Supplemental Information for:

First genomic snapshots of recolonising lineages

following a devastating earthquake

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SUPPLEMENTARY TABLE 1
Sequencing information and results the five GBS libraries used to sequence the 216 *D. antarctica* samples for this study. A new GBS library, FV3, was generated for this study (highlighted in yellow), whereas the other four libraries were produced for previous studies (Parvizi et al. 2020, Vaux et al. 2021, Vaux et al. 2022). The table includes the number of reads removed during quality control using the *process_radtags* component of STACKS 2.53.

GBS library name	CF1	CF2	FV1	FV2	FV3	Total
Total number of multiplexed samples	192	216	96	203	192	899
Multiplexed *D. antarctica* samples for this study	27	12	71	16	90	216
Number of adapter plates	2	3	1	3	2	
Size selection (bp)	250 - 450	300 - 600	200 - 600	200 - 600	200 - 500	
Sequencing platform	Illumina NextSeq 500	Illumina NextSeq 500	Illumina NextSeq 500	Illumina NextSeq 500	Illumina NextSeq 500	
Read length (bp)	75	75	75	75	75	
Paired reads?	Yes	Yes	Yes	Yes	Yes	
PhiX spike-in (approx.)	5%	5%	5%	5%	5%	
Total Sequences	307,797,516	310,206,086	315,678,078	330,627,614	363,842,806	1,628,152,100
Barcode Not Found	152,618,572	37,478,802	26,414,122	45,595,966	42,773,066	304,880,528
Low Quality	79,148	80,258	125,261	71,969	265,853	622,489
RAD Cutsite Not Found	2,868,624	6,485,392	3,029,044	2,753,042	3,302,471	18,438,573
Retained Reads	152,231,172	266,161,634	286,109,651	282,206,637	317,501,416	1,304,210,510
Percentage retained reads	49.5%	85.8%	90.6%	85.4%	87.3%	80.1%

SUPPLEMENTARY TABLE 2

Results of varying certain parameters in *ustacks*, *cstacks* and *populations* components of STACKS 2.53. Complete lists of parameters used for each component are provided in the Methods. The STACKS runs selected for analysis are highlighted in green.

N	ustacks	cstacks	# pops	populations	# variant and invariant loci	# variant loci	Mean missing data per sample
216	-m 3 -M 2 -N 4	-n 2	1	-p 1 -r 0.90	6,177	2,255	5.7%
216	-m 3 -M 2 -N 4	-n 2	1	-p 1 -r 0.80	8,995	3,833	9.4%
216	-m 3 -M 2 -N 4	-n 2	1	-p 1 -r 0.70	10,629	4,872	12.9%
216	-m 3 -M 2 -N 4	-n 2	1	-p 1 -r 0.60	12,035	5,919	17.0%
216	-m 3 -M 2 -N 4	-n 2	1	-p 1 -r 0.50	13,440	7,092	21.8%
216	-m 4 -M 2 -N 4	-n 2	1	-p 1 -r 0.60	11,252	5,549	16.6%
216	-m 3 -M 2 -N 4	-n 1	1	-p 1 -r 0.60	11,976	5,944	17.2%
216	-m 3 -M 2 -N 4	-n 3	1	-p 1 -r 0.60	12,015	5,954	17.1%
216	-m 3 -M 3 -N 5	-n 2	1	-p 1 -r 0.60	11,657	5,763	17.1%

SUPPLEMENTARY TABLE 3

Genetic summary statistics for the sample groups (with pre- and post-earthquake sampling separated for the five uplift locations) in the main dataset (4,629 loci). Estimated values are presented for observed (H_O) and expected heterozygosity (H_E), the inbreeding coefficient (F_{IS}), and allelic richness (AR). 95% confidence intervals are presented for F_{IS} values.

Labels on Figure 1	Sample group	n	Mean H_O	Mean H_E	Mean (CI) F_{IS}	Mean AR
1 – 3	North Island	14	0.13	0.20	0.268 (0.243 – 0.374)	1.20
4	Rārangi	9	0.14	0.13	-0.028 (-0.059 – 0.023)	1.13
5	Cape Campbell 2016	5	0.16	0.18	0.049 (0.039 – 0.110)	1.18
5	Cape Campbell 2018, 20	8	0.17	0.17	0.007 (-0.003 – 0.039)	1.17
6	Ward Beach 2016	17	0.18	0.23	0.173 (0.167 – 0.222)	1.23
6	Ward Beach 2018, 20	21	0.19	0.21	0.090 (0.082 – 0.115)	1.21
7	Wharanui 2016	10	0.17	0.18	0.043 (0.007 – 0.059)	1.18
7	Wharanui 2018, 20	18	0.17	0.17	0.009 (0.007 – 0.039)	1.17
8	Waipapa Bay 2016	21	0.19	0.20	0.081 (0.045 – 0.091)	1.20
8	Waipapa Bay 2018, 20	29	0.19	0.20	0.055 (0.045 – 0.067)	1.20
9	Kaikōura Peninsula 2016	17	0.19	0.23	0.155 (0.137 – 0.198)	1.23
9	Kaikōura Peninsula 2017, 20	16	0.20	0.23	0.099 (0.080 – 0.118)	1.23
10 – 12	Southern Kaikōura	12	0.17	0.20	0.134 (0.1211 – 0.167)	1.20
13, 14	Hurunui	11	0.14	0.16	0.062 (0.053 – 0.112)	1.16
15 – 17	Banks Peninsula	8	0.10	0.12	0.104 (0.128 – 0.174)	1.12

SUPPLEMENTARY TABLE 4

Relative connectivity amongst study sites derived from weighted decadal medians of daily surface currents. The lower triangular matrix represents export from sites listed in column headers to sites listed in row names while the upper triangular matrix represents connectivity in the opposite direction (i.e. columns = export, rows = import). All values are stated as a percentage of system-wide connectivity.

	Cape Campbell	Ward Beach	Wharanui	Waipapa Bay	Kaikōura Peninsula	Southern Kaikōura	Hurunui
Cape Campbell		3.25	2.69	2.71	3.19	2.50	2.04
Ward Beach	3.09		3.57	3.23	3.66	3.03	2.49
Wharanui	2.05	3.11		3.10	3.53	2.84	2.28
Waipapa Bay	1.30	1.73	2.11		4.17	3.62	2.96
Kaikōura Peninsula	1.24	1.39	1.46	2.94		4.28	3.67
Southern Kaikōura	0.75	0.80	0.74	1.86	3.53		3.59
Hurunui	0.15	0.13	0.03	0.85	2.00	2.34	

