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 whole 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 trans-acting 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. When genetic effect sizes are small, 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. 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 whole blood. After stringent filtering and multiple testing correction (Methods) we identified 501 putative genetic interactions influencing the expression levels of 238 genes. 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, we observed that 316 of the remaining 404 discovery SNPs had replication interaction p-values exceeding the one-tailed 2.5% confidence interval under the null distribution of no 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 185 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 four 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 detec-

tion. 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 association²¹ (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 (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 splicing 25) 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. We cross-referenced our epistatic SNPs with a map of chromosome interacting regions (n=96,139) in K562 blood cell lines (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 at least three caveats to this comparison. Firstly, the ratio of additive to epistatic variance may differ at different effect sizes. 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 functional 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 portal to understanding molecular mechanisms and complex trait variation with greater clarity. 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 whole blood samples for 7,339 probes representing 6,158 RefSeq genes. Recent hardware and software¹⁰ ad-

vances 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 whole blood, the Fehrmann dataset¹² (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

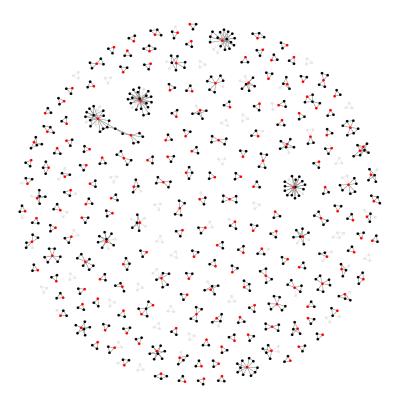


Figure 1: Discovery and replication of epistatic networks All 434 putative genetic interactions (edges) with data common to discovery and replication sets is shown, where black nodes represent SNPs and red nodes represent traits (gene expression probes). Three hundred and forty-five interactions had 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.

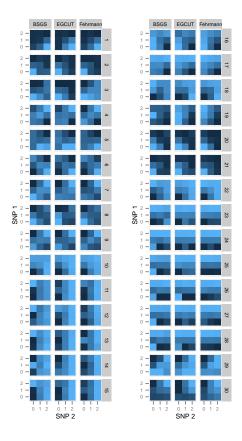


Figure 2: Replication of GP maps in two independent populations The GP maps for each epistatic interaction that is significant at the Bonferroni level in both replication datasets are shown. Each GP map consists of nine tiles where each tile represents the expression level for that two-locus genotype 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.

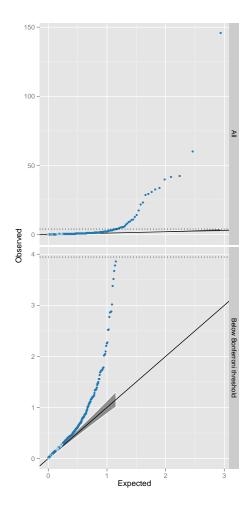


Figure 3: Q-Q plots of interaction p-values from replication datasets. The top panel shows all 434 discovery SNPs that were tested for interactions. Observed p-values (y-axis, $-\log_{10}$ scale) are plotted against the expected p-values (x-axis, $-\log_{10}$ scale). The multiple testing correction threshold 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

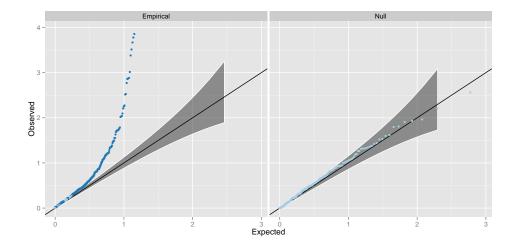


Figure S1: Q-Q plots of interaction p-values from replication datasets, excluding the 30 points significant at the Bonferroni level The right panel (Null) shows the interaction p-values from a meta analysis across two independent datasets on 434 randomly drawn SNP pairs. The left panel (Empirical) shows 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.

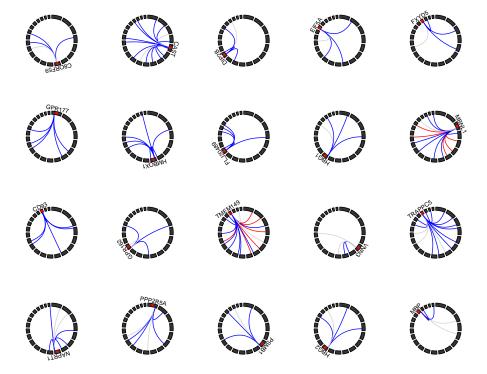


Figure S2: Gene expression traits with four or more genetic interactions Circle plots represent the genomic positions for SNPs (linking lines) and expression probes (red points). Chromosomes are represented by black blocks and ordered from 1 to 22 clockwise, starting from the top. Grey lines represent 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.

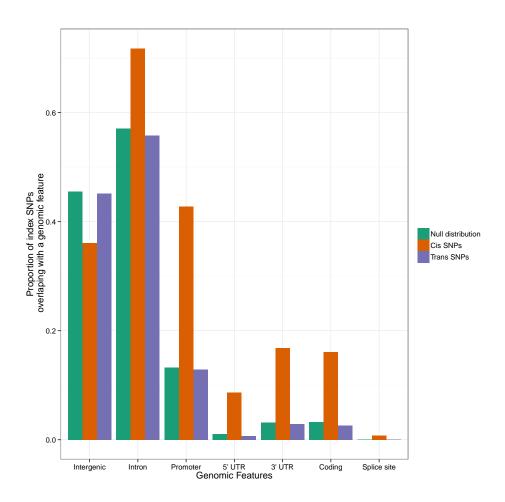


Figure S3: Location of SNPs relative to genomic features All SNPs within 1kb and $r^2 > 0.8$ of each cis- and trans-SNP were taken to find which genomic features (x-axis) were covered by the SNPs that compose the 501 significant interactions. Green bars represent the proportion (y-axis) of the 528,509 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.

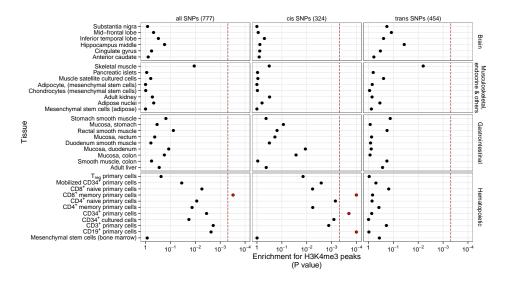


Figure S4: Tissue specific enrichment of SNPs in transcriptionally active regions The locations of transcriptional activity can be predicted by chromatin marks, assayed by H3K4me3.²⁶ Enrichment *p*-values are calculated using permutation analysis for 34 different cell types (*y*-axis) in four tissue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

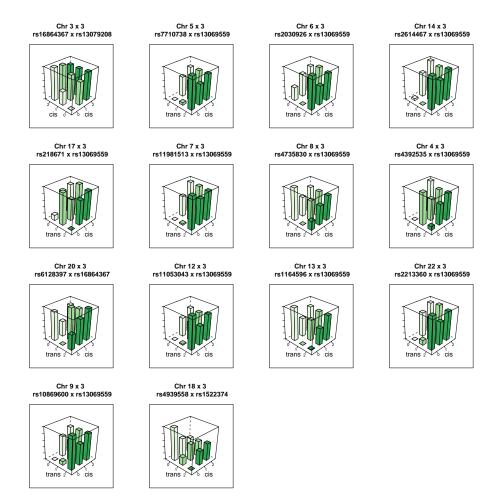


Figure S5: Genotype-phenotype maps for 14 interactions influencing the expression of MBNL1 Each bar represents the mean phenotypic value for individuals in that genotype class. The rs13069559 SNP typically has a *cis*-additive decreasing effect on the expression of MBNL1, but in many of these interactions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

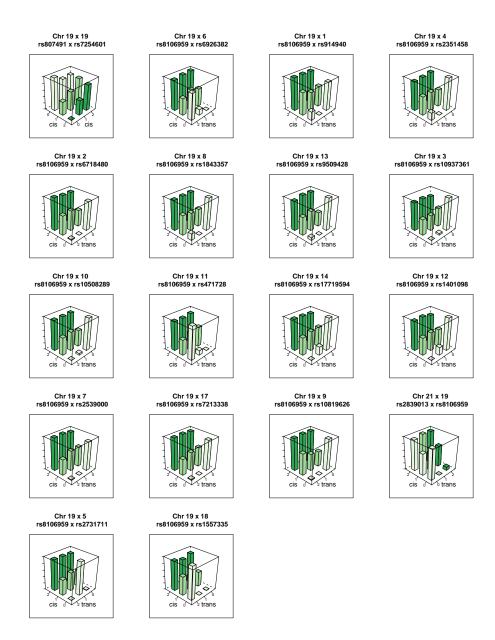


Figure S6: Genotype-phenotype maps for 19 interactions influencing the expression of TMEM149 Each bar represents the mean phenotypic value for individuals in that genotype class. The rs13069559 SNP typically has a *cis*-additive decreasing effect on the expression of TMEM149, but in many of these interactions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

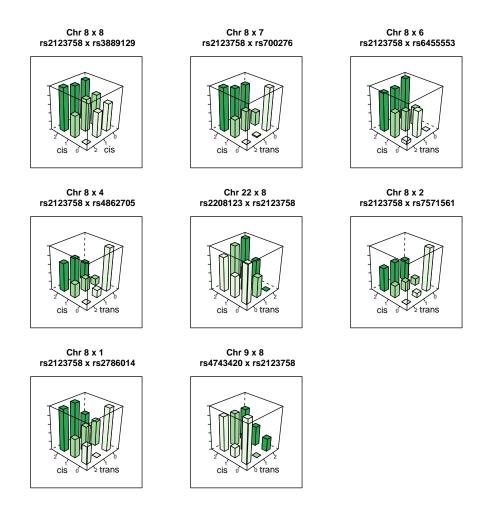


Figure S7: Genotype-phenotype maps for 8 interactions influencing the expression of NAPRT1 Each bar represents the mean phenotypic value for individuals in that genotype class.



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.

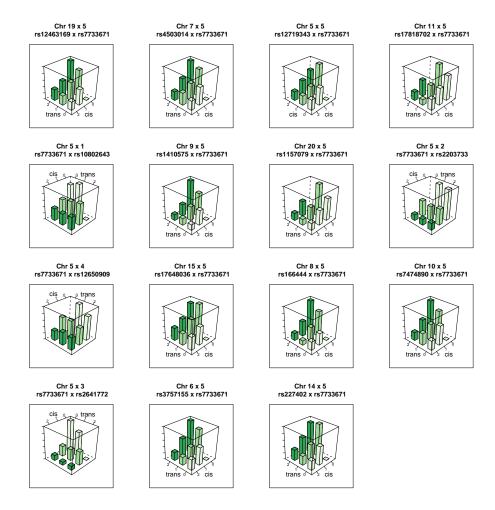


Figure S9: Genotype-phenotype maps for 15 interactions influencing the expression of CAST Each bar represents the mean phenotypic value for individuals in that genotype class.



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.

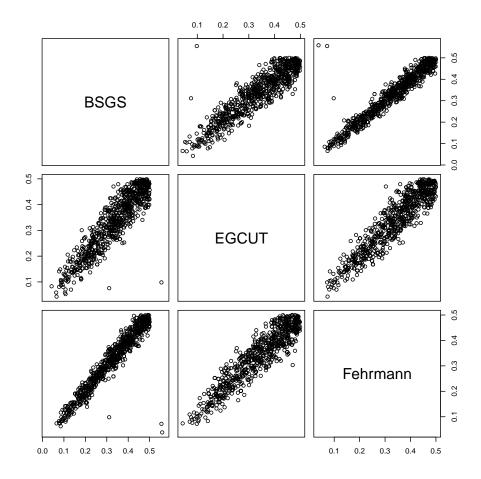


Figure S11: Comparison of allele frequencies for 781 SNPs involved in genetic interactions across independent populations Outliers were removed from the analysis as part of the filtering stage during replication.

