Detection and replication of epistasis influencing transcription in humans

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Abstract

Epistasis is the phenomenon whereby one polymorphism's effect on a trait depends on other polymorphisms present in the genome. The extent to which epistasis influences complex traits¹ and contributes to their variation^{2,3} is a fundamental question in evolution and human genetics. Though epistasis has been demonstrated in artificial gene manipulation studies in model organisms, 4,5 and some examples have been reported in other species,⁶ few convincing examples exist for epistasis amongst natural polymorphisms in human traits.^{7,8} Its absence from empirical findings may simply be due to its low incidence in the genetic control of complex traits,^{2,3} but an alternative view is that it has previously been too technically challenging to detect due to statistical power and computational issues.⁹ Here we show that, using advanced computation techniques¹⁰ and a gene expression study design, many instances of epistasis are found between common single nucleotide polymorphisms (SNPs). In a cohort of 846 individuals with data on 7339 gene expression levels in peripheral blood, we found 501 significant pairwise epistatic interactions between common SNPs acting on the expression levels of 238 genes $(p < 2.91 \times 10^{-16})$. We tested the discovery interactions for replication in two independent data sets. 11,12 Three hundred and forty-five interactions had replication interaction p-values that were more extreme than the 2.5% confidence interval of the distribution under the null hypothesis of no epistasis, with 30 significant at a conservative p < 0.05 Bonferroni level. There was evidence of functional enrichment for the interacting SNPs, for instance 44 of the genetic interactions are located within 2Mb of regions of known intra-cellular chromosome interactions¹³ ($p = 1.8 \times 10^{-10}$). Epistatic networks of three SNPs or more influence the expression levels of 129 genes, whereby one cis-acting SNP is modulated by several transacting SNPs. For example MBNL1 is influenced by an additive effect at rs13069559 which itself is masked by trans-SNPs on 14 different chromosomes, with nearly identical genotype-phenotype (GP) maps for each cis-trans interaction. This study presents the first evidence for multiple instances of epistatic genetic effects emerging from natural genetic variation in humans.

1 Main text

In the genetic analysis of complex traits it is usual for SNP effects to be estimated using an additive model where they are assumed to contribute independently and cumulatively to the mean of a trait. This framework has been successful in identifying thousands of associations, ¹⁴ but to date there is little empirical exploration of the role that epistasis plays in the architecture of complex traits in humans, ^{7,8} though its contribution to phenotypic variance is frequently the subject of debate. ^{1–3} Outside the prism of human association studies there is evidence for epistasis, not only at the molecular scale from artificially induced mutations ⁴ but also at the evolutionary scale in fitness adaptation ¹⁵ and speciation. ¹⁶

Methods are now available to overcome the computational problems involved in searching for epistasis, but its detection still remains problematic due to reduced statistical power. For example increased dependence on linkage disequilibrium (LD) between causal SNPs and observed SNPs, ^{17,18} increased model complexity in fitting interaction terms, 19 and more extreme significance thresholds to account for increased multiple testing⁹ all make it more difficult to detect epistasis in comparison to additive effects. Thus, when combined with small genetic effect sizes, as is expected in most complex traits of interest, ¹⁴ the power to detect epistasis diminishes rapidly. There are two simple ways to overcome this problem. One is by using extremely large sample sizes;²⁰ another is by analysing traits that are likely to have large effect sizes among common variants. Because our focus was to ascertain the extent to which instances of epistasis occur amongst natural genetic variation we designed a study around the latter approach and searched for epistatic genetic effects that influence gene expression levels. Transcription levels can be measured for thousands of genes. These traits are largely heritable but on average less polygenic than high level phenotypes,²¹ thus it is expected that many genetic effects will be relatively large, maximising the chance at detecting epistasis, should it exist.

In our discovery dataset (Brisbane Systems Genetics Study, BSGS²²) of 846 individuals genotyped at 528,509 SNPs, we exhaustively tested every pair of SNPs for genetic interactions against each of 7339 expression traits in peripheral blood. After stringent filtering and multiple testing correction (Methods) we identified 501 putative genetic interactions influencing the expression levels of 238 genes (Supplementary Table 5). Of the 501 discovery interactions, 434 had available data and passed filtering (Methods) in two independent replication datasets, Fehrmann¹² and the Estonian Genomics Centre University of Tartu (EGCUT),¹¹ in which we saw convincing evidence for replication. We used the summary statistics from the replication datasets to perform a meta analysis to obtain an independent p-value for the putative interactions, and 30 were significant after applying a Bonferroni correction for multiple testing (Table 1). These significant interactions exhibited remarkable similarity in GP maps between all three datasets (Figure 2).

In addition, using the meta analysis from the replication samples only, we observed that 316 of the remaining 404 discovery SNPs had replication interaction p-values more extreme than the 2.5% confidence interval of the distribution under the null distribution of no epistatic effects ($p << 1.0 \times 10^{-16}$, Figure 3 and Supplementary Figure S1). The congruence of the epistatic networks in discovery and replication datasets is shown in Figure 1, demonstrating that these complex genetic patterns are common even across independent datasets. A further replication was attempted using the Centre for Health Discovery and Wellbeing (CHDWB) dataset, 23 but only 27 of the SNP pairs passed filtering because the sample size was small (n = 139), and likely due to insufficient power we found no evidence for replication. It should be noted that although it is a necessary step to establish the veracity of the signals from the discovery set, replication of epistasis is theoretically difficult because the dependence on LD between observed SNPs and causal variants is up to three orders of magnitude

higher than it is for independent additive effects.^{17,18} Therefore these results are encouraging with regards to the detection and replication of epistasis.

Though seldom the focus of association studies, SNPs with known main effects are often tested for additive \times additive genetic interactions, but our analysis shows that this is unlikely to be the most effective strategy for its detection. The majority of our discovery interactions comprised of one SNP that was significantly associated with the gene expression level in the discovery dataset, and one SNP that had no previous association (439 out of 501, Methods). Only nine interactions were between SNPs that both had known main effects while 64 were between SNPs that had no known main effects. Additionally, we observed that the largest epistatic variance component for the 501 interactions was equally divided amongst additive \times additive, additive \times dominance, dominance \times additive and dominance \times dominance at the discovery stage (p=0.22 for departure from expectation). This is not surprising because the patterns of epistasis used for statistical decomposition are not designed to resemble biological function. 24

Of the discovery interactions, 47 were cis-cis acting (both SNPs were on the same chromosome as the expression gene), 441 were cis-trans-acting, and 13 were trans-trans-acting. We observed a wide range of significant GP maps (Figure 2) but the most common pattern of epistasis that we detected involved a trans-SNP masking the effect of an additive cis-SNP. For example, MBNL1 (involved in RNA modification and regulation of splicing²⁵) has a cis effect at rs13069559 which in turn is controlled by 13 trans-SNPs and one cis-SNP that each exhibit a masking pattern, such that when the trans-SNP is homozygous for the masking allele the decreasing allele of the cis-SNP no longer has an effect (Supplementary Figure S5. Each of these interactions have evidence for replication in at least one dataset and six are significant at the Bonferroni level (Supplementary Figure S2). We see similar epistatic networks involving multiple trans-acting SNPs for other gene expresson levels too, for example TMEM149 (Supplementary Figure S6), NAPRT1 (Supplementary Figure S7), TRAPPC5 (Supplementary Figure S8), and CAST (Supplementary Figure S9).

In total the 501 interactions comprised 781 unique SNPs, which we analysed for functional enrichment (Methods). We tested the SNPs for cell-type specific overlap with transcriptionally active chromatin regions, tagged by histone-3-lysine-4,3-methylation (H3K4me3) chromatin marks, in 34 cell types²⁶ (Supplementary Figure S4). There was significant enrichment for cis-acting SNPs in haematopoietic cell types only ($p < 1 \times 10^{-4}$ for the three tissues with the strongest enrichment after adjusting for multiple testing). However trans-acting SNPs did not show any tissue specific enrichment (p > 0.1 for all tissues). This difference between cis and trans SNPs suggests different roles in which epistasis might arise where the cis-SNPs provide tissue specificity in these interactions. There is also strong enrichment for SNPs to be localised in enhancer regions,²⁷ consistent for both cis and trans SNPs ($p < 1 \times 10^{-6}$).

We also demonstrate spacial organisation of interacting loci suggesting a mechanism by which biological function can lead to epistatic genetic variance. It has been shown that different chromosomal regions spatially colocalise in the cell through chromatin interactions.¹³ We cross-referenced our epistatic SNPs with a map of chromosome interacting regions (n=96,139) in K562 blood cell lines²⁸ (Methods) and found that 44 epistatic interactions mapped to within 2Mb ($p<1.8\times10^{-10}$), (Supplementary Figure S10). Interaction of distant loci may occur through physical proximity in transcriptional factories that organise across different chromosome regions and can regulate transcription of related genes.^{29,30}

Though we present many instances of epistasis, quantifying its relative importance to complex traits in humans remains an open question. In this study we are able to identify 238 gene expression traits with at least one significant interaction given our experiment-wide threshold. How does this compare to the number of traits influenced by additive effects? The BSGS dataset has been previously analysed for additive effects at all expression traits, 22 and if we take all the additive eQTLs that were significant at the epistatic threshold of $p < 2.91 \times 10^{-16}$ we find that 453 gene expression levels out of the 7339 analysed had at least one significant expression quantitative trait locus (eQTL). Therefore it can be argued that the number of instances of detectable epistasis are substantial.

However in terms of their contribution to complex traits a more important metric might be the proportion of the variance that the epistatic loci explain.² Ideally one would approach this question from a whole genome perspective³¹ but this is intractable for non-additive variance components. Nevertheless, some inference can be made from the ascertained effects in these analyses and it is evident that additive variance is overall a larger component than epistatic variance, as has been argued previously.^{2,3} Taking the additive effects detected in Powell et al (2012) at the $p < 2.91 \times 10^{-16}$ threshold, we calculate that on average they explain 1.73% of the phenotypic variance of each of the 7339 probes. By contrast, the epistatic variance from the interacting SNPs detected in this study on average explain 0.25% of phenotypic variance, approximately seven times lower than the additive variance (Methods). There are several caveats to this comparison. Firstly, the ratio of additive to epistatic variance may differ at different effect sizes, and our estimate is determined by the threshold used. Secondly, the power of a 1 d.f. test exceeds that of an 8 d.f. test. And thirdly, the non-additive variance at causal variants is expected to be underestimated by observed SNPs in comparison to estimates for additive variance, due to differences in the rate of decay of the estimate of the genetic variance of the causal SNPs as LD decreases with the observed SNPs.

Overall, we have demonstrated that it is possible to identify and replicate epistasis in complex traits amongst common human variants. The bioinformatic analysis of the significant epistatic loci suggests that there are a large number of possible mechanisms that can lead to non-additive genetic variation. Further research into such epistatic effects may provide a useful framework to understanding molecular mechanisms and complex trait variation in greater detail. With computational techniques and data now widely available the search for epistasis in larger datasets for traits of broader interest is warranted.

1.1 Methods Summary

We searched for pairwise epistasis exhaustively in the BSGS discovery dataset, ²² which comprises 846 individuals who are genotyped at 528,509 autosomal SNPs and who have gene expression levels measured in peripheral blood samples for 7,339 probes representing 6,158 RefSeq genes. Recent hardware and software ¹⁰ advances made it possible to perform the 1.03×10^{15} statistical tests to complete this analysis. We used permutation analysis³² to calculate an experiment-wide significance threshold of $T_e = 2.91 \times 10^{-16}$ at the 5% family-wise error rate (FWER). SNP pairs were modelled for full genetic effects, including marginal additive and dominance at both SNPs plus four interaction terms. Though we could have used a less complex model to improve statistical efficiency, we deemed it important to be agnostic about the type of epistasis that might exist, and therefore chose not to over-parameterise the test. 18,19 Because there are many large marginal effects present in these data it was necessary to perform several filtering steps to exclude SNP pairs that were significant due to marginal effects alone. All SNP pairs with LD $r^2 > 0.1$ and $D'^2 > 0.1$ were removed to minimise the possibility of haplotype effects. All SNP pairs were required to have at least five data points in all nine genotype classes. If multiple SNP pairs were present on the same chromosomes for a particular expression trait then only the sentinal SNP pair was retained. Finally, a nested test contrasting the full genetic model against the marginal additive and dominance model was performed for each remaining SNP pair (Methods), resulting in 501 significant interactions after Bonferroni correction for multiple testing of the filtered SNPs. The significant SNP pairs were carried forward for replication in two independent datasets that used the same expression assays for analysing transcription in peripheral blood, the Fehrmann dataset (n = 1240) and the Estonian Genome Centre University of the University of Tartu (EGCUT) dataset¹¹ (n = 891). Of these, 434 passed filtering in both replication datasets. A meta analysis on the interaction p-values from each replication dataset was performed to provide an overall replication statistic for each putative interaction.

