

Table S1: Critical values of $|\text{SS-H12}|$ and $|\text{SS-G123}|$ generated from 10^6 neutral replicates (identical for either statistic), used to assign p -values to empirical top candidates across 1000 Genomes Project [Auton et al., 2015] sampled population pairs.

Population	SS-H12	SS-G123
CEU-GBR	0.6151618	0.4017583
CEU-GIH	0.2755997	0.0863085
CEU-JPT	0.2800871	0.0717914
CEU-YRI	0.3924851	0.1569262
LWK-YRI	0.2065271	0.0395899
GIH-YRI	0.2701381	0.0582839
JPT-YRI	0.2408978	0.0450692
JPT-GIH	0.1956585	0.0351749
JPT-KHV	0.4114621	0.1926581

Table S2: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the Central and Western European CEU and GBR populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	ZRANB3	2	0.6138516	0.005253369	2.0×10 ⁻⁶	1
2	SLC12A1	15	0.5964931	0.007102656	4.0×10 ⁻⁶	1
3	R3HDM1	2	0.5907587	0.005776011	4.0×10 ⁻⁶	1
4	DARS	2	0.5605804	0.012398870	1.6×10 ⁻⁵	1
5	MCM6	2	0.5604343	0.010608921	1.6×10 ⁻⁵	1
6	LCT	2	0.5097962	0.009314534	8.9×10 ⁻⁵	1
7	LOC100507600	2	0.5097962	0.009314534	8.9×10 ⁻⁵	1
8	AC093391.2	2	0.4822492	0.008069683	3.14×10 ⁻⁴	1
9	RAB3GAP1	2	0.4788360	0.016863242	3.48×10 ⁻⁴	1
10	UBXN4	2	0.4709547	0.008006012	4.45×10 ⁻⁴	1
11	BCAS3	17	0.4342505	0.024135621	1.43×10 ⁻³	1
12	KAT6B	10	0.4063248	0.010954181	3.11×10 ⁻³	1
13	PPM1D	17	0.4043315	0.013758902	3.27×10 ⁻³	1
14	MYO9A	15	0.3919436	0.014969493	4.55×10 ⁻³	1
15	FAM149B1	10	0.3841613	0.013332285	5.56×10 ⁻³	1
16	ZNF546	19	0.3824392	0.053683499	5.80×10 ⁻³	1
17	MAP3K19	2	0.3807448	0.175652783	6.06×10 ⁻³	3
18	PRMT9	4	0.3782229	0.030300365	6.48×10 ⁻³	1
19	KITLG	12	0.3772852	0.023892213	6.64×10 ⁻³	1
20	MLL3	9	0.3756959	0.085799301	6.92×10 ⁻³	1
21	LAMA3	18	0.3749289	0.327190136	7.04×10 ⁻³	3
22	TMEM116	12	0.3716065	0.023778920	7.60×10 ⁻³	1
23	KMT2A	11	0.3684665	0.034335416	8.22×10 ⁻³	1
24	ADRBK2	22	0.3648397	0.029916410	8.96×10 ⁻³	1
25	ACMSD	2	0.3628647	0.058329766	9.40×10 ⁻³	1
26	CCNT2-AS1	2	0.3628647	0.058329766	9.40×10 ⁻³	1
27	PLAGL2	20	0.3588937	0.315722448	1.03×10 ⁻²	3
28	DIRC3	2	0.3560424	0.021817335	1.10×10 ⁻²	1
29	POLN	4	0.3534160	0.101220872	1.16×10 ⁻²	1
30	AC005592.1	5	0.3518146	0.018718715	1.21×10 ⁻²	1
31	PRKDC	8	0.3491810	0.262222086	1.28×10 ⁻²	4
32	BVES-AS1	6	0.3486739	0.277810748	1.30×10 ⁻²	3
33	PVRL3-AS1	3	0.3470860	0.045461392	1.34×10 ⁻²	1
34	ECD	10	0.3464802	0.201522514	1.36×10 ⁻²	3
35	CLK3	15	0.3446577	0.022635883	1.42×10 ⁻²	1
36	C4orf22	4	0.3430783	0.034845848	1.47×10 ⁻²	1
37	EPN2	17	0.3405261	0.099649864	1.56×10 ⁻²	1
38	NR6A1	9	0.3385413	0.412935867	1.63×10 ⁻²	4
39	CUX2	12	0.3370432	0.466497502	1.68×10 ⁻²	4
40	MIR548O2	8	0.3367965	0.120149341	1.69×10 ⁻²	1

Table S3: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the Western European CEU and South Asian GIH populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	<i>SLC12A1</i>	15	0.4687775	0.01928730	< 10 ⁻⁶	1
2	<i>PRMT9</i>	4	0.3592987	0.02846361	< 10 ⁻⁶	1
3	<i>ZNF546</i>	19	0.3543484	0.01440592	< 10 ⁻⁶	1
4	<i>RNU6-28P</i>	15	0.3328967	0.14154431	< 10 ⁻⁶	2
5	<i>PPIP5K1</i>	15	0.3328967	0.14154431	< 10 ⁻⁶	2
6	<i>CUX2</i>	12	0.3244117	0.01913100	< 10 ⁻⁶	1
7	<i>RUNX1T1</i>	8	0.3239634	0.02660100	< 10 ⁻⁶	1
8	<i>HDAC1</i>	1	0.3000066	0.02793417	< 10 ⁻⁶	1
9	<i>KIAA0947</i>	5	0.2985386	0.09924729	< 10 ⁻⁶	1
10	<i>LINC00478</i>	21	0.2978392	0.03430060	< 10 ⁻⁶	1
11	<i>P4HA1</i>	10	0.2940247	0.02457430	< 10 ⁻⁶	1
12	<i>BCAS3</i>	17	0.2928297	0.01725947	< 10 ⁻⁶	1
13	<i>HS2ST1</i>	1	0.2925146	0.02843537	< 10 ⁻⁶	1
14	<i>USP37</i>	2	0.2841170	0.26690328	1.0×10 ⁻⁶	2
15	<i>EXOC6B</i>	2	0.2839310	0.03022084	1.0×10 ⁻⁶	1
16	<i>TRMT11</i>	6	0.2823063	0.09785459	1.0×10 ⁻⁶	1
17	<i>MYO9A</i>	15	0.2807536	0.02811068	1.0×10 ⁻⁶	1
18	<i>TFAP2E</i>	1	0.2788397	0.19573284	1.0×10 ⁻⁶	2
19	<i>PPM1D</i>	17	0.2780563	0.01891077	1.0×10 ⁻⁶	1
20	<i>METTL25</i>	12	0.2774661	0.02117459	1.0×10 ⁻⁶	1
21	<i>CCDC178</i>	18	0.2756744	0.08725221	1.0×10 ⁻⁶	1
22	<i>USP25</i>	21	0.2754877	0.01694058	2.0×10 ⁻⁶	1
23	<i>KIAA0825</i>	5	0.2741257	0.04268183	2.0×10 ⁻⁶	1
24	<i>CELSR3</i>	3	0.2722865	0.04291467	2.0×10 ⁻⁶	1
25	<i>LOC100188947</i>	10	0.2716363	0.03509440	2.0×10 ⁻⁶	1
26	<i>HECTD2</i>	10	0.2716363	0.03509440	2.0×10 ⁻⁶	1
27	<i>GNA14</i>	9	0.2715994	0.03925893	2.0×10 ⁻⁶	1
28	<i>DNAH6</i>	2	0.2696911	0.02045324	3.0×10 ⁻⁶	1
29	<i>FBN1</i>	15	0.2693902	0.04027675	4.0×10 ⁻⁶	1
30	<i>LYRM7</i>	5	0.2668650	0.04480839	5.0×10 ⁻⁶	1
31	<i>KCNQ5</i>	6	0.2646294	0.01399575	6.0×10 ⁻⁶	1
32	<i>OSBPL9</i>	1	0.2636045	0.04380993	6.0×10 ⁻⁶	1
33	<i>OTUD6B</i>	8	0.2635197	0.16525761	6.0×10 ⁻⁶	2
34	<i>C8orf44-SGK3</i>	8	0.2629975	0.02040620	6.0×10 ⁻⁶	1
35	<i>SGK3</i>	8	0.2629975	0.02040620	6.0×10 ⁻⁶	1
36	<i>FAM69A</i>	1	0.2622265	0.06324476	7.0×10 ⁻⁶	1
37	<i>UNC5D</i>	8	0.2610994	0.03623753	7.0×10 ⁻⁶	1
38	<i>KITLG</i>	12	0.2607259	0.05006524	8.0×10 ⁻⁶	1
39	<i>PSMB2</i>	1	0.2596058	0.02267442	1.0×10 ⁻⁵	1
40	<i>MAP2K5</i>	15	0.2586188	0.33523411	1.1×10 ⁻⁵	2

Table S4: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the Western European CEU and East Asian JPT populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	<i>SPIDR</i>	8	0.4841559	0.13789164	< 10 ⁻⁶	2
2	<i>MRAP2</i>	6	0.3577093	0.05691596	< 10 ⁻⁶	1
3	<i>BVES-AS1</i>	6	0.3550710	0.35553104	< 10 ⁻⁶	2
4	<i>BCAS3</i>	17	0.3003483	0.01124741	< 10 ⁻⁶	1
5	<i>RUNX1T1</i>	8	0.2911443	0.01286325	1.0×10 ⁻⁶	1
6	<i>DIRC3</i>	2	0.2846624	0.02342707	1.0×10 ⁻⁶	1
7	<i>LINC00478</i>	21	0.2845995	0.04674953	1.0×10 ⁻⁶	1
8	<i>CASC4</i>	15	0.2817489	0.28631390	1.0×10 ⁻⁶	2
9	<i>ZNF546</i>	19	0.2775094	0.01187426	2.0×10 ⁻⁶	1
10	<i>C16orf70</i>	16	0.2759704	0.15519459	2.0×10 ⁻⁶	2
11	<i>CUX2</i>	12	0.2711322	0.07265968	3.0×10 ⁻⁶	1
12	<i>C4orf22</i>	4	0.2676980	0.04613398	3.0×10 ⁻⁶	1
13	<i>HDAC1</i>	1	0.2613163	0.01923077	4.0×10 ⁻⁶	1
14	<i>EXOC6B</i>	2	0.2550717	0.02907524	6.0×10 ⁻⁶	1
15	<i>NCAPG</i>	4	0.2540412	0.47979575	6.0×10 ⁻⁶	3
16	<i>DENND1A</i>	9	0.2502850	0.03534972	8.0×10 ⁻⁶	1
17	<i>LRRC29</i>	16	0.2498870	0.01559488	8.0×10 ⁻⁶	1
18	<i>ZNF780B</i>	19	0.2453862	0.01894595	1.2×10 ⁻⁵	1
19	<i>C12orf4</i>	12	0.2413896	0.05908229	1.2×10 ⁻⁵	1
20	<i>MRPS11</i>	15	0.2379901	0.04262436	1.6×10 ⁻⁵	1
21	<i>USP25</i>	21	0.2354323	0.03030037	1.7×10 ⁻⁵	1
22	<i>EPB41L1</i>	20	0.2351457	0.05879280	1.7×10 ⁻⁵	1
23	<i>LCORL</i>	4	0.2345143	0.49844508	1.7×10 ⁻⁵	3
24	<i>NR6A1</i>	9	0.2344024	0.41874136	1.7×10 ⁻⁵	3
25	<i>FOXP2</i>	7	0.2320563	0.06177330	1.8×10 ⁻⁵	1
26	<i>PRKDC</i>	8	0.2316219	0.02158066	1.8×10 ⁻⁵	1
27	<i>CELSR3</i>	3	0.2282892	0.03061224	2.0×10 ⁻⁵	1
28	<i>C2CD5</i>	12	-0.2282773	0.40252754	2.0×10 ⁻⁵	1
29	<i>LOC100130987</i>	11	0.2266829	0.03103294	2.1×10 ⁻⁵	1
30	<i>EPS8</i>	12	0.2262990	0.03675885	2.1×10 ⁻⁵	1
31	<i>C5orf42</i>	5	0.2258946	0.23871429	2.2×10 ⁻⁵	2
32	<i>SGCD</i>	5	0.2248583	0.04520540	2.3×10 ⁻⁵	1
33	<i>PHF20</i>	20	0.2247397	0.03888761	2.3×10 ⁻⁵	1
34	<i>KIAA1324L</i>	7	0.2246612	0.05278810	2.3×10 ⁻⁵	1
35	<i>SPIN1</i>	9	0.2244122	0.02988283	2.5×10 ⁻⁵	1
36	<i>KCND2</i>	7	0.2238942	0.03960568	2.6×10 ⁻⁵	1
37	<i>DNAH6</i>	2	0.2228843	0.04768519	2.6×10 ⁻⁵	1
38	<i>CCBL2</i>	1	0.2220159	0.38969612	2.6×10 ⁻⁵	2
39	<i>DBT</i>	1	0.2211143	0.02032617	2.8×10 ⁻⁵	1
40	<i>CLCF1</i>	11	0.2209926	0.03304531	2.8×10 ⁻⁵	1

Table S5: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the Central European CEU and West African YRI populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	<i>RP11-554F20.1</i>	9	0.4040332	0.011758418	1.0×10 ⁻⁶	1
2	<i>SPRED3</i>	19	0.3495697	0.008281479	2.0×10 ⁻⁶	1
3	<i>CASC4</i>	15	0.3448822	0.018257129	3.0×10 ⁻⁶	1
4	<i>KIAA0825</i>	5	0.3445359	0.023951998	3.0×10 ⁻⁶	1
5	<i>ERLIN2</i>	8	0.3313498	0.020023226	7.0×10 ⁻⁶	1
6	<i>DEDD</i>	1	0.3260732	0.060157676	8.0×10 ⁻⁶	1
7	<i>PHKB</i>	16	0.3236909	0.034041921	1.0×10 ⁻⁵	1
8	<i>CPNE1</i>	20	0.3176717	0.029957092	1.3×10 ⁻⁵	1
9	<i>NNT</i>	5	0.3171650	0.017917746	1.3×10 ⁻⁵	1
10	<i>ATP6V1A</i>	3	0.3132683	0.142126360	1.7×10 ⁻⁵	1
11	<i>DDHD2</i>	8	0.3089642	0.058367643	2.1×10 ⁻⁵	1
12	<i>GLRX2</i>	1	0.3053542	0.233674193	2.7×10 ⁻⁵	2
13	<i>DANCR</i>	4	0.3039967	0.040780000	2.8×10 ⁻⁵	1
14	<i>PIGV</i>	1	0.3036567	0.025363186	2.9×10 ⁻⁵	1
15	<i>USP46</i>	4	0.2995560	0.079339450	3.3×10 ⁻⁵	1
16	<i>RALGAPA2</i>	20	0.2991084	0.025897884	3.4×10 ⁻⁵	1
17	<i>GRIK5</i>	19	0.2981553	0.029953502	3.5×10 ⁻⁵	1
18	<i>PLEKHA8</i>	7	0.2975913	0.086839818	3.6×10 ⁻⁵	1
19	<i>MIR548H3</i>	6	0.2961103	0.037196110	3.7×10 ⁻⁵	1
20	<i>PAWR</i>	12	-0.2904662	0.440909091	4.3×10 ⁻⁵	1
21	<i>ENTHD1</i>	22	0.2886265	0.085943221	4.4×10 ⁻⁵	1
22	<i>GRIA2</i>	4	0.2846541	0.121846119	4.8×10 ⁻⁵	1
23	<i>DKK2</i>	4	0.2823235	0.022479797	5.4×10 ⁻⁵	1
24	<i>C2orf69</i>	2	0.2793307	0.144744191	6.1×10 ⁻⁵	1
25	<i>ATF2</i>	2	0.2722884	0.046899637	7.2×10 ⁻⁵	1
26	<i>PPAPDC1B</i>	8	0.2713097	0.048928393	7.5×10 ⁻⁵	1
27	<i>CNNM2</i>	10	0.2699270	0.042492595	8.0×10 ⁻⁵	1
28	<i>KIAA1244</i>	6	0.2590398	0.023619457	1.21×10 ⁻⁴	1
29	<i>GABRA4</i>	4	0.2587261	0.254620730	1.23×10 ⁻⁴	3
30	<i>SLC4A10</i>	2	0.2583449	0.033468250	1.25×10 ⁻⁴	1
31	<i>TGFBR1</i>	9	0.2583162	0.097024952	1.25×10 ⁻⁴	1
32	<i>CDK6</i>	7	0.2580913	0.019577085	1.26×10 ⁻⁴	1
33	<i>PHF20</i>	20	0.2560493	0.024958371	1.29×10 ⁻⁴	1
34	<i>SEMA3C</i>	7	0.2490896	0.038386148	1.65×10 ⁻⁴	1
35	<i>SPG11</i>	15	0.2474120	0.038898738	1.74×10 ⁻⁴	1
36	<i>EXOC4</i>	7	0.2460852	0.068343293	1.84×10 ⁻⁴	1
37	<i>ABHD17B</i>	9	0.2443668	0.067033633	1.99×10 ⁻⁴	1
38	<i>SYT1</i>	12	0.2427578	0.071155043	2.09×10 ⁻⁴	1
39	<i>ITFG1</i>	16	0.2415787	0.064650360	2.18×10 ⁻⁴	1
40	<i>WHSC1L1</i>	8	0.2411594	0.091198255	2.20×10 ⁻⁴	1

