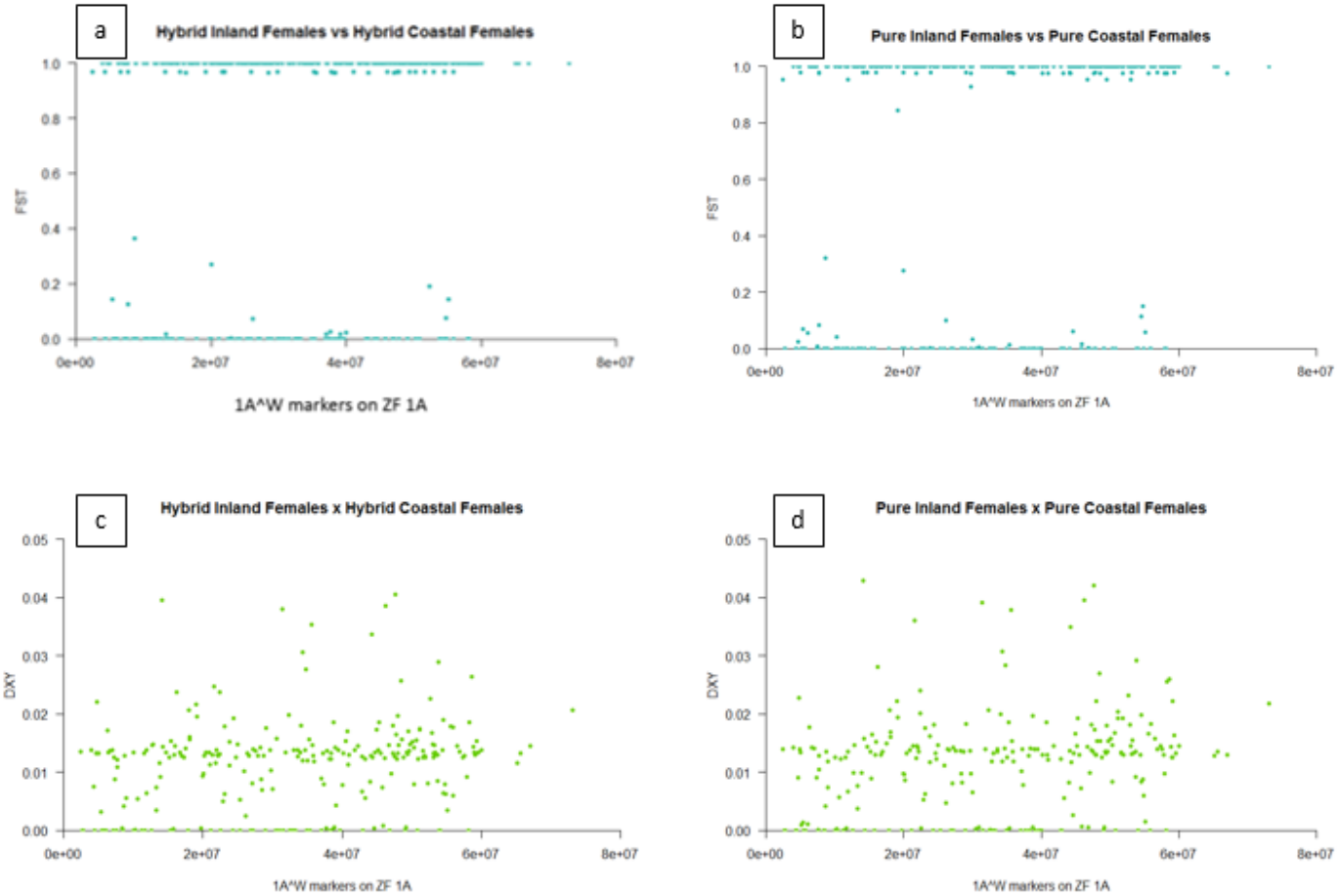


Figure S1: Differentiation and divergence between mitolineages for $1A^W$ markers in females. Plots show F_{ST} values for a) hybrid zone; and b) pure populations differentiation; and D_{XY} values for c) hybrid zone; and d) pure population divergence. The x-axis shows marker position as mapped to Zebra Finch chromosome 1A.

