

Table S1: Critical values of H12, G12, and G123, **each generated from 10^6 replicates**, used to assign *p*-values to empirical top candidates across the CEU, YRI, GIH, and CHB populations.

Population	H12	G12	G123
CEU	0.5030609	0.2445669	0.2927252
YRI	0.4792953	0.2182785	0.2859438
GIH	0.4526817	0.2080309	0.2519559
CHB	0.5069281	0.2715619	0.3015364

Table S2: Correlation of the proportion of individuals in short (classes 2 and 3) and intermediate (class 4) length runs of homozygosity with G123 and $\log_{10}(\text{BF})$ across the combined set of 160 top candidate genes for YRI, CEU, GIH, and CHB (40 top candidates from each population).

Statistic	Run of homozygosity class	Pearson correlation coefficient	<i>P</i> -value
G123	Class 2	-0.01428627	0.857
G123	Class 3	-0.008564582	0.9144
G123	Class 4	0.3202083	3.662×10^{-5}
$\log_{10}(\text{BF})$	Class 2	-0.04705734	0.5546
$\log_{10}(\text{BF})$	Class 3	-0.1185176	0.1355
$\log_{10}(\text{BF})$	Class 4	-0.2573454	1.109×10^{-3}

Table S3: Top 40 sweep candidates for CEU, comparing H12 (left) and G12 (right). Candidates are those that remained after application of a mappability and alignability filter to data. Colored cells in the “Top gene” columns indicate genes that appear as top candidates for both H12 and G12. Target genes that pass the significance threshold are colored in gold in the “*p*-value” columns. Genes whose sweeps are assigned as hard with at least moderate BF support are shaded in red in the “Bayes Factor” columns, while soft sweeps are colored in blue. The “*k* (int)” columns indicate the most probable number of sweeping haplotypes *k* (and the 95% Bayesian credibility interval on *k*) from the posterior distribution of 5×10^6 replicates (see *Materials and methods*), and are colored similarly to the “Bayes Factor” columns.

	Top gene	Maximum H12	P-value	Bayes Factor	<i>k</i> (int)	Top gene	Maximum G12	P-value	Bayes Factor	<i>k</i> (int)
1	ZRANB3	0.6310070	< 10 ⁻⁶	0.0788050	1 (1,6)	DARS	0.4102643	< 10 ⁻⁶	0.06027307	1 (1,6)
2	R3HDM1	0.6153964	< 10 ⁻⁶	0.0911549	1 (1,7)	ZRANB3	0.3986328	< 10 ⁻⁶	0.05887361	1 (1,6)
3	DARS	0.6071829	< 10 ⁻⁶	0.0990382	1 (1,7)	R3HDM1	0.3757780	< 10 ⁻⁶	0.07092850	1 (1,6)
4	AC093391.2	0.5685134	< 10 ⁻⁶	0.1278010	1 (1,8)	LCT	0.3370064	< 10 ⁻⁶	0.08677492	1 (1,7)
5	MCM6	0.5469340	< 10 ⁻⁶	0.1471999	1 (1,9)	LOC100507600	0.3370064	< 10 ⁻⁶	0.08677492	1 (1,7)
6	LCT	0.5246403	1.0×10 ⁻⁶	0.1632331	1 (1,10)	AC093391.2	0.3151719	< 10 ⁻⁶	0.10377629	1 (1,8)
7	LOC100507600	0.5246403	1.0×10 ⁻⁶	0.1632331	1 (1,10)	MCM6	0.3059892	< 10 ⁻⁶	0.11228665	1 (1,9)
8	RAB3GAP1	0.5194878	1.0×10 ⁻⁶	0.1769624	1 (1,10)	RAB3GAP1	0.2749719	< 10 ⁻⁶	0.15380886	1 (1,10)
9	UBXN4	0.5028569	3.0×10 ⁻⁶	0.1826827	1 (1,10)	UBXN4	0.2725232	< 10 ⁻⁶	0.13027204	1 (1,9)
10	AC005592.1	0.4957147	3.0×10 ⁻⁶	0.1901564	1 (1,11)	AC005592.1	0.2327314	3.0×10 ⁻⁶	0.15434080	1 (1,11)
11	SLC12A1	0.4822467	3.0×10 ⁻⁶	0.2181227	1 (1,11)	KMT2A	0.2147740	5.0×10 ⁻⁶	0.18703444	1 (1,12)
12	ZNF546	0.4605142	5.0×10 ⁻⁶	0.2177076	1 (1,12)	SLC12A1	0.2147740	5.0×10 ⁻⁶	0.20681348	1 (1,12)
13	NR6A1	0.4565350	5.0×10 ⁻⁶	4.8614907	3 (1,13)	BMP2K	0.2006938	8.0×10 ⁻⁶	0.21889209	1 (1,12)
14	PRKDC	0.4554637	5.0×10 ⁻⁶	6.0146044	3 (1,13)	KITLG	0.1986532	8.0×10 ⁻⁶	0.22204826	1 (1,12)
15	BCAS3	0.4448526	8.0×10 ⁻⁶	0.2511408	1 (1,12)	BCAS3	0.1984491	9.0×10 ⁻⁶	0.22104975	1 (1,12)
16	RAPGEF6	0.4420467	9.0×10 ⁻⁶	0.2895421	1 (1,13)	RAPGEF6	0.1972248	9.0×10 ⁻⁶	0.32434057	1 (1,13)
17	KMT2A	0.4415366	9.0×10 ⁻⁶	0.2436798	1 (1,12)	ZNF546	0.1953882	1.1×10 ⁻⁵	0.17067860	1 (1,11)
18	BMP2K	0.4305173	1.1×10 ⁻⁵	0.2588261	1 (1,13)	PRKDC	0.1923273	1.1×10 ⁻⁵	0.28448312	1 (1,13)
19	MYO9A	0.4290379	1.4×10 ⁻⁵	0.2525099	1 (1,13)	MYO9A	0.1878380	1.2×10 ⁻⁵	0.19343630	1 (1,12)
20	SLC4A4	0.4225589	1.6×10 ⁻⁵	0.2734554	1 (1,13)	PPM1D	0.1802877	2.0×10 ⁻⁵	0.19622385	1 (1,12)
21	HS2ST1	0.4222528	1.6×10 ⁻⁵	0.2994501	1 (1,13)	C4orf22	0.1796755	2.1×10 ⁻⁵	0.21828940	1 (1,12)
22	PPM1D	0.4163351	1.8×10 ⁻⁵	0.2632907	1 (1,13)	RUNX1T1	0.1729415	2.4×10 ⁻⁵	0.25261326	1 (1,13)
23	LCOR	0.4104173	2.2×10 ⁻⁵	0.2714635	1 (1,13)	LCOR	0.1729415	2.4×10 ⁻⁵	0.21297345	1 (1,12)
24	TMEM163	0.4096521	2.2×10 ⁻⁵	0.2921580	1 (1,13)	KAT6B	0.1717172	2.9×10 ⁻⁵	0.20100413	1 (1,12)
25	C4orf22	0.4095500	2.2×10 ⁻⁵	0.2783512	1 (1,13)	SYT1	0.1715131	2.9×10 ⁻⁵	0.64889005	2 (1,14)
26	FAM149B1	0.4089379	2.2×10 ⁻⁵	0.2651361	1 (1,13)	TMEM116	0.1686563	3.4×10 ⁻⁵	0.27465842	1 (1,13)
27	KAT6B	0.4088358	2.2×10 ⁻⁵	0.26558347	1 (1,13)	MIR548O2	0.1657994	3.5×10 ⁻⁵	3.40628814	3 (1,14)
28	POLN	0.4081216	2.3×10 ⁻⁵	0.2692543	1 (1,13)	SLC4A4	0.1651872	3.6×10 ⁻⁵	0.30164422	1 (1,13)
29	KITLG	0.4050097	2.3×10 ⁻⁵	0.2809663	1 (1,13)	TMEM163	0.1643710	3.8×10 ⁻⁵	0.42027840	1 (1,14)
30	LAMA3	0.4029691	2.6×10 ⁻⁵	7.9062228	3 (2,14)	EPHA6	0.1639629	3.8×10 ⁻⁵	0.28598304	1 (1,13)
31	MIR548O2	0.3985818	3.0×10 ⁻⁵	1.9643483	3 (1,14)	HS2ST1	0.1635547	3.9×10 ⁻⁵	0.32556900	1 (1,14)
32	EPHA6	0.3970003	3.2×10 ⁻⁵	0.3116110	1 (1,13)	CCDC178	0.1625344	4.3×10 ⁻⁵	2.98782457	3 (1,14)
33	NCALD	0.3966942	3.3×10 ⁻⁵	0.5488648	1 (1,14)	ACMSD	0.1598816	4.4×10 ⁻⁵	0.31364737	1 (1,14)
34	ABCB1	0.3923069	4.0×10 ⁻⁵	0.8805725	2 (1,14)	CCNT2-AS1	0.1598816	4.4×10 ⁻⁵	0.31364737	1 (1,14)
35	RUND3B	0.3923069	4.0×10 ⁻⁵	0.8805725	2 (1,14)	FGF12	0.1598816	4.4×10 ⁻⁵	0.31364737	1 (1,14)
36	DIRC3	0.3921028	4.0×10 ⁻⁵	0.2884762	1 (1,13)	NR6A1	0.1576370	4.7×10 ⁻⁵	3.19724734	3 (1,15)
37	PRMT9	0.3916437	4.1×10 ⁻⁵	0.3149462	1 (1,13)	DIRC3	0.1545761	5.9×10 ⁻⁵	0.32579743	1 (1,14)
38	ACMSD	0.3875625	5.1×10 ⁻⁵	0.3242798	1 (1,14)	AUTS2	0.1537598	5.9×10 ⁻⁵	0.28390679	1 (1,13)
39	CCNT2-AS1	0.3875625	5.1×10 ⁻⁵	0.3242798	1 (1,14)	HDAC1	0.1494745	7.0×10 ⁻⁵	0.22529102	1 (1,13)
40	MIR181A2HG	0.3850117	5.4×10 ⁻⁵	3.9897455	3 (1,14)	FAM149B1	0.1494745	7.0×10 ⁻⁵	0.21791736	1 (1,13)

Table S4: Top 40 sweep candidates for CEU, comparing H12 (left) and G123 (right). Coloration and analyzed data are as in Table S3.

	Top gene	Maximum H12	P-value	Bayes Factor	k (int)	Top gene	Maximum G123	P-value	Bayes Factor	k (int)
1	ZRANB3	0.6310070	< 10 ⁻⁶	0.0788050	1 (1,6)	ZRANB3	0.4492399	< 10 ⁻⁶	0.05106634	1 (1,5)
2	R3HDM1	0.6153964	< 10 ⁻⁶	0.0911549	1 (1,7)	DARS	0.4488318	< 10 ⁻⁶	0.05861846	1 (1,6)
3	DARS	0.6071829	< 10 ⁻⁶	0.0990382	1 (1,7)	R3HDM1	0.4369962	< 10 ⁻⁶	0.05790528	1 (1,6)
4	AC093391.2	0.5685134	< 10 ⁻⁶	0.1278010	1 (1,8)	LCT	0.3602694	< 10 ⁻⁶	0.09289292	1 (1,8)
5	MCM6	0.5469340	< 10 ⁻⁶	0.1471999	1 (1,9)	LOC100507600	0.3602694	< 10 ⁻⁶	0.09289292	1 (1,8)
6	LCT	0.5246403	1.0×10 ⁻⁶	0.1632331	1 (1,10)	AC093391.2	0.3600653	< 10 ⁻⁶	0.09811256	1 (1,8)
7	LOC100507600	0.5246403	1.0×10 ⁻⁶	0.1632331	1 (1,10)	MCM6	0.3500663	< 10 ⁻⁶	0.10745858	1 (1,8)
8	RAB3GAP1	0.5194878	1.0×10 ⁻⁶	0.1769624	1 (1,10)	RAB3GAP1	0.3270074	< 10 ⁻⁶	0.14090857	1 (1,9)
9	UBXN4	0.5028569	3.0×10 ⁻⁶	0.1826827	1 (1,10)	UBXN4	0.3037445	< 10 ⁻⁶	0.12768015	1 (1,9)
10	AC005592.1	0.4957147	3.0×10 ⁻⁶	0.1901564	1 (1,11)	KMT2A	0.2629324	4.0×10 ⁻⁶	0.20647879	1 (1,12)
11	SLC12A1	0.4822467	3.0×10 ⁻⁶	0.2181227	1 (1,11)	BMP2K	0.2533415	5.0×10 ⁻⁶	0.20419184	1 (1,12)
12	ZNF546	0.4605142	5.0×10 ⁻⁶	0.2177076	1 (1,12)	AC005592.1	0.2519131	5.0×10 ⁻⁶	0.15638982	1 (1,11)
13	NR6A1	0.4565350	5.0×10 ⁻⁶	4.8614907	3 (1,13)	SLC12A1	0.2515049	5.0×10 ⁻⁶	0.20158514	1 (1,12)
14	PRKDC	0.4554637	5.0×10 ⁻⁶	6.0146044	3 (1,13)	NR6A1	0.2406897	8.0×10 ⁻⁶	4.39917404	3 (1,13)
15	BCAS3	0.4448526	8.0×10 ⁻⁶	0.25111408	1 (1,12)	PRKDC	0.2351801	8.0×10 ⁻⁶	0.30747236	1 (1,13)
16	RAPGEF6	0.4420467	9.0×10 ⁻⁶	0.2895421	1 (1,13)	KITLG	0.2337517	8.0×10 ⁻⁶	0.21584020	1 (1,12)
17	KMT2A	0.4415366	9.0×10 ⁻⁶	0.2436798	1 (1,12)	BCAS3	0.2335476	9.0×10 ⁻⁶	0.21473405	1 (1,12)
18	BMP2K	0.4305173	1.1×10 ⁻⁵	0.2588261	1 (1,13)	RAPGEF6	0.2235486	1.0×10 ⁻⁵	0.32978589	1 (1,13)
19	MYO9A	0.4290379	1.4×10 ⁻⁵	0.2525099	1 (1,13)	TMEM116	0.2164065	1.4×10 ⁻⁵	0.27231272	1 (1,13)
20	SLC4A4	0.4225589	1.6×10 ⁻⁵	0.2734554	1 (1,13)	MYO9A	0.2145699	1.5×10 ⁻⁵	0.20772553	1 (1,12)
21	HS2ST1	0.4222528	1.6×10 ⁻⁵	0.2994501	1 (1,13)	RUNX1T1	0.2139578	1.7×10 ⁻⁵	0.34059214	1 (1,13)
22	PPM1D	0.4163351	1.8×10 ⁻⁵	0.2632907	1 (1,13)	LCOR	0.2137537	1.7×10 ⁻⁵	0.20419408	1 (1,12)
23	LCOR	0.4104173	2.2×10 ⁻⁵	0.2714635	1 (1,13)	SLC4A4	0.2129375	2.1×10 ⁻⁵	0.31255148	1 (1,13)
24	TMEM163	0.4096521	2.2×10 ⁻⁵	0.2921580	1 (1,13)	ZNF546	0.2129375	2.1×10 ⁻⁵	0.17454033	1 (1,11)
25	C4orf22	0.4095500	2.2×10 ⁻⁵	0.2783512	1 (1,13)	FGF12	0.2064075	2.5×10 ⁻⁵	0.32488020	1 (1,13)
26	FAM149B1	0.4089379	2.2×10 ⁻⁵	0.2651361	1 (1,13)	MIR548O2	0.2055913	2.5×10 ⁻⁵	3.85294316	3 (1,14)
27	KAT6B	0.4088358	2.2×10 ⁻⁵	0.2658347	1 (1,13)	PPM1D	0.2053872	2.8×10 ⁻⁵	0.19482740	1 (1,12)
28	POLN	0.4081216	2.3×10 ⁻⁵	0.2692543	1 (1,13)	C4orf22	0.2047750	3.2×10 ⁻⁵	0.21603452	1 (1,12)
29	KITLG	0.4050097	2.3×10 ⁻⁵	0.2809663	1 (1,13)	UNC5D	0.2045710	3.2×10 ⁻⁵	1.25517063	2 (1,14)
30	LAMA3	0.4029691	2.6×10 ⁻⁵	7.9062228	3 (2,14)	DIRC3	0.1998776	3.6×10 ⁻⁵	0.33486055	1 (1,14)
31	MIR548O2	0.3985818	3.0×10 ⁻⁵	1.9643483	3 (1,14)	AUTS2	0.1990613	3.7×10 ⁻⁵	0.27653082	1 (1,13)
32	EPHA6	0.3970003	3.2×10 ⁻⁵	0.3116110	1 (1,13)	ACMSD	0.1986532	3.7×10 ⁻⁵	0.31638941	1 (1,13)
33	NCALD	0.3966942	3.3×10 ⁻⁵	0.5488648	1 (1,14)	CCNT2-AS1	0.1986532	3.7×10 ⁻⁵	0.31638941	1 (1,13)
34	ABCB1	0.3923069	4.0×10 ⁻⁵	0.8805725	2 (1,14)	KAT6B	0.1962045	4.3×10 ⁻⁵	0.19944216	1 (1,12)
35	RUND3B	0.3923069	4.0×10 ⁻⁵	0.8805725	2 (1,14)	EPN2	0.1962045	4.3×10 ⁻⁵	0.37485387	1 (1,14)
36	DIRC3	0.3921028	4.0×10 ⁻⁵	0.2884762	1 (1,13)	SYT1	0.1960004	4.3×10 ⁻⁵	0.65056918	2 (1,14)
37	PRMT9	0.3916437	4.1×10 ⁻⁵	0.3149462	1 (1,13)	EPHA6	0.1957963	4.4×10 ⁻⁵	0.28215730	1 (1,13)
38	ACMSD	0.3875625	5.1×10 ⁻⁵	0.3242798	1 (1,14)	TMEM163	0.1882461	5.3×10 ⁻⁵	0.42479989	1 (1,14)
39	CCNT2-AS1	0.3875625	5.1×10 ⁻⁵	0.3242798	1 (1,14)	HS2ST1	0.1874299	5.6×10 ⁻⁵	0.32403875	1 (1,14)
40	MIR181A2HG	0.3850117	5.4×10 ⁻⁵	3.9897455	3 (1,14)	EDC3	0.1870217	6.0×10 ⁻⁵	0.47605799	1 (1,14)

Table S5: Top 40 sweep candidates for CEU, comparing G123 for the true MLGs of diploid study individuals (left) with those of pseudo-individuals produced from random pairs of study haplotypes (right). Coloration and analyzed data are as in Table S3.

	Top gene	Maximum G123	P-value	Bayes Factor	k (int)	Top gene	Maximum G123a	P-value	Bayes Factor	k (int)
1	ZRANB3	0.4492399	< 10 ⁻⁶	0.05106634	1 (1,5)	ZRANB3	0.4361800	< 10 ⁻⁶	0.05756612	1 (1,6)
2	DARS	0.4488318	< 10 ⁻⁶	0.05861846	1 (1,6)	R3HDM1	0.4357719	< 10 ⁻⁶	0.06189584	1 (1,6)
3	R3HDM1	0.4369962	< 10 ⁻⁶	0.05790528	1 (1,6)	DARS	0.4118967	< 10 ⁻⁶	0.08532860	1 (1,7)
4	LCT	0.3602694	< 10 ⁻⁶	0.09289292	1 (1,8)	AC093391.2	0.3259871	< 10 ⁻⁶	0.11558556	1 (1,9)
5	LOC100507600	0.3602694	< 10 ⁻⁶	0.09289292	1 (1,8)	MCM6	0.3172125	< 10 ⁻⁶	0.14000329	1 (1,10)
6	AC093391.2	0.3600653	< 10 ⁻⁶	0.09811256	1 (1,8)	AC005592.1	0.3157841	< 10 ⁻⁶	0.13022001	1 (1,9)
7	MCM6	0.3500663	< 10 ⁻⁶	0.10745858	1 (1,8)	RAB3GAP1	0.3076217	< 10 ⁻⁶	0.15882140	1 (1,10)
8	RAB3GAP1	0.3270074	< 10 ⁻⁶	0.14090857	1 (1,9)	LCT	0.3061932	< 10 ⁻⁶	0.13601396	1 (1,10)
9	UBXN4	0.3037445	< 10 ⁻⁶	0.12768015	1 (1,9)	LOC100507600	0.2943577	< 10 ⁻⁶	0.13952311	1 (1,10)
10	KMT2A	0.2629324	4.0×10 ⁻⁶	0.20647879	1 (1,12)	SLC12A1	0.2929293	2.0×10 ⁻⁶	0.35402209	1 (1,12)
11	BMP2K	0.2533415	5.0×10 ⁻⁶	0.20419184	1 (1,12)	DIRC3	0.2859912	3.0×10 ⁻⁶	0.46917725	2 (1,12)
12	AC005592.1	0.2519131	5.0×10 ⁻⁶	0.15638982	1 (1,11)	UBXN4	0.2821141	3.0×10 ⁻⁶	0.14250366	1 (1,10)
13	SLC12A1	0.2515049	5.0×10 ⁻⁶	0.20158514	1 (1,12)	BCAS3	0.2733395	3.0×10 ⁻⁶	0.18212457	1 (1,11)
14	NR6A1	0.2406897	8.0×10 ⁻⁶	4.39917404	3 (1,13)	ZNF546	0.2723192	3.0×10 ⁻⁶	0.15021128	1 (1,10)
15	PRKDC	0.2351801	8.0×10 ⁻⁶	0.30747236	1 (1,13)	PPM1D	0.2717070	3.0×10 ⁻⁶	0.15825481	1 (1,11)
16	KITLG	0.2337517	8.0×10 ⁻⁶	0.21584020	1 (1,12)	KMT2A	0.2715029	3.0×10 ⁻⁶	0.16417264	1 (1,11)
17	BCAS3	0.2335476	9.0×10 ⁻⁶	0.21473405	1 (1,12)	FGF12	0.2541577	5.0×10 ⁻⁶	0.51825655	2 (1,13)
18	RAPGEF6	0.2235486	1.0×10 ⁻⁵	0.32978589	1 (1,13)	FAM149B1	0.2515049	5.0×10 ⁻⁶	0.16621949	1 (1,11)
19	TMEM116	0.2164065	1.4×10 ⁻⁵	0.27231272	1 (1,13)	PRKDC	0.2459953	5.0×10 ⁻⁶	0.37782841	1 (1,13)
20	MYO9A	0.2145699	1.5×10 ⁻⁵	0.20772553	1 (1,12)	LCOR	0.2445669	5.0×10 ⁻⁶	0.20819590	1 (1,12)
21	RUNX1T1	0.2139578	1.7×10 ⁻⁵	0.34059214	1 (1,13)	CTNNNA3	0.2439547	5.0×10 ⁻⁶	1.87823990	2 (1,13)
22	LCOR	0.2137537	1.7×10 ⁻⁵	0.20419408	1 (1,12)	AUTS2	0.2345679	8.0×10 ⁻⁶	0.34392030	1 (1,13)
23	SLC4A4	0.2129375	2.1×10 ⁻⁵	0.31255148	1 (1,13)	ADRBK2	0.2333435	9.0×10 ⁻⁶	0.21019687	1 (1,12)
24	ZNF546	0.2129375	2.1×10 ⁻⁵	0.17454033	1 (1,11)	TMEM163	0.2331395	9.0×10 ⁻⁶	0.54482704	2 (1,14)
25	FGF12	0.2064075	2.5×10 ⁻⁵	0.32488020	1 (1,13)	HECTD4	0.2249770	1.0×10 ⁻⁵	2.76790033	3 (1,14)
26	MIR548O2	0.2055913	2.5×10 ⁻⁵	3.85294316	3 (1,14)	SLC4A4	0.2241608	1.0×10 ⁻⁵	0.74146015	2 (1,14)
27	PPM1D	0.2053872	2.8×10 ⁻⁵	0.19482740	1 (1,12)	BMP2K	0.2241608	1.0×10 ⁻⁵	0.19419981	1 (1,12)
28	C4orf22	0.2047750	3.2×10 ⁻⁵	0.21603452	1 (1,12)	PVRL3-AS1	0.2239567	1.0×10 ⁻⁵	0.47818084	1 (1,14)
29	UNC5D	0.2045710	3.2×10 ⁻⁵	1.25517063	2 (1,14)	HS2ST1	0.2233446	1.1×10 ⁻⁵	0.57468141	2 (1,14)
30	DIRC3	0.1998776	3.6×10 ⁻⁵	0.33486055	1 (1,14)	FBN1	0.2233446	1.1×10 ⁻⁵	1.93691765	2 (1,14)
31	AUTS2	0.1990613	3.7×10 ⁻⁵	0.27653082	1 (1,13)	PSMB2	0.2231405	1.1×10 ⁻⁵	0.19120882	1 (1,12)
32	ACMSD	0.1986532	3.7×10 ⁻⁵	0.31638941	1 (1,13)	C4orf22	0.2227324	1.3×10 ⁻⁵	0.20578383	1 (1,12)
33	CCNT2-AS1	0.1986532	3.7×10 ⁻⁵	0.31638941	1 (1,13)	POLK	0.2168146	1.4×10 ⁻⁵	7.84619264	4 (1,14)
34	KAT6B	0.1962045	4.3×10 ⁻⁵	0.19944216	1 (1,12)	C12orf4	0.2168146	1.4×10 ⁻⁵	5.70500399	3 (1,14)
35	EPN2	0.1962045	4.3×10 ⁻⁵	0.37485387	1 (1,14)	RUNX1T1	0.2166105	1.4×10 ⁻⁵	5.88163938	3 (1,14)
36	SYT1	0.1960004	4.3×10 ⁻⁵	0.65056918	2 (1,14)	RAPGEF6	0.2147740	1.5×10 ⁻⁵	1.04417126	2 (1,14)
37	EPHA6	0.1957963	4.4×10 ⁻⁵	0.28215730	1 (1,13)	NR6A1	0.2137537	1.7×10 ⁻⁵	1.56302632	2 (1,14)
38	TMEM163	0.1882461	5.3×10 ⁻⁵	0.42479989	1 (1,14)	KITLG	0.2076319	2.4×10 ⁻⁵	0.22750434	1 (1,13)
39	HS2ST1	0.1874299	5.6×10 ⁻⁵	0.32403875	1 (1,14)	TMEM116	0.2074278	2.4×10 ⁻⁵	0.42560068	1 (1,14)
40	EDC3	0.1870217	6.0×10 ⁻⁵	0.47605799	1 (1,14)	P4HA1	0.2064075	2.5×10 ⁻⁵	0.23153963	1 (1,13)

Table S6: Top 40 sweep candidates for YRI, comparing H12 (**left**) and G12 (**right**). Candidates are those that remained after application of a mappability and alignability filter to data (see *Materials and methods*). Coloration follows the scheme in Table S3.