1.2 Acknowledgements

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Tables 2

Table 1: Epistatic interactions significant at the Bonferroni level in two replication sets

	Gene (chr.)	SNP 1 (chr.)	SNP 2 (chr.)	BSGS^2		-	
1	ADK (10)	rs2395095 (10)	rs10824092 (10)	6.69^{1}	18.33^{1}	21.21^{1}	39.82^{1}
2	ATP13A1 (19)	rs4284750 (19)	rs873870 (19)	5.30	12.18	3.25	14.23
3	C21ORF57 (21)	rs9978658 (21)	rs11701361 (21)	9.42	6.08	16.36	21.67
4	CSTB (21)	rs9979356 (21)	rs3761385 (21)	11.99	25.20	16.72	42.27
5	CTSC (11)	rs7930237 (11)	rs556895 (11)	7.16	18.76	15.06	33.53
6	FN3KRP (17)	rs898095 (17)	rs9892064 (17)	16.16	28.24	29.39	59.95
7	GAA (17)	rs11150847 (17)	rs12602462 (17)	13.91	19.98	12.99	32.60
8	HNRPH1 (5)	rs6894268 (5)	rs4700810 (5)	15.38	8.55	3.01	10.37
9	LAX1 (1)	rs1891432 (1)	rs10900520 (1)	19.16	18.60	11.22	29.24
10	MBNL1(3)	rs16864367 (3)	rs13079208 (3)	13.49	16.25	24.74	41.56
11	MBNL1(3)	rs7710738 (5)	rs13069559 (3)	7.92	2.55	7.89	9.28
12	MBNL1(3)	rs2030926 (6)	rs13069559 (3)	7.10	0.91	5.80	5.53
13	MBNL1(3)	rs2614467 (14)	rs13069559 (3)	5.74	4.13	2.22	5.30
14	MBNL1(3)	rs218671 (17)	rs13069559 (3)	7.63	0.62	5.82	5.23
15	MBNL1(3)	rs11981513 (7)	rs13069559 (3)	7.71	0.43	5.36	4.58
16	MBP (18)	rs8092433 (18)	rs4890876 (18)	5.40	7.06	21.91	28.73
17	NAPRT1 (8)	rs2123758 (8)	rs3889129 (8)	8.45	15.12	16.08	30.77
18	NCL (2)	rs7563453 (2)	rs4973397 (2)	7.31	7.51	6.33	12.70
19	PRMT2 (21)	rs2839372 (21)	rs11701058 (21)	4.81	0.69	4.47	4.06
20	RPL13 (16)	rs352935 (16)	rs2965817 (16)	4.98	3.79	14.41	17.24
21	SNORD14A (11)	rs2634462 (11)	rs6486334 (11)	7.31	13.11	10.96	23.22
22	TMEM149 (19)	rs807491 (19)	rs7254601 (19)	12.16	81.55	45.78	145.78
23	TMEM149 (19)	rs8106959 (19)	rs6926382 (6)	5.80	3.06	8.80	10.72
24	TMEM149 (19)	rs8106959 (19)	rs914940 (1)	6.22	3.36	6.96	9.20
25	TMEM149 (19)	rs8106959 (19)	rs2351458 (4)	7.30	0.04	9.61	8.00
26	TMEM149 (19)	rs8106959 (19)	rs6718480 (2)	8.55	3.31	5.15	7.36
27	TMEM149 (19)	rs8106959 (19)	rs1843357 (8)	6.21	3.72	3.33	6.00
28	TMEM149 (19)	rs8106959 (19)	rs9509428 (13)	9.44	0.10	5.75	4.47
29	TRA2A (7)	rs7776572 (7)	rs11770192 (7)	8.23	3.19	1.89	4.09
30	VASP (19)	rs1264226 (19)	rs2276470 (19)	5.09	0.94	5.14	4.95

 $^{^{1}}$ $-\log_{10} p$ -values for 4 d.f. interaction tests 2 Discovery dataset

 ³ Independent replication dataset
 ⁴ Meta analysis of interaction terms between replication datasets only

3 Figures

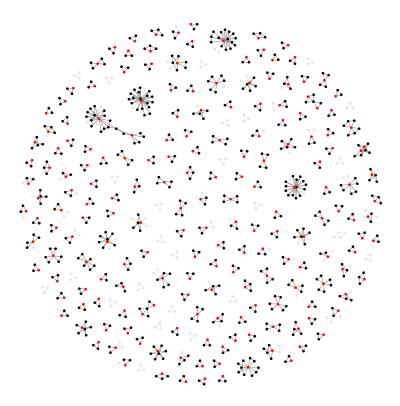


Figure 1: Discovery and replication of epistatic networks All 434 putative genetic interactions (edges) with data common to discovery and replication sets is shown, where black nodes represent SNPs and red nodes represent traits (gene expression probes). Three hundred and forty-five interactions had p-values exceeding the 2.5% confidence interval following meta analysis of the replication data, but the remaining 89 interactions that did not replicate are depicted in grey. It is evident that a large proportion of the complex networks identified in the discovery set also exist in independent populations.

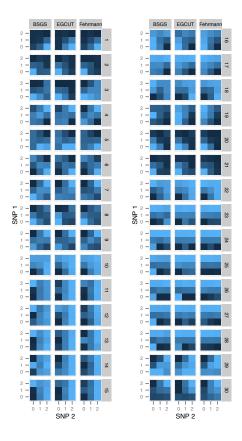


Figure 2: Replication of GP maps in two independent populations The GP maps for each epistatic interaction that is significant at the Bonferroni level in both replication datasets are shown. Each GP map consists of nine tiles where each tile represents the expression level for that two-locus genotype class. Phenotypes are for gene transcript levels (dark coloured tiles = low expression, light coloured tiles = high expression). Columns of GP maps are for each independent population. Rows of GP maps are for each of 30 significantly replicated interactions at the Bonferroni level, corresponding to the rows in Table 1. There is a clear trend of the GP maps replicating across all three datasets.

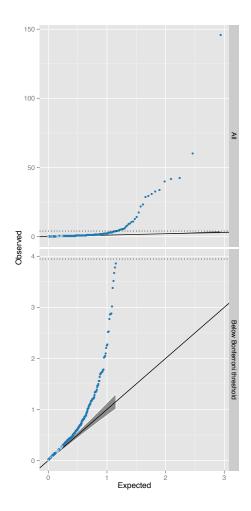


Figure 3: Q-Q plots of interaction p-values from replication datasets. The top panel shows all 434 discovery SNPs that were tested for interactions. Observed p-values (y-axis, $-\log_{10}$ scale) are plotted against the expected p-values (x-axis, $-\log_{10}$ scale). The multiple testing correction threshold for significance following Bonferroni correction is denoted by a dotted line. The bottom panel shows the same data as the top panel but excluding the 30 interactions that were significant at the Bonferroni level in the replication datasets. The shaded grey area represents the 5% confidence interval for the expected distribution of p-values. Dark blue points represent p-values that exceed the confidence interval, light blue are within the confidence interval.

4 Supplementary Figures

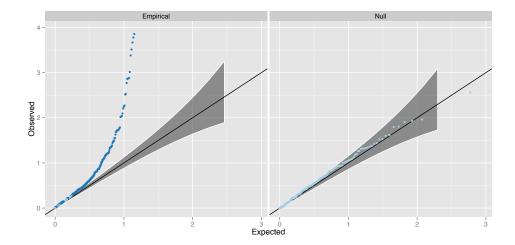


Figure S1: Q-Q plots of interaction p-values from replication datasets, excluding the 30 points significant at the Bonferroni level The right panel (Null) shows the interaction p-values from a meta analysis across two independent datasets on 434 randomly drawn SNP pairs. The left panel (Empirical) shows the interaction p-values from the 404 putative interactions that were not significant at the Bonferroni correction threshold. Dark blue points represent p-values that surpass the 2.5% FDR level, as in Figure 3.

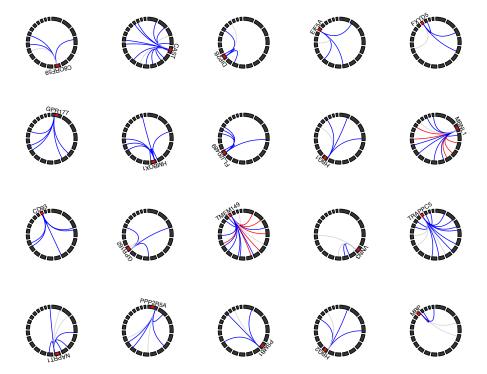


Figure S2: Gene expression traits with four or more genetic interactions Circle plots represent the genomic positions for SNPs (linking lines) and expression probes (red points). Chromosomes are represented by black blocks and ordered from 1 to 22 clockwise, starting from the top. Grey lines represent no evidence for replication, blue lines denote interactions that are outside the 97.5% confidence interval or the Q-Q plot (Figure 3), and red lines denote replication at the Bonferroni correction level. Most interactions are characterised as being *cis-trans* to the expression probe.

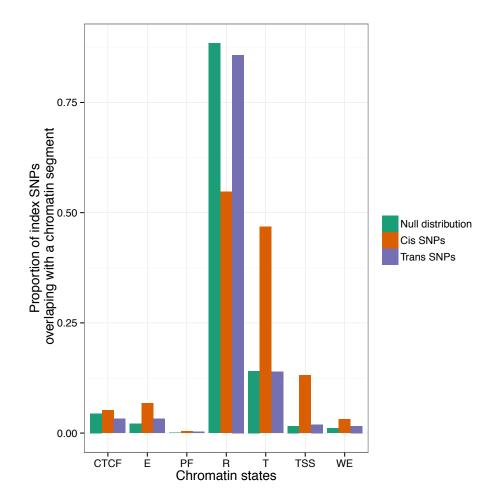


Figure S3: Location of SNPs relative to genomic features All SNPs within 1Mb and $r^2 > 0.8$ of each cis- and trans-SNP were taken to find which genomic features (x-axis) were covered by the SNPs that compose the 501 significant interactions. Green bars represent the proportion (y-axis) of the 528,509 SNPs used in the analysis that fall within the range of the different genomic features. There is enrichment for cis-acting SNPs (red bars) in promotor regions, but trans-acting SNPs (blue bars) are not enriched for genomic features. The labels on the x-axis are as follows: TSS = Predicted promoter region including TSS, PF = Predicted promoter flanking region, E = Predicted enhancer, WE = Predicted weak enhancer or open chromatin cis regulatory element, CTCF = CTCF enriched element, T = Predicted transcribed region, R = Predicted Repressed or Low Activity region

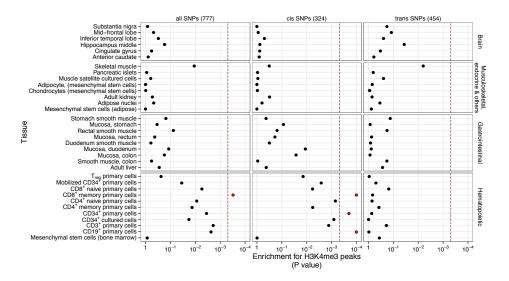


Figure S4: Tissue specific enrichment of SNPs in transcriptionally active regions The locations of transcriptional activity can be predicted by chromatin marks, assayed by H3K4me3.²⁶ Enrichment *p*-values are calculated using permutation analysis for 34 different cell types (*y*-axis) in four tissue types (Rows of boxes). There is enrichment for *cis*-acting SNPs in Haematopoietic tissue types only. *Trans*-acting SNPs have no tissue specificity.