Table S6: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the East African LWK and West African YRI populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	<i>GRIK5</i>	19	0.4257102	0.04258992	< 10 ⁻⁶	1
2	<i>RGS18</i>	1	0.3987118	0.05121985	< 10 ⁻⁶	1
3	<i>RP11-554F20.1</i>	9	0.3888096	0.03007582	< 10 ⁻⁶	1
4	<i>SPIDR</i>	8	0.3877237	0.47505841	< 10 ⁻⁶	2
5	<i>KIAA0825</i>	5	0.3792208	0.06521739	< 10 ⁻⁶	1
6	<i>ARID1A</i>	1	0.3696765	0.05678665	< 10 ⁻⁶	1
7	<i>PPAPDC1B</i>	8	0.3677224	0.02213772	< 10 ⁻⁶	1
8	<i>MIR548AE2</i>	16	0.3602984	0.01837085	< 10 ⁻⁶	1
9	<i>LONP2</i>	16	0.3602984	0.01837085	< 10 ⁻⁶	1
10	<i>NNT</i>	5	0.3578539	0.01703393	< 10 ⁻⁶	1
11	<i>ATF2</i>	2	0.3566302	0.10607443	< 10 ⁻⁶	1
12	<i>CASC4</i>	15	0.3498801	0.02336532	< 10 ⁻⁶	1
13	<i>PIGV</i>	1	0.3469070	0.01980346	< 10 ⁻⁶	1
14	<i>BRIP1</i>	17	0.3454437	0.05989424	< 10 ⁻⁶	1
15	<i>FLJ46284</i>	8	0.3335889	0.34581390	< 10 ⁻⁶	2
16	<i>FER1L6</i>	8	0.3319929	0.36210558	< 10 ⁻⁶	2
17	<i>FER1L6-AS1</i>	8	0.3319929	0.36210558	< 10 ⁻⁶	2
18	<i>PSMD14</i>	2	0.3302383	0.21238349	< 10 ⁻⁶	2
19	<i>EHBP1</i>	2	0.3301406	0.04231345	< 10 ⁻⁶	1
20	<i>SYT1</i>	12	0.3268402	0.02131281	< 10 ⁻⁶	1
21	<i>MAGI3</i>	1	0.3234881	0.03887382	< 10 ⁻⁶	1
22	<i>DDHD2</i>	8	0.3230242	0.03319609	< 10 ⁻⁶	1
23	<i>TCF4</i>	18	0.3221087	0.04095041	< 10 ⁻⁶	1
24	<i>FGFR1</i>	8	0.3219437	0.11190389	< 10 ⁻⁶	1
25	<i>DANCR</i>	4	0.3217441	0.02757380	< 10 ⁻⁶	1
26	<i>DDX19B</i>	16	0.3201310	0.05961249	< 10 ⁻⁶	1
27	<i>PHKB</i>	16	0.3199744	0.14290567	< 10 ⁻⁶	2
28	<i>RRN3P3</i>	16	0.3192156	0.12601099	< 10 ⁻⁶	2
29	<i>ANK3</i>	10	0.3168877	0.41411632	< 10 ⁻⁶	2
30	<i>CNNM2</i>	10	0.3157693	0.04354118	< 10 ⁻⁶	1
31	<i>DKK2</i>	4	0.3148797	0.02507450	< 10 ⁻⁶	1
32	<i>UCHL5</i>	1	0.3148279	0.23817198	< 10 ⁻⁶	2
33	<i>GRIA4</i>	11	0.3093281	0.06513791	< 10 ⁻⁶	1
34	<i>HEMGN</i>	9	0.3087151	0.03213826	< 10 ⁻⁶	1
35	<i>RNLS</i>	10	0.3086794	0.05394666	< 10 ⁻⁶	1
36	<i>TMC1</i>	9	0.3059124	0.05989460	< 10 ⁻⁶	1
37	<i>FAM172A</i>	5	0.3046091	0.36377588	< 10 ⁻⁶	2
38	<i>NANS</i>	9	0.3022555	0.14421537	< 10 ⁻⁶	2
39	<i>SPRED3</i>	19	0.3006544	0.01691324	< 10 ⁻⁶	1
40	<i>CCDC178</i>	18	0.3005286	0.06074190	< 10 ⁻⁶	1

Table S7: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the South Asian GIH and West African YRI populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	<i>RP11-554F20.1</i>	9	0.3771248	0.011770772	< 10 ⁻⁶	1
2	<i>ATP6V1A</i>	3	0.3639640	0.099682934	< 10 ⁻⁶	1
3	<i>DDHD2</i>	8	0.3602952	0.013720551	< 10 ⁻⁶	1
4	<i>CDK6</i>	7	0.3578316	0.071008263	< 10 ⁻⁶	1
5	<i>KIAA0825</i>	5	0.3525741	0.027694560	< 10 ⁻⁶	1
6	<i>SYT1</i>	12	0.3492609	0.012266522	< 10 ⁻⁶	1
7	<i>PSMD14</i>	2	0.3412286	0.135670252	< 10 ⁻⁶	1
8	<i>WHSC1L1</i>	8	0.3283306	0.043503219	< 10 ⁻⁶	1
9	<i>PHKB</i>	16	0.3232317	0.042223410	< 10 ⁻⁶	1
10	<i>NNT</i>	5	0.3223767	0.017984343	< 10 ⁻⁶	1
11	<i>PPAPDC1B</i>	8	0.3196440	0.032132443	< 10 ⁻⁶	1
12	<i>FBXW4</i>	10	0.3196397	0.031138790	< 10 ⁻⁶	1
13	<i>CASC4</i>	15	0.3150844	0.009182066	< 10 ⁻⁶	1
14	<i>PLEKHA8</i>	7	0.3142622	0.083226858	< 10 ⁻⁶	1
15	<i>PIGV</i>	1	0.3115851	0.031716870	< 10 ⁻⁶	1
16	<i>ZNF451</i>	6	0.3085450	0.029623301	< 10 ⁻⁶	1
17	<i>MIR548AE2</i>	16	0.3065668	0.025105816	< 10 ⁻⁶	1
18	<i>LONP2</i>	16	0.3065668	0.025105816	< 10 ⁻⁶	1
19	<i>SLC4A10</i>	2	0.3062220	0.024992628	< 10 ⁻⁶	1
20	<i>DEDD</i>	1	0.2978007	0.043610857	< 10 ⁻⁶	1
21	<i>USP46</i>	4	0.2930645	0.043401898	< 10 ⁻⁶	1
22	<i>ATF2</i>	2	0.2890980	0.042325935	< 10 ⁻⁶	1
23	<i>C10orf76</i>	10	0.2791604	0.241890959	< 10 ⁻⁶	2
24	<i>GRIK5</i>	19	0.2789334	0.026200519	< 10 ⁻⁶	1
25	<i>FRYL</i>	4	0.2770178	0.124549768	< 10 ⁻⁶	1
26	<i>ABHD17B</i>	9	0.2761729	0.019974819	1.0×10 ⁻⁶	1
27	<i>CPNE1</i>	20	0.2749730	0.053890867	1.0×10 ⁻⁶	1
28	<i>RALGAPA2</i>	20	0.2742919	0.031716870	1.0×10 ⁻⁶	1
29	<i>COL7A1</i>	3	0.2710832	0.030527862	1.0×10 ⁻⁶	1
30	<i>PAWR</i>	12	-0.2695280	0.500033047	2.0×10 ⁻⁶	1
31	<i>ERLIN2</i>	8	0.2694367	0.032420110	2.0×10 ⁻⁶	1
32	<i>TYW5</i>	2	0.2662606	0.079070667	2.0×10 ⁻⁶	1
33	<i>KCNIP2</i>	10	0.2654300	0.188650307	2.0×10 ⁻⁶	2
34	<i>ENTHD1</i>	22	0.2648954	0.059516605	2.0×10 ⁻⁶	1
35	<i>CADM1</i>	11	0.2608986	0.130764109	2.0×10 ⁻⁶	1
36	<i>NIT1</i>	1	0.2589696	0.060503570	2.0×10 ⁻⁶	1
37	<i>GRIA4</i>	11	0.2580788	0.177060197	2.0×10 ⁻⁶	2
38	<i>CAMK2G</i>	10	0.2552114	0.145238523	3.0×10 ⁻⁶	1
39	<i>DANCR</i>	4	0.2530703	0.034185402	3.0×10 ⁻⁶	1
40	<i>PLBD2</i>	12	0.2530187	0.025798687	3.0×10 ⁻⁶	1

Table S8: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the East Asian JPT and West African YRI populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	<i>RP11-554F20.1</i>	9	0.3931760	0.106986532	< 10 ⁻⁶	1
2	<i>HEMGN</i>	9	0.3775289	0.024845674	< 10 ⁻⁶	1
3	<i>ATP6V1A</i>	3	0.3612693	0.187013598	< 10 ⁻⁶	3
4	<i>PSMD14</i>	2	0.3478155	0.120552739	< 10 ⁻⁶	1
5	<i>KIAA0825</i>	5	0.3462541	0.042399755	< 10 ⁻⁶	1
6	<i>ENTHD1</i>	22	0.3457729	0.024417586	< 10 ⁻⁶	1
7	<i>UCHL5</i>	1	0.3410178	0.296451830	< 10 ⁻⁶	2
8	<i>EHBP1</i>	2	0.3296022	0.040707208	< 10 ⁻⁶	1
9	<i>DDHD2</i>	8	0.3232796	0.047658115	< 10 ⁻⁶	1
10	<i>GRIK5</i>	19	0.3201569	0.022160505	< 10 ⁻⁶	1
11	<i>CPNE1</i>	20	0.3095707	0.020447795	< 10 ⁻⁶	1
12	<i>CASC4</i>	15	0.3082424	0.008452639	< 10 ⁻⁶	1
13	<i>PIGV</i>	1	0.3080457	0.019652483	< 10 ⁻⁶	1
14	<i>GRIA4</i>	11	0.2877642	0.076983380	< 10 ⁻⁶	1
15	<i>FBXW4</i>	10	0.2812126	0.032817676	< 10 ⁻⁶	1
16	<i>USP46</i>	4	0.2778346	0.050033190	< 10 ⁻⁶	1
17	<i>PPAPDC1B</i>	8	0.2770218	0.067697788	< 10 ⁻⁶	1
18	<i>CSMD3</i>	8	0.2767410	0.025265593	< 10 ⁻⁶	1
19	<i>AUTS2</i>	7	0.2739576	0.048349205	< 10 ⁻⁶	1
20	<i>WDPCP</i>	2	0.2732119	0.160070411	< 10 ⁻⁶	2
21	<i>NNT</i>	5	0.2719657	0.011428056	< 10 ⁻⁶	1
22	<i>WDR75</i>	2	0.2713068	0.477669319	< 10 ⁻⁶	3
23	<i>MAST2</i>	1	0.2710749	0.113317105	< 10 ⁻⁶	1
24	<i>MPHOSPH9</i>	12	-0.2671972	0.500226740	1.0×10 ⁻⁶	1
25	<i>ATF2</i>	2	0.2661096	0.050953776	1.0×10 ⁻⁶	1
26	<i>MIR548H3</i>	6	0.2657886	0.044716955	1.0×10 ⁻⁶	1
27	<i>DKK2</i>	4	0.2654977	0.020832637	1.0×10 ⁻⁶	1
28	<i>RALGAPA2</i>	20	0.2634601	0.018345166	1.0×10 ⁻⁶	1
29	<i>PLEKHA8</i>	7	0.2629720	0.065646654	1.0×10 ⁻⁶	1
30	<i>ABCA17P</i>	16	0.2627850	0.029987576	1.0×10 ⁻⁶	1
31	<i>ERLIN2</i>	8	0.2612417	0.051206414	1.0×10 ⁻⁶	1
32	<i>LOC644554</i>	19	0.2599085	0.046211073	1.0×10 ⁻⁶	1
33	<i>EXOC6B</i>	2	-0.2591453	0.400289321	1.0×10 ⁻⁶	1
34	<i>ARID1A</i>	1	0.2586148	0.012315850	1.0×10 ⁻⁶	1
35	<i>AC016582.2</i>	19	0.2575930	0.184115407	1.0×10 ⁻⁶	2
36	<i>USP31</i>	16	0.2542219	0.048774295	1.0×10 ⁻⁶	1
37	<i>WDR87</i>	19	0.2539212	0.052847194	1.0×10 ⁻⁶	1
38	<i>NCK1</i>	3	0.2533815	0.105668649	1.0×10 ⁻⁶	1
39	<i>MIR548AE2</i>	16	0.2530337	0.012070399	1.0×10 ⁻⁶	1
40	<i>LONP2</i>	16	0.2530337	0.012070399	1.0×10 ⁻⁶	1

Table S9: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the East Asian JPT and South Asian GIH populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	<i>RUNX1T1</i>	8	0.4474761	0.013112088	< 10 ⁻⁶	1
2	<i>P4HTM</i>	3	0.4140126	0.004079071	< 10 ⁻⁶	1
3	<i>TMTC2</i>	12	0.3420391	0.025676243	< 10 ⁻⁶	1
4	<i>EXOC6B</i>	2	0.3326926	0.019515562	< 10 ⁻⁶	1
5	<i>RNF121</i>	11	0.3155150	0.030228890	< 10 ⁻⁶	1
6	<i>BCAS3</i>	17	0.3120734	0.020570739	< 10 ⁻⁶	1
7	<i>HELZ</i>	17	0.3098360	0.111157784	< 10 ⁻⁶	1
8	<i>ADAMTS6</i>	5	0.3076773	0.407162839	< 10 ⁻⁶	3
9	<i>ORC2</i>	2	0.3055687	0.018545289	< 10 ⁻⁶	1
10	<i>CUX2</i>	12	0.3012879	0.114717964	< 10 ⁻⁶	1
11	<i>APPBP2</i>	17	0.2943597	0.018755226	< 10 ⁻⁶	1
12	<i>ZNF546</i>	19	0.2903935	0.026486969	< 10 ⁻⁶	1
13	<i>RP11-682N22.1</i>	7	0.2866539	0.025520555	< 10 ⁻⁶	1
14	<i>LINC00478</i>	21	0.2768036	0.051422319	< 10 ⁻⁶	1
15	<i>DBT</i>	1	0.2754919	0.019618240	< 10 ⁻⁶	1
16	<i>SLC44A1</i>	9	0.2751889	0.027447371	< 10 ⁻⁶	1
17	<i>DPH5</i>	1	0.2734798	0.063964153	< 10 ⁻⁶	1
18	<i>MBOAT2</i>	2	0.2732935	0.022872389	< 10 ⁻⁶	1
19	<i>DR1</i>	1	0.2719058	0.117944872	< 10 ⁻⁶	1
20	<i>ZNF780B</i>	19	0.2710979	0.027775374	< 10 ⁻⁶	1
21	<i>PRPF40B</i>	12	0.2704860	0.009056569	< 10 ⁻⁶	1
22	<i>LOC100188947</i>	10	0.2693331	0.091476681	< 10 ⁻⁶	1
23	<i>HECTD2</i>	10	0.2693331	0.091476681	< 10 ⁻⁶	1
24	<i>USP32</i>	17	0.2668435	0.030825697	< 10 ⁻⁶	1
25	<i>NF1</i>	17	0.2650127	0.446732585	< 10 ⁻⁶	2
26	<i>RP11-53O19.1</i>	5	0.2645393	0.266671012	< 10 ⁻⁶	2
27	<i>HDAC1</i>	1	0.2631774	0.038364271	< 10 ⁻⁶	1
28	<i>ABCB1</i>	7	0.2624699	0.032952008	< 10 ⁻⁶	1
29	<i>RUNDC3B</i>	7	0.2624699	0.032952008	< 10 ⁻⁶	1
30	<i>ADK</i>	10	0.2592457	0.395106884	< 10 ⁻⁶	2
31	<i>CNNM4</i>	2	0.2583070	0.084782739	< 10 ⁻⁶	1
32	<i>DDB1</i>	11	0.2571627	0.012680739	< 10 ⁻⁶	1
33	<i>XXYL1</i>	3	0.2563662	0.022777439	< 10 ⁻⁶	1
34	<i>COMMD3-BMI1</i>	10	0.2549803	0.029266377	< 10 ⁻⁶	1
35	<i>BMI1</i>	10	0.2549803	0.029266377	< 10 ⁻⁶	1
36	<i>PRKAR2A</i>	3	0.2543194	0.029957868	< 10 ⁻⁶	1
37	<i>USP25</i>	21	0.2500539	0.039729584	< 10 ⁻⁶	1
38	<i>ATP6V0D1</i>	16	0.2497646	0.015632539	< 10 ⁻⁶	1
39	<i>GPC5</i>	13	0.2484834	0.088347003	< 10 ⁻⁶	1
40	<i>SPATA31D3</i>	9	0.2473412	0.031572111	< 10 ⁻⁶	1

Table S10: Top 40 SS-H12 sweep candidates at RNA- and protein-coding genes shared between the East Asian JPT and Southeast Asian KHV populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-H12	H2/H1	<i>P</i> -value	Inferred ν
1	<i>EXOC6B</i>	2	0.5264721	0.006772899	< 10^{-6}	1
2	<i>SPAG6</i>	10	0.4968819	0.006607293	< 10^{-6}	1
3	<i>P4HTM</i>	3	0.4842239	0.003800968	< 10^{-6}	1
4	<i>RUNX1T1</i>	8	0.4762151	0.012305665	< 10^{-6}	1
5	<i>C11orf49</i>	11	0.4727695	0.068502981	< 10^{-6}	1
6	<i>RP11-696N14.1</i>	4	0.4622633	0.047157537	< 10^{-6}	1
7	<i>EXD2</i>	14	0.4488191	0.012119385	< 10^{-6}	1
8	<i>BCL2L1</i>	20	0.4334603	0.011505081	1.0×10^{-6}	1
9	<i>SPIDR</i>	8	0.4323823	0.121946971	1.0×10^{-6}	2
10	<i>TMEM33</i>	4	0.4163834	0.013441981	1.0×10^{-6}	1
11	<i>HMCN1</i>	1	0.4139426	0.433746297	1.0×10^{-6}	2
12	<i>TRMT11</i>	6	0.4132626	0.008565410	1.0×10^{-6}	1
13	<i>CSPP1</i>	8	0.4131015	0.370451157	1.0×10^{-6}	2
14	<i>BCL7C</i>	16	0.4116698	0.017374975	1.0×10^{-6}	1
15	<i>AMBRA1</i>	11	0.4078245	0.026064925	3.0×10^{-6}	1
16	<i>ADH1A</i>	4	0.4068527	0.054411554	3.0×10^{-6}	1
17	<i>LINC00536</i>	8	0.4047586	0.319893205	4.0×10^{-6}	2
18	<i>TRUB1</i>	10	0.3960872	0.012888666	8.0×10^{-6}	1
19	<i>SLC25A20</i>	3	0.3951800	0.306872504	1.0×10^{-5}	2
20	<i>NOVA1</i>	14	0.3937128	0.296371985	1.1×10^{-5}	2
21	<i>UBE3A</i>	15	0.3881960	0.421256404	1.3×10^{-5}	2
22	<i>RAD51B</i>	14	0.3877928	0.020655194	1.3×10^{-5}	1
23	<i>C2orf66</i>	2	0.3847481	0.011183304	1.4×10^{-5}	1
24	<i>ARIH2</i>	3	0.3835818	0.011305712	1.5×10^{-5}	1
25	<i>FBXO4</i>	5	0.3830810	0.060543858	1.5×10^{-5}	1
26	<i>PURA</i>	5	0.3821055	0.043743931	1.5×10^{-5}	1
27	<i>LOC100188947</i>	10	0.3819967	0.126665136	1.5×10^{-5}	2
28	<i>HECTD2</i>	10	0.3819967	0.126665136	1.5×10^{-5}	2
29	<i>ZNF282</i>	7	0.3789665	0.013728048	1.5×10^{-5}	1
30	<i>SPATS2</i>	12	0.3779965	0.018103713	1.7×10^{-5}	1
31	<i>DPH6</i>	15	0.3765334	0.016983232	1.7×10^{-5}	1
32	<i>ARIH2OS</i>	3	0.3750646	0.011348289	1.9×10^{-5}	1
33	<i>KCNT2</i>	1	0.3748550	0.093205290	1.9×10^{-5}	1
34	<i>GPHN</i>	14	0.3744098	0.478385232	1.9×10^{-5}	2
35	<i>PHYHIPL</i>	10	0.3737335	0.020357412	2.2×10^{-5}	1
36	<i>CCDC18</i>	1	0.3732415	0.124636275	2.2×10^{-5}	2
37	<i>ABHD17B</i>	9	0.3730153	0.059902525	2.2×10^{-5}	1
38	<i>IFT81</i>	12	0.3714945	0.220865456	2.2×10^{-5}	2
39	<i>FHOD1</i>	16	0.3711776	0.013442943	2.2×10^{-5}	1
40	<i>SYNJ1</i>	21	0.3678745	0.211024411	2.5×10^{-5}	2

