

Table S4. Enrichment analysis of the candidate genes within the CG, Cooper1, and Topig groups was performed using the iHS, CLR, nSL, and XP-EHH methods, along with the GO and KEGG databases.

Group	Term	Database	ID	Count	Background number	Corrected P-Value	Input
CG	cytoplasm	Gene Ontology	GO:0005737	89	2398	0.001	PLK3, DMGDH, ADAD1, ADAD2, CHML, THRA, NAALAD2, CAPN1, PTP4A2, HSPA9, VWA8, RPL11, SERPINB1, PAFAH1B1, TESK2, WDTC1, CCND1, PTPN14, ARHGAP15, PAIP2, MSRA, IL1R2, MC4R, NEK7, SLC9A1, EGR1, GMD5, PPP1R9A, CPSF6, CLUH, CDC25C, SPATA18, NUDT6, SMYD2, FGF4, FGF3, FGF2, FTO, CASC3, RBFOX1, MOS, GCH1, CDC23, MYBBP1A, EEF1E1, SMAD5, FBXO2, FBXO6, ANKRD39, LGALS12, RANBP9, MARK2, RNF150, MAPK9, TPR, LGALS2, PHLPP1, UCHL1, PROX1, JRK, ID3, MAP4K4, ARL2, CD247, RIPK4, NLRP12, NR1D1, UBASH3A, ANKRD6, UTRN, TOB2, MT3, MAPKAPK2, TH, CDCA5, ZCCHC2, DPP3, CNOT6, NR3C1, HSPB3, INTU, PLA2G4A, CCDC172, ROCK1, NEDD4L, KANK1, PPP3CA, PITPNC1, BZW2
	ATP binding	Gene Ontology	GO:0005524	51	1203	0.004	MDN1, STKLD1, MAP4K4, DNAH12, PLK3, PCCA, SCYL3, WRNIP1, PINK1, RIPK4, NLRP12, ATP2C2, MAPKAPK2, KIF2C, FLT1, PAN3, NEK7, CHD1L, MAP3K2, ROR2, DGKH, STK24, PRKG1, TESK2, MARK2, LYN, MAPK9, HSPA9, IGF1R, EPHB1, VWA8, ATP8A1, PDIK1L, PLK4, MAST2, CNM2, UBE2E2, ATP12A, RAD51B, ROR1, ABCG1, AK8, KIF1A, KIF1B, ADCY3, MOS, ROCK1, BBS12, ATP1A1, STK39, KIF20A
	histone H4 acetylation	Gene Ontology	GO:0043967	7	26	0.004	YEATS4, NAA40, NAA50, BRD8, DMAP1, KAT6B, EP300
	nucleus	Gene Ontology	GO:0005634	93	2706	0.004	SAC3D1, PLK3, ADAD1, ADAD2, DLG1, CHML, THRA, CAPN7, LYN, ZNF683, NFIL3, LDB2, MGMT, TESK2, CCND1, KAT5, RABGAP1L, L3MBTL2, KPN2, RBX1, HMG2, DNAJC27, MATR3, PINK1, MAPKAPK2, CHD1L, BACH2, EGR1, NBEA, ZIC5, ZIC2, UBXL2, CAMTA1, NR1H4, TSPYL5, TP63, CDC25C, TSHZ3, LBX1, HSP4A, PMCH, SMYD2, RHOB, FGF2, PRDM16, PRDM15, RBFOX1, EEF1E1, TCEG1L, MIS18A, JAZF1, ANKRD39, LGALS12, TEF, RANBP9, MYT1L, TBX19, MAPK9, TCF20, PHACTR1, PRKN, AGAP1, PROX1, ARID5B, GPBP1L1, OTUB1, JRK, ID3, NAA50, KIF20A, ERCC5, WRNIP1, OVOL1, MYOG, ANKRD6, KLF17, ASAH1, TOB2, DYNCL11, MT3, TH, CDCA5, CNOT6, NR3C2, NR3C1, PDIK1L, EBF2, USP14, FAM53C, POGK, TAB1, KAT6B, POU2F1
