Trajectories of Change in South Africa's Freshwater Fish Fauna

By

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Thesis presented for the degree of Doctor of Philosophy
Department of Biological Sciences
University of Cape Town

July 2024

University of Cape Town

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University of Cape Town

From the river to the sea

To the children of Gaza: you are in my heart. Always.

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DECLARATION

I, Mohammed Kajee (KJXMOH007), confirm that the work presented in this thesis is my own. Where information has been derived from other sources, I confirm that this has been referenced in the thesis.

Signed by candidate

Mohammed Kajee (KJXMOH007)

DECLARATION OF INCLUSION OF PUBLICATIONS

I, Mohammed Kajee (KJXMOH007), confirm that I have been granted permission by the University of Cape Town's Doctoral Degrees Board to include the following publication(s) in my PhD thesis, and where co-authorships are involved, my co-authors have agreed that I may include the publication(s):

1. Kajee, M., Henry, D.A.W., Dallas, H.F., Griffiths, C.L., Pegg, J., Van der Colff, D., Impson, D., Chakona, A., et al. 2023. How the Freshwater Biodiversity Information System (FBIS) is supporting national freshwater fish conservation decisions in South Africa. *Frontiers in Environmental Science*. 11. DOI: 10.3389/fenvs.2023.1122223.

2. Kajee, M., Dallas, H.F., Griffiths, C.L., Kleynhans, C.J. and Shelton, J.M., 2023. The Status of South Africa's freshwater fish fauna: A spatial analysis of diversity, threat, invasion, and protection. *Fishes*, 8(12), p.571.

3. Kajee, M., Dallas, H.F., Swanepoel, A., Griffiths, C.L. and Shelton, J.M. 2023. The Freshwater Biodiversity Information System (FBIS) fish data: a georeferenced dataset of freshwater fishes occurring in South Africa. *Journal of Limnology*. 82(s1). DOI: 10.4081/jlimnol.2023.2133.

My supervisor has testified that I made substantial contributions to the conceptualisation and design of the published articles and that I independently executed the study and wrote the associated manuscripts, with support in the form of comments and suggestions from listed co-authors (see Supplementary S6).

Signed by candidate

Mohammed Kajee (KJXMOH007)

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STATEMENT OF CONTRIBUTIONS BY OTHERS

Chapter 1

This chapter was my own work although my supervisors, Emer. Prof. Charles Griffiths, Dr Helen Dallas, and Dr Jeremy Shelton provided comments and suggestions on earlier drafts. Various aspects of this chapter were included in the introductions of all three published articles associated with this thesis.

Chapter 2

This was my own work although my supervisors, Emer. Prof. Charles Griffiths, Dr Helen Dallas, and Dr Jeremy Shelton provided comments and suggestions on earlier drafts. This chapter was published, in part, in the *Journal of Limnology* in 2023. I am the primary author of this publication, with H.F. Dallas, A. Swanepoel, C.L. Griffiths, and J.M. Shelton as co-authors. I conceptualised and designed the research and independently conducted the study and analysed the data. I wrote the manuscript and dealt with referees comments. A. Swanepoel assisted with some of the data collection under my supervision. All co-authors contributed by providing supervision, comments, and suggestions. Two reviewers from the *Journal of Limnology* provided feedback during the peer-review process, which was used to improve the final manuscript. Components of the methods section were also included in a publication by Dallas et al. (2022), of which I am a co-author. This article is not formally included in this thesis, but presented as a supporting publication, in line with UCT policy (see Supplementary S6).

Chapter 3

This was my own work although my supervisors, Emer. Prof. Charles Griffiths, Dr Helen Dallas, and Dr Jeremy Shelton provided comments and suggestions on earlier drafts This chapter was published in *Fishes* in 2023. I am the primary author of this publication, with H.F. Dallas, C.L. Griffiths, C.J. Kleynhans, and J.M. Shelton serving as co-authors. I conceptualised and designed the research and independently conducted the study and analysed the data. I wrote the manuscript and dealt with referees comments. All co-authors contributed to the publication by providing supervision, comments, and suggestions. Two reviewers from the *Fishes* provided feedback during the peer-review process, which was used to improve the final manuscript.

Chapter 4

This was my own work, with my supervisors (Emer. Prof. Charles Griffiths, Dr Helen Dallas, and Dr Jeremy Shelton) providing comments and suggestions on earlier drafts. Dr Dominic Henry provided statistical advice and training on the modelling processes. Dr Nick Rivers-Moore provided hydrological flow data and advice on including hydrological metrics into the modelling workflow. This chapter has not yet been published and will be prepared for submission during the course of 2024.

Chapter 5

This chapter was published as a short communication in *Frontiers in Environmental Science* in 2023. This chapter was my own work although my supervisors, Emer. Prof. Charles Griffiths, Dr Helen Dallas, and Dr Jeremy Shelton provided comments and suggestions on earlier drafts. I am the primary author of this publication, along with 17 co-authors (see Supplementary S6). This chapter presents a collaborative effort requiring input from multiple national and provincial organisations. I conceptualised and designed the research and independently conducted the study and analysed the data. I wrote the manuscript and dealt with referees comments. Dr Dominic Henry provided statistical advice and training on the modelling processes. The remaining co-authors provided important input, assisting with data cleaning and expert feedback on the final modelled distributions of the taxa included. All co-authors contributed to the publication by providing comments and suggestions on the manuscript. Two reviewers from the *Frontiers in Environmental Science* provided feedback during the peer-review process, which was used to improve the final manuscript.

Chapter 6

The synthesis and conclusions chapter is my own work. My supervisors, Emer. Prof. Charles Griffiths, Dr Helen Dallas, and Dr Jeremy Shelton proof-read this chapter providing minor editorial comments.

Chapter 7

Chapter 7 is a compilation of the references included in this thesis and is my own work.

ABSTRACT

Freshwaters are the most threatened ecosystems in South Africa, facing pressure from water abstraction, land-use change, pollution, invasive species, and climate change. These anthropogenic pressures are directly impacting the diversity, abundance, and survival of freshwater fauna and flora across the country. Freshwater fishes are recognised as South Africa's most threatened species group, with one-third of species classified as threatened (Vulnerable, Endangered, Critically Endangered) by the International Union for the Conservation of Nature (IUCN). Understanding patterns of diversity, threat, invasion, and protection status are vital for management. However, access to reliable and comprehensive long-term data on fish distributions are limited. This thesis aims to collect, collate, and analyse historic and current records for all freshwater fish species (native and non-native) known to occur in South Africa, to better understand distribution, diversity, and threat patterns in space and time.

The country's first *Master Species List for freshwater fishes in South Africa* was developed cataloguing all known primary, secondary, and catadromous native and non-native fishes in South Africa. Following this, a comprehensive freshwater fish occurrence dataset for South Africa was compiled and uploaded to the Freshwater Biodiversity Information System (FBIS, freshwaterbiodiversity.org). An 18-month historic-data collation effort resulted in the accrual of 35 955 records of freshwater fish from South Africa spanning 194 years (1828–2022), that have since also been uploaded to the Global Biodiversity Information Facility (GBIF). Together with pre-existing GBIF records (24 861), a total of 60 837 freshwater fish records are thus now available for South Africa. The data show a marked decline in the number of native fish occurrence records over the last decade relative to the previous five decades. Conversely, the number of occurrences for non-native fishes increased over the past three decades. A breakdown of the data is provided for all native (n = 105) and non-native (n = 24) species, as well as for all endemic (n = 40) and threatened (n = 27) species.

Using occurrence records collected for this thesis, spatial patterns in distribution, richness, threat, invasion, and protection status of freshwater fishes in South Africa were analysed. Few studies have undertaken such analyses at ecologically and politically appropriate spatial scales, largely because of limited access to comprehensive biodiversity data sets. Results show that record density varies spatially, at both primary catchment and provincial scales. The diversity of freshwater fishes also varied spatially: native species hotspots were identified at provincial level in the Limpopo, Mpumalanga and KwaZulu-Natal provinces; endemic species hotspots were identified in the Western Cape; and threatened species hotspots in the Western Cape, Mpumalanga, Eastern Cape, and KwaZulu-Natal. Non-native species distributions mirrored threatened species hotspots in the Western Cape, Mpumalanga, Eastern Cape, and KwaZulu-Natal. Some 47% of threatened species records fell outside of protected areas, and 38% of non-native species records fell within protected

areas. Concerningly, 58% of the distribution ranges of threatened species were invaded by non-native species. A data breakdown is provided for each of South Africa's nine provinces including total number of records, and the numbers of native, non-native, endemic, and threatened species. These data provide a much-needed update of the known status and distribution of freshwater fishes in the country.

To support future spatial modelling of South Africa's freshwater fish species distributions, a robust and repeatable method for applying Species Distribution Models (SDMs) to freshwater fishes was developed. Specifically, this thesis sought to investigate whether SDMs could be applied to a wide range of freshwater fishes in South Africa and whether the inclusion of invasive species spatial data would result in improved model accuracy and performance. Using a Bayesian Additive Regression Trees (BART) algorithm, the distributions of three invasive black bass species (*Micropterus salmoides/ Micropterus nigricans*, *M. dolomieu*, and *M. punctulatus*) and two native species (*Clarias gariepinus* and *Pseudobarbus burgi*) were modelled. A total of 148 hydrological and 16 biological predictor variables were specifically developed for this thesis, along with the collation of 75 environmental predictor variables. The results demonstrated that, with appropriate data cleaning and using a statistically robust method for selecting predictor variables, model outputs performed well, with the resulting modelled distributions congruent with known distributions and historic descriptions of the species' presence. All models for invasive, native, and threatened species performed well, with the area under the receiver operating characteristic curve (AUC) values ranging from 0.923–0.994 and true skill statistic (TSS) ranging from 0.701–0.940. Furthermore, model performance for *P*. *burgi* was not improved by the inclusion of biological predictors (invasive species). The AUC for the original *P. burgi* model (including only climatic, environmental, and hydrological predictors) was 0.994, whereas the adapted model (including both climatic, environmental, and hydrological predictors as well as biological predictors) was marginally lower, with an AUC value of 0.993. This indicates that the inclusion of invasive species as biological predictors may not be necessary to produce accurate predicted species distributions.

This thesis also presents a case study demonstrating how the FBIS system was used to provide freshwater fish spatial data products to a national conservation decision-support tool – The Department of Forestry, Fisheries, and the Environment (DFFE) National Environmental Screening Tool. The Tool uses empirical and modelled biodiversity data to guide Environmental Impact Assessments of proposed developments. Occurrence records for 34 threatened freshwater fishes occurring in South Africa were extracted from the FBIS and verified by taxon specialists, resulting in 6 660 records being used to generate modelled and empirical national distribution layers. This represents the first inclusion of freshwater biodiversity data in the Screening Tool, and future iterations of the Tool will incorporate additional freshwater taxa. This case study demonstrates how systems like the FBIS can play a pivotal role in the data-to-decision pipeline through supporting data-driven conservation and management decisions at a national level.

The collective findings of the thesis are concluded in Chapter 6, which highlights the importance of collecting, collating, and consolidating biodiversity data at a national level. The dataset presents the largest (by number of records) online collection of freshwater fish occurrence records in Africa to date, with data spanning 194 years. This thesis also presents an updated version of South Africa's species list for freshwater fishes, which includes all known native (n = 107) and non-native (n = 27) species occurring in the country, and key species attributes like species origin, endemism, and threat status. By consolidating historical data for all known freshwater fishes, the work also presents the first comprehensive assessment of the status of South Africa's freshwater fish fauna, providing valuable insights into spatial patterns of richness, endemism, threat status and non-native species, as well as assessing how effective the country's protected area network is for protecting freshwater fishes. This thesis addressed the critical need for a deeper, data-driven understanding of spatial and temporal variation in South Africa's freshwater fishes – an essential foundation for sound management of these species and their habitats into the future.

Keywords: freshwater fish; biodiversity data; FBIS; SDM; threatened species; decision-making; freshwater conservation

ACKNOWLEDGEMENTS

Umuntu ngumuntu ngabantu (a person is a person because of others)

There isn't a more apt expression to describe how the African philosophy of inclusiveness sits at the very foundation of this piece of science. I would not have been able to complete this degree were it not for the support I received from my community. It would be near impossible to thank everyone who has had an impact on my life and academic development. Here, I thank just a handful of people who have influenced my life and helped to mould me into the person I am today. This thesis is a testament to the help and support and guidance of the countless wonderful humans who have helped me along my academic journey thus far.

First and foremost, I owe an eternal debt to my parents, who have sacrificed so much to ensure that I was afforded the privilege of attaining a good education. In all of the good times and the bad, I will forever be grateful for what you have given me. I owe much of my academic ability to you. Your unwavering support since I was a child has allowed me to pursue my dreams. جَزَاكَ ٱللَّهُ خَيْرًا.

To my siblings, Fatimah, Med, and X, I don't think that anyone could have wished for better companions to share my life with. I appreciate you all!

Throughout my academic journey, there have been a couple people who have significantly altered how I viewed the world and shaped by scientific thinking. The first of these is Mr Amod, my high school life sciences teacher, my HOD, and a dear friend and mentor. Sir, I don't think I have the words to appropriately articulate just how influential you have been on my life. I am not sure what potential you saw in an arrogant 15-year-old Jeppe Boy, but your faith in me has somehow culminated in this thesis. I am forever grateful for the countless classes, practicals, field trips, and chats that we have had over the years. You ignited in me a love for biology, and more broadly, for science that I did not know I had. Shukran for everything that you have done to help me along this journey! The second person who I'd like to acknowledge is the late Sergeant Gerrit Smit, my first scuba diving instructor. Gerrit, I wish I could have told you just how much your friendship and kindness meant to me. I will never forget the first breath I took underwater and how I knew in an instant that I would spend the rest of my life studying the oceans. My first PADI certifications, first set of diving dear, and first dive computer were all gifted to me by Gerrit. So much of my love for and respect of the ocean exists entirely because he decided help teach a shy Indian kid how to breathe under water. Almost everything that is good in my life today, started off one rainy morning at Bass Lake with Gerrit. I am so incredibly thankful to you for all of the dive trips that you took me on over the years. I owe my career to you. To your wife, Tanya, and children, Zahara, and Justin, I hope you know how much of an impact Gerrit had on my life.

To my supervisors, Charlie, Helen, and Jeremy, I feel incredibly lucky to have you as my supervisors. I do not think I could have wished for a better team of researchers to

help me through this project. I am grateful to each of you for your guidance, advice, and input on this thesis. I am especially grateful to you for your assistance in helping me to secure funding for this work and for paying for me to attend international conferences. Most importantly, thank you for always supporting me, even in moments when I decided to pursue side quests that allowed me to live out my dream of visiting Antarctica.

I would also like to extend my thanks to the plethora of collaborators who have been involved in this research over the years. I am especially grateful to Dr Dominic Henry who provided invaluable assistance and training on my modelling chapters. I would like to thank Nancy Job and the wonderful people at SANBI who initially funded my MSc and gave birth to this project. A special thanks goes out to Prof Olaf Weyl, who had decided to fund my PhD. Selfishly, I am heartbroken that I could not conduct this research under your supervision. Additionally, I would like to thank Dr Josie Pegg and Dr Angus Patterson, who so kindly agreed to honour Olaf's offer, and fund my PhD through SAIAB and the NRF – this work would not be possible without your assistance. At an institutional level, I would like to express my appreciation for all of the remarkable researchers at UCT and the FRC, who have all contributed to this work in some way or the other.

I have been incredibly blessed to have a wonderful community of friends who have all walked this journey with me. There are too many people to mention, but please know that I appreciate each and every one of you. Thank you for all of your love and support and kind words over the past year. Most of all, thank you for still being my friend, despite the fact that I have been in complete hibernation over this past year. To everyone in the Team Griffiths lab, you guys make coming in to work feel easy. I want to make special mention of Jody, who took me under her wing when I first started my MSc. Your friendship over these years has been a source of light and a true blessing in my life. To Ceci, thank you for agreeing to be my work bestie and ADHD manager. There is no chance that I would have been able to finish this PhD were it not for your help and support and friendship. Thank you for always being there for me, for keeping me focussed, and most importantly for being a wonderful friend. You really are the best PhD student I have ever met! Lastly, to Karla, I am so incredibly grateful to you for everything you have done for me. I would not have gotten to this point in my life without your love and support. Thank you for helping to shape my scientific and emotional mind in a way that I didn't know was possible.

Most of all, thank you to Emma. You have been a shining light in my life over the past two years. You have taught me so much and helped me to grow into the person that I am today. Thank you for opening my mind to the social sciences and for fundamentally altering my understanding of how the world works. I can't express how much I appreciate you and all of the support you have given me in this journey. Thank you <3

CHAPTER 1

1. Introduction

1.1. The status of global freshwater ecosystems

Freshwater ecosystems are regarded as some of the most biodiverse habitats on earth (Hughes et al., 2021), covering less than 1% of the planet's total surface area, but accounting for nearly 10% of all described animal species (United Nations Environmental Programme, 2002; Strayer and Dudgeon, 2010; Tickner et al., 2020), including 25% of all vertebrates and more than 50% of all fish species (Hughes et al., 2021; Fricke et al., 2022). Not only are freshwater ecosystems integral for the existence of a wide variety of semi-terrestrial and aquatic life forms (Millennium Ecosystem Assessment, 2005; Nel et al., 2009), but they also fulfil a crucial role in human existence and societies. Rivers, and their associated freshwater habitats, provide crucial ecological infrastructure for water security, which is essential for human health, well-being and socio-economic development (Darwall et al., 2018; Skowno et al., 2019). For example, freshwater ecosystems worldwide provide integral ecosystem services valued at more than US$ 4 trillion per annum (Darwall et al., 2018). These services include the provision of clean drinking water, irrigation of crops, support for recreational activities, and buffering against the impacts of extreme weather events, such as droughts and floods.

However, despite providing essential ecosystem services, the protection of freshwater habitats and their associated biodiversity remain a low priority for policymakers when developing protected areas and legislation (Hughes et al., 2021). Concerningly, only a third of rivers longer than 1 000 km still flow freely from source to sea (Grill et al., 2019), with ~ 30% of freshwater habitats having disappeared in the last 50 years (Tickner et al., 2020). Consequently, freshwater ecosystems across the world are under threat, facing major impacts from human activities, including land-use change, non-native invasive species introductions, water over-abstraction, and climate change (Dudgeon et al., 2006; Darwall, Smith, et al., 2009; Best, 2019; Capon et al., 2021).

As a result of the extreme pressure being exerted on freshwater ecosystems, freshwater biodiversity is declining twice as fast as in either marine or terrestrial ecosystems (Grooten and Almond, 2018). Freshwater habitats have experienced sharp declines in population numbers, diversity, and distributions over the past five decades (Grooten and Almond, 2018; WWF, 2020), with, for example, nearly a third of freshwater fishes now threatened with extinction (WWF, 2020; Hughes et al., 2021). In 2020 alone, 80 freshwater fishes were declared as Extinct, a further 10 being declared Extinct in the Wild and 115 declared as Critically Endangered, Possibly Extinct (IUCN Red List, 2020; Hughes et al., 2021). Furthermore, over the past 50 years, migratory freshwater fish populations have decreased by 76% (He et al., 2019), while large-bodied fishes have declined by 94% (He et al., 2019). Unfortunately, the loss of freshwater fishes is predicted to accelerate in the near future (Strayer and Dudgeon, 2010; Chakona et al., 2022).

1.2. The status of South Africa's freshwater ecosystems

South Africa is one of the most biologically diverse regions on earth (Wynberg, 2002; Van Wilgen et al., 2020), recognised as the third most biologically rich country in the world (World Conservation Monitoring Centre, 1992; Lombard, 1995). Characterised

as a water-scarce country, South Africa's climate ranges from semi-arid to hyper-arid, with few areas considered as humid (receiving >500 mm of rainfall per year). In general, Mean Annual Precipitation (MAP) decreases from east to west and from north to south (Griffiths et al., 2015; Davies and Day, 2023). Rainfall seasonality also varies across the country, with the north-eastern regions typically receiving summer rainfall, while the south-western region typically receives winter rainfall, characteristic of a Mediterranean climate (Davies and Day, 2023). Furthermore, rainfall also varies from year to year, due largely to oscillations in the El Nino/La Nina cycles, resulting in unpredictable periods of flooding and drought (Blamey et al., 2018; Mahlalela et al., 2020). Consequently, South Africa has a variety of freshwater ecosystems occurring in different parts of the country.

1.2.1. Lakes and reservoirs

South Africa is only home to one natural, lentic water body (Lake Fundudzi), which is located in the Limpopo province (Davies and Day, 2023). The lack of natural lakes is attributed to the geological history of the region, with the landscape not having experienced long periods of glaciation, resulting in a flat surface that is generally unsuitable for the formation of lakes (Davies and Day, 2023). Additionally, most of the country is characterised by having evaporation rates that exceed precipitation rates (Otieno et al., 2010), which means that some lentic water bodies in South Africa (for example, Lake Chrissie) occasionally dry out and are consequently classified as wetlands rather than lakes.

While South Africa only has one natural lake, the country has numerous freshwater reservoirs, impoundments, and dams. It is estimated that there are more than 500 000 impoundments and approximately 600 large dams located along the country's rivers (Mantel et al., 2010a; Griffiths et al., 2015). Owing to the unpredictable precipitation and associated flows, these man-made freshwater lakes serve several, critical functions, including the provision of drinking water, irrigation of crops, production of electricity, and servicing of mining and industrial centres of the country (Jackson et al., 2016). The addition of these unnatural water bodies has added extensive new habitat for freshwater (and terrestrial) organisms. However, impoundments and dams often result in the complete transformation of river ecosystems and can also have substantial negative impacts on ecosystem functioning and negatively affect freshwater organisms, specifically migratory species (Mantel et al., 2010a,b). For example, the extensive damming of the Olifants River in the Western Cape has resulted in the complete extirpation of the Clanwilliam sandfish (*Labeo seeberi*) from the system (Cerrilla et al., 2022). Additionally, off-stream impoundments result in water being abstracted from the river system, altering natural river flows and, in some instances, resulting in the drying up of historically perennial rivers (Mantel et al., 2010a,b; Davies and Day, 2023).

1.2.2. Coastal lakes

In total, South Africa has 13 coastal lakes, with seven located along the sandy coastal plain in northern KwaZulu-Natal and five found along the Southern Cape (MacKay et al., 2014). These coastal lakes differ from estuaries since they lack a direct surface water connection with the ocean and are primarily fed by groundwater (MacKay et al., 2014; Davies and Day, 2023). These water bodies are generally brackish, but there are some that contain fresh water. The geological history and faunal composition of

South Africa's coastal lakes indicate that these systems likely had an estuarine past (MacKay et al., 2014; Davies and Day, 2023).

1.2.3. Wetlands

In South Africa, wetlands are defined as land which is transitional between terrestrial and aquatic systems and where the water table is generally near or at the surface, or, as land that is periodically covered with shallow water, and which generally supports vegetation typically adapted to saturated soil (Griffiths et al., 2015; Ellery et al., 2016). The country is home to a range of wetland types, including permanently, seasonally, and ephemerally flooded areas, which are alternatively classified as marine, estuarine, and inland wetlands (Ellery et al., 2016; Ollis et al., 2016). Combined, wetlands cover an area of approximately 29 000 km^2 (Dini and Everard, 2016; Adeeyo et al., 2022). Wetlands provide important ecosystem services, including, flood control and prevention, reducing erosion, groundwater recharge and discharge, and water purification (Ellery et al., 2016; Davies and Day, 2023).

1.2.4. Rivers

South Africa has a wide diversity of river ecosystems, which ranges from sub-tropical in the north-east to semi-arid and arid in the interior and cool Mediterranean in the south-west (Griffiths et al., 2015; Davies and Day, 2023). In total, there are 856 mainstem rivers that drain the 22 primary catchments across a river network that is estimated to span approximately 160 000 km (Nel and Driver, 2015) (Figure 1.1). These rivers have been classified by scientists from a wide range of disciplines for both scientific and management purposes (Rowntree and Wadeson, 1999). A brief overview of the various river classification systems used in South Africa is provided below.

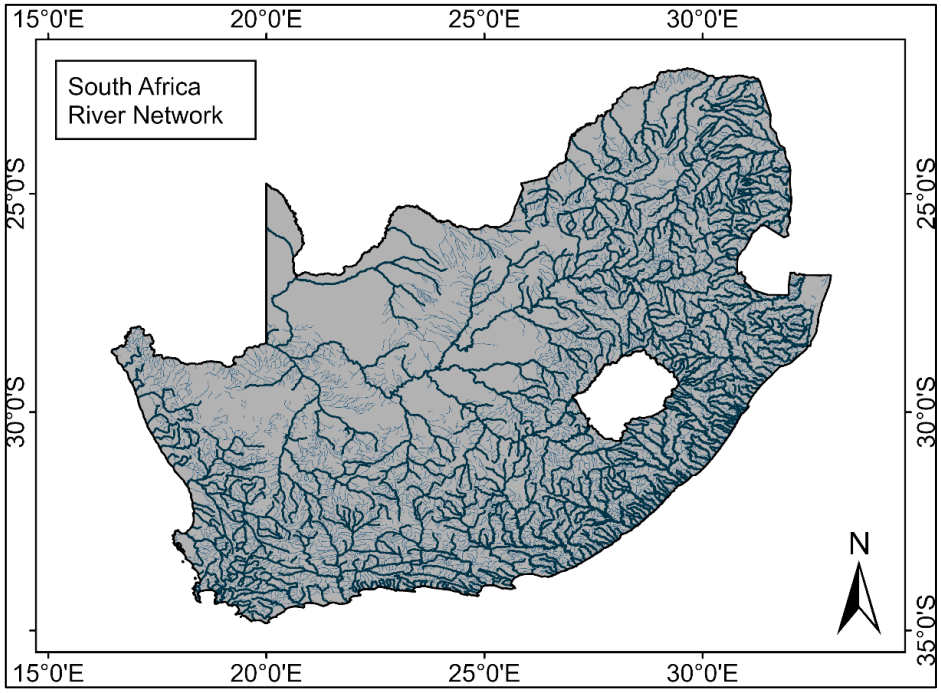


Figure 1. 1. South Africa's 1:500 000 river network (Nel, 2011).

Water Management Areas

The National Water Act (Act 36 of 1998), through the National Water Recourse Strategy (NWRS), provides a framework for the development, protection, management, and control of rivers in the country as a whole. In this regard, the NWRS

provides the framework through which water will be managed at a regional or catchment level, within defined Water Management Areas (WMA). Through an iterative process, the Department of Water and Sanitation (DWS) currently defines nine WMAs within South Africa (Pollard and Du Toit, 2008; Department of Water and Sanitation, 2016), each managed by a Catchment Management Agency (CMA) (Pollard and Du Toit, 2008). This spatial layer delineates each WMA in relation to the drainage boundaries of the region (Figure 1.2). Each WMA is further divided into Sub Water Management Areas (Figure 1.3), which is generally comprised of groups of quaternary catchments for a mainstem river (Pollard and Du Toit, 2008; Nel and Driver, 2015). The sub-WMAs layer is not frequently used by river managers or researchers, but are especially relevant for management of water resources by DWS and policy making (Nel and Driver, 2015).

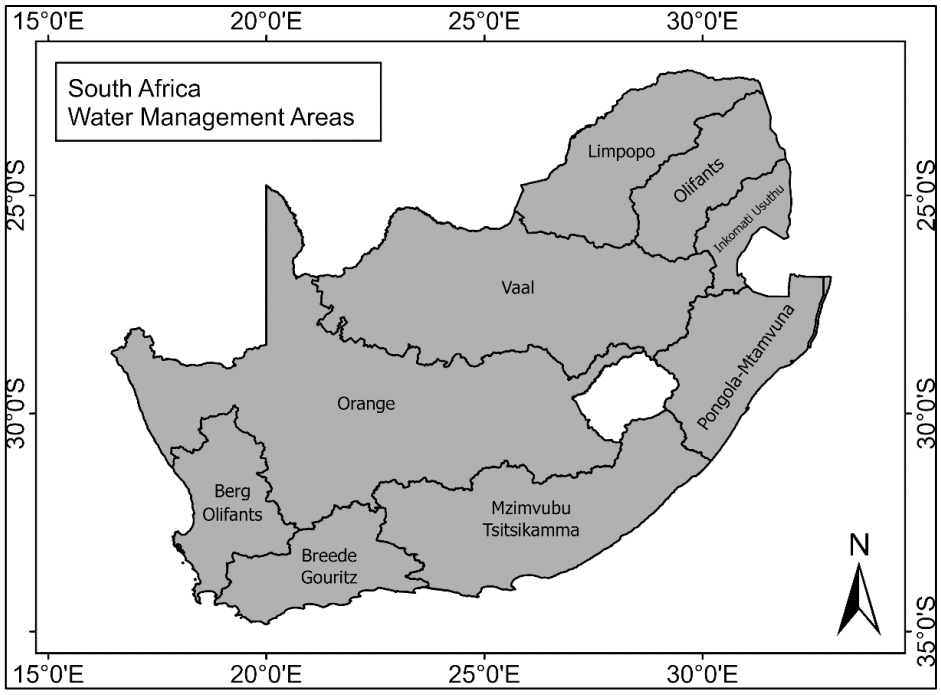
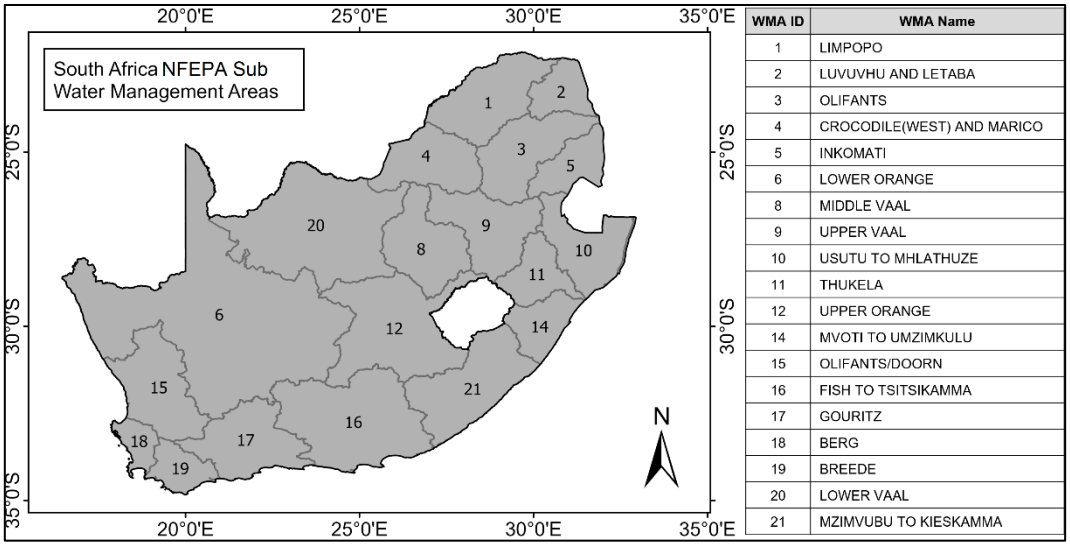


Figure 1. 2. South Africa's Water Management Areas (WMA) (Department of Water and Sanitation, 2016).



WMA ID	WMA Name
1	LIMPOPO
2	LUVUVHU AND LETABA
3	OLIFANTS
4	CROCODILE(WEST) AND MARICO
5	INKOMATI
6	LOWER ORANGE
8	MIDDLE VAAL
9	UPPER VAAL
10	USUTU TO MHLATHUZE
11	THUKELA
12	UPPER ORANGE
14	MVOTI TO UMZIMKULU
15	OLIFANTS/DOORN
16	FISH TO TSITSIKAMMA
17	GOURITZ
18	BERG
19	BREEDE
20	LOWER VAAL
21	MZIMVUBU TO KIESKAMMA

Figure 1. 3. South Africa's NFEPA sub-Water Management Areas (SWMA) Africa (Nel, 2011; Department of Water and Sanitation, 2016).

Longitudinal / Geomorphological Zones

South Africa's river network is also delineated by elevation based on digital elevation models and associated slope classes (Maherry et al., 2013). The most recent, available classification of South African rivers is provided by Rowntree and Wadeson (1999). Under this classification type, rivers in South Africa are classified as either mountain headwater stream, mountain stream, transitional, upper foothill, lower foothill, and lowland river (Rowntree et al., 2000). Most South African rivers are classified as foothill rivers (upper foothill = 45%; lower foothill = 41%), whilst lowland rivers accounting for 9% and mountain streams only making up 4% of the country's total river length (Nel and Driver, 2015).

Ecoregions

The Freshwater Ecoregions of the World (FEOW) spatial layer was published in 2008 (Abell et al., 2008). This global map provides a biogeographic regionalisation of freshwater biodiversity based on available regional information describing freshwater biogeography (broadly including the influences of phylogenetic history, palaeogeography, and ecology) of freshwater fishes (Abell et al., 2008). Based on FEOW's classification, South Africa's rivers fall into one of eight freshwater ecoregions (Abell et al., 2008) (see Figure 1.4).

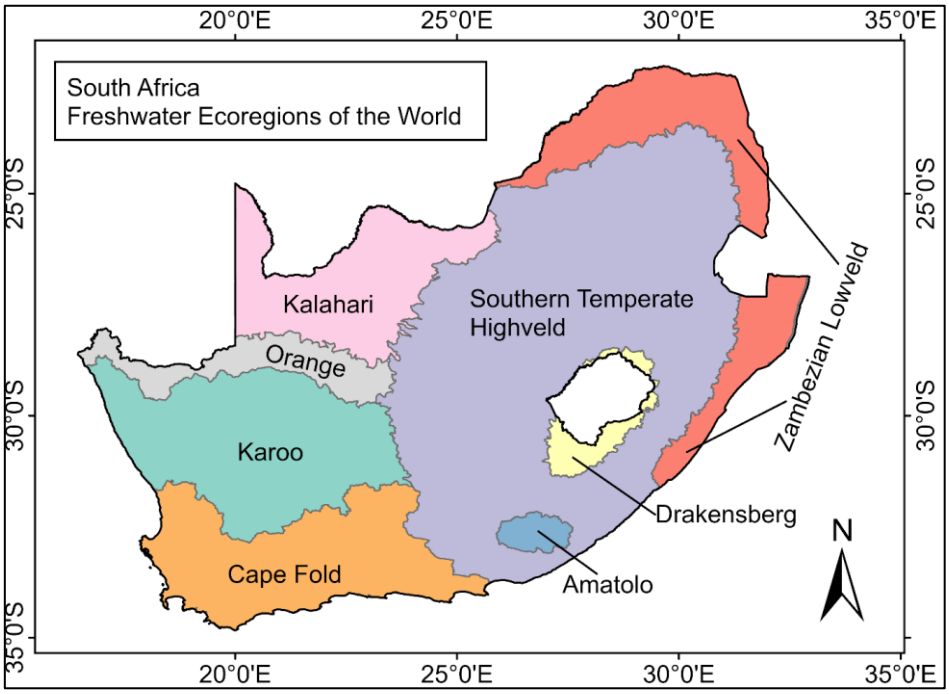


Figure 1. 4. South Africa's freshwater ecoregions based on The Freshwater Ecoregions of the World (FEOW) (Abell et al., 2008).

Catchments

Catchments or drainage basins are defined as areas of land, which are bounded by natural landscape units, where all surface and subsurface water converges (via a network of streams, tributaries, and rivers) to a single point (Sekese, 2019). Catchment boundaries are usually defined by a ridge, which separates hydrological systems (Sekese, 2019). In South Africa, river systems are defined by a series of nested hierarchical catchments or hydrological units (Midgeley et al., 1994; Maherry et al., 2013) and formally endorsed by the DWS (Maherry et al., 2013; CLARK, 2015) (see Figure 1.5). The broadest hydrological catchment area in South Africa is the Primary Catchment (SLIM, 2014a). Nested below this are Secondary Catchments (SLIM,

2014b), followed by Tertiary (SLIM, 2014c) and Quaternary Catchments (SLIM, 2014d). Below the Quaternary Catchment are two sub-catchment categories, namely the Quinary Catchment and the sub-Quaternary Catchment. The Quinary Catchment layer was delineated based on antifungal and hydrological characteristics of the respective river networks (Maherry et al., 2013). The sub-Quaternary Catchment layer was developed for the National Freshwater Ecosystem Priority Area (NFEPA) and delineated catchments using ArcHyrdo (an extension of ArcGIS) based on digital elevation and the rivers network layer (Nel, 2011).

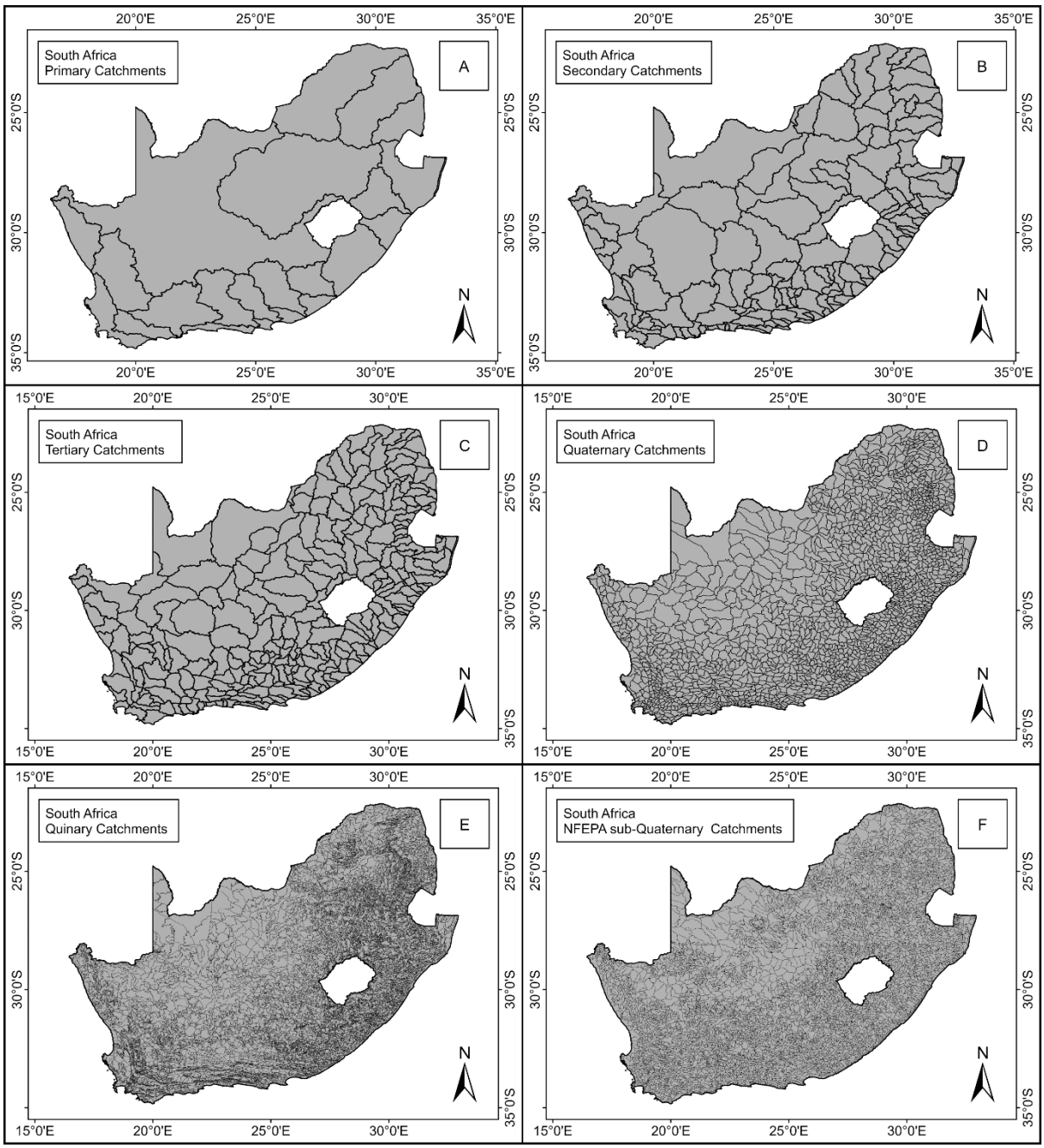


Figure 1. 5. Hydrological catchments of South Africa, showing (A) Primary, (B) Secondary, (C) Tertiary, (D) Quaternary, (E) Quinary, and (F) sub-Quaternary Catchment boundaries.

1.3. Threats to South Africa's rivers

Given the vastness and diversity of South Africa's river network, it is unsurprising that the country's freshwater ecosystems support large amounts of biodiversity (Van Deventer et al., 2019). In addition, South Africa's river ecosystems also play an integral part in supporting a vast array of ecosystem services that are integral to human survival (Van Deventer et al., 2019). However, congruent with global trends (as

described in Section 1.1), the health of South Africa's freshwater ecosystems are in decline. River systems are ranked as the third most threatened ecosystem type in South Africa (Skowno et al., 2019), behind only estuaries and wetlands (also aquatic habitats that are inextricably linked to rivers).

Given that South Africa is a relatively arid and water-stressed country (Zucchini and Nenadić, 2006; DWA, 2013), the pressures being exerted on freshwater ecosystems are further amplified by the heavy reliance on freshwater abstraction for human needs (Skelton et al., 1995). Additionally, anthropogenic climate change has altered temperature and rainfall patterns in South Africa (Dallas and Rivers-Moore, 2014; Ziervogel et al., 2014; Niang et al., 2017), further affecting the stability of these ecosystems. Predicted increases in temperature and changes to rainfall patterns could have substantial negative impacts on freshwater species across the country and hence result in increased extinction rates (Dallas and Rivers-Moore, 2014; Reizenberg, 2017; Shelton et al., 2017). Furthermore, South Africa's rivers are also heavily impacted by biological invasions (Weyl et al., 2020), which have had devastating impacts of freshwater biota and ecosystem functioning as a whole. Consequently, the anthropogenic pressures being exerted on freshwater ecosystems are having direct impacts on the diversity, abundance, and survival of freshwater fauna and flora across the country.

1.4. South Africa's freshwater fishes

According to the most recent National Biodiversity Assessment (NBA), South Africa contains a native freshwater fish fauna comprising approximately 118 species, of which almost 50% are endemic to South Africa (Skowno et al., 2019). However, like many other organisms on earth, freshwater fishes within South Africa face several anthropogenic threats that have resulted in declines in both their abundance and diversity (Dudgeon et al., 2006; Geist, 2011). As a result of the pressures being exerted on South Africa's river ecosystems, freshwater fishes are classified as the country's most threatened species group (Skowno et al., 2019), with almost half of all assessed species listed as threatened (Vulnerable, Endangered, or Critically Endangered) on the IUCN Red List (Darwall, Tweddle, et al., 2009). More recently, Chakona et al. (2022) found that of 105 formally-described native species, 27 are classified as threatened. Of these, at least eight are reported to be in decline, with a negative change in their IUCN Red List status over the past 10 years (Chakona et al., 2022). Additionally, of the 40 endemic freshwater fish species occurring in South Africa, threat level is even higher, with two-thirds of endemics being currently classified as threatened (Chakona et al., 2022). Furthermore, ongoing taxonomic revisions of freshwater fishes indicate that several taxa are genetically distinct and have narrower distribution ranges than previously thought (Chakona et al., 2022). As such, some threatened endemic 'species suites' are likely to be split taxonomically, resulting in individual species being more vulnerable and raising the total number of threatened taxa in the country (Chakona et al., 2022). Concerningly, there have also been several studies recording localised population extinctions of freshwater fishes in South Africa (Cambray, 1997; Skowno et al., 2019; Cerrilla et al., 2022) (see Supplementary Table S.1.1). Evidently, freshwater fishes in South Africa are under immense pressure from several anthropogenic factors, that have the very real possibility of causing the extinction of several species across the country.

The key anthropogenic pressures impacting freshwater fishes in South Africa are land-use change (O'brien et al., 2019; Chakona et al., 2020), pollution (Wepener et al., 2011; Horak et al., 2021), excessive abstraction of water (Dallas and Rivers-Moore,

2014; Cerrilla et al., 2022; Evans et al., 2022), spread of invasive species (Van Rensburg et al., 2011; Ellender and Weyl, 2014; Zengeya et al., 2020; Cerrilla et al., 2022) and climate change (Dallas and Rivers-Moore, 2014; Ziervogel et al., 2014; Niang et al., 2017). Consequently, there is increasing awareness and growing recognition of the need to monitor freshwater fish populations, to develop up-to-date conservation plans, and to formulate policies that can guide effective management and protection of freshwater fishes in South Africa (Chakona et al., 2022; Jordaan et al., 2020). It is thus critical that trends in diversity, distribution, threat status, and protection status of freshwater fishes in South Africa are comprehensively assessed to support management approaches and conservation action.

In light of this, there is a need to establish an easy, efficient, and accurate way to track changes to South Africa's freshwater fish abundance and diversity in both space and time. In order to adequately assess how our freshwater fish fauna is changing, there was a desperate need to consolidate historic freshwater fish data in South Africa. However, the country lacked an informative and accessible platform for hosting freshwater biodiversity data, which impeded the assessment of historic and current freshwater fish abundance and distribution patterns, as well as physical river conditions. This is somewhat surprising, given that South Africa has a rich history of freshwater fish research, with a well-established network of scientific infrastructure, expertise, and funding (Skelton, 2001).

1.4.1. Freshwater fish data in South Africa

South Africa has a rich history of freshwater fish research, dating back more than 200 years to William Burchell's (1822) description of the first species from the region (Skelton, 2001). Throughout the 1800's, several naturalists and scientists (including Henry Lichtenstein, Ludwig Krebbs, Andrew Smith, Wilhelm Peters, Count F. Castelnau, Franz Steindachner, Max Weber, Albert Gunther and George Boulenger) made taxonomic contributions, describing freshwater fish species from across the country (Skelton, 2001). The first comprehensive catalogue of freshwater fishes for southern Africa was written by G.D.F. Gilchrist and W.W. Thompson between 1913 and 1917 (Skelton, 2001). Following on from this, Keppel Barnard revised the known fishes of the South-West Cape in 1938 and 1943, adding several new species (Skelton, 2001). The next major update on freshwater fishes in South Africa was the seminal work – *Freshwater Fishes of Southern* Africa (1967) – published by Rex Jubb (Jubb, 1967; Skelton, 2001). Under colonial and apartheid rule, inland fisheries departments and nature conservation authorities played a role in conducting surveys, studying the biology of species, and sending specimens to museums (Skelton, 2001). Since the 1960's, most freshwater fish research has been conducted via the J.L.B Smith Institute of Ichthyology (Rhodes University), now the South African Institute for Aquatic Biodiversity, NRF-SAIAB, and by the Albany Museum in Grahamstown (Skelton, 2001).

Skelton's – *A Complete Guide to the Freshwater Fishes of Southern Africa* – provided the most up-to-date information on species diversity and distribution of freshwater fishes in southern Africa, in the form of a published field guide in 1993, later revised in 2001 (Skelton, 2001). Using occurrence records from the Albany Museum and J.L.B Smith Institute of Ichthyology, Skelton et al. (1995) presented an analysis of distribution, richness, endemism, and conservation status of freshwater fishes in South Africa, Lesotho, and the Kingdom of eSwatini. He reported 94 native fish taxa and 18 non-native species. Hotspots of endemic fish richness were identified in both the

tropical and temperate regions of South Africa, most notably the Olifants River System in the Western Cape, and in areas of high relief, such as the Amatola-Winterberg Mountains, Drakensberg Escarpment and Cape Fold Mountains (Skelton et al., 1995). In 2011, the Water Research Commission (WRC) published an atlas of the National Freshwater Ecosystem Priority Areas for South Africa (NFEPA), which summarised data and on-the-ground knowledge of regional freshwater ecosystems (Nel, 2011). The NFEPA provides guidance on how best to manage freshwater systems in accordance with South Africa's National Water Act (Republic of South Africa, 2014), National Environmental Management: Biodiversity Act (Republic of South Africa, 2004a), and the National Environmental Management: Protected Areas Act (Republic of South Africa, 2004b). The primary goal of the NFEPA was to keep further freshwater species from becoming threatened and to prevent those fish species already threatened or near threatened from going extinct (Nel, 2011). Included in the NFEPA outputs were maps and associated GIS data, that highlighted locations where threatened and near threatened species occurred ("Fish Sanctuaries") and their associated rivers ("Fish Support Areas") (Nel, 2011). However, the NFEPA outputs did not constitute an assessment of the distribution of freshwater fishes, since these maps were produced using expert knowledge of species distributions, rather than systematically assessing species ranges based on actual occurrence data.

The most recent national-scale assessment of freshwater fishes in South Africa by Chakona et al. (2022), summarised the diversity, distribution, and extinction risk of native freshwater fishes. They assessed the extinction risk for 101 valid species and 18 unique genetic lineages of native fishes, finding that 36% of South Africa's freshwater fishes are threatened with extinction. Important diversity and threat hotspots were also assessed, with the Cape Fold Ecoregion (Abell et al., 2008) being identified as both a high-diversity and high-threat region (Chakona et al., 2022). In addition to peer-reviewed research articles, the South African National Biodiversity Institute (SANBI), which is mandated to assess and monitor the state of South Africa's biodiversity through the National Environmental Management: Biodiversity Act: Act 10 of 2004 (Republic of South Africa, 2004a), also assessed the status of South Africa's freshwater fishes in their NBA conducted in 2004, 2011 and 2018 (Skowno et al., 2019). The most recent NBA (Skowno et al., 2019) assessed the threat status of 118 native freshwater fishes and found that freshwater fishes contained the highest percentage of threatened taxa of any species group in the country (Skowno et al., 2019). Whilst this assessment has been an important update to the status of freshwater fishes in the country, no specific spatio-temporal analyses of the available data were conducted.

1.4.2. Freshwater fish data accessibility in South Africa

Despite the rich history and well-established freshwater fish research infrastructure in South Africa, to date there has been limited sharing of knowledge and data on a national scale. For example, experts within the country have yet to compile and agree upon a comprehensive list of all freshwater fish species known to occur in South Africa (Bills, personal communication, 2018 October 23; Skelton, personal communication, 2018 October 23). Furthermore, the country still does not possess a comprehensive centralised database to store, share, and visualise freshwater fish data. What data do exist are usually only available to small research groups at specific universities, non-government organisations and specific government departments.

Long-term monitoring data sets for South Africa's freshwater fishes are difficult to access or contain limited data and metadata (Chakona et al., 2022; Dallas et al., 2022). Scott (2000), along with Skelton et al. (2000), present the only known Atlas of southern African freshwater fishes, which contained 35 180 georeferenced specimen records covering 735 species from across the region (Scott et al., 2000; Skelton et al., 2000). Scott (2000) and Skelton et al. (2000) used data from the Atlas to assess fish distributions at a regional scale, comparing these with previous studies. Additionally, the Atlas was used to run a rudimentary gradient analysis, investigating the relationship between species distribution and various environmental gradients (Scott, 2000). More recently, however, platforms such as FishBase (Froese and Pauly, 2023) and the Global Biodiversity Information Facility (GIBF) (GBIF.org, 2018) have facilitated the storage of, and access to, large databases via online, open access platforms, which has allowed government and research organisations, as well as private individuals, to share and access data freely online. For example, the South African Institute for Aquatic Biodiversity (SAIAB) has uploaded its entire freshwater fish database to the GBIF platform (SAIAB, 2023), thereby greatly improving the accessibility of this data set (Kajee et al., 2023a,b).

Despite the wealth of freshwater research and biodiversity information available in South Africa, there was no central database for housing freshwater biodiversity data until development of the Freshwater Biodiversity Information System (FBIS; freshwaterbiodiversity.org) (Dallas et al., 2022). The FBIS is a data-rich, open-access online platform that hosts, analyses, and serves freshwater biodiversity data (Dallas et al., 2022). FBIS was developed from 2017 onwards by the Freshwater Research Centre (FRC) in collaboration with SANBI and Kartoza and aims to serve as a platform for the inventory and maintenance of freshwater data. The FBIS will improve access to comprehensive and reliable freshwater biodiversity data and thus facilitate the evaluation of long-term change in freshwater ecosystem condition and guide future monitoring and management efforts (Dallas et al., 2022). Consequently, the FBIS can function as a repository for freshwater biodiversity data in South Africa. However, given that current freshwater fish data are scattered across a variety of key sources, including published scientific literature, government organisations, and online databases (Dallas et al., 2022), undertaking to collect, collate, and consolidate these data are of the utmost importance.

As anthropogenic pressures and the effects of global change on freshwater fishes becomes observable, it is becoming imperative that long-term datasets and baselines are developed, so that critical population trends and ecosystem shifts can be monitored and managed to best protect freshwater fish diversity. Having these data easily accessible to all freshwater stakeholders is of extreme importance and can provide immense benefit in terms of biodiversity planning, conservation management and policy making. Long-term distributional data for freshwater fish species can be vital for detecting critical ecosystem changes, such as species range shifts, new records of non-native invasions and loss of ecosystem services or unique biodiversity. This is especially important when considering the observed (Ellender and Weyl, 2014; Weyl et al., 2020) and predicted (Khosa et al., 2019) expansion of non-native species as well as the translocation of native species outside of their native catchments within South Africa (Ellender and Weyl, 2014; Weyl et al., 2016). Understanding exactly how the abundance and distribution of freshwater fishes (both native and non-native) are changing is pivotal to effectively manage and conserve our unique and threatened freshwater biodiversity and ecosystems. These types of assessments will result in the

production of ‘actionable’ data and information important for conservation planning, species management and policy making. Not being able to effectively observe, record and track critical ecosystem changes can have serious implications for our ability to manage this resource effectively and sustainably. Given the threats to and observed declining trends in South Africa’s freshwater fish fauna, assessing the conservation status and effectiveness of conservation areas at protecting threatened fishes is both imperative and urgent (Jordaan et al., 2020; Chakona et al., 2022).

1.5. Protection of freshwater habitat in South Africa

South Africa’s protected area network (Figure 1.6) is declared under the National Environmental Management: Protected Areas Act (Act 57 of 2003; Republic of South Africa, 2004b; Chakona et al., 2022) and the National Environmental Management: Biodiversity Act (Act 10 of 2004; Republic of South Africa, 2004c), including protected areas that cover less than 10% of South Africa’s total land area (Siegfried, 1989; Skelton et al., 1995; Russell, 2011; Skowno et al., 2019). South Africa has a relatively extensive terrestrial protected area network covering an area of approximately 270 000 km^2 (Department of Forestry Fisheries and the Environment, 2023a,b), including both statutory conservation areas (National Parks, Department of Water Affairs and Forestry (DWAF) Nature Reserves and Provincial Nature Reserves) and non-statutory conservation areas (local authority reserves, Protected Natural Environments, Mountain Catchment Areas Conservancies, Natural Heritage Sites, Private Nature Reserves, DWAF Demarcated Forests and Private Demarcated Forests) (Rouget et al., 2003; DFFE, 2023a,b). Whilst these protected areas do offer some protection to freshwater fishes, few conservation areas and reserves protect entire catchments (Skelton et al., 1995; Acreman et al., 2019), with freshwater systems, in general, being especially neglected (Department of Environmental Affairs, 2016).

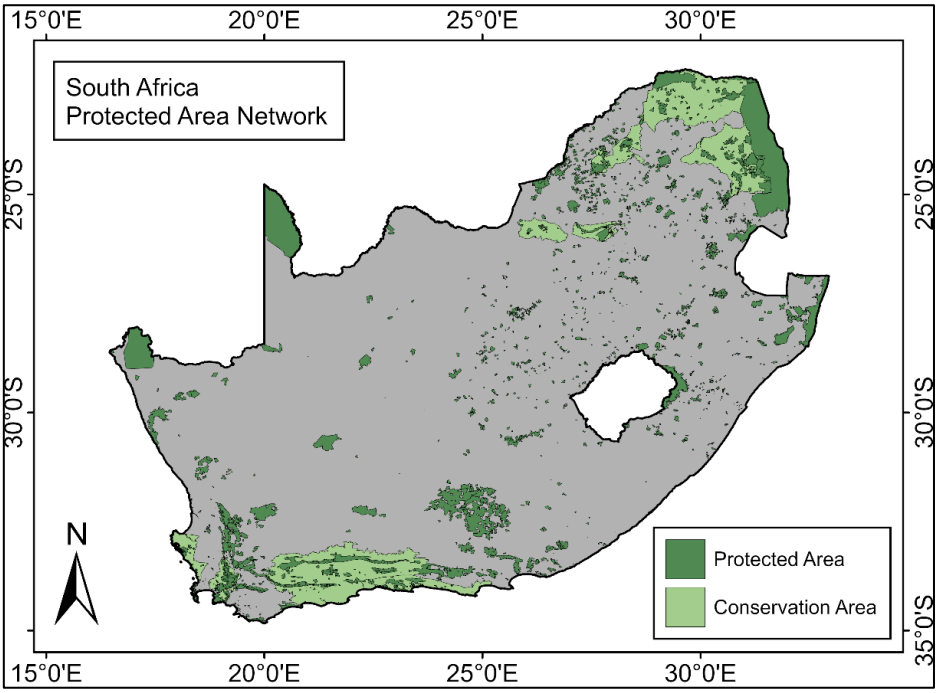


Figure 1. 6. South Africa’s protected area network showing formal protected areas and conservation areas (Department of Forestry Fisheries and the Environment, 2023a,b).

Consistent with global trends (Abell et al., 2007; Nel et al., 2009; Hughes et al., 2021), South Africa’s network of protected areas is severely lacking in terms of adequately conserving freshwater ecosystems, with over 90% of the country’s main rivers falling

outside protected areas (Nel et al., 2004; Abell et al., 2007). A recent national assessment found that, of the country's rivers, only 18% are regarded as Well Protected and 12% as Moderately Protected, with the remainder being classified as Not or Poorly Protected (Department of Environmental Affairs, 2016). However, even rivers that are considered to be Well or Moderately Protected are often not in a pristine or healthy condition. The current network only includes small components of protected river area that form part of much larger, degraded aquatic systems further up and downstream of the parks (Skelton et al., 1995; Russell, 2011). For example, Kleynhans (2000) and Nel et al. (2009) found that almost half of protected river systems occurring in protected areas in South Africa are already degraded upstream as a result of human activities (Kleynhans, 2000; Nel et al., 2009).

Due to the linear nature of river systems, their biotas are particularly vulnerable to point source disturbance events, such as non-native species introductions and pollution further upstream (Impson et al., 2002; Abell et al., 2007; Jordaan et al., 2020). As a result, and consistent with global studies elsewhere (Abell et al., 2007; Nel et al., 2009; Hughes, Harrison, et al., 2021), South Africa's current network of protected areas does not adequately protect freshwater fishes (Nel et al., 2004; Abell et al., 2007; Jordaan et al., 2020). For example, Russell (2011) found that of the 19 national parks managed by South African National Parks, only 13 included habitat for freshwater fishes, with protection being an unintended by-product of the targeted conservation of threatened terrestrial plants and mammals. Similarly, an analysis of protected areas within South Africa's Cape Fold Ecoregion (CFE) found that whilst protected areas do contain populations of several native fish species, actual protection was hindered by non-native species invasions (Impson et al., 2002; Abell et al., 2007). More recently, Jordaan et al. (2020) reported that protected areas in the CFE – one of South Africa's five aquatic regions found along the south-western fringe of the country (Abell et al., 2008; Shelton et al., 2018a) – did not adequately protect native freshwater fish, with 84% of taxa regarded as under-protected (Jordaan et al., 2020). Consequently, very few sites within national parks contain freshwater fishes that are free from human-linked threats (Russell, 2011). Despite the country's extensive Water Act (Republic of South Africa, 2014), there are no clear implementation guidelines and protocols in place to achieve effective conservation of freshwater ecosystems outside of protected areas.

Having recognised the limitations of the current protected areas network, expansion of these areas in South Africa is supported through the country's commitment to the Convention on Biological Diversity (CBD) in The National Protected Area Expansion Strategy (NPAES, 2016; Republic of South Africa, 2010; Department of Environmental Affairs, 2016). The NPAES provides specific additional targets for the protection of freshwater habitats (Department of Environmental Affairs, 2016), with a target to add 1 490 km^2 of protected river habitat (Department of Environmental Affairs, 2016). Importantly, the NPAES includes provisions for using the distribution and needs of threatened aquatic species to guide the development of new protected areas (Department of Environmental Affairs, 2016).

To ensure that freshwater fishes receive the appropriate conservation attention and are included in future conservation plans and policy documents, it is vital that accurate species distribution data and maps are available (Nel, 2011; Skowno et al., 2019; Chakona et al., 2022). However, these data do not exist for all species in the country. As a result, being able to accurately map the distributions of freshwater fishes is an

important part of guaranteeing that these species are adequately protected. This will ensure that conservation plans and interventions are based on accurate and up-to-date data, resulting in improved conservation outcomes. Additionally, accurate species distribution data also enable better assessment of the effectiveness of South Africa's protected area network for conserving freshwater fishes.

1.6. Species distribution modelling

Species distribution models (SDMs), also commonly referred to as ecological niche models, or habitat suitability models, are a suite of statistical models that relate species distribution or occurrence data at known locations to environmental or spatial information in order to predict species spatial distributions across a landscape (Elith and Leathwick, 2009; Hao et al., 2020; Valavi et al., 2021). Broadly speaking, SDMs combine traditional concepts from natural history and ecology, with more recent developments in statistics and computing (Elith and Leathwick, 2009). SDMs are conceptually based on an 'ecological niche' (Gobeyn et al., 2019), which describes the relationship between where a species is recorded to occur (its occurrence) and the suite of environmental conditions that characterise that habitat. According to niche theory, a species can only survive if the local environmental gradients, (collectively termed the niche), enable a positive population growth rate in the absence of immigration (Gobeyn et al., 2019), which allows the species to occupy a distinct niche and exist in a given area (Gobeyn et al., 2019).

SDMs have become one of the most-used tools for understanding patterns in species distributions in relation to environmental factors in recent years (Guisan and Zimmermann, 2000; Guisan and Thuiller, 2005; Fois et al., 2018), benefitting from recent increases in new approaches and methods being developed (Elith and Leathwick, 2009; Papeş et al., 2016). Increasingly, SDMs are becoming an important tool in ecology, biogeography, conservation, and spatial planning, with numerous studies using SDMs for identifying critical habitats (Rufener et al., 2017), managing threatened species reintroductions (Hendricks et al., 2016; Miranda et al., 2019), designing of protected areas (Roos et al., 2015; Kajee et al., 2023a), managing invasive species (Barbet-Massin et al., 2018; Srivastava et al., 2019), and predicting species ranges where comprehensive data are lacking, or in response to climate change (Brown et al., 2016; Booth, 2018; Brun et al., 2020; Santini et al., 2021). As such, SDMs can serve as important tools for ecologists, conservation managers, and policymakers, in light of the urgent need to sustainably manage natural resources and slow-down species extinctions.

There is a steadily growing body of literature focussed on SDMs. Comprehensive reviews of SDM approaches and literature have been conducted by Guisan and Zimmermann (2000), Guisan and Thuiller (2005), Richards et al. (2007), Elith and Leathwich (2009), Martinex-Minaya et al. (2018), and Hao et al. (2019), with several other books, instructional texts, and R packages now readily available online (Thuiller et al., 2009; Naimi and Araújo, 2016; Guisan et al., 2017; Carlson, 2020; Hijmans and Elith, 2023). Consequently, there has been a sharp increase in the number of studies that have utilised SDMs (Zurell et al., 2020). For example, Brotons (2014) found that between 2000 and 2009 the number of studies using SDMs increased consistently, reaching more than 350 published articles in 2009, whilst Peterson and Soberon (2012) found more than 1 000 SDM-related articles published in 2011 alone. The total number of published articles related to SDMs has been reported to range from more than 4 000 (Sequeira et al., 2018) to greater than 6 000 (Araújo et al., 2019). In the

past two decades alone, more than 20 different statistical and machine learning techniques have been applied to species distribution modelling (Carlson, 2020; Norberg et al., 2019).

In addition, there have also been recent developments that focussed on modelling several species at the same time to infer community-level interactions and incorporate these into model outputs. For example, stacked species distribution models (SSDMs) combine (or rather stack) multiple single-species SDMs together to estimate community structure and species richness (Gelfand et al., 2005; Mateo et al., 2012; Wilkinson et al., 2021). Similarly, joint species distribution models (JSDMs), described in detail in Pollock et al. (2014) and Clark et al. (2014b), allow multiple species to be modelled at the same time, accounting for species-to-species correlations not explained by environmental predictors (Wilkinson et al., 2021). In this regard, JSDMs account for the dynamic and multivariate nature of biological communities by assuming that species respond jointly to both the environment and to other species (Warton et al., 2015; Clark et al., 2017; Ovaskainen et al., 2017; Tikhonov et al., 2020). This can be useful since these biological correlations can then be used to generate hypotheses about the potential role of biotic interactions in structuring communities. Additionally, JSDMs can also provide important insight on the strength of co-occurrence patterns between species (Wagner et al., 2020).

However, as the body of knowledge on SDMs has progressively grown over recent years, along with a steady increase in new modelling techniques, so too has the level of complexity and confusion around best practices for modelling species distributions. For example, there is uncertainty around how to access, clean, and process species data, as well as about modelling algorithm choice, tuning of model parameters, selection of background data, and environmental parameters (Araújo et al., 2019; Valavi et al., 2022). Each of these decisions and choices can have substantial impacts on the accuracy, validity, and repeatability of the final model outputs. As such, model predictions can vary significantly depending on an exponentially complex combination of decisions made by modellers, often resulting in knock-on impacts on the conservation and policy decisions being made based on these model predictions (Muscatello et al., 2021). Recent works by Norberg et al. (2019), Hao et al. (2020), and Valavi et al. (2022) have sought to provide some guidance on how to go about selecting modelling algorithms and how to utilise SDMs in a more robust manner, whilst Zurell et al. (2020) provided clarity on how to report SDM results in a standardised manner. Further, recent developments in SDM modelling have sought to account for sampling and sorting biases as well as pseudo-absences to improve the accuracy of model outputs (Rodrigues-Rey et al., 2019; Tao et al., 2023). However, modelling species distributions in both the past, present, and future remains a complex undertaking, one that requires careful considerations of species life history, habitat characteristics, environmental variables, and ecological interactions.

Despite their proven effectiveness and increasingly available scientific literature, until recently, the majority of SDM studies were applied to terrestrial and marine species, with fewer studies focusing on freshwater organisms (Parreira et al., 2019). For example, Papes et al. (2016) found that MaxEnt, one of the most commonly used modelling algorithms, had only been applied in freshwater systems in 23 publications, compared to almost 900 in terrestrial systems. Freshwater species are especially difficult to model for a number of biological, ecological, and logistical reasons. For example, the movement of freshwater organisms is usually restricted to a specific

catchment's drainage network (Valencia-Rodríguez et al., 2021), which makes modelling at broad spatial scales relatively complex. However, in some cases, highly mobile species (for example migratory fish) undertake regular movement between river systems, entire catchments, and even across estuaries into the marine environment (Elith and Leathwick, 2009). As such, modelling freshwater species distributions requires expert knowledge of the target species' biology, life history, and migratory patterns in both space and time. Additionally, species occurrences are strongly influenced by the geographic and physicochemical characteristics of specific river systems (Valencia-Rodríguez et al., 2021), which are in turn susceptible to variation driven by upstream river conditions and human activity (Valencia-Rodríguez et al., 2021). Furthermore, applying SDMs to freshwater systems requires access to large-scale, high-quality climatic and hydrology data, which are often limited and difficult to obtain (Iguchi et al., 2004; McNyset, 2005; Domínguez-Domínguez et al., 2006; McGarvey et al., 2018; Parreira et al., 2019; Domisch et al., 2020). These factors present important methodological challenges to developing SDMs in freshwater systems (Domínguez-Domínguez et al., 2006; Iguchi et al., 2004; McNyset, 2005;) due to the complex interactions between several ecological, climatic, and hydrological drivers in river systems, combined with insufficient biotic and abiotic data to effectively describe the hydro-ecological relationships in freshwater systems (Irving et al., 2022).

As a result, there is a paucity of information available explaining how to approach developing SDMs for freshwater species. Despite these limitations, there has been substantial progress made to model freshwater species' distributions in recent years. For example, da Silva et al. (2023a) modelled the current and future distributions of six mussel species occurring in the Iberian Peninsula. Similarly, da Silva et al. (2023b) used JSDMs to model the co-occurrence of freshwater fishes and mussels, while Nogueira et al. (2023) used these models to identify freshwater priority areas for cross-taxa interactions. Rodriquez-Rey et al. (2019) used five SDM algorithms to assess the predictive performance of models and to predict the distribution of nine freshwater invasive species. Impressively, Tao et al., (2023) used ensemble SDM outputs to predict the distributions of all 1658 freshwater fishes occurring in China. These outputs were then used to assess biodiversity indices and evaluate representativeness if freshwater fishes in China's existing protected area network (Tao et al., 2023). These studies, among others, are indicative of the increasing application of SDMs in freshwater environments for various purposes.

In South Africa, very few studies have attempted to apply SDMs to freshwater fishes. Studies of fish distributions have generally been limited to documenting existing species ranges, based on occurrence data and systematics, or have focussed primarily on linking fish habitat preference to micro-habitat environmental conditions, such as flow and temperature (Dallas et al., 2019). However, in recent years, a handful of studies have attempted to use SDMs to predict the distribution of freshwater fishes in South Africa. The first reported use of SDMs to predict freshwater fish distributions was published by Lübcker et al. (2014) and sought to use MaxEnt to model the potential range of silver carp (*Hypophthalmichthys molitrix*) – a non-native species ranked among the world's 100 worst invasive species (Lowe et al., 2000). Since then, the majority of studies that have applied SDMs to freshwater fishes have focussed on non-native invasives. For example, Khosa et al. (2019) used MaxEnt to model potential distribution ranges for four black bass species occurring in South Africa. Similarly, Rivers-Moore et al. (2019) developed a simplistic univariate model based on thermal threshold exceedances to predict the distribution of two trout species occurring

in the country. More recently, Maimela et al. (2022) used MaxEnt (Phillips et al., 2006; Elith et al., 2011) to model current and future distributions of rainbow trout in the Mpumalanga Province of South Africa. Despite these initial modelling studies returning promising results, information on how to go about applying SDMs to freshwater fishes in South African river systems remains limited.

To date, the most comprehensive modelling effort for freshwater fishes in South Africa was conducted by Dallas et al. (2019), as part of a report commissioned by the Water Research Commission (WRC). Dallas et al. (2019) used SDMs to predict the distribution and responses of endemic freshwater fishes occurring in the CFE to climate change. This report was the first attempt to model native fish distributions in the present and under future climate scenarios in South Africa. Dallas et al. (2019) presented statistically sound and ecologically relevant modelled distributions for 11 native and two non-native taxa. However, the authors also concluded that their study was merely a first step towards being able to accurately model freshwater fish distributions in South Africa in a robust manner (Dallas et al., 2019). Because all modelling was conducted using the original self-contained Java MaxEnt prorgamme (Phillips et al., 2006; Elith et al., 2011), their exact methods and model parameters are difficult to reproduce. Similarly, they used the “Indicators of Hydrological Alteration” (IHA) software package (Richter et al., 1996) to calculate biologically relevant hydrological parameters from time series hydrological data for South Africa. Once again, the methods used to calculate the IHA metrics are not clearly available and difficult to reproduce. Despite these shortcomings, Dallas et al. (2019) did provide an important first step in developing SDMs for freshwater fishes in South Africa, providing important information on how to conduct SDMs in freshwater systems in the country.

Considering the paucity of published literature and available information on how generate SDMs for freshwater taxa (specifically fishes) in South Africa, there is an urgent need to develop a robust and repeatable method for conducting SDMs in freshwater systems in South Africa (Chakona et al., 2022). Consequently, being able to accurately map and model the distributions of South Africa’s threatened freshwater fishes is of utmost importance and can aid in population monitoring, conservation efforts, and policy making (Chakona et al., 2022; Kajee et al., 2023a).

1.7. Thesis aims

This thesis aims to collect, collate, and consolidating historic freshwater fish records for all fish species (native and non-native) known to occur in South Africa, to better understand distribution, diversity, and threat patterns in space and time. This will be underpinned by the objective of being able to provide guidelines to aid better research and publishing practises, improve decision-making in conservation, and improve our understanding of and ability to track fish population changes in response to global change.

Specifically, this thesis aims to:

1. Develop a national database for freshwater fish occurrence and biodiversity data and to consolidate these data into a single, online platform that can be easily accessed and where data can be visualised for analysis of general distribution patterns and species statuses;
2. Analyse these data to understand broadscale patterns in key response variables, such as diversity, threat status, and endemism;

3. Develop a robust and repeatable methodology for modelling freshwater fish distributions in South Africa; and
4. Demonstrate how the use of historic biodiversity data and accurate distribution maps can contribute to improved conservation and management of threatened freshwater fishes.

1.8. Thesis structure

To avoid unnecessary duplication, the thesis is presented in the form of single, overarching Introduction and Conclusions sections. Each data chapter then contains a concise Introduction, followed by the relevant Methods, Results and Discussion sections. References are combined into a single bibliography at the end of the thesis.

Chapter 1 (this chapter) provides and introduction and comprehensive literature review focussing on the status of global and South African freshwater ecosystems, as well as the current status of freshwater fishes in the country. Also included is a brief literature review on South Africa's protected area and conservation network, in relation to freshwater fishes, as well as a comprehensive review of SDMs, as specifically applied to freshwater ecosystems.

Chapter 2 presents a quantitative description of the South African freshwater fish database that was built for this thesis. In doing so, it provides an update on the state of knowledge of freshwater fish fauna in South Africa, including the first *Master Species List for freshwater fishes in South Africa*, along with analyses on the numbers of native and non-native species, threatened species, and rates of endemism at national and provincial scales.

Chapter 3 uses historic and present-day freshwater fish data to assess spatial patterns of distribution, richness, and threat status in South Africa at provincial and primary catchment scales. It also presents an assessment of how well South Africa's protected area network protects threatened species and fish diversity hotspots.

Chapter 4 presents a statistically robust methodology for developing SDMs for freshwater fishes in South Africa using available occurrence records (presence-only data) for a range of species. It also investigates whether the presence of non-native species can influence model accuracy and predicted area of occurrence.

Chapter 5 describes how the FBIS data and SDMs can be used to support freshwater fish conservation in South Africa. It also demonstrates how modelled distributions were used to develop the freshwater fish layer for the National Environmental Screening Tool, which is currently being implemented by the Department of Forestry, Fisheries, and Environment.

Chapter 6 provides a combined synthesis and conclusions for the entire thesis.

Chapter 7 lists the references for the entire thesis.

1.9. Thesis impact

The primary intended impact of this thesis is the improved knowledge and access to data on the status of and changes in South Africa's freshwater fish fauna. It provides a thorough review and analysis of all known, published and unpublished, records of freshwater fishes in South Africa. This consolidation of current knowledge and data

will provide an update on the state of freshwater fishes in South Africa and serve as a reliable baseline for future assessments of change in freshwater fish populations. The consolidated data were used to evaluate patterns of change in freshwater fish populations over the last century. Furthermore, applying a SDM methodology for freshwater fishes in South Africa, with a reproducible workflow, will allow researchers, conservation managers, and policy-makers to accurately map the distributions of freshwater fishes in the country. This will be immensely beneficial for conservation and management strategies across the country. Results from this project will also be used to directly contribute to future national-scale biodiversity assessments (for example, SANBI's National Biodiversity Assessment, NBA) and the IUCN Red List assessments.

In addition, this thesis presents a useful applied contribution to the field of freshwater science in South Africa. For example, all collected data will be uploaded onto the FBIS, which was specifically developed as part of this thesis and, on its own, presents an important contribution to South Africa's available research infrastructure. Furthermore, collating occurrence records on a national scale will allow us to, for the first time, robustly assess long-term change in populations of South African freshwater fish. This has the potential to drive freshwater fish research in South Africa forward, both in terms of the current state of knowledge and to revolutionise how data are stored, shared, and visualised. Indeed, the outputs of this thesis are already being used by researchers, government institutions, and consultants, with more than 500 active users accessing the freshwater fish dataset on FBIS.

CHAPTER 2

2. State of knowledge of South Africa's freshwater fishes

2.1. Introduction

South Africa is one of the most biologically diverse regions on earth (Wynberg, 2002), being formally recognised as the third most biologically rich country in the world (World Conservation Monitoring Centre, 1992; Lombard, 1995). However, compared with other regions, it has a relatively low diversity of freshwater fishes (Skelton, 2001). According to the most recent National Biodiversity Assessment, South Africa hosts 118 species of native freshwater fish, of which almost 50% are endemic (Skowno et al., 2019). As a result of the pressures being exerted on South Africa's river ecosystems, freshwater fishes are regarded as the country's most threatened species group (Skowno et al., 2019), with almost half of all assessed species listed as threatened (Vulnerable, Endangered, Critically Endangered) on the IUCN Red List (Darwall, Tweddle, et al., 2009). As the anthropogenic effects of global change on freshwater fishes becomes observable, it is becoming imperative that long-term datasets and baselines are developed, so that critical population trends and ecosystem shifts can be monitored and managed to best protect freshwater fish diversity.

Despite having a well-established freshwater fish research infrastructure in South Africa (see Chapter 1), to date there has been limited sharing of this knowledge or data on a national scale. Having these data easily accessible to all freshwater stakeholders is critical for biodiversity planning, conservation, management, and decision/policy making. Long-term distributional data for freshwater fish species can be vital for detecting critical ecosystem changes, such as past disturbances resulting in species range shifts, evaluating species resilience to anthropogenic impacts, identifying new records of non-native species invasions, and loss of ecosystem services or unique biodiversity (Dudgeon et al., 2006; Chakona et al., 2020). Understanding exactly how the abundance and distribution of freshwater fishes (both native and non-native) are changing is pivotal to effectively manage and conserve South Africa's unique and threatened freshwater biodiversity and ecosystems.

In short, not being able to effectively observe, record and track trends in freshwater fish populations can have serious implications for our ability to sustainably manage freshwater ecosystems and the services they provide.

This chapter aims to: i) produce a master list for freshwater fishes in South Africa; ii) collect, collate, and consolidating historic freshwater fish records for all fish species (native and non-native) known to occur in South Africa; and iii) analyse these data to better understand distribution, diversity, and threat patterns in space and time. This will be underpinned by the objective of being able to provide guidelines to aid better research and publishing practises, improve decision-making in conservation, and improve our understanding of and ability to track fish population changes in response to global change.

2.2. Methods

A *Master Species List for freshwater fishes in South Africa* was developed and used to build a comprehensive freshwater fish data set, using data from multiple sources, in order to compile all known, accessible records of freshwater fish occurrences in South Africa. Specific details pertaining to how this list was developed, the scope of the data set, as well as the collection and analyses of the data, are provided below. All data were uploaded onto the Freshwater Biodiversity Information System (FBIS) database (Dallas et al., 2022; freshwaterbiodiversity.org). The FBIS database will serve as the long-term storage facility for the data collated for this thesis.

2.2.1. Study area

The geographic scope of this study was restricted to the boundaries of the Republic of South Africa, but also included the Kingdom of Eswatini (formerly Swaziland) and the Kingdom of Lesotho (for convenience purposes, this study area is hereafter referred to as 'South Africa'). Data collection was limited to rivers, dams and freshwater lakes within South Africa. Importantly, estuarine and marine systems were excluded.

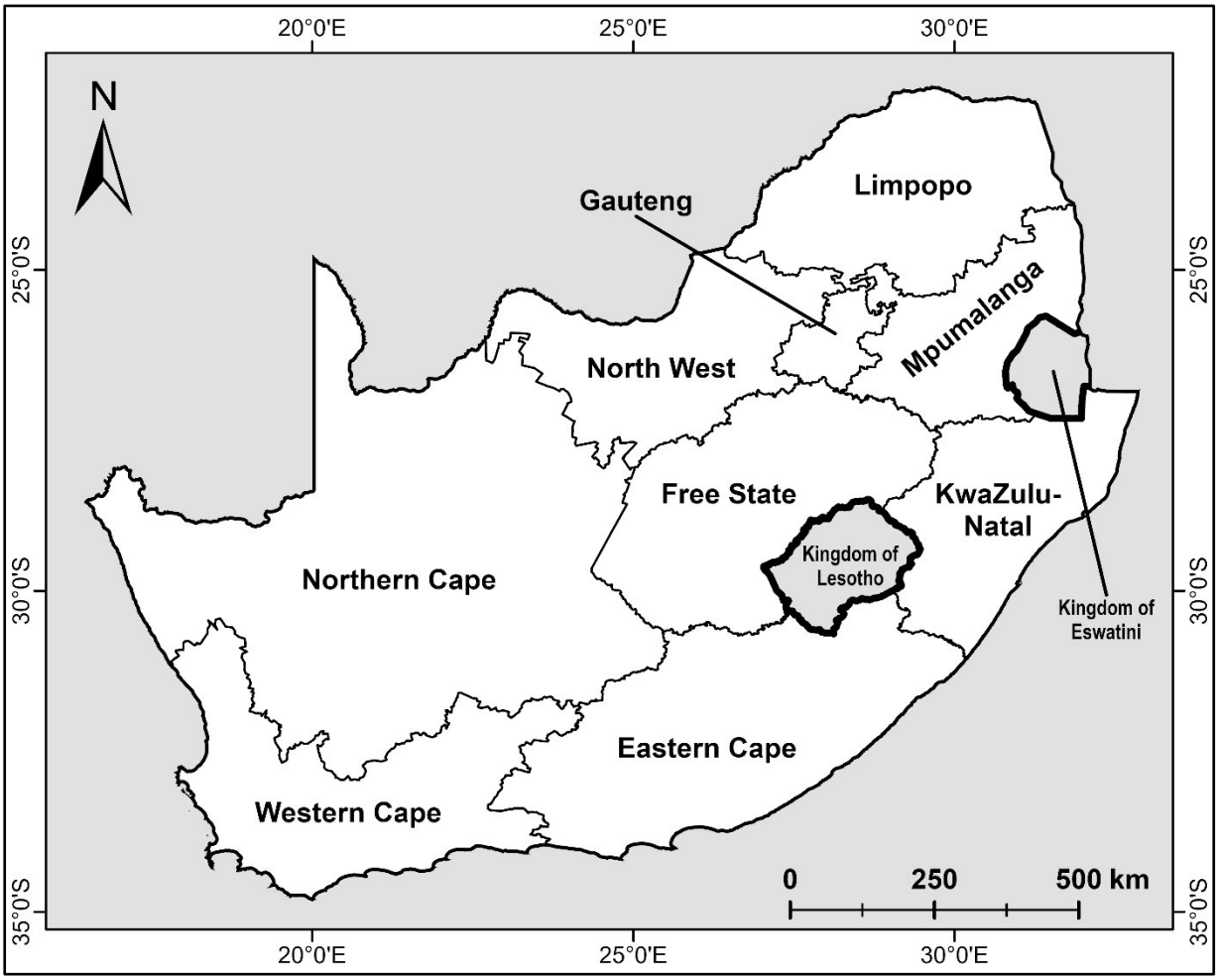


Figure 2. 1. Map of the Republic of South Africa, showing provincial boundaries and including the Kingdom of Eswatini (formerly Swaziland) and the Kingdom of Lesotho, the whole area hereafter referred to as 'South Africa'.

2.2.2. Study species

Coverage included all freshwater fish species known to occur in the wild (species held in captivity were excluded) within South Africa. For the purpose of this chapter, only formally described species recognised using the GBIF taxonomic backbone were

included. All formally described sub-species were also included but listed under their parent taxa. Species in the process of being described, or that belong to groups that are currently under taxonomic review (such as the genera *Enteromius, Galaxias* and *Sandelia*) were omitted completely from the data collection and analyses of this chapter, pending resolution of their taxonomic status. Freshwater fish species are defined as species that spend all, or a critical part, of their lives in either freshwater or brackish environments (IUCN Freshwater Fish Specialist Group, 2015; Arthington et al., 2016). For the purpose of this study, only primary freshwater fish (fishes living in inland waters, with little or no tolerance of saltwater), secondary freshwater fish (fishes relatively tolerant of salt water, but normally living in inland waters) and diadromous fish (fishes that, in the course of their life cycle, regularly migrate between inland waters and the sea, or vice versa) species were included. Importantly, both marine peripheral and sporadic marine species were omitted entirely from both the data collection and analysis (see Skelton (2001) for ecological-tolerance category definitions).

Based on these criteria, a preliminary freshwater fish species list was compiled using the South African Institute for Aquatic Biodiversity's (SAIAB) database and the RHP (River Health Programme) (2015) Rivers Database (Dallas et al., 2007). This preliminary list of taxa was then updated using the freshwater fish field guide by Skelton (2001), as well as subsequent scientific papers, including Skelton (2002), Skelton (2016), Ellender and Weyl (2014) and Weyl et al. (2020). From these sources, a preliminary Master Species List for freshwater fishes was compiled (**see Supplementary Table S2.1**). This contained 297 fish species (comprising both native and non-native fishes) known to occur in the whole of southern Africa (defined by Skelton (2001) as the region "south of the northernmost watershed of the Cunene, Okavango and Zambezi rivers, but excluding Lake Malawi and the Shire River above the Kapachira Falls"). All 297 fish species were included in this preliminary Master Species List to ensure that any recently translocated or introduced species from one of South Africa's neighbouring countries were not mistakenly omitted from the data search.

2.2.3. Data collection

Occurrence data

Published data

A thorough literature search was undertaken for each species included on the preliminary Master Species List, starting in November 2018 and culminating in May 2020. The literature search was conducted using Google Scholar. To ensure that relevant papers were identified, the following search term combination was used for all native freshwater fishes:

"*Genus species" and "South Africa*"
(where "Genus species" represents the current and previous scientific names of each taxon).

A different search term was used for non-native species, to further refine the search. The following search term was used:

"Genus species" and "South Africa" and "study" OR "survey" OR "sample" OR "site" and "map" OR "coordinate" OR "coordinates" OR "latitude" OR "longitude" OR "GPS""

(where "Genus species" represents the current and previous scientific names of each taxon).

Relevant articles were identified based on their titles, abstracts, methods, and results sections. Only the first 500 search results returned by Google Scholar were assessed for relevancy, due to time constraints. This number was selected based on an initial trial phase, which determined that after 500 search results, Google Scholar mostly outputted irrelevant, obscure articles.

Articles (including peer-reviewed publications, theses and published reports) were deemed to be relevant if information from the title, abstract or methods section indicated that the article contained occurrence data for the specific freshwater fish taxon in South Africa. If an article was deemed to be relevant, it was catalogued in a Microsoft Excel (365 ProPlus) spreadsheet and the PDF version of the article downloaded. Data from each relevant article were extracted once all species searches were complete. Detailed explanation of the data extraction process is provided below. If an article was not deemed to be relevant, this was also catalogued in Microsoft Excel and a reason for disregarding the article logged.

Databases

Occurrence data for freshwater fishes in South Africa were also collected from 15 national databases curated within FBIS, and from one international database, the Global Biodiversity Information Facility (GBIF), which included the SAIAB database (**Table 2.1**).

Table 2. 1. Databases accessed to search for freshwater fish occurrence records in South Africa.

#	Name of Database
1	Global Biodiversity Information Facility (GBIF)*
2	South African National Parks Fish Database
3	Limpopo Department of Environmental Affairs Fish Database
4	Rivers Database 2015
5	Mpumalanga Tourism and Parks Agency Fish Database
6	Cape Nature State of Biodiversity Database
7	Clean Stream Biological Services Fish Database
8	Inkomati-Usuthu Catchment Management Agency Database
9	Nepid Fish Database
10	Ecotone Freshwater Consultants Database
11	Ecosun Database
12	Department of Water and Sanitation Regional Fish Database
13	Gauteng Department of Agriculture and Rural Development Database
14	Freshwater Research Centre Monitoring Database
15	The Biodiversity Company SASS and Fish Database

* The Global Biodiversity Information Facility's (GBIF) database. These data included all data uploaded to GBIF by South African and International research institutions like SAIAB, as well as citizen science data from iNaturalist that were classified by GBIF as "Research Grade" data.

Unpublished Data

Several freshwater fish experts and conservation organisations from across the country were identified and contacted to request any additional unpublished data that may exist in analog form, or on private hardware (**see Supplementary Table S2.2**). Additionally, several presentations were delivered at conferences, workshops, and meetings to appeal for data. In October 2019, the FBIS database was launched online and opened for the upload of additional data by approved, registered users. These data were validated by experts and downloaded on 05 October 2022 and incorporated into this study.

2.2.4. Data extraction

Each article that was deemed to be relevant (containing occurrence records of freshwater fishes in South Africa) during the literature search was inspected for species occurrences with GPS coordinates. In cases where GPS coordinates were not provided, the paper was temporarily archived and catalogued, and an email was sent to the listed corresponding author asking whether these were available and if so, requesting a copy. Where site-specific coordinates were provided, these were converted to decimal degrees and entered into the dataset. Available metadata, including collector details, physico-chemical data, sampling method, and abundance measures were also documented for each record. See Supplementary **Table S2.3** for details of the full list of metadata included during data extraction. All data were then uploaded onto the FBIS.

2.2.5. Biological information

Species diversity and origin

Once data collection was complete, species with no known occurrence records in South Africa were removed from the preliminary Master Species List. This list was then sent via email to various freshwater fish experts (**see Table S2.2**) in South Africa for comment. After several iterations, a subset of 134 species were included in the first *Master Species List for freshwater fishes in South Africa* (**see Table S2.4**). The GBIF database (GBIF.org, 2018) was used to ensure that the most recent, accepted scientific name of each species was recorded. All previous scientific names and subspecies names were also included as attributes in the *Master Species List*. In addition, the taxonomic classification (Kingdom, Phylum, Class, Order, Family, Genus and Species) was downloaded for each species using the GBIF database (GBIF.org, 2018) and cross-referenced with current information available on the International Union for the Conservation of Nature (IUCN) Red List of Threatened Species website (IUCN Red List, 2020). Common names for each species were sourced using the SAIAB database, the freshwater field guide of Skelton (2001), or the IUCN Red List of Threatened Species website (IUCN Red List, 2020). Information pertaining to species origin was determined using historic distribution records from the IUCN Red List of Threatened Species website (IUCN Red List, 2020), the GBIF database (GBIF.org, 2018), Skelton (2001) and Ellender and Weyl (2014). Each species was classified as being either ‘native’ (taxon occurring within its natural range – past or present – and dispersal potential) or ‘non-native’ (alien or extralimital taxa) (Dallas et al., 2022).

Ecological tolerance category

Information pertaining to the ecological tolerance of each species was determined using Skelton (2001). Each species was classified as being either 'primary freshwater'; 'secondary freshwater'; or 'diadromous'. This classification was confirmed with relevant fish experts in the country (Skelton, personal communication, 01 April 2020; Chakona et al., personal communication, 14 September 2020).

Endemism

The endemism category of each species was determined using definitions provided on the FBIS (Dallas et al., 2022). Species were classified based on the definitions presented in **Table 2.2** below.

Table 2. 2. Endemism categories for freshwater fishes of South Africa (Dallas et al., 2022).

Endemism Category	Definition
Widespread	Occurring in more than one Freshwater Ecoregion and not restricted to southern Africa.
Subregional endemic	Endemic to southern Africa.
National endemic	Occurring in more than one Freshwater Ecoregion but restricted to South Africa.
Regional endemic level 1	Endemic to South Africa but occurs in more than one primary catchment within a single Freshwater Ecoregion.
Regional endemic level 2	Endemic to one primary catchment in South Africa.
Micro-endemic 1	Endemic to less than five rivers, within one primary catchment in South Africa.
Micro-endemic 2	Endemic to one river in South Africa.

Conservation status

The IUCN Red List of Threatened Species website (IUCN Red List, 2020) classifies species into six main categories based on their extinction risk. Each species was classified as either 'Not Evaluated', 'Data Deficient', 'Least Concern', 'Near Threatened', 'Vulnerable', 'Endangered' or 'Critically Endangered'.

2.2.6. Data analysis

The collected data were standardised (See Supplementary **Table S2.3**) and uploaded onto the FBIS platform, then downloaded from the FBIS on 05 October 2022 and analysed shortly thereafter. Distribution and abundance patterns were assessed and visualised in R Software (Version 3.5.0; R Core Team, Vienna, Austria). The total number of records were calculated for: each data source; each year; each species; each origin category; each ecological tolerance category; each endemism category; and each IUCN conservation category. In addition, the total number of species occurring in each category was also calculated for: each species; each origin category; each ecological tolerance category; each endemism category; and each IUCN conservation category. These calculations were then repeated for each of South Africa's nine provinces.

2.3. Results

2.3.1. Data sources

The data search resulted in the accrual of a total of 60 837 records of freshwater fish from South Africa (**Figure 2.2**) (FBIS, 2022; Dallas et al., 2022). Data for this chapter were collected from four distinct source categories, including published peer-reviewed scientific articles, published reports and university theses, databases, and unpublished data. In terms of origin, most of the data (69.2%) were sourced from databases, followed by unpublished data (13.7%), published reports and theses (8.7%) and peer-reviewed scientific articles (8.5%) (**Figure 2.2**). The majority of records (42 069 records) originated from several separate databases, as shown in **Table 2.3**. Notably, the SAIAB database, harvested from GBIF, accounted for 23 012 records – the largest contribution by any single institution. Of the 60 837 records, 23 835 records (39.2%) also reported abundance values.

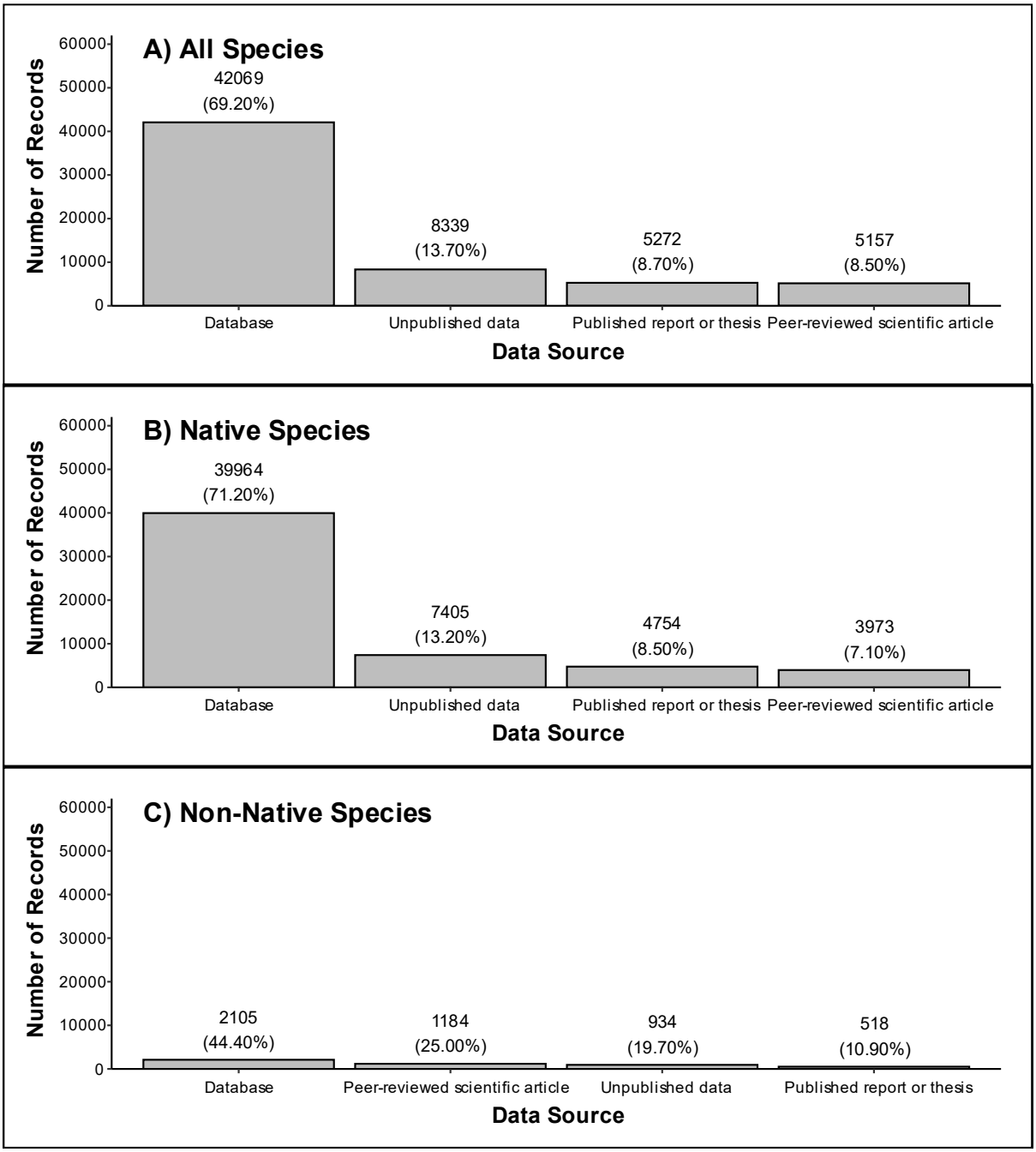


Figure 2. 2. Number of records of freshwater fish species occurring in South Africa collated into FBIS separated according to record category for (A) all species combined

(n = 60 837), for (B) native species only (n = 56 096) and for (C) non-native species only (n = 4 741).

Table 2. 3. Number of records of freshwater fish species occurring in South Africa collected from national and international databases.

#	Name of Database		Number of Records	Percentage Contribution
1	Global Biodiversity Information Facility (GBIF)	SAIAB	23012	54.70%
		iNaturalist	1117	2.66%
		Other	732	1.74%
2	South African National Parks Fish Database		4251	10.10%
3	Limpopo Dept. of Environmental Affairs, Fish Database		3339	7.94%
4	Rivers Database 2015		2845	6.76%
5	Mpumalanga Tourism and Parks Agency		2688	6.39%
6	Cape Nature State of Biodiversity Database		1926	4.58%
7	Clean Stream Biological Services		610	1.45%
8	Inkomati-Usuthu Catchment Management Agency Database		417	0.99%
9	Nepid Fish Database		406	0.97%
10	Ecotone Freshwater Consultants		248	0.59%
11	Ecosun		171	0.41%
12	Dept. of Water and Sanitation Regional Fish Database		151	0.36%
13	Gauteng Dept. of Agriculture and Rural Development		109	0.26%
14	FRC Monitoring Database		31	0.07%
15	The Biodiversity Company SASS and Fish Database		16	0.04%

2.3.2. Temporal patterns

The dataset contains records spanning 194 years (1828–2022), with the vast majority of records (89%) occurring between 1975 and present (**Figure 2.3**). The earliest available records were from 1828, but there were generally few records from the 1800's (n = 43) and between 1900 and 1950 (n = 873), after which numbers started to increase substantially to date (**Figure 2.3**). A total of 6 037 records were available between 1951–1975, while the majority of the data (n = 27 950) were collected between 1976–2000. In the last 21 years (2001-2022), an additional 25 934 records were also added. The earliest records of a non-native species in South Africa comes from 1904–1905 (*Salmo trutta*) and 1912 (*Coptodon zilli*).

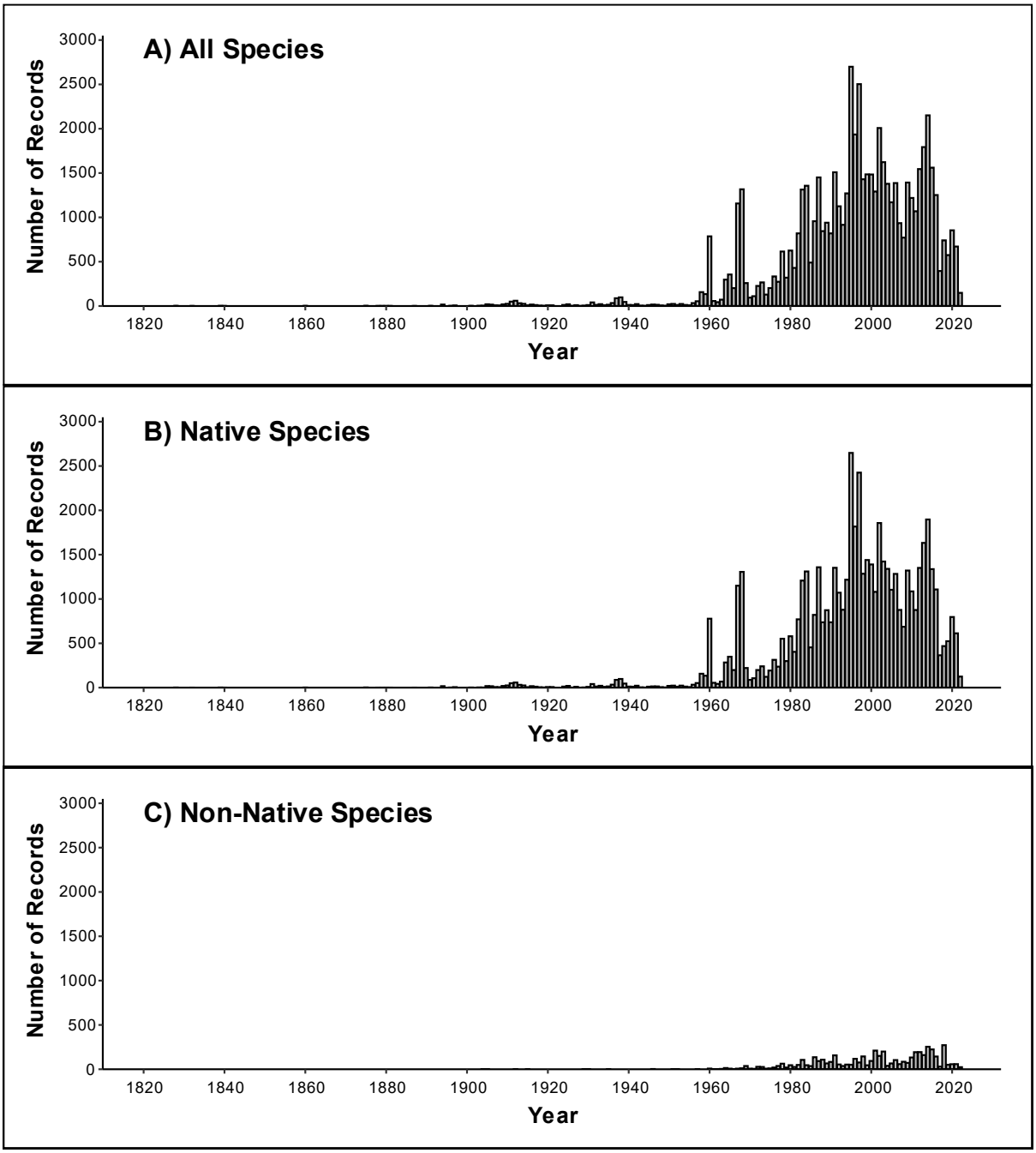


Figure 2. 3. Number of occurrence records of freshwater fish species occurring in South Africa for each year between 1860 and 2020 for (A) all species combined (n = 60 837), for (B) native species only (n = 56 096) and for (C) non-native species only (n = 4 741).

2.3.3. Biological information

Species diversity and origin

Of the 134 species originally on the *Master Species List*, records were found for 129 species, belonging to 51 genera and 22 families (**Table 2.4**). Of the 129 fish species recorded in South Africa, 105 (81%) were native and 24 (19%) non-native. Additionally, of the 60 837 records collected, 56 096 belonged to fishes native to South Africa, whilst 4 741 records were for non-native species. The top five most data-rich species were: *Oreochromis mossambicus* (3 674); *Clarias gariepinus (*2 783); *Pseudocrenilabrus philander* (2 542); *Enteromius trimaculatus* (2 447); and *Labeobarbus marequensis* (2 376). In total, 20 species had more than 1000 records each, while 62 species had

between 100-999 records. Many species were notably data-scarce; 51 species having less than 100 records and 12 species less than 10 records. Five species did not return any occurrence records (see Discussion for details). **Table 2.4** provides a comprehensive list of all the freshwater fishes with occurrence records in freshwater ecosystems in South Africa. It is important to note that the species names used in this table are based on the GBIF taxonomic backbone. As such, some species names have been updated through formally-published peer-reviewed articles, but have not yet been updated on GBIF. For the purpose of this thesis, these names have been kept so as to align with the GBIF taxonomic backbone and what is reflected on the FBIS platform. Taxonomic updates are presented below.

- *Amphilius natalensis* has been split into five species (Mazungula and Chakona, 2021)
    - *A natalensis*
    - *A. zuluorum*
    - *A. engelbrechti*
    - *A. marshalli*
    - *A. leopardus*

- *Enteromius anoplus* has been split into four species (Kamikambi et al., 2019)
    - *E. anoplus*
    - *E. cernuus*
    - *E. oraniensis*
    - *E. mandelai*

- *Pseudobarbus capensis* has been renamed to *Cheilobarbus capensis* (Skelton et al., 2018)

- *Pseudobarbus erubescens* has been renamed to *Sedercypris erubescens* (Skelton et al., 2018)

- *Pseudobarbus trevelyani* has been renamed to *Amatolacypris trevelyani* (Skelton et al., 2018)

- *Pseudobarbus hospes* has been renamed to *Namaquacypris hospes* (Skelton et al., 2018)

- *Schilbe intermedius* does not occur in South Africa, where the species is now given as *Schilbe depressirostris* (Van der Bank et al., 2017)

- *Micropterus salmoides* has been renamed to *Micropterus nigricans* (Ross and Stauffer, 2024)

- *Micropterus floridanus* has been renamed to *Micropterus salmoides* (Ross and Stauffer, 2024)

Table 2. 4. Alphabetical list of 134 freshwater fish species occurring in South Africa and the number of records found for each species. Non-native species are indicated in bold and with an asterisk (*). Species with zero records are highlighted in grey.

Scientific Name	Number of Records	Scientific Name	Number of Records	Scientific Name	Number of Records
Ambassis natalensis	72	*Enteromius paludinosus*	1715	*Opsaridium peringueyi*	474
Amphilius natalensis	444	*Enteromius radiatus*	402	***Oreochromis andersonii****	0
Amphilius uranoscopus	1006	*Enteromius toppini*	590	***Oreochromis aureus****	15
Anguilla bengalensis	26	*Enteromius treurensis*	28	*Oreochromis mossambicus*	3674
Anguilla bicolor	9	*Enteromius trimaculatus*	2447	***Oreochromis niloticus****	80
Anguilla marmorata	195	*Enteromius unitaeniatus*	873	*Oreochromis placidus*	4
Anguilla mossambica	1088	*Enteromius viviparus*	1779	***Pangasius sanitwongsei****	3
Austroglanis barnardi	100	*Galaxias zebratus*	1250	***Perca fluviatilis****	4
Austroglanis gilli	330	***Gambusia affinis****	203	*Petrocephalus wesselsi*	214
Austroglanis sclateri	140	*Hydrocynus vittatus*	367	***Poecilia reticulata****	103
Brycinus imberi	346	***Hypophthalmichthys molitrix****	14	*Protopterus annectens*	0
Brycinus lateralis	72	*Kneria auriculata*	8	*Pseudobarbus afer*	554
Carassius auratus*	31	*Labeo capensis*	416	*Pseudobarbus asper*	379
Chetia brevis	27	*Labeo congoro*	215	*Pseudobarbus burchelli*	655
Chetia flaviventris	123	*Labeo cylindricus*	1292	*Pseudobarbus burgi*	215
Chiloglanis anoterus	571	*Labeo molybdinus*	1771	*Pseudobarbus calidus*	359
Chiloglanis bifurcus	84	*Labeo rosae*	619	*Pseudobarbus capensis*	97
Chiloglanis emarginatus	120	*Labeo rubromaculatus*	227	*Pseudobarbus erubescens*	149
Chiloglanis paratus	957	*Labeo ruddi*	252	*Pseudobarbus hospes*	76
Chiloglanis pretoriae	1540	*Labeo seeberi*	278	*Pseudobarbus phlegethon*	229
Chiloglanis swierstrai	458	*Labeo umbratus*	575	*Pseudobarbus quathlambae*	153
Clarias gariepinus	2783	*Labeobarbus aeneus*	608	*Pseudobarbus senticeps*	17
Clarias ngamensis	9	*Labeobarbus kimberleyensis*	202	*Pseudobarbus serra*	605
Clarias theodorae	98	*Labeobarbus marequensis*	2376	*Pseudobarbus skeltoni*	38
Coptodon rendalli	1152	*Labeobarbus natalensis*	1081	*Pseudobarbus swartzi*	10
Coptodon zilli*	14	*Labeobarbus nelspruitensis*	121	*Pseudobarbus tenuis*	428
Ctenopharyngodon idella*	35	*Labeobarbus polylepis*	360	*Pseudobarbus trevelyani*	89
Ctenopoma multispine	28	*Labeobarbus seeberi*	316	*Pseudobarbus verloreni*	39
Cyprinus carpio*	642	*Lacustricola katangae*	126	*Pseudocrenilabrus philander*	2542
Engraulicypris brevianalis	833	*Lacustricola myaposae*	129	***Pterygoplichthys disjunctivus****	16
Engraulicypris gariepinus	66	***Lepomis macrochirus****	411	***Salmo salar****	0
Enteromius afrohamiltoni	336	*Marcusenius caudisquamatus*	9	*Salmo trutta**	71
Enteromius amatolicus	37	*Marcusenius krameri*	17	***Salvelinus fontinalis****	2
Enteromius annectens	431	*Marcusenius pongolensis*	51	*Sandelia bainsii*	155
Enteromius anoplus	2096	*Megalops cyprinoides*	71	*Sandelia capensis*	1685
Enteromius argenteus	426	*Micralestes acutidens*	1105	*Schilbe intermedius*	461
Enteromius bifrenatus	244	*Microctenopoma intermedium*	6	*Serranochromis jallae*	0
Enteromius brevipinnis	152	*Micropanchax johnstoni*	89	*Serranochromis meridianus*	72
Enteromius eutaenia	658	***Micropterus dolomieu****	657	***Serranochromis robustus****	2
Enteromius gurneyi	170	***Micropterus floridanus****	62	*Synodontis zambezensis*	228
Enteromius lineomaculatus	126	***Micropterus punctulatus****	369	*Tilapia sparrmanii*	2290
Enteromius mattozi	81	***Micropterus salmoides****	1362	*Tinca tinca**	8
Enteromius motebensis	126	*Nothobranchius orthonotus*	48	***Xiphophorus helleri****	45
Enteromius neefi	475	*Nothobranchius pienaari*	0	***Xiphophorus maculatus****	8
Enteromius pallidus	351	***Oncorhynchus mykiss****	584	**Total**	**60837**

Endemism

The number of records belonging to each endemism category is shown in (**Figure 2.4**). In total, 26 020 records were found for species classified as "Subregional endemics" (**Figure 2.4**), the most data-rich endemism category. The second most data-rich category was "Widespread" with 22 515 records. As expected, species belonging to "Micro-endemic level 2" only accounted for 94 records. In addition, the total number of species contained under each category was calculated (**Figure 2.5**). As was the case with the total number of records, the number of species contained within the "Subregional endemic" category was the highest (47 species – 36.4%).

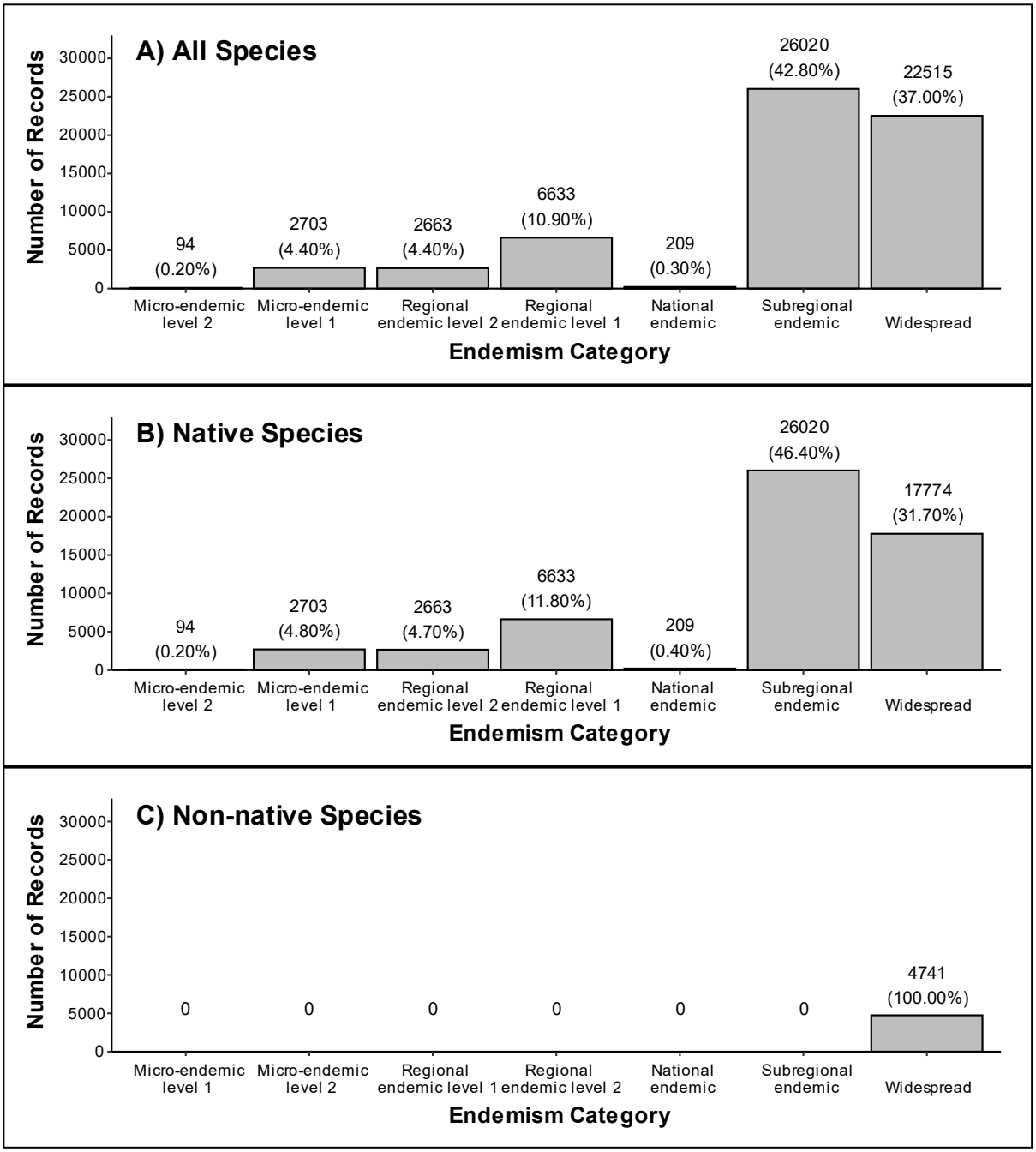


Figure 2. 4. Number of occurrence records of freshwater fish species occurring in South Africa for each endemism category for all species combined (A), for native species only (B) and for non-native species only (C).

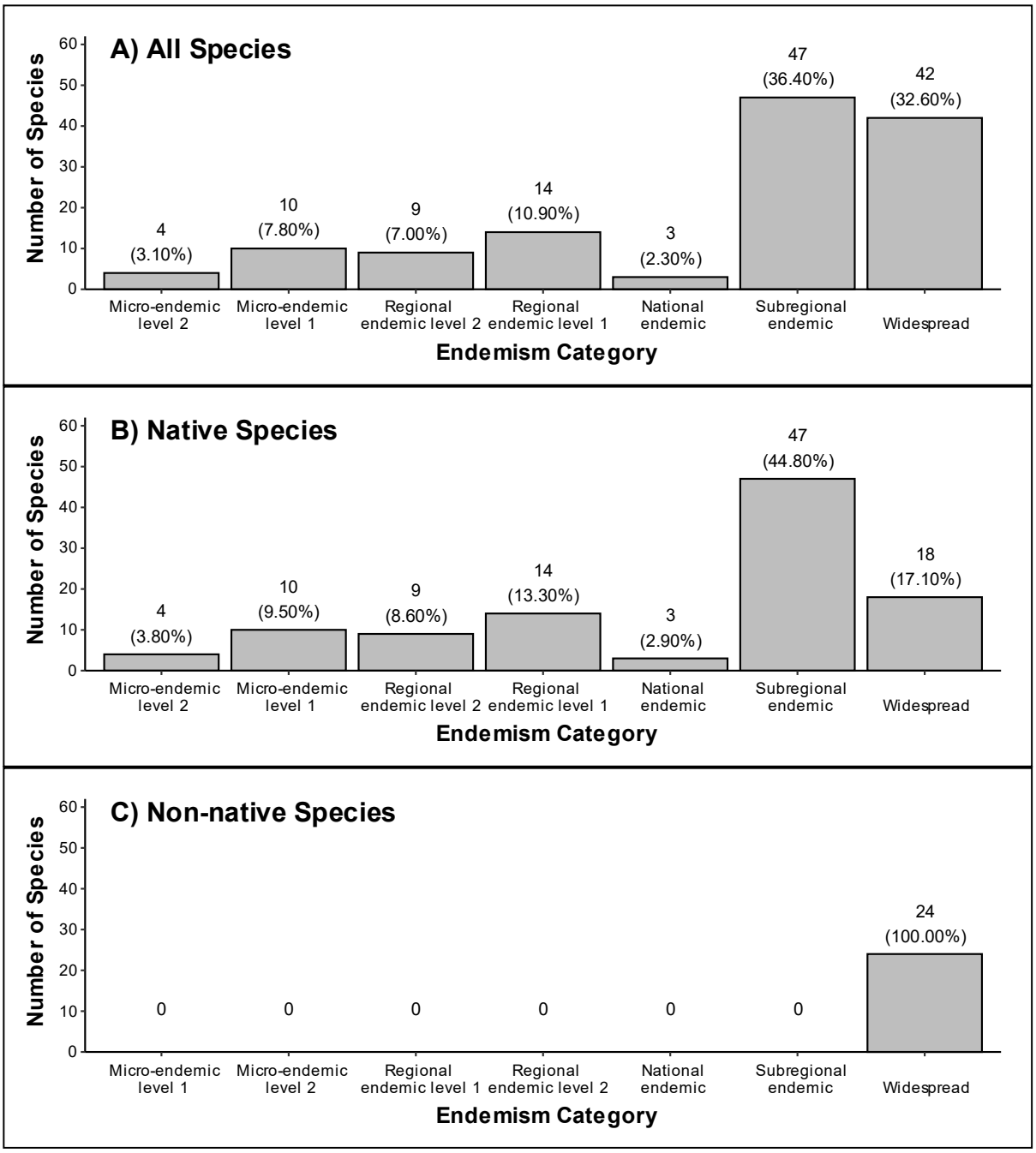


Figure 2. 5. Number of freshwater fish species recorded in South Africa for each of the five endemism categories for all species combined (A), for native species only (B) and for non-native species only (C). Total number of records and percentage (%) composition of each category is provided above each bar.

Conservation status

The number of records for species belonging to each of the IUCN Red List categories is shown in **Figure 2.6**. The category with the most records was “Least Concern” (45 702), followed by “Vulnerable” (5 222). The categories with the least number of records were “Critically endangered” (936) and “Not evaluated” (802). In addition to calculating the number of records, the number of freshwater fish species found within South Africa that lie within each category was also calculated (**Figure 2.7**). Of the native species,

25 (24%) were threatened with extinction, listed as either “Vulnerable” (6 species – 5.7%), “Endangered” (14 species – 13.3%) or “Critically endangered” (5 species – 4.8%). Most of the freshwater fishes found in South Africa were classified as “Least Concern” (63 species – 60%). A further 5 species were categorised as “Not evaluated” or “Data deficient”.

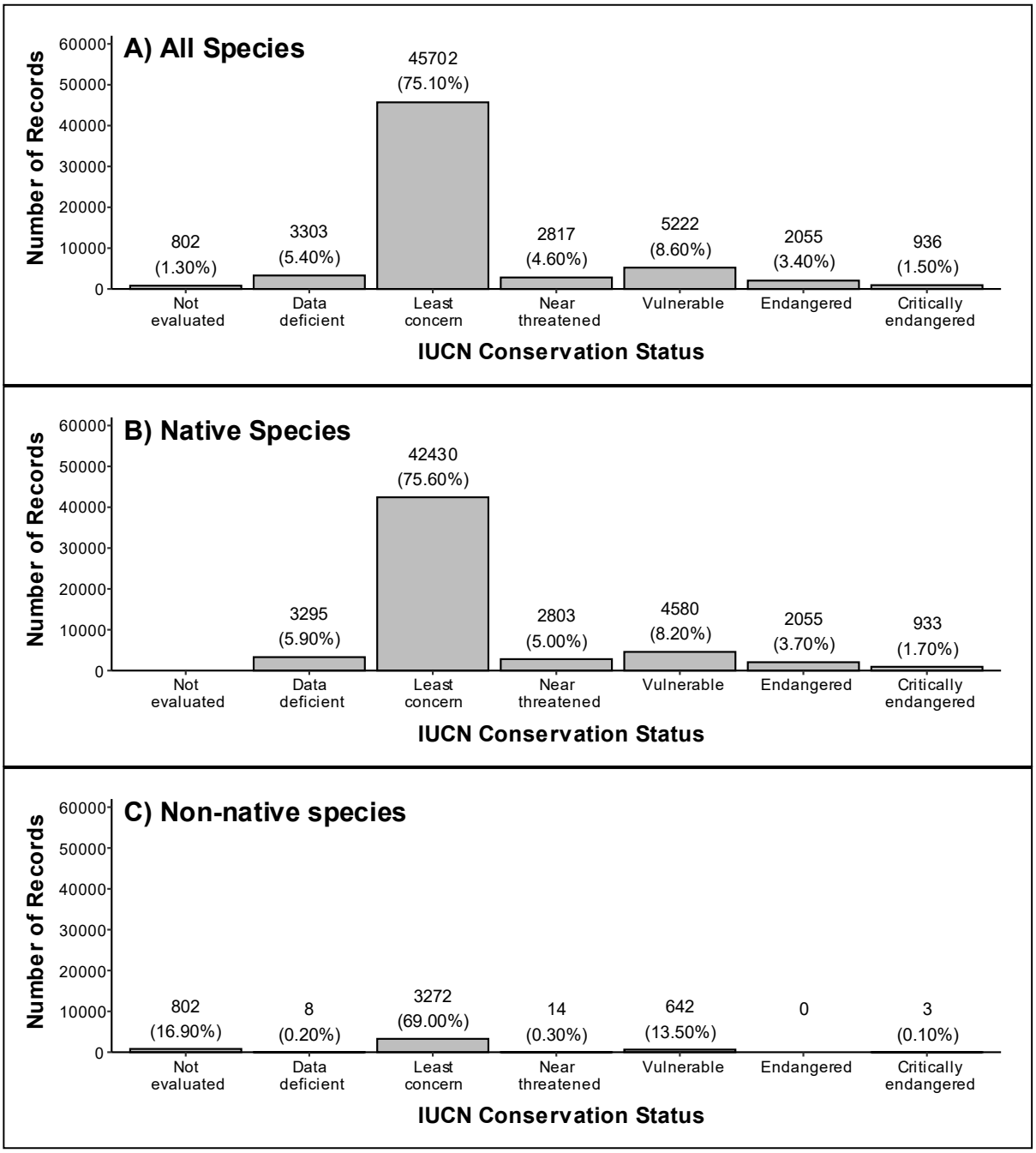


Figure 2. 6. Number of records occurrence records of freshwater fish species occurring in South Africa falling into each of the International Union for the Conservation of Nature (IUCN) conservation category (IUCN Red List, 2020) for all species combined (A), for native species only (B) and for non-native species only (C). Total number of records and percentage (%) composition of each category is provided above each bar.

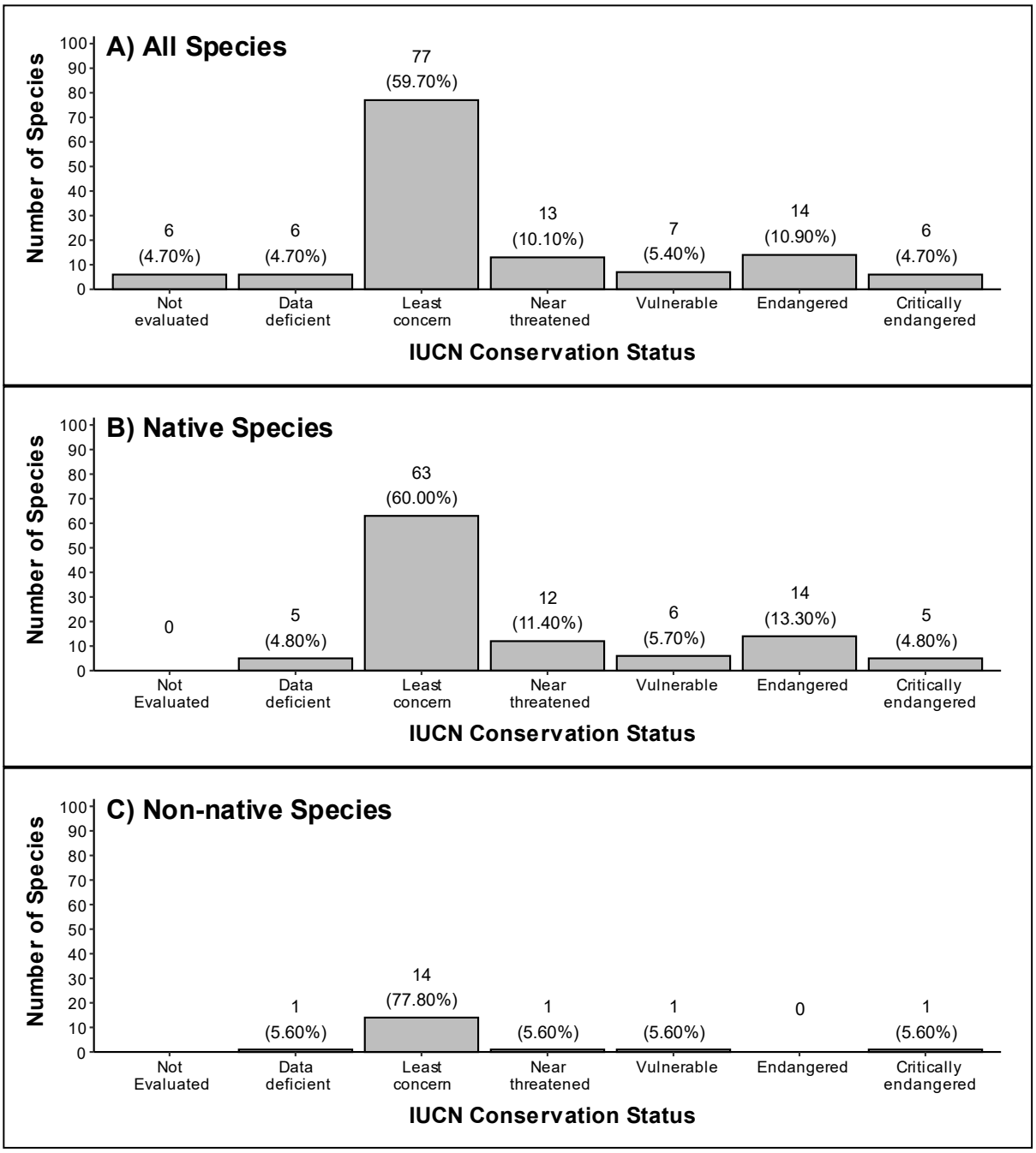


Figure 2. 7. Number of freshwater fish species recorded within South Africa for each of the International Union for the Conservation of Nature (IUCN) conservation categories (IUCN Red List, 2020) for all species combined (A), for native species only (B) and for non-native species only (C). Total number of records and percentage (%) composition of each category is provided above each bar.

2.3.4. Spatial patterns

The province with the greatest number of records was Limpopo (15 332), followed by KwaZulu-Natal (12 615), Mpumalanga (12 300) and the Western Cape (9 236) (**Figure 2.8** and **Figure 2.9**). The provinces with the least number of records were the Free State (964) and Gauteng (989). Non-native species occurred in all nine provinces. KwaZulu-Natal had the greatest number of non-native species (20), followed by the

Western Cape (16) and the Eastern Cape (14). These three provinces also had the largest number of threatened species (KZN = 9 (12%); WC = 16 (43%); EC = 11 (29%)). Endemic species were found in all nine provinces, with the Western Cape showing the highest number of endemic species at 22 (59%) (**Figure 2.9**).

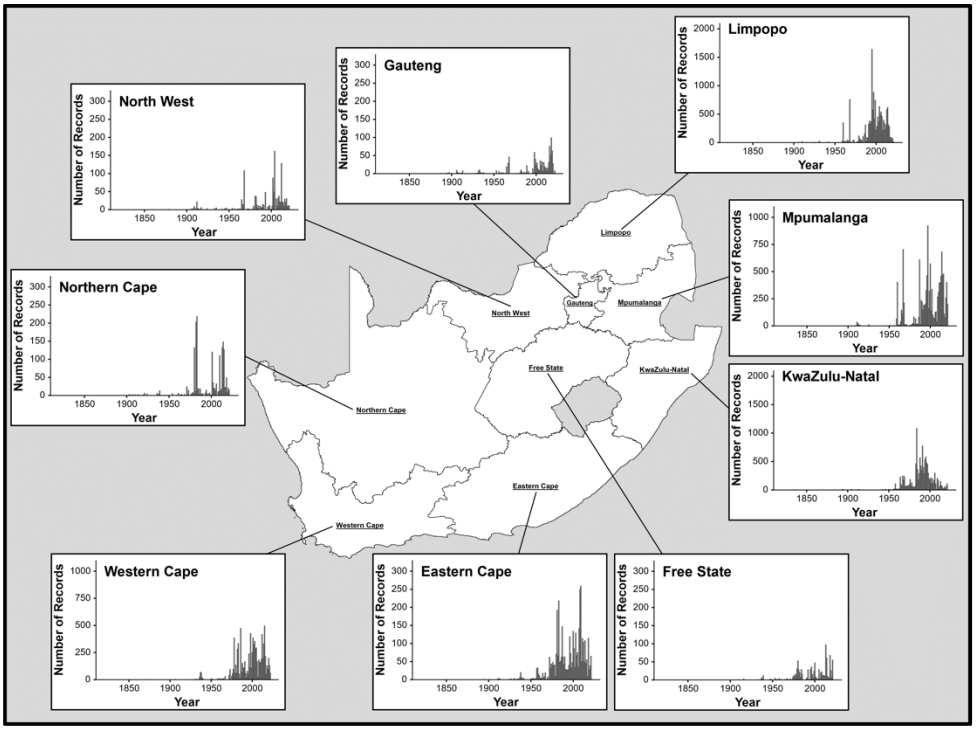


Figure 2. 8. Number of occurrence records of freshwater fish species recorded per year in each of South Africa's nine provinces from 1828 – 2022. Adapted from Frith (2006).

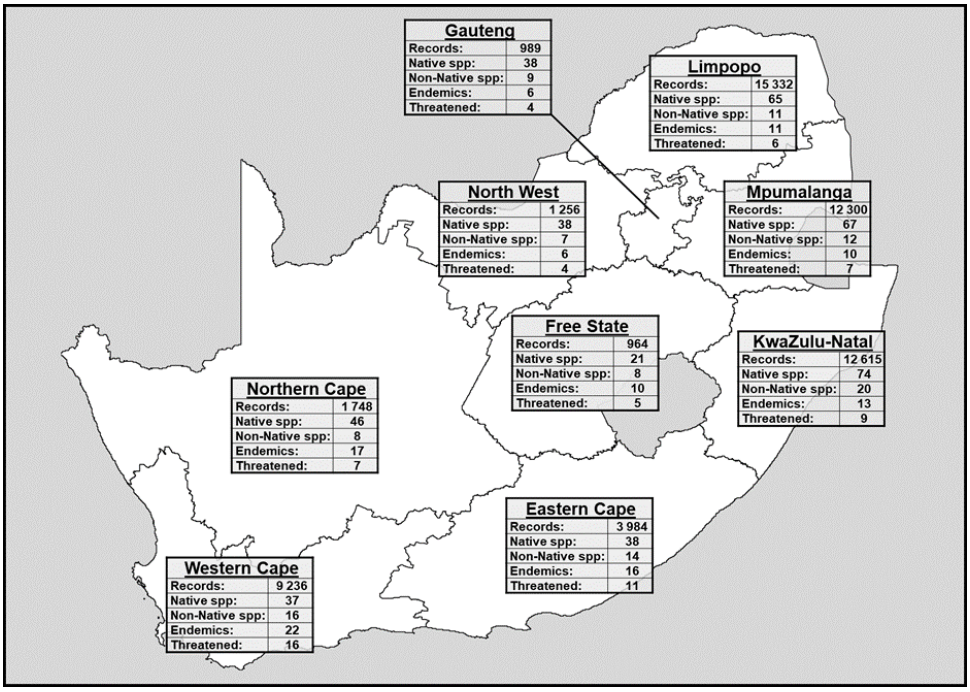


Figure 2. 9. Total number of records and number of native, non-native, endemic and threatened species recorded in each of South Africa's nine provinces. Adapted from Frith (2006).

2.4. Discussion

The primary aims of this chapter were to collect, collate and consolidate historic and current data for freshwater fishes known to occur in South Africa, and to use these data to provide an updated, comprehensive review of the status and distribution of these species. The preliminary analyses provide insights into spatio-temporal patterns in the data set and provide a solid foundation for assessing the diversity, distribution, and status of freshwater fishes in the country.

2.4.1. Data sources

The majority of records available were collected from database records of GBIF (**Figure 2.2**). This is likely attributed to the fact that SAIAB (23 080 records) currently hosts the majority of the freshwater fish occurrence data in the country, which are annually shared and uploaded onto GBIF (Bills, personal communication 2019, November 27). By comparison, there were only 5 157 records collected from peer-reviewed scientific articles, which was surprising, given that this is the primary method of data reporting used by the scientific community. Indeed, during the data collection process, more than 500 articles were flagged as having been relevant, containing data, but lacking any useful geographic information. The relatively low number of records from peer-review articles can be attributed to the lack of standards and requirements for publishing site-specific spatial or geographic information (Wallis et al., 2011; Karl et al., 2013). Consequently, data reporting in many peer-reviewed publications are often condensed for publication, and thus lack accurate geographic descriptions or GPS coordinates for individual species occurrences. This is an area of concern within the scientific community and needs to be addressed. These findings point toward the need for a shift in publication culture within the freshwater fish research community in South Africa to ensure that geographic occurrence data are accurately and adequately reported, or preferably stored in a recognised database where they are accessible for computational and analytical value in the future.

2.4.2. Temporal patterns

The data spanned 194 years, dating back to 1828 (**Figure 2.3**). This timespan, however, excludes the first known fish records from within South Africa, which were collected in 1822 (Skelton, 1993). The low number of records (916) collected between 1828 and 1950 is not surprising, given that many of the earliest records of freshwater fishes in South Africa could not be included in this study, since the geographic information was not detailed enough to accurately determine their location. This has resulted in a substantial number of records being unsuitable for inclusion in the database. One possible solution to deal with these data would be to assign these records with quarter degree square (QDS; 15’ x 15’) values, as was done by Scott et al. (2000) and (Henderson, 1999) when developing the GIS atlas of southern African freshwater fish and the Southern African Plant Invaders Atlas (SAPIA) respectively. Whilst these data lack accuracy, their inclusion could have benefits for a host of applications. It is important to note, however, that these data would need to be clearly marked and added onto the FBIS database as a separate, easily displayable layer, so as not to affect the quality and accuracy of the core dataset. This could serve as an important next step in the development and improvement of the FBIS platform and could yield a plethora of important historical data across South Africa.

2.4.3. Biological information

Species diversity and origin

The comprehensive literature search resulted in 60 837 occurrence records, which currently makes this the largest known database for freshwater fishes in South Africa. Analysis of these records showed that a total of 129 freshwater fish species have data occurrence records in the country (Table 2.4). It is important to note, however, that the *Master Species List for freshwater fishes in South Africa* (see **Table S2.4**) contains 134 species, of which 105 were native and 24 were non-native. This number provides the most up-to-date evaluation for the diversity of freshwater fishes in South Africa. This differs notably from the species list provided in the 2018 National Biodiversity Assessment, which lists only 118 freshwater fishes (Skowno et al., 2019). The NBA species list, however, does not include non-native species. In addition, the NBA species list includes 18 taxa that are yet to be formally described (belonging to the genera *Enteromius*, *Galaxias*, *Kneria*, *Marcusenius* and *Pseudobarbus*) and two species that are categorised as being either marine sporadic or marine peripheral species (*Glossogobius callidus* and *Silhouettea sibayi),* which were hence excluded entirely from this chapter (**see Supplementary Table S2.5**). Accounting for this, the NBA species list contains 98 native freshwater fishes, compared to the 107 native species presented in the *Master Species List*. This important finding (an additional nine native species with known occurrences in South Africa) will no doubt improve the accuracy of future biodiversity assessments in South Africa.

There were five species that are known to have occurred in South Africa and as a result, were included on the *Master Species List*, but did not return any data during the data search (Ellender and Weyl, 2014),. Of these, two are native species (*Nothobranchius pienaari* and *Protopterus annectens)* and are both listed as species of “Least concern” by the IUCN. For *N. pienaari*, the species was only formally described in 2010 (Shidlovskiy et al., 2010), which could account for the lack of records. In addition, three of the species with no occurrence data were non-native species. Of these, two (*Oreochromis andersonii and Salmo salar*) are known to be failed introductions (Ellender and Weyl, 2014). Lastly, it is likely that *Serranochromis jallae* (also a non-native species included in the *Master Species List* but with no available occurrence records) has no known occurrence records in South Africa, as it is often mistaken for *S. robustus* (Skelton, personal communication, 01 April 2020).

Diversity among freshwater fishes is relatively low when compared to other species groups within South Africa (Skowno et al., 2019). The highest diversity was reported for plant species (20 401 species; Skowno et al., 2019) while amongst vertebrates, the most diverse species groups are birds (732 species), followed by reptiles (397) and mammals (336; Skowno et al., 2019). There are ~2000 native marine fish species in South Africa (Griffiths et al., 2010; Skowno et al., 2019), which means that freshwater fishes make up ~5% of fish diversity in the country. Even when accounting for freshwater fishes still needing formal description (Swartz et al., 2007; Linder et al., 2010; Chakona et al., 2013, 2018; Ellender et al., 2017), the proportion of freshwater to marine fish diversity is still low when compared to the rest of the world (Closs et al., 2016; Tickner et al., 2020). For example, global assessments of the disproportionate diversity found in freshwater habitats – ‘freshwater fish paradox’ (Tedesco, Paradis, et al., 2017) – found that approximately 40–50% of total fish diversity is found in freshwater habitats (Tedesco, Beauchard, et al., 2017; Tedesco, Paradis, et al., 2017; Fricke et al., 2022).

Endemism

Most of the records obtained belonged to species categorised as either “Subregional endemic” or “Widespread” (**Figure 2.4**), as expected, given that the majority of species (89 or 69%) are in these categories (**Figure 2.5**). Widespread species are also most likely to be detected in the course of survey work, simply because they occur over a wide range. There are thus both a high number of species listed as “Subregional endemic” or “Widespread” and a high number of records found for each of these species. A comparable pattern is observable across all endemism levels, with Micro-endemic species hence accounting for the lowest number of species and fewest records.

South Africa is recognised as one of the most biodiverse countries in the world (World Conservation Monitoring Centre, 1992; Lombard, 1995; Wynberg, 2002). However, the diversity of freshwater fish found in South Africa is relatively low (**Table 2.3**). Despite this, there is a high level of endemism among the native fishes that occur in the country (Skelton, 2001; Skowno et al., 2019; Van Deventer et al., 2019). This study found that 31% of the native fishes in South African are endemic (**Figure 2.5**). Whilst this still represents a relatively high percentage of endemic species, the number falls short of the endemism level for freshwater fishes reported in the NBA (49%; (Skowno et al., 2019; Van Deventer et al., 2019). A possible explanation for this difference could be attributed to taxa that are yet to be formally described, but which were included in the NBA assessment (Skowno et al., 2019). Once the taxonomic revisions for these taxa are complete and additional species formally described the true number of endemic species and level of endemism within South African freshwater fishes will likely increase and may even exceed the estimate provided in the NBA (Skowno et al., 2019).

An increase in the use of molecular and genetic techniques will also likely result in further taxonomic revisions and additions to South Africa’s freshwater fish fauna (Ellender et al., 2017). More recent studies (Swartz et al., 2007, 2009; Chakona et al., 2013; Chakona, Malherbe, et al., 2015; Chakona, Swartz, et al., 2015) found that genetic differentiation within traditionally recognised species is far higher than previously thought, indicating that biodiversity and endemism has been underestimated (Linder et al., 2010; Ellender et al., 2017). For example, Linder et al. (2010) estimated that there are at least 43 historically isolated lineages currently existing within the Cape Fold Ecoregion (CFE) alone, indicating that species diversity in this ecoregion has been under-estimated and under-studied (Linder et al., 2010; Chakona et al., 2018). Recent taxonomic studies by Chakona and Swartz (2013) and Chakona et al. (2014) resulted in the discovery of two additional species, *Pseudobarbus skeltoni* and *P. verloreni* respectively. Similar studies currently being undertaken in South Africa will likely result in similar new descriptions and lineages (Ellender et al., 2017). There are additional taxonomic reviews being conducted on the genera *Galaxias*, *Pseudobarbus* and *Sandelia* (Swartz et al., 2007, 2009; Linder et al., 2010; Chakona et al., 2015; Ellender et al., 2017). These include at least 10 additional *Galaxias* species (Chakona et al., 2013, 2018; Ellender et al., 2017), seven *Pseudobarbus* species (Swartz et al., 2007; Ellender et al., 2017) and five *Sandelia* species (Chakona et al., 2013; Ellender et al., 2017) that have been identified as needing formal description.

The increase in taxonomic focus will not only result in an increase in overall diversity of described freshwater fish species in South Africa, but also an increase in endemism, given that the main lineages being studied are highly range-restricted endemics. It is likely that any re-description or discovery of new taxa will also include a large proportion of highly range-restricted species, endemic to only a few catchments or tributaries. For example, Chakona et al. (2015) found that one of the newly-identified lineages within the *Galaxias zebratus* species complex is a highly range-restricted endemic comprising fragmented populations found in only six mountain tributaries (Chakona et al., 2015; Chakona et al., 2018). Similar findings will no doubt increase the proportion of endemic species found within South Africa, with serious and urgent impacts on the development of conservation and management plans, given that many of these endemic freshwater fishes are already listed as threatened (**Figure 2.7**).

The limited taxonomic and systematic capacity to rapidly review the diversity and true endemism of freshwater fishes is an impediment to fully describing South Africa's freshwater fauna (Skelton and Swartz, 2011; Ellender et al., 2017). This database, along with the development of a formal *Master Species List*, is an important first step to aid in this process. However, the existence of undescribed, cryptic species may have led to an overestimation of historic distribution ranges, because historic occurrence records may have been incorrectly assigned to single, widespread 'species' (Bickford et al., 2007; Chakona et al., 2020). Reassigning occurrence records to newly-described species in reviewed lineages will prove to be a difficult task and something that needs to be carefully considered as the FBIS database is updated. Further funding, resources and constant refinement and updating is recommended as an important next step to avoid the database from becoming obsolete. Keeping the FBIS database up to date with the most recent taxonomic discoveries and reviews can have ramifications for biodiversity conservation, national and provincial management plans and future ecological studies. For example, revised taxa may require separate management and conservation action (Chakona et al., 2020) to preserve the evolutionary processes that shaped the genetic diversity within each lineage (Moritz, 1994; Chakona et al., 2020).

As additional endemic species are described, the level of endemism found within the freshwater fish species group in South Africa will increase and change in relation to other groups. Currently, based on the NBA assessments, plants show the highest level of endemism (67%), followed by reptiles, (53%), and amphibians (50%), with 13% of marine fishes being endemic (Skowno et al., 2019). Freshwater fishes are currently ranked fifth in the country but will likely see an increase in the description of 'new' endemic species in the coming years, which could see an increase its endemism ranking in the country.

Conservation status

The category with the most records was the "Least Concern" category, which correlates directly with the number of species listed as "Least Concern" (**Figure 2.6**). Similarly, the category with the least records and lowest number of species was "Critically endangered", which could indicate that these species tend to be less common and more difficult to study. This is concerning, given that highly threatened species in South Africa (all of which are endemic) are not receiving the research attention they deserve. A recommendation for immediate research attention and

management action is proposed to ensure that threatened species are adequately protected to ensure their survival.

The results for the IUCN conservation status analysis for this study also differ from those published in the NBA, which reported that 36% of all native taxa and 66% of endemic freshwater fish taxa in South Africa were threatened (Skowno et al., 2019; Van Deventer et al., 2019). This study found that 19% of native taxa are currently categorised as threatened (**Figure 2.7**). As was the case with the total species diversity and endemism, differences between this study and the NBA are likely caused by differences in the species lists used for the NBA. This study did not include 18 taxa that are yet to be formally described. Accounting for this, the number of threatened taxa is likely to be similar. These updated figures, and an agreement on what species should or should not be included in the next NBA report, need to be followed up.

The NBA lists freshwater fishes as South Africa's most threatened species group (36% of native species and 66% of endemics; (Skowno et al., 2019). Of all the taxa assessed in the NBA (n=23 312), 14% (3 157 taxa) are threatened with extinction (Skowno et al., 2019). By comparison, 16% of marine fishes were reported to be threatened, with mammals (17%), plants (14%), and birds (11%) all containing similarly lower percentages of threatened taxa (Skowno et al., 2019). Comparatively, the percentage of threatened native freshwater fish taxa reported in this study (19%; **Figure 2.7**) is still higher than any other species group in the country, likely a reflection of the degraded condition of many of South Africa's rivers (Skowno et al., 2019). Consequently, there have been reports of several localised extinctions of populations of fish belonging to the genera *Pseudobarbus*, *Cheilobarbus*, *Sedercypris*, *Sandelia* and *Galaxias* (Van Deventer et al., 2019; Skowno et al., 2019). Interestingly, targeted conservation and management interventions have prevented any species extinctions from taking place (Ellender et al., 2017; Skowno et al., 2019; Van Deventer et al., 2019). As a result, no freshwater fish species is known to have gone extinct in the wild (Skowno et al., 2019; Van Deventer et al., 2019), which is slightly better than the 0.2% (48 taxa) extinction rate reported for the rest of the country's biodiversity (Skowno et al., 2019). This demonstrates the importance of developing targeted, species-level conservation and management plans for taxa that are regarded as threatened.

2.4.4. Provincial distribution

Provincial-level data showed that the Western Cape had the most records in the country (**Figure 2.8** and **Figure 2.9**). Spikes in number of records per year are noticeable from the late 1970's until present (**Figure 2.8**)). Following on from the Western Cape, KwaZulu-Natal, Limpopo and Mpumalanga all have similarly high number of records (**Figure 2.8** and **Figure 2.9**) and records from all three provinces start to increase rapidly from the 1970's until present (**Figure 2.8**). A possible explanation for this could be linked to funding of national or provincial-level projects that focussed specifically on surveying these river systems. It is also possible that the differences in the number of records across different provinces are influenced by population density or other anthropogenic factors, such as the presence of major universities or road access. Further analysis is needed to understand exactly what drivers impacted the collection of historic occurrence data in each province.

The province with the lowest number of occurrence records was the Free State, which could potentially be attributed to the low levels of diversity and endemism within this province. Additionally, the Free State has relatively few perennial rivers, which could account for low diversity and abundance values. Another potential factor to consider is whether institutional capacity (both provincial conservation authorities and research organisations, such as Universities) are as well funded in the Free State, as in, for example, the Western Cape or Eastern Cape. Gauteng had the second lowest number of records in the country, with no year yielding more than 100 records (**Figure 2.8**). This low number of records could be attributed to the rapid development of the Witwatersrand during the gold rush in the late 1800's (Durand, 2012). The impacts of mining in Gauteng, including water abstraction, acid mine drainage and dumping of mining waste into the surrounding river systems, resulted in the deterioration of water quality in the region and ultimately the decimation of aquatic life that relied on these systems (Durand, 2012). Additionally, the degraded status of these systems may have meant that researchers were less enthusiastic about sampling there. It is also worth noting that Gauteng is the smallest province by area, which could account partly for the low number of records in the province.

The proportions of endemic and threatened species found in each province is an important statistic to consider when assessing conservation and management plans, as well as the potential for localised or widespread extinctions. The Western Cape is home to 22 endemic species (59%), and 46% of native species there are regarded as threatened (**Figure 2.9**). The faunal composition of the Western Cape can be loosely compared to studies that focussed on assessing the diversity, endemism and threat of the CFE. A review of the biology and status of the freshwater fishes of the CFE found that endemism was high, with only a few taxa having wide geographic distributions (Ellender et al., 2017). Additionally, several studies have indicated that the majority (60%) of native freshwater fish species (including several species not formally described) in the CFE are threatened (Abell et al., 2008; Darwall et al., 2009; Ellender et al., 2017; Shelton et al., 2018a). This would place the freshwater fish communities with the CFE among the most threatened in the world (Ellender et al., 2017).

The large proportion of threatened species found within the Western Cape can be attributed to several factors. The primary threats to native fishes in the province are the large number of non-native species that occur there (**Figure 2.9**), many of which are known to be invasive (Ellender and Weyl, 2014; Marr et al., 2017; Weyl et al., 2020). Additional anthropogenic impacts on these river systems, such as unsustainable water abstraction, farming activities and damming of entire catchments, also increase the vulnerability of these species (Ellender et al., 2017). Furthermore, increases in the frequency of unseasonal burns in the Cederberg can result in near complete extirpation of fish populations due to the impacts of increased sedimentation that occurs after burn events (Broom et al., 2023). Climate change and the associated increase in frequency and intensity of extreme weather events, such as floods and drought, have also been known to impact the survival of vulnerable species (Dallas et al., 2019; Shelton et al., 2018a).

Another potential explanation for the large proportion of species classified as threatened could be the high levels of endemism found in this region. The Western Cape (59%) has the highest proportion of endemic species in South Africa (**Figure**

2.9). The large percentage of highly range-restricted endemic species found in the Western Cape is likely a result of the unique characteristics of the catchments found in the CFE. The CFE has many relatively small, short coastal rivers, which are geographically isolated and descend rapidly from high altitudes into the coastal region (Darwall et al., 2009; Ellender et al., 2017). These characteristics create isolated conditions where taxa evolved, resulting in increased levels of endemism, along with limited geographic ranges (Darwall et al., 2009; Chakona et al., 2020). However, while these unique river systems have allowed for the evolution of numerous, isolated freshwater fish taxa, these same river systems are also highly impacted (Ellender et al., 2017), which poses a serious threat to the threatened endemic taxa that live within them. Threats, such as non-native species invasions, water abstraction, flow modifications and climate change (Ellender et al., 2017), that impact species across the country are amplified for the endemics found within the CFE. Highly range-restricted species do not have the luxury of being able to disperse into habitats that are not invaded or are less impacted by human activities. Consequently, disturbances can have disproportion negative impacts on these species. For example, most studies have reported reduced abundance or complete absence of native fishes in the lower reaches of rivers in the CFE (Ellender and Weyl, 2014; Van Der Walt et al., 2016; Ellender et al., 2017). This demonstrates the importance of identifying endemism hotspots within each province in South Africa and incorporating this type of information into future conservation and management planning.

2.4.5. Relevance

The study, along with the development of a nation-wide freshwater fish database in FBIS, has provided a much-needed update on the number and distribution of freshwater fish species in South Africa. Additionally, the comprehensive *Master Species List for freshwater fishes in South Africa*, including all formally described species, all their previous scientific synonyms, sub-species, and taxonomic classification (**see Table S2.4**) is a useful resource that has until now not been available (Bills, personal communication, 2018 October 23; Skelton, personal communication, 2018 October 23). This *Master Species List* will form the foundation for future national and provincial biodiversity assessments and improve the efficiency of current and future taxonomic revisions in the country.

In addition, this study provides a database where all available records for fish occurrence data can be accessed on a single, digital platform. One of the major factors impeding implementation of effective conservation and management intervention is the lack of accurate, reliable and up-to-date data on species distributions (Moyle et al., 2013; Ellender et al., 2017). This study has, through the development of the FBIS database, attended to the urgent need for accurate species distribution data in South Africa and can be used for future assessment of conservation efforts, such as species reintroductions and river rehabilitation. Further to this, the freshwater fish database will allow for the detection of critical ecosystem changes, such as loss of ecosystem services, loss of unique biodiversity and species range shifts, as well as the impacts of non-native species introductions on native species distributions. Additionally, data from this study can be used to identify future long-term monitoring sites and the FBIS platform can serve as an important platform for storing these data. Being able to observe and assess long-term shifts will facilitate more efficient conservation

management interventions and planning. Ultimately, improved access to knowledge and data will result in more informed river management decisions and improved conservation planning. This will support freshwater decision-makers and conservation planners in their decision-making process.

With the onset of the digital revolution and improved access to online infrastructure, this study and the associated FBIS database provides an important step forward in digitising freshwater fish research in South Africa. Species occurrence records mapped on paper, stored in museums, or reported in published materials are rapidly becoming outdated (Scott et al., 2000; Skelton et al., 2000). Updates and changes to scientific names and inaccuracies often reduce the value and usability of data stored on paper. Standardising and digitising these data provide a rapid and efficient way to map the distribution of species. Furthermore, using exact GPS coordinates provides a far more accurate method of describing occurrence sites. The export of the data into other GIS-based software means that distribution maps can also be added to other map layers for enhanced analysis of fish distributions.

As the world transitions into the digital age, the ability to access, store and analyse large datasets will become an integral part of scientific research, conservation and government decision making. By collating data on freshwater fishes into an online, digital platform, the potential for modelling and machine learning-based analysis and future data collection becomes unlimited. This database drives freshwater fish research in South Africa into the 21st Century, allowing for seamless collaboration and computing ability. This study provides occurrence data that are critical to establishing baselines to observe patterns of change, which are, in turn, necessary to help predict the impacts of future changes to the country's freshwater biodiversity. Specifically, this large occurrence dataset, allows for the development of accurate species distribution models. To date, there have only been a handful of studies (Lübcker et al., 2014; Shelton et al., 2017; Dallas et al., 2019; Khosa et al., 2019) that have attempted to model freshwater fish distribution in South Africa. With the collation of occurrence records, this provides the potential to develop these models rapidly across all taxa in the country.

2.4.6. Conclusions and next steps

This chapter presents South Africa's most comprehensive freshwater fish database including data for all species known to occur in the country. Preliminary analysis of the database provides some key insights into the state of South Africa's freshwater fishes, which will no doubt have a positive impact on future research and biodiversity assessments. However, the work presented here is only a first, albeit important, step in understanding the trajectories of change in South Africa's freshwater fish fauna. To better understand the status of the country's freshwater fishes, future research will need to focus on statistically analysing the dataset in a more comprehensive manner, reassessing patterns of richness and invasion, and accurately mapping the distributions of threatened, endemic, and non-native species. In doing so, it is also important to consider what type of analyses and data, and at what spatial scales, are

most urgently needed for conservation and management purposes. The chapters that follow will address some of these questions.

CHAPTER 3

3. The status of South Africa's freshwater fish fauna: A spatial analysis of diversity, threat, invasion and protection

3.1. Introduction

The development of the Freshwater Biodiversity Information System (FBIS; freshwaterbiodiversity.org) (Dallas et al., 2022) freshwater fish database serves as an important platform to collate and appropriately house biodiversity data for freshwater fishes occurring in South Africa. However, unless these data are adequately cleaned and analysed, its potential value remains limited. Given the increasing pressures on freshwater ecosystems and fish, and recent improvements in freshwater fish data access in South Africa, there is now both an urgent need and new opportunity to comprehensively assess trends in diversity, distribution, and threat status of South Africa's freshwater fish fauna to support improved management and conservation decisions. These types of assessments will result in the production of 'actionable' data and information important for conservation planning, species management and policy making. Given the threats to and observed declining trends in South Africa's freshwater fish fauna, assessing the conservation status and effectiveness of conservation areas at protecting threatened fishes is both imperative and urgent (Jordaan et al., 2020; Chakona et al., 2022).

This chapter aims to use historic to present-day freshwater fish data, currently available on the FBIS database, to assess spatial patterns of distribution, diversity, and threat status in South Africa at provincial and primary catchment scales. Additionally, it seeks to assess how well South Africa's protected area network protects threatened species and fish diversity hotspots. It is hypothesized (based on available literature – see Chapter 1.5) that South Africa's current protected area network does not provide adequate protection for all of the country's threatened freshwater fishes.

3.2. Methods

3.2.1. Study site

The geographic scope of this study was restricted to the political boundaries of the Republic of South Africa. Occurrence records were also limited to rivers, dams, and freshwater lakes, with marine and estuarine systems excluded. South Africa's freshwater fish fauna is managed at provincial level (**Figure 3.1B**) via individual provincial conservation authorities. However, primary hydrological catchments (**Figure 3.1C**) and freshwater ecoregions (**Figure 3.1D**) represent more ecologically relevant assessment and management extents, given that the distribution of fishes are strongly impacted by the climate, geomorphological history, and topography of each region (Skelton, 2001). Analyses for this study were therefore conducted at both provincial and primary catchment scales. The primary catchment layer was downloaded from the DFFE (SLIM, 2014a) and is based on a Digital Elevation Model (DEM).

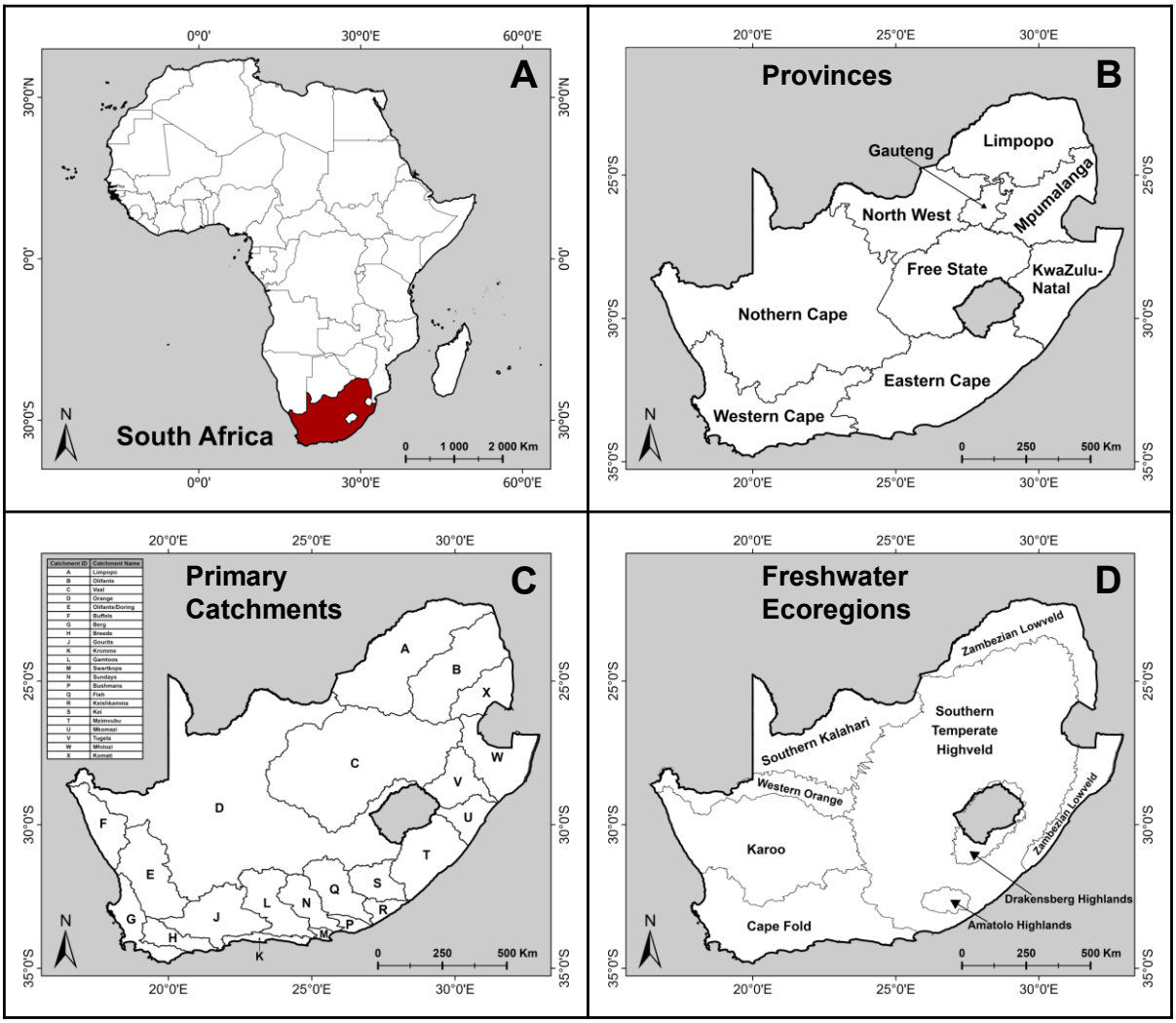


Figure 3. 1. Republic of South Africa (A) showing provincial boundaries (B), primary catchments (C), and freshwater ecoregions (D). Catchment IDs are represented, where: A = Limpopo; B = Olifants; C = Vaal; D = Orange; E = Olifants/Doring; F = Buffels; G = Berg; H= Breede; J = Gourits; K = Kromme; L = Gamtoos; M = Swartkops; N = Sundays; P = Bushmans; Q = Fish; R = Keishkamma; S = Kei; T = Mzimvubu; U = Mkomazi; V = Tugela; W = Mfolozi; and X = Komati.

3.2.2. Data collection and cleaning

Occurrence records for all freshwater fish (all known primary and secondary freshwater fish, as well as for catadromous species) occurring in South Africa were downloaded from the Freshwater Biodiversity Information System (FBIS) on 30 July 2023 (FBIS, 2023) for further analysis.

Preliminary data cleaning was conducted in R Software (R Core Team, 2023; Version 4.2.3) and ArcGIS Pro (Esri Inc, 2022) as follows. First, the data set was clipped to the political boundary of the Republic of South Africa (**Figure 3.1**), ensuring that all records in the ocean were removed from the dataset. Next, a list of native species that have been translocated outside of their native range (**Supplementary Table S3.1**) was

extracted from Ellender & Weyl (2014). For species known to be native but extralimital (Ellender and Weyl, 2014), records occurring outside of the native range of the species – based on IUCN range maps (IUCN, 2018) and expert knowledge – were flagged. These records were not included in the species richness counts for native, threatened, and endemic analyses. The R package, *biogeo* (Robertson et al., 2016; Robertson, 2022) was used to 'autoclean' the dataset prior to final analyses. This was done using the '*quickclean*' function in *biogeo* (Robertson et al., 2016; Robertson, 2022), which performs a check to determine if records are at appropriate spatial resolution, removes records that are deemed to be erroneous, and flags duplicate records per species per grid cell.

3.2.3. Data analysis

All data analyses were conducted using R Software (R Core Team, 2023; Version 4.2.3) and ArcGIS Pro(Esri Inc, 2022). Using the *richnessmap* function from the R package, *biogeo* (Robertson et al., 2016; Robertson, 2022), species richness maps were produced at a quarter degree square (QDS) spatial scale (15' resolution). This was done for all native, non-native, and threatened (listed as Vulnerable, Endangered, or Critically Endangered according to the IUCN Red List of Threatened Species) native species. Species richness was also assessed for species endemic to a single freshwater ecoregion (achieved by combining the Regional endemic level 2, Regional endemic level 1, Micro-endemic level 2, and Micro-endemic level 1 categories in the FBIS (Dallas et al., 2022; Kajee et al., 2023b). Species counts and the number of records for each species were calculated for each province and within each primary catchment, these being considered politically and ecologically useful scales respectively.

A protected area analyses was conducted by overlaying occurrence records and species richness maps at QDS resolution with the protected areas spatial layer downloaded from the South African Protected and Conservation Areas Database on 10 September 2023 (DFFE, 2023a, b). The intersections were then used to calculate number of records and distribution area found within protected and conservation areas for native, non-native, threatened, and endemic species. Additionally, species richness maps at QDS resolution for threatened and non-native species were used to assess spatial overlap between these two species groups. Final maps were produced in ArcGIS Pro (Esri Inc, 2022).

3.3. Results

A total of 57 485 records for freshwater fish were downloaded from the FBIS. After data cleaning, these were reduced to 55 215 records, comprising both native (50 927) and non-native (4 288) fishes occurring in South Africa (**Figure 3. 2.**). The final, cleaned dataset spans 184 years (1839 – 2023) and represent 129 species, of which 105 (81%) were native and 24 (19%) were non-native. A list of species with occurrence records in South African is available in **Table 2.4** and **Supplementary Table S2.4**.

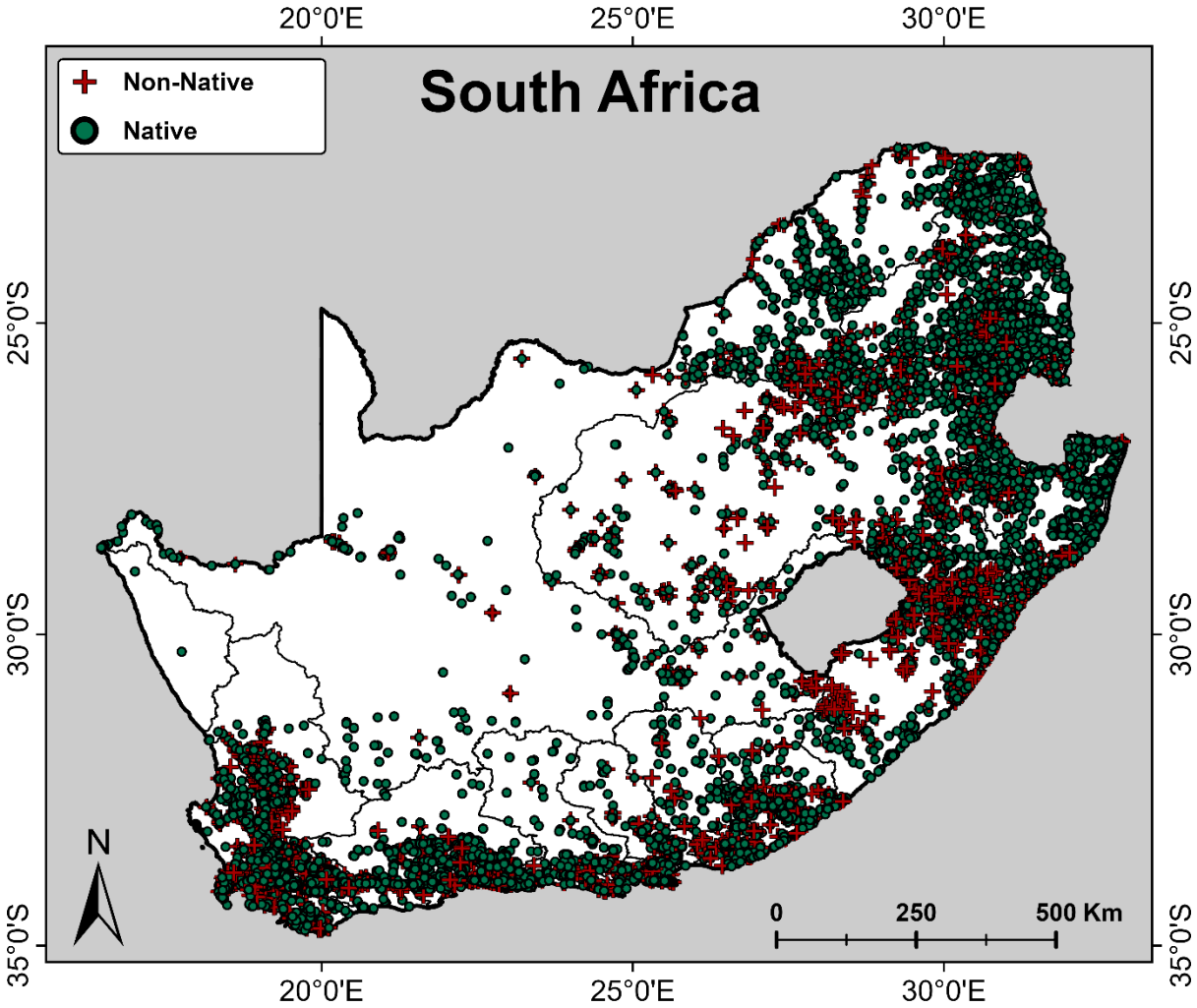


Figure 3. 2. Republic of South Africa showing primary catchment boundaries and the distribution of available, uncleaned freshwater fish occurrence records for native (green circles) and non-native (red crosses) species (n = 57 485 records).

3.3.1. Spatial distribution of records

The density of records per QDS grid cell shows that data were unevenly distributed across the country (**Figure 3. 3.**). At provincial level, fish occurrence records varied substantially between provinces (**Table 3. 1.**). Limpopo (14 353), KwaZulu-Natal (11 411), and Mpumalanga (11 411) each had greater than 10 000 records, whilst Gauteng (907) and Free State (890) both had less than 1 000 records. Similarly, the distribution of records among primary catchments varied widely (**Table 3. 2**). Areas of relatively high density of occurrences (>100 records per QDC grid cell) were in the north-east (Limpopo, Olifants, Komati, Mfolozi, Tugela, and Mkomazi Primary Catchments) and south-west (Olifants/Doring, Berg, Breede, and Gourits Primary Catchments) of South Africa. Conversely, large areas with no records were observed within the central (Orange and Vaal Primary Catchments) and western (Buffels Primary Catchment) parts of the country. On a finer scale, there were noticeable gaps in data in the northern part of the Olifants Doring, Gourits, Mzimvubu, and Limpopo Primary Catchments respectively. The vast majority of grid cells contained low numbers (1–10) of records (represented in violet; **Figure 3. 3.**) or zero records.

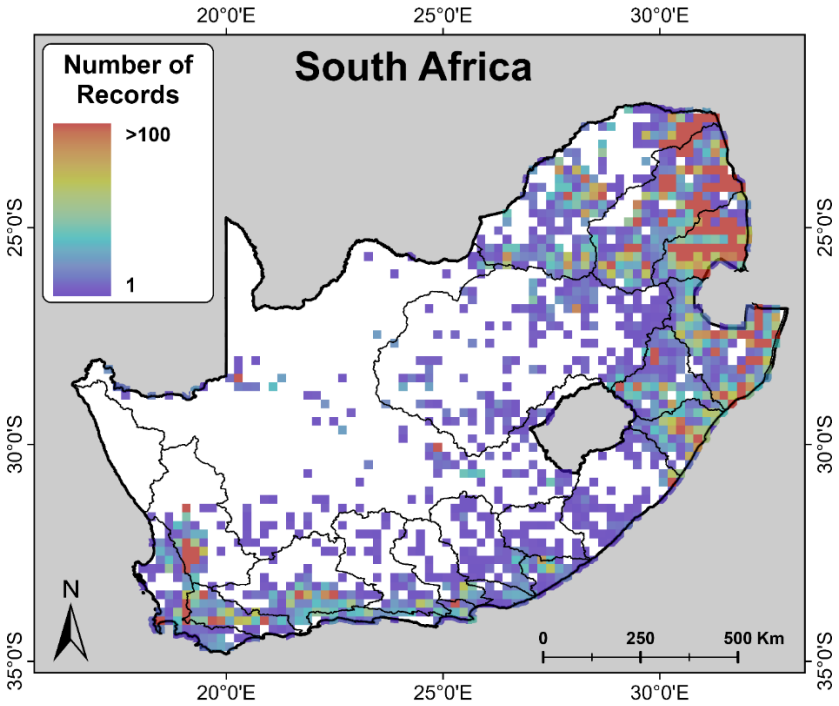


Figure 3. 3. Density of native freshwater fish occurrence records across South Africa per quarter degree square (QDS – 15') grid cell. Primary catchment boundaries are shown.

3.3.2. Species richness

Native species richness per QDS grid cell (**Figure 3. 4.A**) followed a similar pattern to the record density per grid cell (**Figure 3. 3.**) across South Africa. There were noticeable areas of high species richness in Mpumalanga, Limpopo, and northern KwaZulu-Natal (corresponding with the Limpopo, Olifants, Komati, and Mfolozi Primary Catchments). Additionally, species richness was relatively high (10–15 species per QDS grid cell) along the east coast of KwaZulu-Natal (Tugela and Mkomazi Primary Catchments) and in a small cluster in the Western Cape (along the Berg-Olifants/Doring Primary Catchment boundary). As expected, based on recorded occurrence density (**Figure 3. 3.**), species richness was lowest in the Free State, Northern Cape, and North-West Province (Orange, Vaal and Buffels Primary Catchments).

Endemic species richness per QDS grid cell (**Figure 3. 4.B**) was highest in the Western Cape Province (Olfiants/Doring, Berg, and Bree Primary Catchments) and along the south coast of the Eastern Cape (Swartkops, Kromme, and Gamtoos Primary Catchments). There were small clusters of higher endemic species richness in the north-eastern part of the country (Komati, Mfolozi, and Vaal Primary Catchments).

Threatened species were distributed fairly consistently in Limpopo and Mpumalanga (Limpopo, Olifants, and Komati Primary Catchments), along the east coast of KwaZulu-Natal (Mfolozi, Tugela, and Mkomazi Primary Catchments), and south coast of the Eastern Cape (Keishkamma, Bushmans, Swartkops, Fish, Sundays, Gamtoos, Kromme, and Gourits Primary Catchments) (**Figure 3. 4.C**). The Western Cape

(Olifants/Doring, Berg, and Bree Primary Catchments) contained the highest concentration of threatened species, followed by the Komati Primary Catchment in KwaZulu-Natal. There were also notable hotspots within the Kromme and Keishkamma Primary Catchments, as well as within the Mkomazi and Mfolozi Primary Catchments (**Figure 3. 4.C**).

