Table S1: Critical values of H12, G12, and G123 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: Top 40 sweep candidates for CEU, comparing H12 and G12. Candidates presented 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 support are shaded in red in the "Bayes Factor" columns, while soft sweeps are colored in blue.

	Top gene (H12)	Maximum H12	P−value (H12)	Bayes Factor (H12)	Top gene (G12)	Maximum G12	P−value (G12)	Bayes Factor (G12)
1	*SLC12A1*	0.6141210	$< 1.0 \times 10^{-6}$	0.09135782	*DARS*	0.3972044	$< 1.0 \times 10^{-6}$	0.06763033
2	*DARS*	0.5917253	$< 1.0 \times 10^{-6}$	0.11138501	*SLC12A1*	0.3482298	$< 1.0 \times 10^{-6}$	0.08604478
3	*R3HDM1*	0.5766758	$< 1.0 \times 10^{-6}$	0.12045328	*R3HDM1*	0.3402714	$< 1.0 \times 10^{-6}$	0.09004441
4	*ZRANB3*	0.5764718	$< 1.0 \times 10^{-6}$	0.12039326	*ZRANB3*	0.3384349	$< 1.0 \times 10^{-6}$	0.08903317
5	*AC093391.2*	0.5460667	$< 1.0 \times 10^{-6}$	0.14864628	*LCT*	0.3143557	$< 1.0 \times 10^{-6}$	0.10063526
6	*MCM6*	0.5037241	1.0×10^{-6}	0.18500291	*LOC100507600*	0.3143557	$< 1.0 \times 10^{-6}$	0.10063526
7	*LCT*	0.5028569	3.0×10^{-6}	0.18351153	*AC093391.2*	0.3039486	$< 1.0 \times 10^{-6}$	0.11068469
8	*LOC100507600*	0.5028569	3.0×10^{-6}	0.18351153	*MCM6*	0.2941537	$< 1.0 \times 10^{-6}$	0.11979614
9	*RAB3GAP1*	0.4844404	3.0×10^{-6}	0.21222952	*UBXN4*	0.2523212	2.0×10^{-6}	0.14249821
10	*UBXN4*	0.4678094	4.0×10^{-6}	0.21447031	*RAB3GAP1*	0.2447709	2.0×10^{-6}	0.16751196
11	*AC005592.1*	0.4542394	5.0×10^{-6}	0.22397665	*BCAS3*	0.2059994	7.0×10^{-6}	0.20563741
12	*ZNF546*	0.4536782	5.0×10^{-6}	0.22272896	*KMT2A*	0.2053872	7.0×10^{-6}	0.20329658
13	*BCAS3*	0.4437302	8.0×10^{-6}	0.24738011	*AC005592.1*	0.2051831	8.0×10^{-6}	0.17220358
14	*NR6A1*	0.4359759	1.0×10^{-5}	5.61037394	*RAPGEF6*	0.1882461	1.2×10^{-5}	0.26931256
15	*MYO9A*	0.4287318	1.6×10^{-5}	0.25191305	*ZNF546*	0.1868177	1.4×10^{-5}	0.17978931
16	*KMT2A*	0.4225589	1.6×10^{-5}	0.27345539	*KITLG*	0.1823283	1.5×10^{-5}	0.23194485
17	*PRKDC*	0.4222528	1.6×10^{-5}	5.79922352	MYO9A	0.1792674	2.1×10^{-5}	0.19196435
18	*RAPGEF6*	0.4219978	1.7×10^{-5}	0.29212397	*BMP2K*	0.1745740	2.3×10^{-5}	0.23042439
19	*KITLG*	0.4046016	2.3×10^{-5}	0.28034706	*PRKDC*	0.1670238	3.4×10^{-5}	0.33032425
20	*BMP2K*	0.4040404	2.3×10^{-5}	0.27709075	*LCOR*	0.1647791	3.8×10^{-5}	0.22987107
21	*HS2ST1*	0.4030711	2.6×10^{-5}	0.31533815	*PPM1D*	0.1645750	3.8×10^{-5}	0.21045820
22	*PPM1D*	0.3979186	3.0×10^{-5}	0.27862771	*C4orf22*	0.1637588	3.9×10^{-5}	0.23735421
23	*SLC4A4*	0.3975615	3.1×10^{-5}	0.30063092	*COL5A2*	0.1631466	4.1×10^{-5}	0.25038895
24	*ABCB1*	0.3922559	4.0×10^{-5}	1.46545210	*CCDC178*	0.1619223	4.4×10^{-5}	2.91850628
25	*RUNDC3B*	0.3922559	4.0×10^{-5}	1.46545210	*FGF12*	0.1600857	4.4×10^{-5}	0.31678205
26	*MIR548O2*	0.3920008	4.0×10^{-5}	1.70866169	*AUTS2*	0.1596776	4.4×10^{-5}	0.25663324
27	*LCOR*	0.3911336	4.1×10^{-5}	0.28550401	*MIR548O2*	0.1580451	4.7×10^{-5}	2.83888747
28	*C4orf22*	0.3910315	4.1×10^{-5}	0.29382834	*SLC4A4*	0.1572289	4.7×10^{-5}	0.31925621
29	*TMEM163*	0.3908275	4.1×10^{-5}	0.31257078	*HDAC1*	0.1570248	4.7×10^{-5}	0.21831632
30	*COL5A2*	0.3903173	4.2×10^{-5}	0.32809956	*TMEM163*	0.1566167	4.7×10^{-5}	0.44866803
31	*LAMA3*	0.3899092	4.9×10^{-5}	7.96025716	*KAT6B*	0.1560045	5.2×10^{-5}	0.21321408
32	*POLN*	0.3889909	5.0×10^{-5}	0.28210532	*SYT1*	0.1558004	5.4×10^{-5}	0.54254780
33	*PRMT9*	0.3866952	5.1×10^{-5}	6.82260699	*TMEM116*	0.1523314	6.0×10^{-5}	0.29672549
34	*DIRC3*	0.3860320	5.1×10^{-5}	0.29551290	*FAM149B1*	0.1494745	7.0×10^{-5}	0.22529102
35	*NCALD*	0.3841445	5.6×10^{-5}	1.26180258	*KLHL28*	0.1494745	7.0×10^{-5}	0.26700323
36	*FAM149B1*	0.3838384	5.6×10^{-5}	0.28267824	*HS2ST1*	0.1482502	7.8×10^{-5}	0.31840384
37	*MIR181A2HG*	0.3785328	6.4×10^{-5}	5.05064716	*NR6A1*	0.1478421	8.4×10^{-5}	3.80143685
38	*MLLT3*	0.3781247	6.7×10^{-5}	0.38222086	*DIRC3*	0.1472299	8.5×10^{-5}	0.34790287
39	*KAT6B*	0.3776145	7.0×10^{-5}	0.28910670	*ACMSD*	0.1447811	9.1×10^{-5}	0.31179683
40	*AUTS2*	0.3742985	7.2×10^{-5}	0.31964490	*CCNT2−AS1*	0.1447811	9.1×10^{-5}	0.31179683

Table S3: Top 40 sweep candidates for CEU, comparing H12 and G123. Coloration and analyzed data are as in Table S2.

	Top gene (H12)	Maximum H12	P−value (H12)	Bayes Factor (H12)	Top gene (G123)	Maximum G123	P−value (G123)	Bayes Factor (G123)
1	*SLC12A1*	0.6141210	$< 1.0 \times 10^{-6}$	0.09135782	*DARS*	0.4351597	$< 1.0 \times 10^{-6}$	0.07039905
2	*DARS*	0.5917253	$< 1.0 \times 10^{-6}$	0.11138501	*R3HDM1*	0.3984287	$< 1.0 \times 10^{-6}$	0.07776411
3	*R3HDM1*	0.5766758	$< 1.0 \times 10^{-6}$	0.12045328	*ZRANB3*	0.3849607	$< 1.0 \times 10^{-6}$	0.08275510
4	*ZRANB3*	0.5764718	$< 1.0 \times 10^{-6}$	0.12039326	*SLC12A1*	0.3837364	$< 1.0 \times 10^{-6}$	0.08392716
5	*AC093391.2*	0.5460667	$< 1.0 \times 10^{-6}$	0.14864628	*AC093391.2*	0.3480257	$< 1.0 \times 10^{-6}$	0.10593329
6	*MCM6*	0.5037241	1.0×10^{-6}	0.18500291	*MCM6*	0.3374145	$< 1.0 \times 10^{-6}$	0.11454290
7	*LCT*	0.5028569	3.0×10^{-6}	0.18351153	*LCT*	0.3368024	$< 1.0 \times 10^{-6}$	0.10480191
8	*LOC100507600*	0.5028569	3.0×10^{-6}	0.18351153	*LOC100507600*	0.3368024	$< 1.0 \times 10^{-6}$	0.10480191
9	*RAB3GAP1*	0.4844404	3.0×10^{-6}	0.21222952	*RAB3GAP1*	0.2937455	1.0×10^{-6}	0.15468033
10	*UBXN4*	0.4678094	4.0×10^{-6}	0.21447031	*UBXN4*	0.2823181	3.0×10^{-6}	0.14282177
11	*AC005592.1*	0.4542394	5.0×10^{-6}	0.22397665	*KMT2A*	0.2525253	5.0×10^{-6}	0.26656020
12	*ZNF546*	0.4536782	5.0×10^{-6}	0.22272896	*BCAS3*	0.2419141	8.0×10^{-6}	0.19913727
13	*BCAS3*	0.4437302	8.0×10^{-6}	0.24738011	*KITLG*	0.2241608	1.0×10^{-5}	0.22173192
14	*NR6A1*	0.4359759	1.0×10^{-5}	5.61037394	*AC005592.1*	0.2231405	1.1×10^{-5}	0.17430201
15	*MYO9A*	0.4287318	1.6×10^{-5}	0.25191305	*NR6A1*	0.2217121	1.4×10^{-5}	4.33180694
16	*KMT2A*	0.4225589	1.6×10^{-5}	0.27345539	*BMP2K*	0.2153862	1.4×10^{-5}	0.22138463
17	*PRKDC*	0.4222528	1.6×10^{-5}	5.79922352	*RAPGEF6*	0.2139578	1.7×10^{-5}	0.27204479
18	*RAPGEF6*	0.4219978	1.7×10^{-5}	0.29212397	*PRKDC*	0.2068156	2.4×10^{-5}	0.34913534
19	*KITLG*	0.4046016	2.3×10^{-5}	0.28034706	*FGF12*	0.2066116	2.5×10^{-5}	0.32988467
20	*BMP2K*	0.4040404	2.3×10^{-5}	0.27709075	*AUTS2*	0.2062034	2.5×10^{-5}	0.24455636
21	*HS2ST1*	0.4030711	2.6×10^{-5}	0.31533815	*MYO9A*	0.2053872	2.8×10^{-5}	0.20718580
22	*PPM1D*	0.3979186	3.0×10^{-5}	0.27862771	*LCOR*	0.2045710	3.2×10^{-5}	0.22133760
23	*SLC4A4*	0.3975615	3.1×10^{-5}	0.30063092	*ZNF546*	0.2039588	3.6×10^{-5}	0.18239166
24	*ABCB1*	0.3922559	4.0×10^{-5}	1.46545210	*SLC4A4*	0.2037547	3.6×10^{-5}	0.32945098
25	*RUNDC3B*	0.3922559	4.0×10^{-5}	1.46545210	*MIR548O2*	0.1968167	4.1×10^{-5}	3.25438034
26	*MIR548O2*	0.3920008	4.0×10^{-5}	1.70866169	*PPM1D*	0.1964085	4.2×10^{-5}	0.20571009
27	*LCOR*	0.3911336	4.1×10^{-5}	0.28550401	*DIRC3*	0.1913070	4.8×10^{-5}	0.35623922
28	*C4orf22*	0.3910315	4.1×10^{-5}	0.29382834	*TMEM116*	0.1900826	4.8×10^{-5}	0.29087674
29	*TMEM163*	0.3908275	4.1×10^{-5}	0.31257078	*C4orf22*	0.1876339	5.4×10^{-5}	0.23420235
30	*COL5A2*	0.3903173	4.2×10^{-5}	0.32809956	*RUNX1T1*	0.1876339	5.4×10^{-5}	0.41088293
31	*LAMA3*	0.3899092	4.9×10^{-5}	7.96025716	*UNC5D*	0.1874299	5.6×10^{-5}	1.09371130
32	*POLN*	0.3889909	5.0×10^{-5}	0.28210532	*COL5A2*	0.1870217	6.0×10^{-5}	0.24760791
33	*PRMT9*	0.3866952	5.1×10^{-5}	6.82260699	*EDC3*	0.1870217	6.0×10^{-5}	0.47605799
34	*DIRC3*	0.3860320	5.1×10^{-5}	0.29551290	*ACMSD*	0.1815121	6.7×10^{-5}	0.30599100
35	*NCALD*	0.3841445	5.6×10^{-5}	1.26180258	*CCNT2−AS1*	0.1815121	6.7×10^{-5}	0.30599100
36	*FAM149B1*	0.3838384	5.6×10^{-5}	0.28267824	*HDAC1*	0.1802877	7.0×10^{-5}	0.21574470
37	*MIR181A2HG*	0.3785328	6.4×10^{-5}	5.05064716	*TMEM163*	0.1798796	7.4×10^{-5}	0.45123350
38	*MLLT3*	0.3781247	6.7×10^{-5}	0.38222086	*KLHL28*	0.1796755	7.4×10^{-5}	0.26085016
39	*KAT6B*	0.3776145	7.0×10^{-5}	0.28910670	*KAT6B*	0.1792674	8.3×10^{-5}	0.21142890
40	*AUTS2*	0.3742985	7.2×10^{-5}	0.31964490	*EP400NL*	0.1792674	8.3×10^{-5}	0.23851985

Table S4: Top 40 sweep candidates for YRI, comparing G12 and H12. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Coloration follows the scheme in Table S2.

	Top gene (H12)	Maximum H12	P−value (H12)	Bayes Factor (H12)	Top gene (G12)	Maximum G12	P−value (G12)	Bayes Factor (G12)
1	*SYT1*	0.5306499	1.0×10^{-6}	0.3738782	*SYT1*	0.2945816	1.0×10^{-6}	1.4550708
2	*RGS18*	0.5060014	1.0×10^{-6}	0.5279715	*KIAA0825*	0.2352538	1.0×10^{-6}	0.2438008
3	*RP11−554F20.1*	0.4868827	1.0×10^{-6}	0.3231440	*NNT*	0.2205075	2.0×10^{-6}	0.4449099
4	*HEMGN*	0.4612912	4.0×10^{-6}	0.3212904	*HEMGN*	0.2157064	3.0×10^{-6}	0.2205094
5	*ATF2*	0.4500600	5.0×10^{-6}	0.4510632	*RGS18*	0.2107339	4.0×10^{-6}	2.6464951
6	*ATP6V1A*	0.4427298	6.0×10^{-6}	3.6592438	*RP11−554F20.1*	0.2088477	4.0×10^{-6}	0.2889492
7	*NNT*	0.4414866	6.0×10^{-6}	0.3706262	*CDK6*	0.2001029	5.0×10^{-6}	0.3784344
8	*KIAA0825*	0.4397719	6.0×10^{-6}	0.3475407	*MIR548AE2*	0.1989026	7.0×10^{-6}	0.2314425
9	*PRKAR2A*	0.4330418	8.0×10^{-6}	15.6050677	*LONP2*	0.1989026	7.0×10^{-6}	0.2314425
10	*PSMD14*	0.4290552	9.0×10^{-6}	3.5041643	*GRIK5*	0.1985597	7.0×10^{-6}	0.2800724
11	*EHBP1*	0.4269976	9.0×10^{-6}	0.3598746	*EHBP1*	0.1953018	8.0×10^{-6}	0.2916180
12	*CDK6*	0.4269547	9.0×10^{-6}	0.4209465	*ATF2*	0.1922154	9.0×10^{-6}	5.6807807
13	*FBXW4*	0.4265689	9.0×10^{-6}	0.4628400	*SPRED3*	0.1877572	1.1×10^{-5}	0.2253940
14	*RRN3P3*	0.4213392	1.0×10^{-5}	3.2485327	*RRN3P3*	0.1844993	1.1×10^{-5}	2.2105661
15	*ARID1A*	0.4202246	1.4×10^{-5}	0.4004459	*ATP6V1A*	0.1820988	1.2×10^{-5}	5.8264117
16	*LOC102724827*	0.4202246	1.4×10^{-5}	0.4004459	*CASC4*	0.1814129	1.2×10^{-5}	0.2278132
17	*USP46*	0.4192816	1.6×10^{-5}	0.5354838	*DKK2*	0.1736968	2.1×10^{-5}	0.3346187
18	*GRIK5*	0.4154235	1.8×10^{-5}	0.4102029	*DDHD2*	0.1697531	2.3×10^{-5}	0.3706754
19	*MIR548AE2*	0.4077932	2.3×10^{-5}	0.3625203	*FBXW4*	0.1694102	2.3×10^{-5}	0.6899076
20	*LONP2*	0.4077932	2.3×10^{-5}	0.3625203	*DEDD*	0.1683813	2.4×10^{-5}	0.2651601
21	*DDHD2*	0.4027349	2.6×10^{-5}	0.3976449	*ARID1A*	0.1682099	2.5×10^{-5}	0.2398227
22	*UCHL5*	0.4007202	2.7×10^{-5}	10.4588396	*LOC102724827*	0.1682099	2.5×10^{-5}	0.2398227
23	*SGCB*	0.3968193	3.2×10^{-5}	0.7457841	*ABCA17P*	0.1676955	2.6×10^{-5}	0.8073893
24	*PIGV*	0.3962191	3.3×10^{-5}	0.3848330	*PSMD14*	0.1652949	2.9×10^{-5}	9.7400997
25	*ABCA17P*	0.3959191	3.4×10^{-5}	0.4464750	*DANCR*	0.1625514	3.3×10^{-5}	0.3978373
26	*SPRED3*	0.3944187	3.7×10^{-5}	0.3646681	*PARN*	0.1616941	3.6×10^{-5}	0.3787081
27	*PLEKHA8*	0.3912466	4.0×10^{-5}	2.0579230	*PIGV*	0.1608368	3.6×10^{-5}	0.2557738
28	*PAPPA2*	0.3891890	4.8×10^{-5}	15.3123384	*PRKDC*	0.1604938	3.7×10^{-5}	0.2527756
29	*DEDD*	0.3852452	5.6×10^{-5}	0.4049036	*PFDN2*	0.1603224	3.9×10^{-5}	6.1850166
30	*CPNE1*	0.3852023	5.6×10^{-5}	0.4649896	*ABHD17B*	0.1594650	4.0×10^{-5}	0.2353567
31	*KCNIP2*	0.3850737	5.7×10^{-5}	5.7478248	*PLEKHA8*	0.1544925	4.5×10^{-5}	3.0654693
32	*DKK2*	0.3839592	6.5×10^{-5}	0.4086323	*SGCB*	0.1539781	4.5×10^{-5}	1.4914568
33	*FER1L6*	0.3823731	6.7×10^{-5}	12.2287097	*UCHL5*	0.1498628	5.5×10^{-5}	8.7247529
34	*FER1L6−AS1*	0.3823731	6.7×10^{-5}	12.2287097	*USP46*	0.1484911	6.0×10^{-5}	1.3542441
35	*WHSC1L1*	0.3820730	6.7×10^{-5}	3.9143588	*KIAA0226*	0.1474623	6.4×10^{-5}	0.9025792
36	*SLC4A10*	0.3757287	8.7×10^{-5}	0.5038365	*REV3L*	0.1472908	6.4×10^{-5}	3.0680218
37	*ARIH2*	0.3749143	8.9×10^{-5}	42.6034483	*UBE4A*	0.1469479	6.4×10^{-5}	3.1720907
38	*PFDN2*	0.3748714	9.0×10^{-5}	7.1782584	*LOC100131626*	0.1469479	6.4×10^{-5}	3.1720907
39	*CRYBA4*	0.3741427	9.2×10^{-5}	4.1756875	*PRKAR2A*	0.1454047	7.0×10^{-5}	10.7507468
40	*ABHD17B*	0.3739712	9.3×10^{-5}	0.4313744	*CPNE1*	0.1423182	8.1×10^{-5}	1.1703311

