The Molecular Mechanisms of rhIGF1 in the Treatment of Rett Syndrome and Related Disorders: Studies in Patients, Mouse and Cellular Models

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Volume 2 of 2

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Doctor of Philosophy (PhD)

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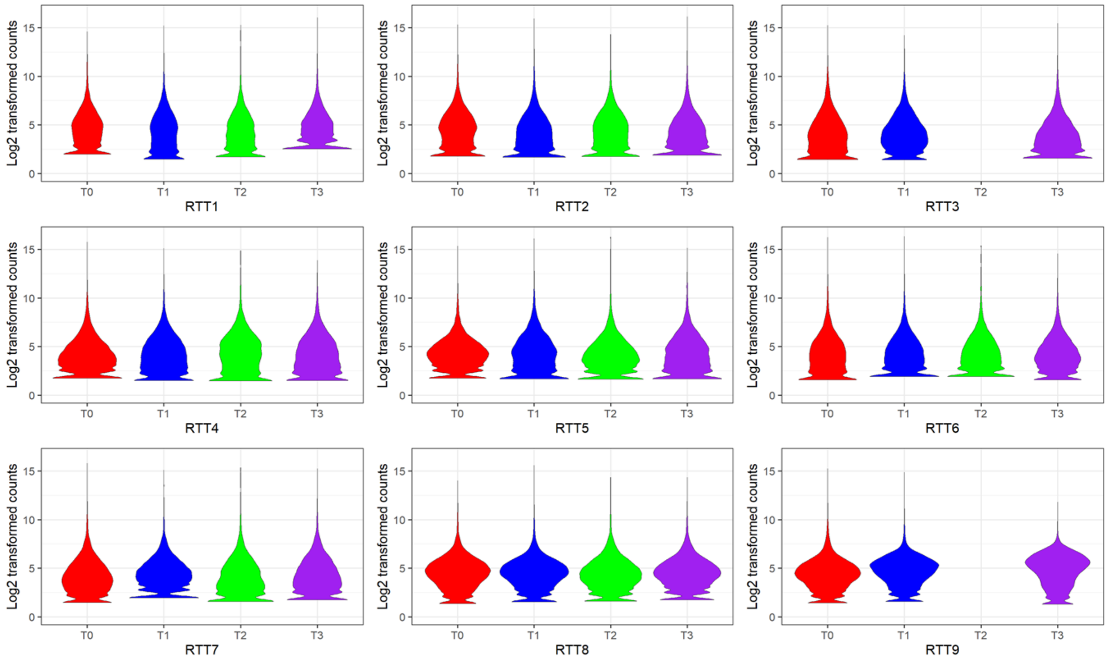
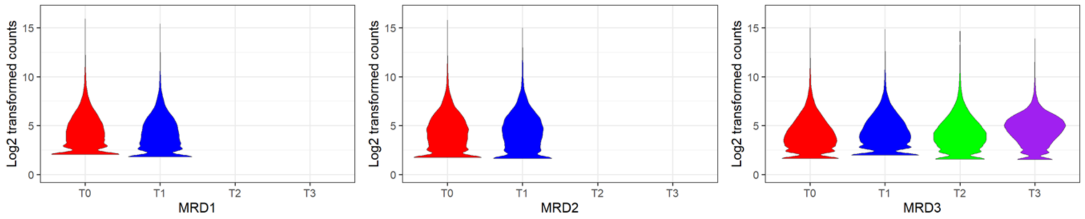
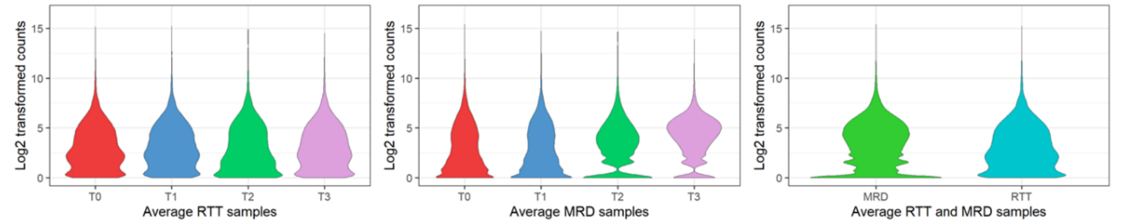


Supplementary Figure 1 - Rett patient's gene distribution for each time-points. Violin plots based on log2 transformed counts for genes in each of the timepoints (T0 = red, T1 = blue, T2 = green, and T3 = purple) in each of the Rett patients (RTT1 to RTT9). Note that RTT3 and RTT 9 do not have a timepoint T2, these samples were from MSR and Responder subgroups respectively.



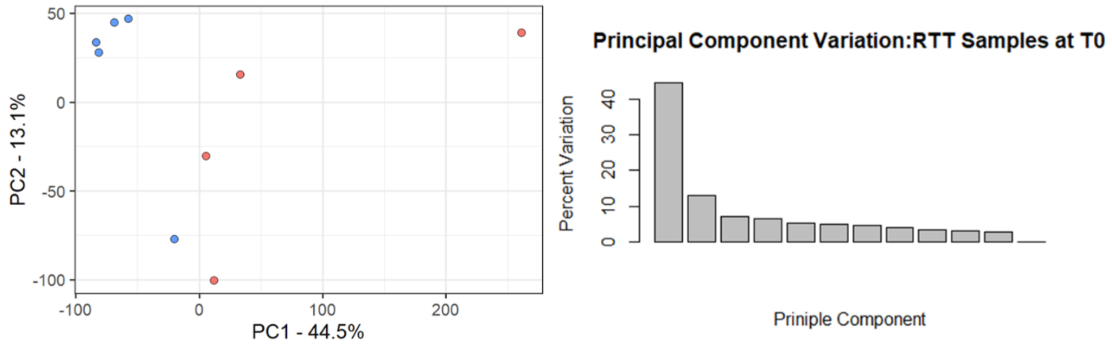
Supplementary Figure 2 - *MECP2* Related Disorder patient's gene distribution for each time-points.

Violin plots based on log2 transformed counts for genes in each of the timepoints (T0 = red, T1 = blue, T2 = green, and T3 = purple) in each of the MRD patients (MRD1 to MRD3). Note that MRD1 and MRD2 patients are monozygotic twins and only MRD3 was treated during both MAD and OLE



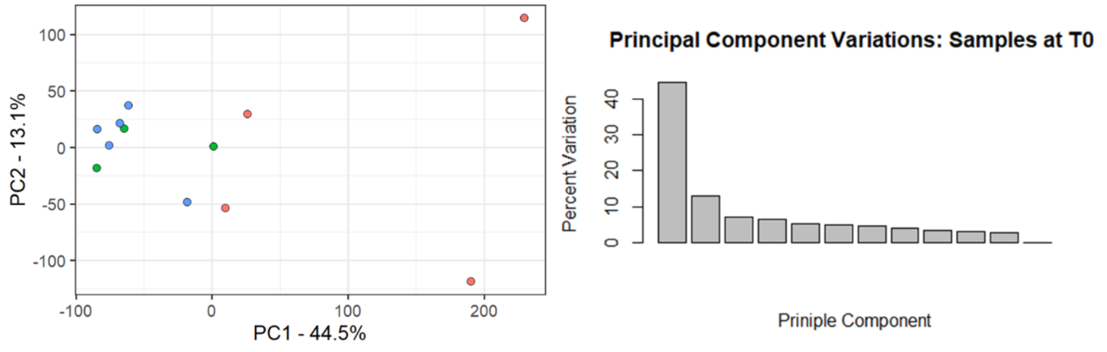
Supplementary Figure 3 - Average Log2 Transformed counts in RTT and MRD patient's gene distribution.

Left and centre panel show Violin plots based on log2 transformed counts for genes in each of the timepoints (T0 = red, T1 = blue, T2 = green, and T3 = purple) in each of the MRD patients (MRD1 to MRD3). Right Panel shows the combined average expression of all MRD and RTT patient samples (all timepoints) in the study. 23,539 average transcripts detected in RTT and 20,610 average transcripts detected in MRD samples



Supplementary Figure 4 - Scree Plot (A) and Principal Component Analysis Plot of Patient samples with RTT (n=9) at baseline (T0).

Principle Components 1 and 2 accounted, respectively, for 44.5% and 13.1% of total variance



Supplementary Figure 5 - Scree Plot (A) and Principle Component Analysis Plot of Patient samples with RTT (n=9) and Patient samples with MRD (n=3) at baseline (T0).

Principle Components 1 and 2 accounted, respectively, for 44.5% and 13.1% of total variance.

Legend:

MSRs = Blue, Responders = Red, MRD = Green

Patient	**Mutation (nucleotide nomenclature)**	**Mutation (amino acid nomenclature)**	***MECP2* domain**	**Mutation type**
RTT1	c.538C>T	R168X	ID, TRD	Nonsense
RTT2	c.790_808del119	-	TRD-NLS	Deletion
RTT3	Deletion of Exons 3 and 4 (min 6.0kb – max 7.1kb)	-	Multiple	Deletion
RTT4	c.1159_1273del	-	C-Term	Frameshift, insertion or deletion
RTT5	c.763C>T	R255X	TRD	Nonsense
RTT6	c.763C>T	R255X	TRD	Nonsense
RTT7	c.473C>T	T158M	MBD	Missense

RTT8	Deletion Exons 1 and 2	-	START codon	Deletion
RTT9	c.965C>T	P322L	C-Term	Missense
MRD1	c.1135_1142delCCCGTGCC	P379T.fs	C-Term	Frameshift, deletion
MRD2	c.1135_1142delCCCGTGCC	P379T.fs	C-Term	Frameshift, deletion
MRD3	c.916C>T	R306C	TRD	Missense

Supplementary Table 1 - Mutations in the Phase I Mecasermin Trial Cohort

Abbreviations: RTT (Rett syndrome, n=9), MRD (MECP2-related disorder, n=3, two of them twins), ID (Interdomain), TRD (Transcriptional Repression Domain), NLS (Nuclear Localisation Signal), C-term (Carboxy-terminus), MBD (Methyl Binding Domain).

Group	Comparison	Gene	LogFC	FDR	Gene	LogFC	FDR
RVMSR	T0	CD177	-5.11	1.86E-19	LOC101928195	2.63	1.72E-02
RVMSR	T0	LINC00273	2.73	8.77E-08	LOC101929583	2.63	1.72E-02
RVMSR	T0	C4B_2	-2.81	6.15E-07	WDR19	2.50	1.72E-02
RVMSR	T0	IFI27	-2.64	1.24E-06	NR2F2	3.67	1.72E-02
RVMSR	T0	CENPV	3.24	1.34E-06	ST7-AS1	3.69	1.72E-02
RVMSR	T0	TMEM221	3.47	1.34E-06	ATXN7L1	1.34	1.72E-02
RVMSR	T0	CCDC175	2.42	1.34E-06	COA7	1.75	1.73E-02
RVMSR	T0	NME5	4.48	1.34E-06	LOC102724738	4.64	1.73E-02
RVMSR	T0	FAM227A	2.99	1.80E-06	BECN2	2.78	1.73E-02
RVMSR	T0	CLPSL1	4.15	2.69E-06	OR10H5	2.02	1.73E-02
RVMSR	T0	DBF4B	3.09	3.60E-06	ALPK2	2.98	1.73E-02
RVMSR	T0	TM4SF5	2.93	6.38E-06	GFRA4	3.69	1.74E-02
RVMSR	T0	DENND5B	2.69	9.29E-06	LOC102724699	3.24	1.74E-02

RVMSR	T0	FLJ40288	4.70	9.29E-06	ZSCAN18	1.59	1.74E-02
RVMSR	T0	PPP1R13L	4.67	1.36E-05	PRC1-AS1	2.39	1.74E-02
RVMSR	T0	LOC101928295	3.39	1.36E-05	STPG1	2.51	1.74E-02
RVMSR	T0	FBN3	3.29	1.36E-05	DDX43	2.98	1.74E-02
RVMSR	T0	IL2	4.00	1.44E-05	PLPP3	2.09	1.74E-02
RVMSR	T0	C4A	-2.83	1.73E-05	WTAPP1	4.62	1.74E-02
RVMSR	T0	TEX26	4.63	1.73E-05	LINC01522	3.24	1.75E-02
RVMSR	T0	CRX	2.79	1.73E-05	PIP5K1P1	2.30	1.75E-02
RVMSR	T0	LOC101927450	4.25	1.79E-05	LINC00864	3.67	1.75E-02
RVMSR	T0	LINC00367	3.78	1.79E-05	BTNL9	2.30	1.75E-02
RVMSR	T0	LOC100996342	2.74	1.89E-05	RPAP2	-1.47	1.75E-02
RVMSR	T0	LINC01296	3.23	1.89E-05	UBOX5-AS1	1.92	1.75E-02
RVMSR	T0	DEFA3	2.32	2.66E-05	FRMPD2B	3.68	1.76E-02
RVMSR	T0	USP12-AS2	2.90	2.85E-05	HNF1A	2.38	1.76E-02
RVMSR	T0	OTOA	2.85	2.85E-05	NOXRED1	2.08	1.76E-02
RVMSR	T0	MIOX	2.70	2.87E-05	TRIM3	2.30	1.76E-02
RVMSR	T0	LOC403312	2.96	2.92E-05	LOC101927142	2.97	1.76E-02
RVMSR	T0	KSR2	3.29	3.04E-05	GNA14	2.78	1.76E-02
RVMSR	T0	LOC101927419	3.10	3.19E-05	CHRND	3.67	1.76E-02
RVMSR	T0	TMEM150C	3.91	3.20E-05	CISD2	-1.23	1.76E-02
RVMSR	T0	UBE2DNL	2.14	4.12E-05	SASH1	1.75	1.76E-02
RVMSR	T0	LINC00092	3.16	4.52E-05	LOC101929607	2.14	1.76E-02
RVMSR	T0	NFIB	2.61	4.59E-05	FADS1	1.98	1.76E-02
RVMSR	T0	TMEM233	2.74	4.67E-05	PLCXD2	4.65	1.76E-02
RVMSR	T0	LOC101928907	3.87	5.03E-05	SMIM21	2.01	1.76E-02
RVMSR	T0	ANO8	5.09	5.52E-05	CEACAM19	2.29	1.76E-02
RVMSR	T0	HOXD1	2.10	5.66E-05	S100A16	3.68	1.76E-02
RVMSR	T0	MB	3.86	5.66E-05	DMRT2	4.65	1.77E-02
RVMSR	T0	ZNF446	2.44	6.13E-05	AKAP5	2.08	1.77E-02

RVMSR	T0	NEUROG1	4.46	6.13E-05	C10orf55	3.64	1.77E-02
RVMSR	T0	ERICH4	2.89	6.18E-05	MROH6	2.08	1.77E-02
RVMSR	T0	OR4D9	3.02	6.68E-05	RTL1	2.96	1.77E-02
RVMSR	T0	PTPRT	5.04	7.09E-05	GJC1	2.30	1.77E-02
RVMSR	T0	RHOD	2.56	7.16E-05	ALG1L2	2.22	1.77E-02
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RVMSR	T0	LOC105372383	3.45	7.47E-05	RASAL2	1.79	1.78E-02
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RVMSR	T0	CA12	3.30	7.98E-05	SORCS1	3.67	1.78E-02
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RVMSR	T0	LOC105369691	3.44	7.98E-05	NKX6-2	3.68	1.78E-02
RVMSR	T0	PLA2G4C-AS1	2.68	8.09E-05	GALR3	3.66	1.78E-02
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RVMSR	T0	LOC100506498	3.18	8.94E-05	OXCT1-AS1	3.23	1.78E-02
RVMSR	T0	HIST1H1D	-2.07	9.17E-05	MIR3927	2.39	1.78E-02
RVMSR	T0	PAX6	2.28	9.75E-05	MIR4296	2.79	1.78E-02
RVMSR	T0	DNAJC9-AS1	2.77	9.75E-05	STEAP2	4.64	1.79E-02
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RVMSR	T0	NOS1	2.28	9.75E-05	AUNIP	4.64	1.79E-02
RVMSR	T0	LOC102725072	2.40	1.02E-04	LOC105369785	3.68	1.79E-02
RVMSR	T0	SMCR5	3.27	1.08E-04	SHANK2-AS1	2.77	1.79E-02
RVMSR	T0	LOC101927572	3.15	1.10E-04	HS6ST3	2.07	1.80E-02
RVMSR	T0	FAT3	2.69	1.21E-04	LOC653786	2.29	1.80E-02
RVMSR	T0	TMEM89	4.00	1.40E-04	LOC100506700	1.65	1.80E-02
RVMSR	T0	SEMA6A	3.99	1.43E-04	MCOLN2	1.70	1.80E-02
RVMSR	T0	LOC100505915	2.54	1.43E-04	TMEM231	2.97	1.80E-02
RVMSR	T0	TSIX	2.21	1.43E-04	RNASE13	4.62	1.80E-02
RVMSR	T0	RHBDL3	3.55	1.43E-04	MC5R	3.24	1.80E-02
RVMSR	T0	OR1A2	3.99	1.43E-04	LOC105375650	1.92	1.80E-02

RVMSR	T0	LOC100506159	6.20	1.57E-04	RNF180	2.97	1.80E-02
RVMSR	T0	LINC00707	2.03	1.65E-04	OR7E24	2.13	1.80E-02
RVMSR	T0	SEMA3B	2.04	1.69E-04	MIR4443	2.77	1.81E-02
RVMSR	T0	KLHL23	3.71	1.77E-04	LEUTX	2.61	1.81E-02
RVMSR	T0	LOC105371766	3.52	1.77E-04	TTC29	4.61	1.81E-02
RVMSR	T0	LINC00312	4.89	1.77E-04	DNAH10	4.61	1.81E-02
RVMSR	T0	FUT2	3.10	1.78E-04	IFT74-AS1	3.23	1.81E-02
RVMSR	T0	ZNF630-AS1	3.00	1.84E-04	LMNB1	-1.69	1.81E-02
RVMSR	T0	C1QTNF1-AS1	3.50	1.93E-04	SNORA52	-1.24	1.81E-02
RVMSR	T0	CYP3A5	6.17	2.04E-04	MIR548T	2.49	1.81E-02
RVMSR	T0	PRTG	2.54	2.05E-04	CYP17A1	2.13	1.81E-02
RVMSR	T0	BBC3	2.36	2.07E-04	LCA5	4.63	1.81E-02
RVMSR	T0	RBPMS-AS1	3.50	2.07E-04	FRGCA	2.95	1.81E-02
RVMSR	T0	LINC00520	3.68	2.07E-04	CA7	2.77	1.81E-02
RVMSR	T0	C11orf16	3.49	2.07E-04	COMMD6	-1.22	1.81E-02
RVMSR	T0	MOG	3.20	2.09E-04	NFASC	2.38	1.81E-02
RVMSR	T0	AJUBA	2.41	2.19E-04	OR1I1	2.20	1.81E-02
RVMSR	T0	GPR32	4.31	2.20E-04	FANCD2OS	2.62	1.81E-02
RVMSR	T0	COPZ2	2.89	2.20E-04	DEFB4B	2.95	1.81E-02
RVMSR	T0	NDRG4	6.14	2.20E-04	MYO15A	2.20	1.81E-02
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RVMSR	T0	GIP	2.61	2.47E-04	RGS20	3.65	1.82E-02
RVMSR	T0	FBLIM1	2.16	2.52E-04	TPRG1-AS2	4.61	1.83E-02
RVMSR	T0	TMEM254-AS1	2.61	2.61E-04	MIR885	3.23	1.83E-02
RVMSR	T0	OR10G3	2.73	2.65E-04	MS4A5	3.65	1.83E-02
RVMSR	T0	UPB1	3.31	2.66E-04	LOC102723883	3.22	1.83E-02
RVMSR	T0	BMPR1B-AS1	3.15	2.83E-04	TMEM51	2.96	1.83E-02
RVMSR	T0	NYAP1	2.60	2.89E-04	GJA3	1.45	1.83E-02

RVMSR	T0	CFAP99	4.83	2.89E-04	IGF1	1.87	1.83E-02
RVMSR	T0	SLC1A6	2.50	2.96E-04	CPLX1	2.96	1.83E-02
RVMSR	T0	BSG	-1.92	2.96E-04	RUNDC3A-AS1	1.62	1.83E-02
RVMSR	T0	RAPGEFL1	2.71	2.96E-04	YWHAEP1	2.96	1.83E-02
RVMSR	T0	EML1	2.22	2.96E-04	LOC101928937	3.23	1.83E-02
RVMSR	T0	ITGA3	4.26	2.96E-04	MIR4718	4.62	1.83E-02
RVMSR	T0	STRA8	3.29	2.96E-04	VTRNA1-2	2.49	1.84E-02
RVMSR	T0	MYADML	3.29	2.97E-04	LINC01567	2.29	1.84E-02
RVMSR	T0	PTPN14	3.15	3.02E-04	BPIFA3	2.38	1.84E-02
RVMSR	T0	CDC25A	3.90	3.02E-04	TERT	3.21	1.84E-02
RVMSR	T0	SMG7-AS1	3.43	3.21E-04	TMEM82	2.48	1.84E-02
RVMSR	T0	CKAP2L	4.24	3.21E-04	KCNG4	3.63	1.84E-02
RVMSR	T0	MCHR1	2.44	3.21E-04	ATP5J2-PTCD1	1.30	1.84E-02
RVMSR	T0	LOC100130849	3.26	3.44E-04	DECR2	1.87	1.84E-02
RVMSR	T0	LOC102724238	2.63	3.49E-04	OR6B2	2.28	1.84E-02
RVMSR	T0	LOC554249	2.63	3.49E-04	HDAC11-AS1	2.62	1.84E-02
RVMSR	T0	GALNT15	3.01	3.52E-04	PMS2	1.42	1.84E-02
RVMSR	T0	PSMA8	2.69	3.52E-04	MIR4746	1.96	1.85E-02
RVMSR	T0	C9orf153	3.42	3.52E-04	NRAV	1.80	1.85E-02
RVMSR	T0	GJA8	3.42	3.52E-04	CLCF1	3.21	1.86E-02
RVMSR	T0	LINC01269	2.57	3.65E-04	MMP7	4.61	1.86E-02
RVMSR	T0	SRR	2.47	3.65E-04	FAM84B	1.87	1.86E-02
RVMSR	T0	RASSF6	3.86	3.65E-04	TIMELESS	1.79	1.87E-02
RVMSR	T0	SOX9-AS1	6.01	3.71E-04	OR7G3	2.37	1.87E-02
RVMSR	T0	BMP8A	2.62	3.71E-04	FOXC2	4.61	1.87E-02
RVMSR	T0	PART1	4.77	3.71E-04	AGAP4	1.62	1.87E-02
RVMSR	T0	PTPRS	2.23	3.71E-04	PCDH11X	2.48	1.87E-02
RVMSR	T0	CELA2A	3.61	3.71E-04	C1orf140	2.48	1.87E-02
RVMSR	T0	PCAT5	2.62	3.71E-04	ELFN2	3.65	1.87E-02

RVMSR	T0	REP15	3.60	3.78E-04	ZNF461	1.71	1.87E-02
RVMSR	T0	PRSS38	2.82	3.78E-04	IQCJ	3.63	1.88E-02
RVMSR	T0	CTBP1-AS	4.76	3.80E-04	SLC25A33	1.83	1.88E-02
RVMSR	T0	OLMALINC	2.68	3.86E-04	TMEM38A	1.40	1.88E-02
RVMSR	T0	RELN	3.84	3.95E-04	DHODH	1.73	1.88E-02
RVMSR	T0	PTK7	2.68	3.95E-04	LINC01028	2.96	1.88E-02
RVMSR	T0	PTPRF	3.40	3.95E-04	COX6A2	2.75	1.89E-02
RVMSR	T0	ECT2L	4.20	3.95E-04	TRAM2-AS1	2.01	1.89E-02
RVMSR	T0	ARSE	2.74	4.00E-04	LOC105376365	4.63	1.89E-02
RVMSR	T0	CHRD	3.10	4.00E-04	OR1F1	3.64	1.89E-02
RVMSR	T0	ICAM5	2.66	4.00E-04	TBX5	2.61	1.89E-02
RVMSR	T0	CDK5R2	2.89	4.00E-04	ZNF230	1.92	1.89E-02
RVMSR	T0	LOC101929159	2.55	4.00E-04	LOC400958	2.76	1.89E-02
RVMSR	T0	TMEM120B	1.82	4.04E-04	PSMA4	-1.21	1.89E-02
RVMSR	T0	ZAN	2.99	4.05E-04	WWTR1	2.59	1.89E-02
RVMSR	T0	DACT3	4.18	4.10E-04	PHOX2B	2.59	1.89E-02
RVMSR	T0	TINCR	2.44	4.10E-04	PGBD4	1.52	1.89E-02
RVMSR	T0	OR8J1	3.84	4.11E-04	SERPINA2	3.21	1.90E-02
RVMSR	T0	GRK7	4.18	4.11E-04	NRIP2	2.76	1.90E-02
RVMSR	T0	CDR2L	2.89	4.11E-04	B3GNT6	2.60	1.90E-02
RVMSR	T0	ATP1A2	2.67	4.11E-04	LOC729950	2.27	1.90E-02
RVMSR	T0	NXNL1	3.83	4.11E-04	SNAR-A2	2.00	1.90E-02
RVMSR	T0	OR5C1	2.81	4.11E-04	C1QTNF1	2.76	1.90E-02
RVMSR	T0	SCRG1	1.78	4.11E-04	HAPLN2	2.27	1.90E-02
RVMSR	T0	LMOD3	2.44	4.16E-04	TMEM161A	1.66	1.90E-02
RVMSR	T0	ELF3	2.65	4.23E-04	CGB8	2.75	1.90E-02
RVMSR	T0	FJX1	4.73	4.31E-04	POTEC	2.47	1.91E-02
RVMSR	T0	BDNF-AS	2.29	4.47E-04	LOC100422737	3.20	1.91E-02
RVMSR	T0	SAPCD1	2.72	4.55E-04	LOC101927686	3.63	1.91E-02

RVMSR	T0	KRT12	3.08	4.55E-04	LOC100507389	3.63	1.91E-02
RVMSR	T0	LINC01144	2.87	4.55E-04	TSKS	2.06	1.92E-02
RVMSR	T0	IFIT1	-1.85	4.69E-04	KCTD14	2.75	1.92E-02
RVMSR	T0	SPOCK1	2.34	4.69E-04	SGSM1	1.68	1.92E-02
RVMSR	T0	FKBP10	3.07	4.69E-04	LHFPL3-AS1	4.59	1.92E-02
RVMSR	T0	CCBE1	2.78	4.96E-04	KCNRG	2.37	1.93E-02
RVMSR	T0	LINC00691	2.47	5.01E-04	CD1B	2.94	1.93E-02
RVMSR	T0	CPZ	2.87	5.03E-04	SLC25A2	4.59	1.93E-02
RVMSR	T0	PMP2	3.36	5.03E-04	DNA2	1.70	1.93E-02
RVMSR	T0	GJB1	2.38	5.03E-04	ANKRD19P	1.95	1.93E-02
RVMSR	T0	LOC550113	4.70	5.03E-04	LIN28A	3.22	1.93E-02
RVMSR	T0	LOC105372397	3.19	5.14E-04	LOC101928140	2.94	1.93E-02
RVMSR	T0	FAM231C	3.06	5.22E-04	ESR1	2.27	1.93E-02
RVMSR	T0	AGBL5-AS1	2.26	5.37E-04	FAM215A	2.19	1.93E-02
RVMSR	T0	SLC1A1	3.80	5.41E-04	HINT1	-1.24	1.93E-02
RVMSR	T0	MSI1	3.06	5.45E-04	BICC1	2.61	1.93E-02
RVMSR	T0	MIR128-2	2.70	5.45E-04	LOC645166	1.82	1.93E-02
RVMSR	T0	LOC285804	2.23	5.51E-04	MIR145	3.64	1.93E-02
RVMSR	T0	MAP1B	2.25	5.85E-04	XYLB	2.36	1.93E-02
RVMSR	T0	NTN5	3.53	5.86E-04	CRYGB	2.92	1.94E-02
RVMSR	T0	MGC34796	2.36	5.86E-04	ZNF462	2.74	1.94E-02
RVMSR	T0	EVPL	3.05	5.86E-04	TRPV1	2.27	1.94E-02
RVMSR	T0	MTMR9LP	2.85	5.86E-04	LOC158435	2.93	1.94E-02
RVMSR	T0	FOSB	2.45	5.86E-04	KRTAP9-4	2.94	1.94E-02
RVMSR	T0	RGL3	2.40	5.99E-04	HTR6	3.20	1.94E-02
RVMSR	T0	FBXO27	2.17	6.03E-04	LOC101928569	3.62	1.94E-02
RVMSR	T0	BSN-AS2	2.84	6.06E-04	SERTAD4	4.59	1.94E-02
RVMSR	T0	BCAR4	2.62	6.11E-04	BMPR1B	3.62	1.94E-02
RVMSR	T0	KCNN3	2.61	6.11E-04	TMEM257	1.99	1.94E-02

RVMSR	T0	CD164L2	2.82	6.18E-04	EFNA5	2.94	1.94E-02
RVMSR	T0	GPR152	2.28	6.25E-04	MIR8485	3.64	1.95E-02
RVMSR	T0	PXDN	2.93	6.25E-04	ACER1	2.75	1.95E-02
RVMSR	T0	PRDM11	3.03	6.25E-04	MIR6086	4.58	1.95E-02
RVMSR	T0	ALPK3	2.67	6.44E-04	OR10K1	4.60	1.95E-02
RVMSR	T0	APOC1P1	2.82	6.45E-04	LTBP1	1.69	1.95E-02
RVMSR	T0	MEX3A	2.74	6.46E-04	LOC105371592	1.56	1.95E-02
RVMSR	T0	LINC01545	3.16	6.50E-04	TDRP	3.64	1.95E-02
RVMSR	T0	SLC7A14	2.27	6.51E-04	LOC642426	2.00	1.95E-02
RVMSR	T0	NCR3	-1.93	6.56E-04	PLEKHG4B	3.62	1.95E-02
RVMSR	T0	TTC23L	2.82	6.56E-04	LOC100129138	2.59	1.95E-02
RVMSR	T0	RSPH6A	3.51	6.81E-04	UTS2R	1.66	1.95E-02
RVMSR	T0	SGCA	5.86	6.82E-04	EID2B	1.55	1.95E-02
RVMSR	T0	CEBPB-AS1	2.39	6.88E-04	SHE	3.19	1.96E-02
RVMSR	T0	CDIPT-AS1	2.91	6.88E-04	KAAG1	2.46	1.96E-02
RVMSR	T0	LINC00905	3.02	6.88E-04	CFAP77	3.61	1.96E-02
RVMSR	T0	MIR3130-1	2.81	6.88E-04	CEMP1	2.94	1.96E-02
RVMSR	T0	LOC101928253	4.09	7.02E-04	RPL17	-1.21	1.96E-02
RVMSR	T0	PRDM14	2.37	7.12E-04	MMP28	3.19	1.96E-02
RVMSR	T0	NAIF1	2.14	7.26E-04	LOC100506860	2.61	1.96E-02
RVMSR	T0	NRSN1	4.10	7.42E-04	U2SURP	-1.20	1.96E-02
RVMSR	T0	LOC100506476	2.32	7.52E-04	SALL4	2.27	1.96E-02
RVMSR	T0	DUOX2	5.83	7.53E-04	SLC9A7P1	2.12	1.96E-02
RVMSR	T0	DUSP21	4.64	7.66E-04	MMP15	3.18	1.97E-02
RVMSR	T0	MORC1	5.85	7.66E-04	WASF3	2.59	1.98E-02
RVMSR	T0	HPCA	4.63	7.73E-04	SMTNL1	3.19	1.98E-02
RVMSR	T0	APOC4-APOC2	2.52	7.77E-04	LOC340107	2.19	1.98E-02
RVMSR	T0	HSPB9	1.97	7.81E-04	PROSER3	1.82	1.98E-02
RVMSR	T0	PYGO1	3.28	7.81E-04	LOC102723661	3.20	1.98E-02

RVMSR	T0	MAPRE3	4.08	7.81E-04	SLC6A20	2.35	1.98E-02
RVMSR	T0	NYAP2	2.41	7.81E-04	ENAH	2.05	1.98E-02
RVMSR	T0	DLG1-AS1	3.48	7.84E-04	EDDM3B	1.81	1.99E-02
RVMSR	T0	LINC00626	4.64	7.91E-04	CADM2	4.57	1.99E-02
RVMSR	T0	MIR4660	2.81	7.94E-04	LOC101929613	2.74	1.99E-02
RVMSR	T0	CYP3A7-CYP3A51P	4.07	8.05E-04	CCDC144NL-AS1	4.59	1.99E-02
RVMSR	T0	LOC101929259	2.13	8.09E-04	SERPINA12	4.59	1.99E-02
RVMSR	T0	SCN3B	4.06	8.18E-04	CELA2B	2.59	1.99E-02
RVMSR	T0	SMIM18	3.00	8.21E-04	LOC105447645	1.55	1.99E-02
RVMSR	T0	LRP5	2.32	8.27E-04	SLC9A1	1.81	1.99E-02
RVMSR	T0	ZMYND15	4.61	8.32E-04	TEX43	2.92	2.00E-02
RVMSR	T0	PPP3R2	3.47	8.42E-04	BMPR2	1.32	2.00E-02
RVMSR	T0	ANO2	4.60	8.42E-04	CCDC190	2.36	2.00E-02
RVMSR	T0	TCF23	2.99	8.52E-04	LOC283332	1.94	2.00E-02
RVMSR	T0	RAB3B	2.89	8.52E-04	PDGFRL	3.63	2.00E-02
RVMSR	T0	LINC00167	2.70	8.52E-04	VCAM1	2.73	2.00E-02
RVMSR	T0	OR2Z1	2.24	8.52E-04	PRG4	2.35	2.01E-02
RVMSR	T0	AKAIN1	5.81	8.52E-04	C6orf15	2.47	2.01E-02
RVMSR	T0	OGN	2.63	8.52E-04	RNF41	1.25	2.01E-02
RVMSR	T0	MAP1S	1.68	8.52E-04	MYLK-AS1	2.93	2.01E-02
RVMSR	T0	PRODH2	2.87	8.52E-04	YES1	2.11	2.01E-02
RVMSR	T0	GPR1	2.20	8.54E-04	ARNT2	2.72	2.01E-02
RVMSR	T0	DENND2A	2.62	8.54E-04	NFATC4	3.61	2.01E-02
RVMSR	T0	C17orf78	2.86	8.62E-04	CLRN2	3.19	2.01E-02
RVMSR	T0	OR4N3P	5.81	8.62E-04	IGSF5	3.61	2.01E-02
RVMSR	T0	KCNAB1-AS2	5.79	8.62E-04	GPX6	3.61	2.03E-02
RVMSR	T0	LOC400710	3.11	8.63E-04	RPS7	-1.20	2.03E-02
RVMSR	T0	DEFB121	5.79	8.63E-04	MFAP5	2.17	2.03E-02
RVMSR	T0	CSPG5	2.77	8.83E-04	XRCC2	1.98	2.03E-02

RVMSR	T0	SLC22A11	3.71	8.83E-04	ZRANB1	-1.31	2.03E-02
RVMSR	T0	MEIS1-AS2	2.78	8.83E-04	MIR7-3HG	2.10	2.03E-02
RVMSR	T0	PDE4A	2.14	8.89E-04	SLC7A11-AS1	2.74	2.03E-02
RVMSR	T0	SPACA5	5.78	8.89E-04	SBSPON	4.55	2.03E-02
RVMSR	T0	SPACA5B	5.78	8.89E-04	CHRDL1	4.55	2.03E-02
RVMSR	T0	MIR4267	2.30	8.89E-04	SHANK2-AS3	2.58	2.04E-02
RVMSR	T0	DCAF12L1	5.78	9.15E-04	FIBIN	2.73	2.04E-02
RVMSR	T0	DPPA4	2.26	9.17E-04	GMCL1P1	2.27	2.04E-02
RVMSR	T0	OR4D10	2.34	9.17E-04	RESP18	2.73	2.04E-02
RVMSR	T0	KANK4	2.30	9.17E-04	SV2A	2.34	2.05E-02
RVMSR	T0	SCUBE3	2.78	9.18E-04	CHEK2P2	2.26	2.05E-02
RVMSR	T0	TXNDC8	2.27	9.24E-04	SNAR-C5	2.91	2.05E-02
RVMSR	T0	SNHG5	-1.73	9.24E-04	PNLIPRP3	3.60	2.05E-02
RVMSR	T0	DEFB4A	5.76	9.26E-04	CDH10	4.57	2.05E-02
RVMSR	T0	LINC01227	3.24	9.26E-04	PXDNL	2.11	2.06E-02
RVMSR	T0	LOC105378614	2.68	9.29E-04	MYHAS	2.72	2.06E-02
RVMSR	T0	IGBP1P1	2.23	9.34E-04	KRTAP3-2	2.72	2.06E-02
RVMSR	T0	MRS2P2	3.25	9.40E-04	LOC101928464	1.26	2.06E-02
RVMSR	T0	CCDC116	2.98	9.42E-04	ATP2B3	3.19	2.06E-02
RVMSR	T0	PDLIM4	5.76	9.42E-04	LOC728290	4.55	2.07E-02
RVMSR	T0	FUT5	5.76	9.42E-04	LINC01352	2.11	2.07E-02
RVMSR	T0	WFDC6	2.76	9.42E-04	LINC00350	2.71	2.07E-02
RVMSR	T0	ENOX1	3.24	9.42E-04	CTLA4	1.99	2.07E-02
RVMSR	T0	SPATS1	2.29	9.44E-04	ALDH4A1	2.25	2.07E-02
RVMSR	T0	LOC100505918	2.67	9.45E-04	LINC01055	2.91	2.08E-02
RVMSR	T0	PDCL3P4	1.97	9.45E-04	ZBTB46-AS1	2.04	2.08E-02
RVMSR	T0	SHROOM1	2.54	9.45E-04	DHDH	1.98	2.08E-02
RVMSR	T0	GHET1	2.33	9.52E-04	LINC00392	2.72	2.08E-02
RVMSR	T0	SULT2A1	2.15	9.58E-04	SVOP	2.03	2.09E-02

RVMSR	T0	IAPP	2.97	9.72E-04	MIR4733	2.91	2.09E-02
RVMSR	T0	CELA3B	2.97	9.74E-04	MIR557	2.92	2.09E-02
RVMSR	T0	DDN	2.76	9.74E-04	DNAI2	2.91	2.09E-02
RVMSR	T0	LOC101928902	2.86	9.81E-04	CKMT1B	1.80	2.09E-02
RVMSR	T0	FGL1	2.54	9.82E-04	LOC101928414	2.26	2.09E-02
RVMSR	T0	POU3F1	4.56	9.89E-04	TNFRSF10D	1.86	2.09E-02
RVMSR	T0	SIX3	5.75	9.90E-04	RPS6KA6	2.35	2.09E-02
RVMSR	T0	RAPGEF4-AS1	4.01	1.01E-03	HKDC1	3.18	2.09E-02
RVMSR	T0	KLRG2	3.44	1.01E-03	C1QTNF4	2.59	2.09E-02
RVMSR	T0	BIRC8	2.96	1.01E-03	RPS3A	-1.21	2.09E-02
RVMSR	T0	LINC00942	3.24	1.01E-03	LOC51145	3.17	2.09E-02
RVMSR	T0	TENM3	4.01	1.01E-03	SPTA1	4.56	2.09E-02
RVMSR	T0	LOC101928696	3.68	1.01E-03	LOC105379176	2.92	2.09E-02
RVMSR	T0	DEFA1B	2.05	1.02E-03	SOX7	3.17	2.09E-02
RVMSR	T0	DEFA1	2.05	1.02E-03	CACNA1G-AS1	3.18	2.09E-02
RVMSR	T0	LOC100129345	5.72	1.04E-03	KIR3DX1	2.34	2.09E-02
RVMSR	T0	MGAT4EP	2.47	1.04E-03	TM4SF19	2.17	2.10E-02
RVMSR	T0	RASGRF1	3.67	1.04E-03	VMO1	2.04	2.10E-02
RVMSR	T0	LOC102724450	2.75	1.04E-03	ABALON	2.45	2.11E-02
RVMSR	T0	CXCL14	2.75	1.04E-03	RUSC1	1.44	2.11E-02
RVMSR	T0	PITX1	3.44	1.04E-03	LOC101927488	3.17	2.11E-02
RVMSR	T0	MND1	2.47	1.07E-03	STOX2	2.72	2.11E-02
RVMSR	T0	EXOC3L2	2.17	1.09E-03	PAGE1	2.72	2.11E-02
RVMSR	T0	GDNF	3.22	1.09E-03	DARS-AS1	3.17	2.11E-02
RVMSR	T0	BSPH1	4.00	1.10E-03	MRGPRF	4.55	2.11E-02
RVMSR	T0	SYT3	2.83	1.12E-03	OR52A5	4.55	2.11E-02
RVMSR	T0	FAM53B-AS1	3.42	1.12E-03	WWC2-AS2	2.33	2.11E-02
RVMSR	T0	MIXL1	2.40	1.12E-03	C8G	3.59	2.11E-02
RVMSR	T0	LINC00964	3.41	1.13E-03	CTB-178M22.2	4.55	2.11E-02

RVMSR	T0	LGI4	3.21	1.13E-03	LOC100507346	3.18	2.12E-02
RVMSR	T0	EBI3	2.03	1.13E-03	ADIPOQ	3.59	2.12E-02
RVMSR	T0	RBKS	2.52	1.13E-03	LINC00158	2.56	2.12E-02
RVMSR	T0	CLUL1	2.52	1.14E-03	MIR4509-3	4.55	2.12E-02
RVMSR	T0	SLC36A3	2.23	1.14E-03	TPD52	-1.42	2.12E-02
RVMSR	T0	MYBPHL	2.31	1.15E-03	ZG16	3.59	2.12E-02
RVMSR	T0	ANKLE1	3.22	1.16E-03	HTR3E-AS1	2.90	2.12E-02
RVMSR	T0	FAM230B	3.39	1.16E-03	LOC101928103	2.03	2.12E-02
RVMSR	T0	LOC643406	3.21	1.17E-03	LOC102723692	1.94	2.12E-02
RVMSR	T0	LOC100129603	3.21	1.18E-03	LOC100506746	1.58	2.13E-02
RVMSR	T0	LOC101927532	1.96	1.18E-03	AWAT1	3.19	2.13E-02
RVMSR	T0	DUSP26	2.93	1.18E-03	TBC1D4	-1.30	2.13E-02
RVMSR	T0	NPAS4	2.45	1.19E-03	KHDRBS3	3.16	2.13E-02
RVMSR	T0	UBE2E1-AS1	3.39	1.20E-03	PRDM15	1.88	2.13E-02
RVMSR	T0	SPDYE3	3.22	1.22E-03	ADAM18	3.17	2.14E-02
RVMSR	T0	MCIDAS	3.21	1.23E-03	C16orf90	2.04	2.14E-02
RVMSR	T0	HTR3E	2.81	1.23E-03	MIR4273	2.72	2.14E-02
RVMSR	T0	ZNF385D	4.51	1.23E-03	SLC37A4	1.76	2.14E-02
RVMSR	T0	ADCY1	3.40	1.23E-03	LOC146795	3.17	2.14E-02
RVMSR	T0	ZNF571-AS1	2.30	1.23E-03	IQSEC3	3.17	2.15E-02
RVMSR	T0	IQCK	3.63	1.23E-03	LOC103191607	4.54	2.15E-02
RVMSR	T0	ZBTB8A	2.34	1.23E-03	PRR23B	1.98	2.15E-02
RVMSR	T0	FGFR4	2.50	1.24E-03	PLCXD3	4.52	2.15E-02
RVMSR	T0	MIR3170	3.39	1.26E-03	CECR3	2.90	2.16E-02
RVMSR	T0	IGF2BP1	2.08	1.26E-03	LOC105376271	2.16	2.16E-02
RVMSR	T0	C9orf106	2.18	1.26E-03	BHMT2	2.57	2.16E-02
RVMSR	T0	CDC42BPG	1.94	1.26E-03	IL13RA2	3.59	2.16E-02
RVMSR	T0	CD70	2.11	1.27E-03	KLK6	2.71	2.16E-02
RVMSR	T0	SV2C	2.49	1.27E-03	PKNOX2	2.09	2.17E-02

RVMSR	T0	KIAA2012	2.72	1.27E-03	FGFBP3	1.61	2.17E-02
RVMSR	T0	WARS2-IT1	3.62	1.28E-03	GIPC3	2.45	2.17E-02
RVMSR	T0	MIR4447	4.49	1.28E-03	OR52I1	3.59	2.17E-02
RVMSR	T0	VSX2	3.95	1.30E-03	FHL5	3.59	2.18E-02
RVMSR	T0	SH2D6	3.63	1.30E-03	ANGPTL3	4.53	2.18E-02
RVMSR	T0	OR6C6	3.39	1.30E-03	LINC01185	2.56	2.18E-02
RVMSR	T0	SPAG4	3.19	1.31E-03	LINC00871	2.71	2.18E-02
RVMSR	T0	FBXO16	2.80	1.33E-03	LENEP	3.17	2.18E-02
RVMSR	T0	NECAB1	4.48	1.33E-03	ZNF205-AS1	1.64	2.18E-02
RVMSR	T0	MEG3	3.20	1.34E-03	ZNF233	3.16	2.18E-02
RVMSR	T0	MMRN2	3.20	1.36E-03	MIR7153	2.57	2.18E-02
RVMSR	T0	ITIH5	3.38	1.36E-03	ITGA8	2.56	2.18E-02
RVMSR	T0	PPP1R26-AS1	3.04	1.36E-03	C3orf35	2.42	2.18E-02
RVMSR	T0	DNAJC22	2.37	1.37E-03	LACTBL1	2.55	2.19E-02
RVMSR	T0	LAMC2	3.04	1.37E-03	GINS3	3.58	2.19E-02
RVMSR	T0	SLC27A2	2.28	1.38E-03	NR0B1	4.53	2.19E-02
RVMSR	T0	GABRE	5.66	1.40E-03	DLC1	2.71	2.20E-02
RVMSR	T0	LOC101928491	3.61	1.41E-03	POM121L2	1.87	2.20E-02
RVMSR	T0	TANC1	3.19	1.41E-03	ODF1	2.44	2.20E-02
RVMSR	T0	CCDC82	-2.04	1.41E-03	EGFLAM-AS2	1.98	2.20E-02
RVMSR	T0	NPIPB15	2.10	1.41E-03	LOC101929413	3.57	2.20E-02
RVMSR	T0	EPN2-AS1	3.38	1.41E-03	PLAC1	2.90	2.20E-02
RVMSR	T0	TAL2	3.18	1.41E-03	LOC101927549	2.56	2.20E-02
RVMSR	T0	LOC730202	2.31	1.42E-03	SSX6	2.43	2.21E-02
RVMSR	T0	NAV2	2.27	1.42E-03	HESX1	3.57	2.21E-02
RVMSR	T0	MIR6718	4.45	1.44E-03	C17orf99	2.57	2.21E-02
RVMSR	T0	SV2B	3.95	1.44E-03	SDC4	2.56	2.21E-02
RVMSR	T0	FERMT1	3.95	1.44E-03	LOC102723335	3.15	2.21E-02
RVMSR	T0	TPTE2P1	2.37	1.44E-03	MIR6124	2.09	2.21E-02

RVMSR	T0	FAM71F2	2.36	1.44E-03	LOC101927230	3.60	2.21E-02
RVMSR	T0	CADM1	2.54	1.45E-03	LOC101929288	3.58	2.21E-02
RVMSR	T0	LOC100101148	4.47	1.45E-03	TRIML2	2.56	2.21E-02
RVMSR	T0	LOC541473	4.47	1.45E-03	MIR4769	2.33	2.21E-02
RVMSR	T0	HTR1D	2.55	1.47E-03	WDR17	2.43	2.22E-02
RVMSR	T0	RHOJ	4.46	1.47E-03	LOC100507406	4.52	2.22E-02
RVMSR	T0	DUXAP8	2.53	1.47E-03	NEURL1B	2.23	2.22E-02
RVMSR	T0	ADAM7	3.94	1.47E-03	MEF2B	2.43	2.22E-02
RVMSR	T0	TMEM52B	2.53	1.49E-03	AMTN	2.09	2.23E-02
RVMSR	T0	ELF5	3.02	1.49E-03	XPNPEP2	2.71	2.24E-02
RVMSR	T0	LY6G6E	2.03	1.49E-03	LOC102723439	2.88	2.24E-02
RVMSR	T0	CDKL3	2.61	1.49E-03	LOC388406	2.90	2.24E-02
RVMSR	T0	SRSF12	2.89	1.49E-03	PPP3CB-AS1	1.21	2.24E-02
RVMSR	T0	EFCC1	3.17	1.49E-03	MIR365A	2.70	2.24E-02
RVMSR	T0	STAR	2.69	1.49E-03	FABP3	1.86	2.24E-02
RVMSR	T0	MYO3B	3.62	1.50E-03	LINC01251	3.15	2.24E-02
RVMSR	T0	LOC101928167	5.62	1.50E-03	CCDC114	1.87	2.24E-02
RVMSR	T0	LOC105374516	3.93	1.50E-03	AOX3P-AOX2P	2.43	2.25E-02
RVMSR	T0	INPP5E	1.96	1.50E-03	PRPH2	3.14	2.25E-02
RVMSR	T0	PIWIL1	4.45	1.50E-03	PRR29-AS1	2.32	2.25E-02
RVMSR	T0	TDRD12	3.60	1.50E-03	NRSN2	2.23	2.25E-02
RVMSR	T0	SNORA101A	5.61	1.51E-03	MIR4429	2.44	2.25E-02
RVMSR	T0	OPRM1	4.46	1.51E-03	KLHL6-AS1	2.16	2.25E-02
RVMSR	T0	PIWIL3	2.90	1.51E-03	FAM46B	4.51	2.25E-02
RVMSR	T0	LOC105369920	4.45	1.51E-03	USH1G	4.51	2.25E-02
RVMSR	T0	LOC101927053	3.01	1.51E-03	PARVA	3.57	2.25E-02
RVMSR	T0	HS3ST2	2.89	1.52E-03	NDUFB2	-1.21	2.25E-02
RVMSR	T0	ABCA3	5.61	1.52E-03	LOC105377682	3.14	2.26E-02
RVMSR	T0	C9orf92	3.17	1.52E-03	WDPCP	1.66	2.26E-02

RVMSR	T0	LINC00543	3.35	1.52E-03	SH3BP4	2.89	2.26E-02
RVMSR	T0	GLTPD2	3.16	1.52E-03	DMRTA2	2.69	2.26E-02
RVMSR	T0	LRRC38	2.53	1.52E-03	MIR6127	2.43	2.26E-02
RVMSR	T0	LOC440300	2.69	1.53E-03	OR4C13	3.56	2.26E-02
RVMSR	T0	FBXO36	2.69	1.54E-03	PGAM1P5	2.31	2.27E-02
RVMSR	T0	MIR6128	3.34	1.54E-03	NXN	2.89	2.27E-02
RVMSR	T0	TRPV4	2.87	1.54E-03	SSTR2	1.56	2.27E-02
RVMSR	T0	MIR4487	2.41	1.54E-03	LINC00887	2.23	2.27E-02
RVMSR	T0	MIR4311	3.34	1.55E-03	CHKB-AS1	1.68	2.27E-02
RVMSR	T0	LOC101928887	5.61	1.56E-03	NDUFAF4P1	2.03	2.27E-02
RVMSR	T0	LEXM	2.11	1.56E-03	OR11H6	2.32	2.28E-02
RVMSR	T0	MIR548Z	3.16	1.56E-03	CREB3L1	2.23	2.28E-02
RVMSR	T0	PCSK2	5.62	1.56E-03	ST8SIA6	2.42	2.28E-02
RVMSR	T0	EPHA3	5.63	1.57E-03	ELN	2.88	2.28E-02
RVMSR	T0	GNG3	2.69	1.58E-03	MIR640	3.15	2.29E-02
RVMSR	T0	LOC339059	2.30	1.59E-03	CLYBL-AS1	2.88	2.29E-02
RVMSR	T0	ZNF554	2.17	1.59E-03	ANKRD63	3.15	2.30E-02
RVMSR	T0	MIR4468	3.33	1.59E-03	TLR3	3.14	2.30E-02
RVMSR	T0	LOC283731	3.16	1.59E-03	PCAT19	2.07	2.30E-02
RVMSR	T0	CACNB1	2.60	1.59E-03	TAZ	1.23	2.30E-02
RVMSR	T0	TSSC2	3.16	1.59E-03	LOC101929297	2.87	2.30E-02
RVMSR	T0	PLIN4	2.47	1.60E-03	LINC01378	2.88	2.30E-02
RVMSR	T0	RPL26	-1.66	1.62E-03	ARHGAP28	2.69	2.30E-02
RVMSR	T0	CGB7	3.15	1.63E-03	PRR22	1.69	2.30E-02
RVMSR	T0	ZNF713	3.14	1.63E-03	GPR139	3.55	2.30E-02
RVMSR	T0	FAM169B	3.33	1.63E-03	LOC375196	2.08	2.30E-02
RVMSR	T0	PRRX2-AS1	5.59	1.63E-03	HP09053	2.08	2.30E-02
RVMSR	T0	FAM153B	3.01	1.63E-03	PBOV1	2.88	2.30E-02
RVMSR	T0	HRH1	2.87	1.63E-03	C6orf118	2.68	2.31E-02

RVMSR	T0	EFHD1	2.34	1.63E-03	MIR215	2.14	2.31E-02
RVMSR	T0	ACSM2A	4.41	1.64E-03	KCTD16	3.56	2.31E-02
RVMSR	T0	OLFML2A	2.20	1.66E-03	LOC100289361	2.55	2.31E-02
RVMSR	T0	SSMEM1	2.77	1.66E-03	IFI44	-1.37	2.31E-02
RVMSR	T0	SRCIN1	2.51	1.67E-03	LOC646268	3.14	2.32E-02
RVMSR	T0	NANOGNB	2.99	1.67E-03	NAXE	-1.25	2.32E-02
RVMSR	T0	WBSCR17	3.56	1.68E-03	FBLN1	2.08	2.32E-02
RVMSR	T0	PLA2G1B	2.76	1.68E-03	CTPS2	1.69	2.32E-02
RVMSR	T0	KLHDC8A	3.90	1.68E-03	NWD1	2.43	2.32E-02
RVMSR	T0	LOC105374266	3.34	1.69E-03	ST6GALNAC1	1.45	2.32E-02
RVMSR	T0	LINC00599	2.66	1.71E-03	LOC101928053	1.48	2.32E-02
RVMSR	T0	STK3	1.58	1.72E-03	LINC00467	1.92	2.32E-02
RVMSR	T0	FGF9	2.75	1.72E-03	MROH2A	4.49	2.33E-02
RVMSR	T0	KLHL29	3.90	1.72E-03	MDH1B	2.88	2.33E-02
RVMSR	T0	MIR193BHG	2.20	1.72E-03	MIR548AJ1	2.42	2.33E-02
RVMSR	T0	SLC30A3	2.99	1.72E-03	LOC101927165	2.07	2.33E-02
RVMSR	T0	TACR2	4.41	1.73E-03	MYL7	2.31	2.33E-02
RVMSR	T0	FBLN2	2.14	1.73E-03	LOC101927211	1.71	2.33E-02
RVMSR	T0	MAPK10	5.56	1.74E-03	EFCAB12	2.69	2.33E-02
RVMSR	T0	CD276	5.57	1.74E-03	NRIP3	2.15	2.34E-02
RVMSR	T0	CYP1A2	2.51	1.79E-03	NOV	2.89	2.34E-02
RVMSR	T0	DEFB107B	3.31	1.81E-03	CRISP3	2.56	2.34E-02
RVMSR	T0	LINC01255	5.54	1.83E-03	RIN1	2.22	2.34E-02
RVMSR	T0	MATN1	5.55	1.83E-03	ITGA10	2.23	2.34E-02
RVMSR	T0	NR2F2-AS1	3.54	1.83E-03	ADAMTS18	3.55	2.34E-02
RVMSR	T0	LOC100128288	2.67	1.85E-03	ANKRD20A1	2.07	2.34E-02
RVMSR	T0	RTBDN	2.27	1.88E-03	OVCH1-AS1	2.16	2.34E-02
RVMSR	T0	TESC-AS1	4.38	1.89E-03	OR10V1	3.14	2.34E-02
RVMSR	T0	LOC494141	3.31	1.92E-03	SHROOM3	3.14	2.34E-02

RVMSR	T0	LOC101927692	3.13	1.93E-03	TRAF3IP1	1.58	2.34E-02
RVMSR	T0	LOC728673	2.27	1.93E-03	MYDGF	-1.20	2.34E-02
RVMSR	T0	MIR3921	5.54	1.93E-03	MARK2P9	2.31	2.34E-02
RVMSR	T0	FAM78B	2.42	1.94E-03	LOC100130698	3.55	2.34E-02
RVMSR	T0	ADAMTS8	2.97	1.94E-03	SEZ6L2	2.42	2.34E-02
RVMSR	T0	GTSE1	2.85	1.95E-03	GPR179	4.48	2.34E-02
RVMSR	T0	MYL2	2.64	1.95E-03	C8orf31	2.32	2.34E-02
RVMSR	T0	LINC00640	5.54	1.95E-03	MIR548H5	3.12	2.35E-02
RVMSR	T0	LAMA2	2.31	1.97E-03	NMNAT1	1.32	2.35E-02
RVMSR	T0	CNGA3	4.39	1.97E-03	SPDYE4	3.56	2.35E-02
RVMSR	T0	CNTNAP1	5.54	1.98E-03	FERMT2	1.96	2.35E-02
RVMSR	T0	UBXN8	2.08	2.01E-03	POM121L1P	3.56	2.35E-02
RVMSR	T0	BATF2	2.11	2.01E-03	POU3F4	4.48	2.35E-02
RVMSR	T0	TRIM67	2.56	2.02E-03	LOC283575	2.31	2.35E-02
RVMSR	T0	LOC101927502	3.53	2.02E-03	HIST1H1E	-1.18	2.35E-02
RVMSR	T0	FSTL3	2.65	2.02E-03	LINC00824	2.69	2.36E-02
RVMSR	T0	MIR520D	4.37	2.03E-03	CST4	3.55	2.36E-02
RVMSR	T0	B3GALT5-AS1	3.53	2.03E-03	TENM2	1.86	2.36E-02
RVMSR	T0	LOC392452	3.87	2.03E-03	TMPO-AS1	1.59	2.36E-02
RVMSR	T0	OR8S1	2.64	2.03E-03	DPH3P1	2.22	2.37E-02
RVMSR	T0	HNF1B	3.12	2.03E-03	SOX2	2.69	2.37E-02
RVMSR	T0	ABCA9	4.37	2.03E-03	LEP	2.08	2.37E-02
RVMSR	T0	LRAT	4.36	2.03E-03	ELMOD1	2.86	2.37E-02
RVMSR	T0	WDR31	2.27	2.03E-03	NDUFAF6	1.58	2.37E-02
RVMSR	T0	BCL2L10	4.38	2.03E-03	ADRA1D	2.41	2.37E-02
RVMSR	T0	ZNRF4	1.96	2.04E-03	JHDM1D-AS1	1.60	2.37E-02
RVMSR	T0	PARD3-AS1	2.96	2.05E-03	KRTAP21-1	4.50	2.37E-02
RVMSR	T0	AQP4	5.52	2.07E-03	MMP24	2.87	2.37E-02
RVMSR	T0	GMDS-AS1	3.11	2.08E-03	FRZB	3.14	2.37E-02

RVMSR	T0	FAM171A1	2.41	2.08E-03	FGF3	2.22	2.37E-02
RVMSR	T0	ATAD3C	2.22	2.08E-03	DOCK9-AS2	2.41	2.38E-02
RVMSR	T0	APOC2	2.55	2.08E-03	HPD	1.67	2.39E-02
RVMSR	T0	BEND7	2.48	2.08E-03	PRAMEF10	3.54	2.39E-02
RVMSR	T0	CLDN19	2.96	2.08E-03	PRAMEF33P	3.54	2.39E-02
RVMSR	T0	FLRT2	3.28	2.09E-03	WNT5A	4.47	2.39E-02
RVMSR	T0	MIR3649	2.83	2.13E-03	MIR4715	1.56	2.39E-02
RVMSR	T0	SLC52A3	3.10	2.14E-03	LINC01372	1.81	2.40E-02
RVMSR	T0	SCGB2A2	5.51	2.14E-03	IRF7	-1.19	2.40E-02
RVMSR	T0	FDPSP2	1.81	2.14E-03	SLC10A1	1.74	2.40E-02
RVMSR	T0	BEND3	2.96	2.15E-03	MIR3675	2.67	2.40E-02
RVMSR	T0	LOC101928841	2.20	2.16E-03	AIRN	2.53	2.40E-02
RVMSR	T0	BEND4	2.30	2.16E-03	FLRT3	2.01	2.40E-02
RVMSR	T0	LINC01568	2.72	2.17E-03	PPIAP30	1.81	2.40E-02
RVMSR	T0	LOC101927257	2.95	2.17E-03	CYP4X1	3.12	2.40E-02
RVMSR	T0	TM4SF4	4.37	2.17E-03	WWP1	-1.36	2.41E-02
RVMSR	T0	LOC100506747	1.93	2.18E-03	SVILP1	2.52	2.41E-02
RVMSR	T0	LOC102724589	2.94	2.20E-03	LYPD3	2.13	2.41E-02
RVMSR	T0	MIR4445	5.50	2.21E-03	LOC101928446	2.86	2.41E-02
RVMSR	T0	HAS2	2.47	2.22E-03	APOB	4.49	2.41E-02
RVMSR	T0	LINC00708	2.63	2.23E-03	PISRT1	4.46	2.42E-02
RVMSR	T0	PHOSPHO2-KLHL23	2.54	2.24E-03	CPM	1.29	2.42E-02
RVMSR	T0	OXGR1	3.85	2.24E-03	SERF1B	-1.58	2.42E-02
RVMSR	T0	TSHZ2	1.95	2.24E-03	THPO	2.14	2.42E-02
RVMSR	T0	PPEF1	2.13	2.26E-03	ELAVL4	2.41	2.42E-02
RVMSR	T0	FSHB	4.35	2.26E-03	TMEM30B	2.66	2.42E-02
RVMSR	T0	MYH16	2.12	2.26E-03	AKR1D1	1.70	2.42E-02
RVMSR	T0	C16orf78	4.33	2.26E-03	AGBL4-IT1	2.22	2.42E-02
RVMSR	T0	HCG24	3.84	2.30E-03	SLC7A13	3.12	2.42E-02

RVMSR	T0	FAM218A	1.88	2.30E-03	CTD-2270F17.1	4.46	2.43E-02
RVMSR	T0	LIM2	1.92	2.30E-03	NACC1	1.52	2.43E-02
RVMSR	T0	LOC400541	2.40	2.30E-03	KLRF2	3.53	2.43E-02
RVMSR	T0	MIR599	2.93	2.41E-03	LOC105374194	3.56	2.43E-02
RVMSR	T0	HMGA1P7	2.94	2.42E-03	ONECUT2	2.12	2.43E-02
RVMSR	T0	TMEM217	3.50	2.44E-03	CCT8L2	2.21	2.43E-02
RVMSR	T0	NPTX2	3.84	2.44E-03	ABCA6	2.68	2.44E-02
RVMSR	T0	RIDA	2.09	2.44E-03	SNAR-B2	2.67	2.44E-02
RVMSR	T0	LOC100506207	4.32	2.44E-03	GABRA5	2.66	2.44E-02
RVMSR	T0	LOC105372653	2.15	2.44E-03	ATP1A3	1.95	2.44E-02
RVMSR	T0	LOC102724927	2.39	2.44E-03	SAA2	3.11	2.45E-02
RVMSR	T0	TDRD1	2.19	2.44E-03	RFPL1S	1.70	2.45E-02
RVMSR	T0	PALM2	2.05	2.44E-03	LOC101928731	2.52	2.45E-02
RVMSR	T0	MIR4419B	4.32	2.46E-03	PDGFRB	4.48	2.45E-02
RVMSR	T0	LOC414300	2.46	2.48E-03	MIR5591	2.52	2.45E-02
RVMSR	T0	SLC39A14	2.70	2.49E-03	FGF19	3.55	2.46E-02
RVMSR	T0	LOC101928700	3.09	2.49E-03	PRPS1L1	4.47	2.46E-02
RVMSR	T0	SRGAP1	3.24	2.54E-03	FMO2	3.53	2.46E-02
RVMSR	T0	AMN	2.19	2.54E-03	OLAH	2.51	2.47E-02
RVMSR	T0	MIR5589	3.83	2.54E-03	PDE11A	2.20	2.47E-02
RVMSR	T0	C4orf36	5.46	2.54E-03	LOC388242	3.54	2.47E-02
RVMSR	T0	TMPRSS12	2.61	2.54E-03	CDH13	2.40	2.47E-02
RVMSR	T0	DCDC2B	3.81	2.55E-03	ZFP82	1.38	2.47E-02
RVMSR	T0	PTGIR	1.96	2.56E-03	CNGA4	3.12	2.48E-02
RVMSR	T0	LINC01104	3.81	2.57E-03	ZC3H7B	1.56	2.48E-02
RVMSR	T0	MYOZ1	3.49	2.57E-03	ZNF658	2.06	2.48E-02
RVMSR	T0	ASB17	5.43	2.58E-03	CMC1	-1.44	2.48E-02
RVMSR	T0	ZNF503	1.73	2.58E-03	GUCY2C	2.07	2.48E-02
RVMSR	T0	VIT	3.49	2.58E-03	LOC100128531	2.13	2.49E-02

RVMSR	T0	TM4SF1-AS1	4.32	2.58E-03	NLGN1-AS1	2.67	2.49E-02
RVMSR	T0	UPK1A	2.92	2.58E-03	LNP1	3.10	2.49E-02
RVMSR	T0	MEG8	3.80	2.58E-03	LOC100506606	1.67	2.49E-02
RVMSR	T0	UMOD	3.47	2.58E-03	LINC01305	2.84	2.49E-02
RVMSR	T0	LINC01618	2.52	2.58E-03	LOC100506885	2.67	2.49E-02
RVMSR	T0	MIR3908	4.31	2.58E-03	LINC00307	2.66	2.50E-02
RVMSR	T0	LOC101926911	3.83	2.58E-03	MIR8057	3.11	2.50E-02
RVMSR	T0	RNU6ATAC	3.49	2.59E-03	DHRS7C	3.55	2.50E-02
RVMSR	T0	SLC25A18	2.69	2.59E-03	PGLYRP4	3.11	2.50E-02
RVMSR	T0	CEACAM5	2.38	2.59E-03	ZNF436-AS1	2.20	2.50E-02
RVMSR	T0	CCDC36	2.69	2.59E-03	KCND3-AS1	2.21	2.50E-02
RVMSR	T0	LOC100505716	2.07	2.60E-03	HIST1H2BL	2.52	2.50E-02
RVMSR	T0	POP3	3.26	2.60E-03	LINC01038	3.54	2.51E-02
RVMSR	T0	MIR610	2.44	2.62E-03	GTF2IP7	1.89	2.51E-02
RVMSR	T0	LOC101929279	2.18	2.63E-03	SNAR-A9	2.06	2.52E-02
RVMSR	T0	ANKRD31	3.07	2.63E-03	MEIOB	2.12	2.52E-02
RVMSR	T0	MIR4462	3.26	2.63E-03	ZNF560	2.67	2.52E-02
RVMSR	T0	MIR7843	4.31	2.63E-03	CADM3-AS1	2.85	2.52E-02
RVMSR	T0	IFI44L	-1.55	2.63E-03	RPL9	-1.15	2.52E-02
RVMSR	T0	MIR4422	3.81	2.63E-03	RBBP5	1.33	2.52E-02
RVMSR	T0	AKR7A2P1	2.38	2.65E-03	LOC105372028	3.11	2.52E-02
RVMSR	T0	LOC105371267	4.31	2.67E-03	FKBP6	3.13	2.52E-02
RVMSR	T0	G6PC	3.48	2.67E-03	LOC100134391	1.73	2.52E-02
RVMSR	T0	CEMIP	3.47	2.67E-03	MICALL1	1.35	2.52E-02
RVMSR	T0	PCDH17	3.47	2.69E-03	LOC101929057	2.28	2.52E-02
RVMSR	T0	ENO3	2.10	2.69E-03	FAM81A	1.80	2.52E-02
RVMSR	T0	LOC101929998	5.44	2.69E-03	CTAGE11P	2.52	2.52E-02
RVMSR	T0	LINC01433	2.27	2.72E-03	LOC107161159	2.39	2.52E-02
RVMSR	T0	ERVV-1	3.80	2.72E-03	MIR4716	2.85	2.52E-02

RVMSR	T0	TUBA3FP	1.63	2.73E-03	STX17-AS1	2.39	2.52E-02
RVMSR	T0	ATP6V1B1-AS1	3.06	2.75E-03	MIR6129	2.51	2.52E-02
RVMSR	T0	GLIS1	3.79	2.76E-03	MIR3160-2	4.46	2.52E-02
RVMSR	T0	DEFB136	2.00	2.77E-03	PWRN2	4.46	2.52E-02
RVMSR	T0	MIR4417	5.41	2.77E-03	EIF3IP1	3.12	2.53E-02
RVMSR	T0	NPPC	4.28	2.77E-03	TMEM52	2.66	2.53E-02
RVMSR	T0	WNT3	4.30	2.77E-03	FAM57B	3.51	2.53E-02
RVMSR	T0	FGF10	5.41	2.77E-03	LINC00482	2.53	2.53E-02
RVMSR	T0	TFR2	2.68	2.78E-03	MIR328	2.52	2.53E-02
RVMSR	T0	LDLR	2.18	2.78E-03	LOC102723604	4.43	2.53E-02
RVMSR	T0	KRT222	3.81	2.78E-03	KCNU1	4.43	2.53E-02
RVMSR	T0	CELA3A	3.47	2.78E-03	FAM217A	2.67	2.53E-02
RVMSR	T0	DLGAP4-AS1	2.69	2.78E-03	AZU1	2.29	2.53E-02
RVMSR	T0	C21orf62	2.51	2.78E-03	CHRNG	3.11	2.53E-02
RVMSR	T0	APOA4	3.79	2.78E-03	CLDN7	2.39	2.53E-02
RVMSR	T0	NPIPB6	2.37	2.78E-03	ZDHHC14	2.31	2.53E-02
RVMSR	T0	LOC285593	3.23	2.78E-03	VWA3B	2.27	2.53E-02
RVMSR	T0	SFTPB	2.37	2.78E-03	NKX2-5	2.66	2.54E-02
RVMSR	T0	PDILT	3.79	2.78E-03	NXF3	2.85	2.54E-02
RVMSR	T0	CLSPN	2.59	2.78E-03	RBPJL	2.84	2.54E-02
RVMSR	T0	FRRS1L	2.37	2.78E-03	BTLA	-1.41	2.55E-02
RVMSR	T0	LOC101927229	2.27	2.78E-03	LOC103312105	3.52	2.55E-02
RVMSR	T0	BBS1	2.02	2.78E-03	DNM3	2.13	2.55E-02
RVMSR	T0	FOXB1	3.78	2.79E-03	TMEM213	2.12	2.55E-02
RVMSR	T0	MYOZ3	2.44	2.80E-03	CMYA5	2.67	2.56E-02
RVMSR	T0	DZANK1	3.06	2.80E-03	CEACAM22P	2.20	2.56E-02
RVMSR	T0	IQCF2	5.41	2.80E-03	F2RL2	2.53	2.56E-02
RVMSR	T0	LOC102725191	5.42	2.80E-03	MIR577	2.66	2.56E-02
RVMSR	T0	ZSCAN2	1.90	2.82E-03	EPB41L4B	4.44	2.57E-02

RVMSR	T0	HNF4A	3.46	2.84E-03	LOC101929154	4.47	2.57E-02
RVMSR	T0	TBC1D12	2.91	2.84E-03	CPA6	1.80	2.57E-02
RVMSR	T0	MAGEA10	4.27	2.84E-03	MUC17	1.79	2.57E-02
RVMSR	T0	CHST6	3.04	2.84E-03	SDHAP2	-2.53	2.58E-02
RVMSR	T0	KCNMB1	2.68	2.84E-03	LOC101927120	4.42	2.58E-02
RVMSR	T0	TSACC	2.43	2.84E-03	C17orf77	2.52	2.58E-02
RVMSR	T0	SNAR-A13	2.50	2.84E-03	SIGLEC12	2.29	2.58E-02
RVMSR	T0	KLB	2.21	2.84E-03	DNM3-IT1	2.39	2.58E-02
RVMSR	T0	NMRK2	2.43	2.84E-03	CCL20	2.52	2.58E-02
RVMSR	T0	HSD17B6	3.22	2.84E-03	PRAME	1.79	2.58E-02
RVMSR	T0	LOC101929227	3.21	2.84E-03	SLC25A4	1.57	2.58E-02
RVMSR	T0	MRLN	4.28	2.84E-03	ZNF232	1.76	2.58E-02
RVMSR	T0	LRRTM2	3.05	2.86E-03	CLCA3P	2.83	2.58E-02
RVMSR	T0	ADCY10	3.46	2.86E-03	LOC729609	2.30	2.58E-02
RVMSR	T0	LOC101927708	3.22	2.87E-03	MIR4327	2.28	2.59E-02
RVMSR	T0	LOC100506142	4.27	2.87E-03	HIST1H3J	2.84	2.59E-02
RVMSR	T0	RNU11	2.50	2.87E-03	LINC00303	4.44	2.59E-02
RVMSR	T0	SCAMP4	2.30	2.89E-03	S100A8	-1.80	2.60E-02
RVMSR	T0	AADACL2-AS1	3.46	2.90E-03	SH2B2	1.84	2.60E-02
RVMSR	T0	SNAR-G2	2.77	2.90E-03	MIR4490	4.44	2.60E-02
RVMSR	T0	LOC101927877	3.04	2.91E-03	KRTAP19-7	3.09	2.60E-02
RVMSR	T0	C12orf54	3.79	2.94E-03	SCARNA21	-1.15	2.60E-02
RVMSR	T0	LINC00842	2.05	2.95E-03	PDE1C	2.28	2.61E-02
RVMSR	T0	RPS17	-1.57	2.95E-03	RADIL	2.19	2.61E-02
RVMSR	T0	LOC644172	2.58	2.95E-03	LOC284379	2.84	2.61E-02
RVMSR	T0	FRMD6-AS1	2.36	2.95E-03	MAGI3	1.72	2.61E-02
RVMSR	T0	MIR4727	3.22	2.96E-03	RIOK3	-1.19	2.61E-02
RVMSR	T0	LOC102723640	2.77	2.96E-03	RPGRIP1	2.21	2.61E-02
RVMSR	T0	LOC101927932	2.30	2.96E-03	HINFP	1.63	2.61E-02

RVMSR	T0	C19orf57	3.78	2.96E-03	LINC00906	4.43	2.61E-02
RVMSR	T0	PKD1L2	3.45	2.96E-03	OR2AT4	4.43	2.61E-02
RVMSR	T0	OR10J3	4.26	2.96E-03	MED4-AS1	1.98	2.62E-02
RVMSR	T0	SLC35G3	2.58	2.97E-03	METTL9	-1.14	2.62E-02
RVMSR	T0	TAT	4.27	2.98E-03	IBA57	1.41	2.63E-02
RVMSR	T0	PRR11	1.52	3.02E-03	KDM4D	2.11	2.63E-02
RVMSR	T0	LINC00458	5.38	3.02E-03	TTPAL	1.55	2.63E-02
RVMSR	T0	C2CD4A	2.36	3.02E-03	MIR211	3.10	2.63E-02
RVMSR	T0	LIMK1	1.94	3.02E-03	TSEN2	1.35	2.63E-02
RVMSR	T0	PPIC	4.25	3.02E-03	UGT3A2	4.45	2.63E-02
RVMSR	T0	SMIM10	2.42	3.03E-03	FLJ31104	2.19	2.64E-02
RVMSR	T0	TTPA	3.44	3.03E-03	SAMD4A	2.30	2.64E-02
RVMSR	T0	C10orf126	2.88	3.05E-03	ZCCHC8	1.31	2.64E-02
RVMSR	T0	MIR1303	2.30	3.07E-03	C1QTNF7	2.27	2.64E-02
RVMSR	T0	UBQLN4	2.29	3.07E-03	DPY30	-1.23	2.64E-02
RVMSR	T0	LOC150051	2.56	3.10E-03	LOC101929748	2.27	2.64E-02
RVMSR	T0	LOC105379143	2.48	3.12E-03	OR6P1	3.50	2.64E-02
RVMSR	T0	CABP7	3.03	3.12E-03	LINC01397	2.66	2.64E-02
RVMSR	T0	EGF	2.41	3.13E-03	LINC00488	2.50	2.64E-02
RVMSR	T0	GOLGA8M	2.24	3.13E-03	MIR3660	3.50	2.64E-02
RVMSR	T0	C1orf195	3.44	3.13E-03	RNF216-IT1	1.33	2.64E-02
RVMSR	T0	DNAH3	2.65	3.13E-03	POLR1D	-1.15	2.65E-02
RVMSR	T0	CRISP1	5.38	3.13E-03	LRRC72	4.42	2.65E-02
RVMSR	T0	SNAI1	2.57	3.13E-03	ADGRA3	4.42	2.65E-02
RVMSR	T0	LINC01015	4.26	3.13E-03	SPATA8-AS1	2.63	2.65E-02
RVMSR	T0	LOC101927131	2.88	3.14E-03	KBTBD12	2.83	2.65E-02
RVMSR	T0	ANO1-AS2	3.19	3.15E-03	MCM2	2.38	2.65E-02
RVMSR	T0	CYB5D1	3.21	3.15E-03	SOST	4.42	2.65E-02
RVMSR	T0	F11	2.29	3.17E-03	CYP2A6	2.50	2.65E-02

RVMSR	T0	TMEM95	2.88	3.17E-03	BLOC1S2	-1.23	2.65E-02
RVMSR	T0	FAM83E	2.24	3.17E-03	LOC440700	1.57	2.65E-02
RVMSR	T0	CASC1	5.37	3.17E-03	PDCD1	2.84	2.65E-02
RVMSR	T0	BPI	2.77	3.18E-03	PTGER3	3.08	2.65E-02
RVMSR	T0	ROM1	1.95	3.19E-03	ASS1	3.50	2.65E-02
RVMSR	T0	PRSS37	3.75	3.20E-03	C1orf210	3.51	2.65E-02
RVMSR	T0	ATE1-AS1	2.48	3.20E-03	OR6C68	3.09	2.65E-02
RVMSR	T0	LOC100289650	4.24	3.20E-03	BARHL1	3.50	2.66E-02
RVMSR	T0	FETUB	3.75	3.22E-03	PLEKHH3	3.08	2.66E-02
RVMSR	T0	PCDHA9	4.25	3.23E-03	MIR5697	1.72	2.66E-02
RVMSR	T0	XGY2	3.43	3.24E-03	CD3EAP	1.68	2.66E-02
RVMSR	T0	LINC01607	2.29	3.24E-03	SOX6	1.60	2.66E-02
RVMSR	T0	PIWIL2	2.23	3.25E-03	ZNF321P	1.19	2.66E-02
RVMSR	T0	CUL7	2.19	3.25E-03	ARTN	1.68	2.66E-02
RVMSR	T0	LDB3	2.56	3.26E-03	LOC643623	2.18	2.66E-02
RVMSR	T0	LINC01413	2.28	3.26E-03	XPNPEP3	1.19	2.67E-02
RVMSR	T0	LINC01300	3.76	3.26E-03	APTR	1.79	2.67E-02
RVMSR	T0	NT5C3B	2.15	3.29E-03	CADPS2	4.39	2.67E-02
RVMSR	T0	PPP5D1	2.40	3.30E-03	CNTN4-AS2	3.49	2.67E-02
RVMSR	T0	ATP6V1C2	3.74	3.31E-03	CGB2	2.39	2.67E-02
RVMSR	T0	BPIFA1	3.43	3.33E-03	CFAP221	3.08	2.67E-02
RVMSR	T0	BAAT	5.33	3.34E-03	PRMT5-AS1	3.50	2.67E-02
RVMSR	T0	LINC00365	3.74	3.34E-03	SYCP2L	3.08	2.67E-02
RVMSR	T0	CCL1	3.41	3.35E-03	CA14	3.50	2.67E-02
RVMSR	T0	MIR4430	3.73	3.36E-03	SNHG12	1.36	2.67E-02
RVMSR	T0	MGARP	2.74	3.36E-03	LOC102724728	2.26	2.67E-02
RVMSR	T0	CNBD2	2.74	3.36E-03	LRP4	2.11	2.67E-02
RVMSR	T0	PGPEP1L	2.86	3.37E-03	OR4P4	2.81	2.67E-02
RVMSR	T0	LINC01593	4.22	3.37E-03	COL4A2	2.39	2.67E-02

RVMSR	T0	C7orf69	3.73	3.38E-03	LOC101928858	4.41	2.67E-02
RVMSR	T0	LOC101929161	3.19	3.38E-03	TRIM63	3.09	2.67E-02
RVMSR	T0	LOC101929431	1.91	3.39E-03	LGALS7	3.48	2.67E-02
RVMSR	T0	XLOC_009911	2.74	3.39E-03	NUGGC	2.49	2.67E-02
RVMSR	T0	ZBED3	3.41	3.39E-03	MIR1302-1	4.41	2.68E-02
RVMSR	T0	LOC101928985	3.73	3.39E-03	LINC00661	2.19	2.68E-02
RVMSR	T0	LOC100508046	3.01	3.39E-03	ALKBH1	1.55	2.68E-02
RVMSR	T0	ADTRP	-4.29	3.40E-03	PRR34	2.49	2.68E-02
RVMSR	T0	GREM1	2.33	3.44E-03	ASB4	3.07	2.68E-02
RVMSR	T0	SHOX	3.73	3.45E-03	ISPD	1.78	2.68E-02
RVMSR	T0	ALPI	3.00	3.46E-03	PCOLCE-AS1	2.64	2.69E-02
RVMSR	T0	JAM2	3.01	3.46E-03	LINC00632	2.62	2.69E-02
RVMSR	T0	CLDN3	2.27	3.47E-03	MOSPD1	-1.36	2.69E-02
RVMSR	T0	MUC16	1.76	3.47E-03	LOC101927269	2.10	2.69E-02
RVMSR	T0	ZCWPW2	2.73	3.47E-03	MIR3121	3.07	2.69E-02
RVMSR	T0	LINC01276	3.72	3.47E-03	MYBPC1	2.27	2.69E-02
RVMSR	T0	MYLK3	3.42	3.47E-03	PTPN3	3.07	2.69E-02
RVMSR	T0	NYX	3.73	3.50E-03	LOC102724360	1.87	2.69E-02
RVMSR	T0	LOC105372440	2.46	3.50E-03	MRPS25	-1.24	2.69E-02
RVMSR	T0	ANKFN1	5.33	3.50E-03	LINC00943	3.08	2.69E-02
RVMSR	T0	ARGFXP2	2.33	3.51E-03	OR4N2	2.83	2.69E-02
RVMSR	T0	UTS2	2.54	3.52E-03	NAALADL2	3.10	2.69E-02
RVMSR	T0	C9orf116	2.09	3.52E-03	EPHB2	2.11	2.69E-02
RVMSR	T0	LOC101927357	3.72	3.52E-03	ZNF192P1	2.83	2.70E-02
RVMSR	T0	NFIC	1.59	3.52E-03	NDP	3.07	2.70E-02
RVMSR	T0	TMEM74	3.41	3.52E-03	ELFN1-AS1	2.50	2.70E-02
RVMSR	T0	LRP11	2.23	3.52E-03	NAP1L2	2.82	2.70E-02
RVMSR	T0	LOC105373044	3.00	3.52E-03	SMOX	-1.18	2.70E-02
RVMSR	T0	MOGAT3	2.13	3.53E-03	LOC101928992	3.09	2.71E-02

RVMSR	T0	HIRA	1.72	3.53E-03	ART1	4.40	2.71E-02
RVMSR	T0	RFX4	2.27	3.53E-03	HIST1H2BA	4.40	2.71E-02
RVMSR	T0	THAP2	1.86	3.54E-03	COL4A2-AS1	4.40	2.71E-02
RVMSR	T0	ADAMTS7P1	3.19	3.54E-03	NDUFA4	-1.16	2.71E-02
RVMSR	T0	LINC00658	5.32	3.54E-03	LOC101928107	3.50	2.71E-02
RVMSR	T0	SRD5A3-AS1	3.17	3.55E-03	C2orf80	4.40	2.72E-02
RVMSR	T0	NANOG	3.18	3.55E-03	PPP2R2B-IT1	2.50	2.72E-02
RVMSR	T0	DLL3	2.33	3.56E-03	C1QTNF9B-AS1	2.82	2.72E-02
RVMSR	T0	DEFB129	4.23	3.57E-03	LINC00244	3.48	2.72E-02
RVMSR	T0	LAMA3	5.31	3.59E-03	CAV1	2.37	2.73E-02
RVMSR	T0	REG3A	5.31	3.59E-03	CSN2	3.07	2.73E-02
RVMSR	T0	CPA4	2.53	3.59E-03	REM2	1.22	2.74E-02
RVMSR	T0	CECR2	2.62	3.59E-03	CLEC4M	2.11	2.74E-02
RVMSR	T0	LOC102723517	4.21	3.59E-03	CAMKK1	1.57	2.74E-02
RVMSR	T0	LOC101929572	2.62	3.62E-03	LOC101928834	1.98	2.74E-02
RVMSR	T0	GPC4	4.21	3.63E-03	MRPS6	-1.19	2.74E-02
RVMSR	T0	PP2D1	3.00	3.65E-03	PRR26	3.49	2.74E-02
RVMSR	T0	SHCBP1L	5.31	3.65E-03	NUMBL	2.29	2.74E-02
RVMSR	T0	LINC00687	3.17	3.65E-03	ZNF286B	1.43	2.75E-02
RVMSR	T0	LOC344967	2.46	3.68E-03	SLC13A4	3.06	2.75E-02
RVMSR	T0	IFNB1	4.21	3.68E-03	ARG1	1.44	2.75E-02
RVMSR	T0	LCE3E	5.30	3.70E-03	UGT2B17	3.06	2.76E-02
RVMSR	T0	FAM183A	2.12	3.71E-03	SMG8	1.50	2.76E-02
RVMSR	T0	LOC441204	4.20	3.71E-03	C14orf2	-1.15	2.76E-02
RVMSR	T0	ZNF311	2.21	3.71E-03	HS3ST5	2.27	2.76E-02
RVMSR	T0	LOC101928043	2.45	3.72E-03	GTSF1L	1.98	2.76E-02
RVMSR	T0	HTRA4	2.53	3.72E-03	STXBP5L	2.80	2.76E-02
RVMSR	T0	SCHLAP1	2.73	3.72E-03	TCEB3CL	3.49	2.76E-02
RVMSR	T0	LRRN4CL	2.21	3.72E-03	GPR82	1.31	2.76E-02

RVMSR	T0	ZNF114	1.98	3.72E-03	TSTA3	-1.14	2.77E-02
RVMSR	T0	KRBOX1-AS1	2.44	3.72E-03	C12orf57	-1.16	2.77E-02
RVMSR	T0	PRSS54	3.39	3.74E-03	MMACHC	1.92	2.77E-02
RVMSR	T0	ELANE	1.96	3.74E-03	ARSH	4.38	2.77E-02
RVMSR	T0	ZNF252P-AS1	2.85	3.76E-03	GNE	1.59	2.77E-02
RVMSR	T0	LOC101929099	5.31	3.76E-03	LINC01582	1.96	2.77E-02
RVMSR	T0	NR2E3	2.98	3.78E-03	PRELID2	1.48	2.78E-02
RVMSR	T0	S100A12	-1.94	3.78E-03	ALG1L	2.62	2.78E-02
RVMSR	T0	DAO	3.17	3.79E-03	CRLF1	1.71	2.78E-02
RVMSR	T0	OR52A1	3.17	3.79E-03	ACSL6	1.48	2.79E-02
RVMSR	T0	SUB1	-1.50	3.81E-03	TARM1	2.49	2.79E-02
RVMSR	T0	MIR3168	2.26	3.82E-03	GZMH	-1.17	2.79E-02
RVMSR	T0	SEMA5A	3.38	3.82E-03	SORBS2	2.09	2.79E-02
RVMSR	T0	TEAD3	2.46	3.82E-03	CYSTM1	-1.14	2.79E-02
RVMSR	T0	SNX8	1.87	3.85E-03	DNAL1	1.87	2.79E-02
RVMSR	T0	KRT80	3.39	3.85E-03	LINC01506	-1.30	2.79E-02
RVMSR	T0	ZNRF3-AS1	1.72	3.86E-03	DEFB108B	2.18	2.79E-02
RVMSR	T0	LINC01356	2.16	3.86E-03	TRAT1	-1.14	2.79E-02
RVMSR	T0	C3orf14	2.09	3.86E-03	SEL1L2	3.06	2.79E-02
RVMSR	T0	ZBTB7C	4.20	3.86E-03	MYO3A	4.41	2.80E-02
RVMSR	T0	LMBRD2	-3.80	3.88E-03	DRD4	2.27	2.80E-02
RVMSR	T0	SPRYD7	1.87	3.89E-03	LOC283856	3.06	2.80E-02
RVMSR	T0	NAT8	3.70	3.89E-03	MAGIX	1.64	2.80E-02
RVMSR	T0	KLHDC9	2.71	3.89E-03	STH	4.38	2.80E-02
RVMSR	T0	VASH2	2.31	3.94E-03	YAP1	2.48	2.80E-02
RVMSR	T0	HID1-AS1	2.97	4.01E-03	SYNE4	1.91	2.80E-02
RVMSR	T0	OR2B3	2.83	4.01E-03	AVPR2	2.81	2.80E-02
RVMSR	T0	ASPG	4.18	4.01E-03	LINC00028	1.86	2.80E-02
RVMSR	T0	CDC25C	2.83	4.01E-03	LINC01030	4.40	2.80E-02

RVMSR	T0	RNF139-AS1	2.98	4.01E-03	SLIT2	2.80	2.80E-02
RVMSR	T0	RNF222	2.15	4.01E-03	MIR125B1	3.47	2.80E-02
RVMSR	T0	C21orf58	1.92	4.02E-03	ANKRD33	3.47	2.80E-02
RVMSR	T0	LOC100506319	2.19	4.02E-03	SNHG6	-1.13	2.80E-02
RVMSR	T0	LOC100132735	2.84	4.02E-03	C1S	2.80	2.80E-02
RVMSR	T0	INHBA	2.42	4.02E-03	REEP6	2.10	2.80E-02
RVMSR	T0	MEIOC	2.19	4.04E-03	LOC105373782	3.47	2.80E-02
RVMSR	T0	AQP6	2.97	4.04E-03	CDH18	3.47	2.80E-02
RVMSR	T0	PGM5	2.04	4.06E-03	KRTAP10-9	3.07	2.80E-02
RVMSR	T0	FABP6	3.69	4.07E-03	PHYHIPL	2.36	2.80E-02
RVMSR	T0	SLC17A5	1.70	4.07E-03	DEFB123	2.63	2.80E-02
RVMSR	T0	LINC00311	4.17	4.07E-03	USP49	1.54	2.80E-02
RVMSR	T0	LOC105372682	3.15	4.07E-03	LOC339260	1.67	2.81E-02
RVMSR	T0	LINC01521	1.99	4.08E-03	PROC	2.82	2.81E-02
RVMSR	T0	SLC26A4	2.81	4.09E-03	FBXW9	2.03	2.81E-02
RVMSR	T0	FOXRED2	1.96	4.10E-03	ASB14	2.36	2.81E-02
RVMSR	T0	TEX15	3.36	4.10E-03	GEMIN2	1.78	2.81E-02
RVMSR	T0	NUP50-AS1	1.86	4.10E-03	CALB2	3.06	2.82E-02
RVMSR	T0	STC1	3.38	4.10E-03	GBX1	3.05	2.82E-02
RVMSR	T0	LOC105369781	2.31	4.10E-03	WDR26	-1.13	2.82E-02
RVMSR	T0	STRIP2	2.71	4.10E-03	OSBPL7	1.44	2.82E-02
RVMSR	T0	NEU2	3.38	4.11E-03	MIR5003	2.17	2.82E-02
RVMSR	T0	SIGLEC11	2.51	4.15E-03	ISPD-AS1	4.37	2.83E-02
RVMSR	T0	LOC101927924	2.19	4.16E-03	CGB1	3.06	2.83E-02
RVMSR	T0	IL5	4.17	4.17E-03	OTUD6A	3.05	2.84E-02
RVMSR	T0	FA2H	2.19	4.17E-03	SNORD19	4.39	2.85E-02
RVMSR	T0	HNF1A-AS1	2.50	4.17E-03	RPL31	-1.19	2.85E-02
RVMSR	T0	SNAR-E	2.24	4.18E-03	CXorf36	1.45	2.85E-02
RVMSR	T0	LOC101929372	2.06	4.22E-03	TH2LCRR	2.09	2.85E-02

RVMSR	T0	PNLIPRP1	5.24	4.25E-03	DUXA	1.96	2.86E-02
RVMSR	T0	RYR1	1.93	4.25E-03	KIAA1462	3.49	2.86E-02
RVMSR	T0	AGR3	4.18	4.29E-03	CENPI	2.62	2.86E-02
RVMSR	T0	ZNF470	2.10	4.30E-03	MIR7849	3.05	2.86E-02
RVMSR	T0	SLC7A4	2.81	4.30E-03	UQCRQ	-1.14	2.87E-02
RVMSR	T0	KIF3C	1.95	4.32E-03	GACAT2	3.47	2.87E-02
RVMSR	T0	SHISA9	2.81	4.32E-03	CPEB1-AS1	2.79	2.88E-02
RVMSR	T0	S100A2	2.96	4.32E-03	CSN1S2BP	4.36	2.88E-02
RVMSR	T0	CX3CL1	2.96	4.32E-03	PVR	1.25	2.88E-02
RVMSR	T0	LINGO2	3.67	4.32E-03	GABPB2	1.28	2.88E-02
RVMSR	T0	MPV17L	2.82	4.33E-03	MIR609	3.47	2.88E-02
RVMSR	T0	LOC100128770	2.18	4.33E-03	SNHG8	-1.46	2.88E-02
RVMSR	T0	ERC2-IT1	2.96	4.33E-03	SALRNA2	3.06	2.88E-02
RVMSR	T0	KIR3DL2	2.51	4.34E-03	LOC101928782	4.36	2.88E-02
RVMSR	T0	CABP2	3.68	4.34E-03	PRSS1	3.46	2.88E-02
RVMSR	T0	TPPP	2.29	4.34E-03	LOC100507194	4.38	2.88E-02
RVMSR	T0	ZNF556	2.51	4.37E-03	LINC00613	2.80	2.88E-02
RVMSR	T0	EFNB2	4.15	4.40E-03	SPRR2D	2.61	2.89E-02
RVMSR	T0	GABRB1	2.95	4.40E-03	MMP12	4.38	2.89E-02
RVMSR	T0	GPX2	3.35	4.40E-03	FAM205A	3.48	2.89E-02
RVMSR	T0	FAM189A2	2.95	4.40E-03	SNORD11B	2.10	2.90E-02
RVMSR	T0	C10orf111	3.37	4.40E-03	AK8	2.02	2.90E-02
RVMSR	T0	LOC400927	2.06	4.41E-03	CELF4	1.42	2.90E-02
RVMSR	T0	LOC101928845	2.50	4.41E-03	MIR7975	1.55	2.90E-02
RVMSR	T0	UNC13A	2.68	4.42E-03	VLDLR-AS1	3.47	2.90E-02
RVMSR	T0	LOC100652999	2.14	4.42E-03	HRK	2.35	2.90E-02
RVMSR	T0	MIR5583-1	2.23	4.42E-03	PDE6H	2.47	2.90E-02
RVMSR	T0	SOWAHC	2.59	4.43E-03	LOC100133091	1.53	2.90E-02
RVMSR	T0	WNT2B	4.14	4.43E-03	LINC00851	2.47	2.90E-02

