

Supplementary table 2 GO and KEGG enrichment analysis.

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_DIRECT	GO:000635 1~transcription, DNA-templated	30	18.63	0.00	CCNT2, BCLAF1, ZNF676, ZNF367, ZEB2, NR3C1, ZEB1, NR2C1, PCGF3, ZNF682, PSIP1, NR2F6, PATZ1, GFI1, KDM5C, ATF7IP, KAT7, ZBTB20, RARG, ARID5B, ZBTB41, PPP1R10, ARNTL, RLF, BAZ1A, ATXN7, BNC2, JMJD1C, LCOR, RERE	149	1955	16792	1.73	0.96	0.80	5.08
GOTERM_BP_DIRECT	GO:000635 5~regulation of transcription, DNA-templated	22	13.66	0.02	KAT7, RREB1, AFF4, ZBTB41, ZNF676, SOX5, NR3C1, AFF1, ARNTL, HMGA2, NR2C1, RLF, PCGF3, BAZ1A, ZNF682, BNC2, PSIP1, PATZ1, JMJD1C, GFI1, ERC1, LCOR	149	1504	16792	1.65	1.00	0.76	30.97
GOTERM_BP_DIRECT	GO:004594 4~positive regulation of transcription from RNA polymerase II promoter	20	12.42	0.00	CCNT2, ARHGEF2, RARG, STRN3, ZEB2, NR3C1, ZEB1, ARNTL, HMGA2, NFATC2IP, RLF, PHIP, TET3, ATXN7, ASH1L, FOXF2, ARF4, PSIP1, TNKS, RERE	149	981	16792	2.30	0.63	0.63	1.59
GOTERM_BP_DIRECT	GO:000012 2~negative regulation of transcription	14	8.70	0.01	ATF7IP, XP01, ZBTB20, RARG, RREB1, STRN3, ARID5B, NR2F6, ZEB2, ZEB1, GFI1, HMGA2, RERE, NR2C1	149	720	16792	2.19	1.00	0.75	16.31

GOTERM_BP_DIRECT	GO:004589 2~negative regulation of transcription	12	7.45	0.00	ATF7IP, BCLAF1, EREG, STRN3, ARID5B, FOXF2, PATZ1, ARNTL, GFI1, ZEB1, HMGA2, KDM5C	149	499	16792	2.71	0.99	0.68	7.19
GOTERM_BP_DIRECT	GO:000646 8~protein phosphorylation	9	5.59	0.05	MAP4K3, CCNT2, SGK1, TAOK1, ROCK2, MMD, WNK3, SIK1, MAP3K11	149	456	16792	2.22	1.00	0.85	54.68
GOTERM_BP_DIRECT	GO:000636 6~transcription from RNA	9	5.59	0.08	CCNT2, RREB1, FOXF2, ASH1L, AFF4, SOX5, CREB5, NR3C1, HMGA2	149	513	16792	1.98	1.00	0.90	74.98
GOTERM_BP_DIRECT	GO:000706 7~mitotic nuclear	8	4.97	0.01	BOD1, SNX18, CLTA, ARHGEF2, TNKS, NR3C1, HMGA2, EML4	149	248	16792	3.64	1.00	0.72	9.72
GOTERM_BP_DIRECT	GO:001503 1~protein transport	8	4.97	0.06	TMEM115, EIF5AL1, ARF4, LRP1B, AAGAB, TNKS, ERC1, MYH9	149	395	16792	2.28	1.00	0.87	62.72
GOTERM_BP_DIRECT	GO:000688 6~intracellular protein	7	4.35	0.02	XPO1, SNX18, CLTA, ARHGEF2, IPO7, STAM, NSF	149	236	16792	3.34	1.00	0.78	25.22
GOTERM_BP_DIRECT	GO:004306 5~positive regulation	7	4.35	0.05	ARHGEF2, BCLAF1, RARG, MTCH1, RAC1, HMGA2, APC	149	300	16792	2.63	1.00	0.84	55.36
GOTERM_BP_DIRECT	GO:005130 1~cell division	7	4.35	0.09	CCNT2, BOD1, CLTA, ARHGEF2, TNKS, NR3C1, HMGA2	149	350	16792	2.25	1.00	0.90	77.21
GOTERM_BP_DIRECT	GO:000726 4~small GTPase mediated	6	3.73	0.07	ARF4, RAC1, RHEB, TRIM23, RAB1A, RHOBTB3	149	246	16792	2.75	1.00	0.87	66.34
GOTERM_BP_DIRECT	GO:000689 7~endocytosis	5	3.11	0.03	C9ORF72, SNX18, USP33, RAB1A, GHR	149	139	16792	4.05	1.00	0.80	42.55
GOTERM_BP_DIRECT	GO:001619 2~vesicle-mediated	5	3.11	0.05	CLTA, VAMP3, NSF, RAB1A, RHOBTB3	149	152	16792	3.71	1.00	0.84	52.04

