₁ **File S1**

₂ SUPPORTING METHODS AND RESULTS

₃ **MCMC algorithm** We developed a Metropolis-Hastings MCMC algorithm (GAMERMAN

₄ and HEDIBERT 2006) to obtain samples from the joint posterior probability distribution for

₅ all model parameters. Haplotype frequencies were estimated using independence or random-

₆ walk chains. When independence chains were used, proposal values for haplotype frequencies

₇ (a vector p_{ij} containing values for each locus and population) were sampled from Dirichlet

₈ distributions that were independent of **p** from the previous time-step and similar in form

₉ to the expected posterior distribution for these parameters. This proposal distribution is

₁₀ very efficient when dealing with few haplotypes and intermediate haplotype frequencies.

₁₁ Random-walk chains were used when these criteria were not met, which involved sampling

₁₂ haplotype frequencies from Dirichlet distributions that were proportional to the vector p_{ij}

₁₃ from the previous MCMC step. At least one of these two proposal algorithms generally

₁₄ worked well with each data set, however, more complicated, alternative proposal distributions

₁₅ might be considered when a very large number of haplotypes are analyzed. The α and β

₁₆ parameters associated with the conditional prior on haplotype frequencies were estimated

₁₇ using random-walk chains. Specifically, new values for each α and β pair were proposed

₁₈ from bivariate Gaussian distributions centered on the previous parameter values with user

₁₉ adjusted variance and covariance. Specification of a high covariance between proposal values

₂₀ of α and β was imposed to increase chain mixing. The MCMC algorithm was written in C++

₂₁ using the GNU Scientific Library (GALASSI *et al.* 2009) and is available from the authors at

₂₂ `http://www.uwyo.edu/buerkle/software/` as the stand-alone software *bamova*.

₂₃ **Simulations: estimation of ϕ statistics** We conducted a series of simulations to deter-

₂₄ mine whether the proposed model provided reasonable estimates of genome-level ϕ-statistics.

₂₅ For these simulations we were solely concerned with genetic differentiation among popula-

26 tions (rather than also considering differentiation among groups of populations). For each

27 of our three likelihood models we simulated sequence data using an infinite sites coalescent

28 model (using R. Hudson's software *ms*; HUDSON 2002). One group of data consisted of

29 sequences from 25 genetic regions, whereas the second group consisted of sequences from

30 500 genetic regions. All simulations assumed five populations split from a common ancestor

31 τ generations in the past, where τ has units of $4N_e$. We varied τ from 0 to 1 in steps of

32 0.05 to produce 21 data sets each for 25 and 500 loci. The ancestral population and all five

33 descendant populations were assigned population mutation rates $\theta = 4N_e\mu$ of 0.5, where μ

34 is the per locus mutation rate. We assumed no migration following population subdivision.

35 Forty gene copies were sampled from each of the five populations. For the *known haplotype*

36 *model* analyses we treated the simulated sequences directly as the sampled data. For *NGS–*

37 *individual model* and *NGS-population model* analyses we re-sampled the simulated sequence

38 data sets such that coverage for each sequence was Poisson distributed ($\lambda = 2$). For the

39 *NGS–individual model* analyses we retained information on which individual each sequence

40 came from, whereas we only retained population identification for *NGS-population model*

41 analyses. Each data set was analyzed using our *bamova* software, with MCMC details as

42 described in the main document.

43   MCMC implementation of the proposed Bayesian models accurately quantified genetic

44 structure among five simulated populations with sequence data from 25 or 500 genetic re-

45 gions (Figure S1). In general, estimates of mean genome-level ϕ_{ST} (μ_{ST}) increased with

46 the time since divergence of the five populations (τ). Credible intervals for genome-level

47 parameters were relatively narrow, particularly when estimates were based on 500 genetic

48 regions (Figure S1, S2). Moreover, credible intervals, and thus the uncertainty in genome-

49 level parameters, were similar for all three first-level likelihood models (*known haplotype*

50 *model*, *NGS-individual model*, and *NGS-population model*). We detected considerable varia-

51 tion in the extent of population structure among genetic regions (and hence non-zero σ_{ST} for

52 genome-level ϕ_{ST}), except when the population divergence time was very low (Fig. S2). Pos-

53 terior probability estimates for μ_{ST} were similar to the empirical mean of the locus-specific ϕ

54 statistics calculated directly from the raw data; however, the estimates of σ_{ST} were generally

55 lower than the empirical standard deviation of ϕ_{ST} from the raw data.

56   In the analyses of simulated data sets, ϕ_{ST} increased reliably and as expected with time

57 since population divergence. Moreover, estimates of genome-level ϕ_{ST} using the *known*

58 *haplotypes model* were very similar to non-Bayesian point estimates of mean ϕ_{ST} (Figure

59 S1). Additionally the estimates of genome-level ϕ_{ST} for the *known haplotypes model*, the

60 *NGS–individual model*, and the *NGS–population model* were similar. This similarity in re-

61 sults among models suggest that high-coverage NGS data can provide parameter estimates

62 with precision and accuracy equivalent to Sanger sequencing. Furthermore, the estimates

63 of genome-level ϕ_{ST} for the SeattleSNPs human sequence data and chromosome-level ϕ_{ST}

64 for the worldwide human SNP data (0.080–0.139) were similar to mean levels of genetic

65 differentiation among human populations based on F_{ST} (e.g., $F_{ST} = 0.09$–0.14 for Yoruba,

66 European, Han Chinese and Japanese populations; WEIR *et al.* 2005; BARREIRO *et al.*

67 2008). An important attribute of the model is that it also provides an accurate estimate

68 of the uncertainty in the parameter estimates. This is an attribute not necessarily shared

69 by non-Bayesian methods of parameter estimation, particularly when hierarchical or derived

70 parameters are involved (LINK and BAKER 2009).

71 **Human SeattleSNP data: alternative data subsets** In addition to analysing the

72 SeattleSNPs data set based on the first five SNPs in each gene we analysed four additional

73 subsets of these data: 1) sequences based on the middle five SNPs in each gene, 2) sequences

74 based on the last five SNPs in each gene, 3) sequences based on five SNPs spaced evenly

75 across each gene, 4) and sequences based on every 12th SNP in each gene (mean number of

76 SNPs = 5.24, sd = 0.423). Analyses of these data sets were as described in the main text

77 for the first five SNPs data set.

78   We classified four genes as high ϕ_{ST} outliers (using $a = 0.5$) in two or more of the data

subsets (Figs. 1, S3). Three of these genes, HSD11B2, FOXA2, and POLG2 were classified as ϕ_{ST} outliers based on the 'first five SNPs' data subset, and are described in the main document. Other outlier gene identified in more than one data subset was CPSF4, which encodes the cleavage polyadenylation specificity factor subunit 4 protein and is an essential component of pre-mRNA 3' processing in mammals (BARABINO *et al.* 1997). Estimates of ϕ_{ST} for CPSF4 were as high as 0.382 (95% ETPI 0.262–0.496; 'last five SNPs' data subset, Fig. S3). Four additional genes were identified as high ϕ_{ST} outliers in single subsets of the data: FUT2, IL1F6, EPPB9, and IKBKB. When classified as outliers these genes had ϕ_{ST} estimates similar to the genes detected as outliers more than once (Figs. 1, S3). Interestingly, FUT2 was classified as a candidate gene experiencing balancing selection in European Americans based on levels of polymorphism and intermediate-frequency alleles by Andres *et al.* (ANDRÉS *et al.* 2009) and is generally regarded as a well-established target of balancing selection (contrary to our findings). Variation among data subsets in whether genes were detected as outliers depended both on the distribution of divergent nucleotides along each gene and the extent of divergence at each of these nucleotides (Fig. 2). No genes were identified as low ϕ_{ST} outliers, nor were any genes identified as high ϕ_{ST} outliers using $a = 0.95$.

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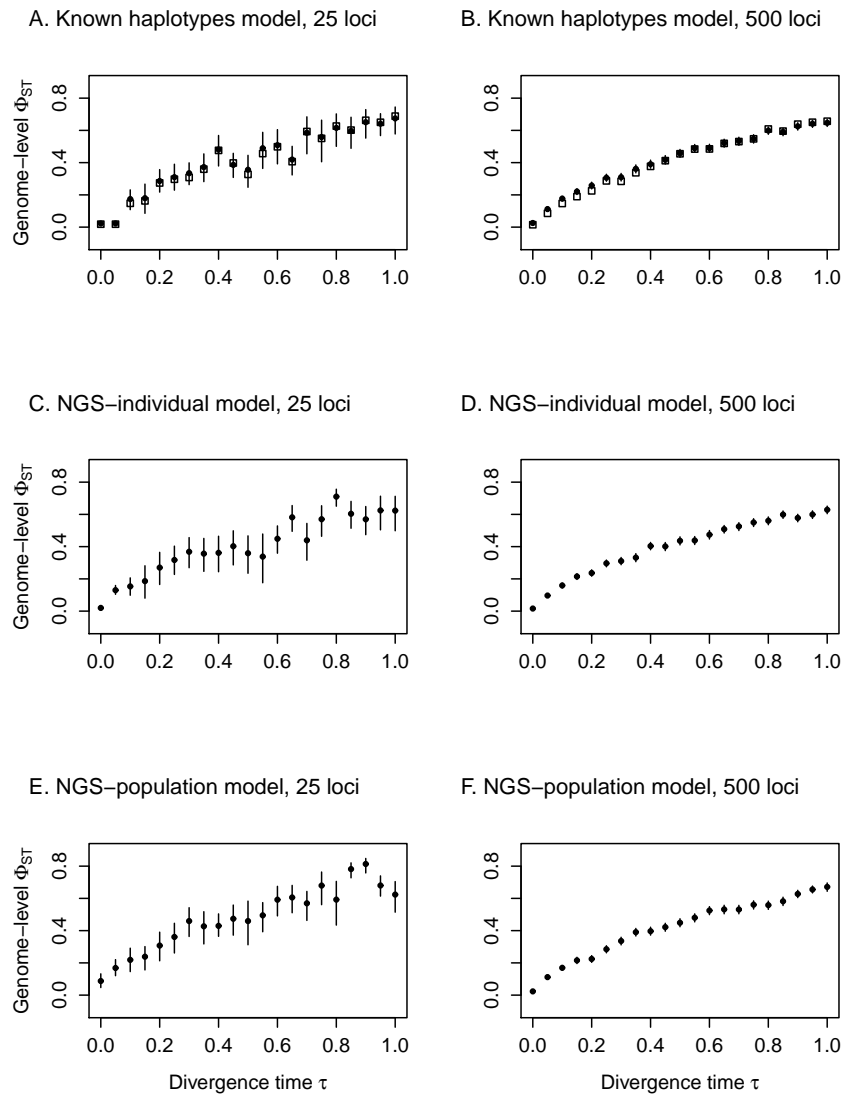
FIGURE S1.—Posterior probability distribution for mean genome-level ϕ_{ST} (μ_{ST}). The median (solid circle), 95% ETPI (vertical lines), and empirical mean ϕ_{ST} (open box, *known haplotypes model*) from a set of simulated data are shown in each plot.

