Supplementary material

Oceanic and coastal populations of a harvested macroinvertebrate *Rochia nilotica* in north-western Australia are isolated and may be locally adapted

Oliver Berry[A,D,H,I]*, Zoe Richards*[B,C,D]*, Glenn Moore*[C,D]*, Udhi Hernawan*[D,E]*,*

Mike Travers[F] *and Bernd Gruber*[G]

[A]CSIRO Oceans and Atmosphere, Indian Ocean Marine Research Centre,
The University of Western Australia, Crawley, WA 6009, Australia.

[B]Trace and Environmental DNA Laboratory, School of Molecular and Life Sciences,
Curtin University, Bentley, WA 6102, Australia.

[C]Department of Aquatic Zoology, Western Australian Museum, Locked Bag 49,
Welshpool DC, WA 6986, Australia.

[D]Western Australian Marine Science Institution. Indian Ocean Marine Research Centre,
The University of Western Australia, Crawley, WA 6009, Australia.

[E]Centre for Marine Ecosystems Research, Edith Cowan University, 270 Joondalup Drive,
Joondalup, WA 6027, Australia.

[F]Fisheries Division, Department of Primary Industries and Regional Development,
39 Northside Drive, Hillarys, WA 6025, Australia.

[G]Institute for Applied Ecology, Faculty of Applied Science,
University of Canberra, ACT 2601, Australia

[H]Present address: CSIRO Environomics Future Science Platform,
The University of Western Australia, Crawley, WA 6009, Australia.

[I]Corresponding author. Email: oliver.berry@csiro.au

Table S1. Descriptive statistics for 5438 neutral SNP markers genotyped in 514 individual *T. niloticus* from Western Australia

N mean number of individuals genotyped per locus; *H*e expected heterozygosity; *H*o observed heterozygosity; *F*is inbreeding coefficient; *A*r allelic richness.

All values are ±standard error in parentheses. Numbers next to site names correspond to labels on Fig. 1*a*, *b*