SUPPLEMENTARY FIGURES

SUPPLEMENTARY FIGURE 1

The percentage of missing data (missingness, estimated in VCFR) per sample in the main dataset (4,629 loci). Sample groups are labelled under samples.
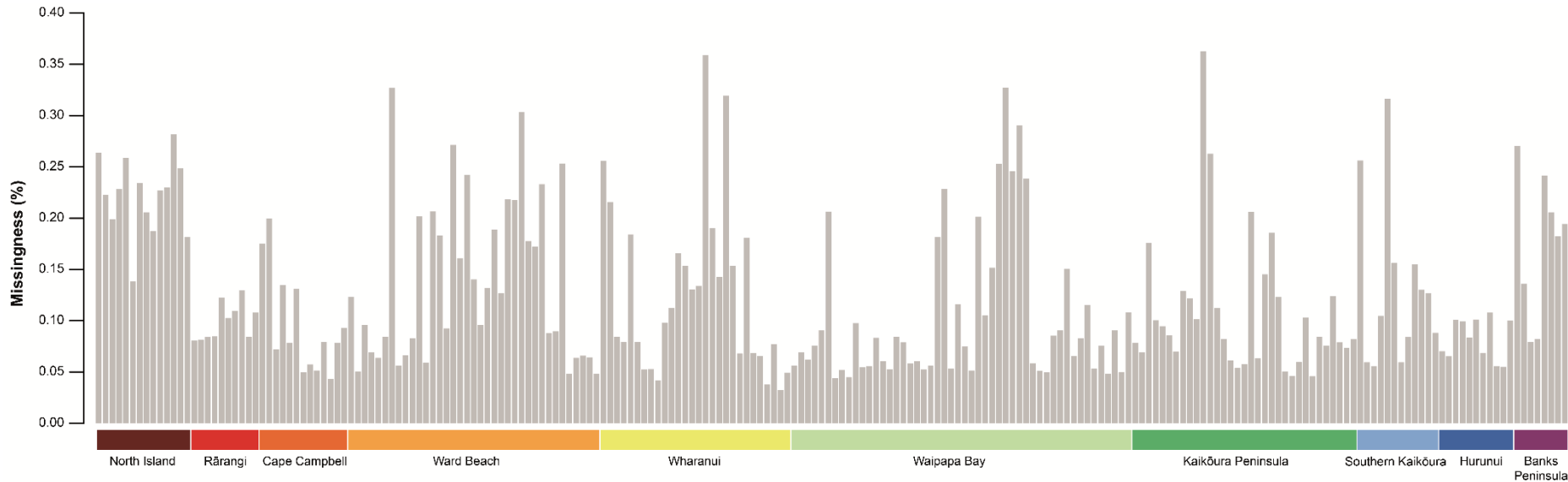
SUPPLEMENTARY FIGURE 2

Histograms of missing data (missingness, estimated in VCFR) per sample in the main dataset
(4,629 loci).
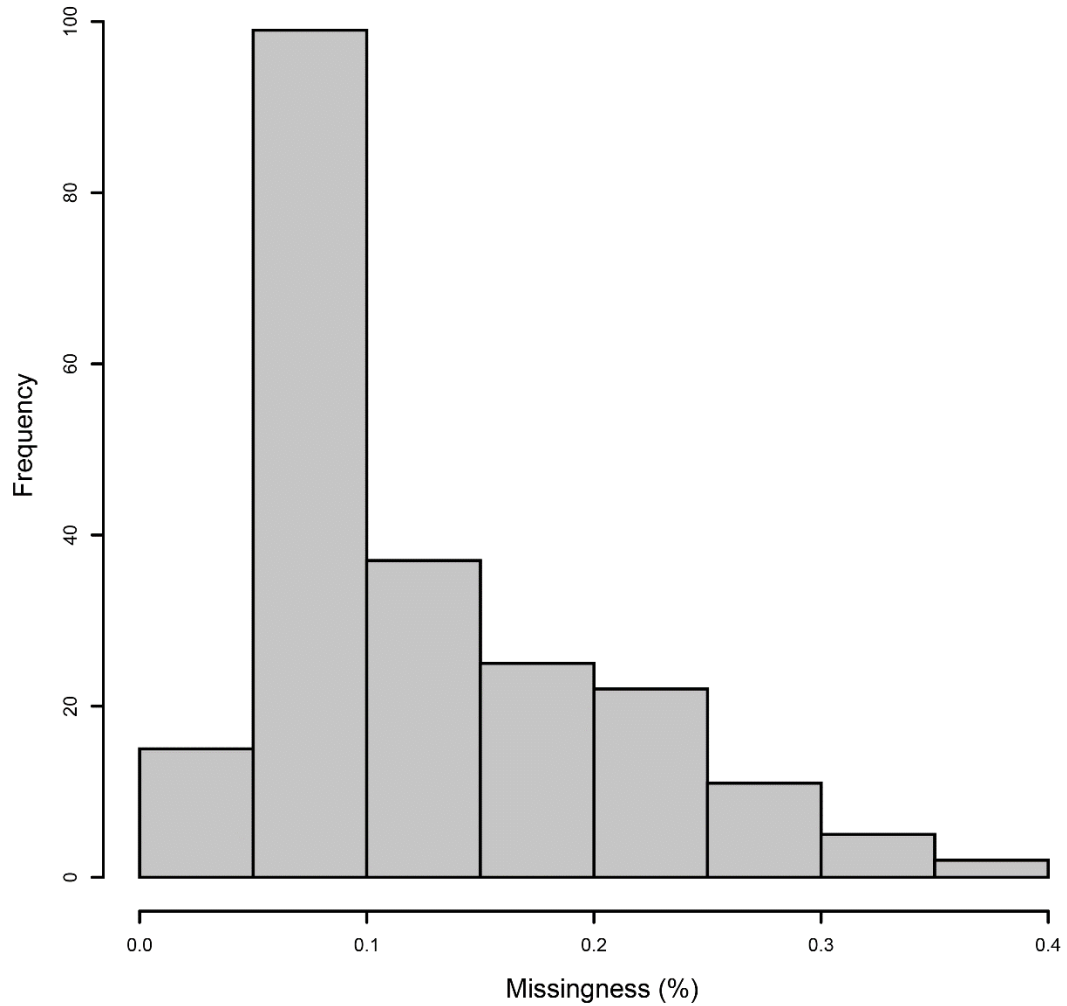
SUPPLEMENTARY FIGURE 3