5 Supplementary Tables

Table S1: Details on 501 interactions discovered in BSGS dataset

	Distance / Mbh					1	0.517			4.231								31.703					0.071																		0.263				
se	ag	60.0	55	2.02	0.87	2.05		88.	0.94	0.57	0.42	0.23	1.01	0.04	0.80	04.	1.16						14.23	0.14	.50	0.54	0.22	0.43	0.24	0.35							0.19	0.13	37	28	.67	0.27	-0.		1.33
- log10 p-values		0.02 0		1.78				1.93 2						0.20			1.02						3.25 14	'				0.50											0.03				0.02 0		0.07
_	_						21.21																															0.0							
Interaction statistic	Fehrmann	0.38	0.02	1.04	0.36	2.04	18.33	1.83	0.92	0.16	0.71	0.27	0.33	0.02	0.44	4.0	08.0						12.18	0.06	0.87	1.15	0.28	0.38	0.90	0.42							0.53	0.01	0.29	0.65	80.9	0.72	0.29	0.31	2.18
Interact	BSGSe	5.82	6.10	6.59	5.59	6.58	6.69	7.15	5.45	6.91	5.93	6.18	6.26	5.75	0.00	5.01	5.60	5.96	6.65	7.64	6.26	5.98	30.72	20.00	6.60	5.66	99.9	3.87	5.02	7.15	4.87	4.32	4.40	3.85	4.61	4.69	6.79	5.90	0 .00 0 00 0 00	4.91	9.42	5.55	5.49	5.45	5.67
	Associationd					ADCK1			AHSA2	AKTIP								ARL17B	ARL17B								C130RF18	C14OBE179	C140RF173								C17ORF60	CIORF86	CIORF86	ZNF641		C5ORF4	CSORF59	CSORF59	CSORF59
SNP 2	Pos/Mb ^c	158100199	136057883	72001517	122933691	78088813	75929517	61119471	61388355	53489705	125543391	179323762	161996349	3032625	154511163	4818792	87918528	44064851	44064851	94722497	125831219	99492045	19738554	129906275	248059423	189150656	46913416	153610164	105189504	238724741	77574438	35427324	63371601	77574438	77574438	77574438	1 6	2082566	2119833	48676038	47764477	154348552	86102223	86102223	86102223
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	rs ID	rs596183	rs914/5/ rs4732202	rs4744894	rs4833241	rs12431896	rs10824092	rs842647	rs1177303	rs13332406	rs1362032	rs1473017	rs11720112	rs4866516	rs3823523	rs4684443	rs2769594	rs8079215	rs8079215	rs1950646	rs2197777	rs2684789	rs873870	rs9804943	rs10888267	rs6553184	rs674754	rs6857876	rs4983382	rs10754644	rs2655991	rs10972462	rs6445340	rs2655991	rs2655991	rs2655991	rs7405659	rs2257182	rs2460002	rs901964	rs11701361	rs286595	rs2896452	rs2896452	rs1004564 rs2896452
	Associationd	ABCA7	ABCA3	ACAT1	ADCK1		ADK	o wow	HLA-G		AKTIP	AKTIP	ALDH3A2	ANG	ANFER	AP3R1	APPI.2			ARL17B	ARL17B	ARLI7B	ARTIE	BID		C11ORF17		C13ORF18		C14ORF173														1000 1000 1000 1000 1000 1000 1000 100	Coone
SNP 1	Pos/Mb ^c	1047161	48771135	108207393	78088813	88462550	76446305	137112421	29938258	57721127	53536345	53536345	19581009	21153299	90363895	77508159	105580918	75768225	35932619	44064851	44064851	44064851	19810050	18213057	18233000	8886260	6259852	46913416	92276674	105189504	13819673	77574438	77574438	70416307	51151724	52083552	63502633	110577257	25711358	48052838	48027084	45866512	36577930	31272238	52273663
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	rs ID	rs3752237	rs9455	rs227064	rs12431896	rs8058066	rs2395095	rs10881585	rs2523971	rs2896940	rs7189819	rs7189819	rs3760489	rs9322855	rs11073891	rs6453374	rs935251	rs12947580	rs2834541	rs8079215	rs8079215	rs8079215	rs4284750	rs8919	rs181405	rs2568061	rs2110603	rs674754	rs11009025 rs3935344	rs4983382	rs1293455	rs2655991	rs2655991	rs4793445	rs6010061	rs7245800	rs9907897	rs2334323	rs2279474 rs7188668	rs4819271	rs9978658	rs1122762	rs12429804	rs12454561	rs7152284
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Expression trait	Probe ID ^b	ILMN_1743205	ILMN 1677814	ILMN_1800008	ILMN_1698777	ILMN_1698777	ILMN-2358626 II.MN 3239130	ILMN_1798308	ILMN_1798308	ILMN_1665982	ILMN_1665982	ILMN_1665982	ILMN_2401641	ILMN_1760727	ILMIN_1763837	II.MN 1768867	ILMN 1765076	ILMN_3231952	ILMN_3231952	ILMN_3231952	ILMN_3231952	ILMN_3231952	II.MN 2134224	ILMN_1763386	ILMN_2372413	ILMN_1752988	ILMN_2196550	ILMN_2196550	ILMN_2393450	ILMN_2393450	ILMN_1804396	ILMN_1804396	ILMIN_1804396	ILMN_1804396	ILMN_1804396	ILMN_1804396	ILMN_1747347	ILMN_1726989	ILMN-2097790	ILMN_1795836	ILMN_1795836	ILMN_1728742	ILMN_1653205	ILMN_1653205	ILMN_1653205
Exp	Gene IDa	ABCA7	ABCA:	ACAT1	ADCK1	ADCK1	ADK	AHSA2	AHSA2	AKTIP	AKTIP	AKTIP	ALDH3A2	ANG	ANFER	AP3R1	APPI.2	ARL17B	ARL17B	ARL17B	ARL17B	ARL17B	ATP13A1	BID	BID	C11ORF17	C13ORF18	C13ORF18	C14ORF173	C14ORF173	C14ORF4	C14ORF4	C14ORF4	C14ORF4	C14ORF4	C14ORF4	C17ORF60	CIORF86	CIORFS6	C21ORF57	C21ORF57	C5ORF4	CSORF59	CSORF59	CSORF59

11.99	SNP 2 SNP
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1 08732819 CPR177 6.04 0.35 0.21 1 08732819 CPR177 6.04 0.05 0.21 1 08732819 CPR177 6.04 0.05 0.21 1 101026374 CSTM1 6.11 0.27 0.19 1 11026574 CSTM1 6.11 0.27 0.19 1 11026574 CSTM1 6.11 0.27 0.19 1 110253241 CSTM1 6.77 0.27 0.19 1 10253246 CSTM1 6.52 0.66 1 5271671 HBC2 5.70 0.25 0.48 1 5271671 HBC2 5.95 0.16 1 213088494 LQK1 6.78 0.06 0.66 1 52808695 HBC2 6.78 0.01 0.24 1 52808695 HBC2 6.06 0.01 0.41 1 52808695 HBC2 0.01 0.41 1 52808695 HBC2 0.01 0.41 1 54808695 HBC2 0.01 0.01 1 54808695 HBC2 0.02 0.02 1 54808695 HB
1 08732819 GPR177 6.04 0.95 0.24 0.34 1 08732819 GPR177 6.86 0.24 0.24 0.34 1 08732819 GPR177 6.86 0.24 0.24 0.34 1 0.25 0.25 0.24 0.24 0.24 0.24 0.24 0.24 0.24 0.24
1 08/32819 GPR177 6.50 0.24 0.24 10 101508261 GSTM1 6.50 0.01 0.24 1 101266754 GSTM1 6.11 0.27 0.19 1 10126574 GSTM1 6.11 0.27 0.19 2 77919015 6.55 0.27 0.31 1 15253246 GSTM1 6.77 0.27 0.31 1 1 15253246 GSTM1 6.55 0.27 0.31 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1 1
1 1026574 GSTM1 5.88 0.64 0.20 1 10266754 GSTM1 6.11 0.27 0.19 1 10265241 GSTM1 6.11 0.27 0.19 1 10263241 GSTM1 6.31 0.27 1.14 2 77919015 6.36 0.57 0.31 3 5877017 6.52 0.27 0.31 1 5277671 HBG2 5.47 0.00 0.66 1 5277671 HBG2 5.98 0.15 0.24 1 51308849 LQK1 6.78 0.08 0.52 1 5309695 HBG2 6.06 0.01 0.41 1 5408695 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.06 0.00 0.00 1 5408605 6.00 0.00 0.00 1 5408605 6.00 0.00 0.00 1 5408605 6.00 0.00 0.00 1 5408605 6.00 0.00 0.00 1 5408605 6.00 0.00 0.00 1 5408605 6.00
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110266754 GSTMI 6.11 0.27 0.19 110253241 GSTMI 6.77 0.27 1.14 110253241 GSTMI 6.77 0.27 1.14 120253241 GSTMI 6.77 0.27 0.31 120253241 GSTMI 6.75 0.27 0.31 120253241 GSTMI 6.75 0.27 0.31 120253241 GSTMI 6.52 0.25 0.48 11 5271671 HBG2 5.95 0.15 0.24 1213088494 LQKI 6.78 0.08 0.52 11 5309695 HBG2 6.42 0.01 0.41
1 110266754 GSTM1 5.91 0.27 1.14 1 110252341 GSTM1 6.77 0.25 1 77919015 6.72 0.66 1 19532546 5.70 0.25 0.48 1 1 5271671 HBG2 5.97 0.00 0.66 1 1 5271671 HBG2 5.98 0.15 0.24 1 1 11 5271671 GCT 6.00 0.66 1 1 527368494 LQK1 6.78 0.08 0.52 1 141533835 HBG2 6.72 0.01 0.41
1 110253241 GSTM1 6.77 0.66 15 7791015 6.36 0.52 0.66 21 1953246 5.70 0.27 0.31 11 5271671 HBG2 5.47 0.00 0.66 11 5271671 HBG2 5.98 0.15 0.24 1 21308849 LQK1 6.78 0.08 0.52 4 141533832 6.42 0.01 0.46 11 5309695 HBG2 6.06 0.01 0.41
2 77919015 6.36 0.52 0.66 1 5.8577017 6.52 0.57 0.31 21 19532546 19632546 0.27 0.31 11 5271671 1HBC2 5.47 0.00 0.66 11 5271671 1HBC2 5.98 0.15 0.24 1 213088494 LQK1 6.78 0.08 0.52 4 141538382 1BG2 6.78 0.01 0.41 11 5306995 1BG2 6.06 0.01 0.41
15 85877017 6.52 0.27 0.31 21 1953246 6.52 0.27 0.31 11 5271671 HBG2 5.47 0.06 0.66 11 5271671 HBG2 5.98 0.15 0.24 1 213088494 LQK1 6.78 0.08 0.52 4 1415383322 6.42 0.01 0.46 11 5309695 HBG2 6.06 0.01 0.41
21 19532546 5.70 0.25 0.48 11 5271671 HBC2 5.47 0.00 0.66 11 5271671 HBC2 5.98 0.15 0.24 1 213088494 LQK1 6.78 0.08 0.52 4 1415838392 6.72 0.01 0.46 11 5309895 HBC2 6.06 0.01 0.41
11 5271671 HBG2 5.47 0.00 0.66 11 5271671 HBG2 5.98 0.15 0.24 1 213088494 LQK1 6.78 0.08 0.52 4 141533832 6.42 0.01 0.46 11 5309695 HBG2 6.06 0.01 0.41
1 5271671 HBG2 5.98 0.15 0.24 1 213088494 LQK1 6.78 0.08 0.52 4 1415383832 6.42 0.01 0.46 11 5309695 HBG2 6.06 0.01 0.41
11 2308695 HBG2 6.06 0.01 0.41
1 213086494 LQK1 0.78 0.05 0.05 0.05 1 1 5309695 HBG2 6.06 0.01 0.46
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11 5309695 HBG2 6.06 0.01 0.41