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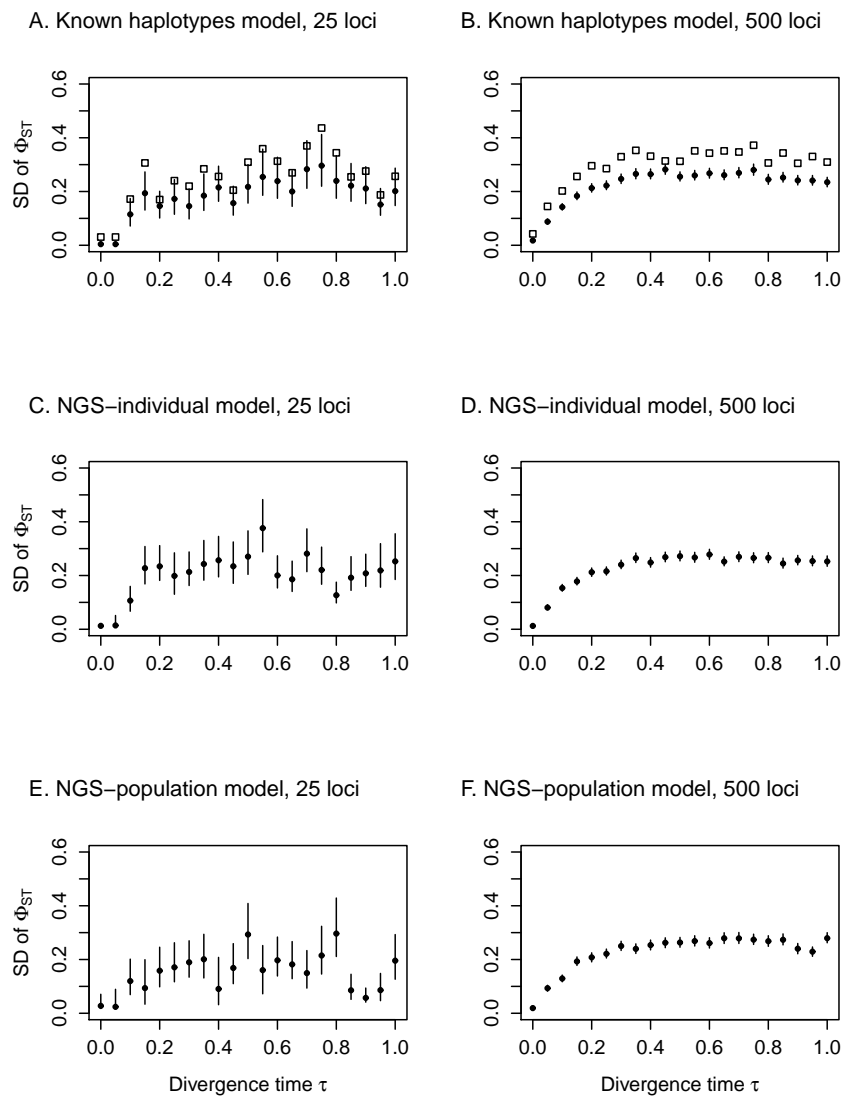
FIGURE S2.—Posterior probability distribution for the standard deviation of the genome-level ϕ_{ST} distribution. The median (solid circle), 95% ETPI (vertical lines), and empirical standard deviation of ϕ_{ST} (open box, known haplotypes model) are shown for each set of simulations.
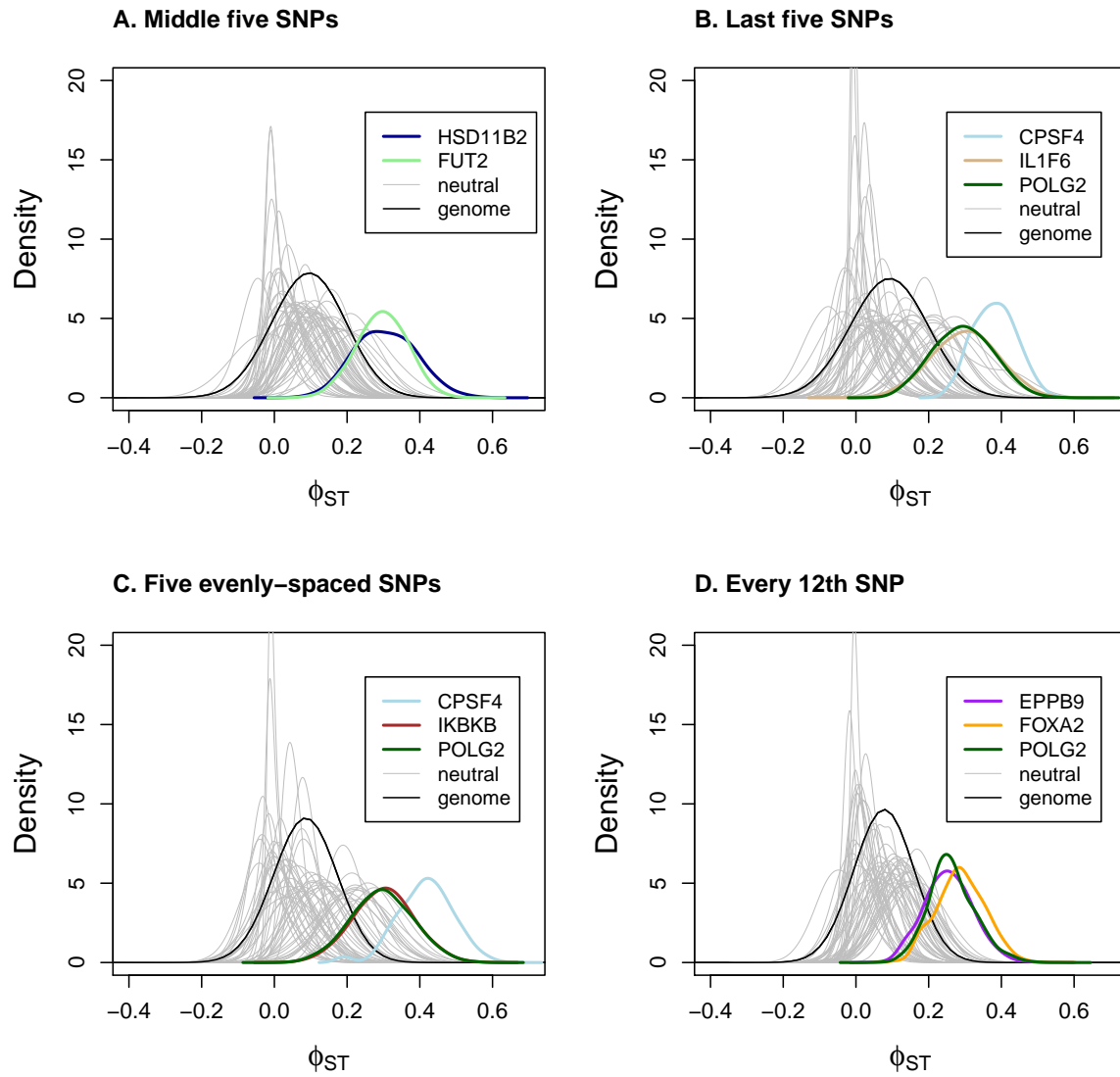
FIGURE S3.—Locus-specific ϕ_{ST} estimates for Africans and Europeans (SeattleSNPs data set). A point estimate of the genome-level ϕ_{ST} distribution (based on the median from the posterior probability distributions of α_{ST} and β_{ST}) is denoted with a solid black line. The posterior probability distributions for the outlier loci (colored lines) and 50 additional randomly chosen genetic regions (gray lines) are shown in each plot. Results from the middle five SNPs in each gene (A), the last five SNPs in each gene (B), five evenly spaced SNPs in each gene (C), and every 12th in each gene (D) are shown.

TABLE S1
Proportion of outlier loci (*known haplotypes model*)

S	No. loci	τ	Neutral								Selective Sweep							
			m=0				m=2				m=0				m=2			
			a=0.5		a=0.95		a=0.5		a=0.95		a=0.5		a=0.95		a=0.5		a=0.95	
			low	high	low	high	low	high	low	high	low	high	low	high	low	high	low	high
1	25	0.25	0.013	0.039	0.000	0.004	0.017	0.004	0.000	0.000	0.000	0.050	0.000	0.000	0.050	0.150	0.000	0.000
		0.50	0.035	0.017	0.000	0.000	0.017	0.017	0.000	0.000	0.150	0.000	0.000	0.000	0.050	0.100	0.000	0.000
		1.00	0.030	0.009	0.000	0.000	0.013	0.026	0.000	0.000	0.050	0.200	0.050	0.000	0.000	0.250	0.000	0.050
	500	0.25	0.022	0.021	0.004	0.002	0.013	0.014	0.001	0.001	0.052	0.084	0.012	0.012	0.028	0.124	0.004	0.044
		0.50	0.017	0.019	0.001	0.001	0.011	0.015	0.000	0.001	0.036	0.072	0.000	0.012	0.020	0.076	0.000	0.040
		1.00	0.029	0.015	0.009	0.000	0.013	0.016	0.000	0.002	0.036	0.052	0.008	0.004	0.072	0.152	0.000	0.076
3	25	0.25	0.013	0.004	0.000	0.000	0.009	0.004	0.000	0.000	0.010	0.300	0.000	0.100	0.000	0.350	0.000	0.250
		0.50	0.030	0.000	0.000	0.000	0.009	0.013	0.000	0.000	0.050	0.300	0.000	0.150	0.000	0.450	0.000	0.100
		1.00	0.026	0.004	0.000	0.000	0.000	0.026	0.000	0.004	0.150	0.100	0.000	0.000	0.100	0.300	0.050	0.000
	500	0.25	0.011	0.008	0.000	0.001	0.009	0.008	0.000	0.001	0.032	0.260	0.000	0.124	0.052	0.324	0.000	0.196
		0.50	0.017	0.010	0.002	0.001	0.009	0.006	0.002	0.001	0.000	0.156	0.000	0.060	0.048	0.376	0.000	0.216
		1.00	0.029	0.012	0.009	0.000	0.013	0.010	0.001	0.001	0.016	0.160	0.004	0.036	0.060	0.340	0.008	0.204
5	25	0.25	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000
		0.50	0.004	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000
		1.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000
	500	0.25	0.003	0.000	0.002	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000
		0.50	0.010	0.003	0.000	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000
		1.00	0.030	0.012	0.010	0.000	0.000	0.000	0.000	0.000	0.000	1.000	0.000	1.000	0.000	1.000	0.000	1.000

Mean proportion of neutrally evolving and selected loci over 10 replicates identified as outliers for the *known haplotypes model*.