	negative regulation of transcription by RNA polymerase II	Gene Ontology	GO:0001122	30	570	0.006	MAD2L2, BPTF, HDAC5, HDAC9, SMAD5, PLK3, OVOL1, NR1D1, SEMA4D, DLG1, ZNF536, BACH2, EGR1, RB1, THRA, DMAP1, NFIL3, MYT1L, TBX19, NR3C1, ZNF202, LDB2, NR1H4, TPR, SMYD2, EP300, PRDM16, CCND1, ID3, SREBF2
	phospholipase A2 activity (consuming 1,2-dipalmitoylphosphatidylcholine)	Gene Ontology	GO:0102567	5	12	0.006	PLA2G2A, PLA2G4A, PLA2G5, PLA2G2D, PLA2G2F
	phospholipase A2 activity consuming 1,2-dioleoylphosphatidylethanolamine)	Gene Ontology	GO:0102568	5	12	0.006	PLA2G2A, PLA2G4A, PLA2G5, PLA2G2D, PLA2G2F
	negative regulation of ERK1 and ERK2 cascade	Gene Ontology	GO:0070373	7	38	0.010	DLG1, GPER1, SPRY1, RANBP9, NLRP12, LYN, PSCA
	adipose tissue development	Gene Ontology	GO:0060612	5	17	0.016	PAXIP1, UMODL1, EBF2, FTO, ARID5B
	spindle	Gene Ontology	GO:0005819	6	30	0.016	MAD2L2, SAC3D1, NR3C1, RB1, PAFAH1B1, KIF2C
	animal organ morphogenesis	Gene Ontology	GO:0009887	8	63	0.018	GREM2, PDGFC, FGF4, ATRNL1, LAMC3, EP300, FGF3, FGF2
	H4 histone acetyltransferase activity	Gene Ontology	GO:0010485	4	9	0.018	KAT6B, NAA50, KAT5, NAA40
	transcription coregulator activity	Gene Ontology	GO:0003712	9	83	0.019	PRDM16, MED13L, MED30, MED24, PTPN14, LDB2, TCEG1L, CAMTA1, KDM3B
	phospholipase A2 activity	Gene Ontology	GO:0004623	5	21	0.022	PLA2G2A, PLA2G4A, PLA2G5, PLA2G2D, PLA2G2F
	protein dimerization activity	Gene Ontology	GO:0046983	11	131	0.023	RILP, ID3, NPAS2, SREBF2, USF3, EBF3, ST13, PPP3CA, ANO3, MYOG, EBF2
	regulation of JNK cascade	Gene Ontology	GO:0046328	4	11	0.023	IGF1R, PHLPP1, MAP4K4, EPHB1
	cellular sodium ion homeostasis	Gene Ontology	GO:0006883	4	12	0.026	TMPPRS3, SLC9A1, ATP1A1, ATP12A
	nervous system development	Gene Ontology	GO:0007399	8	72	0.026	RBFOX1, LDB2, OLFM1, GFRA1, GFRA3, PAFAH1B1, ROR2, ROR1
	protein phosphorylation	Gene Ontology	GO:0006468	17	287	0.026	PAN3, NEK7, STKLD1, MAP3K2, SMAD5, PLK3, ROCK1, SCYL3, PLK4, CCND1, PRKG1, RIPK4, MMD, PINK1, STK39, PDIK1L, TESK2
	cell surface receptor signaling pathway	Gene Ontology	GO:0007166	9	94	0.028	CALCRL, ADGRL2, ADGRG5, CD247, RANBP9, SCTR, TSHR, ADGRB1, ADGRB2