Non-native species richness per QDS grid cell (**Figure 3. 4.D**) was relatively high (4–7 species) along the east coast of KwaZulu-Natal (Mkomazi and Keishkamma Primary Catchments) and highest in the Western Cape (Olifants/Doring, Berg and Bree Primary Catchments). In general, non-native species were present in all provinces and catchments where records were available (**Figure 3. 4.D**). Importantly, 'species richness' hotspots for non-native species indicate grid cells where several non-native species have established successful, self-sustaining (often invasive) populations.

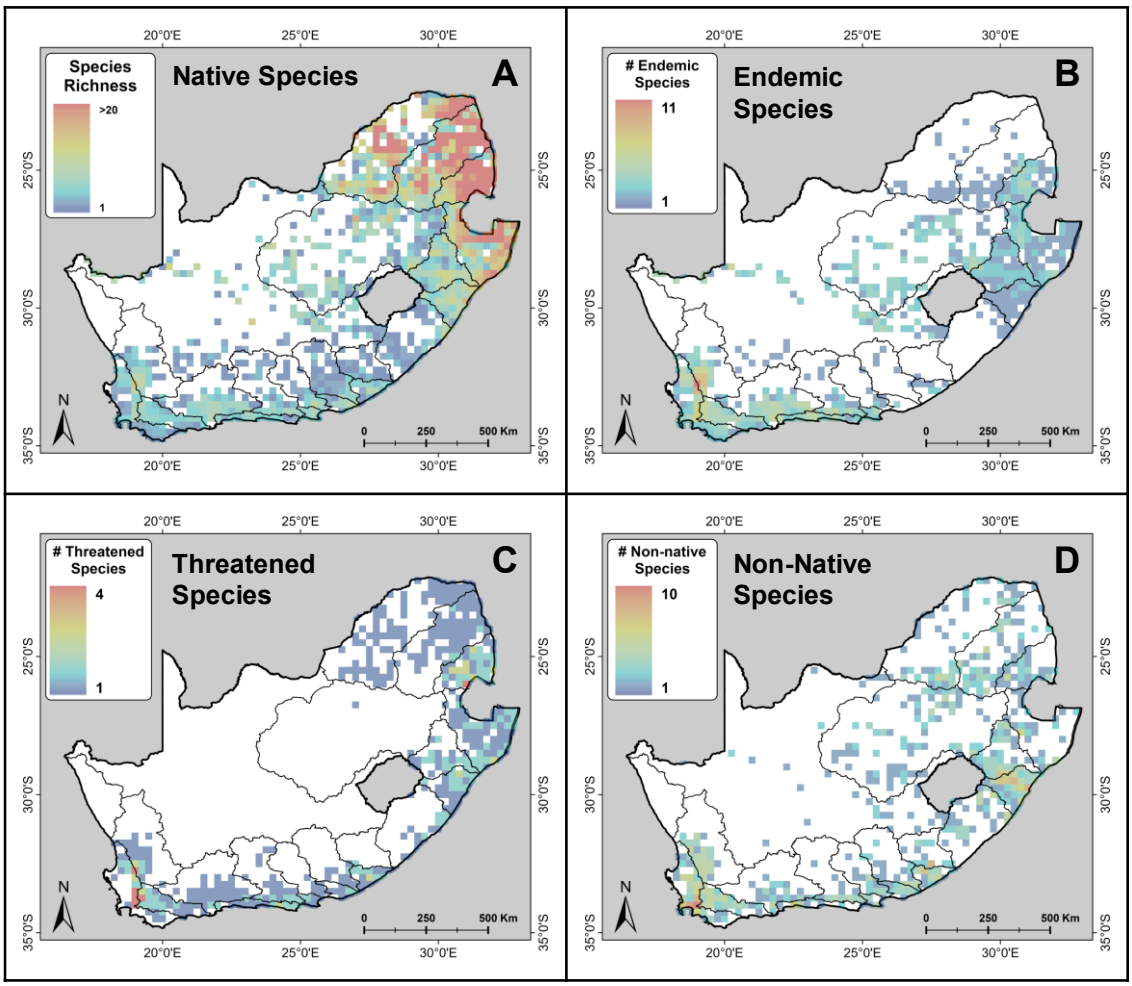


Figure 3. 4. Species richness per quarter degree square (QDS – 15') grid cell for all native (A), endemic* (B), threatened+ (C), and non-native (D) freshwater water fish species occurring in South Africa. Primary catchment boundaries are shown.

* Endemic refers only to includes Regional endemic level 2, Regional endemic level 1, Micro-endemic level 2, and Micro-endemic level 1 species, as defined by Dallas et al. 2022. Nationally endemic species were omitted.

+ Freshwater water fish listed as threatened according to the IUCN Red List of Threatened Species (Vulnerable, Endangered, or Critically Endangered).

Table 3. 1. Number of records and native, extralimital, non-native, endemic, and threatened species occuring in each province of South Africa.

Province	Records	Native Species	Extralimital Species*	Non-Native Species	Endemic Species+	Threatened Species
Eastern Cape	2 725	35	10	14	13	8
Free State	890	19	4	7	8	0
Gauteng	907	38	3	9	5	1
KwaZulu-Natal	11 411	74	8	20	13	8
Limpopo	14 353	61	6	11	7	2
Mpumalanga	11 411	65	7	12	7	6
North West	1 058	37	5	7	6	1
Northern Cape	1 285	39	9	9	13	1
Western Cape	8 159	30	10	16	19	11

* As defined by (Ellender & Weyl, 2014) and occurring outside of their home range.

+ Endemic refers only to includes Regional endemic level 2, Regional endemic level 1, Micro-endemic level 2, and Micro-endemic level 1 species, as defined by Dallas et al. 2022. Nationally endemic species were omitted.

Table 3. 2. Number of records and native, extralimital, non-native, endemic, and threatened species occuring in each Primary Catchment of South Africa.

Catchment ID	Catchment Name	Records	Native Species	Extralimital Species*	Non-Native Species	Endemic Species+	Threatened Species
Region A	Limpopo	8355	60	7	9	7	1
Region B	Olifants	9823	59	7	10	6	4
Region C	Vaal	1240	34	6	10	7	1
Region D	Orange	1100	37	6	8	11	0
Region E	Olifants/Doring	3443	16	7	7	13	6
Region F	Buffels	6	0	3	0	0	0
Region G	Berg	1690	15	8	14	10	4
Region H	Breede	1902	13	5	10	10	3
Region J	Gourits	1269	12	7	7	7	2
Region K	Kromme	488	8	4	9	6	4
Region L	Gamtoos	433	10	4	6	6	2
Region M	Swartkops	309	10	3	6	4	1
Region N	Sundays	342	13	6	4	2	2
Region P	Bushmans	243	14	5	6	3	2
Region Q	Fish	293	11	5	7	2	2
Region R	Keishkamma	444	12	4	11	4	3
Region S	Kei	176	6	5	9	0	1
Region T	Mzimvubu	713	18	5	13	3	3
Region U	Mkomazi	2359	27	4	17	4	3
Region V	Tugela	2089	29	3	11	5	3
Region W	Mfolozi	7017	68	6	12	8	6
Region X	Komati	8471	58	3	12	4	5

* As defined by (Ellender & Weyl, 2014) and occurring outside of their home range.

+ Endemic refers only to includes Regional endemic level 2, Regional endemic level 1, Micro-endemic level 2, and Micro-endemic level 1 species. Nationally endemic species were omitted.

3.3.3. Protected areas

Of the 47 946 records for native fish species analysed, 47% (22 756) occurred outside of protected areas, whilst 53% (25 190) were located inside protected areas (**Figure 3. 5.**). Of these, 28% (6 984) were located within a formally protected area, whereas the remaining 72% (18 206) were located within a conservation area (**Figure 3. 5.**), as defined by the South Africa Protected and Conservation Areas Database (DFFE, 2023a, b). When assessing records for threatened species, a total of 5 740 records were used in the final analyses. Of these, 43% (2 464) were located outside a protected area, and 57% (3 276) within either a formally protected area (32%;1 060) or a conservation area (68%; 2 216) (**Figure 3. 6.A**). Based on the QDS grid cell combined distribution, threatened species covered an area of 328 319 km^2, with only 36% of this range overlapping with South Africa's protected area network (**Figure 3. 6.A**). However, all QDS grid cells that contained more than three threatened species (i.e., the highest density of threatened species) overlapped with a protected area (**Figure 3. 6.C**). Concerningly, 58% of threatened species co-occurred in the same grid cells as non-native species (**Figure 3. 6.D**).

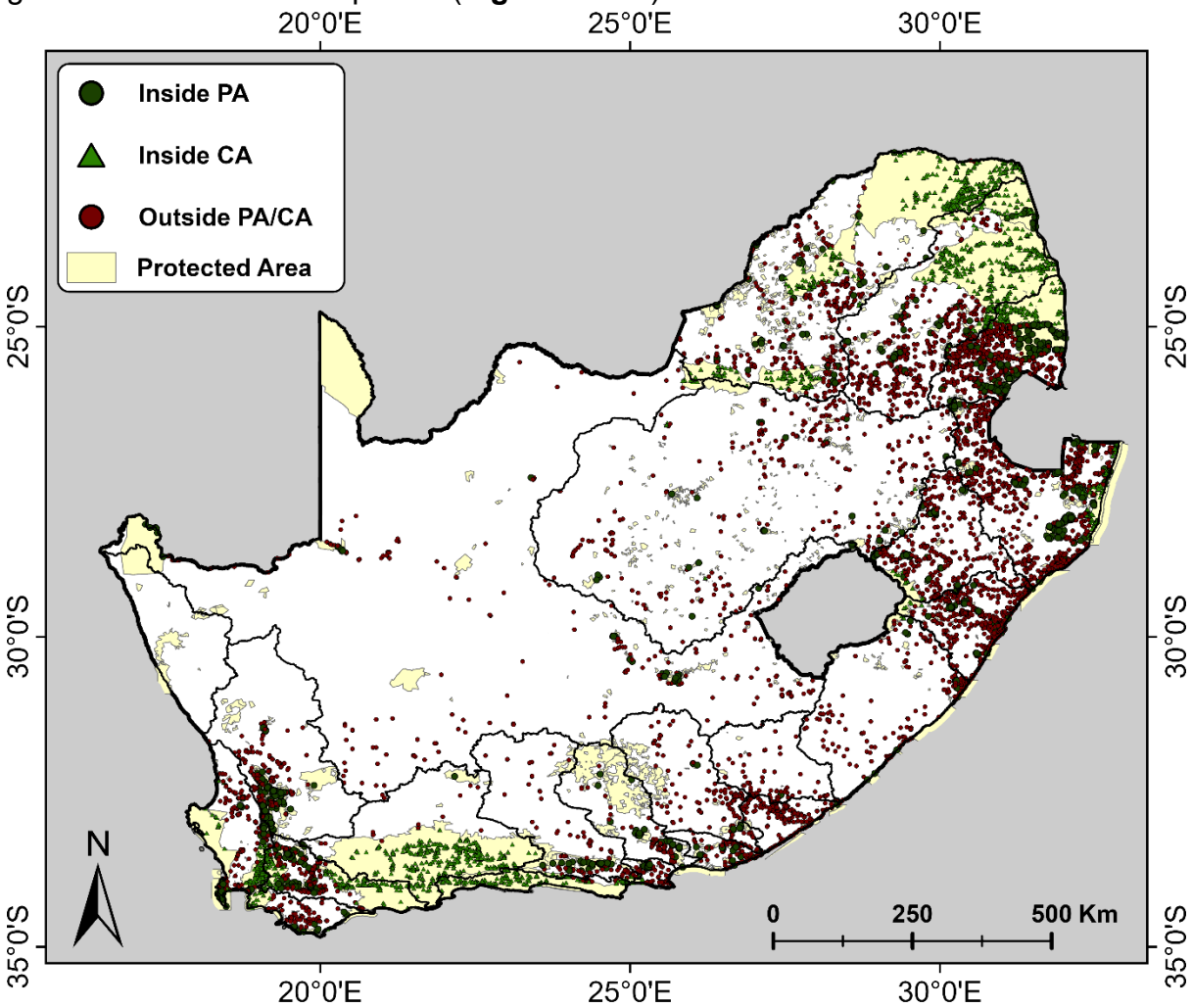


Figure 3. 5. Freshwater fish occurrence records for native freshwater fish occurring withing protected areas (green circles), conservation areas (green triangles), and outside of either protected or conservation areas (red circles) in South Africa. Primary catchment boundaries are shown.

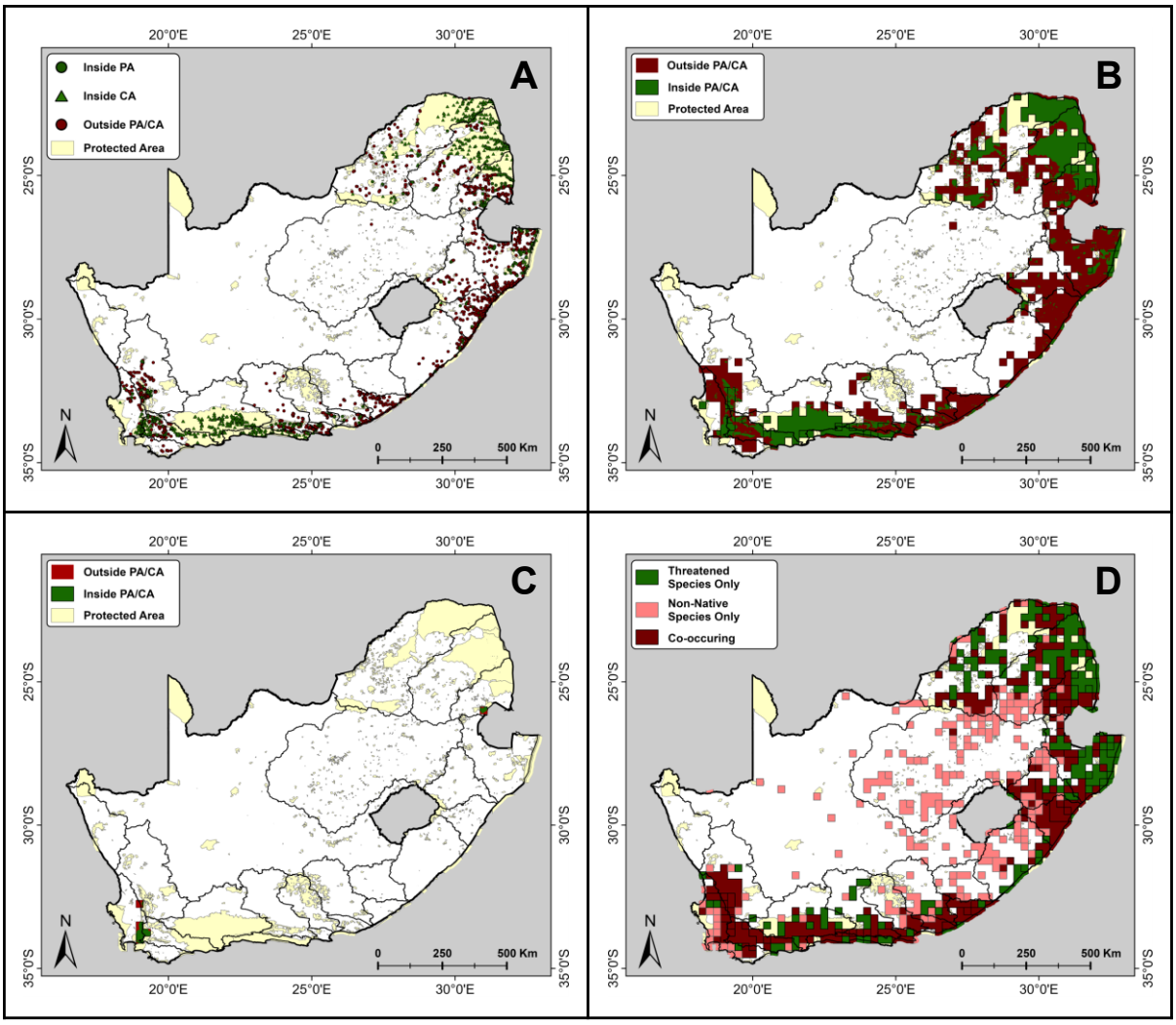


Figure 3. 6. Primary Catchment map of the Republic of South Africa, showing the distribution of threatened freshwater fish (listed as either Vulnerable, Endangered, or Critically Endangered according to the IUCN Red List of Threatened Species) within South Africa's protected areas network. Panel A shows threatened occurrence records within protected areas (green circles), conservation areas (green triangles), and outside of either protected or conservation areas (red circles). Panel B shows QDS grid cell distribution of threatened freshwater fish occurring within protected or conservation areas (green) and outside of protected or conservation areas (red). Panel C shows QDS grid cells that contain the most (n=4) threatened species. Panel D shows QDS grid cell co-distributions for threatened and non-native species, indicating where threatened species do not overlap with non-native species (green), where threatened species overlap with non-native species (red), and where non-native species do not overlap with threatened species (pink).

A total of 4 244 records for non-native species were used in the final analyses. Of these 62% (2 625) were recorded outside a formally protected area, whilst 38% (1 619) were recorded inside either a protected area (53%; 870) or a conservation area (47%; 749) (**Figure 3. 7.**). South Africa's total terrestrial protected area network covers 272 485 km^2, of which 100 815 km^2 (37%) overlaps with non-native species

distributions based on species richness grids generated at quarter degree square (QDS – 15') resolution (**Figure 3. 7.**).

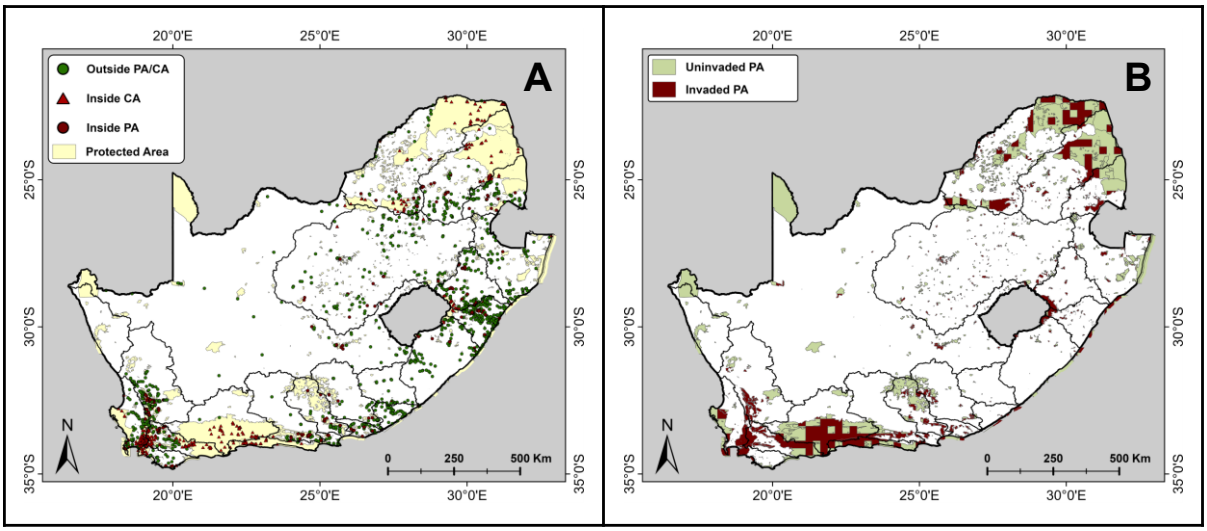


Figure 3. 7. Primary Catchment map of the Republic of South Africa showing (A) records for non-native freshwater fish occurring within protected areas (red circles), conservation areas (red triangles), and outside of either protected or conservation areas (green circles) and (B) QDS grid cell distribution of non-native freshwater fish within protected or conservation areas (red).

3.4. Discussion

The primary aims of this chapter were to assess the spatial patterns of freshwater fish distribution, diversity, threat status, and invasion status in South Africa at national, provincial, and primary catchment scales. Additionally, this chapter sought to assess how well South Africa's protected area network protects threatened species and fish diversity hotspots. This provides a much-needed update on the status of South Africa's freshwater fish fauna, and the first national-level assessment to use actual historic-to-present day occurrence records as the basis for the assessment.

Results showed that record density varied spatially, at both primary catchment and provincial scales. The diversity of freshwater fishes also varied spatially: native fish hotspots were identified in Limpopo, Mpumalanga and KwaZulu-Natal; an endemic species hotspot was identified in the Western Cape and threatened species hotspots were identified in the Western Cape, Mpumalanga, Eastern Cape and KwaZulu-Natal. Non-native species hotspots mirrored threatened species hotspots in the Western Cape, Mpumalanga, Eastern Cape and KwaZulu-Natal. A total of 43% of threatened species records fell outside of protected areas, and 38% of non-native species records fell within protected areas. Lastly, species' summaries (indicating the numbers of native, non-native, extralimital, endemic, and threatened species) at both provincial and primary catchment scales, are presented, along with the first published species lists for the whole country at these scales.

3.4.1. Spatial distribution of records

The spatial distribution of freshwater fish records was uneven across the geographic range of South Africa, indicating that sampling across the country has been biased and concentrated in a few regions. There are several factors that can influence the distribution of these species occurrence data. These include the spatial scale of the original study (Beck et al., 2014; Anderson et al., 2016), how data from individual studies were stored (Beck et al., 2014), accessibility of sites (Hughes et al., 2021), proximity to man-made infrastructure such as roads (Daru et al., 2018; Hughes et al., 2021), cities (Bowler et al., 2022), and research institutions (Daru et al., 2018). Additionally, when dealing with freshwater systems, it is also important to consider the impact of the number and density of perennial rivers within the spatial landscape. In this regard, the spatial distribution of occurrence records in the Northern Cape and North-West Province are likely influenced by relatively low number and density of permanent water bodies characteristic of the Karoo biome. There is also evidence that a higher proportion of occurrence records are generally collected within protected areas, or hotspots of species richness (Hugo and Altwegg, 2017; Jiménez-Valverde et al., 2019). In South Africa, there are noticeable data gaps along the south-east coast and the central western interior, which coincides with a scarcity of formally protected areas (Figures 3.5 and 3.6), which could potentially explain the observed scarcity of data in these areas.

Whilst there have been numerous studies (Ballesteros-Mejia et al., 2013; Yang et al., 2013; Meyer et al., 2016; Daru et al., 2018; Rocha-Ortega et al., 2021; Bowler et al., 2022; Garcia-Rosello et al., 2023) that have sought to identify and quantify inherent bias when using large, publicly available species occurrence datasets, adequately dealing with these biases have proven difficult, and in some cases, impossible (Meyer et al., 2016). One concern with working with large, historic datasets is how these underlying biases influence analyses and ultimately the conclusions drawn. Large species occurrence datasets that are prone to bias can have far-reaching implications for the perception of, and inferences about, macroecological patterns (Yang et al., 2013), which limit the usefulness of these outputs. Another major issue with large historic datasets is that species absences are very rarely reported (Coro et al., 2016). This obviously adds additional uncertainty when interpreting analyses based on these data. For example, a data gap could mean that: i) there is no water body present in the cell ii) a site was not sampled; iii) a site was sampled and did not contain any fish species; or iv) a site was sampled but failed to detect all fish species present. This is especially the case for rare species, i.e., those likely to be represented by only one or two individuals per site (Kanno et al., 2009; Hughes et al., 2021). In this regard, interpretation of results from large, historic datasets should be approached with caution.

Whilst the scope of this study did not include assessing the level of bias and spatial autocorrelation between the distribution of man-made landmarks and the FBIS fish dataset, this is an important next step that should be carried out when conducting future analyses at national, provincial, or catchment scales. Quantifying this will allow for better contextualisation of these results. Additionally, the unevenness in available

freshwater fish data in South Africa speaks to the urgent need for a coordinated national and provincial fish monitoring programme. Unfortunately, however, these sorts of biodiversity data depend on a wealth of scientific, human, and financial resources (Garcia-Rosello et al., 2023), which can be a limiting factor in South Africa's current socio-political and economic landscape. However, given the importance of comprehensive and up-to-date biodiversity data for making informed conservation and management decisions, adequately monitoring river systems across the country should be prioritised.

Additionally, it is important to acknowledge that using a QDS resolution for this assessment provides a useful, but generalised insight into the state of freshwater fishes in South Africa at a national scale. River habitats are linear systems that are not equally distributed across the geographic landscape. As such, Many QDS grid cells are simply not sampled because there are no surface water or drainage regions with regular enough surface water to sustain permanent fish populations. This is obviously valid for a gradient from west to east with many streams draining to the Atlantic (except obviously the Vaal-Orange) not allowing permanent habitat for rheophilic or semi-rheophilic species.

3.4.2. Species richness

The patterns of species richness, endemism, and threatened species are congruent with previously published descriptions of South Africa's freshwater fish diversity. Primary catchments containing the highest freshwater fish species richness in South Africa included: the Limpopo, Olifants, Komati, Mfolozi, Tugela, and Mkomazi Primary Catchments, as well as along the Berg-Olifants/Doring Primary Catchment boundary. Skelton (1995) also identified richness hotspots in the northeastern region of the country, with endemism and threat hotspots in the Western and Eastern Cape (Skelton et al., 1995). Interestingly, Skelton (1995) attributed these hotspots to the relatively high topographical relief characteristic of the Cape Fold Mountains. This hypothesis was supported by more recent work (Chakona et al., 2013; Chakona et al., 2020), which found that South Africa's complex geological and climate history, characterised by tectonism and sea-level fluctuations created unique biogeographic conditions that allowed for diversification of stream-dwelling taxa, particularly obligate freshwater fishes (Chakona et al., 2013). More recently, Chakona et al. (2022) assessed the distribution of freshwater fishes in South Africa, using distribution records from SAIAB's National Fish Collection only (a subset representing ~40% of the raw data included in this study). Whilst they assessed richness at the ecoregion scale, broad patterns in species richness were similar to those presented here. Consequently, it is safe to conclude that the broad patterns of richness identified are an accurate representation of the current state of freshwater fishes in South Africa – despite the concerns regarding the bias contained within the currently available dataset. Similarly, endemic species hotspots were found in the Olifants/Doring, Berg, and Bree Primary Catchments, and, to a lesser degree, the Swartkops, Kromme, Gamtoos, Komati, Mfolozi, and Vaal Primary Catchments. Threatened species hotspots were identified in the Olifants/Doring, Berg, and Bree Primary Catchments, as well as the Mkomazi and Mfolozi catchments, respectively. It is thus recommended that all QDS grid cells

identified as having high levels of species richness, endemism, and threatened species be prioritised for resampling and monitoring to better inform conservation interventions required in these catchments. Focussing effort and resources in this targeted manner could provide the most efficient use of the limited national, provincial, and scientific resources available.

Of particular concern was the large overlap between the distributions of threatened species and of non-native species in South Africa, with the majority (58%) of threatened species co-occurring with non-native species (**Figure** 3. 6.**3.6D**). Non-native species can have profound and devastating impacts on both native threatened species and, more broadly, freshwater habitats as a whole, and are considered a top threat to native freshwater fish in South Africa (Ellender and Weyl, 2014; Marr et al., 2017; Shelton et al., 2018b; Jordaan et al., 2020; Weyl et al., 2020; Chakona et al., 2022). The presence of non-native species has resulted in the widescale extirpation of many native species from their historic distributions (especially in mainstem rivers), with many native species now relegated to the upper reaches of tributaries, surviving in small, fragmented populations above waterfalls or other physical barriers that have prevented invasion by non-native species (Ellender and Weyl, 2014; Van Der Walt et al., 2016; Jordaan et al., 2020).

It is also important to note that this study was limited to formally-described primary and secondary freshwater as well as catadromous fishes based on the GBIF taxonomic backbone and available IUCN Red List assessments. As such, the analyses presented will likely need to be updated in the near future once: i) experts settle on an updated species list for freshwater fishes in the country; ii) all species in South Africa have been had their threat status assessed; and iii) ongoing taxonomic revisions for several species suites are formalised (Chakona and Skelton, 2017; Chakona et al., 2018, 2022; Chakona et al., 2020; Kambikambi et al., 2021; Kajee et al., 2023a).

When compared to other freshwater systems in the world, South Africa's freshwater fish fauna makes up less than 5% of the total diversity of freshwater fishes found in the African continent (Leveque et al., 2008). These findings are congruent with global assessments of freshwater fish species richness, that identified hotspots in South America, Far East Asia, and Central Africa (Granado-Lorencio et al., 2021), with relatively low richness in South Africa. For example, there are at least 100 fish species recorded in the Okavango Delta alone (Cachazo et al., 2023), with central Africa containing more than 1000 species (brooks and Darwall, 2011).

Olden et al. (2008) assembled a present-day species list of native and non-native freshwater fishes in Australia, finding 214 native and 27 non-native freshwater fishes. Of these, seven (3%) were critically endangered, 12 (6%) were endangered and 18 (8%) were vulnerable (Olden et al., 2008). These results contextualise the extent to which South Africa's freshwater fish are disproportionately threatened (**Figure 3.4**) when compared to other regions of the world. Additionally, Olden et al. (2008) found that faunal similarity (fish community heterogeneity) increased over time due to the

introduction of non-native species. While this study did not assess this, it does provide an important recommendation for future research.

Tao et al. (2023) developed a database for 1658 freshwater fish species with occurrence data in China. They found high species richness in the northeastern region and southwestern region, particularly in the middle to lowland areas of large rivers, with species richness higher in large rivers that contained large lakes (Tao et al., 2023). Whilst this study also found a higher richness in the northeastern and southwestern regions of South Africa, there is no plausible connection between these to finding, which a coincidental at best. However, it is interesting to note that native species richness in South African rivers is generally higher in high altitude areas in the upstream/mountain stream region of rivers (Skelton, 2001; Chakona et al., 2013). This difference is, at least in part, due to the fact that South Africa has limited large river systems and is completely devoid of natural lake systems (Griffiths et al., 2015). Additionally, much of the middle and lowland areas of South Africa's river systems are invaded by non-native species and face extreme pressures from anthropogenic activities. This has meant that many native species have been extirpated from their historic distribution ranges.

3.4.3. Protected areas

It was found that South Africa's protected area network (Department of Forestry Fisheries and the Environment, 2023a, b) does not adequately cover the distributions of threatened species in the country. In terms of numbers of records, 57% of records were located within a protected or conservation area, representing a strong bias towards sampling in those areas, which account for only ~20% of South Africa's total land surface area (**Figure 3. 6.**). More concerningly, only 36% of the total area occupied by threatened species occurs within a protected or conservation area (**Figure 3. 6.**). On the one hand, this indicates that the majority of threatened species are not under formal protection and at heightened risk of extinction. Conversely however, this level of protection is relatively high, when compared to the percentage of terrestrial land area under protection globally (Nel et al., 2009; Acreman et al., 2019). Furthermore, 37% of the country's formal protected area network is invaded by non-native species, with a high percentage overlap between threatened and non-native species (**Figure 3. 7.**). As such, threatened freshwater fish in South Africa still face direct threats from non-native species, even though it may appear that they are well-considered in the protected area network. Thus, these findings add further evidence to the growing body of research that considers South Africa's protected area network to provide inadequate protection for sensitive freshwater species. Kleynhans (2000), Nel et al. (2004), Abell et al. (2007), and Nel at al. (2009) all concluded that South Africa's protected areas did not adequately conserve freshwater ecosystems, with the majority of rivers falling outside the protected area network. Of the rivers located in South Africa, 70% are classified as either Not Protected or Poorly Protected (Department of Environmental Affairs, 2016). Furthermore, of the river systems that are protected, almost half of these have already been degraded by human activities upstream of the protected area (Kleynhans, 2000; Nel et al., 2009).

For example, a comprehensive assessment of the 19 National Parks managed by SANParks found that the National Parks protected network only included small components of protected river area that form part of much larger, degraded aquatic systems further up and downstream of the parks (Russell, 2011). Consequently, very few sites within National Parks contained freshwater fishes that were not under direct threat from land-use change, habitat loss, and non-native species invasions (Russell, 2011). Similarly, an analysis of the National Parks and nature reserves within the Cape Floral Kingdom (roughly the same geographic range as the Western Cape Province and the Olifants/Doring, Berg, Breede, and Gourits Primary Catchments) found that, whilst protected areas did contain populations of most native fish, actual protection was impaired due to species ranges extending beyond the boundaries of protection or were protected in rivers with substantial invasion by non-native species (Impson et al., 2002; Abell et al., 2007). More recently, (Jordaan et al., 2020) also found that protected areas in the Cape Fold Ecoregion did not adequately protect native freshwater fish, with 84% of taxa regarded as under-protected (Jordaan et al., 2020).

However, there has been some improvement to the level of protection afforded to South Africa's threatened fish populations. Firstly, the NFEPA project developed a series of strategic spatial maps, prioritising the conservation of the country's freshwater ecosystems (Nel, 2011). Importantly, the NFEPA provides for Fish Sanctuaries and associated Fish Support Areas, which includes rivers that are essential for protecting threatened and near threatened freshwater fish native to South Africa (Nel, 2011). Furthermore, the NFEPA also highlighted important Upstream Management Areas, which flag sub-quaternary catchments where human activities need to be carefully managed to prevent degradation of downstream river Fish Sanctuaries and Fish Support Areas (Nel, 2011). More recently, Kajee et al. (2023a) reported on the first inclusion of freshwater fishes into the DFFE National Environmental Screening Tool (Department of Forestry Fisheries and the Environment, 2021). This process provided an additional layer of protection for South Africa's threatened species, along roughly 50 000 km of river habitat (Kajee, et al., 2023a). However, it is also important to acknowledge that South Africa's freshwater fish fauna has the potential to serve as a vital food and income source for rural communities that face extreme levels of poverty and food insecurity (Hara et al., 2021). Subsistence fishing activities, in response to modern socio-economic circumstances, were recorded at 77% of dams in South Africa, with recent studies indicating that more than 1.5 million people are involved in freshwater angling activities, in an industry worth approximately R9 billion annually (Britz et al., 2015; Hara et al., 2021). Consequently, there is a need to reimagining the country's protected area network to better safeguard freshwater fish – and freshwater habitats in general, whilst also accounting for the socio-economic needs of rural communities in South Africa. In this light, there is a need to reimagine the country's protected area network to better safeguard freshwater fish – and freshwater habitats in general.

3.4.4. Limitations

Whilst these results will no doubt be useful for researchers, catchment and provincial conservation managers, and policymakers, it is acknowledged that there are limitations to the study. Given that the basis of this assessment is occurrence records

sourced from an open-access biodiversity database (Dallas et al., 2022; FBIS, 2023), analyses at national (and even sub-national) scales are quite complicated, due largely to the lack of consistency in the types of metadata available for each record. This made detailed spatio-temporal analysis of fish distribution patterns across South Africa quite difficult. Additionally, working with a large dataset (in our case, more than 50 000 records) can make cleaning raw data unsustainably time-consuming. This study chose to follow the methods of Robertson et al. (2016), and used the *biogeo* R package to 'autoclean' data prior to analysis. Whilst this approach seems to have worked well when assessing species richness patterns across the country, further scrutiny of species lists at provincial and catchment levels revealed some inaccuracies.

For example, when reviewing the final species lists for the Olifants/Doring Primary Catchment there were inaccuracies in the final number of native, endemic, and threatened species reported in the catchment. Most notably, the data indicated that there were 16 native species occurring in the catchment. However, a literature search along with expert consultations revealed 11 such species in this catchment. Further scrutiny revealed that five species (*Labeo rosae*, *Pseudobarbus burchelli*, *Pseudobarbus burgi*, *Pseudobarbus capensis/Cheilobarbus capensis*, and *Sandelia capensis*) had occurrence records in the catchment, when in fact none of these species are known to occur in the area. These records (n <10) are likely a result of misidentifications or inaccurate GPS coordinates. Regardless, their existence undermines the potential benefits of using large, historic datasets to assess species diversity at large spatial extents. Accurate cleaning of the dataset prior to analysis was beyond the scope of this study, but should be a priority for future-such analyses. This would need to be expert-driven and would require substantial time and resources. It is suggested that such a project be planned and coordinated by a national body, such as the SANBI or the SAIAB. As such, this study chose to include these occurrences in the assessment, but to flag them in the final species list reports (see Supplementary **Tables S 3.2 and S3.3**). Additionally, this study focussed only on the spatial patterns of freshwater fishes without conducting a detailed temporal analysis of the data, which fell outside of the scope of the study. It is important acknowledge that these data could, and likely are, influenced by inter-specific temporal variation in the data. Consequently, this study, and the published species list, should act only as a first step towards understanding species richness at national, provincial, and catchment scales. A logical next step would be to repeat this study, after having spent time to thoroughly clean the dataset (as was done for threatened fish taxa only by Kajee et al. (2023a)) and conducting a comprehensive temporal analysis of the data.

3.4.5. Conclusions

This study presents the first assessment of the status of freshwater fish in South Africa using all available data sources from the FBIS. While acknowledging the shortcomings of working with a large, historic dataset the patterns emerging from this assessment identify key fish richness, endemism, and threat hotspots. This provides a much-needed snapshot of the most important geographic areas for freshwater fishes, which could have significant impacts on scientific, conservation, and management priorities in South Africa. Also presented is the first, national-scale assessment of the

effectiveness (in terms of geographic coverage and invasion status) of South Africa's protected area network in protecting threatened freshwater fishes. It is concluded that the current protected area network is not sufficient to functionally conserve threatened species and prevent future population or species extinctions, given that the majority of the distributions of these species are either outside of the protected area network, invaded by non-native species, or do not have adequate upstream protection. Future interventions should prioritise systematically sampling river systems to fill in identified data gaps, developing strategic long-term monitoring programmes in key hotspot catchments (Limpopo, Olifants, Komati, Mfolozi, Mkomazi, Olifants/Doring, Berg, Bree, Swartkops, Kromme, Gamtoos, Keishkamma, Bushmans, Fish, and Sundays catchments), comprehensive cleaning of available data to produce accurate distribution maps for all species, and reimagining protected areas to better conserve freshwater fishes.

CHAPTER 4

4. A stepwise and statistically robust methodology for developing species distribution models for freshwater taxa in South Africa

4.1. Introduction

Species distribution models (SDMs), also commonly referred to as ecological niche models, or habitat suitability models, are a suite of statistical models that relate species distribution or occurrence data at known locations to environmental or spatial information in order to predict species spatial distributions across a landscape (Elith and Leathwick, 2009; Hao et al., 2020; Valavi et al., 2021). Increasingly, SDMs are becoming an important tool in ecology, biogeography, conservation, and spatial planning, with numerous studies using SDMs for identifying critical habitats (Rufener et al., 2017), managing threatened species reintroductions (Hendricks et al., 2016; Miranda et al., 2019), designing protected areas (Roos et al., 2015; Kajee et al., 2023a), managing invasive species (Barbet-Massin et al., 2018; Srivastava et al., 2019), and predicting species range shifts in response to climate change (Brown et al., 2016; Booth, 2018; Brun et al., 2020; Santini et al., 2021). As such, SDMs can serve as important tools for ecologists, conservation managers and policymakers, in light of the urgent need to sustainably manage natural resources and slow-down species extinctions.

Despite their proven effectiveness and increasingly available scientific literature, until recently, the majority of SDM studies were applied to terrestrial and marine species, with fewer focusing on freshwater organisms (Parreira et al., 2019). Indeed, the application of SDMs in freshwater systems to inform policy and conservation decisions remains in its infancy relative to terrestrial and marine systems (Liang et al., 2013; Taylor et al., 2020). However, there has been substantial progress made to model freshwater species' distributions in recent years. For example, da Silva et al. (2023a) modelled the current and future distributions of six mussel species occurring in the Iberian Peninsula. Similarly, da Silva et al. (2023b) used JSDMs to model the co-occurrence of freshwater fishes and mussels, while Nogueira et al. (2023) used these models to identify freshwater priority areas for cross-taxa interactions. These studies, among others, are indicative of the increasing application of SDMs in freshwater environments for various purposes.

In South Africa, very few studies have attempted to apply SDMs to freshwater fishes. Studies of fish distributions have generally been limited to documenting existing species ranges, based on occurrence data and systematics, or have focussed primarily on linking fish habitat preference to micro-habitat environmental conditions, such as flow and temperature (Dallas et al., 2019). However, in recent years, a handful of studies have attempted to use SDMs to predict the distribution of freshwater fishes in South Africa (Lübcker et al., 2014; Dallas et al., 2019; Khosa et al., 2019; Rivers-Moore et al., 2019; Maimela et al., 2022). Despite these initial modelling studies returning promising results, information on how to go about applying SDMs to freshwater fishes in South African river systems remains limited.

Considering the paucity of published literature and available information on how to generate SDMs for freshwater taxa (specifically fishes) in South Africa, there is an urgent need to develop a robust and repeatable method for conducting SDMs in freshwater systems in South Africa (Chakona et al., 2022). Aquatic habitats are listed as the county's most threatened ecosystem types (Skowno et al., 2019), with freshwater fishes assessed to be South Africa's most threatened species group (Skowno et al., 2019). Consequently, being able to accurately map and model the distributions of South Africa's threatened freshwater fishes is of utmost importance and can aid in population monitoring, conservation efforts, and policy making (Chakona et al., 2022; Kajee et al., 2023a).

This chapter aims to develop a stepwise and statistically robust methodology for applying SDMs for freshwater taxa (specifically fishes) in South Africa to determine the current predicted distribution of these species. Additionally, all occurrence, climatic and hydrological data, along with a repeatable R workflow and code, will be made publicly available. This will ensure that the modelling methods presented here can be improved upon in the future and are repeatable and freely available to other researchers, conservation practitioners and policy makers. In setting out to present a modelling workflow for freshwater taxa in South Africa, this chapter also seeks to address the following core questions: i) Can SDMs be practically and reliably applied to a wide range of freshwater fishes occurring in South Africa; and ii) What impact, if any, do the presence of non-native species have on the predicted distribution of native freshwater fishes in South Africa? Based on the findings of Araújo and Luoto (2007) and Meier et al. (2010), it is hypothesized that the inclusion of non-native species distributions as an 'environmental' predictor will improve model performance and the accuracy of predicted distributions of native freshwater fishes.

4.2. Methods

Following the standard procedure proposed by Zurrell et al. (2020), methods for this chapter are presented using the ODMAP protocol (https://odmap.wsl.ch/). The ODMAP protocol follows five basic modelling steps of SDMs: Overview/Conceptualisation, Data, Model Fitting, Assessment, and Prediction (ODMAP) (Zurell et al., 2020). Full details of the ODMAP checklist can be found in **Supplementary Table S4.1**.

4.2.1. Overview

Modelling Objective

The primary objective of the model in this study is species interpolation: the estimated species-predictor relationships are used to map the species distribution within the same geographic area and time period in which the model was built (Zurell et al., 2020). In this specific case, model outputs will be used to map the predicted distribution of each focal taxon. To a lesser extent, the model outputs will also be used to gain insight into the predictor variables that contribute most to a species' current distribution.

Focal taxa

A wide variety of freshwater fish species were modelled, ranging from non-native invasives, to widespread translocated natives and range-restricted threatened species, to test model usefulness and accuracy across a range of species. For non-native species, the black basses were selected as candidate model species, owing to the availability of large numbers of records for these species and the availability of previous models as a point of comparison. A brief description of each species is provided below.

Black bass

Black bass is the collective term used to describe taxa belonging to the genus *Micropterus* (Khosa et al., 2019). Whilst these fishes are native to North America (Taylor et al., 2019), they have been introduced to South Africa to develop sport fisheries (Marr et al., 2017; Khosa et al., 2019). Four black bass species are known to occur in South Africa, namely: largemouth bass (*Micropterus salmoides* now *Micropterus nigricans*), Florida bass (*M. floridanus* now *M. salmoides*), smallmouth bass (*M. dolomieu),* and spotted bass (*M. punctulatus*) (Khosa et al., 2019; Kajee et al., 2023b). Khosa et al. (2019) modelled the distributions of largemouth, smallmouth and spotted bass using MaxEnt. As such, environmental variable selection was informed by Khosa et al. (2019), along with a suite of additional variables. *M. floridanus/ M. salmoides* was not modelled, since there were too few records for the species in the country.

For native taxa, two species (*Clarias gariepinus* and *Pseudobarbus burgi*) were selected for modelling. A brief description of each being provided below.

Clarias gariepinus

The African sharptooth catfish, *Clarias gariepinus*, is widespread throughout much of southern Africa (Skelton 2001). Its native range in South Africa restricted to the north east of the country (Orange River system), but in recent years, it has been translocated beyond its native range and is now considered invasive where it has established outside of its native range (Weyl et al., 2016; Khosa et al., 2023; Mpopetsi and Kadye, 2023; Nelufule et al., 2023; Truter et al., 2023). Sharptooth catfish can grow to a length of 1.4 m and weigh up to 60 kg (Skelton, 2001; Weyl et al., 2016). The species tolerates a wide range of environmental conditions and was selected as a candidate model species owing to its wide distribution range and potential invasive potential into novel habitats currently containing threatened native fish populations.

Pseudobarbus burgi

The Berg River redfin, *Pseudobarbus burgi*, is a small cyprinid fish endemic to the Berg River and its tributaries in the Western Cape, South Africa. The species grows to a maximum size of 120 mm and can be found in a wide range of habitats, from deep, vegetated pools in lowland rivers to clear mountain streams (Skelton, 2001). It is listed as Critically Endangered (IUCN Red List, 2020), and is now extinct across much of its former range, mainly as a result of habitat degradation and impacts of non-native

invasive species such as Rainbow Trout (*Oncorhynchus mykiss*) (Woodford and Impson, 2004), black bass (Bloomer and Impson, 2000) and Bluegill Sunfish (*Lepomis macrochirus).* Predation by the introduced African sharptooth catfish could be an additional threat to the species (Darwall et al., 2009). *P. burgi* was selected as a candidate model species because of its critically endangered conservation status, its relatively small distribution range, and because of the co-occurring impact of several invasive species. Given the severe impact of invasive species on *P. burgi*, two sets of models were run for this species: i) an SDM containing only environmental and hydrological variables; and ii) an SDM containing environmental and hydrological variables as well as biological (invasive species distributions) variables.

Location

The modelling process, predictor variables, and model outputs were restricted to the political boundaries of the Republic of South Africa (**Figure 4.1**) with the following spatial extent: Latitude: 22.13°S, 34.83°S; Longitude: 16.45°E, 32.94°E.

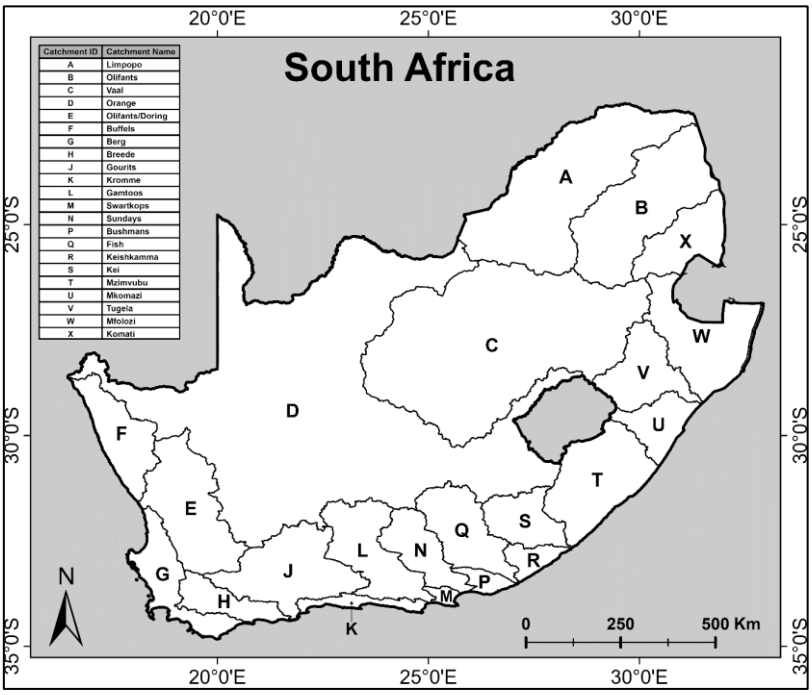


Figure 4. 1. Republic of South Africa showing primary catchment boundaries.

Spatial and temporal scale

In cases where modelled species were widespread across South Africa (black bass and African sharptooth catfish), models were trained and run across the entire country. However, where modelled species occurred in a narrower distribution range (Berg River redfin), the model was trained and run only in the primary catchments (Nel et al., 2011) occupied by the species. Most SDM algorithms require that data all be of the same spatial resolution and that they are geographically congruent (Dallas et al., 2019). All data were thus converted to a resolution of 30 arc-seconds (0.93 X 0.93 km) and saved as GEOTIFF rasters with identical extents and coordinate referencing systems. Models were applied to occurrence data and environmental variables that ranged over time from 1900–2023.

Biodiversity data overview

Historic presence-only data (sourced from peer-reviewed scientific articles, museum records, scientific reports and theses, national and provincial conservation authorities, and privately held expert datasets) were downloaded from the Freshwater Biodiversity Information System (FBIS) database on 30 July 2023 (FBIS, 2023).

Predictor type

Environmental predictors

Atmospheric variables are commonly used as proxies in studies modelling freshwater fishes in situations where there is a lack of accurate and easily-available physicochemical and environmental data for river systems (Iguchi et al., 2004; Lübcker et al., 2014; Khosa et al., 2019). For this study, a comprehensive suite of environmental predictors was included in the modelling process, including climatic variables from the WorldClim database, environmental, landcover, soil, topography, vegetation, fragmentation, and wetland layers. All layers were converted to 30 arc-second resolution and standardised. See **Supplementary Table S4.2** for full list of environmental predictor variables included.

Hydrological predictors

Several studies (Crookes et al., 2020; Dallas et al., 2019; Khosa et al., 2019; McGarvey et al., 2018; Rivers-Moore et al., 2020; Rivers-Moore et al., 2019) have noted the limited availability of accurate environmental data on water quality and hydrological regime for application in SDMs. Despite the increasing availability of fine-scale hydrological data, the majority of SMDs in freshwater systems still use raster data summarised at a coarse, watershed scale (Cao et al., 2013; Liang et al., 2013; Taylor et al., 2020). In many instances, studies that apply SDMs to freshwater habitats used atmospheric variables as proxies for water quality and hydrological variables (Dallas et al., 2017; Khosa et al., 2019; Maimela et al., 2022; Parreira et al., 2019; Valencia-Rodríguez et al., 2021). However, emerging research indicates that these atmospheric and climatic variables are not always accurate or useful proxies to explain river conditions (Parreira et al., 2019; Valencia-Rodríguez et al., 2021). As such, this study sought to calculate specific metrics to describe the hydrological conditions of streams at quinary catchment (Nel et al., 2011) level.

Hydrological metrics for the whole of South Africa were produced in R Studio (R Core Team, 2023) using the *EflowStats* (Thompson et al., 2013) package. *EflowStats* calculates biologically relevant hydrological indicator statistics using daily streamflow data (Thompson et al., 2013). Daily flow data are not available for most river systems in South Africa (Hughes et al., 2014; Rivers-Moore et al., 2020), owing to limited infrastructure in rivers across the region. As such, simulated daily flow data for each quinary catchment in South Africa were sourced from the ACRU model (Schulze, 1995) for the period 1950-1999. The daily flow data (available in mm/day) were then converted to m^3/second using the following calculation, based on Thompson et al. (2013).

$$\frac{[(flow\ value\ in\ mm/day) \times 1000\ \times cumulative\ drainage\ area]}{86400}$$

Converted daily flow data (in m^3/day) for each quinary catchment were then used to calculate 148 biologically-relevant hydrological indicator statistics. These were then converted into raster files (.tif) and included in the final modelling process. See **Supplementary S4.3** for detailed methodology and full R code and workflow. For a full list of hydrological predictor variables, see **Supplementary Table S4.4**.

Biological predictors

Biological predictor variables were developed by applying the SDM workflow presented here to all species listed as invasive in South Africa, as per Ellender & Weyl (2014) and Weyl et al. (2020). The model outputs were converted into raster files (.tif) and included in the final modelling process. See **Supplementary Table S4.5** for full list of available biological predictor variables.

Model hypotheses

Black bass

This study used a suite of statistically selected (see Model Workflow section below) climate, environment, topography and hydrology variables to model the distributions of largemouth bass (*Micropterus salmoides/ Micropterus nigricans*), smallmouth bass (*M. dolomieu*), spotted bass (*M. punctulatus*) in South Africa in an exploratory way.

Clarias gariepinus

This study used a suite of statistically selected (see Model Workflow section below) climate, environment, topography and hydrology variables to model the distribution of *C. gariepinus* in an exploratory way.

Pseudobarbus burgi

This study used a suite of statistically selected (see Model Workflow section below) climate, environment, topography and hydrology variables to model the distribution of *P. burgi* in an exploratory way. In addition, a combination of these variables along with biological variables (the modelled distributions of invasive species) was also used to determine if the inclusion of biological variables could improve the predicted distribution of *P. burgi.* In this case, it was hypothesized that the distribution of *P. burgi* would be correlated with the distribution of black bass species, *C. gariepinus*, and *P. burgi* and thus serve as an accurate way to predict the distribution of non-native invasive species across the whole of South Africa.

Underlying assumptions

Black bass

Given the relatively large occurrence dataset spanning several decades for *Micropterus* spp. in South Africa, it was assumed that the sampling was adequate and representative for these taxa. It was also assumed that the relevant ecological predictors (based on proxy environmental variables) of species distributions were

included in the modelling workflow and that species detectability did not change across the modelling landscape. Lastly, it was assumed that species are at pseudo-equilibrium with the environment and that each 'surveyed' grid square in which a species was not recorded is representative of an absence.

Clarias gariepinus
Given that this is an easily recognisable, well-studied species, it was assumed that the current sampling was both adequate and representative of the known distribution of this species. Where the species had invaded into novel habitats that are yet to be studied, it was assumed that available records represent enough of the true niche signal that the estimated niche is informative about the distributional potential of the species. Further, it was assumed that all relevant ecological drivers (or proxies) impacting species' distribution were included, species are at pseudo-equilibrium with their environment, and detectability does not change across habitat gradients.

Pseudobarbus burgi
Given that this species is Critically Endangered and has been well-studied, and its current distribution is well-known, it was assumed that sampling was adequate and representative. Additionally, it was assumed that all relevant ecological drivers (or proxies) impacting species' distribution were included, species are at pseudo-equilibrium with their environment, and detectability does not change across habitat gradients.

SDM algorithms

Algorithms
SDMs for all species were fitted using Bayesian additive regression trees (BART) in the R package *embarcardero* (Carlson, 2020). BART is a machine-learning model that models the relationship between species occurrences and environmental variables. The model is trained to learn patterns in the data and predict species occurrence based on environmental conditions (Carlson, 2020). BART was selected as the preferred modelling algorithm because it allows for more automated predictor variable selection that is useful for identifying subsets of informative predictors (Tytar et al., 2021), thus providing a statistically robust method for variable selection, making the modelling workflow transparent, repeatable, efficient for modelling large numbers of species. In recent years, BART models have become more common because the process allows for the quantification of uncertainty around predictions and the estimation of marginal effects of individual predictor variables using partial dependency plots and predictor response curves (Carlson, 2020; Pinto-Ledezma and Cavender-Bares, 2021). As a result, BART models have been applied in a number of scenarios, including to model: macroecological patterns (Pinto-Ledezma and Cavender-Bares, 2021), Minke whale distributions (Tytar, 2023), invasive locust (Tytar et al., 2022), vertebrates (Baquero et al., 2021; Cowan et al., 2021), and aquatic crabs (Costa et al., 2023). In recent years, BART models have proven to perform better than MaxEnt and other available modelling algorithms (Baquero et al., 2021; Tytar, 2023)

Model workflow

Occurrence data

Presence-only data were downloaded from the Freshwater Biodiversity Information System (FBIS) database on 30 July 2023 (FBIS, 2023), cleaned and standardised in R (R Core Team, 2023). Duplicate records and records with low accuracy were removed. To minimise the effect of spatial sampling bias, distance-based filtering of occurrence records is often applied to species data prior to modelling (Taylor et al., 2020). Using the *thin* function from the *spThin* package in R (Aiello-Lammens et al., 2015), a spatial thinning protocol was applied (thinning parameter = 0.8 km). This was repeated three times, with the remaining data being included in the final model workflow.

For *P. burgi,* records used in the analysis were restricted to those falling within the known distribution of the species based on the IUCN range map. All additional records were treated as erroneous and deleted. Background point selection and the final model was restricted to primary catchment boundary.

Background points

Background points were sampled from either the entire country (black bass and sharptooth catfish) or from within the boundary of the primary catchment (*P. burgi*). For all species, a total of 10 000 background points (pseudo-absence) were generated from within the modelling landscape.

Environmental and biological variables

All environmental and biological variables were standardised in R using the *stack* function from the *Raster* package in R (Hijmans, 2023), to ensure alignment and consistency. A Pearson correlation test was run to assess collinearity among environmental variables. Using the *vifcor* function in the *usdm* package (Naimi, 2023), the variance inflation factor (VIF) was calculated for the selected variables, excluding highly correlated variables. *vifcor* first finds a pair of variables which has the maximum linear correlation (greater than the threshold; *th*) and excludes the one with a greater VIF (Naimi, 2023). The procedure was repeated until no pair of variables with a high correlation coefficient (greater than the threshold) remained. A threshold value of 0.6 was used for all models. When including biological variables (invasive species modelled distributions), these were included based on available literature, regardless of collinearity with other environmental variables.

Model fitting

Using the *bart* function in the *embarcardero* package in R (Carlson, 2020), an initial model was fitted for each species using 50 iterations. Next, the *varimp.diag* function was used to evaluate which environmental and biological variables have the strongest influence on the species' occurrence patterns. This was followed by repeating the model fitting process using the *variable.step* function, which applies a stepwise variable selection procedure to identify the most important environmental and biological variables that contribute significantly to predicting species occurrence. The

variable.step function employs a stepwise selection algorithm, which iteratively adds or removes variables, based on their importance to model performance. This protocol was followed to select the model with the most informative predictors and the lowest average model root mean square error (RMSE). Finally, a new BART model was fitted using only the most important variables identified in the stepwise selection process. This final BART model was fitted using 200 iterations.

This iterative approach to variable selection, model fitting, and model refinement integrates the insights from the variable selection process, concentrating on the variables deemed most influential for predicting species occurrence. This potentially improves model performance and interpretability. By incorporating variable selection techniques, a more efficient and informative model for understanding species-environment relationships is created (Carlson, 2020).

Model evaluation

Model performance was assessed based on the threshold-independent Receiver Operational Characteristic (ROC), where the Area Under the Curve (AUC) is used to assess predictive performance (Carlson, 2020). AUC values between 0.5–0.7 are an indication of poor prediction, whereas AUC values >0.8 is considered excellent (Hosmer and Lemeshow, 2000). The True Skill Statistics (TSS), which evaluates false positives (type I error) and false negatives (type II error) was also used to assess model accuracy (Carlson, 2020). TSS accounts for the model's specificity (the proportion of absences accurately predicted) and sensitivity (the proportion of presences accurately predicted). Values for TSS range from -1 to +1 where values >0 indicate performance better than random and values >0.7 are considered excellent (Allouche et al., 2006). To determine predicted species distribution, the probability of species presence under the BART model were converted to binary predictions using the recommended threshold value that maximizes true skill statistic (Carlson, 2020).

Software and data availability

Software

Analyses were conducted in R version 4.2.3 (R Core Team, 2023). All codes are provided in the **Supplementary S4.6**.

Data availability

The raw data presented in this study are openly available on the Freshwater Biodiversity Information System (FBIS) at: https://freshwaterbiodiversity.org/

4.3. Results

4.3.1. Current known distributions

Black bass

Micropterus dolomieu

In total, 641 occurrence records were downloaded from the FBIS (**Figure 4.2**). After data cleaning and spatial thinning, 519 records were available, with 230 being used in

the final modelling process. Temporally, records ranged from 1946 to 2020 (74 y), with the most records collected in 2014 (49 records) (**Figure 4.2**).

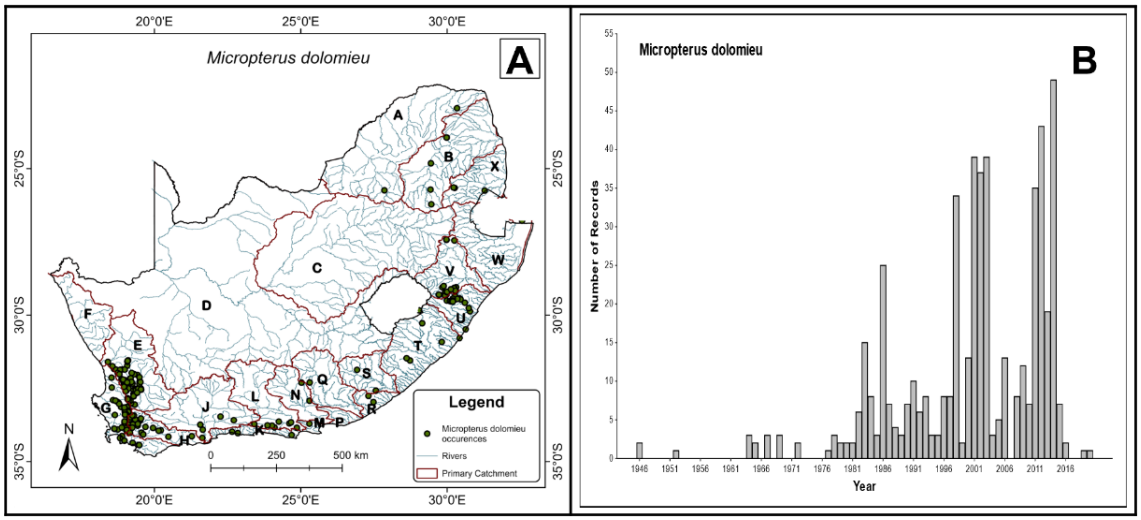


Figure 4. 2. Occurrence records for *Micropterus dolomieu* downloaded from the Freshwater Biodiversity Information System (FBIS) projected onto the primary catchments of South Africa (A) showing the number of records collected per year (B).

Micropterus punctulatus

In total, 363 records were downloaded from the FBIS (**Figure 4.3**). After data cleaning and spatial thinning, 320 records were available, with 124 records included in the final modelling process. Temporally, records ranged from 1968 to 2018 (50 y), with the most records being collected in 2010 (53 records) (**Figure 4.3**).

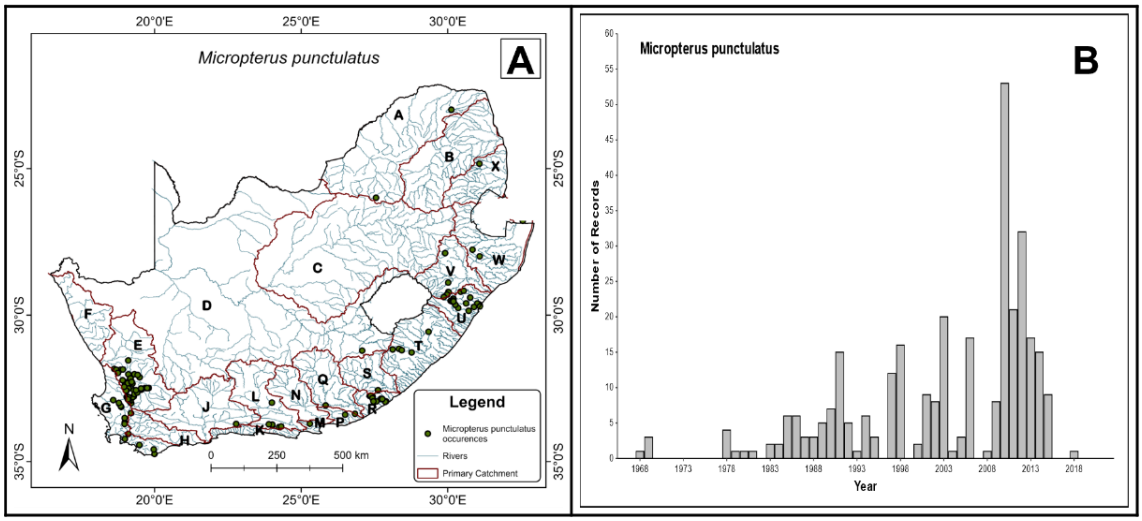


Figure 4. 3. Occurrence records for *Micropterus punctulatus* downloaded from the Freshwater Biodiversity Information System (FBIS) projected onto the primary catchments of South Africa (A) showing the number of records collected per year (B).

Micropterus salmoides/ Micropterus nigricans

In total, 1 126 occurrence records were downloaded from the FBIS (**Figure 4.4**). After data cleaning and spatial thinning, 1 007 records were available with 559 included in the final modelling process. Temporally, records ranged from 1946 to 2020 (74 y), with the most records being collected in 2013 (58 records) (**Figure 4.4**).

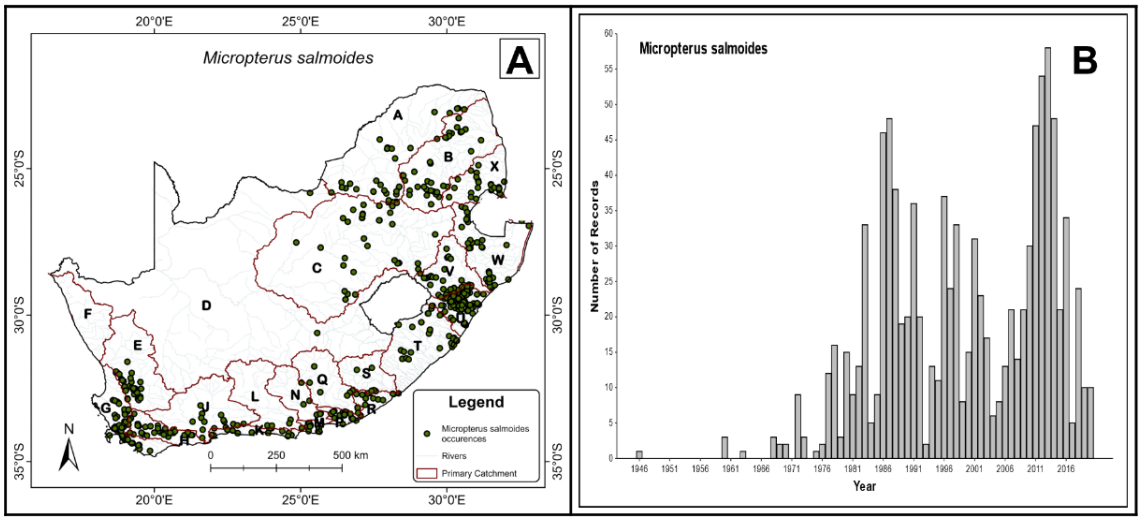


Figure 4. 4. Occurrence records for *Micropterus salmoides/Micropterus nigricans* downloaded from the Freshwater Biodiversity Information System (FBIS) projected onto the primary catchments of South Africa (A) showing the number of records collected per year (B).

Clarias gariepinus

In total, 2 659 records were downloaded from the FBIS (**Figure 4.5**). After data cleaning and spatial thinning, 1 941 records were available with 1 486 records used in the final modelling process. Temporally, records ranged from 1905 to 2023 (118 y). The most records were collected in 1995 (146 records) (**Figure 4.5**).

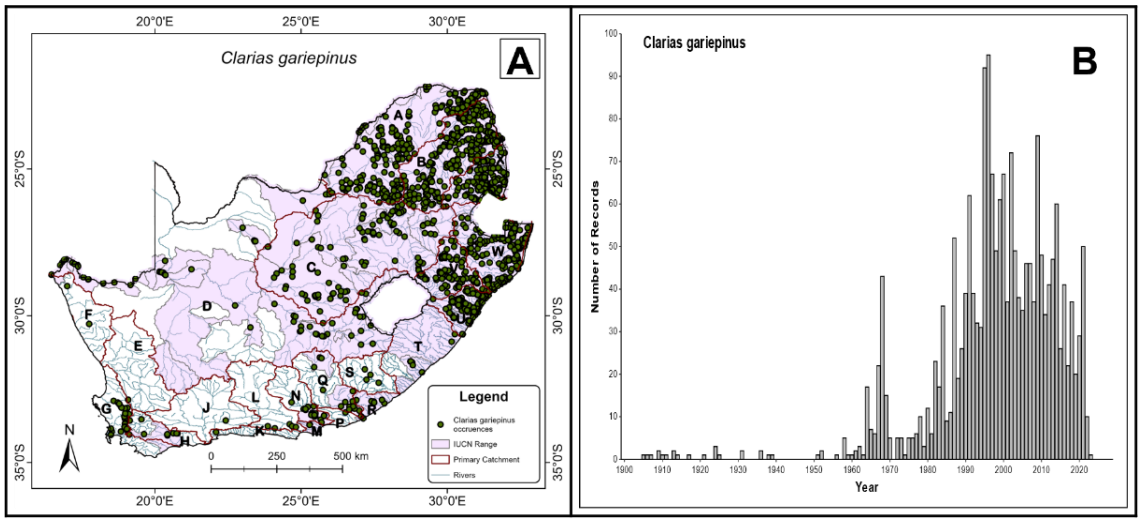


Figure 4. 5. Occurrence records for *Clarias gariepinus* downloaded from the Freshwater Biodiversity Information System (FBIS) projected onto the primary catchments of South Africa (A) showing the number of records collected per year (B).

Pseudobarbus burgi

In total, 212 records were downloaded from the FBIS (**Figure 4.6**). After data cleaning and spatial thinning, 115 records were available with 49 records used included in the final modelling process. Temporally, records ranged from 1971 to 2019 (48 y), with the most records being collected in 1996 (95 records) (**Figure 4.6**).

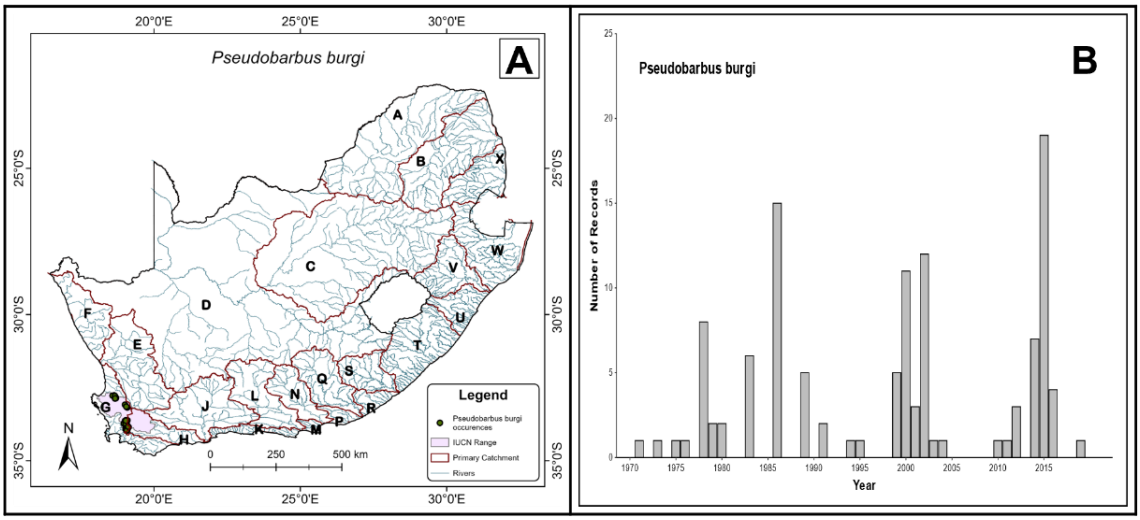


Figure 4. 6. Occurrence records for *Pseudobarbus* burgi downloaded from the Freshwater Biodiversity Information System (FBIS) projected onto the primary catchments of South Africa (A) showing the number of records collected per year (B).

4.3.2. Modelled distributions

Black bass

Micropterus dolomieu

Areas predicted as most suitable (probability of occurrence > 0.6) for *M. dolomieu* were identified in the Berg (G), Breede (H), and Olifants-Doring (E) catchments (**Figure 4.7**). Additionally, there are areas of suitable habitat identified all along the south coast, east coast, and northern parts of South Africa. The total area predicted as suitable for *M. dolomieu* was ca. 144 007 km^2 occupying a total river length of ca. 31 697 km.

For *M. dolomieu*, model performance was good (AUC = 0.968; TSS = 0.803) (**Figure 4.8**). The variables contributing most to model performance were ENVIREM_PETdriestquarter (mean monthly potential evapotranspiration of the driest quarter) (0.117), BIOCLIM_15 (0.116) (precipitation seasonality), dl16 (0.113) (low flow pulse duration), ma31 (0.111) (variability of monthly flow values for August), and TPI (0.109) (difference between elevation of focal cell and the mean of its eight surrounding cells). Response curves indicate that the areas predicted as highly suitable for *M. dolomieu* were mainly associated with a high PET, ranging between 150-200 mm/month and a high precipitation seasonality coefficient, ranging from 60–75 (**see Supplementary S4**.7).

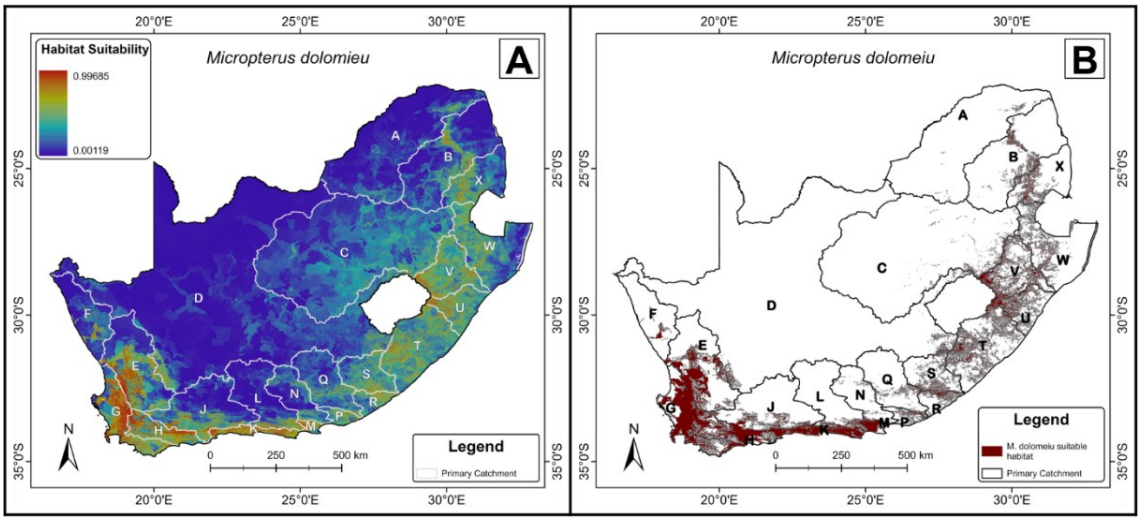


Figure 4. 7. The modelled distribution of *Micropterus dolomieu* in South Africa showing habitat suitability (A) and predicted distribution (B).

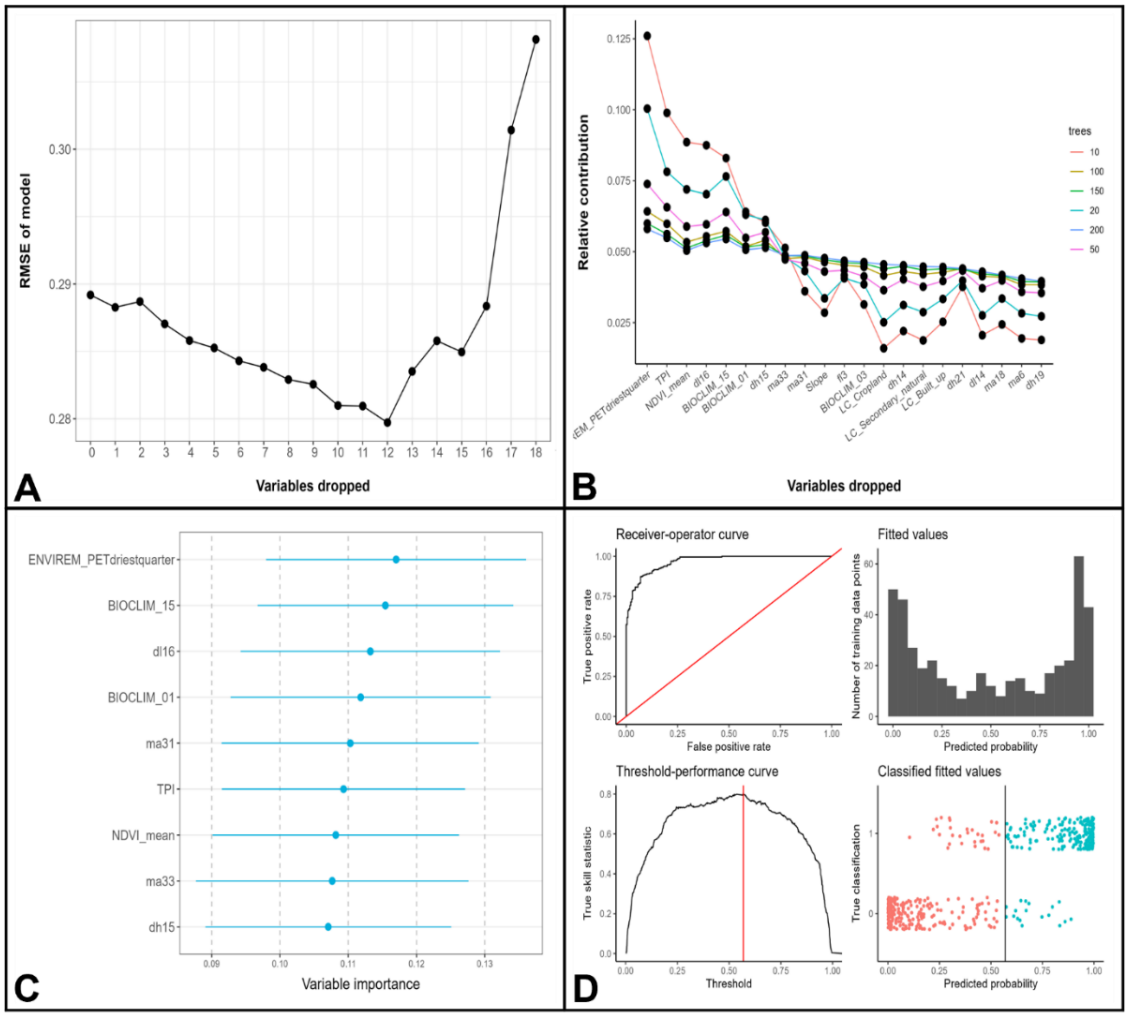


Figure 4. 8. Model diagnostic outputs for *Micropterus dolomieu*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs

(including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

Micropterus punctulatus

Areas predicted as most suitable (probability of occurrence > 0.6) for *M. punctulatus* were identified in the Berg (G), Breede (H), Olifants-Doring (E), western Gourits (J), and Kromme (K) catchments (**Figure 4.9**). Additionally, there are areas of suitable habitat identified all along the south coast and east coast, with patches of suitable habitat in the northern parts of South Africa. The total area predicted as suitable for M. punctulatus was ca. 269 267 km^2 occupying a total river length of ca. 54 388 km.

For *M. punctulatus*, model performance was good (AUC = 0.979; TSS = 0.854) (**Figure 4.10**)**.** The variables contributing most to model performance were ENVIREM_PETdriestquarter (0.111), TPI (0.108), BIOCLIM_19 (0.105) (precipitation of coldest quarter), ENVIREM_aridityindex (0.102) (Thornthwaite aridity index) (0.102)), and ma31 (0.099). Response curves indicate that the areas predicted as highly suitable for *M. punctulatus* were mainly associated with a high PET, ranging between 150-200 mm/month and a low TPI, ranging from -80 to 0 (see **Supplementary S4.8**). Additionally, there is a logarithmic relationship between precipitation of the coldest quarter and *M. punctulatus* habitat suitability (>200 mm) (see **Supplementary S4.8**).

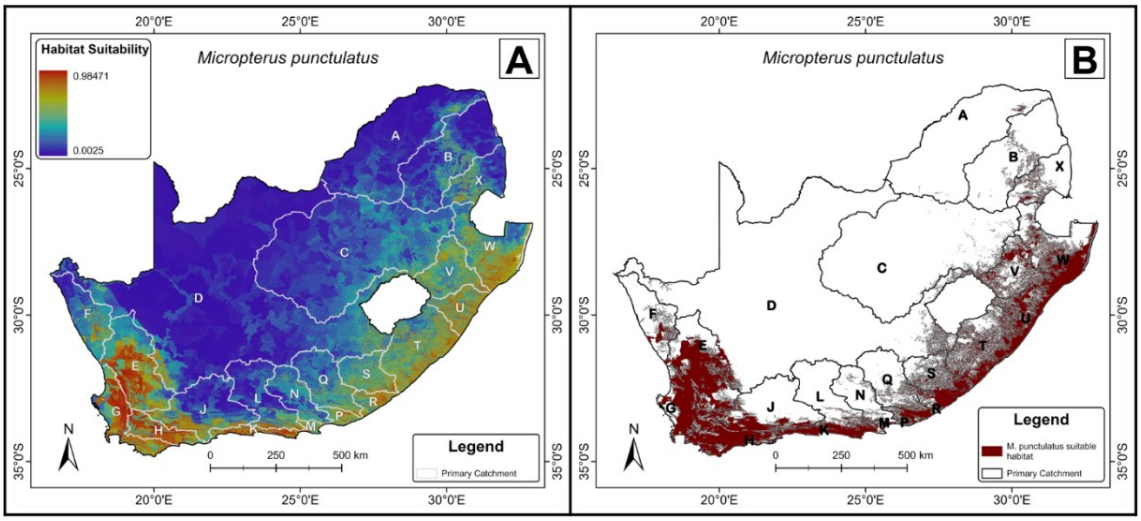


Figure 4. 9. The modelled distribution of *Micropterus punctulatus* in South Africa showing habitat suitability (A) and predicted distribution (B).

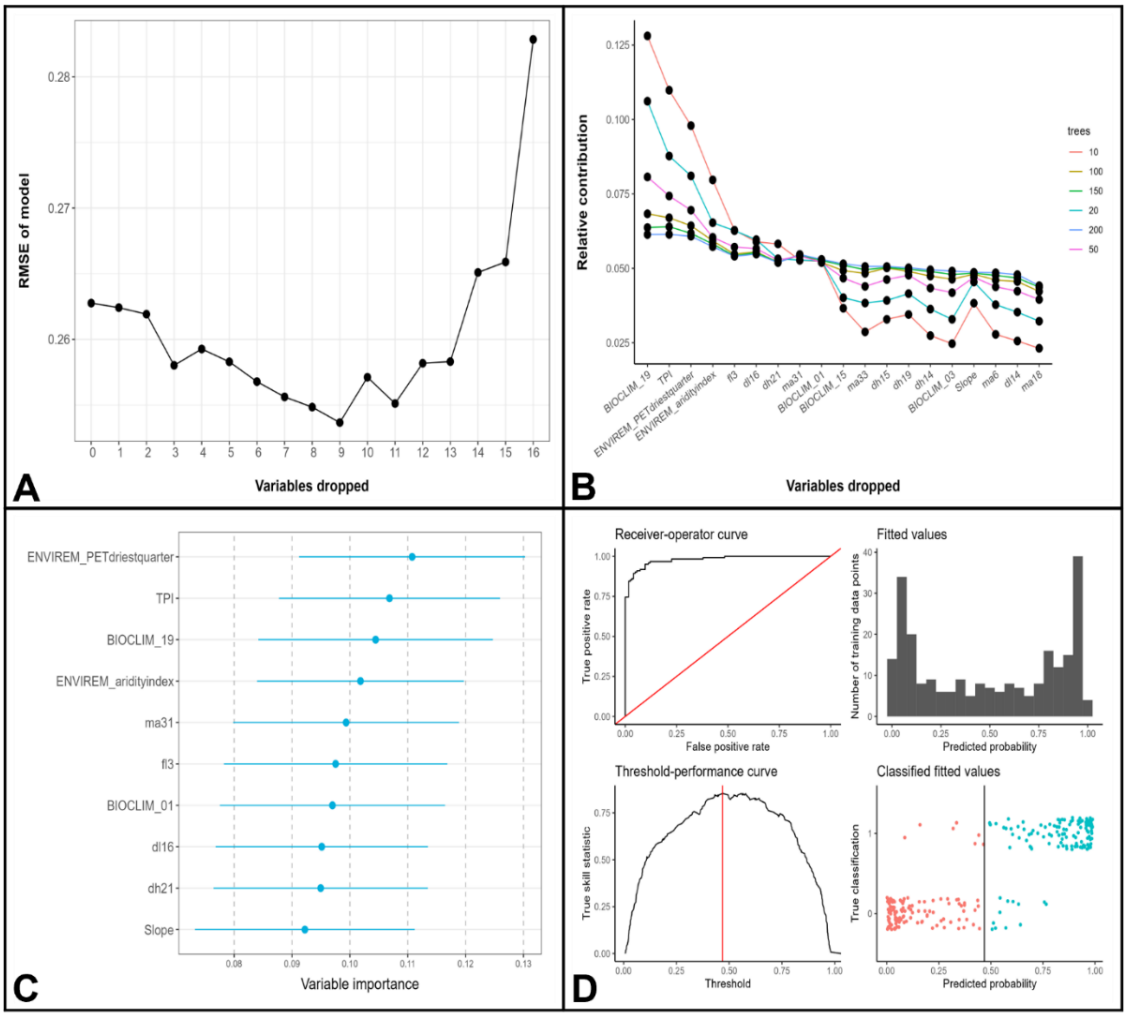


Figure 4. 10. Model diagnostic outputs for *Micropterus punctulatus*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

Micropterus salmoides/*Micropterus nigricans*

Areas predicted as most suitable (probability of occurrence > 0.6) for *M. salmoides//M. nigricans* were identified in the Berg (G), Breede (H), Olifants-Doring (E), western Gourits (J), and Kromme (K) catchments (**Figure 4.11**). Additionally, there are areas of suitable habitat identified all along the south coast, east coast, and the northern and central parts of South Africa. The total area predicted as suitable for *M. salmoides//M. nigricans* was ca. 329 440 km^2 occupying a total river length of ca. 80 847 km.

For *M. salmoides/M. nigricans*, model performance was good (AUC = 0.930; TSS = 0.709) (**Figure 4.12**). The variables contributing most to model performance were TPI (0.09), ma33 (0.084) (variability of monthly flow values), ma31 (0.083), slope (0.081), and dl16 (0.08). Response curves indicate that the areas predicted as highly suitable for *M. salmoides//M. nigricans* were mainly associated with a low TPI, ranging from -

60 to 0 and high monthly flow variability in October (> 30%) and moderate flow variability in August (15–30%) (see **Supplementary S4.9**). Additionally, there is a negative relationship between slope and *M. salmoides/M. nigricans* habitat suitability and a positive relationship between low flow pulse duration (>20 days per year) (see **Supplementary S4.9**).

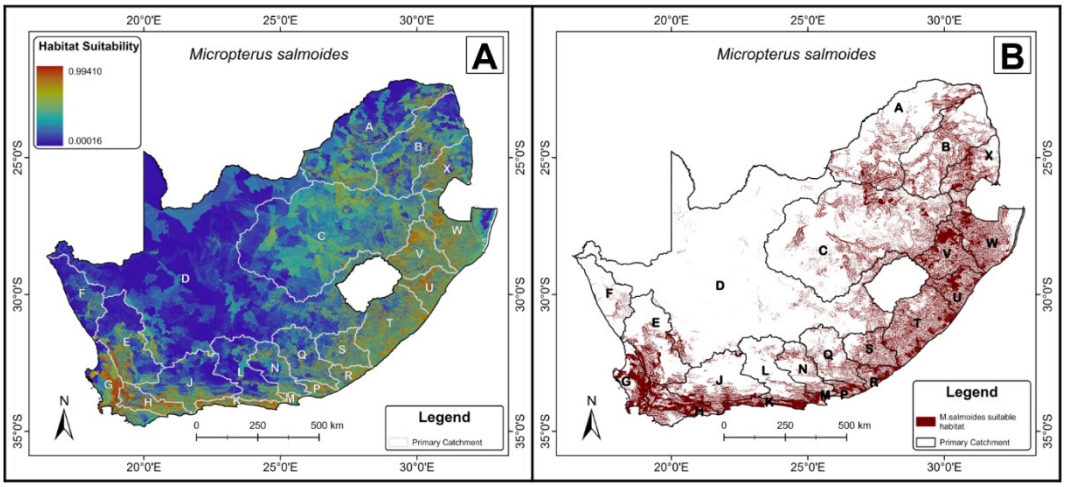


Figure 4. 11. The modelled distribution of *Micropterus salmoides/ Micropterus nigricans* in South Africa showing habitat suitability (A) and predicted distribution (B).

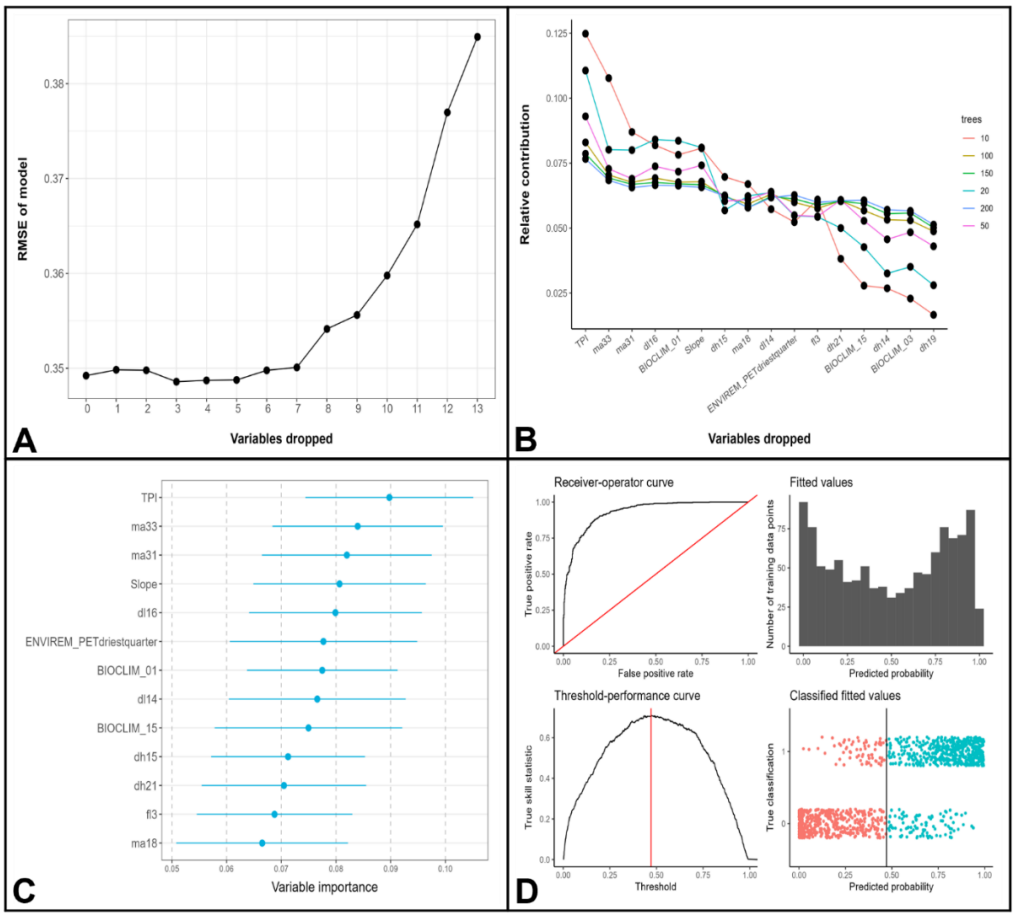


Figure 4. 12. Model diagnostic outputs for *Micropterus salmoides/Micropterus nigricans*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

Clarias gariepinus

Areas predicted as most suitable (probability of occurrence > 0.6) for *C. gariepinus* were identified in the Limpopo (A), Olifants (B), Komati (X), Mfolozi (W) Tugela (V), and Mkomazi (U) catchments (**Figure 4.13**). Additionally, there are sporadic areas of suitable habitat identified all along the east coast and in the western region of South Africa, as well as along the Orange River. The total area predicted as suitable for *C. gariepinus* was ca. 243 357 km^2 occupying a total river length of ca. 55 415 km.

For *C. gariepinus*, model performance was good (AUC = 0.923; TSS = 0.701) (**Figure 4.14**). The variables contributing most to model performance were BIOCLIM_01 (0.108) (Annual Mean Temperature), ENVIREM_PETwarmestquarter (0.093) (mean monthly potential evapotranspiration of the warmest quarter), ENVIREM_PETdriestquarter (0.088), TPI (0.087), and BIOCLIM_15 (0.086). Response curves indicate that the areas predicted as highly suitable for *C. gariepinus* were mainly associated with high temperatures (>20°C), high PET during the warmest quarter (100–150 mm/month) and driest quarter (50–75 mm/month), and low TPI (less than zero) (see **Supplementary S4.10**).

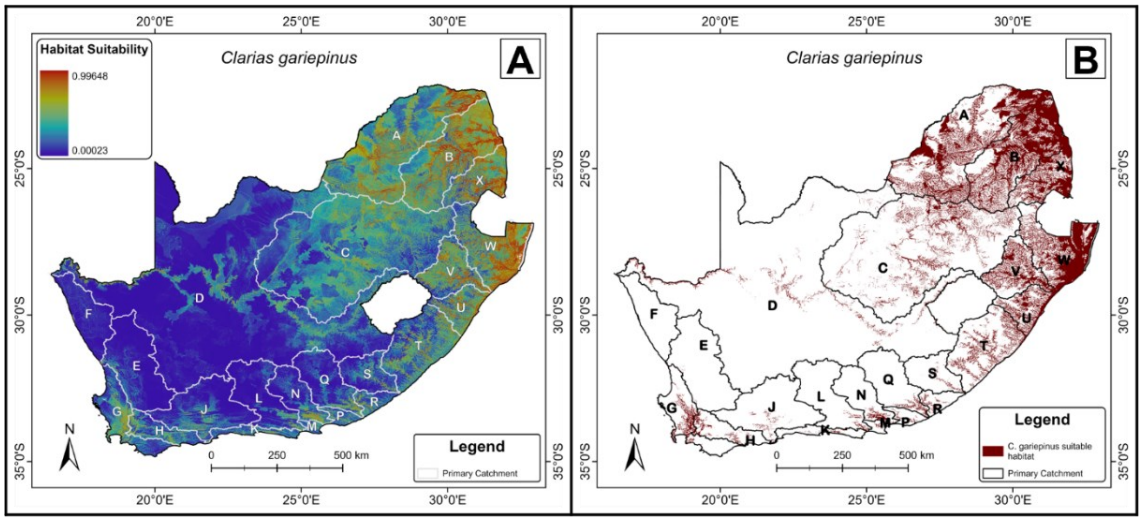


Figure 4. 13. The modelled distribution of *Clarias gariepinus* in South Africa showing habitat suitability (A) and predicted distribution (B).

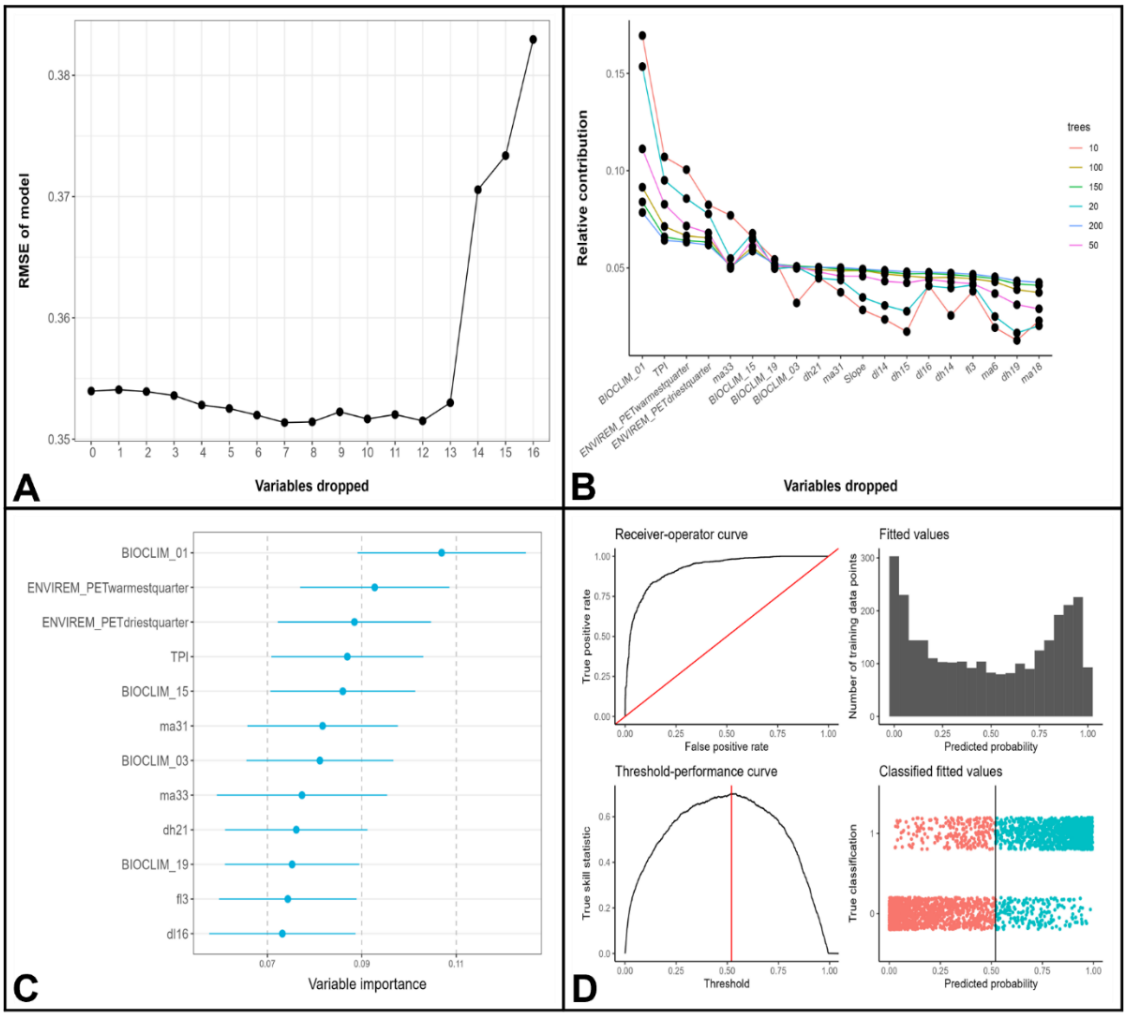


Figure 4. 14. Model diagnostic outputs for *Clarias gariepinus*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

Pseudobarbus burgi

The model for *P. burgi* was limited to the Berg River Catchment. Within the Berg catchment, areas predicted as most suitable (probability of occurrence > 0.6) were identified in the along the eastern boundary of the catchment (**Figure 4.15**). Areas of especially high suitability were identified along the Berg, Boesmans, Drakenstein, Hugos, Franschhoek, Kliphuis, Krom, Leeu, Olifants (tributary), Platkloof, Wemmershoek, and Wolwekloof rivers. The total area predicted as suitable for *P. burgi* was ca. 1815 km^2 occupying a total river length of ca. 297 km.

For the original *P. burgi* model, model performance was good (AUC = 0.994; TSS = 0.940) (**Figure 4.16**). The variables contributing most to model performance were ENVIREM_PETdriestquarter (0.132), slope (0.129), BIOCLIM_03 (0.128) (isothermality = mean diurnal range/annual temperature range*100), TPI (0.127), and

BIOCLIM_15 (0.122). Response curves indicate that the areas predicted as highly suitable for *P. burgi* were mainly associated with high PET during the driest quarter (>140 mm/month) and increasing slope. Additionally, there is a strong negative relationship between isothermality and *P. burgi* habitat suitability (see **Supplementary S4.11**).

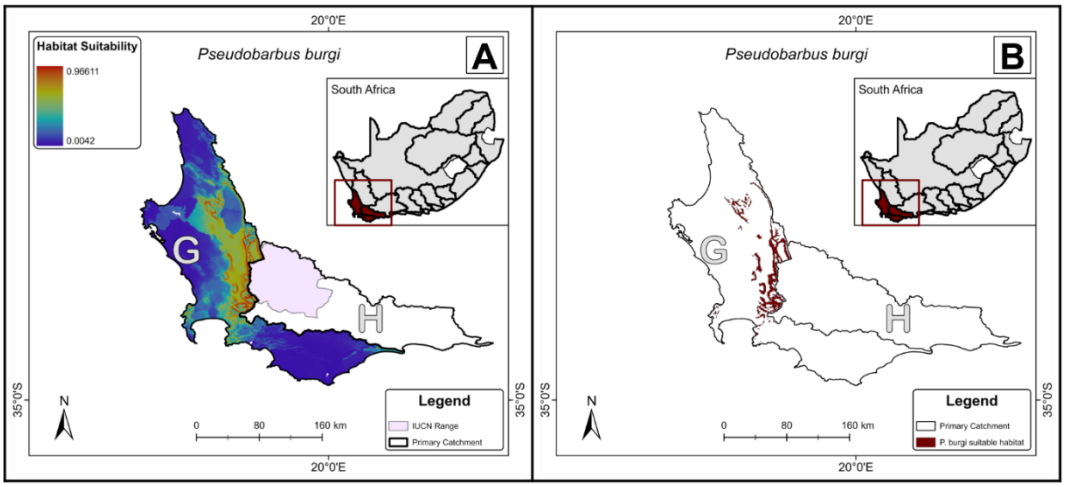


Figure 4. 15. The modelled distribution of *Pseudobarbus burgi* in South Africa showing habitat suitability (A) and predicted distribution (B).

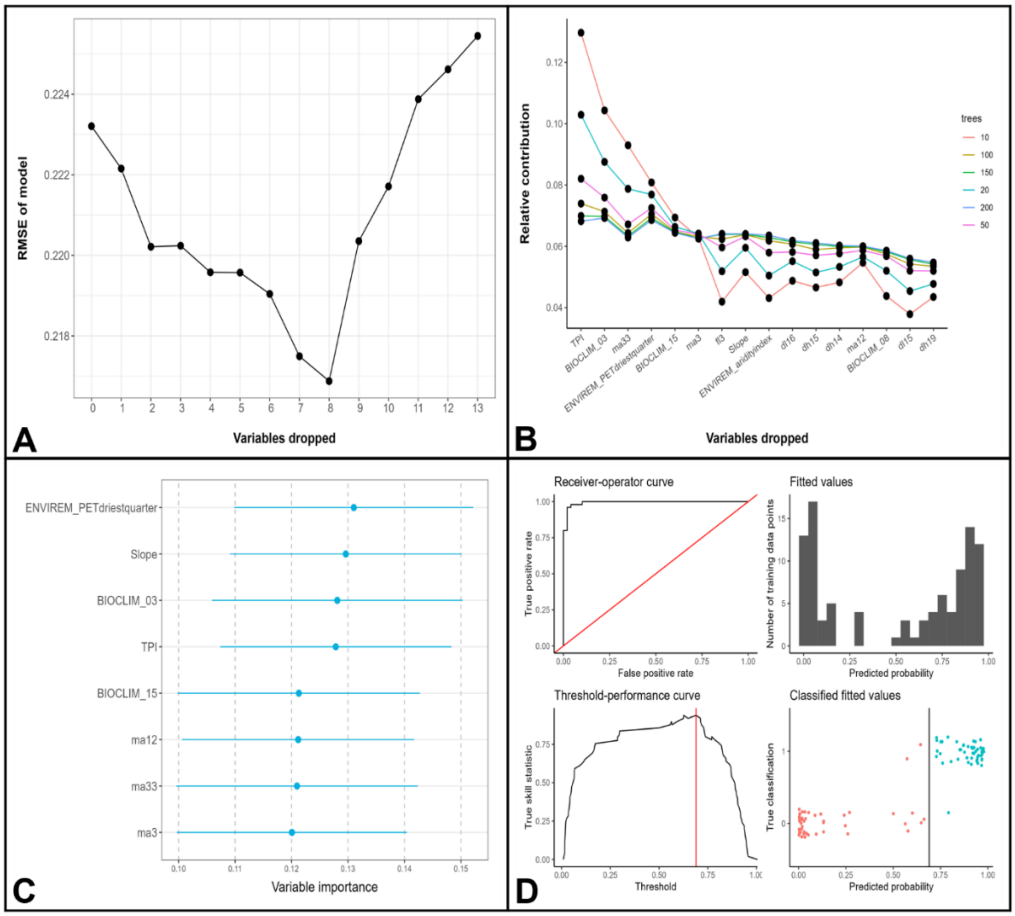


Figure 4. 16. Model diagnostic outputs for *Pseudobarbus burgi,* showing (A) the root-mean square error of the model based on the number of predictor variables dropped,

(B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

Pseudobarbus burgi adapted model

The model for *P. burgi* was limited to the Berg (G) catchment. Within the Berg catchment, areas predicted as most suitable (probability of occurrence > 0.6) were identified in the along the eastern boundary of the catchment (**Figure 4.17**). The total area predicted as suitable for *P. burgi* was larger than in the original *P. burgi* model, covering an area of ca. 2072 km^2 and occupying a total river length of ca. 347 km.

For the adapted *P. burgi* model that included invasive species, model performance was good (AUC = 0.993; TSS = 0.921) (**Figure 4.18**). The variables contributing most to model performance were TPI (0.104), ENVIREM_PETdriestquarter (0.103), slope (0.101), *M. salmoides//M. nigricans* (0.101), *Oreochromis mykiss* (0.10) and ma12 (0.099). Like the original *P. burgi* model, response curves for the adapted model indicate that the areas predicted as highly suitable for *P. burgi* were mainly associated with high PET during the driest quarter and increasing slope. Additionally, there is a strong positive relationship between the presence of *O. mykiss*, *M. salmoides/M. nigricans*, and *M. dolomieu* and *P. burgi* habitat suitability (see **Supplementary S4.12**).

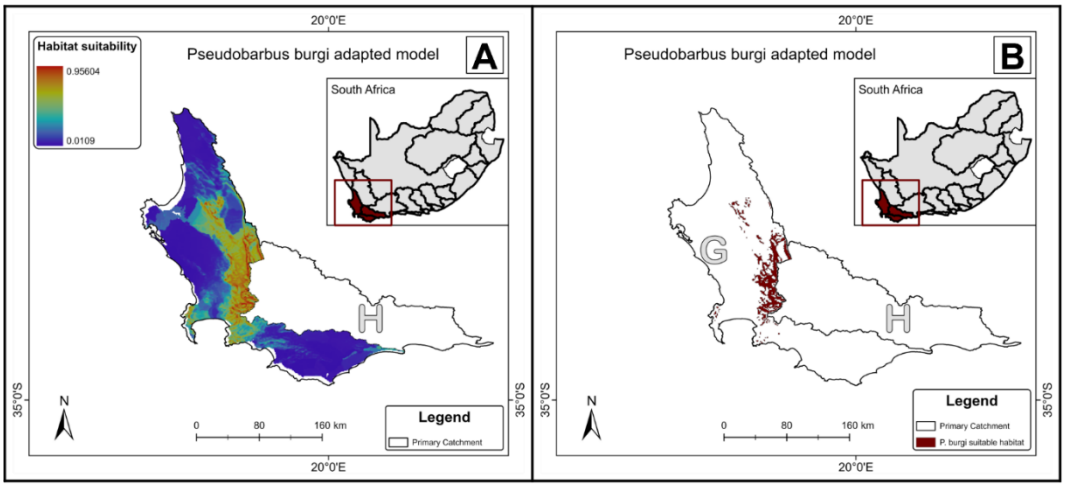


Figure 4. 17. The modelled distribution of *Pseudobarbus burgi* in South Africa showing habitat suitability (A) and predicted distribution (B), using an adapted modelling process that included invasive species distributions as predictor variables.

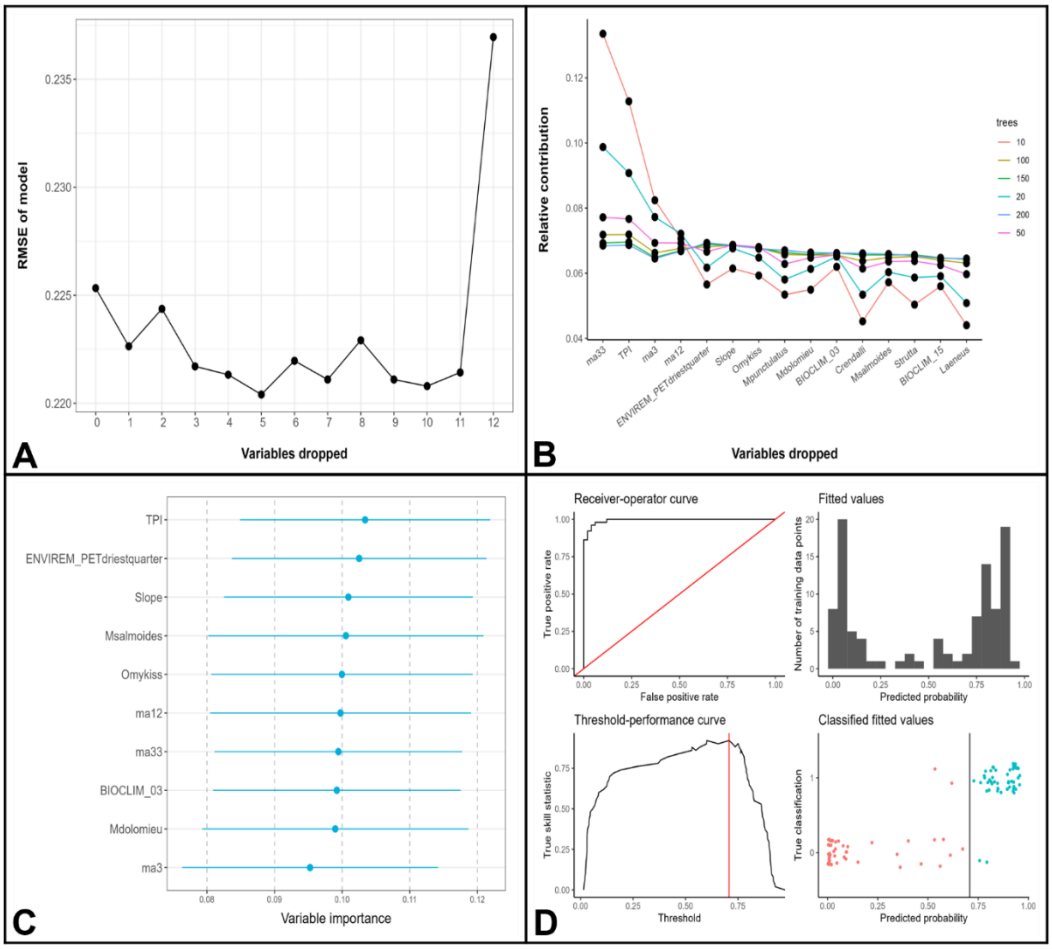


Figure 4. 18. Model diagnostic outputs for *Pseudobarbus burgi*, using an adapted modelling process that included invasive species distributions as predictor variables, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

4.4. Discussion

The aim of this chapter was to develop a stepwise and statistically robust methodology for developing SDMs for freshwater taxa in South Africa. The results demonstrated that, with appropriate data cleaning and using a statistically robust method for selecting predictor variables, the models generally produced outputs that performed well, with the resulting modelled distributions congruent with known distributions and historic descriptions of the species' presence (Skelton, 2001). This chapter thus demonstrates that the proposed modelling workflow can be used to model the distributions of non-native invasives, widespread natives, and range-restricted threatened species, thus providing evidence that SDMs can be used to develop distribution maps easily and efficiently for a wide range of freshwater fishes in South Africa.

4.4.1. Importance of findings

This study provides several important outputs, with implications for researchers, conservation managers, policymakers, and national biodiversity organisations. Firstly, it presents a clear, repeatable, and reliable method for applying SDMs to freshwater species. The collation and standardisation of environmental, hydrological, and biological predictor variables reduces barriers (Elith and Leathwick, 2009; Martínez-Minaya et al., 2018; Hijmans and Elith, 2023) to being able to model species distributions in an efficient manner. This modelling workflow can be used by other researchers, conservation managers, and policy makers without needing to source predictor variables and species occurrence data, and without needing to have expert-level knowledge on how to develop SDMs or detailed knowledge on species' life-histories, ecology, and physiology. Additionally, the modelling workflow presented allows for the modeller to track predictor variable selection and other model parameters to allow for easy repetition of models, in cases where model outputs need to be iteratively improved. Furthermore, with the establishment of the FBIS, which houses accessible occurrence data for all freshwater fishes, this modelling workflow can be applied to all freshwater fishes in South Africa. This will have a positive impact on freshwater research in the country, facilitating improved understanding of diversity patterns, community interactions, and anthropogenic impacts, whilst also informing national and provincial biodiversity assessments, identifying areas in need of additional sampling efforts, and flagging areas that in need of urgent management or protection (Baker et al., 2021; Chakona et al., 2022).

Secondly, calculating hydrological metrics (see **Supplementary Table S4.4**) from modelled daily flow data, sourced from the ACRU database (Schulze, 1995) provides the first, and most comprehensive dataset of hydrological metrics for all quinary catchments in South Africa. These metrics were converted into raster files and are publicly available in GEOTIFF format. Since the inception of this study, Rivers-Moore et al. (2020) has also published a comprehensive dataset using a similar approach. In that study 150 hydrology metrics were calculated using the IHA approach (Indicators of Hydrologic Alteration), whereas this study calculated 148 variables using the *EflowStats* package in R (Thompson et al., 2013). In both instances, the development of a national database containing hydrological metrics is an important first step to being able to more accurately and efficiently apply SDMs in freshwater habitats.

Thirdly, this chapter presents the first attempt to use the modelled distributions of invasive fish species as a predictor variable included in the modelling of native species. The development of biological predictor variables, by applying SDMs to all freshwater fishes classified as invasive in South Africa (Ellender and Weyl, 2014; Weyl et al., 2020), provides the foundation for the development of modelled distributions for all invasive freshwater fishes in the country (see **Supplementary S4.13**). The widespread and often devastating impacts of invasive fishes are well studied (Ellender and Weyl, 2014; Lübcker et al., 2014; Dallas et al., 2017; Cerrilla et al., 2022). Consequently, there is an urgent need to understand both the current and potential

future distributions of invasive species occurring in South Africa (Chakona et al., 2022). In this regard, the production of modelled distribution maps for these species is an important contribution to freshwater research in South Africa. These maps serve as an important first step to i) better understanding the current distribution ranges of invasive species; ii) develop accurate and reliable species range maps in the future; iii) investigate potential invasion risk in uninvaded habitat; and iv) study the impact of invasive species on native species collectively and across broad spatial scales, but especially their impact on threated freshwater fishes. All model outputs, including SDMs and predicted distribution maps, will be made publicly available upon publication of this chapter.

4.4.2. Model performance and interpretation

All models for invasive, native, and threatened species performed well, with AUC values ranging from 0.923–0.994 and TSS ranging from 0.701–0.940. This study shows that BART models are able to accurately model suitable habitat of a wide range of freshwater fishes in South Africa and improve understanding of how environmental factors affect their distribution. The high TSS values were particularly promising, indicating the models' ability to correctly predict true positive rates (an indication of sensitivity) and true negatives (an indication of specificity). Still, model outputs should be thoroughly assessed by experts before their predicted distributions can be used to inform conservation and management decisions and ultimately inform policy.

One of the main positive aspects of using the model workflow presented here is that variable selection is conducted in a manner that is statistically robust and repeatable (Carlson, 2020). However, it is still important to consider that the distribution of freshwater fishes can be influenced by several environmental factors (Skelton et al., 1995; Parreira et al., 2019; Chakona et al., 2022) that often interact with each other and the target species in a manner that is far too complex for any model to handle (Parreira et al., 2019). As such, it is often the case that predictor variables that are statistically selected as important in determining the distribution of any given species may be a proxy for several ecologically relevant predictors, or in some cases may not be ecologically relevant at all. For example, across all models, TPI was repeatedly selected among the five most important predictors. The topographic position index is a semi-automated landform classification that measures the relative topographic position of a central point (or grid cell) in relation to the mean elevation of all (eight) surrounding cells (De Reu et al., 2013). In simple terms, TPI is a quantified the difference in mean elevation. Given that rivers are found in areas that are at a measurably lower elevation than the surrounding environment, it makes sense that TPI would be identified as an important environmental predictor when applying SDMs to freshwater taxa. Considering this, one should proceed with caution when interpreting the relevance of, or drawing ecological conclusions from, model outputs with respect to the variables identified as most important. In this case, the aim of this study was to produce accurate distribution maps for a suite of species, which is something urgently needed for freshwater biodiversity management and conservation planning in South Africa (Jordaan et al., 2020; Chakona et al., 2022). This modelling exercise serves as a first step to better understanding the distribution patterns of the

country's freshwater fishes. In instances where understanding ecological drivers is the main aim of a study, then predictor variable selection needs to be carefully considered, based on the study species' life history and physiology.

The second primary aim of this study was to determine if the inclusion of modelled invasive species distribution as biological environmental predictors would improve model performance and result in more accurate predicted distributions. It was hypothesized that this inclusion would result in improved model performance and more accurate predicted distributions. In this regard, the results showed that model performance for *P. burgi* was not improved by including biological predictors. The AUC for the original *P. burgi* model (including only climatic, environmental, and hydrological predictors) was 0.994, whereas the adapted model (including both climatic, environmental, and hydrological predictors as well as biological predictors) was marginally lower, with an AUC value of 0.993. Similarly, the TSS was lower in the adapted model, when compared to the original model. Furthermore, when assessing the predicted distributions resulting from both models, the original model produced a smaller distribution area (1 815 km^2) compared to the adapted model (2 072 km^2). When compared to the known distribution of the species (Bloomer and Impson, 2000; Impson, 2001; Skelton, 2001; Ellender et al., 2017), the original model produced a more accurate predicted distribution that was also congruent with a previous attempt to model this species (Dallas et al., 2017). Consequently, the results do not support the proposed hypothesis. This could potentially be attributed to the fact that the biological predictors were too course (the invasive species occupy the entire distribution of *P. burgi*) or because other environmental predictors had a stronger correlation with the distribution of the species.

As the SDM field continues to develop, this is an important finding, indicating that the inclusion of biological predictors such as the presence of invasive species may not be necessary to produce accurate predicted species distributions, as was stated by Araújo and Luoto (2007) and Meier et al. (2010). However, these findings should be considered as preliminary, requiring additional studies to apply a similar approach for other species across several groups. Alternatively, it is equally vital to consider that the results were influenced by shortcomings of the modelled invasive distributions themselves. For example, all invasive models were developed at a national scale, which would have resulted in biological predictors that do not contain useful data at a fine resolution. This could be particularly important in the case of *P. burgi*, which was modelled within a single catchment. Developing biological predictors at scales that match the extent of the target species will be time consuming and potentially not feasible when trying to model several species, but it could result in improved model performance and predictive accuracy. Additionally, native-invasive species interactions may be better understood by applying SSDM or JSDM approaches in relevant study contexts (Gelfand et al., 2005; Mateo et al., 2012; Warton et al., 2015; Clark et al., 2017; Ovaskainen et al., 2017; Tikhonov et al., 2020; Wilkinson et al., 2021).

4.4.3. Ecological relevance

Black bass

Micropterus dolomieu

Model outputs for *M. dolomieu* indicated that much of the southwestern catchments (Berg, Breede, and Olifants-Doring) were environmentally suitable (**Figure 4.7**). Additionally, there were scattered areas of environmentally suitable habitat identified along the east coast. In comparison, both Dallas et al., (2017) and Khosa et al. (2019) found suitable habitat (using MAXENT) only in the western region of South Africa, overlapping with the predicted habitat identified in this study in the Berg, Breede, and Olifants-Doring catchments. However, Khosa et al. (2019) allowed their models to forecast suitable habitat in catchments where the species does not exist, thus also identifying suitable habitat extending into the Buffels and Orange catchments (see **Supplementary S4.14**). It is important to highlight that Khosa et al. (2019) used a slightly different modelling objectives, notably their study was focussed on conducting an audit of invasion debt for this species, rather than accurate species prediction of the species' current distribution (interpolation). Given that there are no known records for *M. dolomieu* occurring in either of these catchments and that the species is widely accepted to not occur in these catchments (Skelton, 2001), it is safe to assume that the model produced in this study is correct in not identifying habitat in the Buffels (F) and Orange (D) catchments. Similarly, Khosa et al. (2019) predicted that *M. dolomieu* had a total suitable habitat area of 461 163 km^2 occupying a total river length of ca. 79 976 km, whereas this study found the total areas predicated as suitable to be much smaller at 144 007 km^2 occupying a river length of ca. 31 697 km. This difference can be attributed to the fact that Khosa et al. (2019) did not identify suitable habitat along the east coast and central parts of South Africa, where the species is known to occur (Skelton, 2001), as well as a large area in the central part of the country that was found to be somewhat suitable and included in their final calculations.

In terms of the predictor variables, response curves show that *M. dolomieu* were likely to occur in areas with increasing potential evapotranspiration during the driest quarter (April to June) (**Figure 4.8**). This is likely a reflection of the species' affinity for areas with higher temperatures and increased wind as is the case in the Cape Fold Ecoregion. *M. dolomieu* was also associated with precipitation seasonality ranging between 50–75% and a mean annual temperature of 12 - 18°C (see **Supplementary S4.7**). This is congruent with the known distribution of the species and its thermal preference range needed for spawning and growth (McKinley et al., 2000; Landsman et al., 2011; Ahn et al., 2023). Additionally, *M. dolomieu* are also known to prefer moderate flow rates (Ahn et al., 2023), which this study supports. Response curves show that areas predicted as highly suitable for *M. dolomieu* were associated with long periods of low flow (dl16) and a high flow duration (dh15) ranging from 10 - 30 days per year (see **Supplementary S4.7**).

Micropterus punctulatus

Model outputs for *M. punctulatus* indicated suitable habitat in the Berg (G), Breede (H), Olifants-Doring (E), western Gourits (J), and Kromme (K) (**Figure 4.9**).

Additionally, there were areas of environmentally suitable habitat identified along the south and east coasts. In comparison, Khosa et al. (2019) identified suitable habitat mainly in the western region of South Africa, with some suitability identified along the east and south coasts (see **Supplementary S4.14**). Once again, Khosa et al. (2019) identifies suitable habitat in the Buffels and western Orange catchments, where there are no known *M. punctulatus* records and where the species is not known to occur (Skelton, 2001). When comparing the total area predicted as suitable, Khosa et al. (2019) found *M. punctulatus* to have a total suitable habitat area of 85 976 km^2 occupying a total river length of ca. 18 404 km, whereas this study found the total areas predicated as suitable to be 269 267 km^2 occupying a river length of ca. 54 388 km. Once again, the results from this study produce a larger estimate of suitable habitat compared to Khosa et al. (2019). One possible explanation for this could be that this study used a modelling algorithm that statistically selected predictor variables based on variable importance and contribution rather than selecting predictors based on ecological relevance. This could result in model outputs that more accurately represent the species true distribution in a statistical manner, but that used variables that aren't necessarily ecologically relevant. This has proven to be beneficial when simply trying to map the distribution of the species accurately but could prove to be problematic if the objective of the modelling exercise is to make ecological inferences about what type of habitat the species prefers. Regardless, this notable difference in the predicted area of habitat suitability requires site-sampling to ground-truth model outputs.

Like *M. dolomieu*, response curves show that *M. punctulatus* were likely to occur in areas with increasing potential evapotranspiration during the driest quarter (**Figure 4.10**). In contrast *M. punctulatus* was also associated with increasing precipitation during the winter months and decreasing aridity, indicating that the species be more common in areas with a Mediterranean climate. Additionally, the species was also lower flows (ma31 and fl3) and moderate mean annual temperatures (15°C and 20°C), similar to that of *M. dolomieu*.

Micropterus salmoides/*Micropterus nigricans*

Model outputs for *M. salmoides//M. nigricans* indicated that much of the northern catchments (Limpopo, Olifants, Komati, Mfolozi, and Tugela) was environmentally suitable (**Figure 4.11**). Additionally, almost all of the area along the east, south and west coast was environmentally suitable. In comparison, Khosa et al. (2019) found suitable habitat in broadly similar areas using MAXENT (see **Supplementary S4.14**). However, Khosa et al. (2019) did identify highly suitable habitat (probability of occurrence = 0.86) in the extreme west of the Buffels (F) and Orange (D) catchments, while this study did not. Given that there are no known records for *M. salmoides/M. nigricans* occurring in either of these catchments and that it is widely accepted to not occur in either of these catchments (Skelton, 2001), it is safe to assume that the model produced in this study is correct in not identifying habitat in the Buffels (F) and Orange (D) catchments. Similarly, Khosa et al. (2019) predicted that *M. salmoides/M. nigricans* had a total suitable habitat area of 543 804 km^2 occupying a total river length of ca. 98 253 km, whereas this study found the total areas predicated as suitable to be

329 440 km^2 occupying a river length of ca. 80 847 km. This indicates that the model workflow used in this study has resulted in a predicted distribution that is more conservative than that used by Khosa et al. (2019), but more closely matches the available occurrence records and known distribution range of the species available in the literature (Skelton, 2001).

In terms of the predictor variables, response curves show that *M. salmoides/M. nigricans* were likely to occur in areas with a TPI less than zero (see **Supplementary S4.9**). Once again, this is likely a byproduct of the fact that rivers will generally be found at a slightly lower elevation than the surrounding area (Bernini et al., 2021). More notably, the species was found to have a positive association with high variability of flow in October (>30%), moderate flow variability in August (15-30%), and a low flow pulse duration greater than 20 days per year (see **Supplementary S4.9**). This is in keeping with the species' preference for slow-flowing environments (Jackson, 2002; Claussen, 2015; Khosa et al., 2019). Consequently, with the predicted decrease in rainfall predicted for much of South Africa (Hewitson and Crane, 2006; Ziervogel et al., 2014) and the presence of more than 3 000 impoundments spread across the country (Khosa, 2020), it is likely that more suitable habitat may become available for *M. salmoides/M. nigricans*, facilitating further invasion of the species. From a temperature perspective, *M. salmoides/M. nigricans* was associated with a mean temperature range of 15 - 19°C (see **Supplementary S4.9**). This finding is somewhat misaligned with the available literature on the temperature preference of this species, which tends to do better in higher temperatures, ranging from 20 - 30°C (Tidwell et al., 2003; Bae et al., 2018; Aguilar et al., 2023). A possible explanation is that the other predictors (TPI, slope, and flow metrics) provided enough explanatory power for the model, thus reducing the importance of temperature, which only contributed 7.8% to the final model (**Figure 4.10**). Additionally, the high concentration of *M. salmoides/M. nigricans* records in the Cape Fold Ecoregion (Berg, Breede and Olifants-Doring Catchments) could have influenced the temperature response of the model, since this region is characterised by a Mediterranean climate, with cooler temperatures.

On the whole, the model outputs for *M. salmoides/M. nigricans* needs to be approached with caution and carefully scrutinised, owing to the fact that a large proportion of *M. salmoides/M. nigricans* records come from farm dams scattered across the country, which aren't necessarily representative of the hydrological characteristics of the surrounding habitat. This could mean that model outputs are correlating *M. salmoides/M. nigricans* presence with environment predictors that don't account for microhabitat differences associated with these farm dams. Given that environmental predictors do not currently exist at a fine enough resolution to account for these microhabitat differences, and the fact that developing these sorts of environmental predictors from scratch is currently not feasible, this model output for *M. salmoides/M. nigricans* presents the best available prediction of the species' distribution based on the available environmental data. Additionally, it is important to note that largemouth bass and Florida bass have been found to hybridise in sympatry and are therefore difficult to distinguish and identify (Khosa et al., 2019). This could mean that the current *M. salmoides/M. nigricans* data set includes occurrence records

for both species as well as hybridised individuals. Despite this limitation, these model outputs still provide useful insight into the distribution and some aspects of the environmental preferences of this species.

All three black bass species modelled in this study have similar distributions concentrated in the Cape Fold Ecoregion and extending to varying degrees along the southern and eastern coasts. *M. salmoides/M. nigricans* is the most widely distributed of the three, with *M. dolomieu* having the smallest predicted distribution. When assessed as a suite of invasive species, it is apparent that the distribution of black bass in South Africa overlaps strongly with the distribution of threatened freshwater fishes (see Chapter 3). This once again highlights the impact that black bass have had on the native freshwater fishes of South Africa, which is well-documented (Ellender and Weyl, 2014; Dallas et al., 2017, 2018; Khosa et al., 2019; Weyl et al., 2020; Zengeya et al., 2020; Cerrilla et al., 2022). The convergence of all three species' distributions in the CFE is cause for concern, since this region is characterised by high levels of endemism (Ellender et al., 2017; Shelton et al., 2018a; Jordaan et al., 2020; Chakona et al., 2022) and hosts more threatened species than any other part of the country (Chakona et al., 2022; Kajee et al., 2023b). As such, there is an urgent need to ensure that threatened and endemic species are adequately protected from the negative impacts associated with black bass invasions.

Clarias gariepinus

Model outputs for *C. gariepinus* indicate that much of the north and north east of the country (Limpopo, Olifants, Komati, Mfolozi, and Tugela) is environmentally suitable (**Figure 4.13**). There are also isolated patches of suitable habitat identified in areas along the east coast, western region, and all along the Orange River. This chapter presents the first known attempt to model the distribution of *C. gariepinus* in South Africa. In general, the modelled distribution is similar to distribution ranges presented in Skelton (2001) and Weyl et al. (2016). Importantly, given the recent translocation of *G. gariepinus* and its associated spread into several rivers in the CFE (Weyl et al., 2016), interpreting the suitable habitat presented here, could aid future management efforts. Interestingly, a recently published study by Woodford et al. (2024) reported the first occurrence of *C. gariepinus* in the Wit River (located in the Addo Elephant National Park), which was also predicted by the model (Figure 4.13), despite not having any occurrence records in this system at the time of modelling. Whilst this is only anecdotal evidence at best, it does provide some very preliminary confirmation that the predicted distribution for *C. gariepinus* is accurate, even in novel habitats where the species has not previously been recorded. This also raises the important need for a thorough sampling effort to follow this study to determine the full extent of the expansion of *C. gariepinus*' extralimital distribution, given that this invasion is not over at this point in time – with the species still likely to invade new habitat.

Response curves show that *C. gariepinus* were strongly associated with higher temperatures (>20°C) and high levels of potential evapotranspiration during the warmest and driest quarters, which all indicate that the species is well-suited to warm temperatures. These findings fit well with the published literature on the preferred

temperature ranges for *C. gariepinus* (Weyl et al., 2016). Concerningly, this makes the spread of the species more likely in future as South Africa is predicted to become warmer as a result of climate change (Hewitson and Crane, 2006; Dallas and Rivers-Moore, 2014; Ziervogel et al., 2014). That the species was also found to have a positive association with increased flow variability in August and October and low flow (see **Supplementary S4.10**). indicates is consistent with the known preference of the species for slow-flowing river systems (Skelton, 2001; Weyl et al., 2016).

Pseudobarbus burgi

Model outputs for *P. burgi* indicated that most of the eastern boundary and northern region of the Berg catchment were environmentally suitable habitats for the species (**Figure 4.15**). This is consistent with historic records of its distribution within the catchment (Bloomer and Impson, 2000; Impson, 2001; Skelton, 2001; Ellender and Weyl, 2014). The only previous attempt to model the distribution of *P. burgi* was presented by Dallas et al. (2019), using MAXENT. They also predicted suitable habitat along the eastern boundary, with an additional area of habitat suitability in the central region of the Berg catchment (see **Supplementary 4.15**). Given the strong similarity between the two model outputs, it can be concluded that both MAXENT and BART performed equally well at predicting the distribution of *P. burgi*.

Predictor response curves show that *P. burgi* were likely to occur in areas with high evapotranspiration during the dry season, decreasing isothermality (BIOCLIM_03), and increasing precipitation seasonality (BIONCLIM_15), indicative of the species presence in the Cape Fold Ecoregion, which has a characteristic Mediterranean climate. Interestingly*, P. burgi* is also associated with increasing slope, indicating that the species is likely found in the upper reaches of mountain streams. However, this finding is likely influenced by the fact that *P. burgi* has been extirpated from its historic habitat further downstream. Interestingly, Shelton et al. (2018) also identified elevation as a significant predictor of *P. burgi* presence using a distance-based linear model based on in-situ, site-specific environmental data. However, Shelton et al. (2018) found that instream cover, canopy cover, and areas of relatively slow flows were correlated with *P. burgi* presence. While this study did not have access to instream and canopy cover data at a fine resolution, it did include various measures of flow into the modelling process. Response curves indicates that the species prefers areas of increasing flow (ma12, ma3, and ma33). This difference is likely attributed to the fact that SDMs are not able to account for smaller changes occurring at the microhabitat level. Concerningly, the species' preference for lower temperatures will likely place further pressure on this species, resulting in a potential range shrinking (Dallas et al., 2017), especially when considering the predicted increase in temperature and a decrease in rainfall in the Cape Fold Ecoregion as a result of climate change (Hewitson and Crane, 2006; Ziervogel et al., 2014).

4.4.4. Limitations

While the modelling workflow presented here and the ensuing results present an important first step towards better spatio-temporal understanding of South Africa's

freshwater fish fauna, there are several limitations that need to be discussed. Firstly, although the FBIS platform provides access to large amounts of high-quality occurrence data, working with large datasets can pose complications, since these datasets often include erroneous records which could impact model outputs and interpretation. Indeed, this issue has been studied in several other publications, with erroneous records generally impacting models negatively (Yang et al., 2013; Beck et al., 2014; Taylor et al., 2020). As such, accurate cleaning of occurrence datasets prior to modelling is important and should be conducted following an expert-driven approach (Kajee et al., 2023a). However, this process can require substantial time and resources, which could act as a hindrance to developing SDMs and associated distribution maps.

Another important complication that arises when working with large, publicly available occurrence datasets is the presence of spatial sampling bias within the dataset (Taylor et al., 2020). Spatial sampling bias is recognised as a common issue within the SDM literature (Moua et al., 2020; Taylor et al., 2020; Boyd et al., 2021; Inman et al., 2021; Baker et al., 2022), where areas that are oversampled may result in models that overfit outputs based on those biases (Boria et al., 2014). Furthermore, in river systems, spatial sampling bias may be particularly relevant because differences in river accessibility are often related to other environmental variables, such as elevation, slope, river flow, and anthropogenic infrastructure (Daru et al., 2018; Hughes et al., 2021; Bowler et al., 2022). Additionally, migratory freshwater fishes have life histories that could result in biased sampling effort that could misrepresent their overall distribution within the river system (Taylor et al., 2020). Consequently, it is important that spatial bias in occurrence data be dealt with prior to modelling. In this regard, this study applied a spatial thinning protocol (distance-based filtering) using the *spThin* package in R – the most common applied technique found in the literature (Aiello-Lammens et al., 2015). However, this approach has been criticized, since it rarely considers the unique modelling environments of freshwater fishes and results in the loss of presence data, which makes models more heavily reliant on a smaller subset of records. More recently, Taylor et al. (2020) proposed a novel riverscape filter as a potential alternative to spatial thinning, which could help deal with spatial bias, whilst preserving availability of records. This could be particularly useful for species that are data scarce. In general, however, there is an urgent need for increased long-term monitoring of South Africa's freshwater fish populations (Skowno et al., 2019; Chakona et al., 2022), to improve accuracy and availability of occurrence records and to reduce sampling bias in the existing data. Additionally, a well-thought out and comprehensive monitoring programme can also be used to ground-truth model outputs, thus facilitating better model evaluation and resulting in improved model outputs, which would aid improved conservation management and decision-making.

Secondly, the hydrological variables used in the modelling workflow were generated from simulated flow data available from the ACRU model (Schulze, 1995). The use of simulated flow data, rather than actual flow data, was unavoidable, since South Africa does not have comprehensive, continuous flow data available for most rivers. In essence, this sort of data builds an SDM on top of other modelled data. As a result, it

is important to note that using hydrological metrics calculated from simulated flow data could have introduced additional variability and inaccuracies into the modelling process and potentially resulted in inaccuracies in the final model outputs. A similar issue is encountered when including modelled distributions of invasive species as biological variables. This once again creates a knock-on effect, where any model inaccuracies are carried down through the modelling process and can have an impact on the reliability and accuracy of final model outputs. Additionally, since this study was limited to predictor variables that were readily available, the model workflow did not include all potential predictor variables that could have strong influences of freshwater fish distributions. A potential next step, in all these instances, would be to continue to refine these variable layers for South Africa, so that they may be included in future modelling efforts.

Thirdly, this chapter only included the use of one modelling algorithm (the BART algorithm from the *embarcardero* R package), based on proven improved performance (Baquero et al., 2021; Tytar et al., 2022) and the ability of the BART model to independently select environmental predictor variables in a statistically robust manner (Carlson, 2020; Pinto-Ledezma and Cavender-Bares, 2021; Tytar, 2023). However, limiting the modelling workflow to just one algorithm is not ideal. Due to time constraints, this study could not include additional algorithms. This is an important limitation of this study that needs to be addressed in future studies, given that there is evidence (Norberg et al., 2019; Srivastava et al., 2019; Hao et al., 2020; Valavi et al., 2022) that found that different modelling algorithms performed well in some habitats and poorly in others. As such, the next step in developing a truly robust approach for modelling the distributions of freshwater fauna in South Africa should focus on incorporating several modelling algorithms into the workflow. This is important, especially when considering that there is growing evidence to suggest that ensemble models are able to produce more accurate outputs than any single modelling algorithms (Thuiller et al., 2009; Hao et al., 2019, 2020). As such, it is recommended that this sort of ensemble modelling approach be investigated as an important next step to improve upon the comprehensiveness of this modelling workflow, which could potentially improve model outputs.

4.4.5. Conclusion

Despite some limitations and potential shortcomings, this study provides an important first step in developing a model workflow that can be applied to all freshwater fishes in South Africa. As modelling and computing capabilities improve, there is no doubt that the methods presented here will be further improved. However, the current results provide evidence that the proposed methodology of this study is already suitable for application to all freshwater fish species in South Africa. Expanding this approach to the country's full suite of freshwater fish fauna will provide much needed, timely information to conservation managers and policy makers, allowing for more informed, data-driven freshwater decision making in South Africa.

Key findings of this chapter that are important for conservation managers include that fact that all three black bass species exhibit overlapping distributions, particularly

within the Cape Fold Ecoregion, posing a significant threat to native biodiversity. These overlapping distributions are especially important given the recent reports of hybridisation between largemouth bass and Florida bass (Khosa et al., 2020). Additionally, the distribution of *Clarias gariepinus* is expanding, with potential for further range expansion. The modelled outputs for *C. gariepinus* should be used to inform monitoring and management plans for the species. Lastly, *Pseudobarbus burgi* exhibits strong associations with dry climates and precipitation seasonality. As such, this chapter provided further evidence of the species' vulnerability to climate change, which is predicted to see the Cape Fold Ecoregion become drier and warmer.

These findings further highlight the urgent need for targeted conservation efforts to mitigate the impacts of invasive species and climate change. The distribution maps and associated data generated by this study provide valuable tools for identifying priority areas for conservation action, informing management decisions, and guiding future research. While further research is needed to address limitations (such as spatial bias in occurrence data and the potential impacts of climate change), this study provides a robust foundation for improving our understanding of freshwater fish distributions and developing effective conservation and management plans.

Chapter 5

5. Application of Species Distribution Models (SDMs) to conservation of threatened freshwater fish in South Africa

5.1. Introduction

In South Africa, freshwater fishes are currently recognised as the country's most threatened species group (Skowno et al., 2019), with 27 species threatened with extinction (classified as Vulnerable, Endangered or Critically Endangered according to the IUCN). Of these, at least eight are reported to be in decline, with a negative change in their IUCN Red List status over the past 10 years (Chakona et al., 2022). Ongoing taxonomic revisions of freshwater fishes indicate that several taxa are genetically distinct and have narrower distribution ranges than previously thought (Chakona et al., 2022). As such, some threatened endemic 'species suites' are likely to be split taxonomically, resulting in individual species being more vulnerable and raising the total number of threatened taxa (Chakona et al., 2022). Consequently, there is increasing awareness and growing recognition of the need to develop up-to-date conservation plans and formulate policies to guide effective management and protection of freshwater habitats in South Africa.

South Africa's protected area network covers less than 10% of the total land area (Siegfried, 1989; Skelton et al., 1995; Russell, 2011; Skowno et al., 2019). Of the country's rivers, only 18% are regarded as Well Protected and 12% as Moderately Protected, with the remainder being classified as Not or Poorly Protected (Department of Environmental Affairs, 2016). However, even rivers that are considered Well or Moderately Protected are often not in a pristine or healthy condition. Despite the country's extensive Water Act (Republic of South Africa, 2014), there are no clear implementation guidelines and protocols in place to achieve effective conservation of freshwater ecosystems, outside of protected areas.

In conjunction with the proposed expansion of the protected areas network, the Government of South Africa also published Sections 24(5)(a) and 24 (5)(h) of the National Environmental Management Act, 1998 (Act 107 of 1998; (Republic of South Africa, 1998), stipulating that future developments will need to be guided by an objective Environmental Impact Assessments (EIA) process that takes into consideration presence or absence of threatened taxa (SANBI, 2021). To facilitate this process, the DFFE has developed a National Environmental Screening Tool (screening.environment.gov.za; (SANBI, 2021) – hereafter, the NEST. The NEST is a national web-enabled application that allows applicants seeking environmental authorisation in terms of the EIA Regulations of 2014 to screen their proposed development site for any environmental sensitivities, for example the presence of threatened species (Department of Forestry Fisheries and the Environment, 2021). The development of the NEST, and associated protocols, arose due to the limited availability of standardised approaches and requirements for specialist studies in the EIA process in South Africa, with competent authorities expressing concern regarding the quality of some assessments submitted for decision making (SANBI, 2021).

Furthermore, the lack of readily-available spatial information, specifically biodiversity data, for species of conservation concern limited the ability of competent authorities to make well-informed decisions that adequately consider the ecological needs of threatened taxa (SANBI, 2021). As a result, the development of the NEST, and specifically the Plant and Animal Species Protocols, provide clear requirements and guidelines for specialists undertaking EIAs in accordance with the South Africa's National Environmental Management Act (Department of Environmental Affairs, 2019).

The NEST uses empirical and modelled biodiversity data to guide EIAs of proposed developments – a process that has in the past been criticized for not being sufficiently transparent or robust (data-driven). The NEST is intended to allow for the pre-screening of 'sensitivities' in the environment and for the potential impact of proposed developments to be assessed (SANBI, 2021). The NEST report will identify the environmental sensitivities that intersect with a proposed development and require that specialists provide information on threatened taxa that may be impacted. Under the current NEST Protocols, species listed as Critically Endangered, Endangered, or Vulnerable (IUCN, 2019) should be included in the EIA process. However, whilst the NEST does contain aquatic habitat sensitivity layers, it does not currently include any aquatic/freshwater species-specific layers (SANBI, 2021). This is a gap within the NEST process that potentially leaves freshwater habitats and their associated biota at risk of not being afforded the appropriate considerations and protection required to prevent further decline in river and population health.

Including freshwater taxa into the NEST will provide valuable protection for some of South Africa's most threatened biodiversity. However, this requires access to reliable and comprehensive biodiversity data. Despite a wealth of biodiversity data existing for South Africa's freshwater ecosystems, access to these data has been limited by the lack of a dedicated and resourced freshwater information system (Dallas et al., 2022). What data do exist, are 'locked up' in multiple different organisations, which often have different goals and uses for these data. The development of the FBIS (as described in Chapter 2), along with the development of a robust SDM process for freshwater organisms in South Africa (described in Chapter 4), provide the tools needed to address this knowledge and resource gap.

This chapter describes how data sourced from the FBIS database can be combined with the SDM workflow presented in Chapter 4 to serve freshwater fish spatial data layers to a national conservation decision-support tool. Data sourced from the FBIS were used to develop national freshwater fish sensitivity layers for the NEST, allowing for the first inclusion of freshwater species coverage in the tool. The primary aim is to develop accurate distribution maps and modelled distribution layers that are fit for inclusion in the NEST. In doing so, this chapter seeks to demonstrate the importance of collating, storing, and housing freshwater biodiversity data and to illustrate the importance of being able to use biodiversity data to develop accurate distribution maps for freshwater taxa.

5.2. Methods

5.2.1. Data source

Occurrence records for 34 threatened (Vulnerable, Endangered and Critically Endangered) freshwater fishes occurring in South Africa (**Table 5.1**) were downloaded on 14 September 2022 from the FBIS online database (FBIS, 2022). These taxa included 27 formally described species and seven lineages yet to be formally described (Chakona et al., 2022). Formally described species have been assessed both globally (on the IUCN Red List) and nationally (Red List of South African Species; (SANBI, 2022), whereas undescribed lineages have only been assessed nationally (SANBI, 2022). Only primary, secondary, and catadromous threatened freshwater fishes were included, while marine peripheral/sporadic and primary marine fishes were excluded.

Table 5. 1. List of threatened (Vulnerable, Endangered and Critically Endangered) freshwater fishes occurring in South Africa showing conservation status and the number of occurrence records sourced from the Freshwater Biodiversity Information System (FBIS) pre and post 2002. VU = Vulnerable; EN = Endangered; CR = Critically Endangered.

Scientific name	Common name	IUCN Conser-vation Status	SANBI Conser-vation Status	Number of Records Pre 2002	Number of Records Post 2002
Austroglanis barnardi	Barnard's rock	EN	EN	66	34
Chetia brevis	Orange-fringed	EN	EN	17	27
Chiloglanis bifurcus	Incomati	CR	CR	81	45
Chiloglanis emarginatus	Pongolo	VU	VU	26	27
Ctenopoma multispine	Many-spined	LC	VU	21	3
Enteromius gurneyi	Redtail barb	VU	VU	73	14
Enteromius treurensis	Treur River barb	CR	CR	20	10
Labeo rubromaculatus	Tugela labeo	VU	VU	29	16
Labeo seeberi	Clanwilliam sandfish	EN	EN	42	230
Marcusenius	Natal bulldog	EN	EN	1	8
Oreochromis mossambicus	Mozambique tilapia	VU	VU	1581	1292
Pseudobarbus afer	Eastern Cape redfin	EN	EN	93	95
Pseudobarbus asper	Smallscale redfin	VU	VU	294	54
Pseudobarbus burchelli	Barrydale redfin	CR	CR	18	32
Pseudobarbus burgi	Berg River redfin	EN	EN	84	109
Pseudobarbus capensis/ Cheilobarbus capensis	Berg-Breede River whitefish	EN	EN	45	24
Pseudobarbus erubescens/ Sedercypris erubescens	Twee River redfin	CR	CR	122	20
Pseudobarbus phlegethon	Fiery redfin	EN	EN	118	72
Pseudobarbus	Maloti minnow	EN	EN	94	59
Pseudobarbus senticeps	Krom River redfin	CR	CR	31	4
Pseudobarbus skeltoni	Giant redfin	EN	EN	2	36

Pseudobarbus swartzi	Gamtoos redfin	VU	VU	130	35
Pseudobarbus trevelyani/ Amatolacypris trevelyani	Border barb	EN	EN	23	10
Pseudobarbus verloreni	Verlorenvlei redfin	EN	EN	29	24
Sandelia bainsii	Eastern Cape rocky	EN	EN	83	71
Serranochromis meridianus	Lowveld largemouth	EN	EN	75	10
Silhouettea sibayi	Sibayi Goby	EN	EN	10	2
Kneria sp. nov. south africa		EN	EN	29	19
Marcusenius sp. nov. kosi		EN	EN	0	4
Pseudobarbus sp. nov. breede		N/A	VU	216	324
Pseudobarbus sp. nov. doring		CR	CR	26	19
Pseudobarbus sp. nov. heuningnes		EN	EN	7	48
Pseudobarbus sp. nov. keiskamma		EN	EN	38	9
Pseudobarbus sp. nov. keurbooms		N/A	EN	19	16

5.2.2. Data cleaning and validation

Owing to the issues of data accuracy and reliability reported in Chapters 2 and 3, a thorough data-cleaning protocol was applied to the data used in this chapter. This process spanned more than 12 months and involved freshwater fish experts from across the country. A series of workshops were held with freshwater fish taxon specialists from across South Africa during 2021 and 2022 to verify the quality of the data (**see Supplementary Table S5.1**). Occurrence records for each fish taxon were thoroughly scrutinized and erroneous records removed. Resultant occurrence data sets were used to generate updated distribution maps for each taxon, and these were sent to all specialists for approval prior to further analysis.

5.2.3. Data analysis

All data cleaning, processing and analyses were conducted using R Software (R Core Team, 2020). Data visualizations and final maps were produced using R Software (R Core Team, 2020) and ArcGIS Pro (Esri Inc, 2022). Cleaned and validated occurrence records were used to produce different sensitivity layers, for inclusion into the NEST.

<u>The NEST layers</u>

The NEST consists of theme-specific spatial datasets, which have been assigned a sensitivity level (SANBI, 2021). In this regard, ‘sensitivity’ refers to the potential of negative impacts on species that exist within the proposed development’s zone of impact. The current version of the Screening Tool uses a four-tiered sensitivity rating system for threatened species, which are briefly described below (SANBI, 2021):

- **Very high –** Habitat for species that are threatened endemic taxa where all known occurrences are within an area of 10 km^2. For each taxon, critical habitat is manually mapped at a fine scale. Given that freshwater fish occur in linear river systems, the criteria used to develop the Very high sensitivity layer were adapted as follows: *Historic (pre-2002) and current (post-2002) distribution of fish taxa that are categorised as Critically Endangered.*
- **High –** Recent occurrence records for threatened taxa are included in the high sensitivity level by developing spatial polygons around recent occurrence records (post-2002).
- **Medium –** A modelled distribution, which uses species occurrence records combined with multiple environmental variables to quantify and predict areas of suitable habitat.
- **Low -** Areas where no threatened taxa are known or expected to occur.

These sensitivity layers were developed specifically for terrestrial taxa. As such, this chapter presents a slightly modified definition for each layer. A brief description of how each sensitivity layer was developed is outlined below. Final data and spatial layers were presented to taxon specialists for review before being combined and included in the NEST.

Medium sensitivity layers

Taxa that qualify for inclusion in the 'medium' sensitivity layer were categorised as either Vulnerable or Endangered. For these taxa, species distribution models (SDMs) were used to generate predictive geographic ranges. All valid occurrence records for each freshwater fish were used to independently develop a unique, accurate SDM for each taxon using a Bayesian additive regression trees (BART) algorithm via functions from the *embarcadero* R package (Carlson, 2020). A comprehensive suite of environmental and hydrological variables was used to generate these SDMs (see **Supplementary Table S4.2, S4.4, and S4.5**). Modelled distributions were converted to a binary output (presence/absence) for each species using a threshold that maximizes true skill statistics from the SDM. Detailed methods for the SDM process are described in Chapter 4.

High sensitivity layers

The high sensitivity category was only applied to freshwater fishes that were assessed as Vulnerable or Endangered. The 'high' sensitivity layer is comprised of all valid, post-2002 occurrence records (SANBI, 2021). Occurrence records for each freshwater fish (the assumed, current distribution of the species) were plotted in R (R Core Team, 2020). Occurrence data were then intersected with the River Freshwater Ecosystem Priority Areas (FEPA) Sub-Quaternary Catchment layer (Nel, 2011; SANBI, 2011) to create catchment-specific occurrence polygons, indicating the recent presence of a Vulnerable or Endangered freshwater fish in that catchment.

Very high sensitivity layers

The ‘very high’ sensitivity category was only applied to freshwater fishes that were assessed as Critically Endangered. Here, all known, valid, historic occurrence records were used to build the very high sensitivity layer. Occurrences were intersected with the FEPA Sub-Quaternary Catchment layer (Nel, 2011; SANBI, 2011) to create catchment-specific occurrence polygons, indicating the presence of a Critically Endangered freshwater fish in that catchment.

5.3. Results

The development of the NEST sensitivity layers for freshwater fish was a collaborative effort that included contributions from several organisations: FRC, SANBI, NRF-South African Institute for Aquatic Biodiversity (NRF-SAIAB), CapeNature, Endangered Wildlife Trust (EWT), DFFE, Mpumalanga Tourism and Parks Agency (MTPA), Free State Department: Economic, Small Business Development, Tourism and Environmental Affairs, and University of Cape Town (UCT), as well as multiple other individuals and organisations via SANBI’s National Freshwater Fish Observation Group (**Supplementary Table S5.2 and S5.3**). Initially, 6 068 records were downloaded from the FBIS (FBIS, 2022). Data cleaning, guided by expert consultation, resulted in the deletion of 354 erroneous records (**Figure 5.1**). An additional 946 records provided by the experts were added to the dataset from private, unpublished datasets owned by relevant experts (**Figure 5.1**) and uploaded to the FBIS. The final cleaned dataset was also tagged in FBIS as “DFFE Screening Tool 2022”, which will ensure that expert input and feedback will not be lost and will help streamline this process in the future.

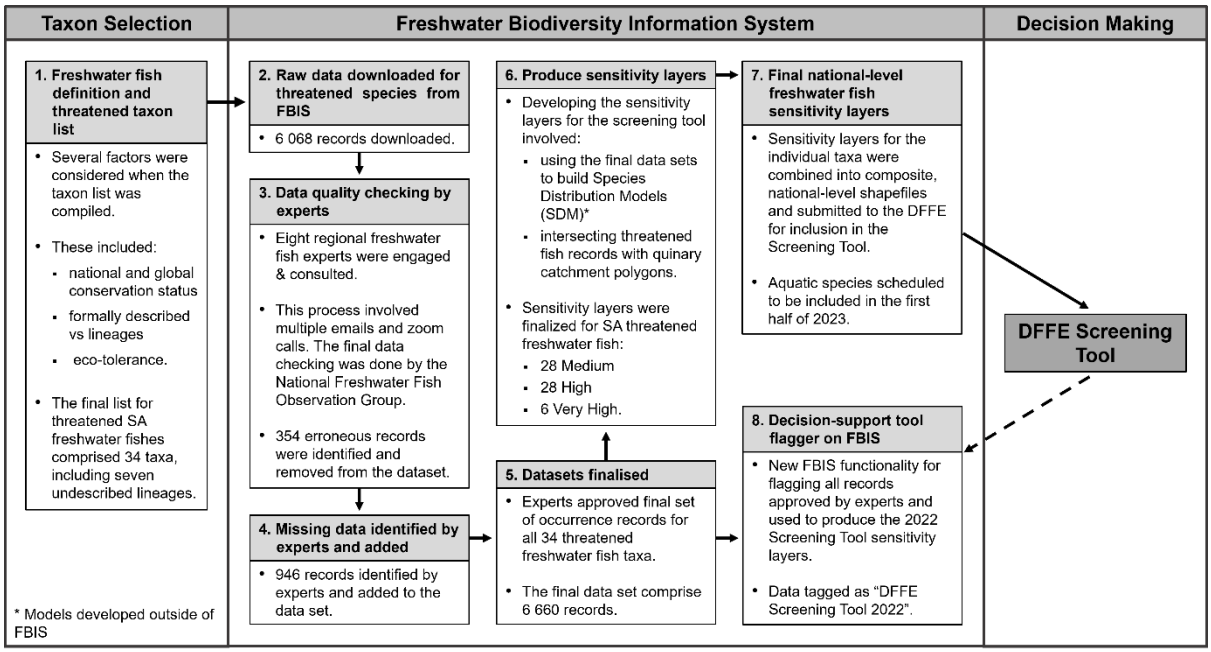


Figure 5. 1. Schematic illustrating the data flow from the Freshwater Biodiversity Information System (FBIS) into the Department of Forestry, Fisheries and Environment (DFFE) Screening Tool and developing the necessary functionality to improve the ease of future such projects.

In total, 6 660 occurrence records for the 34 threatened (Vulnerable = 8; Endangered = 20; Critically Endangered = 6) freshwater fishes were used to develop the Screening Tool layers (**Table 5.1; Figure 5.1**). Of the 34 fishes included, 14 had fewer than 50 records in South Africa (**Table 5.1**). Three threatened taxa had less than 20 records, *Marcusenius caudisquamatus* (9), *Marcusenius* sp nov kosi (4) and *Silhouettea sibayi* (12) . Only two taxa had more than 500 records, *Oreochromis mossambicus* (2 873) and *Pseudobarbus* sp nov breede (540), (**Table 5.1**). Modelled taxon distribution maps (contributing to the medium sensitivity layer) and current taxon distribution maps (high sensitivity layer) were produced for all taxa classified as Vulnerable and Endangered, except for *S. sibayi*, which had no records post-2002. For Critically Endangered taxa, occurrence data were used to develop a single distribution map for each taxon (making up the very high sensitivity layer).

Example outputs are presented for two fish species, namely, *Labeo seeberi* (Endangered) and *Pseudobarbus erubescens/Sedercypris erubescens* (Critically Endangered; **Figure 5.2**), illustrating finalised occurrence data (**Figure 5.2A**; **Figure 5.2E**), SDMs derived from these data (**Figure 5.2B**; **Figure 5.2F**), and how these were used to develop the medium (**Figure 5.2C**), high (**Figure 5.2D**) and very high (**Figure 5.2G**) sensitivity layers for the DFFE Screening Tool. The final composite (combined across all taxa) national sensitivity layers (medium, high, and very high) for all threatened freshwater fishes are presented in **Figure 5.3**. The medium sensitivity layer for freshwater fish spans 49 385 km of river and covers a total area of 251 264 km^2, whilst the high sensitivity layer spans 15 162 km of river and covers an area of 117 412 km^2, with the very high sensitivity layer providing much-needed protection for Critically Endangered freshwater taxa spanning 1024 km of river and covering a total area of 5 992 km^2. Individual taxon maps for all threatened species included in this study are available in **Supplementary S5.4**.

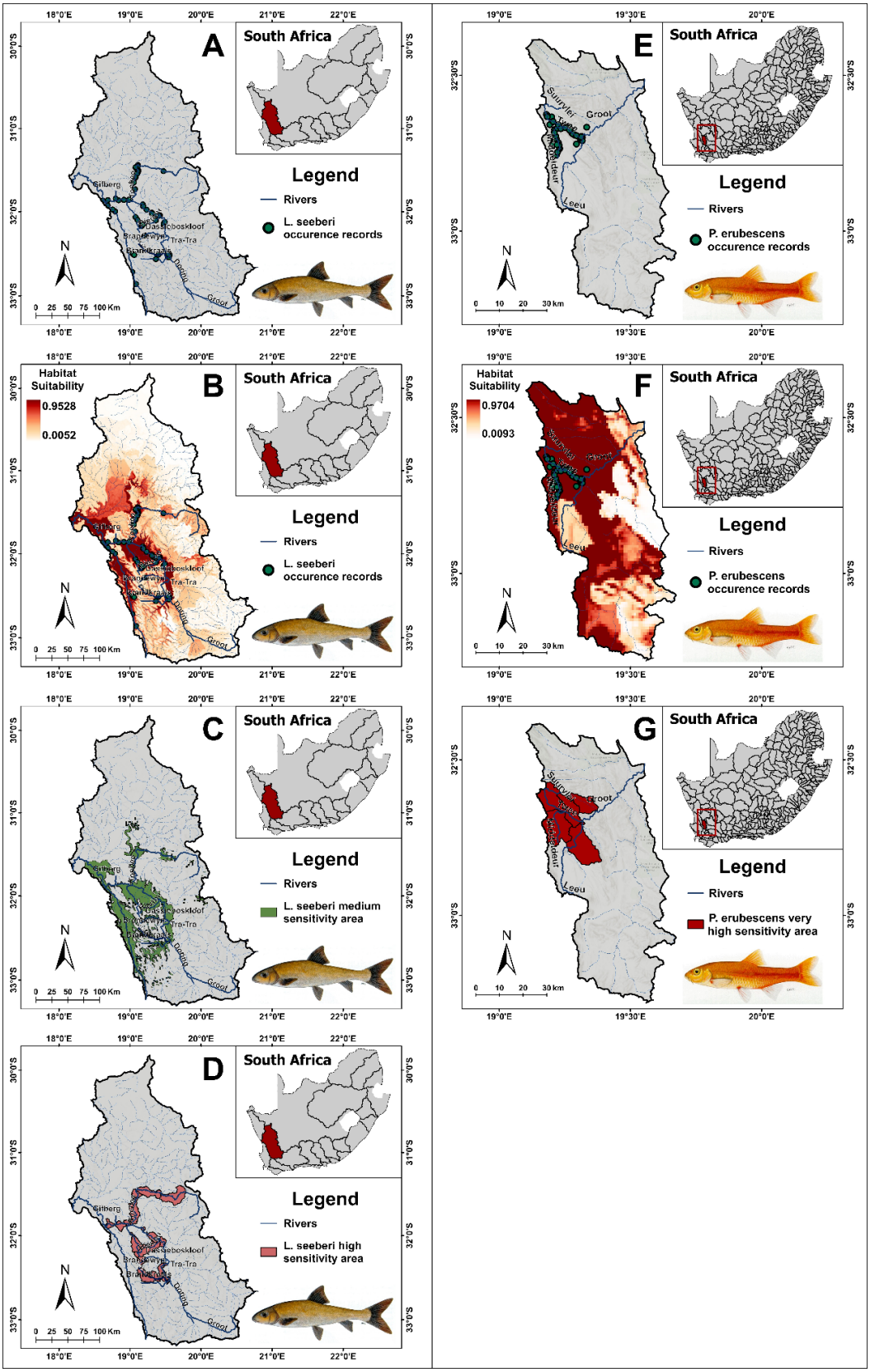


Figure 5. 2. *Labeo seeberi* occurrence records (A), species distribution model (B), medium sensitivity area (C) and high sensitivity area (D) located in the Olifants-Doring primary catchment area of South Africa. *Pseudobarbus erubescens/Sedercypris erubescens* occurrence records (E), species distribution model (F), and very high sensitivity area (G) located in tertiary catchment E21.

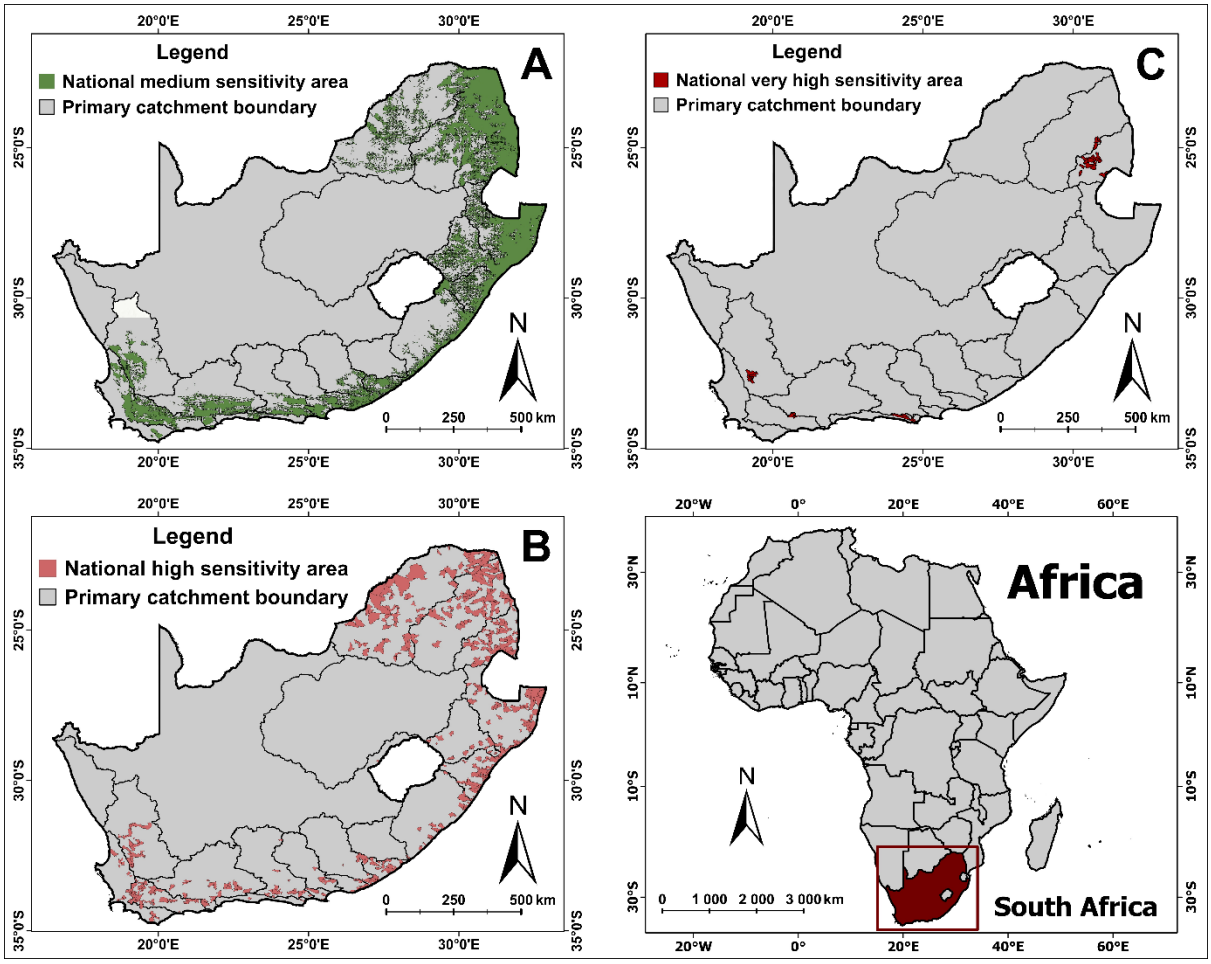


Figure 5. 3. Sensitivity layers for freshwater fishes included in the Department of Forestry, Fisheries and Environment (DFFE) Screening Tool showing medium sensitivity area coverage (A), high sensitivity area coverage (B), and very high sensitivity area coverage (C) across South Africa (D).

5.4. Discussion

This chapter presents the first inclusion of freshwater species coverage in a key national conservation decision-support tool – the NEST - and describes how data from the FBIS were used as the basis for threatened fish sensitivity layers (core elements of the tool) through a multi-stakeholder, collaborative approach (**Supplementary Table S5.2 and S5.3**). Sensitivity layers were successfully developed for 34 threatened freshwater fishes occurring in South Africa. Given that the majority of South Africa's rivers are either poorly protected or not protected (Department of Environmental Affairs, 2016), the updated coverage of freshwater fishes in the Screening Tool should provide much-needed protection for the country's threatened freshwater fishes by preventing or minimising further habitat loss and degradation due to new developments. This will support conservation efforts to halt population declines and reduce extinction risk of these species, especially in locations where threatened taxa occur outside of formal protected areas (Impson et al., 2002; Nel et al., 2004; Abell et al., 2007; Russell, 2011; Jordaan et al., 2020). In addition to the conservation and policy benefits, the distribution maps produced for the medium, high and very high

layers can also help guide the expansion of protected areas and stewardship initiatives and be used in future national biodiversity assessments and in IUCN Red List assessments.

The FBIS supported the development of freshwater fish sensitivity layers through providing quick and easy access to reliable and comprehensive freshwater fish data for South Africa. The relatively large number of records provided is especially noteworthy given that most distribution modelling and mapping of threatened taxa are heavily hampered by limited access to occurrence records (Stockwell and Peterson, 2002; Wisz et al., 2008). Furthermore, the inclusion of various taxon specialists, government organisations and conservation authorities (**Supplementary Table S5.1**) via multiple online workshops was extremely beneficial, ensuring that the final occurrence dataset was cleaned efficiently and included only high-quality, high-certainty records. Additionally, given that the IUCN Red List assessments were done by several scientists, with specialist knowledge relevant to each individual species, including these experts in the development process was imperative.

The inclusion of a freshwater fish component to the Screening Tool provides an additional area of coverage of 251 264 km^2 for the medium sensitivity layer, 117 412 km^2 for the high layer and 5992 km^2 for the very high layer. Given that the majority of South Africa's rivers are either poorly protected or not protected (Department of Environmental Affairs, 2016), the updated coverage of freshwater fishes in the Screening Tool should provide much-needed protection for the country's threatened freshwater fishes. This is especially important in locations where threatened taxa do not occur within the formal protected area network of South Africa (Impson et al., 2002; Nel et al., 2004; Abell et al., 2007; Russell, 2011; Jordaan et al., 2020) and are vulnerable to anthropogenic impacts on rivers and associated catchments. The identification of these areas in the EIA process will provide benefits for other native freshwater species co-occurring in these habitats.

Understandably, there were some limitations encountered whilst developing the NEST sensitivity layers. Firstly, there were 14 taxa with fewer than 50 records in South Africa, with three taxa having less than 20 records each (**Table 5.1**). Data scarcity increased the difficulty of producing accurate SDMs (Stockwell and Peterson, 2002; Wisz et al., 2008) potentially reducing the accuracy of the sensitivity layers for data-scarce taxa. This highlights the urgent need to increase threatened species monitoring efforts at both provincial and national levels (Chakona et al., 2022). It is recommended, based on their low numbers of recent records, that the following taxa be considered as a very high priority for baseline data collection and monitoring: *Chetia brevis*, *Ctenopoma multispine*, *Enteromius treurensis*, *Kneria* sp. nov. south africa, *Labeo rubromaculatus*, *Marcusenius caudisquamatus*, *Marcusenius* sp. nov. kosi, *Pseudobarbus senticeps*, *Pseudobarbus skeltoni, Pseudobarbus* sp. nov. doring, *Pseudobarbus* sp. nov. keiskamma, *Pseudobarbus* sp. nov. keurbooms, *Amatolacypris trevelyani, and Silhouettea sibayi*. In this regard, a standardised sampling protocol for freshwater fishes is currently under development.

Secondly, the NEST sensitivity layers are only restricted to the modelled and current distribution of threatened taxa. Several studies have highlighted the importance of ensuring that catchment-level impacts (Skelton et al., 1995; Kleynhans, 2000; Nel et al., 2004; Abell et al., 2007), specifically upstream-impacts of anthropogenic activities, also be considered when developing protected areas for freshwater systems. The current iteration of the freshwater fish component of the NEST does not fully account for this, providing protection for threatened taxa at the sub-quaternary catchment level only. Future iterations of the tool should consider ways to provide upstream protection at a larger catchment scale. Lastly, the overall success in terms of functionally providing protection to South Africa's threatened freshwater fishes will be dependent on local government authorities correctly and competently interpreting the outputs of the NEST and making responsible land-use change decisions by preventing developments where the risk to threatened taxa are deemed to be too high.

The freshwater fish component of the NEST provides a first step towards adequately incorporating threatened freshwater taxa into the EIA and development application process. However, there are additional steps that could improve upon and update the tool, thereby supporting more effective freshwater conservation in the future. Firstly, there is an urgent need to update and resolve the taxonomy of South Africa's freshwater fishes, as there are a number of distinct genetic lineages that await formal description (Chakona, et al., 2015; Bronaugh et al., 2020; Chakona et al., 2020; Ramoejane et al., 2021). More recent studies have also resulted in the redescription and/or the revalidation of several new species (Martin and Chakona, 2019; Kambikambi et al., 2021; Mazungula and Chakona, 2021). Once the taxonomy of South Africa's freshwater fishes has been resolved and updated, the FBIS and the NEST can be updated accordingly. Secondly, given that the process for developing sensitivity layers for freshwater taxa has now been established, this can easily be replicated for other species groups, such as freshwater invertebrates. Although anurans are already included in the NEST (SANBI, 2021), there is also the potential to use the FBIS and the methodology developed here to improve upon these sensitivity layers. Lastly, the mapping processes used for threatened species should be repeated for non-native freshwater species (specifically invasives) occurring in South Africa. The long-term survival of threatened fishes will not only rely on improved protection of important habitats, but also on accurate information of the distribution and impact of invasive alien species – a top threat to South Africa's native freshwater fishes (Weyl et al., 2020; Zengeya and Wilson, 2020; Chakona et al., 2022). Worryingly, the distributions for many of the country's non-native species are not well known, and a lack of spatial data is holding back reliable system-wide invasive species assessments (De Moor, 1996; Ellender and Weyl, 2014; Zengeya and Wilson, 2020). Although mapping non-native species distributions falls beyond the scope of the NEST, this could provide insights into non-native species impacts on native taxa and assist with identifying key areas for protection and for alien species management interventions (Weyl et al., 2020). Actioning these next steps will amplify the impact that the NEST may have on preventing further population declines in South Africa's freshwater fish fauna.

This case study demonstrates how information systems like the FBIS that provide open access to reliable biodiversity data can play a pivotal role in the data-to-decision pipeline through supporting data-driven conservation and management decisions at a national level. Despite some limitations, the final sensitivity layers produced for the Screening Tool NEST should have far reaching and long-lasting impacts for the improved conservation of South Africa's threatened freshwater fish populations.