	Top gene	Maximum H12	P-value	Bayes Factor	k (int)		Top gene	Maximum G12	P-value	Bayes Factor	k (int)
1	SYT1	0.5928927	< 10 ⁻⁶	0.4447879	1 (1,13)		SYT1	0.3369342	< 10 ⁻⁶	2.3728246	2 (1,13)
2	RGS18	0.5066015	1.0×10 ⁻⁶	0.3711351	1 (1,14)		HEMGN	0.2503429	1.0×10 ⁻⁶	0.2183565	1 (1,13)
3	HEMGN	0.4996571	1.0×10 ⁻⁶	0.3098409	1 (1,14)		RGS18	0.2277092	1.0×10 ⁻⁶	2.2519587	2 (1,15)
4	GRIK5	0.4583762	5.0×10 ⁻⁶	0.3872785	1 (1,14)		KIAA0825	0.2275377	1.0×10 ⁻⁶	0.2658780	1 (1,14)
5	EHBP1	0.4575617	5.0×10 ⁻⁶	0.3425894	1 (1,14)		ENTHD1	0.2266804	2.0×10 ⁻⁶	0.2766130	1 (1,14)
6	RP11-554F20.1	0.4562757	5.0×10 ⁻⁶	0.3427829	1 (1,14)		PARN	0.2253086	2.0×10 ⁻⁶	0.3805620	1 (1,14)
7	SGCB	0.4509174	5.0×10 ⁻⁶	0.6150720	2 (1,15)		GRIK5	0.2247942	2.0×10 ⁻⁶	0.2824735	1 (1,14)
8	ENTHD1	0.4495456	5.0×10 ⁻⁶	0.3397913	1 (1,14)		EHBP1	0.2196502	2.0×10 ⁻⁶	0.2633368	1 (1,14)
9	PFDN2	0.4491598	5.0×10 ⁻⁶	9.3947331	4 (2,15)		CASC4	0.2066187	4.0×10 ⁻⁶	0.2324388	1 (1,14)
10	KIAA0825	0.4465878	6.0×10 ⁻⁶	0.3550147	1 (1,14)		PFDN2	0.2064472	4.0×10 ⁻⁶	5.4107697	3 (2,15)
11	DDHD2	0.4376715	6.0×10 ⁻⁶	0.3617898	1 (1,15)		NNT	0.2057613	4.0×10 ⁻⁶	0.6344531	2 (1,15)
12	RRN3P3	0.4336848	8.0×10 ⁻⁶	4.5822049	4 (1,15)		GSTT1	0.1942730	8.0×10 ⁻⁶	1.1677157	2 (1,15)
13	PARN	0.4329990	8.0×10 ⁻⁶	0.3888889	1 (1,15)		RP11-554F20.1	0.1887860	1.1×10 ⁻⁵	0.3516938	1 (1,14)
14	PPAPDC1B	0.4311986	9.0×10 ⁻⁶	0.3581410	1 (1,15)		SPRED3	0.1886145	1.1×10 ⁻⁵	0.2303388	1 (1,14)
15	SPRED3	0.4300840	9.0×10 ⁻⁶	0.3439192	1 (1,15)		DANCR	0.1868999	1.1×10 ⁻⁵	0.3639476	1 (1,15)
16	SUGCT	0.4251543	1.0×10 ⁻⁵	22.9649416	4 (2,15)		PAWR	0.1856996	1.1×10 ⁻⁵	0.2680580	1 (1,14)
17	NNT	0.4245542	1.0×10 ⁻⁵	0.3944233	1 (1,15)		SGCB	0.1781550	1.3×10 ⁻⁵	1.3358796	2 (1,15)
18	DEDD	0.4196245	1.6×10 ⁻⁵	0.3565987	1 (1,15)		DDHD2	0.1774691	1.3×10 ⁻⁵	0.3533785	1 (1,15)
19	PAPPA2	0.4181241	1.7×10 ⁻⁵	15.6200900	4 (2,15)		DOCK3	0.1771262	1.6×10 ⁻⁵	3.2695864	3 (1,15)
20	ATP6V1A	0.4137946	2.1×10 ⁻⁵	5.2923586	4 (1,15)		DEDD	0.1769547	1.6×10 ⁻⁵	0.2671020	1 (1,14)
21	UCHL5	0.4129372	2.1×10 ⁻⁵	13.1232474	4 (2,15)		EXOC6B	0.1750686	2.0×10 ⁻⁵	0.3584954	1 (1,15)
22	FBXW4	0.4092078	2.2×10 ⁻⁵	0.5710476	1 (1,15)		MIR548AE2	0.1716392	2.2×10 ⁻⁵	0.2965057	1 (1,14)
23	INPP4A	0.4091650	2.2×10 ⁻⁵	0.4160010	1 (1,15)		LONP2	0.1716392	2.2×10 ⁻⁵	0.2965057	1 (1,14)
24	NANS	0.4085219	2.2×10 ⁻⁵	1.2151494	3 (1,15)		SCMH1	0.1704390	2.3×10 ⁻⁵	0.2838627	1 (1,14)
25	DANCR	0.4084362	2.2×10 ⁻⁵	0.3709887	1 (1,15)		INPP4A	0.1704390	2.3×10 ⁻⁵	0.4567950	1 (1,15)
26	ERLIN2	0.4077932	2.3×10 ⁻⁵	0.4624836	1 (1,15)		PPAPDC1B	0.1702675	2.3×10 ⁻⁵	0.3815229	1 (1,15)
27	PRKAR2A	0.4056927	2.3×10 ⁻⁵	21.1686899	4 (2,15)		UCHL5	0.1649520	2.9×10 ⁻⁵	9.6161349	4 (2,15)
28	ATF2	0.4050069	2.3×10 ⁻⁵	1.8540521	4 (1,15)		SEMA3C	0.1634088	3.0×10 ⁻⁵	0.3240110	1 (1,14)
29	PAWR	0.4042781	2.4×10 ⁻⁵	0.4025418	1 (1,15)		AUTS2	0.1623800	3.3×10 ⁻⁵	1.0664386	2 (1,15)
30	ARID1A	0.4040209	2.4×10 ⁻⁵	0.4641650	1 (1,15)		ERLIN2	0.1613512	3.6×10 ⁻⁵	1.3698636	3 (1,15)
31	EXOC6B	0.4030778	2.5×10 ⁻⁵	0.4835229	1 (1,15)		NT5C2	0.1603224	3.9×10 ⁻⁵	0.3112861	1 (1,14)
32	CASC4	0.4018347	2.7×10 ⁻⁵	0.3766653	1 (1,15)		CDK6	0.1594650	4.0×10 ⁻⁵	0.9256024	2 (1,15)
33	ATF6	0.3987054	2.7×10 ⁻⁵	26.7834582	4 (2,15)		ATF2	0.1568930	4.3×10 ⁻⁵	6.1519224	4 (1,15)
34	CPNE1	0.3975480	2.8×10 ⁻⁵	0.4849515	1 (1,15)		ARID1A	0.1555213	4.4×10 ⁻⁵	0.2805995	1 (1,14)
35	USP46	0.3972479	3.0×10 ⁻⁵	1.9972403	4 (1,15)		USP46	0.1548354	4.5×10 ⁻⁵	0.3180625	1 (1,14)
36	F11R	0.3961763	3.3×10 ⁻⁵	0.4006020	1 (1,15)		F11R	0.1539781	4.5×10 ⁻⁵	0.3058407	1 (1,14)
37	PHKB	0.3959619	3.4×10 ⁻⁵	0.6923486	2 (1,15)		NANS	0.1539781	4.5×10 ⁻⁵	2.1153040	3 (1,15)
38	MIR548H3	0.3956619	3.4×10 ⁻⁵	0.3883438	1 (1,15)		ATP6V1A	0.1536351	4.5×10 ⁻⁵	6.8545563	4 (1,15)
39	DDX19B	0.3945902	3.7×10 ⁻⁵	0.7705183	2 (1,15)		ABHD17B	0.1534636	4.5×10 ⁻⁵	0.2476534	1 (1,14)
40	SCMH1	0.3928755	3.8×10 ⁻⁵	0.4214040	1 (1,15)		RALGAPA2	0.1534636	4.5×10 ⁻⁵	0.2599718	1 (1,14)

Table S7: Top 40 sweep candidates for YRI, comparing H12 (left) and G123 (right). Coloration and analyzed data are as in Table S6.

	Top gene	Maximum H12	P-value	Bayes Factor	k (int)		Top gene	Maximum G123	P-value	Bayes Factor	k (int)
1	SYT1	0.5928927	< 10 ⁻⁶	0.4447879	1 (1,13)		SYT1	0.3900892	< 10 ⁻⁶	2.4702450	2 (1,14)
2	RGS18	0.5066015	1.0×10 ⁻⁶	0.3711351	1 (1,14)		RGS18	0.3048697	1.0×10 ⁻⁶	2.4238151	2 (1,15)
3	HEMGN	0.4996571	1.0×10 ⁻⁶	0.3098409	1 (1,14)		ENTHD1	0.2952675	1.0×10 ⁻⁶	0.2622298	1 (1,14)
4	GRIK5	0.4583762	5.0×10 ⁻⁶	0.3872785	1 (1,14)		HEMGN	0.2866941	2.0×10 ⁻⁶	0.2091045	1 (1,13)
5	EHBP1	0.4575617	5.0×10 ⁻⁶	0.3425894	1 (1,14)		PARN	0.2853224	3.0×10 ⁻⁶	0.4019099	1 (1,14)
6	RP11-554F20.1	0.4562757	5.0×10 ⁻⁶	0.3427829	1 (1,14)		GRIK5	0.2848080	3.0×10 ⁻⁶	0.2680215	1 (1,14)
7	SGCB	0.4509174	5.0×10 ⁻⁶	0.6150720	2 (1,15)		KIAA0825	0.2789781	3.0×10 ⁻⁶	0.2525185	1 (1,14)
8	ENTHD1	0.4495456	5.0×10 ⁻⁶	0.3397913	1 (1,14)		EHBP1	0.2700617	3.0×10 ⁻⁶	0.2500839	1 (1,14)
9	PFDN2	0.4491598	5.0×10 ⁻⁶	9.3947331	4 (2,15)		GSTT1	0.2573731	4.0×10 ⁻⁶	1.2947103	2 (1,15)
10	KIAA0825	0.4465878	6.0×10 ⁻⁶	0.3550147	1 (1,14)		CASC4	0.2477709	6.0×10 ⁻⁶	0.2229544	1 (1,14)
11	DDHD2	0.4376715	6.0×10 ⁻⁶	0.3617898	1 (1,15)		NNT	0.2469136	6.0×10 ⁻⁶	0.6227410	2 (1,15)
12	RRN3P3	0.4336848	8.0×10 ⁻⁶	4.5822049	4 (1,15)		DOCK3	0.2434842	6.0×10 ⁻⁶	3.5854984	3 (1,15)
13	PARN	0.4329990	8.0×10 ⁻⁶	0.3888889	1 (1,15)		PFDN2	0.2393690	7.0×10 ⁻⁶	5.3533082	3 (2,15)
14	PPAPDC1B	0.4311986	9.0×10 ⁻⁶	0.3581410	1 (1,15)		RP11-554F20.1	0.2350823	8.0×10 ⁻⁶	0.3315220	1 (1,14)
15	SPRED3	0.4300840	9.0×10 ⁻⁶	0.3439192	1 (1,15)		PAWR	0.2319959	8.0×10 ⁻⁶	0.2539002	1 (1,14)
16	SUGCT	0.4251543	1.0×10 ⁻⁵	22.9649416	4 (2,15)		SGCB	0.2309671	1.0×10 ⁻⁵	1.4206286	2 (1,15)
17	NNT	0.4245542	1.0×10 ⁻⁵	0.3944233	1 (1,15)		DANCR	0.2254801	1.2×10 ⁻⁵	0.3451735	1 (1,15)
18	DEDD	0.4196245	1.6×10 ⁻⁵	0.3565987	1 (1,15)		CDK6	0.2157064	2.2×10 ⁻⁵	0.9848565	2 (1,15)
19	PAPPA2	0.4181241	1.7×10 ⁻⁵	15.6200900	4 (2,15)		UCHL5	0.2153635	2.2×10 ⁻⁵	9.8964791	4 (2,15)
20	ATP6V1A	0.4137946	2.1×10 ⁻⁵	5.2923586	4 (1,15)		DDHD2	0.2151920	2.2×10 ⁻⁵	0.3345744	1 (1,15)
21	UCHL5	0.4129372	2.1×10 ⁻⁵	13.1232474	4 (2,15)		EXOC6B	0.2127915	2.6×10 ⁻⁵	0.3396833	1 (1,15)
22	FBXW4	0.4092078	2.2×10 ⁻⁵	0.5710476	1 (1,15)		SPRED3	0.2127915	2.6×10 ⁻⁵	0.2317636	1 (1,14)
23	INPP4A	0.4091650	2.2×10 ⁻⁵	0.4160010	1 (1,15)		MIR548AE2	0.2085048	2.7×10 ⁻⁵	0.2822482	1 (1,14)
24	NANS	0.4085219	2.2×10 ⁻⁵	1.2151494	3 (1,15)		LONP2	0.2085048	2.7×10 ⁻⁵	0.2822482	1 (1,14)
25	DANCR	0.4084362	2.2×10 ⁻⁵	0.3709887	1 (1,15)		SCMH1	0.2073045	2.7×10 ⁻⁵	0.2713272	1 (1,14)
26	ERLIN2	0.4077932	2.3×10 ⁻⁵	0.4624836	1 (1,15)		INPP4A	0.2073045	2.7×10 ⁻⁵	0.4364079	1 (1,15)
27	PRKAR2A	0.4056927	2.3×10 ⁻⁵	21.1686899	4 (2,15)		DEDD	0.2071331	2.7×10 ⁻⁵	0.2570753	1 (1,14)
28	ATF2	0.4050069	2.3×10 ⁻⁵	1.8540521	4 (1,15)		PPAPDC1B	0.2071331	2.7×10 ⁻⁵	0.3615976	1 (1,15)
29	PAWR	0.4042781	2.4×10 ⁻⁵	0.4025418	1 (1,15)		SEMA3C	0.2066187	2.8×10 ⁻⁵	0.3060949	1 (1,14)
30	ARID1A	0.4040209	2.4×10 ⁻⁵	0.4641650	1 (1,15)		ATF2	0.2061043	2.9×10 ⁻⁵	6.5712030	4 (1,15)
31	EXOC6B	0.4030778	2.5×10 ⁻⁵	0.4835229	1 (1,15)		REV3L	0.2055898	3.0×10 ⁻⁵	6.0703194	4 (1,15)
32	CASC4	0.4018347	2.7×10 ⁻⁵	0.3766653	1 (1,15)		AUTS2	0.1987311	4.2×10 ⁻⁵	0.8548162	2 (1,15)
33	ATF6	0.3987054	2.7×10 ⁻⁵	26.7834582	4 (2,15)		ERLIN2	0.1973594	4.7×10 ⁻⁵	1.3377451	3 (1,15)
34	CPNE1	0.3975480	2.8×10 ⁻⁵	0.4849515	1 (1,15)		SUGCT	0.1963306	4.9×10 ⁻⁵	5.6281072	4 (1,15)
35	USP46	0.3972479	3.0×10 ⁻⁵	1.9972403	4 (1,15)		PRKAR2A	0.1935871	5.2×10 ⁻⁵	11.5443399	5 (2,15)
36	F11R	0.3961763	3.3×10 ⁻⁵	0.4006020	1 (1,15)		PHKB	0.1930727	5.3×10 ⁻⁵	1.7026498	3 (1,15)
37	PHKB	0.3959619	3.4×10 ⁻⁵	0.6923486	2 (1,15)		DDX19B	0.1920439	5.3×10 ⁻⁵	6.2407541	4 (1,15)
38	MIR548H3	0.3956619	3.4×10 ⁻⁵	0.3883438	1 (1,15)		PSMD14	0.1918724	5.3×10 ⁻⁵	14.8763903	5 (2,15)
39	DDX19B	0.3945902	3.7×10 ⁻⁵	0.7705183	2 (1,15)		ARID1A	0.1906722	5.5×10 ⁻⁵	0.2690225	1 (1,14)
40	SCMH1	0.3928755	3.8×10 ⁻⁵	0.4214040	1 (1,15)		KCMF1	0.1901578	5.7×10 ⁻⁵	3.6527913	4 (1,15)

Table S8: Top 40 sweep candidates for YRI, comparing G123 for the true MLGs of diploid study individuals (left) with those of pseudo-individuals produced from random pairs of study haplotypes (right). Coloration and analyzed data are as in Table S6.

	Top gene	Maximum G123	P-value	Bayes Factor	k (int)		Top gene	Maximum G123a	P-value	Bayes Factor	k (int)
1	SYT1	0.3900892	< 10 ⁻⁶	2.4702450	2 (1,14)		SYT1	0.3470508	1.0×10 ⁻⁶	0.5038651	1 (1,14)
2	RGS18	0.3048697	1.0×10 ⁻⁶	2.4238151	2 (1,15)		RGS18	0.3362483	1.0×10 ⁻⁶	2.5337734	2 (1,14)
3	ENTHD1	0.2952675	1.0×10 ⁻⁶	0.2622298	1 (1,14)		HEMGN	0.2873800	2.0×10 ⁻⁶	0.2166109	1 (1,13)
4	HEMGN	0.2866941	2.0×10 ⁻⁶	0.2091045	1 (1,13)		KIAA0825	0.2805213	3.0×10 ⁻⁶	0.2612820	1 (1,14)
5	PARN	0.2853224	3.0×10 ⁻⁶	0.4019099	1 (1,14)		RP11-554F20.1	0.2789781	3.0×10 ⁻⁶	0.9166766	2 (1,15)
6	GRIK5	0.2848080	3.0×10 ⁻⁶	0.2680215	1 (1,14)		EHBP1	0.2788066	3.0×10 ⁻⁶	0.4126420	1 (1,14)
7	KIAA0825	0.2789781	3.0×10 ⁻⁶	0.2525185	1 (1,14)		GRIK5	0.2767490	3.0×10 ⁻⁶	0.2669153	1 (1,14)
8	EHBP1	0.2700617	3.0×10 ⁻⁶	0.2500839	1 (1,14)		ERLIN2	0.2671468	3.0×10 ⁻⁶	1.0724595	2 (1,15)
9	GSTT1	0.2573731	4.0×10 ⁻⁶	1.2947103	2 (1,15)		CDK6	0.2662894	3.0×10 ⁻⁶	0.4373488	1 (1,14)
10	CASC4	0.2477709	6.0×10 ⁻⁶	0.2229544	1 (1,14)		DEDD	0.2501715	4.0×10 ⁻⁶	0.2441348	1 (1,14)
11	NNT	0.2469136	6.0×10 ⁻⁶	0.6227410	2 (1,15)		CASC4	0.2487997	4.0×10 ⁻⁶	0.2359202	1 (1,14)
12	DOCK3	0.2434842	6.0×10 ⁻⁶	3.5854984	3 (1,15)		NNT	0.2481139	5.0×10 ⁻⁶	0.2331367	1 (1,14)
13	PFDN2	0.2393690	7.0×10 ⁻⁶	5.3533082	3 (2,15)		SEMA3C	0.2481139	5.0×10 ⁻⁶	0.2745296	1 (1,14)
14	RP11-554F20.1	0.2350823	8.0×10 ⁻⁶	0.3315220	1 (1,14)		ARID1A	0.2414266	7.0×10 ⁻⁶	2.2620459	3 (1,15)
15	PAWR	0.2319959	8.0×10 ⁻⁶	0.2539002	1 (1,14)		ENTHD1	0.2405693	7.0×10 ⁻⁶	0.2581309	1 (1,14)
16	SGCB	0.2309671	1.0×10 ⁻⁵	1.4206286	2 (1,15)		UCHL5	0.2402263	7.0×10 ⁻⁶	7.6277939	4 (2,15)
17	DANCR	0.2254801	1.2×10 ⁻⁵	0.3451735	1 (1,15)		INPP4A	0.2400549	7.0×10 ⁻⁶	0.3200529	1 (1,14)
18	CDK6	0.2157064	2.2×10 ⁻⁵	0.9848565	2 (1,15)		ZNF451	0.2338820	8.0×10 ⁻⁶	1.5944725	2 (1,15)
19	UCHL5	0.2153635	2.2×10 ⁻⁵	9.8964791	4 (2,15)		PARN	0.2338820	8.0×10 ⁻⁶	0.2442379	1 (1,14)
20	DDHD2	0.2151920	2.2×10 ⁻⁵	0.3345744	1 (1,15)		SPRED3	0.2325103	8.0×10 ⁻⁶	0.2959636	1 (1,14)
21	EXOC6B	0.2127915	2.6×10 ⁻⁵	0.3396833	1 (1,15)		PIGV	0.2323388	8.0×10 ⁻⁶	0.2917220	1 (1,14)
22	SPRED3	0.2127915	2.6×10 ⁻⁵	0.2317636	1 (1,14)		SUGCT	0.2304527	1.1×10 ⁻⁵	10.9488746	4 (2,15)
23	MIR548AE2	0.2085048	2.7×10 ⁻⁵	0.2822482	1 (1,14)		TYW5	0.2253086	1.2×10 ⁻⁵	5.5313275	4 (2,15)
24	LONP2	0.2085048	2.7×10 ⁻⁵	0.2822482	1 (1,14)		SGCB	0.2242798	1.3×10 ⁻⁵	3.7961510	3 (1,15)
25	SCMH1	0.2073045	2.7×10 ⁻⁵	0.2713272	1 (1,14)		PHKB	0.2230796	1.4×10 ⁻⁵	3.7695547	3 (1,15)
26	INPP4A	0.2073045	2.7×10 ⁻⁵	0.4364079	1 (1,15)		F11R	0.2223937	1.6×10 ⁻⁵	0.2445016	1 (1,14)
27	DEDD	0.2071331	2.7×10 ⁻⁵	0.2570753	1 (1,14)		STRBP	0.2170782	1.8×10 ⁻⁵	0.8151397	2 (1,15)
28	PPAPDC1B	0.2071331	2.7×10 ⁻⁵	0.3615976	1 (1,15)		DDHD2	0.2169067	1.8×10 ⁻⁵	0.4397154	1 (1,15)
29	SEMA3C	0.2066187	2.8×10 ⁻⁵	0.3060949	1 (1,14)		SCMH1	0.2155350	2.2×10 ⁻⁵	0.2617500	1 (1,14)
30	ATF2	0.2061043	2.9×10 ⁻⁵	6.5712030	4 (1,15)		BTRC	0.2150206	2.3×10 ⁻⁵	2.3707594	3 (1,15)
31	REV3L	0.2055898	3.0×10 ⁻⁵	6.0703194	4 (1,15)		REV3L	0.2139918	2.6×10 ⁻⁵	7.9262508	4 (2,15)
32	AUTS2	0.1987311	4.2×10 ⁻⁵	0.8548162	2 (1,15)		PAWR	0.2124486	2.7×10 ⁻⁵	0.5433119	2 (1,15)
33	ERLIN2	0.1973594	4.7×10 ⁻⁵	1.3377451	3 (1,15)		ANKRD17	0.2100480	2.7×10 ⁻⁵	4.8416855	4 (1,15)
34	SUGCT	0.1963306	4.9×10 ⁻⁵	5.6281072	4 (1,15)		DANCR	0.2097051	2.7×10 ⁻⁵	0.3551508	1 (1,15)
35	PRKAR2A	0.1935871	5.2×10 ⁻⁵	11.5443399	5 (2,15)		AUTS2	0.2088477	2.7×10 ⁻⁵	1.2540033	2 (1,15)
36	PHKB	0.1930727	5.3×10 ⁻⁵	1.7026498	3 (1,15)		RRN3P3	0.2086763	2.7×10 ⁻⁵	6.1594367	4 (1,15)
37	DDX19B	0.1920439	5.3×10 ⁻⁵	6.2407541	4 (1,15)		FAM172A	0.2069616	2.7×10 ⁻⁵	14.9343066	5 (2,15)
38	PSMD14	0.1918724	5.3×10 ⁻⁵	14.8763903	5 (2,15)		PHF20	0.2059328	2.9×10 ⁻⁵	0.4451930	1 (1,15)
39	ARID1A	0.1906722	5.5×10 ⁻⁵	0.2690225	1 (1,14)		LAMA3	0.2055898	3.0×10 ⁻⁵	4.1582727	4 (1,15)
40	KCMF1	0.1901578	5.7×10 ⁻⁵	3.6527913	4 (1,15)		CNNM2	0.2042181	3.5×10 ⁻⁵	0.3933899	1 (1,15)

Table S9: Top 40 sweep candidates for GIH, comparing H12 (**left**) and G12 (**right**). Candidates are those that remained after application of a mappability and alignability filter to data (see *Materials and methods*). Coloration follows the scheme in Table S3.