RVMSR	T0	CXorf66	2.95	4.46E-03	LINC00937	2.17	2.90E-02
RVMSR	T0	MIR4314	2.80	4.46E-03	SGK3	1.33	2.90E-02
RVMSR	T0	NLN	1.80	4.46E-03	LINC01474	3.06	2.90E-02
RVMSR	T0	PRAMEF19	2.95	4.46E-03	TOB2	1.32	2.90E-02
RVMSR	T0	RSAD2	-1.49	4.46E-03	GRM5	3.04	2.90E-02
RVMSR	T0	MYO1C	2.09	4.46E-03	MIR4753	1.41	2.90E-02
RVMSR	T0	LOC100506679	2.49	4.46E-03	FAM177B	1.33	2.90E-02
RVMSR	T0	IL12A	3.12	4.47E-03	TRY2P	3.46	2.91E-02
RVMSR	T0	FABP5P3	2.50	4.47E-03	RPL17-C18orf32	-1.14	2.91E-02
RVMSR	T0	CNGB1	1.75	4.47E-03	KRT6B	2.61	2.92E-02
RVMSR	T0	ATF5	1.70	4.48E-03	CACNG5	3.46	2.92E-02
RVMSR	T0	SMURF1	1.92	4.52E-03	LOC105376599	4.38	2.92E-02
RVMSR	T0	SLCO1B1	5.23	4.56E-03	HAGLROS	3.04	2.92E-02
RVMSR	T0	CHDH	2.23	4.57E-03	LOC100130172	2.09	2.92E-02
RVMSR	T0	SNCB	3.64	4.57E-03	ST3GAL6-AS1	2.62	2.92E-02
RVMSR	T0	DPYSL5	2.59	4.62E-03	KIF25	4.37	2.92E-02
RVMSR	T0	LOC101928697	2.00	4.67E-03	TUSC5	4.37	2.92E-02
RVMSR	T0	HCN3	3.35	4.67E-03	HSD3BP4	2.10	2.92E-02
RVMSR	T0	SHISA2	3.35	4.67E-03	PWAR1	4.35	2.92E-02
RVMSR	T0	TTYH1	2.41	4.71E-03	OR2H1	2.36	2.92E-02
RVMSR	T0	KLK4	2.57	4.71E-03	C3P1	1.80	2.92E-02
RVMSR	T0	SMIM17	2.04	4.72E-03	LOC101929073	3.46	2.92E-02
RVMSR	T0	SEC1P	1.94	4.74E-03	LOC101928402	1.61	2.92E-02
RVMSR	T0	CT47B1	2.12	4.75E-03	C1QTNF8	2.78	2.92E-02
RVMSR	T0	CELSR2	2.69	4.75E-03	HIP1	1.15	2.92E-02
RVMSR	T0	LOC101927048	4.14	4.76E-03	ZNF816-ZNF321P	1.17	2.93E-02
RVMSR	T0	SULT6B1	2.41	4.76E-03	SNORD116-24	3.46	2.94E-02
RVMSR	T0	TNFRSF9	1.51	4.76E-03	TREH	2.61	2.94E-02
RVMSR	T0	ASB9P1	2.57	4.76E-03	FZD6	2.25	2.94E-02

RVMSR	T0	GABRG3	5.21	4.78E-03	LOC284930	2.59	2.94E-02
RVMSR	T0	ARSD	1.48	4.78E-03	ITGB1BP2	2.79	2.94E-02
RVMSR	T0	OMD	2.41	4.78E-03	CEBPZ	-1.14	2.95E-02
RVMSR	T0	CPXM2	2.21	4.79E-03	LOC100505609	1.90	2.96E-02
RVMSR	T0	MIR4424	2.80	4.79E-03	LOC284412	2.46	2.96E-02
RVMSR	T0	LINC00299	2.94	4.80E-03	EXO1	2.08	2.96E-02
RVMSR	T0	LANCL1-AS1	5.20	4.81E-03	DSG1-AS1	1.65	2.96E-02
RVMSR	T0	RAET1G	5.19	4.86E-03	RNF186	3.03	2.96E-02
RVMSR	T0	NPSR1-AS1	3.34	4.86E-03	LINC00649	-1.52	2.96E-02
RVMSR	T0	LOC102723345	5.19	4.86E-03	LOC101929448	4.36	2.96E-02
RVMSR	T0	SLC38A4	2.78	4.90E-03	TMPRSS7	2.36	2.96E-02
RVMSR	T0	ASIP	2.08	4.90E-03	TMOD4	1.41	2.96E-02
RVMSR	T0	ATP6V1B1	2.40	4.90E-03	DLX1	3.47	2.96E-02
RVMSR	T0	MIR3141	2.94	4.90E-03	NKX6-3	2.36	2.97E-02
RVMSR	T0	LOC554206	1.77	4.91E-03	TBC1D28	4.36	2.97E-02
RVMSR	T0	MIR1253	2.67	4.91E-03	DUSP4	2.01	2.97E-02
RVMSR	T0	LOC442497	4.13	4.95E-03	SEMG1	2.35	2.97E-02
RVMSR	T0	FILIP1	1.94	4.96E-03	POLR3K	-1.23	2.97E-02
RVMSR	T0	AADAT	5.21	4.98E-03	KRT18P55	2.78	2.97E-02
RVMSR	T0	MAOB	4.11	4.98E-03	LINC01490	2.25	2.97E-02
RVMSR	T0	WDR87	2.48	5.00E-03	OR10H1	2.46	2.97E-02
RVMSR	T0	DNAJC18	1.96	5.02E-03	TRPM4	1.90	2.97E-02
RVMSR	T0	MATN2	3.10	5.02E-03	NPAS2	4.36	2.98E-02
RVMSR	T0	WISP2	2.79	5.03E-03	LINC00174	2.47	2.98E-02
RVMSR	T0	BRMS1L	2.68	5.04E-03	MCF2L2	4.36	2.98E-02
RVMSR	T0	BAIAP2L1	2.21	5.04E-03	LAMC1	3.06	2.98E-02
RVMSR	T0	MIR4780	2.79	5.05E-03	INGX	1.38	2.98E-02
RVMSR	T0	ZNF876P	4.13	5.09E-03	EIF2B5-AS1	2.15	2.99E-02
RVMSR	T0	ITPRIPL1	1.80	5.09E-03	LILRP2	2.24	2.99E-02

RVMSR	T0	LOC157273	3.33	5.10E-03	R3HDML	1.85	3.00E-02
RVMSR	T0	PROCR	2.27	5.10E-03	NSUN7	1.90	3.00E-02
RVMSR	T0	NEU4	5.20	5.10E-03	ANXA8	3.03	3.00E-02
RVMSR	T0	TMC7	3.63	5.10E-03	TMEM25	2.09	3.00E-02
RVMSR	T0	KRT27	2.92	5.10E-03	POLE2	2.59	3.00E-02
RVMSR	T0	SLC1A3	5.17	5.10E-03	GATA6	3.03	3.00E-02
RVMSR	T0	MSH5-SAPCD1	1.94	5.10E-03	LMOD2	4.33	3.01E-02
RVMSR	T0	OR2B6	5.19	5.11E-03	LINC00383	2.78	3.01E-02
RVMSR	T0	LIMA1	1.55	5.14E-03	TRPA1	2.33	3.02E-02
RVMSR	T0	LOC101927058	4.12	5.14E-03	LOC645967	1.43	3.02E-02
RVMSR	T0	LOC105371789	2.39	5.14E-03	C16orf47	2.15	3.02E-02
RVMSR	T0	CXADRP3	5.17	5.16E-03	FLJ35934	2.77	3.02E-02
RVMSR	T0	LOC285484	5.18	5.16E-03	TGM7	2.24	3.02E-02
RVMSR	T0	SRD5A1P1	3.10	5.16E-03	MIR4760	3.44	3.02E-02
RVMSR	T0	LOC105372419	2.20	5.16E-03	GCSAML-AS1	2.59	3.04E-02
RVMSR	T0	PCDHB11	3.62	5.18E-03	SMARCA5	-1.12	3.04E-02
RVMSR	T0	ACR	5.19	5.19E-03	TAF7L	3.43	3.04E-02
RVMSR	T0	CAP2	2.26	5.19E-03	LOC100128233	2.59	3.04E-02
RVMSR	T0	LOC105376398	5.16	5.20E-03	CHRNA6	2.60	3.04E-02
RVMSR	T0	PROS1	2.07	5.22E-03	KIAA1211L	2.59	3.04E-02
RVMSR	T0	TFAP2B	2.48	5.24E-03	ERN2	3.03	3.04E-02
RVMSR	T0	LINC01106	3.09	5.24E-03	NDUFV2-AS1	1.66	3.05E-02
RVMSR	T0	DUSP9	2.33	5.25E-03	CATSPERB	3.03	3.05E-02
RVMSR	T0	GUCA1B	2.79	5.25E-03	FAM86B1	2.45	3.05E-02
RVMSR	T0	CAPN14	3.31	5.26E-03	PRDM9	3.03	3.05E-02
RVMSR	T0	IGDCC3	2.65	5.27E-03	RHOXF1	3.44	3.05E-02
RVMSR	T0	KRT79	3.09	5.28E-03	C20orf173	2.78	3.05E-02
RVMSR	T0	CFAP57	2.65	5.32E-03	ATP1A1-AS1	2.25	3.06E-02
RVMSR	T0	COL26A1	5.16	5.35E-03	ZNF565	1.57	3.06E-02

RVMSR	T0	ZFHX4-AS1	3.61	5.35E-03	ANKRD36C	-1.11	3.06E-02
RVMSR	T0	C2orf83	3.60	5.35E-03	LOC100133985	2.08	3.06E-02
RVMSR	T0	NDUFB2-AS1	2.26	5.36E-03	C10orf62	2.34	3.06E-02
RVMSR	T0	MOCOS	2.56	5.37E-03	PAXBP1-AS1	2.15	3.06E-02
RVMSR	T0	ZNF70	3.09	5.37E-03	ASAP1-IT2	1.37	3.06E-02
RVMSR	T0	PRKAR2A-AS1	2.55	5.37E-03	LOC101929596	2.07	3.06E-02
RVMSR	T0	ZWILCH	2.15	5.37E-03	MMP13	3.44	3.07E-02
RVMSR	T0	LOC105369980	2.39	5.40E-03	GART	1.18	3.07E-02
RVMSR	T0	CST11	2.46	5.40E-03	CCT6P3	1.42	3.08E-02
RVMSR	T0	FBF1	2.11	5.40E-03	FOLR3	-1.26	3.08E-02
RVMSR	T0	OR2A20P	2.77	5.41E-03	LTV1	-1.39	3.08E-02
RVMSR	T0	LINC01122	2.54	5.43E-03	MRPL22	-1.22	3.09E-02
RVMSR	T0	MIR3202-2	1.94	5.45E-03	RPL36A-HNRNPH2	-1.15	3.09E-02
RVMSR	T0	PRLH	5.15	5.48E-03	SLC46A1	2.46	3.09E-02
RVMSR	T0	HOXB1	5.15	5.48E-03	LOC400997	2.34	3.09E-02
RVMSR	T0	KCNQ1OT1	1.40	5.50E-03	BAALC-AS2	2.15	3.09E-02
RVMSR	T0	ANKDD1B	2.77	5.50E-03	RAPGEF4	2.78	3.10E-02
RVMSR	T0	SLC8A3	3.29	5.50E-03	PROZ	2.60	3.10E-02
RVMSR	T0	CASP3	-1.61	5.57E-03	F2RL1	1.65	3.10E-02
RVMSR	T0	POU3F2	5.13	5.59E-03	PTGIS	3.43	3.10E-02
RVMSR	T0	CELSR3-AS1	2.10	5.59E-03	COX7C	-1.14	3.10E-02
RVMSR	T0	CCDC177	4.10	5.59E-03	ZSCAN4	2.33	3.11E-02
RVMSR	T0	PARK2	2.19	5.62E-03	LOC728175	2.02	3.12E-02
RVMSR	T0	CLEC19A	3.58	5.63E-03	NMNAT2	4.33	3.12E-02
RVMSR	T0	KCTD21-AS1	3.33	5.64E-03	LINC01289	3.43	3.13E-02
RVMSR	T0	CYP4F24P	5.15	5.65E-03	MAP3K7CL	-1.21	3.13E-02
RVMSR	T0	MARVELD3	2.14	5.65E-03	IL20	2.07	3.14E-02
RVMSR	T0	SHBG	2.46	5.66E-03	LOC101929188	2.77	3.14E-02
RVMSR	T0	LOC643339	2.14	5.68E-03	ZBTB2	1.72	3.14E-02

RVMSR	T0	KIAA0408	1.88	5.68E-03	LOC100131496	2.77	3.14E-02
RVMSR	T0	MTNR1B	3.30	5.68E-03	TNMD	2.14	3.14E-02
RVMSR	T0	FMOD	2.90	5.69E-03	MIR4738	2.07	3.14E-02
RVMSR	T0	PDCD10	-1.43	5.69E-03	SLC9C2	3.03	3.14E-02
RVMSR	T0	AP1M2	2.65	5.69E-03	TRIP13	3.42	3.14E-02
RVMSR	T0	FSD2	2.31	5.69E-03	OR7E5P	2.44	3.14E-02
RVMSR	T0	ITGB6	4.07	5.69E-03	LOC105374205	1.59	3.14E-02
RVMSR	T0	CYS1	5.16	5.69E-03	ZNF645	2.44	3.14E-02
RVMSR	T0	NPHP1	3.59	5.69E-03	MIR4514	2.45	3.15E-02
RVMSR	T0	MAP6	5.16	5.69E-03	LOC100507387	2.60	3.15E-02
RVMSR	T0	FANK1-AS1	2.24	5.69E-03	REXO1L2P	2.76	3.15E-02
RVMSR	T0	ZNF793-AS1	2.55	5.69E-03	MPO	1.94	3.15E-02
RVMSR	T0	P4HA2-AS1	2.65	5.69E-03	TAS2R16	2.77	3.15E-02
RVMSR	T0	LOC100506286	3.29	5.69E-03	TMEM47	2.13	3.15E-02
RVMSR	T0	TUFT1	2.76	5.70E-03	TDGF1	3.42	3.16E-02
RVMSR	T0	WDR97	2.38	5.70E-03	LINC01151	2.78	3.16E-02
RVMSR	T0	SLC25A3P1	5.14	5.72E-03	PPP1R42	2.58	3.16E-02
RVMSR	T0	MRO	5.13	5.73E-03	MIR4670	3.41	3.16E-02
RVMSR	T0	DEFA4	1.66	5.75E-03	NMRAL2P	2.58	3.16E-02
RVMSR	T0	LOC100128494	3.60	5.75E-03	TRPM2	1.44	3.17E-02
RVMSR	T0	ACMSD	3.59	5.76E-03	P2RY6	1.68	3.17E-02
RVMSR	T0	HS6ST2	2.38	5.78E-03	FLT3	2.45	3.17E-02
RVMSR	T0	MIR4529	2.37	5.80E-03	TEX29	2.76	3.17E-02
RVMSR	T0	LRRD1	3.07	5.81E-03	SLC6A1	2.59	3.17E-02
RVMSR	T0	LAMP3	2.06	5.81E-03	NT5C1B	4.35	3.17E-02
RVMSR	T0	GRM4	5.12	5.81E-03	AQP8	1.84	3.17E-02
RVMSR	T0	LOC101060542	2.18	5.81E-03	GTF2IRD1P1	2.06	3.17E-02
RVMSR	T0	KRT34	4.08	5.81E-03	C9orf131	2.15	3.17E-02
RVMSR	T0	HTT-AS	2.64	5.81E-03	C19orf71	-3.47	3.18E-02

RVMSR	T0	LOC100506127	1.68	5.81E-03	C4orf32	1.45	3.18E-02
RVMSR	T0	HIST1H2AA	3.06	5.81E-03	LINC01447	3.01	3.18E-02
RVMSR	T0	LOC102724580	3.28	5.81E-03	RNASE10	2.76	3.18E-02
RVMSR	T0	ZNF341	1.83	5.82E-03	OR10A6	2.76	3.18E-02
RVMSR	T0	IFNA14	5.14	5.85E-03	SEC11C	-1.20	3.18E-02
RVMSR	T0	FUT3	3.06	5.85E-03	APOC1	2.05	3.18E-02
RVMSR	T0	B3GNT4	2.09	5.85E-03	POMC	1.61	3.19E-02
RVMSR	T0	IL18	2.25	5.85E-03	OVOL1	3.01	3.19E-02
RVMSR	T0	C19orf81	3.29	5.86E-03	EFCAB6-AS1	2.33	3.19E-02
RVMSR	T0	SSX1	3.58	5.86E-03	ANKRD20A3	2.23	3.19E-02
RVMSR	T0	41153	2.30	5.86E-03	PDCD1LG2	1.93	3.19E-02
RVMSR	T0	OR13D1	3.29	5.86E-03	LOC101929380	2.57	3.20E-02
RVMSR	T0	OR4D11	2.38	5.86E-03	C21orf140	2.34	3.20E-02
RVMSR	T0	IL1RAPL1	5.14	5.90E-03	KCND2	2.58	3.20E-02
RVMSR	T0	ZBTB20-AS1	4.05	5.94E-03	PLA2G2F	2.14	3.20E-02
RVMSR	T0	LOH12CR2	2.64	5.94E-03	BDKRB2	2.56	3.20E-02
RVMSR	T0	IL17RD	2.62	5.94E-03	PNLIPRP2	2.57	3.20E-02
RVMSR	T0	HTR3B	1.53	5.94E-03	RP1	3.43	3.21E-02
RVMSR	T0	RASSF8-AS1	2.44	5.94E-03	FLT3LG	-1.15	3.21E-02
RVMSR	T0	SERPINA4	5.12	5.94E-03	FAM155A	2.76	3.21E-02
RVMSR	T0	EFCAB6	4.06	5.94E-03	YOD1	-1.13	3.21E-02
RVMSR	T0	KLK8	2.18	5.94E-03	MAGI1-AS1	2.06	3.21E-02
RVMSR	T0	TSR1	1.60	5.97E-03	EIF3E	-1.15	3.21E-02
RVMSR	T0	ZNF562	1.48	5.97E-03	GIF	2.06	3.21E-02
RVMSR	T0	PLA2G2E	3.58	5.98E-03	C7orf65	1.94	3.22E-02
RVMSR	T0	LOC101928118	3.58	5.98E-03	LOC101927550	1.49	3.22E-02
RVMSR	T0	LOC100996415	3.28	5.99E-03	RPL39L	-1.37	3.22E-02
RVMSR	T0	VN1R1	2.24	5.99E-03	C1orf137	4.31	3.22E-02
RVMSR	T0	GHDC	1.71	6.00E-03	LOC401134	3.41	3.22E-02

RVMSR	T0	CDCA2	5.13	6.01E-03	PCAT18	2.22	3.22E-02
RVMSR	T0	LARP6	2.44	6.01E-03	LOC105377458	2.21	3.22E-02
RVMSR	T0	MISP3	2.09	6.01E-03	FOXA3	4.33	3.23E-02
RVMSR	T0	LINC00102	4.06	6.01E-03	CTTNBP2	3.41	3.23E-02
RVMSR	T0	CATSPER2P1	2.53	6.01E-03	AZGP1P1	2.76	3.23E-02
RVMSR	T0	INE2	2.52	6.02E-03	TCEB3CL2	3.42	3.23E-02
RVMSR	T0	STAU2-AS1	2.29	6.02E-03	GPR87	2.14	3.23E-02
RVMSR	T0	LOC101928567	1.81	6.02E-03	CCNA2	2.44	3.23E-02
RVMSR	T0	CPN1	2.63	6.02E-03	LOC101928372	4.33	3.23E-02
RVMSR	T0	LIN28B-AS1	3.28	6.02E-03	RNF165	1.70	3.24E-02
RVMSR	T0	PTPRM	5.14	6.06E-03	HOXC13	2.76	3.24E-02
RVMSR	T0	LOC100288748	1.83	6.06E-03	PRAMENP	2.44	3.24E-02
RVMSR	T0	SYCE2	2.76	6.06E-03	HNF4A-AS1	2.43	3.25E-02
RVMSR	T0	WFDC8	2.74	6.06E-03	PSMD14	-1.34	3.25E-02
RVMSR	T0	LOC101929147	1.90	6.11E-03	EPHX3	2.31	3.26E-02
RVMSR	T0	CXCL11	2.74	6.12E-03	PLEKHS1	3.01	3.26E-02
RVMSR	T0	SPAG17	3.58	6.12E-03	MIR3661	4.30	3.26E-02
RVMSR	T0	C8orf49	3.05	6.16E-03	GNG12	2.43	3.26E-02
RVMSR	T0	LINC01273	3.05	6.18E-03	MIEF2	2.57	3.27E-02
RVMSR	T0	RNFT2	1.99	6.18E-03	LOC100506175	1.83	3.27E-02
RVMSR	T0	MPPED2	2.36	6.20E-03	RIMS3	1.87	3.27E-02
RVMSR	T0	EME1	4.04	6.25E-03	HCRTR1	4.30	3.27E-02
RVMSR	T0	FXYD4	3.07	6.25E-03	SLC22A9	1.82	3.27E-02
RVMSR	T0	PLCD4	2.62	6.25E-03	LOC105371083	1.99	3.27E-02
RVMSR	T0	MAP1LC3C	2.35	6.25E-03	MIR451A	1.74	3.27E-02
RVMSR	T0	DPRX	2.03	6.25E-03	LOC100508631	3.42	3.27E-02
RVMSR	T0	NKAIN3	5.11	6.25E-03	GAS2L2	2.58	3.28E-02
RVMSR	T0	LOC102724579	2.29	6.26E-03	FAM3D	2.77	3.28E-02
RVMSR	T0	SNRPE	-1.64	6.26E-03	RPL39	-1.17	3.28E-02

RVMSR	T0	ALPP	5.11	6.26E-03	ZNF491	2.43	3.28E-02
RVMSR	T0	ACTG1P17	1.63	6.26E-03	LARGE-AS1	1.92	3.29E-02
RVMSR	T0	UCMA	3.05	6.26E-03	CNPPD1	-1.10	3.29E-02
RVMSR	T0	PTGS1	-1.87	6.26E-03	SLC14A2	1.56	3.29E-02
RVMSR	T0	ANO4	4.04	6.26E-03	ZFHX3	1.56	3.29E-02
RVMSR	T0	IL17B	3.26	6.29E-03	PDE8B	2.74	3.29E-02
RVMSR	T0	LINC00836	3.56	6.29E-03	DYNC2H1	2.21	3.29E-02
RVMSR	T0	ENPP7P13	2.87	6.29E-03	SPIRE2	3.41	3.30E-02
RVMSR	T0	TMEM108-AS1	2.87	6.29E-03	LOC388942	3.00	3.30E-02
RVMSR	T0	CYP51A1-AS1	5.09	6.29E-03	SIX5	1.83	3.31E-02
RVMSR	T0	CRISP2	5.12	6.29E-03	TCP11L2	-1.11	3.31E-02
RVMSR	T0	ADRA1B	2.86	6.29E-03	CABP4	1.44	3.31E-02
RVMSR	T0	FLRT1	4.04	6.29E-03	RNU12	1.98	3.31E-02
RVMSR	T0	PRRT2	5.12	6.29E-03	SKP2	-3.45	3.32E-02
RVMSR	T0	PDLIM3	4.03	6.31E-03	YBX2	1.55	3.32E-02
RVMSR	T0	DGKB	2.22	6.35E-03	ULK4P2	2.21	3.32E-02
RVMSR	T0	MAST4-AS1	3.04	6.35E-03	NDUFS4	-1.34	3.32E-02
RVMSR	T0	GABRA1	3.05	6.35E-03	RPL23	-1.16	3.32E-02
RVMSR	T0	ITIH2	2.89	6.38E-03	NEIL3	2.58	3.32E-02
RVMSR	T0	PALD1	2.42	6.39E-03	LOC101928738	3.41	3.33E-02
RVMSR	T0	LOC644189	4.06	6.40E-03	SLC22A6	2.43	3.33E-02
RVMSR	T0	CALB1	2.23	6.40E-03	WFDC13	2.57	3.33E-02
RVMSR	T0	KDELC2	2.51	6.43E-03	MIR103B2	2.43	3.33E-02
RVMSR	T0	NCS1	2.87	6.43E-03	GPRIN2	4.28	3.33E-02
RVMSR	T0	DKFZp434L192	4.03	6.43E-03	KRTAP6-1	4.28	3.33E-02
RVMSR	T0	IP6K3	3.26	6.43E-03	GLYATL1	3.01	3.33E-02
RVMSR	T0	LY6E	-1.40	6.43E-03	SMIM23	2.57	3.33E-02
RVMSR	T0	ATCAY	2.52	6.45E-03	PHYHIP	3.00	3.33E-02
RVMSR	T0	MIR920	2.87	6.48E-03	ANTXRL	2.57	3.34E-02

RVMSR	T0	CFAP206	5.09	6.51E-03	NLRP5	3.38	3.34E-02
RVMSR	T0	MIR4309	4.02	6.53E-03	MCFD2	-1.54	3.34E-02
RVMSR	T0	MIR1254-2	2.43	6.53E-03	PIPOX	2.06	3.34E-02
RVMSR	T0	RERG-AS1	5.10	6.53E-03	PAX3	3.41	3.35E-02
RVMSR	T0	PGR	3.55	6.53E-03	MIR320B2	1.48	3.35E-02
RVMSR	T0	LOC102724153	3.04	6.53E-03	UCP1	4.31	3.35E-02
RVMSR	T0	LOC100506178	5.07	6.53E-03	MFSD4B	1.23	3.35E-02
RVMSR	T0	TMEM178A	2.87	6.54E-03	TTLL13P	2.74	3.35E-02
RVMSR	T0	LINC00678	5.09	6.54E-03	SEC14L4	1.70	3.37E-02
RVMSR	T0	ZNF843	2.87	6.57E-03	GDF7	2.75	3.37E-02
RVMSR	T0	USP29	2.27	6.57E-03	TYMSOS	2.73	3.37E-02
RVMSR	T0	HIPK1-AS1	1.89	6.57E-03	TMEM196	2.99	3.37E-02
RVMSR	T0	SERPINE1	2.07	6.58E-03	SHC4	2.31	3.37E-02
RVMSR	T0	LOC101927503	3.26	6.58E-03	BORCS8-MEF2B	2.12	3.37E-02
RVMSR	T0	RIMKLA	3.26	6.58E-03	AMPH	2.74	3.37E-02
RVMSR	T0	LOC101928174	2.73	6.58E-03	GLUD1P7	2.99	3.37E-02
RVMSR	T0	LOC101928661	2.86	6.59E-03	TDGF1P3	4.27	3.37E-02
RVMSR	T0	STMN2	2.41	6.59E-03	LOC102723344	4.27	3.37E-02
RVMSR	T0	ANXA10	2.86	6.61E-03	PLS3-AS1	2.12	3.37E-02
RVMSR	T0	LOC101928020	1.68	6.62E-03	OR5A1	2.98	3.38E-02
RVMSR	T0	FST	4.02	6.68E-03	CD207	4.27	3.38E-02
RVMSR	T0	COL24A1	2.61	6.70E-03	GSTM2P1	1.92	3.38E-02
RVMSR	T0	TOMM5	-1.43	6.70E-03	CRYBA2	4.27	3.38E-02
RVMSR	T0	C2orf48	2.60	6.74E-03	GEN1	1.73	3.39E-02
RVMSR	T0	PON1	5.10	6.74E-03	GCM1	2.29	3.39E-02
RVMSR	T0	CRTC3-AS1	3.55	6.74E-03	LINC01224	2.57	3.40E-02
RVMSR	T0	PLP1	2.72	6.75E-03	ASAP3	3.38	3.40E-02
RVMSR	T0	CSRP2	3.03	6.75E-03	GUSBP9	1.42	3.41E-02
RVMSR	T0	DOCK9	1.73	6.75E-03	C1orf61	3.40	3.41E-02

RVMSR	T0	ELOVL2	2.73	6.75E-03	LOC100287846	2.04	3.42E-02
RVMSR	T0	ISG15	-1.47	6.75E-03	MIR2467	2.31	3.42E-02
RVMSR	T0	C9orf50	3.26	6.75E-03	CATSPER2	1.66	3.42E-02
RVMSR	T0	LOC101927620	1.73	6.75E-03	MDC1	1.25	3.42E-02
RVMSR	T0	LOC100505588	5.09	6.75E-03	LINC00454	3.38	3.42E-02
RVMSR	T0	BCAN	4.02	6.75E-03	LOC100506472	1.69	3.43E-02
RVMSR	T0	CACNG4	2.49	6.80E-03	NPIPB8	1.81	3.43E-02
RVMSR	T0	SNAR-C4	3.25	6.80E-03	PAK5	2.97	3.43E-02
RVMSR	T0	RD3L	1.54	6.81E-03	PADI3	2.42	3.44E-02
RVMSR	T0	ERVMER34-1	-1.45	6.84E-03	LOC101927795	2.42	3.44E-02
RVMSR	T0	GAS2L3	4.01	6.85E-03	KRTAP20-3	3.39	3.45E-02
RVMSR	T0	LOC100129148	2.72	6.85E-03	PARD3B	2.19	3.45E-02
RVMSR	T0	TCAM1P	2.73	6.86E-03	DFNB59	3.39	3.45E-02
RVMSR	T0	CDH4	3.02	6.88E-03	COLEC12	2.21	3.45E-02
RVMSR	T0	FAM124B	4.01	6.88E-03	MRGPRD	4.26	3.45E-02
RVMSR	T0	FOXM1	3.02	6.91E-03	CCR4	1.53	3.45E-02
RVMSR	T0	CACNA1G	4.01	6.91E-03	GREB1	4.26	3.45E-02
RVMSR	T0	ARMC9	2.27	6.91E-03	GCNT3	2.20	3.45E-02
RVMSR	T0	KIZ-AS1	3.99	6.91E-03	C19orf18	1.98	3.45E-02
RVMSR	T0	TPTE2P6	4.00	6.94E-03	USP2	2.55	3.46E-02
RVMSR	T0	NOVA2	2.06	6.96E-03	CRABP1	2.20	3.46E-02
RVMSR	T0	ACVR2B-AS1	2.86	6.99E-03	LINC00567	3.39	3.46E-02
RVMSR	T0	C8orf86	2.85	7.03E-03	LOC100133286	1.98	3.46E-02
RVMSR	T0	RHPN2	3.03	7.04E-03	NDRG3	1.08	3.47E-02
RVMSR	T0	MIR4692	2.85	7.04E-03	MYCT1	1.57	3.47E-02
RVMSR	T0	ZNF563	1.69	7.04E-03	CEACAM6	2.56	3.47E-02
RVMSR	T0	POM121L4P	3.02	7.04E-03	MIR4711	2.74	3.47E-02
RVMSR	T0	ACAD11	2.85	7.05E-03	BOLA2	-1.09	3.47E-02
RVMSR	T0	TSPAN13	-3.00	7.08E-03	HIF1A-AS2	2.98	3.47E-02

RVMSR	T0	MAP3K9	2.09	7.09E-03	CST7	-1.14	3.47E-02
RVMSR	T0	LOC101929621	2.15	7.10E-03	DUBR	2.11	3.47E-02
RVMSR	T0	FAM229A	1.76	7.10E-03	TXNDC17	-1.15	3.48E-02
RVMSR	T0	DCX	2.70	7.10E-03	NMI	-1.09	3.48E-02
RVMSR	T0	PPP2R2C	4.00	7.12E-03	MIR4770	3.39	3.48E-02
RVMSR	T0	LOC101927575	2.71	7.12E-03	SERPINE3	2.97	3.48E-02
RVMSR	T0	MEOX2	5.06	7.13E-03	LINC00441	2.42	3.48E-02
RVMSR	T0	GALR1	4.01	7.13E-03	DSC1	2.55	3.48E-02
RVMSR	T0	OR56B4	3.01	7.13E-03	APOA2	1.55	3.48E-02
RVMSR	T0	DAND5	2.02	7.13E-03	ADAMTS12	3.37	3.48E-02
RVMSR	T0	FAM230A	2.71	7.14E-03	LOC105376772	2.32	3.48E-02
RVMSR	T0	IFI6	-1.49	7.14E-03	LINC00160	2.54	3.48E-02
RVMSR	T0	CBS	2.11	7.14E-03	SLC7A2	4.25	3.49E-02
RVMSR	T0	CBSL	2.11	7.14E-03	GPC1	4.25	3.50E-02
RVMSR	T0	TCAF2	2.01	7.15E-03	GDF10	4.25	3.50E-02
RVMSR	T0	TTC39A-AS1	2.15	7.15E-03	LINC00377	3.38	3.50E-02
RVMSR	T0	MCM4	1.84	7.15E-03	LINC01173	2.04	3.50E-02
RVMSR	T0	POMZP3	1.90	7.15E-03	LINC01486	3.38	3.50E-02
RVMSR	T0	C11orf45	3.22	7.16E-03	C9orf62	4.24	3.51E-02
RVMSR	T0	HIST1H3I	3.52	7.17E-03	C8orf44-SGK3	1.27	3.51E-02
RVMSR	T0	SERPINB5	3.01	7.17E-03	KREMEN1	1.43	3.51E-02
RVMSR	T0	MIR4531	2.20	7.17E-03	MIR548AP	2.55	3.51E-02
RVMSR	T0	CLIP2	2.15	7.18E-03	SPRR2G	2.99	3.51E-02
RVMSR	T0	SNAR-C3	2.33	7.19E-03	TLDC2	1.73	3.51E-02
RVMSR	T0	DAPK1	2.16	7.21E-03	HLTF-AS1	2.20	3.51E-02
RVMSR	T0	GPX3	2.49	7.23E-03	MIR891A	2.56	3.53E-02
RVMSR	T0	LOC101927619	2.26	7.23E-03	MPHOSPH10	-1.21	3.53E-02
RVMSR	T0	ROBO2	3.99	7.23E-03	RBM12B-AS1	2.21	3.53E-02
RVMSR	T0	PEBP4	2.40	7.27E-03	LOC105373006	2.72	3.53E-02

RVMSR	T0	GPR142	3.03	7.27E-03	EPB41L1	2.73	3.53E-02
RVMSR	T0	DLX6-AS1	5.03	7.29E-03	LOC101928445	2.04	3.53E-02
RVMSR	T0	SNAP25-AS1	5.03	7.29E-03	LINC01120	2.41	3.53E-02
RVMSR	T0	LINC00544	2.48	7.31E-03	CALR3	2.30	3.54E-02
RVMSR	T0	LOC102546229	2.49	7.32E-03	FZD10	2.96	3.54E-02
RVMSR	T0	LINC01094	1.79	7.37E-03	SLC5A5	2.72	3.54E-02
RVMSR	T0	ZFP42	2.59	7.37E-03	ZNF799	1.69	3.54E-02
RVMSR	T0	LOC105377590	2.25	7.37E-03	FAM90A10P	-1.08	3.54E-02
RVMSR	T0	LINC00939	2.70	7.40E-03	KRTAP2-2	4.24	3.54E-02
RVMSR	T0	ADCY6	1.67	7.40E-03	NIPAL1	2.11	3.55E-02
RVMSR	T0	CKMT1A	3.23	7.42E-03	LOC105376975	2.41	3.55E-02
RVMSR	T0	RASL12	2.83	7.44E-03	TAF15	-1.11	3.55E-02
RVMSR	T0	PABPC1P2	2.41	7.44E-03	HAPLN4	2.55	3.55E-02
RVMSR	T0	ART3	3.00	7.45E-03	ADAMTS4	1.85	3.55E-02
RVMSR	T0	C2orf57	3.99	7.46E-03	LOC654342	1.52	3.55E-02
RVMSR	T0	STXBP6	3.52	7.50E-03	SIAH1	-2.52	3.55E-02
RVMSR	T0	ITGAD	2.85	7.51E-03	PDE4C	2.04	3.55E-02
RVMSR	T0	TCF21	3.22	7.51E-03	BOLA2B	-1.09	3.55E-02
RVMSR	T0	SGK494	1.61	7.53E-03	LAMTOR2	-1.09	3.55E-02
RVMSR	T0	FAM92A1P2	2.69	7.53E-03	LPL	2.96	3.55E-02
RVMSR	T0	HTR2A	3.97	7.55E-03	ANGPTL7	2.19	3.55E-02
RVMSR	T0	LRRC2	1.90	7.55E-03	ERICH6	2.97	3.55E-02
RVMSR	T0	SMO	3.51	7.57E-03	MAPT-AS1	2.98	3.55E-02
RVMSR	T0	ACOT2	1.63	7.59E-03	SYBU	4.27	3.55E-02
RVMSR	T0	SPATA1	1.81	7.59E-03	POTEKP	3.39	3.55E-02
RVMSR	T0	HAO2	5.02	7.59E-03	MIR1264	4.26	3.57E-02
RVMSR	T0	SLC35A2	1.90	7.59E-03	GRID2	4.26	3.57E-02
RVMSR	T0	GZMB	-1.38	7.59E-03	LOC102724279	1.57	3.57E-02
RVMSR	T0	LOC101927523	2.39	7.60E-03	LINC01509	2.72	3.57E-02

RVMSR	T0	ZNF490	1.79	7.61E-03	ABCG8	2.30	3.57E-02
RVMSR	T0	LOC101928063	2.84	7.64E-03	OR10G2	2.72	3.58E-02
RVMSR	T0	PRPF40B	2.49	7.64E-03	LINC00977	3.36	3.58E-02
RVMSR	T0	DNAJB7	2.70	7.64E-03	EDDM3A	2.55	3.58E-02
RVMSR	T0	MYBPC2	3.51	7.66E-03	THEGL	2.09	3.58E-02
RVMSR	T0	RAD54L	3.98	7.66E-03	LOC285626	3.37	3.58E-02
RVMSR	T0	WWC2	2.82	7.67E-03	MEGF8	1.85	3.59E-02
RVMSR	T0	LOC100131303	1.89	7.68E-03	CT83	2.71	3.59E-02
RVMSR	T0	CLVS1	5.02	7.68E-03	ICA1L	1.36	3.59E-02
RVMSR	T0	LINC01596	3.00	7.69E-03	LOC100996437	2.42	3.59E-02
RVMSR	T0	LOC101928489	2.84	7.71E-03	ZNF682	1.46	3.60E-02
RVMSR	T0	CBLC	1.86	7.73E-03	RGS9BP	2.96	3.60E-02
RVMSR	T0	C17orf58	2.25	7.75E-03	CBLN3	2.53	3.60E-02
RVMSR	T0	PDE6A	2.31	7.80E-03	SDK1	2.20	3.60E-02
RVMSR	T0	DEFB1	2.99	7.82E-03	SEC14L6	2.40	3.60E-02
RVMSR	T0	DCLK1	2.83	7.82E-03	KCNJ16	2.41	3.60E-02
RVMSR	T0	LOC100288846	2.48	7.82E-03	LHX4	2.71	3.60E-02
RVMSR	T0	GDF3	2.69	7.82E-03	LOC101929541	2.96	3.60E-02
RVMSR	T0	LOC100507144	3.99	7.82E-03	DIGIT	4.23	3.60E-02
RVMSR	T0	UQCRB	-1.44	7.82E-03	LOC100505942	1.86	3.60E-02
RVMSR	T0	SLC4A5	1.60	7.82E-03	RPL29P2	2.74	3.60E-02
RVMSR	T0	LOC101927635	3.20	7.82E-03	CCL16	1.81	3.60E-02
RVMSR	T0	FAM167A	2.83	7.85E-03	FBXL19-AS1	1.27	3.60E-02
RVMSR	T0	LOC90246	3.99	7.89E-03	GHRH	2.03	3.60E-02
RVMSR	T0	MEIKIN	3.00	7.94E-03	ABCB9	1.91	3.61E-02
RVMSR	T0	RPRML	1.80	7.94E-03	HSP90AA1	-1.10	3.61E-02
RVMSR	T0	KRTAP5-1	2.31	7.95E-03	LOC100130880	3.37	3.61E-02
RVMSR	T0	LINC00521	2.82	7.95E-03	DCBLD1	2.53	3.61E-02
RVMSR	T0	HYOU1	1.57	7.96E-03	FAM186B	2.10	3.61E-02

RVMSR	T0	LOC151475	3.98	7.98E-03	MURC	2.54	3.61E-02
RVMSR	T0	TAF1A	2.47	7.98E-03	RNF225	2.96	3.61E-02
RVMSR	T0	LOC101928663	2.58	7.98E-03	SLC51A	2.95	3.61E-02
RVMSR	T0	LINC00298	2.56	8.00E-03	DCC	2.09	3.61E-02
RVMSR	T0	MIR3182	2.68	8.00E-03	RANBP3L	1.97	3.61E-02
RVMSR	T0	CHRNA9	3.96	8.04E-03	OXTR	2.54	3.61E-02
RVMSR	T0	LOC102723471	3.94	8.04E-03	C1GALT1C1L	2.54	3.61E-02
RVMSR	T0	FLJ33534	3.49	8.04E-03	CCIN	3.36	3.61E-02
RVMSR	T0	EYA2	2.99	8.04E-03	KRTAP6-2	1.68	3.61E-02
RVMSR	T0	BPIFB6	3.96	8.04E-03	GP2	2.73	3.61E-02
RVMSR	T0	OR5M10	5.02	8.04E-03	LOC100128361	2.04	3.61E-02
RVMSR	T0	SLC6A2	3.50	8.08E-03	PFN4	2.95	3.61E-02
RVMSR	T0	SIAH2	-1.37	8.08E-03	SPO11	4.25	3.61E-02
RVMSR	T0	CSMD2	2.37	8.08E-03	ZNF610	1.62	3.62E-02
RVMSR	T0	LGR5	3.95	8.13E-03	PORCN	-4.10	3.62E-02
RVMSR	T0	EEF2K	1.73	8.13E-03	HTR1E	2.97	3.62E-02
RVMSR	T0	TFB2M	1.85	8.13E-03	DIS3L	1.17	3.62E-02
RVMSR	T0	SPATA42	3.20	8.13E-03	MIR8059	2.96	3.62E-02
RVMSR	T0	SNORA111	4.99	8.17E-03	LOC105376480	2.11	3.62E-02
RVMSR	T0	ANGPT4	2.82	8.19E-03	RNF141	-1.22	3.62E-02
RVMSR	T0	OOEP	2.38	8.20E-03	EARS2	1.37	3.62E-02
RVMSR	T0	OTUD6B-AS1	-1.46	8.20E-03	BRINP2	2.28	3.63E-02
RVMSR	T0	LOC100288911	3.49	8.21E-03	SCARA5	1.91	3.63E-02
RVMSR	T0	CATIP-AS2	2.81	8.21E-03	NCOA7-AS1	3.36	3.63E-02
RVMSR	T0	LOC105375014	2.81	8.27E-03	C10orf82	2.96	3.64E-02
RVMSR	T0	GVQW2	3.19	8.28E-03	PQLC2L	3.36	3.65E-02
RVMSR	T0	MAMSTR	1.75	8.33E-03	LOC102723769	1.61	3.65E-02
RVMSR	T0	EMCN	2.98	8.33E-03	HEXIM2	1.80	3.65E-02
RVMSR	T0	C9orf64	2.00	8.33E-03	LOC101927274	2.71	3.65E-02

RVMSR	T0	PIP	2.57	8.33E-03	ZNHIT3	-1.20	3.66E-02
RVMSR	T0	RTP3	3.94	8.33E-03	AQP12B	2.41	3.66E-02
RVMSR	T0	VN1R10P	2.98	8.35E-03	H1FX-AS1	1.96	3.66E-02
RVMSR	T0	WT1-AS	3.50	8.35E-03	LOC101927560	2.39	3.67E-02
RVMSR	T0	BRD7P3	1.48	8.35E-03	MIR548XHG	4.24	3.68E-02
RVMSR	T0	MTRNR2L1	-1.46	8.37E-03	MBLAC1	3.36	3.69E-02
RVMSR	T0	SNTN	4.98	8.37E-03	FAM178B	4.24	3.69E-02
RVMSR	T0	KRTAP3-1	3.94	8.37E-03	LINC01411	2.40	3.69E-02
RVMSR	T0	ENO4	5.00	8.39E-03	MAGEB2	1.65	3.69E-02
RVMSR	T0	FITM1	2.68	8.39E-03	PGBD3	2.03	3.69E-02
RVMSR	T0	TEKT1	3.48	8.41E-03	GUSBP3	1.34	3.70E-02
RVMSR	T0	RYR2	3.47	8.42E-03	LOC730183	1.96	3.70E-02
RVMSR	T0	LOC101928231	2.99	8.42E-03	SLIRP	-1.14	3.71E-02
RVMSR	T0	ANKRD20A4	2.37	8.42E-03	CYP19A1	2.95	3.71E-02
RVMSR	T0	PROM2	2.17	8.42E-03	TAAR3	2.96	3.71E-02
RVMSR	T0	SRGAP2-AS1	2.98	8.44E-03	TTLL12	1.33	3.71E-02
RVMSR	T0	LOC105374366	1.73	8.44E-03	PDZD9	4.26	3.72E-02
RVMSR	T0	LOC105376351	3.49	8.44E-03	LOC105374952	1.80	3.72E-02
RVMSR	T0	SPTBN2	2.24	8.47E-03	LINC01203	2.39	3.72E-02
RVMSR	T0	ASTN2	3.94	8.49E-03	MIR5692B	2.70	3.72E-02
RVMSR	T0	KLF5	2.68	8.49E-03	MYH8	2.39	3.73E-02
RVMSR	T0	LOC100499194	3.94	8.49E-03	MLPH	4.23	3.73E-02
RVMSR	T0	SMAD1-AS2	3.47	8.51E-03	DPP10-AS3	4.23	3.73E-02
RVMSR	T0	MIR4419A	2.80	8.51E-03	C1orf64	2.10	3.73E-02
RVMSR	T0	FAM209A	1.87	8.55E-03	LINC01078	4.23	3.74E-02
RVMSR	T0	ITM2A	-1.35	8.57E-03	MIR8058	1.97	3.74E-02
RVMSR	T0	ACOX2	1.82	8.58E-03	LOC101926962	2.94	3.75E-02
RVMSR	T0	SPDYA	2.30	8.59E-03	LGALS16	3.36	3.75E-02
RVMSR	T0	CTCFL	2.80	8.60E-03	LOC100506384	3.35	3.75E-02

RVMSR	T0	RND1	4.97	8.62E-03	ADAMTSL5	2.52	3.75E-02
RVMSR	T0	KLRB1	-1.35	8.66E-03	TTTY16	4.22	3.75E-02
RVMSR	T0	FLJ30679	3.93	8.71E-03	SYNDIG1L	2.53	3.75E-02
RVMSR	T0	DES	3.48	8.74E-03	ANKS1B	2.52	3.75E-02
RVMSR	T0	FUT6	3.18	8.74E-03	MPP3	1.96	3.75E-02
RVMSR	T0	TLX3	4.96	8.78E-03	EXTL3-AS1	2.39	3.75E-02
RVMSR	T0	C16orf45	2.11	8.78E-03	LOC729966	2.94	3.75E-02
RVMSR	T0	APELA	2.98	8.79E-03	LOC105372280	3.36	3.76E-02
RVMSR	T0	GNA11	2.55	8.80E-03	RNASE9	3.36	3.76E-02
RVMSR	T0	TMEM202	2.24	8.81E-03	UPK2	3.33	3.76E-02
RVMSR	T0	FLJ41200	2.66	8.81E-03	CRABP2	1.64	3.76E-02
RVMSR	T0	LSAMP	2.46	8.81E-03	FZD3	1.67	3.76E-02
RVMSR	T0	KRTAP3-3	4.97	8.82E-03	CPNE7	-4.07	3.77E-02
RVMSR	T0	LCE1B	2.37	8.83E-03	EPHB4	1.96	3.77E-02
RVMSR	T0	LOC101928134	2.97	8.86E-03	PRPH	2.02	3.77E-02
RVMSR	T0	COX7B	-1.41	8.86E-03	KIF2A	-1.07	3.77E-02
RVMSR	T0	MIR4504	2.23	8.87E-03	TRIM54	2.18	3.77E-02
RVMSR	T0	MIR4457	2.80	8.87E-03	LINC01312	3.34	3.78E-02
RVMSR	T0	LRRC75B	3.94	8.87E-03	SLC39A10	-1.21	3.78E-02
RVMSR	T0	LZTS1-AS1	4.97	8.87E-03	ADRB1	2.17	3.78E-02
RVMSR	T0	CYP8B1	3.92	8.88E-03	TCF24	2.69	3.78E-02
RVMSR	T0	IL31	3.92	8.89E-03	CEACAM16	1.55	3.79E-02
RVMSR	T0	LOC100505658	2.66	8.89E-03	MIR548AH	3.34	3.79E-02
RVMSR	T0	PON3	2.65	8.91E-03	CSNK1A1P1	2.09	3.79E-02
RVMSR	T0	DSN1	1.64	8.92E-03	ARIH2OS	1.52	3.79E-02
RVMSR	T0	ZNF788	3.17	8.92E-03	DUSP5P1	3.36	3.79E-02
RVMSR	T0	HPX	4.95	8.94E-03	LOC643923	2.94	3.79E-02
RVMSR	T0	MKKS	-1.59	8.94E-03	LOC100133920	2.38	3.79E-02
RVMSR	T0	MIR3123	3.94	8.95E-03	FRMPD1	2.71	3.79E-02

RVMSR	T0	RTN2	1.93	8.95E-03	CCDC38	4.22	3.79E-02
RVMSR	T0	SLC38A7	1.56	8.95E-03	SPC24	2.29	3.79E-02
RVMSR	T0	LOC101927855	2.06	8.95E-03	SNORA107	3.34	3.79E-02
RVMSR	T0	LOC105374389	3.17	8.96E-03	GSG1	2.02	3.79E-02
RVMSR	T0	EPO	4.95	8.96E-03	MT3	2.09	3.79E-02
RVMSR	T0	CRB2	3.91	8.96E-03	LOC100996455	1.79	3.79E-02
RVMSR	T0	ZNF578	2.44	8.96E-03	FAAP24	1.52	3.80E-02
RVMSR	T0	COX6C	-1.35	8.96E-03	LOC285889	4.21	3.80E-02
RVMSR	T0	RABGGTA	-2.78	8.97E-03	LINC01031	2.27	3.80E-02
RVMSR	T0	EXO5	1.81	8.97E-03	LOC440028	2.52	3.80E-02
RVMSR	T0	LOC101929512	3.46	9.04E-03	ABHD11-AS1	4.21	3.80E-02
RVMSR	T0	NCAN	2.36	9.08E-03	LCE2A	4.21	3.80E-02
RVMSR	T0	NOVA1	3.47	9.08E-03	LINC00644	4.21	3.80E-02
RVMSR	T0	KCNJ4	4.96	9.09E-03	OR7A5	2.17	3.81E-02
RVMSR	T0	MEGF11	3.93	9.14E-03	DRC1	2.03	3.81E-02
RVMSR	T0	GABARAPL3	2.66	9.14E-03	TNC	2.18	3.81E-02
RVMSR	T0	PEAR1	2.44	9.24E-03	LOC105375396	2.53	3.82E-02
RVMSR	T0	GGT8P	2.54	9.24E-03	GOLGA6L2	1.37	3.82E-02
RVMSR	T0	RAMP2	1.97	9.24E-03	OR5AP2	2.93	3.82E-02
RVMSR	T0	LINC01150	2.96	9.24E-03	NAPG	-1.47	3.82E-02
RVMSR	T0	HSFX2	2.05	9.24E-03	PGLYRP2	1.58	3.82E-02
RVMSR	T0	C4orf19	2.10	9.29E-03	LGSN	2.38	3.83E-02
RVMSR	T0	MID1	3.90	9.29E-03	LINC01495	2.52	3.83E-02
RVMSR	T0	BCAR3	2.65	9.29E-03	GATSL3	1.45	3.83E-02
RVMSR	T0	MAP7D2	2.54	9.30E-03	HOXD3	2.39	3.83E-02
RVMSR	T0	ULK4P3	2.79	9.31E-03	NOS1AP	2.08	3.83E-02
RVMSR	T0	ERVFRD-1	2.00	9.31E-03	KIF5A	4.24	3.83E-02
RVMSR	T0	ST7L	1.80	9.31E-03	VN1R4	2.93	3.83E-02
RVMSR	T0	SKA1	3.91	9.31E-03	SERPINF2	2.17	3.83E-02

RVMSR	T0	KCNQ5	2.65	9.32E-03	ZBTB26	1.43	3.83E-02
RVMSR	T0	KRTAP5-11	3.91	9.34E-03	AR	1.50	3.83E-02
RVMSR	T0	MOBP	4.93	9.37E-03	KCNJ5	2.51	3.83E-02
RVMSR	T0	ATAD3B	2.44	9.39E-03	MGAT3-AS1	2.70	3.83E-02
RVMSR	T0	KIF2C	2.27	9.40E-03	LOC105378183	3.33	3.84E-02
RVMSR	T0	FLJ13224	2.22	9.40E-03	LOC105372038	2.27	3.84E-02
RVMSR	T0	EFCAB11	2.66	9.40E-03	CDC73	-1.18	3.85E-02
RVMSR	T0	ADAM11	2.44	9.41E-03	GPC5	2.95	3.85E-02
RVMSR	T0	LINC01359	1.83	9.41E-03	TUBB4A	2.02	3.85E-02
RVMSR	T0	LOC102723376	4.94	9.41E-03	FAM120C	2.18	3.85E-02
RVMSR	T0	SLC5A1	4.94	9.41E-03	LINC00462	2.29	3.85E-02
RVMSR	T0	CNDP1	3.15	9.41E-03	FIGNL2	4.20	3.85E-02
RVMSR	T0	TMEM232	3.44	9.46E-03	SRRM3	2.17	3.85E-02
RVMSR	T0	RHOC	-1.39	9.47E-03	FOSL1	4.20	3.85E-02
RVMSR	T0	CTNNAL1	-1.76	9.49E-03	MIR520G	4.20	3.85E-02
RVMSR	T0	RBFOX1	2.93	9.52E-03	MIR1204	1.89	3.85E-02
RVMSR	T0	41883	2.64	9.58E-03	SOX21-AS1	2.27	3.85E-02
RVMSR	T0	DYNC1I1	3.89	9.58E-03	RNF219-AS1	4.20	3.85E-02
RVMSR	T0	LOC100131257	1.89	9.59E-03	LOC107985033	1.94	3.85E-02
RVMSR	T0	SVIP	-1.34	9.59E-03	ZNF474	3.32	3.85E-02
RVMSR	T0	TF	2.78	9.60E-03	OSBPL5	2.09	3.85E-02
RVMSR	T0	GAREM1	2.28	9.62E-03	LINC01363	3.33	3.85E-02
RVMSR	T0	OR6Y1	2.94	9.62E-03	MIR3910-1	3.32	3.85E-02
RVMSR	T0	LRRC74B	1.99	9.64E-03	LOC149373	4.20	3.85E-02
RVMSR	T0	PPP4R1-AS1	2.09	9.64E-03	RPL10L	-3.39	3.85E-02
RVMSR	T0	SSX8	1.79	9.65E-03	WFDC12	2.93	3.85E-02
RVMSR	T0	MIR587	3.45	9.65E-03	ABCA4	2.53	3.85E-02
RVMSR	T0	FAM83D	2.20	9.68E-03	SEMA3F	1.83	3.85E-02
RVMSR	T0	ZNF771	2.15	9.68E-03	NPPA	2.95	3.85E-02

RVMSR	T0	LOC102546228	4.94	9.69E-03	LINC00587	3.33	3.86E-02
RVMSR	T0	MAFG-AS1	3.88	9.71E-03	GPC3	2.69	3.86E-02
RVMSR	T0	FABP1	3.14	9.71E-03	LCMT1-AS2	1.74	3.87E-02
RVMSR	T0	CRYGD	2.95	9.71E-03	ZNF177	1.83	3.87E-02
RVMSR	T0	PROX2	2.15	9.73E-03	AP1S3	1.37	3.87E-02
RVMSR	T0	PRSS48	2.14	9.74E-03	MYCL	2.09	3.87E-02
RVMSR	T0	SAPCD2	1.79	9.74E-03	ANKS4B	3.33	3.87E-02
RVMSR	T0	LRP2BP	4.92	9.74E-03	ZNF750	3.33	3.87E-02
RVMSR	T0	LOC102723617	2.43	9.75E-03	LOC101929237	2.69	3.87E-02
RVMSR	T0	COL27A1	2.21	9.76E-03	DKFZp686K1684	2.92	3.88E-02
RVMSR	T0	DLGAP5	2.33	9.76E-03	ZNF702P	2.09	3.88E-02
RVMSR	T0	SLC8A1-AS1	3.89	9.76E-03	MECOM	2.17	3.88E-02
RVMSR	T0	OLFML3	3.44	9.78E-03	FEZF1	3.32	3.88E-02
RVMSR	T0	TCF15	4.93	9.80E-03	VIP	3.32	3.88E-02
RVMSR	T0	THY1	2.27	9.83E-03	EVI2A	-1.06	3.88E-02
RVMSR	T0	NRXN1	3.16	9.86E-03	TMEM132C	2.50	3.89E-02
RVMSR	T0	DOK6	3.15	9.86E-03	ATG7	-1.56	3.89E-02
RVMSR	T0	FAM124A	2.42	9.86E-03	DIO2	2.93	3.89E-02
RVMSR	T0	WNT8A	3.15	9.90E-03	A2ML1	2.17	3.89E-02
RVMSR	T0	FRMD6	2.94	9.94E-03	SNORA2B	1.38	3.89E-02
RVMSR	T0	NAALADL2-AS2	3.88	9.94E-03	KCNAB3	1.60	3.89E-02
RVMSR	T0	PTCD1	1.45	9.96E-03	ZNF806	2.26	3.89E-02
RVMSR	T0	NPPB	4.93	9.96E-03	NLGN4X	2.52	3.89E-02
RVMSR	T0	C4orf47	2.77	9.96E-03	FLG2	4.19	3.89E-02
RVMSR	T0	MIR548I3	1.99	9.96E-03	MIR4717	4.19	3.89E-02
RVMSR	T0	LINC00499	3.88	9.98E-03	LOC100996635	4.19	3.89E-02
RVMSR	T0	CBR3-AS1	2.43	9.99E-03	LOC101928708	4.19	3.89E-02
RVMSR	T0	ANKRD62	2.34	1.00E-02	VSTM4	2.38	3.89E-02
RVMSR	T0	PRSS58	2.20	1.00E-02	CEP76	2.91	3.89E-02

RVMSR	T0	NCKAP5L	1.74	1.00E-02	SNCAIP	4.19	3.89E-02
RVMSR	T0	LINC00639	3.88	1.00E-02	LOC101927020	4.19	3.89E-02
RVMSR	T0	TINAGL1	3.89	1.00E-02	LINC00460	4.19	3.89E-02
RVMSR	T0	SLC16A14	1.84	1.00E-02	NUTM2G	2.08	3.90E-02
RVMSR	T0	CASP14	2.52	1.00E-02	TXNL4B	1.41	3.90E-02
RVMSR	T0	HS6ST2-AS1	4.90	1.00E-02	LOC101926968	3.33	3.91E-02
RVMSR	T0	ASB16	1.88	1.00E-02	ZRANB3	1.73	3.92E-02
RVMSR	T0	PTRF	3.13	1.00E-02	LINC01553	2.01	3.92E-02
RVMSR	T0	LINC01585	2.20	1.00E-02	FAM96A	-1.09	3.92E-02
RVMSR	T0	RGPD4	2.21	1.00E-02	YPEL4	2.08	3.92E-02
RVMSR	T0	UBE2C	2.04	1.01E-02	FAM172BP	1.59	3.92E-02
RVMSR	T0	NEFH	1.92	1.01E-02	CD81-AS1	2.68	3.93E-02
RVMSR	T0	LOC101927759	2.95	1.01E-02	LTF	1.66	3.94E-02
RVMSR	T0	LINC00621	3.43	1.01E-02	RNASEH1-AS1	1.33	3.94E-02
RVMSR	T0	MYH1	2.94	1.01E-02	LOC105370489	2.17	3.94E-02
RVMSR	T0	LGALS17A	2.94	1.01E-02	CCDC166	2.68	3.94E-02
RVMSR	T0	MRPL47	-1.87	1.01E-02	SLC10A6	2.37	3.94E-02
RVMSR	T0	OR11H4	2.33	1.01E-02	FN1	2.51	3.94E-02
RVMSR	T0	ENPP1	1.46	1.01E-02	RAB39A	2.94	3.94E-02
RVMSR	T0	RCCD1	1.58	1.01E-02	LRRC37A11P	2.26	3.95E-02
RVMSR	T0	ADGRL1	1.73	1.02E-02	MIR548X2	2.69	3.95E-02
RVMSR	T0	OR2D3	3.87	1.02E-02	WDR72	4.18	3.96E-02
RVMSR	T0	COL8A1	2.77	1.02E-02	LOC341056	1.94	3.96E-02
RVMSR	T0	LOC100506085	2.42	1.02E-02	LOC101927018	2.26	3.96E-02
RVMSR	T0	PSMD3	1.81	1.02E-02	PLA2G12B	2.26	3.96E-02
RVMSR	T0	CPS1	3.88	1.02E-02	GCKR	4.18	3.96E-02
RVMSR	T0	OVOL2	3.87	1.02E-02	RGMA	2.69	3.96E-02
RVMSR	T0	CCL19	4.93	1.02E-02	CLVS2	2.69	3.97E-02
RVMSR	T0	MIR4302	3.13	1.02E-02	TMX1	-1.33	3.97E-02

RVMSR	T0	LOC105369332	2.34	1.02E-02	WIF1	1.93	3.97E-02
RVMSR	T0	ATP1B2	1.99	1.02E-02	BAHCC1	4.18	3.97E-02
RVMSR	T0	MIR3200	4.93	1.02E-02	OR4K1	4.18	3.97E-02
RVMSR	T0	CTSG	3.15	1.02E-02	FANCD2	1.34	3.97E-02
RVMSR	T0	POSTN	3.87	1.02E-02	WDR93	2.37	3.97E-02
RVMSR	T0	CARMN	3.13	1.02E-02	FBXW7-AS1	2.26	3.97E-02
RVMSR	T0	HTR3A	4.91	1.02E-02	RNASE1	2.26	3.97E-02
RVMSR	T0	ALPPL2	2.93	1.03E-02	ITLN1	1.96	3.97E-02
RVMSR	T0	LCA5L	1.98	1.03E-02	C14orf132	2.92	3.97E-02
RVMSR	T0	DDX53	3.12	1.03E-02	CYP2A7	1.94	3.98E-02
RVMSR	T0	SAP30L-AS1	3.14	1.03E-02	ZDHHC15	2.25	3.98E-02
RVMSR	T0	PSCA	4.89	1.03E-02	C20orf144	3.32	3.98E-02
RVMSR	T0	LOC642643	2.75	1.04E-02	C15orf48	1.53	3.98E-02
RVMSR	T0	LOC101928168	2.25	1.04E-02	PAPPA	2.36	3.98E-02
RVMSR	T0	STON1-GTF2A1L	2.63	1.04E-02	C1orf168	2.93	3.98E-02
RVMSR	T0	TNN	2.75	1.04E-02	NDUFA6	-1.06	3.98E-02
RVMSR	T0	AVIL	1.91	1.04E-02	S1PR5	1.11	4.00E-02
RVMSR	T0	LOC100288181	2.32	1.04E-02	OPRK1	3.31	4.00E-02
RVMSR	T0	CLDN10	1.97	1.04E-02	TMC3-AS1	2.91	4.00E-02
RVMSR	T0	FAM106B	2.52	1.04E-02	SCARNA10	-1.76	4.00E-02
RVMSR	T0	SPACA4	3.42	1.04E-02	MIR92B	2.15	4.00E-02
RVMSR	T0	LINC00635	4.90	1.04E-02	LOC729461	1.94	4.00E-02
RVMSR	T0	LOC401177	3.14	1.04E-02	LOC105369187	2.37	4.00E-02
RVMSR	T0	ASIC5	4.90	1.04E-02	PRKCE	1.37	4.00E-02
RVMSR	T0	RFWD3	1.72	1.04E-02	BICDL2	2.17	4.01E-02
RVMSR	T0	DLX2-AS1	3.42	1.04E-02	LOC729652	2.08	4.01E-02
RVMSR	T0	MAPK8IP2	1.81	1.04E-02	ANKRD60	3.32	4.01E-02
RVMSR	T0	LOC728752	2.41	1.05E-02	LOC101928254	2.91	4.01E-02
RVMSR	T0	SYTL4	2.19	1.05E-02	C1orf186	1.59	4.01E-02

RVMSR	T0	TLCD2	1.84	1.05E-02	ARHGEF9-IT1	2.50	4.01E-02
RVMSR	T0	LOC105375401	3.86	1.05E-02	CGB5	2.92	4.01E-02
RVMSR	T0	PAX4	2.76	1.05E-02	RPL22L1	-1.31	4.01E-02
RVMSR	T0	SCGB1A1	3.41	1.05E-02	CDS1	2.50	4.01E-02
RVMSR	T0	CNGB3	2.92	1.05E-02	MIR633	4.17	4.01E-02
RVMSR	T0	NEFM	3.41	1.05E-02	LINC01107	2.35	4.01E-02
RVMSR	T0	GLTSCR1	1.87	1.05E-02	PAQR5	2.90	4.01E-02
RVMSR	T0	MTUS2	3.86	1.05E-02	APOBEC3H	1.74	4.02E-02
RVMSR	T0	LAMB1	4.89	1.05E-02	ACRBP	-1.06	4.02E-02
RVMSR	T0	SLC2A7	3.87	1.05E-02	APOM	2.25	4.02E-02
RVMSR	T0	HEXA-AS1	2.25	1.06E-02	FAM174B	2.91	4.02E-02
RVMSR	T0	CSN3	3.40	1.06E-02	MIR486-2	4.17	4.02E-02
RVMSR	T0	RND2	2.25	1.06E-02	DLX3	2.16	4.02E-02
RVMSR	T0	NEURL3	3.87	1.06E-02	RFPL2	2.25	4.02E-02
RVMSR	T0	ZC2HC1C	3.85	1.06E-02	ALX4	4.16	4.02E-02
RVMSR	T0	SETD7	2.74	1.07E-02	OR11L1	2.16	4.03E-02
RVMSR	T0	LOC389705	1.90	1.07E-02	CPLX2	2.90	4.03E-02
RVMSR	T0	FZD10-AS1	4.87	1.07E-02	RAD51D	1.82	4.03E-02
RVMSR	T0	LOC102724571	2.32	1.07E-02	OR8G2	3.32	4.04E-02
RVMSR	T0	RTP1	3.86	1.07E-02	TPST1	1.73	4.04E-02
RVMSR	T0	LSM5	-1.60	1.07E-02	ZFP1	1.82	4.04E-02
RVMSR	T0	LOC101060524	2.50	1.07E-02	ARHGAP31-AS1	3.31	4.04E-02
RVMSR	T0	KCNMA1-AS1	3.85	1.07E-02	SLC6A7	2.91	4.04E-02
RVMSR	T0	MIR548Y	3.86	1.07E-02	SEMA6B	1.82	4.04E-02
RVMSR	T0	LOC100129940	2.51	1.07E-02	LOC152225	2.37	4.04E-02
RVMSR	T0	LOC101926892	2.74	1.07E-02	SNRPD2P2	2.91	4.04E-02
RVMSR	T0	GH2	3.87	1.07E-02	GGT6	2.25	4.04E-02
RVMSR	T0	PARP3	1.66	1.07E-02	LOC101930010	2.91	4.04E-02
RVMSR	T0	SLC25A21	4.88	1.07E-02	CACNG8	1.51	4.04E-02

RVMSR	T0	MUC22	2.42	1.08E-02	KCNAB1	1.88	4.04E-02
RVMSR	T0	ZNF823	1.90	1.08E-02	SPEM1	2.25	4.04E-02
RVMSR	T0	PPY	3.40	1.08E-02	AK5	-2.75	4.05E-02
RVMSR	T0	MBD3L1	3.86	1.08E-02	FGF13-AS1	2.91	4.05E-02
RVMSR	T0	LINC01159	2.92	1.08E-02	TRIM58	-1.08	4.05E-02
RVMSR	T0	PRR23A	2.74	1.08E-02	GAL3ST1	2.90	4.05E-02
RVMSR	T0	CXCL13	2.52	1.08E-02	MIR4280	3.31	4.05E-02
RVMSR	T0	40238	2.50	1.08E-02	DSTYK	1.13	4.05E-02
RVMSR	T0	IFNL1	1.87	1.08E-02	UBXN7-AS1	1.41	4.06E-02
RVMSR	T0	CTNND2	4.89	1.08E-02	AVPR1A	2.36	4.06E-02
RVMSR	T0	MIR3713	4.86	1.08E-02	PPM1E	2.06	4.06E-02
RVMSR	T0	CALN1	2.32	1.08E-02	GPR119	2.66	4.06E-02
RVMSR	T0	SYCN	2.41	1.08E-02	SFTA1P	3.30	4.06E-02
RVMSR	T0	SOGA3	1.69	1.08E-02	LOC102467217	4.16	4.06E-02
RVMSR	T0	LOC101926941	3.40	1.08E-02	MAN1B1-AS1	1.58	4.06E-02
RVMSR	T0	ACSBG2	2.18	1.09E-02	KCNK5	2.50	4.06E-02
RVMSR	T0	ULBP3	3.11	1.09E-02	STAB2	2.14	4.06E-02
RVMSR	T0	CTSV	1.93	1.09E-02	LOC105376633	2.91	4.07E-02
RVMSR	T0	FSTL5	4.87	1.09E-02	C19orf25	-1.29	4.07E-02
RVMSR	T0	CSN1S2AP	3.86	1.09E-02	KRTAP10-10	4.15	4.07E-02
RVMSR	T0	MIR5687	2.60	1.10E-02	C1orf100	2.35	4.07E-02
RVMSR	T0	C1QL4	3.40	1.10E-02	C4orf22	4.15	4.07E-02
RVMSR	T0	MIR548D2	2.24	1.10E-02	MTRNR2L10	-1.06	4.07E-02
RVMSR	T0	KRTAP7-1	2.73	1.10E-02	ZNF295-AS1	4.15	4.08E-02
RVMSR	T0	CTRC	2.92	1.10E-02	CACNB2	1.59	4.08E-02
RVMSR	T0	SMG7	-1.63	1.10E-02	CDRT7	3.30	4.08E-02
RVMSR	T0	ETV2	1.97	1.10E-02	GPR84	1.88	4.08E-02
RVMSR	T0	LOC101927062	2.24	1.10E-02	CHRNA5	2.15	4.08E-02
RVMSR	T0	C15orf65	2.32	1.10E-02	ANLN	1.73	4.08E-02

RVMSR	T0	GTF2IP23	2.50	1.10E-02	C1QL1	1.25	4.08E-02
RVMSR	T0	LRTM1	2.91	1.10E-02	BCL6B	2.91	4.08E-02
RVMSR	T0	LOC101927278	2.50	1.10E-02	DOCK7	1.87	4.08E-02
RVMSR	T0	LOC105372977	3.83	1.10E-02	ARHGAP24	1.48	4.08E-02
RVMSR	T0	MED14OS	2.49	1.10E-02	IRX3	3.31	4.09E-02
RVMSR	T0	ZNF833P	2.50	1.11E-02	SNCG	3.31	4.09E-02
RVMSR	T0	KRT19P2	2.50	1.11E-02	PCNP	-1.08	4.10E-02
RVMSR	T0	MAGEL2	3.84	1.11E-02	LOC105375429	1.93	4.10E-02
RVMSR	T0	FLJ36777	2.18	1.12E-02	LOC101930085	1.76	4.10E-02
RVMSR	T0	HTN3	2.91	1.12E-02	HOXA5	3.32	4.10E-02
RVMSR	T0	HBEGF	1.72	1.12E-02	KCNK15-AS1	1.99	4.10E-02
RVMSR	T0	BVES	2.49	1.13E-02	REEP1	3.30	4.10E-02
RVMSR	T0	LOC90784	2.75	1.13E-02	SLC35G4	1.45	4.10E-02
RVMSR	T0	ZFP90	1.31	1.13E-02	OR3A1	3.31	4.10E-02
RVMSR	T0	PLCE1	2.76	1.13E-02	LIPC-AS1	2.89	4.11E-02
RVMSR	T0	CFC1B	3.11	1.13E-02	RCN3	1.78	4.11E-02
RVMSR	T0	KCNH6	2.74	1.13E-02	GPR143	2.35	4.11E-02
RVMSR	T0	SERHL2	2.91	1.13E-02	LINC00562	2.25	4.11E-02
RVMSR	T0	FILIP1L	1.85	1.13E-02	LOC102723493	2.35	4.11E-02
RVMSR	T0	NTSR2	3.83	1.13E-02	LINC01262	3.30	4.11E-02
RVMSR	T0	COL5A3	1.96	1.13E-02	LOC101929002	2.49	4.11E-02
RVMSR	T0	LOC285696	2.90	1.13E-02	GS1-259H13.2	2.36	4.11E-02
RVMSR	T0	MTOR-AS1	2.17	1.13E-02	MIR8088	2.49	4.11E-02
RVMSR	T0	TRIM9	3.84	1.13E-02	LOC339803	1.31	4.11E-02
RVMSR	T0	NOX4	2.90	1.14E-02	SCN11A	2.67	4.12E-02
RVMSR	T0	EMP2	1.76	1.14E-02	LINC00502	2.91	4.12E-02
RVMSR	T0	AK7	2.39	1.14E-02	SHANK2	2.67	4.12E-02
RVMSR	T0	YY2	1.65	1.14E-02	TUSC3	4.14	4.12E-02
RVMSR	T0	ADPRH	2.31	1.14E-02	LNX1	4.14	4.12E-02

RVMSR	T0	TMIGD1	3.39	1.14E-02	CORT	1.40	4.13E-02
RVMSR	T0	MIR4765	3.83	1.14E-02	LOC101927972	2.66	4.13E-02
RVMSR	T0	RNY4	4.85	1.14E-02	ZDHHC8P1	2.91	4.13E-02
RVMSR	T0	PDZD2	2.61	1.15E-02	MIR548AA1	4.14	4.14E-02
RVMSR	T0	AZIN2	2.60	1.15E-02	SMC5	-1.09	4.14E-02
RVMSR	T0	BNC1	3.10	1.15E-02	PLA2G2D	2.90	4.14E-02
RVMSR	T0	LOC283440	3.84	1.15E-02	SPIN1	1.33	4.15E-02
RVMSR	T0	LINC01152	2.90	1.16E-02	LOC105748977	1.98	4.15E-02
RVMSR	T0	TMEM5-AS1	2.05	1.16E-02	LOC105379194	2.15	4.15E-02
RVMSR	T0	PTPRO	3.83	1.16E-02	IRGC	2.06	4.15E-02
RVMSR	T0	RABL2A	2.01	1.16E-02	SMC1B	2.48	4.15E-02
RVMSR	T0	QPCTL	1.48	1.16E-02	ZNF668	1.33	4.15E-02
RVMSR	T0	BCL2A1	-1.35	1.16E-02	ZNF618	1.81	4.15E-02
RVMSR	T0	KRT40	2.74	1.16E-02	LOC101928710	2.24	4.15E-02
RVMSR	T0	LOC105371433	1.50	1.16E-02	SPATA22	2.14	4.17E-02
RVMSR	T0	SPATA3	2.59	1.16E-02	LOC100505666	2.89	4.17E-02
RVMSR	T0	CRNDE	3.11	1.16E-02	RBM34	-1.06	4.17E-02
RVMSR	T0	PLAC4	2.60	1.16E-02	ZNF770	-1.27	4.17E-02
RVMSR	T0	TGM1	2.24	1.16E-02	AFDN-AS1	2.66	4.17E-02
RVMSR	T0	UGT2B15	3.82	1.16E-02	OR1L4	4.17	4.18E-02
RVMSR	T0	SULT2B1	2.23	1.16E-02	MIR548V	2.90	4.19E-02
RVMSR	T0	SPINT1	1.97	1.16E-02	ZIM2	2.49	4.19E-02
RVMSR	T0	HOGA1	3.83	1.16E-02	LINC00343	2.66	4.19E-02
RVMSR	T0	VCX	3.10	1.16E-02	CYP4F22	2.16	4.21E-02
RVMSR	T0	LOC101928404	4.83	1.17E-02	FAM72B	4.13	4.21E-02
RVMSR	T0	RAB17	3.09	1.17E-02	ARL14EP	-1.08	4.21E-02
RVMSR	T0	RAD51	2.39	1.17E-02	KRT24	2.89	4.21E-02
RVMSR	T0	CBX3P2	2.01	1.17E-02	TRIM31-AS1	2.65	4.21E-02
RVMSR	T0	LINC00574	3.38	1.17E-02	SMKR1	2.15	4.21E-02

RVMSR	T0	LINC00364	2.60	1.17E-02	RGS1	3.29	4.21E-02
RVMSR	T0	CNN1	2.16	1.17E-02	LINC01554	2.48	4.22E-02
RVMSR	T0	TM4SF18	3.83	1.17E-02	LINC00566	2.23	4.22E-02
RVMSR	T0	LINC01301	2.38	1.17E-02	VAT1L	2.50	4.22E-02
RVMSR	T0	GDAP1L1	2.30	1.17E-02	KTN1-AS1	2.47	4.23E-02
RVMSR	T0	FOLR1	2.73	1.17E-02	ZFAT-AS1	2.49	4.23E-02
RVMSR	T0	MIR644A	2.01	1.17E-02	NT5C1A	2.91	4.23E-02
RVMSR	T0	CCL26	3.10	1.18E-02	KRT8P41	2.88	4.23E-02
RVMSR	T0	AP1B1P1	2.88	1.18E-02	TNFSF18	2.89	4.24E-02
RVMSR	T0	ZNF444	1.55	1.18E-02	KLHL10	1.67	4.24E-02
RVMSR	T0	MIR320D2	4.85	1.18E-02	P2RX7	1.15	4.24E-02
RVMSR	T0	PLEKHG1	1.92	1.18E-02	PCLO	2.88	4.24E-02
RVMSR	T0	PTH	2.60	1.18E-02	CACNA2D3	2.49	4.25E-02
RVMSR	T0	LOC101928514	2.89	1.18E-02	LOC101929019	4.16	4.25E-02
RVMSR	T0	SLC7A3	3.80	1.19E-02	ZSCAN22	1.30	4.25E-02
RVMSR	T0	TP53TG5	2.15	1.19E-02	MIR8062	2.06	4.25E-02
RVMSR	T0	POTEB2	2.72	1.19E-02	PRDX3	-1.11	4.25E-02
RVMSR	T0	POTEB3	2.72	1.19E-02	LINC01088	2.23	4.25E-02
RVMSR	T0	CDH12	3.83	1.20E-02	KANK1	1.77	4.25E-02
RVMSR	T0	LINC01483	2.59	1.20E-02	MIR4511	1.99	4.25E-02
RVMSR	T0	SPINK9	4.82	1.20E-02	OR51B2	2.88	4.25E-02
RVMSR	T0	XRCC4	-2.37	1.20E-02	SERPINF1	1.52	4.26E-02
RVMSR	T0	SSX3	3.08	1.20E-02	BMS1P5	1.61	4.26E-02
RVMSR	T0	OPA1-AS1	3.09	1.20E-02	LINC00483	2.04	4.26E-02
RVMSR	T0	ELAC1	2.23	1.20E-02	MMP27	3.29	4.26E-02
RVMSR	T0	C14orf37	4.84	1.20E-02	FAM225B	4.12	4.26E-02
RVMSR	T0	PGA3	2.58	1.20E-02	LOC100287792	1.40	4.26E-02
RVMSR	T0	LOC100134317	3.82	1.20E-02	EBAG9	-1.47	4.26E-02
RVMSR	T0	PPEF1-AS1	2.71	1.20E-02	MELK	4.12	4.26E-02

RVMSR	T0	LINC01523	3.81	1.20E-02	KIAA1210	3.27	4.26E-02
RVMSR	T0	NKX2-6	3.37	1.21E-02	NOTUM	1.80	4.26E-02
RVMSR	T0	FFAR4	3.35	1.21E-02	PHKA1	2.89	4.27E-02
RVMSR	T0	MGAT5B	2.71	1.21E-02	CYP3A43	2.66	4.27E-02
RVMSR	T0	SGCD	2.88	1.21E-02	PCED1A	1.24	4.28E-02
RVMSR	T0	CDX4	3.37	1.21E-02	ASPA	2.23	4.28E-02
RVMSR	T0	WFDC1	2.89	1.21E-02	LOC151174	1.97	4.28E-02
RVMSR	T0	EMX2OS	3.07	1.22E-02	SRSF3	-1.04	4.28E-02
RVMSR	T0	PTH1R	3.83	1.22E-02	SPINT3	1.98	4.28E-02
RVMSR	T0	MKLN1-AS	2.22	1.23E-02	NIPAL4	2.23	4.28E-02
RVMSR	T0	PTPRB	3.09	1.23E-02	CHP2	3.30	4.28E-02
RVMSR	T0	CLEC2A	2.47	1.23E-02	PSMD5-AS1	-1.08	4.29E-02
RVMSR	T0	GLYCAM1	2.89	1.23E-02	FMO4	2.23	4.29E-02
RVMSR	T0	LINC01551	2.72	1.23E-02	LCE3D	2.65	4.30E-02
RVMSR	T0	LINC01622	2.86	1.23E-02	OR10Q1	2.35	4.30E-02
RVMSR	T0	MACROD1	4.83	1.23E-02	LOC100506691	2.64	4.30E-02
RVMSR	T0	ELFN1	3.09	1.23E-02	LOC100507537	2.05	4.30E-02
RVMSR	T0	LOC100507053	3.36	1.23E-02	GABRA6	3.29	4.31E-02
RVMSR	T0	PKD1L3	2.71	1.23E-02	S100A7A	2.64	4.31E-02
RVMSR	T0	LOC102724009	1.81	1.23E-02	LOC101928418	4.14	4.31E-02
RVMSR	T0	KRTAP1-3	4.81	1.23E-02	LOC101929151	2.88	4.32E-02
RVMSR	T0	PCOLCE	2.04	1.23E-02	AP5M1	-1.48	4.32E-02
RVMSR	T0	TBPL1	-1.48	1.23E-02	GOLGA2P9	4.14	4.32E-02
RVMSR	T0	CDH7	4.80	1.24E-02	MST1R	2.64	4.32E-02
RVMSR	T0	LOC102546298	2.88	1.24E-02	DPPA3	3.26	4.32E-02
RVMSR	T0	CXorf40B	-1.87	1.24E-02	TAF1A-AS1	2.06	4.33E-02
RVMSR	T0	PYDC1	3.08	1.24E-02	LYVE1	2.47	4.33E-02
RVMSR	T0	DNAH8	2.71	1.24E-02	LOC100240734	2.05	4.33E-02
RVMSR	T0	ABCC5	1.60	1.24E-02	ZNF559-ZNF177	1.71	4.33E-02

RVMSR	T0	PROSER2-AS1	2.71	1.24E-02	OR52R1	4.11	4.33E-02
RVMSR	T0	ABRA	2.72	1.24E-02	LINC00900	3.26	4.33E-02
RVMSR	T0	CHMP4C	2.47	1.24E-02	APOL5	2.33	4.34E-02
RVMSR	T0	MCEMP1	-1.29	1.24E-02	RSPO3	4.10	4.34E-02
RVMSR	T0	USH2A	3.80	1.25E-02	COG7	1.52	4.34E-02
RVMSR	T0	LYPLA2P2	3.08	1.25E-02	LRRC71	3.27	4.35E-02
RVMSR	T0	MIR548AW	2.88	1.25E-02	LHFPL4	1.55	4.35E-02
RVMSR	T0	SAXO1	2.37	1.25E-02	KRTAP5-5	2.63	4.35E-02
RVMSR	T0	TUB	3.81	1.25E-02	COPS8	-1.22	4.36E-02
RVMSR	T0	SCARNA12	-2.30	1.25E-02	TAS2R39	2.88	4.36E-02
RVMSR	T0	SLC25A21-AS1	2.58	1.26E-02	RAX2	2.34	4.36E-02
RVMSR	T0	AZGP1	3.79	1.26E-02	OIP5	1.98	4.36E-02
RVMSR	T0	GRB7	3.08	1.26E-02	LOC102724908	2.23	4.36E-02
RVMSR	T0	FKBP14	1.83	1.26E-02	KIAA1656	2.34	4.36E-02
RVMSR	T0	LUADT1	2.71	1.26E-02	MIR4481	1.63	4.37E-02
RVMSR	T0	TSC22D1-AS1	2.22	1.26E-02	CCL22	1.98	4.37E-02
RVMSR	T0	PRR7-AS1	3.80	1.26E-02	LINC01063	1.98	4.37E-02
RVMSR	T0	RAB11FIP2	-1.57	1.26E-02	ROR1	1.71	4.37E-02
RVMSR	T0	ITLN2	2.22	1.26E-02	TTLL6	1.90	4.37E-02
RVMSR	T0	FAT4	4.83	1.26E-02	FAM71E1	2.47	4.38E-02
RVMSR	T0	MIR146B	1.47	1.26E-02	B3GNT3	1.44	4.38E-02
RVMSR	T0	TSL	4.81	1.26E-02	OR10T2	3.27	4.38E-02
RVMSR	T0	ACVR1B	1.65	1.26E-02	EEF1B2	-1.04	4.39E-02
RVMSR	T0	KBTBD6	1.71	1.26E-02	SCARNA1	1.44	4.40E-02
RVMSR	T0	PAK3	2.70	1.27E-02	LOC100289561	1.14	4.40E-02
RVMSR	T0	ANGPTL4	1.95	1.27E-02	C14orf178	2.46	4.40E-02
RVMSR	T0	TMEM119	2.57	1.27E-02	LCN1	2.88	4.41E-02
RVMSR	T0	MIR1289-1	2.70	1.28E-02	KCNN1	2.34	4.41E-02
RVMSR	T0	LHX5	2.59	1.28E-02	SLC4A9	1.91	4.41E-02

RVMSR	T0	NLGN1	3.80	1.28E-02	PCDHB6	4.09	4.41E-02
RVMSR	T0	LOC105374972	3.35	1.28E-02	LOC646241	4.09	4.41E-02
RVMSR	T0	HOXB5	3.07	1.28E-02	ENGASE	1.47	4.41E-02
RVMSR	T0	CLCA2	4.82	1.28E-02	HOXA4	4.12	4.41E-02
RVMSR	T0	BARX2	4.82	1.28E-02	THSD4-AS2	3.27	4.41E-02
RVMSR	T0	C12orf77	2.57	1.28E-02	INSL3	1.99	4.41E-02
RVMSR	T0	PLA1A	2.88	1.28E-02	ZNF597	1.58	4.41E-02
RVMSR	T0	KIAA2022	2.58	1.28E-02	DNAJC27-AS1	1.64	4.41E-02
RVMSR	T0	CPLX4	3.78	1.28E-02	SNAR-G1	1.74	4.41E-02
RVMSR	T0	FBLL1	2.28	1.28E-02	SNORA35	2.87	4.41E-02
RVMSR	T0	LCT	2.10	1.29E-02	INSRR	3.28	4.42E-02
RVMSR	T0	LOC101927267	2.14	1.29E-02	SPNS1	-1.46	4.43E-02
RVMSR	T0	SYNPO2L	2.20	1.29E-02	RASGRP3	1.35	4.44E-02
RVMSR	T0	LOC102724849	2.08	1.29E-02	LOC100128993	1.90	4.44E-02
RVMSR	T0	SAA3P	2.20	1.29E-02	LIPM	2.87	4.44E-02
RVMSR	T0	GJD4	2.29	1.29E-02	LYPD6	2.34	4.44E-02
RVMSR	T0	SCOC	-2.21	1.29E-02	KIAA1549	2.22	4.44E-02
RVMSR	T0	L3MBTL4	4.78	1.29E-02	CLDN4	2.33	4.44E-02
RVMSR	T0	AKAP4	4.79	1.29E-02	FAM74A7	2.63	4.44E-02
RVMSR	T0	ADGRF3	2.29	1.29E-02	LYG2	2.22	4.44E-02
RVMSR	T0	COL23A1	3.07	1.29E-02	ZNF433	1.56	4.44E-02
RVMSR	T0	EPN2-IT1	3.35	1.29E-02	MN1	2.87	4.44E-02
RVMSR	T0	MROH7	3.34	1.29E-02	AS3MT	1.37	4.44E-02
RVMSR	T0	NPY5R	3.78	1.29E-02	GLIPR1L2	2.23	4.44E-02
RVMSR	T0	KLK5	3.06	1.30E-02	NPR1	1.42	4.44E-02
RVMSR	T0	LINC01320	3.34	1.30E-02	LINC01584	3.28	4.44E-02
RVMSR	T0	FSD1	2.86	1.30E-02	LRRC3B	2.34	4.45E-02
RVMSR	T0	SEMA3E	2.85	1.30E-02	PGPEP1	1.08	4.45E-02
RVMSR	T0	KLHDC7A	2.70	1.30E-02	MIR606	2.64	4.45E-02

RVMSR	T0	MIR5689HG	2.08	1.31E-02	DRC3	2.04	4.45E-02
RVMSR	T0	LOC100507437	2.58	1.31E-02	TEX264	-1.11	4.45E-02
RVMSR	T0	MIR4802	4.79	1.31E-02	CDKN2A	2.32	4.45E-02
RVMSR	T0	LRRC7	3.06	1.31E-02	GRIK1	3.26	4.45E-02
RVMSR	T0	GDF5	3.05	1.31E-02	PTTG3P	2.34	4.45E-02
RVMSR	T0	OTX2-AS1	2.46	1.31E-02	AQP7P1	2.04	4.45E-02
RVMSR	T0	LOC646029	2.57	1.31E-02	CRYBB2	2.88	4.46E-02
RVMSR	T0	PAX8	3.06	1.32E-02	BEST2	2.13	4.46E-02
RVMSR	T0	POU5F1P3	3.06	1.32E-02	NAALADL2-AS3	2.87	4.46E-02
RVMSR	T0	TSPAN6	2.46	1.32E-02	PRKG1	3.25	4.46E-02
RVMSR	T0	C14orf79	3.05	1.32E-02	GPR50-AS1	2.86	4.46E-02
RVMSR	T0	FHDC1	2.85	1.32E-02	TMEFF2	2.61	4.46E-02
RVMSR	T0	F13B	3.06	1.32E-02	LHX2	3.26	4.46E-02
RVMSR	T0	SNORD115-48	4.80	1.32E-02	LOC100506125	1.46	4.46E-02
RVMSR	T0	LINC00301	3.32	1.32E-02	DNAJC5G	4.08	4.46E-02
RVMSR	T0	FAM71D	3.78	1.32E-02	LOC101929504	4.11	4.46E-02
RVMSR	T0	ANGPT2	2.36	1.32E-02	VRK1	-1.36	4.46E-02
RVMSR	T0	FLJ22763	2.27	1.32E-02	LOC100505515	2.85	4.46E-02
RVMSR	T0	PHLDA3	3.06	1.32E-02	EMB	-1.03	4.46E-02
RVMSR	T0	WWC2-AS1	2.03	1.33E-02	ZNF674-AS1	1.41	4.46E-02
RVMSR	T0	KU-MEL-3	3.05	1.33E-02	SH2D7	2.33	4.46E-02
RVMSR	T0	FAM25A	2.20	1.33E-02	MPP5	1.44	4.47E-02
RVMSR	T0	GABRB3	4.78	1.33E-02	GRP	2.63	4.47E-02
RVMSR	T0	GOLGA8G	1.56	1.33E-02	C1orf105	2.45	4.47E-02
RVMSR	T0	PARTICL	3.05	1.33E-02	MIR367	2.31	4.47E-02
RVMSR	T0	SSTR5-AS1	3.34	1.33E-02	PROK1	2.63	4.47E-02
RVMSR	T0	GXYLT1P3	3.06	1.34E-02	CRNKL1	-1.09	4.47E-02
RVMSR	T0	LOC105373609	2.86	1.34E-02	GSTTP1	2.23	4.47E-02
RVMSR	T0	LGALS2	-1.27	1.34E-02	TSPAN16	1.50	4.47E-02

RVMSR	T0	ERVV-2	2.13	1.34E-02	VN1R2	2.46	4.48E-02
RVMSR	T0	COLCA1	3.06	1.34E-02	ANKRD61	1.84	4.48E-02
RVMSR	T0	C5orf17	4.78	1.34E-02	SLC20A1	-1.39	4.48E-02
RVMSR	T0	SPANXN1	2.56	1.34E-02	RAP1GAP	-1.95	4.48E-02
RVMSR	T0	SCNN1G	3.05	1.34E-02	LOC100130691	2.13	4.48E-02
RVMSR	T0	TMA7	-1.27	1.34E-02	MCMDC2	2.12	4.49E-02
RVMSR	T0	NTRK3	3.34	1.34E-02	NAA38	-1.04	4.49E-02
RVMSR	T0	KRT81	2.13	1.34E-02	FGF1	3.25	4.51E-02
RVMSR	T0	ARHGAP23	2.20	1.34E-02	MIR3158-2	1.80	4.51E-02
RVMSR	T0	MIR4322	2.36	1.34E-02	CRYGC	2.62	4.51E-02
RVMSR	T0	EPHX4	1.47	1.36E-02	TCP10L	2.32	4.51E-02
RVMSR	T0	MAGI2	2.44	1.37E-02	PHYHD1	1.97	4.51E-02
RVMSR	T0	DEPDC4	2.27	1.37E-02	SPON1	2.04	4.51E-02
RVMSR	T0	ENO1-AS1	1.89	1.37E-02	HID1	2.63	4.51E-02
RVMSR	T0	ISM1	4.76	1.37E-02	UBQLNL	2.87	4.51E-02
RVMSR	T0	DMRT3	1.92	1.38E-02	ISYNA1	3.25	4.51E-02
RVMSR	T0	LINC01398	2.69	1.38E-02	LINC01291	2.86	4.51E-02
RVMSR	T0	ITGB4	2.07	1.38E-02	USP16	-1.05	4.52E-02
RVMSR	T0	AACSP1	3.33	1.38E-02	ZNF205	1.53	4.52E-02
RVMSR	T0	FAM183CP	4.78	1.38E-02	SCN4A	3.28	4.52E-02
RVMSR	T0	ZNF436	2.03	1.38E-02	PGLYRP3	4.10	4.52E-02
RVMSR	T0	C4orf26	2.20	1.38E-02	MIR3681HG	4.07	4.52E-02
RVMSR	T0	LOC100506368	1.97	1.38E-02	LOC286238	4.07	4.52E-02
RVMSR	T0	ACKR1	1.90	1.38E-02	LINC01017	4.07	4.52E-02
RVMSR	T0	LOC105376306	3.04	1.38E-02	ABCC2	2.04	4.52E-02
RVMSR	T0	DSG1	3.75	1.38E-02	ODF3L1	4.10	4.52E-02
RVMSR	T0	TSSK6	1.93	1.39E-02	LOC101927798	4.10	4.52E-02
RVMSR	T0	MYH4	3.33	1.39E-02	LUZP2	4.10	4.52E-02
RVMSR	T0	CNNM1	3.31	1.39E-02	LINC00548	4.10	4.52E-02

RVMSR	T0	MIR653	4.77	1.39E-02	CNTN2	2.85	4.52E-02
RVMSR	T0	GAS8-AS1	1.78	1.39E-02	LOC101928269	2.85	4.52E-02
RVMSR	T0	SH3GL2	2.35	1.39E-02	RAB23	1.91	4.53E-02
RVMSR	T0	GRAMD3	1.92	1.40E-02	EDA	2.46	4.53E-02
RVMSR	T0	ADCY2	4.75	1.40E-02	NTM-IT	2.45	4.54E-02
RVMSR	T0	CYGB	1.97	1.40E-02	GOLGA8CP	2.03	4.54E-02
RVMSR	T0	GABRP	3.05	1.40E-02	NPAP1	2.45	4.54E-02
RVMSR	T0	GOLGA6L7P	2.35	1.40E-02	LOC101929340	2.10	4.55E-02
RVMSR	T0	ZNF716	2.55	1.40E-02	ZNF557	1.12	4.55E-02
RVMSR	T0	SPDYE8P	3.04	1.40E-02	ZFP57	2.21	4.55E-02
RVMSR	T0	FOXH1	3.03	1.40E-02	LGALS7B	2.11	4.56E-02
RVMSR	T0	RPS7P5	4.74	1.40E-02	TMEM261	-1.05	4.57E-02
RVMSR	T0	DSG3	2.56	1.40E-02	SNX14	-1.59	4.57E-02
RVMSR	T0	KLK10	2.55	1.40E-02	UNC5D	3.25	4.57E-02
RVMSR	T0	KNG1	1.67	1.40E-02	PLVAP	1.52	4.57E-02
RVMSR	T0	TRIB3	1.67	1.40E-02	LOC103171574	2.62	4.59E-02
RVMSR	T0	LOC101928161	3.77	1.41E-02	LOC101929715	3.24	4.59E-02
RVMSR	T0	LOC101927604	2.55	1.41E-02	MIR3143	1.79	4.59E-02
RVMSR	T0	FAM182A	3.31	1.41E-02	TNP1	2.85	4.59E-02
RVMSR	T0	NNMT	2.83	1.41E-02	CIART	1.90	4.59E-02
RVMSR	T0	MASP1	3.04	1.41E-02	MIR516A1	4.09	4.59E-02
RVMSR	T0	PHKG1	1.78	1.41E-02	MIR3591	4.09	4.59E-02
RVMSR	T0	C10orf95	1.96	1.41E-02	MBLAC2	1.91	4.59E-02
RVMSR	T0	FGFR3	2.35	1.41E-02	ADI1	-1.06	4.59E-02
RVMSR	T0	OPTC	2.55	1.41E-02	DSCAS	4.06	4.59E-02
RVMSR	T0	SMAD9	2.84	1.42E-02	LINC01565	2.21	4.59E-02
RVMSR	T0	NUDT10	3.31	1.42E-02	TEKT4	4.09	4.59E-02
RVMSR	T0	DDR2	3.04	1.42E-02	RARRES1	2.87	4.59E-02
RVMSR	T0	ZDHHC11	4.74	1.42E-02	OR7A17	2.31	4.59E-02

