Table S4 DAVID functional analysis of RefSeq genes with promoters enriched with H3K27me3

Functional analysis of autosomal RefSeq genes containing H3K27me3 promoter enrichment was performed using DAVID (Huang da *et al.* 2009) for the fetal and lamb samples (2,654 and 3,319 genes, respectively). For Functional Annotation Clustering an Enrichment Score (- $\log_{10}$ (mean p-values for cluster terms)) ≥ 1.3 containing ≥ 5 genes for each term was considered significant. KEGG pathway and PFAM enrichments were separately determined. Terms with P-values ≤ 0.05 after Benjamini-Hochberg correction and containing ≥ 10 genes were considered significant.

A. Foetal DAVID clusters

						List	Pop	Benjamini
Category	Term	Count	%	P-value	Genes	Total	Hits	P-value
Annotation Cluster 1 **Enrichment Score: 20.919341115171484**								
SP_PIR_KEYWORDS	Homeobox	50	1.95	1.68E-24	HNF1B, CDX1, CDX2, PAX6, PAX3, HOXD10, CRX, HOXC6, POU5F1, HOXC4, ALX4, PITX1, PITX2, SATB1, NANOG, EMX2, HHEX, MSX1, HOXC11, HOXC13, SIX1, UNCX, IRX3, ONECUT1, MEIS1, OTP, MSX2, DBX2, MEIS2, LHX3, HOXA10, LHX4, LHX5, POU3F2, POU3F1, LHX9, NKX2-5, DBX1, NKX2-3, ISL1, DLX3, HOXB4, ZFHX4, DLX1, MEOX2, LASS4, HOXB7, DLX5, HOXB6, DLX4, HOPX	979	78	3.78E-22
INTERPRO	IPR001356:Homeobox	47	1.83	6.23E-23	IRX3, CDX1, HNF1B, ONECUT1, PAX6, PAX3, MEIS1, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, NKX2-5, LHX9, PITX1, DBX1, NKX2-3, PITX2, SATB1, NANOG, EMX2, ISL1, DLX3, HOXB4, HHEX, DLX1, MSX1, HOXC11, MEOX2, LASS4, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	1185	75	1.01E-19
SMART	SM00389:HOX	47	1.83	1.26E-20	IRX3, CDX1, HNF1B, ONECUT1, PAX6, PAX3, MEIS1, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, NKX2-5, LHX9, PITX1, DBX1, NKX2-3, PITX2, SATB1, NANOG, EMX2, ISL1, DLX3, HOXB4, HHEX, DLX1, MSX1, HOXC11, MEOX2, LASS4, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	649	75	3.39E-18
INTERPRO	IPR017970:Homeobox, conserved site	40	1.56	3.33E-20	IRX3, CDX1, HNF1B, PAX6, PAX3, HOXD10, OTP, CRX, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, LHX9, NKX2-5, PITX1, DBX1, NKX2-3, PITX2, NANOG, EMX2, ISL1, DLX3, HOXB4, HHEX, DLX1, MSX1, MEOX2, LASS4, HOXB7, HOXC13, DLX5, HOXB6, SIX1, HOPX	1185	62	2.70E-17
INTERPRO	IPR012287:Homeodomain-related	45	1.75	5.75E-20	IRX3, CDX1, HNF1B, ONECUT1, PAX6, PAX3, MEIS1, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, MYB, NKX2-5, LHX9, PITX1, DBX1, NKX2-3, PITX2, SATB1, NANOG, EMX2, DLX3, HOXB4, HHEX, HOXC11, MSX1, MEOX2, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	1185	78	3.11E-17

Annotation Cluster 2
Enrichment Score: 15.30920632284991

GOTERM_MF_FAT	GO:0022836~gated channel activity	75	2.92	2.93E-17	KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, GRIK2, GRIK3, GABRB1, GRIN3B, KCNJ10, KCNJ12, KCNIP3, SHKBP1, KCNQ3, GRIN2C, CHRNA5, CHRNA7, KCNG3, CHRNA3, CHRNA2, KCNMA1, KCND2, CACNG2, CNGA3, CLIC5, LOC100139857, KCNH2, KCNH5, SCN1B, KCNA2, KCNA1, KCNA4, KCNA6, CACNB3, CACNB4, KCNA5, KCNS2, KCNE1, SCNN1G, HTR3A, HTR3B, SCN5A, GABRQ, GABRP, KCNE4, GABRD, GABRA2, GLRB, CACNA2D1, GABRA4, LOC100138074, GABRA5, LOC783386, ITPR3, KCNK1, KCNK2, ITPR1, KCNV1, KCTD8, ACCN1, KCNN4, KCNJ9, KCNN1, GRIA2, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, CACNA1D, CACNA1A, CLCN5	1232	204	6.57E-15
GOTERM_MF_FAT	GO:0005216~ion channel activity	87	3.39	6.42E-16	KCNK17, KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, GRIK2, GRIK3, GABRB1, KCNJ10, GRIN3B, KCNJ12, KCNIP3, SHKBP1, KCNQ3, GRIN2C, KCNK6, CHRNA5, CHRNA7, ANO4, KCNG3, CHRNA3, CHRNA2, KCNMA1, TRPM6, KCND2, CFTR, CACNG2, CNGA3, CATSPER4, SLC26A8, CLIC5, LOC100139857, CATSPER1, KCNH2, KCNH5, SCN1B, KCNA2, KCNA1, KCNA4, KCNA6, CACNB3, KCNA5, CACNB4, FXYD7, KCNS2, TTYH1, KCNE1, SCNN1G, HTR3A, SCN5A, HTR3B, GABRQ, KCNE4, GABRP, GABRD, GABRA2, CACNA2D1, GLRB, GABRA4, LOC100138074, GABRA5, LOC783386, ITPR3, KCNK1, KCNK2, ITPR1, KCNV1, KCNK4, KCTD8, ACCN1, KCNN4, KCNJ9, GRIA2, KCNN1, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, LOC505697, CACNA1D, CACNA1A, CLCN5	1232	268	1.19E-13
GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	88	3.43	1.07E-15	KCNK17, KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, GRIK2, GRIK3, GABRB1, GJA1, KCNJ10, GRIN3B, KCNJ12, KCNIP3, SHKBP1, KCNQ3, GRIN2C, KCNK6, CHRNA5, CHRNA7, ANO4, KCNG3, CHRNA3, CHRNA2, KCNMA1, TRPM6, KCND2, CFTR, CACNG2, CNGA3, CATSPER4, SLC26A8, CLIC5, LOC100139857, CATSPER1, KCNH2, KCNH5, SCN1B, KCNA2, KCNA1, KCNA4, KCNA6, CACNB3, KCNA5, CACNB4, FXYD7, KCNS2, TTYH1, KCNE1, SCNN1G, HTR3A, SCN5A, HTR3B, GABRQ, KCNE4, GABRP, GABRD, GABRA2, CACNA2D1, GLRB, GABRA4, LOC100138074, GABRA5, LOC783386, ITPR3, KCNK1, KCNK2, ITPR1, KCNV1, KCNK4, KCTD8, ACCN1, KCNN4, KCNJ9, GRIA2, KCNN1, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, LOC505697, CACNA1D, CACNA1A, CLCN5	1232	275	1.66E-13
GOTERM_MF_FAT	GO:0015267~channel activity	88	3.43	1.07E-15	KCNK17, KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, GRIK2, GRIK3, GABRB1, GJA1, KCNJ10, GRIN3B, KCNJ12, KCNIP3, SHKBP1, KCNQ3, GRIN2C, KCNK6, CHRNA5, CHRNA7, ANO4, KCNG3, CHRNA3, CHRNA2, KCNMA1, TRPM6, KCND2, CFTR, CACNG2, CNGA3, CATSPER4, SLC26A8, CLIC5, LOC100139857, CATSPER1, KCNH2, KCNH5, SCN1B, KCNA2, KCNA1, KCNA4, KCNA6, CACNB3, KCNA5, CACNB4, FXYD7, KCNS2, TTYH1, KCNE1, SCNN1G, HTR3A, SCN5A, HTR3B, GABRQ, KCNE4, GABRP, GABRD, GABRA2, CACNA2D1, GLRB, GABRA4, LOC100138074, GABRA5, LOC783386, ITPR3, KCNK1, KCNK2, ITPR1, KCNV1, KCNK4, KCTD8, ACCN1, KCNN4, KCNJ9, GRIA2, KCNN1,	1232	275	1.66E-13

					KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, LOC505697, CACNA1D, CACNA1A, CLCN5			
GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	87	3.39	1.33E-15	KCNK17, KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, GRIK2, GRIK3, GABRB1, KCNJ10, GRIN3B, KCNJ12, KCNIP3, SHKBP1, KCNQ3, GRIN2C, KCNK6, CHRNA5, CHRNA7, ANO4, KCNG3, CHRNA3, CHRNA2, KCNMA1, TRPM6, KCND2, CFTR, CACNG2, CNGA3, CATSPER4, SLC26A8, CLIC5, LOC100139857, CATSPER1, KCNH2, KCNH5, SCN1B, KCNA2, KCNA1, KCNA4, KCNA6, CACNB3, KCNA5, CACNB4, FXYD7, KCNS2, TTYH1, KCNE1, SCNN1G, HTR3A, SCN5A, HTR3B, GABRQ, KCNE4, GABRP, GABRD, GABRA2, CACNA2D1, GLRB, GABRA4, LOC100138074, GABRA5, LOC783386, ITPR3, KCNK1, KCNK2, ITPR1, KCNV1, KCNK4, KCTD8, ACCN1, KCNN4, KCNJ9, GRIA2, KCNN1, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, LOC505697, CACNA1D, CACNA1A, CLCN5	1232	271	1.71E-13
Annotation Cluster 3 **Enrichment Score: 11.350857115105626**								
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	193	7.52	3.27E-13	CDX1, CDX2, FST, RORB, RORA, HOXD10, PGR, FOXF1, CREB3L3, TWIST2, PITX1, PITX2, PHOX2A, RARG, EMX1, EMX2, BARHL2, RXRG, EOMES, MSX1, HES5, UNCX, LOC783396, OTP, FOXH1, LIF, T, AHRR, LHX3, LHX4, HOXA10, LHX5, LOC789268, LHX9, NKX2-5, NKX2-3, BMP4, KLF5, BMP3, NTF3, ESRRG, DLX3, SHOX2, NR1I3, DLX1, DMRTC2, LOC789959, DLX6, ETS1, DLX5, DLX4, HOPX, CRYM, KLF4, KCNH1, HNF1B, FOXA2, ELF5, LOC783703, GLI1, YBX2, KCNIP3, LOC785085, ZNF540, MKX, FOXB1, NR2F2, MYB, BHLHE41, NR2F1, AR, TBX15, NDUFA13, TLE4, INHBA, LOC539166, FOXC2, KCNH2, KCNH5, LOC522736, ZBTB16, MYCL1, STAT4, LOC787194, TLX2, SIM1, MLLT3, LOC615643, LMX1B, TBX5, TBX4, MYF5, MEOX2, NEUROD1, LOC654400, NR5A2, FOXE3, NR5A1, MYOD1, CBX2, NR2E1, GDNF, LOC782183, TGFB1, HOXC6, ATOH1, GATA5, HOXC4, GATA3, SATB1, SATB2, HES6, PKIA, AHR, HHEX, SIX1, TFAP2A, TFAP2C, NFE2L3, LOC527381, ONECUT1, SOX2, MEIS1, LIN28B, DBX2, VDR, MEIS3, MEIS2, HOXA7, OVOL1, DBX1, TAF1, EPAS1, GSX2, RFX4, MAFB, FOXA1, GSX1, HOXB4, GCM2, HOXB2, ATF3, HOXB7, LASS4, EBF2, HOXB6, PAX6, DMRTA2, PAX3, CRX, FEV, LBH, HEY1, POU5F1, SOX18, PDE8A, ALX4, ALX3, EGR1, NANOG, OTX2, ESR1, MIXL1, ADRB2, HOXC11, HOXC13, NRL, CUX2, CUX1, MAPRE3, IRX3, SBNO2, ABLIM3, LOC618065, MSX2, HAND1, POU2F3, POU3F4, POU3F2, NFATC4, POU3F1, EPO, CEBPA, FOXL2, FOXL1, VSX2, ISL1, ID2, IRF5, ID1, IRF6, IRF8, HEYL, SP7, F2R	1230	845	9.95E-10
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	194	7.55	9.67E-13	CDX1, CDX2, FST, RORB, RORA, HOXD10, PGR, FOXF1, CREB3L3, PITX1, TWIST2, PITX2, PHOX2A, RARG, EMX1, EMX2, BARHL2, RXRG, EOMES, MSX1, HES5, UNCX, LOC783396, OTP, FOXH1, LIF, T, AHRR, LHX3, LHX4, HOXA10, LHX5, LOC789268, LHX9, NKX2-5, NKX2-3, BMP4, KLF5, BMP3, NTF3, ESRRG, DLX3, SHOX2, NR1I3, DLX1, DMRTC2, LOC789959, DLX6, ETS1, DLX5, DLX4, HOPX, CRYM, KLF4, KCNH1, HNF1B, FOXA2, ELF5, LOC783703, GLI1, YBX2, KCNIP3,	1230	860	9.80E-10

