

SUPPLEMENTARY TABLE S4. GSEA RESULTS SUMMARY OF GENESet MIPS_18S_U11_U12_SNRNP

Gene symbol	Gene_title	Rank in gene list	Rank metric score	Running ES	Core enrichment	KO/WT
Dataset						KOvsWTforGSEA.KOvsWT.cls#KO_versus_WT
Phenotype						KOvsWT.cls#KO_versus_WT
Upregulated in class						KO
GeneSet						MIPS_18S_U11_U12_SNRNP
Enrichment score (ES)						0.5717312
Normalized enrichment score (NES)						1.9153707
Nominal P-value						0.0023696683
FDR q-value						0.1871023
FWER P-value						0.731
Gene symbol	Gene_title	Rank in gene list	Rank metric score	Running ES	Core enrichment	KO/WT
ZCRB1	zinc finger CCHC-type and RNA binding motif 1	6	2.379735	0.2199	Yes	4.58
RNPC3	RNA-binding region (RNP1, RRM) containing 3	699	0.879432	0.272856	Yes	18.27
SNRNP25	Small nuclear ribonucleoprotein 25	705	0.877784	0.353854	Yes	4.02
SNRNP3	Small nuclear ribonucleoprotein D3 polypeptide 18 kDa	1020	0.77935	0.413064	Yes	1.93
SNRPD1	Small nuclear ribonucleoprotein D1 polypeptide 16 kDa	2640	0.556754	0.398126	Yes	1.48
SF3B5	Splicing factor 3b, subunit 5, 10 kDa	2667	0.555512	0.448449	Yes	1.52
SNRNPB	Small nuclear ribonucleoprotein polypeptides B and B1	2840	0.541204	0.491456	Yes	2.83
PRPF8	PRP8 pre-mRNA processing factor 8 homolog (<i>S. cerevisiae</i>)	2851	0.540087	0.541009	Yes	1.52
SNRNP35	Small nuclear ribonucleoprotein 35	3286	0.506506	0.570054	Yes	3.22
SNRNP2	Small nuclear ribonucleoprotein D2 polypeptide 16.5 kDa	4232	0.43464	0.57148	Yes	1.22
ZRSR2	Zinc finger (CCCH type), RNA-binding motif and serine/arginine rich 2	5078	0.377578	0.571731	Yes	1.62
DHX15	DEAH (Asp-Glu-Ala-His) box polypeptide 15	6388	0.292184	0.545041	No	1.16
SF3B1	Splicing factor 3b, subunit 1, 155 kDa	6536	0.283142	0.565201	No	1.32
PDCCD7	Programmed cell death 7	9204	0.125078	0.46732	No	1.25
SNRPE	Small nuclear ribonucleoprotein polypeptide E	11254	0.010701	0.384221	No	1.00
SNRPG	Small nuclear ribonucleoprotein polypeptide G	11523	-0.00471	0.373659	No	1.00
YBX1	Y box binding protein 1	12020	-0.03265	0.356324	No	0.98
SF3B2	Splicing factor 3b, subunit 2, 145 kDa	12457	-0.05652	0.343659	No	0.96
ZMAT5	Zinc finger, matrix type 5	12459	-0.05665	0.348859	No	0.86
SF3B4	Splicing factor 3b, subunit 4, 49 kDa	15531	-0.2238	0.243531	No	0.56
SF3B3	Splicing factor 3b, subunit 3, 130 kDa	22121	-0.6362	0.031979	No	0.01
SNRNP48	Small nuclear ribonucleoprotein 48	22337	-0.65957	0.084171	No	0.51

SUPPLEMENTARY TABLE S5. GSEA RESULTS SUMMARY OF GENESet OF INFLAMMATORY GENE VARIATIONS OF HUMAN ENDOTHELIAL CELL RESPONSES TO OXIDIZED LIPIDS

