Table S3: Potentially damaging SNPs found in regions with strong evidence of non-neutral evolution.

Chr	Position	rsID	AA	SIFT	Gene	ENSEMBL	CEU	YRI
1	11090916	rs12711521	D371Y	$p = 0.04$	MASP2	ENST00000400897	0.86	0.1
1	248084909	rs34508376	M197R	p=0.01	OR2T8	ENST00000319968	0.64	0.05
1	248113026	rs10888281	Y289*	—	OR2L8	ENST00000357191	0.94	0.25
1	248129240	rs4478844	V203M	p=0.00	OR2AK2	ENST00000366480	0.67	0.05
2	27424636	rs1395	S481F	p=0.05	SLC5A6	ENST00000310574	0.74	0.16
5	138720108	rs11242462	W45*	—	SLC23A1	ENST00000508270	0.29	0.80
5	177378959	rs7720935	*splice*	—	RP11-423H2.3.1	ENST00000507072	0.94	0.40
8	16043667	rs435815	*splice*	—	MSR1	ENST00000445506	0.11	0.54
19	44932972	rs1434579	G662R	p=0.04	ZNF229	ENST00000291187	0.40	0.04
20	2291722	rs6048066	I163L	p=0.01	TGM3	ENST00000420960	0.006	0.49

SNPs found in the top 0.2% of XP-SFselect regions, deemed damaging by SIFT (nonsynonymous, with p-value ≤ 0.05) or SnpEff (nonsense or splice-site variant). Frequencies in CEU and YRI populations also shown. Splice site donor mutations are indicated by *splice* in the AA column.