Table S1 - continued from previous page

	Expression trait			-4	SNP 1			•1	SNP 2		Interact	Interaction statistic /	- log10 p-values	values	•
Gene ID ^a	Probe ID ^D	Chr.	rs ID	Chr.	Pos/Mb^{c}	Associationd	rs ID	Chr.	Pos/Mb^{c}	Associationd	$BSGS_e$	Fehrmann ^f	$EGCUT^{t}$	Metag	Distance / Mb ⁿ
HBG2	ILMN_2084825	11	rs12975066	19	35723501	нвсэ	rs2855039	11	5271671	HBG2	5.77	0.08	0.13	0.05	
HBG2	ILMN_2084825	11	rs2855039	: :	5271671	HBG2	rs12503379	4 4	141533832	111	86.0	00:00	0.46	0.10	
HDAC7	ILMN_3266186	12	rs2109029	16	6036851		rs4760636	12	48173352	HDAC7	5.75				
HEBP1	ILMN_1802557	12	rs3782567	12	13145613	HEBP1	rs17686635	οο į	135220622		5.98	0.15	0.59	0.32	
HEXDC HI A DBA	ILMN-1741180	17	rs1942719	20 5	71237270		rs7213057	17	80378939	HEXDC HI A DB B 6	5.81	1.61	0.34	1.22	
HLA-F	ILMN_1762861	9	rs11660982	f 00	75467313		rs2523404	9	29695713	HLA-H	5.69	1.00	0.47	0.86	
HMBOX1	ILMN_1720059	oo	rs12435486	14	98670849		rs7837237	00	28876221	HMBOX1	6.54	0.92	1.11	1.34	
HMBOX1	ILMN_1720059	œ	rs2837803	21	42112794		rs4732890	œ	28751381	HMBOX1	6.62	0.02	1.01	0.46	
HMBOX1	ILMN_1720059	œ	rs4765451	12	127237464		rs8180944	œ	28904086	HMBOX1	5.80	0.39	3.13	2.52	
HMBOX1	ILMN_1720059	œ	rs587639	œ	132725731		rs7837237	œ	28876221	HMBOX1	6.58	0.55	0.34	0.44	103.850
HMBOX1	ILMN_1720059	œ	rs8180944	00	28904086	HMBOX1	rs4553956	က	189533772		6.88	3.38	0.03	2.20	
HMBOX1	ILMN_1720059	o o o	rs8180944	œ ç	28904086	HMB0X1	rs7810884	! ~ 0	158276926	13000	6.12	0.34	0.66	0.52	
HMBOAL	ILMIN_1720059	XO 1	rs9521666	υ,	170030488		rs8180944	ю 1	28904086	HMBOAI	0.40	0.00	0.20	0.45	
HODO153	ILMIN-2101920	0 -	150094200	0 -	113032400		rs4700510	0 -	110881184	120001	10.02 0.02 10.02	0.00	9.01	10.01	0.041
HSPC157	ILMN 3194087	-	rs6063164	30	46486900		rs4654783		22439520	HSPC157	5.0				
HSPC157	II.MN 3194087		rs662739	0 -	121229893		rs4654783	-	22439520	HSPC157	6.61				
HSPC157	ILMN 3194087	-	rs7088558	0	101884937	CWF19L1	rs4654783		22439520	HSPC157	6.48				
IL32	ILMN_1778010	16	rs1554999	16	3115628	IL32	rs4759890	12	131757163		6.90	0.19	0.50	0.29	
IL32	ILMN_2368530	16	rs765044	19	2560423		rs1554999	16	3115628	IL32	5.53	69'0	0.23	0.44	
INPP5E	ILMN_1811301	6	rs8044524	16	81603771		rs1127152	6	139335599	INPP5E	5.58	1.46	0.84	1.55	
JAZF1	ILMN_1682727	7	rs757355	12	47970693		rs849341	4	28288174		8.16	0.02	0.26	0.05	
KCNJ15	ILMN_1675756	21	rs2186344	21	39606769	KCNJ15	rs424299	11	5570771		5.64	0.65	0.13	0.33	
KIR2DS5	ILMN_1691803	19	rs649216	19	55324635	KIR2DL1	rs6419960	4	189055298		4.74	0.46	0.89	0.77	
KTELC1	ILMN_1811104	က	rs4349034	13	84597119		rs727905	က	119119433	KTELC1	5.53	0.08	08.0	0.37	
KTELC1	ILMN_1811104	က	rs6815953	4	183109012		rs6414283	က	119195913	KTELC1	5.45	0.64	80.0	0.28	
L3MBTL2	ILMN_2336109	55	rs4822006	22	41519362	L3MBTL2	rs1294338	-	233438952		5.88	0.33	0.04	0.09	
LAP3	ILMN_1683792	4	rs7042087	6	132602868		rs7658240	4	17588950	LAP3	5.72	0.24	0.47	0.31	
LAX1	ILMN_1769782	·	rs1891432	H ;	203877662		rs10900520	٠,	203780591		19.16	18.60	11.22	29.24	0.097
LDLKAPI	ILMN_1809040	- ţ	rs1552032	10	59971635		1121020	⊣ 1	25889632	LDLKAPI	6.00	0	9		
LGALSS	ILMIN-2412214	7.7	rs12450521	10	20083392	111 0 4 5	rs11/49/2/	υ ō	71561407		0.TO	0.35	0.40	0.34	
LINSI	ILMN 2338197	2 12	rs3639332	9 12	101120963	LINSI	rs/1278387	0 0	127804531		0.00	0.43	0.03	0.03	
LRRC25	ILMN 2150196	61	rs6009951	22	51151350		rs8101804	61	18496107	L.B.R.C25	2.68	0.11	0.35	0.15	
LY86	ILMN_1807825	9	rs977785	9	6588881	LY86	rs1543675	н	78946879		5.61	0.13	0.15	0.07	
LYZ	ILMN_1815205	12	rs2168029	12	69734641	LYZ	rs11981725	-1	154137150		5.95	0.15	0.03	0.03	
LYZ	ILMN_2162972	12	rs177820	18	77276964		rs2168029	12	69734641	LYZ	5.71	0.49	0.03	0.16	
LYZ	ILMN_2162972	12	rs2168029	12	69734641	LYZ	rs2253135	6	130319560		6.31	0.61	0.36	0.49	
MADILI	ILMN_2358069	,	rs//83/15	, ,	1923385	MADILI	rs6414306	n	127011798	00.100	5.62	0.25	0.88	0.59	
MADZLIBP	ILMN_1694711	9 6	rs7983718	13	103203146		rs1096699	9 0	43528441	MAD2LIBP	5.93	0.63	1.11	1.09	
MAPILCSA	ILMIN_I776188	20	rs974607	77	70005015		rsb0b0034	0.7	33351864	MAPILC3A	10.0	1.18	0	п 2	
MBNLI	ILMIN-2313138	00	rs10869600	. c	0033070		rs13069559	9 0	152187451	MBNLI	6.70	67:0	0.27	0.04	
MBNL1	ILMN_2313158	0 00	rs1164596	13	97100681		rs13069559		152187431	MBNL1	7.38	1.43	0.63	1.34	
MBNL1	ILMN_2313158	8	rs11981513	7	94648239		rs13069559	က	152187431	MBNL1	7.71	0.43	5.36	4.58	
MBNL1	ILMN_2313158	3	rs16864367	3	152234166		rs13079208	က	152116652		13.49	16.25	24.74	41.56	0.118
MBNL1	ILMN_2313158	က	rs2030926	9	114067127		rs13069559	က	152187431	MBNL1	7.10	0.91	5.80	5.53	
MBNL1	ILMN_2313158	က	rs218671	17	6604708		rs13069559	က	152187431	MBNL1	7.63	0.62	5.82	5.23	
MBNL1	ILMN_2313158	no	rs2213360	22	34291750		rs13069559	ကဂ	152187431	MBNL1	6.05	0.52	0.72	0.70	
MBNLI	ILMN_2313158	0 00	rs2614467	1.5	99770138		rs13069559	0 00	152187431	MBNL1	5.74	4.13	2.22	5.30	
														Continue	Continued on next page

