

## S6 Table. Predictive check of the adjusted 2M demo-genomic model.

Genetic summary statistics derived from the observed probabilistic SFS vs. their prediction under the adjusted 2M scenario.

		<b>Observed</b>	<b>Predicted (mean)</b>	<b>Predicted (CI95% low)<sup>g</sup></b>	<b>Predicted (IC95% up)</b>
<b>Singlet<sup>a</sup></b>	North	<b>6.48E-04</b>	6.94E-04	6.83E-04	7.06E-04
	South	<b>7.54E-04</b>	7.39E-04	7.30E-04	7.48E-04
<b>Private<sup>b</sup></b>	North	<b>1.30E-03</b>	1.32E-03	1.31E-03	1.34E-03
	South	<b>1.52E-03</b>	1.53E-03	1.51E-03	1.54E-03
<b>Shared<sup>c</sup></b>		<b>1.18E-03</b>	1.14E-03	1.13E-03	1.15E-03
<b>S<sup>d</sup></b>	North	<b>2.47E-03</b>	2.46E-03	2.45E-03	2.48E-03
	South	<b>2.69E-03</b>	2.66E-03	2.64E-03	2.68E-03
<b>H<sub>s</sub><sup>e</sup></b>	North	<b>0.2272304</b>	0.2266182	0.225501	0.2277367
	South	<b>0.1882863</b>	0.1892305	0.1883246	0.1901639
<b>F<sub>ST</sub><sup>f</sup></b>		<b>0.1599501</b>	0.1598357	0.1577013	0.1619462

<sup>a</sup> Proportion of singleton SNPs (over all sites).

<sup>b</sup> Proportion of private SNPs (over all sites).

<sup>c</sup> Proportion of shared SNPs (over all sites).

<sup>d</sup> Proportion of SNPs over all sites.

<sup>e</sup> Expected heterozygosity.

<sup>f</sup> Wright's  $F_{ST}$ .

<sup>g</sup> Lower bound of the confidence interval at 95%.