Supplementary materials

Supplementary Table 1. The most significant obesity genes that are common between the different types of diabetes; T1D, T2D, and MODY.

Genes	**Genes**	**Genes**	**Genes**
VDR	*BDNF*	*PPARGC1A*	*SERPINC1*
ACE	*IFNG*	*SERPINE1*	*APOA1*
HMGCR	*ABCA1*	*CYP19A1*	*CCK*
MMP2	*RETN*	*VCAM1*	*ADRB2*
EDN1	*IL4*	*TP53*	*GAPDH*
ABCB7	*BCHE*	*TNF*	*APC*
GSR	*BCL2*	*INSR*	*TLR2*
FASLG	*TNFRSF11B*	*IFNA1*	*VEGFA*
GGT1	*CD36*	*HNF1B*	*CDKN2A*
CYBA	*FGF2*	*GNRH1*	*TGFB1*
IGF1	*CLU*	*HLA-DRB1*	*KCNJ11*
CCL11	*PCK2*	*IL1A*	*TFRC*
PTEN	*HK2*	*LDLR*	*ABCC8*
HMOX1	*G6PD*	*LPL*	*GAST*
HNF1A	*TF*	*CAT*	*TSHR*
NOS2	*GCK*	*MPO*	*JUN*
INS	*IGF1R*	*TCF7L2*	*HCRT*
FLT1	*IRS1*	*LIPC*	*SERPINF2*
SLC6A4	*GHRL*	*SELP*	*TIMP1*
SOD2	*ICAM1*	*GCG*	*CSF2*
BGLAP	*RECK*	*F5*	*GHRH*
MMP3	*RPS27A*	*IL8*	*MMP9*
PPARA	*TNFRSF1B*	*HLA-A*	*CD14*
NGF	*APOB*	*SLC2A2*	*ADIPOQ*
GATA3	*CS*	*AKT1*	
IL2RA	*LTF*	*PIK3R1*	
PAX4	*IL5*	*GRP*	
TTR	*AGT*	*NR1H2*	
LEP	*CGA*	*TNFRSF1A*	
PTPRN2	*PPARG*	*STAT3*	
OXT	*HNF4A*	*SPP1*	
CYP1A2	*CRP*	*F2*	
TG	*HIF1A*	*PTGS2*	
CYP2C19	*CALCA*	*AHSG*	
NOS1	*SERPINA1*	*B2M*	
CRH	*NOS3*	*LRP5*	
IL10	*MAPT*	*OLR1*	
PRL	*GLP1R*	*GH1*	
IGF2	*CASR*	*ITGB3*	
IAPP	*CNR1*	*CYP2C9*	

MTHFR	*DKK1*	*IL1B*	
ISL1	*NFE2L2*	*REN*	
PAX6	*NR3C1*	*VWF*	
TNFSF11	*HP*	*NPY*	
GHR	*OPRM1*	*IL18*	
DPP4	*CYP17A1*	*GAD2*	
NPPB	*TLR4*	*IGFBP2*	
APOC3	*LEPR*	*AR*	
SOD1	*BMP6*	*GAD1*	
IFNA2	*NPPA*	*PCSK9*	
CD79A	*ESR1*	*EPO*	
FOXM1	*SST*	*ACHE*	
PIK3CA	*PRF1*	*CP*	
APOE	*BMP4*	*KLK3*	
IL2	*NEUROD1*	*IL1R1*	
FAS	*SPARC*	*CCL2*	
C3	*AGTR1*	*HGF*	
PDX1	*IGFBP3*	*IL6*	
PON1	*ALB*	*APP*	
NEUROG3	*PTGS1*	*CPT2*	
FOXA2	*LCAT*	*COMT*	
IGFBP1	*APOA4*	*UCP2*	
HSPD1	*POMC*	*PROC*	

Supplementary Table 2. Involved GO terms from ClueGo enrichment analysis for cluster 1 genes.

