**Supplemental Figures**

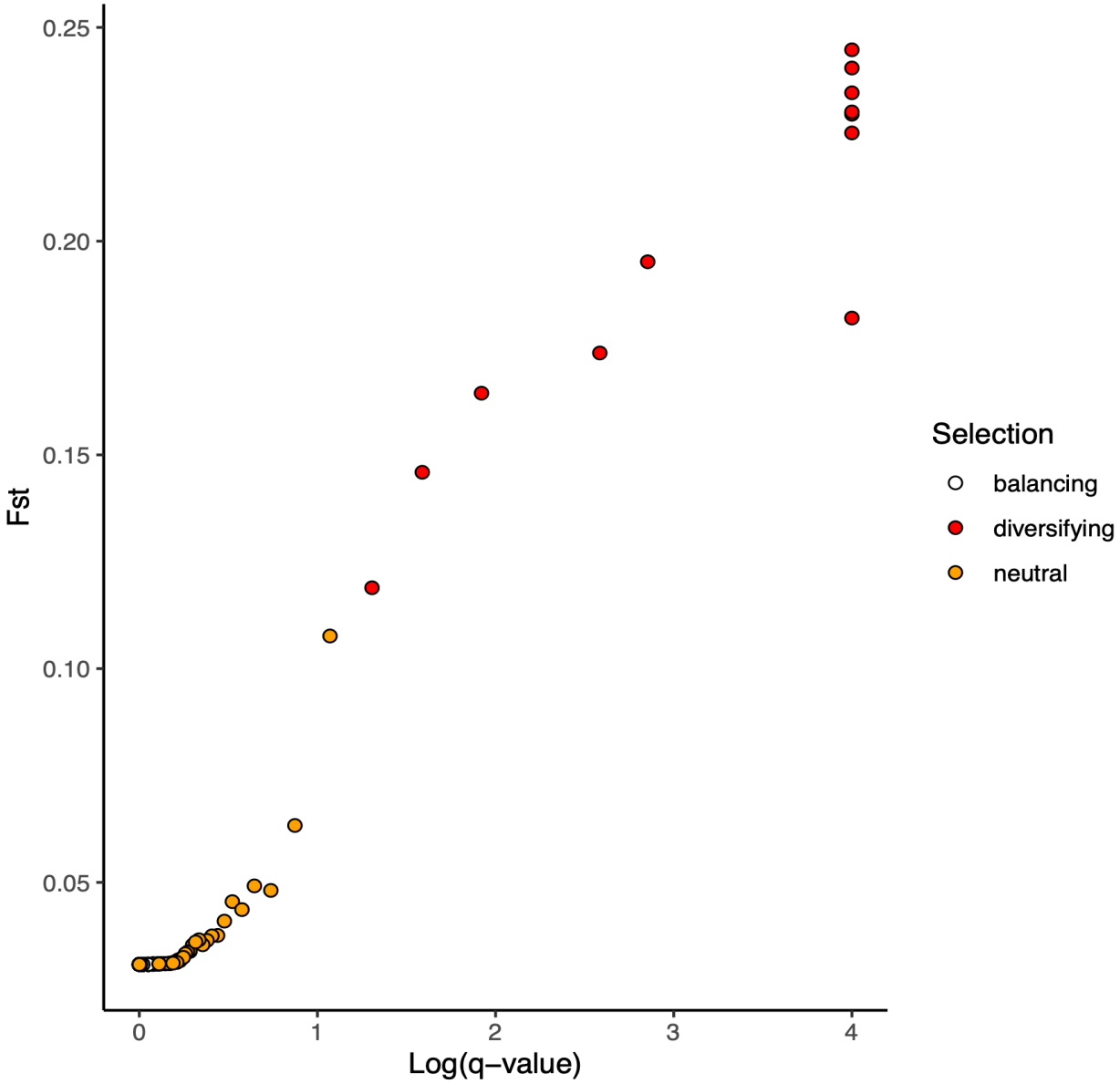


**Figure S1.** Bayescan plot showing outlier loci under diversifying selection

95% HPD Interval low

| | | Source (j) | | | | | |
|---|---|---|---|---|---|---|---|
| | | DC673 | GC852 | KC405 | MC294 | MC297 | MC344 |
| Sink (i) | DC673 | 0.924 | 0.000 | 0.000 | 0.000 | 0.000 | 0.000 |
| | GC852 | 0.050 | 0.809 | 0.000 | 0.000 | 0.000 | 0.000 |
| | KC405 | 0.123 | 0.000 | 0.726 | 0.000 | 0.000 | 0.000 |
| | MC294 | 0.000 | 0.167 | 0.000 | 0.667 | 0.000 | 0.000 |
| | MC297 | 0.028 | 0.071 | 0.000 | 0.000 | 0.667 | 0.000 |
| | MC344 | 0.145 | 0.012 | 0.001 | 0.000 | 0.000 | 0.667 |