Expression trait	i			SNP 1				SNP 2		Interact	Interaction statistic /	- log10 p-values	values	
$^{ m Chr}$		rs ID	Chr.	Pos/Mb^{\sim}	Association	rs ID	Chr.	Pos/Mb^{\sim}	Association	BSGSc	Fehrmann [*]	EGCUT.	Metas	Distance / Mb ^{II}
ကက		rs4392535 rs4735830	4 x	41513423 895841		rs13069559 rs13069559	ကက	152187431 152187431	MBNL1 MBNL1	8.39	0.02	4.33	3.02	
n m		rs4939558	18	46278591		rs1522374	က	152235530		7.72	0.03	0.27	0.07	
က	_	rs6128397	20	57253132		rs16864367	3	152234166		7.22	1.34	1.15	1.73	
e ;		rs7710738	ro i	22101322		rs13069559	8	152187431	MBNL1	7.92	2.55	7.89	9.28	
20 20 20 20		rs6079849	500	15462611		rs2051344	20 00 	74715653	MBP	6.26 7.56	0.10	0.03	0.02	
18		rs2051344	181	74715653	MBP	rs1125539	9 00	155204939		5.79	0.02	0.76	0.27	
18	_	rs2051344	18	74715653	MBP	rs2619046	'n	55097534		6.03	0.15	0.50	0.26	
18		rs4805021	19	33436367		rs2051344	18	74715653	MBP	5.82	0.03	0.47	0.14	
18	_	rs8092433	18	74747424		rs4890876	18	74732087		5.40	7.06	21.91	28.73	0.015
6	_	rs13039689	20	51922071		rs966396	6	123453281	MEGF9	4.63	1.13	1.33	1.71	
П		rs7989895	13	109401737		rs4846085	-	12050634	MFN2	5.76	0.61	0.25	0.41	
7	_	rs12718598	7	50428445	MGC13057	rs11725347	4	171860973		5.81	0.13	0.30	0.14	
71		rs674608	18	69070772		rs12718598	-	50428445	MGC13057	5.57	0.07	1.03	0.50	
7	_	rs8058318	16	82628245		rs12718598	7	50428445	MGC13057	7.05	0.11	0.12	0.05	
20	_	rs845787	20	26197931	MGC72104	rs2660665	œ	137526799		4.17	0.02	80.0	0.02	
1	_	rs740441	17	55779644		rs4147592	-1	165600146	MGST3	5.45	0.57	0.27	0.40	
11		rs1805	11	118076069	MPZL2	rs11771552	-	154708716		5.90	0.01	0.23	0.04	
11		rs7316716	12	19953193		rs1805	11	118076069	MPZL2	5.64	0.97	1.08	1.35	
IJ		rs17469061	10	8436432		rs750495	n	1782046	MRPL36	68.9	0.34	0.18	0.19	
10		rs6564769	16	80641040		rs2863095	10	102746503	MRPL43	5.71	0.26			
14	_	rs1950857	14	26710271		rs3811188	14		MRPL52	6.56	0.14	0.44	0.22	
9	_	rs10955512	œ	110202230		rs722269	9	42194916	MRPS10	7.48	0.46	0.70	0.64	
9	_	rs11698155	20	15063214		rs2395803	9	42158596	MRPS10	6.85	0.31	0.63	0.46	
_	9	rs1420537	16	52453567		rs13217993	9	42164401	MRPS10	6.21	0.41	0.25	0.28	
1	15	rs7178375	15	31215935	MTMR10	rs12431444	14	42068689		5.18	1.87	1.87	2.86	
(1)	21	rs459498	21	42795027		rs11160227	14	95514596		6.31	0.46	0.52	0.50	
.71	7.7	rs459498	7.7	42795027		rs4973801	n	26706382		0.83	0.11	0.50	0.23	
. 4 7	77	rs459498	21	42795027		rs8130120	21.	29363604	0000	6.78	0.29	0.92	0.65	13.431
		rs10134030	1.4	100550110		rs131/149	Ξ.	47480880	MYBPCS	0.00	0.13	0.46	0.23	
	1 2	TS1322100	0 0	109000001	MVOM	rs/124001	- 0	10770014	MIDFO	0.00	40.0	0.0	0.07	
٠.	0 0	rs4/900/0	0 9	007/470	M I OM I	TSZ101422	0 9	104400201	MADDA	0.07	4.00	0.10	0.40	000000
-		rs12444224	10	147638793		rs11049250	0 7	76870220	NADY.	0.0 4.0 4.0	0.20	0.03	i. c	00.940
	, 4	rs2071856	22	37770630		rs6826085	4 4	76870229	NAAA	5.46	0.27	0.43	0.30	
	00	rs2123758	i oc	144663661	NAPRTI	rs2786014	-	234897243		80.9	0.07	0.48	0.18	
	00	rs2123758	00	144663661	NAPRT1	rs3889129	00	144613680		8.45	15.12	16.08	30.77	0.050
	- 00	rs2123758	00	144663661	NAPRT1	rs4862705	4	187445552		5.62	1.27	0.19	0.81	
	œ	rs2123758	œ	144663661	NAPRT1	rs6455553	9	167811764		6.12	0.87	0.76	1.01	
	00	rs2123758	œ	144663661	NAPRT1	rs700276	7	146189057		98.9	1.10	2.58	2.77	
	œ	rs2123758	œ	144663661	NAPRT1	rs7571561	7	213386267		6.03	0.13	0.47	0.23	
	œ	rs2208123	22	48214812		rs2123758	œ	144663661	NAPRT1	6.60	0.29	0.88	0.63	
~	m	rs4743420	6	103488089		rs2123758	œ	144663661	NAPRT1	5.50	0.12	0.17	80.0	
1	19	rs1405655	19	50882619	NAPSB	rs930280	6	98391111		5.58	0.82	0.10	0.40	
19	_	rs1405655	19	50882619	NAPSB	rs10882406	10	95976932		5.58	0.67	1.10	1.12	
-	19	rs1405655	19	50882619	NAPSB	rs7577137	7	234721287		5.58	2.11	0.44	1.71	
	21	rs7563453	73	232301670		rs4973397	7	232291471		7.31	7.51	6.33	12.70	0.010
_	12	rs2746971	22	37101890		rs11107847	12	95386791	NDUFA12	3.88	0.39	0.18	0.22	
_	01	rs10906857	10	15239498	NMT2	rs12490878	3	183114008		6.84	0.42	0.34	0.35	
	9	rs2967636	19	7067773		rs9302752	16	50719103	NOD2	5.90	0.24	0.04	90.0	
	0.0	rs11063498	17	5209048		rs7923609	10	65133822	NRBF2	5.45				
2	1	000000000000000000000000000000000000000	11	***************************************		000000000000000000000000000000000000000	2	10000	7 7777	000			Continu	Continued on next name
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Probe Prop. Prop	Expression trait				SNP 1				SNP 2		Interact	Interaction statistic /	- log10 p-values	values	
10 reduction decided 4	Probe ID ^b	Chr.	rs ID	Chr.	Pos/Mb^{c}	Associationd	rs ID	Chr.	Pos/Mb^{c}	Associationd		Fehrmann ^f	EGCUT	Metag	Distance / Mbh
1 10,000	ILMN_3237385	10	rs6025645	20	56157341		rs7923609	10	65133822	NRBF2 NRBF2	5.45				
8 minoson mino	ILMN_1800897	1	rs4852124	- 61	240680022		rs6588415	1	52334047	MINDE	6.13	0.47	0.05	0.17	
12 nillididadi ilitatis 11 11486050 nillididadi ilitatis 11 11486050 nillididadi ilitatis 11 11486050 0AST 413 0.55 0.00 0AST 0.00 0AST 0.00 <td< td=""><td>ILMN_1787885</td><td>œ</td><td>rs5017351</td><td>11</td><td>25453482</td><td></td><td>rs1005901</td><td>œ</td><td>21964378</td><td>NUDT18</td><td>5.44</td><td>0.03</td><td>0.46</td><td>0.15</td><td></td></td<>	ILMN_1787885	œ	rs5017351	11	25453482		rs1005901	œ	21964378	NUDT18	5.44	0.03	0.46	0.15	
12 mistages m	ILMN_1658247	12	rs11613438	12	113480510		rs1047944	9	163997467		8.59	1.27	1.55	2.03	
10. 1.00 1	ILMN_1658247	17	rs13311	12	113448652		rs2072133	12	113409260		4.13	4.12	0.81	3.86	0.039
1 17,8555507 2 17,755469 CSPP1 CSP	ILMN_1675640	12	rs2892233	13	49160255		rs3741981	15	00000	OASI	4.38	0.87	0.46	0.76	
11 17,220,079 2.1 2.00,024.23 2.00,024.24 2.00	ILMN-2381899	01;	rs7192613	16	74286646		rs17512962	01	13169066	OFTN	5.64	0.42	0.06	0.14	
9 FATABOLIS DE CONTRILIS PATABOLIS DE CONTRILICATION FATABOLIS DE CONTRILICATION </td <td>ILMN_2307032</td> <td>11</td> <td>rs2829679</td> <td>21</td> <td>26662543</td> <td></td> <td>rs998639</td> <td>11</td> <td>3149249</td> <td>OSBPL5</td> <td>5.00</td> <td>0.36</td> <td>0.00</td> <td>0.07</td> <td></td>	ILMN_2307032	11	rs2829679	21	26662543		rs998639	11	3149249	OSBPL5	5.00	0.36	0.00	0.07	
1 FAZZASTYO 10 CAPTA NAME CSTF11 PATABLES 171080823 OVERPL 5.42 1.20 0.03 1 FAZZASTYO 1 20123008 3 101040447 5.64 0.08 0.12 0.12 1 FAZZASATO 1 146726182 PCYOXIL r624030 3 0.08 0.08 0.09 0.01 12 FAZZASAGA 2 40167303 PCYOXIL 12 7.06442 PEXA 6.0 0.0 0.0 13 FAZZASAGA 1 7.076442 PEXA 6.0 0.0	ILMIN_I742456	. מ	rs17780195	Į.Į	70624189		rs22/3/70	ומ	77755469	CSTFI	5.42	0.16	0.87	0.49	
1 0.00000000 1.00000000 1.00000000 1.000000000 1.0000000000	ILMN-1742456	n ,	rs2273770	n ,	77755469	OSTFI	rs7718088	Ω,	179590952		5.42	1.20	80.0	0.62	000
1 1	ILMN_1734542	-	rs10802822	-	240132968		rs1264898	_	111992823	OVGP1	5.43	0.13	1.48	0.88	128.140
5 ##3248340 5 ##324840 6 ##324840 6 ##324840 7 ##324840 7 ##324840 7 ##324840 8 ##324840 9 PAM ##32440 PAM ##324840 PAM PAM PAM PAM <t< td=""><td>ILMN_1734542</td><td>-</td><td>rs347331</td><td>n :</td><td>140148107</td><td></td><td>rs1264894</td><td>-</td><td>111969719</td><td>CVGFI</td><td>6.04</td><td>0.25</td><td>1.21</td><td>0.82</td><td></td></t<>	ILMN_1734542	-	rs347331	n :	140148107		rs1264894	-	111969719	CVGFI	6.04	0.25	1.21	0.82	
15 FRANKSHOUND 1 JARY 2019 PEX.D A.18 A.18 <td>ILMN_2313901</td> <td>io i</td> <td>rs28092</td> <td>io i</td> <td>102149795</td> <td>PAM</td> <td>rs784600</td> <td>- 0</td> <td>40139553</td> <td>HPCAL4</td> <td>5.59</td> <td>0.66</td> <td>0.44</td> <td>0.59</td> <td></td>	ILMN_2313901	io i	rs28092	io i	102149795	PAM	rs784600	- 0	40139553	HPCAL4	5.59	0.66	0.44	0.59	
12 12 12 12 12 12 12 12	ILMN_1815951	ro.	rs2438490	o	148726162	PCYOXIL	rs2731939	n	21395989		6.20	0.19	0.26	0.16	
12 Fig405797 15 74,246,642 Fig4328748 12 7364442 PEX 5 5.74 0.34 0.09 11 rest3288233 12 49151303 rest3284233 12 49151404 rest3284233 19 40029446 PGLYRP1 rest3288233 19 40029446 PGLYRP1 rest3288233 19 40029446 PGLYRP1 rest3288233 19 40029446 PGLYRP1 rest328233 19 70000 0.00 </td <td>ILMN_1660232</td> <td>12</td> <td>rs10444467</td> <td>12</td> <td>128052636</td> <td></td> <td>rs4329748</td> <td>12</td> <td>7364442</td> <td>PEX5</td> <td>5.85</td> <td>0.09</td> <td>0.71</td> <td>0.32</td> <td>120.688</td>	ILMN_1660232	12	rs10444467	12	128052636		rs4329748	12	7364442	PEX5	5.85	0.09	0.71	0.32	120.688
13 18131090 22 401511030 PGTAPRA 5.64 0.87 0.36 21 18131090 22 140151030 PGCS9467 1.4 2195267 PGAPA 6.51 0.65 0.65 22 1847072 22 3167518 PHKRP 182038876 PGAPA 6.51 0.69 0.60 22 1847072 22 3167518 PHKRP 182038876 PGAPA 6.51 0.60 0.00 22 18470672 22 3199917 PHKRP 6.53 0.00 0.00 22 18470672 22 3199917 PHKRP 6.33 0.00 0.00 22 18470674 22 21918284 1870 0.00 0.00 0.00 22 1847064 18 18472700 184706 1870 0.00 0.00 0.00 22 1847064 18 18472700 184706 18470 1870 0.00 0.00 0.00 0.00 </td <td>ILMN_1660232</td> <td>12</td> <td>rs7495797</td> <td>15</td> <td>27246462</td> <td></td> <td>rs4329748</td> <td>12</td> <td>7364442</td> <td>PEX5</td> <td>5.74</td> <td>0.34</td> <td>0.09</td> <td>0.13</td> <td></td>	ILMN_1660232	12	rs7495797	15	27246462		rs4329748	12	7364442	PEX5	5.74	0.34	0.09	0.13	
11 pt.2082333 19 4652466 PCLYRP1 rsi2082336 PCTARBO Feb. 55.1 0.03 0.05 22 rst2082333 11 23097368 PCLYRP1 rsi208634 1 7670806 PPCA 5.51 0.03 0.09 22 rst40440 2 3157185 PPISD rsi206834 1 7778697 PPCA 5.53 0.02 0.09 22 rst40440 2 3157186 PPISD rsi204881 1 1 0.00 </td <td>ILMN_1797893</td> <td>13</td> <td>rs131969</td> <td>22</td> <td>49151303</td> <td></td> <td>rs7328733</td> <td>13</td> <td>33126737</td> <td>PFAAP5</td> <td>5.64</td> <td>0.87</td> <td>0.36</td> <td>0.67</td> <td></td>	ILMN_1797893	13	rs131969	22	49151303		rs7328733	13	33126737	PFAAP5	5.64	0.87	0.36	0.67	
11 response PRADE PRADE <th< td=""><td>ILMN_1704870</td><td>19</td><td>rs12982353</td><td>19</td><td>46529456</td><td>PGLYRP1</td><td>rs1263806</td><td>14</td><td>21982957</td><td></td><td>6.51</td><td>0.03</td><td>0.65</td><td>0.24</td><td></td></th<>	ILMN_1704870	19	rs12982353	19	46529456	PGLYRP1	rs1263806	14	21982957		6.51	0.03	0.65	0.24	
22 read/14/104 22 21/20/51 read/18/52 22 11/20/51 read/18/52 22 11/20/51 read/18/52 22 11/20/51 read/18/52 22 21/20/51 22/20/51 11/20/51 read/18/52 22/20/51 21/20/51 22/20/51 21	ILMN_1812552	11	rs493642	11	123097386		rs10736812	11	76708086	PHCA	5.51	0.36	06.0	0.70	46.389
22 re470072 22 33265131 PISD re1049831 14 3038876 5.23 0.02 0.04 22 re470072 22 33263131 PISD re654874 1 30397775 PISD 4.12 0.00 0.00 22 re715572 22 33234031 PISD re675844 2 32097775 PISD 4.12 0.00 0.00 0.00 2 re11639998 16 46271604 re675844 2 1.018470 6.13 0.01 0.00 0.00 11 re1163998 16 4668225 re102000 1 1.018470 6.14 0.01 0.00 0.01 14 re103908 16 4668225 1 1.0184871 0.01 </td <td>ILMN_1719986</td> <td>22</td> <td>rs4141404</td> <td>22</td> <td>31675185</td> <td>PIK3IP1</td> <td>rs2065841</td> <td>-</td> <td>61728597</td> <td></td> <td>5.60</td> <td>0.20</td> <td>0.01</td> <td>0.03</td> <td></td>	ILMN_1719986	22	rs4141404	22	31675185	PIK3IP1	rs2065841	-	61728597		5.60	0.20	0.01	0.03	