Chapter 6

6. Synthesis and Conclusions

6.1. Introduction

Globally, freshwater ecosystems – and the organisms that rely on these habitats to survive – are under immense pressure from various anthropogenic stressors (Tickner et al., 2020; WWF, 2020; Hughes et al., 2021). Despite covering less than 1% of the earth's surface, these habitats account for nearly 10% of all described animal species and more than half of all fish diversity (Hughes et al., 2021; Fricke et al., 2022). Furthermore, the levels of endemism among freshwater species are notably high compared to marine and terrestrial habitats, with more than half of the fish species assessed for the ecoregions of the world found in a single ecoregion (Tickner et al., 2020). In addition to their importance for biodiversity, freshwater ecosystems are also inextricably linked to human survival, providing important services, such as drinking water, irrigation, and as a source of protein (Hughes et al., 2021). However, despite their importance and the severity of the threats that freshwater habitats face, the management, protection, and conservation of these habitats are often neglected by policymakers and conservation managers (Tickner et al., 2020; Hughes et al., 2021). Consequently, the rate of freshwater habitat loss and associated biodiversity is occurring faster than in marine and terrestrial habitats (Tickner et al., 2020), with 27% of freshwater dependant species listed as threatened according to the IUCN Red List (Tickner et al., 2020).

In South Africa, freshwater fishes are the country's most threatened species group, with almost half of all assessed species listed as threatened in the IUCN Red List (Skowno et al., 2019). These species face several anthropogenic threats that have resulted in declines in both their abundance and diversity (Dudgeon et al., 2006; Geist, 2011), including pressures from land-use change (O'brien et al., 2019; Chakona et al., 2020), pollution (Wepener et al., 2011; Horak et al., 2021), excessive abstraction of water (Dallas and Rivers-Moore, 2014; Cerrilla et al., 2022; Evans et al., 2022), spread of invasive species (Van Rensburg et al., 2011; Ellender and Weyl, 2014; Zengeya et al., 2020; Cerrilla et al., 2022) and climate change (Dallas and Rivers-Moore, 2014; Ziervogel et al., 2014; Niang et al., 2017). Consequently, there is increasing awareness and growing recognition of the need to monitor freshwater fish populations, to develop up-to-date conservation plans, and to formulate policies that can guide effective management and protection of freshwater fishes in South Africa. It is thus critical that trends in diversity, distribution, threat status, and protection status of freshwater fishes in South Africa are comprehensively assessed to support management approaches and conservation action.

However, despite the rich history and well-established freshwater fish research infrastructure in South Africa, to date there has been limited consolidation and sharing of knowledge and data on a national scale. Having these data easily accessible to all freshwater stakeholders is of extreme importance and can provide immense benefit in

terms of biodiversity planning, conservation management, and policy making. Long-term distributional data for freshwater fish species can be vital for detecting critical ecosystem changes, such as species range shifts, new records of non-native invasions and loss of ecosystem services or unique biodiversity (Dallas et al., 2022). Understanding exactly how the abundance and distribution of freshwater fishes (both native and non-native) are changing in space and time is pivotal to effectively manage and conserve our unique and threatened freshwater biodiversity and ecosystems. These types of assessments will result in the production of 'actionable' data products and information important for all freshwater stakeholders. Not being able to effectively observe, record and track critical ecosystem changes can have serious implications for our ability to manage this resource effectively and sustainably.

To provide a much-needed update on the state of knowledge of South Africa's freshwater fish fauna, this thesis collected and consolidated historic freshwater biodiversity data for all primary and secondary freshwater fish species known to occur in the country. Furthermore, it sought to analyse these data to understand broadscale diversity patterns in key response areas, such as threat status, endemism, and invasion, while also presenting a statistically robust and repeatable methodology for modelling the distributions of South Africa's freshwater fishes. Finally, this thesis aimed to demonstrate how access to reliable freshwater biodiversity data and improved geospatial information can contribute to improved policy making and conservation management of freshwater fishes in the country.

Here, the main findings are summarised and important recommendations for future research are put forth.

6.2. The consolidation of historic biodiversity data provides a much-needed update to the state of knowledge of freshwater fishes in South Africa.

In Chapter 2, the primary aims were to collect, collate, and consolidate historic and current data for freshwater fishes known to occur in South Africa, and to use these data to provide an updated, comprehensive review of the status and distribution of these species. This chapter presents the most comprehensive effort to date to harmonise biodiversity data for freshwater fishes in South Africa. A thorough and systematic data search resulted in the accrual of 60 837 freshwater fish occurrence records, which were sourced from peer-reviewed articles, published reports, university theses, databases, and unpublished data. All data are now publicly available on the Freshwater Biodiversity Information System (FBIS), where they can easily be accessed, visualised, and freely downloaded. The dataset presents the largest (by number of records) collection of online freshwater fish records in Africa, with data spanning 194 years and covering 129 formally described species. This dataset enables new insights into trajectories of change in South Africa's freshwater fishes and an opportunity for a more data-driven approach to freshwater fish management in the country.

This thesis also presents South Africa's first comprehensive species list for freshwater fishes, which includes all known native (n = 107) and non-native (n = 27) species

occurring in the country. This list was established using a data-driven approach combined with extensive expert consultation, representing countless hours of work spread over several years. In general, species diversity was found to be relatively low in most parts of the country. However, endemism rates were high, with 31% of native species endemic. Similarly, the percentage of threatened species was high, with 19% of native species currently categorized as threatened (Vulnerable, Endangered, or Critically Endangered), the highest rate of threat of any species group in South Africa (Skowno et al., 2019). These findings will no doubt provide much-needed updates on the status of South Africa's freshwater fish fauna and contribute to future scientific research and conservation efforts in the country, and to management and conservation tools, such as the IUCN Red List assessments and the NBA report.

6.3. Spatial analyses of patterns of diversity, threat, invasion, and protection of South Africa's freshwater fishes reveal uneven distribution of records and a strong correlation between endemism, threat, and non-native hotspots.

Chapter 3 aimed to use historic to present-day freshwater fish data currently available on the FBIS database, to assess spatial patterns of distribution, diversity, and threat status in South Africa at provincial and primary catchment scales. Additionally, this chapter sought to assess how well South Africa's protected area network protects threatened species and fish diversity hotspots. It was hypothesized, based on prior research, that South Africa's current protected area network does not provide adequate protection for all of the country's threatened freshwater fishes.

Spatial analyses indicated that occurrence records for SA freshwater fish were unevenly distributed across the country at both national, provincial, and catchment scales. Areas with relatively low density of occurrences were identified in the Orange, Vaal, and Buffels Primary Catchments, with the vast majority of QDS grid cells containing low numbers of records. Native species richness followed a similar pattern to the density of records. Species richness hotspots were identified in Mpumalanga, Limpopo, and northern KwaZulu-Natal (corresponding with the Limpopo, Olifants, Komati, and Mfolozi Primary Catchments), with areas of relatively high species richness (10–15 species per QDS grid cell) identified along the east coast of KwaZulu-Natal (Tugela and Mkomazi Primary Catchments) and in a small cluster in the Western Cape (along the Berg-Olifants/Doring Primary Catchment boundary). The Western Cape was also found to have the highest level of endemic species richness, threatened species, and non-native species in South Africa. These findings are congruent with previously published assessments of South Africa's freshwater fish diversity (Skelton et al., 1995; Chakona et al., 2013; Chakona et al., 2022). However, having these diversity patterns based on reliable data allows for more effective conservation management decisions and policymaking at national, provincial, and catchment scales. These findings provide a much-needed snapshot into the most important geographic areas for freshwater fishes, highlighting specific regions where species richness is particularly high and areas that contain relatively high numbers of threatened species. Consequently, these findings can (and indeed should) inform both

broadscale and targeted conservation interventions aimed at reducing the rate of population decline observed in many of South Africa's freshwater fish species.

Also presented is the first, national-level assessment of how well South Africa's protected area network protects freshwater fishes. It was found that South Africa's protected area network (Department of Forestry Fisheries and the Environment, 2023a, b) does not adequately cover the distributions of threatened species in the country. Concerningly, only 36% of the total area occupied by threatened species occurred within formally protected areas, the majority of which were also invaded by non-native species. These findings add further evidence to the growing body of research that considers South Africa's protected area network to provide inadequate protection for sensitive freshwater species (Kleynhans, 2000; Nel et al., 2004; Abell et al., 2007, Nel et al., 2009; Russel, 2011; Jordaan et al., 2020). As such, the findings presented in Chapter 3 provide the foundation upon which future assessments of the effectiveness of South Africa's protected areas could be based. Additionally, these findings also have the potential to guide future expansion of the country's protected area network, as laid out in The National Protected Area Expansion Strategy (NPAES, 2016; Republic of South Africa, 2010; Department of Environmental Affairs, 2016), which need to consider the linear nature of river systems and the impacts of upstream disturbances on fish populations located in protected areas further downstream (Impson et al., 2002; Jordaan et al., 2020). This underscores the need for a re-evaluation of protected area management strategies, with a focus on incorporating freshwater fish conservation needs into future planning efforts.

6.4. The development of a stepwise and statistically robust methodology for developing species distribution models (SDMs) improved access to accurate distribution information for freshwater fishes in South Africa.

Chapter 4 presented South Africa's first freely-accessible, robust, and repeatable method for applying SDMs to freshwater species. This will allow for the rapid modelling of other freshwater species for various purposes moving forward. Potential applications include interpolation, diversity assessments, community interaction studies, and anthropogenic impact assessments, whilst also improving access to national environmental, hydrological, and biological spatial datasets. In this regard, this thesis has resulted in the successful development of 148 hydrological spatial layers and the collation of 75 environmental spatial layers. This chapter also hypothesized that the inclusion of invasive species' distributions would result in improved model performance and more accurate predicted distributions. Model outputs indicated that both model performance and model accuracy were not improved by including biological predictor variables, with both the AUC (0.994 vs 0.993) and TSS (0.940 vs 0.921) values being higher when only including environmental and hydrological predictor variables. This finding, although preliminary in nature, indicates that the inclusion of biological predictors may not be necessary to produce accurate predicted species' distributions.

The combined outputs of this thesis (presented in Chapters 2 through 4) were then used to develop accurate species distribution spatial layers as well as SDMs for all

known threatened species, as presented in Chapter 5. This allowed for species' distributions to be more accurately, effectively, and efficiently mapped and modelled using empirical data, rather than distributions based on anecdotal reports from experts. Consequently, modelled distribution maps have been developed for all 34 threatened taxa occurring in South Africa, as well as for all 16 taxa listed as invasive. These outputs address an established knowledge gap (Chakona et al., 2022) and serve as a valuable contribution to the field by improving our understanding of the distribution patterns of important fish species in South Africa. The methodology holds significant value for future research and conservation efforts, enabling the identification of potential habitat suitability for priority species, the prediction of potential impacts from environmental change, and providing much needed data required to inform future protected area expansion planning. Having access to this sort of data, and the associated improved access to reliable and accurate distribution information, will deepen our understanding of changes in species distributions. This is critical for conservation and management decisions and policy making, especially in light of South Africa's limited capacity to physically sample and monitor fish populations (Chakona et al., 2022).

6.5. Implications for freshwater fish conservation

Since the onset of the industrial revolution, the global spread of colonialism, and the consequent establishment of capitalism, anthropogenic activities have increasingly degraded and destroyed natural ecosystems. Since the start of the 20th century, 75% of terrestrial surface area has been significantly altered, the majority of the oceans are polluted, and more than 85% of wetlands and 30% of freshwater habitats have been lost (Tickner et al., 2020; WWF, 2020). In the last 50 years alone, the Global Living Planet Index has shown a 68% decrease in the population size of mammals, birds, reptiles, amphibians, and fish (Hughes et al., 2021). Currently, approximately 1 million species are threatened with extinction (WWF, 2020), with many experts agreeing that we have entered the sixth major mass extinction event (Rampino and Shen, 2021). Globally, nearly one-third of freshwater fish species are threatened with extinction (Hughes et al., 2021;), with large-bodied and migratory species declining between 76–94% since the 1970's (Tickner et a., 2020; Hughes et al., 2021). However, despite their importance and the rapid rates of extinction, freshwater habitats are often not prioritised when making conservation, management, and development decisions (Tickner et al., 2020; Hughes et al., 2021). Freshwater habitats continue to be valued primarily as water pipes for cities (Hughes et al., 2021), and managed as macroeconomic systems that serve human needs (Tickner et al., 2020).

In South Africa, recent studies have concluded that the country's protected area network is severely lacking in terms of adequately conserving freshwater ecosystems and their associated species (Impson et al., 2002; Nel et al., 2004; Abell et al., 2007; Nel et al., 2009; Russel, 2011; Jordaan et al., 2020). As such, there is an urgent need to prioritize the restoration and protection of freshwater habitats to slow the decline of freshwater populations and prevent mass species extinctions.

The successful development of a comprehensive freshwater fish database along with a national assessment of the state of knowledge of South Africa's freshwater fishes will allow for improved conservation planning and management. Having access to accurate information on fish diversity, endemism, threat status, and presence of non-native species at national, provincial, and catchment scales means that national government, provincial conservation authorities, and catchment managers are now better equipped to manage and conserve freshwater fish populations. These findings hold substantial value for future monitoring, management, and conservation efforts, enabling the identification of hotspots of diversity, endemism, invasion, and threat. In this regard, the development of accurate distribution layers at sub-quaternary catchment scale and modelled distribution for all threatened freshwater fishes will be particularly useful for researchers, conservation managers, and policy makers. Similarly, the development of modelled distributions for all invasive species occurring in South Africa will aid in the management of these species and in the assessment of their impacts on native populations across the country.

It is important to highlight that while some hotspots of species richness, endemism, and threatened species do overlap with protected areas, many remain inadequately protected. This thesis also found that a substantial portion of threatened species distributions (43%) fall outside of protected areas, indicating inadequate coverage by the current protected area network. Additionally, 38% of protected areas also have non-native species present, posing a further threat to threatened fish populations within these protected areas. Thus, it is important that South Africa's protected area network is expanded, to ensure adequate coverage of critical habitats (including consideration of upstream impacts) for threatened species along with proactive monitoring and management plans that address the issue of invasive species.

In this regard, the inclusion of threatened freshwater fish into the DFFE NEST provided species-specific conservation consideration for 34 taxa covering an area of 251 264 km^2. This provides much-needed protection for the country's threatened freshwater fishes, especially in locations where these taxa do not occur within the formal protected area network. Furthermore, the SDMs developed for this thesis also provide much needed information on where both threatened and invasive species can occur, highlighting potential future habitats that may be invaded. These SDM outputs can be used to prioritize conservation efforts, identify areas for protected area expansion, and guide the development of effective management strategies for threatened and invasive species.

Overall, this thesis has made significant contributions to understanding and conserving freshwater fishes in South Africa. The established database, modelling framework, and data integration with NEST provide valuable tools for future research and conservation efforts. The inclusion of freshwater fish data ensures that these impacts are more comprehensively evaluated, leading to more informed decisions that balance development needs with biodiversity conservation.

6.6. Recommendations for future research

By constructing a national freshwater fish database and employing a suite of analyses, this thesis provides a much-needed update the current state of South Africa's freshwater fish fauna and provides valuable tools for future research and conservation efforts. The potential for additional research projects, based off this database, are substantial. However, the most important next steps are briefly summarised below.

6.6.1. Taxonomy

There is an urgent need to update and resolve the taxonomy of South Africa's freshwater fishes, as there are a number of distinct genetic lineages that await formal description (Chakona, et al., 2015; Bronaugh et al., 2020; Chakona et al., 2020; Ramoejane et al., 2021). More recent studies have also resulted in the redescription and/or the revalidation of several new species (Martin and Chakona, 2019; Kambikambi et al., 2021; Mazungula and Chakona, 2021). Once the taxonomy of South Africa's freshwater fishes has been resolved and updated, the freshwater fish species list and the FBIS fish database can also be updated. The first step in this process should focus on updating the species list presented in this thesis to include all potential lineage taxa and all marine peripheral and marine sporadic species. These updates would then need to be transposed to other important management outputs, for example, the NEST layer for freshwater fishes (presented in Chapter 5) and require additional analyses identifying hotspots of endemism, threat, and richness (as presented in Chapter 3). Another important point to consider is that fully resolving the taxonomy of South Africa's freshwater fishes will take substantial time and effort. In some instances, formally describing all of the taxa contained within some of these species suites may take many years, despite the fact that taxonomists already know that these are definitely distinct species. As such, it is important to improve lines of communication between taxonomists and management bodies, to ensure that appropriate considerations for newly described species are incorporated into planning, management, and decision making in a proactive manner.

6.6.2. Spatio-temporal analyses and monitoring

There is scope to undertake additional analyses to gain new insights about the distributions of freshwater fishes and their associated drivers. This will require additional, thorough cleaning of the dataset prior to analysis – a process that would need to be driven by experts from across the country. At a national level, the country would benefit immensely from workshops and training programmes to build capacity for cleaning and analysing biodiversity data. Importantly, it is recommended substantial investment be made to allow for the cleaning of data for all species that that have not yet been scrutinised by experts, as was done for threatened species included in the NEST presented in Chapter 3. Additionally, it is recommended that specific focus be placed on identifying sampling bias contained within the current dataset (such as the correlation and aggregation of records around anthropogenic features, such as human settlements, road networks, and research institutions), assessment of sampling effort at species level, and identifying potential data gaps. Where data gaps are identified, it is important that these areas be flagged, so that they

may be prioritised for ground-truthing through a concerted sampling effort. Additionally, there is scope to interrogate that dataset temporally to identify patterns of change at relevant temporal intervals. This could potentially shed light on how species populations have changed over time in response to increasing anthropogenic pressures and the introduction of non-native species. There is also scope to conduct detailed analyses of the fish composition characterising each catchment, as was done by Khosa et al. (2023) in the Kowie Catchment.

Additionally, there is a need to quantify the impacts of non-native species on threatened native species within protected areas. Findings from this thesis indicate that there is a large overlap between the distribution of threatened and non-native species, especially within protected areas. However, this serves only as a first step towards understanding the relationships and impacts of non-native invasions on native populations. Future studies could use SSDMs or JSDMs to quantify the relation between native and non-native species, while focus should also be given towards understanding how the introduction of non-native species in South African structures impacts community structure and similarity over time.

Separately, this thesis also provided extremely valuable analyses, identifying data gaps in fish records in various parts of the country. As such, future research should prioritise systematically sampling river systems (especially within protected areas) and developing strategic long-term monitoring programmes to shed light on how native populations are changing and the extent and magnitude of the presence of non-native species in these areas. There is also an immediate and urgent need to undertake a national study on the current invasion of C. gariepinus into catchments where it historically did not occur. This is especially important given the shortage of capacity for monitoring freshwater fish populations in South Africa (Impson, 2016).

6.6.3. Species distribution modelling

The modelling methodology and associated DFFE NEST sensitivity layers developed in this thesis open up the opportunity for numerous research projects that will improve the reliability and accuracy of SDMs for freshwater taxa. Various studies (Norberg et al., 2019; Srivastava et al., 2019; Hao et al., 2020; Valavi et al., 2022) have found that different modelling algorithms performed well in some habitats and poorly in others. Additionally, there is growing evidence to suggest that ensemble models can produce more accurate outputs than any single modelling algorithms (Thuiller et al., 2009; Hao et al., 2019, 2020). As such, it is recommended that this sort of ensemble modelling approach be investigated as an important next step to improve upon the modelling workflow presented. There is also potential to apply these SDMs to other important freshwater species groups, such as invertebrates, plants, and frogs.

6.6.4. Data-based hypothesis testing

Given that the data accumulated for this thesis presents a rare example of a database not from North American rivers, these is substantial opportunity to use the dataset for meta-ecology hypothesis testing specifically dealing with ecological and invasion

theoretical frameworks. For example, there is scope for the dataset to be used to assess population or community trends in different catchments or rivers, broadening the representation of existing indicators of the status of global biodiversity and drivers of biodiversity changes in freshwater systems. Additionally, these data could also be integrated into ecological models and used to forecast how fish communities will respond to future environmental change, paving the way for better management. Furthermore, the FBIS dataset could also offer new insights into how fish invasions spread over time and what the impacts of these invasions have been on the community structure of natives fishes.

6.7. Conclusions

In summary, the research presented in this thesis represents the most comprehensive harmonisation of biodiversity data to date for all formally described freshwater fishes occurring in South Africa. This thesis presents the first comprehensive, data-driven assessment of the status of South Africa's freshwater fish fauna, providing valuable insights into spatial patterns of richness, endemism, threat status, and non-native species, as well as assessing how effective the country's protected area network is for protecting freshwater fishes. These findings have important applications for conservation and management, providing an important baseline for future research and monitoring efforts. The development of a robust and repeatable methodology for modelling freshwater fish distributions allows for the prediction of current species distributions based on historical data, climate variables, and hydrological information. The modelling workflow presented holds considerable value for identifying potentially suitable habitat for species of conservation concern and for assessing potential impacts of environmental change. Importantly, this workflow allows for the rapid development of SDMs for all freshwater fishes, but can also be applied to any freshwater species, where appropriate occurrence data are available. Finally, the thesis demonstrated the importance of collating historic biodiversity data and being able to accurately map and model species' distributions. In this regard, this thesis was not only able to contribute data and published research outputs to the field of freshwater science, but also improve drive data-driven conservation planning on a national scale at government level (through the development of the DFFE NEST). Consequently, this thesis has provided scientific outputs that will result in more informed biodiversity management and conservation decisions and contribute towards much-needed protection for South Africa's most threatened species group. This highlights the importance of incorporating applied conservation elements within traditional scientific research that is normally the focus of PhD research. Although this thesis addressed the critical need for comprehensive biodiversity information for freshwater fishes in South Africa, its greatest value is to provide a platform upon which further research can be based, improving decision-making in conservation, and our understanding of and ability to track fish population changes in response to global change.

Chapter 7

7. References

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Supplementary S1

Table S. 1.1 Published records of localised, native freshwater fish population extinctions occurring in South Africa.

#	Species	Location	Cause	Citation	Source
1	*Amatolacypris trevelyani*	Rooikrantz River	Trout invasion	Cambray, 2003.	https://doi.org/10.2989/16085914.2003.9626601
2	*Labeo seeberi*	Olifants/Doring Rivers	Non-native invasions	Cerrilla, 2020.	http://hdl.handle.net/11427/32205
3	*Pseudobarbus afer*	Swartkops River	*M. salmoides* and *M. dolomieu* predation	Ellender et al. 2018.	https://doi.org/10.1111/jfb.13562
4	*Pseudobarbus andrewi*	Berg river	Non-native invasions	Woodford and Impson, 2004.	https://doi.org/10.2989/16085910409503799
5	*Pseudobarbus andrewi*	Berg river	Non-native invasions	Clark et al., 2009.	https://doi.org/10.1080/00359190909519249
6	*Pseudobarbus burgi*	Eerste River	Non-native invasions	Schmidt et al., 2017.	https://doi.org/10.1002/aqc.2851
7	*Pseudobarbus capensis*	Berg River	Non-native invasions	Chakona et al., 2017.	https://doi.org/10.1002/aqc.2850
8	*Pseudobarbus quathlambae*	Umkomazana River	*S. trutta* and habitat degradation	Cambray, 2003.	https://doi.org/10.2989/16085914.2003.9626601
9	*Pseudobarbus quathlambae*	Mkomazana Rive	Non-native invasions	Quintela-Alonso et al., 2017.	https://doi.org/10.1002/aqc.2852
10	*Pseudobarbus serra*	Olifants/Doring	Non-native invasions	Impson, 2007.	https://www.wrc.org.za/wp-content/uploads/mdocs/KV212-web-conservation.pdf#page=27
11	*Sandelia bainsii*	Fish River	*Clarias gariepinus* translocation	Cambray, 1997.	https://doi.org/10.1023/A:1018300104631

Supplementary S2

Table S.2.1. Preliminary Master Species List for Freshwater Fishes in South Africa

Kingdom	Phylum	Class	Order	Family	Genus	Species	Taxon	Scientific name and authority	Common name	Tolerance
Animalia	Chordata	Actinopterygii	Perciformes	Sparidae	Acanthopagrus	berda	*Acanthopagrus berda*	Acanthopagrus berda (Forsskål, 1775)	Picnic seabream	M
Animalia	Chordata	Actinopterygii	Perciformes	Ambassidae	Ambassis	ambassis	*Ambassis ambassis*	Ambassis ambassis (Lacepède, 1802)	Longspine glassy	M
Animalia	Chordata	Actinopterygii	Perciformes	Ambassidae	Ambassis	dussumieri	*Ambassis dussumieri*	Ambassis dussumieri Cuvier, 1828	Bald glassy	M
Animalia	Chordata	Actinopterygii	Perciformes	Ambassidae	Ambassis	natalensis	*Ambassis natalensis*	Ambassis natalensis Gilchrist & Thompson, 1908	Slender glassy	1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Amphilius	laticaudatus	*Amphilius laticaudatus*	Amphilius laticaudatus Skelton, 1984	Broadtail mountain catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Amphilius	natalensis	*Amphilius natalensis*	Amphilius natalensis Boulenger, 1917	Natal mountain catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Amphilius	uranoscopus	*Amphilius uranoscopus*	Amphilius uranoscopus (Pfeffer, 1889)	Stargazer mountain catfish	1
Animalia	Chordata	Actinopterygii	Anguilliformes	Anguillidae	Anguilla	bengalensis	*Anguilla bengalensis*	Anguilla bengalensis (Gray, 1831)	Indian mottled eel	D
Animalia	Chordata	Actinopterygii	Anguilliformes	Anguillidae	Anguilla	bicolor	*Anguilla bicolor*	Anguilla bicolor McClelland, 1844	Shortfin eel	D
Animalia	Chordata	Actinopterygii	Anguilliformes	Anguillidae	Anguilla	marmorata	*Anguilla marmorata*	Anguilla marmorata Quoy & Gaimard 1824	Giant mottled eel	D
Animalia	Chordata	Actinopterygii	Anguilliformes	Anguillidae	Anguilla	mossambica	*Anguilla mossambica*	Anguilla mossambica (Peters, 1852)	African longfin eel	D
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Astatotilapia	calliptera	*Astatotilapia calliptera*	Astatotilapia calliptera (Günther, 1893)	Eastern river bream	2
Animalia	Chordata	Actinopterygii	Characiformes	Hepsetidae	Astyanax	orthodus	*Astyanax orthodus*	Astyanax orthodus Eigenmann, 1907		1
Animalia	Chordata	Actinopterygii	Atheriniformes	Atherinidae	Atherina	breviceps	*Atherina breviceps*	Atherina breviceps Valenciennes, 1835	Cape silverside	M
Animalia	Chordata	Actinopterygii	Atheriniformes	Atherinidae	Atherinomorus	lacunosus	*Atherinomorus lacunosus*	Atherinomorus lacunosus (Forster, 1801)	Hardyhead silverside	M
Animalia	Chordata	Actinopterygii	Siluriformes	Austroglanididae	Austroglanis	barnardi	*Austroglanis barnardi*	Austroglanis barnardi (Skelton, 1981)	Barnard's rock catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Austroglanididae	Austroglanis	gilli	*Austroglanis gilli*	Austroglanis gilli (Barnard, 1943)	Clanwilliam rock catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Austroglanididae	Austroglanis	sclateri	*Austroglanis sclateri*	Austroglanis sclateri (Boulenger, 1901)	Rock catfish	1
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Awaous	aeneofuscus	*Awaous aeneofuscus*	Awaous aeneofuscus (Peters, 1852)	Freshwater goby	M
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Awaous	lateristriga	*Awaous lateristriga*	Awaous lateristriga (Peters, 1876)	Brown goby	M
Animalia	Chordata	Actinopterygii	Perciformes	Eleotridae	Dormitator	lebretonis	*Dormitator lebretonis*	Batanga lebretonis (Steindachner, 1870)	Deep sleeper	M
Animalia	Chordata	Actinopterygii	Characiformes	Characidae	Brycinus	imberi	*Brycinus imberi*	Brycinus imberi (Peters, 1852)	Imberi	1
Animalia	Chordata	Actinopterygii	Characiformes	Characidae	Brycinus	lateralis	*Brycinus lateralis*	Brycinus lateralis (Boulenger, 1900)	Astriped robber	1
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Caffrogobius	gilchristi	*Caffrogobius gilchristi*	Caffrogobius gilchristi (Boulenger, 1898)	Prison goby	M
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Carassius	auratus	*Carassius auratus*	Carassius auratus (Linnaeus, 1758)	Goldfish	1
Animalia	Chordata	Chondrichthyes	Carcharhiniformes	Carcharhinidae	Carcharhinus	leucas	*Carcharhinus leucas*	Carcharhinus leucas (Valenciennes, 1839)	Bull shark	M
Animalia	Chordata	Actinopterygii	Scorpaeniformes	Triglidae	Chelidonichthys	kumu	*Chelidonichthys kumu*	Chelidonichthys kumu (Cuvier, 1829)	Bluefin gurnard	M
Animalia	Chordata	Actinopterygii	Mugiliformes	Mugilidae	Chelon	richardsonii	*Chelon richardsonii*	Chelon richardsonii (Smith, 1846)	South African mullet	M
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Chetia	brevicauda	*Chetia brevicauda*	Chetia brevicauda Bills and Weyl, 2002		2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Chetia	brevis	*Chetia brevis*	Chetia brevis Jubb, 1968	Orange-fringed largemouth	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Chetia	flaviventris	*Chetia flaviventris*	Chetia flaviventris Trewavas, 1961	Canary kurper	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Chetia	gracilis	*Chetia gracilis*	Chetia gracilis (Greenwood, 1984)	Slender river bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Chetia	welwitschi	*Chetia welwitschi*	Chetia welwitschi (Boulenger, 1898)	Angolan river bream	2
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	anoterus	*Chiloglanis anoterus*	Chiloglanis anoterus Crass, 1960	Pennant-tail suckermouth / Rock catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	bifurcus	*Chiloglanis bifurcus*	Chiloglanis bifurcus Jubb & le Roux, 1969	Incomati suckermouth / Rock catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	emarginatus	*Chiloglanis emarginatus*	Chiloglanis emarginatus Jubb & le Roux, 1969	Pongolo suckermouth / Rock catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	fasciatus	*Chiloglanis fasciatus*	Chiloglanis fasciatus Pellegrin, 1936	Okavango suckermouth / Rock catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	neumanni	*Chiloglanis neumanni*	Chiloglanis neumanni Boulenger, 1911	Neumann's suckermouth / Rock catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	paratus	*Chiloglanis paratus*	Chiloglanis paratus Crass, 1960	Sawfin suckermouth / Rock catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	pretoriae	*Chiloglanis pretoriae*	Chiloglanis pretoriae van der Horst, 1931	Shortspine suckermouth / Rock catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	swierstrai	*Chiloglanis swierstrai*	Chiloglanis swierstrai van der Horst, 1931	Lowveld suckermouth / Rock catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Claroteidae	Chrysichthys	hildae	*Chrysichthys hildae*	Chrysichthys hildae Bell-Cross, 1973	Hilda's grunter / Buzi grunter	1
Animalia	Chordata	Actinopterygii	Siluriformes	Clariidae	Clariallabes	platyprosopos	*Clariallabes platyprosopos*	Clariallabes platyprosopos Jubb, 1964	Broadhead catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Clariidae	Clarias	cavernicola	*Clarias cavernicola*	Clarias cavernicola Trewavas, 1936	Cave catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Clariidae	Clarias	gariepinus	*Clarias gariepinus*	Clarias gariepinus (Burchell, 1822)	Sharptooth catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Clariidae	Clarias	liocephalus	*Clarias liocephalus*	Clarias liocephalus Boulenger, 1898	Smoothhead catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Clariidae	Clarias	ngamensis	*Clarias ngamensis*	Clarias ngamensis Castelnau, 1861	Blunttooth catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Clariidae	Clarias	stappersii	*Clarias stappersii*	Clarias stappersii Boulenger, 1915	Blotched catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Clariidae	Clarias	theodorae	*Clarias theodorae*	Clarias theodorae Weber, 1897	Snake catfish	1
Animalia	Chordata	Actinopterygii	Perciformes	Clinidae	Clinus	superciliosus	*Clinus superciliosus*	Clinus superciliosus (Linnaeus, 1758)	Super klipfish (MS)	M
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Clypeobarbus	bellcrossi	*Clypeobarbus bellcrossi*	Clypeobarbus bellcrossi (Conway and Stiassny, 2008)	Gorgeous barb	1
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Coptodon	rendalli	*Coptodon rendalli*	Coptodon rendalli (Boulenger, 1897)	Redbreast tilapia	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Coptostomabarbus	wittei	*Coptostomabarbus wittei*	Coptostomabarbus wittei David & Poll, 1937	Upjaw barb	1
Animalia	Chordata	Actinopterygii	Mugiliformes	Mugilidae	Crenimugil	buchanani	*Crenimugil buchanani*	Crenimugil buchanani (Bleeker, 1853)	Bluetail Mullet	M
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Croilia	mossambica	*Croilia mossambica*	Croilia mossambica Smith, 1955	Burrowing goby	M
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Ctenopharyngodon	idella	*Ctenopharyngodon idella*	Ctenopharyngodon idella (Valenciennes, 1844)	Grass carp	1
Animalia	Chordata	Actinopterygii	Perciformes	Anabantidae	Ctenopoma	multispine	*Ctenopoma multispine*	Ctenopoma multispine Peters, 1844	Many-spined climbing perch	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Cyphomyrus	discorhynchus	*Cyphomyrus discorhynchus*	Cyphomyrus discorhynchus (Pellegrin, 1936)	Zambezi parrotfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Cyprinus	carpio	*Cyprinus carpio*	Cyprinus carpio Linnaeus, 1758	Common carp	1

Kingdom	Phylum	Class	Order	Family	Genus	Species	Taxon	Scientific name and authority	Common name	Tolerance
Animalia	Chordata	Actinopterygii	Characiformes	Distichodontidae	Distichodus	mossambicus	*Distichodus mossambicus*	Distichodus mossambicus Peters, 1852	Nkupe	1
Animalia	Chordata	Actinopterygii	Characiformes	Distichodontidae	Distichodus	schenga	*Distichodus schenga*	Distichodus schenga Peters, 1852	Chessa	1
Animalia	Chordata	Actinopterygii	Perciformes	Eleotridae	Eleotris	fusca	*Eleotris fusca*	Eleotris fusca (Schneider, 1801)	Dusky sleeper	M
Animalia	Chordata	Actinopterygii	Perciformes	Eleotridae	Eleotris	melanosoma	*Eleotris melanosoma*	Eleotris melanosoma Bleeker, 1852	Broadhead sleeper	M
Animalia	Chordata	Actinopterygii	Perciformes	Eleotridae	Eleotris	vittata	*Eleotris vittata*	Eleotris vittata Duméril, 1858	Striped sleeper	M
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Engraulicypris	brevianalis	*Engraulicypris brevianalis*	Engraulicypris brevianalis (Boulenger, 1908)	Hyphen barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Engraulicypris	gariepinus	*Engraulicypris gariepinus*	Engraulicypris gariepinus Barnard, 1943		1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	afrohamiltoni	*Enteromius afrohamiltoni*	Enteromius afrohamiltoni (Crass, 1960)	Hamilton's barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	afrovernayi	*Enteromius afrovernayi*	Enteromius afrovernayi (Nichols & Boulton, 1927)	Spottail barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	amatolicus	*Enteromius amatolicus*	Enteromius amatolicus (Skelton, 1990)	Amatola barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	annectens	*Enteromius annectens*	Enteromius annectens (Gilchrist & Thompson, 1917)	Broadstriped barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	anoplus	*Enteromius anoplus*	Enteromius anoplus (Weber, 1897)	Chubbyhead barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	argenteus	*Enteromius argenteus*	Enteromius argenteus (Günther, 1868)	Rosefin barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	atkinsoni	*Enteromius atkinsoni*	Enteromius atkinsoni (Bailey, 1969)	Dash-dot barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	barnardi	*Enteromius barnardi*	Enteromius barnardi (Jubb, 1965)	Blackback barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	barotseensis	*Enteromius barotseensis*	Enteromius barotseensis (Pellegrin, 1920)	Barotse barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	bifrenatus	*Enteromius bifrenatus*	Enteromius bifrenatus (Fowler, 1935)	Hyphen barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	breviceps	*Enteromius breviceps*	Enteromius breviceps (Trewavas, 1936)	Shorthead barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	brevidorsalis	*Enteromius brevidorsalis*	Enteromius brevidorsalis (Boulenger, 1915)	Dwarf barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	brevipinnis	*Enteromius brevipinnis*	Enteromius brevipinnis (Jubb, 1966)	Shortfin barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	choloensis	*Enteromius choloensis*	Enteromius choloensis (Norman, 1925)	Silver barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	dorsolineatus	*Enteromius dorsolineatus*	Enteromius dorsolineatus (Trewavas, 1936)	Topstripe barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	eutaenia	*Enteromius eutaenia*	Enteromius eutaenia (Boulenger, 1904)	Orangefin barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	fasciolatus	*Enteromius fasciolatus*	Enteromius fasciolatus (Günther, 1868)	Red barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	gurneyi	*Enteromius gurneyi*	Enteromius gurneyi (Günther, 1868)	Redtail barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	haasianus	*Enteromius haasianus*	Enteromius haasianus (David, 1936)	Sicklefin barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	hospes	*Enteromius hospes*	Enteromius hospes (Barnard, 1938)	Namaqua barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	kerstenii	*Enteromius kerstenii*	Enteromius kerstenii (Peters, 1868)	Redspot barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	kessleri	*Enteromius kessleri*	Enteromius kessleri (Steindachner, 1866)	Gillbar barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	lineomaculatus	*Enteromius lineomaculatus*	Enteromius lineomaculatus (Boulenger, 1903)	Line-spotted barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	macrotaenia	*Enteromius macrotaenia*	Enteromius macrotaenia (Worthington, 1933)	Broadband barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	manicensis	*Enteromius manicensis*	Enteromius manicensis (Pellegrin, 1919)	Yellow barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	mattozi	*Enteromius mattozi*	Enteromius mattozi (Guimaraes, 1884)	Papermouth	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	miolepis	*Enteromius miolepis*	Enteromius miolepis (Boulenger, 1902)	Zig-zag barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	motebensis	*Enteromius motebensis*	Enteromius motebensis (Steindachner, 1894)	Marico barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	multilineatus	*Enteromius multilineatus*	Enteromius multilineatus (Worthington, 1933)	Copperstripe barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	neefi	*Enteromius neefi*	Enteromius neefi (Greenwood, 1962)	Sidespot barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	pallidus	*Enteromius pallidus*	Enteromius pallidus (Smith, 1841)	Goldie barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	paludinosus	*Enteromius paludinosus*	Enteromius paludinosus (Peters, 1852)	Straightfin barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	poechii	*Enteromius poechii*	Enteromius poechii (Steindachner, 1911)	Dashtail barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	radiatus	*Enteromius radiatus*	Enteromius radiatus (Peters, 1853)	Beira barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	thamalakanensis	*Enteromius thamalakanensis*	Enteromius thamalakanensis (Fowler, 1935)	Thamalakane barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	toppini	*Enteromius toppini*	Enteromius toppini (Boulenger, 1916)	East-coast barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	treurensis	*Enteromius treurensis*	Enteromius treurensis (Groenewald, 1958)	Treur River barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	trimaculatus	*Enteromius trimaculatus*	Enteromius trimaculatus (Peters, 1852)	Threespot barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	unitaeniatus	*Enteromius unitaeniatus*	Enteromius unitaeniatus (Günther, 1866)	Longbeard barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	viviparus	*Enteromius viviparus*	Enteromius viviparus (Weber, 1897)	Bowstripe barb	1
Animalia	Chordata	Actinopterygii	Gadiformes	Lotidae	Gaidropsarus	capensis	*Gaidropsarus capensis*	Gaidropsarus capensis (Kaup, 1858)	Cape rockling	M
Animalia	Chordata	Actinopterygii	Osmeriformes	Galaxiidae	Galaxias	zebratus	*Galaxias zebratus*	Galaxias zebratus (Castelnau, 1861)	Cape galaxias	2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Gambusia	affinis	*Gambusia affinis*	Gambusia affinis (Baird & Girard, 1853)	Mosquitofish	1
Animalia	Chordata	Actinopterygii	Clupeiformes	Clupeidae	Gilchristella	aestuaria	*Gilchristella aestuaria*	Gilchristella aestuaria (Gilchrist, 1913)	Estuarine round herring	M
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Glossogobius	callidus	*Glossogobius callidus*	Glossogobius callidus (Smith, 1937)	River goby	M
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Glossogobius	giuris	*Glossogobius giuris*	Glossogobius giuris (Hamilton-Buchanan, 1822)	Tank goby	M
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Gobionellus	lepturus	*Gobionellus lepturus*	Gobionellus lepturus Pfaff, 1933	Slender goby	M
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Hemichromis	elongatus	*Hemichromis elongatus*	Hemichromis elongatus (Guichenot, 1859)	Banded jewelfish	2
Animalia	Chordata	Actinopterygii	Characiformes	Characidae	Hemigrammopetersius	barnardi	*Hemigrammopetersius barnardi*	Hemigrammopetersius barnardi (Herre, 1936)	Barnard's robber	1
Animalia	Chordata	Actinopterygii	Characiformes	Hepsetidae	Hepsetus	odoe	*Hepsetus odoe*	Hepsetus odoe (Bloch, 1794)	African pike	1
Animalia	Chordata	Actinopterygii	Siluriformes	Clariidae	Heterobranchus	longifilis	*Heterobranchus longifilis*	Heterobranchus longifilis Valenciennes, 1840	Vundu	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Hippopotamyrus	ansorgii	*Hippopotamyrus ansorgii*	Hippopotamyrus ansorgii (Boulenger,1905)	Slender stonebasher	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Hippopotamyrus	longilateralis	*Hippopotamyrus longilateralis*	Hippopotamyrus longilateralis Kramer and Swartz 2010		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Hippopotamyrus	szaboi	*Hippopotamyrus szaboi*	Hippopotamyrus szaboi Kramer van der Bank & Wink, 2004		1
Animalia	Chordata	Actinopterygii	Characiformes	Characidae	Hydrocynus	vittatus	*Hydrocynus vittatus*	Hydrocynus vittatus Castelnau, 1861	Tigerfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Hypophthalmichthys	molitrix	*Hypophthalmichthys molitrix*	Hypophthalmichthys molitrix (Valenciennes, 1844)	Silver carp	1
Animalia	Chordata	Actinopterygii	Beloniformes	Hemirhamphidae	Hyporhamphus	capensis	*Hyporhamphus capensis*	Hyporhamphus capensis (Thominot, 1886)	Cape halfbeak	M
Animalia	Chordata	Actinopterygii	Perciformes	Eleotridae	Hypseleotris	dayi	*Hypseleotris dayi*	Hypseleotris dayi Smith, 1950	Golden sleeper	M
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Hypsopanchax	jubbi	*Hypsopanchax jubbi*	Hypsopanchax jubbi Poll & Lambert, 1965	Southern deepbody	2

Kingdom	Phylum	Class	Order	Family	Genus	Species	Taxon	Scientific name and authority	Common name	Tolerance
Animalia	Chordata	Actinopterygii	Gonorynchiformes	Kneriidae	Kneria	angolensis	*Kneria angolensis*	Kneria angolensis Steindachner, 1866	Angola kneria	1
Animalia	Chordata	Actinopterygii	Gonorynchiformes	Kneriidae	Kneria	auriculata	*Kneria auriculata*	Kneria auriculata (Pellegrin, 1905)	Southern kneria	1
Animalia	Chordata	Actinopterygii	Gonorynchiformes	Kneriidae	Kneria	maydelli	*Kneria maydelli*	Kneria maydelli Ladiges & Voelker, 1961	Cunene kneria	1
Animalia	Chordata	Actinopterygii	Gonorynchiformes	Kneriidae	Kneria	polli	*Kneria polli*	Kneria polli Trewavas, 1936	Northern kneria	1
Animalia	Chordata	Actinopterygii	Perciformes	Kuhliidae	Kuhlia	rupestris	*Kuhlia rupestris*	Kuhlia rupestris (Lacepède, 1801)	Rock flagtail	M
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	altivelis	*Labeo altivelis*	Labeo altivelis Peters, 1852	Manyame labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	ansorgii	*Labeo ansorgii*	Labeo ansorgii Boulenger, 1907	Cunene labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	capensis	*Labeo capensis*	Labeo capensis (Smith, 1841)	Orange River mudfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	congoro	*Labeo congoro*	Labeo congoro Peters, 1852	Purple labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	cylindricus	*Labeo cylindricus*	Labeo cylindricus Peters, 1852	Redeye labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	lunatus	*Labeo lunatus*	Labeo lunatus Jubb, 1963	Upper Zambezi labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	molybdinus	*Labeo molybdinus*	Labeo molybdinus du Plessis, 1963	Leaden labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	rosae	*Labeo rosae*	Labeo rosae Steindachner, 1894	Rednose labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	rubromaculatus	*Labeo rubromaculatus*	Labeo rubromaculatus Gilchrist & Thompson, 1913	Tugela labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	ruddi	*Labeo ruddi*	Labeo ruddi Boulenger, 1907	Silver labeo	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	seeberi	*Labeo seeberi*	Labeo seeberi Gilchrist & Thompson, 1911	Clanwilliam sandfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeo	umbratus	*Labeo umbratus*	Labeo umbratus (Smith, 1841)	Moggel	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	aeneus	*Labeobarbus aeneus*	Labeobarbus aeneus (Burchell, 1822)	Vaal-Orange smallmouth yellowfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	codringtonii	*Labeobarbus codringtonii*	Labeobarbus codringtonii Boulenger, 1908	Upper Zambezi yellowfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	dimidiatus	*Labeobarbus dimidiatus*	Labeobarbus dimidiatus Tweddle & Skelton, 1998	Blacktop chiselmouth	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	kimberleyensis	*Labeobarbus kimberleyensis*	Labeobarbus kimberleyensis Gilchrist & Thompson, 1913	Vaal-Orange largemouth yellowfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	marequensis	*Labeobarbus marequensis*	Labeobarbus marequensis Smith, 1841	Lowveld largescale yellowfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	natalensis	*Labeobarbus natalensis*	Labeobarbus natalensis Castelnau, 1861	Scaly Kwa-Zulu Natal yellowfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	nelspruitensis	*Labeobarbus nelspruitensis*	Labeobarbus nelspruitensis (Gilchrist & Thompson, 1911)	Incomati chiselmouth	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	polylepis	*Labeobarbus polylepis*	Labeobarbus polylepis Boulenger, 1907	Bushveld smallscale yellowfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	pungweensis	*Labeobarbus pungweensis*	Labeobarbus pungweensis Jubb, 1959	Pungwe chiselmouth	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	seeberi	*Labeobarbus seeberi*	Labeobarbus seeberi (Gilchrist & Thompson, 1913)	Clanwilliam yellowfish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	xyrocheilus	*Labeobarbus xyrocheilus*	Labeobarbus xyrocheilus Tweddle & Skelton, 1998	Razorlip chiselmouth	1
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Lacustricola	katangae	*Lacustricola katangae*	Lacustricola katangae (Boulenger, 1912)	Striped topminnow	2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Lacustricola	macrurus	*Lacustricola macrurus*	Lacustricola macrurus (Boulenger, 1904)	Big tailed lampeye	2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Lacustricola	myaposae	*Lacustricola myaposae*	Lacustricola myaposae (Boulenger, 1912)	Natal topminnow	2
Animalia	Chordata	Actinopterygii	Perciformes	Centrarchidae	Lepomis	macrochirus	*Lepomis macrochirus*	Lepomis macrochirus Rafinesque, 1819	Bluegill sunfish	1
Animalia	Chordata	Actinopterygii	Perciformes	Carangidae	Lichia	amia	*Lichia amia*	Lichia amia (Linnaeus, 1758)	Leerfish	M
Animalia	Chordata	Actinopterygii	Clupeiformes	Clupeidae	Limnothrissa	miodon	*Limnothrissa miodon*	Limnothrissa miodon (Boulenger, 1906)	Kapenta	1
Animalia	Chordata	Actinopterygii	Perciformes	Sparidae	Lithognathus	Lithognathus	*Lithognathus Lithognathus*	Lithognathus lithognathus (Cuvier, 1829)	White steenbras	M
Animalia	Chordata	Actinopterygii	Perciformes	Lutjanidae	Lutjanus	argentimaculatus	*Lutjanus argentimaculatus*	Lutjanus argentimaculatus (Forsskål, 1775)	River snapper	M
Animalia	Chordata	Actinopterygii	Siluriformes	Malapteruridae	Malapterurus	electricus	*Malapterurus electricus*	Malapterurus electricus (Gmelin, 1789)	Electric catfish	
Animalia	Chordata	Actinopterygii	Siluriformes	Malapteruridae	Malapterurus	shirensis	*Malapterurus shirensis*	Malapterurus shirensis Roberts, 2000	Zambezi electric catfish	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	altisambesi	*Marcusenius altisambesi*	Marcusenius altisambesi Kramer, Skelton, van der Bank & Wink, 2007		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	caudisquamatus	*Marcusenius caudisquamatus*	Marcusenius caudisquamatus Maake, Gon & Swartz, 2014		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	cubangoensis	*Marcusenius cubangoensis*	Marcusenius cubangoensis Pellegrin, 1936	Elephantfish	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	desertus	*Marcusenius desertus*	Marcusenius desertus Kramer, van der Bank & Wink, 2016		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	krameri	*Marcusenius krameri*	Marcusenius krameri Maake, Gon & Swartz, 2014		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	macrolepidotus	*Marcusenius macrolepidotus*	Marcusenius macrolepidotus (Peters, 1852)	Bulldog	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	multisquamatus	*Marcusenius multisquamatus*	Marcusenius multisquamatus Kramer and Wink 2013		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	pongolensis	*Marcusenius pongolensis*	Marcusenius pongolensis (Fowler, 1934)		1
Animalia	Chordata	Actinopterygii	Synbranchiformes	Mastacembelidae	Mastacembelus	frenatus	*Mastacembelus frenatus*	Mastacembelus frenatus (Boulenger, 1901)	Longtail spinyeel	1
Animalia	Chordata	Actinopterygii	Synbranchiformes	Mastacembelidae	Mastacembelus	shiranus	*Mastacembelus shiranus*	Mastacembelus shiranus (Günther, 1896)	Malawi spinyeel	1
Animalia	Chordata	Actinopterygii	Synbranchiformes	Mastacembelidae	Mastacembelus	vanderwaali	*Mastacembelus vanderwaali*	Mastacembelus vanderwaali (Skelton, 1976)	Ocellate spinyeel	1
Animalia	Chordata	Actinopterygii	Elopiformes	Megalopidae	Megalops	cyprinoides	*Megalops cyprinoides*	Megalops cyprinoides (Broussonet, 1782)	Oxeye tarpon	3
Animalia	Chordata	Actinopterygii	Characiformes	Characidae	Micralestes	acutidens	*Micralestes acutidens*	Micralestes acutidens (Peters, 1852)	Silver robber	1
Animalia	Chordata	Actinopterygii	Perciformes	Anabantidae	Microctenopoma	intermedium	*Microctenopoma intermedium*	Microctenopoma intermedium (Pellegrin, 1920)	Blackspot climbing perch	1
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Micropanchax	hutereaui	*Micropanchax hutereaui*	Micropanchax hutereaui Ghedotti, 2000	Meshscaled topminnow	2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Micropanchax	johnstoni	*Micropanchax johnstoni*	Micropanchax johnstoni Ghedotti, 2000	Johnston's topminnow	2
Animalia	Chordata	Actinopterygii	Sygnathiformes	Syngnathidae	Microphis	brachyurus	*Microphis brachyurus*	Microphis brachyurus Bleeker, 1853	Opossum pipefish	M
Animalia	Chordata	Actinopterygii	Sygnathiformes	Syngnathidae	Microphis	fluviatilis	*Microphis fluviatilis*	Microphis fluviatilis (Peters, 1852)	freshwater pipefish	M
Animalia	Chordata	Actinopterygii	Perciformes	Centrarchidae	Micropterus	dolomieu	*Micropterus dolomieu*	Micropterus dolomieu Lacepède, 1802	Smallmouth bass	1
Animalia	Chordata	Actinopterygii	Perciformes	Centrarchidae	Micropterus	floridanus	*Micropterus floridanus*	Micropterus floridanus Lesueur, 1822	Florida bass	1
Animalia	Chordata	Actinopterygii	Perciformes	Centrarchidae	Micropterus	punctulatus	*Micropterus punctulatus*	Micropterus punctulatus (Rafinesque, 1819)	Spotted bass	1
Animalia	Chordata	Actinopterygii	Perciformes	Centrarchidae	Micropterus	salmoides	*Micropterus salmoides*	Micropterus salmoides (Lacepède, 1802)	Largemouth bass	1
Animalia	Chordata	Actinopterygii	Perciformes	Monodactylidae	Monodactylus	argenteus	*Monodactylus argenteus*	Monodactylus argenteus (Linnaeus, 1758)	Natal moony	M
Animalia	Chordata	Actinopterygii	Perciformes	Monodactylidae	Monodactylus	falciformis	*Monodactylus falciformis*	Monodactylus falciformis Lacepède, 1801	Full moony	M
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Mormyrops	anguilloides	*Mormyrops anguilloides*	Mormyrops anguilloides (Linnaeus, 1758)	Cornish jack	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Mormyrus	lacerda	*Mormyrus lacerda*	Mormyrus lacerda Castelnau, 1861	Western bottlenose	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Mormyrus	longirostris	*Mormyrus longirostris*	Mormyrus longirostris Peters, 1852	Eastern bottelnose	1
Animalia	Chordata	Actinopterygii	Mugiliformes	Mugilidae	Mugil	cephalus	*Mugil cephalus*	Mugil cephalus Linnaeus, 1758	Flathead grey mullet	M

Kingdom	Phylum	Class	Order	Family	Genus	Species	Taxon	Scientific name and authority	Common name	Tolerance
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Mugilogobius	durbanensis	*Mugilogobius durbanensis*	Mugilogobius durbanensis (Barnard, 1927)	Durban goby	M
Animalia	Chordata	Actinopterygii	Characiformes	Distichodontidae	Nannocharax	machadoi	*Nannocharax machadoi*	Nannocharax machadoi Poll, 1967	Dwarf citharine	1
Animalia	Chordata	Actinopterygii	Characiformes	Distichodontidae	Nannocharax	macropterus	*Nannocharax macropterus*	Nannocharax macropterus Pellegrin, 1925	Broadbarred citharine	1
Animalia	Chordata	Actinopterygii	Characiformes	Distichodontidae	Nannocharax	multifasciatus	*Nannocharax multifasciatus*	Nannocharax multifasciatus Boulenger, 1923	Multibar citharine	1
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Nematogobius	maindroni	*Nematogobius maindroni*	Nematogobiusmaindroni Sauvage, 1880	Spotfin goby	M
Animalia	Chordata	Actinopterygii	Mugiliformes	Mugilidae	Neochelon	falcipinnis	*Neochelon falcipinnis*	Neochelon falcipinnis (Valenciennes, 1836)	Sicklefin Mullet	M
Animalia	Chordata	Actinopterygii	Characiformes	Distichodontidae	Neolebias	lozii	*Neolebias lozii*	Neolebias lozii Winemiller & Kelso-Winemiller, 1993	Banded neolebias	1
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	boklundi	*Nothobranchius boklundi*	Nothobranchius boklundi Valdesalici 2010		2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	capriviensis	*Nothobranchius capriviensis*	Nothobranchius capriviensis Watters, Wildekamp & Shidlovskiy, 2015		2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	furzeri	*Nothobranchius furzeri*	Nothobranchius furzeri Jubb, 1971	Turquoise killifish	2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	kadleci	*Nothobranchius kadleci*	Nothobranchius kadleci Reichard 2010		2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	kafuensis	*Nothobranchius kafuensis*	Nothobranchius kafuensis Wildekamp & Rosenstock, 1989	Caprivi killifish	2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	krysanovi	*Nothobranchius krysanovi*	Nothobranchius krysanovi Schidlovskiy, Watters & Wildekamp, 2010		2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	kuhntae	*Nothobranchius kuhntae*	Nothobranchius kuhntae (Ahl, 1926)	Beira killifish	2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	orthonotus	*Nothobranchius orthonotus*	Nothobranchius orthonotus (Peters, 1844)	Spotted killifish	2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	pienaari	*Nothobranchius pienaari*	Nothobranchius pienaari Schidlovskiy, Watters & Wildekamp, 2010		2
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	rachovii	*Nothobranchius rachovii*	Nothobranchius rachovii Ahl, 1926	Rainbow killifish	2
Animalia	Chordata	Actinopterygii	Beloniformes	Blenniidae	Omobranchus	ferox	*Omobranchus ferox*	Omobranchus ferox (Herre, 1927)	Gossamer blenny	
Animalia	Chordata	Actinopterygii	Salmoniformes	Salmonidae	Oncorhynchus	mykiss	*Oncorhynchus mykiss*	Oncorhynchus mykiss (Walbaum, 1792)	Rainbow trout	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Opsaridium	peringueyi	*Opsaridium peringueyi*	Opsaridium peringueyi (Gilchrist & Thompson, 1913)	Southern barred minnow	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Opsaridium	tweddleorum	*Opsaridium tweddleorum*	Opsaridium tweddleorum (Skelton, 1996)	Dwarf sanjika	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Opsaridium	zambezense	*Opsaridium zambezense*	Opsaridium zambezense (Peters, 1852)	Barred minnow	1
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Oreochromis	macrochir	*Oreochromis macrochir*	Oreochromis (Nyasalapia) macrochir (Boulenger, 1912)	Greenhead tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Oreochromis	andersonii	*Oreochromis andersonii*	Oreochromis andersonii (Castelnau, 1861)	Threespot tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Oreochromis	aureus	*Oreochromis aureus*	Oreochromis aureus (Steindachner, 1864)	Israeli tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Oreochromis	mortimeri	*Oreochromis mortimeri*	Oreochromis mortimeri (Trewavas, 1966)	Kariba tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Oreochromis	mossambicus	*Oreochromis mossambicus*	Oreochromis mossambicus (Peters, 1852)	Mozambique tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Oreochromis	niloticus	*Oreochromis niloticus*	Oreochromis niloticus (Linnaeus, 1758)	Nile tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Oreochromis	placidus	*Oreochromis placidus*	Oreochromis placidus (Trewavas, 1941)	Black tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Oreochromis	shiranus	*Oreochromis shiranus*	Oreochromis shiranus (Boulenger, 1896)	Shire tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Orthochromis	machadoi	*Orthochromis machadoi*	Orthochromis machadoi (Poll, 1967)		2
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Pandaka	silvana	*Pandaka silvana*	Pandaka silvana (Barnard, 1943)	Dwarf goby	M
Animalia	Chordata	Actinopterygii	Gonorynchiformes	Kneriidae	Parakneria	fortuita	*Parakneria fortuita*	Parakneria fortuita Penrith, 1973	Cubango kneria	1
Animalia	Chordata	Actinopterygii	Gonorynchiformes	Kneriidae	Parakneria	mossambica	*Parakneria mossambica*	Parakneria mossambica Jubb & Bell-Cross, 1974	Gorongoza kneria	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Paramormyrops	jacksoni	*Paramormyrops jacksoni*	Paramormyrops jacksoni (Poll, 1967)	Ghost stonebasher	1
Animalia	Chordata	Actinopterygii	Siluriformes	Claroteidae	Parauchenoglanis	ngamensis	*Parauchenoglanis ngamensis*	Parauchenoglanis ngamensis (Boulenger, 1911)	Zambezi grunter	1
Animalia	Chordata	Actinopterygii	Perciformes	Percidae	Perca	fluviatilis	*Perca fluviatilis*	Perca fluviatilis Linnaeus, 1758	European perch	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	catostoma	*Petrocephalus catostoma*	Petrocephalus catostoma (Günther, 1866)	Churchill	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	longianalis	*Petrocephalus longianalis*	Petrocephalus longianalis Kramer, Bills, Skelton & Wink, 2012		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	longicapitis	*Petrocephalus longicapitis*	Petrocephalus longicapitis Kramer, Bills, Skelton & Wink, 2012		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	magnitrunci	*Petrocephalus magnitrunci*	Petrocephalus magnitrunci Kramer, Bills, Skelton & Wink, 2012		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	magnoculis	*Petrocephalus magnoculis*	Petrocephalus magnoculis Kramer, Bills, Skelton & Wink, 2012		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	okavangoensis	*Petrocephalus okavangoensis*	Petrocephalus okavangoensis Kramer, Bills, Skelton & Wink, 2012		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	petersi	*Petrocephalus petersi*	Petrocephalus petersi Kramer, Bills, Skelton & Wink, 2012		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	wesselsi	*Petrocephalus wesselsi*	Petrocephalus wesselsi (Kramer & van der Bank, 2000)	Southern churchill	1
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Phalloceros	caudimaculatus	*Phalloceros caudimaculatus*	Phalloceros caudimaculatus (Hensel, 1868)	Dusky millions fish	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Pharyngochromis	acuticeps	*Pharyngochromis acuticeps*	Pharyngochromis acuticeps (Steindachner, 1866)	Zambezi river bream	2
Animalia	Chordata	Actinopterygii	Mugiliformes	Mugilidae	Planiliza	macrolepis	*Planiliza macrolepis*	Planiliza macrolepis (Smith, 1846)	Large-scale mullet	M
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Poecilia	reticulata	*Poecilia reticulata*	Poecilia reticulata Peters, 1859	Guppy	2
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Pollimyrus	castelnaui	*Pollimyrus castelnaui*	Pollimyrus castelnaui (Boulenger, 1911)	Dwarf stonebasher	1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Pollimyrus	cuandoensis	*Pollimyrus cuandoensis*	Pollimyrus cuandoensis Kramer, van der Bank & Wink, 2013		1
Animalia	Chordata	Actinopterygii	Osteoglossiformes	Mormyridae	Pollimyrus	marianne	*Pollimyrus marianne*	Pollimyrus marianne Kramer, van der Bank, Flint, Sauer-Gürth & Wink, 2003		1
Animalia	Chordata	Chondrichthyes	Rhinopristiformes	Pristidae	Pristis	microdon	*Pristis microdon*	Pristis microdon Latham, 1794	smalltooth sawfish	M
Animalia	Chordata	Sacropterygii	Lepidosireniformes	Protopteridae	Protopterus	amphibius	*Protopterus amphibius*	Protopterus amphibius (Peters, 1844)	East coast lungfish	2
Animalia	Chordata	Sacropterygii	Lepidosireniformes	Protopteridae	Protopterus	annectens	*Protopterus annectens*	Protopterus annectens brieni Poll, 1961	African lungfish	2
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Psammogobius	knysnaensis	*Psammogobius knysnaensis*	Psammogobius knysnaensis Smith, 1935	Knysna sand goby	M
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	afer	*Pseudobarbus afer*	Pseudobarbus afer (Peters, 1864)	Eastern Cape redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	asper	*Pseudobarbus asper*	Pseudobarbus asper (Boulenger, 1911)	Smallscale redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	burchelli	*Pseudobarbus burchelli*	Pseudobarbus burchelli (Smith, 1841)	Breede River redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	burgi	*Pseudobarbus burgi*	Pseudobarbus burgi (Boulenger, 1911)	Berg River redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	calidus	*Pseudobarbus calidus*	Pseudobarbus calidus (Barnard, 1938)	Clanwilliam redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	capensis	*Pseudobarbus capensis*	Pseudobarbus capensis (Smith, 1841)	Berg-breede river whitefish	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	erubescens	*Pseudobarbus erubescens*	Pseudobarbus erubescens (Skelton, 1974)	Twee river redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	phlegethon	*Pseudobarbus phlegethon*	Pseudobarbus phlegethon (Barnard, 1938)	Fiery redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	quathlambae	*Pseudobarbus quathlambae*	Pseudobarbus quathlambae (Barnard, 1938)	Maloti minnow	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	senticeps	*Pseudobarbus senticeps*	Pseudobarbus senticeps (Smith, 1936)		1

Kingdom	Phylum	Class	Order	Family	Genus	Species	Taxon	Scientific name and authority	Common name	Tolerance
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	serra	*Pseudobarbus serra*	Pseudobarbus serra (Peters, 1864)	Sawfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	skeltoni	*Pseudobarbus skeltoni*	Pseudobarbus skeltoni Chakona and Swartz 2013	Giant redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	swartzi	*Pseudobarbus swartzi*	Pseudobarbus swartzi Chakona & Skelton, 2017	Gamtoos redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	tenuis	*Pseudobarbus tenuis*	Pseudobarbus tenuis (Barnard, 1938)	Slender redfin	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	trevelyani	*Pseudobarbus trevelyani*	Pseudobarbus trevelyani Günther, 1877	Border barb	1
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	verloreni	*Pseudobarbus verloreni*	Pseudobarbus verloreni Chakona, Swartz & Skelton, 2014		1
Animalia	Chordata	Actinopterygii	Cichliformes	Cichlidae	Pseudocrenilabrus	philander	*Pseudocrenilabrus philander*	Pseudocrenilabrus philander (Weber, 1897)	Southern mouthbrooder	2
Animalia	Chordata	Actinopterygii	Mugiliformes	Mugilidae	Pseudomyxus	capensis	*Pseudomyxus capensis*	Pseudomyxus capensis (Valenciennes, 1836)	Freshwater mullet	M
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Redigobius	dewaali	*Redigobius dewaali*	Redigobius dewaali (Weber, 1897)	Checked goby	M
Animalia	Chordata	Actinopterygii	Characiformes	Characidae	Rhabdalestes	maunensis	*Rhabdalestes maunensis*	Rhabdalestes maunensis (Fowler, 1935)	Slender robber	1
Animalia	Chordata	Actinopterygii	Salmoniformes	Salmonidae	Salmo	trutta	*Salmo trutta*	Salmo trutta Linnaeus, 1758	Brown trout	1
Animalia	Chordata	Actinopterygii	Salmoniformes	Salmonidae	Salvelinus	fontinalis	*Salvelinus fontinalis*	Salvelinus fontinalis (Mitchill, 1815)	Brook trout	1
Animalia	Chordata	Actinopterygii	Perciformes	Anabantidae	Sandelia	bainsii	*Sandelia bainsii*	Sandelia bainsii Castelnau, 1861	Eastern Cape rocky	1
Animalia	Chordata	Actinopterygii	Perciformes	Anabantidae	Sandelia	capensis	*Sandelia capensis*	Sandelia capensis (Cuvier, 1829)	Cape kurper	1
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Sargochromis	carlottae	*Sargochromis carlottae*	Sargochromis carlottae (Boulenger, 1905)	Rainbow bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Sargochromis	codringtonii	*Sargochromis codringtonii*	Sargochromis codringtonii (Boulenger, 1908)	Green bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Sargochromis	coulteri	*Sargochromis coulteri*	Sargochromis coulteri (Bell-Cross, 1975)	Cunene bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Sargochromis	giardi	*Sargochromis giardi*	Sargochromis giardi (Pellegrin, 1903)	Pink bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Sargochromis	greenwoodi	*Sargochromis greenwoodi*	Sargochromis greenwoodi (Bell-Cross, 1975)	Greenwood's bream / Deepcheek bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Sargochromis	mortimeri	*Sargochromis mortimeri*	Sargochromis mortimeri (Bell-Cross, 1975)	Mortimer's bream / Kafue bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Sparidae	Sarpa	salpa	*Sarpa salpa*	Sarpa salpa (Linnaeus, 1758)	Karanteen	M
Animalia	Chordata	Actinopterygii	Siluriformes	Schilbeidae	Schilbe	intermedius	*Schilbe intermedius*	Schilbe intermedius Rüppell, 1832	Butter catfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Schilbeidae	Schilbe	yangambianus	*Schilbe yangambianus*	Schilbe yangambianus (Poll, 1954)	Yangambi buttercatfish	1
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Serranochromis	altus	*Serranochromis altus*	Serranochromis altus Winemiller & Kelso-Winemiller, 1991	Humpback largemouth	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Serranochromis	angusticeps	*Serranochromis angusticeps*	Serranochromis angusticeps (Boulenger, 1907)	Thinface largemouth	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Serranochromis	longimanus	*Serranochromis longimanus*	Serranochromis longimanus (Boulenger, 1911)	Longfin largemouth	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Serranochromis	macrocephalus	*Serranochromis macrocephalus*	Serranochromis macrocephalus (Boulenger, 1899)	Purpleface largemouth	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Serranochromis	meridianus	*Serranochromis meridianus*	Serranochromis meridianus Jubb, 1967	Lowveld largemouth	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Serranochromis	robustus	*Serranochromis robustus*	Serranochromis robustus (Boulenger, 1896)	Nembwe	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Serranochromis	thumbergi	*Serranochromis thumbergi*	Serranochromis thumbergi (Castelnau, 1861)	Brownspot largemouth	2
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Silhouettea	sibayi	*Silhouettea sibayi*	Silhouettea sibayi Farquharson, 1970	Sibayi goby	M
Animalia	Chordata	Actinopterygii	Perciformes	Gobiidae	Stenogobius	kenyae	*Stenogobius kenyae*	Stenogobius kenyae Smith 1959	Kenyan river goby	M
Animalia	Chordata	Actinopterygii	Beloniformes	Belonidae	Strongylura	leiura	*Strongylura leiura*	Strongylura leiura (Bleeker, 1851)	Yellowfin needlefish	M
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	leopardinus	*Synodontis leopardinus*	Synodontis leopardinus Pellegrin, 1914	Leopard squeaker	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	macrostigma	*Synodontis macrostigma*	Synodontis macrostigma Boulenger, 1911	Large-spot squeaker	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	macrostoma	*Synodontis macrostoma*	Synodontis macrostoma Skelton & White, 1990	Largemouth squeaker	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	nebulosus	*Synodontis nebulosus*	Synodontis nebulosus Peters, 1852	Cloudy squeaker	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	nigromaculatus	*Synodontis nigromaculatus*	Synodontis nigromaculatus Boulenger, 1905	Spotted squeaker	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	thamalakanensis	*Synodontis thamalakanensis*	Synodontis thamalakanensis Fowler, 1935	Bubblebarb squeaker	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	vanderwaali	*Synodontis vanderwaali*	Synodontis vanderwaali Skelton & White, 1990	Finetooth squeaker	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	woosnami	*Synodontis woosnami*	Synodontis woosnami Boulenger, 1911	Upper Zambezi squeaker	1
Animalia	Chordata	Actinopterygii	Siluriformes	Mochokidae	Synodontis	zambezensis	*Synodontis zambezensis*	Synodontis zambezensis Peters, 1852	Brown squeaker	1
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Thoracochromis	albolabris	*Thoracochromis albolabris*	Thoracochromis albolabris (Trewavas & Thys van den Audenaerde, 1969)	Thicklipped river bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Thoracochromis	buysi	*Thoracochromis buysi*	Thoracochromis buysi (Penrith, 1970)	Namibriver bream	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Tilapia	guinasana	*Tilapia guinasana*	Tilapia guinasana Trewavas, 1936	Otjikoto tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Tilapia	ruweti	*Tilapia ruweti*	Tilapia ruweti (Poll & Thys van den Audenaerde, 1965)	Okavango tilapia	2
Animalia	Chordata	Actinopterygii	Perciformes	Cichlidae	Tilapia	sparrmanii	*Tilapia sparrmanii*	Tilapia sparrmanii Smith, 1840	Banded tilapia	2
Animalia	Chordata	Actinopterygii	Cypriniformes	Cyprinidae	Tinca	tinca	*Tinca tinca*	Tinca tinca (Linnaeus, 1758)	Tench	1
Animalia	Chordata	Actinopterygii	Perciformes	Anabantidae	Trichopodus	trichopterus	*Trichopodus trichopterus*	Trichogaster trichopterus	Gourami	M
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Xiphophorus	helleri	*Xiphophorus helleri*	Xiphophorus helleri Heckel, 1848	Swordtail	1
Animalia	Chordata	Actinopterygii	Cyprinodontiformes	Poeciliidae	Xiphophorus	maculatus	*Xiphophorus maculatus*	Xiphophorus maculatus (Gunther, 1866)	Southern platyfish	1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Zaireichthys	conspicuus	*Zaireichthys conspicuus*	Zaireichthys conspicuus Eccles, Tweddle & Skelton, 2011	Blotched sand catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Zaireichthys	dorae	*Zaireichthys dorae*	Zaireichthys dorae (Poll, 1967)	Chobe sand catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Zaireichthys	kafuensis	*Zaireichthys kafuensis*	Zaireichthys kafuensis Eccles, Tweddle & Skelton, 2011		1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Zaireichthys	kavangoensis	*Zaireichthys kavangoensis*	Zaireichthys kavangoensis Eccles, Tweddle & Skelton, 2011		1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Zaireichthys	kunenensis	*Zaireichthys kunenensis*	Zaireichthys kunenensis Eccles, Tweddle & Skelton, 2011		1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Zaireichthys	pallidus	*Zaireichthys pallidus*	Zaireichthys pallidus Eccles Eccles, Tweddle & Skelton, 2011	Pale sand catlet	1
Animalia	Chordata	Actinopterygii	Siluriformes	Amphiliidae	Zaireichthys	rotundiceps	*Zaireichthys rotundiceps*	Zaireichthys rotundiceps (Hilgendorf, 1905)	Sand catlet	1

Table S. 2.2. List of freshwater fish experts and conservation organisations contacted requesting freshwater fish occurrence data.

#	Name and Surname	Province	Email Address
1	Albert Chakona	Eastern Cape	A.Chakona@saiab.ac.za
2	Andrew Deacon	SANPARKS	andrewd@sanparks.org
3	Andrew Husted	Gauteng	andrew@thebiodiversitycompany.com
4	Barry Clarke	Western Cape	barry@anchorenvironmental.co.za
5	Basi Diole	North-West Province	bdiole@nwpg.gov.za
6	Brent Coverdale	KwaZulu-Natal	Brent.coverdale@kznwildlife.com
7	Bruce Paxton	Western Cape	Did not email. These are collaborators.
8	Darragh Woodford	Gauteng	darragh.woodford@wits.ac.za
9	Dean Impson	Western Cape	Did not email. These are collaborators.
10	Dr Gordon O'Brien	Kwa Zulu Natal	gordon.obrien@ump.ac.za
11	Dr Paul Fouche	Limpopo	psofouche@gmail.com
12	Erasmus Nkabinde	Gauteng	erasmus.nkabinde@gauteng.gov.za
13	Francois Roux	Mpumalanga	hydrocynus@mweb.co.za
14	Ian Russell	SANPARKS	ian.russell@sanparks.org
15	Jaco van Deventer	Western Cape	jvdeventer@capenature.co.za
16	Jeremy Shelton	Western Cape	Did not email. These are collaborators.
17	Leon Barkhuizen	Free State	barkhl@detea.fs.gov.za
18	Magdel Boshoff	Dept. of Environmental Affairs	mboshoff@environment.gov.za
19	Mandy Schumann	Northern Cape	bokkeveld@gmail.com
20	Martine Jordaan	Western Cape	Did not email. These are collaborators.
21	Mick Angliss	Northen Province	ma24@mweb.co.za
22	Mr R van der Walt	Western Cape	Did not email. These are collaborators.
23	Neels Kleynhans	Gauteng/ Mpumalanga	kneria@gmail.com
24	Nico Smit	North-West Province	nico.smit@nwu.ac.za
25	Nicola Van Wilgen	SANPARKS	nicola.vanwilgen@sanparks.org
26	Olaf Weyl	Eastern Cape	O.Weyl@saiab.ac.za
27	Peter Ramollo	Northern Cape	ramollopp@gmail.co.za
28	Phumla Mzazi	Eastern Cape	phumla.mzazi@deaet.ecape.gov.za
29	Pieter Kotze	SANPARKS	pieter@cleanstream.co.za pk@rau.ac.za
30	Riaan de Lange	Mpumalanga	riaan@mtpa.co.za
31	Roger Bills	Eastern Cape	R.Bills@saiab.ac.za
32	Sam Mkubele	Limpopo	bopapecn@ledet.gov.za
33	Skhumbuzo Kubheka	Kwazulu-Natal	Skhumbuzo.Kubheka@kznwildlife.com
34	Stanley Rodgers	Limpopo	rodgersssm@ledet.gov.za
35	Warren Aken	Free State	WAken@golder.co.za
36	Wessel Jacobs	Limpopo	ncph@vodamail.co.za
37	Wynand Vlok	Various	wynand.vlok@gmail.com

Table S.2.3. List of parameters extracted from occurrence data sources and uploaded onto the Freshwater Biodiversity Information System (FBIS; freshwaterbiodiversity.org).

Parameter	Description
UUID	Unique identifier assigned by the FBIS platform.
River	Current river name based on GPS location.
Original Site Code	Original site code described by the original data collector.
FBIS Site Code	Unique site code assigned by the FBIS platform which combines the Secondary Catchment ID, the river name, and the site locality.
Site description	Original site description described by the original data collector.
Geomorphological zone - Ground truthed	Description of Geomorphological zone.
Latitude	In decimal degrees
Longitude	In decimal degrees
Sampling Date	DD-MM-YYYY
Kingdom	Kingdom
Phylum	Phylum
Class	Class
Order	Order
Family	Family
Genus	Genus
Species	Species
Taxon	Genus and species combined
Scientific Name and Authority	Scientific Name and Authority
Former Scientific Name	Any previous scientific names of the species
Common Name	Common name of species described in original data source.
Habitat	freshwater; euryhaline
Origin	native; non-native; translocated
Endemism	Widespread; Regional endemic level 1; Regional endemic level 2; Micro-endemic level 1; Micro-endemic level 2; national endemic; sub-regional endemic
Present	Yes; No
Sampling method	Fyke net; seine net; gill net; electrofishing; snorkelling; video analyses; rod and line angling; hand net; multiple
Effort (area, m^2)	Sampling effort measured in m2
Effort (time, min)	Sampling effort measure in minutes

Effort (number, throws)	Sampling effort measured as the number of net throws
Catch/number	Total number of individuals of the same species
Catch Per Unit Effort (CPUE)	CPUE where available
Number of replicates	Number of replicates
Hydraulic biotope	fast-deep; fast-shallow; slow-deep; slow-shallow
Substratum	River substratum
Depth (m)	River depth measured in meters
Near Bed Velocity (m/s)	Near bed velocity measured in m/s
Conductivity (mS m^{-1})	Water conductivity (mS m-1)
pH	Water pH
Dissolved Oxygen (%)	Dissolved Oxygen (%)
Dissolved Oxygen (mg/L)	Dissolved Oxygen (mg/L)
Temperature (°C)	Temperature (°C)
Turbidity (NTU)	Turbidity (NTU)
Collector/Assessor	Name of person who collected the data
Institute	Institution of the data collector
Reference	Full reference indicating where the data were sourced from
Reference category	Database, peer-reviewed article, report or thesis, unpublished data
DOI	Digital Object Identifier
Notes	Any notes recorded by the data extractor.

Table S.2.4. Master Species List for freshwater fishes in South Africa.

Class	Order	Family	Genus	Species	Taxon	Scientific name and authority	Common name	Origin	Endemism	Conservation status	Eco-tolerance	Status in SA
Actinopterygii	Cypriniformes	Cyprinidae	Amatolacypris	trevelyani	Amatolacypris trevelyani	Amatolacypris trevelyani Günther, 1877	Border barb	Native	Regional endemic level 1	Endangered	1	Extant
Actinopterygii	Perciformes	Ambassidae	Ambassis	natalensis	Ambassis natalensis	Ambassis natalensis Gilchrist & Thompson, 1908	Slender glassy	Native	Widespread	Least concern	1	Extant
Actinopterygii	Siluriformes	Amphiliidae	Amphilius	natalensis	Amphilius natalensis	Amphilius natalensis Boulenger, 1917	Natal mountain catfish	Native	Widespread	Least concern	1	Extant
Actinopterygii	Siluriformes	Amphiliidae	Amphilius	uranoscopus	Amphilius uranoscopus	Amphilius uranoscopus (Pfeffer, 1889)	Stargazer mountain catfish	Native	Widespread	Least concern	1	Extant
Actinopterygii	Anguilliformes	Anguillidae	Anguilla	bengalensis	Anguilla bengalensis	Anguilla bengalensis (Gray, 1831)	Indian mottled eel	Native	Widespread	Near threatened	3	Extant
Actinopterygii	Anguilliformes	Anguillidae	Anguilla	bicolor	Anguilla bicolor	Anguilla bicolor McClelland, 1844	Shortfin eel	Native	Widespread	Near threatened	3	Extant
Actinopterygii	Anguilliformes	Anguillidae	Anguilla	marmorata	Anguilla marmorata	Anguilla marmorata Quoy & Gaimard 1824	Giant mottled eel	Native	Widespread	Least concern	3	Extant
Actinopterygii	Anguilliformes	Anguillidae	Anguilla	mossambica	Anguilla mossambica	Anguilla mossambica (Peters, 1852)	African longfin eel	Native	Widespread	Least concern	3	Extant
Actinopterygii	Siluriformes	Austroglanididae	Austroglanis	barnardi	Austroglanis barnardi	Austroglanis barnardi (Skelton, 1981)	Barnard's rock catfish	Native	Regional endemic level 1	Endangered	1	Extant
Actinopterygii	Siluriformes	Austroglanididae	Austroglanis	gilli	Austroglanis gilli	Austroglanis gilli (Barnard, 1943)	Clanwilliam rock catfish	Native	Regional endemic level 1	Near threatened	1	Extant
Actinopterygii	Siluriformes	Austroglanididae	Austroglanis	sclateri	Austroglanis sclateri	Austroglanis sclateri (Boulenger, 1901)	Rock catfish	Native	Regional endemic level 2	Least concern	1	Extant
Actinopterygii	Characiformes	Characidae	Brycinus	imberi	Brycinus imberi	Brycinus imberi (Peters, 1852)	Imberi	Native	Widespread	Least concern	1	Extant
Actinopterygii	Characiformes	Characidae	Brycinus	lateralis	Brycinus lateralis	Brycinus lateralis (Boulenger, 1900)	Striped robber	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Carassius	auratus	Carassius auratus	Carassius auratus (Linnaeus, 1758)	Goldfish	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Cheilobarbus	capensis	Cheilobarbus capensis	Cheilobarbus capensis (Smith, 1841)	Berg-breede river whitefish	Native	Regional endemic level 1	Endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Cheilobarbus	serra	Cheilobarbus serra	Cheilobarbus serra (Peters, 1864)	Sawfin	Native	Micro-endemic level 1	Near threatened	1	Extant
Actinopterygii	Perciformes	Cichlidae	Chetia	brevis	Chetia brevis	Chetia brevis Jubb, 1968	Orange-fringed largemouth	Native	Widespread	Endangered	2	Extant
Actinopterygii	Perciformes	Cichlidae	Chetia	flaviventris	Chetia flaviventris	Chetia flaviventris Trewavas, 1961	Canary kurper	Native	Widespread	Least concern	2	Extant
Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	anoterus	Chiloglanis anoterus	Chiloglanis anoterus Crass, 1960	Pennant-tail suckermouth	Native	Regional endemic level 1	Least concern	1	Extant
Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	bifurcus	Chiloglanis bifurcus	Chiloglanis bifurcus Jubb & le Roux, 1969	Incomati suckermouth	Native	Micro-endemic level 1	Critically endangered	1	Extant
Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	emarginatus	Chiloglanis emarginatus	Chiloglanis emarginatus Jubb & le Roux, 1969	Pongolo suckermouth	Native	Widespread	Vulnerable	1	Extant
Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	paratus	Chiloglanis paratus	Chiloglanis paratus Crass, 1960	Sawfin suckermouth	Native	Widespread	Least concern	1	Extant
Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	pretoriae	Chiloglanis pretoriae	Chiloglanis pretoriae van der Horst, 1931	Shortspine suckermouth	Native	Widespread	Least concern	1	Extant
Actinopterygii	Siluriformes	Mochokidae	Chiloglanis	swierstrai	Chiloglanis swierstrai	Chiloglanis swierstrai van der Horst, 1931	Lowveld suckermouth	Native	Widespread	Least concern	1	Extant
Actinopterygii	Siluriformes	Clariidae	Clarias	gariepinus	Clarias gariepinus	Clarias gariepinus (Burchell, 1822)	Sharptooth catfish	Native	Widespread	Least concern	1	Extant
Actinopterygii	Siluriformes	Clariidae	Clarias	ngamensis	Clarias ngamensis	Clarias ngamensis Castelnau, 1861	Blunttooth catfish	Native	Widespread	Least concern	1	Extant
Actinopterygii	Siluriformes	Clariidae	Clarias	theodorae	Clarias theodorae	Clarias theodorae Weber, 1897	Snake catfish	Native	Widespread	Least concern	1	Extant
Actinopterygii	Perciformes	Cichlidae	Coptodon	rendalli	Coptodon rendalli	Coptodon rendalli (Boulenger, 1897)	Redbreast tilapia	Native	Widespread	Least concern	1	Extant
Actinopterygii	Perciformes	Cichlidae	Coptodon	zilli	Coptodon zilli	Coptodon zillii (Gervais, 1848)	Banded tilapia	Non-native	Widespread	Least concern	1	Extinct
Actinopterygii	Cypriniformes	Cyprinidae	Ctenopharyngodon	idella	Ctenopharyngodon idella	Ctenopharyngodon idella (Valenciennes, 1844)	Grass carp	Non-native	Widespread	Not evaluated	1	Extant
Actinopterygii	Perciformes	Anabantidae	Ctenopoma	multispine	Ctenopoma multispine	Ctenopoma multispine Peters, 1844	Many-spined climbing perch	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Cyprinus	carpio	Cyprinus carpio	Cyprinus carpio Linnaeus, 1758	Common carp	Non-native	Widespread	Vulnerable	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Engraulicypris	gariepinus	Engraulicypris gariepinus	Engraulicypris gariepinus Barnard, 1943	Orange river sardine	Native	Regional endemic level 2	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Engraulicypris	brevianalis	Engraulicypris brevianalis	Engraulicypris brevianalis (Boulenger, 1908)	Eastern river sardine	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	afrohamiltoni	Enteromius afrohamiltoni	Enteromius afrohamiltoni (Crass, 1960)	Hamilton's barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	amatolicus	Enteromius amatolicus	Enteromius amatolicus (Skelton, 1990)	Amatola barb	Native	Widespread	Data deficient	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	annectens	Enteromius annectens	Enteromius annectens (Gilchrist & Thompson, 1917)	Broadstriped barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	anoplus	Enteromius anoplus	Enteromius anoplus (Weber, 1897)	Chubbyhead barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	argenteus	Enteromius argenteus	Enteromius argenteus (Günther, 1868)	Rosefin barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	bifrenatus	Enteromius bifrenatus	Enteromius bifrenatus (Fowler, 1935)	Hyphen barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	brevipinnis	Enteromius brevipinnis	Enteromius brevipinnis (Jubb, 1966)	Shortfin barb	Native	Widespread	Near threatened	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	eutaenia	Enteromius eutaenia	Enteromius eutaenia (Boulenger, 1904)	Orangefin barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	gurneyi	Enteromius gurneyi	Enteromius gurneyi (Günther, 1868)	Redtail barb	Native	Widespread	Vulnerable	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	lineomaculatus	Enteromius lineomaculatus	Enteromius lineomaculatus (Boulenger, 1903)	Line-spotted barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	mattozi	Enteromius mattozi	Enteromius mattozi (Guimaraes, 1884)	Papermouth	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	motebensis	Enteromius motebensis	Enteromius motebensis (Steindachner, 1894)	Marico barb	Native	Widespread	Near threatened	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	neefi	Enteromius neefi	Enteromius neefi (Greenwood, 1962)	Sidespot barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	pallidus	Enteromius pallidus	Enteromius pallidus (Smith, 1841)	Goldie barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	paludinosus	Enteromius paludinosus	Enteromius paludinosus (Peters, 1852)	Straightfin barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	radiatus	Enteromius radiatus	Enteromius radiatus (Peters, 1853)	Beira barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	toppini	Enteromius toppini	Enteromius toppini (Boulenger, 1916)	East-coast barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	treurensis	Enteromius treurensis	Enteromius treurensis (Groenewald, 1958)	Treur River barb	Native	Micro-endemic level 2	Critically endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	trimaculatus	Enteromius trimaculatus	Enteromius trimaculatus (Peters, 1852)	Threespot barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	unitaeniatus	Enteromius unitaeniatus	Enteromius unitaeniatus (Günther, 1866)	Longbeard barb	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Enteromius	viviparus	Enteromius viviparus	Enteromius viviparus (Weber, 1897)	Bowstripe barb	Native	Widespread	Least concern	1	Extant

Class	Order	Family	Genus	Species	Taxon	Scientific name and authority	Common name	Origin	Endemism	Conservation status	Eco-tolerance	Status in SA
Actinopterygii	Osmeriformes	Galaxiidae	Galaxias	zebratus	Galaxias zebratus	Galaxias zebratus (Castelnau, 1861)	Cape galaxias	Native	Regional endemic level 1	Data deficient	2	Extant
Actinopterygii	Cyprinodontiformes	Poeciliidae	Gambusia	affinis	Gambusia affinis	Gambusia affinis (Baird & Girard, 1853)	Mosquitofish	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Characiformes	Characidae	Hydrocynus	vittatus	Hydrocynus vittatus	Hydrocynus vittatus Castelnau, 1861	Tigerfish	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Hypophthalmichthys	molitrix	Hypophthalmichthys molitrix	Hypophthalmichthys molitrix (Valenciennes, 1844)	Silver carp	Non-native	Widespread	Near threatened	1	Extant
Actinopterygii	Gonorynchiformes	Kneriidae	Kneria	auriculata	Kneria auriculata	Kneria auriculata (Pellegrin, 1905)	Southern kneria	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	capensis	Labeo capensis	Labeo capensis (Smith, 1841)	Orange River mudfish	Native	Regional endemic level 2	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	congoro	Labeo congoro	Labeo congoro Peters, 1852	Purple labeo	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	cylindricus	Labeo cylindricus	Labeo cylindricus Peters, 1852	Redeye labeo / African Carp	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	molybdinus	Labeo molybdinus	Labeo molybdinus du Plessis, 1963	Leaden labeo	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	rosae	Labeo rosae	Labeo rosae Steindachner, 1894	Rednose labeo	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	rubromaculatus	Labeo rubromaculatus	Labeo rubromaculatus Gilchrist & Thompson, 1913	Tugela labeo	Native	Micro-endemic level 1	Vulnerable	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	ruddi	Labeo ruddi	Labeo ruddi Boulenger, 1907	Silver labeo	Native	Widespread	Data deficient	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	seeberi	Labeo seeberi	Labeo seeberi Gilchrist & Thompson, 1911	Clanwilliam sandfish	Native	Regional endemic level 2	Endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeo	umbratus	Labeo umbratus	Labeo umbratus (Smith, 1841)	Moggel	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	aeneus	Labeobarbus aeneus	Labeobarbus aeneus (Burchell, 1822)	Vaal-Orange smallmouth yellowfish	Native	Regional endemic level 2	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	kimberleyensis	Labeobarbus kimberleyensis	Labeobarbus kimberleyensis Gilchrist & Thompson, 1913	Vaal-Orange largemouth yellowfish	Native	Regional endemic level 2	Near threatened	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	marequensis	Labeobarbus marequensis	Labeobarbus marequensis Smith, 1841	Lowveld largescale yellowfish	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	natalensis	Labeobarbus natalensis	Labeobarbus natalensis Castelnau, 1861	Scaly Kwa-Zulu Natal yellowfish	Native	Regional endemic level 1	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	nelspruitensis	Labeobarbus nelspruitensis	Labeobarbus nelspruitensis (Gilchrist & Thompson, 1911)	Incomati chiselmouth	Native	Regional endemic level 1	Near threatened	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	polylepis	Labeobarbus polylepis	Labeobarbus polylepis Boulenger, 1907	Bushveld smallscale yellowfish	Native	Regional endemic level 1	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Labeobarbus	seeberi	Labeobarbus seeberi	Labeobarbus seeberi (Gilchrist & Thompson, 1913)	Clanwilliam yellowfish	Native	Regional endemic level 1	Near threatened	1	Extant
Actinopterygii	Cyprinodontiformes	Poeciliidae	Lacustricola	katangae	Lacustricola katangae	Lacustricola katangae (Boulenger, 1912)	Striped topminnow	Native	Widespread	Least concern	2	Extant
Actinopterygii	Cyprinodontiformes	Poeciliidae	Lacustricola	myaposae	Lacustricola myaposae	Lacustricola myaposae (Boulenger, 1912)	Natal topminnow	Native	Regional endemic level 1	Near threatened	2	Extant
Actinopterygii	Perciformes	Centrarchidae	Lepomis	macrochirus	Lepomis macrochirus	Lepomis macrochirus Rafinesque, 1819	Bluegill sunfish	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	caudisquamatus	Marcusenius caudisquamatus	Marcusenius caudisquamatus Maake, Gon & Swartz, 2014		Native	Micro-endemic level 1	Endangered	1	Extant
Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	krameri	Marcusenius krameri	Marcusenius krameri Maake, Gon & Swartz, 2014		Native	Widespread	Least concern	1	Extant
Actinopterygii	Osteoglossiformes	Mormyridae	Marcusenius	pongolensis	Marcusenius pongolensis	Marcusenius pongolensis (Fowler, 1934)		Native	Widespread	Least concern	1	Extant
Actinopterygii	Elopiformes	Megalopidae	Megalops	cyprinoides	Megalops cyprinoides	Megalops cyprinoides (Broussonet, 1782)	Oxeye tarpon	Native	Widespread	Data deficient	3	Extant
Actinopterygii	Characiformes	Characidae	Micralestes	acutidens	Micralestes acutidens	Micralestes acutidens (Peters, 1852)	Silver robber	Native	Widespread	Least concern	1	Extant
Actinopterygii	Perciformes	Anabantidae	Microctenopoma	intermedium	Microctenopoma intermedium	Microctenopoma intermedium (Pellegrin, 1920)	Blackspot climbing perch	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cyprinodontiformes	Poeciliidae	Micropanchax	johnstoni	Micropanchax johnstoni	Micropanchax johnstoni Ghedotti, 2000	Johnston's topminnow	Native	Widespread	Least concern	2	Extant
Actinopterygii	Perciformes	Centrarchidae	Micropterus	dolomieu	Micropterus dolomieu	Micropterus dolomieu Lacepède, 1802	Smallmouth bass	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Perciformes	Centrarchidae	Micropterus	floridanus	Micropterus floridanus	Micropterus floridanus Lesueur, 1822	Florida bass	Non-native	Widespread	Not evaluated	1	Extant
Actinopterygii	Perciformes	Centrarchidae	Micropterus	punctulatus	Micropterus punctulatus	Micropterus punctulatus (Rafinesque, 1819)	Spotted bass	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Perciformes	Centrarchidae	Micropterus	salmoides	Micropterus salmoides	Micropterus salmoides (Lacepède, 1802)	Largemouth bass	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Namaquacypris	hospes	Namaquacypris hospes	Namaquacypris hospes (Barnard, 1938)	Namaqua barb	Native	Regional endemic level 1	Least concern	1	Extant
Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	orthonotus	Nothobranchius orthonotus	Nothobranchius orthonotus (Peters, 1844)	Spotted killifish	Native	Widespread	Least concern	2	Extant
Actinopterygii	Cyprinodontiformes	Aplocheilidae	Nothobranchius	pienaari	Nothobranchius pienaari	Nothobranchius pienaari Schidlovskiy, Watters & Wildekamp, 2010		Native	Widespread	Least concern	2	Extant
Actinopterygii	Salmoniformes	Salmonidae	Oncorhynchus	mykiss	Oncorhynchus mykiss	Oncorhynchus mykiss (Walbaum, 1792)	Rainbow trout	Non-native	Widespread	Not evaluated	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Opsaridium	peringueyi	Opsaridium peringueyi	Opsaridium peringueyi (Gilchrist & Thompson, 1913)	Southern barred minnow	Native	Widespread	Extinct	1	Extant
Actinopterygii	Perciformes	Cichlidae	Oreochromis	andersonii	Oreochromis andersonii	Oreochromis andersonii (Castelnau, 1861)	Threespot tilapia	Non-native	Widespread	Vulnerable	2	Extinct - failed introduction
Actinopterygii	Perciformes	Cichlidae	Oreochromis	aureus	Oreochromis aureus	Oreochromis aureus (Steindachner, 1864)	Blue Tilapia	Non-native	Widespread	Least concern	2	Extant
Actinopterygii	Perciformes	Cichlidae	Oreochromis	mossambicus	Oreochromis mossambicus	Oreochromis mossambicus (Peters, 1852)	Mozambique tilapia	Native	Widespread	Vulnerable	2	Extant
Actinopterygii	Perciformes	Cichlidae	Oreochromis	niloticus	Oreochromis niloticus	Oreochromis niloticus (Linnaeus, 1758)	Nile tilapia	Non-native	Widespread	Oreochromis niloticus	2	Extant

Class	Order	Family	Genus	Species	Taxon	Scientific name and authority	Common name	Origin	Endemism	Conservation status	Eco-tolerance	Status in SA
Actinopterygii	Perciformes	Cichlidae	Oreochromis	placidus	Oreochromis placidus	Oreochromis placidus (Trewavas, 1941)	Black tilapia	Native	Widespread	Least concern	2	Extant
Actinopterygii	Siluriformes	Pangasiidae	Pangasius	sanitwongsei	Pangasius sanitwongsei	Pangasius sanitwongsei Smith, 1931	Chao Phraya giant catfish	Non-native	Widespread	Critically endangered	1	Extant
Actinopterygii	Perciformes	Percidae	Perca	fluviatilis	Perca fluviatilis	Perca fluviatilis Linnaeus, 1758	European perch	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Osteoglossiformes	Mormyridae	Petrocephalus	wesselsi	Petrocephalus wesselsi	Petrocephalus wesselsi (Kramer & van der Bank, 2000)	Southern churchill	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cyprinodontiformes	Poeciliidae	Poecilia	reticulata	Poecilia reticulata	Poecilia reticulata Peters, 1859	Guppy	Non-native	Widespread	Not evaluated	2	Extant
Sacropterygii	Lepidosireniformes	Protopteridae	Protopterus	annectens	Protopterus annectens	Protopterus annectens, Poll, 1961	African lungfish	Native	Widespread	Least concern	2	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	afer	Pseudobarbus afer	Pseudobarbus afer (Peters, 1864)	Eastern Cape redfin	Native	Micro-endemic level 1	Endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	asper	Pseudobarbus asper	Pseudobarbus asper (Boulenger, 1911)	Smallscale redfin	Native	Regional endemic level 2	Vulnerable	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	burchelli	Pseudobarbus burchelli	Pseudobarbus burchelli (Smith, 1841)	Breede River redfin	Native	Micro-endemic level 1	Critically endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	burgi	Pseudobarbus burgi	Pseudobarbus burgi (Boulenger, 1911)	Berg River redfin	Native	Regional endemic level 2	Endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	phlegethon	Pseudobarbus phlegethon	Pseudobarbus phlegethon (Barnard, 1938)	Fiery redfin	Native	Micro-endemic level 1	Endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	quathlambae	Pseudobarbus quathlambae	Pseudobarbus quathlambae (Barnard, 1938)	Maloti minnow	Native	Micro-endemic level 1	Endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	senticeps	Pseudobarbus senticeps	Pseudobarbus senticeps (Smith, 1936)		Native	Micro-endemic level 2	Critically endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	skeltoni	Pseudobarbus skeltoni	Pseudobarbus skeltoni Chakona and Swartz 2013	Giant redfin	Native	Micro-endemic level 1	Endangered	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	swartzi	Pseudobarbus swartzi	Pseudobarbus swartzi Chakona & Skelton, 2017	Gamtoos redfin	Native	Micro-endemic level 2	Vulnerable	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	tenuis	Pseudobarbus tenuis	Pseudobarbus tenuis (Barnard, 1938)	Slender redfin	Native	Regional endemic level 1	Near threatened	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Pseudobarbus	verloreni	Pseudobarbus verloreni	Pseudobarbus verloreni Chakona, Swartz & Skelton, 2014		Native	Micro-endemic level 2	Endangered	1	Extant
Actinopterygii	Perciformes	Cichlidae	Pseudocrenilabrus	philander	Pseudocrenilabrus philander	Pseudocrenilabrus philander (Weber, 1897)	Southern mouthbrooder	Native	Widespread	Least concern	2	Extant
Actinopterygii	Siluriformes	Loricariidae	Pterygoplichthys	disjunctivus	Pterygoplichthys disjunctivus	Pterygoplichthys disjunctivus (Weber, 1991)	Vermiculated sailfin catfish	Non-native	Widespread	Not evaluated	1	Extant
Actinopterygii	Salmoniformes	Salmonidae	Salmo	salar	Salmo salar	Salmo salar Linnaeus, 1758	Atlantic salmon	Non-native	Widespread	Vulnerable	1	Extinct - failed introduction
Actinopterygii	Salmoniformes	Salmonidae	Salmo	trutta	Salmo trutta	Salmo trutta Linnaeus, 1758	Brown trout	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Salmoniformes	Salmonidae	Salvelinus	fontinalis	Salvelinus fontinalis	Salvelinus fontinalis (Mitchill, 1815)	Brook trout	Non-native	Widespread	Not evaluated	1	Extant
Actinopterygii	Perciformes	Anabantidae	Sandelia	bainsii	Sandelia bainsii	Sandelia bainsii Castelnau, 1861	Eastern Cape rocky	Native	Widespread	Endangered	1	Extant
Actinopterygii	Perciformes	Anabantidae	Sandelia	capensis	Sandelia capensis	Sandelia capensis (Cuvier, 1829)	Cape kurper	Native	Regional endemic level 1	Data deficient	1	Extant
Actinopterygii	Siluriformes	Schilbeidae	Schilbe	depressirostris	Schilbe depressirostris	Schilbe depressirostris (Peters, 1852)	Butter catfish	Native	Widespread	Least concern	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Sedercypris	calidus	Sedercypris calidus	Sedercypris calidus (Barnard, 1938)	Clanwilliam redfin	Native	Regional endemic level 2	Near threatened	1	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Sedercypris	erubescens	Sedercypris erubescens	Sedercypris erubescens (Skelton, 1974)	Twee river redfin	Native	Micro-endemic level 1	Critically endangered	1	Extant
Actinopterygii	Perciformes	Cichlidae	Serranochromis	jallae	Serranochromis jallae	Serranochromis jallae (Boulenger, 1896)		Non-native	Widespread	Least concern	2	Extant
Actinopterygii	Perciformes	Cichlidae	Serranochromis	meridianus	Serranochromis meridianus	Serranochromis meridianus Jubb, 1967	Lowveld largemouth	Native	Widespread	Endangered	2	Extant
Actinopterygii	Perciformes	Cichlidae	Serranochromis	robustus	Serranochromis robustus	Serranochromis robustus (Boulenger, 1896)	Nembwe	Non-native	Widespread	Least concern	2	Extinct - failed introduction
Actinopterygii	Siluriformes	Mochokidae	Synodontis	zambezensis	Synodontis zambezensis	Synodontis zambezensis Peters, 1852	Brown squeaker	Native	Widespread	Least concern	1	Extant
Actinopterygii	Perciformes	Cichlidae	Tilapia	sparrmanii	Tilapia sparrmanii	Tilapia sparrmanii Smith, 1840	Banded tilapia	Native	Widespread	Least concern	2	Extant
Actinopterygii	Cypriniformes	Cyprinidae	Tinca	tinca	Tinca tinca	Tinca tinca (Linnaeus, 1758)	Tench	Non-native	Widespread	Least concern	1	Extant
Actinopterygii	Cyprinodontiformes	Poeciliidae	Xiphophorus	maculatus	Xiphophorus maculatus	Xiphophorus maculatus (Gunther, 1866)	Southern platyfish	Non-native	Widespread	Data deficient	1	Extant
Actinopterygii	Cyprinodontiformes	Poeciliidae	Xiphophorus	helleri	Xiphophorus helleri	Xiphophorus helleri Heckel, 1848	Swordtail	Non-native	Widespread	Least concern	1	Extant

Table S. 2.5. Comparison between the species listed in the National Biodiversity Assessments (Skowno et al., 2019) and fish species contained on the Master Species List for Freshwater Fishes in South Africa. Yellow shading indicates a species that was listed not listed on the NBA list, but included in this study. Green shading indicates 'species' that aren't yet formally described and were omitted from this study but included in the NBA list. Blue shading indicates marine sporadic or marine peripheral species that were not included for this study but included on the NBA list.

NBA Species List	Master Species List for freshwater fishes in SA	Origin	NBA Species List	Master Species List for freshwater fishes in SA	Origin	NBA Species List	Master Species List for freshwater fishes in SA	Origin
X	Ambassis natalensis	Native	X	Enteromius trimaculatus	Native	X	Nothobranchius pienaari	Native
Amphilius natalensis	Amphilius natalensis	Native	X	Enteromius unitaeniatus	Native	X	Oncorhynchus mykiss	Non-native
Amphilius uranoscopus	Amphilius uranoscopus	Native	X	Enteromius viviparus	Native	Opsaridium peringueyi	Opsaridium peringueyi	Native
X	Anguilla bengalensis	Native	Galaxias sp nov breede	X	Native	X	Oreochromis aureus	Non-native
X	Anguilla bicolor	Native	Galaxias sp nov goukou	X	Native	Oreochromis mossambicus	Oreochromis mossambicus	Native
X	Anguilla marmorata	Native	Galaxias sp nov gourits	X	Native	X	Oreochromis niloticus	Non-native
X	Anguilla mossambica	Native	Galaxias sp nov heuningnes	X	Native	Oreochromis placidus	Oreochromis placidus	Native
Austroglanis barnardi	Austroglanis barnardi	Native	Galaxias sp nov klein	X	Native	X	Perca fluviatilis	Non-native
Austroglanis gilli	Austroglanis gilli	Native	Galaxias sp nov riviersonderend	X	Native	X	Petrocephalus catostoma	Non-native
Austroglanis sclateri	Austroglanis sclateri	Native	Galaxias sp nov slender	X	Native	Petrocephalus wesselsi	Petrocephalus wesselsi	Native
Brycinus imberi	Brycinus imberi	Native	Galaxias sp nov verlorenvlei	X	Native	X	Poecilia reticulata	Non-native
Brycinus lateralis	Brycinus lateralis	Native	Galaxias zebratus	Galaxias zebratus	Native	Protopterus annectens brieni	Protopterus annectens	Native
X	Carassius auratus	Non-native	X	Gambusia affinis	Non-native	Pseudobarbus afer	Pseudobarbus afer	Native
Chetia brevis	Chetia brevis	Native	Glossogobius callidus	X	Marine	Pseudobarbus asper	Pseudobarbus asper	Native
Chetia flaviventris	Chetia flaviventris	Native	Hydrocynus vittatus	Hydrocynus vittatus	Native	Pseudobarbus burchelli	Pseudobarbus burchelli	Native
Chiloglanis anoterus	Chiloglanis anoterus	Native	X	Hypophthalmichthys molitrix	Non-native	Pseudobarbus burgi	Pseudobarbus burgi	Native
Chiloglanis bifurcus	Chiloglanis bifurcus	Native	X	Kneria auriculata	Native	Pseudobarbus calidus	Sedercypris calidus	Native
Chiloglanis emarginatus	Chiloglanis emarginatus	Native	Kneria sp nov south africa	X	Native	Pseudobarbus capensis	Cheilobarbus capensis	Native
Chiloglanis paratus	Chiloglanis paratus	Native	Labeo capensis	Labeo capensis	Native	Pseudobarbus erubescens	Sedercypris erubescens	Native
Chiloglanis pretoriae	Chiloglanis pretoriae	Native	Labeo congoro	Labeo congoro	Native	Pseudobarbus phlegethon	Pseudobarbus phlegethon	Native
Chiloglanis swierstrai	Chiloglanis swierstrai	Native	Labeo cylindricus	Labeo cylindricus	Native	Pseudobarbus quathlambae	Pseudobarbus quathlambae	Native
Clarias gariepinus	Clarias gariepinus	Native	Labeo molybdinus	Labeo molybdinus	Native	Pseudobarbus senticeps	Pseudobarbus senticeps	Native
Clarias ngamensis	Clarias ngamensis	Native	Labeo rosae	Labeo rosae	Native	Pseudobarbus serra	Cheilobarbus serra	Native
Clarias theodorae	Clarias theodorae	Native	Labeo rubromaculatus	Labeo rubromaculatus	Native	Pseudobarbus skeltoni	Pseudobarbus skeltoni	Native
Coptodon rendalli	Coptodon rendalli	Native	Labeo ruddi	Labeo ruddi	Native	Pseudobarbus sp nov breede	X	Native
X	Ctenopharyngodon idella	Non-native	Labeo seeberi	Labeo seeberi	Native	Pseudobarbus sp nov doring	X	Native
Ctenopoma multispine	Ctenopoma multispine	Native	Labeo umbratus	Labeo umbratus	Native	Pseudobarbus sp nov forest	X	Native
X	Cyprinus carpio	Non-native	Labeobarbus aeneus	Labeobarbus aeneus	Native	Pseudobarbus sp nov heuningnes	X	Native
Engraulicypris gariepinus	Engraulicypris gariepinus	Native	Labeobarbus kimberleyensis	Labeobarbus kimberleyensis	Native	Pseudobarbus sp nov keiskamma	X	Native
Engraulicypris brevianalis	Engraulicypris brevianalis	Native	Labeobarbus marequensis	Labeobarbus marequensis	Native	Pseudobarbus sp nov keurbooms	X	Native
Enteromius afrohamiltoni	Enteromius afrohamiltoni	Native	Labeobarbus natalensis	Labeobarbus natalensis	Native	Pseudobarbus swartzi	Pseudobarbus swartzi	Native
Enteromius amatolicus	Enteromius amatolicus	Native	Labeobarbus nelspruitensis	Labeobarbus nelspruitensis	Native	Pseudobarbus tenuis	Pseudobarbus tenuis	Native
Enteromius annectens	Enteromius annectens	Native	Labeobarbus polylepis	Labeobarbus polylepis	Native	Pseudobarbus trevelyani	Amatolacypris trevelyani	Native
Enteromius anoplus	Enteromius anoplus	Native	Labeobarbus seeberi	Labeobarbus seeberi	Native	Pseudobarbus verloreni	Pseudobarbus verloreni	Native
X	Enteromius argenteus	Non-native	Micropanchax katangae	Lacustricola katangae	Native	Pseudocrenilabrus philander	Pseudocrenilabrus philander	Native
Enteromius bifrenatus	Enteromius bifrenatus	Native	Micropanchax myaposae	Lacustricola myaposae	Native	X	Salmo trutta	Non-native
Enteromius brevipinnis	Enteromius brevipinnis	Native	X	Lepomis macrochirus	Non-native	X	Salvelinus fontinalis	Non-native
Enteromius eutaenia	Enteromius eutaenia	Native	Marcusenius caudisquamatus	Marcusenius caudisquamatus	Native	Sandelia bainsii	Sandelia bainsii	Native
Enteromius gurneyi	Enteromius gurneyi	Native	Marcusenius krameri	Marcusenius krameri	Native	Sandelia capensis	Sandelia capensis	Native
Enteromius hospes	Namaquacypris hospes	Native	X	Marcusenius macrolepidotus	Non-native	Schilbe intermedius	Schilbe depressirostris	Native
Enteromius lineomaculatus	Enteromius lineomaculatus	Native	Marcusenius pongolensis	Marcusenius pongolensis	Native	Serranochromis meridianus	Serranochromis meridianus	Native
Enteromius crocodilensis	Enteromius mattozi	Native	X	Megalops cyprinoides	Native	Silhouettea sibayi	X	Marine
Enteromius motebensis	Enteromius motebensis	Native	Marcusenius sp nov kosi	X	Native	X	Serranochromis robustus	Non-native
X	Enteromius neefi	Native	Micralestes acutidens	Micralestes acutidens	Native	X	Serranochromis jallae	Non-native
Enteromius pallidus	Enteromius pallidus	Native	Microctenopoma intermedium	Microctenopoma intermedium	Native	Synodontis zambezensis	Synodontis zambezensis	Native
Enteromius paludinosus	Enteromius paludinosus	Native	Micropanchax johnstoni	Micropanchax johnstoni	Native	Tilapia sparrmanii	Tilapia sparrmanii	Native
Enteromius radiatus	Enteromius radiatus	Native	X	Micropterus dolomieu	Non-native	X	Tinca tinca	Non-native

Enteromius sp nov south africa	X	Native	X	Micropterus floridanus	Non-native	X	Xiphophorus maculatus	Non-native
Enteromius sp nov waterberg	X	Native	X	Micropterus punctulatus	Non-native	X	Xiphophorus helleri	Non-native
Enteromius toppini	Enteromius toppini	Native	X	Micropterus salmoides	Non-native			
Enteromius treurensis	Enteromius treurensis	Native	Nothobranchius orthonotus	Nothobranchius orthonotus	Native			

Supplementary S3

Table S. 3.1. List of native species that have been translocated outside of their native range, extracted from Ellender and Weyl (2014).

#	Species Name	Status
1	Tilapia sparrmanii	Established, widespread
2	Oreochromis mossambicus	Established, widespread
3	Coptedon rendalli	Established, widespread
4	Enteromius anoplus	Established, widespread
5	Clarias gariepinus	Established, widespread
6	Labeobarbus aeneus	Established
7	Pseudocrenilabrus philander	Established
8	Barbus treurensis	Established
9	Kneria auriculata	Established
10	Labeobarbus natalensis	Established
11	Labeo capensis	Established
12	Labeo umbratus	Established
13	Sandelia capensis	Established, localised
14	Hydrocynus vittatus	Established, localised
15	Labeobarbus capensis	Established, localised
16	Barbus calidus	Established, localised
17	Barbus serra	Established, localised
18	Chetia brevis	Established, localised

Table S. 3.2a. List of all native freshwater fishes occurring in each province in South Africa.

Province	Species Name	Number of Records	IUCN Conservation Status	Endemism Category
Eastern Cape	Ambassis natalensis	12	Least concern	Subregional endemic
Eastern Cape	Anguilla bicolor	3	Near threatened	Widespread
Eastern Cape	Anguilla marmorata	25	Least concern	Widespread
Eastern Cape	Anguilla mossambica	202	Least concern	Widespread
Eastern Cape	Austroglanis sclateri	21	Least concern	Regional endemic level 2
Eastern Cape	Clarias gariepinus	11	Least concern	Widespread
Eastern Cape	Engraulicypris brevianalis	2	Least concern	Subregional endemic
Eastern Cape	Enteromius afrohamiltoni	1	Least concern	Subregional endemic
Eastern Cape	Enteromius amatolicus	31	Data deficient	National endemic
Eastern Cape	Enteromius anoplus	432	Least concern	Subregional endemic
Eastern Cape	Enteromius eutaenia	4	Least concern	Widespread
Eastern Cape	Enteromius gurneyi	6	Vulnerable	Subregional endemic
Eastern Cape	Enteromius pallidus	192	Least concern	Subregional endemic
Eastern Cape	Enteromius radiatus	1	Least concern	Subregional endemic
Eastern Cape	Enteromius trimaculatus	3	Least concern	Subregional endemic
Eastern Cape	Enteromius viviparus	3	Least concern	Subregional endemic
Eastern Cape	Galaxias zebratus	28	Data deficient	Regional endemic level 1
Eastern Cape	Labeo capensis	10	Least concern	Regional endemic level 2
Eastern Cape	Labeo umbratus	154	Least concern	Subregional endemic
Eastern Cape	Labeobarbus aeneus	52	Least concern	Regional endemic level 2
Eastern Cape	Labeobarbus kimberleyensis	13	Near threatened	Regional endemic level 2
Eastern Cape	Labeobarbus marequensis	14	Least concern	Subregional endemic
Eastern Cape	Labeobarbus natalensis	3	Least concern	Regional endemic level 1
Eastern Cape	Megalops cyprinoides	3	Data deficient	Widespread
Eastern Cape	Opsaridium peringueyi	2	Least concern	Subregional endemic
Eastern Cape	Oreochromis mossambicus	128	Vulnerable	Widespread
Eastern Cape	Pseudobarbus afer	352	Endangered	Micro-endemic level 1
Eastern Cape	Pseudobarbus asper	37	Vulnerable	Regional endemic level 2
Eastern Cape	Pseudobarbus capensis	1	Endangered	Regional endemic level 1
Eastern Cape	Pseudobarbus senticeps	5	Critically endangered	Micro-endemic level 2
Eastern Cape	Pseudobarbus swartzi	9	Vulnerable	Micro-endemic level 2
Eastern Cape	Pseudobarbus trevelyani	79	Endangered	Regional endemic level 1

Eastern Cape	Pseudocrenilabrus philander	20	Least concern	Subregional endemic
Eastern Cape	Sandelia bainsii	103	Endangered	National endemic
Eastern Cape	Sandelia capensis	202	Data deficient	Regional endemic level 1
Free State	Anguilla mossambica	1	Least concern	Widespread
Free State	Austroglanis sclateri	19	Least concern	Regional endemic level 2
Free State	Clarias gariepinus	97	Least concern	Widespread
Free State	Enteromius anoplus	89	Least concern	Subregional endemic
Free State	Enteromius argenteus	1	Least concern	Subregional endemic
Free State	Enteromius pallidus	12	Least concern	Subregional endemic
Free State	Enteromius paludinosus	19	Least concern	Widespread
Free State	Enteromius trimaculatus	1	Least concern	Subregional endemic
Free State	Galaxias zebratus	1	Data deficient	Regional endemic level 1
Free State	Labeo capensis	145	Least concern	Regional endemic level 2
Free State	Labeo umbratus	97	Least concern	Subregional endemic
Free State	Labeobarbus aeneus	159	Least concern	Regional endemic level 2
Free State	Labeobarbus kimberleyensis	82	Near threatened	Regional endemic level 2
Free State	Labeobarbus marequensis	1	Least concern	Subregional endemic
Free State	Pseudobarbus asper	5	Vulnerable	Regional endemic level 2
Free State	Pseudobarbus phlegethon	1	Endangered	Micro-endemic level 1
Free State	Pseudobarbus quathlambae	1	Endangered	Micro-endemic level 1
Free State	Pseudocrenilabrus philander	22	Least concern	Subregional endemic
Free State	Tilapia sparrmanii	12	Least concern	Widespread
Gauteng	Amphilius natalensis	1	Least concern	Widespread
Gauteng	Amphilius uranoscopus	13	Least concern	Subregional endemic
Gauteng	Anguilla mossambica	1	Least concern	Widespread
Gauteng	Austroglanis sclateri	5	Least concern	Regional endemic level 2
Gauteng	Chetia flaviventris	11	Least concern	Subregional endemic
Gauteng	Chiloglanis emarginatus	1	Vulnerable	Subregional endemic
Gauteng	Chiloglanis pretoriae	40	Least concern	Subregional endemic
Gauteng	Clarias gariepinus	93	Least concern	Widespread
Gauteng	Coptodon rendalli	1	Least concern	Widespread
Gauteng	Engraulicypris brevianalis	4	Least concern	Subregional endemic
Gauteng	Enteromius annectens	1	Least concern	Subregional endemic
Gauteng	Enteromius anoplus	91	Least concern	Subregional endemic

Gauteng	Enteromius argenteus	1	Least concern	Subregional endemic
Gauteng	Enteromius brevipinnis	1	Near threatened	Subregional endemic
Gauteng	Enteromius eutaenia	1	Least concern	Widespread
Gauteng	Enteromius mattozi	6	Least concern	Subregional endemic
Gauteng	Enteromius motebensis	14	Near threatened	Subregional endemic
Gauteng	Enteromius neefi	3	Least concern	Subregional endemic
Gauteng	Enteromius pallidus	11	Least concern	Subregional endemic
Gauteng	Enteromius paludinosus	66	Least concern	Widespread
Gauteng	Enteromius trimaculatus	17	Least concern	Subregional endemic
Gauteng	Enteromius unitaeniatus	20	Least concern	Subregional endemic
Gauteng	Labeo capensis	8	Least concern	Regional endemic level 2
Gauteng	Labeo cylindricus	6	Least concern	Widespread
Gauteng	Labeo molybdinus	10	Least concern	Subregional endemic
Gauteng	Labeo umbratus	3	Least concern	Subregional endemic
Gauteng	Labeobarbus aeneus	10	Least concern	Regional endemic level 2
Gauteng	Labeobarbus kimberleyensis	8	Near threatened	Regional endemic level 2
Gauteng	Labeobarbus marequensis	97	Least concern	Subregional endemic
Gauteng	Labeobarbus polylepis	23	Least concern	Regional endemic level 1
Gauteng	Lacustricola katangae	2	Least concern	Subregional endemic
Gauteng	Opsaridium peringueyi	1	Least concern	Subregional endemic
Gauteng	Oreochromis mossambicus	19	Vulnerable	Widespread
Gauteng	Pseudocrenilabrus philander	108	Least concern	Subregional endemic
Gauteng	Schilbe intermedius	4	Least concern	Widespread
Gauteng	Serranochromis meridianus	2	Endangered	Subregional endemic
Gauteng	Synodontis zambezensis	2	Least concern	Subregional endemic
Gauteng	Tilapia sparrmanii	103	Least concern	Widespread
Kwazulu Natal	Ambassis natalensis	44	Least concern	Subregional endemic
Kwazulu Natal	Amphilius natalensis	232	Least concern	Widespread
Kwazulu Natal	Amphilius uranoscopus	87	Least concern	Subregional endemic
Kwazulu Natal	Anguilla bengalensis	20	Near threatened	Widespread
Kwazulu Natal	Anguilla bicolor	5	Near threatened	Widespread
Kwazulu Natal	Anguilla marmorata	93	Least concern	Widespread
Kwazulu Natal	Anguilla mossambica	427	Least concern	Widespread
Kwazulu Natal	Austroglanis sclateri	4	Least concern	Regional endemic level 2

Kwazulu Natal	Brycinus imberi	100	Least concern	Widespread
Kwazulu Natal	Brycinus lateralis	62	Least concern	Subregional endemic
Kwazulu Natal	Chetia flaviventris	1	Least concern	Subregional endemic
Kwazulu Natal	Chiloglanis anoterus	72	Least concern	Regional endemic level 1
Kwazulu Natal	Chiloglanis emarginatus	30	Vulnerable	Subregional endemic
Kwazulu Natal	Chiloglanis paratus	56	Least concern	Subregional endemic
Kwazulu Natal	Chiloglanis pretoriae	1	Least concern	Subregional endemic
Kwazulu Natal	Chiloglanis swierstrai	63	Least concern	Subregional endemic
Kwazulu Natal	Clarias gariepinus	530	Least concern	Widespread
Kwazulu Natal	Clarias ngamensis	7	Least concern	Subregional endemic
Kwazulu Natal	Clarias theodorae	79	Least concern	Widespread
Kwazulu Natal	Coptodon rendalli	104	Least concern	Widespread
Kwazulu Natal	Ctenopoma multispine	27	Least concern	Subregional endemic
Kwazulu Natal	Engraulicypris brevianalis	170	Least concern	Subregional endemic
Kwazulu Natal	Enteromius afrohamiltoni	84	Least concern	Subregional endemic
Kwazulu Natal	Enteromius annectens	112	Least concern	Subregional endemic
Kwazulu Natal	Enteromius anoplus	463	Least concern	Subregional endemic
Kwazulu Natal	Enteromius argenteus	90	Least concern	Subregional endemic
Kwazulu Natal	Enteromius bifrenatus	21	Least concern	Subregional endemic
Kwazulu Natal	Enteromius brevipinnis	2	Near threatened	Subregional endemic
Kwazulu Natal	Enteromius eutaenia	13	Least concern	Widespread
Kwazulu Natal	Enteromius gurneyi	149	Vulnerable	Subregional endemic
Kwazulu Natal	Enteromius lineomaculatus	9	Least concern	Subregional endemic
Kwazulu Natal	Enteromius mattozi	2	Least concern	Subregional endemic
Kwazulu Natal	Enteromius neefi	2	Least concern	Subregional endemic
Kwazulu Natal	Enteromius pallidus	52	Least concern	Subregional endemic
Kwazulu Natal	Enteromius paludinosus	579	Least concern	Widespread
Kwazulu Natal	Enteromius radiatus	46	Least concern	Subregional endemic
Kwazulu Natal	Enteromius toppini	233	Least concern	Subregional endemic
Kwazulu Natal	Enteromius trimaculatus	503	Least concern	Subregional endemic
Kwazulu Natal	Enteromius unitaeniatus	71	Least concern	Subregional endemic
Kwazulu Natal	Enteromius viviparus	701	Least concern	Subregional endemic
Kwazulu Natal	Galaxias zebratus	1	Data deficient	Regional endemic level 1
Kwazulu Natal	Hydrocynus vittatus	94	Least concern	Widespread

Kwazulu Natal	Labeo capensis	11	Least concern	Regional endemic level 2
Kwazulu Natal	Labeo congoro	18	Least concern	Subregional endemic
Kwazulu Natal	Labeo cylindricus	131	Least concern	Widespread
Kwazulu Natal	Labeo molybdinus	268	Least concern	Subregional endemic
Kwazulu Natal	Labeo rosae	127	Least concern	Subregional endemic
Kwazulu Natal	Labeo rubromaculatus	223	Vulnerable	Micro-endemic level 1
Kwazulu Natal	Labeo umbratus	2	Least concern	Subregional endemic
Kwazulu Natal	Labeobarbus aeneus	11	Least concern	Regional endemic level 2
Kwazulu Natal	Labeobarbus marequensis	95	Least concern	Subregional endemic
Kwazulu Natal	Labeobarbus natalensis	1032	Least concern	Regional endemic level 1
Kwazulu Natal	Labeobarbus nelspruitensis	7	Near threatened	Regional endemic level 1
Kwazulu Natal	Labeobarbus polylepis	48	Least concern	Regional endemic level 1
Kwazulu Natal	Lacustricola katangae	100	Least concern	Subregional endemic
Kwazulu Natal	Lacustricola myaposae	122	Near threatened	Regional endemic level 1
Kwazulu Natal	Marcusenius caudisquamatus	7	Endangered	Micro-endemic level 1
Kwazulu Natal	Marcusenius pongolensis	7	Least concern	Subregional endemic
Kwazulu Natal	Megalops cyprinoides	45	Data deficient	Widespread
Kwazulu Natal	Micralestes acutidens	122	Least concern	Widespread
Kwazulu Natal	Microctenopoma intermedium	6	Least concern	Subregional endemic
Kwazulu Natal	Micropanchax johnstoni	24	Least concern	Subregional endemic
Kwazulu Natal	Nothobranchius orthonotus	30	Least concern	Subregional endemic
Kwazulu Natal	Opsaridium peringueyi	42	Least concern	Subregional endemic
Kwazulu Natal	Oreochromis mossambicus	1167	Vulnerable	Widespread
Kwazulu Natal	Oreochromis placidus	3	Least concern	Subregional endemic
Kwazulu Natal	Petrocephalus wesselsi	23	Least concern	Subregional endemic
Kwazulu Natal	Pseudobarbus quathlambae	2	Endangered	Micro-endemic level 1
Kwazulu Natal	Pseudobarbus trevelyani	1	Endangered	Regional endemic level 1
Kwazulu Natal	Pseudocrenilabrus philander	637	Least concern	Subregional endemic
Kwazulu Natal	Schilbe intermedius	116	Least concern	Widespread
Kwazulu Natal	Serranochromis meridianus	2	Endangered	Subregional endemic
Kwazulu Natal	Synodontis zambezensis	68	Least concern	Subregional endemic
Kwazulu Natal	Tilapia sparrmanii	295	Least concern	Widespread
Limpopo	Amphilius natalensis	25	Least concern	Widespread
Limpopo	Amphilius uranoscopus	321	Least concern	Subregional endemic

Limpopo	Anguilla bengalensis	3	Near threatened	Widespread
Limpopo	Anguilla marmorata	8	Least concern	Widespread
Limpopo	Anguilla mossambica	86	Least concern	Widespread
Limpopo	Brycinus imberi	148	Least concern	Widespread
Limpopo	Brycinus lateralis	2	Least concern	Subregional endemic
Limpopo	Chetia flaviventris	86	Least concern	Subregional endemic
Limpopo	Chiloglanis anoterus	2	Least concern	Regional endemic level 1
Limpopo	Chiloglanis paratus	506	Least concern	Subregional endemic
Limpopo	Chiloglanis pretoriae	727	Least concern	Subregional endemic
Limpopo	Chiloglanis swierstrai	94	Least concern	Subregional endemic
Limpopo	Clarias gariepinus	798	Least concern	Widespread
Limpopo	Clarias ngamensis	1	Least concern	Subregional endemic
Limpopo	Clarias theodorae	18	Least concern	Widespread
Limpopo	Coptodon rendalli	504	Least concern	Widespread
Limpopo	Engraulicypris brevianalis	312	Least concern	Subregional endemic
Limpopo	Enteromius afrohamiltoni	182	Least concern	Subregional endemic
Limpopo	Enteromius annectens	123	Least concern	Subregional endemic
Limpopo	Enteromius anoplus	35	Least concern	Subregional endemic
Limpopo	Enteromius bifrenatus	181	Least concern	Subregional endemic
Limpopo	Enteromius brevipinnis	94	Near threatened	Subregional endemic
Limpopo	Enteromius eutaenia	255	Least concern	Widespread
Limpopo	Enteromius lineomaculatus	93	Least concern	Subregional endemic
Limpopo	Enteromius mattozi	32	Least concern	Subregional endemic
Limpopo	Enteromius motebensis	8	Near threatened	Subregional endemic
Limpopo	Enteromius neefi	324	Least concern	Subregional endemic
Limpopo	Enteromius pallidus	15	Least concern	Subregional endemic
Limpopo	Enteromius paludinosus	444	Least concern	Widespread
Limpopo	Enteromius radiatus	190	Least concern	Subregional endemic
Limpopo	Enteromius toppini	200	Least concern	Subregional endemic
Limpopo	Enteromius trimaculatus	871	Least concern	Subregional endemic
Limpopo	Enteromius unitaeniatus	449	Least concern	Subregional endemic
Limpopo	Enteromius viviparus	603	Least concern	Subregional endemic
Limpopo	Galaxias zebratus	1	Data deficient	Regional endemic level 1
Limpopo	Hydrocynus vittatus	113	Least concern	Widespread

Limpopo	Labeo congoro	62	Least concern	Subregional endemic
Limpopo	Labeo cylindricus	712	Least concern	Widespread
Limpopo	Labeo molybdinus	851	Least concern	Subregional endemic
Limpopo	Labeo rosae	269	Least concern	Subregional endemic
Limpopo	Labeo rubromaculatus	1	Vulnerable	Micro-endemic level 1
Limpopo	Labeo ruddi	172	Data deficient	Subregional endemic
Limpopo	Labeobarbus marequensis	1097	Least concern	Subregional endemic
Limpopo	Labeobarbus nelspruitensis	1	Near threatened	Regional endemic level 1
Limpopo	Labeobarbus polylepis	20	Least concern	Regional endemic level 1
Limpopo	Lacustricola katangae	8	Least concern	Subregional endemic
Limpopo	Lacustricola myaposae	1	Near threatened	Regional endemic level 1
Limpopo	Marcusenius krameri	14	Least concern	National endemic
Limpopo	Marcusenius pongolensis	8	Least concern	Subregional endemic
Limpopo	Micralestes acutidens	501	Least concern	Widespread
Limpopo	Micropanchax johnstoni	56	Least concern	Subregional endemic
Limpopo	Nothobranchius orthonotus	3	Least concern	Subregional endemic
Limpopo	Opsaridium peringueyi	139	Least concern	Subregional endemic
Limpopo	Oreochromis mossambicus	981	Vulnerable	Widespread
Limpopo	Petrocephalus wesselsi	110	Least concern	Subregional endemic
Limpopo	Pseudobarbus capensis	2	Endangered	Regional endemic level 1
Limpopo	Pseudocrenilabrus philander	633	Least concern	Subregional endemic
Limpopo	Schilbe intermedius	170	Least concern	Widespread
Limpopo	Serranochromis meridianus	4	Endangered	Subregional endemic
Limpopo	Synodontis zambezensis	101	Least concern	Subregional endemic
Limpopo	Tilapia sparrmanii	415	Least concern	Widespread
Mpumalanga	Ambassis natalensis	1	Least concern	Subregional endemic
Mpumalanga	Amphilius natalensis	157	Least concern	Widespread
Mpumalanga	Amphilius uranoscopus	509	Least concern	Subregional endemic
Mpumalanga	Anguilla bengalensis	2	Near threatened	Widespread
Mpumalanga	Anguilla marmorata	21	Least concern	Widespread
Mpumalanga	Anguilla mossambica	104	Least concern	Widespread
Mpumalanga	Austroglanis sclateri	5	Least concern	Regional endemic level 2
Mpumalanga	Brycinus imberi	56	Least concern	Widespread
Mpumalanga	Brycinus lateralis	2	Least concern	Subregional endemic

Mpumalanga	Chetia brevis	19	Endangered	Subregional endemic
Mpumalanga	Chetia flaviventris	3	Least concern	Subregional endemic
Mpumalanga	Chiloglanis anoterus	350	Least concern	Regional endemic level 1
Mpumalanga	Chiloglanis bifurcus	72	Critically endangered	Micro-endemic level 1
Mpumalanga	Chiloglanis emarginatus	30	Vulnerable	Subregional endemic
Mpumalanga	Chiloglanis paratus	276	Least concern	Subregional endemic
Mpumalanga	Chiloglanis pretoriae	616	Least concern	Subregional endemic
Mpumalanga	Chiloglanis swierstrai	202	Least concern	Subregional endemic
Mpumalanga	Clarias gariepinus	507	Least concern	Widespread
Mpumalanga	Clarias ngamensis	1	Least concern	Subregional endemic
Mpumalanga	Coptodon rendalli	274	Least concern	Widespread
Mpumalanga	Engraulicypris brevianalis	157	Least concern	Subregional endemic
Mpumalanga	Enteromius afrohamiltoni	42	Least concern	Subregional endemic
Mpumalanga	Enteromius annectens	146	Least concern	Subregional endemic
Mpumalanga	Enteromius anoplus	494	Least concern	Subregional endemic
Mpumalanga	Enteromius argenteus	286	Least concern	Subregional endemic
Mpumalanga	Enteromius bifrenatus	5	Least concern	Subregional endemic
Mpumalanga	Enteromius brevipinnis	47	Near threatened	Subregional endemic
Mpumalanga	Enteromius eutaenia	309	Least concern	Widespread
Mpumalanga	Enteromius lineomaculatus	14	Least concern	Subregional endemic
Mpumalanga	Enteromius mattozi	10	Least concern	Subregional endemic
Mpumalanga	Enteromius motebensis	40	Near threatened	Subregional endemic
Mpumalanga	Enteromius neefi	114	Least concern	Subregional endemic
Mpumalanga	Enteromius pallidus	42	Least concern	Subregional endemic
Mpumalanga	Enteromius paludinosus	219	Least concern	Widespread
Mpumalanga	Enteromius radiatus	130	Least concern	Subregional endemic
Mpumalanga	Enteromius toppini	74	Least concern	Subregional endemic
Mpumalanga	Enteromius treurensis	20	Critically endangered	Micro-endemic level 2
Mpumalanga	Enteromius trimaculatus	526	Least concern	Subregional endemic
Mpumalanga	Enteromius unitaeniatus	262	Least concern	Subregional endemic
Mpumalanga	Enteromius viviparus	316	Least concern	Subregional endemic
Mpumalanga	Hydrocynus vittatus	97	Least concern	Widespread
Mpumalanga	Kneria auriculata	7	Least concern	Subregional endemic
Mpumalanga	Labeo congoro	102	Least concern	Subregional endemic

Mpumalanga	Labeo cylindricus	279	Least concern	Widespread
Mpumalanga	Labeo molybdinus	442	Least concern	Subregional endemic
Mpumalanga	Labeo rosae	149	Least concern	Subregional endemic
Mpumalanga	Labeo ruddi	38	Data deficient	Subregional endemic
Mpumalanga	Labeo umbratus	2	Least concern	Subregional endemic
Mpumalanga	Labeobarbus kimberleyensis	7	Near threatened	Regional endemic level 2
Mpumalanga	Labeobarbus marequensis	828	Least concern	Subregional endemic
Mpumalanga	Labeobarbus nelspruitensis	86	Near threatened	Regional endemic level 1
Mpumalanga	Labeobarbus polylepis	244	Least concern	Regional endemic level 1
Mpumalanga	Marcusenius krameri	1	Least concern	National endemic
Mpumalanga	Marcusenius pongolensis	34	Least concern	Subregional endemic
Mpumalanga	Micralestes acutidens	337	Least concern	Widespread
Mpumalanga	Micropanchax johnstoni	1	Least concern	Subregional endemic
Mpumalanga	Nothobranchius orthonotus	3	Least concern	Subregional endemic
Mpumalanga	Opsaridium peringueyi	194	Least concern	Subregional endemic
Mpumalanga	Oreochromis mossambicus	530	Vulnerable	Widespread
Mpumalanga	Petrocephalus wesselsi	70	Least concern	Subregional endemic
Mpumalanga	Pseudocrenilabrus philander	674	Least concern	Subregional endemic
Mpumalanga	Schilbe intermedius	71	Least concern	Widespread
Mpumalanga	Serranochromis meridianus	62	Endangered	Subregional endemic
Mpumalanga	Synodontis zambezensis	31	Least concern	Subregional endemic
Mpumalanga	Tilapia sparrmanii	456	Least concern	Widespread
North West	Amphilius uranoscopus	41	Least concern	Subregional endemic
North West	Anguilla mossambica	1	Least concern	Widespread
North West	Austroglanis sclateri	3	Least concern	Regional endemic level 2
North West	Brycinus imberi	1	Least concern	Widespread
North West	Brycinus lateralis	3	Least concern	Subregional endemic
North West	Chetia flaviventris	21	Least concern	Subregional endemic
North West	Chiloglanis pretoriae	42	Least concern	Subregional endemic
North West	Chiloglanis swierstrai	1	Least concern	Subregional endemic
North West	Clarias gariepinus	76	Least concern	Widespread
North West	Coptodon rendalli	5	Least concern	Widespread
North West	Engraulicypris brevianalis	22	Least concern	Subregional endemic
North West	Enteromius anoplus	5	Least concern	Subregional endemic

North West	Enteromius brevipinnis	6	Near threatened	Subregional endemic
North West	Enteromius lineomaculatus	1	Least concern	Subregional endemic
North West	Enteromius mattozi	12	Least concern	Subregional endemic
North West	Enteromius motebensis	47	Near threatened	Subregional endemic
North West	Enteromius neefi	1	Least concern	Subregional endemic
North West	Enteromius pallidus	13	Least concern	Subregional endemic
North West	Enteromius paludinosus	104	Least concern	Widespread
North West	Enteromius trimaculatus	57	Least concern	Subregional endemic
North West	Enteromius unitaeniatus	39	Least concern	Subregional endemic
North West	Labeo capensis	2	Least concern	Regional endemic level 2
North West	Labeo cylindricus	6	Least concern	Widespread
North West	Labeo molybdinus	27	Least concern	Subregional endemic
North West	Labeo rosae	1	Least concern	Subregional endemic
North West	Labeo umbratus	31	Least concern	Subregional endemic
North West	Labeobarbus aeneus	1	Least concern	Regional endemic level 2
North West	Labeobarbus kimberleyensis	4	Near threatened	Regional endemic level 2
North West	Labeobarbus marequensis	89	Least concern	Subregional endemic
North West	Labeobarbus polylepis	15	Least concern	Regional endemic level 1
North West	Micralestes acutidens	3	Least concern	Widespread
North West	Micropanchax johnstoni	4	Least concern	Subregional endemic
North West	Oreochromis mossambicus	45	Vulnerable	Widespread
North West	Pseudobarbus phlegethon	1	Endangered	Micro-endemic level 1
North West	Pseudocrenilabrus philander	121	Least concern	Subregional endemic
North West	Schilbe intermedius	1	Least concern	Widespread
North West	Tilapia sparrmanii	115	Least concern	Widespread
Northern Cape	Anguilla mossambica	1	Least concern	Widespread
Northern Cape	Austroglanis gilli	3	Near threatened	Regional endemic level 1
Northern Cape	Austroglanis sclateri	12	Least concern	Regional endemic level 2
Northern Cape	Clarias gariepinus	53	Least concern	Widespread
Northern Cape	Engraulicypris brevianalis	23	Least concern	Subregional endemic
Northern Cape	Engraulicypris gariepinus	21	Least concern	Regional endemic level 2
Northern Cape	Enteromius annectens	1	Least concern	Subregional endemic
Northern Cape	Enteromius anoplus	141	Least concern	Subregional endemic
Northern Cape	Enteromius bifrenatus	4	Least concern	Subregional endemic

Northern Cape	Enteromius eutaenia	2	Least concern	Widespread
Northern Cape	Enteromius lineomaculatus	1	Least concern	Subregional endemic
Northern Cape	Enteromius mattozi	1	Least concern	Subregional endemic
Northern Cape	Enteromius pallidus	1	Least concern	Subregional endemic
Northern Cape	Enteromius paludinosus	72	Least concern	Widespread
Northern Cape	Enteromius radiatus	1	Least concern	Subregional endemic
Northern Cape	Enteromius toppini	1	Least concern	Subregional endemic
Northern Cape	Enteromius trimaculatus	48	Least concern	Subregional endemic
Northern Cape	Enteromius unitaeniatus	2	Least concern	Subregional endemic
Northern Cape	Enteromius viviparus	1	Least concern	Subregional endemic
Northern Cape	Galaxias zebratus	4	Data deficient	Regional endemic level 1
Northern Cape	Labeo capensis	78	Least concern	Regional endemic level 2
Northern Cape	Labeo cylindricus	1	Least concern	Widespread
Northern Cape	Labeo molybdinus	2	Least concern	Subregional endemic
Northern Cape	Labeo rosae	1	Least concern	Subregional endemic
Northern Cape	Labeo ruddi	2	Data deficient	Subregional endemic
Northern Cape	Labeo seeberi	160	Endangered	Regional endemic level 2
Northern Cape	Labeo umbratus	31	Least concern	Subregional endemic
Northern Cape	Labeobarbus aeneus	101	Least concern	Regional endemic level 2
Northern Cape	Labeobarbus kimberleyensis	35	Near threatened	Regional endemic level 2
Northern Cape	Labeobarbus marequensis	3	Least concern	Subregional endemic
Northern Cape	Labeobarbus seeberi	48	Near threatened	Regional endemic level 1
Northern Cape	Petrocephalus wesselsi	3	Least concern	Subregional endemic
Northern Cape	Pseudobarbus erubescens	1	Critically endangered	Micro-endemic level 1
Northern Cape	Pseudobarbus hospes	31	Least concern	Regional endemic level 1
Northern Cape	Pseudobarbus senticeps	1	Critically endangered	Micro-endemic level 2
Northern Cape	Pseudobarbus serra	171	Near threatened	Micro-endemic level 1
Northern Cape	Pseudocrenilabrus philander	45	Least concern	Subregional endemic
Northern Cape	Schilbe intermedius	1	Least concern	Widespread
Northern Cape	Tilapia sparrmanii	60	Least concern	Widespread
Western Cape	Anguilla bicolor	1	Near threatened	Widespread
Western Cape	Anguilla marmorata	5	Least concern	Widespread
Western Cape	Anguilla mossambica	44	Least concern	Widespread
Western Cape	Austroglanis barnardi	94	Endangered	Regional endemic level 1

Western Cape	Austroglanis gilli	300	Near threatened	Regional endemic level 1
Western Cape	Ctenopoma multispine	1	Least concern	Subregional endemic
Western Cape	Enteromius anoplus	254	Least concern	Subregional endemic
Western Cape	Enteromius lineomaculatus	1	Least concern	Subregional endemic
Western Cape	Enteromius mattozi	2	Least concern	Subregional endemic
Western Cape	Enteromius pallidus	1	Least concern	Subregional endemic
Western Cape	Galaxias zebratus	1129	Data deficient	Regional endemic level 1
Western Cape	Labeo cylindricus	2	Least concern	Widespread
Western Cape	Labeo rosae	1	Least concern	Subregional endemic
Western Cape	Labeo seeberi	113	Endangered	Regional endemic level 2
Western Cape	Labeo umbratus	65	Least concern	Subregional endemic
Western Cape	Labeobarbus seeberi	257	Near threatened	Regional endemic level 1
Western Cape	Pseudobarbus afer	137	Endangered	Micro-endemic level 1
Western Cape	Pseudobarbus asper	305	Vulnerable	Regional endemic level 2
Western Cape	Pseudobarbus burchelli	641	Critically endangered	Micro-endemic level 2
Western Cape	Pseudobarbus burgi	212	Endangered	Regional endemic level 2
Western Cape	Pseudobarbus calidus	334	Near threatened	Regional endemic level 2
Western Cape	Pseudobarbus capensis	76	Endangered	Regional endemic level 1
Western Cape	Pseudobarbus erubescens	139	Critically endangered	Micro-endemic level 1
Western Cape	Pseudobarbus phlegethon	225	Endangered	Micro-endemic level 1
Western Cape	Pseudobarbus serra	415	Near threatened	Micro-endemic level 1
Western Cape	Pseudobarbus skeltoni	38	Endangered	Micro-endemic level 1
Western Cape	Pseudobarbus tenuis	416	Near threatened	Regional endemic level 1
Western Cape	Pseudobarbus trevelyani	2	Endangered	Regional endemic level 1
Western Cape	Pseudobarbus verloreni	35	Endangered	Micro-endemic level 2
Western Cape	Sandelia capensis	1215	Data deficient	Regional endemic level 1

Table S. 3.2b. List of all non-native freshwater fishes occurring in each province in South Africa.

Province	Species Name	Number of Records	IUCN Conservation Status	Endemism Category
Eastern Cape	Carassius auratus	5	Least concern	Widespread
Eastern Cape	Cyprinus carpio	82	Vulnerable	Widespread
Eastern Cape	Gambusia affinis	33	Least concern	Widespread
Eastern Cape	Hypophthalmichthys molitrix	2	Near threatened	Widespread
Eastern Cape	Lepomis macrochirus	43	Least concern	Widespread
Eastern Cape	Micropterus dolomieu	45	Least concern	Widespread
Eastern Cape	Micropterus floridanus	5	Not evaluated	Widespread
Eastern Cape	Micropterus punctulatus	61	Least concern	Widespread
Eastern Cape	Micropterus salmoides	225	Least concern	Widespread
Eastern Cape	Oncorhynchus mykiss	53	Not evaluated	Widespread
Eastern Cape	Oreochromis niloticus	2	Least concern	Widespread
Eastern Cape	Perca fluviatilis	2	Least concern	Widespread
Eastern Cape	Salmo trutta	2	Least concern	Widespread
Eastern Cape	Salvelinus fontinalis	1	Not evaluated	Widespread
Free State	Carassius auratus	1	Least concern	Widespread
Free State	Ctenopharyngodon idella	4	Not evaluated	Widespread
Free State	Cyprinus carpio	72	Vulnerable	Widespread
Free State	Gambusia affinis	9	Least concern	Widespread
Free State	Lepomis macrochirus	2	Least concern	Widespread
Free State	Micropterus salmoides	27	Least concern	Widespread
Free State	Oncorhynchus mykiss	10	Not evaluated	Widespread
Gauteng	Ctenopharyngodon idella	2	Not evaluated	Widespread
Gauteng	Cyprinus carpio	33	Vulnerable	Widespread
Gauteng	Gambusia affinis	31	Least concern	Widespread
Gauteng	Micropterus dolomieu	1	Least concern	Widespread
Gauteng	Micropterus floridanus	1	Not evaluated	Widespread
Gauteng	Micropterus punctulatus	2	Least concern	Widespread
Gauteng	Micropterus salmoides	27	Least concern	Widespread
Gauteng	Oreochromis niloticus	1	Least concern	Widespread
Gauteng	Xiphophorus maculatus	1	Data deficient	Widespread
Kwazulu Natal	Carassius auratus	15	Least concern	Widespread
Kwazulu Natal	Ctenopharyngodon idella	23	Not evaluated	Widespread

Kwazulu Natal	Cyprinus carpio	206	Vulnerable	Widespread
Kwazulu Natal	Gambusia affinis	9	Least concern	Widespread
Kwazulu Natal	Hypophthalmichthys molitrix	2	Near threatened	Widespread
Kwazulu Natal	Lepomis macrochirus	97	Least concern	Widespread
Kwazulu Natal	Micropterus dolomieu	75	Least concern	Widespread
Kwazulu Natal	Micropterus floridanus	4	Not evaluated	Widespread
Kwazulu Natal	Micropterus punctulatus	77	Least concern	Widespread
Kwazulu Natal	Micropterus salmoides	405	Least concern	Widespread
Kwazulu Natal	Oncorhynchus mykiss	66	Not evaluated	Widespread
Kwazulu Natal	Oreochromis aureus	1	Least concern	Widespread
Kwazulu Natal	Oreochromis niloticus	8	Least concern	Widespread
Kwazulu Natal	Perca fluviatilis	2	Least concern	Widespread
Kwazulu Natal	Poecilia reticulata	98	Not evaluated	Widespread
Kwazulu Natal	Pterygoplichthys disjunctivus	6	Not evaluated	Widespread
Kwazulu Natal	Salmo trutta	39	Least concern	Widespread
Kwazulu Natal	Serranochromis robustus	1	Least concern	Widespread
Kwazulu Natal	Xiphophorus helleri	38	Least concern	Widespread
Kwazulu Natal	Xiphophorus maculatus	6	Data deficient	Widespread
Limpopo	Cyprinus carpio	28	Vulnerable	Widespread
Limpopo	Gambusia affinis	8	Least concern	Widespread
Limpopo	Hypophthalmichthys molitrix	10	Near threatened	Widespread
Limpopo	Lepomis macrochirus	3	Least concern	Widespread
Limpopo	Micropterus dolomieu	6	Least concern	Widespread
Limpopo	Micropterus floridanus	1	Not evaluated	Widespread
Limpopo	Micropterus punctulatus	2	Least concern	Widespread
Limpopo	Micropterus salmoides	49	Least concern	Widespread
Limpopo	Oncorhynchus mykiss	7	Not evaluated	Widespread
Limpopo	Oreochromis niloticus	50	Least concern	Widespread
Limpopo	Salmo trutta	4	Least concern	Widespread
Mpumalanga	Coptodon zilli	6	Least concern	Widespread
Mpumalanga	Cyprinus carpio	28	Vulnerable	Widespread
Mpumalanga	Gambusia affinis	37	Least concern	Widespread
Mpumalanga	Lepomis macrochirus	3	Least concern	Widespread
Mpumalanga	Micropterus dolomieu	7	Least concern	Widespread

Mpumalanga	Micropterus punctulatus	3	Least concern	Widespread
Mpumalanga	Micropterus salmoides	65	Least concern	Widespread
Mpumalanga	Oncorhynchus mykiss	47	Not evaluated	Widespread
Mpumalanga	Poecilia reticulata	2	Not evaluated	Widespread
Mpumalanga	Salmo trutta	1	Least concern	Widespread
Mpumalanga	Serranochromis robustus	1	Least concern	Widespread
Mpumalanga	Xiphophorus helleri	6	Least concern	Widespread
North West	Ctenopharyngodon idella	1	Not evaluated	Widespread
North West	Cyprinus carpio	27	Vulnerable	Widespread
North West	Gambusia affinis	11	Least concern	Widespread
North West	Micropterus dolomieu	2	Least concern	Widespread
North West	Micropterus floridanus	2	Not evaluated	Widespread
North West	Micropterus punctulatus	1	Least concern	Widespread
North West	Micropterus salmoides	47	Least concern	Widespread
Northern Cape	Carassius auratus	1	Least concern	Widespread
Northern Cape	Cyprinus carpio	16	Vulnerable	Widespread
Northern Cape	Gambusia affinis	10	Least concern	Widespread
Northern Cape	Lepomis macrochirus	35	Least concern	Widespread
Northern Cape	Micropterus dolomieu	40	Least concern	Widespread
Northern Cape	Micropterus punctulatus	10	Least concern	Widespread
Northern Cape	Micropterus salmoides	2	Least concern	Widespread
Northern Cape	Poecilia reticulata	1	Not evaluated	Widespread
Northern Cape	Salmo trutta	2	Least concern	Widespread
Western Cape	Carassius auratus	9	Least concern	Widespread
Western Cape	Ctenopharyngodon idella	3	Not evaluated	Widespread
Western Cape	Cyprinus carpio	124	Vulnerable	Widespread
Western Cape	Gambusia affinis	42	Least concern	Widespread
Western Cape	Lepomis macrochirus	220	Least concern	Widespread
Western Cape	Micropterus dolomieu	461	Least concern	Widespread
Western Cape	Micropterus floridanus	1	Not evaluated	Widespread
Western Cape	Micropterus punctulatus	208	Least concern	Widespread
Western Cape	Micropterus salmoides	267	Least concern	Widespread
Western Cape	Oncorhynchus mykiss	326	Not evaluated	Widespread
Western Cape	Oreochromis aureus	5	Least concern	Widespread

Western Cape	Oreochromis niloticus	4	Least concern	Widespread
Western Cape	Pangasius sanitwongsei	3	Critically endangered	Widespread
Western Cape	Salmo trutta	17	Least concern	Widespread
Western Cape	Salvelinus fontinalis	1	Not evaluated	Widespread
Western Cape	Tinca tinca	8	Least concern	Widespread

Table S. 3.2c. List of all extralimital freshwater fishes occurring in each province in South Africa.

Province	Species Name	Number of Records	IUCN Conservation Status	Endemism Category
Eastern Cape	Clarias gariepinus	96	Least concern	Widespread
Eastern Cape	Coptodon rendalli	1	Least concern	Widespread
Eastern Cape	Enteromius anoplus	1	Least concern	Subregional endemic
Eastern Cape	Labeo capensis	38	Least concern	Regional endemic level 2
Eastern Cape	Labeo umbratus	80	Least concern	Subregional endemic
Eastern Cape	Labeobarbus aeneus	109	Least concern	Regional endemic level 2
Eastern Cape	Oreochromis mossambicus	94	Vulnerable	Widespread
Eastern Cape	Pseudocrenilabrus philander	1	Least concern	Subregional endemic
Eastern Cape	Sandelia capensis	13	Data deficient	Regional endemic level 1
Eastern Cape	Tilapia sparrmanii	220	Least concern	Widespread
Free State	Labeo capensis	1	Least concern	Regional endemic level 2
Free State	Labeo umbratus	3	Least concern	Subregional endemic
Free State	Labeobarbus aeneus	3	Least concern	Regional endemic level 2
Free State	Pseudobarbus serra	1	Near threatened	Micro-endemic level 1
Gauteng	Labeo capensis	7	Least concern	Regional endemic level 2
Gauteng	Labeo umbratus	4	Least concern	Subregional endemic
Gauteng	Labeobarbus aeneus	18	Least concern	Regional endemic level 2
Kwazulu Natal	Clarias gariepinus	228	Least concern	Widespread
Kwazulu Natal	Coptodon rendalli	170	Least concern	Widespread
Kwazulu Natal	Enteromius anoplus	8	Least concern	Subregional endemic
Kwazulu Natal	Hydrocynus vittatus	1	Least concern	Widespread
Kwazulu Natal	Labeo capensis	2	Least concern	Regional endemic level 2
Kwazulu Natal	Labeobarbus aeneus	2	Least concern	Regional endemic level 2
Kwazulu Natal	Labeobarbus natalensis	1	Least concern	Regional endemic level 1
Kwazulu Natal	Tilapia sparrmanii	134	Least concern	Widespread
Limpopo	Enteromius anoplus	3	Least concern	Subregional endemic
Limpopo	Hydrocynus vittatus	17	Least concern	Widespread
Limpopo	Labeo umbratus	1	Least concern	Subregional endemic
Limpopo	Labeobarbus natalensis	2	Least concern	Regional endemic level 1
Limpopo	Oreochromis mossambicus	13	Vulnerable	Widespread
Limpopo	Sandelia capensis	2	Data deficient	Regional endemic level 1
Mpumalanga	Chetia brevis	4	Endangered	Subregional endemic

Mpumalanga	Enteromius treurensis	1	Critically endangered	Micro-endemic level 2
Mpumalanga	Hydrocynus vittatus	31	Least concern	Widespread
Mpumalanga	Labeo capensis	18	Least concern	Regional endemic level 2
Mpumalanga	Labeo umbratus	38	Least concern	Subregional endemic
Mpumalanga	Labeobarbus aeneus	32	Least concern	Regional endemic level 2
Mpumalanga	Oreochromis mossambicus	1	Vulnerable	Widespread
North West	Enteromius anoplus	13	Least concern	Subregional endemic
North West	Labeo capensis	41	Least concern	Regional endemic level 2
North West	Labeo umbratus	3	Least concern	Subregional endemic
North West	Labeobarbus aeneus	24	Least concern	Regional endemic level 2
North West	Oreochromis mossambicus	7	Vulnerable	Widespread
Northern Cape	Clarias gariepinus	4	Least concern	Widespread
Northern Cape	Coptodon rendalli	2	Least concern	Widespread
Northern Cape	Labeo capensis	4	Least concern	Regional endemic level 2
Northern Cape	Labeo umbratus	2	Least concern	Subregional endemic
Northern Cape	Labeobarbus aeneus	6	Least concern	Regional endemic level 2
Northern Cape	Oreochromis mossambicus	15	Vulnerable	Widespread
Northern Cape	Pseudocrenilabrus philander	41	Least concern	Subregional endemic
Northern Cape	Sandelia capensis	1	Data deficient	Regional endemic level 1
Northern Cape	Tilapia sparrmanii	118	Least concern	Widespread
Western Cape	Clarias gariepinus	49	Least concern	Widespread
Western Cape	Enteromius anoplus	5	Least concern	Subregional endemic
Western Cape	Labeo capensis	10	Least concern	Regional endemic level 2
Western Cape	Labeo umbratus	4	Least concern	Subregional endemic
Western Cape	Labeobarbus aeneus	35	Least concern	Regional endemic level 2
Western Cape	Oreochromis mossambicus	172	Vulnerable	Widespread
Western Cape	Pseudobarbus calidus	1	Near threatened	Regional endemic level 2
Western Cape	Pseudobarbus serra	5	Near threatened	Micro-endemic level 1
Western Cape	Sandelia capensis	72	Data deficient	Regional endemic level 1
Western Cape	Tilapia sparrmanii	283	Least concern	Widespread
Mpumalanga	Cyprinus carpio	28	Vulnerable	Widespread
Mpumalanga	Gambusia affinis	37	Least concern	Widespread
Mpumalanga	Lepomis macrochirus	3	Least concern	Widespread
Mpumalanga	Micropterus dolomieu	7	Least concern	Widespread

Mpumalanga	Micropterus punctulatus	3	Least concern	Widespread
Mpumalanga	Micropterus salmoides	65	Least concern	Widespread
Mpumalanga	Oncorhynchus mykiss	47	Not evaluated	Widespread
Mpumalanga	Poecilia reticulata	2	Not evaluated	Widespread
Mpumalanga	Salmo trutta	1	Least concern	Widespread
Mpumalanga	Serranochromis robustus	1	Least concern	Widespread
Mpumalanga	Xiphophorus helleri	6	Least concern	Widespread
North West	Ctenopharyngodon idella	1	Not evaluated	Widespread
North West	Cyprinus carpio	27	Vulnerable	Widespread
North West	Gambusia affinis	11	Least concern	Widespread
North West	Micropterus dolomieu	2	Least concern	Widespread
North West	Micropterus floridanus	2	Not evaluated	Widespread
North West	Micropterus punctulatus	1	Least concern	Widespread
North West	Micropterus salmoides	47	Least concern	Widespread
Northern Cape	Carassius auratus	1	Least concern	Widespread
Northern Cape	Cyprinus carpio	16	Vulnerable	Widespread
Northern Cape	Gambusia affinis	10	Least concern	Widespread
Northern Cape	Lepomis macrochirus	35	Least concern	Widespread
Northern Cape	Micropterus dolomieu	40	Least concern	Widespread
Northern Cape	Micropterus punctulatus	10	Least concern	Widespread
Northern Cape	Micropterus salmoides	2	Least concern	Widespread
Northern Cape	Poecilia reticulata	1	Not evaluated	Widespread
Northern Cape	Salmo trutta	2	Least concern	Widespread
Western Cape	Carassius auratus	9	Least concern	Widespread
Western Cape	Ctenopharyngodon idella	3	Not evaluated	Widespread
Western Cape	Cyprinus carpio	124	Vulnerable	Widespread
Western Cape	Gambusia affinis	42	Least concern	Widespread
Western Cape	Lepomis macrochirus	220	Least concern	Widespread
Western Cape	Micropterus dolomieu	461	Least concern	Widespread
Western Cape	Micropterus floridanus	1	Not evaluated	Widespread
Western Cape	Micropterus punctulatus	208	Least concern	Widespread
Western Cape	Micropterus salmoides	267	Least concern	Widespread
Western Cape	Oncorhynchus mykiss	326	Not evaluated	Widespread
Western Cape	Oreochromis aureus	5	Least concern	Widespread

Western Cape	Oreochromis niloticus	4	Least concern	Widespread
Western Cape	Pangasius sanitwongsei	3	Critically endangered	Widespread
Western Cape	Salmo trutta	17	Least concern	Widespread
Western Cape	Salvelinus fontinalis	1	Not evaluated	Widespread
Western Cape	Tinca tinca	8	Least concern	Widespread

Table S. 3.3a. List of all native freshwater fishes occuring in each primary catchment in South Africa.