GOTERM_BP_DIRECT	GO:004584 0~positive regulation of mitotic	3	1.86	0.02	PHIP, EREG, SH2B1	149	26	16792	13.00	1.00	0.76	29.36
GOTERM_BP_DIRECT	GO:200014 5~regulation of cell	3	1.86	0.03	EREG, ROCK2, INPP5F	149	28	16792	12.07	1.00	0.77	32.99
GOTERM_BP_DIRECT	GO:000028 1~mitotic	3	1.86	0.03	SNX18, APC, MYH10	149	29	16792	11.66	1.00	0.75	34.82
GOTERM_BP_DIRECT	GO:004800 8~platelet-derived growth factor	3	1.86	0.03	ARID5B, GAB1, TIPARP	149	29	16792	11.66	1.00	0.75	34.82
GOTERM_BP_DIRECT	GO:200123 7~negative regulation of extrinsic apoptotic	3	1.86	0.04	PHIP, ITGAV, SGMS1	149	38	16792	8.90	1.00	0.84	50.85
GOTERM_BP_DIRECT	GO:004586 0~positive regulation of protein	3	1.86	0.06	EREG, MMD, TAB2	149	47	16792	7.19	1.00	0.88	64.98
GOTERM_BP_DIRECT	GO:004364 7~inositol phosphate metabolic	3	1.86	0.06	ITPKB, IPMK, INPP5A	149	47	16792	7.19	1.00	0.88	64.98
GOTERM_BP_DIRECT	GO:000725 4~JNK	3	1.86	0.07	MAP4K3, TAB2, MAP3K11	149	49	16792	6.90	1.00	0.87	67.75
GOTERM_BP_DIRECT	GO:004851 1~rhythmic	3	1.86	0.08	ROCK2, SIK1, KDM5C	149	54	16792	6.26	1.00	0.90	74.02
GOTERM_BP_DIRECT	GO:000717 3~epidermal growth factor	3	1.86	0.09	EREG, ARF4, GAB1	149	56	16792	6.04	1.00	0.90	76.27

GOTERM_BP_DIRECT	GO:004340 1~steroid hormone mediated	3	1.86	0.09	RARG, NR2F6, NR2C1	149	57	16792	5.93	1.00	0.89	77.34
GOTERM_BP_DIRECT	GO:004573 2~positive regulation of protein	3	1.86	0.10	TIPARP, NSF, APC	149	60	16792	5.63	1.00	0.90	80.34
GOTERM_BP_DIRECT	GO:004423 6~multicellular organism	2	1.24	0.02	TIPARP, GHR	149	2	16792	#####	1.00	0.79	24.33
GOTERM_BP_DIRECT	GO:000645 2~translational	2	1.24	0.03	EIF5AL1, EIF5A	149	3	16792	75.13	1.00	0.76	34.18
GOTERM_BP_DIRECT	GO:200007 4~regulation of type B pancreatic	2	1.24	0.03	RHEB, ARNTL	149	3	16792	75.13	1.00	0.76	34.18
GOTERM_BP_DIRECT	GO:004590 5~positive regulation of	2	1.24	0.03	EIF5AL1, EIF5A	149	3	16792	75.13	1.00	0.76	34.18
GOTERM_BP_DIRECT	GO:004297 7~activation of JAK2	2	1.24	0.03	PRLR, GHR	149	3	16792	75.13	1.00	0.76	34.18
GOTERM_BP_DIRECT	GO:004590 1~positive regulation of	2	1.24	0.03	EIF5AL1, EIF5A	149	4	16792	56.35	1.00	0.79	42.74
GOTERM_BP_DIRECT	GO:006061 3~fat pad	2	1.24	0.05	ARID5B, HMGA2	149	6	16792	37.57	1.00	0.84	56.67
GOTERM_BP_DIRECT	GO:007238 3~plus-ended- directed vesicle	2	1.24	0.06	KIF5B, FYCO1	149	7	16792	32.20	1.00	0.88	62.31