Table S5: Top 40 sweep candidates for YRI, comparing H12 and G123. Coloration and analyzed data are as in Table S4.

	Top gene (H12)	Maximum H12	P−value (H12)	Bayes Factor (H12)	Top gene (G123)	Maximum G123	P−value (G123)	Bayes Factor (G123)
1	*SYT1*	0.5306499	1.0×10^{-6}	0.3738782	*SYT1*	0.3343621	1.0×10^{-6}	1.3430611
2	*RGS18*	0.5060014	1.0×10^{-6}	0.5279715	*GSTT1*	0.3043553	1.0×10^{-6}	0.3131835
3	*RP11−554F20.1*	0.4868827	1.0×10^{-6}	0.3231440	*KIAA0825*	0.2877229	1.0×10^{-6}	0.2336808
4	*HEMGN*	0.4612912	4.0×10^{-6}	0.3212904	*RGS18*	0.2683471	3.0×10^{-6}	2.6928661
5	*ATF2*	0.4500600	5.0×10^{-6}	0.4510632	*CDK6*	0.2565158	4.0×10^{-6}	0.3706977
6	*ATP6V1A*	0.4427298	6.0×10^{-6}	3.6592438	*RP11−554F20.1*	0.2500000	4.0×10^{-6}	0.2745741
7	*NNT*	0.4414866	6.0×10^{-6}	0.3706262	*HEMGN*	0.2493141	4.0×10^{-6}	0.2121993
8	*KIAA0825*	0.4397719	6.0×10^{-6}	0.3475407	*NNT*	0.2469136	6.0×10^{-6}	0.2471558
9	*PRKAR2A*	0.4330418	8.0×10^{-6}	15.6050677	*GRIK5*	0.2469136	6.0×10^{-6}	0.2636660
10	*PSMD14*	0.4290552	9.0×10^{-6}	3.5041643	*EHBP1*	0.2426269	7.0×10^{-6}	0.2741587
11	*EHBP1*	0.4269976	9.0×10^{-6}	0.3598746	*ENTHD1*	0.2393690	7.0×10^{-6}	0.6314805
12	*CDK6*	0.4269547	9.0×10^{-6}	0.4209465	*ATF2*	0.2316529	9.0×10^{-6}	5.6199092
13	*FBXW4*	0.4265689	9.0×10^{-6}	0.4628400	*MIR548AE2*	0.2311385	1.0×10^{-5}	0.2219055
14	*RRN3P3*	0.4213392	1.0×10^{-5}	3.2485327	*LONP2*	0.2311385	1.0×10^{-5}	0.2219055
15	*ARID1A*	0.4202246	1.4×10^{-5}	0.4004459	*RRN3P3*	0.2230796	1.4×10^{-5}	2.1197559
16	*LOC102724827*	0.4202246	1.4×10^{-5}	0.4004459	*ATP6V1A*	0.2206790	1.8×10^{-5}	5.7804848
17	*USP46*	0.4192816	1.6×10^{-5}	0.5354838	*DOCK3*	0.2163923	2.0×10^{-5}	5.3277637
18	*GRIK5*	0.4154235	1.8×10^{-5}	0.4102029	*FBXW4*	0.2136488	2.6×10^{-5}	0.6782700
19	*MIR548AE2*	0.4077932	2.3×10^{-5}	0.3625203	*CASC4*	0.2122771	2.7×10^{-5}	0.2201954
20	*LONP2*	0.4077932	2.3×10^{-5}	0.3625203	*PSMD14*	0.2090192	2.7×10^{-5}	9.3563698
21	*DDHD2*	0.4027349	2.6×10^{-5}	0.3976449	*DDHD2*	0.2066187	2.8×10^{-5}	0.3521398
22	*UCHL5*	0.4007202	2.7×10^{-5}	10.4588396	*RBBP4*	0.2054184	3.1×10^{-5}	5.2702311
23	*SGCB*	0.3968193	3.2×10^{-5}	0.7457841	*PARN*	0.2049040	3.3×10^{-5}	0.3575007
24	*PIGV*	0.3962191	3.3×10^{-5}	0.3848330	*GSTTP2*	0.2047325	3.3×10^{-5}	0.3081970
25	*ABCA17P*	0.3959191	3.4×10^{-5}	0.4464750	*DKK2*	0.2038752	3.7×10^{-5}	0.3192281
26	*SPRED3*	0.3944187	3.7×10^{-5}	0.3646681	*SPRED3*	0.2035322	3.7×10^{-5}	0.2190593
27	*PLEKHA8*	0.3912466	4.0×10^{-5}	2.0579230	*REV3L*	0.2007888	3.8×10^{-5}	3.6532096
28	*PAPPA2*	0.3891890	4.8×10^{-5}	15.3123384	*PRKAR2A*	0.1989026	4.2×10^{-5}	12.7732636
29	*DEDD*	0.3852452	5.6×10^{-5}	0.4049036	*ARID1A*	0.1987311	4.2×10^{-5}	1.9304365
30	*CPNE1*	0.3852023	5.6×10^{-5}	0.4649896	*DEDD*	0.1978738	4.5×10^{-5}	0.2557345
31	*KCNIP2*	0.3850737	5.7×10^{-5}	5.7478248	*PRKDC*	0.1965021	4.9×10^{-5}	0.2435841
32	*DKK2*	0.3839592	6.5×10^{-5}	0.4086323	*DANCR*	0.1913580	5.3×10^{-5}	0.3795499
33	*FER1L6*	0.3823731	6.7×10^{-5}	12.2287097	*UCHL5*	0.1910151	5.4×10^{-5}	9.4329238
34	*FER1L6−AS1*	0.3823731	6.7×10^{-5}	12.2287097	*ABCA17P*	0.1898148	5.9×10^{-5}	0.7351430
35	*WHSC1L1*	0.3820730	6.7×10^{-5}	3.9143588	*PIGV*	0.1896433	6.0×10^{-5}	0.2480200
36	*SLC4A10*	0.3757287	8.7×10^{-5}	0.5038365	*USP46*	0.1896433	6.0×10^{-5}	1.3618489
37	*ARIH2*	0.3749143	8.9×10^{-5}	42.6034483	*PLEKHA8*	0.1896433	6.0×10^{-5}	3.1010413
38	*PFDN2*	0.3748714	9.0×10^{-5}	7.1782584	*PFDN2*	0.1891289	6.5×10^{-5}	6.0955235
39	*CRYBA4*	0.3741427	9.2×10^{-5}	4.1756875	*SGCB*	0.1891289	6.5×10^{-5}	1.4620129
40	*ABHD17B*	0.3739712	9.3×10^{-5}	0.4313744	*UBE4A*	0.1881001	6.8×10^{-5}	3.4887179

Table S6: Top 40 sweep candidates for GIH, comparing G12 and H12. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Coloration follows the scheme in Table S2.

	Top gene (H12)	Maximum H12	P–value (H12)	Bayes Factor (H12)	Top gene (G12)	Maximum G12	P–value (G12)	Bayes Factor (G12)
1	*SLC12A1*	0.5426996	$< 1.0 \times 10^{-6}$	0.1864263	*SLC12A1*	0.2660948	1.0×10^{-6}	0.4167995
2	*RUNX1T1*	0.5267697	$< 1.0 \times 10^{-6}$	0.1898326	*RUNX1T1*	0.2642096	1.0×10^{-6}	0.8529346
3	*EEF1G*	0.4922707	1.0×10^{-6}	0.2957677	*KDM2A*	0.2434725	1.0×10^{-6}	0.1756071
4	*KDM2A*	0.4852012	1.0×10^{-6}	0.2127236	*EEF1G*	0.2182110	1.0×10^{-6}	3.7996676
5	*P4HA1*	0.4784617	1.0×10^{-6}	1.6086290	*P4HA1*	0.2067113	5.0×10^{-6}	2.3742676
6	*P4HTM*	0.4520219	4.0×10^{-6}	0.2320159	*SMAD5*	0.1999246	7.0×10^{-6}	0.5048051
7	*SPATA31D3*	0.4431615	8.0×10^{-6}	0.2660423	*KCNQ5*	0.1927609	1.0×10^{-5}	0.2156955
8	*SMAD5*	0.4398624	9.0×10^{-6}	0.2588064	*P4HTM*	0.1910642	1.0×10^{-5}	0.1931029
9	*KCNQ5*	0.4338769	9.0×10^{-6}	0.2485570	*CUX2*	0.1901216	1.0×10^{-5}	0.2147554
10	*ZNF546*	0.4256763	2.0×10^{-5}	0.2714188	*KIAA0947*	0.1835234	1.4×10^{-5}	1.8672459
11	*CUX2*	0.4209162	2.1×10^{-5}	0.2705478	*NLK*	0.1822038	1.5×10^{-5}	1.2885710
12	*KCND2*	0.4164389	2.2×10^{-5}	0.3705526	*SPATA31D3*	0.1812612	1.5×10^{-5}	0.2912047
13	*NLK*	0.4150721	2.5×10^{-5}	0.3258362	*ZNF546*	0.1739089	1.8×10^{-5}	0.3156611
14	*CELSR3*	0.4150250	2.5×10^{-5}	0.2792874	*KIAA0825*	0.1708926	2.2×10^{-5}	0.5791245
15	*EXOC6B*	0.4082854	3.3×10^{-5}	0.2663773	*KCND2*	0.1691960	2.2×10^{-5}	2.2220460
16	*PRMT9*	0.4032897	3.6×10^{-5}	0.2772317	*FABP5*	0.1652371	2.8×10^{-5}	0.1966055
17	*RALGAPB*	0.3975398	4.0×10^{-5}	0.2981996	*EXOC6B*	0.1646715	2.8×10^{-5}	0.2787438
18	*KIAA0825*	0.3809501	5.9×10^{-5}	0.3209327	*CELSR3*	0.1601470	3.3×10^{-5}	0.2439441
19	*SSH2*	0.3800547	6.1×10^{-5}	2.1497524	*BCAS3*	0.1595815	3.7×10^{-5}	0.2282339
20	*BCAS3*	0.3789707	6.4×10^{-5}	0.2904880	*USP46*	0.1592044	3.8×10^{-5}	0.2167963
21	*PRPF40B*	0.3788293	6.5×10^{-5}	0.3078750	*RALGAPB*	0.1535489	4.3×10^{-5}	0.3149341
22	*FMNL3*	0.3788293	6.5×10^{-5}	0.3078750	*PRMT9*	0.1527948	4.9×10^{-5}	0.2283227
23	*RNF121*	0.3783109	6.8×10^{-5}	0.3671037	*PATL1*	0.1518522	5.4×10^{-5}	0.2228148
24	*VPS45*	0.3750118	7.1×10^{-5}	0.3298900	*PRPF40B*	0.1445000	8.2×10^{-5}	0.2287922
25	*KIAA0947*	0.3737393	7.9×10^{-5}	0.4148649	*FMNL3*	0.1445000	8.2×10^{-5}	0.2287922
26	*SLC26A6*	0.3719483	8.7×10^{-5}	0.3398815	*RNU6−28P*	0.1422377	8.4×10^{-5}	2.2626032
27	*GREB1L*	0.3655387	1.0×10^{-4}	12.1135612	*PPIP5K1*	0.1422377	8.4×10^{-5}	2.2626032
28	*ADK*	0.3636064	1.1×10^{-4}	9.3488372	*MACF1*	0.1377133	1.0×10^{-4}	0.2272245
29	*SNAP91*	0.3628994	1.2×10^{-4}	5.1138761	*HS2ST1*	0.1377133	1.0×10^{-4}	0.2496698
30	*CASC4*	0.3624281	1.2×10^{-4}	11.5340094	*PTPRK*	0.1377133	1.0×10^{-4}	0.2672836
31	*PTPRK*	0.3613913	1.3×10^{-4}	0.3263333	*MBOAT2*	0.1371477	1.1×10^{-4}	0.3728418
32	*RNU6−28P*	0.3612028	1.3×10^{-4}	1.0654490	*RNF121*	0.1369592	1.1×10^{-4}	0.2839225
33	*PPIP5K1*	0.3612028	1.3×10^{-4}	1.0654490	*TSPAN12*	0.1339429	1.2×10^{-4}	0.3149508
34	*ADAMTS6*	0.3568668	1.5×10^{-4}	8.9631458	*FBN1*	0.1337544	1.2×10^{-4}	0.4851509
35	*ORC2*	0.3561599	1.6×10^{-4}	0.3379306	*USP25*	0.1320577	1.4×10^{-4}	0.2525881
36	*MBOAT2*	0.3544632	1.7×10^{-4}	0.3583785	*METTL25*	0.1314921	1.5×10^{-4}	0.2481290
37	*ZMYM1*	0.3529550	1.7×10^{-4}	0.3475098	*DPH6−AS1*	0.1314921	1.5×10^{-4}	0.4277112
38	*TBXAS1*	0.3529550	1.7×10^{-4}	2.8622010	*KLHL28*	0.1311151	1.6×10^{-4}	0.2347874
39	*GPC5*	0.3513055	1.8×10^{-4}	0.3697656	*HDAC1*	0.1307381	1.6×10^{-4}	0.4102046
40	*USP46*	0.3510227	1.8×10^{-4}	0.3200877	*PARD3B*	0.1303610	1.6×10^{-4}	0.2401545

Table S7: Top 40 sweep candidates for GIH, comparing H12 and G123. Coloration and analyzed data are as in Table S6.