RVMSR	T0	CEL	2.55	1.42E-02	PNPLA3	1.84	4.60E-02
RVMSR	T0	LOC100996447	2.67	1.43E-02	NRCAM	2.32	4.60E-02
RVMSR	T0	MIR5708	2.19	1.43E-02	C17orf97	1.62	4.60E-02
RVMSR	T0	HARBI1	1.72	1.43E-02	FOXP4-AS1	3.26	4.60E-02
RVMSR	T0	LINC00254	3.03	1.44E-02	KRTAP4-12	4.09	4.60E-02
RVMSR	T0	RAI2	3.03	1.44E-02	TBX2	4.09	4.60E-02
RVMSR	T0	FAM84A	4.74	1.44E-02	DDO	2.46	4.60E-02
RVMSR	T0	TIGD4	3.75	1.44E-02	C22orf31	2.61	4.61E-02
RVMSR	T0	LOC283299	2.44	1.45E-02	SNTA1	1.62	4.61E-02
RVMSR	T0	GPNMB	1.92	1.45E-02	MIR3912	1.65	4.61E-02
RVMSR	T0	LINC01517	2.84	1.46E-02	DBIL5P	2.21	4.61E-02
RVMSR	T0	LY86-AS1	2.06	1.46E-02	SPZ1	2.11	4.62E-02
RVMSR	T0	CYP2A13	4.73	1.46E-02	UGT3A1	2.31	4.63E-02
RVMSR	T0	MIR4264	2.67	1.46E-02	ATG16L1	1.31	4.64E-02
RVMSR	T0	RIMBP3	2.83	1.46E-02	P2RX3	2.21	4.64E-02
RVMSR	T0	HEYL	3.03	1.46E-02	AVPI1	1.79	4.65E-02
RVMSR	T0	ZNF566	1.43	1.46E-02	FAM74A1	2.45	4.65E-02
RVMSR	T0	PROSER2	3.02	1.46E-02	FAM74A6	2.45	4.65E-02
RVMSR	T0	RBMS3-AS1	4.73	1.46E-02	AKR1C4	2.02	4.65E-02
RVMSR	T0	ACSM5	3.31	1.47E-02	LOC100506497	2.31	4.65E-02
RVMSR	T0	LOC101559451	3.32	1.47E-02	TEX22	2.46	4.65E-02
RVMSR	T0	LINC00950	4.74	1.47E-02	SNORA105C	1.78	4.65E-02
RVMSR	T0	SLC6A4	1.87	1.47E-02	TEAD4	2.30	4.65E-02
RVMSR	T0	CDH5	3.75	1.47E-02	LOC101928540	4.12	4.65E-02
RVMSR	T0	NCCRP1	3.30	1.47E-02	SLC23A1	2.62	4.65E-02
RVMSR	T0	CAPN9	3.02	1.47E-02	OR4E1	3.23	4.66E-02
RVMSR	T0	SNORA95	3.02	1.47E-02	MIR4754	1.96	4.66E-02
RVMSR	T0	LOC100131347	2.43	1.47E-02	GLIDR	1.84	4.66E-02
RVMSR	T0	HOXC11	3.73	1.47E-02	CABP5	2.03	4.66E-02

RVMSR	T0	KISS1	2.84	1.47E-02	DHX30	-1.21	4.66E-02
RVMSR	T0	TMEM59L	2.53	1.47E-02	MUC21	1.95	4.66E-02
RVMSR	T0	IQGAP3	2.83	1.48E-02	SDR16C5	2.85	4.66E-02
RVMSR	T0	LINC00924	3.30	1.48E-02	PLD6	1.35	4.66E-02
RVMSR	T0	SYT5	2.18	1.48E-02	LINC01338	3.27	4.66E-02
RVMSR	T0	ARFGEF3	1.88	1.48E-02	BTNL2	4.08	4.66E-02
RVMSR	T0	GUCA1A	2.67	1.48E-02	LIN54	1.25	4.66E-02
RVMSR	T0	LMNTD1	4.74	1.49E-02	TP53INP2	1.55	4.66E-02
RVMSR	T0	LOC105374988	2.53	1.49E-02	PGM5P3-AS1	3.25	4.67E-02
RVMSR	T0	MYO1H	4.72	1.49E-02	SPDYE7P	4.08	4.67E-02
RVMSR	T0	GJA1	2.34	1.49E-02	DPY19L2	4.08	4.67E-02
RVMSR	T0	LOC105371998	3.30	1.49E-02	LOC441081	1.53	4.67E-02
RVMSR	T0	A4GALT	3.30	1.49E-02	MKRN2OS	2.11	4.67E-02
RVMSR	T0	LINC01350	4.72	1.49E-02	LOC101928304	2.21	4.67E-02
RVMSR	T0	EDRF1-AS1	2.68	1.49E-02	RBP4	4.07	4.67E-02
RVMSR	T0	IFITM3	-1.52	1.49E-02	SNORD121A	2.04	4.67E-02
RVMSR	T0	LOC101928272	2.82	1.49E-02	MIR1471	2.31	4.68E-02
RVMSR	T0	FGG	3.74	1.49E-02	CHGB	2.43	4.68E-02
RVMSR	T0	SPIC	2.83	1.49E-02	DAGLB	1.06	4.69E-02
RVMSR	T0	LOC100507140	2.66	1.49E-02	TXNDC2	2.44	4.69E-02
RVMSR	T0	CLEC4GP1	2.66	1.49E-02	ZNF260	1.23	4.69E-02
RVMSR	T0	NARS2	1.50	1.49E-02	ENPP7	1.77	4.70E-02
RVMSR	T0	FAM81B	3.73	1.49E-02	GOLGA2P11	3.24	4.70E-02
RVMSR	T0	LOC100132781	2.53	1.50E-02	LOC100129307	2.60	4.70E-02
RVMSR	T0	FAM161A	1.84	1.50E-02	LINC00176	2.10	4.70E-02
RVMSR	T0	MIR4777	2.25	1.50E-02	SDK2	2.31	4.70E-02
RVMSR	T0	RPL34	-1.29	1.50E-02	DNMBP-AS1	1.49	4.70E-02
RVMSR	T0	TSHR	3.74	1.50E-02	ECHS1	-1.13	4.70E-02
RVMSR	T0	CASC16	3.30	1.50E-02	FGB	1.84	4.70E-02

RVMSR	T0	TMEM88B	2.83	1.50E-02	LOC101929295	2.21	4.70E-02
RVMSR	T0	MIR3186	2.06	1.50E-02	DNAJC15	-1.04	4.70E-02
RVMSR	T0	LOC101929767	2.11	1.50E-02	NMRK1	-1.23	4.70E-02
RVMSR	T0	SYNGR4	1.91	1.50E-02	CRNN	2.59	4.70E-02
RVMSR	T0	PRRT1	2.24	1.50E-02	PTCHD1	2.85	4.71E-02
RVMSR	T0	PCDH18	2.68	1.50E-02	PRICKLE2-AS2	2.59	4.71E-02
RVMSR	T0	LOC105376554	2.24	1.50E-02	HAP1	1.69	4.71E-02
RVMSR	T0	ARGFX	2.24	1.50E-02	CA5A	1.62	4.71E-02
RVMSR	T0	PLAT	2.05	1.50E-02	LOC105372288	1.52	4.71E-02
RVMSR	T0	OIT3	2.41	1.50E-02	FLJ40194	2.43	4.71E-02
RVMSR	T0	C1orf194	1.56	1.50E-02	CBLN4	3.24	4.71E-02
RVMSR	T0	CHPT1	-1.29	1.50E-02	SCGB2A1	4.04	4.72E-02
RVMSR	T0	HTT	-1.77	1.51E-02	PCDH7	2.61	4.72E-02
RVMSR	T0	ZGLP1	1.81	1.51E-02	LOC286297	2.11	4.72E-02
RVMSR	T0	HP09025	2.42	1.52E-02	BRINP3	4.10	4.72E-02
RVMSR	T0	MIR136	4.72	1.52E-02	TMEM207	3.24	4.72E-02
RVMSR	T0	ZBED8	2.32	1.53E-02	LOC108783645	2.44	4.72E-02
RVMSR	T0	SNORD32B	2.54	1.53E-02	SLC25A10	2.21	4.72E-02
RVMSR	T0	DTL	4.70	1.53E-02	TAS2R13	4.07	4.72E-02
RVMSR	T0	C17orf112	3.71	1.53E-02	LOC100506551	2.19	4.72E-02
RVMSR	T0	LOC102724502	2.66	1.53E-02	CAPN11	1.95	4.72E-02
RVMSR	T0	SALL2	2.17	1.54E-02	PUM3	-1.18	4.72E-02
RVMSR	T0	ARHGEF15	2.33	1.54E-02	FOXE1	4.07	4.72E-02
RVMSR	T0	S100G	2.41	1.54E-02	ADRB3	1.83	4.72E-02
RVMSR	T0	ZNF280B	1.66	1.54E-02	LINC01037	2.61	4.73E-02
RVMSR	T0	HAND2	3.74	1.54E-02	FBN1	2.61	4.73E-02
RVMSR	T0	LINC01549	3.30	1.54E-02	ATP4B	4.06	4.73E-02
RVMSR	T0	TSPAN11	3.28	1.54E-02	CACTIN-AS1	2.84	4.73E-02
RVMSR	T0	AICDA	1.70	1.54E-02	CASP16P	2.10	4.73E-02

RVMSR	T0	LOC101928725	3.29	1.54E-02	AA06	4.06	4.74E-02
RVMSR	T0	LOC100506107	4.71	1.55E-02	CISTR	2.45	4.74E-02
RVMSR	T0	TEX35	3.28	1.55E-02	ABL2	1.29	4.74E-02
RVMSR	T0	EHHADH-AS1	1.89	1.55E-02	LOC101929130	2.60	4.74E-02
RVMSR	T0	LOC101928896	1.77	1.55E-02	MIR4438	2.30	4.74E-02
RVMSR	T0	MIR1302-3	2.99	1.55E-02	RHOXF1P1	2.32	4.74E-02
RVMSR	T0	MIR98	3.73	1.56E-02	ZEB1	-1.05	4.74E-02
RVMSR	T0	TRPC1	2.05	1.56E-02	BRWD1	-1.05	4.74E-02
RVMSR	T0	BCL2L15	3.01	1.56E-02	ZNF350	-1.99	4.74E-02
RVMSR	T0	BFSP2	3.01	1.56E-02	MSTN	3.24	4.74E-02
RVMSR	T0	FLJ46284	4.70	1.56E-02	FAM153A	1.84	4.74E-02
RVMSR	T0	PSMC3IP	2.67	1.56E-02	A1CF	2.31	4.74E-02
RVMSR	T0	MPP2	2.32	1.56E-02	IL3	2.44	4.75E-02
RVMSR	T0	TNFSF15	2.65	1.56E-02	CYP26C1	2.59	4.75E-02
RVMSR	T0	CCDC8	2.41	1.57E-02	GABRR1	2.44	4.75E-02
RVMSR	T0	LOC101929473	3.73	1.57E-02	HAGLR	2.59	4.77E-02
RVMSR	T0	HAMP	1.68	1.57E-02	LOC283177	2.85	4.77E-02
RVMSR	T0	ZNF730	2.53	1.57E-02	NAT16	2.84	4.77E-02
RVMSR	T0	MIR518A1	3.71	1.57E-02	CBY3	1.44	4.78E-02
RVMSR	T0	HTR2A-AS1	3.01	1.57E-02	MIR4795	4.03	4.78E-02
RVMSR	T0	LOC101928885	2.80	1.57E-02	LOC101928837	3.22	4.78E-02
RVMSR	T0	NEDD4	2.66	1.58E-02	MIER1	-1.03	4.78E-02
RVMSR	T0	DPPA2	2.41	1.58E-02	ZNF813	1.44	4.78E-02
RVMSR	T0	TCEB3C	2.51	1.59E-02	LELP1	2.60	4.78E-02
RVMSR	T0	ADA	-1.55	1.59E-02	LINC00533	3.23	4.78E-02
RVMSR	T0	LOC644656	1.68	1.59E-02	DPM3	-1.03	4.78E-02
RVMSR	T0	DEFB103B	3.27	1.60E-02	GIMAP7	-1.10	4.78E-02
RVMSR	T0	FAM74A4	3.01	1.60E-02	MIR3622A	4.05	4.78E-02
RVMSR	T0	AIPL1	2.41	1.60E-02	LINC01246	4.09	4.78E-02

RVMSR	T0	GPX8	2.81	1.60E-02	KRTAP9-3	2.85	4.78E-02
RVMSR	T0	MORC2-AS1	1.76	1.60E-02	KLLN	2.44	4.78E-02
RVMSR	T0	TYRO3	2.04	1.60E-02	MIR371B	1.18	4.78E-02
RVMSR	T0	SSX2	2.52	1.60E-02	WDR86-AS1	1.51	4.79E-02
RVMSR	T0	SSX2B	2.52	1.60E-02	DGKZ	-1.42	4.79E-02
RVMSR	T0	NPIPB9	2.10	1.60E-02	FGFR2	1.78	4.79E-02
RVMSR	T0	LINC01093	2.42	1.60E-02	TNFRSF19	4.05	4.79E-02
RVMSR	T0	LOC101928453	2.16	1.61E-02	STX19	4.05	4.79E-02
RVMSR	T0	SOAT2	3.00	1.61E-02	LYZL1	2.11	4.79E-02
RVMSR	T0	TMEM81	2.80	1.61E-02	MIR3910-2	4.05	4.80E-02
RVMSR	T0	FOXS1	4.69	1.61E-02	USP33	-1.08	4.80E-02
RVMSR	T0	TRIM71	3.00	1.61E-02	YIF1B	1.12	4.80E-02
RVMSR	T0	EGOT	3.00	1.61E-02	CBLL1	-1.44	4.80E-02
RVMSR	T0	MLXIPL	3.71	1.61E-02	TEX11	2.61	4.80E-02
RVMSR	T0	AMHR2	1.99	1.61E-02	AQP7	2.60	4.80E-02
RVMSR	T0	C22orf24	3.28	1.61E-02	BTBD19	1.49	4.81E-02
RVMSR	T0	MIRLET7BHG	2.10	1.61E-02	OR7D4	2.59	4.81E-02
RVMSR	T0	PGA4	2.40	1.62E-02	LOC101927668	2.59	4.83E-02
RVMSR	T0	BCDIN3D	1.41	1.62E-02	LINC01381	3.23	4.83E-02
RVMSR	T0	DLG5-AS1	2.80	1.62E-02	LOC646743	2.42	4.83E-02
RVMSR	T0	C7orf77	2.41	1.62E-02	TISP43	2.42	4.83E-02
RVMSR	T0	CST2	2.81	1.62E-02	E2F6	2.11	4.83E-02
RVMSR	T0	C20orf194	1.99	1.62E-02	PKD2L2	2.30	4.83E-02
RVMSR	T0	LINC00933	2.24	1.62E-02	APOA1-AS	2.10	4.84E-02
RVMSR	T0	LINC01491	4.68	1.63E-02	SPNS2	2.87	4.84E-02
RVMSR	T0	PRKCA-AS1	1.89	1.63E-02	SLC52A1	1.65	4.84E-02
RVMSR	T0	LALBA	3.27	1.63E-02	ANKRD20A12P	2.01	4.85E-02
RVMSR	T0	FOXN1	2.51	1.63E-02	MAMDC2	2.83	4.85E-02
RVMSR	T0	ACTR6	1.25	1.63E-02	MIR5700	1.94	4.85E-02

RVMSR	T0	LOC100130331	4.70	1.63E-02	PCSK4	4.08	4.85E-02
RVMSR	T0	LOC101928303	2.51	1.63E-02	LOC100379224	2.19	4.85E-02
RVMSR	T0	HOXB-AS3	3.27	1.63E-02	LOC101928471	4.04	4.85E-02
RVMSR	T0	MYOM1	2.04	1.63E-02	PYCR1	-3.89	4.86E-02
RVMSR	T0	LOC105369911	3.00	1.64E-02	VENTXP7	2.20	4.86E-02
RVMSR	T0	DISC2	4.66	1.64E-02	PAX2	2.82	4.86E-02
RVMSR	T0	UBE2U	2.79	1.64E-02	NDFIP2-AS1	4.04	4.87E-02
RVMSR	T0	MANEAL	2.31	1.64E-02	MUC1	4.04	4.87E-02
RVMSR	T0	NAE1	-1.80	1.64E-02	MIR652	2.02	4.87E-02
RVMSR	T0	MT2A	-1.26	1.64E-02	GRIN3A	4.04	4.87E-02
RVMSR	T0	LYRM4-AS1	1.95	1.65E-02	HIST3H3	2.58	4.87E-02
RVMSR	T0	LOC101929718	3.28	1.65E-02	LINC00559	4.04	4.87E-02
RVMSR	T0	MIR130B	3.01	1.65E-02	ABCB11	2.09	4.88E-02
RVMSR	T0	THEG	3.70	1.66E-02	OR5B17	2.81	4.88E-02
RVMSR	T0	KCP	2.98	1.67E-02	CTAGE6	2.59	4.88E-02
RVMSR	T0	SRGAP3-AS2	3.69	1.67E-02	TIGD3	1.57	4.88E-02
RVMSR	T0	DEFA9P	2.09	1.67E-02	MIR4502	2.30	4.88E-02
RVMSR	T0	TMEM17	3.26	1.67E-02	GSTO1	-1.03	4.88E-02
RVMSR	T0	HCG22	2.79	1.67E-02	MIR454	1.95	4.88E-02
RVMSR	T0	IFNA13	3.26	1.67E-02	RBM5-AS1	2.31	4.88E-02
RVMSR	T0	CASC23	3.69	1.68E-02	ATP2C2	2.19	4.91E-02
RVMSR	T0	MIR1295A	2.64	1.68E-02	BNC2	2.10	4.91E-02
RVMSR	T0	TEX101	2.30	1.68E-02	STAM-AS1	1.23	4.91E-02
RVMSR	T0	GUCA2A	4.68	1.68E-02	COX17	-1.05	4.91E-02
RVMSR	T0	CCL4	-1.23	1.68E-02	LOC100507670	1.55	4.91E-02
RVMSR	T0	DRC7	3.26	1.68E-02	RNF183	1.73	4.91E-02
RVMSR	T0	KRTAP15-1	2.99	1.68E-02	SOD1	-1.02	4.91E-02
RVMSR	T0	PCDH15	2.51	1.68E-02	ECE2	1.20	4.91E-02
RVMSR	T0	LOC101928510	2.16	1.69E-02	ALOX15B	1.87	4.92E-02

RVMSR	T0	CDH15	4.68	1.69E-02	MIR4662A	1.82	4.92E-02
RVMSR	T0	LINC01541	4.68	1.69E-02	MEF2C-AS1	1.88	4.92E-02
RVMSR	T0	MIR2117	3.70	1.69E-02	LOC105375483	4.03	4.92E-02
RVMSR	T0	UNC79	3.70	1.69E-02	KRTAP13-3	4.03	4.93E-02
RVMSR	T0	MYOCD	2.23	1.69E-02	TJP2	1.64	4.93E-02
RVMSR	T0	LOC100506393	2.99	1.69E-02	LOC101928894	2.42	4.93E-02
RVMSR	T0	LINC01429	1.77	1.69E-02	TAF8	1.40	4.94E-02
RVMSR	T0	KHDC1	2.31	1.69E-02	ATP5I	-1.02	4.94E-02
RVMSR	T0	MIR548A2	2.98	1.69E-02	LINC00927	3.20	4.94E-02
RVMSR	T0	ASPHD1	2.99	1.69E-02	ERICH1-AS1	4.06	4.94E-02
RVMSR	T0	C17orf98	1.89	1.69E-02	TOPAZ1	4.03	4.94E-02
RVMSR	T0	SLC25A16	1.56	1.70E-02	OR4Q3	1.82	4.94E-02
RVMSR	T0	GPR158-AS1	2.15	1.70E-02	RMI1	1.57	4.94E-02
RVMSR	T0	MIR3937	3.69	1.70E-02	MIR613	1.49	4.95E-02
RVMSR	T0	NPTX1	3.26	1.70E-02	TOMM7	-1.02	4.95E-02
RVMSR	T0	LOC105371730	2.15	1.71E-02	TCEA1	-1.03	4.95E-02
RVMSR	T0	DCT	4.67	1.71E-02	LINC00448	1.87	4.95E-02
RVMSR	T0	MARK1	1.89	1.71E-02	GRM3	2.01	4.96E-02
RVMSR	T0	DCTN1-AS1	2.79	1.71E-02	RGS18	-1.01	4.97E-02
RVMSR	T0	GPR88	4.65	1.71E-02	LOC106699570	1.88	4.97E-02
RVMSR	T0	RNU5D-1	2.99	1.71E-02	LRRN4	3.21	4.98E-02
RVMSR	T0	RNU5E-1	2.99	1.71E-02	LOC101929625	2.29	4.98E-02
RVMSR	T0	ENTHD1	3.68	1.71E-02	LINC01046	2.57	4.98E-02
RVMSR	T0	WFDC5	2.79	1.72E-02	DEFB134	2.42	4.98E-02
RVMSR	T0	TOP1P2	1.69	1.72E-02	MX1	-1.02	4.99E-02
RVMSR	T0	GLB1L3	2.79	1.72E-02	LOC644919	2.43	4.99E-02
RVMSR	T0	LOC105371506	2.98	1.72E-02	LINC01563	1.45	4.99E-02
RVMSR	T0	LOC101928535	2.79	1.72E-02	JPH1	3.21	5.00E-02
RVMSR	T0	ADAMTSL1	2.40	1.72E-02	CASC8	1.49	5.00E-02

RVMSR	T0	NTNG1	2.39	1.72E-02	CYP3A7	2.57	5.00E-02
RVMSR	T1	MIR8078	4.17	6.82E-12	LEF1	-1.63	3.37E-02
RVMSR	T1	HLA-DRB5	-3.63	1.22E-09	MIR3186	2.12	3.43E-02
RVMSR	T1	CD177	-3.86	2.70E-09	LINC01120	3.26	3.43E-02
RVMSR	T1	TMEM176B	-3.02	1.61E-07	BMPR1B-AS1	1.93	3.43E-02
RVMSR	T1	TMEM176A	-2.76	7.33E-06	CALN1	2.36	3.43E-02
RVMSR	T1	ARFRP1	-2.91	1.64E-04	SVEP1	5.40	3.43E-02
RVMSR	T1	MCEMP1	-2.36	2.76E-04	FOXN1	3.45	3.43E-02
RVMSR	T1	IFI27	-2.17	2.32E-03	ZNRF3-AS1	1.65	3.43E-02
RVMSR	T1	LOC100996342	2.15	6.33E-03	HOXD1	1.52	3.43E-02
RVMSR	T1	FBLIM1	2.04	6.33E-03	OR4D9	2.19	3.43E-02
RVMSR	T1	TSIX	2.03	6.48E-03	LOC102725072	1.79	3.43E-02
RVMSR	T1	LOC100288748	2.34	6.48E-03	LOC105378614	2.42	3.61E-02
RVMSR	T1	KRT10	-2.01	6.48E-03	TRHDE-AS1	4.45	3.61E-02
RVMSR	T1	ZNF618	3.80	1.10E-02	FAM134C	-1.86	3.63E-02
RVMSR	T1	LINC00273	1.82	1.10E-02	FBXO27	1.83	3.64E-02
RVMSR	T1	UBXN7-AS1	2.08	1.10E-02	TMEM233	1.78	3.67E-02
RVMSR	T1	SLC1A6	2.08	1.10E-02	LMOD3	1.82	3.74E-02
RVMSR	T1	CLYBL-AS1	5.97	1.11E-02	CEP55	3.93	3.83E-02
RVMSR	T1	DEFA4	2.00	1.82E-02	STIP1	-2.51	3.83E-02
RVMSR	T1	HNF1A-AS1	2.23	1.87E-02	KRT1	-1.61	3.83E-02
RVMSR	T1	CPZ	2.75	1.87E-02	GIP	1.80	3.83E-02
RVMSR	T1	ERC2-IT1	2.73	2.06E-02	ID3	-1.59	3.83E-02
RVMSR	T1	FOSB	2.63	2.06E-02	LOC105376398	5.35	3.83E-02
RVMSR	T1	ADCY6	2.13	2.06E-02	NLN	1.87	3.83E-02
RVMSR	T1	WIF1	2.94	2.14E-02	RTN2	2.26	3.83E-02
RVMSR	T1	SEMA3B	1.73	2.14E-02	FLJ13224	2.40	3.83E-02
RVMSR	T1	CCDC175	1.72	2.22E-02	LRRC74B	2.38	3.83E-02
RVMSR	T1	SNAR-A13	2.86	2.22E-02	LINC00707	1.52	3.83E-02

RVMSR	T1	PLK5	2.35	2.32E-02	C19orf12	-2.01	3.83E-02
RVMSR	T1	MIOX	1.88	2.32E-02	CCR7	-1.79	3.83E-02
RVMSR	T1	ATP1A2	2.77	2.32E-02	LOC101929646	1.93	3.83E-02
RVMSR	T1	TOB2P1	2.85	2.33E-02	LOC101928766	5.32	3.84E-02
RVMSR	T1	FAT3	2.01	2.46E-02	FAM218A	1.70	3.94E-02
RVMSR	T1	LINC00383	3.63	2.46E-02	LOC374890	5.30	3.94E-02
RVMSR	T1	CYP1A2	2.75	2.46E-02	P2RX5	-1.65	3.96E-02
RVMSR	T1	MIR7-3HG	2.90	2.46E-02	LINC01015	4.38	3.96E-02
RVMSR	T1	CEBPZ	-1.75	2.60E-02	LOC101928841	1.86	3.96E-02
RVMSR	T1	LINC00566	3.41	2.60E-02	ITPK1-AS1	2.58	4.04E-02
RVMSR	T1	TMEM221	1.97	2.60E-02	CREB3L1	2.95	4.08E-02
RVMSR	T1	PRR11	1.64	2.60E-02	BRIP1	4.35	4.13E-02
RVMSR	T1	DEFA3	1.99	2.60E-02	DGKB	2.28	4.13E-02
RVMSR	T1	LOC101928917	4.65	2.60E-02	LINC01122	2.61	4.13E-02
RVMSR	T1	NFIB	1.91	2.60E-02	CNGB1	1.70	4.13E-02
RVMSR	T1	LOC101927619	3.01	2.60E-02	C10orf126	3.39	4.13E-02
RVMSR	T1	ELK2AP	-1.73	2.60E-02	SNORA52	-1.71	4.22E-02
RVMSR	T1	LOC102723640	2.71	2.60E-02	GHET1	1.82	4.34E-02
RVMSR	T1	LINC00167	2.00	2.60E-02	KNG1	2.42	4.34E-02
RVMSR	T1	IGF1	2.58	2.60E-02	FEZF2	5.22	4.36E-02
RVMSR	T1	ZBTB8A	2.22	2.60E-02	FGL1	2.54	4.36E-02
RVMSR	T1	LINC00842	2.48	2.60E-02	MUC4	2.02	4.36E-02
RVMSR	T1	ALDH4A1	4.13	2.60E-02	IGDCC3	3.08	4.36E-02
RVMSR	T1	VASH2	2.89	2.60E-02	TUBA3FP	1.53	4.36E-02
RVMSR	T1	GOLGA8M	2.46	2.60E-02	PTPN1	-1.55	4.49E-02
RVMSR	T1	SLC36A3	2.02	2.60E-02	MIR5700	4.33	4.50E-02
RVMSR	T1	ZNF630-AS1	2.32	2.60E-02	IL10RA	-1.53	4.52E-02
RVMSR	T1	UBE2DNL	1.59	2.60E-02	C1orf194	1.74	4.52E-02
RVMSR	T1	FCRL1	-2.15	2.60E-02	DENND2A	2.31	4.52E-02

RVMSR	T1	PCAT5	2.16	2.60E-02	CCNYL2	4.34	4.52E-02
RVMSR	T1	OR4D10	2.23	2.60E-02	TLL1	5.21	4.52E-02
RVMSR	T1	CFD	-1.89	2.63E-02	LOC101929259	1.67	4.52E-02
RVMSR	T1	HSPB9	1.82	2.68E-02	LOC105373044	2.61	4.52E-02
RVMSR	T1	MIR3168	2.62	2.68E-02	CXXC5	-1.79	4.52E-02
RVMSR	T1	LOC440700	1.99	2.68E-02	CRYM-AS1	2.21	4.52E-02
RVMSR	T1	ORC6	4.57	2.68E-02	HSF1	-1.73	4.52E-02
RVMSR	T1	DUSP9	2.22	2.71E-02	HPD	2.23	4.52E-02
RVMSR	T1	SNRNP25	-2.08	2.71E-02	LY6G6E	1.65	4.52E-02
RVMSR	T1	LOC403312	2.00	2.71E-02	CRX	1.73	4.52E-02
RVMSR	T1	38047	4.56	2.76E-02	NOS1	1.53	4.52E-02
RVMSR	T1	CD79A	-1.66	2.90E-02	GJA3	1.64	4.61E-02
RVMSR	T1	SGSM1	2.65	2.90E-02	LOC105372653	1.73	4.61E-02
RVMSR	T1	PDLIM2	-1.79	2.90E-02	TTC23L	2.12	4.61E-02
RVMSR	T1	LAMC2	2.73	2.90E-02	LOC100499484	-5.31	4.64E-02
RVMSR	T1	PALM2	1.97	2.90E-02	KCNN3	2.22	4.64E-02
RVMSR	T1	SULT2A1	1.92	2.90E-02	LINC00317	5.17	4.74E-02
RVMSR	T1	LOC100288254	5.50	2.90E-02	NLGN1	5.17	4.74E-02
RVMSR	T1	RYR2	3.74	2.91E-02	PDE4A	1.65	4.77E-02
RVMSR	T1	C15orf48	2.20	3.01E-02	TMEM18	-1.63	4.79E-02
RVMSR	T1	SELENOM	-1.70	3.18E-02	CST7	-1.65	4.79E-02
RVMSR	T1	LINC01433	2.14	3.18E-02	GPR152	1.75	4.79E-02
RVMSR	T1	MZB1	-1.64	3.18E-02	GMIP	-1.54	4.87E-02
RVMSR	T1	FDPSP2	1.65	3.21E-02	UBOX5-AS1	2.07	4.89E-02
RVMSR	T1	MRAP	5.50	3.21E-02	EFHD1	1.88	4.99E-02
RVMSR	T1	MIR3130-1	2.76	3.30E-02	MGAT5B	3.33	4.99E-02
RVMSR	T1	PPP3R2	2.43	3.33E-02			
RVMSR	T2	CCDC175	1.87	2.24E-04	LOC101927532	2.15	2.57E-02
RVMSR	T2	DEFA1B	1.82	2.24E-04	LIM2	2.81	2.61E-02

RVMSR	T2	DEFA1	1.82	2.24E-04	FBLIM1	2.05	2.71E-02
RVMSR	T2	IFI27	-1.83	3.57E-04	LY6E	-1.34	2.84E-02
RVMSR	T2	DEFA3	1.66	3.57E-04	LOC100131303	2.64	2.84E-02
RVMSR	T2	HLA-DRB5	-2.09	4.81E-04	SLC26A5	5.61	2.94E-02
RVMSR	T2	SEMA3B	2.12	1.70E-03	OR2V1	5.60	3.01E-02
RVMSR	T2	TARP	-1.71	1.92E-03	CNGB1	2.18	3.01E-02
RVMSR	T2	CELA2A	4.70	3.40E-03	LINC00543	3.33	3.82E-02
RVMSR	T2	CPZ	4.01	8.83E-03	TM4SF5	2.14	3.82E-02
RVMSR	T2	MIR193BHG	2.90	9.15E-03	ZNF571-AS1	2.89	3.82E-02
RVMSR	T2	GZMH	-1.72	9.15E-03	HOPX	-1.41	3.82E-02
RVMSR	T2	PTPRS	2.44	9.77E-03	MYH1	4.21	3.82E-02
RVMSR	T2	LINC00707	1.99	1.23E-02	TENM3	2.74	3.82E-02
RVMSR	T2	LINC00273	1.65	1.23E-02	ST7-AS2	5.52	4.09E-02
RVMSR	T2	KCNN3	3.32	1.23E-02	HEATR9	3.66	4.12E-02
RVMSR	T2	LOC105371789	3.33	1.23E-02	STC1	4.20	4.18E-02
RVMSR	T2	TSIX	1.93	1.24E-02	FAM227A	2.17	4.18E-02
RVMSR	T2	MGC34796	3.29	1.24E-02	LINC01206	5.46	4.18E-02
RVMSR	T2	CCL4L1	-2.05	1.24E-02	PALM2	2.39	4.18E-02
RVMSR	T2	CCL4L2	-2.05	1.24E-02	CATIP-AS1	5.48	4.18E-02
RVMSR	T2	MIR4267	2.82	1.24E-02	SYNC	1.32	4.18E-02
RVMSR	T2	NKG7	-1.40	1.33E-02	PPP3CB-AS1	1.39	4.18E-02
RVMSR	T2	SEC1P	2.91	1.34E-02	HMGCS2	5.47	4.18E-02
RVMSR	T2	TMEM120B	1.54	1.34E-02	FAT3	2.30	4.18E-02
RVMSR	T2	UBE2DNL	1.64	1.34E-02	CAPN14	5.46	4.18E-02
RVMSR	T2	ROM1	2.46	1.76E-02	CXorf66	5.46	4.18E-02
RVMSR	T2	ICAM5	3.80	2.11E-02	MAP1S	1.29	4.18E-02
RVMSR	T2	GZMA	-1.38	2.11E-02	LOC102723692	3.62	4.18E-02
RVMSR	T2	MIR4777	3.80	2.11E-02	ALOX15B	4.15	4.18E-02
RVMSR	T2	MIR3912	3.80	2.11E-02	PRDM15	2.47	4.18E-02

RVMSR	T2	ENPP7P13	3.45	2.11E-02	MTFP1	-1.91	4.32E-02
RVMSR	T2	MIR1253	3.79	2.11E-02	C1orf105	5.44	4.56E-02
RVMSR	T2	LEMD1-AS1	5.71	2.11E-02	ZAN	3.01	4.58E-02
RVMSR	T2	TMEM109	-1.94	2.18E-02	CLIC3	-1.41	4.58E-02
RVMSR	T2	MYL1	5.64	2.18E-02	GSTTP1	5.43	4.62E-02
RVMSR	T2	CCEPR	1.40	2.18E-02	GGA1	-1.86	4.71E-02
RVMSR	T2	GZMB	-1.36	2.18E-02	ZNF565	2.16	4.71E-02
RVMSR	T2	CYP17A1	3.17	2.18E-02	CTSV	2.81	4.77E-02
RVMSR	T2	LINC00842	2.69	2.28E-02	PLCB2	-1.30	4.87E-02
RVMSR	T2	DHH	4.31	2.57E-02	NLRP11	5.40	4.94E-02
RVMSR	T3	DEFA4	-3.40	2.03E-04	CHPT1	-2.45	1.69E-02
RVMSR	T3	C4B_2	-3.41	2.03E-04	GLRX5	-2.48	1.97E-02
RVMSR	T3	GPR146	-3.05	6.32E-04	RETN	-2.53	2.21E-02
RVMSR	T3	SIAH2	-3.07	1.49E-03	TMOD1	-2.39	2.52E-02
RVMSR	T3	PTTG1	-3.14	1.49E-03	MKI67	-2.30	2.52E-02
RVMSR	T3	OR2W3	-2.82	1.92E-03	GZMH	-2.28	3.23E-02
RVMSR	T3	C4A	-3.33	3.68E-03	STOM	-2.27	3.92E-02
RVMSR	T3	FECH	-2.73	6.14E-03	MPP1	-2.47	3.92E-02
RVMSR	T3	CENPF	-2.85	8.47E-03	MAP3K21	5.99	3.92E-02
RVMSR	T3	KRT1	-2.62	8.47E-03	SLC6A8	-2.22	4.49E-02
RVMSR	T3	CA1	-2.78	8.47E-03	TK1	-2.97	4.49E-02
RVMSR	T3	BSG	-2.73	8.47E-03	ANK1	-2.28	4.49E-02
RVMSR	T3	FAM46C	-2.60	1.38E-02	TNS1	-2.21	4.49E-02
RVMSR	T3	LTF	-2.72	1.65E-02	PITHD1	-2.24	4.49E-02
RVMSR	T3	CKS2	-2.64	1.65E-02	RNU12	4.10	4.49E-02
All RTT	T1 to T2	TMEM176B	-2.53	3.41E-07	TMEM176A	-2.72	3.41E-07
All RTT	T2 to T3	ERVMER34-1	2.35	7.81E-05	RRM2	2.06	2.98E-02
All RTT	T2 to T3	TMEM176B	2.07	7.81E-05	CENPF	1.98	3.31E-02
Responders	T0 to T1	HLA-DRB5	-3.14	3.49E-04			

Responders	T0 to T2	HLA-DRB5	-2.38	2.57E-04	SMCR5	-3.00	3.66E-02
Responders	T2 to T3	HLA-DRB5	3.04	3.33E-07			
MSRs	T0 to T1	ERVMER34-1	-3.13	2.33E-09	CD177	-1.47	2.73E-02
MSRs	T0 to T1	C4B_2	-2.80	2.33E-09	CISD2	-1.51	3.08E-02
MSRs	T0 to T1	C4A	-2.90	1.47E-06	UQCRB	-1.59	3.08E-02
MSRs	T0 to T1	ELK2AP	1.80	1.30E-03	SERPING1	-1.67	4.07E-02
MSRs	T0 to T1	RPL26	-1.65	5.15E-03	RAP1GAP	-3.64	4.47E-02
MSRs	T0 to T1	TUBB2A	-1.67	9.31E-03	RPL22L1	-1.91	4.53E-02
MSRs	T0 to T1	IFI44L	-1.48	2.73E-02			
MSRs	T0 to T2	ERVMER34-1	-4.33	3.05E-12	IGF2BP2	-2.02	1.13E-02
MSRs	T0 to T2	CHPT1	-2.29	1.53E-04	ALAS2	-1.83	1.13E-02
MSRs	T0 to T2	TRIM58	-2.00	1.53E-04	RIOK3	-1.57	1.56E-02
MSRs	T0 to T2	OSBP2	-2.24	1.53E-04	LCMT2	-1.70	1.56E-02
MSRs	T0 to T2	SIAH2	-2.00	1.53E-04	RAP1GAP	-3.93	1.56E-02
MSRs	T0 to T2	C4B_2	-1.90	2.07E-03	MAP2K3	-1.56	1.56E-02
MSRs	T0 to T2	BPGM	-1.77	4.43E-03	SELENBP1	-1.55	1.63E-02
MSRs	T0 to T2	CA1	-1.66	9.28E-03	GPR146	-1.74	2.34E-02
MSRs	T0 to T2	YOD1	-1.81	9.37E-03	AHSP	-1.51	2.34E-02
MSRs	T0 to T2	SLC4A1	-1.64	9.44E-03	MXI1	-1.49	3.38E-02
MSRs	T0 to T2	C4A	-1.99	1.03E-02	OR2W3	-1.59	3.39E-02
MSRs	T0 to T2	PITHD1	-1.66	1.13E-02	FAM46C	-1.48	3.45E-02
MSRs	T0 to T3	CD177	-4.09	3.04E-16	FCGR1A	-2.02	4.63E-03
MSRs	T0 to T3	DEFA3	3.84	2.95E-12	S100A12	-2.09	4.68E-03
MSRs	T0 to T3	DEFA4	3.31	5.14E-12	CAMP	1.69	5.37E-03
MSRs	T0 to T3	DEFA1B	3.64	4.67E-08	LCMT2	-1.77	1.45E-02
MSRs	T0 to T3	DEFA1	3.64	4.67E-08	MKI67	1.87	1.45E-02
MSRs	T0 to T3	IFI44L	-2.19	2.38E-05	CENPF	2.05	1.79E-02
MSRs	T0 to T3	FAM90A10P	-1.93	9.25E-04	ZFHX2	-3.17	1.81E-02
MSRs	T0 to T3	RSAD2	-2.00	1.19E-03	PTTG1	1.97	1.81E-02
MSRs	T0 to T3	SMIM1	-1.96	1.77E-03	TXNDC5	1.88	2.02E-02
MSRs	T0 to T3	CHI3L1	1.86	1.92E-03	TIMD4	4.37	2.98E-02
MSRs	T0 to T3	ELANE	2.31	2.06E-03	UBE2C	2.25	3.16E-02
MSRs	T0 to T3	MCEMP1	-1.82	2.97E-03	RRM2	2.02	3.16E-02
MSRs	T0 to T3	LTF	2.40	3.08E-03	LOC100130520	-1.72	3.36E-02
MSRs	T0 to T3	ELK2AP	1.77	4.30E-03	BCL2A1	-1.60	4.20E-02
MSRs	T1 to T2	TMEM176B	-3.54	3.39E-19	E2F2	-1.72	6.82E-03
MSRs	T1 to T2	TMEM176A	-3.62	5.28E-15	ALAS2	-1.24	7.69E-03
MSRs	T1 to T2	SLC4A1	-2.03	2.71E-10	DCAF12	-1.15	9.61E-03
MSRs	T1 to T2	KRT1	-2.14	2.79E-10	LOC101927697	-1.17	9.61E-03
MSRs	T1 to T2	AHSP	-1.70	8.63E-07	HBM	-1.22	9.78E-03
MSRs	T1 to T2	TRIM58	-1.51	1.19E-04	EPB42	-1.27	1.05E-02
MSRs	T1 to T2	FAM210B	-1.40	4.07E-04	RPL17	1.15	1.19E-02

MSRs	T1 to T2	RSAD2	-2.26	4.07E-04	C7orf73	-1.13	1.26E-02
MSRs	T1 to T2	SMIM1	-1.68	4.07E-04	TESC	-1.12	1.81E-02
MSRs	T1 to T2	BLVRB	-1.37	5.01E-04	HBQ1	-1.10	1.89E-02
MSRs	T1 to T2	PAX8-AS1	-3.15	6.01E-04	BAG1	-1.09	1.89E-02
MSRs	T1 to T2	SNCA	-1.32	8.15E-04	PSMF1	-1.09	1.89E-02
MSRs	T1 to T2	UBXN6	-1.32	9.15E-04	PCGF5	-1.07	2.50E-02
MSRs	T1 to T2	HOPX	1.66	9.15E-04	CA1	-1.13	2.61E-02
MSRs	T1 to T2	RBM38	-1.35	9.15E-04	YBX3	-1.07	2.65E-02
MSRs	T1 to T2	DMTN	-1.31	9.15E-04	RUNDC3A	-1.54	2.65E-02
MSRs	T1 to T2	HEMGN	-1.49	1.07E-03	GUK1	-1.11	3.55E-02
MSRs	T1 to T2	SELENBP1	-1.30	1.14E-03	RPL26	1.06	4.16E-02
MSRs	T1 to T2	BCL2L1	-1.30	1.62E-03	RNF10	-1.06	4.24E-02
MSRs	T1 to T2	SLC25A39	-1.34	1.73E-03	FAM46C	-1.13	4.34E-02
MSRs	T1 to T2	BRSK1	-1.61	3.16E-03	LOC105372626	-1.12	4.34E-02
MSRs	T1 to T2	JCHAIN	1.22	4.10E-03	PHOSPHO1	-1.11	4.34E-02
MSRs	T1 to T2	STRADB	-1.23	5.78E-03	MKRN1	-1.02	4.34E-02
MSRs	T1 to T2	GSPT1	-1.20	5.80E-03	PDHX	2.36	4.99E-02
MSRs	T1 to T2	GYPB	-1.48	6.56E-03			
MSRs	T1 to T3	DEFA4	3.60	3.90E-18	RRM2	2.13	2.30E-03
MSRs	T1 to T3	DEFA3	3.68	4.87E-16	SMIM1	-1.68	3.59E-03
MSRs	T1 to T3	DEFA1B	3.58	4.22E-11	GZMA	1.45	4.55E-03
MSRs	T1 to T3	DEFA1	3.58	4.22E-11	RNASE3	2.04	5.38E-03
MSRs	T1 to T3	ERVMER34-1	2.89	7.82E-08	ELANE	1.87	5.38E-03
MSRs	T1 to T3	CD177	-2.60	3.42E-06	CENPF	1.90	5.66E-03
MSRs	T1 to T3	C4B_2	2.29	9.77E-06	CKS2	1.83	8.34E-03
MSRs	T1 to T3	CAMP	1.78	5.44E-05	ASPM	2.46	9.07E-03
MSRs	T1 to T3	TMEM176A	-2.08	1.60E-04	LTF	1.82	2.32E-02
MSRs	T1 to T3	SMOX	1.75	5.98E-04	FAM90A10P	-1.39	3.10E-02
MSRs	T1 to T3	C4A	2.48	6.19E-04	SLC8A1	-2.97	3.86E-02
MSRs	T1 to T3	MKI67	1.94	9.04E-04	SIAH2	1.26	4.94E-02
MSRs	T1 to T3	RPS24	1.54	1.76E-03	MCEMP1	-1.35	4.94E-02
MSRs	T1 to T3	HIST1H2AM	1.60	2.30E-03			
MSRs	T2 to T3	DEFA3	4.80	9.43E-27	CENPM	2.02	3.92E-03
MSRs	T2 to T3	DEFA1B	4.72	2.79E-22	RNASE3	2.22	4.58E-03
MSRs	T2 to T3	DEFA1	4.72	2.79E-22	TOP2A	2.55	7.64E-03
MSRs	T2 to T3	DEFA4	4.09	3.92E-19	CDKN3	2.87	9.33E-03
MSRs	T2 to T3	CAMP	2.88	1.13E-11	ASPM	2.58	1.08E-02
MSRs	T2 to T3	ERVMER34-1	4.12	4.82E-11	CEACAM8	3.60	1.15E-02
MSRs	T2 to T3	ELANE	3.18	1.58E-06	SHISA4	2.50	1.58E-02
MSRs	T2 to T3	AHSP	2.05	3.52E-06	PTTG1	1.90	1.63E-02
MSRs	T2 to T3	SLC4A1	2.03	4.40E-06	UBE2C	2.22	1.94E-02
MSRs	T2 to T3	LTF	2.89	5.04E-05	NUSAP1	1.95	1.94E-02

MSRs	T2 to T3	LCN2	2.28	6.44E-05	HLA-DRB5	-1.70	2.01E-02
MSRs	T2 to T3	CENPF	2.64	7.15E-05	RETN	1.84	2.32E-02
MSRs	T2 to T3	IFI27	1.84	7.15E-05	HIST1H2AH	2.55	2.44E-02
MSRs	T2 to T3	TK1	2.90	1.09E-03	CCNB2	2.84	2.63E-02
MSRs	T2 to T3	GYPB	1.82	2.49E-03	ESCO2	2.99	3.08E-02
MSRs	T2 to T3	TMEM176B	2.24	2.49E-03	CEBPE	2.86	3.33E-02
MSRs	T2 to T3	AURKB	3.47	2.93E-03	KIAA0101	1.94	4.30E-02
MSRs	T2 to T3	RRM2	2.29	3.83E-03	HIST1H2AM	1.42	4.90E-02
MSRs	T2 to T3	MKI67	1.90	3.83E-03			

Supplementary Table 2 –Differential Gene Expression Analysis from Chapter I
All significant DEG from Hypothesis Free Testing. Comparisons include; RVMSR at T0, T1, T2 and T3 (n= 4 vs. 5), and All RTT (n = 9), Responders (n = 4), and MSRs (n = 5) at T0 to T1, T0 to T2, T0 to T3, T1 to T2, T1 to T3, and T2 to T3.
Legend:
FDR = False Discovery Rate, LogFC = Log$_2$ Fold Change

Group	Comparison	GO biological process complete	FDR
All RTT	T1 to T2	negative regulation of dendritic cell differentiation (GO:2001199)	2.09E-03
All RTT	T1 to T2	regulation of dendritic cell differentiation (GO:2001198)	3.40E-03
MSR	T0 to T2	erythrocyte development (GO:0048821)	3.33E-02
MSR	T0 to T2	erythrocyte differentiation (GO:0030218)	3.71E-02
MSR	T0 to T2	erythrocyte homeostasis (GO:0034101)	2.65E-02
MSR	T0 to T2	myeloid cell homeostasis (GO:0002262)	3.94E-02
MSR	T0 to T3	membrane disruption in other organism (GO:0051673)	1.41E-06
MSR	T0 to T3	antifungal humoral response (GO:0019732)	2.41E-04
MSR	T0 to T3	innate immune response in mucosa (GO:0002227)	4.02E-07
MSR	T0 to T3	response to yeast (GO:0001878)	2.59E-02
MSR	T0 to T3	defense response to fungus (GO:0050832)	3.18E-09
MSR	T0 to T3	mucosal immune response (GO:0002385)	7.22E-07
MSR	T0 to T3	organ or tissue specific immune response (GO:0002251)	1.07E-06
MSR	T0 to T3	T cell chemotaxis (GO:0010818)	4.15E-02
MSR	T0 to T3	killing by host of symbiont cells (GO:0051873)	1.38E-03
MSR	T0 to T3	killing of cells in other organism involved in symbiotic interaction (GO:0051883)	1.71E-03
MSR	T0 to T3	response to fungus (GO:0009620)	9.79E-09
MSR	T0 to T3	antibacterial humoral response (GO:0019731)	4.05E-07
MSR	T0 to T3	killing of cells of other organism (GO:0031640)	6.24E-08
MSR	T0 to T3	antimicrobial humoral immune response mediated by antimicrobial peptide (GO:0061844)	1.93E-07
MSR	T0 to T3	defense response to Gram-negative bacterium (GO:0050829)	1.31E-06
MSR	T0 to T3	cell killing (GO:0001906)	3.82E-07
MSR	T0 to T3	defense response to Gram-positive bacterium (GO:0050830)	8.71E-05

MSR	T0 to T3	regulation of mitotic sister chromatid separation (GO:0010965)	2.26E-02
MSR	T0 to T3	regulation of chromosome segregation (GO:0051983)	1.76E-03
MSR	T0 to T3	biological process involved in interaction with symbiont (GO:0051702)	1.73E-03
MSR	T0 to T3	antimicrobial humoral response (GO:0019730)	8.61E-07
MSR	T0 to T3	regulation of sister chromatid segregation (GO:0033045)	2.83E-02
MSR	T0 to T3	regulation of chromosome separation (GO:1905818)	2.79E-02
MSR	T0 to T3	modulation of process of other organism (GO:0035821)	3.97E-04
MSR	T0 to T3	cellular response to lipopolysaccharide (GO:0071222)	2.18E-02
MSR	T0 to T3	cellular response to molecule of bacterial origin (GO:0071219)	2.59E-02
MSR	T0 to T3	neutrophil degranulation (GO:0043312)	3.61E-07
MSR	T0 to T3	neutrophil activation involved in immune response (GO:0002283)	3.51E-07
MSR	T0 to T3	defense response to bacterium (GO:0042742)	8.67E-05
MSR	T0 to T3	neutrophil mediated immunity (GO:0002446)	3.66E-07
MSR	T0 to T3	neutrophil activation (GO:0042119)	3.49E-07
MSR	T0 to T3	granulocyte activation (GO:0036230)	3.48E-07
MSR	T0 to T3	leukocyte degranulation (GO:0043299)	3.69E-07
MSR	T0 to T3	myeloid leukocyte mediated immunity (GO:0002444)	4.07E-07
MSR	T0 to T3	myeloid cell activation involved in immune response (GO:0002275)	4.50E-07
MSR	T0 to T3	defense response to symbiont (GO:0140546)	3.49E-02
MSR	T0 to T3	defense response to virus (GO:0051607)	3.44E-02
MSR	T0 to T3	cellular response to biotic stimulus (GO:0071216)	3.57E-02
MSR	T0 to T3	humoral immune response (GO:0006959)	1.73E-04
MSR	T0 to T3	myeloid leukocyte activation (GO:0002274)	1.11E-06
MSR	T0 to T3	leukocyte activation involved in immune response (GO:0002366)	1.80E-06
MSR	T0 to T3	cell activation involved in immune response (GO:0002263)	1.83E-06
MSR	T0 to T3	response to lipopolysaccharide (GO:0032496)	1.27E-02
MSR	T0 to T3	response to molecule of bacterial origin (GO:0002237)	1.60E-02
MSR	T0 to T3	regulated exocytosis (GO:0045055)	4.07E-06
MSR	T0 to T3	leukocyte mediated immunity (GO:0002443)	8.43E-06
MSR	T0 to T3	leukocyte migration (GO:0050900)	2.61E-02
MSR	T0 to T3	immune effector process (GO:0002252)	4.32E-08
MSR	T0 to T3	exocytosis (GO:0006887)	1.09E-05
MSR	T0 to T3	leukocyte activation (GO:0045321)	4.45E-06
MSR	T0 to T3	innate immune response (GO:0045087)	2.08E-04
MSR	T0 to T3	defense response to other organism (GO:0098542)	1.10E-05
MSR	T0 to T3	secretion by cell (GO:0032940)	5.75E-05
MSR	T0 to T3	cell activation (GO:0001775)	1.69E-05
MSR	T0 to T3	export from cell (GO:0140352)	8.55E-05
MSR	T0 to T3	response to bacterium (GO:0009617)	7.04E-03

MSR	T0 to T3	secretion (GO:0046903)	1.45E-04
MSR	T0 to T3	positive regulation of transferase activity (GO:0051347)	4.14E-02
MSR	T0 to T3	defense response (GO:0006952)	2.22E-05
MSR	T0 to T3	response to other organism (GO:0051707)	2.01E-04
MSR	T0 to T3	response to external biotic stimulus (GO:0043207)	1.99E-04
MSR	T0 to T3	response to biotic stimulus (GO:0009607)	2.36E-04
MSR	T0 to T3	immune response (GO:0006955)	1.01E-05
MSR	T0 to T3	vesicle-mediated transport (GO:0016192)	3.61E-03
MSR	T0 to T3	biological process involved in interspecies interaction between organisms (GO:0044419)	7.16E-03
MSR	T0 to T3	establishment of localization in cell (GO:0051649)	3.44E-03
MSR	T0 to T3	immune system process (GO:0002376)	6.25E-04
MSR	T0 to T3	response to external stimulus (GO:0009605)	6.04E-03
MSR	T0 to T3	cellular localization (GO:0051641)	2.97E-02
MSR	T0 to T3	response to stress (GO:0006950)	9.30E-03
MSR	T1 to T2	hemoglobin metabolic process (GO:0020027)	7.29E-03
MSR	T1 to T2	erythrocyte development (GO:0048821)	2.62E-04
MSR	T1 to T2	myeloid cell development (GO:0061515)	5.98E-04
MSR	T1 to T2	erythrocyte differentiation (GO:0030218)	2.47E-04
MSR	T1 to T2	erythrocyte homeostasis (GO:0034101)	2.78E-04
MSR	T1 to T2	myeloid cell homeostasis (GO:0002262)	6.81E-04
MSR	T1 to T2	myeloid cell differentiation (GO:0030099)	1.46E-03
MSR	T1 to T2	homeostasis of number of cells (GO:0048872)	1.40E-02
MSR	T1 to T2	hemopoiesis (GO:0030097)	4.24E-02
MSR	T1 to T2	regulation of developmental process (GO:0050793)	4.26E-02
MSR	T1 to T3	membrane disruption in other organism (GO:0051673)	3.04E-06
MSR	T1 to T3	antifungal humoral response (GO:0019732)	0.000392
MSR	T1 to T3	innate immune response in mucosa (GO:0002227)	2.04E-08
MSR	T1 to T3	positive regulation of apoptotic cell clearance (GO:2000427)	0.0208
MSR	T1 to T3	regulation of apoptotic cell clearance (GO:2000425)	0.0249
MSR	T1 to T3	response to yeast (GO:0001878)	0.0289
MSR	T1 to T3	mucosal immune response (GO:0002385)	3.30E-08
MSR	T1 to T3	organ or tissue specific immune response (GO:0002251)	4.77E-08
MSR	T1 to T3	T cell chemotaxis (GO:0010818)	0.0498
MSR	T1 to T3	defense response to fungus (GO:0050832)	9.82E-08
MSR	T1 to T3	killing by host of symbiont cells (GO:0051873)	0.00174
MSR	T1 to T3	killing of cells in other organism involved in symbiotic interaction (GO:0051883)	0.00205
MSR	T1 to T3	antibacterial humoral response (GO:0019731)	1.48E-08
MSR	T1 to T3	response to fungus (GO:0009620)	3.53E-07
MSR	T1 to T3	defense response to Gram-negative bacterium (GO:0050829)	9.85E-08
MSR	T1 to T3	killing of cells of other organism (GO:0031640)	2.30E-06

MSR	T1 to T3	antimicrobial humoral immune response mediated by antimicrobial peptide (GO:0061844)	1.86E-07
MSR	T1 to T3	defense response to Gram-positive bacterium (GO:0050830)	5.26E-06
MSR	T1 to T3	cell killing (GO:0001906)	1.39E-05
MSR	T1 to T3	biological process involved in interaction with symbiont (GO:0051702)	0.0022
MSR	T1 to T3	antimicrobial humoral response (GO:0019730)	2.08E-06
MSR	T1 to T3	modulation of process of other organism (GO:0035821)	0.000592
MSR	T1 to T3	humoral immune response (GO:0006959)	1.92E-06
MSR	T1 to T3	cellular response to lipopolysaccharide (GO:0071222)	0.0255
MSR	T1 to T3	cellular response to molecule of bacterial origin (GO:0071219)	0.0302
MSR	T1 to T3	defense response to bacterium (GO:0042742)	0.000166
MSR	T1 to T3	cellular response to biotic stimulus (GO:0071216)	0.0464
MSR	T1 to T3	response to molecule of bacterial origin (GO:0002237)	0.00167
MSR	T1 to T3	neutrophil degranulation (GO:0043312)	0.000133
MSR	T1 to T3	neutrophil activation involved in immune response (GO:0002283)	0.000134
MSR	T1 to T3	neutrophil mediated immunity (GO:0002446)	0.000141
MSR	T1 to T3	neutrophil activation (GO:0042119)	0.000138
MSR	T1 to T3	granulocyte activation (GO:0036230)	0.00014
MSR	T1 to T3	leukocyte degranulation (GO:0043299)	0.000148
MSR	T1 to T3	response to lipopolysaccharide (GO:0032496)	0.0157
MSR	T1 to T3	myeloid leukocyte mediated immunity (GO:0002444)	0.000155
MSR	T1 to T3	myeloid cell activation involved in immune response (GO:0002275)	0.000163
MSR	T1 to T3	myeloid leukocyte activation (GO:0002274)	0.000353
MSR	T1 to T3	leukocyte mediated immunity (GO:0002443)	2.33E-05
MSR	T1 to T3	leukocyte activation involved in immune response (GO:0002366)	0.000492
MSR	T1 to T3	cell activation involved in immune response (GO:0002263)	0.0005
MSR	T1 to T3	response to bacterium (GO:0009617)	0.000145
MSR	T1 to T3	regulated exocytosis (GO:0045055)	0.000914
MSR	T1 to T3	innate immune response (GO:0045087)	0.000411
MSR	T1 to T3	exocytosis (GO:0006887)	0.00201
MSR	T1 to T3	immune effector process (GO:0002252)	5.84E-05
MSR	T1 to T3	defense response to other organism (GO:0098542)	0.000233
MSR	T1 to T3	export from cell (GO:0140352)	0.00128
MSR	T1 to T3	leukocyte activation (GO:0045321)	0.00622
MSR	T1 to T3	secretion by cell (GO:0032940)	0.0066
MSR	T1 to T3	response to other organism (GO:0051707)	0.000401
MSR	T1 to T3	response to external biotic stimulus (GO:0043207)	0.000394
MSR	T1 to T3	response to biotic stimulus (GO:0009607)	0.000485
MSR	T1 to T3	secretion (GO:0046903)	0.0139
MSR	T1 to T3	cell activation (GO:0001775)	0.0158

MSR	T1 to T3	defense response (GO:0006952)	0.00236
MSR	T1 to T3	immune response (GO:0006955)	0.00111
MSR	T1 to T3	biological process involved in interspecies interaction between organisms (GO:0044419)	0.00206
MSR	T1 to T3	establishment of localization in cell (GO:0051649)	0.00589
MSR	T1 to T3	response to external stimulus (GO:0009605)	0.00985
MSR	T1 to T3	immune system process (GO:0002376)	0.0066
MSR	T1 to T3	cellular localization (GO:0051641)	0.0111
MSR	T2 to T3	membrane disruption in other organism (GO:0051673)	1.14E-05
MSR	T2 to T3	antifungal humoral response (GO:0019732)	6.54E-04
MSR	T2 to T3	innate immune response in mucosa (GO:0002227)	1.58E-07
MSR	T2 to T3	response to yeast (GO:0001878)	3.32E-02
MSR	T2 to T3	mucosal immune response (GO:0002385)	2.55E-07
MSR	T2 to T3	organ or tissue specific immune response (GO:0002251)	3.68E-07
MSR	T2 to T3	defense response to fungus (GO:0050832)	7.55E-07
MSR	T2 to T3	killing by host of symbiont cells (GO:0051873)	2.93E-03
MSR	T2 to T3	killing of cells in other organism involved in symbiotic interaction (GO:0051883)	3.55E-03
MSR	T2 to T3	antibacterial humoral response (GO:0019731)	1.66E-07
MSR	T2 to T3	response to fungus (GO:0009620)	1.97E-06
MSR	T2 to T3	negative regulation of mitotic sister chromatid separation (GO:2000816)	6.11E-03
MSR	T2 to T3	negative regulation of mitotic sister chromatid segregation (GO:0033048)	6.03E-03
MSR	T2 to T3	negative regulation of sister chromatid segregation (GO:0033046)	5.95E-03
MSR	T2 to T3	negative regulation of chromosome segregation (GO:0051985)	6.93E-03
MSR	T2 to T3	negative regulation of chromosome separation (GO:1905819)	6.84E-03
MSR	T2 to T3	defense response to Gram-negative bacterium (GO:0050829)	7.83E-07
MSR	T2 to T3	killing of cells of other organism (GO:0031640)	1.37E-05
MSR	T2 to T3	antimicrobial humoral immune response mediated by antimicrobial peptide (GO:0061844)	1.44E-06
MSR	T2 to T3	regulation of mitotic sister chromatid segregation (GO:0033047)	1.66E-02
MSR	T2 to T3	regulation of mitotic sister chromatid separation (GO:0010965)	2.00E-03
MSR	T2 to T3	defense response to Gram-positive bacterium (GO:0050830)	3.21E-05
MSR	T2 to T3	regulation of chromosome segregation (GO:0051983)	3.09E-04
MSR	T2 to T3	biological process involved in interaction with symbiont (GO:0051702)	3.00E-04
MSR	T2 to T3	regulation of sister chromatid segregation (GO:0033045)	2.69E-03
MSR	T2 to T3	regulation of chromosome separation (GO:1905818)	2.65E-03
MSR	T2 to T3	antimicrobial humoral response (GO:0019730)	8.40E-07
MSR	T2 to T3	negative regulation of chromosome organization (GO:2001251)	3.47E-03
MSR	T2 to T3	cell killing (GO:0001906)	7.60E-05

MSR	T2 to T3	regulation of mitotic metaphase/anaphase transition (GO:0030071)	3.22E-02
MSR	T2 to T3	regulation of metaphase/anaphase transition of cell cycle (GO:1902099)	3.62E-02
MSR	T2 to T3	protein localization to chromosome (GO:0034502)	4.59E-02
MSR	T2 to T3	modulation of process of other organism (GO:0035821)	1.51E-04
MSR	T2 to T3	regulation of mitotic nuclear division (GO:0007088)	9.88E-03
MSR	T2 to T3	sister chromatid segregation (GO:0000819)	2.20E-03
MSR	T2 to T3	cellular response to lipopolysaccharide (GO:0071222)	3.71E-04
MSR	T2 to T3	anaphase (GO:0051322)	2.71E-03
MSR	T2 to T3	mitotic anaphase (GO:0000090)	2.67E-03
MSR	T2 to T3	cellular response to molecule of bacterial origin (GO:0071219)	4.91E-04
MSR	T2 to T3	M phase (GO:0000279)	2.78E-03
MSR	T2 to T3	mitotic M phase (GO:0000087)	2.73E-03
MSR	T2 to T3	nuclear chromosome segregation (GO:0098813)	1.25E-04
MSR	T2 to T3	regulation of nuclear division (GO:0051783)	1.98E-02
MSR	T2 to T3	cellular response to biotic stimulus (GO:0071216)	7.84E-04
MSR	T2 to T3	biological phase (GO:0044848)	1.96E-04
MSR	T2 to T3	mitotic cell cycle phase (GO:0098763)	1.90E-04
MSR	T2 to T3	cell cycle phase (GO:0022403)	1.84E-04
MSR	T2 to T3	defense response to bacterium (GO:0042742)	1.15E-05
MSR	T2 to T3	chromosome segregation (GO:0007059)	3.29E-04
MSR	T2 to T3	mitotic prometaphase (GO:0000236)	3.87E-02
MSR	T2 to T3	mitotic nuclear division (GO:0140014)	7.51E-03
MSR	T2 to T3	spindle organization (GO:0007051)	1.03E-02
MSR	T2 to T3	response to lipopolysaccharide (GO:0032496)	5.31E-04
MSR	T2 to T3	response to molecule of bacterial origin (GO:0002237)	7.15E-04
MSR	T2 to T3	humoral immune response (GO:0006959)	1.82E-04
MSR	T2 to T3	nuclear division (GO:0000280)	7.84E-04
MSR	T2 to T3	organelle fission (GO:0048285)	1.25E-03
MSR	T2 to T3	neutrophil degranulation (GO:0043312)	1.23E-04
MSR	T2 to T3	neutrophil activation involved in immune response (GO:0002283)	1.26E-04
MSR	T2 to T3	cell division (GO:0051301)	1.27E-04
MSR	T2 to T3	neutrophil mediated immunity (GO:0002446)	1.24E-04
MSR	T2 to T3	neutrophil activation (GO:0042119)	1.23E-04
MSR	T2 to T3	granulocyte activation (GO:0036230)	1.27E-04
MSR	T2 to T3	leukocyte degranulation (GO:0043299)	1.37E-04
MSR	T2 to T3	regulation of chromosome organization (GO:0033044)	2.65E-02
MSR	T2 to T3	mitotic cell cycle phase transition (GO:0044772)	2.71E-02
MSR	T2 to T3	myeloid leukocyte mediated immunity (GO:0002444)	1.47E-04
MSR	T2 to T3	myeloid cell activation involved in immune response (GO:0002275)	1.64E-04

MSR	T2 to T3	cell cycle phase transition (GO:0044770)	3.04E-02
MSR	T2 to T3	mitotic cell cycle process (GO:1903047)	2.51E-05
MSR	T2 to T3	myeloid leukocyte activation (GO:0002274)	3.22E-04
MSR	T2 to T3	mitotic cell cycle (GO:0000278)	6.35E-05
MSR	T2 to T3	leukocyte activation involved in immune response (GO:0002366)	5.20E-04
MSR	T2 to T3	cell activation involved in immune response (GO:0002263)	5.35E-04
MSR	T2 to T3	cell cycle process (GO:0022402)	5.94E-07
MSR	T2 to T3	regulated exocytosis (GO:0045055)	9.50E-04
MSR	T2 to T3	cellular response to lipid (GO:0071396)	3.22E-02
MSR	T2 to T3	response to bacterium (GO:0009617)	1.24E-03
MSR	T2 to T3	microtubule cytoskeleton organization (GO:0000226)	1.15E-02
MSR	T2 to T3	leukocyte mediated immunity (GO:0002443)	1.79E-03
MSR	T2 to T3	cell cycle (GO:0007049)	1.15E-06
MSR	T2 to T3	exocytosis (GO:0006887)	2.31E-03
MSR	T2 to T3	innate immune response (GO:0045087)	3.46E-03
MSR	T2 to T3	defense response to other organism (GO:0098542)	4.99E-04
MSR	T2 to T3	immune effector process (GO:0002252)	7.73E-04
MSR	T2 to T3	regulation of cell cycle (GO:0051726)	3.15E-04
MSR	T2 to T3	leukocyte activation (GO:0045321)	6.95E-03
MSR	T2 to T3	secretion by cell (GO:0032940)	7.34E-03
MSR	T2 to T3	export from cell (GO:0140352)	1.02E-02
MSR	T2 to T3	chromosome organization (GO:0051276)	1.60E-02
MSR	T2 to T3	secretion (GO:0046903)	1.59E-02
MSR	T2 to T3	cell activation (GO:0001775)	1.82E-02
MSR	T2 to T3	defense response (GO:0006952)	6.09E-03
MSR	T2 to T3	response to other organism (GO:0051707)	6.08E-03
MSR	T2 to T3	response to external biotic stimulus (GO:0043207)	6.07E-03
MSR	T2 to T3	response to biotic stimulus (GO:0009607)	6.91E-03
MSR	T2 to T3	immune system process (GO:0002376)	6.15E-05
MSR	T2 to T3	immune response (GO:0006955)	1.97E-02
MSR	T2 to T3	cellular localization (GO:0051641)	5.95E-03
MSR	T2 to T3	response to stress (GO:0006950)	1.25E-02
RVMSR	T2 to T3	multicellular organismal process (GO:0032501)	4.64E-12
RVMSR	T2 to T3	gene expression (GO:0010467)	1.40E-10
RVMSR	T2 to T3	cellular macromolecule metabolic process (GO:0044260)	3.16E-08
RVMSR	T2 to T3	anatomical structure morphogenesis (GO:0009653)	4.78E-08
RVMSR	T2 to T3	macromolecule metabolic process (GO:0043170)	5.12E-08
RVMSR	T2 to T3	RNA processing (GO:0006396)	1.78E-07
RVMSR	T2 to T3	system process (GO:0003008)	2.14E-07
RVMSR	T2 to T3	cellular metabolic process (GO:0044237)	3.82E-07
RVMSR	T2 to T3	cellular protein metabolic process (GO:0044267)	6.00E-07

RVMSR	T2 to T3	primary metabolic process (GO:0044238)	9.56E-07
RVMSR	T2 to T3	nitrogen compound metabolic process (GO:0006807)	2.43E-06
RVMSR	T2 to T3	multicellular organism development (GO:0007275)	3.81E-06
RVMSR	T2 to T3	RNA metabolic process (GO:0016070)	4.09E-06
RVMSR	T2 to T3	anatomical structure development (GO:0048856)	4.19E-06
RVMSR	T2 to T3	organic substance metabolic process (GO:0071704)	5.51E-06
RVMSR	T2 to T3	nucleic acid metabolic process (GO:0090304)	7.19E-06
RVMSR	T2 to T3	macromolecule modification (GO:0043412)	8.44E-06
RVMSR	T2 to T3	developmental process (GO:0032502)	1.06E-05
RVMSR	T2 to T3	metabolic process (GO:0008152)	2.30E-05
RVMSR	T2 to T3	cell-cell signaling (GO:0007267)	2.42E-05
RVMSR	T2 to T3	mRNA processing (GO:0006397)	4.62E-05
RVMSR	T2 to T3	intracellular transport (GO:0046907)	4.67E-05
RVMSR	T2 to T3	cellular nitrogen compound metabolic process (GO:0034641)	4.96E-05
RVMSR	T2 to T3	protein modification process (GO:0036211)	5.08E-05
RVMSR	T2 to T3	tissue development (GO:0009888)	5.17E-05
RVMSR	T2 to T3	cellular protein modification process (GO:0006464)	5.27E-05
RVMSR	T2 to T3	system development (GO:0048731)	5.31E-05
RVMSR	T2 to T3	cell adhesion (GO:0007155)	7.12E-05
RVMSR	T2 to T3	adaptive immune response (GO:0002250)	7.36E-05
RVMSR	T2 to T3	cell junction organization (GO:0034330)	7.81E-05
RVMSR	T2 to T3	biological adhesion (GO:0022610)	9.41E-05
RVMSR	T2 to T3	mRNA metabolic process (GO:0016071)	9.41E-05
RVMSR	T2 to T3	nucleobase-containing compound metabolic process (GO:0006139)	9.95E-05
RVMSR	T2 to T3	phagocytosis, engulfment (GO:0006911)	1.08E-04
RVMSR	T2 to T3	protein modification by small protein conjugation or removal (GO:0070647)	1.97E-04
RVMSR	T2 to T3	protein metabolic process (GO:0019538)	2.79E-04
RVMSR	T2 to T3	viral process (GO:0016032)	3.72E-04
RVMSR	T2 to T3	cell morphogenesis (GO:0000902)	3.88E-04
RVMSR	T2 to T3	nervous system process (GO:0050877)	3.93E-04
RVMSR	T2 to T3	plasma membrane invagination (GO:0099024)	5.86E-04
RVMSR	T2 to T3	RNA splicing (GO:0008380)	5.99E-04
RVMSR	T2 to T3	heterocycle metabolic process (GO:0046483)	6.83E-04
RVMSR	T2 to T3	cell development (GO:0048468)	7.16E-04
RVMSR	T2 to T3	biological process involved in symbiotic interaction (GO:0044403)	1.04E-03
RVMSR	T2 to T3	animal organ development (GO:0048513)	1.26E-03
RVMSR	T2 to T3	cell differentiation (GO:0030154)	1.31E-03
RVMSR	T2 to T3	activation of immune response (GO:0002253)	1.41E-03
RVMSR	T2 to T3	trans-synaptic signaling (GO:0099537)	1.50E-03

RVMSR	T2 to T3	protein-containing complex subunit organization (GO:0043933)	1.53E-03
RVMSR	T2 to T3	cellular localization (GO:0051641)	1.62E-03
RVMSR	T2 to T3	immune response-regulating cell surface receptor signaling pathway (GO:0002768)	1.62E-03
RVMSR	T2 to T3	immune response-regulating signaling pathway (GO:0002764)	1.62E-03
RVMSR	T2 to T3	cellular developmental process (GO:0048869)	1.66E-03
RVMSR	T2 to T3	immune system process (GO:0002376)	1.68E-03
RVMSR	T2 to T3	movement of cell or subcellular component (GO:0006928)	1.69E-03
RVMSR	T2 to T3	membrane invagination (GO:0010324)	1.76E-03
RVMSR	T2 to T3	protein modification by small protein conjugation (GO:0032446)	1.83E-03
RVMSR	T2 to T3	cellular aromatic compound metabolic process (GO:0006725)	1.85E-03
RVMSR	T2 to T3	vesicle-mediated transport (GO:0016192)	1.87E-03
RVMSR	T2 to T3	cellular nitrogen compound biosynthetic process (GO:0044271)	2.00E-03
RVMSR	T2 to T3	anatomical structure formation involved in morphogenesis (GO:0048646)	2.03E-03
RVMSR	T2 to T3	reproductive process (GO:0022414)	2.03E-03
RVMSR	T2 to T3	vascular process in circulatory system (GO:0003018)	2.06E-03
RVMSR	T2 to T3	cellular macromolecule biosynthetic process (GO:0034645)	2.17E-03
RVMSR	T2 to T3	animal organ morphogenesis (GO:0009887)	2.19E-03
RVMSR	T2 to T3	regulation of system process (GO:0044057)	2.29E-03
RVMSR	T2 to T3	reproduction (GO:0000003)	2.31E-03
RVMSR	T2 to T3	cellular component morphogenesis (GO:0032989)	2.42E-03
RVMSR	T2 to T3	synapse organization (GO:0050808)	3.09E-03
RVMSR	T2 to T3	immune response-activating signal transduction (GO:0002757)	3.65E-03
RVMSR	T2 to T3	immune response-activating cell surface receptor signaling pathway (GO:0002429)	3.70E-03
RVMSR	T2 to T3	immune response (GO:0006955)	3.73E-03
RVMSR	T2 to T3	cell morphogenesis involved in differentiation (GO:0000904)	3.93E-03
RVMSR	T2 to T3	regulation of tube diameter (GO:0035296)	4.29E-03
RVMSR	T2 to T3	synaptic signaling (GO:0099536)	4.30E-03
RVMSR	T2 to T3	cell-cell adhesion (GO:0098609)	4.34E-03
RVMSR	T2 to T3	blood vessel diameter maintenance (GO:0097746)	4.35E-03
RVMSR	T2 to T3	anterograde trans-synaptic signaling (GO:0098916)	4.38E-03
RVMSR	T2 to T3	chemical synaptic transmission (GO:0007268)	4.44E-03
RVMSR	T2 to T3	regulation of tube size (GO:0035150)	4.47E-03
RVMSR	T2 to T3	establishment of localization in cell (GO:0051649)	4.52E-03
RVMSR	T2 to T3	intracellular protein transport (GO:0006886)	4.56E-03
RVMSR	T2 to T3	protein-containing complex assembly (GO:0065003)	4.57E-03
RVMSR	T2 to T3	neuron projection morphogenesis (GO:0048812)	5.20E-03
RVMSR	T2 to T3	ncRNA processing (GO:0034470)	5.45E-03
RVMSR	T2 to T3	complement activation (GO:0006956)	5.77E-03

RVMSR	T2 to T3	cell projection morphogenesis (GO:0048858)	5.82E-03
RVMSR	T2 to T3	axon guidance (GO:0007411)	6.33E-03
RVMSR	T2 to T3	regulation of catabolic process (GO:0009894)	6.41E-03
RVMSR	T2 to T3	complement activation, classical pathway (GO:0006958)	6.44E-03
RVMSR	T2 to T3	peptidyl-lysine modification (GO:0018205)	6.58E-03
RVMSR	T2 to T3	axon development (GO:0061564)	6.64E-03
RVMSR	T2 to T3	plasma membrane bounded cell projection morphogenesis (GO:0120039)	6.65E-03
RVMSR	T2 to T3	chromatin organization (GO:0006325)	6.85E-03
RVMSR	T2 to T3	B cell receptor signaling pathway (GO:0050853)	6.90E-03
RVMSR	T2 to T3	cellular macromolecule localization (GO:0070727)	6.97E-03
RVMSR	T2 to T3	Fc-epsilon receptor signaling pathway (GO:0038095)	7.22E-03
RVMSR	T2 to T3	locomotion (GO:0040011)	7.26E-03
RVMSR	T2 to T3	axonogenesis (GO:0007409)	7.43E-03
RVMSR	T2 to T3	neuron projection guidance (GO:0097485)	7.89E-03
RVMSR	T2 to T3	cell morphogenesis involved in neuron differentiation (GO:0048667)	7.92E-03
RVMSR	T2 to T3	neuron development (GO:0048666)	7.95E-03
RVMSR	T2 to T3	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile (GO:0000377)	7.95E-03
RVMSR	T2 to T3	antigen receptor-mediated signaling pathway (GO:0050851)	7.99E-03
RVMSR	T2 to T3	mRNA splicing, via spliceosome (GO:0000398)	8.03E-03
RVMSR	T2 to T3	sensory organ development (GO:0007423)	8.16E-03
RVMSR	T2 to T3	organic cyclic compound metabolic process (GO:1901360)	8.23E-03
RVMSR	T2 to T3	negative regulation of developmental process (GO:0051093)	8.33E-03
RVMSR	T2 to T3	cell-cell adhesion via plasma-membrane adhesion molecules (GO:0098742)	8.35E-03
RVMSR	T2 to T3	cellular protein localization (GO:0034613)	8.36E-03
RVMSR	T2 to T3	cell activation (GO:0001775)	8.67E-03
RVMSR	T2 to T3	nervous system development (GO:0007399)	8.74E-03
RVMSR	T2 to T3	epithelium development (GO:0060429)	9.86E-03
RVMSR	T2 to T3	cell part morphogenesis (GO:0032990)	1.02E-02
RVMSR	T2 to T3	generation of neurons (GO:0048699)	1.04E-02
RVMSR	T2 to T3	protein localization (GO:0008104)	1.05E-02
RVMSR	T2 to T3	regulation of cytosolic calcium ion concentration (GO:0051480)	1.09E-02
RVMSR	T2 to T3	immune effector process (GO:0002252)	1.09E-02
RVMSR	T2 to T3	cell migration (GO:0016477)	1.10E-02
RVMSR	T2 to T3	RNA splicing, via transesterification reactions (GO:0000375)	1.16E-02
RVMSR	T2 to T3	protein ubiquitination (GO:0016567)	1.17E-02
RVMSR	T2 to T3	humoral immune response mediated by circulating immunoglobulin (GO:0002455)	1.17E-02
RVMSR	T2 to T3	neuron projection development (GO:0031175)	1.27E-02
RVMSR	T2 to T3	response to organic cyclic compound (GO:0014070)	1.28E-02
RVMSR	T2 to T3	neurogenesis (GO:0022008)	1.34E-02

RVMSR	T2 to T3	phagocytosis (GO:0006909)	1.34E-02
RVMSR	T2 to T3	ribonucleoprotein complex biogenesis (GO:0022613)	1.35E-02
RVMSR	T2 to T3	chromosome organization (GO:0051276)	1.41E-02
RVMSR	T2 to T3	blood circulation (GO:0008015)	1.43E-02
RVMSR	T2 to T3	cellular protein-containing complex assembly (GO:0034622)	1.43E-02
RVMSR	T2 to T3	external encapsulating structure organization (GO:0045229)	1.44E-02
RVMSR	T2 to T3	organelle organization (GO:0006996)	1.44E-02
RVMSR	T2 to T3	inorganic ion transmembrane transport (GO:0098660)	1.51E-02
RVMSR	T2 to T3	leukocyte mediated immunity (GO:0002443)	1.52E-02
RVMSR	T2 to T3	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains (GO:0002460)	1.53E-02
RVMSR	T2 to T3	regulation of telomere maintenance (GO:0032204)	1.54E-02
RVMSR	T2 to T3	cell junction assembly (GO:0034329)	1.69E-02
RVMSR	T2 to T3	extracellular matrix organization (GO:0030198)	1.69E-02
RVMSR	T2 to T3	protein transport (GO:0015031)	1.69E-02
RVMSR	T2 to T3	immunoglobulin production (GO:0002377)	1.69E-02
RVMSR	T2 to T3	extracellular structure organization (GO:0043062)	1.71E-02
RVMSR	T2 to T3	response to endogenous stimulus (GO:0009719)	1.76E-02
RVMSR	T2 to T3	sensory perception of light stimulus (GO:0050953)	1.83E-02
RVMSR	T2 to T3	establishment of protein localization (GO:0045184)	1.83E-02
RVMSR	T2 to T3	immunoglobulin mediated immune response (GO:0016064)	1.84E-02
RVMSR	T2 to T3	Fc receptor signaling pathway (GO:0038093)	1.90E-02
RVMSR	T2 to T3	mRNA transport (GO:0051028)	1.90E-02
RVMSR	T2 to T3	production of molecular mediator of immune response (GO:0002440)	1.92E-02
RVMSR	T2 to T3	leukocyte activation (GO:0045321)	1.93E-02
RVMSR	T2 to T3	ncRNA metabolic process (GO:0034660)	1.99E-02
RVMSR	T2 to T3	multicellular organism reproduction (GO:0032504)	2.00E-02
RVMSR	T2 to T3	regulation of blood circulation (GO:1903522)	2.39E-02
RVMSR	T2 to T3	circulatory system process (GO:0003013)	2.40E-02
RVMSR	T2 to T3	negative regulation of multicellular organismal process (GO:0051241)	2.41E-02
RVMSR	T2 to T3	RNA localization (GO:0006403)	2.44E-02
RVMSR	T2 to T3	killing of cells of other organism (GO:0031640)	2.46E-02
RVMSR	T2 to T3	peptide biosynthetic process (GO:0043043)	2.50E-02
RVMSR	T2 to T3	cell motility (GO:0048870)	2.51E-02
RVMSR	T2 to T3	localization of cell (GO:0051674)	2.53E-02
RVMSR	T2 to T3	antimicrobial humoral response (GO:0019730)	2.54E-02
RVMSR	T2 to T3	camera-type eye development (GO:0043010)	2.54E-02
RVMSR	T2 to T3	skin development (GO:0043588)	2.63E-02
RVMSR	T2 to T3	regulation of vascular permeability (GO:0043114)	2.69E-02
RVMSR	T2 to T3	antimicrobial humoral immune response mediated by antimicrobial peptide (GO:0061844)	2.69E-02

RVMSR	T2 to T3	cell killing (GO:0001906)	2.73E-02
RVMSR	T2 to T3	positive regulation of immune system process (GO:0002684)	2.74E-02
RVMSR	T2 to T3	positive regulation of B cell activation (GO:0050871)	2.74E-02
RVMSR	T2 to T3	multicellular organismal reproductive process (GO:0048609)	2.75E-02
RVMSR	T2 to T3	macromolecule biosynthetic process (GO:0009059)	2.83E-02
RVMSR	T2 to T3	vesicle organization (GO:0016050)	2.85E-02
RVMSR	T2 to T3	heterophilic cell-cell adhesion via plasma membrane cell adhesion molecules (GO:0007157)	2.89E-02
RVMSR	T2 to T3	B cell mediated immunity (GO:0019724)	2.89E-02
RVMSR	T2 to T3	positive regulation of vasoconstriction (GO:0045907)	2.97E-02
RVMSR	T2 to T3	peptide transport (GO:0015833)	2.97E-02
RVMSR	T2 to T3	cellular response to endogenous stimulus (GO:0071495)	2.98E-02
RVMSR	T2 to T3	regulation of cellular catabolic process (GO:0031329)	2.98E-02
RVMSR	T2 to T3	tissue morphogenesis (GO:0048729)	3.29E-02
RVMSR	T2 to T3	translation (GO:0006412)	3.39E-02
RVMSR	T2 to T3	developmental growth (GO:0048589)	3.43E-02
RVMSR	T2 to T3	neuron differentiation (GO:0030182)	3.46E-02
RVMSR	T2 to T3	visual perception (GO:0007601)	3.69E-02
RVMSR	T2 to T3	positive regulation of immune response (GO:0050778)	3.69E-02
RVMSR	T2 to T3	nucleic acid transport (GO:0050657)	3.69E-02
RVMSR	T2 to T3	response to chemical (GO:0042221)	3.71E-02
RVMSR	T2 to T3	RNA transport (GO:0050658)	3.71E-02
RVMSR	T2 to T3	establishment of RNA localization (GO:0051236)	3.73E-02
RVMSR	T2 to T3	regulation of multicellular organismal process (GO:0051239)	3.74E-02
RVMSR	T2 to T3	regulation of nucleobase-containing compound metabolic process (GO:0019219)	3.74E-02
RVMSR	T2 to T3	vasculature development (GO:0001944)	3.86E-02
RVMSR	T2 to T3	tube development (GO:0035295)	4.08E-02
RVMSR	T2 to T3	regulation of response to wounding (GO:1903034)	4.09E-02
RVMSR	T2 to T3	endomembrane system organization (GO:0010256)	4.12E-02
RVMSR	T2 to T3	regulation of wound healing (GO:0061041)	4.31E-02
RVMSR	T2 to T3	growth (GO:0040007)	4.34E-02
RVMSR	T2 to T3	endosomal transport (GO:0016197)	4.44E-02
RVMSR	T2 to T3	negative regulation of cell differentiation (GO:0045596)	4.58E-02
RVMSR	T2 to T3	mitotic nuclear division (GO:0140014)	4.59E-02
RVMSR	T2 to T3	regulation of proteasomal protein catabolic process (GO:0061136)	4.60E-02
RVMSR	T2 to T3	regulation of cellular macromolecule biosynthetic process (GO:2000112)	4.63E-02
RVMSR	T2 to T3	biological process involved in interspecies interaction between organisms (GO:0044419)	4.68E-02
RVMSR	T2 to T3	amide transport (GO:0042886)	4.68E-02
RVMSR	T2 to T3	eye development (GO:0001654)	4.83E-02
RVMSR	T2 to T3	regulation of RNA metabolic process (GO:0051252)	4.83E-02

RVMSR	T2 to T3	circulatory system development (GO:0072359)	4.96E-02
RVMSR	T2 to T3	embryonic morphogenesis (GO:0048598)	4.97E-02

Supplementary Table 3 – GO Analysis from Chapter I Hypothesis Free Testing
All significant ontologies from Hypothesis Free Testing. Comparisons include; RVMSR at T0, T1, T2 and T3 (n= 4 vs. 5), and All RTT (n = 9), Responders (n = 4), and MSRs (n = 5) at T0 to T1, T0 to T2, T0 to T3, T1 to T2, T1 to T3, and T2 to T3. The list of significant DEG, filtered for gene that were not recognised, were used as input for the analysis.
Legend:
FDR = False Discovery Rate

Group	**Comparison**	**Pathway name**	**FDR**
All RTT	T2 to T3	Cell Cycle, Mitotic	8.06E-05
All RTT	T2 to T3	Cell Cycle	9.27E-05
All RTT	T2 to T3	Polo-like kinase mediated events	1.46E-04
All RTT	T2 to T3	G1/S-Specific Transcription	3.50E-04
All RTT	T2 to T3	Transcriptional Regulation by E2F6	3.50E-04
All RTT	T2 to T3	G1/S Transition	3.07E-03
All RTT	T2 to T3	Mitotic G1 phase and G1/S transition	3.26E-03
All RTT	T2 to T3	G2/M Transition	3.66E-03
All RTT	T2 to T3	Mitotic G2-G2/M phases	3.73E-03
All RTT	T2 to T3	Interconversion of nucleotide di- and triphosphates	3.99E-02
All RTT	T2 to T3	Amplification of signal from the kinetochores	3.99E-02
All RTT	T2 to T3	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	3.99E-02
All RTT	T2 to T3	Mitotic Spindle Checkpoint	3.99E-02
All RTT	T2 to T3	EML4 and NUDC in mitotic spindle formation	3.99E-02
All RTT	T2 to T3	Resolution of Sister Chromatid Cohesion	3.99E-02
All RTT	T2 to T3	RHO GTPases Activate Formins	3.99E-02
Responders	T0 to T1	Interferon gamma signaling	3.90E-03
Responders	T0 to T1	Interferon Signaling	4.45E-03
Responders	T0 to T1	Cytokine Signaling in Immune system	8.00E-03
Responders	T0 to T1	Translocation of ZAP-70 to Immunological synapse	8.00E-03
Responders	T0 to T1	Phosphorylation of CD3 and TCR zeta chains	8.00E-03
Responders	T0 to T1	PD-1 signaling	8.00E-03
Responders	T0 to T1	Generation of second messenger molecules	8.00E-03
Responders	T0 to T1	Costimulation by the CD28 family	1.35E-02
Responders	T0 to T1	Downstream TCR signaling	1.68E-02
Responders	T0 to T1	TCR signaling	1.99E-02
Responders	T0 to T1	MHC class II antigen presentation	2.00E-02
Responders	T0 to T1	Immune System	3.40E-02
Responders	T0 to T2	Interferon gamma signaling	3.90E-03
Responders	T0 to T2	Interferon Signaling	4.45E-03
Responders	T0 to T2	Cytokine Signaling in Immune system	8.00E-03

Responders	T0 to T2	Translocation of ZAP-70 to Immunological synapse	8.00E-03
Responders	T0 to T2	Phosphorylation of CD3 and TCR zeta chains	8.00E-03
Responders	T0 to T2	PD-1 signaling	8.00E-03
Responders	T0 to T2	Generation of second messenger molecules	8.00E-03
Responders	T0 to T2	Costimulation by the CD28 family	1.35E-02
Responders	T0 to T2	Downstream TCR signaling	1.68E-02
Responders	T0 to T2	TCR signaling	1.99E-02
Responders	T0 to T2	MHC class II antigen presentation	2.00E-02
Responders	T0 to T2	Immune System	3.40E-02
Responders	T2 to T3	Interferon gamma signaling	3.90E-03
Responders	T2 to T3	Interferon Signaling	4.45E-03
Responders	T2 to T3	Cytokine Signaling in Immune system	8.00E-03
Responders	T2 to T3	Translocation of ZAP-70 to Immunological synapse	8.00E-03
Responders	T2 to T3	Phosphorylation of CD3 and TCR zeta chains	8.00E-03
Responders	T2 to T3	PD-1 signaling	8.00E-03
Responders	T2 to T3	Generation of second messenger molecules	8.00E-03
Responders	T2 to T3	Costimulation by the CD28 family	1.35E-02
Responders	T2 to T3	Downstream TCR signaling	1.68E-02
Responders	T2 to T3	TCR signaling	1.99E-02
Responders	T2 to T3	MHC class II antigen presentation	2.00E-02
Responders	T2 to T3	Immune System	3.40E-02
MSRs	T0 to T1	Axon guidance	4.26E-04
MSRs	T0 to T1	Nervous system development	4.26E-04
MSRs	T0 to T1	Activation of C3 and C5	8.83E-04
MSRs	T0 to T1	Peptide chain elongation	8.95E-04
MSRs	T0 to T1	Eukaryotic Translation Termination	8.95E-04
MSRs	T0 to T1	Selenocysteine synthesis	8.95E-04
MSRs	T0 to T1	Eukaryotic Translation Elongation	8.95E-04
MSRs	T0 to T1	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	8.95E-04
MSRs	T0 to T1	Cellular responses to stress	8.95E-04
MSRs	T0 to T1	Viral mRNA Translation	8.95E-04
MSRs	T0 to T1	Formation of a pool of free 40S subunits	8.95E-04
MSRs	T0 to T1	Response of EIF2AK4 (GCN2) to amino acid deficiency	8.95E-04
MSRs	T0 to T1	Cellular responses to external stimuli	8.95E-04
MSRs	T0 to T1	L13a-mediated translational silencing of Ceruloplasmin expression	8.95E-04
MSRs	T0 to T1	SRP-dependent cotranslational protein targeting to membrane	8.95E-04
MSRs	T0 to T1	GTP hydrolysis and joining of the 60S ribosomal subunit	8.95E-04
MSRs	T0 to T1	Nonsense-Mediated Decay (NMD)	8.95E-04
MSRs	T0 to T1	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	8.95E-04

MSRs	T0 to T1	Microtubule-dependent trafficking of connexons from Golgi to the plasma membrane	8.95E-04
MSRs	T0 to T1	Selenoamino acid metabolism	8.95E-04
MSRs	T0 to T1	Eukaryotic Translation Initiation	8.95E-04
MSRs	T0 to T1	Cap-dependent Translation Initiation	8.95E-04
MSRs	T0 to T1	Transport of connexons to the plasma membrane	9.17E-04
MSRs	T0 to T1	Post-chaperonin tubulin folding pathway	1.10E-03
MSRs	T0 to T1	Developmental Biology	1.12E-03
MSRs	T0 to T1	Regulation of Complement cascade	1.12E-03
MSRs	T0 to T1	Formation of tubulin folding intermediates by CCT/TriC	1.12E-03
MSRs	T0 to T1	Complement cascade	1.27E-03
MSRs	T0 to T1	Prefoldin mediated transfer of substrate to CCT/TriC	1.27E-03
MSRs	T0 to T1	Activation of AMPK downstream of NMDARs	1.27E-03
MSRs	T0 to T1	Influenza Viral RNA Transcription and Replication	1.27E-03
MSRs	T0 to T1	RHO GTPases activate IQGAPs	1.27E-03
MSRs	T0 to T1	Sealing of the nuclear envelope (NE) by ESCRT-III	1.27E-03
MSRs	T0 to T1	Cooperation of Prefoldin and TriC/CCT in actin and tubulin folding	1.35E-03
MSRs	T0 to T1	Regulation of expression of SLITs and ROBOs	1.54E-03
MSRs	T0 to T1	Influenza Infection	1.54E-03
MSRs	T0 to T1	Gap junction assembly	1.74E-03
MSRs	T0 to T1	Major pathway of rRNA processing in the nucleolus and cytosol	1.74E-03
MSRs	T0 to T1	Formation of Fibrin Clot (Clotting Cascade)	1.74E-03
MSRs	T0 to T1	rRNA processing in the nucleus and cytosol	1.74E-03
MSRs	T0 to T1	Aggrephagy	1.74E-03
MSRs	T0 to T1	Assembly and cell surface presentation of NMDA receptors	1.74E-03
MSRs	T0 to T1	rRNA processing	1.74E-03
MSRs	T0 to T1	Carboxyterminal post-translational modifications of tubulin	1.74E-03
MSRs	T0 to T1	Gap junction trafficking	1.97E-03
MSRs	T0 to T1	Recycling pathway of L1	1.97E-03
MSRs	T0 to T1	Signaling by ROBO receptors	2.04E-03
MSRs	T0 to T1	Gap junction trafficking and regulation	2.13E-03
MSRs	T0 to T1	COPI-independent Golgi-to-ER retrograde traffic	2.30E-03
MSRs	T0 to T1	Intraflagellar transport	2.38E-03
MSRs	T0 to T1	HSP90 chaperone cycle for steroid hormone receptors (SHR)	2.65E-03
MSRs	T0 to T1	Kinesins	3.33E-03
MSRs	T0 to T1	Immune System	3.51E-03
MSRs	T0 to T1	Translocation of SLC2A4 (GLUT4) to the plasma membrane	4.15E-03
MSRs	T0 to T1	Translation	4.15E-03
MSRs	T0 to T1	Nuclear Envelope (NE) Reassembly	4.15E-03
MSRs	T0 to T1	The role of GTSE1 in G2/M progression after G2 checkpoint	4.15E-03