	adenylate cyclase-activating G protein-coupled receptor signaling	Gene Ontology	GO:0007189	9	97	0.033	CALCRL, ADCY3, GPER1, ADGRG5, MC4R, TSHR, GPR161, ADGRB1, ADGRB2
	cellular response to DNA damage stimulus	Gene Ontology	GO:0006974	9	98	0.033	PLK3, CHD1L, RNF169, SPATA18, UBE2E2, MACROD1, LYN, OTUB1, MAPKAPK2

	cellular response to steroid hormone stimulus	Gene Ontology	GO:0071383	3	5	0.034	<i>NR3C1, ATP1A1, TFPI</i>
	dynein complex binding	Gene Ontology	GO:0070840	4	14	0.034	<i>CENPF, PAFAH1B1, TPR, DNAAF1</i>
	GTPase activator activity	Gene Ontology	GO:0005096	12	170	0.034	<i>TBC1D8, TBC1D9, CHML, RANGAP1, RABGAP1L, AGAP1, RGS6, ARHGAP15, SGSM3, ARHGAP26, RAPIGDS1, USP6NL</i>
	negative regulation of inflammatory response	Gene Ontology	GO:0050728	7	60	0.034	<i>RB1, GPER1, NRIH4, IL2, NLRP12, WFDC1, PROC</i>
	carbohydrate binding	Gene Ontology	GO:0030246	9	101	0.034	<i>LGALS12, GALNTL6, ADGRL2, GALNT18, FBXO2, COLEC12, FBXO6, GALNT4, LGALS2</i>
	histone H2A acetylation	Gene Ontology	GO:0043968	4	15	0.034	<i>NAA40, BRD8, DMAP1, YEATS4</i>
	positive regulation of cell migration	Gene Ontology	GO:0030335	10	124	0.034	<i>IGF1R, PDGFC, MAP4K4, SYNE2, INS, GPER1, PPP3CA, LYN, SEMA4D, ROR2</i>
	positive regulation of ERK1 and ERK2 cascade	Gene Ontology	GO:0070374	10	130	0.042	<i>PLA2G2A, PDGFC, DNAJC27, MT3, GPER1, FGF19, PLA2G5, FGF4, ROR2, ROR1</i>
	nucleoplasm	Gene Ontology	GO:0005654	53	1546	0.043	<i>MDN1, BPTF, MFSD8, MIS18A, SLC44A1, SMAD5, SPRY1, TNRC6B, UROD, WDR3, NAALADL2, POLR3H, UBASH3A, NEK7, CHML, FASTKD2, SLC9A1, ELAC2, PARPBP, MAP3K2, BACH2, EGR1, NPAS2, CBR3, MAPKAPK2, MARK2, CDC45, RPGRIPI1, TSHZ3, TAF1C, ZNF202, NUB1, CENPF, GGA1, RPL11, MACROD1, MGMT, CHD1L, PRDM16, NR3C2, TRPS1, CCND1, RBX1, GCH1, MCUB, NUP37, PTPN14, SREBF2, KPNA2, PPP3CA, STEAP4, HIVEP2, POU2F1</i>
	protein kinase activity	Gene Ontology	GO:0004672	10	131	0.043	<i>PAN3, STKLD1, MAP3K2, SCYL3, PDIK1L, MOS, CCND1, RIPK4, PINK1, MMD</i>
	negative regulation of cell population proliferation	Gene Ontology	GO:0008285	12	182	0.045	<i>EEF1E1, ROR2, KIFAP3, TOB2, LBX1, NUDT6, PROX1, SPRY1, SLIT3, SMYD2, PTPN14, PTPRJ</i>
	positive regulation of neuron projection development	Gene Ontology	GO:0010976	6	48	0.045	<i>SCARF1, MARK2, LYN, EP300, ROR2, ROR1</i>