GO ID	**GO Term**	**Group p-Value Corrected with Bonferroni step down**	**% Associated Genes**	**Nr. Genes**	**Associated Genes Found**
R-HSA:375276	Peptide ligand-binding receptors	7.15293E-47	18.42	35.00	*[AGT, AGTR1, APLN, APLNR, APP, BDKRB2, C3, CCK, CCKAR, CCL5, CCR2, CCR5, CX3CR1, CXCL5, CXCL8, CXCR4, EDN1, EDNRA, F2, GAL, GHSR, GRP, HCRT, KNG1, MLN, NPY, NTS, OPRM1, OXT, POMC, PPY, PYY, SST, TAC1, TRH]*
R-HSA:373076	Class A/1 (Rhodopsin-like receptors)	7.15293E-47	14.81	48.00	*[ADORA1, ADRA2A, ADRA2B, AGT, AGTR1, APLN, APLNR, APP, BDKRB2, C3, CCK, CCKAR, CCL5, CCR2, CCR5, CNR1, CNR2, CX3CR1, CXCL5, CXCL8, CXCR4, DRD2, DRD4, EDN1, EDNRA, F2, GAL, GHSR, GNRH1, GPR39, GRP, HCRT, HTR1A, HTR2A, KNG1, MLN, MTNR1A, MTNR1B, NPY, NTS, OPRM1, OXT, POMC, PPY, PYY, SST, TAC1, TRH]*
KEGG:04080	Neuroactive ligand-receptor interaction	7.15293E-47	12.13	41.00	*[ADORA1, ADRA2A, ADRA2B, AGT, AGTR1, APLN, APLNR, BDKRB2, C3, CCK, CCKAR, CNR1, CNR2, DRD2, DRD4, EDN1, EDNRA, F2, GAL, GCG, GCGR, GHSR, GNRH1, GRP, HCRT, HTR1A, HTR2A, KNG1, MLN, MTNR1A, MTNR1B, NPY, NTS, OPRM1, OXT, POMC, PPY, PYY, SST, TAC1, TRH]*
R-HSA:500792	GPCR ligand binding	7.15293E-47	11.16	51.00	*[ADORA1, ADRA2A, ADRA2B, AGT, AGTR1, APLN, APLNR, APP, BDKRB2, C3, CASR, CCK, CCKAR, CCL5, CCR2, CCR5, CNR1, CNR2, CX3CR1, CXCL5, CXCL8, CXCR4, DRD2, DRD4, EDN1, EDNRA, F2, GAL, GCG, GCGR, GHSR, GNRH1, GPR39, GRP, HCRT, HTR1A, HTR2A, KNG1, MLN, MTNR1A, MTNR1B, NPY, NTS, OPRM1, OXT, POMC, PPY, PYY, SST, TAC1, TRH]*
R-HSA:418594	G alpha (i) signalling events	7.15293E-47	9.09	37.00	*[ADORA1, ADRA2A, ADRA2B, AGT, APLN, APLNR, APOA1, APOA2, APOB, APOE, APP, BDKRB2, C3, CASR, CCL5, CCR2, CCR5, CNR1, CNR2, CX3CR1, CXCL5, CXCL8, CXCR4, DRD2, DRD4, GAL, GNAI1, HTR1A, KNG1, MTNR1A, MTNR1B, NPY, OPRM1, POMC, PPY, PYY, SST]*
R-HSA:8957275	Post-translational protein phosphorylation	7.24486E-42	28.70	31.00	*[AHSG, ALB, APOA1, APOA2, APOA5, APOB, APOE, APP, BMP4, C3, CP, CSF1, CST3, F5, FGA, FGF23, IGFBP1, IGFBP3, IGFBP5, IGFBP7, IL6, KNG1, PCSK9, PNPLA2, PROC, SERPINA1, SERPINC1, SPP1, TF, TIMP1, TNC]*
R-HSA:381426	Regulation of Insulin-like Growth Factor (IGF) transport and uptake by	7.24486E-42	25.60	32.00	*[AHSG, ALB, APOA1, APOA2, APOA5, APOB, APOE, APP, BMP4, C3, CP, CSF1, CST3, F2, F5, FGA, FGF23, IGFBP1, IGFBP3,*