MSRs	T0 to T1	Selective autophagy	4.15E-03
MSRs	T0 to T1	Post NMDA receptor activation events	4.15E-03
MSRs	T0 to T1	Defective SERPING1 causes hereditary angioedema	4.15E-03
MSRs	T0 to T1	Infectious disease	4.15E-03
MSRs	T0 to T1	Recruitment of NuMA to mitotic centrosomes	4.15E-03
MSRs	T0 to T1	Chaperonin-mediated protein folding	4.15E-03
MSRs	T0 to T1	Hemostasis	4.15E-03
MSRs	T0 to T1	Activation of NMDA receptors and postsynaptic events	4.15E-03
MSRs	T0 to T1	Protein folding	4.15E-03
MSRs	T0 to T1	COPI-mediated anterograde transport	4.15E-03
MSRs	T0 to T1	COPI-dependent Golgi-to-ER retrograde traffic	4.23E-03
MSRs	T0 to T1	Metabolism of amino acids and derivatives	4.81E-03
MSRs	T0 to T1	Initial triggering of complement	4.89E-03
MSRs	T0 to T1	Disease	5.03E-03
MSRs	T0 to T1	Hedgehog 'off' state	5.15E-03
MSRs	T0 to T1	EML4 and NUDC in mitotic spindle formation	5.41E-03
MSRs	T0 to T1	L1CAM interactions	5.78E-03
MSRs	T0 to T1	Metabolism of proteins	6.17E-03
MSRs	T0 to T1	Resolution of Sister Chromatid Cohesion	6.25E-03
MSRs	T0 to T1	Golgi-to-ER retrograde transport	7.35E-03
MSRs	T0 to T1	Macroautophagy	7.35E-03
MSRs	T0 to T1	RHO GTPases Activate Formins	7.76E-03
MSRs	T0 to T1	MHC class II antigen presentation	7.87E-03
MSRs	T0 to T1	Signaling by Hedgehog	8.75E-03
MSRs	T0 to T1	Autophagy	8.97E-03
MSRs	T0 to T1	ER to Golgi Anterograde Transport	9.31E-03
MSRs	T0 to T1	Factors involved in megakaryocyte development and platelet production	9.90E-03
MSRs	T0 to T1	Transport to the Golgi and subsequent modification	1.32E-02
MSRs	T0 to T1	Separation of Sister Chromatids	1.39E-02
MSRs	T0 to T1	G2/M Transition	1.49E-02
MSRs	T0 to T1	Mitotic G2-G2/M phases	1.51E-02
MSRs	T0 to T1	Diseases of hemostasis	1.53E-02
MSRs	T0 to T1	Defects of contact activation system (CAS) and kallikrein/kinin system (KKS)	1.53E-02
MSRs	T0 to T1	Rap1 signalling	1.53E-02
MSRs	T0 to T1	Cilium Assembly	1.54E-02
MSRs	T0 to T1	Mitotic Prometaphase	1.56E-02
MSRs	T0 to T1	Intra-Golgi and retrograde Golgi-to-ER traffic	1.60E-02
MSRs	T0 to T1	HCMV Early Events	1.63E-02
MSRs	T0 to T1	Neurotransmitter receptors and postsynaptic signal transmission	1.63E-02
MSRs	T0 to T1	Mitotic Anaphase	2.09E-02

MSRs	T0 to T1	Common Pathway of Fibrin Clot Formation	2.10E-02
MSRs	T0 to T1	Mitotic Metaphase and Anaphase	2.10E-02
MSRs	T0 to T1	Innate Immune System	2.10E-02
MSRs	T0 to T1	Intrinsic Pathway of Fibrin Clot Formation	2.19E-02
MSRs	T0 to T1	Metabolism of RNA	2.37E-02
MSRs	T0 to T1	HCMV Infection	2.52E-02
MSRs	T0 to T1	Transmission across Chemical Synapses	2.72E-02
MSRs	T0 to T1	RHO GTPase Effectors	3.13E-02
MSRs	T0 to T1	Organelle biogenesis and maintenance	3.19E-02
MSRs	T0 to T1	Asparagine N-linked glycosylation	3.33E-02
MSRs	T0 to T1	RET signaling	3.87E-02
MSRs	T0 to T2	Activation of C3 and C5	5.62E-03
MSRs	T0 to T2	Erythrocytes take up oxygen and release carbon dioxide	1.44E-02
MSRs	T0 to T2	O2/CO2 exchange in erythrocytes	1.46E-02
MSRs	T0 to T2	Erythrocytes take up carbon dioxide and release oxygen	1.46E-02
MSRs	T0 to T3	Neutrophil degranulation	4.67E-07
MSRs	T0 to T3	Antimicrobial peptides	4.22E-06
MSRs	T0 to T3	Immune System	4.22E-06
MSRs	T0 to T3	Innate Immune System	2.06E-05
MSRs	T0 to T3	Alpha-defensins	3.13E-05
MSRs	T0 to T3	Defensins	2.44E-03
MSRs	T0 to T3	Cell Cycle, Mitotic	9.21E-03
MSRs	T0 to T3	Interferon Signaling	1.01E-02
MSRs	T0 to T3	Polo-like kinase mediated events	1.29E-02
MSRs	T0 to T3	Cell Cycle	1.91E-02
MSRs	T0 to T3	G1/S-Specific Transcription	3.63E-02
MSRs	T0 to T3	Transcriptional Regulation by E2F6	3.63E-02
MSRs	T0 to T3	Cross-presentation of soluble exogenous antigens (endosomes)	4.42E-02
MSRs	T0 to T3	Separation of Sister Chromatids	4.73E-02
MSRs	T1 to T2	Regulation of expression of SLITs and ROBOs	3.53E-04
MSRs	T1 to T2	Nonsense Mediated Decay (NMD) independent of the Exon Junction Complex (EJC)	3.53E-04
MSRs	T1 to T2	Eukaryotic Translation Termination	3.53E-04
MSRs	T1 to T2	Nonsense-Mediated Decay (NMD)	4.46E-04
MSRs	T1 to T2	Nonsense Mediated Decay (NMD) enhanced by the Exon Junction Complex (EJC)	4.46E-04
MSRs	T1 to T2	Signaling by ROBO receptors	5.69E-04
MSRs	T1 to T2	BH3-only proteins associate with and inactivate anti-apoptotic BCL-2 members	1.13E-02
MSRs	T1 to T2	Erythrocytes take up oxygen and release carbon dioxide	2.01E-02
MSRs	T1 to T2	Reversible hydration of carbon dioxide	2.01E-02
MSRs	T1 to T2	Cellular responses to stress	2.01E-02

MSRs	T1 to T2	Translation	2.01E-02
MSRs	T1 to T2	Cellular responses to external stimuli	2.01E-02
MSRs	T1 to T2	STAT5 activation downstream of FLT3 ITD mutants	2.19E-02
MSRs	T1 to T2	O2/CO2 exchange in erythrocytes	2.25E-02
MSRs	T1 to T2	Erythrocytes take up carbon dioxide and release oxygen	2.25E-02
MSRs	T1 to T2	Peptide chain elongation	2.29E-02
MSRs	T1 to T2	Eukaryotic Translation Elongation	2.40E-02
MSRs	T1 to T2	Formation of a pool of free 40S subunits	2.40E-02
MSRs	T1 to T2	Axon guidance	2.40E-02
MSRs	T1 to T2	Selenocysteine synthesis	2.40E-02
MSRs	T1 to T2	Signaling by FLT3 ITD and TKD mutants	2.40E-02
MSRs	T1 to T2	Viral mRNA Translation	2.40E-02
MSRs	T1 to T2	Response of EIF2AK4 (GCN2) to amino acid deficiency	2.40E-02
MSRs	T1 to T2	Nervous system development	2.40E-02
MSRs	T1 to T2	SRP-dependent cotranslational protein targeting to membrane	2.40E-02
MSRs	T1 to T2	GTP hydrolysis and joining of the 60S ribosomal subunit	2.46E-02
MSRs	T1 to T2	L13a-mediated translational silencing of Ceruloplasmin expression	2.46E-02
MSRs	T1 to T2	Eukaryotic Translation Initiation	2.77E-02
MSRs	T1 to T2	Cap-dependent Translation Initiation	2.77E-02
MSRs	T1 to T2	Oncogene Induced Senescence	3.65E-02
MSRs	T1 to T3	Antimicrobial peptides	8.31E-08
MSRs	T1 to T3	Neutrophil degranulation	2.70E-05
MSRs	T1 to T3	Alpha-defensins	3.21E-05
MSRs	T1 to T3	Innate Immune System	5.24E-05
MSRs	T1 to T3	Activation of C3 and C5	1.48E-03
MSRs	T1 to T3	Defensins	1.54E-03
MSRs	T1 to T3	Immune System	5.15E-03
MSRs	T1 to T3	Polo-like kinase mediated events	9.67E-03
MSRs	T1 to T3	Regulation of Complement cascade	1.81E-02
MSRs	T1 to T3	Complement cascade	2.34E-02
MSRs	T1 to T3	G1/S-Specific Transcription	2.49E-02
MSRs	T1 to T3	Transcriptional Regulation by E2F6	2.60E-02
MSRs	T1 to T3	Formation of the ternary complex, and subsequently, the 43S complex	3.23E-02
MSRs	T1 to T3	Translation initiation complex formation	3.60E-02
MSRs	T1 to T3	Ribosomal scanning and start codon recognition	3.60E-02
MSRs	T1 to T3	Activation of the mRNA upon binding of the cap-binding complex and eIFs, and subsequent binding to 43S	3.82E-02
MSRs	T2 to T3	Cell Cycle, Mitotic	5.60E-10
MSRs	T2 to T3	Cell Cycle	6.15E-09
MSRs	T2 to T3	Antimicrobial peptides	1.28E-07

MSRs	T2 to T3	Polo-like kinase mediated events	2.80E-05
MSRs	T2 to T3	Alpha-defensins	1.64E-04
MSRs	T2 to T3	Neutrophil degranulation	1.86E-04
MSRs	T2 to T3	G1/S-Specific Transcription	1.86E-04
MSRs	T2 to T3	Mitotic G1 phase and G1/S transition	2.11E-04
MSRs	T2 to T3	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	1.17E-03
MSRs	T2 to T3	Mitotic Anaphase	1.19E-03
MSRs	T2 to T3	Mitotic Metaphase and Anaphase	1.19E-03
MSRs	T2 to T3	APC/C-mediated degradation of cell cycle proteins	1.84E-03
MSRs	T2 to T3	Regulation of mitotic cell cycle	1.84E-03
MSRs	T2 to T3	Separation of Sister Chromatids	2.77E-03
MSRs	T2 to T3	Mitotic Spindle Checkpoint	3.17E-03
MSRs	T2 to T3	G2/M Transition	3.53E-03
MSRs	T2 to T3	Mitotic G2-G2/M phases	3.53E-03
MSRs	T2 to T3	SUMOylation of DNA replication proteins	3.67E-03
MSRs	T2 to T3	Defensins	3.88E-03
MSRs	T2 to T3	Resolution of Sister Chromatid Cohesion	4.66E-03
MSRs	T2 to T3	Metal sequestration by antimicrobial proteins	5.25E-03
MSRs	T2 to T3	G1/S Transition	7.09E-03
MSRs	T2 to T3	M Phase	7.80E-03
MSRs	T2 to T3	Cell Cycle Checkpoints	8.25E-03
MSRs	T2 to T3	Immune System	1.42E-02
MSRs	T2 to T3	Transcription of E2F targets under negative control by DREAM complex	1.42E-02
MSRs	T2 to T3	Amplification of signal from the kinetochores	1.49E-02
MSRs	T2 to T3	Amplification of signal from unattached kinetochores via a MAD2 inhibitory signal	1.49E-02
MSRs	T2 to T3	Mitotic Prometaphase	1.79E-02
MSRs	T2 to T3	Innate Immune System	1.79E-02
MSRs	T2 to T3	Metalloprotease DUBs	1.92E-02
MSRs	T2 to T3	EML4 and NUDC in mitotic spindle formation	2.51E-02
MSRs	T2 to T3	G0 and Early G1	2.68E-02
MSRs	T2 to T3	Transcriptional Regulation by E2F6	3.49E-02
MSRs	T2 to T3	Defective SLC4A1 causes hereditary spherocytosis type 4 (HSP4), distal renal tubular acidosis (dRTA) and dRTA with hemolytic anemia (dRTA-HA)	3.49E-02
MSRs	T2 to T3	FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes	3.49E-02
MSRs	T2 to T3	RHO GTPases Activate Formins	3.55E-02
MSRs	T2 to T3	RMTs methylate histone arginines	4.06E-02
MSRs	T2 to T3	Interaction between PHLDA1 and AURKA	4.54E-02

Supplementary Table 4 – Reactome Pathway Analysis from Chapter I Hypothesis Free Testing All significant pathways from Hypothesis Free Testing. Comparisons include; RVMSR at T0, T1, T2 and T3 (n= 4 vs. 5), and All RTT (n = 9), Responders (n = 4), and MSRs (n = 5) at T0 to T1, T0 to T2,

T0 to T3, T1 to T2, T1 to T3, and T2 to T3. The list of significant DEG, filtered for gene that were not recognised, were used as input for the analysis.
Legend:
FDR = False Discovery Rate

Comparison	Group	Gene Set	ID	N	FDR
RVMSR	T0	brain-derived neurotrophic factor receptor signaling pathway	GO.0031547	5	2.34E-02
RVMSR	T0	serotonin receptor signaling pathway	GO.0007210	9	5.96E-03
RVMSR	T0	dopamine receptor signaling pathway	GO.0007212	13	3.27E-03
RVMSR	T0	response to catecholamine	GO.0071869	71	5.96E-03
RVMSR	T0	respiratory electron transport chain	GO.0022904	15	8.95E-03
RVMSR	T0	Marchetto.ASD_Chronic	Marchetto.ASD_Chronic	99	6.03E-03
RVMSR	T0	MAPK cascade	GO.0000165	261	5.96E-03
RVMSR	T0	phosphatidylinositol 3-kinase signaling	GO.0014065	33	6.21E-03
RVMSR	T0	inflammatory response	GO.0006954	361	5.96E-03
RVMSR	T0	protein ubiquitination	GO.0016567	408	5.96E-03
RVMSR	T0	Marchetto.Control_Acute	Marchetto.Control_Acute	122	6.21E-03
RVMSR	T0	reactive oxygen species metabolic process	GO.0072593	27	5.96E-03
RVMSR	T0	insulin-like growth factor receptor signaling pathway	GO.0048009	13	2.02E-02
RVMSR	T0	chromatin organization	GO.0006325	105	1.08E-02
RVMSR	T0	Marchetto.Control_Chronic	Marchetto.Control_Chronic	83	6.21E-03
RVMSR	T0	Marchetto.ASD_Acute	Marchetto.ASD_Acute	75	2.34E-02
RVMSR	T1	insulin-like growth factor receptor signaling pathway	GO.0048009	13	8.81E-03
RVMSR	T2	phosphatidylinositol 3-kinase signaling	GO.0014065	33	3.13E-03
RVMSR	T2	response to catecholamine	GO.0071869	71	5.20E-04
RVMSR	T2	brain-derived neurotrophic factor receptor signaling pathway	GO.0031547	5	2.20E-02
RVMSR	T2	dopamine receptor signaling pathway	GO.0007212	13	2.02E-02
RVMSR	T2	serotonin receptor signaling pathway	GO.0007210	9	2.49E-02
RVMSR	T2	reactive oxygen species metabolic process	GO.0072593	27	2.02E-02
Responders	T1 to T2	insulin-like growth factor receptor signaling pathway	GO.0048009	13	1.79E-02
MSRs	T1 to T2	Marchetto.ASD_Chronic	Marchetto.ASD_Chronic	99	1.18E-07

Supplementary Table 5 – EdgeR fry Analysis from Chapter I Hypothesis Driven Testing
All gene set differentially expressed from Hypothesis Driven Testing. Comparisons include; RVMSR at T0, T1, T2 and T3 (n= 4 vs. 5), and All RTT (n = 9), Responders (n = 4), and MSRs (n = 5) at T0 to T1, T0 to T2, T0 to T3, T1 to T2, T1 to T3, and T2 to T3. This analysis was conducted using EdgeR's Fry Function.

Legend:
FDR = False Discovery Rate, ID = Identifier

Group	Comparison	ID	FDR
RVMSR	T0	GO.0007423	3.46E-02
RVMSR	T0	GO.0000904	3.46E-02
RVMSR	T0	GO.0019730	3.46E-02
RVMSR	T0	GO.0046483	3.46E-02
RVMSR	T0	GO.0031640	3.46E-02
RVMSR	T0	GO.0050953	3.46E-02
RVMSR	T0	GO.0048513	3.46E-02
RVMSR	T0	GO.0061844	3.46E-02
RVMSR	T0	GO.0061041	3.46E-02
RVMSR	T0	GO.0048699	3.46E-02
RVMSR	T0	GO.0050778	3.46E-02
RVMSR	T0	GO.0007157	3.46E-02
RVMSR	T0	GO.0034645	3.46E-02
RVMSR	T0	GO.0098742	3.46E-02
RVMSR	T0	GO.0050877	3.46E-02
RVMSR	T0	GO.0043114	3.46E-02
RVMSR	T0	GO.0009888	3.46E-02
RVMSR	T0	GO.0000902	3.46E-02
RVMSR	T0	GO.0050851	3.46E-02
RVMSR	T0	GO.0007601	3.46E-02
RVMSR	T0	GO.0030198	3.46E-02
RVMSR	T0	GO.0031175	3.46E-02
RVMSR	T0	GO.0045907	3.46E-02
RVMSR	T0	GO.0032502	3.46E-02
RVMSR	T0	GO.0048667	3.46E-02
RVMSR	T0	GO.0044267	3.46E-02
RVMSR	T0	GO.0007399	3.46E-02
RVMSR	T0	GO.0009887	3.46E-02
RVMSR	T0	GO.0007268	3.46E-02
RVMSR	T0	GO.0098609	3.46E-02
RVMSR	T0	GO.0008152	3.46E-02
RVMSR	T0	GO.0022008	3.46E-02
RVMSR	T0	GO.0043588	3.46E-02
RVMSR	T0	GO.0050808	3.46E-02
RVMSR	T0	GO.0001654	3.46E-02
RVMSR	T0	GO.0048812	3.46E-02
RVMSR	T0	GO.0007155	3.46E-02

RVMSR	T0	GO.0048731	3.46E-02
RVMSR	T0	GO.0007267	3.46E-02
RVMSR	T0	GO.0016477	3.46E-02
RVMSR	T0	GO.0002757	3.48E-02
RVMSR	T0	GO.0045596	3.50E-02
RVMSR	T0	GO.0007275	3.58E-02
RVMSR	T0	GO.0042886	3.58E-02
RVMSR	T0	GO.0019538	3.62E-02
RVMSR	T0	GO.0007409	3.66E-02
RVMSR	T0	GO.0030154	3.66E-02
RVMSR	T0	GO.0035150	3.66E-02
RVMSR	T0	GO.0009653	3.83E-02
RVMSR	T0	GO.0048856	3.83E-02
RVMSR	T0	GO.0007411	3.83E-02
RVMSR	T0	GO.0045184	3.83E-02
RVMSR	T0	GO.0051276	3.88E-02
RVMSR	T0	GO.0072359	3.88E-02
RVMSR	T0	GO.0034641	3.90E-02
RVMSR	T0	GO.0097746	3.91E-02
RVMSR	T0	GO.0034470	3.92E-02
RVMSR	T0	GO.0050871	4.21E-02
RVMSR	T0	GO.0051480	4.21E-02
RVMSR	T0	GO.0006996	4.22E-02
RVMSR	T0	GO.0040011	4.25E-02
RVMSR	T0	GO.0048598	4.25E-02
RVMSR	T0	GO.0061564	4.50E-02
RVMSR	T0	GO.0010467	4.50E-02
RVMSR	T0	GO.0006956	4.57E-02
RVMSR	T0	GO.0002376	4.57E-02
RVMSR	T0	GO.0065003	4.58E-02
RVMSR	T0	GO.0002253	4.65E-02
RVMSR	T0	GO.0008104	4.74E-02
RVMSR	T0	GO.0030182	4.77E-02
RVMSR	T0	GO.0001944	4.77E-02
RVMSR	T0	R.HSA.1474228	1.55E-02
RVMSR	T0	R.HSA.1474244	1.55E-02
RVMSR	T0	R.HSA.6805567	1.72E-02
RVMSR	T0	R.HSA.1266738	1.90E-02
RVMSR	T2	R.HSA.1474228	3.62E-02
RVMSR	T2	R.HSA.1462054	3.62E-02
RVMSR	T2	R.HSA.1474244	3.92E-02

Supplementary Table 6 – Validation of Reactome and GO Analysis with EdgeR Fry Function
All significant pathways and ontologies identified in Hypothesis Free Testing that were subsequently significant when analysed using EdgeR's Fry Function.. Comparisons include; RVMSR at T0, T1, T2 and T3 (n= 4 vs. 5), and All RTT (n = 9), Responders (n = 4), and MSRs (n = 5) at T0 to T1, T0 to T2, T0 to T3, T1 to T2, T1 to T3, and T2 to T3.
Legend:
FDR = False Discovery Rate

Appendix II

Tissue	Comparison	Gene	logFC	FDR	Gene	logFC	FDR
CRB	HET.IGF1_VEH	Crym	-6.91	5.54E-71	Nefm	0.76	2.79E-04
CRB	HET.IGF1_VEH	Rpl31-ps8	9.93	1.11E-44	Icam5	-4.64	3.53E-04
CRB	HET.IGF1_VEH	Spink8	-5.30	1.64E-37	Rasgrp1	-0.96	3.76E-04
CRB	HET.IGF1_VEH	Gm4767	-9.31	6.77E-33	Smoc2	-2.17	3.92E-04
CRB	HET.IGF1_VEH	Neurod6	-2.10	5.51E-31	Cck	-0.78	6.99E-04
CRB	HET.IGF1_VEH	Ptk2b	-2.82	8.02E-27	Syt17	-1.80	7.89E-04
CRB	HET.IGF1_VEH	Pcdha5	8.85	2.41E-22	Egr3	-4.14	8.98E-04
CRB	HET.IGF1_VEH	Camk2a	-2.17	3.03E-22	Kcnj13	-0.72	1.01E-03
CRB	HET.IGF1_VEH	Foxg1	-5.69	2.31E-19	Chn1	-0.69	1.24E-03
CRB	HET.IGF1_VEH	Scn3b	-1.88	1.91E-18	Ak5	-1.47	1.56E-03
CRB	HET.IGF1_VEH	Enc1	-2.09	2.13E-16	Gm49337	1.20	1.63E-03
CRB	HET.IGF1_VEH	Npy2r	-3.80	2.22E-16	Gm36742	-6.22	1.87E-03
CRB	HET.IGF1_VEH	Hpca	-1.79	1.33E-15	Slc10a4	4.75	2.14E-03
CRB	HET.IGF1_VEH	Ddn	-4.62	1.98E-14	Vamp1	0.72	2.17E-03
CRB	HET.IGF1_VEH	Pde1a	-1.80	2.88E-13	Dlx6os1	-6.17	2.67E-03
CRB	HET.IGF1_VEH	Bcl11b	-2.45	1.56E-10	Syt16	-1.74	2.70E-03
CRB	HET.IGF1_VEH	Crhbp	-2.53	1.66E-10	Gm12666	6.30	3.59E-03
CRB	HET.IGF1_VEH	Rgs14	-4.15	1.66E-10	Gal	1.32	4.15E-03
CRB	HET.IGF1_VEH	C1ql2	-3.19	3.40E-10	Gabra5	-1.18	4.15E-03
CRB	HET.IGF1_VEH	Cpne6	-1.95	1.04E-09	3110039M20Rik	-4.89	4.17E-03
CRB	HET.IGF1_VEH	Calcb	4.30	2.48E-09	2900040C04Rik	-1.06	4.21E-03
CRB	HET.IGF1_VEH	Myo5b	-2.80	1.14E-08	Slc17a6	0.74	4.44E-03
CRB	HET.IGF1_VEH	St6galnac5	-2.03	1.28E-08	Slc6a5	1.05	5.01E-03
CRB	HET.IGF1_VEH	Grin2b	-1.41	9.69E-08	Lrrc10b	-4.86	5.32E-03
CRB	HET.IGF1_VEH	Kcne2	-1.13	1.02E-07	Nefh	0.70	5.34E-03
CRB	HET.IGF1_VEH	Gm10095	-0.99	1.22E-07	Gm42566	0.65	5.38E-03
CRB	HET.IGF1_VEH	Hpcal4	-1.47	1.22E-07	Gh	0.95	7.23E-03
CRB	HET.IGF1_VEH	Mas1	-4.55	2.67E-07	Enpp2	-0.65	7.24E-03
CRB	HET.IGF1_VEH	Vxn	-1.70	2.67E-07	Wipf3	-0.96	8.62E-03
CRB	HET.IGF1_VEH	Camkv	-2.36	2.86E-07	Lhx6	-5.95	9.43E-03
CRB	HET.IGF1_VEH	Cpne7	-3.32	3.30E-07	Pcdha9	6.18	9.83E-03

CRB	HET.IGF1_VEH	Lmo3	-1.52	5.95E-07	Kctd4	-1.01	9.83E-03
CRB	HET.IGF1_VEH	Snca	-0.90	1.23E-06	Gm47486	-1.47	9.83E-03
CRB	HET.IGF1_VEH	Nrgn	-1.88	1.46E-06	Epha7	-0.68	1.04E-02
CRB	HET.IGF1_VEH	Gda	-2.26	1.50E-06	Steap1	-1.03	1.07E-02
CRB	HET.IGF1_VEH	Prl	0.99	2.61E-06	Calca	1.21	1.07E-02
CRB	HET.IGF1_VEH	Gm10600	-6.99	2.61E-06	Cpne4	-1.21	1.12E-02
CRB	HET.IGF1_VEH	Plk2	-1.18	2.65E-06	Slc26a4	-3.87	1.19E-02
CRB	HET.IGF1_VEH	Ecrg4	-0.87	3.97E-06	Dkk3	-0.84	1.22E-02
CRB	HET.IGF1_VEH	Lamp5	1.09	3.97E-06	Npy	-0.67	1.22E-02
CRB	HET.IGF1_VEH	Gm32687	2.48	4.32E-06	Grm5	-0.93	1.27E-02
CRB	HET.IGF1_VEH	Ptgs2	-3.85	4.42E-06	Rps13-ps1	1.77	1.27E-02
CRB	HET.IGF1_VEH	Pcdha12	7.06	4.49E-06	Prph	2.74	1.28E-02
CRB	HET.IGF1_VEH	Pcdha8	-2.79	6.05E-06	Nr4a2	-0.95	1.28E-02
CRB	HET.IGF1_VEH	Rasl10a	-3.93	7.19E-06	Hemk1	-0.83	1.32E-02
CRB	HET.IGF1_VEH	Calml4	-1.17	7.23E-06	Grp	-2.03	1.47E-02
CRB	HET.IGF1_VEH	Folr1	-1.15	7.23E-06	Lpl	-1.62	1.53E-02
CRB	HET.IGF1_VEH	Slc5a7	3.00	7.23E-06	Kcnv1	-3.01	1.55E-02
CRB	HET.IGF1_VEH	Fezf2	-5.53	9.08E-06	Tph2	1.65	1.75E-02
CRB	HET.IGF1_VEH	Iqgap2	-1.92	1.36E-05	Mpped1	-1.32	1.77E-02
CRB	HET.IGF1_VEH	Ttr	-1.03	1.36E-05	Tafa1	-1.16	2.27E-02
CRB	HET.IGF1_VEH	Vip	-1.87	2.08E-05	Tbr1	-3.30	2.32E-02
CRB	HET.IGF1_VEH	Mal2	-1.69	2.39E-05	Gm14648	-0.91	2.49E-02
CRB	HET.IGF1_VEH	Gm5796	6.86	3.02E-05	Gm34466	-4.60	2.67E-02
CRB	HET.IGF1_VEH	Uts2	6.83	3.29E-05	Snhg7os	-3.36	2.87E-02
CRB	HET.IGF1_VEH	Pcdha1	6.73	6.76E-05	Emx2	-5.70	3.14E-02
CRB	HET.IGF1_VEH	Chrm1	-3.63	8.43E-05	Meis2	1.26	3.18E-02
CRB	HET.IGF1_VEH	Otos	2.98	8.72E-05	Fosl2	-1.04	3.91E-02
CRB	HET.IGF1_VEH	Fam131a	-1.19	1.01E-04	Runx1	5.82	3.99E-02
CRB	HET.IGF1_VEH	Ctxn1	-2.21	1.16E-04	Cdh9	-1.64	4.20E-02
CRB	HET.IGF1_VEH	Gm20754	-6.54	1.51E-04	Epha4	-0.70	4.42E-02
CRB	HET.IGF1_VEH	Alkal2	-3.58	1.69E-04	Sst	-1.00	4.57E-02
CRB	HET.IGF1_VEH	Pcdha3	-2.09	2.05E-04	Gm48690	5.80	4.98E-02
CRB	HET.IGF1_VEH	Sostdc1	-0.88	2.15E-04			
CRB	WTF.IGF1_VEH	Gm14648	2.87	9.23E-34	Gm3755	-6.65	6.62E-03
CRB	WTF.IGF1_VEH	Tcea1-ps1	8.61	1.89E-17	Gm13301	6.54	8.64E-03
CRB	WTF.IGF1_VEH	Pcdha1	-8.27	4.37E-13	Bpifa2	-6.54	9.61E-03
CRB	WTF.IGF1_VEH	Mamdc4	-4.23	8.79E-13	Pcdha11	6.60	1.24E-02
CRB	WTF.IGF1_VEH	Cers1	7.44	7.49E-07	Gm4739	1.26	1.60E-02
CRB	WTF.IGF1_VEH	Pcdha8	-7.21	4.19E-05	Tgtp1	2.25	2.26E-02
CRB	WTF.IGF1_VEH	Gm10095	0.94	1.47E-04	Tmem45b	4.99	2.77E-02
CRB	WTF.IGF1_VEH	Prl	-0.88	2.24E-04	Gm17081	-2.65	2.77E-02
CRB	WTF.IGF1_VEH	nan	1.84	2.41E-04	Gm10340	6.27	3.08E-02
CRB	WTF.IGF1_VEH	Fxyd2	2.19	2.68E-04	Brms1	6.41	3.70E-02
CRB	WTF.IGF1_VEH	Tph2	-1.51	2.68E-04	Gm9104	-6.31	3.70E-02

CRB	WTF.IGF1_VEH	Gdf1	-2.96	3.59E-03	Pcdha3	-6.28	4.47E-02
CRB	WTF.IGF1_VEH	Pcdha11	2.06	5.17E-03	nan	6.24	4.59E-02
CRB	IGF1.HET_WTF	Gm4767	-9.23	1.10E-31	Calca	-0.95	5.88E-03
CRB	IGF1.HET_WTF	Prl	-1.67	2.28E-26	Plac9a	-6.14	5.88E-03
CRB	IGF1.HET_WTF	Gm32687	8.71	2.28E-20	Tmem91	-1.11	5.88E-03
CRB	IGF1.HET_WTF	Gh	-1.69	1.67E-19	Tgtp2	-1.15	7.36E-03
CRB	IGF1.HET_WTF	Mamdc4	-4.55	4.69E-18	Fabp7	-0.61	7.60E-03
CRB	IGF1.HET_WTF	Lamp5	-1.45	3.27E-17	Prl2c3	-1.03	8.41E-03
CRB	IGF1.HET_WTF	Ighm	-1.82	3.24E-14	A2ml1	-1.16	9.44E-03
CRB	IGF1.HET_WTF	Tcea1-ps1	7.89	5.00E-11	Pcdha9	6.19	9.73E-03
CRB	IGF1.HET_WTF	Bc1	-0.99	1.17E-10	Cd200	-0.66	1.01E-02
CRB	IGF1.HET_WTF	Resp18	-1.02	1.42E-09	Hoxb7	-2.67	1.01E-02
CRB	IGF1.HET_WTF	Pcdha5	2.84	1.46E-08	Rasgrp2	-1.06	1.08E-02
CRB	IGF1.HET_WTF	Sst	-1.63	1.46E-08	Msmo1	-0.58	1.14E-02
CRB	IGF1.HET_WTF	Gal	-1.39	6.30E-08	Cdk19	0.67	1.14E-02
CRB	IGF1.HET_WTF	Pomc	-1.76	1.10E-07	Cd59a	-0.67	1.14E-02
CRB	IGF1.HET_WTF	Sncg	-1.15	1.18E-07	6330403K07Rik	-0.74	1.25E-02
CRB	IGF1.HET_WTF	Tatdn1	-0.86	2.46E-07	Slc6a1	0.64	1.32E-02
CRB	IGF1.HET_WTF	Gm15500	-1.10	2.83E-07	Serpina3n	-1.46	1.34E-02
CRB	IGF1.HET_WTF	Tph2	-1.60	5.96E-07	Malat1	0.55	1.34E-02
CRB	IGF1.HET_WTF	Cartpt	-2.42	7.90E-07	Tango2	-0.58	1.61E-02
CRB	IGF1.HET_WTF	Tac1	-1.31	1.08E-06	Hmgcs1	-0.58	1.68E-02
CRB	IGF1.HET_WTF	Arhgdig	-1.31	5.55E-06	Pcdha1	-1.63	1.74E-02
CRB	IGF1.HET_WTF	Pcdha12	7.09	6.12E-06	Mcf2	-1.11	2.20E-02
CRB	IGF1.HET_WTF	Minar2	-1.04	7.90E-06	Kcnmb4os2	1.32	2.23E-02
CRB	IGF1.HET_WTF	Otos	3.38	9.81E-06	Slc17a6	-0.61	2.25E-02
CRB	IGF1.HET_WTF	AW551984	-1.59	9.81E-06	Calml4	-0.83	2.34E-02
CRB	IGF1.HET_WTF	Gm29216	-0.75	1.12E-05	Gm10599	-5.82	2.60E-02
CRB	IGF1.HET_WTF	Gm3755	-6.83	3.47E-05	Car5b	-1.93	2.82E-02
CRB	IGF1.HET_WTF	Hoxb2	-1.81	4.87E-05	nan	-0.69	2.82E-02
CRB	IGF1.HET_WTF	Gm2897	-6.77	4.96E-05	Dgkd	0.71	2.86E-02
CRB	IGF1.HET_WTF	Kcne2	-0.95	5.65E-05	2900052N01Rik	-1.00	2.92E-02
CRB	IGF1.HET_WTF	Bpifa2	-6.71	6.18E-05	Sbk1	0.66	2.92E-02
CRB	IGF1.HET_WTF	Gm42566	0.77	1.33E-04	Gm3005	-5.77	2.99E-02
CRB	IGF1.HET_WTF	Crhbp	-1.93	1.33E-04	Nrxn3	0.56	3.02E-02
CRB	IGF1.HET_WTF	Vstm2a	-0.89	1.81E-04	Hoxa5	-1.69	3.09E-02
CRB	IGF1.HET_WTF	Slc5a7	-1.44	1.84E-04	Gm20754	-5.78	3.20E-02
CRB	IGF1.HET_WTF	Basp1	-1.28	1.96E-04	Gm49883	2.49	3.24E-02
CRB	IGF1.HET_WTF	Xlr3b	1.27	2.12E-04	Fmod	1.11	3.32E-02
CRB	IGF1.HET_WTF	Zcchc12	-0.88	2.27E-04	Pcca	0.60	3.37E-02
CRB	IGF1.HET_WTF	Vip	-1.72	2.66E-04	Mgat4c	-0.90	3.37E-02
CRB	IGF1.HET_WTF	Nrsn1	-0.77	2.92E-04	nan	-5.75	3.37E-02

CRB	IGF1.HET_WTF	Gm13301	6.70	2.96E-04	Fcrls	-1.11	3.37E-02
CRB	IGF1.HET_WTF	Nefm	-0.71	2.96E-04	Klhl1	-0.99	3.52E-02
CRB	IGF1.HET_WTF	Rab3b	-0.99	4.68E-04	Lyz2	-0.64	3.60E-02
CRB	IGF1.HET_WTF	Elavl2	-0.77	8.82E-04	Pmch	-3.28	3.60E-02
CRB	IGF1.HET_WTF	Clvs2	-1.09	9.10E-04	Sgk1	-0.55	3.63E-02
CRB	IGF1.HET_WTF	Hoxb3os	-2.22	1.18E-03	2610005L07Rik	1.17	3.63E-02
CRB	IGF1.HET_WTF	Hoxa4	-2.98	1.20E-03	Cd1d1	-1.77	3.83E-02
CRB	IGF1.HET_WTF	Pak3	-0.75	1.36E-03	Nefl	-0.51	4.01E-02
CRB	IGF1.HET_WTF	Glra3	-1.98	1.41E-03	Shisa6	0.67	4.08E-02
CRB	IGF1.HET_WTF	Itpr1	0.64	1.47E-03	Calcb	-1.09	4.09E-02
CRB	IGF1.HET_WTF	Adcyap1	-1.43	1.49E-03	Cdh1	1.43	4.09E-02
CRB	IGF1.HET_WTF	B230312C02Rik	-0.91	1.99E-03	Fat2	0.63	4.09E-02
CRB	IGF1.HET_WTF	Scg2	-0.63	1.99E-03	Rgs10	-0.61	4.14E-02
CRB	IGF1.HET_WTF	Chodl	-2.00	2.19E-03	Kcnj13	-0.56	4.19E-02
CRB	IGF1.HET_WTF	Serpinb1b	-0.86	2.56E-03	Epb41l4b	0.85	4.30E-02
CRB	IGF1.HET_WTF	Folr1	-0.92	2.57E-03	Kit	0.64	4.30E-02
CRB	IGF1.HET_WTF	Rgs4	-0.79	2.62E-03	Gm49337	0.91	4.30E-02
CRB	IGF1.HET_WTF	Uchl1	-0.69	2.73E-03	Rpl31-ps8	-0.76	4.30E-02
CRB	IGF1.HET_WTF	Nts	-1.10	2.76E-03	Cbln3	0.53	4.30E-02
CRB	IGF1.HET_WTF	Klk6	-0.73	3.33E-03	Htr2a	-1.70	4.58E-02
CRB	IGF1.HET_WTF	Scn3b	-0.96	3.65E-03	Lgals1	-0.56	4.64E-02
CRB	IGF1.HET_WTF	Ifi27l2a	-1.06	3.68E-03	Cpne8	0.53	4.64E-02
CRB	IGF1.HET_WTF	Foxj2	1.02	4.73E-03	Mog	-0.55	4.64E-02
CRB	IGF1.HET_WTF	Pdlim2	-0.76	4.81E-03	Tac2	-2.25	4.69E-02
CRB	IGF1.HET_WTF	Pcp4l1	-0.65	5.18E-03	Kctd12	0.58	4.75E-02
CRB	IGF1.HET_WTF	Reln	0.72	5.50E-03	Tgtp1	1.86	4.93E-02
CRB	IGF1.HET_WTF	Col19a1	1.83	5.74E-03	Speer4a	-5.62	4.93E-02
CRB	IGF1.HET_WTF	Rps16-ps2	-0.89	5.75E-03	Mecp2	-0.68	4.93E-02
CRB	VEH.HET_WTF	Rpl31-ps8	-11.16	3.55E-86	Gm15500	-1.01	9.05E-04
CRB	VEH.HET_WTF	Crym	4.89	1.65E-39	Serpinb1b	-0.98	9.05E-04
CRB	VEH.HET_WTF	Lamp5	-2.25	2.39E-26	Plk2	1.05	1.02E-03
CRB	VEH.HET_WTF	Neurod6	2.19	6.49E-24	Uts2b	-3.82	1.19E-03
CRB	VEH.HET_WTF	Calcb	-5.55	1.84E-22	Pcp4l1	-0.83	1.19E-03
CRB	VEH.HET_WTF	Sncg	-2.21	2.13E-22	Nr4a3	1.82	1.23E-03
CRB	VEH.HET_WTF	Ptk2b	2.92	5.95E-22	Gdf1	2.91	1.29E-03
CRB	VEH.HET_WTF	Calca	-2.69	6.29E-21	Chrm1	3.65	1.34E-03
CRB	VEH.HET_WTF	Gh	-2.21	1.08E-20	Gm9104	6.61	1.62E-03
CRB	VEH.HET_WTF	Spink8	3.71	1.01E-19	Nefh	-0.84	1.78E-03
CRB	VEH.HET_WTF	Prl	-1.77	3.57E-18	Tppp3	-0.84	2.31E-03
CRB	VEH.HET_WTF	Gal	-2.60	1.72E-17	Pcdh11x	-1.46	2.45E-03
CRB	VEH.HET_WTF	Foxg1	6.69	9.13E-17	Pcdha11	-6.56	3.28E-03
CRB	VEH.HET_WTF	Pcdha3	8.41	1.08E-15	Slc6a5	-1.16	3.28E-03
CRB	VEH.HET_WTF	Prph	-4.58	3.63E-15	Chn1	0.78	3.29E-03

CRB	VEH.HET_WTF	Camk2a	2.00	9.18E-15	Hpcal4	1.07	3.88E-03
CRB	VEH.HET_WTF	Nr4a2	2.62	5.87E-14	Cpne6	1.24	3.88E-03
CRB	VEH.HET_WTF	Pcdha8	8.15	8.28E-13	Gm3095	-6.37	3.88E-03
CRB	VEH.HET_WTF	Gm14648	-1.59	9.43E-12	Gm3558	-1.85	4.42E-03
CRB	VEH.HET_WTF	Nefm	-1.38	1.07E-11	Gm7271	-6.46	4.43E-03
CRB	VEH.HET_WTF	Pcdha5	-7.91	2.73E-11	Nr4a1	1.84	4.74E-03
CRB	VEH.HET_WTF	Grin2b	1.92	8.35E-11	Fosl2	1.36	4.85E-03
CRB	VEH.HET_WTF	Slc5a7	-3.71	1.91E-10	Meis2	-1.49	4.94E-03
CRB	VEH.HET_WTF	Ddn	4.26	2.20E-10	Rassf4	-1.28	5.69E-03
CRB	VEH.HET_WTF	Hoxa5	-4.40	8.69E-10	Lmo3	1.11	6.94E-03
CRB	VEH.HET_WTF	Fos	1.73	2.97E-09	Ppp1r1c	-4.34	7.15E-03
CRB	VEH.HET_WTF	St6galnac5	2.38	3.81E-09	Fam131a	1.06	7.77E-03
CRB	VEH.HET_WTF	Hoxb2	-3.21	3.81E-09	Arhgap36	-3.90	8.61E-03
CRB	VEH.HET_WTF	Hoxb7	-7.62	1.01E-08	Wasf1	0.99	8.61E-03
CRB	VEH.HET_WTF	Tac1	-1.72	1.76E-08	Tac2	-2.24	9.32E-03
CRB	VEH.HET_WTF	Hpca	1.49	2.49E-08	Gm10340	-6.24	9.32E-03
CRB	VEH.HET_WTF	Iqgap2	2.77	2.49E-08	Cracdl	1.43	9.54E-03
CRB	VEH.HET_WTF	Enc1	1.63	3.45E-08	3110039M20Rik	6.24	1.10E-02
CRB	VEH.HET_WTF	Npy2r	2.67	4.85E-08	Cpne4	1.34	1.12E-02
CRB	VEH.HET_WTF	C1ql2	3.12	4.85E-08	Tmem91	-1.34	1.12E-02
CRB	VEH.HET_WTF	Mas1	7.51	5.23E-08	Gm8258	-3.42	1.19E-02
CRB	VEH.HET_WTF	Cpne7	4.40	6.32E-08	Nmu	-4.77	1.23E-02
CRB	VEH.HET_WTF	Rgs14	3.99	7.51E-08	Lrrc10b	6.21	1.34E-02
CRB	VEH.HET_WTF	Cers1	-7.40	1.79E-07	Ttr	0.98	1.35E-02
CRB	VEH.HET_WTF	Bcl11b	2.21	2.88E-07	Grin2a	0.78	1.51E-02
CRB	VEH.HET_WTF	Resp18	-1.09	3.52E-07	Slc10a4	-4.76	1.67E-02
CRB	VEH.HET_WTF	AW551984	-2.38	3.87E-07	Prrxl1	-4.73	1.67E-02
CRB	VEH.HET_WTF	Ighm	-1.53	6.04E-07	Sertm1	1.78	1.67E-02
CRB	VEH.HET_WTF	Slc17a6	-1.15	6.37E-07	Mal2	1.29	1.75E-02
CRB	VEH.HET_WTF	Pde1a	1.45	6.46E-07	Zcchc12	-0.82	1.75E-02
CRB	VEH.HET_WTF	Crh	-4.02	1.37E-06	Tph2	-1.78	1.77E-02
CRB	VEH.HET_WTF	Nrgn	2.09	1.45E-06	Hoxb3os	-2.47	1.91E-02
CRB	VEH.HET_WTF	Fxyd2	-2.65	1.84E-06	Gm44503	-2.96	1.97E-02
CRB	VEH.HET_WTF	Epha7	1.12	4.84E-06	Pomc	-1.33	2.09E-02
CRB	VEH.HET_WTF	Myo5b	2.52	5.88E-06	Fstl1	-0.84	2.10E-02
CRB	VEH.HET_WTF	Ctxn1	2.91	6.61E-06	Egr1	1.14	2.12E-02
CRB	VEH.HET_WTF	Chodl	-4.01	9.87E-06	Hoxc5	-6.20	2.17E-02
CRB	VEH.HET_WTF	Wipf3	1.52	1.18E-05	Mef2c	0.75	2.22E-02
CRB	VEH.HET_WTF	Uts2	-7.03	2.93E-05	Neurl1b	3.92	2.38E-02
CRB	VEH.HET_WTF	Scn3b	1.13	3.64E-05	Bcas1	-0.69	2.45E-02
CRB	VEH.HET_WTF	F2rl2	-4.45	3.65E-05	Ptgs2	2.42	2.59E-02
CRB	VEH.HET_WTF	Mpped1	2.15	3.98E-05	Zdhhc23	2.73	2.59E-02
CRB	VEH.HET_WTF	Chrm2	-1.74	4.73E-05	Gm3099	-6.20	2.61E-02

CRB	VEH.HET_WTF	Smoc2	2.81	4.82E-05	Rims3	0.83	2.73E-02
CRB	VEH.HET_WTF	Fezf2	6.90	7.87E-05	Tnfaip8l3	3.56	2.81E-02
CRB	VEH.HET_WTF	Vxn	1.54	8.72E-05	Trh	-4.73	2.84E-02
CRB	VEH.HET_WTF	Klk6	-0.99	1.04E-04	Adcyap1	-1.42	2.84E-02
CRB	VEH.HET_WTF	Epha4	1.14	1.05E-04	Gm10045	-6.03	2.84E-02
CRB	VEH.HET_WTF	Gda	2.08	1.13E-04	Glra3	-1.78	2.86E-02
CRB	VEH.HET_WTF	Gm45799	-4.69	1.27E-04	Mog	-0.68	2.96E-02
CRB	VEH.HET_WTF	Crhbp	1.76	1.38E-04	Camkv	1.39	3.38E-02
CRB	VEH.HET_WTF	Gm16056	6.82	1.67E-04	Rfx3	0.91	3.41E-02
CRB	VEH.HET_WTF	Gm10600	6.80	2.47E-04	Dlx6os1	6.00	3.72E-02
CRB	VEH.HET_WTF	Cartpt	-2.52	3.03E-04	Syt17	1.48	3.89E-02
CRB	VEH.HET_WTF	Rasgrp1	1.10	4.06E-04	Gm42772	0.97	3.99E-02
CRB	VEH.HET_WTF	Nefl	-0.87	4.36E-04	Rasgrp2	-1.22	4.05E-02
CRB	VEH.HET_WTF	Icam5	6.70	4.97E-04	Rasl10a	2.39	4.06E-02
CRB	VEH.HET_WTF	Mrap2	-1.61	5.45E-04	Hs3st5	-1.46	4.15E-02
CRB	VEH.HET_WTF	Olfr729	-1.29	5.60E-04	Gm32687	5.98	4.23E-02
CRB	VEH.HET_WTF	Slc18a2	-3.19	5.81E-04	Armcx6	-1.28	4.23E-02
CRB	VEH.HET_WTF	Gm48799	6.70	5.81E-04	Gm42912	1.00	4.39E-02
CRB	VEH.HET_WTF	Pdlim2	-0.97	5.92E-04	Uchl1	-0.66	4.52E-02
CRB	VEH.HET_WTF	Sostdc1	0.95	7.45E-04			
CRB	HETIGF1_WTF VEH	Gm14648	-2.52	1.47E-35	Gdf1	2.76	1.99E-03
CRB	HETIGF1_WTF VEH	Gm4767	-8.99	6.98E-29	Cartpt	-2.02	1.99E-03
CRB	HETIGF1_WTF VEH	Gm32687	8.60	3.36E-18	nan	-6.31	1.99E-03
CRB	HETIGF1_WTF VEH	Sncg	-1.50	4.75E-14	nan	-6.31	1.99E-03
CRB	HETIGF1_WTF VEH	Lamp5	-1.21	3.02E-10	Pdlim2	-0.80	2.79E-03
CRB	HETIGF1_WTF VEH	Rpl31-ps8	-1.41	8.05E-10	Pcdha3	6.38	3.24E-03
CRB	HETIGF1_WTF VEH	Ighm	-1.59	1.29E-09	Glra3	-1.96	3.31E-03
CRB	HETIGF1_WTF VEH	Calca	-1.50	1.29E-09	Nefm	-0.65	3.48E-03
CRB	HETIGF1_WTF VEH	Gh	-1.28	1.77E-09	Calcb	-1.28	4.44E-03
CRB	HETIGF1_WTF VEH	Gm10095	-1.05	1.63E-08	Gm10045	-6.14	4.44E-03
CRB	HETIGF1_WTF VEH	Fxyd2	-2.83	1.90E-08	Tppp3	-0.72	4.56E-03
CRB	HETIGF1_WTF VEH	Gm5898	-7.37	2.66E-08	Rgs4	-0.78	4.56E-03
CRB	HETIGF1_WTF VEH	Bc1	-0.86	1.18E-06	Dock4	0.92	4.56E-03
CRB	HETIGF1_WTF VEH	Tac1	-1.31	2.04E-06	Olfr729	-0.99	5.05E-03
CRB	HETIGF1_WTF VEH	Gal	-1.30	2.09E-06	Cd59a	-0.72	5.05E-03
CRB	HETIGF1_WTF VEH	Resp18	-0.88	2.09E-06	Gm9104	6.31	5.21E-03

CRB	HETIGF1_WTF VEH	Serpinb1b	-1.12	3.10E-06	Gm53013	-2.30	7.62E-03
CRB	HETIGF1_WTF VEH	Sst	-1.38	3.38E-05	Pcdha11	-1.65	8.49E-03
CRB	HETIGF1_WTF VEH	Tac2	-3.03	3.38E-05	Minar2	-0.79	8.59E-03
CRB	HETIGF1_WTF VEH	Pcdha12	6.99	5.19E-05	Rab3b	-0.87	8.59E-03
CRB	HETIGF1_WTF VEH	Tatdn1	-0.75	7.39E-05	Ocrl	0.91	8.59E-03
CRB	HETIGF1_WTF VEH	Prph	-1.87	7.39E-05	F2rl2	-2.53	8.59E-03
CRB	HETIGF1_WTF VEH	2900064K03Rik	1.38	7.64E-05	Pomc	-1.24	1.03E-02
CRB	HETIGF1_WTF VEH	Rims3	1.03	9.89E-05	AW551984	-1.24	1.08E-02
CRB	HETIGF1_WTF VEH	Gm17081	2.87	1.44E-04	Gm12666	6.22	1.08E-02
CRB	HETIGF1_WTF VEH	Prl	-0.81	1.47E-04	Vstm2a	-0.73	1.27E-02
CRB	HETIGF1_WTF VEH	Nr4a2	1.65	1.50E-04	Serpina3n	-1.48	1.70E-02
CRB	HETIGF1_WTF VEH	mt-Nd4l	-0.72	1.58E-04	Arhgdig	-0.96	1.73E-02
CRB	HETIGF1_WTF VEH	Gm10599	-6.64	1.58E-04	Gm42919	1.08	1.83E-02
CRB	HETIGF1_WTF VEH	Prl2c3	-1.23	2.30E-04	Gm42770	1.27	1.95E-02
CRB	HETIGF1_WTF VEH	Hoxb7	-3.12	3.23E-04	Slamf1	-0.82	1.95E-02
CRB	HETIGF1_WTF VEH	Crh	-2.65	3.49E-04	Tmem45b	-3.61	1.95E-02
CRB	HETIGF1_WTF VEH	Gm3055	-1.18	3.74E-04	Lgals1	-0.62	2.06E-02
CRB	HETIGF1_WTF VEH	Pcdha11	-6.68	3.98E-04	Vip	-1.44	2.26E-02
CRB	HETIGF1_WTF VEH	Cers1	-3.40	4.01E-04	mt-Nd3	-0.54	2.59E-02
CRB	HETIGF1_WTF VEH	Pcdha1	6.64	4.55E-04	Gm42912	0.94	2.66E-02
CRB	HETIGF1_WTF VEH	Gm42566	0.74	5.89E-04	Arid1b	0.78	2.77E-02
CRB	HETIGF1_WTF VEH	Gm48799	6.67	6.80E-04	nan	-0.69	3.64E-02
CRB	HETIGF1_WTF VEH	Ifi27l2a	-1.16	6.80E-04	Clvs2	-0.89	4.14E-02
CRB	HETIGF1_WTF VEH	Hoxb2	-1.70	7.72E-04	Rpl31	-0.52	4.24E-02
CRB	HETIGF1_WTF VEH	Hoxa5	-2.06	7.75E-04	mt-Rnr1	-0.54	4.32E-02
CRB	HETIGF1_WTF VEH	Gm10340	-6.35	1.24E-03	Lum	-0.92	4.32E-02
CRB	HETIGF1_WTF VEH	Klk6	-0.79	1.32E-03	Rbm11	-1.20	4.42E-02
CRB	HETIGF1_WTF VEH	Otos	2.64	1.38E-03	mt-Nd5	-0.52	4.43E-02
CRB	HETIGF1_WTF VEH	Gm16056	6.50	1.50E-03	Nrxn3	0.56	4.48E-02

CRB	HETIGF1_WTF VEH	Fos	1.10	1.89E-03	Nfib	0.61	4.86E-02
CRB	HETIGF1_WTF VEH	Nts	-1.12	1.99E-03	D830030 K20Rik	-0.98	4.95E-02
CRB	HETIGF1_WTF VEH	Gm42772	1.06	1.99E-03	Cbx7	0.78	4.95E-02
CRB	HETIGF1_WTF VEH	Pcp4l1	-0.70	1.99E-03			
BL	HET.IGF1_VEH	Alb	-3.29	2.03E-04	Ccl5	-2.18	1.32E-03
BL	HET.IGF1_VEH	Fabp1	-4.58	5.01E-04	Rps13-ps1	3.04	3.56E-03
BL	HET.IGF1_VEH	Rps16-ps2	-6.89	9.03E-04	Gm10240	-2.01	1.37E-02
BL	HET.IGF1_VEH	Apoa2	-3.32	1.32E-03	Ipo11	-2.11	4.56E-02
BL	VEH.HET_WTF	Mup3	-6.54	2.62E-16	Cyp4a10	-5.22	3.30E-04
BL	VEH.HET_WTF	Serpina1d	-7.61	2.62E-16	Gm13842	4.77	4.09E-04
BL	VEH.HET_WTF	Serpina1b	-6.45	5.51E-15	Inafm2	5.23	4.11E-04
BL	VEH.HET_WTF	Serpina1a	-6.48	1.42E-14	Pls1	6.76	4.17E-04
BL	VEH.HET_WTF	Mup19	-6.63	3.39E-14	Slc10a1	-4.31	4.30E-04
BL	VEH.HET_WTF	Mup14	-5.90	9.81E-14	Spp2	-4.30	4.73E-04
BL	VEH.HET_WTF	Hpx	-6.84	4.36E-13	Cyp2a12	-6.59	4.81E-04
BL	VEH.HET_WTF	Mup11	-6.27	1.08E-12	Acaa2	-3.23	4.84E-04
BL	VEH.HET_WTF	Mup9	-9.02	1.47E-12	Abcb11	-6.57	5.50E-04
BL	VEH.HET_WTF	Serpina1c	-5.51	2.02E-12	Gm21596	6.70	5.96E-04
BL	VEH.HET_WTF	Arg1	-8.78	1.62E-11	Cyp2c70	-4.26	6.25E-04
BL	VEH.HET_WTF	Serpina3k	-5.56	3.17E-11	Uba7	3.01	6.56E-04
BL	VEH.HET_WTF	Kng1	-7.21	4.64E-11	Ang	-4.22	7.10E-04
BL	VEH.HET_WTF	Rbp4	-5.35	5.54E-11	Proz	-6.52	7.16E-04
BL	VEH.HET_WTF	Adh1	-5.75	5.55E-11	Cfh	-4.03	7.16E-04
BL	VEH.HET_WTF	Ahsg	-5.43	5.77E-11	Mylk	4.68	7.20E-04
BL	VEH.HET_WTF	Car3	-5.52	5.77E-11	Rny1	5.22	7.20E-04
BL	VEH.HET_WTF	Apoc3	-5.01	6.10E-11	Rny3	3.98	7.27E-04
BL	VEH.HET_WTF	Gc	-5.21	1.07E-10	Capn3	3.85	7.27E-04
BL	VEH.HET_WTF	Gng11	4.68	3.77E-10	Asgr1	-3.62	7.66E-04
BL	VEH.HET_WTF	Alb	-4.64	4.89E-10	Ugt2b36	-3.83	7.74E-04
BL	VEH.HET_WTF	Apoa2	-4.60	6.18E-10	Ly6g2	-4.51	8.37E-04
BL	VEH.HET_WTF	Gsta3	-6.04	6.20E-10	Ly6g6c	5.19	8.37E-04
BL	VEH.HET_WTF	Clec1b	4.60	7.83E-10	C4bp	-6.47	9.20E-04
BL	VEH.HET_WTF	Ambp	-5.80	8.36E-10	Pxmp2	-4.52	9.33E-04
BL	VEH.HET_WTF	Fgb	-5.50	9.18E-10	Hsd3b7	-3.66	9.54E-04
BL	VEH.HET_WTF	Azgp1	-5.98	1.03E-09	Gstz1	-3.48	1.04E-03
BL	VEH.HET_WTF	Igf1	-6.85	1.03E-09	Serpina3m	-6.44	1.04E-03
BL	VEH.HET_WTF	Apoc1	-4.55	1.34E-09	Cyp1a2	-6.44	1.04E-03
BL	VEH.HET_WTF	F2	-6.79	1.76E-09	Selenop	-2.59	1.04E-03
BL	VEH.HET_WTF	Slc27a5	-8.22	1.76E-09	Cd302	-3.21	1.08E-03
BL	VEH.HET_WTF	Bhmt	-5.18	1.92E-09	Rarres2	-3.33	1.12E-03
BL	VEH.HET_WTF	Mat1a	-6.19	2.82E-09	Cyp2d26	-3.93	1.15E-03

BL	VEH.HET_WTF	Cyp2e1	-5.38	3.01E-09	Kng2	-6.42	1.18E-03
BL	VEH.HET_WTF	Sult2a8	-6.15	3.93E-09	C9	-6.42	1.18E-03
BL	VEH.HET_WTF	Fabp1	-4.37	3.93E-09	Retnla	-2.90	1.19E-03
BL	VEH.HET_WTF	Cyp3a11	-5.14	4.21E-09	Pemt	-3.93	1.23E-03
BL	VEH.HET_WTF	Lsm12	4.62	4.24E-09	Nnmt	-5.01	1.26E-03
BL	VEH.HET_WTF	Cyp2f2	-8.09	4.65E-09	Gm49391	3.42	1.30E-03
BL	VEH.HET_WTF	Fgg	-5.29	5.90E-09	Cyp2c23	-6.39	1.35E-03
BL	VEH.HET_WTF	Gp9	4.82	6.06E-09	Pcbd1	-3.33	1.43E-03
BL	VEH.HET_WTF	Ctla2a	4.50	6.06E-09	Cyp2j5	-4.97	1.43E-03
BL	VEH.HET_WTF	Uox	-5.17	6.61E-09	Tpm4	2.81	1.52E-03
BL	VEH.HET_WTF	Aldob	-4.91	6.61E-09	BC024386	-6.36	1.54E-03
BL	VEH.HET_WTF	Rpl31-ps9	-8.01	8.53E-09	Ces1f	-6.36	1.54E-03
BL	VEH.HET_WTF	Mup20	-6.03	9.12E-09	Retnlg	2.73	1.63E-03
BL	VEH.HET_WTF	Mup10	-5.49	1.08E-08	Tmem86b	-6.39	1.69E-03
BL	VEH.HET_WTF	Apoc4	-5.47	1.15E-08	Vsig4	-4.96	1.72E-03
BL	VEH.HET_WTF	Hamp	-6.01	1.15E-08	Kif2a	2.88	1.74E-03
BL	VEH.HET_WTF	Ctla2b	4.33	1.23E-08	Apob	-4.41	1.78E-03
BL	VEH.HET_WTF	Apoa5	-7.91	1.78E-08	Nrgn	3.71	1.86E-03
BL	VEH.HET_WTF	Apoa1	-4.89	1.82E-08	Vwf	4.51	1.96E-03
BL	VEH.HET_WTF	Akr1c6	-5.14	1.85E-08	Ifitm1	3.31	1.98E-03
BL	VEH.HET_WTF	Ppbp	4.08	2.19E-08	Itih2	-4.91	2.00E-03
BL	VEH.HET_WTF	Apom	-7.87	2.48E-08	Ces2a	-6.31	2.02E-03
BL	VEH.HET_WTF	Hpd	-4.77	3.01E-08	S100a9	2.58	2.08E-03
BL	VEH.HET_WTF	Cavin2	4.81	3.02E-08	S100a8	2.50	2.18E-03
BL	VEH.HET_WTF	Pf4	4.09	3.73E-08	Rps13-ps1	-3.23	2.26E-03
BL	VEH.HET_WTF	Orm1	-5.50	5.45E-08	Pdlim1	2.70	2.31E-03
BL	VEH.HET_WTF	Myl9	4.27	5.49E-08	Oaf	-6.28	2.32E-03
BL	VEH.HET_WTF	Fbp1	-5.28	5.49E-08	Itga2b	4.14	2.93E-03
BL	VEH.HET_WTF	Ces1c	-5.09	8.35E-08	Aldh7a1	-4.32	3.00E-03
BL	VEH.HET_WTF	Itih4	-7.73	8.88E-08	Cyp4v3	-4.84	3.04E-03
BL	VEH.HET_WTF	Cps1	-5.24	9.59E-08	Slc6a4	6.36	3.23E-03
BL	VEH.HET_WTF	Serpinc1	-4.94	1.04E-07	Mup17	-4.84	3.25E-03
BL	VEH.HET_WTF	Tsc22d1	3.94	1.39E-07	Rab27b	3.39	3.54E-03
BL	VEH.HET_WTF	Ugt2b5	-6.23	1.43E-07	F13a1	3.24	3.76E-03
BL	VEH.HET_WTF	Angptl3	-6.20	1.63E-07	Sult1a1	-3.17	3.78E-03
BL	VEH.HET_WTF	Cd9	3.84	1.73E-07	Plg	-4.27	3.78E-03
BL	VEH.HET_WTF	Pzp	-7.63	2.16E-07	Sh3bgrl2	2.88	3.78E-03
BL	VEH.HET_WTF	Mctp1	6.25	2.44E-07	Bcl2a1d	-6.20	3.86E-03
BL	VEH.HET_WTF	Rnase4	-5.31	2.64E-07	Pbld2	-6.16	4.34E-03
BL	VEH.HET_WTF	Aadac	-5.62	2.65E-07	F13b	-6.16	4.34E-03
BL	VEH.HET_WTF	Urah	-7.60	2.88E-07	Mbnl1	2.48	4.91E-03
BL	VEH.HET_WTF	Gm15501	-7.66	3.74E-07	Ipo11	2.69	4.93E-03
BL	VEH.HET_WTF	Apof	-6.09	4.00E-07	Fli1	3.63	5.05E-03

BL	VEH.HET_WTF	Pon1	-6.06	4.94E-07	Mug1	-4.20	5.29E-03
BL	VEH.HET_WTF	Fga	-5.53	5.25E-07	Pecr	-3.91	5.30E-03
BL	VEH.HET_WTF	Rdh7	-4.85	5.25E-07	Rhoj	6.24	5.53E-03
BL	VEH.HET_WTF	Fgl1	-7.52	5.99E-07	Birc2	2.71	5.54E-03
BL	VEH.HET_WTF	Mbl2	-5.49	7.14E-07	Odc1	2.69	5.71E-03
BL	VEH.HET_WTF	Trf	-3.65	7.60E-07	Ubap1	2.66	5.79E-03
BL	VEH.HET_WTF	Otc	-7.49	7.77E-07	Hsd17b13	-6.09	6.05E-03
BL	VEH.HET_WTF	Alox12	4.17	7.77E-07	Skap2	2.70	6.13E-03
BL	VEH.HET_WTF	Apoh	-4.28	8.59E-07	Tmem37	-4.74	6.13E-03
BL	VEH.HET_WTF	Cyp2c29	-5.14	1.04E-06	F2rl2	3.14	6.36E-03
BL	VEH.HET_WTF	H2-Q10	-4.64	1.20E-06	Mup7	-4.70	6.71E-03
BL	VEH.HET_WTF	Dap	3.69	2.36E-06	Ston2	4.74	6.80E-03
BL	VEH.HET_WTF	Gnmt	-4.39	2.37E-06	Igfbp4	-4.16	7.06E-03
BL	VEH.HET_WTF	Inmt	-4.65	2.79E-06	0610005C13Rik	-6.05	7.06E-03
BL	VEH.HET_WTF	P2ry12	4.02	2.97E-06	Ftcd	-6.05	7.06E-03
BL	VEH.HET_WTF	Tmem40	4.48	3.01E-06	Cyp2b9	-6.05	7.06E-03
BL	VEH.HET_WTF	Rgs18	3.66	3.32E-06	Clic4	2.81	7.13E-03
BL	VEH.HET_WTF	Cfhr2	-4.95	4.27E-06	Saa3	-2.68	7.21E-03
BL	VEH.HET_WTF	Hpse	7.41	5.15E-06	Pttg1ip	2.52	7.33E-03
BL	VEH.HET_WTF	Fhl1	3.71	5.61E-06	Serping1	-3.32	7.38E-03
BL	VEH.HET_WTF	Cfb	-5.19	6.95E-06	Cxcl13	-2.78	7.38E-03
BL	VEH.HET_WTF	Cd226	3.66	6.95E-06	Rap1b	2.48	7.63E-03
BL	VEH.HET_WTF	Rgs10	3.44	8.71E-06	Gsr	3.47	7.71E-03
BL	VEH.HET_WTF	Slco1b2	-5.70	9.58E-06	Hamp2	-2.74	8.22E-03
BL	VEH.HET_WTF	Pah	-7.18	1.09E-05	Ces3b	-6.02	8.22E-03
BL	VEH.HET_WTF	Rps23-ps1	-7.25	1.37E-05	Mup12	-6.02	8.22E-03
BL	VEH.HET_WTF	Cideb	-7.15	1.38E-05	Ugt2b34	-4.64	8.22E-03
BL	VEH.HET_WTF	Cfi	-7.15	1.38E-05	Cd1d1	-3.43	8.55E-03
BL	VEH.HET_WTF	Cyp2c68	-5.63	1.74E-05	Cyp2c54	-4.13	8.68E-03
BL	VEH.HET_WTF	Rdh16f2	-7.11	1.78E-05	Myct1	3.94	9.08E-03
BL	VEH.HET_WTF	Ces3a	-7.10	2.02E-05	Gp6	2.89	9.10E-03
BL	VEH.HET_WTF	Tdo2	-4.72	2.16E-05	Apol7a	-5.98	9.76E-03
BL	VEH.HET_WTF	C3	-4.03	2.16E-05	Ugt2a3	-5.98	9.76E-03
BL	VEH.HET_WTF	Proc	-7.08	2.23E-05	Cd84	2.66	9.98E-03
BL	VEH.HET_WTF	Hsd17b6	-7.08	2.23E-05	Phyh	-2.58	1.07E-02
BL	VEH.HET_WTF	Hmgcs2	-4.51	2.29E-05	Ddt	-2.53	1.09E-02
BL	VEH.HET_WTF	C8g	-3.97	2.36E-05	Crp	-5.94	1.18E-02
BL	VEH.HET_WTF	Mup16	-7.07	2.49E-05	Cyp2b13	-5.94	1.18E-02
BL	VEH.HET_WTF	Rgn	-4.14	2.81E-05	Cd44	2.47	1.29E-02
BL	VEH.HET_WTF	Agxt	-7.05	2.81E-05	Slamf1	2.74	1.34E-02
BL	VEH.HET_WTF	Ugt1a7c	-4.66	2.92E-05	Stx11	2.84	1.34E-02
BL	VEH.HET_WTF	Ass1	-3.76	3.25E-05	Apcs	-5.91	1.41E-02
BL	VEH.HET_WTF	Parvb	7.16	3.40E-05	Rasgrp2	2.96	1.41E-02
BL	VEH.HET_WTF	Hgd	-7.01	3.55E-05	Slc25a47	-5.90	1.42E-02

BL	VEH.HET_WTF	Ephx2	-7.00	3.99E-05	Iyd	-5.90	1.42E-02
BL	VEH.HET_WTF	Hal	-7.00	3.99E-05	Apon	-5.90	1.42E-02
BL	VEH.HET_WTF	Plek	3.24	3.99E-05	Mcur1	3.49	1.50E-02
BL	VEH.HET_WTF	Gstt1	-4.43	3.99E-05	Mmrn1	3.35	1.52E-02
BL	VEH.HET_WTF	Cdo1	-4.43	3.99E-05	Nudt7	-3.05	1.52E-02
BL	VEH.HET_WTF	Cth	-4.61	4.20E-05	Cald1	2.45	1.53E-02
BL	VEH.HET_WTF	Cyp2c50	-4.95	4.56E-05	Tmem140	3.10	1.53E-02
BL	VEH.HET_WTF	Leap2	-5.51	4.61E-05	Col18a1	-5.90	1.53E-02
BL	VEH.HET_WTF	Rps16-ps2	7.09	5.28E-05	Asl	-3.35	1.60E-02
BL	VEH.HET_WTF	Wfdc21	-3.25	5.46E-05	Sh3bgrl3	2.13	1.71E-02
BL	VEH.HET_WTF	Hacd4	3.39	5.67E-05	Akr1c14	-5.86	1.72E-02
BL	VEH.HET_WTF	Hacl1	-4.60	5.89E-05	Fah	-2.79	1.77E-02
BL	VEH.HET_WTF	Acaa1b	-5.46	5.89E-05	Cd151	2.78	1.79E-02
BL	VEH.HET_WTF	Mmd	3.66	6.07E-05	Cyp4a14	-3.44	1.83E-02
BL	VEH.HET_WTF	Aldh8a1	-6.92	6.28E-05	Ptpn18	2.33	1.83E-02
BL	VEH.HET_WTF	Upb1	-5.46	6.65E-05	H2bc4	2.26	1.84E-02
BL	VEH.HET_WTF	Ghr	-6.91	7.12E-05	Mtarc1	-3.95	1.85E-02
BL	VEH.HET_WTF	Ces1d	-4.32	7.58E-05	Pipox	-4.48	1.88E-02
BL	VEH.HET_WTF	Mettl7b	-6.90	7.69E-05	Cpb2	-3.93	2.08E-02
BL	VEH.HET_WTF	Mup1	-6.89	8.02E-05	Ugt3a2	-5.82	2.08E-02
BL	VEH.HET_WTF	Cyp2c37	-4.31	8.79E-05	I830077J02Rik	2.87	2.19E-02
BL	VEH.HET_WTF	Nat8f2	-6.87	8.95E-05	Cbs	-3.43	2.22E-02
BL	VEH.HET_WTF	Pck1	-6.87	8.95E-05	Acat3	-4.40	2.47E-02
BL	VEH.HET_WTF	Mbl1	-6.87	8.95E-05	Morrbid	4.45	2.53E-02
BL	VEH.HET_WTF	Litaf	3.20	8.95E-05	Pank1	-3.42	2.53E-02
BL	VEH.HET_WTF	Cyp2d10	-5.40	9.85E-05	F9	-5.77	2.55E-02
BL	VEH.HET_WTF	Mgst1	-3.03	1.04E-04	Hsd3b3	-5.77	2.55E-02
BL	VEH.HET_WTF	Vtn	-3.53	1.06E-04	Irag1	5.88	2.66E-02
BL	VEH.HET_WTF	Gm13775	-6.83	1.16E-04	Cmbl	-3.11	2.81E-02
BL	VEH.HET_WTF	Reep6	-6.82	1.27E-04	Khk	-2.70	2.82E-02
BL	VEH.HET_WTF	Ahcy	-3.68	1.30E-04	Clu	2.06	2.82E-02
BL	VEH.HET_WTF	Cela1	3.65	1.31E-04	Apoe	-2.03	2.91E-02
BL	VEH.HET_WTF	H1f2	3.70	1.37E-04	H2bc24	5.84	2.91E-02
BL	VEH.HET_WTF	4930486L24Rik	4.85	1.48E-04	Pla2g12b	-5.75	2.96E-02
BL	VEH.HET_WTF	Cyp3a25	-6.79	1.49E-04	Gm26569	5.85	3.00E-02
BL	VEH.HET_WTF	Rac1	3.17	1.63E-04	Tagln2	2.06	3.05E-02
BL	VEH.HET_WTF	Itgb3	3.38	1.63E-04	Slc22a1	-5.73	3.08E-02
BL	VEH.HET_WTF	Dpyd	-6.77	1.69E-04	Hrg	-5.73	3.08E-02
BL	VEH.HET_WTF	Tat	-4.05	1.77E-04	Cyp2c40	-5.73	3.08E-02
BL	VEH.HET_WTF	Treml1	4.88	1.77E-04	Timd2	-5.73	3.08E-02
BL	VEH.HET_WTF	Zyx	3.29	1.96E-04	Gatad1	2.88	3.10E-02
BL	VEH.HET_WTF	Thbs1	3.53	2.01E-04	Gls2	-3.87	3.11E-02
BL	VEH.HET_WTF	Smim3	3.95	2.01E-04	Rtn4ip1	2.76	3.15E-02

BL	VEH.HET_WTF	Slc38a4	-5.27	2.24E-04	Slc27a2	-3.85	3.25E-02
BL	VEH.HET_WTF	Angpt1	5.31	2.35E-04	Sult1d1	-3.85	3.25E-02
BL	VEH.HET_WTF	Pigr	-5.27	2.42E-04	Pros1	3.96	3.33E-02
BL	VEH.HET_WTF	Mup22	-4.36	2.42E-04	Clec4d	2.59	3.39E-02
BL	VEH.HET_WTF	Mpig6b	4.51	2.59E-04	Snap23	2.20	3.49E-02
BL	VEH.HET_WTF	Itga6	3.44	2.59E-04	Gsn	3.03	3.51E-02
BL	VEH.HET_WTF	Baat	-6.70	2.62E-04	Fcer1g	2.03	3.52E-02
BL	VEH.HET_WTF	Gm30411	4.01	2.62E-04	Ly6g6f	4.33	3.93E-02
BL	VEH.HET_WTF	Tmsb4x	3.11	2.76E-04	Zfp664	4.40	4.12E-02
BL	VEH.HET_WTF	Ttpa	-6.67	3.12E-04	Acad11	-3.78	4.31E-02
BL	VEH.HET_WTF	Glyat	-6.66	3.23E-04	Cd59b	2.60	4.92E-02
BL	VEH.HET_WTF	Serpina1e	-5.23	3.23E-04			
BL	HETIGF1_WTF VEH	Fabp1	-8.97	1.81E-18	Tdo2	-4.72	7.20E-04
BL	HETIGF1_WTF VEH	Mup3	-8.04	5.06E-18	Pah	-6.88	7.43E-04
BL	HETIGF1_WTF VEH	Alb	-7.87	5.06E-18	Clec1b	3.14	7.97E-04
BL	HETIGF1_WTF VEH	Apoa2	-7.90	9.16E-18	Urah	-5.24	8.42E-04
BL	HETIGF1_WTF VEH	Apoc3	-8.35	1.42E-16	Slc38a4	-6.85	8.84E-04
BL	HETIGF1_WTF VEH	Serpina1c	-8.31	1.72E-16	Cyp2c50	-5.23	8.92E-04
BL	HETIGF1_WTF VEH	Mup14	-7.29	3.57E-16	H2-Q10	-3.78	1.02E-03
BL	HETIGF1_WTF VEH	Serpina1b	-7.81	1.09E-15	Pigr	-6.82	1.05E-03
BL	HETIGF1_WTF VEH	Ahsg	-10.24	1.49E-15	Rdh16f2	-6.82	1.05E-03
BL	HETIGF1_WTF VEH	Serpina3k	-10.22	1.77E-15	Ces3a	-6.80	1.15E-03
BL	HETIGF1_WTF VEH	Mup11	-10.05	8.91E-15	Mctp1	5.31	1.15E-03
BL	HETIGF1_WTF VEH	Rbp4	-8.37	1.60E-14	Cyp4a10	-6.80	1.17E-03
BL	HETIGF1_WTF VEH	Serpina1d	-8.32	2.02E-14	Proc	-6.79	1.23E-03
BL	HETIGF1_WTF VEH	Gc	-8.31	2.10E-14	Hsd17b6	-6.79	1.23E-03
BL	HETIGF1_WTF VEH	Apoc1	-6.71	6.42E-14	Rnase4	-3.88	1.26E-03
BL	HETIGF1_WTF VEH	Fgb	-9.35	8.25E-12	Serpina1e	-6.77	1.33E-03
BL	HETIGF1_WTF VEH	Hpd	-9.31	1.15E-11	Mup16	-6.77	1.33E-03
BL	HETIGF1_WTF VEH	Adh1	-7.64	1.51E-11	Agxt	-6.75	1.47E-03
BL	HETIGF1_WTF VEH	Fgg	-9.05	1.37E-10	Apob	-6.74	1.60E-03
BL	HETIGF1_WTF VEH	Apoh	-9.04	1.39E-10	Cyp4a14	-6.74	1.60E-03
BL	HETIGF1_WTF VEH	Aldob	-7.38	1.39E-10	Hgd	-6.72	1.77E-03

BL	HETIGF1_WTF VEH	Hpx	-6.84	1.46E-10	Hal	-6.70	1.95E-03
BL	HETIGF1_WTF VEH	Serpina1a	-5.68	2.52E-10	Ctla2b	3.09	2.02E-03
BL	HETIGF1_WTF VEH	Cyp3a11	-7.32	2.55E-10	Itga6	3.48	2.05E-03
BL	HETIGF1_WTF VEH	Gsta3	-8.93	3.16E-10	Alox12	3.43	2.15E-03
BL	HETIGF1_WTF VEH	Akr1c6	-8.90	4.01E-10	Pf4	2.72	2.80E-03
BL	HETIGF1_WTF VEH	Azgp1	-8.87	5.51E-10	Aldh8a1	-6.63	2.86E-03
BL	HETIGF1_WTF VEH	Apoa1	-7.16	8.87E-10	Plg	-6.63	2.86E-03
BL	HETIGF1_WTF VEH	Kng1	-8.77	1.29E-09	Ghr	-6.61	3.17E-03
BL	HETIGF1_WTF VEH	Mup9	-8.73	1.83E-09	Mettl7b	-6.60	3.34E-03
BL	HETIGF1_WTF VEH	Uox	-7.07	2.12E-09	Mup1	-6.59	3.46E-03
BL	HETIGF1_WTF VEH	Mup19	-5.45	3.98E-09	Mug1	-6.59	3.46E-03
BL	HETIGF1_WTF VEH	Cyp2e1	-6.98	4.07E-09	Ppbp	2.73	3.50E-03
BL	HETIGF1_WTF VEH	Fbp1	-8.56	7.20E-09	Nat8f2	-6.57	3.76E-03
BL	HETIGF1_WTF VEH	Mat1a	-8.52	9.84E-09	Pck1	-6.57	3.76E-03
BL	HETIGF1_WTF VEH	Arg1	-8.49	1.24E-08	Mbl1	-6.57	3.76E-03
BL	HETIGF1_WTF VEH	Sult2a8	-8.48	1.32E-08	Nnmt	-6.55	4.14E-03
BL	HETIGF1_WTF VEH	Bhmt	-5.94	1.37E-08	Cyp2j5	-6.55	4.14E-03
BL	HETIGF1_WTF VEH	Rdh7	-8.44	1.79E-08	Selenop	-2.66	4.33E-03
BL	HETIGF1_WTF VEH	Cps1	-8.44	1.82E-08	Acaa1b	-4.91	4.36E-03
BL	HETIGF1_WTF VEH	C8g	-8.42	2.08E-08	Gm13775	-6.53	4.53E-03
BL	HETIGF1_WTF VEH	Mup20	-8.42	2.08E-08	Tmem40	3.69	4.85E-03
BL	HETIGF1_WTF VEH	Ambp	-6.19	3.10E-08	Itih2	-6.49	5.53E-03
BL	HETIGF1_WTF VEH	F2	-8.34	3.60E-08	Vsig4	-6.49	5.53E-03
BL	HETIGF1_WTF VEH	Hamp	-8.34	3.60E-08	Cyp3a25	-6.49	5.53E-03
BL	HETIGF1_WTF VEH	Serpinc1	-6.65	6.03E-08	Fah	-4.02	5.64E-03
BL	HETIGF1_WTF VEH	Inmt	-8.24	7.92E-08	Dpyd	-6.47	6.10E-03
BL	HETIGF1_WTF VEH	Hamp2	-8.22	8.94E-08	Cfh	-4.32	6.23E-03
BL	HETIGF1_WTF VEH	Mup10	-6.57	1.03E-07	Cyp2c54	-6.45	6.69E-03
BL	HETIGF1_WTF VEH	Rgn	-8.14	1.62E-07	Parvb	6.29	7.12E-03

BL	HETIGF1_WTF VEH	Ces1c	-6.50	1.81E-07	Ly6g2	-4.84	7.40E-03
BL	HETIGF1_WTF VEH	Car3	-4.73	2.68E-07	Baat	-6.41	8.35E-03
BL	HETIGF1_WTF VEH	Gnmt	-6.42	3.20E-07	Pcbd1	-3.53	8.49E-03
BL	HETIGF1_WTF VEH	Wfdc21	-4.63	4.71E-07	Tsc22d1	2.71	8.58E-03
BL	HETIGF1_WTF VEH	Apoc4	-5.79	6.34E-07	Mup17	-6.39	8.83E-03
BL	HETIGF1_WTF VEH	Orm1	-6.35	6.37E-07	Cmbl	-4.79	9.24E-03
BL	HETIGF1_WTF VEH	Aadac	-7.95	6.48E-07	Glyat	-6.37	9.71E-03
BL	HETIGF1_WTF VEH	Slc27a5	-7.93	7.47E-07	Cfi	-4.72	1.19E-02
BL	HETIGF1_WTF VEH	C3	-6.28	9.49E-07	Cpb2	-6.32	1.19E-02
BL	HETIGF1_WTF VEH	Fga	-7.88	1.02E-06	Hsd3b7	-3.69	1.27E-02
BL	HETIGF1_WTF VEH	Mbl2	-7.84	1.41E-06	Cyp2a12	-6.30	1.31E-02
BL	HETIGF1_WTF VEH	Cfhr2	-7.83	1.47E-06	Serpinf1	-6.29	1.40E-02
BL	HETIGF1_WTF VEH	Cyp2f2	-7.80	1.84E-06	Ahcy	-3.13	1.61E-02
BL	HETIGF1_WTF VEH	Angptl3	-7.78	2.03E-06	Mup7	-6.25	1.61E-02
BL	HETIGF1_WTF VEH	Ugt2b5	-7.77	2.13E-06	Rarres2	-3.28	1.72E-02
BL	HETIGF1_WTF VEH	Rpl31-ps9	-7.72	3.20E-06	Rnaset2a	-6.23	1.75E-02
BL	HETIGF1_WTF VEH	Lsm12	4.18	3.34E-06	Aqp8	-6.23	1.75E-02
BL	HETIGF1_WTF VEH	Mgst1	-3.95	4.89E-06	Ugt2b34	-6.23	1.75E-02
BL	HETIGF1_WTF VEH	Apof	-7.64	5.54E-06	Proz	-6.23	1.75E-02
BL	HETIGF1_WTF VEH	Apoa5	-7.62	6.27E-06	Mfap3l	4.80	1.78E-02
BL	HETIGF1_WTF VEH	Pon1	-7.61	6.63E-06	Kel	-3.67	1.78E-02
BL	HETIGF1_WTF VEH	Ces1d	-7.59	7.53E-06	Hacl1	-3.60	1.84E-02
BL	HETIGF1_WTF VEH	Tat	-7.57	9.17E-06	Cd226	2.78	1.97E-02
BL	HETIGF1_WTF VEH	Ass1	-4.88	1.18E-05	Nudt7	-3.79	2.08E-02
BL	HETIGF1_WTF VEH	Cfb	-7.52	1.28E-05	Gm42522	-6.21	2.08E-02
BL	HETIGF1_WTF VEH	Cyp2c37	-7.51	1.36E-05	Gls2	-6.18	2.08E-02
BL	HETIGF1_WTF VEH	Itih4	-7.44	2.26E-05	Slc27a2	-6.18	2.08E-02
BL	HETIGF1_WTF VEH	Gm15501	-7.44	3.58E-05	C4bp	-6.18	2.08E-02
BL	HETIGF1_WTF VEH	Ugt2b36	-7.34	4.34E-05	Sult1d1	-6.18	2.08E-02

BL	HETIGF1_WTF VEH	Pzp	-7.34	4.34E-05	Angpt1	4.76	2.09E-02
BL	HETIGF1_WTF VEH	Hmgcs2	-5.72	4.50E-05	Serpina3m	-6.15	2.29E-02
BL	HETIGF1_WTF VEH	Gng11	3.39	5.37E-05	Cyp1a2	-6.15	2.29E-02
BL	HETIGF1_WTF VEH	Igf1	-4.65	6.10E-05	Retsat	-6.12	2.53E-02
BL	HETIGF1_WTF VEH	Slco1b2	-7.28	6.20E-05	Kng2	-6.12	2.53E-02
BL	HETIGF1_WTF VEH	Mup22	-7.27	6.67E-05	C9	-6.12	2.53E-02
BL	HETIGF1_WTF VEH	Fgl1	-7.22	9.35E-05	Ugt1a7c	-3.28	2.67E-02
BL	HETIGF1_WTF VEH	Cyp2c68	-7.21	1.01E-04	Itih1	-6.10	2.80E-02
BL	HETIGF1_WTF VEH	Otc	-7.20	1.13E-04	Cyp2c23	-6.10	2.80E-02
BL	HETIGF1_WTF VEH	Cavin2	4.12	1.40E-04	Dap	2.58	3.10E-02
BL	HETIGF1_WTF VEH	Cyp2d26	-7.15	1.52E-04	BC024386	-6.07	3.10E-02
BL	HETIGF1_WTF VEH	Slc10a1	-7.14	1.64E-04	Ces1f	-6.07	3.10E-02
BL	HETIGF1_WTF VEH	Pemt	-7.14	1.64E-04	Acaa2	-2.77	3.10E-02
BL	HETIGF1_WTF VEH	Apom	-5.51	1.65E-04	Lyz1	-2.71	3.10E-02
BL	HETIGF1_WTF VEH	Spp2	-7.12	1.75E-04	Cideb	-4.00	3.17E-02
BL	HETIGF1_WTF VEH	Ang	-7.10	2.08E-04	Masp2	-6.04	3.43E-02
BL	HETIGF1_WTF VEH	Cyp2c70	-7.08	2.25E-04	Cxcl13	-2.90	3.50E-02
BL	HETIGF1_WTF VEH	Gp9	3.87	2.27E-04	Mylk	4.25	3.70E-02
BL	HETIGF1_WTF VEH	Trf	-3.19	2.27E-04	Asgr1	-3.19	3.79E-02
BL	HETIGF1_WTF VEH	Leap2	-7.06	2.63E-04	Ces2a	-6.01	3.79E-02
BL	HETIGF1_WTF VEH	Cth	-5.43	2.67E-04	Mmd	2.91	3.79E-02
BL	HETIGF1_WTF VEH	Ctla2a	3.16	2.67E-04	Cd302	-2.85	3.83E-02
BL	HETIGF1_WTF VEH	Saa3	-4.03	3.53E-04	Gm21596	5.86	3.95E-02
BL	HETIGF1_WTF VEH	Vtn	-3.97	4.27E-04	Slc6a4	5.85	4.18E-02
BL	HETIGF1_WTF VEH	Myl9	3.46	4.64E-04	Oaf	-5.98	4.18E-02
BL	HETIGF1_WTF VEH	Rps23-ps1	-7.03	5.00E-04	Acat3	-5.98	4.18E-02
BL	HETIGF1_WTF VEH	Cyp2d10	-6.95	5.00E-04	Reep6	-4.47	4.20E-02
BL	HETIGF1_WTF VEH	Cyp2c29	-4.45	5.26E-04	Gm14327	-6.03	4.21E-02
BL	HETIGF1_WTF VEH	Cdo1	-4.73	6.57E-04	Cyp2a5	-5.95	4.68E-02

BL	HETIGF1_WTFVEH	Sap18b	-6.91	6.82E-04	Treml1	4.19	4.74E-02

Supplementary Table 7 – DEG Analysis in Female rhIGF1 Treated Mice from Chapter II
All significant DEG found in the analysis of Female mice treated with rhIGF1 or vehicle. These results were calculated using EdgeR's QLFT function. The
Legend:
CRB = Cerebellum, BL = Blood, HET.IGF1_VEH = rhIGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{-/+}$, WTF.IGF1_VEH = rhIGF1 treated *Mecp2*$^{+/+}$ vs. VEH treated *Mecp2*$^{+/+}$, IGF1.HET_WTF= rhIGF1 treated *Mecp2*$^{-/+}$ vs. rhIGF1 treated *Mecp2*$^{+/+}$, VEH.HET_WTF = VEH treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/+}$, HETIGF1_WTFVEH = IGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/+}$

Tissue	Comparison	Gene	logFC	FDR	Gene	logFC	FDR
CRB	KO.IGF1_VEH	Mir6236	-2.51	3.32E-33	Sgk1	0.48	6.32E-03
CRB	KO.IGF1_VEH	Usp1	-2.30	3.78E-22	Th	-1.01	6.37E-03
CRB	KO.IGF1_VEH	Tmem59l	-1.14	3.58E-17	AK010878	-0.73	6.76E-03
CRB	KO.IGF1_VEH	Fam213b	-0.98	3.84E-12	Hist1h4h	-1.32	6.98E-03
CRB	KO.IGF1_VEH	Gpx4	-0.85	1.59E-09	Psmd4	-0.48	6.98E-03
CRB	KO.IGF1_VEH	Caly	-1.08	2.25E-08	Gnai1	-0.50	6.99E-03
CRB	KO.IGF1_VEH	Tppp3	-0.93	4.72E-08	Psmb5	-0.52	7.25E-03
CRB	KO.IGF1_VEH	Necap2	-1.32	7.18E-08	Mt2	0.52	7.62E-03
CRB	KO.IGF1_VEH	Ywhaq	-0.77	1.09E-07	Hmgxb3	1.41	8.67E-03
CRB	KO.IGF1_VEH	Isca1	-0.78	1.36E-07	Mal	0.51	8.81E-03
CRB	KO.IGF1_VEH	Wsb1	-0.90	2.45E-07	Zc3h6	-0.90	9.07E-03
CRB	KO.IGF1_VEH	Vcp	-0.85	5.32E-07	9130401M01Rik	-0.70	9.07E-03
CRB	KO.IGF1_VEH	Arhgdia	-0.76	6.65E-07	2310057M21Rik	-0.86	9.31E-03
CRB	KO.IGF1_VEH	Glrx5	-1.05	7.08E-07	Cnn2	-1.11	9.43E-03
CRB	KO.IGF1_VEH	Cdk5	-0.80	7.78E-07	Spg7	-0.95	9.64E-03
CRB	KO.IGF1_VEH	Trappc5	-0.90	7.78E-07	Uqcc2	-0.46	1.09E-02
CRB	KO.IGF1_VEH	Acbd3	-1.33	9.56E-07	Vim	-0.60	1.09E-02
CRB	KO.IGF1_VEH	Psmd8	-0.80	9.67E-07	2700094K13Rik	-0.50	1.09E-02
CRB	KO.IGF1_VEH	Bag1	-1.27	9.67E-07	BC030336	1.02	1.09E-02
CRB	KO.IGF1_VEH	Tmem59	-0.73	1.06E-06	Mrps12	-0.51	1.09E-02
CRB	KO.IGF1_VEH	Wdr45	-0.92	1.71E-06	Ing4	-0.59	1.12E-02
CRB	KO.IGF1_VEH	Fuca1	-0.92	1.71E-06	Pam16	-0.56	1.12E-02

CRB	KO.IGF1_VEH	Pkn2	-1.16	2.03E-06	Tspyl4	-0.46	1.16E-02
CRB	KO.IGF1_VEH	Tmem160	-1.19	2.04E-06	Scrn1	-0.50	1.31E-02
CRB	KO.IGF1_VEH	Pgrmc1	-0.76	4.07E-06	Scrn2	-1.85	1.35E-02
CRB	KO.IGF1_VEH	Atp6v1g2	-0.69	4.28E-06	Atp5g3	-0.50	1.35E-02
CRB	KO.IGF1_VEH	B4gat1	-0.89	5.88E-06	Ncaph2	-0.54	1.35E-02
CRB	KO.IGF1_VEH	Ndufb6	-0.68	6.08E-06	Sppl2b	-1.21	1.42E-02
CRB	KO.IGF1_VEH	Rpl27a	-0.76	6.73E-06	Ctcf	-0.53	1.42E-02
CRB	KO.IGF1_VEH	Acin1	-0.74	6.73E-06	Gtf2f1	-0.62	1.42E-02
CRB	KO.IGF1_VEH	Zmat5	-0.91	7.86E-06	Gm5617	-1.17	1.46E-02
CRB	KO.IGF1_VEH	Mpdu1	-0.78	1.22E-05	Tars	-0.51	1.51E-02
CRB	KO.IGF1_VEH	Golph3l	-0.67	1.57E-05	Pnrc1	-0.81	1.51E-02
CRB	KO.IGF1_VEH	Tssc4	-0.96	1.58E-05	Metrn	-0.53	1.52E-02
CRB	KO.IGF1_VEH	Cfl1	-0.66	1.63E-05	Dnajc30	-0.75	1.56E-02
CRB	KO.IGF1_VEH	Gabrd	-0.70	1.63E-05	Hagh	-0.45	1.58E-02
CRB	KO.IGF1_VEH	Hexb	-0.80	2.32E-05	Slc35b4	-0.87	1.58E-02
CRB	KO.IGF1_VEH	Fabp4	3.10	2.32E-05	Cmc2	-0.72	1.60E-02
CRB	KO.IGF1_VEH	Pef1	-0.96	2.65E-05	Thap3	-0.92	1.60E-02
CRB	KO.IGF1_VEH	Id3	-0.69	2.65E-05	BC005561	-0.99	1.69E-02
CRB	KO.IGF1_VEH	Rab7	-0.63	2.81E-05	Gnptg	-0.46	1.80E-02
CRB	KO.IGF1_VEH	Ucp1	3.74	4.13E-05	Ak1	-0.45	1.90E-02
CRB	KO.IGF1_VEH	Snrpb	-0.66	4.40E-05	Acadl	-0.75	1.90E-02
CRB	KO.IGF1_VEH	Cd81	-0.71	7.49E-05	Ccdc115	-0.78	1.90E-02
CRB	KO.IGF1_VEH	Rraga	-0.67	9.08E-05	Rab24	-0.60	1.93E-02
CRB	KO.IGF1_VEH	Saa3	3.26	9.08E-05	Wdr18	-0.76	1.98E-02
CRB	KO.IGF1_VEH	Sec61b	-0.66	9.32E-05	Smarcd3	-1.56	2.05E-02
CRB	KO.IGF1_VEH	Metap2	-0.61	9.42E-05	Dctn3	-0.45	2.14E-02
CRB	KO.IGF1_VEH	Pdcd6	-0.62	1.34E-04	Rnd1	-1.09	2.15E-02
CRB	KO.IGF1_VEH	Fkbp2	-0.60	1.49E-04	Cst6	-0.92	2.22E-02
CRB	KO.IGF1_VEH	Cbx1	-0.77	1.61E-04	Dhdds	-0.85	2.25E-02