22 rid51875 2 3199917 PISD rid51875 2 3199917 PISD rid51875 2 100 110 2 rid51875 2 3199917 PISD rid51875 2 10182481 PINED 6.35 0.16 0.42 1 rid589411 5 18781004 rid587 PINED 6.35 0.16 0.13 0.04 1 rid50308 6 457109 rid588048 1 0.18 0.13 0.13 0.03 1 rid5030170 1 5885086 rid5120009 1 2144716 PPPRARA 6.16 0.03 0.13 1 rid528677 1 12244716 PPPRARA 5.75 0.05 0.13 1 rid580083 rid5120009 1 21244716 PPPRARA 5.75 0.03 0.13 1 rid580084 rid5120009 1 21244716 PPPRARA 5.75 0.03 0.13 1 <td>II.MN 1793934</td> <td>66</td> <td>rs470072</td> <td>22</td> <td>32263131</td> <td>PISD</td> <td>rs10498313</td> <td>14</td> <td>30398876</td> <td></td> <td>5 23</td> <td>0.00</td> <td>0.87</td> <td>0.33</td> <td></td>	II.MN 1793934	66	rs470072	22	32263131	PISD	rs10498313	14	30398876		5 23	0.00	0.87	0.33	
22 re651875 2 32097775 PISD 4.12 0.05 0.42 2 re715572 2 3324931 re6518784 2 219087775 PISD 4.12 0.05 0.04 9 re16880411 5 18781004 re572109 re572844 2 219182481 PNRLA 6.35 0.05 0.04 14 re101019 2 45682056 re11156875 1 755930 PPPERS 4.44 0.23 0.04 14 re102303775 2 10.8503064 re1120009 1 212447167 PPPERS 4.44 0.03 0.04 1 re622861 1 1747287 1 1747208 re1120009 1 21244767 PPPERS 5.44 0.05 0.04 1 re622861 1 1747787 PPPERS 5.44 0.03 0.04 1 re622861 1 121244767 PPPERS 5.44 0.09 0.04 <	II.MN 1793934		re6518752	000	31999197	DISD	re954697	-	18236681		1.0	00.0	01.1	0.00	
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9 Figure 100 Common Name Figure 100	II MIN 1774604	4 0	1110012	4 4 1	150701504		190019104	4 0	10101010	GING	1 0	91.0	7.0	0.10	101.1
11 FFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFFF	TIMIN TOUGHOUT	110	110000411		100/01004		184012004	N (140401100	LIND TATUM	0.5	0.10	70.0	70.0	
11 FF911019 20 49902230 FFF1010 7.5199310 FFF1010 0.29 0.442 0.429 0.429 0.442 0.429 0.442 0.429 0.442 0.442 0.442 0.444	ILMIN-1662587	, .	rs11039998	910	4527109		rs928046	n -	14048/108	PNFLA/	0.10	0.31	0.0	0.00	
14 FF12914003 15 38201991 FF12741ATG PFP2RAG 5.81 0.12 0.48 1 F812914003 15 121447167 PPP2RAG 5.63 0.72 0.48 1 F81202003 1 212447167 PPP2RAG 5.63 0.03 0.03 1 F81202003 1 212447167 PPP2RAG 5.63 0.03 0.03 1 F862234 1 10741728 F812120009 1 212447167 PPP2RAG 5.63 0.03 0.03 1 F862234 1 10741728 F812120009 1 212447167 PPP2RAG 5.63 0.03 0.03 1 F86019823 4 5.64 5.67 0.06 0.13 0.14 1 F87619823 4 5.64 5.73 0.05 0.13 0.14 1 F87619823 4 5.64 5.73 0.05 0.13 0.14 2 1 F876108034	1LMIN_16/5656	1;	1901199	07:	49008255		rs4/58001	1;	0.000000	PFFIBF2	4.44	0.29	0.33	0.20	
1 FF12030170 2 10539404 FF12120009 1 21447167 FFP2R5A 5.03 0.72 0.75 1 FF12032150 2 15505064 FF12120009 1 21447167 PPP2R5A 5.75 0.05 0.75 1 FF1263255 13 66222691 FF12120009 1 21447167 PPP2R5A 5.65 1.05 0.05 1 FF757871 6 135030045 FF12120009 1 21447167 PPP2R5A 5.65 1.05 0.05 1 FF757871 6 135030045 FF12120009 1 212447167 PPP2R5A 5.65 0.05 0.05 1 FF757871 6 135030045 FF12120009 1 212447167 PPP2R5A 5.72 0.05 0.03 1 FF7040482 7 1400099 1 212447167 PPP2R5A 5.72 0.06 0.03 1 FF7040482 7 1400099 1 212447167	ILMIN_1662617	14	10000170	15	58350896		rs11156875	14	35619816	PPPZK3C	10.01	0.12	0.42	0.19	
1 F812429633 1 C12324064 F812120009 1 212447167 PPP2R5A 5.77 0.08 0.13 1 F8582334 1 107417238 F812120009 1 212447167 PPP2R5A 5.61 0.08 0.13 1 F8582334 1 107417238 F812120009 1 212447167 PPP2R5A 5.65 1.69 0.03 1 F87871778 9 27144847 F812120009 1 212447167 PPP2R5A 5.65 0.16 0.03 1 F8787177 9 27144876 F812120009 1 212447167 PPP2R5A 5.60 0.16 0.03 1 F88019823 1 95040482 F812120009 1 212447167 PPP2R5A 5.61 0.06 0.13 1 F8801982 1 4508830 1 450880 1 0.14 0.03 0.11 2 F8802864 1 1 12447167 PPP2R5A 5.	ILMIN_1,50,04	٠,	0/1000181	۷ (100288401		FS12120009	٠,	101/44717	FFFZNSA	0.00	0.72	0.40	00.00	
1 rs682934 13 06222091 rs12120009 1 212447167 PPP2R6A 5.61 0.36 0.13 1 rs623304 3 13 107417238 rs12120009 1 212447167 PPP2R6A 5.65 1.06 0.28 1 rs6757871 6 135030045 rs12120009 1 212447167 PPP2R6A 5.65 0.06 0.028 1 rs6019823 14 95040482 rs11200009 11 61447167 PPP2R6A 5.65 0.37 0.06 1 rs2883357 16 28867776 rs10600990 11 61482807 PPP2R6A 5.65 0.37 0.06 2 rs2883372 2 47931652 rs10600990 11 6148280 7.34 0.53 0.03 2 rs2883377 2 47836864 5 7.84 0.53 0.03 4 rs386064 18 439883854 rs61 rs60384 rs11 7.74 <	ILMIN_1738784	-	rs12423255	7.7	123595064		rs12120009	-	212447167	PPPZR5A	5.72	0.08	0.95	0.46	
1 rse622334 1 10741738 rse12120009 1 212447167 PPP2R5A 5.65 1.69 0.28 1 rse7871374 9 27144475 rse12120009 1 21447167 PPP2R5A 5.65 0.16 0.06 1 rse7871378 9 27144475 rse12120009 1 21447167 PPP2R5A 5.95 0.16 0.06 1 rse1218355 16 23867776 rse10600990 1 21447167 PPP2R5A 5.72 0.16 0.06 1 rse1283571 2 1 47931663 C21ORF57 rse10492793 16 12639807 6.73 0.01 0.14 2 rse266937 1 47931663 C21ORF57 rse1204044 PSMB1 5.73 0.01 0.03 6 rse3660937 2 47931663 1 4775824 4.81 0.03 0.04 0.14 6 rse610936 2 1 4775824 4.81	ILMN_1738784	-	rs1889083	13	66222691		rs12120009	-	212447167	PPP2R5A	5.61	0.36	0.13	0.17	
1 rsy757871 6 136030045 rsy12120009 1 212447167 PPP2R5A 5.95 0.37 0.06 11 rs98019823 14 95040482 rs11600990 11 64082807 PRDX5 5.95 0.37 0.01 11 rs8019823 14 95040482 rs11600990 11 64082807 PRDX5 6.43 0.31 0.14 1 rs28039323 21 47931653 C21ORF57 rs98817 6.43 0.03 0.03 2 rs28239372 21 4508362 C21ORF57 rs958174 PSMB1 0.00 0.03 6 rs2839372 22 14083682 C21ORF57 rs958174 PSMB1 0.00 0.03 6 rs4890648 18 43983954 rs922843 6 170890384 PSMB1 5.79 0.04 0.04 6 rs6069890 10 170829379 1 170829379 PSMB1 5.79 0.04 0.04	ILMN_1738784	-	rs682334	11	107417238		rs12120009	-	212447167	PPP2R5A	5.65	1.69	0.28	1.21	
1 rsp87193178 9 27144475 rs12120009 1 21244167 PPP2R5A 5.72 0.16 0.30 1 rs20198375 16 2286776 rs1040970 1 6.443807 F.73 0.16 0.13 21 rs2188355 16 2286776 rs1049773 16 1263880 7.34 0.15 0.14 21 rs2288372 21 47931653 C210RF57 rs11701058 1 4.776882 C210RF57 4.81 0.63 4.47 21 rs28802648 1 121774705 rs11701058 1 4.776882 C210RF57 4.81 0.05 0.13 6 rs28602603 2 3034782 rs1170144 FSMB1 5.79 0.04 0.26 6 rs6060330 2 3034782 rs1082375 FSMB1 5.44 0.44 0.21 7 1 1.7685423 rs1080384 FSMB1 rs276989 1 1.7587744 FSMB1 5.44 <td>ILMN_1738784</td> <td>-</td> <td>rs7757871</td> <td>9</td> <td>135030045</td> <td></td> <td>rs12120009</td> <td>-</td> <td>212447167</td> <td>PPP2R5A</td> <td>5.95</td> <td>0.37</td> <td>90.0</td> <td>0.12</td> <td></td>	ILMN_1738784	-	rs7757871	9	135030045		rs12120009	-	212447167	PPP2R5A	5.95	0.37	90.0	0.12	
11 rs8818352 14 95040482 rs1160990 11 64082807 PRDX5 6.43 0.81 0.11 21 rs2188352 1 47931653 C210RF57 1811009793 16 16838800 7.34 0.53 0.11 21 rs21029331 21 47931653 C210RF57 1811701058 21 4777334 5.79 0.19 0.03 6 rs4800648 11 12174705 rs13207114 PSMB1 5.79 0.04 0.04 6 rs4800648 18 43983854 PSMB1 17087444 PSMB1 5.74 0.09 0.26 6 rs6028843 6 170890384 PSMB1 5.14 0.00 0.26 6 rs6028843 6 170890384 PSMB1 rs12079757 4.45 0.01 0.21 6 rs6028843 6 170890384 PSMB1 rs12079757 4.58 1.95 0.01 0.01 1 rs6028843	ILMN_1738784	-	rs7871178	6	27148475		rs12120009	-	212447167	PPP2R5A	5.72	0.16	0.30	0.16	
16 res288355 16 22867776 res1049273 16 12639360 7.34 0.53 0.11 21 res1089355 16 4381653 C210RF57 res10497346 5.60 0.03 0.03 21 res283972 21 48063862 C210RF57 res11701058 21 47776382 C210RF57 4.81 0.69 4.47 6 res3802648 18 43803854 res028843 6 17080384 pSMB1 5.14 0.09 0.26 6 res060830 20 3034782 res0298415 6 17082379 PSMB1 5.14 0.00 0.26 6 res060830 20 3034782 res0296415 6 17087744 PSMB1 5.14 0.04 0.26 12 res060830 20 3034782 res1020714 6 17087744 PSMB1 6.147 0.00 0.05 12 res031562 17 7568912 11 521825 PTDSS1	ILMN_1711606	11	rs8019823	14	95040482		rs11600990	11	64082807	PRDX5	6.43	0.81	0.14	0.44	
21 rss1292921 21 47931653 C21ORF57 rss95817 18 31497368 C21ORF57 48 14 0.03 0.19 0.03 6 rss286267 11 12177470 rss13207114 6 17089034 5.60 0.19 0.44 6 rss286267 11 12177470 rss12207114 6 17089034 5.14 0.00 0.26 6 rss286267 11 121774762 rss286245 6 17089034 5.14 0.00 0.21 6 rss6228843 6 17089034 8 17089034 9.01 0.21 0.21 6 rs6228843 6 17089034 9 1.03 0.21 0.	ILMN_1713603	16	rs2188355	16	23867776		rs10492793	16	12639800		7.34	0.53	0.11	0.25	11.228
21 rs2839372 21 48063862 rs1710158 21 4777632 C210RF57 4.81 0.69 4.47 6 rs3839372 11 12/74705 rs13207114 6 170890384 PSMB1 5.79 0.04 0.44 6 rs608030 10 3034782 rs6928843 6 170890384 PSMB1 5.14 0.00 0.26 6 rs608030 20 30347822 rs6080384 6 170890384 PSMB1 5.14 0.00 0.26 6 rs608030 20 30347822 rs7080345 6 170890384 PSMB1 5.14 0.04 0.26 1 rs6080384 1 405478823 rs11036212 11 5221825 FDDSS1 5.00 0.03 0.03 1 rs631562 1 7658423 rs11036212 11 521825 PTDSS1 5.90 0.08 0.08 1 rs631562 1 1 7521825 PTDSS1	ILMN_1675038	21	rs1029231	21	47931653	C21ORF57	rs958127	18	31497346		5.60	0.19	0.03	0.04	
6 res8862667 11 121774705 res13207114 6 17087744 PSMB1 5.79 0.44 6 res606036 20 31347832 re6928843 6 170823379 PSMB1 5.14 0.00 0.26 6 re606036 20 31347832 re9295415 6 170823379 PSMB1 5.14 0.04 0.21 6 re606036 20 31347832 re2769689 1 22579787 4.58 1.98 1.36 12 re40692843 6 170850324 1 72579787 4.58 1.38 0.32 12 re4069286 17 7521825 PTDSS1 5.00 0.03 0.48 12 re406926 1 7521825 PTDSS1 5.70 0.02 0.04 12 re404670 6 106348246 1 1 7221825 PTDSS1 5.70 0.02 13 re404670 6 106348246 1 <td< td=""><td>ILMN_1675038</td><td>21</td><td>rs2839372</td><td>21</td><td>48063862</td><td></td><td>rs11701058</td><td>21</td><td>47776382</td><td>C21ORF57</td><td>4.81</td><td>0.69</td><td>4.47</td><td>4.06</td><td>0.287</td></td<>	ILMN_1675038	21	rs2839372	21	48063862		rs11701058	21	47776382	C21ORF57	4.81	0.69	4.47	4.06	0.287
6 rs4890648 18 4988954 rs6928843 6 170890384 PSMB1 5.14 0.00 0.26 6 rs6928843 6 rs6928843 6 170890384 PSMB1 5.14 0.00 0.21 6 rs6928843 6 170890384 PSMB1 rs2797957 4.58 1.95 0.021 1 rs6228843 6 170890384 PSMB1 rs2797957 4.58 1.95 0.64 1 rs7253676 1 1.25521825 PTDSS1 5.00 0.03 0.48 1.2 rs4369205 1 7.05541825 PTDSS1 5.00 0.03 0.48 1.2 rs431622 1 5221825 PTDSS1 5.70 0.03 0.04 1.2 rs63166 1 1 5221825 PTDSS1 5.70 0.03 0.04 1.2 rs63166 1 1 5221825 PTDSS1 5.70 0.03 0.08 1.2	ILMN_1789176	9	rs3862607	11	121774705		rs13207114	9	170877444	PSMB1	5.79		0.44		
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12 rs241730 22 33375704 rs7305307 12 70235726 6.55 0.25 0.08 19 rs1075728 16 43262788 RAFAP rs765344 15 26938488 6.38 0.03 0.31 11 rs1087702 16 5352651 AKTIP rs4892879 11 32136436 RCNI 6.38 0.03 0.31 11 rs4922579 11 32136436 RCNI rs11416997 8 11177468 4.32 0.41 0.09 11 rs4922579 11 32136436 RCNI rs1341899 1 102740645 5.40 0.04 0.26	ILMN_1672443	4	rs4946705	9	106348246		rs10020773	4	17526682	QDPR	5.75	1.03	1.25	1.55	
19 rs1075728 19 42467788 RABACI rs7951628 11 120161117 6.42 0.28 0.84 16 rs9931702 16 53526551 AKTIP rs18633464 15 26938488 6.42 0.28 0.31 1 rs1927313 12 41147155 rs4922579 11 32136436 RCN1 rs11177468 4.32 0.41 0.09 1 rs4922579 11 32136436 RCN1 rs1341899 1 102740645 5.40 0.04 0.26	ILMN_1803197	12	rs241730	22	33375704		rs7305307	12	70235726		6.55	0.25	0.08	0.09	
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	ILMN_1800276	11	rs4922579	11	32136436	RCN1	rs1341899	1	102740645		5.40	0.04	0.26	0.02	