Table S11: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the Central and Western European CEU and GBR populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	ZRANB3	2	0.4036658	0.01992548	2.0×10 ⁻⁶	1
2	R3HDM1	2	0.4001688	0.03074343	3.0×10 ⁻⁶	1
3	DARS	2	0.3939288	0.04113419	4.0×10 ⁻⁶	1
4	SLC12A1	15	0.3494603	0.03411498	1.2×10 ⁻⁵	1
5	MCM6	2	0.3425388	0.04473161	1.8×10 ⁻⁵	1
6	AC093391.2	2	0.2944935	0.04039653	8.0×10 ⁻⁵	1
7	LCT	2	0.2864912	0.02114967	1.00×10 ⁻⁴	1
8	UBXN4	2	0.2740023	0.02600907	1.47×10 ⁻⁴	1
9	LOC100507600	2	0.2706452	0.02798382	1.68×10 ⁻⁴	1
10	RAB3GAP1	2	0.2506534	0.06432749	3.48×10 ⁻⁴	1
11	KMT2A	11	0.2041324	0.10449343	1.73×10 ⁻³	1
12	BCAS3	17	0.1859900	0.09758002	3.05×10 ⁻³	1
13	PPM1D	17	0.1800870	0.07265290	3.63×10 ⁻³	1
14	UNC5D	8	0.1780280	0.39270231	3.86×10 ⁻³	3
15	KAT6B	10	0.1707262	0.05624037	4.80×10 ⁻³	1
16	TMEM116	12	0.1651175	0.18743961	5.66×10 ⁻³	1
17	PRKDC	8	0.1628838	0.14634787	6.00×10 ⁻³	1
18	MYO9A	15	0.1598302	0.06094675	6.56×10 ⁻³	1
19	ACMSD	2	0.1572425	0.15455562	7.09×10 ⁻³	1
20	CCNT2-AS1	2	0.1572425	0.15455562	7.09×10 ⁻³	1
21	ZNF546	19	0.1563353	0.28800989	7.27×10 ⁻³	2
22	C4orf22	4	0.1548723	0.17300057	7.57×10 ⁻³	1
23	COL5A2	2	0.1531146	0.07664563	7.97×10 ⁻³	1
24	KITLG	12	0.1507429	0.09976581	8.55×10 ⁻³	1
25	MRPS31	13	0.1404181	0.66863672	1.17×10 ⁻²	6
26	LAMA3	18	0.1397230	0.41137771	1.19×10 ⁻²	3
27	AGO3	1	0.1389525	0.18726491	1.22×10 ⁻²	1
28	RALGAPA1	14	0.1372367	0.10397132	1.28×10 ⁻²	1
29	RALGAPA1P	14	0.1372367	0.10397132	1.28×10 ⁻²	1
30	SYT1	12	0.1368878	0.18617021	1.29×10 ⁻²	1
31	GFRA2	8	0.1354658	0.51413190	1.35×10 ⁻²	4
32	CNBD2	20	0.1345655	0.10348771	1.39×10 ⁻²	1
33	PIK3R4	3	0.1315715	0.31331699	1.51×10 ⁻²	2
34	CDK6	7	0.1302599	0.19966667	1.57×10 ⁻²	1
35	DIRC3	2	0.1301000	0.13940724	1.58×10 ⁻²	1
36	GNA14	9	0.1297811	0.11111111	1.59×10 ⁻²	1
37	EXOC5	14	0.1292055	0.27603759	1.62×10 ⁻²	1
38	SPATA5L1	15	0.1291950	0.50091659	1.62×10 ⁻²	4
39	AC005592.1	5	0.1283393	0.05882353	1.66×10 ⁻²	1
40	TMEM163	2	0.1271473	0.27047556	1.72×10 ⁻²	1

Table S12: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the Western European CEU and South Asian GIH populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	SLC12A1	15	0.24849898	0.07039983	< 10 ⁻⁶	1
2	RUNX1T1	8	0.16146633	0.14275121	< 10 ⁻⁶	1
3	ZNF546	19	0.13139163	0.31590106	< 10 ⁻⁶	2
4	RNU6-28P	15	0.12412153	0.49297753	< 10 ⁻⁶	2
5	PPIP5K1	15	0.12412153	0.49297753	< 10 ⁻⁶	2
6	PRMT9	4	0.12362840	0.12395833	< 10 ⁻⁶	1
7	BCAS3	17	0.12155652	0.05834652	< 10 ⁻⁶	1
8	HDAC1	1	0.11263346	0.10144553	< 10 ⁻⁶	1
9	P4HA1	10	0.10999698	0.16650149	1.0×10 ⁻⁶	1
10	PITPNB	22	0.10563578	0.35822785	1.0×10 ⁻⁶	2
11	CUX2	12	0.10209057	0.06924939	2.0×10 ⁻⁶	1
12	NECAB1	8	0.10197638	0.25569620	2.0×10 ⁻⁶	1
13	HS2ST1	1	0.10041528	0.10199005	2.0×10 ⁻⁶	1
14	METTL25	12	0.09952687	0.08587185	2.0×10 ⁻⁶	1
15	CELSR3	3	0.09761571	0.12500000	2.0×10 ⁻⁶	1
16	KCNQ5	6	0.09516938	0.08284819	2.0×10 ⁻⁶	1
17	USP25	21	0.09485193	0.11653037	2.0×10 ⁻⁶	1
18	OSBPL9	1	0.09477321	0.16461204	2.0×10 ⁻⁶	1
19	PPM1D	17	0.09457751	0.08187773	2.0×10 ⁻⁶	1
20	PSMB2	1	0.09368669	0.10872127	2.0×10 ⁻⁶	1
21	KITLG	12	0.09321913	0.10938491	2.0×10 ⁻⁶	1
22	PTPRK	6	0.09238986	0.15235110	2.0×10 ⁻⁶	1
23	PRPF40B	12	0.08811411	0.10312899	2.0×10 ⁻⁶	1
24	EXOC5	14	0.08680119	0.14383562	2.0×10 ⁻⁶	1
25	NF1	17	0.08654684	0.53987730	2.0×10 ⁻⁶	2
26	KIAA0825	5	0.08651185	0.13956568	2.0×10 ⁻⁶	1
27	KLHL28	14	0.08623216	0.08287895	3.0×10 ⁻⁶	1
28	UNC5D	8	0.08584013	0.23278008	4.0×10 ⁻⁶	1
29	C8orf44-SGK3	8	0.08500952	0.10876730	4.0×10 ⁻⁶	1
30	SGK3	8	0.08500952	0.10876730	4.0×10 ⁻⁶	1
31	GNA14	9	0.08464131	0.20441989	4.0×10 ⁻⁶	1
32	POLN	4	0.08228096	0.25619469	4.0×10 ⁻⁶	1
33	FMNL3	12	0.08227142	0.09967949	4.0×10 ⁻⁶	1
34	IFT80	3	0.08224157	0.65133172	4.0×10 ⁻⁶	4
35	TFAP2E	1	0.08005606	0.45766932	6.0×10 ⁻⁶	2
36	KIAA0947	5	0.08003881	0.33080329	6.0×10 ⁻⁶	1
37	LINC00478	21	0.07852482	0.16499666	6.0×10 ⁻⁶	1
38	EXOC6B	2	0.07730652	0.14328063	6.0×10 ⁻⁶	1
39	FAM149B1	10	0.07630036	0.14383562	6.0×10 ⁻⁶	1
40	CCDC178	18	0.07628428	0.33479106	6.0×10 ⁻⁶	1

Table S13: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the Western European CEU and East Asian JPT populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	<i>SPIDR</i>	8	0.19359701	0.31787351	< 10 ⁻⁶	3
2	<i>RUNX1T1</i>	8	0.11275519	0.05393330	< 10 ⁻⁶	1
3	<i>MRAP2</i>	6	0.11102258	0.25897350	< 10 ⁻⁶	1
4	<i>BVES-AS1</i>	6	0.10952935	0.51920530	< 10 ⁻⁶	2
5	<i>LINC00478</i>	21	0.10122097	0.27387331	< 10 ⁻⁶	1
6	<i>USP25</i>	21	0.09815414	0.14385858	< 10 ⁻⁶	1
7	<i>BCAS3</i>	17	0.09127146	0.06342583	< 10 ⁻⁶	1
8	<i>DNAH6</i>	2	0.08296677	0.20867526	< 10 ⁻⁶	1
9	<i>BEND4</i>	4	0.08124753	0.09624478	< 10 ⁻⁶	1
10	<i>ZNF546</i>	19	0.07817327	0.06845577	2.0×10 ⁻⁶	1
11	<i>HDAC1</i>	1	0.07768263	0.06808180	2.0×10 ⁻⁶	1
12	<i>DENND1A</i>	9	0.07496250	0.22050376	2.0×10 ⁻⁶	1
13	<i>ZRANB3</i>	2	-0.07278140	0.49384359	2.0×10 ⁻⁶	2
14	<i>C16orf70</i>	16	0.07075091	0.43935927	3.0×10 ⁻⁶	1
15	<i>EXOC6B</i>	2	0.06885796	0.10195948	3.0×10 ⁻⁶	1
16	<i>DIRC3</i>	2	0.06861035	0.13584514	3.0×10 ⁻⁶	1
17	<i>C4orf22</i>	4	0.06847775	0.22222222	3.0×10 ⁻⁶	1
18	<i>NR6A1</i>	9	0.06812268	0.55860716	4.0×10 ⁻⁶	2
19	<i>LRRC29</i>	16	0.06519534	0.13352580	6.0×10 ⁻⁶	1
20	<i>TMEM116</i>	12	-0.06340056	0.44410413	6.0×10 ⁻⁶	1
21	<i>C2CD5</i>	12	-0.06292884	0.36420361	6.0×10 ⁻⁶	1
22	<i>PRKDC</i>	8	0.06144151	0.09442680	7.0×10 ⁻⁶	1
23	<i>PRPF40B</i>	12	0.05952341	0.09292184	8.0×10 ⁻⁶	1
24	<i>CELSR3</i>	3	0.05950715	0.15054195	8.0×10 ⁻⁶	1
25	<i>MTOR</i>	1	0.05841437	0.34873239	1.1×10 ⁻⁵	1
26	<i>ANGPTL7</i>	1	0.05841437	0.34873239	1.1×10 ⁻⁵	1
27	<i>KIAA1324L</i>	7	0.05770516	0.16563659	1.1×10 ⁻⁵	1
28	<i>EPB41L1</i>	20	0.05760458	0.24740228	1.1×10 ⁻⁵	1
29	<i>EPS8</i>	12	0.05647792	0.23065250	1.4×10 ⁻⁵	1
30	<i>LOC100188947</i>	10	0.05452677	0.26400000	1.8×10 ⁻⁵	1
31	<i>HECTD2</i>	10	0.05452677	0.26400000	1.8×10 ⁻⁵	1
32	<i>R3HDM1</i>	2	-0.05448265	0.31076443	1.8×10 ⁻⁵	1
33	<i>ZNF106</i>	15	0.05420983	0.10975158	1.9×10 ⁻⁵	1
34	<i>C8orf44-SGK3</i>	8	0.05260365	0.54661301	2.2×10 ⁻⁵	2
35	<i>SGK3</i>	8	0.05260365	0.54661301	2.2×10 ⁻⁵	2
36	<i>CCBL2</i>	1	0.05220339	0.37208039	2.3×10 ⁻⁵	1
37	<i>LYRM7</i>	5	0.05213381	0.12161647	2.4×10 ⁻⁵	1
38	<i>C5orf42</i>	5	0.05108960	0.57542225	2.7×10 ⁻⁵	2
39	<i>RCBTB2</i>	13	0.05067259	0.52998066	2.8×10 ⁻⁵	2
40	<i>ARL13B</i>	3	0.05000593	0.54782609	3.3×10 ⁻⁵	2

Table S14: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the Central European CEU and West African YRI populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	KIAA0825	5	0.16262192	0.09800692	2.0×10 ⁻⁶	1
2	RP11-554F20.1	9	0.14328641	0.07170707	3.0×10 ⁻⁶	1
3	SPRED3	19	0.13648875	0.04008778	3.0×10 ⁻⁶	1
4	CASC4	15	0.13642990	0.06088150	3.0×10 ⁻⁶	1
5	DEDD	1	0.12323306	0.19270458	6.0×10 ⁻⁶	1
6	GSTT1	22	0.11632223	0.07518328	7.0×10 ⁻⁶	1
7	ENTHD1	22	0.11574899	0.29510665	7.0×10 ⁻⁶	1
8	NNT	5	0.11500267	0.09709843	8.0×10 ⁻⁶	1
9	ATP6V1A	3	0.11487292	0.46656145	9.0×10 ⁻⁶	1
10	DANCR	4	0.10908564	0.16342225	1.1×10 ⁻⁵	1
11	MIR548H3	6	0.10678068	0.11806435	1.5×10 ⁻⁵	1
12	GRIA2	4	0.10578392	0.36923077	1.7×10 ⁻⁵	1
13	GRIK5	19	0.10082463	0.14846599	1.9×10 ⁻⁵	1
14	TYW5	2	0.10050784	0.52092831	1.9×10 ⁻⁵	1
15	PIGV	1	0.09740419	0.10112360	2.3×10 ⁻⁵	1
16	RALGAPA2	20	0.09590598	0.09440637	2.7×10 ⁻⁵	1
17	PLEKHA8	7	0.09390530	0.29760666	3.3×10 ⁻⁵	1
18	GLRX2	1	0.09374561	0.53420670	3.3×10 ⁻⁵	1
19	PAWR	12	-0.09282636	0.41657077	3.4×10 ⁻⁵	1
20	PHKB	16	0.09044005	0.10755993	3.6×10 ⁻⁵	1
21	ERLIN2	8	0.08847504	0.09065880	3.9×10 ⁻⁵	1
22	SPG11	15	0.08398508	0.14916585	5.5×10 ⁻⁵	1
23	RRN3P3	16	-0.08384446	0.67088036	5.6×10 ⁻⁵	8
24	DKK2	4	0.08252351	0.13276618	6.1×10 ⁻⁵	1
25	ABHD17B	9	0.08249391	0.08387291	6.1×10 ⁻⁵	1
26	CNNM2	10	0.08094510	0.15631825	6.4×10 ⁻⁵	1
27	TGFBR1	9	0.07873090	0.42549372	7.4×10 ⁻⁵	1
28	CPNE1	20	0.07384179	0.19304797	1.03×10 ⁻⁴	1
29	PRKAR2A	3	0.07271481	0.59669161	1.14×10 ⁻⁴	2
30	NLK	17	0.07079549	0.24630342	1.30×10 ⁻⁴	1
31	CDK6	7	0.07054583	0.07748561	1.32×10 ⁻⁴	1
32	SYT1	12	0.06986742	0.27157762	1.38×10 ⁻⁴	1
33	GABRA4	4	0.06971220	0.52556668	1.38×10 ⁻⁴	1
34	ZNF451	6	0.06885744	0.19779485	1.46×10 ⁻⁴	1
35	ITFG1	16	0.06882713	0.16926617	1.46×10 ⁻⁴	1
36	FRYL	4	0.06828603	0.56018307	1.52×10 ⁻⁴	2
37	EXOC6B	2	-0.06782534	0.46576537	1.62×10 ⁻⁴	1
38	USP46	4	0.06639854	0.25667307	1.75×10 ⁻⁴	1
39	LGSN	6	0.06638067	0.19928826	1.76×10 ⁻⁴	1
40	ATF2	2	0.06592706	0.26808614	1.83×10 ⁻⁴	1

Table S15: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the East African LWK and West African YRI populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	<i>GRIK5</i>	19	0.2415148	0.12482020	< 10 ⁻⁶	1
2	<i>GSTT1</i>	22	0.2247992	0.23472029	< 10 ⁻⁶	3
3	<i>RP11-554F20.1</i>	9	0.2067291	0.10210615	< 10 ⁻⁶	1
4	<i>KIAA0825</i>	5	0.2003773	0.29785697	< 10 ⁻⁶	2
5	<i>RGS18</i>	1	0.1739911	0.21109123	< 10 ⁻⁶	2
6	<i>RRN3P3</i>	16	0.1675603	0.40424178	< 10 ⁻⁶	2
7	<i>PPAPDC1B</i>	8	0.1654046	0.11850615	< 10 ⁻⁶	1
8	<i>SPRED3</i>	19	0.1609167	0.05899437	< 10 ⁻⁶	1
9	<i>NNT</i>	5	0.1564619	0.09173050	< 10 ⁻⁶	1
10	<i>ARID1A</i>	1	0.1540840	0.14330287	< 10 ⁻⁶	1
11	<i>CASC4</i>	15	0.1429575	0.05820969	< 10 ⁻⁶	1
12	<i>EHBP1</i>	2	0.1429198	0.17335159	< 10 ⁻⁶	1
13	<i>ATF2</i>	2	0.1396078	0.54310604	< 10 ⁻⁶	2
14	<i>DKK2</i>	4	0.1378883	0.12261259	< 10 ⁻⁶	1
15	<i>MIR548AE2</i>	16	0.1372927	0.09054441	< 10 ⁻⁶	1
16	<i>LONP2</i>	16	0.1372927	0.09054441	< 10 ⁻⁶	1
17	<i>DDHD2</i>	8	0.1343500	0.11662586	< 10 ⁻⁶	1
18	<i>PHKB</i>	16	0.1315935	0.39985719	< 10 ⁻⁶	2
19	<i>FER1L6</i>	8	0.1274631	0.42668677	< 10 ⁻⁶	2
20	<i>FER1L6-AS1</i>	8	0.1274631	0.42668677	< 10 ⁻⁶	2
21	<i>SPIDR</i>	8	0.1269844	0.47826087	< 10 ⁻⁶	2
22	<i>GRIA4</i>	11	0.1268945	0.16182811	< 10 ⁻⁶	1
23	<i>DANCR</i>	4	0.1260421	0.15609221	< 10 ⁻⁶	1
24	<i>TCF4</i>	18	0.1243683	0.20357244	< 10 ⁻⁶	1
25	<i>PIGV</i>	1	0.1237784	0.09449782	< 10 ⁻⁶	1
26	<i>RALGAPA2</i>	20	0.1233941	0.09403724	< 10 ⁻⁶	1
27	<i>TMC1</i>	9	0.1218435	0.28051683	< 10 ⁻⁶	1
28	<i>PSMD14</i>	2	0.1205903	0.43648469	< 10 ⁻⁶	2
29	<i>CNNM2</i>	10	0.1205598	0.13187097	< 10 ⁻⁶	1
30	<i>FAM172A</i>	5	0.1204877	0.46349206	< 10 ⁻⁶	2
31	<i>BRIP1</i>	17	0.1186024	0.25193076	< 10 ⁻⁶	1
32	<i>GSTTP2</i>	22	0.1184177	0.16994022	< 10 ⁻⁶	1
33	<i>MAGI3</i>	1	0.1173924	0.17789681	< 10 ⁻⁶	1
34	<i>METTL25</i>	12	0.1168971	0.23853844	< 10 ⁻⁶	1
35	<i>CCDC178</i>	18	0.1152967	0.27341227	< 10 ⁻⁶	1
36	<i>DDX19B</i>	16	0.1146779	0.23421127	< 10 ⁻⁶	1
37	<i>RBBP4</i>	1	0.1145007	0.63782696	< 10 ⁻⁶	2
38	<i>C10orf32-ASMT</i>	10	0.1138325	0.38839475	< 10 ⁻⁶	2
39	<i>AS3MT</i>	10	0.1138325	0.38839475	< 10 ⁻⁶	2
40	<i>ZNF451</i>	6	0.1137655	0.21774436	< 10 ⁻⁶	1