TABLE S2

Proportion of outlier loci (*NGS−individual model*)

			Neutral								Selective Sweep							
			$m=0$				$m=2$				$m=0$				$m=2$			
			$a=0.5$		$a=0.95$		$a=0.5$		$a=0.95$		$a=0.5$		$a=0.95$		$a=0.5$		$a=0.95$	
S	No. loci	τ	low	high	low	high	low	high	low	high	low	high	low	high	low	high	low	high
1	25	0.25	0.009	0.022	0.000	0.000	0.013	0.009	0.000	0.000	0.000	0.100	0.000	0.000	0.050	0.150	0.000	0.000
		0.50	0.022	0.013	0.000	0.004	0.000	0.013	0.000	0.000	0.000	0.050	0.000	0.000	0.050	0.050	0.000	0.000
		1.00	0.030	0.017	0.009	0.004	0.013	0.017	0.000	0.000	0.100	0.000	0.000	0.000	0.100	0.050	0.000	0.000
	500	0.25	0.012	0.021	0.001	0.003	0.005	0.017	0.000	0.003	0.008	0.044	0.000	0.008	0.012	0.064	0.000	0.012
		0.50	0.023	0.016	0.003	0.002	0.011	0.019	0.000	0.002	0.016	0.036	0.004	0.000	0.008	0.064	0.000	0.000
		1.00	0.031	0.007	0.008	0.001	0.011	0.018	0.000	0.002	0.036	0.004	0.008	0.000	0.028	0.076	0.000	0.008
3	25	0.25	0.004	0.022	0.000	0.000	0.004	0.026	0.000	0.000	0.050	0.250	0.050	0.000	0.000	0.100	0.000	0.050
		0.50	0.018	0.022	0.004	0.004	0.017	0.004	0.000	0.000	0.050	0.000	0.000	0.000	0.000	0.400	0.000	0.100
		1.00	0.043	0.009	0.000	0.000	0.009	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.100	0.250	0.000	0.0500
	500	0.25	0.009	0.015	0.001	0.002	0.008	0.013	0.000	0.003	0.024	0.160	0.000	0.032	0.012	0.248	0.000	0.072
		0.50	0.018	0.014	0.001	0.002	0.009	0.013	0.000	0.002	0.036	0.076	0.004	0.008	0.044	0.220	0.000	0.056
		1.00	0.032	0.009	0.008	0.001	0.010	0.013	0.001	0.001	0.056	0.032	0.004	0.008	0.036	0.216	0.000	0.044
5	25	0.25	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.650	0.000	0.150	0.000	0.850	0.000	0.350
		0.50	0.013	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.300	0.000	0.100	0.000	0.950	0.000	0.3000
		1.00	0.022	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.200	0.000	0.100	0.000	0.850	0.000	0.400
	500	0.25	0.011	0.006	0.000	0.001	0.006	0.002	0.000	0.000	0.000	0.656	0.000	0.2888	0.000	0.888	0.000	0.440
		0.50	0.018	0.007	0.002	0.001	0.005	0.003	0.000	0.001	0.000	0.308	0.000	0.108	0.000	0.824	0.000	0.416
		1.00	0.031	0.008	0.009	0.001	0.009	0.004	0.000	0.001	0.000	0.060	0.000	0.004	0.000	0.792	0.000	0.324

Mean proportion of neutrally evolving and selected loci over 10 replicates identified as outliers for the *NGS-individual model*.

TABLE S3

Proportion of outlier loci (*NGS-population model*)

			Neutral								Selective Sweep							
			$m=0$				$m=2$				$m=0$				$m=2$			
			$a=0.5$		$a=0.95$		$a=0.5$		$a=0.95$		$a=0.5$		$a=0.95$		$a=0.5$		$a=0.95$	
S	No. loci	τ	low	high	low	high	low	high	low	high	low	high	low	high	low	high	low	high
1	25	0.25	0.030	0.013	0.000	0.000	0.000	0.017	0.000	0.000	0.050	0.100	0.000	0.050	0.000	0.150	0.000	0.000
		0.50	0.013	0.009	0.000	0.000	0.004	0.017	0.000	0.000	0.050	0.050	0.000	0.000	0.000	0.200	0.000	0.000
		1.00	0.052	0.013	0.000	0.000	0.009	0.009	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.050	0.100	0.000
	500	0.25	0.014	0.018	0.000	0.002	0.006	0.012	0.000	0.001	0.024	0.108	0.000	0.016	0.012	0.084	0.000	0.016
		0.50	0.020	0.013	0.001	0.001	0.008	0.015	0.000	0.001	0.036	0.048	0.008	0.004	0.016	0.096	0.000	0.016
		1.00	0.036	0.006	0.004	0.000	0.009	0.017	0.000	0.002	0.044	0.016	0.008	0.000	0.020	0.084	0.000	0.032
3	25	0.25	0.013	0.009	0.000	0.000	0.004	0.000	0.000	0.000	0.000	0.350	0.000	0.050	0.000	0.350	0.000	0.050
		0.50	0.022	0.013	0.000	0.000	0.009	0.004	0.000	0.000	0.000	0.100	0.000	0.000	0.100	0.150	0.000	0.000
		1.00	0.030	0.004	0.009	0.000	0.004	0.004	0.000	0.000	0.000	0.050	0.000	0.000	0.050	0.300	0.000	0.050
	500	0.25	0.019	0.014	0.000	0.002	0.007	0.010	0.000	0.000	0.028	0.248	0.000	0.080	0.044	0.308	0.000	0.132
		0.50	0.016	0.013	0.001	0.000	0.009	0.009	0.000	0.000	0.048	0.140	0.012	0.024	0.048	0.388	0.000	0.160
		1.00	0.033	0.005	0.004	0.000	0.006	0.011	0.000	0.001	0.036	0.040	0.000	0.004	0.028	0.336	0.000	0.136
5	25	0.25	0.004	0.000	0.000	0.000	0.000	0.004	0.000	0.000	0.000	0.800	0.000	0.250	0.000	0.750	0.000	0.350
		0.50	0.022	0.004	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.450	0.000	0.050	0.000	0.850	0.000	0.550
		1.00	0.030	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.000	0.250	0.000	0.100	0.000	0.900	0.000	0.4000
	500	0.25	0.003	0.001	0.000	0.000	0.001	0.001	0.000	0.000	0.000	0.420	0.000	0.240	0.000	0.724	0.000	0.552
		0.50	0.009	0.000	0.000	0.000	0.002	0.000	0.000	0.000	0.000	0.240	0.000	0.160	0.000	0.676	0.000	0.532
		1.00	0.028	0.002	0.005	0.000	0.001	0.000	0.000	0.000	0.000	0.096	0.000	0.052	0.000	0.520	0.000	0.368

Mean proportion of neutrally evolving and selected loci over 10 replicates identified as outliers for the *NGS-population model*.

TABLE S4

Proportion of outlier loci (group structure) with the *NGS–individual model*

S_G	No. loci	ϕ	Neutral				Selective Sweep			
			$a = 0.5$	$a = 0.5$	$a = 0.95$	$a = 0.95$	$a = 0.5$	$a = 0.5$	$a = 0.95$	$a = 0.95$
			low	high	low	high	low	high	low	high
1	25	ϕ_{ST}	0.004	0.030	0.002	0.009	0.000	0.025	0.000	0.000
		ϕ_{CT}	0.009	0.028	0.000	0.004	0.025	0.025	0.000	0.000
		ϕ_{SC}	0.007	0.024	0.000	0.000	0.000	0.150	0.000	0.025
	500	ϕ_{ST}	0.014	0.032	0.003	0.008	0.016	0.012	0.000	0.000
		ϕ_{CT}	0.019	0.032	0.003	0.009	0.048	0.008	0.012	0.000
		ϕ_{SC}	0.009	0.010	0.000	0.000	0.004	0.120	0.000	0.044
2	25	ϕ_{ST}	0.004	0.002	0.000	0.000	0.000	0.925	0.000	0.875
		ϕ_{CT}	0.020	0.017	0.002	0.000	0.225	0.100	0.175	0.025
		ϕ_{SC}	0.000	0.000	0.000	0.000	0.000	0.950	0.000	0.900
	500	ϕ_{ST}	0.006	0.002	0.000	0.000	0.000	1.000	0.000	0.988
		ϕ_{CT}	0.020	0.029	0.004	0.009	0.164	0.108	0.160	0.100
		ϕ_{SC}	0.000	0.000	0.000	0.000	0.000	1.000	0.000	0.988

Mean proportion of neutrally evolving and selected loci over 10 replicates identified as outliers with group structure for the *NGS-individual model*.

Z. Gompert and C. A. Buerkle

TABLE S5

Summary of outlier analysis for the worldwide human SNP data (JAKOBSSON *et al.* 2008). For each genetic region we give the chromosome number (Chrom.), gene ID (Gene), and classification as a low (l) or high (h) ϕ_{ST} outlier as well as whether outlier status was at $a = 0.5$ or $a = 0.95$. Additionally we provide the median and credible intervals for each locus's ϕ_{ST} and quantile in the genome-level distribution.

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
1	AKT3	l–0.5	0.0015	0.0167	0.1217	-0.1017	-0.0455	0.0201
1	C1orf116	l–0.5	0.0016	0.0190	0.1253	-0.1007	-0.0420	0.0209
1	C1orf117	l–0.5	0.0018	0.0137	0.0711	-0.0981	-0.0508	-0.0009
1	GPR161	l–0.5	0.0001	0.0061	0.1521	-0.1631	-0.0712	0.0297
1	GSTM4	l–0.5	0.0011	0.0205	0.1673	-0.1089	-0.0399	0.0335
1	MYCBP	l–0.5	0.0019	0.0146	0.0828	-0.0969	-0.0493	0.0048
1	PLA2G2D	l–0.5	0.0014	0.0243	0.1920	-0.1036	-0.0351	0.0399
1	ACADM	h–0.5	0.9536	0.9938	0.9995	0.2119	0.2655	0.3168
1	AIM1L	h–0.5	0.9249	0.9851	0.9981	0.1960	0.2441	0.2906
1	AP4B1	h–0.5	0.9489	0.9951	0.9997	0.2087	0.2710	0.3267
1	ASPM	h–0.5	0.8376	0.9752	0.9981	0.1653	0.2304	0.2903
1	ATPAF1	h–0.5	0.9639	0.9971	0.9999	0.2192	0.2824	0.3420
1	C1orf113	h–0.5	0.9074	0.9882	0.9992	0.1883	0.2500	0.3076
1	C1orf114	h–0.5	0.8921	0.9770	0.9973	0.1825	0.2325	0.2834
1	C1orf123	h–0.5	0.9202	0.9903	0.9994	0.1935	0.2550	0.3111
1	C1orf161	h–0.5	0.9433	0.9886	0.9987	0.2055	0.2510	0.2984
1	C1orf83	h–0.5	0.8171	0.9774	0.9987	0.1603	0.2330	0.2983
1	C1orf83	h–0.5	0.9513	0.9960	0.9998	0.2101	0.2755	0.3345
1	CD34	h–0.5	0.9540	0.9915	0.9990	0.2125	0.2581	0.3017
1	ELA3B	h–0.5	0.8788	0.9763	0.9973	0.1782	0.2318	0.2832
1	FCER1A	h–0.5	0.9222	0.9829	0.9975	0.1951	0.2405	0.2846
1	GPR88	h–0.5	0.9547	0.9900	0.9984	0.2127	0.2540	0.2942

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
1	HMCN1	h–0.5	0.9608	0.9982	1.0000	0.2174	0.2915	0.3563
1	HNRPR	h–0.5	0.9246	0.9884	0.9989	0.1960	0.2506	0.3016
1	ILF2	h–0.5	0.9176	0.9845	0.9981	0.1926	0.2431	0.2907
1	INSRR	h–0.5	0.8887	0.9753	0.9965	0.1814	0.2304	0.2779
1	KCNT2	h–0.5	0.9559	0.9981	1.0000	0.2131	0.2912	0.3615
1	KIAA0319L	h–0.5	0.8693	0.9802	0.9986	0.1750	0.2366	0.2958
1	LRRC7	h–0.5	0.9286	0.9898	0.9993	0.1978	0.2539	0.3104
1	MEF2D	h–0.5	0.9292	0.9855	0.9982	0.1980	0.2449	0.2914
1	NBL1	h–0.5	0.9640	0.9929	0.9991	0.2204	0.2627	0.3031
1	NBPF3	h–0.5	0.9042	0.9777	0.9967	0.1870	0.2334	0.2789
1	ORC1L	h–0.5	0.9018	0.9832	0.9985	0.1860	0.2410	0.2956
1	PHTF1	h–0.5	0.9478	0.9909	0.9991	0.2078	0.2563	0.3049
1	PSMA5	h–0.5	0.9569	0.9947	0.9996	0.2142	0.2688	0.3209
1	RGL1	h–0.5	0.9513	0.9930	0.9995	0.2103	0.2627	0.3141
1	SNX27	h–0.5	0.9244	0.9779	0.9954	0.1959	0.2337	0.2721
1	TRIM46	h–0.5	0.9376	0.9838	0.9971	0.2023	0.2420	0.2815
1	TM2D1	l–0.95	0.0008	0.0051	0.0273	-0.1154	-0.0755	-0.0320
1	C1orf41	h–0.95	0.9968	0.9998	1.0000	0.2798	0.3322	0.3808
1	CLCNKB	h–0.95	0.9859	0.9988	0.9999	0.2456	0.2997	0.3505
1	CLSPN	h–0.95	0.9975	0.9998	1.0000	0.2855	0.3343	0.3793
1	EIF2C1	h–0.95	0.9999	1.0000	1.0000	0.3387	0.3881	0.4335
1	EIF2C3	h–0.95	0.9961	0.9997	1.0000	0.2760	0.3237	0.3695
1	EPS15	h–0.95	0.9862	0.9989	1.0000	0.2461	0.3010	0.3552
1	FRRS1	h–0.95	0.9710	0.9957	0.9997	0.2256	0.2740	0.3218
1	KHDRBS1	h–0.95	0.9757	0.9984	1.0000	0.2309	0.2947	0.3554
1	KIAA0319L	h–0.95	0.9664	0.9963	0.9998	0.2214	0.2768	0.3306
1	KIAA0907	h–0.95	0.9712	0.9989	1.0000	0.2261	0.3016	0.3673
1	MASP2	h–0.95	0.9899	0.9989	0.9999	0.2540	0.3015	0.3473
1	OSBPL9	h–0.95	0.9796	0.9986	1.0000	0.2354	0.2974	0.3520