	Top gene (H12)	Maximum H12	P−value (H12)	Bayes Factor (H12)	Top gene (G123)	Maximum G123	P−value (G123)	Bayes Factor (G123)
1	*SLC12A1*	0.5426996	$< 1.0 \times 10^{-6}$	0.1864263	*SLC12A1*	0.3347158	1.0×10^{-6}	0.4654927
2	*RUNX1T1*	0.5267697	$< 1.0 \times 10^{-6}$	0.1898326	*RUNX1T1*	0.3230276	1.0×10^{-6}	0.9277338
3	*EEF1G*	0.4922707	1.0×10^{-6}	0.2957677	*KDM2A*	0.2717504	1.0×10^{-6}	0.1759464
4	*KDM2A*	0.4852012	1.0×10^{-6}	0.2127236	*EEF1G*	0.2536526	2.0×10^{-6}	4.3730713
5	*P4HA1*	0.4784617	1.0×10^{-6}	1.6086290	*SPATA31D3*	0.2446036	4.0×10^{-6}	0.3331732
6	*P4HTM*	0.4520219	4.0×10^{-6}	0.2320159	*KCNQ5*	0.2425299	6.0×10^{-6}	0.2025376
7	*SPATA31D3*	0.4431615	8.0×10^{-6}	0.2660423	*SMAD5*	0.2423414	6.0×10^{-6}	0.5566015
8	*SMAD5*	0.4398624	9.0×10^{-6}	0.2588064	*KIAA0825*	0.2327269	8.0×10^{-6}	0.8065777
9	*KCNQ5*	0.4338769	9.0×10^{-6}	0.2485570	*KIAA0947*	0.2321614	9.0×10^{-6}	2.1821009
10	*ZNF546*	0.4256763	2.0×10^{-5}	0.2714188	*P4HTM*	0.2242436	1.1×10^{-5}	0.1884389
11	*CUX2*	0.4209162	2.1×10^{-5}	0.2705478	*P4HA1*	0.2240550	1.1×10^{-5}	3.1190441
12	*KCND2*	0.4164389	2.2×10^{-5}	0.3705526	*EXOC6B*	0.2174569	1.4×10^{-5}	0.2752025
13	*NLK*	0.4150721	2.5×10^{-5}	0.3258362	*KCND2*	0.2155717	1.5×10^{-5}	2.5976748
14	*CELSR3*	0.4150250	2.5×10^{-5}	0.2792874	*CUX2*	0.2150061	1.7×10^{-5}	0.2135333
15	*EXOC6B*	0.4082854	3.3×10^{-5}	0.2663773	*NLK*	0.2065228	2.0×10^{-5}	1.2182411
16	*PRMT9*	0.4032897	3.6×10^{-5}	0.2772317	*ZNF546*	0.1976624	2.6×10^{-5}	0.3161810
17	*RALGAPB*	0.3975398	4.0×10^{-5}	0.2981996	*CELSR3*	0.1903101	3.5×10^{-5}	0.2389775
18	*KIAA0825*	0.3809501	5.9×10^{-5}	0.3209327	*USP46*	0.1893675	4.3×10^{-5}	0.2124142
19	*SSH2*	0.3800547	6.1×10^{-5}	2.1497524	*RNU6−28P*	0.1840890	4.7×10^{-5}	2.8750497
20	*BCAS3*	0.3789707	6.4×10^{-5}	0.2904880	*PPIP5K1*	0.1840890	4.7×10^{-5}	2.8750497
21	*PRPF40B*	0.3788293	6.5×10^{-5}	0.3078750	*RALGAPB*	0.1829579	5.2×10^{-5}	0.3106026
22	*FMNL3*	0.3788293	6.5×10^{-5}	0.3078750	*PRMT9*	0.1822038	6.2×10^{-5}	0.2240557
23	*RNF121*	0.3783109	6.8×10^{-5}	0.3671037	*BCAS3*	0.1822038	6.2×10^{-5}	0.2263247
24	*VPS45*	0.3750118	7.1×10^{-5}	0.3298900	*RNF121*	0.1814497	6.8×10^{-5}	3.2951850
25	*KIAA0947*	0.3737393	7.9×10^{-5}	0.4148649	*PATL1*	0.1812612	7.1×10^{-5}	0.2188847
26	*SLC26A6*	0.3719483	8.7×10^{-5}	0.3398815	*FABP5*	0.1806956	7.7×10^{-5}	0.1984930
27	*GREB1L*	0.3655387	1.1×10^{-4}	12.1135612	*FBXO4*	0.1748515	8.7×10^{-5}	0.6082372
28	*ADK*	0.3636064	1.1×10^{-4}	9.3488372	*FBN1*	0.1744745	9.0×10^{-5}	0.5041701
29	*SNAP91*	0.3628994	1.2×10^{-4}	5.1138761	*TUT1*	0.1680649	1.1×10^{-4}	2.1210219
30	*CASC4*	0.3624281	1.2×10^{-4}	11.5340094	*TSPAN12*	0.1678763	1.2×10^{-4}	0.3075874
31	*PTPRK*	0.3613913	1.3×10^{-4}	0.3263333	*TRMT11*	0.1663682	1.3×10^{-4}	0.3629881
32	*RNU6−28P*	0.3612028	1.3×10^{-4}	1.0654490	*PRPF40B*	0.1659911	1.5×10^{-4}	0.2267868
33	*PPIP5K1*	0.3612028	1.3×10^{-4}	1.0654490	*FMNL3*	0.1659911	1.5×10^{-4}	0.2267868
34	*ADAMTS6*	0.3568668	1.5×10^{-4}	8.9631458	*MACF1*	0.1656141	1.5×10^{-4}	0.2234625
35	*ORC2*	0.3561599	1.6×10^{-4}	0.3379306	*HS2ST1*	0.1656141	1.5×10^{-4}	0.2451918
36	*MBOAT2*	0.3544632	1.7×10^{-4}	0.3583785	*PTPRK*	0.1656141	1.5×10^{-4}	0.2619477
37	*ZMYM1*	0.3529550	1.7×10^{-4}	0.3475098	*MBOAT2*	0.1650485	1.6×10^{-4}	0.3659225
38	*TBXAS1*	0.3529550	1.7×10^{-4}	2.8622010	*VPS45*	0.1620322	1.6×10^{-4}	0.3164293
39	*GPC5*	0.3513055	1.8×10^{-4}	0.3697656	*CEP350*	0.1610896	1.6×10^{-4}	0.3348170
40	*USP46*	0.3510227	1.8×10^{-4}	0.3200877	*NECAB1*	0.1605241	1.6×10^{-4}	0.8283894

Table S8: Top 40 sweep candidates for CHB, comparing G12 and H12. Candidates presented are those that remained after application of a mappability and alignability filter to data (see *Materials and Methods*). Coloration follows the scheme in Table S2.

	Top gene (H12)	Maximum H12	P−value (H12)	Bayes Factor (H12)	Top gene (G12)	Maximum G12	P−value (G12)	Bayes Factor (G12)
1	*MIR548AE2*	0.5321897	2.0×10^{-6}	4.4547386	*FMNL3*	0.2610048	5.0×10^{-6}	0.1458074
2	*SPIDR*	0.5094260	2.0×10^{-6}	0.2891520	*SPIDR*	0.2498822	6.0×10^{-6}	1.9686499
3	*LOC100507577*	0.4975964	7.0×10^{-6}	5.3878702	*RANBP10*	0.2442266	6.0×10^{-6}	1.0012687
4	*EXOC6B*	0.4911867	8.0×10^{-6}	0.2265323	*ZNF660*	0.2429070	7.0×10^{-6}	0.2672693
5	*FMNL3*	0.4910925	8.0×10^{-6}	0.2070728	*EXOC6B*	0.2348006	1.3×10^{-5}	0.2158991
6	*ZNF660*	0.4780846	1.3×10^{-5}	0.2435286	*MIR548AE2*	0.2334810	1.7×10^{-5}	3.4664213
7	*RANBP10*	0.4778019	1.5×10^{-5}	5.8416275	*ATP6V0D1*	0.2334810	1.7×10^{-5}	0.1831550
8	*PRPF40B*	0.4711094	1.9×10^{-5}	0.2285023	*PRPF40B*	0.2327269	1.9×10^{-5}	0.1688298
9	*RP11−696N14.1*	0.4655481	2.1×10^{-5}	0.2719284	*RP11−696N14.1*	0.2263173	2.5×10^{-5}	1.1556109
10	*ATP6V0D1*	0.4581487	3.3×10^{-5}	0.2473506	*LIMS1*	0.2155717	3.7×10^{-5}	0.2084669
11	*SLC9A5*	0.4459893	4.7×10^{-5}	3.7969444	*EXD2*	0.2153832	3.8×10^{-5}	0.2001885
12	*ADH1A*	0.4428787	5.4×10^{-5}	0.2795167	*ADH1A*	0.2129324	3.9×10^{-5}	0.2472917
13	*LONP2*	0.4398624	6.2×10^{-5}	5.4293395	*NETO2*	0.2055802	5.8×10^{-5}	0.1917678
14	*LIMS1*	0.4321802	9.3×10^{-5}	0.2715267	*CCDC138*	0.2053916	5.8×10^{-5}	0.1860869
15	*PTPRK*	0.4274201	9.7×10^{-5}	3.5131299	*BEND4*	0.2053916	5.8×10^{-5}	0.2372168
16	*BEND4*	0.4253464	1.2×10^{-4}	0.2792847	*LOC100507577*	0.1987935	6.7×10^{-5}	3.4238083
17	*ZBTB20*	0.4199736	1.4×10^{-4}	0.3437485	*SLC9A5*	0.1986050	6.7×10^{-5}	0.2103430
18	*LINC00535*	0.4161090	1.5×10^{-4}	5.1225440	*FBXO4*	0.1980394	7.1×10^{-5}	0.1962185
19	*SLC25A20*	0.4134697	1.7×10^{-4}	3.7670028	*FBXL19*	0.1978509	7.2×10^{-5}	0.1926042
20	*RUNX1T1*	0.4133283	1.7×10^{-4}	0.3245736	*FHOD1*	0.1978509	7.2×10^{-5}	0.2078746
21	*CCDC138*	0.4130455	1.7×10^{-4}	0.2801925	*MON1A*	0.1910642	8.5×10^{-5}	0.2424354
22	*RANBP2*	0.4106419	1.8×10^{-4}	1.5181123	*SLC25A20*	0.1888020	1.1×10^{-4}	1.1637530
23	*FBXO4*	0.4091809	1.8×10^{-4}	0.2954225	*RANBP2*	0.1857857	1.1×10^{-4}	4.6608315
24	*FHOD1*	0.4091338	1.8×10^{-4}	0.2968677	*SLC4A7*	0.1837119	1.1×10^{-4}	0.2328856
25	*EXD2*	0.4072957	2.1×10^{-4}	0.2941817	*BCL7C*	0.1818268	1.3×10^{-4}	0.2469314
26	*AMBRA1*	0.4032897	2.2×10^{-4}	0.3078374	*DCAF4L1*	0.1814497	1.3×10^{-4}	0.2449140
27	*PGAP1*	0.4029126	2.2×10^{-4}	0.3191557	*ESRP2*	0.1814497	1.3×10^{-4}	0.2099606
28	*SPATA31D3*	0.4028655	2.2×10^{-4}	0.3190796	*BCL2L1*	0.1812612	1.4×10^{-4}	0.2598905
29	*FAF1*	0.4026298	2.3×10^{-4}	0.3184828	*PHF20*	0.1812612	1.4×10^{-4}	0.2225617
30	*MON1A*	0.4025827	2.3×10^{-4}	0.3104087	*ZBTB20*	0.1810727	1.4×10^{-4}	1.2589909
31	*STX4*	0.4019700	2.4×10^{-4}	0.2945809	*SPATA31D3*	0.1765482	1.5×10^{-4}	0.2586918
32	*SYNJ1*	0.4019229	2.4×10^{-4}	7.0123907	*PGAP1*	0.1761712	1.5×10^{-4}	0.3481103
33	*PRKAR2A*	0.4014045	2.5×10^{-4}	0.3255329	*ABCC11*	0.1756056	1.5×10^{-4}	0.2412494
34	*UHRF1BP1L*	0.4012631	2.5×10^{-4}	8.0027033	*HS2ST1*	0.1750401	1.6×10^{-4}	0.3925843
35	*PHF20*	0.4011688	2.5×10^{-4}	0.3044839	*LRRC29*	0.1740975	1.8×10^{-4}	0.2338983
36	*BCL7C*	0.4011217	2.5×10^{-4}	0.3067340	*LONP2*	0.1739089	1.9×10^{-4}	0.2183530
37	*ABCC11*	0.3966915	2.7×10^{-4}	0.3112945	*HOOK1*	0.1733434	1.9×10^{-4}	0.7246261
38	*NETO2*	0.3950419	3.0×10^{-4}	0.3358649	*FAF1*	0.1695730	2.0×10^{-4}	0.3947007
39	*FBXL19*	0.3948534	3.0×10^{-4}	0.2974847	*PTPRK*	0.1688189	2.1×10^{-4}	3.3992039
40	*BCL2L1*	0.3903290	3.3×10^{-4}	0.3315043	*AMBRA1*	0.1688189	2.1×10^{-4}	0.2920880

Table S9: Top 40 sweep candidates for CHB, comparing H12 and G123. Coloration and analyzed data are as in Table S8.

	Top gene (H12)	Maximum H12	P−value (H12)	Bayes Factor (H12)	Top gene (G123)	Maximum G123	P−value (G123)	Bayes Factor (G123)
1	*MIR548AE2*	0.5321897	2.0×10^{-6}	4.4547386	*MIR548AE2*	0.3330191	$< 1.0 \times 10^{-6}$	3.7777426
2	*SPIDR*	0.5094260	2.0×10^{-6}	0.2891520	*SPIDR*	0.3158639	1.0×10^{-6}	2.2592666
3	*LOC100507577*	0.4975964	7.0×10^{-6}	5.3878702	*RANBP10*	0.2913564	5.0×10^{-6}	1.0676830
4	*EXOC6B*	0.4911867	8.0×10^{-6}	0.2265323	*FMNL3*	0.2904138	5.0×10^{-6}	0.1453509
5	*FMNL3*	0.4910925	8.0×10^{-6}	0.2070728	*ZNF660*	0.2900368	5.0×10^{-6}	0.2892879
6	*ZNF660*	0.4780846	1.3×10^{-5}	0.2435286	*LOC100507577*	0.2900368	5.0×10^{-6}	4.1273204
7	*RANBP10*	0.4778019	1.5×10^{-5}	5.8416275	*RP11−696N14.1*	0.2817419	6.0×10^{-6}	0.1993062
8	*PRPF40B*	0.4711094	1.9×10^{-5}	0.2285023	*EXOC6B*	0.2809878	1.0×10^{-5}	0.2025320
9	*RP11−696N14.1*	0.4655481	2.1×10^{-5}	0.2719284	*ADH1A*	0.2736356	1.4×10^{-5}	0.2398620
10	*ATP6V0D1*	0.4581487	3.3×10^{-5}	0.2473506	*ATP6V0D1*	0.2611933	2.5×10^{-5}	0.1815591
11	*SLC9A5*	0.4459893	4.7×10^{-5}	3.7969444	*PRPF40B*	0.2604392	3.2×10^{-5}	0.1650375
12	*ADH1A*	0.4428787	5.4×10^{-5}	0.2795167	*LIMS1*	0.2598737	3.2×10^{-5}	0.1944867
13	*LONP2*	0.4398624	6.2×10^{-5}	5.4293395	*EXD2*	0.2508248	4.0×10^{-5}	0.1918154
14	*LIMS1*	0.4321802	9.3×10^{-5}	0.2715267	*RANBP2*	0.2425299	4.6×10^{-5}	5.7853860
15	*PTPRK*	0.4274201	9.7×10^{-5}	3.5131299	*SLC9A5*	0.2410218	5.5×10^{-5}	0.1979254
16	*BEND4*	0.4253464	1.2×10^{-4}	0.2792847	*CCDC138*	0.2334810	6.1×10^{-5}	5.4284787
17	*ZBTB20*	0.4199736	1.4×10^{-4}	0.3437485	*FHOD1*	0.2317843	8.3×10^{-5}	0.2006812
18	*LINC00535*	0.4161090	1.5×10^{-4}	5.1225440	*LONP2*	0.2257517	8.4×10^{-5}	4.6142815
19	*SLC25A20*	0.4134697	1.7×10^{-4}	3.7670028	*SLC4A7*	0.2242436	9.2×10^{-5}	0.2219778
20	*RUNX1T1*	0.4133283	1.7×10^{-4}	0.3245736	*MON1A*	0.2242436	9.2×10^{-5}	0.2351749
21	*CCDC138*	0.4130455	1.7×10^{-4}	0.2801925	*FBXO4*	0.2234895	1.0×10^{-4}	0.1957779
22	*RANBP2*	0.4106419	1.8×10^{-4}	1.5181123	*FBXL19*	0.2233010	1.0×10^{-4}	0.1912010
23	*FBXO4*	0.4091809	1.8×10^{-4}	0.2954225	*ABCC11*	0.2231125	1.0×10^{-4}	0.2252419
24	*FHOD1*	0.4091338	1.8×10^{-4}	0.2968677	*NETO2*	0.2229239	1.0×10^{-4}	0.1954909
25	*EXD2*	0.4072957	2.1×10^{-4}	0.2941817	*BEND4*	0.2227354	1.0×10^{-4}	0.2405979
26	*AMBRA1*	0.4032897	2.2×10^{-4}	0.3078374	*PTPRK*	0.2151946	1.2×10^{-4}	3.9762170
27	*PGAP1*	0.4029126	2.2×10^{-4}	0.3191557	*BCL7C*	0.2142521	1.4×10^{-4}	0.2396246
28	*SPATA31D3*	0.4028655	2.2×10^{-4}	0.3190796	*DCAF4L1*	0.2138750	1.5×10^{-4}	0.2379868
29	*FAF1*	0.4026298	2.3×10^{-4}	0.3184828	*PHF20*	0.2136865	1.5×10^{-4}	0.2156139
30	*MON1A*	0.4025827	2.3×10^{-4}	0.3104087	*ADH6*	0.2085965	1.5×10^{-4}	8.4319644
31	*STX4*	0.4019700	2.4×10^{-4}	0.2945809	*FAF1*	0.2082194	1.5×10^{-4}	0.4183259
32	*SYNJ1*	0.4019229	2.4×10^{-4}	7.0123907	*SPATA31D3*	0.2082194	1.5×10^{-4}	0.2508514
33	*PRKAR2A*	0.4014045	2.5×10^{-4}	0.3255329	*PGAP1*	0.2078424	1.5×10^{-4}	0.3566613
34	*UHRF1BP1L*	0.4012631	2.5×10^{-4}	8.0027033	*AMBRA1*	0.2074654	1.5×10^{-4}	0.2814520
35	*PHF20*	0.4011688	2.5×10^{-4}	0.3044839	*LINC00535*	0.2070883	1.6×10^{-4}	3.0714645
36	*BCL7C*	0.4011217	2.5×10^{-4}	0.3067340	*C2CD5*	0.2070883	1.6×10^{-4}	0.3194495
37	*ABCC11*	0.3966915	2.7×10^{-4}	0.3112945	*HS2ST1*	0.2067113	1.6×10^{-4}	0.4074141
38	*NETO2*	0.3950419	3.0×10^{-4}	0.3358649	*ESRP2*	0.2057687	1.9×10^{-4}	0.2077222
39	*FBXL19*	0.3948534	3.0×10^{-4}	0.2974847	*BCL2L1*	0.2055802	1.9×10^{-4}	0.2565834
40	*BCL2L1*	0.3903290	3.3×10^{-4}	0.3315043	*SLC25A20*	0.2053916	1.9×10^{-4}	1.0383075