Table S16: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the South Asian GIH and West African YRI populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	CASC4	15	0.16711386	0.03621655	< 10 ⁻⁶	1
2	NNT	5	0.14575420	0.04650487	< 10 ⁻⁶	1
3	KIAA0825	5	0.14498089	0.07326733	< 10 ⁻⁶	1
4	CDK6	7	0.13787179	0.23060483	< 10 ⁻⁶	1
5	ATP6V1A	3	0.12981556	0.28721584	< 10 ⁻⁶	1
6	DDHD2	8	0.12639095	0.06514875	< 10 ⁻⁶	1
7	SYT1	12	0.12432490	0.04995287	< 10 ⁻⁶	1
8	DEDD	1	0.12425622	0.15489439	< 10 ⁻⁶	1
9	RP11-554F20.1	9	0.12160852	0.05718271	< 10 ⁻⁶	1
10	PSMD14	2	0.11708713	0.43952713	< 10 ⁻⁶	1
11	FBXW4	10	0.11552344	0.12795875	< 10 ⁻⁶	1
12	PIGV	1	0.11324551	0.10666977	< 10 ⁻⁶	1
13	MIR548AE2	16	0.10772443	0.11468505	< 10 ⁻⁶	1
14	LONP2	16	0.10772443	0.11468505	< 10 ⁻⁶	1
15	ABHD17B	9	0.10372984	0.05366309	< 10 ⁻⁶	1
16	GRIK5	19	0.10341289	0.11576916	< 10 ⁻⁶	1
17	PPAPDC1B	8	0.10317107	0.12980421	< 10 ⁻⁶	1
18	C10orf76	10	0.10178019	0.51611553	< 10 ⁻⁶	1
19	PLEKHA8	7	0.10177351	0.30315058	< 10 ⁻⁶	1
20	PHKB	16	0.09939696	0.15921020	< 10 ⁻⁶	1
21	RALGAPA2	20	0.09639928	0.13588492	< 10 ⁻⁶	1
22	TULP4	6	0.09480228	0.14873493	< 10 ⁻⁶	1
23	ERLIN2	8	0.09254210	0.13007499	< 10 ⁻⁶	1
24	EXOC6B	2	-0.09028512	0.55109110	1.0×10 ⁻⁶	2
25	ZNF451	6	0.08854748	0.09354446	1.0×10 ⁻⁶	1
26	CADM1	11	0.08766952	0.35196436	1.0×10 ⁻⁶	1
27	COL7A1	3	0.08603112	0.12098249	1.0×10 ⁻⁶	1
28	PAWR	12	-0.08580547	0.44387569	1.0×10 ⁻⁶	1
29	CAMK2G	10	0.08306775	0.43884563	2.0×10 ⁻⁶	1
30	FRYL	4	0.08153959	0.50101833	2.0×10 ⁻⁶	1
31	SIRPB1	20	0.07908564	0.23271969	2.0×10 ⁻⁶	1
32	USP46	4	0.07871925	0.11263519	2.0×10 ⁻⁶	1
33	SLC4A10	2	0.07705620	0.12719176	2.0×10 ⁻⁶	1
34	CPNE1	20	0.07523397	0.32026984	2.0×10 ⁻⁶	1
35	FER1L6	8	0.07413957	0.50163815	2.0×10 ⁻⁶	1
36	FER1L6-AS1	8	0.07413957	0.50163815	2.0×10 ⁻⁶	1
37	UBE4A	11	0.07396793	0.50684932	2.0×10 ⁻⁶	1
38	LOC100131626	11	0.07396793	0.50684932	2.0×10 ⁻⁶	1
39	NLK	17	0.07380719	0.33165253	2.0×10 ⁻⁶	1
40	ENTHD1	22	0.07378007	0.20033285	2.0×10 ⁻⁶	1

Table S17: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the East Asian JPT and West African YRI populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	<i>UCHL5</i>	1	0.16261045	0.54330176	< 10 ⁻⁶	2
2	<i>CASC4</i>	15	0.15414538	0.02859798	< 10 ⁻⁶	1
3	<i>GRIK5</i>	19	0.15077705	0.08571429	< 10 ⁻⁶	1
4	<i>ATP6V1A</i>	3	0.14779863	0.51696607	< 10 ⁻⁶	2
5	<i>SIRPB1</i>	20	0.14373282	0.17088899	< 10 ⁻⁶	1
6	<i>HEMGN</i>	9	0.14078020	0.07985481	< 10 ⁻⁶	1
7	<i>KIAA0825</i>	5	0.13892611	0.14634146	< 10 ⁻⁶	1
8	<i>EHBP1</i>	2	0.13344376	0.15266860	< 10 ⁻⁶	1
9	<i>RP11-554F20.1</i>	9	0.12449166	0.28106373	< 10 ⁻⁶	1
10	<i>ENTHD1</i>	22	0.11764075	0.12615588	< 10 ⁻⁶	1
11	<i>PSMD14</i>	2	0.10605231	0.32749562	< 10 ⁻⁶	1
12	<i>NNT</i>	5	0.10287121	0.02879851	< 10 ⁻⁶	1
13	<i>EXOC6B</i>	2	-0.09657734	0.32384649	< 10 ⁻⁶	1
14	<i>DDHD2</i>	8	0.09268298	0.17119048	< 10 ⁻⁶	1
15	<i>MIR548AE2</i>	16	0.09252061	0.04543263	< 10 ⁻⁶	1
16	<i>LONP2</i>	16	0.09252061	0.04543263	< 10 ⁻⁶	1
17	<i>PIGV</i>	1	0.09246271	0.08195141	< 10 ⁻⁶	1
18	<i>GRIA4</i>	11	0.09091467	0.24805339	< 10 ⁻⁶	1
19	<i>RALGAPA2</i>	20	0.09018390	0.06541614	< 10 ⁻⁶	1
20	<i>CSMD3</i>	8	0.08642643	0.10669975	< 10 ⁻⁶	1
21	<i>AUTS2</i>	7	0.08609979	0.23589894	< 10 ⁻⁶	1
22	<i>MPHOSPH9</i>	12	-0.08463466	0.52033195	< 10 ⁻⁶	1
23	<i>PPAPDC1B</i>	8	0.08450565	0.28654354	< 10 ⁻⁶	1
24	<i>MIR548H3</i>	6	0.08341730	0.14782609	< 10 ⁻⁶	1
25	<i>ABCB1</i>	7	0.08225091	0.50471294	< 10 ⁻⁶	1
26	<i>RUNDC3B</i>	7	0.08225091	0.50471294	< 10 ⁻⁶	1
27	<i>SIPA1L3</i>	19	0.08082831	0.16331995	< 10 ⁻⁶	1
28	<i>NLK</i>	17	0.08023741	0.25966716	< 10 ⁻⁶	1
29	<i>CPNE1</i>	20	0.07997871	0.11175373	< 10 ⁻⁶	1
30	<i>GRIA2</i>	4	0.07905065	0.40514076	< 10 ⁻⁶	1
31	<i>CDK6</i>	7	0.07856601	0.11933861	< 10 ⁻⁶	1
32	<i>PLEKHA8</i>	7	0.07799249	0.29088472	< 10 ⁻⁶	1
33	<i>DKK2</i>	4	0.07704189	0.07856381	< 10 ⁻⁶	1
34	<i>SYT1</i>	12	0.07684115	0.12255668	< 10 ⁻⁶	1
35	<i>COL7A1</i>	3	0.07658377	0.07582045	< 10 ⁻⁶	1
36	<i>GSTT1</i>	22	0.07574164	0.10880196	< 10 ⁻⁶	1
37	<i>FBXW4</i>	10	0.07431220	0.15773660	1.0×10 ⁻⁶	1
38	<i>USP46</i>	4	0.07174521	0.19367210	1.0×10 ⁻⁶	1
39	<i>AC016582.2</i>	19	0.07004390	0.18775372	1.0×10 ⁻⁶	1
40	<i>ARID1A</i>	1	0.06960214	0.02739301	1.0×10 ⁻⁶	1

Table S18: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the East Asian JPT and South Asian GIH populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	<i>RUNX1T1</i>	8	0.19081280	0.08034745	< 10 ⁻⁶	1
2	<i>P4HTM</i>	3	0.17561530	0.02724586	< 10 ⁻⁶	1
3	<i>EXOC6B</i>	2	0.11912726	0.09503897	< 10 ⁻⁶	1
4	<i>TMTC2</i>	12	0.11638215	0.18265334	< 10 ⁻⁶	1
5	<i>SUGCT</i>	7	0.11594031	0.12736706	< 10 ⁻⁶	1
6	<i>HELZ</i>	17	0.11386077	0.35123207	< 10 ⁻⁶	2
7	<i>DBT</i>	1	0.11216524	0.06377143	< 10 ⁻⁶	1
8	<i>BCAS3</i>	17	0.10947050	0.06812121	< 10 ⁻⁶	1
9	<i>RP11-53O19.1</i>	5	0.10879938	0.52299606	< 10 ⁻⁶	2
10	<i>ZNF546</i>	19	0.09867813	0.13472000	< 10 ⁻⁶	1
11	<i>ADAMTS6</i>	5	0.09839895	0.49891634	< 10 ⁻⁶	2
12	<i>APPBP2</i>	17	0.09796838	0.09183407	< 10 ⁻⁶	1
13	<i>DR1</i>	1	0.09702526	0.42016095	< 10 ⁻⁶	1
14	<i>USP25</i>	21	0.09547922	0.16971106	< 10 ⁻⁶	1
15	<i>RNF121</i>	11	0.09440660	0.09574218	< 10 ⁻⁶	1
16	<i>NEGR1</i>	1	0.09420501	0.28005997	< 10 ⁻⁶	1
17	<i>RNU6-28P</i>	15	0.09050468	0.27059635	< 10 ⁻⁶	1
18	<i>PPIP5K1</i>	15	0.09050468	0.27059635	< 10 ⁻⁶	1
19	<i>ORC2</i>	2	0.08524372	0.07114440	< 10 ⁻⁶	1
20	<i>HDAC1</i>	1	0.08444452	0.12845175	< 10 ⁻⁶	1
21	<i>USP32</i>	17	0.08419480	0.14071582	< 10 ⁻⁶	1
22	<i>CCDC18</i>	1	0.08341467	0.34291581	< 10 ⁻⁶	1
23	<i>LYRM7</i>	5	0.08066234	0.07455296	< 10 ⁻⁶	1
24	<i>LOC100188947</i>	10	0.08039944	0.38098427	< 10 ⁻⁶	1
25	<i>HECTD2</i>	10	0.08039944	0.38098427	< 10 ⁻⁶	1
26	<i>SSH2</i>	17	0.07918183	0.29931234	< 10 ⁻⁶	1
27	<i>ZNF780B</i>	19	0.07884324	0.14236707	< 10 ⁻⁶	1
28	<i>NLK</i>	17	0.07866030	0.15058966	< 10 ⁻⁶	1
29	<i>MTF2</i>	1	0.07827113	0.56458636	< 10 ⁻⁶	2
30	<i>ATP6V0D1</i>	16	0.07404407	0.08471815	< 10 ⁻⁶	1
31	<i>MBOAT2</i>	2	0.07358927	0.11950505	< 10 ⁻⁶	1
32	<i>BCL2L1</i>	20	0.07326540	0.13298940	< 10 ⁻⁶	1
33	<i>CENPW</i>	6	0.07324676	0.21777778	< 10 ⁻⁶	1
34	<i>BEND4</i>	4	0.07308935	0.08658982	< 10 ⁻⁶	1
35	<i>LINC00478</i>	21	0.07294715	0.17406645	< 10 ⁻⁶	1
36	<i>XXYLT1</i>	3	0.07133674	0.10906096	< 10 ⁻⁶	1
37	<i>ABCB1</i>	7	0.07111757	0.14704879	< 10 ⁻⁶	1
38	<i>RUNDC3B</i>	7	0.07111757	0.14704879	< 10 ⁻⁶	1
39	<i>NGLY1</i>	3	0.06960764	0.15325248	< 10 ⁻⁶	1
40	<i>CELSR3</i>	3	0.06809979	0.09836612	< 10 ⁻⁶	1

Table S19: Top 40 SS-G123 sweep candidates at RNA- and protein-coding genes shared between the East Asian JPT and Southeast Asian KHV populations. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Target genes that pass the significance threshold are colored in gold in the “*P*-value” column. Genes whose sweeps are assigned as hard ($\nu = 1$) are shaded in red in the “Inferred ν ” column, while soft sweeps ($\nu \geq 2$) are colored in blue.

	Top gene	Chromosome	Maximum SS-G123	G2/G1	<i>P</i> -value	Inferred ν
1	<i>SPIDR</i>	8	0.2784003	0.38334810	< 10 ⁻⁶	2
2	<i>RP11-696N14.1</i>	4	0.2744507	0.20046722	< 10 ⁻⁶	2
3	<i>EXOC6B</i>	2	0.2617294	0.03631803	< 10 ⁻⁶	1
4	<i>RUNX1T1</i>	8	0.2599384	0.06254055	< 10 ⁻⁶	1
5	<i>SPAG6</i>	10	0.2444433	0.03124657	< 10 ⁻⁶	1
6	<i>EXD2</i>	14	0.2338336	0.06551773	< 10 ⁻⁶	1
7	<i>P4HTM</i>	3	0.2265336	0.02184214	< 10 ⁻⁶	1
8	<i>AMBRA1</i>	11	0.2041819	0.07887964	< 10 ⁻⁶	1
9	<i>BCL7C</i>	16	0.2019106	0.04684318	< 10 ⁻⁶	1
10	<i>BCL2L1</i>	20	0.1971090	0.09232554	< 10 ⁻⁶	1
11	<i>ADH1A</i>	4	0.1963534	0.27346115	< 10 ⁻⁶	2
12	<i>PGAP1</i>	2	0.1945704	0.09764099	< 10 ⁻⁶	1
13	<i>C11orf49</i>	11	0.1898302	0.18259828	3.0×10 ⁻⁶	2
14	<i>PRPF40B</i>	12	0.1861633	0.03307622	6.0×10 ⁻⁶	1
15	<i>LOC100188947</i>	10	0.1858056	0.47456664	6.0×10 ⁻⁶	2
16	<i>HECTD2</i>	10	0.1858056	0.47456664	6.0×10 ⁻⁶	2
17	<i>NOVA1</i>	14	0.1830759	0.49632253	7.0×10 ⁻⁶	2
18	<i>ZNF282</i>	7	0.1813378	0.05366309	7.0×10 ⁻⁶	1
19	<i>HMCN1</i>	1	0.1764870	0.47648708	8.0×10 ⁻⁶	2
20	<i>PHYHIPL</i>	10	0.1743157	0.07840000	8.0×10 ⁻⁶	1
21	<i>LINC01024</i>	5	0.1742617	0.13723019	8.0×10 ⁻⁶	1
22	<i>ARIH2</i>	3	0.1734230	0.06296852	8.0×10 ⁻⁶	1
23	<i>PURA</i>	5	0.1727126	0.13155916	9.0×10 ⁻⁶	1
24	<i>ARIH2OS</i>	3	0.1680339	0.05414495	1.2×10 ⁻⁵	1
25	<i>TRUB1</i>	10	0.1677889	0.06171946	1.2×10 ⁻⁵	1
26	<i>CEP112</i>	17	0.1663139	0.06596257	1.4×10 ⁻⁵	1
27	<i>USP38</i>	4	0.1643823	0.14698163	1.5×10 ⁻⁵	1
28	<i>C2orf66</i>	2	0.1629327	0.04013059	1.5×10 ⁻⁵	1
29	<i>LINC01088</i>	4	0.1622231	0.12088799	1.5×10 ⁻⁵	1
30	<i>TRMT11</i>	6	0.1609308	0.04417217	1.6×10 ⁻⁵	1
31	<i>CCDC18</i>	1	0.1591868	0.39498058	1.6×10 ⁻⁵	2
32	<i>LINC00536</i>	8	0.1575138	0.53060485	1.6×10 ⁻⁵	3
33	<i>CSPP1</i>	8	0.1570753	0.46273402	1.6×10 ⁻⁵	2
34	<i>RAD51B</i>	14	0.1546937	0.07764864	1.6×10 ⁻⁵	1
35	<i>SPATS2</i>	12	0.1543295	0.07337854	1.6×10 ⁻⁵	1
36	<i>FBXO4</i>	5	0.1535929	0.03908674	1.6×10 ⁻⁵	1
37	<i>PKIA</i>	8	0.1529611	0.23342175	1.7×10 ⁻⁵	2
38	<i>GPHN</i>	14	0.1511221	0.41336881	1.7×10 ⁻⁵	2
39	<i>ZNF660</i>	3	0.1509682	0.12457299	1.7×10 ⁻⁵	1
40	<i>OXCT1</i>	5	0.1500597	0.04652922	1.8×10 ⁻⁵	1