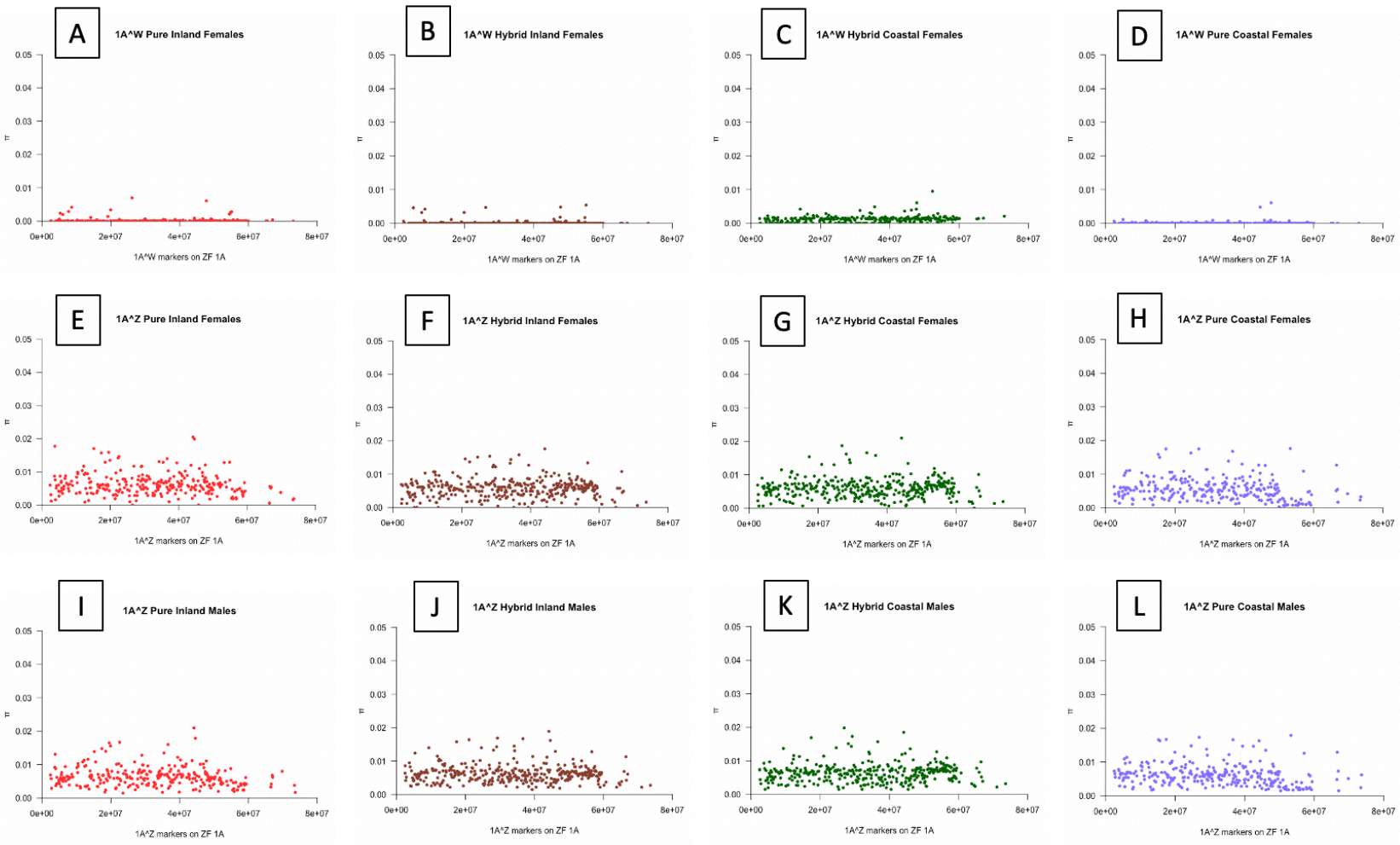


Figure S2: P_i values of $1A^W$ markers in females for a) pure inland; b) hybrid inland; c) hybrid coastal; and d) pure coastal populations; $1A^Z$ markers in females for e) pure inland; f) hybrid inland; g) hybrid coastal; and h) pure coastal populations; and $1A^Z$ markers in males for i) pure inland; j) hybrid inland; k) hybrid coastal; and l) pure coastal populations. The x-axis shows marker position as mapped to Zebra Finch chromosome 1A.

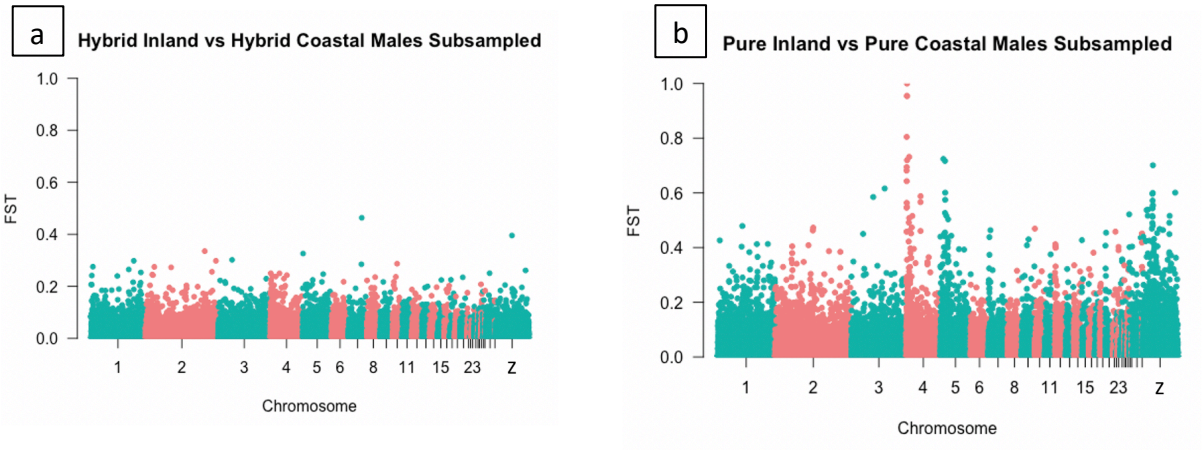


Figure S3: Differentiation between males between mitolineages for markers mapping to ZF autosomes (excluding 1A) and chromosome Z. Here, males have been subsampled to replicate female sample sizes. Plots show F_{ST} values for a) hybrid inland and b) hybrid coastal populations.

