




trait	min(p-value)	source DB	source entry/link	variant(s)
3-(4-hydroxyphenyl)lactate	3.53×10 <sup>-5</sup>	Metabolomics GWAS Server	24816252 	3









### Direct effect on transcript

#### Amino acid sequence alteration

gene	effect type	affected transcript	RefSeq id	protein	exchanged AA's	exchanged codons	SIFT prediction	PolyPhen prediction	variant(s)
LILRB1 <i>e!</i>	missense variant	ENST00000421584 ?		ENSP00000410165	5	5			5
LILRB1 <i>e!</i>	missense variant	ENST00000396315 ?		ENSP00000379608	5	5			5
LILRB1 <i>e!</i>	missense variant	ENST00000427581 ?		ENSP00000395004	5	5			5
LILRB1 <i>e!</i>	missense variant	ENST00000396332	NM_001081639.2	ENSP00000379623	5	5			5
LILRB1 <i>e!</i>	missense variant	ENST00000396327	NM_001081638.2	ENSP00000379618	5	5			5
LILRB1 <i>e!</i>	missense variant	ENST00000324602	NM_001081637.1	ENSP00000315997	5	5			5
LILRB1 <i>e!</i>	missense variant	ENST00000396317	NM_001278398.1	ENSP00000379610	5	5			5
LILRB1 <i>e!</i>	missense variant	ENST00000396331	NM_006669.5	ENSP00000379622	5	5			5
LILRB1 <i>e!</i>	missense variant	ENST00000418536 ?		ENSP00000391514	A/T	Gcc/Acc	?	?	1
LILRB1 <i>e!</i>	missense variant	ENST00000396321 ?		ENSP00000379614	A/T	Gcc/Acc	?	?	1

### Direct effect on regulation

#### cis-eQTL

gene	transcript	probe	tissue	min(statistic) (type)	source	variant(s)
LILRA1 <i>e!</i>	?	ENSG00000104974 <i>e!</i>	lung	4.15×10 <sup>-7</sup> (p-value)	GTEx Portal V6 	39
LILRA2 <i>e!</i>	?	ENSG00000239998 <i>e!</i>	lung	1.26×10 <sup>-7</sup> (p-value)	GTEx Portal V6 	61
LILRP1 <i>e!</i>	?	ENSG00000186152 <i>e!</i>	EBV lymphocytes	6.26×10 <sup>-8</sup> (p-value)	GTEx Portal V6 	13
LILRB5 <i>e!</i>	?	ENSG00000105609 <i>e!</i>	EBV lymphocytes	1.02×10 <sup>-7</sup> (p-value)	GTEx Portal V6 	51
LILRB2 <i>e!</i>	?	ENSG00000131042 <i>e!</i>	EBV lymphocytes	5.43×10 <sup>-9</sup> (p-value)	GTEx Portal V6 	56
CTB-83J4.2 <i>e!</i>	?	ENSG00000269271 <i>e!</i>	blood	4.50×10 <sup>-8</sup> (p-value)	GTEx Portal V6 	38
LILRA1 <i>e!</i>	?	ENSG00000104974 <i>e!</i>	blood	2.28×10 <sup>-9</sup> (p-value)	GTEx Portal V6 	52
LILRA2 <i>e!</i>	?	ENSG00000239998 <i>e!</i>	subcutaneous adipocytes	1.86×10 <sup>-8</sup> (p-value)	GTEx Portal V6 	5

### Putative effect on regulation

#### FANTOM5 expressed promoter

SNiPA promoter id	variant(s)	associated transcript(s)	gene
FFCP00000344796 <i>e!</i>	1	ENST00000418536 <i>e!</i> , ENST00000396321 <i>e!</i>	LILRB1 <i>e!</i>