Gene symbol	Gene_title	Rank in gene list	Rank metric score	Running ES	Core enrichment	KO/WT
CCDC68	Coiled-coil domain containing 68	1699	0.646615	0.058796	Yes	1.67
IRAK2	Interleukin-1 receptor-associated kinase 2	2197	0.590166	0.155688	Yes	6.37
DUSP5	Dual specificity phosphatase 5	2294	0.580959	0.267203	Yes	2.04
HERPUD2	HERPUD family member 2	2312	0.579404	0.38165	Yes	1.74
ADAMTS1	ADAM metalloproteinase with thrombospondin type 1 motif, 1	2366	0.576131	0.49397	Yes	12.27
RORA	RAR-related orphan receptor A	2372	0.575657	0.608164	Yes	13.54
EMP1	Epithelial membrane protein 1	4975	0.383721	0.577668	No	3.49
ADAMTS9	ADAM metalloproteinase with thrombospondin type 1 motif, 9	10115	0.075885	0.381909	No	1.06
LBH	Limb bud and heart development	11289	0.009029	0.335578	No	1.01
SOS1	Son of sevenless homolog 1 (Drosophila)	12781	-0.07456	0.289223	No	0.89
NAV3	Neuron navigator 3	13183	-0.09554	0.291758	No	0.82
FNIP1	Folliculin interacting protein 1	13580	-0.11815	0.298991	No	0.73
TFEC	Transcription factor EC	14492	-0.16639	0.294681	No	0.78
TRIM16	Tripartite motif-containing 16	15869	-0.24185	0.28629	No	0.78
ARRDC4	Arrestin domain containing 4	17165	-0.31793	0.296341	No	0.53

Dataset
 KOvsWTforGSEA.KOvsWT.cls#KO_vsus_WT
 Phenotype
 Upregulated in class
 GeneSet
 KOvsWT.cls#KO_vsus_WT
 ES
 KO
 GARGALOVIC_RESPONSE_TO_OXIDIZED_PHOSPHOLIPIDS_GREY_UP
 NES
 0.60816413
 1.845696
 Nominal P-value
 0.0023094688
 FDR q-value
 0.22862837
 FWER P-Value
 0.94