	Insulin-like Growth Factor Binding Proteins (IGFBPs)				*IGFBP5, IGFBP7, IL6, KNG1, PCSK9, PNPLA2, PROC, SERPINA1, SERPINC1, SPP1, TF, TIMP1, TNC]*
R-HSA:416476	G alpha (q) signalling events	6.88134E-26	12.44	27.00	*[AGT, AGTR1, APP, BDKRB2, CASR, CCK, CCKAR, EDN1, EDNRA, F2, GAST, GCG, GCGR, GHSR, GNRH1, GPR39, GRP, HCRT, HTR2A, KNG1, MLN, NTS, OXT, PIK3CA, PIK3R1, TAC1, TRH]*
R-HSA:392023	Adrenaline signalling through Alpha-2 adrenergic receptor	6.72026E-10	66.67	2.00	*[ADRA2A, ADRA2B]*
R-HSA:390651	Dopamine receptors	6.72026E-10	40.00	2.00	*[DRD2, DRD4]*
R-HSA:140875	Common Pathway of Fibrin Clot Formation	6.72026E-10	22.73	5.00	*[F2, F5, FGA, PROC, SERPINC1]*
R-HSA:390696	Adrenoceptors	6.72026E-10	22.22	2.00	*[ADRA2A, ADRA2B]*
R-HSA:390666	Serotonin receptors	6.72026E-10	16.67	2.00	*[HTR1A, HTR2A]*
R-HSA:375280	Amine ligand-binding receptors	6.72026E-10	14.29	6.00	*[ADRA2A, ADRA2B, DRD2, DRD4, HTR1A, HTR2A]*
R-HSA:76009	Platelet Aggregation (Plug Formation)	6.72026E-10	10.26	4.00	*[ADRA2A, ADRA2B, F2, FGA]*
R-HSA:140875	Common Pathway of Fibrin Clot Formation	1.1004E-08	22.73	5.00	*[F2, F5, FGA, PROC, SERPINC1]*
R-HSA:159763	Transport of gamma-carboxylated protein precursors from the endoplasmic reticulum to the Golgi apparatus	1.1004E-08	22.22	2.00	*[F2, PROC]*
R-HSA:159740	Gamma-carboxylation of protein precursors	1.1004E-08	20.00	2.00	*[F2, PROC]*
R-HSA:159782	Removal of aminoterminal propeptides from gamma-carboxylated proteins	1.1004E-08	20.00	2.00	*[F2, PROC]*
R-HSA:140837	Intrinsic Pathway of Fibrin Clot Formation	1.1004E-08	18.18	4.00	*[F2, KNG1, PROC, SERPINC1]*
R-HSA:159854	Gamma-carboxylation, transport, and amino-terminal cleavage of proteins	1.1004E-08	18.18	2.00	*[F2, PROC]*