					LOC785085, ZNF540, MKX, FOXB1, NR2F2, MYB, BHLHE41, NR2F1, AR, TBX15, NDUFA13, TLE4, INHBA, LOC539166, FOXC2, KCNH2, KCNH5, LOC522736, ZBTB16, MYCL1, STAT4, LOC787194, TLX2, SIM1, MLLT3, LOC615643, LMX1B, TBX5, TBX4, MYF5, MEOX2, NEUROD1, LOC654400, NR5A2, FOXE3, NR5A1, MYOD1, CBX2, NR2E1, GDNF, LOC782183, TGFB1, HOXC6, ATOH1, GATA5, HOXC4, GATA3, SATB1, SATB2, HES6, PKIA, AHR, HHEX, SIX1, TFAP2A, TFAP2C, NFE2L3, LOC527381, ONECUT1, SOX2, MEIS1, LIN28B, DBX2, VDR, MEIS3, MEIS2, HOXA7, OVOL1, DBX1, TAF1, EPAS1, GSX2, RFX4, MAFB, FOXA1, GSX1, HOXB4, GCM2, HOXB2, ATF3, HOXB7, LASS4, EBF2, HOXB6, PAX6, DMRTA2, PAX3, CRX, FEV, LBH, HEY1, POU5F1, SOX18, PDE8A, ALX4, ALX3, EGR1, NANOG, OTX2, ESR1, MIXL1, ADRB2, HOXC11, HOXC13, NRL, CUX2, CUX1, MAPRE3, CALCR, IRX3, SBNO2, ABLIM3, LOC618065, MSX2, HAND1, POU2F3, POU3F4, POU3F2, NFATC4, POU3F1, EPO, CEBPA, FOXL2, FOXL1, VSX2, ISL1, ID2, IRF5, ID1, IRF6, IRF8, HEYL, SP7, F2R			
GOTERM_BP_FAT	GO:0045449~regulation of transcription	236	9.19	2.80E-10	CDX1, CDX2, GDF6, FST, RORB, PDLIM1, RORA, HOXD10, PGR, FOXF1, CREB3L3, PITX1, TWIST2, PITX2, TWIST1, PHOX2A, RARG, EMX1, EMX2, BARHL2, RXRG, EOMES, MSX1, HES5, ECOP, PRDM6, UNCX, LOC783396, OTP, FOXH1, LIF, T, TCF21, AHRR, LHX3, HOXA10, LHX4, LHX5, LOC789268, NKX2-5, LHX9, NKX2-3, KLF5, BMP4, BMP3, IKZF3, NTF3, ESRRG, SHOX2, DLX3, NR1I3, DLX1, DMRTC2, ETS1, LOC789959, DLX6, DLX5, DLX4, HOPX, CRYM, KLF4, TCF15, KCNH1, HNF1B, FOXA2, ELF5, LOC783703, KCNIP3, GLI1, YBX2, FERD3L, LOC785085, LOC789450, ZNF540, MKX, FOXB1, BHLHE41, MYB, NR2F2, NR2F1, AR, TBX15, TLE4, NDUFA13, INHBA, LOC539166, FOXC2, KCNH2, KCNH5, LOC281370, LOC522736, ZBTB16, SEC14L2, MYCL1, STAT4, LOC787194, ACTL6B, TLX2, SIM1, LOC615643, MLLT3, LMX1B, TBX5, MYF5, TBX4, SNAI2, MEOX2, NEUROD1, NR5A2, LOC654400, ZNF572, FOXE3, NR5A1, MYOD1, LMO3, CBX2, GDNF, NR2E1, LOC782183, TGFB1, HOXC6, ATOH1, OLIG3, GATA5, GATA3, HOXC4, OLIG1, ATOH7, SATB1, SATB2, MLXIPL, HES6, PKIA, AHR, PTHLH, ASCL2, ASCL1, HHEX, SIX1, TFAP2A, RIPK2, TFAP2C, NFE2L3, ASCL4, LOC527381, ONECUT1, LOC781206, SOX2, MEIS1, LIN28B, DBX2, VDR, MEIS3, MEIS2, HOXA7, OVOL1, DBX1, TAF1, RFX4, EPAS1, GSX2, MAFB, FOXA1, GSX1, NEUROG1, NEUROG3, FEZF2, HOXB4, GCM2, HOXB2, ATF3, HOXB7, LASS4, EBF2, HOXB6, EAF2, BMI1, HR, PAX6, PAX5, DMRTA2, PAX3, PAX1, FEV, CRX, LBH, HEY1, PAX9, LOC509704, POU5F1, PAX8, SOX18, PDE8A, ALX4, ALX3, EGR1, NANOG, EGR4, OTX2, ESR1, PCGF1, MIXL1, ADRB2, HOXC11, HOXC13, NRL, LOC617563, CUX2, CUX1, MAPRE3, IRX3, SBNO2, ABLIM3, TRIB3, LOC618065, MSX2, HAND1, POU2F3, POU3F4, PYCARD, NFATC4, POU3F2, POU3F1, EPO, CEBPA, INSM1, FOXL2, FOXL1, ISL1, VSX2, ID2, IRF5, ID1, IRF6, IRF8, HEYL, SP7, F2R	1230	1166	1.70E-07
Annotation Cluster 4 **Enrichment Score: 10.944754470318188**								
SP_PIR_KEY	g-protein coupled receptor	62	2.41	2.90E-13	CASR, TACR3, F2RL1, LHCGR, VIPR1, S1PR2, AGTR1, EDNRB, S1PR3,	979	177	1.87E-11

WORDS					PTGIR, CXCR4, LTB4R, CXCR7, GALR2, LOC781367, MC5R, LPHN1, C5AR1, PTGER3, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, CRHR1, SSTR2, GRM3, ADRB2, ADRB1, PTGDR, NK1R, TSHR, CALCR, DRD1, PRLHR, GPRC5C, ADORA2B, ADCYAP1R1, FFAR2, OPRK1, NPY2R, PTH1R, GPR6, OXTR, BDKRB2, GPR4, ADRB3, HCRTR1, ADRA2A, FZD3, PTGFR, FZD6, FZD10, AVPR1B, ADRA1B, MC4R, AVPR1A, UTS2R, GHSR, F2R, HTR2A			
INTERPRO	IPR000276:7TM GPCR, rhodopsin-like	54	2.1	6.25E-11	MCHR1, GPR162, TACR3, F2RL1, LHCGR, S1PR2, AGTR1, EDNRB, S1PR3, PTGIR, HTR1A, CXCR4, LTB4R, CXCR7, GALR2, LOC781367, MC5R, PTGER3, C5AR1, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, SSTR2, ADRB2, ADRB1, PTGDR, NK1R, TSHR, DRD1, PRLHR, ADORA2B, FFAR2, OPRK1, NPY2R, GPR6, OXTR, BDKRB2, GPR4, ADRB3, HCRTR1, ADRA2A, PTGFR, GPR37, AVPR1B, ADRA1B, MC4R, AVPR1A, UTS2R, GHSR, F2R, HTR2A	1185	164	2.53E-08
INTERPRO	IPR017452:GPCR, rhodopsin-like superfamily	54	2.1	8.08E-11	MCHR1, GPR162, TACR3, F2RL1, LHCGR, S1PR2, AGTR1, EDNRB, S1PR3, PTGIR, HTR1A, CXCR4, LTB4R, CXCR7, GALR2, LOC781367, MC5R, PTGER3, C5AR1, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, SSTR2, ADRB2, ADRB1, PTGDR, NK1R, TSHR, DRD1, PRLHR, ADORA2B, FFAR2, OPRK1, NPY2R, GPR6, OXTR, BDKRB2, GPR4, ADRB3, HCRTR1, ADRA2A, PTGFR, GPR37, AVPR1B, ADRA1B, MC4R, AVPR1A, UTS2R, GHSR, F2R, HTR2A	1185	165	2.62E-08
Annotation Cluster 5 **Enrichment Score: 8.164708874769264**								
GOTERM_MF_FAT	GO:0015276~ligand-gated ion channel activity	35	1.36	2.10E-09	GRIK1, GLRA1, GRIK2, GRIK3, GABRB1, KCNJ10, GRIN3B, KCNJ12, GRIN2C, CHRNA5, CHRNA7, SCNN1G, HTR3A, HTR3B, GABRQ, CHRNA3, CHRNA2, GABRP, GABRD, GLRB, GABRA2, LOC100138074, GABRA4, GABRA5, LOC783386, CNGA3, ITPR3, ITPR1, ACCN1, KCNJ9, GRIA2, LOC100139857, CHRNB4, CHRND, CHRNB2	1232	88	1.71E-07
GOTERM_MF_FAT	GO:0022834~ligand-gated channel activity	35	1.36	2.10E-09	GRIK1, GLRA1, GRIK2, GRIK3, GABRB1, KCNJ10, GRIN3B, KCNJ12, GRIN2C, CHRNA5, CHRNA7, SCNN1G, HTR3A, HTR3B, GABRQ, CHRNA3, CHRNA2, GABRP, GABRD, GLRB, GABRA2, LOC100138074, GABRA4, GABRA5, LOC783386, CNGA3, ITPR3, ITPR1, ACCN1, KCNJ9, GRIA2, LOC100139857, CHRNB4, CHRND, CHRNB2	1232	88	1.71E-07
GOTERM_MF_FAT	GO:0005230~extracellular ligand-gated ion channel activity	26	1.01	7.26E-08	GLRA1, GRIK1, GRIK2, GABRB1, GRIK3, GRIN3B, GRIN2C, CHRNA5, CHRNA7, HTR3A, HTR3B, GABRQ, CHRNA3, GABRP, CHRNA2, GABRD, GLRB, GABRA2, LOC100138074, GABRA4, GABRA5, LOC783386, GRIA2, CHRNB4, CHRND, CHRNB2	1232	61	4.65E-06
Annotation Cluster 6 **Enrichment Score: 7.457119967464377**								
GOTERM_BP_FAT	GO:0050801~ion homeostasis	56	2.18	3.45E-10	CASR, JPH2, GLRA1, EDN2, SLC9A3, SNCA, EDN1, LOC785842, CKB, AGTR1, EDNRB, LOC531957, APOE, AQP11, HMOX1, LTF, CHRNA7, MT3, FTL, KCNMA1, PRKCA, PTGER3, LOC786683, CCKBR, LOC783224, SLC34A1, CACNG2, PRKCB, RHCG, LOC100139857, LOC525947, CALCR, PTH1R, GPR6, TAC1, CLDN11, KCNA5, CACNB4, ATP6V1B1, CCL28, SYPL2, FKBP1B, CD9, VDR, KCNE1, GAL3ST1, GLRB, UPK3A, LOC783993, AFG3L2, TNNI3, ITPR1, KDR, CHRNB4, CACNA1G, CHRNB2,	1230	168	1.75E-07