	NuA4 histone acetyltransferase complex	Gene Ontology	GO:0035267	4	18	0.050	<i>BRD8, DMAP1, YEATS4, KAT5</i>
	Progesterone-mediated oocyte maturation	KEGG PATHWAY	ssc04914	10	88	0.010	<i>MAD2L2, IGF1R, CCNA2, ADCY3, CDC25C, SPDYC, CDC23, INS, MOS, MAPK9</i>
	Cytokine-cytokine receptor interaction	KEGG PATHWAY	ssc04060	17	259	0.016	<i>IL19, IFNLR1, IL1RL1, IL18RAP, IFN-ALPHA-9, IL1RL2, IL18R1, CSF3, IL21, IL20, XCL1, IL2, TNFRSF11A, IL22RA1, IL1R2, IL1R1, IFN-ALPHA-15</i>
	MAPK signaling pathway	KEGG PATHWAY	ssc04010	18	286	0.016	<i>LAMTOR3, IGF1R, PDGFC, MAP4K4, MAP3K2, MAPK9, TAB1, MAPKAPK2, FGF19, INS, PPP3CA, CACNA2D3, PLA2G4A, FGF4, FGF3, FGF2, IL1R1, FLT1</i>
	Human T-cell leukemia virus 1 infection	KEGG PATHWAY	ssc05166	15	220	0.020	<i>DLG1, MAPK9, CCNA2, ADCY3, CCND1, IL2, EGR1, CDC23, KAT5, RB1, SLC25A31, PPP3CA, EP300, IL1R2, IL1R1</i>
	Melanoma	KEGG PATHWAY	ssc05218	8	69	0.023	<i>IGF1R, PDGFC, CCND1, RB1, FGF19, FGF4, FGF3, FGF2</i>
	Oocyte meiosis	KEGG PATHWAY	ssc04114	10	115	0.028	<i>MAD2L2, IGF1R, ADCY3, CDC25C, SPDYC, CDC23, INS, MOS, RBX1, PPP3CA</i>
	Pathways in cancer	KEGG PATHWAY	ssc05200	24	506	0.033	<i>PTGS2, ITGA2, IFN-ALPHA-15, EP300, RB1, FGF2, WNT8A, FGF19, MAPK9, IGF1R, TPR, LAMC3, FGF4, FGF3, CTNNA1, IFN-ALPHA-9, CCND1, ADCY3, ROCK1, IL2, PTCH2, RBX1, LPAR6, WNT7B</i>
	PI3K-Akt signaling pathway	KEGG PATHWAY	ssc04151	18	335	0.034	<i>IGF1R, PDGFC, FGF4, IFN-ALPHA-9, CCND1, FGF3, ITGA2, CSF3, FGF19, IL2, IFN-ALPHA-15, INS, ITGA1, LAMC3, PHLPP1, LPAR6, FGF2, FLT1</i>
	Ether lipid metabolism	KEGG PATHWAY	ssc00565	6	45	0.038	<i>PLA2G5, CHPT1, PLA2G2D, PLA2G2F, PLA2G4A, PAFAH1B1</i>
	Jak-STAT signaling pathway	KEGG PATHWAY	ssc04630	11	151	0.038	<i>IL19, IFNLR1, IFN-ALPHA-9, CCND1, CSF3, IL21, IL20, IL2, IFN-ALPHA-15, IL22RA1, EP300</i>
	Ras signaling pathway	KEGG PATHWAY	ssc04014	14	229	0.039	<i>EXOC2, IGF1R, PDGFC, MAPK9, INS, FGF19, PLA2G5, PLA2G2D, PLA2G2F, PLA2G4A, FGF4, FGF3, FGF2, FLT1</i>