SUPPLEMENTARY TABLE S6. GSEA RESULTS SUMMARY OF GENE EXPRESSION PROFILING OF PEDIATRIC ACUTE MYELOGENOUS LEUKEMIA

Dataset		KOvsWTforGSEA.KOvsWT.cls#KO_ versus_WT				
Phenotype		KOvsWT.cls#KO_ versus_WT				
Upregulated in class		KO				
GeneSet		ROSS_AML_WITH_CBFB_MYH11_FUSION				
ES		0.4514762				
NES		1.8177781				
Nominal P-value		0.0024875621				
FDR q-value		0.2690509				
FWER P-value		0.974				
<i>Gene symbol</i>	<i>Gene_title</i>	<i>Rank in gene list</i>	<i>Rank metric score</i>	<i>Running ES</i>	<i>Core enrichment</i>	<i>KO/WT</i>
HPCAL1	Hippocalcin-like 1	49	1.649472356	0.07114862	Yes	2.24
CFP	Complement factor properdin	176	1.239297748	0.12094103	Yes	2.47
TGFB1	Transforming growth factor, beta-induced, 68 kDa	1434	0.692949951	0.10003945	Yes	7.48
CTSS	Cathepsin S	1493	0.683476031	0.12797207	Yes	2.87
CLEC10A	C-type lectin domain family 10, member A	1545	0.675664723	0.15584579	Yes	12.34
SLC38A1	Solute carrier family 38, member 1	1575	0.670774043	0.18440633	Yes	2.66
PLBD1	Phospholipase B domain containing 1	1600	0.665722013	0.21294819	Yes	5.77
CCR2	Chemokine (C-C motif) receptor 2	1792	0.635456264	0.23328732	Yes	4.09
LGALS2	Lectin, galactoside-binding, soluble, 2 (galectin 2)	2019	0.608251929	0.25098205	Yes	1.74
GIMAP4	GTPase, IMAP family member 4	2370	0.575773001	0.26214233	Yes	2.21
CH13L1	Chitinase 3-like 1 (cartilage glycoprotein-39)	2793	0.545612037	0.2690071	Yes	2.34
MEGF9	Multiple EGF-like-domains 9	2823	0.543178141	0.29190817	Yes	2.23
CYBB	Cytochrome b-245, beta polypeptide (chronic granulomatous disease)	2926	0.534000516	0.31144034	Yes	8.87
ST18	Suppression of tumorigenicity 18 (breast carcinoma) (zinc finger protein)	3117	0.519149125	0.32662487	Yes	1.74
CBFB	Core-binding factor, beta subunit	3120	0.518837154	0.34955546	Yes	1.59
CEBPD	CCAAT/enhancer binding protein (C/EBP), delta	3338	0.502948821	0.36294925	Yes	2.54
CD52	CD52 molecule	3608	0.482027024	0.37327892	Yes	2.12
NRP1	Neuropilin 1	3620	0.481240988	0.39417222	Yes	2.45
ANXA11	Annexin A11	3938	0.456828654	0.4014124	Yes	4.64
SPARC	Secreted protein, acidic, cysteine-rich (osteonectin)	3948	0.456404716	0.42128628	Yes	2.67
AK5	Adenylate kinase 5	4009	0.451549619	0.43884978	Yes	2.17
SLC7A7	Solute carrier family 7 (cationic amino acid transporter, y+ system), member 7	4178	0.440265894	0.4514762	Yes	3.99
NAGA	N-acetylgalactosaminidase, alpha-	4782	0.397178382	0.44432184	No	1.97
TES	Testis derived transcript (3 LIM domains)	5502	0.350123972	0.4303152	No	1.62
FYB	FYN binding protein (FYB-120/130)	6089	0.311039805	0.42003858	No	2.00
KCID12	Potassium channel tetramerisation domain containing 12	6310	0.297059417	0.42417702	No	1.99
PTPRM	Protein tyrosine phosphatase, receptor type, M	6731	0.271892458	0.41898325	No	1.48
MYH11	Myosin, heavy chain 11, smooth muscle	6826	0.267038643	0.42696613	No	1.27
LPAR1	Lysophosphatidic acid receptor 1	8319	0.179532111	0.37363845	No	1.13
S100A8	S100 calcium binding protein A8	9429	0.11423514	0.33314806	No	1.18
S100A9	S100 calcium binding protein A9	11606	-0.009887209	0.24419744	No	0.98
NACC2	Nucleus accumbens associated 2, BEN and BTB (POZ) domain containing	11851	-0.023757331	0.23522778	No	0.99

(continued)

SUPPLEMENTARY TABLE S6. (CONTINUED)

<i>Gene symbol</i>	<i>Gene_title</i>	<i>Rank in gene list</i>	<i>Rank metric score</i>	<i>Running ES</i>	<i>Core enrichment</i>	<i>KO/WT</i>
GRHRP	Glyoxylate reductase/hydroxypyruvate reductase	12353	-0.050696608	0.21689554	No	0.85
IL13RA1	Interleukin 13 receptor, alpha 1	12523	-0.060985543	0.21265808	No	0.95
PLXNB2	Plexin B2	16029	-0.250425041	0.079781644	No	0.69
DUSP6	Dual specificity phosphatase 6	16361	-0.270227253	0.0781701	No	0.77
MEF2A	MADS box transcription enhancer factor 2, polypeptide A (myocyte enhancer factor 2A)	17019	-0.309347481	0.06490178	No	0.45
TNFAIP2	Tumor necrosis factor, alpha-induced protein 2	17828	-0.35370788	0.047398016	No	0.37
CLEC7A	C-type lectin domain family 7, member A	19973	-0.478776753	-0.019440688	No	0.17
QPCT	Glutaminyl-peptide cyclotransferase (glutaminyl cyclase)	19980	-0.47925958	0.001570153	No	0.65
IL10RA	Interleukin 10 receptor, alpha	20430	-0.501668096	0.005376662	No	0.02
MN1	Meningioma (disrupted in balanced translocation) 1	21427	-0.571854532	-0.010174272	No	0.41
PGM1	Phosphoglucomutase 1	22404	-0.667900324	-0.02064355	No	0.18
KIF17	Kinesin family member 17	22527	-0.68552202	0.004750726	No	0.61
MTMR11	Myotubularin related protein 11	22801	-0.729974508	0.025913656	No	0.42
MDFIC	MyoD family inhibitor domain containing	23539	-0.884654582	0.03487642	No	0.42