#### ENCODE promoter-associated DHS

SNiPA promoter id	variant(s)	associated gene(s)
ENCP00000024800 <i>e!</i>		





	KIR2DL4 <i>e!</i>
	KIR2DL4 <i>e!</i>
-----	KIR2DL4 <i>e!</i>
ENCP00000024772	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>
-----	LAIR1 <i>e!</i>
ENCP00000024825	FCAR <i>e!</i>
	FCAR <i>e!</i>
	FCAR <i>e!</i>
	FCAR <i>e!</i>
	FCAR <i>e!</i>
	FCAR <i>e!</i>
	FCAR <i>e!</i>
	FCAR <i>e!</i>
	FCAR <i>e!</i>
-----	FCAR <i>e!</i>
ENCP00000024771	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>
-----	LAIR1 <i>e!</i>
ENCP00000024810	LILRB4 <i>e!</i>
	LILRB4 <i>e!</i>
	LILRB4 <i>e!</i>
	LILRB4 <i>e!</i>
-----	LILRB4 <i>e!</i>
ENCP00000024759	AC010518.3 <i>e!</i>
-----	AC010518.3 <i>e!</i>
ENCP00000024819	KIR2DL1 <i>e!</i>
	KIR2DL1 <i>e!</i>
	KIR2DL1 <i>e!</i>
	KIR2DL1 <i>e!</i>
	KIR2DL1 <i>e!</i>
	KIR2DL1 <i>e!</i>
	KIR2DL1 <i>e!</i>
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	KIR2DL1 <i>e!</i>
	KIR2DL1 <i>e!</i>
-----	KIR2DL1 <i>e!</i>
ENCP00000024799	LILRA1 <i>e!</i>
	LILRA1 <i>e!</i>
	LILRA1 <i>e!</i>
-----	LILRA1 <i>e!</i>
ENCP00000024751	AC012314.19 <i>e!</i>
-----	AC012314.19 <i>e!</i>
ENCP00000024811	LILRB4 <i>e!</i>
	LILRB4 <i>e!</i>
	LILRB4 <i>e!</i>
	LILRB4 <i>e!</i>
-----	LILRB4 <i>e!</i>
ENCP00000024768	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>
	LAIR1 <i>e!</i>





		ENCP00000024766	AC008984.6 <i>e!</i> AC008984.6 <i>e!</i>
		ENCP00000024801	LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i>
		ENCP00000024826	NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i>
		ENCP00000024795	KIR3DX1 <i>e!</i> KIR3DX1 <i>e!</i> KIR3DX1 <i>e!</i> KIR3DX1 <i>e!</i>
ENCE00000233675 <i>e!</i>	1	ENCP00000024805	LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i>
		ENCP00000024796	AC009892.2 <i>e!</i> AC009892.2 <i>e!</i>
		ENCP00000024766	AC008984.6 <i>e!</i> AC008984.6 <i>e!</i>
		ENCP00000024801	LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i>
		ENCP00000024826	NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i>
		ENCP00000024795	KIR3DX1 <i>e!</i> KIR3DX1 <i>e!</i> KIR3DX1 <i>e!</i> KIR3DX1 <i>e!</i>
ENCE00000233680 <i>e!</i>	3	ENCP00000024805	LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i> LILRB1 <i>e!</i>
		ENCP00000024796	AC009892.2 <i>e!</i> AC009892.2 <i>e!</i>
		ENCP00000024766	AC008984.6 <i>e!</i> AC008984.6 <i>e!</i>
		ENCP00000024826	NLRP2 <i>e!</i> NLRP2 <i>e!</i>  NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i> NLRP2 <i>e!</i>
		ENCP00000024801	NLRP2 <i>e!</i> LILRB1 <i>e!</i>