Coverage depth per locus in the main dataset, as estimated in VCFR, including highly correlated loci. (*a*) a histogram of mean coverage depth per locus, (*b*) a box and whisker plot of mean coverage depth per locus, (*c*) a histogram of the standard deviation (SD) in coverage depth per locus, (*d*) a box and whisker plot of the standard deviation in coverage depth per locus. Plots for the alternative dataset without highly correlated loci were very similar and are not presented.
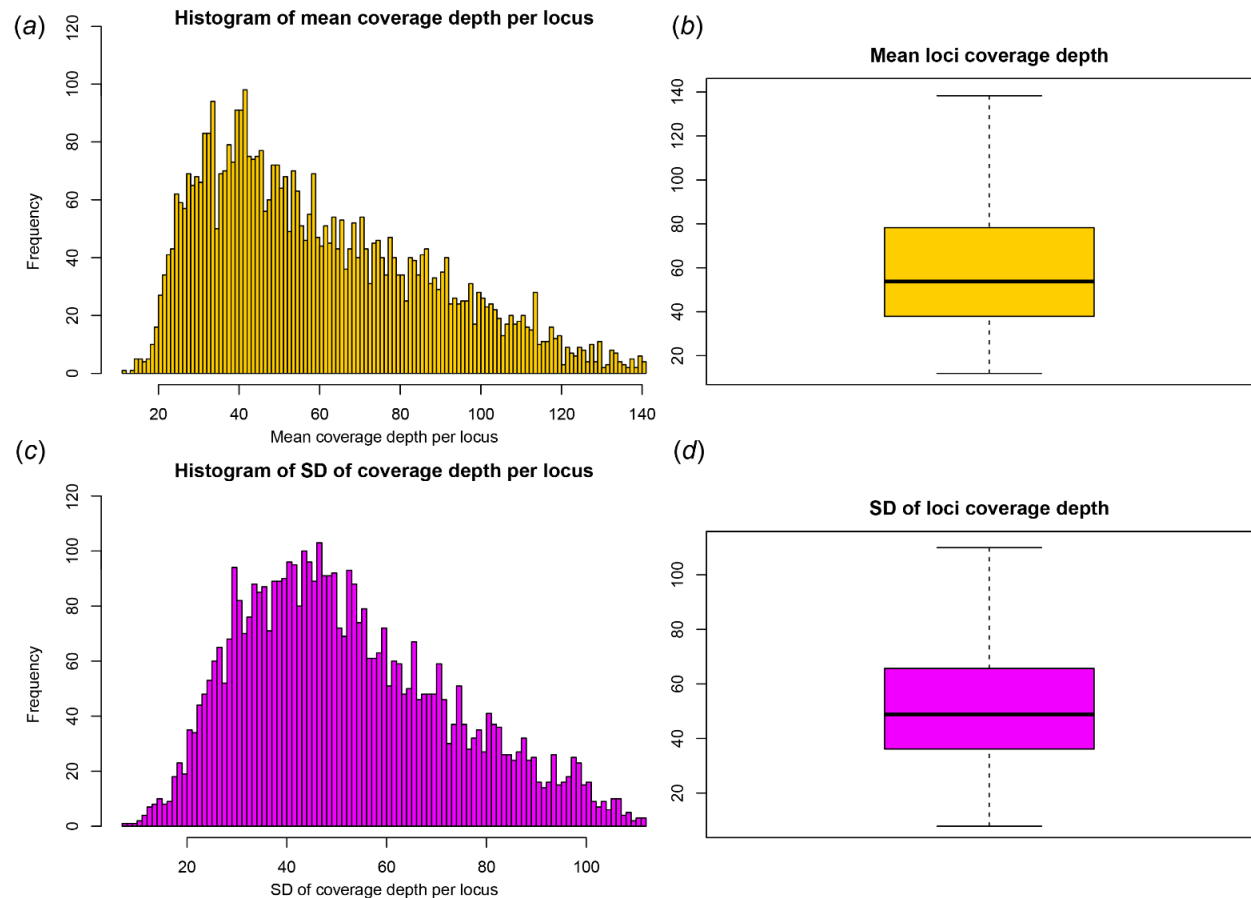
SUPPLEMENTARY FIGURE 4