					SCARA5, CACNA1A, F2R			
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	49	1.91	1.36E-08	CASR, JPH2, GLRA1, EDN2, SNCA, EDN1, LOC785842, CKB, AGTR1, LOC531957, APOE, AQP11, LTF, CHRNA7, MT3, FTL, KCNMA1, PRKCA, PTGER3, LOC786683, CCKBR, LOC783224, CACNG2, PRKCB, RHCG, LOC100139857, LOC525947, CALCR, PTH1R, GPR6, TAC1, CACNB4, CLDN11, KCNA5, FKBP1B, CCL28, SYPL2, CD9, VDR, KCNE1, GAL3ST1, GLRB, LOC783993, AFG3L2, TNNI3, ITPR1, CHRNB4, CACNA1G, CHRNB2, SCARA5, CACNA1A, F2R	1230	151	3.17E-06
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	63	2.45	1.40E-08	CASR, JPH2, GLRA1, EDN2, SLC9A3, EDN1, SNCA, LOC785842, CKB, EDNRB, AGTR1, LOC531957, SLC2A4, AQP11, APOE, HMOX1, LTF, CHRNA7, MT3, FTL, KCNMA1, PRKCA, PTGER3, LOC786683, CCKBR, LOC783224, SLC34A1, CACNG2, PRKCB, PTHLH, G6PC, RHCG, LOC100139857, LOC525947, CALCR, PTH1R, GPR6, TAC1, KCNA5, CLDN11, CACNB4, ATP6V1B1, SYPL2, CCL28, FKBP1B, CD9, VDR, KCNE1, GAL3ST1, LPL, GLRB, EPAS1, FOXA1, UPK3A, LOC783993, TNNI3, AFG3L2, ITPR1, KDR, CHRNB4, CACNA1G, CHRNB2, CACNA1E, SCARA5, CACNA1A, F2R	1230	218	3.04E-06
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	49	1.91	2.17E-08	CASR, JPH2, GLRA1, EDN2, SNCA, EDN1, LOC785842, CKB, AGTR1, LOC531957, APOE, AQP11, LTF, CHRNA7, MT3, FTL, KCNMA1, PRKCA, PTGER3, LOC786683, CCKBR, LOC783224, CACNG2, PRKCB, RHCG, LOC100139857, LOC525947, CALCR, PTH1R, GPR6, TAC1, CACNB4, CLDN11, KCNA5, FKBP1B, CCL28, SYPL2, CD9, VDR, KCNE1, GAL3ST1, GLRB, LOC783993, AFG3L2, TNNI3, ITPR1, CHRNB4, CACNA1G, CHRNB2, SCARA5, CACNA1A, F2R	1230	153	3.89E-06
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	53	2.06	3.64E-05	CASR, JPH2, GLRA1, PDIA2, EDN2, SNCA, EDN1, LOC785842, LOC539389, CKB, AGTR1, LOC531957, APOE, AQP11, LTF, CHRNA7, MT3, FTL, KCNMA1, PRKCA, PTGER3, AIFM3, LOC786683, CCKBR, LOC783224, CACNG2, PRKCB, RHCG, LOC100139857, LOC525947, CALCR, PTH1R, GPR6, TAC1, CLDN11, KCNA5, CACNB4, FKBP1B, CCL28, SYPL2, CD9, VDR, KCNE1, GAL3ST1, GLRB, LOC783993, AFG3L2, TNNI3, ITPR1, KCNN4, CHRNB4, CACNA1G, CHRNB2, SCARA5, CACNA1A, F2R	1230	215	0.00156039
Annotation Cluster 7 **Enrichment Score: 7.3651838608178215**								
GOTERM_MF_FAT	GO:0022832~voltage-gated channel activity	40	1.56	3.23E-08	KCNH1, KCNC1, SCN1B, KCNAB1, KCNA2, KCNA1, KCNA4, CACNB3, KCNJ10, KCNA6, CACNB4, KCNA5, KCNJ12, KCNIP3, SHKBP1, KCNS2, KCNQ3, KCNE1, KCNG3, SCN5A, KCNE4, KCNMA1, CACNA2D1, KCND2, CACNG2, KCNK1, KCNK2, KCNV1, KCTD8, KCNJ9, CLIC5, CACNA1G, KCNF1, SCN4B, CACNA1E, KCNH2, CACNA1D, CACNA1A, KCNH5, CLCN5	1232	119	2.23E-06
GOTERM_MF_FAT	GO:0005244~voltage-gated ion channel activity	40	1.56	3.23E-08	KCNH1, KCNC1, SCN1B, KCNAB1, KCNA2, KCNA1, KCNA4, CACNB3, KCNJ10, KCNA6, CACNB4, KCNA5, KCNJ12, KCNIP3, SHKBP1, KCNS2, KCNQ3, KCNE1, KCNG3, SCN5A, KCNE4, KCNMA1, CACNA2D1, KCND2, CACNG2, KCNK1, KCNK2, KCNV1, KCTD8, KCNJ9, CLIC5, CACNA1G, KCNF1, SCN4B, CACNA1E, KCNH2, CACNA1D, CACNA1A, KCNH5, CLCN5	1232	119	2.23E-06

GOTERM_MF_FAT	GO:0022843~voltage-gated cation channel activity	34	1.32	7.68E-08	KCNH1, KCNC1, KCNAB1, KCNA2, KCNA1, KCNA4, CACNB3, KCNJ10, KCNA6, CACNB4, KCNA5, KCNJ12, SHKBP1, KCNS2, KCNQ3, KCNE1, KCNG3, SCN5A, KCNE4, KCNMA1, CACNA2D1, KCND2, CACNG2, KCNK2, KCNV1, KCTD8, KCNJ9, CACNA1G, KCNF1, CACNA1E, KCNH2, CACNA1D, CACNA1A, KCNH5	1232	95	4.59E-06
Annotation Cluster 8 **Enrichment Score: 6.898048750641291**								
GOTERM_BP_FAT	GO:0055065~metal ion homeostasis	30	1.17	6.91E-09	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, AGTR1, VDR, APOE, CHRNA7, MT3, PRKCA, KCNMA1, LOC786683, PTGER3, CCKBR, UPK3A, TNNI3, ITPR1, KDR, PRKCB, LOC100139857, CACNA1A, F2R	1230	68	2.63E-06
GOTERM_BP_FAT	GO:0055080~cation homeostasis	41	1.6	1.31E-08	CALCR, CASR, JPH2, EDN2, SLC9A3, PTH1R, EDN1, GPR6, LOC785842, TAC1, CACNB4, ATP6V1B1, FKBP1B, CCL28, SYPL2, VDR, AGTR1, EDNRB, LOC531957, APOE, AQP11, HMOX1, LTF, CHRNA7, FTL, MT3, PRKCA, KCNMA1, PTGER3, LOC786683, CCKBR, LOC783224, LOC783993, UPK3A, TNNI3, ITPR1, PRKCB, KDR, RHCG, LOC100139857, LOC525947, SCARA5, CACNA1A, F2R	1230	115	3.32E-06
GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	28	1.09	4.49E-08	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, AGTR1, VDR, APOE, CHRNA7, MT3, PRKCA, KCNMA1, LOC786683, PTGER3, CCKBR, TNNI3, ITPR1, PRKCB, LOC100139857, CACNA1A, F2R	1230	65	7.19E-06
GOTERM_BP_FAT	GO:0055074~calcium ion homeostasis	27	1.05	6.32E-08	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, AGTR1, VDR, APOE, CHRNA7, PRKCA, LOC786683, PTGER3, CCKBR, TNNI3, ITPR1, KDR, PRKCB, LOC100139857, CACNA1A, F2R	1230	62	9.15E-06
GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	26	1.01	1.32E-07	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, AGTR1, VDR, APOE, CHRNA7, PRKCA, LOC786683, PTGER3, CCKBR, TNNI3, ITPR1, PRKCB, LOC100139857, CACNA1A, F2R	1230	60	1.74E-05
GOTERM_BP_FAT	GO:0030003~cellular cation homeostasis	34	1.32	7.48E-07	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, LOC785842, TAC1, CACNB4, FKBP1B, SYPL2, CCL28, AGTR1, VDR, LOC531957, APOE, AQP11, LTF, CHRNA7, FTL, MT3, PRKCA, KCNMA1, PTGER3, LOC786683, CCKBR, LOC783224, LOC783993, TNNI3, ITPR1, PRKCB, LOC100139857, LOC525947, SCARA5, CACNA1A, F2R	1230	99	8.12E-05
GOTERM_BP_FAT	GO:0055066~di-, tri-valent inorganic cation homeostasis	33	1.29	8.43E-07	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, LOC785842, TAC1, CACNB4, FKBP1B, SYPL2, CCL28, AGTR1, VDR, LOC531957, APOE, HMOX1, LTF, CHRNA7, FTL, PRKCA, LOC786683, PTGER3, CCKBR, LOC783224, LOC783993, TNNI3, ITPR1, KDR, PRKCB, LOC100139857, LOC525947, SCARA5, CACNA1A, F2R	1230	95	8.84E-05
GOTERM_BP_FAT	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	31	1.21	3.07E-06	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, LOC785842, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, AGTR1, VDR, LOC531957, APOE, LTF, CHRNA7, FTL, PRKCA, LOC786683, PTGER3, CCKBR, LOC783224, LOC783993, TNNI3, ITPR1, PRKCB, LOC100139857, LOC525947, SCARA5, CACNA1A, F2R	1230	91	2.17E-04
Annotation Cluster 9 **Enrichment Score: 6.866826564798346**								

GOTERM_MF_FAT	GO:0001653~peptide receptor activity	31	1.21	7.94E-08	GPR83, PRLHR, TACR3, NPY2R, OPRK1, F2RL1, OXTR, BDKRB2, HCRTR2, EDNRB, AGTR1, HCRTR1, CXCR4, GALR2, MC5R, XCR1, C5AR1, CCKBR, PROKR2, NPR1, PROKR1, NPR3, NTSR1, SSTR2, NK1R, AVPR1B, MC4R, AVPR1A, UTS2R, F2R, OPRD1	1232	82	4.45E-06
GOTERM_MF_FAT	GO:0008528~peptide receptor activity, G-protein coupled	31	1.21	7.94E-08	GPR83, PRLHR, TACR3, NPY2R, OPRK1, F2RL1, OXTR, BDKRB2, HCRTR2, EDNRB, AGTR1, HCRTR1, CXCR4, GALR2, MC5R, XCR1, C5AR1, CCKBR, PROKR2, NPR1, PROKR1, NPR3, NTSR1, SSTR2, NK1R, AVPR1B, MC4R, AVPR1A, UTS2R, F2R, OPRD1	1232	82	4.45E-06
GOTERM_MF_FAT	GO:0042277~peptide binding	34	1.32	3.98E-07	GPR83, CALCR, PRLHR, TACR3, NPY2R, CRHBP, OPRK1, F2RL1, OXTR, BDKRB2, HCRTR2, EDNRB, AGTR1, HCRTR1, CXCR4, GALR2, MC5R, XCR1, KDELR1, C5AR1, CCKBR, PROKR2, NPR1, PROKR1, NPR3, NTSR1, SSTR2, NK1R, AVPR1B, MC4R, AVPR1A, UTS2R, F2R, OPRD1	1232	101	1.98E-05
Annotation Cluster 10 **Enrichment Score: 5.593557646836122**								
GOTERM_MF_FAT	GO:0005267~potassium channel activity	33	1.29	1.17E-07	KCNK17, KCNH1, KCNC1, KCNAB1, KCNA2, KCNA1, KCNA4, KCNJ10, KCNA6, KCNA5, KCNJ12, KCNIP3, SHKBP1, KCNS2, KCNQ3, KCNK6, KCNE1, KCNG3, KCNE4, KCNMA1, KCND2, KCNK1, KCNK2, KCNV1, KCNK4, KCTD8, KCNN4, KCNN1, KCNJ9, KCNN2, KCNF1, KCNH2, KCNH5	1232	92	6.15E-06
GOTERM_MF_FAT	GO:0005249~voltage-gated potassium channel activity	25	0.97	1.02E-05	KCNH1, KCNC1, KCNAB1, KCNA2, KCNA1, KCNA4, KCNJ10, KCNA6, KCNA5, KCNJ12, SHKBP1, KCNQ3, KCNS2, KCNE1, KCNG3, KCNE4, KCNMA1, KCND2, KCNK2, KCNV1, KCTD8, KCNJ9, KCNF1, KCNH2, KCNH5	1232	72	4.82E-04
GOTERM_BP_FAT	GO:0006813~potassium ion transport	32	1.25	1.39E-05	KCNK17, KCNH1, KCNC1, KCNAB1, KCNA2, KCNA1, KCNA4, KCNJ10, KCNA6, KCNA5, KCNJ12, KCNIP3, SHKBP1, KCNQ3, KCNS2, KCNK6, KCNE1, KCNG3, KCNE4, KCNMA1, KCND2, KCNK1, KCNK2, KCNV1, KCNK4, KCTD8, KCNN1, KCNJ9, KCNN2, KCNF1, KCNH2, KCNH5	1230	102	7.17E-04
Annotation Cluster 11 **Enrichment Score: 5.185949619099902**								
INTERPRO	IPR006201:Neurotransmitter-gated ion-channel	15	0.58	2.28E-06	GABRD, GABRA2, GLRB, GLRA1, GABRA4, LOC100138074, GABRB1, GABRA5, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	1185	28	4.62E-04
INTERPRO	IPR006202:Neurotransmitter-gated ion-channel ligand-binding	15	0.58	2.28E-06	GABRD, GABRA2, GLRB, GLRA1, GABRA4, LOC100138074, GABRB1, GABRA5, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	1185	28	4.62E-04
INTERPRO	IPR006029:Neurotransmitter-gated ion-channel transmembrane region	14	0.55	5.29E-06	GABRD, GABRA2, GLRB, GLRA1, GABRA4, GABRB1, GABRA5, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	1185	26	9.53E-04
INTERPRO	IPR018000:Neurotransmitter-gated ion-channel, conserved site	14	0.55	5.29E-06	GABRD, GABRA2, GLRB, GLRA1, GABRA4, GABRB1, GABRA5, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	1185	26	9.53E-04
SP_PIR_KEYWORDS	postsynaptic cell membrane	18	0.7	7.35E-06	GABRD, GABRA2, GLRB, GLRA1, GABRA4, GRIK1, GABRB1, CABP1, GABRA5, CAMK2N1, GRIA2, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	979	41	1.44E-04
PIR_SUPERFAMILY	PIRSF002443:acetylcholine receptor	12	0.47	7.16E-05	GLRB, GABRA2, GABRA4, GLRA1, GABRB1, GABRA5, CHRNA5, CHRNB4, CHRND, CHRNA7, CHRNA3, GABRP	556	22	0.01935007