Cooperl	cytoplasm	Gene Ontology	GO:0005737	110	2398	0.000	<i>HSPA5, PLK3, POLG2, IKBKB, ASS1, ADAD2, KNCN, SNRNP200, CHML, CPEB2, SCAF8, FLII, MKLN1, EPS15L1, MKKS, RAB5A, VW48, MDFIC, LLGL2, KITLG, TESK2, TRAPPC9, CCNY, PTPN14, DDX5, TTC17, NCAPG, RNFB4, STARD7, POLB, SLBP, FUBP3, TRAK1, HABP4, NDRG4, NEK11, SMURF2, TEK3, DRC7, HECA, MYD88, CDC25C, EFS, VILL, TK2, DYNCL12, EIF4E, NELL1, ACTB, PTPN4, SRXN1, MOS, CDC23, PSMD12, STK33, MEF2D, IPO5, NUDCD2, FARS2, SMYD2, SMAD5, MSRB2, CCNG1, CTNND2, MEOX2, LGALS12, FNIP2, BMP2K, CNKSR3, MAPK7, RNF150, RANBP3, BSRPY, SPATS2L, IRAK3, CHP2, UCHL1, PROX1, FSCN1, DICER1, LLGL1, SNRK, MTF2, SREBF1, RNF144A, PPID, PPIC, NEU2, SCAI, HMGB4, ANGEL2, DRG2, CASQ2, CPNE2, CMPK2, ARL4C, CRACR2A, NR3C1, ARHGAP44, CARD11, TXLNB, CFL2, THTPA, SEC22C, UPPI, KATNB1, ROCK2, UPF3A, PTPNC1, BZW2</i>

nucleus	Gene Ontology	GO:0005634	111	2706	0.000	HSPA5, PLK3, SUMO2, SF1, SCRT2, ADAD2, CHML, USB1, DDX31, PROX1, ZNF782, DGK1, FLII, TESK2, IRAK3, MKKS, LYN, MDFIC, SAFB, GATA5, SHMT1, SETD6, MYD88, BARHL1, RABGAP1L, AHR, DDX5, L3MBTL2, ACTB, NHLH2, SLBP, FOXK2, FUBP3, ZNF219, NR3C1, HABP4, NEK11, TCF15, HSPH1, NT5C, USP40, CDC25C, HECA, ZNF510, GTF2I, PLCB4, CHRA1, GTF2IRD1, CUX1, CPEB2, SMYD2, MTF2, STK33, MEF2D, IPO5, ALKBH3, AGO2, HMX1, ZFHX2, MUTYH, CCNG1, CTNND2, FIGN, CCNK, LGALS12, BMP2K, MAPK7, RBM15, FOXN3, RANBP3, TOX4, AGAP1, SATB2, SALL2, CHP2, MYC, API5, DICER1, ARID5A, SNRK, METTL3, SREBF1, KIF20A, SCAI, ZNF319, PRKN, BCL11B, CACYBP, NOCT, LTA4H, FAM83G, DMBX1, CPNE2, CRY1, RAI1, ETS1, TRMT10A, KLF2, EYA4, AJUBA, ESRRG, ZNHIT6, USP14, FAM53C, FAM53A, NFIA, ALKBH5, ROCK2, ZNF713, COQ7, ATXN1
ATP binding	Gene Ontology	GO:0005524	57	1203	0.000	FARS2, DNAH9, HSPA5, PLK3, TTF2, DDX31, RIPK1, ATP11A, MAP2K4, TPK1, ASS1, NEK11, KIF2C, SNRNP200, VW48, DDX39A, CHD8, BMP2K, KIFC3, FIGN, DGK1, TLL11, MAPK7, JAK1, DGKB, DICER1, MKKS, RPS6KC1, ERN2, DGKD, ULK2, KIF16B, LYN, ULK4, PKN1, PRKCB, ROR2, MAST3, DYNC1L2, IRAK3, DNAH6, FGF3, TESK2, MYH7, IKKBK, ABCG2, AK8, RPS6KA4, MOS, SNRK, MTHFD1L, ROCK2, DDX5, STK33, ACTB, SRXN1, KIF20A
negative regulation of transcription by RNA polymerase II	Gene Ontology	GO:0000122	33	570	0.001	HMX1, BPTF, FOXK2, HDAC9, SMAD5, PLK3, SALL2, ZFHX2, SCRT2, NR1D2, FNIP2, DMBX1, CRY1, KLF2, RBM15, MYC, NR3C1, CUX1, SATB2, SMYD2, PPARA, EP300, CNOT1, NFIA, ARID5A, MTF2, NOTCH2, AHR, DDX5, SREBF1, PPID, TGIF1, ATXN1