- 1	Distance / Mb ⁿ										0.135																								0.324	14.040												
alues	Metag	1.17	0.06	0.21	0.26	0.70	0.0	0.64	0.13	1.28	17.24	0.38	0.02	0.19	0.15	0.22		1.17	0.15	0.10	0.31	0.35	0.30	0.0	0.17	0.09	90.0	0.19	1.24	0.40	0.26	0.00	1	0.72	23.22			0.83	90.0		0.33	0.31	0.30		0.14	0.24	0.03	C 10
$-\log_{10} p$ -values	$EGCUT^{t}$	1.23	0.10	0.33	0.60	0.21	0.44	0.46	0.30	0.52	14.41	0.73	90.0	0.20	0.37	0.45		1.73	0.51	0.06	0.51	0.12	0.51	0.18	0.18	0.24	0.10	0.13	0.82	0.07	0.58	0.03	1	1.03	10.96			1.41	0.00		0.12	0.17	0.24	0.00	0.16	0.31	0.15	0.76
Interaction statistic /	$Fehrmann^{I}$	0.61	0.14	0.21	0.08	0.42	60.0	0.71	0.11	1.48	3.79	0.13	0.09	0.32	0.10	0.13		0.22	0.02	0.31	0.21	0.70	0.20	0.32	0.29	0.00	0.15	0.39	1.10	0.86	0.09	0.39		0.29	13.11			0.13	0.34		0.67	0.57	0.40	0.01	0.26	0.28	0.03	16.0
Interacti	BSGS ^e I	5.66	5.74	5.12	5.71	0.48 8 - 1	0.11	- 0: 10: - 0: 10:	6.27	4.32	86.4	5.55	5.46	5.86	4.59	4.33	6.48	5.70	5.50	5.67	5.60	5.52	5.97	7.40	5.74	5.47	5.70	6.15	88.0	5.95	5.52	0.10	6.11	09.9	7.31	6.08	0.33	6.45	5.59	5.44	5.65	00 i	0.01	0.00	6.14	5.47	5.55	E 0
-	Association	RERE	KEKE	REKE	KEKE	DNACEG	DIN ASEO					RPL23AP7				RPL8	SEC13	SEMA4A	SESN3	SESN3		PPBP	PFBF	SH3GLB2		SLC22A18			SLC41A3		SLC46A3	SMC	SNHG8	SNORD14A		SNOKD89	SNORD89			SPATA5L1		STYXL1	TITEM	TUFM	SURF6	SYTL2	THBS3	COULTE
SNF 2	Pos/Mb^{c}	8501786	82.1008	8501786	820T.V86	21182800	54668512	36348968	201983242	201983242	89513234	114450028	138038093	66137260	234585790	145984615	10342876	156147326	94906111	94906111	134606425	56849749	56849749	131785369	60489510	2923826	153224179	241678528	125801067	174598073	29259349	65800982	119225940	17291499	17015557	101889306	101889306	81888905	193706323	45652086	72509713	75616105	180439235	28550667	136281753	85495269	155162067	000000
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	rs ID	rs301819	rs301819	rs301819	rs301819	rs/324305	rs4884857	rs11706900	rs2819365	rs2819365	rs2965817	rs4849261	rs17495030	rs1502991	rs1619856	rs2958482	rs696221	rs7695	rs684856	rs684856	rs7004947	rs1354034	rs1354034	rs17455517	rs6842739	rs367035	rs3110874	rs3772054	rs6771703	rs7701916	rs7981190	rs11677815	rs705837	rs214097	rs6486334	rs750783	rs750783	rs7185362	rs1472075	rs4774580	rs1000620	rs17685	18939294 100707084	rs3785354	rs3118663	rs485485	rs4072037	2000100
	Association					KNASEO		RNF167					RPL36AL	RPL36AL	RPL8						NEW NS				SIRPG		SLC22A18	SLC22A18		SLC45A4		SMOX						SNUPN	SNUPN			-	SOLFZ					
SNF I	Pos/Mb^{c}	24987865	135248366	13174312	112844086	8106591	487556	4839930	46127549	67153386	89648580	80320056	50103816	50020817	145984615	4741304	80913946	95388015	104412137	46591793	94906111	43893658	00383979	18196922	1612819	52181798	2923826	2923826	24616743	142337734	55602091	4161500	133050233	46259108	17339127	115929241	26778066	46376528	46376528	41117869	90174526	104947517	40153148 74999054	40119768	56013994	103410782	95422867	00000000
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	rs ID	rs4982958	rs/69/290	rs11085829	rs3852011	rs11628398	re238230	rs400688	rs1107121	rs8071611	rs352935	rs1401202	rs3007033	rs4900928	rs2958482	rs4143674	rs4889214	rs17085428	rs12147460	rs355391	rs684856	rs10838191	rs2545385	rs1034120	rs1535883	rs11673260	rs367035	rs367035	rs1912136	rs6985508	rs949805	rs8118315	rs1105621	rs1520429	rs2634462	rs10445863	rs2135064	rs8134646	rs8134646	rs1131620	rs2221406	rs4073164	rs11700065	rs2836657	rs6099626	rs1375719	rs1939875	02014080
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Expression trait	Probe ID ^b	ILMN_1802380	ILMN-1802380	ILMN_2327795	ILMIN_2327795	ILMIN-1780533	II.MN 1794726	ILMN-1794726	ILMN 1738347	II.MN 1738347	ILMN_2413278	ILMN_2222750	ILMN_2189933	ILMN_2189936	ILMN_1764721	ILMN_1764721	ILMN-3297880	ILMN_1702787	ILMN_1694027	ILMN_1694027	ILMN_1694027	ILMN_1762764	ILMIN-1762764	ILMN 2158336	ILMN_1771801	ILMN_2382505	ILMN_2382505	ILMN_2382505	ILMN_2356111	ILMN_1745778	ILMN_1658639	ILMN 1775380	ILMN_3309349	ILMN_1799381	ILMN_1799381	ILMIN-3238662	ILMN 3238662	ILMN_1733932	ILMN_2364535	ILMN_1729179	ILMN_1717052	ILMN_2210729	ILMIN_2345142	ILMN 2336133	ILMN_1778032	ILMN_2336609	ILMN_1804663	11 MAN 100 4009
	Gene ID ^a	RERE	KEKE	KEKE	KEKE	KNASEO	RNF167	RNF167	RNPEP	RNPEP	RPL13	RPL23AP7	RPL36AL	RPL36AL	RPL8	RPL8	SEC13	SEMA4A	SESN3	SESN3	SESN3	SH3BGRL2	SH3BGRLZ	SH3GLB2	SIRPG	SLC22A18	SLC22A18	SLC22A18	SLC41A3	SLC45A4	SLC46A3	SMOX	SNHG8	SNORD14A	SNORD14A	SNOKD89	SNORD89	SNUPN	SNUPN	SPATA5L1	STARD10	STYXL1	SULFZ	SULTIA4	SURF6	SYTL2	THBS3	TIDES