Annotation Cluster 12 **Enrichment Score: 4.866990506119727**								
GOTERM_BP_FAT	GO:0048666~neuron development	34	1.32	9.69E-07	CCK, UCHL1, PAX6, GJA1, GDNF, HOXD10, LIF, EFHD1, ATOH1, SLC1A3, CXCR4, GALR2, LHX4, NEFL, LOC506110, NTF3, KIF5C, STXBP1, NTNG2, ISL1, AFG3L2, THY1, LEP, EPHA4, FEZF2, RND1, S100B, CLIC5, DLX5, CHRNB2, NGFR, CACNA1A, GAP43, GFRA3	1230	100	9.82E-05
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	25	0.97	1.66E-06	CCK, UCHL1, PAX6, ATOH1, SLC1A3, CXCR4, LHX4, NEFL, LOC506110, NTF3, KIF5C, STXBP1, NTNG2, AFG3L2, ISL1, EPHA4, FEZF2, S100B, CLIC5, DLX5, CHRNB2, NGFR, GAP43, CACNA1A, GFRA3	1230	63	1.48E-04
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	24	0.93	1.71E-06	LOC506110, CCK, NTF3, KIF5C, UCHL1, PAX6, STXBP1, NTNG2, GJA1, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, S100B, CXCR4, DLX5, LHX4, CHRNB2, NGFR, NEFL, CACNA1A, GAP43, GFRA3	1230	59	1.44E-04
GOTERM_BP_FAT	GO:0031175~neuron projection development	27	1.05	2.74E-06	CCK, UCHL1, PAX6, GJA1, GDNF, EFHD1, ATOH1, CXCR4, GALR2, LHX4, NEFL, LOC506110, NTF3, KIF5C, STXBP1, NTNG2, ISL1, AFG3L2, EPHA4, FEZF2, S100B, DLX5, CHRNB2, NGFR, GAP43, CACNA1A, GFRA3	1230	73	2.03E-04
GOTERM_BP_FAT	GO:0007409~axonogenesis	22	0.86	9.83E-06	LOC506110, CCK, NTF3, KIF5C, UCHL1, PAX6, STXBP1, NTNG2, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, S100B, CXCR4, DLX5, LHX4, CHRNB2, NGFR, NEFL, GAP43, GFRA3	1230	56	5.25E-04
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	24	0.93	1.16E-05	LOC506110, CCK, NTF3, KIF5C, UCHL1, PAX6, STXBP1, NTNG2, GJA1, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, S100B, CXCR4, DLX5, LHX4, CHRNB2, NGFR, NEFL, CACNA1A, GAP43, GFRA3	1230	65	6.07E-04
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	26	1.01	2.10E-05	CCK, UCHL1, PAX6, CRYGB, ATOH1, SLC1A3, CXCR4, LHX4, NEFL, LOC506110, NTF3, KIF5C, STXBP1, NTNG2, AFG3L2, ISL1, EPHA4, FEZF2, S100B, CLIC5, DLX5, CHRNB2, NGFR, GAP43, CACNA1A, GFRA3	1230	76	9.97E-04
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	24	0.93	5.84E-05	LOC506110, CCK, NTF3, KIF5C, UCHL1, PAX6, STXBP1, NTNG2, GJA1, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, S100B, CXCR4, DLX5, LHX4, CHRNB2, NGFR, NEFL, CACNA1A, GAP43, GFRA3	1230	71	0.00211325
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	30	1.17	2.11E-04	CCK, UCHL1, PAX6, GJA1, CRYGB, ATOH1, SLC1A3, CXCR4, LHX4, NEFL, LOC506110, NTF3, PDPN, KIF5C, STXBP1, NTNG2, UPK3A, ISL1, AFG3L2, EPHA4, FEZF2, S100B, DLX5, CLIC5, MAP7, CHRNB2, NGFR, CACNA1A, GAP43, GFRA3	1230	106	0.00587529
GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	32	1.25	9.66E-04	CCK, UCHL1, PAX6, GJA1, CD9, CRYGB, ATOH1, SLC1A3, CXCR4, LHX4, NEFL, LOC506110, ACTA1, NTF3, PDPN, KIF5C, STXBP1, NTNG2, UPK3A, ISL1, AFG3L2, EPHA4, FEZF2, S100B, DLX5, CLIC5, MAP7, CHRNB2, NGFR, CACNA1A, GAP43, GFRA3	1230	126	0.02201727
Annotation Cluster 13 **Enrichment Score: 4.820705305913005**								
INTERPRO	IPR000742:EGF-like, type 3	27	1.05	7.05E-06	PEAR1, PTGS2, LTBP2, NELL2, BCAN, DLK2, DLK1, PROZ, ACAN, TGFA, MRCL, NRG1, THBS2, THBS4, TMEFF2, TNXB, ADAM23, EFEMP1, NTNG2, EGFLAM, THBD, DLL4, MGC139448, VCAN, WIF1, AREG, VLDLR	1185	82	0.00114324
INTERPRO	IPR006210:EGF-like	28	1.09	7.41E-06	PEAR1, PTGS2, LTBP2, NELL2, ITGB5, BCAN, DLK2, DLK1, CSPG5, RSPO3, PROZ, TGFA, MRCL, NRG1, THBS2, THBS4, TMEFF2, TNXB, ADAM23, NTNG2, EGFLAM, THBD, DLL4, MGC139448, VCAN, WIF1, CLEC14A, VLDLR	1185	87	0.00109271
INTERPRO	IPR013032:EGF-like region,	33	1.29	1.17E-05	PEAR1, PTGS2, LTBP2, NELL2, ITGB5, BCAN, SPOCK1, DLK2, DLK1,	1185	114	0.001454

	conserved site				ITGB7, PROZ, ACAN, TGFA, MRCL, NRG1, THBS2, THBS4, TMEFF2, TNXB, ADAM23, EFEMP1, NTNG2, LAMA4, THBD, EGFLAM, MGC139448, DLL4, VCAN, WIF1, AREG, NGFR, CLEC14A, VLDLR			29
SMART	SM00181:EGF	28	1.09	8.55E-05	PEAR1, PTGS2, LTBP2, NELL2, ITGB5, BCAN, DLK2, DLK1, CSPG5, RSPO3, PROZ, TGFA, MRCL, NRG1, THBS2, THBS4, TMEFF2, TNXB, ADAM23, NTNG2, EGFLAM, THBD, DLL4, MGC139448, VCAN, WIF1, CLEC14A, VLDLR	649	87	0.005732 84
Annotation Cluster 14 **Enrichment Score: 4.785654654970917**								
GOTERM_BP _FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	61	2.38	1.68E-06	MYOD1, CDX1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, TGFB1, HOXD10, CRX, GLI1, ATOH1, GATA5, APOE, GATA3, EGR1, AR, RARG, RXRG, PRKCG, CD40, AHR, INHBA, ADRB2, HES5, GHRH, SIX1, MAPRE3, LOC281370, ADORA2B, ABLIM3, SOX2, FOXH1, LIF, T, MEIS2, HAND1, LOC510369, PTX3, NKX2-5, EPO, NKX2-3, BMP4, KLF5, BMP3, FOXL2, NTF3, EPAS1, FOXA1, MYF5, GSX1, ISL1, IRF6, ETS1, NEUROD1, EAF2, LOC654400, KLF4, F2R, NR5A1	1230	236	1.46E-04
GOTERM_BP _FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	59	2.3	2.85E-06	MYOD1, CDX1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, TGFB1, HOXD10, CRX, GLI1, ATOH1, GATA5, APOE, GATA3, EGR1, AR, RARG, RXRG, PRKCG, CD40, AHR, INHBA, ADRB2, HES5, GHRH, SIX1, MAPRE3, LOC281370, ADORA2B, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, NKX2-5, EPO, NKX2-3, BMP4, KLF5, BMP3, FOXL2, NTF3, EPAS1, FOXA1, MYF5, GSX1, ISL1, IRF6, ETS1, NEUROD1, EAF2, LOC654400, KLF4, F2R, NR5A1	1230	229	2.07E-04
GOTERM_BP _FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	42	1.64	6.78E-06	MYOD1, CDX1, HNF1B, ABLIM3, SOX2, PAX6, PAX3, GDNF, HOXD10, GLI1, CRX, LIF, FOXH1, T, ATOH1, MEIS2, HAND1, GATA3, NKX2-5, NKX2-3, BMP4, BMP3, AR, FOXL2, RARG, NTF3, EPAS1, MYF5, FOXA1, GSX1, RXRG, ISL1, AHR, INHBA, ADRB2, HES5, ETS1, SIX1, NEUROD1, LOC654400, KLF4, NR5A1	1230	147	4.12E-04
GOTERM_BP _FAT	GO:0010628~positive regulation of gene expression	55	2.14	8.15E-06	MYOD1, CDX1, HNF1B, GDF6, PAX6, PAX3, GDNF, HOXD10, TGFB1, GLI1, CRX, ATOH1, GATA5, GATA3, EGR1, AR, RARG, RXRG, AHR, INHBA, ADRB2, TNFSF13B, HES5, SIX1, MAPRE3, LOC281370, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, NKX2-5, EPO, NKX2-3, BMP4, KLF5, BMP3, FOXL2, NTF3, EPAS1, FOXA1, MYF5, GSX1, ISL1, CDH13, IRF6, ETS1, NEUROD1, EAF2, LOC654400, KLF4, F2R, NR5A1	1230	215	4.77E-04
GOTERM_BP _FAT	GO:0045941~positive regulation of transcription	53	2.06	8.85E-06	MYOD1, CDX1, HNF1B, GDF6, PAX6, PAX3, GDNF, HOXD10, TGFB1, GLI1, CRX, ATOH1, GATA5, GATA3, EGR1, AR, RARG, RXRG, AHR, INHBA, ADRB2, HES5, SIX1, MAPRE3, LOC281370, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, NKX2-5, EPO, NKX2-3, BMP4, KLF5, BMP3, FOXL2, EPAS1, NTF3, FOXA1, MYF5, GSX1, ISL1, IRF6, ETS1, NEUROD1, EAF2, LOC654400, KLF4, F2R, NR5A1	1230	205	4.89E-04
GOTERM_BP _FAT	GO:0045893~positive regulation of transcription, DNA-dependent	46	1.79	1.52E-05	MYOD1, CDX1, HNF1B, ABLIM3, SOX2, PAX6, PAX3, GDNF, HOXD10, TGFB1, GLI1, CRX, FOXH1, LIF, T, ATOH1, MEIS2, HAND1, GATA3, NKX2-5, NKX2-3, EPO, BMP4, BMP3, FOXL2, AR, RARG, NTF3, EPAS1, MYF5, FOXA1, GSX1, RXRG, ISL1, AHR, INHBA, ADRB2, HES5, ETS1, SIX1, NEUROD1, LOC654400, MAPRE3, KLF4, F2R, NR5A1	1230	172	7.70E-04
GOTERM_BP	GO:0051254~positive	46	1.79	1.52E-05	MYOD1, CDX1, HNF1B, ABLIM3, SOX2, PAX6, PAX3, GDNF, HOXD10,	1230	172	7.70E-04