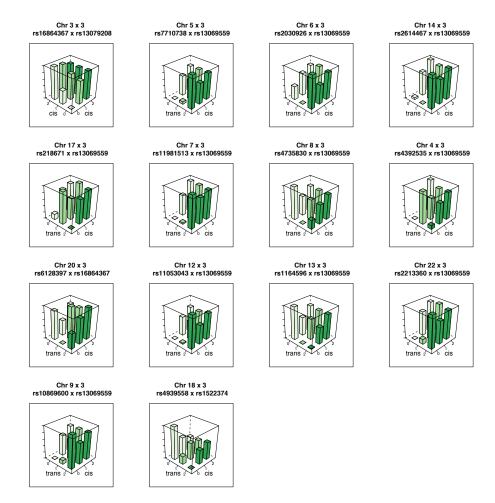


Figure S5: Genotype-phenotype maps for 14 interactions influencing the expression of MBNL1 Each bar represents the mean phenotypic value for individuals in that genotype class. The rs13069559 SNP typically has a *cis*-additive decreasing effect on the expression of MBNL1, but in many of these interactions the *cis* effect is masked when the *trans* SNP is homozygous.

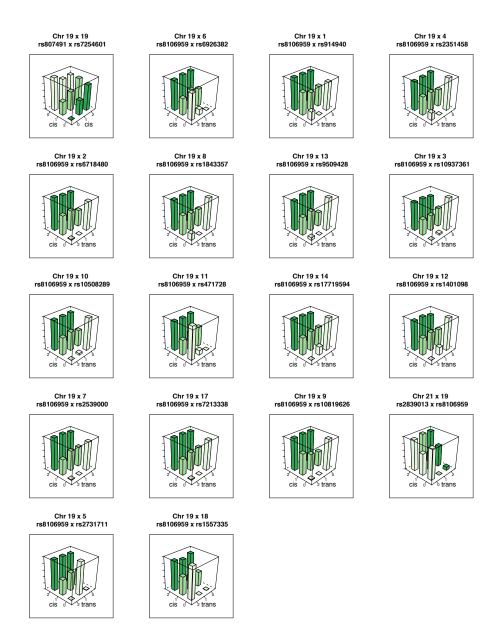


Figure S6: Genotype-phenotype maps for 19 interactions influencing the expression of TMEM149 Each bar represents the mean phenotypic value for individuals in that genotype class. The rs13069559 SNP typically has a *cis*-additive decreasing effect on the expression of TMEM149, but in many of these interactions the *cis* effect is masked when the *trans* SNP is homozygous.

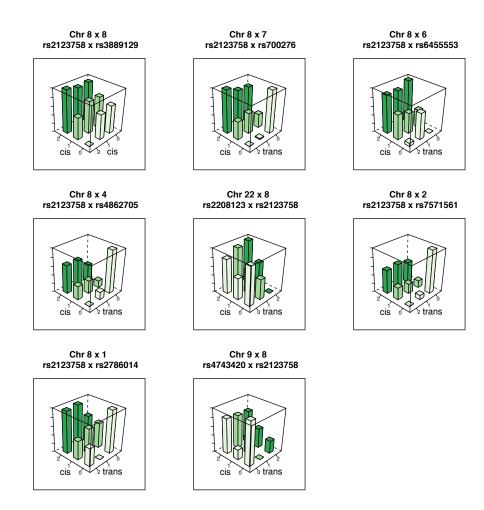


Figure S7: Genotype-phenotype maps for 8 interactions influencing the expression of NAPRT1 Each bar represents the mean phenotypic value for individuals in that genotype class.

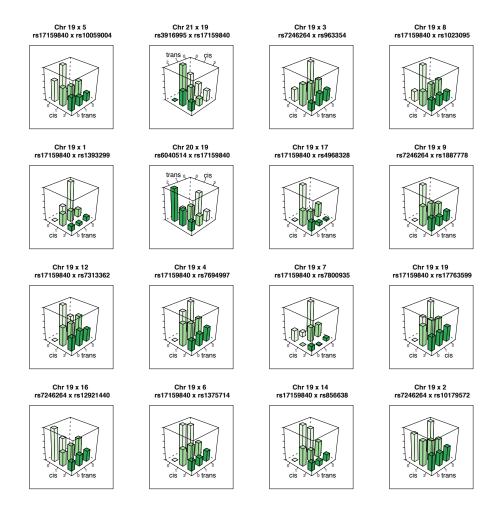


Figure S8: Genotype-phenotype maps for 16 interactions influencing the expression of TRAPPC5 Each bar represents the mean phenotypic value for individuals in that genotype class.

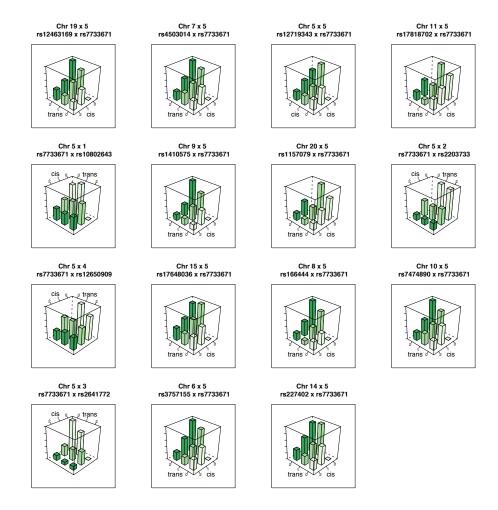


Figure S9: Genotype-phenotype maps for 15 interactions influencing the expression of CAST Each bar represents the mean phenotypic value for individuals in that genotype class.

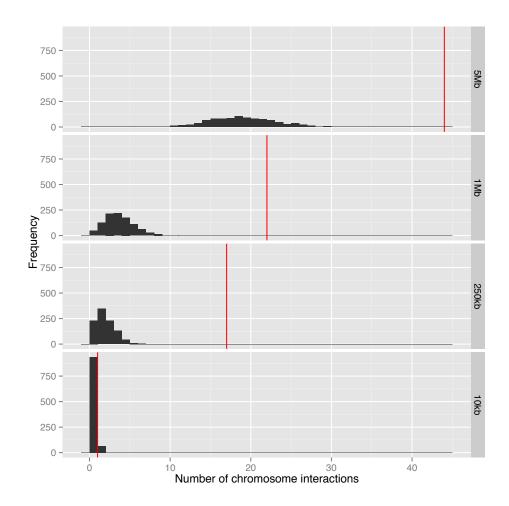


Figure S10: Number of overlaps between chromosome interactions and epistatic interactions Interacting chromosome regions may be a possible mechanism underlying epistatic interactions. The number of epistatic interactions within 20kb, 500kb, 2Mb and 10Mb of known chromosome interacting regions are shown by red vertical lines. The histograms represent the null distribution based on random sampling of 10,000 datasets for each window size.

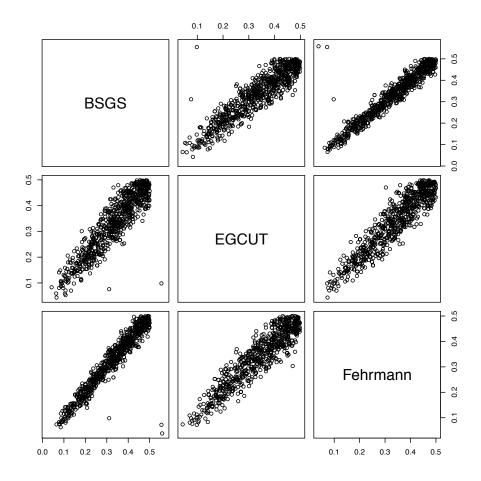


Figure S11: Comparison of allele frequencies for 781 SNPs involved in genetic interactions across independent populations Outliers were removed from the analysis as part of the filtering stage during replication.

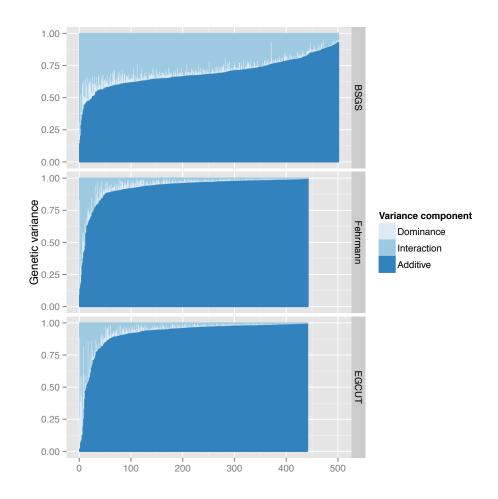


Figure S12: Comparison of variance distribution from different cohorts How does the estimated variance decomposition change in different cohorts? The cumulative proportion of the genetic variance that is additive, dominant, or epistatic for each putative interaction is shown on the y-axis. BSGS has 501 interactions whereas Fehrmann and EGCUT have 434 (x-axis). The variance estimates are ordered from lowest additive to highest additive proportion. This is done independently for each cohort to depict the distribution of estimated effects.