| Site (north–south)	Region	N		*H*e		*H*o		*F*is		*A*r	
1 Bathurst Is. North	Coastal	27.836	(0.006)	0.304	(0.002)	0.280	(0.002)	0.073	(0.003)	1.550	(0.004)
2 Bowles Reef	Coastal	32.799	(0.007)	0.307	(0.002)	0.282	(0.002)	0.079	(0.003)	1.553	(0.004)
3 Irvine Island	Coastal	5.964	(0.003)	0.306	(0.003)	0.278	(0.003)	0.064	(0.005)	1.553	(0.004)
4 Frazer Island	Coastal	13.916	(0.004)	0.304	(0.002)	0.280	(0.002)	0.068	(0.004)	1.554	(0.004)
5 Barrett Rock	Coastal	38.779	(0.008)	0.307	(0.002)	0.282	(0.002)	0.078	(0.003)	1.554	(0.004)
6 Longitude Island	Coastal	5.962	(0.003)	0.303	(0.003)	0.281	(0.003)	0.049	(0.005)	1.554	(0.004)
7 Asshlyn Island	Coastal	39.779	(0.008)	0.307	(0.002)	0.286	(0.002)	0.066	(0.003)	1.555	(0.004)
8 Pope Rock	Coastal	30.824	(0.007)	0.304	(0.002)	0.281	(0.002)	0.073	(0.003)	1.537	(0.004)
9 Tide Rip Island	Coastal	37.772	(0.008)	0.304	(0.002)	0.279	(0.002)	0.081	(0.003)	1.537	(0.005)
10 Jalan	Coastal	53.693	(0.010)	0.305	(0.002)	0.284	(0.002)	0.072	(0.003)	1.556	(0.004)
11 Janinko	Coastal	38.765	(0.008)	0.305	(0.002)	0.283	(0.002)	0.073	(0.003)	1.551	(0.004)
12 Ngoorroodool	Coastal	34.801	(0.008)	0.306	(0.002)	0.285	(0.002)	0.068	(0.003)	1.550	(0.004)