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TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
1	PMVK	h–0.95	0.9848	0.9998	1.0000	0.2434	0.3282	0.4002
1	POLR3GL	h–0.95	0.9871	0.9997	1.0000	0.2475	0.3256	0.3922
1	RABGAP1L	h–0.95	0.9755	0.9974	0.9999	0.2311	0.2844	0.3359
1	RABGGTB	h–0.95	0.9757	0.9961	0.9996	0.2311	0.2757	0.3174
1	RBBP5	h–0.95	0.9943	0.9996	1.0000	0.2673	0.3194	0.3679
1	RC3H1	h–0.95	0.9912	0.9994	1.0000	0.2571	0.3129	0.3632
1	SH3BP5L	h–0.95	0.9982	0.9999	1.0000	0.2922	0.3371	0.3799
1	SHE	h–0.95	0.9889	0.9990	0.9999	0.2514	0.3028	0.3492
1	SLC16A1	h–0.95	0.9896	0.9993	1.0000	0.2533	0.3095	0.3599
1	SLC9A11	h–0.95	0.9987	1.0000	1.0000	0.2977	0.3642	0.4257
1	SYF2	h–0.95	0.9998	1.0000	1.0000	0.3325	0.4019	0.4630
1	UBE2J2	h–0.95	0.9767	0.9996	1.0000	0.2321	0.3199	0.3941
1	YY1AP1	h–0.95	0.9811	0.9996	1.0000	0.2375	0.3189	0.3886
1	ZBTB41	h–0.95	0.9975	0.9998	1.0000	0.2856	0.3355	0.3850
1	ZMYM4	h–0.95	0.9860	0.9982	0.9999	0.2458	0.2920	0.3372
1	ZMYM6	h–0.95	0.9997	1.0000	1.0000	0.3267	0.3962	0.4585
2	EIF2AK2	l–0.5	0.0010	0.0145	0.1055	-0.0956	-0.0384	0.0216
2	MGC39518	l–0.5	0.0003	0.0125	0.1879	-0.1204	-0.0421	0.0451
2	SMYD5	l–0.5	0.0049	0.0219	0.0819	-0.0632	-0.0278	0.0123
2	XPO1	l–0.5	0.0003	0.0164	0.2286	-0.1175	-0.0352	0.0541
2	ALK	h–0.5	0.8903	0.9772	0.9971	0.1800	0.2279	0.2737
2	CAB39	h–0.5	0.9596	0.9938	0.9996	0.2123	0.2590	0.3075
2	CHST10	h–0.5	0.8857	0.9832	0.9988	0.1785	0.2357	0.2910
2	CREG2	h–0.5	0.8386	0.9791	0.9986	0.1645	0.2304	0.2885
2	CTDSP1	h–0.5	0.9642	0.9928	0.9990	0.2160	0.2556	0.2937
2	FLJ20758	h–0.5	0.9261	0.9873	0.9987	0.1937	0.2427	0.2892
2	KYNU	h–0.5	0.9414	0.9933	0.9997	0.2005	0.2571	0.3138
2	LOC51252	h–0.5	0.9550	0.9897	0.9984	0.2096	0.2476	0.2849
2	MALL	h–0.5	0.9563	0.9971	0.9999	0.2097	0.2747	0.3367

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
2	MKI67IP	h–0.5	0.9526	0.9959	0.9998	0.2076	0.2674	0.3228
2	ORMDL1	h–0.5	0.8793	0.9895	0.9997	0.1765	0.2470	0.3128
2	REEP1	h–0.5	0.8450	0.9847	0.9994	0.1661	0.2382	0.3043
2	REEP1	h–0.5	0.9332	0.9911	0.9994	0.1968	0.2507	0.3046
2	RHBDD1	h–0.5	0.9498	0.9937	0.9995	0.2065	0.2583	0.3075
2	RNF149	h–0.5	0.9336	0.9899	0.9989	0.1970	0.2478	0.2930
2	SELI	h–0.5	0.9476	0.9964	0.9999	0.2044	0.2702	0.3299
2	STK11IP	h–0.5	0.8709	0.9848	0.9991	0.1736	0.2381	0.2956
2	SULT1C2	h–0.5	0.9477	0.9948	0.9997	0.2048	0.2625	0.3164
2	TMEFF2	h–0.5	0.9186	0.9854	0.9981	0.1904	0.2391	0.2841
2	TRPM8	h–0.5	0.8220	0.9842	0.9995	0.1605	0.2373	0.3055
2	ZNF512	h–0.5	0.9559	0.9948	0.9997	0.2100	0.2627	0.3143
2	RIF1	l–0.95	0.0006	0.0048	0.0267	-0.1051	-0.0646	-0.0226
2	AOX2	h–0.95	0.9840	0.9980	0.9999	0.2371	0.2823	0.3275
2	BIN1	h–0.95	0.9919	0.9994	1.0000	0.2525	0.3044	0.3556
2	C2orf13	h–0.95	0.9994	1.0000	1.0000	0.3041	0.3569	0.4085
2	CMKOR1	h–0.95	0.9707	0.9967	0.9998	0.2216	0.2720	0.3213
2	KIAA1212	h–0.95	0.9818	0.9990	1.0000	0.2333	0.2946	0.3490
2	PROKR1	h–0.95	0.9948	0.9997	1.0000	0.2625	0.3165	0.3658
2	PSCDBP	h–0.95	0.9968	0.9998	1.0000	0.2725	0.3220	0.3735
2	RAB3GAP1	h–0.95	0.9625	0.9986	1.0000	0.2137	0.2881	0.3572
2	SMC6L1	h–0.95	0.9960	1.0000	1.0000	0.2677	0.3464	0.4152
2	SMYD1	h–0.95	1.0000	1.0000	1.0000	0.3423	0.3974	0.4457
2	ZRANB3	h–0.95	0.9765	0.9992	1.0000	0.2268	0.2993	0.3597
3	CEP63	l–0.5	0.0015	0.0108	0.0543	-0.0848	-0.0445	-0.0017
3	GPR156	l–0.5	0.0023	0.0122	0.0503	-0.0767	-0.0415	-0.0044
3	ARL6	h–0.5	0.9189	0.9826	0.9977	0.1864	0.2296	0.2720
3	B3GNT5	h–0.5	0.9435	0.9935	0.9996	0.1977	0.2522	0.3032
3	BCL6	h–0.5	0.9323	0.9882	0.9987	0.1927	0.2388	0.2832

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
3	C3orf17	h–0.5	0.9370	0.9900	0.9991	0.1943	0.2426	0.2906
3	C3orf25	h–0.5	0.9158	0.9838	0.9983	0.1847	0.2315	0.2776
3	DNAH1	h–0.5	0.9268	0.9860	0.9985	0.1898	0.2347	0.2800
3	FLJ25996	h–0.5	0.9350	0.9882	0.9986	0.1935	0.2389	0.2821
3	MAPKAPK3	h–0.5	0.8826	0.9899	0.9997	0.1736	0.2424	0.3076
3	NGLY1	h–0.5	0.9304	0.9885	0.9990	0.1910	0.2392	0.2876
3	NR2C2	h–0.5	0.9094	0.9770	0.9961	0.1831	0.2227	0.2617
3	PCAF	h–0.5	0.9187	0.9856	0.9985	0.1866	0.2340	0.2793
3	PLCXD2	h–0.5	0.9041	0.9751	0.9963	0.1803	0.2207	0.2623
3	PLS1	h–0.5	0.9424	0.9894	0.9989	0.1976	0.2415	0.2861
3	RASA2	h–0.5	0.8803	0.9806	0.9986	0.1725	0.2271	0.2824
3	RBP2	h–0.5	0.8786	0.9843	0.9991	0.1718	0.2322	0.2907
3	UNQ846	h–0.5	0.9097	0.9806	0.9975	0.1829	0.2271	0.2704
3	BTLA	h–0.95	0.9910	0.9993	1.0000	0.2450	0.2953	0.3438
3	C3orf23	h–0.95	0.9959	0.9997	1.0000	0.2624	0.3097	0.3539
3	C3orf37	h–0.95	0.9697	0.9977	0.9999	0.2157	0.2733	0.3248
3	C3orf58	h–0.95	0.9842	0.9992	1.0000	0.2326	0.2921	0.3468
3	COPG	h–0.95	0.9941	0.9997	1.0000	0.2541	0.3098	0.3629
3	GNAI2	h–0.95	0.9980	0.9999	1.0000	0.2761	0.3260	0.3715
3	GORASP1	h–0.95	0.9995	1.0000	1.0000	0.2997	0.3492	0.3956
3	LMLN	h–0.95	0.9778	0.9981	0.9999	0.2234	0.2769	0.3268
3	LTF	h–0.95	0.9766	0.9978	0.9999	0.2225	0.2743	0.3243
3	MSL2L1	h–0.95	0.9707	0.9983	1.0000	0.2165	0.2792	0.3377
3	NPCDR1	h–0.95	0.9794	0.9985	0.9999	0.2254	0.2813	0.3323
3	RBP1	h–0.95	0.9772	0.9971	0.9998	0.2232	0.2689	0.3134
3	TRAK1	h–0.95	0.9983	1.0000	1.0000	0.2783	0.3344	0.3882
4	KLHL8	l–0.5	0.0001	0.0080	0.1424	-0.1536	-0.0674	0.0264
4	C4orf18	h–0.5	0.9279	0.9814	0.9966	0.2011	0.2425	0.2824
4	CCDC4	h–0.5	0.9555	0.9926	0.9993	0.2178	0.2660	0.3140