_FAT	regulation of RNA metabolic process				TGFB1, GLI1, CRX, FOXH1, LIF, T, ATOH1, MEIS2, HAND1, GATA3, NKX2-5, NKX2-3, EPO, BMP4, BMP3, FOXL2, AR, RARG, NTF3, EPAS1, MYF5, FOXA1, GSX1, RXRG, ISL1, AHR, INHBA, ADRB2, HES5, ETS1, SIX1, NEUROD1, LOC654400, MAPRE3, KLF4, F2R, NR5A1			
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	69	2.69	4.30E-05	MYOD1, CDX1, HNF1B, PDGFA, GDF6, SNCA, PAX6, GJA1, PAX3, GDNF, TGFB1, HOXD10, CRX, GLI1, AGTR1, ATOH1, GATA5, APOE, GATA3, SYK, EGR1, PRKCA, AR, RARG, RXRG, PRKCG, CD40, AHR, INHBA, CARD11, CCND1, ADRB2, TNFSF13B, HES5, CCND2, SIX1, MAPRE3, LOC281370, FGFR3, ABLIM3, SOX2, FOXH1, LIF, T, MEIS2, HAND1, NKX2-5, EPO, NKX2-3, BMP4, KLF5, BMP3, FOXL2, NTF3, EPAS1, FOXA1, MYF5, GSX1, ISL1, CDH13, S100B, IRF6, ETS1, NEUROD1, EAF2, LOC654400, KLF4, F2R, NR5A1	1230	305	0.00176503
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	60	2.34	5.72E-05	MYOD1, CDX1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, TGFB1, HOXD10, CRX, GLI1, ATOH1, GATA5, APOE, GATA3, SYK, EGR1, AR, RARG, RXRG, AHR, CARD11, INHBA, ADRB2, HES5, GHRH, SIX1, MAPRE3, LOC281370, ADORA2B, ABLIM3, SOX2, FOXH1, LIF, T, MEIS2, HAND1, PTX3, NKX2-5, EPO, NKX2-3, BMP4, KLF5, BMP3, FOXL2, NTF3, EPAS1, FOXA1, MYF5, GSX1, ISL1, IRF6, ETS1, NEUROD1, EAF2, LOC654400, KLF4, F2R, NR5A1	1230	257	0.00217396
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	60	2.34	8.11E-05	MYOD1, CDX1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, TGFB1, HOXD10, CRX, GLI1, ATOH1, GATA5, APOE, GATA3, SYK, EGR1, AR, RARG, RXRG, AHR, CARD11, INHBA, ADRB2, HES5, GHRH, SIX1, MAPRE3, LOC281370, ADORA2B, ABLIM3, SOX2, FOXH1, LIF, T, MEIS2, HAND1, PTX3, NKX2-5, EPO, NKX2-3, BMP4, KLF5, BMP3, FOXL2, NTF3, EPAS1, FOXA1, MYF5, GSX1, ISL1, IRF6, ETS1, NEUROD1, EAF2, LOC654400, KLF4, F2R, NR5A1	1230	260	0.00280008
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	56	2.18	2.11E-04	MYOD1, CDX1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, TGFB1, HOXD10, GLI1, CRX, ATOH1, GATA5, GATA3, SYK, EGR1, AR, RARG, RXRG, AHR, CARD11, INHBA, ADRB2, HES5, SIX1, MAPRE3, LOC281370, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, NKX2-5, EPO, NKX2-3, BMP4, KLF5, BMP3, FOXL2, NTF3, EPAS1, FOXA1, MYF5, GSX1, ISL1, IRF6, ETS1, NEUROD1, EAF2, LOC654400, KLF4, F2R, NR5A1	1230	246	0.00591941
Annotation Cluster 15 **Enrichment Score: 4.73282584958233**								
SP_PIR_KEYWORDS	potassium channel	13	0.51	1.30E-06	KCNH1, KCNMA1, KCNC1, KCNA2, KCNA4, KCNA5, KCNK1, KCNV1, KCNIP3, KCNQ3, KCNE1, KCNF1, KCNE4	979	20	2.93E-05
SP_PIR_KEYWORDS	potassium transport	16	0.62	1.57E-05	KCNH1, KCNMA1, KCNC1, KCNAB1, KCNA2, KCNA4, KCNJ10, KCNA5, KCNK1, KCNJ12, KCNV1, KCNIP3, KCNQ3, KCNE1, KCNF1, KCNE4	979	35	2.83E-04
GOTERM_MF_FAT	GO:0030955~potassium ion binding	18	0.7	6.16E-05	KCNMA1, KCNH1, KCNC1, KCNAB1, KCNA2, KCNA4, KCNJ10, KCNA5, KCNK1, KCNJ12, GMPR, KCNV1, KCNIP3, KCNQ3, PKLR, KCNE1, KCNF1, KCNE4	1232	47	0.00250756
SP_PIR_KEYWORDS	potassium	17	0.66	9.26E-05	KCNMA1, KCNH1, KCNC1, KCNAB1, KCNA2, KCNA4, KCNJ10, KCNA5, KCNK1, KCNJ12, GMPR, KCNV1, KCNIP3, KCNQ3, KCNE1, KCNF1, KCNE4	979	44	0.00134315
Annotation Cluster 16 **Enrichment Score: 4.617880851622108**								

GOTERM_BP_FAT	GO:0001944~vasculature development	37	1.44	4.98E-06	FGFR2, FGF18, CDX2, PDGFA, EDN1, GJA1, CDH2, GJA4, SHH, T, TCF21, HEY1, HAND1, APOE, CXCR4, TGFA, SOX18, LOX, ADRA2B, NR2F2, ANGPT2, NKX2-5, BMP4, KLF5, EPAS1, PDPN, ITGA4, TNNI3, KDR, THY1, CDH13, PROK2, LAMA4, MEOX2, DLL4, COL1A2, COL1A1	1230	121	3.22E-04
GOTERM_BP_FAT	GO:0001568~blood vessel development	35	1.36	1.93E-05	FGFR2, FGF18, CDX2, PDGFA, EDN1, GJA1, CDH2, GJA4, SHH, T, HEY1, HAND1, APOE, CXCR4, TGFA, SOX18, LOX, ADRA2B, NR2F2, ANGPT2, NKX2-5, KLF5, BMP4, EPAS1, ITGA4, TNNI3, KDR, THY1, CDH13, PROK2, LAMA4, MEOX2, DLL4, COL1A2, COL1A1	1230	118	9.47E-04
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	29	1.13	1.46E-04	FGFR2, FGF18, PDGFA, EDN1, GJA1, CDH2, SHH, T, HEY1, HAND1, APOE, CXCR4, TGFA, SOX18, ADRA2B, NR2F2, ANGPT2, NKX2-5, KLF5, BMP4, EPAS1, ITGA4, TNNI3, KDR, THY1, CDH13, PROK2, MEOX2, DLL4	1230	99	0.00442632
Annotation Cluster 17 **Enrichment Score: 4.485258720861838**								
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	14	0.55	2.16E-06	CALCR, PTGER3, ADORA2B, PTH1R, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, APOE, GHRH, TSHR	1230	23	1.73E-04
GOTERM_BP_FAT	GO:0007188~G-protein signaling, coupled to cAMP nucleotide second messenger	13	0.51	4.61E-06	CALCR, PTGER3, ADORA2B, PTH1R, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, GHRH, TSHR	1230	21	3.12E-04
GOTERM_BP_FAT	GO:0007187~G-protein signaling, coupled to cyclic nucleotide second messenger	13	0.51	4.61E-06	CALCR, PTGER3, ADORA2B, PTH1R, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, GHRH, TSHR	1230	21	3.12E-04
GOTERM_BP_FAT	GO:0010578~regulation of adenylate cyclase activity involved in G-protein signaling	10	0.39	8.39E-06	CALCR, ADRB3, GNAL, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	13	4.73E-04
GOTERM_BP_FAT	GO:0010579~positive regulation of adenylate cyclase activity by G-protein signaling pathway	10	0.39	8.39E-06	CALCR, ADRB3, GNAL, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	13	4.73E-04
GOTERM_BP_FAT	GO:0007189~activation of adenylate cyclase activity by G-protein signaling pathway	10	0.39	8.39E-06	CALCR, ADRB3, GNAL, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	13	4.73E-04
GOTERM_BP_FAT	GO:0019933~cAMP-mediated signaling	13	0.51	8.86E-06	CALCR, PTGER3, ADORA2B, PTH1R, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, GHRH, TSHR	1230	22	4.81E-04
GOTERM_BP_FAT	GO:0007190~activation of adenylate cyclase activity	10	0.39	2.06E-05	CALCR, ADRB3, GNAL, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	14	9.93E-04
GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	19	0.74	3.03E-05	CALCR, CASR, PTGER3, ADORA2B, EDN2, EDN1, PTH1R, AGTR1, ADRB3, GNAL, S1PR3, ADRB2, SSTR2, UCN3, ADRB1, APOE, GHRH, CA8, TSHR	1230	47	0.00135329
GOTERM_BP_FAT	GO:0045761~regulation of adenylate cyclase activity	12	0.47	3.52E-05	CALCR, ADRB3, S1PR3, GNAL, SSTR2, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	21	0.00154954
GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	14	0.55	3.57E-05	CALCR, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, PDE2A, GHRH, TSHR	1230	28	0.00154877
GOTERM_BP_FAT	GO:0045762~positive regulation of adenylate	10	0.39	4.51E-05	CALCR, ADRB3, GNAL, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	15	0.00180172