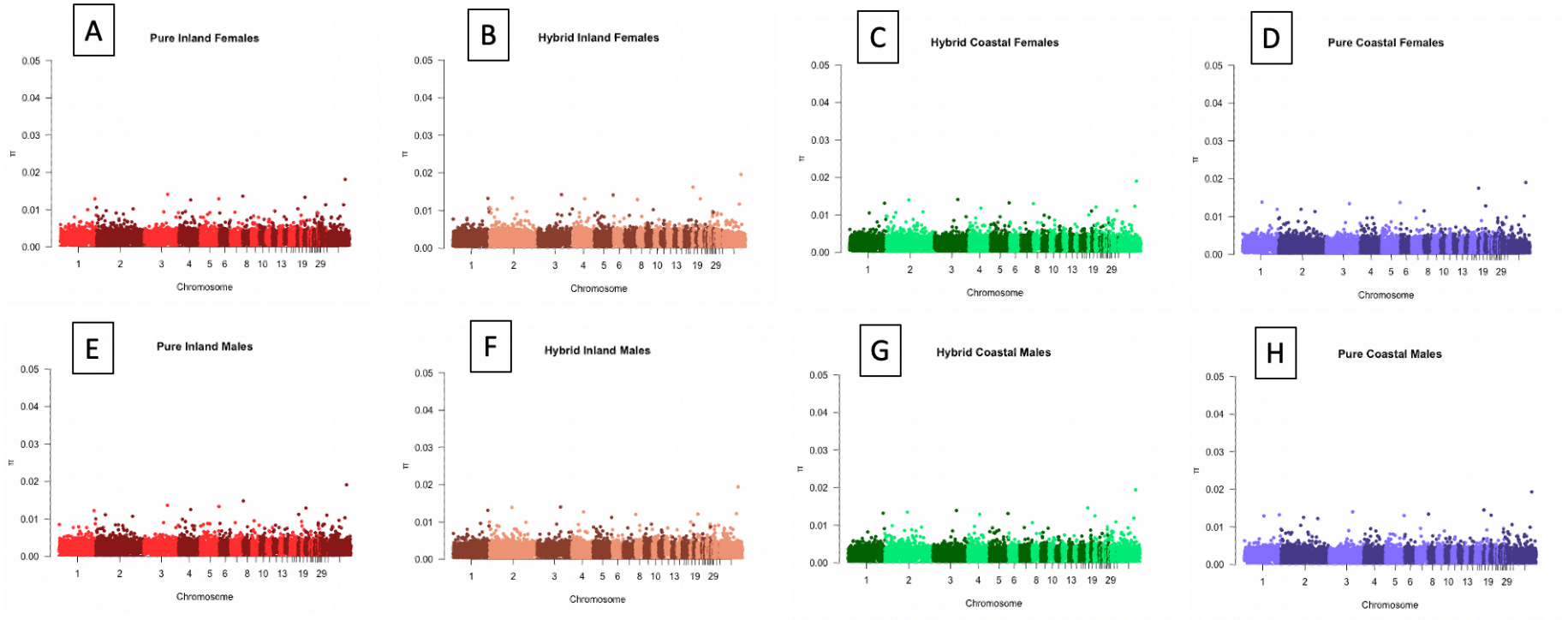


Figure S4: P_i values for markers that map to ZF autosomes (excluding 1A) and chromosome Z a) pure inland females; b) hybrid inland females; c) hybrid coastal females; d) pure coastal females; e) pure inland males; f) hybrid inland males; g) hybrid coastal males; and h) pure coastal males.