	Top gene	Maximum H12	P-value	Bayes Factor	k (int)		Top gene	Maximum G12	P-value	Bayes Factor	k (int)
1	SLC12A1	0.5498162	< 10 ⁻⁶	0.1868307	1 (1,10)		SLC12A1	0.2758978	1.0×10 ⁻⁶	0.6851279	2 (1,12)
2	RUNX1T1	0.5264869	< 10 ⁻⁶	0.1879192	1 (1,10)		RUNX1T1	0.2634556	1.0×10 ⁻⁶	0.6216055	2 (1,12)
3	EEF1G	0.5060797	1.0×10 ⁻⁶	0.2740524	1 (1,11)		KDM2A	0.2525214	1.0×10 ⁻⁶	0.1598400	1 (1,11)
4	KDM2A	0.4918937	1.0×10 ⁻⁶	0.2052141	1 (1,11)		EEF1G	0.2187765	1.0×10 ⁻⁶	3.8405285	3 (1,12)
5	P4HA1	0.4724762	1.0×10 ⁻⁶	1.7435802	2 (1,13)		P4HTM	0.1999246	7.0×10 ⁻⁶	0.1889226	1 (1,12)
6	SPATA31D3	0.4623433	1.0×10 ⁻⁶	0.2461002	1 (1,12)		SMAD5	0.1993590	7.0×10 ⁻⁶	0.4794483	1 (1,13)
7	P4HTM	0.4587143	1.0×10 ⁻⁶	0.2267931	1 (1,12)		P4HA1	0.1989820	7.0×10 ⁻⁶	2.5768515	2 (1,13)
8	SMAD5	0.4460835	4.0×10 ⁻⁶	0.2541345	1 (1,12)		CUX2	0.1986050	8.0×10 ⁻⁶	0.2068006	1 (1,12)
9	CUX2	0.4399095	9.0×10 ⁻⁶	0.2588838	1 (1,12)		SPATA31D3	0.1978509	9.0×10 ⁻⁶	0.2669687	1 (1,13)
10	KCNQ5	0.4338769	9.0×10 ⁻⁶	0.2497948	1 (1,12)		KIAA0825	0.1944575	1.0×10 ⁻⁵	0.2594823	1 (1,13)
11	CELSR3	0.4334056	1.0×10 ⁻⁵	0.2643386	1 (1,13)		KCNQ5	0.1929494	1.0×10 ⁻⁵	0.2285045	1 (1,12)
12	ZNF546	0.4258177	2.0×10 ⁻⁵	0.2780846	1 (1,13)		KIAA0947	0.1916297	1.0×10 ⁻⁵	1.7655200	2 (1,14)
13	KCND2	0.4176171	2.1×10 ⁻⁵	0.3824129	1 (1,13)		NLK	0.1823923	1.5×10 ⁻⁵	0.6814040	2 (1,14)
14	KIAA0825	0.4099821	3.0×10 ⁻⁵	0.2823101	1 (1,13)		KCND2	0.1769253	1.5×10 ⁻⁵	2.1068939	2 (1,14)
15	NLK	0.4090395	3.1×10 ⁻⁵	0.3179821	1 (1,13)		CELSR3	0.1752286	1.5×10 ⁻⁵	0.2257331	1 (1,13)
16	EXOC6B	0.4085682	3.2×10 ⁻⁵	0.2651058	1 (1,13)		ZNF546	0.1740975	1.8×10 ⁻⁵	0.3194599	1 (1,13)
17	PRMT9	0.4035253	3.6×10 ⁻⁵	0.2808257	1 (1,13)		FABP5	0.1733434	2.1×10 ⁻⁵	0.1935290	1 (1,12)
18	VPS45	0.3982939	4.0×10 ⁻⁵	0.3038464	1 (1,13)		EXOC6B	0.1718352	2.2×10 ⁻⁵	0.2619755	1 (1,13)
19	RNF121	0.3961259	4.2×10 ⁻⁵	0.3452225	1 (1,13)		BCAS3	0.1661797	2.7×10 ⁻⁵	0.2165031	1 (1,12)
20	RALGAPB	0.3922613	4.5×10 ⁻⁵	0.3037277	1 (1,13)		USP46	0.1518522	5.4×10 ⁻⁵	0.2334447	1 (1,13)
21	SSH2	0.3921199	4.5×10 ⁻⁵	2.3548763	3 (1,14)		PATL1	0.1518522	5.4×10 ⁻⁵	0.2228148	1 (1,13)
22	KIAA0947	0.3913658	4.6×10 ⁻⁵	0.3838530	1 (1,14)		SUGCT	0.1514752	5.7×10 ⁻⁵	0.3290481	1 (1,14)
23	ADAMTS6	0.3870770	5.1×10 ⁻⁵	9.1600799	4 (1,14)		FBXO4	0.1505326	6.6×10 ⁻⁵	0.4900826	1 (1,14)
24	SLC26A6	0.3840136	5.6×10 ⁻⁵	0.3339177	1 (1,14)		PRMT9	0.1465737	7.1×10 ⁻⁵	0.2412547	1 (1,13)
25	GREB1L	0.3716184	8.8×10 ⁻⁵	10.8010130	4 (1,14)		APPBP2	0.1452540	7.7×10 ⁻⁵	0.2333901	1 (1,13)
26	ADK	0.3694033	9.0×10 ⁻⁵	8.2307308	4 (1,14)		HS2ST1	0.1445000	8.2×10 ⁻⁵	0.2398467	1 (1,13)
27	SNAP91	0.3689320	9.1×10 ⁻⁵	5.0447150	4 (2,15)		RNF121	0.1445000	8.2×10 ⁻⁵	0.2768325	1 (1,13)
28	GPC5	0.3683194	9.4×10 ⁻⁵	0.3490552	1 (1,14)		PPP1R12A	0.1441229	8.3×10 ⁻⁵	0.2725638	1 (1,13)
29	BCAS3	0.3676124	9.9×10 ⁻⁵	0.3015640	1 (1,14)		FADS2	0.1433688	8.3×10 ⁻⁵	0.2462957	1 (1,13)
30	FABP5	0.3664813	1.06×10 ⁻⁴	0.3115463	1 (1,14)		VPS45	0.1424262	8.4×10 ⁻⁵	0.2908501	1 (1,13)
31	SLC23A1	0.3659157	1.07×10 ⁻⁴	8.5683998	4 (1,14)		CEP350	0.1422377	8.4×10 ⁻⁵	0.2892411	1 (1,13)
32	TBXAS1	0.3653973	1.09×10 ⁻⁴	3.1805930	3 (1,15)		RALGAPB	0.1414836	8.5×10 ⁻⁵	0.3067448	1 (1,14)
33	RNU6-28P	0.3630879	1.17×10 ⁻⁴	1.2943940	2 (1,15)		PRKAR2A	0.1405411	8.8×10 ⁻⁵	0.2731190	1 (1,13)
34	PPIP5K1	0.3630879	1.17×10 ⁻⁴	1.2943940	2 (1,15)		PTPRK	0.1388444	9.9×10 ⁻⁵	0.2788808	1 (1,13)
35	CEP350	0.3629937	1.18×10 ⁻⁴	0.3154847	1 (1,14)		METTL25	0.1388444	9.9×10 ⁻⁵	0.2442649	1 (1,13)
36	DPH6-AS1	0.3620040	1.23×10 ⁻⁴	6.7453791	4 (2,15)		CHRN3	0.1386559	9.9×10 ⁻⁵	0.2766622	1 (1,13)
37	COMM3-BMI1	0.3614855	1.25×10 ⁻⁴	0.3210330	1 (1,14)		DPH6-AS1	0.1384673	1.01×10 ⁻⁴	0.4010478	1 (1,14)
38	BMI1	0.3614855	1.25×10 ⁻⁴	0.3210330	1 (1,14)		MTF2	0.1380903	1.03×10 ⁻⁴	0.7534079	2 (1,15)
39	ZMYM1	0.3596475	1.37×10 ⁻⁴	0.3508923	1 (1,14)		KIAA0556	0.1377133	1.03×10 ⁻⁴	0.2272245	1 (1,13)
40	HELZ	0.3571496	1.43×10 ⁻⁴	1.5539256	3 (1,15)		RNU6-28P	0.1371477	1.08×10 ⁻⁴	1.5540063	3 (1,15)

Table S10: Top 40 sweep candidates for GIH, comparing H12 (**left**) and G123 (**right**). Coloration and analyzed data are as in Table S9.

	Top gene	Maximum H12	P-value	Bayes Factor	k (int)	Top gene	Maximum G123	P-value	Bayes Factor	k (int)
1	SLC12A1	0.5498162	< 10 ⁻⁶	0.1868307	1 (1,10)	SLC12A1	0.3458384	1.0×10 ⁻⁶	0.7401583	2 (1,11)
2	RUNX1T1	0.5264869	< 10 ⁻⁶	0.1879192	1 (1,10)	RUNX1T1	0.3124705	1.0×10 ⁻⁶	0.6575972	2 (1,12)
3	EEF1G	0.5060797	1.0×10 ⁻⁶	0.2740524	1 (1,11)	KDM2A	0.2813649	1.0×10 ⁻⁶	0.1592963	1 (1,11)
4	KDM2A	0.4918937	1.0×10 ⁻⁶	0.2052141	1 (1,11)	KIAA0825	0.2708078	1.0×10 ⁻⁶	0.7820495	2 (1,13)
5	P4HA1	0.4724762	1.0×10 ⁻⁶	1.7435802	2 (1,13)	SPATA31D3	0.2642096	1.0×10 ⁻⁶	0.3020106	1 (1,12)
6	SPATA31D3	0.4623433	1.0×10 ⁻⁶	0.2461002	1 (1,12)	EEF1G	0.2542181	2.0×10 ⁻⁶	4.4004005	3 (1,13)
7	P4HTM	0.4587143	1.0×10 ⁻⁶	0.2267931	1 (1,12)	KCNQ5	0.2427184	5.0×10 ⁻⁶	0.2163047	1 (1,12)
8	SMAD5	0.4460835	4.0×10 ⁻⁶	0.2541345	1 (1,12)	P4HTM	0.2423414	6.0×10 ⁻⁶	0.1800392	1 (1,11)
9	CUX2	0.4399095	9.0×10 ⁻⁶	0.2588838	1 (1,12)	KIAA0947	0.2413988	6.0×10 ⁻⁶	2.0221779	2 (1,14)
10	KCNQ5	0.4338769	9.0×10 ⁻⁶	0.2497948	1 (1,12)	SMAD5	0.2332925	8.0×10 ⁻⁶	0.5006187	1 (1,13)
11	CELSR3	0.4334056	1.0×10 ⁻⁵	0.2643386	1 (1,13)	KCND2	0.2244321	1.1×10 ⁻⁵	2.4688336	2 (1,14)
12	ZNF546	0.4258177	2.0×10 ⁻⁵	0.2780846	1 (1,13)	P4HA1	0.2244321	1.1×10 ⁻⁵	2.5651789	3 (1,14)
13	KCND2	0.4176171	2.1×10 ⁻⁵	0.3824129	1 (1,13)	CUX2	0.2240550	1.1×10 ⁻⁵	0.2060792	1 (1,12)
14	KIAA0825	0.4099821	3.0×10 ⁻⁵	0.2823101	1 (1,13)	EXOC6B	0.2182110	1.4×10 ⁻⁵	0.2543031	1 (1,13)
15	NLK	0.4090395	3.1×10 ⁻⁵	0.3179821	1 (1,13)	FBXO4	0.2078424	1.9×10 ⁻⁵	0.6262816	2 (1,14)
16	EXOC6B	0.4085682	3.2×10 ⁻⁵	0.2651058	1 (1,13)	CELSR3	0.2068998	1.9×10 ⁻⁵	0.2206053	1 (1,12)
17	PRMT9	0.4035253	3.6×10 ⁻⁵	0.2808257	1 (1,13)	NLK	0.2067113	1.9×10 ⁻⁵	0.6632448	2 (1,14)
18	VPS45	0.3982939	4.0×10 ⁻⁵	0.3038464	1 (1,13)	ZNF546	0.1978509	2.6×10 ⁻⁵	0.3200392	1 (1,13)
19	RNF121	0.3961259	4.2×10 ⁻⁵	0.3452225	1 (1,13)	BCAS3	0.1893675	4.3×10 ⁻⁵	0.2143972	1 (1,12)
20	RALGAPB	0.3922613	4.5×10 ⁻⁵	0.3037277	1 (1,13)	FABP5	0.1891790	4.5×10 ⁻⁵	0.1945499	1 (1,12)
21	SSH2	0.3921199	4.5×10 ⁻⁵	2.3548763	3 (1,14)	RNU6-28P	0.1846545	4.5×10 ⁻⁵	2.1387075	3 (1,15)
22	KIAA0947	0.3913658	4.6×10 ⁻⁵	0.3838530	1 (1,14)	PPIP5K1	0.1846545	4.5×10 ⁻⁵	2.1387075	3 (1,15)
23	ADAMTS6	0.3870770	5.1×10 ⁻⁵	9.1600799	4 (1,14)	CEP350	0.1840890	4.7×10 ⁻⁵	0.2801608	1 (1,13)
24	SLC26A6	0.3840136	5.6×10 ⁻⁵	0.3339177	1 (1,14)	RNF121	0.1818268	6.6×10 ⁻⁵	3.3519127	3 (1,15)
25	GREB1L	0.3716184	8.8×10 ⁻⁵	10.8010130	4 (1,14)	USP46	0.1812612	7.1×10 ⁻⁵	0.2291151	1 (1,13)
26	ADK	0.3694033	9.0×10 ⁻⁵	8.2307308	4 (1,14)	PATL1	0.1812612	7.1×10 ⁻⁵	0.2188847	1 (1,13)
27	SNAP91	0.3689320	9.1×10 ⁻⁵	5.0447150	4 (2,15)	VPS45	0.1773023	7.8×10 ⁻⁵	0.2836972	1 (1,13)
28	GPC5	0.3683194	9.4×10 ⁻⁵	0.3490552	1 (1,14)	RALGAPB	0.1763597	7.8×10 ⁻⁵	0.2996623	1 (1,13)
29	BCAS3	0.3676124	9.9×10 ⁻⁵	0.3015640	1 (1,14)	PRKAR2A	0.1754171	8.1×10 ⁻⁵	0.2652970	1 (1,13)
30	FABP5	0.3664813	1.06×10 ⁻⁴	0.3115463	1 (1,14)	GPC5	0.1754171	8.1×10 ⁻⁵	0.4353939	1 (1,14)
31	SLC23A1	0.3659157	1.07×10 ⁻⁴	8.5683998	4 (1,14)	PRMT9	0.1752286	8.3×10 ⁻⁵	0.2365477	1 (1,13)
32	TBXAS1	0.3653973	1.09×10 ⁻⁴	3.1805930	3 (1,15)	FBXL19	0.1750401	8.4×10 ⁻⁵	2.8933491	3 (1,15)
33	RNU6-28P	0.3630879	1.17×10 ⁻⁴	1.2943940	2 (1,15)	PTPRK	0.1737204	9.7×10 ⁻⁵	0.2707310	1 (1,13)
34	PPIP5K1	0.3630879	1.17×10 ⁻⁴	1.2943940	2 (1,15)	SUGCT	0.1735319	9.8×10 ⁻⁵	0.3238500	1 (1,14)
35	CEP350	0.3629937	1.18×10 ⁻⁴	0.3154847	1 (1,14)	HS2ST1	0.1731549	1.00×10 ⁻⁴	0.2355341	1 (1,13)
36	DPH6-AS1	0.3620040	1.23×10 ⁻⁴	6.7453791	4 (2,15)	PPP1R12A	0.1727778	1.03×10 ⁻⁴	0.2672769	1 (1,13)
37	COMM3-BMI1	0.3614855	1.25×10 ⁻⁴	0.3210330	1 (1,14)	GREB1L	0.1682534	1.08×10 ⁻⁴	1.6145271	3 (1,15)
38	BMI1	0.3614855	1.25×10 ⁻⁴	0.3210330	1 (1,14)	TUT1	0.1680649	1.09×10 ⁻⁴	2.1210219	3 (1,15)
39	ZMYM1	0.3596475	1.37×10 ⁻⁴	0.3508923	1 (1,14)	TSPAN12	0.1673108	1.14×10 ⁻⁴	0.3322767	1 (1,14)
40	HELZ	0.3571496	1.43×10 ⁻⁴	1.5539256	3 (1,15)	METTL25	0.1667452	1.25×10 ⁻⁴	0.2401106	1 (1,13)

Table S11: Top 40 sweep candidates for GIH, comparing G123 for the true MLGs of diploid study individuals (left) with those of pseudo-individuals produced from random pairs of study haplotypes (right). Coloration and analyzed data are as in Table S9.

Top gene	Maximum G123	P-value	Bayes Factor	k (int)	Top gene	Maximum G123a	P-value	Bayes Factor	k (int)
1 <i>SLC12A1</i>	0.3458384	1.0×10^{-6}	0.7401583	2 (1,11)	<i>KDM2A</i>	0.3692148	< 10^{-6}	0.2410049	1 (1,10)
2 <i>RUNX1T1</i>	0.3124705	1.0×10^{-6}	0.6575972	2 (1,12)	<i>SLC12A1</i>	0.3607315	< 10^{-6}	3.1777778	2 (1,9)
3 <i>KDM2A</i>	0.2813649	1.0×10^{-6}	0.1592963	1 (1,11)	<i>RUNX1T1</i>	0.3251013	1.0×10^{-6}	0.1994129	1 (1,10)
4 <i>KIAA0825</i>	0.2708078	1.0×10^{-6}	0.7820495	2 (1,13)	<i>SPATA31D3</i>	0.3156754	1.0×10^{-6}	0.1929338	1 (1,10)
5 <i>SPATA31D3</i>	0.2642096	1.0×10^{-6}	0.3020106	1 (1,12)	<i>EEF1G</i>	0.3019135	1.0×10^{-6}	1.5241856	2 (1,12)
6 <i>EEF1G</i>	0.2542181	2.0×10^{-6}	4.4004005	3 (1,13)	<i>RALGAPB</i>	0.2540296	2.0×10^{-6}	0.2023247	1 (1,12)
7 <i>KCNQ5</i>	0.2427184	5.0×10^{-6}	0.2163047	1 (1,12)	<i>P4HA1</i>	0.2534640	2.0×10^{-6}	4.9063792	3 (1,13)
8 <i>P4HTM</i>	0.2423414	6.0×10^{-6}	0.1800392	1 (1,11)	<i>SMAD5</i>	0.2451692	4.0×10^{-6}	0.4545719	1 (1,13)
9 <i>KIAA0947</i>	0.2413988	6.0×10^{-6}	2.0221779	2 (1,14)	<i>PPP1R42</i>	0.2449807	4.0×10^{-6}	0.7695942	2 (1,14)
10 <i>SMAD5</i>	0.2332925	8.0×10^{-6}	0.5006187	1 (1,13)	<i>KIAA0825</i>	0.2438496	4.0×10^{-6}	0.1983985	1 (1,12)
11 <i>KCND2</i>	0.2244321	1.1×10^{-5}	2.4688336	2 (1,14)	<i>EXOC6B</i>	0.2355547	7.0×10^{-6}	0.2076274	1 (1,12)
12 <i>P4HA1</i>	0.2244321	1.1×10^{-5}	2.5651789	3 (1,14)	<i>KCNQ5</i>	0.2338580	7.0×10^{-6}	0.1791274	1 (1,11)
13 <i>CUX2</i>	0.2240550	1.1×10^{-5}	0.2060792	1 (1,12)	<i>P4HTM</i>	0.2246206	1.1×10^{-5}	0.1813244	1 (1,12)
14 <i>EXOC6B</i>	0.2182110	1.4×10^{-5}	0.2543031	1 (1,13)	<i>CEP350</i>	0.2165143	1.4×10^{-5}	0.2642069	1 (1,13)
15 <i>FBXO4</i>	0.2078424	1.9×10^{-5}	0.6262816	2 (1,14)	<i>VPS45</i>	0.2161372	1.4×10^{-5}	0.3057306	1 (1,13)
16 <i>CELSR3</i>	0.2068998	1.9×10^{-5}	0.2206053	1 (1,12)	<i>DDB1</i>	0.2159487	1.5×10^{-5}	0.2935921	1 (1,13)
17 <i>NLK</i>	0.2067113	1.9×10^{-5}	0.6632448	2 (1,14)	<i>KCND2</i>	0.2080309	1.9×10^{-5}	3.3576880	3 (1,14)
18 <i>ZNF546</i>	0.1978509	2.6×10^{-5}	0.3200392	1 (1,13)	<i>NLK</i>	0.2070883	1.9×10^{-5}	0.6823070	2 (1,14)
19 <i>BCAS3</i>	0.1893675	4.3×10^{-5}	0.2143972	1 (1,12)	<i>RAD51B</i>	0.1999246	2.2×10^{-5}	0.3359709	1 (1,14)
20 <i>FABP5</i>	0.1891790	4.5×10^{-5}	0.1945499	1 (1,12)	<i>USP46</i>	0.1995476	2.3×10^{-5}	0.2333471	1 (1,13)
21 <i>RNU6-28P</i>	0.1846545	4.5×10^{-5}	2.1387075	3 (1,15)	<i>CUX2</i>	0.1938920	2.9×10^{-5}	0.3760942	1 (1,14)
22 <i>PPIP5K1</i>	0.1846545	4.5×10^{-5}	2.1387075	3 (1,15)	<i>RNU6-28P</i>	0.1927609	3.0×10^{-5}	1.6261752	2 (1,14)
23 <i>CEP350</i>	0.1840890	4.7×10^{-5}	0.2801608	1 (1,13)	<i>PPIP5K1</i>	0.1927609	3.0×10^{-5}	1.6261752	2 (1,14)
24 <i>RNF121</i>	0.1818268	6.6×10^{-5}	3.3519127	3 (1,15)	<i>RNF121</i>	0.1914412	3.1×10^{-5}	2.4062690	3 (1,14)
25 <i>USP46</i>	0.1812612	7.1×10^{-5}	0.2291151	1 (1,13)	<i>SSH2</i>	0.1914412	3.1×10^{-5}	2.1816189	3 (1,14)
26 <i>PATL1</i>	0.1812612	7.1×10^{-5}	0.2188847	1 (1,13)	<i>GABRB2</i>	0.1910642	3.1×10^{-5}	0.5451186	1 (1,14)
27 <i>VPS45</i>	0.1773023	7.8×10^{-5}	0.2836972	1 (1,13)	<i>NR2F1-AS1</i>	0.1908757	3.1×10^{-5}	2.6491451	3 (1,15)
28 <i>RALGAPB</i>	0.1763597	7.8×10^{-5}	0.2996623	1 (1,13)	<i>FBXL19</i>	0.1908757	3.1×10^{-5}	3.0358582	3 (1,15)
29 <i>PRKAR2A</i>	0.1754171	8.1×10^{-5}	0.2652970	1 (1,13)	<i>APPBP2</i>	0.1904986	3.4×10^{-5}	0.2180203	1 (1,12)
30 <i>GPC5</i>	0.1754171	8.1×10^{-5}	0.4353939	1 (1,14)	<i>LOC100188947</i>	0.1903101	3.5×10^{-5}	0.7331984	2 (1,14)
31 <i>PRMT9</i>	0.1752286	8.3×10^{-5}	0.2365477	1 (1,13)	<i>HECTD2</i>	0.1903101	3.5×10^{-5}	0.7331984	2 (1,14)
32 <i>FBXL19</i>	0.1750401	8.4×10^{-5}	2.8933491	3 (1,15)	<i>ANXA7</i>	0.1901216	3.7×10^{-5}	0.5953063	2 (1,14)
33 <i>PTPRK</i>	0.1737204	9.7×10^{-5}	0.2707310	1 (1,13)	<i>KIAA0947</i>	0.1889905	4.5×10^{-5}	0.7238604	2 (1,14)
34 <i>SUGCT</i>	0.1735319	9.8×10^{-5}	0.3238500	1 (1,14)	<i>ZMYM1</i>	0.1861627	4.5×10^{-5}	0.9655766	2 (1,14)
35 <i>HS2ST1</i>	0.1731549	1.00×10^{-4}	0.2355341	1 (1,13)	<i>CLASP2</i>	0.1837119	4.9×10^{-5}	0.8844948	2 (1,14)
36 <i>PPP1R12A</i>	0.1727778	1.03×10^{-4}	0.2672769	1 (1,13)	<i>BCAS3</i>	0.1837119	4.9×10^{-5}	0.2422994	1 (1,13)
37 <i>GREB1L</i>	0.1682534	1.08×10^{-4}	1.6145271	3 (1,15)	<i>SPAG6</i>	0.1835234	4.9×10^{-5}	0.2235184	1 (1,13)
38 <i>TUT1</i>	0.1680649	1.09×10^{-4}	2.1210219	3 (1,15)	<i>TBXAS1</i>	0.1833349	4.9×10^{-5}	2.5473840	3 (1,15)
39 <i>TSPAN12</i>	0.1673108	1.14×10^{-4}	0.3322767	1 (1,14)	<i>ORA13</i>	0.1831464	5.1×10^{-5}	2.3325488	3 (1,15)
40 <i>METTL25</i>	0.1667452	1.25×10^{-4}	0.2401106	1 (1,13)	<i>RP11-682N22.1</i>	0.1829579	5.2×10^{-5}	0.2506462	1 (1,13)

Table S12: Top 40 sweep candidates for CHB, comparing H12 (left) and G12 (right). Candidates are those that remained after application of a mappability and alignability filter to data (see *Materials and methods*). Coloration follows the scheme in Table S3.