Unrooted maximum likelihood (ML) phylogeny produced by IQTREE for the main dataset
(4,629 loci).
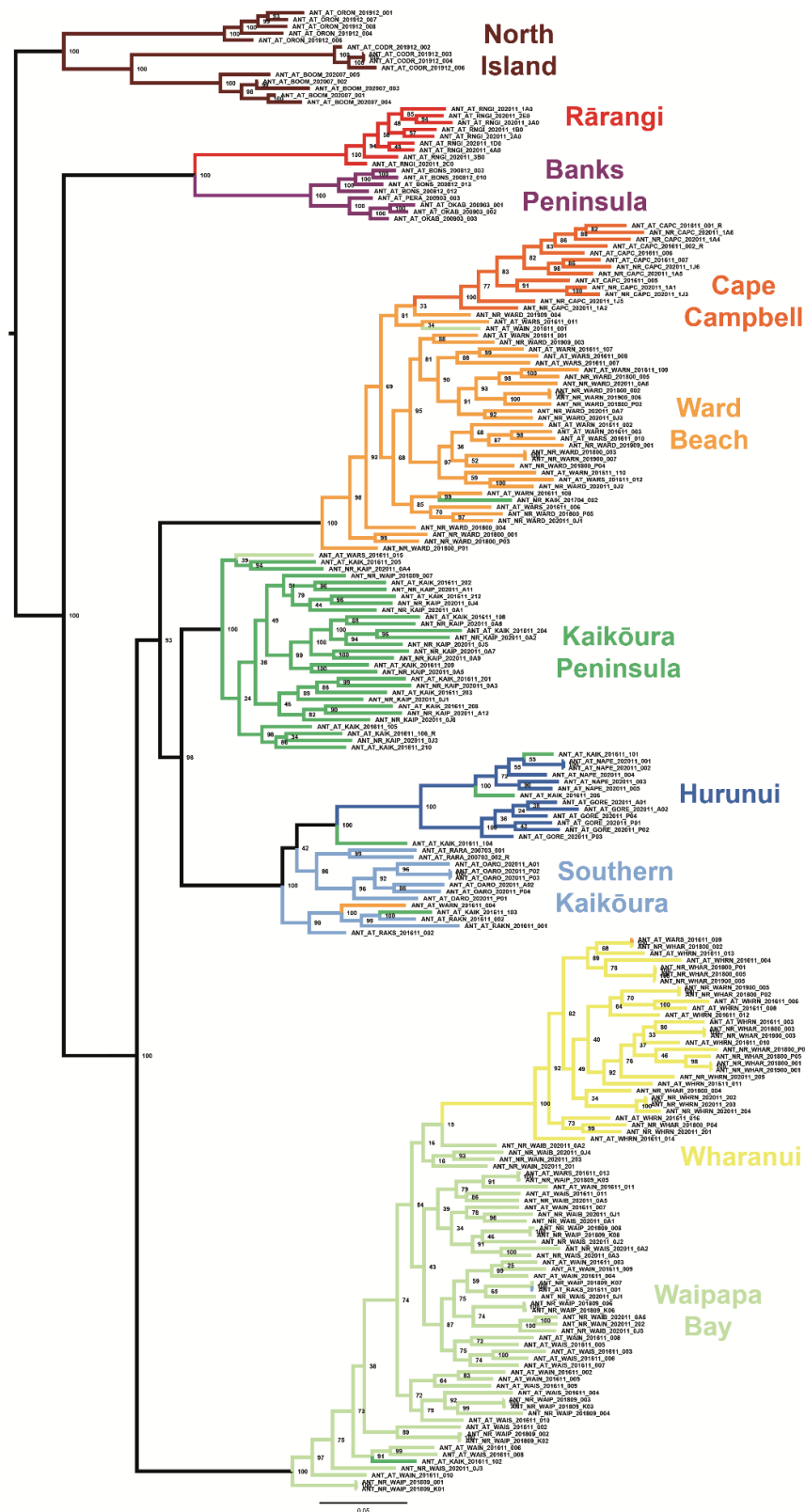
SUPPLEMENTARY FIGURE 5
Unrooted maximum likelihood (ML) phylogeny produced by IQTREE for the alternative
dataset without highly correlated loci (2,851 loci).
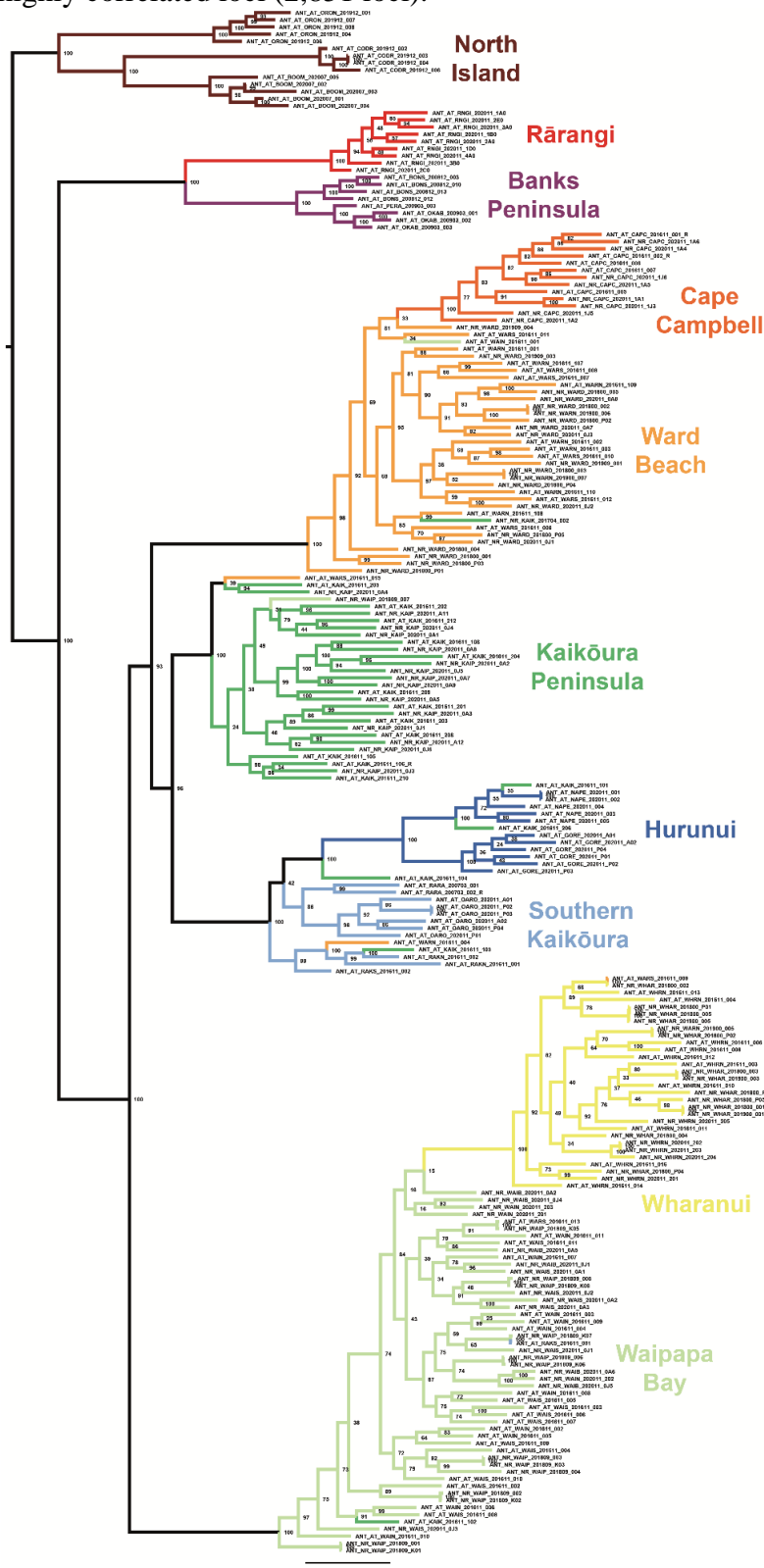
SUPPLEMENTARY FIGURE 6
Unrooted neighbour-joining (NJ) phylogeny produced by VCF-KIT for the main dataset (4,629 loci).
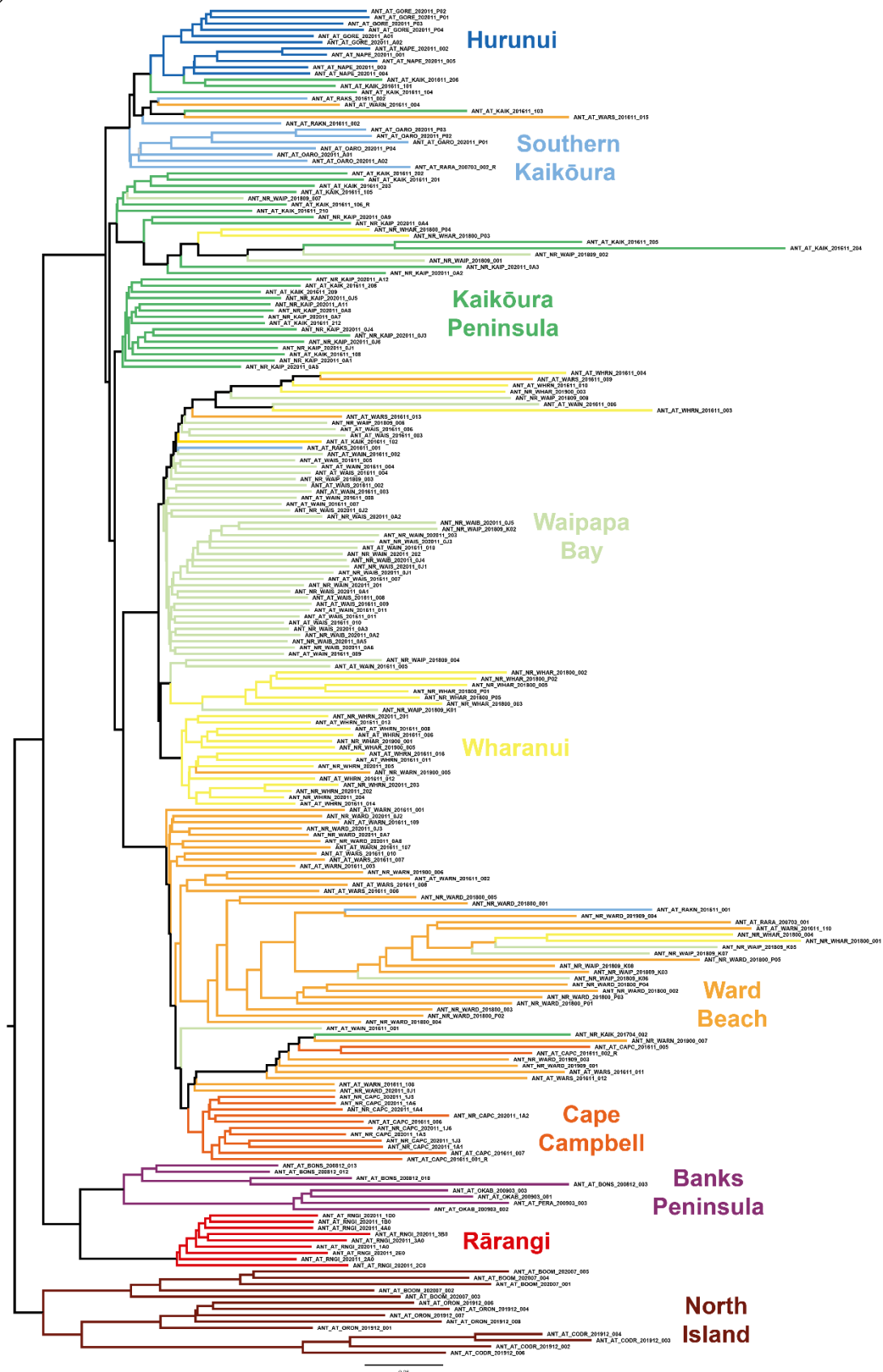
SUPPLEMENTARY FIGURE 7