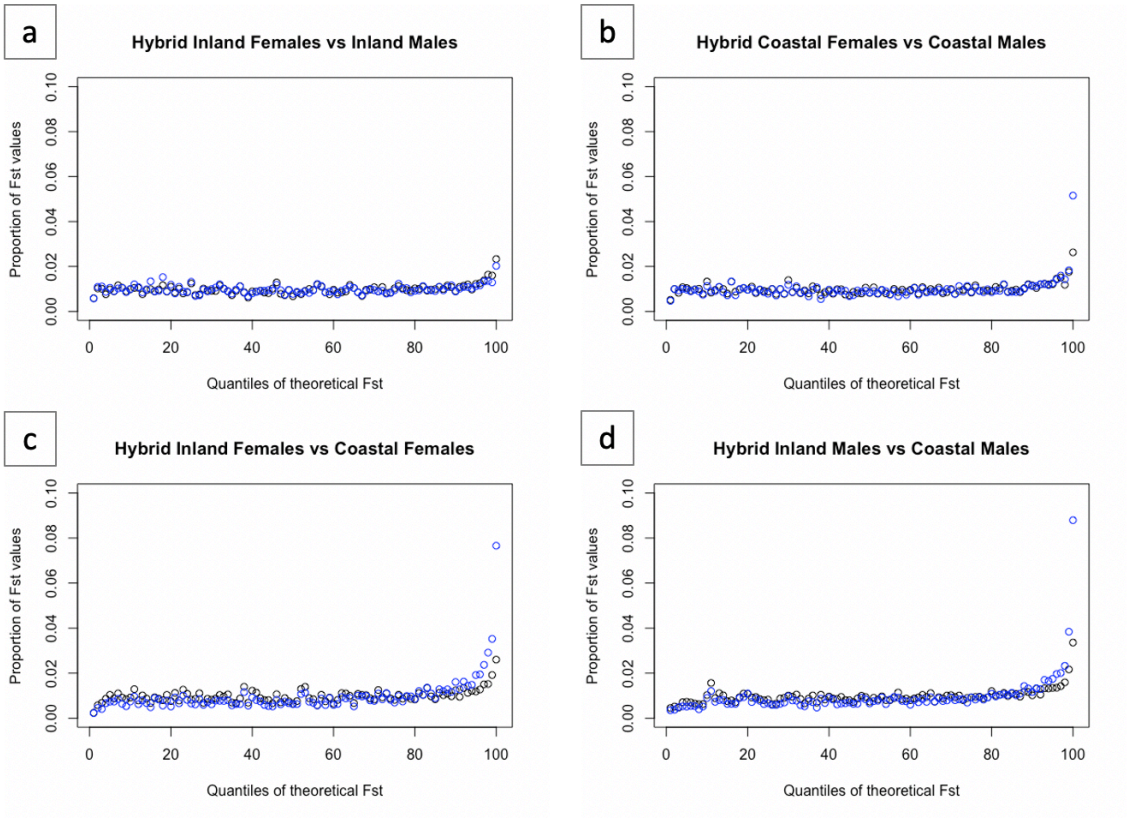


Figure S5: Observed (blue) and expected under permutation (black) distributions of F_{ST} for a) hybrid inland females and hybrid inland males; b) hybrid coastal females and hybrid coastal males; c) hybrid inland females and hybrid coastal females; and d) hybrid inland males and hybrid coastal males.

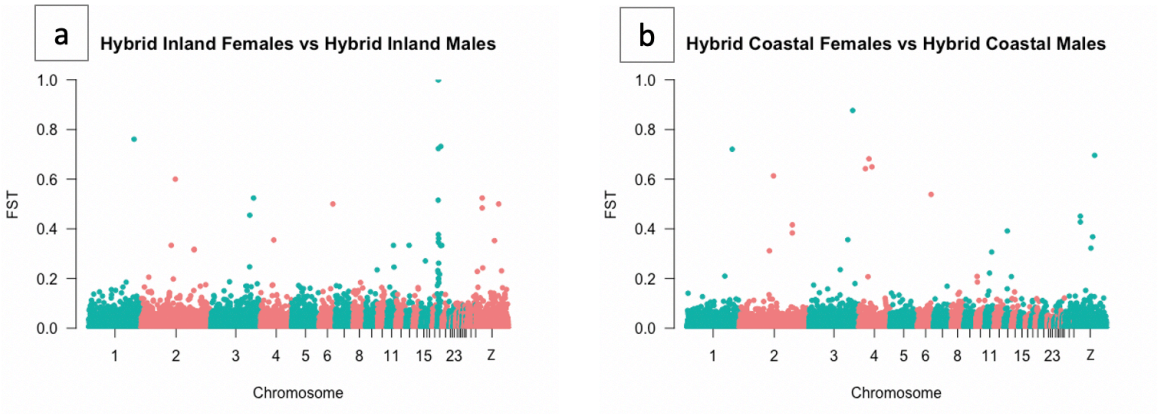
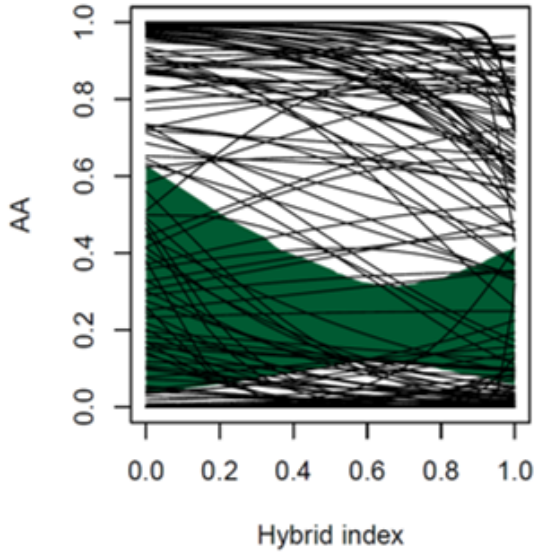
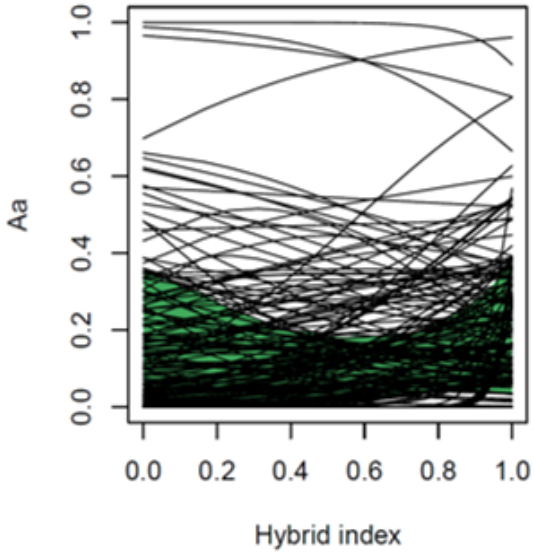
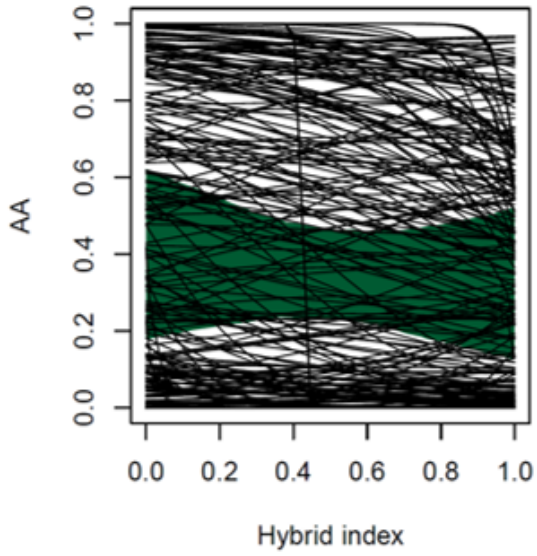