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TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
4	HCAP-G	h–0.5	0.9144	0.9843	0.9984	0.1941	0.2475	0.2979
4	LEF1	h–0.5	0.9273	0.9826	0.9974	0.2010	0.2444	0.2878
4	MOBKL1A	h–0.5	0.9038	0.9853	0.9990	0.1899	0.2490	0.3071
4	NUDT6	h–0.5	0.9562	0.9924	0.9992	0.2182	0.2652	0.3109
4	NUP54	h–0.5	0.9501	0.9935	0.9996	0.2135	0.2693	0.3228
4	STX18	h–0.5	0.9399	0.9877	0.9986	0.2078	0.2536	0.3022
4	TBC1D19	h–0.5	0.9401	0.9911	0.9993	0.2076	0.2618	0.3156
4	TLR10	h–0.5	0.8653	0.9763	0.9978	0.1768	0.2357	0.2920
4	ARHGAP10	h–0.95	0.9977	0.9998	1.0000	0.2930	0.3374	0.3778
4	CENTD1	h–0.95	0.9902	0.9984	0.9999	0.2597	0.3007	0.3447
4	DCK	h–0.95	0.9999	1.0000	1.0000	0.3526	0.4099	0.4624
4	ENAM	h–0.95	0.9993	1.0000	1.0000	0.3171	0.3827	0.4396
4	ESSPL	h–0.95	0.9755	0.9970	0.9998	0.2361	0.2863	0.3362
4	ETFDH	h–0.95	0.9992	1.0000	1.0000	0.3127	0.3954	0.4679
4	LRBA	h–0.95	0.9765	0.9975	0.9999	0.2361	0.2906	0.3455
4	NPNT	h–0.95	0.9859	0.9989	1.0000	0.2508	0.3070	0.3613
4	PHF22	h–0.95	0.9985	0.9999	1.0000	0.3024	0.3501	0.3943
4	POLN	h–0.95	0.9869	0.9984	0.9999	0.2516	0.3001	0.3454
4	SLC30A9	h–0.95	0.9916	0.9991	1.0000	0.2641	0.3107	0.3573
4	TMEM34	h–0.95	0.9989	1.0000	1.0000	0.3075	0.3612	0.4108
5	DNAJA5	l–0.5	0.0010	0.0071	0.0386	-0.0917	-0.0542	-0.0132
5	C6	h–0.5	0.8581	0.9869	0.9996	0.1593	0.2280	0.2928
5	CD180	h–0.5	0.8830	0.9792	0.9981	0.1674	0.2171	0.2665
5	GMCL1L	h–0.5	0.9080	0.9871	0.9991	0.1753	0.2284	0.2809
5	HSPA4	h–0.5	0.9065	0.9840	0.9984	0.1748	0.2236	0.2694
5	IL4	h–0.5	0.9003	0.9792	0.9975	0.1729	0.2173	0.2615
5	LOC51334	h–0.5	0.9439	0.9887	0.9986	0.1908	0.2315	0.2708
5	LOC90624	h–0.5	0.9509	0.9917	0.9993	0.1951	0.2384	0.2826
5	MARCH6	h–0.5	0.9528	0.9897	0.9985	0.1963	0.2336	0.2703

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
5	SKP2	h–0.5	0.9493	0.9936	0.9996	0.1934	0.2439	0.2916
5	SRFBP1	h–0.5	0.8352	0.9788	0.9988	0.1541	0.2166	0.2760
5	GPBP1	l–0.95	0.0002	0.0023	0.0206	-0.1175	-0.0774	-0.0293
5	RBM22	l–0.95	0.0000	0.0004	0.0386	-0.1900	-0.1092	-0.0118
5	HINT1	h–0.95	0.9818	0.9987	1.0000	0.2207	0.2745	0.3265
5	LOC92270	h–0.95	0.9862	0.9994	1.0000	0.2273	0.2886	0.3431
5	MGC23985	h–0.95	0.9958	0.9998	1.0000	0.2533	0.3026	0.3497
5	MSX2	h–0.95	0.9929	0.9997	1.0000	0.2417	0.2991	0.3511
5	NSUN2	h–0.95	0.9796	0.9961	0.9996	0.2176	0.2540	0.2929
5	PITX1	h–0.95	0.9988	1.0000	1.0000	0.2753	0.3344	0.3864
5	ROPN1L	h–0.95	0.9688	0.9952	0.9996	0.2080	0.2498	0.2925
5	SDHA	h–0.95	0.9773	0.9974	0.9998	0.2159	0.2619	0.3059
5	SLC36A2	h–0.95	0.9893	0.9996	1.0000	0.2325	0.2929	0.3505
5	WDR70	h–0.95	0.9943	0.9997	1.0000	0.2455	0.2979	0.3491
6	FRS3	l–0.5	0.0003	0.0041	0.0388	-0.1045	-0.0605	-0.0098
6	GCM2	l–0.5	0.0014	0.0173	0.1098	-0.0787	-0.0300	0.0207
6	KIFC1	l–0.5	0.0003	0.0099	0.1468	-0.1083	-0.0425	0.0312
6	MYCT1	l–0.5	0.0026	0.0239	0.1380	-0.0682	-0.0222	0.0287
6	TDRD6	l–0.5	0.0004	0.0053	0.0448	-0.1009	-0.0555	-0.0063
6	ZNF187	l–0.5	0.0030	0.0223	0.1170	-0.0654	-0.0239	0.0232
6	C6orf146	h–0.5	0.9155	0.9867	0.9989	0.1696	0.2166	0.2631
6	C6orf70	h–0.5	0.8524	0.9768	0.9985	0.1509	0.2040	0.2573
6	CDC40	h–0.5	0.8677	0.9762	0.9979	0.1548	0.2034	0.2521
6	CYB5R4	h–0.5	0.9572	0.9951	0.9997	0.1886	0.2369	0.2827
6	FNDC1	h–0.5	0.9051	0.9779	0.9969	0.1658	0.2051	0.2448
6	IHPK3	h–0.5	0.8933	0.9791	0.9975	0.1624	0.2062	0.2490
6	IL20RA	h–0.5	0.8823	0.9753	0.9972	0.1591	0.2024	0.2471
6	PEX6	h–0.5	0.9103	0.9771	0.9958	0.1682	0.2044	0.2388
6	PGBD1	h–0.5	0.8928	0.9843	0.9990	0.1622	0.2132	0.2650

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
6	POPDC3	h–0.5	0.9417	0.9948	0.9998	0.1799	0.2359	0.2923
6	SRPK1	h–0.5	0.8672	0.9891	0.9997	0.1547	0.2210	0.2831
6	TAGAP	h–0.5	0.9185	0.9893	0.9993	0.1706	0.2214	0.2709
6	UBD	h–0.5	0.9104	0.9962	0.9999	0.1672	0.2418	0.3070
6	VIP	h–0.5	0.9282	0.9951	0.9999	0.1743	0.2367	0.2935
6	ZNF435	h–0.5	0.9373	0.9855	0.9978	0.1788	0.2147	0.2508
6	C6orf125	h–0.95	0.9783	0.9984	0.9999	0.2060	0.2567	0.3038
6	C6orf167	h–0.95	0.9725	0.9968	0.9998	0.2003	0.2447	0.2880
6	C6orf206	h–0.95	0.9992	1.0000	1.0000	0.2669	0.3475	0.4119
6	GSTA5	h–0.95	0.9781	0.9986	1.0000	0.2057	0.2587	0.3096
6	KIAA0408	h–0.95	0.9932	0.9998	1.0000	0.2305	0.2864	0.3374
6	PAK1IP1	h–0.95	0.9994	1.0000	1.0000	0.2722	0.3395	0.3991
6	SNRPC	h–0.95	0.9881	0.9994	1.0000	0.2194	0.2732	0.3227
6	VNN3	h–0.95	0.9711	0.9976	0.9999	0.1988	0.2501	0.2996
7	IGF2BP3	l–0.5	0.0001	0.0043	0.0569	-0.1411	-0.0728	-0.0046
7	PIP	l–0.5	0.0012	0.0186	0.1446	-0.0982	-0.0374	0.0290
7	C7orf34	h–0.5	0.8282	0.9763	0.9989	0.1589	0.2243	0.2905
7	CREB3L2	h–0.5	0.9083	0.9757	0.9961	0.1840	0.2240	0.2661
7	EPHB6	h–0.5	0.9386	0.9912	0.9994	0.1967	0.2488	0.3030
7	FAM3C	h–0.5	0.9403	0.9912	0.9993	0.1978	0.2488	0.2993
7	MDH2	h–0.5	0.9449	0.9929	0.9995	0.2003	0.2537	0.3039
7	PBEF1	h–0.5	0.9085	0.9791	0.9969	0.1837	0.2276	0.2701
7	PSCD3	h–0.5	0.8635	0.9754	0.9976	0.1680	0.2233	0.2764
7	NYD-SP18	h–0.5	0.8941	0.9879	0.9994	0.1778	0.2413	0.3028
7	RPA3	h–0.5	0.9227	0.9784	0.9956	0.1896	0.2269	0.2628
7	SP4	h–0.5	0.9258	0.9846	0.9982	0.1911	0.2354	0.2805
7	TRIM24	h–0.5	0.9181	0.9852	0.9985	0.1871	0.2364	0.2843
7	CYP3A43	h–0.95	0.9678	0.9963	0.9998	0.2160	0.2674	0.3187
7	CYP3A4	h–0.95	0.9896	0.9990	0.9999	0.2453	0.2928	0.3384

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
7	CYP3A5	h–0.95	0.9997	1.0000	1.0000	0.3147	0.3589	0.4011
7	DDX56	h–0.95	0.9896	0.9996	1.0000	0.2449	0.3094	0.3660
7	FLJ10324	h–0.95	0.9736	0.9969	0.9998	0.2214	0.2714	0.3188
7	FLJ12571	h–0.95	0.9949	0.9997	1.0000	0.2615	0.3126	0.3597
7	ING3	h–0.95	0.9839	0.9980	0.9999	0.2349	0.2804	0.3245
7	KCND2	h–0.95	0.9762	0.9966	0.9998	0.2249	0.2692	0.3172
7	MYH16	h–0.95	0.9936	0.9997	1.0000	0.2565	0.3131	0.3663
7	SMURF1	h–0.95	0.9961	0.9997	1.0000	0.2674	0.3123	0.3575
7	SVH	h–0.95	0.9999	1.0000	1.0000	0.3252	0.4036	0.4681
7	TRIAD3	h–0.95	0.9990	1.0000	1.0000	0.2925	0.3765	0.4434
7	TRIM4	h–0.95	0.9893	0.9995	1.0000	0.2441	0.3060	0.3639
7	ZFP95	h–0.95	0.9999	1.0000	1.0000	0.3291	0.3757	0.4177
8	EXTL3	l–0.5	0.0017	0.0111	0.0564	-0.0708	-0.0363	0.0030
8	ZHX1	l–0.5	0.0000	0.0037	0.1125	-0.1293	-0.0582	0.0243
8	ADCK5	h–0.5	0.8071	0.9781	0.9991	0.1410	0.2044	0.2643
8	ASH2L	h–0.5	0.8827	0.9764	0.9972	0.1596	0.2027	0.2447
8	C8orf72	h–0.5	0.8684	0.9757	0.9982	0.1553	0.2021	0.2531
8	CHRNA6	h–0.5	0.8063	0.9830	0.9995	0.1409	0.2101	0.2734
8	CNOT7	h–0.5	0.8986	0.9773	0.9968	0.1640	0.2036	0.2418
8	FLJ23356	h–0.5	0.8522	0.9829	0.9991	0.1508	0.2100	0.2644
8	KIAA0196	h–0.5	0.8861	0.9781	0.9975	0.1599	0.2044	0.2474
8	KIAA1967	h–0.5	0.9152	0.9847	0.9986	0.1693	0.2124	0.2558
8	LRP12	h–0.5	0.8505	0.9780	0.9986	0.1508	0.2044	0.2569
8	POTE8	h–0.5	0.8039	0.9887	0.9998	0.1404	0.2188	0.2901
8	SAMD12	h–0.5	0.9250	0.9859	0.9984	0.1738	0.2142	0.2533
8	SDCBP	h–0.5	0.8948	0.9832	0.9986	0.1628	0.2105	0.2566
8	SLA	h–0.5	0.9488	0.9922	0.9994	0.1847	0.2264	0.2685
8	SLC30A8	h–0.5	0.8587	0.9754	0.9979	0.1530	0.2019	0.2495
8	TEX15	h–0.5	0.9448	0.9947	0.9998	0.1815	0.2340	0.2851

