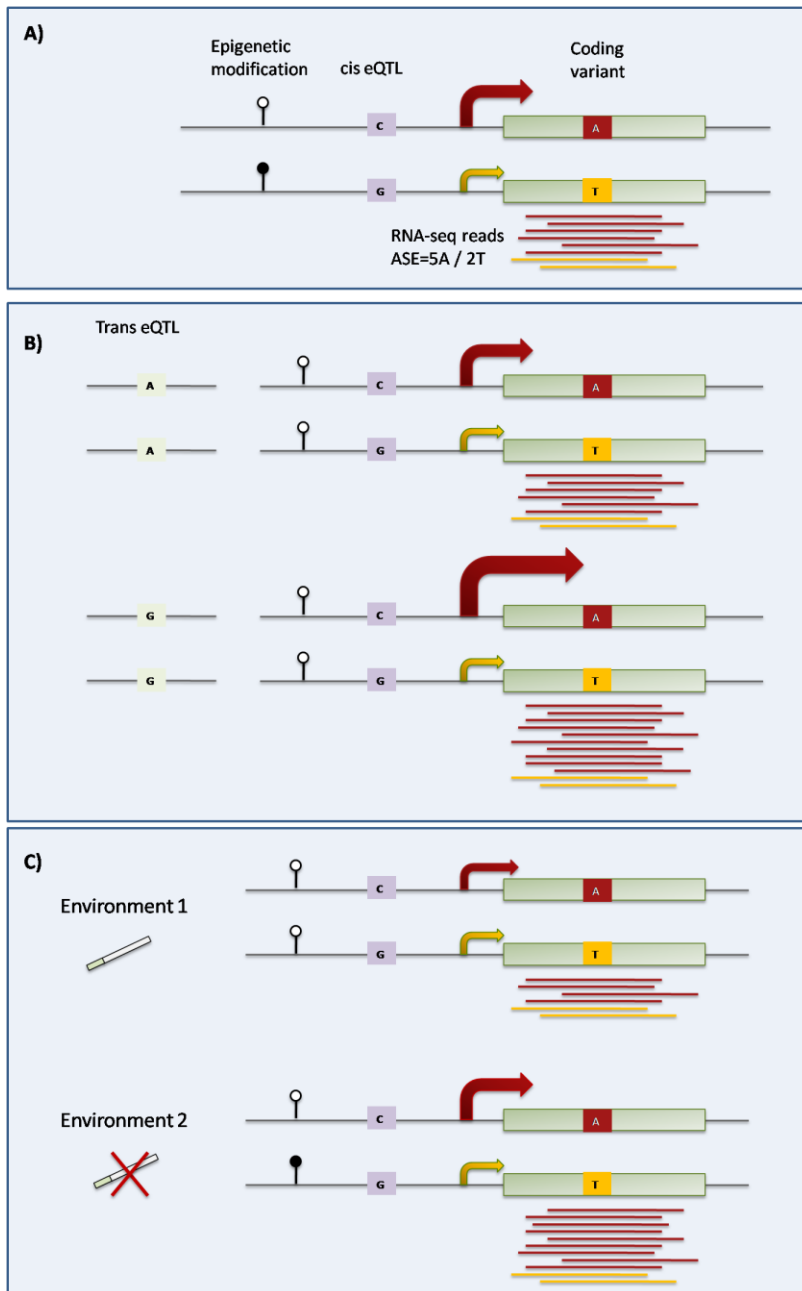


## Supplementary Materials

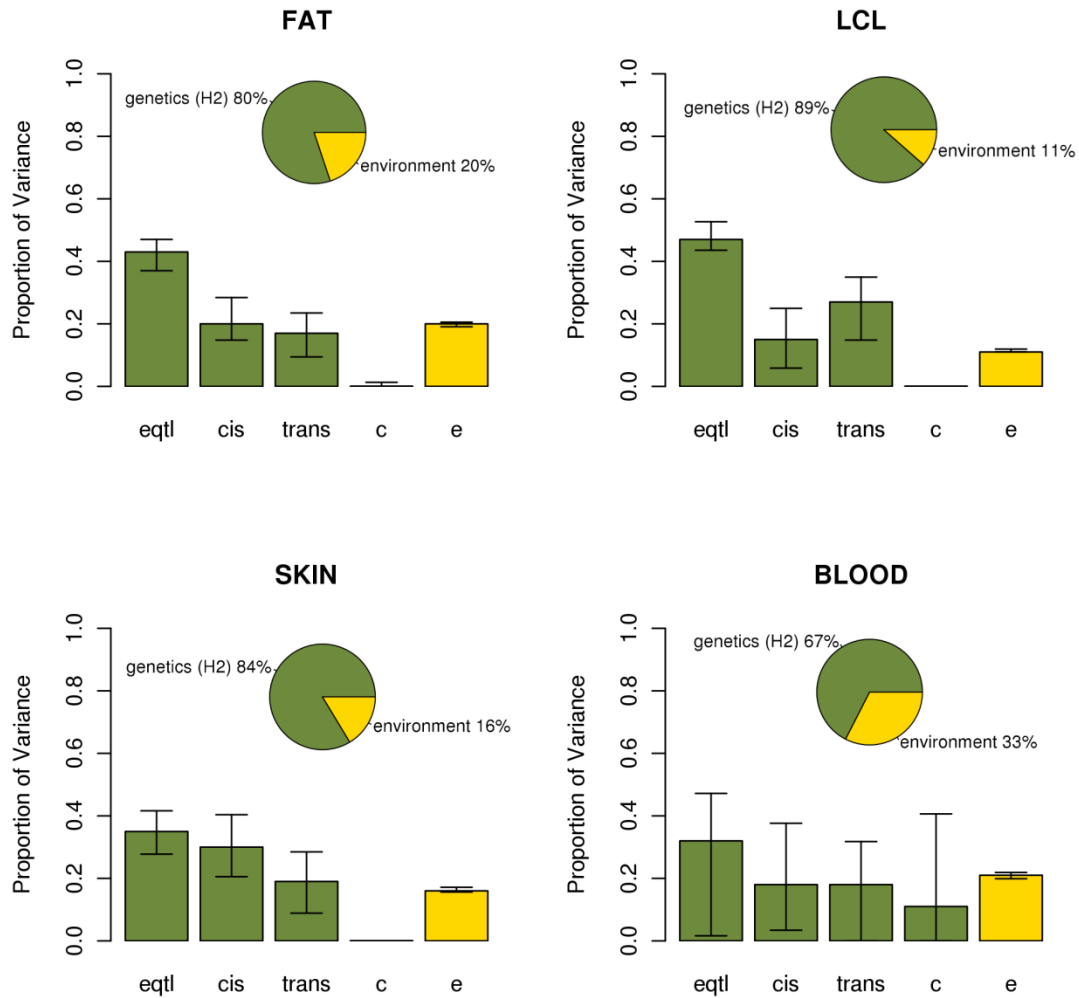
### Transcriptome Sequencing Reveals Widespread Gene-Gene and Gene-Environment Interactions

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Supplementary Figure 1. ASE models. A) Basic model of ASE: genetic variants in cis or epigenetic modifications cause a difference in the expression of the haplotypes. B) GxG effects of ASE: the effect on ASE of the genetic variants in cis depends on the genotype of a locus in trans. C) GxE effects on ASE: the magnitude of the ASE caused by genetic variants in cis depends on the effect of an environmental factor.



Supplementary Figure 2. Variance components of ASE: 'H2' (equal to eqtl + cis + trans) is the heritability of ASE, 'eqtl' is the proportion of variance explained by a common eQTL, 'cis' is the proportion of variance explained by other variants in cis, 'trans' is the proportion of variance explained by genetic variants in trans, 'c' is the proportion of variance explained by the shared environment and 'e' is the proportion of variance explained by the individual environment. The 95% confidence intervals were calculated using 1000 bootstrap permutations.