13 Noyon	Coastal	44.744	(0.009)	0.306	(0.002)	0.284	(0.002)	0.071	(0.003)	1.555	(0.004)
14 Mermaid_Island	Coastal	47.708	(0.009)	0.306	(0.002)	0.281	(0.002)	0.078	(0.003)	1.545	(0.005)
15 Ardinoogoon	Coastal	27.859	(0.006)	0.307	(0.002)	0.290	(0.002)	0.055	(0.003)	1.556	(0.004)
16 Rowley Shoals	Oceanic	26.658	(0.012)	0.297	(0.002)	0.272	(0.002)	0.083	(0.003)	1.551	(0.004)
17 Scott Reefs	Oceanic	4.937	(0.004)	0.301	(0.003)	0.264	(0.003)	0.084	(0.006)	1.551	(0.004)
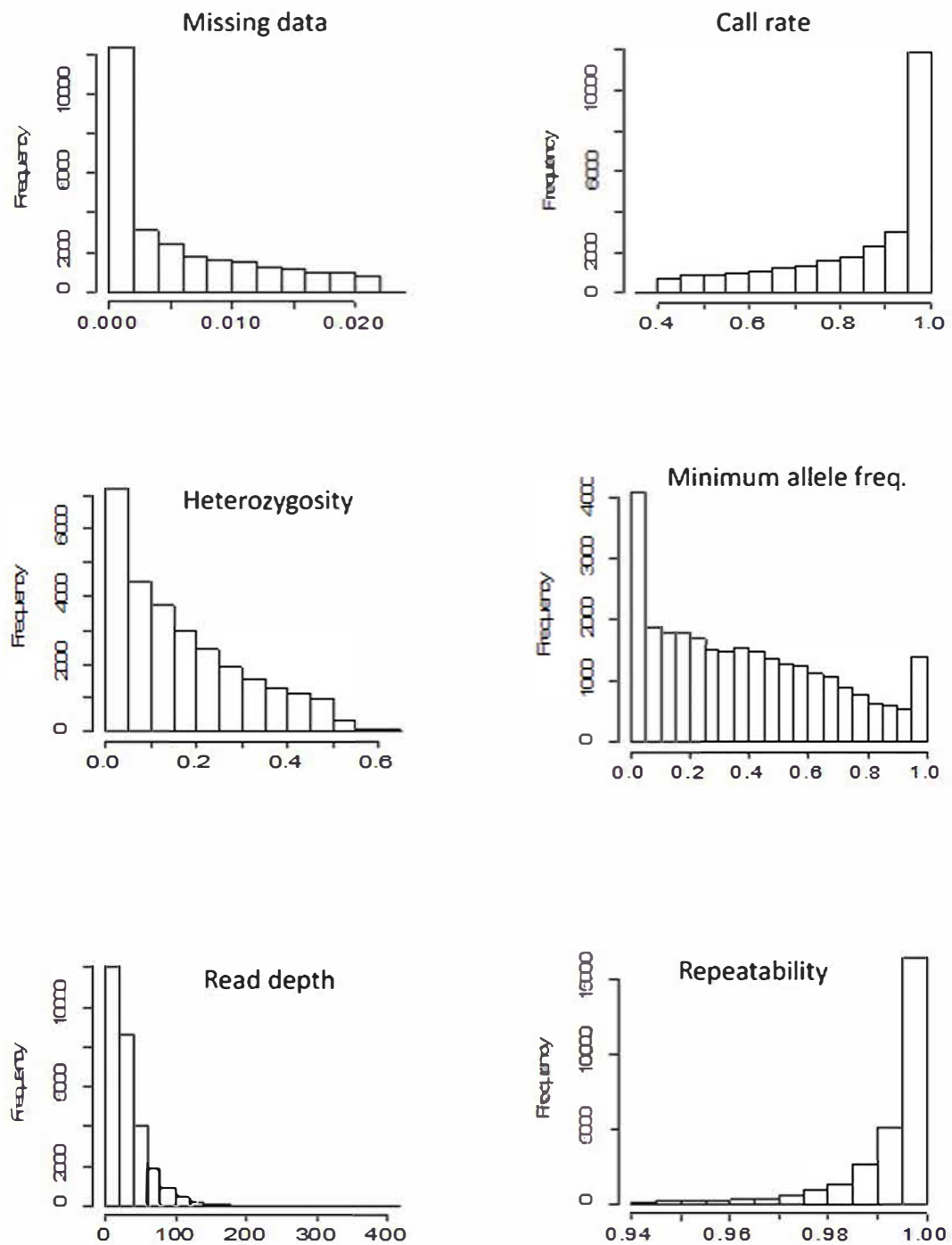
Fig. S1. Frequency histograms of descriptive statistics used to filter 29 552 single nucleotide polymorphisms in *Rochia nilotica.*
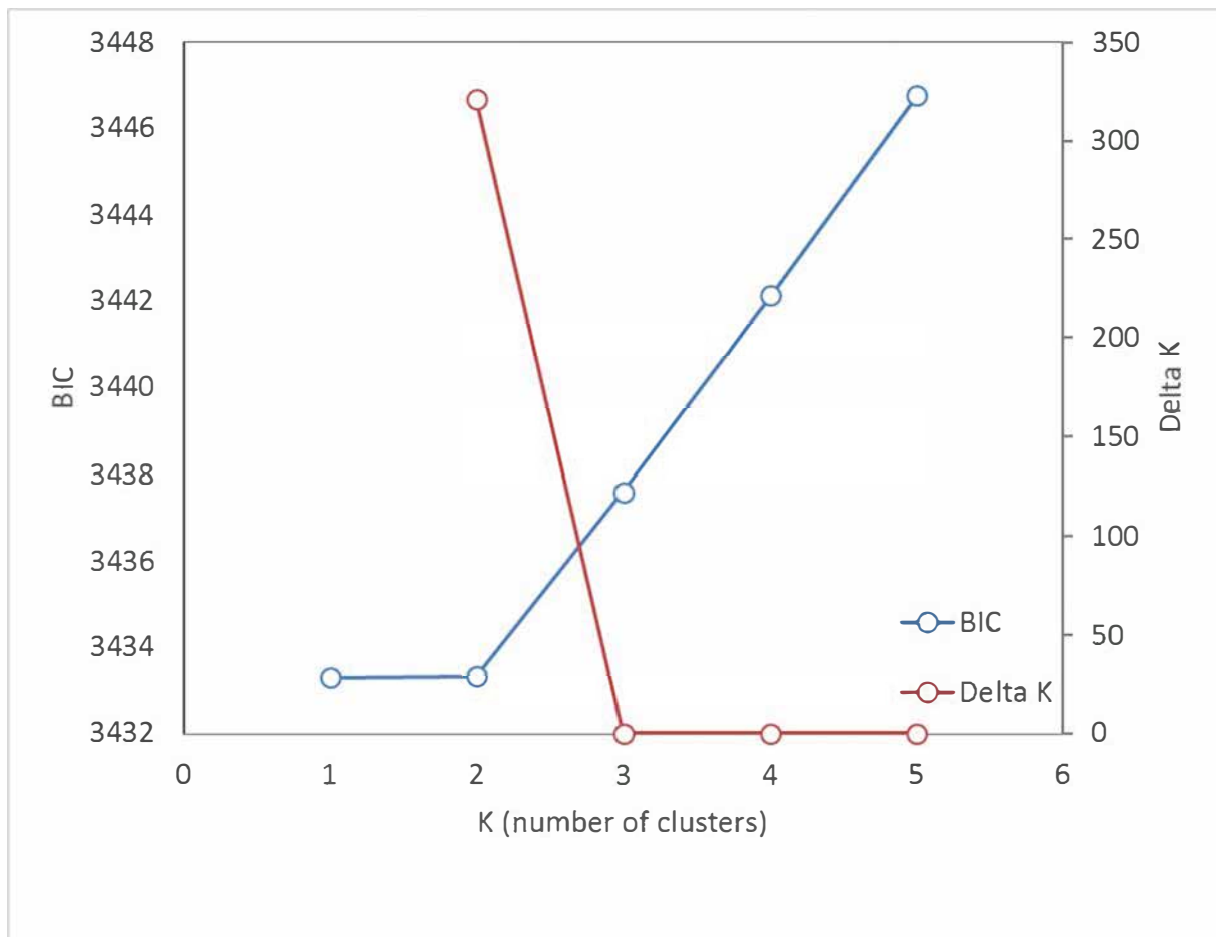
Fig. S2. Blue line shows change in Bayesian Information Content (BIC) for increasing numbers of clusters in the data generated by the find.clusters function in the R package adegenet (ver. 2.0, see https://cran.r-project.org/web/packages/adegenet/index.html, accessed March 2019, Jombart *et al*. 2010). The best supported number of clusters is indicated by the inflection point (Jombart *et al*. 2010). Red line shows change in Δ*K* for different numbers of clusters in the data. Maximal ΔK indicates the best-supported solution (Evanno *et al*. 2005).