Unrooted neighbour-joining (NJ) phylogeny produced by VCF-KIT for the alternative dataset without highly correlated loci (2,851 loci).
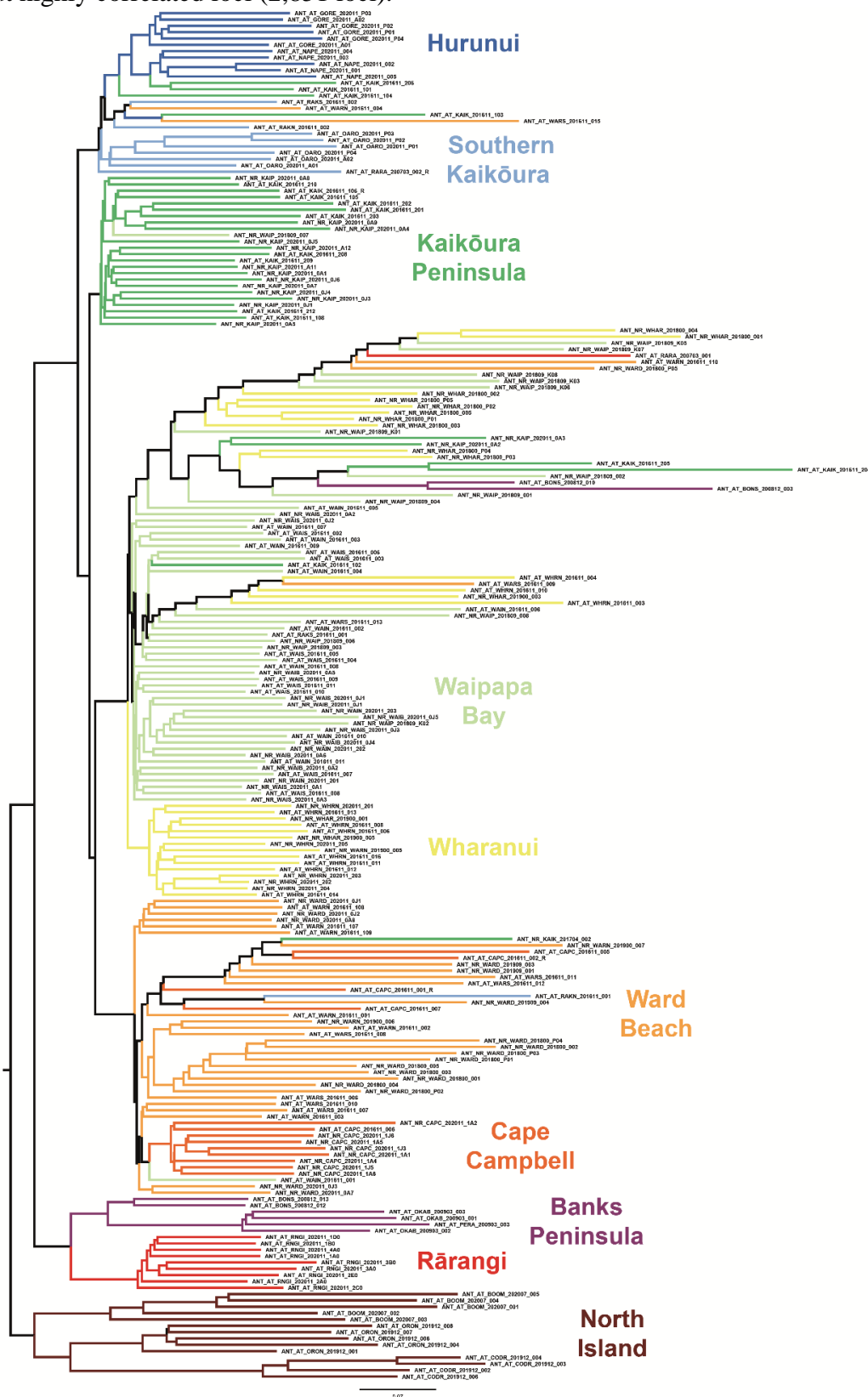
SUPPLEMENTARY FIGURE 8
The selection of retained principal components (PCs) for principal components analysis. Each graph shows the Eigenvalues for all PCs in a) the main dataset (4,629 loci), b) the alternative dataset without highly correlated loci (2,851 loci). The red line shows the broken-stick test, the number of PCs above the broken-stick line that were retained for analysis are labelled in red.