Supplementary Table 1. Results of MZ twins discordant analysis in Fat: 'snpASE' is the SNP in which we measured ASE, 'snpAssoc' is the SNP that shows the association, 'p' is the raw p value of the test, 'p\_adj' is the adjusted p value taking into account the number of tests, 'gene' is the name of the analyzed gene.

snpASE	snpAssoc	p	p_adj	gene	
rs8086	rs34710824	3.6e-06	0.00089	ACSL1	acyl-CoA synthetase long-chain family member 1
rs4686804	rs4686817	4.4e-06	0.0011	ADIPOQ	adiponectin, C1Q and collagen domain containing
rs3185480	rs1940232	4.8e-06	0.0012	APCDD1	adenomatosis polyposis coli down-regulated 1
rs35880596	rs11230908	8.4e-06	0.0021	EML3	echinoderm microtubule associated protein like 3
rs487098	rs10447415	1.3e-05	0.0033	SERINC1	serine incorporator 1
rs1059288	rs28383423	1.7e-05	0.0043	TAPBP	TAP binding protein (tapasin)
rs1129448	rs5756639	2.1e-05	0.0054	TRIOBP	TRIO and F-actin binding protein
rs2257269	rs116714571	2.4e-05	0.0059	HLA-B	major histocompatibility complex, class I, B
rs7473	rs2477202	2.5e-05	0.0063	LAMC1	laminin, gamma 1
rs3821083	rs12185692	2.6e-05	0.0066	CYBRD1	cytochrome b reductase 1
rs1801214	rs12645004	2.8e-05	0.007	WFS1	Wolfram syndrome 1 (wolframin)
rs7612	rs2942558	3.3e-05	0.0082	ACTB	actin, beta
rs1043943	rs7648762	3.4e-05	0.0085	TMEM43	transmembrane protein 43
rs8130574	rs11702317	3.7e-05	0.0092	PDXK	pyridoxal (pyridoxine, vitamin B6) kinase
rs3206576	rs58617429	4e-05	0.01	TBC1D16	TBC1 domain family, member 16