	Top gene	Maximum H12	P-value	Bayes Factor	k (int)	Top gene	Maximum G12	P-value	Bayes Factor	k (int)
1	MIR548AE2	0.5900650	< 10 ⁻⁶	3.4614860	2 (1,9)	RANBP10	0.2730700	2.0×10 ⁻⁶	1.0283806	2 (1,12)
2	LOC100507577	0.5535866	1.0×10 ⁻⁶	4.2906216	2 (1,10)	EXOC6B	0.2630785	5.0×10 ⁻⁶	0.1924576	1 (1,11)
3	EXOC6B	0.5466585	2.0×10 ⁻⁶	0.1676242	1 (1,10)	ZNF660	0.2619474	5.0×10 ⁻⁶	0.2123802	1 (1,11)
4	RANBP10	0.5326609	2.0×10 ⁻⁶	4.8778325	2 (1,10)	FMNL3	0.2617589	5.0×10 ⁻⁶	0.1468601	1 (1,10)
5	ZNF660	0.5259214	2.0×10 ⁻⁶	0.1894574	1 (1,11)	ATP6V0D1	0.2617589	5.0×10 ⁻⁶	0.1615796	1 (1,11)
6	FMNL3	0.5188519	2.0×10 ⁻⁶	0.1819477	1 (1,11)	MIR548AE2	0.2538411	6.0×10 ⁻⁶	3.0419833	2 (1,11)
7	ATP6V0D1	0.5118767	2.0×10 ⁻⁶	0.1938132	1 (1,11)	RP11-696N14.1	0.2474314	6.0×10 ⁻⁶	0.2033525	1 (1,12)
8	RP11-696N14.1	0.5057498	3.0×10 ⁻⁶	0.2205014	1 (1,11)	EXD2	0.2430955	7.0×10 ⁻⁶	0.1813310	1 (1,11)
9	ADH1A	0.4957583	7.0×10 ⁻⁶	0.2216801	1 (1,12)	PRPF40B	0.2425299	9.0×10 ⁻⁶	0.1597707	1 (1,11)
10	LONP2	0.4924121	7.0×10 ⁻⁶	5.0084185	3 (1,12)	ADH1A	0.2406447	1.2×10 ⁻⁵	0.2401296	1 (1,12)
11	PRPF40B	0.4915638	8.0×10 ⁻⁶	0.2074760	1 (1,11)	BEND4	0.2321614	2.0×10 ⁻⁵	0.2045374	1 (1,12)
12	BEND4	0.4772363	1.5×10 ⁻⁵	0.2266500	1 (1,12)	NETO2	0.2321614	2.0×10 ⁻⁵	0.1706640	1 (1,11)
13	SLC9A5	0.4721463	1.7×10 ⁻⁵	3.9931687	3 (1,13)	LIMS1	0.2253747	2.5×10 ⁻⁵	0.2023350	1 (1,12)
14	LIMS1	0.4645584	2.5×10 ⁻⁵	0.2391615	1 (1,12)	LOC100507577	0.2176454	3.3×10 ⁻⁵	3.1893823	2 (1,13)
15	ZBTB20	0.4583844	3.1×10 ⁻⁵	0.3099972	1 (1,13)	FBXL19	0.2150061	3.8×10 ⁻⁵	0.1776796	1 (1,12)
16	EXD2	0.4581959	3.3×10 ⁻⁵	0.2486788	1 (1,12)	CCDC138	0.2146291	3.9×10 ⁻⁵	0.1798582	1 (1,12)
17	PTPRK	0.4527759	3.7×10 ⁻⁵	3.2681424	3 (1,14)	MON1A	0.2082194	4.2×10 ⁻⁵	0.2363243	1 (1,13)
18	UHFR1BP1L	0.4517391	4.1×10 ⁻⁵	7.3556538	3 (1,13)	ESRP2	0.2067113	5.2×10 ⁻⁵	0.1898930	1 (1,12)
19	RUNX1T1	0.4514563	4.1×10 ⁻⁵	0.2853657	1 (1,13)	FHOD1	0.2063342	5.5×10 ⁻⁵	0.2004936	1 (1,12)
20	LINC00535	0.4488642	4.3×10 ⁻⁵	5.2622160	3 (1,13)	SLC25A20	0.2057687	5.8×10 ⁻⁵	1.4328953	2 (1,14)
21	CCDC138	0.4485343	4.3×10 ⁻⁵	1.7837674	3 (1,14)	FBXO4	0.1987935	6.7×10 ⁻⁵	0.1986722	1 (1,12)
22	RANBP2	0.4484871	4.3×10 ⁻⁵	1.5089434	2 (1,14)	SLC9A5	0.1987935	6.7×10 ⁻⁵	0.2109907	1 (1,12)
23	AMBRA1	0.4471204	4.3×10 ⁻⁵	0.2669763	1 (1,13)	LONP2	0.1982279	7.1×10 ⁻⁵	0.1968969	1 (1,12)
24	SPIDR	0.4442926	5.4×10 ⁻⁵	0.3250062	1 (1,13)	ZBTB20	0.1978509	7.2×10 ⁻⁵	1.5525411	2 (1,14)
25	PGAP1	0.4407107	5.7×10 ⁻⁵	0.2827285	1 (1,13)	BCL2L1	0.1976624	7.2×10 ⁻⁵	0.2370220	1 (1,13)
26	MON1A	0.4405693	5.7×10 ⁻⁵	0.2823235	1 (1,13)	SPIDR	0.1946461	7.6×10 ⁻⁵	0.9691856	2 (1,14)
27	BCL7C	0.4387784	7.4×10 ⁻⁵	0.2720877	1 (1,13)	RANBP2	0.1940805	7.8×10 ⁻⁵	4.2847257	3 (1,14)
28	NETO2	0.4387313	7.5×10 ⁻⁵	0.2862753	1 (1,13)	SLC4A7	0.1929494	7.8×10 ⁻⁵	0.2292313	1 (1,13)
29	SLC25A20	0.4386841	7.5×10 ⁻⁵	3.5381513	3 (1,14)	PGAP1	0.1927609	7.8×10 ⁻⁵	0.3167656	1 (1,13)
30	FBXO4	0.4344896	7.8×10 ⁻⁵	0.2712723	1 (1,13)	C2CD5	0.1923838	7.8×10 ⁻⁵	0.2688265	1 (1,13)
31	SPATA31D3	0.4343011	7.8×10 ⁻⁵	0.2922907	1 (1,13)	ABCC11	0.1916297	8.0×10 ⁻⁵	0.2233366	1 (1,13)
32	FHOD1	0.4341597	7.9×10 ⁻⁵	0.2718403	1 (1,13)	BCL7C	0.1904986	8.9×10 ⁻⁵	0.2393384	1 (1,13)
33	VRK1	0.4329343	8.3×10 ⁻⁵	0.2751153	1 (1,13)	LRRC29	0.1903101	9.1×10 ⁻⁵	0.2182267	1 (1,13)
34	PRKAR2A	0.4326515	8.7×10 ⁻⁵	0.2914096	1 (1,13)	CEP350	0.1897446	9.9×10 ⁻⁵	0.2718989	1 (1,13)
35	ABCC11	0.4278443	9.5×10 ⁻⁵	0.2801485	1 (1,13)	PLA2G15	0.1897446	9.9×10 ⁻⁵	0.2162242	1 (1,13)
36	GOLGA4	0.4275144	9.7×10 ⁻⁵	2.2342218	3 (1,14)	HOOK1	0.1893675	1.00×10 ⁻⁴	0.6672593	2 (1,14)
37	BCL2L1	0.4271845	9.8×10 ⁻⁵	0.2945582	1 (1,13)	LINC00535	0.1850316	1.09×10 ⁻⁴	3.1223691	3 (1,14)
38	STX4	0.4269017	1.00×10 ⁻⁴	0.2714921	1 (1,13)	AMBRA1	0.1844660	1.11×10 ⁻⁴	0.2873597	1 (1,13)
39	CEP350	0.4261476	1.15×10 ⁻⁴	0.3675222	1 (1,13)	HS2ST1	0.1835234	1.14×10 ⁻⁴	0.3846791	1 (1,14)
40	HECW2	0.4260534	1.15×10 ⁻⁴	0.2733157	1 (1,13)	DCAF4L1	0.1822038	1.23×10 ⁻⁴	0.2492549	1 (1,13)

Table S13: Top 40 sweep candidates for CHB, comparing H12 (left) and G123 (right). Coloration and analyzed data are as in Table S12.

	Top gene	Maximum H12	P-value	Bayes Factor	k (int)		Top gene	Maximum G123	P-value	Bayes Factor	k (int)
1	MIR548AE2	0.5900650	< 10 ⁻⁶	3.4614860	2 (1,9)		MIR548AE2	0.3669526	< 10 ⁻⁶	3.1043339	2 (1,9)
2	LOC100507577	0.5535866	1.0×10 ⁻⁶	4.2906216	2 (1,10)		RANBP10	0.3230276	< 10 ⁻⁶	1.1246310	2 (1,12)
3	EXOC6B	0.5466585	2.0×10 ⁻⁶	0.1676242	1 (1,10)		LOC100507577	0.3217080	1.0×10 ⁻⁶	3.5741514	2 (1,11)
4	RANBP10	0.5326609	2.0×10 ⁻⁶	4.8778325	2 (1,10)		RP11-696N14.1	0.3134131	1.0×10 ⁻⁶	0.1790092	1 (1,11)
5	ZNF660	0.5259214	2.0×10 ⁻⁶	0.1894574	1 (1,11)		EXOC6B	0.3120935	2.0×10 ⁻⁶	0.1818818	1 (1,11)
6	FMNL3	0.5188519	2.0×10 ⁻⁶	0.1819477	1 (1,11)		ZNF660	0.3109624	2.0×10 ⁻⁶	0.2173031	1 (1,11)
7	ATP6V0D1	0.5118767	2.0×10 ⁻⁶	0.1938132	1 (1,11)		ADH1A	0.3053068	2.0×10 ⁻⁶	0.2601613	1 (1,12)
8	RP11-696N14.1	0.5057498	3.0×10 ⁻⁶	0.2205014	1 (1,11)		FMNL3	0.2911679	5.0×10 ⁻⁶	0.1464355	1 (1,10)
9	ADH1A	0.4957583	7.0×10 ⁻⁶	0.2216801	1 (1,12)		ATP6V0D1	0.2911679	5.0×10 ⁻⁶	0.1605230	1 (1,11)
10	LONP2	0.4924121	7.0×10 ⁻⁶	5.0084185	3 (1,12)		EXD2	0.2807993	1.0×10 ⁻⁵	0.1733082	1 (1,11)
11	PRPF40B	0.4915638	8.0×10 ⁻⁶	0.2074760	1 (1,11)		LIMS1	0.2796682	1.4×10 ⁻⁵	0.1817935	1 (1,11)
12	BEND4	0.4772363	1.5×10 ⁻⁵	0.2266500	1 (1,12)		PRPF40B	0.2708078	1.7×10 ⁻⁵	0.1559721	1 (1,11)
13	SLC9A5	0.4721463	1.7×10 ⁻⁵	3.9931687	3 (1,13)		LONP2	0.2534640	3.3×10 ⁻⁵	4.2028387	3 (1,13)
14	LIMS1	0.4645584	2.5×10 ⁻⁵	0.2391615	1 (1,12)		RANBP2	0.2521444	3.4×10 ⁻⁵	5.1860538	3 (1,13)
15	ZBTB20	0.4583844	3.1×10 ⁻⁵	0.3099972	1 (1,13)		BEND4	0.2506363	4.1×10 ⁻⁵	0.2088174	1 (1,12)
16	EXD2	0.4581959	3.3×10 ⁻⁵	0.2486788	1 (1,12)		NETO2	0.2506363	4.1×10 ⁻⁵	0.1731087	1 (1,11)
17	PTPRK	0.4527759	3.7×10 ⁻⁵	3.2681424	3 (1,14)		SPIDR	0.2444151	4.3×10 ⁻⁵	1.1416553	2 (1,14)
18	UHFR1BP1L	0.4517391	4.1×10 ⁻⁵	7.3556538	3 (1,13)		CCDC138	0.2429070	4.4×10 ⁻⁵	6.4060463	3 (1,13)
19	RUNX1T1	0.4514563	4.1×10 ⁻⁵	0.2853657	1 (1,13)		MON1A	0.2429070	4.4×10 ⁻⁵	0.2289236	1 (1,12)
20	LINC00535	0.4488642	4.3×10 ⁻⁵	5.2622160	3 (1,13)		SLC4A7	0.2427184	4.4×10 ⁻⁵	0.2107451	1 (1,12)
21	CCDC138	0.4485343	4.3×10 ⁻⁵	1.7837674	3 (1,14)		FBXL19	0.2415873	5.3×10 ⁻⁵	0.1776357	1 (1,12)
22	RANBP2	0.4484871	4.3×10 ⁻⁵	1.5089434	2 (1,14)		ABCC11	0.2413988	5.4×10 ⁻⁵	0.2064761	1 (1,12)
23	AMBRA1	0.4471204	4.3×10 ⁻⁵	0.2669763	1 (1,13)		SLC9A5	0.2412103	5.5×10 ⁻⁵	0.1984343	1 (1,12)
24	SPIDR	0.4442926	5.4×10 ⁻⁵	0.3250062	1 (1,13)		FHOD1	0.2410218	5.5×10 ⁻⁵	0.1929885	1 (1,12)
25	PGAP1	0.4407107	5.7×10 ⁻⁵	0.2827285	1 (1,13)		C2CD5	0.2338580	5.9×10 ⁻⁵	0.2617569	1 (1,13)
26	MON1A	0.4405693	5.7×10 ⁻⁵	0.2823235	1 (1,13)		LINC00535	0.2336695	6.0×10 ⁻⁵	3.5982326	3 (1,14)
27	BCL7C	0.4387784	7.4×10 ⁻⁵	0.2720877	1 (1,13)		FBXO4	0.2327269	7.4×10 ⁻⁵	0.1923462	1 (1,12)
28	NETO2	0.4387313	7.5×10 ⁻⁵	0.2862753	1 (1,13)		ESRP2	0.2327269	7.4×10 ⁻⁵	0.1891129	1 (1,12)
29	SLC25A20	0.4386841	7.5×10 ⁻⁵	3.5381513	3 (1,14)		ADH6	0.2261288	8.3×10 ⁻⁵	14.6556873	4 (2,14)
30	FBXO4	0.4344896	7.8×10 ⁻⁵	0.2712723	1 (1,13)		PGAP1	0.2259402	8.4×10 ⁻⁵	0.3287068	1 (1,13)
31	SPATA31D3	0.4343011	7.8×10 ⁻⁵	0.2922907	1 (1,13)		AGRP	0.2255632	8.4×10 ⁻⁵	0.2860129	1 (1,13)
32	FHOD1	0.4341597	7.9×10 ⁻⁵	0.2718403	1 (1,13)		AMBRA1	0.2249976	8.6×10 ⁻⁵	0.2861734	1 (1,13)
33	VRK1	0.4329343	8.3×10 ⁻⁵	0.2751153	1 (1,13)		ZNF282	0.2244321	9.1×10 ⁻⁵	0.2639356	1 (1,13)
34	PRKAR2A	0.4326515	8.7×10 ⁻⁵	0.2914096	1 (1,13)		PTPRK	0.2242436	9.2×10 ⁻⁵	4.6862841	3 (1,14)
35	ABCC11	0.4278443	9.5×10 ⁻⁵	0.2801485	1 (1,13)		HS2ST1	0.2238665	9.6×10 ⁻⁵	0.3836981	1 (1,14)
36	GOLGA4	0.4275144	9.7×10 ⁻⁵	2.2342218	3 (1,14)		BCL7C	0.2236780	9.9×10 ⁻⁵	0.2320706	1 (1,13)
37	BCL2L1	0.4271845	9.8×10 ⁻⁵	0.2945582	1 (1,13)		CEP112	0.2234895	1.00×10 ⁻⁴	0.2889956	1 (1,13)
38	STX4	0.4269017	1.00×10 ⁻⁴	0.27114921	1 (1,13)		ZBTB20	0.2233010	1.01×10 ⁻⁴	1.4914960	2 (1,14)
39	CEP350	0.4261476	1.15×10 ⁻⁴	0.3675222	1 (1,13)		SLC25A20	0.2231125	1.02×10 ⁻⁴	1.2669874	2 (1,14)
40	HECW2	0.4260534	1.15×10 ⁻⁴	0.2733157	1 (1,13)		BCL2L1	0.2231125	1.02×10 ⁻⁴	0.2347724	1 (1,13)

Table S14: Top 40 sweep candidates for CHB, comparing G123 for the true MLGs of diploid study individuals (left) with those of pseudo-individuals produced from random pairs of study haplotypes (right). Coloration and analyzed data are as in Table S12.

	Top gene	Maximum G123	P-value	Bayes Factor	k (int)		Top gene	Maximum G123a	P-value	Bayes Factor	k (int)
1	MIR548AE2	0.3669526	< 10 ⁻⁶	3.1043339	2 (1,9)		MIR548AE2	0.4033368	< 10 ⁻⁶	3.09110473	2 (1,8)
2	RANBP10	0.3230276	< 10 ⁻⁶	1.1246310	2 (1,12)		ATP6V0D1	0.3805260	< 10 ⁻⁶	0.08764229	1 (1,7)
3	LOC100507577	0.3217080	1.0×10 ⁻⁶	3.5741514	2 (1,11)		LOC100507577	0.3567726	< 10 ⁻⁶	3.45557730	2 (1,9)
4	RP11-696N14.1	0.3134131	1.0×10 ⁻⁶	0.1790092	1 (1,11)		FMNL3	0.3565840	< 10 ⁻⁶	0.10901353	1 (1,9)
5	EXOC6B	0.3120935	2.0×10 ⁻⁶	0.1818818	1 (1,11)		RANBP10	0.3465925	< 10 ⁻⁶	3.21395806	2 (1,10)
6	ZNF660	0.3109624	2.0×10 ⁻⁶	0.2173031	1 (1,11)		RP11-696N14.1	0.3458384	< 10 ⁻⁶	0.12064908	1 (1,9)
7	ADH1A	0.3053068	2.0×10 ⁻⁶	0.2601613	1 (1,12)		ADH1A	0.3458384	< 10 ⁻⁶	0.12064908	1 (1,9)
8	FMNL3	0.2911679	5.0×10 ⁻⁶	0.1464355	1 (1,10)		PRPF40B	0.3458384	< 10 ⁻⁶	0.11815304	1 (1,9)
9	ATP6V0D1	0.2911679	5.0×10 ⁻⁶	0.1605230	1 (1,11)		ZNF660	0.3445188	< 10 ⁻⁶	0.91456206	2 (1,12)
10	EXD2	0.2807993	1.0×10 ⁻⁵	0.1733082	1 (1,11)		EXOC6B	0.3235932	< 10 ⁻⁶	0.58026850	2 (1,12)
11	LIMS1	0.2796682	1.4×10 ⁻⁵	0.1817935	1 (1,11)		AMBRA1	0.3235932	< 10 ⁻⁶	0.13931079	1 (1,10)
12	PRPF40B	0.2708078	1.7×10 ⁻⁵	0.1559721	1 (1,11)		FBXO4	0.3130361	2.0×10 ⁻⁶	0.14170242	1 (1,10)
13	LONP2	0.2534640	3.3×10 ⁻⁵	4.2028387	3 (1,13)		BCL7C	0.2907908	5.0×10 ⁻⁶	0.18303122	1 (1,11)
14	RANBP2	0.2521444	3.4×10 ⁻⁵	5.1860538	3 (1,13)		AGRP	0.2841927	5.0×10 ⁻⁶	0.25922411	1 (1,12)
15	BEND4	0.2506363	4.1×10 ⁻⁵	0.2088174	1 (1,12)		SPATA31D3	0.2828730	5.0×10 ⁻⁶	0.43513173	1 (1,13)
16	NETO2	0.2506363	4.1×10 ⁻⁵	0.1731087	1 (1,11)		EXD2	0.2819304	6.0×10 ⁻⁶	0.19673780	1 (1,11)
17	SPIDR	0.2444151	4.3×10 ⁻⁵	1.1416553	2 (1,14)		CCDC138	0.2817419	6.0×10 ⁻⁶	3.73523387	3 (1,12)
18	CCDC138	0.2429070	4.4×10 ⁻⁵	6.4060463	3 (1,13)		BEND4	0.2813649	7.0×10 ⁻⁶	0.19744993	1 (1,12)
19	MON1A	0.2429070	4.4×10 ⁻⁵	0.2289236	1 (1,12)		CDR2	0.2806108	1.2×10 ⁻⁵	3.90798283	3 (1,12)
20	SLC4A7	0.2427184	4.4×10 ⁻⁵	0.2107451	1 (1,12)		LONP2	0.2738241	1.4×10 ⁻⁵	3.92208618	3 (1,13)
21	FBXL19	0.2415873	5.3×10 ⁻⁵	0.1776357	1 (1,12)		ZBTB20	0.2706193	1.7×10 ⁻⁵	2.00544348	2 (1,13)
22	ABCC11	0.2413988	5.4×10 ⁻⁵	0.2064761	1 (1,12)		RANBP2	0.2619474	2.2×10 ⁻⁵	3.86428959	3 (1,13)
23	SLC9A5	0.2412103	5.5×10 ⁻⁵	0.1984343	1 (1,12)		C2CD5	0.2540296	3.3×10 ⁻⁵	0.28872994	1 (1,13)
24	FHOD1	0.2410218	5.5×10 ⁻⁵	0.1929885	1 (1,12)		STX4	0.2538411	3.3×10 ⁻⁵	0.19340146	1 (1,12)
25	C2CD5	0.2338580	5.9×10 ⁻⁵	0.2617569	1 (1,13)		ABCC11	0.2528985	3.3×10 ⁻⁵	0.19762591	1 (1,12)
26	LINC00535	0.2336695	6.0×10 ⁻⁵	3.5982326	3 (1,14)		CENPW	0.2513903	3.7×10 ⁻⁵	1.91376518	2 (1,14)
27	FBXO4	0.2327269	7.4×10 ⁻⁵	0.1923462	1 (1,12)		DPH6-AS1	0.2513903	3.7×10 ⁻⁵	1.13788114	2 (1,14)
28	ESRP2	0.2327269	7.4×10 ⁻⁵	0.1891129	1 (1,12)		LIMS1	0.2512018	3.9×10 ⁻⁵	3.76678734	3 (1,13)
29	ADH6	0.2261288	8.3×10 ⁻⁵	14.6556873	4 (2,14)		FBXL19	0.2512018	3.9×10 ⁻⁵	0.16897531	1 (1,11)
30	PGAP1	0.2259402	8.4×10 ⁻⁵	0.3287068	1 (1,13)		PHF20	0.2504477	4.2×10 ⁻⁵	0.22332104	1 (1,12)
31	AGRP	0.2255632	8.4×10 ⁻⁵	0.2860129	1 (1,13)		ARIH2OS	0.2440381	4.3×10 ⁻⁵	0.20829187	1 (1,12)
32	AMBRA1	0.2249976	8.6×10 ⁻⁵	0.2861734	1 (1,13)		RP11-682N22.1	0.2434725	4.3×10 ⁻⁵	0.19945643	1 (1,12)
33	ZNF282	0.2244321	9.1×10 ⁻⁵	0.2639356	1 (1,13)		SPECC1	0.2434725	4.3×10 ⁻⁵	0.24088478	1 (1,13)
34	PTPRK	0.2242436	9.2×10 ⁻⁵	4.6862841	3 (1,14)		WDTC1	0.2427184	4.4×10 ⁻⁵	0.55141534	2 (1,14)
35	HS2ST1	0.2238665	9.6×10 ⁻⁵	0.3836981	1 (1,14)		ZKSCAN7	0.2423414	4.7×10 ⁻⁵	1.23316905	2 (1,14)
36	BCL7C	0.2236780	9.9×10 ⁻⁵	0.2320706	1 (1,13)		EXOC6	0.2421529	4.9×10 ⁻⁵	0.34946761	1 (1,13)
37	CEP112	0.2234895	1.00×10 ⁻⁴	0.2889956	1 (1,13)		FAF1	0.2364973	5.6×10 ⁻⁵	0.47716663	1 (1,14)
38	ZBTB20	0.2233010	1.01×10 ⁻⁴	1.4914960	2 (1,14)		LINC01088	0.2359318	5.6×10 ⁻⁵	0.21429452	1 (1,12)
39	SLC25A20	0.2231125	1.02×10 ⁻⁴	1.2669874	2 (1,14)		PGAP1	0.2342351	5.8×10 ⁻⁵	0.23964544	1 (1,13)
40	BCL2L1	0.2231125	1.02×10 ⁻⁴	0.2347724	1 (1,13)		HS2ST1	0.2340466	5.9×10 ⁻⁵	0.42397482	1 (1,14)

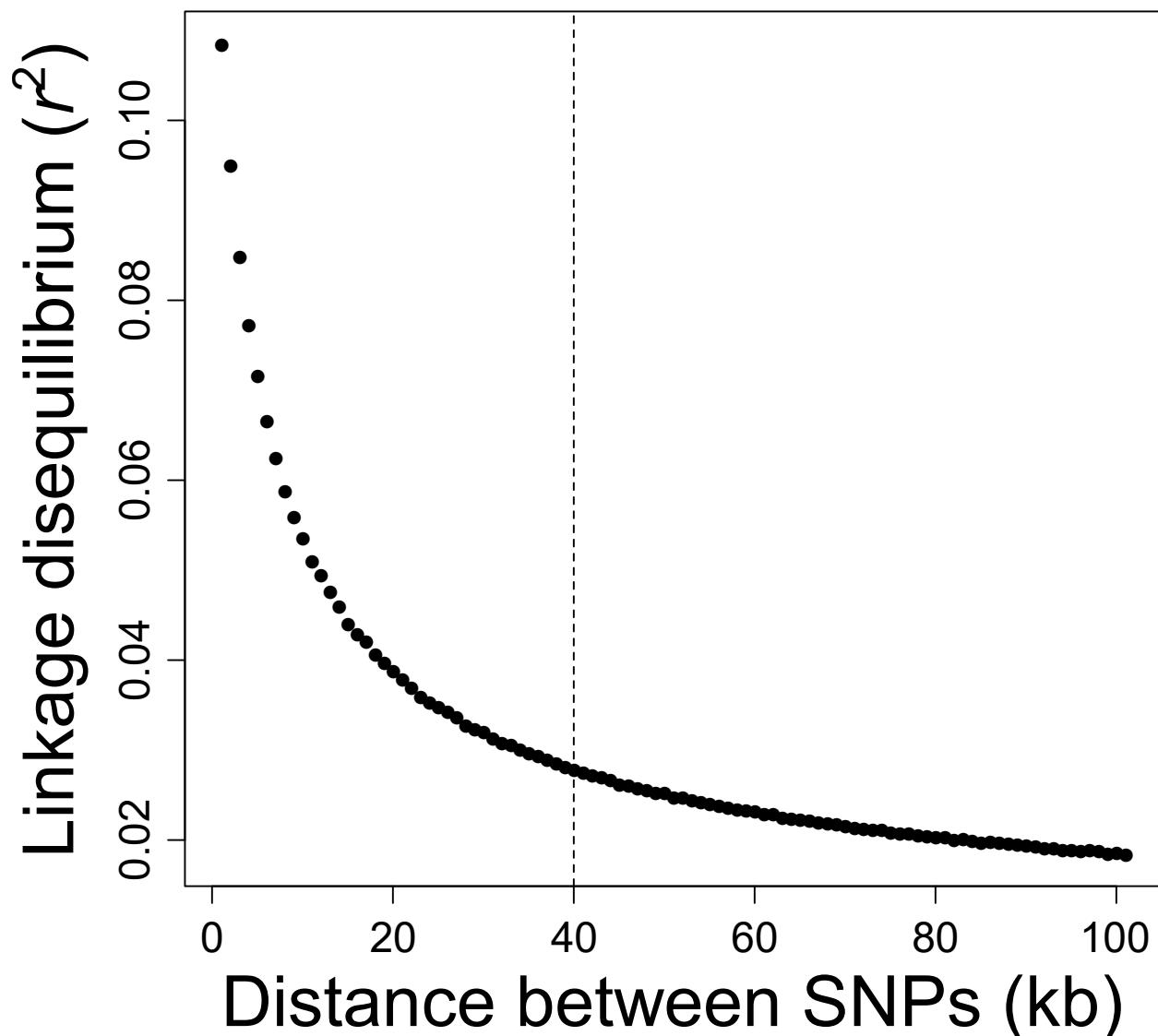


Figure S1: Mean decay of the r^2 measure of linkage disequilibrium between pairs of loci in simulated 500 kb chromosomes across 10^3 replicates. Dashed vertical line indicates window size used in selection scans.