Figure S6: Differentiation between sexes within mitolineages for markers mapping to ZF autosomes (excluding 1A) and chromosome Z. Plots show F_{ST} values for a) hybrid inland and b) hybrid coastal populations.

Figure S7: Correlation of F_{ST} value with proportion of missing data for a) hybrid inland females vs hybrid coastal females; b) hybrid inland males vs hybrid coastal males; c) pure inland females vs pure coastal females; d) pure inland males vs pure coastal males; e) hybrid inland females vs hybrid inland males; and f) hybrid coastal females vs hybrid coastal males. F_{ST} values are for markers that map to autosomes (excluding 1A) or the Z chromosome on ZF.


AA
0.0
0.2
0.4
0.6
0.8
1.0
Hybrid index


Aa
0.0
0.2
0.4
0.6
0.8
1.0
Hybrid index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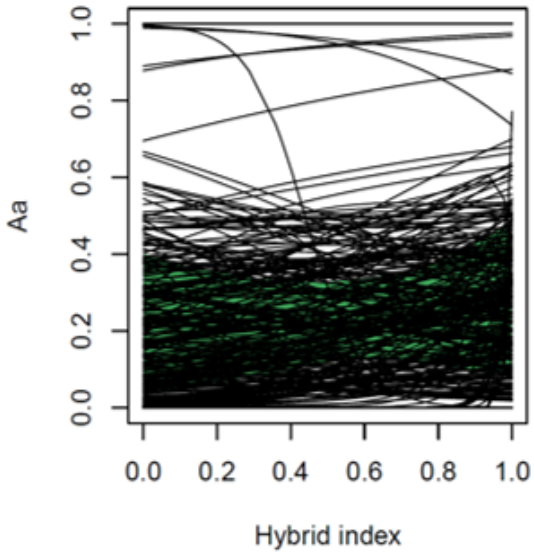
0.2
0.4
0.6
0.8
1.0
Hybrid index


Aa
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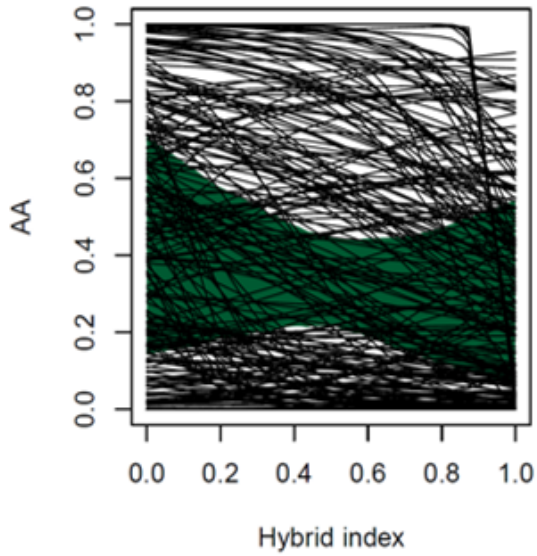
0.2
0.4
0.6
0.8
1.0
Hybrid index


