

## Additional file 4

### Tables

**Table S4 Association between variant effect and cline steepness (v).** Variant effects predicted by VEP (McLaren et al. [61]) were tested for their effect on v using a linear regression ( $y \sim x$ ) where  $y = \ln(v)$  and  $x = \text{effect category}$ . The table shows number of variants (n) and the effect estimate for  $\ln(v)$ . Higher estimated  $\ln(v)$  indicates stronger evidence for restricted introgression.

	<i>European taurine SI</i>		<i>African taurine SI</i>	
Effect category	n	Estimated $\ln(v) \pm \text{SE}$	n	Estimated $\ln(v) \pm \text{SE}$
3_prime_UTR_variant	21,234	0.17 $\pm$ 0.009	15,232	-0.59 $\pm$ 0.013
5_prime_UTR_variant	3,207	0.19 $\pm$ 0.023	2,329	-0.54 $\pm$ 0.032
downstream_gene_variant	10,059	0.20 $\pm$ 0.013	7,281	-0.62 $\pm$ 0.018
intergenic_variant	4,873,627	0.19 $\pm$ 0.001	3,492,131	-0.64 $\pm$ 0.001
intron_variant	2,634,414	0.21 $\pm$ 0.001	1,912,359	-0.60 $\pm$ 0.001
missense_variant	10,968	0.25 $\pm$ 0.013	7,825	-0.58 $\pm$ 0.017
non_coding_transcript_exon_variant	4,735	0.22 $\pm$ 0.019	3,535	-0.53 $\pm$ 0.026
splice_polypyrimidine_tract_variant	3,575	0.19 $\pm$ 0.022	2,594	-0.59 $\pm$ 0.030
splice_region_variant	1,899	0.18 $\pm$ 0.030	1,356	-0.55 $\pm$ 0.042
synonymous_variant	14,161	0.22 $\pm$ 0.011	10,501	-0.58 $\pm$ 0.015
upstream_gene_variant	5,500	0.20 $\pm$ 0.018	3,943	-0.60 $\pm$ 0.025