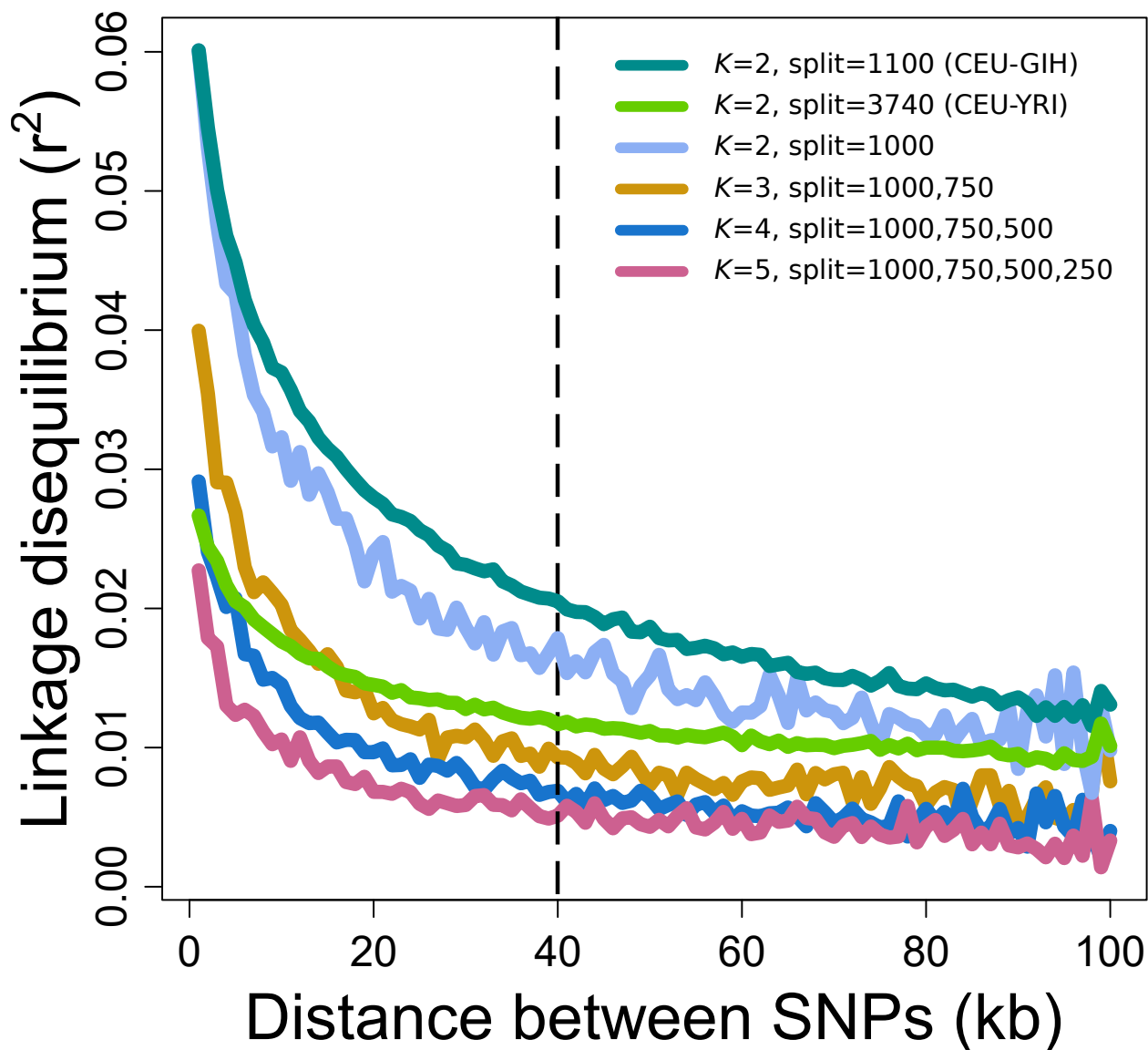


Figure S1: Decay of pairwise LD measured as r^2 over 100 kb for pooled samples simulated under neutrality containing two to five populations. For pairs of populations (cyan, chartreuse, and sky blue), we simulated under the CEU-GIH ($\tau = 1100$) or CEU-YRI ($\tau = 3740$) human demographic models, or a simplified constant demographic history model ($\tau = 1000$) with $N = 10^4$, where the ancestral population splits once. For trios of populations (goldenrod), two splits underlie the sample phylogeny, occurring $\tau_1 = 1000$ and $\tau_2 = 750$ generations before sampling. For quartets of populations (dark blue), there are three splits occurring at $\tau_1 = 1000$, $\tau_2 = 750$, and $\tau_3 = 500$ generations before sampling. Finally, $K = 5$ phylogenies result from four splits, at $\tau_1 = 1000$, $\tau_2 = 750$, $\tau_3 = 500$, and $\tau_4 = 250$ generations before sampling. All samples are identical to those analyzed in the main text.

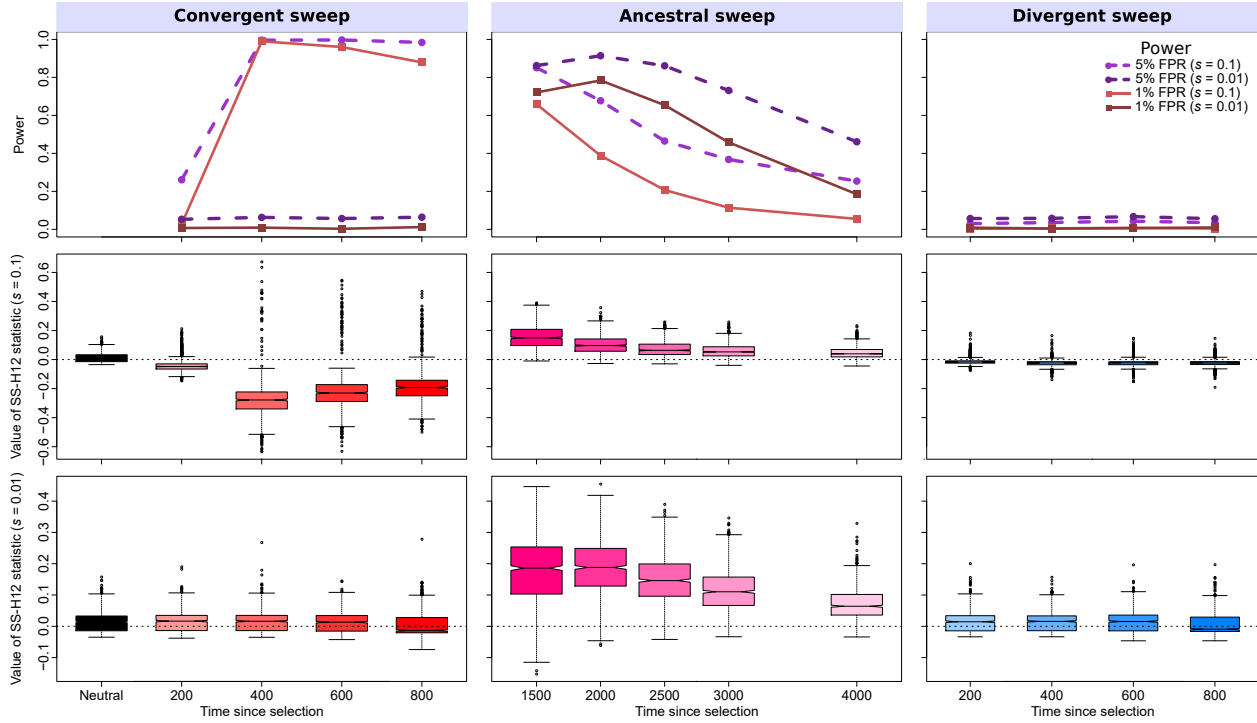


Figure S2: Properties of SS-H12 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) soft sweep ($\nu = 4$) scenarios under the CEU-GIH model ($\tau = 1100$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent soft sweeps from selection on standing genetic variation as a function of time at which selection of the favored haplotypes initiated (t), with FPR based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-H12 values from windows of maximum $|\text{SS-H12}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-H12} = 0$. (Bottom row) Box plots summarizing the distribution of SS-H12 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. All replicate samples for the CEU-GIH model contain 99 simulated CEU individuals and 103 simulated GIH individuals, as in the 1000 Genomes Project dataset [Auton et al., 2015], and we performed 1000 replicates for each scenario.

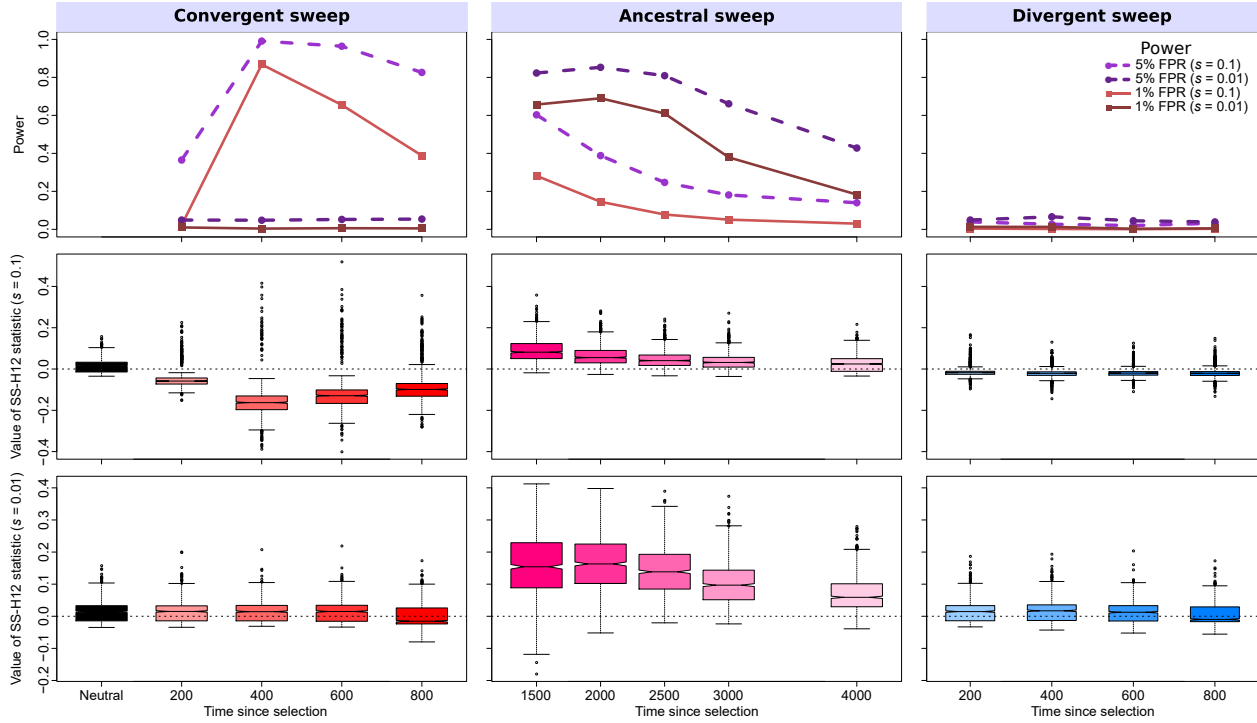


Figure S3: Properties of SS-H12 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) soft sweep ($\nu = 8$) scenarios under the CEU-GIH model ($\tau = 1100$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent soft sweeps from selection on standing genetic variation as a function of time at which selection of the favored haplotypes initiated (t), with FPR based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-H12 values from windows of maximum $|\text{SS-H12}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-H12} = 0$. (Bottom row) Box plots summarizing the distribution of SS-H12 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. All replicate samples for the CEU-GIH model contain 99 simulated CEU individuals and 103 simulated GIH individuals, as in the 1000 Genomes Project dataset [Auton et al., 2015], and we performed 1000 replicates for each scenario.

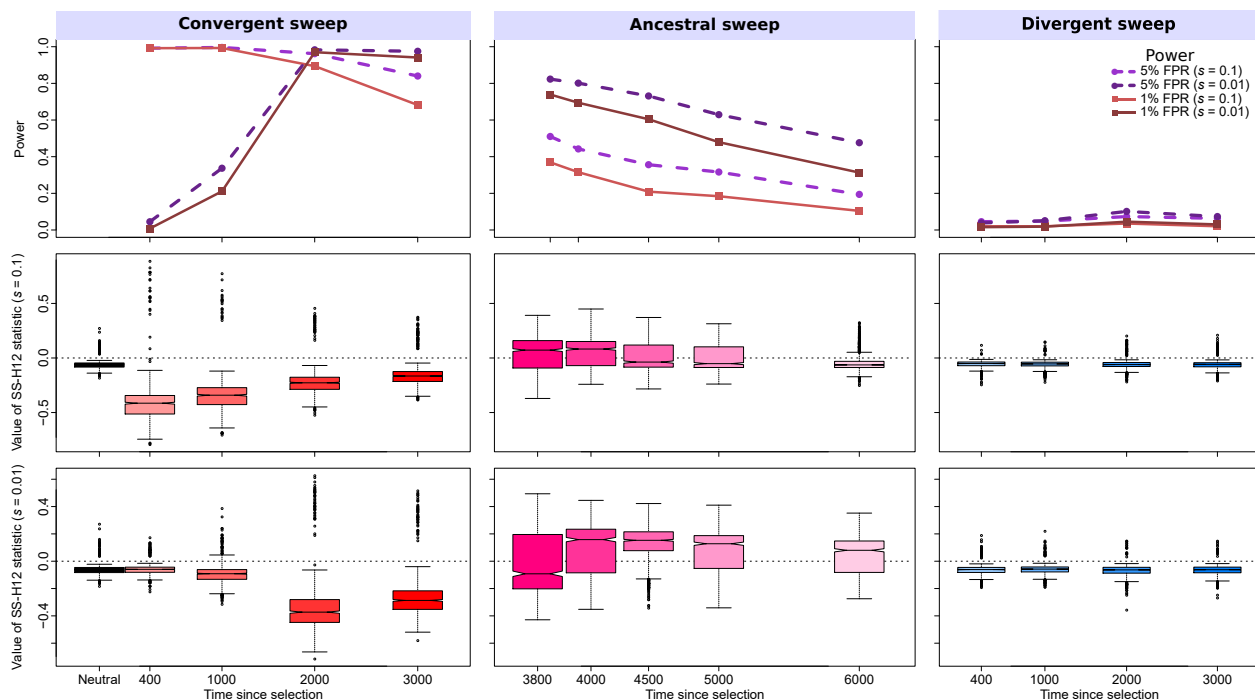


Figure S4: Properties of SS-H12 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) soft sweep ($\nu = 4$) scenarios under the CEU-YRI model ($\tau = 3740$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent soft sweeps from selection on standing genetic variation as a function of time at which selection of the favored haplotypes initiated (t), with FPR based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-H12 values from windows of maximum $|\text{SS-H12}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-H12} = 0$. (Bottom row) Box plots summarizing the distribution of SS-H12 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. All replicate samples for the CEU-YRI model contain 99 simulated CEU individuals and 108 simulated YRI individuals, as in the 1000 Genomes Project dataset [Auton et al., 2015], and we performed 1000 replicates for each scenario.

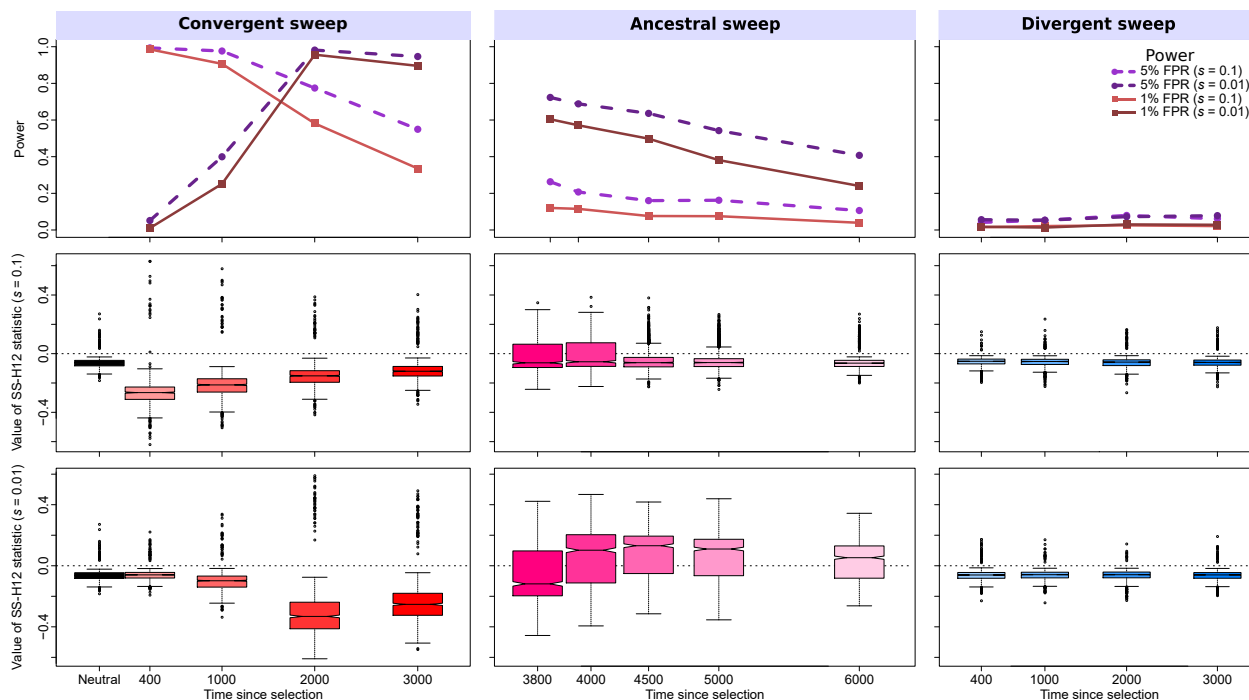


Figure S5: Properties of SS-H12 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) soft sweep ($\nu = 8$) scenarios under the CEU-YRI model ($\tau = 3740$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent soft sweeps from selection on standing genetic variation as a function of time at which selection of the favored haplotypes initiated (t), with FPR based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-H12 values from windows of maximum $|\text{SS-H12}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-H12} = 0$. (Bottom row) Box plots summarizing the distribution of SS-H12 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. All replicate samples for the CEU-YRI model contain 99 simulated CEU individuals and 108 simulated YRI individuals, as in the 1000 Genomes Project dataset [Auton et al., 2015], and we performed 1000 replicates for each scenario.