SUPPLEMENTARY TABLE S7. GSEA RESULTS SUMMARY FROM ANALYSIS OF THE HUMAN AND MOUSE TRANSCRIPTOMES

<i>Gene symbol</i>	<i>Gene_title</i>	<i>Rank in gene list</i>	<i>Rank metric score</i>	<i>Running ES</i>	<i>Core enrichment</i>	<i>KO/WT</i>
ETS1	v-ets erythroblastosis virus E26 oncogene homolog 1 (avian)	64	1.533523	0.151507	Yes	2.04
MYB	v-myb myeloblastosis viral oncogene homolog (avian)	238	1.15292	0.260288	Yes	1.70
MMP12	Matrix metalloproteinase 12 (macrophage elastase)	466	0.979138	0.349386	Yes	1.52
CCR9	Chemokine (C-C motif) receptor 9	626	0.909821	0.434307	Yes	2.94
SLAMF1	Signaling lymphocytic activation molecule family member 1	1167	0.745323	0.487063	Yes	4.55
IRF8	Interferon regulatory factor 8	1753	0.640505	0.527436	Yes	3.34
ITK	IL2-inducible T-cell kinase	2100	0.600001	0.573545	Yes	6.11
CYTIP	Cytohesin 1 interacting protein	2698	0.552692	0.6046	Yes	9.16
RHOH	Ras homolog gene family, member H	4915	0.387292	0.552603	No	3.60
NCK2	NCK adaptor protein 2	5434	0.35464	0.566993	No	2.82
TRAF3IP3	TRAF3 interacting protein 3	6890	0.262645	0.533692	No	1.38
PAX1	Paired box gene 1	11970	-0.03044	0.328356	No	0.96
PIK3CD	Phosphoinositide-3-kinase, catalytic, delta polypeptide	14426	-0.16321	0.24403	No	0.75
ADAMDEC1	ADAM-like, decysin 1	14631	-0.17464	0.253213	No	0.78
IRF4	Interferon regulatory factor 4	17712	-0.34725	0.16174	No	0.69
GNA13	Guanine nucleotide binding protein (G protein), alpha 13	20512	-0.50679	0.097832	No	0.42
SH2D1A	SH2 domain protein 1A, Duncan's disease (lymphoproliferative syndrome)	21825	-0.60852	0.105162	No	0.37

Dataset KOvsWTforGSEA.KOvsWT.cls#KO_versus_WT
 Phenotype KOvsWT.cls#KO_versus_WT
 Upregulated in class KO
 GeneSet SU_THYMUS
 ES 0.60460025
 NES 1.8951225
 Nominal P-value 0.0043196543
 FDR q-value 0.19467275
 FWER P-value 0.8

SUPPLEMENTARY TABLE S8. GSEA RESULTS SUMMARY FROM GENE-EXPRESSION PROFILE OF AGEING, HEATSHOCK TREATMENT, AND IN VIVO TOTAL ANTIOXIDANT STATUS AND PROTEIN SYNTHESIS IN HUMAN PERIPHERAL LYMPHOCYTES

Gene symbol	Gene_title	Rank in gene list	Rank metric score	Running ES	Core enrichment	KO/WT
SOAT1	Sterol O-acyltransferase (acyl-coenzyme A: cholesterol acyltransferase) 1	2040	0.605698	-0.00296	No	1.89
FDFT1	Farnesyl-diphosphate farnesyltransferase 1	4245	0.433794	-0.03557	No	2.86
CDC16	GDC16 cell division cycle 16 homolog (<i>S. cerevisiae</i>)	4508	0.416594	0.009221	No	1.95
STAT4	Signal transducer and activator of transcription 4	6479	0.2869	-0.03337	No	1.46
LGALS3	Lectin, galactoside-binding, soluble, 3 (galectin 3)	7929	0.199467	-0.06623	No	1.59
NDUFS4	NADH dehydrogenase (ubiquinone) Fe-S protein 4, 18 kDa (NADH-coenzyme Q reductase)	8226	0.184476	-0.05378	No	1.16
PLIN2	Perilipin 2	8732	0.153073	-0.0541	No	1.38
SDC4	Syndecan 4 (amphiglycan, ryudocan)	11411	0.001504	-0.16378	No	1.00
COL9A3	Collagen, type IX, alpha 3	11986	-0.03132	-0.18316	No	0.97
PLA2G16	Phospholipase A2, group XVI	12485	-0.0585	-0.19579	No	0.89
RUNX3	Runt-related transcription factor 3	20939	-0.53332	-0.47154	Yes	0.45
GNAI5	Guanine nucleotide binding protein (G protein), alpha 15 (Gq class)	21227	-0.5544	-0.40941	Yes	0.37
PCMT1	Protein-L-isoaspartate (D-aspartate) O-methyltransferase	21444	-0.57335	-0.34184	Yes	0.24
UFDL1	Ubiquitin fusion degradation 1 like (yeast)	21818	-0.60805	-0.27609	Yes	0.21
KDM6A	Lysine (K)-specific demethylase 6A	22218	-0.64574	-0.20637	Yes	0.29
CDK18	Cyclin-dependent kinase 18	22446	-0.67368	-0.12588	Yes	0.59
TXK	TXK tyrosine kinase	22603	-0.699	-0.03909	Yes	0.52
NRG2	Neuregulin 2	23380	-0.84236	0.041361	Yes	0.64