cytosol	Gene Ontology	GO:0005829	79	2056	0.003	NUDCD2, SNX2, MTHFD1L, ALAD, TBC1D5, TRERF1, DESI1, SMAD5, ANO6, SRXN1, TTF2, PRKN, HELZ, HABP4, UROD, RNF216, AKAP10, UPF2, CACYBP, DNAAF1, HSPA5, FAM83G, ARL4C, LLGL2, GAPVD1, CHML, SPECC1, HSPH1, LHPP, ASS1, NT5C, SHMT1, USP40, NR3C1, FLII, MAPK7, MKLN1, PPP6C, CNOT1, MYD88, RAB14, DGKD, ATPAF2, CENPM, RAB5A, USP14, HOMEZ, FNIP2, PPP2R2C, NUP85, DLEC1, SLC35F6, KLHL3, SMYD2, PLCD1, EIF4E, RPS6KA4, EP300, UCHL1, FSCN1, ECSCR, TNIP2, CARMIL1, ALKBH5, RGS12, ADH5, ADH4, MOS, WDR91, NAA11, ATXN1, UPF3A, NCAPH, LAMTOR5, PPID, OSBP, TRMT10A, NEU2, LTA4H
signal transduction	Gene Ontology	GO:0007165	25	435	0.013	SH3BP2, RASD1, LRPAP1, RIPK1, ARHGAP8, CCK, FAM13B, FAM83G, THOC1, ARHGAP44, PDE1C, SAG, ARHGAP21, ARHGAP26, GAPVD1, PKN1, GLRB, RANGAP1, AGAP1, KITLG, RGS12, MOS, TOMIL2, RHEB, IL9
metal ion binding	Gene Ontology	GO:0046872	41	915	0.014	BPTF, IDO1, METAP1, ZFYVE28, PRKN, PHF21B, MUTYH, POLB, RSAD2, SH3RF3, HDAC9, RAI1, PDE1C, PPM1K, ZNF782, ANKMY2, NEURL3, RNF112, RNF220, EYA4, ZNF510, AJUBA, ZNHIT6, ZC3H7B, ETFDH, BAZ1A, AGAP1, LPL, HBE1, SMYD2, HELZ, HBB, ZNF662, TOE1, MTF2, ROCK2, ZNF713, RNF144A, COQ7, XPNPEP1, AGO2
calcium ion binding	Gene Ontology	GO:0005509	28	542	0.021	ADGRE5, LETM1, NCS1, CHP2, PKD2L2, FBLN1, ACER3, CASQ2, CDH8, LRP1B, DGKB, CDH5, SYT6, CRACR2A, PLCB4, CAPS, ASTN2, LPL, EPS15L1, PLCD1, NELL1, NOTCH4, PKD2, NOTCH2, SPOCK1, SYT1, CALR3, GUCA1B
peptidyl-lysine monomethylation	Gene Ontology	GO:0018026	4	8	0.021	SETD3, SETD7, SMYD2, SETD6
calcium channel regulator activity	Gene Ontology	GO:0005246	5	19	0.027	CACNG1, TSPAN13, CACNG4, PRKCB, GRM3
protein serine/threonine kinase activity	Gene Ontology	GO:0004674	16	234	0.027	ULK2, PLK3, RPS6KA4, MOS, SNRK, BMP2K, MAST3, ERN2, IKKBK, PKN1, STK33, ROCK2, MAP2K4, IRAK3, NEK11, TESK2
RNA polymerase II cis-regulatory region sequence-specific DNA binding	Gene Ontology	GO:0000978	27	532	0.027	BPTF, FOXK2, SMAD5, EP300, ZNF219, ZFHX2, NHLH2, NR1D2, MEOX2, GATA5, PROX1, ZNF782, KLF2, ZNF662, NR3C1, SAFB, ZNF367, SATB2, PPARA, BCL11B, MYC, NFIA, ZNF713, TCF15, SREBF1, MEF2D, TGIF1