Catchment ID	Species Name	Number of Records	IUCN Conservation Status	Endemism Category
Region A	Amphilius natalensis	18	Least concern	Widespread
Region A	Amphilius uranoscopus	292	Least concern	Subregional endemic
Region A	Anguilla bengalensis	3	Near threatened	Widespread
Region A	Anguilla marmorata	4	Least concern	Widespread
Region A	Anguilla mossambica	75	Least concern	Widespread
Region A	Brycinus imberi	52	Least concern	Widespread
Region A	Brycinus lateralis	5	Least concern	Subregional endemic
Region A	Chetia flaviventris	111	Least concern	Subregional endemic
Region A	Chiloglanis emarginatus	1	Vulnerable	Subregional endemic
Region A	Chiloglanis paratus	179	Least concern	Subregional endemic
Region A	Chiloglanis pretoriae	435	Least concern	Subregional endemic
Region A	Chiloglanis swierstrai	33	Least concern	Subregional endemic
Region A	Clarias gariepinus	390	Least concern	Widespread
Region A	Clarias theodorae	18	Least concern	Widespread
Region A	Coptodon rendalli	212	Least concern	Widespread
Region A	Engraulicypris brevianalis	180	Least concern	Subregional endemic
Region A	Enteromius afrohamiltoni	60	Least concern	Subregional endemic
Region A	Enteromius annectens	58	Least concern	Subregional endemic
Region A	Enteromius anoplus	36	Least concern	Subregional endemic
Region A	Enteromius bifrenatus	177	Least concern	Subregional endemic
Region A	Enteromius brevipinnis	96	Near threatened	Subregional endemic
Region A	Enteromius eutaenia	137	Least concern	Widespread
Region A	Enteromius lineomaculatus	47	Least concern	Subregional endemic
Region A	Enteromius mattozi	24	Least concern	Subregional endemic
Region A	Enteromius motebensis	60	Near threatened	Subregional endemic
Region A	Enteromius neefi	190	Least concern	Subregional endemic
Region A	Enteromius pallidus	10	Least concern	Subregional endemic
Region A	Enteromius paludinosus	431	Least concern	Widespread
Region A	Enteromius radiatus	97	Least concern	Subregional endemic
Region A	Enteromius toppini	37	Least concern	Subregional endemic
Region A	Enteromius trimaculatus	462	Least concern	Subregional endemic
Region A	Enteromius unitaeniatus	314	Least concern	Subregional endemic

Region A	Enteromius viviparus	277	Least concern	Subregional endemic
Region A	Galaxias zebratus	1	Data deficient	Regional endemic level 1
Region A	Hydrocynus vittatus	58	Least concern	Widespread
Region A	Labeo congoro	23	Least concern	Subregional endemic
Region A	Labeo cylindricus	329	Least concern	Widespread
Region A	Labeo molybdinus	433	Least concern	Subregional endemic
Region A	Labeo rosae	77	Least concern	Subregional endemic
Region A	Labeo rubromaculatus	1	Vulnerable	Micro-endemic level 1
Region A	Labeo ruddi	36	Data deficient	Subregional endemic
Region A	Labeobarbus marequensis	673	Least concern	Subregional endemic
Region A	Labeobarbus nelspruitensis	1	Near threatened	Regional endemic level 1
Region A	Labeobarbus polylepis	38	Least concern	Regional endemic level 1
Region A	Lacustricola katangae	4	Least concern	Subregional endemic
Region A	Lacustricola myaposae	1	Near threatened	Regional endemic level 1
Region A	Marcusenius krameri	14	Least concern	National endemic
Region A	Marcusenius pongolensis	2	Least concern	Subregional endemic
Region A	Micralestes acutidens	317	Least concern	Widespread
Region A	Micropanchax johnstoni	60	Least concern	Subregional endemic
Region A	Opsaridium peringueyi	65	Least concern	Subregional endemic
Region A	Oreochromis mossambicus	454	Vulnerable	Widespread
Region A	Petrocephalus wesselsi	82	Least concern	Subregional endemic
Region A	Pseudobarbus capensis	2	Endangered	Regional endemic level 1
Region A	Pseudobarbus phlegethon	1	Endangered	Micro-endemic level 1
Region A	Pseudocrenilabrus philander	459	Least concern	Subregional endemic
Region A	Schilbe intermedius	64	Least concern	Widespread
Region A	Serranochromis meridianus	3	Endangered	Subregional endemic
Region A	Synodontis zambezensis	33	Least concern	Subregional endemic
Region A	Tilapia sparrmanii	419	Least concern	Widespread
Region B	Amphilius natalensis	20	Least concern	Widespread
Region B	Amphilius uranoscopus	134	Least concern	Subregional endemic
Region B	Anguilla marmorata	5	Least concern	Widespread
Region B	Anguilla mossambica	18	Least concern	Widespread
Region B	Austroglanis sclateri	1	Least concern	Regional endemic level 2
Region B	Brycinus imberi	107	Least concern	Widespread

Region B	Chetia flaviventris	7	Least concern	Subregional endemic
Region B	Chiloglanis anoterus	3	Least concern	Regional endemic level 1
Region B	Chiloglanis paratus	403	Least concern	Subregional endemic
Region B	Chiloglanis pretoriae	468	Least concern	Subregional endemic
Region B	Chiloglanis swierstrai	100	Least concern	Subregional endemic
Region B	Clarias gariepinus	728	Least concern	Widespread
Region B	Clarias ngamensis	1	Least concern	Subregional endemic
Region B	Coptodon rendalli	324	Least concern	Widespread
Region B	Engraulicypris brevianalis	172	Least concern	Subregional endemic
Region B	Enteromius afrohamiltoni	124	Least concern	Subregional endemic
Region B	Enteromius annectens	66	Least concern	Subregional endemic
Region B	Enteromius anoplus	240	Least concern	Subregional endemic
Region B	Enteromius argenteus	3	Least concern	Subregional endemic
Region B	Enteromius bifrenatus	8	Least concern	Subregional endemic
Region B	Enteromius brevipinnis	4	Near threatened	Subregional endemic
Region B	Enteromius eutaenia	145	Least concern	Widespread
Region B	Enteromius lineomaculatus	54	Least concern	Subregional endemic
Region B	Enteromius mattozi	35	Least concern	Subregional endemic
Region B	Enteromius motebensis	42	Near threatened	Subregional endemic
Region B	Enteromius neefi	212	Least concern	Subregional endemic
Region B	Enteromius pallidus	29	Least concern	Subregional endemic
Region B	Enteromius paludinosus	246	Least concern	Widespread
Region B	Enteromius radiatus	100	Least concern	Subregional endemic
Region B	Enteromius toppini	187	Least concern	Subregional endemic
Region B	Enteromius treurensis	20	Critically endangered	Micro-endemic level 2
Region B	Enteromius trimaculatus	556	Least concern	Subregional endemic
Region B	Enteromius unitaeniatus	213	Least concern	Subregional endemic
Region B	Enteromius viviparus	377	Least concern	Subregional endemic
Region B	Hydrocynus vittatus	55	Least concern	Widespread
Region B	Kneria auriculata	2	Least concern	Subregional endemic
Region B	Labeo congoro	72	Least concern	Subregional endemic
Region B	Labeo cylindricus	467	Least concern	Widespread
Region B	Labeo molybdinus	538	Least concern	Subregional endemic
Region B	Labeo rosae	259	Least concern	Subregional endemic

Region B	Labeo ruddi	157	Data deficient	Subregional endemic
Region B	Labeobarbus kimberleyensis	6	Near threatened	Regional endemic level 2
Region B	Labeobarbus marequensis	788	Least concern	Subregional endemic
Region B	Labeobarbus nelspruitensis	3	Near threatened	Regional endemic level 1
Region B	Labeobarbus polylepis	64	Least concern	Regional endemic level 1
Region B	Lacustricola katangae	5	Least concern	Subregional endemic
Region B	Marcusenius krameri	1	Least concern	National endemic
Region B	Marcusenius pongolensis	7	Least concern	Subregional endemic
Region B	Micralestes acutidens	200	Least concern	Widespread
Region B	Micropanchax johnstoni	1	Least concern	Subregional endemic
Region B	Nothobranchius orthonotus	4	Least concern	Subregional endemic
Region B	Opsaridium peringueyi	79	Least concern	Subregional endemic
Region B	Oreochromis mossambicus	703	Vulnerable	Widespread
Region B	Petrocephalus wesselsi	39	Least concern	Subregional endemic
Region B	Pseudocrenilabrus philander	526	Least concern	Subregional endemic
Region B	Schilbe intermedius	130	Least concern	Widespread
Region B	Serranochromis meridianus	5	Endangered	Subregional endemic
Region B	Synodontis zambezensis	89	Least concern	Subregional endemic
Region B	Tilapia sparrmanii	280	Least concern	Widespread
Region C	Austroglanis sclateri	27	Least concern	Regional endemic level 2
Region C	Brycinus imberi	1	Least concern	Widespread
Region C	Chetia flaviventris	1	Least concern	Subregional endemic
Region C	Clarias gariepinus	147	Least concern	Widespread
Region C	Coptodon rendalli	2	Least concern	Widespread
Region C	Enteromius annectens	2	Least concern	Subregional endemic
Region C	Enteromius anoplus	122	Least concern	Subregional endemic
Region C	Enteromius bifrenatus	3	Least concern	Subregional endemic
Region C	Enteromius lineomaculatus	1	Least concern	Subregional endemic
Region C	Enteromius mattozi	1	Least concern	Subregional endemic
Region C	Enteromius neefi	2	Least concern	Subregional endemic
Region C	Enteromius pallidus	36	Least concern	Subregional endemic
Region C	Enteromius paludinosus	78	Least concern	Widespread
Region C	Enteromius radiatus	1	Least concern	Subregional endemic
Region C	Enteromius trimaculatus	17	Least concern	Subregional endemic

Region C	Enteromius unitaeniatus	1	Least concern	Subregional endemic
Region C	Labeo capensis	108	Least concern	Regional endemic level 2
Region C	Labeo cylindricus	1	Least concern	Widespread
Region C	Labeo molybdinus	3	Least concern	Subregional endemic
Region C	Labeo ruddi	1	Data deficient	Subregional endemic
Region C	Labeo umbratus	115	Least concern	Subregional endemic
Region C	Labeobarbus aeneus	121	Least concern	Regional endemic level 2
Region C	Labeobarbus kimberleyensis	56	Near threatened	Regional endemic level 2
Region C	Labeobarbus marequensis	3	Least concern	Subregional endemic
Region C	Labeobarbus polylepis	1	Least concern	Regional endemic level 1
Region C	Lacustricola katangae	1	Least concern	Subregional endemic
Region C	Micralestes acutidens	1	Least concern	Widespread
Region C	Oreochromis mossambicus	1	Vulnerable	Widespread
Region C	Petrocephalus wesselsi	3	Least concern	Subregional endemic
Region C	Pseudobarbus asper	3	Vulnerable	Regional endemic level 2
Region C	Pseudobarbus phlegethon	1	Endangered	Micro-endemic level 1
Region C	Pseudocrenilabrus philander	96	Least concern	Subregional endemic
Region C	Schilbe intermedius	4	Least concern	Widespread
Region C	Tilapia sparrmanii	93	Least concern	Widespread
Region D	Anguilla mossambica	3	Least concern	Widespread
Region D	Austroglanis sclateri	33	Least concern	Regional endemic level 2
Region D	Chiloglanis pretoriae	1	Least concern	Subregional endemic
Region D	Clarias gariepinus	67	Least concern	Widespread
Region D	Engraulicypris brevianalis	23	Least concern	Subregional endemic
Region D	Engraulicypris gariepinus	21	Least concern	Regional endemic level 2
Region D	Enteromius anoplus	119	Least concern	Subregional endemic
Region D	Enteromius argenteus	1	Least concern	Subregional endemic
Region D	Enteromius bifrenatus	1	Least concern	Subregional endemic
Region D	Enteromius brevipinnis	3	Near threatened	Subregional endemic
Region D	Enteromius eutaenia	2	Least concern	Widespread
Region D	Enteromius lineomaculatus	1	Least concern	Subregional endemic
Region D	Enteromius mattozi	1	Least concern	Subregional endemic
Region D	Enteromius motebensis	1	Near threatened	Subregional endemic
Region D	Enteromius pallidus	4	Least concern	Subregional endemic

Region D	Enteromius paludinosus	63	Least concern	Widespread
Region D	Enteromius toppini	1	Least concern	Subregional endemic
Region D	Enteromius trimaculatus	44	Least concern	Subregional endemic
Region D	Enteromius unitaeniatus	2	Least concern	Subregional endemic
Region D	Enteromius viviparus	1	Least concern	Subregional endemic
Region D	Galaxias zebratus	1	Data deficient	Regional endemic level 1
Region D	Labeo capensis	135	Least concern	Regional endemic level 2
Region D	Labeo cylindricus	1	Least concern	Widespread
Region D	Labeo molybdinus	1	Least concern	Subregional endemic
Region D	Labeo rosae	1	Least concern	Subregional endemic
Region D	Labeo ruddi	1	Data deficient	Subregional endemic
Region D	Labeo umbratus	61	Least concern	Subregional endemic
Region D	Labeobarbus aeneus	202	Least concern	Regional endemic level 2
Region D	Labeobarbus kimberleyensis	86	Near threatened	Regional endemic level 2
Region D	Labeobarbus marequensis	4	Least concern	Subregional endemic
Region D	Pseudobarbus asper	2	Vulnerable	Regional endemic level 2
Region D	Pseudobarbus erubescens	1	Critically endangered	Micro-endemic level 1
Region D	Pseudobarbus hospes	31	Least concern	Regional endemic level 1
Region D	Pseudobarbus quathlambae	1	Endangered	Micro-endemic level 1
Region D	Pseudobarbus senticeps	1	Critically endangered	Micro-endemic level 2
Region D	Pseudocrenilabrus philander	52	Least concern	Subregional endemic
Region D	Tilapia sparrmanii	63	Least concern	Widespread
Region E	Austroglanis barnardi	94	Endangered	Regional endemic level 1
Region E	Austroglanis gilli	303	Near threatened	Regional endemic level 1
Region E	Enteromius anoplus	111	Least concern	Subregional endemic
Region E	Galaxias zebratus	206	Data deficient	Regional endemic level 1
Region E	Labeo cylindricus	2	Least concern	Widespread
Region E	Labeo rosae	1	Least concern	Subregional endemic
Region E	Labeo seeberi	269	Endangered	Regional endemic level 2
Region E	Labeobarbus seeberi	304	Near threatened	Regional endemic level 1
Region E	Pseudobarbus burchelli	2	Critically endangered	Micro-endemic level 2
Region E	Pseudobarbus burgi	1	Endangered	Regional endemic level 2
Region E	Pseudobarbus calidus	334	Near threatened	Regional endemic level 2
Region E	Pseudobarbus capensis	9	Endangered	Regional endemic level 1

Region E	Pseudobarbus erubescens	139	Critically endangered	Micro-endemic level 1
Region E	Pseudobarbus phlegethon	224	Endangered	Micro-endemic level 1
Region E	Pseudobarbus serra	586	Near threatened	Micro-endemic level 1
Region E	Sandelia capensis	1	Data deficient	Regional endemic level 1
Region G	Anguilla marmorata	1	Least concern	Widespread
Region G	Anguilla mossambica	7	Least concern	Widespread
Region G	Ctenopoma multispine	1	Least concern	Subregional endemic
Region G	Enteromius mattozi	2	Least concern	Subregional endemic
Region G	Enteromius pallidus	1	Least concern	Subregional endemic
Region G	Galaxias zebratus	460	Data deficient	Regional endemic level 1
Region G	Labeo seeberi	4	Endangered	Regional endemic level 2
Region G	Pseudobarbus afer	1	Endangered	Micro-endemic level 1
Region G	Pseudobarbus asper	1	Vulnerable	Regional endemic level 2
Region G	Pseudobarbus burchelli	36	Critically endangered	Micro-endemic level 2
Region G	Pseudobarbus burgi	207	Endangered	Regional endemic level 2
Region G	Pseudobarbus capensis	21	Endangered	Regional endemic level 1
Region G	Pseudobarbus trevelyani	2	Endangered	Regional endemic level 1
Region G	Pseudobarbus verloreni	35	Endangered	Micro-endemic level 2
Region G	Sandelia capensis	389	Data deficient	Regional endemic level 1
Region H	Anguilla bicolor	1	Near threatened	Widespread
Region H	Anguilla marmorata	2	Least concern	Widespread
Region H	Anguilla mossambica	16	Least concern	Widespread
Region H	Galaxias zebratus	335	Data deficient	Regional endemic level 1
Region H	Labeobarbus seeberi	1	Near threatened	Regional endemic level 1
Region H	Pseudobarbus afer	1	Endangered	Micro-endemic level 1
Region H	Pseudobarbus asper	1	Vulnerable	Regional endemic level 2
Region H	Pseudobarbus burchelli	602	Critically endangered	Micro-endemic level 2
Region H	Pseudobarbus burgi	4	Endangered	Regional endemic level 2
Region H	Pseudobarbus capensis	45	Endangered	Regional endemic level 1
Region H	Pseudobarbus phlegethon	1	Endangered	Micro-endemic level 1
Region H	Pseudobarbus skeltoni	38	Endangered	Micro-endemic level 1
Region H	Sandelia capensis	577	Data deficient	Regional endemic level 1
Region J	Anguilla marmorata	2	Least concern	Widespread
Region J	Anguilla mossambica	2	Least concern	Widespread

Region J	Enteromius anoplus	210	Least concern	Subregional endemic
Region J	Enteromius lineomaculatus	1	Least concern	Subregional endemic
Region J	Galaxias zebratus	74	Data deficient	Regional endemic level 1
Region J	Labeo umbratus	63	Least concern	Subregional endemic
Region J	Pseudobarbus afer	13	Endangered	Micro-endemic level 1
Region J	Pseudobarbus asper	289	Vulnerable	Regional endemic level 2
Region J	Pseudobarbus burchelli	1	Critically endangered	Micro-endemic level 2
Region J	Pseudobarbus capensis	1	Endangered	Regional endemic level 1
Region J	Pseudobarbus tenuis	386	Near threatened	Regional endemic level 1
Region J	Sandelia capensis	152	Data deficient	Regional endemic level 1
Region K	Anguilla mossambica	22	Least concern	Widespread
Region K	Enteromius pallidus	2	Least concern	Subregional endemic
Region K	Galaxias zebratus	72	Data deficient	Regional endemic level 1
Region K	Pseudobarbus afer	169	Endangered	Micro-endemic level 1
Region K	Pseudobarbus asper	14	Vulnerable	Regional endemic level 2
Region K	Pseudobarbus senticeps	1	Critically endangered	Micro-endemic level 2
Region K	Pseudobarbus tenuis	29	Near threatened	Regional endemic level 1
Region K	Sandelia capensis	119	Data deficient	Regional endemic level 1
Region L	Anguilla mossambica	6	Least concern	Widespread
Region L	Enteromius anoplus	23	Least concern	Subregional endemic
Region L	Enteromius pallidus	37	Least concern	Subregional endemic
Region L	Galaxias zebratus	10	Data deficient	Regional endemic level 1
Region L	Labeo umbratus	30	Least concern	Subregional endemic
Region L	Pseudobarbus afer	132	Endangered	Micro-endemic level 1
Region L	Pseudobarbus asper	35	Vulnerable	Regional endemic level 2
Region L	Pseudobarbus swartzi	9	Vulnerable	Micro-endemic level 2
Region L	Pseudobarbus tenuis	1	Near threatened	Regional endemic level 1
Region L	Sandelia capensis	76	Data deficient	Regional endemic level 1
Region M	Anguilla marmorata	2	Least concern	Widespread
Region M	Anguilla mossambica	14	Least concern	Widespread
Region M	Enteromius anoplus	1	Least concern	Subregional endemic
Region M	Enteromius pallidus	59	Least concern	Subregional endemic
Region M	Galaxias zebratus	3	Data deficient	Regional endemic level 1
Region M	Labeo umbratus	1	Least concern	Subregional endemic

Region M	Pseudobarbus afer	79	Endangered	Micro-endemic level 1
Region M	Pseudobarbus senticeps	3	Critically endangered	Micro-endemic level 2
Region M	Pseudocrenilabrus philander	17	Least concern	Subregional endemic
Region M	Sandelia capensis	103	Data deficient	Regional endemic level 1
Region N	Anguilla marmorata	5	Least concern	Widespread
Region N	Anguilla mossambica	42	Least concern	Widespread
Region N	Enteromius anoplus	21	Least concern	Subregional endemic
Region N	Enteromius eutaenia	4	Least concern	Widespread
Region N	Enteromius pallidus	51	Least concern	Subregional endemic
Region N	Enteromius trimaculatus	3	Least concern	Subregional endemic
Region N	Labeo umbratus	52	Least concern	Subregional endemic
Region N	Labeobarbus marequensis	2	Least concern	Subregional endemic
Region N	Megalops cyprinoides	1	Data deficient	Widespread
Region N	Opsaridium peringueyi	2	Least concern	Subregional endemic
Region N	Oreochromis mossambicus	1	Vulnerable	Widespread
Region N	Pseudobarbus afer	93	Endangered	Micro-endemic level 1
Region N	Pseudobarbus asper	1	Vulnerable	Regional endemic level 2
Region P	Anguilla bicolor	2	Near threatened	Widespread
Region P	Anguilla marmorata	2	Least concern	Widespread
Region P	Anguilla mossambica	24	Least concern	Widespread
Region P	Engraulicypris brevianalis	1	Least concern	Subregional endemic
Region P	Enteromius amatolicus	1	Data deficient	National endemic
Region P	Enteromius anoplus	28	Least concern	Subregional endemic
Region P	Enteromius pallidus	27	Least concern	Subregional endemic
Region P	Galaxias zebratus	1	Data deficient	Regional endemic level 1
Region P	Labeo umbratus	10	Least concern	Subregional endemic
Region P	Oreochromis mossambicus	30	Vulnerable	Widespread
Region P	Pseudobarbus afer	1	Endangered	Micro-endemic level 1
Region P	Pseudobarbus senticeps	1	Critically endangered	Micro-endemic level 2
Region P	Pseudocrenilabrus philander	3	Least concern	Subregional endemic
Region P	Sandelia bainsii	31	Endangered	National endemic
Region Q	Anguilla bicolor	1	Near threatened	Widespread
Region Q	Anguilla marmorata	5	Least concern	Widespread
Region Q	Anguilla mossambica	23	Least concern	Widespread

Region Q	Austroglanis sclateri	4	Least concern	Regional endemic level 2
Region Q	Enteromius anoplus	99	Least concern	Subregional endemic
Region Q	Enteromius pallidus	8	Least concern	Subregional endemic
Region Q	Labeo umbratus	51	Least concern	Subregional endemic
Region Q	Labeobarbus marequensis	12	Least concern	Subregional endemic
Region Q	Oreochromis mossambicus	8	Vulnerable	Widespread
Region Q	Pseudobarbus trevelyani	1	Endangered	Regional endemic level 1
Region Q	Sandelia bainsii	30	Endangered	National endemic
Region R	Anguilla marmorata	4	Least concern	Widespread
Region R	Anguilla mossambica	55	Least concern	Widespread
Region R	Engraulicypris brevianalis	1	Least concern	Subregional endemic
Region R	Enteromius amatolicus	1	Data deficient	National endemic
Region R	Enteromius anoplus	127	Least concern	Subregional endemic
Region R	Enteromius pallidus	3	Least concern	Subregional endemic
Region R	Labeobarbus kimberleyensis	1	Near threatened	Regional endemic level 2
Region R	Oreochromis mossambicus	44	Vulnerable	Widespread
Region R	Pseudobarbus asper	1	Vulnerable	Regional endemic level 2
Region R	Pseudobarbus capensis	1	Endangered	Regional endemic level 1
Region R	Pseudobarbus trevelyani	78	Endangered	Regional endemic level 1
Region R	Sandelia bainsii	42	Endangered	National endemic
Region S	Anguilla mossambica	12	Least concern	Widespread
Region S	Enteromius afrohamiltoni	1	Least concern	Subregional endemic
Region S	Enteromius amatolicus	14	Data deficient	National endemic
Region S	Enteromius anoplus	67	Least concern	Subregional endemic
Region S	Enteromius radiatus	1	Least concern	Subregional endemic
Region S	Oreochromis mossambicus	2	Vulnerable	Widespread
Region T	Ambassis natalensis	14	Least concern	Subregional endemic
Region T	Anguilla bengalensis	1	Near threatened	Widespread
Region T	Anguilla marmorata	28	Least concern	Widespread
Region T	Anguilla mossambica	90	Least concern	Widespread
Region T	Enteromius amatolicus	15	Data deficient	National endemic
Region T	Enteromius annectens	1	Least concern	Subregional endemic
Region T	Enteromius anoplus	84	Least concern	Subregional endemic
Region T	Enteromius brevipinnis	1	Near threatened	Subregional endemic

Region T	Enteromius gurneyi	16	Vulnerable	Subregional endemic
Region T	Enteromius pallidus	5	Least concern	Subregional endemic
Region T	Enteromius paludinosus	7	Least concern	Widespread
Region T	Enteromius viviparus	51	Least concern	Subregional endemic
Region T	Galaxias zebratus	1	Data deficient	Regional endemic level 1
Region T	Labeobarbus natalensis	67	Least concern	Regional endemic level 1
Region T	Megalops cyprinoides	6	Data deficient	Widespread
Region T	Oreochromis mossambicus	110	Vulnerable	Widespread
Region T	Pseudobarbus quathlambae	2	Endangered	Micro-endemic level 1
Region T	Pseudocrenilabrus philander	25	Least concern	Subregional endemic
Region U	Ambassis natalensis	14	Least concern	Subregional endemic
Region U	Amphilius natalensis	102	Least concern	Widespread
Region U	Anguilla bengalensis	8	Near threatened	Widespread
Region U	Anguilla marmorata	19	Least concern	Widespread
Region U	Anguilla mossambica	171	Least concern	Widespread
Region U	Chetia flaviventris	1	Least concern	Subregional endemic
Region U	Clarias theodorae	4	Least concern	Widespread
Region U	Engraulicypris brevianalis	1	Least concern	Subregional endemic
Region U	Enteromius anoplus	58	Least concern	Subregional endemic
Region U	Enteromius gurneyi	91	Vulnerable	Subregional endemic
Region U	Enteromius mattozi	1	Least concern	Subregional endemic
Region U	Enteromius paludinosus	32	Least concern	Widespread
Region U	Enteromius toppini	3	Least concern	Subregional endemic
Region U	Enteromius trimaculatus	50	Least concern	Subregional endemic
Region U	Enteromius unitaeniatus	1	Least concern	Subregional endemic
Region U	Enteromius viviparus	272	Least concern	Subregional endemic
Region U	Labeo molybdinus	2	Least concern	Subregional endemic
Region U	Labeo rubromaculatus	2	Vulnerable	Micro-endemic level 1
Region U	Labeobarbus marequensis	1	Least concern	Subregional endemic
Region U	Labeobarbus natalensis	372	Least concern	Regional endemic level 1
Region U	Labeobarbus polylepis	1	Least concern	Regional endemic level 1
Region U	Lacustricola myaposae	2	Near threatened	Regional endemic level 1
Region U	Megalops cyprinoides	16	Data deficient	Widespread
Region U	Nothobranchius orthonotus	1	Least concern	Subregional endemic

Region U	Oreochromis mossambicus	346	Vulnerable	Widespread
Region U	Pseudocrenilabrus philander	149	Least concern	Subregional endemic
Region U	Schilbe intermedius	1	Least concern	Widespread
Region V	Amphilius natalensis	122	Least concern	Widespread
Region V	Amphilius uranoscopus	1	Least concern	Subregional endemic
Region V	Anguilla bengalensis	4	Near threatened	Widespread
Region V	Anguilla marmorata	3	Least concern	Widespread
Region V	Anguilla mossambica	94	Least concern	Widespread
Region V	Austroglanis sclateri	4	Least concern	Regional endemic level 2
Region V	Chiloglanis paratus	1	Least concern	Subregional endemic
Region V	Clarias gariepinus	196	Least concern	Widespread
Region V	Enteromius anoplus	313	Least concern	Subregional endemic
Region V	Enteromius gurneyi	10	Vulnerable	Subregional endemic
Region V	Enteromius lineomaculatus	1	Least concern	Subregional endemic
Region V	Enteromius motebensis	1	Near threatened	Subregional endemic
Region V	Enteromius pallidus	43	Least concern	Subregional endemic
Region V	Enteromius paludinosus	31	Least concern	Widespread
Region V	Enteromius trimaculatus	58	Least concern	Subregional endemic
Region V	Enteromius unitaeniatus	1	Least concern	Subregional endemic
Region V	Enteromius viviparus	32	Least concern	Subregional endemic
Region V	Labeo capensis	11	Least concern	Regional endemic level 2
Region V	Labeo molybdinus	76	Least concern	Subregional endemic
Region V	Labeo rosae	1	Least concern	Subregional endemic
Region V	Labeo rubromaculatus	217	Vulnerable	Micro-endemic level 1
Region V	Labeo umbratus	2	Least concern	Subregional endemic
Region V	Labeobarbus aeneus	11	Least concern	Regional endemic level 2
Region V	Labeobarbus marequensis	2	Least concern	Subregional endemic
Region V	Labeobarbus natalensis	425	Least concern	Regional endemic level 1
Region V	Micralestes acutidens	2	Least concern	Widespread
Region V	Oreochromis mossambicus	63	Vulnerable	Widespread
Region V	Pseudocrenilabrus philander	20	Least concern	Subregional endemic
Region V	Tilapia sparrmanii	35	Least concern	Widespread
Region W	Ambassis natalensis	28	Least concern	Subregional endemic
Region W	Amphilius natalensis	14	Least concern	Widespread

Region W	Amphilius uranoscopus	151	Least concern	Subregional endemic
Region W	Anguilla bengalensis	7	Near threatened	Widespread
Region W	Anguilla bicolor	5	Near threatened	Widespread
Region W	Anguilla marmorata	50	Least concern	Widespread
Region W	Anguilla mossambica	100	Least concern	Widespread
Region W	Brycinus imberi	100	Least concern	Widespread
Region W	Brycinus lateralis	62	Least concern	Subregional endemic
Region W	Chiloglanis anoterus	153	Least concern	Regional endemic level 1
Region W	Chiloglanis emarginatus	44	Vulnerable	Subregional endemic
Region W	Chiloglanis paratus	56	Least concern	Subregional endemic
Region W	Chiloglanis pretoriae	3	Least concern	Subregional endemic
Region W	Chiloglanis swierstrai	72	Least concern	Subregional endemic
Region W	Clarias gariepinus	341	Least concern	Widespread
Region W	Clarias ngamensis	7	Least concern	Subregional endemic
Region W	Clarias theodorae	75	Least concern	Widespread
Region W	Coptodon rendalli	105	Least concern	Widespread
Region W	Ctenopoma multispine	27	Least concern	Subregional endemic
Region W	Engraulicypris brevianalis	171	Least concern	Subregional endemic
Region W	Enteromius afrohamiltoni	84	Least concern	Subregional endemic
Region W	Enteromius annectens	111	Least concern	Subregional endemic
Region W	Enteromius anoplus	114	Least concern	Subregional endemic
Region W	Enteromius argenteus	134	Least concern	Subregional endemic
Region W	Enteromius bifrenatus	21	Least concern	Subregional endemic
Region W	Enteromius brevipinnis	3	Near threatened	Subregional endemic
Region W	Enteromius eutaenia	13	Least concern	Widespread
Region W	Enteromius gurneyi	38	Vulnerable	Subregional endemic
Region W	Enteromius lineomaculatus	8	Least concern	Subregional endemic
Region W	Enteromius mattozi	1	Least concern	Subregional endemic
Region W	Enteromius motebensis	1	Near threatened	Subregional endemic
Region W	Enteromius neefi	3	Least concern	Subregional endemic
Region W	Enteromius pallidus	21	Least concern	Subregional endemic
Region W	Enteromius paludinosus	513	Least concern	Widespread
Region W	Enteromius radiatus	46	Least concern	Subregional endemic
Region W	Enteromius toppini	231	Least concern	Subregional endemic

Region W	Enteromius trimaculatus	402	Least concern	Subregional endemic
Region W	Enteromius unitaeniatus	75	Least concern	Subregional endemic
Region W	Enteromius viviparus	351	Least concern	Subregional endemic
Region W	Hydrocynus vittatus	94	Least concern	Widespread
Region W	Labeo congoro	18	Least concern	Subregional endemic
Region W	Labeo cylindricus	132	Least concern	Widespread
Region W	Labeo molybdinus	191	Least concern	Subregional endemic
Region W	Labeo rosae	127	Least concern	Subregional endemic
Region W	Labeo rubromaculatus	4	Vulnerable	Micro-endemic level 1
Region W	Labeobarbus marequensis	122	Least concern	Subregional endemic
Region W	Labeobarbus natalensis	171	Least concern	Regional endemic level 1
Region W	Labeobarbus nelspruitensis	19	Near threatened	Regional endemic level 1
Region W	Labeobarbus polylepis	104	Least concern	Regional endemic level 1
Region W	Lacustricola katangae	100	Least concern	Subregional endemic
Region W	Lacustricola myaposae	120	Near threatened	Regional endemic level 1
Region W	Marcusenius caudisquamatus	7	Endangered	Micro-endemic level 1
Region W	Marcusenius pongolensis	9	Least concern	Subregional endemic
Region W	Megalops cyprinoides	25	Data deficient	Widespread
Region W	Micralestes acutidens	122	Least concern	Widespread
Region W	Microctenopoma intermedium	6	Least concern	Subregional endemic
Region W	Micropanchax johnstoni	24	Least concern	Subregional endemic
Region W	Nothobranchius orthonotus	29	Least concern	Subregional endemic
Region W	Opsaridium peringueyi	48	Least concern	Subregional endemic
Region W	Oreochromis mossambicus	695	Vulnerable	Widespread
Region W	Oreochromis placidus	3	Least concern	Subregional endemic
Region W	Petrocephalus wesselsi	23	Least concern	Subregional endemic
Region W	Pseudobarbus trevelyani	1	Endangered	Regional endemic level 1
Region W	Pseudocrenilabrus philander	478	Least concern	Subregional endemic
Region W	Schilbe intermedius	116	Least concern	Widespread
Region W	Serranochromis meridianus	2	Endangered	Subregional endemic
Region W	Synodontis zambezensis	68	Least concern	Subregional endemic
Region W	Tilapia sparrmanii	290	Least concern	Widespread
Region X	Ambassis natalensis	1	Least concern	Subregional endemic
Region X	Amphilius natalensis	139	Least concern	Widespread

Region X	Amphilius uranoscopus	393	Least concern	Subregional endemic
Region X	Anguilla bengalensis	2	Near threatened	Widespread
Region X	Anguilla marmorata	20	Least concern	Widespread
Region X	Anguilla mossambica	93	Least concern	Widespread
Region X	Brycinus imberi	45	Least concern	Widespread
Region X	Brycinus lateralis	2	Least concern	Subregional endemic
Region X	Chetia brevis	19	Endangered	Subregional endemic
Region X	Chetia flaviventris	2	Least concern	Subregional endemic
Region X	Chiloglanis anoterus	268	Least concern	Regional endemic level 1
Region X	Chiloglanis bifurcus	72	Critically endangered	Micro-endemic level 1
Region X	Chiloglanis emarginatus	16	Vulnerable	Subregional endemic
Region X	Chiloglanis paratus	199	Least concern	Subregional endemic
Region X	Chiloglanis pretoriae	519	Least concern	Subregional endemic
Region X	Chiloglanis swierstrai	155	Least concern	Subregional endemic
Region X	Clarias gariepinus	296	Least concern	Widespread
Region X	Clarias ngamensis	1	Least concern	Subregional endemic
Region X	Coptodon rendalli	245	Least concern	Widespread
Region X	Engraulicypris brevianalis	141	Least concern	Subregional endemic
Region X	Enteromius afrohamiltoni	40	Least concern	Subregional endemic
Region X	Enteromius annectens	145	Least concern	Subregional endemic
Region X	Enteromius anoplus	231	Least concern	Subregional endemic
Region X	Enteromius argenteus	240	Least concern	Subregional endemic
Region X	Enteromius bifrenatus	1	Least concern	Subregional endemic
Region X	Enteromius brevipinnis	43	Near threatened	Subregional endemic
Region X	Enteromius eutaenia	283	Least concern	Widespread
Region X	Enteromius lineomaculatus	6	Least concern	Subregional endemic
Region X	Enteromius motebensis	4	Near threatened	Subregional endemic
Region X	Enteromius neefi	37	Least concern	Subregional endemic
Region X	Enteromius pallidus	3	Least concern	Subregional endemic
Region X	Enteromius paludinosus	102	Least concern	Widespread
Region X	Enteromius radiatus	123	Least concern	Subregional endemic
Region X	Enteromius toppini	49	Least concern	Subregional endemic
Region X	Enteromius trimaculatus	434	Least concern	Subregional endemic
Region X	Enteromius unitaeniatus	236	Least concern	Subregional endemic

Region X	Enteromius viviparus	263	Least concern	Subregional endemic
Region X	Hydrocynus vittatus	97	Least concern	Widespread
Region X	Kneria auriculata	5	Least concern	Subregional endemic
Region X	Labeo congoro	69	Least concern	Subregional endemic
Region X	Labeo cylindricus	205	Least concern	Widespread
Region X	Labeo molybdinus	356	Least concern	Subregional endemic
Region X	Labeo rosae	82	Least concern	Subregional endemic
Region X	Labeo ruddi	17	Data deficient	Subregional endemic
Region X	Labeobarbus marequensis	617	Least concern	Subregional endemic
Region X	Labeobarbus nelspruitensis	71	Near threatened	Regional endemic level 1
Region X	Labeobarbus polylepis	142	Least concern	Regional endemic level 1
Region X	Marcusenius pongolensis	31	Least concern	Subregional endemic
Region X	Micralestes acutidens	321	Least concern	Widespread
Region X	Nothobranchius orthonotus	2	Least concern	Subregional endemic
Region X	Opsaridium peringueyi	184	Least concern	Subregional endemic
Region X	Oreochromis mossambicus	413	Vulnerable	Widespread
Region X	Petrocephalus wesselsi	59	Least concern	Subregional endemic
Region X	Pseudocrenilabrus philander	435	Least concern	Subregional endemic
Region X	Schilbe intermedius	48	Least concern	Widespread
Region X	Serranochromis meridianus	60	Endangered	Subregional endemic
Region X	Synodontis zambezensis	12	Least concern	Subregional endemic
Region X	Tilapia sparrmanii	276	Least concern	Widespread

Table S. 3.3b. List of all non-native freshwater fishes occurring in each primary catchment in South Africa.

Catchment ID	Species Name	Number of Records	IUCN Conservation Status	Endemism Category
Region A	Ctenopharyngodon idella	1	Not evaluated	Widespread
Region A	Cyprinus carpio	52	Vulnerable	Widespread
Region A	Gambusia affinis	13	Least concern	Widespread
Region A	Lepomis macrochirus	3	Least concern	Widespread
Region A	Micropterus dolomieu	4	Least concern	Widespread
Region A	Micropterus floridanus	2	Not evaluated	Widespread
Region A	Micropterus punctulatus	5	Least concern	Widespread
Region A	Micropterus salmoides	56	Least concern	Widespread
Region A	Oreochromis niloticus	48	Least concern	Widespread
Region B	Cyprinus carpio	41	Vulnerable	Widespread
Region B	Gambusia affinis	47	Least concern	Widespread
Region B	Hypophthalmichthys molitrix	10	Near threatened	Widespread
Region B	Micropterus dolomieu	7	Least concern	Widespread
Region B	Micropterus floridanus	1	Not evaluated	Widespread
Region B	Micropterus punctulatus	1	Least concern	Widespread
Region B	Micropterus salmoides	57	Least concern	Widespread
Region B	Oncorhynchus mykiss	20	Not evaluated	Widespread
Region B	Oreochromis niloticus	3	Least concern	Widespread
Region B	Salmo trutta	4	Least concern	Widespread
Region C	Carassius auratus	1	Least concern	Widespread
Region C	Ctenopharyngodon idella	6	Not evaluated	Widespread
Region C	Cyprinus carpio	73	Vulnerable	Widespread
Region C	Gambusia affinis	37	Least concern	Widespread
Region C	Lepomis macrochirus	2	Least concern	Widespread
Region C	Micropterus dolomieu	1	Least concern	Widespread
Region C	Micropterus floridanus	1	Not evaluated	Widespread
Region C	Micropterus salmoides	54	Least concern	Widespread
Region C	Oncorhynchus mykiss	10	Not evaluated	Widespread
Region C	Xiphophorus maculatus	1	Data deficient	Widespread
Region D	Carassius auratus	3	Least concern	Widespread
Region D	Cyprinus carpio	40	Vulnerable	Widespread
Region D	Gambusia affinis	3	Least concern	Widespread

Region D	Micropterus punctulatus	2	Least concern	Widespread
Region D	Micropterus salmoides	3	Least concern	Widespread
Region D	Oncorhynchus mykiss	10	Not evaluated	Widespread
Region D	Poecilia reticulata	1	Not evaluated	Widespread
Region D	Salmo trutta	2	Least concern	Widespread
Region E	Cyprinus carpio	2	Vulnerable	Widespread
Region E	Lepomis macrochirus	192	Least concern	Widespread
Region E	Micropterus dolomieu	348	Least concern	Widespread
Region E	Micropterus punctulatus	187	Least concern	Widespread
Region E	Micropterus salmoides	79	Least concern	Widespread
Region E	Oncorhynchus mykiss	45	Not evaluated	Widespread
Region E	Salmo trutta	4	Least concern	Widespread
Region G	Carassius auratus	2	Least concern	Widespread
Region G	Ctenopharyngodon idella	1	Not evaluated	Widespread
Region G	Cyprinus carpio	84	Vulnerable	Widespread
Region G	Gambusia affinis	32	Least concern	Widespread
Region G	Lepomis macrochirus	27	Least concern	Widespread
Region G	Micropterus dolomieu	86	Least concern	Widespread
Region G	Micropterus punctulatus	26	Least concern	Widespread
Region G	Micropterus salmoides	77	Least concern	Widespread
Region G	Oncorhynchus mykiss	168	Not evaluated	Widespread
Region G	Oreochromis aureus	5	Least concern	Widespread
Region G	Oreochromis niloticus	4	Least concern	Widespread
Region G	Salmo trutta	8	Least concern	Widespread
Region G	Salvelinus fontinalis	1	Not evaluated	Widespread
Region G	Tinca tinca	1	Least concern	Widespread
Region H	Cyprinus carpio	12	Vulnerable	Widespread
Region H	Lepomis macrochirus	28	Least concern	Widespread
Region H	Micropterus dolomieu	56	Least concern	Widespread
Region H	Micropterus floridanus	1	Not evaluated	Widespread
Region H	Micropterus punctulatus	1	Least concern	Widespread
Region H	Micropterus salmoides	64	Least concern	Widespread
Region H	Oncorhynchus mykiss	104	Not evaluated	Widespread
Region H	Pangasius sanitwongsei	3	Critically endangered	Widespread

Region H	Salmo trutta	2	Least concern	Widespread
Region H	Tinca tinca	7	Least concern	Widespread
Region J	Cyprinus carpio	14	Vulnerable	Widespread
Region J	Lepomis macrochirus	1	Least concern	Widespread
Region J	Micropterus dolomieu	6	Least concern	Widespread
Region J	Micropterus punctulatus	4	Least concern	Widespread
Region J	Micropterus salmoides	41	Least concern	Widespread
Region J	Oncorhynchus mykiss	8	Not evaluated	Widespread
Region J	Salmo trutta	1	Least concern	Widespread
Region K	Carassius auratus	7	Least concern	Widespread
Region K	Ctenopharyngodon idella	2	Not evaluated	Widespread
Region K	Cyprinus carpio	13	Vulnerable	Widespread
Region K	Gambusia affinis	10	Least concern	Widespread
Region K	Lepomis macrochirus	8	Least concern	Widespread
Region K	Micropterus dolomieu	2	Least concern	Widespread
Region K	Micropterus salmoides	15	Least concern	Widespread
Region K	Oncorhynchus mykiss	1	Not evaluated	Widespread
Region K	Salmo trutta	2	Least concern	Widespread
Region L	Cyprinus carpio	7	Vulnerable	Widespread
Region L	Lepomis macrochirus	12	Least concern	Widespread
Region L	Micropterus dolomieu	26	Least concern	Widespread
Region L	Micropterus punctulatus	15	Least concern	Widespread
Region L	Micropterus salmoides	13	Least concern	Widespread
Region L	Oncorhynchus mykiss	1	Not evaluated	Widespread
Region M	Carassius auratus	1	Least concern	Widespread
Region M	Cyprinus carpio	1	Vulnerable	Widespread
Region M	Gambusia affinis	1	Least concern	Widespread
Region M	Micropterus dolomieu	3	Least concern	Widespread
Region M	Micropterus punctulatus	3	Least concern	Widespread
Region M	Micropterus salmoides	18	Least concern	Widespread
Region N	Cyprinus carpio	19	Vulnerable	Widespread
Region N	Gambusia affinis	25	Least concern	Widespread
Region N	Micropterus dolomieu	2	Least concern	Widespread
Region N	Micropterus salmoides	18	Least concern	Widespread

Region P	Cyprinus carpio	3	Vulnerable	Widespread
Region P	Gambusia affinis	1	Least concern	Widespread
Region P	Lepomis macrochirus	16	Least concern	Widespread
Region P	Micropterus punctulatus	2	Least concern	Widespread
Region P	Micropterus salmoides	57	Least concern	Widespread
Region P	Oreochromis niloticus	2	Least concern	Widespread
Region Q	Carassius auratus	2	Least concern	Widespread
Region Q	Cyprinus carpio	12	Vulnerable	Widespread
Region Q	Gambusia affinis	3	Least concern	Widespread
Region Q	Lepomis macrochirus	1	Least concern	Widespread
Region Q	Micropterus dolomieu	1	Least concern	Widespread
Region Q	Micropterus punctulatus	5	Least concern	Widespread
Region Q	Micropterus salmoides	27	Least concern	Widespread
Region R	Cyprinus carpio	16	Vulnerable	Widespread
Region R	Gambusia affinis	3	Least concern	Widespread
Region R	Hypophthalmichthys molitrix	2	Near threatened	Widespread
Region R	Lepomis macrochirus	9	Least concern	Widespread
Region R	Micropterus dolomieu	3	Least concern	Widespread
Region R	Micropterus floridanus	1	Not evaluated	Widespread
Region R	Micropterus punctulatus	22	Least concern	Widespread
Region R	Micropterus salmoides	26	Least concern	Widespread
Region R	Oncorhynchus mykiss	1	Not evaluated	Widespread
Region R	Perca fluviatilis	1	Least concern	Widespread
Region R	Salmo trutta	2	Least concern	Widespread
Region S	Cyprinus carpio	13	Vulnerable	Widespread
Region S	Lepomis macrochirus	4	Least concern	Widespread
Region S	Micropterus dolomieu	4	Least concern	Widespread
Region S	Micropterus floridanus	4	Not evaluated	Widespread
Region S	Micropterus punctulatus	3	Least concern	Widespread
Region S	Micropterus salmoides	45	Least concern	Widespread
Region S	Oncorhynchus mykiss	4	Not evaluated	Widespread
Region S	Perca fluviatilis	1	Least concern	Widespread
Region S	Salvelinus fontinalis	1	Not evaluated	Widespread
Region T	Carassius auratus	5	Least concern	Widespread

Region T	Ctenopharyngodon idella	2	Not evaluated	Widespread
Region T	Cyprinus carpio	8	Vulnerable	Widespread
Region T	Lepomis macrochirus	15	Least concern	Widespread
Region T	Micropterus dolomieu	10	Least concern	Widespread
Region T	Micropterus floridanus	1	Not evaluated	Widespread
Region T	Micropterus punctulatus	13	Least concern	Widespread
Region T	Micropterus salmoides	67	Least concern	Widespread
Region T	Oncorhynchus mykiss	56	Not evaluated	Widespread
Region T	Perca fluviatilis	2	Least concern	Widespread
Region T	Poecilia reticulata	5	Not evaluated	Widespread
Region T	Serranochromis robustus	1	Least concern	Widespread
Region T	Xiphophorus helleri	4	Least concern	Widespread
Region U	Carassius auratus	7	Least concern	Widespread
Region U	Ctenopharyngodon idella	16	Not evaluated	Widespread
Region U	Cyprinus carpio	98	Vulnerable	Widespread
Region U	Gambusia affinis	5	Least concern	Widespread
Region U	Hypophthalmichthys molitrix	2	Near threatened	Widespread
Region U	Lepomis macrochirus	52	Least concern	Widespread
Region U	Micropterus dolomieu	34	Least concern	Widespread
Region U	Micropterus floridanus	2	Not evaluated	Widespread
Region U	Micropterus punctulatus	52	Least concern	Widespread
Region U	Micropterus salmoides	232	Least concern	Widespread
Region U	Oncorhynchus mykiss	2	Not evaluated	Widespread
Region U	Oreochromis aureus	1	Least concern	Widespread
Region U	Oreochromis niloticus	8	Least concern	Widespread
Region U	Poecilia reticulata	71	Not evaluated	Widespread
Region U	Salmo trutta	17	Least concern	Widespread
Region U	Xiphophorus helleri	33	Least concern	Widespread
Region U	Xiphophorus maculatus	6	Data deficient	Widespread
Region V	Carassius auratus	2	Least concern	Widespread
Region V	Ctenopharyngodon idella	5	Not evaluated	Widespread
Region V	Cyprinus carpio	75	Vulnerable	Widespread
Region V	Gambusia affinis	2	Least concern	Widespread
Region V	Lepomis macrochirus	28	Least concern	Widespread

Region V	Micropterus dolomieu	40	Least concern	Widespread
Region V	Micropterus punctulatus	16	Least concern	Widespread
Region V	Micropterus salmoides	75	Least concern	Widespread
Region V	Oncorhynchus mykiss	42	Not evaluated	Widespread
Region V	Poecilia reticulata	3	Not evaluated	Widespread
Region V	Salmo trutta	21	Least concern	Widespread
Region W	Carassius auratus	1	Least concern	Widespread
Region W	Cyprinus carpio	30	Vulnerable	Widespread
Region W	Gambusia affinis	2	Least concern	Widespread
Region W	Lepomis macrochirus	3	Least concern	Widespread
Region W	Micropterus floridanus	1	Not evaluated	Widespread
Region W	Micropterus punctulatus	5	Least concern	Widespread
Region W	Micropterus salmoides	56	Least concern	Widespread
Region W	Oncorhynchus mykiss	3	Not evaluated	Widespread
Region W	Poecilia reticulata	19	Not evaluated	Widespread
Region W	Pterygoplichthys disjunctivus	6	Not evaluated	Widespread
Region W	Salmo trutta	1	Least concern	Widespread
Region W	Xiphophorus helleri	1	Least concern	Widespread
Region X	Coptodon zilli	6	Least concern	Widespread
Region X	Cyprinus carpio	3	Vulnerable	Widespread
Region X	Gambusia affinis	6	Least concern	Widespread
Region X	Lepomis macrochirus	2	Least concern	Widespread
Region X	Micropterus dolomieu	4	Least concern	Widespread
Region X	Micropterus punctulatus	2	Least concern	Widespread
Region X	Micropterus salmoides	34	Least concern	Widespread
Region X	Oncorhynchus mykiss	34	Not evaluated	Widespread
Region X	Poecilia reticulata	2	Not evaluated	Widespread
Region X	Salmo trutta	1	Least concern	Widespread
Region X	Serranochromis robustus	1	Least concern	Widespread
Region X	Xiphophorus helleri	6	Least concern	Widespread

Table S. 3.3c. List of all extralimital freshwater fishes occuring in each primary catchment in South Africa.

Catchment ID	Species Name	Number of Records	IUCN Conservation Status
Region A	Enteromius anoplus	16	Least concern
Region A	Hydrocynus vittatus	15	Least concern
Region A	Labeo capensis	1	Least concern
Region A	Labeo umbratus	2	Least concern
Region A	Labeobarbus aeneus	7	Least concern
Region A	Oreochromis mossambicus	15	Vulnerable
Region A	Sandelia capensis	2	Data deficient
Region B	Chetia brevis	1	Endangered
Region B	Hydrocynus vittatus	33	Least concern
Region B	Labeo capensis	5	Least concern
Region B	Labeo umbratus	36	Least concern
Region B	Labeobarbus aeneus	16	Least concern
Region B	Labeobarbus natalensis	2	Least concern
Region B	Oreochromis mossambicus	1	Vulnerable
Region C	Coptodon rendalli	2	Least concern
Region C	Labeo capensis	61	Least concern
Region C	Labeo umbratus	11	Least concern
Region C	Labeobarbus aeneus	48	Least concern
Region C	Oreochromis mossambicus	1	Vulnerable
Region C	Pseudobarbus serra	1	Near threatened
Region D	Labeo capensis	16	Least concern
Region D	Labeo umbratus	5	Least concern
Region D	Labeobarbus aeneus	7	Least concern
Region D	Oreochromis mossambicus	19	Vulnerable
Region D	Pseudocrenilabrus philander	41	Least concern
Region D	Sandelia capensis	1	Data deficient
Region E	Clarias gariepinus	1	Least concern
Region E	Labeo capensis	9	Least concern
Region E	Oreochromis mossambicus	15	Vulnerable
Region E	Pseudobarbus calidus	1	Near threatened
Region E	Pseudobarbus serra	3	Near threatened
Region E	Sandelia capensis	69	Data deficient

Region E	Tilapia sparrmanii	169	Least concern
Region F	Clarias gariepinus	4	Least concern
Region F	Labeobarbus aeneus	1	Least concern
Region F	Oreochromis mossambicus	1	Vulnerable
Region G	Clarias gariepinus	32	Least concern
Region G	Enteromius anoplus	2	Least concern
Region G	Labeo capensis	1	Least concern
Region G	Labeo umbratus	1	Least concern
Region G	Labeobarbus aeneus	1	Least concern
Region G	Oreochromis mossambicus	80	Vulnerable
Region G	Pseudobarbus serra	2	Near threatened
Region G	Tilapia sparrmanii	73	Least concern
Region H	Clarias gariepinus	14	Least concern
Region H	Enteromius anoplus	3	Least concern
Region H	Labeo umbratus	1	Least concern
Region H	Oreochromis mossambicus	6	Vulnerable
Region H	Tilapia sparrmanii	46	Least concern
Region J	Clarias gariepinus	1	Least concern
Region J	Labeo capensis	1	Least concern
Region J	Labeo umbratus	2	Least concern
Region J	Labeobarbus aeneus	34	Least concern
Region J	Oreochromis mossambicus	3	Vulnerable
Region J	Sandelia capensis	3	Data deficient
Region J	Tilapia sparrmanii	106	Least concern
Region K	Clarias gariepinus	1	Least concern
Region K	Labeo umbratus	1	Least concern
Region K	Oreochromis mossambicus	67	Vulnerable
Region K	Tilapia sparrmanii	8	Least concern
Region L	Clarias gariepinus	6	Least concern
Region L	Enteromius anoplus	1	Least concern
Region L	Oreochromis mossambicus	14	Vulnerable
Region L	Tilapia sparrmanii	35	Least concern
Region M	Clarias gariepinus	6	Least concern
Region M	Oreochromis mossambicus	6	Vulnerable

Region M	Tilapia sparrmanii	30	Least concern
Region N	Clarias gariepinus	31	Least concern
Region N	Labeo capensis	8	Least concern
Region N	Labeobarbus aeneus	16	Least concern
Region N	Oreochromis mossambicus	72	Vulnerable
Region N	Sandelia capensis	2	Data deficient
Region N	Tilapia sparrmanii	19	Least concern
Region P	Clarias gariepinus	1	Least concern
Region P	Coptodon rendalli	1	Least concern
Region P	Labeobarbus aeneus	4	Least concern
Region P	Sandelia capensis	7	Data deficient
Region P	Tilapia sparrmanii	22	Least concern
Region Q	Clarias gariepinus	32	Least concern
Region Q	Labeo capensis	13	Least concern
Region Q	Labeobarbus aeneus	19	Least concern
Region Q	Sandelia capensis	3	Data deficient
Region Q	Tilapia sparrmanii	27	Least concern
Region R	Clarias gariepinus	8	Least concern
Region R	Labeo umbratus	76	Least concern
Region R	Sandelia capensis	1	Data deficient
Region R	Tilapia sparrmanii	57	Least concern
Region S	Clarias gariepinus	4	Least concern
Region S	Labeobarbus aeneus	38	Least concern
Region S	Oreochromis mossambicus	2	Vulnerable
Region S	Pseudocrenilabrus philander	1	Least concern
Region S	Tilapia sparrmanii	14	Least concern
Region T	Clarias gariepinus	10	Least concern
Region T	Coptodon rendalli	26	Least concern
Region T	Labeo capensis	4	Least concern
Region T	Labeobarbus aeneus	31	Least concern
Region T	Tilapia sparrmanii	18	Least concern
Region U	Clarias gariepinus	224	Least concern
Region U	Coptodon rendalli	89	Least concern
Region U	Enteromius anoplus	2	Least concern

Region U	Tilapia sparrmanii	131	Least concern
Region V	Coptodon rendalli	1	Least concern
Region V	Labeo capensis	2	Least concern
Region V	Labeobarbus aeneus	2	Least concern
Region W	Clarias gariepinus	2	Least concern
Region W	Coptodon rendalli	54	Least concern
Region W	Enteromius anoplus	6	Least concern
Region W	Hydrocynus vittatus	1	Least concern
Region W	Labeobarbus aeneus	1	Least concern
Region W	Labeobarbus natalensis	1	Least concern
Region X	Chetia brevis	3	Endangered
Region X	Enteromius treurensis	1	Critically endangered
Region X	Labeobarbus aeneus	4	Least concern

Supplementary S4

Table S4.1. ODMAP checklist for modelling process followed in this study.

ODMAP protocol		Obligatory
		Objective: Explanation/Inference
		Objective: Mapping/Interpolation
		Objective: Transfer/Forecast
		Optional

ODMAP section	ODMAP subsection	ODMAP elements
Overview	Authorship	· Authors: Mohammed Kajee, Dominic Henry, Helen Dallas, Charles Griffiths, Jeremy Shelton · Contact email: kjxmoh007@myuct.ac.za · Title: A stepwise, robust methodology for developing species distribution models for freshwater taxa in South Africa · DOI: TBD
	Model objective	· SDM objective/purpose: species interpolation ecological inference / explanation | Mapping / interpolation | Forecast / transfer · Main target output: In this specific case, model outputs will be used to map the predicted distribution of each focal taxon. To a lesser extent, the model outputs will also be used to gain insight into the predictor variables that contribute most to a species' current distribution.
	Taxon	· A wide variety of freshwater fish species were modelled, ranging from non-native invasives, to widespread translocated natives, and range-restricted threatened species.
	Location	· Republic of South Africa
	Scale of analysis	· Spatial Extent: Latitude: 22.13°S, 34.83°S; Longitude: 16.45°E, 32.94°E · Spatial resolution: 30 arc-seconds (0.93 X 0.93 km) · Temporal extent/time period: 1900-2023 · Temporal resolution, if applicable: Year · Type of extent boundary: Political or hydrological

Biodiversity data overview	· Observation type: Historic · Response/data type: Presence-only
Type of predictors	· Climate, topographic, landcover, soil, vegetation cover, wetlands, hydroligcal, biological
Conceptual model	· Hypotheses about species-environment relationships: This study used a suite of statistically selected climate, environment, topography and hydrology variables to model the distributions of freshwater fishes in South Africa in an exploratory way. It was hypothesized that certain of these variables would be correlated with the distribution of Black Bass species and thus serve as an accurate way to predict the distribution of non-native invasive species across the whole of South Africa.
Assumptions	· State critical model assumptions: It is assumed that the sampling is adequate and representative for these taxa. It is also assumed that the relevant ecological predictors (based on proxy environmental variables) of species distributions are included in the modelling workflow and that species detectability does not change across the modelling landscape. Lastly, it is assumed that species are at pseudo-equilibrium with the environment and that each 'surveyed' grid square in which a species was not recorded is representative of an absence. . Further, it is also assumed that all relevant ecological drivers (or proxies) impacting species' distribution are included, species are at pseudo-equilibrium with their environment, and detectability does not change across habitat gradients.
SDM algorithms	· Model algorithms: SDMs for all species were fitted using Bayesian additive regression trees (BART) in the R package embarcardero (Carlson, 2020a). BART is a machine-learning model that models the relationship between species occurrences and environmental variables. The model is trained to learn patterns in the data and predict species occurrence based on environmental conditions (Carlson, 2020a). BART was selected as the preferred modelling algorithm because it allows for more automated predictor variable selection that is useful for identifying subsets of informative predictors (Tytar et al., 2021), thus providing a statistically robust method for variable selection, making the modelling workflow transparent, repeatable, efficient for modelling large numbers of species. · Justification of model complexity: We chose different modelling parameters to optimise each statistical technique. Model settings were chosen to yield intermediately complex response surfaces but prevent excessive overfitting · Is model averaging/ensemble modelling used: Yes

	Model workflow	· Presence-only data were downloaded from the Freshwater Biodiversity Information System (FBIS) database on 30 July 2023 (FBIS, 2023) and cleaned. Background points were sampled from either the entire country (black bass and Sharptooth Catfish) or from within the boundary of the primary catchment (P. burgi). For all species, a total of 10 000 background points (pseudo-absence) were generated from within the modelling landscape. Using the bart function in the embarcardero package in R (Carlson, 2020), an initial model was fitted for each species using 50 iterations. Next, the varimp.diag function was used to evaluate which environmental and biological variables have the strongest influence on the species' occurrence patterns. This was followed by repeating the model fitting process using the variable.step function, which applies a stepwise variable selection procedure to identify the most important environmental and biological variables that contribute significantly to predicting species occurrence. Finally, a new BART model was fitted using only the most important variables identified in the stepwise selection process. This final BART model was fitted using 200 iterations. Model performance was assessed based on the threshold-independent Receiver Operational Characteristic (ROC), where the Area Under the Curve (AUC) is used to assess predictive performance (Carlson, 2020). The True Skill Statistics (TSS), which evaluates false positives (type I error) and false negatives (type II error) was also used to assess model accuracy (Carlson, 2020).
	Software, codes and data	· Specify modelling platform incl. version, key packages used: Using the *bart* function in the *embarcardero* package in R (Carlson, 2020a), an initial model was fitted for each species · Specify availability of codes: TBD · Specify availability of data, e.g. data links: The raw data presented in this study are openly available on the Freshwater Biodiversity Information System (FBIS) at: https://freshwaterbiodiversity.org/
Data	Biodiversity data	· Taxon names: · Black bass (Micropterus salmoides, M. dolomieu, M. punctulatus) · Clarias gariepinus · Pseudobarbus burgi
		· Details on taxonomic reference system: ITIS (Interagency Taxonomic Information System) via the GBIF Taxonomic Backbone
		· Ecological level (ind., pop, comm?): Species
		· Biodiversity data source: reference, accession date: Presence-only data were downloaded from the Freshwater Biodiversity Information System (FBIS) database on 30 July 2023 (FBIS, 2023)

	· Sampling design: spatial design (e.g. random, uniform, stratified), temporal design, nestedness
	· Sample size per taxon: e.g., number of observations/counts, prevalence
	· Country/region masl, if applicable: Republic of South Africa
	· Details on scaling, if applicable: e.g., rasterisation of polygon maps, spatial and temporal thinning, measures to address spatial uncertainties: Duplicate records and records with low accuracy were removed. To minimise the effect of spatial sampling bias, distance-based filtering of occurrence records is often applied to species data prior to modelling (Taylor et al., 2020). Using the thin function from the spThin package in R (Aiello-Lammens et al., 2015), a spatial thinning protocol was applied (thinning parameter = 0.8 km). This was repeated three times, with the remaining data being included in the final model workflow. For P. burgi, records used in the analysis were restricted to those falling within the known distribution of the species based on the IUCN range map. All additional records were treated as erroneous and deleted. Background point selection and the final model was restricted to primary catchment boundary.
	· Details on data cleaning/filtering steps, if applicable: e.g., taxonomically, spatially, temporally, outlier presence/treatment: Presence-only data were downloaded from the Freshwater Biodiversity Information System (FBIS) database on 30 July 2023 (FBIS, 2023), cleaned and standardised in R (R Core Team, 2023). Duplicate records and records with low accuracy were removed. To minimise the effect of spatial sampling bias, distance-based filtering of occurrence records is often applied to species data prior to modelling (Taylor et al., 2020). Using the thin function from the spThin package in R (Aiello-Lammens et al., 2015), a spatial thinning protocol was applied (thinning parameter = 0.8km). This was repeated three times, with the remaining data being included in the final model workflow. For P. burgi, records used in the analysis were restricted to those falling within the known distribution of the species based on the IUCN range map. All additional records were treated as erroneous and deleted. Background point selection and the final model was restricted to primary catchment boundary.
	· Details on absence data collection, if applicable: N/A

	· Details on background data derivation, if applicable: e.g., spatial and temporal extent, spatial and temporal buffer, bias correction (e.g. target group sampling): Background points were sampled from either the entire country (Black Bass and Sharptooth Catfish) or from within the boundary of the primary catchment (P. burgi). For all species, a total of 10 000 background points (pseudo-absence) were generated from within the modelling landscape.
	· Details on potential errors and biases in data, if applicable: e.g., detection probability, misidentification potential, geo-referencing errors, sampling bias
Data partitioning	· Selection of training data (for model fitting)
	· Selection of validation data (withheld from model fitting, used for estimating prediction error for model selection, model averaging or ensemble): e.g., cross-validation method
	· Selection of test (truly independent) data, *sensu* Hastie, et al. (2009): No data partitioning was applied;
Predictor variables	· State predictor variables used: See Supplementary S4.2, S4.4, and S4.5.
	· Details on data sources: e.g., URL/DOI, accession date, database version: See Supplementary S4.2, S4.4, and S4.5.
	· Spatial resolution and spatial extent of raw data, if different from biodiversity data: All data were thus converted to a resolution of 30 arc-seconds (0.93 X 0.93 km) and saved as GEOTIFF rasters with identical extents and coordinate referencing systems
	· Map projection (coordinate reference system): WGS84
	· Temporal resolution and temporal extent of raw data, if applicable: 1950-1999
	· Details on data processing and on spatial, temporal and thematic scaling: e.g. upscaling/downscaling, transformations, normalisations, thematic aggregations (e.g. of land cover classes), measures to address spatial uncertainties: N/A

					· Details on measurements errors and bias, when known: N/A
					· Details on dimension reduction of variable set, if applicable – if model-based, this should be contained in **M**odel section (element: Details on pre-selection of variables): All variables were allowed into the modelling workflow. A Pearson correlation test was run to assess collinearity among environmental variables. Using the vifcor function in the usdm package (Naimi, 2023), the variance inflation factor (VIF) was calculated for the selected variables, excluding highly correlated variables. vifcor first finds a pair of variables which has the maximum linear correlation (greater than the threshold; th) and excludes the one with a greater VIF (Naimi, 2023). The procedure was repeated until no pair of variables with a high correlation coefficient (greater than the threshold) remained. A threshold value of 0.6 was used for all models.
			Transfer data for projection		· Details on data sources: e.g., URL/DOI, accession date, database version
					· Spatial extent · Spatial resolution · temporal extent/time period · temporal resolution
					· Models and scenarios used
					· Details on data processing and scaling (see above): N/A
					· Quantification of novel environmental conditions and novel environmental combinations: e.g., distance to training data
	Model		Variable pre-selection		· Details on pre-selection of variables, if applicable: A comprehensive suite of 75 environmental predictors, 148 hydrological predictors, and 16 biological predictors were used in the model workflow.
			Multicollinearity		· Methods for identifying and dealing with multicollinearity (Dormann, et al. 2013) or justification if multicollinearity is not explicitly dealt with: A Pearson correlation test was run to assess collinearity among environmental variables. Using the vifcor function in the usdm package (Naimi, 2023), the variance inflation factor (VIF) was calculated for the selected variables, excluding highly correlated variables. vifcor first finds a pair of variables which has the maximum linear correlation (greater than the threshold; th) and excludes the one with a greater VIF (Naimi, 2023). The procedure was repeated until no pair of variables with a high correlation coefficient (greater than the threshold) remained. A threshold value of 0.6 was used for all models.

			Model settings	· Models settings for all selected algorithms (including default settings of specific platforms/packages, weighting of data etc.): Using the bart function in the embarcardero package in R (Carlson, 2020), an initial model was fitted for each species using 50 iterations. Next, the varimp.diag function was used to evaluate which environmental and biological variables have the strongest influence on the species' occurrence patterns. This was followed by repeating the model fitting process using the variable.step function, which applies a stepwise variable selection procedure to identify the most important environmental and biological variables that contribute significantly to predicting species occurrence. The variable.step function employs a stepwise selection algorithm, which iteratively adds or removes variables, based on their importance to model performance. This protocol was followed to select the model with the most informative predictors and the lowest average model root mean square error (RMSE). Finally, a new BART model was fitted using only the most important variables identified in the stepwise selection process. This final BART model was fitted using 200 iterations.
				· Details on relevant model settings for extrapolation beyond sample range, if applicable: e.g., clamping
			Model estimates	· Assessment of model coefficients: Covariate importance calculated as averaged model drop contributions (explained deviance loss when variable dropped)
				· Details on quantification of uncertainty in model coefficients, e.g. resampling
				· Assessment of variable importance
			Model selection / Model averaging / Ensembles	· Model selection strategy: e.g. information-theoretic approach for variable selection, shrinkage and regularization: N/A
				· Method for model averaging: e.g. derivation of weights: N/A
				· Ensemble method: N/A
			Non-independence correction/analyses	· Method for addressing spatial autocorrelation in residuals: Potential non-independence in the data was not accounted for in the models
				· Method for addressing temporal autocorrelation in residuals: N/A

			· Method to account for nested data: e.g., fixed and random effects: N/A
		Threshold selection	· Details on threshold selection, if applicable: transforming continuous predictions into binary predictions
	Assessment	Performance statistics	· Performance statistics estimated on training data: N/A
			· Performance statistics estimated on validation data (from data partitioning): Area under curve (AUC) of the receiver operating characteristic (ROC). Model performance was assessed based on the average true skill statistic (TSS) from **50 bootstrap runs,** calculated based on a TSS-maximisation threshold.
			· Performance statistics estimated on test (truly independent) data, if applicable: N/A
		Plausibility check	· Response plots, e.g. partial response plots, evaluation strips, inflated response plots: Partial dependence plots
			· Expert judgements, e.g. map display: Maps were checked with previous modelled distributions for each species. Additionally, maps were compared to the current known distribution of the species and sent to relevant experts for approval/comment.
	Prediction	Prediction output	· Prediction unit: Predictions of probability of presence expressed on a continuous scale.
			· Post-processing, e.g. clipping, reprojection: The model was limited to interpolation within catchments where the species is kown to occur (i.e. no prediction or projection was allowed in new habitat). Model outputs were reprojected in ARC GIS Pro.
		Uncertainty quantification	· Algorithmic uncertainty, if applicable: N/A
			· Uncertainty in input data, if applicable: N/A
			· Effect of parameter uncertainty, error propagation, if applicable; N/A
			· Uncertainty in scenarios (e.g. climate models, land use models, storylines)
			· Visualisation/treatment of novel environments: e.g., masking

Table S4.2. List of environmental predictor variables used in SDM workflow.

Layer name	Relevance	Description
BIOCLIM_01.tif	high	Annual Mean Temperature
BIOCLIM_02.tif	high	Mean Diurnal Range (Mean of monthly (max temp - min temp))
BIOCLIM_03.tif	low	Isothermality (BIO2/BIO7) (* 100)
BIOCLIM_04.tif	high	Temperature Seasonality (standard deviation *100)
BIOCLIM_05.tif	high	Max Temperature of Warmest Month
BIOCLIM_06.tif	high	Min Temperature of Coldest Month
BIOCLIM_07.tif	low	Temperature Annual Range (BIO5-BIO6)
BIOCLIM_08.tif	low	Mean Temperature of Wettest Quarter
BIOCLIM_09.tif	low	Mean Temperature of Driest Quarter
BIOCLIM_10.tif	low	Mean Temperature of Warmest Quarter
BIOCLIM_11.tif	low	Mean Temperature of Coldest Quarter
BIOCLIM_12.tif	low	Annual Precipitation
BIOCLIM_13.tif	low	Precipitation of Wettest Month
BIOCLIM_14.tif	low	Precipitation of Driest Month
BIOCLIM_15.tif	high	Precipitation Seasonality (Coefficient of Variation)
BIOCLIM_16.tif	low	Precipitation of Wettest Quarter
BIOCLIM_17.tif	low	Precipitation of Driest Quarter
BIOCLIM_18.tif	low	Precipitation of Warmest Quarter
BIOCLIM_19.tif	low	Precipitation of Coldest Quarter
ENVIREM_annualPET.tif	high	annual potential evapotranspiration: a measure of the ability of the atmosphere to remove water through evapotranspiration processes, given unlimited moisture
ENVIREM_arideityindex.tif	low	Thornthwaite aridity index: Index of the degree of water deficit below water need
ENVIREM_climaticmoisture index.tif	high	a metric of relative wetness and aridity
ENVIREM_continentality.tif	high	average temp. of warmest month - average temp. of coldest month
ENVIREM_embergerQ.tif	low	Emberger's pluviothermic quotient: a metric that was designed to differentiate among Mediterranean type climates
ENVIREM_growingdegday s0.tif	low	sum of mean monthly temperature for months with mean temperature greater than 0? multiplied by number of days
ENVIREM_growingdegday s5.tif	low	sum of mean monthly temperature for months with mean temperature greater than 5? multiplied by number of days
ENVIREM_maxtempcoldes t.tif	low	max. temp. of the coldest month

ENVIREM_mintempwarmest.tif	low	min. temp. of the warmest month
ENVIREM_monthcountbytemp.tif	low	count of the number of months with mean temp greater than 10?
ENVIREM_PETcoldestquarter.tif	high	mean monthly PET of coldest quarter
ENVIREM_PETdriestquarter.tif	high	mean monthly PET of driest quarter
ENVIREM_PETseasonality.tif	high	monthly variability in potential evapotranspiration
ENVIREM_PETwarmestquarter.tif	high	mean monthly PET of warmest quarter
ENVIREM_PETwettestquarter.tif	high	mean monthly PET of wettest quarter
ENVIREM_thermicityindex.tif	low	compensated thermicity index: sum of mean annual temp., min. temp. of coldest month, max. temp. of the coldest month, x 10, with compensations for better comparability across the globe
LC_Built_up.tif	high	
LC_Cropland.tif	high	
LC_Natural.tif	high	
LC_Secondary_natural.tif	high	
NDVI_mean.tif	high	
BDRICM_Clipped.tif	low	Depth to bedrock (R horizon) up to 200 cm
BLDFIE_Clipped.tif	low	Bulk density (fine earth) in kg / cubic-meter
CLYPPT_Clipped.tif	high	Clay content (0-2 micro meter) mass fraction in %
CRFVOL_Clipped.tif	high	Coarse fragments volumetric in %
ORCDRC_Clipped.tif	high	Soil organic carbon content (fine earth fraction) in g per kg
PHIHOX_Clipped.tif	low	Soil pH x 10 in H2O
SLTPPT_Clipped.tif	high	Silt content (2-50 micro meter) mass fraction in %
SNDPPT_Clipped.tif	high	Sand content (50-2000 micro meter) mass fraction in %
Aspect_East.tif	high	
Aspect_North.tif	high	
Elevation.tif	high	
Slope.tif	high	In degrees?
TPI.tif	high	Difference between elevation of focal cell and the mean of it's 8 surrounding cells. Positive and negative values correspond to ridges and valleys respectively, while zero value correspond to flat

TRI.tif	high	Quantifies total elevation change of 3 by 3 cell (flat areas have zero where mountainous areas with steep ridges have positive values).
TWI.tif	high	High values indicate areas with high potential runoff (such as water courses and rivers).
vm_Albany_Thicket.tif	high	
vm_Azonal_Vegetation.tif	high	
vm_Desert.tif	high	
vm_Forests.tif	high	
vm_Fynbos_montane.tif	high	
vm_Fynbos_plain.tif	high	
vm_Grassland.tif	high	
vm_Indian_Ocean_Coastal_Belt.tif	high	
vm_Nama.Karoo.tif	high	
vm_Savanna.tif	high	
vm_Sub.Escarpment_Grassland.tif	high	
vm_Sub.Escarpment_Savanna.tif	high	
vm_Succulent_Karoo.tif	high	
frag_clumpy.tif	high	CLUMPY is an 'Aggregation metric'. It equals the proportional deviation of the proportion of like adjacencies involving the corresponding class from that expected under a spatially random distribution. Equals -1 for maximally disaggregated, 0 for randomly distributed and 1 for maximally aggregated classes.
frag_cai_mn.tif	high	CAI_MN is a 'Core area metric'. The mean core area index is the mean percentage of core area in relation to patch area. A cell is defined as core area if the cell has no neighbour with a different value than itself. CAI_MN = 0 when all patches have no core area and approaches CAI_MN = 100 with increasing percentage of core area within patches.
frag_shape_mn.tif	high	SHAPE_MN is a 'Shape metric'. SHAPE describes the ratio between the actual perimeter of the patch and the hypothetical minimum perimeter of the patch. The minimum perimeter equals the perimeter if the patch would be maximally compact. Equals SHAPE_MN = 0 if all patches are squares. Increases, without limit, as the shapes of patches become more complex.
frag_pd.tif	high	Number of patches per 100 hectares. Increases as the landscape gets more patchy. Reaches its maximum if every cell is a different patch.
frag_area_mn.tif	high	Mean Patch Area. Approaches AREA_MN = 0 if all patches are small. Increases, without limit, as the patch areas increase.
wetlands_natural.tif	high	
wetlands_all.tif	high	

Supplementary S4.3. R code used to calculate hydrological metrics for South Africa.

```
##_____________________________________________________________________________

## Title: SA flow data conversion
## Purpose: Convert the modelled flow data from the ACRU model from mm/day to m3/second. (Advice from Nick RIvers-Moore)
## Author: Mohammed Kajee & Dominic Henry
## Date: 14/11/2020

## Explantion: To convert flow data from mm/day to m3/second, the following calculation was used:
## (flow value x 1000 x cumulative drainage area)/86400

##_____________________________________________________________________________

#Libraries
library(tidyverse)
library(lubridate)
library(janitor)
library(stringr)
library(glue)
library(renv)

##_____________________________________________________________________________

# Add renv workflow - stores package versions.
# renv::init() - run this once project code is ready for first commit
# renv::snapshot() - run when new packages are installed (to update renv.lock file)

renv::init()

##_____________________________________________________________________________

################################### START ###################################

# Import layare.csv - File containing the quinary layare numbers and the cummulative drainage area.
cum_area <- read.csv("input data/ACRU_flows_hist/layare.csv",header=T,sep=",") %>%
  janitor::clean_names() %>%
  mutate(subc = sprintf("%04d", subc)) #Adds leading zeros to the first 999 quinaries - needed to match quinary name to quinary csv file.


# Create file list for all quinary csv files
file_list <- dir("input data/ACRU_flows_hist/",
                 full.names = TRUE,
                 pattern = ".csv")

x <- file_list[2:3] #this needs to start at 2 because the first file is the quinary area file
```

```
# Function to convert ACRU flow data
flow_conversion <- function (x){

  station <- (x)  # Takes the csv file name for each quinary and keeps only the quinary number. Quinary number = 'station'
  station <-word(station, 2, sep = "obs_") # Use the pipe operator to avoid having to keep writing new objects. Pipe was not working here. So went old school.
  station <-str_replace(station, "s", "")
  station <-str_replace(station, ".csv", "")

  area <- cum_area %>%
    filter(subc == station) # Matches the quinary number to the file name.

  flow_calc <- read_csv(x) %>%  # Reads in the csv file for specific quinary.
    janitor::clean_names() %>%
    rename_if(str_detect(names(.),"dd.mm.yyyy"), ~ "date") %>%
    mutate(date = parse_date_time(date, c("Ymd","dmY"))) %>%  # sets the date format
    mutate(date = ymd(date)) %>%  # Adds new formatted date to the csv
    dplyr::select(date, celrun) %>% # keeps only the date and the flow data
    filter(date > "1952-09-30") %>% #Removes first two years of data - ACRU model does not calculate the first two years
    mutate(station)%>% # Adds quinary station number
    mutate(area$conare_km2) %>% #Adds collumn for cumulative area - extracted from cum_area
    mutate(flow = (celrun*1000*area$conare_km2)/86400) %>% # formula to convert flow data to m3/second
    as.data.frame()

}

# Runs function on all files listed in X
converted_flow <- map_dfr(x,
                  flow_conversion)

# Creates list of quinary numbers
station_names <- unique(converted_flow$station)

# Function writes the converted flow values to individual csv files for each quinary.
write_file <- function(x){

  new_files %>%
    filter(station == x) %>%
    write_csv(glue("input data/new_flow_data/{x}.csv")) # You'll need to customise the path and actual file name prefix

}

# Runs function on all files listed in station_names
walk(station_names,
     write_file)

## End ##
## Script working - 19/01/2021
```

```
##_____________________________________________________________________

## Title: SA flow data conversion
## Purpose: Convert the modelled flow data from the ACRU model from mm/day to m3/second. (Advice from Nick RIvers-Moore)
## Author: Mohammed Kajee & Dominic Henry
## Date: 14/11/2020

## Explantion: To convert flow data from mm/day to m3/second, the following calculation was used:
## (flow value x 1000 x cumulative drainage area)/86400

##_____________________________________________________________________

#Libraries

# #Make sure RTools is installed
# # Follow install instructions found here: https://cran.r-project.org/bin/windows/Rtools/
# #Once Rtools is installed, you need to put the location of the Rtools make utilities (bash, make, etc) on the PATH
# #To do this, use the code below:
# writeLines('PATH="${RTOOLS40_HOME}\\usr\\bin;${PATH}"', con = "~/.Renviron")
# install.packages("installr")
# library("installr")
# install.Rtools()
#
# #Then install devtools
# install.packages("devtools")
# library(devtools)
#
# ####### Installing EflowStats ######
#
# #Option 1 to install EflowStats
# install.packages("remotes")
# remotes::install_github("USGS-R/EflowStats")

#This worked for me

# library(dataRetrieval) # Why do we need this?
library(EflowStats)
library(tidyverse)
library(lubridate) # dmy() wont work unless this is loaded
library(janitor)
library (dplyr)

##_____________________________________________________________________

# Add renv workflow - stores package versions.
# renv::init() - run this once project code is ready for first commit
```

```
# renv::snapshot() - run when new packages are installed (to update renv.lock file)

renv::init()

##_____________________________________________________________________________

################################### START ###################################

# Creates a list of files in the new_flow_data folder. Each file represents one quinary.
quart_list <- dir("input data/new_flow_data/",
                  full.names = TRUE,
                  pattern = ".csv")

# 1 station = 1 quinary
#x <- quart_list[215] # Use only if you want to run on a subset of the quinaries

start <- Sys.time()

quinary_metrics <- function (x){ # Fucntion to calculate hydrological metrics for each quinary

  df <- read_csv(x) %>%  # Creates dataframe for each quinary and formats data to run in eflowstats.
    janitor::clean_names() %>%
    rename_if(str_detect(names(.),"dd_mm_yyyy"), ~ "date") %>%
    rename_if(str_detect(names(.),"flow"), ~ "flow_cumecs") %>%
    #mutate(date = parse_date_time(date, c("Ymd","dmY"))) %>% # Remedy for inconsitent date formats. Do not use. Now part of Step 00.
    #mutate(date = ymd(date)) %>%
    select(date, flow_cumecs, station) %>%
    #mutate(quart = str_match(x, "Flows\\/(.*?).csv")[,2]) %>% # actually quart
    filter(date > "1954-12-31") %>%  #must start at 1955 because some stations have the same value for the first few years. First data value is 01 Jan because we use calendar years and not
water years.
    #filter(date < "1999-01-01" ) %>%
    as.data.frame()


  df[which(is.na(df$flow_cumecs)),] # Finds NA values and replaces it with the mean.

  if (length(which(is.na(df$flow_cumecs))) > 0) {

    mean_flow <- mean(df$flow_cumecs, na.rm = TRUE)
    df[which(is.na(df$flow_cumecs)),"flow_cumecs"] <- mean_flow

  }

  uni_station <- unique(df$station)

  # y <- uni_station[1]
```

```
  calc_metrics <- function(y){ # calculates hydrology metrics using eflowstats

    station_data <- df %>%
      filter(station == y)

    #data validation step required to use calc_allHITOUT
    data_validated <-  validate_data(station_data[c("date","flow_cumecs")],yearType="calendar")

    #Actual hyrdology metrics calcuation.
    calc_allHITOut <- calc_allHIT(data_validated,
                                  yearType = "calendar", # Year types is calendar. Data must run from 01 Jan to 31 Dec. When using 'water years', function returns an error.
                                  stats= c("calc_magAverage",
                                           "calc_magLow",
                                           "calc_magHigh",
                                           "calc_frequencyLow",
                                           "calc_frequencyHigh",
                                           "calc_durationLow",
                                           "calc_durationHigh",
                                           "calc_timingAverage",
                                           "calc_timingLow",
                                           "calc_timingHigh"),  #When using "All", function returns an error for some stations. We dont know why. Error dissapears when we remove the calc_rateChange.
                                           # the calc_rateChange - removed because it causes an error. We lose 9 metrics.
                                  pref = "mean",
                                  drainArea=0, # Drainage area is set to 0, since the drainage are is included in our flow values.
                                  floodThreshold=NULL
                                  ) %>%
      mutate(station = y)


    # Error in na_locf(x, option, na.remaining, maxgap) :
    # Input data has only NAs. Input data needs at least 1 non-NA data point for applying na_locf

  }

# Runs function for all quinaries in each file
  metrics_df <- map_dfr(uni_station,
                        calc_metrics)
}

# Runs function on all files in the file list
metrics_all <- map(quart_list,
             safely(quinary_metrics))

warnings()

#Checks for erros
err_check <- transpose(metrics_all)[["error"]] %>%
```

```
  map(is.null) %>%
  unlist

err_stations <- quart_list[which(err_check == "FALSE")] #this doesnt return the correct file if not run from the first file in the folder.
err_stations

clean_metrics <- transpose(metrics_all)[["result"]] %>%
  discard(is.null) %>%
  as.data.frame() %>%
  map_dfr(rbind)


help(rbind)

clean_metrics %>%
  group_by(station) %>%
  tally() %>%
  print(n="all")

clean_metrics %>%
  as.data.frame()

clean_metrics %>%
  write_csv("output data/hydro_metrics.csv")

end <- Sys.time()

print(glue("SUCCESSFULLY COMPLETED - RUNTIME: {round(end-start,2)} {attr(end-start, 'units')}"))
system('CMD /C "ECHO GREAT SUCCESS. I LIKE. THE MODEL HAS FINISHED RUNNING! && PAUSE"',
       invisible=FALSE, wait=FALSE)

################################### END ###################################

# #Check for errors in individual datasheets
#
#checkdf <- read_csv("input data/Simulated Daily Flows/J35.csv", skip = 1)
#
# checkdf %>%
#   group_by(Station) %>%
#   tally() %>%
#   print(n = "all")
#
# checkdf %>%
#   filter(is.na(Flow))
#
# ############################## Troubleshooting ############################
# #Make sure ONLY Error file has been run through first code
```

```
#
test <- read_csv("input data/new_flow_data/0215.csv")  %>%
    janitor::clean_names() %>%
    rename_if(str_detect(names(.),"dd_mm_yyyy"), ~ "date") %>%
    rename_if(str_detect(names(.),"flow"), ~ "flow_cumecs") %>%
    #mutate(date = dmy(date)) %>%
    select (date, flow_cumecs, station) %>%
    #mutate(quart = str_match(x, "Flows\\/(.*?).csv")[,2]) %>% # actually quart
    filter(date > "1953-12-31" ) %>%
    filter(date < "1999-01-01" ) %>%
    as.data.frame
#
#
 Quinarytest <- subset(test, station=="0215", select=-station)
#
 data_validated <-  validate_data(Quinarytest[c("date","flow_cumecs")],yearType="calendar")
#
 calc_allHITOut <- calc_allHIT(data_validated,
                               yearType = "calendar",
                              stats= c("calc_magAverage",
                                    "calc_magLow",
                                    "calc_magHigh",
                                    "calc_frequencyLow",
                                    "calc_frequencyHigh",
                                    "calc_durationLow",
                                    "calc_durationHigh",
                                    "calc_timingAverage",
                                    "calc_timingLow",
                                    "calc_timingHigh") ,
                                 pref = "mean",
                                 drainArea=0,
                                 floodThreshold=NULL)
```

Table S4.4. List of hydrological predictor variables used in SDM workflow.

Layer	Description
dh1.tif	Annual maximum daily flow. Compute the maximum of a 1-day moving average flow for each year. DH1 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dh10.tif	Variability of annual maximum of 90-day moving average flows. Compute the standard deviation for the maximum 90-day moving averages. DH10 is 100 times the standard deviation divided by the mean (percent – spatial).
dh11.tif	Annual maximum of 1-day moving average flows divided by the median for the entire record. Compute the maximum of a 1-day moving average flow for each year. DL11 is the mean of these values divided by the median for the entire record (dimensionless – temporal).
dh12.tif	Annual maximum of 7-day moving average flows divided by the median for the entire record. Compute the maximum daily average flow for each year. DL12 is the mean of these values divided by the median for the entire record (dimensionless – temporal).
dh13.tif	Annual maximum of 30-day moving average flows divided by the median for the entire record. Compute the maximum of a 30-day moving average flow for each year. DL13 is the mean of these values divided by the median for the entire record (dimensionless – temporal).
dh14.tif	Flood duration. Compute the mean of the mean monthly flow values. Find the 95th percentile for the mean monthly flows. DH14 is the 95th percentile value divided by the mean of the monthly means (dimensionless – spatial).
dh15.tif	High flow pulse duration. Compute the average duration for flow events with flows above a threshold equal to the 75th percentile value for each year in the flow record. DH15 is the median of the yearly average durations (days/year – temporal).
dh16.tif	Variability in high flow pulse duration. Compute the standard deviation for the yearly average high pulse durations. DH16 is 100 times the standard deviation divided by the mean of the yearly average high pulse durations (percent – spatial).
dh17.tif	High flow duration. Compute the average duration of flow events with flows above a threshold equal to the median flow value for the entire flow record. DH17 is the average (or median - Use Preference option) duration of the events (days – temporal).
dh18.tif	High flow duration. Compute the average duration of flow events with flows above a threshold equal to three times the median flow value for the entire flow record. DH18 is the average (or median - Use Preference option) duration of the events (days – temporal).
dh19.tif	High flow duration. Compute the average duration of flow events with flows above a threshold equal to seven times the median flow value for the entire flow record. DH19 is the average (or median - Use Preference option) duration of the events (days – temporal).
dh2.tif	Annual maximum of 3-day moving average flows. Compute the maximum of a 3day moving average flow for each year. DH2 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dh20.tif	High flow duration. Compute the 75th percentile value for the entire flow record. Compute the average duration of flow events with flows above a threshold equal to the 75th percentile value for the median annual flows. DH20 is the average (or median - Use Preference option) duration of the events (days – temporal).
dh21.tif	High flow duration. Compute the 25th percentile value for the entire flow record. Compute the average duration of flow events with flows above a threshold equal to the 25th percentile value for the entire set of flows. DH21 is the average (or median - Use Preference option) duration of the events (days – temporal).
dh3.tif	Annual maximum of 7-day moving average flows. Compute the maximum of a 7day moving average flow for each year. DH3 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dh4.tif	Annual maximum of 30-day moving average flows. Compute the maximum of 30day moving average flows. Compute the maximum of a 30-day moving average flow for each year. DH4 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dh5.tif	Annual maximum of 90-day moving average flows. Compute the maximum of a 90day moving average flow for each year. DH5 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dh6.tif	Variability of annual maximum daily flows. Compute the standard deviation for the maximum 1-day moving averages. DH6 is 100 times the standard deviation divided by the mean (percent – spatial).

dh7.tif	Variability of annual maximum of 3-day moving average flows. Compute the standard deviation for the maximum 3-day moving averages. DH7 is 100 times the standard deviation divided by the mean (percent – spatial).
dh8.tif	Variability of annual maximum of 7-day moving average flows. Compute the standard deviation for the maximum 7-day moving averages. DH8 is 100 times the standard deviation divided by the mean (percent – spatial).
dh9.tif	Variability of annual maximum of 30-day moving average flows. Compute the standard deviation for the maximum 30-day moving averages. DH9 is 100 times the standard deviation divided by the mean (percent – spatial).
dl1.tif	Annual minimum daily flow. Compute the minimum 1-day average flow for each year. DL1 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dl10.tif	Variability of annual minimum of 90-day moving average flow. Compute the standard deviation for the minimum 90-day moving averages. DL10 is 100 times the standard deviation divided by the mean (percent - spatial).
dl11.tif	Annual minimum daily flow divided by the median for the entire record. Compute the minimum daily flow for each year. DL11 is the mean of these values divided by the median for the entire record (dimensionless – temporal).
dl12.tif	Annual minimum of 7-day moving average flow divided by the median for the entire record. Compute the minimum of a 7-day moving average flow for each year. DL12 is the mean of these values divided by the median for the entire record (dimensionless – temporal).
dl13.tif	Annual minimum of 30-day moving average flow divided by the median for the entire record. Compute the minimum of a 30-day moving average flow for each year. DL13 is the mean of these values divided by the median for the entire record (dimensionless – temporal).
dl14.tif	Low exceedence flows. Compute the 75 percent exceedence value for the entire flow record. DL14 is the exceedence value divided by the median for the entire record (dimensionless – spatial).
dl15.tif	Low exceedence flows. Compute the 90 percent exceedence value for the entire flow record. DL14 is the exceedence value divided by the median for the entire record (dimensionless – spatial).
dl16.tif	Low flow pulse duration. Compute the average pulse duration for each year for flow events below a threshold equal to the 25th percentile value for the entire flow record. DL16 is the median of the yearly average durations (number of days – temporal).
dl18.tif	Number of zero-flow days. Count the number of zero-flow days for the entire flow record. DL18 is the mean (or median - Use Preference option) annual number of zero flow days (number of days/year – temporal). DO NOT USE. ALL VALUES ARE 0.
dl2.tif	Annual minimum of 3-day moving average flow. Compute the minimum of a 3-day moving average flow for each year. DL2 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dl20.tif	Number of zero-flow months. While computing the mean monthly flow values, count the number of months in which there was no flow over the entire flow record (percent – spatial). DO NOT USE. ALL VALUES ARE 0.
dl3.tif	Annual minimum of 7-day moving average flow. Compute the minimum of a 7-day moving average flow for each year. DL3 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dl4.tif	Annual minimum of 30-day moving average flow. Compute the minimum of a 30day moving average flow for each year. DL4 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dl5.tif	Annual minimum of 90-day moving average flow. Compute the minimum of a 90day moving average flow for each year. DL5 is the mean (or median - Use Preference option) of these values (cubic feet per second – temporal).
dl6.tif	Variability of annual minimum daily average flow. Compute the standard deviation for the minimum daily average flow. DL6 is 100 times the standard deviation divided by the mean (percent – spatial).
dl7.tif	Variability of annual minimum of 3-day moving average flow. Compute the standard deviation for the minimum 3-day moving averages. DL7 is 100 times the standard deviation divided by the mean (percent - spatial).
dl8.tif	Variability of annual minimum of 7-day moving average flow. Compute the standard deviation for the minimum 7-day moving averages. DL8 is 100 times the standard deviation divided by the mean (percent - spatial).
dl9.tif	Variability of annual minimum of 30-day moving average flow. Compute the standard deviation for the minimum 30-day moving averages. DL9 is 100 times the standard deviation divided by the mean (percent - spatial).

fh1.tif	High flood pulse count. Compute the average number of flow events with flows above a threshold equal to the 75th percentile value for the entire flow record. FH1 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
fh10.tif	Flood frequency. Compute the average number of flow events with flows above a threshold equal to median of the annual minima for the entire flow record. FH10 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
fh2.tif	Variability in high pulse count. Compute the standard deviation in the annual pulse counts for FH1. FH2 is 100 times the standard deviation divided by the mean pulse count (number of events/year – spatial).
fh3.tif	High flood pulse count. Compute the average number of days per year that the flow is above a threshold equal to three times the median flow for the entire record. FH3 is the mean (or median – Use Preference option) of the annual number of days for all years (number of days/year – temporal).
fh4.tif	High flood pulse count. Compute the average number of days per year that the flow is above a threshold equal to seven times the median flow for the entire record. FH4 is the mean (or median - Use Preference option) of the annual number of days for all years (number of days/year – temporal).
fh5.tif	Flood frequency. Compute the average number of flow events with flows above a threshold equal to the median flow value for the entire flow record. FH5 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
fh6.tif	Flood frequency. Compute the average number of flow events with flows above a threshold equal to three times the median flow value for the entire flow record. FH6 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
fh7.tif	Flood frequency. Compute the average number of flow events with flows above a threshold equal to seven times the median flow value for the entire flow record. FH6 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
fh8.tif	Flood frequency. Compute the average number of flow events with flows above a threshold equal to 25 percent exceedence value for the entire flow record. FH8 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
fh9.tif	Flood frequency. Compute the average number of flow events with flows above a threshold equal to 75 percent exceedence value for the entire flow record. FH9 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
fl1.tif	Low flood pulse count. Compute the average number of flow events with flows below a threshold equal to the 25th percentile value for the entire flow record. FL1 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
fl3.tif	Frequency of low pulse spells. Compute the average number of flow events with flows below a threshold equal to 5 percent of the mean flow value for the entire flow record. FL3 is the average (or median - Use Preference option) number of events (number of events/year – temporal).
ma1.tif	Mean of the daily mean flow values for the entire flow record (cubic feet per second – temporal).
ma10.tif	Spread in daily flows is computed like MA9 except using the 20th and 80th percentiles (dimensionless – spatial).
ma11.tif	Spread in daily flows is computed like MA9 except using the 25th and 75th percentiles (dimensionless – spatial).
ma12.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma13.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma14.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma15.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma16.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma17.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma18.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).

ma19.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma2.tif	Median of the daily mean flow values for the entire flow record (cubic feet per second – temporal).
ma20.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma21.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma22.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma23.tif	Means (or medians - Use Preference option) of monthly flow values. Compute the means for each month over the entire flow record. For example, MA12 is the mean of all January flow values over the entire record (cubic feet per second – temporal).
ma24.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma25.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma26.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma27.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma28.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma29.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma3.tif	Mean (or median - Use Preference option) of the coefficients of variation (standard deviation/mean) for each year. Compute the coefficient of variation for each year of daily flows. Compute the mean of the annual coefficients of variation (percent - temporal).
ma30.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma31.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma32.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).

ma33.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma34.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma35.tif	Variability (coefficient of variation) of monthly flow values. Compute the standard deviation for each month in each year over the entire flow record. Divide the standard deviation by the mean for each month. Average (or median - Use Preference option) these values for each month across all years (percent – temporal).
ma36.tif	Variability across monthly flows. Compute the minimum, maximum, and mean flows for each month in the entire flow record. MA36 is the maximum monthly flow minus the minimum monthly flow divided by the median monthly flow (dimensionless – spatial).
ma37.tif	Variability across monthly flows. Compute the first (25th percentile) and the third (75th percentile) quartiles (every month in the flow record). MA37 is the third quartile minus the first quartile divided by the median of the monthly means (dimensionless – spatial).
ma38.tif	Variability across monthly flows. Compute the 10th and 90th percentiles for the monthly means (every month in the flow record). MA38 is the 90th percentile minus the 10thpercentile divided by the median of the monthly means (dimensionless – spatial).
ma39.tif	Variability across monthly flows. Compute the standard deviation for the monthly means. MA39 is the standard deviation times 100 divided by the mean of the monthlymeans (percent – spatial).
ma4.tif	Standard deviation of the percentiles of the logs of the entire flow record divided by the mean of percentiles of the logs. Compute the log10 of the daily flows for the entire record. Compute the 5th, 10th, 15th, 20th, 25th, 30th, 35th, 40th, 45th, 50th, 55th, 60th, 65th, 70th, 75th, 80th, 85th, 90th, and 95th percentiles for the logs of the entire flow record. Percentiles are computed by interpolating between the ordered (ascending) logs of the flow values. Compute the standard deviation and mean for the percentile values. Divide the standard deviation by the mean (percent - spatial).
ma40.tif	Skewness in the monthly flows. MA40 is the mean of the monthly flow means minus the median of the monthly means divided by the median of the monthly means (dimensionless – spatial).
ma42.tif	Variability across annual flows. MA42 is the maximum annual flow minus the minimum annual flow divided by the median annual flow (dimensionless – spatial).
ma43.tif	Variability across annual flows. Compute the first (25th percentile) and third (75th percentile) quartiles and the 10th and 90th percentiles for the annual means (every year in the flow record). MA43 is the third quartile minus the first quartile divided by the median of the annual means (dimensionless –spatial).
ma44.tif	Variability across annual flows. Compute the first (25th percentile) and third (75th percentile) quartiles and the 10th and 90th percentiles for the annual means (every year in the flow record). MA44 is the 90th percentile minus the 10th percentile divided by the median of the annual means (dimensionless – spatial).
ma45.tif	Skewness in the annual flows. MA45 is the mean of the annual flow means minus the median of the annual means divided by the median of the annual means (dimensionless – spatial).
ma5.tif	The skewness of the entire flow record is computed as the mean for the entire flow record (MA1) divided by the median (MA2) for the entire flow record (dimensionless - spatial).
ma6.tif	Range in daily flows is the ratio of the 10 percent to 90 percent exceedence values for the entire flow record. Compute the 5 percent to 95 percent exceedence values for the entire flow record. Exceedence is computed by interpolating between the ordered (descending) flow values. Divide the 10 percent exceedence value by the 90 percent value (dimensionless – spatial).
ma7.tif	Range in daily flows is computed like MA6 except using the 20 percent and 80 percent exceedence values. Divide the 20 percent exceedence value by the 80 percent value (dimensionless - spatial).
ma8.tif	Range in daily flows is computed like MA6 except using the 25 percent and 75 percent exceedence values. Divide the 25 percent exceedence value by the 75 percent value (dimensionless – spatial).

ma9.tif	Spread in daily flows is the ratio of the difference between the 90th and 10th percentile of the logs of the flow data to the log of the median of the entire flow record. Compute the log10 of the daily flows for the entire record. Compute the 5th, 10th, 15th, 20th, 25th, 30th, 35th, 40th, 45th, 50th, 55th, 60th, 65th, 70th, 75th, 80th, 85th, 90th, and 95th percentiles for the logs of the entire flow record. Percentiles are computed by interpolating between the ordered (ascending) logs of the flow values. Compute MA9 as (90th – 10th) /log10(MA2) (dimensionless – spatial).
mh1.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh10.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh11.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh12.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh13.tif	Variability (coefficient of variation) across maximum monthly flow values. Compute the mean and standard deviation for the maximum monthly flows over the entire flow record. MH13 is the standard deviation times 100 divided by the mean maximum monthly flow for all years (percent – spatial).
mh14.tif	Median of annual maximum flows. Compute the annual maximum flows from monthly maximum flows. Compute the ratio of annual maximum flow to median annual flow for each year. MH14 is the median of these ratios (dimensionless – temporal).
mh15.tif	High flow discharge index. Compute the 1 percent exceedence value for the entire data record. MH15 is the 1 percent exceedence value divided by the median flow for the entire record (dimensionless – spatial).
mh16.tif	High flow discharge index. Compute the 10 percent exceedence value for the entire data record. MH16 is the 10 percent exceedence value divided by the median flow for the entire record (dimensionless – spatial).
mh17.tif	High flow discharge index. Compute the 25 percent exceedence value for the entire data record. MH17 is the 25 percent exceedence value divided by the median flow for the entire record (dimensionless – spatial).
mh18.tif	Variability across annual maximum flows. Compute the logs (log10) of the maximum annual flows. Find the standard deviation and mean for these values. MH18 is the standard deviation times 100 divided by the mean (percent – spatial).
mh19.tif	Skewness in annual maximum flows.
mh2.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh21.tif	High flow volume index. Compute the average volume for flow events above a threshold equal to the median flow for the entire record. MH21 is the average volume divided by the median flow for the entire record (days – temporal).
mh22.tif	High flow volume. Compute the average volume for flow events above a threshold equal to three times the median flow for the entire record. MH22 is the average volume divided by the median flow for the entire record (days - temporal).
mh23.tif	High flow volume. Compute the average volume for flow events above a threshold equal to seven times the median flow for the entire record. MH23 is the average volume divided by the median flow for the entire record (days - temporal).
mh24.tif	High peak flow. Compute the average peak flow value for flow events above a threshold equal to the median flow for the entire record. MH24 is the average peak flow divided by the median flow for the entire record (dimensionless – temporal).
mh25.tif	High peak flow. Compute the average peak-flow value for flow events above a threshold equal to three times the median flow for the entire record. MH25 is the average peak flow divided by the median flow for the entire record (dimensionless – temporal).
mh26.tif	High peak flow. Compute the average peak flow value for flow events above a threshold equal to seven times the median flow for the entire record. MH26 is the average peak flow divided by the median flow for the entire record (dimensionless – temporal).
mh27.tif	High peak flow. Compute the average peak flow value for flow events above a threshold equal to 75th percentile value for the entire flow record. MH27 is the average peak flow divided by the median flow for the entire record (dimensionless – temporal).

mh3.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh4.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh5.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh6.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh7.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh8.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
mh9.tif	Mean (or median - Use Preference option) maximum flows for each month across all years. Compute the maximums for each month over the entire flow record. For example, MH1 is the mean of the maximums of all January flow values over the entire record (cubic feet per second – temporal).
ml1.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml10.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml11.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml12.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml13.tif	Variability (coefficient of variation) across minimum monthly flow values. Compute the mean and standard deviation for the minimum monthly flows over the entire flow record. ML13 is the standard deviation times 100 divided by the mean minimum monthly flow for all years (percent – spatial).
ml14.tif	Compute the minimum annual flow for each year. ML14 is the mean of the ratios of minimum annual flows to the median flow for each year (dimensionless – temporal).
ml15.tif	Low flow index. ML15 is the mean of the ratios of minimum annual flows to the mean flow for each year (dimensionless – temporal).
ml16.tif	Median of annual minimum flows. ML16 is the median of the ratios of minimum annual flows to the median flow for each year (dimensionless – temporal).
ml17.tif	Base flow. Compute the mean annual flows. Compute the minimum of a 7-day moving average flow for each year and divide them by the mean annual flow for that year. ML17 is the mean (or median - Use Preference option) of those ratios (dimensionless – temporal).
ml18.tif	Variability in base flow. Compute the standard deviation for the ratios of 7-day moving average flows to mean annual flows for each year. ML18 is the standard deviation times 100 divided by the mean of the ratios (percent – spatial).
ml19.tif	Base flow. Compute the ratios of the minimum annual flow to mean annual flow for each year. ML19 is the mean (or median - Use Preference option) of these ratios times 100 (dimensionless – temporal).
ml2.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml20.tif	Base flow. Divide the daily flow record into 5-day blocks. Find the minimum flow for each block. Assign the minimum flow as a base flow for that block if 90 percent of that minimum flow is less than the minimum flows for the blocks on either side. Otherwise, set it to zero. Fill in the zero values using linear interpolation. Compute the total flow for the entire record and the total base flow for the entire record. ML20 is the ratio of total flow to total base flow (dimensionless – spatial).

ml21.tif	Variability across annual minimum flows. Compute the mean and standard deviation for the annual minimum flows. ML21 is the standard deviation times 100 divided by the mean (percent – spatial).
ml3.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml4.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml5.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml6.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml7.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml8.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ml9.tif	Mean (or median - Use Preference option) minimum flows for each month across all years. Compute the minimums for each month over the entire flow record. For example, ML1 is the mean of the minimums of all January flow values over the entire record (cubic feet per second – temporal).
ta1.tif	Constancy. Constancy is computed via the formulation of Colwell (see example in Colwell, 1974). A matrix of values is compiled where the rows are 11 flow categories and the columns are 365 (no February 29th) days of the year. The cell values are the number of times that a flow falls into a category on each day.
ta2.tif	Predictability. Predictability is computed from the same matrix as constancy (see example in Colwell, 1974).
th1.tif	Julian date of annual maximum. Determine the Julian date that the maximum flow occurs for each year. Transform the dates to relative values on a circular scale (radians or degrees). Compute the x and y components for each year and average them across all years. Compute the mean angle as the arc tangent of y-mean divided by x-mean. Transform the resultant angle back to Julian date (Julian day – spatial).
th2.tif	Variability in Julian date of annual maxima. Compute the coefficient of variation for the mean x and y components and convert to a date (Julian days - spatial).
tl1.tif	Julian date of annual minimum. Determine the Julian date that the minimum flow occurs for each water year. Transform the dates to relative values on a circular scale (radians or degrees). Compute the x and y components for each year and average them across all years. Compute the mean angle as the arc tangent of y-mean divided by x-mean. Transform the resultant angle back to Julian date (Julian day – spatial).
tl2.tif	Variability in Julian date of annual minima. Compute the coefficient of variation for the mean x and y components and convert to a date (Julian day – spatial).

Table S4.5. List of biological predictor variables used in SDM workflow.

Layer	Description
Ccarpio.tif	Modelled distribution for Cyprinus caprio. Measured as probability of occurrence (0-1).
Cgariepinus.tif	Modelled distribution for Claria gariepinus. Measured as probability of occurrence (0-1).
Cidella.tif	Modelled distribution for Ctenopharyngodon idella. Measured as probability of occurrence (0-1).
Crendalli.tif	Modelled distribution for Coptedon rendalli. Measured as probability of occurrence (0-1).
Gaffinis.tif	Modelled distribution for Gambusia affinis. Measured as probability of occurrence (0-1).
Lumbratus.tif	Modelled distribution for Labeo umbratus. Measured as probability of occurrence (0-1).
Laeneus.tif	Modelled distribution for Labeo aeneus. Measured as probability of occurrence (0-1).
Lmacrochirus.tif	Modelled distribution for Lepichromis macrochirus. Measured as probability of occurrence (0-1).
Mdolomieu.tif	Modelled distribution for Micropterus dolomieu. Measured as probability of occurrence (0-1).
Mpunctulatus.tif	Modelled distribution for Micropterus punctulatus. Measured as probability of occurrence (0-1).
Msalmoides.tif	Modelled distribution for Micropterus salmoides. Measured as probability of occurrence (0-1).
Omossambicus.tif	Modelled distribution for Oreochromis mossambicus. Measured as probability of occurrence (0-1).
Omykiss.tif	Modelled distribution for Oncorhynchus mykiss. Measured as probability of occurrence (0-1).
Oniloticus.tif	Modelled distribution for Oreochromis niloticus. Measured as probability of occurrence (0-1).
Strutta.tif	Modelled distribution for Salmo trutta. Measured as probability of occurrence (0-1).
Tsparrmanii.tif	Modelled distribution for Tilapia sparmanii. Measured as probability of occurrence (0-1).

Supplementary S4.6. R Code used to develop species distribution models.

```
## ____________________________________________________________________________

## Title:   Import data
## Purpose: Import and process occurrence data for freshwater fish
## Author:  Dominic Henry & Mo Kajee
## Date:    02/12/2020

## Libraries
library(tidyverse)
library(readxl)
library(sf)
library(janitor)
## ____________________________________________________________________________

## renv::init() - run this once project code is ready for first commit
## renv::snapshot() - run when new packages are installed (to update renv.lock file)


# Import occurrence data ----------------------------------------------------
# occ_data_all <- map_dfr(dir("data input/species data/", full.names = TRUE),
#                         read_csv)

occ_data_all <- read_csv("data input/OccurrenceData.csv") %>%
  janitor::clean_names() %>%
  mutate(occurrence_id = str_sub(uuid, 1, 8)) %>%
  select(occurrence_id, taxon, latitude, longitude, sampling_date, conservation_status_global) %>%
  rename(scientific_name = taxon,
         decimal_latitude = latitude,
         decimal_longitude = longitude)


## Check number of records
occ_data_all %>%
  group_by(scientific_name) %>%
  tally() %>%
  print(n = 140)

# Filter records ------------------------------------------------------------

## Add quality filters (obvs will need to keep more of the original cols to do this)


# Create spatial data -------------------------------------------------------
latlongCRS <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
```

```
za <- st_read("data input/RSA_fixed.shp")

## Create sf object (first filter non-valid lat/long values)
occ_data_sf <- occ_data_all %>%
  filter(!(is.na(decimal_latitude) | is.na(decimal_longitude))) %>%
  filter(!(decimal_latitude == "NULL" | decimal_longitude == "NULL")) %>%
  mutate_at(c("decimal_latitude", "decimal_longitude"), as.numeric) %>%
  st_as_sf(coords = c("decimal_longitude","decimal_latitude"), crs = latlongCRS)

## Plot check
ggplot()+
  geom_sf(data = occ_data_sf)+
  geom_sf(data = za, fill = NA, color = "black")

# Write workspaces ----------------------------------------------------------
save(list = c("occ_data_all","occ_data_sf"), file = "data output/occ_data_clean.RData")


## _____________________________________________________________________________

## Title:   SDM data import
## Purpose: Process raster and occurrence data in prep for fish SDMs
## Author:  Dominic Henry & Mo Kajee
## Date:    08/09/2021

## Libraries
library(lubridate)
library(gridExtra)
library(ggpubr)
library(sf)
library(viridis)
library(readxl)
library(raster) #this has been replaced by terra
library(terra)
library(tidyverse)
library(glue)
## _____________________________________________________________________________

#memory.limit(size=100000) # increases available RAM usage

## Error in dl18 and dl20 - these rasters are empty! Need to check hydrological data generation step
x <- "data input/Queries/SDM_query_Pseudobarbus burgi.xlsx"

load("data output/occ_data_clean.RData")
start <- Sys.time()

# Import query details ------------------------------------------------------
```

```
query <- read_xlsx(x) %>%
  print

sppselect <- query$Value[which(query$Input == "Species")]

occ_data_sf_all <- occ_data_sf %>%
  filter(scientific_name %in% sppselect)

plot(occ_data_sf_all$geometry)

# Temporal filter ------------------------------------------------------------

## Keep all records for now -- No temporal filter ##
occ_data_sf_all <- occ_data_sf_all %>%
  mutate(year = year(sampling_date)) %>%
  filter(year >= as.numeric(query$Value[which(query$Input == "Start year")])) %>%
  filter(year <= as.numeric(query$Value[which(query$Input == "End year")]))


# Create output folder -------------------------------------------------------
if(dir.exists(glue("data output/sdm data processing/{sppselect}"))) {
  print("Folder exists")
} else {
  print("Folder created")
  dir.create(glue("data output/sdm data processing/{sppselect}"))
}

# Spatial filter -------------------------------------------------------------
##Skip for invasives
# Read in IUCN map
tempfile <- tempfile()
unzip(zipfile = glue("data input/Fish Distribution Map_IUCN/{sppselect}.zip"),
      exdir = tempfile)

range_files <- list.files(tempfile, pattern = ".shp$",full.names=TRUE)
range <- st_read(range_files) %>%
  mutate(ASSESSMENT = as.character(ASSESSMENT)) %>%
  mutate(ID_NO = as.integer(ID_NO))

## Write range map to file
range %>%
  st_write(glue("data output/sdm data processing/{sppselect}/IUCN_range_{sppselect}.shp"),
           delete_dsn = TRUE)

## Check plots
plot(occ_data_sf_all$geometry)
plot(range$geometry, add = TRUE)
```

```
plot(st_buffer(range,1)$geometry, add = TRUE)

## Intersect range and keep points within range and buffer
occ_data_sf <- st_intersection(occ_data_sf_all, st_buffer(range,1))

## Write outlying points to file
occ_data_sf_all %>%
 filter(!(occurrence_id %in% occ_data_sf$occurrence_id)) %>%
  st_write(glue("data output/sdm data processing/{sppselect}/Outlier_occ_{sppselect}.shp"),
           delete_dsn = TRUE)

### If invasives and you have skipped spatial filter, run this code

#occ_data_sf <- occ_data_sf_all

# Spatial projections  ----------------------------------------------------
geo_proj <- query$Value[which(query$Input == "Geographic projection")]

aeaproj <- "+proj=aea +lat_1=20 +lat_2=-23 +lat_0=0 +lon_0=25 +x_0=0 +y_0=0 +datum=WGS84 +units=m +no_defs +ellps=WGS84 +towgs84=0,0,0"

latlongCRS <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

if (geo_proj == "Yes") {
  occ_points <- occ_data_sf %>%
    st_transform(aeaproj)
} else {
  occ_points <- occ_data_sf %>%
    st_transform(latlongCRS)
}

## Remove duplicate coordinate values
occ_points <- occ_points %>%
  distinct(geometry, .keep_all = TRUE)

# Create background points -----------------------------------------------

## Read in catchment file
catchments <- st_read("data input/primary_catchment_latlong.shp", crs = latlongCRS) %>%
  st_transform(crs = aeaproj)

## Select catchments of interest
catch_vals <- query$Value[which(query$Input == "Catchments")]
regions <- str_c("Region ", str_split(catch_vals, pattern = ",")[[1]]) %>%
  str_replace(., "  ", " ")

catchment <- catchments %>%
  filter(name %in% regions) %>%
```

```
  st_union()

catchment %>%
  st_transform(crs = latlongCRS) %>%
  st_write(glue("data output/sdm data processing/{sppselect}/catchments_{sppselect}.shp"), delete_layer = TRUE)

# plot(catchment)

## Read in value of background points from query
n_points <- as.numeric(query$Value[which(query$Input == "Background points")])

## Randomly sample points within buffer (returns sfc object - use st_sf() to convert to sf)
bck_points <- st_sample(catchment, n_points) %>%
  st_sf()

## Write temporary files used in Python processing
bck_points %>%
  st_transform(crs = latlongCRS) %>%
  st_write("data output/temp_bck_dir/bck_points.shp", delete_layer = TRUE)

catchment %>%
  st_transform(crs = latlongCRS) %>%
  st_write("data output/temp_bck_dir/occ_buffer.shp", delete_layer = TRUE)

occ_points %>%
  st_transform(crs = latlongCRS) %>%
  st_write("data output/temp_bck_dir/occ_points.shp", delete_layer = TRUE)

## Run python background point processing
system('"C:/Program Files/ArcGIS/Pro/bin/Python/envs/arcgispro-py3/python" src/bck_points_processing.py',
       intern = TRUE)

## Read in adjusted background points
bck_points <- st_read("data output/temp_bck_dir/bck_points_updated.shp") %>%
  st_transform(aeaproj)

## Read in RSA grid
if (geo_proj == "Yes") {
  zagrid_sf <- readRDS("data input/zagrid_aea_sf.rds")
} else {
  ## Add non-projected sf ZA grid at some point
}

## Create a background point unique ID
bck_points <- mutate(bck_points, ID = str_c("B", 1:nrow(bck_points)))

## Assign a polygonID to each background point
```

```
bck_grid <- st_join(bck_points, zagrid_sf, join = st_intersects, left = FALSE)

## Group by polygons and keep first point (i.e. remove duplicate points)
bck_points <- bck_grid %>% #
  group_by(ID) %>%
  filter(row_number() == 1) %>%
  ungroup

## Import RSA shapefile
if (geo_proj == "Yes") {
  za <- st_read("data input/RSA_fixed.shp", crs = latlongCRS) %>%
    st_transform(aeaproj)
} else {
  za <- st_read("data input/RSA_fixed.shp", crs = latlongCRS)
}

# Occurrence and BP plot checks ------------------------------------------

## Create a bounding box for map inset
occ_bbox <- st_make_grid(catchment, n = 1)

p1 <- ggplot() +
  geom_sf(data = za, fill = alpha("grey",0.5))+
  geom_sf(data = occ_points, size = 1.5)+
  geom_sf(data = occ_bbox, fill = NA, col = "dodgerblue", size = 1.3) +
  theme_bw()+
  theme(legend.text = element_text(size = 14))+
  ggtitle(glue("{query$Value[which(query$Input == 'Species')]} - {nrow(occ_points)} occurrence points"))

p2 <- ggplot() +
  geom_sf(data = za, fill = alpha("grey",0.5), size = 1.0)+
  geom_sf(data = zagrid_sf, fill = alpha("grey",0.3))+
  geom_sf(data = bck_points, size = 0.2, col = "red")+
  geom_sf(data = occ_points, size = 0.8, col = "blue")+
  coord_sf(xlim = c(st_bbox(occ_bbox)$xmin,st_bbox(occ_bbox)$xmax),
           ylim = c(st_bbox(occ_bbox)$ymin,st_bbox(occ_bbox)$ymax))+
  theme_bw()+
  theme(panel.border = element_rect(colour = "dodgerblue", fill=NA, size=1.6))+
  ggtitle(query$Value[which(query$Input == "Species")])

p3 <- ggplot() +
  geom_sf(data = za, fill = alpha("grey",0.5), size = 1.0)+
  geom_sf(data = occ_points, size = 1.5)+
  geom_sf(data = catchment, fill = alpha("red",0.1))+
  coord_sf(xlim = c(st_bbox(occ_bbox)$xmin,st_bbox(occ_bbox)$xmax),
           ylim = c(st_bbox(occ_bbox)$ymin,st_bbox(occ_bbox)$ymax))+
  theme_bw()+
```

```
  theme(panel.border = element_rect(colour = "dodgerblue", fill=NA, size=1.6))+
  theme(legend.text = element_text(size = 14))+
  ggtitle(glue("{query$Value[which(query$Input == 'Species')]}"))

p4 <- ggplot() +
  geom_sf(data = za, fill = alpha("grey",0.5), size = 1.0)+
  geom_sf(data = bck_points, size = 0.3)+
  coord_sf(xlim = c(st_bbox(occ_bbox)$xmin,st_bbox(occ_bbox)$xmax),
           ylim = c(st_bbox(occ_bbox)$ymin,st_bbox(occ_bbox)$ymax))+
  theme_bw()+
  theme(panel.border = element_rect(colour = "dodgerblue", fill=NA, size=1.6))+
  ggtitle(glue("{query$Value[which(query$Input == 'Species')]} - {nrow(bck_points)} background points"))

pdf(glue("data output/sdm data processing/{sppselect}/fig1.pdf"), width = 16, height = 9)
grid.arrange(grobs = list(p1,p2,p3,p4), ncol = 2) # Also see ggarrange
dev.off()

# p <- arrangeGrob(grobs = list(p1,p2,p3,p4), ncol = 2)
# ggsave(glue("data output/sdm data processing/{sppselect}/fig1.png"),
#        p,
#        width = 12, height = 6)

# Environmental data ----------------------------------------------------
env_layer_list <- read_xlsx(x, sheet = "env_var_list") %>%
  filter(.data[[glue("select - {sppselect}")]] == 1) %>% # .data[[]] is tidy eval for a string input
  dplyr::select(folder,layer) %>%
  mutate(path = glue("data input/Environmental data 30s reduced/{folder}/{layer}")) %>%
  dplyr::select(path) %>%
  pull

env_layer_list

hydro_layer_list <- read_xlsx(x, sheet = "hydro_var_list") %>%
  filter(.data[[glue("select - {sppselect}")]] == 1) %>% # .data[[]] is tidy eval for a string input
  dplyr::select(folder,layer) %>%
  mutate(path = glue("data input/Environmental data 30s reduced/{folder}/{layer}")) %>%
  dplyr::select(path) %>%
  pull

hydro_layer_list

envstack <- readAll(stack(env_layer_list))


hydrostack <- readAll(stack(hydro_layer_list))

envstack <- stack(envstack,hydrostack)
```

```
names(envstack)



# Project rasters ------------------------------------------------------

## Project the rasters to AEA and crop (20% buffer added) to occurrence buffer
projenv_aea <- function(x){
  projection(x) <- latlongCRS
  projectRaster(x, crs=aeaproj)
}

projenv_latlong <- function(x){
  projection(x) <- latlongCRS
  projectRaster(x, crs=latlongCRS)
}

if (geo_proj == "Yes") {
  envstack <- stack(envstack)
  envstack <- stack(map(envstack@layers,projenv_aea))
  envstack <- readAll(stack(crop(envstack,extent(bck_points)*1.10))) # Add a 10% buffer
} else {
  envstack <- stack(envstack)
  envstack <- stack(map(envstack@layers,projenv_latlong))
  envstack <- readAll(stack(crop(envstack,extent(bck_points)*1.10)))
}


# Center and scale envstack ------------------------------------------------

## Create an option in the query file as to whether variables should be scaled?
# envstack <- scale(envstack)

# Collinearity of environemental predictors ----------------------------------
cormatrix <- raster::layerStats(envstack, "pearson", na.rm = TRUE)

cormatrix <- as_tibble(cormatrix$`pearson correlation coefficient`) %>%
  mutate(var = colnames(cormatrix$`pearson correlation coefficient`)) %>%
  dplyr::select(var, everything()) %>%
  write_csv(glue("data output/sdm data processing/{sppselect}/raster_corr_matrix.csv"))

## This method seems fairly robust and easy to understand
envstack <- terra::rast(envstack) #must use the rast fucntion from terra in order to use vifcor
 var_reduced <- usdm::vifcor(envstack, th=0.6)
var_reduced@results$Variables
```

```
# Alternative
# vif_reduced <- usdm::vifstep(envstack, th=10)

# Exclude the collinear variables that were identified in the previous step
envstack <- usdm::exclude(envstack,var_reduced)

usdm::vif(envstack) %>%
  as_tibble %>%
  write_csv(glue("data output/sdm data processing/{sppselect}/vif_check.csv")) %>%
  print(n = 20)

envstack <- stack(envstack) #converts envstack back into a RasterStack
# Raster predictor plots ----------------------------------------------------
enlen <- 1:nlayers(envstack)
plists <- split(enlen, ceiling(seq_along(enlen)/4))
plotras <- function(x){plot(envstack[[x]])}

pdf(glue("data output/sdm data processing/{sppselect}/fig3.pdf"), width = 16, height = 9)
map(plists, plotras)
dev.off()

# Write query file ----------------------------------------------------------
copyfrom <- x
copyto <- glue("data output/sdm data processing/{sppselect}/")
file.copy(copyfrom, copyto, recursive=TRUE)

# Write occurrence points to shapefile --------------------------------------
occ_points %>%
  st_write(glue("data output/sdm data processing/{sppselect}/occ_points_{sppselect}.shp"),
           delete_dsn=TRUE)

# Write workspace -----------------------------------------------------------
envstack <- readAll(stack(envstack))

save(list = c("occ_points","bck_points","envstack"),
     file = glue("data output/sdm data processing/{sppselect}/sdm_input_data.RData"))

end <- Sys.time()

print(glue("SUCCESSFULLY COMPLETED - RUNTIME: {round(end-start,2)} {attr(end-start, 'units')}"))
system('CMD /C "ECHO GREAT SUCCESS. I LIKE. THE MODEL HAS FINISHED RUNNING! && PAUSE"',
       invisible=FALSE, wait=FALSE)


## ____________________________________________________________________________

## Title:   BART SDMs
```

```
## Purpose: Run regression tree analysis on reptiles develop SDM predictions
## Author:  Dominic Henry
## Date:    08/09/2021

## Libraries
# install.packages('devtools')
#devtools::install_github('cjcarlson/embarcadero')
library(embarcadero)
library(dismo)
library(glue)
library(rasterVis)
library(RColorBrewer)
library(readxl)
library(sf)
library(raster)
library(tidyverse)
library(dplyr)
library(rstatix) #needed to solve the "select" issue
## ____________________________________________________________________________

#memory.limit(size=100000) # increases available RAM usage

start <- Sys.time()

# Select species ------------------------------------------------------------
(folder_list <- dir("data output/sdm data processing/"))
(sppselect <- folder_list[16])

# Import species and environmental data -------------------------------------
load(glue("data output/sdm data processing/{sppselect}/sdm_input_data.RData"))

# Create output folder ------------------------------------------------------
BART_dir <- glue("data output/sdm BART results/{sppselect}")
if(dir.exists(BART_dir)) {
  print("Folder exists")
} else {
  print("Folder created")
  dir.create(BART_dir)
}

plot(envstack)

# Extract PB data and create input dataframe ---------------------------------

## Thin data
latlongCRS <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"
```

```
op <- occ_points %>%
  sf::st_transform(crs = latlongCRS)

op <- as.data.frame(as(op, "Spatial")) %>%
  dplyr::select(coords.x1, coords.x2, occurrence_id, scientific_name)

op_thin <- spThin::thin(loc.data = op,
                        lat.col = "coords.x1",
                        long.col = "coords.x2",
                        spec.col = "scientific_name",
                        thin.par = 0.8, # units = km
                        reps = 3,
                        locs.thinned.list.return = TRUE,
                        write.files = FALSE)

keep_ref <- as.numeric(row.names(op_thin[[1]]))

occ_points <- occ_points %>%
  filter(row_number() %in% keep_ref)

occ_points %>%
  sf::st_write(glue("{BART_dir}/occ_points_thinned.shp"), delete_dsn = TRUE)

PB_data <- occ_points %>%
  ungroup %>%
  mutate(Species = 1) %>%
  dplyr::select(Species) %>%
  rbind(bck_points %>%
          ungroup %>%
          mutate(Species = 0) %>%
          dplyr::select(Species)
  )

num_occ_points <- nrow(PB_data %>%
                         filter(Species == 1))

occ <- as(PB_data, 'Spatial')
occ.df <- cbind(PB_data$Species,
                raster::extract(envstack, occ))

occ.df <- as.data.frame(occ.df) # VERY NB - occ.df needs to be a data frame (not matrix)
colnames(occ.df)[1] <- "Observed"
head(occ.df)

## Small random sample of background points
num_bck <- num_occ_points
```

```
if(num_bck < 35){
  num_bck_small <- 70
  keepabs <- sample(2000:8500, num_bck_small)
} else {
  keepabs <- sample(2000:8500, num_bck)
}

occ.df <- occ.df[c(1:num_occ_points,keepabs),]
head(occ.df)

# Run full model BART -------------------------------------------------------
sdm_full <- bart(y.train=occ.df['Observed'],
                 x.train=occ.df[,-1],
                 keeptrees = TRUE)


# Check variable importance -------------------------------------------------
varimp.diag(occ.df[,-1], occ.df['Observed'], iter=50, quiet=TRUE)
ggsave(glue("{BART_dir}/variable_importance_diag.png"), width = 8, height = 6)
dev.off()

# Run stepwise variable selection -------------------------------------------
step.model <- variable.step(x.data=occ.df[,-1],
                            y.data=occ.df['Observed'],
                            quiet=TRUE)
step.model
ggsave(glue("{BART_dir}/RMSE_var_selection.png"), width = 8, height = 6)

# Retrain the model after variable selection --------------------------------
sdm <- bart(x.train=occ.df[, step.model],
            y.train=occ.df['Observed'],
            keeptrees = TRUE)

# Model summary and diagnostics ---------------------------------------------
summary(sdm)
ggsave(glue("{BART_dir}/model_diagnostics.png"), width = 8, height = 6)
capture.output(summary(sdm), file = glue("{BART_dir}/model_summary_capture.txt"))
sum_text <- read_lines(glue("{BART_dir}/model_summary_capture.txt"))
tss_threshold <- as.numeric(word(sum_text[10],4))
auc <- as.numeric(word(sum_text[7],3))

# Select prediction area ----------------------------------------------------
aeaproj <- "+proj=aea +lat_1=20 +lat_2=-23 +lat_0=0 +lon_0=25 +x_0=0 +y_0=0 +datum=WGS84 +units=m +no_defs"
latlongCRS <- "+proj=longlat +datum=WGS84 +no_defs +ellps=WGS84 +towgs84=0,0,0"

x <- glue("data input/Queries/SDM_query_{sppselect}.xlsx")
```

```
env_layer_list <- read_xlsx(x, sheet = "env_var_list") %>%
  filter(.data[[glue("select - {sppselect}")]] == 1) %>% # .data[[]] is tidy eval for a string input
  dplyr::select(folder,layer)

hydro_layer_list <- read_xlsx(x, sheet = "hydro_var_list") %>%
  filter(.data[[glue("select - {sppselect}")]] == 1) %>% # .data[[]] is tidy eval for a string input
  dplyr::select(folder,layer)

envpaths <- env_layer_list[which(str_detect(env_layer_list$layer, paste(step.model, collapse = '|'))),] %>%
  bind_rows(hydro_layer_list[which(str_detect(hydro_layer_list$layer, paste(step.model, collapse = '|'))),]) %>%
  mutate(path = glue("data input/Environmental data 30s reduced/{folder}/{layer}")) %>%
  dplyr::select(path) %>%
  pull

envpaths

catchments <- st_read(glue("data output/sdm data processing/{sppselect}/catchments_{sppselect}.shp")) %>%
  st_transform(aeaproj)

catchments <- as(catchments, "Spatial")

projenv_aea <- function(x){
  projection(x) <- latlongCRS
  projectRaster(x, crs=aeaproj)
}

envstack_rsa <- readAll(stack(envpaths))
envstack_rsa <- stack(map(envstack_rsa@layers,projenv_aea))
envstack_rsa <- stack(envstack_rsa)

envstack_catchment <- mask(envstack_rsa, catchments)
envstack_catchment <- crop(envstack_catchment,catchments)
envstack_catchment <- stack(envstack_catchment)
plot(envstack_catchment)

# Run model prediction with 95% CIs ----------------------------------------
map <- predict(sdm,
               envstack_catchment,
               quantiles=c(0.025, 0.975),
               quiet=FALSE,
               splitby=10)

# Map plotting -------------------------------------------------------------

## Mean SDM probability
mapTheme <- rasterTheme(region = rev(brewer.pal(11, "Spectral")),
                        layout.widths = list(right.padding = 10),
```

```
                    axis.line = list(col = "transparent"),
                    tick = list(col = 'transparent'))

## Change the scale to occur on left of plot
pdf(glue("{BART_dir}/SDM_mean_probability.pdf"), width = 16, height = 9)

#Getting an error here. Have hashed out some stuff


#Code from chat GPT. Ask Dom about this. Is this ok.
#occurence_points <- SpatialPoints(occ[1:num_occ_points,])

#levelplot(map[[1]],
#maxpixels = 1e10,
#margin = FALSE,
#par.settings = mapTheme,
#scales = list(x = list(draw = FALSE),
#              y = list(draw = FALSE)),
#zlim = c(0, 1)) +
#  layer(sp.points(occurence_points, pch=20, col="black", cex = 0.8),
#        data = list(occurence_points=occurence_points),
#        geom = "sp.points",
#        stat = "identity")

levelplot(map[[1]],
          maxpixels = 1e10,
          margin = FALSE,
          par.settings = mapTheme,
          scales = list(x = list(draw = FALSE),
                        y = list(draw = FALSE)),
          zlim = c(0, 1)) #+
 # layer(sp.points(occurence_points, pch=20, col="black", cex = 0.8),
      # data = list(occurence_points=SpatialPoints(occ[1:num_occ_points,])))

grid::grid.text('Probability of presence',
                rot = 90,
                y = unit(0.5, "npc"),
                x = unit(0.925, "npc"),
                gp = grid::gpar(fontsize = 15)
)

## Background points
# points(occ[keepabs,], col = "red", cex = 0.5)
dev.off()

## Posterior width
mapTheme <- rasterTheme(region = brewer.pal(9, "Blues"),
```

```
                    layout.widths = list(right.padding = 10),
                    axis.line = list(col = "transparent"),
                    tick = list(col = 'transparent'))

pdf(glue("{BART_dir}/SDM_posterior_width.pdf"), width = 16, height = 9)
levelplot(map[[3]] - map[[2]],
        maxpixels = 1e10,
        margin = FALSE,
        par.settings = mapTheme,
        scales = list(x = list(draw = FALSE),
                    y = list(draw = FALSE)),
        zlim = c(0, 1))

grid::grid.text('Posterior width',
              rot = 90,
              y = unit(0.5, "npc"),
              x = unit(0.925, "npc"),
              gp = grid::gpar(fontsize = 15))
dev.off()

## Four measure SDM plots
pdf(glue("{BART_dir}/SDM_four_panel_probability.pdf"), width = 16, height = 9)
par(mfrow=c(2,2))
par(mar=c(2,1,2,5))
plot(map[[1]], main = 'Posterior mean',
    box=F, axes=F)
plot(map[[2]], main = 'Lower 95% CI bound',
    box=F, axes=F)
plot(map[[3]], main = 'Upper 95% CI bound',
    box=F, axes=F)
plot(map[[3]]-map[[2]], main = 'Credible interval width',
    box=F, axes=F)
dev.off()

## Binary predictions
pdf(glue("{BART_dir}/SDM_four_panel_binary.pdf"), width = 16, height = 9)
par(mfrow=c(2,2))
plot(map[[1]] > tss_threshold, main = 'Posterior mean',
    box=F, axes=F)
plot(map[[2]] > tss_threshold, main = 'Lower 95% CI bound',
    box=F, axes=F)
plot(map[[3]] > tss_threshold, main = 'Upper 95% CI bound',
    box=F, axes=F)
quant <- quantile(values(map[[3]] - map[[2]]),
                0.75,
                na.rm = TRUE)
plot((map[[3]] - map[[2]]) > quant,
```

```
    box = FALSE,
    axes = FALSE,
    main = "Highest uncertainty zones",
    axis.args=list(at=pretty(0:1), labels=pretty(0:1)),
    legend.args=list(text='', side=2, line=1.3)
)
dev.off()


## Mean binary
pdf(glue("{BART_dir}/SDM_mean_binary.pdf"), width = 16, height = 9)
par(mfrow = c(1,1))
plot(map[[1]] > tss_threshold, main='Predicted presence',
    box=F, axes=F)
points(points(occ[1:num_occ_points,], col = "blue", pch = 20))
dev.off()

# Variable importance ------------------------------------------------------
varimp(sdm, plot=TRUE)
ggsave(glue("{BART_dir}/variable_importance.png"), width = 8, height = 6)

# Partial dependence plots -------------------------------------------------
p <- partial(sdm,
             trace=FALSE,
             ci=TRUE,
             smooth=10,
             equal=TRUE,
             panels=TRUE)
p

ggsave(glue("{BART_dir}/partial_dep.png"), width = 12, height = 8)

# Spatial partial maps -----------------------------------------------------
spa <- spartial(
  model = sdm,
  envs = envstack_catchment,
  x.vars = NULL,
  equal = FALSE,
  smooth = 1,
  transform = TRUE,
  save = TRUE
)

pdf(glue("{BART_dir}/spartial_maps.pdf"), width = 8, height = 6)
plot(spa)
dev.off()
```

```
# Write rasters ------------------------------------------------------------
writeRaster(map[[1]],
            glue("{BART_dir}/SDM_prob_mean{sppselect}.tif"),
            format = "GTiff",overwrite = TRUE)

writeRaster(map[[2]],
            glue("{BART_dir}/SDM_prob_lower{sppselect}.tif"),
            format = "GTiff",overwrite = TRUE)

writeRaster(map[[3]],
            glue("{BART_dir}/SDM_prob_upper{sppselect}.tif"),
            format = "GTiff",overwrite = TRUE)

writeRaster(map[[1]] > tss_threshold,
            glue("{BART_dir}/SDM_bin_mean{sppselect}.tif"),
            format = "GTiff",overwrite = TRUE)

writeRaster(map[[2]] > tss_threshold,
            glue("{BART_dir}/SDM_bin_lower{sppselect}.tif"),
            format = "GTiff",overwrite = TRUE)

writeRaster(map[[3]] > tss_threshold,
            glue("{BART_dir}/SDM_bin_upper{sppselect}.tif"),
            format = "GTiff",overwrite = TRUE)

writeRaster(map[[3]]- map[[2]],
            glue("{BART_dir}/SDM_cred_int_width{sppselect}.tif"),
            format = "GTiff",overwrite = TRUE)


# Write BART objects -------------------------------------------------------

saveRDS(object = occ.df, file = glue("{BART_dir}/bart_occdf.rds"))
# occ.df <- readRDS(glue("{BART_dir}/bart_occdf.rds"))

saveRDS(object = sdm, file = glue("{BART_dir}/bart_sdm.rds"))
# sdm <- readRDS(glue("{BART_dir}/bart_sdm.rds"))

saveRDS(object = map, file = glue("{BART_dir}/bart_predict_maps.rds"))
# map <- readRDS(glue("{BART_dir}/bart_predict_maps.rds"))

saveRDS(object = p, file = glue("{BART_dir}/bart_partial_plots.rds"))
# p <- readRDS(glue("{BART_dir}/bart_partial_plots.rds"))

saveRDS(object = spa, file = glue("{BART_dir}/bart_spartial_maps.rds"))
# spp <- readRDS(glue("{BART_dir}/bart_partial_spartial_maps.rds"))
```

```
# Timings ----------------------------------------------------------------
print("SUCCESSFULLY COMPLETED")
end <- Sys.time()
print(glue("SUCCESSFULLY COMPLETED - RUNTIME: {round(end-start,2)} {attr(end-start, 'units')}"))
# system('CMD /C "ECHO GREAT SUCCESS. I LIKE. THE MODEL HAS FINISHED RUNNING! && PAUSE"',
#        invisible=FALSE, wait=FALSE)
```

Supplementary S4.7. Model outputs for *Micropterus dolomieu*.

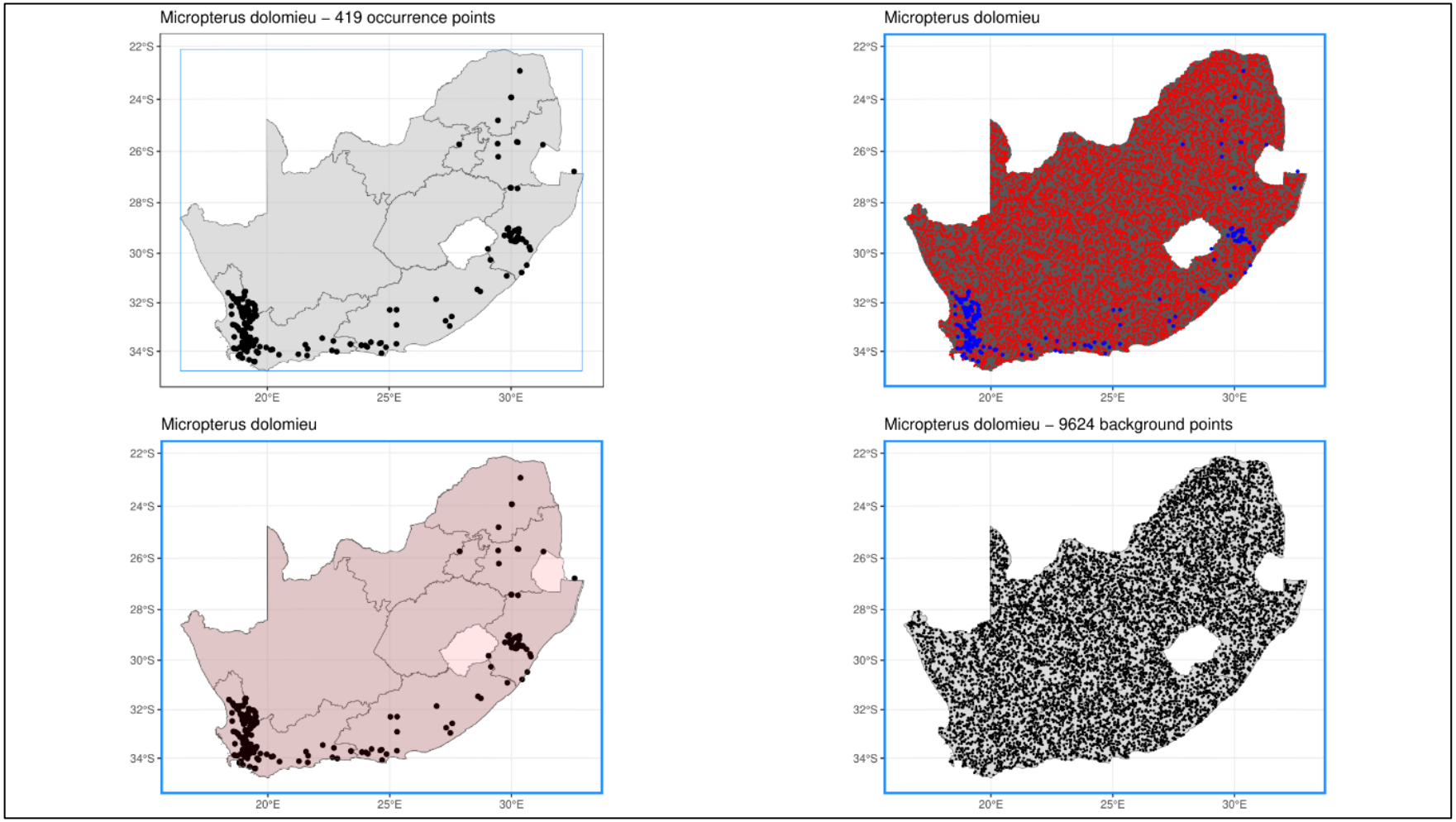


Figure S4.7a. Occurrence records and background points for *Micropterus dolomieu*.

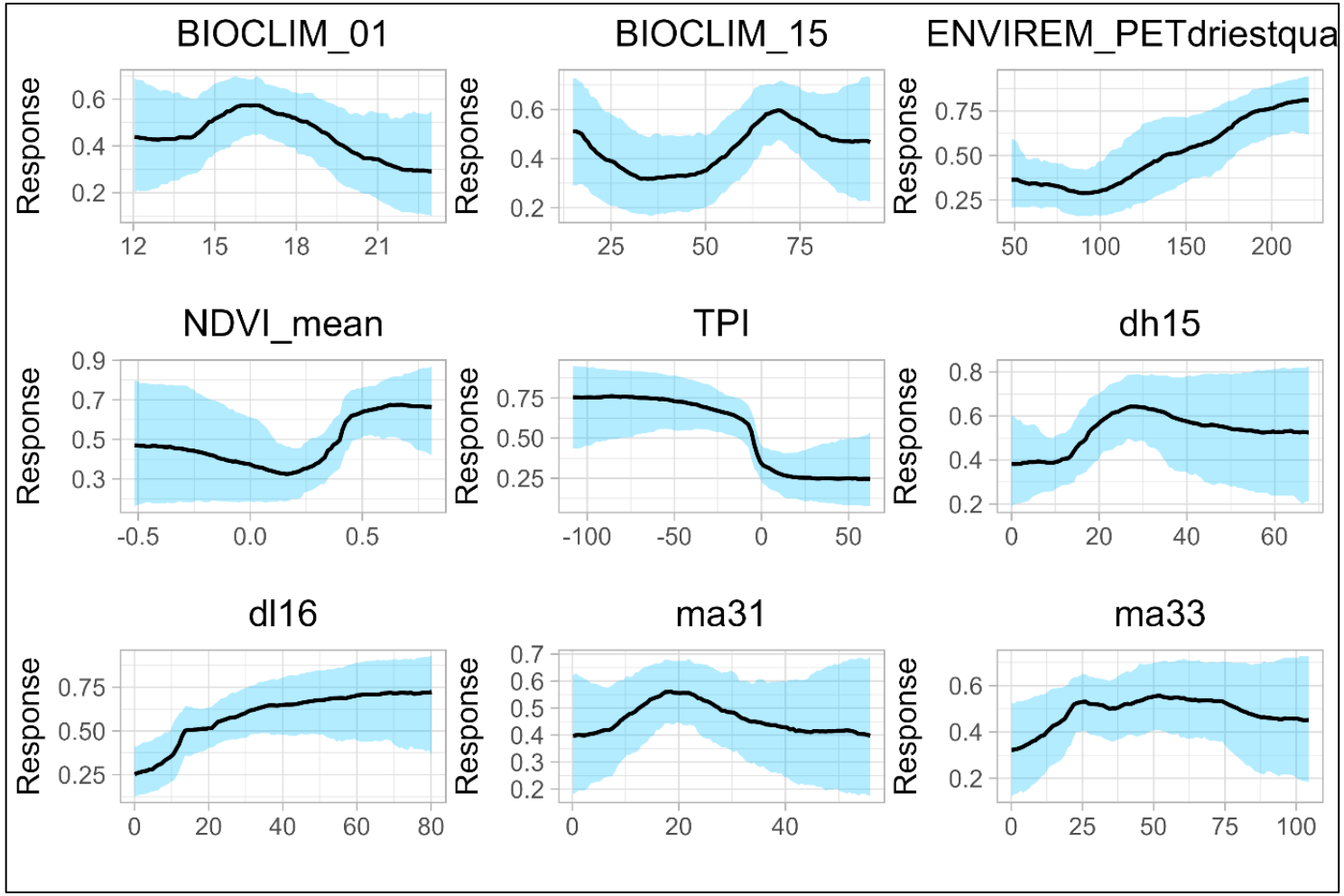


Figure S4.7b. Partial dependence plots for *Micropterus dolomieu*.

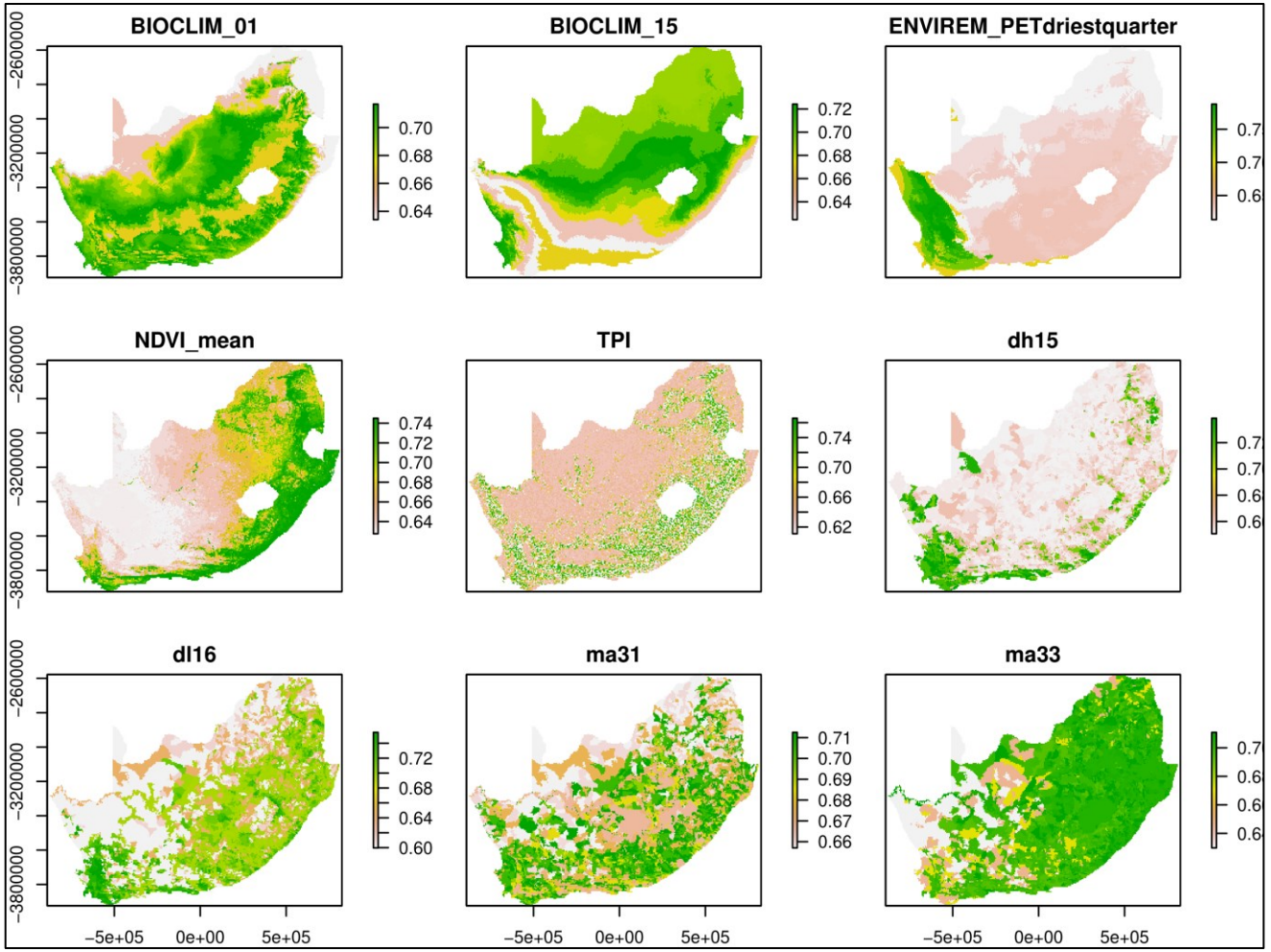


Figure S4.7c. Univariate probability model for *Micropterus dolomieu*.

Supplementary S4.8. Model outputs for *Micropterus punctulatus*.

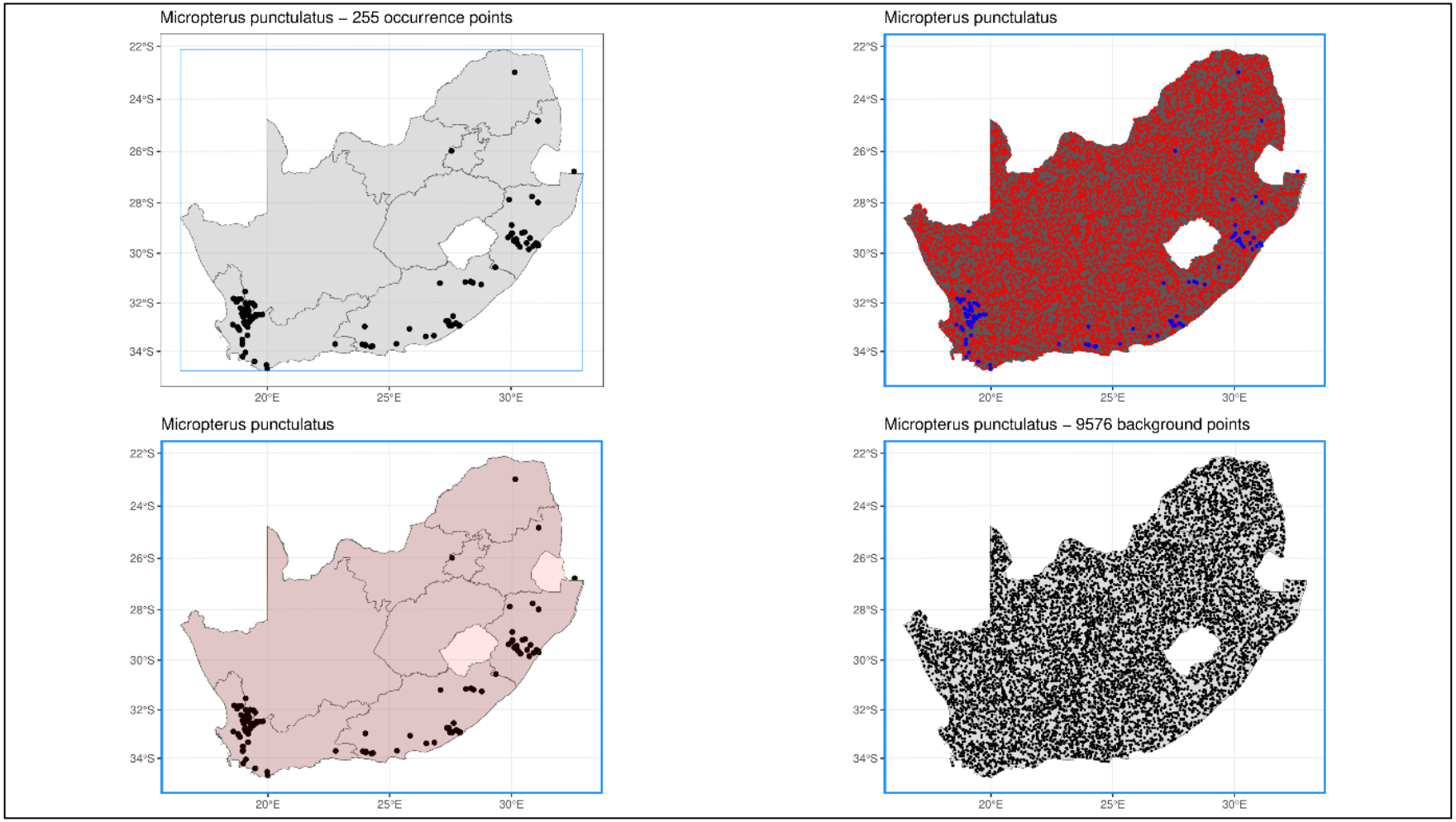


Figure S4.8a. Occurrence records and background points for *Micropterus punctulatus*.

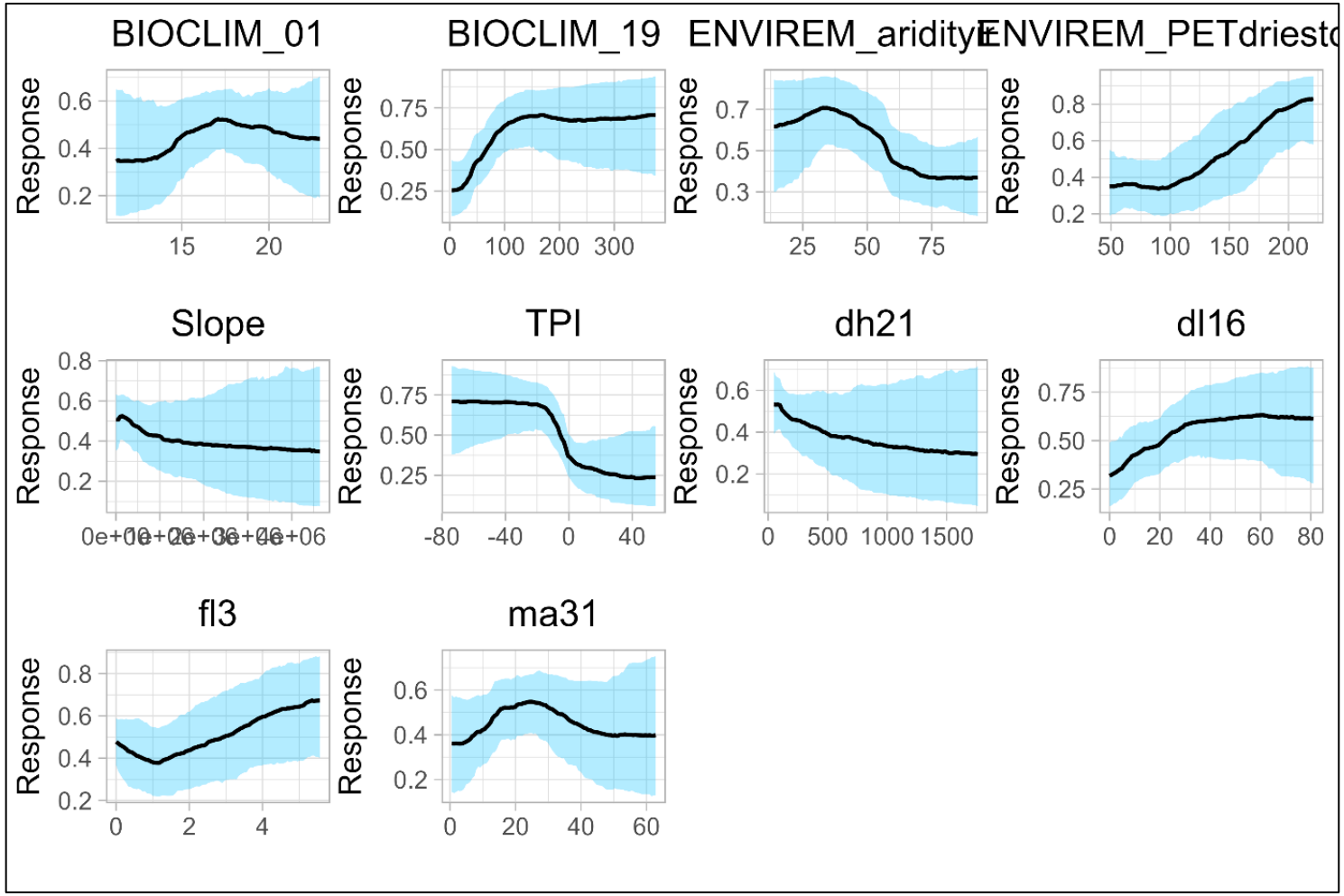


Figure S4.8b. Partial dependence plots for *Micropterus punctulatus*.

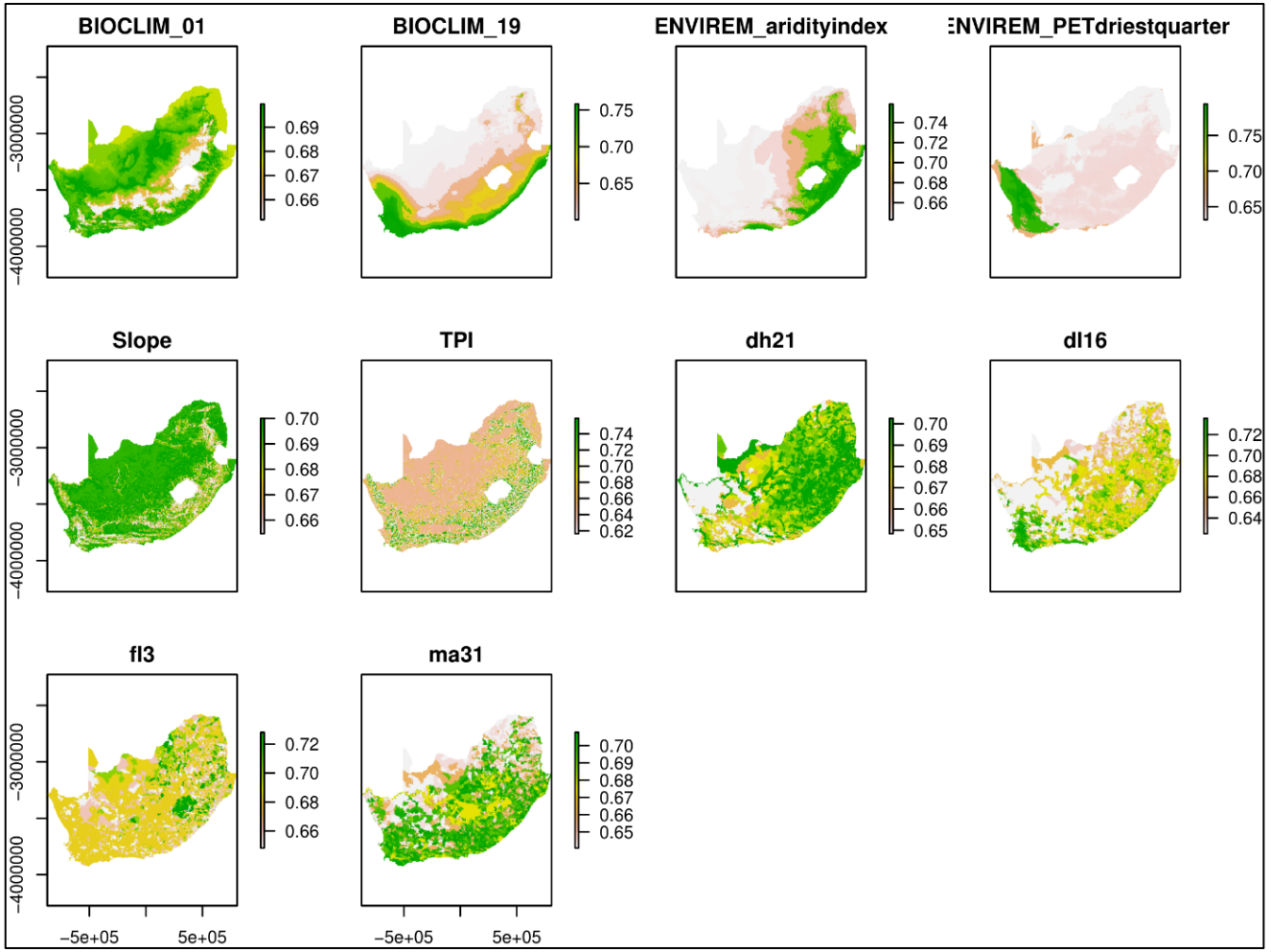


Figure S4.8c. Univariate probability model for *Micropterus punctulatus*.

Supplementary S4.9. Model outputs for *Micropterus salmoides*.

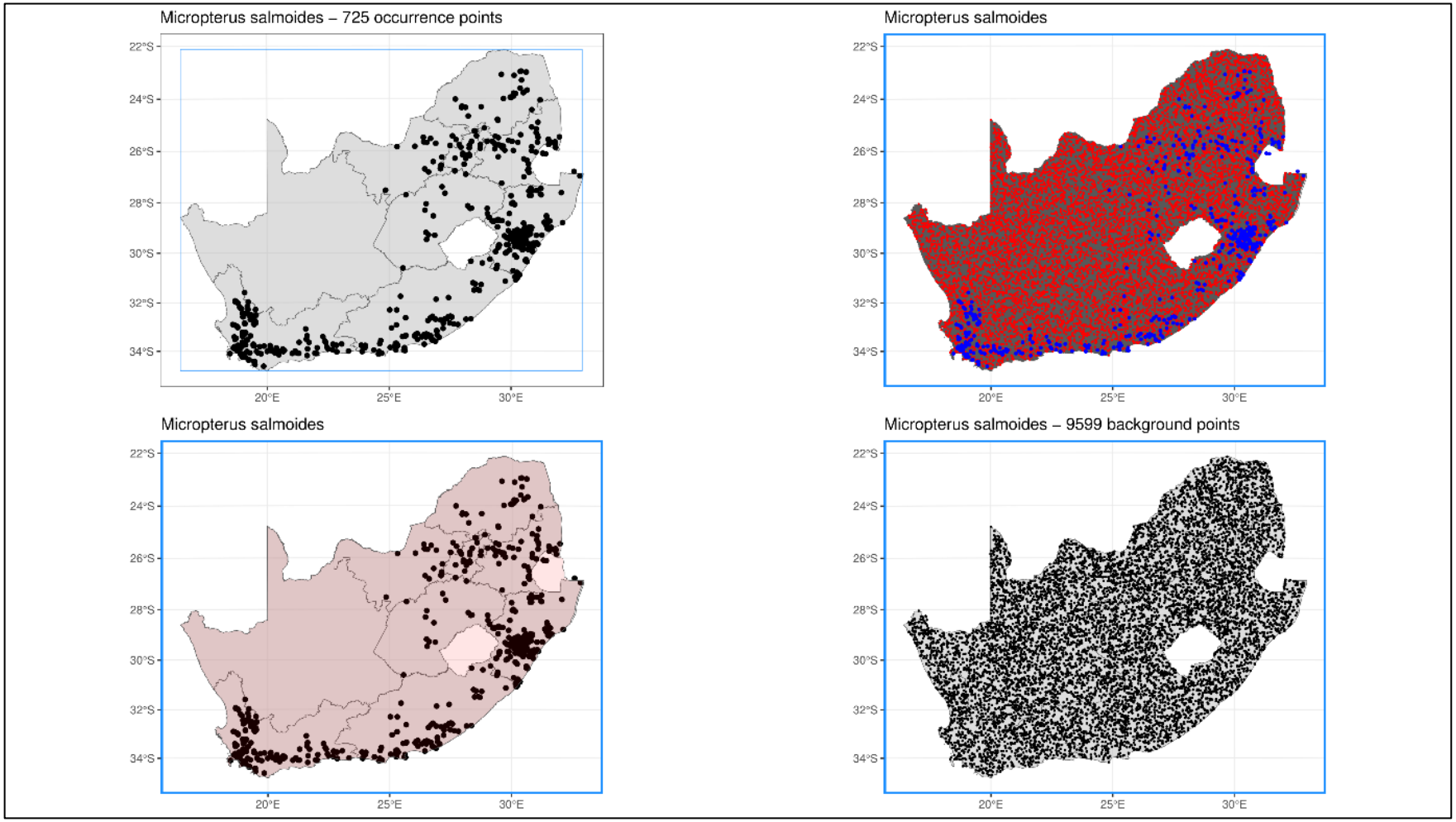


Figure S4.9a. Occurrence records and background points for *Micropterus salmoides*.

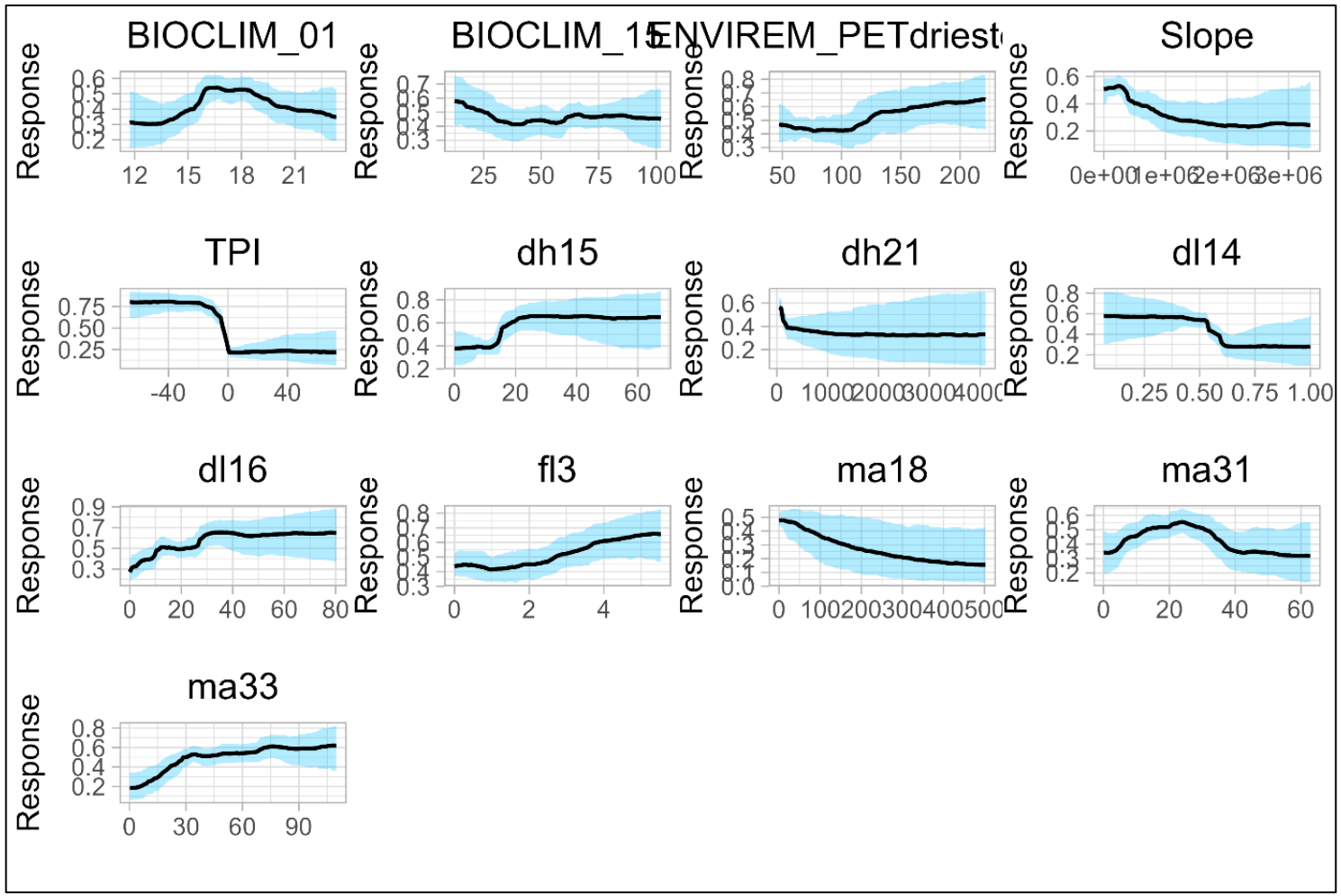


Figure S4.9b. Partial dependence plots for *Micropterus salmoides*.

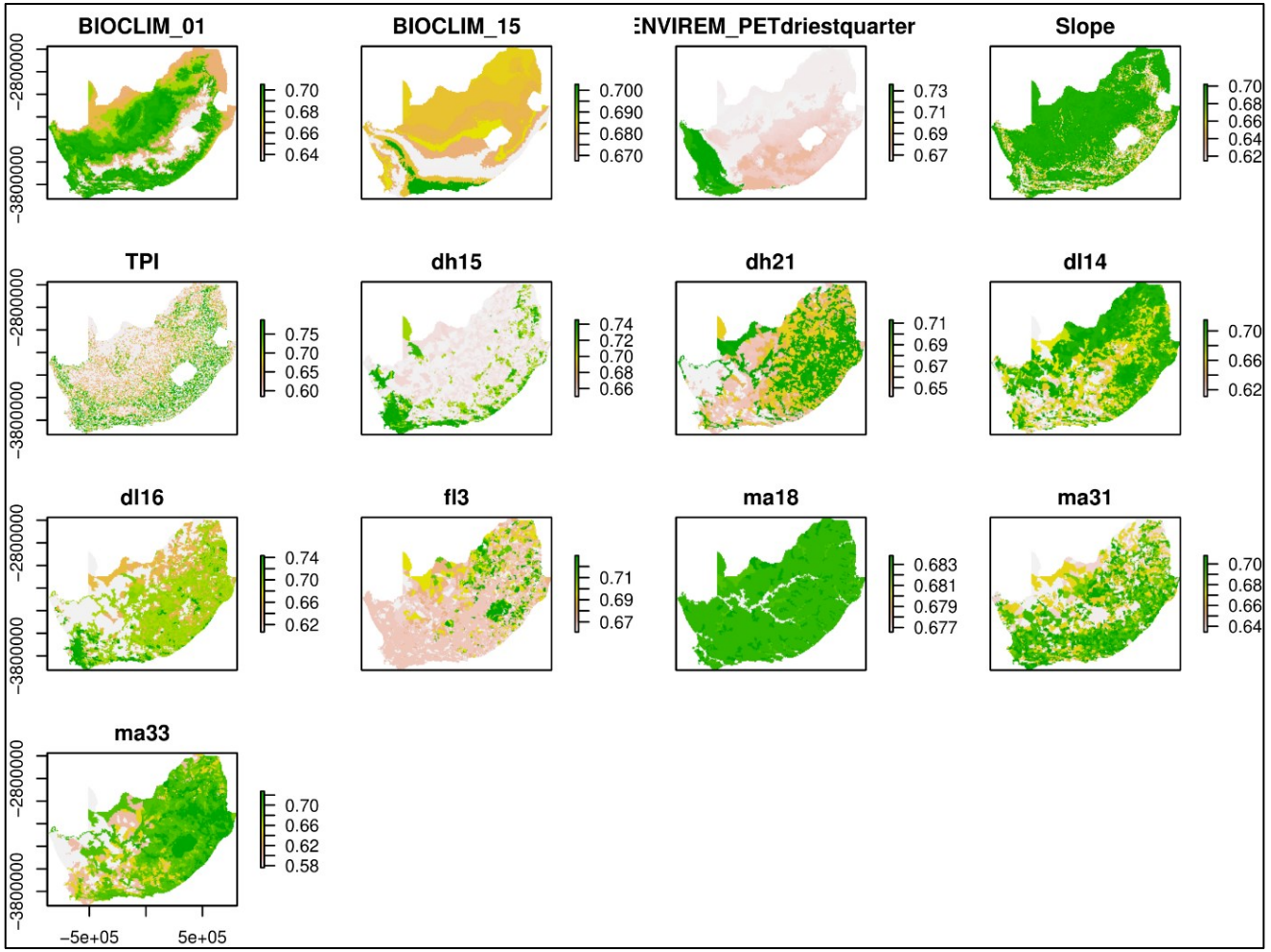


Figure S4.9c. Univariate probability model for *Micropterus salmoides*.

Supplementary S4.10. Model outputs for *Clarias gariepinus*.

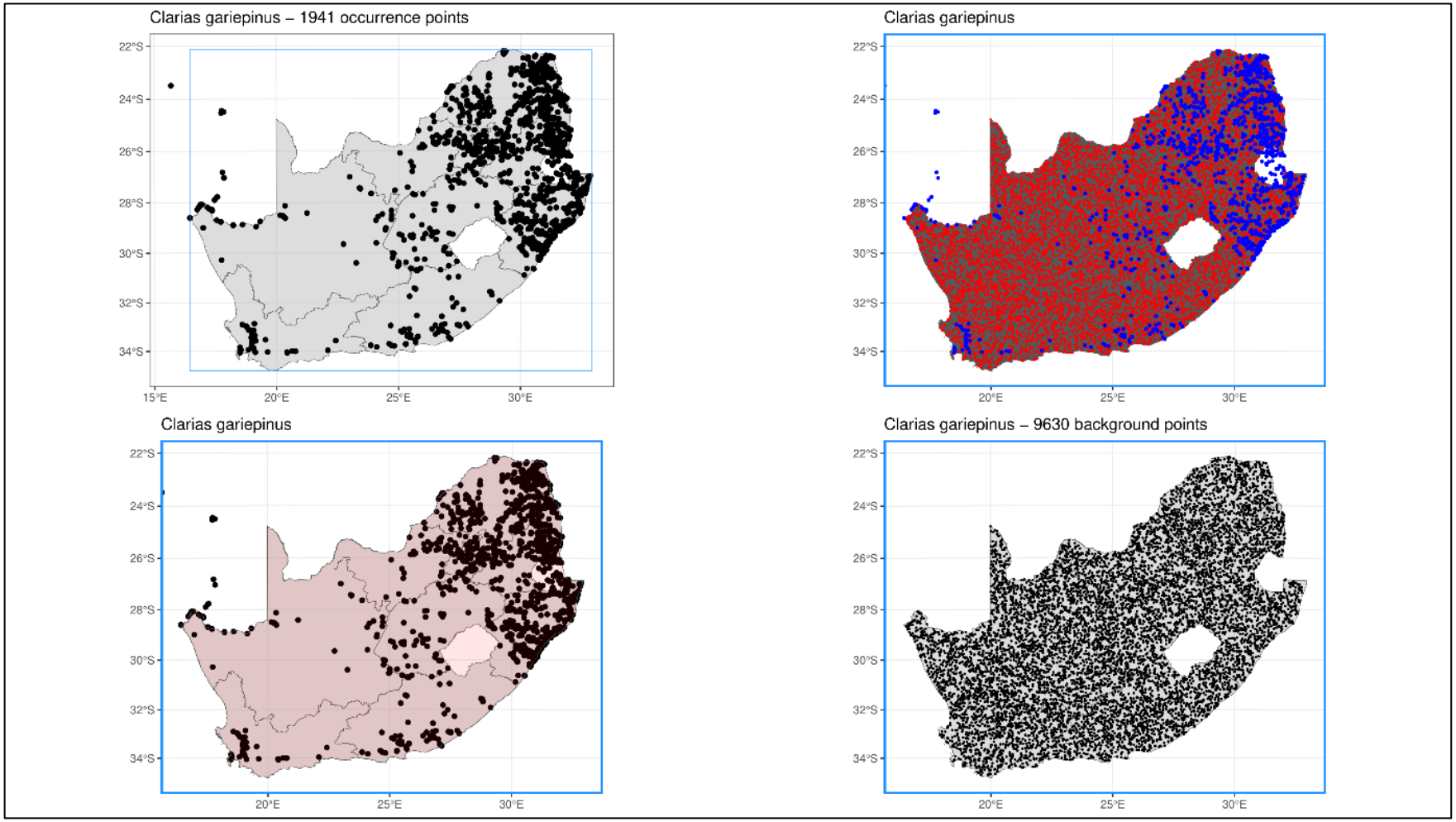


Figure S4.10a. Occurrence records and background points for *Clarias gariepinus*.

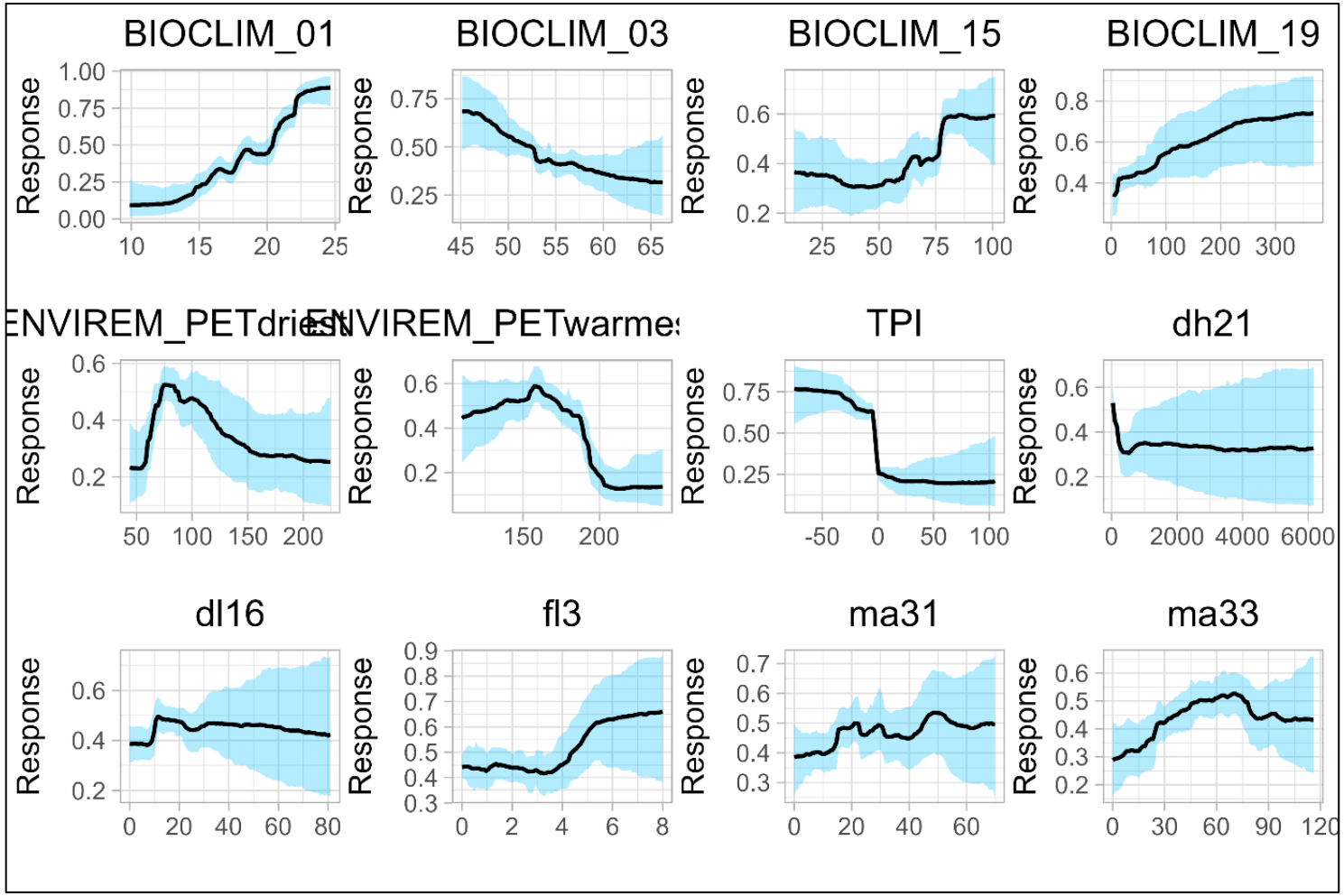


Figure S4.10b. Partial dependence plots for *Clarias gariepinus*.

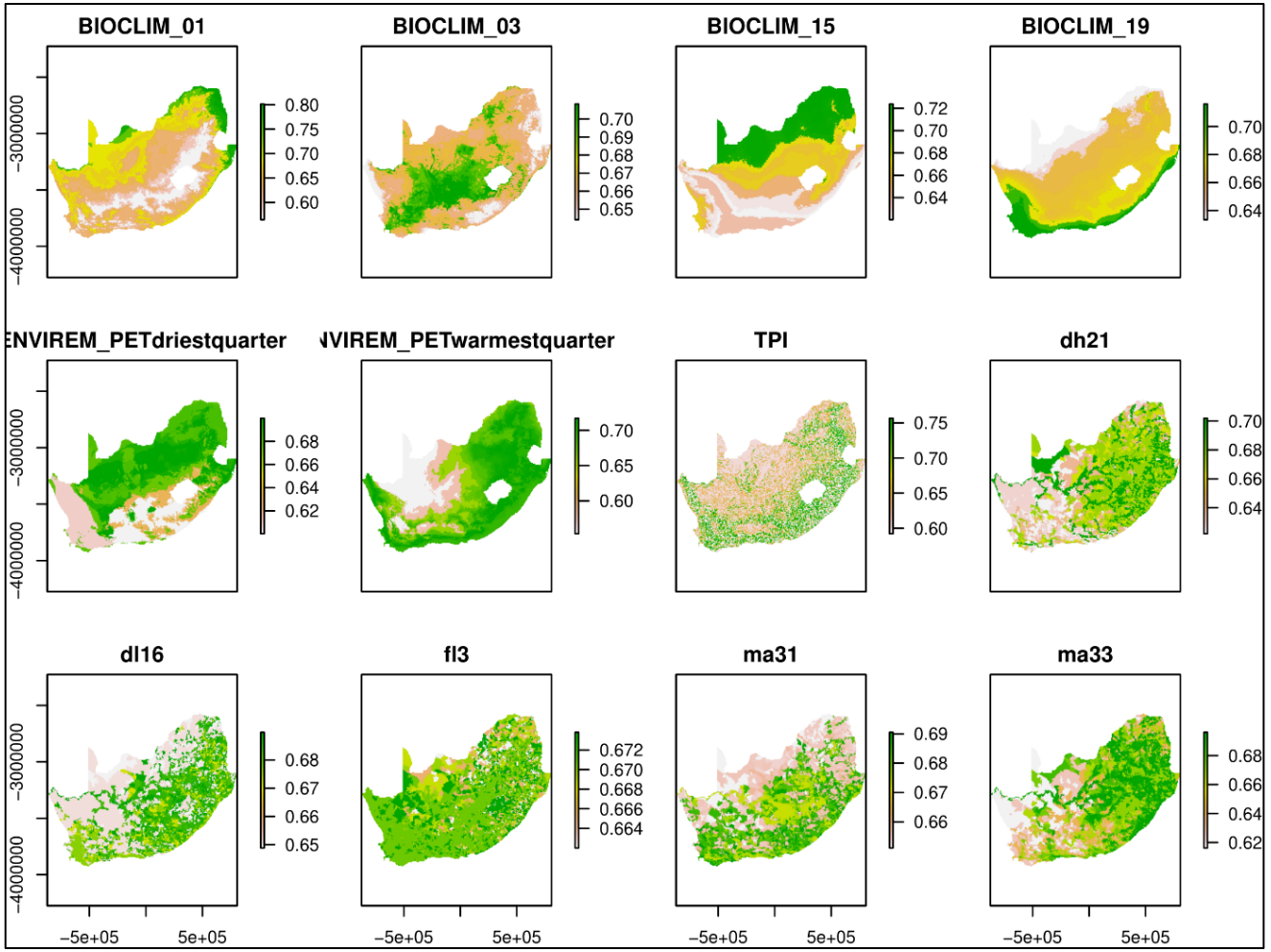


Figure S4.10c. Univariate probability model for *Clarias gariepinus*.