R-HSA:140877	Formation of Fibrin Clot (Clotting Cascade)	1.1004E-08	15.38	6.00	*[F2, F5, FGA, KNG1, PROC, SERPINC1]*
KEGG:04610	Complement and coagulation cascades	1.1004E-08	11.39	9.00	*[BDKRB2, C3, F2, F5, FGA, KNG1, PROC, SERPINA1, SERPINC1]*
R-HSA:76009	Platelet Aggregation (Plug Formation)	1.1004E-08	10.26	4.00	*[ADRA2A, ADRA2B, F2, FGA]*
R-HSA:173107	Binding and entry of HIV virion	2.31219E-08	20.00	2.00	*[CCR5, CXCR4]*
R-HSA:6783783	Interleukin-10 signaling	2.31219E-08	14.89	7.00	*[CCL5, CCR2, CCR5, CSF1, CXCL8, IL6, TIMP1]*
R-HSA:380108	Chemokine receptors bind chemokines	2.31219E-08	14.58	7.00	*[CCL5, CCR2, CCR5, CX3CR1, CXCL5, CXCL8, CXCR4]*
R-HSA:162594	Early Phase of HIV Life Cycle	2.31219E-08	10.00	2.00	*[CCR5, CXCR4]*
KEGG:05142	Chagas disease (American trypanosomiasis)	3.50978E-07	8.74	9.00	*[BDKRB2, C3, CCL5, CXCL8, GNAI1, IL6, KNG1, PIK3CA, PIK3R1]*
KEGG:04614	Renin-angiotensin system	0.000272724	8.70	2.00	*[AGT, AGTR1]*
KEGG:04924	Renin secretion	0.000272724	8.70	6.00	*[ADORA1, AGT, AGTR1, EDN1, EDNRA, GNAI1]*
R-HSA:8963901	Chylomicron remodeling	0.000437865	55.56	5.00	*[APOA1, APOA2, APOA5, APOB, APOE]*
R-HSA:8963888	Chylomicron assembly	0.000437865	44.44	4.00	*[APOA1, APOA2, APOB, APOE]*
R-HSA:8964026	Chylomicron clearance	0.000437865	40.00	2.00	*[APOB, APOE]*
R-HSA:3000471	Scavenging by Class B Receptors	0.000437865	33.33	2.00	*[APOA1, APOB]*
R-HSA:8964058	HDL remodeling	0.000437865	30.00	3.00	*[ALB, APOA1, APOE]*
R-HSA:8963898	Plasma lipoprotein assembly	0.000437865	22.22	4.00	*[APOA1, APOA2, APOB, APOE]*
R-HSA:8963899	Plasma lipoprotein remodeling	0.000437865	20.00	6.00	*[ALB, APOA1, APOA2, APOA5, APOB, APOE]*
R-HSA:3000480	Scavenging by Class A Receptors	0.000437865	15.79	3.00	*[APOA1, APOB, APOE]*
R-HSA:2168880	Scavenging of heme from plasma	0.000437865	15.38	2.00	*[ALB, APOA1]*
R-HSA:8964043	Plasma lipoprotein clearance	0.000437865	12.12	4.00	*[APOA1, APOB, APOE, PCSK9]*
R-HSA:5686938	Regulation of TLR by endogenous ligand	0.000437865	10.53	2.00	*[APOB, FGA]*

R-HSA:8964038	LDL clearance	0.000437865	10.53	2.00	*[APOB, PCSK9]*
R-HSA:174824	Plasma lipoprotein assembly, remodeling, and clearance	0.000437865	10.14	7.00	*[ALB, APOA1, APOA2, APOA5, APOB, APOE, PCSK9]*
KEGG:04979	Cholesterol metabolism	0.000437865	10.00	5.00	*[APOA1, APOA2, APOB, APOE, PCSK9]*
R-HSA:2173782	Binding and Uptake of Ligands by Scavenger Receptors	0.000437865	9.52	4.00	*[ALB, APOA1, APOB, APOE]*
R-HSA:975634	Retinoid metabolism and transport	0.000437865	9.30	4.00	*[APOA1, APOA2, APOB, APOE]*
R-HSA:6806667	Metabolism of fat-soluble vitamins	0.000437865	8.51	4.00	*[APOA1, APOA2, APOB, APOE]*
KEGG:04977	Vitamin digestion and absorption	0.000437865	8.33	2.00	*[APOA1, APOB]*
R-HSA:8851907	MET activates PI3K/AKT signaling	0.004786962	33.33	2.00	*[PIK3CA, PIK3R1]*
R-HSA:9603381	Activated NTRK3 signals through PI3K	0.004786962	33.33	2.00	*[PIK3CA, PIK3R1]*
R-HSA:9028335	Activated NTRK2 signals through PI3K	0.004786962	28.57	2.00	*[PIK3CA, PIK3R1]*
R-HSA:198203	PI3K/AKT activation	0.004786962	22.22	2.00	*[PIK3CA, PIK3R1]*
R-HSA:1250342	PI3K events in ERBB4 signaling	0.004786962	20.00	2.00	*[PIK3CA, PIK3R1]*
R-HSA:8853334	Signaling by FGFR3 fusions in cancer	0.004786962	20.00	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5655291	Signaling by FGFR4 in disease	0.004786962	18.18	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5654710	PI-3K cascade:FGFR3	0.004786962	16.67	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:9027276	Erythropoietin activates Phosphoinositide-3-kinase (PI3K)	0.004786962	16.67	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5654720	PI-3K cascade:FGFR4	0.004786962	15.00	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:5654689	PI-3K cascade:FGFR1	0.004786962	14.29	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:5655332	Signaling by FGFR3 in disease	0.004786962	13.64	3.00	*[FGF23, PIK3CA, PIK3R1]*