Dataset KOvsWTforGSEA.KOvsWT.cls#KO_versus_WT
 Phenotype KOvsWT.cls#KO_versus_WT
 Upregulated in class WT
 GeneSet VISALA_AGING_LYMPHOCYTE_DN
 ES -0.54264146
 NES -1.6509995
 Nominal P-value 0.011299435
 FDR q-value 1.0
 FWER P-value 1.0

SUPPLEMENTARY TABLE S9. GSEA RESULTS SUMMARY FROM GENE EXPRESSION IN PLEURIPOTENT STEM CELLS FROM HUMAN TESTIS

Gene symbol	Gene_title	Rank in gene list	Rank metric score	Running ES	Core enrichment	KO/WT
MYC	v-myc myelocytomatosis viral oncogene homolog (avian)	1295	0.719384	-0.00981	No	1.88
HSPA4	Heat shock 70 kDa protein 4	1681	0.64919	0.013511	No	2.05
KLF4	Kruppel-like factor 4 (gut)	2336	0.577699	0.021479	No	12.31
POU6F1	POU domain, class 6, transcription factor 1	2917	0.534371	0.029874	No	1.93
REXO1	REX1, RNA exonuclease 1 homolog (<i>S. cerevisiae</i>)	2954	0.531518	0.060436	No	2.37
GDF3	Growth differentiation factor 3	3593	0.483325	0.063372	No	2.22
TEP1	Telomerase-associated protein 1	4754	0.399166	0.039799	No	3.62
TERF1	Telomeric repeat binding factor (NIMA-interacting) 1	6870	0.263992	-0.03114	No	1.66
TINF2	TERF1 (TRF1)-interacting nuclear factor 2	7655	0.215658	-0.05033	No	1.51
PHTF2	Putative homeodomain transcription factor 2	9292	0.120357	-0.11026	No	1.71
CD9	CD9 molecule	10010	0.081359	-0.1348	No	1.20
GABRB3	Gamma-aminobutyric acid (GABA) A receptor, beta 3	10181	0.072388	-0.13741	No	1.05
DKK3	Dickkopf homolog 3 (<i>Xenopus laevis</i>)	10966	0.027335	-0.16796	No	1.03
TTL4	Tubulin tyrosine ligase-like family, member 4	11568	-0.00746	-0.19219	No	0.99
LIN28A	Lin-28 homolog A (<i>Caenorhabditis elegans</i>)	11597	-0.00943	-0.19277	No	0.99
ZFP42	Zinc finger protein 42 homolog (mouse)	11934	-0.02867	-0.20484	No	0.97
SOX2	SRY (sex determining region Y)-box 2	12134	-0.03865	-0.21068	No	0.96
DPPA4	Developmental pluripotency associated 4	13529	-0.11541	-0.26097	No	0.83
AKT3	v-akt murine thymoma viral oncogene homolog 3 (protein kinase B, gamma)	14513	-0.16766	-0.29123	No	0.78
UTF1	Undifferentiated embryonic cell transcription factor 1	14992	-0.19433	-0.29914	No	0.70
PRRX1	Paired related homeobox 1	15222	-0.2062	-0.29612	No	0.73
DPPA2	Developmental pluripotency associated 2	15309	-0.21108	-0.28693	No	0.90
LIN28B	Lin-28 homolog B (<i>C. elegans</i>)	15767	-0.23519	-0.29152	No	0.64
PHC1	Polyhomeotic homolog 1 (<i>Drosophila</i>)	16294	-0.26601	-0.29708	No	0.67
DNMT3B	DNA (cytosine-5)-methyltransferase 3 beta	16956	-0.30607	-0.30577	No	0.59
GJA1	Gap junction protein, alpha 1, 43 kDa (connexin 43)	17480	-0.33493	-0.30706	No	0.47
MYCBP	c-myc binding protein	17734	-0.3485	-0.29644	No	0.52
RET	Ret proto-oncogene (multiple endocrine neoplasia and medullary thyroid carcinoma 1, Hirschsprung disease)	17889	-0.35774	-0.2812	No	0.66
SALL2	Sal-like 2 (<i>Drosophila</i>)	19606	-0.4597	-0.32396	No	0.35
PTWIL2	Ptvi-like 2 (<i>Drosophila</i>)	22310	-0.65571	-0.39543	Yes	0.43
ELOVL6	ELOVL family member 6, elongation of long chain fatty acids (FEN1/Elo2, SUR4/Elo3-like, yeast)	23128	-0.78707	-0.38153	Yes	0.22
KLF5	Kruppel-like factor 5 (intestinal)	23628	-0.91083	-0.34712	Yes	0.45
CXCL5	Chemokine (C-X-C motif) ligand 5	23776	-0.96513	-0.29497	Yes	0.45
NANOG	Nanog homeobox	23864	-1.0092	-0.23771	Yes	0.27
PROM1	Prominin 1	24035	-1.10322	-0.17819	Yes	0.58
POU5F1	POU domain, class 5, transcription factor 1	24171	-1.22526	-0.10987	Yes	0.31
MYBL2	v-myb myeloblastosis viral oncogene homolog (avian)-like 2	24367	-1.96982	0.000863	Yes	0.12