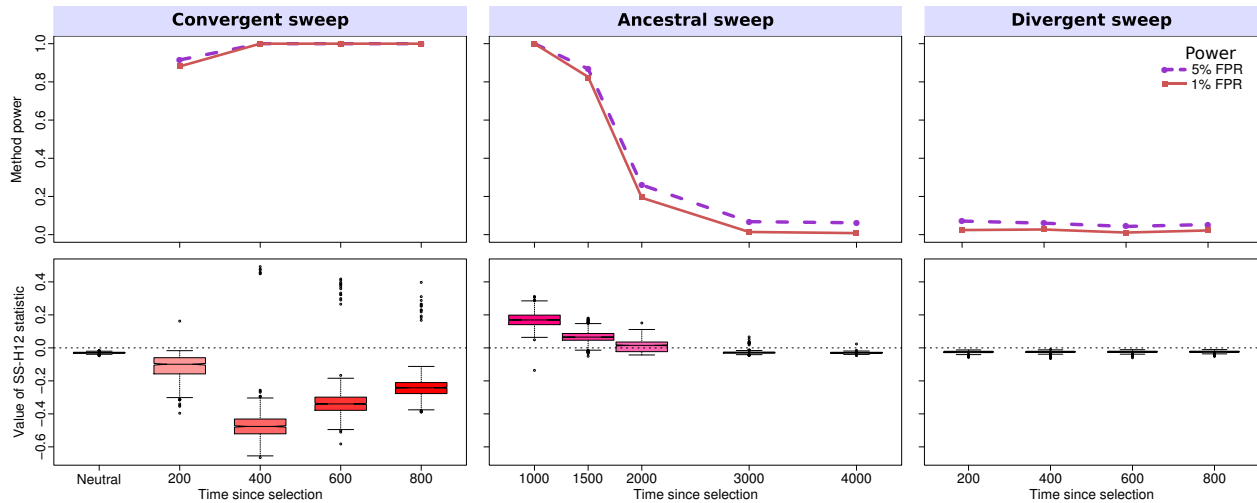


Figure S6: Properties of SS-H12 for simulated hard sweep scenarios for samples drawn from $K = 2$ equally-sized populations in which $\tau = 1000$ generations before sampling, for a constant demographic history in which $N = 10^4$ for the duration of the simulation. (Top) Power at 1 and 5% false positive rates (FPRs) to detect recent ancestral, convergent, and divergent hard sweeps (see Figure 1) as a function of time at which selection initiated, with false positive rate based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-H12 values from windows of maximum $|\text{SS-H12}|$ for each replicate, corresponding to each point in the power curve, with dashed lines in each panel representing $\text{SS-H12} = 0$. Convergent and divergent sweeps occur after this time (200-800 generations before sampling), while ancestral sweeps occur before this time (1100-4000 generations before sampling). All sweeps are strong ($s = 0.1$) for a sample of $n = 100$ diploid individuals per population, with 1000 replicates performed for each scenario.

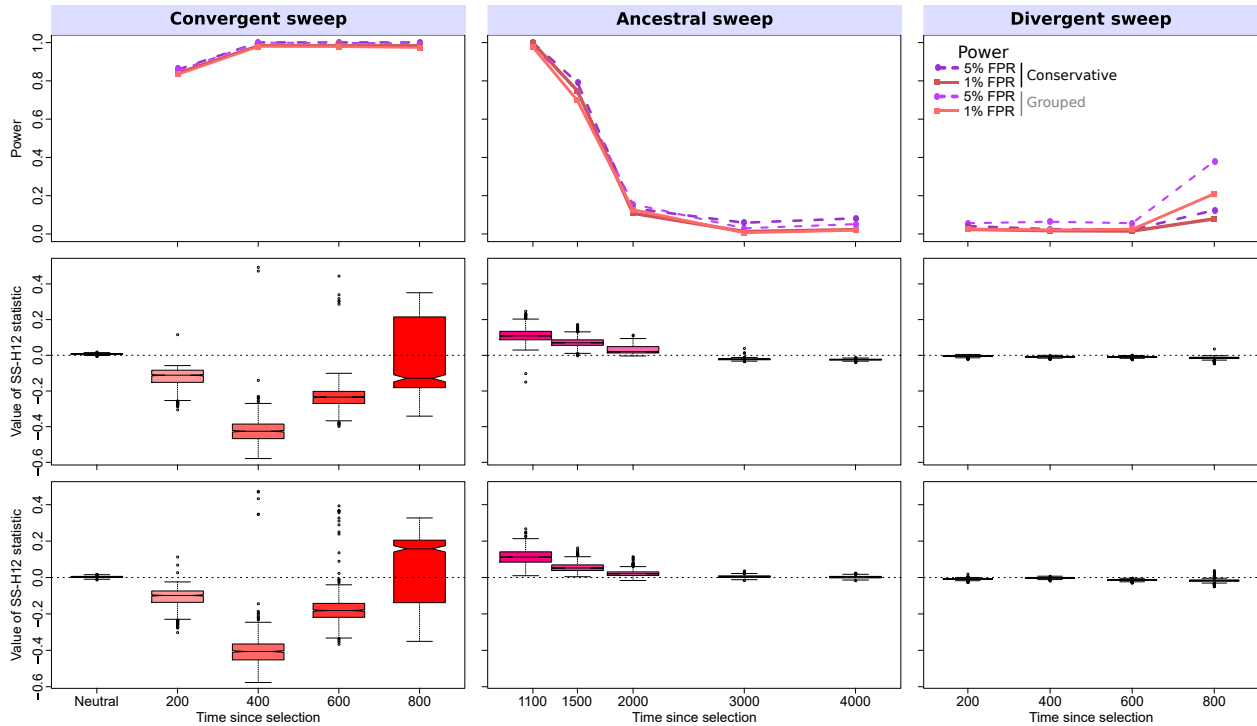


Figure S7: Properties of SS-H12 for simulated hard sweep scenarios for samples drawn from $K = 3$ equally-sized populations in which $\tau_1 = 1000$ and $\tau_2 = 750$ generations before sampling. (Top) Power at 1 and 5% false positive rates (FPRs) to detect recent ancestral, convergent, and divergent hard sweeps (see Figure 1) as a function of time at which selection initiated, with false positive rate based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates. (Middle and bottom rows) Box plots summarizing the distribution of SS-H12 values from windows of maximum $|\text{SS-H12}|$ for each replicate, corresponding to each point in the power curve for conservative (middle row) and grouped (bottom row) approaches, with dashed lines in each panel representing $\text{SS-H12} = 0$. Convergent and divergent sweeps occur after this time (200-800 generations before sampling), while ancestral sweeps occur before this time (1100-4000 generations before sampling). All sweeps are strong ($s = 0.1$) for a sample of $n = 100$ diploid individuals per population, with 1000 replicates performed for each scenario.

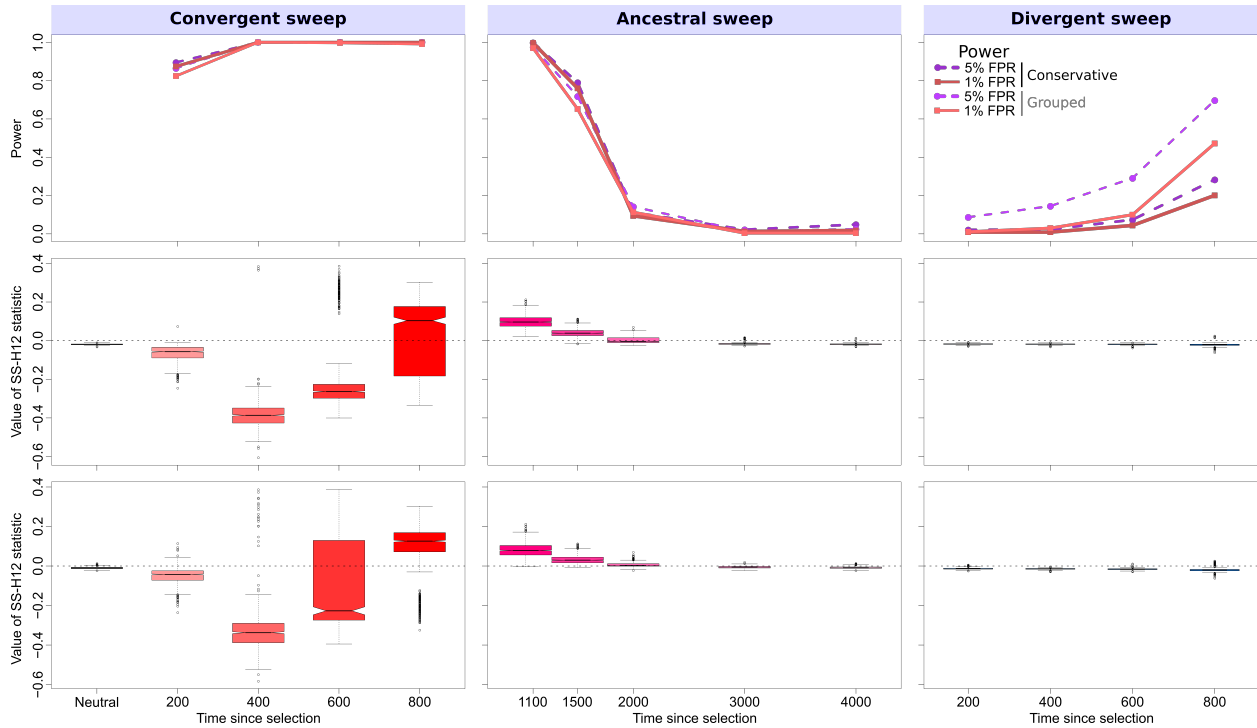


Figure S8: Properties of SS-H12 for simulated hard sweep scenarios for samples drawn from $K = 4$ equally-sized populations in which $\tau_1 = 1000$, $\tau_2 = 750$, and $\tau_3 = 500$ generations before sampling. (Top row) Power at 1 and 5% false positive rates (FPRs) to detect recent ancestral, convergent, and divergent hard sweeps (see Figure 1) as a function of time at which selection initiated, with false positive rate based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates. (Middle and bottom rows) Box plots summarizing the distribution of SS-H12 values from windows of maximum $|\text{SS-H12}|$ for each replicate, corresponding to each point in the power curve for conservative (middle row) and grouped (bottom row) approaches, with dashed lines in each panel representing $\text{SS-H12} = 0$. Convergent and divergent sweeps occur after this time (200-800 generations before sampling), while ancestral sweeps occur before this time (1100-4000 generations before sampling). All sweeps are strong ($s = 0.1$) for a sample of $n = 100$ diploid individuals per population, with 1000 replicates performed for each scenario.

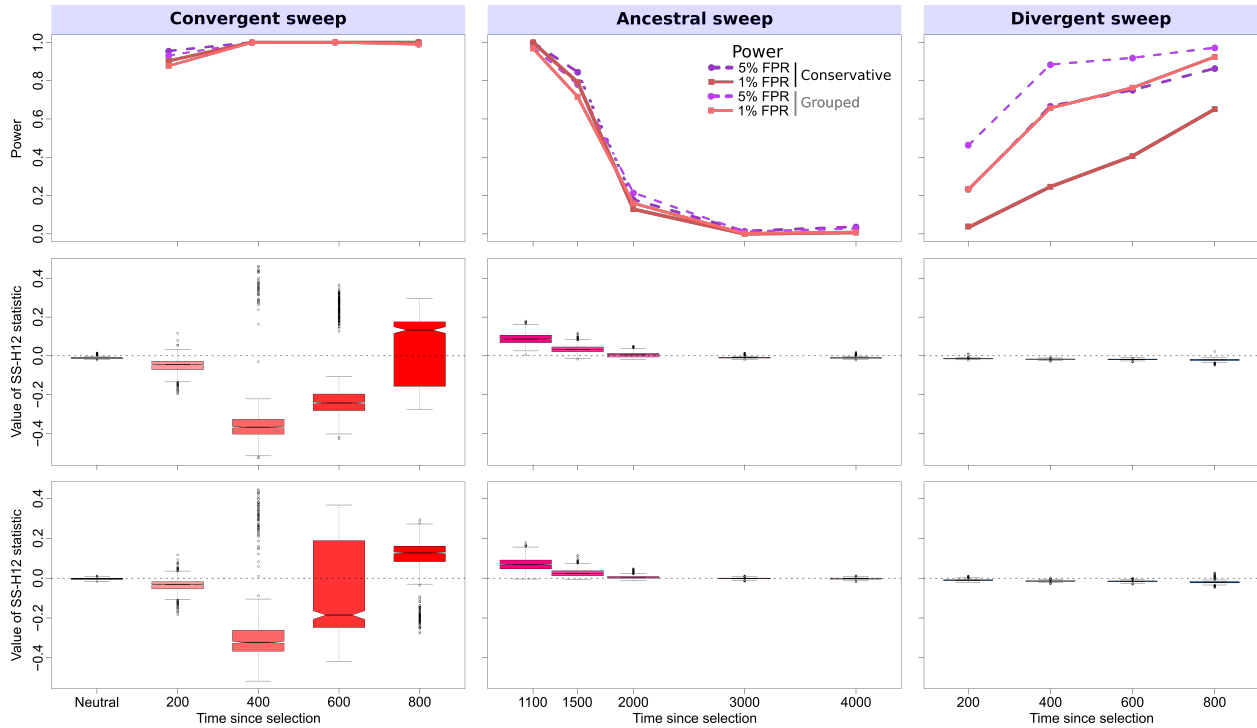


Figure S9: Properties of SS-H12 for simulated hard sweep scenarios for samples drawn from $K = 5$ equally-sized populations in which $\tau_1 = 1000$, $\tau_2 = 750$, $\tau_3 = 500$, and $\tau_4 = 250$ generations before sampling. (Top row) Power at 1 and 5% false positive rates (FPRs) to detect recent ancestral, convergent, and divergent hard sweeps (see Figure 1) as a function of time at which selection initiated, with false positive rate based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates. (Middle and bottom rows) Box plots summarizing the distribution of SS-H12 values from windows of maximum $|\text{SS-H12}|$ for each replicate, corresponding to each point in the power curve for conservative (middle row) and grouped (bottom row) approaches, with dashed lines in each panel representing $\text{SS-H12} = 0$. Convergent and divergent sweeps occur after this time (200-800 generations before sampling), while ancestral sweeps occur before this time (1100-4000 generations before sampling). All sweeps are strong ($s = 0.1$) for a sample of $n = 100$ diploid individuals per population, with 1000 replicates performed for each scenario.

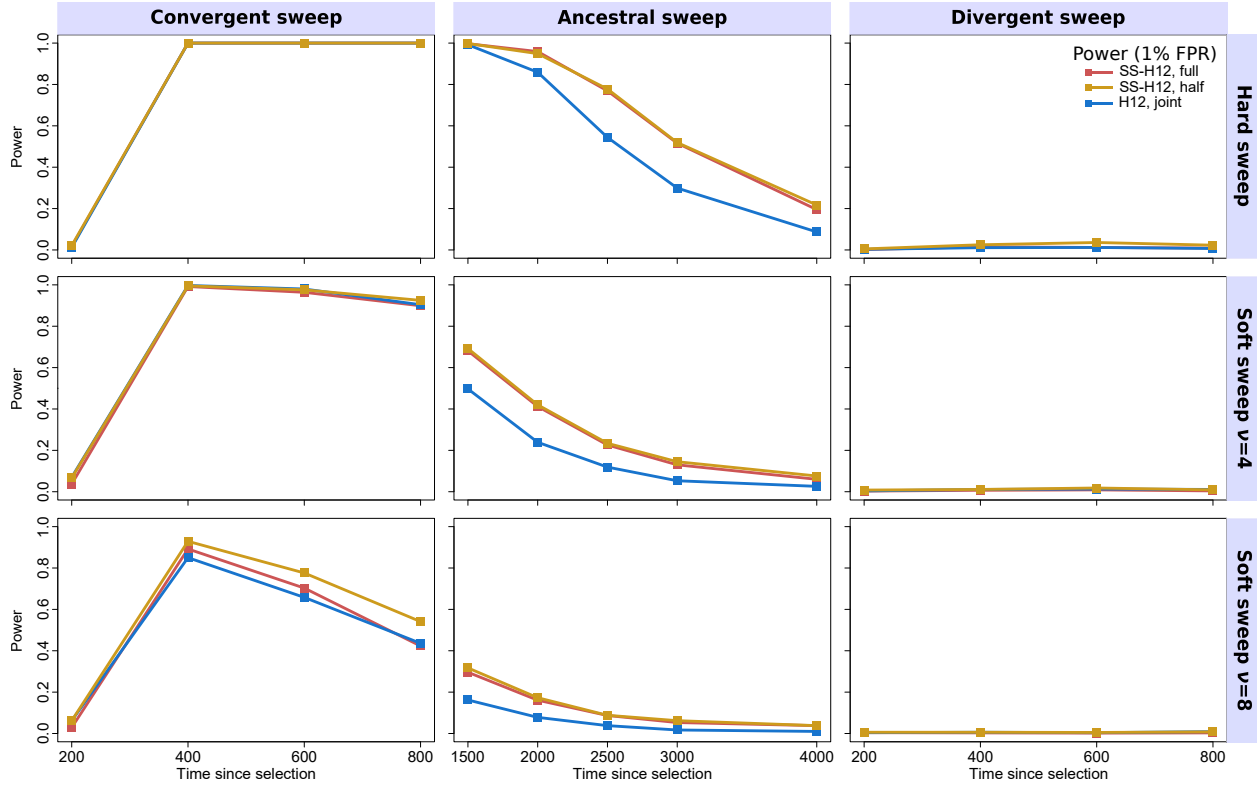


Figure S10: Powers of SS-H12 and H12 at a 1% false positive rate to detect recent ancestral, convergent, and divergent simulated strong ($s = 0.1$) selective sweeps under the CEU-GIH model ($\tau = 1100$ generations before sampling) for hard (top) and soft ($\nu = 4$, middle; $\nu = 8$, bottom) sweeps as a function of time at which positive selection of the favored allele initiated (t), with FPR based on the distribution of maximum $|\text{SS-H12}|$ or H12 across simulated neutral replicates. “SS-H12, full” refers to analyses in which we generated full-size pooled samples consisting of 99 simulated CEU individuals and 103 simulated GIH individuals, whereas “SS-H12, half” used only half of the alleles in each sample. “H12, joint” analyses used the full sample size for both populations. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. We performed 1000 replicates for each scenario.