R-HSA:8853338	Signaling by FGFR3 point mutants in cancer	0.004786962	13.64	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:5637810	Constitutive Signaling by EGFRvIII	0.004786962	13.33	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5637812	Signaling by EGFRvIII in Cancer	0.004786962	13.33	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5654695	PI-3K cascade:FGFR2	0.004786962	13.04	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:1963642	PI3K events in ERBB2 signaling	0.004786962	12.50	2.00	*[PIK3CA, PIK3R1]*
R-HSA:2730905	Role of LAT2/NTAL/LAB on calcium mobilization	0.004786962	12.50	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5654708	Downstream signaling of activated FGFR3	0.004786962	12.00	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:180292	GAB1 signalosome	0.004786962	11.76	2.00	*[PIK3CA, PIK3R1]*
R-HSA:9034015	Signaling by NTRK3 (TRKC)	0.004786962	11.76	2.00	*[PIK3CA, PIK3R1]*
R-HSA:1839117	Signaling by cytosolic FGFR1 fusion mutants	0.004786962	11.11	2.00	*[PIK3CA, PIK3R1]*
R-HSA:210993	Tie2 Signaling	0.004786962	11.11	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5654716	Downstream signaling of activated FGFR4	0.004786962	11.11	3.00	*[FGF23, PIK3CA, PIK3R1]*
KEGG:04923	Regulation of lipolysis in adipocytes	0.004786962	10.91	6.00	*[ADORA1, GNAI1, NPY, PIK3CA, PIK3R1, PNPLA2]*
R-HSA:1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	0.004786962	10.53	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	0.004786962	10.53	2.00	*[PIK3CA, PIK3R1]*
R-HSA:5654696	Downstream signaling of activated FGFR2	0.004786962	10.00	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:1839124	FGFR1 mutant receptor activation	0.004786962	9.68	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:5654687	Downstream signaling of activated FGFR1	0.004786962	9.68	3.00	*[FGF23, PIK3CA, PIK3R1]*
R-HSA:389357	CD28 dependent PI3K/Akt signaling	0.004786962	9.09	2.00	*[PIK3CA, PIK3R1]*