	cyclase activity							
GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	13	0.51	4.74E-05	CALCR, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, GHRH, TSHR	1230	25	0.00187247
GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	14	0.55	8.69E-05	CALCR, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, APOE, GHRH, TSHR	1230	30	0.00296599
GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	14	0.55	8.69E-05	CALCR, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, APOE, GHRH, TSHR	1230	30	0.00296599
GOTERM_BP_FAT	GO:0031281~positive regulation of cyclase activity	10	0.39	9.02E-05	CALCR, ADRB3, GNAL, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	16	0.00304439
GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	15	0.58	9.17E-05	CALCR, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, PDE2A, APOE, GHRH, TSHR	1230	34	0.00306094
GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	15	0.58	1.33E-04	CALCR, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB2, ADRB1, PDE2A, APOE, GHRH, TSHR	1230	35	0.00408921
GOTERM_BP_FAT	GO:0031279~regulation of cyclase activity	12	0.47	1.66E-04	CALCR, ADRB3, S1PR3, GNAL, SSTR2, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	24	0.00494752
GOTERM_BP_FAT	GO:0051349~positive regulation of lyase activity	10	0.39	2.94E-04	CALCR, ADRB3, GNAL, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	18	0.00782491
GOTERM_BP_FAT	GO:0051339~regulation of lyase activity	12	0.47	3.94E-04	CALCR, ADRB3, S1PR3, GNAL, SSTR2, ADRB2, UCN3, ADRB1, ADORA2B, GHRH, PTH1R, TSHR	1230	26	0.01018527
Annotation Cluster 18 **Enrichment Score: 4.3624918520918605**								
INTERPRO	IPR001839:Transforming growth factor beta	11	0.43	1.02E-05	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, BMP7, GDNF, TGFB1	1185	17	0.00137741
SMART	SM00204:TGFB	11	0.43	3.52E-05	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, BMP7, GDNF, TGFB1	649	17	0.00315406
INTERPRO	IPR015615:Transforming growth factor-beta-related	10	0.39	4.72E-05	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, BMP7, TGFB1	1185	16	0.00477384
INTERPRO	IPR017948:Transforming growth factor beta, conserved site	9	0.35	2.09E-04	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, TGFB1	1185	15	0.01682853
Annotation Cluster 19 **Enrichment Score: 4.182775871040769**								
GOTERM_MF_FAT	GO:0005539~glycosaminoglycan binding	21	0.82	1.75E-05	BMP4, HAPLN2, LPL, HAPLN1, HAPLN4, HAPLN3, TNXB, CXCL5, PGLYRP1, TLR2, BCAN, PF4, LYVE1, EGFLAM, APOE, CRISPLD2, RSPO3, ACAN, PTN, VCAN, THBS2	1232	56	7.47E-04
GOTERM_MF_FAT	GO:0001871~pattern binding	22	0.86	1.27E-04	HAPLN2, BMP4, LPL, HAPLN1, HAPLN4, HAPLN3, TNXB, CXCL5, PGLYRP1, TLR2, BCAN, PF4, LYVE1, EGFLAM, APOE, CRISPLD2, RSPO3, ACAN, PTN, VCAN, PTX3, THBS2	1232	68	0.00436983
GOTERM_MF_FAT	GO:0030247~polysaccharide binding	22	0.86	1.27E-04	HAPLN2, BMP4, LPL, HAPLN1, HAPLN4, HAPLN3, TNXB, CXCL5, PGLYRP1, TLR2, BCAN, PF4, LYVE1, EGFLAM, APOE, CRISPLD2, RSPO3, ACAN, PTN, VCAN, PTX3, THBS2	1232	68	0.00436983
Annotation Cluster 20								

Enrichment Score: 4.044949671500718								
INTERPRO	IPR000742:EGF-like, type 3	27	1.05	7.05E-06	PEAR1, PTGS2, LTBP2, NELL2, BCAN, DLK2, DLK1, PROZ, ACAN, TGFA, MRCL, NRG1, THBS2, THBS4, TMEFF2, TNXB, ADAM23, EFEMP1, NTNG2, EGFLAM, THBD, DLL4, MGC139448, VCAN, WIF1, AREG, VLDLR	1185	82	0.00114324
INTERPRO	IPR006209:EGF	20	0.78	1.72E-05	TMEFF2, PTGS2, LTBP2, NTNG2, BCAN, DLK2, DLK1, THBD, EGFLAM, DLL4, PROZ, ACAN, TGFA, VCAN, WIF1, AREG, NRG1, THBS2, VLDLR, THBS4	1185	53	0.00198883
SP_PIR_KEYWORDS	egf-like domain	21	0.82	0.006049	TMEFF2, TNXB, LTBP2, NELL2, EFEMP1, BCAN, DLK2, DLK1, THBD, EGFLAM, DLL4, PROZ, ACAN, TGFA, VCAN, WIF1, AREG, NRG1, THBS2, VLDLR, THBS4	979	84	0.07504902
Annotation Cluster 21 **Enrichment Score: 3.9489232478152796**								
GOTERM_BP_FAT	GO:0060541~respiratory system development	19	0.74	5.80E-05	LOC790682, FGFR2, BMP4, FGF18, FGFR4, EPAS1, PDPN, PDGFA, FOXA1, SOX2, GLI1, KDR, PTHLH, TCF21, PDGFRA, HOPX, LOX, CUX1, LOC654400	1230	49	0.00215096
GOTERM_BP_FAT	GO:0030324~lung development	18	0.7	1.57E-04	LOC790682, FGFR2, BMP4, FGF18, FGFR4, EPAS1, PDPN, PDGFA, FOXA1, GLI1, KDR, PTHLH, TCF21, PDGFRA, HOPX, LOX, CUX1, LOC654400	1230	48	0.00470536
GOTERM_BP_FAT	GO:0030323~respiratory tube development	18	0.7	1.57E-04	LOC790682, FGFR2, BMP4, FGF18, FGFR4, EPAS1, PDPN, PDGFA, FOXA1, GLI1, KDR, PTHLH, TCF21, PDGFRA, HOPX, LOX, CUX1, LOC654400	1230	48	0.00470536
Annotation Cluster 22 **Enrichment Score: 3.926639528548549**								
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	21	0.82	6.52E-05	IRX3, DTX1, FOXA1, SOX2, PAX6, ISL1, GLI1, THY1, METRN, DLX1, ATOH1, HES5, LOC787355, SIX1, LHX5, CHRNB2, GHSR, NKX2-5, NEFL, CACNA1A, MT3	1230	58	0.00230338
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	16	0.62	9.23E-05	IRX3, DTX1, SOX2, FOXA1, PAX6, ISL1, THY1, ATOH1, METRN, HES5, LOC787355, SIX1, CHRNB2, NKX2-5, NEFL, CACNA1A	1230	38	0.00304718
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	18	0.7	2.76E-04	IRX3, DTX1, SOX2, FOXA1, PAX6, ISL1, THY1, DLX1, ATOH1, METRN, HES5, LOC787355, SIX1, CHRNB2, NKX2-5, NEFL, CACNA1A, MT3	1230	50	0.00746613
Annotation Cluster 23 **Enrichment Score: 3.242013610386458**								
GOTERM_BP_FAT	GO:0003018~vascular process in circulatory system	13	0.51	5.73E-04	CASR, ADORA2B, EDN2, EDN1, LOC784945, ADRB3, CALCB, EDNRB, ECE2, ADRB2, ADRB1, APOE, NPPC	1230	31	0.01384637
GOTERM_BP_FAT	GO:0035150~regulation of tube size	13	0.51	5.73E-04	CASR, ADORA2B, EDN2, EDN1, LOC784945, ADRB3, CALCB, EDNRB, ECE2, ADRB2, ADRB1, APOE, NPPC	1230	31	0.01384637
GOTERM_BP_FAT	GO:0050880~regulation of blood vessel size	13	0.51	5.73E-04	CASR, ADORA2B, EDN2, EDN1, LOC784945, ADRB3, CALCB, EDNRB, ECE2, ADRB2, ADRB1, APOE, NPPC	1230	31	0.01384637
Annotation Cluster 24 **Enrichment Score: 3.204477505607967**								
GOTERM_MF_FAT	GO:0005540~hyaluronic acid binding	8	0.31	3.13E-04	HAPLN2, HAPLN1, HAPLN4, LYVE1, HAPLN3, ACAN, BCAN, VCAN	1232	12	0.0096165
INTERPRO	IPR000538:Link	7	0.27	6.04E-04	HAPLN2, HAPLN1, LYVE1, HAPLN3, ACAN, BCAN, VCAN	1185	10	0.03844392
SMART	SM00445:LINK	7	0.27	0.001289	HAPLN2, HAPLN1, LYVE1, HAPLN3, ACAN, BCAN, VCAN	649	10	0.06705613

Annotation Cluster 25 **Enrichment Score: 3.091617934927488**								
SP_PIR_KEYWORDS	chloride channel	11	0.43	8.68E-05	GLRB, GABRA2, GABRA4, GLRA1, CLIC5, GABRB1, TTYH1, GABRA5, CFTR, ANO4, GABRP	979	20	0.00134585
GOTERM_CC_FAT	GO:0034707~chloride channel complex	11	0.43	1.03E-04	GLRB, GABRA2, GABRA4, GLRA1, CLIC5, GABRB1, TTYH1, GABRA5, CFTR, ANO4, GABRP	947	20	0.00220122
SP_PIR_KEYWORDS	chloride	11	0.43	3.68E-04	GLRB, GABRA2, GABRA4, GLRA1, CLIC5, GABRB1, TTYH1, GABRA5, CFTR, ANO4, GABRP	979	23	0.00500942
GOTERM_MF_FAT	GO:0031404~chloride ion binding	11	0.43	5.60E-04	GLRB, GABRA2, GABRA4, GLRA1, CLIC5, GABRB1, TTYH1, GABRA5, CFTR, ANO4, GABRP	1232	24	0.01659293
GOTERM_MF_FAT	GO:0043168~anion binding	12	0.47	0.001469	GLRB, GABRA2, G6PC, GABRA4, GLRA1, CLIC5, GABRB1, TTYH1, GABRA5, CFTR, ANO4, GABRP	1232	31	0.03912634
GOTERM_MF_FAT	GO:0005254~chloride channel activity	13	0.51	0.005657	GABRA2, GLRB, GLRA1, GABRA4, GABRB1, GABRA5, CFTR, SLC26A8, CLIC5, TTYH1, ANO4, CLCN5, GABRP	1232	41	0.1090974
GOTERM_MF_FAT	GO:0005253~anion channel activity	13	0.51	0.014868	GABRA2, GLRB, GLRA1, GABRA4, GABRB1, GABRA5, CFTR, SLC26A8, CLIC5, TTYH1, ANO4, CLCN5, GABRP	1232	46	0.22748922
Annotation Cluster 26 **Enrichment Score: 2.917937282913537**								
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	23	0.9	3.39E-04	PRKCA, ICAM1, LOC785455, HS3ST5, PDGFB, PDGFA, MMP9, EDN2, SNCA, F2RL1, PAX6, ITGB3, THY1, KDR, CDH13, LAMA4, APOE, CXCR4, DLL4, CXCL16, TSHR, SST, F2R	1230	74	0.00893906
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	19	0.74	0.001891	ICAM1, LOC785455, PDGFB, PDGFA, MMP9, EDN2, F2RL1, PAX6, ITGB3, THY1, KDR, CDH13, LAMA4, APOE, CXCR4, DLL4, CXCL16, SST, F2R	1230	63	0.0391969
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	20	0.78	0.002747	ICAM1, LOC785455, PDGFB, PDPN, PDGFA, MMP9, EDN2, F2RL1, PAX6, ITGB3, THY1, KDR, CDH13, LAMA4, APOE, CXCR4, DLL4, CXCL16, SST, F2R	1230	70	0.05287823
Annotation Cluster 27 **Enrichment Score: 2.7331708488118642**								
INTERPRO	IPR018933:Netrin module, non-TIMP type	7	0.27	6.04E-04	SFRP5, SFRP1, C3, SFRP2, SFRP4, FRZB, PCOLCE2	1185	10	0.03844392
SMART	SM00643:C345C	7	0.27	0.001289	SFRP5, SFRP1, C3, SFRP2, SFRP4, FRZB, PCOLCE2	649	10	0.06705613
INTERPRO	IPR001134:Netrin domain	7	0.27	0.008111	SFRP5, SFRP1, C3, SFRP2, SFRP4, FRZB, PCOLCE2	1185	15	0.2593353
Annotation Cluster 28 **Enrichment Score: 2.6807933708202594**								
GOTERM_CC_FAT	GO:0005624~membrane fraction	45	1.75	9.91E-04	GAL3ST4, JPH2, GLRA1, PTGS2, SNCB, SNCA, ACSBG2, ATP6V1B1, APLP1, ADRB3, SLC2A4, RASGRP4, PTGES, HMOX1, RASGRP2, HSD17B6, CHRNA7, NT5E, SNAP25, PRKCA, LOC790682, MOGAT1, GLRB, STX1A, CYP1A1, CCKBR, CPNE6, ITGA3, ITPR3, CAMK2N1, BCL2L11, ITPR1, SLC17A7, CD38, SSTR2, ADRB2, G6PC, ADRB1, SLC17A6, DGAT1, CLIC5, HSD11B2, SLC13A3, VAMP1, GRB14	947	204	0.01641153
GOTERM_CC_FAT	GO:0005626~insoluble fraction	45	1.75	0.002221	GAL3ST4, JPH2, GLRA1, PTGS2, SNCB, SNCA, ACSBG2, ATP6V1B1, APLP1, ADRB3, SLC2A4, RASGRP4, PTGES, HMOX1, RASGRP2, HSD17B6, CHRNA7, NT5E, SNAP25, PRKCA, LOC790682, MOGAT1,	947	212	0.02900643