Supplementary S4.11. Model outputs for *Pseudobarbus burgi*.

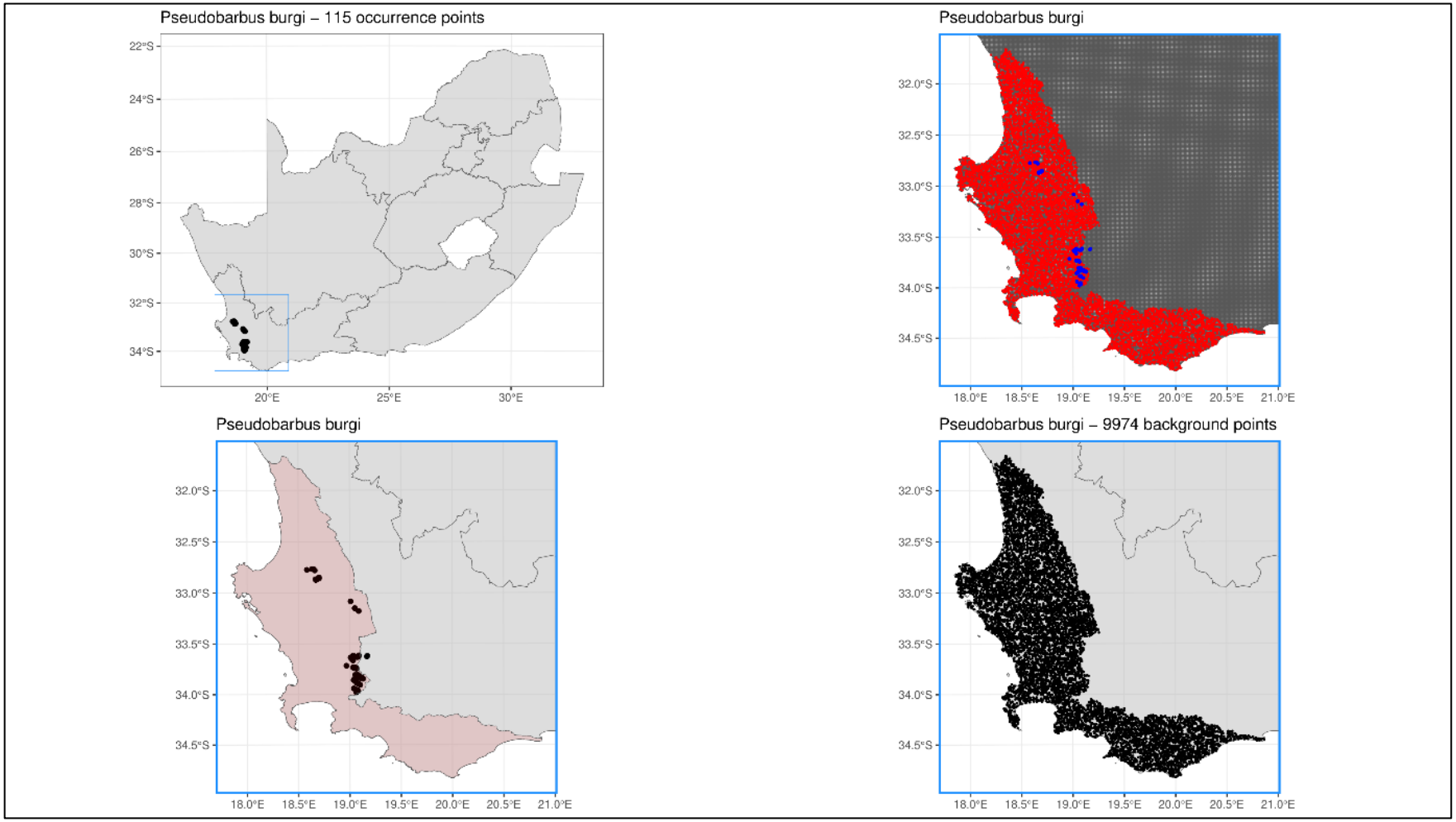


Figure S4.11a. Occurrence records and background points for *Pseudobarbus burgi*.

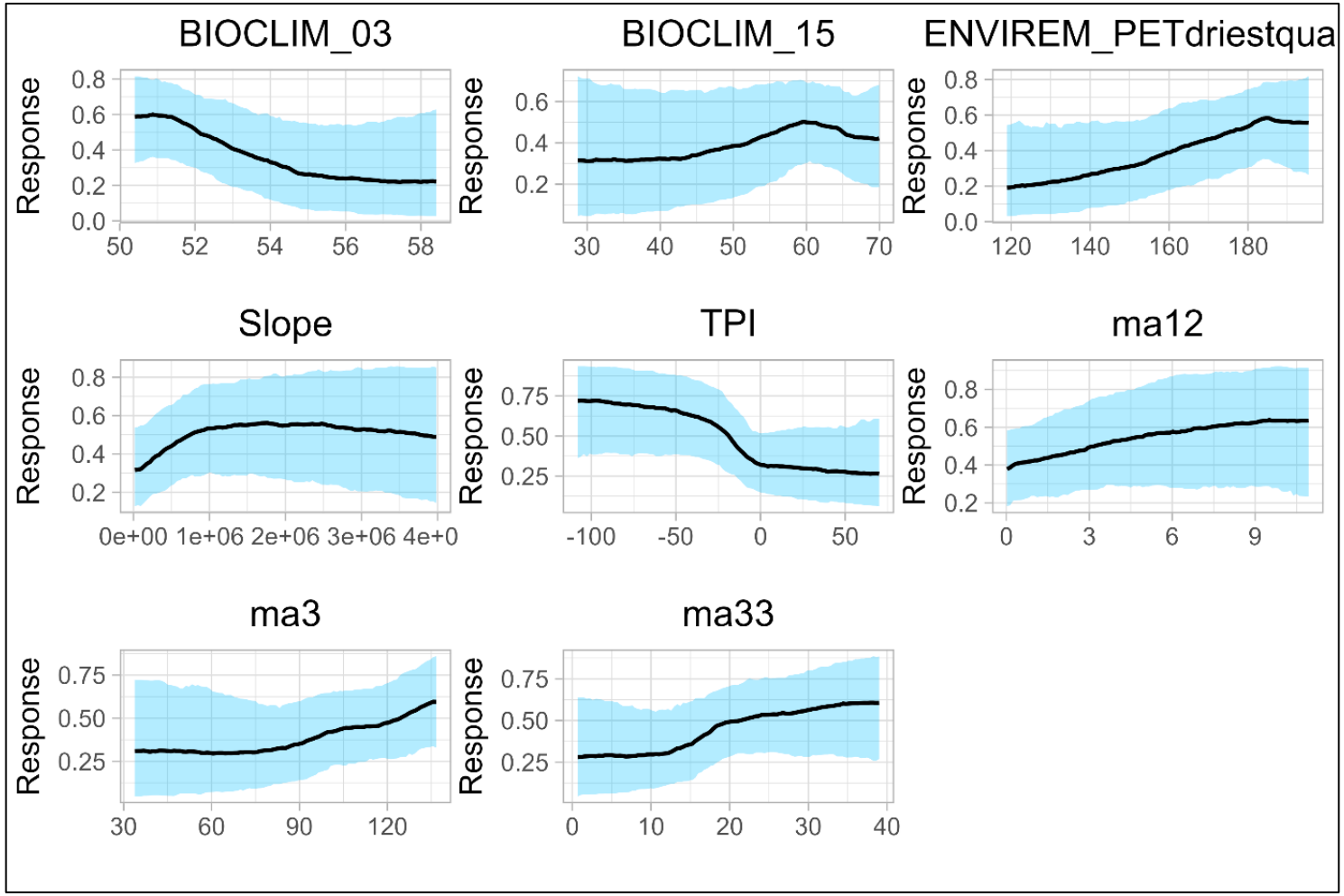


Figure S4.11b. Partial dependence plots for *Pseudobarbus burgi*.

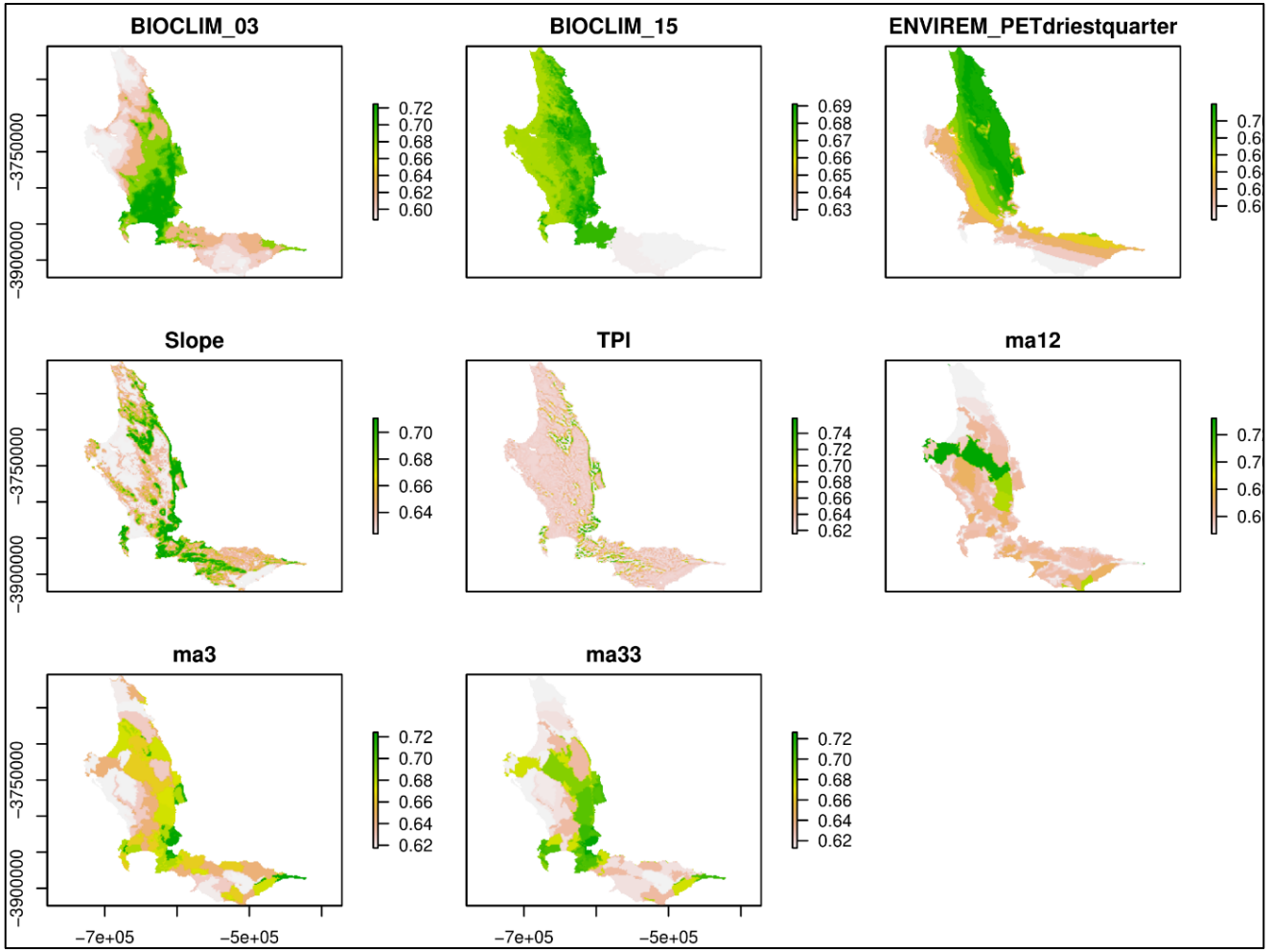


Figure S4.11c. Univariate probability model for *Pseudobarbus burgi*.

Supplementary S4.12. Model outputs for *Pseudobarbus burgi* adapted model.

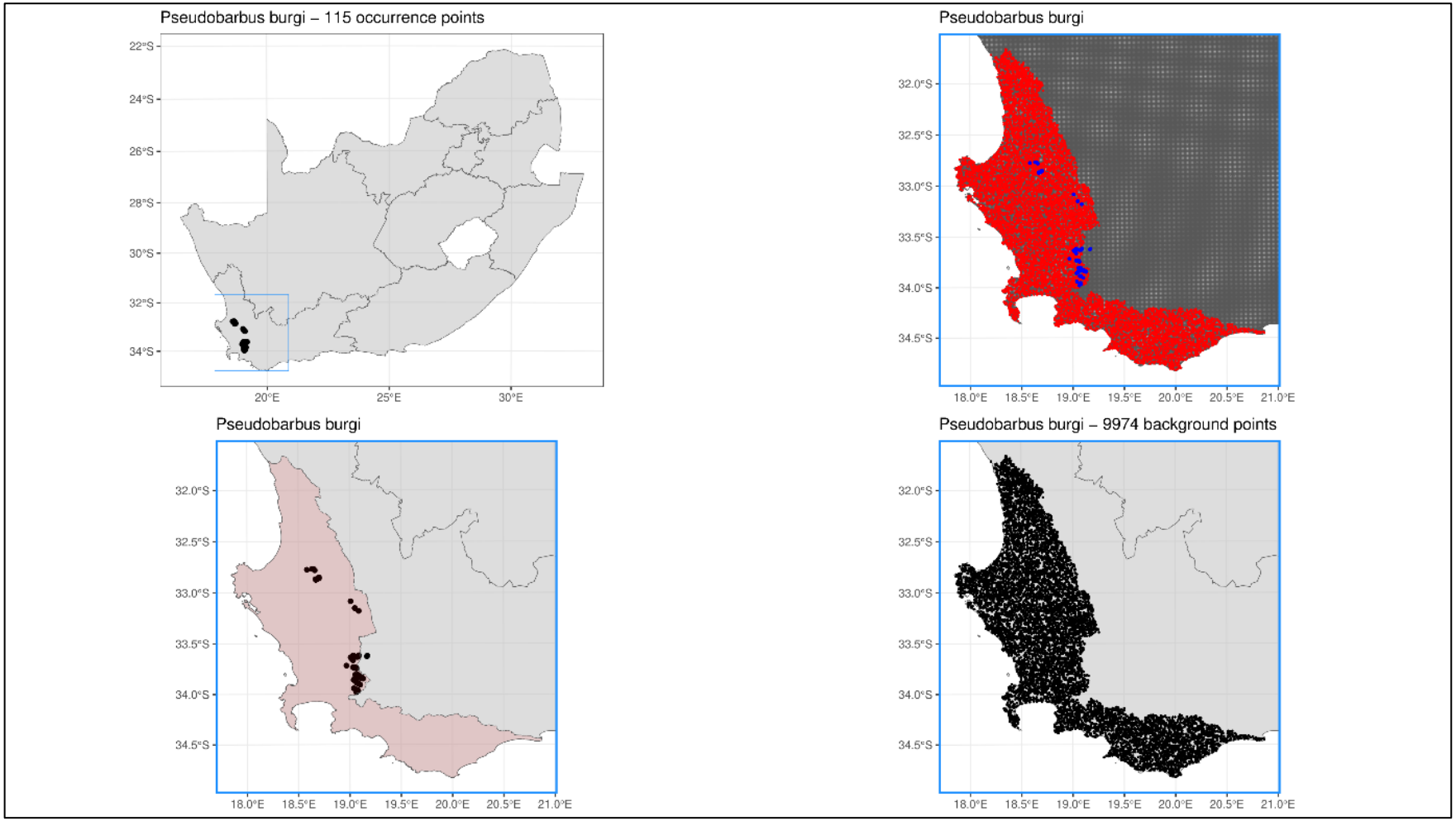


Figure S4.12a. Occurrence records and background points for *Pseudobarbus burgi* adapted model.

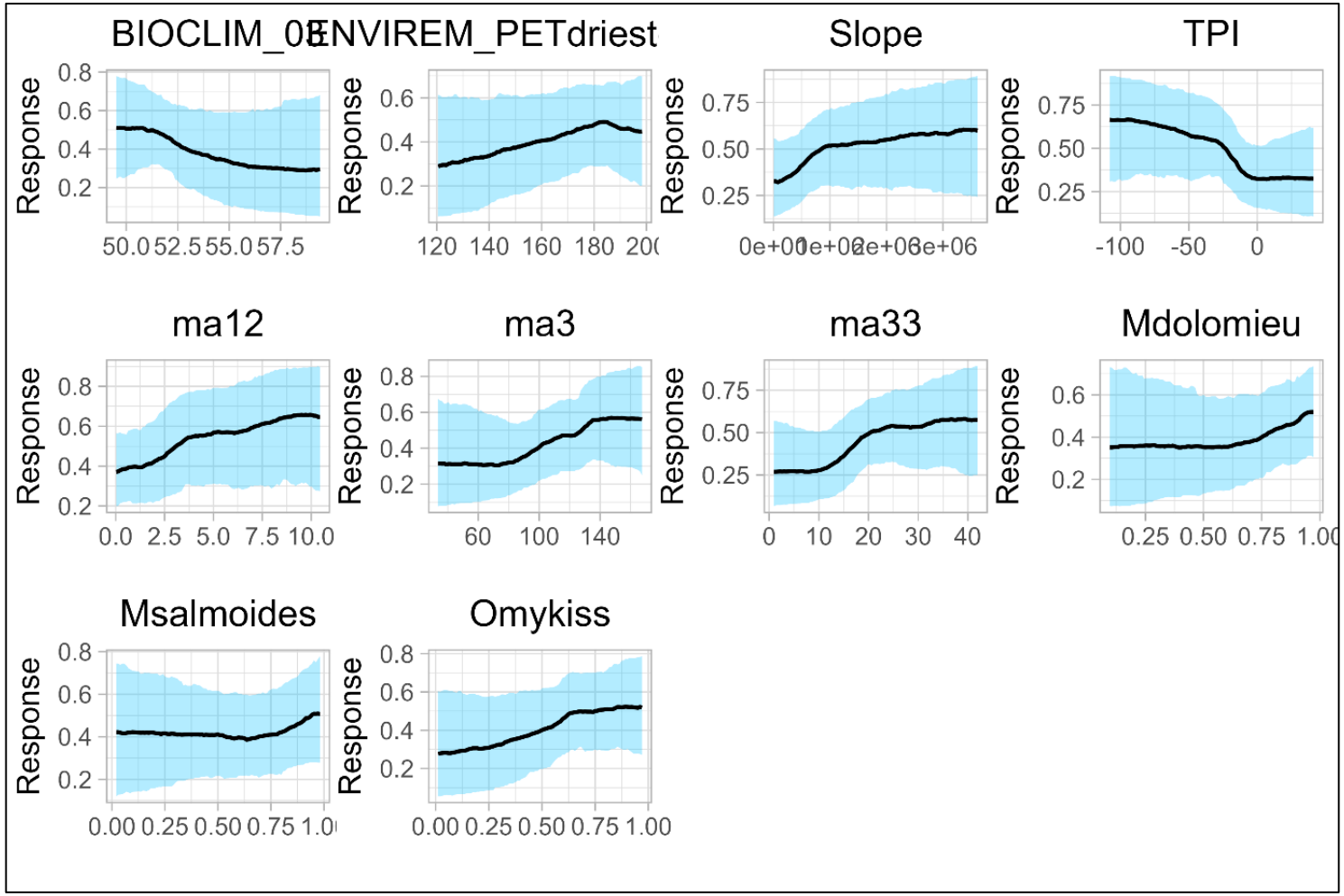


Figure S4.12b. Partial dependence plots for *Pseudobarbus burgi* adapted model.

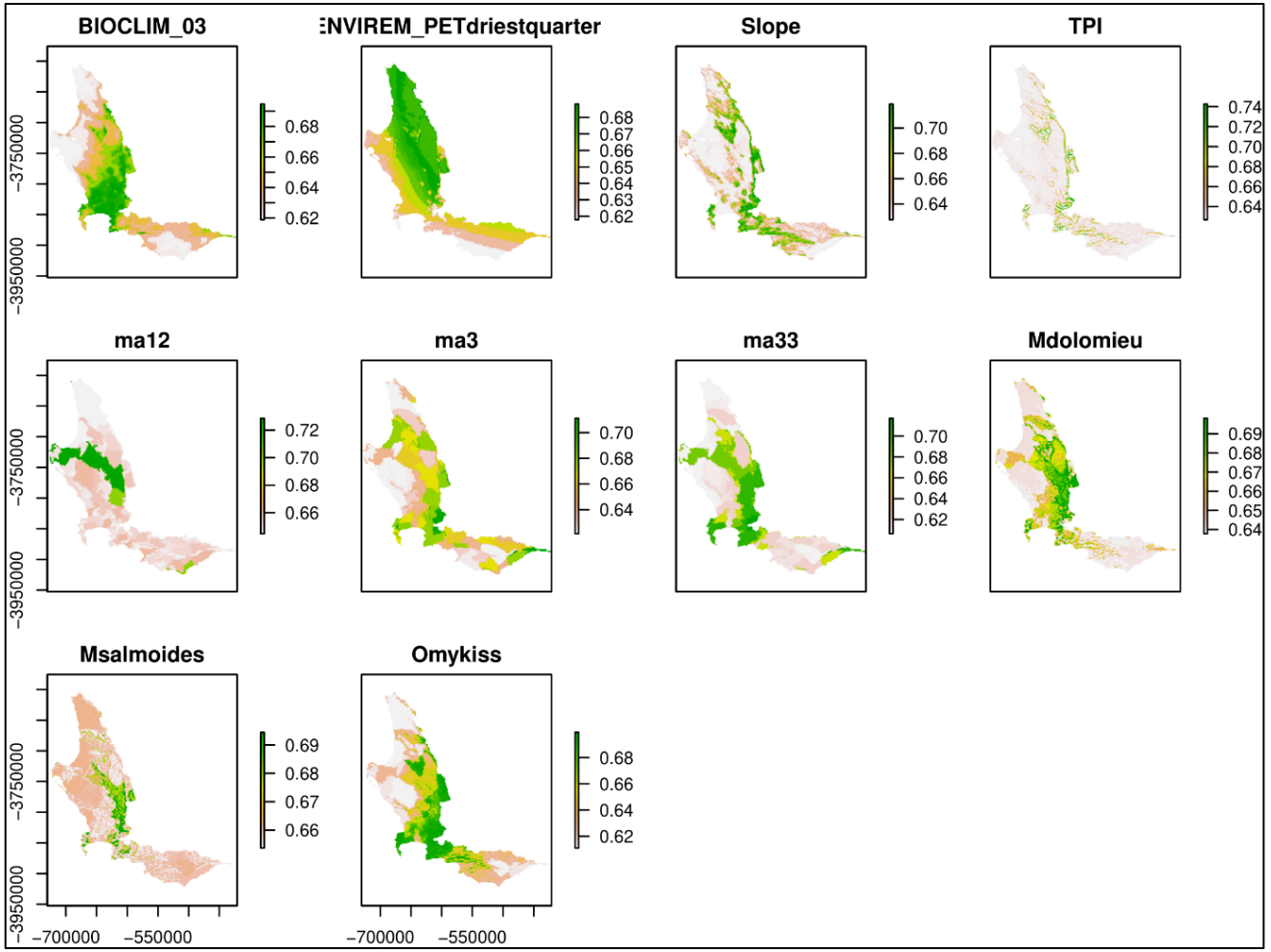


Figure S4.12c. Univariate probability model for *Pseudobarbus burgi* adapted model.

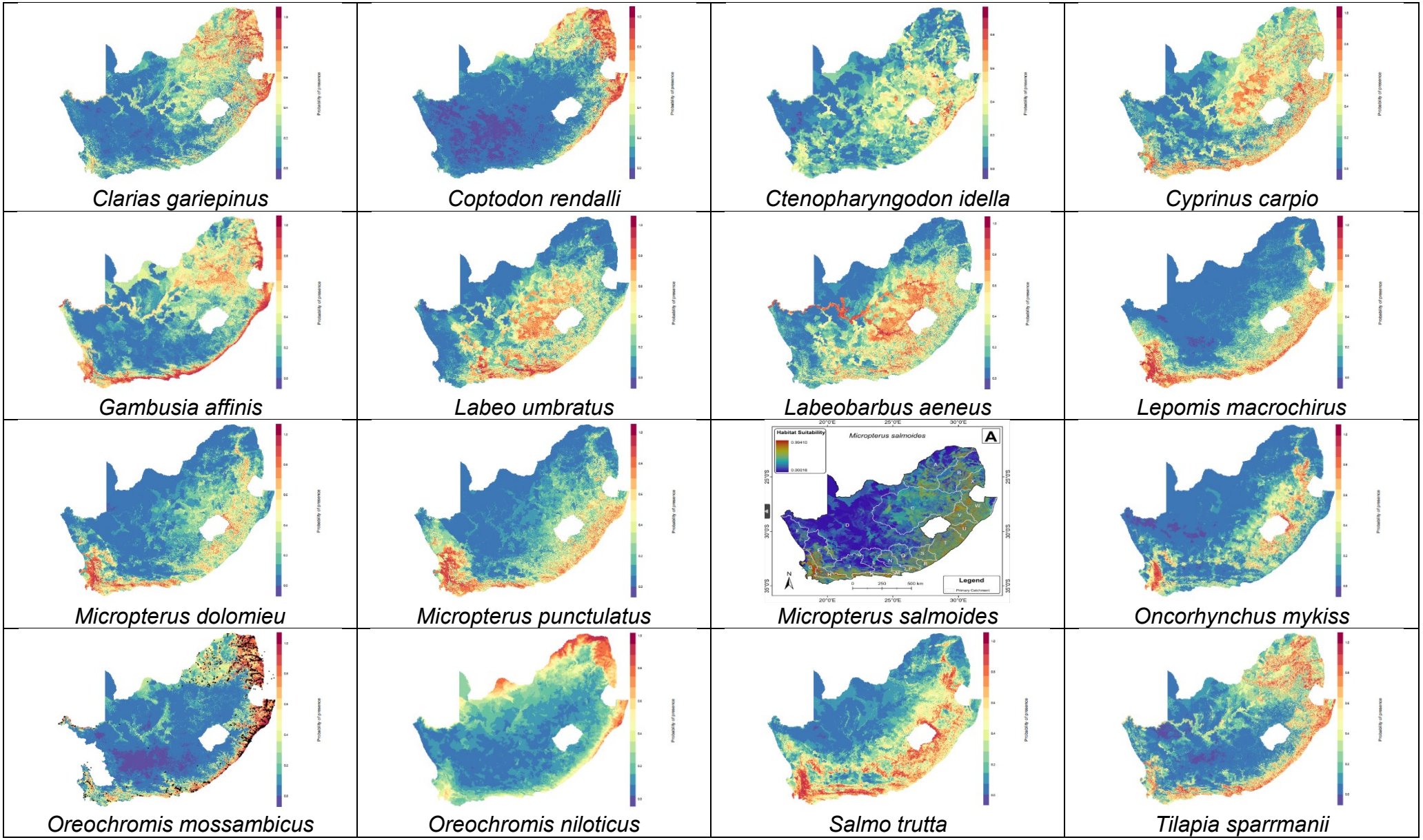


Figure S4.13. Modelled distributions for invasive species occurring in South Africa.

Supplementary S4.14. Modelled black bass distributions extracted from Khosa (2020).

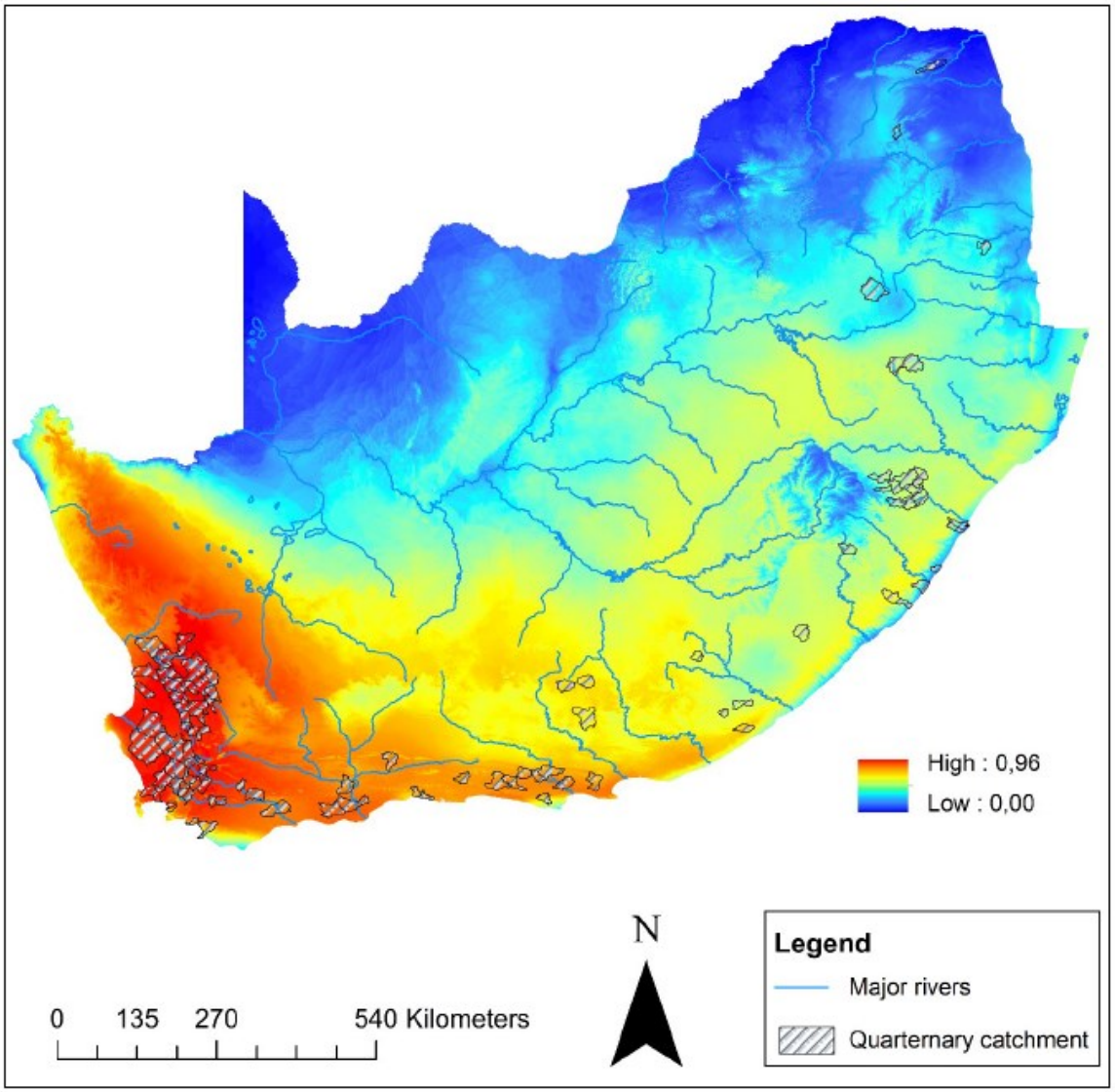


Figure S4.14.a. *Micropterus dolomieu* modelled distribution extracted from Khosa (2020).

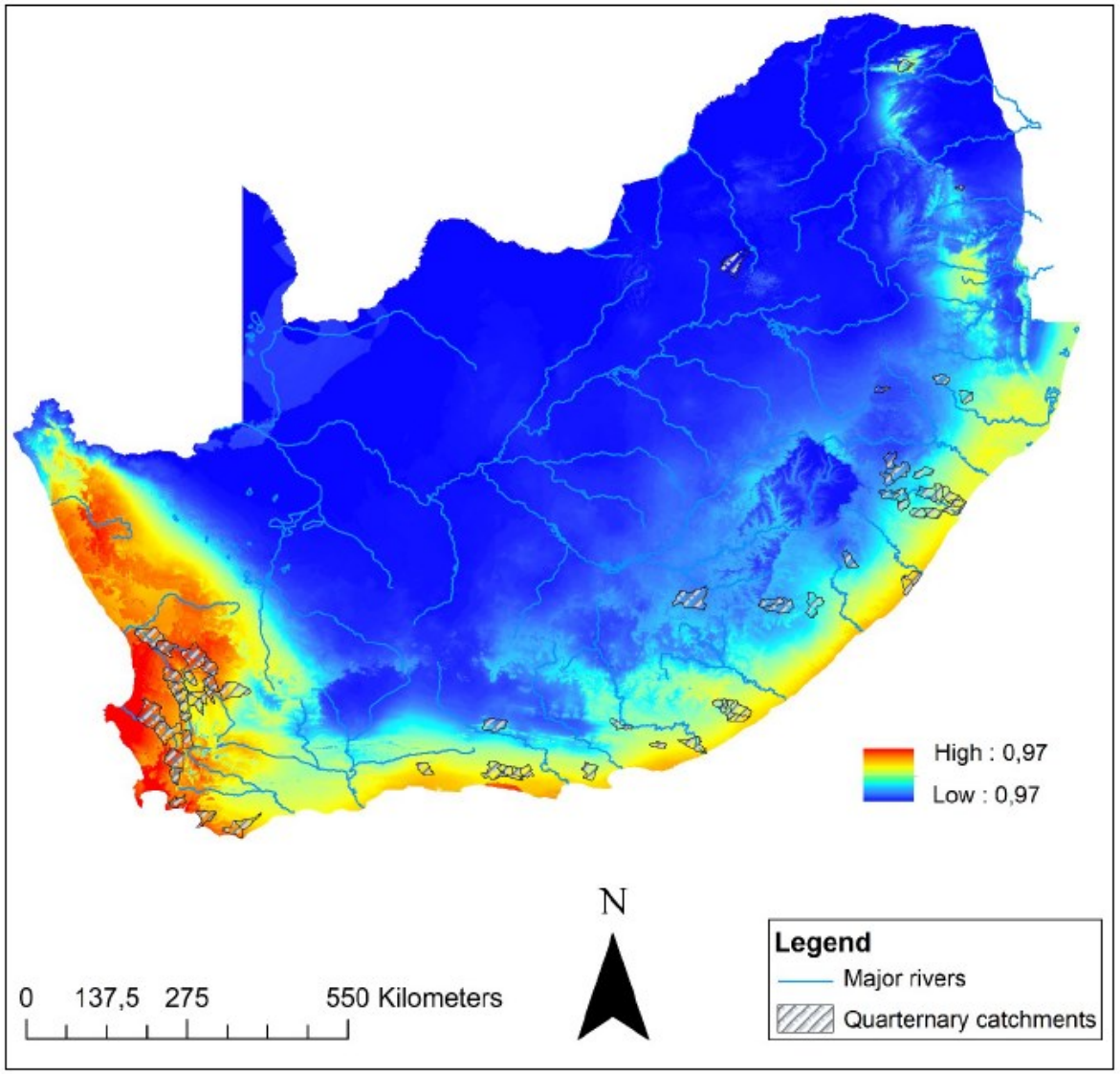


Figure S4.14.b. *Micropterus punctulatus* modelled distribution extracted from Khosa (2020).

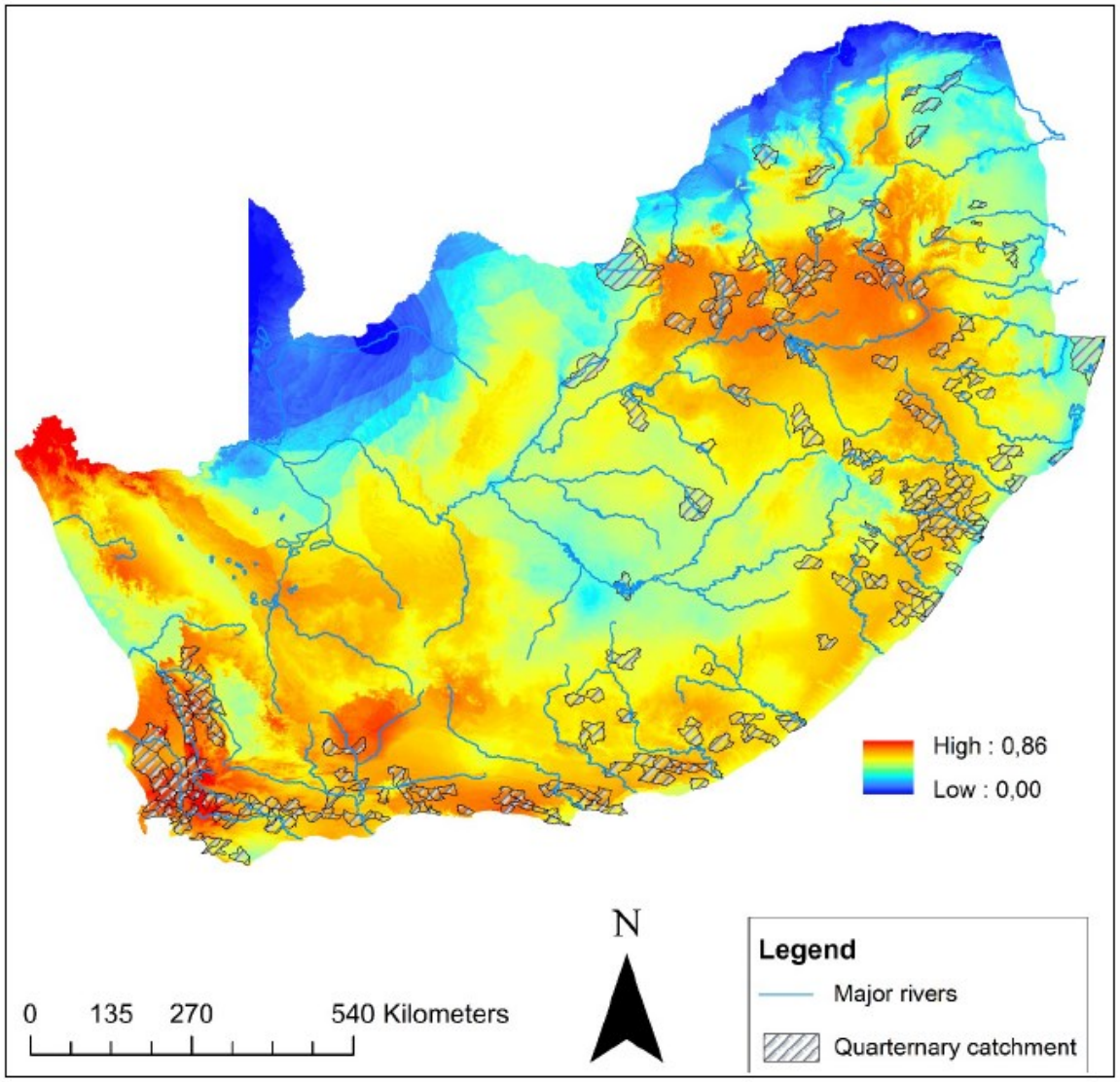
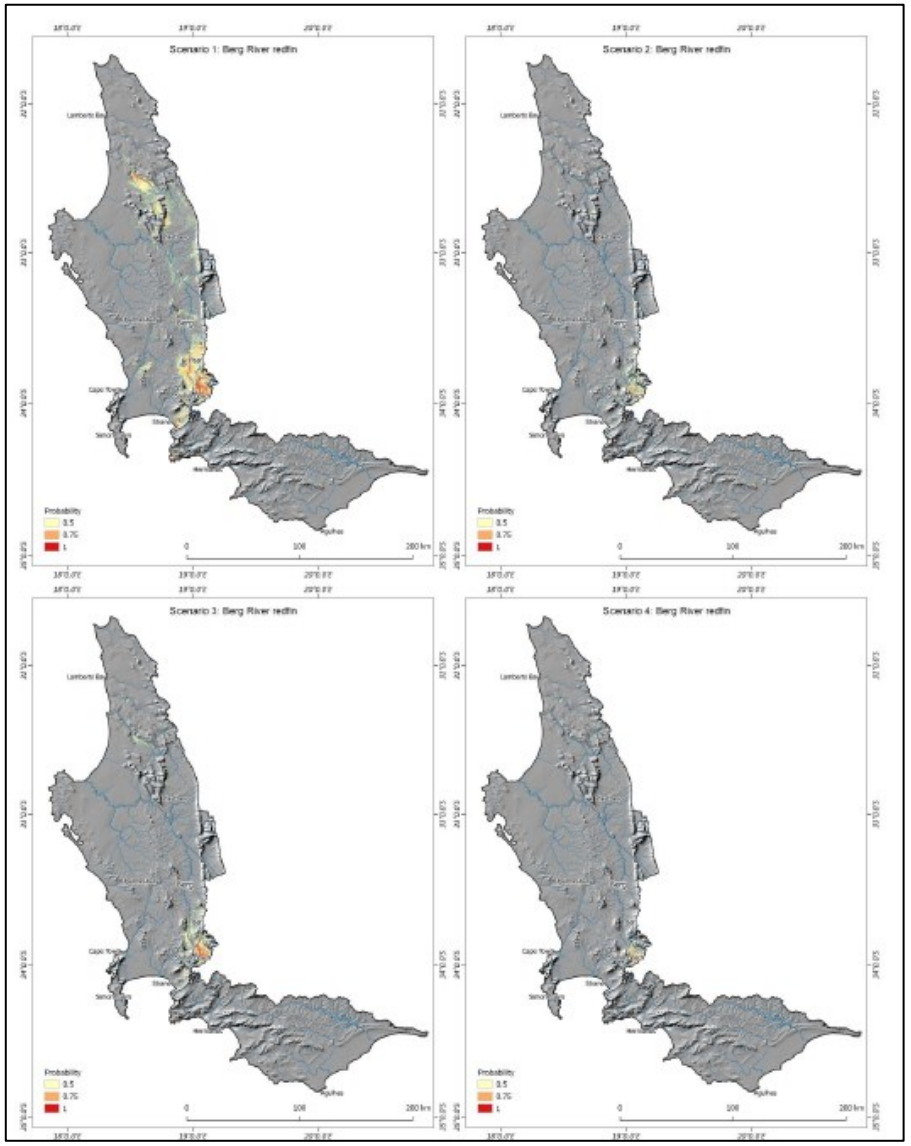


Figure S4.14.c. *Micropterus salmoides* modelled distribution extracted from Khosa (2020).

Supplementary S4.15. Modelled *Pseudobarbus burgi* distributions extracted from Dallas et al. (2017)



Supplementary S4.15.a. Predicted probabilities of occurrence for the Berg River redfin *Pseudobarbus burgi* for four scenarios. Warmer colours (orange and red) show areas predicted by the model to be more suitable for the species. Extracted from Dallas et al. (2017).

Supplementary S5

Table S5.1. List of freshwater fish experts included in data cleaning process.

#	Name	Organisation / Institution	Email Address
1	Dean Impson	Freshwater Research Centre / CapeNature	ndimpson@gmail.com
2	Albert Chakona	South African Institute for Aquatic Biodiversity	a.chakona@saiab.nrf.ac.za
3	Martine Jordaan	CapeNature	mjordaan@capenature.co.za
4	Bruce Paxton	Freshwater Research Centre	bruce@frcsa.org.za
5	Roger Bills	South African Institute for Aquatic Biodiversity	ir.bills@saiab.nrf.ac.za
6	Andre Hoffman	Mpumalanga Tourism and Parks Agency	27824125756@vodamail.co.za
7	Tsungai Zengeya	South African National Biodiversity Institute / University of Pretoria	t.zengeya@sanbi.org.za
8	Francious Roux	Mpumalanga Tourism and Parks Agency	hydrocynus@mweb.co.za
9	Jeremy Shelton	Freshwater Research Centr	jeremy@frcsa.org.za

Table S5.2. Data sources and number of records for freshwater fish data used in the NEST.

Reference Category	Source	Number of Records	Percentage Contribution	Total Number of Records	Percentage Contribution
Database	Global Biodiversity Information Facility (GBIF) -SAIAB	3016	45.29%	4866	73.06%
	Global Biodiversity Information Facility (GBIF) - iNaturalist	213	3.20%		
	Global Biodiversity Information Facility (GBIF) - Other	87	1.31%		
	Cape Nature State of Biodiversity Database	625	9.38%		
	South African National Parks Fish Database	331	4.97%		
	Limpopo Department of Environmental Affairs, Fish Database	227	3.41%		
	Rivers Database 2015	159	2.39%		
	Mpumalanga Tourism and Parks Agency	113	1.70%		
	Clean Stream Biological Services	38	0.57%		
	Department of Water and Sanitation Regional Fish Database	25	0.38%		
	Nepid fish database	16	0.24%		
	FRC monitoring database	13	0.20%		
	Ecotone Freshwater Consultants	3	0.05%		
Unpublished data	M Schumann	117	1.76%	284	4.26%
	Bruce Paxton	80	1.20%		
	Neels Kleynhans	14	0.21%		
	Albert Chakona	13	0.20%		
	Johan Engelbrecht	12	0.18%		
	Paul Fouche	7	0.11%		
	Andrew Deacon	6	0.09%		
	Andre Hoffman	5	0.08%		
	Francois Roux	5	0.08%		
	Mick Angliss	5	0.08%		
	Jeremy Shelton	4	0.06%		
	S. Lamberth	4	0.06%		
	Gerhard Diedericks	3	0.05%		

	Jim Cambray	3	0.05%		
	Dale Kindler	2	0.03%		
	Francois Roux & Andre Hoffman	2	0.03%		
	Francois Roux & Gerhard Diedericks	1	0.02%		
	Keir Lynch	1	0.02%		
Published Data	Published report or thesis	850	12.76%	850	12.76%
	Peer-reviewed scientific article	660	9.91%	660	9.91%

Table S5.3. Data contribution by different institutions and number of records for freshwater fish data used in the Department of Forestry, Fisheries, and Environment National Environmental Screening Tool.

Institution name	Number of Records	Percentage Contribution
The South African Institute for Aquatic Biodiversity	3227	48.45%
Cape Nature	629	9.44%
Freshwater Research Centre	613	9.20%
Department of Economic Development, Environment and Tourism Limpopo	279	4.19%
Council for Scientific and Industrial Research	243	3.65%
iNaturalist	213	3.20%
South African National Parks	169	2.54%
University of Pretoria	148	2.22%
Department of Water and Sanitation	119	1.79%
Department of Environment and Nature Conservation	117	1.76%
Ecosun	89	1.34%
Rhodes University	85	1.28%
University of Limpopo	66	0.99%
Stellenbosch University	54	0.81%
University of Venda	53	0.80%
Mpumalanga Parks Board	47	0.71%
University of Cape Town	45	0.68%
Mpumalanga Tourism and Parks Agency	41	0.62%
Clean Stream Biological Services	38	0.57%
South African Environment Observation Network	38	0.57%
University of Johannesburg	38	0.57%
Rivers Database 2015	33	0.50%
North-West University	25	0.38%
Golder Associates	24	0.36%
FishBase	23	0.35%
River Health Programme	19	0.29%
Nepid Consultants	14	0.21%
University of Stellenbosch	14	0.21%
Advance Africa Management Services	10	0.15%
University of South Africa	10	0.15%
Other	137	2.06%

Supplementary S5.4. Species distribution model outputs and distribution maps for threatened freshwater fishes occurring in South Africa.

Austroglanis barnardi

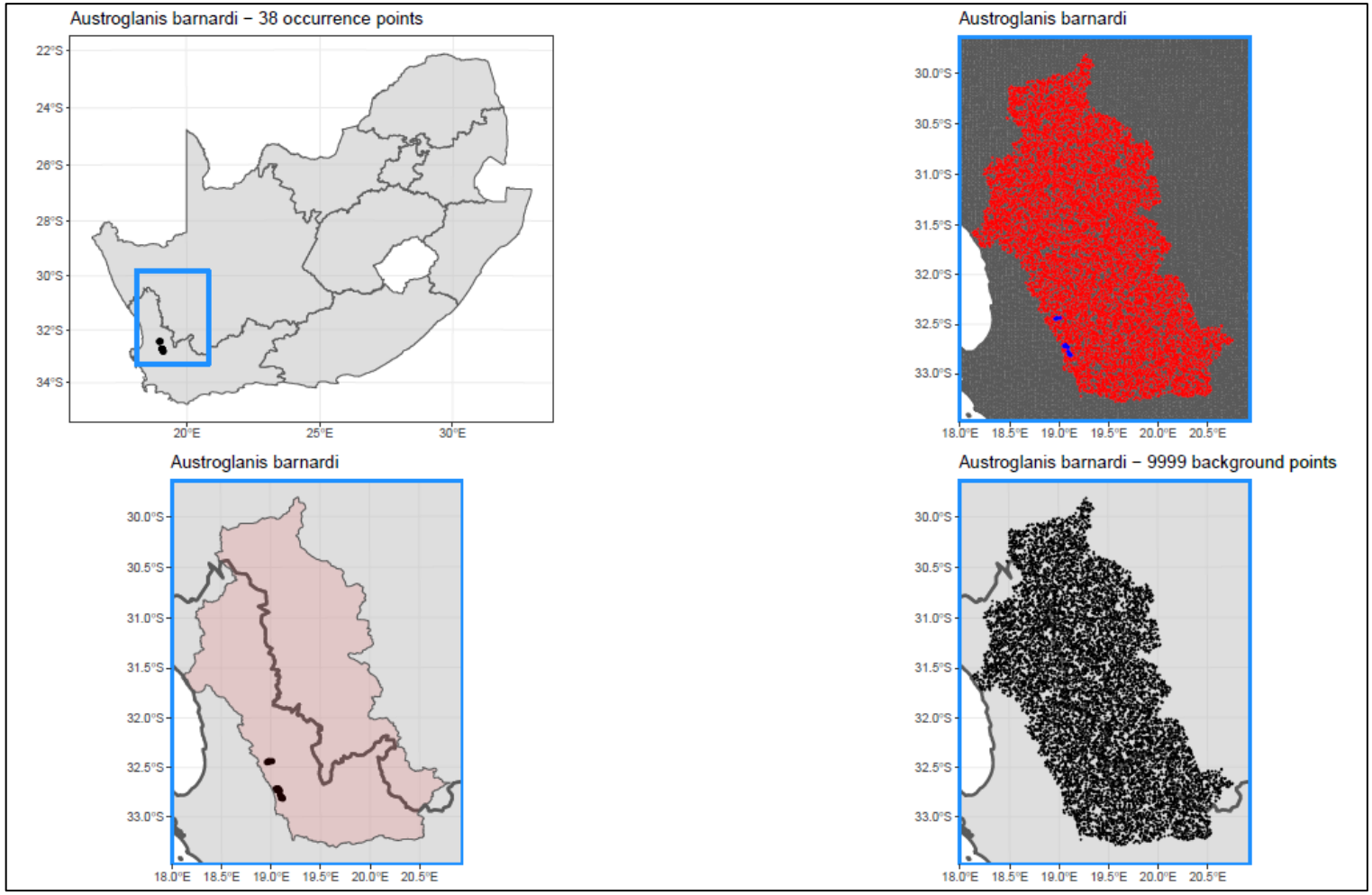


Figure S5.4.1. Occurrence records and background points for *Austroglanis barnardi.*

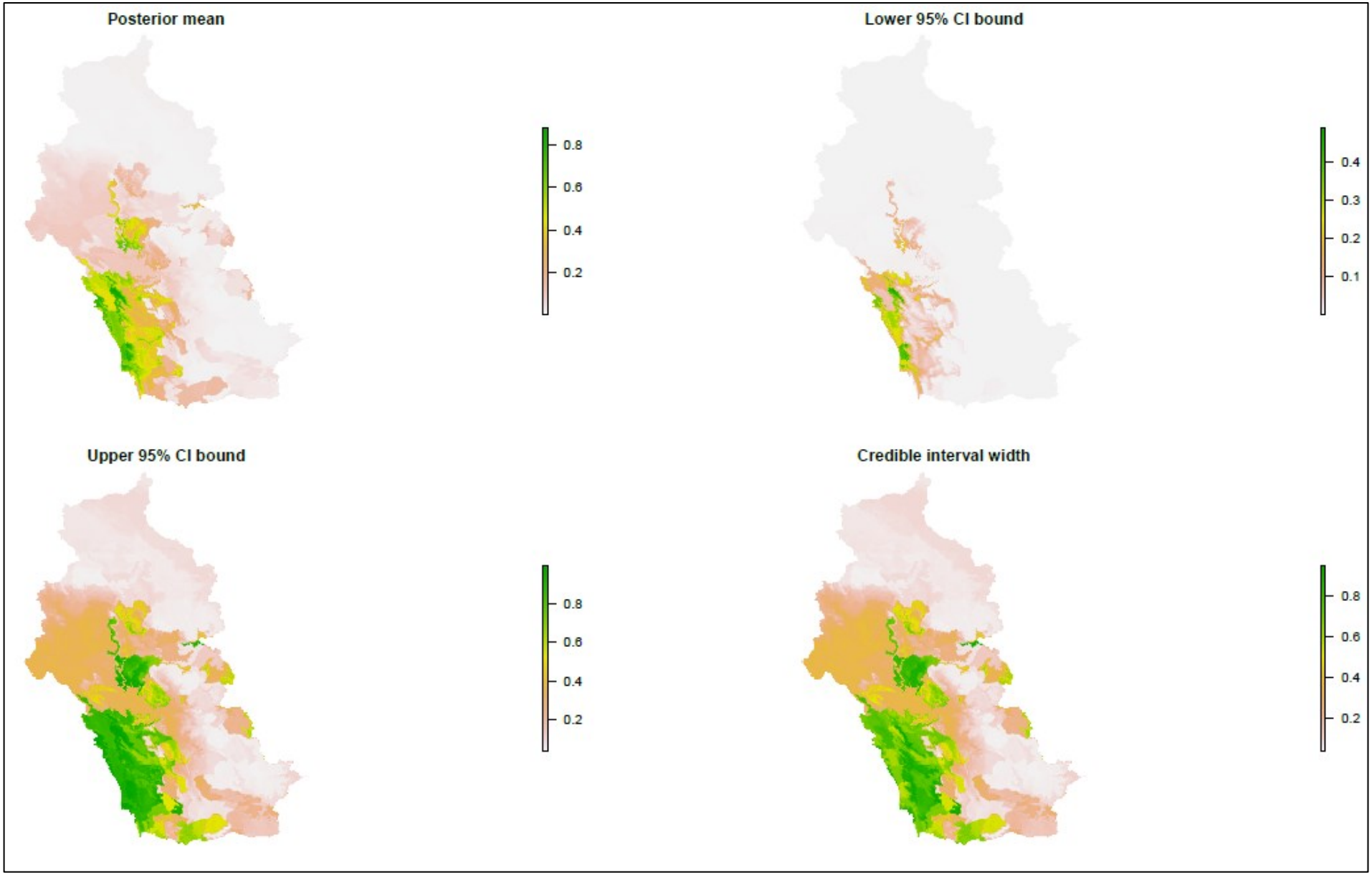


Figure S5.4.2. The modelled distribution of *Austroglanis barnardi* in South Africa showing habitat suitability.

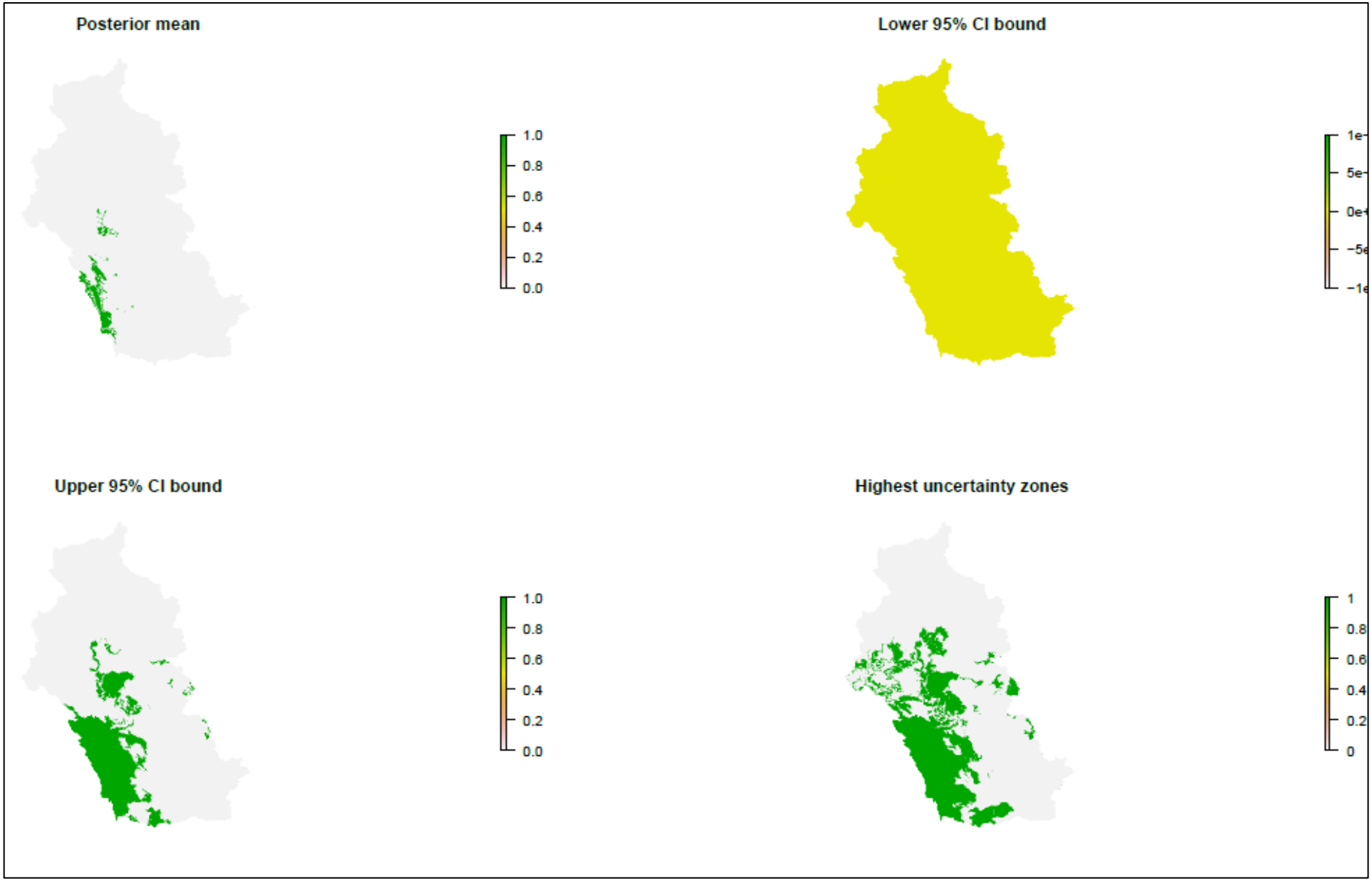


Figure S5.4.3. The modelled distribution of *Austroglanis barnardi* in South Africa showing predicted distribution as a binary output.

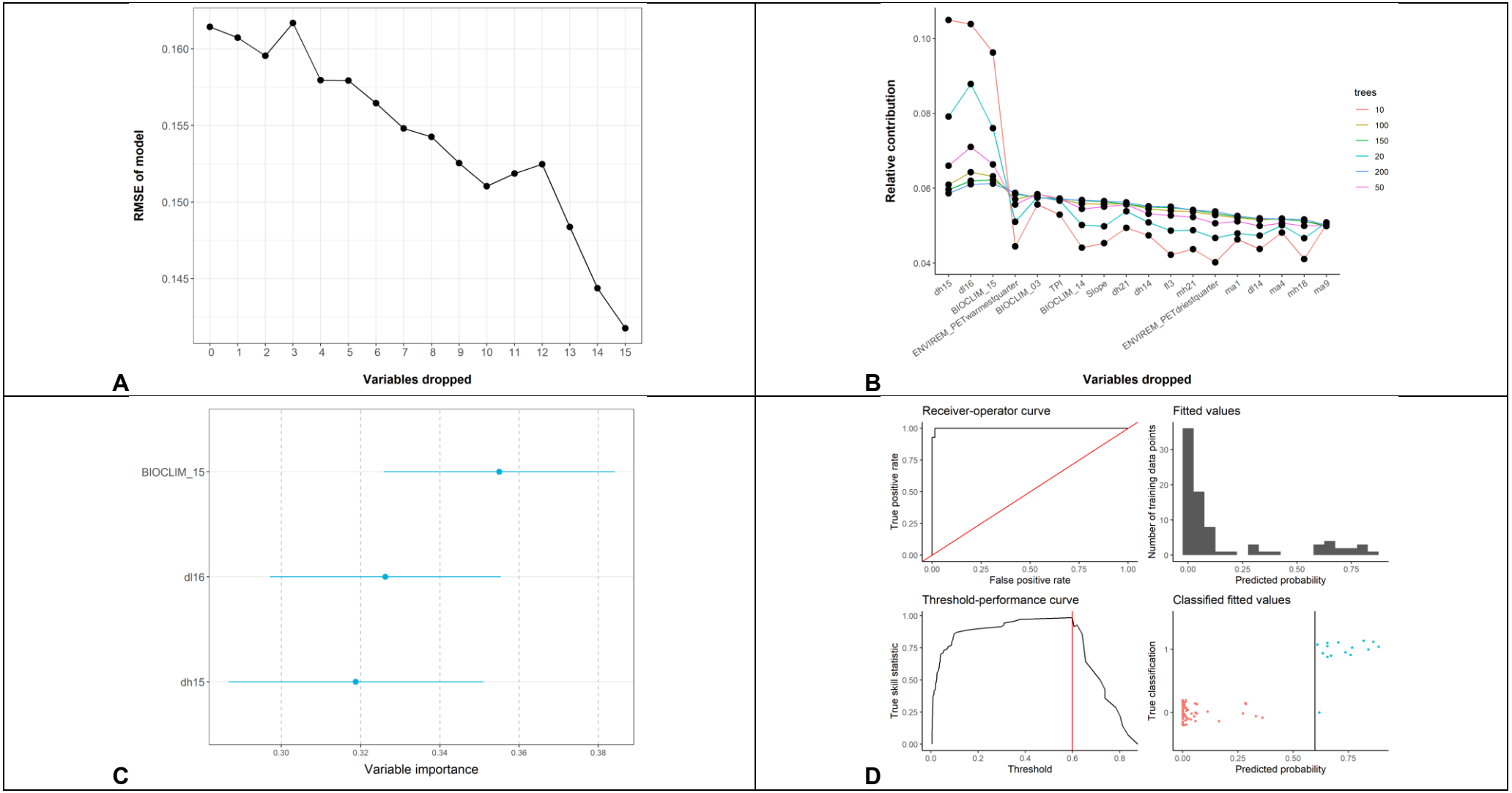


Figure S5.4.4. Model diagnostic outputs for *Austroglanis barnardi*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

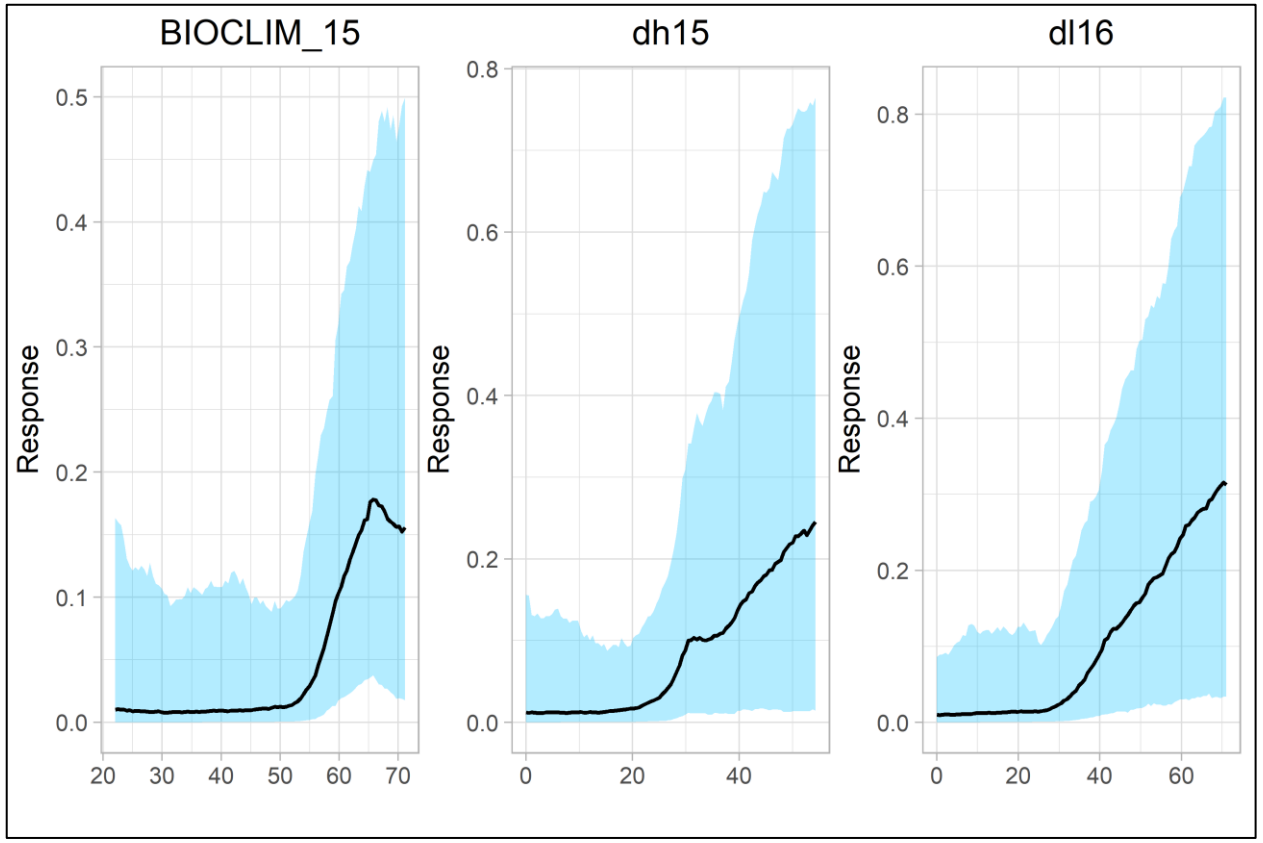


Figure S5.4.5. Partial dependence plots for *Austroglanis barnardi.*

Chetia brevis

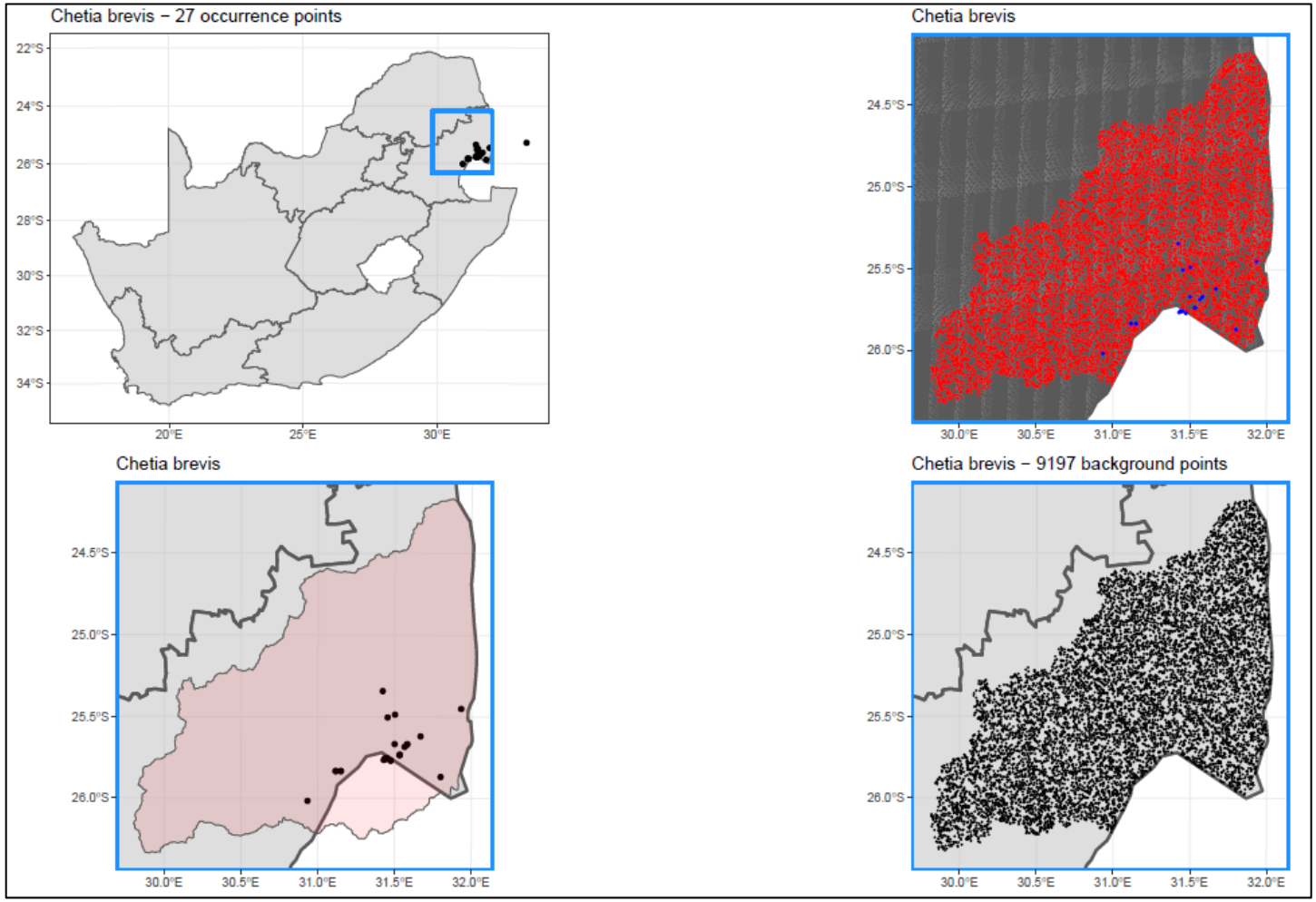


Figure S5.4.6. Occurrence records and background points for *Chetia brevis*.

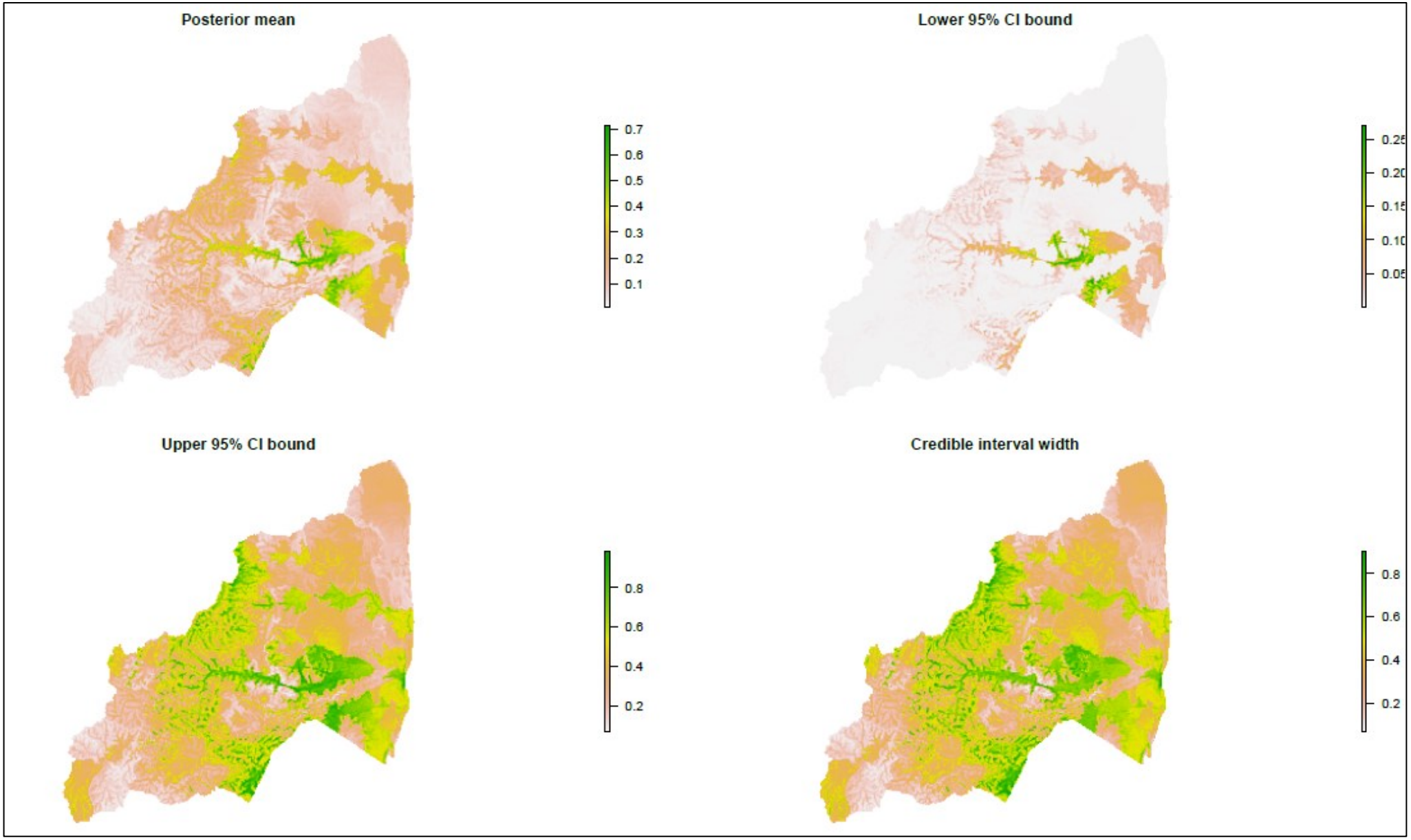


Figure S5.4.7. The modelled distribution of *Chetia brevis* in South Africa showing habitat suitability.

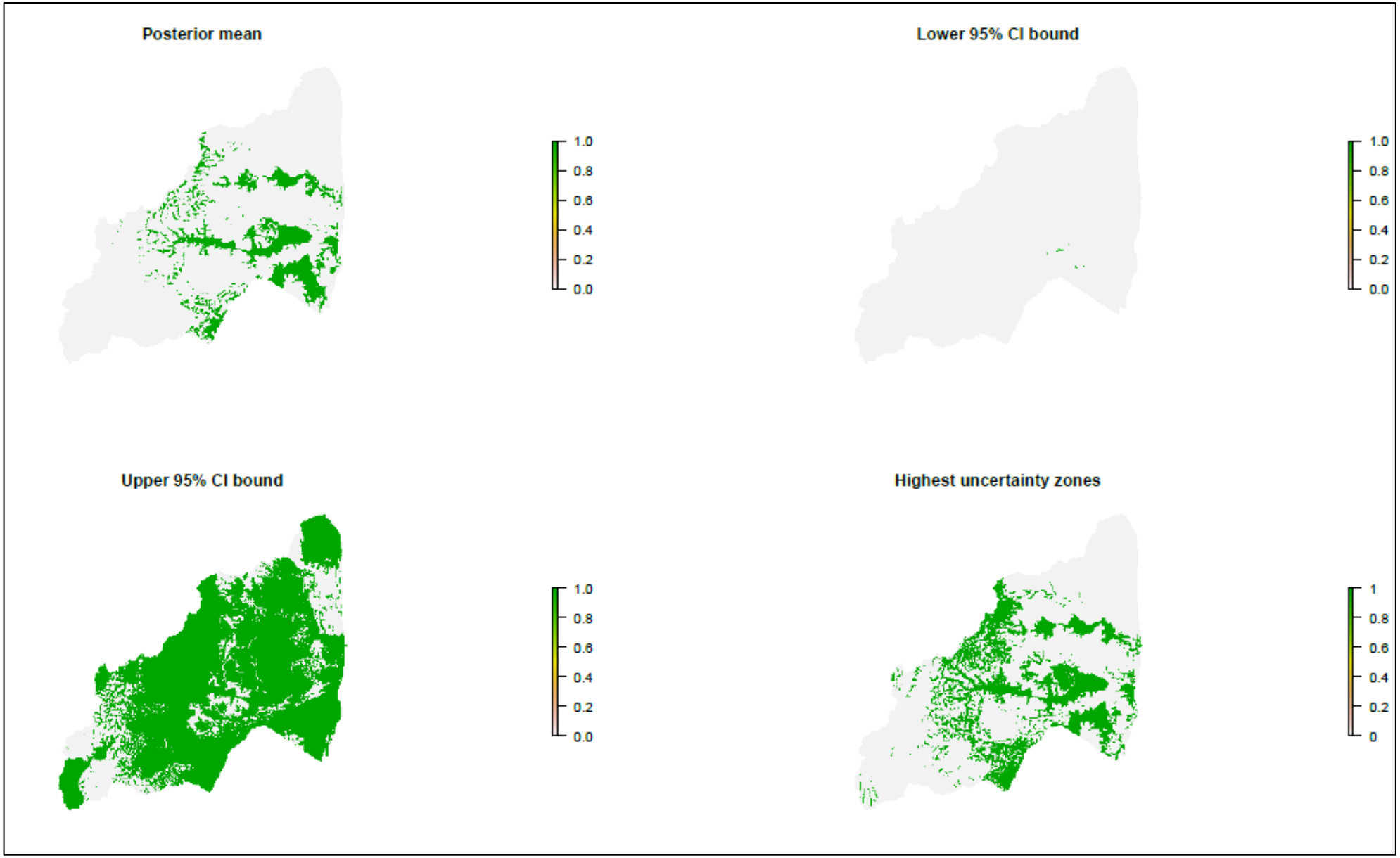


Figure S5.4.8. The modelled distribution of *Chetia brevis* in South Africa showing predicted distribution as a binary output.

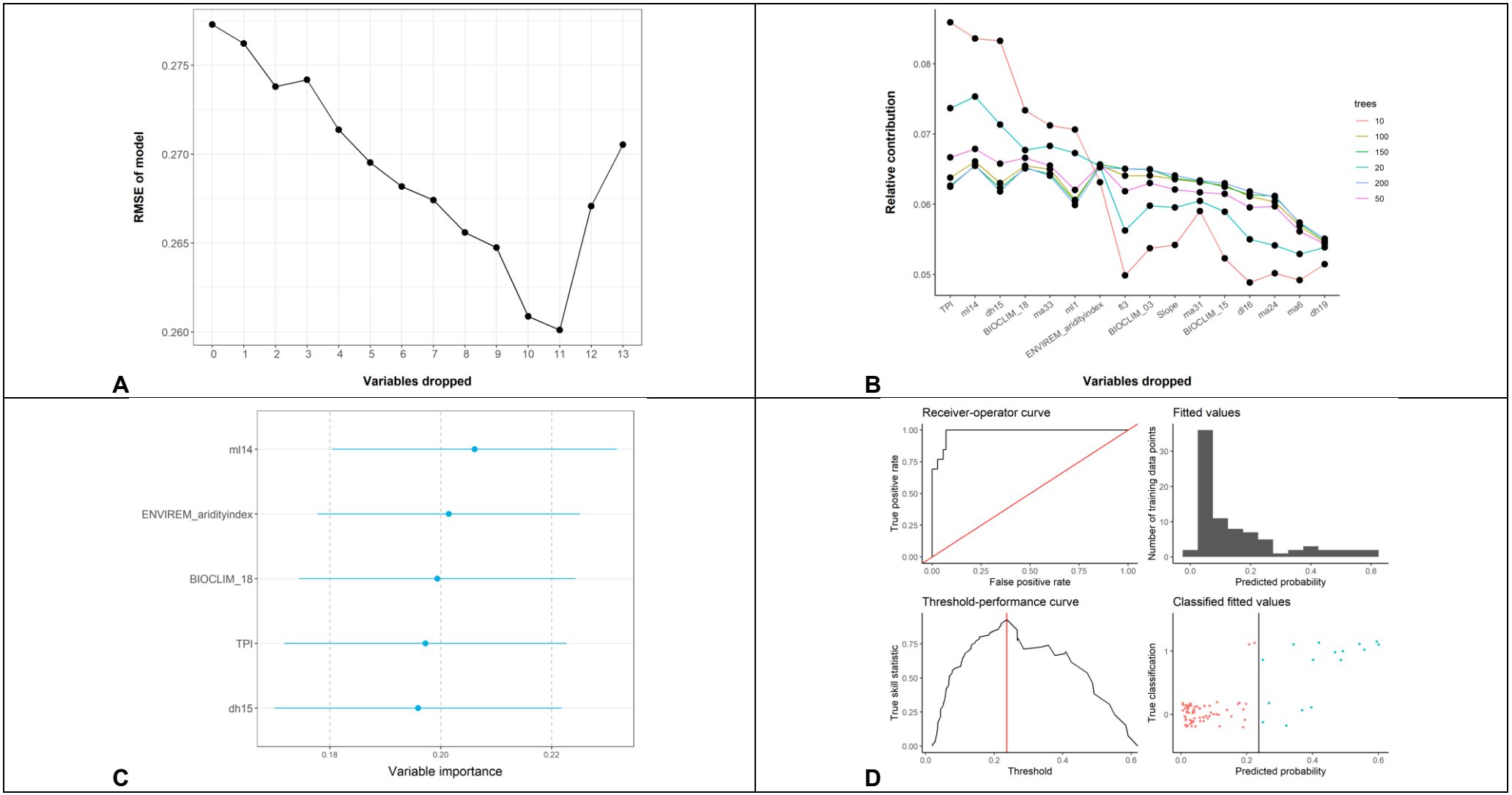


Figure S5.4.9. Model diagnostic outputs for *Chetia brevis*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

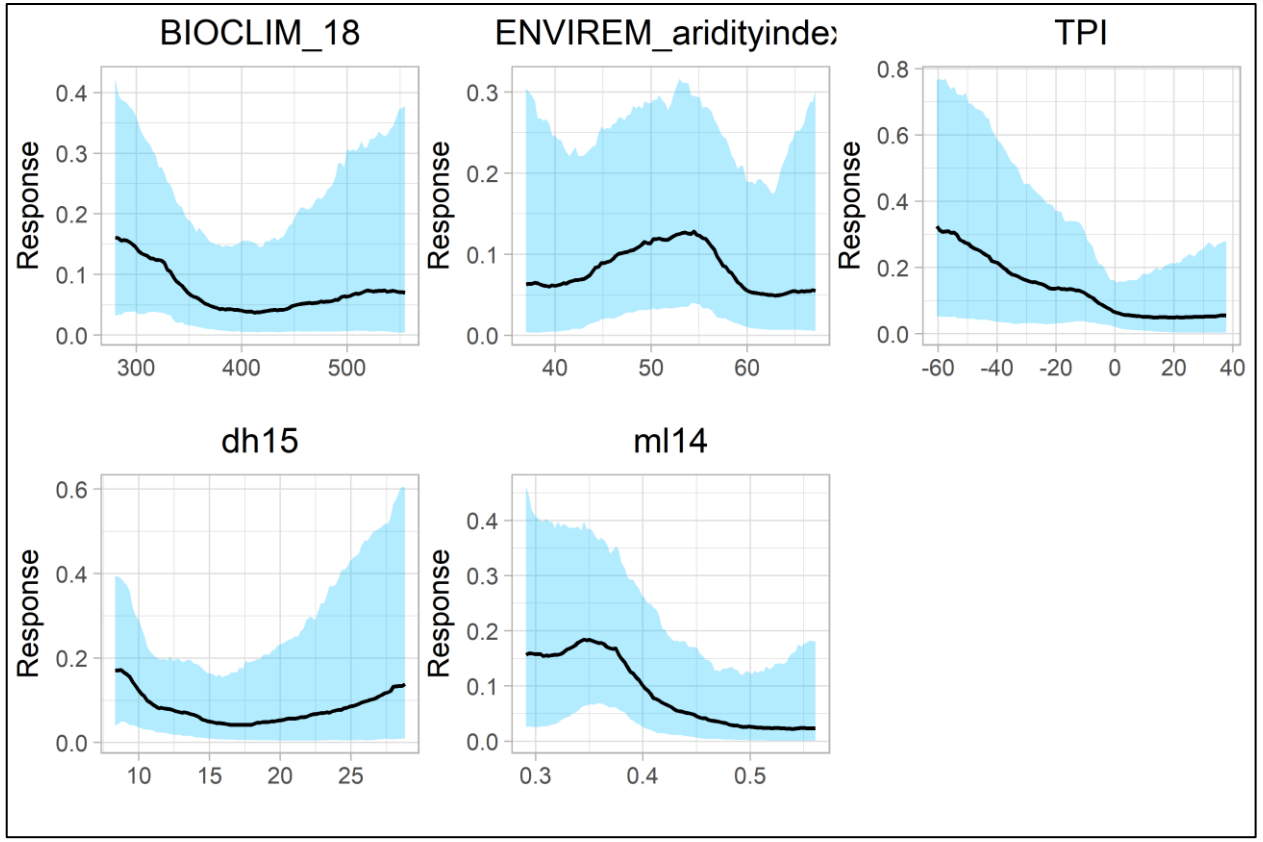


Figure S5.4.10. Partial dependence plots for *Chetia brevis.*

Chiloglanis bifurcus

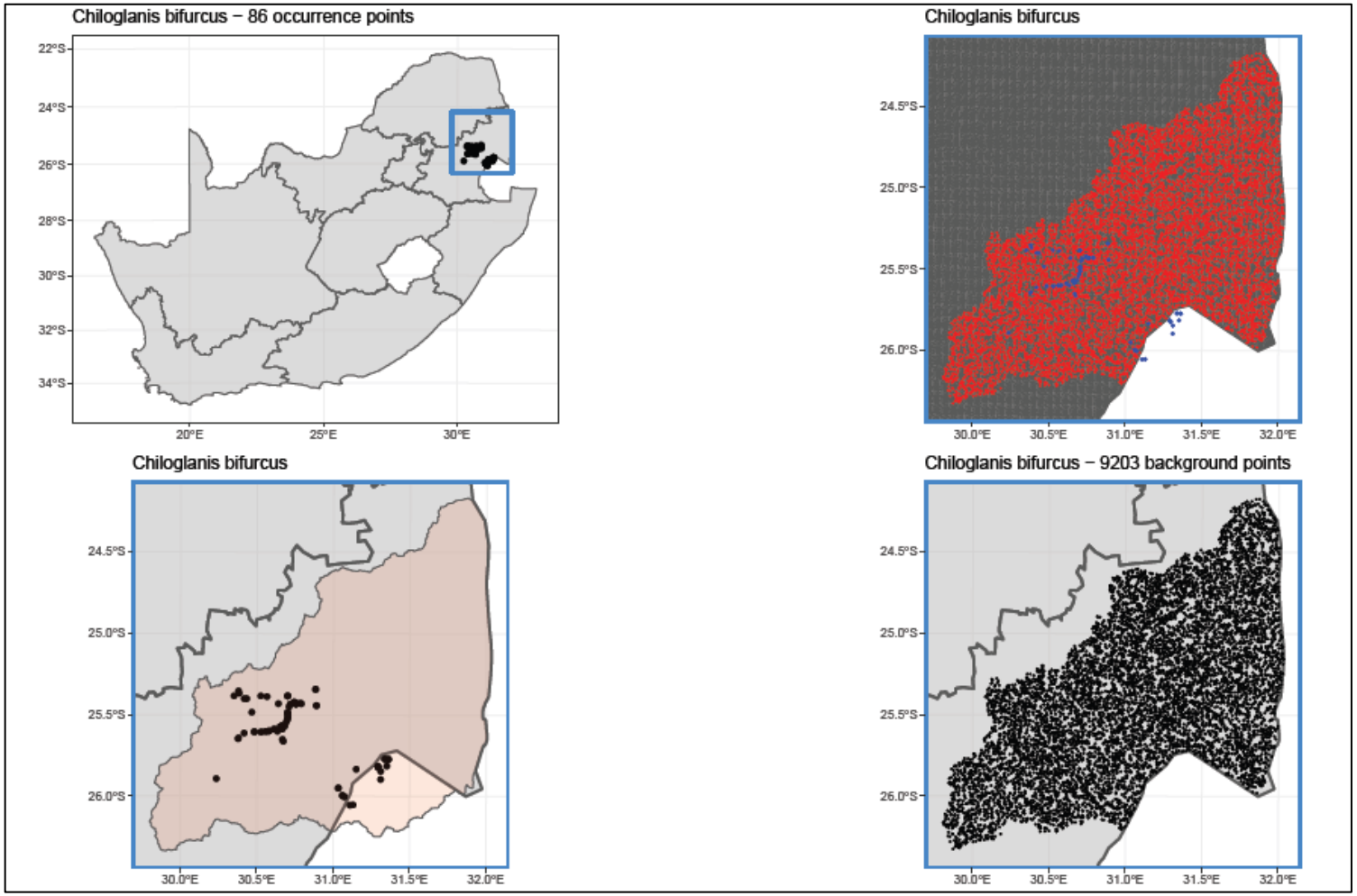


Figure S5.4.11. Occurrence records and background points for *Chiloglanis bifurcus.*

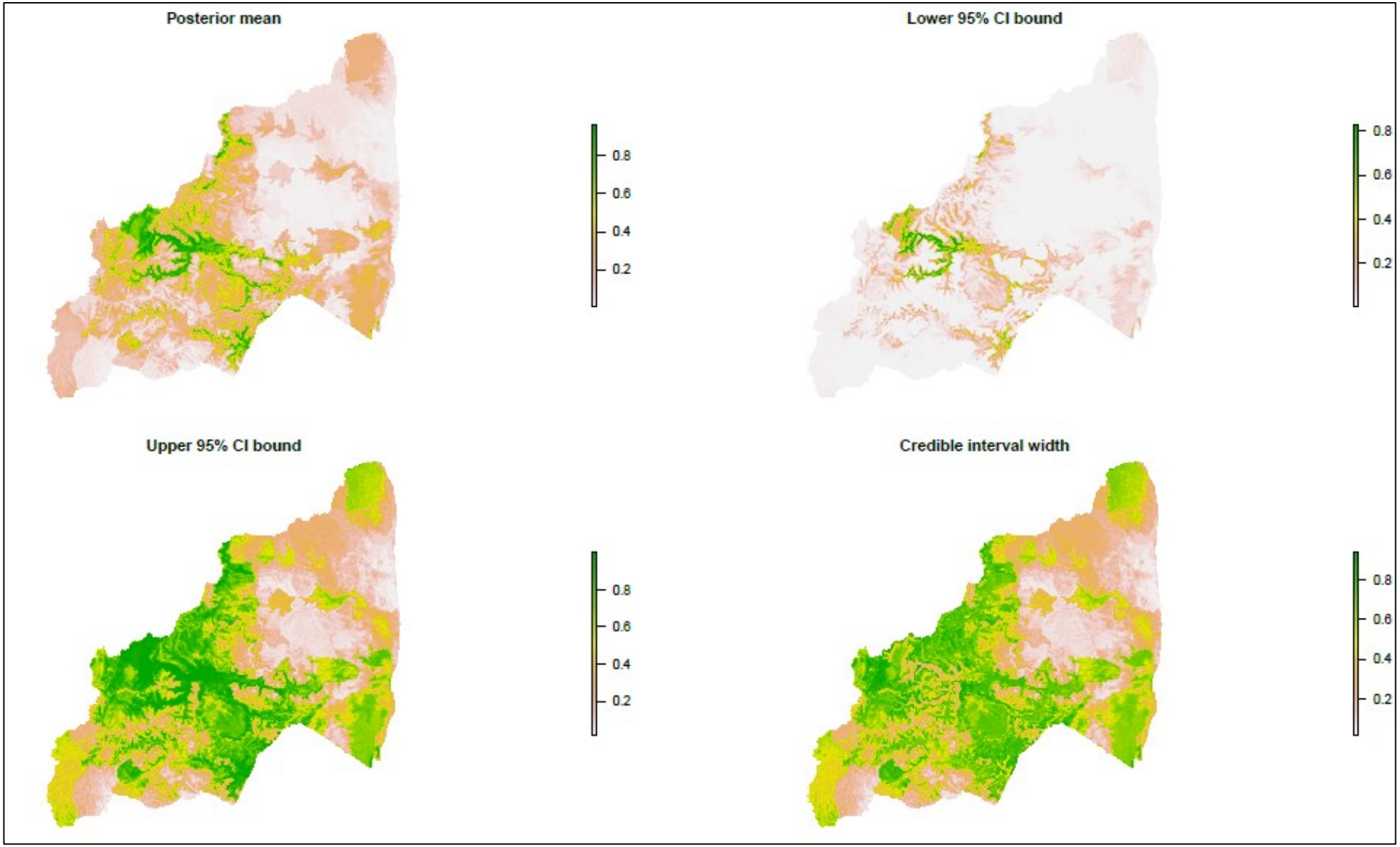


Figure S5.4.12. The modelled distribution of *Chiloglanis bifurcus* in South Africa showing habitat suitability.

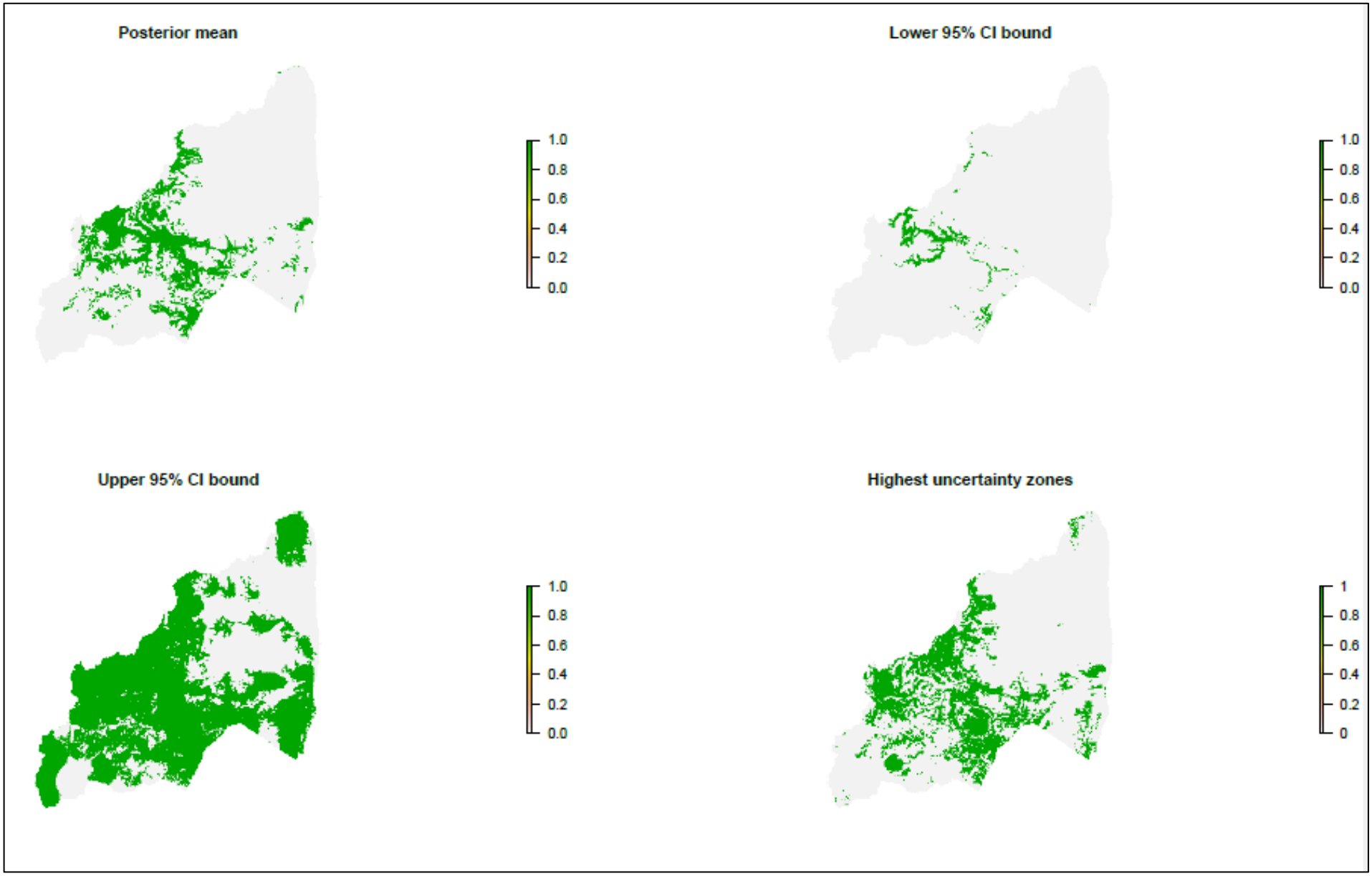


Figure S5.4.13. The modelled distribution of *Chiloglanis bifurcus* in South Africa showing predicted distribution as a binary output.

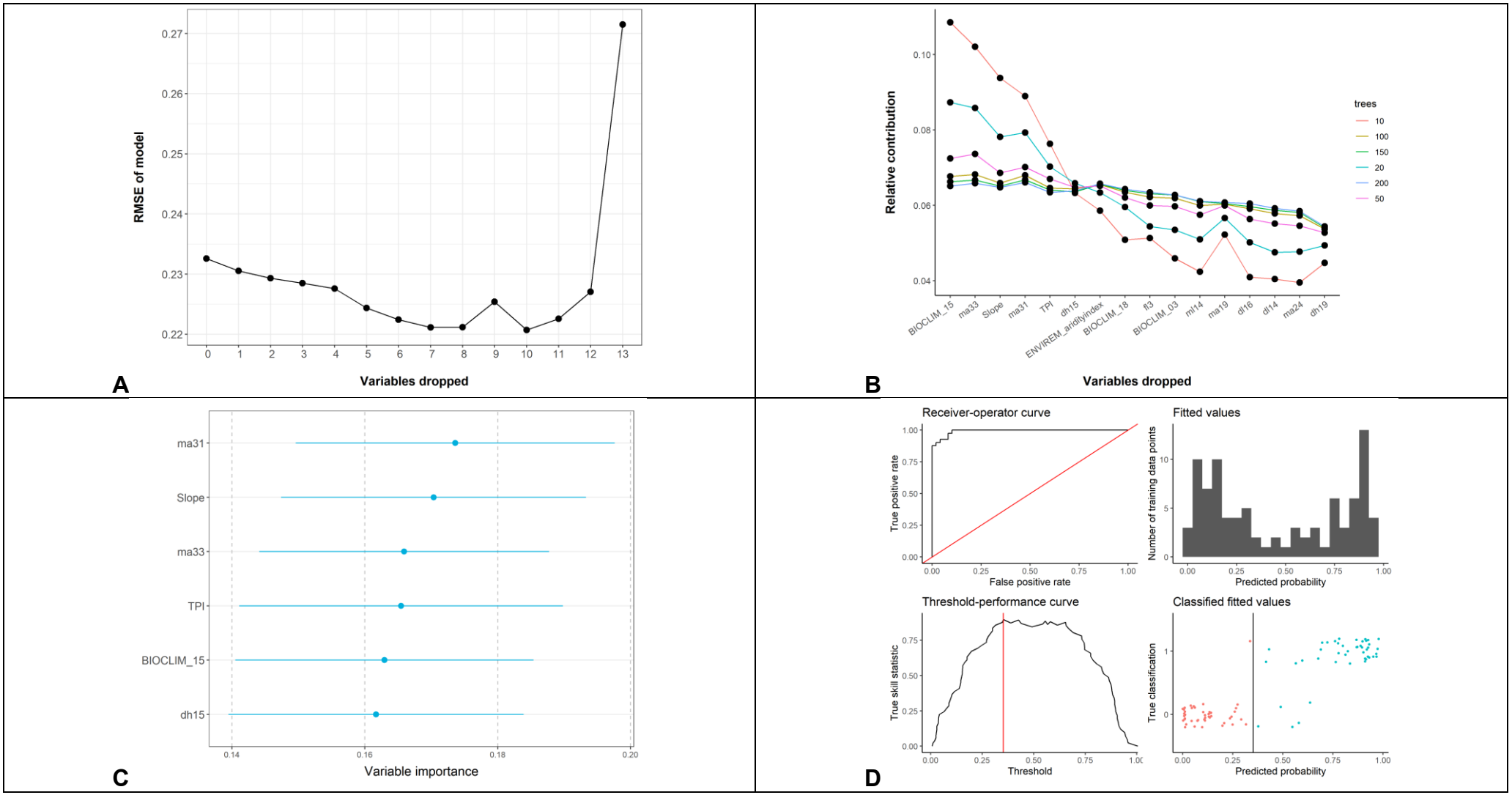


Figure S5.4.14. Model diagnostic outputs for *Chiloglanis bifurcus*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

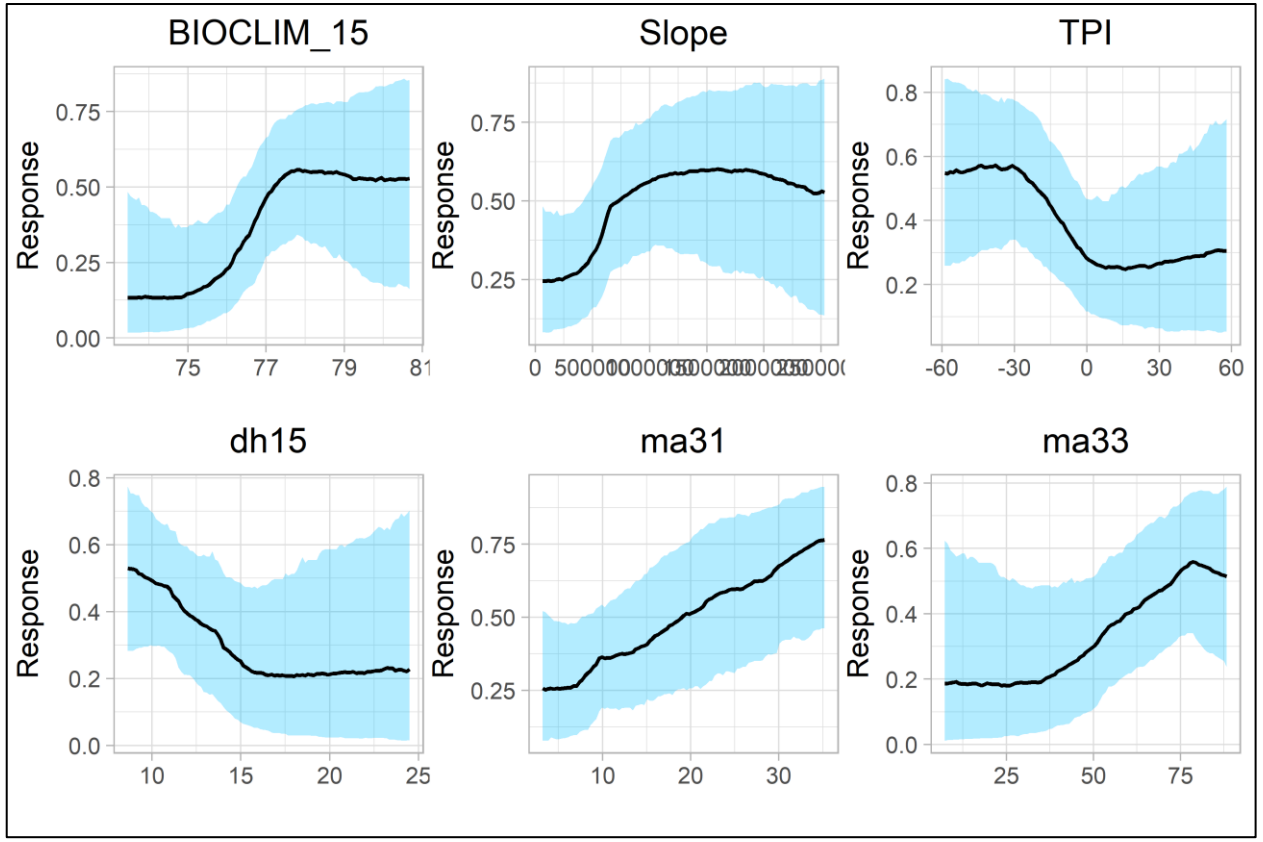


Figure S5.4.15. Partial dependence plots for *Chiloglanis bifurcus*.

Chiloglanis emarginatus

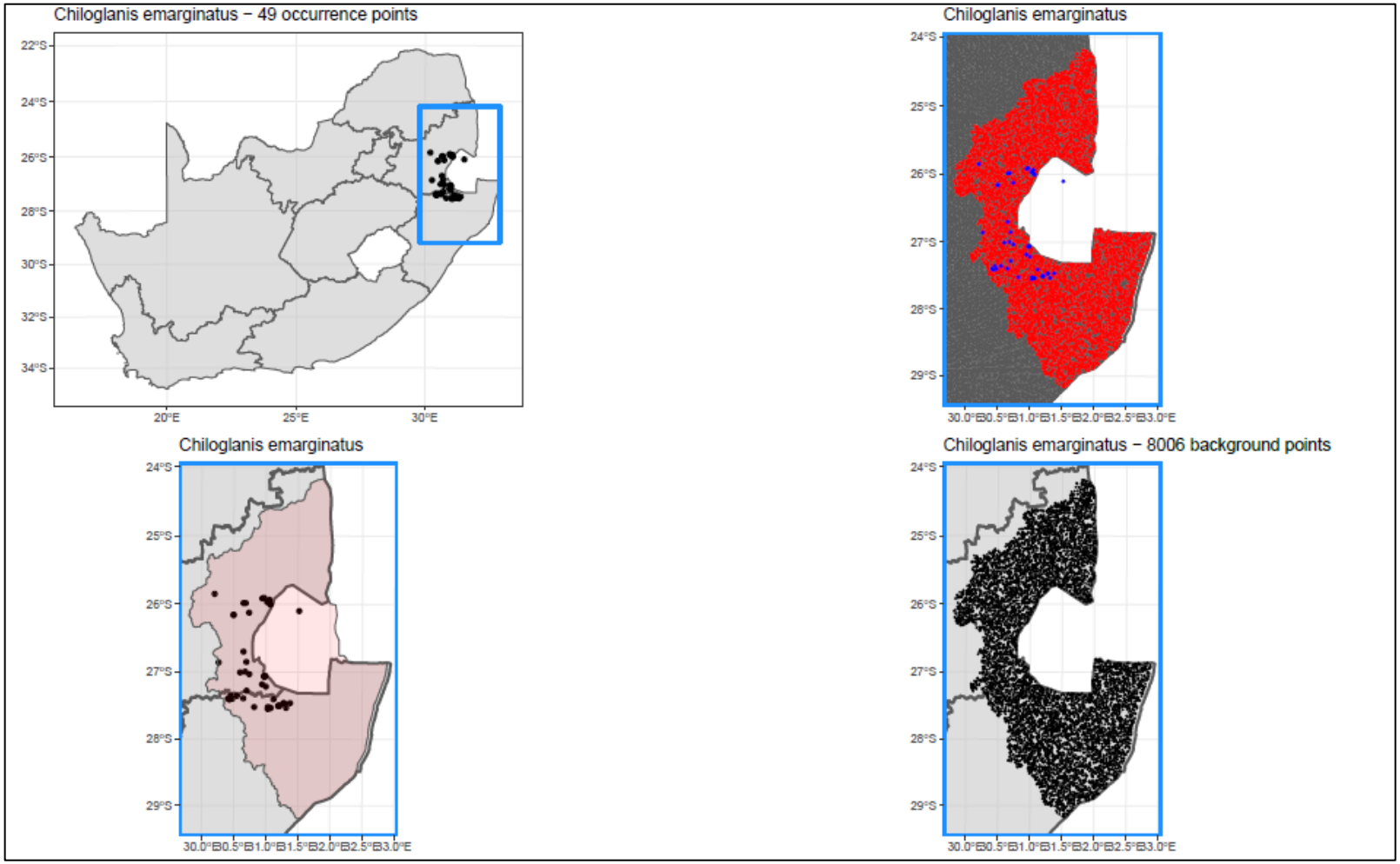


Figure S5.4.16. Occurrence records and background points for *Chiloglanis emarginatus.*

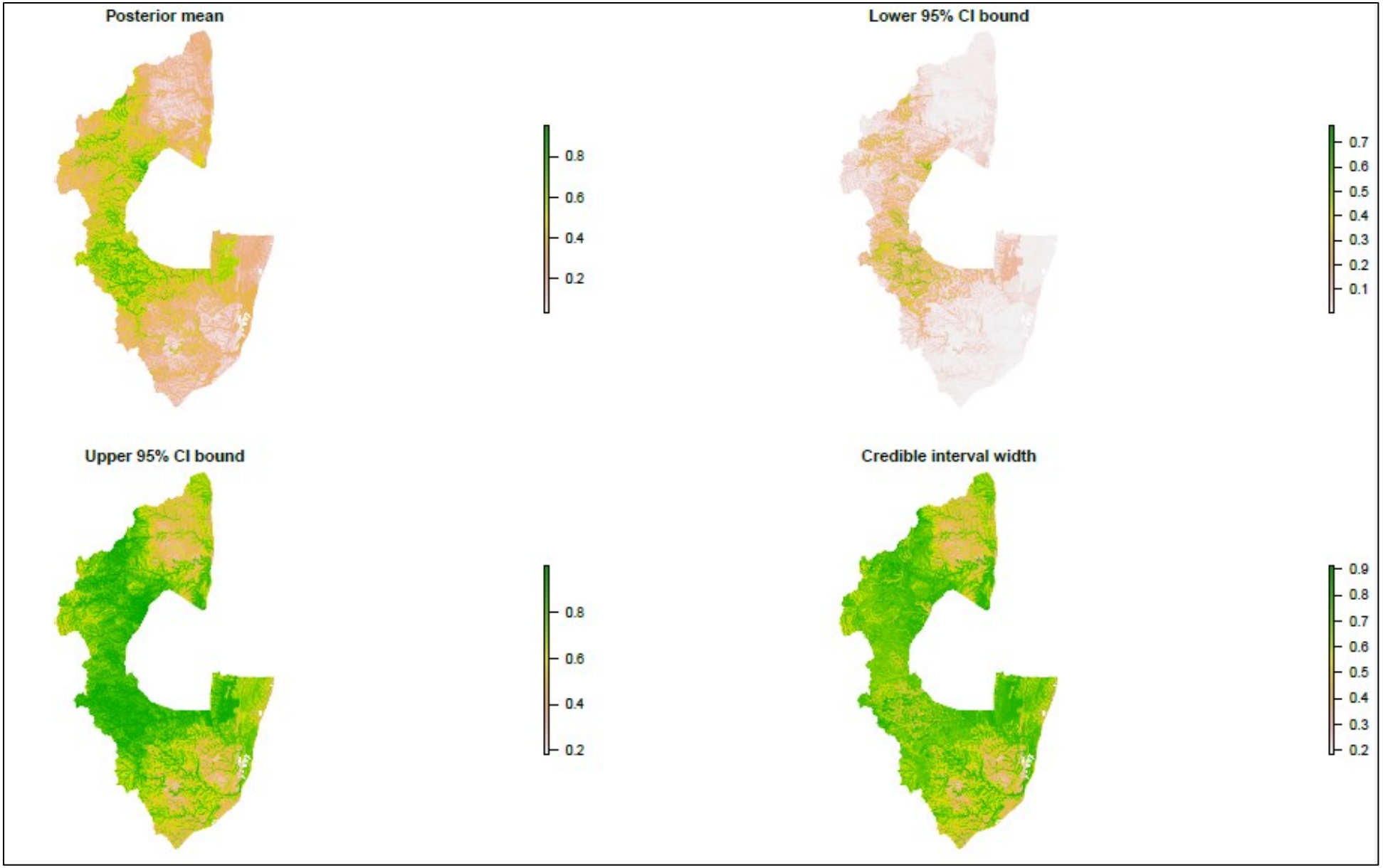


Figure S5.4.17. The modelled distribution of *Chiloglanis emarginatus* in South Africa showing habitat suitability.

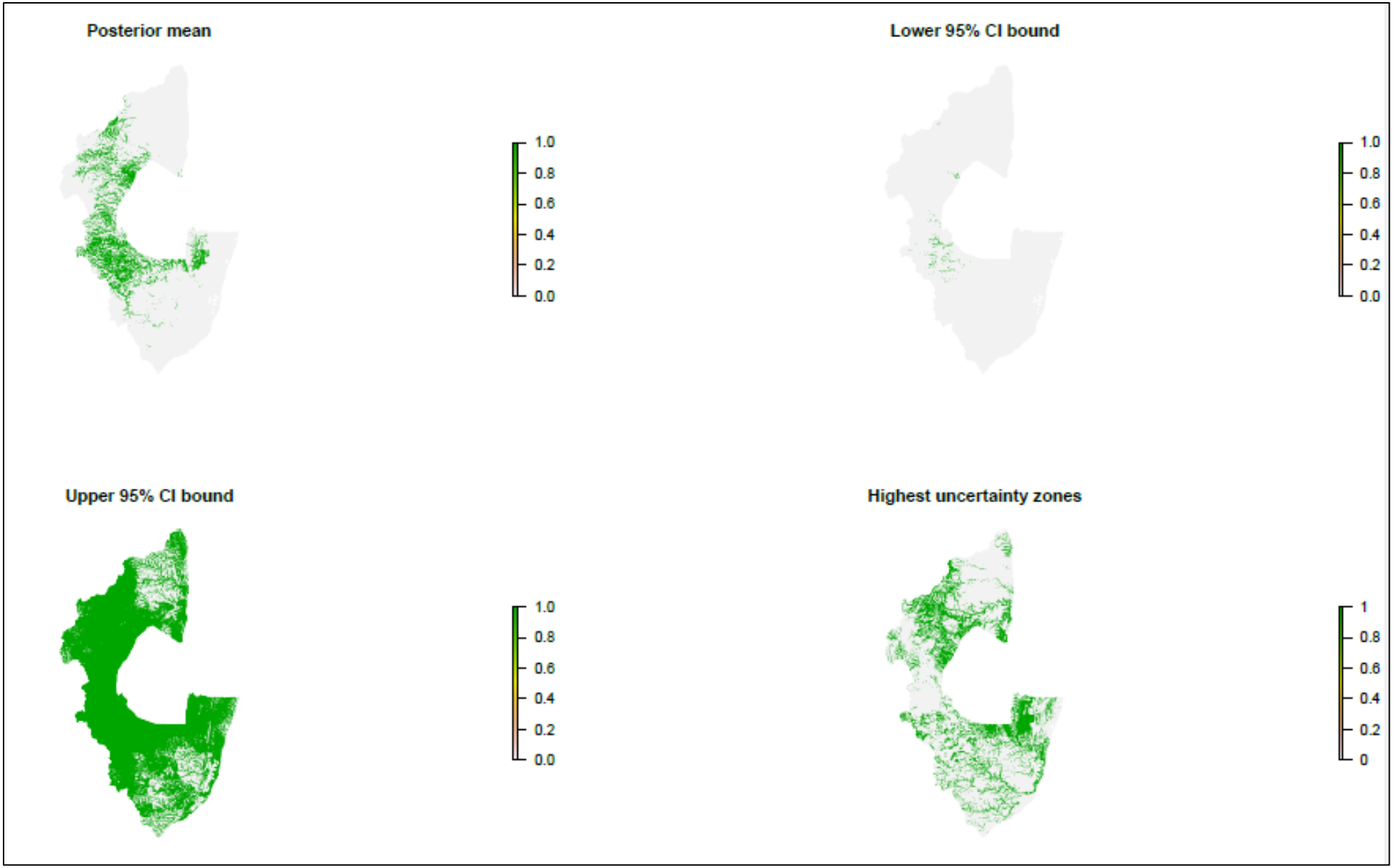


Figure S5.4.18. The modelled distribution of *Chiloglanis emarginatus* in South Africa showing predicted distribution as a binary output.

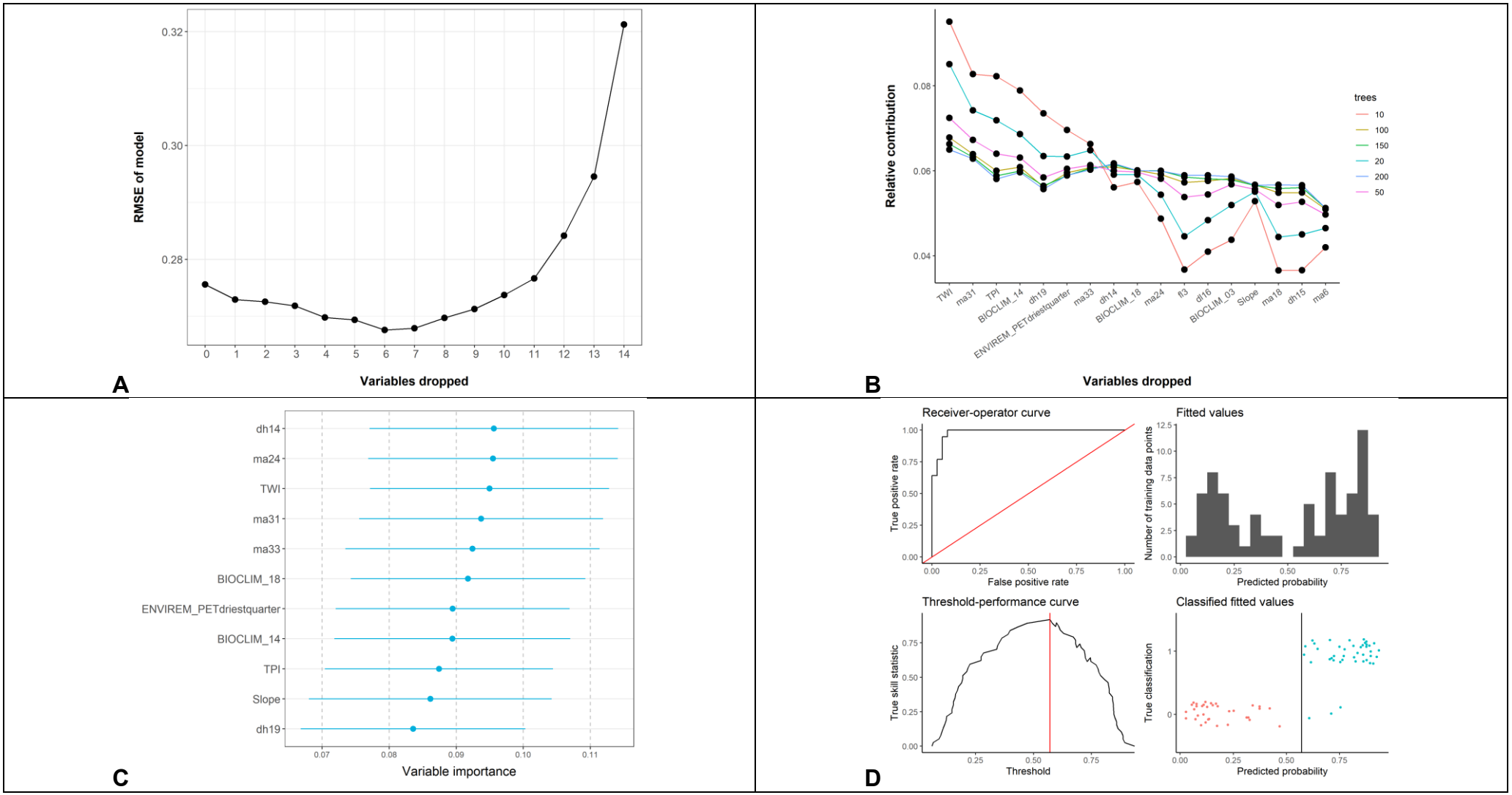


Figure S5.4.19. Model diagnostic outputs for *Chiloglanis emarginatus*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

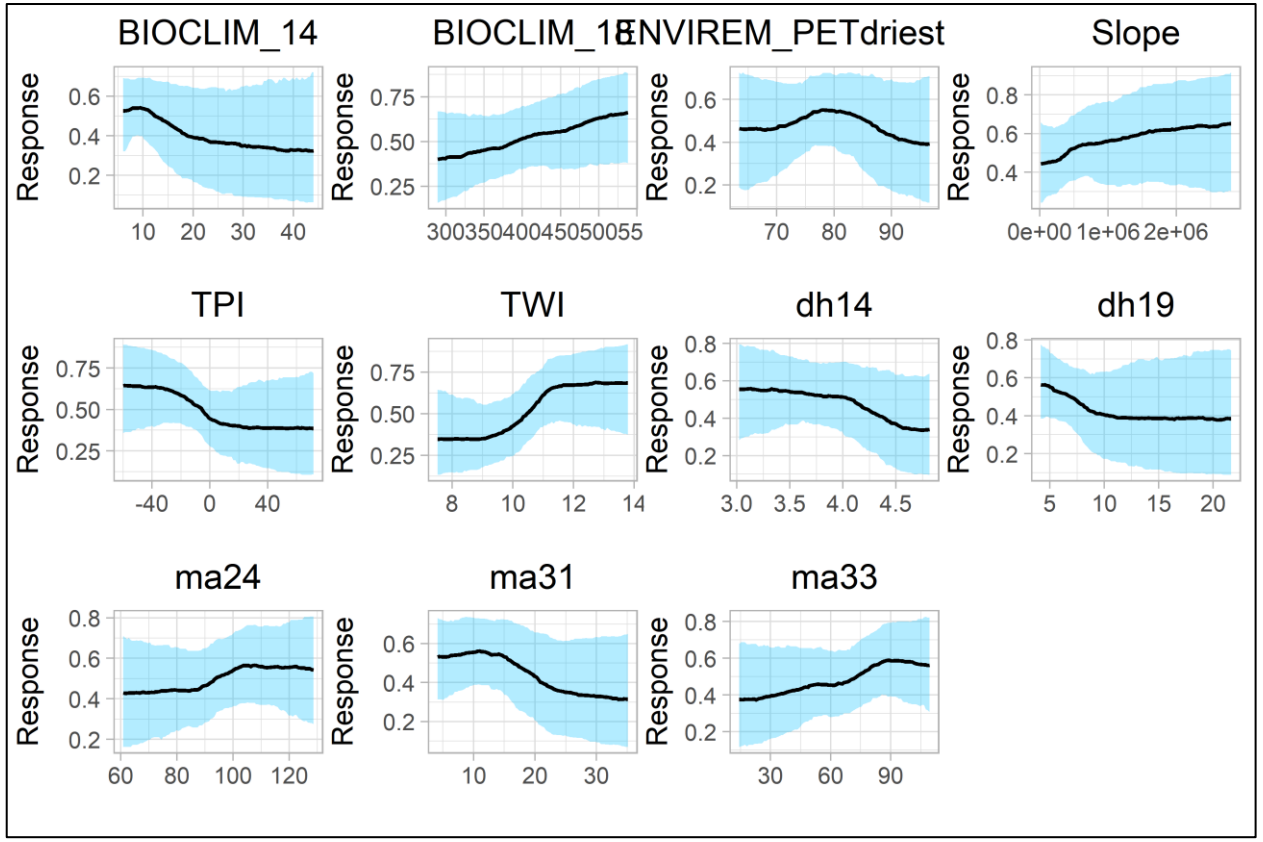


Figure S5.4.20. Partial dependence plots for *Chiloglanis emarginatus.*

Ctenopoma multispine

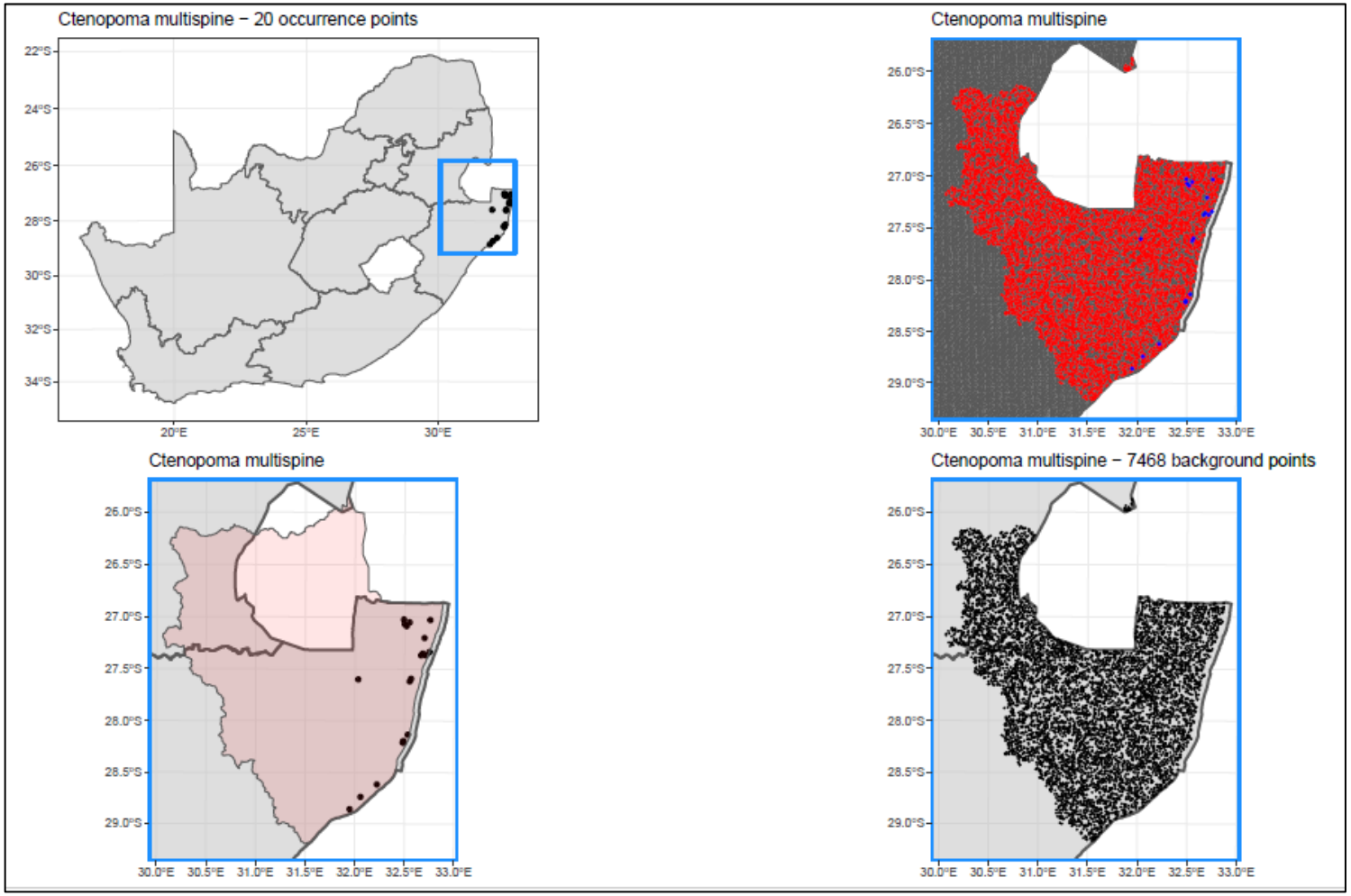


Figure S5.4.21. Occurrence records and background points for *Ctenopoma multispine*.

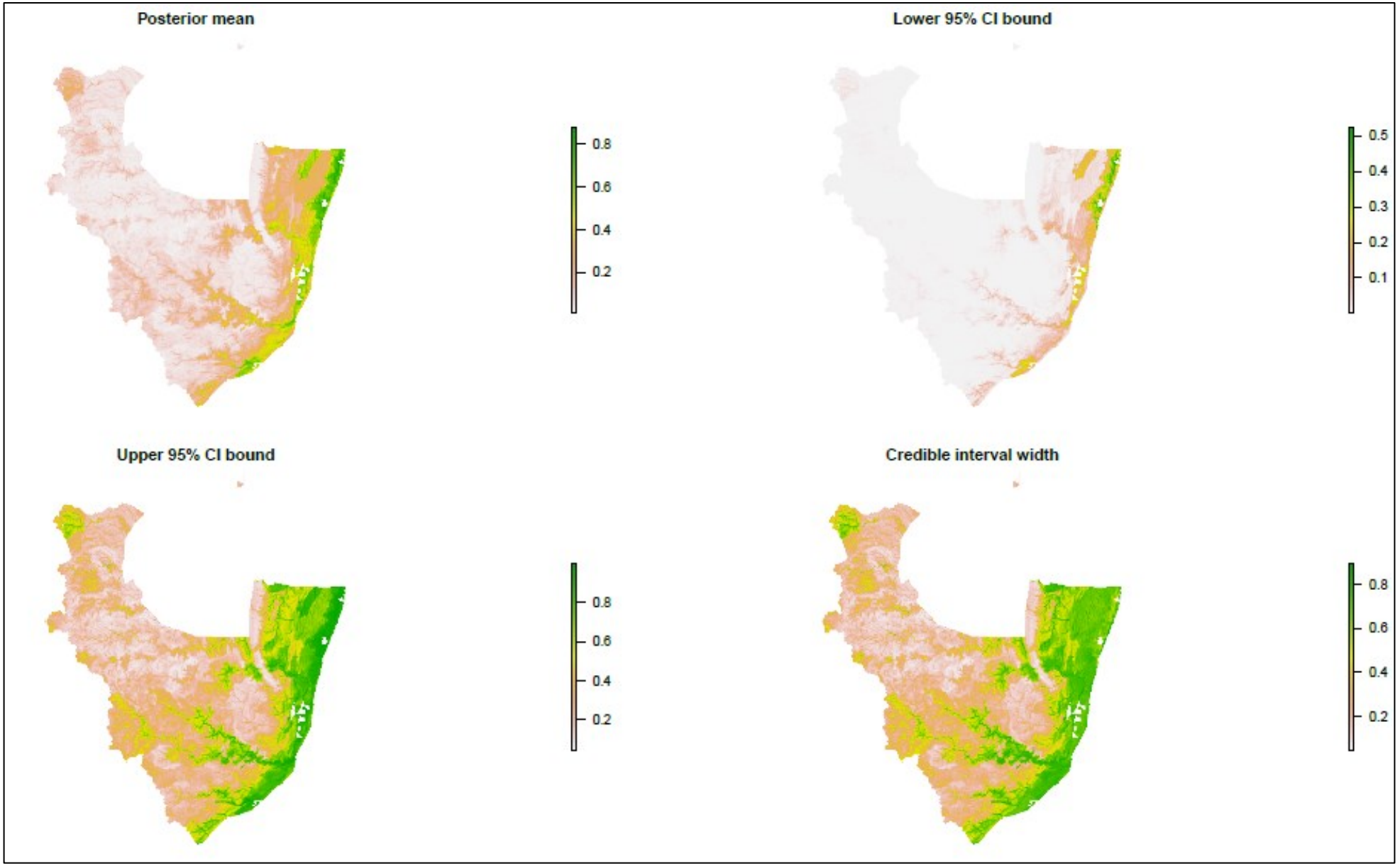


Figure S5.4.22. The modelled distribution of *Ctenopoma multispine* in South Africa showing habitat suitability.

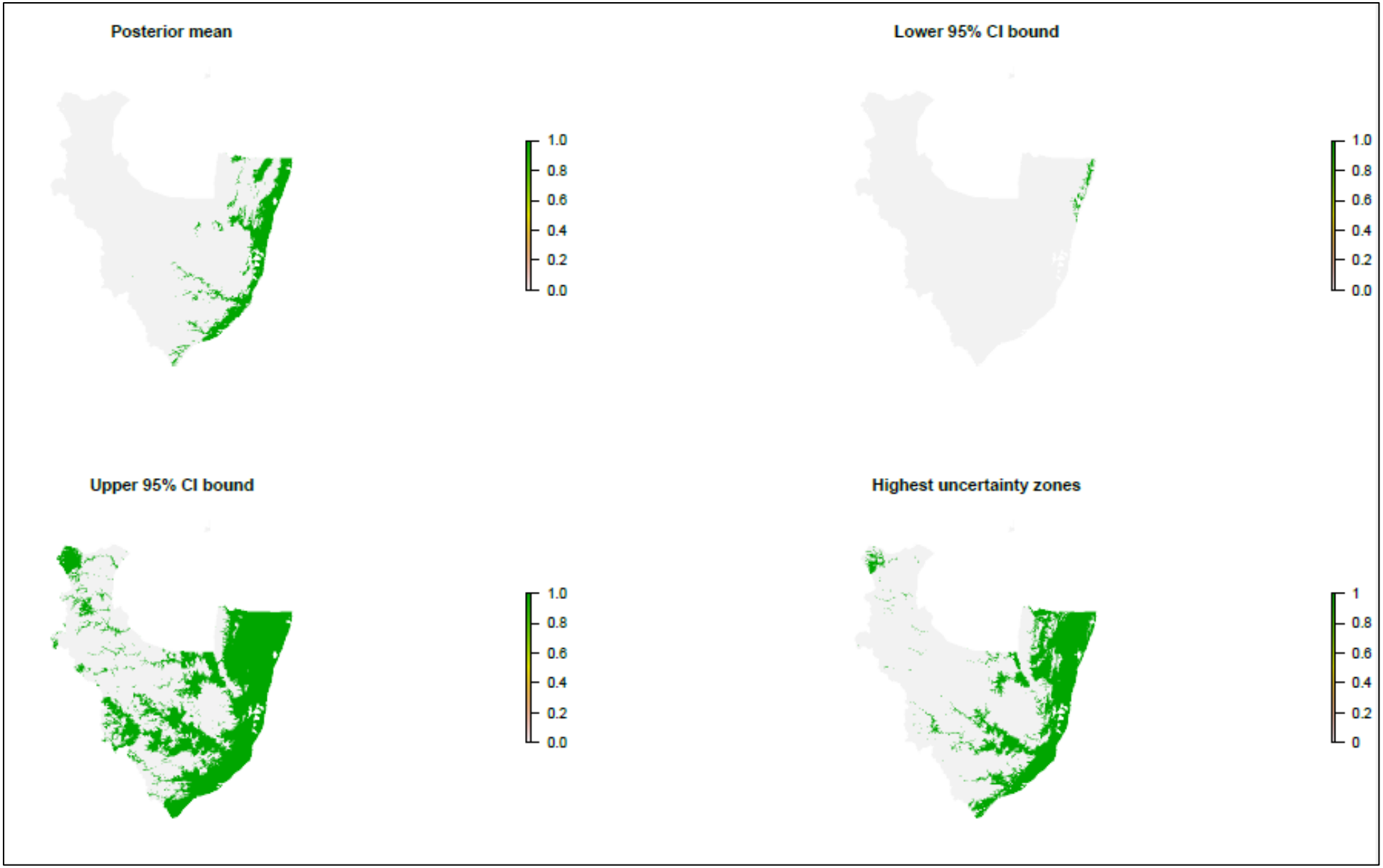


Figure S5.4.23. The modelled distribution of *Ctenopoma multispine* in South Africa showing predicted distribution as a binary output.

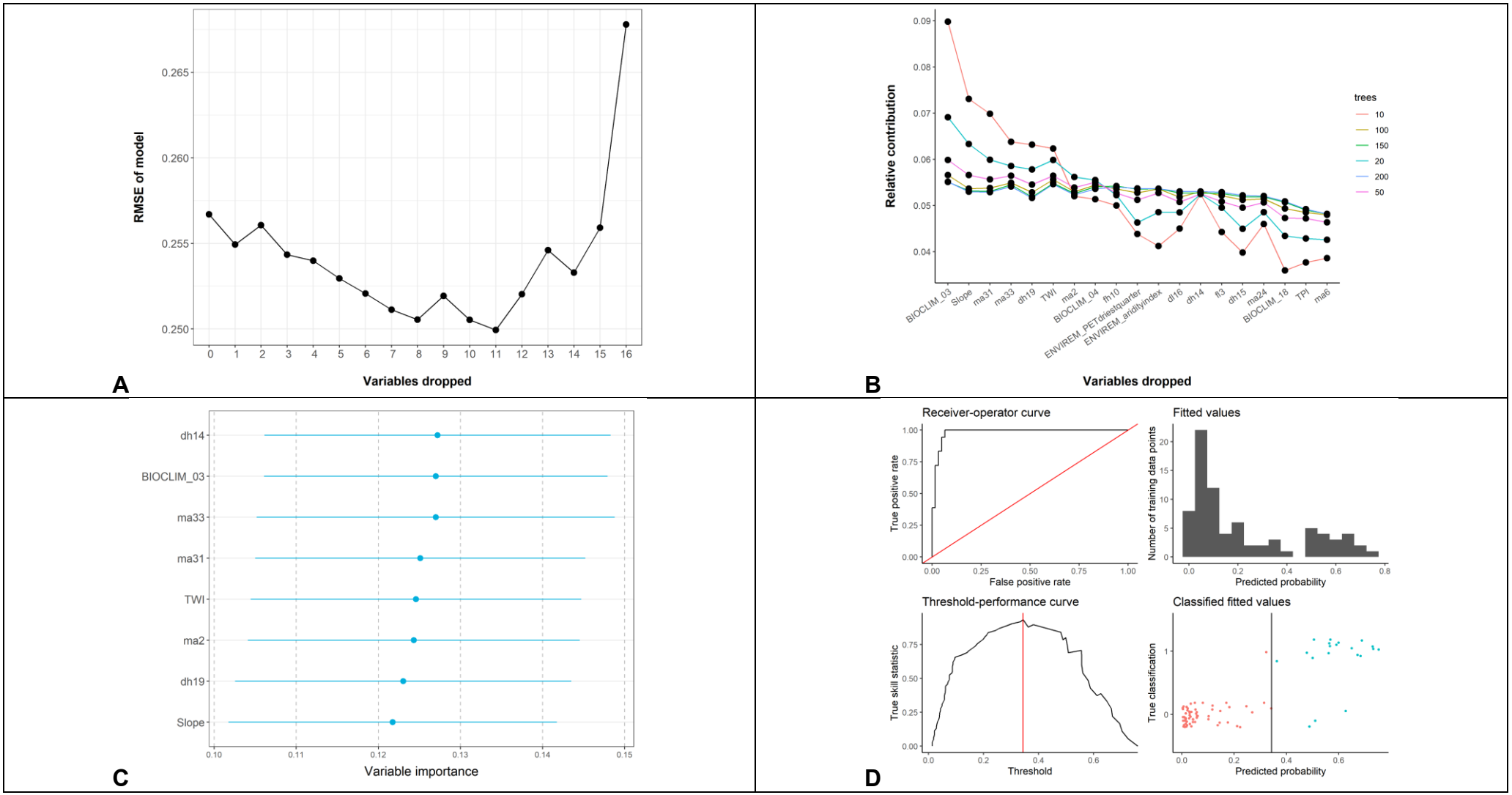


Figure S5.4.24. Model diagnostic outputs for *Ctenopoma multispine,* showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

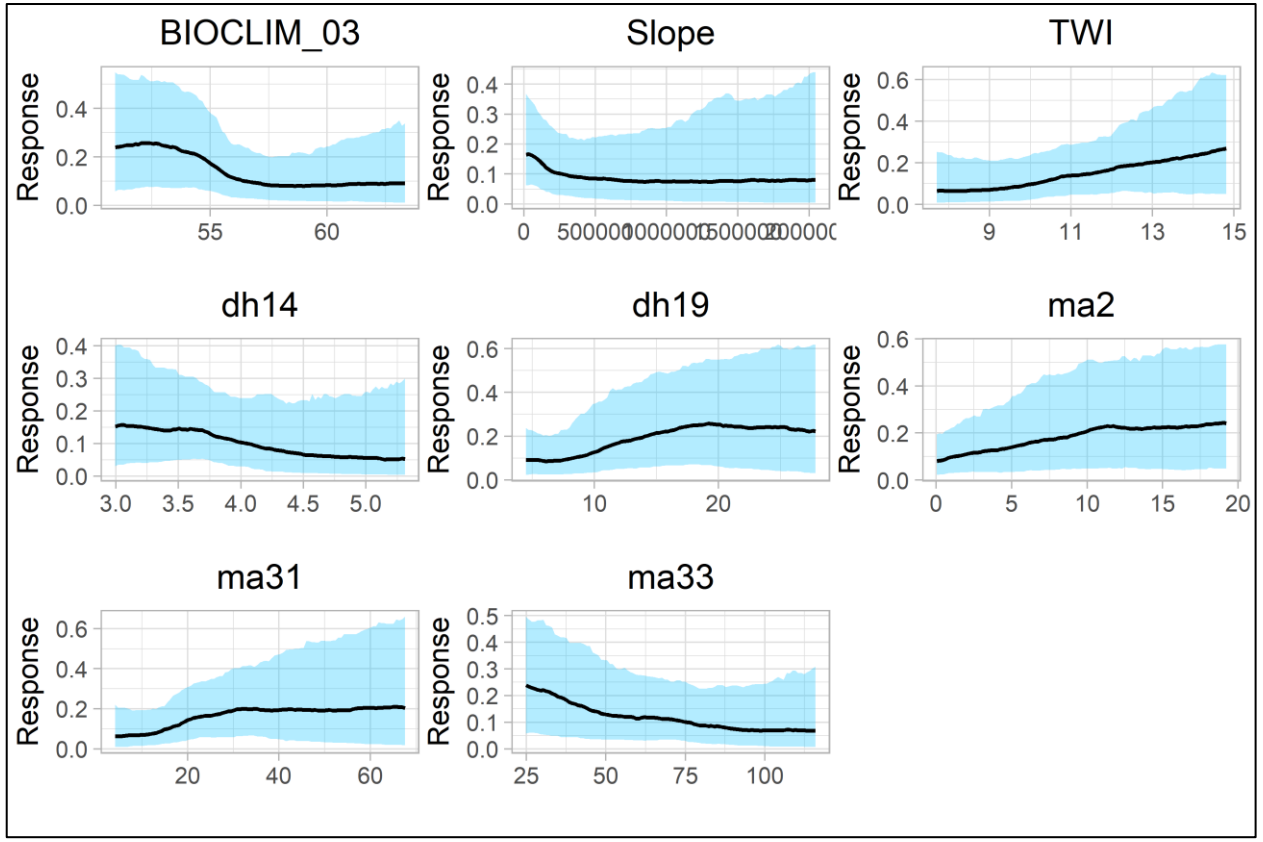


Figure S5.4.25. Partial dependence plots for *Ctenopoma multispine*.

Enteromius gurneyi

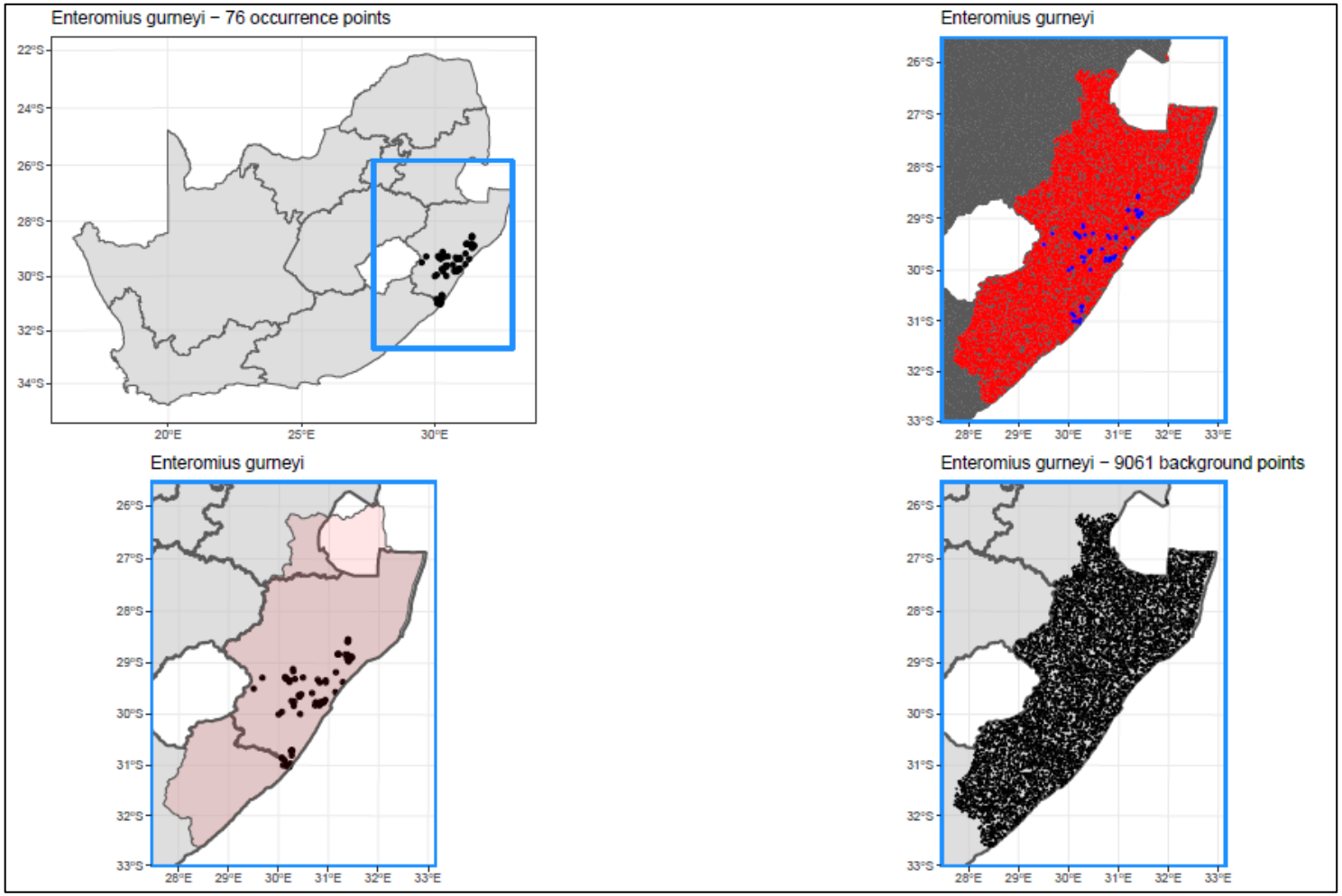


Figure S5.4.26. Occurrence records and background points for *Enteromius gurneyi.*

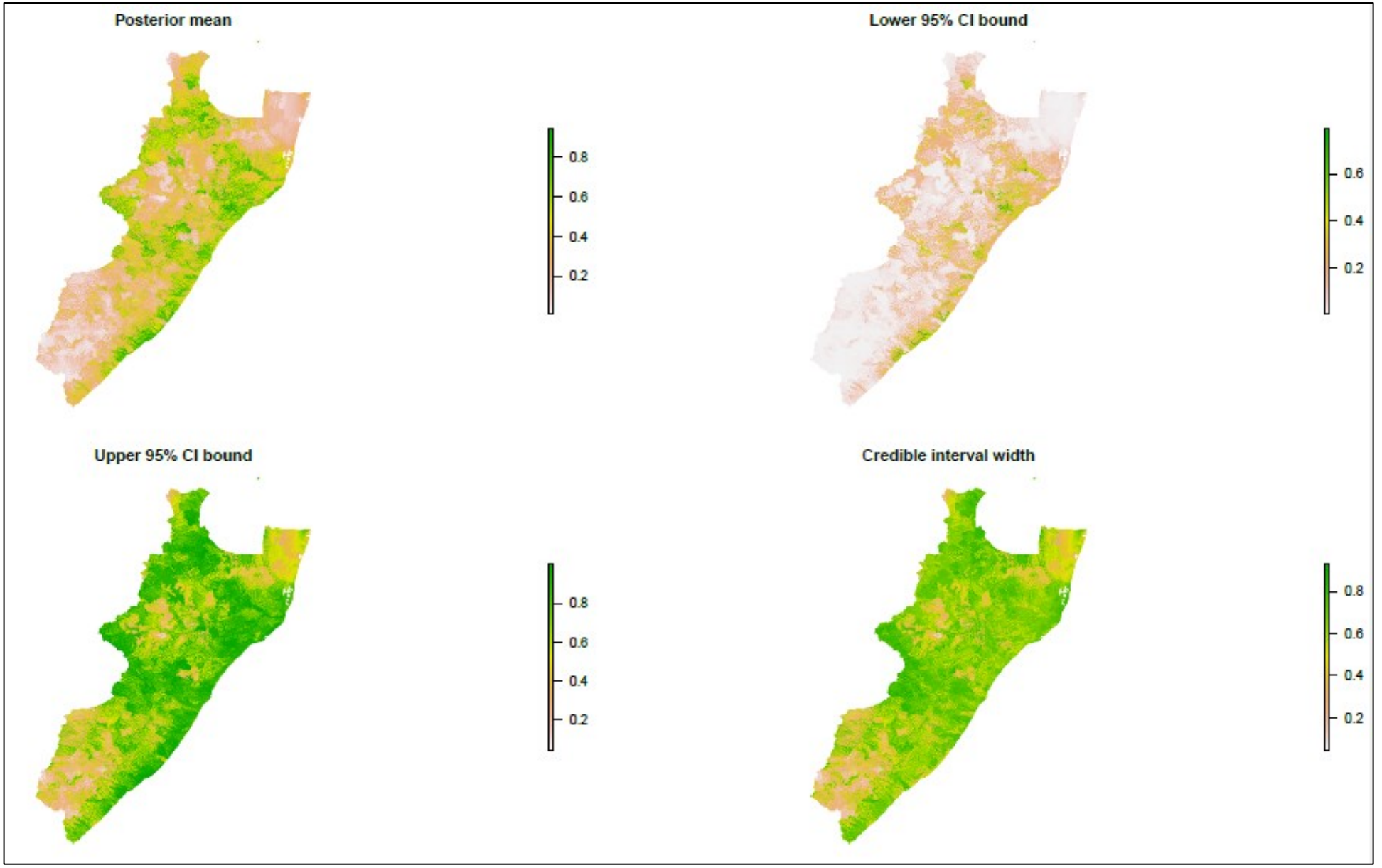


Figure S5.4.27. The modelled distribution of *Enteromius gurneyi* in South Africa showing habitat suitability.

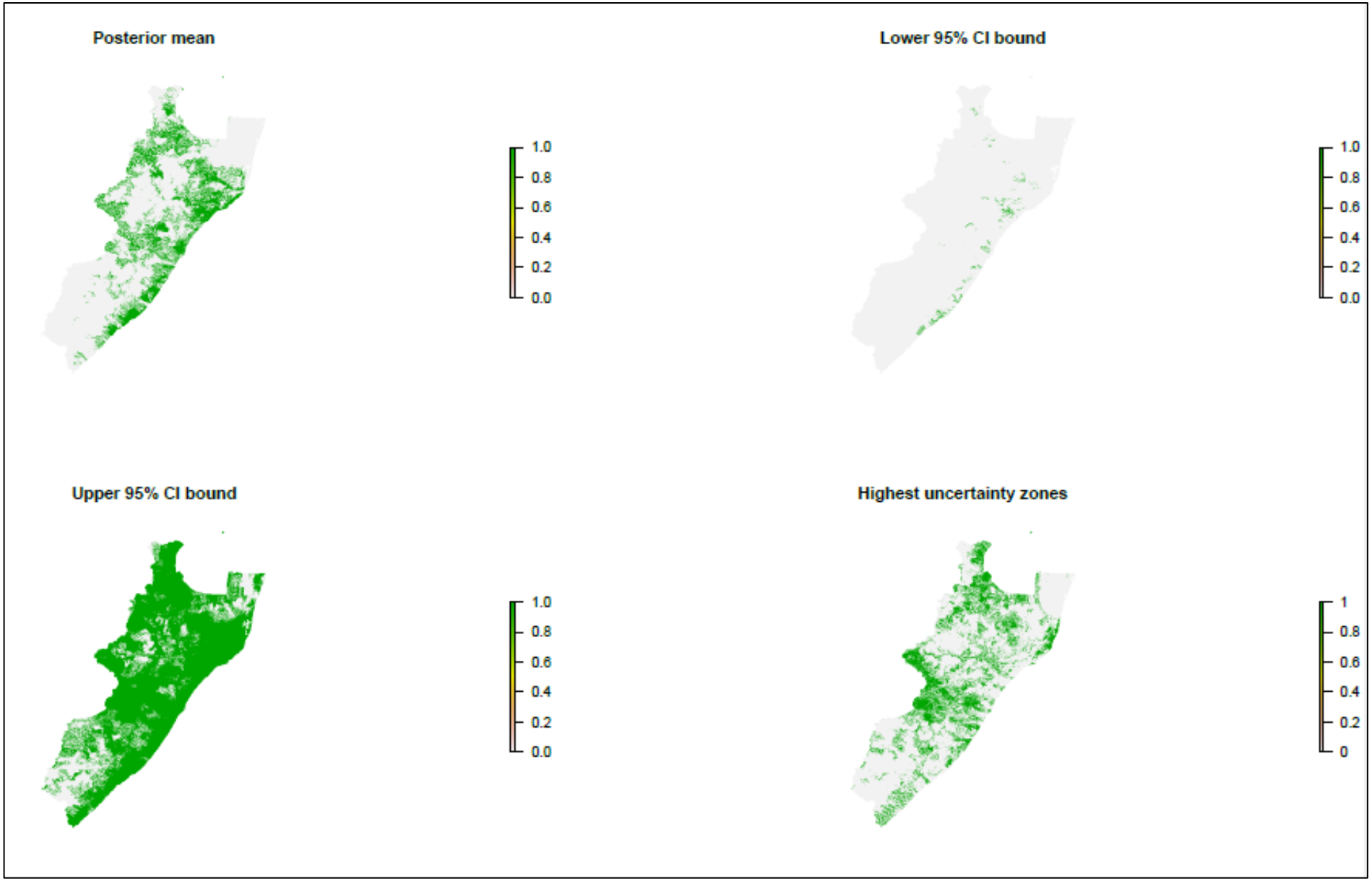


Figure S5.4.28. The modelled distribution of *Enteromius gurneyi* in South Africa showing predicted distribution as a binary output.

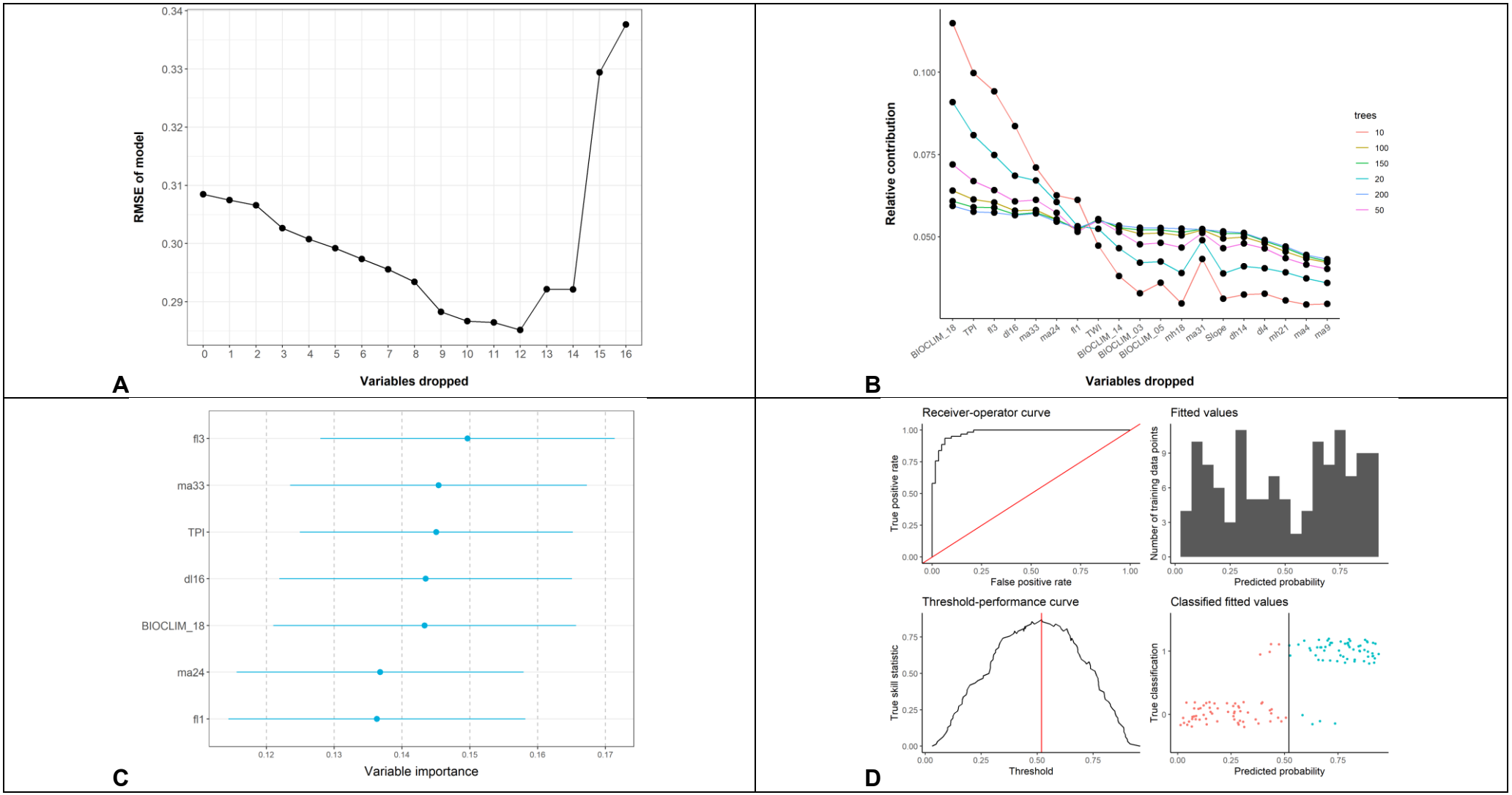


Figure S5.4.29. Model diagnostic outputs for *Enteromius gurneyi*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

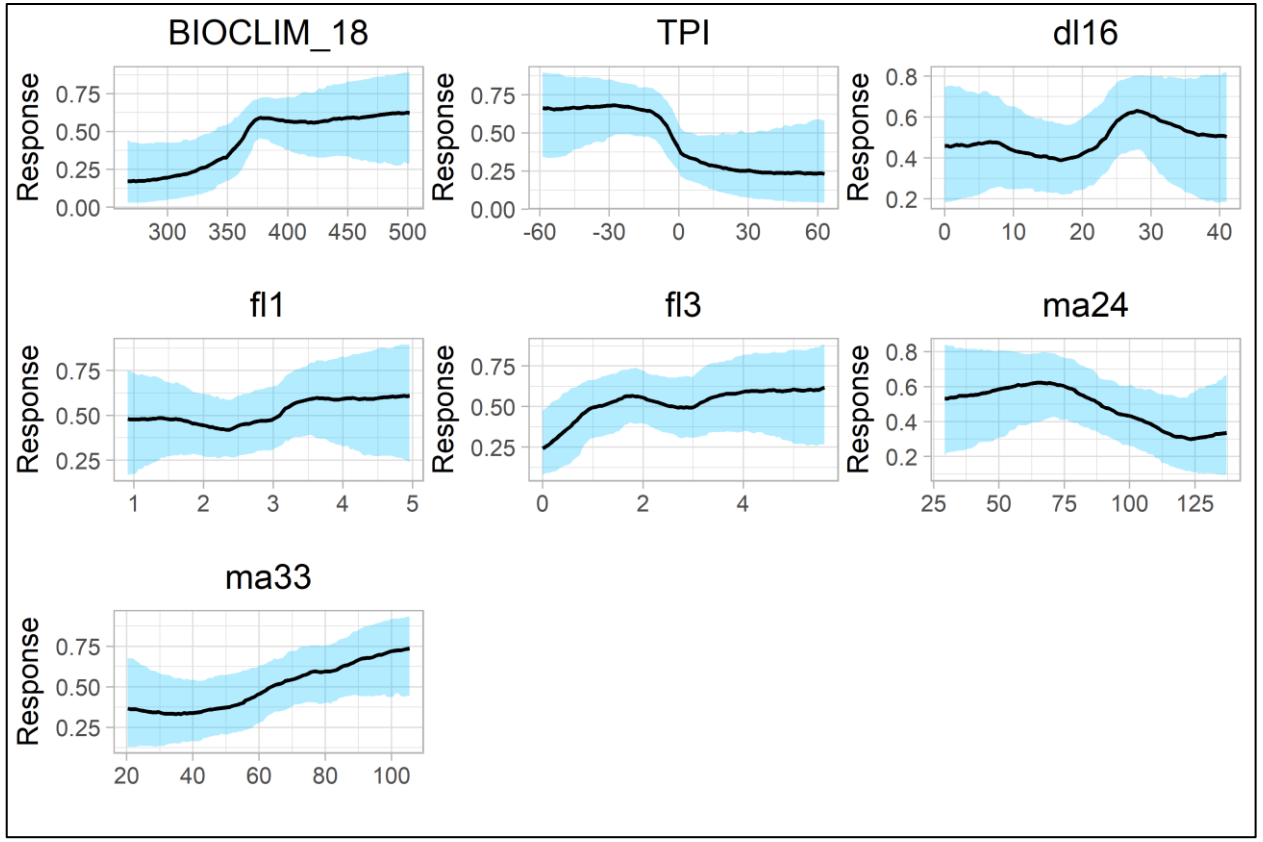


Figure S5.4.30. Partial dependence plots for *Enteromius gurneyi.*

Enteromius treurensis

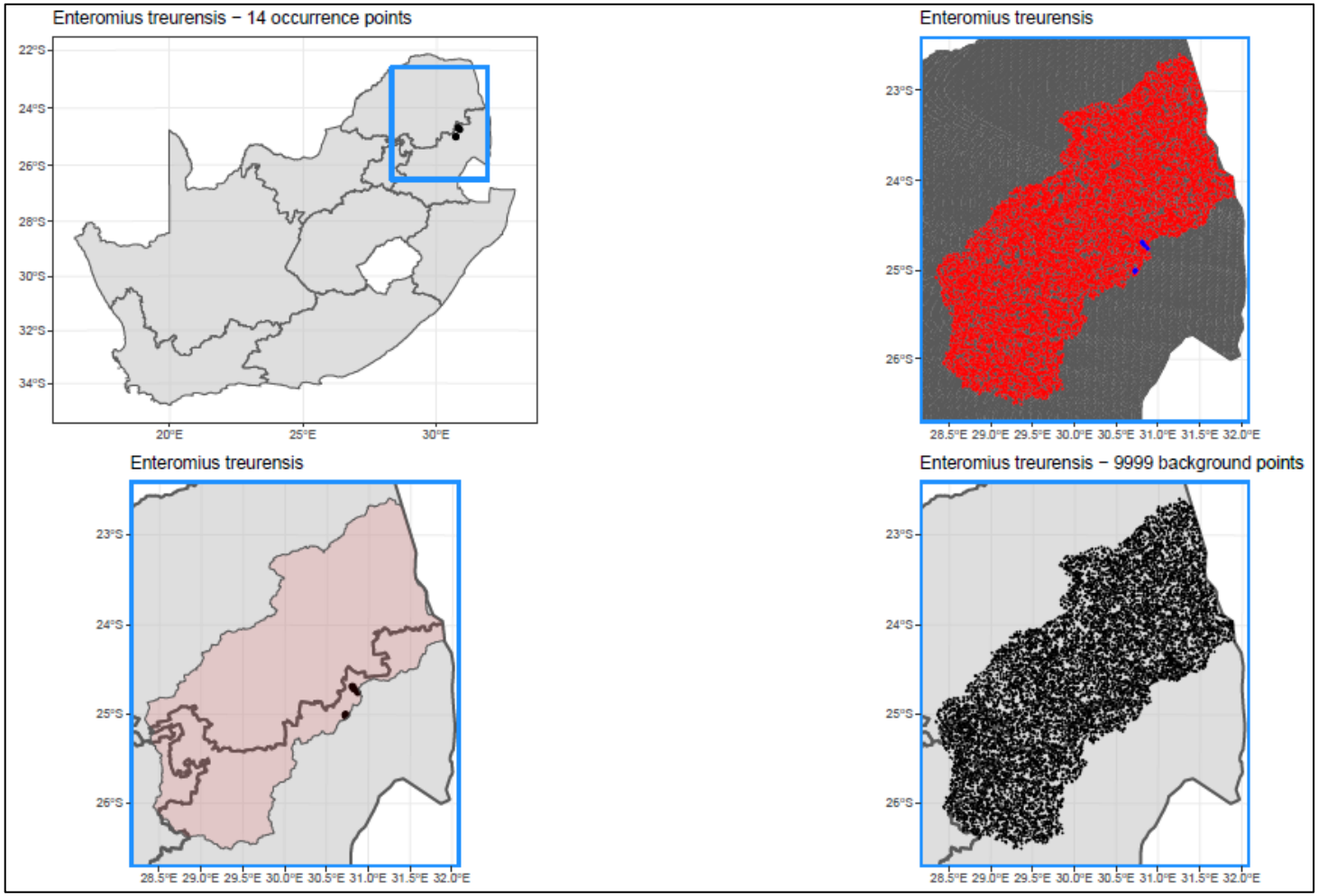


Figure S5.4.31. Occurrence records and background points for *Enteromius treurensis.*

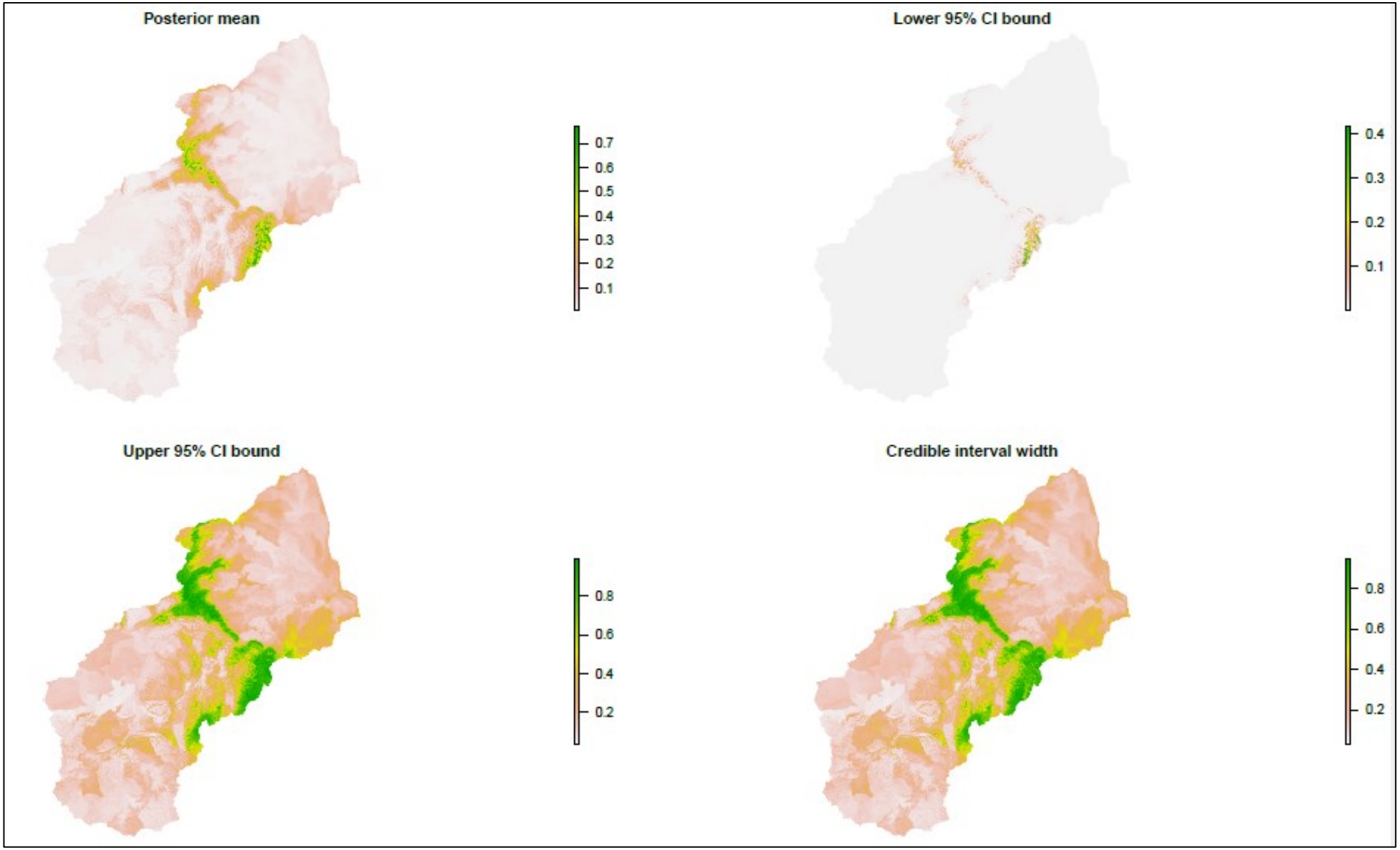


Figure S5.4.32. The modelled distribution of *Enteromius treurensis* in South Africa showing habitat suitability.

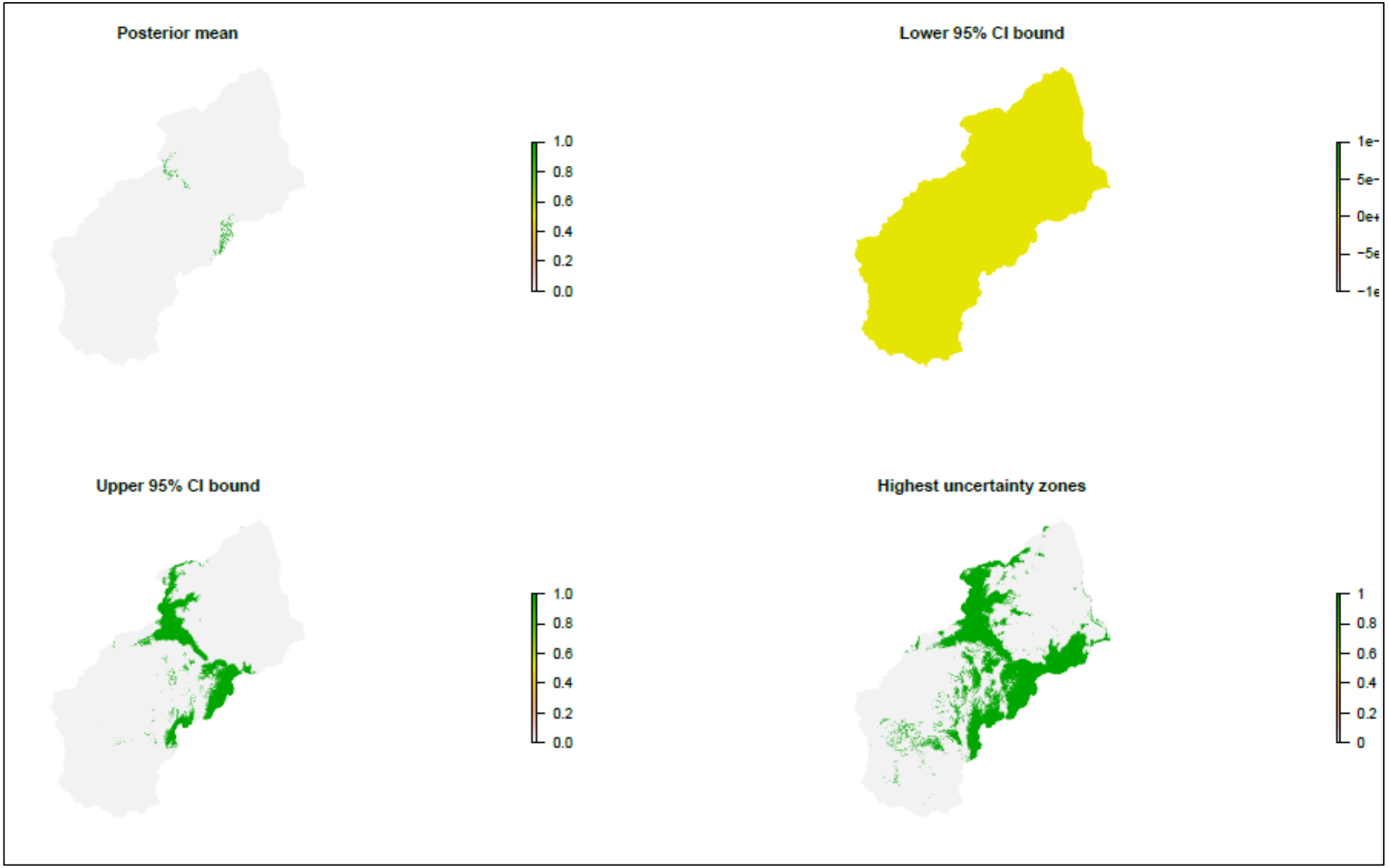


Figure S5.4.33. The modelled distribution of *Enteromius treurensis* in South Africa showing predicted distribution as a binary output.