GOTERM_ BP_DIRECT	GO:002179 9~cerebral cortex radially	2	1.24	0.08	RAC1, FBXO45	149	9	16792	25.04	1.00	0.89	71.49
GOTERM_ BP_DIRECT	GO:200102 2~positive regulation of response	2	1.24	0.08	BCLAF1, HMGA2	149	10	16792	22.54	1.00	0.90	75.20
GOTERM_ BP_DIRECT	GO:004801 6~inositol phosphate- mediated	2	1.24	0.09	ITPR3, INPP5A	149	11	16792	20.49	1.00	0.90	78.43

GOTERM_ GO:000563
CC_DIRECT 4~nucleus
T

72 44.72

0.00

CCNT2, XPO1, C9ORF72, OSBP, CPEB2, FIGNL1,
ZNF676, EIF5A, ITPKB, ZEB2, ZEB1, SGMS1,
ACBD5, NFATC2IP, DIP2A, PCGF3, ZNF682,
FOXF2, NR2F6, PSIP1, QKI, RBM47, PATZ1, SIK1,
IPMK, KDM5C, MTUS1, RBMS1, GHR, ATF7IP,
SGK1, ZBTB20, RARG, RREB1, ROCK2, ARID5B,
STRN3, MBD6, BTBD7, ARNTL, HMGA2, MYH9,
BRWD3, ASH1L, JMJD1C, LCOR, BCLAF1, TIPARP,
SOX5, ZNF367, NR3C1, NR2C1, PHIP, RAC1,
SH2B1, GFI1, TSEN34, HECTD1, APC, KAT7, PELI1,
ZBTB41, PPP1R10, CREB5, TRIM23, TMEM115,
RLF, TET3, ATXN7, BNC2, RERE, MYH10

153 5415 18224 1.58 0.00 0.00 0.01

GOTERM_ CC_DIRECT	GO:0005829~cytosol	42	26.09	0.00	XPO1, CLTA, OSBP, EIF5A, ITPKB, RAB1A, ARHGAP12, TAGAP, AKT1S1, GAB1, RAC1, PUM1, AAGAB, PSIP1, TNKS, STAM, SH2B1, FBXO3, PIK3R6, FNDC3A, NSF, RHOBTB3, APC, FMNL2, SGK1, PELI1, ARHGEF2, OSBPL3, TAOK1, CEP192, ROCK2, WNK3, PFKM, MARK3, MYH9, TAB2, IPO7, ARF4, PGM1, RHEB, VAMP3, MYH10	153	3315	18224	1.51	0.66	0.14	5.83
GOTERM_ CC_DIRECT	GO:0016020~membrane	30	18.63	0.01	XPO1, CLTA, OSBP, MMGT1, UTRN, MMD, EIF5A, ITPKB, SGMS1, ACBD5, STAU1, ITGAV, RAC1, MTCH1, PIK3R6, SH2B1, FYCO1, FNDC3A, INPP5A, MGAT4A, OSBPL3, KIF5B, MYH9, ITPR3, EML4, ATP2A2, IPO7, ARF4, RHEB, MAP3K11	153	2200	18224	1.62	0.85	0.21	9.93
GOTERM_ CC_DIRECT	GO:0005622~intracellular	23	14.29	0.00	XPO1, TWF1, ARHGEF2, ROCK2, ZNF676, RAB1A, MAP4K3, ZNF682, EREG, IPO7, ITGAV, MTCH1, RAC1, ARF4, RHEB, VAMP3, STAM, JMJD1C, SH2B1, INPP5A, GHR, MAP3K11, RHOBTB3	153	1332	18224	2.06	0.31	0.07	2.01