AA
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0.2
0.4
0.6
0.8
1.0
Hybrid index

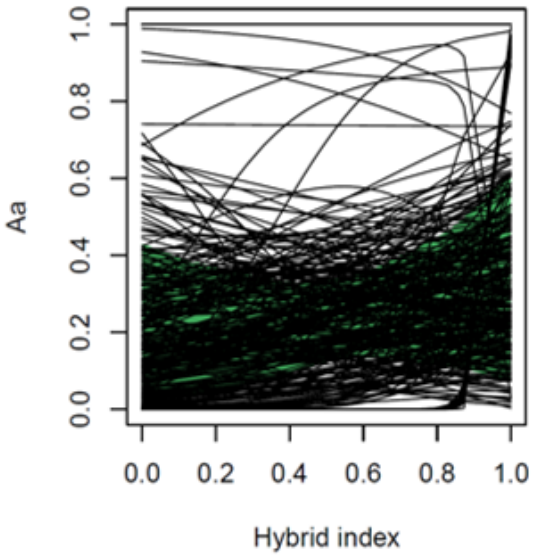
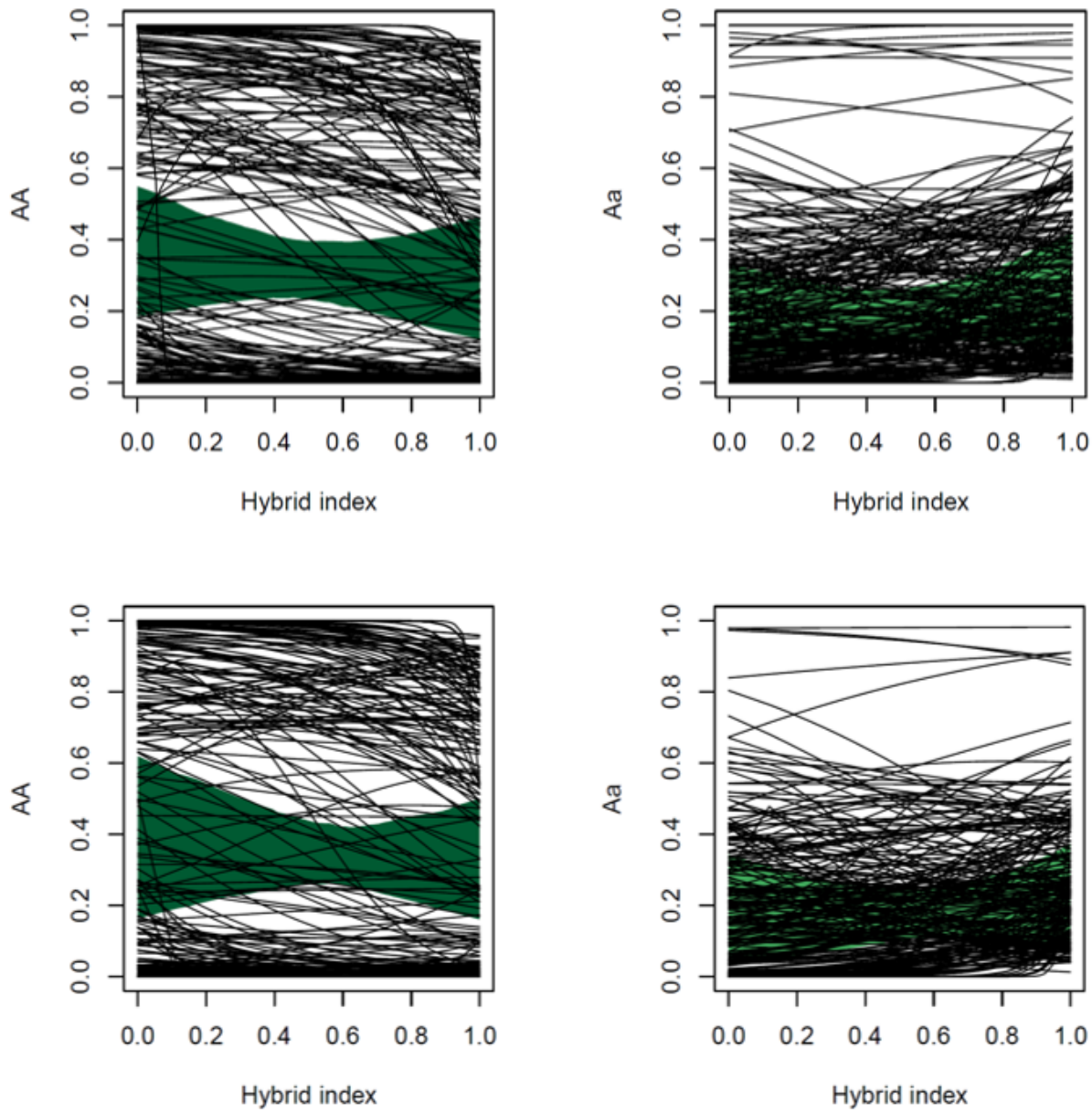

Aa
0.0
0.2
0.4
0.6
0.8
1.0
Hybrid index

Figure S8: Genomic clines of autosomal loci in females. Alleles have been filtered for missing data and linkage. The dark green shaded area represents the neutral expectation of homozygous genotypes in admixed populations based on allele frequencies in the parental populations, while the medium green shaded area represents the neutral expectation of heterozygous genotypes. In order to increase plot readability, loci are grouped into multiple displays.



