Table S2: The top 40 non-overlapping regions identified genome-wide by XP-SFselect.

Chr	Position (Mb)	Max XP-SFselect	Genes	Study
X	66.10-66.56	4.38657		
12	88.24-88.36	4.38258		
X	99.00-99.16	4.34082	LOC442459	Frazer *et al.* (2007)
8	52.67-52.82	4.31338	PXDNL, PCMTD1	(Frazer *et al.* 2007)
X	35.27-35.38	4.27039		
12	123.61-123.78	4.20905	MPHOSPH9, C12orf65, CDK2AP1, SBNO1	
12	88.90-89.00	4.20736	KITLG	(Pickrell *et al.* 2009)
4	148.54-148.79	4.19501	TMEM184C, PRMT10, ARHGAP10	
10	100.78-100.94	4.19111	HPSE2	
10	31.47-31.55	4.14863		(Chen *et al.* 2010)
X	110.08-110.37	4.13684	PAK3	(Sabeti *et al.* 2007); (Frazer *et al.* 2007)
2	13.69-13.90	4.12967		
11	105.99-106.22	4.11825		
X	80.24-80.38	4.10921	HMGN5	
13	71.98-72.12	4.10127	DACH1	
4	52.88-53.14	4.09292	LRRC66, SGCB, SPATA18	
2	150.39-150.49	4.07069	MMADHC	
15	44.29-44.39	4.05108	FRMD5	
1	142.66-142.87	4.04074		
11	40.22-40.32	4.02215	LRRC4C	
16	15.14-15.30	4.01629	NTAN1, RRN3, MIR3180-4	
2	97.68-97.85	3.99585	FAHD2B, ANKRD36	
4	159.35-159.44	3.9884		
2	104.76-104.83	3.97891		
17	73.30-73.44	3.96581	GRB2, MIR3678	
20	60.66-60.73	3.93865	LSM14B, PSMA7, SS18L1	
4	41.96-42.11	3.93681	TMEM33, DCAF4L1, SLC30A9	
15	28.19-28.27	3.91923	OCA2	(Chen *et al.* 2010)
1	158.15-158.24	3.89804	CD1D, CD1A	
13	41.39-41.54	3.8952	SUGT1P3, ELF1	
1	100.67-100.77	3.88985	DBT,RTCD1, MIR553	
X	65.54-65.91	3.87444	EDA2R	
17	53.79-53.87	3.87161	TMEM100, PCTP	
18	30.40-30.58	3.86989	C18orf34	
1	248.07-248.16	3.86911	OR2T8, OR2L13, OR2L81, OR2AK2, OR2L1P	
16	79.80-79.88	3.86909		(Chen *et al.* 2010); (Frazer *et al.* 2007)
X	108.00-108.15	3.82083		
18	15.04-15.15	3.81846		(Frazer *et al.* 2007)
2	167.50-167.60	3.81693		
X	74.42-74.72	3.80593	UPRT, ZDHHC15	

The right-most column specifies the studies, if any, in which the corresponding regions were reported as showing signal of selection.