					GLRB, STX1A, CYP1A1, CCKBR, CPNE6, ITGA3, ITPR3, CAMK2N1, BCL2L11, ITPR1, SLC17A7, CD38, SSTR2, ADRB2, G6PC, ADRB1, SLC17A6, DGAT1, CLIC5, HSD11B2, SLC13A3, VAMP1, GRB14			
GOTERM_CC_FAT	GO:0000267~cell fraction	48	1.87	0.004123	GAL3ST4, JPH2, GLRA1, PTGS2, SNCB, SNCA, ACSBG2, ATP6V1B1, APLP1, PCSK2, ADRB3, SLC2A4, RASGRP4, PTGES, HMOX1, RASGRP2, HSD17B6, CHRNA7, NT5E, SNAP25, PRKCA, LOC790682, MOGAT1, GLRB, STX1A, CYP1A1, CCKBR, CPNE6, ITGA3, ITPR3, PKIA, CAMK2N1, BCL2L11, ITPR1, SLC17A7, CD38, SSTR2, ADRB2, G6PC, ADRB1, SLC17A6, DGAT1, TPPP, CLIC5, HSD11B2, SLC13A3, VAMP1, GRB14	947	237	0.05151334

Annotation Cluster 29
Enrichment Score: 2.6115526569903538

GOTERM_CC_FAT	GO:0005923~tight junction	15	0.58	6.56E-04	PRKCZ, CLDN7, F11R, PARD3, OCLN, CLDN9, CLDN4, CLDN3, CLDN6, CLDN5, CLDN10, CLDN11, CLDN23, CLDN1, LOC536606	947	41	0.01193367
GOTERM_CC_FAT	GO:0070160~occluding junction	15	0.58	6.56E-04	PRKCZ, CLDN7, F11R, PARD3, OCLN, CLDN9, CLDN4, CLDN3, CLDN6, CLDN5, CLDN10, CLDN11, CLDN23, CLDN1, LOC536606	947	41	0.01193367
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	16	0.62	0.006345	PRKCZ, F11R, CLDN7, PARD3, OCLN, CLDN9, CLDN4, CLDN3, CLDN6, CLDN5, CLDN10, CLDN11, CLDN23, FZD6, CLDN1, LOC536606	947	56	0.06074852
GOTERM_CC_FAT	GO:0043296~apical junction complex	15	0.58	0.013095	PRKCZ, CLDN7, F11R, PARD3, OCLN, CLDN9, CLDN4, CLDN3, CLDN6, CLDN5, CLDN10, CLDN11, CLDN23, CLDN1, LOC536606	947	55	0.11354025

Annotation Cluster 30
Enrichment Score: 2.5848272376399577

GOTERM_MF_FAT	GO:0004955~prostaglandin receptor activity	6	0.23	0.001636	PTGER3, PTGER4, PTGDR, LOC781367, PTGFR, HPGD	1232	8	0.04106147
GOTERM_MF_FAT	GO:0004953~icosanoid receptor activity	6	0.23	0.003279	PTGER3, PTGER4, PTGDR, LOC781367, PTGFR, HPGD	1232	9	0.0726901
GOTERM_MF_FAT	GO:0004954~prostanoid receptor activity	6	0.23	0.003279	PTGER3, PTGER4, PTGDR, LOC781367, PTGFR, HPGD	1232	9	0.0726901

Annotation Cluster 31
Enrichment Score: 2.530668426882812

INTERPRO	IPR000008:C2 calcium-dependent membrane targeting	15	0.58	0.001805	PRKCA, CPNE8, CPNE9, SYT1, SYT5, CPNE6, PRKCH, PRKCG, RPH3A, RIMS2, PRKCB, CADPS, DOC2A, CADPS2, SYT13	1185	47	0.0902185
INTERPRO	IPR018029:C2 membrane targeting protein	13	0.51	0.002181	CPNE8, PRKCA, CPNE9, SYT1, SYT5, CPNE6, PRKCH, PRKCG, RIMS2, RPH3A, PRKCB, DOC2A, SYT13	1185	38	0.1047829
SMART	SM00239:C2	15	0.58	0.006497	PRKCA, CPNE8, CPNE9, SYT1, SYT5, CPNE6, PRKCH, PRKCG, RPH3A, RIMS2, PRKCB, CADPS, DOC2A, CADPS2, SYT13	649	47	0.17700694

Annotation Cluster 32
Enrichment Score: 2.4996825403757463

GOTERM_BP_FAT	GO:0009914~hormone transport	10	0.39	4.90E-04	LEP, CPLX3, HNF1B, LY6E, GHRH, EDN1, MC4R, GHSR, FKBP1B, CRYM	1230	19	0.01195716
GOTERM_BP_FAT	GO:0030072~peptide hormone secretion	8	0.31	0.002373	LEP, CPLX3, HNF1B, GHRH, EDN1, MC4R, GHSR, FKBP1B	1230	15	0.04703487
GOTERM_BP_FAT	GO:0002790~peptide secretion	8	0.31	0.003714	LEP, CPLX3, HNF1B, GHRH, EDN1, MC4R, GHSR, FKBP1B	1230	16	0.06748301
GOTERM_BP	GO:0046879~hormone	8	0.31	0.00556	LEP, CPLX3, HNF1B, GHRH, EDN1, MC4R, GHSR, FKBP1B	1230	17	0.090895

_FAT	secretion			1				33
GOTERM_BP_FAT	GO:0015833~peptide transport	9	0.35	0.013213	LEP, CPLX3, HNF1B, GHRH, TAP1, EDN1, MC4R, GHSR, FKBP1B	1230	24	0.17374625

Annotation Cluster 33
Enrichment Score: 2.445141953693394

GOTERM_CC_FAT	GO:0034704~calcium channel complex	8	0.31	0.001197	CACNA2D1, CACNA1G, CACNA1E, CACNB3, CACNB4, FKBP1B, CACNA1D, CACNA1A	947	14	0.01823067
GOTERM_CC_FAT	GO:0005891~voltage-gated calcium channel complex	7	0.27	0.004521	CACNA2D1, CACNA1G, CACNA1E, CACNB3, CACNB4, CACNA1D, CACNA1A	947	13	0.05135959
GOTERM_MF_FAT	GO:0005245~voltage-gated calcium channel activity	8	0.31	0.008535	CACNA2D1, CACNA1G, CACNA1E, CACNB3, CACNG2, CACNB4, CACNA1D, CACNA1A	1232	19	0.15075884

Annotation Cluster 34
Enrichment Score: 2.4403597803093837

GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	28	1.09	4.08E-05	CDX2, FST, SOX2, CBX2, PAX3, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, TLE4, PKIA, DLX1, MSX1, ID2, HES5, ID1, HOPX, CUX1, CRYM	1230	88	0.0017222
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-dependent	32	1.25	3.95E-04	SBNO2, CDX2, SOX2, FST, CBX2, PAX3, ZBTB16, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, DLX1, MSX1, ID2, HES5, ID1, HOPX, CUX1, CRYM	1230	120	0.01014472
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	32	1.25	4.62E-04	SBNO2, CDX2, SOX2, FST, CBX2, PAX3, ZBTB16, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, DLX1, MSX1, ID2, HES5, ID1, HOPX, CUX1, CRYM	1230	121	0.01136371
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	35	1.36	0.004429	SBNO2, CDX2, SOX2, FST, HR, CBX2, PAX3, ZBTB16, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, CUX1, CRYM	1230	155	0.07678628
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	41	1.6	0.007296	SBNO2, CDX2, PDGFA, SOX2, EDN1, FST, HR, CBX2, PAX3, ZBTB16, ITGB3, KCNIP3, FOXH1, VDR, HAND1, APOE, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, INHBB, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, CUX1, CACNA1A, CRYM	1230	195	0.10953606
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	36	1.4	0.00753	SBNO2, CDX2, SOX2, EDN1, FST, HR, CBX2, PAX3, ZBTB16, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, CUX1, CRYM	1230	166	0.11231033
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic process	36	1.4	0.009099	SBNO2, CDX2, SOX2, EDN1, FST, HR, CBX2, PAX3, ZBTB16, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, CUX1, CRYM	1230	168	0.13163592
GOTERM_BP_FAT	GO:0010629~negative regulation of gene expression	36	1.4	0.010929	SBNO2, CDX2, SOX2, FST, HR, CBX2, PAX3, ZBTB16, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, BMP4, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, NR1I3, DLX1,	1230	170	0.15182825

					MSX1, HES5, ID2, ID1, PRDM6, HOPX, CUX1, CRYM			
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	39	1.52	0.012117	SBNO2, CDX2, PDGFA, SOX2, EDN1, FST, HR, CBX2, PAX3, ZBTB16, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, INHBB, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, CUX1, CACNA1A, CRYM	1230	189	0.1625937
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	38	1.48	0.015519	SBNO2, CDX2, SOX2, EDN1, FST, HR, CBX2, PAX3, ZBTB16, ITGB3, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, EGR1, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PKIA, INHBB, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, CUX1, CRYM	1230	186	0.19527054
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	43	1.67	0.042241	SBNO2, CDX2, SOX2, EDN1, SNCA, FST, HR, CBX2, PAX3, ZBTB16, ITGB3, BDKRB2, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, TWIST2, NR2F1, PRKCA, EGR1, BMP4, SATB1, NANOG, RARG, FOXA1, NDUFA13, TLE4, PRKCG, PKIA, INHBB, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, CUX1, CRYM	1230	231	0.40241949
Annotation Cluster 35 **Enrichment Score: 2.423278225785902**								
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	30	1.17	0.002131	BMI1, CALCR, CD8A, SFXN1, CACNB4, ZBTB16, TGFB1, BCL11A, HOXA9, NKX2-5, NKX2-3, SYK, EPO, EGR1, BMP4, SATB1, EPAS1, CD3D, IL7, OSTM1, BCL2L11, KDR, CARD11, HOXB7, ID2, SIX1, IRF8, CD79A, KLF1, TSHR	1230	121	0.04318329
GOTERM_BP_FAT	GO:0002520~immune system development	31	1.21	0.003758	BMI1, CALCR, NBN, CD8A, SFXN1, CACNB4, ZBTB16, TGFB1, BCL11A, HOXA9, NKX2-5, NKX2-3, SYK, EPO, EGR1, BMP4, SATB1, EPAS1, CD3D, IL7, OSTM1, BCL2L11, KDR, CARD11, HOXB7, ID2, SIX1, IRF8, CD79A, KLF1, TSHR	1230	131	0.0678627
GOTERM_BP_FAT	GO:0030097~hemopoiesis	26	1.01	0.006708	BMI1, CALCR, CD8A, SFXN1, ZBTB16, BCL11A, HOXA9, NKX2-5, NKX2-3, SYK, EPO, BMP4, EGR1, SATB1, EPAS1, CD3D, IL7, OSTM1, KDR, CARD11, HOXB7, ID2, IRF8, CD79A, TSHR, KLF1	1230	108	0.10423526
Annotation Cluster 36 **Enrichment Score: 2.3775176637788813**								
GOTERM_BP_FAT	GO:0035094~response to nicotine	6	0.23	8.73E-04	HMOX1, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1230	7	0.02008395
GOTERM_BP_FAT	GO:0043279~response to alkaloid	8	0.31	0.005561	GNAL, SLC6A3, HMOX1, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1230	17	0.09089533
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	8	0.31	0.015176	GNAL, SLC6A3, HMOX1, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1230	20	0.19456145
Annotation Cluster 37 **Enrichment Score: 2.3665924788187938**								
INTERPRO	IPR017974:Claudin, conserved site	8	0.31	0.00147	CLDN7, TMEM37, CLDN4, CLDN3, CLDN5, CLDN1, CLDN10, CLDN11	1185	15	0.07644617
INTERPRO	IPR006187:Claudin	7	0.27	0.003495	CLDN7, CLDN4, CLDN3, CLDN5, CLDN1, CLDN10, CLDN11	1185	13	0.13879584
SP_PIR_KEYWORDS	Tight junction	8	0.31	0.015473	CLDN7, F11R, CLDN4, CLDN3, CLDN5, CLDN1, CLDN10, CLDN11	979	21	0.1573057
Annotation Cluster 38								