5 Supplementary Tables

Table S1: Details on 501 interactions discovered in BSGS dataset

E	Expression trait				SNP 1				SNP 2		Intera	ction statistic	/ - log10 p-	values	
Gene IDa	Probe ID ^b	Chr.	rs ID	Chr.	Pos/Mb ^c	Associationd	rs ID	Chr.	Pos/Mb ^c	Associationd	BSGS ^e	Fehrmannf	EGCUT	Metag	Distance / Mbh
ABCA7	ILMN_1743205	19	rs3752237	19	1047161	ABCA7	rs596183	6	158100199	1100001401011	5.82	0.38	0.02	0.09	Bistance / Mis
ABCA7	ILMN_1743205	19	rs3752237	19	1047161	ABCA7	rs914737	9	139522101		5.50	0.00	0.02	0.00	
ABCC3	ILMN_1677814	17	rs9455	17	48771135	ABCC3	rs4732202	7	136057883		6.10	0.02	1.81	0.95	
ACAT1	ILMN_1800008	11	rs227064	11	108207393	ACAT1	rs4744894	9	72001517		6.59	1.04	1.78	2.02	
ADCK1	ILMN_1698777	14	rs12431896	14	78088813	ADCK1	rs4833241	4	122933691		5.59	0.36	1.14	0.87	
ADCK1	ILMN_1698777	14	rs8058066	16	88462550	MDOMI	rs12431896	14	78088813	ADCK1	6.58	2.04	0.83	2.05	
ADK	ILMN_2358626	10	rs2395095	10	76446305	ADK	rs10824092	10	75929517	ADORT	6.69	18.33	21.21	39.82	0.517
AGAP6	ILMN_3239130	10	rs2611512	10	51515534	AGAP8	rs2547996	5	95174319		6.22	10.00	21.21	33.02	0.011
AHSA2	ILMN_1798308	2	rs10881585	9	137112421	710711 0	rs842647	2	61119471		7.15	1.83	1.93	2.88	
AHSA2	ILMN_1798308	2	rs2523971	6	29938258	HLA-G	rs1177303	2	61388355	AHSA2	5.45	0.92	0.64	0.94	
AKTIP	ILMN_1665982	16	rs2896940	16	57721127	IILA-G	rs13332406	16	53489705	AKTIP	6.91	0.16	0.99	0.54	4.231
AKTIP	ILMN_1665982	16	rs7189819	16	53536345	AKTIP	rs1362032	7	125543391	AKIII	5.93	0.71	0.20	0.42	4.231
AKTIP	ILMN_1665982	16	rs7189819	16	53536345	AKTIP	rs1473017	4	179323762		6.18	0.71	0.20	0.42	
ALDH3A2	ILMN_2401641	17		17	19581009	ALDH3A2	rs11720112	3	161996349		6.26	0.27	1.37	1.01	
ANG	ILMN_1760727	14	rs3760489		21153299	ALDHSAZ	rs4866516		3032625		5.75	0.02	0.20		
ANPEP		14	rs9322855	14		ANPEP		5 7						0.04	
ANPEP	ILMN_1763837	15	rs11073891	15 15	90363995	ANPEP	rs3823523		154511163		5.85 6.31	$0.44 \\ 0.47$	1.09	0.90	
AP3B1	ILMN_1763837	15 5	rs11073891		90363995	AP3B1	rs6846031	4	178019148		5.94		0.17	0.26	
	ILMN_1768867		rs6453374	5	77508159		rs4684443	3	4818792			0.05	1.00	1.10	
APPL2 ARL17B	ILMN_1765076	12 17	rs935251	12 17	105580918	APPL2	rs2769594	9	87918528	ADI 15D	5.60	0.80	1.02	1.16	01 700
	ILMN_3231952		rs12947580		75768225		rs8079215	17	44064851	ARL17B	5.96				31.703
ARL17B	ILMN_3231952	17	rs2834541	21	35932619	4 D7 4 ED	rs8079215	17	44064851	ARL17B	6.65				
ARL17B	ILMN_3231952	17	rs8079215	17	44064851	ARL17B	rs1950646	14	94722497		7.64				
ARL17B	ILMN_3231952	17	rs8079215	17	44064851	ARL17B	rs2197777	12	125831219		6.26				
ARL17B	ILMN_3231952	17	rs8079215	17	44064851	ARL17B	rs2684789	15	99492045		5.98				
ARL17B	ILMN_3231952	17	rs8079215	17	44064851	ARL17B	rs9834627	3	191203546		5.72				
ATP13A1	ILMN_2134224	19	rs4284750	19	19810050		rs873870	19	19738554		5.30	12.18	3.25	14.23	0.071
BID	ILMN_1763386	22	rs8919	22	18213057	BID	rs9804943	12	129906275		5.84	0.06	0.40	0.14	
BID	ILMN_2372413	22	rs181405	22	18233000		rs10888267	1	248059423		6.60	0.87	0.16	0.50	
C11ORF17	ILMN_1752988	11	rs2568061	11	8886260	C11ORF17	rs6553184	4	189150656		5.66	1.15	0.04	0.54	
C13ORF18	ILMN_2196550	13	rs2110603	16	6259852		rs674754	13	46913416	C13ORF18	6.66	0.28	0.28	0.22	
C13ORF18	ILMN_2196550	13	rs674754	13	46913416	C13ORF18	rs6857876	4	153610164		3.87	0.38	0.50	0.43	
C14ORF173	ILMN_2393450	14	rs11089825	22	37575398		rs4983382	14	105189504	C14ORF173	6.02	0.60	0.84	0.85	
C14ORF173	ILMN_2393450	14	rs3935344	15	92276674		rs4983382	14	105189504	C14ORF173	5.98	0.31	0.28	0.24	
C14ORF173	ILMN_2393450	14	rs4983382	14	105189504	C14ORF173	rs10754644	1	238724741		7.15	0.42	0.34	0.35	
C14ORF4	ILMN_1804396	14	rs1293455	18	13819673		rs2655991	14	77574438		4.87				
C14ORF4	ILMN_1804396	14	rs2655991	14	77574438		rs10972462	9	35427324		4.32				
C14ORF4	ILMN_1804396	14	rs2655991	14	77574438		rs6445340	3	63371601		4.40				
C14ORF4	ILMN_1804396	14	rs2655991	14	77574438		rs9787151	1	63179138		4.05				
C14ORF4	ILMN_1804396	14	rs4793445	17	70416307		rs2655991	14	77574438		3.85				
C14ORF4	ILMN_1804396	14	rs6010061	22	51151724		rs2655991	14	77574438		4.61				
C14ORF4	ILMN_1804396	14	rs7245800	19	52083552		rs2655991	14	77574438		4.69				
C17ORF60	ILMN_1747347	17	rs9907897	17	63502633		rs7405659	17		C17ORF60	6.79	0.53	0.05	0.19	
C1ORF86	ILMN_1726989	1	rs2334323	6	110577257		rs2257182	1	2082566	C1ORF86	5.90	0.01	0.50	0.13	
C1ORF86	ILMN_2097790	1	rs2279474	18	46384412		rs2460002	1	2119833	C1ORF86	5.65		0.03		
C1ORF86	ILMN_2097790	1	rs7188668	16	25711358		rs2460002	1	2119833	C1ORF86	5.59	0.29	0.50	0.37	
C21ORF57	ILMN_1795836	21	rs4819271	21	48052838		rs901964	12	48676038	ZNF641	4.91	0.65	0.08	0.28	
C21ORF57	ILMN_1795836	21	rs9978658	21	48027084		rs11701361	21	47764477		9.42	6.08	16.36	21.67	0.263
C5ORF4	ILMN_1728742	5	rs1122762	18	45866512		rs286595	5	154348552	C5ORF4	5.55	0.72	0.04	0.27	
C8ORF59	ILMN_1653205	8	rs12429804	13	36577930		rs2896452	8	86102223	C8ORF59	5.49	0.29	0.02	0.07	
C8ORF59	ILMN_1653205	8	rs12454561	18	31272238		rs2896452	8	86102223	C8ORF59	5.45	0.31			
C8ORF59	ILMN_1653205	8	rs2896452	8	86102223	C8ORF59	rs1004564	4	55242625		7.62	0.38	0.18	0.21	
C8ORF59	ILMN_1653205	8	rs7152284	14	52273663		rs2896452	8	86102223	C8ORF59	5.67	2.18	0.07	1.33	