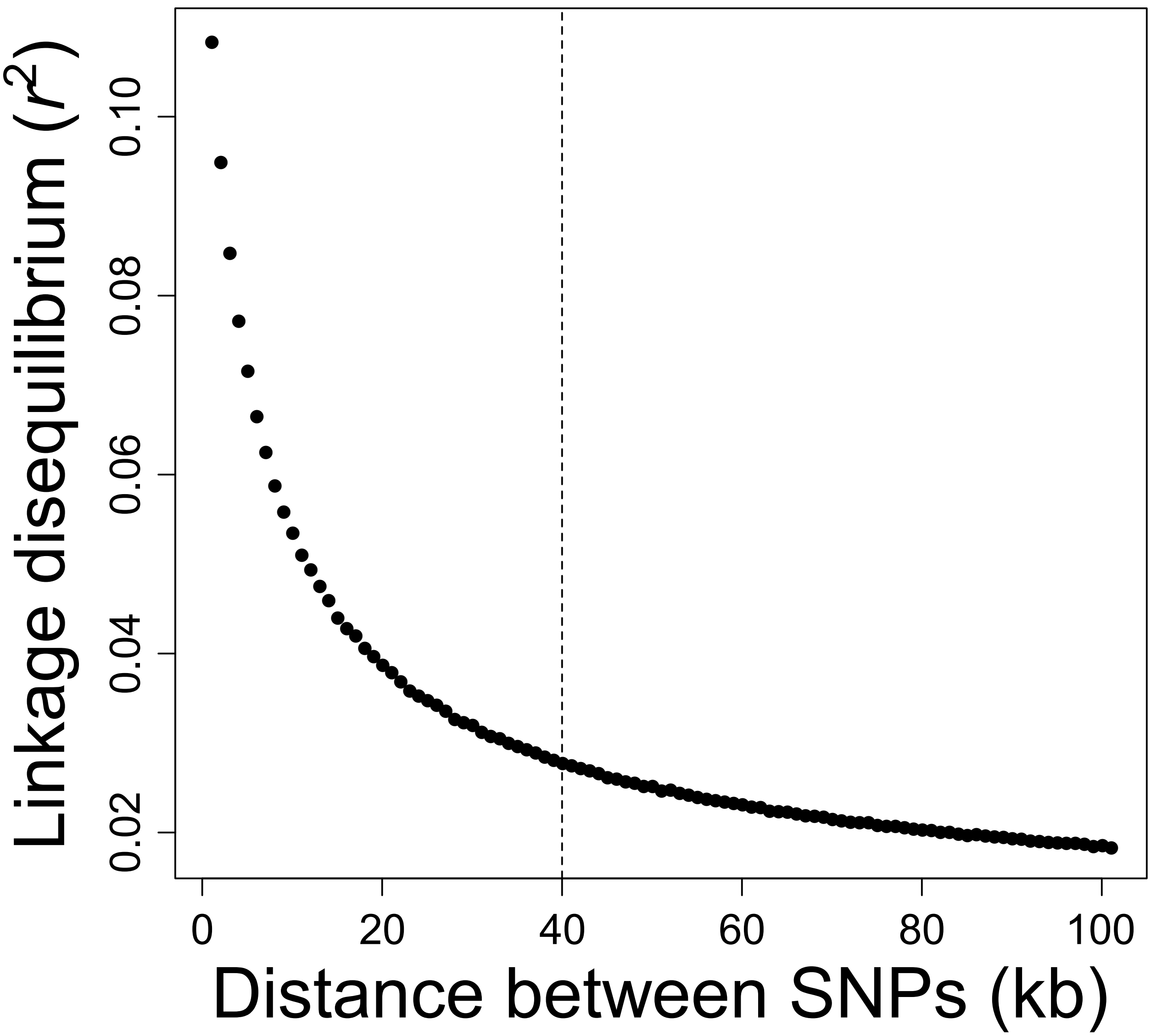


Figure S1: Mean decay of the r^2 measured of linkage disequilibrium between pairs of loci in simulated 500 kb chromsomes across 10^3 replicates. Dashed vertical line indicates window size used in selection scans.

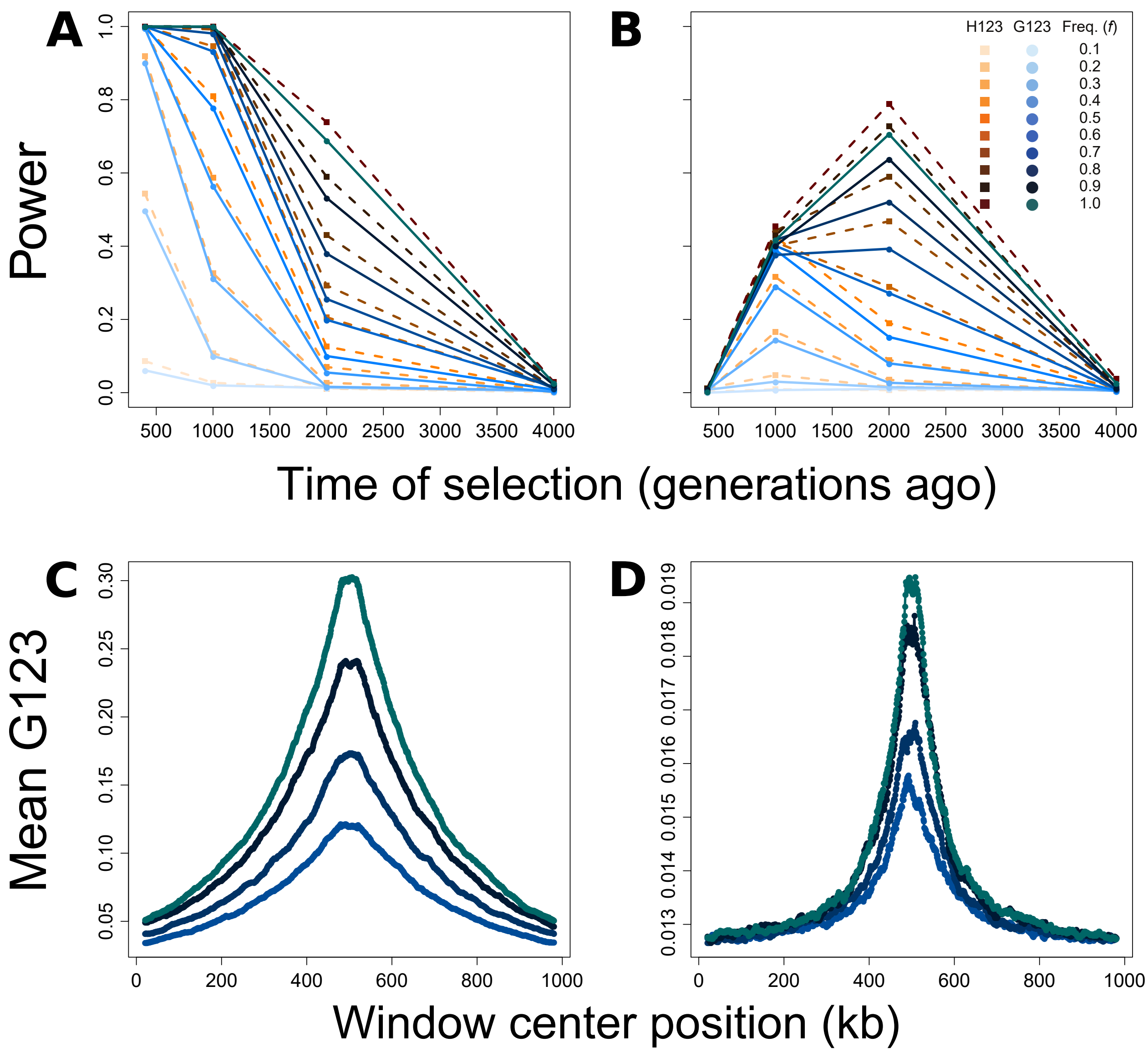


Figure S2: Signal of hard sweeps from simulated 100 kb chromosome generated for selection across identical time points and sweep frequencies (f, frequency to which the selected allele rises before becoming selectively neutral) as in Figure 3. (A) Powers of H123 (orange) and G123 (blue) to detect strong sweeps ($s = 0.1$). (B) Powers of H123 (orange) and G123 (blue) to detect moderate sweeps ($s = 0.01$). (C) Spatial G123 signal for strong sweeps occurring 400 generations prior to sampling. (D) Spatial G123 signal 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 (A) and (B).

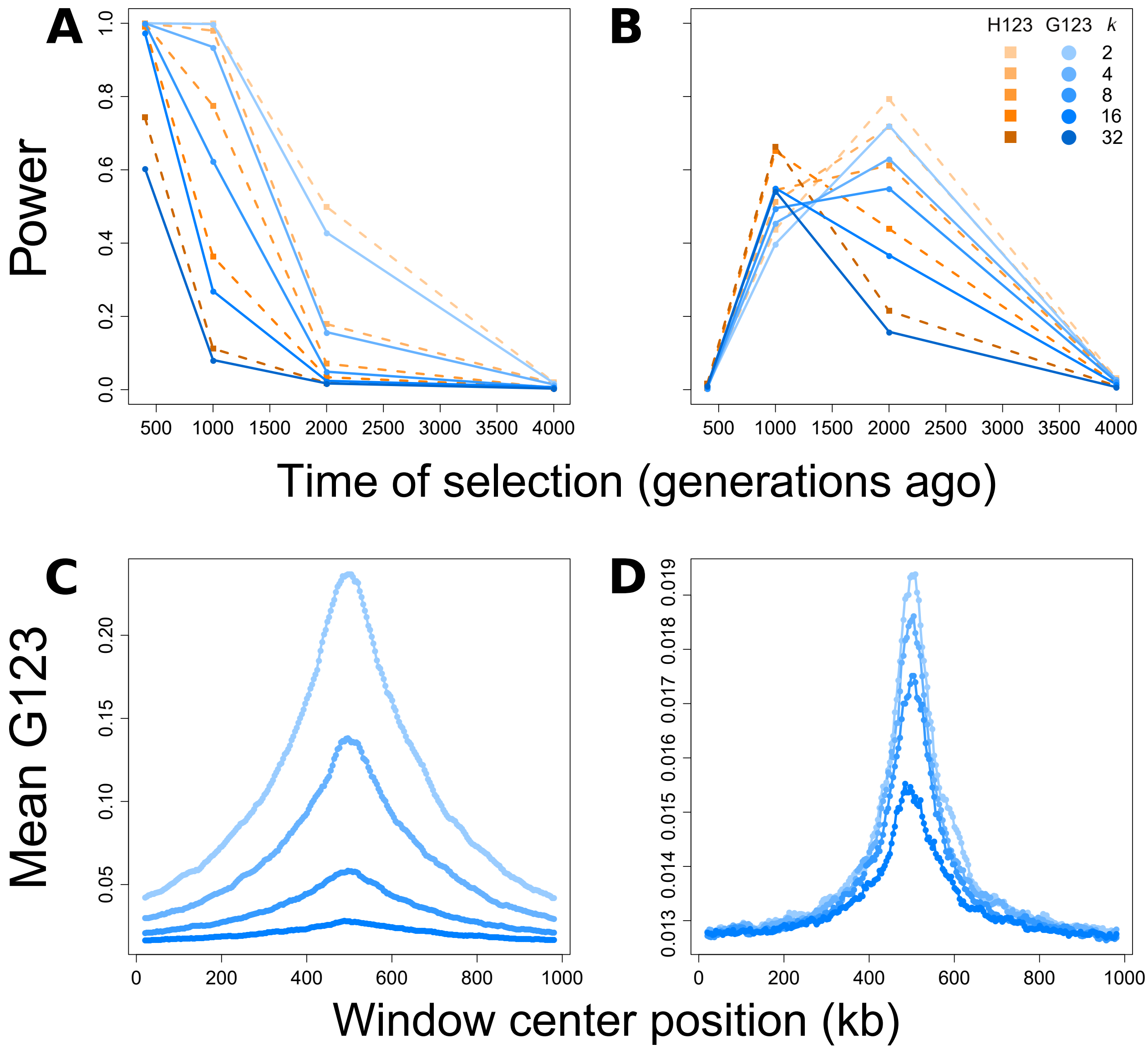


Figure S3: Signal of soft sweeps from selection on standing variation (SSV) from simulated 100 kb chromosome generated for selection across identical time points and initially selected haplotypes (k, number of haplotypes on which the selected allele arises at time of selection) as in Figure 4. (A) Powers of H123 (orange) and G123 (blue) to detect strong sweeps ($s = 0.1$). (B) Powers of H123 (orange) and G123 (blue) to detect moderate sweeps ($s = 0.01$). (C) Spatial G123 signal for strong sweeps occurring 400 generations prior to sampling. (D) Spatial G123 signal 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 (A) and (B).

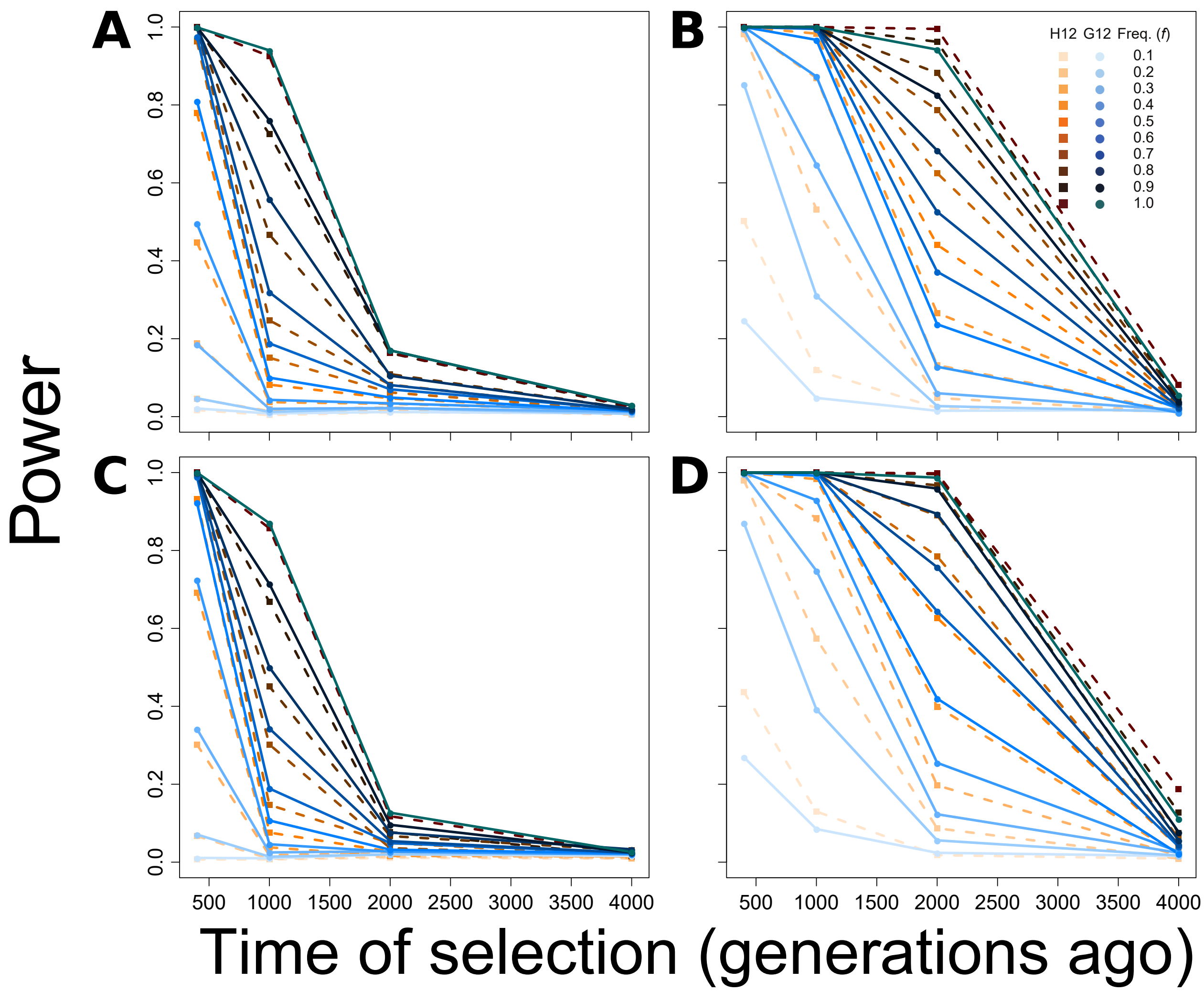


Figure S4: Powers of H12 (orange) and G12 (blue) to detect strong hard sweeps across the same time points and parameters as described previously (Figure 3), under population bottleneck and population expansion demographic histories (Figures 2B and C). (A) Powers of H12 and G12 in the presence of a population 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.