KOvsWTforGSEA.KOvsWT.cls#KO_versus_WT
 KOvsWT.cls#KO_versus_WT
 WT
 CONRAD_STEM_CELL
 -0.43495297
 -1.6443975
 0.010869565
 1.0
 1.0

SUPPLEMENTARY TABLE S10. GSEA RESULTS SUMMARY OF GENE EXPRESSION IN WNT CANONICAL PATHWAY

<i>Gene symbol</i>	<i>Gene_title</i>	<i>Rank in gene list</i>	<i>Rank metric score</i>	<i>Running ES</i>	<i>Core enrichment</i>	<i>KO/WT</i>
CSNK1G1	Casein kinase 1, gamma 1	1558	0.674078226	0.009545445	No	3.10
KLHL12	Kelch-like 12 (Drosophila)	2581	0.561615646	0.028826853	No	1.50
DVL3	Dishevelled, dsh homolog 3 (Drosophila)	9013	0.134897277	-0.22036928	No	1.29
CUL3	Cullin 3	9737	0.09571591	-0.23960444	No	1.11
DVL2	Dishevelled, dsh homolog 2 (Drosophila)	12277	-0.04648336	-0.33872718	No	0.95
RANBP3	RAN binding protein 3	13154	-0.09388889	-0.36443996	No	0.96
AXIN1	Axin 1	15220	-0.20587587	-0.4267369	No	0.65
PIP5K1B	Phosphatidylinositol-4-phosphate 5-kinase, type 1, beta	15661	-0.23007240	-0.41971317	No	
GSK3A	Glycogen synthase kinase 3 alpha	17367	-0.32761386	-0.45396695	Yes	0.73
WNT3A	Wingless-type MMTV integration site family, member 3A	17743	-0.34871229	-0.43134335	Yes	0.71
CTNNB1	Catenin (cadherin-associated protein), beta 1, 88 kDa	18939	-0.41966083	-0.43463516	Yes	0.64
APC	Adenomatosis polyposis coli	19290	-0.44061285	-0.40096787	Yes	0.17
NKD2	Naked cuticle homolog 2 (Drosophila)	19451	-0.45028683	-0.35844925	Yes	0.50
GSK3B	Glycogen synthase kinase 3 beta	20193	-0.49002999	-0.3354401	Yes	0.42
LRP6	Low density lipoprotein receptor-related protein 6	21784	-0.60416477	-0.33482885	Yes	0.28
PPP2R5A	Protein phosphatase 2, regulatory subunit B (B56), alpha isoform	22786	-0.72745746	-0.29660782	Yes	0.54
PI4K2A	Phosphatidylinositol 4-kinase type 2 alpha	23009	-0.76296937	-0.22254887	Yes	0.28
FZD5	Frizzled homolog 5 (Drosophila)	23382	-0.84298586	-0.14592296	Yes	0.35
CAV1	Caveolin 1, caveolae protein, 22 kDa	23393	-0.84527677	-0.05419238	Yes	0.43
DVL1	Dishevelled, dsh homolog 1 (Drosophila)	23490	-0.87133818	0.03684999	Yes	0.39