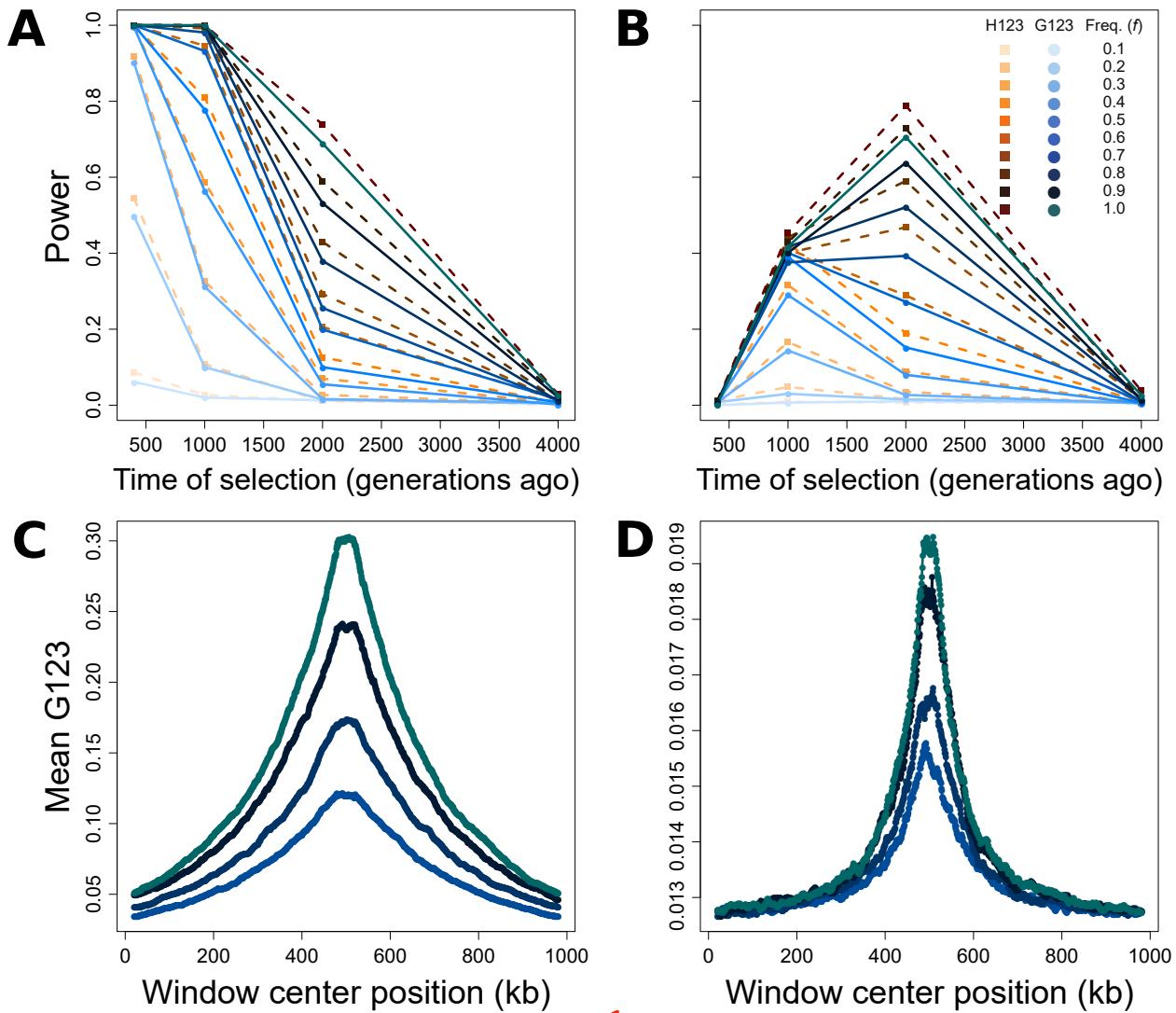


Figure S2: Capabilities of H123 (orange) and G123 (blue) to detect hard sweeps from simulated chromosome generated for selection across identical time points and sweep frequencies (f , frequency to which the selected allele rises before becoming selectively neutral) as in Figure 3. (A) Powers of H123 (orange) and G123 (blue) to detect strong sweeps ($s = 0.1$) in a 100 kb chromosome. (B) Powers of H123 (orange) and G123 (blue) to detect moderate sweeps ($s = 0.01$) in a 100 kb chromosome. (C) Spatial G123 signal across a one Mb chromosome for strong sweeps occurring 400 generations prior to sampling. (D) Spatial G123 signal across a one Mb chromosome for moderate sweeps occurring 2,000 generations prior to sampling. Lines in (C) and (D) are mean values generated from the same set of simulations as panels A and B, and contain only results for $f \geq 0.7$. Note that vertical axes in panels C and D differ.

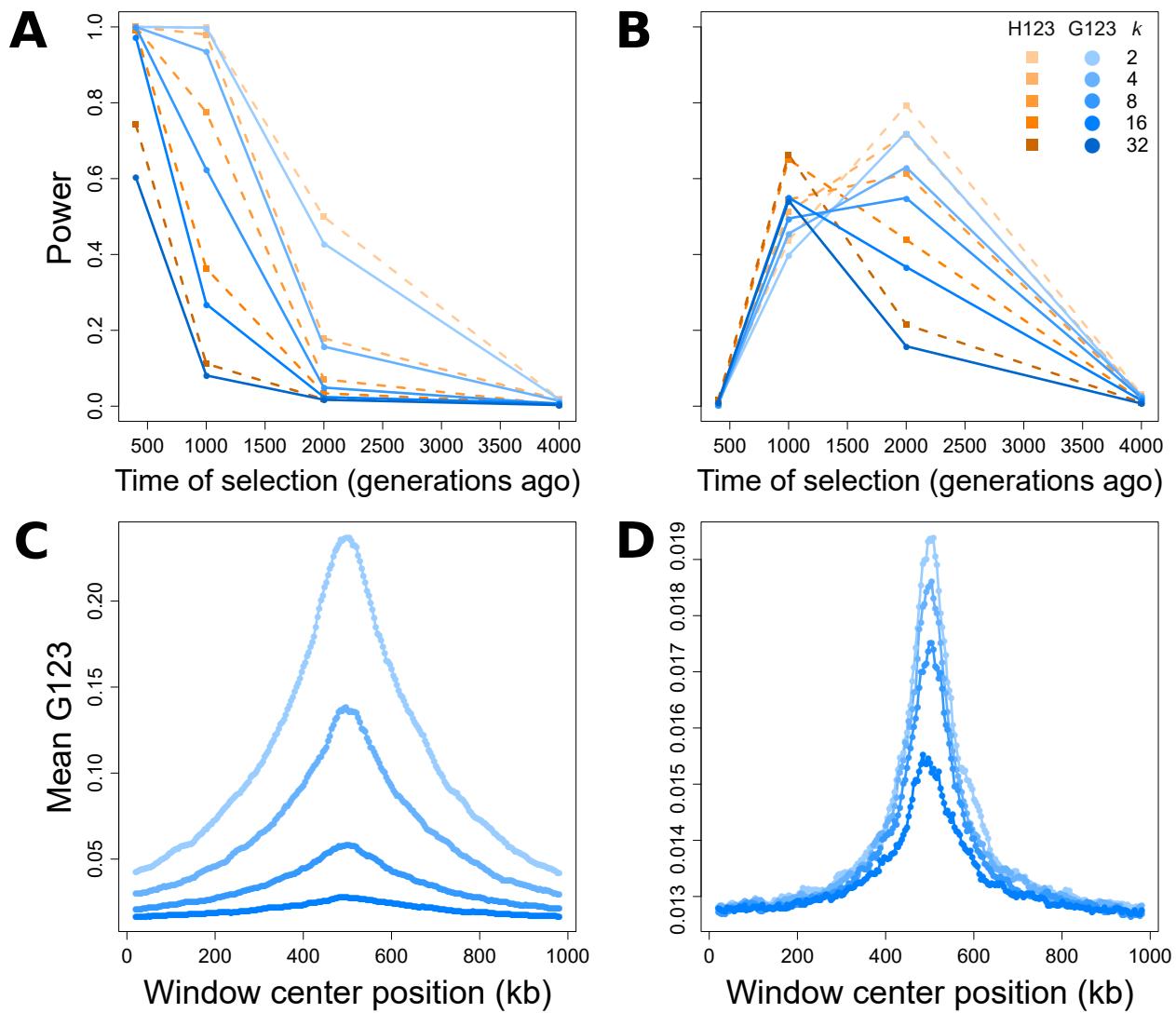


Figure S3: Capabilities of H123 (orange) and G123 (blue) to detect soft sweeps from selection on standing variation (SSV) from simulated chromosomes generated for selection across identical time points and initially selected haplotypes (k , number of haplotypes on which the selected allele arises at time of selection) as in Figure 4. (A) Powers of H123 (orange) and G123 (blue) to detect strong sweeps ($s = 0.1$) in a 100 kb chromosome. (B) Powers of H123 (orange) and G123 (blue) to detect moderate sweeps ($s = 0.01$) in a 100 kb chromosome. (C) Spatial G123 signal across a one Mb chromosome for strong sweeps occurring 400 generations prior to sampling. (D) Spatial G123 signal across a one Mb chromosome for moderate sweeps occurring 2,000 generations prior to sampling. Lines in (C) and (D) are mean values generated from the same set of simulations as panels A and B, and contain only results for $k \leq 16$. Note that vertical axes in panels C and D differ.

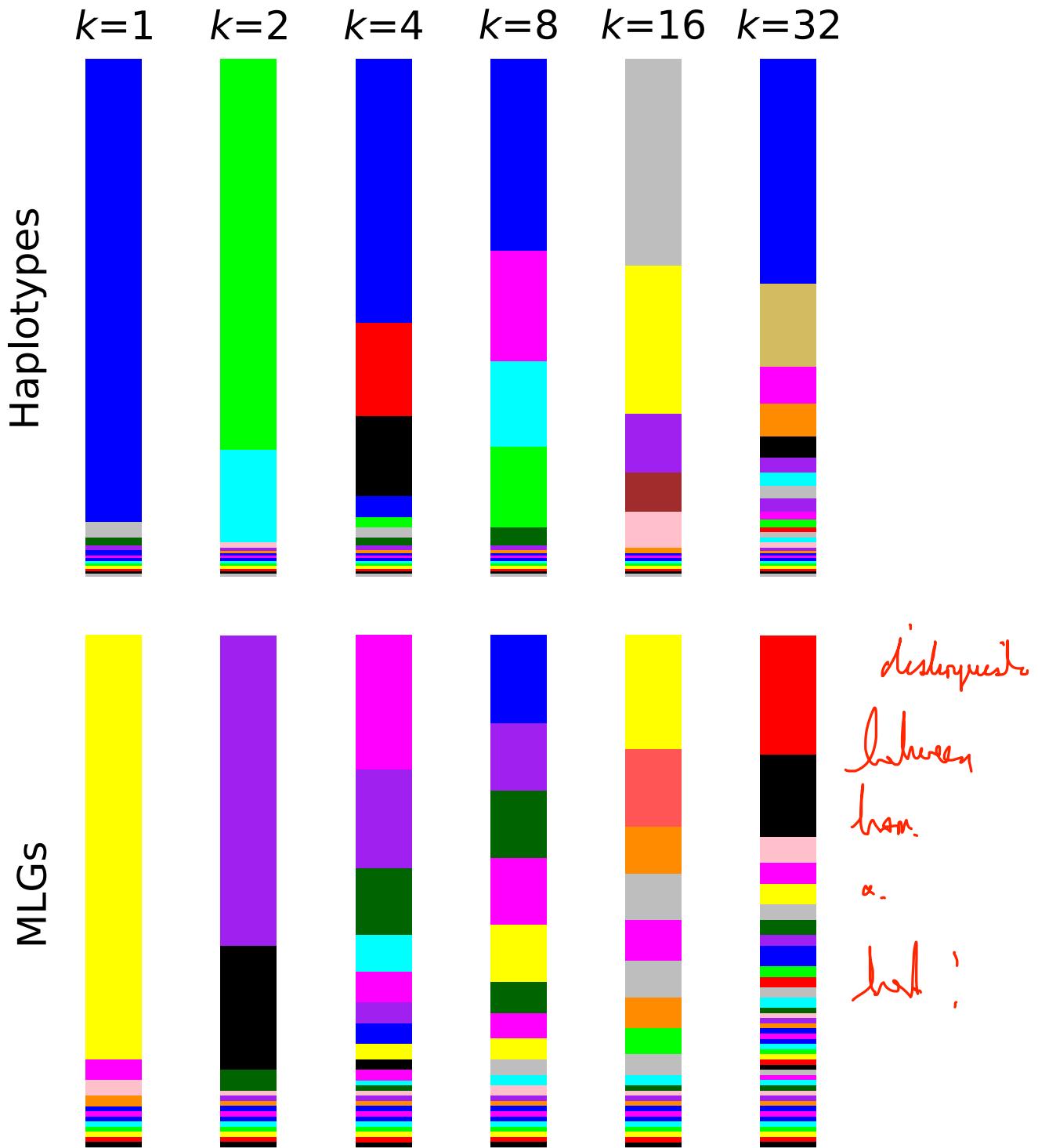


Figure S4: Example haplotype (top) and MLG (bottom) frequency spectra of random single replicate sweep simulations on $k \in \{1, 2, 4, 8, 16, 32\}$ different haplotypes and sample size $n = 100$ diploids. Each plot represents one of the 10^3 replicate simulations featured in the power curve computations of Figures 3 and S2 ($k = 1$) or Figures 4 and S3 ($k > 1$). Each colored block within a plot represents the proportion of individuals in the sample carrying a particular haplotype, with blocks arranged in descending order of frequency.

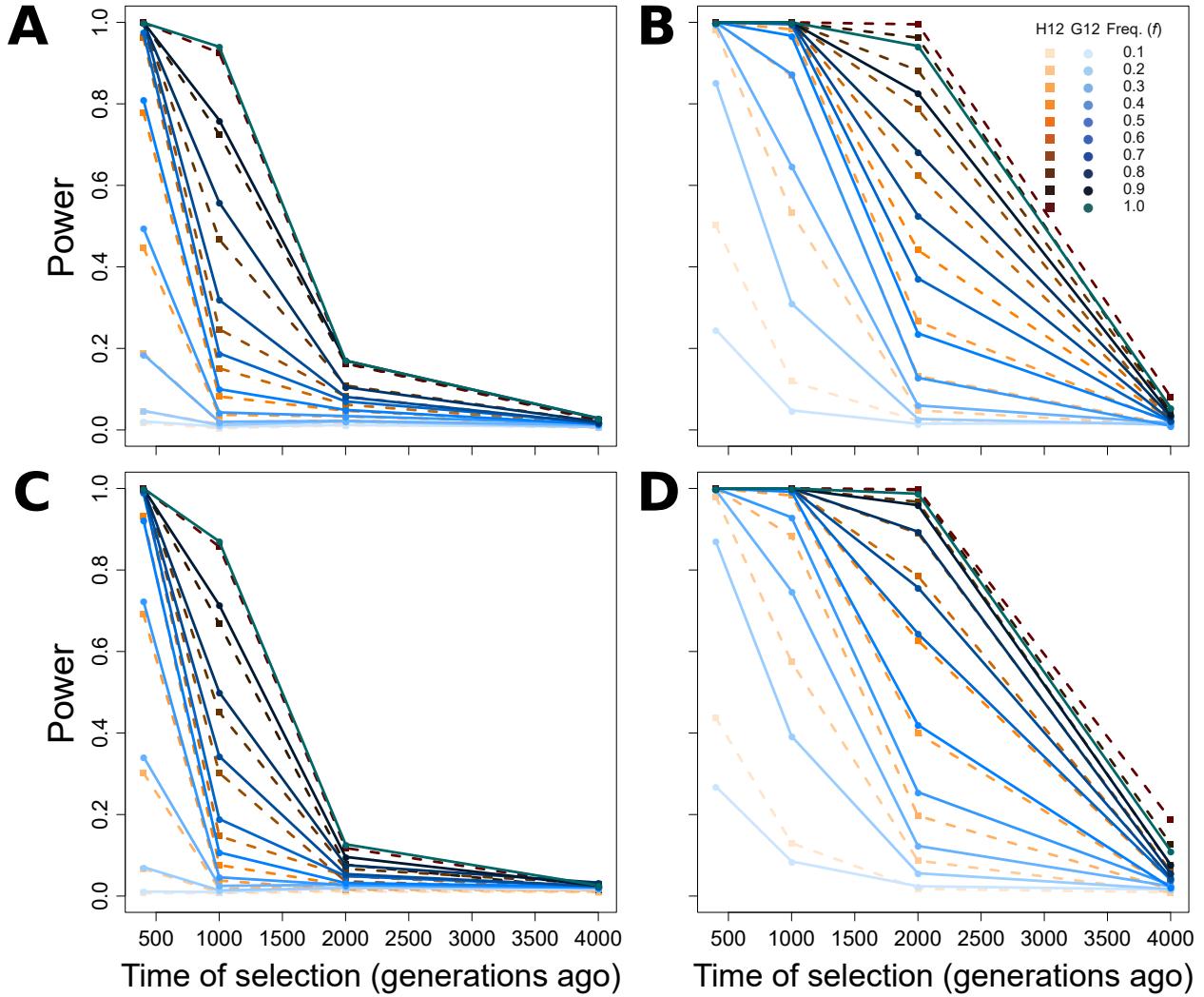


Figure S5: Powers of H12 (orange) and G12 (blue) to detect strong ($s = 0.1$) hard sweeps across the same time points and parameters as described previously (Figure 3), under population bottleneck and population expansion demographic histories (Figures 2B and C). (A) Powers of H12 and G12 in the presence of a population bottleneck occurring between 1,200 and 880 generations ago, for unadjusted window size of 40 kb. (B) Powers of H12 and G12 in the presence of a population expansion beginning 1,920 generations before the time of sampling, for unadjusted window size of 40 kb. (C) Powers of H12 and G12 in the presence of a population bottleneck, for adjusted window size of 56,060 bases. (D) Powers of H12 and G12 in the presence of a population expansion, for adjusted window size of 35,048 bases.

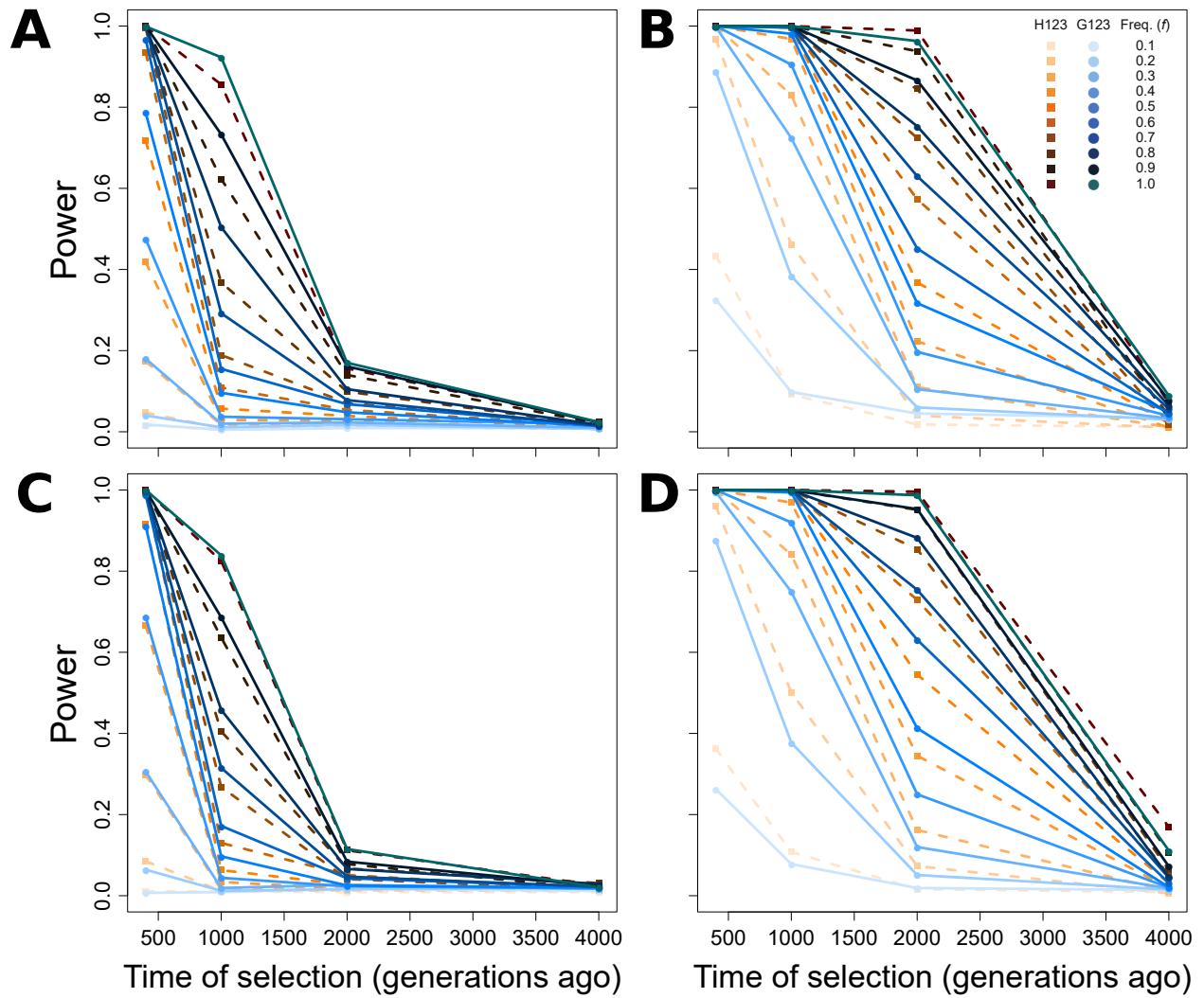


Figure S6: Powers of H123 (orange) and G123 (blue) to detect strong hard sweeps across the same time points and parameters as described previously (Figure 3), under population bottleneck and population expansion demographic histories (Figures 2B and C). Data and panels are as in Figure S5, but using G123 and H123 to analyze data.