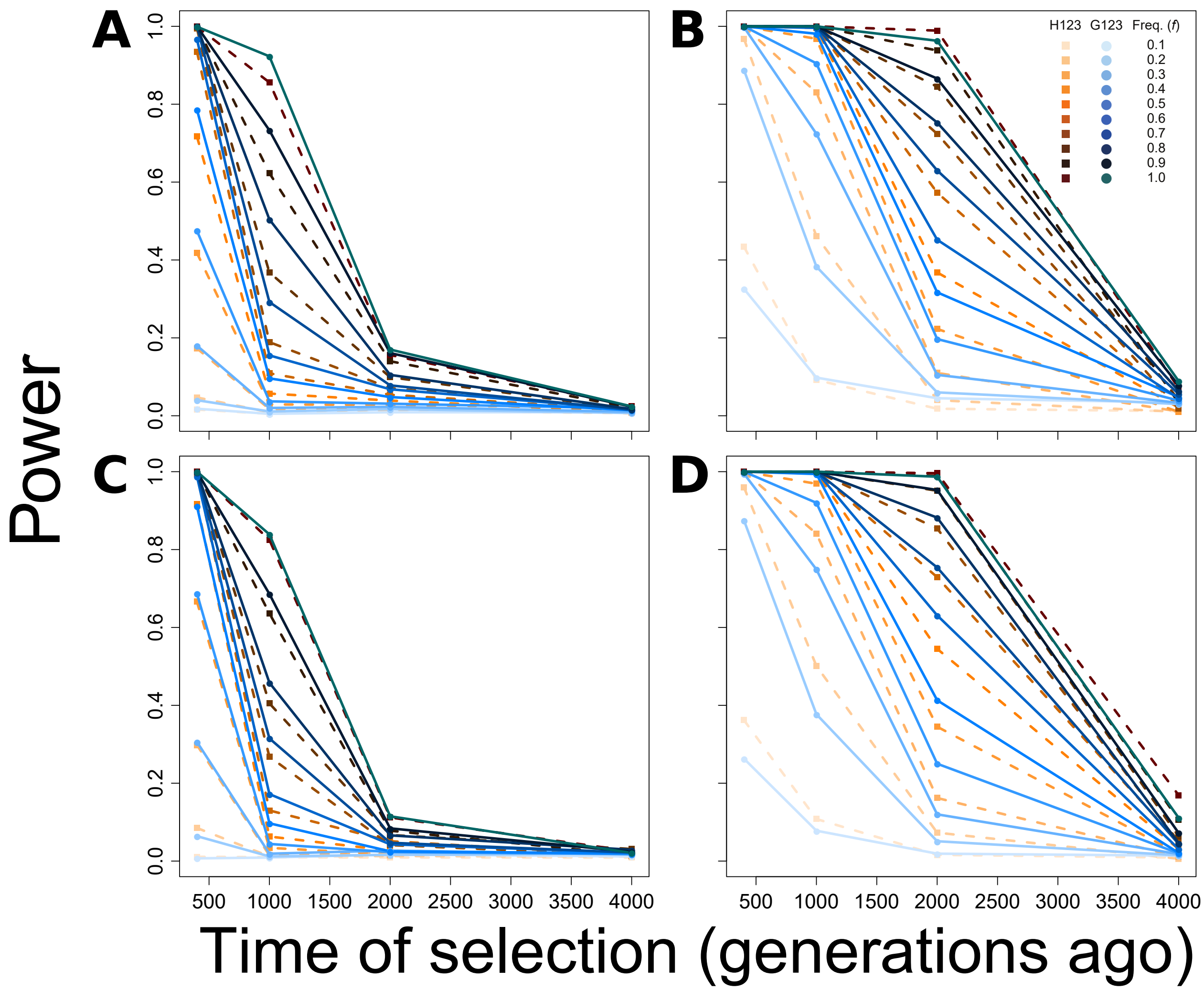


Figure S5: Powers of H123 (orange) and G123 (blue) to detect strong hard sweeps across the same time points and parameters as described previously (Figure 3), under population bottleneck and population expansion demographic histories (Figures 2B and C). Data and panels are as in Figure S4, but using G123 and H123 to analyze data.

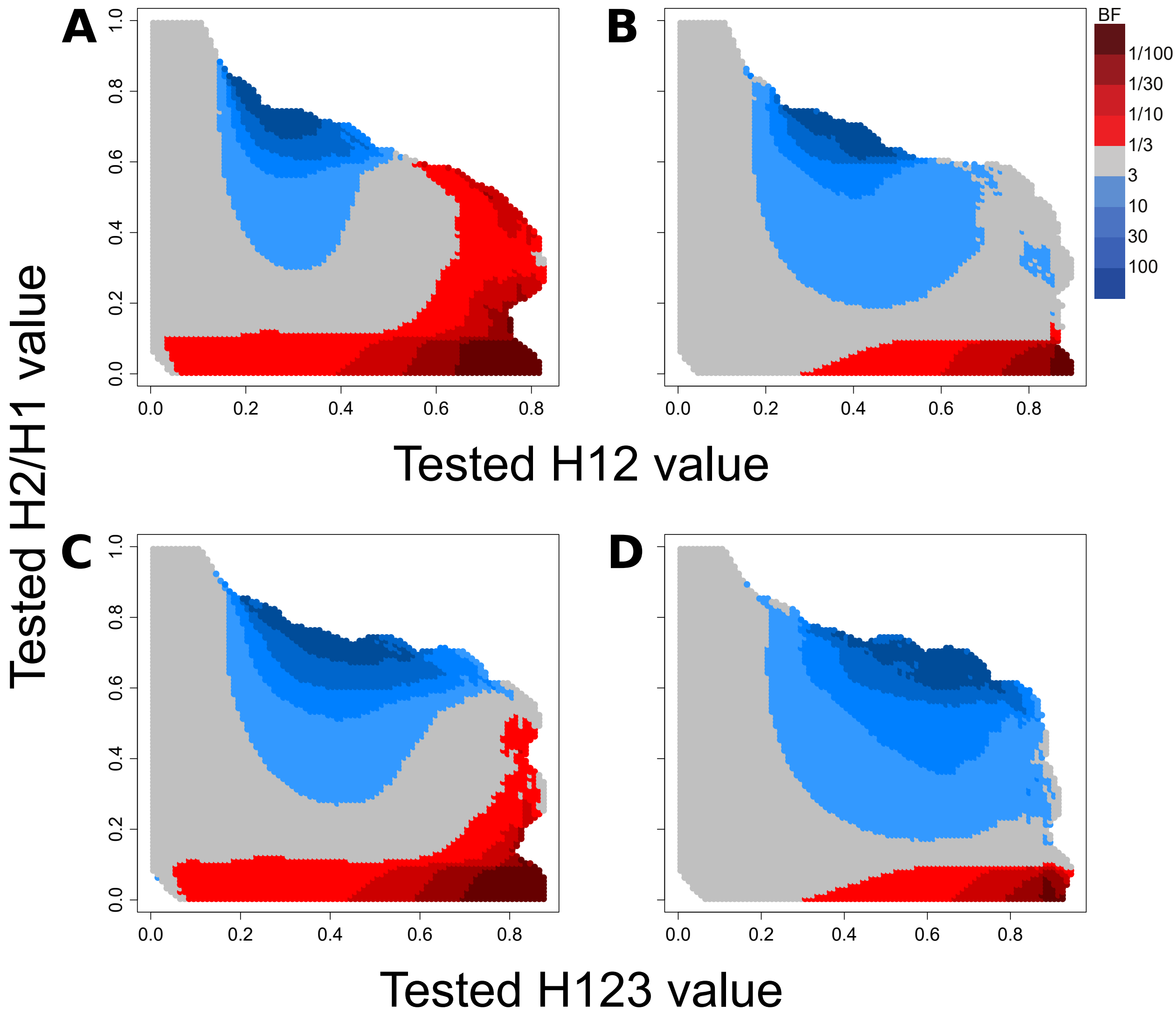
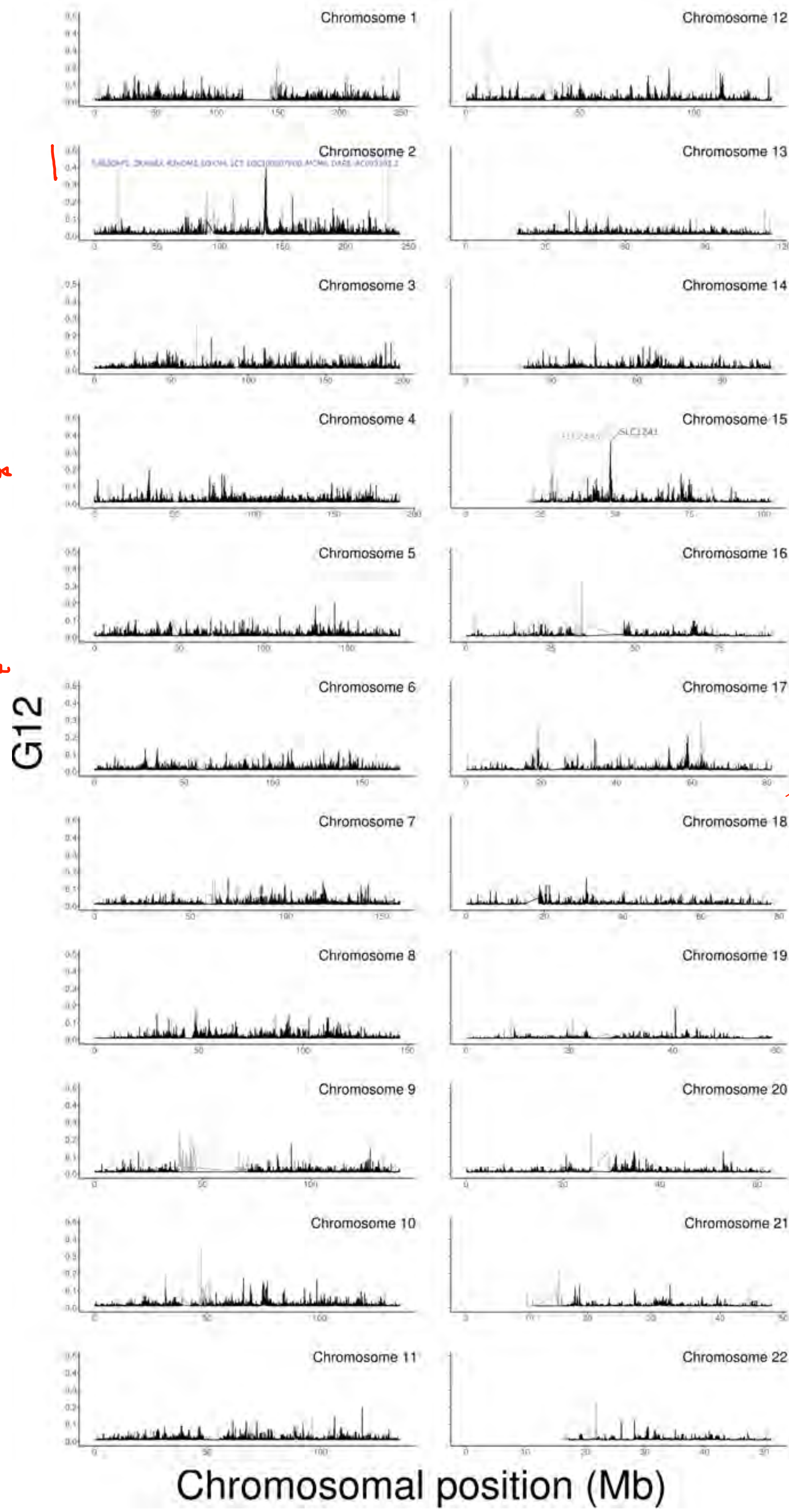


Figure S6: Ability of H12 or H123 with H2/H1 to distinguish between hard and soft sweeps, as measured by Bayes factors (BFs). Plots represent the relative probability of obtaining a paired (H12, H2/H1) or (H123, H2/H1) value within a Euclidean distance of 0.1 from a test point for a particular selection type, determined as described in the *Materials and Methods*. Selection coefficients (s) and times of selection (t) were drawn as described in the *Materials and Methods*. Red-shaded regions represent a higher likelihood for hard sweeps, while blue-shaded regions represent a higher likelihood for soft sweeps. (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).

- It is not clear if all genes refer to the peak around ~136 Mb, unless one also considers Fig. 7.

- What's the difference between the black a. grey lines ?



It is a detail, but gaps of missing information should not be spanned by a line (unless these are in fact the true G values).

Figure S7: Manhattan plots of G12 for the CEU population. The top 10 G12 candidate genes are labeled following their designations in Table S2.

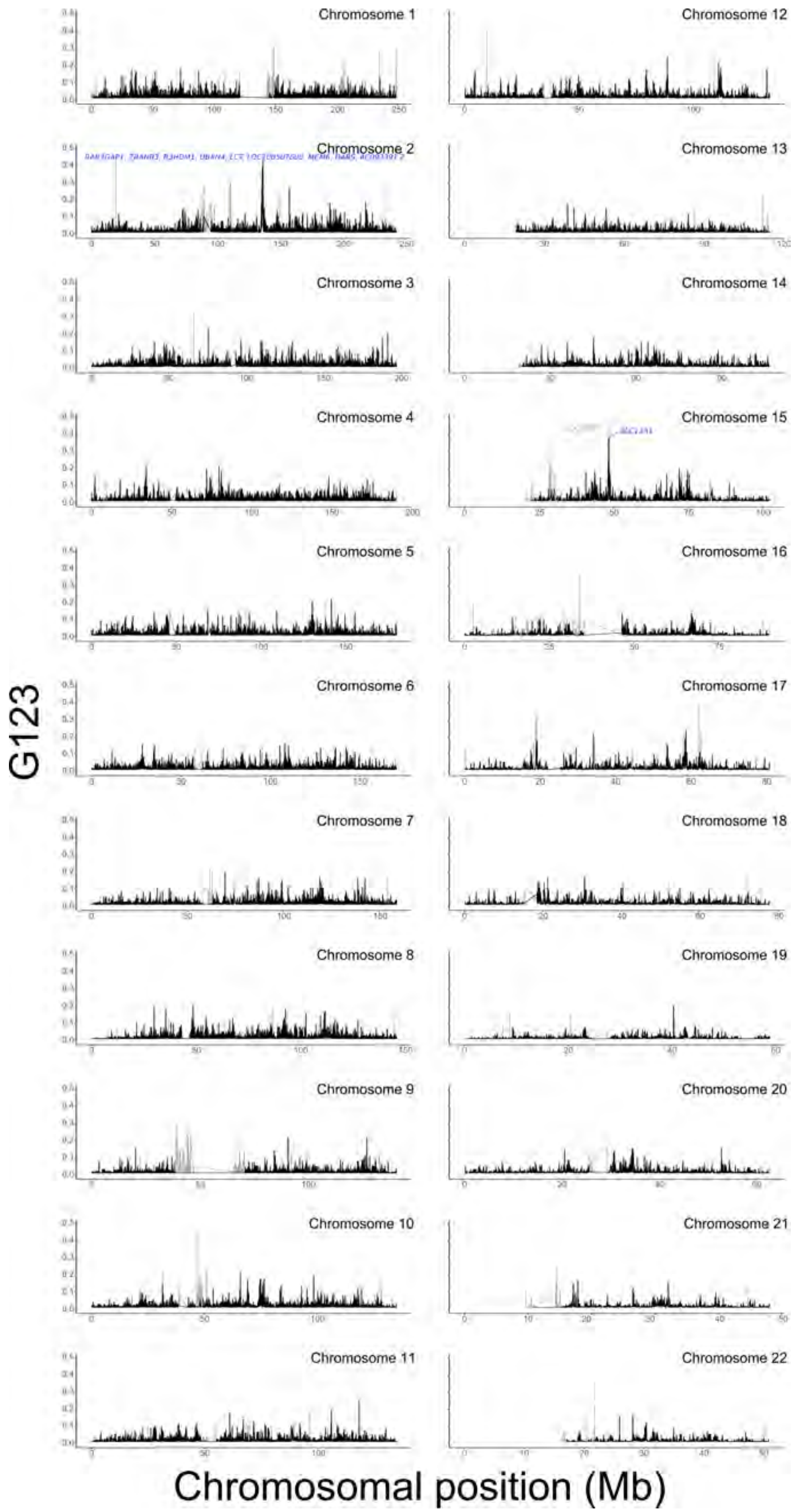


Figure S8: Manhattan plots of G123 for the CEU population. The top 10 G123 candidate genes are labeled following their designations in Table S3.