Continued on next page

Column C	Expression trait				SNP 1				SNP 2		Interact	Interaction statistic /	$-\log_{10} p$ -values	values	
ILANY 172232 1	Probe ID ^b	Chr.	rs ID	Chr.	$\mathrm{Pos/Mb}^{\mathrm{c}}$	Associationd	rs ID	Chr.	Pos/Mb^{c}		$BSGS^{e}$	$Fehrmann^{f}$	$EGCUT^{f}$	Metag	Distance / Mbh
ILANI 177234 1 147266847 10 19398885 1 14706680 1 1470680	ILMN_165320	ω c	rs8051751	16	7188323	000 000 000 000 000 000 000 000 000 00	rs2896452	∞ -	86102223	C8ORF59	5.79	1.39	0.18	0.87	
ILMN 1772233 0 mis2077364 10 10020601 10020	ILMN-174188	- -	rs12765847	6 C	4353908	CSORFIZ	rs25256598		227174210	CABC1	6.36	0.95	0.01	0.37	
ILMN.177234	ILMN_171253	2 9	rs4266763	6	139289825	INPP5E	rs684040	-	82128660		5.81			,	
HANKLYTYTA A STATEMAN	ILMN_171253	2 9	rs4573661	11	6026661		rs4077515	6	139266496	INPP5E	6.61	0.09	0.86	0.42	
ILMN 1777234 5 mi21090344 10 5 5 5 5 5 5 5 5 5	ILMN_171723	4 ·	rs1157079	50	6778978		rs7733671	ı, ı	96000269	CAST	7.07	0.23	0.96	0.62	
ILANIA 177234 5 First 17524 5 Fi	ILMN-171723	4. 44 0. 70	rs12463169	19	81840122		rs7733671	010	96000269	CASI	2.73	0.02	2.00	1.79	
ILMN.177234 5 mi10f644 8 78936769 mi773871 5 90000260 CAST 7 6 5 0 13 144 14	ILMN_171723	. 4-	rs12719343	2 10	125369113		rs7733671	, rc	96000269	CAST	7.68	0.36	1.57	1.20	29.369
ILMN.177234 5	ILMN_171723	4 5	rs1410575	6	78255630		rs7733671	n	96000269	CAST	6.55	0.13	1.34	0.78	
ILMN.177244 5 mid746905 15 27311111 mid733671 5 5 5 5 5 5 5 5 5	ILMN_171723		rs166444	œ	78392770		rs7733671	ıO	96000269	CAST	7.01	0.27	0.52	0.37	
ILMN.177234	ILMN_171723		rs17648036	15	27311111		rs7733671	ю	96000269	CAST	7.81	0.97	0.03	0.41	
Image: column Image: colum	ILMN_171723	4 5	rs17818702	11	86107920		rs7733671	ю	96000269	CAST	6.62	1.15	0.59	1.09	
ILANIA 177234 5 ma22212 6 136448509 ma7733671 5 96000260 CAST 6.87 0.07 0.33 ma7733671 1.06 0.000260 CAST 0.87 0.07 0.03 ma7733671 0.05 0.0000260 CAST 0.07 0.03 ma7733671 0.05 0.0000260 CAST 0.07 0	ILMN_171723		rs227402	14	70496867		rs7733671	ю	96000269	CAST	6.12	0.11	0.01	0.01	
ILANN_1717234 5 ms4577155 6 104654869 ms7733671 5 90000269 CAST 5.84 0.07 0.12 ILANN_1717234 5 ms4577155 ms4773671 5 90000269 CAST 5.84 0.07 0.12 ILANN_1717234 5 ms4773671 5 90000269 CAST ms7733671 5 90000269 CAST 7.42 0.23 0.78 ILANN_1717234 5 ms7733671 5 90000269 CAST ms2733671 5 90000269 CAST ms27056009 4 17012880 CAST ms2705609 4 17012880 CAST ms270599 Ms2705609 4 17012880 CAST ms270599	ILMN_171723		rs2822124	21	15166804		rs7733671	ю	96000269	CAST	6.87				
ILANN 1717234 5 m ² 4744890 7 311944 m ² 47733671 5 96000269 CAST 5 85.8 0.92 1.66 1.1	ILMN_171723		rs3757155	9	136458593		rs7733671	ю	96000269	CAST	7.24	0.07	0.33	0.12	
ILMN_177234 5 rar733671 5 specimen rar732671 5 specimen rar732671 5 specimen rar732671 5 specimen rar	ILMN_171723		rs4503014	-1	31149140		rs7733671	10	96000269	CAST	800	0.92	1.56	1.72	
ILMN.177234 5 irity234 5 irity2345 5 irity2345 5 irity234 5	II.MN 171723		rs7474890	10	59590078		rs7733671	r:	96000269	CAST	6.74	0.49	0.12	0.23	
ILMN.1777244	II.MN 171723		rs7733671	100	96000369	TSAC	rs10802643	-	238120177		7 42	0.75	0.78	0 93	
IMAN_177724	ILMN 171753		1223671	'n	08000000	FV	re19650a0a		170102800		7 45	0.00	4 - 0	25.0	
ILMN.1772244 5 ar77732671 18 ar7772248 1 ar772248 ar7	00111111111111111111111111111111111111	# -	1200011) M	08000080	Euro	1012000000	* 0	224002101		110	000	0.0	0.0	
Image: Cape	00111111111111111111111111111111111111	# -	1200011) M	08000080	Euro	2000000	10	105591941		0.0	200	90.0	. O	
IMAN_177208	TI NEW TOTAGE	0 -	127.000.1 1000.1	0 0	90000209	CASI	1100001	0 :	190001041	E	0.30	0.19	0.20	0.10	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	٠,		rs872311	x0 ;	98867.199		rs11032695	Π;	34447586	CAI	6.41	0.26	0.30	0.22	
Image: Column Image: Colum	-		rs2353203	19	17099980		rs541207	11	64125142	CCDC88B	2.68	0.33	0.37	0.31	
LIMN.1764763 7 ra3211834 7 re02011 ref700168 1 7 re3211834 7 re02011 ref700163 1 7 red201834 7 red20400 2 854565 2 0.058 0.018 0.024 ILMN.1704730 20 re1884655 2.0 2.2074375 CD93 re46067266 4 157182040 6.06 1.74 0.024 ILMN.1704730 20 re1884655 2.0 2.2074375 CD93 re46067266 4 7.075025 6.06 1.74 0.024 ILMN.170470 20 re1884655 2.0 2.2074375 CD93 re4843472 2.0 0.04 0.024 ILMN.170470 20 re4813479 2.0 2.20776914 CD93 re1884655 2.0 2.0076914 CD93 re1884655 2.0 2.0076914 CD93 re1884656 0.04 0.71 0.04 0.07 ILMN.170470 20 re4813479 2.0 2.20776914 CD93	_		rs694739	11	64097233	CCDC88B	rs12771349	10	96998193		5.62	0.23	0.18	0.14	
ILMN 1.1804730 1 ref506601 1 ref5062334 CD55 5 0.9 0.03 0.03 ILMN 1.1804730 2 ref106601 1 ref10625470 7 1 207620234 CD55 5 0.9 0.04 0.24 ILMN 1.704730 20 ref1864655 2 2 2.0 23974375 CD93 ref22566 3 1 20542639 5 5.71 0.04 0.24 ILMN 1.704730 20 ref186465 2 0 23774775 CD93 ref186465 2 0 23774775 CD93 ref186463 2 0 23774775 0 23774775 0 23774747 0 23774747 0 23774747 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 2377474 0 237747	ILMN_178486	3	rs3211834	-	80280117		rs1254900	7	85816334	VAMP8	6.93	0.15	0.01	0.02	
LIMN.1704730 20 rsi884655 20 23074375 CD93 rsi025540 4 157182040 6.06 1.74 0.24 ILMN.1704730 20 rsi884655 20 23074375 CD93 rs4696756 4 16721395 5.71 0.13 0.80 ILMN.1704730 20 rsi884655 20 23074375 CD93 rs88875 13 16671395 6.06 0.71 0.80 ILMN.1704730 20 rsi884655 20 23074375 CD93 rs8884654 1 288889900 6.06 0.71 0.20 ILMN.1704730 20 rs4813479 20 23076914 CD93 rs4884347 1 288889900 7.43 0.71 0.22 ILMN.1704730 20 rs4813479 20 23076914 CD93 rs473485 8 16506054 7.02 0.71 0.75 ILMN.1704730 20 rs4813479 20 23076914 CD93 rs474482 CD93 7.43	ILMN_180054		rs750801	11	76033374		rs6700168	1	207502534	CD55	5.09	80.0	0.03	0.02	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	ILMN_170473		rs1884655	20	23074375	CD93	rs10255470	-	157182040		90.9	1.74	0.24	1.20	
HANN LY07430 20 rst884655 20 23074375 CD93 rst7622560 3 196721395 5.56 0.04 0.27 HANN LY074730 20 rst884655 20 23074375 CD93 rst854658 13 15.54 0.71 0.27 HANN LY074730 20 rst813479 20 23076914 CD93 rst834475 CD93 15.68 0.71 0.75 HAN LY074730 20 rst813479 20 23076914 CD93 rst82899903 7.72 0.07 0.75 HAN LY04730 20 rst813479 20 23076914 CD93 rst8265420 8 15600054 0.75 0.76 HAN LY04730 20 rst813479 20 23076914 CD93 rst826542 0.36 6.13 0.74 0.75 HAN LYARSA 20 23076914 CD93 rst8285421 1 7.7864482 6.13 0.04 0.75 HAN LYARSA 20 23076914 CD93	ILMN_170473		rs1884655	20	23074375	CD93	rs4696726	4	7992632		5.71	0.13	08.0	0.42	
ILMN 1704730 20 rsl888465 20 23074375 CD93 rss88865 12 25145594 6.31 0.24 1.67 ILMN 1704730 20 rsl884655 20 23074375 CD93 rsl884655 20 23074375 CD93 rsl884655 20 23074375 CD93 rsl884655 20 23076914 CD93 rsl884969 7.02 30	ILMN_170473		rs1884655	20	23074375	CD93	rs7622580	က	196721395		5.56	0.04	0.27	80.0	
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	ILMN_170473		rs1884655	20	23074375	CD93	rs838875	12	125145394		6.31	0.24	1.67	1.16	
ILMN.1704730 20 rs2866504 20 37771578 Code 0.75 ILMN.1704730 20 rs286504 20 37771578 1 28898903 7.43 0.64 0.75 ILMN.1704730 20 rs4813479 20 23076914 CD93 rs4813470 1 28899903 7.43 0.75 ILMN.1704730 20 rs4813479 20 23076914 CD93 rs485981 18 74439642 6.13 6.13 0.75 ILMN.1704730 20 rs4813479 20 23076914 CD93 rs485981 18 74439642 6.18 6.18 0.21 0.75 ILMN.173704780 13 rs861544 14 104162263 HOXB2 rs4803481 19 4206656 CEACAM21 6.15 0.07 0.12 ILMN.1745949 19 rs6605780 14 101360228 rs4803481 19 4206656 CEACAM21 6.15 0.24 0.05 ILMN.1763794 15	ILMN_170473		rs1884655	20	23074375	CD93	rs9576388	13	38434472		7.88	0.71	0.22	0.45	
ILMN 1704730 20 rs4813479 20 23076914 CD93 rs28393003 7.43 7.43 ILMN 1704730 20 rs4813479 20 23076914 CD93 rs2873420 8 15600554 7.02 ILMN 1704730 20 rs4813479 20 23076914 CD93 rs438531 18 7443642 6.13 7.03 ILMN 1704730 20 rs4813479 20 23076914 CD93 rs438531 18 7443642 6.13 6.13 ILMN 1704730 20 rs481474 CD93 rs4324744 17 7726448 6.13 7.03 ILMN 1704734 17 rs48048 17 464102 HOXB2 rs4324744 17 7726488 6.15 0.13 ILMN 170474 18 rs480481 19 42066556 CEACAM21 18 4147766 AIA 6.15 0.12 ILMN 1704764 18 rs480481 19 42066556 CEACAM21 18 4147766	ILMN_170473		rs2868504	20	37771578		rs1884655	20	23074375	CD93	5.71	0.64	0.75	0.81	14.697
$ \begin{array}{l l l l l l l l l l l l l l l l l l l $	ILMN_170473		rs4813479	20	23076914	CD93	rs10925747	Т	238899903		7.43				
ILMN_1709730 20 rs4813479 20 23076914 CD93 rs438531 18 74435642 6.13 ILMN_1704730 20 rs4813479 20 23076914 CD93 rs438531 17 7746482 6.13 6.13 ILMN_1704730 13 rs861544 14 104162263 CD93 rs4732474 13 715008038 CDC16 5.46 0.21 0.14 ILMN_1776349 19 rs8010699 20 51966250 CDC16 5.47 0.99 0.12 ILMN_1776349 19 rs8010699 12 4104102 HOXB2 rs41050 5 15843044 6.15 0.10 0.12 ILMN_176949 19 rs820569 14 101350298 CEP192 rs133719 3 13424770 ANAPC13 6.36 0.23 0.10 ILMN_176379 12 rs8196778 13 38883122 CEP192 rs2324868 0.02 0.12 0.10 ILMN_176379 12	ILMN_170473		rs4813479	20	23076914	CD93	rs2873420	œ	136500554		7.02				
$ \begin{array}{c ccccccccccccccccccccccccccccccccccc$	ILMN_170473		rs4813479	20	23076914	CD93	rs4328531	18	74439542		6.13				
ILMN 1239096 13 rs861644 14 104162263 Fr7324744 13 115008038 CDC16 5,46 0.21 0.01 ILMN 1230928 17 rs906090 20 51956250 CEACAM21 19 4206656 CEACAM21 6,15 0.07 0.07 ILMN 1745949 19 rs8205690 10 51956250 CEACAM21 19 4206656 CEACAM21 6,15 0.09 0.12 ILMN 1745949 19 rs820569 14 101300288 rs1332719 4 10466566 CEACAM21 6,15 0.09 0.15 ILMN 170374 16 rs820569 14 101330298 rs1332719 3 13447706 ANAPC13 6,36 0.23 0.10 ILMN 1202294 12 rs813122 rs201077 12 rs201077 12 rs20107	ILMN_170473		rs4813479	20	23076914	CD93	rs4789981	17	77264482		80.9				
ILMN_175028 17 re9905640 17 46614102 HOXB2 re1165631 17 30833162 CDK6R11 5.47 0.95 0.07 ILMN_1745949 19 re3600699 20 4206656 CEACAM21 4 18026566 CEACAM21 6.15 0.12 0.12 ILMN_1745949 19 re3600699 18 13069782 CEP192 re2431060 5 18 13069782 CEP192 re343044 6.67 2.16 0.12 ILMN_1757084 18 re361967 13 3883812 CEP192 13424770 3444770 6.36 0.10 0.10 ILMN_1250240 12 re361967 13 3883812 CEP192 re370788 2.3554862 CEP7 0.10 0.10 ILMN_250240 12 re5639014 12 10227772 CEP7 1 0.10 0.10 ILMN_163142 12 10156646 re53903088 10 13423668 CEPC12A 5.55 0.05 0.07	ILMN_233979		rs861544	14	104162263		rs7324744	13	115008038	CDC16	5.46	0.21	0.14	0.11	
ILMN_1745949 19 rs200669 20 5196526 CEACAM21 rs24803481 19 4206656 CEACAM21 6.15 0.90 0.12 ILMN_1745949 19 rs200656 CEACAM21 rs2490344 6.15 0.16 0.16 ILMN_175949 18 rs6505780 18 13069782 CEP192 rs1313719 4 18026526 6.75 0.15 0.16 ILMN_177808 18 rs6819267 13 3888122 CEP192 3 13424706 ANAPC13 6.36 0.23 0.10 ILMN_2502940 12 rs691967 13 3888122 ceS1 7 7 0.15 0.24 ILMN_2502940 12 rs673788 12 10208784 CHPT1 5,74 0,72 0.20 ILMN_263122 12 rs73788 12 10208784 CHPT1 5,74 0,72 0.20 ILMN_163142 12 10247782 rs7332388 10 13423668 CICE12A	_		rs9905940	17	46614102	HOXB2	rs11655031	17	30833162	CDK5R1	5.47	0.95	0.07	0.45	15.781
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ILMN.17037804	_		rs4803481	19	42066556	CEACAM21	rs2421050	ю	158943044		6.67	2.16	0.16	1.44	
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ILMN.2202945 16 rss8192935 16 5864794 CES1 rss20652900 12 rss2048562 15 5.65 0.77 0.20 ILMN.2202940 12 rss203014 12 102277782 rss2065290 12 10227782 13 10227782 14 15 10227782 15 10227782 15 10227782 17 10227782 17 10227782 17 1026646 rss2065304 18 rss205054 19 rss705054 19 rss705054 19 rss705054 19 rss705054 19 rss705057 19 rss705057 19 rss705057 19 rss705057 19 rss705057 10 rss705057 19 rss705057 10 rs	ILMN_178780		rs3825569	14	101350298		rs13079012	3	134247706	ANAPC13	6.36	0.23	0.10	0.09	
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FLIZO489	Expression trait		l			SNP 1	:			SNP 2	:	Intera	Interaction statistic	/ -log10 p-values	values	
FL FL FL FL FL FL FL FL	Probe ID ^D Chr. rs ID Chr.	rs ID		Chr.		Pos/Mb^{c}	Association	rs ID	Chr.	Pos/Mb^{c}	Association	$BSGS^{e}$	$Fehrmann^{I}$	$EGCUT^{I}$	Metag	Distance / Mb ⁿ
FL120489	2 rs2356400 19	. 19	. 19		44	44321776		rs13406184	2	36791226	FEZ2	5.78	0.14	0.33	0.16	
PLJ20489 H8572208	ILMIN_1739586	1 4 1	1 4 1	_	4620	3132		rs11691600	N (C	35810133	FEZZ FGD2	5.59	0.14	0.28	0.14	
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FXYD5 FYSBS2004 T 8082709 FYD7	6 rs6906101 6	rs6906101 6			3666761	2 :	FLJ43093	rs13214069	10	32705248		5.44	0.00	0.64		3.962
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CAA FXTDS TATTORGES TATTORGE	19 rs2285515 19	rs2285515 19	6.0		3566045	ے د	FXYDS	rs13067700	o et	95331048		9.00	0.09	0.51	0.22	
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CASDMB Trial Tri	12 122707210 12	rs2707210 12	1 5		02020	200	GPR162	rs9827054	on	188880113		6.21	0.96	0.0	0.44	
CASDMB Fig1005581 1 68723819 CPR177 5.76 0.17 0.40	1 rs11057383 12 12	rs11057383 12 12	12 12	12	1243694	121		rs12065581		68732819	GPR177	5.45	0.72	0.67	0.81	
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CADMB Page	1 rs725613	16	16		1116968	33		rs12065581	1	68732819	GPR177	5.43	0.31	0.11	0.13	
GSDMB rs12065581 1 68723819 GPR177 5.86 0.24 0.34 GSDMB rs4965745 15 101568261 GPR177 6.50 0.024 0.24 rs410101992 1 10266754 GSTM1 6.11 0.27 0.19 rs111011992 1 10266754 GSTM1 6.11 0.27 0.19 rs1120101992 1 10266754 GSTM1 6.11 0.27 0.19 rs485333 2 7391015 GSTM1 6.36 0.27 0.14 rs4856039 1 10253241 GSTM1 6.50 0.27 0.31 rs2856039 1 5271671 HBG2 5.47 0.06 rs2856039 1 5271671 HBG2 5.98 0.15 0.24 HBG2 rs12042179 1 121308849 LQK1 6.78 0.08 0.46 rs16912979 1 5309695 HBG2 6.06 0.01 0.46 rs16912979 1 5309695 HBG2 6.06 0.01 0.41 rs16912979 1 5309695 HBG2 6.06 0.01 0.41 rs16912979 1 6309695 HBG2 0.06 0.01 0.04 rs16912979 1 6309695 HBG2 0.06 0.01 0.04 rs16912979 1 630695 HBG2 0.06 0.01 0.04 rs16012979 1 630695 HBG2 0.06 0.01 0.04 rs16012979 1 630695 HBG2 0.06 0.01 0.04 rs16012979 1 630695 HBG2 0.06 0.01 0.06 rs16012979 0.06 0.06 0.01 0.06 rs16012979 0.06 0.06 0.06 0.06 rs1	1 rs9575097 13	13	13		829862	38		rs12065581	1	68732819	GPR177	6.04	0.95	0.21	09.0	
GSDMB rest2005581 1 68723819 GPR177 6.550 0.01 0.24	1 rs6566669 18	18	18		705060	Ξ		rs12065581	1	68732819	GPR177	5.86	0.24	0.34	0.23	
GSDMB rs4965745 10 10 10 10 10 10 10 10 rs11101992 1 10 10 10 10 rs11101992 1 10 10 10 10 rs11101992 1 10 10 10 10 rs11101992 1 10 10 10 10 rs11101992 1 10 10 10 10 rs485333 2 7791015 6.52 0.27 rs9983949 21 1953241 6.52 0.27 rs985039 1 5271671 HBG2 5.47 0.00 rs12032181 2 13 0 88494 LQK1 6.78 0.01 rs1203187 4 141533832 HBG2 6.00 0.00 rs12031979 1 5309695 HBG2 6.00 0.01 0.46 rs10912979 1 5309695 HBG2 6.00 0.01 rs10912979 1 5309695 HBG2 6.00 0.01 0.41 rs10912979 1 60000 0.00 rs10912979 1 60000 0.00 rs10912979 1 60000 0.00 rs10912979 1 60000 0.00 rs10912979 1 600000 0.00 rs10912979 0.00000000 0.000000000000000000000	1 rs9290426 3 1	3 1	3 1	1	17139932	_		rs12065581	1	68732819	GPR177	6.50	0.01	0.24	0.04	
Test	17 rs11557467 17	17	17		38028634		GSDMB	rs4965745	12	101508261		5.88	89.0	0.20	0.41	
100 100	1 rs12248673 10	10	10		53192833			rs11101992	1	110266754	GSTM1	6.11	0.27	0.19	0.16	
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rs4855333 2 77919015 6.36 0.52 0.66 rs96497007 15 85877017 6.36 0.27 0.67 rs98583049 11 15271671 HBG2 5.47 0.00 0.66 rs12050318 11 2571671 HBG2 5.98 0.15 0.24 rs12042181 1 23088494 LQK1 6.78 0.03 0.52 rs12053379 4 141533832 HBG2 6.42 0.01 0.46 rs16912979 11 5309695 HBG2 6.06 0.01 0.41	ILMN_2201580 1 rs6492807 13 96159560	13	13		96159560			rs3754446	1	110253241	GSTM1	6.77				
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$\begin{array}{c ccccccccccccccccccccccccccccccccccc$	11 rs2855039 11	Ξ	Ξ		52716	121	HBG2	rs12042181	-	213088494	LOK1	6.78	0.08	0.52	0.21	
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3 152187431 MBNL1 7.63 0.62 5.82 152187431 MBNL1 6.95 0.52 0.72 3 152187431 MBNL1 6.94 1.67 2.22 3 152187431 MBNL1 5.74 4.13 2.22			114067127
3 152187431 MBNL1 6.05 0.52 0.72 3 122187431 MBNL1 6.94 1.67 3 152187431 MBNL1 5.74 4.13 2.22			6604708
3 152187431 MBNL1 6.94 1.67 2.22 3.22			
77.7 CT:4 4.10 THINDIN TO4.101701 C			10038030
	o I		