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
8	TSPYL5	h–0.5	0.9590	0.9968	0.9999	0.1892	0.2428	0.2921
8	UBXD6	h–0.5	0.9613	0.9926	0.9991	0.1916	0.2274	0.2617
8	ZNF34	h–0.5	0.9154	0.9893	0.9994	0.1692	0.2201	0.2701
8	C8orf77	h–0.95	0.9849	0.9988	1.0000	0.2131	0.2595	0.3041
8	CRISPLD1	h–0.95	0.9872	0.9989	1.0000	0.2174	0.2610	0.3049
8	IKBKB	h–0.95	0.9750	0.9982	1.0000	0.2016	0.2532	0.3034
8	TCEA1	h–0.95	0.9806	0.9987	1.0000	0.2077	0.2587	0.3090
8	TMEM64	h–0.95	0.9744	0.9986	1.0000	0.2008	0.2575	0.3133
8	ZNF395	h–0.95	0.9868	0.9995	1.0000	0.2152	0.2740	0.3292
9	C9orf152	l–0.5	0.0009	0.0089	0.0591	-0.0869	-0.0446	0.0029
9	PMPCA	l–0.5	0.0009	0.0204	0.1845	-0.0880	-0.0255	0.0422
9	C5	h–0.5	0.9506	0.9921	0.9993	0.1909	0.2349	0.2771
9	CDC14B	h–0.5	0.8811	0.9847	0.9992	0.1639	0.2203	0.2762
9	CDKN2A	h–0.5	0.9539	0.9925	0.9994	0.1933	0.2355	0.2798
9	CTSL2	h–0.5	0.9390	0.9887	0.9987	0.1855	0.2271	0.2674
9	DAB2IP	h–0.5	0.9607	0.9987	1.0000	0.1964	0.2680	0.3335
9	DBC1	h–0.5	0.9401	0.9892	0.9989	0.1860	0.2279	0.2691
9	GARNL3	h–0.5	0.8711	0.9861	0.9995	0.1609	0.2225	0.2838
9	IARS	h–0.5	0.9418	0.9869	0.9980	0.1871	0.2237	0.2596
9	KIAA1539	h–0.5	0.9371	0.9869	0.9985	0.1844	0.2235	0.2645
9	LAMC3	h–0.5	0.9604	0.9935	0.9993	0.1979	0.2381	0.2778
9	NDUFA8	h–0.5	0.9580	0.9927	0.9992	0.1959	0.2358	0.2757
9	NPR2	h–0.5	0.9598	0.9960	0.9998	0.1968	0.2479	0.2943
9	NR6A1	h–0.5	0.8937	0.9890	0.9995	0.1670	0.2275	0.2846
9	C9orf114	h–0.95	0.9843	0.9979	0.9998	0.2203	0.2594	0.2969
9	C9orf89	h–0.95	0.9873	0.9987	0.9999	0.2247	0.2679	0.3117
9	FLJ16636	h–0.95	0.9999	1.0000	1.0000	0.3092	0.4013	0.4717
9	PRG-3	h–0.95	0.9976	1.0000	1.0000	0.2567	0.3238	0.3828
9	RABGAP1	h–0.95	0.9970	1.0000	1.0000	0.2525	0.3159	0.3742

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TABLE S5 – continued from previous page

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Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
9	STRBP	h–0.95	0.9809	0.9984	0.9999	0.2151	0.2649	0.3138
9	TBC1D13	h–0.95	0.9953	0.9995	1.0000	0.2463	0.2850	0.3239
9	TRPM6	h–0.95	0.9984	1.0000	1.0000	0.2647	0.3209	0.3727
9	ZBTB26	h–0.95	0.9937	0.9998	1.0000	0.2394	0.2991	0.3526
10	IFIT2	l–0.5	0.0002	0.0085	0.1270	-0.1137	-0.0483	0.0254
10	ANKRD2	h–0.5	0.8747	0.9838	0.9991	0.1592	0.2166	0.2709
10	CDNF	h–0.5	0.9584	0.9935	0.9994	0.1939	0.2360	0.2780
10	BMPR1A	h–0.5	0.8985	0.9796	0.9975	0.1673	0.2110	0.2530
10	C10orf70	h–0.5	0.9145	0.9863	0.9989	0.1722	0.2202	0.2691
10	C10orf99	h–0.5	0.8952	0.9784	0.9974	0.1658	0.2098	0.2530
10	CHUK	h–0.5	0.8947	0.9844	0.9990	0.1653	0.2173	0.2697
10	GDF2	h–0.5	0.8063	0.9813	0.9993	0.1428	0.2133	0.2757
10	HECTD2	h–0.5	0.9484	0.9957	0.9999	0.1872	0.2441	0.2992
10	ITGB1	h–0.5	0.8937	0.9778	0.9976	0.1650	0.2092	0.2540
10	KIAA1754	h–0.5	0.8782	0.9786	0.9982	0.1605	0.2098	0.2602
10	PPP3CB	h–0.5	0.9238	0.9923	0.9997	0.1754	0.2327	0.2890
10	REEP3	h–0.5	0.9600	0.9956	0.9998	0.1944	0.2437	0.2926
10	SEPHS1	h–0.5	0.8384	0.9810	0.9992	0.1499	0.2126	0.2729
10	TTC18	h–0.5	0.8960	0.9774	0.9972	0.1660	0.2085	0.2511
10	ECHDC3	l–0.95	0.0000	0.0009	0.0123	-0.1395	-0.0916	-0.0406
10	USP54	l–0.95	0.0000	0.0003	0.0486	-0.1953	-0.1090	-0.0052
10	ADD3	h–0.95	0.9648	0.9979	1.0000	0.1972	0.2573	0.3121
10	CTNNA3	h–0.95	0.9988	0.9999	1.0000	0.2673	0.3114	0.3530
10	ECHS1	h–0.95	0.9660	0.9975	0.9999	0.1983	0.2546	0.3083
10	IPMK	h–0.95	0.9927	0.9997	1.0000	0.2339	0.2876	0.3400
10	OIT3	h–0.95	0.9966	0.9998	1.0000	0.2490	0.2946	0.3391
10	POLR3A	h–0.95	0.9976	1.0000	1.0000	0.2552	0.3211	0.3815
11	PRDX5	l–0.5	0.0002	0.0230	0.3628	-0.1124	-0.0215	0.0759
11	BAD	h–0.5	0.8636	0.9865	0.9994	0.1606	0.2250	0.2827

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Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
11	C11orf49	h–0.5	0.8937	0.9779	0.9977	0.1696	0.2135	0.2592
11	C11orf56	h–0.5	0.9421	0.9864	0.9983	0.1886	0.2250	0.2633
11	CCS	h–0.5	0.9536	0.9896	0.9983	0.1950	0.2306	0.2647
11	CKAP5	h–0.5	0.9338	0.9890	0.9990	0.1845	0.2295	0.2747
11	FADS3	h–0.5	0.9348	0.9859	0.9980	0.1854	0.2241	0.2624
11	FLJ12529	h–0.5	0.8833	0.9794	0.9981	0.1662	0.2152	0.2637
11	GTF2H1	h–0.5	0.9245	0.9887	0.9991	0.1803	0.2288	0.2756
11	MGC34821	h–0.5	0.8774	0.9786	0.9981	0.1645	0.2144	0.2633
11	NRXN2	h–0.5	0.9228	0.9851	0.9983	0.1798	0.2228	0.2661
11	SART1	h–0.5	0.8403	0.9882	0.9996	0.1548	0.2278	0.2900
11	SDHD	h–0.5	0.9500	0.9981	1.0000	0.1924	0.2637	0.3260
11	SF1	h–0.5	0.9482	0.9906	0.9990	0.1919	0.2328	0.2729
11	SF3B2	h–0.5	0.9418	0.9911	0.9993	0.1883	0.2342	0.2795
11	SIAE	h–0.5	0.9499	0.9943	0.9997	0.1929	0.2433	0.2934
11	SLC43A1	h–0.5	0.9208	0.9863	0.9988	0.1792	0.2247	0.2705
11	SYT7	h–0.5	0.9650	0.9946	0.9996	0.2019	0.2443	0.2873
11	DDB1	h–0.95	1.0000	1.0000	1.0000	0.3472	0.4089	0.4610
11	DKFZP564J0863	h–0.95	0.9754	0.9993	1.0000	0.2105	0.2809	0.3416
11	FADS1	h–0.95	0.9958	0.9995	1.0000	0.2500	0.2868	0.3201
11	FBXL11	h–0.95	0.9935	0.9998	1.0000	0.2406	0.2968	0.3522
11	FLJ20294	h–0.95	0.9689	0.9976	0.9999	0.2052	0.2592	0.3103
11	HRASLS5	h–0.95	0.9878	0.9995	1.0000	0.2271	0.2846	0.3406
11	MGC2574	h–0.95	0.9694	0.9965	0.9998	0.2061	0.2527	0.2988
12	CCDC65	l–0.5	0.0062	0.0243	0.0830	-0.0681	-0.0341	0.0044
12	RAB5B	l–0.5	0.0022	0.0206	0.1205	-0.0915	-0.0387	0.0195
12	BAZ2A	h–0.5	0.9248	0.9887	0.9992	0.1925	0.2472	0.3020
12	C12orf44	h–0.5	0.9647	0.9947	0.9995	0.2167	0.2644	0.3092
12	C12orf51	h–0.5	0.9439	0.9917	0.9993	0.2025	0.2545	0.3048
12	CUTL2	h–0.5	0.9607	0.9944	0.9996	0.2139	0.2633	0.3122

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TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
12	DPY19L2	h–0.5	0.8293	0.9834	0.9994	0.1603	0.2373	0.3063
12	EP400NL	h–0.5	0.9365	0.9867	0.9984	0.1984	0.2430	0.2880
12	EPS8	h–0.5	0.9156	0.9898	0.9993	0.1883	0.2495	0.3068
12	IFT81	h–0.5	0.9400	0.9850	0.9975	0.2006	0.2399	0.2790
12	KERA	h–0.5	0.9284	0.9831	0.9973	0.1948	0.2368	0.2782
12	KIAA0789	h–0.5	0.9388	0.9844	0.9974	0.1999	0.2389	0.2787
12	LOC196463	h–0.5	0.8520	0.9869	0.9995	0.1665	0.2433	0.3109
12	LYZ	h–0.5	0.8838	0.9856	0.9993	0.1761	0.2410	0.3033
12	MBD6	h–0.5	0.8855	0.9814	0.9986	0.1773	0.2343	0.2910
12	NAP1L1	h–0.5	0.9429	0.9892	0.9989	0.2018	0.2483	0.2944
12	NOL1	h–0.5	0.9249	0.9929	0.9997	0.1923	0.2578	0.3162
12	NR4A1	h–0.5	0.9583	0.9956	0.9997	0.2116	0.2686	0.3207
12	OACT5	h–0.5	0.9479	0.9928	0.9994	0.2048	0.2578	0.3082
12	SLC15A4	h–0.5	0.9033	0.9789	0.9973	0.1834	0.2310	0.2790
12	SLCO1C1	h–0.5	0.9353	0.9838	0.9972	0.1984	0.2378	0.2772
12	SMARCC2	h–0.5	0.8367	0.9758	0.9985	0.1627	0.2273	0.2900
12	UBE2N	h–0.5	0.9420	0.9906	0.9992	0.2014	0.2513	0.3010
12	ULK1	h–0.5	0.9188	0.9853	0.9984	0.1901	0.2405	0.2883
12	ACTR6	h–0.95	0.9832	0.9981	0.9999	0.2378	0.2858	0.3319
12	ANAPC5	h–0.95	0.9906	0.9994	1.0000	0.2514	0.3080	0.3631
12	AQP6	h–0.95	0.9872	0.9983	0.9999	0.2447	0.2882	0.3300
12	C12orf30	h–0.95	0.9764	0.9966	0.9997	0.2285	0.2743	0.3197
12	CART1	h–0.95	0.9881	0.9986	0.9999	0.2464	0.2916	0.3334
12	CEP290	h–0.95	0.9750	0.9969	0.9998	0.2269	0.2763	0.3260
12	CMAS	h–0.95	0.9786	0.9976	0.9999	0.2304	0.2813	0.3307
12	EIF4B	h–0.95	0.9993	1.0000	1.0000	0.3036	0.3599	0.4132
12	GABARAPL1	h–0.95	0.9846	0.9983	0.9999	0.2399	0.2879	0.3336
12	MPHOSPH9	h–0.95	0.9687	0.9962	0.9997	0.2200	0.2720	0.3211
12	PAWR	h–0.95	0.9962	0.9999	1.0000	0.2718	0.3351	0.3930