LILRB1 *e!*  
 LILRB1 *e!*  
 LILRB1 *e!*  
 LILRB1 *e!*

ENCP00000024795

KIR3DX1 *e!*  
 KIR3DX1 *e!*  
 KIR3DX1 *e!*  
 KIR3DX1 *e!*

### Regulatory feature cluster

element id	variant(s)	tissue/cell	factors
ENSR00000348881 <i>e!</i> (open chromatin region)	6	blood (GM12878) blood (K562) A549	H3K4me3, H3K27ac, H3K4me2 H3K27me3 H3K27me3
ENSR00000348884 <i>e!</i> (promoter)	3	cervix (HeLa-S3) embryonic stem cell (H1ESC) blood (GM12878) A549 blood (K562)	H3K27me3 DNase1 Yy1, PU1, PolII, BATF, DNase1, IRF4, H3K79me2, H3K4me3, BCL11A, Pax5, H3K27ac, H3K4me2, H3K9ac H3K27me3 H3K27me3
ENSR00001649225 <i>e!</i> (promoter)	1	cervix (HeLa-S3) monocytes (Monocytes-CD14+) blood (GM12878) blood (K562) blood (DND-41) A549	H3K27me3 H3K4me3, H3K36me3, H3K9ac, DNase1, H3K4me1, H3K4me2, H3K27ac PolII, H3K36me3 H3K27me3 H3K27me3 H3K27me3
ENSR00000348890 <i>e!</i> (open chromatin region)	2	blood (K562) A549	USF1, H3K27me3 H3K27me3

### Variation proximal to gene

gene	variant type	min(distance)	transcript	RefSeq id	protein	variant(s)
AC009892.10 <i>e!</i>	downstream gene variant, upstream gene variant	347	ENST00000456337 <i>e!</i> ?	?	?	14
AC009892.5 <i>e!</i>	upstream gene variant, downstream gene variant	72	ENST00000432400 <i>e!</i> ?	?	?	15
AC009892.9 <i>e!</i>	upstream gene variant, downstream gene variant	2348	ENST00000429259 <i>e!</i> ?	?	?	5
AC245036.1 <i>e!</i>	downstream gene variant, upstream gene variant	20	ENST00000578908 <i>e!</i> ?	?	?	22
AC245036.2 <i>e!</i>	upstream gene variant, downstream gene variant	1613	ENST00000618840 <i>e!</i> ?	?	?	4
AC245036.3 <i>e!</i>	upstream gene variant, downstream gene variant	2000	ENST00000610849 <i>e!</i> ?	?	?	4
AC245036.4 <i>e!</i>	upstream gene variant, downstream gene variant	1785	ENST00000622837 <i>e!</i> ?	?	?	4
AC245036.5 <i>e!</i>	upstream gene variant, downstream gene variant	1871	ENST00000616955 <i>e!</i> ?	?	?	4
AC245036.6 <i>e!</i>	upstream gene variant, downstream gene variant	2086	ENST00000614474 <i>e!</i> ?	?	?	4
LILRA1 <i>e!</i>	downstream gene variant	4407	ENST00000473156 <i>e!</i> ?	?	?	3
LILRA1 <i>e!</i>	downstream gene variant	4194	ENST00000453777 <i>e!</i> NM_001278318.1	ENSP00000413715 <i>e!</i>	?	4
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	195	ENST00000487425 <i>e!</i> ?	?	?	22
LILRB1 <i>e!</i>	upstream gene variant	225	ENST00000630741 <i>e!</i> ?	?	ENSP00000485956 <i>e!</i>	11
LILRB1 <i>e!</i>	upstream gene variant	187	ENST00000418536 <i>e!</i> ?	?	ENSP00000391514 <i>e!</i>	11
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	37	ENST00000480375 <i>e!</i> ?	?	?	20
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	225	ENST00000396315 <i>e!</i> ?	?	ENSP00000379608 <i>e!</i>	13
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	275	ENST00000396332 <i>e!</i> NM_001081639.2	ENSP00000379623 <i>e!</i>	?	12
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	275	ENST00000324602 <i>e!</i> NM_001081637.1	ENSP00000315997 <i>e!</i>	?	12
LILRB1 <i>e!</i>	upstream gene variant	225	ENST00000396321 <i>e!</i> ?	?	ENSP00000379614 <i>e!</i>	11
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	275	ENST00000396331 <i>e!</i> NM_006669.5	ENSP00000379622 <i>e!</i>	?	6
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	613	ENST00000427581 <i>e!</i> ?	?	ENSP00000395004 <i>e!</i>	12
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	225	ENST00000396317 <i>e!</i> NM_001278308.1	ENSP00000379610 <i>e!</i>	?	13

LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	423	ENST00000396317 <i>e!</i>	NM_001278398.1	ENSP00000379610 <i>e!</i>	13
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	275	ENST00000462628 <i>e!</i>	?	?	10
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	477	ENST00000473412 <i>e!</i>	?	?	16
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	275	ENST00000396327 <i>e!</i>	NM_001081638.2	ENSP00000379618 <i>e!</i>	12
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	225	ENST00000421584 <i>e!</i>	?	ENSP00000410165 <i>e!</i>	13
LILRB1 <i>e!</i>	upstream gene variant, downstream gene variant	333	ENST00000480257 <i>e!</i>	?	?	28
LILRB4 <i>e!</i>	upstream gene variant, downstream gene variant	137	ENST00000461839 <i>e!</i>	?	?	2
LILRB4 <i>e!</i>	upstream gene variant	4977	ENST00000391736 <i>e!</i>	NM_001278426.2	ENSP00000375616 <i>e!</i>	1
LILRB4 <i>e!</i>	upstream gene variant	3684	ENST00000270452 <i>e!</i>	?	ENSP00000270452 <i>e!</i>	1
MIR8061 <i>e!</i>	downstream gene variant	1485	ENST00000618936 <i>e!</i>	?	?	3
VN1R105P <i>e!</i>	upstream gene variant, downstream gene variant	117	ENST00000486595 <i>e!</i>	?	?	3

### Putative effect on transcript

#### Synonymous coding variant

gene	affected transcript	RefSeq id	protein	AA's	exchanged codons	variant(s)
LILRB1 <i>e!</i>	ENST00000396331 <i>e!</i>	NM_006669.5	ENSP00000379622 <i>e!</i>	2	3	3
LILRB1 <i>e!</i>	ENST00000324602 <i>e!</i>	NM_001081637.1	ENSP00000315997 <i>e!</i>	2	3	3
LILRB1 <i>e!</i>	ENST00000427581 <i>e!</i>	?	ENSP00000395004 <i>e!</i>	2	3	3
LILRB1 <i>e!</i>	ENST00000396332 <i>e!</i>	NM_001081639.2	ENSP00000379623 <i>e!</i>	2	3	3
LILRB1 <i>e!</i>	ENST00000396327 <i>e!</i>	NM_001081638.2	ENSP00000379618 <i>e!</i>	2	3	3
LILRB1 <i>e!</i>	ENST00000421584 <i>e!</i>	?	ENSP00000410165 <i>e!</i>	2	2	3
LILRB1 <i>e!</i>	ENST00000396315 <i>e!</i>	?	ENSP00000379608 <i>e!</i>	2	3	3
LILRB1 <i>e!</i>	ENST00000396317 <i>e!</i>	NM_001278398.1	ENSP00000379610 <i>e!</i>	2	2	3