	Distance / Mbh				1	0.039					128.140				120.688				46.389				1.137											11000	11.220	0.587	1														Continued on next page
/alues	ಶ್ಚಿ		0.17	0.15	2.03	3.86	0.70	0.07	0.49	0.62	0.88	0.82	0.59	0.16	0.32	0.13	0.67	0.24	0.70	0.03	0.33	0.48	0.15	0.04	0.56	0.26	0.19	0.66	0.46	0.17	1.21	0.12	0.10	4.0	0.43	40.0	,	0.04	0.27	1.78	98.0	0.15	0.38	0.11	1.55	0.09	0.59	0.08	0.47	0.17	Continued
- log10 p-values	EGCUT		0.05	0.46	1.55	0.81	0.46	00.0	0.87	0.08	1.48	1.21	0.44	0.26	0.71	0.09	0.36	0.65	0.90	0.01	0.87	1.19	0.42	0.04	0.78	0.33	0.42	0.48	0.95	0.13	0.28	0.00	0.30	0.14	0.03	0.03	0.44	0.26	0.21	0.64	0.32	0.48	0.08	0.40	1.25	0.08	0.84	0.31	0.37	0.09	
Interaction statistic /	Fehrmannf		0.47	0.03	1.27	4.12	0.87	0.36	0.16	1.20	0.13	0.25	99.0	0.19	0.09	0.34	0.87	0.03	0.36	0.20	0.02	0.00	0.02	0.16	0.31	0.29	0.12	0.72	0.08	0.36	L.09	0.37	0.10	0.0	0.00	0.13		0.00	0.44	1.95	1.18	0.03	08.0	0.02	1.03	0.25	0.28	0.03	0.58	0.04	
Interactio	BSGSe F	5.45	6.13	5.44	8.59	4.13	4. 5. 6. 5.	2.00	5.42	5.42	5.43	6.04	5.59	6.20	5.85	5.74	5.64	6.51	5.51	5.60	5.23	7.11	4.12	6.35	5.15	4.44	5.81	5.63	5.72	5.61	0.00	0.60	0.72	0.40	40.7	200.0	5.79	5.14	5.44	4.58	5.42	5.00	5.90	5.70	5.75	6.55	6.42	6.38	5.23 2.23	5.40	
	Associationd	NRBF2 NRBF2		NUDT18			DASI	OSBPLE	OSTF1		OVGP1	OVGP1	HPCAL4		PEX5	PEX5	PFAAP5		PHCA				PISD	PNKD	PNPLA7	PPFIBP2	PPP2R3C	PPPZR5A	PPP2R5A	PPP2R5A	PFZR5A	PPPZR5A	PFFZR5A	0 V C V C		091OBER7	PSMB1	PSMB1	PSMB1		PSMB1	PTDSS1	PTDSS1	PTDSS1	2DPR				RCN1		
SNP 2	Pos/Mbc	65133822		21964378	163997467	113409260	13169066			179590952	111992823 (111969719 (40139553	21395989	_	7364442	33126737			61728597	30398876				140487108								212447167	100700701	21407946	77776380			170823379	225797957	170877444	5221825		5221825	17526682 (70235726	120161117			141177468 102740645	
S	Chr.	10		œ	9	2 5	7 0	2 -	5	10	1	т	Т	က	12	12	13	14	11	-	14	-	22	71	6	11	14	۰,	н,	н,	٠,	٠.	٠,	101	0 0	210	9 9	9	9	1	9	11	11	11	4	12	11	12	 	α	
	rs ID	rs7923609	rs6588415	rs1005901	rs1047944	rs2072133	rs3/41981	rs998639	rs2273770	rs7718088	rs1264898	rs1264894	rs784600	rs2731939	rs4329748	rs4329748	rs7328733	rs1263806	rs10736812	rs2065841	rs10498313	rs954627	rs6518754	rs4672884	rs928046	rs4758001	rs11156875	rs12120009	rs12120009	rs12120009	rs12120009	rs12120009	rs12120009	rs11000990	rs10492795	re11701058	rs13207114	rs6928843	rs9295415	rs2769689	rs13207114	rs11036212	rs11036212	rs11036212	rs10020773	rs7305307	rs7951628	rs1863464	rs4922579	rs11166957 rs1341899	
	Associationd									OSTF1			PAM	PCYOX1L				PGLYRP1		PIK3IP1	PISD	PISD													731000107	OZIOITE OI				PSMB1							RABACI	AKTIP	BCN1	RCN1	
SNP 1	Pos/Mb^{c}	56157341	240680022	25453482	113480510	113448652	49160255 74286646	26662543	70624189	77755469	240132968	140148107	102149795	148726162	128052636	27246462	49151303	46529456	123097386	31675185	32263131	31999127	33234931	158781604	4527109	49668255	58350896	166399467	123595064	66222691	107417238	135030045	27148475	90040404	47091659	48063869	121774705	43983954	30347832	170890384	131727816	95478823	76598123	126852438	106348246	33375704	42462788	53526551	41147155	32136436 32136436	
00	Chr.	20	1 01	11	12	7 5	61	2.5	17	6	1	3	ю	ю	12	15	22	19	11	22	22	22	22	ı,	16	20	15	21 (12	13	II	٥٥	. <u>.</u>	7 .	31	2 6	i =	18	20	9	12	14	17	11	9	55	19	16	17	1 1	i
	rs ID	rs6025645	rs4852124	rs5017351	rs11613438	rs13311	rs2892233	rs2829679	rs17780195	rs2273770	rs10802822	rs347331	rs28092	rs2438490	rs10444467	rs7495797	rs131969	rs12982353	rs493642	rs4141404	rs470072	rs6518752	rs715572	rs6869411	rs11639998	rs911019	rs12914603	rs10930170	rs12423255	rs1889083	rs082334	TS/(5/8/1	rs/8/11/8	120013023	rs21000000	157675757	rs3862607	rs4890648	rs6060930	rs6928843	rs7299749	rs2353567	rs4969205	rs631562	rs4946705	rs241730	rs1075728	rs9931702	rs10879131	rs4922579 rs4922579	1
	Chr.	10	7	œ	12	21 5	7 0	2 -	5 6	. 6	1		ю	ю	12	12	13	19	11	55	22	55	22	61	o :	11	14				۰,	٠,	- ;	1 .	210	1.0	9 9	9	9	9	9	12	12	12	4	12	13	16	===		-
Expression trait	Probe ID ^b	ILMN_3237385	ILMN_1800897	ILMN_1787885	ILMN_1658247	ILMN_1658247	ILMN-16/5640	II.MN 2307032	ILMN_1742456	ILMN_1742456	ILMN_1734542	ILMN_1734542	ILMN_2313901	ILMN_1815951	ILMN_1660232	ILMN_1660232	ILMN_1797893	ILMN_1704870	ILMN_1812552	ILMN_1719986	ILMN_1793934	ILMN_1793934	ILMN_1793934	ILMN_1774604	ILMN_1662587	ILMN_1675656	ILMN_1662617	ILMN_1738784	ILMN_1738784	ILMN_1738784	ILMIN-1738784	ILMIN_1738784	ILMIN_1738784	TEMINAL TEROOP	ILMIN-1715003	II.MN 1675038	11.MN 1789176	ILMN_1789176	ILMN_1789176	ILMN_1789176	ILMN_1789176	ILMN_1743049	ILMN_1743049	ILMN_1743049	ILMN_1672443	ILMN_1803197	ILMN_2207363	ILMN_1756999	ILMN_1800276	ILMN_1800276	
Exp	Gene IDa	NRBF2 NRBF2	NRD1	NUDT18	OAS1	OASI	OPEN	OSBPL5	OSTF1	OSTF1	OVGP1	OVGP1	PAM	PCYOX1L	PEX5	PEX5	PFAAP5	PGLYRP1	PHCA	PIK3IP1	PISD	PISD	PISD	PNKD	PNPLA7	PPFIBP2	PPP2R3C	PPPZR5A	PPP2R5A	PPP2R5A	PPP2R5A	PPPZK5A	PPPZK5A	rhbys inches	PDMT9	PRMT2	PSMB1	PSMB1	PSMB1	PSMB1	PSMB1	PWP1	PWP1	PWP1	QDPR	RAB3IP	RABAC1	RBL2	RCN1	RCN1	