R-HSA:912631	Regulation of signaling by CBL	0.004786962	9.09	2.00	*[PIK3CA, PIK3R1]*
R-HSA:373753	Nephrin family interactions	0.004786962	8.70	2.00	*[PIK3CA, PIK3R1]*
R-HSA:1643713	Signaling by EGFR in Cancer	0.004786962	8.00	2.00	*[PIK3CA, PIK3R1]*
R-HSA:2029485	Role of phospholipids in phagocytosis	0.004786962	8.00	2.00	*[PIK3CA, PIK3R1]*
R-HSA:9006115	Signaling by NTRK2 (TRKB)	0.004786962	8.00	2.00	*[PIK3CA, PIK3R1]*
R-HSA:9006335	Signaling by Erythropoietin	0.004786962	8.00	2.00	*[PIK3CA, PIK3R1]*
R-HSA:9615017	FOXO-mediated transcription of oxidative stress, metabolic and neuronal genes	0.005339022	10.34	3.00	*[IGFBP1, NPY, POMC]*
R-HSA:202040	G-protein activation	0.005773145	10.71	3.00	*[GNAI1, OPRM1, POMC]*
KEGG:05143	African trypanosomiasis	0.006542366	8.11	3.00	*[APOA1, IL6, KNG1]*
R-HSA:380994	ATF4 activates genes	0.013149546	8.00	2.00	*[CXCL8, IGFBP1]*
R-HSA:381771	Synthesis, secretion, and inactivation of Glucagon-like Peptide-1 (GLP-1)	0.022380594	10.00	2.00	*[GCG, GRP]*
R-HSA:400508	Incretin synthesis, secretion, and inactivation	0.022380594	8.70	2.00	*[GCG, GRP]*

Supplementary Table 3. Involved GO terms from ClueGo enrichment analysis for cluster 2 genes.

GO ID	GO Term	Term p-Value Corrected with Bonferroni step down	% Associated Genes	Nr. Genes	Associated Genes Found
R-HSA:114608	Platelet degranulation	3.48546E-20	11.63	15.00	*[A2M, CLU, F13A1, FGB, HGF, IGF1, IGF2, PROS1, SERPINE1, SERPINF2, SPARC, TGFB1, THBS1, VEGFA, VWF]*

R-HSA:76005	Response to elevated platelet cytosolic Ca2+	5.87143E-20	11.19	15.00	*[A2M, CLU, F13A1, FGB, HGF, IGF1, IGF2, PROS1, SERPINE1, SERPINF2, SPARC, TGFB1, THBS1, VEGFA, VWF]*
R-HSA:373080	Class B/2 (Secretin family receptors)	9.2479E-13	10.53	10.00	*[ADM, CALCA, CRH, GHRH, GIP, GLP1R, GNAS, IAPP, PTH, RAMP1]*
KEGG:04610	Complement and coagulation cascades	4.78905E-10	10.13	8.00	*[A2M, CLU, F13A1, FGB, PROS1, SERPINE1, SERPINF2, VWF]*
KEGG:04923	Regulation of lipolysis in adipocytes	9.30048E-08	10.91	6.00	*[ADRB1, ADRB2, ADRB3, CGA, GNAS, TSHR]*
R-HSA:419812	Calcitonin-like ligand receptors	1.06302E-07	40.00	4.00	*[ADM, CALCA, IAPP, RAMP1]*
R-HSA:140877	Formation of Fibrin Clot (Clotting Cascade)	6.20737E-07	12.82	5.00	*[A2M, F13A1, FGB, PROS1, VWF]*
R-HSA:390696	Adrenoceptors	1.26179E-05	33.33	3.00	*[ADRB1, ADRB2, ADRB3]*
R-HSA:420092	Glucagon-type ligand receptors	1.31787E-05	12.12	4.00	*[GHRH, GIP, GLP1R, GNAS]*
R-HSA:140875	Common Pathway of Fibrin Clot Formation	0.000161063	13.64	3.00	*[F13A1, FGB, PROS1]*
R-HSA:8866910	TFAP2 (AP-2) family regulates transcription of growth factors and their receptors	0.00082292	13.33	2.00	*[CGA, VEGFA]*
R-HSA:354194	GRB2:SOS provides linkage to MAPK signaling for Integrins	0.00082292	13.33	2.00	*[FGB, VWF]*
R-HSA:372708	p130Cas linkage to MAPK signaling for integrins	0.00082292	13.33	2.00	*[FGB, VWF]*
R-HSA:2428933	SHC-related events triggered by IGF1R	0.001140851	22.22	2.00	*[IGF1, IGF2]*
R-HSA:75205	Dissolution of Fibrin Clot	0.001227039	15.38	2.00	*[SERPINE1, SERPINF2]*
R-HSA:375281	Hormone ligand-binding receptors	0.001560206	16.67	2.00	*[CGA, TSHR]*

Supplementary Table 4. Involved GO terms from ClueGo enrichment analysis for cluster 3 genes.