#### Intron variant (splice region)

gene	affected transcript	RefSeq id	protein	variant(s)
LILRB1 <i>e!</i>	ENST00000462628 <i>e!</i>	?	?	1
LILRB1 <i>e!</i>	ENST00000396331 <i>e!</i>	NM_006669.5	ENSP00000379622 <i>e!</i>	1
LILRB1 <i>e!</i>	ENST00000324602 <i>e!</i>	NM_001081637.1	ENSP00000315997 <i>e!</i>	1
LILRB1 <i>e!</i>	ENST00000427581 <i>e!</i>	?	ENSP00000395004 <i>e!</i>	1
LILRB1 <i>e!</i>	ENST00000396332 <i>e!</i>	NM_001081639.2	ENSP00000379623 <i>e!</i>	1
LILRB1 <i>e!</i>	ENST00000396327 <i>e!</i>	NM_001081638.2	ENSP00000379618 <i>e!</i>	1
LILRB1 <i>e!</i>	ENST00000421584 <i>e!</i>	?	ENSP00000410165 <i>e!</i>	1
LILRB1 <i>e!</i>	ENST00000396315 <i>e!</i>	?	ENSP00000379608 <i>e!</i>	1
LILRB1 <i>e!</i>	ENST00000396317 <i>e!</i>	NM_001278398.1	ENSP00000379610 <i>e!</i>	1

#### Intron variant

gene	affected transcript	RefSeq id	protein	variant(s)
AC009892.10 <i>e!</i>	ENST00000456337 <i>e!</i>	?	?	7
LILRB1 <i>e!</i>	ENST00000462628 <i>e!</i>	?	?	15
LILRB1 <i>e!</i>	ENST00000396331 <i>e!</i>	NM_006669.5	ENSP00000379622 <i>e!</i>	39
LILRB1 <i>e!</i>	ENST00000324602 <i>e!</i>	NM_001081637.1	ENSP00000315997 <i>e!</i>	14
LILRB1 <i>e!</i>	ENST00000480257 <i>e!</i>	?	?	1

LILRB1 <i>e!</i>	ENST00000427581 <i>e!</i>	?	ENSP00000395004 <i>e!</i>	14
LILRB1 <i>e!</i>	ENST00000480375 <i>e!</i>	?	?	1
LILRB1 <i>e!</i>	ENST00000396332 <i>e!</i>	NM_001081639.2	ENSP00000379623 <i>e!</i>	14
LILRB1 <i>e!</i>	ENST00000396327 <i>e!</i>	NM_001081638.2	ENSP00000379618 <i>e!</i>	14
LILRB1 <i>e!</i>	ENST00000421584 <i>e!</i>	?	ENSP00000410165 <i>e!</i>	13
LILRB1 <i>e!</i>	ENST00000396315 <i>e!</i>	?	ENSP00000379608 <i>e!</i>	13
LILRB1 <i>e!</i>	ENST00000396321 <i>e!</i>	?	ENSP00000379614 <i>e!</i>	25
LILRB1 <i>e!</i>	ENST00000396317 <i>e!</i>	NM_001278398.1	ENSP00000379610 <i>e!</i>	13
LILRB1 <i>e!</i>	ENST00000418536 <i>e!</i>	?	ENSP00000391514 <i>e!</i>	25
LILRB1 <i>e!</i>	ENST00000487425 <i>e!</i>	?	?	1
LILRB1 <i>e!</i>	ENST00000630741 <i>e!</i>	?	ENSP00000485956 <i>e!</i>	26
LILRB4 <i>e!</i>	ENST00000270452 <i>e!</i>	?	ENSP00000270452 <i>e!</i>	6
LILRB4 <i>e!</i>	ENST00000461839 <i>e!</i>	?	?	2

### 3'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
LILRB1 <i>e!</i>	ENST00000421584 <i>e!</i>	?	ENSP00000410165 <i>e!</i>	1

### 5'-UTR variant

gene	affected transcript	RefSeq id	protein	variant(s)
LILRB1 <i>e!</i>	ENST00000427581 <i>e!</i>	?	ENSP00000395004 <i>e!</i>	1

### Non-coding exon variant

gene	affected transcript	RefSeq id	variant(s)
AC009892.5 <i>e!</i>	ENST00000432400 <i>e!</i>	?	3
LILRB1 <i>e!</i>	ENST00000462628 <i>e!</i>	?	13
LILRB1 <i>e!</i>	ENST00000473412 <i>e!</i>	?	8
LILRB4 <i>e!</i>	ENST00000461839 <i>e!</i>	?	1