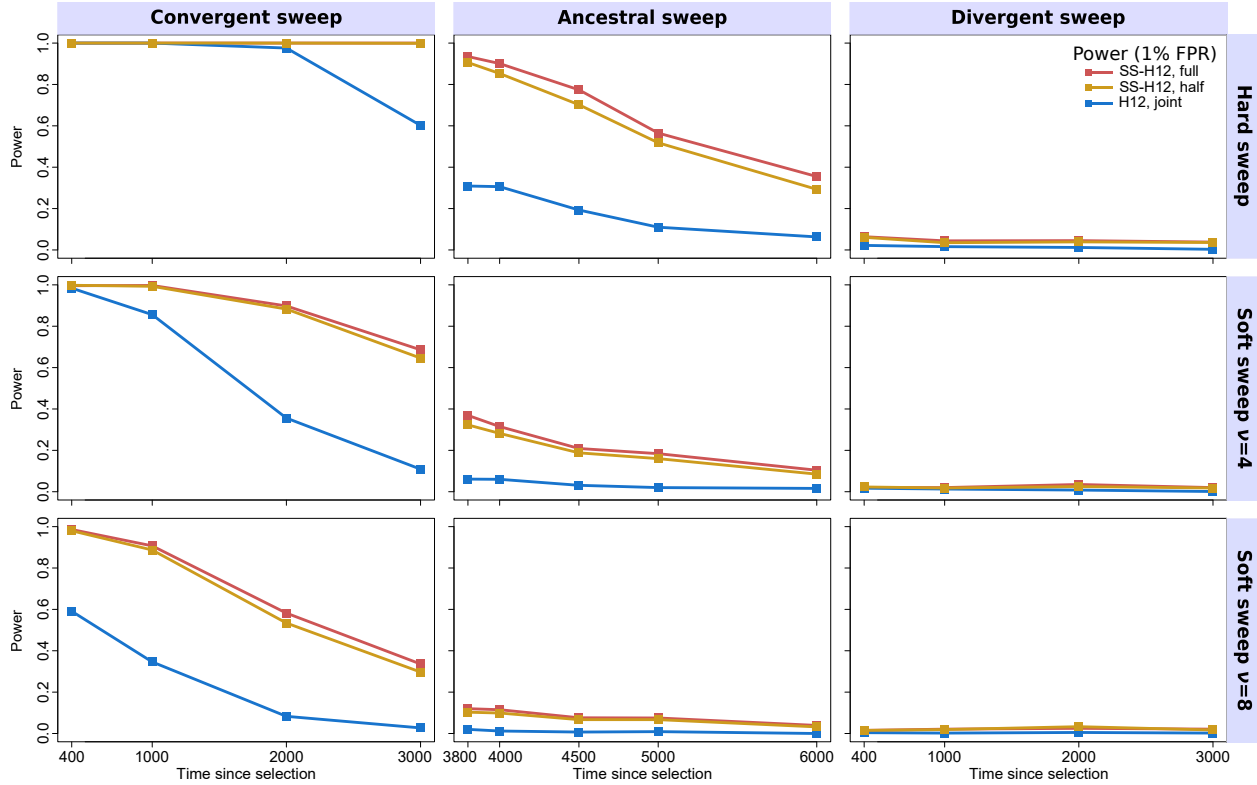


Figure S11: Powers of SS-H12 and H12 at a 1% false positive rate to detect recent ancestral, convergent, and divergent simulated strong ($s = 0.1$) selective sweeps under the CEU-YRI model ($\tau = 3740$ generations before sampling) for hard (top) and soft ($\nu = 4$, middle; $\nu = 8$, bottom) sweeps as a function of time at which positive selection of the favored allele initiated (t), with FPR based on the distribution of maximum |SS-H12| or H12 across simulated neutral replicates. “SS-H12, full” refers to analyses in which we generated full-size pooled samples consisting of 99 simulated CEU individuals and 108 simulated GIH individuals, while “SS-H12, half” used only half of the alleles in each sample. “H12, joint” analyses used the full sample size for both populations. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. We performed 1000 replicates for each scenario.

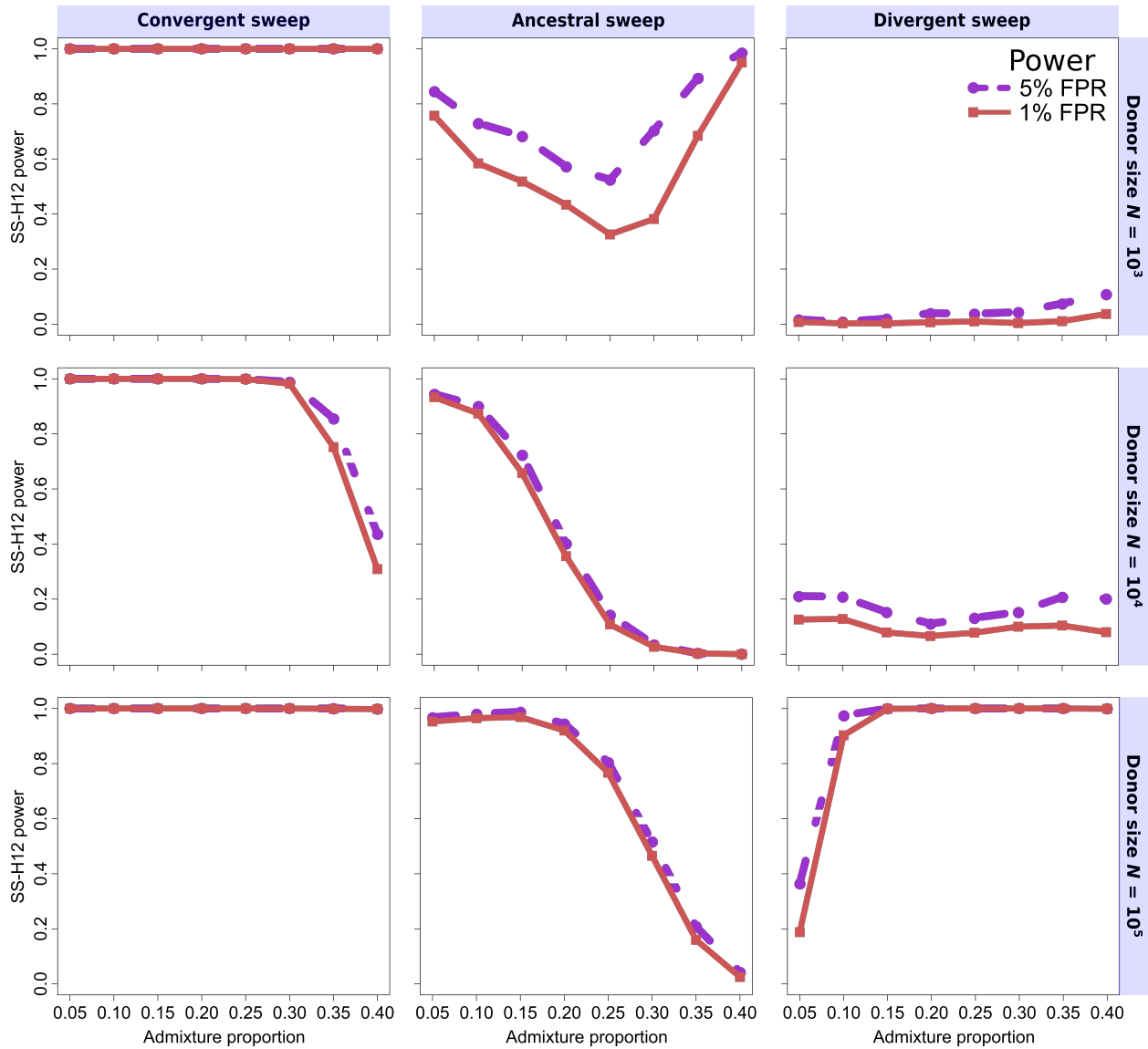


Figure S12: Power at 1 and 5% false positive rates (FPRs) to detect recent strong ($s = 0.1$) ancestral, convergent, and divergent hard sweeps (see Figure 1) as a function of admixture proportion, with false positive rate based on the distribution of maximum $|\text{SS-H12}|$ across simulated neutral replicates under a given admixture scenario. Data here are simulated as in Figure 4, with scenarios of admixture proportion 0.2, 0.3, and 0.4 identical to Figure 4.

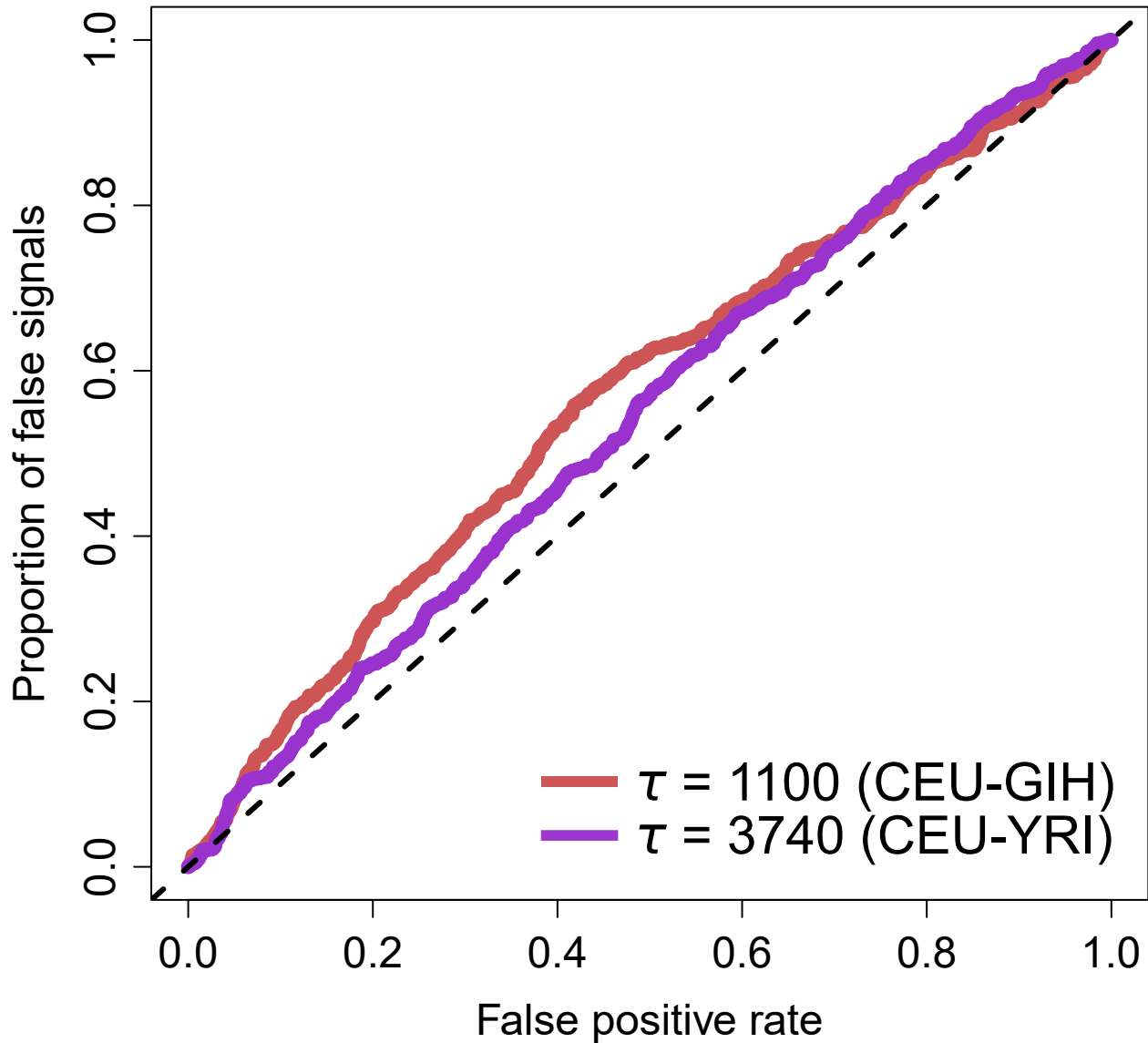


Figure S13: Proportion of false signals generated by background selection as a function of false positive rate based on neutrality for SS-H12 under CEU-GIH (red) or CEU-YRI (purple) demographic models. Neutral replicates used here are identical to those used across Figures 2, 3, and S2-S5. Background selection simulations, totaling 1000 replicates, were generated according to the procedure described in the *Materials and Methods*.

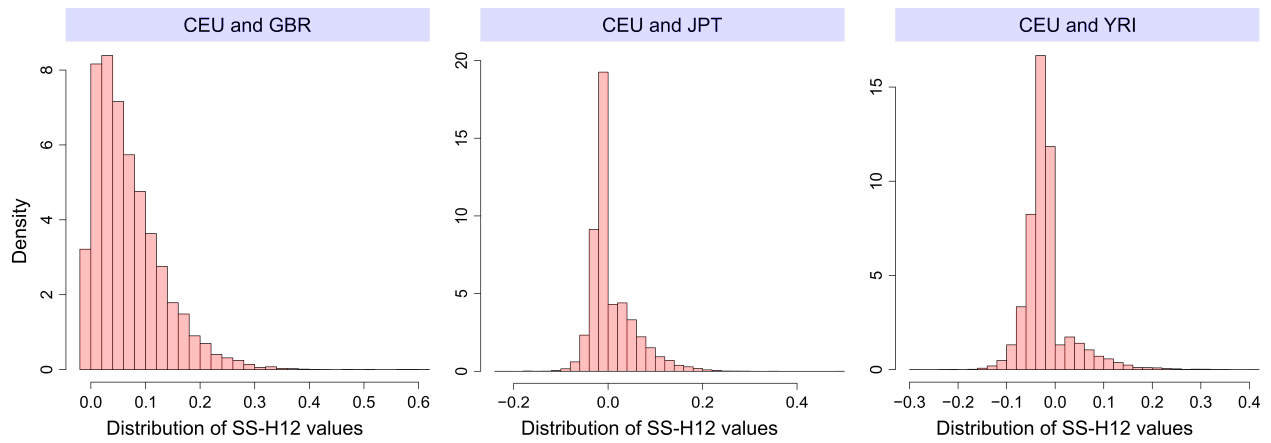


Figure S14: Empirical distributions of SS-H12 values assigned to each protein- and mRNA-coding gene based on the analysis of individuals from the 1000 Genomes Project Consortium [Auton et al., 2015] for three population comparisons with CEU. (Left) Distribution of SS-H12 values between the closely-related CEU and GBR populations of European descent. (Middle) Distribution of SS-H12 values between CEU and the East Asian JPT populations, representing a pair that diverged after the out-of-Africa event. (Right) Distribution of SS-H12 values between CEU and the sub-Saharan African YRI populations, representing a distantly-related population pair. SS-H12 is assigned to each gene from the window of maximum $|\text{SS-H12}|$ falling between the transcription start and stop of the gene.

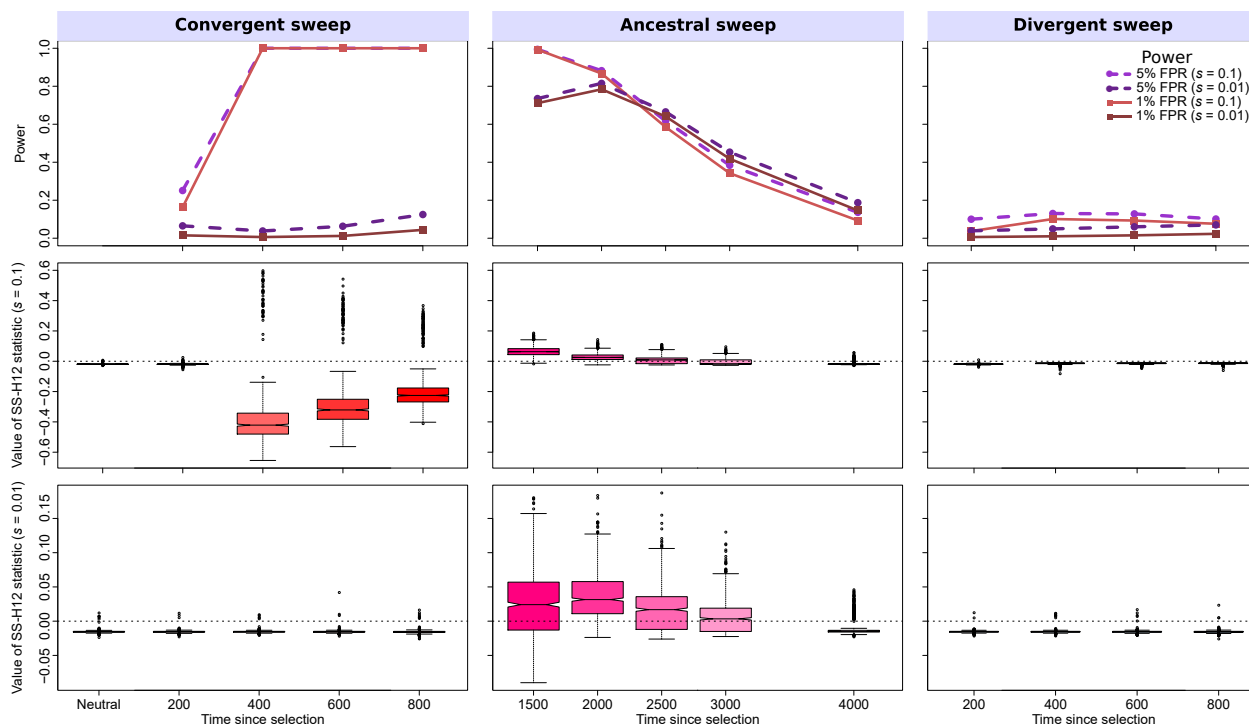


Figure S15: Properties of SS-G123 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) hard sweep scenarios under the CEU-GIH model ($\tau = 1100$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent hard sweeps (see Figure 1) as a function of time at which positive selection of the favored allele initiated (t), with FPR based on the distribution of maximum $|\text{SS-G123}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-G123 values from windows of maximum $|\text{SS-G123}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-G123} = 0$. (Bottom row) Box plots summarizing the distribution of SS-G123 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. Simulated replicates are identical to those in Figure 2, but with each individual's two haplotypes merged into their multilocus genotypes.

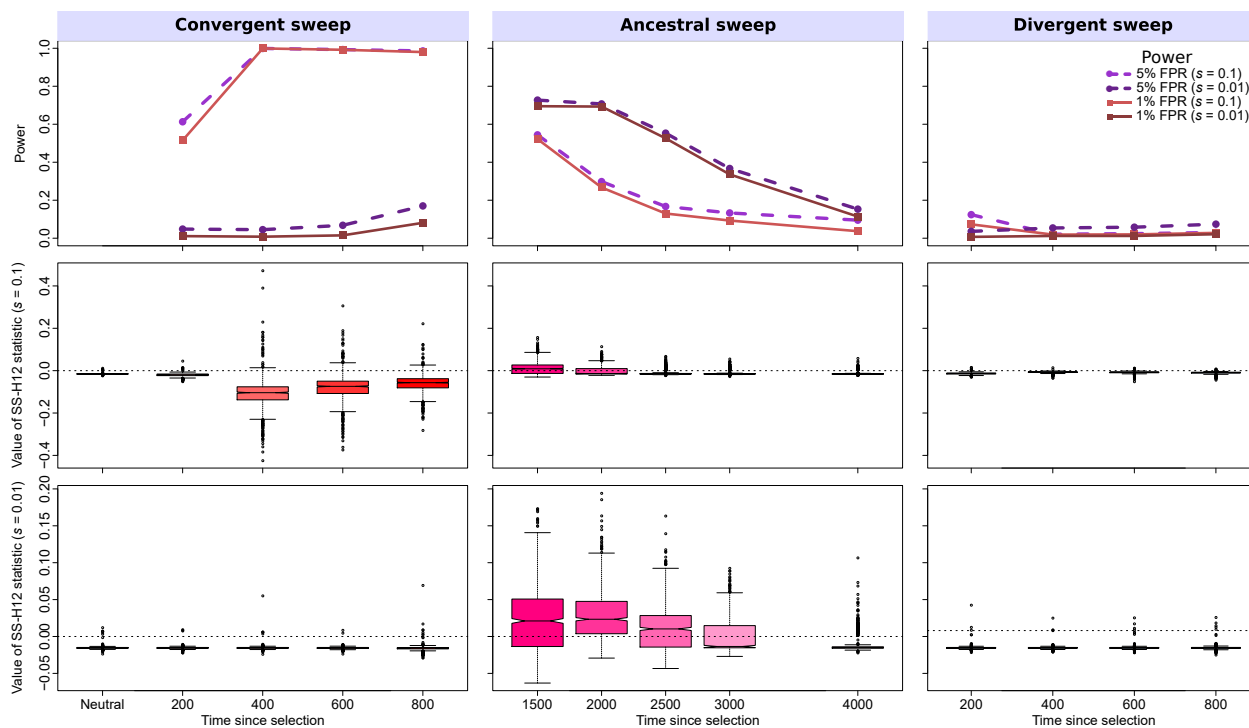


Figure S16: Properties of SS-G123 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) soft sweep ($\nu = 4$) scenarios under the CEU-GIH model ($\tau = 1100$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent soft sweeps from selection on standing genetic variation as a function of time at which selection of the favored haplotypes initiated (t), with FPR based on the distribution of maximum $|\text{SS-G123}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-G123 values from windows of maximum $|\text{SS-G123}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-G123} = 0$. (Bottom row) Box plots summarizing the distribution of SS-G123 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. Simulated replicates are identical to those in Figure S2, but with each individual's two haplotypes merged into their multilocus genotypes.