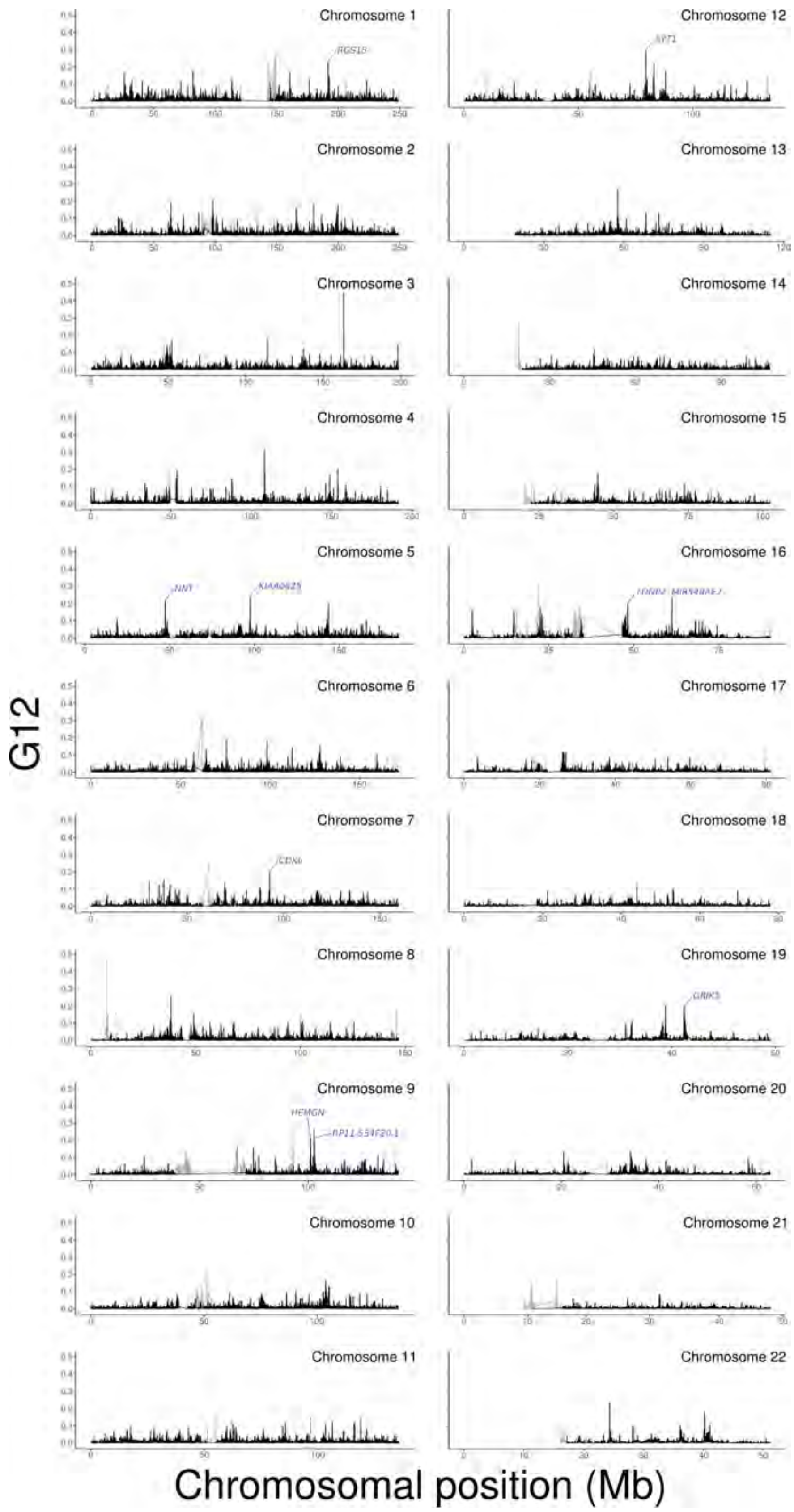


Figure S9: Manhattan plots of G12 for the YRI population. The top 10 G12 candidate genes are labeled following their designations in Table S4.

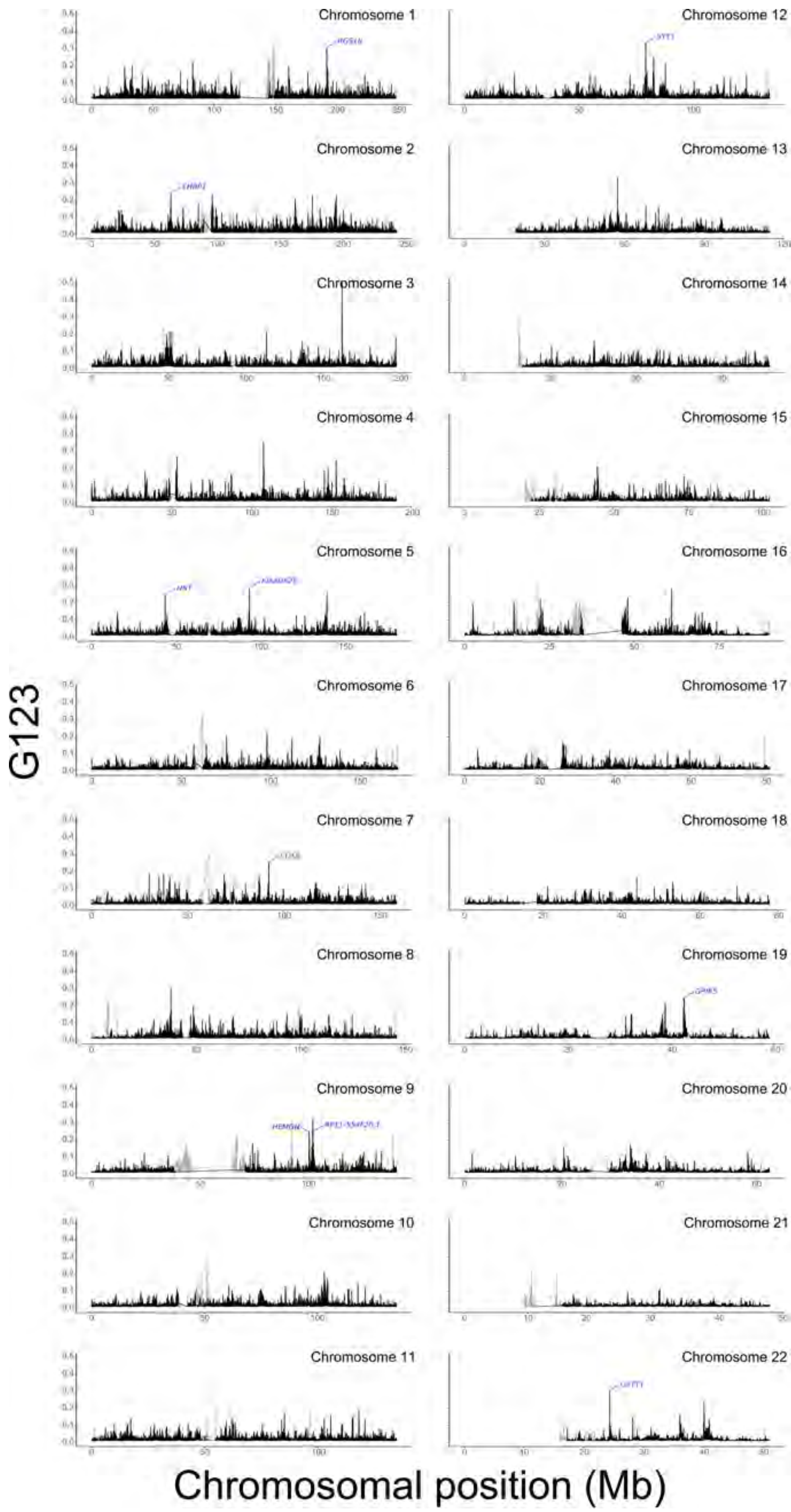


Figure S10: Manhattan plots of G123 for the YRI population. The top 10 G123 candidate genes are labeled following their designations in Table S5.

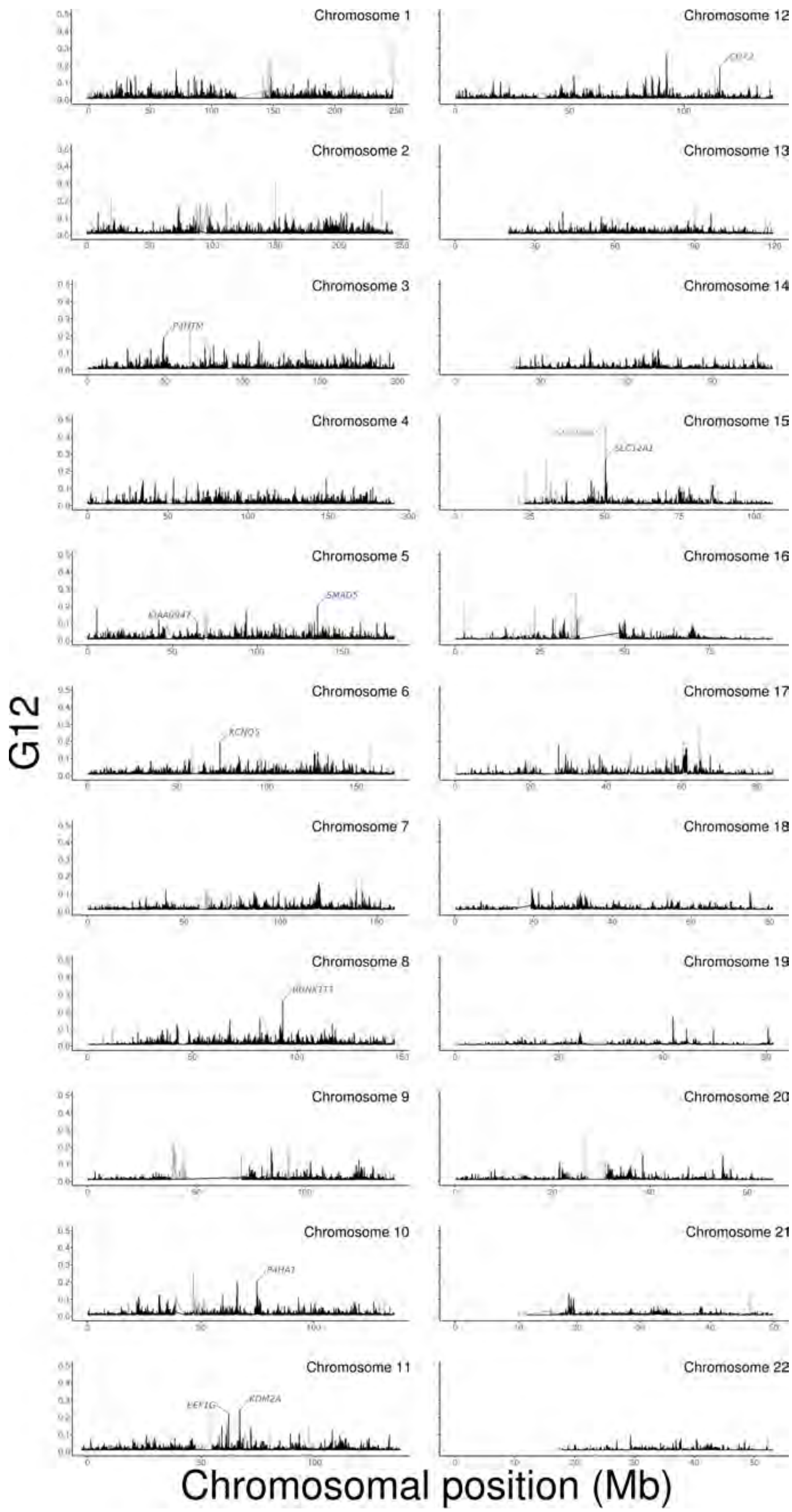


Figure S11: Manhattan plots of G12 for the GIH population. The top 10 G12 candidate genes are labeled following their designations in Table S6.

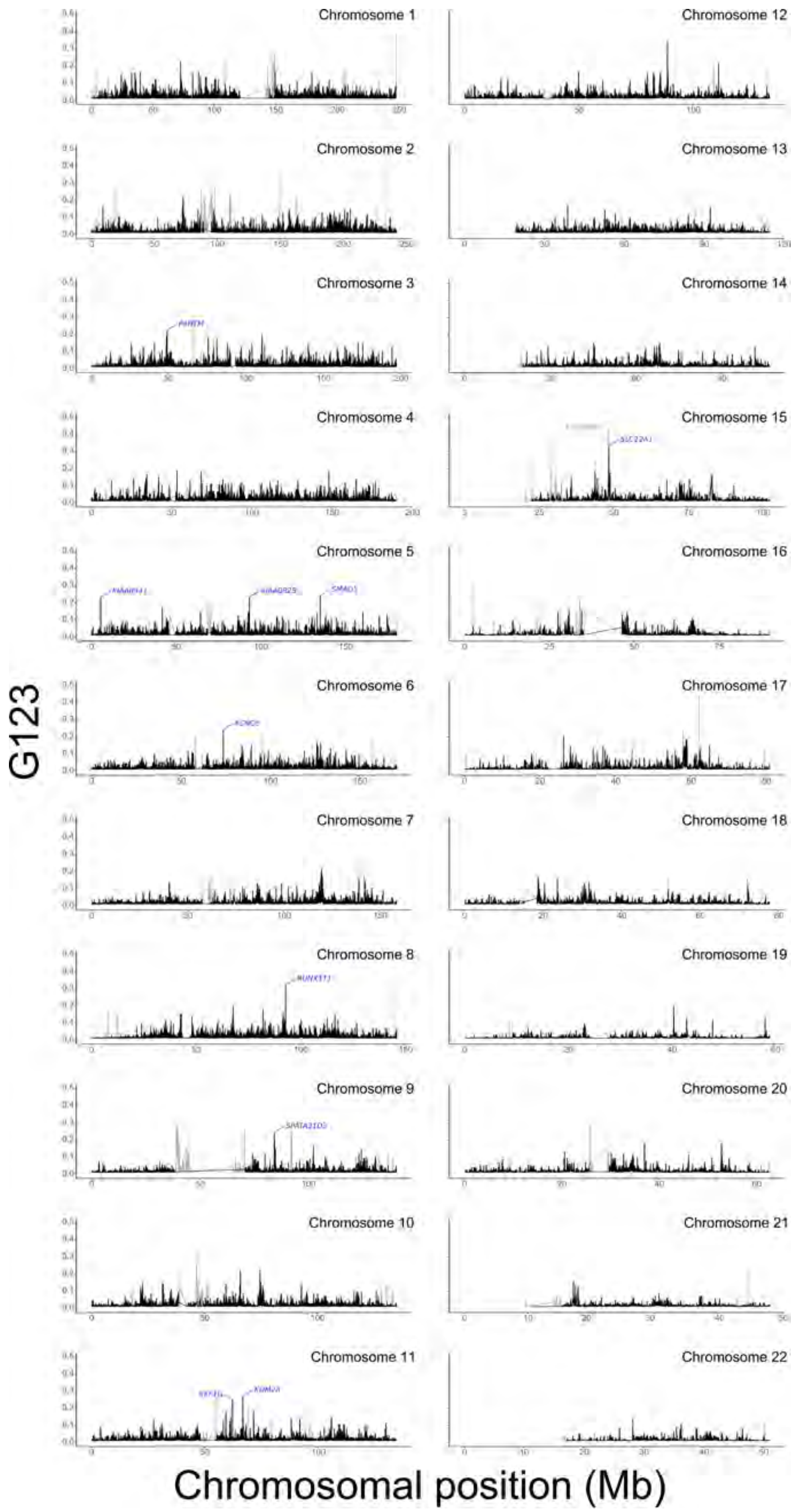


Figure S12: Manhattan plots of G123 for the GIH population. The top 10 G123 candidate genes are labeled following their designations in Table S7.

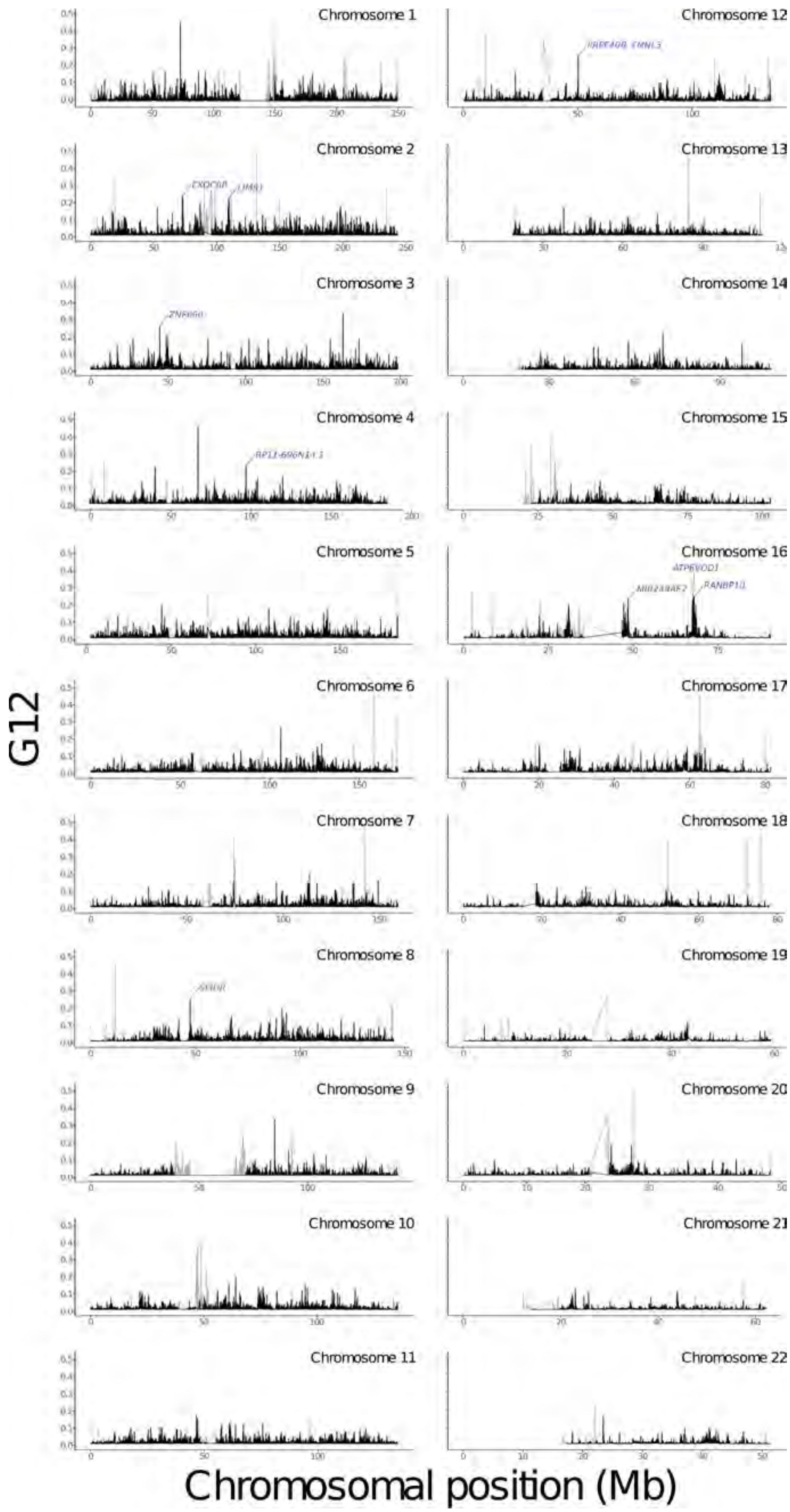


Figure S13: Manhattan plots of G12 for the CHB population. The top 10 G12 candidate genes are labeled following their designations in Table S8.