nucleoplasm	Gene Ontology	GO:0005654	58	1546	0.030	BPTF, FOXK2, TRERF1, PCSK2, SMAD5, ZNF219, NUP85, SPECC1, UROD, RNF216, CACYBP, NR1D2, NEK11, SNRNP200, CHML, ELAC2, USB1, RAI1, FLII, MKLN1, GPR107, TRMT10A, MYC, GTF2I, CDH5, RANBP3, LTA4H, PRKCB, TRMU, HOMEZ, NCAPH, SAFB, NFIA, ZNF367, JPT1, TNIP2, SLC35F6, B4GALT2, PPARA, ITPR2, RPS6KA4, TAF1C, ABCG2, NARF, RGS12, DPH6, ARID5A, ADH4, NAA11, MCUB, NOTCH2, PTPN14, UPF3A, MEF2D, PPID, OSBP, TGIF1, ATXN1
GTPase activator activity	Gene Ontology	GO:0005096	13	170	0.035	ARHGAP44, CHML, LLGL2, LLGL1, TBC1D22A, RANGAP1, RABGAP1L, TBC1D5, AGAP1, ARHGAP21, ARHGAP26, RAPGEF2, RANBP3
mitochondrion	Gene Ontology	GO:0005739	30	647	0.042	FOXK2, HSPA5, TRAK1, POLG2, PRKN, MSRB2, DHTKD1, NOCT, AKAP10, ASS1, RSAD2, LGALS12, CMPK2, HADHA, CRY1, GRAMD4, GOT2, NR3C1, TRMU, VW48, ETFDH, BRD8, BCAT1, BPHL, ABHD4, SLC35F6, MRRF, ADH5, MTHFD1L, FGGY
circadian rhythm	Gene Ontology	GO:0007623	5	23	0.043	EP300, SREBF1, ASS1, PROX1, MTTP
Wnt signaling pathway	KEGG PATHWAY	ssc04310	14	155	0.010	PLCB4, FZD8, CHD8, DKK4, PRKCB, ROCK2, CTNNB1, WNT8A, CTNND2, CACYBP, VANG1, MYC, EP300, ROR2

Topigs	Thyroid hormone signaling pathway	KEGG PATHWAY	ssc04919	12	117	0.010	<i>RHEB, PLCB4, MYH7, NOTCH4, PRKCB, KAT2B, NOTCH2, CTNNB1, PLCD1, MYC, EP300, ACTB</i>
							<i>BCL2L1, WWP2, ZYX, USP20, OTUD7A, CHML, ARHGEF5, MIB1, CSNK1D, NAALAD2, CDH3, MTMR3, CDKN2C, PRMT9, FNTA, VWA8, WRN, DYNLRB2, RBP2, HECA, ADRA1A, WDR55, ADRA1B, PNLD1, SOCS2, PPP2CB, RNF181, KPNA7, DND1, UBB, TCF12, NCAPG, APC, CAPZB, TRIM38, PCMT1, KATNA1, MAPKAPK5, LRRC75A, NEK11, PER2, TEKT3, CCNE1, ARHGAP15, JAK2, NF1, GRM5, MYD88, PPP1R14C, WNT2, DST, SPATA18, VILL, PTPN3, TRIM44, ESPNL, RBFOX1, UBE2B, DTYMK, IPO5, NUDCD3, PIWIL4, SDCCAG8, CARS2, CTNND2, GAD2, OPTN, CTPS1, SKP1, NEDD1, REPS1, PSMA7, PSMA5, MAGI3, RANBP6, GPCPD1, POMP, PFDN6, TRAPPC9, MYLK2, CELSR2, TRIM68, CLU, PAWR, SCAF8, FHOD3, LLGL2, AK3, NTN1, AK7, AATF, NEU4, PPID, ARL1, CPEB3, FOXO6, ARL4D, CDC37L1, CEBPB, CCNA1, SLAH3, CDK17, CDK14, ACTL7B, ACTL7A, NRG1, EYA1, AQP11, CNTF, NR3C1, TXLNB, ATG4B, METTL21C, IL33, ATF4, SASH1, CASP6, PARD3, MTUS1, NSUN2, PER1, ANK1, WBP2</i>