<div align="center">TABLE S5 – continued from previous page</div>

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
12	SPATS2	h–0.95	0.9999	1.0000	1.0000	0.3465	0.3944	0.4380
12	STRAP	h–0.95	0.9966	0.9999	1.0000	0.2746	0.3368	0.3933
12	WDR66	h–0.95	0.9826	0.9985	0.9999	0.2362	0.2901	0.3448
13	WBP4	l–0.5	0.0008	0.0147	0.1256	-0.1006	-0.0426	0.0212
13	RB1	h–0.5	0.9494	0.9963	0.9999	0.1894	0.2510	0.3053
13	C13orf12	h–0.95	0.9902	0.9991	1.0000	0.2324	0.2771	0.3200
13	FAM48A	h–0.95	0.9972	1.0000	1.0000	0.2557	0.3291	0.3980
13	FBXL3	h–0.95	0.9992	1.0000	1.0000	0.2792	0.3340	0.3856
13	GTF2F2	h–0.95	0.9942	0.9996	1.0000	0.2444	0.2911	0.3377
13	KLF5	h–0.95	0.9993	1.0000	1.0000	0.2817	0.3346	0.3838
13	NDFIP2	h–0.95	0.9984	1.0000	1.0000	0.2685	0.3216	0.3695
13	TGDS	h–0.95	0.9835	0.9983	0.9999	0.2202	0.2661	0.3100
14	C14orf165	l–0.5	0.0001	0.0066	0.1247	-0.1503	-0.0683	0.0226
14	FOS	l–0.5	0.0012	0.0187	0.1340	-0.1041	-0.0414	0.0246
14	C14orf174	h–0.5	0.9462	0.9882	0.9984	0.2094	0.2514	0.2926
14	DLK1	h–0.5	0.9429	0.9921	0.9994	0.2068	0.2611	0.3118
14	DLST	h–0.5	0.9431	0.9890	0.9986	0.2075	0.2531	0.2954
14	GPHN	h–0.5	0.9125	0.9801	0.9974	0.1924	0.2376	0.2848
14	KIAA0423	h–0.5	0.8789	0.9807	0.9985	0.1792	0.2385	0.2965
14	PSEN1	h–0.5	0.8692	0.9765	0.9980	0.1762	0.2332	0.2901
14	RAB2B	h–0.5	0.9103	0.9801	0.9974	0.1917	0.2376	0.2840
14	SEC10L1	h–0.5	0.9293	0.9856	0.9983	0.1999	0.2461	0.2923
14	BRF1	h–0.95	0.9960	0.9996	1.0000	0.2777	0.3227	0.3675
14	EFS	h–0.95	0.9841	0.9975	0.9997	0.2458	0.2863	0.3260
14	IL17E	h–0.95	0.9890	0.9985	0.9999	0.2549	0.2970	0.3367
14	JPH4	h–0.95	0.9972	0.9999	1.0000	0.2839	0.3437	0.3976
14	MTA1	h–0.95	0.9992	1.0000	1.0000	0.3105	0.3607	0.4061
14	RBM23	h–0.95	0.9993	0.9999	1.0000	0.3142	0.3511	0.3843
14	SIX4	h–0.95	0.9705	0.9989	1.0000	0.2264	0.3029	0.3691

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TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
14	TDP1	h–0.95	0.9675	0.9959	0.9998	0.2245	0.2759	0.3272
15	DYX1C1	h–0.5	0.9427	0.9866	0.9978	0.2258	0.2705	0.3146
15	FURIN	h–0.5	0.9098	0.9795	0.9971	0.2090	0.2584	0.3074
15	HERC2	h–0.5	0.9329	0.9915	0.9994	0.2197	0.2828	0.3389
15	ARPP-19	h–0.5	0.9645	0.9928	0.9990	0.2425	0.2869	0.3301
15	PDIA3	h–0.5	0.9641	0.9923	0.9989	0.2422	0.2854	0.3267
15	PEX11A	h–0.5	0.9113	0.9877	0.9990	0.2085	0.2730	0.3310
15	SLC28A2	h–0.5	0.9498	0.9913	0.9991	0.2300	0.2826	0.3326
15	SNRPN	h–0.5	0.9585	0.9948	0.9997	0.2368	0.2954	0.3536
15	TMEM87A	h–0.5	0.9278	0.9893	0.9991	0.2169	0.2767	0.3334
15	ZNF690	h–0.5	0.9388	0.9757	0.9923	0.2251	0.2533	0.2824
15	ARIH1	h–0.95	0.9877	0.9989	0.9999	0.2728	0.3290	0.3828
15	CDAN1	h–0.95	0.9959	0.9996	1.0000	0.3016	0.3500	0.3959
15	DUOX2	h–0.95	1.0000	1.0000	1.0000	0.3899	0.4480	0.4977
15	FRMD5	h–0.95	0.9892	0.9988	0.9999	0.2784	0.3275	0.3731
15	NIP	h–0.95	0.9729	0.9973	0.9999	0.2507	0.3107	0.3657
15	RBPMS2	h–0.95	0.9911	0.9989	0.9999	0.2832	0.3304	0.3761
15	SLC24A5	h–0.95	0.9757	0.9959	0.9996	0.2545	0.3008	0.3466
15	SPATA5L1	h–0.95	0.9700	0.9995	1.0000	0.2462	0.3471	0.4295
15	TP53BP1	h–0.95	0.9939	0.9992	0.9999	0.2933	0.3369	0.3800
15	TRIP4	h–0.95	0.9866	0.9987	0.9999	0.2710	0.3257	0.3788
16	HAS3	l–0.5	0.0011	0.0091	0.0560	-0.1321	-0.0778	-0.0154
16	ADAT1	h–0.5	0.9233	0.9847	0.9983	0.2271	0.2832	0.3398
16	ARHGAP17	h–0.5	0.8884	0.9775	0.9973	0.2099	0.2710	0.3289
16	C16orf34	h–0.5	0.8907	0.9787	0.9975	0.2115	0.2726	0.3301
16	CCL22	h–0.5	0.8749	0.9819	0.9985	0.2047	0.2782	0.3424
16	FLJ20581	h–0.5	0.9630	0.9931	0.9992	0.2543	0.3059	0.3564
16	LONPL	h–0.5	0.9167	0.9857	0.9984	0.2237	0.2851	0.3405
16	LRRC36	h–0.5	0.9125	0.9859	0.9987	0.2214	0.2854	0.3454

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
16	MGC33367	h–0.5	0.9190	0.9803	0.9968	0.2247	0.2753	0.3238
16	MPFL	h–0.5	0.9211	0.9761	0.9947	0.2263	0.2692	0.3106
16	SPIN1	h–0.5	0.9085	0.9892	0.9994	0.2188	0.2934	0.3623
16	TRAF7	h–0.5	0.8984	0.9771	0.9970	0.2147	0.2706	0.3267
16	ZNF23	h–0.5	0.9333	0.9962	0.9999	0.2322	0.3217	0.3969
16	ABCC12	h–0.95	0.9821	0.9981	0.9999	0.2796	0.3377	0.3919
16	CCL17	h–0.95	0.9877	0.9987	0.9999	0.2904	0.3469	0.3991
16	CORO7	h–0.95	0.9854	0.9986	0.9999	0.2849	0.3454	0.4005
16	CREBBP	h–0.95	0.9904	0.9995	1.0000	0.2973	0.3667	0.4290
16	GABARAPL2	h–0.95	0.9817	0.9983	0.9999	0.2788	0.3404	0.3962
16	GLIS2	h–0.95	0.9931	0.9992	0.9999	0.3074	0.3586	0.4062
16	PLEKHG4	h–0.95	0.9993	1.0000	1.0000	0.3621	0.4125	0.4598
16	POLR3E	h–0.95	0.9665	0.9977	0.9999	0.2579	0.3339	0.4015
16	SLC9A5	h–0.95	0.9974	0.9999	1.0000	0.3318	0.3985	0.4603
17	TUSC5	l–0.5	0.0047	0.0207	0.0685	-0.0761	-0.0376	0.0015
17	ADORA2B	h–0.5	0.9079	0.9800	0.9978	0.2013	0.2512	0.3036
17	CASC3	h–0.5	0.9093	0.9876	0.9991	0.2019	0.2643	0.3230
17	CD300LF	h–0.5	0.9182	0.9817	0.9975	0.2062	0.2535	0.3021
17	CDR2L	h–0.5	0.9264	0.9908	0.9994	0.2094	0.2717	0.3298
17	DDX5	h–0.5	0.8575	0.9949	1.0000	0.1829	0.2859	0.3739
17	ERN1	h–0.5	0.9634	0.9917	0.9988	0.2343	0.2743	0.3163
17	ET	h–0.5	0.9080	0.9885	0.9993	0.2016	0.2662	0.3271
17	GRB2	h–0.5	0.9599	0.9926	0.9992	0.2309	0.2771	0.3224
17	KIAA1618	h–0.5	0.9183	0.9776	0.9960	0.2066	0.2480	0.2901
17	NDEL1	h–0.5	0.8524	0.9774	0.9984	0.1820	0.2477	0.3106
17	NLGN2	h–0.5	0.9421	0.9899	0.9989	0.2189	0.2693	0.3183
17	RSAD1	h–0.5	0.8919	0.9862	0.9990	0.1947	0.2614	0.3193
17	SCARF1	h–0.5	0.9176	0.9853	0.9986	0.2056	0.2597	0.3129
17	TTC25	h–0.5	0.8478	0.9839	0.9992	0.1797	0.2571	0.3250