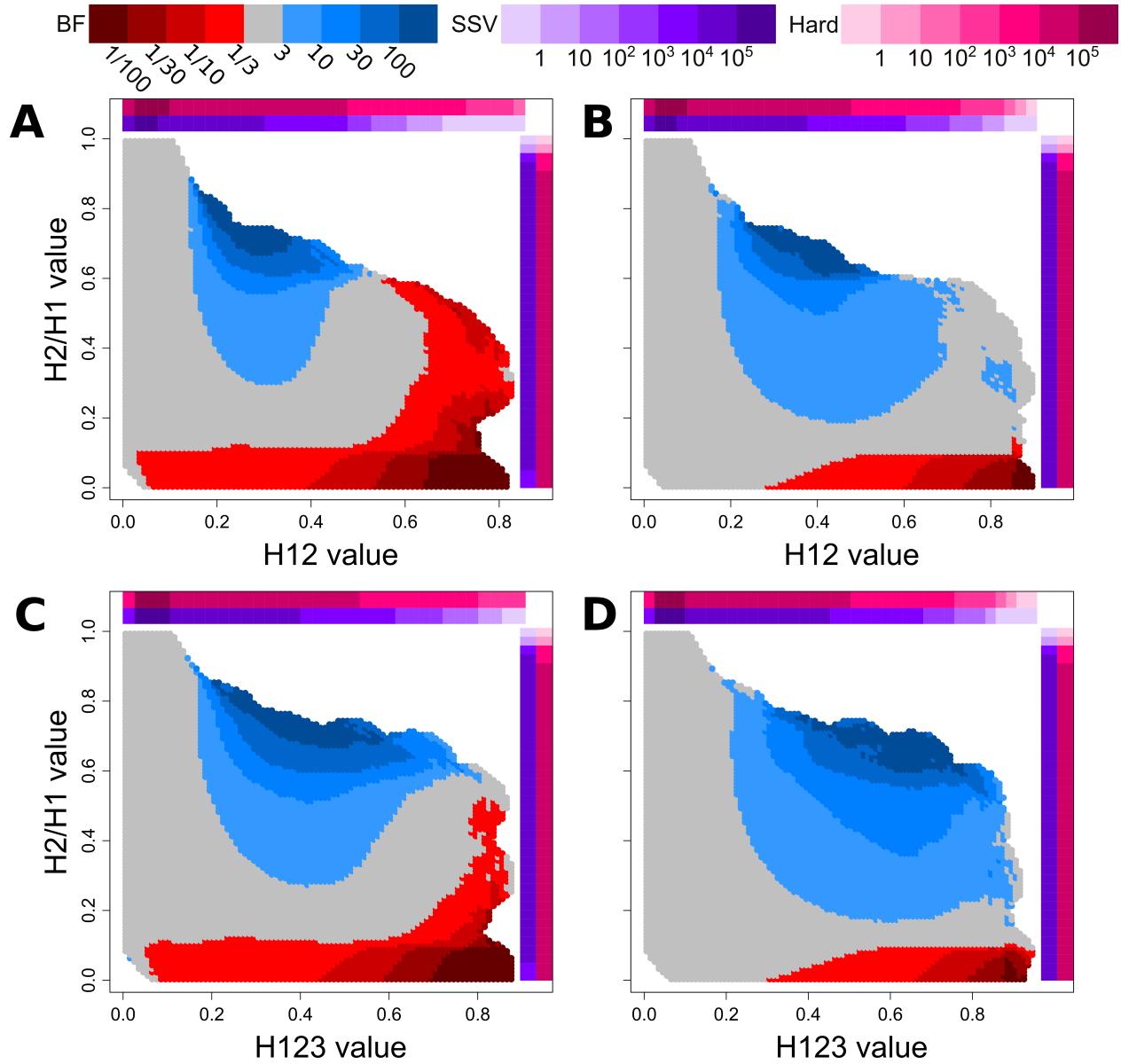


Figure S7: Assignment of Bayes factors (BFs) to tested paired values of (H12, H2/H1) and (H123, H2/H1). Plots represent the relative probability of obtaining a paired (H12, H2/H1) or (H123, H2/H1) value within a Euclidean distance of 0.1 from a test point for **hard** versus **soft** sweeps, determined as described in the *Materials and methods*. Selection coefficients (s) and times (t) were drawn as described in the *Materials and methods*. Red regions represent a higher likelihood for hard sweeps, while blue regions represent a higher likelihood for soft sweeps. Colored bars along the axes indicate the density of H12 or H123 (horizontal) and H2/H1 (vertical) observations within consecutive intervals of size 0.025 for hard sweep (magenta) and SSV (purple) simulations. (A) BFs of paired (H12, H2/H1) values for hard sweep scenarios and SSV scenarios ($k = 5$). (B) BFs of paired (H12, H2/H1) values for hard sweep scenarios and SSV scenarios ($k = 3$). (C) BFs of paired (H123, H2/H1) values for hard sweep scenarios and SSV scenarios ($k = 5$). (D) BFs of paired (H123, H2/H1) values for hard sweep scenarios and SSV scenarios ($k = 3$). Only test points for which at least one simulation of each type was within a Euclidean distance of 0.1 were counted (and therefore colored).

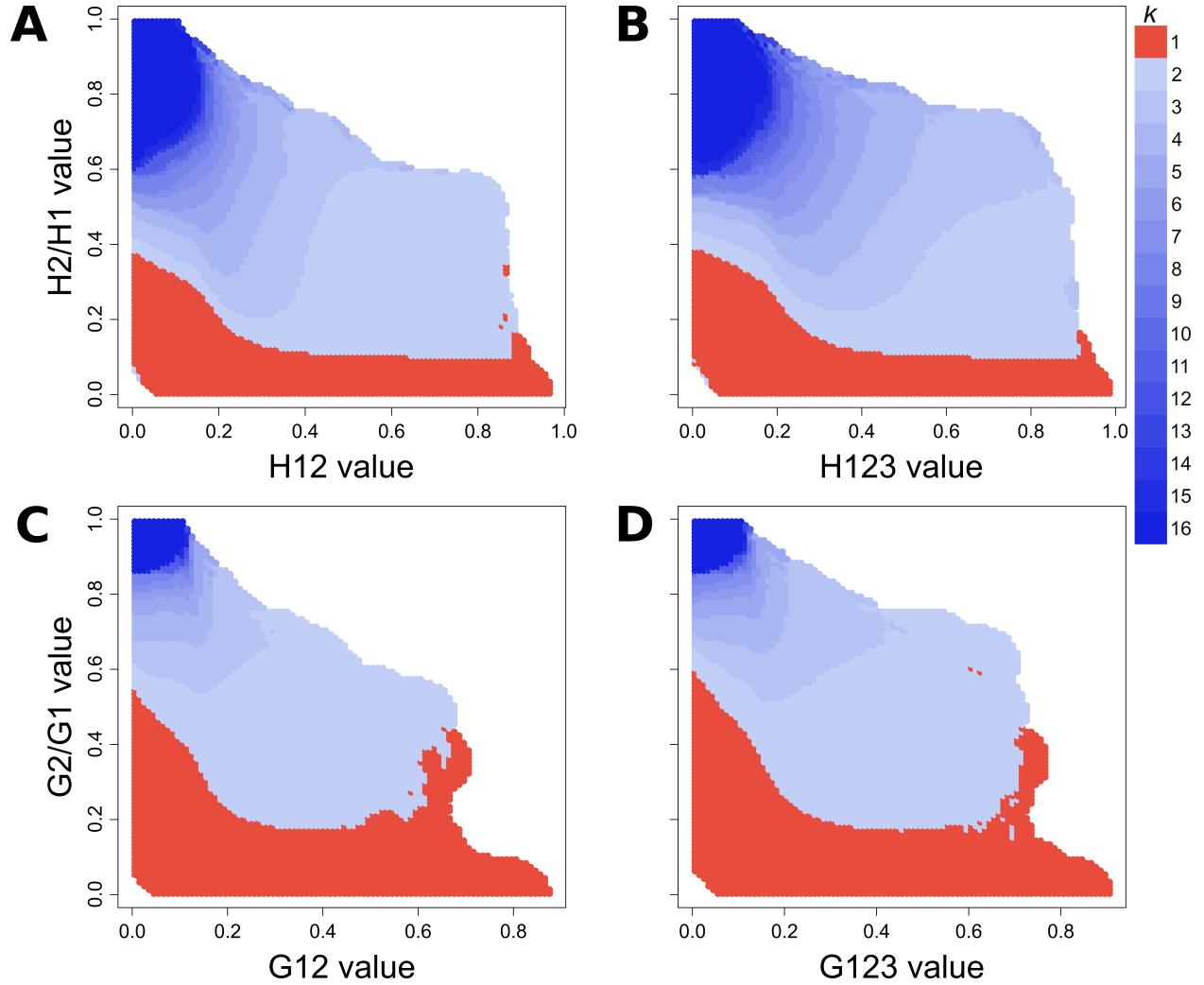


Figure S8: Assignment of a most probable number of sweeping haplotypes (k), between 1 and 16, to paired expected homozygosity statistic test points. Test points are colored according to the most probable k among simulated replicates within a Euclidean distance of 0.1 from 5×10^6 replicates of sweeps with $k \in \{1, 2, \dots, 16\}$ drawn uniformly at random. Test points with no nearby simulated replicates are left uncolored. (A) Most probable k for test points in $(H_{12}, H_{2/H_1})$ distribution. (B) Most probable k for test points in $(H_{123}, H_{2/H_1})$ distribution. (C) Most probable k for test points in $(G_{12}, G_{2/G_1})$ distribution. (D) Most probable k for test points in $(G_{123}, G_{2/G_1})$ distribution.

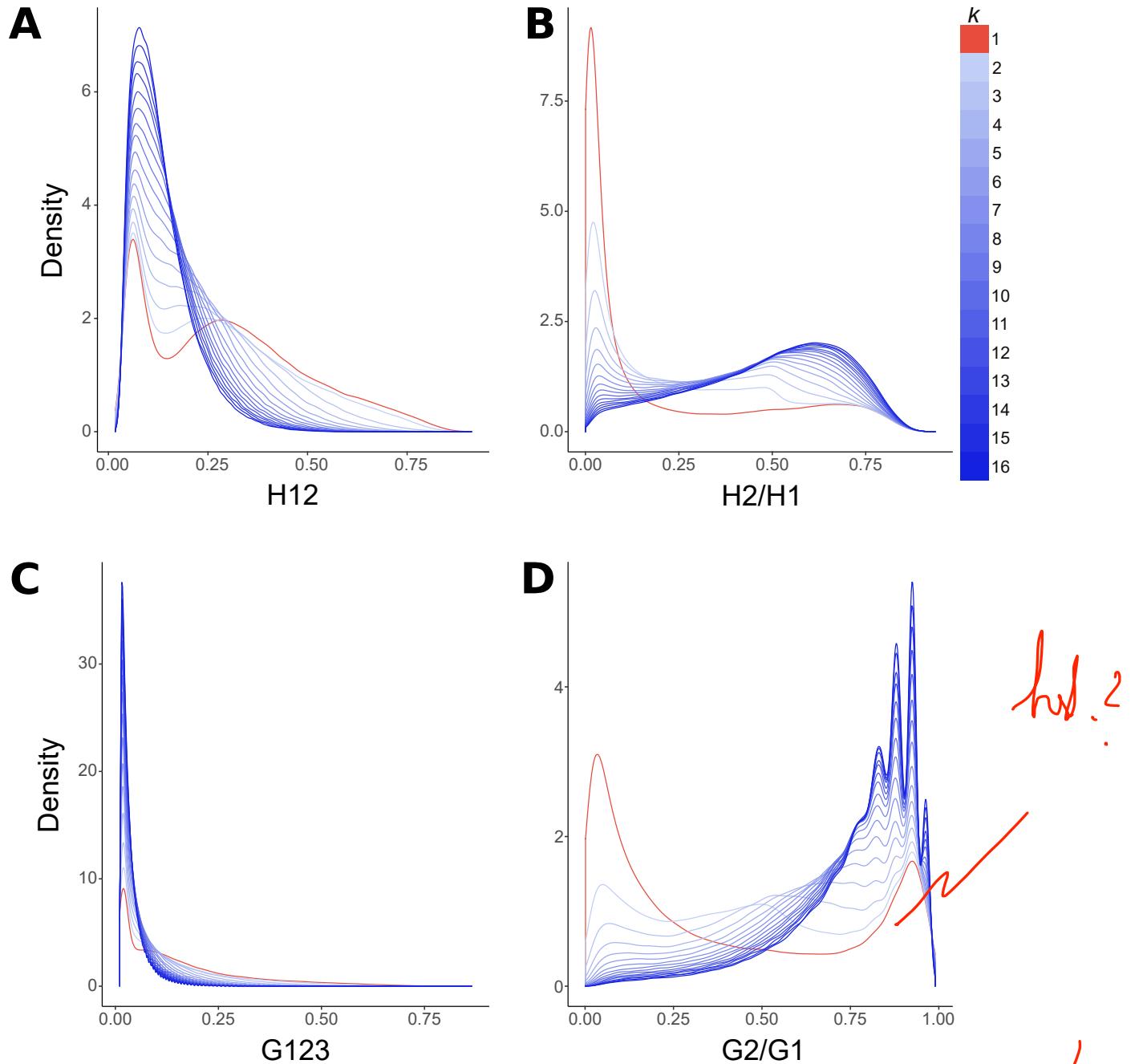


Figure S9: Probability density functions of expected homozygosity statistics across 5×10^6 simulated replicates for which k was drawn uniformly at random. The data displayed here are identical to those in Figure S8. Curves represent the probability density functions of (A) H12, (B) H2/H1, (C) G123, and (D) G2/G1 for $k \in \{1, 2, \dots, 16\}$. MLGs in (C) and (D) were assembled from the haplotypes in (A) and (B).

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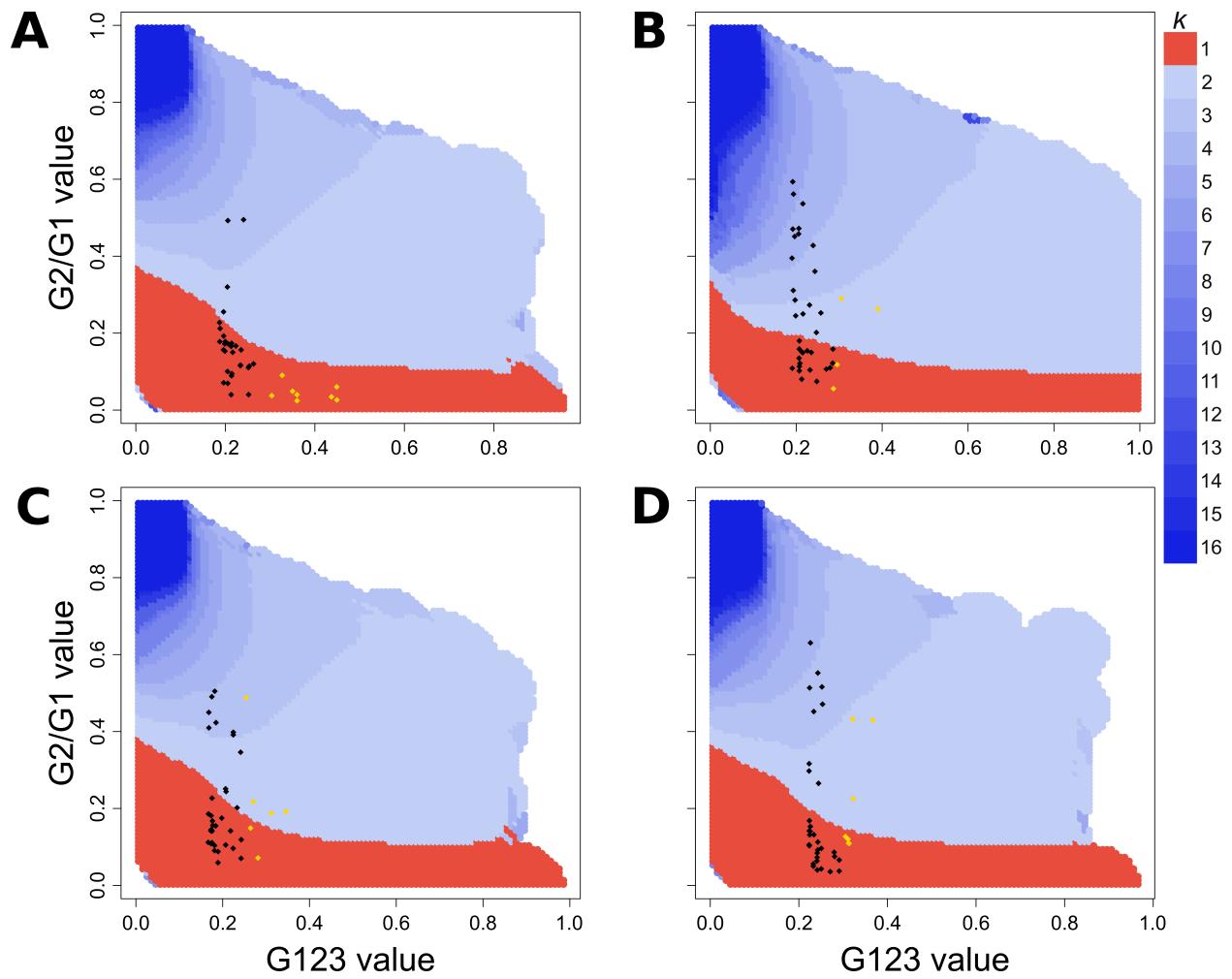


Figure S10: $(G_{123}, G_{2/G1})$ values used to assign a most probable number of sweeping haplotypes (k), between 1 and 16, in human empirical data using demographic models inferred with `smc++` [Terhorst et al., 2017] as in Figure 6. Replicates were otherwise generated in the same manner as in Figure S8. Points representing the top 40 G_{123} selection candidates (Tables S4, S7, S10, and S13) for the (A) CEU, (B) YRI, (C) GIH, and (D) CHB populations are overlayed onto each population's specific $(G_{123}, G_{2/G1})$ distribution. Candidates exceeding the significance threshold (Table S1; different for each population) are colored in gold.

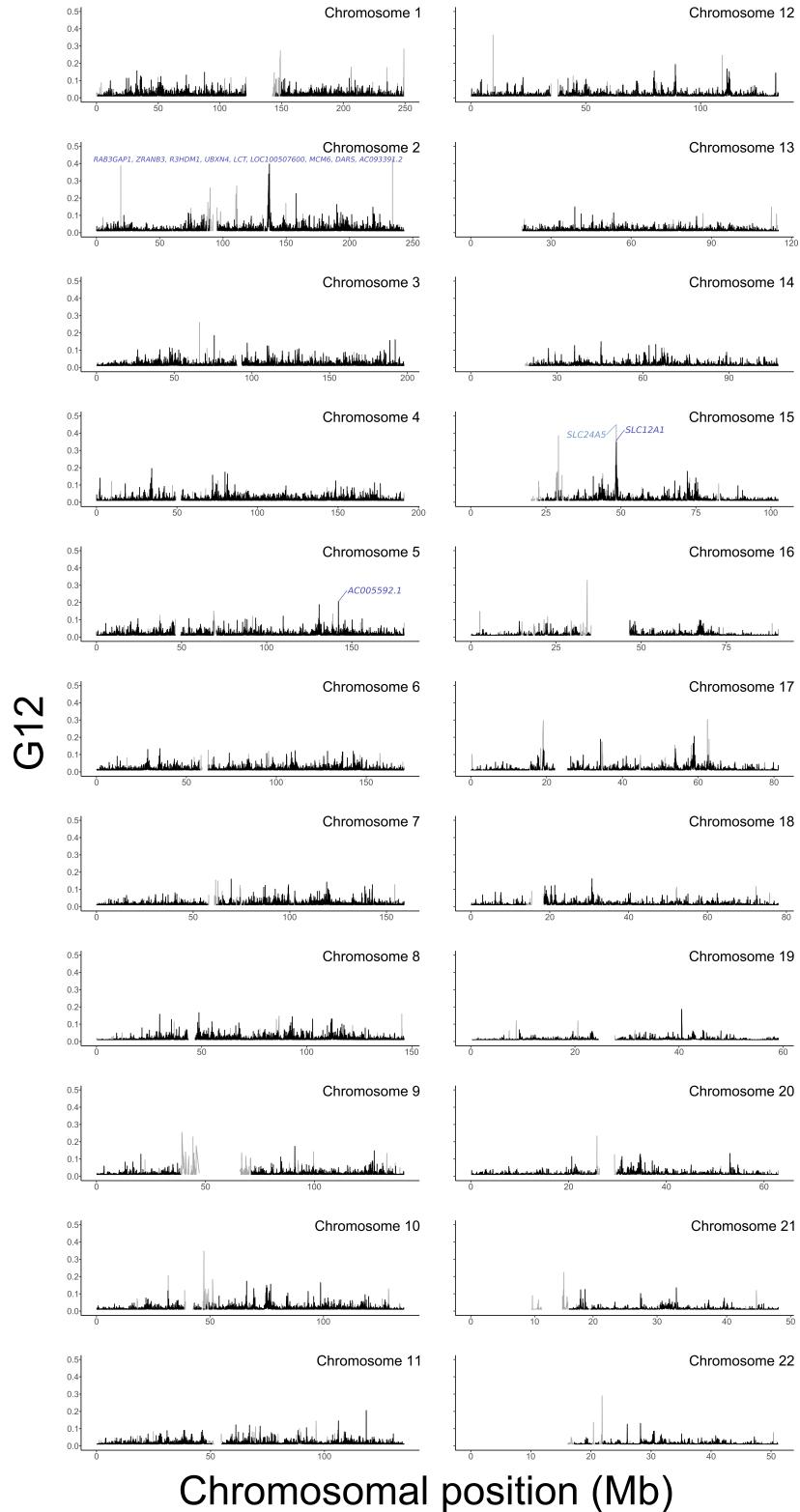


Figure S11: Manhattan plots of G12 for the CEU population. The top 10 G12 candidate genes, as well as the *SLC12A1/SLC24A5* peak, are labeled following their designations in Table S3. Candidates labeled on chromosome 2 belong to the same peak. Gray lines represent the G12 signal of filtered regions.

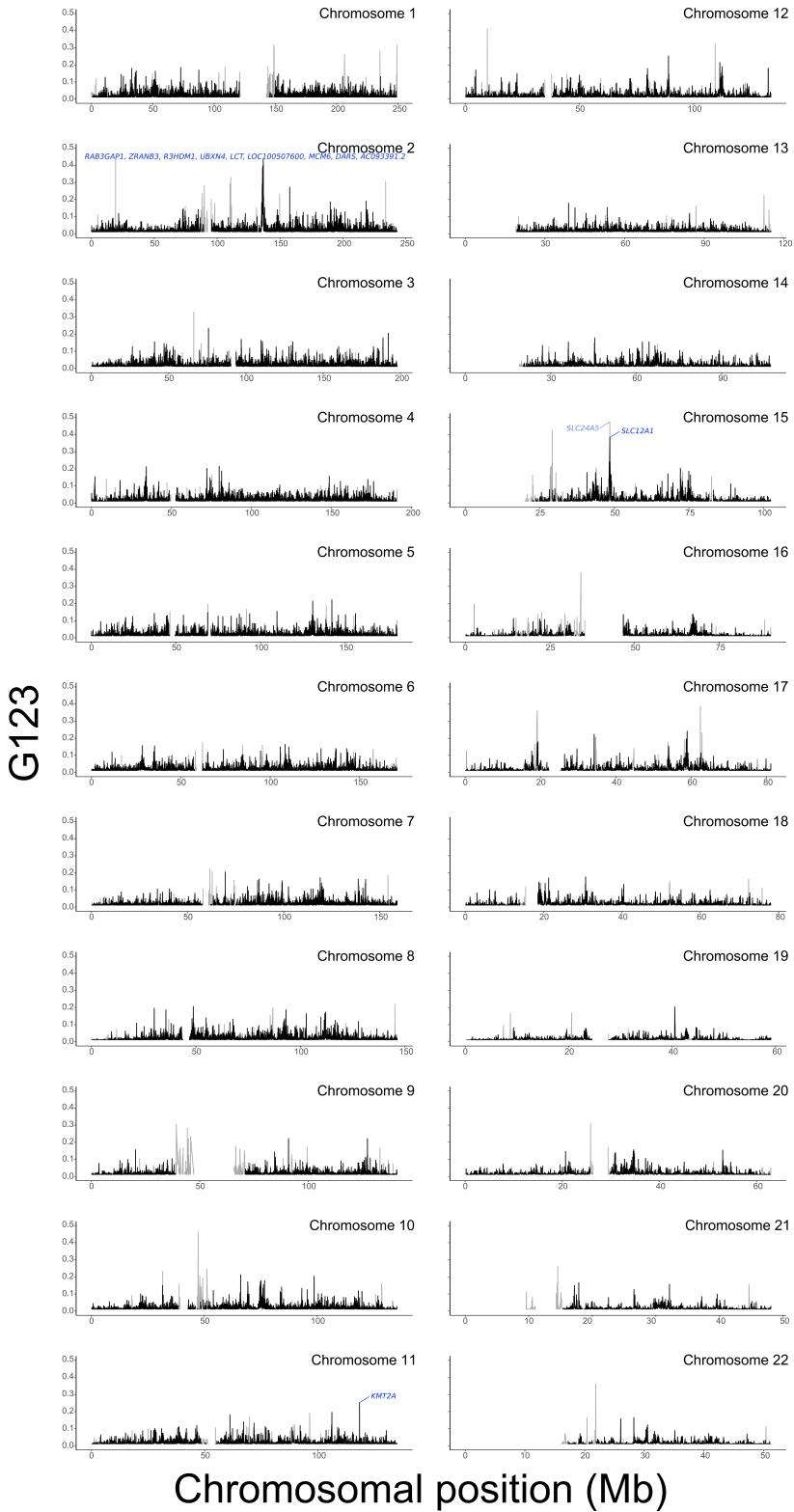


Figure S12: Manhattan plots of G123 for the CEU population. The top 10 G123 candidate genes, as well as the *SLC12A1/SLC24A5* peak, are labeled following their designations in Table S4. Candidates labeled on chromosome 2 belong to the same peak. Gray lines represent the G123 signal of filtered regions.