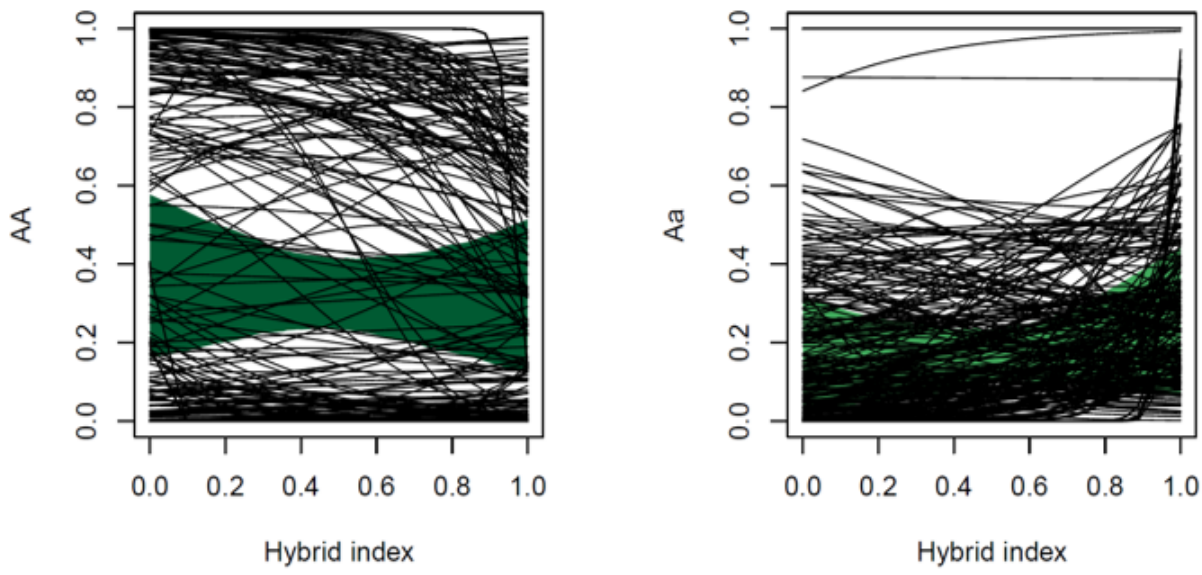


Figure S9: Genomic clines of autosomal loci in males. Alleles have been filtered for missing data and linkage. The dark green shaded area represents the neutral expectation of homozygous genotypes in admixed populations based on allele frequencies in the parental populations, while the medium green shaded area represents the neutral expectation of heterozygous genotypes. In order to increase plot readability, loci are grouped into multiple displays.

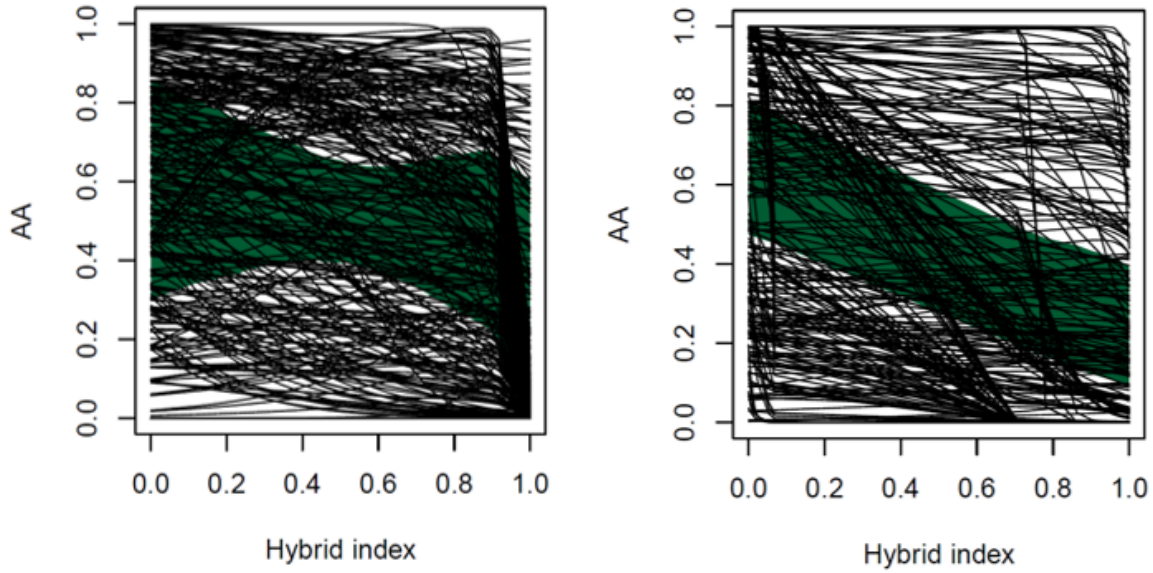


Figure S10: Genomic clines of Z-behaving loci that map to ZF chromosome 1A in females. The dark green shaded area represents the neutral expectation of homozygous genotypes in admixed populations based on allele frequencies in the parental populations, while the medium green shaded area represents the neutral expectation of heterozygous genotypes. In order to increase plot readability, loci are grouped into multiple displays.