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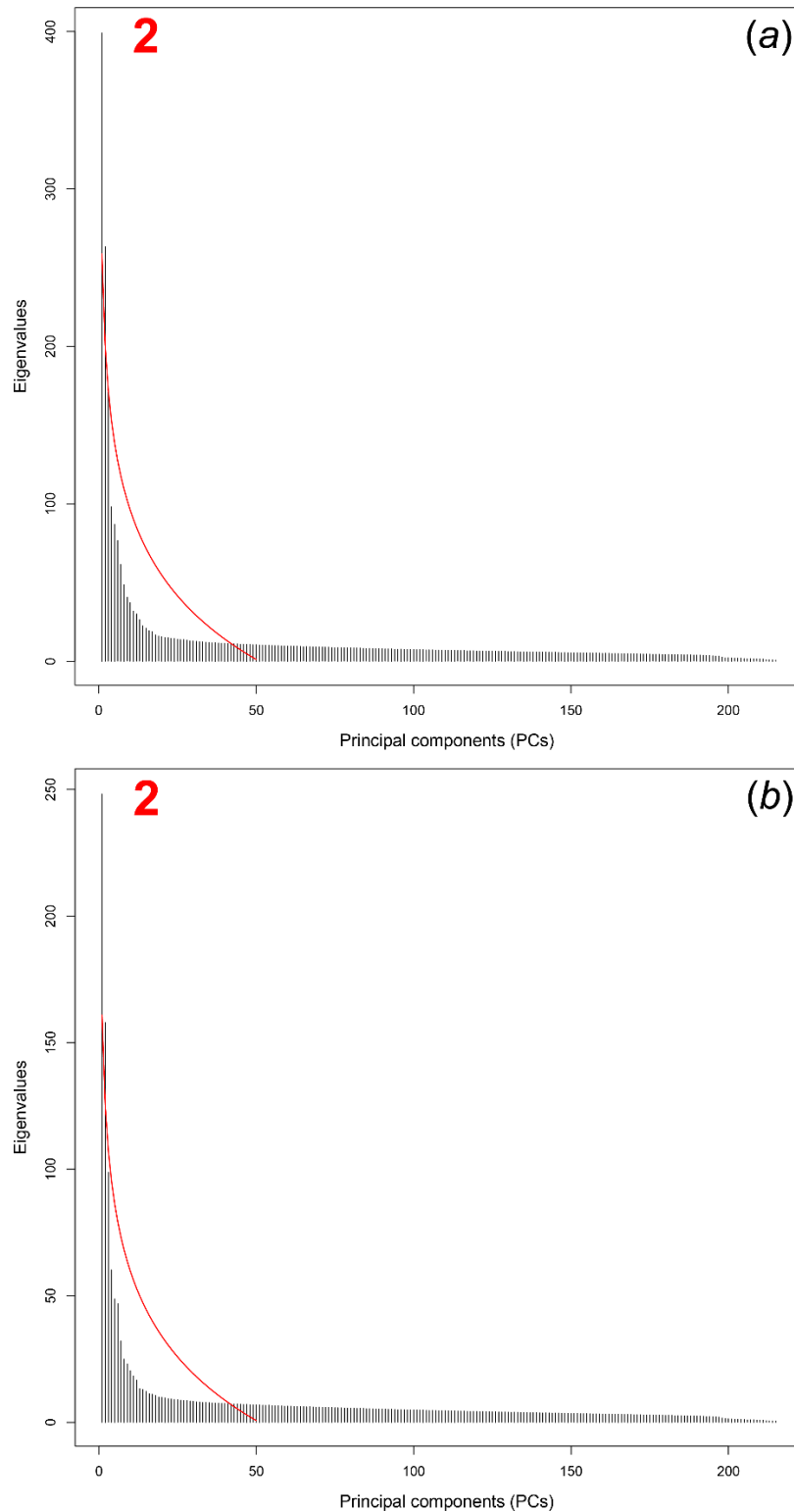
SUPPLEMENTARY FIGURE 9
Principal components analysis plots produced in ADEGENET for the alternative dataset without highly correlated loci (4,629 loci), showing PC1 (13.9% of variation) and PC2 (8.8%).
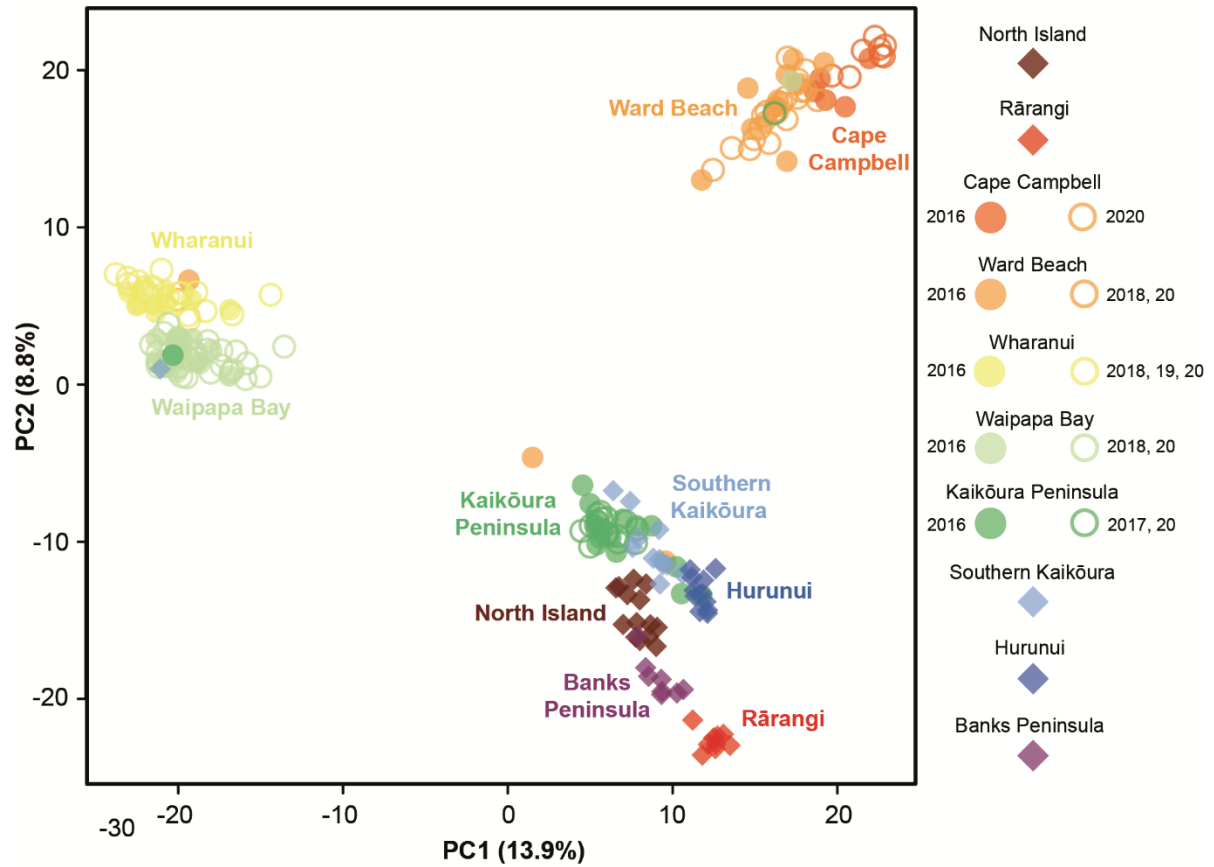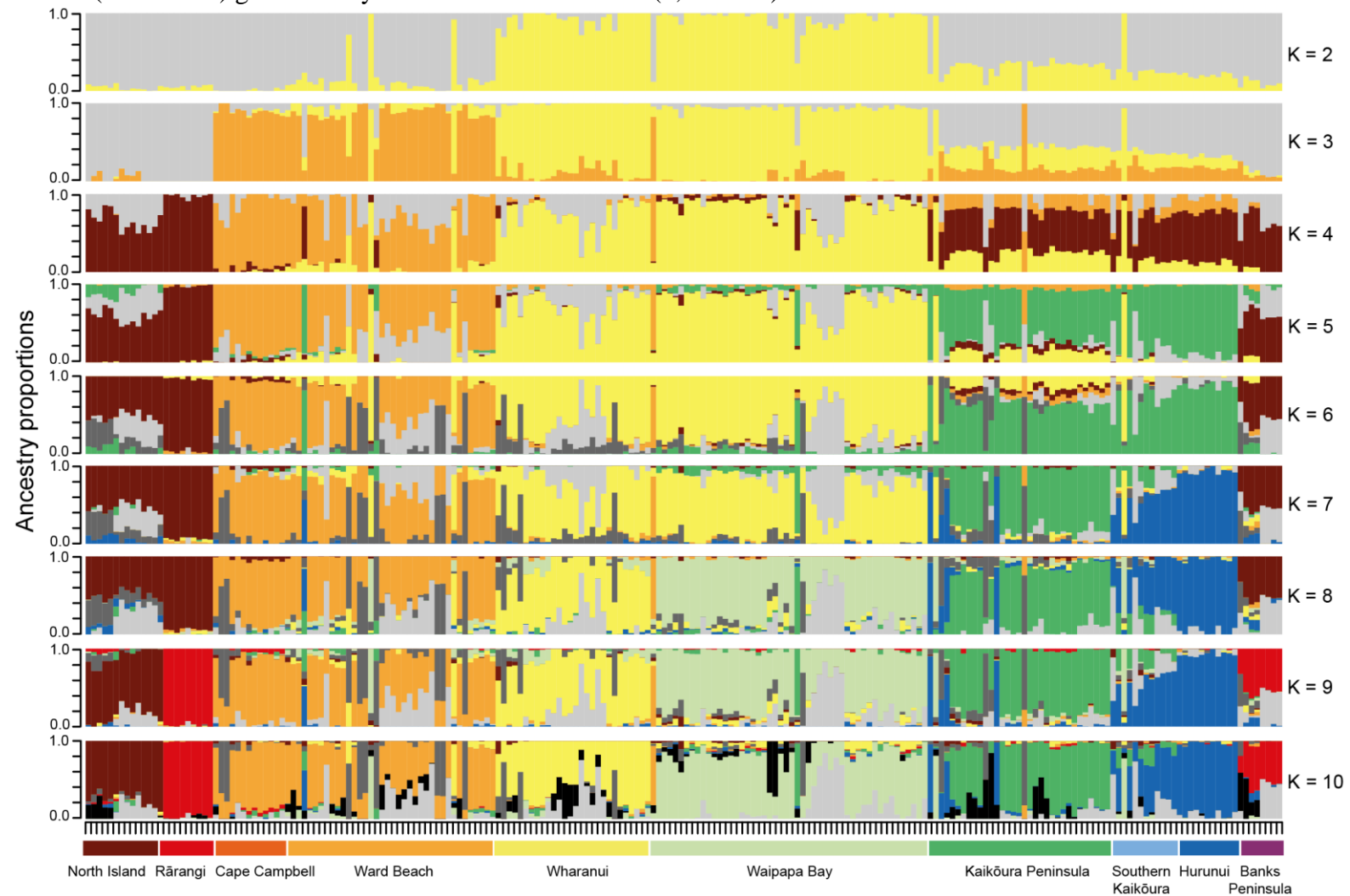