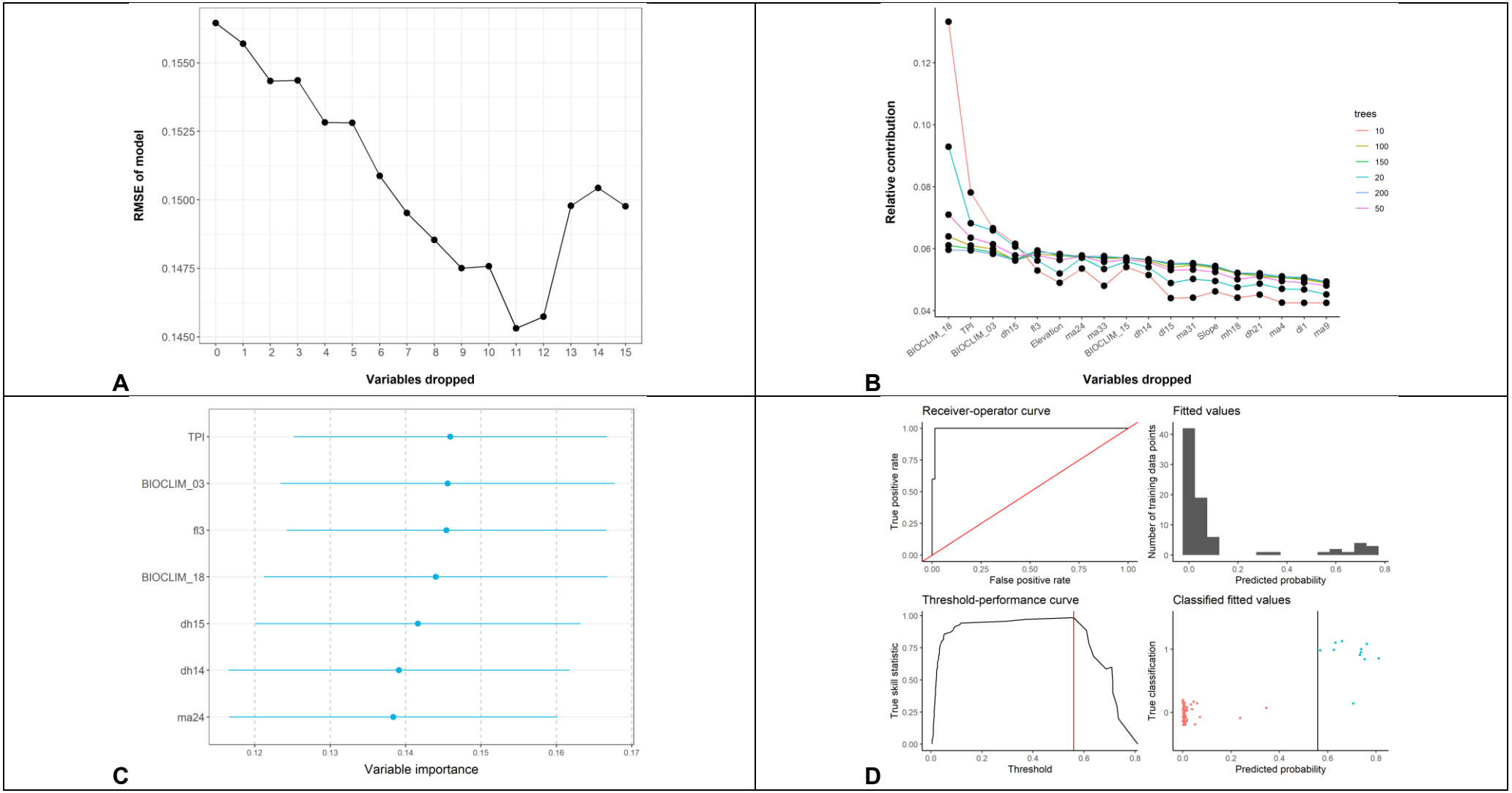


Figure S5.4.34. Model diagnostic outputs for *Enteromius treurensis*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

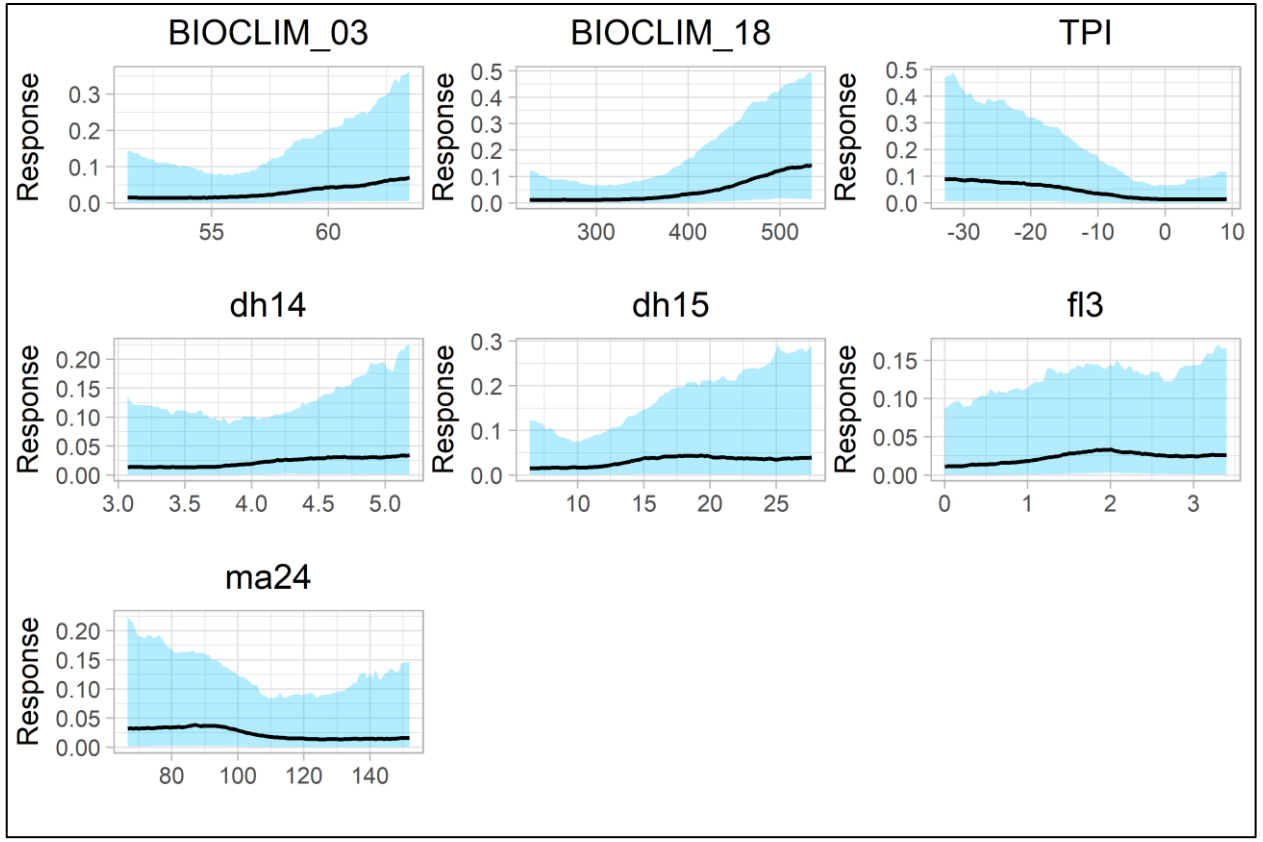


Figure S5.4.35. Partial dependence plots for *Enteromius treurensis.*

Labeo rubromaculatus

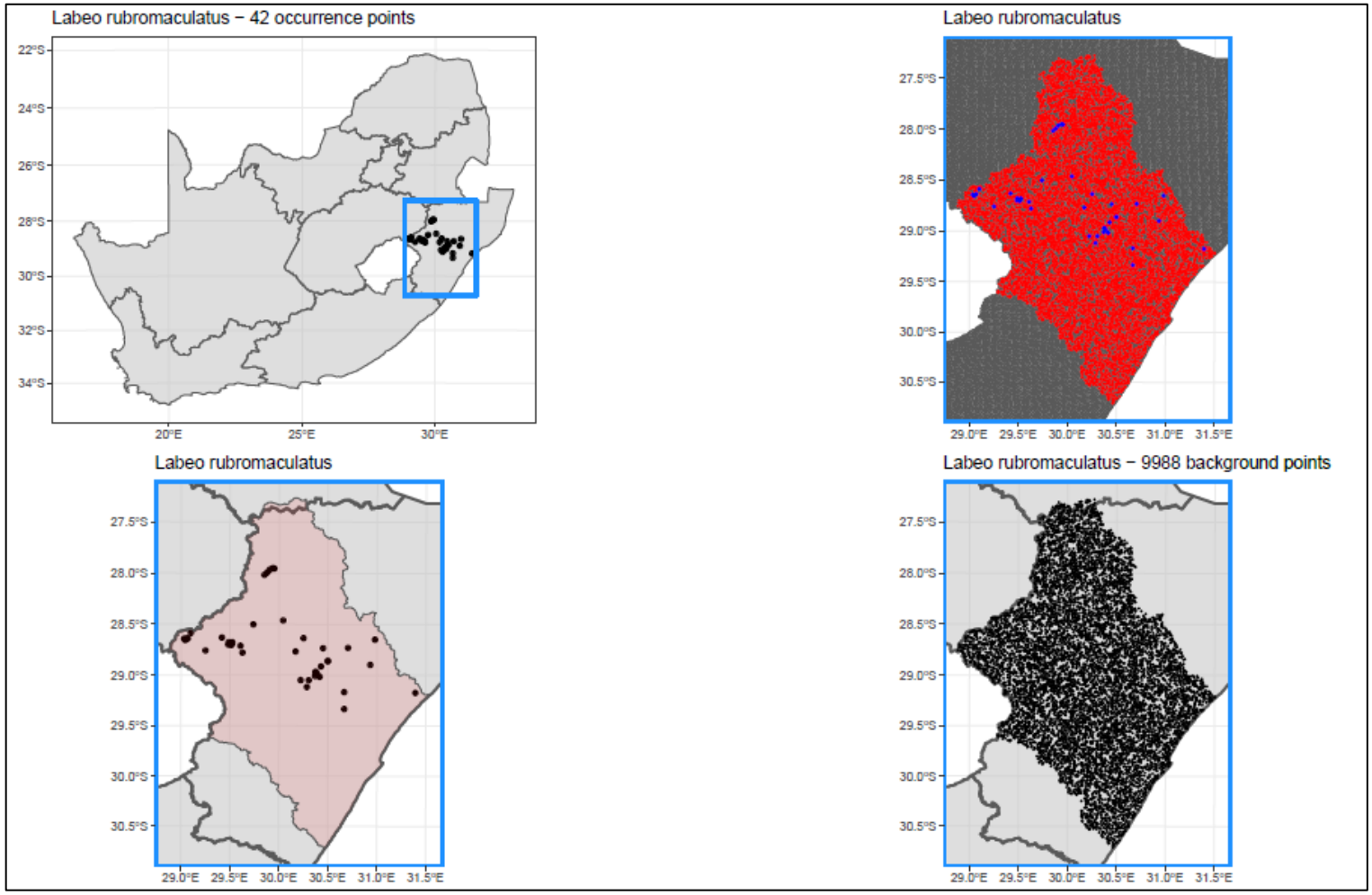


Figure S5.4.36. Occurrence records and background points for *Labeo rubromaculatus*.

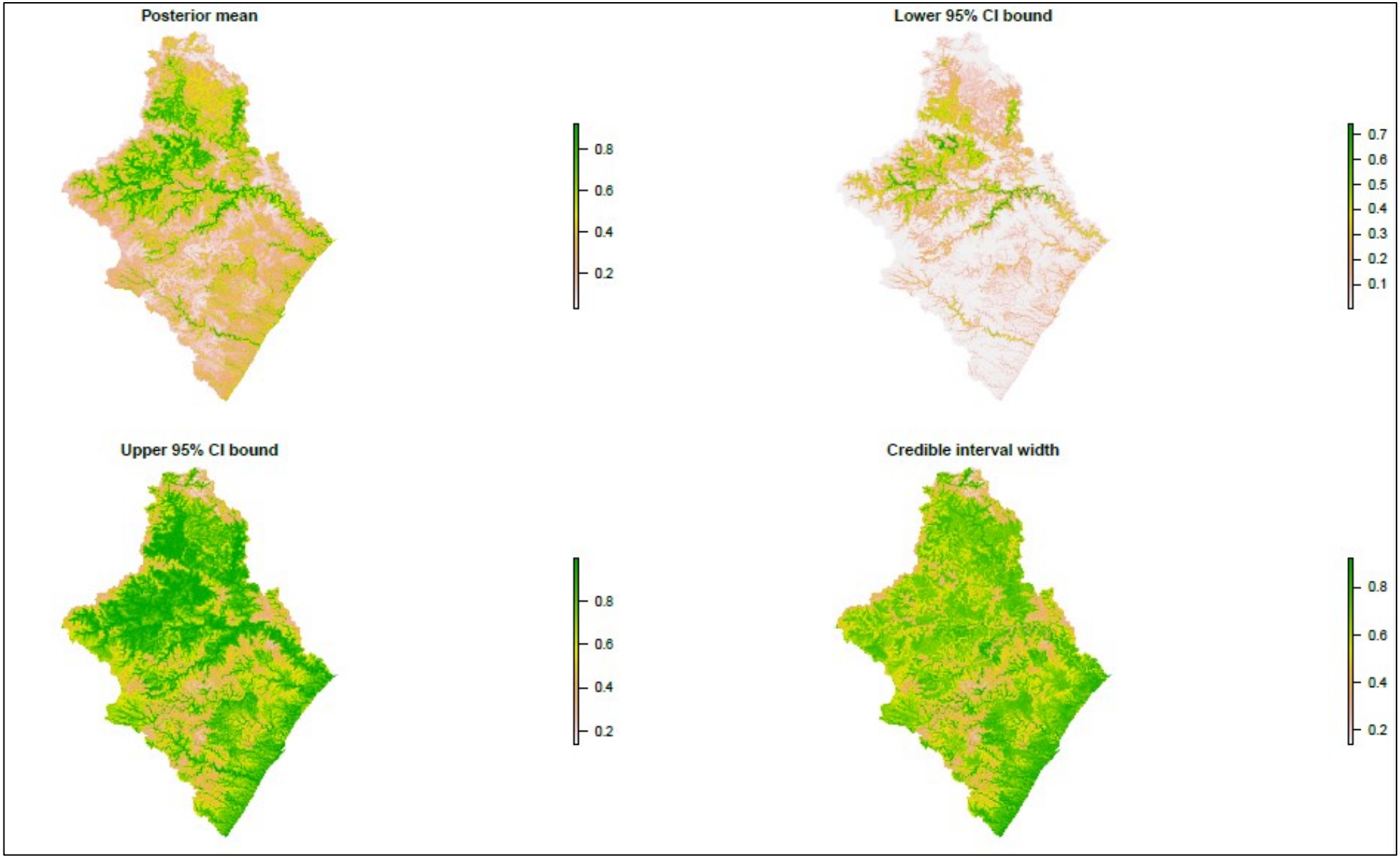


Figure S5.4.37. The modelled distribution of *Labeo rubromaculatus* in South Africa showing habitat suitability.

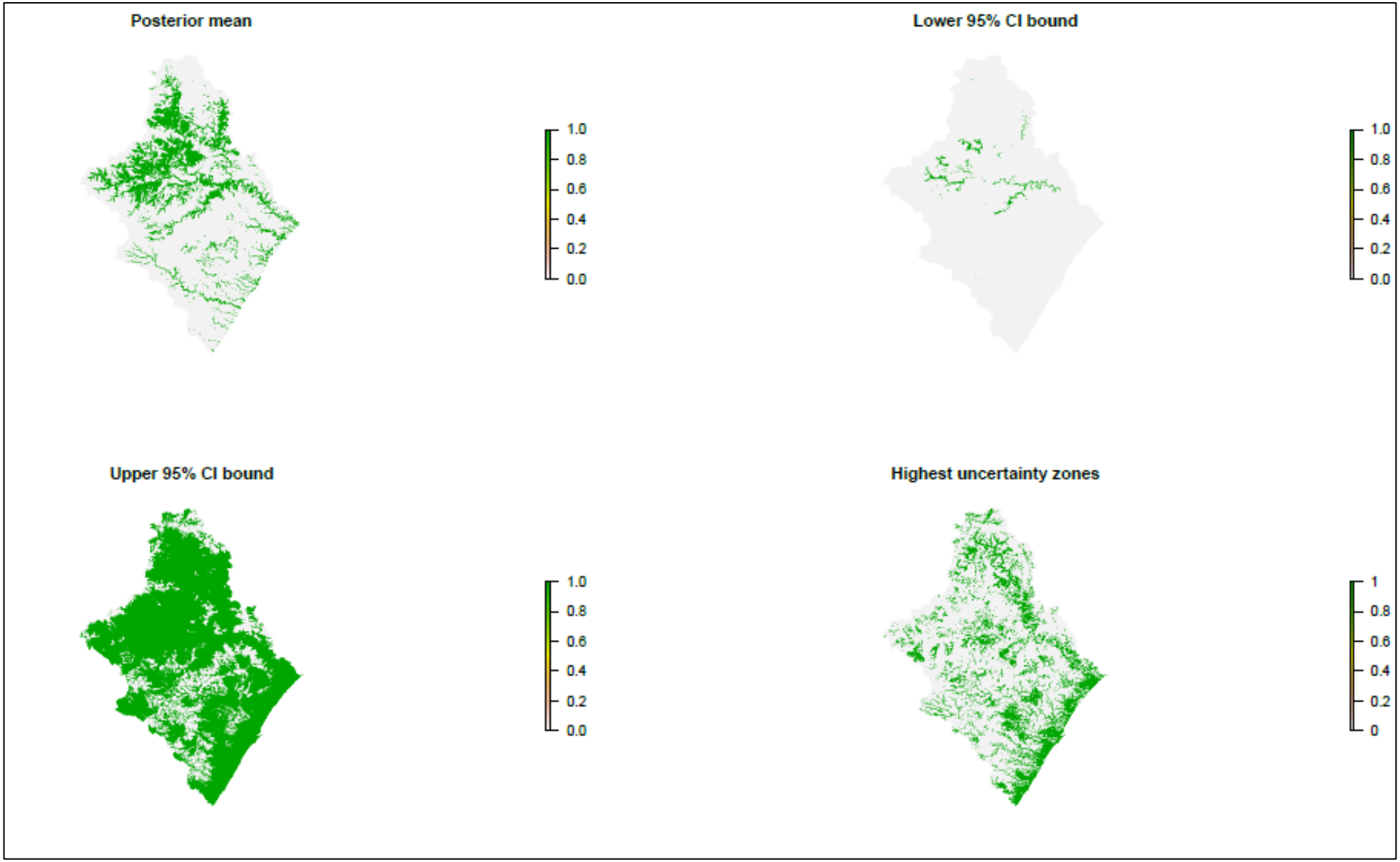


Figure S5.4.38. The modelled distribution of *Labeo rubromaculatus* in South Africa showing predicted distribution as a binary output.

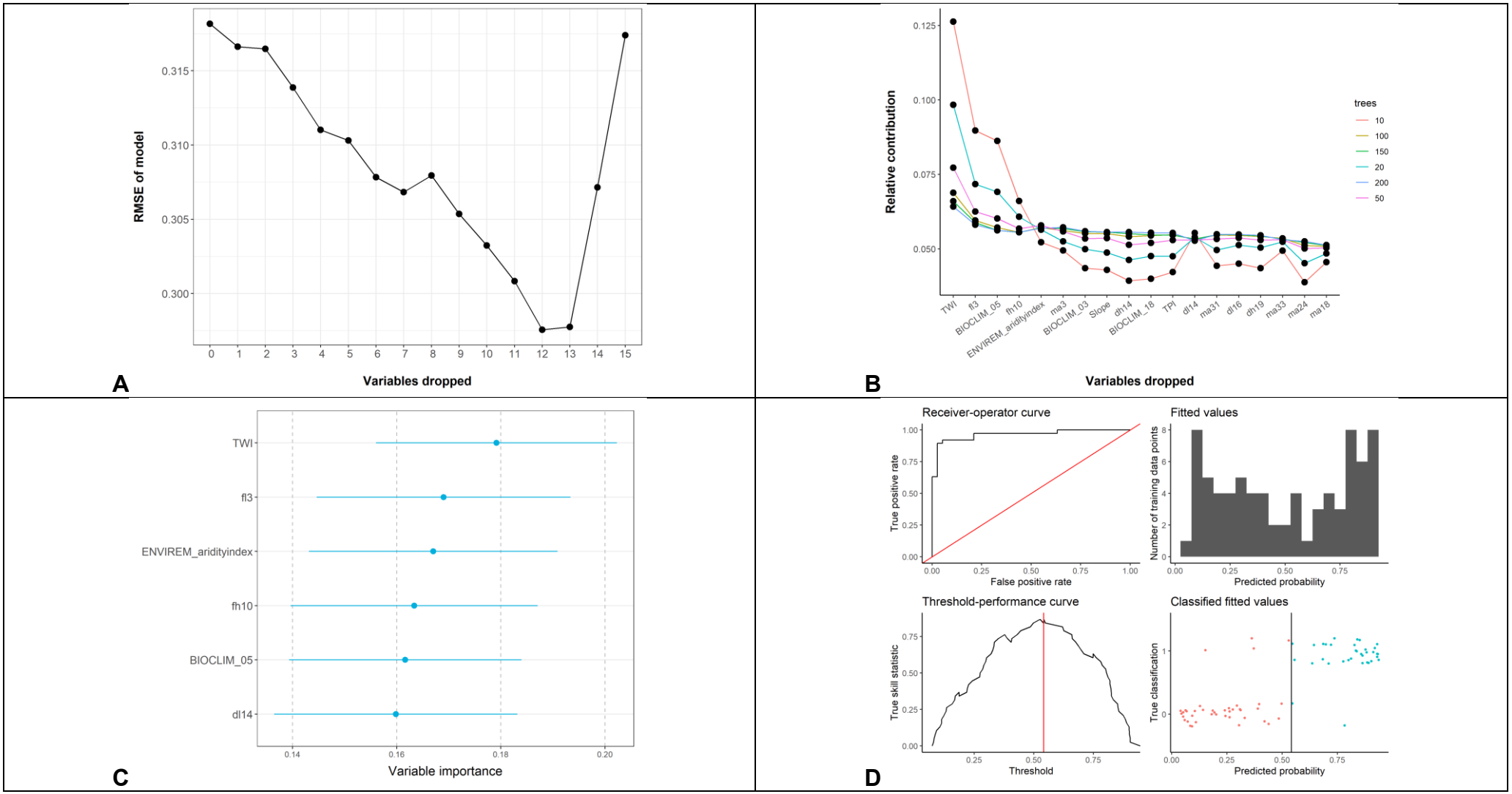


Figure S5.4.39. Model diagnostic outputs for *Labeo rubromaculatus,* showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

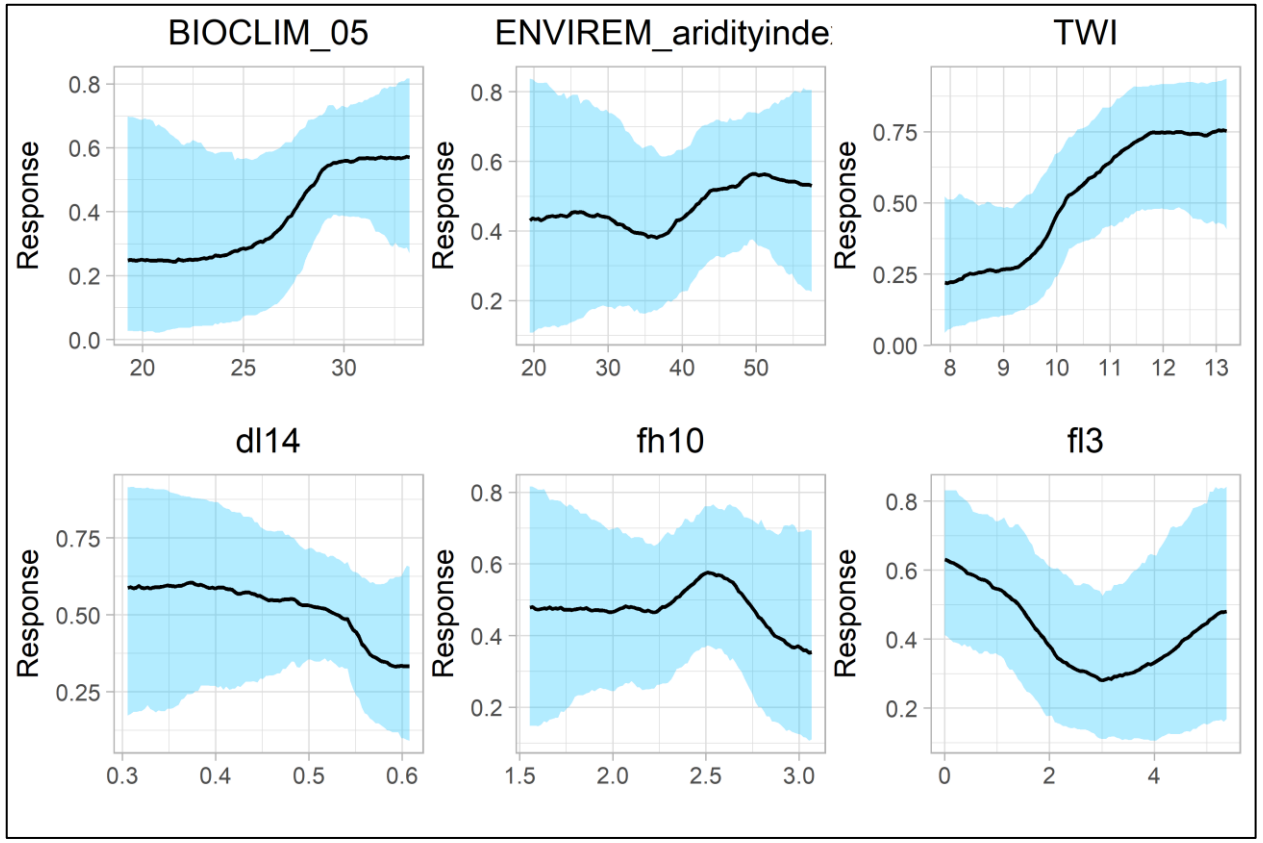


Figure S5.4.40. Partial dependence plots for *Labeo rubromaculatus*.

Labeo seeberi

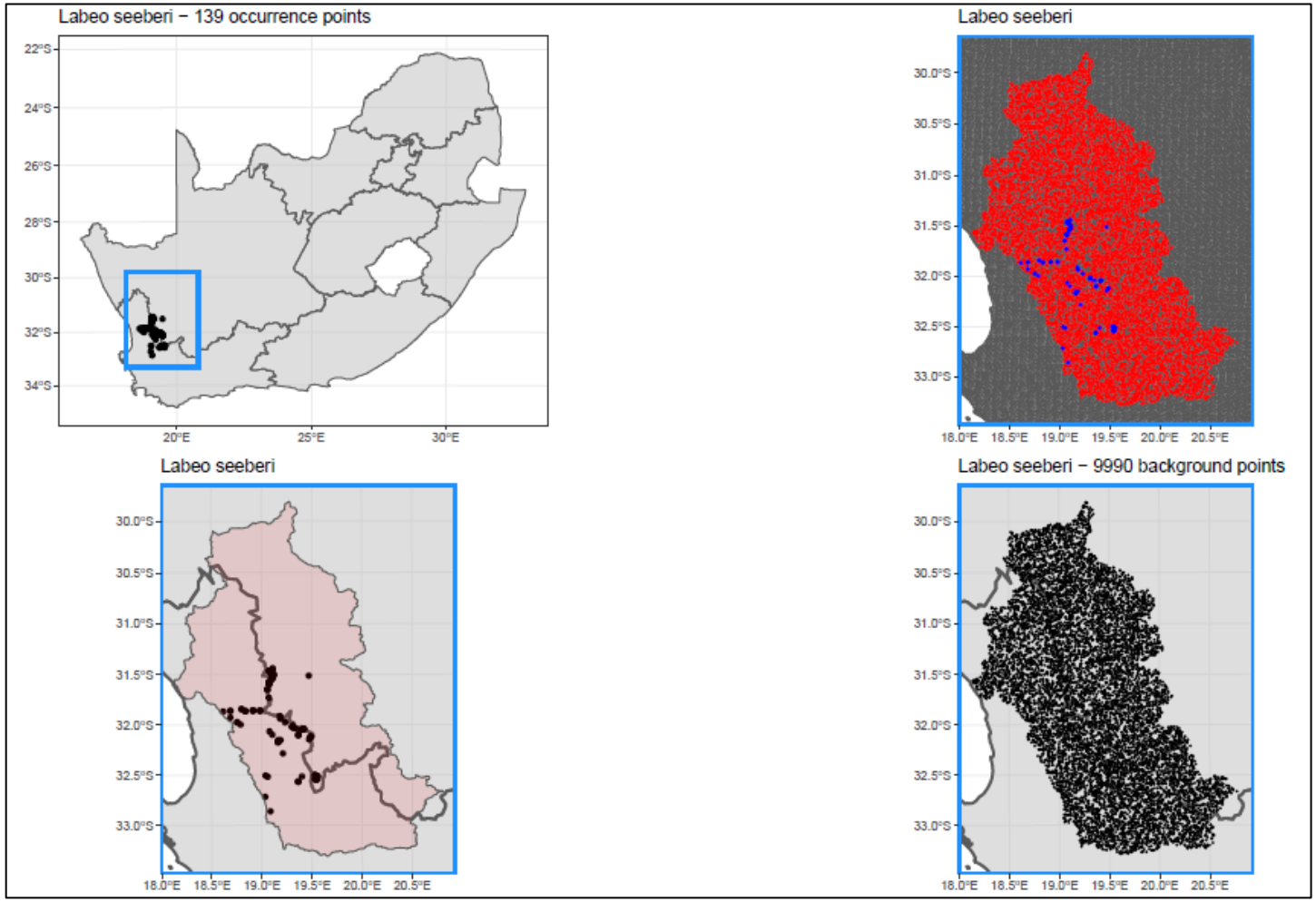


Figure S5.4.41. Occurrence records and background points for *Labeo seeberi.*

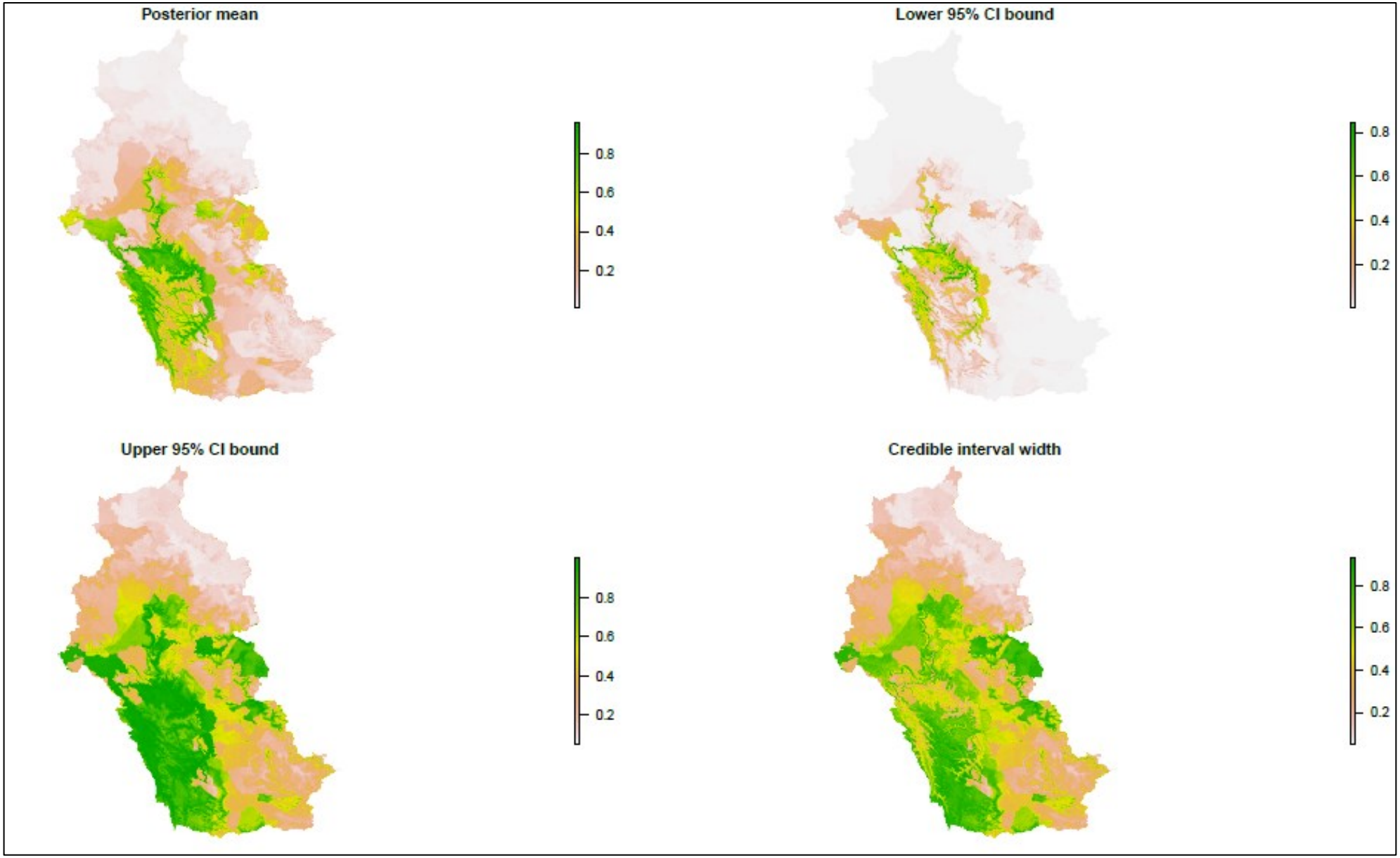


Figure S5.4.42. The modelled distribution of *Labeo seeberi* in South Africa showing habitat suitability.

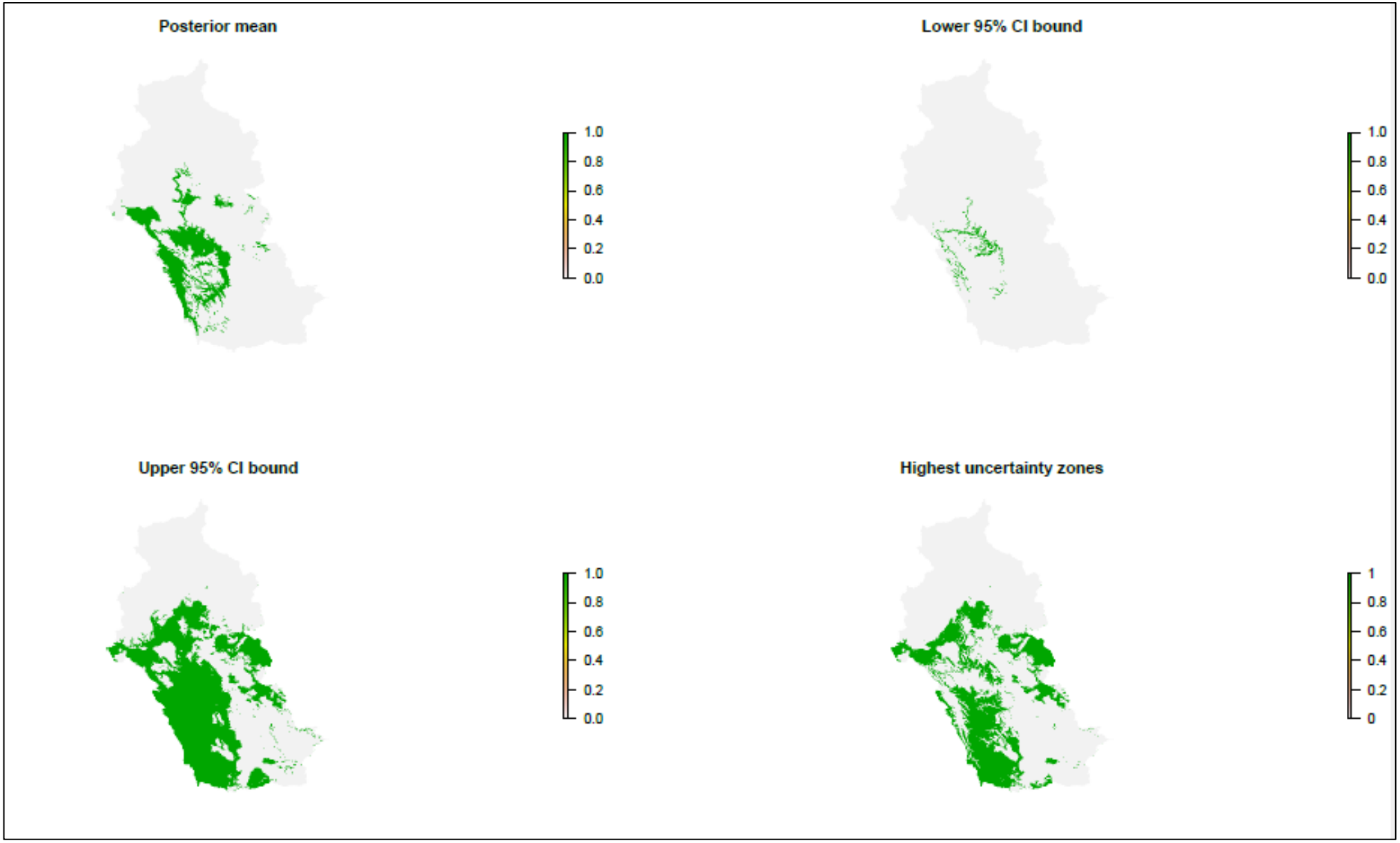


Figure S5.4.43. The modelled distribution of *Labeo seeberi* in South Africa showing predicted distribution as a binary output.

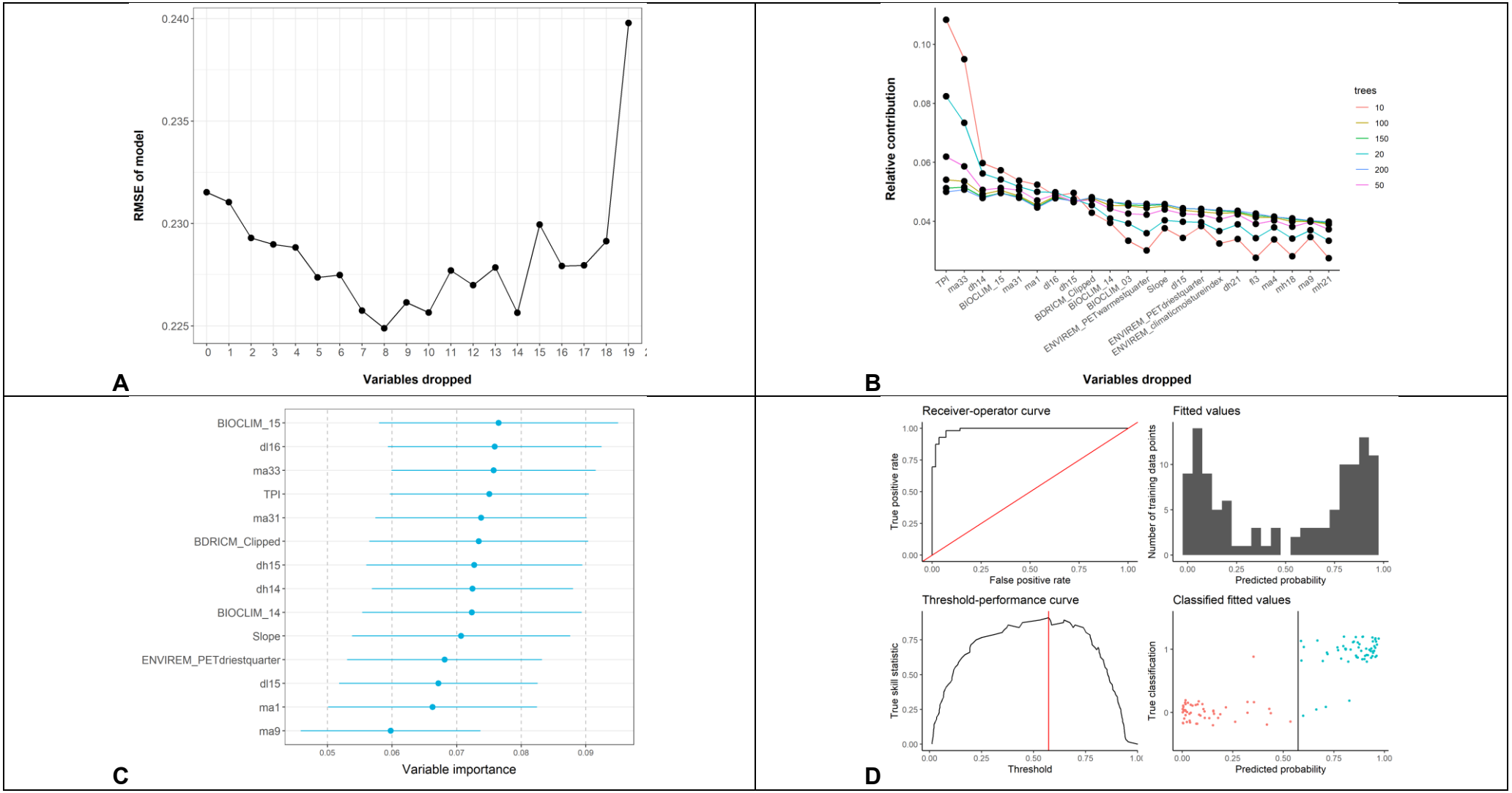


Figure S5.4.44. Model diagnostic outputs for *Labeo seeberi*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

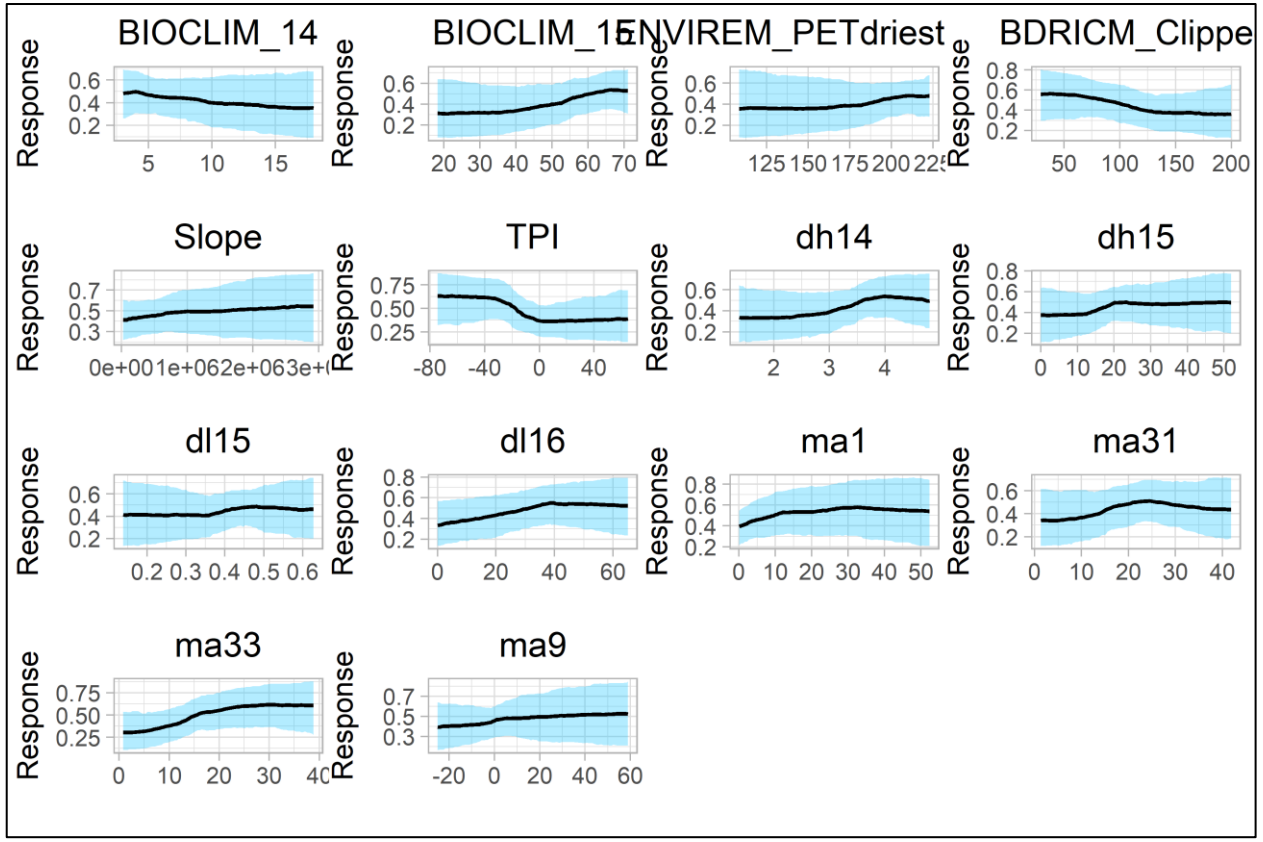


Figure S5.4.45. Partial dependence plots for *Labeo seeberi.*

Marcusenius caudisquamatus

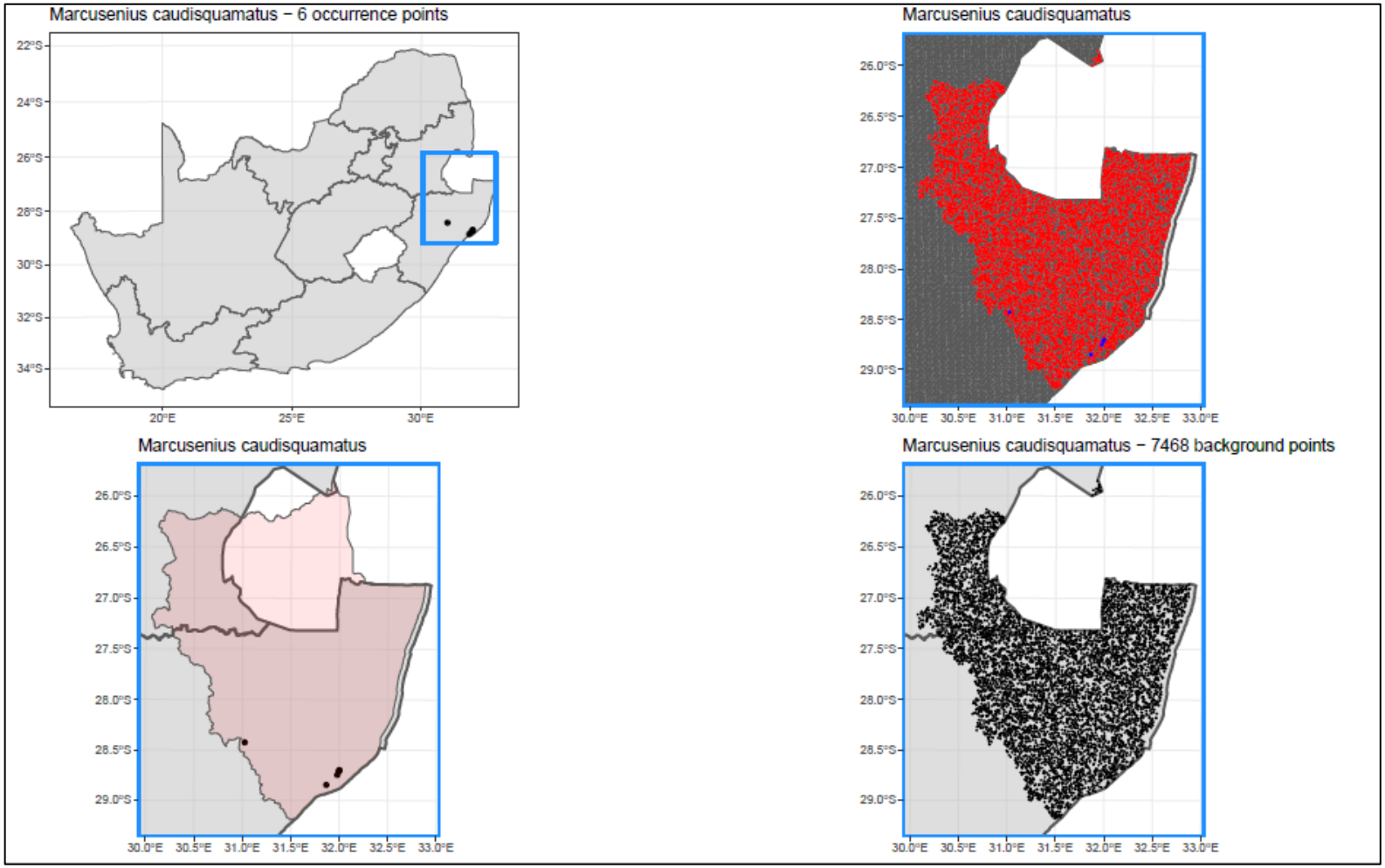


Figure S5.4.46. Occurrence records and background points for *Marcusenius caudisquamatus.*

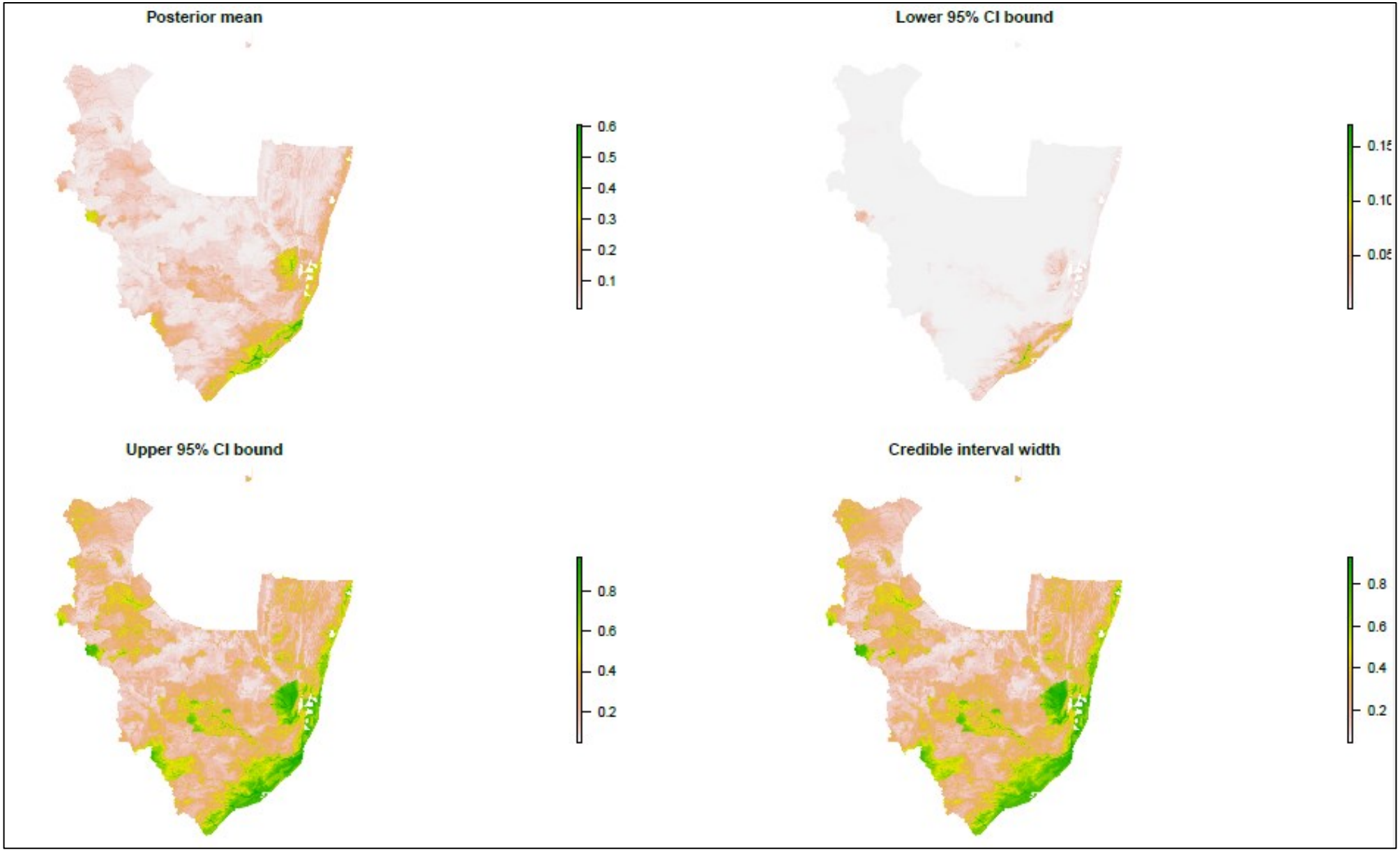


Figure S5.4.47. The modelled distribution of *Marcusenius caudisquamatus* in South Africa showing habitat suitability.

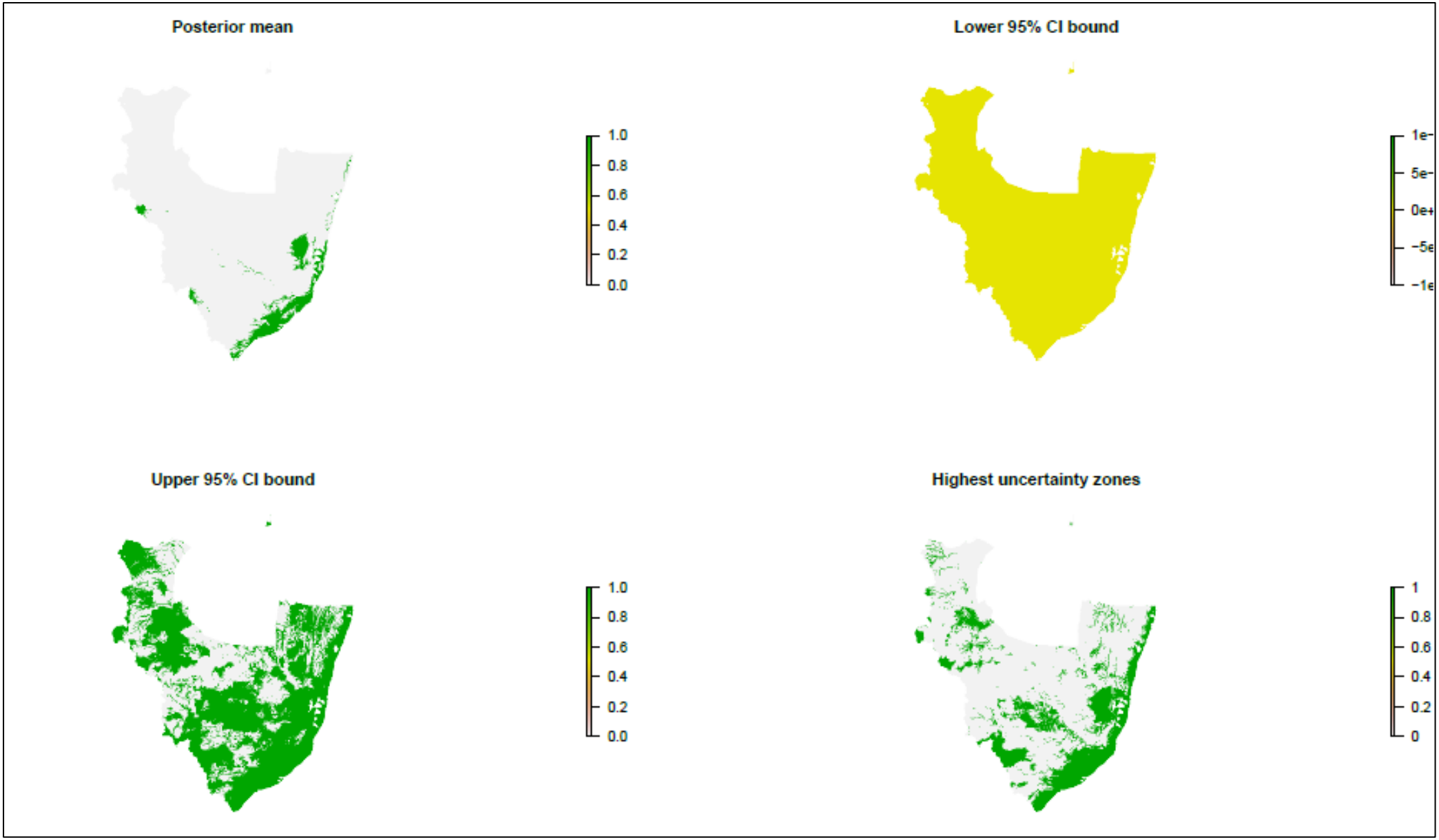


Figure S5.4.48. The modelled distribution of *Marcusenius caudisquamatus* in South Africa showing predicted distribution as a binary output.

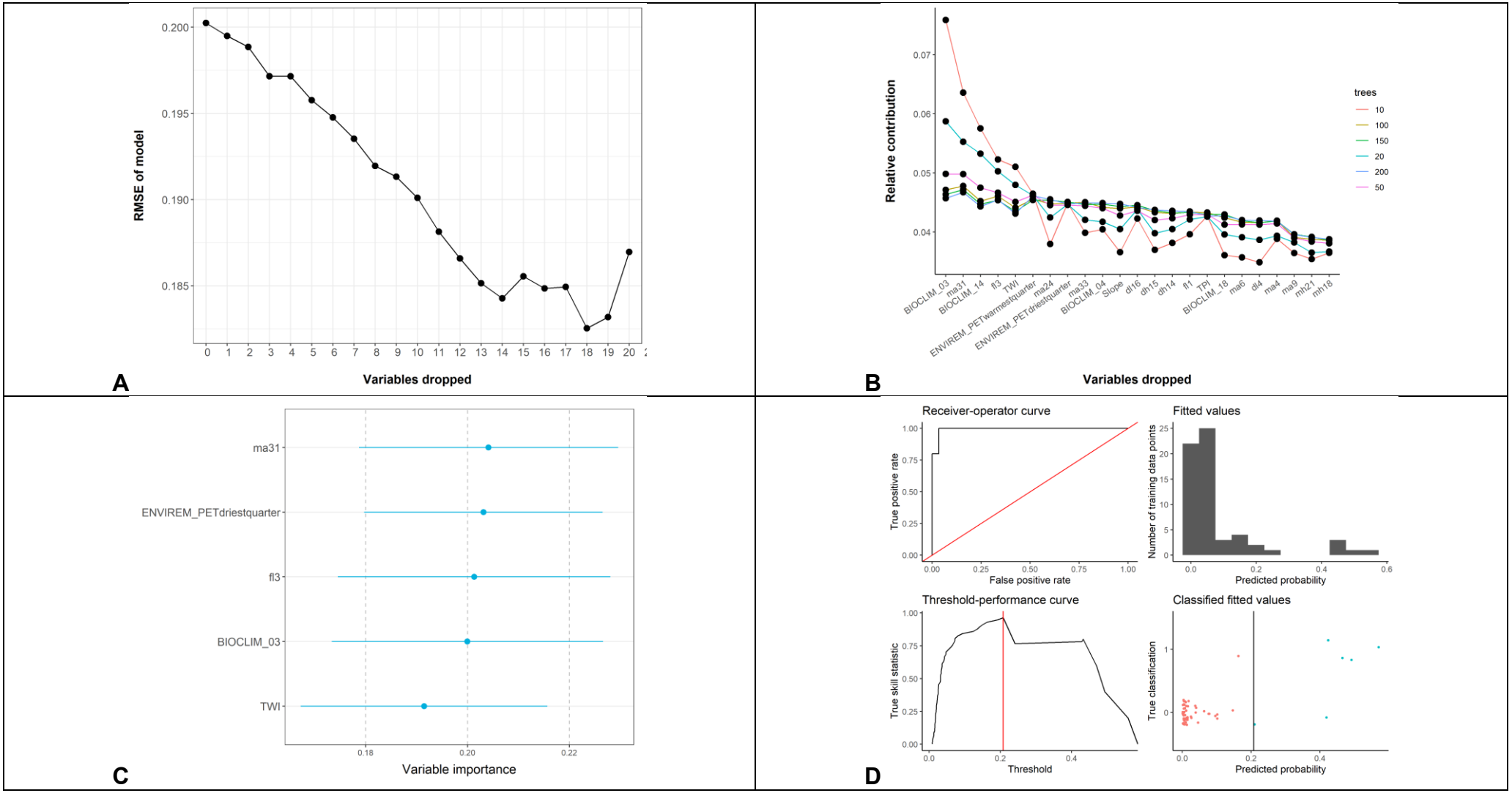


Figure S5.4.49. Model diagnostic outputs for *Marcusenius caudisquamatus*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

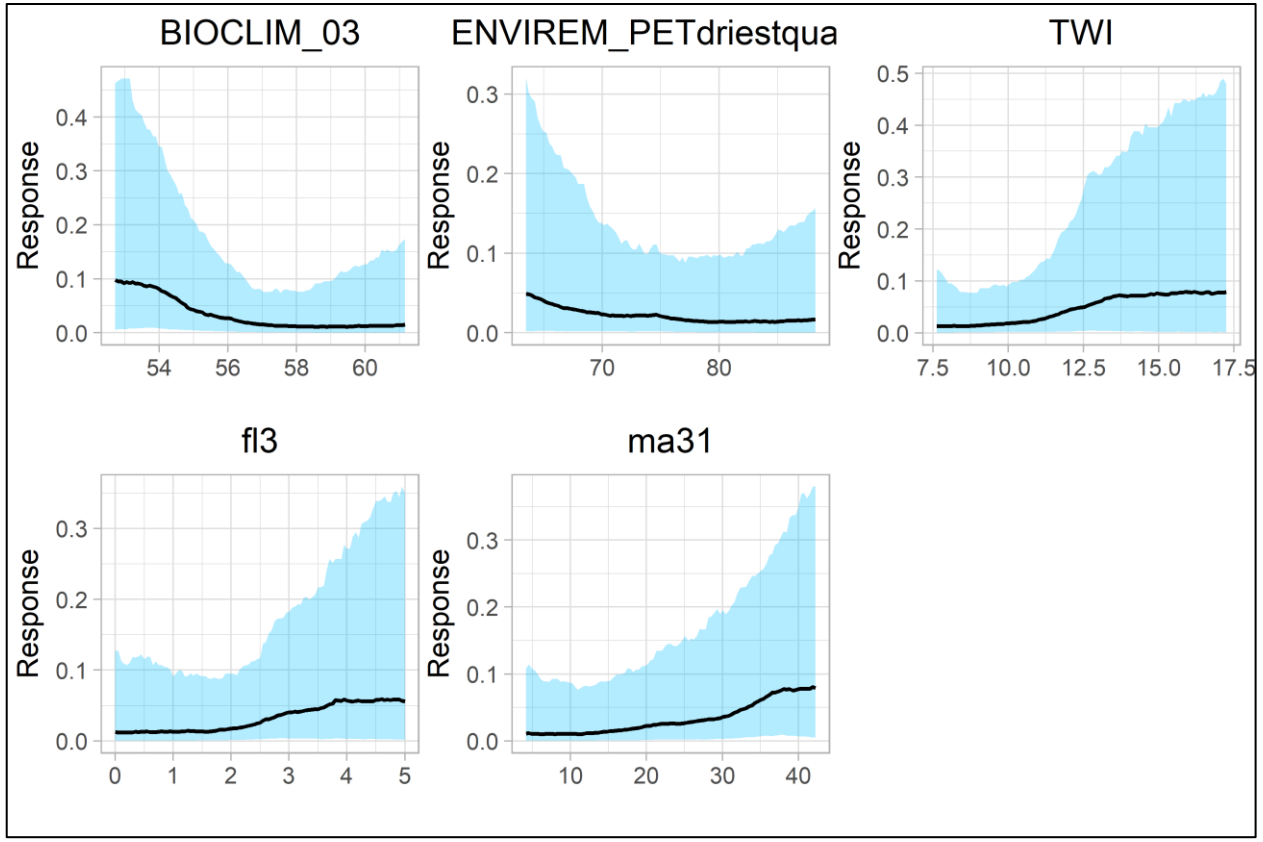


Figure S5.4.50. Partial dependence plots for *Marcusenius caudisquamatus.*

Oreochromis mossambicus

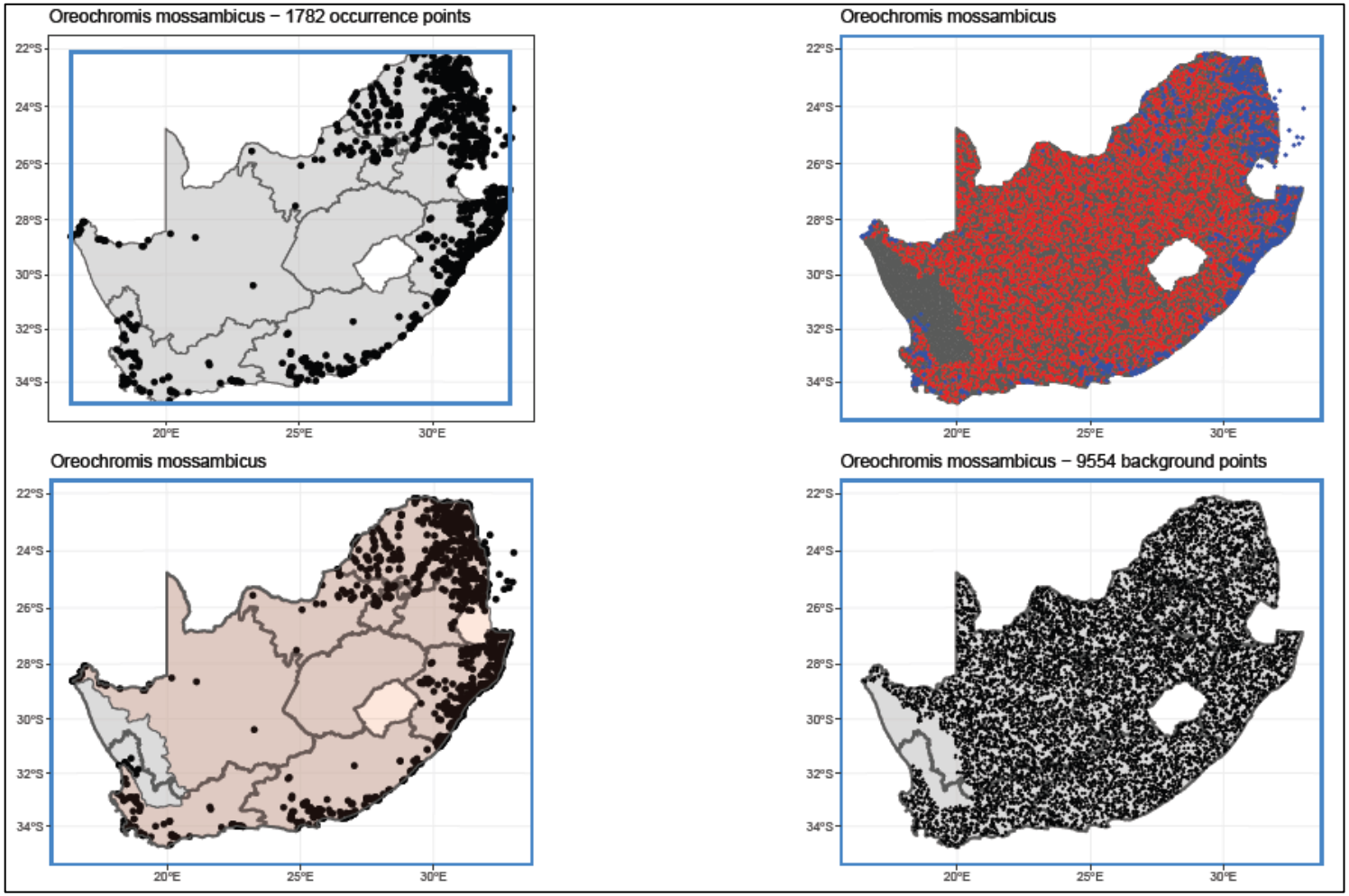


Figure S5.4.51. Occurrence records and background points for *Oreochromis mossambicus.*

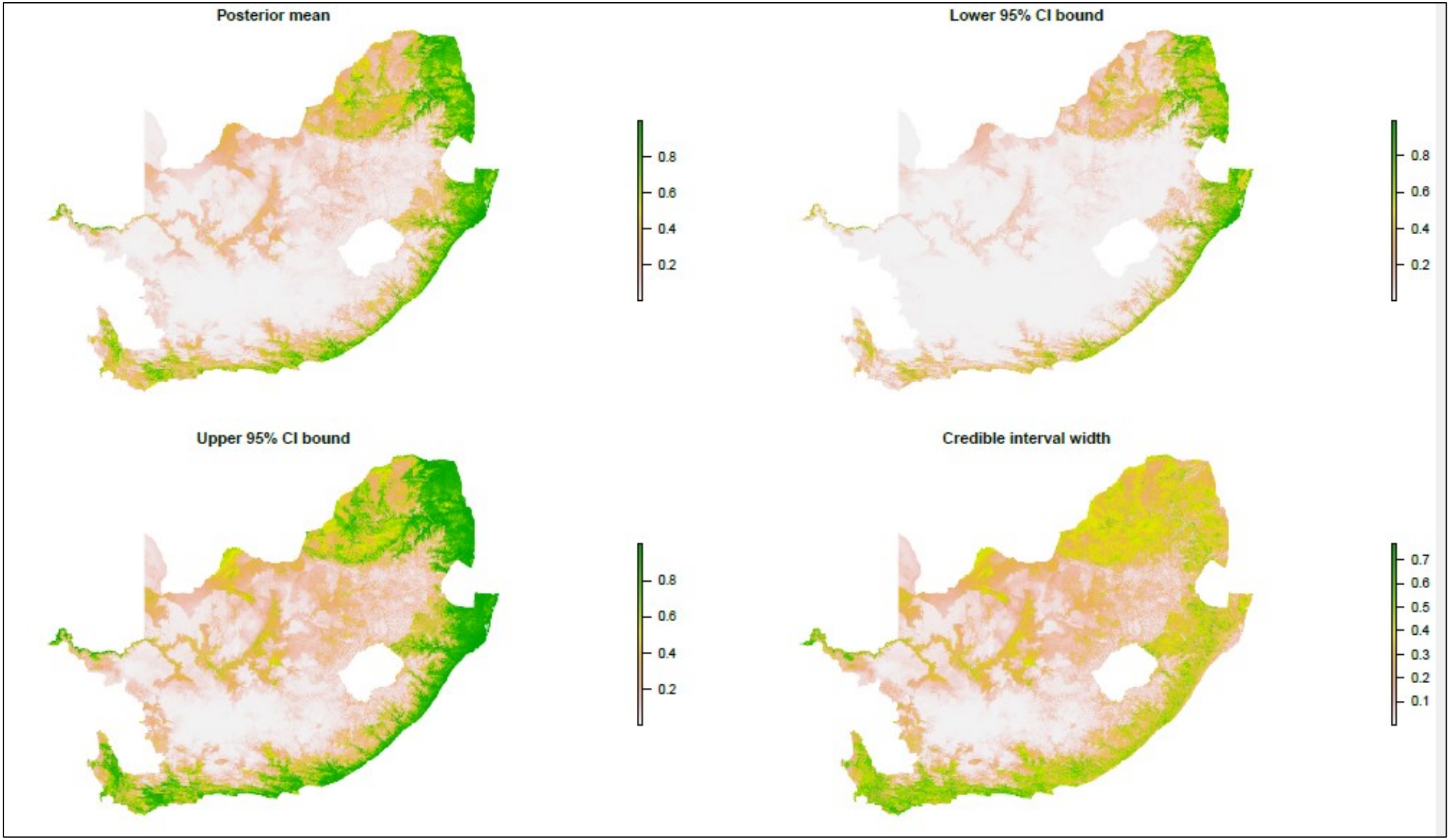


Figure S5.4.52. The modelled distribution of *Oreochromis mossambicus* in South Africa showing habitat suitability.

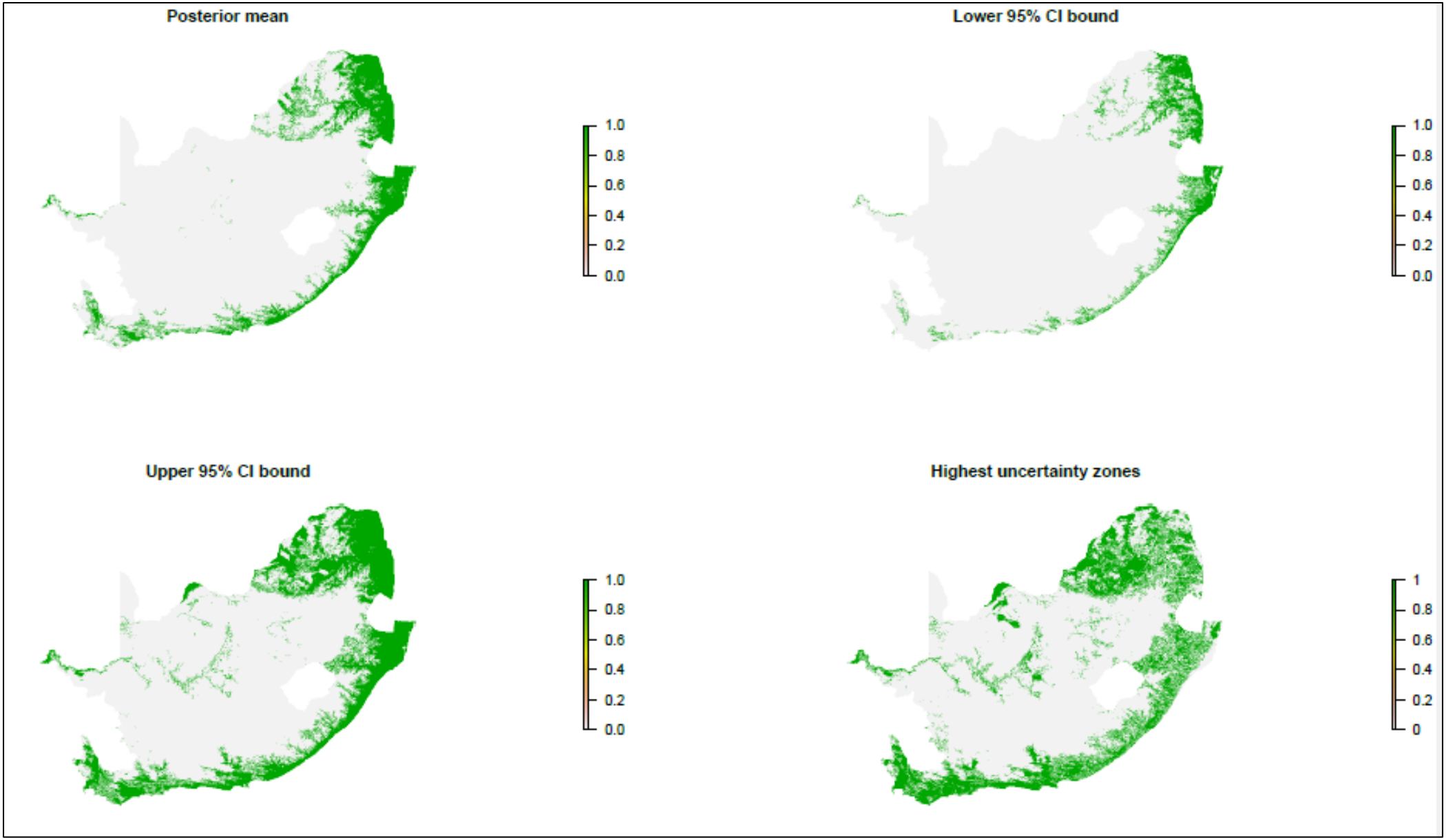


Figure S5.4.53. The modelled distribution of *Oreochromis mossambicus* in South Africa showing predicted distribution as a binary output.

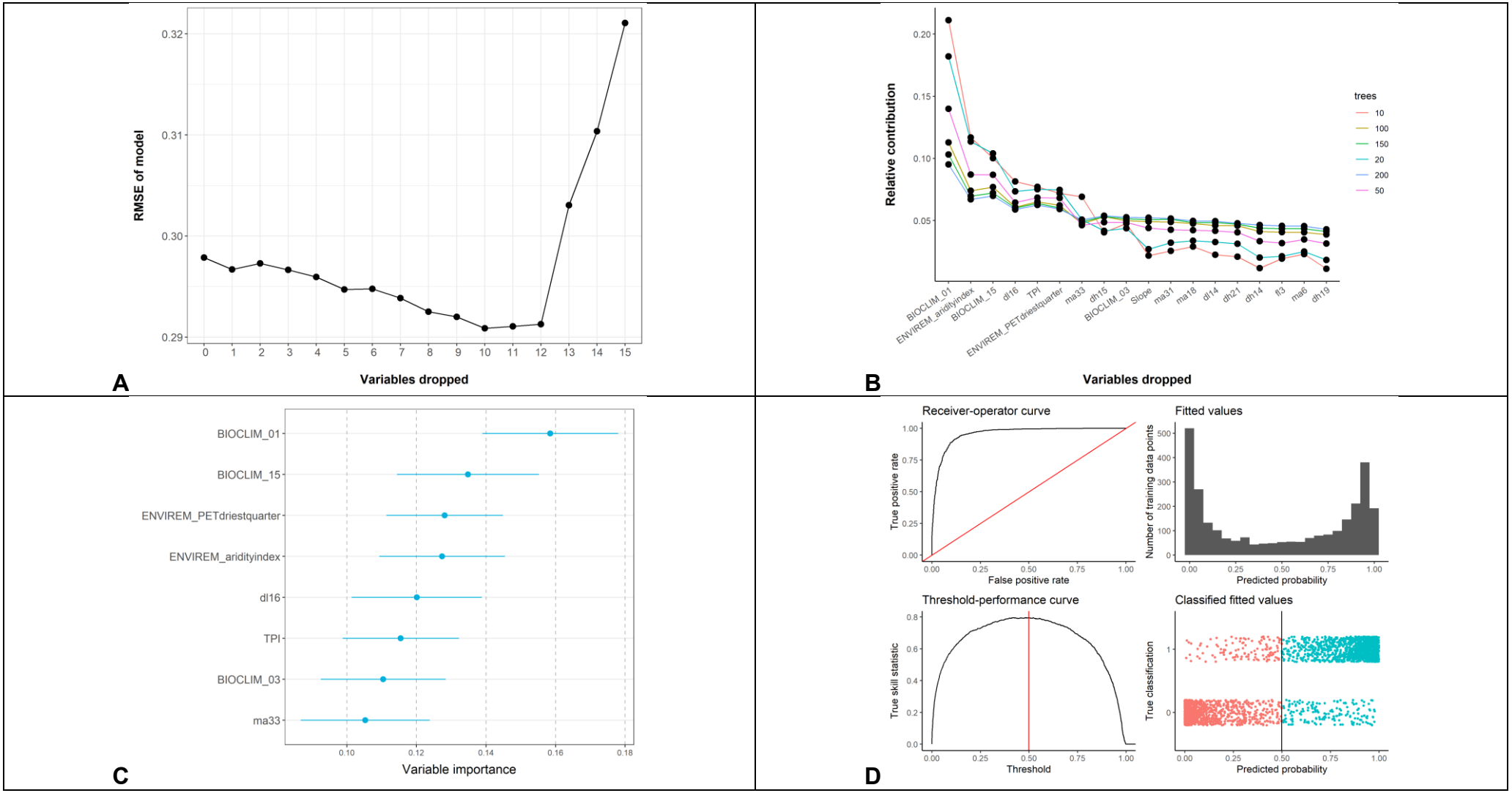


Figure S5.4.54. Model diagnostic outputs for *Oreochromis mossambicus*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

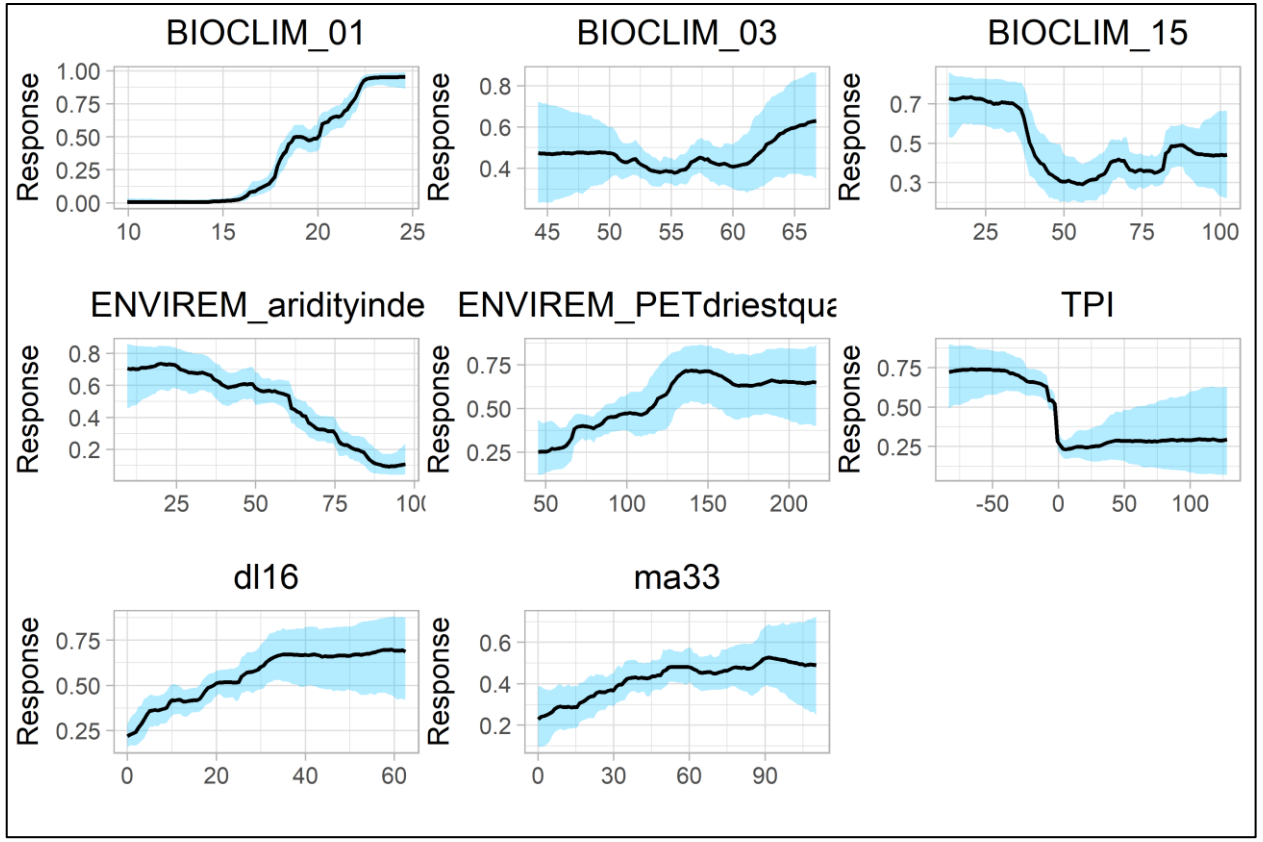


Figure S5.4.55. Partial dependence plots for *Oreochromis mossambicus.*

Pseudobarbus afer

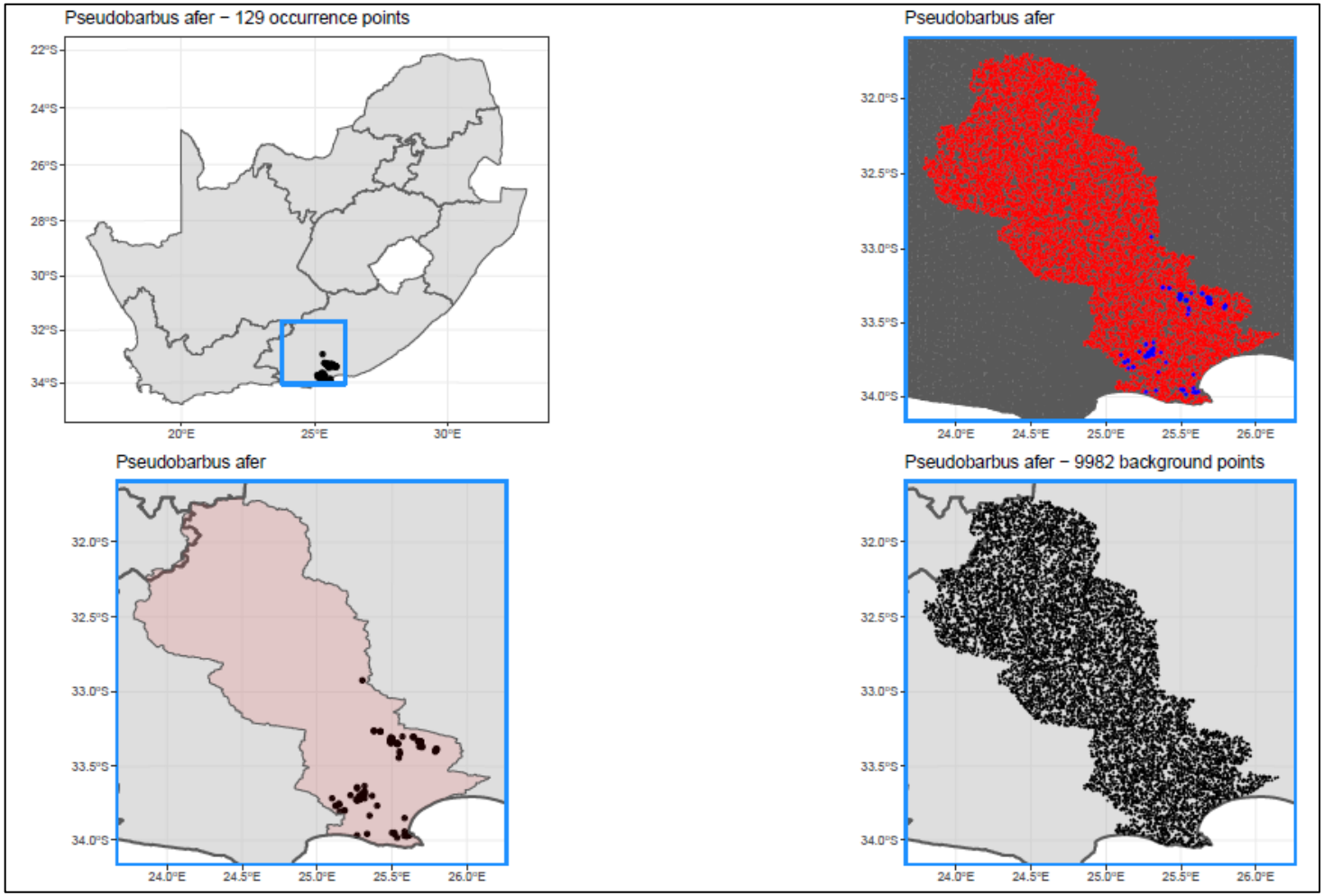


Figure S5.4.56. Occurrence records and background points for *Pseudobarbus afer.*

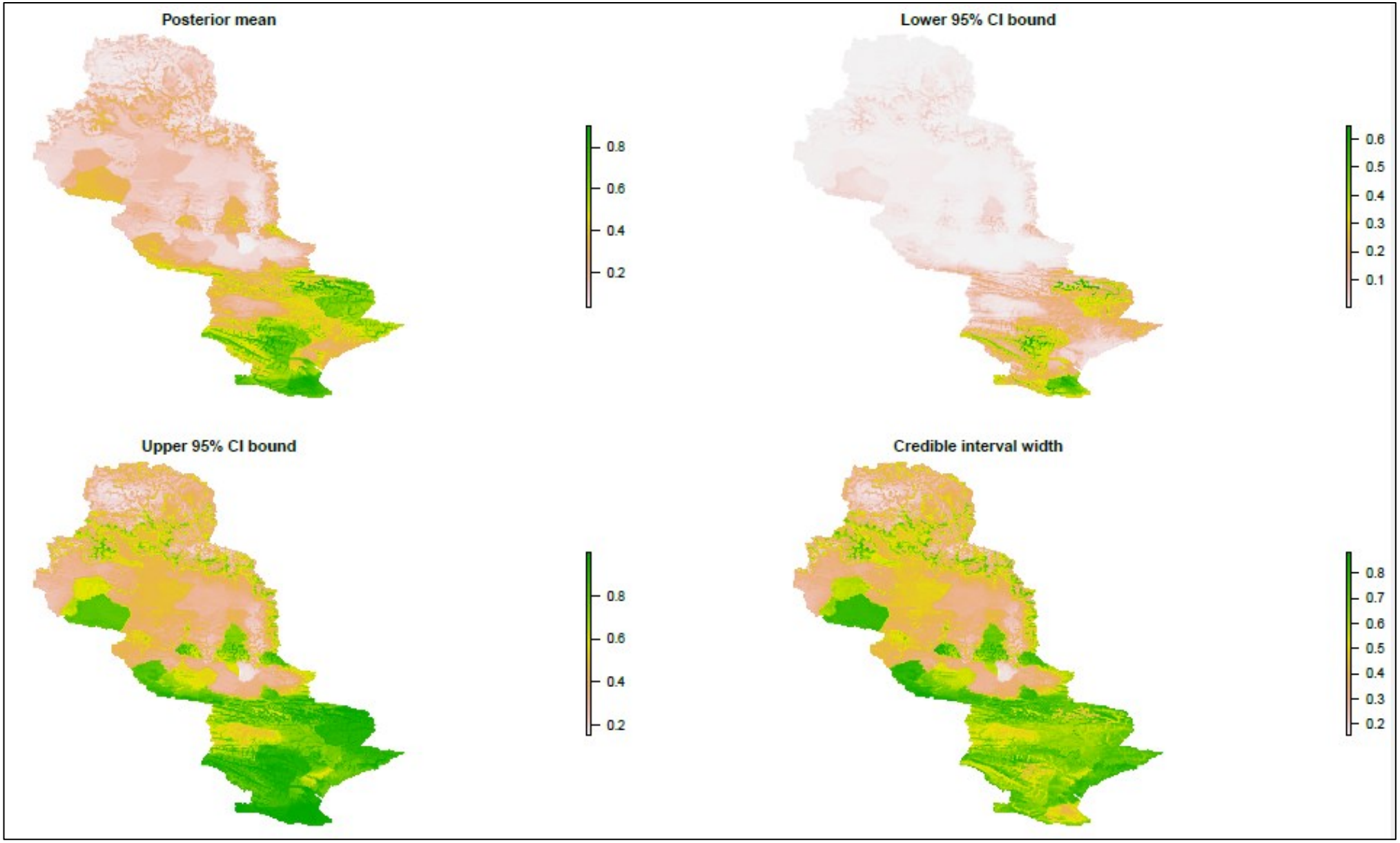


Figure S5.4.57. The modelled distribution of *Pseudobarbus afer* in South Africa showing habitat suitability.

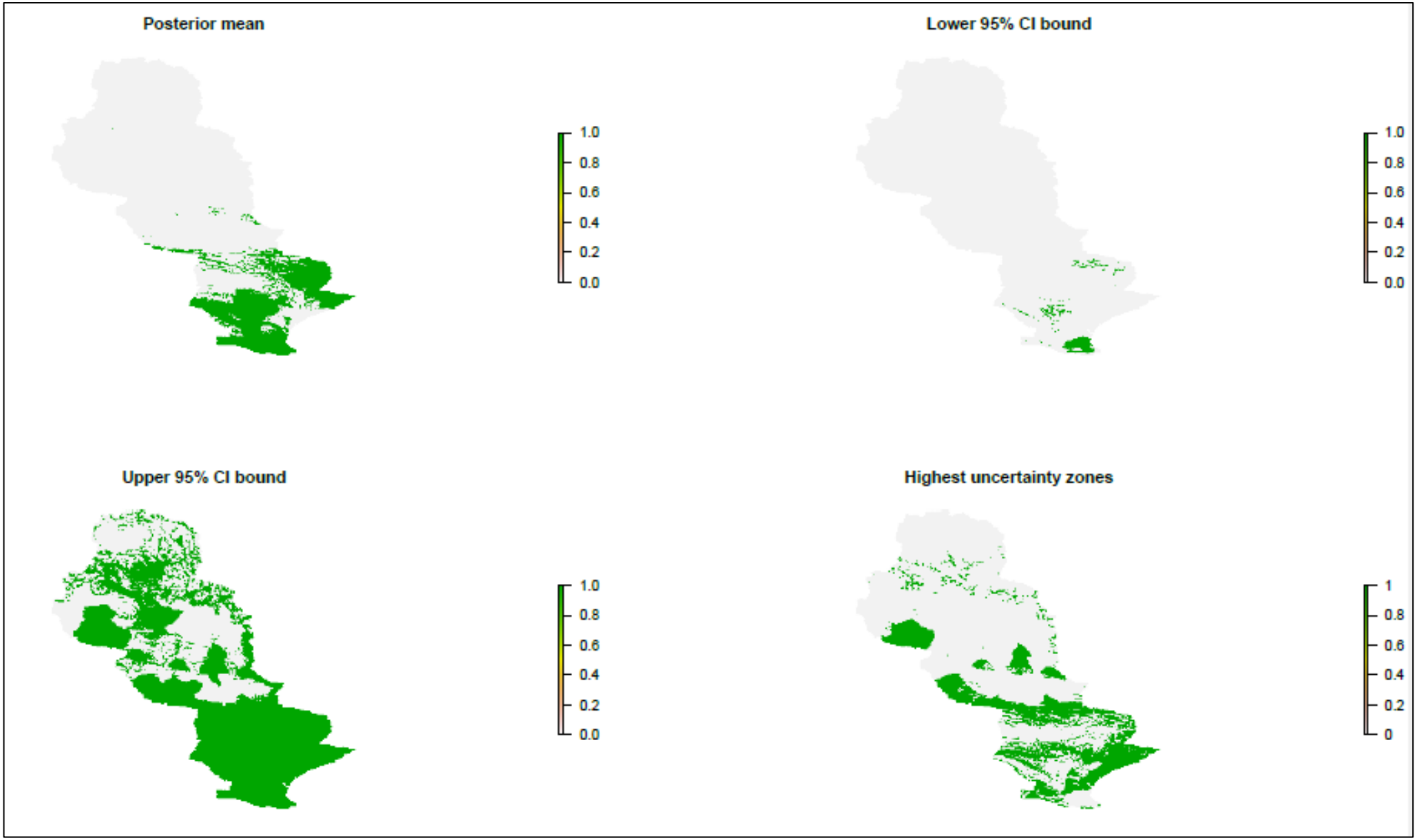


Figure S5.4.58. The modelled distribution of *Pseudobarbus afer* in South Africa showing predicted distribution as a binary output.

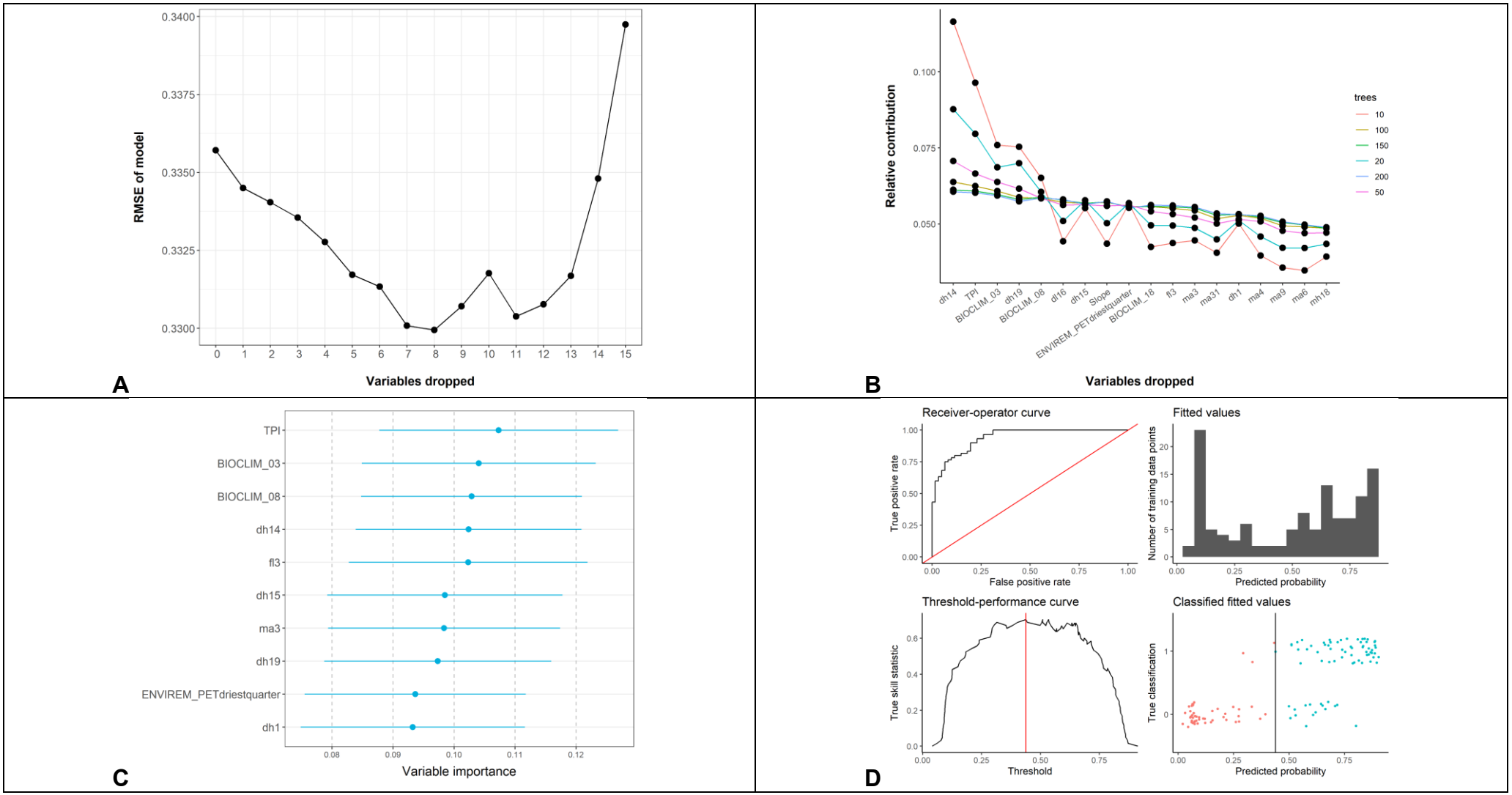


Figure S5.4.59. Model diagnostic outputs for *Pseudobarbus afer,* showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

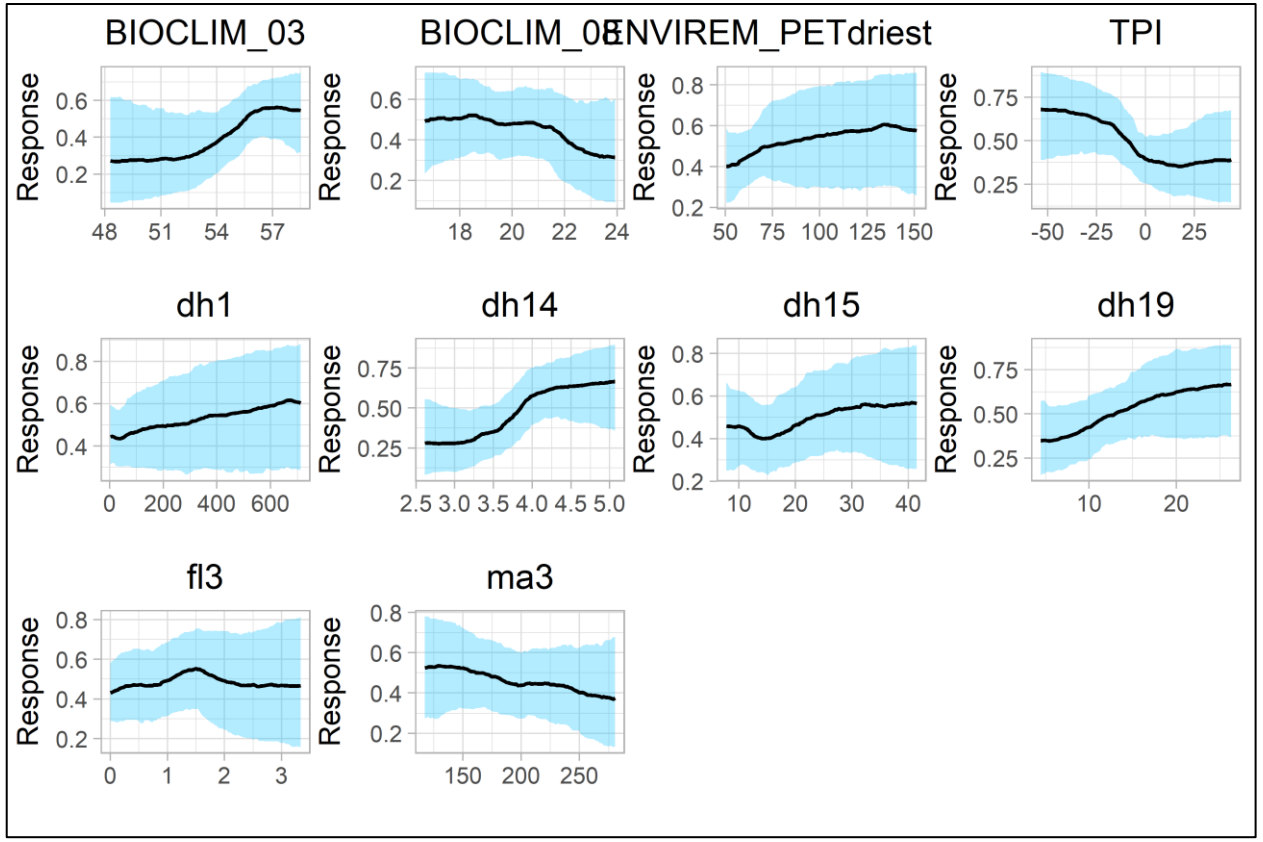


Figure S5.4.60. Partial dependence plots for *Pseudobarbus afer.*

Pseudobarbus asper

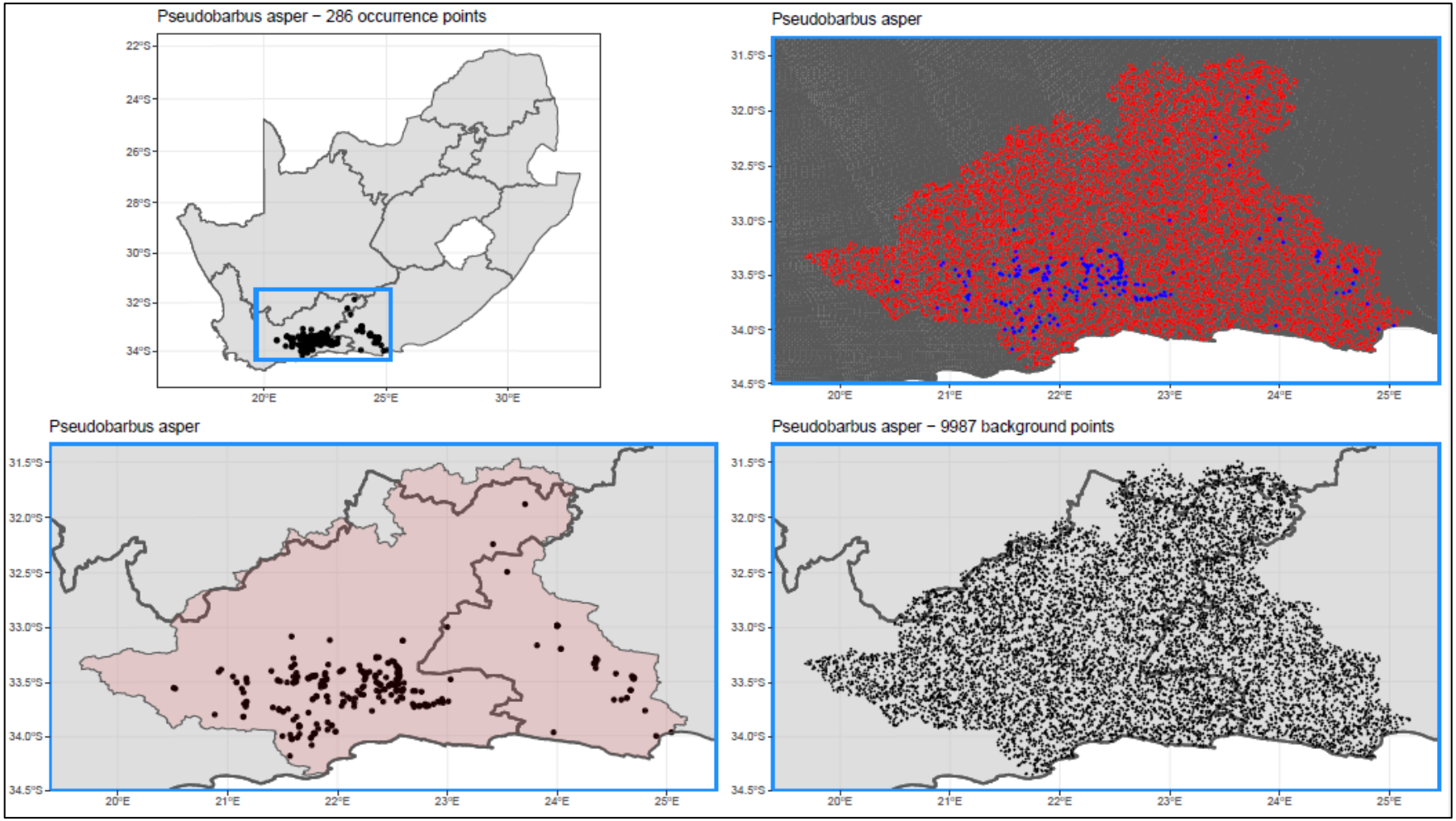


Figure S5.4.61. Occurrence records and background points for *Pseudobarbus asper*.

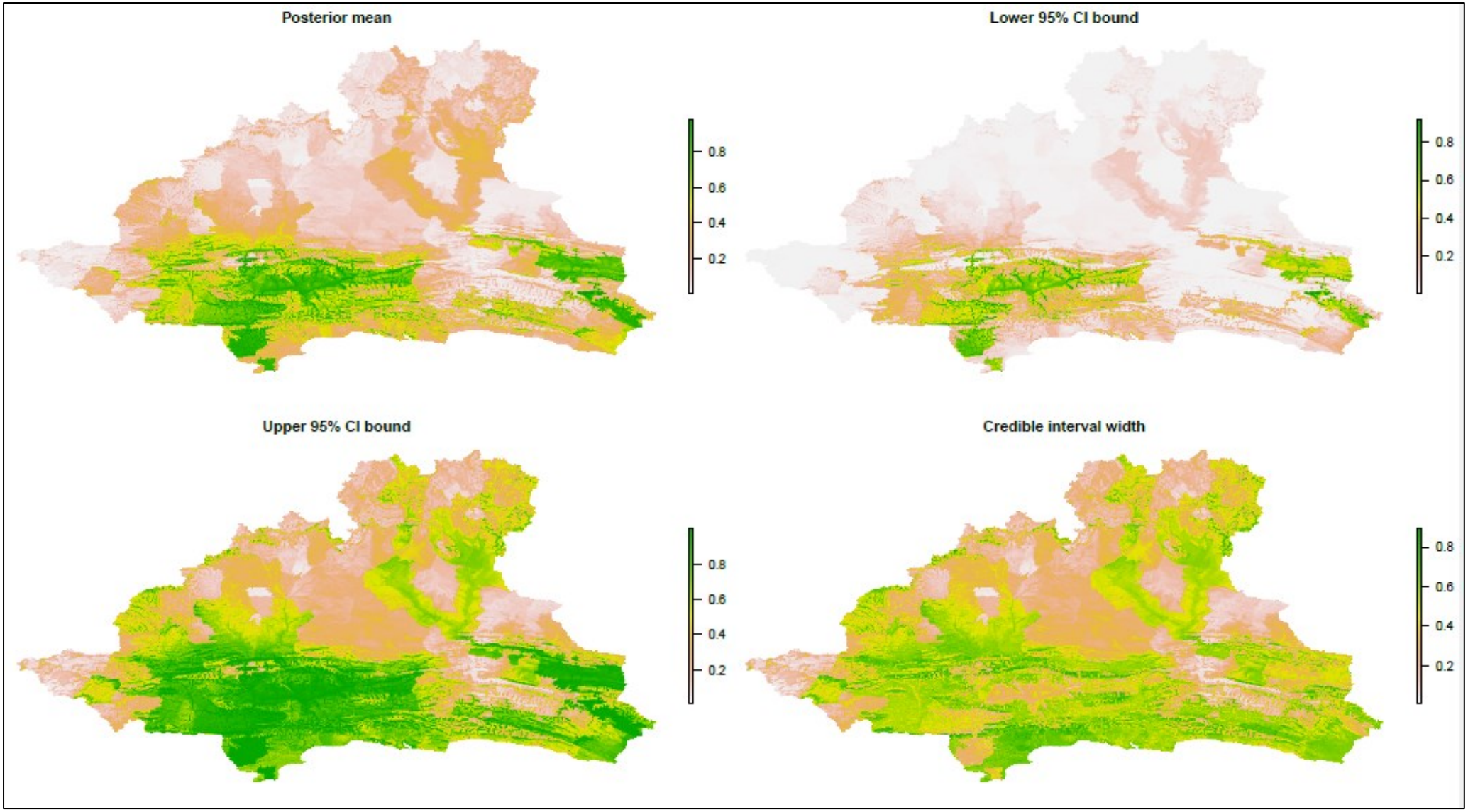


Figure S5.4.62. The modelled distribution of *Pseudobarbus asper* in South Africa showing habitat suitability.

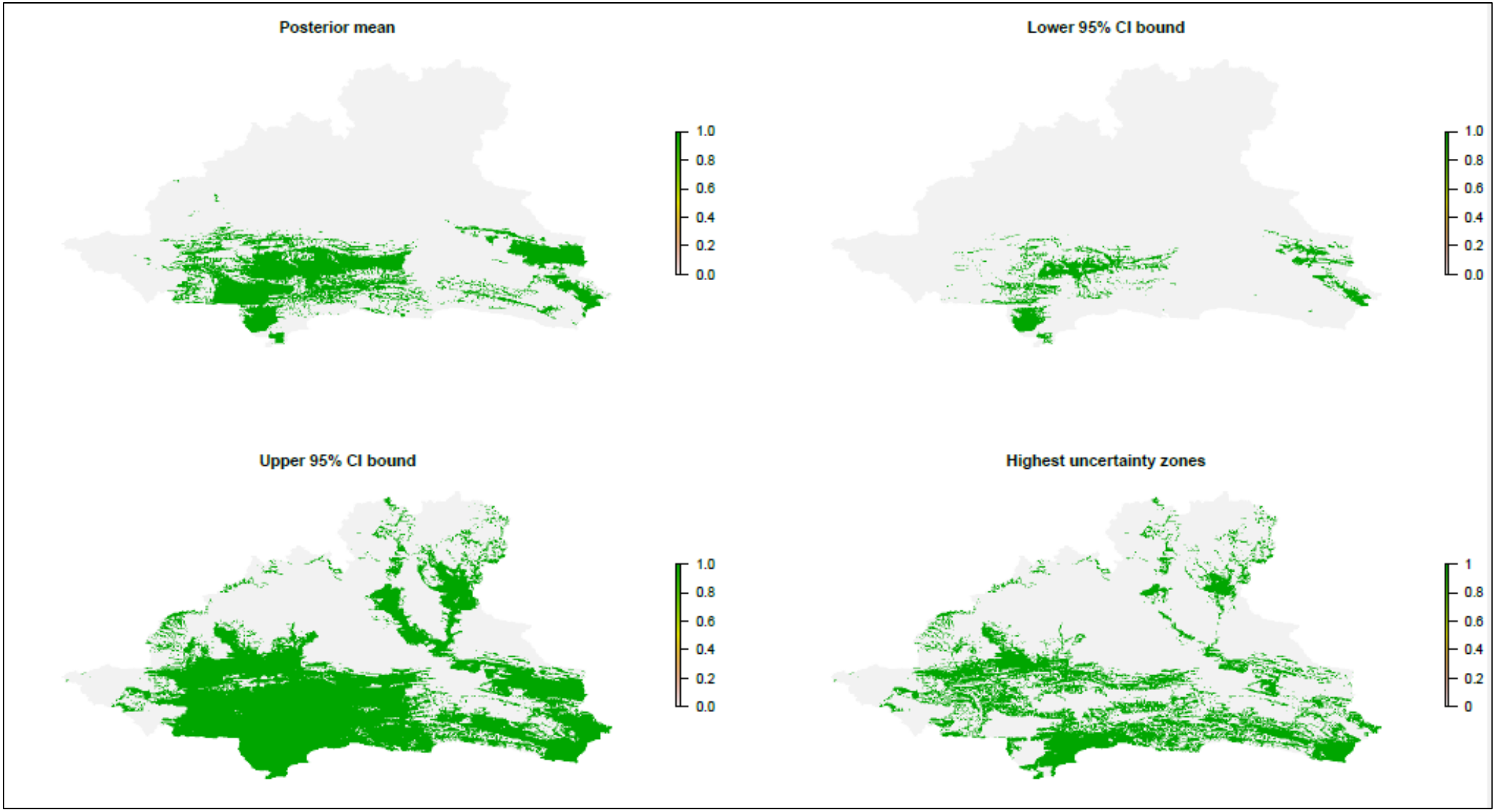


Figure S5.4.63. The modelled distribution of *Pseudobarbus asper* in South Africa showing predicted distribution as a binary output.

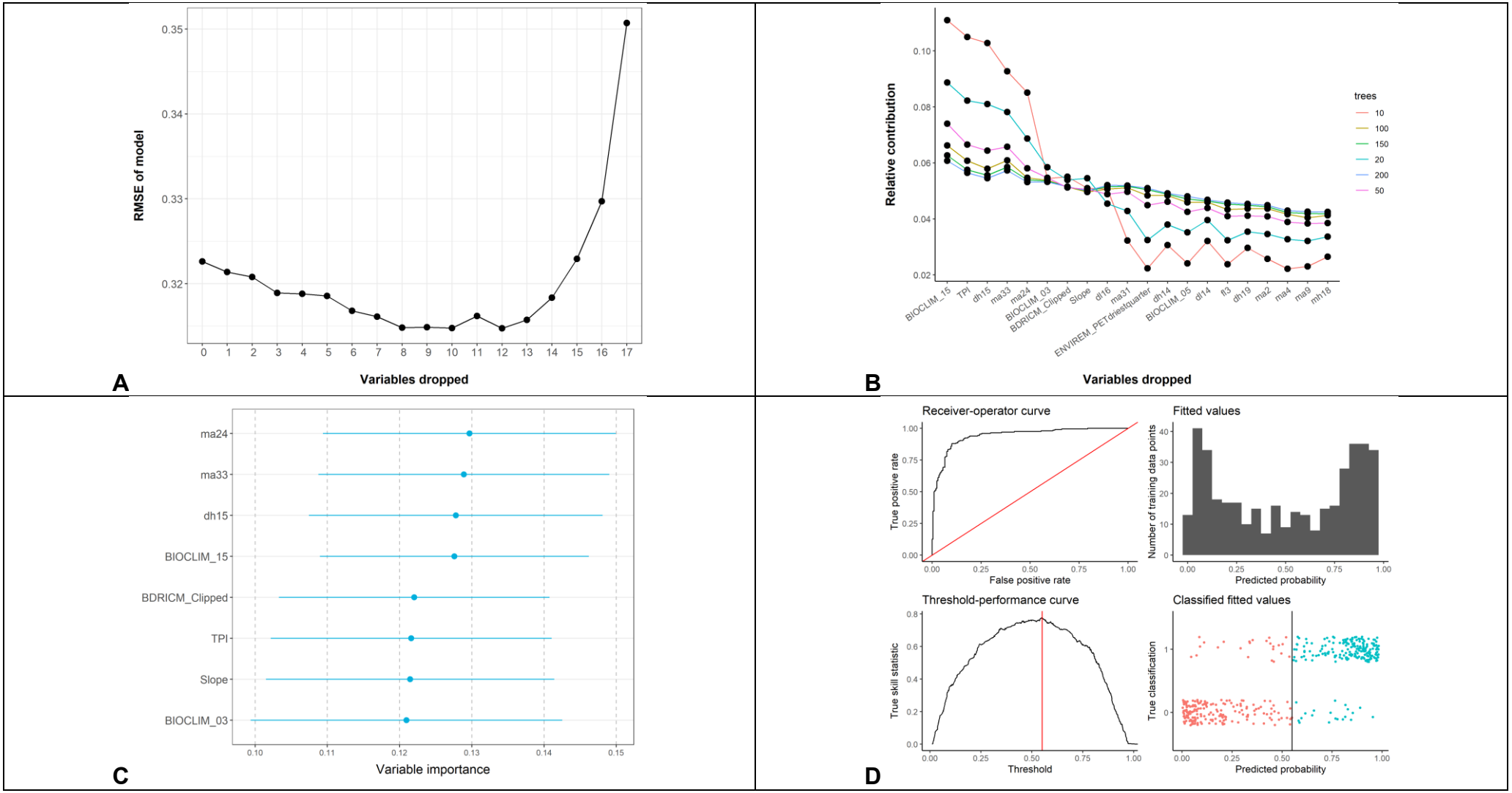


Figure S5.4.64. Model diagnostic outputs for *Pseudobarbus asper*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

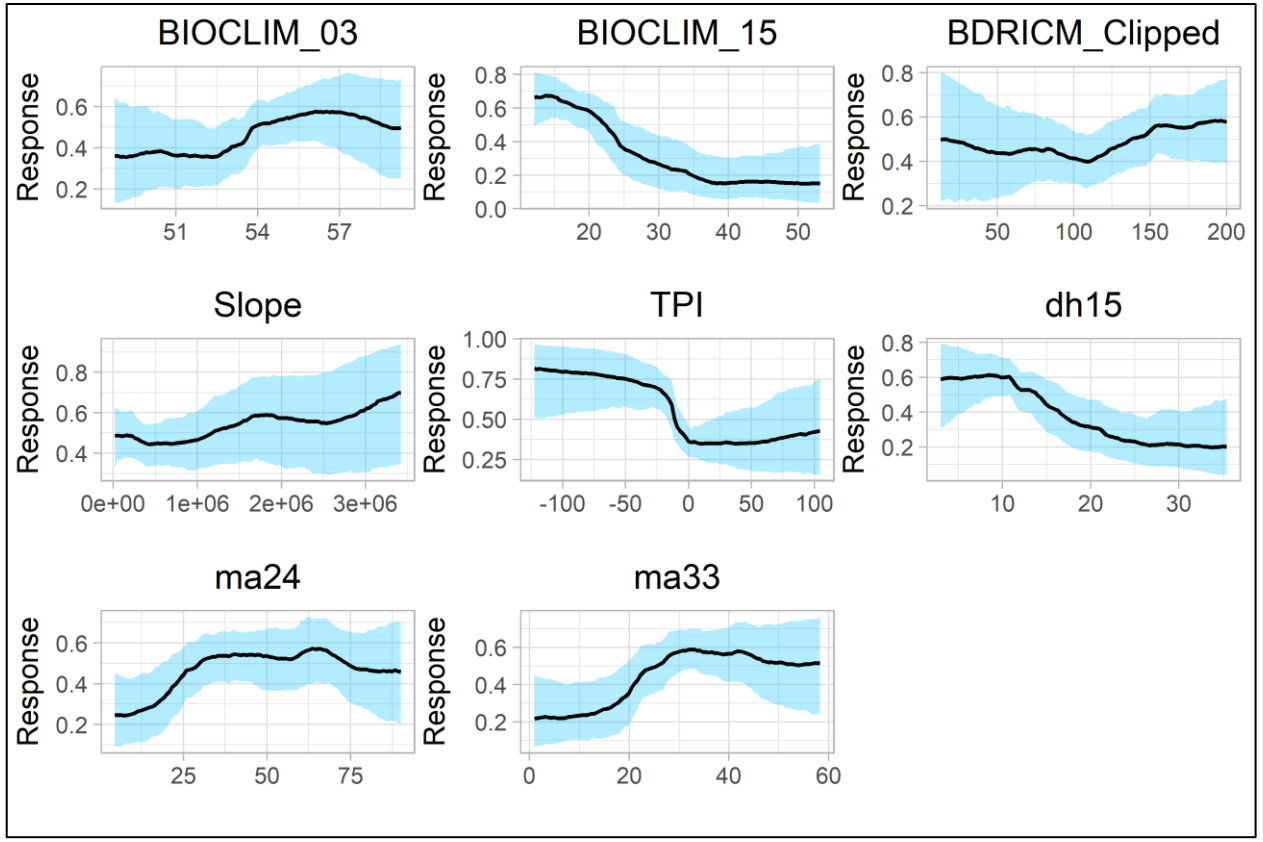


Figure S5.4.65. Partial dependence plots for *Pseudobarbus asper.*

Pseudobarbus burgi

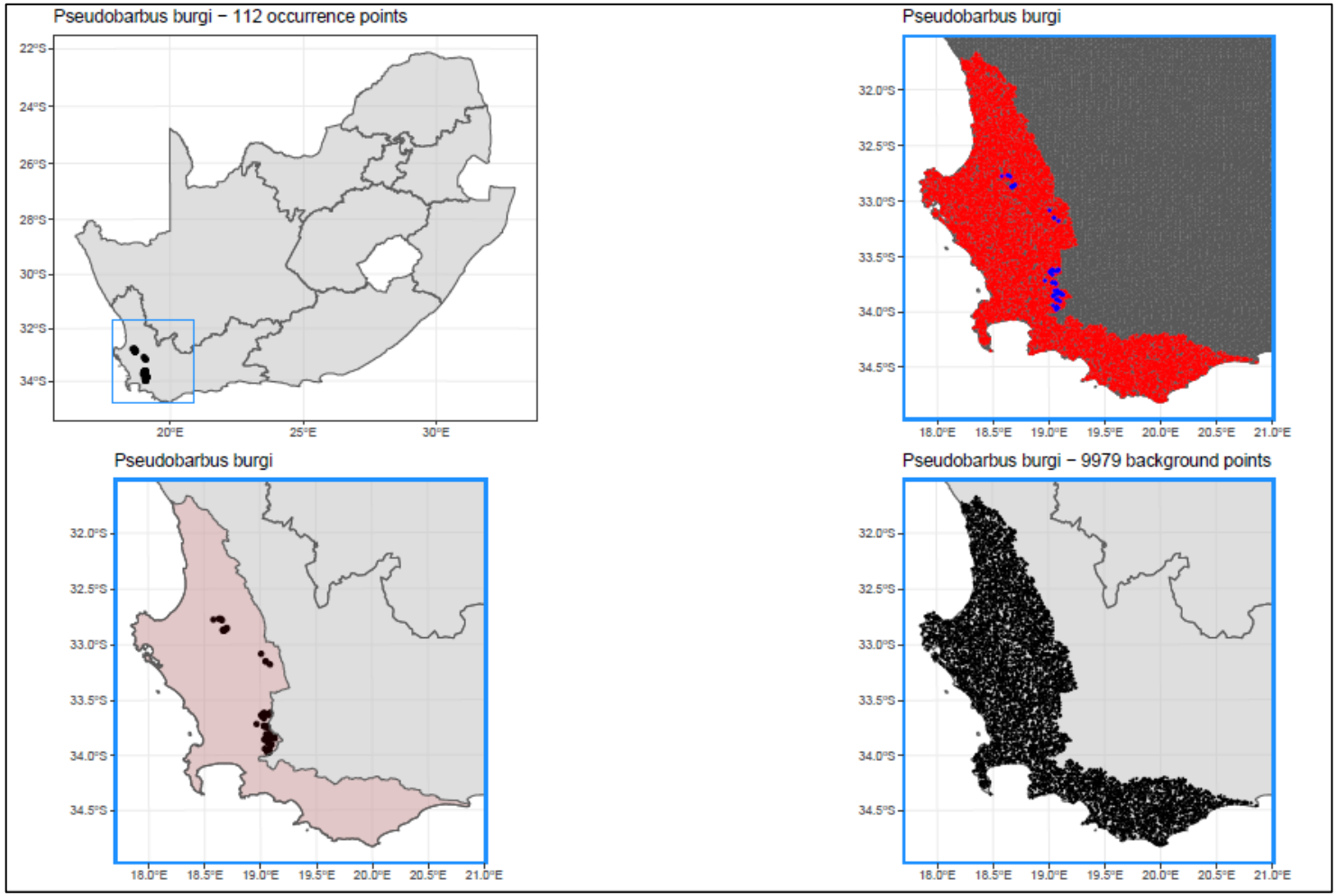


Figure S5.4.66. Occurrence records and background points for *Pseudobarbus burgi.*

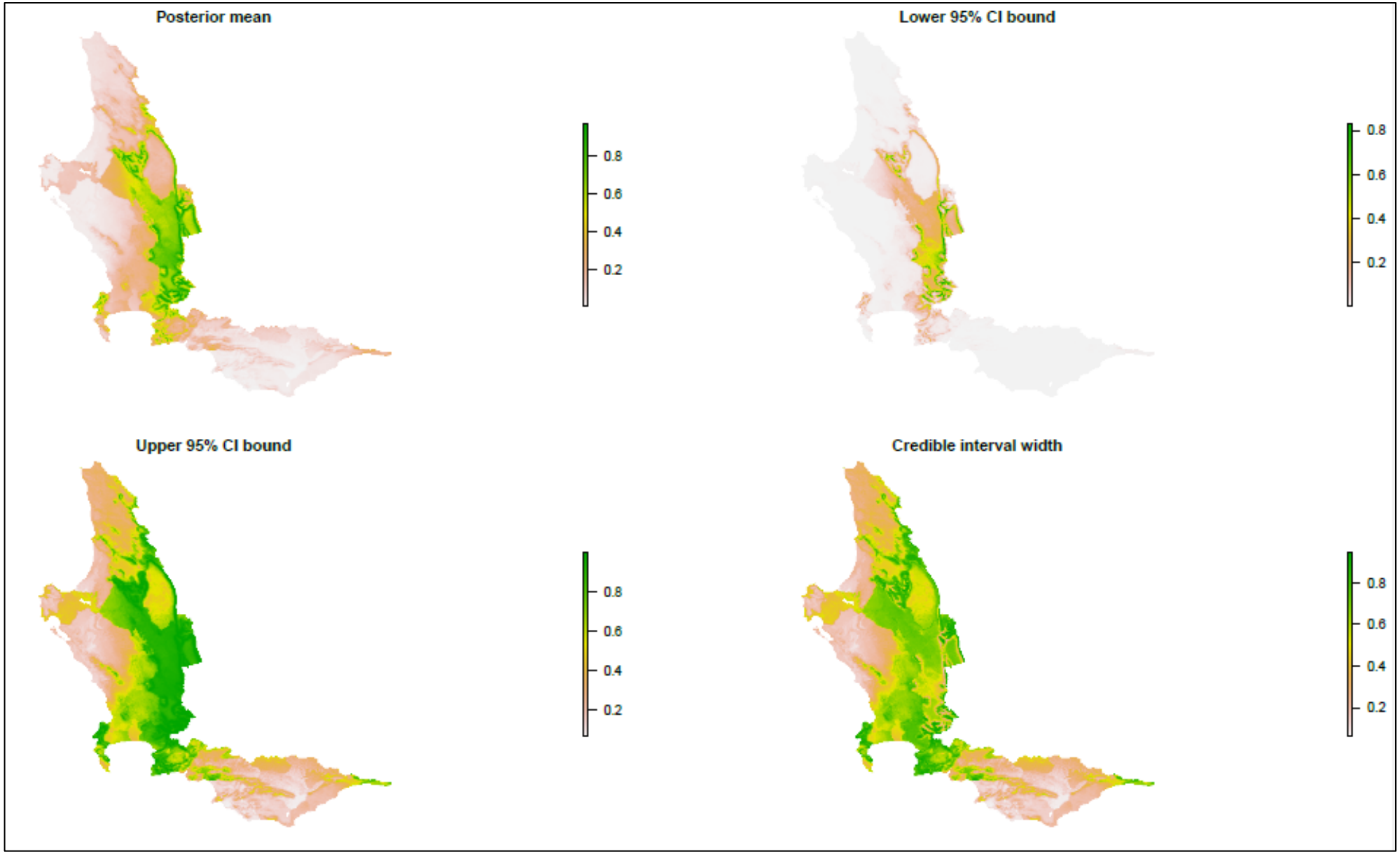


Figure S5.4.67. The modelled distribution of *Pseudobarbus burgi* in South Africa showing habitat suitability.

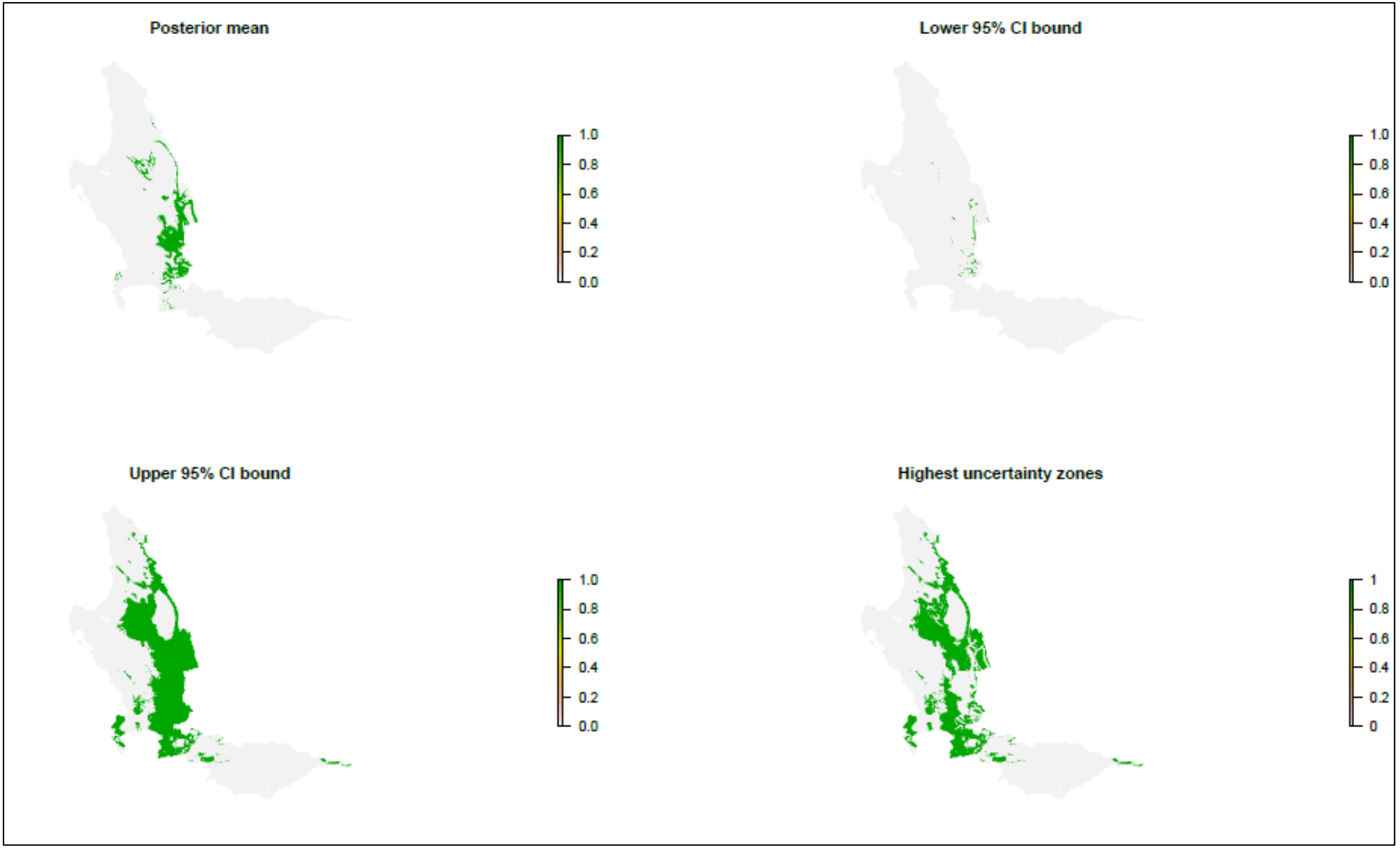


Figure S5.4.68. The modelled distribution of *Pseudobarbus burgi* in South Africa showing predicted distribution as a binary output.

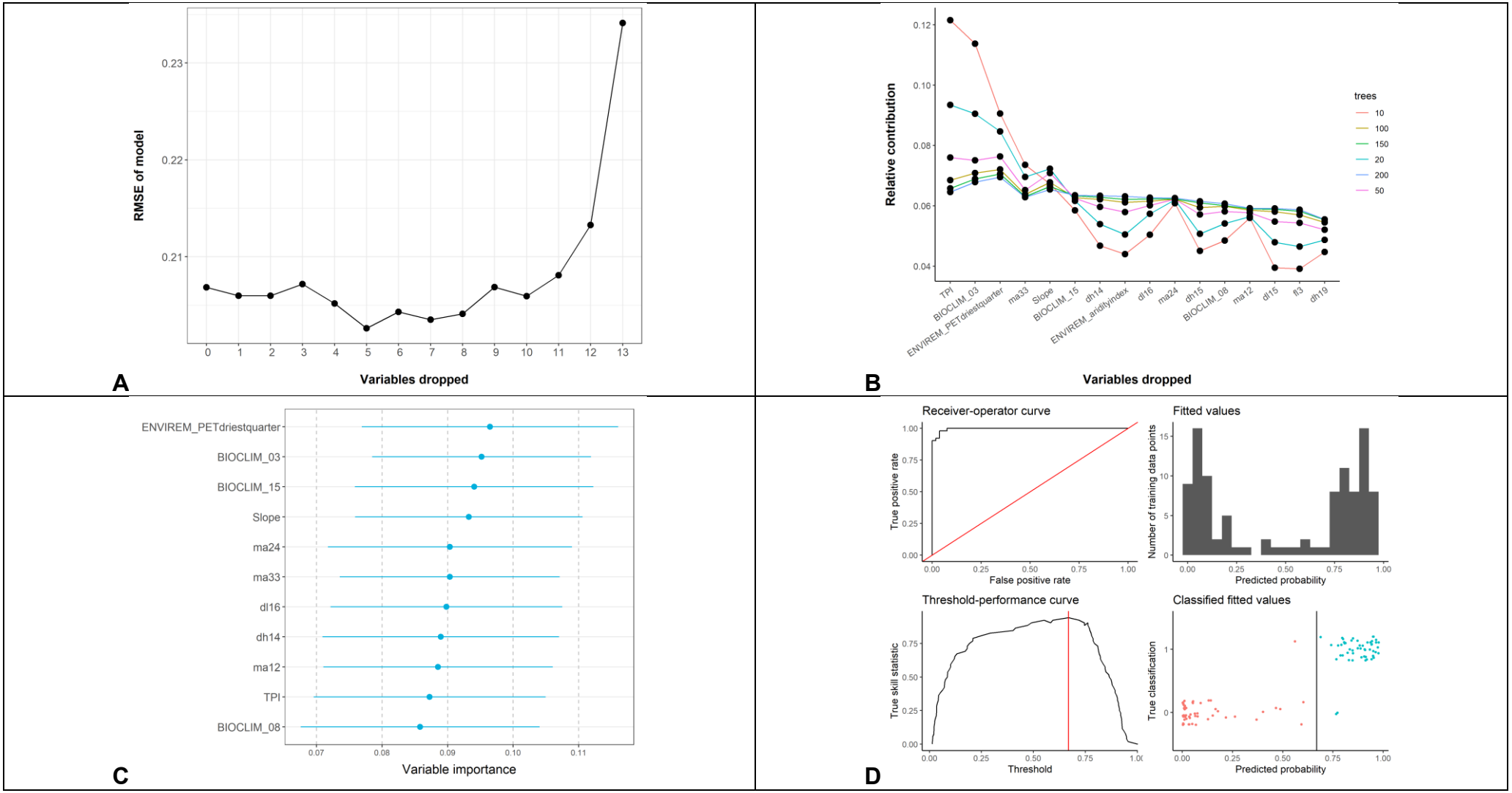


Figure S5.4.69. Model diagnostic outputs for *Pseudobarbus burgi*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

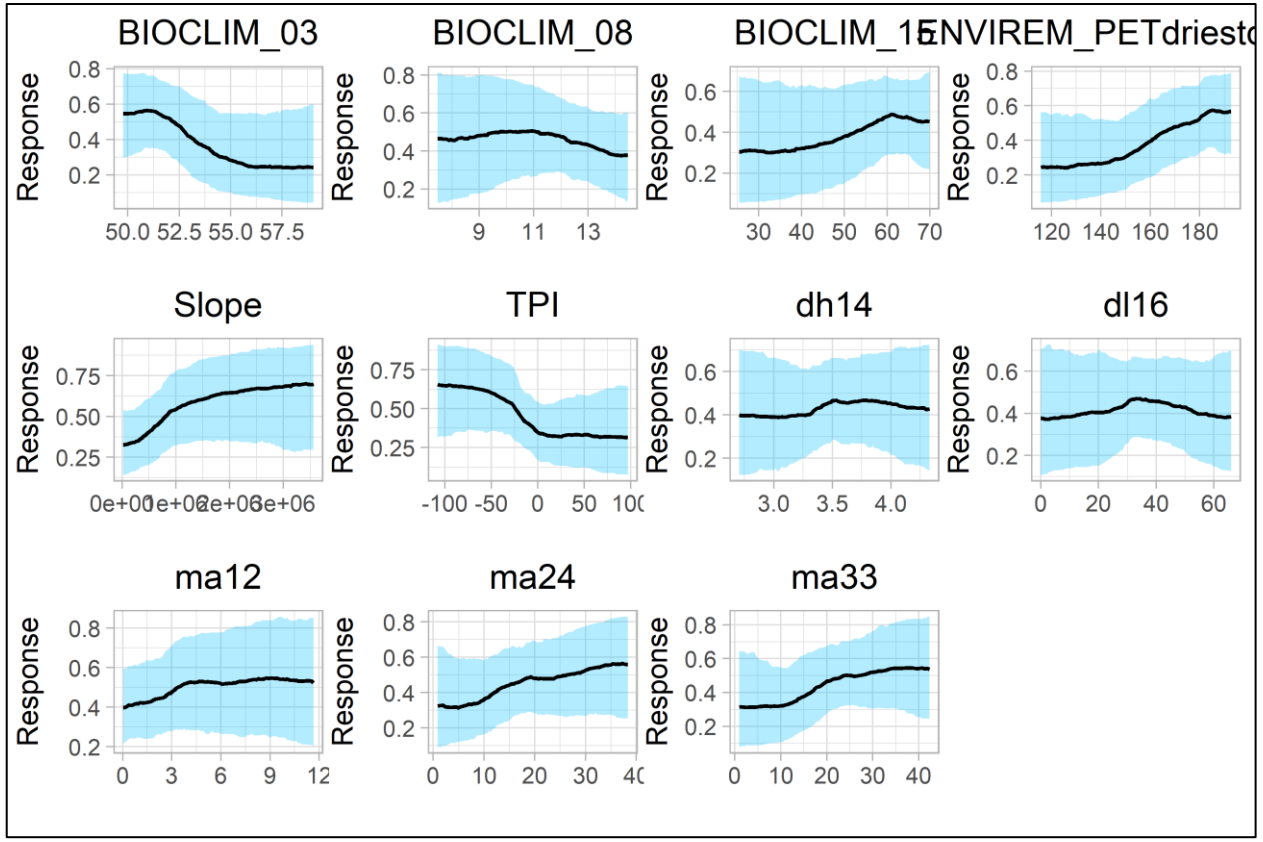


Figure S5.4.70. Partial dependence plots for *Pseudobarbus burgi.*

Pseudobarbus capensis

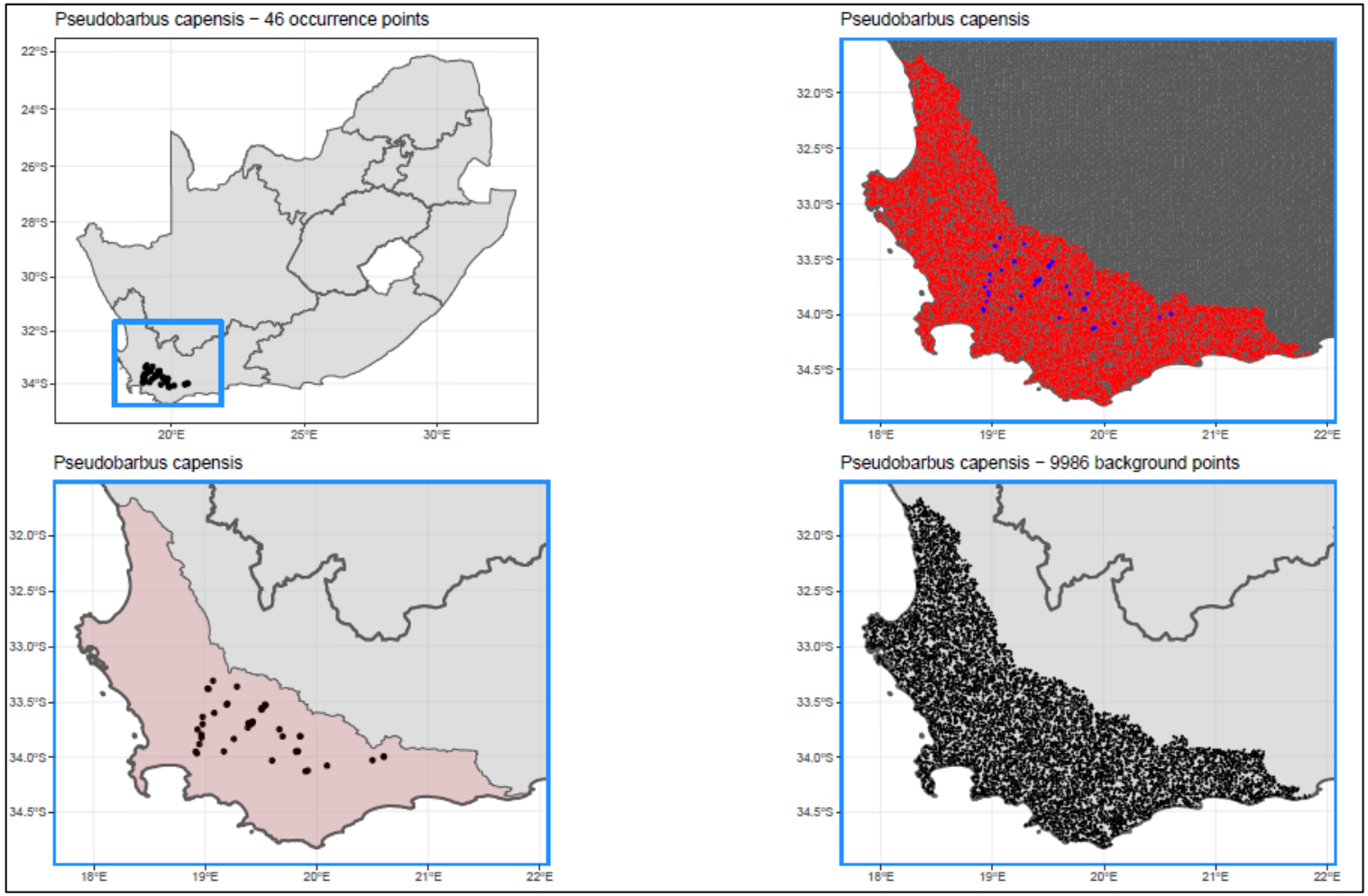


Figure S5.4.71. Occurrence records and background points for *Pseudobarbus capensis.*

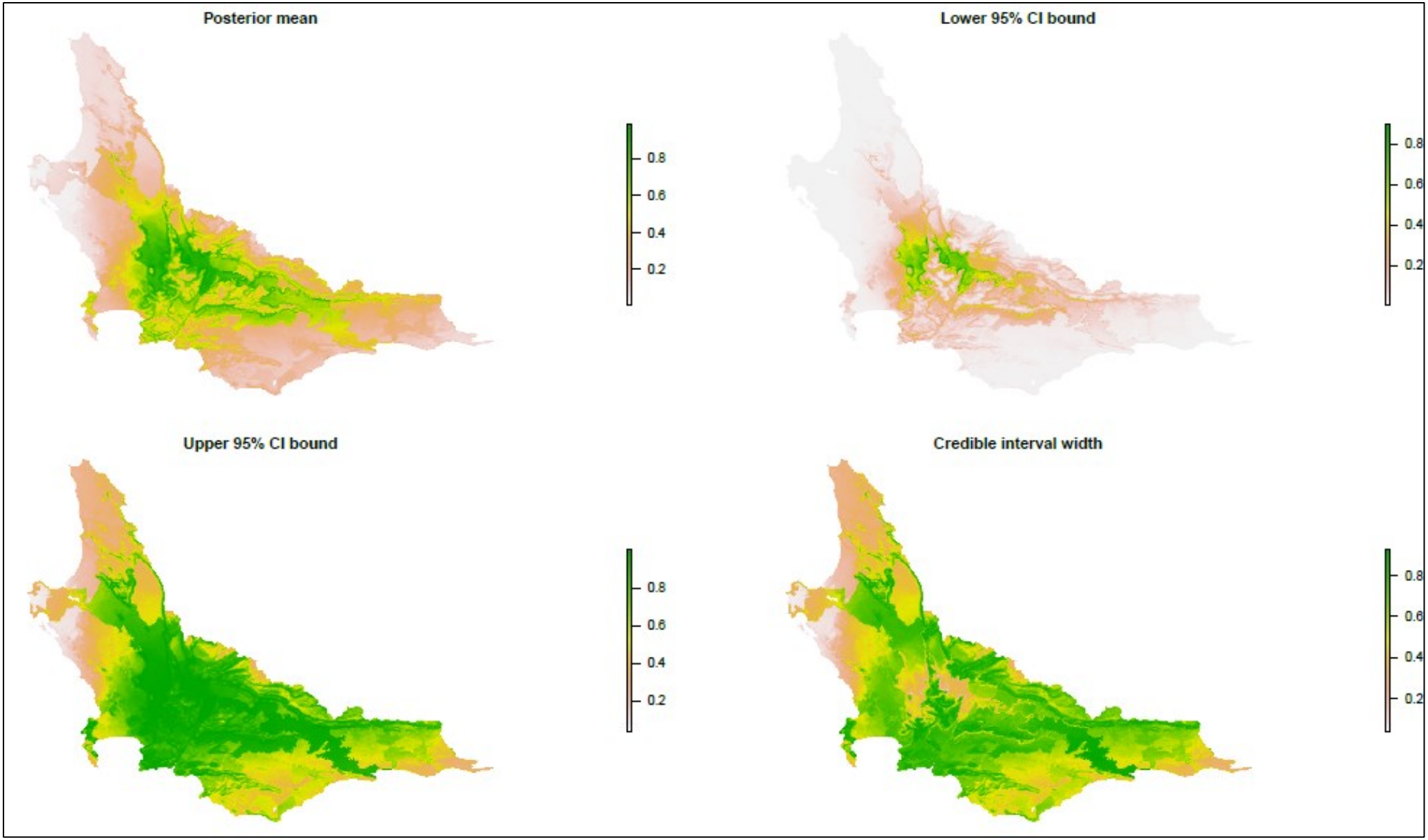


Figure S5.4.72. The modelled distribution of *Pseudobarbus capensis* in South Africa showing habitat suitability.

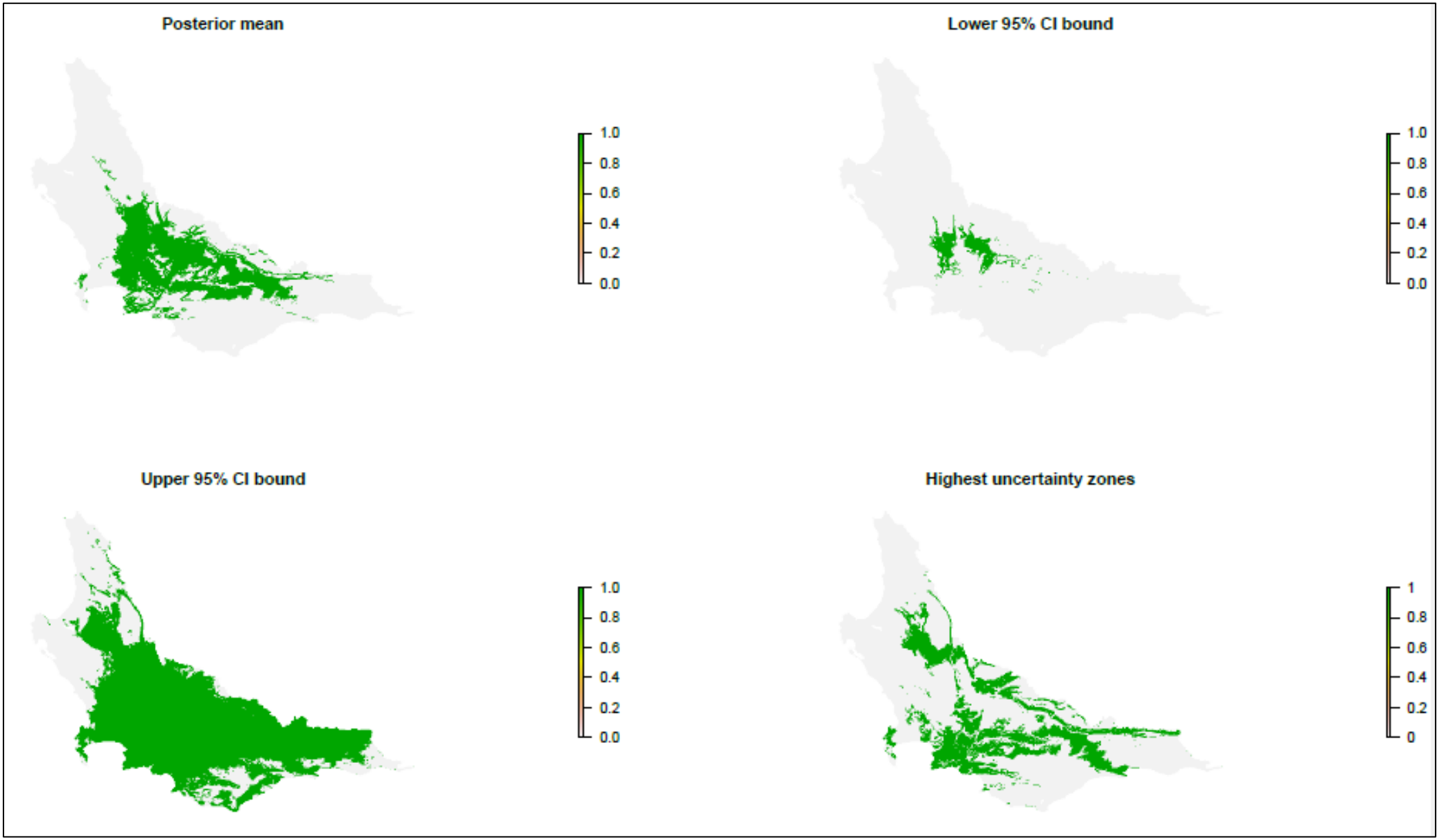


Figure S5.4.73. The modelled distribution of *Pseudobarbus capensis* in South Africa showing predicted distribution as a binary output.

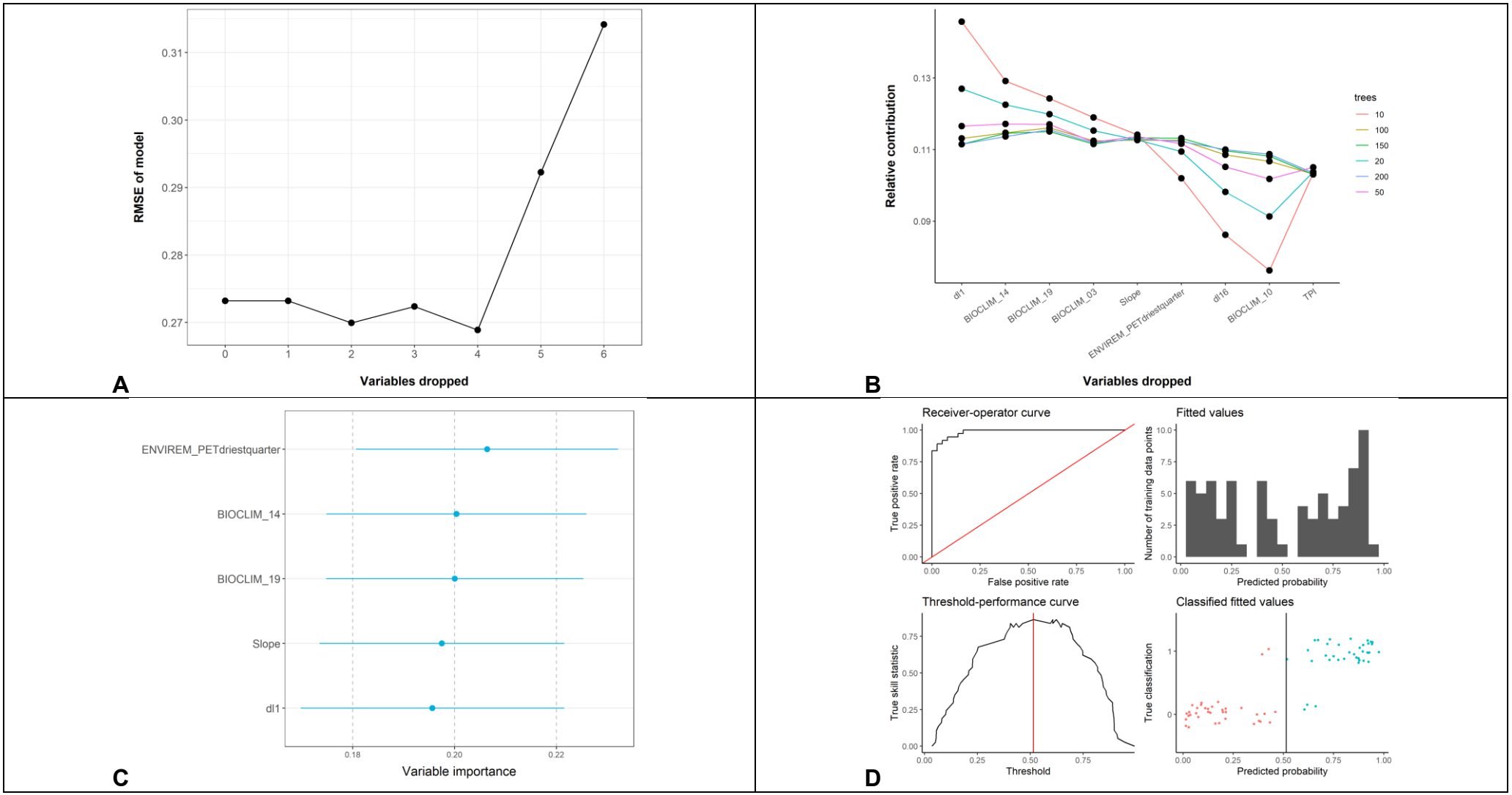


Figure S5.4.74. Model diagnostic outputs for *Pseudobarbus capensis*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

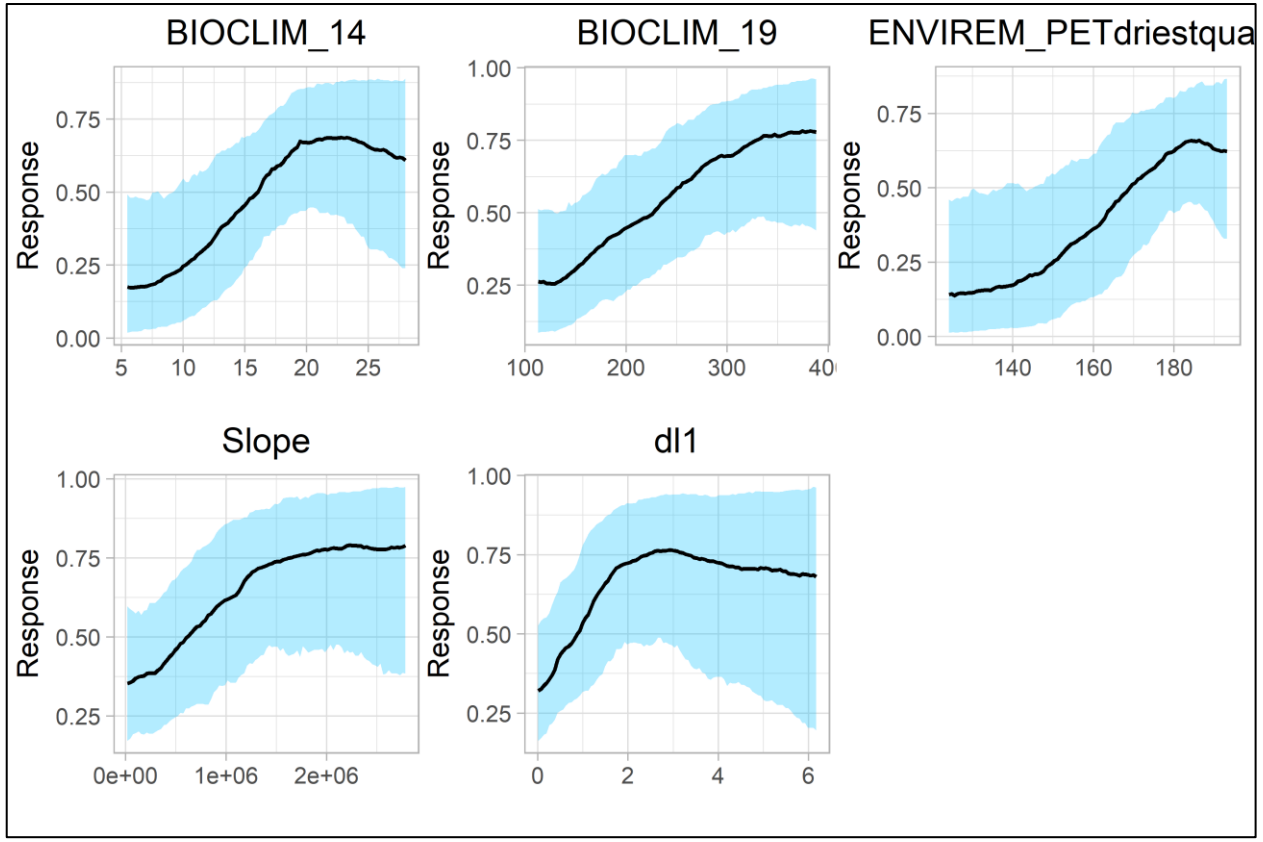


Figure S5.4.75. Partial dependence plots for *Pseudobarbus capensis.*

Pseudobarbus erubescens

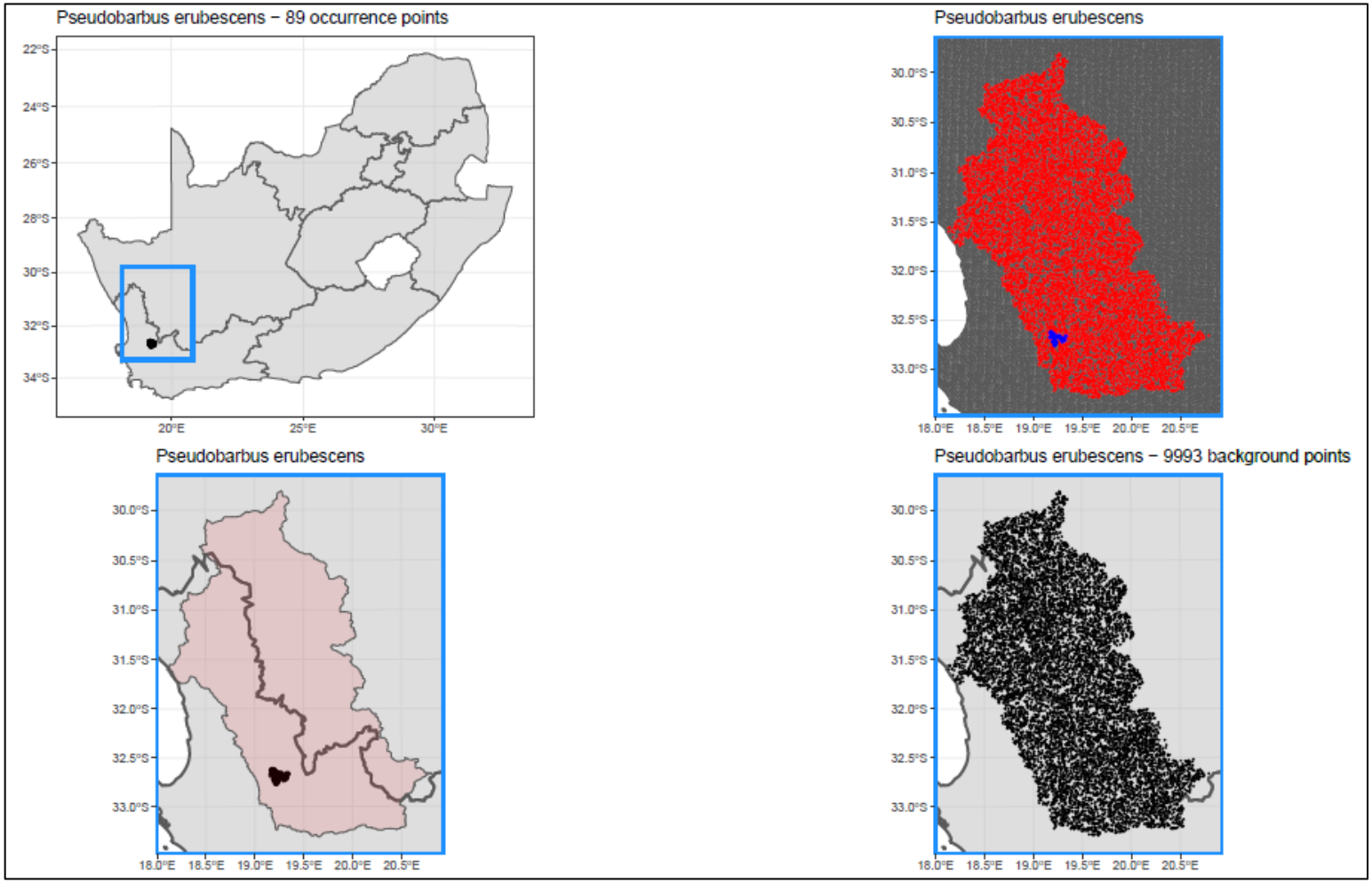


Figure S5.4.76. Occurrence records and background points for *Pseudobarbus erubescens.*

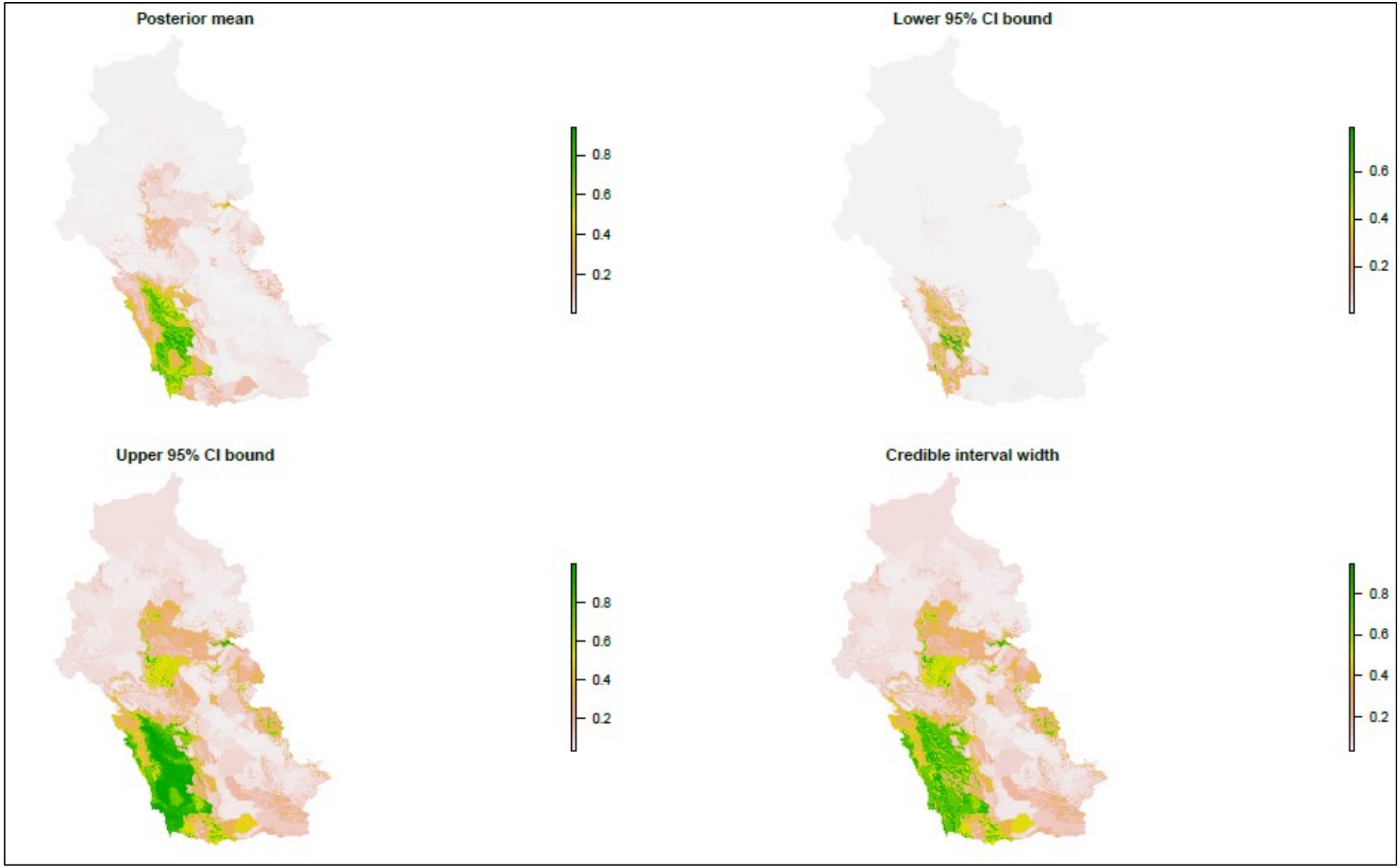


Figure S5.4.77. The modelled distribution of *Pseudobarbus erubescens* in South Africa showing habitat suitability.

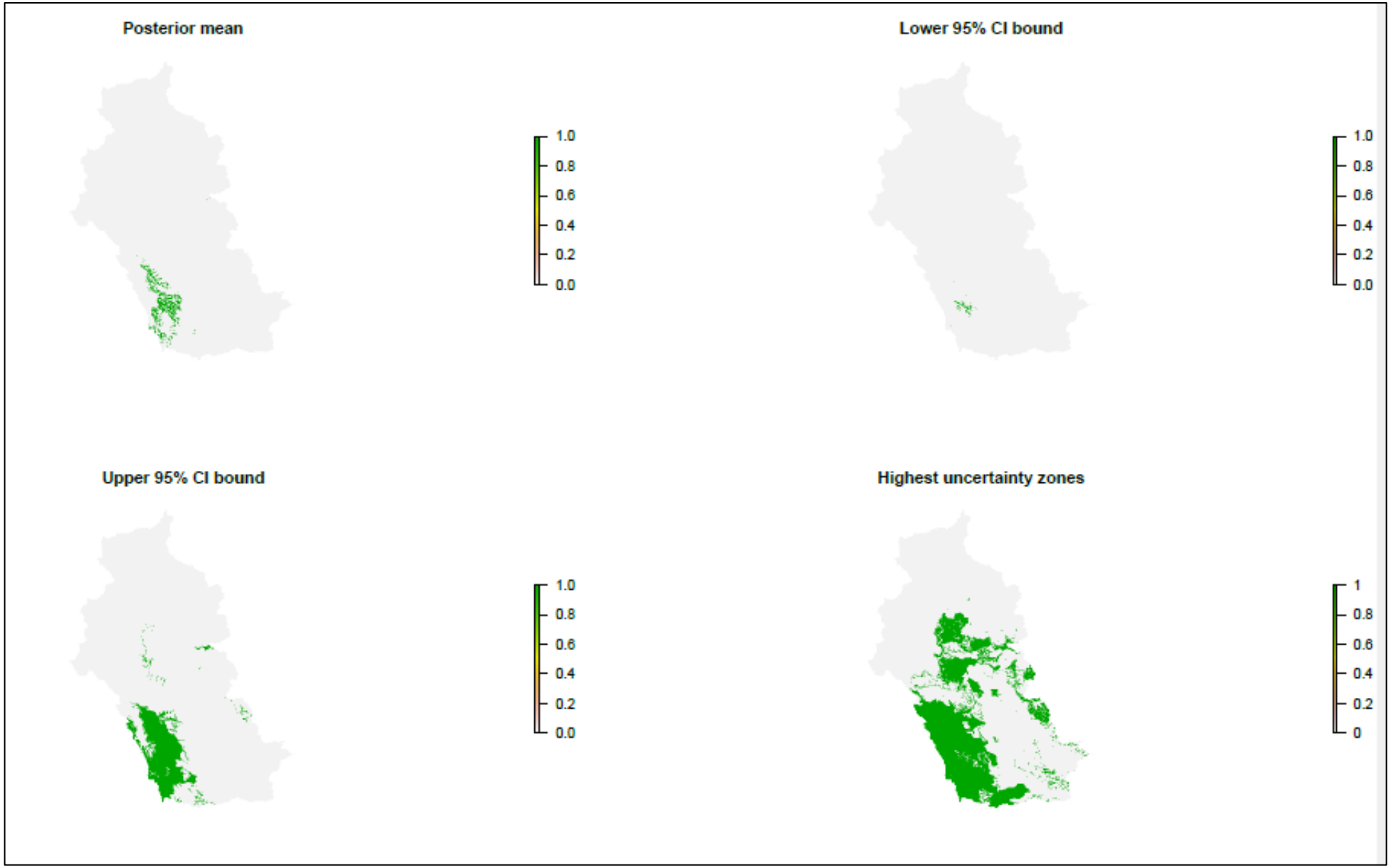


Figure S5.4.78. The modelled distribution of *Pseudobarbus erubescens* in South Africa showing predicted distribution as a binary output.