Ex	Expression trait				SNP 1		SNP 2		SNP 2		Interac	Interaction statistic	/ - log10 p-values	ralues	
Gene IDa	Probe ID ^b	Chr.	rs ID	Chr.	Pos/Mb ^c	Associationd	rs ID	Chr.	Pos/Mb ^c	Associationd	BSGSe	Fehrmann ^f	$EGCUT^{f}$	Metag	Distance / Mbh
RERE	ILMN_1802380		rs4982958	14	24987865		rs301819	1	8501786	RERE	5.66	0.61	1.23	1.17	
RERE	ILMN_1802380	1	rs7697290	4	135248366		rs301819	-	8501786	RERE	5.74	0.14	0.10	90.0	
RERE	ILMN_2327795	1	rs11085829	19	13174312		rs301819	1	8501786	RERE	5.12	0.21	0.33	0.21	
RERE	ILMN_2327795	-	rs3852011	က	112844086		rs301819	П	8501786	RERE	5.71	80.0	09.0	0.26	
RNASE6	ILMN_1780533	14	rs11628398	14	21182800	RNASE6	rs7324365	13	100601327		5.48	0.42	0.21	0.26	
RNASE6	ILMN_1780533	14	rs6603134	19	8106521		rs11628398	14	21182800	RNASE6	5.11	0.09	0.22	0.08	
KNF167	ILMN_1794726	17	rs238230	17	4875566		rs4884857	13	54668512		4.37	i			
RNF167	ILMN_1794726	17	rs400688	17	4839930	RNF167	rs11706900	η,	36348968		5.59	0.71	0.46	0.64	
RNPEP	ILMN_1738347	-	rs1107121	21	46127549		rs2819365	Η,	201983242		6.27	0.11	0.30	0.13	
RNPEP	ILMN_1738347	-	rs8071611	17	67153386		rs2819365	-	201983242		4.32	1.48	0.52	1.28	
RPL13	ILMN_2413278	16	rs352935	16	89648580		rs2965817	16	89513234		4.98	3.79	14.41	17.24	0.135
RPL23AP7	ILMN_2222750	61	rs1401202	16	80320056		rs4849261	61	114450028	RPL23AP7	5.55	0.13	0.73	0.38	
RPL36AL	ILMN_2189933	14	rs3007033	14	50103816	RPL36AL	rs17495030	6	138038093		5.46	0.00	90.0	0.05	
RPL36AL	ILMN_2189936	14	rs4900928	14	50020817	RPL36AL	rs1502991	9	66137260		5.86	0.32	0.20	0.19	
RPL8	ILMN_1764721	00	rs2958482	oo j	145984615	RPL8	rs1619856	-	234585790		4.59	0.10	0.37	0.15	
RPL8	ILMN_1764721	∞	rs4143674	20	4741304		rs2958482	œ	145984615	RPL8	4.33	0.13	0.45	0.55	
SEC13	ILMN_3297880	n	rs4889214	16	80913946		rs696221	က	10342876	SEC13	6.48				
SEMA4A	ILMN_1702787	1	rs17085428	rO	95388015		rs7695	-	156147326	SEMA4A	5.70	0.22	1.73	1.17	
SESN3	ILMN_1694027	11	rs12147460	14	104412137		rs684856	11	94906111	SESN3	5.50	0.03	0.51	0.15	
SESN3	ILMN_1694027	11	rs355391	15	46591793		rs684856	11	94906111	SESN3	5.67	0.31	90.0	0.10	
SESN3	ILMN_1694027	11	rs684856	11	94906111	SESN3	rs7004947	œ	134606425		5.60	0.21	0.51	0.31	
SH3BGRL2	ILMN_1762764	9	rs10838191	11	43893658		rs1354034	8	56849749	PPBP	5.52	0.70	0.12	0.35	
SH3BGRL2	ILMN_1762764	9	rs2545385	70	66383979		rs1354034	8	56849749	PPBP	5.97	0.20	0.51	0.30	
SH3BGRL2	ILMN_1762764	9	rs6845304	4	88280502		rs1354034	8	56849749	PPBP	5.23	0.32	0.71	0.53	
SH3GLB2	ILMN_2158336	6	rs1034120	21	18196922		rs17455517	6	131785369	SH3GLB2	7.40	0.22	0.18	0.13	
SIRPG	ILMN_1771801	20	rs1535883	20	1612819	SIRPG	rs6842739	4	60489510		5.74	0.29	0.18	0.17	
SLC22A18	ILMN_2382505	11	rs11673260	19	52181798		rs367035	11	2923826	SLC22A18	5.47	0.09	0.24	0.09	
SLC22A18	ILMN_2382505	11	rs367035	11	2923826	SLC22A18	rs3110874	7	153224179		5.70	0.15	0.10	90.0	
SLC22A18	ILMN_2382505	11	rs367035	11	2923826	SLC22A18	rs3772054	7	241678528		6.15	0.39	0.13	0.19	
SLC41A3	ILMN_2356111	က	rs1912136	11	24616743		rs6771703	6	125801067	SLC41A3	5.88	1.10	0.82	1.24	
SLC45A4	ILMN_1745778	œ	rs6985508	œ	142337734	SLC45A4	rs7701916	ю	174598073		5.95	0.86	0.02	0.40	
SLC46A3	ILMN_1658639	13	rs949805	17	55602091		rs7981190	13	29259349	SLC46A3	5.52	0.09	0.58	0.26	
SMG7	ILMN_1706553	-	rs8035259	12	97403923		rs10911353	-	183489203	SMG7	6.52	0.17	0.09	90.0	
SMOX	ILMN_1775380	20	rs8118315	20	4161500	SMOX	rs11677815	61	65800982	0	5.68	0.39	0.62	0.52	
SNHCS	ILMIN_3309349	4.	rs1105621	י מ	133050233		rs/05837	4.	119225940	SNHGS	6.11	0		i	
SNORD14A	ILMIN-1799381	::	rs1520429	112	46259108		rs214097	1 :	17015557	SNORD14A	0.00	19 11	10.06	20.02	1000
SNORD89	II.MN 3238662	7.6	rs10445863	77	115929241		rs750783	77	101889306	SNOBDRA	80.6	10:01	10:30	44.0	14 040
SNORD89	II.MN 3238662	10	rs11605822	-	122986326		rs750783	10	101889306	SNORD89	5.96				
SNORD89	ILMN_3238662	61	rs2135064	r0	26778066		rs750783	61	101889306	SNORD89	6.33				
SNUPN	ILMN_1733932	15	rs8134646	21	46376528	SNUPN	rs7185362	16	81888905		6.45	0.13	1.41	0.83	
SNUPN	ILMN_2364535	15	rs8134646	21	46376528	SNUPN	rs1472075	33	193706323		5.59	0.34	0.00	90.0	
SPATA5L1	ILMN_1729179	12	rs1131620	19	41117869		rs4774580	15	45652086	SPATA5L1	5.44				
STARD10	ILMN_1717052	11	rs2221406	13	90174526		rs1000620	11	72509713		5.65	0.67	0.12	0.33	
STYXL1	ILMN_2210729	7	rs4073164	14	104947517		rs17685	7	75616105	STYXL1	2.88	0.57	0.17	0.31	
SULFZ	ILMN-2345142	07.	rs11700063	07.	46153148	SOLFZ	rs939294	4.	180439236		5.51	0.46	0.24	0.30	
SULTIA4	ILMN_2336133	91	rs1463965	x ;	74332954		rs3785354	16	28550667	TUFM	7.05	0.01	0.02	0.00	
SULTIA4	ILMN-2336133	91	rs2836657	17.0	40119768		rs3785354	16	28550667	TUFM	5.83	0		,	
SURFE	ILMIN_I778032	n :	rs0099626	0.77	103410760		rs3118003	n :	130281753	SCRF6	0.14	0.26	0.10	0.14	
THES3	ILMN-2336609		rs1375719	21.	95422867		rs485485	TT -	155162067	THRS	74.0 74.7	0.28	0.31	0.04	
THESS	II.MN 1804663		rs1959675	11	20687978		rs2049805		155194980	THESS	5.00 5.00 5.00 5.00	0.03	0.13	0.00	
TIPRI	II.MN 1781457		rs2823245	21	16745523		rs1320993		168154599	TIPRI	5 22	0.31	0.76	0.00	
			1	i	1		-		1		1	0		, , , ,	Continued on next nage

Gene ID ^a Probe ID ^b TMED4 ILMN_1804148 TMEM149 ILMN_1786426	Chr.	Tra ID	Chr.	Pos/Mb^{c}	Associationd	rs ID	Chr.	Pos /Mbc	Pacitation4	PSC26	Fehrmannf	RGCUT	Meta8	,
								T CO TAT C	Tago Cranton				300744	Distance / Mb.
	7	rs1940400	11	132389627		rs17725246	7	44581986	TMED4		90.0	1.34	0.70	
	19	rs2839013	21	47248981		rs8106959	19	36219525	TMEM149	8.11	0.16	0.48	0.26	
	19	rs5762235	22	27925288		rs8106959	19	36219525	TMEM149	6.79				
TMEM149 ILMN_1786426	61	rs6090518	50	45207005	000	rs8106959	13	36219525	TMEM149	11.09	0.76	i i	i i	0
TMEM149 ILMIN-1/86426	D C	rs807491	1.0	30208923	TMEMIAO	rs/254601	5 -	4700150	I MEMI49	12.10	81.00 81.00	87.08	145.78	0.122
	61	rs8106959	61	36219525	TMEM149	rs10819626	0,7	133025756		8.02	0.40	66.0	08.0	
	13	rs8106959	19	36219525	TMEM149	rs10937361	0	188359436		8.39	3.61	1.18	3.78	
	19	rs8106959	19	36219525	TMEM149	rs1401098	12	128884559		7.37	2.41	1.00	2.52	
TMEM149 ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs1557335	18	64268976		6.95	80.0	0.07	0.03	
TMEM149 ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs17719594	14	90932598		6.93	3.06	0.77	2.87	
	19	rs8106959	19	36219525	TMEM149	rs1843357	œ	13822381		6.21	3.72	3.33	6.00	
TMEM149 ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs2351458	4	113317583		7.30	0.04	9.61	8.00	
TMEM149 ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs2539000	7	147619772		6.70	1.57	1.52	2.27	
	19	rs8106959	19	36219525	TMEM149	rs2731711	10	171792273		5.92	0.19	0.33	0.19	
	19	rs8106959	19	36219525	TMEM149	rs471728	11	129595460		8.89	0.90	3.62	3.51	
	13	rs8106959	19	36219525	TMEM149	rs6718480	2	233879066		20.00	3.31	5.15	7.36	
_	6.	rs8106959	61	36219525	TMEM149	rs6926382	ı c	161683974		5.80	3.06	08.80	10.72	
	61	rs8106959	61	36219525	TMEM149	rs7213338	17	80357420		5.49	0.07	3.14	2.10	
	13	rs8106959	19	36219525	TMEM149	rs914940	;	242889492		6.22	3.36	96.9	9.20	
TMEM149 ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs9509428	13	21473952		9.44	0.10	5.75	4.47	
TMEM63A ILMN_1719649	-	rs1254086	13	72890603		rs4149226	1	226027323	TMEM63A	5.60				
TMEM80 ILMN_1708482	11	rs1548475	19	58058246		rs4963126	11	656845	TMEM80	5.79	0.64	0.12	0.32	
ILMN_1683811	-1	rs1537146	6	4859303		rs10488630	-1	128593948	IRF5	5.61	0.11	0.15	0.07	
ILMN_1683811	-	rs199793	20	22287303		rs10488630	7	128593948	IRF5	5.52	1.03	0.17	0.62	
	-	rs7776572	7	23528927		rs11770192	4	23498358		8.23	3.19	1.89	4.09	0.031
_	11	rs1278760	13	113531675		rs3916581	11	118887887	TRAPPC4	5.61	0.28	0.40	0.29	
	11	rs1793823	11	131018917		rs3916581	11	118887887	TRAPPC4	5.52	0.93	0.01	0.36	12.131
	19	rs17159840	19	7758194	TRAPPC5	rs10059004	n	166970604		5.97	0.21	1.60	1.07	
	13	rs17159840	19	7758194	TRAPPC5	rs1023095	00	132022957		6.92	0.37	0.87	0.68	
	n ,	rs17159840	61	7758194	TRAPPCS	rs1375714	φ,	156404902		7.79	0.12	0.18	0.08	
	n ,	rs17159840	61	7758194	TRAPPCS	rs1393299	۰,	242329791		6.43	0.63	0.47	0.59	0 0
	57 .	rs17159840	61	7758194	TRAPPOS	rs17763599	51.5	2369415		6.38	0.21	0.24	0.16	5.389
TRAFFC5 ILMIN-23/2639 TRAFFC5 ILMIN 2372639	n 0	rs17159840	S C	7758194	TRAPPCS	rs4908328	12	19964437		0.01	0.50	0.38	0.44 4.0 7.0	
	6.	rs17159840	61	7758194	TRAPPOS	rs7694997	4	9947811		8.80	0.20	0.36	0.22	
	19	rs17159840	19	7758194	TRAPPC5	rs7800935	7	146690926		6.27	0.15	0.33	0.16	
TRAPPC5 ILMN_2372639	19	rs17159840	19	7758194	TRAPPC5	rs856638	14	85439550		6.73	0.24	0.07	0.08	
TRAPPC5 ILMN_2372639	19	rs380708	22	22740855		rs17159840	19	7758194	TRAPPC5	7.58				
_	19	rs3916995	21	45128454		rs17159840	19	7758194	TRAPPC5	7.73	0.85	0.78	1.01	
	19	rs6040514	20	11272861		rs17159840	19	7758194	TRAPPC5	8.10	0.51	0.55	0.56	
	13	rs7246264	19	7762978		rs10179572	21 5	228504503		6.71	0.14	0.02	0.02	
	61	rs7246264	61	7762978		rs12921440	16	30408765		7.34	0.14	0.26	0.13	
	61	rs7246264	61	7762978		rs1887778	n 0	134635088	KAPGEF1	7.05	80.0	0.86	0.40	
TRAFFC5 ILMN_2372639	67	rs/246264	61.	7.1629.78		rs963354	n	41064577	13/11/11	7.41	0.36	0.90	0.69	
ILMIN_1688231	٥	rs10862975	7 7	85749398		rs2395771	٥٥	41204577	TREMI	5.42	1.00	0.25	1.00	
ILMIN_1688231	φ 0	rs12412964	10	108256422		rs2395771	9	41264577	TREMI	5.92	1.20	1.23	1.69	
	٥	rs2527180	- !	158808416		rs2032447	٥	20044309	TRIMISS	0.40	0.04	0.91	0.39	
TSFANIA ILMIN-1785060	2 :	rs908726	7 :	27194634 47669040	00000000	rs1048526	0 :	822/30/9	TSPAN14	0.00	0.07	0.18	0.00	200
	: :	rs10838/38	11	9317051	TSPAN39	rs12800998	11	137947208	1 SPAIN 92	0.0 r				40.040
	22	rs140522	2.2	50971266	ECTE 1	rs1198819	00	238746880		6.34				
II.MN 3223126	4 0	rs470119	4 6	50966914	1500	rs4783126	4 6	85147633		6.04				