SUPPLEMENTARY FIGURE 10
Cross entropy values for each iteration of K (1 – 10) applied in LEA for a) the main dataset (2,851 loci), b) the alternative dataset without highly correlated loci (2,851 loci).
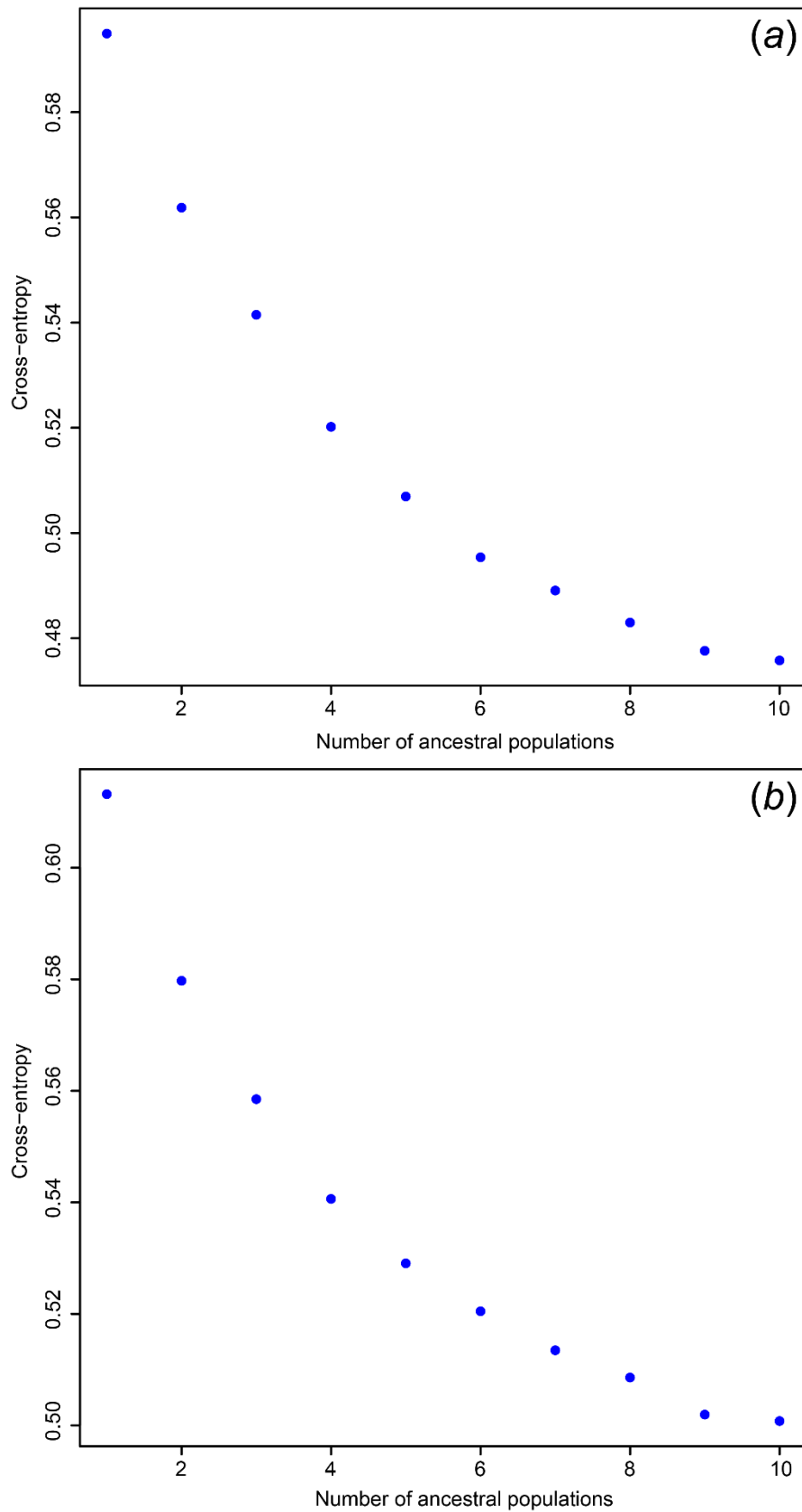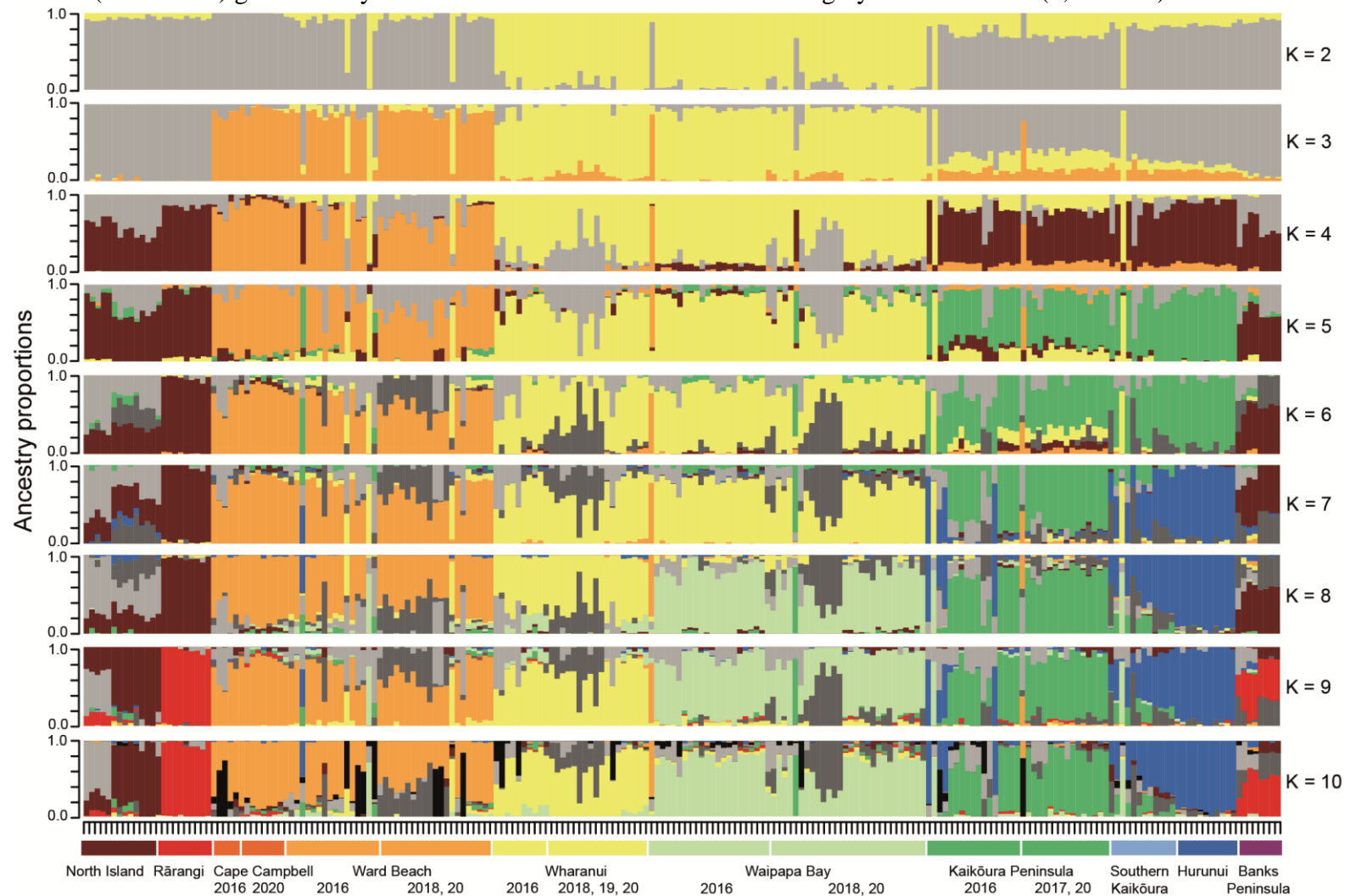
SUPPLEMENTARY FIGURE 11