Probe Dr. Probe Dr. Probe Dr. Probe Dr. Prob Dr. Probe Dr. Dr. Probe Dr.	Chr. rill Chr. Pos/MbF Association of a 1D Chr. Pos/MbF Thill and a 1D <	田	Expression trait			01	SNP 1			.51	SNP 2		Interact	Interaction statistic /	/ - log10 p-values	values	
INAN 1994	LIMN.1786426 19 102359012 1 12335902 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 17226481 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 172264881 1 17226488 1 172264881 1	D^{a}	Probe ID ^b	Chr.	rs ID	Chr.	Pos/Mb ^c	Associationd	rs ID	Chr.	Pos/Mbc	Associationd	BSGSe	Fehrmann ^f	$EGCUT^{f}$	Metag	\
INAN_INFEGRED 10 1970-1979 20 20 20 20 20 20 20 2	ILANIA 1786420 19 17825288 19 17825288 188100050 19 3021025 TMEM149 188100250 19 3021025 TMEM149 18810025 TMEM149 TMEM149 18810025 TMEM149 TMEM14	4	ILMN_1804148	7	rs1940400	11	132389627		rs17725246	7	44581986	TMED4	5.70	90.0	1.34	0.70	
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INAN_1756426	ILAN 1786426 19 1800000518 19 0 452070005 18 180000528 19 0 180000528 10 0 180000528 10 0 180000528 10 0 180000528 10 0 180000528	149	ILMN_1786426	19	rs5762235	22	27925288		rs8106959	19	36219525	TMEM149	6.79				
INAN_1764560 10 10 10 10 10 10 10	LINKLITROGRAM 19 SERIORAD 10 SERIORA	149	ILMN_1786426	13	rs6090518	20	45207005		rs8106959	19	36219525	TMEM149	11.09	0.76	:	1	
INVALITY 1985 198	ILMN 1766426 19 18510650 19 18010622 19 18010623 19 18010623 19 18010623 19 18010623 19 18010620 10 18010620 10 18010620	49	ILMN_1786426	61	rs807491	61	36268923	SNX26	rs7254601	61	36147315	TMEM149	12.16	81.55	45.78	145.78	0.122
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ILANIA TYPOGRAFIA 19 FAMILY 19 F	IMAN_1766426 19 res100696 19 30213052 TMEM.149 res2054648 19 19032508 TMEM.140 res2054648 19 res100696 19 30213052 TMEM.149 res2054648 19 1202373 TMEM.140 res2054648 19 res100696 19 30213052 TMEM.149 res2054648 19 res100696 10 res100696 10	49	II.MN 1786426	61	rs8106959	61	36219525	TMEM149	rs10937361	n on	188359436		10.00 0.00 0.00 0.00	3.61	20.00	3 00 00	
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ILMN 1786426 19 F88100000 19 30210025 TNEM140 ILMN 1786426 19 F88100000 ILMN 1786426 19 F88100000 ILMN 1786426	LANN_1786426 19 188106059 19 32219525 TMEM149 11843376 1 1892281 LANN_1786426 19 188106059 19 32219525 TMEM149 122554456 1 14719227 1 1 1 1 1 1 1 1 1	49	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs1557335	18	64268976		6.95	0.08	0.07	0.03	
ILMN 1786426 19 188100909 19 36210225 TNEM149 TS258101 19 181100509 19 36210225 TNEM149 TS258000 19 13317862 19 181100509 19 36210225 TNEM149 TS258000 19 120005464 19 181100509 19 36210225 TNEM149 TS258000 19 120005460 19 181100509 19 36210225 TNEM149 TS258000 19 120005460 19 181100509 19 36210225 TNEM149 TS258000 19 120005460 19 181100509 19 36210225 TNEM149 TS258000 19 TS25800	LWN 1786426 19 188106059 19 36219525 TMEMI49 19255436 4 113317683 1 118116625 1 188106059 19 36219525 TMEMI49 192554360 7 14719722 1 17719223 1 17719223 1 17719223 1 17719223 1 17719223 1 17719223 1 17719223 1 17719223 1 17719223 1 1 17719223 1 1 17719223 1 1 17719223 1 1 17719223 1 1 17719223 1 1 17719223 1 1 17719223 1 1 1 1 1 1 1 1 1	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs17719594	14	90932598		6.93	3.06	0.77	2.87	
ILANIA 1786445 19 188100050 19 3021052 TMEBALI49 122551458 4 11337753 7 7 0 0 0 0 0 0 0 0	LANN L.786426 19 188106059 19 32219525 TMEM149 192351456 4 11377583 19 188106059 19 32219525 TMEM149 192373711 5 17772223 17772233 17772223 1777223	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs1843357	œ	13822381		6.21	3.72	3.33	6.00	
ILMN.1786426 19 188100650 19 36210552 TMEBA149 17223300 1 147019723 6 70 15.7 15.2 2.7 15.2	ILMN 176426 19 rest100950 9 38219525 TMEM149 re2559000 7 147197272 171792273 171792273 171792274 176426 19 rest100950 19 38219525 TMEM149 re271711 176426 19 rest100950 19 38219525 TMEM149 re271874 1 17792274 1 1779274	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs2351458	4	113317583		7.30	0.04	9.61	8.00	
ILMN.1764426 19 rest100509 19 30510525 TMEM149 rest71281 11 11702273 15 15 10 10 10 10 10 10	IMANIATION TO CONTINUE AND INTEGRACE 19 93219325 TIMEMIAGO TO THE TOTAL TO	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs2539000	7	147619772		6.70	1.57	1.52	2.27	
Image: column Image: colum	ILWN_1786426 19	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs2731711	10	171792273		5.92	0.19	0.33	0.19	
ILANN.1786426 19 rest 1000500 19 36219025 TMEM140 ref 718400 2 233879066 8.55 3.11 5.15 7.36 10. ILANN.1786426 19 rest 1000500 19 36219025 TMEM140 ref 713338 17 81509374 5.60 5.70 5.40 5.10 5.70 ILANN.1786426 19 rest 1000500 19 36219025 TMEM140 ref 713338 17 81509374 5.60 5.70 5.40 5.10 5.70 ILANN.1786426 11 relicator 19 rest 1000500 19 36219025 TMEM140 ref 713338 17 81509374 5.60 5.70 5.40 5.70 ILANN.1706420 11 relicator 19 7250000 19 36219025 TMEM140 ref 71850000 10 relicator 10 relicato	ILMN.1786426 19 res100659 19 36219255 TMEM149 res926382 6 1610889740 ILMN.1786426 19 res100659 19 36219255 TMEM149 res926382 6 1610889742 ILMN.1786426 19 res100659 19 36219255 TMEM149 res913388 17 36957420 ILMN.1786426 19 res106659 19 36219255 TMEM149 res913388 17 36957420 ILMN.178642 11 res124066 13 272806923 18 res146926 13 24388949 ILMN.178640 11 res157446 9 4859334 res1469216 11 res6845 RFF ILMN.1781043 7 res96346 11 1148884 18 71760899 18 1876889 17 18768787 TRAPPCA ILMN.1781045 11 res170884 18 7768194 7768194 7768194 7768194 7768194 7768194 7768194 7768194	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs471728	11	129595460		8.89	0.90	3.62	3.51	
ILANI 1786426 19 rest	ILMN 1786426 19 re81009559 19 36219225 TMEM149 re8003383 1 50377420 ILMN 1786426 19 re81009559 19 36219225 TMEM149 re910440 11 21473952 ILMN 1786426 19 re81009550 19 36219225 TMEM149 re9500428 13 21473952 ILMN 1708459 11 res1254476 19 56058346 res1068630 7 12859348 IRFE ILMN 1708451 7 res108763 12 2287703 res106863 7 128653948 IRFE ILMN 1708451 7 res108763 13 13531675 7 2346863 7 128653948 IRFE ILMN 1708451 7 res108763 13 13531675 7 2346863 18 1784PPC ILMN 1708451 7 res108860 13 17788194 7788194 7788194 7788194 7788194 7788194 7788194 7788194 7788194 7788194 <td< td=""><td>149</td><td>ILMN_1786426</td><td>19</td><td>rs8106959</td><td>19</td><td>36219525</td><td>TMEM149</td><td>rs6718480</td><td>7</td><td>233879066</td><td></td><td>8.55</td><td>3.31</td><td>5.15</td><td>7.36</td><td></td></td<>	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs6718480	7	233879066		8.55	3.31	5.15	7.36	
ILIAN 1.77664.56 19 RESTIGGESO 11 RESTIGGESO 12 RESTIGGESO 12 RESTIGGESO 13 RESTIGGESO 14 RESTIGGESO 15 REST	ILMN 17766426 19 re81009550 19 36219225 TMEM149 re713338 17 80377420 ILMN 17766426 19 re8109550 19 36219225 TMEM149 re914440 1 242889402 ILMN 17706426 19 re8109550 19 36219225 TMEM149 re914426 11 re1548475 19 58058246 re914402 1 226027233 TMEM170849 11 re1548475 19 58058246 re1449226 11 re1548475 12 25287303 re1449226 11 re1548475 12 12 25287303 re1449226 11 re1548475 12 12 25287303 re1449286 11 re144940 re144926 11 re144940 re144926 11 re144940 re144926	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs6926382	9	161683974		5.80	3.06	8.80	10.72	
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LIMALITORAGE 1 PAGENGRAGE 13 TOTAL SAGE AND COLOR AND C	LIMN.1710649 1 res154486 13 72890003 res149226 1 2608133 TMEMINITY ILMN.1708482 1 res1544475 19 58058204 res148830 7 128503948 IRFE ILMN.168831 7 res19973 2 22287303 res10488630 7 128503948 IRFE ILMN.168831 7 res19973 7 22387303 7 128503948 IRFE ILMN.1814650 11 res177652 7 22387307 7 128503948 IRFE ILMN.237639 19 res1776540 18 </td <td>149</td> <td>ILMN_1786426</td> <td>19</td> <td>rs8106959</td> <td>19</td> <td>36219525</td> <td>TMEM149</td> <td>rs9509428</td> <td>13</td> <td>21473952</td> <td></td> <td>9.44</td> <td>0.10</td> <td>5.75</td> <td>4.47</td> <td></td>	149	ILMN_1786426	19	rs8106959	19	36219525	TMEM149	rs9509428	13	21473952		9.44	0.10	5.75	4.47	
ILMN L 1708481	ILMN_1708482 11 re1548475 19 56062346 re1648620 7 12869348 IRF5 ILMN_1688811 7 re157146 9 4859303 re10488630 7 12869348 IRF5 ILMN_188811 7 re157746 9 22287303 re10488630 7 12869348 IRF5 ILMN_184450 11 re1776572 7 22287305 re10488630 7 12869348 IRF5 ILMN_181450 11 re1776540 13 13331675 re208638 re2087887 TRAPPC re2080688 11 118887887 TRAPPC ILMN_287639 19 re1715940 19 7758194 TRAPPC5 re1069004 5 166070604 1 RAPPC4 ILMN_287639 19 re1715940 19 7758194 TRAPPC5 re1069002 1 1769402 1 7758194 TRAPPC5 re1069326 1 17694432 1 1769494 1 1769494 1 1769494 <td< td=""><td>63A</td><td>ILMN_1719649</td><td>Н</td><td>rs1254086</td><td>13</td><td>72890603</td><td></td><td>rs4149226</td><td>1</td><td>226027323</td><td>TMEM63A</td><td>5.60</td><td></td><td></td><td></td><td></td></td<>	63A	ILMN_1719649	Н	rs1254086	13	72890603		rs4149226	1	226027323	TMEM63A	5.60				
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ILMN_1291091 7 128089148 ILMS 17100801 7 128089148 ILMS 17100801 1 10.23 0.17 0.022 ILMN_1291049 7 12808265 1 1 11177015 7 23408358 1 1 0.22 0.03 0.01 0.02 ILMN_12814650 1 1 1 1 1 1 1 0.22 0.03 0.01 0.02 ILMN_12870530 1 1 1 1 1 1 0.02 0.03 0.01 0.02 ILMN_2370530 1 1 1 1 1 1 0.02 0.03 0.01 0.02 ILMN_2370530 1	ILMN 1083811 7 res199703 2 22528927 res10486830 7 12859348 IRF5 ILMN 1181456 11 res1076672 7 res1048831 7 13493358 IRF5 ILMN 1181466 11 res1775672 7 13531675 res1076831 11 118887887 TRAPPC4 ILMN 1281466 11 res1758840 19		ILMN_1683811	-	rs1537146	6	4859303		rs10488630	7	128593948	IRF5	5.61	0.11	0.15	0.07	
LMN_1281043 7 ray775042 7 23428285 1118887887 TRAPPCA 5.51 0.28 0.40 0.29 LMN_1281450 11 raf775870 13 13.018817 TRAPPCA 11 118887887 TRAPPCA 5.51 0.29 0.40 0.29 LMN_1287639 13 raf75840 13 7758194 TRAPPCA 11 118887887 TRAPPCA 5.52 0.37 0.01 0.36 LMN_227639 19 raf75840 19 7758194 TRAPPCA raf3299 1 11888787 TRAPPCA 5.52 0.37 0.21 0.01 0.36 LMN_227639 19 raf758194 TRAPPCA raf37574 6 12 0.37 0.14 0.03 0.03 0.03 0.03 0.04 0.05 LMN_227639 19 raf7158840 19 7758194 TRAPPCA raf765399 12 2369415 7.08 0.04 0.05 LMN_227639 19 raf7158840 <td>ILMN 1731043 7 187778572 7 2353827 131731678 14 158216581 11 118887887 TRAPPC4 ILMN 1844660 11 rs1728842 11 13531675 rs105316781 11 118887887 TRAPPC4 ILMN 1844660 11 rs17158840 19 r7758194 TRAPPC5 rs10023095 1 118887887 TRAPPC4 ILMN 2372639 19 rs17158840 19 r7758194 TRAPPC5 rs1023095 1 242229791 ILMN 2372639 19 rs17158840 19 r7758194 TRAPPC5 rs13322997 1 4749447 ILMN 2372639 19 rs17158840 19 r7758194 TRAPPC5 rs1775899 19 rs17158840 19 r7758194 TRAPPC5 rs1775899 19 rs17158840 19 r7758194 TRAPPC5 rs700399 19 rs17758940 19 r7758194 TRAPPC5 rs700399 19 rs17758940 19 r7758194 TRAPPC5 rs700399</td> <td></td> <td>ILMN_1683811</td> <td>-1</td> <td>rs199793</td> <td>20</td> <td>22287303</td> <td></td> <td>rs10488630</td> <td>-1</td> <td>128593948</td> <td>IRF5</td> <td>5.52</td> <td>1.03</td> <td>0.17</td> <td>0.62</td> <td></td>	ILMN 1731043 7 187778572 7 2353827 131731678 14 158216581 11 118887887 TRAPPC4 ILMN 1844660 11 rs1728842 11 13531675 rs105316781 11 118887887 TRAPPC4 ILMN 1844660 11 rs17158840 19 r7758194 TRAPPC5 rs10023095 1 118887887 TRAPPC4 ILMN 2372639 19 rs17158840 19 r7758194 TRAPPC5 rs1023095 1 242229791 ILMN 2372639 19 rs17158840 19 r7758194 TRAPPC5 rs13322997 1 4749447 ILMN 2372639 19 rs17158840 19 r7758194 TRAPPC5 rs1775899 19 rs17158840 19 r7758194 TRAPPC5 rs1775899 19 rs17158840 19 r7758194 TRAPPC5 rs700399 19 rs17758940 19 r7758194 TRAPPC5 rs700399 19 rs17758940 19 r7758194 TRAPPC5 rs700399		ILMN_1683811	-1	rs199793	20	22287303		rs10488630	-1	128593948	IRF5	5.52	1.03	0.17	0.62	
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ILMN 12372639 19 Fill 19840 19 7758194 TRAPPC5 Fill 198540 19 7758194 TRAPPC5 Trapped TRAPPC5 Trapped TRAPPC5 Trapped Trap	ILMN 2372639 19 7758194 <t< td=""><td>3 5</td><td>ILMIN-2372639</td><td>67.</td><td>rs17159840</td><td>1.0</td><td>7758194</td><td>TRAPPOS</td><td>rs1375714</td><td>٥٠</td><td>156404902</td><td></td><td>6, 6</td><td>0.12</td><td>0.18</td><td>0.08</td><td></td></t<>	3 5	ILMIN-2372639	67.	rs17159840	1.0	7758194	TRAPPOS	rs1375714	٥٠	156404902		6, 6	0.12	0.18	0.08	
ILMN 12372639 19 Fill 1984-0 19 7758194 TRAPPC5 Fish 1984-0 19 7758194 TRAPPC5 Trap 1984-0	ILMN L2372639 19 rs17153840 19 r758194 TMAPPCS rs17153849 19 rs17153840 19 rr758194 TMAPPCS rs17153849 17 rs7494547 TMAPPCS rs7403432 17 rs7404541 TMAPPCS rs7403432 17 rs7404541 TMAPPCS rs7403432 17 rs7404432 18 rs7403432 18 rs740343 18 rs740343 18 rs7404032 18 rs77173 18 rs740403 18 rs740403 18 rs740403 18 rs740403 18 rs740403 18 rs740403 18	ŝ	ILMIN-2372639	2 5	rs1/159840	5 -	7758194	TRAPPCS	rs1393299	٠,	242329791		0.43	0.63	0.47	0.59	i i
ILMN 12372639 19 1817159840 19 7758194 TRAPPC5 187809325 11 18000000000000000000000000000000	ILMN 2372639 19 rs17153840 19 r758194 TRAPPCS rs733382 12 1944442 ILMN 2372639 19 rs17153840 19 r758194 TRAPPCS rs7664937 4 9947811 ILMN 2372639 19 rs17153840 19 r758194 TRAPPCS rs766438 14 85439550 ILMN 2372639 19 rs17153840 19 r7758194 TRAPPCS rs766338 14 85439550 ILMN 2372639 19 rs380708 2 2 2274865 rs8766388 19 7758194 TRAPPCS ILMN 2372639 19 rs7246244 19 7762978 rs17159840 19 7758194 TRAPPCS ILMN 2372639 19 rs7246244 19 7762978 rs10176572 2 255604633 RAPPCS ILMN 2372639 19 rs7246244 19 7762978 rs12827440 16 7758194 TRAPPCS ILMN 12372639 19 rs7246244 19 <t< td=""><td>3 5</td><td>ILMIN-2372639</td><td>2 5</td><td>rs17159840</td><td>n -</td><td>7750104</td><td>TRAPPOS</td><td>rs17703599</td><td>1 0</td><td>2309415</td><td></td><td>0.38</td><td>0.21</td><td>92.0</td><td>0. TO</td><td>0.389</td></t<>	3 5	ILMIN-2372639	2 5	rs17159840	n -	7750104	TRAPPOS	rs17703599	1 0	2309415		0.38	0.21	92.0	0. TO	0.389