<p>GOTERM_ GO:000551 MF_DIREC 5~protein T binding</p>	<p>110 68.32 0.00</p>	<p>XPO1, UTRN, EIF5A, ITPKB, RAB1A, GAB1, PUM1, AAGAB, PSIP1, STAM, ELOVL7, RBMS1, FLVCR1, PPP1R37, RPUUSD4, RARG, KIF5B, ROCK2, STRN3, WNK3, SYNJ2BP, ARNTL, MYH9, MARK3, MAP4K3, CCDC6, BAZ1A, PGM1, VAMP3, ERC1, EP400, SOX5, NR2C1, ALCAM, AKT1S1, ITGAV, MTCH1, RAC1, TNKS, FBXO3, FBXO45, HECTD1, RHOBTB3, KAT7, PELI1, OSBPL3, TAOK1, TEAD1, TMEM115, TET3, ATP2A2, ARF4, RERE, MYH10, CCNT2, C9ORF72, CLTA, OSBP, FIGNL1, ZEB2, ZEB1, DIP2A, PCGF3, TMEM59, NR2F6, QKI, SIK1, NSF, GHR, ATF7IP, SGK1, ARHGEF2, ARID5B, PFKM, HMGA2, FAM114A1, EREG, IPO7, JMJD1C, LCOR, MAP3K11, SNX18, BCLAF1, NR3C1, SMUG1, STAU1, PHIP, INPP5F, MTMR9, SH2B1, PIK3R6, GFI1, FYCO1, MANBAL, USP33, INPP5A, APC, CEP192, AFF4, CREB5, AFF1, TRIM23, ITPR3, TAB2, RASSF3, RLF, PPP1R2, PRLR, ATXN7, TMTC3</p>	<p>149 8785 16881 1.42 0.00 0.00 0.00</p>
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GOTERM_ MF_DIREC T	GO:000367 7~DNA binding	28	17.39	0.00	BCLAF1, SOX5, ZNF367, ZEB2, NR3C1, ZEB1, SMUG1, NR2C1, FOXF2, NR2F6, PATZ1, KDM5C, ZBTB20, RARG, ARID5B, MBD6, ZBTB41, PPP1R10, TEAD1, ARNTL, HMGA2, RLF, TET3, BNC2, ASH1L, LCOR, EP400, RERE	149	1674	16881	1.90	0.34	0.19	1.76
GOTERM_ MF_DIREC T	GO:004687 2~metal ion binding	27	16.77	0.04	TIPARP, ZNF676, ZNF367, ZEB2, ZEB1, PCGF3, ZNF682, ITGAV, PATZ1, GFI1, FYCO1, NSF, HECTD1, MGAT4A, ARHGEF2, ZBTB20, RREB1, ROCK2, ZBTB41, PPP1R10, CREB5, PFKM, PRLR, ATP2A2, BNC2, RHEB, JMJD1C	149	2069	16881	1.48	1.00	0.62	39.45
GOTERM_ MF_DIREC T	GO:000827 0~zinc ion binding	20	12.42	0.01	ARHGEF2, KAT7, RARG, UTRN, NR3C1, ZEB1, TRIM23, TAB2, NR2C1, RLF, TET3, PCGF3, BAZ1A, BNC2, ASH1L, NR2F6, TNKS, USP33, KDM5C, RERE	149	1169	16881	1.94	0.88	0.50	8.63
GOTERM_ MF_DIREC T	GO:000552 4~ATP binding	20	12.42	0.06	TWF1, SGK1, KIF5B, ROCK2, FIGNL1, TAOK1, ITPKB, WNK3, PFKM, MYH9, MARK3, MAP4K3, ATP2A2, SIK1, IPMK, NSF, EP400, MAP3K11, MYH10, RHOBTB3	149	1495	16881	1.52	1.00	0.72	58.90