Dataset KOvsWTforGSEA.KOvsWT.cls#KO_versus_WT
 Phenotype KOvsWT.cls#KO_versus_WT
 Upregulated in class WT
 GeneSet PID_WNT_CANONICAL_PATHWAY
 ES -0.4896791
 NES -1.5536127
 Nominal P-value 0.043165468
 FDR q-value 1.0
 FWER P-value 1.0

SUPPLEMENTARY TABLE S11. GSEA RESULTS SUMMARY OF GENE EXPRESSION IN BETA CATENIN DEGRADATION PATHWAY

Dataset		KOvsWTforGSEA.KOvsWT.cls#KO_versus_WT				
Phenotype		KOvsWT.cls#KO_versus_WT				
Upregulated in class		WT				
GeneSet		PID_BETACATENIN_DEG_PATHWAY				
ES		-0.51706684				
NES		-1.5547533				
Nominal P-value		0.038043477				
FDR q-value		1.0				
FWER P-value		1.0				
<i>Gene symbol</i>	<i>Gene_title</i>	<i>Rank in gene list</i>	<i>Rank metric score</i>	<i>Running ES</i>	<i>Core enrichment</i>	<i>KO/WT</i>
CUL1	Cullin 1	1237	0.730244	0.050141	No	3.53
DVL3	Dishevelled, dsh homolog 3 (Drosophila)	9013	0.134897	-0.25023	No	1.29
DVL2	Dishevelled, dsh homolog 2 (Drosophila)	12277	-0.04648	-0.37769	No	0.95
CSNK1E	Casein kinase 1, epsilon	14035	-0.14249	-0.4301	No	0.79
CSNK1A1	Casein kinase 1, alpha 1	14230	-0.15327	-0.41688	No	0.91
AXIN1	Axin 1	15220	-0.20588	-0.42901	No	0.65
GSK3A	Glycogen synthase kinase 3 alpha	17367	-0.32761	-0.4718	Yes	0.66
WNT3A	Wingless-type MMTV integration site family, member 3A	17743	-0.34871	-0.43901	Yes	0.71
CSNK1D	Casein kinase 1, delta	18713	-0.40611	-0.42265	Yes	0.71
CTNNB1	Catenin (cadherin-associated protein), beta 1, 88 kDa	18939	-0.41966	-0.3739	Yes	0.64
APC	Adenomatosis polyposis coli	19290	-0.44061	-0.32739	Yes	0.17
AXIN2	Axin 2 (conductin, axil)	19983	-0.47968	-0.2895	Yes	0.39
GSK3B	Glycogen synthase kinase 3 beta	20193	-0.49003	-0.23037	Yes	0.42
SSPO	SCO-spondin homolog (Bos taurus)	21664	-0.59341	-0.2087	Yes	0.36
LRP6	Low density lipoprotein receptor-related protein 6	21784	-0.60416	-0.1301	Yes	0.28
FZD5	Frizzled homolog 5 (Drosophila)	23382	-0.84299	-0.07915	Yes	0.35
DVL1	Dishevelled, dsh homolog 1 (Drosophila)	23490	-0.87134	0.036846	Yes	0.39