ILMN 2372639 19 rs17159840 19 7758194 TRAPPC5 rs7694997 4 9947811 5.86 0.20 0.36 0.22 ILMN 2372639 19 rs17159840 19 7758194 TRAPPC5 rs780926 6.27 0.15 0.36 0.02 ILMN 2372639 19 rs17159840 19 7758194 TRAPPC5 rs775194 TRAPPC5 7.58 0.04 0.05 0.06 ILMN 2372639 19 rs17159840 19 7758194 TRAPPC5 7.73 0.05 0.05 0.05 ILMN 2372639 19 rs6040514 2 2244685 rs17159840 19 7758194 TRAPPC5 7.73 0.05 0.05 0.05 ILMN 2372639 19 rs7246264 19 7762978 rs17159840 19 7758194 TRAPPC5 7.78 0.04 0.05 0.05 ILMN 2372639 19 rs7246264 19 7762978 rs12891778 1 1741 0.05	ILMN_2372639 19 rs17159840 19 7758194 TRAPPC5 rs7694997 4 9947811 ILMN_2372639 19 rs17159840 19 7758194 TRAPPC5 rs760335 7 1469026 ILMN_2372639 19 rs187159840 19 7758194 TRAPPC5 rs866638 14 8453550 ILMN_2372639 19 rs28016995 2 27476454 TRAPPC5 rs87159840 19 7758194 TRAPPC5 ILMN_2372639 19 rs78016995 2 11272861 rs17159840 19 7758194 TRAPPC5 ILMN_2372639 19 rs7246344 19 7762978 rs17159840 19 7758194 TRAPPC5 ILMN_2372639 19 rs7246344 19 7762978 rs12159840 19 7753978 RAPCEF1 ILMN_2372639 19 rs7246344 19 7762978 rs12867778 9 1466577 TREMI ILMN_128272639 19 rs7246344 19) C	ILMN 2372639	61	rs17159840	61	7758194	TRAPPOS	rs7313362	12	129644342		70.0	0.03	0.65	0.25	
ILMN 2372639 19 rs/17159840 19 7758194 TRAPPC5 rs/800936 7 14609026 6.27 0.15 0.33 0.16 ILMN 2372639 19 rs/817159840 19 7758194 TRAPPC5 rs/810986 19 7758194 TRAPPC5 7.73 0.24 0.07 0.08 ILMN 2372639 19 rs/830708 2 22740856 2 14728454 rs/1759840 19 7758194 TRAPPC5 7.73 0.24 0.07 0.08 ILMN 2372639 19 rs/8246264 19 7762978 rs/1759840 19 7758194 TRAPPC5 7.73 0.58 0.78 1.01 ILMN 2372639 19 rs/7246264 19 7762978 rs/109476 1 776819 7.34 0.04 0.07 0.03 ILMN 2372639 19 rs/7246264 19 7762978 rs/109476 1 7741 0.05 0.05 0.05 ILMN 1288231 6 12	ILMN 2372639 19 rs/17159840 19 7758194 TRAPPC5 rs/76038 7 14690926 ILMN 2372639 19 rs/380708 2 22740855 rs/380708 19 7758194 TRAPPC5 rs/385638 19 7758194 TRAPPC5 ILMN 2372639 19 rs/380708 2 22740855 19 7758194 TRAPPC5 ILMN 2372639 19 rs/346564 19 7762978 rs/1758940 19 7758194 TRAPPC5 ILMN 2372639 19 rs/246264 19 7762978 rs/1758940 19 7758194 TRAPPC5 ILMN 2372639 19 rs/246264 19 7762978 rs/187778 17640876 RAPG576 ILMN 2372639 19 rs/246264 19 7762978 rs/1887778 178408765 1 ILMN 1088231 6 rs/246264 19 7762978 rs/246264 19 7762978 rs/246264 10 7762477 REBM1 ILMN 1088231	CS	ILMN_2372639	19	rs17159840	19	7758194	TRAPPC5	rs7694997	4	9947811		5.86	0.20	0.36	0.22	
ILMN 2372639 19 rst7159840 TRAPPC5 rss87059 14 55439550 C73 0.24 0.07 0.08 ILMN 2372639 19 rst80708 27748194 TRAPPC5 7758194 TRAPPC5 7758194 TRAPPC5 775 0.24 0.07 0.08 ILMN 2372639 19 rst8010595 21 45128454 TRAPPC5 7.75 0.51 0.51 0.07 0.08 ILMN 2372639 19 rst74654 19 7762978 rst17199840 19 7778194 TRAPPC5 7.73 0.85 0.78 1.01 ILMN 2372639 19 rst746264 19 7762978 rst12416944 16 3048765 1.1 0.14 0.26 0.13 ILMN 2372639 19 rst746264 19 7762978 rst12412964 1778977 14 0.14 0.05 0.05 ILMN 108821 6 rst12412964 10 108256422 15 12339577 14 1426457 TREMI<	ILMN 12372639 19 rs97159840 19 7758194 TRAPPC5 rs856638 14 84393550 ILMN 12372639 19 rs73159840 19 7758194 TRAPPC5 ILMN 12372639 19 rs60400514 2 22740855 rs7159840 19 7758194 TRAPPC5 ILMN 12372639 19 rs60400514 2 11272861 rs7159840 19 7758194 TRAPPC5 ILMN 12372639 19 rs6040514 10 7762978 rs11758840 19 7758194 TRAPPC5 ILMN 12372639 19 rs7246264 19 7762978 rs12921440 16 7408765 ILMN 12472639 19 rs7246324 19 7762978 rs12921440 16 7408765 ILMN 1088231 6 rs12412964 10 10825422 1762978 15229571 6 4126457 7REM1 ILMN 1088231 6 rs12412964 10 10825422 6 26044369 178A178	Q2	ILMN_2372639	19	rs17159840	19	7758194	TRAPPC5	rs7800935	7	146690926		6.27	0.15	0.33	0.16	
ILMN 2372639 19 res772639 19 res772639 19 res772639 19 res772639 19 res772639 19 res78194 TRAPPC5 7.58 0.55 0.75 1.01 ILMN 2372639 19 res9816995 21 11272861 res17159840 19 7758194 TRAPPC5 7.73 0.55 0.56 ILMN 2372639 19 res7246264 19 7762978 res17159840 19 7778194 TRAPPC5 8.10 0.51 0.55 0.02 ILMN 2372639 19 res7246264 19 7762978 res102921440 16 7762978 0.14 0.02 0.02 ILMN 2372639 19 res10292440 16 7762978 18465508 RAPGEF1 7.05 0.08 0.86 0.40 ILMN 1268231 6 res10292440 16 41264577 TREMI 5.92 1.03 0.13 ILMN 1268231 6 res1024264 10 7762978 res1024477	ILMN 2372639 19 re380708 2 2740855 re31158840 19 7758194 TRAPPC5 ILMN 2372639 19 re36040514 2 11272861 re17158840 19 7758194 TRAPPC5 ILMN 2372639 19 re7624624 19 776278 re17158840 19 7758194 TRAPPC5 ILMN 2372639 19 re7246364 19 7762978 re12021440 16 70408765 ILMN 2372639 19 re7246364 19 7762978 re12021440 16 70408765 ILMN 1268231 6 re1204564 19 7762978 re2395771 6 4126457 TREM1 ILMN 1688231 6 re124657 1 102256422 re2395771 6 4126457 TREM1 ILMN 1688231 6 re1264564 1 7765978 re2395771 6 4126457 TREM1 ILMN 1688231 6 re126457 7 7580442 1 7276397 re2395771	Q5	ILMN_2372639	19	rs17159840	19	7758194	TRAPPC5	rs856638	14	85439550		6.73	0.24	0.07	80.0	
ILMN 2372639 19 res040695 21 45128464 res17159840 19 7758194 TRAPPC5 7.73 0.85 0.78 1.01 ILMN 2372639 19 res040514 22 228504503 7758194 TRAPPC5 6.71 0.51 0.56 0.00 ILMN 2372639 19 res246264 19 7762978 res1291440 16 30408765 6.71 0.14 0.05 0.02 ILMN 2372639 19 res7246264 19 7762978 res1291440 16 30408765 6.71 0.14 0.05 0.05 0.01 0.05	ILMN 2372639 19 res0404014 20 41228454 19 7758194 19 7758194 178APPC5 ILMN 2372639 19 res744564 19 776978 res1017957 2 225604503 TRAPPC5 ILMN 2372639 19 re7246264 19 776978 re1017957 2 225604503 TRAPPC5 ILMN 2372639 19 re7246264 19 7762978 re1017957 2 225604503 TRAPPC5 ILMN 2372639 19 re7246264 19 7762978 re10291440 16 34048765 RAPGEF1 ILMN 1688231 6 re10863975 1 8574398 re2395771 6 4126457 TREM1 ILMN 168701 6 re227180 7 719634 re2032447 6 26044369 TREM3 ILMN 178506 10 re266349 MYBPC3 re12806998 11 2317951 re280607 6 137947208 ILMN 2323126 2 re4106889 1 <td>Q2</td> <td>ILMN_2372639</td> <td>19</td> <td>rs380708</td> <td>22</td> <td>22740855</td> <td></td> <td>rs17159840</td> <td>19</td> <td>7758194</td> <td>TRAPPC5</td> <td>7.58</td> <td></td> <td></td> <td></td> <td></td>	Q2	ILMN_2372639	19	rs380708	22	22740855		rs17159840	19	7758194	TRAPPC5	7.58				
ILIMN 1.2372363 19 re2740264 19 re2772363 19 re2760264 10	ILMN.2372639 19 rsf246264 19 7762978 rs1019572 2 226504503 rs7246264 19 7762978 rs1019572 2 226504503 rs7246264 19 7762978 rs1019572 2 226504503 rs7246264 19 7762978 rs10291440 16 34068765 rs10262976 rs10262976 rs10262976 rs10262976 rs10262976 rs10262977 rs10263747 rs10263747 rs10263747 rs10263747 rs10263747 rs10263747 rs10263748 rs1026374 rs10263748 rs10263748 rs1026374 rs1026374 rs10263744 rs1026374	Ç	ILMN_2372639	19	rs3916995	21	45128454		rs17159840	19	7758194	TRAPPC5	7.73	0.85	0.78	1.01	
ILMN 2372659 19 F87246264 19 T762978 rs10179572 2 228604503 6.71 0.14 0.02 0.02 ILMN 2372639 19 rs7246264 19 7762978 rs188778 9 13465508 RAPGEF1 7.05 0.08 0.08 0.03 ILMN 2372639 19 rs7246264 19 7762978 rs188778 9 13465508 RAPGEF1 7.05 0.08 0.08 0.03 ILMN 1287631 6 rs10862977 rs2396771 6 4126457 TREMI 5.92 0.11 0.25 0.01 0.02 <	ILMN 12372639 19 187246364 19 7762978 1819021440 16 30408765 187246364 19 7762978 1818921440 16 30408765 187246364 19 7762978 1818921440 16 30408765 18188772839 19 187246264 19 7762978 18683544 19 34365088 RAPGEF1 1MN 1688231 16 1810862975 12 85749398 182395771 16 41264577 TREM1 182239577 182239577 182239577 182239577 182239577 182239577 182239578 18223328 18223328 18223328 182232328 182232	0.5	ILMN_2372639	13	rs6040514	20	11272861		rs17159840	19	7758194	TRAPPC5	8.10	0.51	0.55	0.56	
ILMN_12372639 19 Fi2/246564 19 7762378 Fi2/24738 19 7762378 Fi2/2440 10 5 5 5 5 5 5 5 5 5	ILMN-12372639 19 rs72462244 19 r762978 rs1887778 9 34043688 RAPCEFT ILMN-12372639 19 rs72462244 19 r762978 rs18877778 9 134635688 RAPCEFT ILMN-12372639 19 rs72462242 19 rs762978 rs2295771 6 41264577 rrEM1 rs2295771 rs22959771 rs22959771 rs22959771 rs2295977 rs2295978 rs2295978	C	ILMN-2372639	61	rs7246264	61	7762978		rs10179572	21 .	228504503		6.71	0.14	0.02	0.02	
ILMN-1272639 19 F476274 19 7762378 F4585374 19 776278 F4585374 19 776278 F4585374 19 7762378 F4585374 19 7762378 F4585374 19 7762378 F4585374 19 7762378 F4585374 10 76256422 F4585642 10 76256422 F4585642 10 76256422 F4585642 10 76256422 F4585642 10 76256422 F4585641 F458566 10 72527180 F458566 10 72527180 F458566 10 727194634 F458566 11 7410638738 11 74106349 MYBPC3 F4585667 11 74106349 MYBPC3 F4585667 12 74106349 F4585687 F4	ILMN_1088231 9 1876246.544 19 7762378 187628771 19 134023708 14 14 14 14 14 14 14 1	ŝŧ	ILMIN-2372639	5	rs/246264	. T	7762978		rs12921440	91	30408765	4	7.34	0.14	0.26	0.13	
ILMN-13523156 1 1810862975 1 1810862975 1 1810862975 1 1810862975 1 1810862975 1 1810862975 1 1810862975 1 1810862975 1 1810862975 1 181088231 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108889 1 18108898 1 18108889 1 18108889 1 18108889 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 18108898 1 181088888 1 181088888 1 181088888 1 181088888 1 181088888 1 1810888888 1 181088888 1 181088888 1 181088888 1 181088888 1 181088888 1 1810888888 1 181088888 1 1810888888 1 1810888888 1 18108888888 1 1810888888 1 18108888888 1 18108888888 1 1810888888	ILMN_1088231 6 re10862245 12 8743939 re2395771 6 41264577 TREM1 ILMN_1088231 6 re12821864 10 108256422 re2395771 6 41264577 TREM1 re2295771 6 41264577 TREM1 re229571 re229577 re229579 re229577 re22957	3 5	ILMIN-23/2639	6 6	FS/240204	6.	7763076		TSIOO///O	n o	154055088	RAFGEFI	7.43	0.08	0.00	0.40	
ILMN-1688231 6 rs12412964 10 108256422 rs2395771 6 41264577 TREM1 5.92 1.20 1.23 1.69 1.20	ILMN-1688231 6 rs12412964 10 108256422 rs2395771 6 41264577 TREM1 ILMN-1785060 10 rs987718 7 158808416 rs10748526 10 82273079 TSPAN14 ILMN-1786501 rs10838738 11 rs10838738 11 rs10838738 11 rs10800998 11 rs10800998 11 rs10800998 11 rs10800998 11 rs10800998 12 rs1074852 rs1074852 rs107452 rs107619 rs108200998 13 rs108500998 13 rs108500998 14 rs108500998 15 rs108500998 15	3	ILMN 1688231	6.0	rs10862975	12	85749398		re2395771	o (c	41264577	TREM1	5 42	0.30	0.90	0.03	
ILMN-1697971 6 re2527180 7 158808416 re2032447 6 26044489 TRIM38 6.46 0.04 0.91 0.39 1.810748526 10 re968726 17 27194634 re12280098 11 re12800998 11 re12800998 11 2317951 TSPAN32 re22800998 12 2317951 TSPAN32 re12800998 13 2317951 TSPAN32 re12800998 13 re12800998 14 re20607 re1198819 2 23874880 6.34 re1198819 2 re1198819	ILMN-1697971 6 re2527180 7 158808416 re2032447 6 26044369 TRIM38 re2082447 6 26044369 TRIM38 re2082848 1 re108888738 1 24766349 MYBPC3 re10800998 11 2317951 TSPAN14 TSPAN32 ILMN-2389970 11 re12800998 11 2317951 TSPAN32 re208007 re208007 re208007 re20807 re208007 re208007 re208007 re208007 re208007 re20807 re208007 re20807 re2080		II.MN 1688231		rs12412964	1 -	108256422		re2395771	0 0	41264577	TREMI	200	1.20	200	1 69	
ILMN_1785060 10 18968726 17 27194634 1810748526 10 82273079 TSPAN14 6.00 0.07 0.18 0.06 1.18	ILMN.178626 10 rs988726 17 27194634 rs10748526 10 82278079 TSPAN14 rs108038738 11 47663049 MYBPC3 rs12800998 11 2317951 TSPAN32 rs2080998 12 2317951 TSPAN32 rs2080998 13 2317951 TSPAN32 rs2080998 14 2317951 TSPAN32 rs2080998 14 2317951 TSPAN32 rs2080998 15 2317951 TSPAN32 rs2080998 16 2317951 TSPAN32 rs400119 22 50966914 ECGF1 rs4783126 16 85147633 16 Rs4783126 17 Rs4783126 18 Rs4783126	~	ILMN_1697971	9	rs2527180	-	158808416		rs2032447	9	26044369	TRIM38	6.46	0.04	0.91	0.39	
ILMN_1784621 11 res10850998 11 47663049 WYBPC3 res128009998 12 2317951 TSPAN32 res20067 137947208 5.01 res10650298 11 res106522 5.0971266 ECGF1 res1088819 2 238746880 6.34 6.34	ILMN-1718621 11 rs10838738 11 47663049 MYBPC3 rs12800998 11 2317951 TSPAN32 ILMN-2383970 rs12800998 11 2317951 TSPAN32 rs628067 6 137947208 ILMN-3223126 rs470119 22 50971266 EGGF1 rs4783126 S43746880 ILMN-3223126 rs470119 22 50966914 EGGF1 rs4783126 16 85147633 EGGF1 Rs4783126 Rs47	14	ILMN_1785060	10	rs968726	17	27194634		rs10748526	10	82273079	TSPAN14	6.00	0.07	0.18	0.00	
ILMN-2389970	ILMN_2289970	32	ILMN_1718621	11	rs10838738	11	47663049	MYBPC3	rs12800998	11	2317951	TSPAN32	5.01				45.345
22 rs140522 22 50971266 ECGF1 rs1198819 2 238746880	22 rs140522 22 50971266 ECGF1 rs1198819 2 238746880	32	ILMN_2389970	11	rs12800998	11	2317951	TSPAN32	rs620607	9	137947208		5.51				
The second secon	$22 \mid rs470119 \qquad 22 50966914 ECGF1 \mid rs4783126 16 85147633 \qquad \mid$		ILMN_3223126	22	rs140522	22	50971266	ECGF1	rs1198819	7	238746880		6.34				

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	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
$-\log_{10} p$ -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	0.05	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	BSGSe	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	7
	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	7	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	-
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 by Illumina probe ID used to measure gene expression of Physical SNP position in base pairs (HG19) defeded Gene ID of gene expression level that is influenced by the SNP (BSGS discovery dataset, 10^{-11}) of the reaction of the special problem of the replication dataset form replication dataset form an analysis of replication datasets af Interaction of 10810 problem from meta analysis of replication datasets only historical in Mb between interacting SNPs for cis-cis acting SNP pairs

6 References

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).
- ¹⁵ 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).