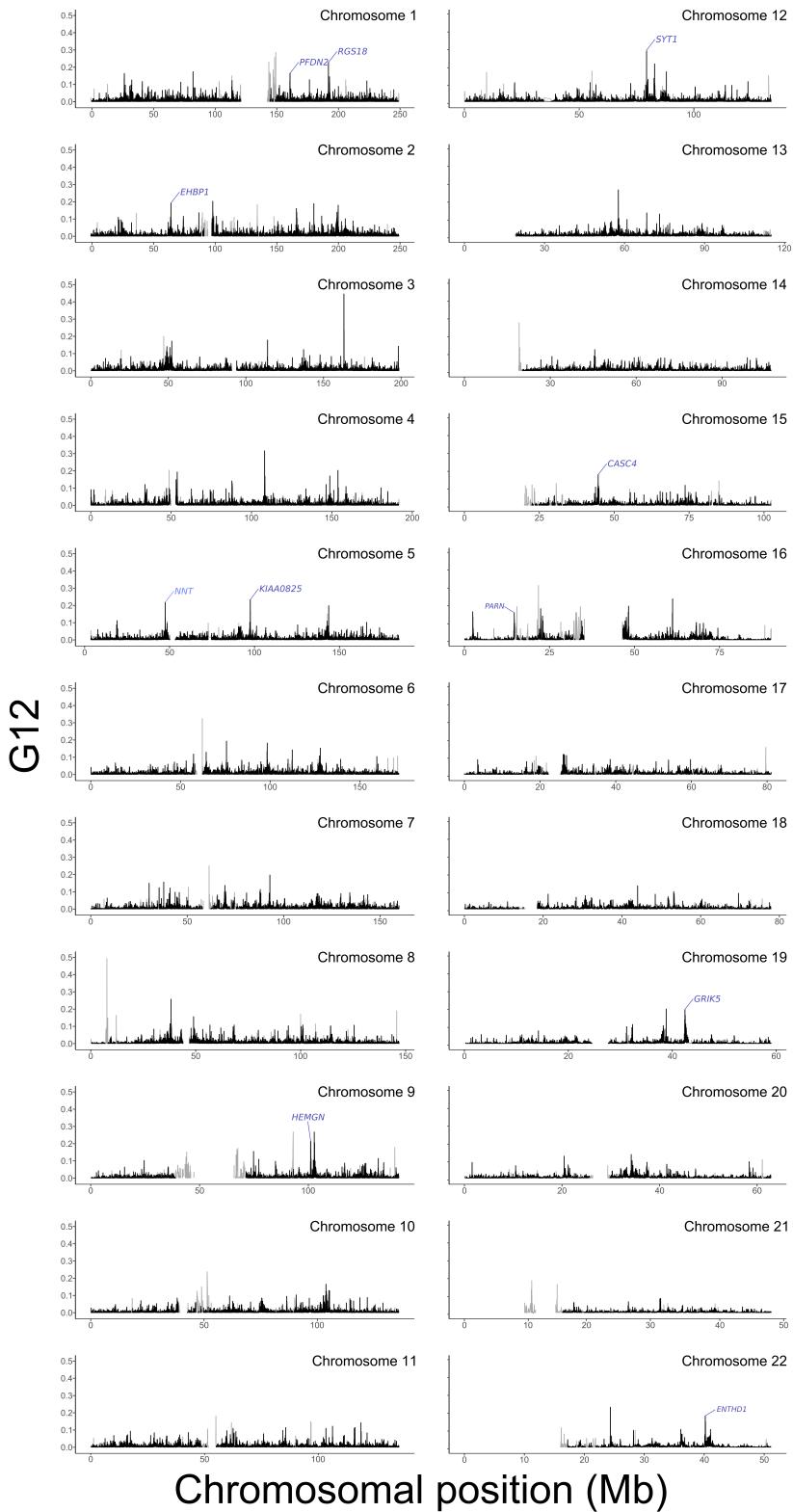


Figure S13: Manhattan plots of G12 for the YRI population. The top 10 G12 candidate genes, as well as *NNT*, are labeled following their designations in Table S6. Gray lines represent the G12 signal of filtered regions.

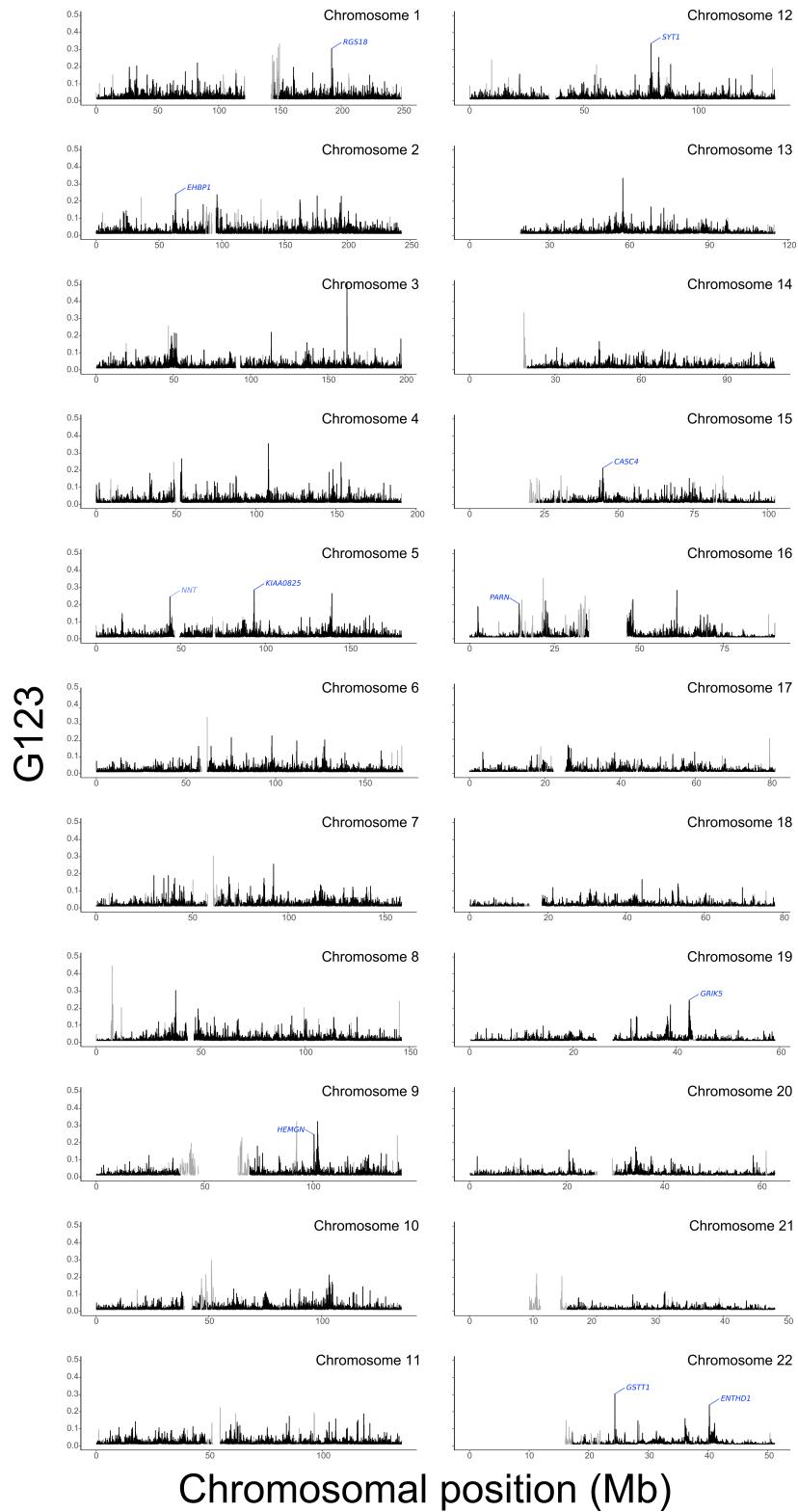


Figure S14: Manhattan plots of G123 for the YRI population. The top 10 G123 candidate genes, as well as *NNT*, are labeled following their designations in Table S7. **Gray lines represent the G123 signal of filtered regions.**

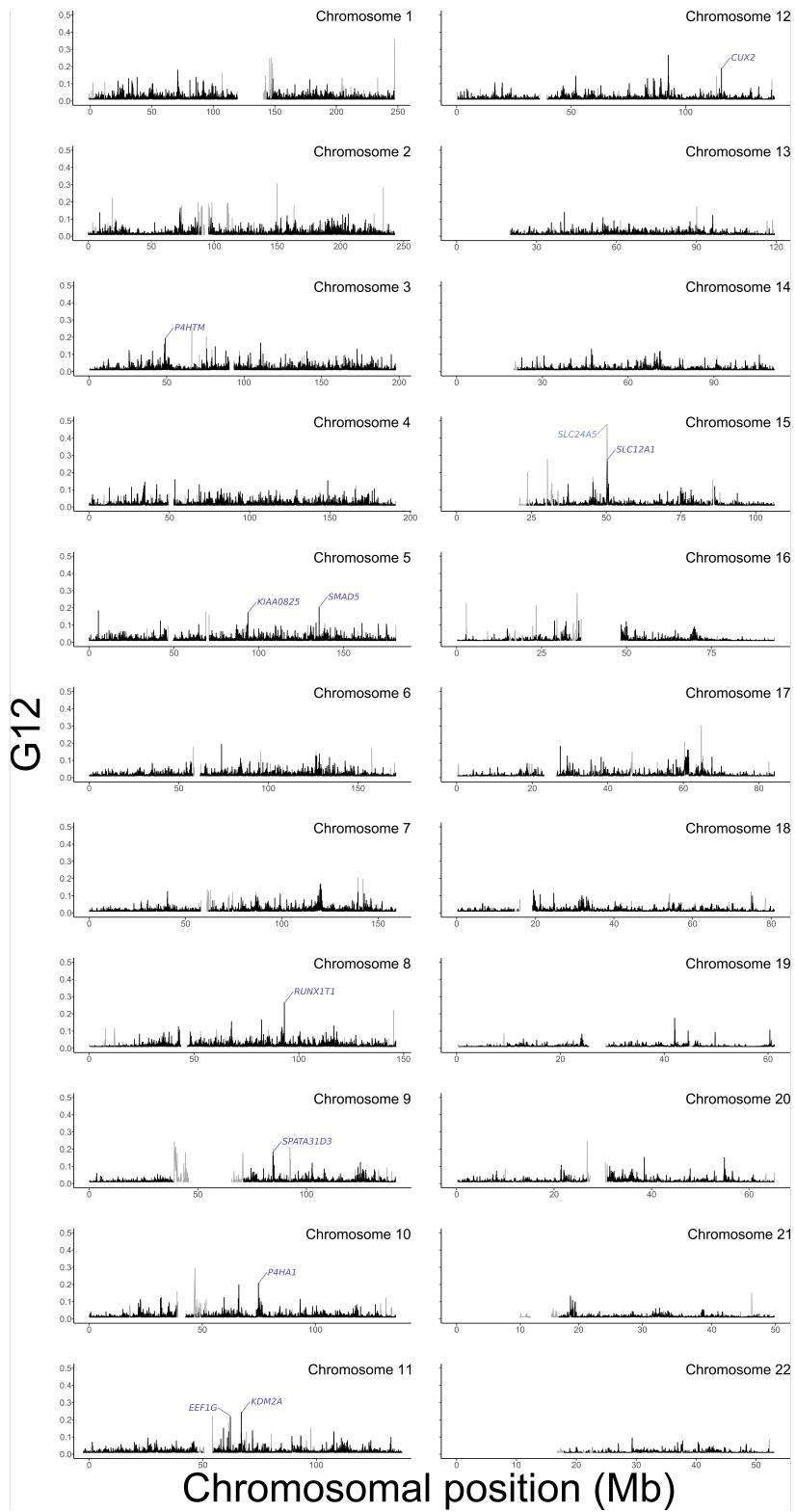


Figure S15: Manhattan plots of G12 for the GIH population. The top 10 G12 candidate genes are labeled following their designations in Table S9. **Gray lines represent the G12 signal of filtered regions.**

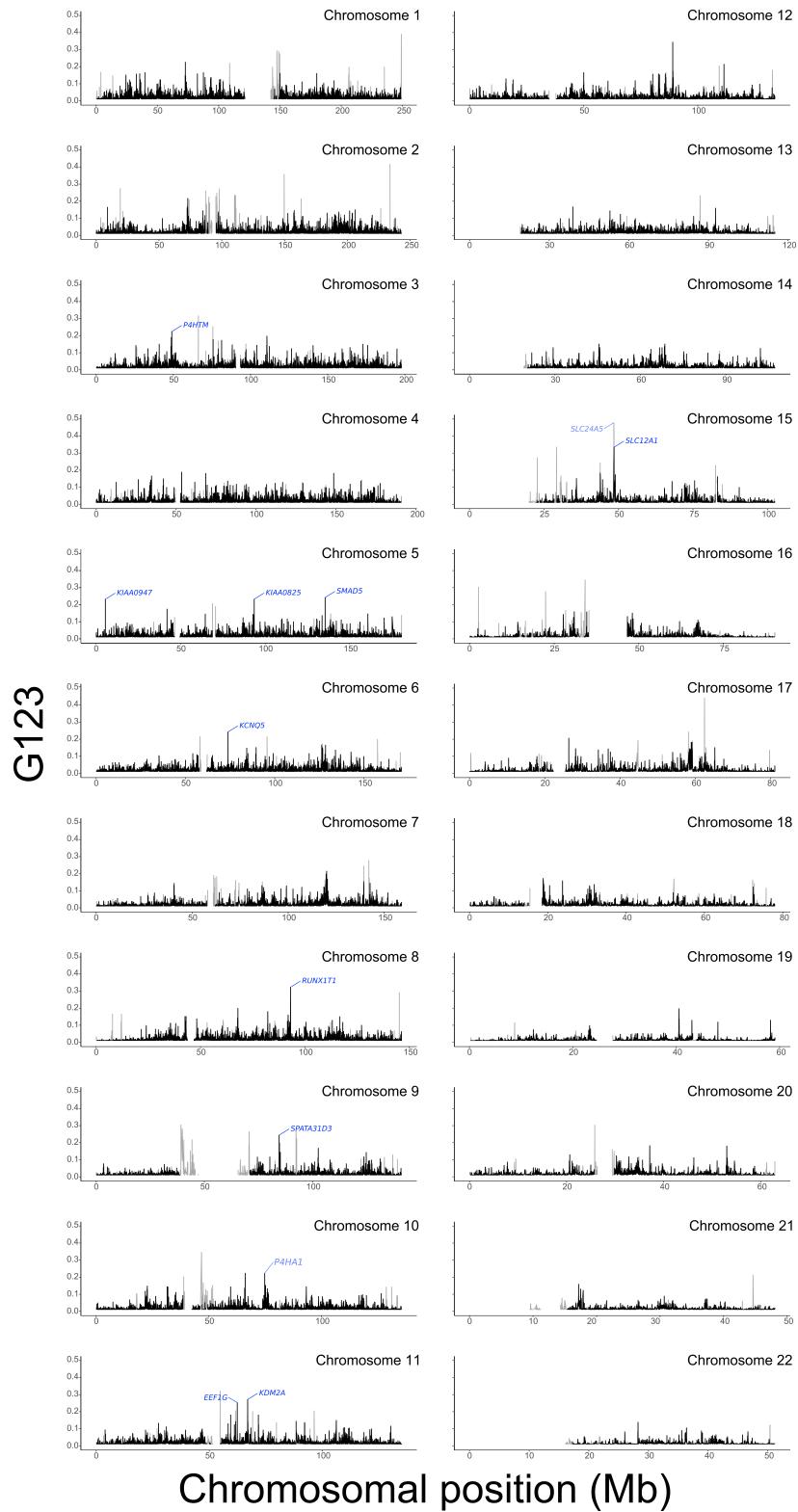


Figure S16: Manhattan plots of G123 for the GIH population. The top 10 G123 candidate genes, as well as *P4HA1*, are labeled following their designations in Table S10. **Gray lines represent the G123 signal of filtered regions.**

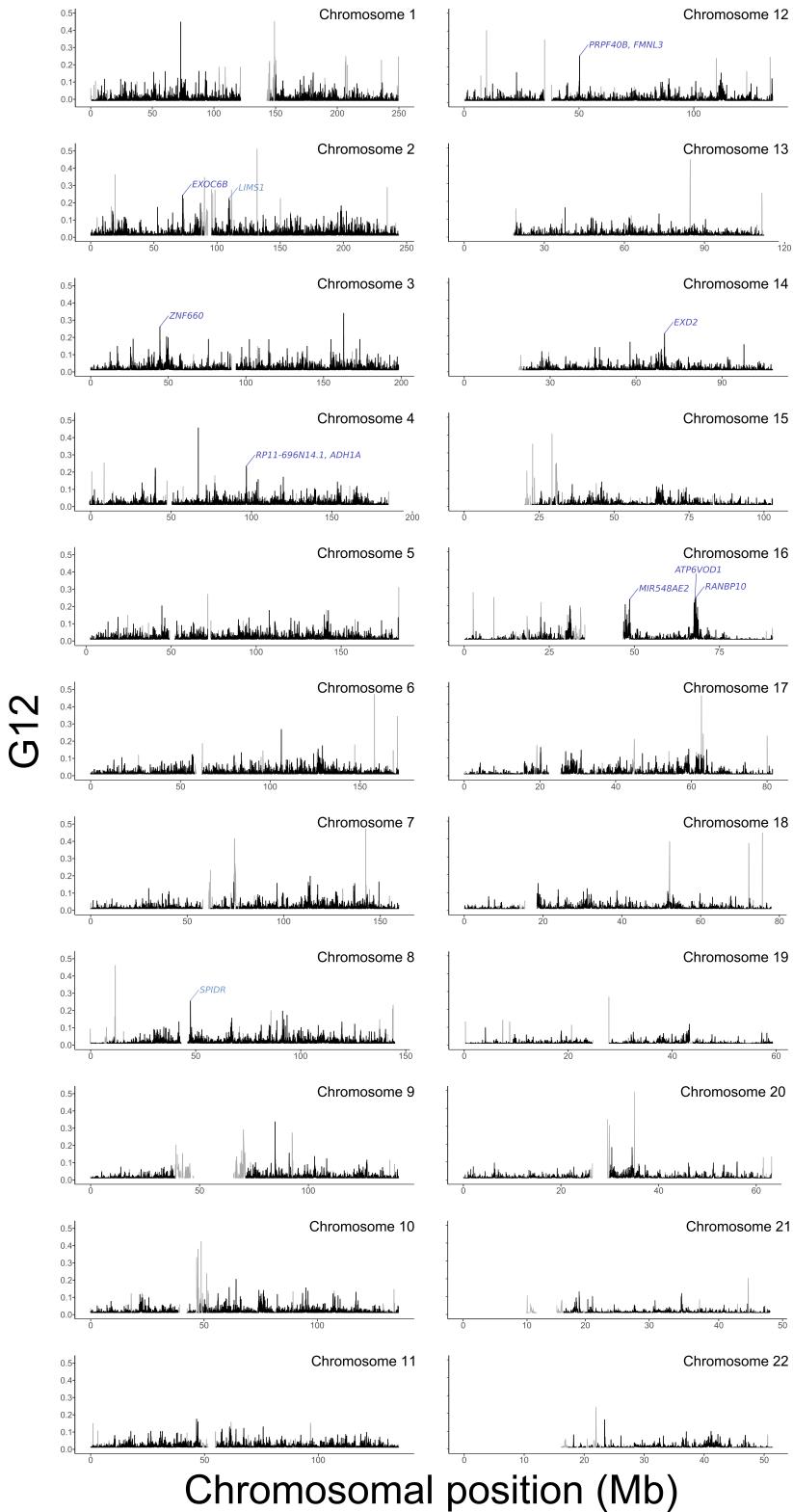


Figure S17: Manhattan plots of G12 for the CHB population. The top 10 G12 candidate genes, as well as *LIMS1*, are labeled following their designations in Table S12. **Gray lines represent the G12 signal of filtered regions.**

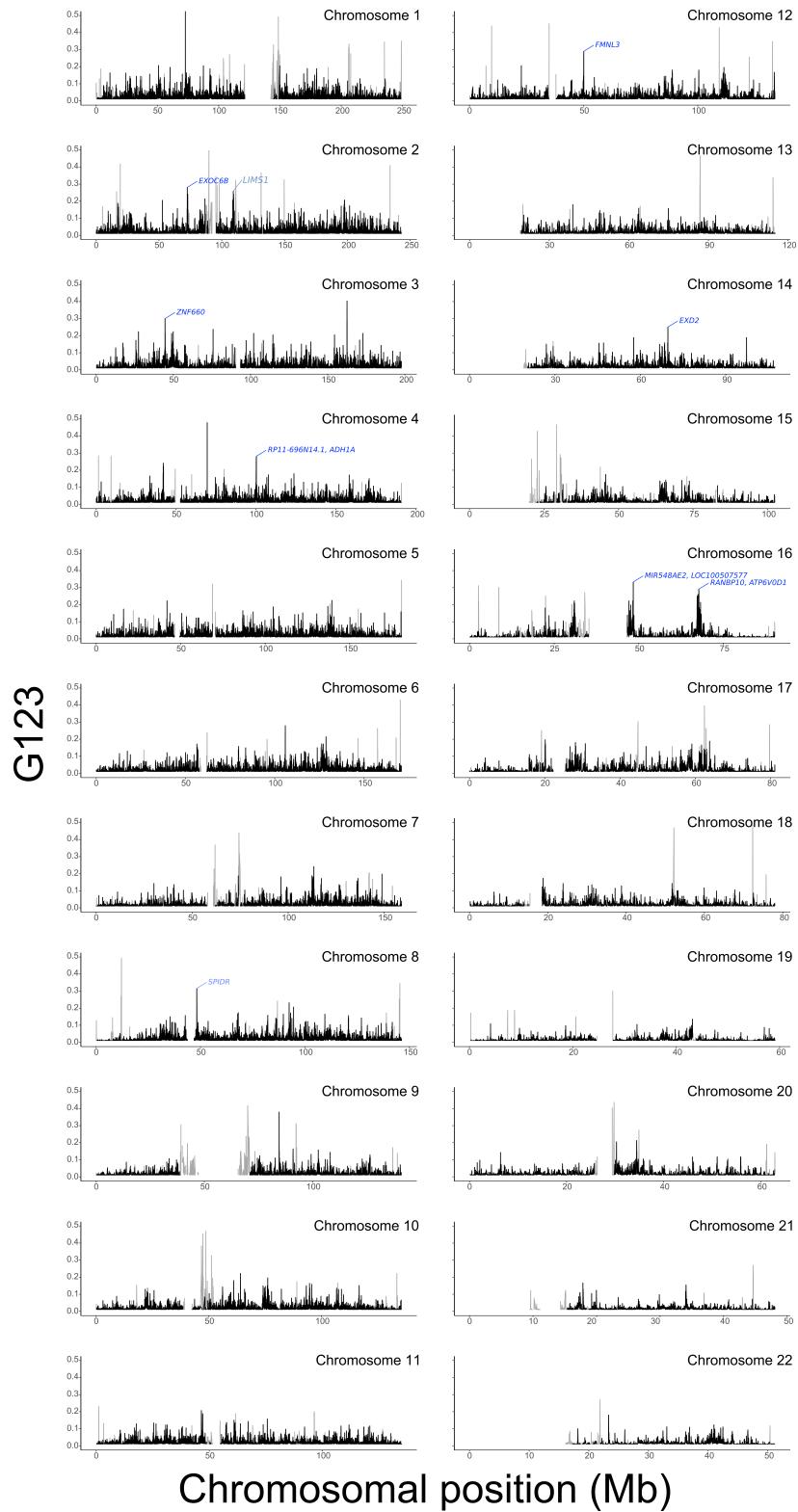


Figure S18: Manhattan plots of G123 for the CHB population. The top 10 G123 candidate genes, as well as *SPIDR* and *LIMS1*, are labeled following their designations in Table S13. Gray lines represent the G123 signal of filtered regions.

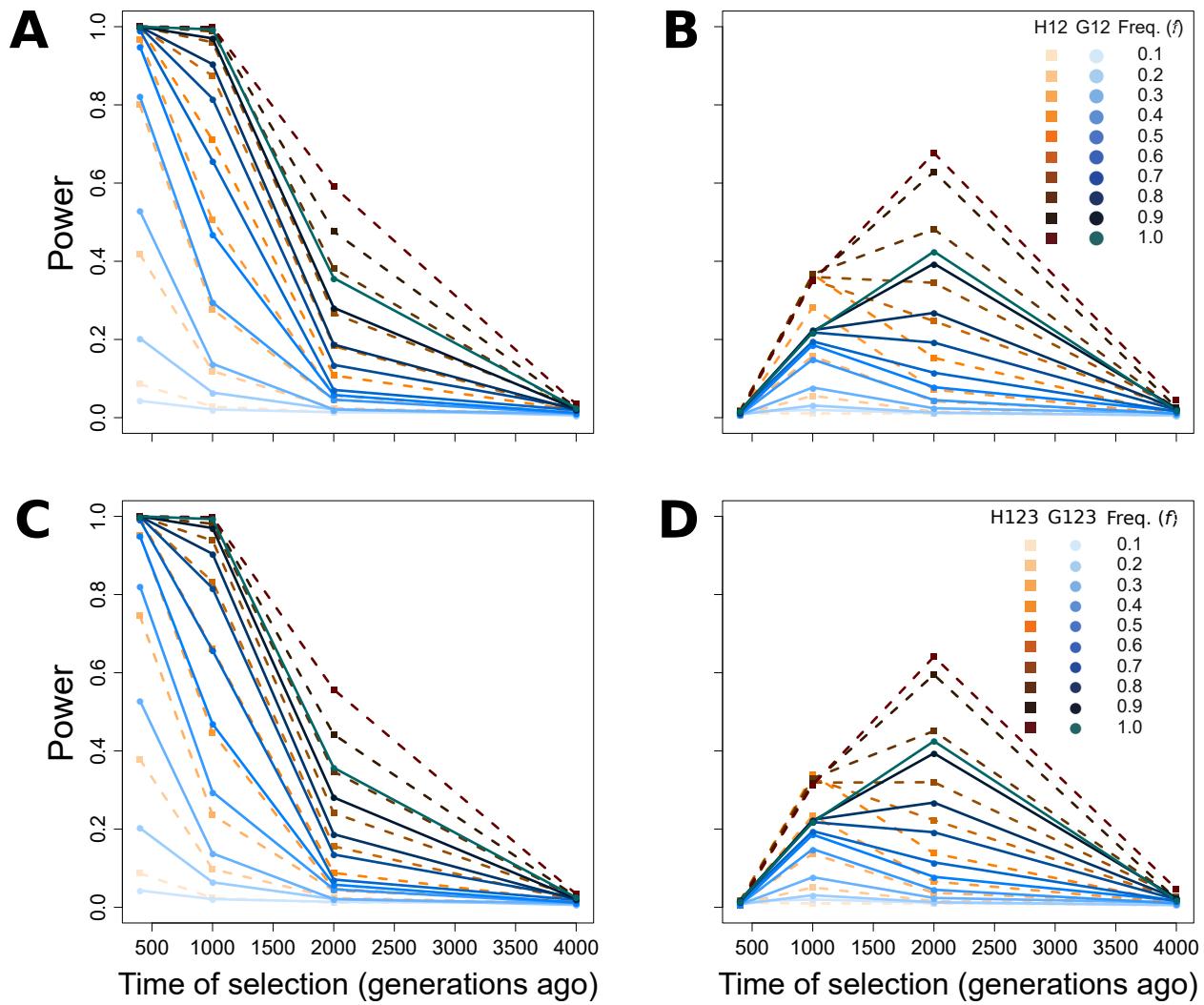


Figure S19: G12, G123, H12, and H123 maintain comparable power to detect sweeps for smaller sample sizes. For the same times of selection, values of s , and values of f as in Figure 3, we reduced the sample size for hard sweep scenarios to $n = 25$ individuals. Powers of H12 (orange) and G12 (blue) to detect strong (A) and moderate (B) hard sweeps. Powers of H123 (orange) and G123 (blue) to detect strong (C) and moderate (D) hard sweeps.