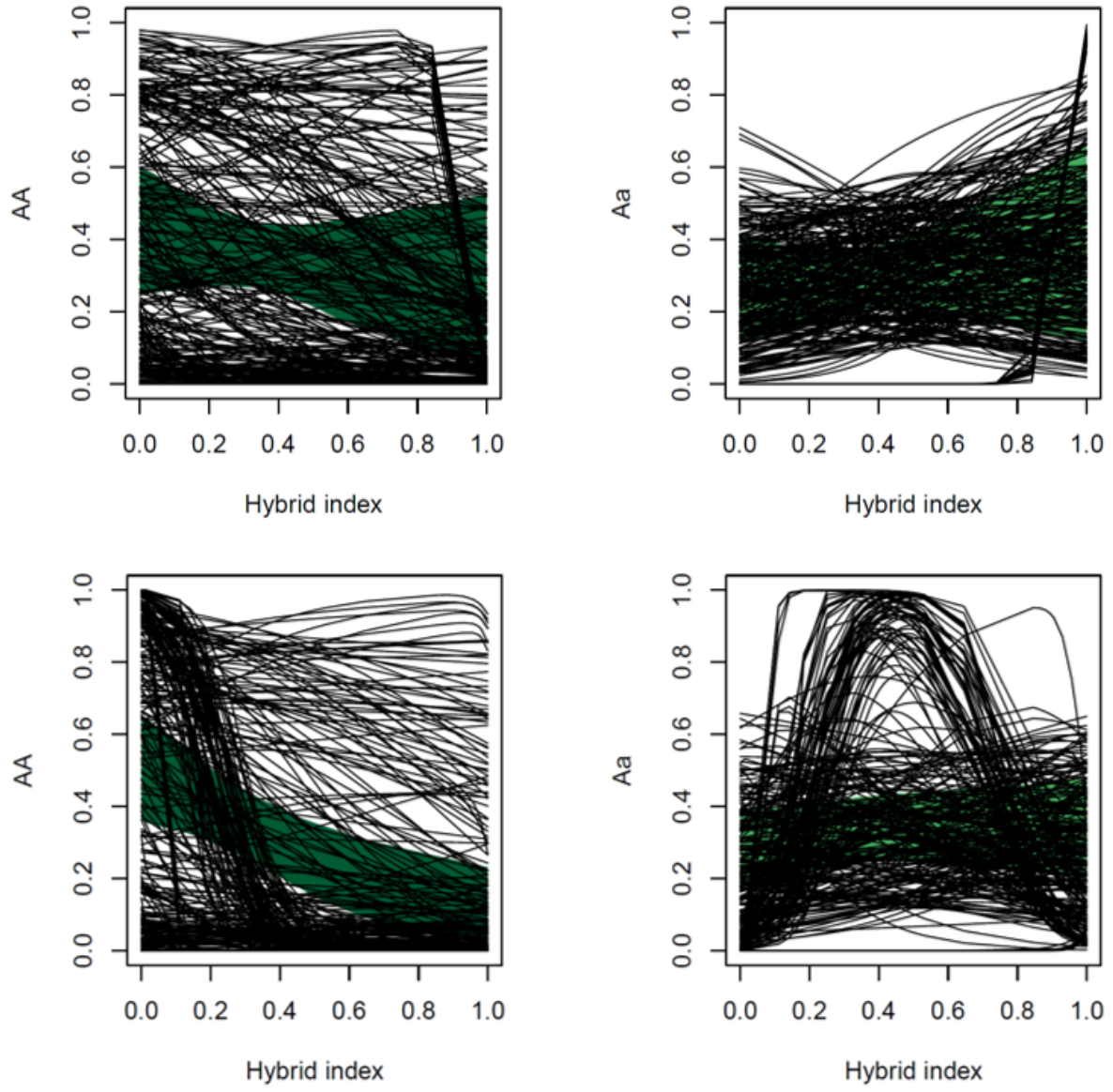


Figure S11: Genomic clines of Z-behaving loci that map to ZF chromosome 1A in males. The dark green shaded area represents the neutral expectation of homozygous genotypes in admixed populations based on allele frequencies in the parental populations, while the medium green shaded area represents the neutral expectation of heterozygous genotypes. In order to increase plot readability, loci are grouped into multiple displays.