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TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
17	ZNF232	h–0.5	0.9295	0.9856	0.9983	0.2115	0.2604	0.3080
17	AATF	h–0.95	0.9977	0.9998	1.0000	0.3051	0.3484	0.3962
17	C17orf64	h–0.95	0.9999	1.0000	1.0000	0.3710	0.4266	0.4791
17	CENTA2	h–0.95	0.9763	0.9973	0.9999	0.2473	0.3002	0.3529
17	CSNK1D	h–0.95	0.9919	0.9995	1.0000	0.2754	0.3355	0.3891
17	DERL2	h–0.95	0.9941	0.9995	1.0000	0.2832	0.3350	0.3831
17	G6PC	h–0.95	0.9675	0.9953	0.9996	0.2367	0.2881	0.3382
17	GNA13	h–0.95	0.9927	0.9995	1.0000	0.2782	0.3348	0.3885
17	ITGAE	h–0.95	0.9968	0.9999	1.0000	0.2965	0.3706	0.4349
17	PRPF8	h–0.95	0.9816	0.9978	0.9999	0.2539	0.3047	0.3557
17	TTC19	h–0.95	0.9934	0.9996	1.0000	0.2813	0.3379	0.3916
17	USP32	h–0.95	0.9955	0.9999	1.0000	0.2885	0.3654	0.4355
17	WDR68	h–0.95	0.9936	0.9996	1.0000	0.2810	0.3392	0.3897
18	ANKRD30B	l–0.5	0.0043	0.0219	0.0782	-0.0497	-0.0194	0.0130
18	C18orf10	l–0.5	0.0001	0.0031	0.0419	-0.1105	-0.0594	-0.0030
18	SERPINB12	l–0.5	0.0008	0.0138	0.1152	-0.0809	-0.0295	0.0253
18	GATA6	h–0.5	0.9591	0.9941	0.9996	0.1882	0.2291	0.2702
18	GNAL	h–0.5	0.8948	0.9777	0.9970	0.1617	0.2019	0.2391
18	KIAA1328	h–0.5	0.9065	0.9869	0.9992	0.1653	0.2128	0.2610
18	ME2	h–0.5	0.8918	0.9802	0.9983	0.1593	0.2045	0.2502
18	KIAA1772	h–0.95	0.9898	0.9997	1.0000	0.2174	0.2765	0.3330
18	PSMA8	h–0.95	0.9796	0.9980	0.9999	0.2043	0.2484	0.2909
18	RTTN	h–0.95	0.9898	0.9995	1.0000	0.2183	0.2688	0.3188
18	TXNDC10	h–0.95	0.9982	1.0000	1.0000	0.2497	0.3032	0.3559
19	FLJ23447	l–0.5	0.0005	0.0130	0.1581	-0.1151	-0.0449	0.0347
19	MYBPC2	l–0.5	0.0073	0.0239	0.0674	-0.0575	-0.0288	0.0017
19	SFRS16	l–0.5	0.0050	0.0195	0.0612	-0.0651	-0.0343	-0.0013
19	ZNF599	l–0.5	0.0018	0.0110	0.0486	-0.0873	-0.0490	-0.0082
19	BPY2IP1	h–0.5	0.9530	0.9955	0.9998	0.2065	0.2650	0.3216

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
19	C19orf25	h–0.5	0.8690	0.9769	0.9980	0.1713	0.2264	0.2813
19	CBLC	h–0.5	0.9506	0.9935	0.9995	0.2049	0.2568	0.3073
19	DDX49	h–0.5	0.8839	0.9773	0.9973	0.1760	0.2269	0.2747
19	EEF2	h–0.5	0.8921	0.9756	0.9969	0.1795	0.2249	0.2717
19	EMR1	h–0.5	0.9506	0.9897	0.9986	0.2059	0.2463	0.2866
19	EPN1	h–0.5	0.9660	0.9949	0.9996	0.2165	0.2622	0.3069
19	FCAR	h–0.5	0.8873	0.9835	0.9987	0.1772	0.2351	0.2895
19	GTF2F1	h–0.5	0.9585	0.9937	0.9994	0.2102	0.2578	0.3025
19	LIM2	h–0.5	0.9221	0.9916	0.9996	0.1906	0.2511	0.3098
19	LOC115098	h–0.5	0.9420	0.9908	0.9992	0.2004	0.2493	0.2969
19	LOC126208	h–0.5	0.9280	0.9912	0.9994	0.1930	0.2501	0.3027
19	MAP4K1	h–0.5	0.9053	0.9799	0.9973	0.1840	0.2300	0.2741
19	MGC11271	h–0.5	0.9626	0.9926	0.9992	0.2137	0.2541	0.2957
19	PGPEP1	h–0.5	0.9147	0.9859	0.9988	0.1873	0.2390	0.2894
19	PIAS4	h–0.5	0.9618	0.9946	0.9996	0.2131	0.2611	0.3074
19	PPP1R15A	h–0.5	0.9009	0.9758	0.9963	0.1824	0.2253	0.2681
19	PRKCSH	h–0.5	0.8978	0.9827	0.9984	0.1808	0.2339	0.2852
19	RASGRP4	h–0.5	0.9242	0.9823	0.9972	0.1918	0.2332	0.2741
19	TNPO2	h–0.5	0.9010	0.9833	0.9986	0.1820	0.2346	0.2871
19	TYROBP	h–0.5	0.6729	0.9752	0.9994	0.1284	0.2245	0.3048
19	ZNF444	h–0.5	0.9335	0.9857	0.9980	0.1960	0.2388	0.2799
19	ZNF560	h–0.5	0.9269	0.9905	0.9994	0.1925	0.2485	0.3039
19	ZNF653	h–0.5	0.9179	0.9932	0.9998	0.1884	0.2560	0.3192
19	ARHGEF1	h–0.95	0.9832	0.9990	1.0000	0.2348	0.2938	0.3495
19	CDC34	h–0.95	0.9784	0.9961	0.9995	0.2290	0.2677	0.3053
19	CNN1	h–0.95	0.9996	1.0000	1.0000	0.3092	0.3651	0.4170
19	FKBP8	h–0.95	0.9974	1.0000	1.0000	0.2755	0.3567	0.4256
19	LOC112703	h–0.95	0.9694	0.9975	0.9999	0.2187	0.2771	0.3310
19	PSMC4	h–0.95	0.9700	0.9961	0.9997	0.2196	0.2678	0.3142

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
19	SAMD4B	h–0.95	0.9939	0.9998	1.0000	0.2580	0.3197	0.3779
19	ZNF440L	h–0.95	0.9952	0.9998	1.0000	0.2639	0.3204	0.3741
19	ZNF93	h–0.95	0.9660	0.9985	1.0000	0.2155	0.2869	0.3506
19	ZNRF4	h–0.95	0.9748	0.9983	0.9999	0.2243	0.2847	0.3394
20	BCAS4	h–0.5	0.9511	0.9871	0.9982	0.2194	0.2588	0.3027
20	CST9	h–0.5	0.9204	0.9826	0.9976	0.2023	0.2507	0.2971
20	DEFB123	h–0.5	0.9249	0.9947	0.9999	0.2038	0.2810	0.3526
20	FLJ33706	h–0.5	0.9489	0.9961	0.9999	0.2175	0.2880	0.3500
20	PDYN	h–0.5	0.9562	0.9901	0.9985	0.2238	0.2653	0.3060
20	RNPC1	h–0.5	0.9103	0.9812	0.9974	0.1979	0.2481	0.2950
20	STK35	h–0.5	0.9651	0.9938	0.9993	0.2313	0.2767	0.3207
20	AHCY	h–0.95	0.9995	1.0000	1.0000	0.3291	0.4079	0.4767
20	BCL2L1	h–0.95	0.9709	0.9941	0.9992	0.2373	0.2781	0.3197
20	C20orf4	h–0.95	0.9998	1.0000	1.0000	0.3469	0.4151	0.4748
20	CBLN4	h–0.95	0.9986	0.9999	1.0000	0.3127	0.3579	0.3995
20	HM13	h–0.95	0.9999	1.0000	1.0000	0.3653	0.4175	0.4648
20	PSMA7	h–0.95	0.9946	0.9994	1.0000	0.2818	0.3277	0.3707
20	SRMS	h–0.95	0.9688	0.9952	0.9996	0.2337	0.2834	0.3308
20	TPX2	h–0.95	0.9697	0.9956	0.9997	0.2356	0.2848	0.3349
21	BRWD1	l–0.5	0.0016	0.0211	0.1346	-0.0542	-0.0123	0.0316
21	CHODL	h–0.5	0.7998	0.9759	0.9990	0.1226	0.1753	0.2261
21	NDUFV3	h–0.5	0.9511	0.9941	0.9997	0.1615	0.2003	0.2384
21	USP16	h–0.5	0.8572	0.9769	0.9984	0.1334	0.1761	0.2187
21	C21orf33	h–0.95	0.9733	0.9976	0.9999	0.1743	0.2142	0.2534
21	DSCR8	h–0.95	0.9715	0.9981	1.0000	0.1715	0.2174	0.2606
21	MRAP	h–0.95	0.9902	0.9994	1.0000	0.1914	0.2332	0.2736
22	PDGFB	l–0.5	0.0049	0.0232	0.0820	-0.0823	-0.0425	-0.0000
22	ADRBK2	h–0.5	0.9624	0.9939	0.9994	0.2303	0.2791	0.3269
22	CARD10	h–0.5	0.9206	0.9815	0.9969	0.2042	0.2501	0.2928

TABLE S5 – continued from previous page

Chrom.	Gene	Class.	Quant. (lb)	Quant. (median)	Quant. (ub)	ϕ_{ST} (lb)	ϕ_{ST} (median)	ϕ_{ST} (ub)
22	FAM83F	h–0.5	0.8972	0.9915	0.9997	0.1924	0.2711	0.3406
22	LIF	h–0.5	0.7590	0.9832	0.9995	0.1523	0.2531	0.3337
22	ZNF278	h–0.5	0.9363	0.9899	0.9992	0.2118	0.2670	0.3202
22	FLJ10945	h–0.95	0.9759	0.9956	0.9995	0.2442	0.2871	0.3283
22	FLJ20699	h–0.95	0.9802	0.9994	1.0000	0.2476	0.3275	0.3993
22	FLJ27365	h–0.95	0.9739	0.9937	0.9990	0.2419	0.2787	0.3157
22	MMP11	h–0.95	0.9848	0.9986	0.9999	0.2565	0.3119	0.3625
22	PKDREJ	h–0.95	1.0000	1.0000	1.0000	0.3964	0.4547	0.5044
22	ZBED4	h–0.95	0.9974	0.9998	1.0000	0.3005	0.3498	0.3996
X	CRSP2	h–0.5	0.9387	0.9837	0.9971	0.2888	0.3411	0.3935
X	EDA2R	h–0.5	0.9130	0.9907	0.9996	0.2697	0.3607	0.4439
X	FLJ20298	h–0.5	0.8873	0.9848	0.9990	0.2563	0.3435	0.4233
X	HEPH	h–0.5	0.9445	0.9910	0.9991	0.2930	0.3618	0.4247
X	IGBP1	h–0.5	0.9262	0.9779	0.9951	0.2806	0.3297	0.3778
X	ITIH5L	h–0.5	0.9379	0.9912	0.9993	0.2863	0.3625	0.4313
X	LOC158957	h–0.5	0.9322	0.9817	0.9967	0.2833	0.3369	0.3886
X	NRK	h–0.5	0.8801	0.9806	0.9981	0.2524	0.3348	0.4065
X	PRRG1	h–0.5	0.9661	0.9961	0.9998	0.3144	0.3877	0.4564
X	AR	h–0.95	0.9983	0.9998	1.0000	0.4152	0.4645	0.5098
X	GNL3L	h–0.95	0.9762	0.9980	0.9999	0.3276	0.4068	0.4786
X	GPKOW	h–0.95	0.9983	1.0000	1.0000	0.4117	0.4910	0.5563
X	MSN	h–0.95	0.9834	0.9985	0.9999	0.3410	0.4138	0.4804
X	PHKA1	h–0.95	0.9713	0.9954	0.9995	0.3207	0.3828	0.4396
X	RPL10	h–0.95	0.9726	0.9957	0.9996	0.3227	0.3850	0.4414
X	TSC22D3	h–0.95	0.9724	0.9968	0.9998	0.3217	0.3930	0.4590