GO ID	**GO Term**	**Term p-Value Corrected with Bonferroni step down**	**% Associated Genes**	**Nr. Genes**	**Associated Genes Found**
R-HSA:74749	Signal attenuation	1.00541E-07	40.00	4.00	*[INS, INSR, IRS1, SHC1]*
R-HSA:74749	Signal attenuation	1.00541E-07	40.00	4.00	*[INS, INSR, IRS1, SHC1]*

KEGG:04910	Insulin signaling pathway	2.53779E-07	5.11	7.00	*[INPPL1, INS, INSR, IRS1, PRKCZ, PTPN1, SHC1]*
R-HSA:8856825	Cargo recognition for clathrin-mediated endocytosis	1.85804E-06	5.66	6.00	*[IGF2R, LDLR, RPS27A, SH3GL2, TFRC, WNT5A]*
R-HSA:74713	IRS activation	2.49046E-06	60.00	3.00	*[INS, INSR, IRS1]*
R-HSA:432722	Golgi Associated Vesicle Biogenesis	2.59797E-06	8.93	5.00	*[FTH1, IGF2R, PIK3C2A, SH3GL2, TFRC]*
R-HSA:199992	trans-Golgi Network Vesicle Budding	9.03152E-06	6.94	5.00	*[FTH1, IGF2R, PIK3C2A, SH3GL2, TFRC]*
R-HSA:421837	Clathrin derived vesicle budding	9.03152E-06	6.94	5.00	*[FTH1, IGF2R, PIK3C2A, SH3GL2, TFRC]*
KEGG:04930	Type II diabetes mellitus	6.23421E-05	8.70	4.00	*[INS, INSR, IRS1, PRKCZ]*
R-HSA:512988	Interleukin-3, Interleukin-5 and GM-CSF signaling	7.17434E-05	8.33	4.00	*[IL5, INPPL1, RPS27A, SHC1]*
KEGG:04913	Ovarian steroidogenesis	7.54143E-05	8.16	4.00	*[IGF1R, INS, INSR, LDLR]*
R-HSA:74751	Insulin receptor signalling cascade	0.00010795	7.41	4.00	*[INS, INSR, IRS1, SHC1]*
R-HSA:74751	Insulin receptor signalling cascade	0.00010795	7.41	4.00	*[INS, INSR, IRS1, SHC1]*
KEGG:04213	Longevity regulating pathway	0.000181635	6.45	4.00	*[IGF1R, INS, INSR, IRS1]*
R-HSA:6807004	Negative regulation of MET activity	0.00024795	14.29	3.00	*[PTPN1, RPS27A, SH3GL2]*
R-HSA:74752	Signaling by Insulin receptor	0.000420816	5.13	4.00	*[INS, INSR, IRS1, SHC1]*
R-HSA:74752	Signaling by Insulin receptor	0.000420816	5.13	4.00	*[INS, INSR, IRS1, SHC1]*
R-HSA:6806834	Signaling by MET	0.000424953	5.06	4.00	*[PTPN1, RPS27A, SH3GL2, SHC1]*
R-HSA:912526	Interleukin receptor SHC signaling	0.000478543	11.11	3.00	*[IL5, INPPL1, SHC1]*
R-HSA:1592389	Activation of Matrix Metalloproteinases	0.000847019	9.09	3.00	*[MMP8, MMP9, TIMP2]*
KEGG:04960	Aldosterone-regulated sodium reabsorption	0.001145307	8.11	3.00	*[INS, INSR, IRS1]*
R-HSA:451927	Interleukin-2 family signaling	0.001841966	6.82	3.00	*[IL5, INPPL1, SHC1]*
R-HSA:177929	Signaling by EGFR	0.002418122	6.12	3.00	*[RPS27A, SH3GL2, SHC1]*
R-HSA:2428933	SHC-related events triggered by IGF1R	0.002535729	22.22	2.00	*[IGF1R, SHC1]*
R-HSA:2428933	SHC-related events triggered by IGF1R	0.002535729	22.22	2.00	*[IGF1R, SHC1]*
KEGG:04923	Regulation of lipolysis in adipocytes	0.002696766	5.45	3.00	*[INS, INSR, IRS1]*
R-HSA:2404192	Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	0.002723271	5.56	3.00	*[IGF1R, IRS1, SHC1]*