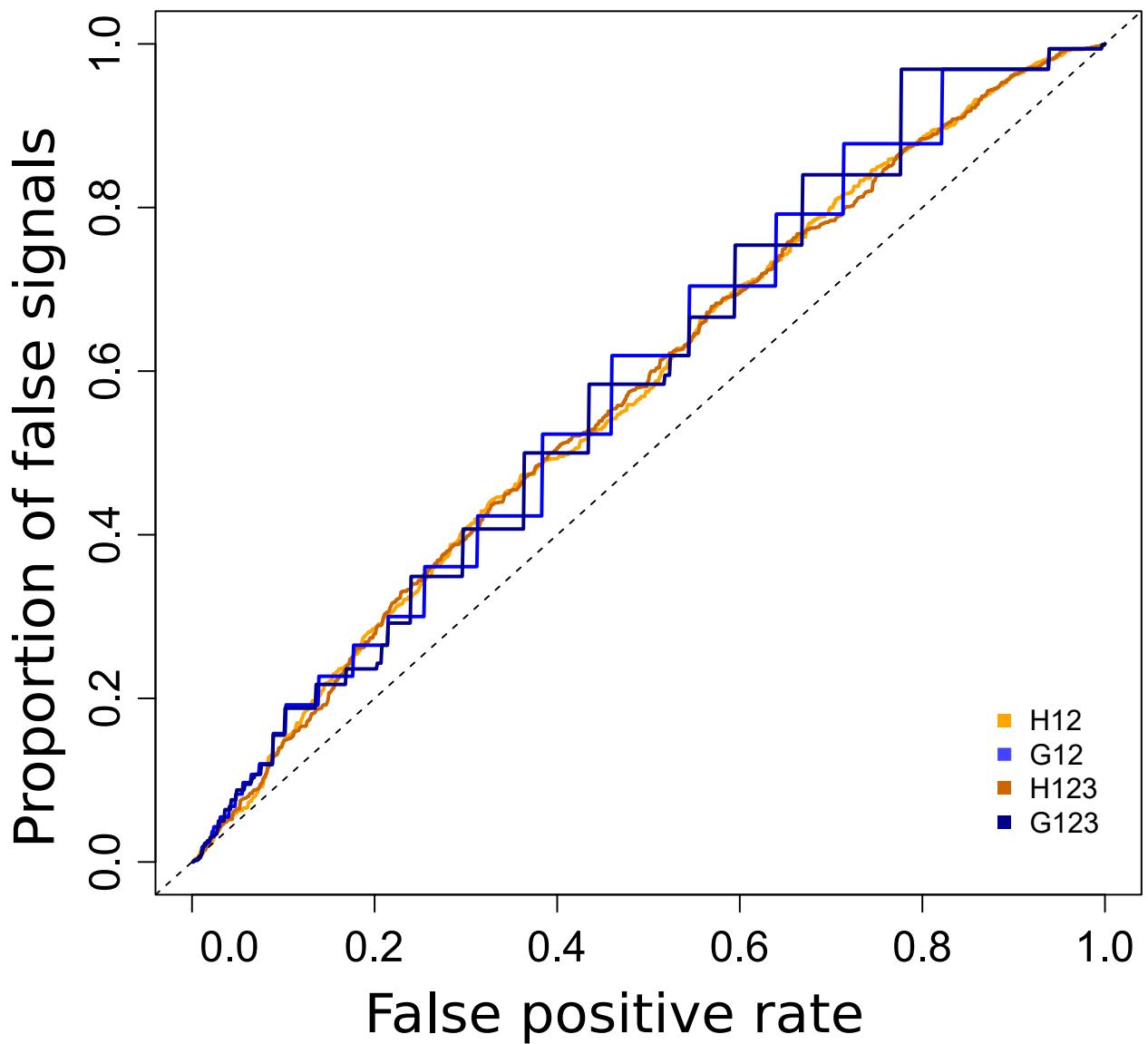


Figure S20: Proportion of false signals generated by background selection as a function of false positive rate based on neutrality for each expected homozygosity ~~✓~~ method.

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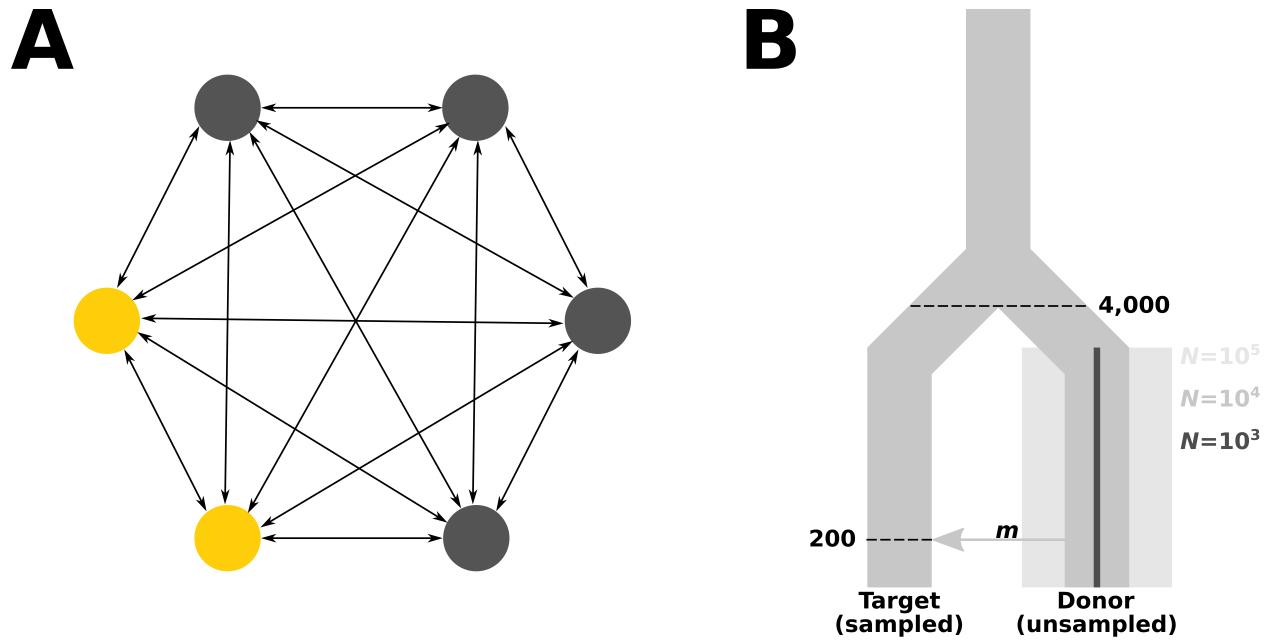


Figure S21: Demographic models of potentially-confounding non-adaptive scenarios. (A) Model of population substructure as symmetric island migration wherein members of each deme migrate to all other demes. Each generation, individuals migrate between six equally-sized demes ($N = 1,660$) at rate $m \in \{0.05, 0.10, 0.15, 0.20, 0.25, 0.30, 0.35, 0.40\}$. Two demes are sampled (indicated as gold) with equal sample sizes of $n = 50$ diploids. (B) Model of pulse admixture in which an ancestral population splits 4,000 generations ago into two modern populations, one of which (donor) is unsampled and admixes into a sampled population (target) at rate m , 200 generations ago. We varied the size of the donor population across values 10^3 , 10^4 , and 10^5 diploids, with the target retaining a constant size equal to the ancestral size of 10^4 diploids. Note that dashed line positions and population sizes in the figure are not to scale.

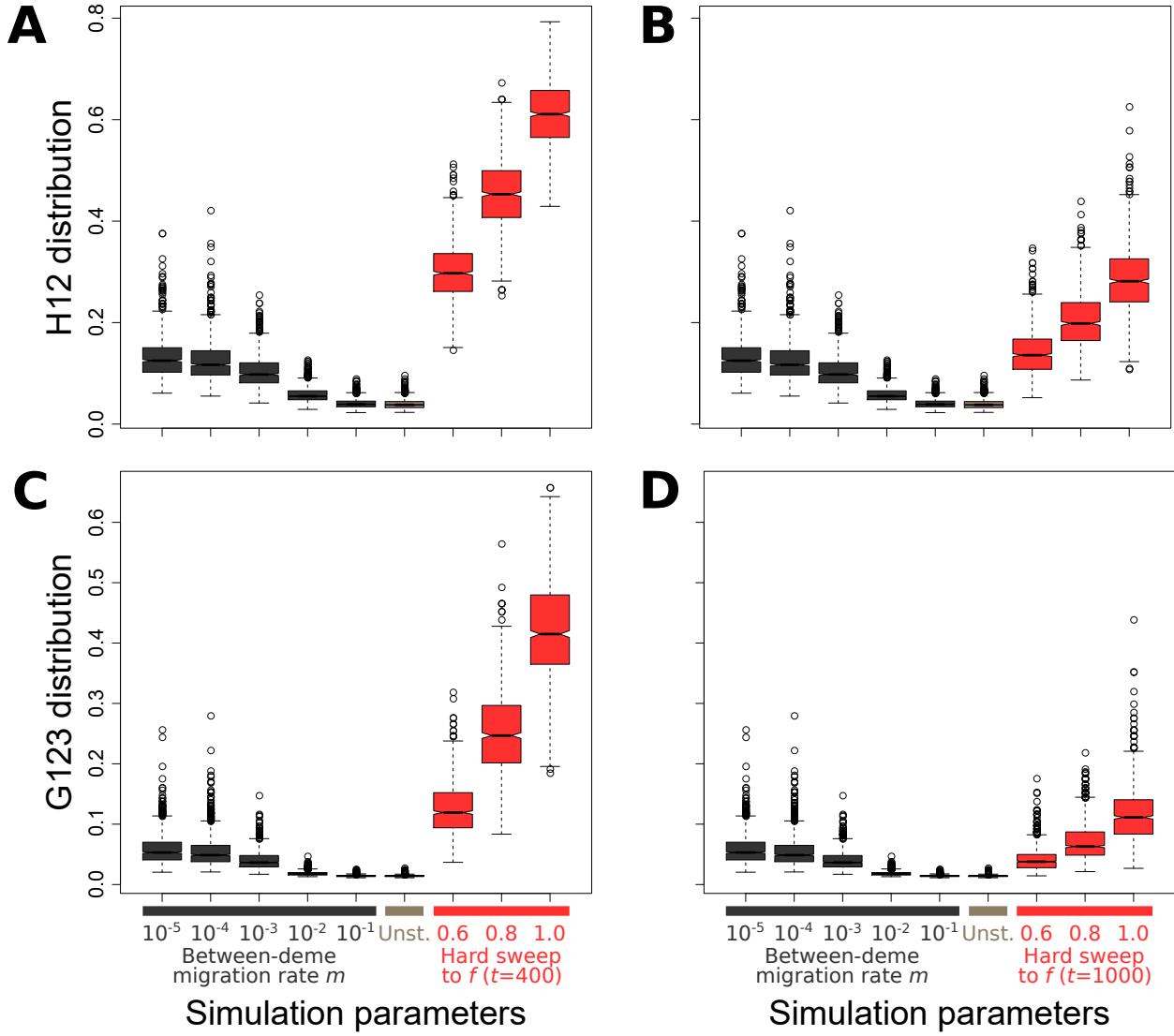


Figure S22: Distribution of H12 and G123 values under a symmetric island migration population substructure model with six demes (Figure S21A), relative to an unstructured model (Figure 2A). Each deme has size $N = 1,660$ diploids and per-generation migration rates (m) between demes of 10^{-5} , 10^{-4} , 10^{-3} , 10^{-2} , and 10^{-1} are indicated in black. Migration rates reflect the fraction of a deme made up of a specific other deme. Thus, a rate of $m = 10^{-2}$ indicates that each deme contributes 1% of the next generation's haplotypes in each other deme, and a total of 5% of a deme's haplotypes come from the other demes each generation. Results for an unstructured population of size $6N$ (“Unst.”) with no migration are indicated in light gray. Results for strong hard sweeps to frequency $f = 0.6$, 0.8 , and 1.0 are indicated in red. (A, B) Distributions of H12 values, with sweeps beginning 400 (A) or 1,000 (B) generations prior to sampling. (C, D) Distributions of G123 values, with sweeps beginning 400 (C) or 1,000 (D) generations prior to sampling.

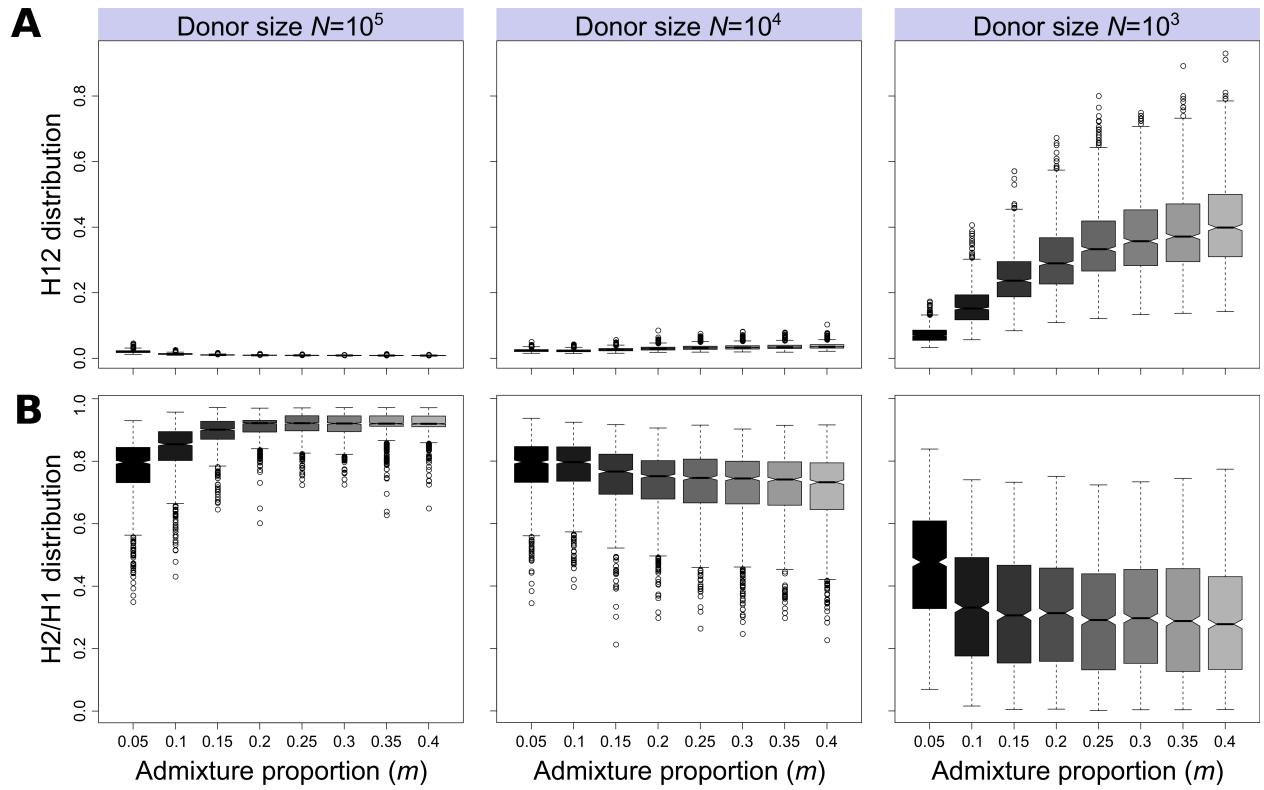


Figure S23: Distributions of maximum H12 values (A) and their associated H2/H1 (B) generated under admixture (Figure S21B) from a donor population of size 10^5 (left), 10^4 (center), or 10^3 diploids (right) into a target population of size 10^4 diploids. Admixture occurred as a single pulse 200 generations before sampling, with $m \in \{0.05, 0.10, 0.15, 0.20, 0.25, 0.30, 0.35, 0.40\}$.

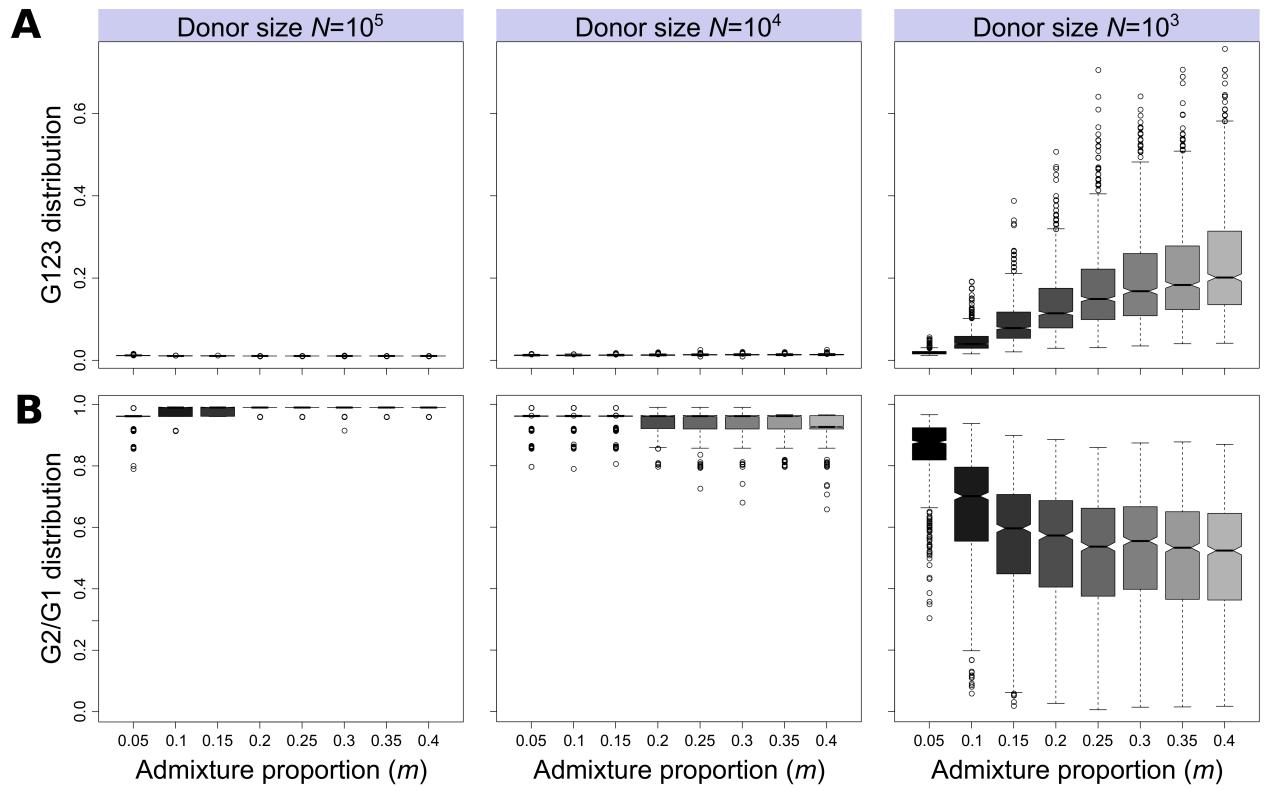


Figure S24: Distributions of maximum G123 values (A) and their associated G2/G1 (B) generated under admixture (Figure S21B) from a donor population of size 10^5 (left), 10^4 (center), or 10^3 diploids (right) into a target population of size 10^4 diploids. Admixture occurred as a single pulse 200 generations before sampling, with $m \in \{0.05, 0.10, 0.15, 0.20, 0.25, 0.30, 0.35, 0.40\}$.

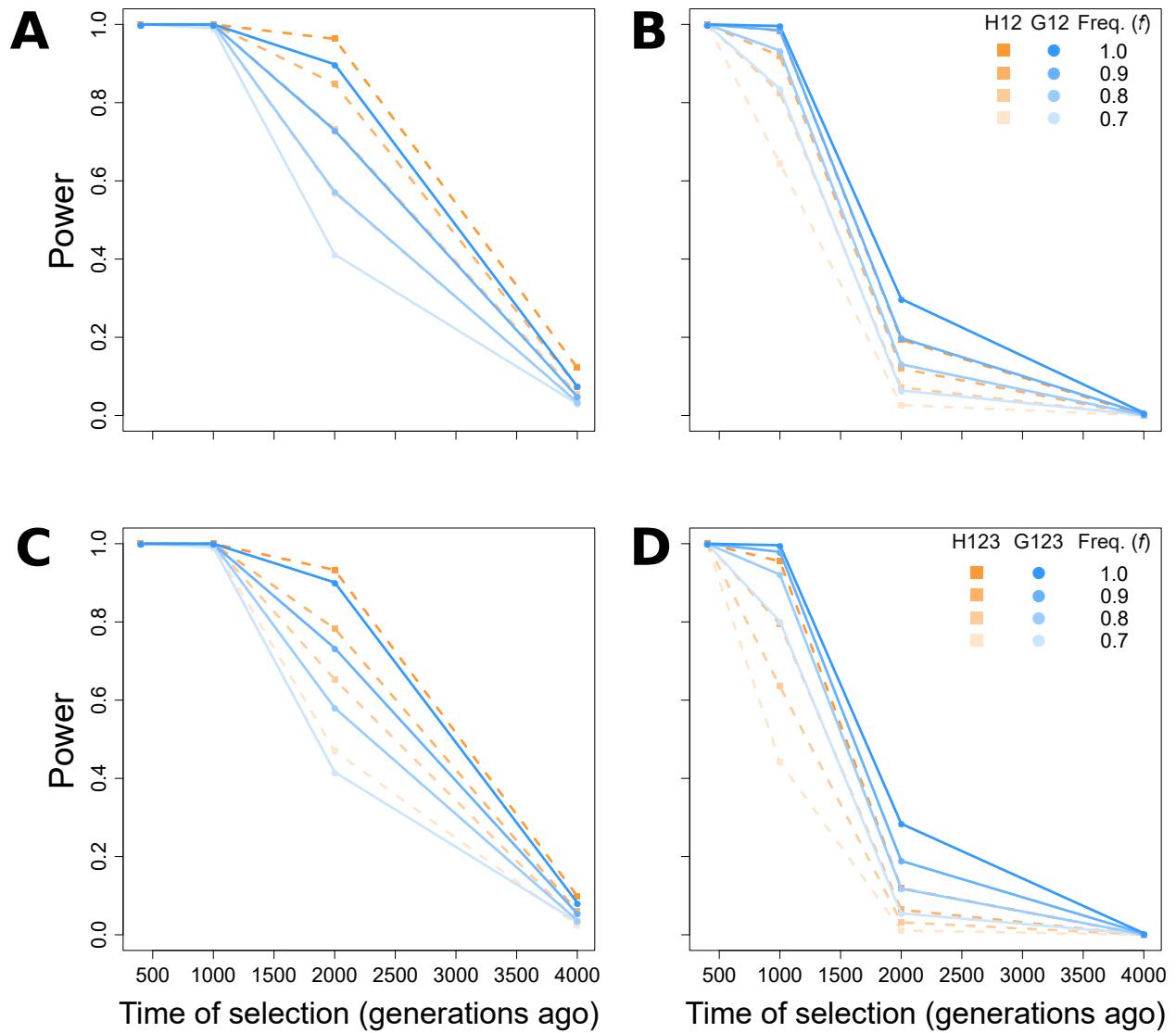


Figure S25: Effects of two strategies to account for missing data in sampled individuals on powers of G12 and H12, as well as G123 and H123. Data are identical to those in Figure 3. (A) Powers of G12 (blue) and H12 (orange) to detect strong hard sweeps when sites with missing data are removed. (B) Powers of G12 (blue) and H12 (orange) to detect strong hard sweeps when MLGs and haplotypes (respectively) with missing data are counted as new sequences. (C) Equivalent to (A), but with G123 (blue) and H123 (orange). (D) Equivalent to (B), but with G123 (blue) and H123 (orange).