Ancestry matrices (K = 2 – 10) generated by LEA for the main dataset (4,629 loci).

SUPPLEMENTARY FIGURE 12

Ancestry matrices (K = 2 – 10) generated by LEA for the alternative dataset without highly correlated loci (2,851 loci).

SUPPLEMENTARY FIGURE 13

A chord plot visualising estimated oceanographic connectivity among the five earthquake comparison sites in the first reproductive season following the November 2016 Kaikōura earthquake. A map of the South Island of New Zealand, with the sample locations used for the connectivity analysis, is shown on the left. See Figure 3 for an alternative Sankey plot visualisation of the same results, and values associated with the plots are listed in Supplementary Table 4.
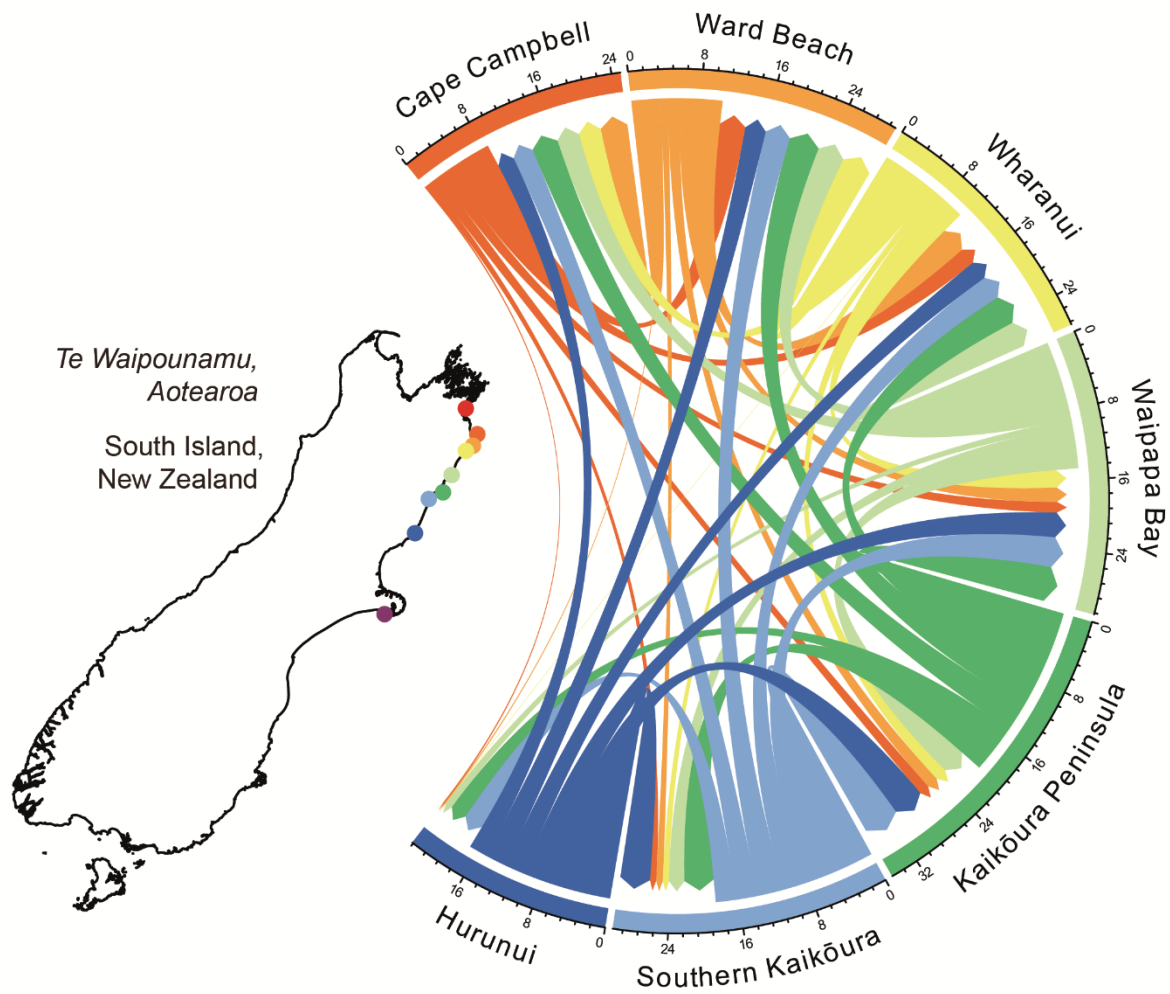
SUPPLEMENTARY REFERENCES

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