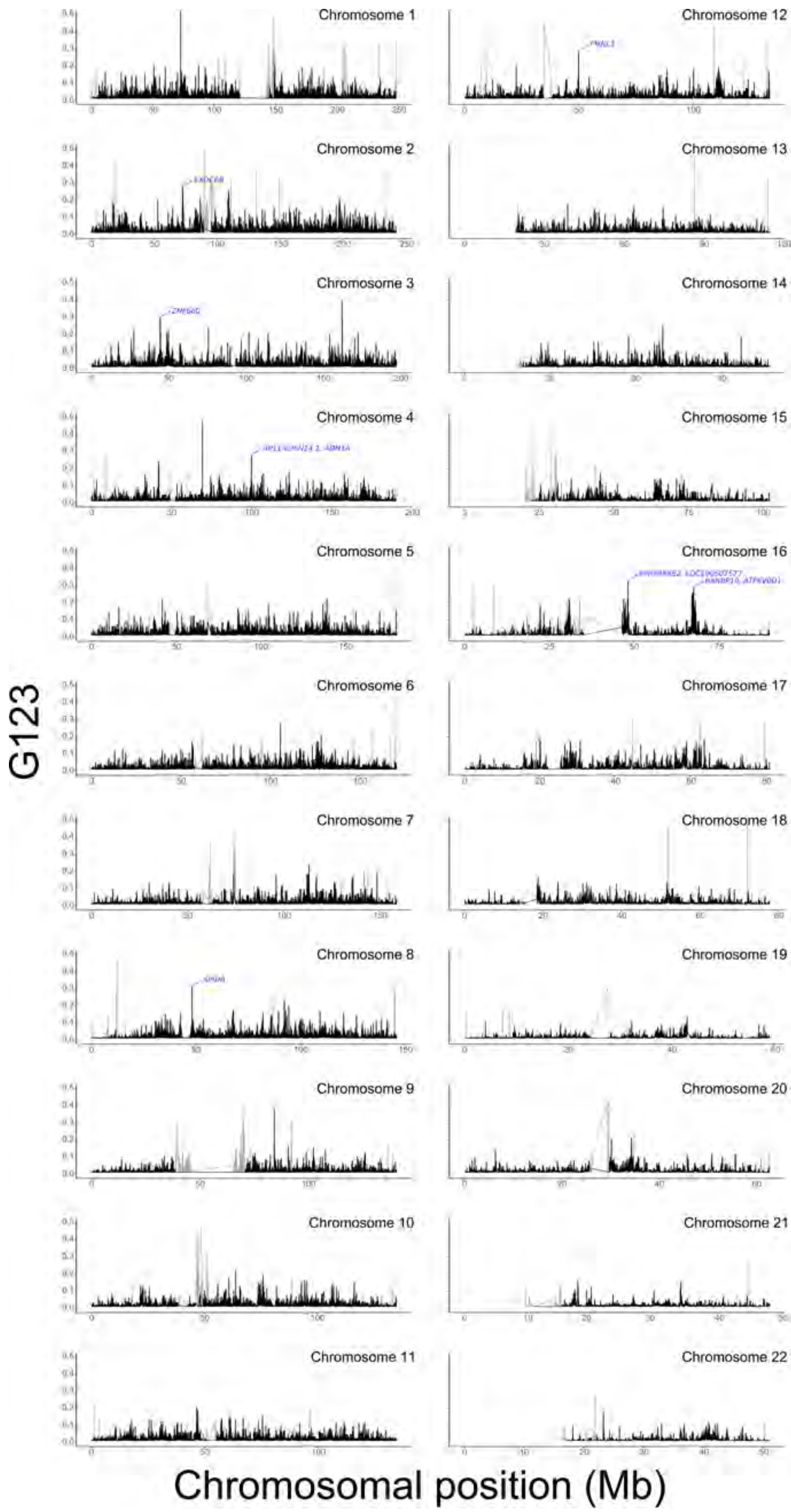


Figure S14: Manhattan plots of G123 for the CHB population. The top 10 G123 candidate genes are labeled following their designations in Table S9.

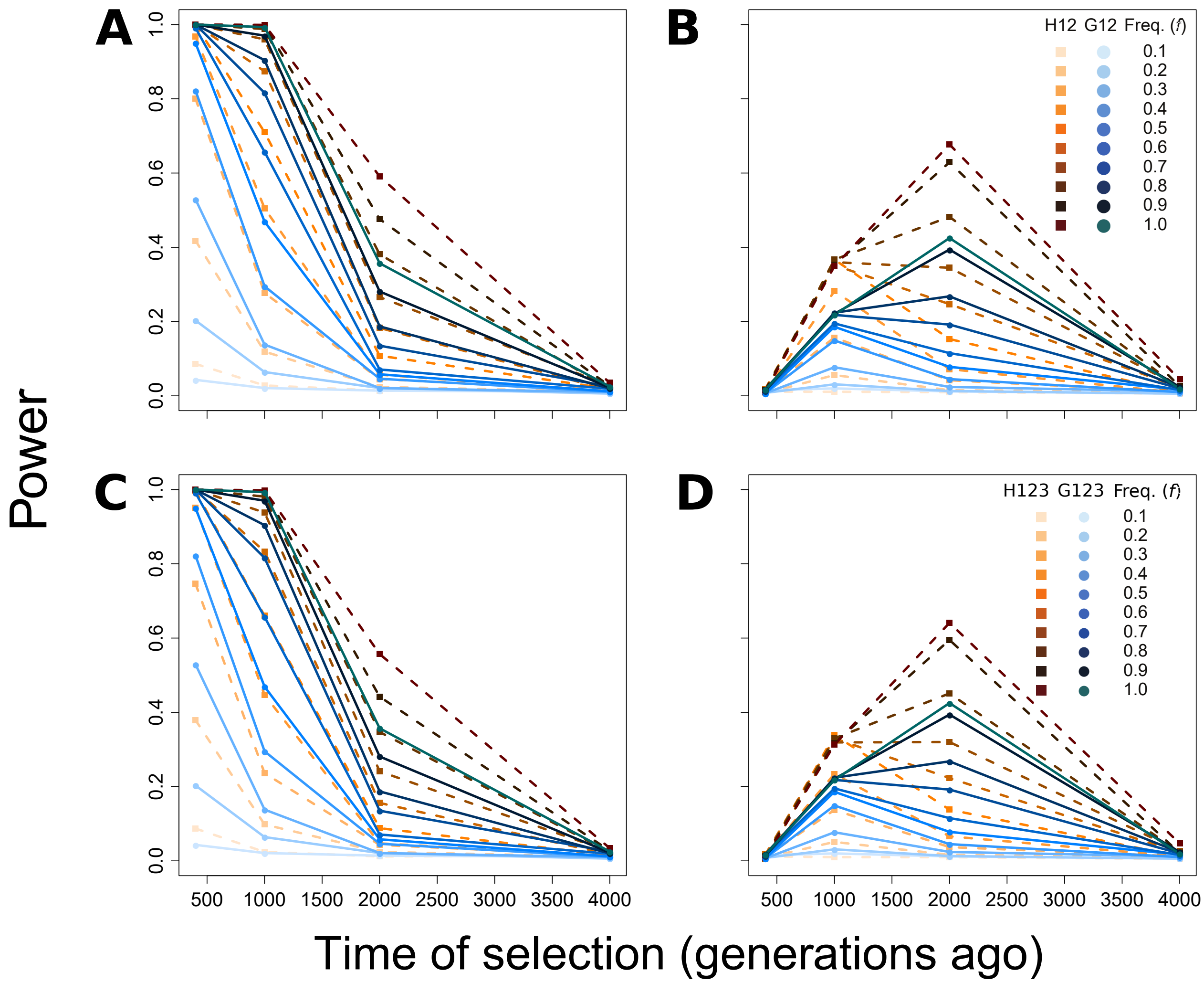


Figure S15: G12, G123, H12, and H123 maintain comparable power to detect sweeps for smaller sample sizes. For the same times of selection, values of s, and values of f as in Figure 3, we reduced the sample size for hard sweep scenarios to $n = 25$ individuals. Powers of H12 (orange) and G12 (blue) to detect strong (A) and moderate (B) hard sweeps. Powers of H123 (orange) and G123 (blue) to detect strong (C) and moderate (D) hard sweeps.

Probably worth mentioning that there are combinations of h and f such that there is no power to distinguish.

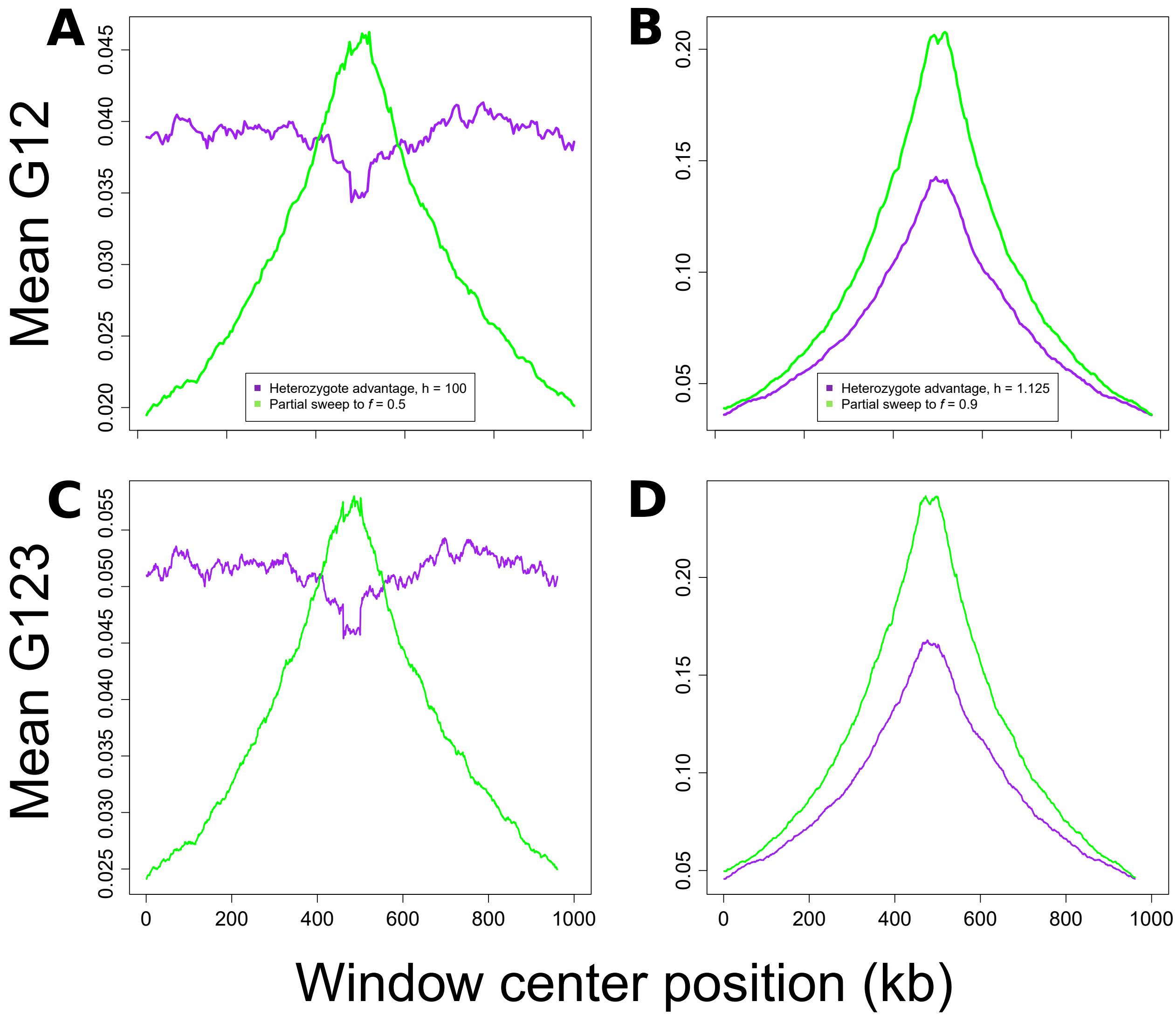


Figure S16: Recent balancing selection modeled as heterozygote advantage produces an elevated expected homozygosity signal that may spuriously resemble recent sweeps for smaller values of dominance coefficient h. (A) Spatial mean G12 signal of recent heterozygote advantage for $h = 100$ (equilibrium frequency of selected allele approximately 0.5) compared with signal of recent partial hard sweep to $f = 0.5$ for strong selection ($s = 0.1$) occurring 400 generations prior to sampling across a 1 Mb simulated region. (B) Spatial mean G12 signal of recent heterozygote advantage for $h = 1.125$ (equilibrium frequency of selected allele 0.9) compared with signal of recent partial hard sweep to $f = 0.9$ for strong selection ($s = 0.1$) occurring 400 generations prior to sampling across 1 Mb simulated region. (C) and (D) represent the same parameters as in (A) and (B), respectively, but with G123 displayed on the vertical axes.

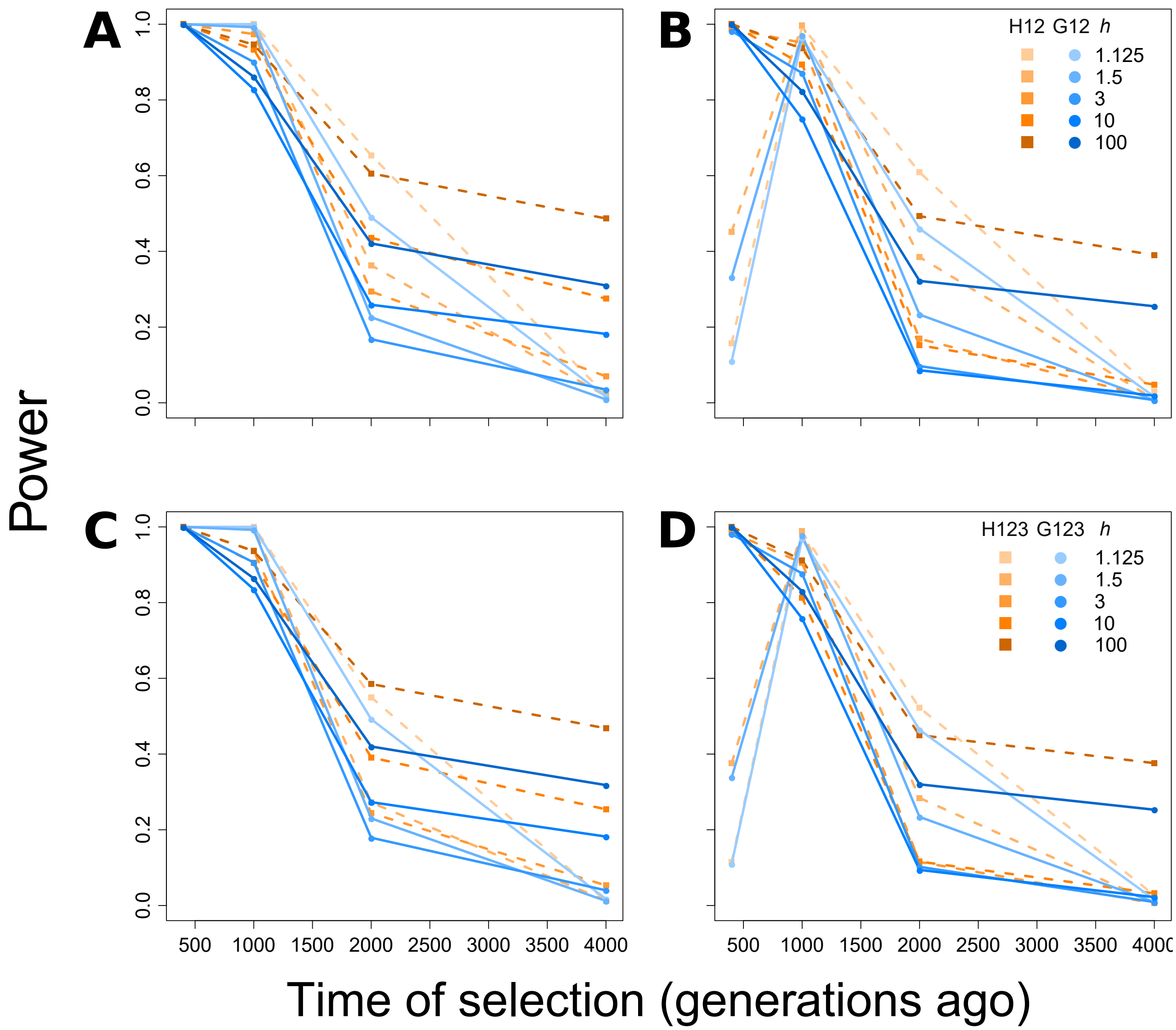


Figure S17: Powers of H12 and H123 (orange), and G12 and G123 (blue) to detect recent balancing selection modeled as heterozygote advantage from simulated 100 kb chromosomes generated for selection across identical time points as Figure 3 and values of dominance coefficient $h = 1.125$, 1.5, 3, 10, and 100, producing equilibrium frequencies for the selected allele of 0.9, 0.75, 0.6, 0.526, and 0.503, respectively. Selection simulations conditioned on the selected allele not being lost. Powers of H12 and G12 to detect strong (A) and moderate (B) balancing selection spuriously as a sweep. Powers of H123 and G123 to detect strong (C) and moderate (D) balancing selection spuriously as a sweep.