GOTERM_MF_DIRECT	GO:000370 0~transcription factor activity, sequence-specific	17	10.56	0.01	KAT7, RARG, RREB1, STRN3, AFF4, SOX5, TEAD1, ZNF367, CREB5, NR3C1, AFF1, ARNTL, ZEB1, NR2C1, FOXF2, NR2F6, RERE	149	961	16881	2.00	0.96	0.55	12.85
GOTERM_MF_DIRECT	GO:000367 6~nucleic acid binding	14	8.70	0.09	ZBTB20, CPEB2, RREB1, ZNF676, ZBTB41, CREB5, ZEB2, ZEB1, ZNF682, PATZ1, RBM47, GF11, TSEN34, RBMS1	149	985	16881	1.61	1.00	0.78	72.62
GOTERM_MF_DIRECT	GO:000467 4~protein serine/threonine kinase	9	5.59	0.02	MAP4K3, CCNT2, SGK1, TAOK1, ROCK2, WNK3, MARK3, SIK1, MAP3K11	149	376	16881	2.71	1.00	0.55	21.55
GOTERM_MF_DIRECT	GO:000368 2~chromatin binding	9	5.59	0.02	CCNT2, ATXN7, ASH1L, PSIP1, MBD6, PATZ1, ZEB1, EP400, RERE	149	391	16881	2.61	1.00	0.58	25.87
GOTERM_MF_DIRECT	GO:001990 1~protein kinase	8	4.97	0.05	CCNT2, UTRN, RAC1, RHEB, SIK1, NSF, GHR, APC	149	376	16881	2.41	1.00	0.69	48.32
GOTERM_MF_DIRECT	GO:000392 4~GTPase activity	6	3.73	0.06	ARF4, RAC1, RHEB, TRIM23, RAB1A, MMAA	149	234	16881	2.91	1.00	0.72	53.43
GOTERM_MF_DIRECT	GO:001630 1~kinase activity	6	3.73	0.06	MAP4K3, TAOK1, SGMS1, PIK3R6, TAB2, MAP3K11	149	241	16881	2.82	1.00	0.73	57.19
GOTERM_MF_DIRECT	GO:001713 7~Rab	5	3.11	0.03	C9ORF72, RAC1, ERC1, NSF, RHOBTB3	149	134	16881	4.23	1.00	0.62	33.90
GOTERM_MF_DIRECT	GO:000370 7~steroid hormone	4	2.48	0.01	RARG, NR2F6, NR3C1, NR2C1	149	56	16881	8.09	0.98	0.56	16.16

GOTERM_MF_DIRECT	GO:000122 7~transcriptional repressor activity, RNA polymerase II	4	2.48	0.02	ARID5B, NR2F6, ZEB2, ZEB1	149	59	16881	7.68	0.99	0.54	18.38
GOTERM_MF_DIRECT	GO:000107 8~transcriptional repressor activity, RNA polymerase II core	4	2.48	0.07	ZBTB20, GFI1, HMGA2, NR2C1	149	111	16881	4.08	1.00	0.73	64.39
GOTERM_MF_DIRECT	GO:001704 8~Rho	3	1.86	0.02	FMNL2, ARHGEF2, ROCK2	149	28	16881	12.14	1.00	0.58	28.69
GOTERM_MF_DIRECT	GO:000486 4~protein phosphatases	3	1.86	0.03	PPP1R37, PPP1R2, PPP1R10	149	33	16881	10.30	1.00	0.62	36.95
GOTERM_MF_DIRECT	GO:004302 2~ribosomal	3	1.86	0.07	CPEB2, EIF5AL1, EIF5A	149	51	16881	6.66	1.00	0.75	64.22
GOTERM_MF_DIRECT	GO:000844 0~inositol-1,4,5-trisphosphate	2	1.24	0.08	ITPKB, IPMK	149	10	16881	22.66	1.00	0.76	69.36
KEGG_PATHWAY	hsa04151:PI3K-Akt signaling	7	4.35	0.06	SGK1, PRLR, ITGAV, RAC1, RHEB, CREB5, GHR	57	345	6879	2.45	1.00	0.95	52.23
KEGG_PATHWAY	hsa05205:Proteoglycans	5	3.11	0.08	ROCK2, ITGAV, GAB1, RAC1, ITPR3	57	200	6879	3.02	1.00	0.91	62.52
KEGG_PATHWAY	hsa04972:Pancreatic	4	2.48	0.04	ATP2A2, PLA2G12A, RAC1, ITPR3	57	93	6879	5.19	1.00	1.00	38.23
KEGG_PATHWAY	hsa04070:Phosphatidylinositol	4	2.48	0.05	ITPKB, ITPR3, IPMK, INPP5A	57	98	6879	4.93	1.00	0.97	42.34

KEGG_PATHWAY	hsa04152:A	4	2.48	0.08	AKT1S1, RHEB, CREB5, PFKM	57	123	6879	3.92	1.00	0.95	62.05
KEGG_PATHWAY	hsa04728:D	4	2.48	0.09	KIF5B, CREB5, ARNTL, ITPR3	57	128	6879	3.77	1.00	0.89	65.61