Supplementary Table 2. Results of MZ twins discordant analysis in LCLs: 'snpASE' is the SNP in which we measured ASE, 'snpAssoc' is the SNP that shows the association, 'p' is the raw p value of the test, 'p\_adj' is the adjusted p value taking into account the number of tests, 'gene' is the name of the analyzed gene.

snpASE	snpAssoc	p	p_adj	gene	
rs9919	rs4394929	5.1e-07	0.00013	EIF2B1	eukaryotic translation initiation factor 2B, subunit 1 alpha
rs348389	rs12710084	1.2e-06	3e-04	TNFSF9	tumor necrosis factor (ligand) superfamily, member 9
rs1803382	rs9935402	5.1e-06	0.0013	PIEZO1	piezo-type mechanosensitive ion channel component 1
rs34653729	rs10760665	1.5e-05	0.0037	FNBP1	formin binding protein 1
rs4905	rs67782188	1.5e-05	0.0037	EBI3	Epstein-Barr virus induced 3
rs9038	rs56146203	1.6e-05	0.0039	SEPT9	septin 9
rs1545837	rs75371758	1.7e-05	0.0044	KIAA1967	
rs11136344	rs57665959	2.1e-05	0.0052	PARP10	poly (ADP-ribose) polymerase family, member 10
rs7612	rs28508548	2.4e-05	0.0061	ACTB	actin, beta
rs11115	rs76286165	2.6e-05	0.0066	MRPL4	mitochondrial ribosomal protein L4
rs241448	rs2856997	3e-05	0.0076	TAP2	transporter 2, ATP-binding cassette, sub-family B
rs836	rs7515302	3e-05	0.0074	F11R	F11 receptor
rs9616	rs10908452	3e-05	0.0076	ADAR	adenosine deaminase, RNA-specific
rs4937333	rs66726214	3.2e-05	0.008	ETS1	v-etserythroblastosis virus E26 oncogene homolog 1 (avian)
rs699517	rs12954127	3.2e-05	0.008	ENOSF1	enolase superfamily member 1
rs699517	rs12954127	3.2e-05	0.008	TYMS	thymidylatesynthetase
rs1057902	rs8064938	3.8e-05	0.0094	UBE2Z	ubiquitin-conjugating enzyme E2Z
rs11609	rs6496760	3.8e-05	0.0096	IQGAP1	IQ motif containing GTPase activating protein 1
rs660339	rs4121668	3.8e-05	0.0095	UCP2	uncoupling protein 2 (mitochondrial, proton carrier)
rs1049961	rs6583964	3.9e-05	0.0097	PDLIM1	PDZ and LIM domain 1

Supplementary Table 3. Results of MZ twins discordant analysis in Skin: 'snpASE' is the SNP in which we measured ASE, 'snpAssoc' is the SNP that shows the association, 'p' is the raw p value of the test, 'p\_adj' is the adjusted p value taking into account the number of tests, 'gene' is the name of the analyzed gene.

snpASE	snpAssoc	p	p_adj	gene	
rs3185480	rs62078925	1e-05	0.0026	APCDD1	adenomatosis polyposis coli down-regulated 1
rs7734	rs61063076	2.3e-05	0.0058	GLUL	glutamate-ammonia ligase
rs7018	rs6036766	2.5e-05	0.0061	PYGB	phosphorylase, glycogen;
rs1131264	rs145607607	3.8e-05	0.0094	FLNB	filamin B, beta

Supplementary Table 4. Results of MZ twins discordant analysis in Blood: 'snpASE' is the SNP in which we measured ASE, 'snpAssoc' is the SNP that shows the association, 'p' is the raw p value of the test, 'p\_adj' is the adjusted p value taking into account the number of tests, 'gene' is the name of the analyzed gene.

snpASE	snpAssoc	p	p_adj	gene	
rs1044059	rs204293	2.9e-05	0.0072	RNASET2	ribonuclease T2