CRB	KO.IGF1_VEH	Rps10	-0.83	1.62E-04	Ddah2	-0.51	2.31E-02
CRB	KO.IGF1_VEH	2810013P06Rik	-0.75	1.89E-04	Hmgcr	0.59	2.40E-02
CRB	KO.IGF1_VEH	Ddrgk1	-0.64	2.23E-04	Znhit1	-0.68	2.44E-02
CRB	KO.IGF1_VEH	Ndufa8	-0.58	2.23E-04	Lactb	-1.30	2.47E-02
CRB	KO.IGF1_VEH	Mrps6	-0.72	3.26E-04	H3f3b	-0.52	2.47E-02
CRB	KO.IGF1_VEH	Yipf5	-0.70	3.41E-04	BC031361	2.98	2.47E-02
CRB	KO.IGF1_VEH	Ckb	-0.80	3.41E-04	P4ha1	-0.99	2.49E-02
CRB	KO.IGF1_VEH	Alb	-1.37	3.41E-04	Irf2bp2	0.82	2.60E-02
CRB	KO.IGF1_VEH	Mapk6	-0.91	3.42E-04	Pafah1b3	-0.79	2.69E-02
CRB	KO.IGF1_VEH	Yif1b	-0.62	3.46E-04	Cct6a	-0.45	2.77E-02
CRB	KO.IGF1_VEH	Mrpl2	-0.63	3.67E-04	Sec22b	-0.58	2.78E-02
CRB	KO.IGF1_VEH	Eif3h	-0.57	3.71E-04	Bbs7	-0.81	2.87E-02
CRB	KO.IGF1_VEH	Specc1	-0.71	3.88E-04	Id1	-1.13	2.87E-02
CRB	KO.IGF1_VEH	Fos	1.19	4.31E-04	Pgm1	-1.16	3.01E-02
CRB	KO.IGF1_VEH	Trim32	-0.61	4.37E-04	Spns1	-0.70	3.03E-02
CRB	KO.IGF1_VEH	Herpud1	-0.63	4.45E-04	Bckdk	-0.55	3.03E-02
CRB	KO.IGF1_VEH	Rab11fip2	-0.89	4.49E-04	Wapl	-0.58	3.03E-02
CRB	KO.IGF1_VEH	Coq8a	-1.08	4.89E-04	Senp7	-0.73	3.06E-02
CRB	KO.IGF1_VEH	Tprgl	-0.66	6.78E-04	Rn45s	0.66	3.06E-02
CRB	KO.IGF1_VEH	BC003965	-0.91	6.78E-04	Nrn1	0.42	3.06E-02
CRB	KO.IGF1_VEH	Car8	-0.68	6.78E-04	Ubl7	-0.61	3.06E-02
CRB	KO.IGF1_VEH	Isoc1	-1.10	7.04E-04	Apopt1	-0.52	3.18E-02
CRB	KO.IGF1_VEH	Ndufa12	-0.56	8.33E-04	Mxra7	-2.07	3.26E-02
CRB	KO.IGF1_VEH	Trim23	-0.72	8.98E-04	Hars2	-0.82	3.39E-02
CRB	KO.IGF1_VEH	Uchl1	-0.57	1.02E-03	Yod1	0.71	3.40E-02
CRB	KO.IGF1_VEH	Snhg10	-1.26	1.04E-03	Gnb5	-0.45	3.48E-02
CRB	KO.IGF1_VEH	Mtpn	-0.55	1.07E-03	Apbb1	-0.42	3.57E-02
CRB	KO.IGF1_VEH	Polr3e	0.89	1.07E-03	Mrpl12	-0.57	3.57E-02
CRB	KO.IGF1_VEH	Tsc22d1	-0.54	1.18E-03	Bola1	-0.54	3.57E-02

CRB	KO.IGF1_VEH	Tsc22d3	0.52	1.52E-03	Cd79b	3.17	3.69E-02
CRB	KO.IGF1_VEH	Gap43	-0.55	1.64E-03	Bst1	3.21	3.69E-02
CRB	KO.IGF1_VEH	Anxa7	-0.74	2.03E-03	Mir544	3.24	3.69E-02
CRB	KO.IGF1_VEH	Cend1	-0.52	2.18E-03	Grb14	0.47	3.80E-02
CRB	KO.IGF1_VEH	4931408D14Rik	3.73	2.18E-03	Sesn1	-0.47	3.80E-02
CRB	KO.IGF1_VEH	Slc28a2	1.01	2.30E-03	Pfkl	-0.79	3.80E-02
CRB	KO.IGF1_VEH	Cnp	-0.51	2.33E-03	Vps25	-0.48	3.80E-02
CRB	KO.IGF1_VEH	Mrpl52	-0.81	3.05E-03	Ide	0.71	3.85E-02
CRB	KO.IGF1_VEH	Vps53	-0.72	3.06E-03	Rtn3	0.47	3.96E-02
CRB	KO.IGF1_VEH	Habp4	-0.84	3.10E-03	Avpi1	-0.53	4.00E-02
CRB	KO.IGF1_VEH	Psmd6	-0.55	3.10E-03	Nr1i2	-1.62	4.00E-02
CRB	KO.IGF1_VEH	Zfp830	-0.65	3.14E-03	R3hcc1	-0.62	4.09E-02
CRB	KO.IGF1_VEH	Pigyl	-0.51	3.33E-03	Arhgap25	2.68	4.15E-02
CRB	KO.IGF1_VEH	Gh	0.93	3.36E-03	Plekhg4	0.91	4.15E-02
CRB	KO.IGF1_VEH	Coq9	-0.58	3.48E-03	Gpx3	-0.92	4.15E-02
CRB	KO.IGF1_VEH	Mir22hg	0.76	3.64E-03	Gmpr	-0.61	4.17E-02
CRB	KO.IGF1_VEH	Thap7	-0.95	3.95E-03	9630013A20Rik	0.89	4.21E-02
CRB	KO.IGF1_VEH	Sh3bgr	-0.82	4.07E-03	Srsf10	-0.50	4.29E-02
CRB	KO.IGF1_VEH	Tbc1d17	-0.92	4.07E-03	Cdh9	2.82	4.33E-02
CRB	KO.IGF1_VEH	Sucla2	-0.51	4.16E-03	Wbscr22	-0.64	4.45E-02
CRB	KO.IGF1_VEH	Mettl14	-1.02	4.16E-03	Fth1	-0.63	4.45E-02
CRB	KO.IGF1_VEH	Mycbp2	-0.53	4.31E-03	Scx	-1.46	4.47E-02
CRB	KO.IGF1_VEH	Maea	-0.67	4.34E-03	Arpc4	-0.43	4.47E-02
CRB	KO.IGF1_VEH	Sumo3	-0.50	4.62E-03	Mobp	0.43	4.47E-02
CRB	KO.IGF1_VEH	Ndufs5	-0.49	4.88E-03	Atg14	-0.63	4.47E-02
CRB	KO.IGF1_VEH	BC002163	-0.49	4.88E-03	Dap	-0.65	4.48E-02
CRB	KO.IGF1_VEH	Cst3	-0.57	5.35E-03	Lamtor1	-0.47	4.68E-02
CRB	KO.IGF1_VEH	1810043G02Rik	-1.16	5.42E-03	Cuedc2	-0.40	4.68E-02
CRB	KO.IGF1_VEH	Cdkn1c	-1.33	5.62E-03	Hmgcs1	0.40	4.72E-02

CRB	KO.IGF1_VEH	Cldn5	-0.98	5.80E-03	Mfsd10	-1.51	4.84E-02
CRB	KO.IGF1_VEH	Hikeshi	-0.56	5.80E-03	Ppp3cb	0.53	4.89E-02
CRB	KO.IGF1_VEH	Faim2	-0.61	6.16E-03	Rfxap	-0.61	4.99E-02
CRB	KO.IGF1_VEH	Hist3h2ba	-0.73	6.17E-03			
CRB	WTM.IGF1_VEH	Mir6236	2.30	4.71E-30	Akr1c6	-3.66	7.91E-03
CRB	WTM.IGF1_VEH	Usp1	2.13	5.15E-20	Dnajb11	0.69	7.92E-03
CRB	WTM.IGF1_VEH	Hspa5	0.85	9.07E-15	Txn1	-0.29	8.02E-03
CRB	WTM.IGF1_VEH	Lamp5	-3.07	1.09E-10	Hoxa5	-3.65	8.27E-03
CRB	WTM.IGF1_VEH	Acbd3	1.54	5.26E-10	5730522E02Rik	-3.57	8.76E-03
CRB	WTM.IGF1_VEH	Tmem59l	0.50	2.61E-08	Atp9a	0.68	8.94E-03
CRB	WTM.IGF1_VEH	Manf	1.00	1.02E-06	Gpx4	0.32	8.94E-03
CRB	WTM.IGF1_VEH	Car8	0.44	1.85E-06	Mycbp2	0.43	8.94E-03
CRB	WTM.IGF1_VEH	Wapl	0.90	6.37E-06	Mog	-0.35	1.12E-02
CRB	WTM.IGF1_VEH	Apoa2	-1.73	6.94E-06	Tekt2	-3.56	1.27E-02
CRB	WTM.IGF1_VEH	Pdia3	0.58	8.50E-06	Ywhaz	0.29	1.28E-02
CRB	WTM.IGF1_VEH	Ttr	-0.69	1.03E-05	Tagln3	-0.28	1.31E-02
CRB	WTM.IGF1_VEH	Spp1	-0.56	1.46E-05	Ahr	3.22	1.37E-02
CRB	WTM.IGF1_VEH	Ckb	0.41	1.52E-05	Myh4	3.66	1.47E-02
CRB	WTM.IGF1_VEH	Ywhaq	0.43	2.05E-05	Ckm	3.22	1.48E-02
CRB	WTM.IGF1_VEH	Alb	-1.74	2.05E-05	Habp4	0.72	1.48E-02
CRB	WTM.IGF1_VEH	Pgrmc1	0.60	2.13E-05	Exd2	0.58	1.54E-02
CRB	WTM.IGF1_VEH	Chgb	0.42	2.74E-05	Arhgdia	0.36	1.55E-02
CRB	WTM.IGF1_VEH	Cd81	0.38	4.04E-05	Necap2	0.70	1.66E-02
CRB	WTM.IGF1_VEH	Serinc3	-0.52	5.19E-05	Psip1	0.43	1.66E-02
CRB	WTM.IGF1_VEH	Hsd17b11	-0.42	1.14E-04	Hmgcs1	-0.32	1.66E-02
CRB	WTM.IGF1_VEH	Ipo7	0.68	1.25E-04	Yars	0.48	1.66E-02
CRB	WTM.IGF1_VEH	Cfl1	0.39	1.45E-04	Plp1	-0.29	1.68E-02
CRB	WTM.IGF1_VEH	Atp6v1g2	0.46	1.55E-04	Pdia4	0.37	1.68E-02
CRB	WTM.IGF1_VEH	Bag1	0.95	1.55E-04	Rock2	0.49	1.93E-02

CRB	WTM.IGF1_VEH	Tpm4	0.80	1.60E-04	Slain2	1.09	2.03E-02
CRB	WTM.IGF1_VEH	Enpp2	-0.48	2.35E-04	Atp1b2	0.36	2.11E-02
CRB	WTM.IGF1_VEH	1500015O10Rik	-0.54	3.02E-04	Cyp3a11	-2.02	2.11E-02
CRB	WTM.IGF1_VEH	Gh	1.70	3.13E-04	Camk2b	0.38	2.17E-02
CRB	WTM.IGF1_VEH	Pkn2	0.91	3.20E-04	G530011O06Rik	-1.09	2.36E-02
CRB	WTM.IGF1_VEH	Tmem160	0.93	3.32E-04	Map1lc3a	0.41	2.36E-02
CRB	WTM.IGF1_VEH	Sncg	-1.21	3.95E-04	Szrd1	0.58	2.36E-02
CRB	WTM.IGF1_VEH	Glrx5	0.74	3.99E-04	Hsp90b1	0.29	2.51E-02
CRB	WTM.IGF1_VEH	Xbp1	0.64	4.06E-04	Cetn3	-0.29	3.00E-02
CRB	WTM.IGF1_VEH	Ywhah	0.38	5.02E-04	Pmvk	-0.39	3.01E-02
CRB	WTM.IGF1_VEH	Grb14	-0.59	9.51E-04	Bola1	0.50	3.05E-02
CRB	WTM.IGF1_VEH	Resp18	-0.60	1.30E-03	Eml4	0.95	3.05E-02
CRB	WTM.IGF1_VEH	Tprgl	0.60	1.37E-03	Shisa3	-2.99	3.11E-02
CRB	WTM.IGF1_VEH	Metap2	0.39	1.54E-03	Lactb	1.09	3.30E-02
CRB	WTM.IGF1_VEH	Polr2m	0.55	1.94E-03	B2m	-0.28	3.48E-02
CRB	WTM.IGF1_VEH	Ubqln1	0.63	2.64E-03	Cstb	-0.29	3.51E-02
CRB	WTM.IGF1_VEH	Fam213b	0.41	2.86E-03	Mapk6	0.65	3.52E-02
CRB	WTM.IGF1_VEH	Tsc22d1	0.33	2.86E-03	Sostdc1	-0.65	3.71E-02
CRB	WTM.IGF1_VEH	Mir219a-2	-0.47	3.41E-03	Snx20	3.27	3.71E-02
CRB	WTM.IGF1_VEH	Folr1	-0.77	3.48E-03	Rif1	0.49	3.71E-02
CRB	WTM.IGF1_VEH	Cnih2	2.03	4.30E-03	Tmem59	0.27	3.73E-02
CRB	WTM.IGF1_VEH	Metrn	0.49	4.30E-03	Pilra	3.26	3.73E-02
CRB	WTM.IGF1_VEH	Aar2	0.62	4.66E-03	Nefl	-0.33	3.77E-02
CRB	WTM.IGF1_VEH	Ndufb6	0.36	4.79E-03	Myl1	2.78	3.78E-02
CRB	WTM.IGF1_VEH	Herpud1	0.47	5.32E-03	Phf20l1	0.63	3.78E-02
CRB	WTM.IGF1_VEH	Rbfox3	0.40	5.32E-03	Gnb5	0.37	3.78E-02
CRB	WTM.IGF1_VEH	Ssr1	0.51	5.32E-03	Cyp2c29	-2.40	3.78E-02
CRB	WTM.IGF1_VEH	Ccdc115	0.89	5.43E-03	Cebpg	0.71	3.96E-02
CRB	WTM.IGF1_VEH	Spns1	0.75	5.43E-03	Pdlim2	-0.39	4.45E-02

CRB	WTM.IGF1_VEH	Gm14322	-1.01	5.66E-03	Trf	-0.25	4.58E-02
CRB	WTM.IGF1_VEH	Dlgap4	0.60	6.13E-03	Zfp212	1.64	4.60E-02
CRB	WTM.IGF1_VEH	Calcb	-3.71	6.20E-03	Kcnj13	-0.44	4.60E-02
CRB	WTM.IGF1_VEH	Sst	-0.87	6.24E-03	Dtnbp1	0.67	4.77E-02
CRB	WTM.IGF1_VEH	Cd63	-0.33	7.41E-03	Upp2	-2.38	4.87E-02
CRB	WTM.IGF1_VEH	Hoxb5	-3.71	7.65E-03			
CRB	IGF1.KO_WTM	Mir6236	-2.56	1.52E-35	Mrpl12	-0.63	8.32E-03
CRB	IGF1.KO_WTM	Tmem59l	-1.04	4.14E-19	Ing4	-0.58	8.37E-03
CRB	IGF1.KO_WTM	Usp1	-2.16	1.24E-18	Mien1	-0.45	8.73E-03
CRB	IGF1.KO_WTM	Rbm3	1.04	6.98E-16	Mboat4	2.90	8.77E-03
CRB	IGF1.KO_WTM	Sgk1	1.01	9.85E-16	Nrip3	-0.56	8.83E-03
CRB	IGF1.KO_WTM	Etnppl	1.05	2.34E-15	Car4	-0.41	8.95E-03
CRB	IGF1.KO_WTM	Hspa5	-0.86	1.36E-12	Snrnp35	-0.86	9.86E-03
CRB	IGF1.KO_WTM	Fkbp2	-0.74	2.17E-09	Dap	-0.73	9.95E-03
CRB	IGF1.KO_WTM	Cirbp	0.90	6.34E-09	Cgrrf1	-0.58	9.95E-03
CRB	IGF1.KO_WTM	Fabp7	-0.75	7.09E-09	Mrpl43	-0.48	1.02E-02
CRB	IGF1.KO_WTM	Car8	-0.83	7.73E-09	Mettl14	-0.96	1.03E-02
CRB	IGF1.KO_WTM	Grb14	0.92	1.06E-08	Calr	-0.44	1.03E-02
CRB	IGF1.KO_WTM	Pdia3	-0.81	1.06E-08	Hist1h4h	-1.28	1.06E-02
CRB	IGF1.KO_WTM	Fabp4	4.73	1.87E-08	Spock3	-0.47	1.07E-02
CRB	IGF1.KO_WTM	Ywhaq	-0.70	2.38E-08	Ptgds	0.53	1.07E-02
CRB	IGF1.KO_WTM	Gpx4	-0.69	3.87E-08	Churc1	0.51	1.08E-02
CRB	IGF1.KO_WTM	Isca1	-0.71	1.20E-07	Phb	-0.43	1.11E-02
CRB	IGF1.KO_WTM	Bdnf	-0.84	2.09E-07	Myh4	-3.60	1.19E-02
CRB	IGF1.KO_WTM	Fam213b	-0.73	2.18E-07	Vstm2a	-0.75	1.28E-02
CRB	IGF1.KO_WTM	Sult1a1	1.30	2.44E-07	Cmc2	-0.72	1.30E-02
CRB	IGF1.KO_WTM	Hexb	-0.90	2.52E-07	Ywhah	-0.40	1.32E-02
CRB	IGF1.KO_WTM	Mt2	0.67	2.52E-07	Mrps12	-0.48	1.32E-02
CRB	IGF1.KO_WTM	Pdia4	-0.71	2.60E-07	Atl2	-0.42	1.34E-02

CRB	IGF1.KO_WTM	Cbx1	-0.92	3.02E-07	Cyp2j6	0.85	1.34E-02
CRB	IGF1.KO_WTM	Cd81	-0.70	3.17E-07	Gabrd	-0.46	1.37E-02
CRB	IGF1.KO_WTM	Acbd3	-1.35	3.17E-07	Cebpg	-0.82	1.37E-02
CRB	IGF1.KO_WTM	Pdcd6	-0.70	7.23E-07	Ciart	0.55	1.37E-02
CRB	IGF1.KO_WTM	Cfl1	-0.63	8.15E-07	Fuca1	-0.60	1.37E-02
CRB	IGF1.KO_WTM	Caly	-0.94	1.64E-06	Mrpl34	-0.49	1.37E-02
CRB	IGF1.KO_WTM	Bag1	-1.25	1.89E-06	2700094K13Rik	-0.46	1.37E-02
CRB	IGF1.KO_WTM	Txnip	1.08	3.33E-06	BC005561	-0.98	1.37E-02
CRB	IGF1.KO_WTM	Spp1	0.62	3.45E-06	Szrd1	-0.65	1.39E-02
CRB	IGF1.KO_WTM	Manf	-0.93	3.75E-06	Atat1	-0.93	1.39E-02
CRB	IGF1.KO_WTM	Rmdn3	-0.89	5.14E-06	Klk6	-0.59	1.40E-02
CRB	IGF1.KO_WTM	Mir219a-2	0.66	5.26E-06	Specc1	-0.55	1.43E-02
CRB	IGF1.KO_WTM	Arhgdia	-0.65	5.85E-06	Ctsz	-0.59	1.46E-02
CRB	IGF1.KO_WTM	Tmem59	-0.59	6.71E-06	Rangap1	-0.71	1.47E-02
CRB	IGF1.KO_WTM	Ndufb6	-0.60	1.18E-05	Pigyl	-0.41	1.50E-02
CRB	IGF1.KO_WTM	H1f0	0.70	1.20E-05	Zfp946	-0.81	1.54E-02
CRB	IGF1.KO_WTM	Gjb6	0.63	1.54E-05	Rasl11a	0.71	1.56E-02
CRB	IGF1.KO_WTM	Rgs8	-0.58	1.61E-05	Cend1	-0.39	1.58E-02
CRB	IGF1.KO_WTM	Tpm4	-0.96	1.70E-05	Uqcc2	-0.39	1.60E-02
CRB	IGF1.KO_WTM	Vcp	-0.73	1.96E-05	Tulp2	3.39	1.64E-02
CRB	IGF1.KO_WTM	Glrx5	-0.94	1.96E-05	Cd70	-1.11	1.64E-02
CRB	IGF1.KO_WTM	Necap2	-1.13	1.96E-05	Ppp1r16b	-0.65	1.65E-02
CRB	IGF1.KO_WTM	Pgrmc1	-0.69	1.96E-05	Gpx1	-0.43	1.66E-02
CRB	IGF1.KO_WTM	P4ha1	-1.36	2.15E-05	Dclk1	-0.41	1.69E-02
CRB	IGF1.KO_WTM	B4gat1	-0.83	2.18E-05	Naa60	-0.56	1.70E-02
CRB	IGF1.KO_WTM	Mecp2	-1.55	2.83E-05	Lcat	-0.45	1.70E-02
CRB	IGF1.KO_WTM	Mtpn	-0.60	2.97E-05	Coro1a	-0.68	1.70E-02
CRB	IGF1.KO_WTM	Saa3	3.47	3.28E-05	Nefm	-0.48	1.70E-02
CRB	IGF1.KO_WTM	Kcng4	-0.87	3.65E-05	Capsl	-1.91	1.75E-02

CRB	IGF1.KO_WTM	Hsp90b1	-0.54	4.79E-05	Dars	-0.44	1.79E-02
CRB	IGF1.KO_WTM	Mettl16	-0.97	5.58E-05	Mgp	0.40	1.82E-02
CRB	IGF1.KO_WTM	Kif5a	-0.55	5.58E-05	Taf9	0.40	1.84E-02
CRB	IGF1.KO_WTM	Reep2	-0.69	7.13E-05	Grcc10	-0.38	1.84E-02
CRB	IGF1.KO_WTM	Pkn2	-1.04	7.25E-05	Phgdh	-0.63	1.84E-02
CRB	IGF1.KO_WTM	Zfp830	-0.75	7.69E-05	Mpdu1	-0.51	1.84E-02
CRB	IGF1.KO_WTM	Cdk5	-0.65	8.74E-05	Prdx6	0.38	1.88E-02
CRB	IGF1.KO_WTM	Hsph1	-0.77	8.90E-05	Id3	-0.46	1.88E-02
CRB	IGF1.KO_WTM	Phyhd1	1.06	9.20E-05	Rapgef6	-0.88	1.89E-02
CRB	IGF1.KO_WTM	Tsc22d1	-0.52	1.11E-04	Selt	-0.50	1.95E-02
CRB	IGF1.KO_WTM	Tex264	-0.78	1.23E-04	Mir9-3hg	0.93	1.97E-02
CRB	IGF1.KO_WTM	Cthrc1	-0.98	1.23E-04	Sparc	0.38	2.00E-02
CRB	IGF1.KO_WTM	Tmem160	-1.05	1.23E-04	Creld2	-0.95	2.00E-02
CRB	IGF1.KO_WTM	Rab7	-0.53	1.61E-04	9630013A20Rik	0.94	2.01E-02
CRB	IGF1.KO_WTM	Rpl27a	-0.65	1.81E-04	Trim23	-0.58	2.06E-02
CRB	IGF1.KO_WTM	Ube2a	-0.65	1.81E-04	Zfp93	-1.08	2.13E-02
CRB	IGF1.KO_WTM	Scg2	-0.51	2.26E-04	Eif2s3y	0.46	2.19E-02
CRB	IGF1.KO_WTM	Gap43	-0.51	2.44E-04	Atp2b2	-0.39	2.25E-02
CRB	IGF1.KO_WTM	Stk17b	-0.64	2.85E-04	Rab18	-0.39	2.26E-02
CRB	IGF1.KO_WTM	Fubp1	-0.61	2.94E-04	Spx	-2.73	2.33E-02
CRB	IGF1.KO_WTM	Tpm2	-1.03	3.60E-04	Apoa2	1.10	2.34E-02
CRB	IGF1.KO_WTM	Lactb	-1.63	3.66E-04	1700086L19Rik	-1.67	2.35E-02
CRB	IGF1.KO_WTM	Hsd17b11	0.50	3.66E-04	Dctn3	-0.41	2.43E-02
CRB	IGF1.KO_WTM	Lnpk1	-0.73	3.68E-04	Gpr165	-2.26	2.43E-02
CRB	IGF1.KO_WTM	Bhlhe40	0.60	4.18E-04	Nsfl1c	-0.39	2.46E-02
CRB	IGF1.KO_WTM	Trappc5	-0.70	4.18E-04	Cars	-0.75	2.50E-02
CRB	IGF1.KO_WTM	Sec61b	-0.58	4.21E-04	Srsf5	0.36	2.50E-02
CRB	IGF1.KO_WTM	Tfrc	0.59	5.53E-04	Mgst1	0.42	2.51E-02
CRB	IGF1.KO_WTM	4930447F24Rik	-2.08	6.17E-04	Igfbp2	-0.75	2.51E-02

CRB	IGF1.KO_WTM	Metap2	-0.51	6.78E-04	Wapl	-0.57	2.51E-02
CRB	IGF1.KO_WTM	Lamp5	2.06	6.78E-04	Smim12	-0.52	2.51E-02
CRB	IGF1.KO_WTM	Ncor1	0.50	7.36E-04	Gchfr	-0.97	2.54E-02
CRB	IGF1.KO_WTM	Hikeshi	-0.60	7.72E-04	Pcca	0.46	2.57E-02
CRB	IGF1.KO_WTM	Mt1	0.58	7.77E-04	Agpat5	-0.44	2.61E-02
CRB	IGF1.KO_WTM	Myl1	-4.24	9.68E-04	Tars	-0.45	2.61E-02
CRB	IGF1.KO_WTM	Tekt2	3.85	9.97E-04	Uqcr11	-0.39	2.63E-02
CRB	IGF1.KO_WTM	Ucp1	2.78	1.18E-03	Psmd7	-0.39	2.63E-02
CRB	IGF1.KO_WTM	Gpbp1	-0.52	1.18E-03	Sez6l2	-0.44	2.63E-02
CRB	IGF1.KO_WTM	Necab3	-1.00	1.18E-03	Gstm5	0.37	2.63E-02
CRB	IGF1.KO_WTM	Trim32	-0.55	1.20E-03	Tfap4	-3.41	2.63E-02
CRB	IGF1.KO_WTM	Pam16	-0.62	1.30E-03	Adamts4	-0.75	2.74E-02
CRB	IGF1.KO_WTM	Ndrg4	-0.47	1.43E-03	Gdf11	-1.98	2.74E-02
CRB	IGF1.KO_WTM	Paqr6	-0.94	1.51E-03	Ndrg1	-0.54	2.77E-02
CRB	IGF1.KO_WTM	Pef1	-0.80	1.59E-03	Ubqln1	-0.55	2.82E-02
CRB	IGF1.KO_WTM	Thap7	-0.99	1.66E-03	Tssc4	-0.64	2.84E-02
CRB	IGF1.KO_WTM	Scd1	0.64	1.66E-03	Ywhaz	-0.36	2.86E-02
CRB	IGF1.KO_WTM	Zmat5	-0.72	1.66E-03	Pdia6	-0.37	2.86E-02
CRB	IGF1.KO_WTM	Atp6v1g2	-0.49	1.77E-03	Ifit3	0.62	2.87E-02
CRB	IGF1.KO_WTM	Znhit1	-0.80	1.78E-03	Armc1	-0.45	3.00E-02
CRB	IGF1.KO_WTM	Itih3	0.73	1.78E-03	Fam107b	-0.51	3.03E-02
CRB	IGF1.KO_WTM	Tnfrsf12a	-0.68	1.91E-03	Itgad	2.00	3.05E-02
CRB	IGF1.KO_WTM	Tsc22d3	0.45	1.91E-03	Ndufaf8	-0.52	3.06E-02
CRB	IGF1.KO_WTM	Hspa4l	-0.50	1.96E-03	Itgav	1.13	3.06E-02
CRB	IGF1.KO_WTM	Cnih2	-2.23	2.00E-03	Pcnx4	-0.78	3.06E-02
CRB	IGF1.KO_WTM	Polr3e	0.86	2.00E-03	C1qtnf4	0.65	3.06E-02
CRB	IGF1.KO_WTM	Wdr18	-0.87	2.00E-03	Mapk6	-0.68	3.06E-02
CRB	IGF1.KO_WTM	Nfib	0.58	2.09E-03	Nap1l5	0.36	3.06E-02
CRB	IGF1.KO_WTM	S100a8	0.70	2.17E-03	Nrsn1	-0.55	3.06E-02

CRB	IGF1.KO_WTM	Metrn	-0.57	2.18E-03	Stard3	-0.76	3.06E-02
CRB	IGF1.KO_WTM	Ndufs5	-0.45	2.18E-03	Faim2	-0.52	3.06E-02
CRB	IGF1.KO_WTM	BC002163	-0.45	2.18E-03	Naa38	-0.39	3.06E-02
CRB	IGF1.KO_WTM	AK010878	-0.78	2.46E-03	Scrn1	-0.43	3.06E-02
CRB	IGF1.KO_WTM	Anxa7	-0.72	2.71E-03	Rpe	-0.63	3.06E-02
CRB	IGF1.KO_WTM	Commd7	-0.80	2.77E-03	Mal	0.42	3.06E-02
CRB	IGF1.KO_WTM	Rbm4b	-0.75	2.85E-03	Rab3b	0.72	3.06E-02
CRB	IGF1.KO_WTM	Fam107a	0.44	3.31E-03	Myl12a	0.38	3.06E-02
CRB	IGF1.KO_WTM	Rps10	-0.71	3.34E-03	Lrrc36	3.14	3.06E-02
CRB	IGF1.KO_WTM	Ndufa8	-0.44	3.56E-03	Wnt5b	3.14	3.06E-02
CRB	IGF1.KO_WTM	Hsdl2	-0.57	3.63E-03	Hs3st6	3.16	3.06E-02
CRB	IGF1.KO_WTM	Agt	0.48	3.69E-03	Mir544	3.20	3.06E-02
CRB	IGF1.KO_WTM	BC003965	-0.83	3.69E-03	Psmd8	-0.45	3.10E-02
CRB	IGF1.KO_WTM	Cnp	-0.43	3.79E-03	Col1a2	0.59	3.13E-02
CRB	IGF1.KO_WTM	Ncoa7	-0.70	3.87E-03	Cog6	-0.82	3.20E-02
CRB	IGF1.KO_WTM	Tppp3	-0.58	3.94E-03	Sucla2	-0.39	3.20E-02
CRB	IGF1.KO_WTM	Gstm1	0.43	3.94E-03	Stmn4	-0.47	3.25E-02
CRB	IGF1.KO_WTM	Ppargc1a	0.51	3.95E-03	Prl2c4	-1.75	3.25E-02
CRB	IGF1.KO_WTM	Rraga	-0.52	4.08E-03	Wfdc2	-2.63	3.28E-02
CRB	IGF1.KO_WTM	Hoxb7	3.67	4.14E-03	Alkbh6	-0.37	3.29E-02
CRB	IGF1.KO_WTM	Snhg3	0.57	4.14E-03	Gm10033	-0.59	3.30E-02
CRB	IGF1.KO_WTM	Psmd6	-0.51	4.14E-03	Fndc4	-0.57	3.31E-02
CRB	IGF1.KO_WTM	Cox6b2	-1.00	4.41E-03	Lrrn4cl	2.61	3.31E-02
CRB	IGF1.KO_WTM	Cox6a2	-1.47	4.41E-03	Calml4	-0.87	3.31E-02
CRB	IGF1.KO_WTM	Ngp	0.77	4.41E-03	AU022252	-1.54	3.31E-02
CRB	IGF1.KO_WTM	2810468N07Rik	0.89	4.43E-03	Fam198b	-2.08	3.46E-02
CRB	IGF1.KO_WTM	Synpr	0.46	4.43E-03	4931440P22Rik	2.60	3.57E-02
CRB	IGF1.KO_WTM	Chil3	1.96	4.46E-03	Fkbp5	1.69	3.69E-02
CRB	IGF1.KO_WTM	Tspyl4	-0.43	4.46E-03	Cldn10	0.37	3.74E-02

CRB	IGF1.KO_WTM	Acin1	-0.52	4.71E-03	2810013P06Rik	-0.52	3.74E-02
CRB	IGF1.KO_WTM	Rnaseh1	-1.09	4.72E-03	Ywhag	-0.45	3.76E-02
CRB	IGF1.KO_WTM	Kcnj13	-0.54	4.88E-03	Cox14	-0.35	3.76E-02
CRB	IGF1.KO_WTM	Dlgap4	-0.65	4.99E-03	Hist3h2ba	-0.61	3.79E-02
CRB	IGF1.KO_WTM	Gsn	-0.52	4.99E-03	Phtf1	-1.18	3.80E-02
CRB	IGF1.KO_WTM	Wbscr22	-0.74	5.01E-03	Yipf5	-0.49	3.80E-02
CRB	IGF1.KO_WTM	Spns1	-0.79	5.01E-03	Mfge8	-0.46	3.81E-02
CRB	IGF1.KO_WTM	Pmp22	0.50	5.18E-03	Polr2m	-0.47	3.84E-02
CRB	IGF1.KO_WTM	Golph3l	-0.47	5.30E-03	Baiap3	-3.19	3.84E-02
CRB	IGF1.KO_WTM	Chd3	-1.00	5.65E-03	Rab4a	0.66	3.91E-02
CRB	IGF1.KO_WTM	Mia	0.77	5.65E-03	Aqp4	-0.35	3.93E-02
CRB	IGF1.KO_WTM	Gfap	-0.62	5.68E-03	Pfkl	-0.77	3.98E-02
CRB	IGF1.KO_WTM	Herpud1	-0.52	5.83E-03	Fxyd3	2.56	3.99E-02
CRB	IGF1.KO_WTM	S100a9	0.86	5.93E-03	Eif3h	-0.36	4.05E-02
CRB	IGF1.KO_WTM	Ndufa12	-0.42	6.01E-03	Rnf152	-0.78	4.06E-02
CRB	IGF1.KO_WTM	Atp5g3	-0.43	6.05E-03	Fabp1	1.47	4.15E-02
CRB	IGF1.KO_WTM	Arpc1a	0.43	6.10E-03	Fech	0.57	4.18E-02
CRB	IGF1.KO_WTM	Habp4	-0.80	6.10E-03	Chordc1	-0.40	4.20E-02
CRB	IGF1.KO_WTM	Bag5	0.50	6.60E-03	Hexa	-0.65	4.24E-02
CRB	IGF1.KO_WTM	Ran	-0.42	6.60E-03	Inpp5k	0.48	4.26E-02
CRB	IGF1.KO_WTM	Lpcat1	0.43	6.90E-03	Adk	0.36	4.28E-02
CRB	IGF1.KO_WTM	Ckb	-0.51	7.41E-03	Gabrr2	2.42	4.28E-02
CRB	IGF1.KO_WTM	Chgb	-0.41	7.41E-03	Plaa	0.75	4.52E-02
CRB	IGF1.KO_WTM	Errfi1	0.82	7.63E-03	Calm1	-0.48	4.92E-02
CRB	IGF1.KO_WTM	Scn2b	-0.48	7.99E-03	Fam173a	-0.38	4.93E-02
CRB	IGF1.KO_WTM	Cnn2	-1.11	8.12E-03	Psen2	-1.33	4.93E-02
CRB	IGF1.KO_WTM	Exd2	-0.66	8.12E-03	Gprin1	0.43	4.96E-02
CRB	IGF1.KO_WTM	Il17rc	3.46	8.12E-03	Dnaja1	-0.34	4.96E-02
CRB	IGF1.KO_WTM	Hoxa5	3.47	8.12E-03	Fth1	-0.46	4.96E-02

CRB	IGF1.KO_WTM	Prrt4	3.49	8.12E-03	Gna11	-0.82	4.96E-02
CRB	IGF1.KO_WTM	Rab24	-0.62	8.21E-03			
CRB	VEH.KO_WTM	Mir6236	2.24	5.13E-29	Tdgf1	0.98	9.83E-03
CRB	VEH.KO_WTM	Usp1	2.25	2.55E-23	Emc2	-0.36	9.86E-03
CRB	VEH.KO_WTM	Kcnj13	-1.14	2.42E-14	A830018L16Rik	-1.89	9.89E-03
CRB	VEH.KO_WTM	Fabp7	-0.87	4.09E-14	Kitl	-0.36	1.02E-02
CRB	VEH.KO_WTM	Scg2	-0.75	6.35E-12	Npy	0.44	1.02E-02
CRB	VEH.KO_WTM	Mecp2	-2.13	2.10E-11	Cct6a	0.40	1.03E-02
CRB	VEH.KO_WTM	Klk6	-1.07	4.61E-11	Pink1	0.44	1.04E-02
CRB	VEH.KO_WTM	Snrpb	0.84	7.44E-11	Luzp2	-0.34	1.05E-02
CRB	VEH.KO_WTM	Etnppl	0.84	1.39E-10	Tsc22d1	0.33	1.13E-02
CRB	VEH.KO_WTM	Acbd3	1.51	1.06E-09	Dnajc30	0.68	1.13E-02
CRB	VEH.KO_WTM	Sst	-1.64	1.76E-09	Atoh7	0.71	1.13E-02
CRB	VEH.KO_WTM	Ckb	0.68	1.10E-08	Acyp2	-0.36	1.15E-02
CRB	VEH.KO_WTM	Atp6v1g2	0.66	1.38E-08	Vcp	0.42	1.15E-02
CRB	VEH.KO_WTM	Tmem59l	0.59	2.48E-08	Henmt1	-3.07	1.16E-02
CRB	VEH.KO_WTM	Serpinb1a	-0.88	3.72E-08	Pgm2	0.46	1.16E-02
CRB	VEH.KO_WTM	Fam213b	0.65	4.62E-08	Pik3r2	1.32	1.16E-02
CRB	VEH.KO_WTM	Pdlim2	-0.79	4.74E-08	Ubqln1	0.53	1.22E-02
CRB	VEH.KO_WTM	Tprgl	0.83	5.07E-08	Cox20	-0.36	1.22E-02
CRB	VEH.KO_WTM	Cirbp	0.75	5.59E-08	Gm10638	3.43	1.23E-02
CRB	VEH.KO_WTM	Itm2a	-0.62	2.13E-07	Lxn	-0.33	1.28E-02
CRB	VEH.KO_WTM	Rbm3	0.65	4.95E-07	Rgs8	-0.35	1.30E-02
CRB	VEH.KO_WTM	Tppp3	0.70	1.77E-06	Id1	1.08	1.34E-02
CRB	VEH.KO_WTM	Tmem160	1.07	2.15E-06	4930447F24Rik	-1.41	1.34E-02
CRB	VEH.KO_WTM	Pgrmc1	0.66	2.45E-06	Dnaja1	-0.33	1.34E-02
CRB	VEH.KO_WTM	Wapl	0.90	2.84E-06	Dpysl4	0.72	1.43E-02
CRB	VEH.KO_WTM	Kif5a	-0.54	2.84E-06	Zfp937	-1.11	1.43E-02
CRB	VEH.KO_WTM	Ptn	-0.51	2.90E-06	Lsm6	-0.33	1.44E-02

CRB	VEH.KO_WTM	Mycbp2	0.64	3.27E-06	Hist1h1e	1.38	1.44E-02
CRB	VEH.KO_WTM	Pkn2	1.03	3.39E-06	St8sia2	-3.24	1.44E-02
CRB	VEH.KO_WTM	Isoc1	1.32	3.70E-06	Fam213a	0.34	1.48E-02
CRB	VEH.KO_WTM	Glrx5	0.84	6.87E-06	Metrn	0.43	1.52E-02
CRB	VEH.KO_WTM	Gpx3	1.63	7.41E-06	Yif1b	0.39	1.56E-02
CRB	VEH.KO_WTM	Gnptg	0.59	7.44E-06	Spns1	0.65	1.59E-02
CRB	VEH.KO_WTM	Drap1	0.87	8.11E-06	Cdkn1c	1.06	1.59E-02
CRB	VEH.KO_WTM	Cst3	0.52	1.21E-05	Taldo1	-0.33	1.59E-02
CRB	VEH.KO_WTM	Ddrgk1	0.61	1.23E-05	Rab7	0.33	1.59E-02
CRB	VEH.KO_WTM	Ywhaq	0.49	1.36E-05	Rps5	0.32	1.64E-02
CRB	VEH.KO_WTM	Kcne2	-1.08	1.53E-05	Krt15	-2.76	1.64E-02
CRB	VEH.KO_WTM	Fuca1	0.73	1.57E-05	Timp4	0.33	1.66E-02
CRB	VEH.KO_WTM	Gstm1	0.48	1.84E-05	Gtf2f1	0.51	1.67E-02
CRB	VEH.KO_WTM	Txn1	-0.48	1.84E-05	Rdh5	-0.59	1.67E-02
CRB	VEH.KO_WTM	Hmgcr	-0.76	2.02E-05	Slain2	1.01	1.67E-02
CRB	VEH.KO_WTM	Aqp4	-0.47	2.56E-05	Tmem41b	0.64	1.67E-02
CRB	VEH.KO_WTM	Bag1	0.97	3.85E-05	Cept1	-0.41	1.67E-02
CRB	VEH.KO_WTM	S100a9	1.09	5.88E-05	Hagh	0.33	1.67E-02
CRB	VEH.KO_WTM	Gpx4	0.47	6.99E-05	Rida	-0.32	1.67E-02
CRB	VEH.KO_WTM	Gnb5	0.55	7.17E-05	Mcee	-0.43	1.69E-02
CRB	VEH.KO_WTM	Coch	-2.05	7.65E-05	Rab33a	0.59	1.69E-02
CRB	VEH.KO_WTM	Necap2	0.88	8.10E-05	Sncg	-0.82	1.81E-02
CRB	VEH.KO_WTM	Mapk6	0.86	9.08E-05	Cdkn1a	0.68	1.87E-02
CRB	VEH.KO_WTM	E130102H24Rik	0.69	9.22E-05	Pdia6	-0.34	1.88E-02
CRB	VEH.KO_WTM	Rbfox3	0.51	9.82E-05	Trpc3	-0.76	1.89E-02
CRB	VEH.KO_WTM	Metap2	0.48	9.82E-05	Krt12	3.28	1.93E-02
CRB	VEH.KO_WTM	Hmgcs1	-0.48	9.82E-05	Gtf3c6	-0.42	1.95E-02
CRB	VEH.KO_WTM	Herpud1	0.57	1.02E-04	Drg1	0.38	1.95E-02
CRB	VEH.KO_WTM	Zc3h6	1.11	1.18E-04	Gstt1	-0.52	1.99E-02

CRB	VEH.KO_WTM	Gabrd	0.54	1.24E-04	Sppl2b	1.02	2.00E-02
CRB	VEH.KO_WTM	Ccdc115	1.01	1.24E-04	Gng11	-0.37	2.00E-02
CRB	VEH.KO_WTM	Psmd8	0.55	1.25E-04	Mrps12	0.39	2.00E-02
CRB	VEH.KO_WTM	Cycs	-0.44	1.42E-04	Mfge8	-0.43	2.01E-02
CRB	VEH.KO_WTM	Rab11fip2	0.84	1.47E-04	Nipsnap3b	-0.59	2.01E-02
CRB	VEH.KO_WTM	Sh3bgr	0.90	1.50E-04	Isca1	0.33	2.01E-02
CRB	VEH.KO_WTM	Cmtm5	-0.47	1.59E-04	Ctrb1	-2.93	2.06E-02
CRB	VEH.KO_WTM	Patj	0.52	1.62E-04	Poldip3	0.47	2.06E-02
CRB	VEH.KO_WTM	Stk17b	-0.60	1.66E-04	Nrip1	0.65	2.07E-02
CRB	VEH.KO_WTM	Sult1a1	0.98	1.72E-04	Vim	0.48	2.07E-02
CRB	VEH.KO_WTM	Eif2s1	-0.53	1.73E-04	Traf6	0.95	2.08E-02
CRB	VEH.KO_WTM	Fads1	-0.65	2.04E-04	Ptgds	0.38	2.12E-02
CRB	VEH.KO_WTM	H3f3b	0.46	2.08E-04	Rrp1	0.35	2.14E-02
CRB	VEH.KO_WTM	Trappc5	0.62	2.08E-04	Wfdc18	-2.02	2.15E-02
CRB	VEH.KO_WTM	Snrnp70	0.57	2.37E-04	Myeov2	-0.32	2.16E-02
CRB	VEH.KO_WTM	Cldn5	1.10	2.52E-04	Pdia4	-0.37	2.16E-02
CRB	VEH.KO_WTM	Th	1.16	2.53E-04	Atp5k	-0.32	2.16E-02
CRB	VEH.KO_WTM	Ddah2	0.59	2.56E-04	Ttc5	-0.39	2.16E-02
CRB	VEH.KO_WTM	Wsb1	0.58	2.63E-04	Calml4	-0.79	2.18E-02
CRB	VEH.KO_WTM	Mrpl2	0.53	3.22E-04	Atg14	0.59	2.19E-02
CRB	VEH.KO_WTM	Golph3l	0.47	3.30E-04	Homer2	1.02	2.21E-02
CRB	VEH.KO_WTM	Phyhip	0.62	3.49E-04	B4gat1	0.46	2.21E-02
CRB	VEH.KO_WTM	Bdnf	-0.59	3.50E-04	B9d1	-0.53	2.25E-02
CRB	VEH.KO_WTM	Tubb2a	-0.42	3.50E-04	Hist3h2ba	0.55	2.28E-02
CRB	VEH.KO_WTM	1500015O10Rik	-0.53	4.11E-04	Apip	-0.36	2.31E-02
CRB	VEH.KO_WTM	Snhg10	1.23	4.11E-04	Agt	0.36	2.34E-02
CRB	VEH.KO_WTM	Wbp2	0.46	4.12E-04	Adrbk1	0.75	2.34E-02
CRB	VEH.KO_WTM	Pcsk1	-0.98	4.39E-04	Copz1	-0.35	2.36E-02
CRB	VEH.KO_WTM	Arhgdia	0.46	4.40E-04	Chd7	0.42	2.37E-02

CRB	VEH.KO_WTM	Cd63	-0.43	4.48E-04	Eif4e	-0.32	2.37E-02
CRB	VEH.KO_WTM	Irak1	1.13	5.16E-04	Cuedc2	0.32	2.40E-02
CRB	VEH.KO_WTM	Mapk12	0.63	5.16E-04	Phyhd1	0.67	2.41E-02
CRB	VEH.KO_WTM	Plp1	-0.47	5.16E-04	Car4	-0.33	2.41E-02
CRB	VEH.KO_WTM	Serinc3	-0.48	5.21E-04	Nap1l5	0.32	2.42E-02
CRB	VEH.KO_WTM	Arpc4	0.49	5.23E-04	Tuba1a	-0.33	2.43E-02
CRB	VEH.KO_WTM	Prl2c4	-2.10	5.41E-04	Sptb	0.63	2.43E-02
CRB	VEH.KO_WTM	Il33	-0.56	6.96E-04	Fbxo7	0.75	2.43E-02
CRB	VEH.KO_WTM	Camk2b	0.47	7.01E-04	Defb11	-1.19	2.43E-02
CRB	VEH.KO_WTM	Prl2c3	-2.08	7.29E-04	Mir682	0.32	2.43E-02
CRB	VEH.KO_WTM	1810037I17Rik	-0.41	7.41E-04	Ormdl2	-0.50	2.44E-02
CRB	VEH.KO_WTM	Cfl1	0.40	7.64E-04	Trim32	0.37	2.44E-02
CRB	VEH.KO_WTM	Lrrc49	0.54	7.64E-04	Gm1673	-0.56	2.46E-02
CRB	VEH.KO_WTM	Necab1	0.95	7.64E-04	Uqcrq	-0.33	2.47E-02
CRB	VEH.KO_WTM	Ndufb6	0.43	8.33E-04	Endog	0.79	2.49E-02
CRB	VEH.KO_WTM	Mcrs1	1.03	8.67E-04	Rundc1	-0.93	2.49E-02
CRB	VEH.KO_WTM	Nrgn	-2.08	8.67E-04	Car2	-0.31	2.53E-02
CRB	VEH.KO_WTM	Psmb5	0.49	8.67E-04	Ecel1	-3.23	2.54E-02
CRB	VEH.KO_WTM	Ahr	3.59	8.96E-04	Rnf113a2	0.73	2.63E-02
CRB	VEH.KO_WTM	9130401M01Rik	0.72	8.96E-04	Cldn11	0.34	2.63E-02
CRB	VEH.KO_WTM	Tmem59	0.40	9.29E-04	Phf20l1	0.60	2.63E-02
CRB	VEH.KO_WTM	Scaf11	0.55	9.94E-04	Caly	0.45	2.68E-02
CRB	VEH.KO_WTM	Dynll1	-0.40	1.01E-03	Atl2	-0.34	2.72E-02
CRB	VEH.KO_WTM	Hsph1	-0.65	1.01E-03	Mocs1	2.32	2.75E-02
CRB	VEH.KO_WTM	Tst	-0.55	1.08E-03	Blcap	0.49	2.79E-02
CRB	VEH.KO_WTM	Sesn1	0.52	1.08E-03	Cox6b2	-0.74	2.86E-02
CRB	VEH.KO_WTM	Klhdc9	1.75	1.14E-03	Sec14l1	0.44	2.93E-02
CRB	VEH.KO_WTM	2300009A05Rik	0.71	1.14E-03	Cyb5r3	0.39	3.02E-02
CRB	VEH.KO_WTM	Rps10	0.63	1.18E-03	Ndufc1	-0.31	3.04E-02

CRB	VEH.KO_WTM	Amigo2	2.06	1.20E-03	Kif24	3.13	3.13E-02
CRB	VEH.KO_WTM	Vps53	0.65	1.26E-03	Ddx5	0.31	3.15E-02
CRB	VEH.KO_WTM	Rpl27a	0.50	1.36E-03	Fndc4	-0.54	3.20E-02
CRB	VEH.KO_WTM	Msmo1	-0.43	1.37E-03	Wdr45	0.44	3.22E-02
CRB	VEH.KO_WTM	Nrsn1	-0.61	1.47E-03	Capza1	-0.46	3.40E-02
CRB	VEH.KO_WTM	Ssr1	0.54	1.47E-03	Tmem107	-0.66	3.46E-02
CRB	VEH.KO_WTM	Apbb1	0.42	1.54E-03	Tbc1d17	0.65	3.46E-02
CRB	VEH.KO_WTM	Fam21	0.44	1.65E-03	AI593442	0.71	3.46E-02
CRB	VEH.KO_WTM	Pnrc1	0.85	1.66E-03	Eif5a2	-0.69	3.48E-02
CRB	VEH.KO_WTM	Ipo7	0.58	1.66E-03	Cthrc1	-0.59	3.51E-02
CRB	VEH.KO_WTM	Vps25	0.52	2.00E-03	Cnp	0.30	3.53E-02
CRB	VEH.KO_WTM	Stoml2	0.47	2.08E-03	Soga1	0.56	3.53E-02
CRB	VEH.KO_WTM	Calcb	-3.75	2.20E-03	Cacybp	-0.33	3.53E-02
CRB	VEH.KO_WTM	Necab3	-0.86	2.21E-03	Trafd1	0.71	3.53E-02
CRB	VEH.KO_WTM	Ndufa8	0.38	2.29E-03	Vstm2a	-0.60	3.53E-02
CRB	VEH.KO_WTM	Habp4	0.75	2.31E-03	Eif2b2	0.50	3.53E-02
CRB	VEH.KO_WTM	4931408D14Rik	-3.67	2.37E-03	Spon1	0.57	3.53E-02
CRB	VEH.KO_WTM	Ovgp1	1.94	2.54E-03	Slit2	-1.94	3.53E-02
CRB	VEH.KO_WTM	Meis2	-1.86	2.81E-03	Pfkp	-0.34	3.53E-02
CRB	VEH.KO_WTM	Tnfrsf12a	-0.61	2.85E-03	Nkain4	-0.36	3.53E-02
CRB	VEH.KO_WTM	Ctcf	0.50	2.89E-03	Chkb	0.89	3.53E-02
CRB	VEH.KO_WTM	Bcl6	1.02	3.11E-03	Auts2	0.49	3.53E-02
CRB	VEH.KO_WTM	Cxcl1	3.83	3.30E-03	2310057M21Rik	0.65	3.53E-02
CRB	VEH.KO_WTM	Ttll3	0.51	3.34E-03	Tamm41	1.17	3.53E-02
CRB	VEH.KO_WTM	Fam234a	0.91	3.34E-03	Tpp1	-0.35	3.53E-02
CRB	VEH.KO_WTM	Gfpt1	-0.53	3.42E-03	2810013P06Rik	0.43	3.53E-02
CRB	VEH.KO_WTM	Eml4	1.03	3.61E-03	Micu3	0.46	3.54E-02
CRB	VEH.KO_WTM	Tssc4	0.62	3.63E-03	Shox2	-2.57	3.61E-02
CRB	VEH.KO_WTM	Tppp	-0.44	3.67E-03	AW551984	-2.56	3.64E-02

CRB	VEH.KO_WTM	S100a10	-0.41	3.80E-03	Rbp1	-0.52	3.66E-02
CRB	VEH.KO_WTM	Spx	-2.71	3.80E-03	Zbtb18	0.35	3.68E-02
CRB	VEH.KO_WTM	Cd81	0.37	3.96E-03	Slc5a7	-2.72	3.72E-02
CRB	VEH.KO_WTM	Synpr	0.40	4.02E-03	Mut	-0.41	3.74E-02
CRB	VEH.KO_WTM	Slc6a12	1.65	4.21E-03	Sparc	0.30	3.75E-02
CRB	VEH.KO_WTM	Atp9a	0.67	4.26E-03	Scrn1	0.37	3.77E-02
CRB	VEH.KO_WTM	Rraga	0.44	4.41E-03	Deaf1	0.84	3.77E-02
CRB	VEH.KO_WTM	Tssk5	0.86	4.42E-03	Mrps30	0.96	3.83E-02
CRB	VEH.KO_WTM	Smarcd3	1.64	4.63E-03	Ube2n	-0.34	3.83E-02
CRB	VEH.KO_WTM	Coq8a	0.82	4.64E-03	Cables2	-1.23	3.86E-02
CRB	VEH.KO_WTM	Ndufa1	-0.36	4.86E-03	Afap1	0.90	3.86E-02
CRB	VEH.KO_WTM	Rpl17	0.46	5.11E-03	Zfas1	0.47	3.86E-02
CRB	VEH.KO_WTM	Il20rb	0.54	5.16E-03	Abhd16a	0.36	3.87E-02
CRB	VEH.KO_WTM	Fxyd6	0.40	5.16E-03	Snhg8	0.41	3.97E-02
CRB	VEH.KO_WTM	Tomm40l	-0.56	5.16E-03	Uqcrh	-0.29	4.07E-02
CRB	VEH.KO_WTM	Mrpl52	0.69	5.16E-03	9430038I01Rik	-1.66	4.07E-02
CRB	VEH.KO_WTM	Bola1	0.54	5.23E-03	Pnisr	0.30	4.07E-02
CRB	VEH.KO_WTM	Yars	0.50	5.24E-03	Ube2w	-0.30	4.16E-02
CRB	VEH.KO_WTM	Igf2	-0.90	5.24E-03	Caln1	0.30	4.19E-02
CRB	VEH.KO_WTM	Ghitm	-0.36	5.32E-03	Ggact	0.38	4.27E-02
CRB	VEH.KO_WTM	Eef1akmt1	-0.44	5.65E-03	Rbm33	0.90	4.31E-02
CRB	VEH.KO_WTM	Kbtbd11	0.42	5.88E-03	Pxylp1	0.48	4.35E-02
CRB	VEH.KO_WTM	Sec61b	0.42	6.07E-03	Folr1	-0.55	4.45E-02
CRB	VEH.KO_WTM	Mog	-0.38	6.09E-03	Ufm1	-0.37	4.49E-02
CRB	VEH.KO_WTM	Ccpg1os	-0.71	6.09E-03	Gpx8	-0.48	4.55E-02
CRB	VEH.KO_WTM	Mid1ip1	0.66	6.09E-03	Mrps33	-0.29	4.55E-02
CRB	VEH.KO_WTM	Trim23	0.55	6.15E-03	Bcat1	-0.40	4.55E-02
CRB	VEH.KO_WTM	Fmod	1.16	6.15E-03	Slc25a33	0.79	4.55E-02
CRB	VEH.KO_WTM	Serf2	-0.36	6.15E-03	3110056K07Rik	-0.64	4.55E-02

CRB	VEH.KO_WTM	Mobp	-0.35	6.17E-03	Fam49a	0.51	4.57E-02
CRB	VEH.KO_WTM	Rims3	0.72	6.71E-03	Pqlc2	0.68	4.57E-02
CRB	VEH.KO_WTM	Megf11	-0.65	6.76E-03	Klhl4	-0.51	4.64E-02
CRB	VEH.KO_WTM	Cdc37	0.54	6.87E-03	Pef1	0.49	4.65E-02
CRB	VEH.KO_WTM	Chordc1	-0.42	6.96E-03	Mturn	0.56	4.65E-02
CRB	VEH.KO_WTM	Bbip1	-0.38	6.98E-03	Zcchc12	-0.83	4.65E-02
CRB	VEH.KO_WTM	Mt1	0.38	7.01E-03	Clec12a	-2.66	4.65E-02
CRB	VEH.KO_WTM	Kcnmb4	0.96	7.12E-03	Gsdma	-2.92	4.65E-02
CRB	VEH.KO_WTM	Jup	0.72	7.18E-03	Kcnt2	-2.92	4.65E-02
CRB	VEH.KO_WTM	Acin1	0.42	7.32E-03	Otor	-2.93	4.65E-02
CRB	VEH.KO_WTM	Prl2c2	-1.82	7.32E-03	Ripk3	-2.93	4.65E-02
CRB	VEH.KO_WTM	Ppp1cc	0.50	7.32E-03	Gzma	-2.96	4.65E-02
CRB	VEH.KO_WTM	Mpp3	0.60	7.32E-03	Mfsd4b1	-2.98	4.65E-02
CRB	VEH.KO_WTM	St6galnac4	0.74	7.41E-03	Gabrg3	-3.01	4.65E-02
CRB	VEH.KO_WTM	Enpp2	-0.42	7.42E-03	Senp6	0.54	4.68E-02
CRB	VEH.KO_WTM	Krt24	1.28	7.46E-03	Gjb1	-0.46	4.70E-02
CRB	VEH.KO_WTM	Cdh9	-3.16	7.50E-03	Srsf10	0.40	4.75E-02
CRB	VEH.KO_WTM	Spg7	0.86	8.33E-03	Mmd2	-0.32	4.79E-02
CRB	VEH.KO_WTM	Sgk1	0.45	8.38E-03	Mrps23	0.54	4.79E-02
CRB	VEH.KO_WTM	Crtc1	1.23	8.45E-03	Rian	-0.42	4.79E-02
CRB	VEH.KO_WTM	Nme1	-0.34	8.47E-03	4930528A17Rik	3.01	4.79E-02
CRB	VEH.KO_WTM	1810043G02Rik	0.98	8.47E-03	Smpd5	2.99	4.79E-02
CRB	VEH.KO_WTM	Sh3glb2	0.42	8.49E-03	Sh2d4a	3.02	4.79E-02
CRB	VEH.KO_WTM	Tnc	-1.45	8.49E-03	Tas2r135	3.07	4.79E-02
CRB	VEH.KO_WTM	Ndufaf3	-0.41	8.50E-03	Mybpc2	3.16	4.79E-02
CRB	VEH.KO_WTM	Gyg	-0.64	8.81E-03	Hook1	0.50	4.81E-02
CRB	VEH.KO_WTM	Slc7a3	-0.89	9.33E-03	Rasl11a	0.64	4.84E-02
CRB	VEH.KO_WTM	Coq9	0.45	9.33E-03	Scx	1.26	4.95E-02
CRB	VEH.KO_WTM	Spcs1	-0.34	9.49E-03	Slco4a1	0.63	4.95E-02

CRB	VEH.KO_WTM	Cetn2	-0.39	9.49E-03	Resp18	-0.44	4.95E-02
CRB	VEH.KO_WTM	Upp2	-2.69	9.73E-03	Crem	-0.61	4.96E-02
CRB	VEH.KO_WTM	Lpar1	-0.51	9.83E-03	Tspyl4	0.29	4.96E-02
CRB	KOIGF1_WTMVEH	Fabp7	-0.91	4.28E-15	Phyhd1	0.81	9.69E-03
CRB	KOIGF1_WTMVEH	Etnppl	1.01	4.88E-15	Prl2c2	-2.13	9.69E-03
CRB	KOIGF1_WTMVEH	Sgk1	0.95	4.88E-15	Rdh5	-0.72	9.69E-03
CRB	KOIGF1_WTMVEH	Kcnj13	-0.97	5.83E-12	Itm2a	-0.42	1.02E-02
CRB	KOIGF1_WTMVEH	Gh	1.90	4.26E-10	Rgs8	-0.41	1.03E-02
CRB	KOIGF1_WTMVEH	Mt2	0.73	1.12E-09	Tango2	-0.52	1.07E-02
CRB	KOIGF1_WTMVEH	Alb	-1.70	5.73E-08	Ttyh1	0.45	1.34E-02
CRB	KOIGF1_WTMVEH	Klk6	-0.95	8.48E-08	Gstm1	0.39	1.35E-02
CRB	KOIGF1_WTMVEH	Sst	-1.35	8.52E-08	Cthrc1	-0.78	1.49E-02
CRB	KOIGF1_WTMVEH	Mecp2	-1.73	4.83E-07	Spx	-2.96	1.49E-02
CRB	KOIGF1_WTMVEH	Rbm3	0.67	6.73E-07	Kif24	3.57	1.49E-02
CRB	KOIGF1_WTMVEH	Folr1	-1.09	8.96E-07	Hoxb7	3.59	1.49E-02
CRB	KOIGF1_WTMVEH	Scg2	-0.60	9.06E-07	Mir5121	-2.58	1.49E-02
CRB	KOIGF1_WTMVEH	Sult1a1	1.21	2.01E-06	Isca1	-0.43	1.49E-02
CRB	KOIGF1_WTMVEH	Ngp	1.13	5.62E-06	Fam173a	-0.44	1.50E-02
CRB	KOIGF1_WTMVEH	S100a8	0.94	1.08E-05	Zbtb33	1.69	1.58E-02
CRB	KOIGF1_WTMVEH	Fkbp2	-0.55	1.20E-05	Capsl	-1.97	1.96E-02
CRB	KOIGF1_WTMVEH	Ciart	0.83	1.36E-05	Nap1l5	0.38	2.15E-02
CRB	KOIGF1_WTMVEH	Serpinb1a	-0.80	1.43E-05	B9d1	-0.63	2.23E-02
CRB	KOIGF1_WTMVEH	Txnip	0.99	2.33E-05	Ndrg4	-0.38	2.24E-02
CRB	KOIGF1_WTMVEH	Ucp1	4.09	2.82E-05	Mapk13	1.56	2.56E-02
CRB	KOIGF1_WTMVEH	Kcne2	-1.09	2.90E-05	Cbx1	-0.57	2.66E-02
CRB	KOIGF1_WTMVEH	Il33	-0.74	2.90E-05	Rpe	-0.68	2.73E-02
CRB	KOIGF1_WTMVEH	Polr3e	1.09	3.52E-05	Yipf5	-0.53	2.74E-02
CRB	KOIGF1_WTMVEH	Tmem59l	-0.53	3.65E-05	Calcb	-3.55	2.75E-02
CRB	KOIGF1_WTMVEH	Fabp4	3.08	4.45E-05	Rnf187	0.61	2.75E-02

CRB	KOIGF1_WTMVEH	Fam107a	0.52	4.66E-05	Gfap	-0.57	2.75E-02
CRB	KOIGF1_WTMVEH	Kif5a	-0.53	4.84E-05	Ppp3r2	3.32	2.89E-02
CRB	KOIGF1_WTMVEH	Mt1	0.63	4.84E-05	Ctsg	3.46	2.89E-02
CRB	KOIGF1_WTMVEH	Tsc22d3	0.50	1.24E-04	Itih3	0.60	2.99E-02
CRB	KOIGF1_WTMVEH	Rasl11a	1.01	1.24E-04	Gpr165	-2.33	3.01E-02
CRB	KOIGF1_WTMVEH	Cirbp	0.62	1.96E-04	Sparc	0.36	3.07E-02
CRB	KOIGF1_WTMVEH	1500015O10Rik	-0.55	2.07E-04	Lamp5	-1.00	3.28E-02
CRB	KOIGF1_WTMVEH	Sostdc1	-0.87	2.77E-04	Gpx4	-0.37	3.33E-02
CRB	KOIGF1_WTMVEH	Coch	-2.01	3.23E-04	Ttr	-0.63	3.33E-02
CRB	KOIGF1_WTMVEH	Saa3	3.02	5.43E-04	Caly	-0.60	3.36E-02
CRB	KOIGF1_WTMVEH	Gng11	-0.53	7.86E-04	Mfge8	-0.48	3.36E-02
CRB	KOIGF1_WTMVEH	S100a9	1.03	9.33E-04	Wfdc2	-2.80	3.36E-02
CRB	KOIGF1_WTMVEH	Car2	-0.47	9.33E-04	Mup1	2.13	3.36E-02
CRB	KOIGF1_WTMVEH	Id3	-0.56	1.09E-03	Cdca8	-2.57	3.85E-02
CRB	KOIGF1_WTMVEH	Phactr3	0.66	1.27E-03	Gm10033	-0.61	4.01E-02
CRB	KOIGF1_WTMVEH	Nrsn1	-0.69	1.52E-03	Col1a2	0.61	4.07E-02
CRB	KOIGF1_WTMVEH	Gjb6	0.50	1.69E-03	Cep162	-0.91	4.07E-02
CRB	KOIGF1_WTMVEH	4930447F24Rik	-2.05	1.69E-03	Ccpg1os	-0.70	4.07E-02
CRB	KOIGF1_WTMVEH	Calml4	-1.10	1.72E-03	Cmtm5	-0.37	4.07E-02
CRB	KOIGF1_WTMVEH	Enpp2	-0.47	1.72E-03	Tmem50b	0.37	4.07E-02
CRB	KOIGF1_WTMVEH	Slco1a5	-4.19	1.94E-03	Tnfrsf12a	-0.56	4.07E-02
CRB	KOIGF1_WTMVEH	Aqp4	-0.44	2.31E-03	Psmd6	-0.43	4.16E-02
CRB	KOIGF1_WTMVEH	Stk17b	-0.58	2.47E-03	Mettl26	-0.49	4.17E-02
CRB	KOIGF1_WTMVEH	Rmdn3	-0.69	3.05E-03	Lpar1	-0.52	4.17E-02
CRB	KOIGF1_WTMVEH	H1f0	0.53	3.70E-03	Ctsz	-0.55	4.25E-02
CRB	KOIGF1_WTMVEH	Prl2c4	-2.06	5.19E-03	Cox6a2	-1.30	4.25E-02
CRB	KOIGF1_WTMVEH	Necab3	-0.95	5.43E-03	Hmgn2	-0.56	4.25E-02
CRB	KOIGF1_WTMVEH	Bdnf	-0.56	6.33E-03	Vstm2b	-2.06	4.27E-02
CRB	KOIGF1_WTMVEH	Rpl17	0.50	6.52E-03	Tomm40l	-0.53	4.27E-02

CRB	KOIGF1_WTMVEH	Prl2c3	-2.04	6.52E-03	Ins2	-3.01	4.43E-02
CRB	KOIGF1_WTMVEH	Chil3	2.03	6.89E-03	Pdcd6	-0.41	4.67E-02
CRB	KOIGF1_WTMVEH	Slc4a4	0.46	6.89E-03	Cdk5	-0.44	4.89E-02
CRB	KOIGF1_WTMVEH	Scd1	0.58	7.38E-03	Atp5s	-0.64	4.91E-02
CRB	KOIGF1_WTMVEH	Cd63	-0.42	7.49E-03	Gjb1	-0.55	4.96E-02
CRB	KOIGF1_WTMVEH	Hexb	-0.60	7.53E-03	Mrpl43	-0.42	4.96E-02
CRB	KOIGF1_WTMVEH	Cox6b2	-1.00	7.86E-03	Serf2	-0.35	4.96E-02
CRB	KOIGF1_WTMVEH	Lhfp	0.54	8.29E-03			
BL	KO.IGF1_VEH	Alb	-8.29	8.92E-30	Trf	-1.75	6.15E-03
BL	KO.IGF1_VEH	Apoa2	-7.76	1.86E-23	Tmcc2	1.68	6.79E-03
BL	KO.IGF1_VEH	Mir6236	2.92	5.30E-16	Nme2	-1.52	1.43E-02
BL	KO.IGF1_VEH	Ttr	-4.67	2.13E-13	Ccl6	-1.19	1.56E-02
BL	KO.IGF1_VEH	Saa3	-2.69	1.63E-12	Sepp1	-1.34	2.04E-02
BL	KO.IGF1_VEH	Apoc1	-4.36	5.28E-09	Fam46c	1.00	2.04E-02
BL	KO.IGF1_VEH	Apoa1	-6.12	6.37E-09	Mrpl33	-1.57	2.04E-02
BL	KO.IGF1_VEH	Ahsg	-5.91	1.12E-07	Yod1	1.30	2.04E-02
BL	KO.IGF1_VEH	Wfdc17	-1.79	5.56E-06	Ybx3	1.11	2.08E-02
BL	KO.IGF1_VEH	Fabp1	-5.58	6.44E-06	Wdr26	1.11	2.28E-02
BL	KO.IGF1_VEH	Cyp3a11	-5.40	4.27E-05	Apoh	-4.39	2.43E-02
BL	KO.IGF1_VEH	Fgb	-5.33	8.47E-05	Txn1	-1.20	2.65E-02
BL	KO.IGF1_VEH	Serpina1d	-5.22	2.11E-04	Cd5l	-2.26	2.82E-02
BL	KO.IGF1_VEH	Apoc3	-5.19	2.64E-04	Ccl24	-3.24	2.95E-02
BL	KO.IGF1_VEH	Serpina1b	-5.17	2.92E-04	Isca1	0.99	3.04E-02
BL	KO.IGF1_VEH	Rbp4	-5.15	3.21E-04	Ube2c	1.21	3.04E-02
BL	KO.IGF1_VEH	Serpina3k	-5.14	3.39E-04	Ly86	-1.51	3.18E-02
BL	KO.IGF1_VEH	Retnla	-1.65	3.39E-04	Cps1	-4.31	3.37E-02
BL	KO.IGF1_VEH	Rsad2	1.32	3.52E-04	Timd4	-2.10	3.70E-02
BL	KO.IGF1_VEH	Aldob	-5.11	3.70E-04	Thumpd3	-4.29	3.70E-02
BL	KO.IGF1_VEH	Gpx1	1.21	7.76E-04	Alox15	-1.29	3.70E-02

BL	KO.IGF1_VEH	Serpina1c	-4.98	1.02E-03	Msr1	-1.91	3.79E-02
BL	KO.IGF1_VEH	Cxcl13	-1.81	1.12E-03	Crip1	-1.11	3.91E-02
BL	KO.IGF1_VEH	Ces1c	-4.92	1.53E-03	Mup2	-4.26	3.92E-02
BL	KO.IGF1_VEH	Slc25a37	1.20	1.56E-03	Dcaf12	0.99	3.92E-02
BL	KO.IGF1_VEH	Hpx	-4.88	1.73E-03	Nupr1	-2.56	4.05E-02
BL	KO.IGF1_VEH	Serpina1a	-4.87	1.85E-03	Fech	0.95	4.16E-02
BL	KO.IGF1_VEH	Tmem176b	-2.83	1.85E-03	S100a9	-1.10	4.16E-02
BL	KO.IGF1_VEH	Slc4a1	1.28	1.86E-03	Timp2	-2.24	4.29E-02
BL	KO.IGF1_VEH	Epb41	1.19	1.94E-03	Rfk	1.18	4.30E-02
BL	KO.IGF1_VEH	Apob	-4.84	1.94E-03	Oas3	1.95	4.30E-02
BL	KO.IGF1_VEH	Gc	-4.78	3.09E-03	Mt1	-1.74	4.53E-02
BL	KO.IGF1_VEH	Ube2o	1.31	3.09E-03	C1qc	-1.59	4.53E-02
BL	KO.IGF1_VEH	Arf5	1.29	3.25E-03	Uox	-4.21	4.53E-02
BL	KO.IGF1_VEH	E2f2	1.28	3.25E-03	Rbm38	1.50	4.54E-02
BL	KO.IGF1_VEH	Apoc4	-4.75	3.25E-03	Ednrb	-1.75	4.57E-02
BL	KO.IGF1_VEH	Ociad2	-4.66	4.87E-03	Rpl14	-1.08	4.86E-02
BL	KO.IGF1_VEH	Slc25a51	1.21	6.01E-03			
BL	WTM.IGF1_VEH	Prg4	-2.69	2.25E-10	Alox15	-1.43	2.27E-02
BL	WTM.IGF1_VEH	Fn1	-1.99	2.18E-08	Itgam	-1.69	3.04E-02
BL	WTM.IGF1_VEH	Ednrb	-2.77	9.62E-04	Mup2	-4.31	3.44E-02
BL	WTM.IGF1_VEH	Saa3	-1.74	9.62E-04	Cfd	-3.20	3.55E-02
BL	WTM.IGF1_VEH	Car3	-3.18	1.43E-02			
BL	IGF1.KO_WTM	Mir6236	3.09	3.22E-19	B2m	-1.22	7.52E-03
BL	IGF1.KO_WTM	Gzma	-2.80	1.44E-08	Tbrg1	-2.71	8.00E-03
BL	IGF1.KO_WTM	Prg4	2.49	2.06E-06	Slc25a37	1.21	8.00E-03
BL	IGF1.KO_WTM	Ccl5	-1.81	6.27E-06	Ppbp	-1.20	8.85E-03
BL	IGF1.KO_WTM	Tgtp2	-2.49	1.42E-05	Rn45s	1.24	1.30E-02
BL	IGF1.KO_WTM	Cox5a	-1.80	4.91E-05	Rac2	-1.27	1.30E-02
BL	IGF1.KO_WTM	Nkg7	-2.12	4.91E-05	Lars2	1.18	1.34E-02

BL	IGF1.KO_WTM	Ifi27l2a	-1.91	9.66E-05	Klra18	-4.52	2.31E-02
BL	IGF1.KO_WTM	Arf5	1.50	1.73E-04	Cxcl13	2.05	2.74E-02
BL	IGF1.KO_WTM	E2f2	1.46	3.51E-04	Ccl4	-4.48	2.80E-02
BL	IGF1.KO_WTM	Tgtp1	-2.69	1.31E-03	Srp14	-1.22	3.17E-02
BL	IGF1.KO_WTM	Ifi27	-1.74	1.38E-03	Irf7	-1.26	3.31E-02
BL	IGF1.KO_WTM	AW112010	-1.68	2.12E-03	Ifi35	-2.06	4.53E-02
BL	IGF1.KO_WTM	Prr13	-1.39	2.30E-03	Il2rg	-1.30	4.53E-02
BL	IGF1.KO_WTM	Pkn2	1.47	3.02E-03	Cxx1a	-2.05	4.53E-02
BL	IGF1.KO_WTM	Fn1	1.53	3.02E-03	Fam46c	1.09	4.53E-02
BL	IGF1.KO_WTM	Ms4a4b	-1.49	5.81E-03	Ikzf1	-1.79	4.53E-02
BL	VEH.KO_WTM	Alb	4.77	7.30E-31	Cps1	3.85	5.37E-03
BL	VEH.KO_WTM	Apoa2	4.63	4.12E-25	Gm5483	2.70	5.50E-03
BL	VEH.KO_WTM	Ttr	4.78	2.58E-21	Ypel3	-1.25	5.64E-03
BL	VEH.KO_WTM	Apoc1	4.04	2.77E-13	Alox15	1.22	7.02E-03
BL	VEH.KO_WTM	Irf7	-2.73	3.17E-13	Klre1	-4.44	7.02E-03
BL	VEH.KO_WTM	Saa3	2.30	7.46E-13	Atg4a	-1.40	7.28E-03
BL	VEH.KO_WTM	Gzma	-2.87	2.16E-11	Cyp2d26	4.18	8.19E-03
BL	VEH.KO_WTM	Cxcl13	2.65	2.35E-11	Timd4	1.87	8.29E-03
BL	VEH.KO_WTM	Wfdc17	2.04	4.70E-11	Ifit1	-2.26	8.29E-03
BL	VEH.KO_WTM	Ccl5	-2.10	1.94E-10	Cryl1	2.81	8.29E-03
BL	VEH.KO_WTM	S100a8	1.92	2.67E-10	Stfa2	4.12	8.29E-03
BL	VEH.KO_WTM	Apoa1	4.06	3.76E-10	Cyp4b1-ps2	-1.10	9.10E-03
BL	VEH.KO_WTM	BC100530	4.58	4.53E-08	Uox	3.74	9.97E-03
BL	VEH.KO_WTM	Ahsg	3.75	4.84E-08	Cyp4a10	4.10	1.06E-02
BL	VEH.KO_WTM	Ifi27	-2.38	6.22E-08	Arg1	2.88	1.08E-02
BL	VEH.KO_WTM	S100a9	1.70	1.88E-07	Apoe	1.15	1.14E-02
BL	VEH.KO_WTM	Cyp3a11	4.43	5.36E-07	Fga	3.71	1.14E-02
BL	VEH.KO_WTM	Isg15	-2.23	1.30E-06	Fbp1	4.06	1.21E-02
BL	VEH.KO_WTM	Apoc3	4.75	1.30E-06	Herc6	-2.07	1.21E-02

BL	VEH.KO_WTM	Ces1c	5.33	1.82E-06	Vmn2r26	2.95	1.48E-02
BL	VEH.KO_WTM	Apol11b	-1.51	1.82E-06	Fgg	3.67	1.48E-02
BL	VEH.KO_WTM	Rbp4	4.71	1.82E-06	Slco1b2	3.96	1.69E-02
BL	VEH.KO_WTM	Fabp1	3.61	3.28E-06	Cox5a	-1.25	1.74E-02
BL	VEH.KO_WTM	Stfa1	4.18	1.09E-05	Slpi	1.07	1.81E-02
BL	VEH.KO_WTM	Rsad2	-1.39	1.39E-05	Acsl1	-1.19	1.97E-02
BL	VEH.KO_WTM	Aldob	4.13	2.05E-05	Klra23	-4.16	1.99E-02
BL	VEH.KO_WTM	Fgb	3.65	2.20E-05	Apoa5	3.88	2.19E-02
BL	VEH.KO_WTM	Mthfd2	-2.11	2.46E-05	Cmas	-1.10	2.26E-02
BL	VEH.KO_WTM	Ifi27l2a	-1.68	4.45E-05	Pzp	3.86	2.26E-02
BL	VEH.KO_WTM	Serpina1a	4.42	5.07E-05	Stat1	-1.61	2.39E-02
BL	VEH.KO_WTM	Apob	4.40	5.51E-05	Rbbp9	3.87	2.61E-02
BL	VEH.KO_WTM	Serpina1d	3.54	7.72E-05	Rdh7	3.54	2.94E-02
BL	VEH.KO_WTM	Chil3	1.62	7.72E-05	Serpinb2	1.42	3.05E-02
BL	VEH.KO_WTM	Serpina1c	3.98	8.77E-05	Retnlg	1.00	3.21E-02
BL	VEH.KO_WTM	Rtp4	-3.04	1.39E-04	Rnf114	-1.27	3.21E-02
BL	VEH.KO_WTM	Mt1	2.09	1.45E-04	Ccl6	0.96	3.32E-02
BL	VEH.KO_WTM	Hpx	3.90	1.99E-04	Cyb5b	2.42	3.33E-02
BL	VEH.KO_WTM	Apoh	4.79	2.52E-04	Nusap1	-0.97	3.47E-02
BL	VEH.KO_WTM	Gm4070	-1.41	2.59E-04	Lipn	3.72	3.61E-02
BL	VEH.KO_WTM	Gvin1	-1.41	2.59E-04	Hn1	-0.98	3.61E-02
BL	VEH.KO_WTM	S100a6	1.38	2.92E-04	Gsta3	3.70	3.61E-02
BL	VEH.KO_WTM	Oas3	-2.22	2.92E-04	Creg1	-0.93	3.61E-02
BL	VEH.KO_WTM	Serpina1b	3.24	3.47E-04	Mat2b	-1.18	3.61E-02
BL	VEH.KO_WTM	Serpina3k	3.20	5.13E-04	Klra13-ps	-3.96	3.61E-02
BL	VEH.KO_WTM	Apoc4	3.72	9.03E-04	Lncpint	-3.96	3.61E-02
BL	VEH.KO_WTM	S100a4	1.63	1.23E-03	Xaf1	-2.31	3.61E-02
BL	VEH.KO_WTM	Trf	1.53	1.78E-03	Inmt	3.66	3.81E-02
BL	VEH.KO_WTM	Vtn	4.52	1.89E-03	Tmbim1	1.93	4.09E-02

BL	VEH.KO_WTM	Gc	3.39	2.14E-03	Tgtp2	-1.32	4.09E-02
BL	VEH.KO_WTM	Gnmt	4.49	2.25E-03	Oasl2	-1.98	4.38E-02
BL	VEH.KO_WTM	Ccl24	2.97	2.58E-03	Mki67	1.55	4.38E-02
BL	VEH.KO_WTM	Serpinc1	4.43	2.80E-03	C1qb	1.19	4.55E-02
BL	VEH.KO_WTM	Wfdc21	1.98	2.88E-03	Anxa1	1.19	4.56E-02
BL	VEH.KO_WTM	Cyp2c29	4.39	3.55E-03	Ctsb	-0.90	4.83E-02
BL	VEH.KO_WTM	1600020E01Rik	-1.68	4.36E-03	Asb17os	-2.23	4.83E-02
BL	VEH.KO_WTM	Mat1a	4.34	4.54E-03	Pon1	3.56	4.84E-02
BL	VEH.KO_WTM	Cyp2d10	4.31	4.97E-03	Mb	-3.84	4.84E-02
BL	VEH.KO_WTM	Nkg7	-1.37	5.23E-03	1500011B03Rik	2.06	4.90E-02
BL	VEH.KO_WTM	Pdzk1ip1	1.20	5.28E-03			
BL	KOIGF1_WTMVEH	Mir6236	3.19	1.13E-22	Nxpe2	1.25	2.32E-02
BL	KOIGF1_WTMVEH	Arf5	2.00	9.26E-10	Cd8b1	-1.93	2.46E-02
BL	KOIGF1_WTMVEH	Gzma	-2.67	1.64E-07	Slc25a51	1.02	2.48E-02
BL	KOIGF1_WTMVEH	Ifi27l2a	-2.12	4.14E-06	Ly6d	-1.09	2.88E-02
BL	KOIGF1_WTMVEH	Nkg7	-2.25	5.53E-06	Ly6a	-1.90	3.21E-02
BL	KOIGF1_WTMVEH	Ccl5	-1.74	5.53E-06	Ssrp1	-2.42	3.27E-02
BL	KOIGF1_WTMVEH	Sftpc	-5.57	6.76E-05	Ift140	1.17	3.27E-02
BL	KOIGF1_WTMVEH	E2f2	1.39	2.52E-04	Ifi35	-2.08	3.41E-02
BL	KOIGF1_WTMVEH	Pkn2	1.63	2.52E-04	Ybx3	0.98	3.42E-02
BL	KOIGF1_WTMVEH	Slc25a37	1.21	8.37E-04	H2-K1	-1.18	3.47E-02
BL	KOIGF1_WTMVEH	Mki67	2.14	8.37E-04	Tnk2os	1.86	3.56E-02
BL	KOIGF1_WTMVEH	Ppp1cb	1.21	8.37E-04	Fech	0.93	3.58E-02
BL	KOIGF1_WTMVEH	Malat1	-1.25	8.86E-04	Sft2d2	1.05	3.62E-02
BL	KOIGF1_WTMVEH	Gpx1	1.19	9.15E-04	2310057J18Rik	1.03	3.62E-02
BL	KOIGF1_WTMVEH	Tgtp2	-2.16	1.13E-03	Snord58b	1.23	3.62E-02
BL	KOIGF1_WTMVEH	Memo1	1.29	1.57E-03	Oasl2	-2.51	3.62E-02
BL	KOIGF1_WTMVEH	Fam46c	1.15	1.57E-03	Ctse	1.06	3.62E-02
BL	KOIGF1_WTMVEH	Prdx2	1.14	1.94E-03	Zfp707	-4.45	3.65E-02

BL	KOIGF1_WTMVEH	Lars2	1.21	2.23E-03	Ube2e3	1.40	3.74E-02
BL	KOIGF1_WTMVEH	Fcrl1	-3.27	2.46E-03	Thumpd3	-4.45	3.74E-02
BL	KOIGF1_WTMVEH	Gstm5	1.30	2.95E-03	Rhox8	0.93	3.74E-02
BL	KOIGF1_WTMVEH	Bag1	1.43	2.95E-03	Cd3g	-1.49	3.74E-02
BL	KOIGF1_WTMVEH	Epb41	1.05	9.68E-03	Mc1r	3.74	3.74E-02
BL	KOIGF1_WTMVEH	Isca1	1.05	9.68E-03	Slfn2	-1.17	3.74E-02
BL	KOIGF1_WTMVEH	Cfd	-4.86	1.02E-02	Psme2b	-1.21	3.74E-02
BL	KOIGF1_WTMVEH	Rac2	-1.23	1.02E-02	Ccl4	-4.43	3.75E-02
BL	KOIGF1_WTMVEH	Riok3	1.07	1.02E-02	Pink1	1.09	3.93E-02
BL	KOIGF1_WTMVEH	Wapl	1.18	1.14E-02	Slc38a5	1.20	3.93E-02
BL	KOIGF1_WTMVEH	Ifi27	-1.54	1.18E-02	Cox6b2	1.03	3.94E-02
BL	KOIGF1_WTMVEH	AW112010	-1.50	1.30E-02	Galnt1	1.11	4.16E-02
BL	KOIGF1_WTMVEH	Tgtp1	-2.43	1.30E-02	Sp110	-2.81	4.40E-02
BL	KOIGF1_WTMVEH	Mcf2l	1.40	1.30E-02	Gm10371	1.03	4.40E-02
BL	KOIGF1_WTMVEH	Irf7	-1.29	1.30E-02	0610007P14Rik	-3.06	4.40E-02
BL	KOIGF1_WTMVEH	Pde1c	1.17	1.30E-02	Klra18	-4.38	4.40E-02
BL	KOIGF1_WTMVEH	Tbrg1	-2.67	1.30E-02	Ifi209	-1.47	4.40E-02
BL	KOIGF1_WTMVEH	Ms4a4b	-1.37	1.30E-02	Cd48	-1.47	4.46E-02
BL	KOIGF1_WTMVEH	Rn45s	1.00	1.30E-02	Numa1	-3.49	4.53E-02
BL	KOIGF1_WTMVEH	Ltb	-2.14	1.52E-02	Acp5	-1.69	4.83E-02
BL	KOIGF1_WTMVEH	H2-Ob	-1.61	1.62E-02	Cd2	-1.57	4.83E-02
BL	KOIGF1_WTMVEH	4930513N10Rik	-1.91	1.74E-02	Vbp1	-1.20	4.88E-02
BL	KOIGF1_WTMVEH	Fam213a	1.00	1.90E-02	Tatdn2	1.67	4.88E-02
BL	KOIGF1_WTMVEH	Smarca4	-3.26	2.24E-02			

Supplementary Table 8 – DEG Analysis of Male Mice from Chapter II
All significant DEG found in the analysis of Male mice treated with rhIGF1 or vehicle. These results were calculated using EdgeR's QLFT function.
Legend:
CRB = Cerebellum, BL = Blood,
KO.IGF1_VEH = rhIGF1 treated *Mecp2*$^{-/y}$ vs. VEH treated *Mecp2*$^{-/y}$,
WTM.IGF1_VEH = rhIGF1 treated *Mecp2*$^{+/y}$ vs. VEH treated *Mecp2*$^{+/y}$,
IGF1.KO_WTM= rhIGF1 treated *Mecp2*$^{-/y}$ vs. rhIGF1 treated *Mecp2*$^{+/y}$,
VEH.KO_WTM = VEH treated *Mecp2*$^{-/y}$ vs. VEH treated *Mecp2*$^{+/y}$,
KOIGF1_WTMVEH = IGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/y}$

Tissue	Gene	Baseline LogFC	Baseline FDR	rhIGF1 LogFC	rhIGF1 FDR
CRB	3110039M20Rik	6.24	1.31E-02	-4.89	5.35E-03
CRB	Bcl11b	2.21	6.72E-07	-2.45	8.01E-10
CRB	C1ql2	3.12	1.29E-07	-3.19	1.45E-09
CRB	Calca	-2.69	6.92E-20	1.21	1.21E-02
CRB	Calcb	-5.55	2.83E-21	4.30	9.57E-09
CRB	Camk2a	2.00	4.71E-14	-2.17	3.33E-21
CRB	Camkv	1.39	3.57E-02	-2.36	8.15E-07
CRB	Chn1	0.78	4.37E-03	-0.69	1.71E-03
CRB	Chrm1	3.65	1.87E-03	-3.63	1.41E-04
CRB	Cpne4	1.34	1.30E-02	-1.21	1.25E-02
CRB	Cpne6	1.24	4.98E-03	-1.95	4.20E-09
CRB	Cpne7	4.40	1.57E-07	-3.32	9.07E-07
CRB	Crhbp	1.76	2.16E-04	-2.53	8.00E-10
CRB	Crym	4.89	6.33E-38	-6.91	4.26E-69
CRB	Ctxn1	2.91	1.31E-05	-2.21	1.87E-04
CRB	Ddn	4.26	7.38E-10	-4.62	1.17E-13
CRB	Dlx6os1	6.00	3.87E-02	-6.17	3.55E-03
CRB	Enc1	1.63	9.85E-08	-2.09	1.64E-15
CRB	Epha4	1.14	1.72E-04	-0.70	4.42E-02
CRB	Epha7	1.12	1.01E-05	-0.68	1.20E-02
CRB	Fam131a	1.06	9.35E-03	-1.19	1.65E-04
CRB	Fezf2	6.90	1.35E-04	-5.53	1.71E-05
CRB	Fosl2	1.36	6.12E-03	-1.04	3.96E-02
CRB	Foxg1	6.69	5.86E-16	-5.69	2.22E-18
CRB	Gal	-2.60	1.20E-16	1.32	5.41E-03
CRB	Gda	2.08	1.81E-04	-2.26	3.73E-06
CRB	Gh	-2.21	1.04E-19	0.95	8.57E-03
CRB	Gm10600	6.80	3.80E-04	-6.99	6.10E-06
CRB	Gm14648	-1.59	4.04E-11	-0.91	2.59E-02
CRB	Gm32687	5.98	4.23E-02	2.48	9.25E-06
CRB	Grin2b	1.92	3.06E-10	-1.41	3.25E-07
CRB	Hpca	1.49	7.66E-08	-1.79	8.55E-15
CRB	Hpcal4	1.07	5.07E-03	-1.47	3.92E-07
CRB	Icam5	6.70	7.36E-04	-4.64	5.23E-04
CRB	Iqgap2	2.77	7.36E-08	-1.92	2.49E-05
CRB	Lamp5	-2.25	6.14E-25	1.09	8.73E-06
CRB	Lmo3	1.11	8.48E-03	-1.52	1.58E-06
CRB	Lrrc10b	6.21	1.54E-02	-4.86	6.50E-03
CRB	Mal2	1.29	1.93E-02	-1.69	4.18E-05
CRB	Mas1	7.51	1.34E-07	-4.55	8.23E-07
CRB	Meis2	-1.49	6.13E-03	1.26	3.27E-02
CRB	Mpped1	2.15	7.12E-05	-1.32	1.87E-02
CRB	Myo5b	2.52	1.19E-05	-2.80	4.16E-08

CRB	Nefh	-0.84	2.45E-03	0.70	6.43E-03
CRB	Nefm	-1.38	4.35E-11	0.76	4.21E-04
CRB	Neurod6	2.19	1.25E-22	-2.10	1.06E-29
CRB	Npy2r	2.67	1.33E-07	-3.80	1.56E-15
CRB	Nr4a2	2.62	2.83E-13	-0.95	1.39E-02
CRB	Nrgn	2.09	3.11E-06	-1.88	3.75E-06
CRB	Pcdha3	8.41	6.37E-15	-2.09	3.22E-04
CRB	Pcdha5	-7.91	1.05E-10	8.85	3.10E-21
CRB	Pcdha8	8.15	3.75E-12	-2.79	1.23E-05
CRB	Pde1a	1.45	1.42E-06	-1.80	1.58E-12
CRB	Plk2	1.05	1.45E-03	-1.18	6.01E-06
CRB	Prl	-1.77	2.75E-17	0.99	6.29E-06
CRB	Prph	-4.58	2.00E-14	2.74	1.41E-02
CRB	Ptgs2	2.42	2.77E-02	-3.85	9.20E-06
CRB	Ptk2b	2.92	7.63E-21	-2.82	1.23E-25
CRB	Rasgrp1	1.10	6.13E-04	-0.96	5.47E-04
CRB	Rasl10a	2.39	4.12E-02	-3.93	1.42E-05
CRB	Rgs14	3.99	1.81E-07	-4.15	7.53E-10
CRB	Rpl31-ps8	-11.16	2.74E-84	9.93	4.28E-43
CRB	Scn3b	1.13	6.68E-05	-1.88	1.63E-17
CRB	Slc10a4	-4.76	1.87E-02	4.75	2.89E-03
CRB	Slc17a6	-1.15	1.44E-06	0.74	5.61E-03
CRB	Slc5a7	-3.71	6.67E-10	3.00	1.39E-05
CRB	Slc6a5	-1.16	4.44E-03	1.05	6.22E-03
CRB	Smoc2	2.81	8.44E-05	-2.17	5.59E-04
CRB	Sostdc1	0.95	1.08E-03	-0.88	3.31E-04
CRB	Spink8	3.71	8.67E-19	-5.30	4.22E-36
CRB	St6galnac5	2.38	1.22E-08	-2.03	4.49E-08
CRB	Syt17	1.48	3.99E-02	-1.80	1.10E-03
CRB	Tph2	-1.78	1.91E-02	1.65	1.87E-02
CRB	Ttr	0.98	1.53E-02	-1.03	2.43E-05
CRB	Uts2	-7.03	5.51E-05	6.83	5.62E-05
CRB	Vxn	1.54	1.46E-04	-1.70	7.91E-07
CRB	Wipf3	1.52	2.27E-05	-0.96	1.01E-02
BL	Rps13-ps1	-3.23	6.78E-03	3.04	1.07E-02
BL	Ipo11	2.69	7.40E-03	-2.11	6.83E-02
BL	Rps16-ps2	7.09	5.28E-05	-6.89	9.03E-04

Supplementary Table 9 – Target Genes of rhIGF1 Action in female $Mecp2^{-/+}$ Mice
Overlapping DEG found in both vehicle treated $Mecp2^{-/+}$ vs $Mecp2^{+/+}$ mice and in rhIGF1 treated $Mecp2^{-/+}$ vs *vehicle treated* $Mecp2^{-/+}$ mice comparisons but regulated in different directions.
Legend:
CRB = Cerebellum, BL = Blood