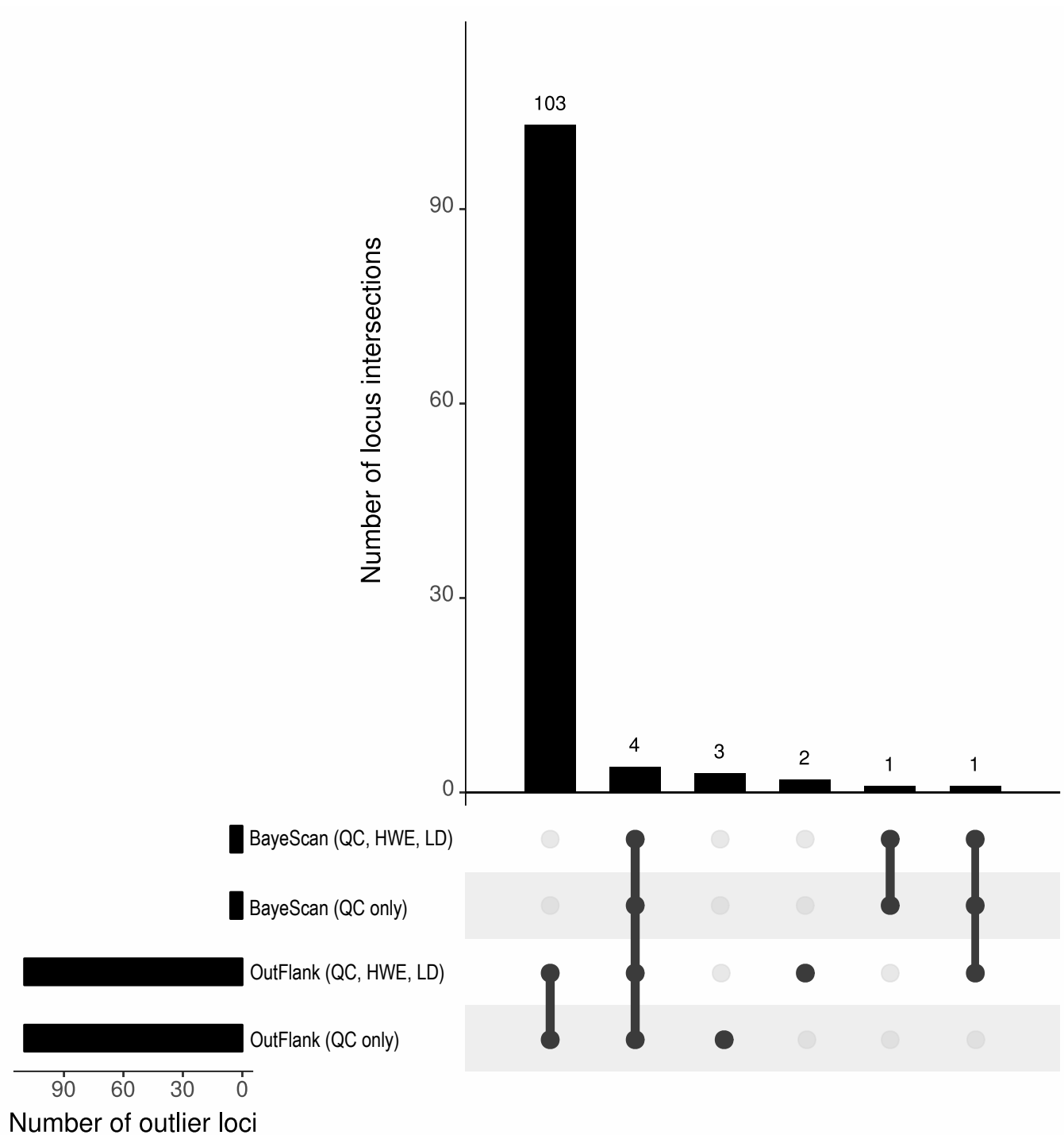
Fig. S3. Upset plot (Conway *et al*. 2017) illustrating intersections in the identification of outlier SNP loci using OutFlank and BayeScan methods. Also illustrated are results for datasets where loci were filtered based on Hardy–Weinberg equilibrium and gametic-phase disequilibrium (QC, HWE, LD), and where they were not (QC only).

References

Conway, J. R., Lex, A., and Gehlenborg, N. (2017). UpSetR: an R package for the visualization of intersecting sets and their properties. *Bioinformatics* **33**(18), 2938–2940 . doi:10.1093/bioinformatics/btx364

Evanno, G., Regnaut, S., and Goudet, J. (2005). Detecting the number of clusters of individuals using the software structure: a simulation study. *Molecular Ecology* **14**(8), 2611–2620 . doi:10.1111/j.1365-294X.2005.02553.x

Jombart, T., Devillard, S., and Balloux, F. (2010). Discriminant analysis of principal components: a new method for the analysis of genetically structured populations. *BMC Genetics* **11**, 94 . doi:10.1186/1471-2156-11-94