95% HPD Interval high

| | | Source (j) | | | | | |
|---|---|---|---|---|---|---|---|
| | | DC673 | GC852 | KC405 | MC294 | MC297 | MC344 |
| Sink (i) | DC673 | 0.988 | 0.025 | 0.025 | 0.025 | 0.025 | 0.025 |
| | GC852 | 0.149 | 0.916 | 0.029 | 0.029 | 0.029 | 0.029 |
| | KC405 | 0.236 | 0.031 | 0.833 | 0.031 | 0.031 | 0.031 |
| | MC294 | 0.076 | 0.295 | 0.049 | 0.715 | 0.049 | 0.049 |
| | MC297 | 0.153 | 0.212 | 0.051 | 0.051 | 0.718 | 0.051 |
| | MC344 | 0.269 | 0.105 | 0.063 | 0.041 | 0.040 | 0.707 |

**Figure S2. 95%** HPD confidence intervals of migration rates (*m*) estimated in BayesAss

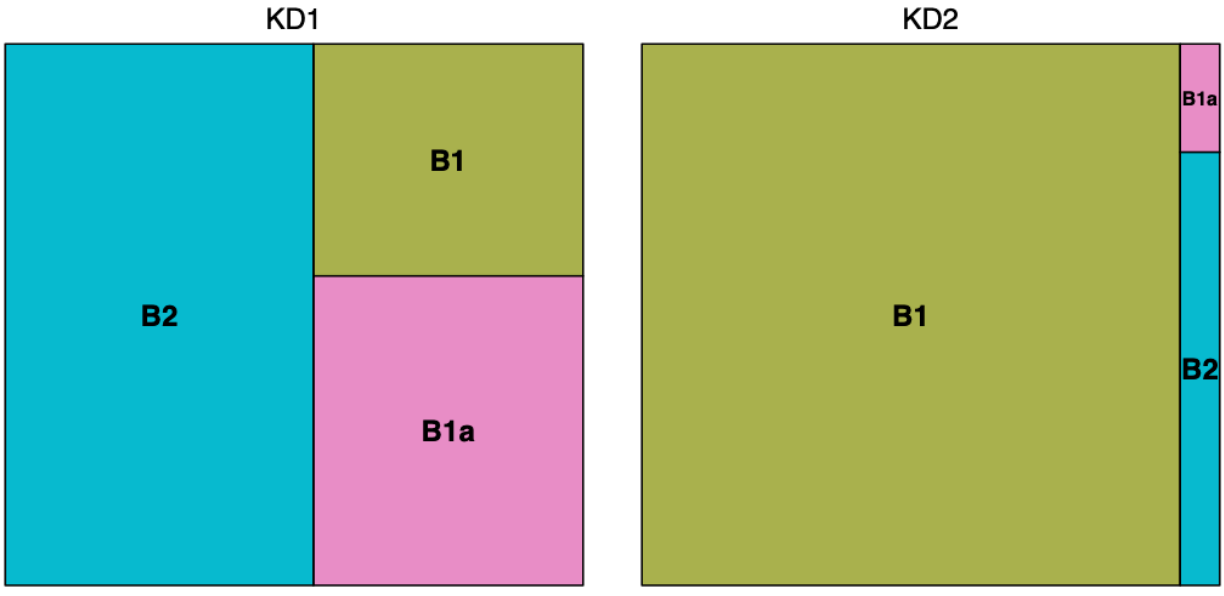


**Figure S3. Treemap showing the correspondence between** mitochondrial haplotypes defined by Doughty et al. (2014) and genomic clusters identified by DAPC analyses (left: $K_{D1}$ and right: $K_{D2}$). The size of each rectangle is proportional to the number of individuals with a given mitochondrial haplotype.