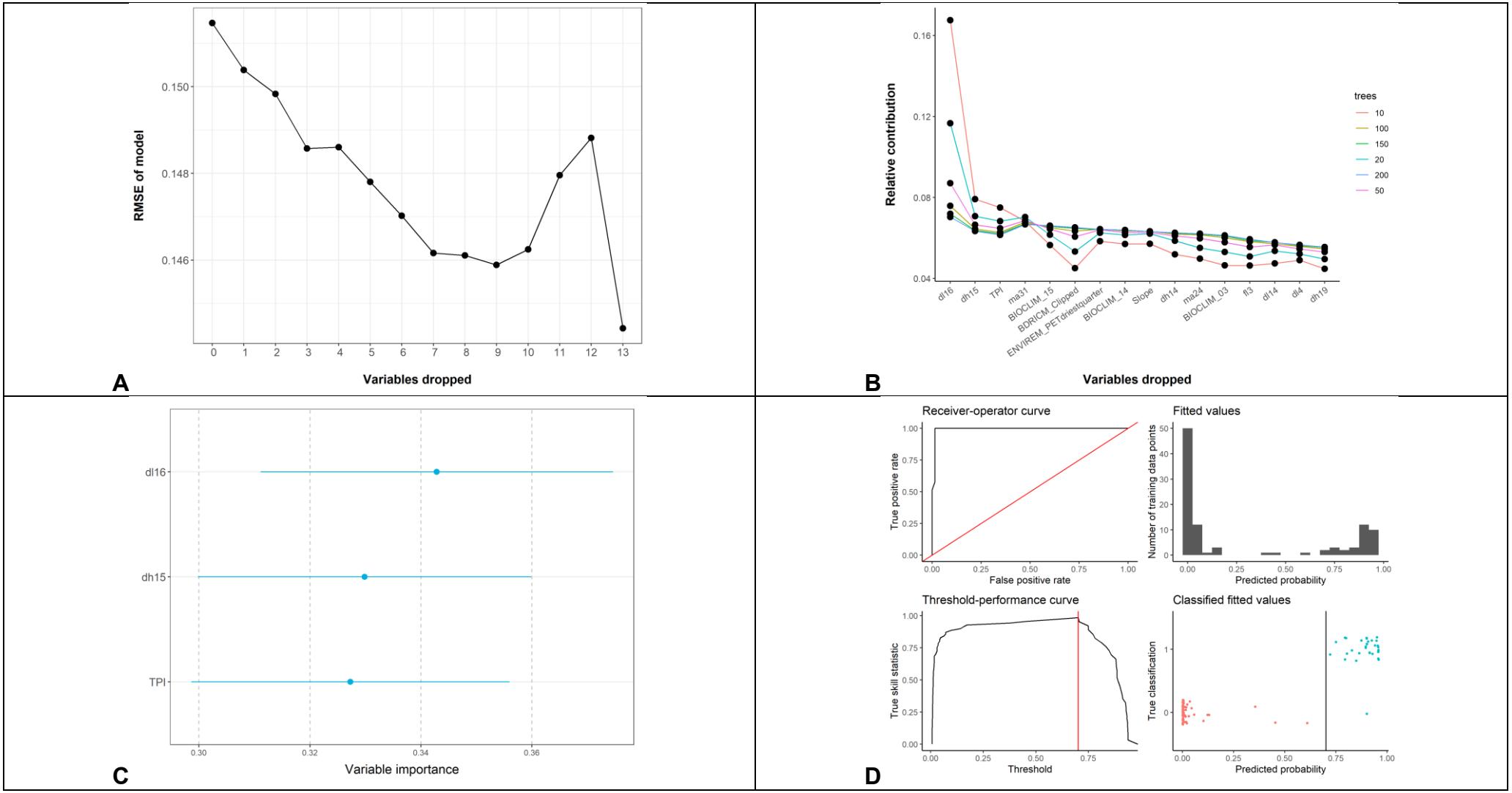


Figure S5.4.79. Model diagnostic outputs for *Pseudobarbus erubescens*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

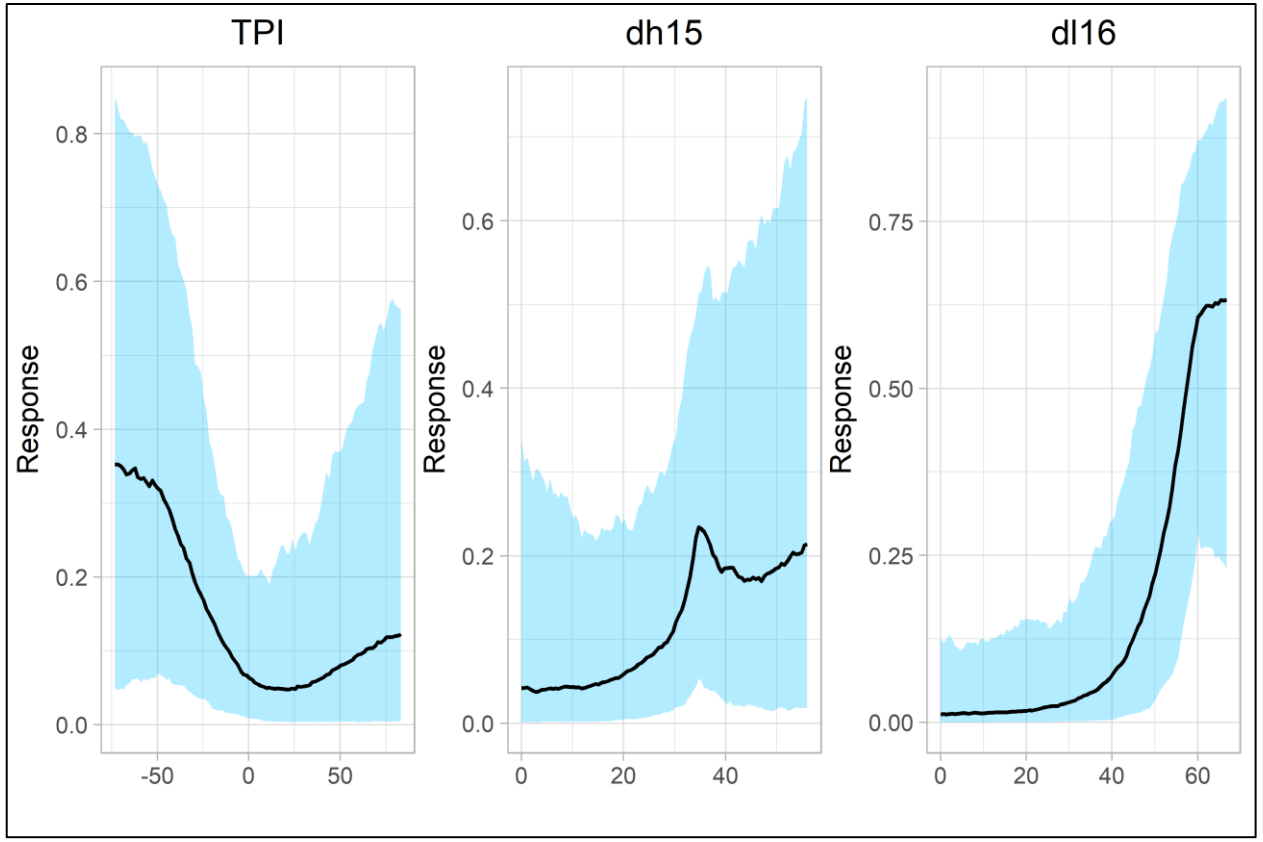


Figure S5.4.80. Partial dependence plots for *Pseudobarbus erubescens.*

Pseudobarbus quathlambae

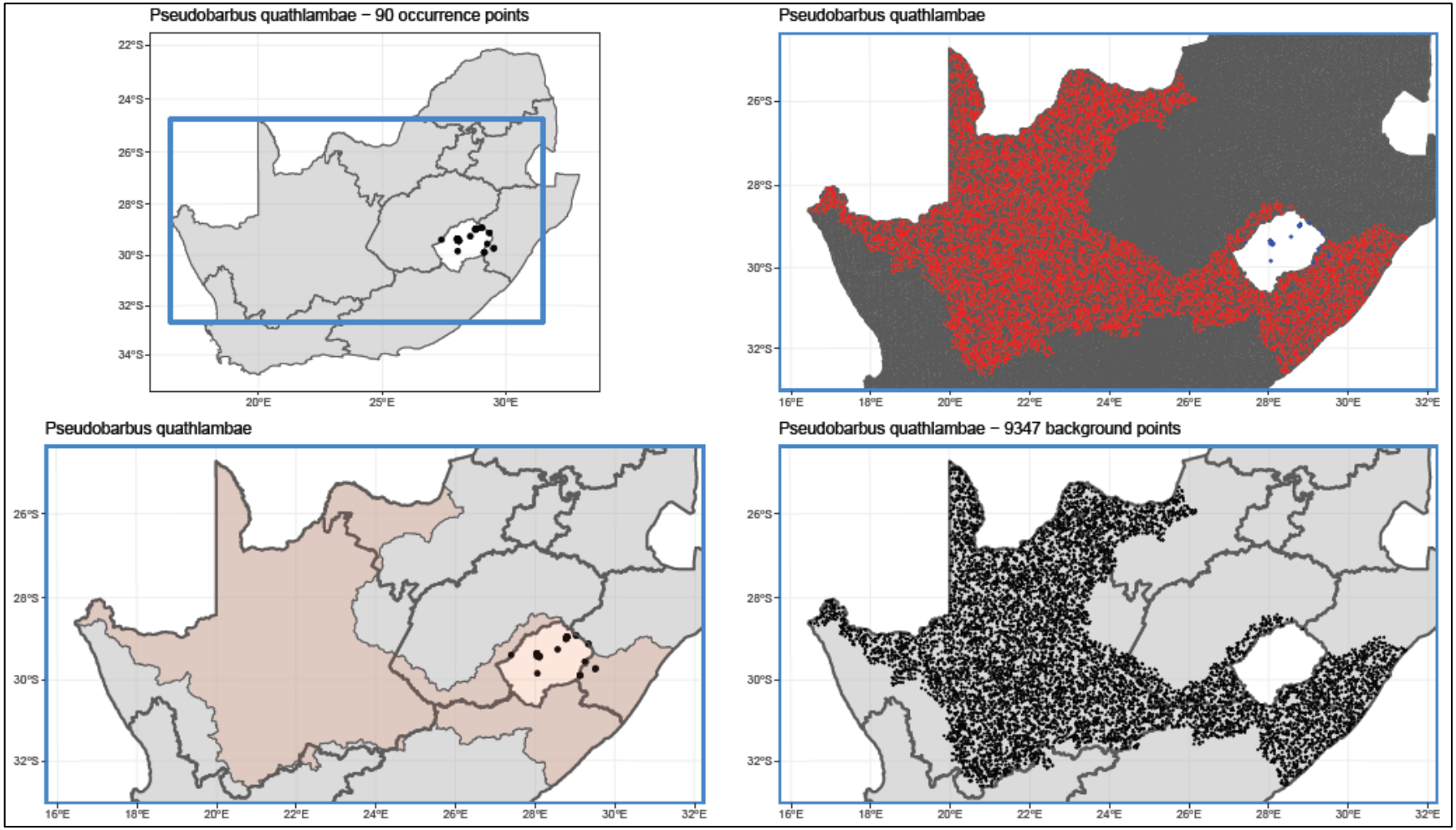


Figure S5.4.81. Occurrence records and background points for *Pseudobarbus quathlambae.*

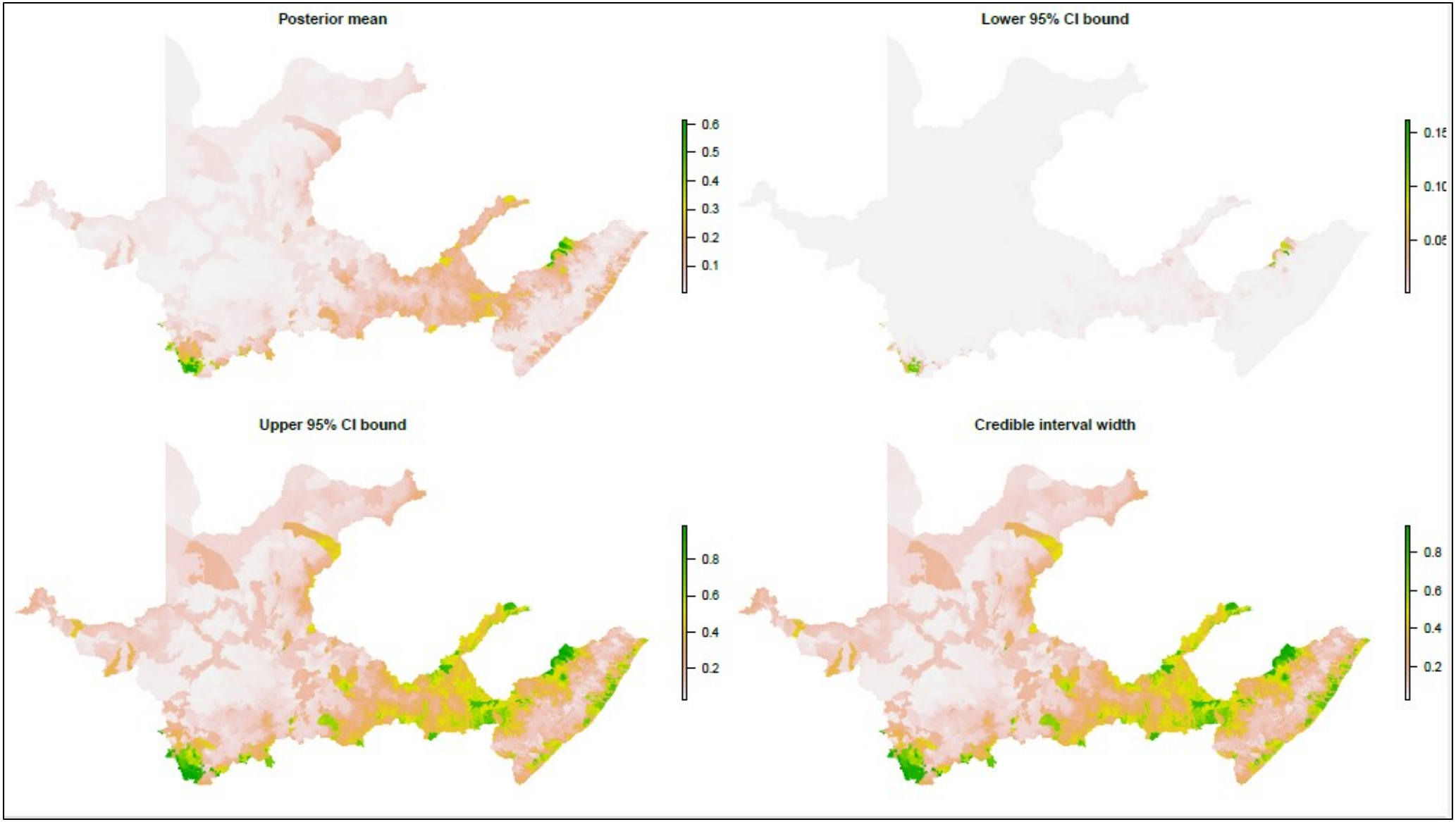


Figure S5.4.82. The modelled distribution of *Pseudobarbus quathlambae* in South Africa showing habitat suitability.

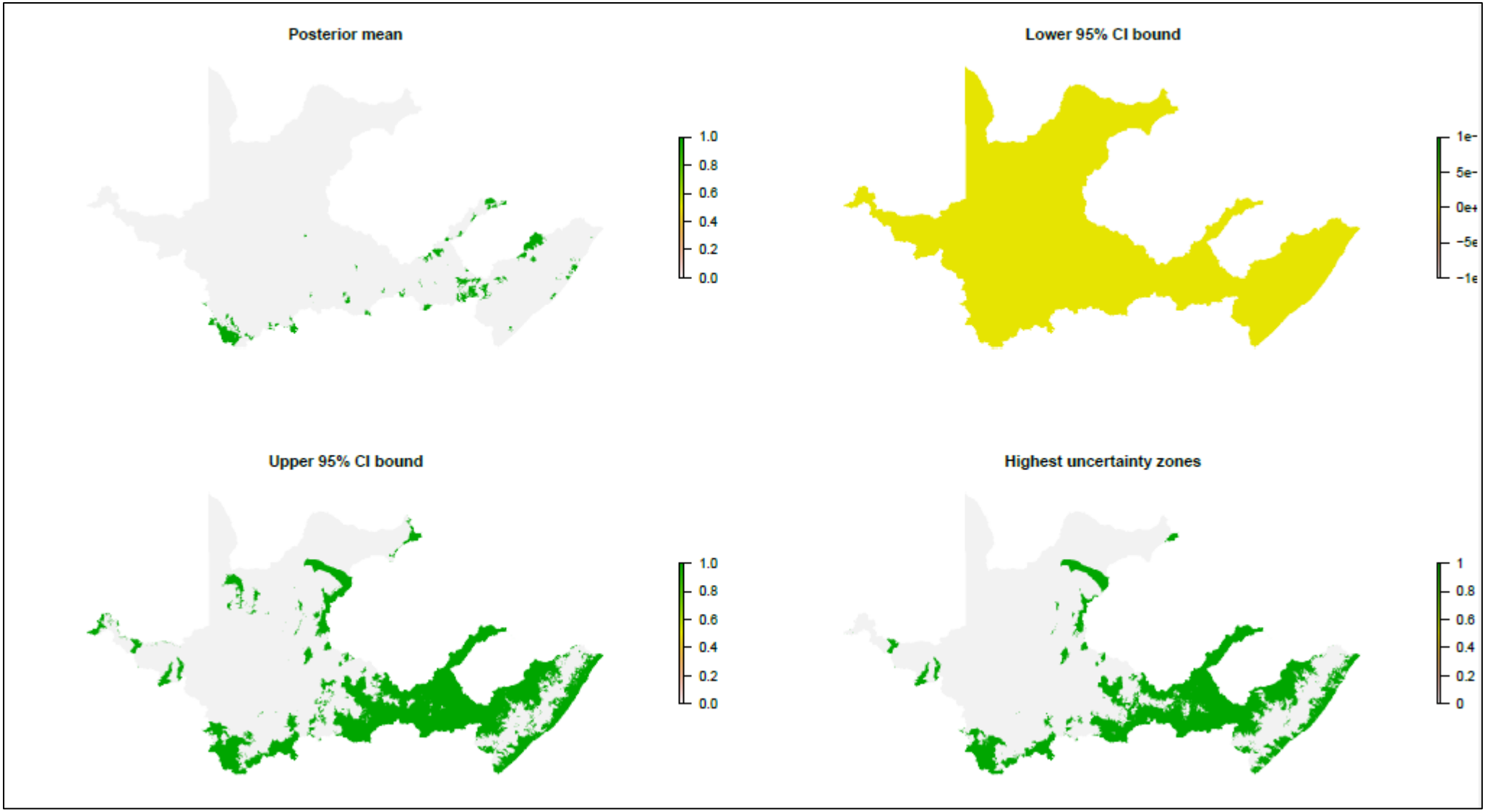


Figure S5.4.83. The modelled distribution of *Pseudobarbus quathlambae* in South Africa showing predicted distribution as a binary output.

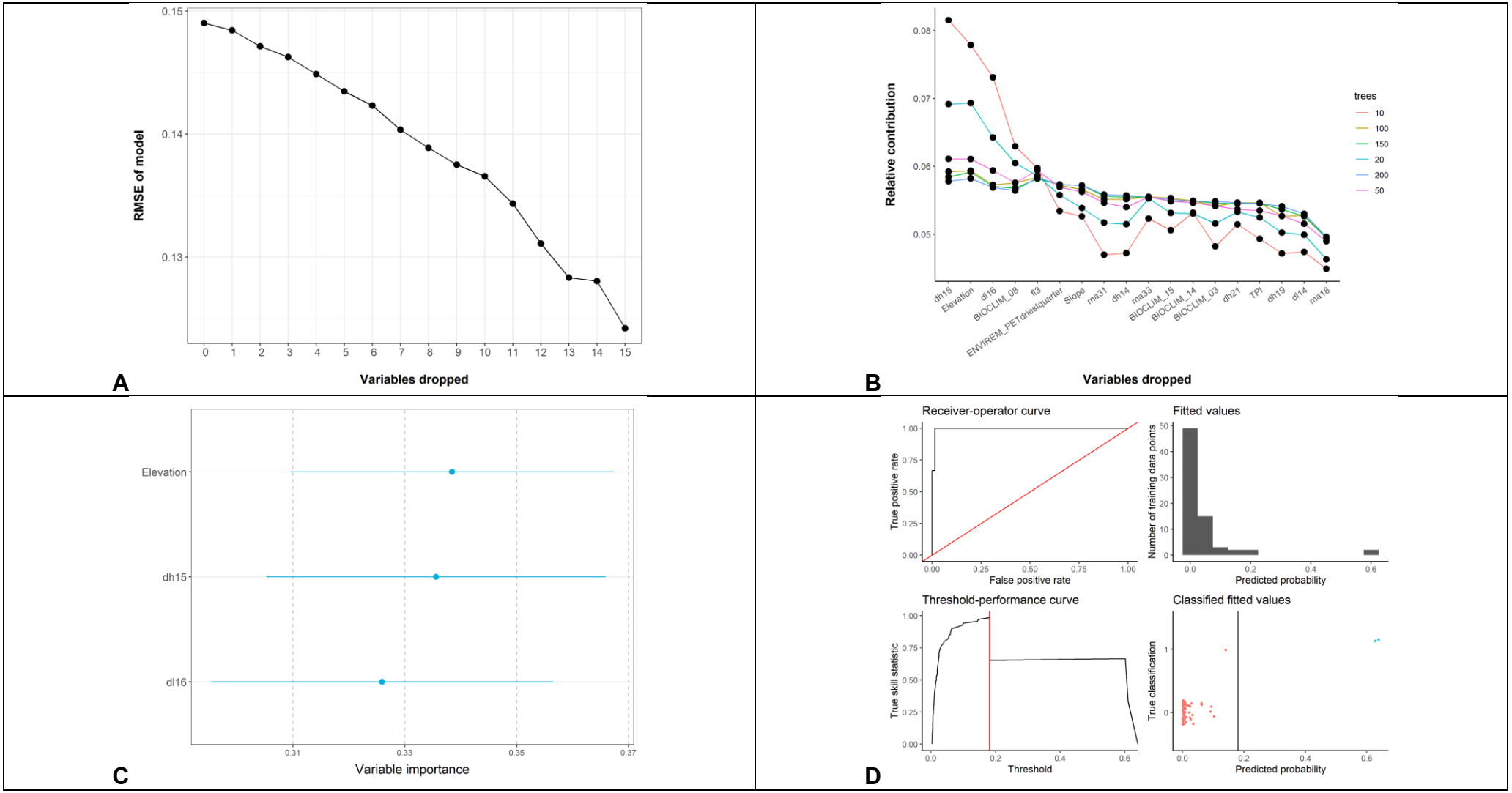


Figure S5.4.84. Model diagnostic outputs for *Pseudobarbus quathlambae*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

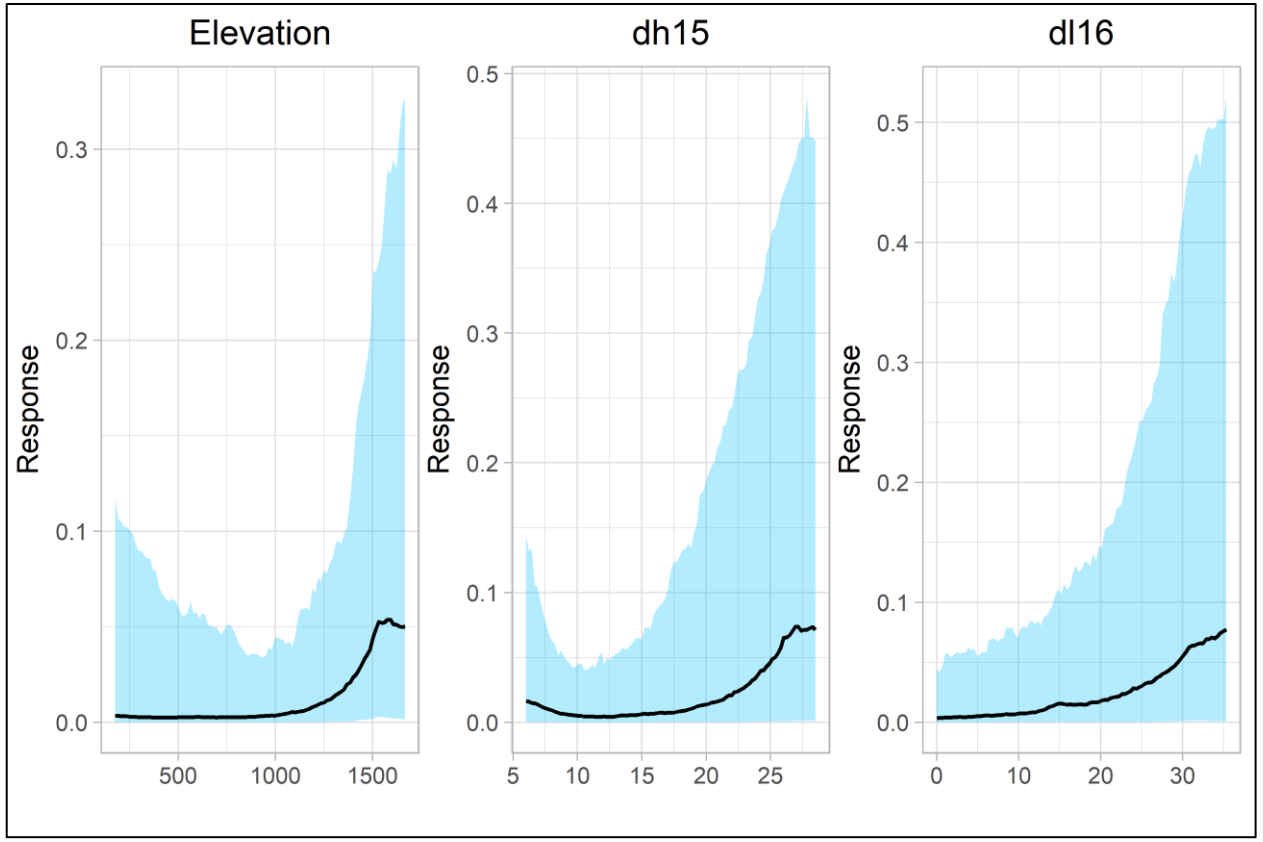


Figure S5.4.85. Partial dependence plots for *Pseudobarbus quathlambae.*

Pseudobarbus senticeps

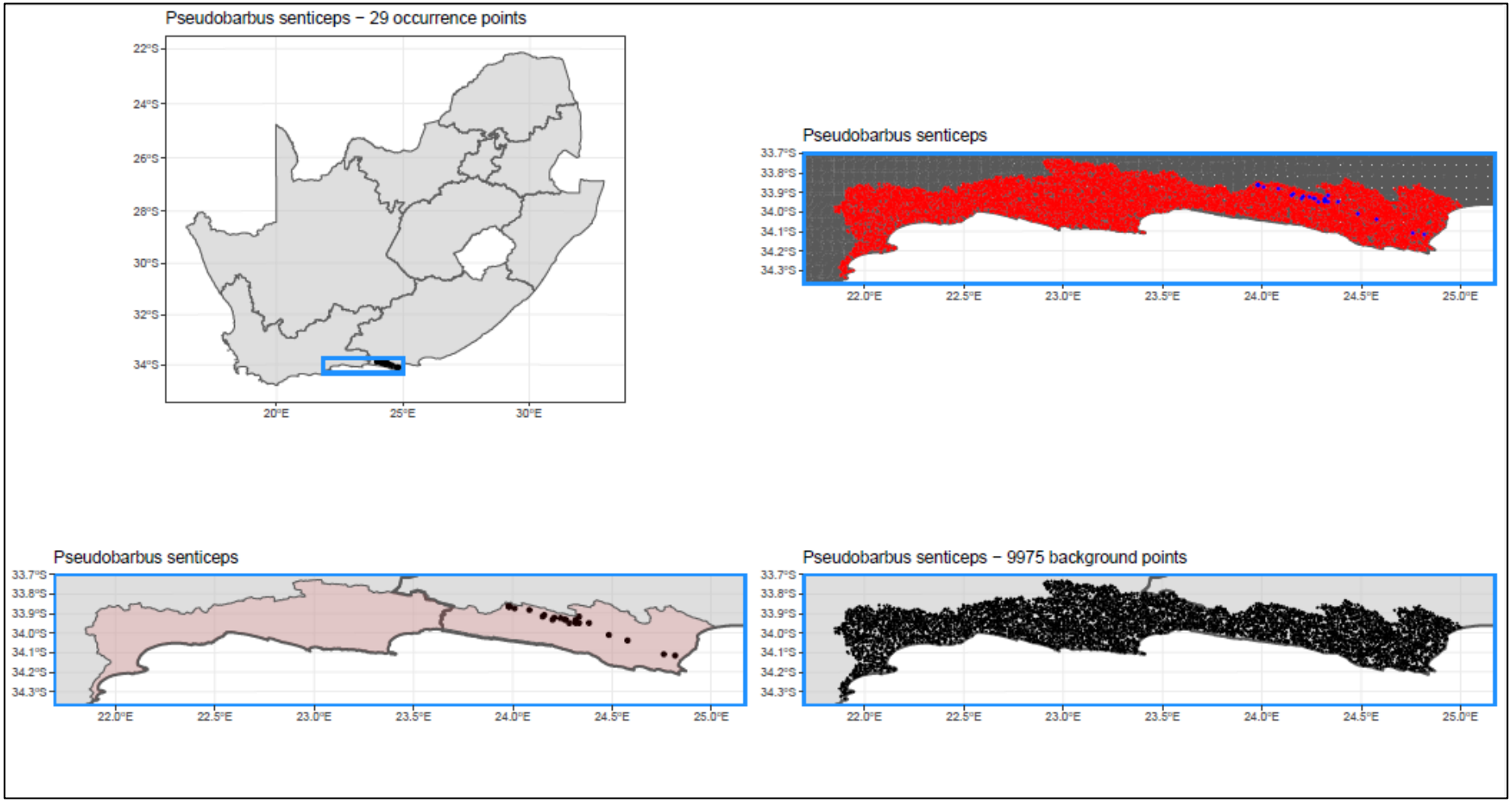


Figure S5.4.86. Occurrence records and background points for *Pseudobarbus senticeps.*

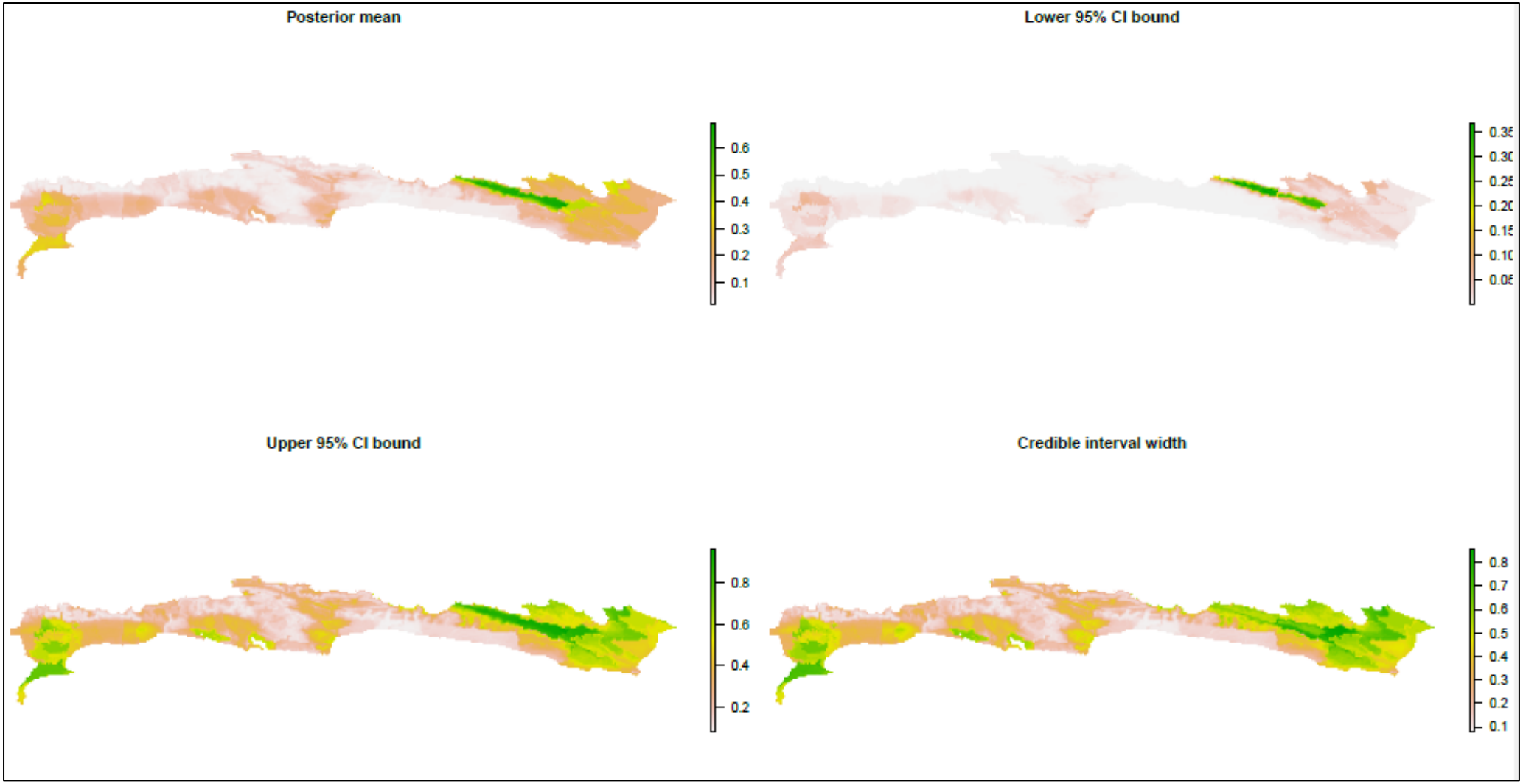


Figure S5.4.87. The modelled distribution of *Pseudobarbus senticeps* in South Africa showing habitat suitability.

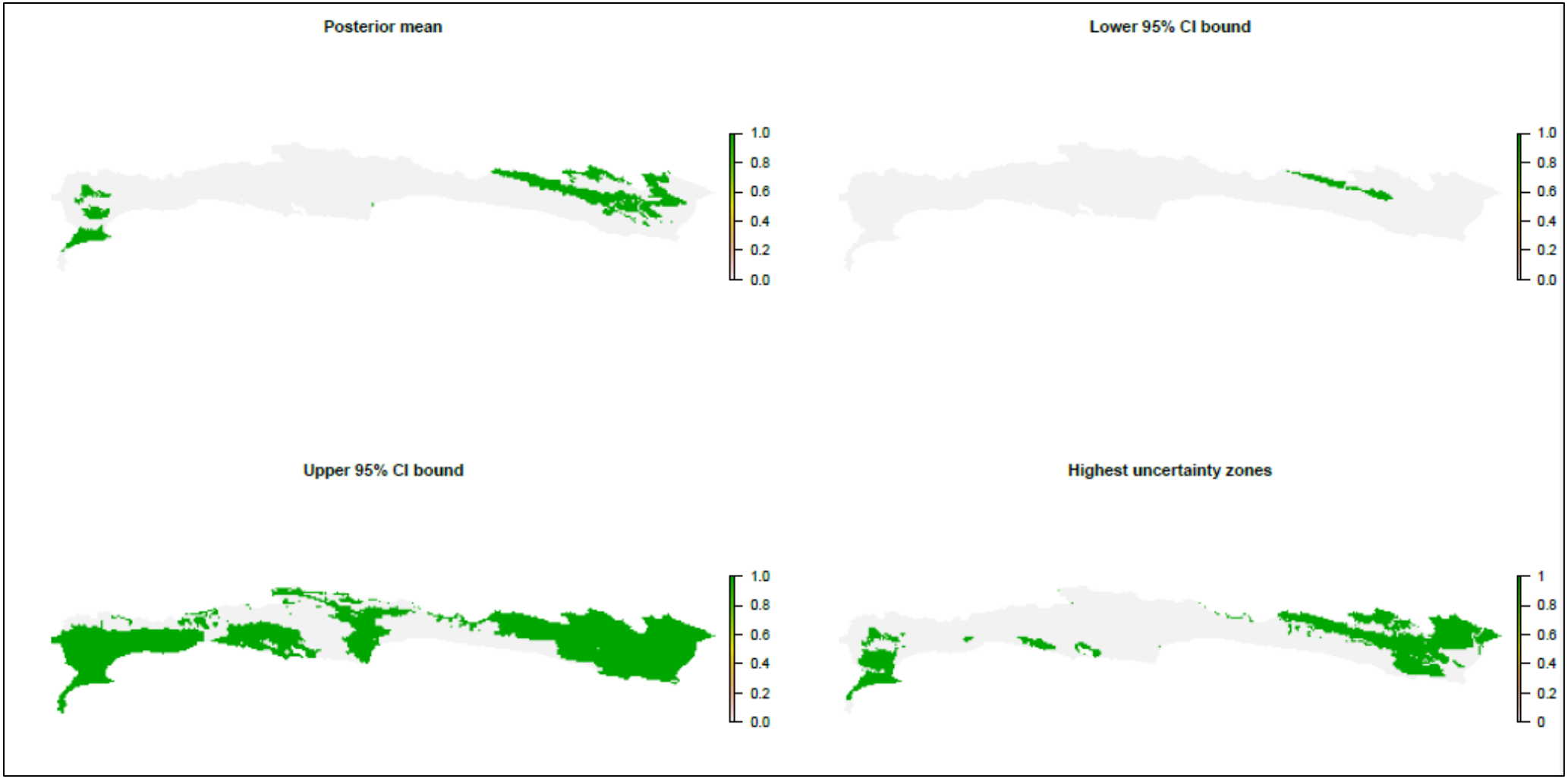


Figure S5.4.88. The modelled distribution of *Pseudobarbus senticeps* in South Africa showing predicted distribution as a binary output.

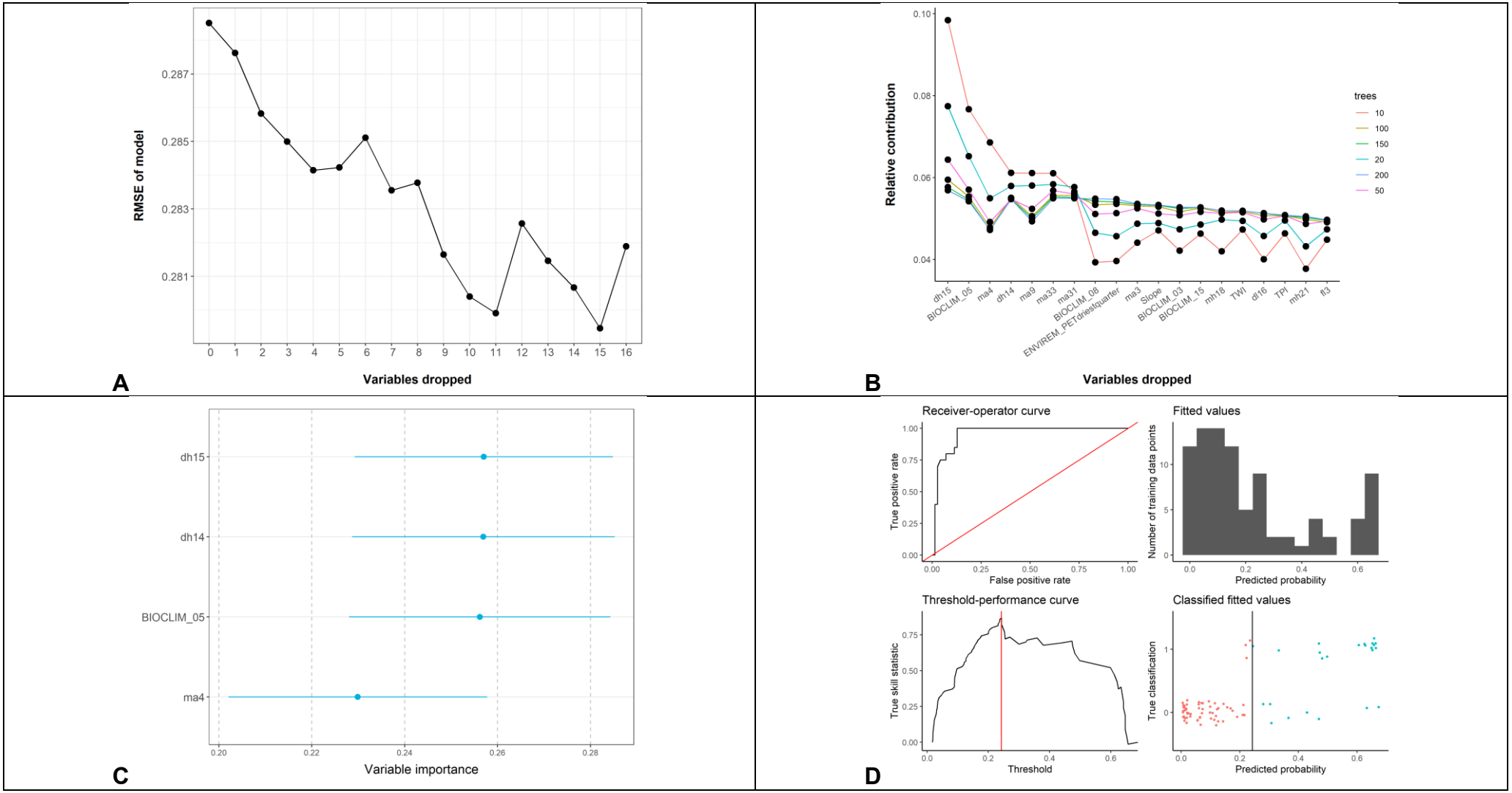


Figure S5.4.89. Model diagnostic outputs for *Pseudobarbus senticeps,* showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

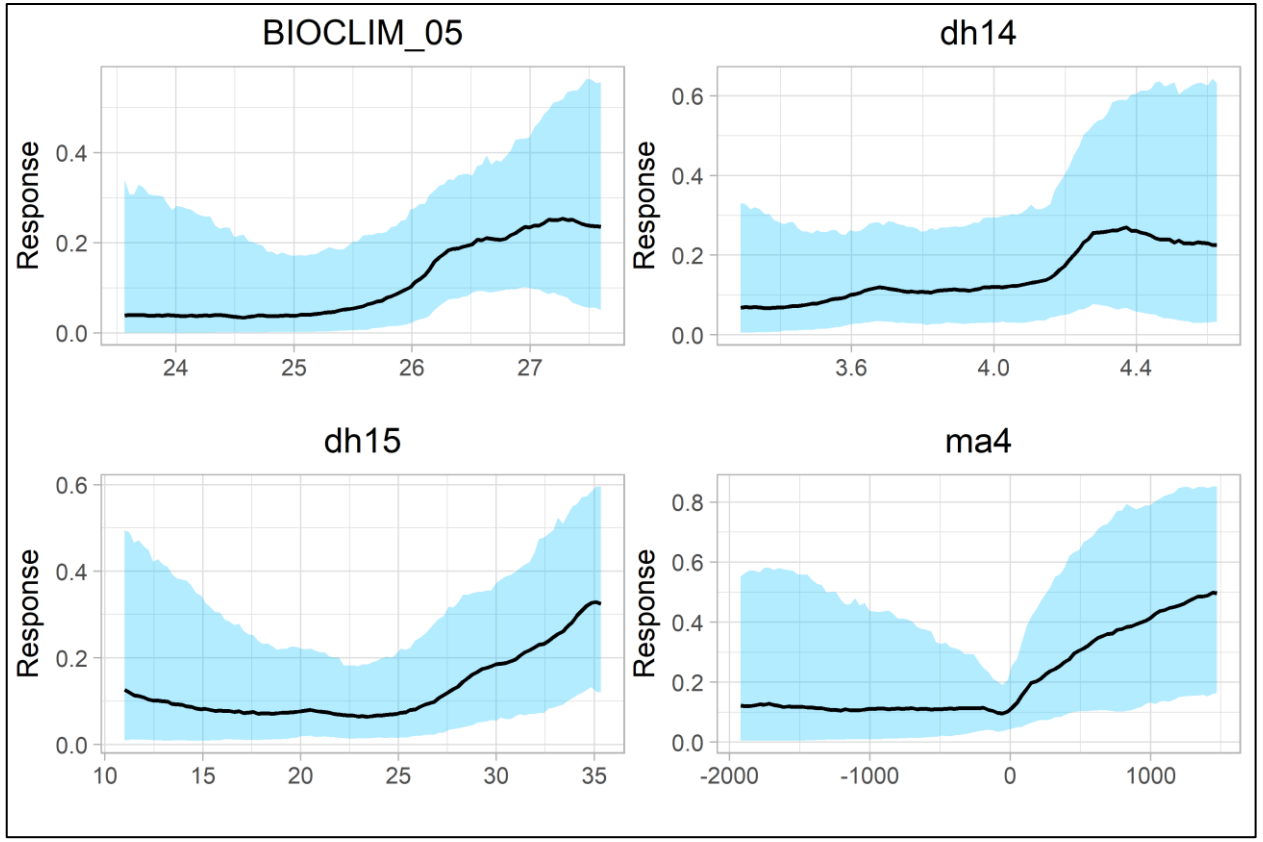


Figure S5.4.90. Partial dependence plots for *Pseudobarbus senticeps.*

Pseudobarbus skeltoni

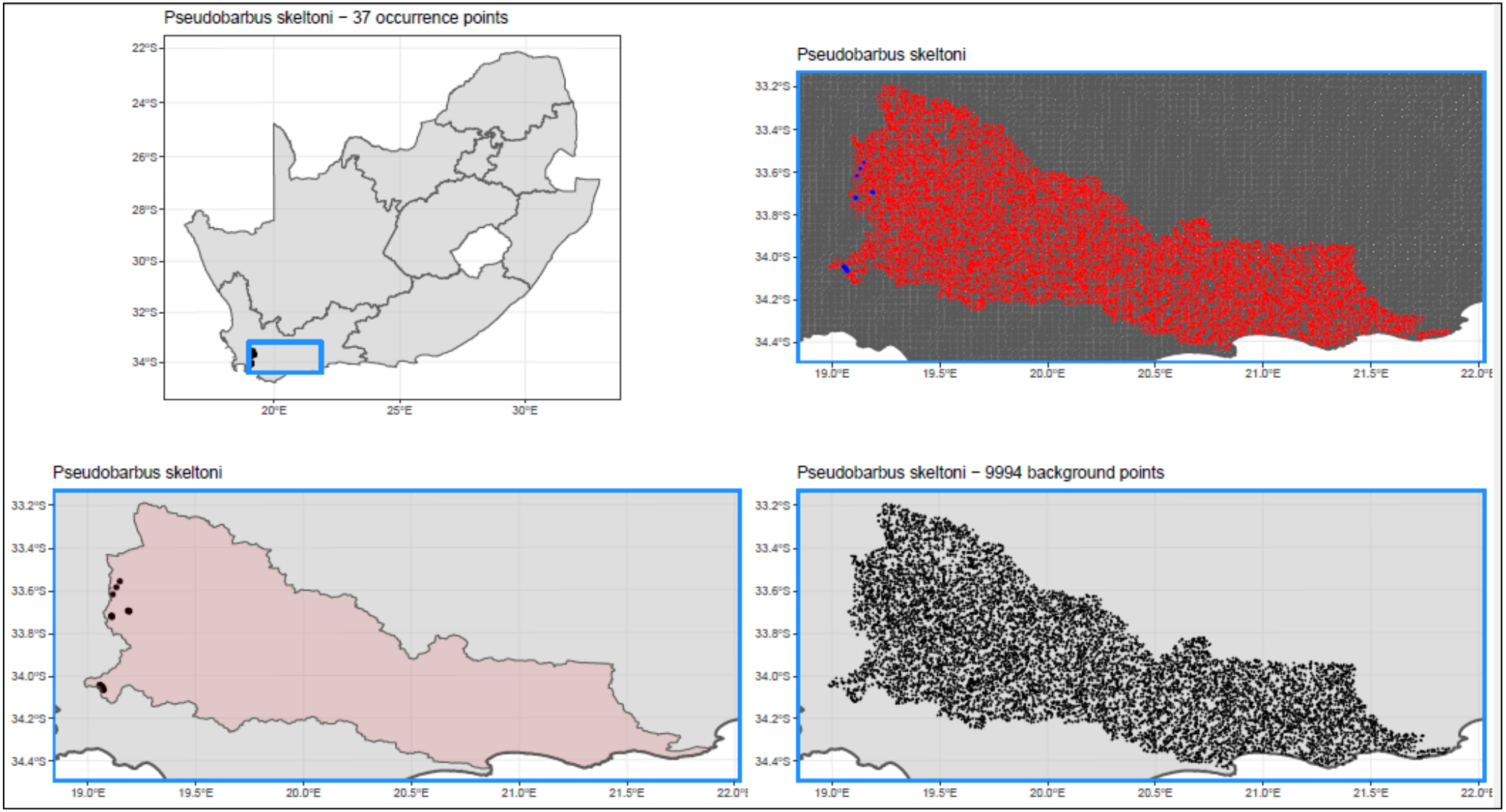


Figure S5.4.19. Occurrence records and background points for *Pseudobarbus skeltoni.*

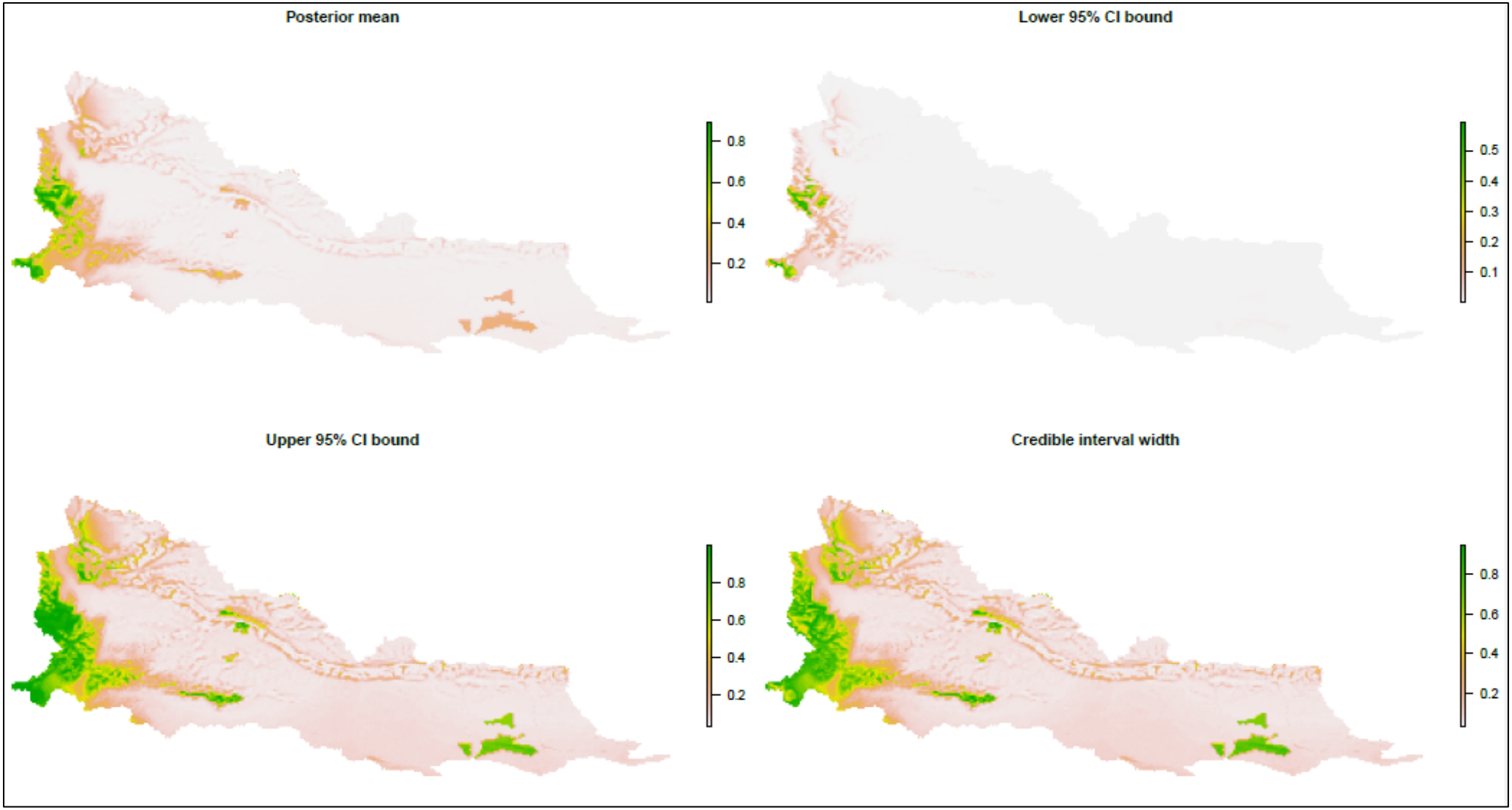


Figure S5.4.92. The modelled distribution of *Pseudobarbus skeltoni* in South Africa showing habitat suitability.

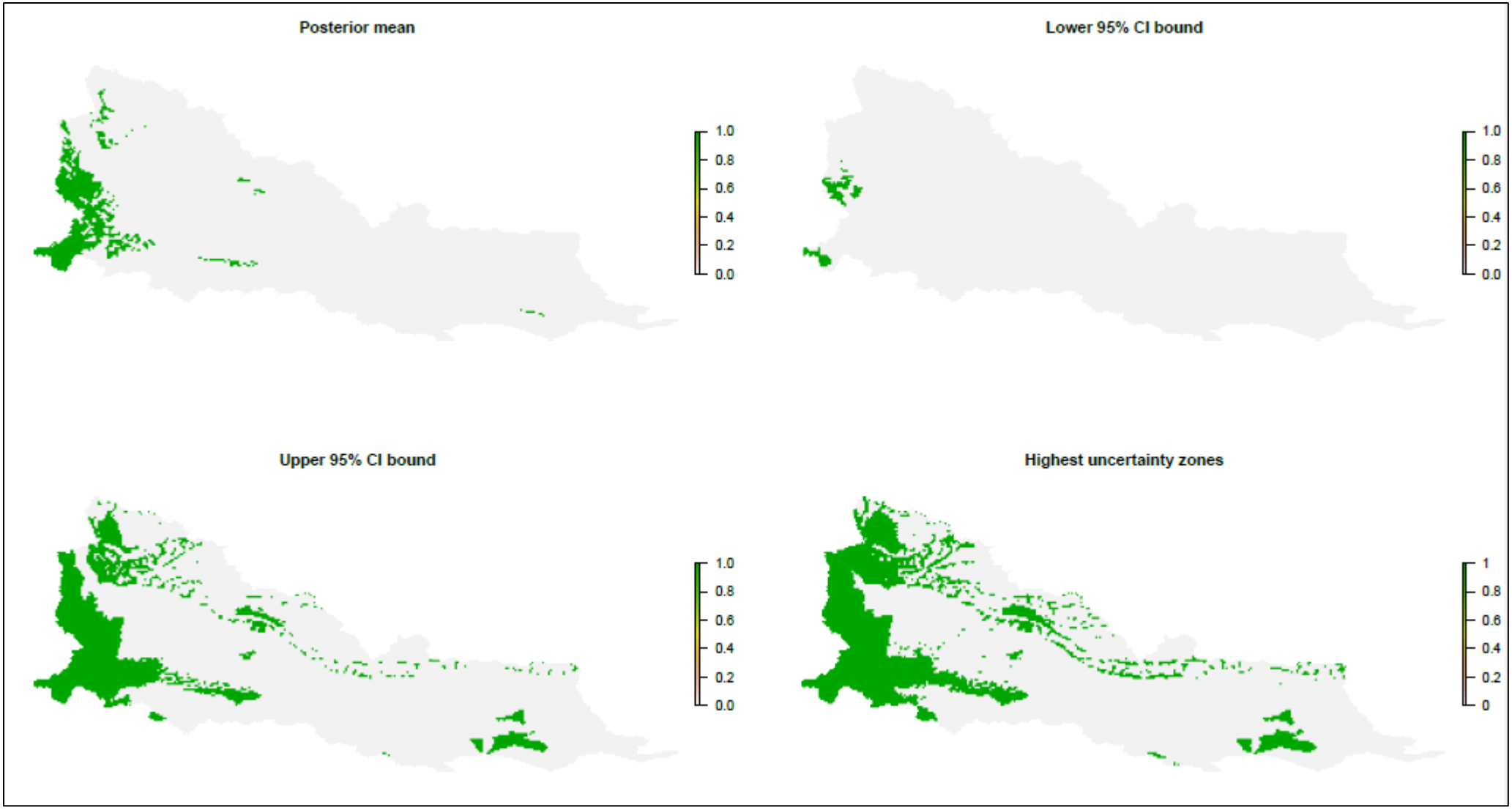


Figure S5.4.93. The modelled distribution of *Pseudobarbus skeltoni* in South Africa showing predicted distribution as a binary output.

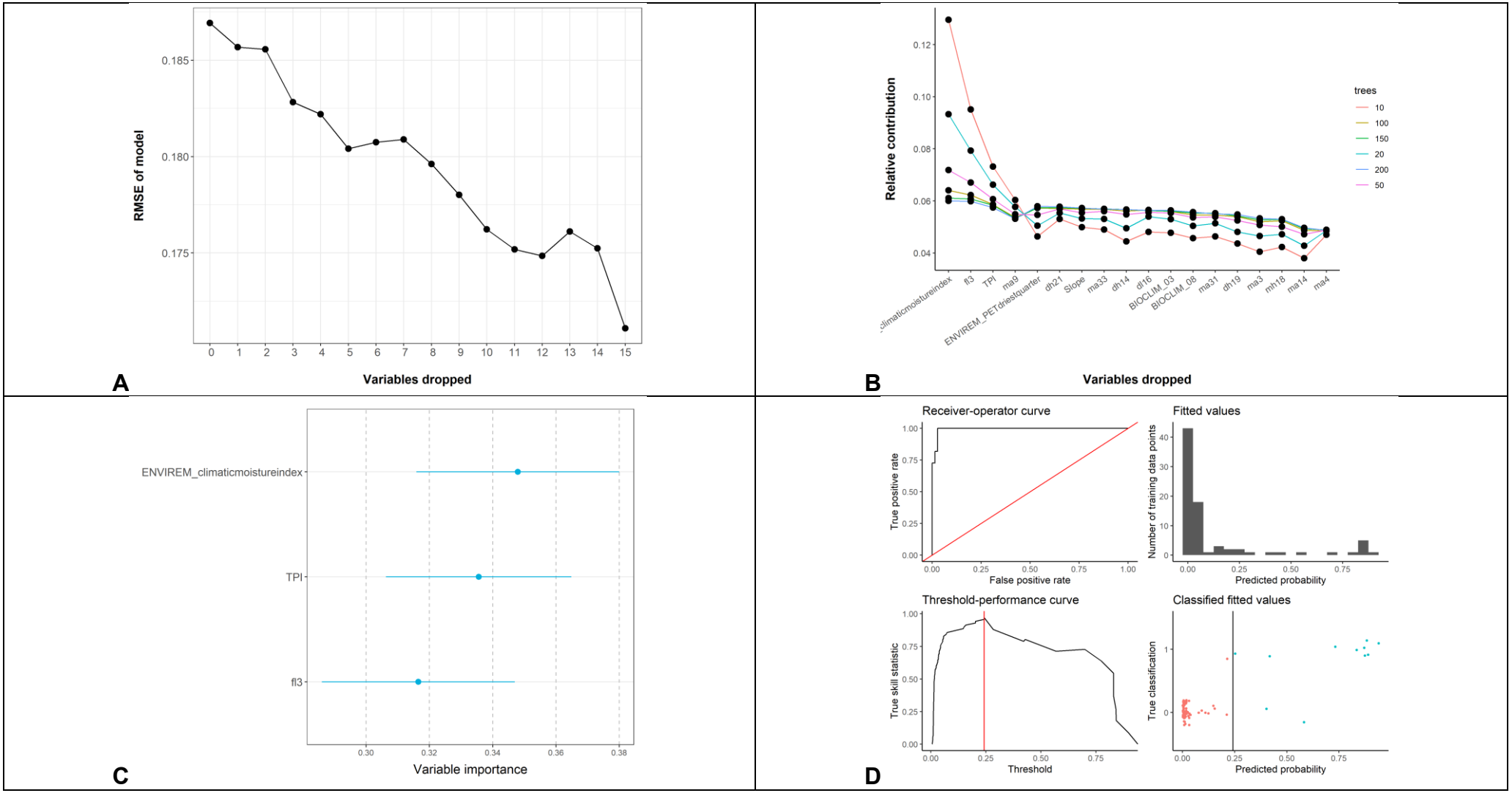


Figure S5.4.94. Model diagnostic outputs for *Pseudobarbus skeltoni*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

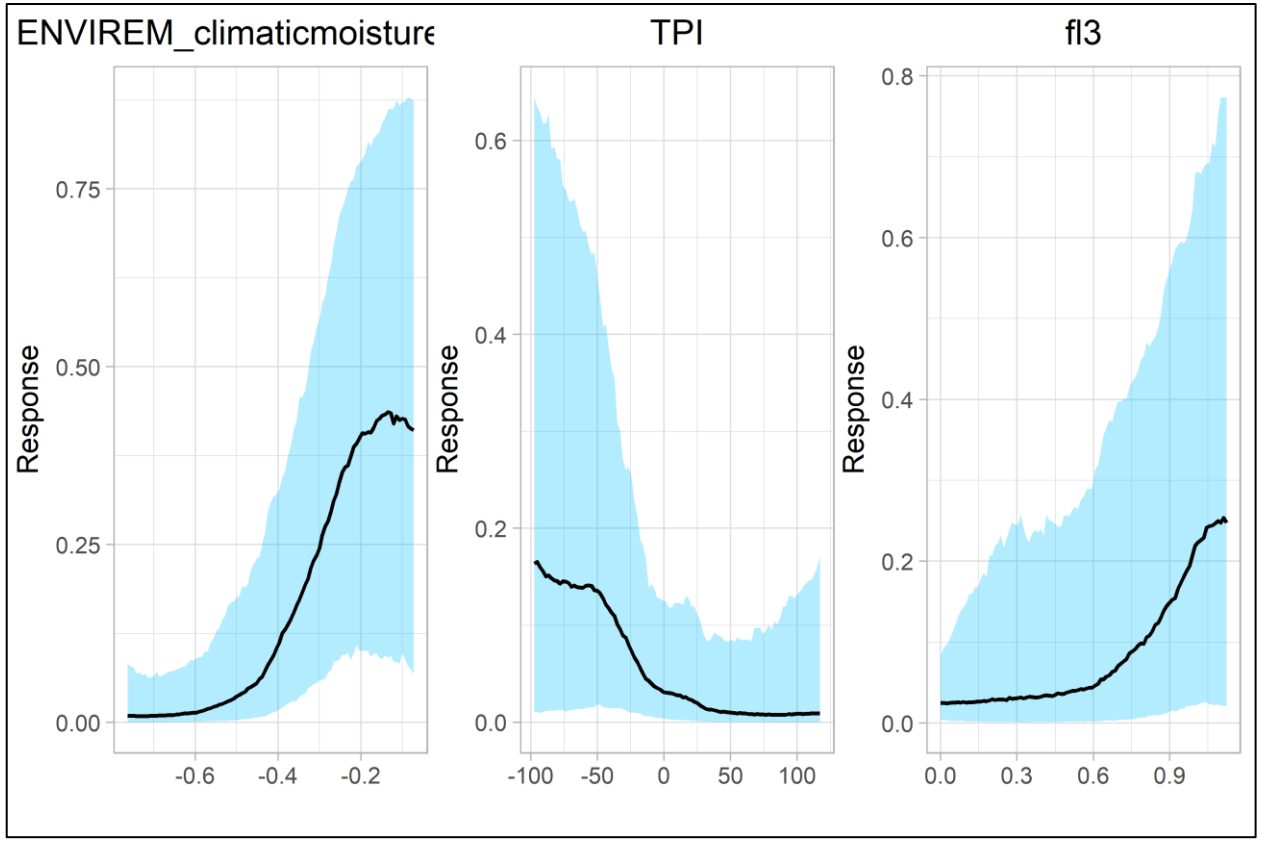


Figure S5.4.95. Partial dependence plots for *Pseudobarbus skeltoni.*

Pseudobarbus swartzi

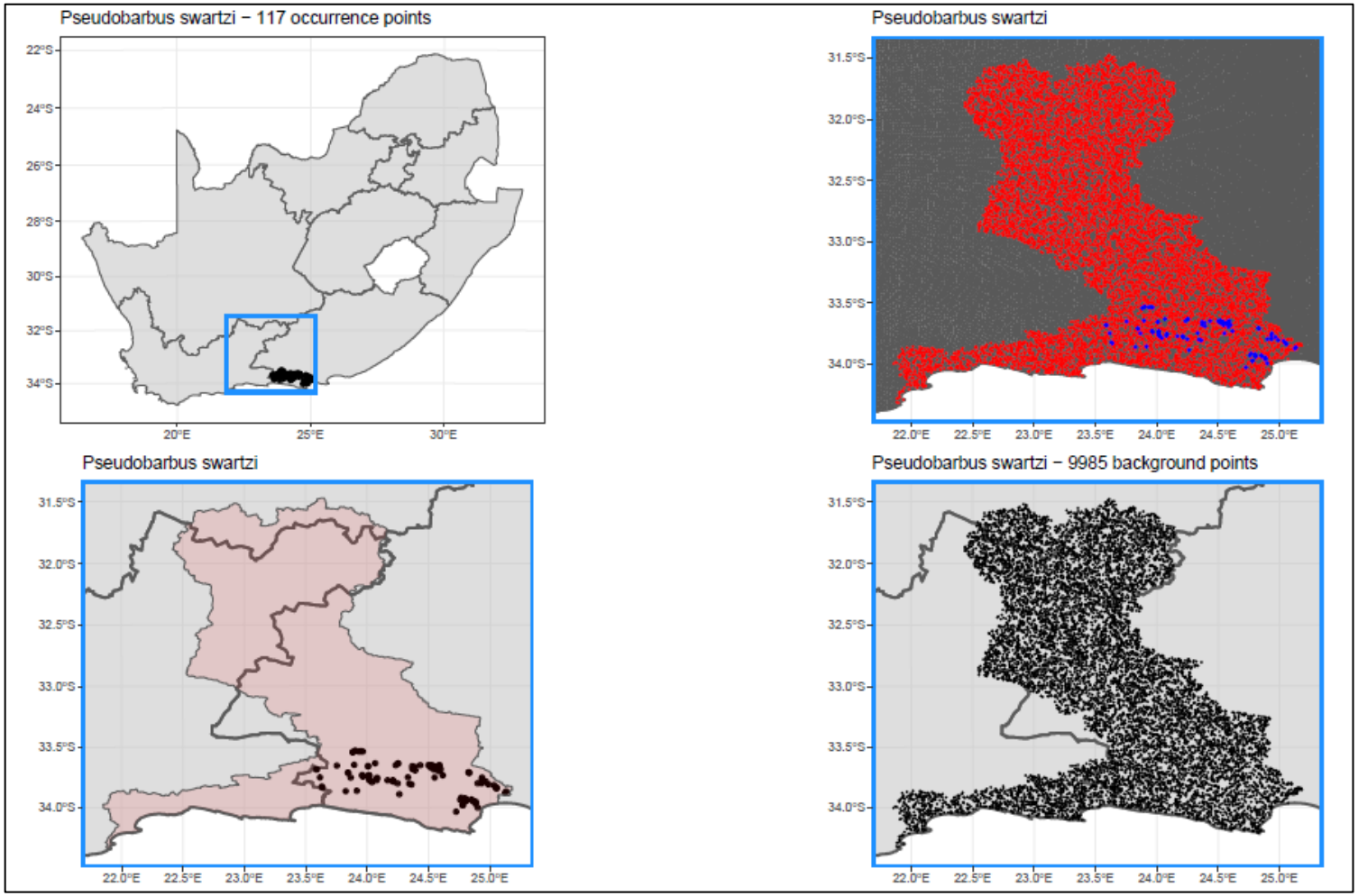


Figure S5.4.96. Occurrence records and background points for *Pseudobarbus swartzi.*

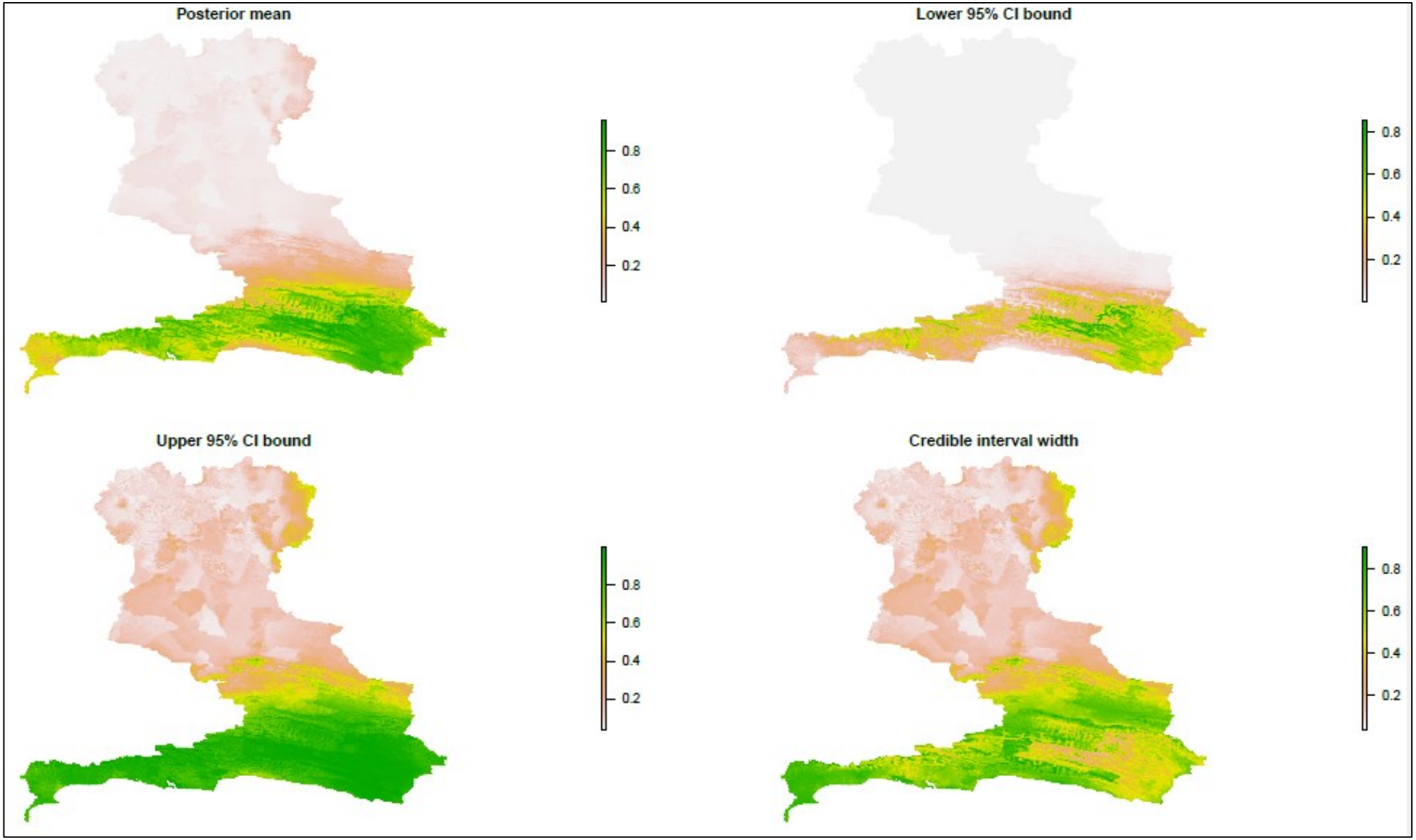


Figure S5.4.97. The modelled distribution of *Pseudobarbus swartzi* in South Africa showing habitat suitability

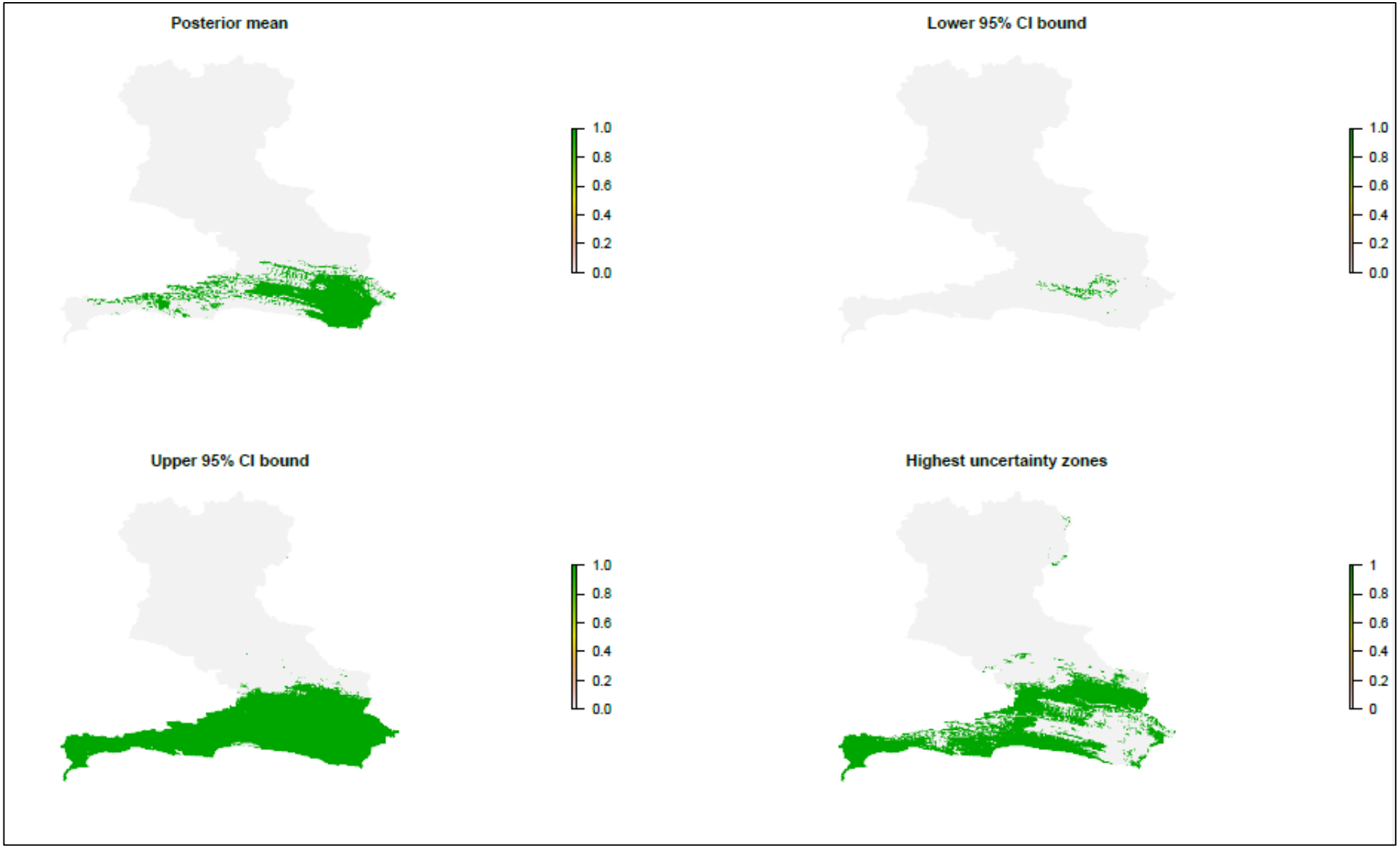


Figure S5.4.98. The modelled distribution of *Pseudobarbus swartzi* in South Africa showing predicted distribution as a binary output.

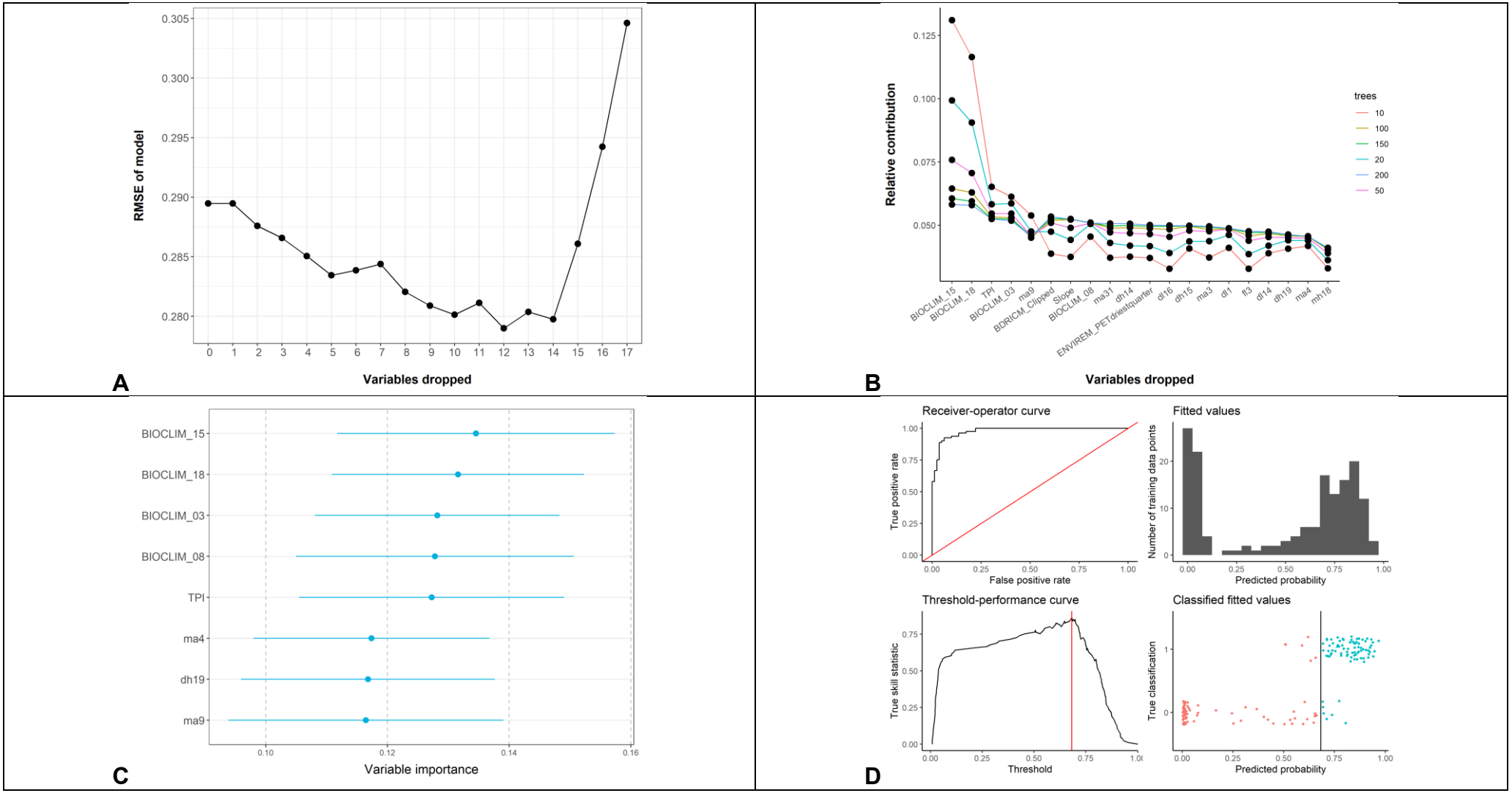


Figure S5.4.99. Model diagnostic outputs for *Pseudobarbus swartzi*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

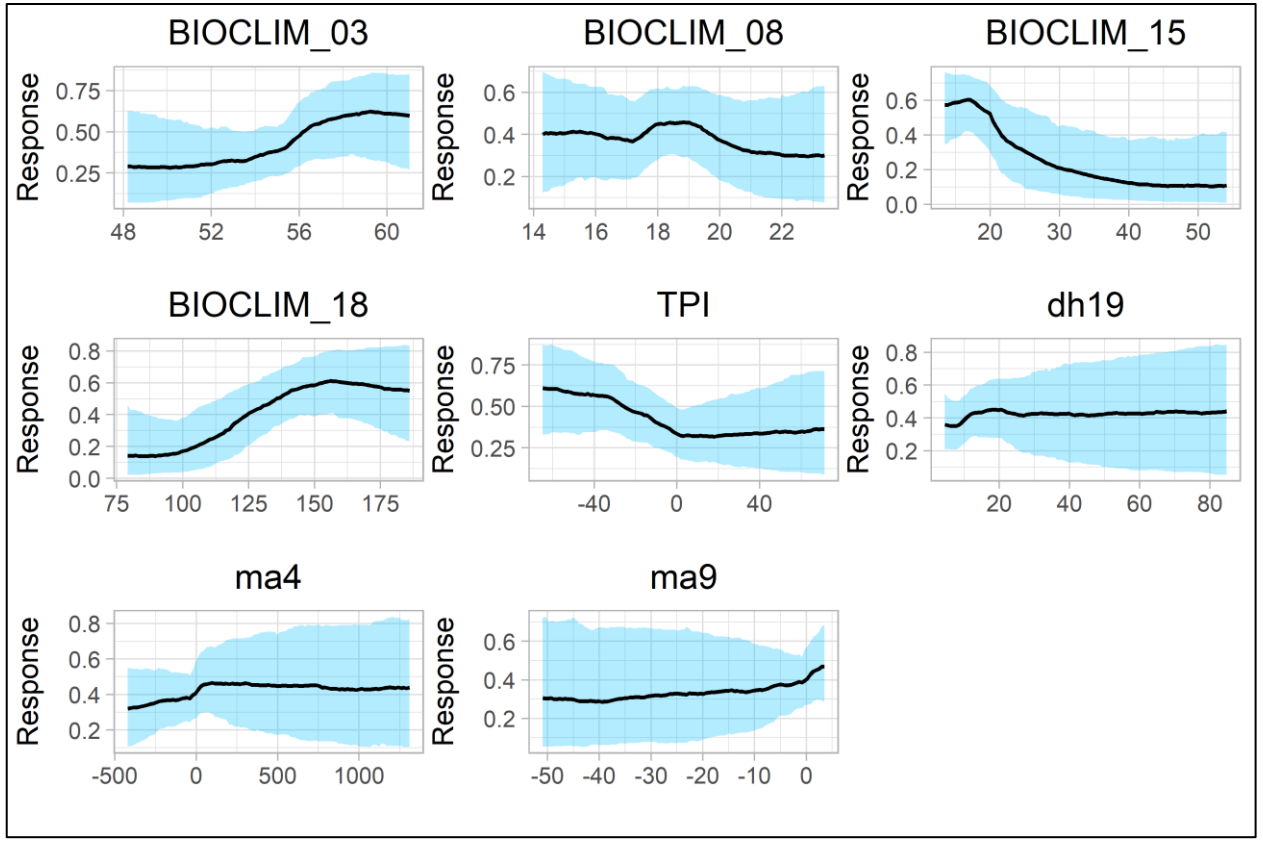


Figure S5.4.100. Partial dependence plots for *Pseudobarbus swartzi.*

Pseudobarbus verloreni

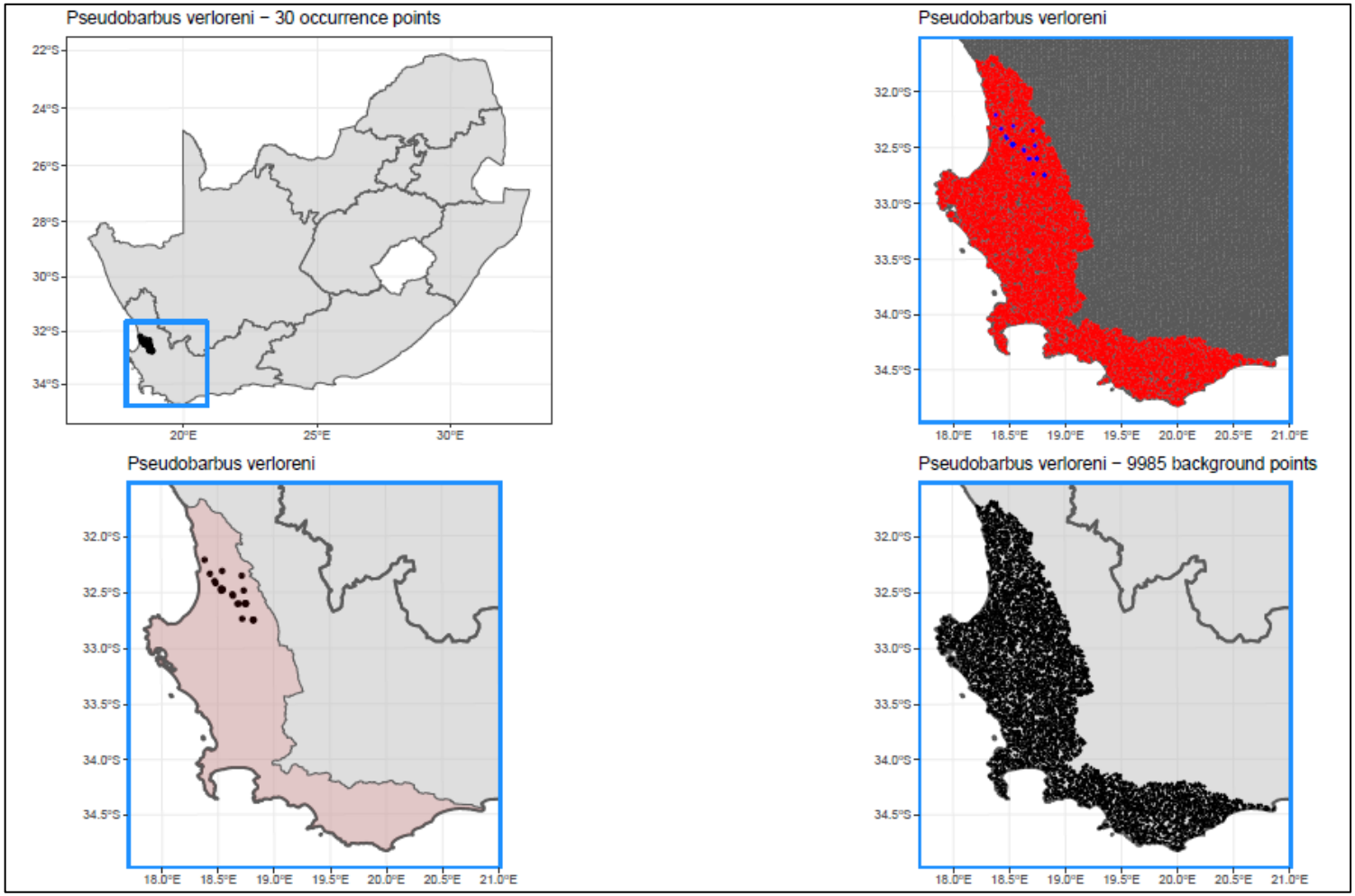


Figure S5.4.101. Occurrence records and background points for *Pseudobarbus verloreni.*

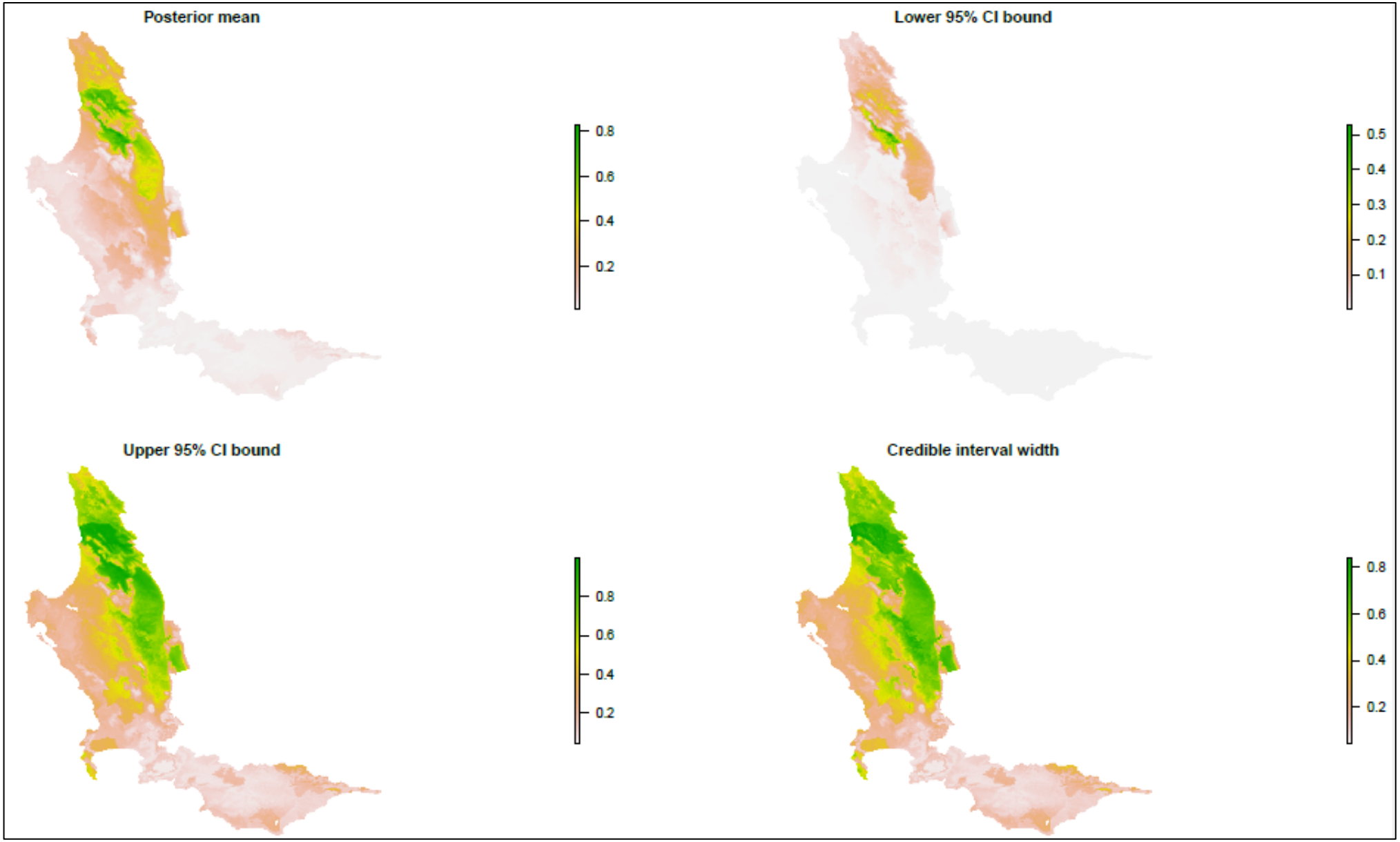


Figure S5.4.102. The modelled distribution of *Pseudobarbus verloreni* in South Africa showing habitat suitability.

Figure S5.4.103. The modelled distribution of *Pseudobarbus verloreni* in South Africa showing predicted distribution as a binary output.

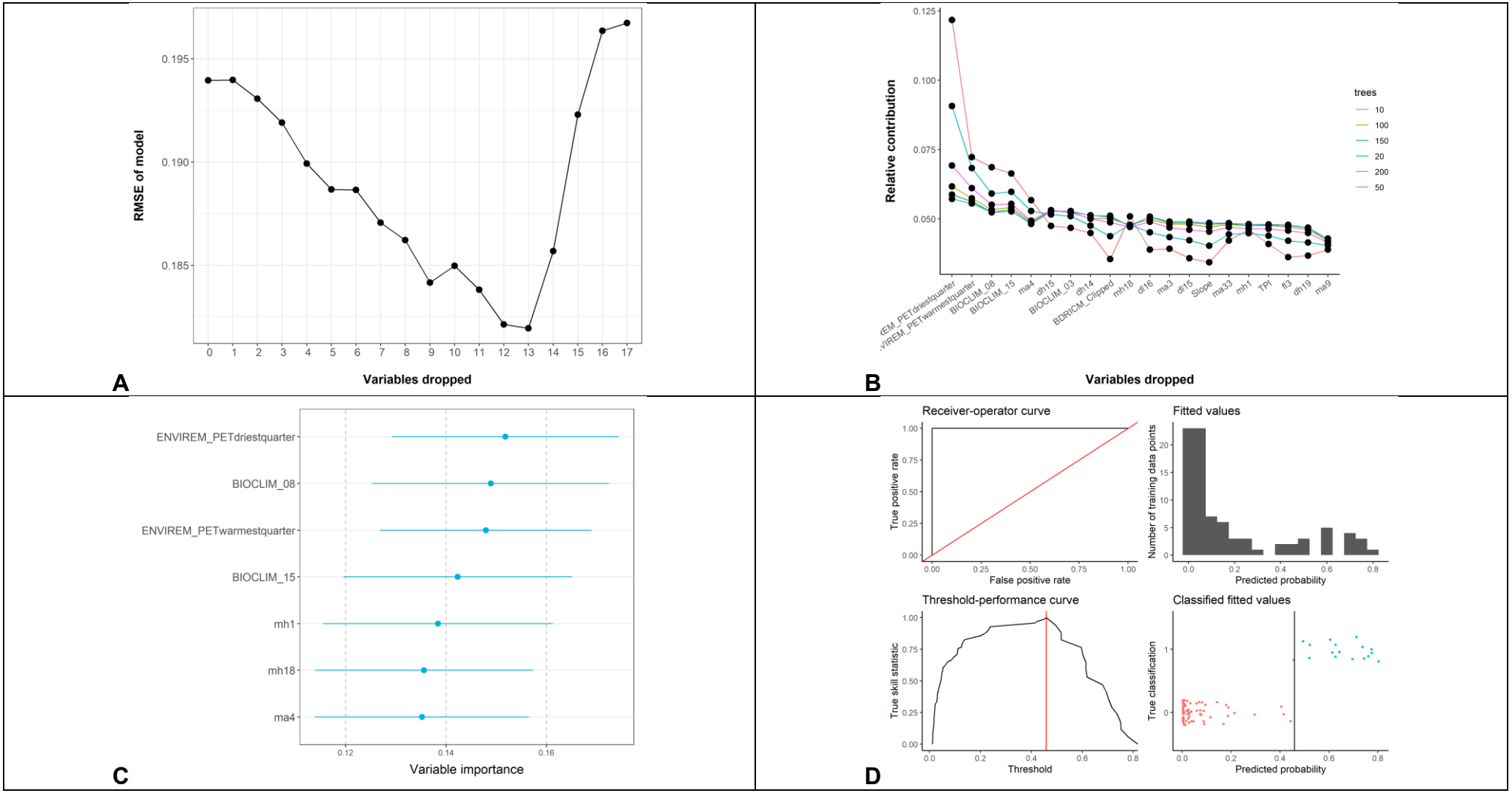


Figure S5.4.104. Model diagnostic outputs for *Pseudobarbus verloreni,* showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

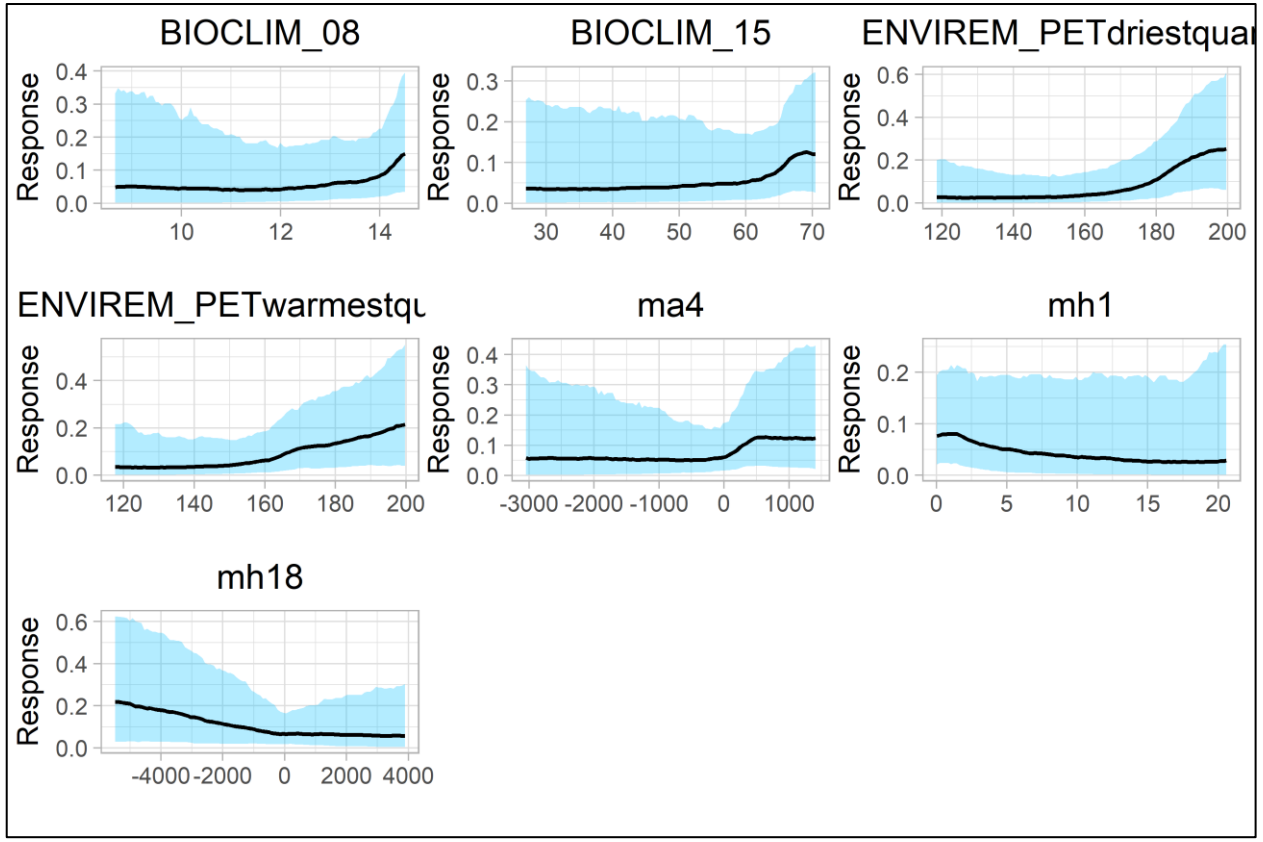


Figure S5.4.105. Partial dependence plots for *Pseudobarbus verloreni.*

Sandelia bainsii

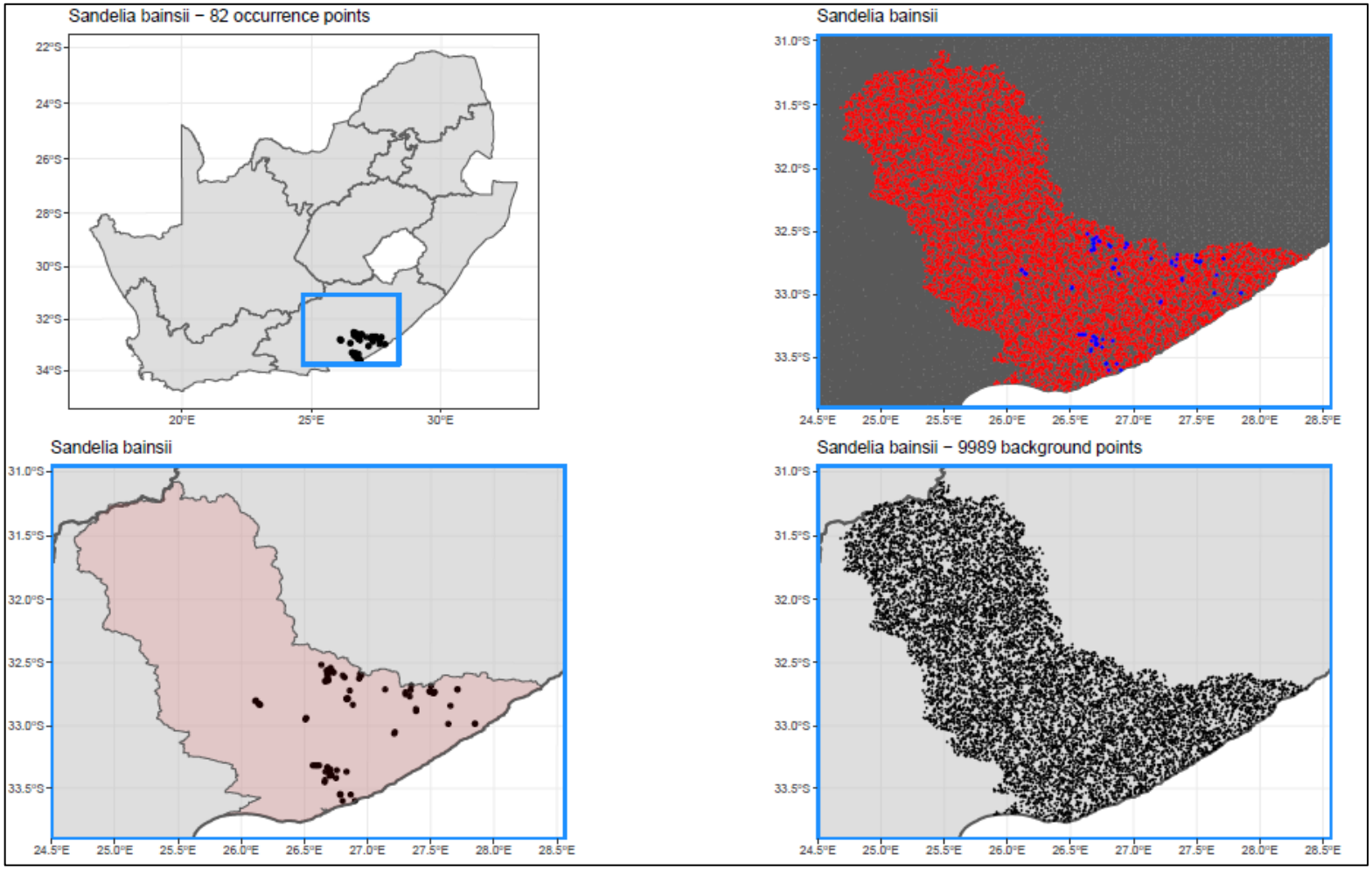


Figure S5.4.106. Occurrence records and background points for *Sandelia bainsii.*

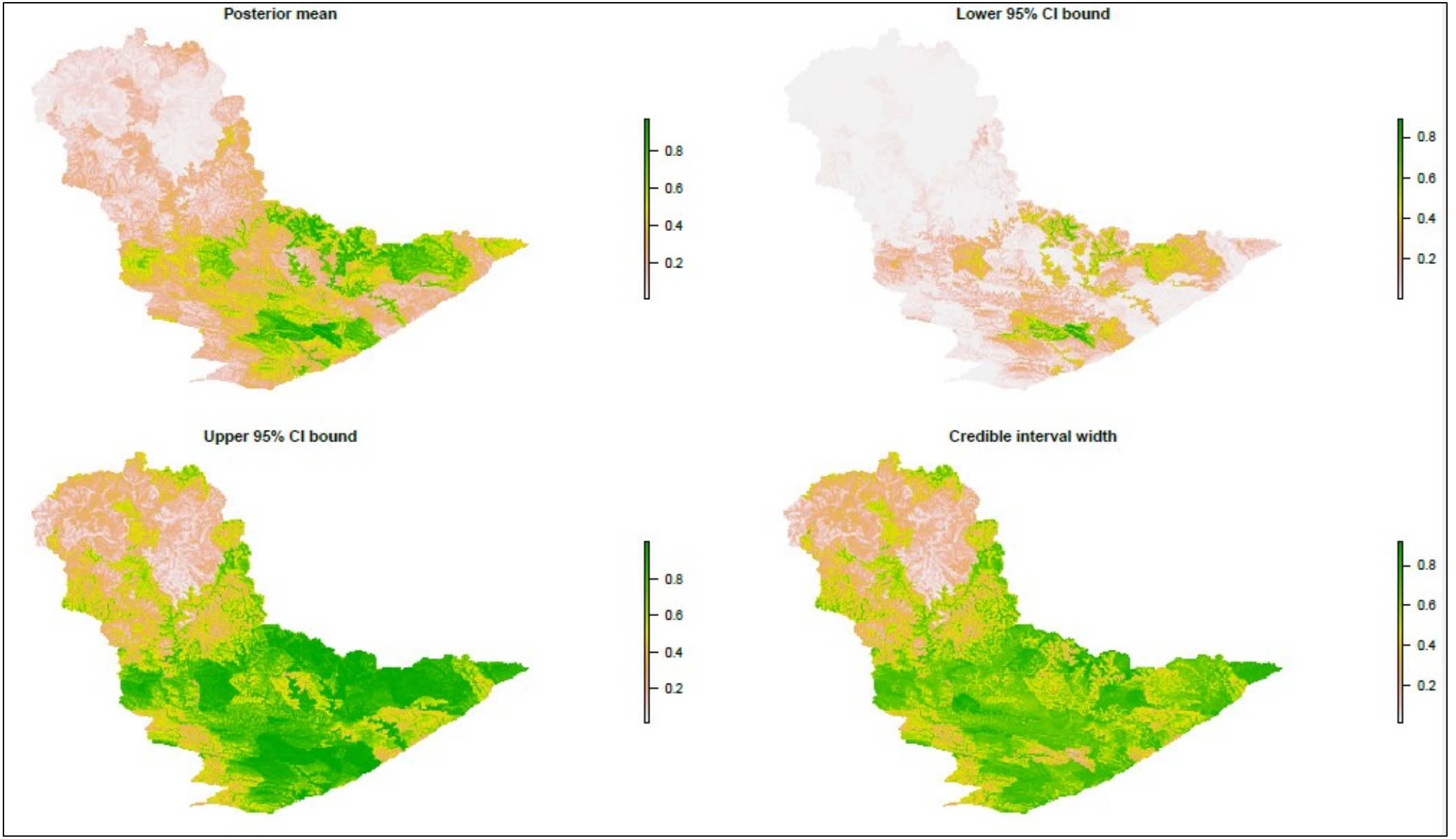


Figure S5.4.107. The modelled distribution of *Sandelia bainsii* in South Africa showing habitat suitability.

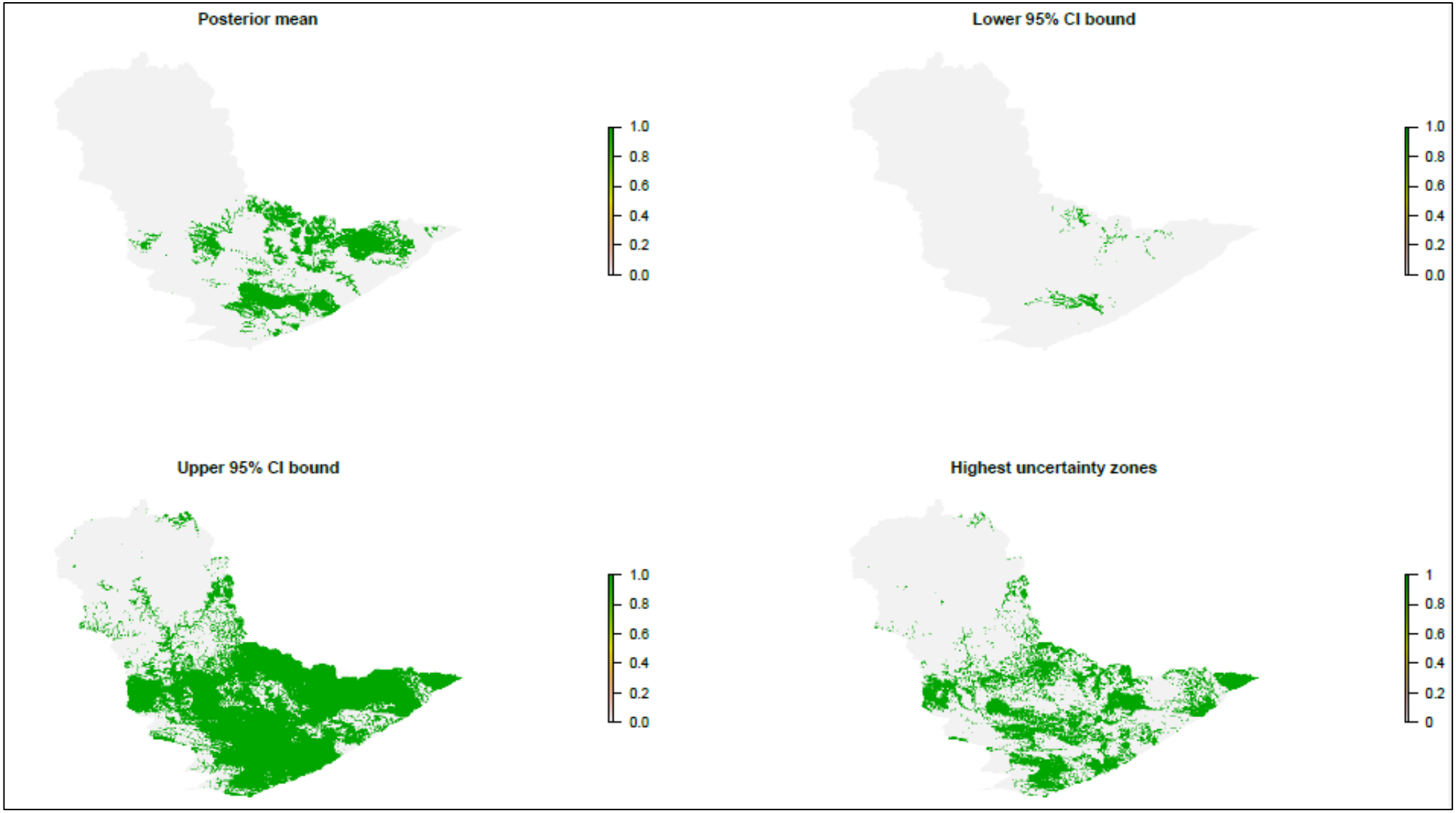


Figure S5.4.108. The modelled distribution of *Sandelia bainsii* in South Africa showing predicted distribution as a binary output.

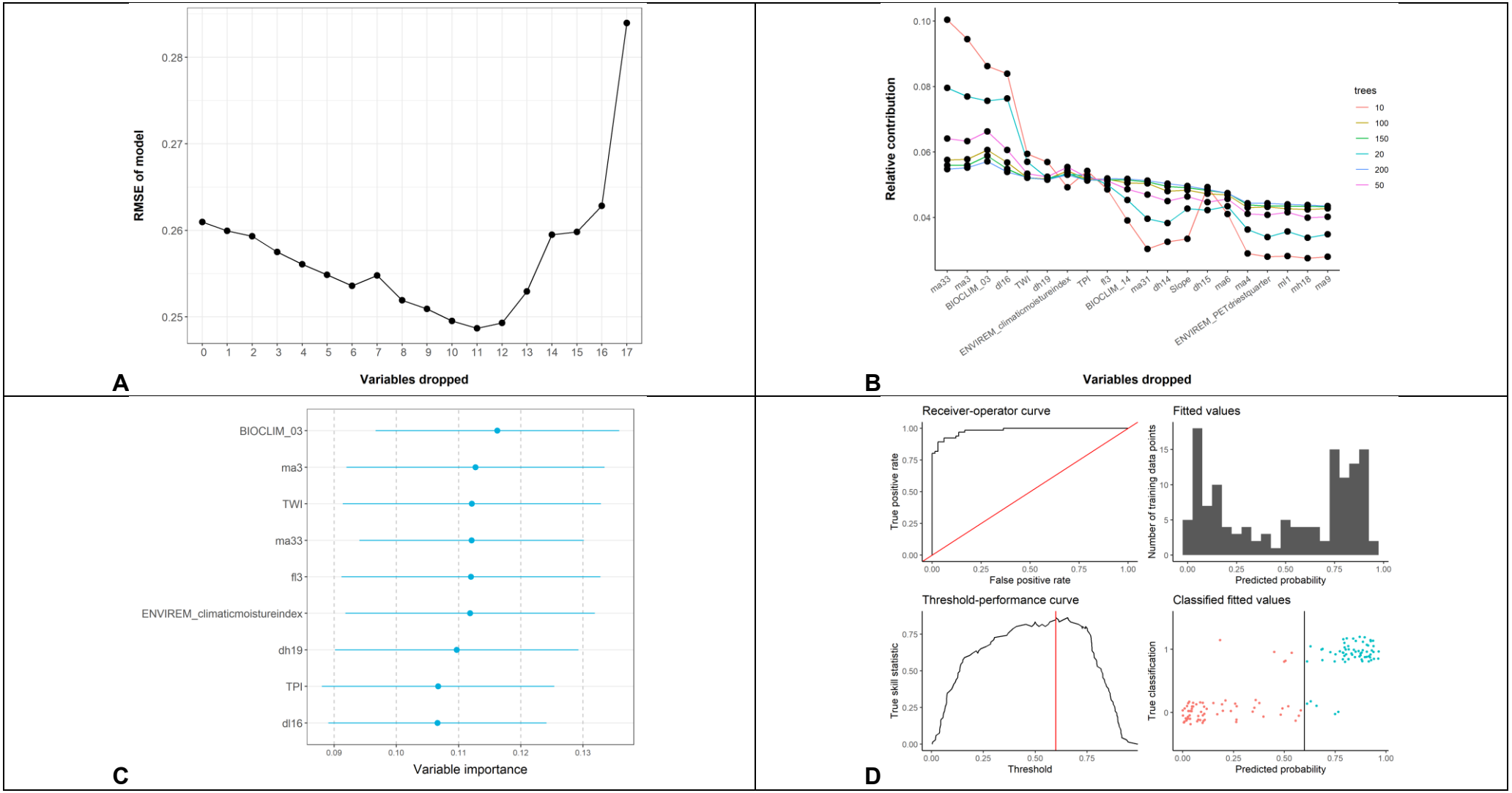


Figure S5.4.109. Model diagnostic outputs for *Sandelia bainsii*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

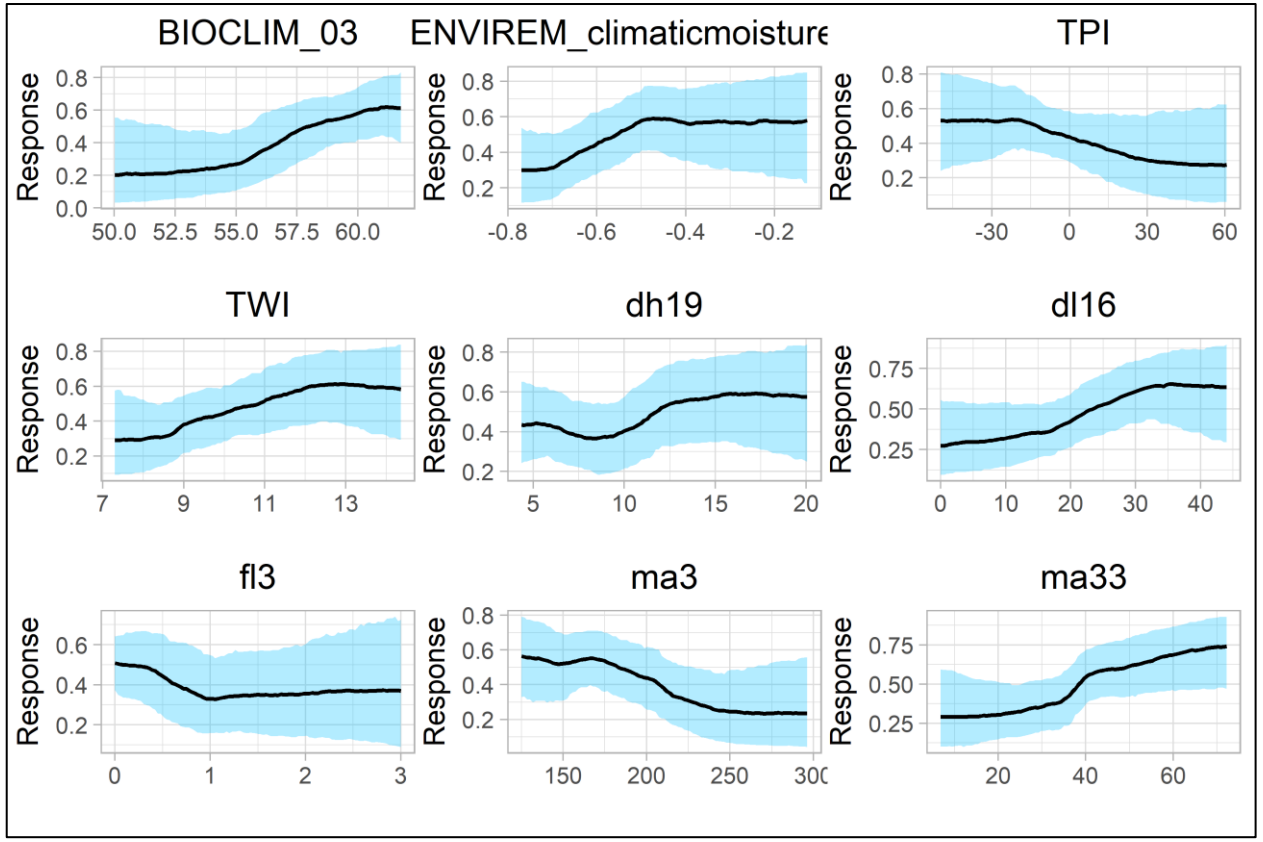


Figure S5.4.110. Partial dependence plots for *Sandelia bainsii.*

Serranochromis meridianus

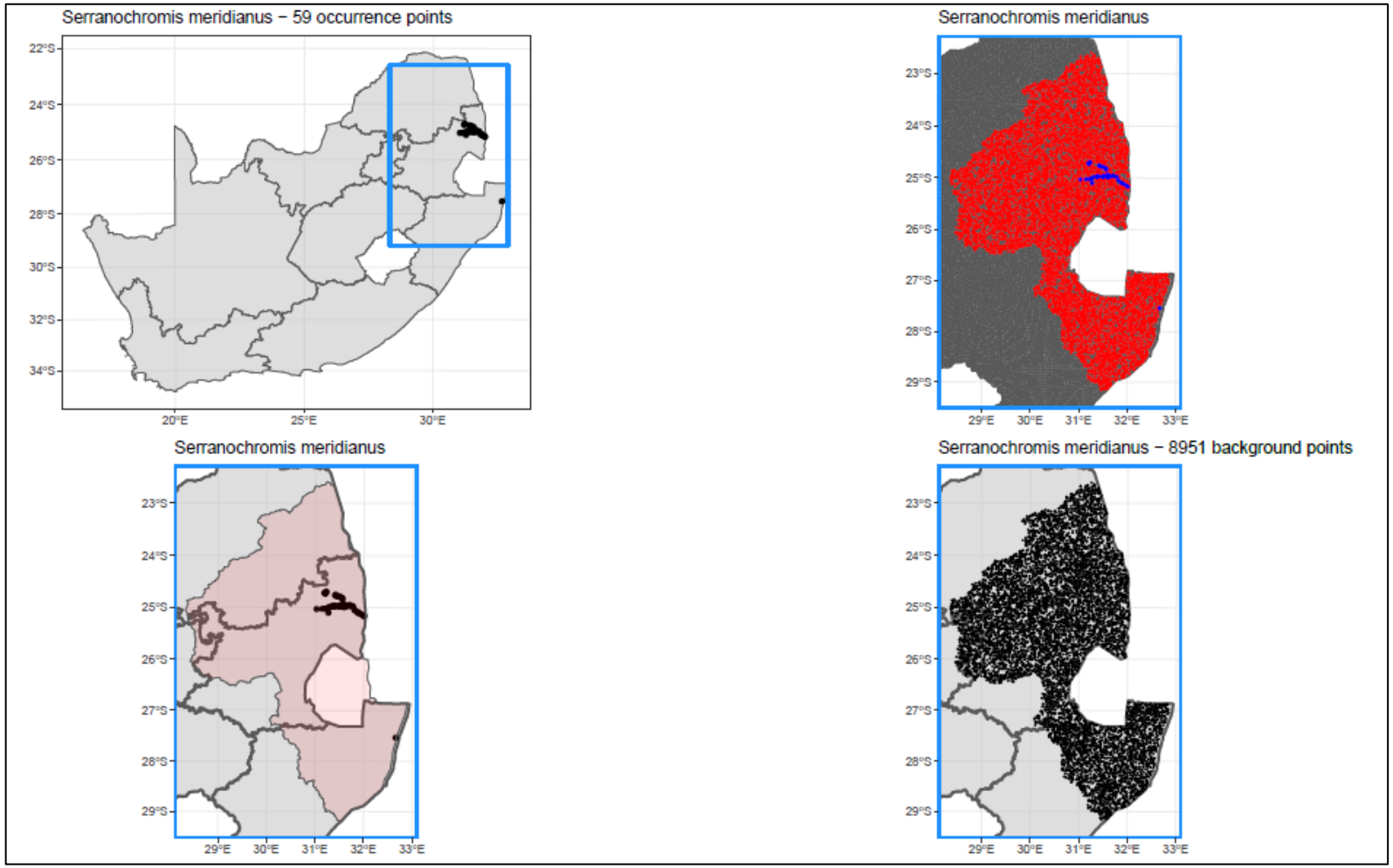


Figure S5.4.111. Occurrence records and background points for *Serranochromis meridianus.*

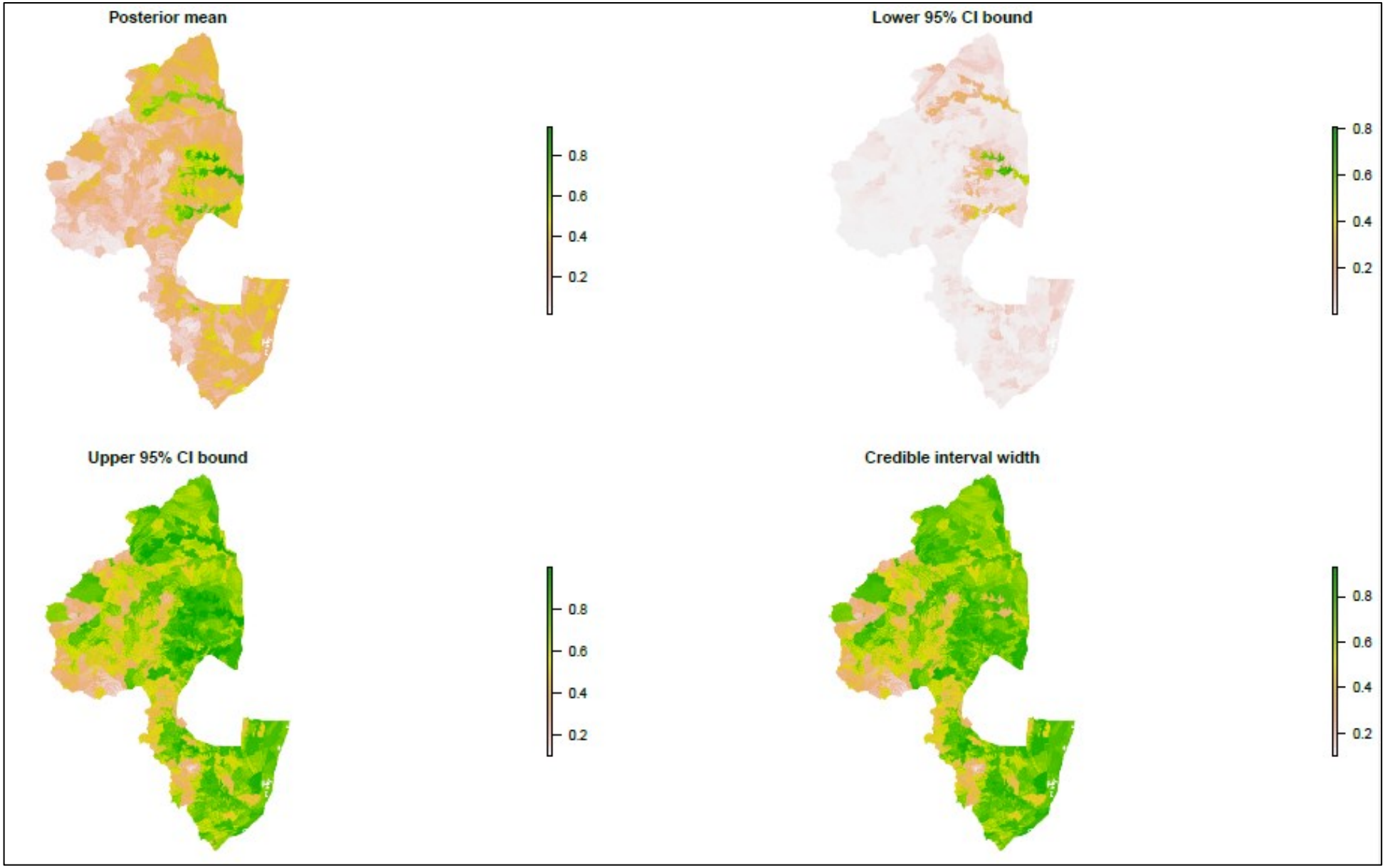


Figure S5.4.112. The modelled distribution of *Serranochromis meridianus* in South Africa showing habitat suitability.

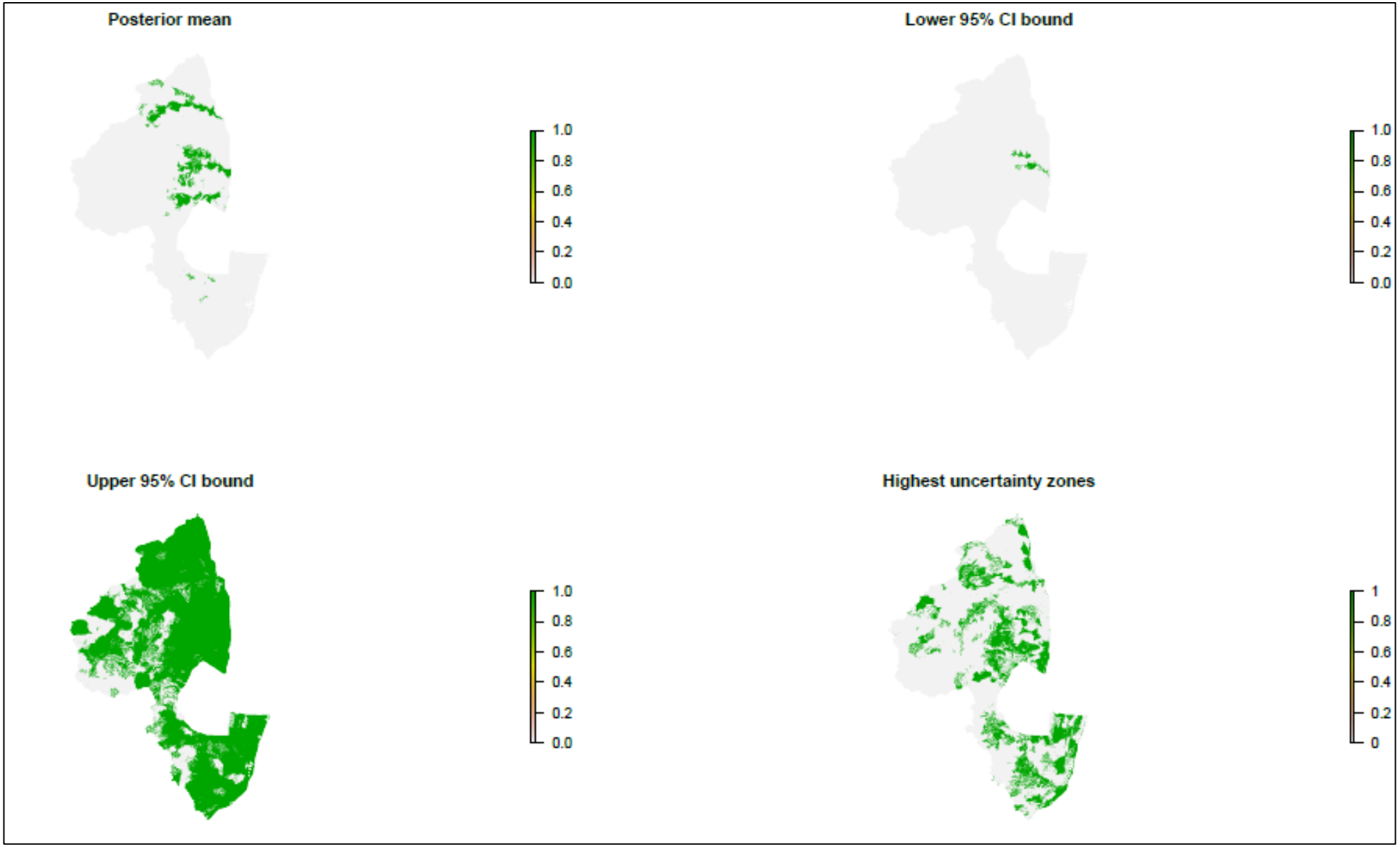


Figure S5.4.113. The modelled distribution of *Serranochromis meridianus* in South Africa showing predicted distribution as a binary output.

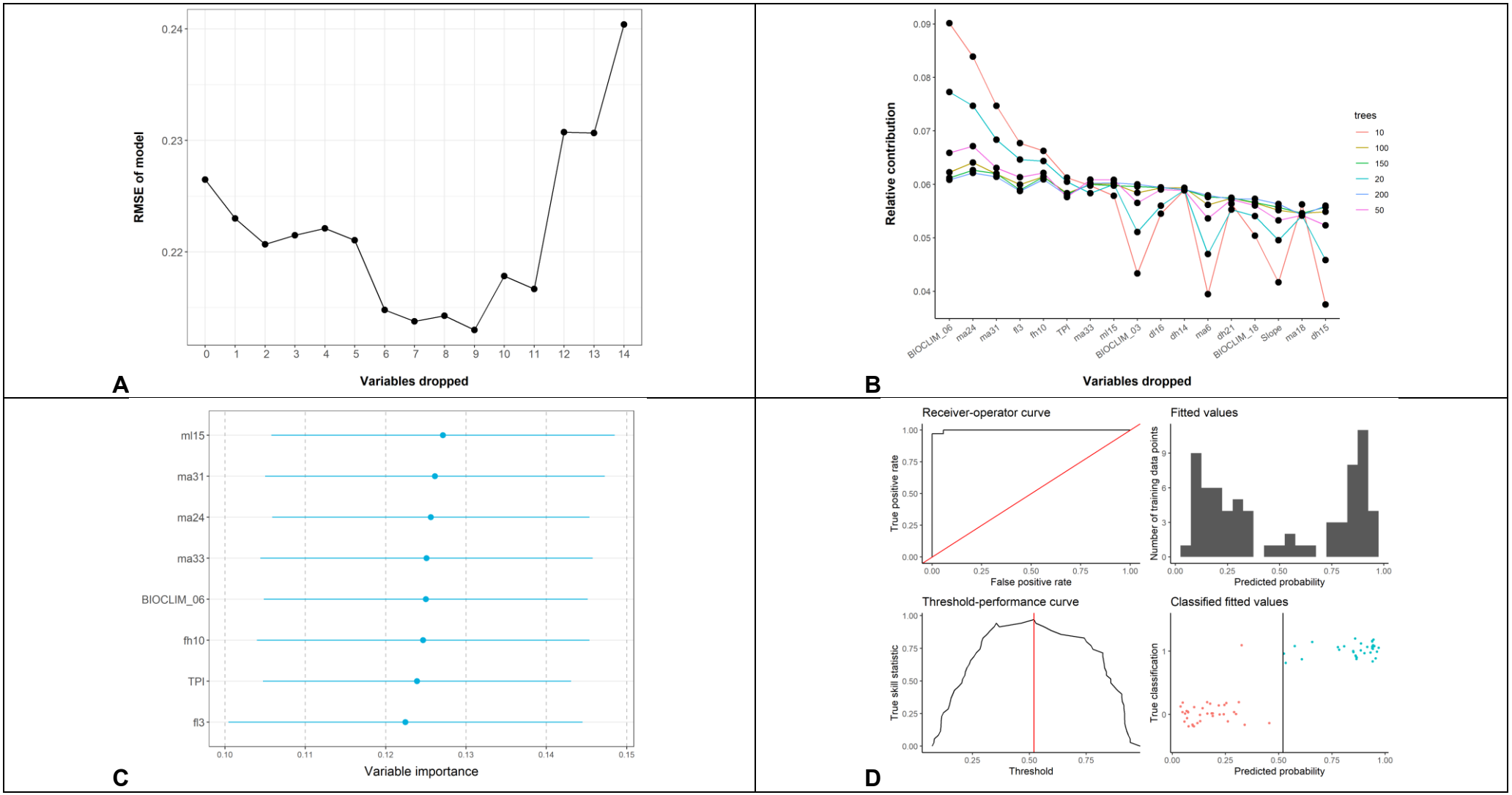


Figure S5.4.114. Model diagnostic outputs for *Serranochromis meridianus*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

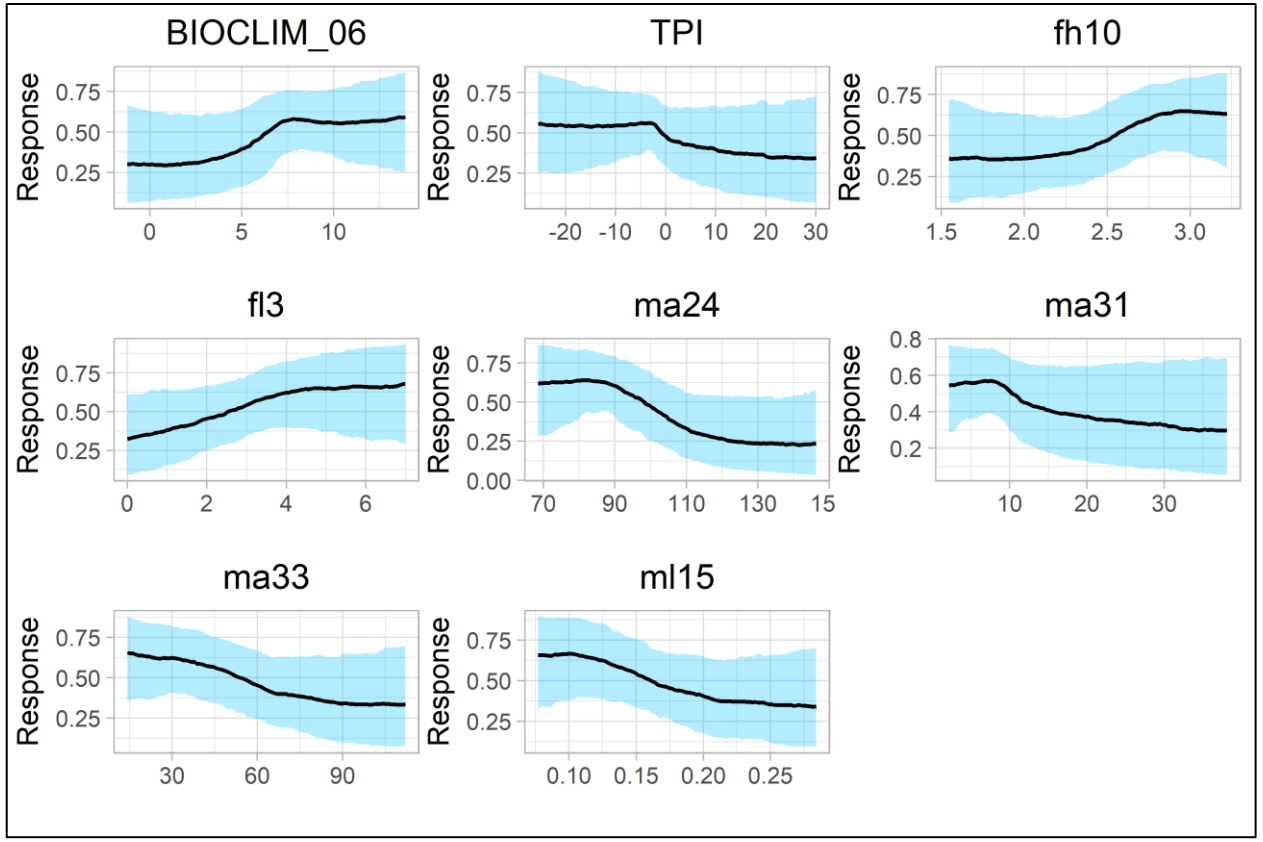


Figure S5.4.115. Partial dependence plots for *Serranochromis meridianus.*

Silhouettea sibayi

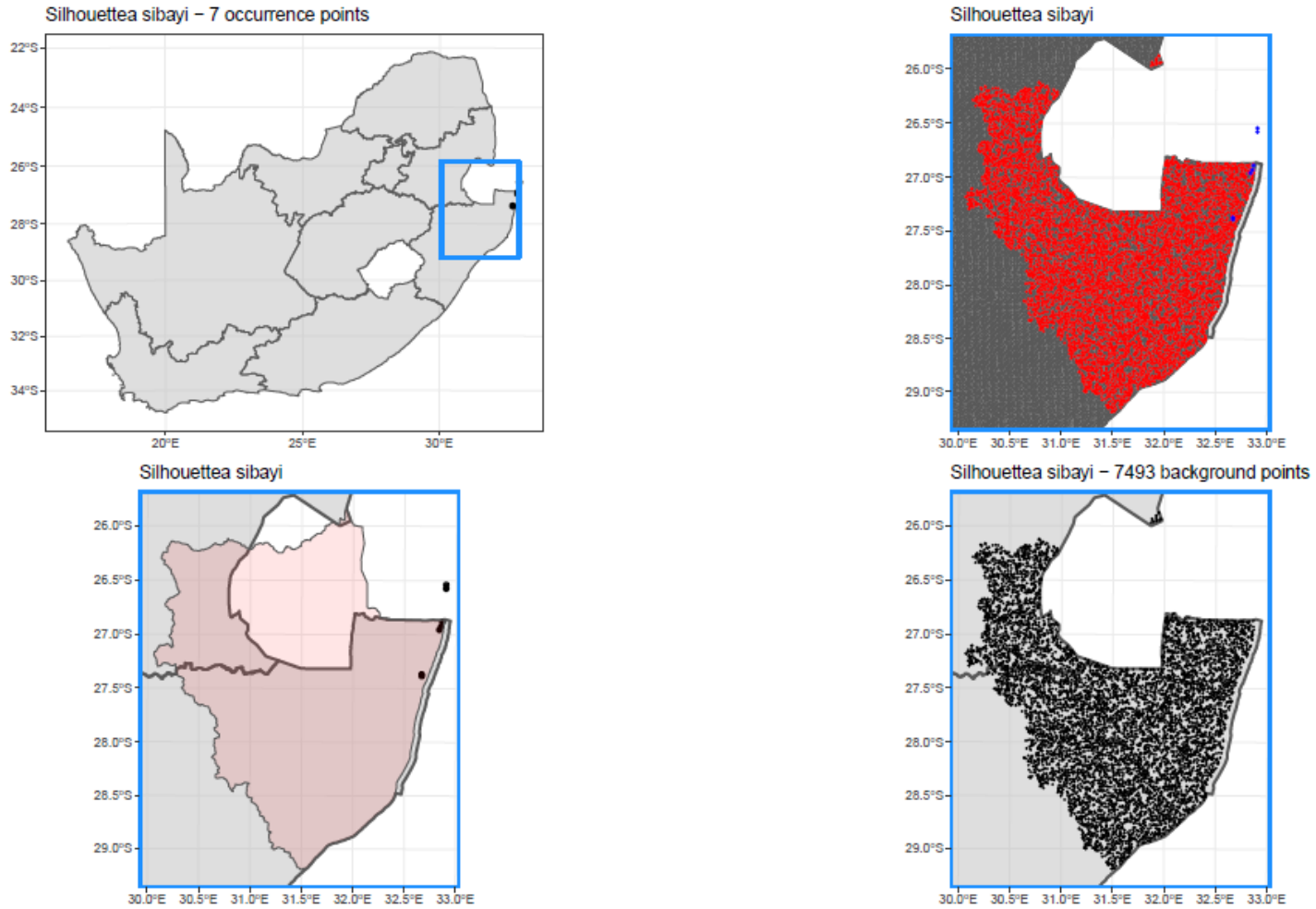


Figure S5.4.116. Occurrence records and background points for *Silhouettea sibayi.*

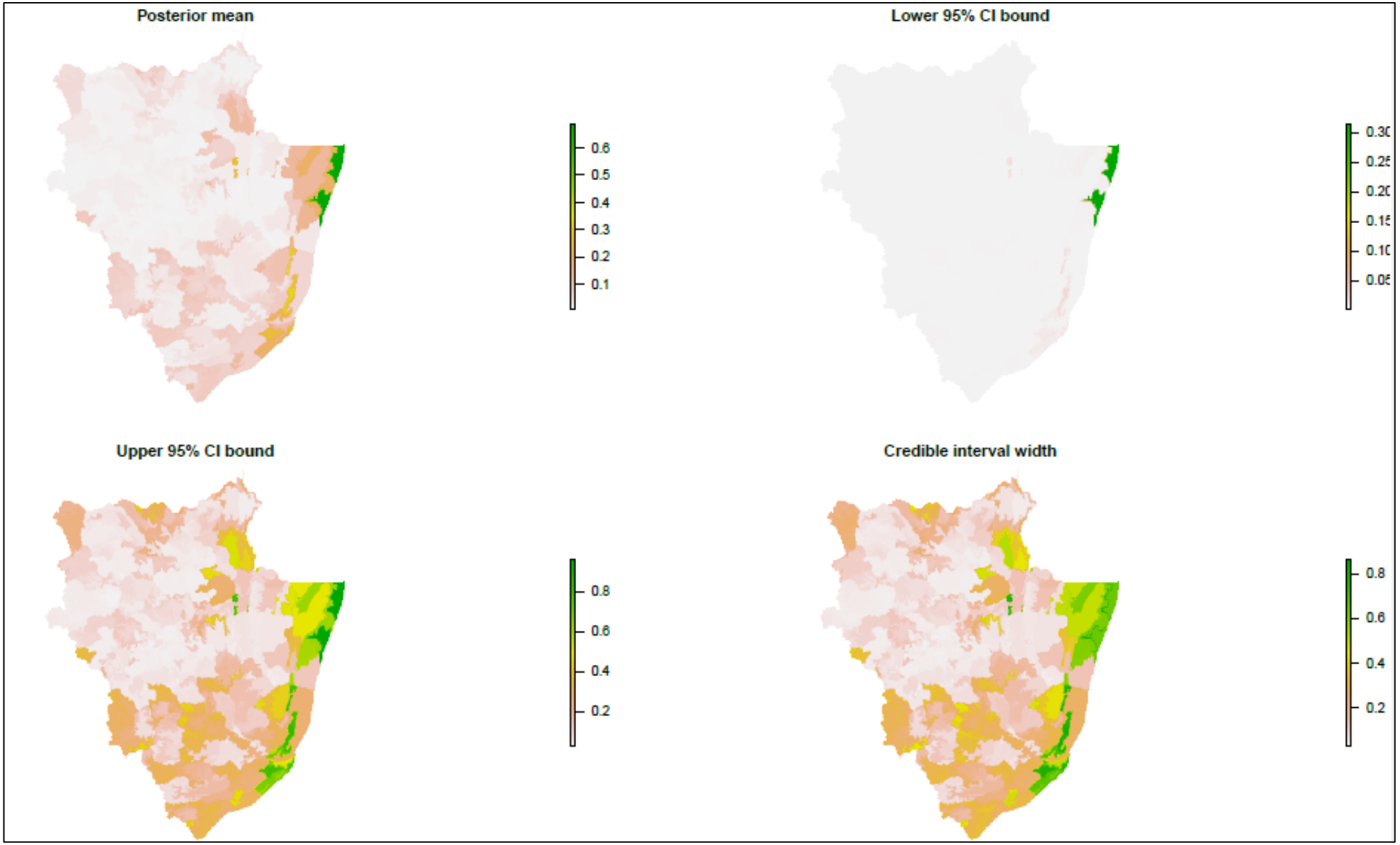


Figure S5.4.117. The modelled distribution of *Silhouettea sibayi* in South Africa showing habitat suitability.

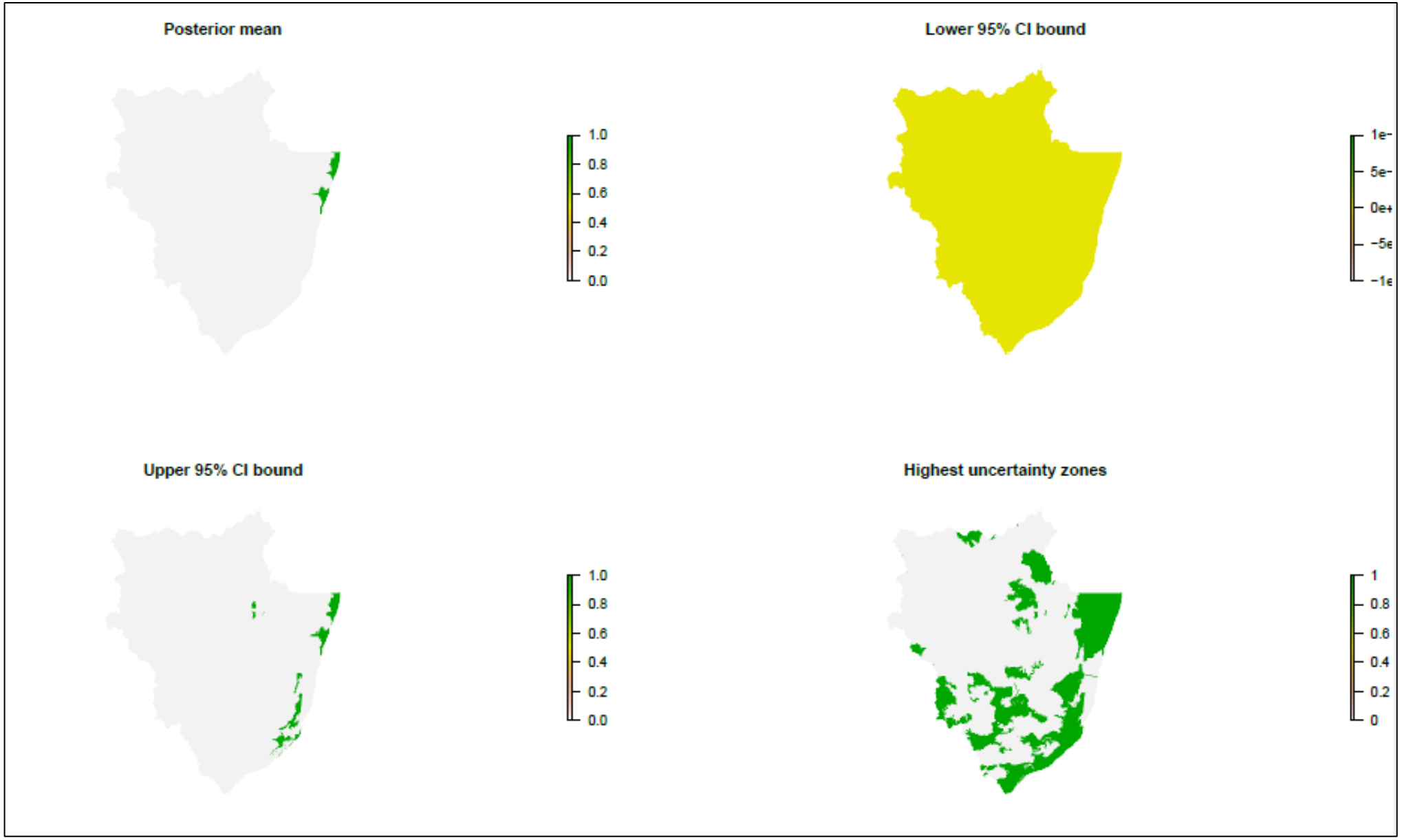


Figure S5.4.118. The modelled distribution of *Silhouettea sibayi* in South Africa showing predicted distribution as a binary output.

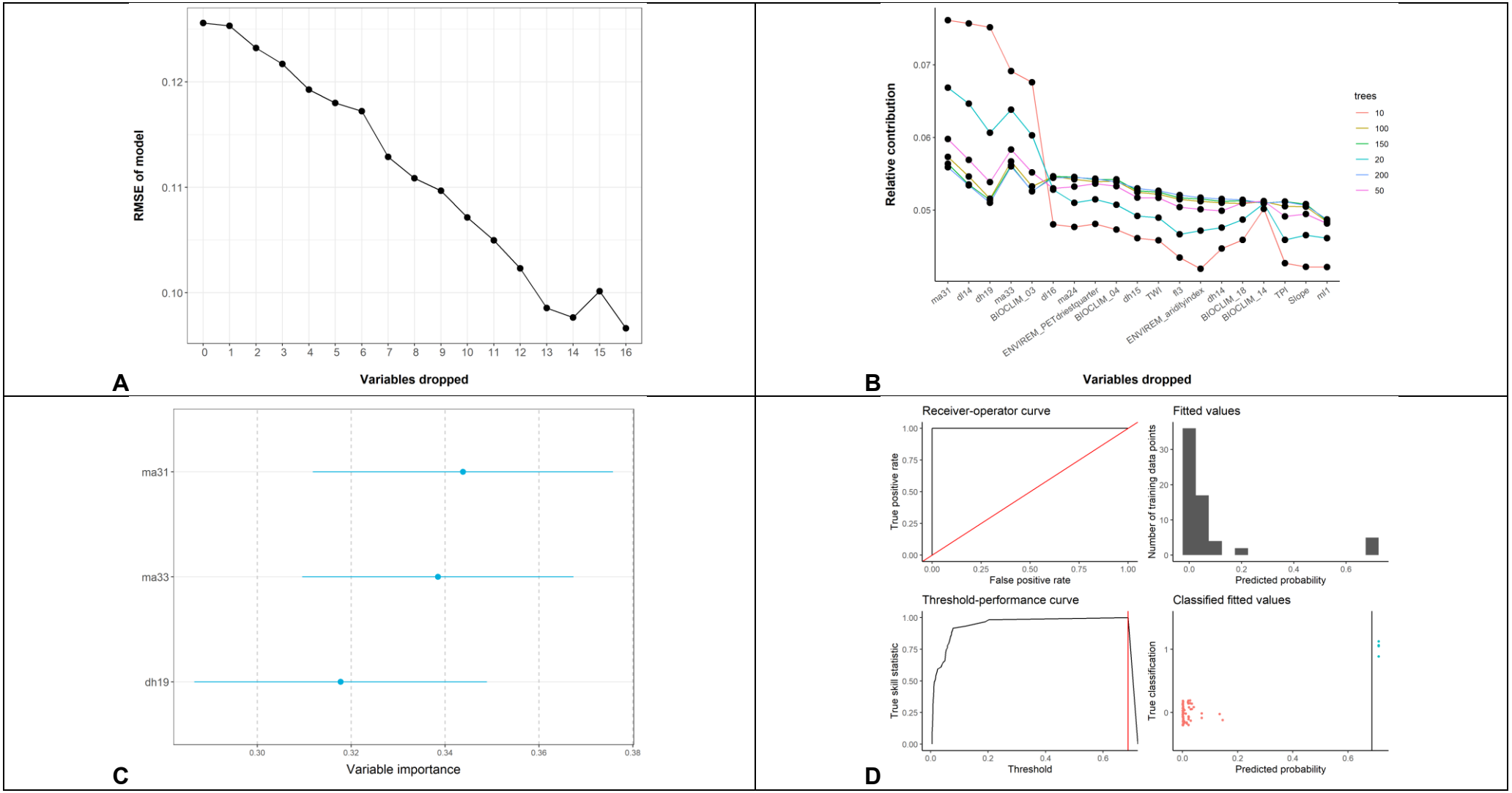


Figure S5.4.119. Model diagnostic outputs for *Silhouettea sibayi*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

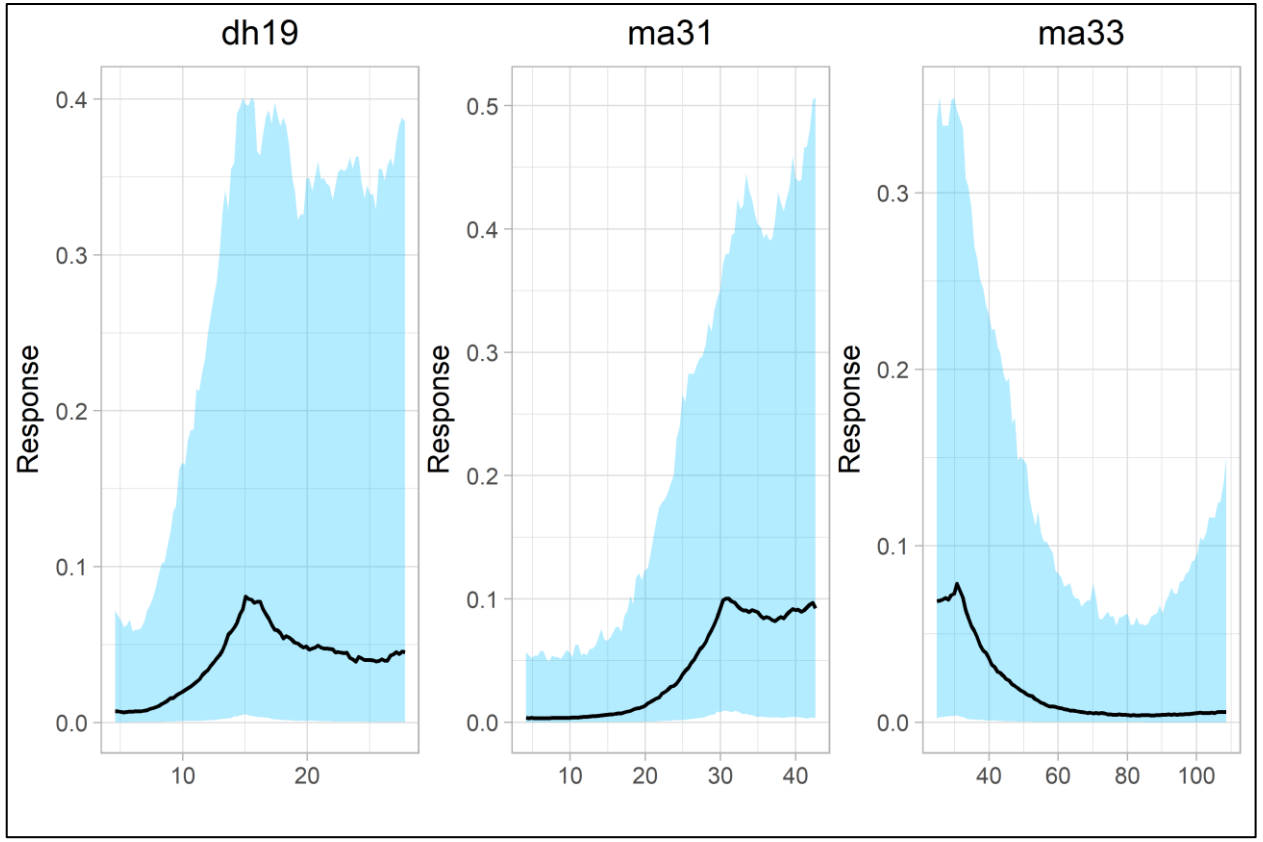


Figure S5.4.120. Partial dependence plots for *Silhouettea sibayi.*

Kneria sp nov south africa

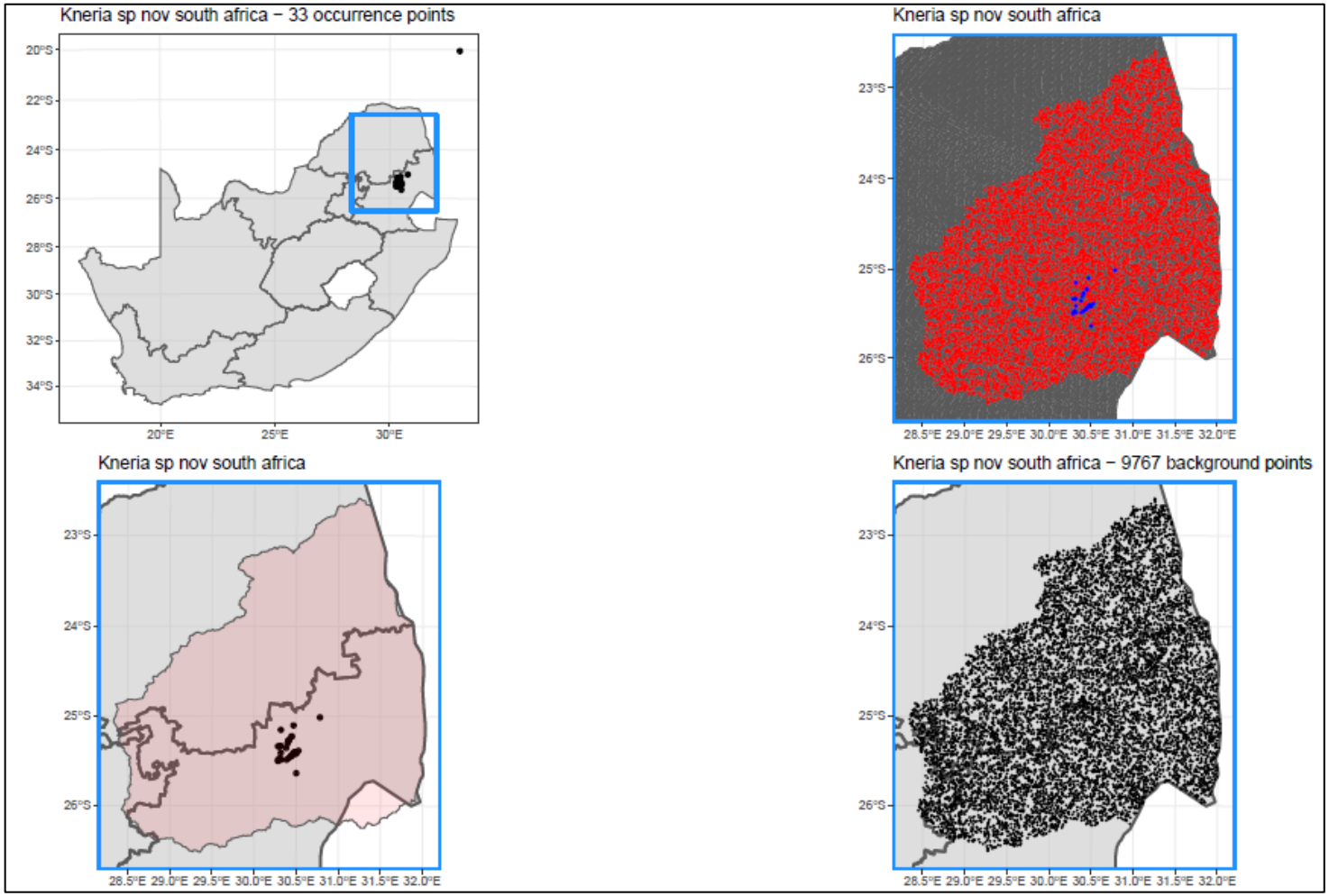


Figure S5.4.121. Occurrence records and background points for *Kneria* sp nov south africa.

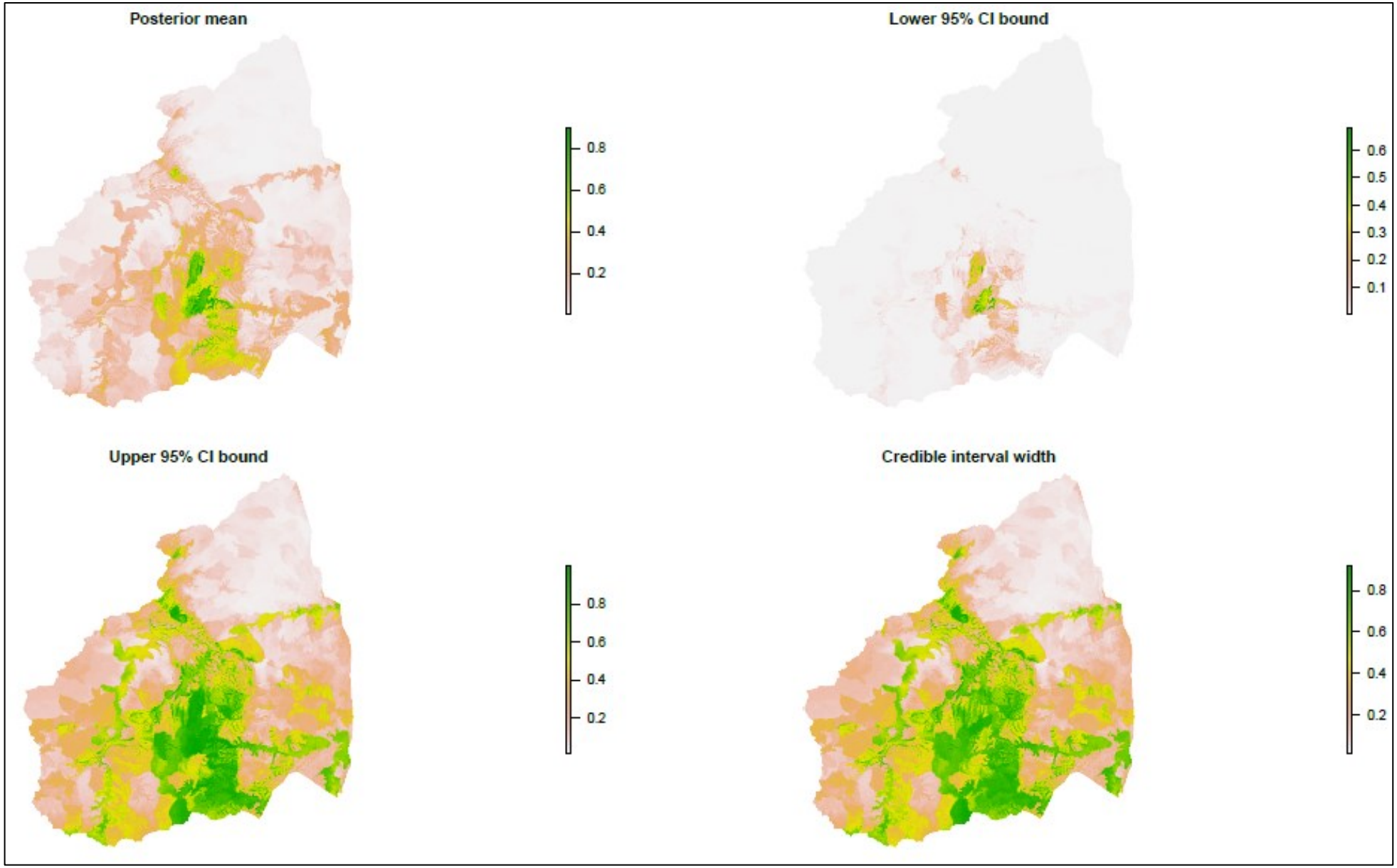


Figure S5.4.122. The modelled distribution of *Kneria* sp nov south africa in South Africa showing habitat suitability.

Figure S5.4.123. The modelled distribution of *Kneria* sp nov south africa in South Africa showing predicted distribution as a binary output.

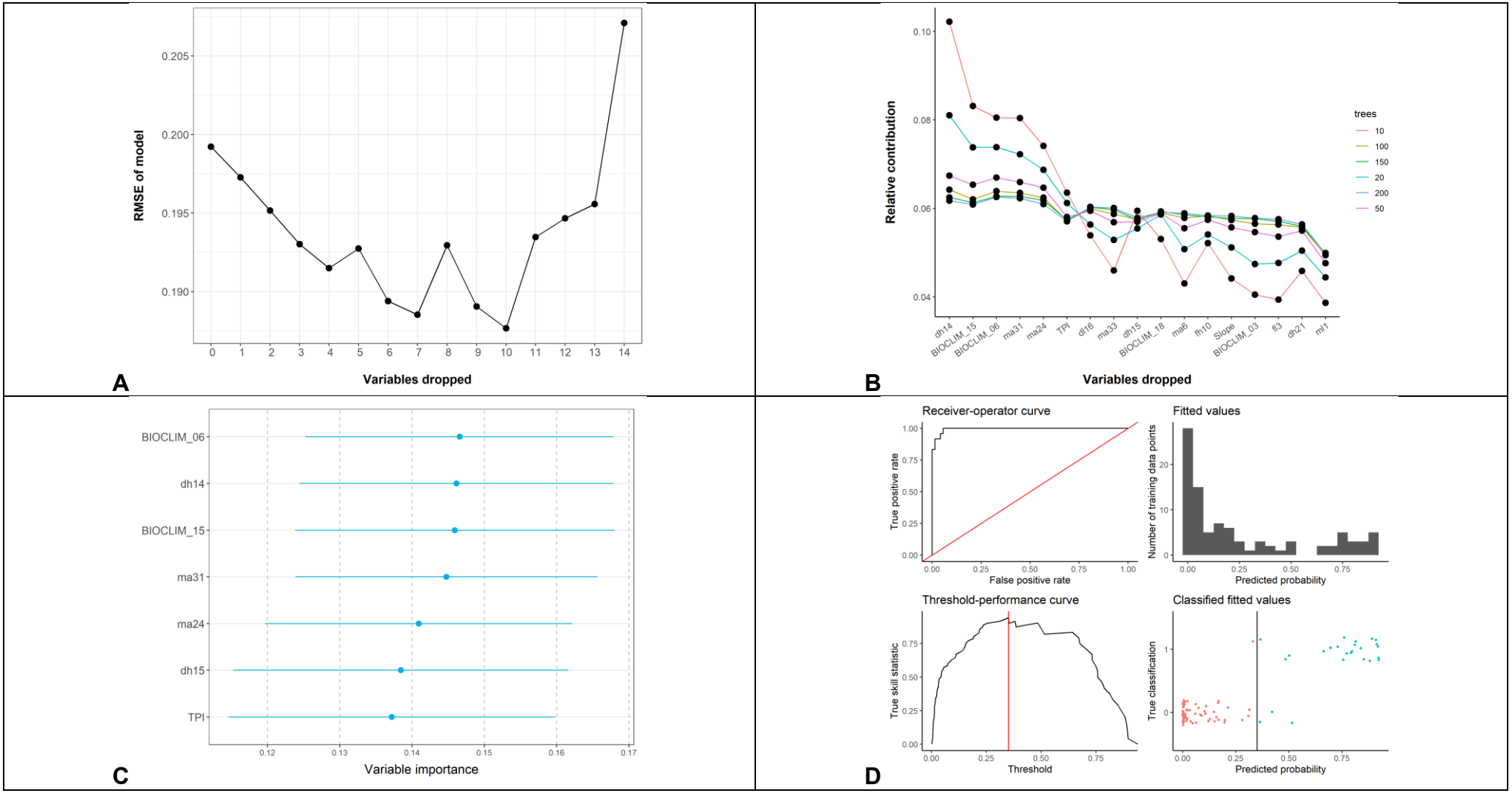


Figure S5.4.124. Model diagnostic outputs for *Kneria* sp nov south africa, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

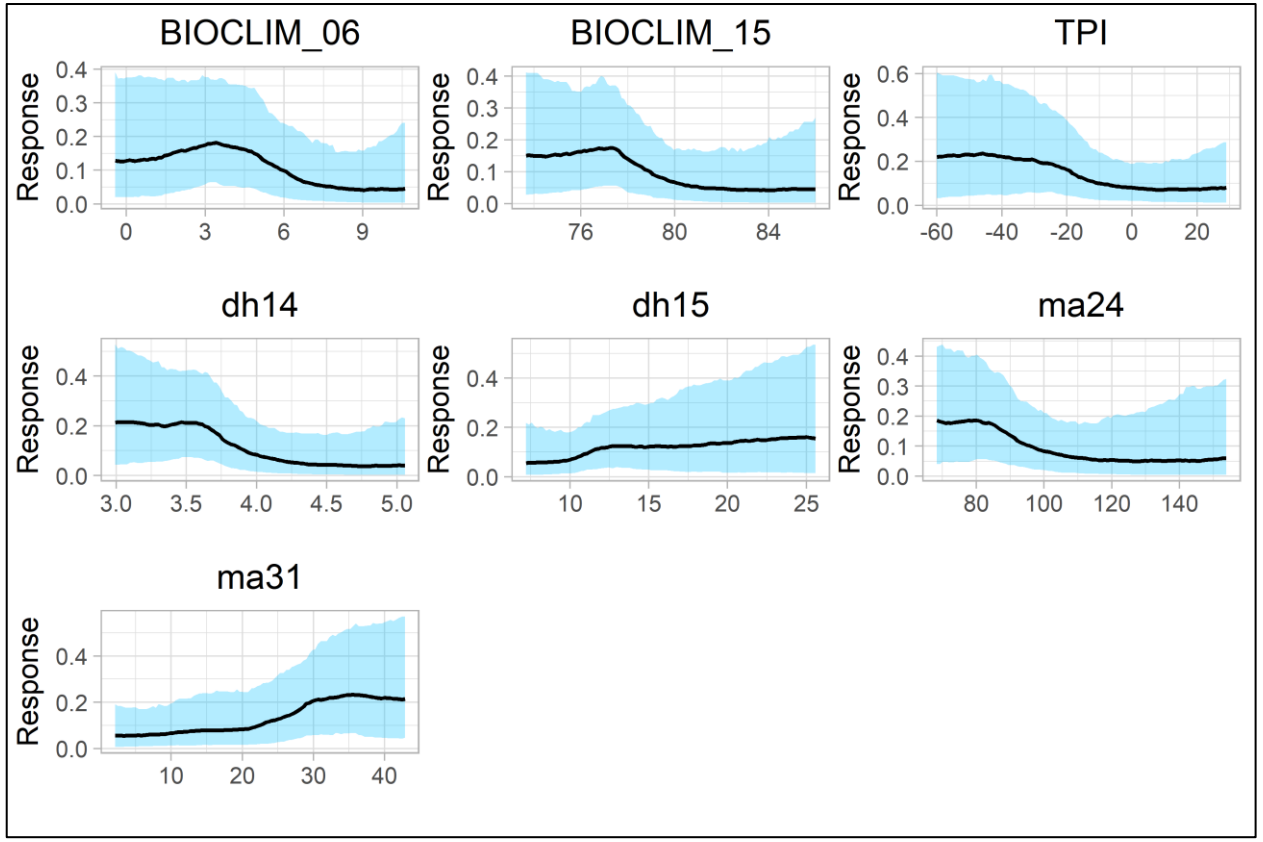


Figure S5.4.125. Partial dependence plots for *Kneria* sp nov south africa.

Marcusenius sp nov kosi

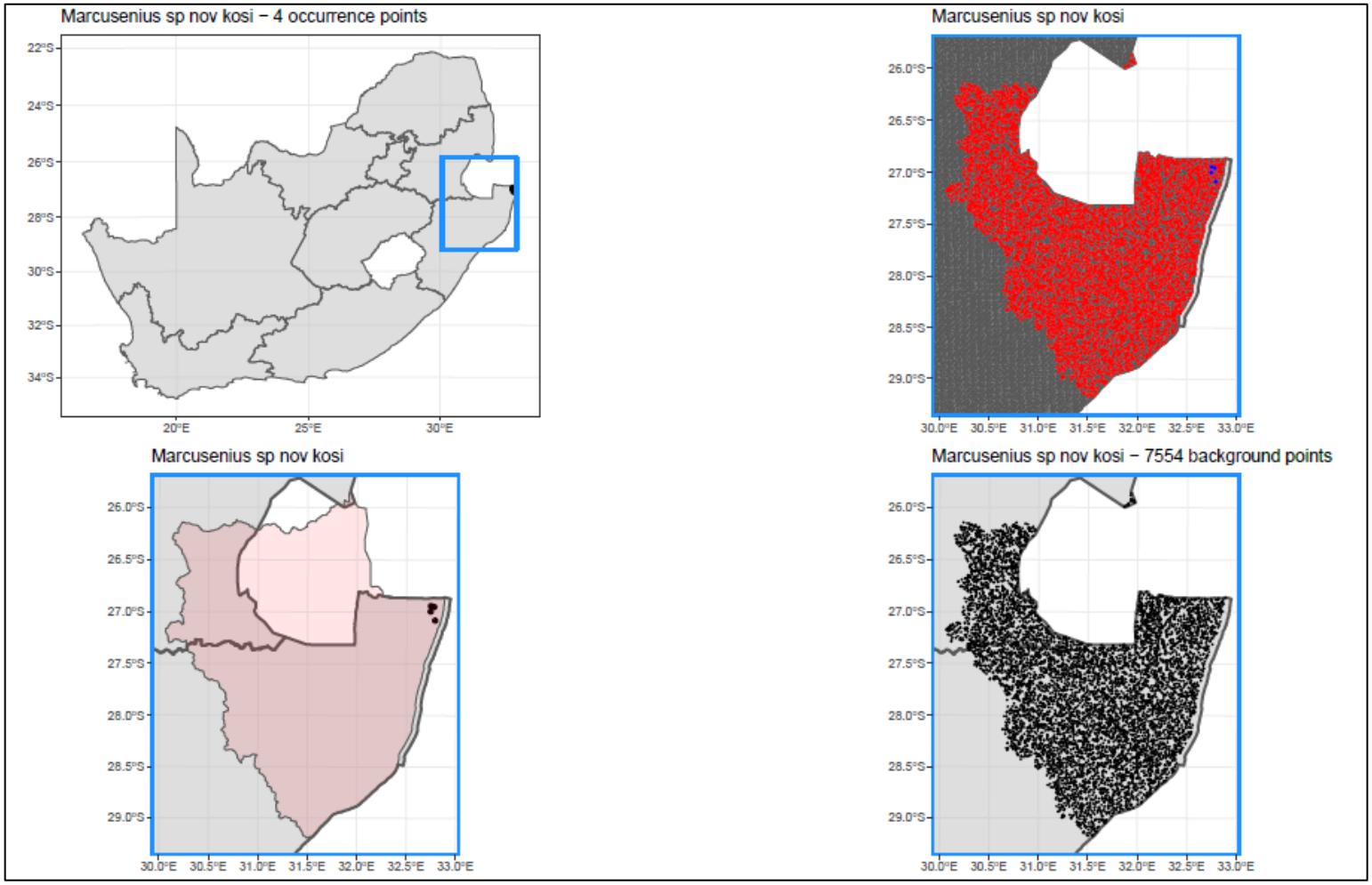


Figure S5.4.126. Occurrence records and background points for *Marcusenius* sp nov kosi.

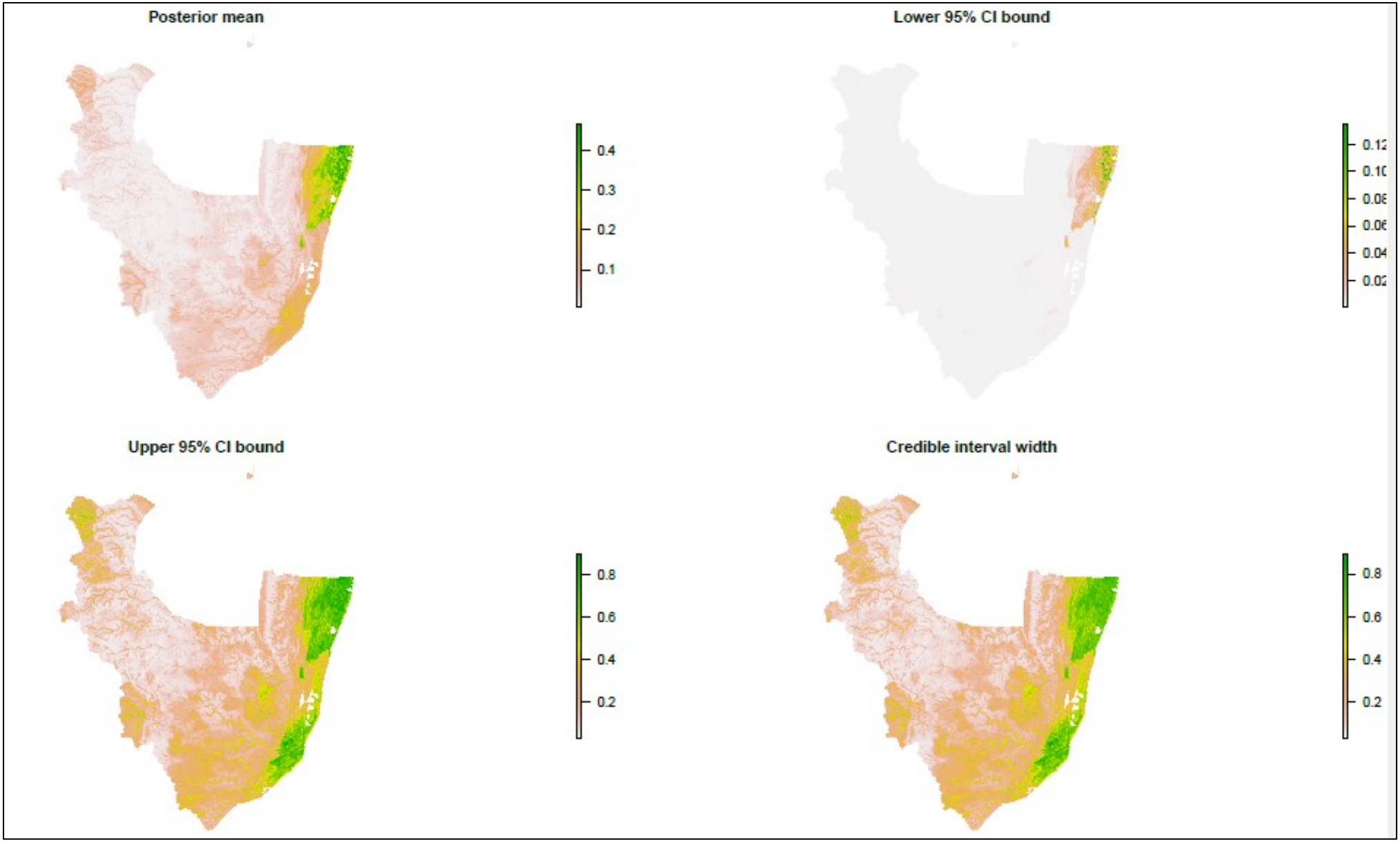


Figure S5.4.127. The modelled distribution of *Marcusenius* sp nov kosi in South Africa showing habitat suitability.