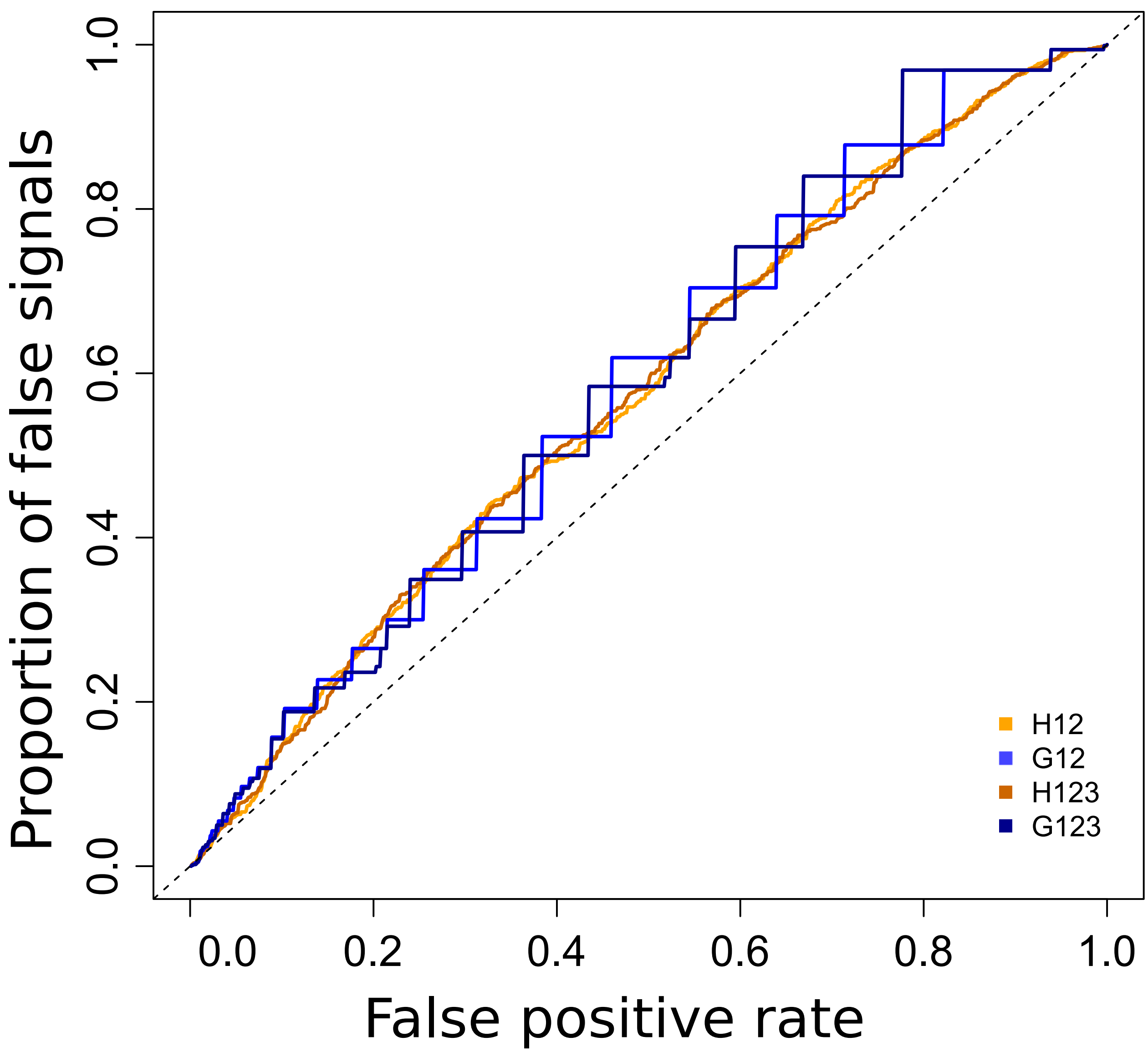


Figure S18: Proportion of false signals generated by background selection as a function of false positive rate based on neutrality for each expected homozygosity method.

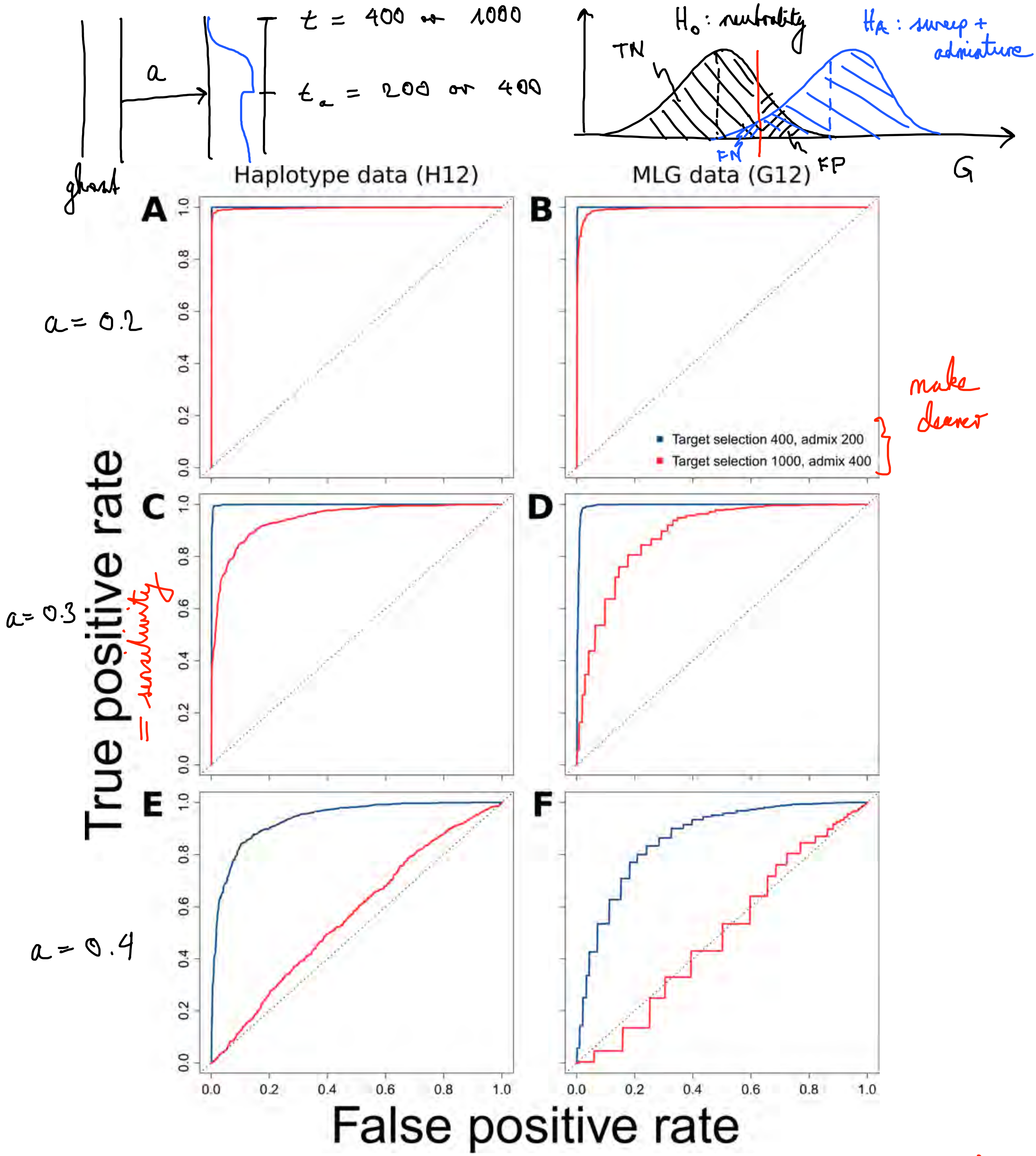


Figure S19: Effect of admixture on abilities of H12 (left panels) and G12 (right panels) to detect sweeps. Admixture occurs as a single pulse after a strong ($s = 0.1$) hard sweep has completed in the target population. Powers of H12 (A) and G12 (B) to detect sweeps in the sampled target population following 20% admixture from the donor. Powers of H12 (C) and G12 (D) to detect sweeps in the sample following 30% admixture from the donor. Powers of H12 (E) and G12 (F) to detect sweeps in the sample following 40% admixture from the donor.

V hard [sweeps]

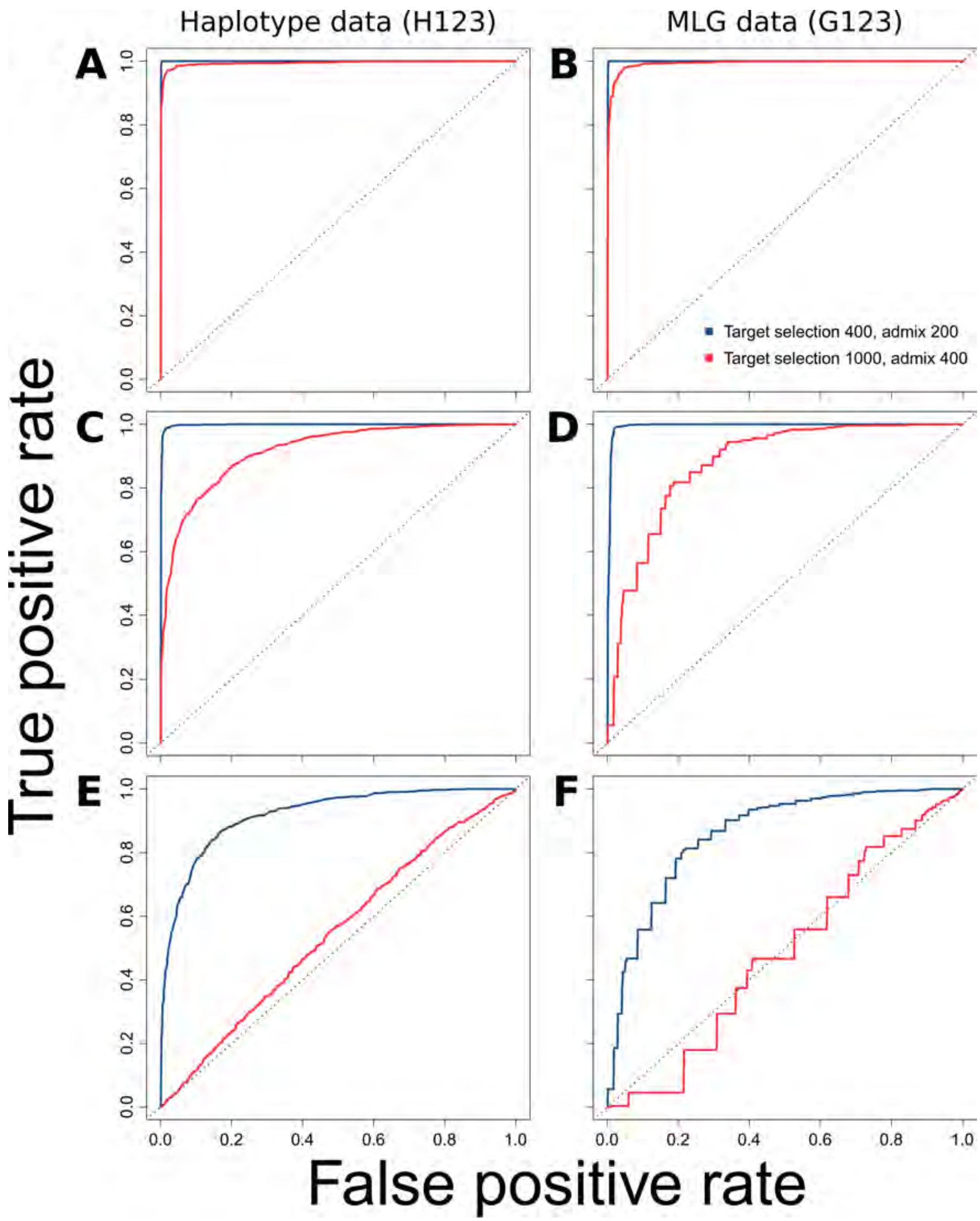


Figure S20: Effect of admixture on ability of H123 (left panels) and G123 (right panels) to detect sweeps. Data are identical to those in Figure S19, but analyzed with the alternate statistics.

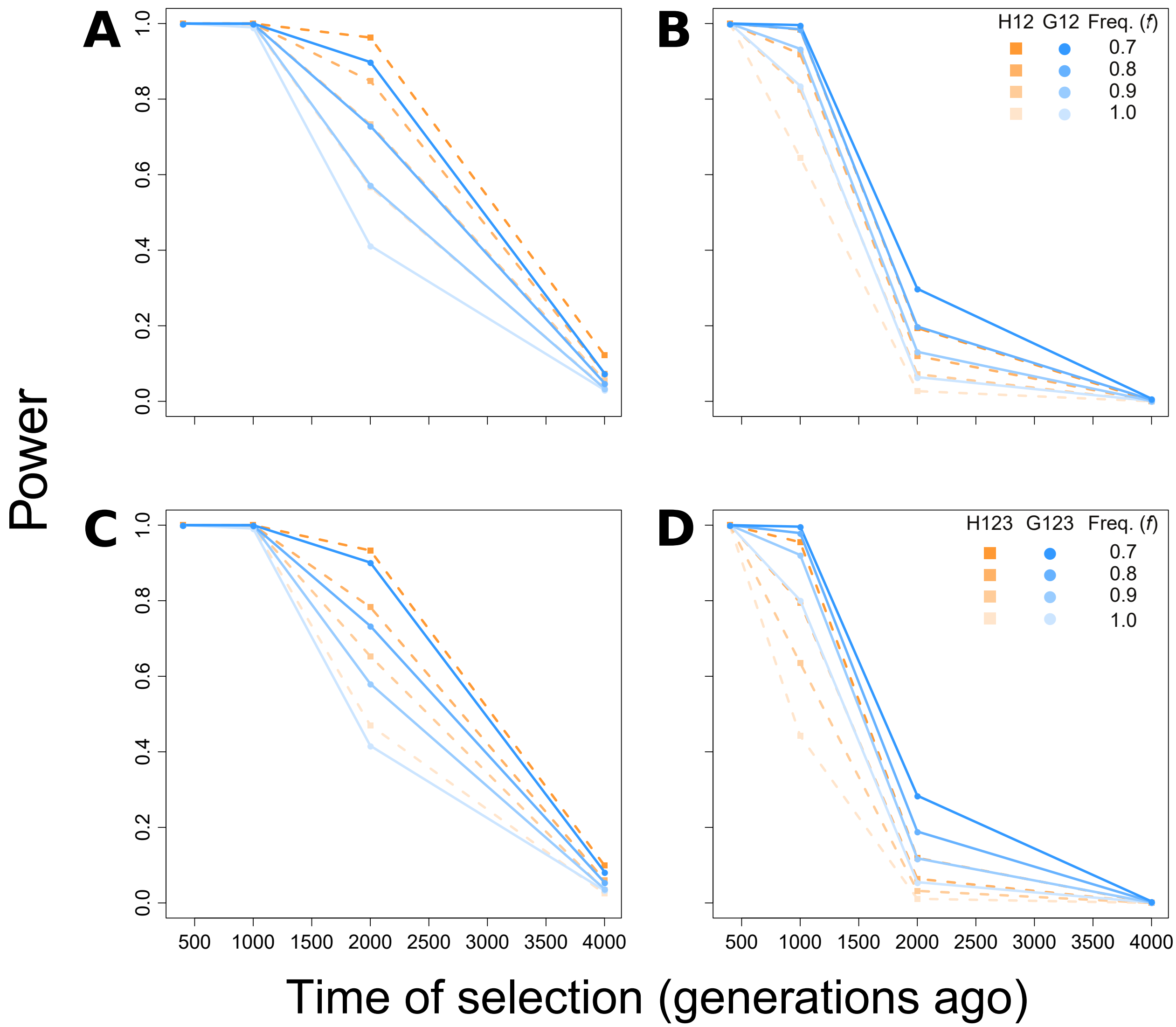


Figure S21: Effects of two strategies to account for missing data in sampled individuals on powers of G12 and H12, as well as G123 and H123. Data are identical to those in Figure 3. (A) Powers of G12 (blue) and H12 (orange) to detect strong hard sweeps when sites with missing data are removed. (B) Powers 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).