	cytoplasm	Gene Ontology	GO:0005737	123	2398	0.000	<i>CDKL3, WWP2, PPIL4, EVC2, ZYX, OTUD7A, LHX1, CHML, CCNA1, ARHGEF5, CSNK1D, DRAP1, CDKN2C, WRN, PGBD5, MTUS1, PER1, USP36, PPP2CA, PPP2CB, KPNA7, SCGN, DND1, UBB, TCF12, APC, CFTR, CCNK, FOXP2, NCAPG2, GLIS3, KATNA1, MAPKAPK5, NEK11, DDX51, CCNE1, JAK2, SMARCA1, HECA, MYD88, TCF7, MIER1, FOXS1, OPTN, SOX13, SCMHI, ING5, ING1, ING2, RBFOX1, DNAJC1, DTYMK, TOX2, ASCC2, IPO5, HES6, HES7, PIWIL4, SMYD3, RCOR3, CTNND2, TNPO1, SKP2, SKP1, ZHX3, SS18L1, FOSL1, PBK, PSMA5, CITED2, RANBP6, PSMA7, POMP, FBXO43, RXRA, HMGAI, SPIC, CLU, TJP2, LEO1, CCDC85B, RPS18, CPEB3, FOXO6, ELF1, ZC3H12D, ARL4D, KLF13, CEBPB, ASAH1, USP46, TWIST2, CDK17, CDK14, ACTL7B, ACTL7A, DGK1, EYA1, NR3C1, MCM10, TRAF6, PTGIS, IK, METTL21C, EBF2, MCM8, THAP1, NFIA, PER2, TAB1, NSUN2, ZNF713, ZBTB43, PURG, WBP2</i>
	nucleus	Gene Ontology	GO:0005634	115	2706	0.000	<i>IYD, TMC3, EPHA4, CDH4, TENM3, TENM2, INSRR, P2RX2, AXL, LMBR1, KCNK9, SLC16A3, HBEGF, CHRN3, NTRK1, KCNK2, TMEM150A, FOLH1B, SLC16A10, NRG1, GRM5, TRPM1, TRPV2, OTOPI, ADGRG1, SLC38A2, CLCN1, CELSR2, ADGRD1, SLC8A1, CHRNA6, ROR2, ADRA1A, VAMP5, ADRA1D, HCN3, DRD5, PLGRKT, CFTR, ADGRG5, ADGRG3, TLR4, AMIGO1, SLC1A1</i>
	integral component of plasma membrane	Gene Ontology	GO:0005887	44	684	0.000	<i>UBE2B, CDKL3, DNAH12, EPHA4, NTRK1, KIF14, KATNA1, DNAH17, EP400, INSRR, RRM1, DHX15, MAT2A, MAPKAPK5, P2RX2, NEK11, AXL, DDX59, CTPS1, DNAH9, RYR1, GRK4, DDX51, CDK17, CDK14, ROR2, NADK2, DGKH, DGKI, JAK2, SMARCA1, RPS6KC1, GUCY2D, VWA8, WRN, MYLK2, CSNK1D, BTA1, PBK, MCM8, STK32B, DDX20, KIF1A, DNAH5, AK3, PIP5K1B, CARS2, MTHFD1L, AK7, LATS1, TCPI1, DTYMK, CLK2, MYO7A, CFTR</i>
	ATP binding	Gene Ontology	GO:0005524	55	1203	0.005	<i>STX8, JCAD, VAMP5, LGMN, TRAF6, CD34, FBXL5, THBS3, RAP1A, GTPBP4, TMEM192, DGK1, NOX4, LPXN, CLU, SORT1, VPS52, ALOX12B, AQP11, GALNT2</i>
	perinuclear region of cytoplasm	Gene Ontology	GO:0048471	20	279	0.014	<i>WWP2, TRIM71, TRAF6, UBE2B, RNF181, TRIM68, UHRF2, RNF11</i>
	protein autoubiquitination	Gene Ontology	GO:0051865	8	50	0.023	<i>PDLIM5, JCAD, PARD3, PDLIM3, PGM5, CDH8, CDH12, CTNND2, CDH3, ZYX</i>
	adherens junction	Gene Ontology	GO:0005912	10	85	0.025	<i>SLC38A2, COL22A1, COL9A1, COL21A1, COL27A1, PRSS2, COL4A3, SLC16A10, SLC8A1, SLC1A1</i>
	Protein digestion and absorption	KEGG PATHWAY	ssc04974	10	86	0.025	