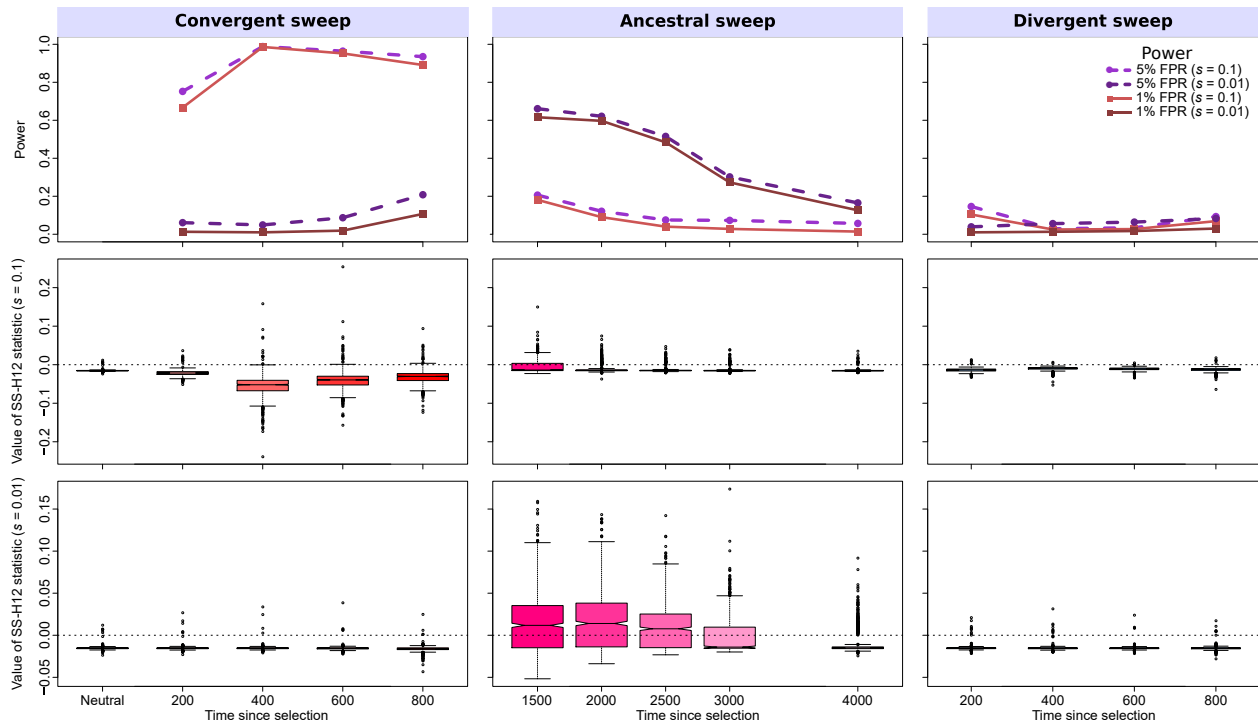


Figure S17: Properties of SS-G123 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) soft sweep ($\nu = 8$) scenarios under the CEU-GIH model ($\tau = 1100$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent soft sweeps from selection on standing genetic variation as a function of time at which selection of the favored haplotypes initiated (t), with FPR based on the distribution of maximum $|\text{SS-G123}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-G123 values from windows of maximum $|\text{SS-G123}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-G123} = 0$. (Bottom row) Box plots summarizing the distribution of SS-G123 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. Simulated replicates are identical to those in Figure S3, but with each individual's two haplotypes merged into their multilocus genotypes.

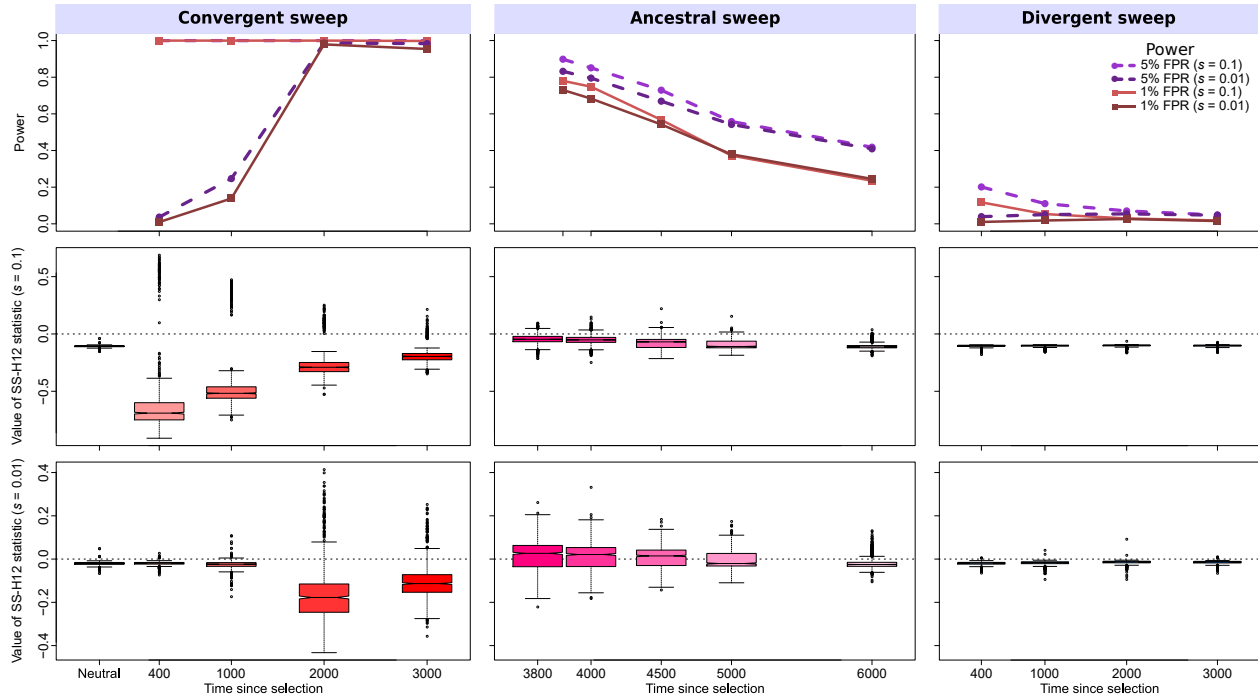


Figure S18: Properties of SS-G123 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) hard sweep scenarios under the CEU-YRI model ($\tau = 3740$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent hard sweeps (see Figure 1) as a function of time at which positive selection of the favored allele initiated (t), with FPR based on the distribution of maximum $|\text{SS-G123}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-G123 values from windows of maximum $|\text{SS-G123}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-G123} = 0$. (Bottom row) Box plots summarizing the distribution of SS-G123 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. Simulated replicates are identical to those in Figure 3, but with each individual's two haplotypes merged into their multilocus genotypes.

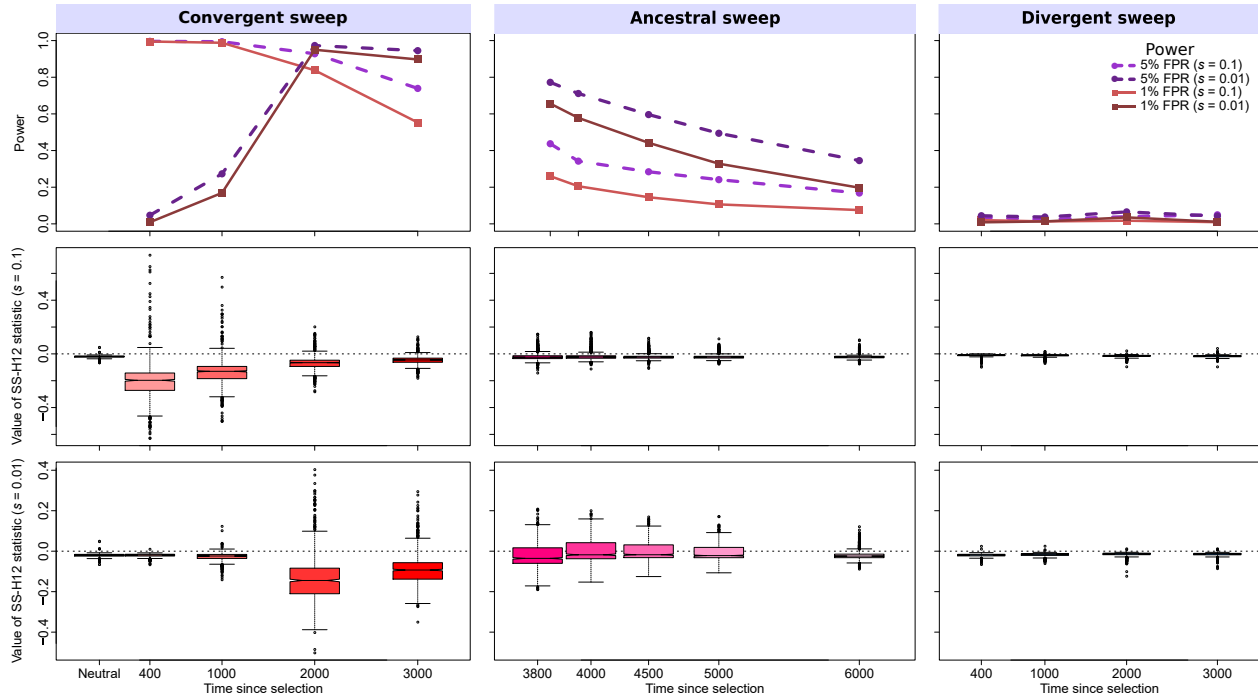


Figure S19: Properties of SS-G123 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) soft sweep ($\nu = 4$) scenarios under the CEU-YRI model ($\tau = 3740$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent soft sweeps from selection on standing genetic variation as a function of time at which selection of the favored haplotypes initiated (t), with FPR based on the distribution of maximum $|\text{SS-G123}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-G123 values from windows of maximum $|\text{SS-G123}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-G123} = 0$. (Bottom row) Box plots summarizing the distribution of SS-G123 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. Simulated replicates are identical to those in Figure S4, but with each individual's two haplotypes merged into their multilocus genotypes.

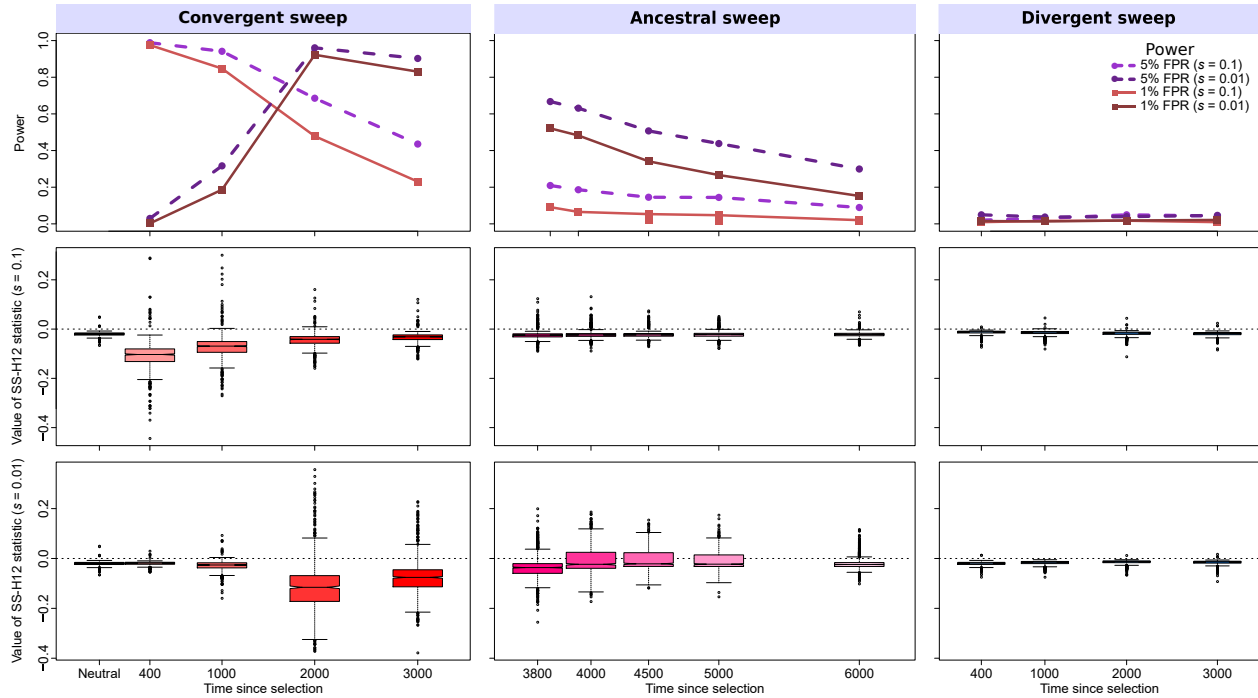


Figure S20: Properties of SS-G123 for simulated strong ($s = 0.1$) and moderate ($s = 0.01$) soft sweep ($\nu = 8$) scenarios under the CEU-YRI model ($\tau = 3740$ generations before sampling). (Top row) Power at 1% (red lines) and 5% (purple lines) false positive rates (FPRs) to detect recent ancestral, convergent, and divergent soft sweeps from selection on standing genetic variation as a function of time at which selection of the favored haplotypes initiated (t), with FPR based on the distribution of maximum $|\text{SS-G123}|$ across simulated neutral replicates. (Middle row) Box plots summarizing the distribution of SS-G123 values from windows of maximum $|\text{SS-G123}|$ across strong sweep replicates, corresponding to each time point in the power curves, with dashed lines in each panel representing $\text{SS-G123} = 0$. (Bottom row) Box plots summarizing the distribution of SS-G123 values across moderate sweep replicates. For convergent and divergent sweeps, $t < \tau$, while for ancestral sweeps, $t > \tau$. Simulated replicates are identical to those in Figure S5, but with each individual's two haplotypes merged into their multilocus genotypes.

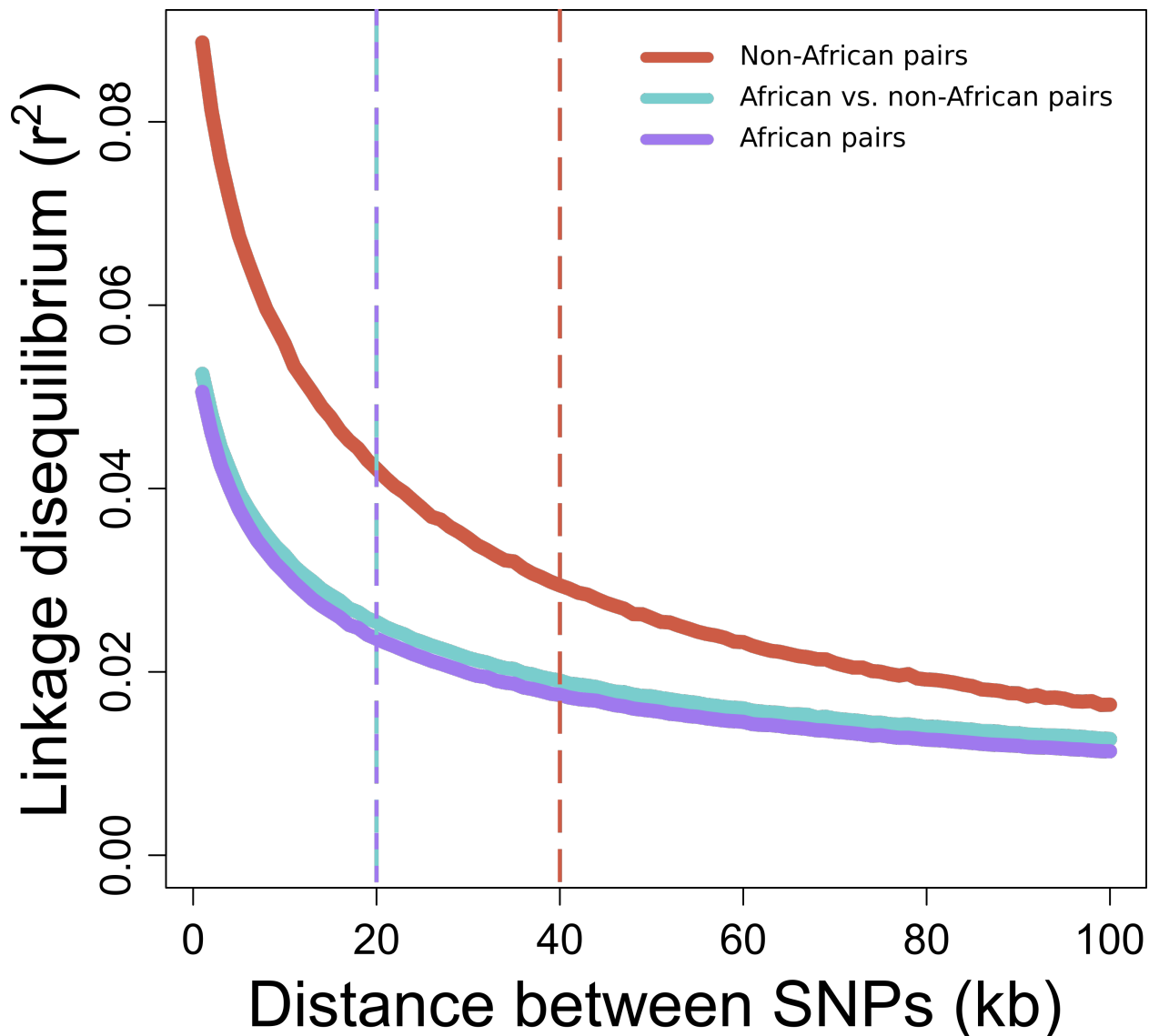


Figure S21: Mean decay of pairwise linkage disequilibrium (LD) measured by r^2 over one to 100 kb intervals downstream of each SNP for pooled population pair samples from the 1000 Genomes Project dataset [Auton et al., 2015]. We used the pooled CEU-JPT sample as representative of LD between non-African population pairs (red), the pooled CEU-YRI population as representative of LD between African and non-African population pairs (cyan), and the pooled LWK-YRI population as representative of the LD between African population pairs (purple). All samples are identical to those analyzed in the *Results* section.