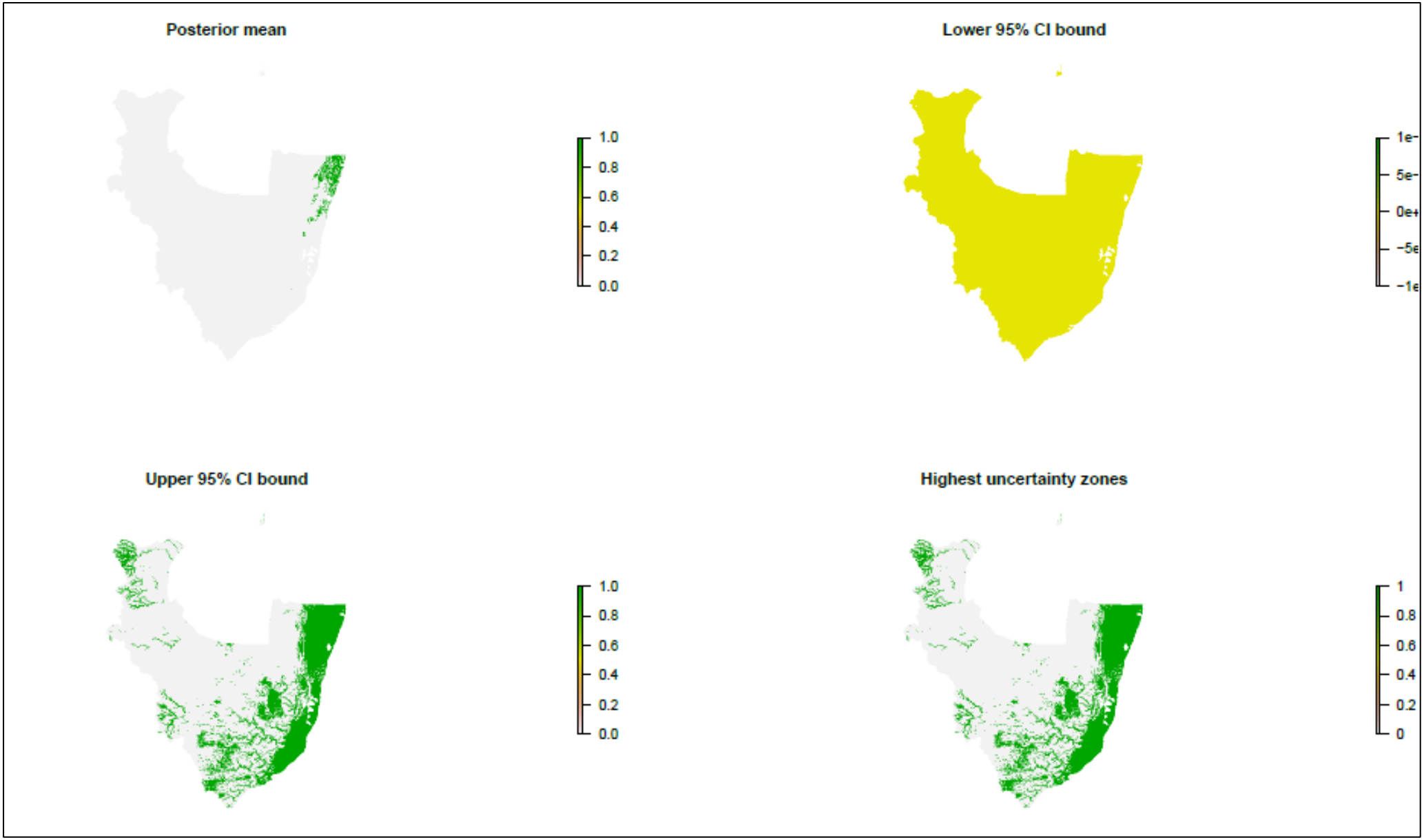


Figure S5.4.128. The modelled distribution of *Marcusenius* sp nov kosi in South Africa showing predicted distribution as a binary output.

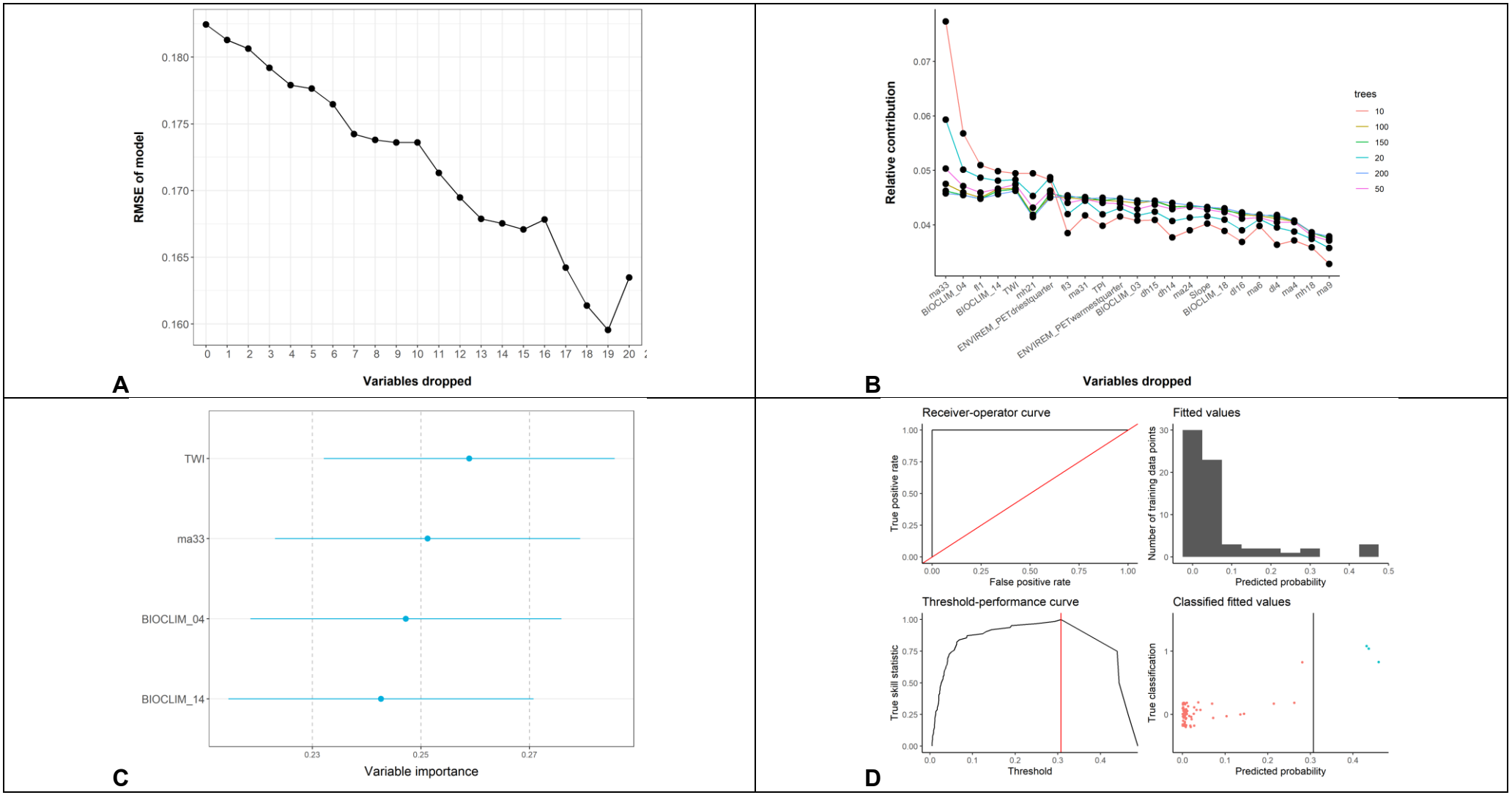


Figure S5.4.129. Model diagnostic outputs for *Marcusenius* sp nov kosi, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

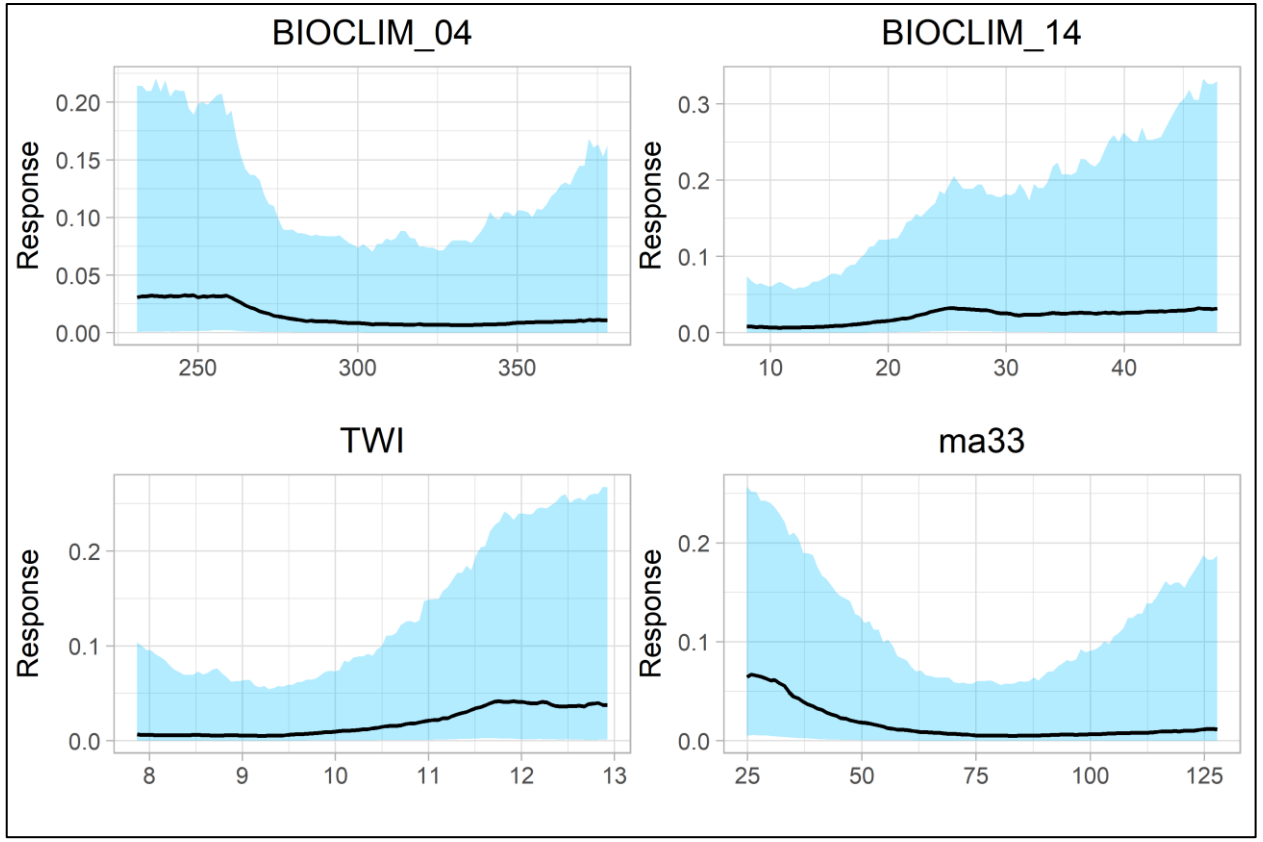


Figure S5.4.130. Partial dependence plots for *Marcusenius* sp nov kosi.

Pseudobarbus burchelli Breede

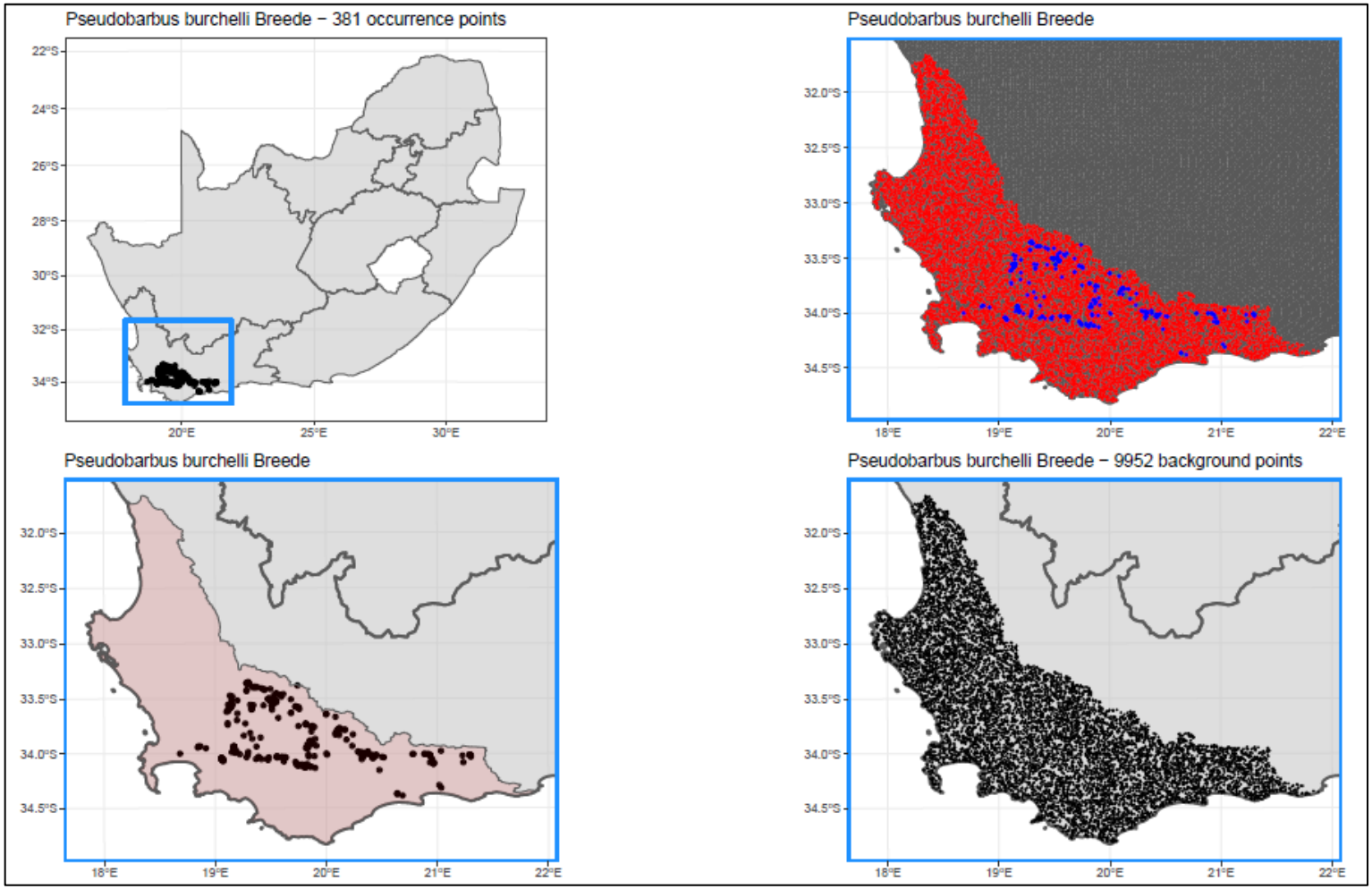


Figure S5.4.131. Occurrence records and background points for *Pseudobarbus burchelli* Breede.

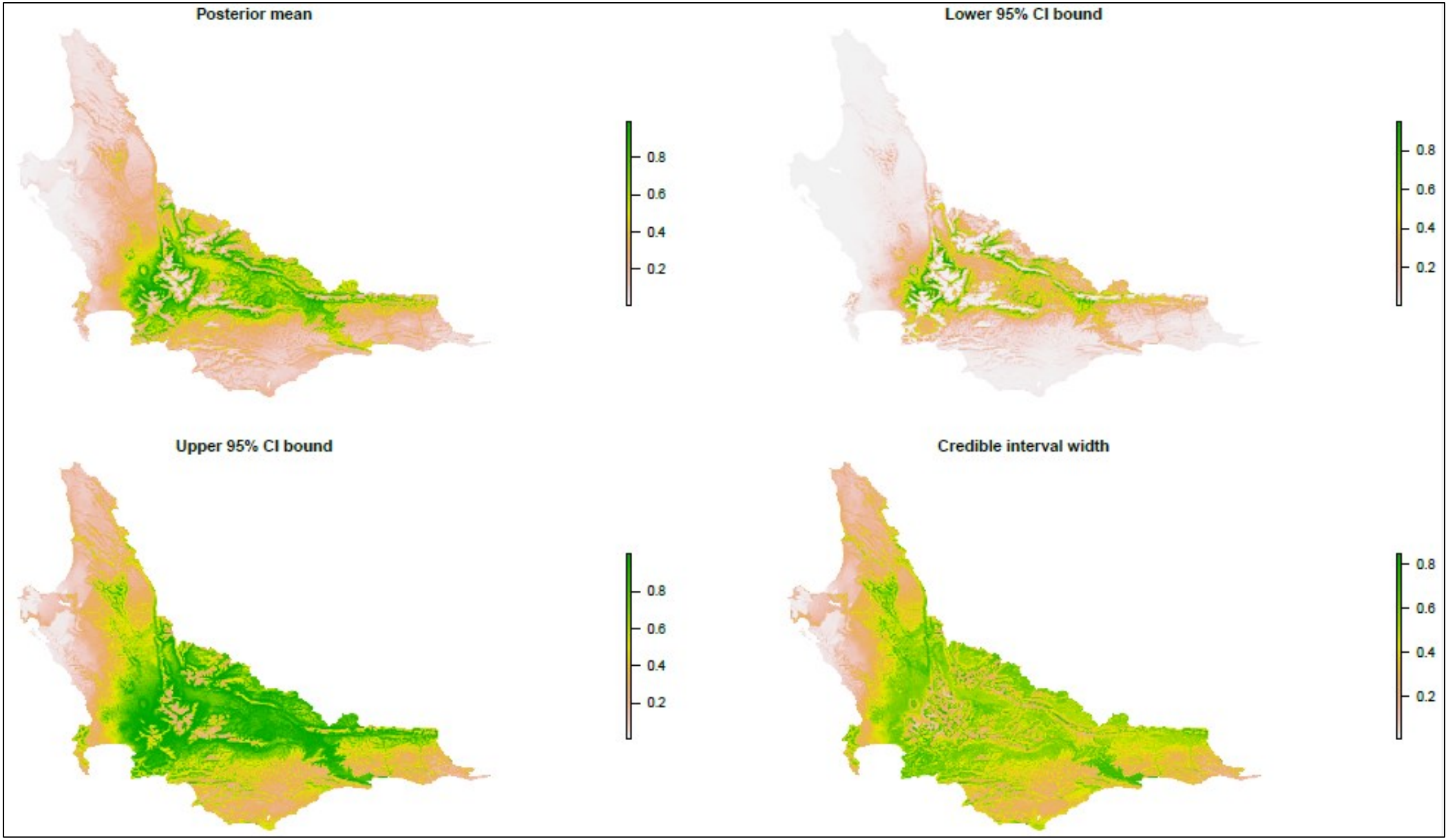


Figure S5.4.132. The modelled distribution of *Pseudobarbus burchelli* Breede in South Africa showing habitat suitability.

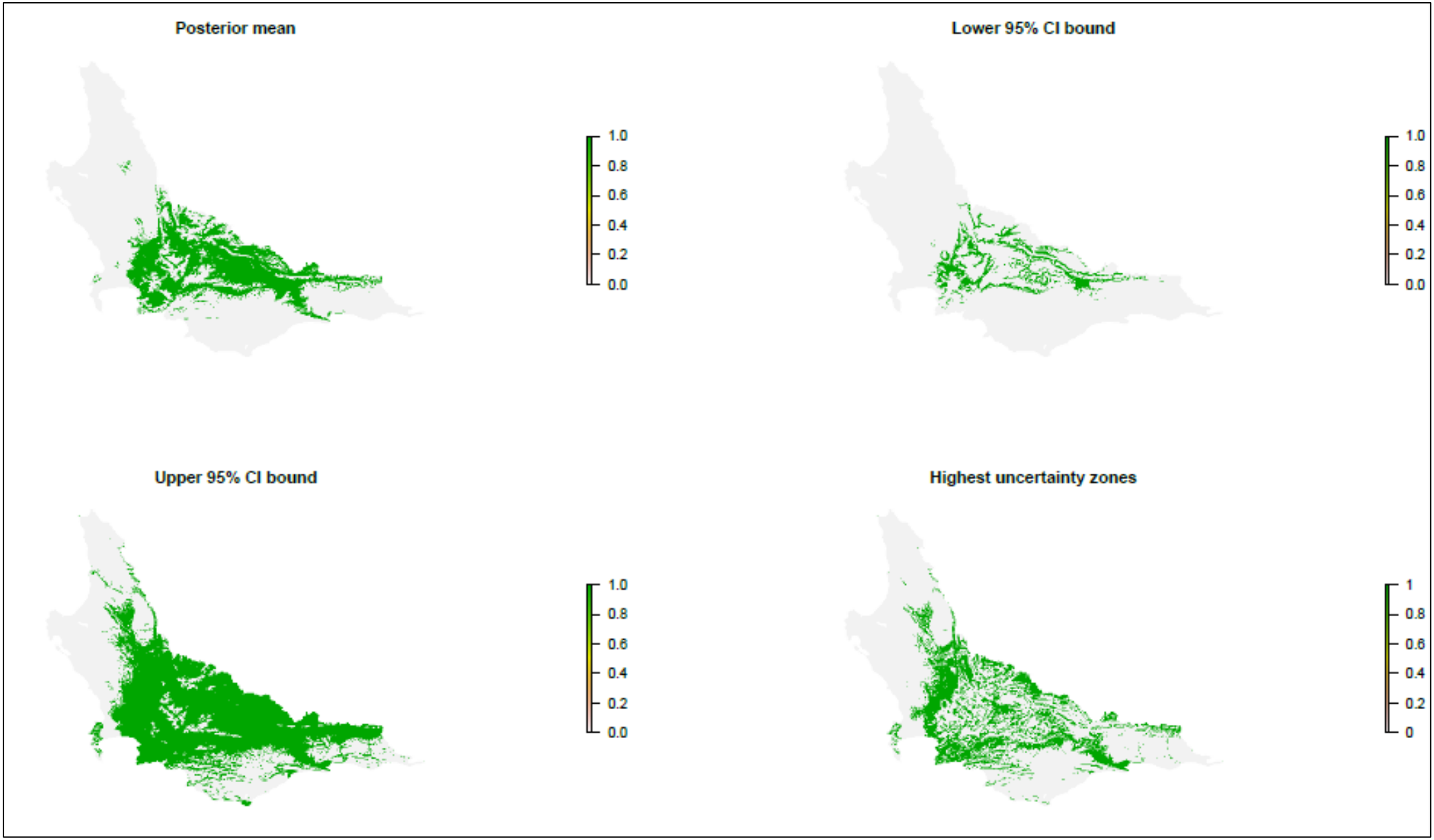


Figure S5.4.133. The modelled distribution of *Pseudobarbus burchelli* Breede in South Africa showing predicted distribution as a binary output.

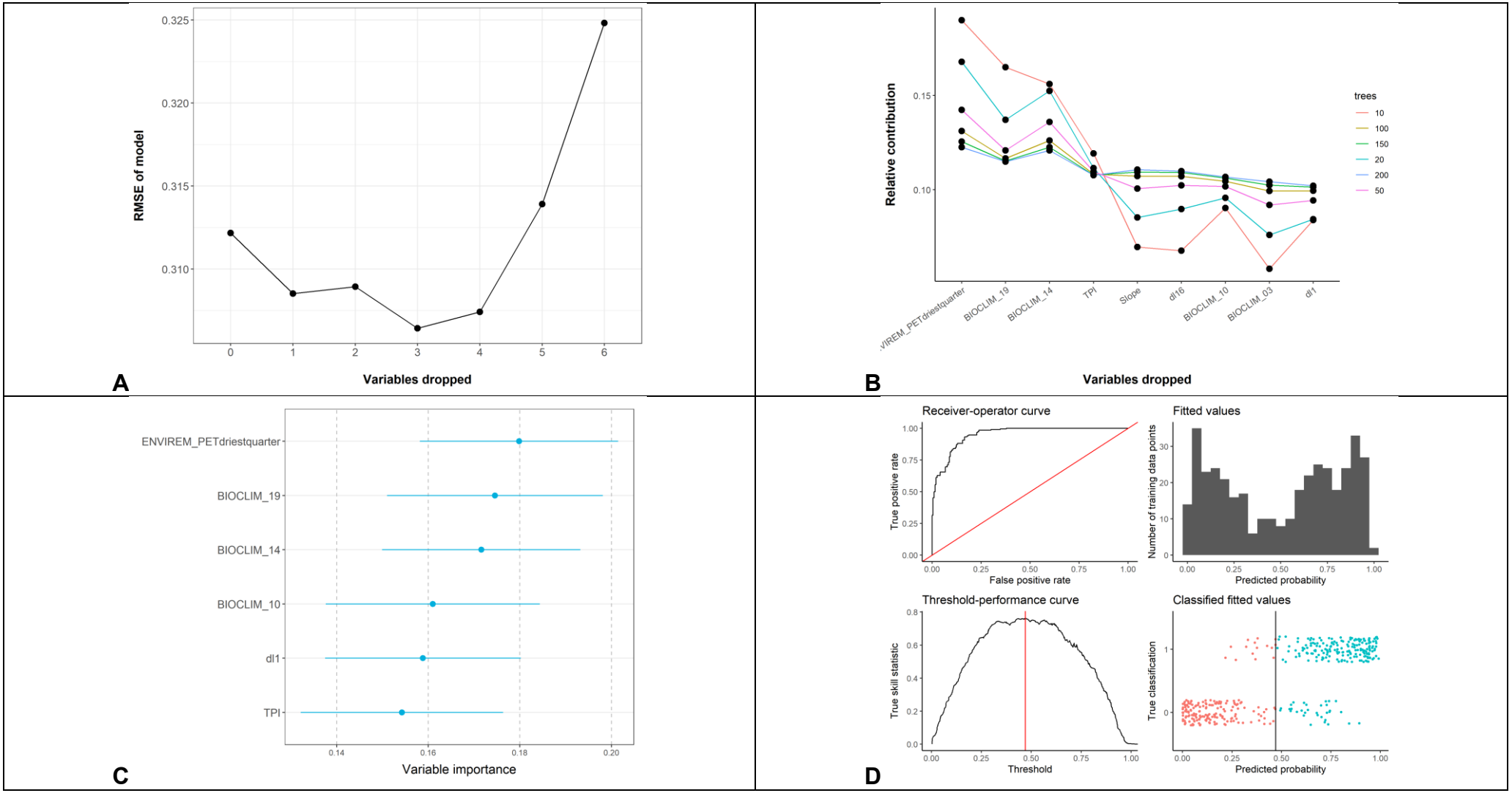


Figure S5.4.134. Model diagnostic outputs for *Pseudobarbus burchelli* Breede, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

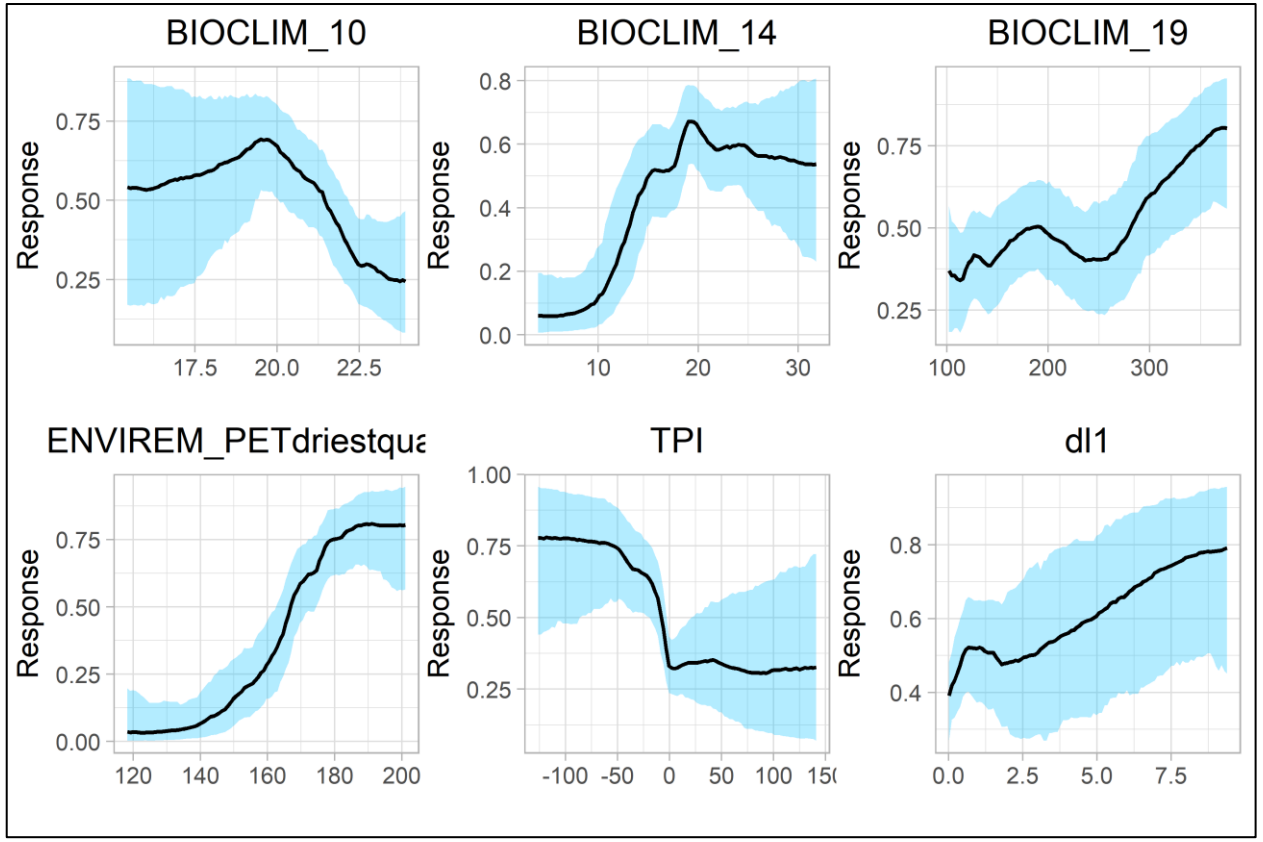


Figure S5.4.135. Partial dependence plots for *Pseudobarbus burchelli* Breede.

Pseudobarbus burchelli Heuningnes

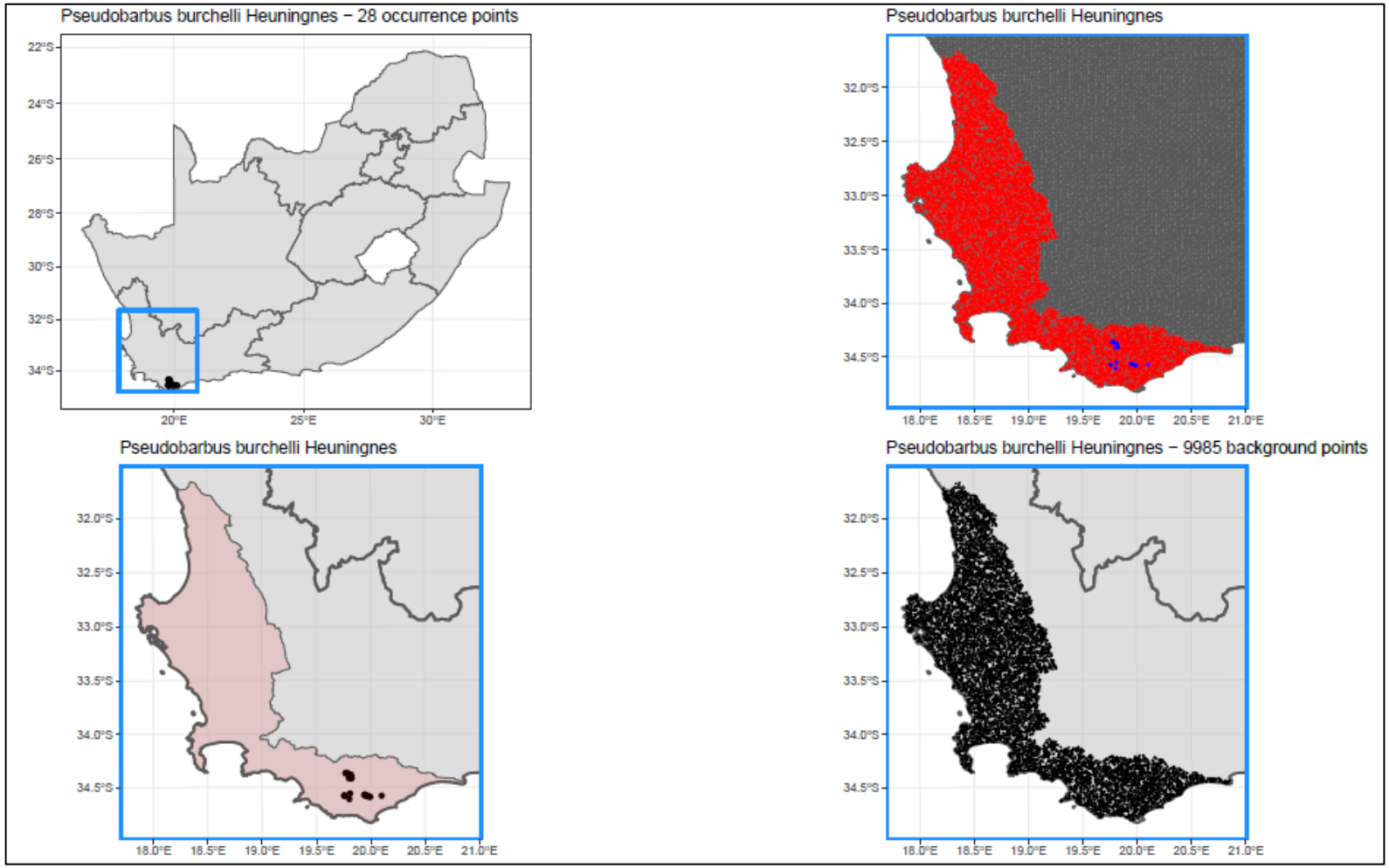


Figure S5.4.136. Occurrence records and background points for *Pseudobarbus burchelli* Heuningnes.

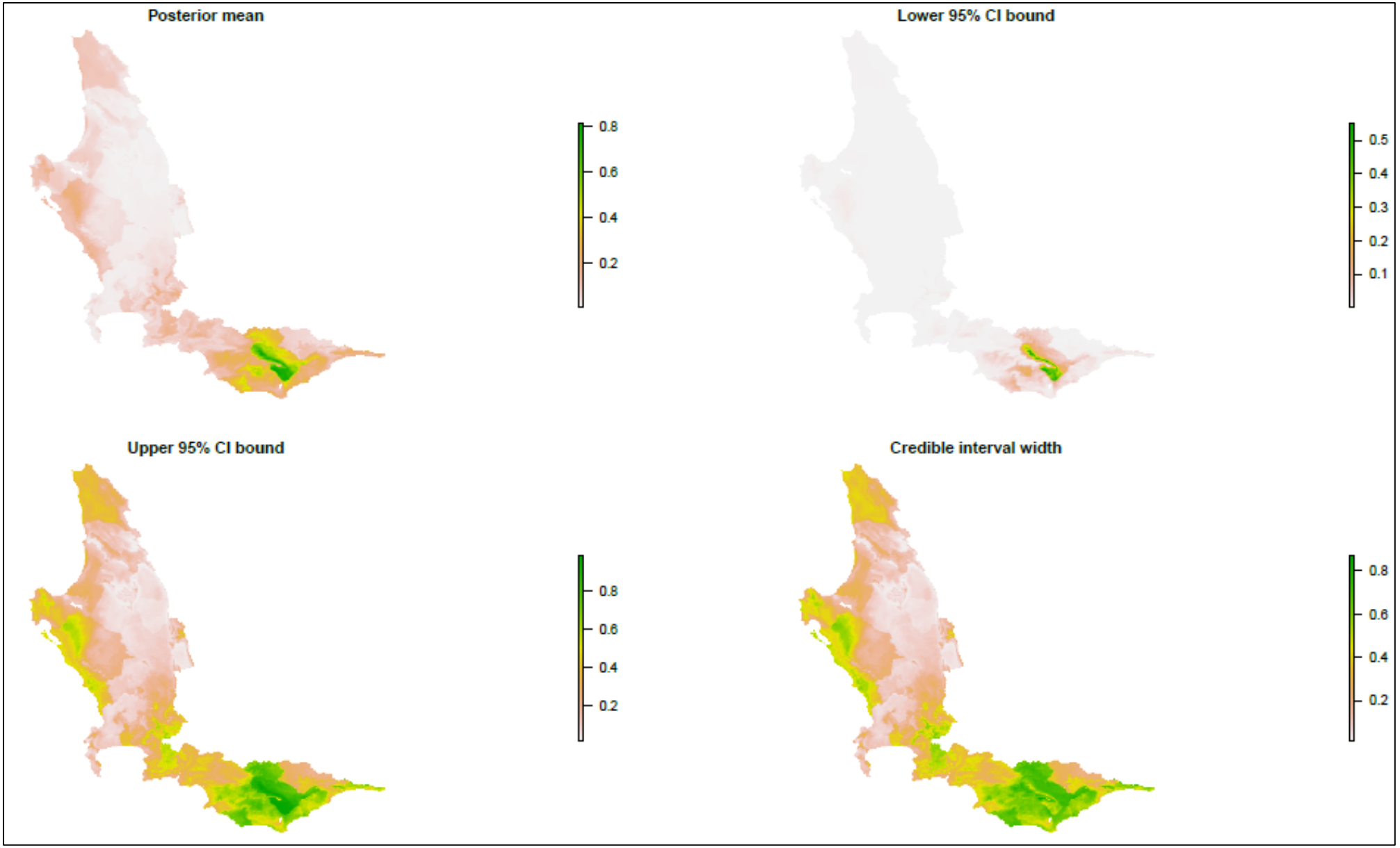


Figure S5.4.137. The modelled distribution of *Pseudobarbus burchelli* Heuningnes in South Africa showing habitat suitability.

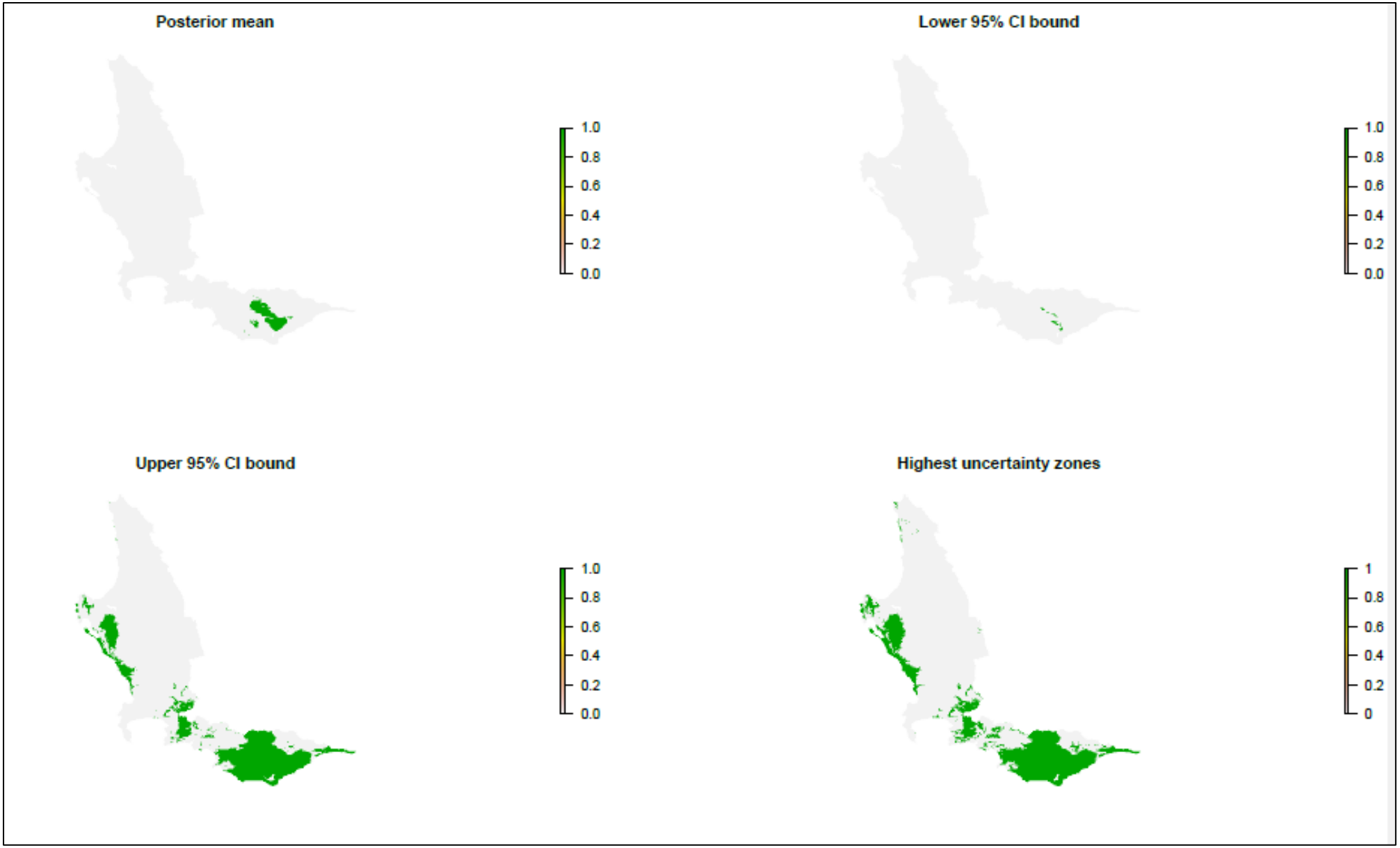


Figure S5.4.138. The modelled distribution of *Pseudobarbus burchelli* Heuningnes in South Africa showing predicted distribution as a binary output.

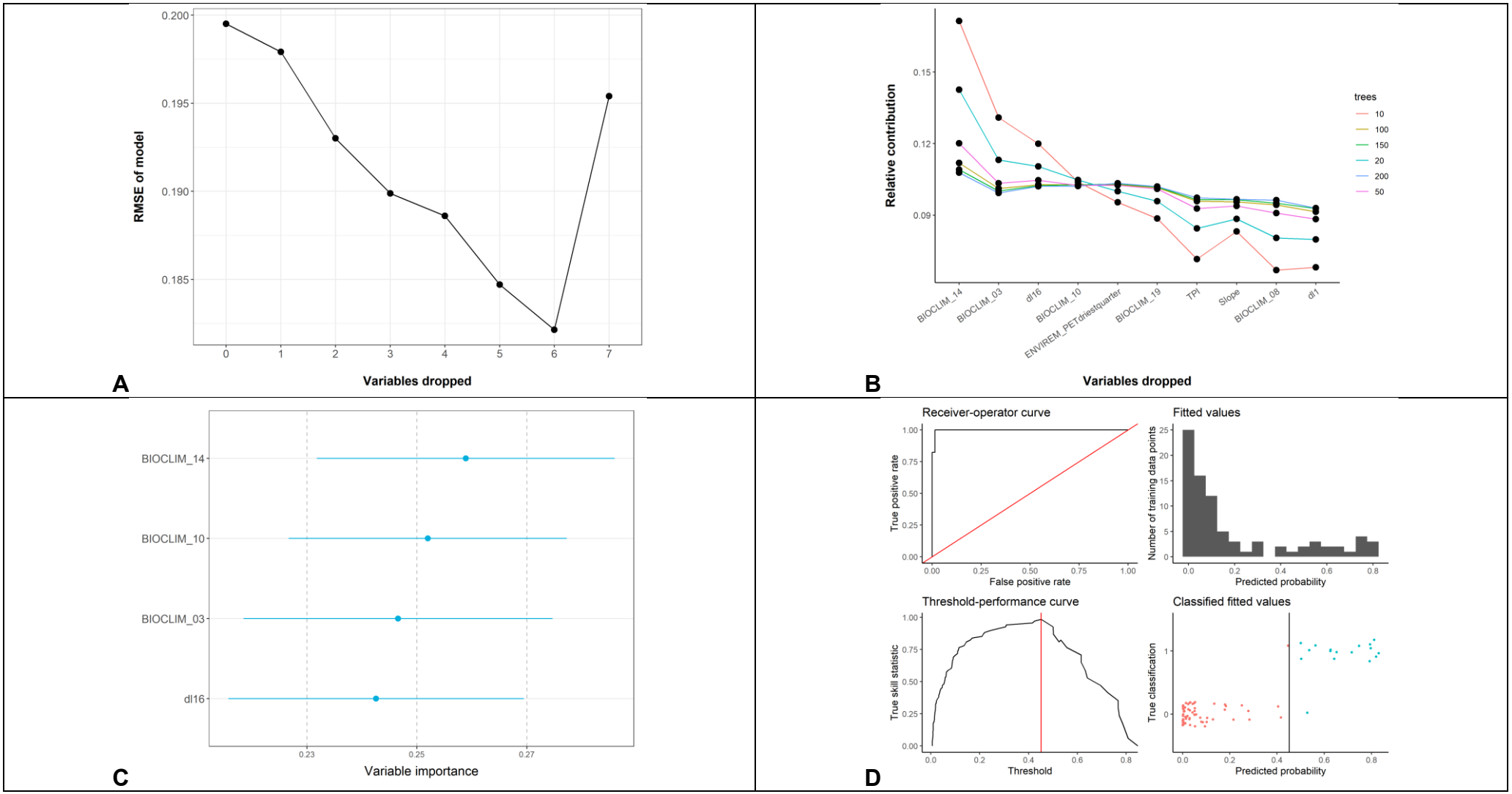


Figure S5.4.139. Model diagnostic outputs for *Pseudobarbus burchelli* Heuningnes, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

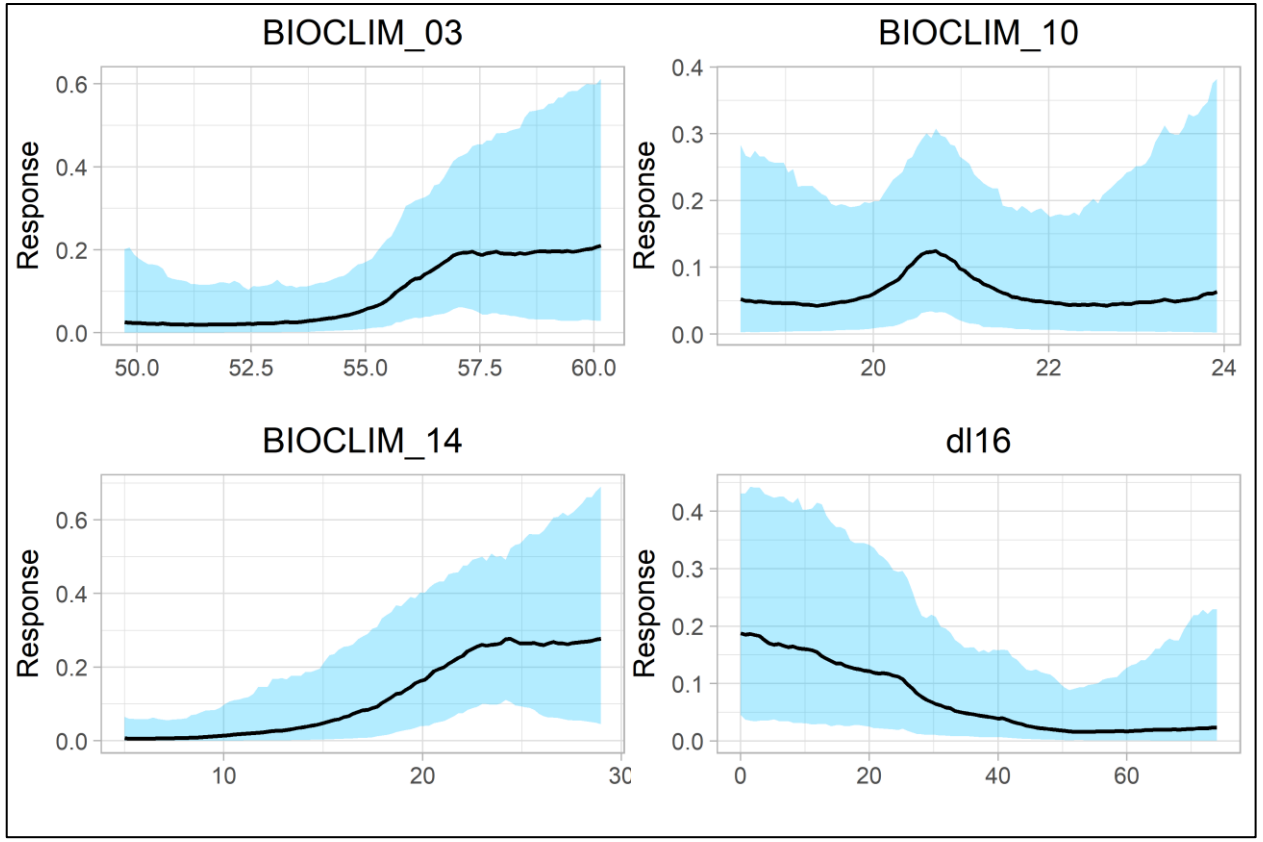


Figure S5.4.140. Partial dependence plots for *Pseudobarbus burchelli* Heuningnes.

Pseudobarbus burchelli Tradou

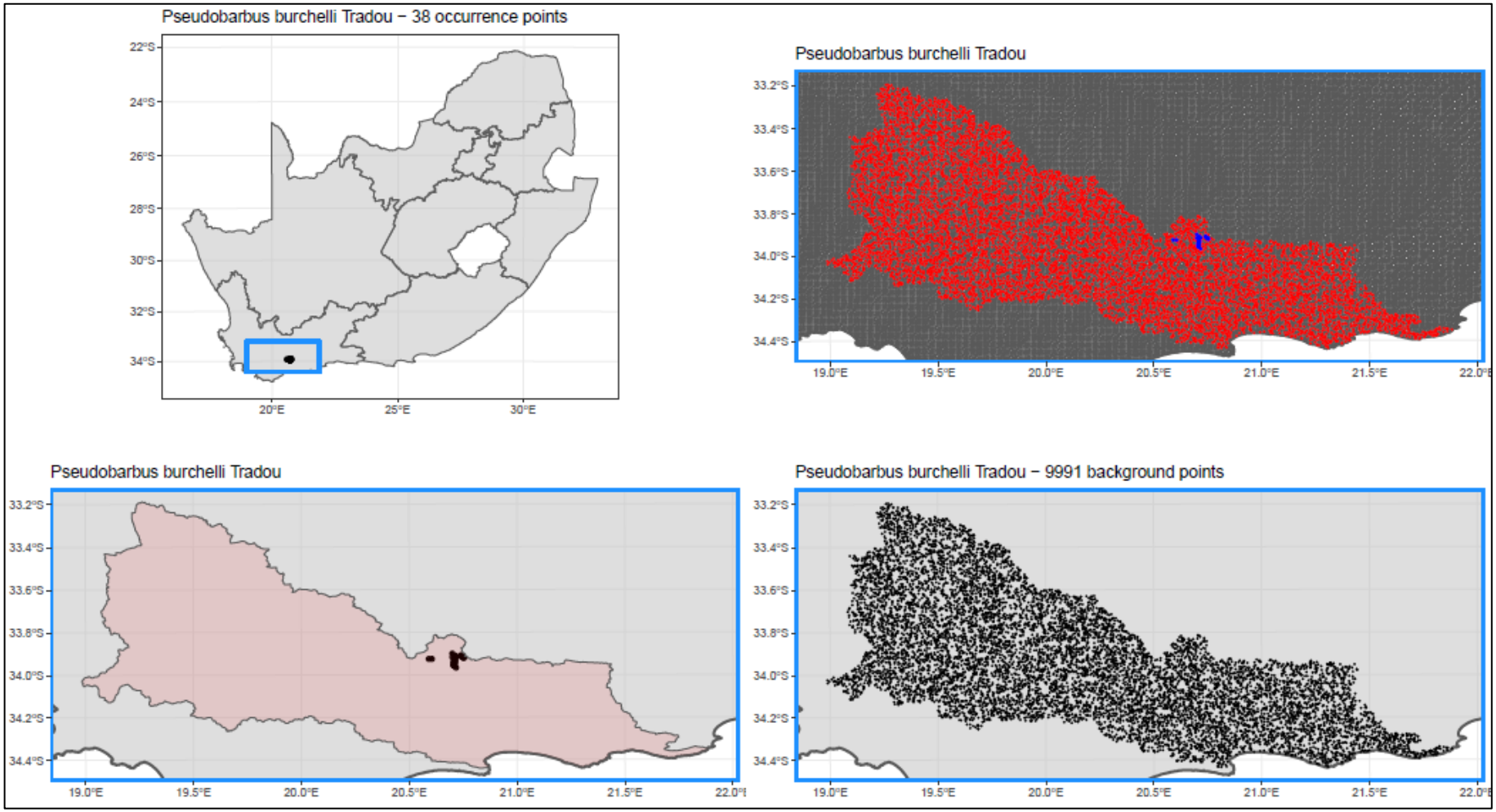


Figure S5.4.141. Occurrence records and background points for *Pseudobarbus burchelli Tradou*.

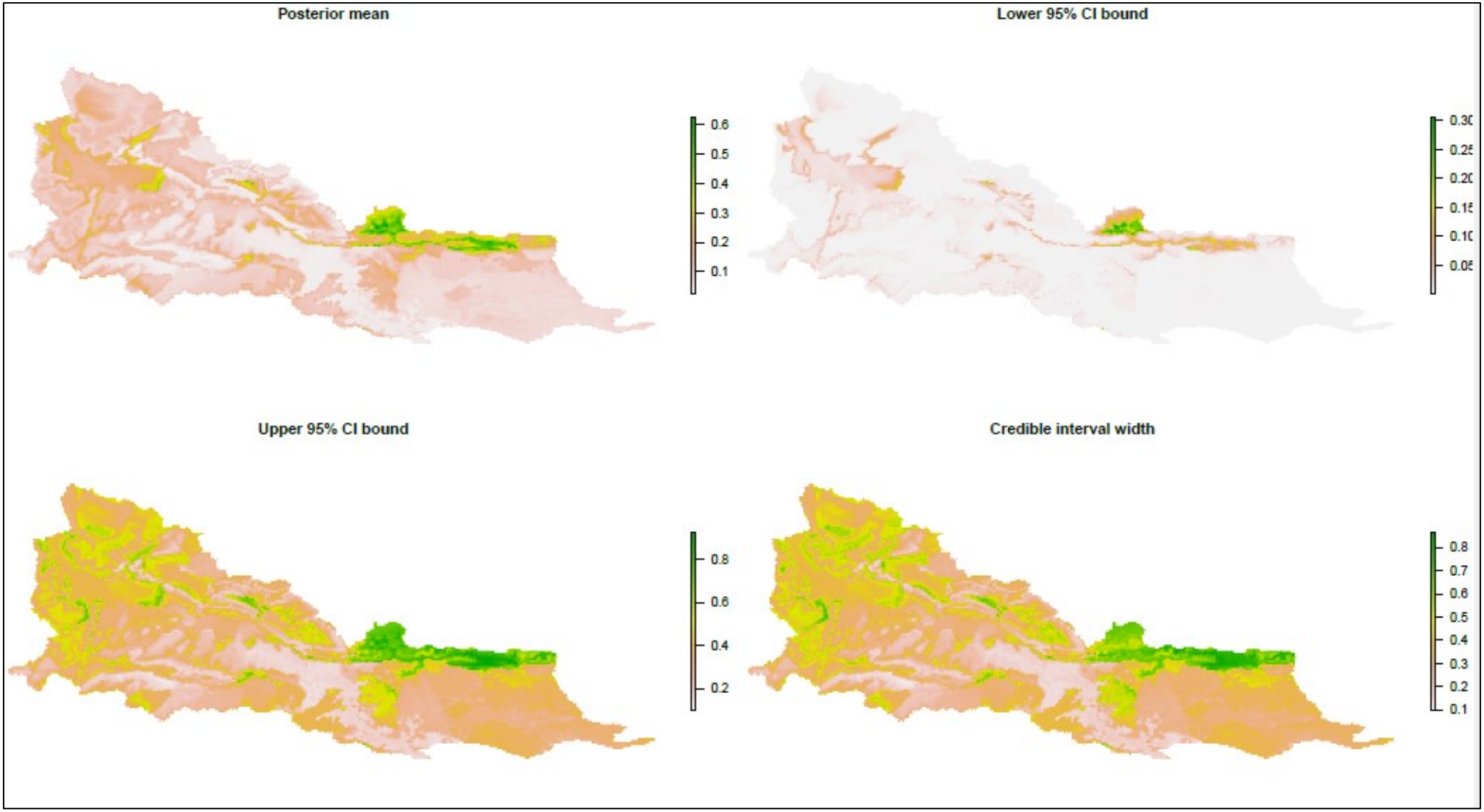


Figure S5.4.142. The modelled distribution of *Pseudobarbus burchelli Tradou* in South Africa showing habitat suitability.

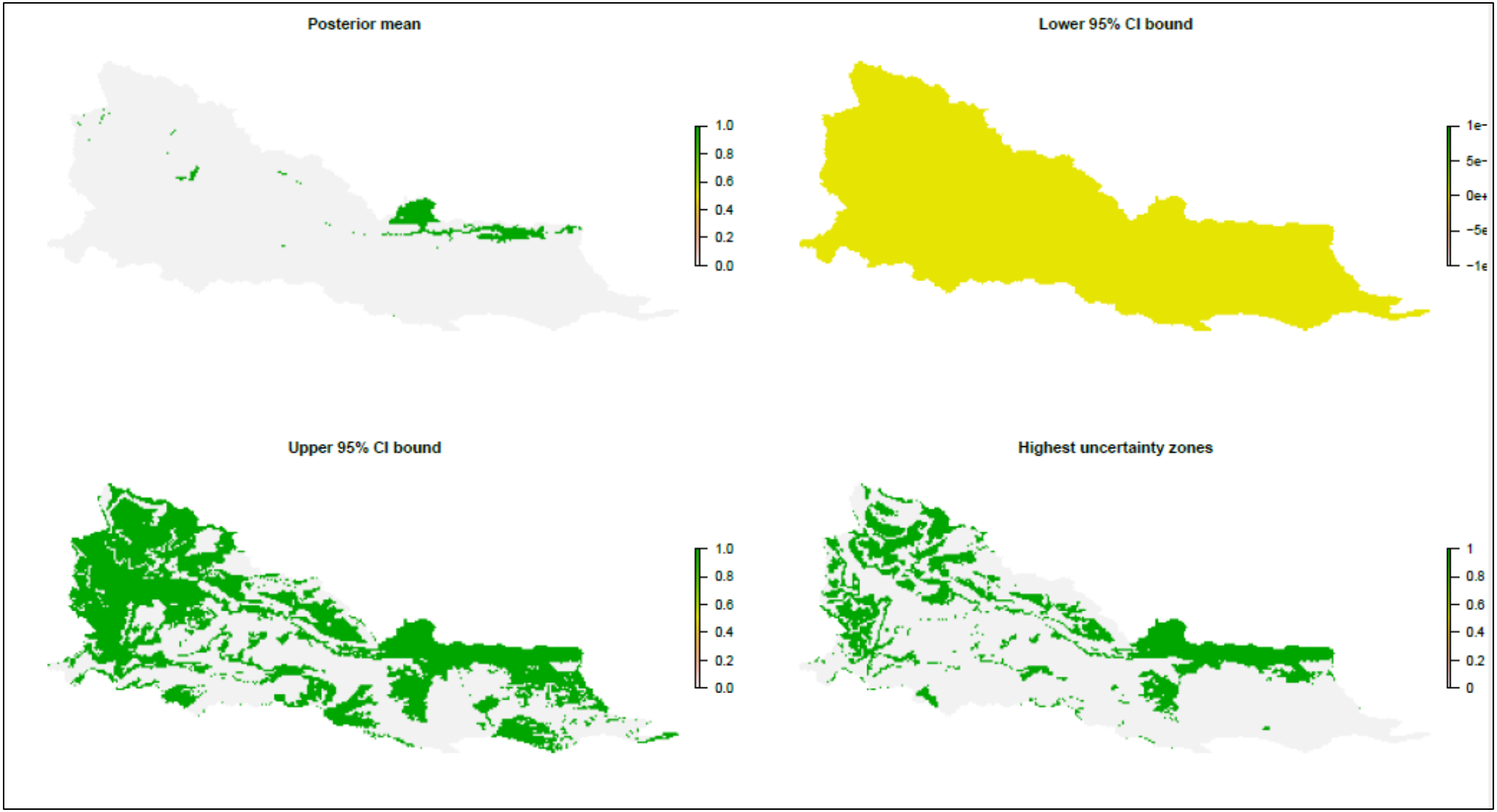


Figure S5.4.143. The modelled distribution of *Pseudobarbus burchelli Tradou* in South Africa showing predicted distribution as a binary output.

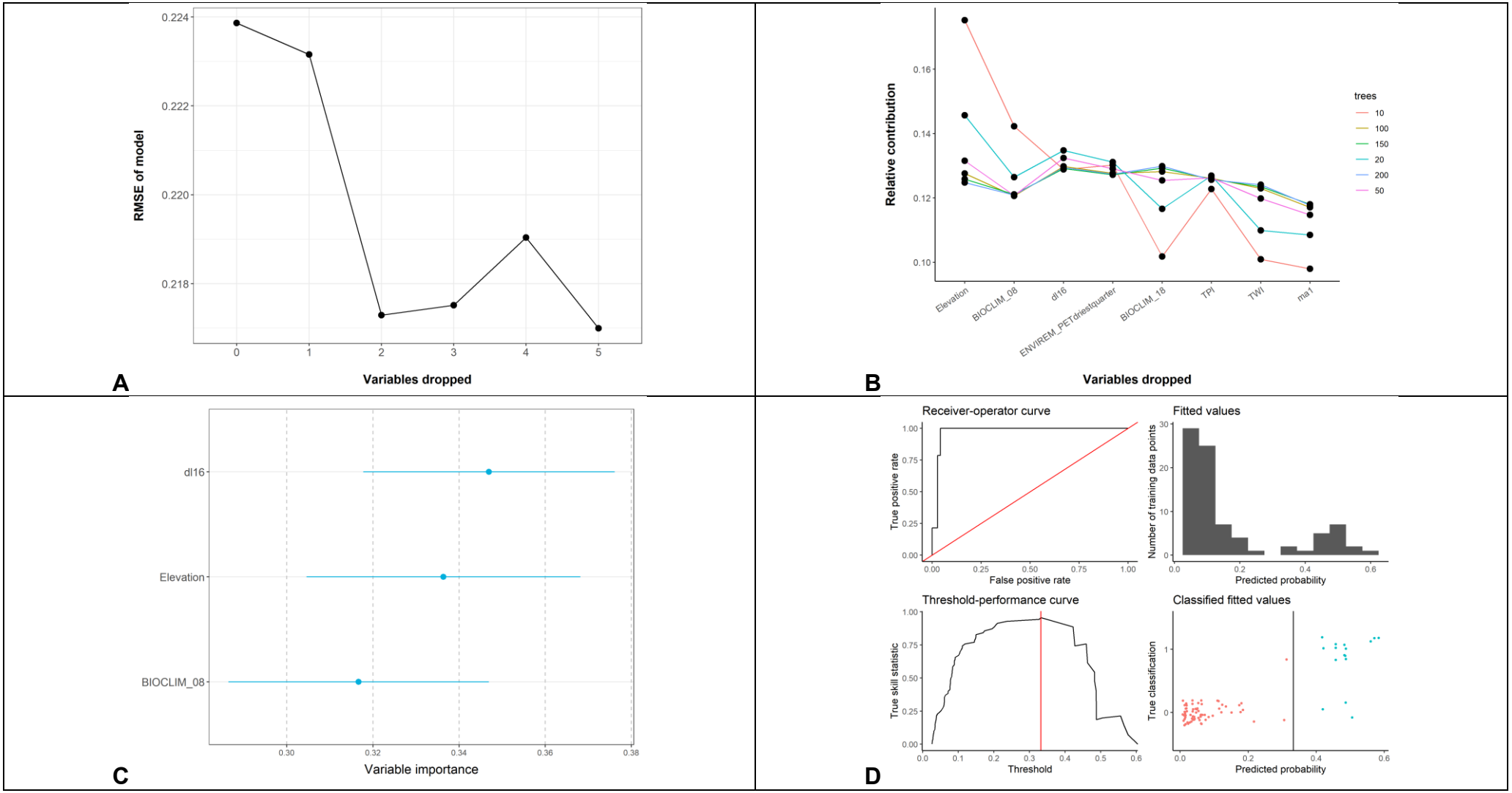


Figure S5.4.144. Model diagnostic outputs for *Pseudobarbus burchelli Tradou*, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

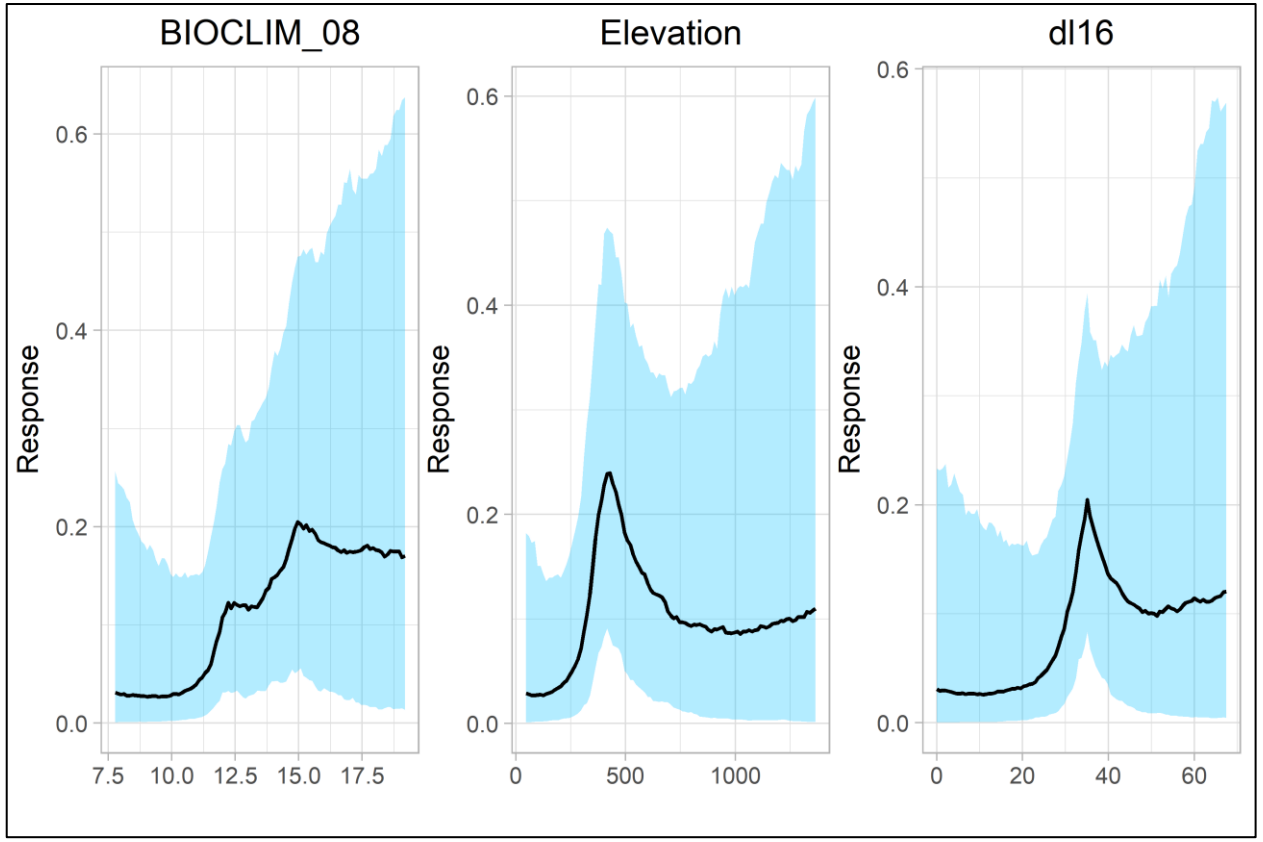


Figure S5.4.145. Partial dependence plots for *Pseudobarbus burchelli Tradou*.

Pseudobarbus phlegethon Doring

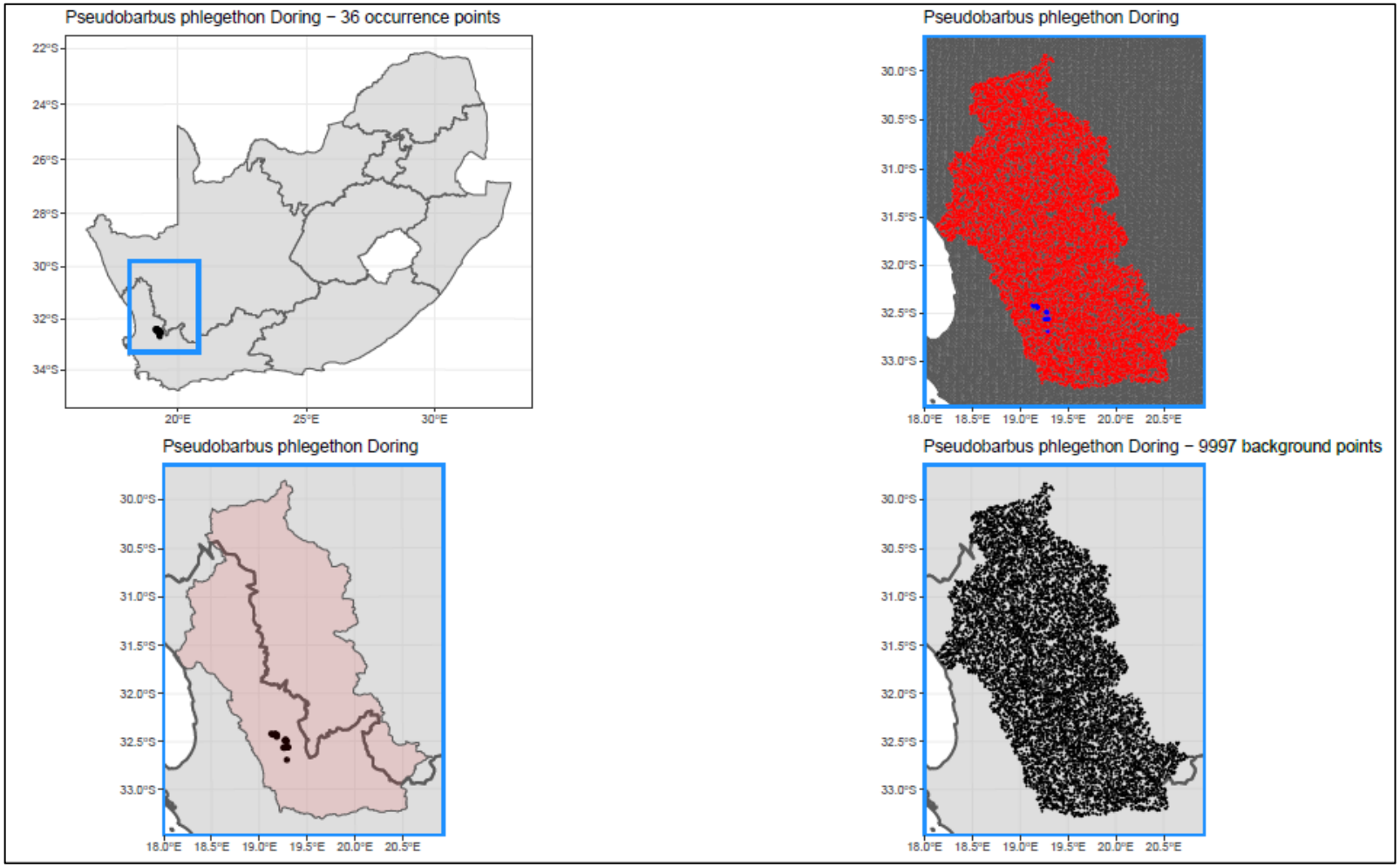


Figure S5.4.146. Occurrence records and background points for *Pseudobarbus phlegethon* Doring.

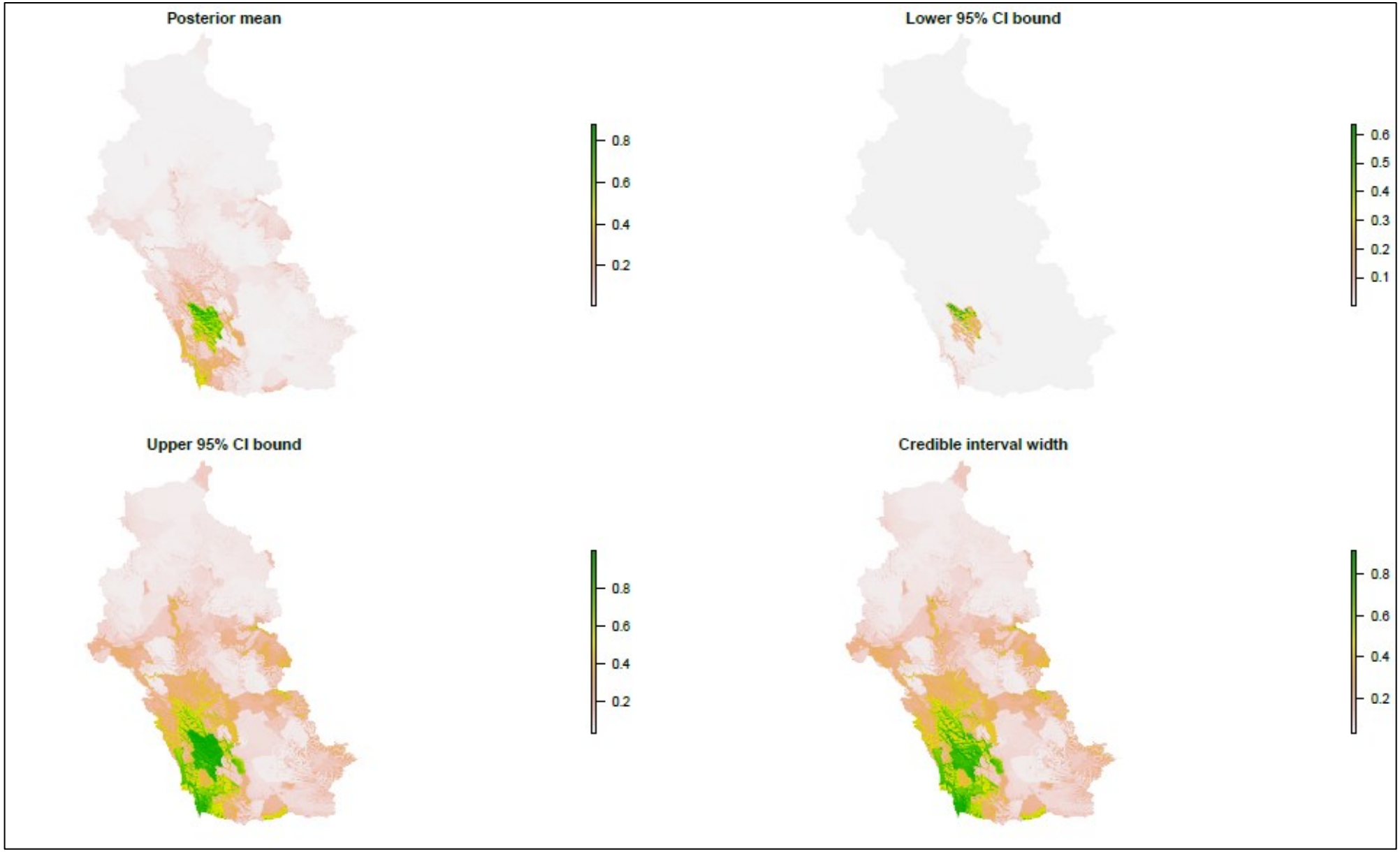


Figure S5.4.147. The modelled distribution of *Pseudobarbus phlegethon* Doring in South Africa showing habitat suitability.

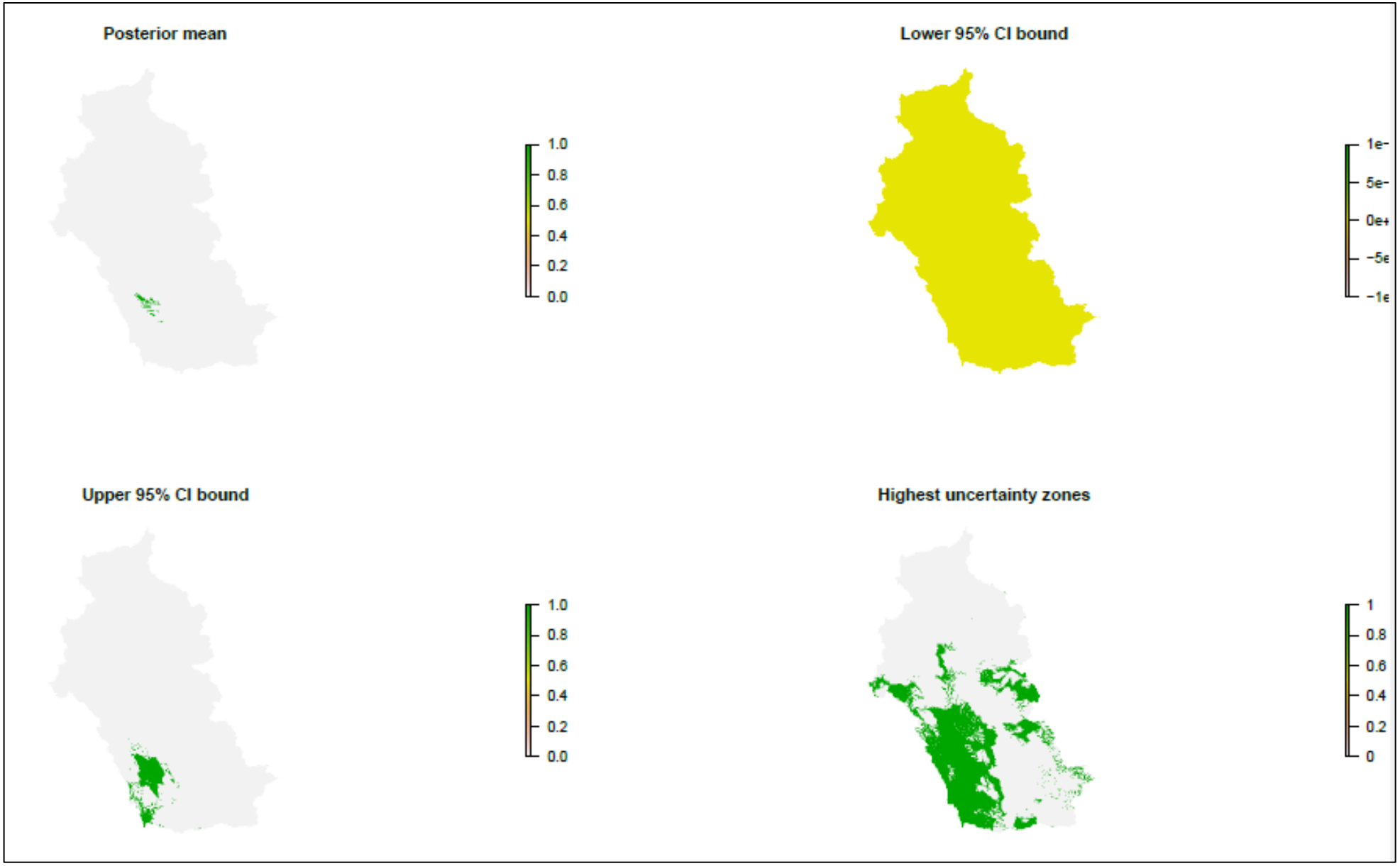


Figure S5.4.148. The modelled distribution of Pseudobarbus phlegethon Doring in South Africa showing predicted distribution as a binary output.

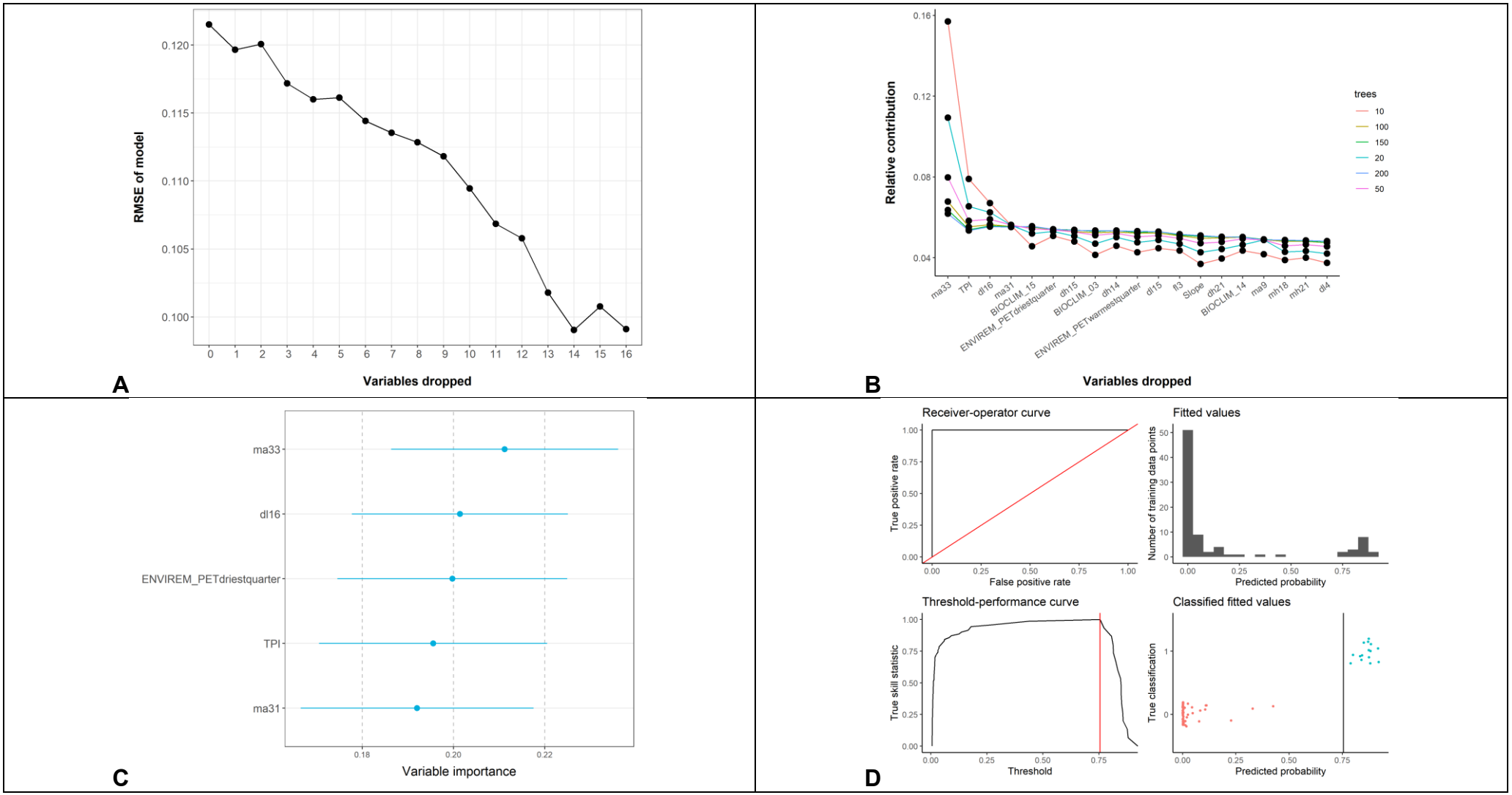


Figure S5.4.149. Model diagnostic outputs for *Pseudobarbus phlegethon* Doring, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

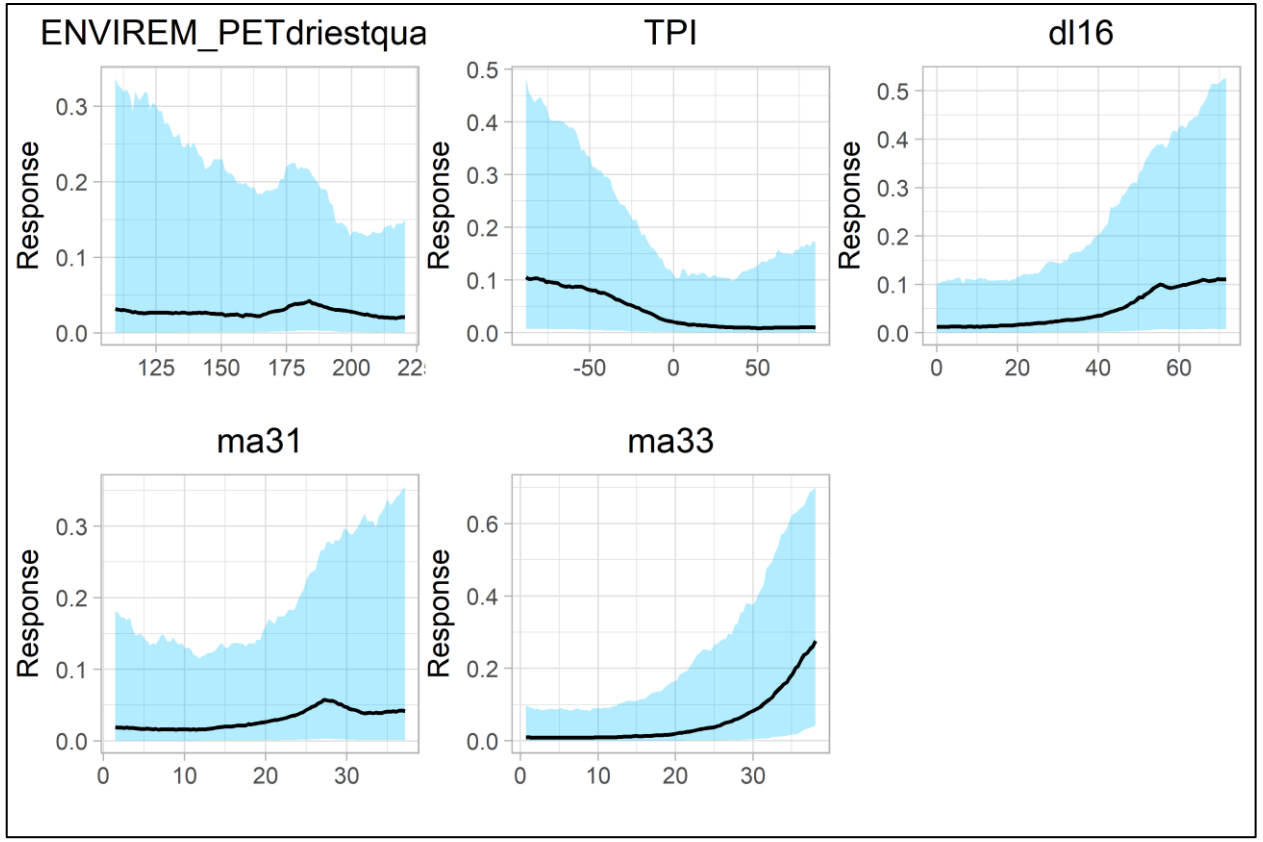


Figure S5.4.150. Partial dependence plots for *Pseudobarbus phlegethon* Doring.

Pseudobarbus phlegethon Olifants

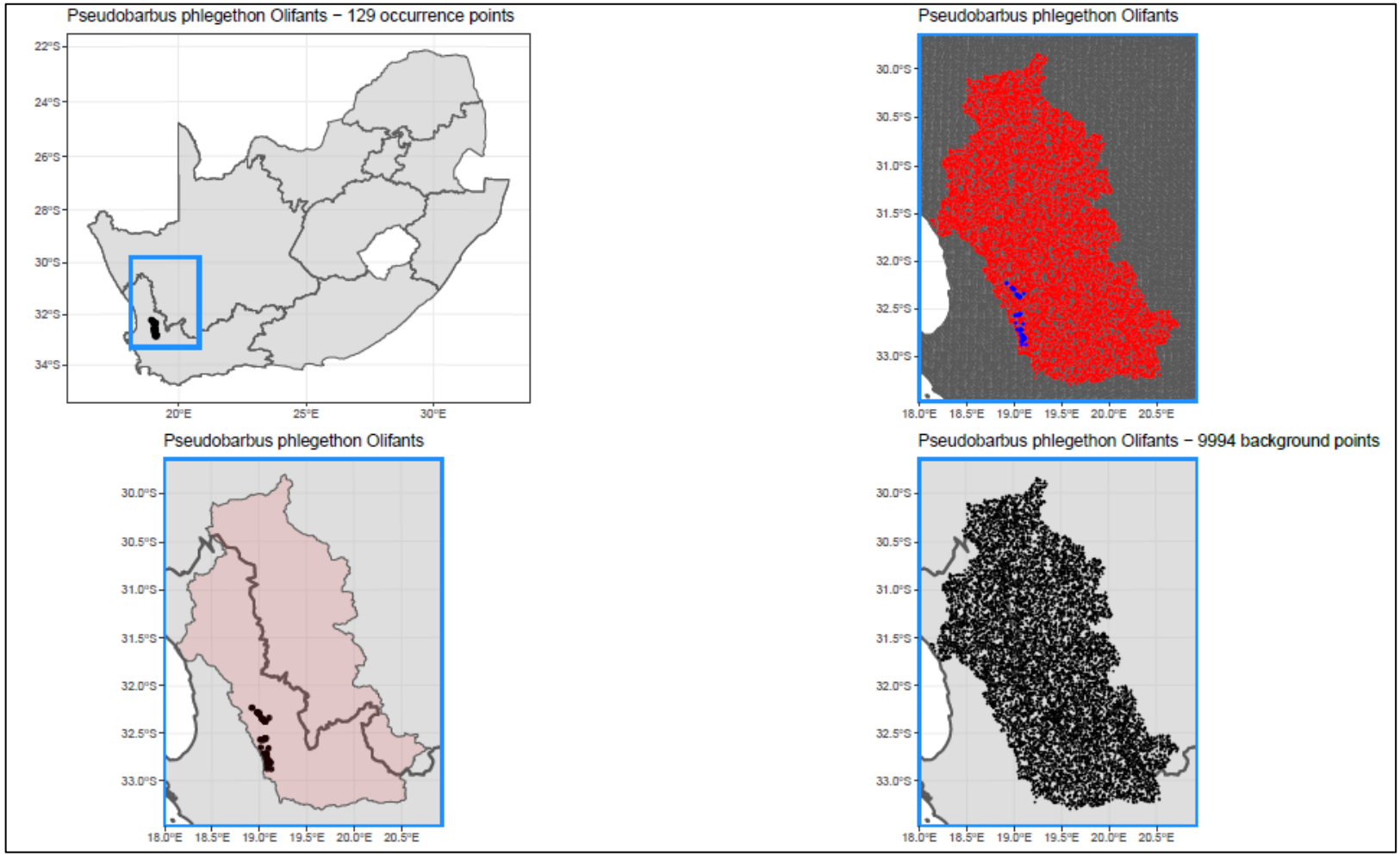


Figure S5.4.151. Occurrence records and background points for *Pseudobarbus phlegethon* Olifants.

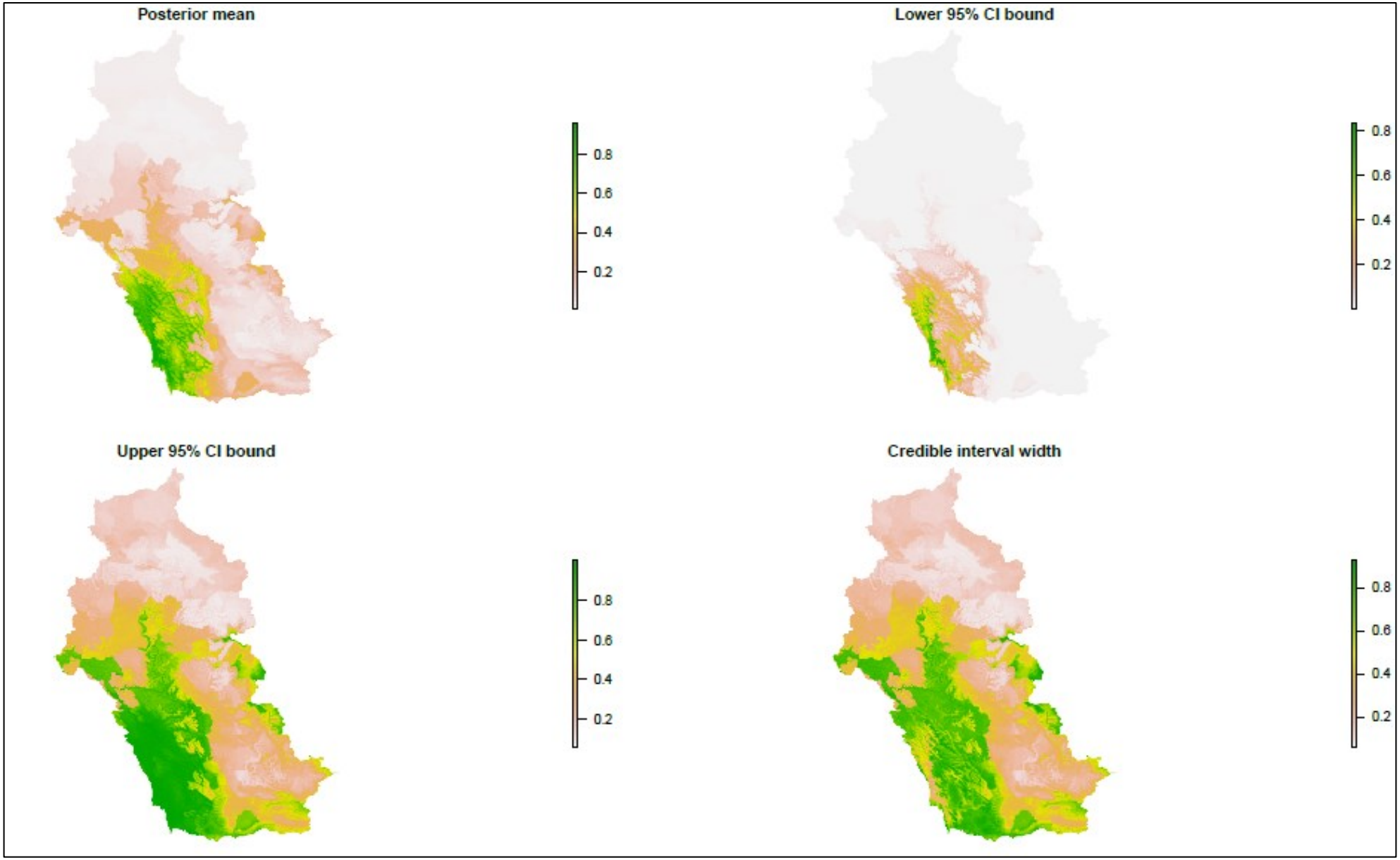


Figure S5.4.152. The modelled distribution of *Pseudobarbus phlegethon* Olifants in South Africa showing habitat suitability.

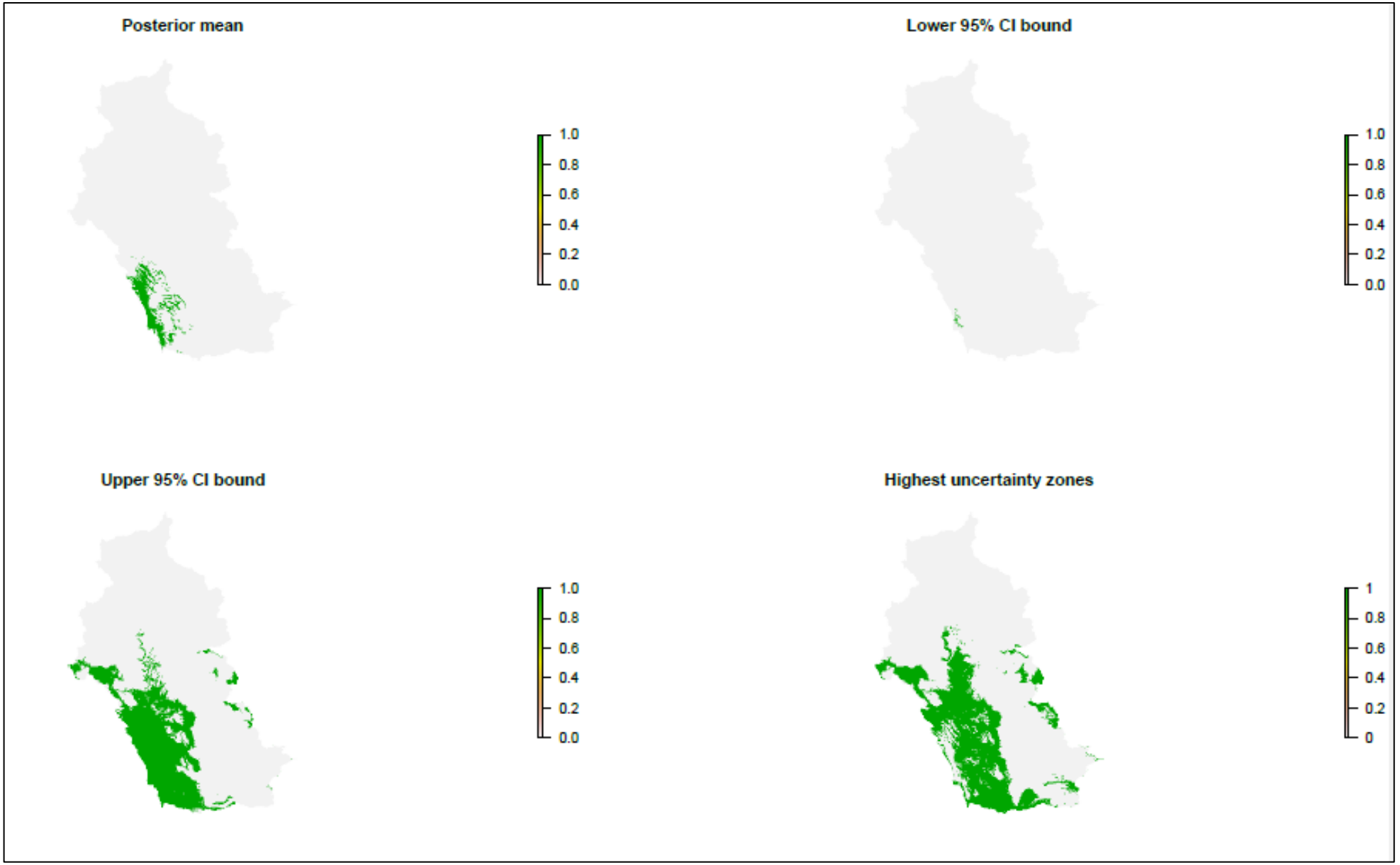


Figure S5.4.153. The modelled distribution of *Pseudobarbus phlegethon* Olifants in South Africa showing predicted distribution as a binary output.

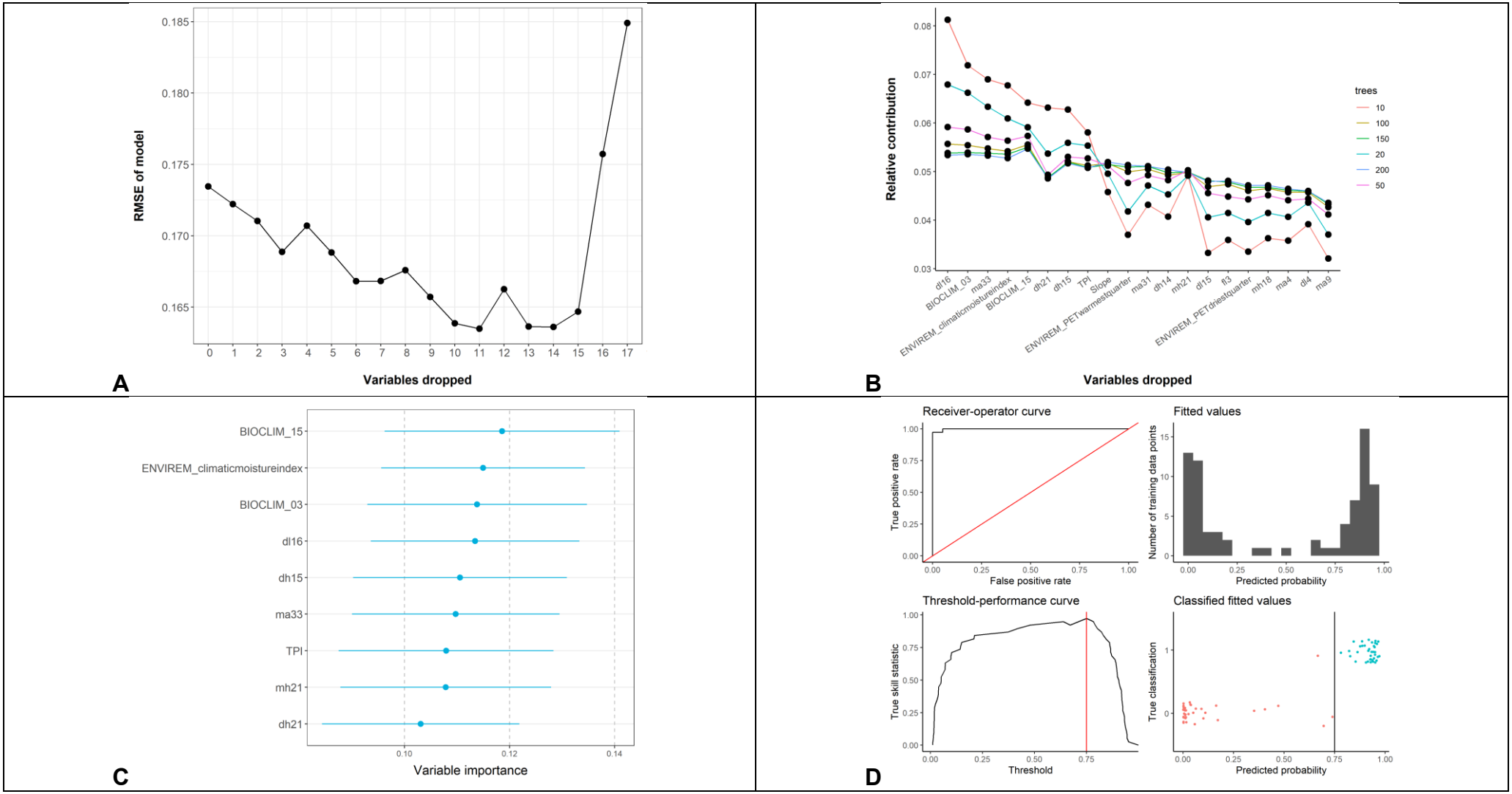


Figure S5.4.154. Model diagnostic outputs for *Pseudobarbus phlegethon* Olifants, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

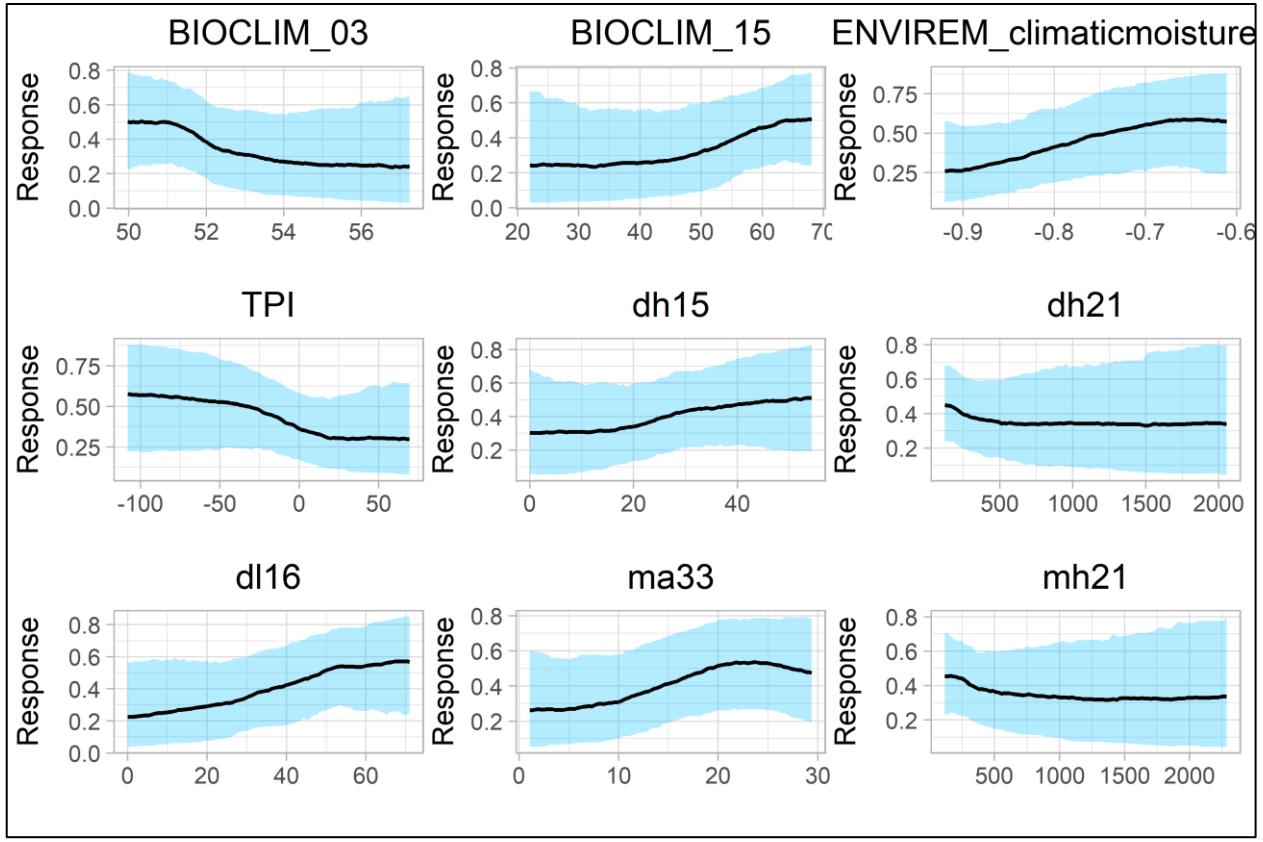


Figure S5.4.155. Partial dependence plots for *Pseudobarbus phlegethon* Olifants.

Pseudobarbus tenuis Keurbooms

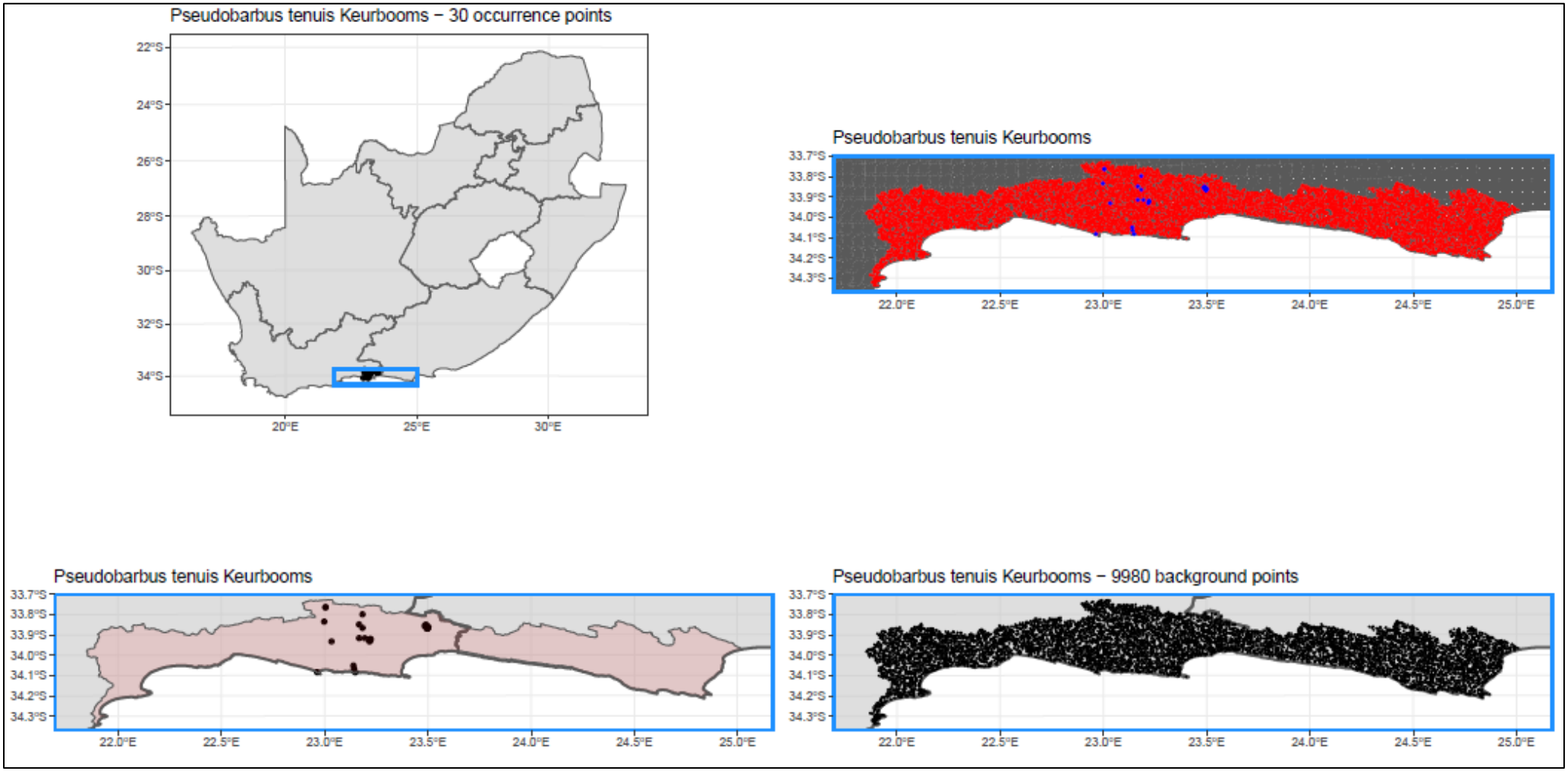


Figure S5.4.156. Occurrence records and background points for *Pseudobarbus tenuis* Keurbooms.

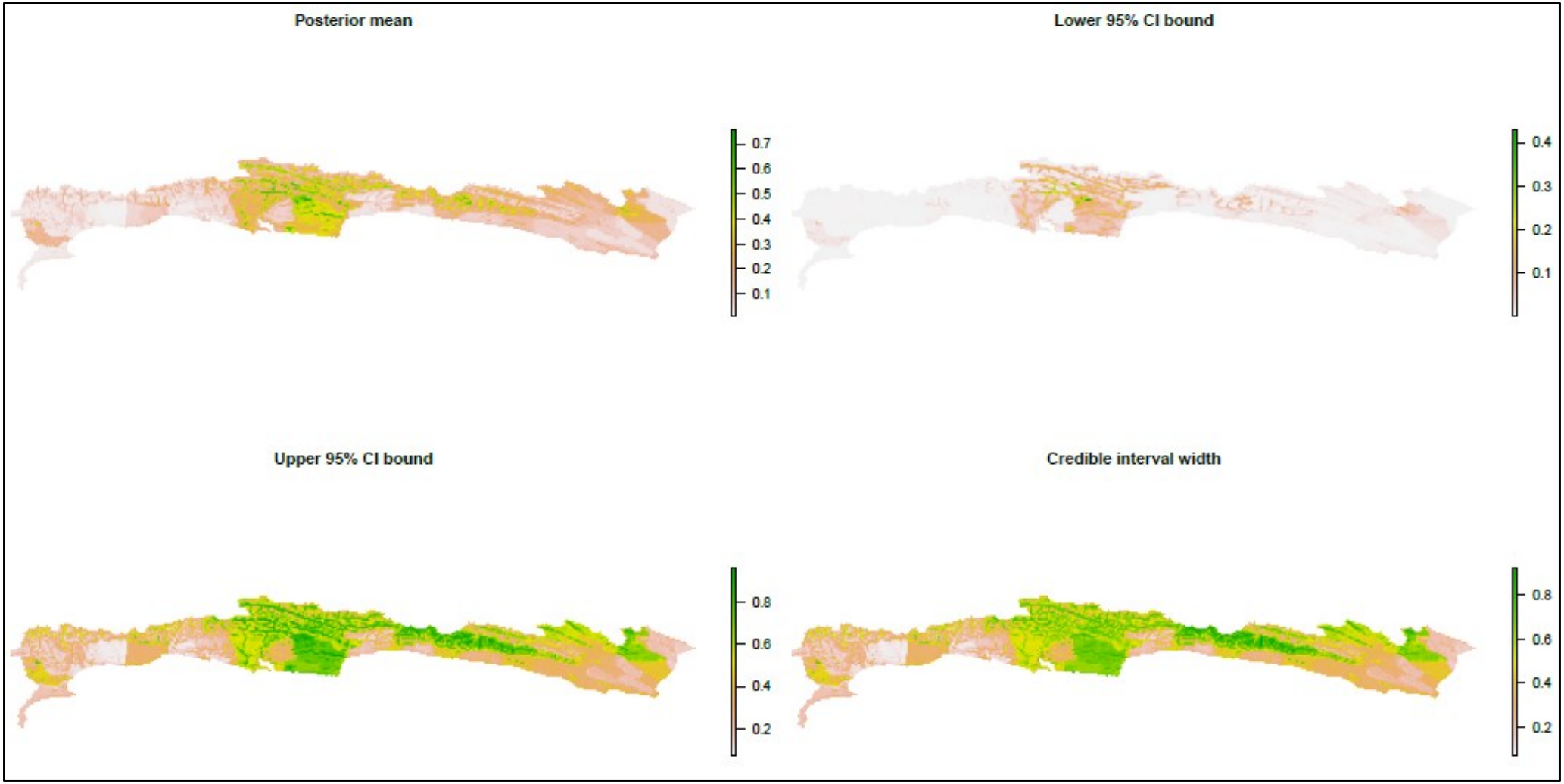


Figure S5.4.157. The modelled distribution of *Pseudobarbus tenuis* Keurbooms in South Africa showing habitat suitability.

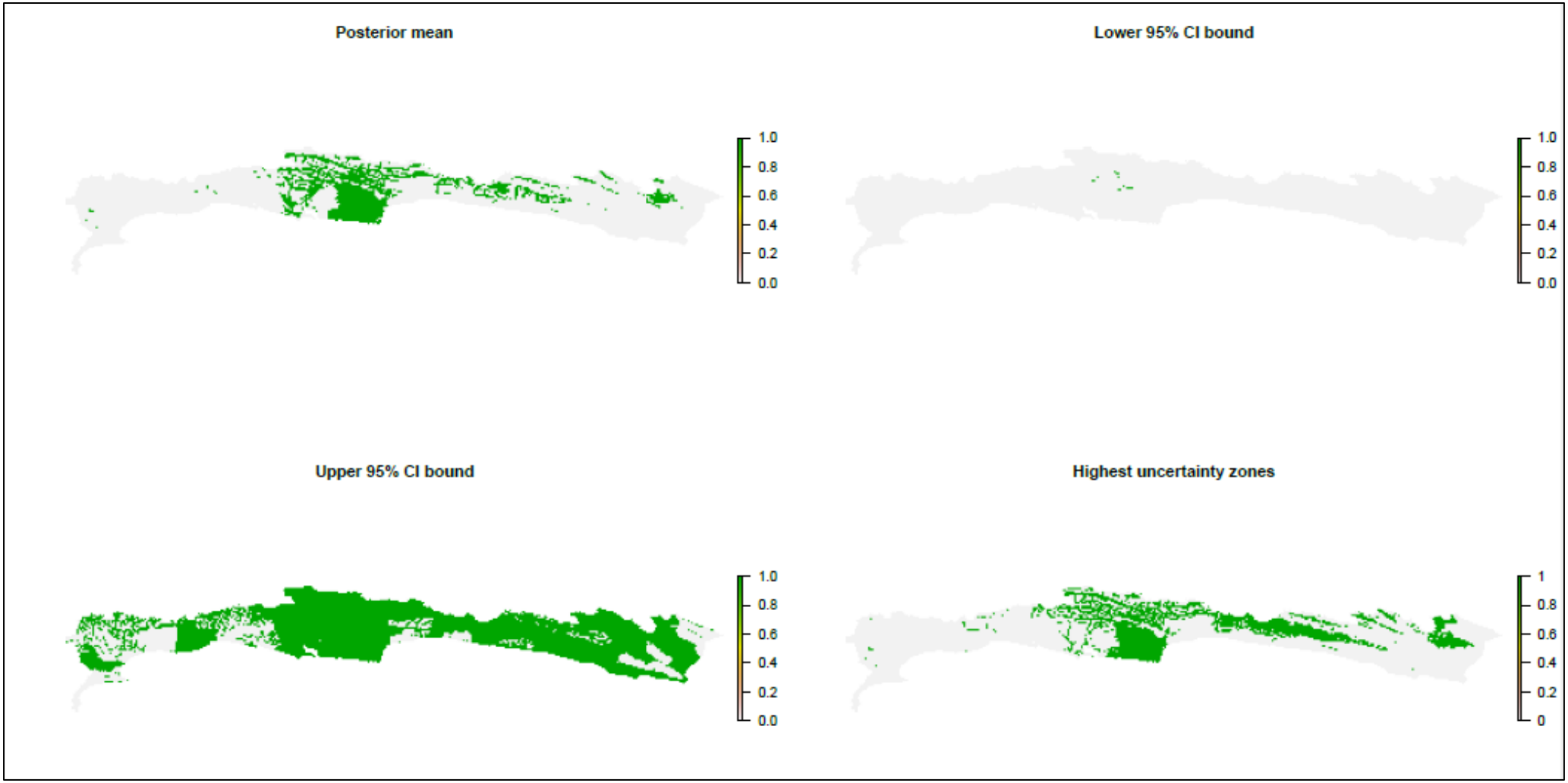


Figure S5.4.158. The modelled distribution of *Pseudobarbus tenuis* Keurbooms in South Africa showing predicted distribution as a binary output.

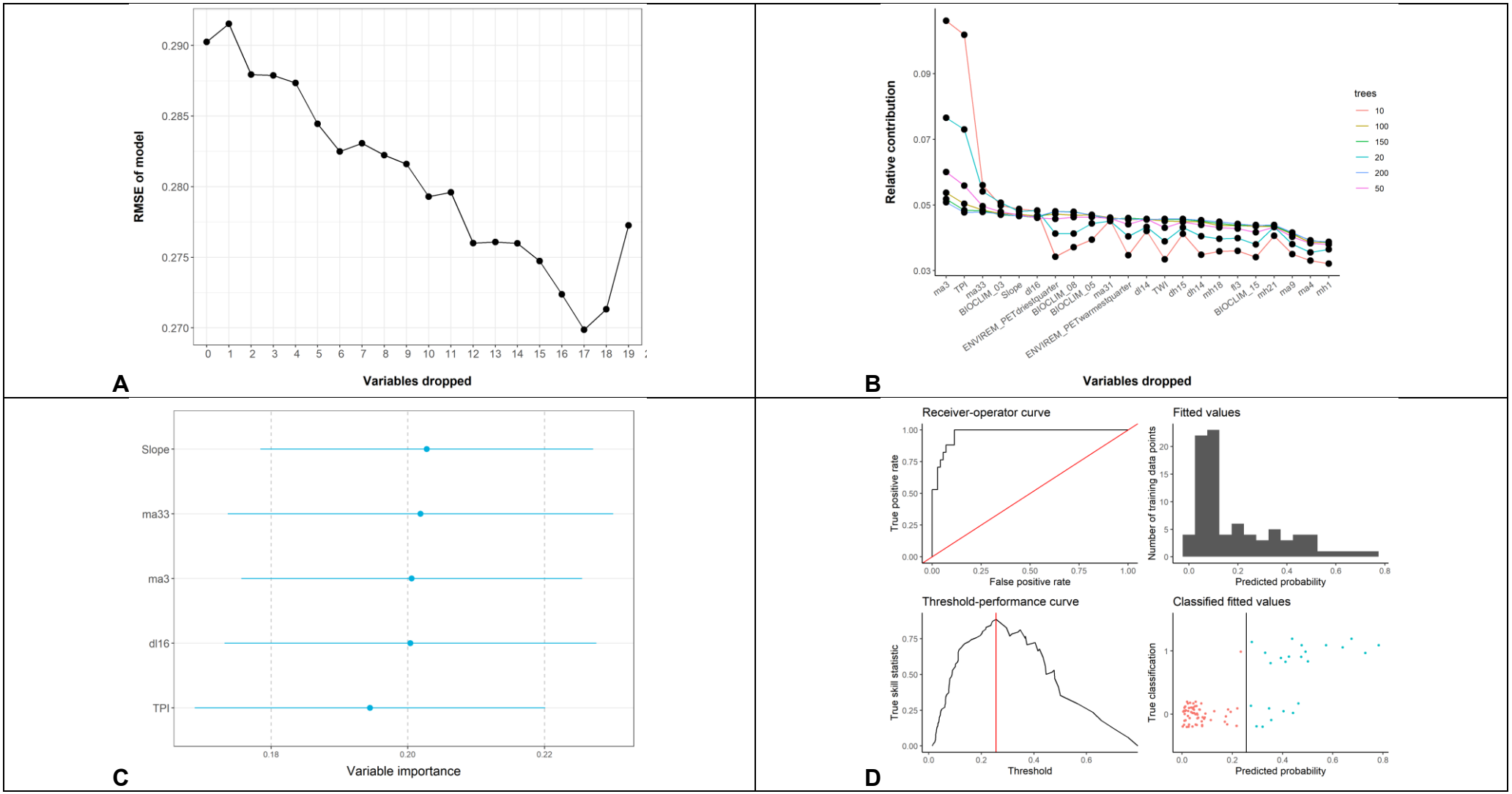


Figure S5.4.159. Model diagnostic outputs for *Pseudobarbus tenuis* Keurbooms, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

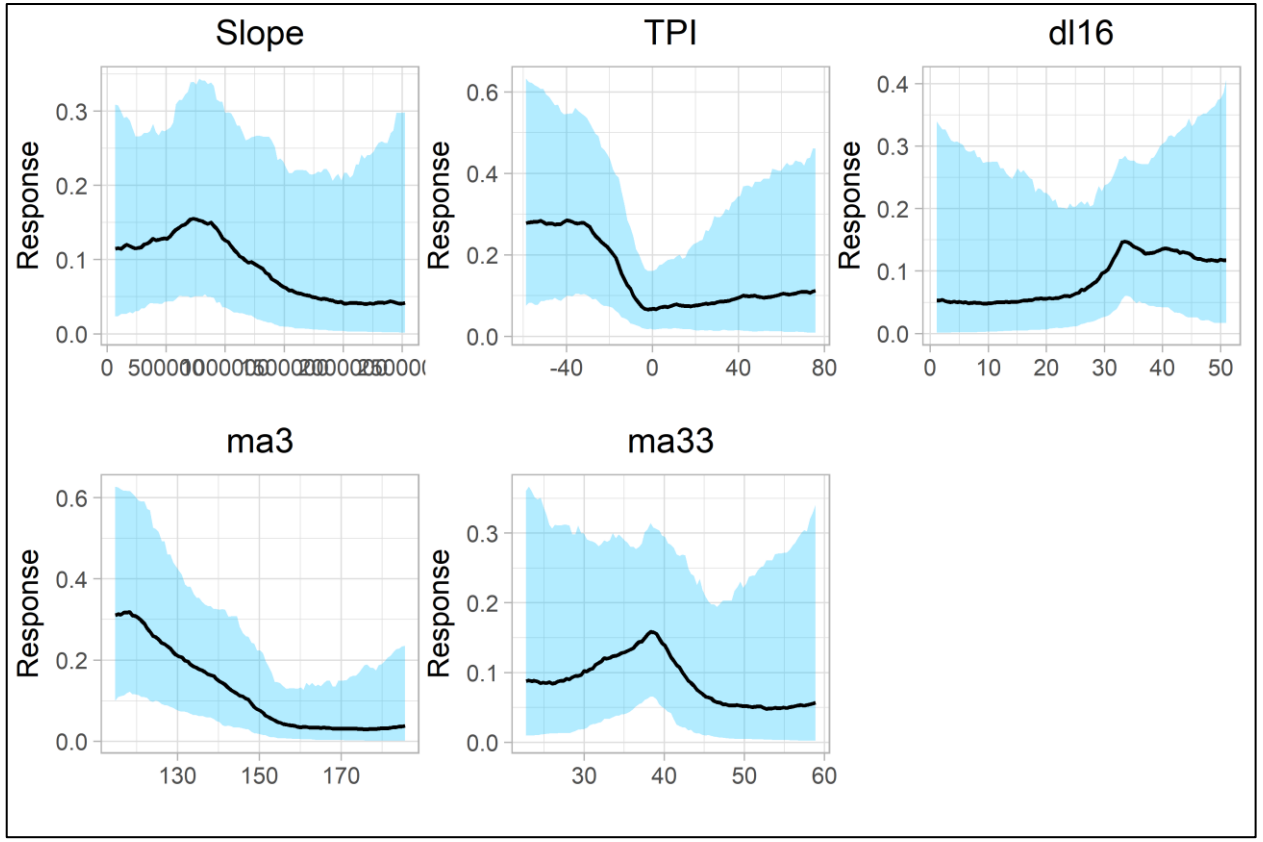


Figure S5.4.160. Partial dependence plots for *Pseudobarbus tenuis* Keurbooms.

Pseudobarbus trevelyani Buffalo

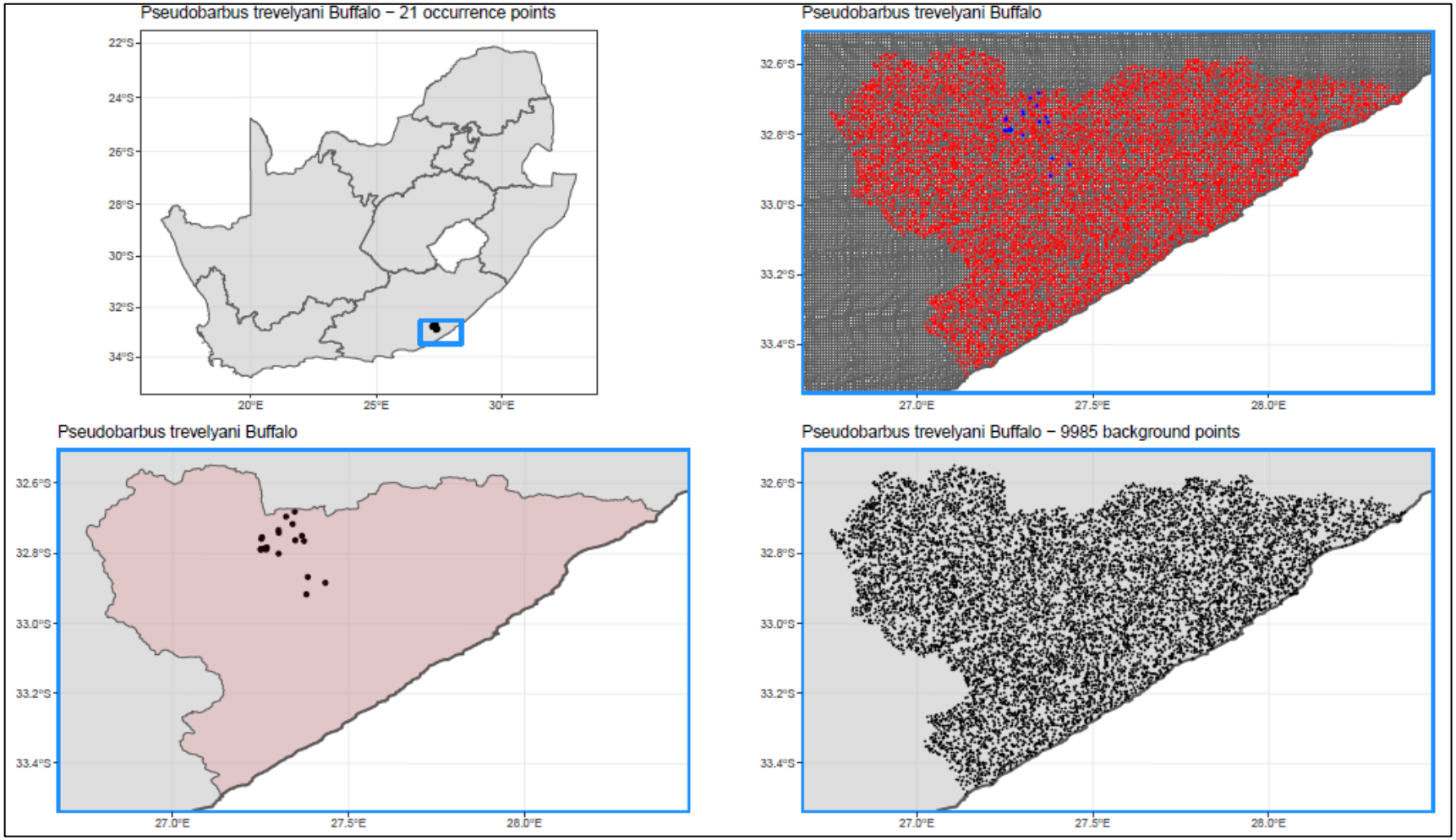


Figure S5.4.161. Occurrence records and background points for *Pseudobarbus trevelyani* Buffalo.

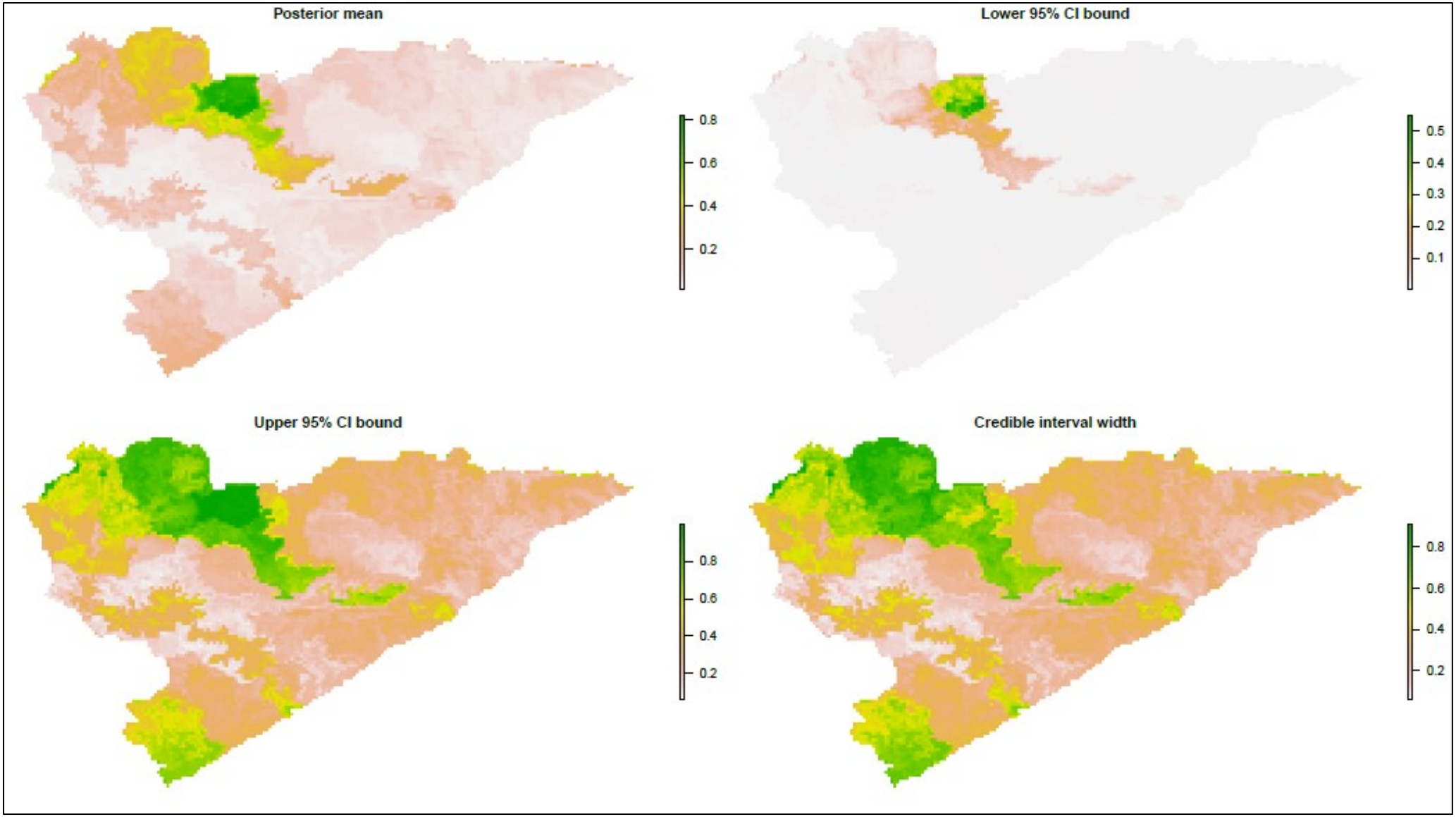


Figure S5.4.162. The modelled distribution of *Pseudobarbus trevelyani* Buffalo in South Africa showing habitat suitability.

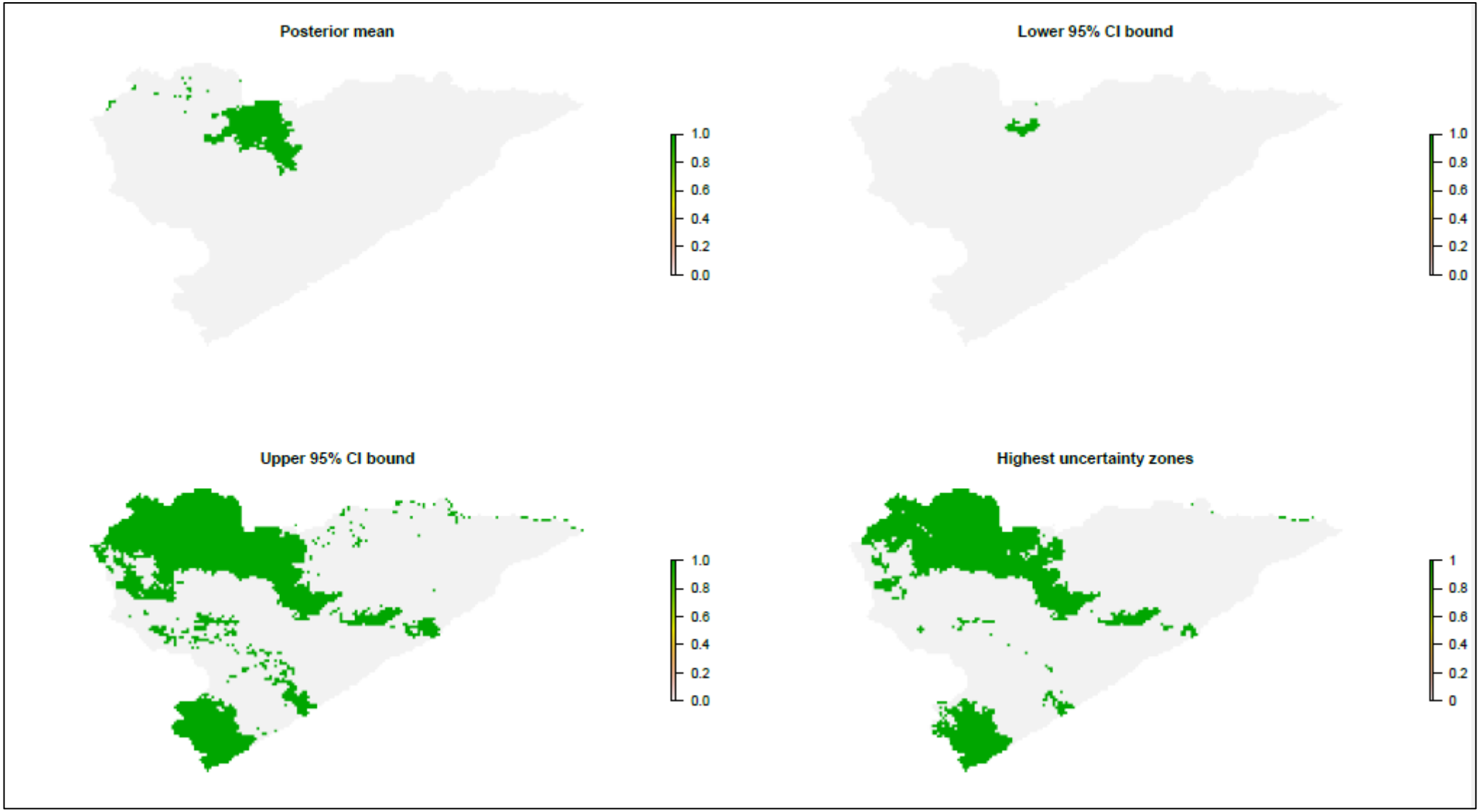


Figure S5.4.163. The modelled distribution of *Pseudobarbus trevelyani* Buffalo in South Africa showing predicted distribution as a binary output.

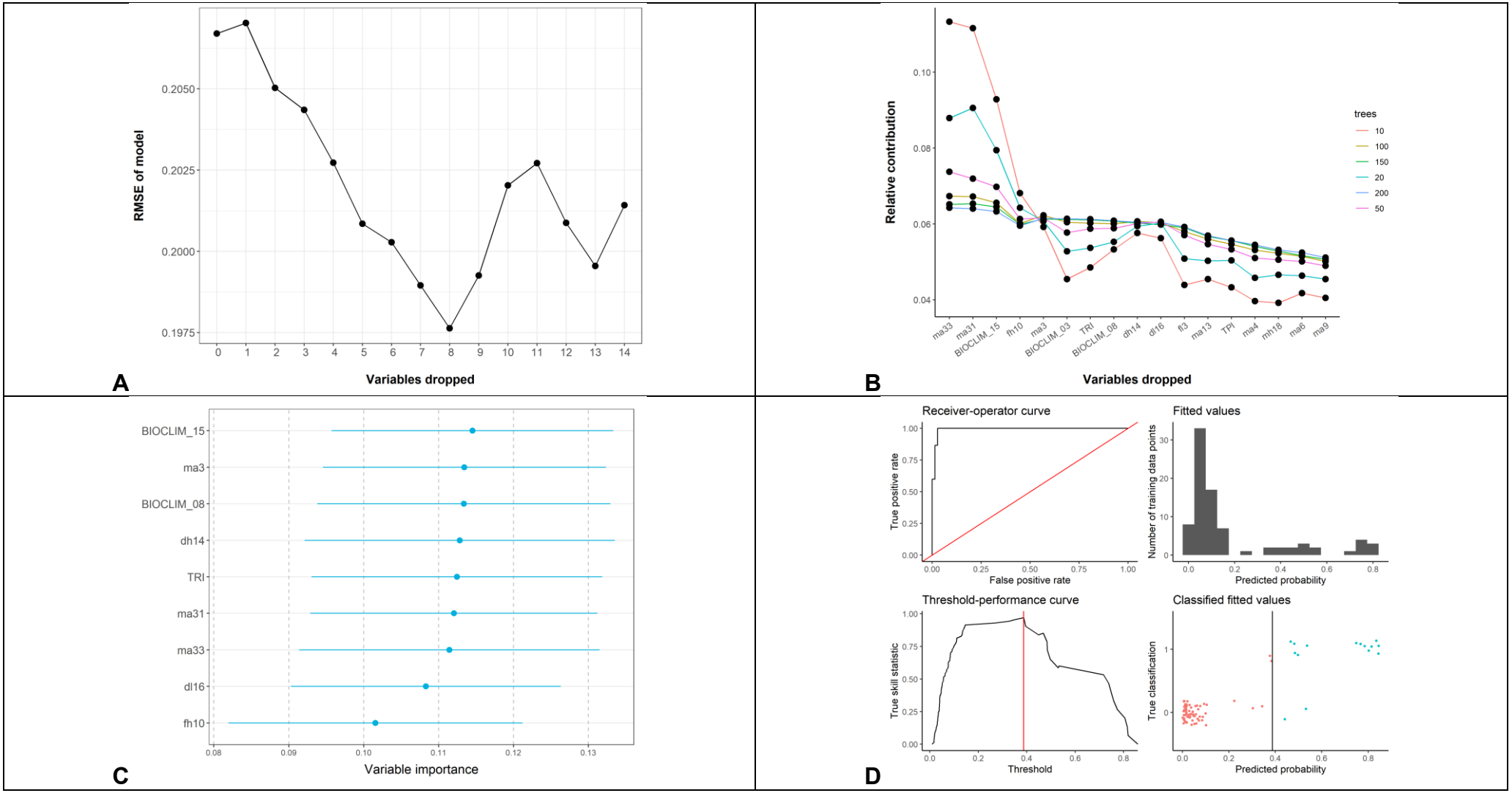


Figure S5.4.164. Model diagnostic outputs for *Pseudobarbus trevelyani* Buffalo, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

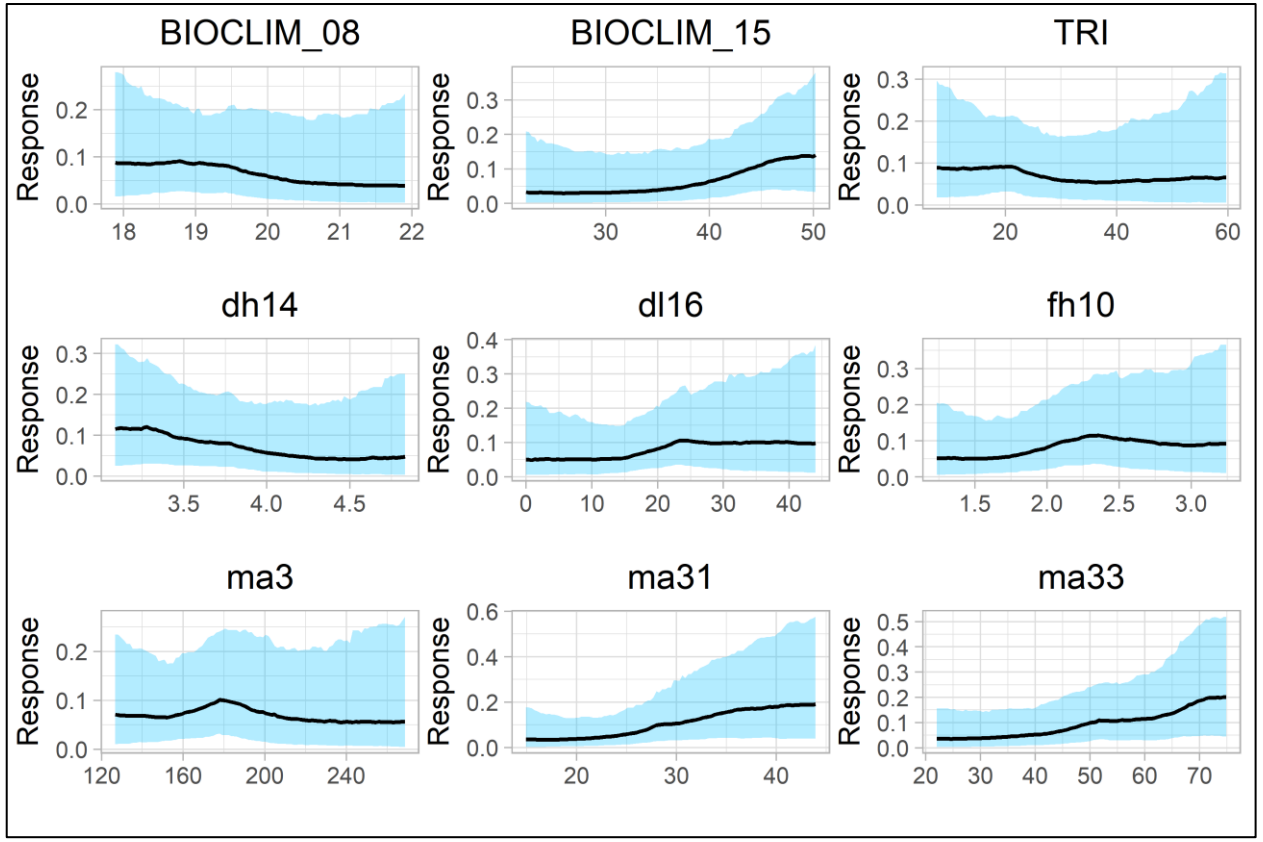


Figure S5.4.165. Partial dependence plots for *Pseudobarbus trevelyani* Buffalo.

Pseudobarbus trevelyani Kieskamma

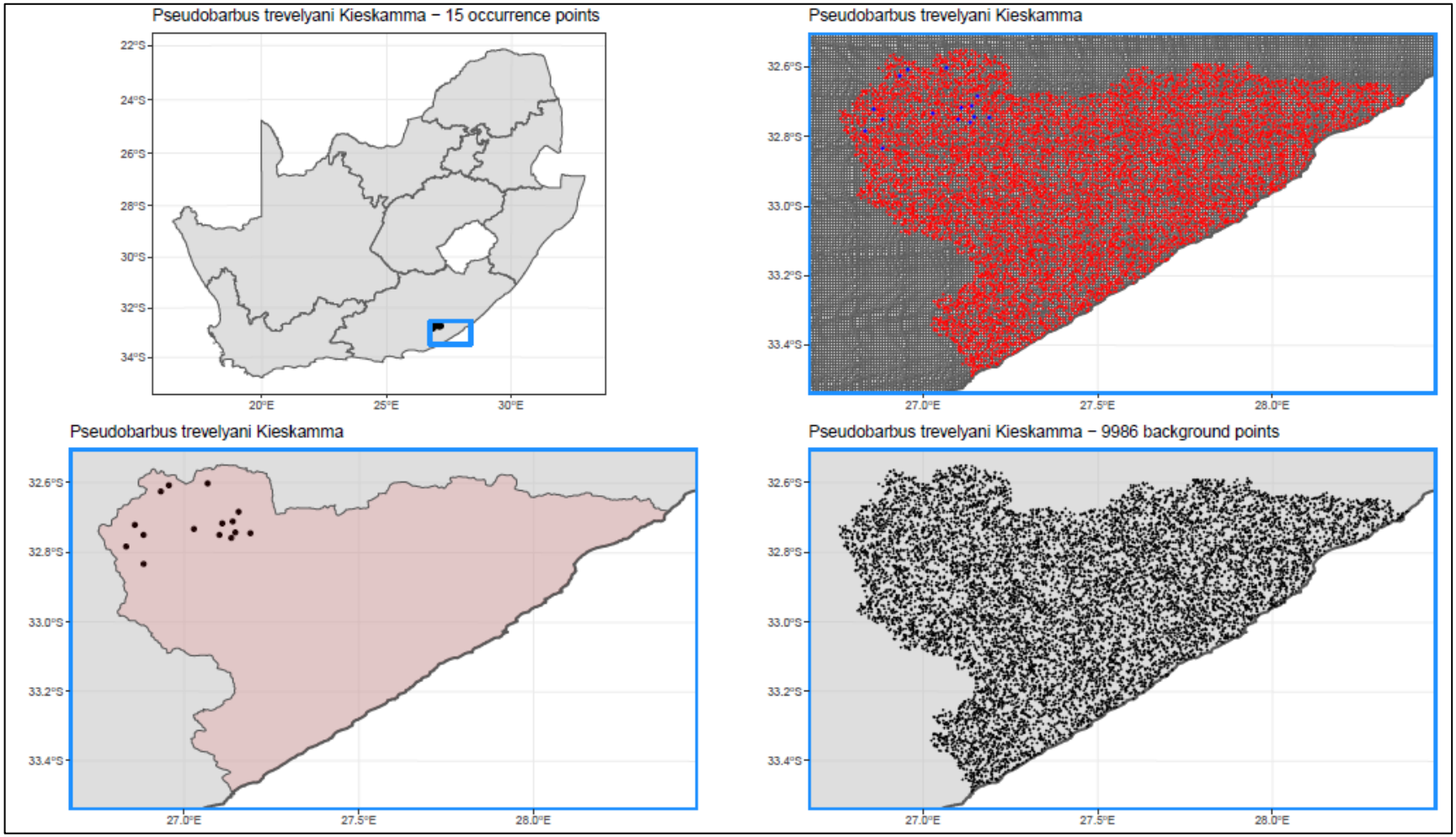


Figure S5.4.166. Occurrence records and background points for *Pseudobarbus trevelyani* Kieskamma.

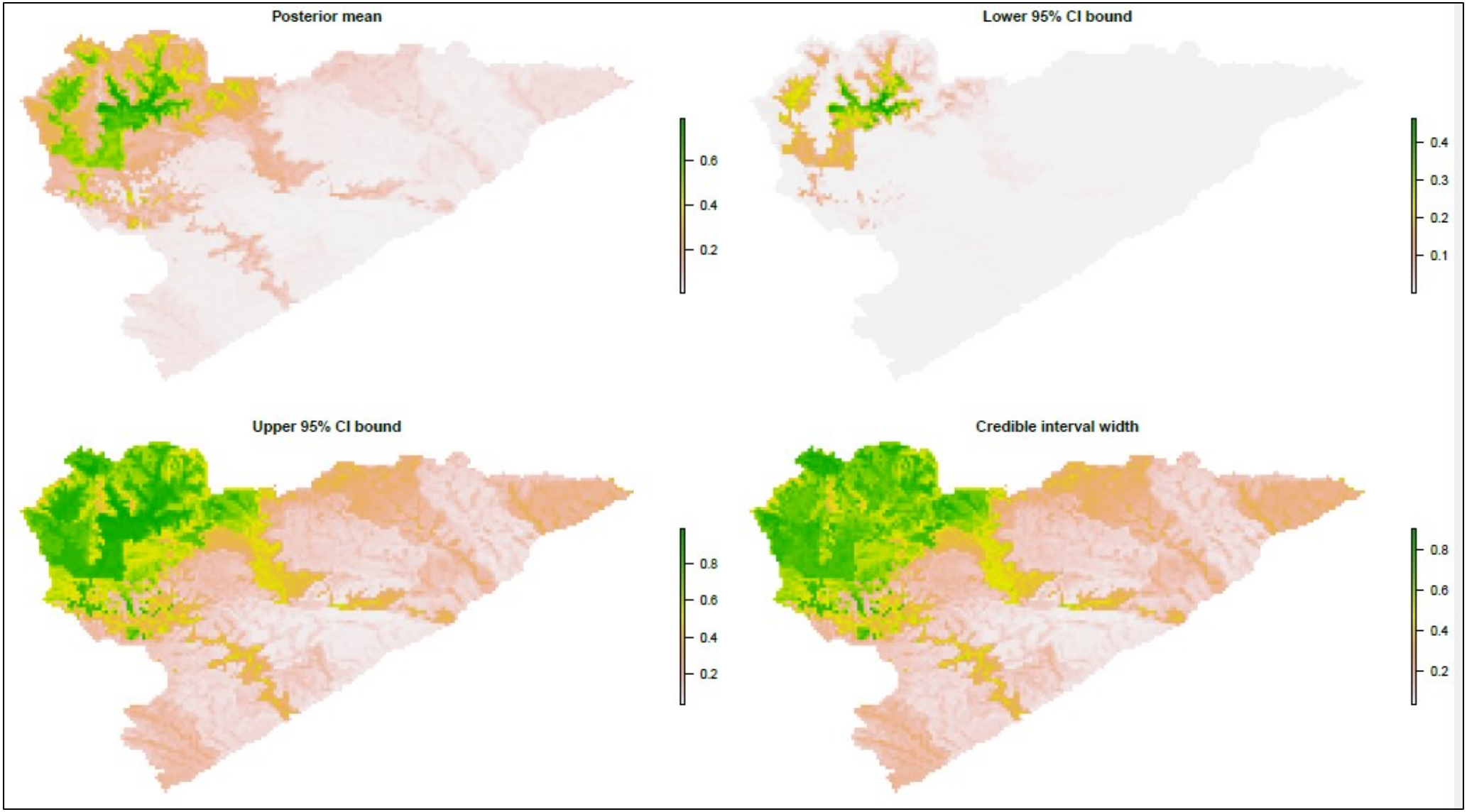


Figure S5.4.167. The modelled distribution of *Pseudobarbus trevelyani* Kieskamma in South Africa showing habitat suitability.

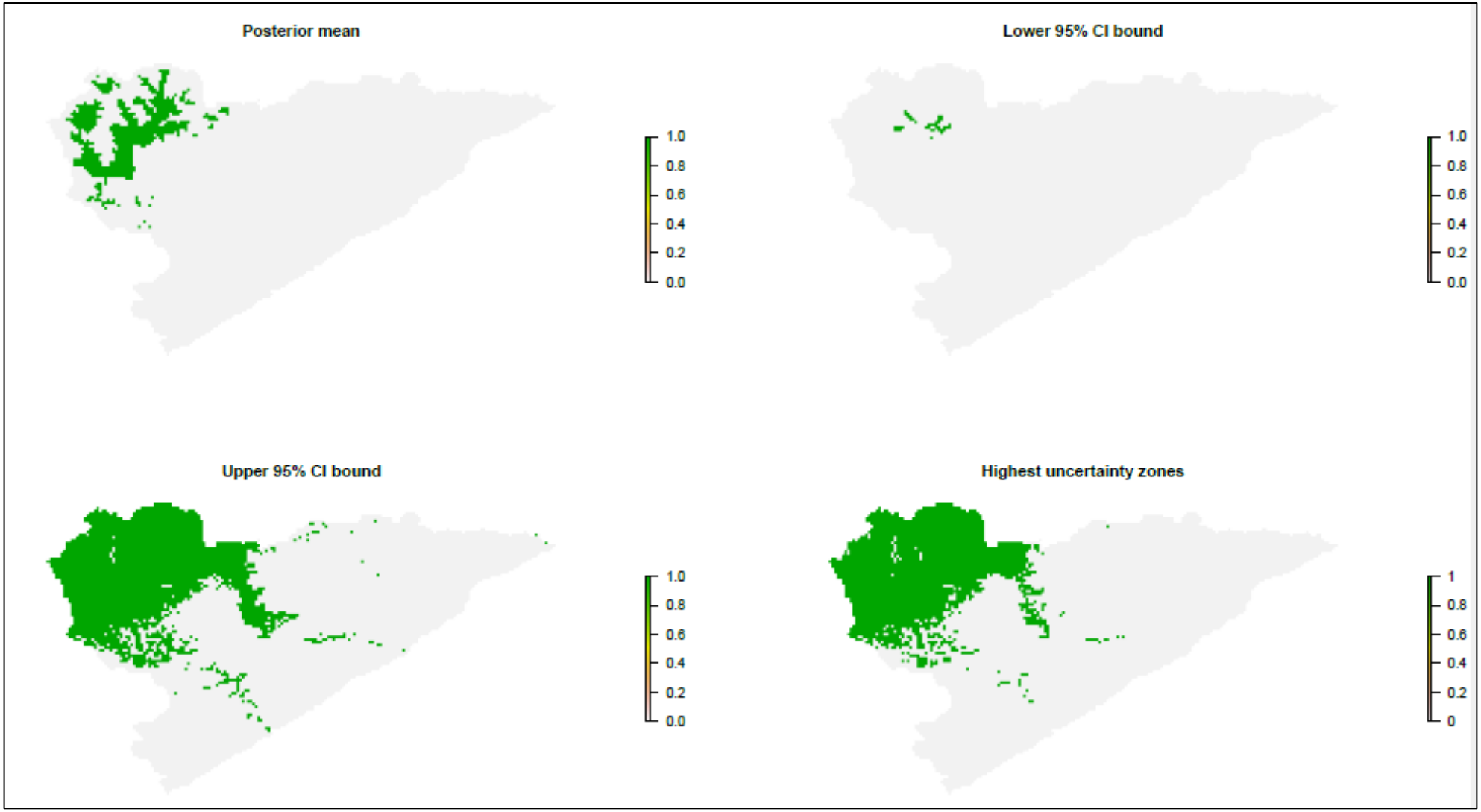


Figure S5.4.168. The modelled distribution of *Pseudobarbus trevelyani* Kieskamma in South Africa showing predicted distribution as a binary output.

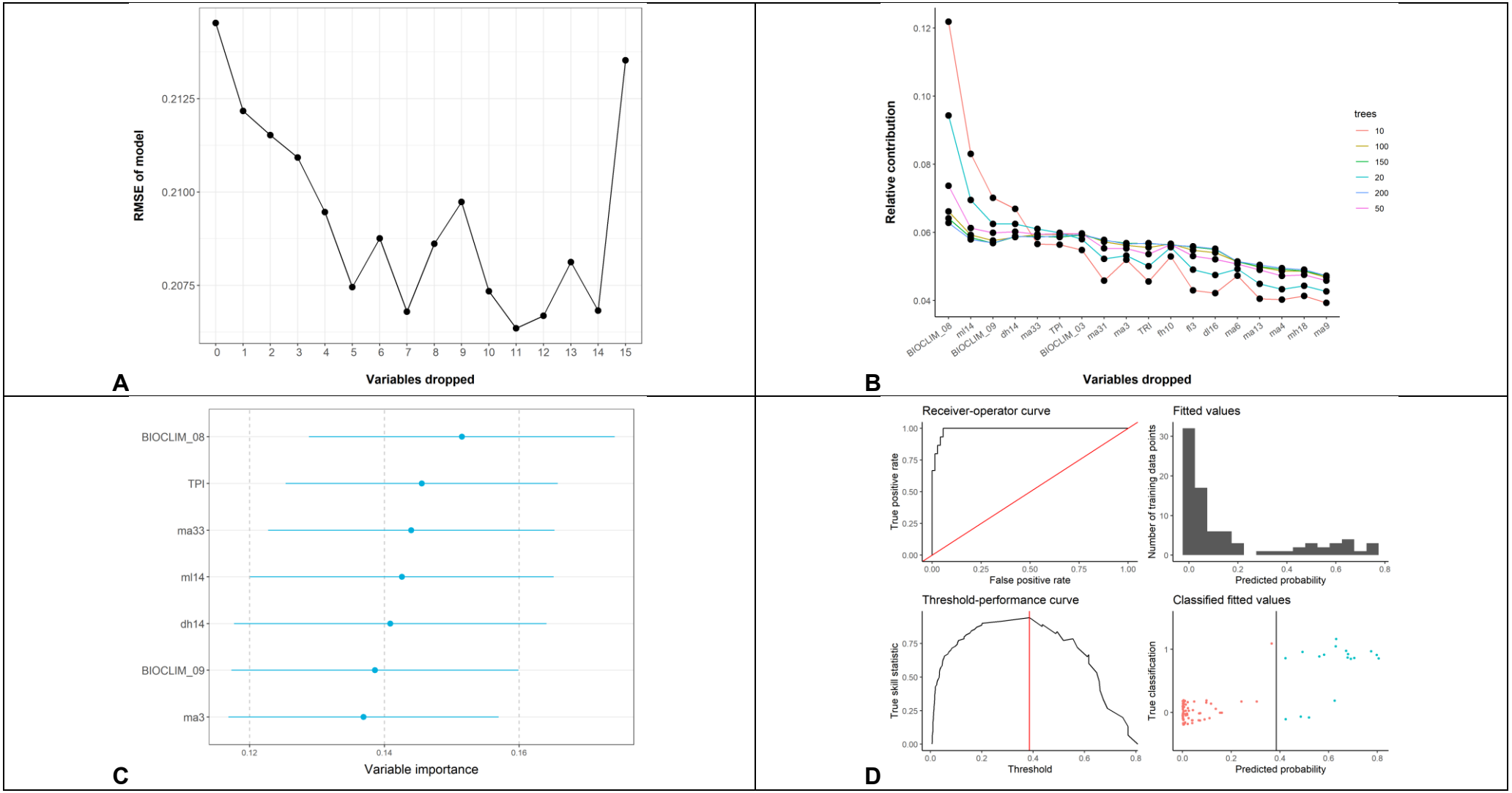


Figure S5.4.169. Model diagnostic outputs for *Pseudobarbus trevelyani* Kieskamma, showing (A) the root-mean square error of the model based on the number of predictor variables dropped, (B) relative contribution of predictor variables during model variable selection, (C) variable importance for the final model output, and (D) model diagnostic outputs (including the model's receiver-operator cure, fitted values, threshold-performance curve, and classified fitted values).

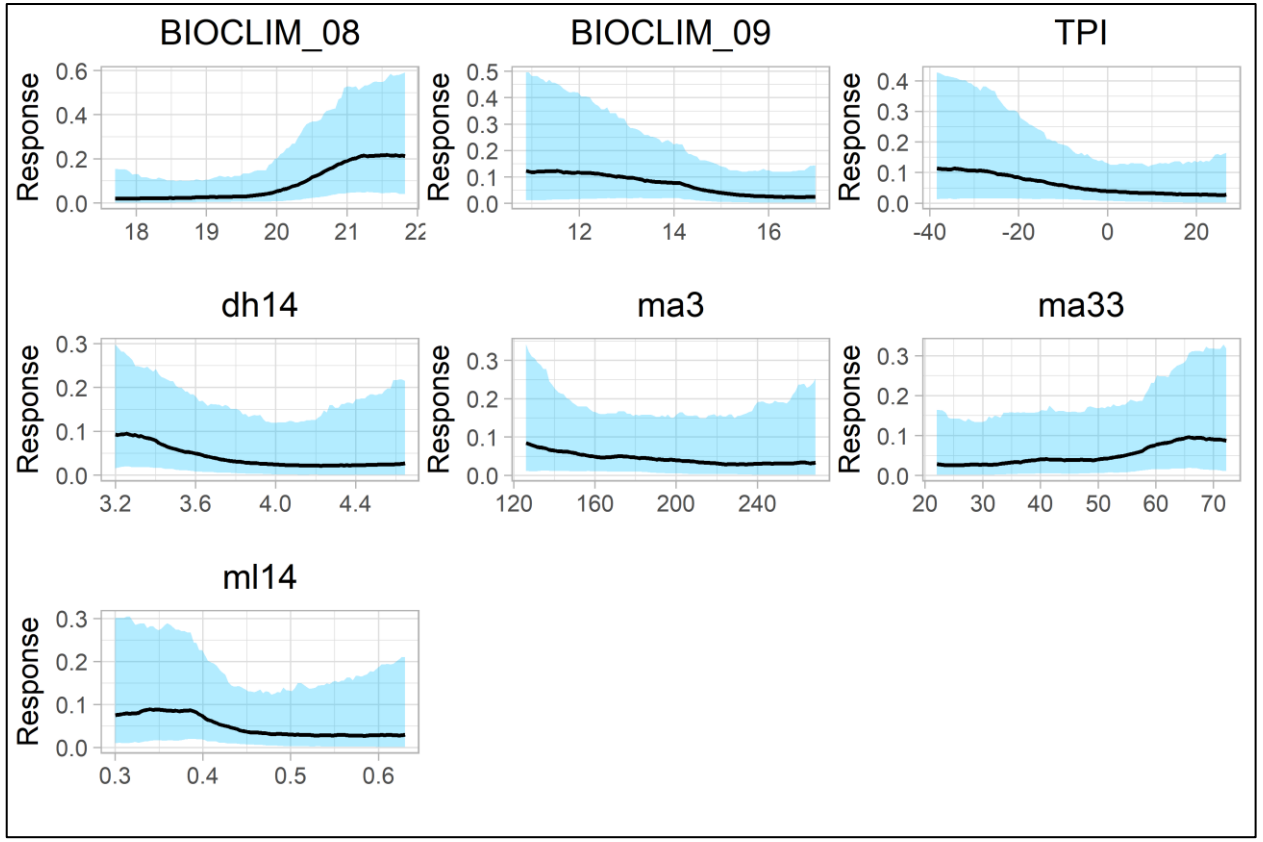


Figure S5.4.170. Partial dependence plots for *Pseudobarbus trevelyani* Kieskamma.

Supplementary S6

Supplementary S6.1. Author permission letter for Kajee et al. (2023) published in *Frontiers in Environmental Science*. 11. DOI: 10.3389/fenvs.2023.1122223.

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20 June 2024

To whom it may concern,

I hereby testify that I am a co-author of the following article, in which Mr Mohammed Kajee (KXJMOH007) was the lead researcher and first author.

Kajee, M., Henry, D.A.W., Dallas, H.F., Griffiths, C.L., Pegg, J., Van der Colff, D., Impson, D., Chakona, A., et al. 2023. How the Freshwater Biodiversity Information System (FBIS) is supporting national freshwater fish conservation decisions in South Africa. Frontiers in Environmental Science. 11. DOI: 10.3389/fenvs.2023.1122223.

Mr Kajee conceptualised and designed the research and independently conducted the study and analysed the data. He wrote the manuscript and dealt with referees comments. As a co-author, I provided specialised expertise and input, supervision, and comments for the final published manuscript.

I am aware that this publication formed part of Mr Kajee's PhD thesis in the Department of Biological Sciences at the University of Cape Town. As such, I am providing permission for him to include aspects of this article as part of his PhD thesis.

Yours sincerely,

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Supplementary S6.2. Author permission letter for Kajee et al. (2023) published in *Fishes* 8(12), p.571.

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20 June 2024

To whom it may concern,

I hereby testify that I am a co-author of the following article, in which Mr Mohammed Kajee (KXJMOH007) was the lead researcher and first author.

Kajee, M., Dallas, H.F., Griffiths, C.L., Kleynhans, C.J. and Shelton, J.M., 2023. The Status of South Africa's Freshwater Fish Fauna: A Spatial Analysis of Diversity, Threat, Invasion, and Protection. Fishes, 8(12), p.571.

Mr Kajee conceptualised and designed the research and independently conducted the study and analysed the data. He wrote the manuscript and dealt with referees comments. As a co-author, I provided specialised expertise and input, supervision, and comments for the final published manuscript.

I am aware that this publication formed part of Mr Kajee's PhD thesis in the Department of Biological Sciences at the University of Cape Town. As such, I am providing permission for him to include aspects of this article as par of his PhD thesis.

Yours sincerely,

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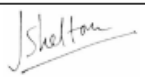
J.M. Shelton	jeremy@frcsa.org.za	

Supplementary S6.3. Author permission letter for Kajee et al. (2023) published in *Journal of Limnology*. 82(s1). DOI: 10.4081/jlimnol.2023.2133.

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20 June 2024

To whom it may concern,

I hereby testify that I am a co-author of the following article, in which Mr Mohammed Kajee (KXJMOH007) was the lead researcher and first author.

Kajee, M., Dallas, H.F., Swanepoel, A., Griffiths, C.L. and Shelton, J.M. 2023. The Freshwater Biodiversity Information System (FBIS) fish data: a georeferenced dataset of freshwater fishes occurring in South Africa. Journal of Limnology. 82(s1). DOI: 10.4081/jlimnol.2023.2133.

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Yours sincerely,

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Supplementary S6.4. Supervisor permission letter acknowledging contributions to all publications included in this thesis.

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2 July 2024

To whom it may concern,

I hereby testify that the Mohammed Kajee (KXJMOH007) was the first author and lead researcher in the work done towards completing the following articles included in his PhD thesis:

1. Kajee, M., Henry, D.A.W., Dallas, H.F., Griffiths, C.L., Pegg, J., Van der Colff, D., Impson, D., Chakona, A., et al. 2023. How the Freshwater Biodiversity Information System (FBIS) is supporting national freshwater fish conservation decisions in South Africa. *Frontiers in Environmental Science*. 11. DOI: 10.3389/fenvs.2023.1122223.

2. Kajee, M., Dallas, H.F., Griffiths, C.L., Kleynhans, C.J. and Shelton, J.M., 2023. The Status of South Africa's Freshwater Fish Fauna: A Spatial Analysis of Diversity, Threat, Invasion, and Protection. *Fishes*, 8(12), p.571.

3. Kajee, M., Dallas, H.F., Swanepoel, A., Griffiths, C.L. and Shelton, J.M. 2023. The Freshwater Biodiversity Information System (FBIS) fish data: a georeferenced dataset of freshwater fishes occurring in South Africa. *Journal of Limnology*. 82(s1). DOI: 10.4081/jlimnol.2023.2133.

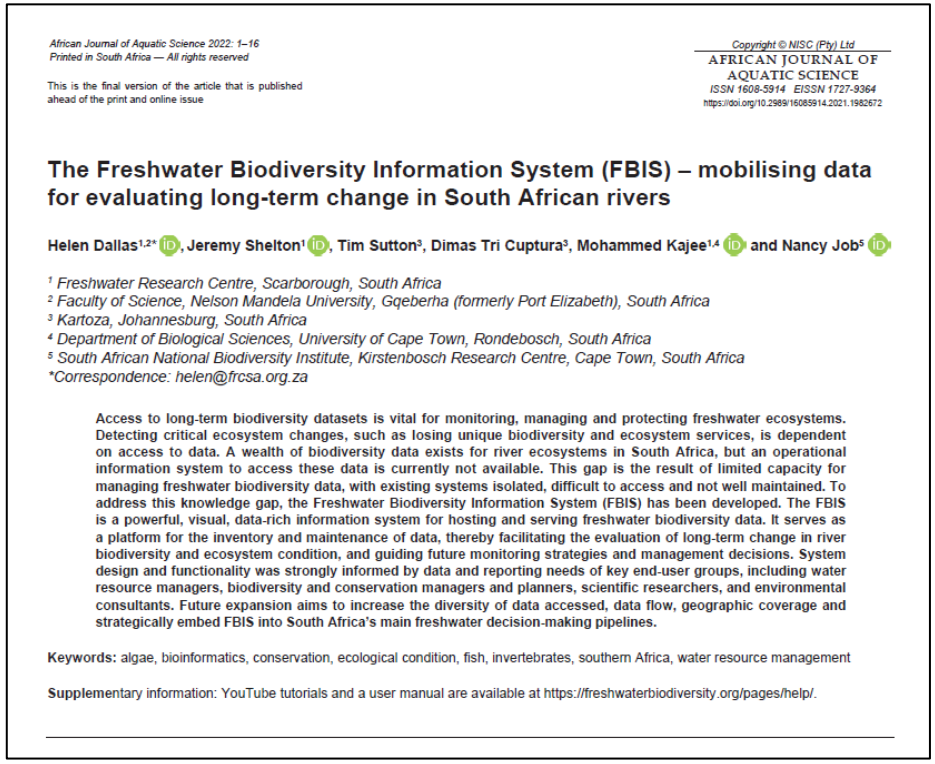
Mohammed Kajee conceptualised and designed the research and independently conducted the study and analysed the data. He wrote the manuscript and dealt with referees comments. The co-authors contributed by facilitating the work through providing special expertise, funds, facilities, supervision, and comments and suggestions on the manuscript.

Yours sincerely,

Emer Prof Charles Griffiths, Principal Supervisor

Supplementary S6.5. Supporting publication included in this thesis.

Dallas, H., Shelton, J., Sutton, T., Tri Cuptura, D., Kajee, M. and Job, N., 2022. The Freshwater Biodiversity Information System (FBIS)–mobilising data for evaluating long-term change in South African rivers. African Journal of Aquatic Science, 47(3), pp.291-306.



African Journal of Aquatic Science 2022: 1–16
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This is the final version of the article that is published ahead of the print and online issue

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AFRICAN JOURNAL OF AQUATIC SCIENCE
ISSN 1608-5914 EISSN 1727-9364
https://doi.org/10.2989/16085914.2021.1982672

The Freshwater Biodiversity Information System (FBIS) – mobilising data for evaluating long-term change in South African rivers

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Access to long-term biodiversity datasets is vital for monitoring, managing and protecting freshwater ecosystems. Detecting critical ecosystem changes, such as losing unique biodiversity and ecosystem services, is dependent on access to data. A wealth of biodiversity data exists for river ecosystems in South Africa, but an operational information system to access these data is currently not available. This gap is the result of limited capacity for managing freshwater biodiversity data, with existing systems isolated, difficult to access and not well maintained. To address this knowledge gap, the Freshwater Biodiversity Information System (FBIS) has been developed. The FBIS is a powerful, visual, data-rich information system for hosting and serving freshwater biodiversity data. It serves as a platform for the inventory and maintenance of data, thereby facilitating the evaluation of long-term change in river biodiversity and ecosystem condition, and guiding future monitoring strategies and management decisions. System design and functionality was strongly informed by data and reporting needs of key end-user groups, including water resource managers, biodiversity and conservation managers and planners, scientific researchers, and environmental consultants. Future expansion aims to increase the diversity of data accessed, data flow, geographic coverage and strategically embed FBIS into South Africa's main freshwater decision-making pipelines.

Keywords: algae, bioinformatics, conservation, ecological condition, fish, invertebrates, southern Africa, water resource management

Supplementary information: YouTube tutorials and a user manual are available at https://freshwaterbiodiversity.org/pages/help/.

Available at: https://www.tandfonline.com/doi/pdf/10.2989/16085914.2021.1982672

PDF

Dallas et al_2021_African Jour