R-HSA:2404192	Signaling by Type 1 Insulin-like Growth Factor 1 Receptor (IGF1R)	0.002723271	5.56	3.00	*[IGF1R, IRS1, SHC1]*
R-HSA:2428924	IGF1R signaling cascade	0.002736368	5.66	3.00	*[IGF1R, IRS1, SHC1]*
R-HSA:2428924	IGF1R signaling cascade	0.002736368	5.66	3.00	*[IGF1R, IRS1, SHC1]*
R-HSA:1236977	Endosomal/Vacuolar pathway	0.002790979	18.18	2.00	*[B2M, CTSS]*
KEGG:04216	Ferroptosis	0.002937287	5.00	2.00	*[FTH1, TFRC]*
R-HSA:5654741	Signaling by FGFR3	0.002937287	5.00	2.00	*[RPS27A, SHC1]*
R-HSA:917937	Iron uptake and transport	0.002948518	5.17	3.00	*[FTH1, RPS27A, TFRC]*
R-HSA:182971	EGFR downregulation	0.005312053	6.45	2.00	*[RPS27A, SH3GL2]*
R-HSA:2173791	TGF-beta receptor signaling in EMT (epithelial to mesenchymal transition)	0.005586252	12.50	2.00	*[PRKCZ, RPS27A]*
R-HSA:8875360	InlB-mediated entry of Listeria monocytogenes into host cell	0.005586252	12.50	2.00	*[RPS27A, SH3GL2]*
R-HSA:76009	Platelet Aggregation (Plug Formation)	0.005587752	5.13	2.00	*[PTPN1, SHC1]*
R-HSA:9034015	Signaling by NTRK3 (TRKC)	0.005796306	11.76	2.00	*[IRS1, SHC1]*
R-HSA:9034015	Signaling by NTRK3 (TRKC)	0.005796306	11.76	2.00	*[IRS1, SHC1]*
R-HSA:1236382	Constitutive Signaling by Ligand-Responsive EGFR Cancer Variants	0.006609053	10.53	2.00	*[RPS27A, SHC1]*
R-HSA:5637815	Signaling by Ligand-Responsive EGFR Variants in Cancer	0.006609053	10.53	2.00	*[RPS27A, SHC1]*
R-HSA:2424491	DAP12 signaling	0.006633994	6.67	2.00	*[B2M, SHC1]*
R-HSA:354192	Integrin alphaIIb beta3 signaling	0.006716084	7.41	2.00	*[PTPN1, SHC1]*
R-HSA:9006921	Integrin signaling	0.006716084	7.41	2.00	*[PTPN1, SHC1]*
R-HSA:77387	Insulin receptor recycling	0.007471563	7.69	2.00	*[INS, INSR]*
R-HSA:8876384	Listeria monocytogenes entry into host cells	0.008005403	9.09	2.00	*[RPS27A, SH3GL2]*
R-HSA:1643713	Signaling by EGFR in Cancer	0.008056271	8.00	2.00	*[RPS27A, SHC1]*
R-HSA:982772	Growth hormone receptor signaling	0.008481092	8.33	2.00	*[IRS1, PTPN1]*