Table S1 - continued from previous page

_																										
	Distance / Mb ^h			1.643	0.088																					
values	Metag	0.52	1.10	0.03	4.95	0.46	0.57		0.19	0.41	0.31	0.17	0.04	1.21	0.16	0.57	0.26	1.47	0.09	1.22	0.35	2.25	1.63	0.15	0.46	0.05
- log10 p-values	$EGCUT^{f}$	0.42	1.29	0.14	5.14	0.15	0.69		0.19	0.74	0.48	0.17	0.19	1.15	0.02	0.54	0.17	1.38	0.13	1.35	0.61	1.43	0.17	0.36	0.27	0.01
Interaction statistic /	$Fehrmann^f$	0.59	0.48	0.03	0.94	0.84	0.39		0.33	0.16	0.23	0.31	0.03	0.73	0.46	0.53	0.48	0.81	0.19	0.57	0.18	1.64	2.38	0.09	0.67	0.26
Interacti	BSGS _e	5.91	6.01	5.71	5.09	5.64	5.44	5.72	5.77	6.44	5.74	6.44	5.82	6.12	4.83	5.60	5.71	5.88	5.88	6.34	5.85	4.86	5.48	5.79	5.29	6.04
	Associationd					VNN2	VNN2	VNN2	VNN2	VNN3	VNN3	VNN3	VNN3	VNN3	VNN3			VSTM1	WDR48	WDR48	WDR48	WDR6		ZFP90	ZNF500	ZYX
SNP 2	Pos/Mb ^c	83600397	214514361	75151717	45974668	133077063	133072650	133072650	133072650	133067782	133067782	133067782	133067782	133067782	133067782	71024750	123098249	54553697	39091812	39067925	39044116	49194331	93119799	68573945	4799041	143093824
	Chr.	16	1	17	19	9	9	9	9	9	9	9	9	9	9	18	10	19	8	8	8	8	15	16	16	-1
	rs ID	rs7201194	rs7512594	rs7225546	rs2276470	rs1883613	rs1883617	rs1883617	rs1883617	rs2267952	rs2267952	rs2267952	rs2267952	rs2267952	rs2267952	rs4552100	rs7895870	rs10500316	rs6778963	rs883349	rs7619193	rs11715581	rs12591171	rs1182968	rs2290560	rs2242601
	Associationd	UBASH3A	UBASH3A	USP36												VSTM1	VSTM1			RAPGEF1			XAF1			
SNP 1	Pos/Mb^{c}	43855067	43855067	76794981	46063167	105252718	9116155	49927332	16834510	151662184	73006453	75547169	83262064	16594253	51692548	54553697	54553697	30261219	188927822	134635088	102624790	123371708	6673170	37040648	48283177	8935312
S	Chr.	21	21	17	19	7	20	22	11	-	œ	6	14	21	13	19	19	22	4	6	13	11	17	21	22	20
	rs ID	rs1893592	rs1893592	rs2279308	rs1264226	rs10435352	rs13044386	rs134447	rs216495	rs10278073	rs1443946	rs348462	rs7157055	rs2823165	rs9596457	rs10500316	rs10500316	rs9625870	rs1388935	rs1887778	rs9554833	rs12362253	rs1533031	rs909446	rs4823723	rs6056281
	Chr.	21	21	17	19	9	9	9	9	9	9	9	9	9	9	19	19	19	8	8	8	8	17	16	16	-1
Expression trait	Probe ID ^b	ILMN_2338348	ILMN_2338348	ILMN_1697227	ILMN_1743646	ILMN_1678939	ILMN_1678939	ILMN_1678939	ILMN_1678939	ILMN_1804935	ILMN_1804935	ILMN_1804935	ILMN_1804935	ILMN_2387680	ILMN_2387680	ILMN_1763455	ILMN_1763455	ILMN_1763455	ILMN_1762103	ILMN_1762103	ILMN_1762103	ILMN_1669484	ILMN_2370573	ILMN_1684628	ILMN_1700238	ILMN_1701875
Ex	Gene ID ^a	UBASH3A	UBASH3A	USP36	VASP	VNN2	VNN2	VNN2	VNN2	VNN3	VNN3	VNN3	VNN3	VNN3	VNN3	VSTM1	VSTM1	VSTM1	WDR48	WDR48	WDR48	WDR6	XAF1	ZFP90	ZNF500	ZYX

Table S1-continued from previous page

a Phenotypes are expression levels of RefSeq Genes billumina probe ID used to measure gene expression (Physical SNP position in base pairs (HG19) and RefSeq Gene ID of gene expression level that is influenced by the SNP (BSGS discovery dataset, significance threshold = 1.29 \times 10^{-11} , thereaction - log₁₀ p-value from replication dataset for interaction - log₁₀ p-value from meta analysis of replication datasets functoraction - log₁₀ p-value from meta analysis of replication datasets only historic in Mb between interacting SNPs for cis-cis acting SNP pairs

References

- ¹ Carlborg, O. & Haley, C. S. Epistasis: too often neglected in complex trait studies? *Nature Reviews Genetics* **5**, 618–25 (2004).
- ² Hill, W. G., Goddard, M. E. & Visscher, P. M. Data and Theory Point to Mainly Additive Genetic Variance for Complex Traits. *PLoS Genetics* 4 (2008).
- ³ Crow, J. F. On epistasis: why it is unimportant in polygenic directional selection. *Philosophical transactions of the Royal Society of London. Series B, Biological sciences* **365**, 1241–4 (2010).
- ⁴ Costanzo, M. *et al.* The genetic landscape of a cell. *Science (New York, N.Y.)* **327**, 425–31 (2010).
- ⁵ Bloom, J. S., Ehrenreich, I. M., Loo, W. T., Lite, T.-L. V. o. & Kruglyak, L. Finding the sources of missing heritability in a yeast cross. *Nature* 1–6 (2013).
- ⁶ Carlborg, O., Jacobsson, L., Ahgren, P., Siegel, P. & Andersson, L. Epistasis and the release of genetic variation during long-term selection. *Nature Genetics* 38, 418–420 (2006).
- ⁷ Strange, A. *et al.* A genome-wide association study identifies new psoriasis susceptibility loci and an interaction between HLA-C and ERAP1. *Nature Genetics* **42**, 985–90 (2010).
- ⁸ Evans, D. M. *et al.* Interaction between ERAP1 and HLA-B27 in ankylosing spondylitis implicates peptide handling in the mechanism for HLA-B27 in disease susceptibility. *Nature Genetics* **43** (2011).
- ⁹ Cordell, H. J. Detecting gene-gene interactions that underlie human diseases. *Nature Reviews Genetics* **10**, 392–404 (2009).
- ¹⁰ Hemani, G., Theocharidis, A., Wei, W. & Haley, C. EpiGPU: exhaustive pairwise epistasis scans parallelized on consumer level graphics cards. *Bioin-formatics (Oxford, England)* 27, 1462–5 (2011).
- ¹¹ Metspalu, A. The Estonian Genome Project. Drug Development Research 62, 97–101 (2004).
- ¹² Fehrmann, R. S. N. et al. Trans-eQTLs reveal that independent genetic variants associated with a complex phenotype converge on intermediate genes, with a major role for the HLA. PLoS genetics 7, e1002197 (2011).
- ¹³ Lieberman-Aiden, E. et al. Comprehensive mapping of long-range interactions reveals folding principles of the human genome. Science (New York, N.Y.) 326, 289–93 (2009).

- ¹⁴ Visscher, P. M., Brown, M. a., McCarthy, M. I. & Yang, J. Five years of GWAS discovery. *American journal of human genetics* **90**, 7–24 (2012).
- Weinreich, D. M., Delaney, N. F., Depristo, M. a. & Hartl, D. L. Darwinian evolution can follow only very few mutational paths to fitter proteins. *Science (New York, N.Y.)* 312, 111–4 (2006).
- ¹⁶ Breen, M. S., Kemena, C., Vlasov, P. K., Notredame, C. & Kondrashov, F. a. Epistasis as the primary factor in molecular evolution. *Nature* **490**, 535–538 (2012).
- ¹⁷ Weir, B. S. Linkage disequilibrium and association mapping. *Annual review of genomics and human genetics* **9**, 129–42 (2008).
- ¹⁸ Hemani, G., Knott, S. & Haley, C. An Evolutionary Perspective on Epistasis and the Missing Heritability. *PLoS Genetics* **9**, e1003295 (2013).
- ¹⁹ Marchini, J., Donnelly, P. & Cardon, L. R. Genome-wide strategies for detecting multiple loci that influence complex diseases. *Nature Genetics* 37, 413–417 (2005).
- ²⁰ Lango Allen, H. et al. Hundreds of variants clustered in genomic loci and biological pathways affect human height. Nature 467, 832–8 (2010).
- ²¹ Powell, J. E. et al. Congruence of Additive and Non-Additive Effects on Gene Expression Estimated from Pedigree and SNP Data. PLoS Genetics 9, e1003502 (2013).
- ²² Powell, J. E. *et al.* The Brisbane Systems Genetics Study: genetical genomics meets complex trait genetics. *PloS one* **7**, e35430 (2012).
- ²³ Preininger, M. et al. Blood-informative transcripts define nine common axes of peripheral blood gene expression. PLoS genetics 9, e1003362 (2013).
- ²⁴ Cockerham, C. C. An extension of the concept of partitioning hereditary variance for analysis of covariances among relatives when epistasis is present. *Genetics* 39, 859–882 (1954).
- ²⁵ Ho, T. H. et al. Muscleblind proteins regulate alternative splicing. The EMBO journal 23, 3103–12 (2004).
- 26 Trynka, G. et al. Chromatin marks identify critical cell types for fine mapping complex trait variants. Nature genetics ${\bf 45},\,124\text{--}30$ (2013).
- ²⁷ Ward, L. D. & Kellis, M. HaploReg: a resource for exploring chromatin states, conservation, and regulatory motif alterations within sets of genetically linked variants. *Nucleic acids research* 40, D930–4 (2012).
- ²⁸ Lan, X. et al. Integration of Hi-C and ChIP-seq data reveals distinct types of chromatin linkages. Nucleic acids research 40, 7690–704 (2012).

- ²⁹ Osborne, C. S. *et al.* Active genes dynamically colocalize to shared sites of ongoing transcription. *Nature genetics* **36**, 1065–71 (2004).
- ³⁰ Rieder, D., Trajanoski, Z. & McNally, J. G. Transcription factories. Frontiers in genetics 3, 221 (2012).
- ³¹ Visscher, P. M., Hill, W. G. & Wray, N. R. Heritability in the genomics eraconcepts and misconceptions. *Nature Reviews Genetics* 9, 255–66 (2008).
- ³² Churchill, G. A. & Doerge, R. W. Empirical threshold values for quantitative trait mapping. *Genetics* **138**, 963–71 (1994).