Tissue	Gene	Baseline LogFC	Baseline FDR	rhIGF1 LogFC	rhIGF1 FDR

CRB	1810043G02Rik	0.98	1.20E-02	-1.16	9.01E-03
CRB	2310057M21Rik	0.65	3.73E-02	-0.86	1.37E-02
CRB	2810013P06Rik	0.43	3.70E-02	-0.75	5.10E-04
CRB	4931408D14Rik	-3.67	4.19E-03	3.73	4.25E-03
CRB	9130401M01Rik	0.72	1.91E-03	-0.70	1.35E-02
CRB	Acbd3	1.51	2.99E-08	-1.33	6.75E-06
CRB	Acin1	0.42	1.09E-02	-0.74	2.62E-05
CRB	Apbb1	0.42	2.95E-03	-0.42	3.99E-02
CRB	Arhgdia	0.46	1.04E-03	-0.76	5.78E-06
CRB	Arpc4	0.49	1.21E-03	-0.43	4.63E-02
CRB	Atg14	0.59	2.53E-02	-0.63	4.56E-02
CRB	Atp6v1g2	0.66	2.60E-07	-0.69	1.93E-05
CRB	B4gat1	0.46	2.52E-02	-0.89	2.56E-05
CRB	Bag1	0.97	1.74E-04	-1.27	6.07E-06
CRB	Bola1	0.54	8.21E-03	-0.54	3.95E-02
CRB	Caly	0.45	2.93E-02	-1.08	4.24E-07
CRB	Ccdc115	1.01	4.01E-04	-0.78	2.36E-02
CRB	Cct6a	0.40	1.43E-02	-0.45	3.26E-02
CRB	Cd81	0.37	6.67E-03	-0.71	2.29E-04
CRB	Cdh9	-3.16	1.10E-02	2.82	4.57E-02
CRB	Cdkn1c	1.06	1.99E-02	-1.33	9.20E-03
CRB	Cfl1	0.40	1.73E-03	-0.66	5.76E-05
CRB	Ckb	0.68	2.48E-07	-0.80	8.55E-04
CRB	Cldn5	1.10	6.95E-04	-0.98	9.36E-03
CRB	Cnp	0.30	3.77E-02	-0.51	4.46E-03
CRB	Coq8a	0.82	7.49E-03	-1.08	1.06E-03
CRB	Coq9	0.45	1.30E-02	-0.58	6.25E-03
CRB	Cst3	0.52	6.85E-05	-0.57	9.02E-03
CRB	Ctcf	0.50	5.03E-03	-0.53	1.91E-02
CRB	Cuedc2	0.32	2.69E-02	-0.40	4.72E-02
CRB	Ddah2	0.59	6.74E-04	-0.51	2.81E-02
CRB	Ddrgk1	0.61	6.61E-05	-0.64	5.85E-04
CRB	Dnajc30	0.68	1.53E-02	-0.75	2.00E-02
CRB	Fam213b	0.65	6.53E-07	-0.98	1.08E-10
CRB	Fuca1	0.73	7.69E-05	-0.92	9.22E-06
CRB	Gabrd	0.54	4.13E-04	-0.70	5.58E-05
CRB	Glrx5	0.84	4.57E-05	-1.05	5.72E-06
CRB	Gnb5	0.55	3.00E-04	-0.45	3.93E-02
CRB	Gnptg	0.59	4.42E-05	-0.46	2.26E-02
CRB	Golph3l	0.47	8.11E-04	-0.67	5.90E-05
CRB	Gpx3	1.63	4.65E-05	-0.92	4.47E-02
CRB	Gpx4	0.47	3.04E-04	-0.85	3.60E-08
CRB	Gtf2f1	0.51	2.05E-02	-0.62	1.88E-02
CRB	H3f3b	0.46	6.03E-04	-0.52	2.94E-02

CRB	Habp4	0.75	4.14E-03	-0.84	5.64E-03
CRB	Hagh	0.33	2.03E-02	-0.45	2.00E-02
CRB	Herpud1	0.57	3.58E-04	-0.63	1.01E-03
CRB	Hist3h2ba	0.55	2.58E-02	-0.73	9.83E-03
CRB	Hmgcr	-0.76	9.50E-05	0.59	2.88E-02
CRB	Hmgcs1	-0.48	3.58E-04	0.40	4.72E-02
CRB	Id1	1.08	1.76E-02	-1.13	3.34E-02
CRB	Isca1	0.33	2.36E-02	-0.78	1.53E-06
CRB	Isoc1	1.32	2.61E-05	-1.10	1.47E-03
CRB	Mapk6	0.86	3.54E-04	-0.91	8.41E-04
CRB	Metap2	0.48	3.70E-04	-0.61	2.66E-04
CRB	Metrn	0.43	1.97E-02	-0.53	1.98E-02
CRB	Mir6236	2.24	5.79E-27	-2.51	3.75E-31
CRB	Mobp	-0.35	9.29E-03	0.43	4.59E-02
CRB	Mrpl2	0.53	8.08E-04	-0.63	8.64E-04
CRB	Mrpl52	0.69	8.22E-03	-0.81	5.74E-03
CRB	Mrps12	0.39	2.37E-02	-0.51	1.54E-02
CRB	Mycbp2	0.64	2.64E-05	-0.53	7.39E-03
CRB	Ndufa8	0.38	4.17E-03	-0.58	5.72E-04
CRB	Ndufb6	0.43	1.85E-03	-0.68	2.55E-05
CRB	Necap2	0.88	3.27E-04	-1.32	1.01E-06
CRB	Pef1	0.49	4.78E-02	-0.96	8.79E-05
CRB	Pgrmc1	0.66	2.30E-05	-0.76	1.91E-05
CRB	Pkn2	1.03	2.55E-05	-1.16	1.04E-05
CRB	Pnrc1	0.85	3.12E-03	-0.81	1.98E-02
CRB	Psmb5	0.49	1.88E-03	-0.52	1.11E-02
CRB	Psmd8	0.55	3.91E-04	-0.80	6.43E-06
CRB	Rab11fip2	0.84	4.48E-04	-0.89	9.94E-04
CRB	Rab7	0.33	1.97E-02	-0.63	9.07E-05
CRB	Rpl27a	0.50	2.65E-03	-0.76	2.72E-05
CRB	Rps10	0.63	2.39E-03	-0.83	4.47E-04
CRB	Rraga	0.44	7.32E-03	-0.67	2.70E-04
CRB	Scrn1	0.37	3.91E-02	-0.50	1.80E-02
CRB	Scx	1.26	5.00E-02	-1.46	4.68E-02
CRB	Sec61b	0.42	9.39E-03	-0.66	2.70E-04
CRB	Sesn1	0.52	2.22E-03	-0.47	4.17E-02
CRB	Sgk1	0.45	1.20E-02	0.48	9.93E-03
CRB	Sh3bgr	0.90	4.47E-04	-0.82	7.19E-03
CRB	Smarcd3	1.64	7.58E-03	-1.56	2.52E-02
CRB	Snhg10	1.23	9.89E-04	-1.26	2.10E-03
CRB	Snrpb	0.84	2.80E-09	-0.66	1.38E-04
CRB	Spg7	0.86	1.21E-02	-0.95	1.40E-02
CRB	Spns1	0.65	2.01E-02	-0.70	3.50E-02
CRB	Sppl2b	1.02	2.40E-02	-1.21	1.93E-02

CRB	Srsf10	0.40	4.84E-02	-0.50	4.57E-02
CRB	Tbc1d17	0.65	3.72E-02	-0.92	7.08E-03
CRB	Th	1.16	6.81E-04	-1.01	9.85E-03
CRB	Tmem160	1.07	2.21E-05	-1.19	1.00E-05
CRB	Tmem59	0.40	1.94E-03	-0.73	6.30E-06
CRB	Tmem59l	0.59	4.00E-07	-1.14	1.35E-15
CRB	Tppp3	0.70	2.00E-05	-0.93	7.61E-07
CRB	Tprgl	0.83	6.37E-07	-0.66	1.44E-03
CRB	Trappc5	0.62	5.88E-04	-0.90	5.86E-06
CRB	Trim23	0.55	9.39E-03	-0.72	1.85E-03
CRB	Trim32	0.37	2.70E-02	-0.61	1.01E-03
CRB	Tsc22d1	0.33	1.54E-02	-0.54	2.35E-03
CRB	Tspyl4	0.29	4.96E-02	-0.46	1.62E-02
CRB	Tssc4	0.62	6.21E-03	-0.96	5.77E-05
CRB	Usp1	2.25	1.44E-21	-2.30	2.14E-20
CRB	Vcp	0.42	1.53E-02	-0.85	5.01E-06
CRB	Vim	0.48	2.41E-02	-0.60	1.56E-02
CRB	Vps25	0.52	3.70E-03	-0.48	4.13E-02
CRB	Vps53	0.65	2.49E-03	-0.72	5.66E-03
CRB	Wapl	0.90	2.47E-05	-0.58	3.46E-02
CRB	Wdr45	0.44	3.50E-02	-0.92	9.68E-06
CRB	Wsb1	0.58	6.76E-04	-0.90	2.52E-06
CRB	Yif1b	0.39	2.00E-02	-0.62	8.31E-04
CRB	Ywhaq	0.49	7.00E-05	-0.77	1.37E-06
CRB	Zc3h6	1.11	4.05E-04	-0.90	1.37E-02
BL	Ahsg	3.75	1.99E-07	-5.91	5.93E-07
BL	Alb	4.77	2.70E-29	-8.29	3.30E-28
BL	Aldob	4.13	4.45E-05	-5.11	7.61E-04
BL	Alox15	1.22	7.64E-03	-1.29	4.15E-02
BL	Apoa1	4.06	1.74E-09	-6.12	3.93E-08
BL	Apoa2	4.63	7.62E-24	-7.76	3.44E-22
BL	Apob	4.40	1.02E-04	-4.84	3.00E-03
BL	Apoc1	4.04	2.56E-12	-4.36	3.90E-08
BL	Apoc3	4.75	4.00E-06	-5.19	7.52E-04
BL	Apoc4	3.72	1.15E-03	-4.75	4.62E-03
BL	Apoh	4.79	3.72E-04	-4.39	3.10E-02
BL	Ccl24	2.97	2.98E-03	-3.24	3.64E-02
BL	Ccl6	0.96	3.32E-02	-1.19	2.06E-02
BL	Ces1c	5.33	5.17E-06	-4.92	2.69E-03
BL	Cps1	3.85	6.02E-03	-4.31	4.03E-02
BL	Cxcl13	2.65	1.45E-10	-1.81	2.08E-03
BL	Cyp3a11	4.43	1.80E-06	-5.40	1.58E-04
BL	Fabp1	3.61	8.09E-06	-5.58	2.65E-05
BL	Fgb	3.65	4.51E-05	-5.33	2.85E-04

BL	Gc	3.39	2.55E-03	-4.78	4.58E-03
BL	Hpx	3.90	3.07E-04	-4.88	2.91E-03
BL	Mt1	2.09	2.33E-04	-1.74	4.66E-02
BL	Oas3	-2.22	4.15E-04	1.95	4.54E-02
BL	Rbp4	4.71	4.80E-06	-5.15	7.91E-04
BL	Rsad2	-1.39	3.22E-05	1.32	7.66E-04
BL	S100a9	1.70	6.95E-07	-1.10	4.53E-02
BL	Saa3	2.30	5.52E-12	-2.69	1.51E-11
BL	Serpina1a	4.42	9.88E-05	-4.87	2.98E-03
BL	Serpina1b	3.24	4.75E-04	-5.17	7.72E-04
BL	Serpina1c	3.98	1.47E-04	-4.98	1.98E-03
BL	Serpina1d	3.54	1.36E-04	-5.22	6.51E-04
BL	Serpina3k	3.20	6.78E-04	-5.14	7.85E-04
BL	Timd4	1.87	8.77E-03	-2.10	4.28E-02
BL	Trf	1.53	2.20E-03	-1.75	8.43E-03
BL	Ttr	4.78	3.18E-20	-4.67	2.63E-12
BL	Uox	3.74	1.02E-02	-4.21	4.53E-02
BL	Wfdc17	2.04	2.48E-10	-1.79	2.57E-05

Supplementary Table 10 – Target genes of rhIGF1 Action in *Mecp2$^{-/y}$* Mice
Overlapping DEG found in both vehicle treated *Mecp2$^{-/y}$* vs *Mecp2$^{+/y}$* mice and in rhIGF1 treated *Mecp2$^{-/y}$* vs *vehicle treated Mecp2$^{-/y}$* mice comparisons but regulated in different directions.
Legend:
CRB = Cerebellum, BL = Blood

Tissue	Comparison	Pathway identifier	Pathway name	FDR
CRB	HET.IGF1_VEH	R-HSA-372790	Signaling by GPCR	4.08E-05
CRB	HET.IGF1_VEH	R-HSA-388396	GPCR downstream signalling	4.08E-05
CRB	HET.IGF1_VEH	R-HSA-500792	GPCR ligand binding	1.25E-04
CRB	HET.IGF1_VEH	R-HSA-375276	Peptide ligand-binding receptors	1.49E-03
CRB	HET.IGF1_VEH	R-HSA-8986944	Transcriptional Regulation by MECP2	1.49E-03
CRB	HET.IGF1_VEH	R-HSA-419812	Calcitonin-like ligand receptors	2.01E-03
CRB	HET.IGF1_VEH	R-HSA-373080	Class B/2 (Secretin family receptors)	1.05E-02
CRB	HET.IGF1_VEH	R-HSA-8951911	RUNX3 regulates RUNX1-mediated transcription	1.05E-02
CRB	HET.IGF1_VEH	R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	1.80E-02
CRB	HET.IGF1_VEH	R-HSA-9620244	Long-term potentiation	2.31E-02
CRB	HET.IGF1_VEH	R-HSA-5250989	Toxicity of botulinum toxin type G (botG)	2.31E-02
CRB	HET.IGF1_VEH	R-HSA-5250981	Toxicity of botulinum toxin type F (botF)	3.20E-02
CRB	HET.IGF1_VEH	R-HSA-5250955	Toxicity of botulinum toxin type D (botD)	3.20E-02
CRB	HET.IGF1_VEH	R-HSA-977225	Amyloid fiber formation	3.92E-02
CRB	WTF.IGF1_VEH	R-HSA-9679191	Potential therapeutics for SARS	1.11E-03

CRB	WTF.IGF1_VEH	R-HSA-9013508	NOTCH3 Intracellular Domain Regulates Transcription	4.67E-03
CRB	WTF.IGF1_VEH	R-HSA-9679506	SARS-CoV Infections	4.67E-03
CRB	WTF.IGF1_VEH	R-HSA-9012852	Signaling by NOTCH3	6.19E-03
CRB	WTF.IGF1_VEH	R-HSA-5578775	Ion homeostasis	6.19E-03
CRB	WTF.IGF1_VEH	R-HSA-936837	Ion transport by P-type ATPases	6.51E-03
CRB	WTF.IGF1_VEH	R-HSA-5576891	Cardiac conduction	2.00E-02
CRB	WTF.IGF1_VEH	R-HSA-983712	Ion channel transport	3.47E-02
CRB	WTF.IGF1_VEH	R-HSA-397014	Muscle contraction	3.48E-02
CRB	WTF.IGF1_VEH	R-HSA-1170546	Prolactin receptor signaling	3.48E-02
CRB	WTF.IGF1_VEH	R-HSA-157118	Signaling by NOTCH	3.48E-02
CRB	WTF.IGF1_VEH	R-HSA-209931	Serotonin and melatonin biosynthesis	3.48E-02
CRB	WTF.IGF1_VEH	R-HSA-1181150	Signaling by NODAL	3.48E-02
CRB	WTF.IGF1_VEH	R-HSA-982772	Growth hormone receptor signaling	4.03E-02
CRB	IGF1.HET_WTF	R-HSA-8986944	Transcriptional Regulation by MECP2	7.21E-05
CRB	IGF1.HET_WTF	R-HSA-372790	Signaling by GPCR	1.12E-04
CRB	IGF1.HET_WTF	R-HSA-388396	GPCR downstream signalling	1.12E-04
CRB	IGF1.HET_WTF	R-HSA-9022702	MECP2 regulates transcription of neuronal ligands	1.31E-04
CRB	IGF1.HET_WTF	R-HSA-5619507	Activation of HOX genes during differentiation	4.53E-04
CRB	IGF1.HET_WTF	R-HSA-5617472	Activation of anterior HOX genes in hindbrain development during early embryogenesis	4.53E-04
CRB	IGF1.HET_WTF	R-HSA-373080	Class B/2 (Secretin family receptors)	1.76E-03
CRB	IGF1.HET_WTF	R-HSA-419812	Calcitonin-like ligand receptors	2.10E-03
CRB	IGF1.HET_WTF	R-HSA-500792	GPCR ligand binding	2.48E-03
CRB	IGF1.HET_WTF	R-HSA-9022534	Loss of MECP2 binding ability to 5hmC-DNA	2.48E-03
CRB	IGF1.HET_WTF	R-HSA-9013508	NOTCH3 Intracellular Domain Regulates Transcription	2.48E-03
CRB	IGF1.HET_WTF	R-HSA-9022692	Regulation of MECP2 expression and activity	3.07E-03
CRB	IGF1.HET_WTF	R-HSA-416476	G alpha (q) signalling events	9.53E-03
CRB	IGF1.HET_WTF	R-HSA-162582	Signal Transduction	1.01E-02
CRB	IGF1.HET_WTF	R-HSA-9660821	ADORA2B mediated anti-inflammatory cytokines production	1.01E-02
CRB	IGF1.HET_WTF	R-HSA-9022538	Loss of MECP2 binding ability to 5mC-DNA	1.01E-02
CRB	IGF1.HET_WTF	R-HSA-9012852	Signaling by NOTCH3	1.27E-02
CRB	IGF1.HET_WTF	R-HSA-9022927	MECP2 regulates transcription of genes involved in GABA signaling	1.27E-02
CRB	IGF1.HET_WTF	R-HSA-418555	G alpha (s) signalling events	1.27E-02
CRB	IGF1.HET_WTF	R-HSA-9022535	Loss of phosphorylation of MECP2 at T308	1.63E-02

CRB	IGF1.HET_WTF	R-HSA-9022537	Loss of MECP2 binding ability to the NCoR/SMRT complex	2.00E-02
CRB	IGF1.HET_WTF	R-HSA-375276	Peptide ligand-binding receptors	2.51E-02
CRB	IGF1.HET_WTF	R-HSA-9022707	MECP2 regulates transcription factors	2.76E-02
CRB	IGF1.HET_WTF	R-HSA-114508	Effects of PIP2 hydrolysis	2.84E-02
CRB	IGF1.HET_WTF	R-HSA-9664433	Leishmania parasite growth and survival	3.03E-02
CRB	IGF1.HET_WTF	R-HSA-9662851	Anti-inflammatory response favouring Leishmania parasite infection	3.03E-02
CRB	VEH.HET_WTF	R-HSA-8986944	Transcriptional Regulation by MECP2	7.35E-07
CRB	VEH.HET_WTF	R-HSA-388396	GPCR downstream signalling	7.07E-06
CRB	VEH.HET_WTF	R-HSA-372790	Signaling by GPCR	7.07E-06
CRB	VEH.HET_WTF	R-HSA-500792	GPCR ligand binding	5.82E-05
CRB	VEH.HET_WTF	R-HSA-9620244	Long-term potentiation	1.98E-04
CRB	VEH.HET_WTF	R-HSA-375276	Peptide ligand-binding receptors	5.75E-04
CRB	VEH.HET_WTF	R-HSA-162582	Signal Transduction	5.75E-04
CRB	VEH.HET_WTF	R-HSA-438066	Unblocking of NMDA receptors, glutamate binding and activation	1.59E-03
CRB	VEH.HET_WTF	R-HSA-9617324	Negative regulation of NMDA receptor-mediated neuronal transmission	1.59E-03
CRB	VEH.HET_WTF	R-HSA-373080	Class B/2 (Secretin family receptors)	2.17E-03
CRB	VEH.HET_WTF	R-HSA-419812	Calcitonin-like ligand receptors	2.17E-03
CRB	VEH.HET_WTF	R-HSA-9022699	MECP2 regulates neuronal receptors and channels	2.28E-03
CRB	VEH.HET_WTF	R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	3.21E-03
CRB	VEH.HET_WTF	R-HSA-416476	G alpha (q) signalling events	3.74E-03
CRB	VEH.HET_WTF	R-HSA-418555	G alpha (s) signalling events	4.49E-03
CRB	VEH.HET_WTF	R-HSA-212436	Generic Transcription Pathway	5.11E-03
CRB	VEH.HET_WTF	R-HSA-9609736	Assembly and cell surface presentation of NMDA receptors	8.26E-03
CRB	VEH.HET_WTF	R-HSA-438064	Post NMDA receptor activation events	1.06E-02
CRB	VEH.HET_WTF	R-HSA-73857	RNA Polymerase II Transcription	1.41E-02
CRB	VEH.HET_WTF	R-HSA-9660821	ADORA2B mediated anti-inflammatory cytokines production	1.41E-02
CRB	VEH.HET_WTF	R-HSA-390648	Muscarinic acetylcholine receptors	1.41E-02
CRB	VEH.HET_WTF	R-HSA-442982	Ras activation upon Ca2+ influx through NMDA receptor	1.44E-02
CRB	VEH.HET_WTF	R-HSA-166520	Signaling by NTRKs	1.60E-02
CRB	VEH.HET_WTF	R-HSA-442755	Activation of NMDA receptors and postsynaptic events	1.68E-02
CRB	VEH.HET_WTF	R-HSA-9658195	Leishmania infection	2.56E-02
CRB	VEH.HET_WTF	R-HSA-9022707	MECP2 regulates transcription factors	3.05E-02
CRB	VEH.HET_WTF	R-HSA-198725	Nuclear Events (kinase and transcription factor activation)	3.05E-02
CRB	VEH.HET_WTF	R-HSA-112315	Transmission across Chemical Synapses	3.14E-02

CRB	VEH.HET_WTF	R-HSA-442742	CREB1 phosphorylation through NMDA receptor-mediated activation of RAS signaling	3.14E-02
CRB	VEH.HET_WTF	R-HSA-74160	Gene expression (Transcription)	3.18E-02
CRB	VEH.HET_WTF	R-HSA-383280	Nuclear Receptor transcription pathway	3.38E-02
CRB	VEH.HET_WTF	R-HSA-187037	Signaling by NTRK1 (TRKA)	3.43E-02
CRB	VEH.HET_WTF	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	3.43E-02
CRB	VEH.HET_WTF	R-HSA-9022702	MECP2 regulates transcription of neuronal ligands	3.93E-02
CRB	VEH.HET_WTF	R-HSA-9664433	Leishmania parasite growth and survival	4.02E-02
CRB	VEH.HET_WTF	R-HSA-9662851	Anti-inflammatory response favouring Leishmania parasite infection	4.02E-02
CRB	VEH.HET_WTF	R-HSA-112314	Neurotransmitter receptors and postsynaptic signal transmission	4.93E-02
CRB	HETIGF1_WTFVEH	R-HSA-9022702	MECP2 regulates transcription of neuronal ligands	5.25E-05
CRB	HETIGF1_WTFVEH	R-HSA-419812	Calcitonin-like ligand receptors	1.06E-03
CRB	HETIGF1_WTFVEH	R-HSA-500792	GPCR ligand binding	1.06E-03
CRB	HETIGF1_WTFVEH	R-HSA-8868766	rRNA processing in the mitochondrion	1.07E-03
CRB	HETIGF1_WTFVEH	R-HSA-388396	GPCR downstream signalling	1.07E-03
CRB	HETIGF1_WTFVEH	R-HSA-6785470	tRNA processing in the mitochondrion	1.07E-03
CRB	HETIGF1_WTFVEH	R-HSA-9660821	ADORA2B mediated anti-inflammatory cytokines production	1.07E-03
CRB	HETIGF1_WTFVEH	R-HSA-373080	Class B/2 (Secretin family receptors)	1.15E-03
CRB	HETIGF1_WTFVEH	R-HSA-418555	G alpha (s) signalling events	1.30E-03
CRB	HETIGF1_WTFVEH	R-HSA-372790	Signaling by GPCR	1.70E-03
CRB	HETIGF1_WTFVEH	R-HSA-375276	Peptide ligand-binding receptors	2.57E-03
CRB	HETIGF1_WTFVEH	R-HSA-8986944	Transcriptional Regulation by MECP2	1.18E-02
CRB	HETIGF1_WTFVEH	R-HSA-9664433	Leishmania parasite growth and survival	1.49E-02
CRB	HETIGF1_WTFVEH	R-HSA-9662851	Anti-inflammatory response favouring Leishmania parasite infection	1.49E-02
CRB	HETIGF1_WTFVEH	R-HSA-5619507	Activation of HOX genes during differentiation	1.49E-02
CRB	HETIGF1_WTFVEH	R-HSA-5617472	Activation of anterior HOX genes in hindbrain development during early embryogenesis	1.49E-02
CRB	HETIGF1_WTFVEH	R-HSA-1170546	Prolactin receptor signaling	3.15E-02
CRB	HETIGF1_WTFVEH	R-HSA-72312	rRNA processing	3.24E-02
CRB	HETIGF1_WTFVEH	R-HSA-2022857	Keratan sulfate degradation	4.35E-02
CRB	HETIGF1_WTFVEH	R-HSA-9658195	Leishmania infection	4.99E-02
CRB	HETIGF1_WTFVEH	R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	4.99E-02
BL	HET.IGF1_VEH	R-HSA-1989781	PPARA activates gene expression	4.30E-05

BL	HET.IGF1_VEH	R-HSA-400206	Regulation of lipid metabolism by PPARalpha	4.30E-05
BL	HET.IGF1_VEH	R-HSA-189483	Heme degradation	3.92E-03
BL	HET.IGF1_VEH	R-HSA-8963899	Plasma lipoprotein remodeling	5.02E-03
BL	HET.IGF1_VEH	R-HSA-556833	Metabolism of lipids	5.02E-03
BL	HET.IGF1_VEH	R-HSA-189445	Metabolism of porphyrins	6.95E-03
BL	HET.IGF1_VEH	R-HSA-6783783	Interleukin-10 signaling	6.95E-03
BL	HET.IGF1_VEH	R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	7.71E-03
BL	HET.IGF1_VEH	R-HSA-8957275	Post-translational protein phosphorylation	9.51E-03
BL	HET.IGF1_VEH	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	1.07E-02
BL	HET.IGF1_VEH	R-HSA-9707564	Cytoprotection by HMOX1	1.64E-02
BL	HET.IGF1_VEH	R-HSA-9711123	Cellular response to chemical stress	2.33E-02
BL	HET.IGF1_VEH	R-HSA-8963888	Chylomicron assembly	2.85E-02
BL	HET.IGF1_VEH	R-HSA-8963901	Chylomicron remodeling	2.85E-02
BL	HET.IGF1_VEH	R-HSA-8964058	HDL remodeling	4.01E-02
BL	VEH.HET_WTF	R-HSA-140877	Formation of Fibrin Clot (Clotting Cascade)	1.65E-14
BL	VEH.HET_WTF	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	1.65E-14
BL	VEH.HET_WTF	R-HSA-76002	Platelet activation, signaling and aggregation	1.65E-14
BL	VEH.HET_WTF	R-HSA-114608	Platelet degranulation	1.65E-14
BL	VEH.HET_WTF	R-HSA-109582	Hemostasis	1.65E-14
BL	VEH.HET_WTF	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	2.72E-10
BL	VEH.HET_WTF	R-HSA-140875	Common Pathway of Fibrin Clot Formation	6.03E-10
BL	VEH.HET_WTF	R-HSA-8957275	Post-translational protein phosphorylation	1.09E-08
BL	VEH.HET_WTF	R-HSA-140837	Intrinsic Pathway of Fibrin Clot Formation	1.57E-08
BL	VEH.HET_WTF	R-HSA-166658	Complement cascade	2.61E-07
BL	VEH.HET_WTF	R-HSA-1430728	Metabolism	2.61E-07
BL	VEH.HET_WTF	R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	9.61E-07
BL	VEH.HET_WTF	R-HSA-977606	Regulation of Complement cascade	1.62E-06
BL	VEH.HET_WTF	R-HSA-76009	Platelet Aggregation (Plug Formation)	7.89E-06
BL	VEH.HET_WTF	R-HSA-354194	GRB2:SOS provides linkage to MAPK signaling for Integrins	8.83E-06
BL	VEH.HET_WTF	R-HSA-8963898	Plasma lipoprotein assembly	8.83E-06

BL	VEH.HET_WTF	R-HSA-8963899	Plasma lipoprotein remodeling	1.01E-05
BL	VEH.HET_WTF	R-HSA-372708	p130Cas linkage to MAPK signaling for integrins	1.38E-05
BL	VEH.HET_WTF	R-HSA-71291	Metabolism of amino acids and derivatives	1.77E-05
BL	VEH.HET_WTF	R-HSA-211859	Biological oxidations	2.17E-05
BL	VEH.HET_WTF	R-HSA-159740	Gamma-carboxylation of protein precursors	2.23E-05
BL	VEH.HET_WTF	R-HSA-159854	Gamma-carboxylation, transport, and amino-terminal cleavage of proteins	3.13E-05
BL	VEH.HET_WTF	R-HSA-9033241	Peroxisomal protein import	3.46E-05
BL	VEH.HET_WTF	R-HSA-159763	Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus	3.46E-05
BL	VEH.HET_WTF	R-HSA-8963901	Chylomicron remodeling	3.59E-05
BL	VEH.HET_WTF	R-HSA-354192	Integrin signaling	3.59E-05
BL	VEH.HET_WTF	R-HSA-216083	Integrin cell surface interactions	3.79E-05
BL	VEH.HET_WTF	R-HSA-168249	Innate Immune System	4.29E-05
BL	VEH.HET_WTF	R-HSA-159782	Removal of aminoterminal propeptides from gamma-carboxylated proteins	4.74E-05
BL	VEH.HET_WTF	R-HSA-6798695	Neutrophil degranulation	9.77E-05
BL	VEH.HET_WTF	R-HSA-9671793	Diseases of hemostasis	9.98E-05
BL	VEH.HET_WTF	R-HSA-9651496	Defects of contact activation system (CAS) and kallikrein/kinin system (KKS)	9.98E-05
BL	VEH.HET_WTF	R-HSA-156580	Phase II - Conjugation of compounds	1.36E-04
BL	VEH.HET_WTF	R-HSA-428359	Insulin-like Growth Factor-2 mRNA Binding Proteins (IGF2BPs/IMPs/VICKZs) bind RNA	1.46E-04
BL	VEH.HET_WTF	R-HSA-5686938	Regulation of TLR by endogenous ligand	1.76E-04
BL	VEH.HET_WTF	R-HSA-9024446	NR1H2 and NR1H3-mediated signaling	1.84E-04
BL	VEH.HET_WTF	R-HSA-8963888	Chylomicron assembly	1.87E-04
BL	VEH.HET_WTF	R-HSA-8963691	Phenylalanine and tyrosine metabolism	5.15E-04
BL	VEH.HET_WTF	R-HSA-8936459	RUNX1 regulates genes involved in megakaryocyte differentiation and platelet function	5.31E-04
BL	VEH.HET_WTF	R-HSA-6802948	Signaling by high-kinase activity BRAF mutants	5.62E-04
BL	VEH.HET_WTF	R-HSA-8963684	Tyrosine catabolism	8.99E-04
BL	VEH.HET_WTF	R-HSA-5674135	MAP2K and MAPK activation	1.03E-03
BL	VEH.HET_WTF	R-HSA-9656223	Signaling by RAF1 mutants	1.03E-03
BL	VEH.HET_WTF	R-HSA-6806667	Metabolism of fat-soluble vitamins	1.27E-03

BL	VEH.HET_WTF	R-HSA-9649948	Signaling downstream of RAS mutants	1.64E-03
BL	VEH.HET_WTF	R-HSA-6802946	Signaling by moderate kinase activity BRAF mutants	1.64E-03
BL	VEH.HET_WTF	R-HSA-6802955	Paradoxical activation of RAF signaling by kinase inactive BRAF	1.64E-03
BL	VEH.HET_WTF	R-HSA-6802949	Signaling by RAS mutants	1.64E-03
BL	VEH.HET_WTF	R-HSA-2408508	Metabolism of ingested SeMet, Sec, MeSec into H2Se	2.03E-03
BL	VEH.HET_WTF	R-HSA-159418	Recycling of bile acids and salts	2.03E-03
BL	VEH.HET_WTF	R-HSA-9609507	Protein localization	2.30E-03
BL	VEH.HET_WTF	R-HSA-5602498	MyD88 deficiency (TLR2/4)	2.46E-03
BL	VEH.HET_WTF	R-HSA-975634	Retinoid metabolism and transport	2.58E-03
BL	VEH.HET_WTF	R-HSA-8964043	Plasma lipoprotein clearance	2.58E-03
BL	VEH.HET_WTF	R-HSA-5603041	IRAK4 deficiency (TLR2/4)	2.70E-03
BL	VEH.HET_WTF	R-HSA-75892	Platelet Adhesion to exposed collagen	3.82E-03
BL	VEH.HET_WTF	R-HSA-156590	Glutathione conjugation	5.60E-03
BL	VEH.HET_WTF	R-HSA-70635	Urea cycle	5.83E-03
BL	VEH.HET_WTF	R-HSA-166665	Terminal pathway of complement	6.38E-03
BL	VEH.HET_WTF	R-HSA-202733	Cell surface interactions at the vascular wall	7.76E-03
BL	VEH.HET_WTF	R-HSA-6802952	Signaling by BRAF and RAF1 fusions	7.76E-03
BL	VEH.HET_WTF	R-HSA-8866423	VLDL assembly	8.95E-03
BL	VEH.HET_WTF	R-HSA-9662001	Defective factor VIII causes hemophilia A	8.95E-03
BL	VEH.HET_WTF	R-HSA-194068	Bile acid and bile salt metabolism	9.81E-03
BL	VEH.HET_WTF	R-HSA-1474244	Extracellular matrix organization	9.93E-03
BL	VEH.HET_WTF	R-HSA-8964046	VLDL clearance	1.10E-02
BL	VEH.HET_WTF	R-HSA-8964058	HDL remodeling	1.42E-02
BL	VEH.HET_WTF	R-HSA-5602358	Diseases associated with the TLR signaling cascade	1.61E-02
BL	VEH.HET_WTF	R-HSA-5260271	Diseases of Immune System	1.61E-02
BL	VEH.HET_WTF	R-HSA-114604	GPVI-mediated activation cascade	1.79E-02
BL	VEH.HET_WTF	R-HSA-9029569	NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	1.97E-02
BL	VEH.HET_WTF	R-HSA-9668250	Defective factor IX causes hemophilia B	2.08E-02
BL	VEH.HET_WTF	R-HSA-6802957	Oncogenic MAPK signaling	2.46E-02
BL	VEH.HET_WTF	R-HSA-1614635	Sulfur amino acid metabolism	2.46E-02
BL	VEH.HET_WTF	R-HSA-9018682	Biosynthesis of maresins	2.46E-02

BL	VEH.HET_WTF	R-HSA-3000170	Syndecan interactions	2.46E-02
BL	VEH.HET_WTF	R-HSA-1989781	PPARA activates gene expression	2.46E-02
BL	VEH.HET_WTF	R-HSA-9672391	Defective F8 cleavage by thrombin	2.46E-02
BL	VEH.HET_WTF	R-HSA-400206	Regulation of lipid metabolism by PPARalpha	2.46E-02
BL	VEH.HET_WTF	R-HSA-445355	Smooth Muscle Contraction	2.50E-02
BL	VEH.HET_WTF	R-HSA-389599	Alpha-oxidation of phytanate	2.85E-02
BL	VEH.HET_WTF	R-HSA-163841	Gamma carboxylation, hypusine formation and arylsulfatase activation	3.06E-02
BL	VEH.HET_WTF	R-HSA-556833	Metabolism of lipids	3.56E-02
BL	VEH.HET_WTF	R-HSA-9673240	Defective gamma-carboxylation of F9	3.65E-02
BL	VEH.HET_WTF	R-HSA-193368	Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol	3.94E-02
BL	HETIGF1_WTFVEH	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	1.03E-13
BL	HETIGF1_WTFVEH	R-HSA-114608	Platelet degranulation	2.56E-13
BL	HETIGF1_WTFVEH	R-HSA-76002	Platelet activation, signaling and aggregation	3.71E-12
BL	HETIGF1_WTFVEH	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	3.74E-12
BL	HETIGF1_WTFVEH	R-HSA-8957275	Post-translational protein phosphorylation	6.07E-10
BL	HETIGF1_WTFVEH	R-HSA-140877	Formation of Fibrin Clot (Clotting Cascade)	6.07E-10
BL	HETIGF1_WTFVEH	R-HSA-1430728	Metabolism	5.96E-09
BL	HETIGF1_WTFVEH	R-HSA-140875	Common Pathway of Fibrin Clot Formation	6.02E-08
BL	HETIGF1_WTFVEH	R-HSA-109582	Hemostasis	1.08E-07
BL	HETIGF1_WTFVEH	R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	1.62E-07
BL	HETIGF1_WTFVEH	R-HSA-166658	Complement cascade	3.57E-07
BL	HETIGF1_WTFVEH	R-HSA-8963899	Plasma lipoprotein remodeling	1.32E-06
BL	HETIGF1_WTFVEH	R-HSA-8963898	Plasma lipoprotein assembly	3.52E-06
BL	HETIGF1_WTFVEH	R-HSA-977606	Regulation of Complement cascade	5.06E-06
BL	HETIGF1_WTFVEH	R-HSA-140837	Intrinsic Pathway of Fibrin Clot Formation	2.70E-05
BL	HETIGF1_WTFVEH	R-HSA-71291	Metabolism of amino acids and derivatives	4.46E-05
BL	HETIGF1_WTFVEH	R-HSA-8963901	Chylomicron remodeling	6.31E-05
BL	HETIGF1_WTFVEH	R-HSA-211859	Biological oxidations	7.83E-05
BL	HETIGF1_WTFVEH	R-HSA-975634	Retinoid metabolism and transport	1.40E-04
BL	HETIGF1_WTFVEH	R-HSA-9024446	NR1H2 and NR1H3-mediated signaling	2.26E-04
BL	HETIGF1_WTFVEH	R-HSA-6806667	Metabolism of fat-soluble vitamins	3.00E-04

BL	HETIGF1_WTFVEH	R-HSA-8963691	Phenylalanine and tyrosine metabolism	3.11E-04
BL	HETIGF1_WTFVEH	R-HSA-168249	Innate Immune System	3.85E-04
BL	HETIGF1_WTFVEH	R-HSA-8963888	Chylomicron assembly	5.03E-04
BL	HETIGF1_WTFVEH	R-HSA-159740	Gamma-carboxylation of protein precursors	6.20E-04
BL	HETIGF1_WTFVEH	R-HSA-159854	Gamma-carboxylation, transport, and amino-terminal cleavage of proteins	7.96E-04
BL	HETIGF1_WTFVEH	R-HSA-1989781	PPARA activates gene expression	9.25E-04
BL	HETIGF1_WTFVEH	R-HSA-400206	Regulation of lipid metabolism by PPARalpha	9.52E-04
BL	HETIGF1_WTFVEH	R-HSA-5686938	Regulation of TLR by endogenous ligand	1.24E-03
BL	HETIGF1_WTFVEH	R-HSA-556833	Metabolism of lipids	1.38E-03
BL	HETIGF1_WTFVEH	R-HSA-8963684	Tyrosine catabolism	1.54E-03
BL	HETIGF1_WTFVEH	R-HSA-2408508	Metabolism of ingested SeMet, Sec, MeSec into H2Se	1.56E-03
BL	HETIGF1_WTFVEH	R-HSA-159418	Recycling of bile acids and salts	1.56E-03
BL	HETIGF1_WTFVEH	R-HSA-194068	Bile acid and bile salt metabolism	1.96E-03
BL	HETIGF1_WTFVEH	R-HSA-9033241	Peroxisomal protein import	2.11E-03
BL	HETIGF1_WTFVEH	R-HSA-8866423	VLDL assembly	2.28E-03
BL	HETIGF1_WTFVEH	R-HSA-159763	Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus	2.28E-03
BL	HETIGF1_WTFVEH	R-HSA-2187338	Visual phototransduction	2.51E-03
BL	HETIGF1_WTFVEH	R-HSA-8964046	VLDL clearance	2.84E-03
BL	HETIGF1_WTFVEH	R-HSA-159782	Removal of aminoterminal propeptides from gamma-carboxylated proteins	2.84E-03
BL	HETIGF1_WTFVEH	R-HSA-211981	Xenobiotics	2.91E-03
BL	HETIGF1_WTFVEH	R-HSA-211945	Phase I - Functionalization of compounds	2.91E-03
BL	HETIGF1_WTFVEH	R-HSA-76009	Platelet Aggregation (Plug Formation)	4.87E-03
BL	HETIGF1_WTFVEH	R-HSA-211999	CYP2E1 reactions	5.08E-03
BL	HETIGF1_WTFVEH	R-HSA-70635	Urea cycle	6.45E-03
BL	HETIGF1_WTFVEH	R-HSA-6798695	Neutrophil degranulation	6.54E-03
BL	HETIGF1_WTFVEH	R-HSA-1614635	Sulfur amino acid metabolism	8.77E-03
BL	HETIGF1_WTFVEH	R-HSA-156580	Phase II - Conjugation of compounds	1.25E-02
BL	HETIGF1_WTFVEH	R-HSA-189483	Heme degradation	1.32E-02
BL	HETIGF1_WTFVEH	R-HSA-8964043	Plasma lipoprotein clearance	1.51E-02
BL	HETIGF1_WTFVEH	R-HSA-354194	GRB2:SOS provides linkage to MAPK signaling for Integrins	1.51E-02
BL	HETIGF1_WTFVEH	R-HSA-9027307	Biosynthesis of maresin-like SPMs	1.72E-02

BL	HETIGF1_WTFVEH	R-HSA-9651496	Defects of contact activation system (CAS) and kallikrein/kinin system (KKS)	1.72E-02
BL	HETIGF1_WTFVEH	R-HSA-9671793	Diseases of hemostasis	1.72E-02
BL	HETIGF1_WTFVEH	R-HSA-193775	Synthesis of bile acids and bile salts via 24-hydroxycholesterol	1.72E-02
BL	HETIGF1_WTFVEH	R-HSA-173736	Alternative complement activation	1.72E-02
BL	HETIGF1_WTFVEH	R-HSA-372708	p130Cas linkage to MAPK signaling for integrins	1.73E-02
BL	HETIGF1_WTFVEH	R-HSA-9006931	Signaling by Nuclear Receptors	1.83E-02
BL	HETIGF1_WTFVEH	R-HSA-193368	Synthesis of bile acids and bile salts via 7alpha-hydroxycholesterol	1.85E-02
BL	HETIGF1_WTFVEH	R-HSA-5423646	Aflatoxin activation and detoxification	2.12E-02
BL	HETIGF1_WTFVEH	R-HSA-8964058	HDL remodeling	2.21E-02
BL	HETIGF1_WTFVEH	R-HSA-174577	Activation of C3 and C5	2.32E-02
BL	HETIGF1_WTFVEH	R-HSA-156581	Methylation	2.37E-02
BL	HETIGF1_WTFVEH	R-HSA-5602498	MyD88 deficiency (TLR2/4)	2.37E-02
BL	HETIGF1_WTFVEH	R-HSA-216083	Integrin cell surface interactions	2.40E-02
BL	HETIGF1_WTFVEH	R-HSA-166665	Terminal pathway of complement	2.57E-02
BL	HETIGF1_WTFVEH	R-HSA-5603041	IRAK4 deficiency (TLR2/4)	2.63E-02
BL	HETIGF1_WTFVEH	R-HSA-9609507	Protein localization	2.82E-02
BL	HETIGF1_WTFVEH	R-HSA-211935	Fatty acids	3.20E-02
BL	HETIGF1_WTFVEH	R-HSA-9018682	Biosynthesis of maresins	3.20E-02
BL	HETIGF1_WTFVEH	R-HSA-8963889	Assembly of active LPL and LIPC lipase complexes	3.51E-02
BL	HETIGF1_WTFVEH	R-HSA-9632974	NR1H2 & NR1H3 regulate gene expression linked to gluconeogenesis	3.96E-02
BL	HETIGF1_WTFVEH	R-HSA-8964041	LDL remodeling	3.96E-02
BL	HETIGF1_WTFVEH	R-HSA-211897	Cytochrome P450 - arranged by substrate type	4.27E-02
BL	HETIGF1_WTFVEH	R-HSA-9029569	NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	4.27E-02
BL	HETIGF1_WTFVEH	R-HSA-156590	Glutathione conjugation	4.73E-02

Supplementary Table 11 – Reactome Analysis for Chapter II Female Mice
All significant pathways found in Reactome analysis of Female mice treated with rhIGF1 or vehicle.
Legend:
CRB = Cerebellum, BL = Blood,
HET.IGF1_VEH = rhIGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{-/+}$,
WTF.IGF1_VEH = rhIGF1 treated *Mecp2*$^{+/+}$ vs. VEH treated *Mecp2*$^{+/+}$,
IGF1.HET_WTF= rhIGF1 treated *Mecp2*$^{-/+}$ vs. rhIGF1 treated *Mecp2*$^{+/+}$,
VEH.HET_WTF = VEH treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/+}$,
HETIGF1_WTFVEH = IGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/+}$

Tissue	Comparison	Pathway identifier	Pathway name	Entities FDR

CRB	KO.IGF1_VEH	R-HSA-9031628	NGF-stimulated transcription	0.01
CRB	KO.IGF1_VEH	R-HSA-198725	Nuclear Events (kinase and transcription factor activation)	0.03
CRB	KO.IGF1_VEH	R-HSA-8953897	Cellular responses to stimuli	0.03
CRB	KO.IGF1_VEH	R-HSA-9013407	RHOH GTPase cycle	0.03
CRB	KO.IGF1_VEH	R-HSA-383280	Nuclear Receptor transcription pathway	0.03
CRB	KO.IGF1_VEH	R-HSA-5362768	Hh mutants are degraded by ERAD	0.03
CRB	KO.IGF1_VEH	R-HSA-5387390	Hh mutants abrogate ligand secretion	0.03
CRB	KO.IGF1_VEH	R-HSA-1168372	Downstream signaling events of B Cell Receptor (BCR)	0.03
CRB	KO.IGF1_VEH	R-HSA-2262752	Cellular responses to stress	0.03
CRB	KO.IGF1_VEH	R-HSA-5678895	Defective CFTR causes cystic fibrosis	0.03
CRB	KO.IGF1_VEH	R-HSA-5358346	Hedgehog ligand biogenesis	0.03
CRB	KO.IGF1_VEH	R-HSA-68867	Assembly of the pre-replicative complex	0.03
CRB	KO.IGF1_VEH	R-HSA-211733	Regulation of activated PAK-2p34 by proteasome mediated degradation	0.03
CRB	KO.IGF1_VEH	R-HSA-5687128	MAPK6/MAPK4 signaling	0.03
CRB	KO.IGF1_VEH	R-HSA-8939236	RUNX1 regulates transcription of genes involved in differentiation of HSCs	0.03
CRB	KO.IGF1_VEH	R-HSA-350562	Regulation of ornithine decarboxylase (ODC)	0.03
CRB	KO.IGF1_VEH	R-HSA-180534	Vpu mediated degradation of CD4	0.03
CRB	KO.IGF1_VEH	R-HSA-1236978	Cross-presentation of soluble exogenous antigens (endosomes)	0.03
CRB	KO.IGF1_VEH	R-HSA-72766	Translation	0.03
CRB	KO.IGF1_VEH	R-HSA-69613	p53-Independent G1/S DNA damage checkpoint	0.03
CRB	KO.IGF1_VEH	R-HSA-69601	Ubiquitin Mediated Degradation of Phosphorylated Cdc25A	0.03
CRB	KO.IGF1_VEH	R-HSA-69610	p53-Independent DNA Damage Response	0.03
CRB	KO.IGF1_VEH	R-HSA-349425	Autodegradation of the E3 ubiquitin ligase COP1	0.03
CRB	KO.IGF1_VEH	R-HSA-75815	Ubiquitin-dependent degradation of Cyclin D	0.03
CRB	KO.IGF1_VEH	R-HSA-169911	Regulation of Apoptosis	0.03
CRB	KO.IGF1_VEH	R-HSA-8854050	FBXL7 down-regulates AURKA during mitotic entry and in early mitosis	0.03
CRB	KO.IGF1_VEH	R-HSA-174113	SCF-beta-TrCP mediated degradation of Emi1	0.03
CRB	KO.IGF1_VEH	R-HSA-180585	Vif-mediated degradation of APOBEC3G	0.03
CRB	KO.IGF1_VEH	R-HSA-450408	AUF1 (hnRNP D0) binds and destabilizes mRNA	0.03

CRB	KO.IGF1_VEH	R-HSA-4641258	Degradation of DVL	0.03
CRB	KO.IGF1_VEH	R-HSA-4641257	Degradation of AXIN	0.03
CRB	KO.IGF1_VEH	R-HSA-68827	CDT1 association with the CDC6:ORC:origin complex	0.03
CRB	KO.IGF1_VEH	R-HSA-69541	Stabilization of p53	0.03
CRB	KO.IGF1_VEH	R-HSA-5607764	CLEC7A (Dectin-1) signaling	0.03
CRB	KO.IGF1_VEH	R-HSA-69002	DNA Replication Pre-Initiation	0.03
CRB	KO.IGF1_VEH	R-HSA-8932339	ROS sensing by NFE2L2	0.03
CRB	KO.IGF1_VEH	R-HSA-9639288	Amino acids regulate mTORC1	0.03
CRB	KO.IGF1_VEH	R-HSA-5676590	NIK-->noncanonical NF-kB signaling	0.03
CRB	KO.IGF1_VEH	R-HSA-5610780	Degradation of GLI1 by the proteasome	0.03
CRB	KO.IGF1_VEH	R-HSA-5610783	Degradation of GLI2 by the proteasome	0.03
CRB	KO.IGF1_VEH	R-HSA-5610785	GLI3 is processed to GLI3R by the proteasome	0.03
CRB	KO.IGF1_VEH	R-HSA-5628897	TP53 Regulates Metabolic Genes	0.04
CRB	KO.IGF1_VEH	R-HSA-194315	Signaling by Rho GTPases	0.04
CRB	KO.IGF1_VEH	R-HSA-5419276	Mitochondrial translation termination	0.04
CRB	KO.IGF1_VEH	R-HSA-5389840	Mitochondrial translation elongation	0.04
CRB	KO.IGF1_VEH	R-HSA-5368286	Mitochondrial translation initiation	0.04
CRB	KO.IGF1_VEH	R-HSA-3858494	Beta-catenin independent WNT signaling	0.04
CRB	KO.IGF1_VEH	R-HSA-392499	Metabolism of proteins	0.04
CRB	KO.IGF1_VEH	R-HSA-4608870	Asymmetric localization of PCP proteins	0.04
CRB	KO.IGF1_VEH	R-HSA-5607761	Dectin-1 mediated noncanonical NF-kB signaling	0.04
CRB	KO.IGF1_VEH	R-HSA-5689603	UCH proteinases	0.04
CRB	KO.IGF1_VEH	R-HSA-9716542	Signaling by Rho GTPases, Miro GTPases and RHOBTB3	0.04
CRB	KO.IGF1_VEH	R-HSA-174154	APC/C:Cdc20 mediated degradation of Securin	0.04
CRB	KO.IGF1_VEH	R-HSA-5619084	ABC transporter disorders	0.04
CRB	KO.IGF1_VEH	R-HSA-6807070	PTEN Regulation	0.04
CRB	KO.IGF1_VEH	R-HSA-6798695	Neutrophil degranulation	0.04
CRB	KO.IGF1_VEH	R-HSA-9711123	Cellular response to chemical stress	0.04
CRB	KO.IGF1_VEH	R-HSA-1236974	ER-Phagosome pathway	0.04

CRB	KO.IGF1_VEH	R-HSA-69563	p53-Dependent G1 DNA Damage Response	0.04
CRB	KO.IGF1_VEH	R-HSA-69580	p53-Dependent G1/S DNA damage checkpoint	0.04
CRB	KO.IGF1_VEH	R-HSA-5368287	Mitochondrial translation	0.04
CRB	KO.IGF1_VEH	R-HSA-5658442	Regulation of RAS by GAPs	0.04
CRB	KO.IGF1_VEH	R-HSA-2426168	Activation of gene expression by SREBF (SREBP)	0.04
CRB	KO.IGF1_VEH	R-HSA-9711097	Cellular response to starvation	0.04
CRB	KO.IGF1_VEH	R-HSA-1169091	Activation of NF-kappaB in B cells	0.04
CRB	KO.IGF1_VEH	R-HSA-1234176	Oxygen-dependent proline hydroxylation of Hypoxia-inducible Factor Alpha	0.04
CRB	KO.IGF1_VEH	R-HSA-69615	G1/S DNA Damage Checkpoints	0.04
CRB	KO.IGF1_VEH	R-HSA-174184	Cdc20:Phospho-APC/C mediated degradation of Cyclin A	0.04
CRB	KO.IGF1_VEH	R-HSA-68949	Orc1 removal from chromatin	0.04
CRB	KO.IGF1_VEH	R-HSA-8878171	Transcriptional regulation by RUNX1	0.04
CRB	KO.IGF1_VEH	R-HSA-174178	APC/C:Cdh1 mediated degradation of Cdc20 and other APC/C:Cdh1 targeted proteins in late mitosis/early G1	0.04
CRB	KO.IGF1_VEH	R-HSA-179419	APC:Cdc20 mediated degradation of cell cycle proteins prior to satisfation of the cell cycle checkpoint	0.04
CRB	KO.IGF1_VEH	R-HSA-8948751	Regulation of PTEN stability and activity	0.04
CRB	KO.IGF1_VEH	R-HSA-187037	Signaling by NTRK1 (TRKA)	0.04
CRB	KO.IGF1_VEH	R-HSA-69017	CDK-mediated phosphorylation and removal of Cdc6	0.04
CRB	KO.IGF1_VEH	R-HSA-9707587	Regulation of HMOX1 expression and activity	0.04
CRB	KO.IGF1_VEH	R-HSA-9010553	Regulation of expression of SLITs and ROBOs	0.04
CRB	KO.IGF1_VEH	R-HSA-176409	APC/C:Cdc20 mediated degradation of mitotic proteins	0.04
CRB	KO.IGF1_VEH	R-HSA-176814	Activation of APC/C and APC/C:Cdc20 mediated degradation of mitotic proteins	0.04
CRB	KO.IGF1_VEH	R-HSA-9012999	RHO GTPase cycle	0.05
CRB	KO.IGF1_VEH	R-HSA-983705	Signaling by the B Cell Receptor (BCR)	0.05
CRB	KO.IGF1_VEH	R-HSA-1632852	Macroautophagy	0.05
CRB	KO.IGF1_VEH	R-HSA-351202	Metabolism of polyamines	0.05
CRB	KO.IGF1_VEH	R-HSA-109581	Apoptosis	0.05
CRB	KO.IGF1_VEH	R-HSA-8935964	RUNX1 regulates expression of components of tight junctions	0.05
CRB	KO.IGF1_VEH	R-HSA-163200	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	0.05

CRB	KO.IGF1_VEH	R-HSA-376176	Signaling by ROBO receptors	0.05
CRB	KO.IGF1_VEH	R-HSA-69481	G2/M Checkpoints	0.05
CRB	KO.IGF1_VEH	R-HSA-1236975	Antigen processing-Cross presentation	0.05
CRB	KO.IGF1_VEH	R-HSA-8939902	Regulation of RUNX2 expression and activity	0.05
CRB	KO.IGF1_VEH	R-HSA-8852276	The role of GTSE1 in G2/M progression after G2 checkpoint	0.05
CRB	KO.IGF1_VEH	R-HSA-176408	Regulation of APC/C activators between G1/S and early anaphase	0.05
CRB	KO.IGF1_VEH	R-HSA-1428517	The citric acid (TCA) cycle and respiratory electron transport	0.05
CRB	WTM.IGF1_VEH	R-HSA-381119	Unfolded Protein Response (UPR)	0.00
CRB	WTM.IGF1_VEH	R-HSA-381183	ATF6 (ATF6-alpha) activates chaperone genes	0.00
CRB	WTM.IGF1_VEH	R-HSA-381033	ATF6 (ATF6-alpha) activates chaperones	0.00
CRB	WTM.IGF1_VEH	R-HSA-381070	IRE1alpha activates chaperones	0.00
CRB	WTM.IGF1_VEH	R-HSA-2262752	Cellular responses to stress	0.00
CRB	WTM.IGF1_VEH	R-HSA-8953897	Cellular responses to stimuli	0.00
CRB	WTM.IGF1_VEH	R-HSA-75035	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	0.01
CRB	WTM.IGF1_VEH	R-HSA-381042	PERK regulates gene expression	0.02
CRB	WTM.IGF1_VEH	R-HSA-76002	Platelet activation, signaling and aggregation	0.02
CRB	WTM.IGF1_VEH	R-HSA-111447	Activation of BAD and translocation to mitochondria	0.02
CRB	WTM.IGF1_VEH	R-HSA-114608	Platelet degranulation	0.03
CRB	WTM.IGF1_VEH	R-HSA-381038	XBP1(S) activates chaperone genes	0.03
CRB	WTM.IGF1_VEH	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	0.03
CRB	WTM.IGF1_VEH	R-HSA-8957275	Post-translational protein phosphorylation	0.04
CRB	IGF1.KO_WTM	R-HSA-8986944	Transcriptional Regulation by MECP2	0.00
CRB	IGF1.KO_WTM	R-HSA-8953897	Cellular responses to stimuli	0.00
CRB	IGF1.KO_WTM	R-HSA-2262752	Cellular responses to stress	0.00
CRB	IGF1.KO_WTM	R-HSA-381183	ATF6 (ATF6-alpha) activates chaperone genes	0.00
CRB	IGF1.KO_WTM	R-HSA-381033	ATF6 (ATF6-alpha) activates chaperones	0.00
CRB	IGF1.KO_WTM	R-HSA-9005891	Loss of function of MECP2 in Rett syndrome	0.00
CRB	IGF1.KO_WTM	R-HSA-9697154	Disorders of Nervous System Development	0.00
CRB	IGF1.KO_WTM	R-HSA-9005895	Pervasive developmental disorders	0.00

CRB	IGF1.KO_WTM	R-HSA-9675151	Disorders of Developmental Biology	0.00
CRB	IGF1.KO_WTM	R-HSA-9022699	MECP2 regulates neuronal receptors and channels	0.00
CRB	IGF1.KO_WTM	R-HSA-9013407	RHOH GTPase cycle	0.01
CRB	IGF1.KO_WTM	R-HSA-9022692	Regulation of MECP2 expression and activity	0.01
CRB	IGF1.KO_WTM	R-HSA-9022702	MECP2 regulates transcription of neuronal ligands	0.01
CRB	IGF1.KO_WTM	R-HSA-9022538	Loss of MECP2 binding ability to 5mC-DNA	0.01
CRB	IGF1.KO_WTM	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	0.01
CRB	IGF1.KO_WTM	R-HSA-381119	Unfolded Protein Response (UPR)	0.01
CRB	IGF1.KO_WTM	R-HSA-75035	Chk1/Chk2(Cds1) mediated inactivation of Cyclin B:Cdk1 complex	0.01
CRB	IGF1.KO_WTM	R-HSA-8957275	Post-translational protein phosphorylation	0.01
CRB	IGF1.KO_WTM	R-HSA-1251985	Nuclear signaling by ERBB4	0.01
CRB	IGF1.KO_WTM	R-HSA-6798695	Neutrophil degranulation	0.01
CRB	IGF1.KO_WTM	R-HSA-9022535	Loss of phosphorylation of MECP2 at T308	0.01
CRB	IGF1.KO_WTM	R-HSA-111447	Activation of BAD and translocation to mitochondria	0.02
CRB	IGF1.KO_WTM	R-HSA-9022537	Loss of MECP2 binding ability to the NCoR/SMRT complex	0.02
CRB	IGF1.KO_WTM	R-HSA-9022534	Loss of MECP2 binding ability to 5hmC-DNA	0.03
CRB	IGF1.KO_WTM	R-HSA-195258	RHO GTPase Effectors	0.05
CRB	VEH.KO_WTM	R-HSA-8986944	Transcriptional Regulation by MECP2	0.00
CRB	VEH.KO_WTM	R-HSA-8953897	Cellular responses to stimuli	0.00
CRB	VEH.KO_WTM	R-HSA-2262752	Cellular responses to stress	0.00
CRB	VEH.KO_WTM	R-HSA-9022702	MECP2 regulates transcription of neuronal ligands	0.00
CRB	VEH.KO_WTM	R-HSA-9614085	FOXO-mediated transcription	0.02
CRB	VEH.KO_WTM	R-HSA-9646399	Aggrephagy	0.03
CRB	VEH.KO_WTM	R-HSA-72766	Translation	0.03
CRB	VEH.KO_WTM	R-HSA-9022538	Loss of MECP2 binding ability to 5mC-DNA	0.03
CRB	VEH.KO_WTM	R-HSA-392499	Metabolism of proteins	0.03
CRB	VEH.KO_WTM	R-HSA-1632852	Macroautophagy	0.04
CRB	VEH.KO_WTM	R-HSA-69895	Transcriptional activation of cell cycle inhibitor p21	0.04
CRB	VEH.KO_WTM	R-HSA-69560	Transcriptional activation of p53 responsive genes	0.04

CRB	KOIGF1_WTMVEH	R-HSA-9022702	MECP2 regulates transcription of neuronal ligands	0.00
CRB	KOIGF1_WTMVEH	R-HSA-8986944	Transcriptional Regulation by MECP2	0.00
CRB	KOIGF1_WTMVEH	R-HSA-9022538	Loss of MECP2 binding ability to 5mC-DNA	0.00
CRB	KOIGF1_WTMVEH	R-HSA-9022534	Loss of MECP2 binding ability to 5hmC-DNA	0.01
CRB	KOIGF1_WTMVEH	R-HSA-9022692	Regulation of MECP2 expression and activity	0.01
CRB	KOIGF1_WTMVEH	R-HSA-9005891	Loss of function of MECP2 in Rett syndrome	0.01
CRB	KOIGF1_WTMVEH	R-HSA-9675151	Disorders of Developmental Biology	0.01
CRB	KOIGF1_WTMVEH	R-HSA-9697154	Disorders of Nervous System Development	0.01
CRB	KOIGF1_WTMVEH	R-HSA-9005895	Pervasive developmental disorders	0.01
CRB	KOIGF1_WTMVEH	R-HSA-5661231	Metallothioneins bind metals	0.01
CRB	KOIGF1_WTMVEH	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	0.01
CRB	KOIGF1_WTMVEH	R-HSA-1251985	Nuclear signaling by ERBB4	0.01
CRB	KOIGF1_WTMVEH	R-HSA-5660526	Response to metal ions	0.02
CRB	KOIGF1_WTMVEH	R-HSA-9031628	NGF-stimulated transcription	0.02
CRB	KOIGF1_WTMVEH	R-HSA-9022927	MECP2 regulates transcription of genes involved in GABA signaling	0.03
CRB	KOIGF1_WTMVEH	R-HSA-8957275	Post-translational protein phosphorylation	0.03
CRB	KOIGF1_WTMVEH	R-HSA-166520	Signaling by NTRKs	0.03
CRB	KOIGF1_WTMVEH	R-HSA-9022535	Loss of phosphorylation of MECP2 at T308	0.03
CRB	KOIGF1_WTMVEH	R-HSA-9022537	Loss of MECP2 binding ability to the NCoR/SMRT complex	0.04
BL	KO.IGF1_VEH	R-HSA-8963898	Plasma lipoprotein assembly	0.00
BL	KO.IGF1_VEH	R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	0.00
BL	KO.IGF1_VEH	R-HSA-8963888	Chylomicron assembly	0.00
BL	KO.IGF1_VEH	R-HSA-8963901	Chylomicron remodeling	0.00
BL	KO.IGF1_VEH	R-HSA-975634	Retinoid metabolism and transport	0.00
BL	KO.IGF1_VEH	R-HSA-6806667	Metabolism of fat-soluble vitamins	0.00
BL	KO.IGF1_VEH	R-HSA-114608	Platelet degranulation	0.00
BL	KO.IGF1_VEH	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	0.00
BL	KO.IGF1_VEH	R-HSA-8963899	Plasma lipoprotein remodeling	0.00
BL	KO.IGF1_VEH	R-HSA-8957275	Post-translational protein phosphorylation	0.00

BL	KO.IGF1_VEH	R-HSA-8866423	VLDL assembly	0.00
BL	KO.IGF1_VEH	R-HSA-8964046	VLDL clearance	0.00
BL	KO.IGF1_VEH	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	0.00
BL	KO.IGF1_VEH	R-HSA-8964043	Plasma lipoprotein clearance	0.00
BL	KO.IGF1_VEH	R-HSA-2187338	Visual phototransduction	0.00
BL	KO.IGF1_VEH	R-HSA-1989781	PPARA activates gene expression	0.00
BL	KO.IGF1_VEH	R-HSA-400206	Regulation of lipid metabolism by PPARalpha	0.00
BL	KO.IGF1_VEH	R-HSA-8964058	HDL remodeling	0.00
BL	KO.IGF1_VEH	R-HSA-9029569	NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	0.00
BL	KO.IGF1_VEH	R-HSA-76002	Platelet activation, signaling and aggregation	0.01
BL	KO.IGF1_VEH	R-HSA-9024446	NR1H2 and NR1H3-mediated signaling	0.01
BL	KO.IGF1_VEH	R-HSA-5686938	Regulation of TLR by endogenous ligand	0.01
BL	KO.IGF1_VEH	R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	0.01
BL	KO.IGF1_VEH	R-HSA-8953897	Cellular responses to stimuli	0.01
BL	KO.IGF1_VEH	R-HSA-3000480	Scavenging by Class A Receptors	0.02
BL	KO.IGF1_VEH	R-HSA-196854	Metabolism of vitamins and cofactors	0.02
BL	KO.IGF1_VEH	R-HSA-1430728	Metabolism	0.03
BL	KO.IGF1_VEH	R-HSA-5661231	Metallothioneins bind metals	0.03
BL	KO.IGF1_VEH	R-HSA-2142712	Synthesis of 12-eicosatetraenoic acid derivatives	0.04
BL	KO.IGF1_VEH	R-HSA-3000471	Scavenging by Class B Receptors	0.04
BL	KO.IGF1_VEH	R-HSA-5660526	Response to metal ions	0.04
BL	KO.IGF1_VEH	R-HSA-2142770	Synthesis of 15-eicosatetraenoic acid derivatives	0.05
BL	WTF.IGF1_VEH	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	0.00
BL	WTF.IGF1_VEH	R-HSA-449147	Signaling by Interleukins	0.00
BL	WTF.IGF1_VEH	R-HSA-1280215	Cytokine Signaling in Immune system	0.00
BL	WTF.IGF1_VEH	R-HSA-168256	Immune System	0.00
BL	WTF.IGF1_VEH	R-HSA-216083	Integrin cell surface interactions	0.02
BL	WTF.IGF1_VEH	R-HSA-114608	Platelet degranulation	0.03
BL	WTF.IGF1_VEH	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	0.03

BL	WTF.IGF1_VEH	R-HSA-173736	Alternative complement activation	0.03
BL	WTF.IGF1_VEH	R-HSA-1566977	Fibronectin matrix formation	0.03
BL	WTF.IGF1_VEH	R-HSA-9025106	Biosynthesis of DPAn-6 SPMs	0.03
BL	WTF.IGF1_VEH	R-HSA-9700645	ALK mutants bind TKIs	0.03
BL	WTF.IGF1_VEH	R-HSA-9026286	Biosynthesis of DPAn-3-derived protectins and resolvins	0.03
BL	WTF.IGF1_VEH	R-HSA-202733	Cell surface interactions at the vascular wall	0.03
BL	WTF.IGF1_VEH	R-HSA-9018681	Biosynthesis of protectins	0.03
BL	WTF.IGF1_VEH	R-HSA-9023661	Biosynthesis of E-series 18(R)-resolvins	0.03
BL	WTF.IGF1_VEH	R-HSA-109582	Hemostasis	0.03
BL	WTF.IGF1_VEH	R-HSA-419408	Lysosphingolipid and LPA receptors	0.03
BL	WTF.IGF1_VEH	R-HSA-2142712	Synthesis of 12-eicosatetraenoic acid derivatives	0.03
BL	WTF.IGF1_VEH	R-HSA-354194	GRB2:SOS provides linkage to MAPK signaling for Integrins	0.03
BL	WTF.IGF1_VEH	R-HSA-76002	Platelet activation, signaling and aggregation	0.03
BL	WTF.IGF1_VEH	R-HSA-372708	p130Cas linkage to MAPK signaling for integrins	0.03
BL	WTF.IGF1_VEH	R-HSA-2142770	Synthesis of 15-eicosatetraenoic acid derivatives	0.03
BL	WTF.IGF1_VEH	R-HSA-9018896	Biosynthesis of E-series 18(S)-resolvins	0.03
BL	WTF.IGF1_VEH	R-HSA-9725371	Nuclear events stimulated by ALK signaling in cancer	0.03
BL	WTF.IGF1_VEH	R-HSA-1474244	Extracellular matrix organization	0.03
BL	WTF.IGF1_VEH	R-HSA-3000170	Syndecan interactions	0.03
BL	WTF.IGF1_VEH	R-HSA-9025094	Biosynthesis of DPAn-3 SPMs	0.03
BL	WTF.IGF1_VEH	R-HSA-8874081	MET activates PTK2 signaling	0.03
BL	WTF.IGF1_VEH	R-HSA-9018679	Biosynthesis of EPA-derived SPMs	0.03
BL	WTF.IGF1_VEH	R-HSA-9018683	Biosynthesis of DPA-derived SPMs	0.03
BL	WTF.IGF1_VEH	R-HSA-2129379	Molecules associated with elastic fibres	0.03
BL	WTF.IGF1_VEH	R-HSA-354192	Integrin signaling	0.03
BL	WTF.IGF1_VEH	R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	0.03
BL	WTF.IGF1_VEH	R-HSA-6802948	Signaling by high-kinase activity BRAF mutants	0.03
BL	WTF.IGF1_VEH	R-HSA-8875878	MET promotes cell motility	0.03
BL	WTF.IGF1_VEH	R-HSA-1566948	Elastic fibre formation	0.03

BL	WTF.IGF1_VEH	R-HSA-5674135	MAP2K and MAPK activation	0.03
BL	WTF.IGF1_VEH	R-HSA-9656223	Signaling by RAF1 mutants	0.03
BL	WTF.IGF1_VEH	R-HSA-2142691	Synthesis of Leukotrienes (LT) and Eoxins (EX)	0.03
BL	WTF.IGF1_VEH	R-HSA-76009	Platelet Aggregation (Plug Formation)	0.03
BL	WTF.IGF1_VEH	R-HSA-9649948	Signaling downstream of RAS mutants	0.03
BL	WTF.IGF1_VEH	R-HSA-6802946	Signaling by moderate kinase activity BRAF mutants	0.03
BL	WTF.IGF1_VEH	R-HSA-6802955	Paradoxical activation of RAF signaling by kinase inactive BRAF	0.03
BL	WTF.IGF1_VEH	R-HSA-6802949	Signaling by RAS mutants	0.03
BL	WTF.IGF1_VEH	R-HSA-6798695	Neutrophil degranulation	0.03
BL	WTF.IGF1_VEH	R-HSA-3000171	Non-integrin membrane-ECM interactions	0.04
BL	WTF.IGF1_VEH	R-HSA-9725370	Signaling by ALK fusions and activated point mutants	0.04
BL	WTF.IGF1_VEH	R-HSA-9700206	Signaling by ALK in cancer	0.04
BL	WTF.IGF1_VEH	R-HSA-6802952	Signaling by BRAF and RAF1 fusions	0.05
BL	WTF.IGF1_VEH	R-HSA-3000178	ECM proteoglycans	0.05
BL	IGF1.KO_WTM	R-HSA-1280215	Cytokine Signaling in Immune system	0.00
BL	IGF1.KO_WTM	R-HSA-380108	Chemokine receptors bind chemokines	0.00
BL	IGF1.KO_WTM	R-HSA-168256	Immune System	0.00
BL	IGF1.KO_WTM	R-HSA-6783783	Interleukin-10 signaling	0.00
BL	IGF1.KO_WTM	R-HSA-913531	Interferon Signaling	0.00
BL	IGF1.KO_WTM	R-HSA-909733	Interferon alpha/beta signaling	0.00
BL	IGF1.KO_WTM	R-HSA-375276	Peptide ligand-binding receptors	0.00
BL	IGF1.KO_WTM	R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	0.00
BL	IGF1.KO_WTM	R-HSA-449147	Signaling by Interleukins	0.00
BL	IGF1.KO_WTM	R-HSA-500792	GPCR ligand binding	0.01
BL	IGF1.KO_WTM	R-HSA-418594	G alpha (i) signalling events	0.01
BL	IGF1.KO_WTM	R-HSA-372790	Signaling by GPCR	0.01
BL	IGF1.KO_WTM	R-HSA-9701898	STAT3 nuclear events downstream of ALK signaling	0.01
BL	IGF1.KO_WTM	R-HSA-162582	Signal Transduction	0.01
BL	IGF1.KO_WTM	R-HSA-877300	Interferon gamma signaling	0.03

BL	IGF1.KO_WTM	R-HSA-114608	Platelet degranulation	0.04
BL	IGF1.KO_WTM	R-HSA-76002	Platelet activation, signaling and aggregation	0.04
BL	IGF1.KO_WTM	R-HSA-201556	Signaling by ALK	0.04
BL	IGF1.KO_WTM	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	0.04
BL	VEH.KO_WTM	R-HSA-909733	Interferon alpha/beta signaling	0.00
BL	VEH.KO_WTM	R-HSA-8957275	Post-translational protein phosphorylation	0.00
BL	VEH.KO_WTM	R-HSA-8963898	Plasma lipoprotein assembly	0.00
BL	VEH.KO_WTM	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	0.00
BL	VEH.KO_WTM	R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	0.00
BL	VEH.KO_WTM	R-HSA-168256	Immune System	0.00
BL	VEH.KO_WTM	R-HSA-8963901	Chylomicron remodeling	0.00
BL	VEH.KO_WTM	R-HSA-913531	Interferon Signaling	0.00
BL	VEH.KO_WTM	R-HSA-8963899	Plasma lipoprotein remodeling	0.00
BL	VEH.KO_WTM	R-HSA-1280215	Cytokine Signaling in Immune system	0.00
BL	VEH.KO_WTM	R-HSA-8963888	Chylomicron assembly	0.00
BL	VEH.KO_WTM	R-HSA-5686938	Regulation of TLR by endogenous ligand	0.00
BL	VEH.KO_WTM	R-HSA-1989781	PPARA activates gene expression	0.00
BL	VEH.KO_WTM	R-HSA-400206	Regulation of lipid metabolism by PPARalpha	0.00
BL	VEH.KO_WTM	R-HSA-114608	Platelet degranulation	0.00
BL	VEH.KO_WTM	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	0.00
BL	VEH.KO_WTM	R-HSA-5602498	MyD88 deficiency (TLR2/4)	0.00
BL	VEH.KO_WTM	R-HSA-5603041	IRAK4 deficiency (TLR2/4)	0.00
BL	VEH.KO_WTM	R-HSA-975634	Retinoid metabolism and transport	0.00
BL	VEH.KO_WTM	R-HSA-6806667	Metabolism of fat-soluble vitamins	0.00
BL	VEH.KO_WTM	R-HSA-9029569	NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	0.00
BL	VEH.KO_WTM	R-HSA-8964043	Plasma lipoprotein clearance	0.00
BL	VEH.KO_WTM	R-HSA-5602358	Diseases associated with the TLR signaling cascade	0.00
BL	VEH.KO_WTM	R-HSA-5260271	Diseases of Immune System	0.00
BL	VEH.KO_WTM	R-HSA-140877	Formation of Fibrin Clot (Clotting Cascade)	0.00

BL	VEH.KO_WTM	R-HSA-8964058	HDL remodeling	0.00
BL	VEH.KO_WTM	R-HSA-140875	Common Pathway of Fibrin Clot Formation	0.00
BL	VEH.KO_WTM	R-HSA-9024446	NR1H2 and NR1H3-mediated signaling	0.00
BL	VEH.KO_WTM	R-HSA-8866423	VLDL assembly	0.00
BL	VEH.KO_WTM	R-HSA-8964046	VLDL clearance	0.00
BL	VEH.KO_WTM	R-HSA-168898	Toll-like Receptor Cascades	0.00
BL	VEH.KO_WTM	R-HSA-189483	Heme degradation	0.00
BL	VEH.KO_WTM	R-HSA-2187338	Visual phototransduction	0.00
BL	VEH.KO_WTM	R-HSA-76002	Platelet activation, signaling and aggregation	0.00
BL	VEH.KO_WTM	R-HSA-354194	GRB2:SOS provides linkage to MAPK signaling for Integrins	0.00
BL	VEH.KO_WTM	R-HSA-372708	p130Cas linkage to MAPK signaling for integrins	0.01
BL	VEH.KO_WTM	R-HSA-6798695	Neutrophil degranulation	0.01
BL	VEH.KO_WTM	R-HSA-166016	Toll Like Receptor 4 (TLR4) Cascade	0.01
BL	VEH.KO_WTM	R-HSA-168249	Innate Immune System	0.01
BL	VEH.KO_WTM	R-HSA-166058	MyD88:MAL(TIRAP) cascade initiated on plasma membrane	0.01
BL	VEH.KO_WTM	R-HSA-168188	Toll Like Receptor TLR6:TLR2 Cascade	0.01
BL	VEH.KO_WTM	R-HSA-196854	Metabolism of vitamins and cofactors	0.01
BL	VEH.KO_WTM	R-HSA-168179	Toll Like Receptor TLR1:TLR2 Cascade	0.01
BL	VEH.KO_WTM	R-HSA-181438	Toll Like Receptor 2 (TLR2) Cascade	0.01
BL	VEH.KO_WTM	R-HSA-8964026	Chylomicron clearance	0.01
BL	VEH.KO_WTM	R-HSA-1430728	Metabolism	0.01
BL	VEH.KO_WTM	R-HSA-189445	Metabolism of porphyrins	0.01
BL	VEH.KO_WTM	R-HSA-354192	Integrin signaling	0.02
BL	VEH.KO_WTM	R-HSA-216083	Integrin cell surface interactions	0.02
BL	VEH.KO_WTM	R-HSA-977225	Amyloid fiber formation	0.02
BL	VEH.KO_WTM	R-HSA-6799990	Metal sequestration by antimicrobial proteins	0.02
BL	VEH.KO_WTM	R-HSA-6802948	Signaling by high-kinase activity BRAF mutants	0.02
BL	VEH.KO_WTM	R-HSA-6785807	Interleukin-4 and Interleukin-13 signaling	0.02
BL	VEH.KO_WTM	R-HSA-1169410	Antiviral mechanism by IFN-stimulated genes	0.02

BL	VEH.KO_WTM	R-HSA-5674135	MAP2K and MAPK activation	0.03
BL	VEH.KO_WTM	R-HSA-9656223	Signaling by RAF1 mutants	0.03
BL	VEH.KO_WTM	R-HSA-3000480	Scavenging by Class A Receptors	0.03
BL	VEH.KO_WTM	R-HSA-5661231	Metallothioneins bind metals	0.03
BL	VEH.KO_WTM	R-HSA-449147	Signaling by Interleukins	0.03
BL	VEH.KO_WTM	R-HSA-76009	Platelet Aggregation (Plug Formation)	0.03
BL	VEH.KO_WTM	R-HSA-1059683	Interleukin-6 signaling	0.03
BL	VEH.KO_WTM	R-HSA-556833	Metabolism of lipids	0.03
BL	VEH.KO_WTM	R-HSA-6802946	Signaling by moderate kinase activity BRAF mutants	0.03
BL	VEH.KO_WTM	R-HSA-9649948	Signaling downstream of RAS mutants	0.03
BL	VEH.KO_WTM	R-HSA-6802955	Paradoxical activation of RAF signaling by kinase inactive BRAF	0.03
BL	VEH.KO_WTM	R-HSA-6802949	Signaling by RAS mutants	0.03
BL	VEH.KO_WTM	R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	0.03
BL	VEH.KO_WTM	R-HSA-8963896	HDL assembly	0.03
BL	VEH.KO_WTM	R-HSA-1236974	ER-Phagosome pathway	0.03
BL	VEH.KO_WTM	R-HSA-1474244	Extracellular matrix organization	0.04
BL	VEH.KO_WTM	R-HSA-3000471	Scavenging by Class B Receptors	0.04
BL	VEH.KO_WTM	R-HSA-5660526	Response to metal ions	0.04
BL	KOIGF1_WTMVEH	R-HSA-6783783	Interleukin-10 signaling	0.01
BL	KOIGF1_WTMVEH	R-HSA-909733	Interferon alpha/beta signaling	0.02
BL	KOIGF1_WTMVEH	R-HSA-1280215	Cytokine Signaling in Immune system	0.03
BL	KOIGF1_WTMVEH	R-HSA-111957	Cam-PDE 1 activation	0.03

Supplementary Table 12 – Reactome Analysis from Chapter II Male Mice
All significant pathways found in Reactome analysis of Male mice treated with rhIGF1 or vehicle.
Legend:
CRB = Cerebellum, BL = Blood,
KO.IGF1_VEH = rhIGF1 treated *Mecp2*$^{-/y}$ vs. VEH treated *Mecp2*$^{-/y}$,
WTM.IGF1_VEH = rhIGF1 treated *Mecp2*$^{+/y}$ vs. VEH treated *Mecp2*$^{+/y}$,
IGF1.KO_WTM= rhIGF1 treated *Mecp2*$^{-/y}$ vs. rhIGF1 treated *Mecp2*$^{+/y}$,
VEH.KO_WTM = VEH treated *Mecp2*$^{-/y}$ vs. VEH treated *Mecp2*$^{+/y}$,
KOIGF1_WTMVEH = IGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/y}$

Tissue	Comparison	GO biological process complete	upload_1 (FDR)
CRB	HET.IGF1_VEH	neurofilament bundle assembly (GO:0033693)	4.75E-02

CRB	HET.IGF1_VEH	NMDA selective glutamate receptor signaling pathway (GO:0098989)	4.70E-02
CRB	HET.IGF1_VEH	commitment of neuronal cell to specific neuron type in forebrain (GO:0021902)	7.73E-03
CRB	HET.IGF1_VEH	forebrain neuron fate commitment (GO:0021877)	8.18E-04
CRB	HET.IGF1_VEH	positive regulation of steroid hormone secretion (GO:2000833)	2.17E-02
CRB	HET.IGF1_VEH	regulation of inositol phosphate biosynthetic process (GO:0010919)	3.09E-02
CRB	HET.IGF1_VEH	regulation of modification of synaptic structure (GO:1905244)	3.35E-02
CRB	HET.IGF1_VEH	dentate gyrus development (GO:0021542)	3.72E-02
CRB	HET.IGF1_VEH	regulation of dopamine metabolic process (GO:0042053)	4.88E-02
CRB	HET.IGF1_VEH	positive regulation of behavior (GO:0048520)	2.01E-02
CRB	HET.IGF1_VEH	long-term synaptic potentiation (GO:0060291)	7.76E-03
CRB	HET.IGF1_VEH	forebrain neuron differentiation (GO:0021879)	8.77E-03
CRB	HET.IGF1_VEH	regulation of alcohol biosynthetic process (GO:1902930)	3.29E-02
CRB	HET.IGF1_VEH	neuron fate commitment (GO:0048663)	2.59E-03
CRB	HET.IGF1_VEH	positive regulation of amine transport (GO:0051954)	3.77E-02
CRB	HET.IGF1_VEH	cellular response to calcium ion (GO:0071277)	3.01E-03
CRB	HET.IGF1_VEH	regulation of endocrine process (GO:0044060)	3.99E-02
CRB	HET.IGF1_VEH	multicellular organismal response to stress (GO:0033555)	8.60E-04
CRB	HET.IGF1_VEH	negative regulation of G protein-coupled receptor signaling pathway (GO:0045744)	4.84E-02
CRB	HET.IGF1_VEH	forebrain generation of neurons (GO:0021872)	1.52E-02
CRB	HET.IGF1_VEH	feeding behavior (GO:0007631)	8.78E-03
CRB	HET.IGF1_VEH	neuropeptide signaling pathway (GO:0007218)	2.73E-02
CRB	HET.IGF1_VEH	associative learning (GO:0008306)	1.22E-02
CRB	HET.IGF1_VEH	regulation of amine transport (GO:0051952)	1.28E-02
CRB	HET.IGF1_VEH	central nervous system neuron development (GO:0021954)	4.26E-02
CRB	HET.IGF1_VEH	positive regulation of synaptic transmission (GO:0050806)	2.42E-03
CRB	HET.IGF1_VEH	response to calcium ion (GO:0051592)	1.86E-02
CRB	HET.IGF1_VEH	regulation of G protein-coupled receptor signaling pathway (GO:0008277)	2.19E-02
CRB	HET.IGF1_VEH	learning (GO:0007612)	3.99E-03
CRB	HET.IGF1_VEH	regulation of synaptic plasticity (GO:0048167)	6.08E-04
CRB	HET.IGF1_VEH	cellular response to metal ion (GO:0071248)	1.10E-02
CRB	HET.IGF1_VEH	cellular response to inorganic substance (GO:0071241)	1.90E-02
CRB	HET.IGF1_VEH	learning or memory (GO:0007611)	8.34E-04
CRB	HET.IGF1_VEH	cognition (GO:0050890)	7.07E-04
CRB	HET.IGF1_VEH	chemical synaptic transmission (GO:0007268)	6.47E-04
CRB	HET.IGF1_VEH	anterograde trans-synaptic signaling (GO:0098916)	5.82E-04
CRB	HET.IGF1_VEH	behavior (GO:0007610)	3.04E-08
CRB	HET.IGF1_VEH	central nervous system neuron differentiation (GO:0021953)	3.22E-02
CRB	HET.IGF1_VEH	trans-synaptic signaling (GO:0099537)	7.89E-04
CRB	HET.IGF1_VEH	synaptic signaling (GO:0099536)	1.60E-03

CRB	HET.IGF1_VEH	regulation of transmembrane transporter activity (GO:0022898)	2.90E-02
CRB	HET.IGF1_VEH	response to metal ion (GO:0010038)	3.16E-02
CRB	HET.IGF1_VEH	positive regulation of ion transport (GO:0043270)	1.77E-02
CRB	HET.IGF1_VEH	regulation of transporter activity (GO:0032409)	3.59E-02
CRB	HET.IGF1_VEH	axon development (GO:0061564)	1.34E-02
CRB	HET.IGF1_VEH	regulation of ion transport (GO:0043269)	9.02E-05
CRB	HET.IGF1_VEH	positive regulation of secretion by cell (GO:1903532)	2.75E-02
CRB	HET.IGF1_VEH	modulation of chemical synaptic transmission (GO:0050804)	2.51E-03
CRB	HET.IGF1_VEH	regulation of trans-synaptic signaling (GO:0099177)	2.45E-03
CRB	HET.IGF1_VEH	response to inorganic substance (GO:0010035)	8.76E-03
CRB	HET.IGF1_VEH	positive regulation of secretion (GO:0051047)	1.86E-02
CRB	HET.IGF1_VEH	regulation of metal ion transport (GO:0010959)	2.68E-02
CRB	HET.IGF1_VEH	cell morphogenesis involved in neuron differentiation (GO:0048667)	3.09E-02
CRB	HET.IGF1_VEH	secretion (GO:0046903)	1.84E-02
CRB	HET.IGF1_VEH	positive regulation of cell adhesion (GO:0045785)	3.71E-02
CRB	HET.IGF1_VEH	regulation of system process (GO:0044057)	1.01E-02
CRB	HET.IGF1_VEH	neuron projection morphogenesis (GO:0048812)	4.80E-02
CRB	HET.IGF1_VEH	regulation of ion transmembrane transport (GO:0034765)	4.87E-02
CRB	HET.IGF1_VEH	plasma membrane bounded cell projection morphogenesis (GO:0120039)	5.04E-02
CRB	HET.IGF1_VEH	regulation of secretion by cell (GO:1903530)	1.45E-02
CRB	HET.IGF1_VEH	cell-cell signaling (GO:0007267)	4.66E-03
CRB	HET.IGF1_VEH	regulation of secretion (GO:0051046)	1.29E-02
CRB	HET.IGF1_VEH	regulation of transmembrane transport (GO:0034762)	4.99E-02
CRB	HET.IGF1_VEH	neuron differentiation (GO:0030182)	8.33E-04
CRB	HET.IGF1_VEH	generation of neurons (GO:0048699)	1.42E-04
CRB	HET.IGF1_VEH	neuron projection development (GO:0031175)	2.40E-02
CRB	HET.IGF1_VEH	neuron development (GO:0048666)	7.51E-03
CRB	HET.IGF1_VEH	neurogenesis (GO:0022008)	5.04E-04
CRB	HET.IGF1_VEH	positive regulation of transport (GO:0051050)	1.16E-02
CRB	HET.IGF1_VEH	central nervous system development (GO:0007417)	3.68E-02
CRB	HET.IGF1_VEH	positive regulation of cell differentiation (GO:0045597)	2.86E-02
CRB	HET.IGF1_VEH	nervous system development (GO:0007399)	9.24E-05
CRB	HET.IGF1_VEH	regulation of transport (GO:0051049)	7.40E-04
CRB	HET.IGF1_VEH	positive regulation of developmental process (GO:0051094)	7.40E-03
CRB	HET.IGF1_VEH	positive regulation of multicellular organismal process (GO:0051240)	5.08E-03
CRB	HET.IGF1_VEH	movement of cell or subcellular component (GO:0006928)	8.88E-03
CRB	HET.IGF1_VEH	regulation of multicellular organismal development (GO:2000026)	1.87E-02
CRB	HET.IGF1_VEH	regulation of cell differentiation (GO:0045595)	2.02E-02
CRB	HET.IGF1_VEH	regulation of localization (GO:0032879)	2.94E-04
CRB	HET.IGF1_VEH	regulation of developmental process (GO:0050793)	1.40E-02

CRB	HET.IGF1_VEH	regulation of multicellular organismal process (GO:0051239)	7.35E-03
CRB	HET.IGF1_VEH	regulation of biological quality (GO:0065008)	8.91E-04
CRB	HET.IGF1_VEH	regulation of cell communication (GO:0010646)	7.65E-03
CRB	HET.IGF1_VEH	regulation of signaling (GO:0023051)	7.53E-03
CRB	HET.IGF1_VEH	positive regulation of nitrogen compound metabolic process (GO:0051173)	4.46E-02
CRB	HET.IGF1_VEH	system development (GO:0048731)	2.65E-03
CRB	HET.IGF1_VEH	multicellular organism development (GO:0007275)	5.90E-03
CRB	HET.IGF1_VEH	localization (GO:0051179)	1.03E-02
CRB	HET.IGF1_VEH	developmental process (GO:0032502)	8.18E-03
CRB	HET.IGF1_VEH	anatomical structure development (GO:0048856)	2.16E-02
CRB	HET.IGF1_VEH	positive regulation of cellular process (GO:0048522)	2.59E-02
CRB	HET.IGF1_VEH	multicellular organismal process (GO:0032501)	7.23E-03
CRB	IGF1.HET_WTF	positive regulation of epinephrine secretion (GO:0032812)	4.84E-02
CRB	IGF1.HET_WTF	intermediate filament polymerization or depolymerization (GO:0045105)	4.75E-02
CRB	IGF1.HET_WTF	regulation of glucocorticoid secretion (GO:2000849)	2.61E-02
CRB	IGF1.HET_WTF	negative regulation of potassium ion transport (GO:0043267)	3.13E-03
CRB	IGF1.HET_WTF	neuropeptide signaling pathway (GO:0007218)	1.60E-06
CRB	IGF1.HET_WTF	long-term memory (GO:0007616)	3.39E-02
CRB	IGF1.HET_WTF	multicellular organismal response to stress (GO:0033555)	8.06E-03
CRB	IGF1.HET_WTF	associative learning (GO:0008306)	3.26E-03
CRB	IGF1.HET_WTF	regulation of amine transport (GO:0051952)	3.09E-03
CRB	IGF1.HET_WTF	sensory perception of pain (GO:0019233)	1.26E-02
CRB	IGF1.HET_WTF	regulation of heart rate (GO:0002027)	1.62E-02
CRB	IGF1.HET_WTF	regulation of potassium ion transport (GO:0043266)	1.58E-02
CRB	IGF1.HET_WTF	regulation of G protein-coupled receptor signaling pathway (GO:0008277)	3.39E-02
CRB	IGF1.HET_WTF	learning (GO:0007612)	5.27E-03
CRB	IGF1.HET_WTF	regulation of nervous system process (GO:0031644)	5.23E-03
CRB	IGF1.HET_WTF	adult behavior (GO:0030534)	5.03E-03
CRB	IGF1.HET_WTF	regulation of blood pressure (GO:0008217)	1.28E-02
CRB	IGF1.HET_WTF	chemical synaptic transmission (GO:0007268)	8.60E-04
CRB	IGF1.HET_WTF	anterograde trans-synaptic signaling (GO:0098916)	7.74E-04
CRB	IGF1.HET_WTF	trans-synaptic signaling (GO:0099537)	1.05E-03
CRB	IGF1.HET_WTF	learning or memory (GO:0007611)	5.41E-03
CRB	IGF1.HET_WTF	regulation of neurotransmitter levels (GO:0001505)	2.63E-02
CRB	IGF1.HET_WTF	synaptic signaling (GO:0099536)	8.43E-04
CRB	IGF1.HET_WTF	synapse organization (GO:0050808)	1.95E-02
CRB	IGF1.HET_WTF	cognition (GO:0050890)	1.18E-02
CRB	IGF1.HET_WTF	behavior (GO:0007610)	8.81E-06
CRB	IGF1.HET_WTF	blood circulation (GO:0008015)	3.17E-03
CRB	IGF1.HET_WTF	modulation of chemical synaptic transmission (GO:0050804)	1.21E-03

CRB	IGF1.HET_WTF	regulation of trans-synaptic signaling (GO:0099177)	1.13E-03
CRB	IGF1.HET_WTF	regulation of system process (GO:0044057)	2.05E-04
CRB	IGF1.HET_WTF	circulatory system process (GO:0003013)	5.28E-03
CRB	IGF1.HET_WTF	regulation of ion transport (GO:0043269)	2.56E-04
CRB	IGF1.HET_WTF	export from cell (GO:0140352)	4.09E-02
CRB	IGF1.HET_WTF	regulation of metal ion transport (GO:0010959)	4.39E-02
CRB	IGF1.HET_WTF	regulation of neurogenesis (GO:0050767)	4.38E-02
CRB	IGF1.HET_WTF	regulation of secretion (GO:0051046)	2.90E-03
CRB	IGF1.HET_WTF	regulation of neuron projection development (GO:0010975)	4.93E-02
CRB	IGF1.HET_WTF	cell-cell signaling (GO:0007267)	2.84E-03
CRB	IGF1.HET_WTF	regulation of secretion by cell (GO:1903530)	2.57E-02
CRB	IGF1.HET_WTF	response to organonitrogen compound (GO:0010243)	2.56E-02
CRB	IGF1.HET_WTF	positive regulation of transport (GO:0051050)	3.28E-03
CRB	IGF1.HET_WTF	cell adhesion (GO:0007155)	2.46E-02
CRB	IGF1.HET_WTF	biological adhesion (GO:0022610)	2.57E-02
CRB	IGF1.HET_WTF	response to nitrogen compound (GO:1901698)	2.59E-02
CRB	IGF1.HET_WTF	regulation of transport (GO:0051049)	6.34E-05
CRB	IGF1.HET_WTF	response to endogenous stimulus (GO:0009719)	1.28E-02
CRB	IGF1.HET_WTF	positive regulation of multicellular organismal process (GO:0051240)	3.14E-03
CRB	IGF1.HET_WTF	regulation of multicellular organismal development (GO:2000026)	3.28E-02
CRB	IGF1.HET_WTF	regulation of localization (GO:0032879)	1.97E-04
CRB	IGF1.HET_WTF	regulation of multicellular organismal process (GO:0051239)	8.98E-04
CRB	IGF1.HET_WTF	regulation of cell communication (GO:0010646)	2.60E-02
CRB	IGF1.HET_WTF	regulation of signaling (GO:0023051)	2.65E-02
CRB	IGF1.HET_WTF	multicellular organismal process (GO:0032501)	1.44E-02
CRB	IGF1.HET_WTF	nucleic acid metabolic process (GO:0090304)	3.39E-02
CRB	VEH.HET_WTF	neurofilament bundle assembly (GO:0033693)	0.00138
CRB	VEH.HET_WTF	intermediate filament polymerization or depolymerization (GO:0045105)	0.0236
CRB	VEH.HET_WTF	cellular response to corticotropin-releasing hormone stimulus (GO:0071376)	0.00202
CRB	VEH.HET_WTF	response to corticotropin-releasing hormone (GO:0043435)	0.00199
CRB	VEH.HET_WTF	positive regulation of corticosterone secretion (GO:2000854)	0.0341
CRB	VEH.HET_WTF	NMDA selective glutamate receptor signaling pathway (GO:0098989)	0.0339
CRB	VEH.HET_WTF	regulation of corticosterone secretion (GO:2000852)	0.00402
CRB	VEH.HET_WTF	positive regulation of glucocorticoid secretion (GO:2000851)	0.00397
CRB	VEH.HET_WTF	positive regulation of cortisol secretion (GO:0051464)	0.0457
CRB	VEH.HET_WTF	intermediate filament bundle assembly (GO:0045110)	0.00498
CRB	VEH.HET_WTF	regulation of glucocorticoid secretion (GO:2000849)	0.000821
CRB	VEH.HET_WTF	positive regulation of corticosteroid hormone secretion (GO:2000848)	0.00801
CRB	VEH.HET_WTF	response to salt (GO:1902074)	0.00999

CRB	VEH.HET_WTF	neurofilament cytoskeleton organization (GO:0060052)	0.0122
CRB	VEH.HET_WTF	positive regulation of steroid hormone secretion (GO:2000833)	0.0181
CRB	VEH.HET_WTF	regulation of corticosteroid hormone secretion (GO:2000846)	0.00264
CRB	VEH.HET_WTF	ionotropic glutamate receptor signaling pathway (GO:0035235)	0.0209
CRB	VEH.HET_WTF	negative regulation of feeding behavior (GO:2000252)	0.0236
CRB	VEH.HET_WTF	regulation of NMDA receptor activity (GO:2000310)	0.000563
CRB	VEH.HET_WTF	response to amphetamine (GO:0001975)	0.00402
CRB	VEH.HET_WTF	cellular response to fluid shear stress (GO:0071498)	0.0255
CRB	VEH.HET_WTF	response to amine (GO:0014075)	0.00497
CRB	VEH.HET_WTF	regulation of modification of synaptic structure (GO:1905244)	0.0282
CRB	VEH.HET_WTF	regulation of steroid hormone secretion (GO:2000831)	0.00555
CRB	VEH.HET_WTF	mitochondrion transport along microtubule (GO:0047497)	0.0461
CRB	VEH.HET_WTF	establishment of mitochondrion localization, microtubule-mediated (GO:0034643)	0.0459
CRB	VEH.HET_WTF	ammonium ion metabolic process (GO:0097164)	0.0457
CRB	VEH.HET_WTF	positive regulation of behavior (GO:0048520)	0.00216
CRB	VEH.HET_WTF	cellular response to calcium ion (GO:0071277)	5.46E-06
CRB	VEH.HET_WTF	long-term synaptic potentiation (GO:0060291)	0.000989
CRB	VEH.HET_WTF	neuropeptide signaling pathway (GO:0007218)	1.17E-05
CRB	VEH.HET_WTF	regulation of feeding behavior (GO:0060259)	0.0197
CRB	VEH.HET_WTF	regulation of endocrine process (GO:0044060)	0.00567
CRB	VEH.HET_WTF	regulation of cAMP-mediated signaling (GO:0043949)	0.0316
CRB	VEH.HET_WTF	positive regulation of synaptic transmission (GO:0050806)	4.5E-07
CRB	VEH.HET_WTF	intermediate filament cytoskeleton organization (GO:0045104)	0.0353
CRB	VEH.HET_WTF	sensory perception of pain (GO:0019233)	0.000262
CRB	VEH.HET_WTF	response to ethanol (GO:0045471)	0.0119
CRB	VEH.HET_WTF	positive regulation of amine transport (GO:0051954)	0.037
CRB	VEH.HET_WTF	intermediate filament-based process (GO:0045103)	0.0368
CRB	VEH.HET_WTF	feeding behavior (GO:0007631)	0.000265
CRB	VEH.HET_WTF	regulation of neurotransmitter receptor activity (GO:0099601)	0.0137
CRB	VEH.HET_WTF	regulation of catecholamine secretion (GO:0050433)	0.0136
CRB	VEH.HET_WTF	positive regulation of blood pressure (GO:0045777)	0.0436
CRB	VEH.HET_WTF	regulation of smooth muscle contraction (GO:0006940)	0.0138
CRB	VEH.HET_WTF	response to calcium ion (GO:0051592)	0.00014
CRB	VEH.HET_WTF	regulation of behavior (GO:0050795)	0.00147
CRB	VEH.HET_WTF	cellular response to metal ion (GO:0071248)	1.64E-05
CRB	VEH.HET_WTF	multicellular organismal response to stress (GO:0033555)	0.00653
CRB	VEH.HET_WTF	regulation of synaptic transmission, glutamatergic (GO:0051966)	0.0208
CRB	VEH.HET_WTF	regulation of amine transport (GO:0051952)	0.00288

CRB	VEH.HET_WTF	negative regulation of myeloid cell differentiation (GO:0045638)	0.0272
CRB	VEH.HET_WTF	cellular response to inorganic substance (GO:0071241)	4.56E-05
CRB	VEH.HET_WTF	regulation of synaptic plasticity (GO:0048167)	5.98E-06
CRB	VEH.HET_WTF	regulation of neurotransmitter transport (GO:0051588)	0.00139
CRB	VEH.HET_WTF	associative learning (GO:0008306)	0.0148
CRB	VEH.HET_WTF	hormone transport (GO:0009914)	0.0387
CRB	VEH.HET_WTF	regulation of blood pressure (GO:0008217)	0.00014
CRB	VEH.HET_WTF	adult behavior (GO:0030534)	0.00126
CRB	VEH.HET_WTF	regulation of neurotransmitter secretion (GO:0046928)	0.0208
CRB	VEH.HET_WTF	regulation of systemic arterial blood pressure (GO:0003073)	0.0217
CRB	VEH.HET_WTF	chemical synaptic transmission (GO:0007268)	4.07E-06
CRB	VEH.HET_WTF	anterograde trans-synaptic signaling (GO:0098916)	3.56E-06
CRB	VEH.HET_WTF	regulation of G protein-coupled receptor signaling pathway (GO:0008277)	0.0272
CRB	VEH.HET_WTF	memory (GO:0007613)	0.0126
CRB	VEH.HET_WTF	regulation of neurotransmitter levels (GO:0001505)	0.000407
CRB	VEH.HET_WTF	trans-synaptic signaling (GO:0099537)	5.52E-06
CRB	VEH.HET_WTF	modulation of chemical synaptic transmission (GO:0050804)	3.92E-08
CRB	VEH.HET_WTF	regulation of trans-synaptic signaling (GO:0099177)	2.71E-08
CRB	VEH.HET_WTF	response to metal ion (GO:0010038)	0.000265
CRB	VEH.HET_WTF	female pregnancy (GO:0007565)	0.0352
CRB	VEH.HET_WTF	response to inorganic substance (GO:0010035)	2.77E-06
CRB	VEH.HET_WTF	locomotory behavior (GO:0007626)	0.00164
CRB	VEH.HET_WTF	behavior (GO:0007610)	2.65E-10
CRB	VEH.HET_WTF	regulation of cation channel activity (GO:2001257)	0.0215
CRB	VEH.HET_WTF	synaptic signaling (GO:0099536)	1.42E-05
CRB	VEH.HET_WTF	regulation of peptide secretion (GO:0002791)	0.00462
CRB	VEH.HET_WTF	regulation of peptide transport (GO:0090087)	0.00477
CRB	VEH.HET_WTF	learning (GO:0007612)	0.0231
CRB	VEH.HET_WTF	regulation of nervous system process (GO:0031644)	0.0238
CRB	VEH.HET_WTF	regulation of axonogenesis (GO:0050770)	0.0236
CRB	VEH.HET_WTF	regulation of hormone secretion (GO:0046883)	0.00136
CRB	VEH.HET_WTF	regulation of peptide hormone secretion (GO:0090276)	0.0158
CRB	VEH.HET_WTF	negative regulation of secretion (GO:0051048)	0.0316
CRB	VEH.HET_WTF	learning or memory (GO:0007611)	0.00186
CRB	VEH.HET_WTF	cognition (GO:0050890)	0.0011
CRB	VEH.HET_WTF	axon guidance (GO:0007411)	0.0209
CRB	VEH.HET_WTF	neuron projection guidance (GO:0097485)	0.0211
CRB	VEH.HET_WTF	axon development (GO:0061564)	0.000653
CRB	VEH.HET_WTF	regulation of ion transmembrane transporter activity (GO:0032412)	0.0121
CRB	VEH.HET_WTF	regulation of myeloid cell differentiation (GO:0045637)	0.0454
CRB	VEH.HET_WTF	positive regulation of cytosolic calcium ion concentration (GO:0007204)	0.00632

CRB	VEH.HET_WTF	response to peptide hormone (GO:0043434)	0.0139
CRB	VEH.HET_WTF	regulation of transmembrane transporter activity (GO:0022898)	0.0138
CRB	VEH.HET_WTF	regulation of muscle system process (GO:0090257)	0.0267
CRB	VEH.HET_WTF	negative regulation of neuron death (GO:1901215)	0.0266
CRB	VEH.HET_WTF	regulation of neuron death (GO:1901214)	0.00204
CRB	VEH.HET_WTF	regulation of secretion by cell (GO:1903530)	4.68E-06
CRB	VEH.HET_WTF	regulation of cytosolic calcium ion concentration (GO:0051480)	0.0041
CRB	VEH.HET_WTF	axonogenesis (GO:0007409)	0.00473
CRB	VEH.HET_WTF	neuron projection morphogenesis (GO:0048812)	0.000377
CRB	VEH.HET_WTF	regulation of transporter activity (GO:0032409)	0.0178
CRB	VEH.HET_WTF	blood circulation (GO:0008015)	0.00138
CRB	VEH.HET_WTF	plasma membrane bounded cell projection morphogenesis (GO:0120039)	0.000405
CRB	VEH.HET_WTF	cell projection morphogenesis (GO:0048858)	0.000447
CRB	VEH.HET_WTF	regulation of synapse structure or activity (GO:0050803)	0.0351
CRB	VEH.HET_WTF	regulation of secretion (GO:0051046)	5.76E-06
CRB	VEH.HET_WTF	response to peptide (GO:1901652)	0.0127
CRB	VEH.HET_WTF	regulation of hormone levels (GO:0010817)	0.000298
CRB	VEH.HET_WTF	response to xenobiotic stimulus (GO:0009410)	0.0237
CRB	VEH.HET_WTF	cell morphogenesis involved in neuron differentiation (GO:0048667)	0.00215
CRB	VEH.HET_WTF	regulation of system process (GO:0044057)	0.000117
CRB	VEH.HET_WTF	circulatory system process (GO:0003013)	0.00234
CRB	VEH.HET_WTF	cell part morphogenesis (GO:0032990)	0.000732
CRB	VEH.HET_WTF	negative regulation of transport (GO:0051051)	0.00141
CRB	VEH.HET_WTF	secretion (GO:0046903)	0.00145
CRB	VEH.HET_WTF	positive regulation of secretion by cell (GO:1903532)	0.0158
CRB	VEH.HET_WTF	positive regulation of secretion (GO:0051047)	0.0125
CRB	VEH.HET_WTF	cellular response to nitrogen compound (GO:1901699)	0.00217
CRB	VEH.HET_WTF	cellular response to organonitrogen compound (GO:0071417)	0.00693
CRB	VEH.HET_WTF	cell-cell signaling (GO:0007267)	2.49E-05
CRB	VEH.HET_WTF	secretion by cell (GO:0032940)	0.0248
CRB	VEH.HET_WTF	regulation of ion transport (GO:0043269)	0.000223
CRB	VEH.HET_WTF	neuron projection development (GO:0031175)	0.000417
CRB	VEH.HET_WTF	cellular component morphogenesis (GO:0032989)	0.00285
CRB	VEH.HET_WTF	cellular calcium ion homeostasis (GO:0006874)	0.0238
CRB	VEH.HET_WTF	positive regulation of kinase activity (GO:0033674)	0.0436
CRB	VEH.HET_WTF	export from cell (GO:0140352)	0.0467
CRB	VEH.HET_WTF	calcium ion homeostasis (GO:0055074)	0.0291
CRB	VEH.HET_WTF	cellular divalent inorganic cation homeostasis (GO:0072503)	0.0319
CRB	VEH.HET_WTF	response to hormone (GO:0009725)	0.0138
CRB	VEH.HET_WTF	cell morphogenesis involved in differentiation (GO:0000904)	0.0149
CRB	VEH.HET_WTF	positive regulation of cell death (GO:0010942)	0.00635

CRB	VEH.HET_WTF	divalent inorganic cation homeostasis (GO:0072507)	0.0444
CRB	VEH.HET_WTF	cellular response to endogenous stimulus (GO:0071495)	0.00136
CRB	VEH.HET_WTF	regulation of anatomical structure size (GO:0090066)	0.0343
CRB	VEH.HET_WTF	response to organonitrogen compound (GO:0010243)	0.00682
CRB	VEH.HET_WTF	response to nitrogen compound (GO:1901698)	0.00349
CRB	VEH.HET_WTF	neuron development (GO:0048666)	0.00405
CRB	VEH.HET_WTF	regulation of transmembrane transport (GO:0034762)	0.0435
CRB	VEH.HET_WTF	cell morphogenesis (GO:0000902)	0.015
CRB	VEH.HET_WTF	regulation of transport (GO:0051049)	2.34E-06
CRB	VEH.HET_WTF	response to endogenous stimulus (GO:0009719)	0.00213
CRB	VEH.HET_WTF	positive regulation of protein phosphorylation (GO:0001934)	0.0352
CRB	VEH.HET_WTF	neuron differentiation (GO:0030182)	0.00481
CRB	VEH.HET_WTF	cellular response to oxygen-containing compound (GO:1901701)	0.0159
CRB	VEH.HET_WTF	positive regulation of transport (GO:0051050)	0.00831
CRB	VEH.HET_WTF	positive regulation of phosphorylation (GO:0042327)	0.0318
CRB	VEH.HET_WTF	plasma membrane bounded cell projection organization (GO:0120036)	0.00682
CRB	VEH.HET_WTF	positive regulation of phosphorus metabolic process (GO:0010562)	0.0284
CRB	VEH.HET_WTF	positive regulation of phosphate metabolic process (GO:0045937)	0.0283
CRB	VEH.HET_WTF	positive regulation of cell communication (GO:0010647)	0.000266
CRB	VEH.HET_WTF	regulation of anatomical structure morphogenesis (GO:0022603)	0.0222
CRB	VEH.HET_WTF	positive regulation of signaling (GO:0023056)	0.000258
CRB	VEH.HET_WTF	positive regulation of multicellular organismal process (GO:0051240)	0.000559
CRB	VEH.HET_WTF	regulation of hydrolase activity (GO:0051336)	0.0241
CRB	VEH.HET_WTF	negative regulation of multicellular organismal process (GO:0051241)	0.0139
CRB	VEH.HET_WTF	cell projection organization (GO:0030030)	0.012
CRB	VEH.HET_WTF	positive regulation of cell differentiation (GO:0045597)	0.0388
CRB	VEH.HET_WTF	generation of neurons (GO:0048699)	0.00499
CRB	VEH.HET_WTF	response to oxygen-containing compound (GO:1901700)	0.00799
CRB	VEH.HET_WTF	regulation of multicellular organismal development (GO:2000026)	0.00457
CRB	VEH.HET_WTF	positive regulation of transcription by RNA polymerase II (GO:0045944)	0.0167
CRB	VEH.HET_WTF	movement of cell or subcellular component (GO:0006928)	0.00497
CRB	VEH.HET_WTF	positive regulation of catalytic activity (GO:0043085)	0.0386
CRB	VEH.HET_WTF	neurogenesis (GO:0022008)	0.00633
CRB	VEH.HET_WTF	positive regulation of developmental process (GO:0051094)	0.00852
CRB	VEH.HET_WTF	nervous system development (GO:0007399)	0.00125
CRB	VEH.HET_WTF	regulation of localization (GO:0032879)	2.58E-05
CRB	VEH.HET_WTF	regulation of multicellular organismal process (GO:0051239)	3.77E-05
CRB	VEH.HET_WTF	regulation of cell death (GO:0010941)	0.0136

CRB	VEH.HET_WTF	regulation of cell communication (GO:0010646)	3.13E-05
CRB	VEH.HET_WTF	regulation of signaling (GO:0023051)	3.25E-05
CRB	VEH.HET_WTF	regulation of cell differentiation (GO:0045595)	0.0272
CRB	VEH.HET_WTF	regulation of biological quality (GO:0065008)	4.52E-06
CRB	VEH.HET_WTF	positive regulation of biosynthetic process (GO:0009891)	0.0154
CRB	VEH.HET_WTF	regulation of catalytic activity (GO:0050790)	0.0271
CRB	VEH.HET_WTF	positive regulation of cellular biosynthetic process (GO:0031328)	0.0224
CRB	VEH.HET_WTF	positive regulation of macromolecule biosynthetic process (GO:0010557)	0.0392
CRB	VEH.HET_WTF	cellular response to chemical stimulus (GO:0070887)	0.00631
CRB	VEH.HET_WTF	regulation of developmental process (GO:0050793)	0.0136
CRB	VEH.HET_WTF	regulation of molecular function (GO:0065009)	0.0183
CRB	VEH.HET_WTF	system development (GO:0048731)	0.000238
CRB	VEH.HET_WTF	response to chemical (GO:0042221)	0.00203
CRB	VEH.HET_WTF	positive regulation of nitrogen compound metabolic process (GO:0051173)	0.0138
CRB	VEH.HET_WTF	multicellular organism development (GO:0007275)	0.000118
CRB	VEH.HET_WTF	positive regulation of cellular metabolic process (GO:0031325)	0.0135
CRB	VEH.HET_WTF	regulation of signal transduction (GO:0009966)	0.0311
CRB	VEH.HET_WTF	animal organ development (GO:0048513)	0.0254
CRB	VEH.HET_WTF	cell communication (GO:0007154)	0.000265
CRB	VEH.HET_WTF	signaling (GO:0023052)	0.000513
CRB	VEH.HET_WTF	positive regulation of cellular process (GO:0048522)	0.000142
CRB	VEH.HET_WTF	cell differentiation (GO:0030154)	0.0235
CRB	VEH.HET_WTF	anatomical structure development (GO:0048856)	0.000731
CRB	VEH.HET_WTF	transport (GO:0006810)	0.0237
CRB	VEH.HET_WTF	developmental process (GO:0032502)	0.000381
CRB	VEH.HET_WTF	cellular developmental process (GO:0048869)	0.0254
CRB	VEH.HET_WTF	establishment of localization (GO:0051234)	0.0281
CRB	VEH.HET_WTF	multicellular organismal process (GO:0032501)	9.67E-06
CRB	VEH.HET_WTF	positive regulation of biological process (GO:0048518)	0.000503
CRB	VEH.HET_WTF	localization (GO:0051179)	0.0146
CRB	VEH.HET_WTF	signal transduction (GO:0007165)	0.0245
CRB	VEH.HET_WTF	cellular response to stimulus (GO:0051716)	0.0234
CRB	VEH.HET_WTF	regulation of cellular process (GO:0050794)	0.0151
CRB	VEH.HET_WTF	biological regulation (GO:0065007)	0.00769
CRB	VEH.HET_WTF	regulation of biological process (GO:0050789)	0.029
CRB	HETIG1_WTFVEH	positive regulation of epinephrine secretion (GO:0032812)	5.01E-02
CRB	HETIG1_WTFVEH	regulation of corticosterone secretion (GO:2000852)	6.40E-03
CRB	HETIG1_WTFVEH	positive regulation of glucocorticoid secretion (GO:2000851)	5.69E-03
CRB	HETIG1_WTFVEH	regulation of epinephrine secretion (GO:0014060)	9.10E-03
CRB	HETIG1_WTFVEH	regulation of glucocorticoid secretion (GO:2000849)	1.81E-03

CRB	HETIG1_WTFVEH	positive regulation of corticosteroid hormone secretion (GO:2000848)	1.11E-02
CRB	HETIG1_WTFVEH	positive regulation of steroid hormone secretion (GO:2000833)	2.71E-02
CRB	HETIG1_WTFVEH	regulation of corticosteroid hormone secretion (GO:2000846)	5.75E-03
CRB	HETIG1_WTFVEH	regulation of steroid hormone secretion (GO:2000831)	6.51E-03
CRB	HETIG1_WTFVEH	neuropeptide signaling pathway (GO:0007218)	2.22E-05
CRB	HETIG1_WTFVEH	regulation of endocrine process (GO:0044060)	3.71E-02
CRB	HETIG1_WTFVEH	regulation of amine transport (GO:0051952)	6.34E-03
CRB	HETIG1_WTFVEH	regulation of nervous system process (GO:0031644)	3.86E-02
CRB	HETIG1_WTFVEH	regulation of blood pressure (GO:0008217)	1.48E-02
CRB	HETIG1_WTFVEH	chemical synaptic transmission (GO:0007268)	3.09E-02
CRB	HETIG1_WTFVEH	anterograde trans-synaptic signaling (GO:0098916)	2.92E-02
CRB	HETIG1_WTFVEH	trans-synaptic signaling (GO:0099537)	3.85E-02
CRB	HETIG1_WTFVEH	regulation of secretion (GO:0051046)	6.33E-03
CRB	HETIG1_WTFVEH	regulation of secretion by cell (GO:1903530)	2.32E-02
CRB	HETIG1_WTFVEH	regulation of system process (GO:0044057)	4.83E-02
CRB	HETIG1_WTFVEH	behavior (GO:0007610)	3.14E-02
CRB	HETIG1_WTFVEH	regulation of transport (GO:0051049)	5.45E-03
CRB	HETIG1_WTFVEH	regulation of localization (GO:0032879)	7.34E-03
BL	VEH.HET_WTF	negative regulation of sterol import (GO:2000910)	0.0429
BL	VEH.HET_WTF	4-nitrophenol metabolic process (GO:0018960)	0.0428
BL	VEH.HET_WTF	cysteine biosynthetic process via cystathionine (GO:0019343)	0.0427
BL	VEH.HET_WTF	alkaloid metabolic process (GO:0009820)	0.0426
BL	VEH.HET_WTF	argininosuccinate metabolic process (GO:0000053)	0.0425
BL	VEH.HET_WTF	arginine biosynthetic process via ornithine (GO:0042450)	0.0425
BL	VEH.HET_WTF	negative regulation of iron ion transmembrane transporter activity (GO:1904255)	0.0424
BL	VEH.HET_WTF	monoterpenoid metabolic process (GO:0016098)	0.0423
BL	VEH.HET_WTF	negative regulation of iron export across plasma membrane (GO:1904039)	0.0422
BL	VEH.HET_WTF	regulation of iron export across plasma membrane (GO:1904038)	0.0421
BL	VEH.HET_WTF	response to methanol (GO:0033986)	0.000279
BL	VEH.HET_WTF	positive regulation of neurofibrillary tangle assembly (GO:1902998)	0.042
BL	VEH.HET_WTF	negative regulation of cholesterol import (GO:0060621)	0.0419
BL	VEH.HET_WTF	tyrosine catabolic process (GO:0006572)	3.49E-05
BL	VEH.HET_WTF	regulation of very-low-density lipoprotein particle remodeling (GO:0010901)	0.000452
BL	VEH.HET_WTF	response to chromate (GO:0046687)	0.00045
BL	VEH.HET_WTF	L-cysteine catabolic process (GO:0019448)	0.00535
BL	VEH.HET_WTF	negative regulation of endothelial cell chemotaxis (GO:2001027)	0.00534
BL	VEH.HET_WTF	L-phenylalanine catabolic process (GO:0006559)	4.03E-06
BL	VEH.HET_WTF	arginine biosynthetic process (GO:0006526)	0.00532

BL	VEH.HET_WTF	erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process (GO:1902222)	3.99E-06
BL	VEH.HET_WTF	negative regulation of very-low-density lipoprotein particle remodeling (GO:0010903)	0.0053
BL	VEH.HET_WTF	cysteine catabolic process (GO:0009093)	0.00529
BL	VEH.HET_WTF	L-cysteine metabolic process (GO:0046439)	0.00527
BL	VEH.HET_WTF	methyl-branched fatty acid metabolic process (GO:0097089)	0.00526
BL	VEH.HET_WTF	L-phenylalanine metabolic process (GO:0006558)	4.61E-07
BL	VEH.HET_WTF	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process (GO:1902221)	4.56E-07
BL	VEH.HET_WTF	negative regulation of fibrinolysis (GO:0051918)	0.000694
BL	VEH.HET_WTF	short-chain fatty acid catabolic process (GO:0019626)	0.000691
BL	VEH.HET_WTF	fibrinolysis (GO:0042730)	6.08E-09
BL	VEH.HET_WTF	blood coagulation, fibrin clot formation (GO:0072378)	8.87E-05
BL	VEH.HET_WTF	high-density lipoprotein particle assembly (GO:0034380)	8.81E-05
BL	VEH.HET_WTF	sulfur amino acid catabolic process (GO:0000098)	0.001
BL	VEH.HET_WTF	tyrosine metabolic process (GO:0006570)	2.26E-06
BL	VEH.HET_WTF	nitrogen cycle metabolic process (GO:0071941)	0.000174
BL	VEH.HET_WTF	triglyceride-rich lipoprotein particle clearance (GO:0071830)	0.011
BL	VEH.HET_WTF	triglyceride mobilization (GO:0006642)	0.0109
BL	VEH.HET_WTF	fatty acid alpha-oxidation (GO:0001561)	0.0109
BL	VEH.HET_WTF	purine nucleobase catabolic process (GO:0006145)	0.0109
BL	VEH.HET_WTF	monocyte aggregation (GO:0070487)	0.0109
BL	VEH.HET_WTF	regulation of bile acid secretion (GO:0120188)	0.00142
BL	VEH.HET_WTF	urea cycle (GO:0000050)	0.000173
BL	VEH.HET_WTF	S-adenosylhomocysteine metabolic process (GO:0046498)	0.0108
BL	VEH.HET_WTF	urea metabolic process (GO:0019627)	0.000172
BL	VEH.HET_WTF	high-density lipoprotein particle clearance (GO:0034384)	0.0108
BL	VEH.HET_WTF	chylomicron remnant clearance (GO:0034382)	0.0108
BL	VEH.HET_WTF	triglyceride-rich lipoprotein particle remodeling (GO:0034370)	0.00142
BL	VEH.HET_WTF	aromatic amino acid family catabolic process (GO:0009074)	3.21E-06
BL	VEH.HET_WTF	phospholipid efflux (GO:0033700)	2.87E-05
BL	VEH.HET_WTF	complement activation, alternative pathway (GO:0006957)	0.000244
BL	VEH.HET_WTF	negative regulation of serine-type peptidase activity (GO:1902572)	0.00197
BL	VEH.HET_WTF	regulation of serine-type peptidase activity (GO:1902571)	0.00196
BL	VEH.HET_WTF	regulation of fibrinolysis (GO:0051917)	0.00195
BL	VEH.HET_WTF	negative regulation of serine-type endopeptidase activity (GO:1900004)	0.00195
BL	VEH.HET_WTF	regulation of serine-type endopeptidase activity (GO:1900003)	0.00194
BL	VEH.HET_WTF	negative regulation of lipoprotein lipase activity (GO:0051005)	0.0145

BL	VEH.HET_WTF	alkanesulfonate metabolic process (GO:0019694)	0.0144
BL	VEH.HET_WTF	very-low-density lipoprotein particle remodeling (GO:0034372)	0.0144
BL	VEH.HET_WTF	taurine metabolic process (GO:0019530)	0.0144
BL	VEH.HET_WTF	protein activation cascade (GO:0072376)	0.000322
BL	VEH.HET_WTF	ornithine metabolic process (GO:0006591)	0.00256
BL	VEH.HET_WTF	positive regulation of cholesterol esterification (GO:0010873)	0.00256
BL	VEH.HET_WTF	epoxygenase P450 pathway (GO:0019373)	4.73E-12
BL	VEH.HET_WTF	high-density lipoprotein particle remodeling (GO:0034375)	0.000416
BL	VEH.HET_WTF	nucleobase catabolic process (GO:0046113)	0.019
BL	VEH.HET_WTF	regulation of Cdc42 protein signal transduction (GO:0032489)	0.019
BL	VEH.HET_WTF	thrombin-activated receptor signaling pathway (GO:0070493)	0.019
BL	VEH.HET_WTF	negative regulation of iron ion transport (GO:0034757)	0.0189
BL	VEH.HET_WTF	reverse cholesterol transport (GO:0043691)	1.04E-05
BL	VEH.HET_WTF	cysteine metabolic process (GO:0006534)	0.00329
BL	VEH.HET_WTF	positive regulation of triglyceride catabolic process (GO:0010898)	0.00328
BL	VEH.HET_WTF	plasma lipoprotein particle remodeling (GO:0034369)	2.4E-07
BL	VEH.HET_WTF	protein-lipid complex remodeling (GO:0034368)	2.37E-07
BL	VEH.HET_WTF	leukocyte aggregation (GO:0070486)	0.000532
BL	VEH.HET_WTF	negative regulation of blood coagulation (GO:0030195)	2.36E-13
BL	VEH.HET_WTF	regulation of lipoprotein lipase activity (GO:0051004)	9.04E-05
BL	VEH.HET_WTF	positive regulation of hemostasis (GO:1900048)	1.37E-05
BL	VEH.HET_WTF	positive regulation of blood coagulation (GO:0030194)	1.36E-05
BL	VEH.HET_WTF	negative regulation of hemostasis (GO:1900047)	3.05E-13
BL	VEH.HET_WTF	negative regulation of coagulation (GO:0050819)	3.92E-13
BL	VEH.HET_WTF	arginine metabolic process (GO:0006525)	0.000681
BL	VEH.HET_WTF	plasminogen activation (GO:0031639)	0.00406
BL	VEH.HET_WTF	glutamine family amino acid biosynthetic process (GO:0009084)	0.00405
BL	VEH.HET_WTF	purine ribonucleoside catabolic process (GO:0046130)	0.024
BL	VEH.HET_WTF	deoxyribonucleoside catabolic process (GO:0046121)	0.0239
BL	VEH.HET_WTF	protein-containing complex remodeling (GO:0034367)	3.87E-07
BL	VEH.HET_WTF	cholesterol efflux (GO:0033344)	4.89E-07
BL	VEH.HET_WTF	regulation of triglyceride catabolic process (GO:0010896)	0.000831
BL	VEH.HET_WTF	aromatic amino acid family metabolic process (GO:0009072)	6.2E-07
BL	VEH.HET_WTF	response to lead ion (GO:0010288)	0.00505
BL	VEH.HET_WTF	positive regulation of integrin activation (GO:0033625)	0.00503
BL	VEH.HET_WTF	regulation of cholesterol esterification (GO:0010872)	0.00502
BL	VEH.HET_WTF	low-density lipoprotein particle remodeling (GO:0034374)	0.005
BL	VEH.HET_WTF	positive regulation of coagulation (GO:0050820)	0.000028
BL	VEH.HET_WTF	regulation of blood coagulation (GO:0030193)	9.32E-16

BL	VEH.HET_WTF	positive regulation of receptor catabolic process (GO:2000646)	0.0302
BL	VEH.HET_WTF	Fc receptor signaling pathway (GO:0038093)	0.0301
BL	VEH.HET_WTF	positive regulation of lipoprotein lipase activity (GO:0051006)	0.0301
BL	VEH.HET_WTF	plasma lipoprotein particle clearance (GO:0034381)	0.000175
BL	VEH.HET_WTF	plasma lipoprotein particle assembly (GO:0034377)	0.000174
BL	VEH.HET_WTF	regulation of hemostasis (GO:1900046)	1.36E-15
BL	VEH.HET_WTF	regulation of complement activation (GO:0030449)	3.45E-05
BL	VEH.HET_WTF	positive regulation of heterotypic cell-cell adhesion (GO:0034116)	0.00598
BL	VEH.HET_WTF	negative regulation of cholesterol transport (GO:0032375)	0.00596
BL	VEH.HET_WTF	negative regulation of sterol transport (GO:0032372)	0.00595
BL	VEH.HET_WTF	regulation of coagulation (GO:0050818)	2.04E-15
BL	VEH.HET_WTF	short-chain fatty acid metabolic process (GO:0046459)	0.00593
BL	VEH.HET_WTF	negative regulation of complement activation (GO:0045916)	0.00591
BL	VEH.HET_WTF	negative regulation of lipase activity (GO:0060192)	0.00127
BL	VEH.HET_WTF	sulfur amino acid metabolic process (GO:0000096)	8.08E-06
BL	VEH.HET_WTF	purine nucleoside catabolic process (GO:0006152)	0.0363
BL	VEH.HET_WTF	regulation of intestinal cholesterol absorption (GO:0030300)	0.0362
BL	VEH.HET_WTF	positive regulation of triglyceride lipase activity (GO:0061365)	0.0361
BL	VEH.HET_WTF	coagulation (GO:0050817)	1.48E-23
BL	VEH.HET_WTF	blood coagulation (GO:0007596)	1.31E-23
BL	VEH.HET_WTF	hemostasis (GO:0007599)	1.85E-23
BL	VEH.HET_WTF	plasma lipoprotein particle organization (GO:0071827)	3.46E-07
BL	VEH.HET_WTF	regulation of intestinal absorption (GO:1904478)	0.00156
BL	VEH.HET_WTF	platelet aggregation (GO:0070527)	6.38E-05
BL	VEH.HET_WTF	xenobiotic catabolic process (GO:0042178)	4.65E-13
BL	VEH.HET_WTF	acute-phase response (GO:0006953)	1.46E-05
BL	VEH.HET_WTF	protein-lipid complex assembly (GO:0065005)	0.000379
BL	VEH.HET_WTF	glycine metabolic process (GO:0006544)	0.00864
BL	VEH.HET_WTF	fructose metabolic process (GO:0006000)	0.0423
BL	VEH.HET_WTF	sulfur compound catabolic process (GO:0044273)	0.000377
BL	VEH.HET_WTF	S-adenosylmethionine metabolic process (GO:0046500)	0.00861
BL	VEH.HET_WTF	arachidonic acid metabolic process (GO:0019369)	1.55E-13
BL	VEH.HET_WTF	protein-lipid complex subunit organization (GO:0071825)	7.08E-07
BL	VEH.HET_WTF	nucleoside catabolic process (GO:0009164)	0.00221
BL	VEH.HET_WTF	triglyceride catabolic process (GO:0019433)	0.0103
BL	VEH.HET_WTF	alpha-amino acid catabolic process (GO:1901606)	3.78E-11
BL	VEH.HET_WTF	platelet activation (GO:0030168)	3.15E-08
BL	VEH.HET_WTF	linoleic acid metabolic process (GO:0043651)	0.000107
BL	VEH.HET_WTF	negative regulation of lipid storage (GO:0010888)	0.000527
BL	VEH.HET_WTF	negative regulation of wound healing (GO:0061045)	5.46E-11

BL	VEH.HET_WTF	cellular response to low-density lipoprotein particle stimulus (GO:0071404)	0.00261
BL	VEH.HET_WTF	response to stilbenoid (GO:0035634)	0.0026
BL	VEH.HET_WTF	negative regulation of humoral immune response (GO:0002921)	0.0119
BL	VEH.HET_WTF	bile acid metabolic process (GO:0008206)	0.00063
BL	VEH.HET_WTF	positive regulation of lipid catabolic process (GO:0050996)	0.000148
BL	VEH.HET_WTF	regulation of integrin activation (GO:0033623)	0.0139
BL	VEH.HET_WTF	regulation of bile acid metabolic process (GO:1904251)	0.0139
BL	VEH.HET_WTF	negative regulation of platelet activation (GO:0010544)	0.0139
BL	VEH.HET_WTF	nucleobase-containing small molecule catabolic process (GO:0034656)	0.00353
BL	VEH.HET_WTF	positive regulation of triglyceride metabolic process (GO:0090208)	0.000838
BL	VEH.HET_WTF	acylglycerol catabolic process (GO:0046464)	0.000834
BL	VEH.HET_WTF	neutral lipid catabolic process (GO:0046461)	0.00083
BL	VEH.HET_WTF	cellular amino acid catabolic process (GO:0009063)	9.45E-12
BL	VEH.HET_WTF	xenobiotic metabolic process (GO:0006805)	1.24E-15
BL	VEH.HET_WTF	deoxyribonucleoside monophosphate catabolic process (GO:0009159)	0.0159
BL	VEH.HET_WTF	regulation of heterotypic cell-cell adhesion (GO:0034114)	0.00405
BL	VEH.HET_WTF	medium-chain fatty acid metabolic process (GO:0051791)	0.00403
BL	VEH.HET_WTF	negative regulation of cytokine production involved in immune response (GO:0002719)	0.00402
BL	VEH.HET_WTF	negative regulation of lipid localization (GO:1905953)	7E-07
BL	VEH.HET_WTF	regulation of plasma lipoprotein particle levels (GO:0097006)	3.26E-06
BL	VEH.HET_WTF	olefinic compound metabolic process (GO:0120254)	1.82E-15
BL	VEH.HET_WTF	triglyceride homeostasis (GO:0070328)	0.000278
BL	VEH.HET_WTF	acylglycerol homeostasis (GO:0055090)	0.000276
BL	VEH.HET_WTF	serine family amino acid metabolic process (GO:0009069)	0.000275
BL	VEH.HET_WTF	positive regulation of cholesterol efflux (GO:0010875)	0.00111
BL	VEH.HET_WTF	purine ribonucleoside metabolic process (GO:0046128)	0.00463
BL	VEH.HET_WTF	unsaturated fatty acid metabolic process (GO:0033559)	1.63E-14
BL	VEH.HET_WTF	long-chain fatty acid metabolic process (GO:0001676)	1.85E-14
BL	VEH.HET_WTF	steroid catabolic process (GO:0006706)	0.00517
BL	VEH.HET_WTF	sterol transport (GO:0015918)	2.91E-07
BL	VEH.HET_WTF	cholesterol transport (GO:0030301)	2.88E-07
BL	VEH.HET_WTF	ribonucleoside monophosphate catabolic process (GO:0009158)	0.0209
BL	VEH.HET_WTF	regulation of cholesterol storage (GO:0010885)	0.0209
BL	VEH.HET_WTF	positive regulation of steroid metabolic process (GO:0045940)	9.75E-05
BL	VEH.HET_WTF	negative regulation of response to wounding (GO:1903035)	1.24E-09
BL	VEH.HET_WTF	negative regulation of lipid transport (GO:0032369)	0.0017
BL	VEH.HET_WTF	regulation of platelet activation (GO:0010543)	0.000458

BL	VEH.HET_WTF	alpha-amino acid biosynthetic process (GO:1901607)	3.38E-05
BL	VEH.HET_WTF	glycosyl compound catabolic process (GO:1901658)	0.00645
BL	VEH.HET_WTF	alpha-amino acid metabolic process (GO:1901605)	7.73E-17
BL	VEH.HET_WTF	cellular amino acid biosynthetic process (GO:0008652)	9.91E-06
BL	VEH.HET_WTF	triglyceride metabolic process (GO:0006641)	6.37E-07
BL	VEH.HET_WTF	benzene-containing compound metabolic process (GO:0042537)	0.0273
BL	VEH.HET_WTF	regulation of humoral immune response (GO:0002920)	0.000162
BL	VEH.HET_WTF	regulation of lipid storage (GO:0010883)	4.31E-05
BL	VEH.HET_WTF	icosanoid metabolic process (GO:0006690)	7.22E-13
BL	VEH.HET_WTF	regulation of lipid catabolic process (GO:0050994)	3.27E-06
BL	VEH.HET_WTF	regulation of wound healing (GO:0061041)	4.52E-12
BL	VEH.HET_WTF	acetyl-CoA metabolic process (GO:0006084)	0.00829
BL	VEH.HET_WTF	carboxylic acid catabolic process (GO:0046395)	4.47E-18
BL	VEH.HET_WTF	regulation of triglyceride metabolic process (GO:0090207)	0.000205
BL	VEH.HET_WTF	nucleoside monophosphate catabolic process (GO:0009125)	0.0307
BL	VEH.HET_WTF	cytolysis (GO:0019835)	0.0306
BL	VEH.HET_WTF	homotypic cell-cell adhesion (GO:0034109)	0.00074
BL	VEH.HET_WTF	defense response to fungus (GO:0050832)	0.000737
BL	VEH.HET_WTF	organic acid catabolic process (GO:0016054)	5.55E-18
BL	VEH.HET_WTF	response to lipoprotein particle (GO:0055094)	0.00932
BL	VEH.HET_WTF	ribonucleoside metabolic process (GO:0009119)	0.00929
BL	VEH.HET_WTF	cellular response to xenobiotic stimulus (GO:0071466)	2.01E-15
BL	VEH.HET_WTF	leukocyte migration involved in inflammatory response (GO:0002523)	0.0344
BL	VEH.HET_WTF	deoxyribose phosphate catabolic process (GO:0046386)	0.0343
BL	VEH.HET_WTF	secondary alcohol biosynthetic process (GO:1902653)	0.00303
BL	VEH.HET_WTF	cholesterol biosynthetic process (GO:0006695)	0.00302
BL	VEH.HET_WTF	purine nucleoside metabolic process (GO:0042278)	0.0104
BL	VEH.HET_WTF	regulation of cholesterol metabolic process (GO:0090181)	0.00337
BL	VEH.HET_WTF	steroid metabolic process (GO:0008202)	5.69E-22
BL	VEH.HET_WTF	deoxyribonucleotide catabolic process (GO:0009264)	0.0378
BL	VEH.HET_WTF	cellular response to lipoprotein particle stimulus (GO:0071402)	0.0114
BL	VEH.HET_WTF	glutamine family amino acid metabolic process (GO:0009064)	0.000357
BL	VEH.HET_WTF	cholesterol metabolic process (GO:0008203)	1.38E-09
BL	VEH.HET_WTF	positive regulation of wound healing (GO:0090303)	0.000393
BL	VEH.HET_WTF	regulation of cholesterol transport (GO:0032374)	0.000036
BL	VEH.HET_WTF	regulation of sterol transport (GO:0032371)	3.58E-05
BL	VEH.HET_WTF	retinol metabolic process (GO:0042572)	0.042
BL	VEH.HET_WTF	wound healing (GO:0042060)	1.24E-19
BL	VEH.HET_WTF	acylglycerol metabolic process (GO:0006639)	7.54E-08
BL	VEH.HET_WTF	regulation of cholesterol efflux (GO:0010874)	0.00404
BL	VEH.HET_WTF	neutral lipid metabolic process (GO:0006638)	9.19E-08

BL	VEH.HET_WTF	secondary metabolic process (GO:0019748)	0.00143
BL	VEH.HET_WTF	monocarboxylic acid catabolic process (GO:0072329)	3.49E-07
BL	VEH.HET_WTF	terpenoid metabolic process (GO:0006721)	0.000148
BL	VEH.HET_WTF	fatty acid catabolic process (GO:0009062)	1.45E-05
BL	VEH.HET_WTF	cholesterol homeostasis (GO:0042632)	1.35E-06
BL	VEH.HET_WTF	sterol homeostasis (GO:0055092)	1.48E-06
BL	VEH.HET_WTF	sterol metabolic process (GO:0016125)	3.76E-09
BL	VEH.HET_WTF	vitamin transport (GO:0051180)	0.0153
BL	VEH.HET_WTF	aspartate family amino acid metabolic process (GO:0009066)	0.0153
BL	VEH.HET_WTF	organic hydroxy compound transport (GO:0015850)	1.18E-09
BL	VEH.HET_WTF	small molecule catabolic process (GO:0044282)	1.25E-21
BL	VEH.HET_WTF	positive regulation of cholesterol transport (GO:0032376)	0.00537
BL	VEH.HET_WTF	positive regulation of sterol transport (GO:0032373)	0.00535
BL	VEH.HET_WTF	sterol biosynthetic process (GO:0016126)	0.00533
BL	VEH.HET_WTF	secondary alcohol metabolic process (GO:1902652)	5.16E-09
BL	VEH.HET_WTF	negative regulation of production of molecular mediator of immune response (GO:0002701)	0.0169
BL	VEH.HET_WTF	nucleoside metabolic process (GO:0009116)	0.00208
BL	VEH.HET_WTF	cellular amino acid metabolic process (GO:0006520)	1.3E-15
BL	VEH.HET_WTF	response to nutrient (GO:0007584)	0.00229
BL	VEH.HET_WTF	response to fungus (GO:0009620)	0.00253
BL	VEH.HET_WTF	regulation of response to wounding (GO:1903034)	4.4E-10
BL	VEH.HET_WTF	fatty acid metabolic process (GO:0006631)	6.04E-22
BL	VEH.HET_WTF	killing of cells of other organism (GO:0031640)	0.000127
BL	VEH.HET_WTF	isoprenoid metabolic process (GO:0006720)	0.000139
BL	VEH.HET_WTF	diterpenoid metabolic process (GO:0016101)	0.00324
BL	VEH.HET_WTF	acute inflammatory response (GO:0002526)	0.00119
BL	VEH.HET_WTF	primary alcohol metabolic process (GO:0034308)	0.00118
BL	VEH.HET_WTF	glycerolipid catabolic process (GO:0046503)	0.00973
BL	VEH.HET_WTF	fatty acid oxidation (GO:0019395)	0.00048
BL	VEH.HET_WTF	glycosyl compound metabolic process (GO:1901657)	0.000477
BL	VEH.HET_WTF	steroid biosynthetic process (GO:0006694)	2.34E-05
BL	VEH.HET_WTF	ribonucleotide catabolic process (GO:0009261)	0.0291
BL	VEH.HET_WTF	purine-containing compound catabolic process (GO:0072523)	0.029
BL	VEH.HET_WTF	regulation of endothelial cell apoptotic process (GO:2000351)	0.0106
BL	VEH.HET_WTF	regulation of body fluid levels (GO:0050878)	3.97E-18
BL	VEH.HET_WTF	regulation of macrophage migration (GO:1905521)	0.0312
BL	VEH.HET_WTF	response to wounding (GO:0009611)	4.83E-17
BL	VEH.HET_WTF	cellular aldehyde metabolic process (GO:0006081)	0.0122
BL	VEH.HET_WTF	positive regulation of response to wounding (GO:1903036)	0.00194
BL	VEH.HET_WTF	carboxylic acid metabolic process (GO:0019752)	2.21E-41
BL	VEH.HET_WTF	organic acid metabolic process (GO:0006082)	4.31E-43

BL	VEH.HET_WTF	lipid oxidation (GO:0034440)	0.000759
BL	VEH.HET_WTF	oxoacid metabolic process (GO:0043436)	1.5E-41
BL	VEH.HET_WTF	regulation of fatty acid biosynthetic process (GO:0042304)	0.0363
BL	VEH.HET_WTF	monocarboxylic acid metabolic process (GO:0032787)	1.91E-24
BL	VEH.HET_WTF	retinoid metabolic process (GO:0001523)	0.0141
BL	VEH.HET_WTF	cell killing (GO:0001906)	2.02E-05
BL	VEH.HET_WTF	positive regulation of lipid metabolic process (GO:0045834)	5.26E-08
BL	VEH.HET_WTF	negative regulation of endopeptidase activity (GO:0010951)	6.68E-08
BL	VEH.HET_WTF	long-chain fatty acid transport (GO:0015909)	0.0419
BL	VEH.HET_WTF	antimicrobial humoral response (GO:0019730)	1.35E-06
BL	VEH.HET_WTF	integrin-mediated signaling pathway (GO:0007229)	0.00301
BL	VEH.HET_WTF	regulation of lipid localization (GO:1905952)	2.66E-07
BL	VEH.HET_WTF	response to xenobiotic stimulus (GO:0009410)	6.33E-13
BL	VEH.HET_WTF	protein homotetramerization (GO:0051289)	0.0469
BL	VEH.HET_WTF	organic hydroxy compound metabolic process (GO:1901615)	4.57E-18
BL	VEH.HET_WTF	antimicrobial humoral immune response mediated by antimicrobial peptide (GO:0061844)	9.96E-05
BL	VEH.HET_WTF	acyl-CoA metabolic process (GO:0006637)	0.00365
BL	VEH.HET_WTF	positive regulation of phagocytosis (GO:0050766)	0.00364
BL	VEH.HET_WTF	thioester metabolic process (GO:0035383)	0.00363
BL	VEH.HET_WTF	cellular hormone metabolic process (GO:0034754)	0.000633
BL	VEH.HET_WTF	alcohol metabolic process (GO:0006066)	2.89E-11
BL	VEH.HET_WTF	positive regulation of receptor-mediated endocytosis (GO:0048260)	0.0215
BL	VEH.HET_WTF	sulfur compound metabolic process (GO:0006790)	4.13E-12
BL	VEH.HET_WTF	regulation of lipase activity (GO:0060191)	0.00388
BL	VEH.HET_WTF	purine nucleoside bisphosphate metabolic process (GO:0034032)	0.000681
BL	VEH.HET_WTF	ribonucleoside bisphosphate metabolic process (GO:0033875)	0.000677
BL	VEH.HET_WTF	nucleoside bisphosphate metabolic process (GO:0033865)	0.000674
BL	VEH.HET_WTF	regulation of steroid metabolic process (GO:0019218)	0.000291
BL	VEH.HET_WTF	cellular modified amino acid metabolic process (GO:0006575)	5.28E-07
BL	VEH.HET_WTF	response to toxic substance (GO:0009636)	0.000352
BL	VEH.HET_WTF	negative regulation of peptidase activity (GO:0010466)	2.74E-09
BL	VEH.HET_WTF	cellular lipid catabolic process (GO:0044242)	1.85E-06
BL	VEH.HET_WTF	carboxylic acid biosynthetic process (GO:0046394)	7.35E-08
BL	VEH.HET_WTF	organic acid biosynthetic process (GO:0016053)	7.59E-08
BL	VEH.HET_WTF	glutathione metabolic process (GO:0006749)	0.0125
BL	VEH.HET_WTF	response to glucocorticoid (GO:0051384)	0.0125
BL	VEH.HET_WTF	lipid catabolic process (GO:0016042)	6.84E-09
BL	VEH.HET_WTF	regulation of epithelial cell apoptotic process (GO:1904035)	0.006
BL	VEH.HET_WTF	dicarboxylic acid metabolic process (GO:0043648)	0.0142

BL	VEH.HET_WTF	organic hydroxy compound catabolic process (GO:1901616)	0.0339
BL	VEH.HET_WTF	regulation of lipid transport (GO:0032368)	0.000126
BL	VEH.HET_WTF	alcohol biosynthetic process (GO:0046165)	0.00675
BL	VEH.HET_WTF	regulation of nitric oxide biosynthetic process (GO:0045428)	0.0359
BL	VEH.HET_WTF	phospholipid transport (GO:0015914)	0.0158
BL	VEH.HET_WTF	lipid homeostasis (GO:0055088)	6.41E-05
BL	VEH.HET_WTF	lipid transport (GO:0006869)	1.52E-08
BL	VEH.HET_WTF	negative regulation of hydrolase activity (GO:0051346)	3.49E-11
BL	VEH.HET_WTF	cell-matrix adhesion (GO:0007160)	0.00181
BL	VEH.HET_WTF	zymogen activation (GO:0031638)	0.0399
BL	VEH.HET_WTF	response to corticosteroid (GO:0031960)	0.0189
BL	VEH.HET_WTF	positive regulation of lipid localization (GO:1905954)	0.002
BL	VEH.HET_WTF	regulation of nitric oxide metabolic process (GO:0080164)	0.0421
BL	VEH.HET_WTF	neutrophil chemotaxis (GO:0030593)	0.0433
BL	VEH.HET_WTF	regulation of lipid biosynthetic process (GO:0046890)	2.35E-05
BL	VEH.HET_WTF	response to metal ion (GO:0010038)	8.27E-08
BL	VEH.HET_WTF	small molecule biosynthetic process (GO:0044283)	1.05E-10
BL	VEH.HET_WTF	organic hydroxy compound biosynthetic process (GO:1901617)	0.000268
BL	VEH.HET_WTF	negative regulation of immune effector process (GO:0002698)	0.00277
BL	VEH.HET_WTF	small molecule metabolic process (GO:0044281)	2.73E-43
BL	VEH.HET_WTF	lipid localization (GO:0010876)	2.7E-08
BL	VEH.HET_WTF	cell-substrate adhesion (GO:0031589)	0.000146
BL	VEH.HET_WTF	hormone metabolic process (GO:0042445)	0.000323
BL	VEH.HET_WTF	cellular lipid metabolic process (GO:0044255)	4.71E-24
BL	VEH.HET_WTF	positive regulation of lipid biosynthetic process (GO:0046889)	0.0124
BL	VEH.HET_WTF	negative regulation of proteolysis (GO:0045861)	8.49E-09
BL	VEH.HET_WTF	regulation of blood vessel endothelial cell migration (GO:0043535)	0.0278
BL	VEH.HET_WTF	regulation of cellular ketone metabolic process (GO:0010565)	0.002
BL	VEH.HET_WTF	leukocyte chemotaxis (GO:0030595)	0.00406
BL	VEH.HET_WTF	lipid modification (GO:0030258)	0.0011
BL	VEH.HET_WTF	lipid metabolic process (GO:0006629)	5.11E-28
BL	VEH.HET_WTF	regulation of cytokine production involved in immune response (GO:0002718)	0.0339
BL	VEH.HET_WTF	regulation of receptor-mediated endocytosis (GO:0048259)	0.00851
BL	VEH.HET_WTF	phenol-containing compound metabolic process (GO:0018958)	0.0355
BL	VEH.HET_WTF	regulation of fatty acid metabolic process (GO:0019217)	0.0368
BL	VEH.HET_WTF	response to calcium ion (GO:0051592)	0.00978
BL	VEH.HET_WTF	regulation of endopeptidase activity (GO:0052548)	1.54E-07
BL	VEH.HET_WTF	regulation of phagocytosis (GO:0050764)	0.0193
BL	VEH.HET_WTF	lipoprotein metabolic process (GO:0042157)	0.0192

BL	VEH.HET_WTF	positive regulation of lipid transport (GO:0032370)	0.0386
BL	VEH.HET_WTF	regeneration (GO:0031099)	0.0405
BL	VEH.HET_WTF	regulation of glucose metabolic process (GO:0010906)	0.0108
BL	VEH.HET_WTF	regulation of lipid metabolic process (GO:0019216)	1.03E-07
BL	VEH.HET_WTF	regulation of peptidase activity (GO:0052547)	7.47E-09
BL	VEH.HET_WTF	organic cyclic compound catabolic process (GO:1901361)	2.42E-06
BL	VEH.HET_WTF	positive regulation of small molecule metabolic process (GO:0062013)	0.00377
BL	VEH.HET_WTF	response to alcohol (GO:0097305)	0.00376
BL	VEH.HET_WTF	humoral immune response (GO:0006959)	7.51E-08
BL	VEH.HET_WTF	blood vessel diameter maintenance (GO:0097746)	0.00507
BL	VEH.HET_WTF	regulation of tube diameter (GO:0035296)	0.00505
BL	VEH.HET_WTF	regulation of endothelial cell migration (GO:0010594)	0.00504
BL	VEH.HET_WTF	regulation of tube size (GO:0035150)	0.00516
BL	VEH.HET_WTF	positive regulation of peptide secretion (GO:0002793)	0.0332
BL	VEH.HET_WTF	aromatic compound catabolic process (GO:0019439)	4.34E-05
BL	VEH.HET_WTF	negative regulation of response to external stimulus (GO:0032102)	9.02E-07
BL	VEH.HET_WTF	regulation of small molecule metabolic process (GO:0062012)	3.44E-06
BL	VEH.HET_WTF	myeloid leukocyte migration (GO:0097529)	0.0343
BL	VEH.HET_WTF	carbohydrate derivative catabolic process (GO:1901136)	0.0193
BL	VEH.HET_WTF	positive regulation of endocytosis (GO:0045807)	0.0359
BL	VEH.HET_WTF	regulation of cellular carbohydrate metabolic process (GO:0010675)	0.012
BL	VEH.HET_WTF	glycerolipid metabolic process (GO:0046486)	4.01E-05
BL	VEH.HET_WTF	purine-containing compound metabolic process (GO:0072521)	8.96E-05
BL	VEH.HET_WTF	response to inorganic substance (GO:0010035)	1.77E-06
BL	VEH.HET_WTF	positive regulation of adaptive immune response (GO:0002821)	0.0301
BL	VEH.HET_WTF	regulation of production of molecular mediator of immune response (GO:0002700)	0.0183
BL	VEH.HET_WTF	ribonucleotide metabolic process (GO:0009259)	0.000486
BL	VEH.HET_WTF	response to peptide hormone (GO:0043434)	0.000874
BL	VEH.HET_WTF	vascular process in circulatory system (GO:0003018)	0.00483
BL	VEH.HET_WTF	regulation of endocytosis (GO:0030100)	0.00524
BL	VEH.HET_WTF	ribose phosphate metabolic process (GO:0019693)	0.000739
BL	VEH.HET_WTF	leukocyte migration (GO:0050900)	0.00924
BL	VEH.HET_WTF	cellular response to metal ion (GO:0071248)	0.0428
BL	VEH.HET_WTF	purine ribonucleotide metabolic process (GO:0009150)	0.00254
BL	VEH.HET_WTF	inflammatory response (GO:0006954)	1.73E-05
BL	VEH.HET_WTF	regulation of immune effector process (GO:0002697)	8.98E-05
BL	VEH.HET_WTF	cellular response to inorganic substance (GO:0071241)	0.032
BL	VEH.HET_WTF	cell chemotaxis (GO:0060326)	0.0193
BL	VEH.HET_WTF	positive regulation of ERK1 and ERK2 cascade (GO:0070374)	0.0119
BL	VEH.HET_WTF	complement activation (GO:0006956)	0.0122

BL	VEH.HET_WTF	regulation of carbohydrate metabolic process (GO:0006109)	0.0383
BL	VEH.HET_WTF	purine nucleotide metabolic process (GO:0006163)	0.00406
BL	VEH.HET_WTF	regulation of proteolysis (GO:0030162)	1.22E-07
BL	VEH.HET_WTF	organic acid transport (GO:0015849)	0.0193
BL	VEH.HET_WTF	negative regulation of cell adhesion (GO:0007162)	0.0059
BL	VEH.HET_WTF	cellular catabolic process (GO:0044248)	3.83E-16
BL	VEH.HET_WTF	nucleobase-containing small molecule metabolic process (GO:0055086)	0.000481
BL	VEH.HET_WTF	negative regulation of catalytic activity (GO:0043086)	3.33E-06
BL	VEH.HET_WTF	regulation of adaptive immune response (GO:0002819)	0.0359
BL	VEH.HET_WTF	catabolic process (GO:0009056)	3.77E-18
BL	VEH.HET_WTF	response to peptide (GO:1901652)	0.00558
BL	VEH.HET_WTF	regulation of hydrolase activity (GO:0051336)	1.22E-08
BL	VEH.HET_WTF	regulation of cysteine-type endopeptidase activity (GO:2000116)	0.0446
BL	VEH.HET_WTF	regulation of epithelial cell migration (GO:0010632)	0.0445
BL	VEH.HET_WTF	regulation of vesicle-mediated transport (GO:0060627)	4.66E-05
BL	VEH.HET_WTF	nucleotide metabolic process (GO:0009117)	0.00501
BL	VEH.HET_WTF	response to extracellular stimulus (GO:0009991)	0.00517
BL	VEH.HET_WTF	regulation of response to external stimulus (GO:0032101)	1.55E-07
BL	VEH.HET_WTF	positive regulation of immune effector process (GO:0002699)	0.0271
BL	VEH.HET_WTF	nucleoside phosphate metabolic process (GO:0006753)	0.00592
BL	VEH.HET_WTF	organic substance catabolic process (GO:1901575)	5.17E-12
BL	VEH.HET_WTF	response to hormone (GO:0009725)	0.000424
BL	VEH.HET_WTF	positive regulation of response to external stimulus (GO:0032103)	0.00651
BL	VEH.HET_WTF	lipid biosynthetic process (GO:0008610)	0.00283
BL	VEH.HET_WTF	adaptive immune response (GO:0002250)	0.0031
BL	VEH.HET_WTF	response to nutrient levels (GO:0031667)	0.0369
BL	VEH.HET_WTF	response to organic cyclic compound (GO:0014070)	0.000802
BL	VEH.HET_WTF	positive regulation of cell adhesion (GO:0045785)	0.00784
BL	VEH.HET_WTF	carbohydrate derivative metabolic process (GO:1901135)	8.98E-05
BL	VEH.HET_WTF	regulation of hormone levels (GO:0010817)	0.00341
BL	VEH.HET_WTF	response to lipid (GO:0033993)	0.000935
BL	VEH.HET_WTF	blood circulation (GO:0008015)	0.0171
BL	VEH.HET_WTF	regulation of cell-cell adhesion (GO:0022407)	0.014
BL	VEH.HET_WTF	circulatory system process (GO:0003013)	0.0143
BL	VEH.HET_WTF	positive regulation of transport (GO:0051050)	1.46E-05
BL	VEH.HET_WTF	positive regulation of secretion (GO:0051047)	0.03
BL	VEH.HET_WTF	organonitrogen compound catabolic process (GO:1901565)	7.04E-05
BL	VEH.HET_WTF	cell activation (GO:0001775)	0.00395
BL	VEH.HET_WTF	regulation of cell adhesion (GO:0030155)	0.00111
BL	VEH.HET_WTF	response to nitrogen compound (GO:1901698)	0.000332

BL	VEH.HET_WTF	organophosphate metabolic process (GO:0019637)	0.00178
BL	VEH.HET_WTF	response to bacterium (GO:0009617)	0.000414
BL	VEH.HET_WTF	negative regulation of molecular function (GO:0044092)	0.00014
BL	VEH.HET_WTF	response to organonitrogen compound (GO:0010243)	0.00217
BL	VEH.HET_WTF	positive regulation of immune system process (GO:0002684)	0.000136
BL	VEH.HET_WTF	negative regulation of multicellular organismal process (GO:0051241)	0.000106
BL	VEH.HET_WTF	response to chemical (GO:0042221)	4.7E-18
BL	VEH.HET_WTF	positive regulation of immune response (GO:0050778)	0.00644
BL	VEH.HET_WTF	response to other organism (GO:0051707)	5.07E-06
BL	VEH.HET_WTF	response to external biotic stimulus (GO:0043207)	5.12E-06
BL	VEH.HET_WTF	response to oxygen-containing compound (GO:1901700)	2.95E-05
BL	VEH.HET_WTF	defense response (GO:0006952)	8.62E-06
BL	VEH.HET_WTF	innate immune response (GO:0045087)	0.00296
BL	VEH.HET_WTF	cellular amide metabolic process (GO:0043603)	0.00785
BL	VEH.HET_WTF	defense response to other organism (GO:0098542)	0.000312
BL	VEH.HET_WTF	regulation of secretion (GO:0051046)	0.00934
BL	VEH.HET_WTF	response to biotic stimulus (GO:0009607)	8.05E-06
BL	VEH.HET_WTF	immune effector process (GO:0002252)	0.0429
BL	VEH.HET_WTF	response to endogenous stimulus (GO:0009719)	0.000376
BL	VEH.HET_WTF	negative regulation of protein metabolic process (GO:0051248)	0.000691
BL	VEH.HET_WTF	biological process involved in interspecies interaction between organisms (GO:0044419)	8.13E-06
BL	VEH.HET_WTF	cell adhesion (GO:0007155)	0.00502
BL	VEH.HET_WTF	biological adhesion (GO:0022610)	0.00552
BL	VEH.HET_WTF	cellular response to chemical stimulus (GO:0070887)	1.86E-08
BL	VEH.HET_WTF	chemical homeostasis (GO:0048878)	0.00157
BL	VEH.HET_WTF	negative regulation of cellular protein metabolic process (GO:0032269)	0.00498
BL	VEH.HET_WTF	regulation of cell activation (GO:0050865)	0.024
BL	VEH.HET_WTF	regulation of catalytic activity (GO:0050790)	2.77E-05
BL	VEH.HET_WTF	regulation of immune response (GO:0050776)	0.00721
BL	VEH.HET_WTF	regulation of transport (GO:0051049)	3.01E-05
BL	VEH.HET_WTF	regulation of response to stress (GO:0080134)	0.00203
BL	VEH.HET_WTF	response to external stimulus (GO:0009605)	6.52E-07
BL	VEH.HET_WTF	regulation of immune system process (GO:0002682)	0.000269
BL	VEH.HET_WTF	organic cyclic compound metabolic process (GO:1901360)	2.39E-07
BL	VEH.HET_WTF	response to stress (GO:0006950)	6.37E-09
BL	VEH.HET_WTF	protein-containing complex assembly (GO:0065003)	0.0245
BL	VEH.HET_WTF	protein-containing complex subunit organization (GO:0043933)	0.0105
BL	VEH.HET_WTF	regulation of biological quality (GO:0065008)	3E-09
BL	VEH.HET_WTF	immune response (GO:0006955)	0.00242
BL	VEH.HET_WTF	response to organic substance (GO:0010033)	9.16E-05

BL	VEH.HET_WTF	negative regulation of response to stimulus (GO:0048585)	0.00666
BL	VEH.HET_WTF	homeostatic process (GO:0042592)	0.00701
BL	VEH.HET_WTF	regulation of localization (GO:0032879)	9.17E-05
BL	VEH.HET_WTF	biosynthetic process (GO:0009058)	0.00342
BL	VEH.HET_WTF	regulation of molecular function (GO:0065009)	0.000955
BL	VEH.HET_WTF	organic substance biosynthetic process (GO:1901576)	0.0136
BL	VEH.HET_WTF	positive regulation of response to stimulus (GO:0048584)	0.00658
BL	VEH.HET_WTF	organic substance transport (GO:0071702)	0.0334
BL	VEH.HET_WTF	organonitrogen compound metabolic process (GO:1901564)	5.7E-06
BL	VEH.HET_WTF	primary metabolic process (GO:0044238)	3.61E-10
BL	VEH.HET_WTF	organic substance metabolic process (GO:0071704)	5.28E-12
BL	VEH.HET_WTF	immune system process (GO:0002376)	0.00532
BL	VEH.HET_WTF	metabolic process (GO:0008152)	9.04E-13
BL	VEH.HET_WTF	cellular metabolic process (GO:0044237)	1.21E-08
BL	VEH.HET_WTF	regulation of multicellular organismal process (GO:0051239)	0.00937
BL	VEH.HET_WTF	regulation of protein metabolic process (GO:0051246)	0.0199
BL	VEH.HET_WTF	regulation of cellular protein metabolic process (GO:0032268)	0.0422
BL	VEH.HET_WTF	regulation of response to stimulus (GO:0048583)	0.00106
BL	VEH.HET_WTF	response to stimulus (GO:0050896)	1.35E-08
BL	VEH.HET_WTF	nitrogen compound metabolic process (GO:0006807)	0.0217
BL	VEH.HET_WTF	negative regulation of biological process (GO:0048519)	0.0432
BL	VEH.HET_WTF	cellular process (GO:0009987)	0.0125
BL	VEH.HET_WTF	signal transduction (GO:0007165)	0.039
BL	VEH.HET_WTF	cellular macromolecule metabolic process (GO:0044260)	0.0218
BL	VEH.HET_WTF	cellular protein metabolic process (GO:0044267)	0.0365
BL	VEH.HET_WTF	regulation of cellular macromolecule biosynthetic process (GO:2000112)	0.00263
BL	VEH.HET_WTF	organelle organization (GO:0006996)	0.0059
BL	VEH.HET_WTF	regulation of RNA biosynthetic process (GO:2001141)	0.00589
BL	VEH.HET_WTF	regulation of macromolecule biosynthetic process (GO:0010556)	0.00169
BL	VEH.HET_WTF	regulation of RNA metabolic process (GO:0051252)	0.0026
BL	VEH.HET_WTF	regulation of transcription, DNA-templated (GO:0006355)	0.00355
BL	VEH.HET_WTF	regulation of nucleic acid-templated transcription (GO:1903506)	0.00354
BL	VEH.HET_WTF	regulation of nucleobase-containing compound metabolic process (GO:0019219)	0.000388
BL	VEH.HET_WTF	G protein-coupled receptor signaling pathway (GO:0007186)	0.0304
BL	VEH.HET_WTF	gene expression (GO:0010467)	0.00855
BL	VEH.HET_WTF	negative regulation of RNA metabolic process (GO:0051253)	0.0435
BL	VEH.HET_WTF	negative regulation of RNA biosynthetic process (GO:1902679)	0.0438

BL	VEH.HET_WTF	negative regulation of nucleobase-containing compound metabolic process (GO:0045934)	0.0159
BL	VEH.HET_WTF	regulation of transcription by RNA polymerase II (GO:0006357)	0.000311
BL	VEH.HET_WTF	negative regulation of cellular macromolecule biosynthetic process (GO:2000113)	0.0159
BL	VEH.HET_WTF	negative regulation of macromolecule biosynthetic process (GO:0010558)	0.0123
BL	VEH.HET_WTF	nervous system process (GO:0050877)	0.00069
BL	VEH.HET_WTF	sensory perception (GO:0007600)	0.00441
BL	VEH.HET_WTF	negative regulation of transcription, DNA-templated (GO:0045892)	0.0202
BL	VEH.HET_WTF	negative regulation of nucleic acid-templated transcription (GO:1903507)	0.0204
BL	VEH.HET_WTF	nucleic acid metabolic process (GO:0090304)	0.000121
BL	VEH.HET_WTF	negative regulation of transcription by RNA polymerase II (GO:0000122)	0.02
BL	VEH.HET_WTF	cell cycle process (GO:0022402)	0.0412
BL	VEH.HET_WTF	sensory perception of chemical stimulus (GO:0007606)	0.00105
BL	VEH.HET_WTF	RNA metabolic process (GO:0016070)	0.000754
BL	VEH.HET_WTF	chromosome organization (GO:0051276)	0.00514
BL	VEH.HET_WTF	cell cycle (GO:0007049)	0.000303
BL	VEH.HET_WTF	RNA processing (GO:0006396)	0.00609
BL	VEH.HET_WTF	sensory perception of smell (GO:0007608)	8.97E-05
BL	KOIGF1_WTFVEH	negative regulation of sterol import (GO:2000910)	2.31E-02
BL	KOIGF1_WTFVEH	alkaloid metabolic process (GO:0009820)	2.30E-02
BL	KOIGF1_WTFVEH	negative regulation of iron ion transmembrane transporter activity (GO:1904255)	2.29E-02
BL	KOIGF1_WTFVEH	monoterpenoid metabolic process (GO:0016098)	2.29E-02
BL	KOIGF1_WTFVEH	negative regulation of iron export across plasma membrane (GO:1904039)	2.28E-02
BL	KOIGF1_WTFVEH	regulation of iron export across plasma membrane (GO:1904038)	2.27E-02
BL	KOIGF1_WTFVEH	response to methanol (GO:0033986)	6.24E-05
BL	KOIGF1_WTFVEH	negative regulation of cholesterol import (GO:0060621)	2.27E-02
BL	KOIGF1_WTFVEH	regulation of very-low-density lipoprotein particle remodeling (GO:0010901)	1.02E-04
BL	KOIGF1_WTFVEH	response to chromate (GO:0046687)	1.01E-04
BL	KOIGF1_WTFVEH	negative regulation of very-low-density lipoprotein particle remodeling (GO:0010903)	1.84E-03
BL	KOIGF1_WTFVEH	tyrosine catabolic process (GO:0006572)	1.57E-04
BL	KOIGF1_WTFVEH	regulation of iron ion transmembrane transporter activity (GO:1904254)	3.50E-02
BL	KOIGF1_WTFVEH	urate catabolic process (GO:0019628)	3.49E-02
BL	KOIGF1_WTFVEH	L-phenylalanine catabolic process (GO:0006559)	1.17E-05
BL	KOIGF1_WTFVEH	erythrose 4-phosphate/phosphoenolpyruvate family amino acid catabolic process (GO:1902222)	1.16E-05
BL	KOIGF1_WTFVEH	L-phenylalanine metabolic process (GO:0006558)	8.99E-07
BL	KOIGF1_WTFVEH	erythrose 4-phosphate/phosphoenolpyruvate family amino acid metabolic process (GO:1902221)	8.89E-07
BL	KOIGF1_WTFVEH	L-cysteine catabolic process (GO:0019448)	4.91E-02
BL	KOIGF1_WTFVEH	blood coagulation, fibrin clot formation (GO:0072378)	3.26E-04

BL	KOIGF1_WTFVEH	triglyceride mobilization (GO:0006642)	4.07E-03
BL	KOIGF1_WTFVEH	arginine biosynthetic process (GO:0006526)	4.90E-02
BL	KOIGF1_WTFVEH	purine nucleobase catabolic process (GO:0006145)	4.05E-03
BL	KOIGF1_WTFVEH	xanthine catabolic process (GO:0009115)	4.89E-02
BL	KOIGF1_WTFVEH	hypoxanthine catabolic process (GO:0009114)	4.88E-02
BL	KOIGF1_WTFVEH	ketone body biosynthetic process (GO:0046951)	4.86E-02
BL	KOIGF1_WTFVEH	negative regulation of very-low-density lipoprotein particle clearance (GO:0010916)	4.85E-02
BL	KOIGF1_WTFVEH	regulation of very-low-density lipoprotein particle clearance (GO:0010915)	4.84E-02
BL	KOIGF1_WTFVEH	cysteine catabolic process (GO:0009093)	4.83E-02
BL	KOIGF1_WTFVEH	S-adenosylhomocysteine metabolic process (GO:0046498)	4.04E-03
BL	KOIGF1_WTFVEH	L-cysteine metabolic process (GO:0046439)	4.82E-02
BL	KOIGF1_WTFVEH	short-chain fatty acid catabolic process (GO:0019626)	4.02E-03
BL	KOIGF1_WTFVEH	high-density lipoprotein particle assembly (GO:0034380)	3.24E-04
BL	KOIGF1_WTFVEH	methyl-branched fatty acid metabolic process (GO:0097089)	4.81E-02
BL	KOIGF1_WTFVEH	complement activation, alternative pathway (GO:0006957)	3.54E-05
BL	KOIGF1_WTFVEH	negative regulation of serine-type peptidase activity (GO:1902572)	4.31E-04
BL	KOIGF1_WTFVEH	regulation of serine-type peptidase activity (GO:1902571)	4.28E-04
BL	KOIGF1_WTFVEH	negative regulation of serine-type endopeptidase activity (GO:1900004)	4.26E-04
BL	KOIGF1_WTFVEH	regulation of serine-type endopeptidase activity (GO:1900003)	4.24E-04
BL	KOIGF1_WTFVEH	coumarin metabolic process (GO:0009804)	5.56E-03
BL	KOIGF1_WTFVEH	phenylpropanoid metabolic process (GO:0009698)	5.54E-03
BL	KOIGF1_WTFVEH	negative regulation of lipoprotein lipase activity (GO:0051005)	5.52E-03
BL	KOIGF1_WTFVEH	fibrinolysis (GO:0042730)	3.61E-06
BL	KOIGF1_WTFVEH	sulfur amino acid catabolic process (GO:0000098)	5.50E-03
BL	KOIGF1_WTFVEH	alkanesulfonate metabolic process (GO:0019694)	5.48E-03
BL	KOIGF1_WTFVEH	taurine metabolic process (GO:0019530)	5.46E-03
BL	KOIGF1_WTFVEH	nitrogen cycle metabolic process (GO:0071941)	5.64E-04
BL	KOIGF1_WTFVEH	urea cycle (GO:0000050)	5.61E-04
BL	KOIGF1_WTFVEH	aromatic amino acid family catabolic process (GO:0009074)	4.83E-06
BL	KOIGF1_WTFVEH	urea metabolic process (GO:0019627)	5.58E-04
BL	KOIGF1_WTFVEH	phospholipid efflux (GO:0033700)	6.59E-05
BL	KOIGF1_WTFVEH	nucleobase catabolic process (GO:0046113)	7.22E-03
BL	KOIGF1_WTFVEH	regulation of bile acid secretion (GO:0120188)	7.20E-03
BL	KOIGF1_WTFVEH	triglyceride-rich lipoprotein particle remodeling (GO:0034370)	7.17E-03
BL	KOIGF1_WTFVEH	positive regulation of triglyceride catabolic process (GO:0010898)	7.34E-04
BL	KOIGF1_WTFVEH	tyrosine metabolic process (GO:0006570)	8.44E-05
BL	KOIGF1_WTFVEH	regulation of lipoprotein lipase activity (GO:0051004)	8.37E-06

BL	KOIGF1_WTFVEH	purine ribonucleoside catabolic process (GO:0046130)	9.21E-03
BL	KOIGF1_WTFVEH	deoxyribonucleoside catabolic process (GO:0046121)	9.18E-03
BL	KOIGF1_WTFVEH	epoxygenase P450 pathway (GO:0019373)	8.96E-12
BL	KOIGF1_WTFVEH	protein activation cascade (GO:0072376)	9.33E-04
BL	KOIGF1_WTFVEH	complement activation, lectin pathway (GO:0001867)	9.15E-03
BL	KOIGF1_WTFVEH	plasminogen activation (GO:0031639)	9.28E-04
BL	KOIGF1_WTFVEH	reverse cholesterol transport (GO:0043691)	1.33E-05
BL	KOIGF1_WTFVEH	regulation of triglyceride catabolic process (GO:0010896)	1.35E-04
BL	KOIGF1_WTFVEH	response to lead ion (GO:0010288)	1.17E-03
BL	KOIGF1_WTFVEH	high-density lipoprotein particle remodeling (GO:0034375)	1.16E-03
BL	KOIGF1_WTFVEH	positive regulation of lipoprotein lipase activity (GO:0051006)	1.13E-02
BL	KOIGF1_WTFVEH	positive regulation of cholesterol esterification (GO:0010873)	1.12E-02
BL	KOIGF1_WTFVEH	cholesterol efflux (GO:0033344)	2.70E-07
BL	KOIGF1_WTFVEH	plasma lipoprotein particle remodeling (GO:0034369)	2.83E-06
BL	KOIGF1_WTFVEH	protein-lipid complex remodeling (GO:0034368)	2.81E-06
BL	KOIGF1_WTFVEH	negative regulation of lipase activity (GO:0060192)	2.06E-04
BL	KOIGF1_WTFVEH	cysteine metabolic process (GO:0006534)	1.37E-02
BL	KOIGF1_WTFVEH	purine nucleoside catabolic process (GO:0006152)	1.36E-02
BL	KOIGF1_WTFVEH	regulation of intestinal cholesterol absorption (GO:0030300)	1.36E-02
BL	KOIGF1_WTFVEH	positive regulation of triglyceride lipase activity (GO:0061365)	1.35E-02
BL	KOIGF1_WTFVEH	arginine metabolic process (GO:0006525)	1.77E-03
BL	KOIGF1_WTFVEH	regulation of intestinal absorption (GO:1904478)	2.50E-04
BL	KOIGF1_WTFVEH	protein-containing complex remodeling (GO:0034367)	4.08E-06
BL	KOIGF1_WTFVEH	glycine metabolic process (GO:0006544)	2.12E-03
BL	KOIGF1_WTFVEH	glutamine family amino acid biosynthetic process (GO:0009084)	1.63E-02
BL	KOIGF1_WTFVEH	S-adenosylmethionine metabolic process (GO:0046500)	2.12E-03
BL	KOIGF1_WTFVEH	plasma lipoprotein particle clearance (GO:0034381)	3.01E-04
BL	KOIGF1_WTFVEH	plasma lipoprotein particle assembly (GO:0034377)	3.00E-04
BL	KOIGF1_WTFVEH	negative regulation of blood coagulation (GO:0030195)	1.48E-09
BL	KOIGF1_WTFVEH	sulfur amino acid metabolic process (GO:0000096)	5.90E-06
BL	KOIGF1_WTFVEH	aromatic amino acid family metabolic process (GO:0009072)	5.84E-06
BL	KOIGF1_WTFVEH	negative regulation of hemostasis (GO:1900047)	1.78E-09
BL	KOIGF1_WTFVEH	triglyceride catabolic process (GO:0019433)	2.56E-03
BL	KOIGF1_WTFVEH	negative regulation of coagulation (GO:0050819)	2.14E-09
BL	KOIGF1_WTFVEH	regulation of intestinal lipid absorption (GO:1904729)	1.95E-02
BL	KOIGF1_WTFVEH	deoxyribonucleoside metabolic process (GO:0009120)	1.94E-02
BL	KOIGF1_WTFVEH	regulation of cholesterol esterification (GO:0010872)	1.94E-02
BL	KOIGF1_WTFVEH	response to stilbenoid (GO:0035634)	4.11E-04
BL	KOIGF1_WTFVEH	xenobiotic catabolic process (GO:0042178)	1.03E-13
BL	KOIGF1_WTFVEH	positive regulation of lipid catabolic process (GO:0050996)	1.01E-05

BL	KOIGF1_WTFVEH	arachidonic acid metabolic process (GO:0019369)	2.10E-14
BL	KOIGF1_WTFVEH	positive regulation of heterotypic cell-cell adhesion (GO:0034116)	2.30E-02
BL	KOIGF1_WTFVEH	methionine metabolic process (GO:0006555)	2.29E-02
BL	KOIGF1_WTFVEH	negative regulation of cholesterol transport (GO:0032375)	2.28E-02
BL	KOIGF1_WTFVEH	negative regulation of sterol transport (GO:0032372)	2.28E-02
BL	KOIGF1_WTFVEH	short-chain fatty acid metabolic process (GO:0046459)	2.27E-02
BL	KOIGF1_WTFVEH	plasma lipoprotein particle organization (GO:0071827)	1.87E-06
BL	KOIGF1_WTFVEH	protein-lipid complex assembly (GO:0065005)	5.69E-04
BL	KOIGF1_WTFVEH	sulfur compound catabolic process (GO:0044273)	5.66E-04
BL	KOIGF1_WTFVEH	regulation of complement activation (GO:0030449)	5.63E-04
BL	KOIGF1_WTFVEH	positive regulation of triglyceride metabolic process (GO:0090208)	9.62E-05
BL	KOIGF1_WTFVEH	acylglycerol catabolic process (GO:0046464)	9.56E-05
BL	KOIGF1_WTFVEH	neutral lipid catabolic process (GO:0046461)	9.49E-05
BL	KOIGF1_WTFVEH	bile acid biosynthetic process (GO:0006699)	2.58E-02
BL	KOIGF1_WTFVEH	medium-chain fatty acid metabolic process (GO:0051791)	6.43E-04
BL	KOIGF1_WTFVEH	linoleic acid metabolic process (GO:0043651)	1.09E-04
BL	KOIGF1_WTFVEH	ribonucleoside catabolic process (GO:0042454)	2.58E-02
BL	KOIGF1_WTFVEH	negative regulation of cholesterol storage (GO:0010887)	2.57E-02
BL	KOIGF1_WTFVEH	purine ribonucleoside metabolic process (GO:0046128)	7.53E-04
BL	KOIGF1_WTFVEH	alpha-amino acid catabolic process (GO:1901606)	2.78E-10
BL	KOIGF1_WTFVEH	protein-lipid complex subunit organization (GO:0071825)	3.40E-06
BL	KOIGF1_WTFVEH	nucleoside catabolic process (GO:0009164)	4.99E-03
BL	KOIGF1_WTFVEH	acute-phase response (GO:0006953)	1.47E-04
BL	KOIGF1_WTFVEH	phosphatidylcholine biosynthetic process (GO:0006656)	2.99E-02
BL	KOIGF1_WTFVEH	regulation of bile acid biosynthetic process (GO:0070857)	2.98E-02
BL	KOIGF1_WTFVEH	bile acid metabolic process (GO:0008206)	8.74E-04
BL	KOIGF1_WTFVEH	regulation of cholesterol storage (GO:0010885)	5.62E-03
BL	KOIGF1_WTFVEH	regulation of blood coagulation (GO:0030193)	2.90E-09
BL	KOIGF1_WTFVEH	retinol metabolic process (GO:0042572)	9.90E-04
BL	KOIGF1_WTFVEH	response to testosterone (GO:0033574)	3.42E-02
BL	KOIGF1_WTFVEH	positive regulation of cholesterol metabolic process (GO:0090205)	3.42E-02
BL	KOIGF1_WTFVEH	regulation of hemostasis (GO:1900046)	3.69E-09
BL	KOIGF1_WTFVEH	positive regulation of cell growth involved in cardiac muscle cell development (GO:0061051)	3.41E-02
BL	KOIGF1_WTFVEH	regulation of coagulation (GO:0050818)	4.67E-09
BL	KOIGF1_WTFVEH	sterol transport (GO:0015918)	3.51E-08
BL	KOIGF1_WTFVEH	cholesterol transport (GO:0030301)	3.46E-08
BL	KOIGF1_WTFVEH	fatty acid derivative biosynthetic process (GO:1901570)	3.89E-02
BL	KOIGF1_WTFVEH	serine family amino acid metabolic process (GO:0009069)	2.51E-04
BL	KOIGF1_WTFVEH	nucleobase-containing small molecule catabolic process (GO:0034656)	7.33E-03

BL	KOIGF1_WTFVEH	long-chain fatty acid metabolic process (GO:0001676)	5.97E-15
BL	KOIGF1_WTFVEH	olefinic compound metabolic process (GO:0120254)	5.66E-15
BL	KOIGF1_WTFVEH	positive regulation of cholesterol efflux (GO:0010875)	1.46E-03
BL	KOIGF1_WTFVEH	regulation of heterotypic cell-cell adhesion (GO:0034114)	8.35E-03
BL	KOIGF1_WTFVEH	cytolysis (GO:0019835)	8.32E-03
BL	KOIGF1_WTFVEH	negative regulation of cytokine production involved in immune response (GO:0002719)	8.29E-03
BL	KOIGF1_WTFVEH	cellular amino acid catabolic process (GO:0009063)	3.25E-10
BL	KOIGF1_WTFVEH	positive regulation of steroid metabolic process (GO:0045940)	6.01E-05
BL	KOIGF1_WTFVEH	xenobiotic metabolic process (GO:0006805)	5.00E-14
BL	KOIGF1_WTFVEH	oxidative demethylation (GO:0070989)	4.38E-02
BL	KOIGF1_WTFVEH	regulation of bile acid metabolic process (GO:1904251)	4.37E-02
BL	KOIGF1_WTFVEH	negative regulation of wound healing (GO:0061045)	6.82E-08
BL	KOIGF1_WTFVEH	regulation of plasma lipoprotein particle levels (GO:0097006)	1.12E-05
BL	KOIGF1_WTFVEH	ribonucleoside metabolic process (GO:0009119)	1.63E-03
BL	KOIGF1_WTFVEH	unsaturated fatty acid metabolic process (GO:0033559)	6.30E-14
BL	KOIGF1_WTFVEH	triglyceride metabolic process (GO:0006641)	7.70E-08
BL	KOIGF1_WTFVEH	negative regulation of lipid storage (GO:0010888)	9.28E-03
BL	KOIGF1_WTFVEH	secondary alcohol biosynthetic process (GO:1902653)	3.53E-04
BL	KOIGF1_WTFVEH	cholesterol biosynthetic process (GO:0006695)	3.52E-04
BL	KOIGF1_WTFVEH	purine nucleoside metabolic process (GO:0042278)	1.84E-03
BL	KOIGF1_WTFVEH	cellular response to cholesterol (GO:0071397)	4.92E-02
BL	KOIGF1_WTFVEH	purine nucleobase metabolic process (GO:0006144)	4.91E-02
BL	KOIGF1_WTFVEH	deoxyribonucleoside monophosphate catabolic process (GO:0009159)	4.90E-02
BL	KOIGF1_WTFVEH	positive regulation of hemostasis (GO:1900048)	4.89E-02
BL	KOIGF1_WTFVEH	positive regulation of blood coagulation (GO:0030194)	4.88E-02
BL	KOIGF1_WTFVEH	regulation of lipid catabolic process (GO:0050994)	5.55E-07
BL	KOIGF1_WTFVEH	steroid catabolic process (GO:0006706)	1.04E-02
BL	KOIGF1_WTFVEH	platelet aggregation (GO:0070527)	1.03E-02
BL	KOIGF1_WTFVEH	coagulation (GO:0050817)	4.32E-12
BL	KOIGF1_WTFVEH	blood coagulation (GO:0007596)	4.20E-12
BL	KOIGF1_WTFVEH	hemostasis (GO:0007599)	5.26E-12
BL	KOIGF1_WTFVEH	icosanoid metabolic process (GO:0006690)	2.26E-13
BL	KOIGF1_WTFVEH	regulation of triglyceride metabolic process (GO:0090207)	1.15E-04
BL	KOIGF1_WTFVEH	triglyceride homeostasis (GO:0070328)	2.56E-03
BL	KOIGF1_WTFVEH	acylglycerol homeostasis (GO:0055090)	2.55E-03
BL	KOIGF1_WTFVEH	terpenoid metabolic process (GO:0006721)	5.00E-06
BL	KOIGF1_WTFVEH	glycosyl compound catabolic process (GO:1901658)	1.28E-02
BL	KOIGF1_WTFVEH	platelet activation (GO:0030168)	1.29E-04
BL	KOIGF1_WTFVEH	alpha-amino acid biosynthetic process (GO:1901607)	1.44E-04
BL	KOIGF1_WTFVEH	alpha-amino acid metabolic process (GO:1901605)	5.33E-15
BL	KOIGF1_WTFVEH	acylglycerol metabolic process (GO:0006639)	2.37E-09

BL	KOIGF1_WTFVEH	sterol biosynthetic process (GO:0016126)	6.46E-04
BL	KOIGF1_WTFVEH	neutral lipid metabolic process (GO:0006638)	2.93E-09
BL	KOIGF1_WTFVEH	regulation of lipid storage (GO:0010883)	1.73E-04
BL	KOIGF1_WTFVEH	carboxylic acid catabolic process (GO:0046395)	7.92E-17
BL	KOIGF1_WTFVEH	negative regulation of endothelial cell apoptotic process (GO:2000352)	1.55E-02
BL	KOIGF1_WTFVEH	acetyl-CoA metabolic process (GO:0006084)	1.55E-02
BL	KOIGF1_WTFVEH	cholesterol metabolic process (GO:0008203)	1.42E-10
BL	KOIGF1_WTFVEH	regulation of cholesterol transport (GO:0032374)	8.46E-06
BL	KOIGF1_WTFVEH	regulation of sterol transport (GO:0032371)	8.39E-06
BL	KOIGF1_WTFVEH	organic acid catabolic process (GO:0016054)	9.16E-17
BL	KOIGF1_WTFVEH	glutamine family amino acid metabolic process (GO:0009064)	1.91E-04
BL	KOIGF1_WTFVEH	negative regulation of lipid localization (GO:1905953)	2.11E-04
BL	KOIGF1_WTFVEH	regulation of humoral immune response (GO:0002920)	8.72E-04
BL	KOIGF1_WTFVEH	negative regulation of response to wounding (GO:1903035)	5.46E-07
BL	KOIGF1_WTFVEH	retinoid metabolic process (GO:0001523)	2.32E-04
BL	KOIGF1_WTFVEH	cellular response to xenobiotic stimulus (GO:0071466)	1.28E-13
BL	KOIGF1_WTFVEH	nucleobase metabolic process (GO:0009112)	1.85E-02
BL	KOIGF1_WTFVEH	killing of cells of other organism (GO:0031640)	3.11E-06
BL	KOIGF1_WTFVEH	sterol metabolic process (GO:0016125)	3.53E-10
BL	KOIGF1_WTFVEH	secondary metabolic process (GO:0019748)	1.04E-03
BL	KOIGF1_WTFVEH	regulation of cholesterol efflux (GO:0010874)	4.79E-03
BL	KOIGF1_WTFVEH	monocarboxylic acid catabolic process (GO:0072329)	1.83E-07
BL	KOIGF1_WTFVEH	cellular amino acid biosynthetic process (GO:0008652)	2.80E-04
BL	KOIGF1_WTFVEH	diterpenoid metabolic process (GO:0016101)	2.78E-04
BL	KOIGF1_WTFVEH	steroid metabolic process (GO:0008202)	3.58E-20
BL	KOIGF1_WTFVEH	secondary alcohol metabolic process (GO:1902652)	4.72E-10
BL	KOIGF1_WTFVEH	glycerolipid catabolic process (GO:0046503)	1.24E-03
BL	KOIGF1_WTFVEH	defense response to fungus (GO:0050832)	5.65E-03
BL	KOIGF1_WTFVEH	purine-containing compound catabolic process (GO:0072523)	5.63E-03
BL	KOIGF1_WTFVEH	organic hydroxy compound transport (GO:0015850)	7.63E-10
BL	KOIGF1_WTFVEH	fatty acid catabolic process (GO:0009062)	2.18E-05
BL	KOIGF1_WTFVEH	nucleoside metabolic process (GO:0009116)	1.48E-03
BL	KOIGF1_WTFVEH	positive regulation of cholesterol transport (GO:0032376)	6.14E-03
BL	KOIGF1_WTFVEH	positive regulation of sterol transport (GO:0032373)	6.12E-03
BL	KOIGF1_WTFVEH	monosaccharide biosynthetic process (GO:0046364)	2.35E-02
BL	KOIGF1_WTFVEH	vitamin transport (GO:0051180)	2.56E-02
BL	KOIGF1_WTFVEH	aspartate family amino acid metabolic process (GO:0009066)	2.56E-02
BL	KOIGF1_WTFVEH	isoprenoid metabolic process (GO:0006720)	3.12E-05
BL	KOIGF1_WTFVEH	regulation of fatty acid biosynthetic process (GO:0042304)	7.24E-03
BL	KOIGF1_WTFVEH	negative regulation of production of molecular mediator of immune response (GO:0002701)	2.75E-02

BL	KOIGF1_WTFVEH	steroid biosynthetic process (GO:0006694)	2.38E-06
BL	KOIGF1_WTFVEH	small molecule catabolic process (GO:0044282)	1.83E-19
BL	KOIGF1_WTFVEH	primary alcohol metabolic process (GO:0034308)	5.71E-04
BL	KOIGF1_WTFVEH	fatty acid derivative metabolic process (GO:1901568)	3.23E-02
BL	KOIGF1_WTFVEH	regulation of cholesterol metabolic process (GO:0090181)	3.22E-02
BL	KOIGF1_WTFVEH	regulation of wound healing (GO:0061041)	2.33E-07
BL	KOIGF1_WTFVEH	negative regulation of epithelial cell apoptotic process (GO:1904036)	1.04E-02
BL	KOIGF1_WTFVEH	phosphatidylcholine metabolic process (GO:0046470)	1.04E-02
BL	KOIGF1_WTFVEH	cell killing (GO:0001906)	1.34E-06
BL	KOIGF1_WTFVEH	regulation of lipase activity (GO:0060191)	2.51E-04
BL	KOIGF1_WTFVEH	cholesterol homeostasis (GO:0042632)	7.56E-05
BL	KOIGF1_WTFVEH	fatty acid metabolic process (GO:0006631)	1.45E-19
BL	KOIGF1_WTFVEH	cellular amino acid metabolic process (GO:0006520)	5.60E-13
BL	KOIGF1_WTFVEH	sterol homeostasis (GO:0055092)	8.15E-05
BL	KOIGF1_WTFVEH	homotypic cell-cell adhesion (GO:0034109)	4.31E-02
BL	KOIGF1_WTFVEH	cellular aldehyde metabolic process (GO:0006081)	1.29E-02
BL	KOIGF1_WTFVEH	regulation of digestive system process (GO:0044058)	1.28E-02
BL	KOIGF1_WTFVEH	ribonucleotide catabolic process (GO:0009261)	4.30E-02
BL	KOIGF1_WTFVEH	response to nutrient (GO:0007584)	1.28E-02
BL	KOIGF1_WTFVEH	glycosyl compound metabolic process (GO:1901657)	1.15E-03
BL	KOIGF1_WTFVEH	response to fungus (GO:0009620)	1.35E-02
BL	KOIGF1_WTFVEH	antimicrobial humoral response (GO:0019730)	2.30E-07
BL	KOIGF1_WTFVEH	acute inflammatory response (GO:0002526)	4.37E-03
BL	KOIGF1_WTFVEH	positive regulation of lipid metabolic process (GO:0045834)	2.08E-08
BL	KOIGF1_WTFVEH	positive regulation of glucose metabolic process (GO:0010907)	4.91E-02
BL	KOIGF1_WTFVEH	alcohol biosynthetic process (GO:0046165)	4.73E-04
BL	KOIGF1_WTFVEH	alcohol metabolic process (GO:0006066)	3.11E-13
BL	KOIGF1_WTFVEH	acyl-CoA metabolic process (GO:0006637)	1.60E-03
BL	KOIGF1_WTFVEH	thioester metabolic process (GO:0035383)	1.59E-03
BL	KOIGF1_WTFVEH	carboxylic acid metabolic process (GO:0019752)	5.45E-37
BL	KOIGF1_WTFVEH	monocarboxylic acid metabolic process (GO:0032787)	1.54E-22
BL	KOIGF1_WTFVEH	organic acid metabolic process (GO:0006082)	1.28E-38
BL	KOIGF1_WTFVEH	oxoacid metabolic process (GO:0043436)	1.29E-36
BL	KOIGF1_WTFVEH	negative regulation of peptidase activity (GO:0010466)	1.35E-10
BL	KOIGF1_WTFVEH	cellular lipid catabolic process (GO:0044242)	1.99E-07
BL	KOIGF1_WTFVEH	antimicrobial humoral immune response mediated by antimicrobial peptide (GO:0061844)	7.21E-05
BL	KOIGF1_WTFVEH	negative regulation of endopeptidase activity (GO:0010951)	1.96E-07
BL	KOIGF1_WTFVEH	response to xenobiotic stimulus (GO:0009410)	1.16E-12
BL	KOIGF1_WTFVEH	positive regulation of receptor-mediated endocytosis (GO:0048260)	2.11E-02
BL	KOIGF1_WTFVEH	organic hydroxy compound metabolic process (GO:1901615)	5.59E-18

BL	KOIGF1_WTFVEH	cellular hormone metabolic process (GO:0034754)	8.64E-04
BL	KOIGF1_WTFVEH	fatty acid oxidation (GO:0019395)	8.07E-03
BL	KOIGF1_WTFVEH	regulation of lipid localization (GO:1905952)	1.06E-06
BL	KOIGF1_WTFVEH	purine nucleoside bisphosphate metabolic process (GO:0034032)	9.10E-04
BL	KOIGF1_WTFVEH	ribonucleoside bisphosphate metabolic process (GO:0033875)	9.05E-04
BL	KOIGF1_WTFVEH	nucleoside bisphosphate metabolic process (GO:0033865)	9.01E-04
BL	KOIGF1_WTFVEH	regulation of response to wounding (GO:1903034)	3.71E-06
BL	KOIGF1_WTFVEH	positive regulation of lipid localization (GO:1905954)	4.05E-04
BL	KOIGF1_WTFVEH	sulfur compound metabolic process (GO:0006790)	7.49E-11
BL	KOIGF1_WTFVEH	lipid catabolic process (GO:0016042)	2.29E-09
BL	KOIGF1_WTFVEH	organic hydroxy compound biosynthetic process (GO:1901617)	1.71E-05
BL	KOIGF1_WTFVEH	negative regulation of hydrolase activity (GO:0051346)	7.17E-13
BL	KOIGF1_WTFVEH	positive regulation of phagocytosis (GO:0050766)	1.05E-02
BL	KOIGF1_WTFVEH	wound healing (GO:0042060)	2.92E-08
BL	KOIGF1_WTFVEH	lipid oxidation (GO:0034440)	1.10E-02
BL	KOIGF1_WTFVEH	organic hydroxy compound catabolic process (GO:1901616)	3.01E-02
BL	KOIGF1_WTFVEH	lipid transport (GO:0006869)	4.34E-09
BL	KOIGF1_WTFVEH	regulation of lipid biosynthetic process (GO:0046890)	3.12E-06
BL	KOIGF1_WTFVEH	regulation of steroid metabolic process (GO:0019218)	1.62E-03
BL	KOIGF1_WTFVEH	zymogen activation (GO:0031638)	3.51E-02
BL	KOIGF1_WTFVEH	carboxylic acid biosynthetic process (GO:0046394)	4.81E-07
BL	KOIGF1_WTFVEH	organic acid biosynthetic process (GO:0016053)	5.04E-07
BL	KOIGF1_WTFVEH	response to toxic substance (GO:0009636)	1.88E-03
BL	KOIGF1_WTFVEH	negative regulation of proteolysis (GO:0045861)	1.10E-10
BL	KOIGF1_WTFVEH	positive regulation of small molecule metabolic process (GO:0062013)	1.01E-04
BL	KOIGF1_WTFVEH	small molecule biosynthetic process (GO:0044283)	1.36E-11
BL	KOIGF1_WTFVEH	regulation of cellular ketone metabolic process (GO:0010565)	2.88E-04
BL	KOIGF1_WTFVEH	regulation of lipid transport (GO:0032368)	3.17E-04
BL	KOIGF1_WTFVEH	lipid localization (GO:0010876)	4.42E-09
BL	KOIGF1_WTFVEH	response to glucocorticoid (GO:0051384)	4.72E-02
BL	KOIGF1_WTFVEH	lipoprotein metabolic process (GO:0042157)	8.48E-03
BL	KOIGF1_WTFVEH	cellular lipid metabolic process (GO:0044255)	5.96E-24
BL	KOIGF1_WTFVEH	response to alcohol (GO:0097305)	5.33E-04
BL	KOIGF1_WTFVEH	regulation of fatty acid metabolic process (GO:0019217)	2.23E-02
BL	KOIGF1_WTFVEH	lipid homeostasis (GO:0055088)	5.61E-04
BL	KOIGF1_WTFVEH	positive regulation of lipid transport (GO:0032370)	2.31E-02
BL	KOIGF1_WTFVEH	small molecule metabolic process (GO:0044281)	5.17E-41
BL	KOIGF1_WTFVEH	regeneration (GO:0031099)	2.37E-02
BL	KOIGF1_WTFVEH	hormone metabolic process (GO:0042445)	6.45E-04
BL	KOIGF1_WTFVEH	organic cyclic compound catabolic process (GO:1901361)	1.95E-07

BL	KOIGF1_WTFVEH	regulation of body fluid levels (GO:0050878)	8.26E-08
BL	KOIGF1_WTFVEH	cellular modified amino acid metabolic process (GO:0006575)	3.51E-04
BL	KOIGF1_WTFVEH	lipid metabolic process (GO:0006629)	3.00E-28
BL	KOIGF1_WTFVEH	positive regulation of lipid biosynthetic process (GO:0046889)	2.79E-02
BL	KOIGF1_WTFVEH	response to wounding (GO:0009611)	2.49E-07
BL	KOIGF1_WTFVEH	aromatic compound catabolic process (GO:0019439)	1.83E-06
BL	KOIGF1_WTFVEH	regulation of receptor-mediated endocytosis (GO:0048259)	1.32E-02
BL	KOIGF1_WTFVEH	humoral immune response (GO:0006959)	3.19E-09
BL	KOIGF1_WTFVEH	regulation of lipid metabolic process (GO:0019216)	5.81E-08
BL	KOIGF1_WTFVEH	response to metal ion (GO:0010038)	5.73E-06
BL	KOIGF1_WTFVEH	regulation of peptidase activity (GO:0052547)	4.74E-09
BL	KOIGF1_WTFVEH	regulation of glucose metabolic process (GO:0010906)	1.59E-02
BL	KOIGF1_WTFVEH	response to peptide hormone (GO:0043434)	2.28E-05
BL	KOIGF1_WTFVEH	regulation of phagocytosis (GO:0050764)	3.98E-02
BL	KOIGF1_WTFVEH	glycerolipid metabolic process (GO:0046486)	5.60E-06
BL	KOIGF1_WTFVEH	circadian rhythm (GO:0007623)	2.15E-02
BL	KOIGF1_WTFVEH	regulation of endopeptidase activity (GO:0052548)	3.25E-06
BL	KOIGF1_WTFVEH	cell-matrix adhesion (GO:0007160)	4.99E-02
BL	KOIGF1_WTFVEH	organophosphate catabolic process (GO:0046434)	2.58E-02
BL	KOIGF1_WTFVEH	lipid modification (GO:0030258)	1.29E-02
BL	KOIGF1_WTFVEH	negative regulation of response to external stimulus (GO:0032102)	2.86E-06
BL	KOIGF1_WTFVEH	purine-containing compound metabolic process (GO:0072521)	8.13E-05
BL	KOIGF1_WTFVEH	regulation of small molecule metabolic process (GO:0062012)	1.95E-05
BL	KOIGF1_WTFVEH	response to peptide (GO:1901652)	4.53E-05
BL	KOIGF1_WTFVEH	defense response to Gram-positive bacterium (GO:0050830)	3.36E-02
BL	KOIGF1_WTFVEH	regulation of production of molecular mediator of immune response (GO:0002700)	1.66E-02
BL	KOIGF1_WTFVEH	cell-substrate adhesion (GO:0031589)	2.08E-02
BL	KOIGF1_WTFVEH	complement activation (GO:0006956)	5.68E-03
BL	KOIGF1_WTFVEH	positive regulation of protein secretion (GO:0050714)	4.56E-02
BL	KOIGF1_WTFVEH	response to inorganic substance (GO:0010035)	1.26E-05
BL	KOIGF1_WTFVEH	regulation of cellular carbohydrate metabolic process (GO:0010675)	4.70E-02
BL	KOIGF1_WTFVEH	cellular response to extracellular stimulus (GO:0031668)	1.65E-02
BL	KOIGF1_WTFVEH	negative regulation of catalytic activity (GO:0043086)	1.22E-07
BL	KOIGF1_WTFVEH	ribonucleotide metabolic process (GO:0009259)	2.76E-03
BL	KOIGF1_WTFVEH	purine ribonucleotide metabolic process (GO:0009150)	6.27E-03
BL	KOIGF1_WTFVEH	ribose phosphate metabolic process (GO:0019693)	3.94E-03
BL	KOIGF1_WTFVEH	regulation of immune effector process (GO:0002697)	3.51E-04
BL	KOIGF1_WTFVEH	response to hormone (GO:0009725)	1.01E-05
BL	KOIGF1_WTFVEH	regulation of proteolysis (GO:0030162)	2.30E-07
BL	KOIGF1_WTFVEH	purine nucleotide metabolic process (GO:0006163)	9.39E-03

BL	KOIGF1_WTFVEH	response to extracellular stimulus (GO:0009991)	1.59E-03
BL	KOIGF1_WTFVEH	organic acid transport (GO:0015849)	2.99E-02
BL	KOIGF1_WTFVEH	cellular catabolic process (GO:0044248)	4.70E-16
BL	KOIGF1_WTFVEH	nucleobase-containing small molecule metabolic process (GO:0055086)	5.63E-04
BL	KOIGF1_WTFVEH	regulation of hydrolase activity (GO:0051336)	3.32E-09
BL	KOIGF1_WTFVEH	negative regulation of cell adhesion (GO:0007162)	1.29E-02
BL	KOIGF1_WTFVEH	cellular response to external stimulus (GO:0071496)	3.81E-02
BL	KOIGF1_WTFVEH	catabolic process (GO:0009056)	1.57E-16
BL	KOIGF1_WTFVEH	lipid biosynthetic process (GO:0008610)	7.99E-04
BL	KOIGF1_WTFVEH	organic substance catabolic process (GO:1901575)	7.66E-11
BL	KOIGF1_WTFVEH	nucleotide metabolic process (GO:0009117)	1.62E-02
BL	KOIGF1_WTFVEH	response to nutrient levels (GO:0031667)	2.59E-02
BL	KOIGF1_WTFVEH	nucleoside phosphate metabolic process (GO:0006753)	1.95E-02
BL	KOIGF1_WTFVEH	response to organic cyclic compound (GO:0014070)	5.01E-04
BL	KOIGF1_WTFVEH	regulation of hormone levels (GO:0010817)	2.10E-03
BL	KOIGF1_WTFVEH	response to lipid (GO:0033993)	5.56E-04
BL	KOIGF1_WTFVEH	carbohydrate derivative metabolic process (GO:1901135)	7.09E-05
BL	KOIGF1_WTFVEH	response to bacterium (GO:0009617)	2.81E-05
BL	KOIGF1_WTFVEH	response to organonitrogen compound (GO:0010243)	2.10E-04
BL	KOIGF1_WTFVEH	inflammatory response (GO:0006954)	1.15E-02
BL	KOIGF1_WTFVEH	negative regulation of molecular function (GO:0044092)	8.64E-06
BL	KOIGF1_WTFVEH	response to nitrogen compound (GO:1901698)	1.84E-04
BL	KOIGF1_WTFVEH	regulation of cell-cell adhesion (GO:0022407)	2.60E-02
BL	KOIGF1_WTFVEH	cellular amide metabolic process (GO:0043603)	1.83E-03
BL	KOIGF1_WTFVEH	adaptive immune response (GO:0002250)	2.21E-02
BL	KOIGF1_WTFVEH	negative regulation of cellular protein metabolic process (GO:0032269)	1.51E-04
BL	KOIGF1_WTFVEH	regulation of response to external stimulus (GO:0032101)	3.99E-04
BL	KOIGF1_WTFVEH	response to oxygen-containing compound (GO:1901700)	4.64E-06
BL	KOIGF1_WTFVEH	organophosphate metabolic process (GO:0019637)	3.35E-03
BL	KOIGF1_WTFVEH	positive regulation of transport (GO:0051050)	1.62E-04
BL	KOIGF1_WTFVEH	regulation of vesicle-mediated transport (GO:0060627)	1.55E-02
BL	KOIGF1_WTFVEH	negative regulation of multicellular organismal process (GO:0051241)	1.44E-04
BL	KOIGF1_WTFVEH	negative regulation of protein metabolic process (GO:0051248)	3.99E-04
BL	KOIGF1_WTFVEH	response to endogenous stimulus (GO:0009719)	3.40E-04
BL	KOIGF1_WTFVEH	chemical homeostasis (GO:0048878)	3.55E-04
BL	KOIGF1_WTFVEH	response to other organism (GO:0051707)	3.56E-05
BL	KOIGF1_WTFVEH	response to external biotic stimulus (GO:0043207)	3.62E-05
BL	KOIGF1_WTFVEH	response to chemical (GO:0042221)	1.52E-14
BL	KOIGF1_WTFVEH	response to biotic stimulus (GO:0009607)	8.29E-05
BL	KOIGF1_WTFVEH	organonitrogen compound catabolic process (GO:1901565)	4.42E-03

BL	KOIGF1_WTFVEH	organic cyclic compound metabolic process (GO:1901360)	5.48E-09
BL	KOIGF1_WTFVEH	regulation of cell adhesion (GO:0030155)	2.46E-02
BL	KOIGF1_WTFVEH	biological process involved in interspecies interaction between organisms (GO:0044419)	1.70E-04
BL	KOIGF1_WTFVEH	regulation of catalytic activity (GO:0050790)	9.70E-05
BL	KOIGF1_WTFVEH	defense response to other organism (GO:0098542)	9.90E-03
BL	KOIGF1_WTFVEH	response to external stimulus (GO:0009605)	2.35E-06
BL	KOIGF1_WTFVEH	defense response (GO:0006952)	1.35E-03
BL	KOIGF1_WTFVEH	positive regulation of immune system process (GO:0002684)	4.19E-02
BL	KOIGF1_WTFVEH	biosynthetic process (GO:0009058)	3.62E-04
BL	KOIGF1_WTFVEH	organic substance biosynthetic process (GO:1901576)	1.11E-03
BL	KOIGF1_WTFVEH	immune response (GO:0006955)	5.47E-03
BL	KOIGF1_WTFVEH	regulation of transport (GO:0051049)	2.54E-03
BL	KOIGF1_WTFVEH	regulation of response to stress (GO:0080134)	3.97E-02
BL	KOIGF1_WTFVEH	cellular response to chemical stimulus (GO:0070887)	3.94E-04
BL	KOIGF1_WTFVEH	regulation of immune system process (GO:0002682)	1.44E-02
BL	KOIGF1_WTFVEH	homeostatic process (GO:0042592)	1.56E-02
BL	KOIGF1_WTFVEH	primary metabolic process (GO:0044238)	2.09E-13
BL	KOIGF1_WTFVEH	organonitrogen compound metabolic process (GO:1901564)	2.35E-07
BL	KOIGF1_WTFVEH	regulation of molecular function (GO:0065009)	1.28E-03
BL	KOIGF1_WTFVEH	response to organic substance (GO:0010033)	1.02E-03
BL	KOIGF1_WTFVEH	metabolic process (GO:0008152)	1.04E-16
BL	KOIGF1_WTFVEH	organic substance metabolic process (GO:0071704)	6.11E-15
BL	KOIGF1_WTFVEH	regulation of cellular protein metabolic process (GO:0032268)	9.60E-03
BL	KOIGF1_WTFVEH	cellular biosynthetic process (GO:0044249)	2.90E-02
BL	KOIGF1_WTFVEH	regulation of protein metabolic process (GO:0051246)	1.01E-02
BL	KOIGF1_WTFVEH	cellular metabolic process (GO:0044237)	3.35E-09
BL	KOIGF1_WTFVEH	response to stress (GO:0006950)	1.59E-03
BL	KOIGF1_WTFVEH	cellular aromatic compound metabolic process (GO:0006725)	3.38E-02
BL	KOIGF1_WTFVEH	regulation of biological quality (GO:0065008)	1.15E-03
BL	KOIGF1_WTFVEH	regulation of localization (GO:0032879)	1.55E-02
BL	KOIGF1_WTFVEH	nitrogen compound metabolic process (GO:0006807)	4.00E-04
BL	KOIGF1_WTFVEH	response to stimulus (GO:0050896)	4.70E-07
BL	KOIGF1_WTFVEH	cell communication (GO:0007154)	4.68E-02
BL	KOIGF1_WTFVEH	signal transduction (GO:0007165)	5.24E-03
BL	KOIGF1_WTFVEH	signaling (GO:0023052)	1.94E-03
BL	KOIGF1_WTFVEH	regulation of RNA biosynthetic process (GO:2001141)	1.81E-02
BL	KOIGF1_WTFVEH	regulation of RNA metabolic process (GO:0051252)	7.80E-03
BL	KOIGF1_WTFVEH	regulation of cellular macromolecule biosynthetic process (GO:2000112)	2.55E-03
BL	KOIGF1_WTFVEH	regulation of transcription, DNA-templated (GO:0006355)	9.27E-03
BL	KOIGF1_WTFVEH	regulation of nucleic acid-templated transcription (GO:1903506)	9.28E-03

BL	KOIGF1_WTFVEH	regulation of macromolecule biosynthetic process (GO:0010556)	2.56E-03
BL	KOIGF1_WTFVEH	regulation of nucleobase-containing compound metabolic process (GO:0019219)	1.89E-03
BL	KOIGF1_WTFVEH	regulation of transcription by RNA polymerase II (GO:0006357)	1.15E-02
BL	KOIGF1_WTFVEH	cellular localization (GO:0051641)	1.15E-02
BL	KOIGF1_WTFVEH	G protein-coupled receptor signaling pathway (GO:0007186)	2.50E-02
BL	KOIGF1_WTFVEH	nucleic acid metabolic process (GO:0090304)	9.85E-03
BL	KOIGF1_WTFVEH	establishment of localization in cell (GO:0051649)	1.15E-02
BL	KOIGF1_WTFVEH	intracellular transport (GO:0046907)	4.39E-02
BL	KOIGF1_WTFVEH	organelle organization (GO:0006996)	5.72E-07
BL	KOIGF1_WTFVEH	sensory perception of smell (GO:0007608)	1.77E-02
BL	KOIGF1_WTFVEH	cytoskeleton organization (GO:0007010)	1.77E-02
BL	KOIGF1_WTFVEH	cell cycle (GO:0007049)	1.22E-03
BL	KOIGF1_WTFVEH	RNA processing (GO:0006396)	3.91E-02
BL	KOIGF1_WTFVEH	chromosome organization (GO:0051276)	7.18E-03
BL	KOIGF1_WTFVEH	cell cycle process (GO:0022402)	3.87E-02

Supplementary Table 13 – GO Analysis of Treated Female Mice from Chapter II
All significant ontologies found in GO analysis of Female mice treated with rhIGF1 or vehicle.
Legend:
CRB = Cerebellum, BL = Blood,
HET.IGF1_VEH = rhIGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{-/+}$,
WTF.IGF1_VEH = rhIGF1 treated *Mecp2*$^{+/+}$ vs. VEH treated *Mecp2*$^{+/+}$,
IGF1.HET_WTF= rhIGF1 treated *Mecp2*$^{-/+}$ vs. rhIGF1 treated *Mecp2*$^{+/+}$,
VEH.HET_WTF = VEH treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/+}$,
HETIGF1_WTFVEH = IGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/+}$

Tissue	Comparison	GO biological process complete	FDR
CRB	KO.IGF1_VEH	ATP metabolic process (GO:0046034)	2.08E-02
CRB	KO.IGF1_VEH	autophagy (GO:0006914)	3.98E-02
CRB	KO.IGF1_VEH	process utilizing autophagic mechanism (GO:0061919)	3.70E-02
CRB	KO.IGF1_VEH	cellular response to external stimulus (GO:0071496)	4.46E-02
CRB	KO.IGF1_VEH	protein-containing complex subunit organization (GO:0043933)	4.37E-02
CRB	KO.IGF1_VEH	intracellular transport (GO:0046907)	4.36E-02
CRB	KO.IGF1_VEH	cellular catabolic process (GO:0044248)	1.37E-02
CRB	KO.IGF1_VEH	catabolic process (GO:0009056)	1.51E-02
CRB	KO.IGF1_VEH	cellular localization (GO:0051641)	4.01E-02
CRB	KO.IGF1_VEH	organonitrogen compound metabolic process (GO:1901564)	1.18E-04
CRB	KO.IGF1_VEH	cellular protein metabolic process (GO:0044267)	4.79E-02
CRB	KO.IGF1_VEH	protein metabolic process (GO:0019538)	4.31E-02
CRB	KO.IGF1_VEH	cellular metabolic process (GO:0044237)	7.77E-06
CRB	KO.IGF1_VEH	nitrogen compound metabolic process (GO:0006807)	3.56E-04
CRB	KO.IGF1_VEH	metabolic process (GO:0008152)	3.97E-06
CRB	KO.IGF1_VEH	primary metabolic process (GO:0044238)	1.23E-03
CRB	KO.IGF1_VEH	organic substance metabolic process (GO:0071704)	1.46E-03

CRB	KO.IGF1_VEH	cellular process (GO:0009987)	3.64E-02
CRB	KO.IGF1_VEH	G protein-coupled receptor signaling pathway (GO:0007186)	3.67E-02
CRB	KO.IGF1_VEH	sensory perception of smell (GO:0007608)	3.37E-02
CRB	KO.IGF1_VEH	sensory perception of chemical stimulus (GO:0007606)	2.06E-02
CRB	WTM.IGF1_VEH	response to organonitrogen compound (GO:0010243)	7.21E-02
CRB	WTM.IGF1_VEH	response to nitrogen compound (GO:1901698)	4.61E-02
CRB	IGF1.KO_WTM	response to toxic substance (GO:0009636)	3.96E-02
CRB	IGF1.KO_WTM	protein folding (GO:0006457)	7.52E-03
CRB	IGF1.KO_WTM	glial cell differentiation (GO:0010001)	7.70E-03
CRB	IGF1.KO_WTM	gliogenesis (GO:0042063)	1.35E-02
CRB	IGF1.KO_WTM	autophagy (GO:0006914)	3.72E-02
CRB	IGF1.KO_WTM	process utilizing autophagic mechanism (GO:0061919)	3.63E-02
CRB	IGF1.KO_WTM	regulation of apoptotic signaling pathway (GO:2001233)	4.46E-03
CRB	IGF1.KO_WTM	intracellular protein transport (GO:0006886)	4.02E-02
CRB	IGF1.KO_WTM	protein-containing complex subunit organization (GO:0043933)	3.85E-04
CRB	IGF1.KO_WTM	negative regulation of programmed cell death (GO:0043069)	1.04E-02
CRB	IGF1.KO_WTM	negative regulation of apoptotic process (GO:0043066)	1.38E-02
CRB	IGF1.KO_WTM	response to organonitrogen compound (GO:0010243)	4.47E-02
CRB	IGF1.KO_WTM	negative regulation of molecular function (GO:0044092)	9.70E-03
CRB	IGF1.KO_WTM	negative regulation of cell death (GO:0060548)	1.06E-02
CRB	IGF1.KO_WTM	response to nitrogen compound (GO:1901698)	3.78E-02
CRB	IGF1.KO_WTM	regulation of apoptotic process (GO:0042981)	7.60E-04
CRB	IGF1.KO_WTM	protein-containing complex assembly (GO:0065003)	1.69E-02
CRB	IGF1.KO_WTM	regulation of programmed cell death (GO:0043067)	7.32E-04
CRB	IGF1.KO_WTM	regulation of cell death (GO:0010941)	5.78E-04
CRB	IGF1.KO_WTM	response to oxygen-containing compound (GO:1901700)	1.23E-02
CRB	IGF1.KO_WTM	establishment of protein localization (GO:0045184)	4.79E-02
CRB	IGF1.KO_WTM	regulation of cell population proliferation (GO:0042127)	1.39E-02
CRB	IGF1.KO_WTM	regulation of protein metabolic process (GO:0051246)	1.08E-03
CRB	IGF1.KO_WTM	cellular component assembly (GO:0022607)	7.69E-03
CRB	IGF1.KO_WTM	catabolic process (GO:0009056)	2.75E-02
CRB	IGF1.KO_WTM	regulation of cellular protein metabolic process (GO:0032268)	5.18E-03
CRB	IGF1.KO_WTM	response to organic substance (GO:0010033)	2.03E-03
CRB	IGF1.KO_WTM	cellular component biogenesis (GO:0044085)	8.53E-03
CRB	IGF1.KO_WTM	response to chemical (GO:0042221)	2.91E-04
CRB	IGF1.KO_WTM	cellular response to chemical stimulus (GO:0070887)	1.09E-02
CRB	IGF1.KO_WTM	cellular localization (GO:0051641)	2.22E-02
CRB	IGF1.KO_WTM	regulation of molecular function (GO:0065009)	1.29E-02
CRB	IGF1.KO_WTM	response to stress (GO:0006950)	7.50E-03
CRB	IGF1.KO_WTM	regulation of localization (GO:0032879)	2.20E-02
CRB	IGF1.KO_WTM	cellular component organization (GO:0016043)	3.52E-04
CRB	IGF1.KO_WTM	organelle organization (GO:0006996)	3.96E-02

CRB	IGF1.KO_WTM	cellular component organization or biogenesis (GO:0071840)	3.87E-04
CRB	IGF1.KO_WTM	negative regulation of cellular process (GO:0048523)	1.02E-03
CRB	IGF1.KO_WTM	regulation of biological quality (GO:0065008)	1.38E-02
CRB	IGF1.KO_WTM	negative regulation of biological process (GO:0048519)	2.34E-03
CRB	IGF1.KO_WTM	organonitrogen compound metabolic process (GO:1901564)	2.18E-02
CRB	IGF1.KO_WTM	localization (GO:0051179)	3.99E-02
CRB	IGF1.KO_WTM	cellular metabolic process (GO:0044237)	2.76E-02
CRB	IGF1.KO_WTM	metabolic process (GO:0008152)	6.56E-03
CRB	IGF1.KO_WTM	cellular process (GO:0009987)	4.06E-03
CRB	IGF1.KO_WTM	G protein-coupled receptor signaling pathway (GO:0007186)	5.22E-03
CRB	IGF1.KO_WTM	sensory perception of chemical stimulus (GO:0007606)	8.43E-04
CRB	IGF1.KO_WTM	sensory perception of smell (GO:0007608)	2.61E-04
CRB	VEH.KO_WTM	aerobic electron transport chain (GO:0019646)	4.55E-02
CRB	VEH.KO_WTM	oxidative phosphorylation (GO:0006119)	3.11E-02
CRB	VEH.KO_WTM	cellular component disassembly (GO:0022411)	2.89E-02
CRB	VEH.KO_WTM	response to organonitrogen compound (GO:0010243)	1.38E-02
CRB	VEH.KO_WTM	response to nitrogen compound (GO:1901698)	2.25E-02
CRB	VEH.KO_WTM	positive regulation of cell population proliferation (GO:0008284)	3.99E-02
CRB	VEH.KO_WTM	positive regulation of cellular component organization (GO:0051130)	3.73E-02
CRB	VEH.KO_WTM	regulation of cellular component organization (GO:0051128)	2.80E-02
CRB	VEH.KO_WTM	organonitrogen compound metabolic process (GO:1901564)	1.51E-02
CRB	VEH.KO_WTM	positive regulation of cellular process (GO:0048522)	1.87E-02
CRB	VEH.KO_WTM	cellular metabolic process (GO:0044237)	6.74E-03
CRB	VEH.KO_WTM	nitrogen compound metabolic process (GO:0006807)	4.61E-02
CRB	VEH.KO_WTM	metabolic process (GO:0008152)	5.65E-03
CRB	VEH.KO_WTM	cellular process (GO:0009987)	1.35E-02
CRB	VEH.KO_WTM	sensory perception (GO:0007600)	2.86E-02
CRB	VEH.KO_WTM	sensory perception of chemical stimulus (GO:0007606)	9.80E-05
CRB	VEH.KO_WTM	sensory perception of smell (GO:0007608)	7.02E-05
CRB	KOIGF1_WTM VEH	response to oxygen-containing compound (GO:1901700)	9.96E-03
CRB	KOIGF1_WTM VEH	response to external stimulus (GO:0009605)	1.10E-02
CRB	KOIGF1_WTM VEH	cellular response to chemical stimulus (GO:0070887)	1.68E-02
CRB	KOIGF1_WTM VEH	response to stimulus (GO:0050896)	3.39E-02
BL	IGF1.KO_WTM	positive regulation of cell-cell adhesion mediated by integrin (GO:0033634)	3.03E-02
BL	IGF1.KO_WTM	regulation of mast cell chemotaxis (GO:0060753)	4.33E-02
BL	IGF1.KO_WTM	lymphocyte chemotaxis (GO:0048247)	1.99E-02
BL	IGF1.KO_WTM	chemokine-mediated signaling pathway (GO:0070098)	1.91E-03
BL	IGF1.KO_WTM	cellular response to chemokine (GO:1990869)	2.85E-03
BL	IGF1.KO_WTM	response to chemokine (GO:1990868)	2.59E-03
BL	IGF1.KO_WTM	neutrophil chemotaxis (GO:0030593)	3.87E-03
BL	IGF1.KO_WTM	granulocyte chemotaxis (GO:0071621)	5.01E-03

BL	IGF1.KO_WTM	lymphocyte migration (GO:0072676)	4.17E-02
BL	IGF1.KO_WTM	neutrophil migration (GO:1990266)	6.09E-03
BL	IGF1.KO_WTM	granulocyte migration (GO:0097530)	8.91E-03
BL	IGF1.KO_WTM	myeloid leukocyte migration (GO:0097529)	1.82E-02
BL	IGF1.KO_WTM	leukocyte chemotaxis (GO:0030595)	2.10E-02
BL	IGF1.KO_WTM	positive regulation of chemotaxis (GO:0050921)	2.64E-02
BL	IGF1.KO_WTM	cytokine-mediated signaling pathway (GO:0019221)	5.06E-04
BL	IGF1.KO_WTM	positive regulation of cell-cell adhesion (GO:0022409)	2.18E-02
BL	IGF1.KO_WTM	regulation of T cell activation (GO:0050863)	3.52E-02
BL	IGF1.KO_WTM	cellular response to cytokine stimulus (GO:0071345)	1.11E-04
BL	IGF1.KO_WTM	positive regulation of response to external stimulus (GO:0032103)	1.33E-02
BL	IGF1.KO_WTM	response to cytokine (GO:0034097)	2.02E-04
BL	IGF1.KO_WTM	positive regulation of cell adhesion (GO:0045785)	1.93E-02
BL	IGF1.KO_WTM	regulation of cell adhesion (GO:0030155)	2.65E-02
BL	IGF1.KO_WTM	innate immune response (GO:0045087)	4.19E-02
BL	IGF1.KO_WTM	biological process involved in interspecies interaction between organisms (GO:0044419)	8.45E-04
BL	IGF1.KO_WTM	defense response (GO:0006952)	2.82E-03
BL	IGF1.KO_WTM	response to other organism (GO:0051707)	2.48E-03
BL	IGF1.KO_WTM	response to external biotic stimulus (GO:0043207)	2.16E-03
BL	IGF1.KO_WTM	positive regulation of immune system process (GO:0002684)	2.56E-02
BL	IGF1.KO_WTM	defense response to other organism (GO:0098542)	2.79E-02
BL	IGF1.KO_WTM	response to biotic stimulus (GO:0009607)	2.12E-03
BL	IGF1.KO_WTM	cellular response to organic substance (GO:0071310)	8.43E-03
BL	IGF1.KO_WTM	immune response (GO:0006955)	2.26E-02
BL	IGF1.KO_WTM	response to external stimulus (GO:0009605)	1.59E-02
BL	VEH.KO_WTM	negative regulation of sterol import (GO:2000910)	1.06E-02
BL	VEH.KO_WTM	negative regulation of cholesterol import (GO:0060621)	1.05E-02
BL	VEH.KO_WTM	regulation of very-low-density lipoprotein particle remodeling (GO:0010901)	2.10E-05
BL	VEH.KO_WTM	response to chromate (GO:0046687)	2.06E-05
BL	VEH.KO_WTM	negative regulation of very-low-density lipoprotein particle remodeling (GO:0010903)	5.88E-04
BL	VEH.KO_WTM	response to methanol (GO:0033986)	5.83E-04
BL	VEH.KO_WTM	neutrophil aggregation (GO:0070488)	1.63E-02
BL	VEH.KO_WTM	very-low-density lipoprotein particle clearance (GO:0034447)	1.62E-02
BL	VEH.KO_WTM	triglyceride-rich lipoprotein particle clearance (GO:0071830)	1.16E-03
BL	VEH.KO_WTM	chylomicron remnant clearance (GO:0034382)	1.15E-03
BL	VEH.KO_WTM	blood coagulation, fibrin clot formation (GO:0072378)	6.56E-05
BL	VEH.KO_WTM	S-adenosylmethionine biosynthetic process (GO:0006556)	2.27E-02
BL	VEH.KO_WTM	negative regulation of very-low-density lipoprotein particle clearance (GO:0010916)	2.26E-02
BL	VEH.KO_WTM	regulation of very-low-density lipoprotein particle clearance (GO:0010915)	2.25E-02
BL	VEH.KO_WTM	positive regulation of phospholipid efflux (GO:1902995)	2.24E-02
BL	VEH.KO_WTM	regulation of phospholipid efflux (GO:1902994)	2.23E-02

BL	VEH.KO_WTM	high-density lipoprotein particle assembly (GO:0034380)	6.47E-05
BL	VEH.KO_WTM	triglyceride-rich lipoprotein particle remodeling (GO:0034370)	6.38E-05
BL	VEH.KO_WTM	phospholipid efflux (GO:0033700)	2.50E-07
BL	VEH.KO_WTM	very-low-density lipoprotein particle remodeling (GO:0034372)	1.55E-03
BL	VEH.KO_WTM	interleukin-27-mediated signaling pathway (GO:0070106)	2.87E-02
BL	VEH.KO_WTM	induction of bacterial agglutination (GO:0043152)	2.86E-02
BL	VEH.KO_WTM	positive regulation of cholesterol esterification (GO:0010873)	1.16E-04
BL	VEH.KO_WTM	regulation of Cdc42 protein signal transduction (GO:0032489)	2.06E-03
BL	VEH.KO_WTM	protein activation cascade (GO:0072376)	1.90E-04
BL	VEH.KO_WTM	negative regulation of serine-type peptidase activity (GO:1902572)	2.62E-03
BL	VEH.KO_WTM	regulation of serine-type peptidase activity (GO:1902571)	2.61E-03
BL	VEH.KO_WTM	triglyceride mobilization (GO:0006642)	3.63E-02
BL	VEH.KO_WTM	plasminogen activation (GO:0031639)	1.88E-04
BL	VEH.KO_WTM	negative regulation of serine-type endopeptidase activity (GO:1900004)	2.59E-03
BL	VEH.KO_WTM	regulation of serine-type endopeptidase activity (GO:1900003)	2.57E-03
BL	VEH.KO_WTM	high-density lipoprotein particle clearance (GO:0034384)	3.62E-02
BL	VEH.KO_WTM	regulation of cholesterol esterification (GO:0010872)	2.23E-04
BL	VEH.KO_WTM	high-density lipoprotein particle remodeling (GO:0034375)	2.21E-04
BL	VEH.KO_WTM	positive regulation of lipoprotein lipase activity (GO:0051006)	3.13E-03
BL	VEH.KO_WTM	regulation of lipoprotein lipase activity (GO:0051004)	2.11E-05
BL	VEH.KO_WTM	regulation of sterol import (GO:2000909)	4.52E-02
BL	VEH.KO_WTM	positive regulation of heterotypic cell-cell adhesion (GO:0034116)	2.77E-04
BL	VEH.KO_WTM	positive regulation of cell-cell adhesion mediated by integrin (GO:0033634)	4.51E-02
BL	VEH.KO_WTM	peptidyl-cysteine S-nitrosylation (GO:0018119)	4.49E-02
BL	VEH.KO_WTM	negative regulation of cholesterol transport (GO:0032375)	2.74E-04
BL	VEH.KO_WTM	negative regulation of sterol transport (GO:0032372)	2.72E-04
BL	VEH.KO_WTM	negative regulation of lipoprotein lipase activity (GO:0051005)	4.48E-02
BL	VEH.KO_WTM	regulation of cholesterol import (GO:0060620)	4.46E-02
BL	VEH.KO_WTM	plasma lipoprotein particle remodeling (GO:0034369)	1.70E-07
BL	VEH.KO_WTM	protein-lipid complex remodeling (GO:0034368)	1.62E-07
BL	VEH.KO_WTM	negative regulation of lipase activity (GO:0060192)	2.43E-05
BL	VEH.KO_WTM	positive regulation of triglyceride catabolic process (GO:0010898)	3.79E-03
BL	VEH.KO_WTM	regulation of intestinal cholesterol absorption (GO:0030300)	3.77E-03
BL	VEH.KO_WTM	positive regulation of triglyceride lipase activity (GO:0061365)	3.75E-03
BL	VEH.KO_WTM	protein-containing complex remodeling (GO:0034367)	2.34E-07
BL	VEH.KO_WTM	cholesterol efflux (GO:0033344)	2.57E-07
BL	VEH.KO_WTM	plasma lipoprotein particle clearance (GO:0034381)	3.52E-05
BL	VEH.KO_WTM	regulation of triglyceride catabolic process (GO:0010896)	4.07E-04

BL	VEH.KO_WTM	triglyceride catabolic process (GO:0019433)	4.84E-04
BL	VEH.KO_WTM	response to lead ion (GO:0010288)	5.46E-03
BL	VEH.KO_WTM	regulation of intestinal lipid absorption (GO:1904729)	5.44E-03
BL	VEH.KO_WTM	low-density lipoprotein particle remodeling (GO:0034374)	5.41E-03
BL	VEH.KO_WTM	fibrinolysis (GO:0042730)	6.26E-03
BL	VEH.KO_WTM	reverse cholesterol transport (GO:0043691)	6.53E-04
BL	VEH.KO_WTM	plasma lipoprotein particle assembly (GO:0034377)	7.39E-04
BL	VEH.KO_WTM	regulation of heterotypic cell-cell adhesion (GO:0034114)	8.16E-05
BL	VEH.KO_WTM	S-adenosylmethionine metabolic process (GO:0046500)	8.52E-03
BL	VEH.KO_WTM	plasma lipoprotein particle organization (GO:0071827)	1.40E-06
BL	VEH.KO_WTM	acylglycerol catabolic process (GO:0046464)	1.42E-04
BL	VEH.KO_WTM	neutral lipid catabolic process (GO:0046461)	1.40E-04
BL	VEH.KO_WTM	protein-lipid complex subunit organization (GO:0071825)	2.18E-06
BL	VEH.KO_WTM	protein-lipid complex assembly (GO:0065005)	1.27E-03
BL	VEH.KO_WTM	regulation of intestinal absorption (GO:1904478)	1.24E-02
BL	VEH.KO_WTM	positive regulation of lipid catabolic process (GO:0050996)	1.96E-04
BL	VEH.KO_WTM	triglyceride homeostasis (GO:0070328)	2.94E-04
BL	VEH.KO_WTM	acylglycerol homeostasis (GO:0055090)	2.91E-04
BL	VEH.KO_WTM	positive regulation of triglyceride metabolic process (GO:0090208)	2.28E-03
BL	VEH.KO_WTM	regulation of plasma lipoprotein particle levels (GO:0097006)	5.78E-06
BL	VEH.KO_WTM	positive regulation of cholesterol efflux (GO:0010875)	2.72E-03
BL	VEH.KO_WTM	negative regulation of extrinsic apoptotic signaling pathway via death domain receptors (GO:1902042)	2.96E-03
BL	VEH.KO_WTM	sterol transport (GO:0015918)	1.60E-06
BL	VEH.KO_WTM	cholesterol transport (GO:0030301)	1.55E-06
BL	VEH.KO_WTM	response to type I interferon (GO:0034340)	3.23E-03
BL	VEH.KO_WTM	type I interferon signaling pathway (GO:0060337)	2.23E-02
BL	VEH.KO_WTM	cellular response to type I interferon (GO:0071357)	2.22E-02
BL	VEH.KO_WTM	negative regulation of cytokine production involved in immune response (GO:0002719)	2.22E-02
BL	VEH.KO_WTM	monocyte chemotaxis (GO:0002548)	3.50E-03
BL	VEH.KO_WTM	negative regulation of lipid transport (GO:0032369)	3.48E-03
BL	VEH.KO_WTM	positive regulation of fatty acid biosynthetic process (GO:0045723)	2.42E-02
BL	VEH.KO_WTM	regulation of cholesterol transport (GO:0032374)	2.38E-06
BL	VEH.KO_WTM	regulation of sterol transport (GO:0032371)	2.32E-06
BL	VEH.KO_WTM	positive regulation of steroid metabolic process (GO:0045940)	6.25E-04
BL	VEH.KO_WTM	triglyceride metabolic process (GO:0006641)	2.51E-06
BL	VEH.KO_WTM	negative regulation of blood coagulation (GO:0030195)	6.75E-04
BL	VEH.KO_WTM	platelet aggregation (GO:0070527)	2.62E-02
BL	VEH.KO_WTM	regulation of nuclease activity (GO:0032069)	2.61E-02
BL	VEH.KO_WTM	animal organ regeneration (GO:0031100)	2.60E-02
BL	VEH.KO_WTM	negative regulation of hemostasis (GO:1900047)	7.28E-04
BL	VEH.KO_WTM	vitamin transport (GO:0051180)	4.52E-03
BL	VEH.KO_WTM	negative regulation of lipid catabolic process (GO:0050995)	2.83E-02

BL	VEH.KO_WTM	negative regulation of coagulation (GO:0050819)	7.84E-04
BL	VEH.KO_WTM	regulation of fatty acid biosynthetic process (GO:0042304)	7.78E-04
BL	VEH.KO_WTM	regulation of blood coagulation (GO:0030193)	2.27E-05
BL	VEH.KO_WTM	regulation of lipid catabolic process (GO:0050994)	2.42E-05
BL	VEH.KO_WTM	negative regulation of viral genome replication (GO:0045071)	1.58E-04
BL	VEH.KO_WTM	sulfur amino acid metabolic process (GO:0000096)	3.05E-02
BL	VEH.KO_WTM	regulation of hemostasis (GO:1900046)	2.61E-05
BL	VEH.KO_WTM	one-carbon metabolic process (GO:0006730)	5.72E-03
BL	VEH.KO_WTM	regulation of triglyceride metabolic process (GO:0090207)	9.99E-04
BL	VEH.KO_WTM	regulation of coagulation (GO:0050818)	3.09E-05
BL	VEH.KO_WTM	peptide cross-linking (GO:0018149)	6.10E-03
BL	VEH.KO_WTM	negative regulation of endothelial cell apoptotic process (GO:2000352)	3.54E-02
BL	VEH.KO_WTM	glycerolipid catabolic process (GO:0046503)	1.17E-03
BL	VEH.KO_WTM	regulation of lipase activity (GO:0060191)	7.25E-06
BL	VEH.KO_WTM	lymphocyte chemotaxis (GO:0048247)	6.59E-03
BL	VEH.KO_WTM	regulation of cholesterol efflux (GO:0010874)	6.56E-03
BL	VEH.KO_WTM	acute-phase response (GO:0006953)	3.78E-02
BL	VEH.KO_WTM	regulation of myeloid cell apoptotic process (GO:0033032)	4.08E-02
BL	VEH.KO_WTM	nucleobase metabolic process (GO:0009112)	4.07E-02
BL	VEH.KO_WTM	regulation of type 2 immune response (GO:0002828)	4.06E-02
BL	VEH.KO_WTM	negative regulation of lipid localization (GO:1905953)	1.52E-03
BL	VEH.KO_WTM	positive regulation of cholesterol transport (GO:0032376)	8.25E-03
BL	VEH.KO_WTM	positive regulation of sterol transport (GO:0032373)	8.22E-03
BL	VEH.KO_WTM	acylglycerol metabolic process (GO:0006639)	2.48E-06
BL	VEH.KO_WTM	granulocyte chemotaxis (GO:0071621)	7.30E-05
BL	VEH.KO_WTM	positive regulation of fatty acid metabolic process (GO:0045923)	9.44E-03
BL	VEH.KO_WTM	neutral lipid metabolic process (GO:0006638)	2.83E-06
BL	VEH.KO_WTM	regulation of type I interferon-mediated signaling pathway (GO:0060338)	4.96E-02
BL	VEH.KO_WTM	long-chain fatty acid transport (GO:0015909)	1.06E-02
BL	VEH.KO_WTM	neutrophil chemotaxis (GO:0030593)	4.83E-04
BL	VEH.KO_WTM	regulation of extrinsic apoptotic signaling pathway via death domain receptors (GO:1902041)	1.27E-02
BL	VEH.KO_WTM	phosphatidylcholine metabolic process (GO:0046470)	1.26E-02
BL	VEH.KO_WTM	cholesterol homeostasis (GO:0042632)	1.58E-04
BL	VEH.KO_WTM	sterol homeostasis (GO:0055092)	1.67E-04
BL	VEH.KO_WTM	cholesterol metabolic process (GO:0008203)	8.25E-06
BL	VEH.KO_WTM	phospholipid transport (GO:0015914)	7.41E-04
BL	VEH.KO_WTM	chemokine-mediated signaling pathway (GO:0070098)	1.60E-02
BL	VEH.KO_WTM	negative regulation of wound healing (GO:0061045)	3.46E-03
BL	VEH.KO_WTM	organic hydroxy compound transport (GO:0015850)	2.12E-06
BL	VEH.KO_WTM	granulocyte migration (GO:0097530)	1.96E-04
BL	VEH.KO_WTM	regulation of viral genome replication (GO:0045069)	8.64E-04
BL	VEH.KO_WTM	fatty acid transport (GO:0015908)	1.76E-02

BL	VEH.KO_WTM	negative regulation of viral process (GO:0048525)	2.20E-04
BL	VEH.KO_WTM	neutrophil migration (GO:1990266)	9.72E-04
BL	VEH.KO_WTM	sterol metabolic process (GO:0016125)	1.37E-05
BL	VEH.KO_WTM	secondary alcohol metabolic process (GO:1902652)	1.62E-05
BL	VEH.KO_WTM	mononuclear cell migration (GO:0071674)	1.18E-03
BL	VEH.KO_WTM	negative regulation of cytokine-mediated signaling pathway (GO:0001960)	2.18E-02
BL	VEH.KO_WTM	negative regulation of endopeptidase activity (GO:0010951)	2.44E-07
BL	VEH.KO_WTM	arachidonic acid metabolic process (GO:0019369)	5.29E-03
BL	VEH.KO_WTM	response to interferon-beta (GO:0035456)	2.26E-02
BL	VEH.KO_WTM	myeloid leukocyte migration (GO:0097529)	8.86E-05
BL	VEH.KO_WTM	positive regulation of lipase activity (GO:0060193)	2.30E-02
BL	VEH.KO_WTM	lymphocyte migration (GO:0072676)	2.42E-02
BL	VEH.KO_WTM	regulation of wound healing (GO:0061041)	1.02E-04
BL	VEH.KO_WTM	lipoprotein metabolic process (GO:0042157)	4.03E-04
BL	VEH.KO_WTM	regulation of fatty acid metabolic process (GO:0019217)	1.63E-03
BL	VEH.KO_WTM	cellular response to chemokine (GO:1990869)	2.52E-02
BL	VEH.KO_WTM	response to chemokine (GO:1990868)	2.51E-02
BL	VEH.KO_WTM	negative regulation of response to cytokine stimulus (GO:0060761)	2.50E-02
BL	VEH.KO_WTM	regulation of lipid localization (GO:1905952)	1.81E-06
BL	VEH.KO_WTM	regulation of lipid transport (GO:0032368)	3.19E-05
BL	VEH.KO_WTM	leukocyte chemotaxis (GO:0030595)	1.39E-04
BL	VEH.KO_WTM	positive regulation of type I interferon production (GO:0032481)	2.84E-02
BL	VEH.KO_WTM	negative regulation of peptidase activity (GO:0010466)	1.52E-08
BL	VEH.KO_WTM	positive regulation of lipid localization (GO:1905954)	5.95E-04
BL	VEH.KO_WTM	negative regulation of hydrolase activity (GO:0051346)	5.36E-12
BL	VEH.KO_WTM	xenobiotic catabolic process (GO:0042178)	3.08E-02
BL	VEH.KO_WTM	negative regulation of response to wounding (GO:1903035)	8.58E-03
BL	VEH.KO_WTM	positive regulation of peptide secretion (GO:0002793)	6.59E-04
BL	VEH.KO_WTM	zymogen activation (GO:0031638)	3.34E-02
BL	VEH.KO_WTM	response to interleukin-1 (GO:0070555)	1.02E-02
BL	VEH.KO_WTM	antibacterial humoral response (GO:0019731)	1.01E-02
BL	VEH.KO_WTM	cellular response to interleukin-1 (GO:0071347)	3.78E-02
BL	VEH.KO_WTM	lipid transport (GO:0006869)	4.11E-08
BL	VEH.KO_WTM	regulation of steroid metabolic process (GO:0019218)	3.29E-03
BL	VEH.KO_WTM	organophosphate ester transport (GO:0015748)	3.27E-03
BL	VEH.KO_WTM	positive regulation of lipid transport (GO:0032370)	1.32E-02
BL	VEH.KO_WTM	regeneration (GO:0031099)	1.38E-02
BL	VEH.KO_WTM	negative regulation of innate immune response (GO:0045824)	4.59E-02
BL	VEH.KO_WTM	regulation of cytokine-mediated signaling pathway (GO:0001959)	4.07E-03
BL	VEH.KO_WTM	positive regulation of lipid metabolic process (GO:0045834)	1.16E-04
BL	VEH.KO_WTM	long-chain fatty acid metabolic process (GO:0001676)	4.23E-03
BL	VEH.KO_WTM	olefinic compound metabolic process (GO:0120254)	4.21E-03

BL	VEH.KO_WTM	lipid homeostasis (GO:0055088)	4.19E-04
BL	VEH.KO_WTM	positive regulation of lipid biosynthetic process (GO:0046889)	1.59E-02
BL	VEH.KO_WTM	regulation of response to wounding (GO:1903034)	4.99E-04
BL	VEH.KO_WTM	regulation of cellular ketone metabolic process (GO:0010565)	1.61E-03
BL	VEH.KO_WTM	lipid localization (GO:0010876)	1.47E-07
BL	VEH.KO_WTM	steroid metabolic process (GO:0008202)	5.22E-06
BL	VEH.KO_WTM	modulation of process of other organism (GO:0035821)	5.79E-03
BL	VEH.KO_WTM	regulation of response to cytokine stimulus (GO:0060759)	5.76E-03
BL	VEH.KO_WTM	defense response to symbiont (GO:0140546)	2.06E-04
BL	VEH.KO_WTM	defense response to virus (GO:0051607)	2.04E-04
BL	VEH.KO_WTM	antimicrobial humoral response (GO:0019730)	2.16E-03
BL	VEH.KO_WTM	coagulation (GO:0050817)	2.24E-02
BL	VEH.KO_WTM	blood coagulation (GO:0007596)	2.23E-02
BL	VEH.KO_WTM	cell chemotaxis (GO:0060326)	2.64E-04
BL	VEH.KO_WTM	hemostasis (GO:0007599)	2.30E-02
BL	VEH.KO_WTM	regulation of endopeptidase activity (GO:0052548)	3.74E-07
BL	VEH.KO_WTM	response to toxic substance (GO:0009636)	2.44E-02
BL	VEH.KO_WTM	negative regulation of proteolysis (GO:0045861)	3.75E-07
BL	VEH.KO_WTM	xenobiotic metabolic process (GO:0006805)	2.52E-02
BL	VEH.KO_WTM	regulation of viral process (GO:0050792)	2.96E-03
BL	VEH.KO_WTM	unsaturated fatty acid metabolic process (GO:0033559)	2.65E-02
BL	VEH.KO_WTM	positive regulation of peptide hormone secretion (GO:0090277)	2.64E-02
BL	VEH.KO_WTM	regulation of peptidase activity (GO:0052547)	2.05E-08
BL	VEH.KO_WTM	regulation of viral life cycle (GO:1903900)	1.01E-02
BL	VEH.KO_WTM	regulation of production of molecular mediator of immune response (GO:0002700)	3.38E-03
BL	VEH.KO_WTM	regulation of lipid biosynthetic process (GO:0046890)	1.25E-03
BL	VEH.KO_WTM	negative regulation of immune effector process (GO:0002698)	3.22E-02
BL	VEH.KO_WTM	response to virus (GO:0009615)	2.04E-04
BL	VEH.KO_WTM	icosanoid metabolic process (GO:0006690)	3.62E-02
BL	VEH.KO_WTM	alcohol metabolic process (GO:0006066)	8.78E-05
BL	VEH.KO_WTM	glycerolipid metabolic process (GO:0046486)	3.86E-05
BL	VEH.KO_WTM	leukocyte migration (GO:0050900)	2.16E-03
BL	VEH.KO_WTM	response to peptide hormone (GO:0043434)	3.61E-04
BL	VEH.KO_WTM	positive regulation of ERK1 and ERK2 cascade (GO:0070374)	2.61E-03
BL	VEH.KO_WTM	cellular response to xenobiotic stimulus (GO:0071466)	1.91E-02
BL	VEH.KO_WTM	response to metal ion (GO:0010038)	4.21E-04
BL	VEH.KO_WTM	negative regulation of catalytic activity (GO:0043086)	1.71E-09
BL	VEH.KO_WTM	regulation of peptide secretion (GO:0002791)	2.86E-03
BL	VEH.KO_WTM	regulation of peptide transport (GO:0090087)	2.98E-03
BL	VEH.KO_WTM	response to inorganic substance (GO:0010035)	3.78E-06
BL	VEH.KO_WTM	regulation of hydrolase activity (GO:0051336)	7.42E-14
BL	VEH.KO_WTM	cytokine-mediated signaling pathway (GO:0019221)	5.91E-04

BL	VEH.KO_WTM	regulation of innate immune response (GO:0045088)	1.04E-02
BL	VEH.KO_WTM	organic hydroxy compound metabolic process (GO:1901615)	2.13E-05
BL	VEH.KO_WTM	regulation of protein secretion (GO:0050708)	2.45E-03
BL	VEH.KO_WTM	regulation of small molecule metabolic process (GO:0062012)	4.59E-04
BL	VEH.KO_WTM	positive regulation of defense response (GO:0031349)	6.73E-03
BL	VEH.KO_WTM	response to cytokine (GO:0034097)	1.78E-08
BL	VEH.KO_WTM	negative regulation of immune response (GO:0050777)	3.76E-02
BL	VEH.KO_WTM	lipid catabolic process (GO:0016042)	7.22E-03
BL	VEH.KO_WTM	regulation of lipid metabolic process (GO:0019216)	5.94E-04
BL	VEH.KO_WTM	response to peptide (GO:1901652)	1.38E-03
BL	VEH.KO_WTM	negative regulation of response to external stimulus (GO:0032102)	8.23E-04
BL	VEH.KO_WTM	wound healing (GO:0042060)	2.19E-02
BL	VEH.KO_WTM	positive regulation of cell-cell adhesion (GO:0022409)	1.01E-02
BL	VEH.KO_WTM	positive regulation of immune effector process (GO:0002699)	1.04E-02
BL	VEH.KO_WTM	response to lipopolysaccharide (GO:0032496)	1.11E-02
BL	VEH.KO_WTM	regulation of defense response (GO:0031347)	2.05E-05
BL	VEH.KO_WTM	regulation of response to biotic stimulus (GO:0002831)	5.40E-03
BL	VEH.KO_WTM	regulation of inflammatory response (GO:0050727)	5.53E-03
BL	VEH.KO_WTM	innate immune response (GO:0045087)	8.99E-08
BL	VEH.KO_WTM	regulation of proteolysis (GO:0030162)	3.04E-06
BL	VEH.KO_WTM	response to molecule of bacterial origin (GO:0002237)	1.62E-02
BL	VEH.KO_WTM	regulation of ERK1 and ERK2 cascade (GO:0070372)	1.91E-02
BL	VEH.KO_WTM	regulation of immune effector process (GO:0002697)	5.14E-03
BL	VEH.KO_WTM	response to wounding (GO:0009611)	2.17E-02
BL	VEH.KO_WTM	regulation of response to external stimulus (GO:0032101)	1.14E-06
BL	VEH.KO_WTM	positive regulation of response to external stimulus (GO:0032103)	5.87E-03
BL	VEH.KO_WTM	regulation of hormone secretion (GO:0046883)	4.73E-02
BL	VEH.KO_WTM	inflammatory response (GO:0006954)	3.03E-03
BL	VEH.KO_WTM	defense response to other organism (GO:0098542)	2.08E-07
BL	VEH.KO_WTM	negative regulation of molecular function (GO:0044092)	1.01E-06
BL	VEH.KO_WTM	cellular lipid metabolic process (GO:0044255)	8.30E-06
BL	VEH.KO_WTM	response to hormone (GO:0009725)	1.11E-03
BL	VEH.KO_WTM	fatty acid metabolic process (GO:0006631)	3.05E-02
BL	VEH.KO_WTM	positive regulation of hydrolase activity (GO:0051345)	2.47E-03
BL	VEH.KO_WTM	regulation of cell-cell adhesion (GO:0022407)	1.01E-02
BL	VEH.KO_WTM	cell-cell adhesion (GO:0098609)	2.17E-02
BL	VEH.KO_WTM	small molecule metabolic process (GO:0044281)	1.39E-08
BL	VEH.KO_WTM	response to bacterium (GO:0009617)	3.83E-05
BL	VEH.KO_WTM	lipid metabolic process (GO:0006629)	1.44E-06
BL	VEH.KO_WTM	positive regulation of cell adhesion (GO:0045785)	1.21E-02
BL	VEH.KO_WTM	response to biotic stimulus (GO:0009607)	7.72E-09
BL	VEH.KO_WTM	response to other organism (GO:0051707)	1.69E-08
BL	VEH.KO_WTM	response to external biotic stimulus (GO:0043207)	1.43E-08

BL	VEH.KO_WTM	biological process involved in interspecies interaction between organisms (GO:0044419)	6.08E-09
BL	VEH.KO_WTM	cellular response to cytokine stimulus (GO:0071345)	1.27E-03
BL	VEH.KO_WTM	regulation of catalytic activity (GO:0050790)	4.17E-10
BL	VEH.KO_WTM	defense response (GO:0006952)	4.63E-08
BL	VEH.KO_WTM	positive regulation of cytokine production (GO:0001819)	1.62E-02
BL	VEH.KO_WTM	chemotaxis (GO:0006935)	1.72E-02
BL	VEH.KO_WTM	taxis (GO:0042330)	1.85E-02
BL	VEH.KO_WTM	regulation of vesicle-mediated transport (GO:0060627)	5.78E-03
BL	VEH.KO_WTM	organic acid metabolic process (GO:0006082)	6.96E-04
BL	VEH.KO_WTM	carboxylic acid metabolic process (GO:0019752)	1.38E-03
BL	VEH.KO_WTM	oxoacid metabolic process (GO:0043436)	1.68E-03
BL	VEH.KO_WTM	regulation of protein transport (GO:0051223)	2.83E-02
BL	VEH.KO_WTM	response to oxygen-containing compound (GO:1901700)	2.09E-05
BL	VEH.KO_WTM	regulation of establishment of protein localization (GO:0070201)	3.93E-02
BL	VEH.KO_WTM	negative regulation of cellular protein metabolic process (GO:0032269)	1.39E-03
BL	VEH.KO_WTM	regulation of response to stress (GO:0080134)	1.19E-04
BL	VEH.KO_WTM	response to lipid (GO:0033993)	3.04E-02
BL	VEH.KO_WTM	negative regulation of protein metabolic process (GO:0051248)	2.71E-03
BL	VEH.KO_WTM	immune response (GO:0006955)	1.31E-05
BL	VEH.KO_WTM	positive regulation of transport (GO:0051050)	2.74E-03
BL	VEH.KO_WTM	regulation of secretion (GO:0051046)	2.84E-02
BL	VEH.KO_WTM	response to external stimulus (GO:0009605)	1.11E-07
BL	VEH.KO_WTM	regulation of cytokine production (GO:0001817)	3.20E-02
BL	VEH.KO_WTM	response to organonitrogen compound (GO:0010243)	3.31E-02
BL	VEH.KO_WTM	regulation of molecular function (GO:0065009)	8.86E-08
BL	VEH.KO_WTM	response to chemical (GO:0042221)	8.21E-11
BL	VEH.KO_WTM	response to nitrogen compound (GO:1901698)	3.23E-02
BL	VEH.KO_WTM	response to endogenous stimulus (GO:0009719)	1.20E-02
BL	VEH.KO_WTM	catabolic process (GO:0009056)	2.00E-04
BL	VEH.KO_WTM	response to organic substance (GO:0010033)	1.37E-06
BL	VEH.KO_WTM	negative regulation of multicellular organismal process (GO:0051241)	1.25E-02
BL	VEH.KO_WTM	positive regulation of multicellular organismal process (GO:0051240)	2.39E-03
BL	VEH.KO_WTM	cellular catabolic process (GO:0044248)	3.83E-03
BL	VEH.KO_WTM	organic substance catabolic process (GO:1901575)	5.72E-03
BL	VEH.KO_WTM	positive regulation of catalytic activity (GO:0043085)	4.96E-02
BL	VEH.KO_WTM	chemical homeostasis (GO:0048878)	4.97E-02
BL	VEH.KO_WTM	regulation of transport (GO:0051049)	2.82E-03
BL	VEH.KO_WTM	response to stress (GO:0006950)	1.60E-05
BL	VEH.KO_WTM	regulation of immune system process (GO:0002682)	1.47E-02
BL	VEH.KO_WTM	cellular response to chemical stimulus (GO:0070887)	6.95E-04
BL	VEH.KO_WTM	immune system process (GO:0002376)	5.92E-04

BL	VEH.KO_WTM	regulation of cellular protein metabolic process (GO:0032268)	2.04E-02
BL	VEH.KO_WTM	regulation of multicellular organismal process (GO:0051239)	7.51E-03
BL	VEH.KO_WTM	positive regulation of response to stimulus (GO:0048584)	3.05E-02
BL	VEH.KO_WTM	regulation of localization (GO:0032879)	9.33E-03
BL	VEH.KO_WTM	organonitrogen compound metabolic process (GO:1901564)	1.98E-04
BL	VEH.KO_WTM	organic cyclic compound metabolic process (GO:1901360)	2.30E-02
BL	VEH.KO_WTM	regulation of protein metabolic process (GO:0051246)	4.75E-02
BL	VEH.KO_WTM	organic substance metabolic process (GO:0071704)	5.94E-05
BL	VEH.KO_WTM	primary metabolic process (GO:0044238)	1.06E-03
BL	VEH.KO_WTM	metabolic process (GO:0008152)	8.19E-05
BL	VEH.KO_WTM	negative regulation of cellular process (GO:0048523)	2.23E-02
BL	VEH.KO_WTM	negative regulation of biological process (GO:0048519)	1.60E-02
BL	VEH.KO_WTM	response to stimulus (GO:0050896)	6.03E-05
BL	VEH.KO_WTM	nitrogen compound metabolic process (GO:0006807)	1.52E-02
BL	VEH.KO_WTM	cellular metabolic process (GO:0044237)	1.60E-02
BL	VEH.KO_WTM	organelle organization (GO:0006996)	1.57E-02
BL	KOIGF1_WTM VEH	response to toxic substance (GO:0009636)	8.17E-03
BL	KOIGF1_WTM VEH	response to other organism (GO:0051707)	4.20E-03
BL	KOIGF1_WTM VEH	response to external biotic stimulus (GO:0043207)	3.21E-03
BL	KOIGF1_WTM VEH	biological process involved in interspecies interaction between organisms (GO:0044419)	3.90E-03
BL	KOIGF1_WTM VEH	response to biotic stimulus (GO:0009607)	3.62E-03
BL	KOIGF1_WTM VEH	immune system process (GO:0002376)	3.72E-03
BL	KOIGF1_WTM VEH	response to external stimulus (GO:0009605)	4.03E-02

Supplementary Table 14 – GO Analysis of Treated Male Mice from Chapter II
All significant pathways found in Reactome analysis of Male mice treated with rhIGF1 or vehicle.
Legend:
CRB = Cerebellum, BL = Blood,
KO.IGF1_VEH = rhIGF1 treated *Mecp2*$^{-/y}$ vs. VEH treated *Mecp2*$^{-/y}$,
WTM.IGF1_VEH = rhIGF1 treated *Mecp2*$^{+/y}$ vs. VEH treated *Mecp2*$^{+/y}$,
IGF1.KO_WTM= rhIGF1 treated *Mecp2*$^{-/y}$ vs. rhIGF1 treated *Mecp2*$^{+/y}$,
VEH.KO_WTM = VEH treated *Mecp2*$^{-/y}$ vs. VEH treated *Mecp2*$^{+/y}$,
KOIGF1_WTMVEH = IGF1 treated *Mecp2*$^{-/+}$ vs. VEH treated *Mecp2*$^{+/y}$

Comparison	**ID**	**Pathway name**	**FDR**
CRB.KO	R-HSA-2262752	Cellular responses to stress	0.03
CRB.KO	R-HSA-8953897	Cellular responses to stimuli	0.03
CRB.KO	R-HSA-9013407	RHOH GTPase cycle	0.03
CRB.KO	R-HSA-2426168	Activation of gene expression by SREBF (SREBP)	0.03
CRB.KO	R-HSA-9711097	Cellular response to starvation	0.04
CRB.KO	R-HSA-5628897	TP53 Regulates Metabolic Genes	0.04
CRB.KO	R-HSA-1655829	Regulation of cholesterol biosynthesis by SREBP (SREBF)	0.04

BL.KO	R-HSA-8963898	Plasma lipoprotein assembly	0.00
BL.KO	R-HSA-174824	Plasma lipoprotein assembly, remodeling, and clearance	0.00
BL.KO	R-HSA-8963888	Chylomicron assembly	0.00
BL.KO	R-HSA-975634	Retinoid metabolism and transport	0.00
BL.KO	R-HSA-8963901	Chylomicron remodeling	0.00
BL.KO	R-HSA-6806667	Metabolism of fat-soluble vitamins	0.00
BL.KO	R-HSA-8963899	Plasma lipoprotein remodeling	0.00
BL.KO	R-HSA-8957275	Post-translational protein phosphorylation	0.00
BL.KO	R-HSA-381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Proteins (IGFBPs)	0.00
BL.KO	R-HSA-8866423	VLDL assembly	0.00
BL.KO	R-HSA-114608	Platelet degranulation	0.00
BL.KO	R-HSA-76005	Response to elevated platelet cytosolic Ca2+	0.00
BL.KO	R-HSA-8964046	VLDL clearance	0.00
BL.KO	R-HSA-8964043	Plasma lipoprotein clearance	0.00
BL.KO	R-HSA-2187338	Visual phototransduction	0.00
BL.KO	R-HSA-1989781	PPARA activates gene expression	0.00
BL.KO	R-HSA-400206	Regulation of lipid metabolism by PPARalpha	0.00
BL.KO	R-HSA-9029569	NR1H3 & NR1H2 regulate gene expression linked to cholesterol transport and efflux	0.00
BL.KO	R-HSA-8964058	HDL remodeling	0.00
BL.KO	R-HSA-9024446	NR1H2 and NR1H3-mediated signaling	0.00
BL.KO	R-HSA-76002	Platelet activation, signaling and aggregation	0.00
BL.KO	R-HSA-5686938	Regulation of TLR by endogenous ligand	0.00
BL.KO	R-HSA-196854	Metabolism of vitamins and cofactors	0.00
BL.KO	R-HSA-5661231	Metallothioneins bind metals	0.01
BL.KO	R-HSA-2173782	Binding and Uptake of Ligands by Scavenger Receptors	0.01
BL.KO	R-HSA-556833	Metabolism of lipids	0.01
BL.KO	R-HSA-3000471	Scavenging by Class B Receptors	0.01
BL.KO	R-HSA-5660526	Response to metal ions	0.01
BL.KO	R-HSA-909733	Interferon alpha/beta signaling	0.01
BL.KO	R-HSA-9709957	Sensory Perception	0.01
BL.KO	R-HSA-5602498	MyD88 deficiency (TLR2/4)	0.02
CRB.HET	R-HSA-5603041	IRAK4 deficiency (TLR2/4)	0.02
BL.KO	R-HSA-2168880	Scavenging of heme from plasma	0.02
BL.KO	R-HSA-2474795	Diseases associated with visual transduction	0.02
BL.KO	R-HSA-9675143	Diseases of the neuronal system	0.02
BL.KO	R-HSA-2453864	Retinoid cycle disease events	0.02
BL.KO	R-HSA-1430728	Metabolism	0.02
BL.KO	R-HSA-189483	Heme degradation	0.03
BL.KO	R-HSA-5657560	Hereditary fructose intolerance	0.03
BL.KO	R-HSA-6809583	Retinoid metabolism disease events	0.03
BL.KO	R-HSA-109582	Hemostasis	0.03
BL.KO	R-HSA-5602358	Diseases associated with the TLR signaling cascade	0.03

BL.KO	R-HSA-5260271	Diseases of Immune System	0.03
BL.KO	R-HSA-3000480	Scavenging by Class A Receptors	0.03
BL.KO	R-HSA-2453902	The canonical retinoid cycle in rods (twilight vision)	0.04
CRB.HET	R-HSA-419812	Calcitonin-like ligand receptors	0.00
CRB.HET	R-HSA-372790	Signaling by GPCR	0.00
CRB.HET	R-HSA-388396	GPCR downstream signalling	0.01
CRB.HET	R-HSA-9620244	Long-term potentiation	0.01
CRB.HET	R-HSA-373080	Class B/2 (Secretin family receptors)	0.02
CRB.HET	R-HSA-8986944	Transcriptional Regulation by MECP2	0.02
CRB.HET	R-HSA-500792	GPCR ligand binding	0.04

Supplementary Table 15 – Reactome Analysis of Targets of rhIGF1 Action in Mice
All significant pathways found in Reactome analysis of Male mice treated with rhIGF1 or vehicle.
Legend:
CRB.KO = Cerebellum *Mecp2*$^{-/y}$ targets, BL.KO = Blood *Mecp2*$^{-/y}$ targets, CRB.HET = Cerebellum *Mecp2*$^{-+y}$ targets

Comparison	**GO biological process complete**	**upload_1 (FDR)**
CRB.KO	organonitrogen compound metabolic process (GO:1901564)	2.52E-02
CRB.KO	cellular metabolic process (GO:0044237)	2.37E-03
CRB.KO	metabolic process (GO:0008152)	7.51E-03
BL.KO	negative regulation of sterol import (GO:2000910)	2.50E-03
BL.KO	negative regulation of cholesterol import (GO:0060621)	2.46E-03
BL.KO	negative regulation of very-low-density lipoprotein particle remodeling (GO:0010903)	5.48E-05
BL.KO	regulation of sterol import (GO:2000909)	5.10E-03
BL.KO	negative regulation of very-low-density lipoprotein particle clearance (GO:0010916)	5.04E-03
BL.KO	regulation of very-low-density lipoprotein particle clearance (GO:0010915)	4.98E-03
BL.KO	regulation of very-low-density lipoprotein particle remodeling (GO:0010901)	9.11E-05
BL.KO	regulation of cholesterol import (GO:0060620)	4.93E-03
BL.KO	triglyceride-rich lipoprotein particle clearance (GO:0071830)	6.34E-03
BL.KO	chylomicron remnant clearance (GO:0034382)	6.27E-03
BL.KO	phospholipid efflux (GO:0033700)	6.85E-06
BL.KO	negative regulation of lipoprotein lipase activity (GO:0051005)	7.74E-03
BL.KO	positive regulation of cholesterol esterification (GO:0010873)	2.14E-04
BL.KO	high-density lipoprotein particle clearance (GO:0034384)	9.59E-03
BL.KO	very-low-density lipoprotein particle assembly (GO:0034379)	3.22E-04
BL.KO	regulation of Cdc42 protein signal transduction (GO:0032489)	1.14E-02
BL.KO	regulation of cholesterol esterification (GO:0010872)	3.84E-04
BL.KO	high-density lipoprotein particle remodeling (GO:0034375)	1.39E-05
BL.KO	negative regulation of lipase activity (GO:0060192)	1.62E-05
BL.KO	blood coagulation, fibrin clot formation (GO:0072378)	1.36E-02
BL.KO	positive regulation of lipoprotein lipase activity (GO:0051006)	1.35E-02
BL.KO	regulation of lipoprotein lipase activity (GO:0051004)	1.70E-05

BL.KO	negative regulation of cholesterol transport (GO:0032375)	5.61E-04
BL.KO	negative regulation of sterol transport (GO:0032372)	5.49E-04
BL.KO	plasma lipoprotein particle clearance (GO:0034381)	2.32E-06
BL.KO	plasma lipoprotein particle assembly (GO:0034377)	1.74E-06
BL.KO	cholesterol efflux (GO:0033344)	1.67E-06
BL.KO	negative regulation of lipoprotein particle clearance (GO:0010985)	1.57E-02
BL.KO	regulation of intestinal cholesterol absorption (GO:0030300)	1.56E-02
BL.KO	positive regulation of triglyceride lipase activity (GO:0061365)	1.55E-02
BL.KO	triglyceride-rich lipoprotein particle remodeling (GO:0034370)	1.53E-02
BL.KO	protein activation cascade (GO:0072376)	1.77E-02
BL.KO	plasminogen activation (GO:0031639)	1.76E-02
BL.KO	regulation of intestinal lipid absorption (GO:1904729)	1.74E-02
BL.KO	protein-lipid complex assembly (GO:0065005)	1.73E-06
BL.KO	plasma lipoprotein particle remodeling (GO:0034369)	1.81E-06
BL.KO	protein-lipid complex remodeling (GO:0034368)	1.62E-06
BL.KO	triglyceride catabolic process (GO:0019433)	9.69E-04
BL.KO	protein oxidation (GO:0018158)	1.99E-02
BL.KO	reverse cholesterol transport (GO:0043691)	9.51E-04
BL.KO	high-density lipoprotein particle assembly (GO:0034380)	1.97E-02
BL.KO	protein-containing complex remodeling (GO:0034367)	2.00E-06
BL.KO	peptidyl-methionine modification (GO:0018206)	2.21E-02
BL.KO	regulation of intestinal absorption (GO:1904478)	2.19E-02
BL.KO	chronic inflammatory response (GO:0002544)	2.45E-02
BL.KO	regulation of triglyceride catabolic process (GO:0010896)	2.44E-02
BL.KO	acylglycerol catabolic process (GO:0046464)	5.98E-05
BL.KO	neutral lipid catabolic process (GO:0046461)	5.78E-05
BL.KO	negative regulation of fatty acid biosynthetic process (GO:0045717)	2.72E-02
BL.KO	positive regulation of heterotypic cell-cell adhesion (GO:0034116)	3.00E-02
BL.KO	low-density lipoprotein particle remodeling (GO:0034374)	2.98E-02
BL.KO	regulation of heterotypic cell-cell adhesion (GO:0034114)	1.93E-03
BL.KO	negative regulation of lipid catabolic process (GO:0050995)	1.90E-03
BL.KO	plasma lipoprotein particle organization (GO:0071827)	6.58E-06
BL.KO	positive regulation of lipid catabolic process (GO:0050996)	2.42E-03
BL.KO	protein-lipid complex subunit organization (GO:0071825)	9.32E-06
BL.KO	regulation of lipoprotein particle clearance (GO:0010984)	4.10E-02
BL.KO	positive regulation of steroid metabolic process (GO:0045940)	2.74E-03
BL.KO	negative regulation of lipid transport (GO:0032369)	2.89E-03
BL.KO	regulation of nuclease activity (GO:0032069)	4.56E-02
BL.KO	regulation of plasma lipoprotein particle levels (GO:0097006)	1.64E-05
BL.KO	triglyceride metabolic process (GO:0006641)	1.88E-06
BL.KO	regulation of lipid catabolic process (GO:0050994)	2.20E-05
BL.KO	cholesterol transport (GO:0030301)	2.28E-05
BL.KO	triglyceride homeostasis (GO:0070328)	4.70E-03
BL.KO	acylglycerol homeostasis (GO:0055090)	4.64E-03

BL.KO	glycerolipid catabolic process (GO:0046503)	3.57E-04
BL.KO	regulation of fatty acid biosynthetic process (GO:0042304)	5.27E-03
BL.KO	regulation of cholesterol transport (GO:0032374)	6.72E-04
BL.KO	regulation of sterol transport (GO:0032371)	6.59E-04
BL.KO	sterol transport (GO:0015918)	6.13E-05
BL.KO	acylglycerol metabolic process (GO:0006639)	7.15E-06
BL.KO	neutral lipid metabolic process (GO:0006638)	6.51E-06
BL.KO	negative regulation of lipid localization (GO:1905953)	7.75E-03
BL.KO	positive regulation of immunoglobulin production (GO:0002639)	8.05E-03
BL.KO	intermembrane lipid transfer (GO:0120009)	7.98E-03
BL.KO	regulation of lipase activity (GO:0060191)	8.89E-05
BL.KO	cholesterol homeostasis (GO:0042632)	1.86E-03
BL.KO	positive regulation of phagocytosis (GO:0050766)	1.45E-02
BL.KO	sterol homeostasis (GO:0055092)	1.85E-03
BL.KO	regulation of fatty acid metabolic process (GO:0019217)	2.25E-03
BL.KO	regulation of phagocytosis (GO:0050764)	2.31E-03
BL.KO	phospholipid transport (GO:0015914)	2.27E-03
BL.KO	regulation of steroid metabolic process (GO:0019218)	2.33E-03
BL.KO	lipoprotein metabolic process (GO:0042157)	3.03E-04
BL.KO	regulation of immunoglobulin production (GO:0002637)	1.91E-02
BL.KO	neutrophil chemotaxis (GO:0030593)	2.22E-02
BL.KO	organic hydroxy compound transport (GO:0015850)	5.69E-05
BL.KO	regulation of lipid localization (GO:1905952)	5.91E-05
BL.KO	granulocyte chemotaxis (GO:0071621)	2.53E-02
BL.KO	regulation of production of molecular mediator of immune response (GO:0002700)	6.13E-05
BL.KO	neutrophil migration (GO:1990266)	2.93E-02
BL.KO	positive regulation of production of molecular mediator of immune response (GO:0002702)	4.71E-03
BL.KO	cholesterol metabolic process (GO:0008203)	4.94E-03
BL.KO	lipid homeostasis (GO:0055088)	7.90E-04
BL.KO	cellular oxidant detoxification (GO:0098869)	3.32E-02
BL.KO	granulocyte migration (GO:0097530)	3.52E-02
BL.KO	regulation of cytokine production involved in immune response (GO:0002718)	3.68E-02
BL.KO	negative regulation of lipid metabolic process (GO:0045833)	3.75E-02
BL.KO	regulation of cellular ketone metabolic process (GO:0010565)	6.13E-03
BL.KO	secondary alcohol metabolic process (GO:1902652)	6.24E-03
BL.KO	lipid transport (GO:0006869)	4.22E-06
BL.KO	regulation of lipid transport (GO:0032368)	6.23E-03
BL.KO	organophosphate ester transport (GO:0015748)	6.71E-03
BL.KO	sterol metabolic process (GO:0016125)	6.83E-03
BL.KO	positive regulation of peptide hormone secretion (GO:0090277)	4.39E-02
BL.KO	cellular detoxification (GO:1990748)	4.52E-02
BL.KO	positive regulation of lipid localization (GO:1905954)	4.50E-02
BL.KO	positive regulation of peptide secretion (GO:0002793)	4.56E-02

BL.KO	lipid localization (GO:0010876)	1.76E-06
BL.KO	positive regulation of lipid metabolic process (GO:0045834)	8.69E-03
BL.KO	regulation of lipid biosynthetic process (GO:0046890)	1.11E-02
BL.KO	glycerolipid metabolic process (GO:0046486)	1.98E-05
BL.KO	cellular lipid catabolic process (GO:0044242)	1.54E-02
BL.KO	positive regulation of protein-containing complex assembly (GO:0031334)	3.35E-03
BL.KO	steroid metabolic process (GO:0008202)	5.16E-03
BL.KO	alcohol metabolic process (GO:0006066)	1.25E-03
BL.KO	negative regulation of hydrolase activity (GO:0051346)	2.62E-04
BL.KO	regulation of lipid metabolic process (GO:0019216)	1.62E-03
BL.KO	regulation of immune effector process (GO:0002697)	1.86E-03
BL.KO	organic hydroxy compound metabolic process (GO:1901615)	8.82E-05
BL.KO	positive regulation of immune effector process (GO:0002699)	3.30E-02
BL.KO	response to toxic substance (GO:0009636)	3.76E-02
BL.KO	regulation of protein secretion (GO:0050708)	4.53E-02
BL.KO	regulation of small molecule metabolic process (GO:0062012)	1.25E-02
BL.KO	regulation of inflammatory response (GO:0050727)	1.45E-02
BL.KO	inflammatory response (GO:0006954)	1.41E-03
BL.KO	negative regulation of response to external stimulus (GO:0032102)	1.97E-02
BL.KO	regulation of vesicle-mediated transport (GO:0060627)	1.85E-03
BL.KO	regulation of hydrolase activity (GO:0051336)	3.41E-06
BL.KO	regulation of defense response (GO:0031347)	2.73E-03
BL.KO	positive regulation of response to external stimulus (GO:0032103)	2.93E-02
BL.KO	positive regulation of hydrolase activity (GO:0051345)	2.91E-03
BL.KO	response to wounding (GO:0009611)	3.21E-02
BL.KO	positive regulation of cellular component biogenesis (GO:0044089)	1.01E-02
BL.KO	negative regulation of transport (GO:0051051)	3.26E-02
BL.KO	regulation of protein-containing complex assembly (GO:0043254)	3.27E-02
BL.KO	cellular lipid metabolic process (GO:0044255)	1.09E-04
BL.KO	regulation of response to external stimulus (GO:0032101)	1.09E-04
BL.KO	lipid metabolic process (GO:0006629)	1.71E-05
BL.KO	negative regulation of multicellular organismal process (GO:0051241)	2.29E-04
BL.KO	negative regulation of catalytic activity (GO:0043086)	1.13E-02
BL.KO	chemical homeostasis (GO:0048878)	5.47E-04
BL.KO	cellular response to cytokine stimulus (GO:0071345)	3.73E-02
BL.KO	response to lipid (GO:0033993)	1.53E-02
BL.KO	response to bacterium (GO:0009617)	4.23E-02
BL.KO	regulation of response to stress (GO:0080134)	5.78E-03
BL.KO	defense response (GO:0006952)	2.55E-03
BL.KO	homeostatic process (GO:0042592)	1.27E-03
BL.KO	regulation of immune system process (GO:0002682)	2.85E-03
BL.KO	small molecule metabolic process (GO:0044281)	5.16E-03
BL.KO	positive regulation of cell communication (GO:0010647)	7.30E-03
BL.KO	positive regulation of signaling (GO:0023056)	7.50E-03

BL.KO	regulation of localization (GO:0032879)	5.92E-05
BL.KO	response to other organism (GO:0051707)	4.37E-02
BL.KO	response to external biotic stimulus (GO:0043207)	4.36E-02
BL.KO	regulation of transport (GO:0051049)	1.10E-02
BL.KO	regulation of catalytic activity (GO:0050790)	1.95E-03
BL.KO	organic substance transport (GO:0071702)	2.22E-02
BL.KO	response to stress (GO:0006950)	1.08E-04
BL.KO	regulation of multicellular organismal process (GO:0051239)	3.41E-03
BL.KO	regulation of biological quality (GO:0065008)	8.52E-05
BL.KO	positive regulation of response to stimulus (GO:0048584)	3.57E-02
BL.KO	regulation of molecular function (GO:0065009)	4.08E-03
BL.KO	response to organic substance (GO:0010033)	1.73E-02
BL.KO	cellular response to chemical stimulus (GO:0070887)	4.25E-02
BL.KO	organic cyclic compound metabolic process (GO:1901360)	3.29E-02
BL.KO	establishment of localization (GO:0051234)	3.01E-03
BL.KO	regulation of cell communication (GO:0010646)	2.25E-02
BL.KO	transport (GO:0006810)	7.12E-03
BL.KO	regulation of signaling (GO:0023051)	2.34E-02
BL.KO	localization (GO:0051179)	1.16E-03
BL.KO	response to chemical (GO:0042221)	1.52E-02
BL.KO	positive regulation of biological process (GO:0048518)	2.67E-03
BL.KO	positive regulation of cellular process (GO:0048522)	4.25E-02
BL.KO	primary metabolic process (GO:0044238)	4.55E-02
BL.KO	response to stimulus (GO:0050896)	1.02E-02
BL.KO	organic substance metabolic process (GO:0071704)	3.47E-02
BL.KO	biological regulation (GO:0065007)	4.55E-02
CRB.HET	neurofilament bundle assembly (GO:0033693)	5.09E-02
CRB.HET	response to lithium ion (GO:0010226)	4.98E-02
CRB.HET	long-term synaptic potentiation (GO:0060291)	2.54E-02
CRB.HET	intermediate filament cytoskeleton organization (GO:0045104)	2.61E-02
CRB.HET	intermediate filament-based process (GO:0045103)	2.64E-02
CRB.HET	cellular response to calcium ion (GO:0071277)	1.85E-03
CRB.HET	negative regulation of synaptic transmission (GO:0050805)	4.13E-02
CRB.HET	multicellular organismal response to stress (GO:0033555)	5.00E-02
CRB.HET	response to calcium ion (GO:0051592)	5.96E-04
CRB.HET	positive regulation of synaptic transmission (GO:0050806)	1.62E-02
CRB.HET	regulation of synaptic plasticity (GO:0048167)	1.39E-03
CRB.HET	cellular response to metal ion (GO:0071248)	1.67E-03
CRB.HET	cellular response to inorganic substance (GO:0071241)	3.31E-03
CRB.HET	sodium ion transport (GO:0006814)	2.65E-02
CRB.HET	learning or memory (GO:0007611)	2.58E-02
CRB.HET	cognition (GO:0050890)	1.96E-02
CRB.HET	response to metal ion (GO:0010038)	2.38E-03
CRB.HET	behavior (GO:0007610)	5.44E-04

CRB.HET	chemical synaptic transmission (GO:0007268)	1.98E-02
CRB.HET	anterograde trans-synaptic signaling (GO:0098916)	1.86E-02
CRB.HET	response to peptide hormone (GO:0043434)	3.10E-02
CRB.HET	trans-synaptic signaling (GO:0099537)	2.02E-02
CRB.HET	axon development (GO:0061564)	3.50E-02
CRB.HET	modulation of chemical synaptic transmission (GO:0050804)	2.53E-02
CRB.HET	regulation of trans-synaptic signaling (GO:0099177)	2.47E-02
CRB.HET	synaptic signaling (GO:0099536)	2.60E-02
CRB.HET	response to peptide (GO:1901652)	2.52E-02
CRB.HET	response to inorganic substance (GO:0010035)	2.61E-02
CRB.HET	regulation of ion transport (GO:0043269)	2.45E-02
CRB.HET	brain development (GO:0007420)	2.13E-02
CRB.HET	head development (GO:0060322)	2.63E-02
CRB.HET	neuron development (GO:0048666)	2.67E-02
CRB.HET	central nervous system development (GO:0007417)	1.78E-02
CRB.HET	neuron differentiation (GO:0030182)	1.80E-02
CRB.HET	nervous system development (GO:0007399)	1.52E-06
CRB.HET	cell-cell signaling (GO:0007267)	2.06E-02
CRB.HET	generation of neurons (GO:0048699)	2.55E-02
CRB.HET	positive regulation of developmental process (GO:0051094)	2.72E-02
CRB.HET	neurogenesis (GO:0022008)	4.96E-02
CRB.HET	regulation of developmental process (GO:0050793)	2.50E-02
CRB.HET	system development (GO:0048731)	9.90E-05
CRB.HET	multicellular organism development (GO:0007275)	2.03E-04
CRB.HET	anatomical structure development (GO:0048856)	1.58E-03
CRB.HET	regulation of biological quality (GO:0065008)	4.99E-02
CRB.HET	developmental process (GO:0032502)	1.15E-03
CRB.HET	multicellular organismal process (GO:0032501)	1.53E-03

Supplementary Table 16 – GO Analysis of Targets of rhIGF1 Action in Mice
All significant ontologies found in GO analysis of Male mice treated with rhIGF1 or vehicle.
Legend:
CRB.KO = Cerebellum *Mecp2*$^{-/y}$ targets, BL.KO = Blood *Mecp2*$^{-/y}$ targets, CRB.HET = Cerebellum *Mecp2*$^{-+y}$ targets

Appendix III

Analysis of SH-SY5Y Cell Line Immunofluorescence Data:

Antibody	Group1	Group2	n1	N2	p	p.Adj	Significance
pCREB	Con	IGF1_24hr	1285	724	5.69e-13	8.54e-13	***
pCREB	Con	IGF1_24hr_PPP	1285	327	4.89e-17	9.78e-17	***
pCREB	Con	PPP	1285	1008	5.59e-12	6.71e-12	***
pCREB	IGF1_24hr	IGF1_24hr_PPP	724	327	6.00e-03	6.00e-03	*
pCREB	IGF1_24hr	PPP	724	1008	7.43e-37	4.46e-36	***

pCREB	IGF1_24hr_PPP	PPP	327	1008	1.26e-34	3.78e-34	***

Supplementary Table 17 – Nuclear Localisation for pCREB in SH-SY5Y Cells Treated with rhIGF1 in the Presence or Absence of PPP Blocker

Immunofluorescence confocal analysis detecting nuclear pCREB levels

Legend:

PPP = Cells pre-treated with 1uM PPP
IGF1_24hr = Cell treated with rhIGF1 for 24 hours
IGF1_24hr_PPP = Cells pre-treated with 1uM of PPP then treated with rhIGF1 for 24hr,
*** = adjusted p-value <0.00005
* = adjusted p-value <0.05

Antibody	Group1	Group2	n1	n2	P-Value	Adjusted P-Value	Significance
pCREB	Con	GPE_24hr	1285	970	7.00e-03	7.00e-03	*
pCREB	Con	GPE_24hr_PPP	1285	423	3.78e-24	1.13e-23	***
pCREB	Con	PPP	1285	1008	5.59e-12	8.39e-12	***
pCREB	GPE_24hr	GPE_24hr_PPP	970	423	3.66e-33	2.20e-32	***
pCREB	GPE_24hr	PPP	970	1008	2.96e-20	5.92e-20	***
pCREB	GPE_24hr_PPP	PPP	423	1008	3.08e-08	3.70e-08	***

Supplementary Table 18 – Nuclear Localisation for pCREB in SH-SY5Y Cells Treated with GPE in the Presence or Absence of PPP Blocker

Immunofluorescence confocal analysis detecting nuclear pCREB levels

Legend:

PPP = Cells pre-treated with 1uM PPP
GPE_24hr = Cell treated with GPR for 24 hours
GPE_24hr_PPP = Cells pre-treated with 1uM of PPP then treated with GPR for 24hr,
*** = adjusted p-value <0.00005,
* = adjusted p-value <0.05

Antibody	Group1	Group2	N1	N2	P-Value	Adjusted P-Value	Significance
pAKT	Con	IGF1_24hr	7565	4945	1.20e-96	7.20e-96	***
pAKT	Con	IGF1_24hr_PPP	7565	2676	6.28e-01	6.82e-01	NS
pAKT	Con	PPP	7565	2405	6.50e-02	9.75e-02	NS
pAKT	IGF1_24hr	IGF1_24hr_PPP	4945	2676	4.82e-48	9.64e-48	***
pAKT	IGF1_24hr	PPP	4945	2405	1.78e-50	5.34e-50	***
pAKT	IGF1_24hr_PPP	PPP	2676	2405	2.13e-01	2.56e-01	NS

Supplementary Table 19 – Cytosolic pAKT in SH-SY5Y Cells Treated with rhIGF1 in the Presence or Absence of PPP Blocker

Immunofluorescence confocal analysis detecting cytosolic pAKT levels

Legend:

PPP = Cells pre-treated with 1uM PPP,
GPE_24hr = Cell treated with rhIGF1 for 24 hours,
GPE_24hr_PPP = Cells pre-treated with 1uM of PPP then treated with rhIGF1 for 24 hours,
*** = adjusted p-value <0.00005 (asterisks directly over individual bars were relative to control),
NS = Not Significant

Antibody	Group1	Group2	N1	N2	P-Value	Adjusted P-Value	Significance
pAKT	Con	GPE_24hr	7565	4243	0.00	0.00	***
pAKT	Con	GPE_24hr_PPP	7565	4221	6.31e-100	9.47e-100	***
pAKT	Con	PPP	7565	2405	6.50e-02	6.50e-02	NS
pAKT	GPE_24hr	GPE_24hr_PPP	4243	4221	0.00	0.00	***
pAKT	GPE_24hr	PPP	4243	2405	0.00	0.00	***
pAKT	GPE_24hr_PPP	PPP	4221	2405	9.40e-40	1.13e-39	***

Supplementary Table 20 – Cytosolic pAKT in SH-SY5Y Cells Treated with GPE in the presence or absence of PPP Blocker

Immunofluorescence confocal analysis detecting cytosolic pAKT levels

Legend:

PPP = Cells pre-treated with 1uM PPP,
GPE_24hr = Cell treated with GPE for 24 hours,
GPE_24hr_PPP = Cells pre-treated with 1uM of PPP then treated with GPE for 24 hours,
*** = adjusted p-value <0.00005 (asterisks directly over individual bars were relative to control),
NS = Not Significant

Antibody	Group1	Group2	N1	N2	P-Value	Adjusted P-Value	Significance
pERK1/2	Con	IGF1_24hr	2026	1234	2.19e-15	2.91e-15	***
pERK1/2	Con	IGF1_24hr_PPP	2026	489	1.19e-96	2.38e-96	***
pERK1/2	Con	PPP	2026	970	1.17e-192	7.02e-192	***
pERK1/2	IGF1_24hr	IGF1_24hr_PPP	1234	489	1.62e-84	2.43e-84	***
pERK1/2	IGF1_24hr	PPP	1234	970	1.63e-168	4.89e-168	***
pERK1/2	IGF1_24hr_PPP	PPP	489	970	1.17e-17	1.40e-17	***

Supplementary Table 21 – Cytosolic pERK1/2 in SH-SY5Y Cells Treated with rhIGF1 in the Presence or Absence of PPP Blocker

Immunofluorescence confocal analysis detecting cytosolic pERK1/2 levels

Legend:

PPP = Cells pre-treated with 1uM PPP,
GPE_24hr = Cell treated with rhIGF1 for 24 hours,
GPE_24hr_PPP = Cells pre-treated with 1uM of PPP then treated with rhIGF1 for 24 hours,
*** = adjusted p-value <0.00005 (asterisks directly over individual bars were relative to control),
NS = Not Significant

Antibody	Group1	Group2	N1	N2	P-Value	Adjusted P-Value	Significance
pERK1/2	Con	GPE_24hr	2026	789	1.71e-64	4.20e-64	***
pERK1/2	Con	GPE_24hr_PPP	2026	721	1.50e-98	4.50e-98	***
pERK1/2	Con	PPP	2026	970	1.17e-192	7.02e-192	***
pERK1/2	GPE_24hr	GPE_24hr_PPP	789	721	2.84e-09	2.84e-09	***
pERK1/2	GPE_24hr	PPP	789	970	2.86e-61	4.29e-61	***
pERK1/2	GPE_24hr_PPP	PPP	721	970	1.47e-33	1.76e-33	***

Supplementary Table 22 – Cytosolic pERK1/2 in SH-SY5Y Cells Treated with GPE in the Presence or Absence of PPP Blocker

Immunofluorescence confocal analysis detecting cytosolic pERK1/2 levels

Legend:

PPP = Cells pre-treated with 1uM PPP,
GPE_24hr = Cell treated with GPE for 24 hours,
GPE_24hr_PPP = Cells pre-treated with 1uM of PPP then treated with GPE for 24 hours,
*** = adjusted p-value <0.00005 (asterisks directly over individual bars were relative to control),
NS = Not Significant