Enrichment Score: 2.341104912387001								
GOTERM_BP_FAT	GO:0007517~muscle organ development	23	0.9	0.002998	MYOD1, FOXL2, ACTA1, MYF5, PAX3, CACNG2, CACNB4, AFG3L2, TNNI3, HOXD10, LIF, MSX1, LY6E, MEOX2, HAND1, SIX1, PDGFRB, NR2F2, LOC654400, NKX2-5, PITX1, TCF15, SNTA1	1230	86	0.0568651
GOTERM_BP_FAT	GO:0060537~muscle tissue development	19	0.74	0.004695	MYOD1, FOXL2, ACTA1, MYF5, CACNG2, CACNB4, TNNI3, AFG3L2, HOXD10, LY6E, MEOX2, HAND1, SIX1, PDGFRB, NR2F2, LOC654400, NKX2-5, PITX1, SNTA1	1230	68	0.07942401
GOTERM_BP_FAT	GO:0014706~striated muscle tissue development	18	0.7	0.006733	MYOD1, FOXL2, ACTA1, MYF5, CACNG2, CACNB4, TNNI3, AFG3L2, HOXD10, LY6E, MEOX2, HAND1, SIX1, NR2F2, LOC654400, NKX2-5, PITX1, SNTA1	1230	65	0.10407571
Annotation Cluster 39 **Enrichment Score: 2.2168492736382124**								
INTERPRO	IPR017983:GPCR, family 2, secretin-like, conserved site	7	0.27	0.003495	CALCR, CRHR1, GPR133, ADCYAP1R1, PTH1R, VIPR1, LPHN1	1185	13	0.13879584
INTERPRO	IPR001879:GPCR, family 2, extracellular region	6	0.23	0.00511	CALCR, CRHR1, ADCYAP1R1, PTH1R, VIPR1, LPHN1	1185	10	0.18759658
INTERPRO	IPR000832:GPCR, family 2, secretin-like	7	0.27	0.008111	CALCR, CRHR1, GPR133, ADCYAP1R1, PTH1R, VIPR1, LPHN1	1185	15	0.2593353
SMART	SM00008:HormR	6	0.23	0.009369	CALCR, CRHR1, ADCYAP1R1, PTH1R, VIPR1, LPHN1	649	10	0.22370124
Annotation Cluster 40 **Enrichment Score: 2.16928042552493**								
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	12	0.47	0.006422	CPLX3, SLC1A3, GLRA1, S100B, SNCA, EDN1, ACTN1, CHRNA7, CHRNB2, CSPG5, GDNF, CACNA1A	1230	35	0.10104076
GOTERM_BP_FAT	GO:0031644~regulation of neurological system process	12	0.47	0.006422	CPLX3, SLC1A3, GLRA1, S100B, SNCA, EDN1, ACTN1, CHRNA7, CHRNB2, CSPG5, GDNF, CACNA1A	1230	35	0.10104076
GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	11	0.43	0.00753	CPLX3, SLC1A3, S100B, SNCA, EDN1, ACTN1, CHRNA7, CHRNB2, CSPG5, GDNF, CACNA1A	1230	31	0.11176634
Annotation Cluster 41 **Enrichment Score: 2.0252985361375844**								
GOTERM_BP_FAT	GO:0048736~appendage development	14	0.55	0.003662	RARG, CRABP2, ZBTB16, GREM1, HOXD10, MSX2, MSX1, HOXC11, MEOX2, DLX5, KIAA1715, HOXA9, NR2F2, PITX1	1230	42	0.06696789
GOTERM_BP_FAT	GO:0060173~limb development	14	0.55	0.003662	RARG, CRABP2, ZBTB16, GREM1, HOXD10, MSX2, MSX1, HOXC11, MEOX2, DLX5, KIAA1715, HOXA9, NR2F2, PITX1	1230	42	0.06696789
GOTERM_BP_FAT	GO:0030326~embryonic limb morphogenesis	11	0.43	0.015048	MSX2, RARG, HOXC11, MSX1, DLX5, CRABP2, KIAA1715, HOXA9, ZBTB16, GREM1, HOXD10	1230	34	0.1938876
GOTERM_BP_FAT	GO:0035113~embryonic appendage morphogenesis	11	0.43	0.015048	MSX2, RARG, HOXC11, MSX1, DLX5, CRABP2, KIAA1715, HOXA9, ZBTB16, GREM1, HOXD10	1230	34	0.1938876
GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	12	0.47	0.015238	MSX2, RARG, HOXC11, MSX1, DLX5, CRABP2, KIAA1715, HOXA9, ZBTB16, GREM1, PITX1, HOXD10	1230	39	0.19446767
GOTERM_BP_FAT	GO:0035108~limb morphogenesis	12	0.47	0.015238	MSX2, RARG, HOXC11, MSX1, DLX5, CRABP2, KIAA1715, HOXA9, ZBTB16, GREM1, PITX1, HOXD10	1230	39	0.19446767
Annotation Cluster 42 **Enrichment Score: 2.0088843539861765**								

GOTERM_BP_FAT	GO:0016477~cell migration	27	1.05	0.007074	CCK, PDGFB, EDN2, PAX6, GJA1, PF4, CDH2, PAX3, GDNF, EDNRB, ATOH1, CXCR4, NR2F2, NKX2-3, NR2F1, PRKCA, ICAM1, LOC786683, EMX2, ITGA3, ITGA4, ISL1, KDR, CDH13, CD34, SIX1, GFRA3	1230	114	0.10744591
GOTERM_BP_FAT	GO:0048870~cell motility	28	1.09	0.01153	CCK, PDGFB, EDN2, PAX6, GJA1, PF4, CDH2, PAX3, GDNF, EDNRB, ATOH1, CXCR4, CHRNA7, NR2F2, NKX2-3, NR2F1, PRKCA, ICAM1, LOC786683, EMX2, ITGA3, ITGA4, ISL1, KDR, CDH13, CD34, SIX1, GFRA3	1230	124	0.15809418
GOTERM_BP_FAT	GO:0051674~localization of cell	28	1.09	0.01153	CCK, PDGFB, EDN2, PAX6, GJA1, PF4, CDH2, PAX3, GDNF, EDNRB, ATOH1, CXCR4, CHRNA7, NR2F2, NKX2-3, NR2F1, PRKCA, ICAM1, LOC786683, EMX2, ITGA3, ITGA4, ISL1, KDR, CDH13, CD34, SIX1, GFRA3	1230	124	0.15809418
Annotation Cluster 43 **Enrichment Score: 1.9615645059690543**								
GOTERM_BP_FAT	GO:0035095~behavioral response to nicotine	5	0.19	0.004519	CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1230	6	0.07784201
INTERPRO	IPR002394:Nicotinic acetylcholine receptor, N-terminal	6	0.23	0.00511	CHRNA5, CHRNB4, CHRND, CHRNA7, CHRNB2, CHRNA3	1185	10	0.18759658
GOTERM_CC_FAT	GO:0005892~nicotinic acetylcholine-gated receptor-channel complex	5	0.19	0.015029	CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	947	8	0.12648241
GOTERM_MF_FAT	GO:0015464~acetylcholine receptor activity	6	0.23	0.021179	CHRM1, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1232	13	0.28572928
GOTERM_MF_FAT	GO:0042166~acetylcholine binding	6	0.23	0.021179	CHRM1, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1232	13	0.28572928
Annotation Cluster 44 **Enrichment Score: 1.9498434880037865**								
GOTERM_BP_FAT	GO:0031128~developmental induction	6	0.23	0.007268	BMP4, FGFR4, HOXC11, SIX1, SOX2, GDNF	1230	10	0.10967667
GOTERM_BP_FAT	GO:0045168~cell-cell signaling involved in cell fate specification	6	0.23	0.007268	BMP4, FGFR4, HOXC11, SIX1, SOX2, GDNF	1230	10	0.10967667
GOTERM_BP_FAT	GO:0001759~induction of an organ	5	0.19	0.026773	BMP4, FGFR4, HOXC11, SIX1, GDNF	1230	9	0.29622025
Annotation Cluster 45 **Enrichment Score: 1.9181553165038465**								
GOTERM_BP_FAT	GO:0006584~catecholamine metabolic process	8	0.31	0.011188	LY6E, SNCB, EPAS1, PNMT, GATA3, SLC6A3, SNCA, GCH1	1230	19	0.15445048
GOTERM_BP_FAT	GO:0009712~catechol metabolic process	8	0.31	0.011188	LY6E, SNCB, EPAS1, PNMT, GATA3, SLC6A3, SNCA, GCH1	1230	19	0.15445048
GOTERM_BP_FAT	GO:0034311~diol metabolic process	8	0.31	0.011188	LY6E, SNCB, EPAS1, PNMT, GATA3, SLC6A3, SNCA, GCH1	1230	19	0.15445048
GOTERM_BP_FAT	GO:0018958~phenol metabolic process	8	0.31	0.015176	LY6E, SNCB, EPAS1, PNMT, GATA3, SLC6A3, SNCA, GCH1	1230	20	0.19456145
Annotation Cluster 46								

Enrichment Score: 1.9037186225978304								
INTERPRO	IPR001781:Zinc finger, LIM-type	13	0.51	0.008163	LMO1, LIMS2, LMO2, LMO3, ABLIM3, PDLIM3, PDLIM1, ISL1, LHX3, LHX4, LHX5, LHX9, TES	1185	44	0.25579161
SP_PIR_KEYWORDS	LIM domain	13	0.51	0.010301	LMO1, LIMS2, LMO2, LMO3, ABLIM3, PDLIM3, PDLIM1, ISL1, LHX3, LHX4, LHX5, LHX9, TES	979	44	0.11539998
SMART	SM00132:LIM	13	0.51	0.023127	LMO1, LIMS2, LMO2, LMO3, ABLIM3, PDLIM3, PDLIM1, ISL1, LHX3, LHX4, LHX5, LHX9, TES	649	44	0.4081574
Annotation Cluster 47 **Enrichment Score: 1.7564192382686643**								
UP_SEQ_FEATURE	metal ion-binding site:Calcium 3	6	0.23	0.00608	PRKCA, SYT1, MMP9, PRKCG, COLEC12, PRKCB	677	11	0.59915998
UP_SEQ_FEATURE	metal ion-binding site:Calcium 1; via carbonyl oxygen	6	0.23	0.013802	PRKCA, SYT1, CABP1, PRKCG, COLEC12, PRKCB	677	13	0.76126924
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	7	0.27	0.019999	PRKCA, SYT1, MMP9, CABP1, PRKCG, COLEC12, PRKCB	677	19	0.81092347
UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	7	0.27	0.019999	PRKCA, SYT1, MMP9, CABP1, PRKCG, COLEC12, PRKCB	677	19	0.81092347
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	7	0.27	0.049211	PRKCA, SYT1, MMP9, CABP1, PRKCG, COLEC12, PRKCB	677	23	0.93757382
Annotation Cluster 48 **Enrichment Score: 1.740367314416787**								
GOTERM_MF_FAT	GO:0008066~glutamate receptor activity	7	0.27	0.0134	GRM3, GRIK1, GRIA2, GRIN2C, GRIK2, GRIK3, GRIN3B	1232	16	0.21474289
GOTERM_MF_FAT	GO:0004970~ionotropic glutamate receptor activity	6	0.23	0.021179	GRIK1, GRIA2, GRIN2C, GRIK2, GRIK3, GRIN3B	1232	13	0.28572928
GOTERM_MF_FAT	GO:0005234~extracellular-glutamate-gated ion channel activity	6	0.23	0.021179	GRIK1, GRIA2, GRIN2C, GRIK2, GRIK3, GRIN3B	1232	13	0.28572928
Annotation Cluster 49 **Enrichment Score: 1.7402310335516**								
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	52	2.02	0.0054	SYT1, SYT5, SYT7, CSPG5, AP1S3, SLC2A8, PACSIN1, AP1S1, SLC2A4, SMAGP, NECAP1, RAB6B, MT3, SCAMP5, SEC23A, SVOP, STX1A, STXBP2, RPH3A, CHGA, DOC2A, RHCG, CLIC5, NRSN2, VAMP1, CHGB, CALCR, HCRT, RAB3B, AP1M2, CLU, RHBG, POMC, SYPL2, GCH1, PCSK2, PCSK1, ECE2, CRISPLD2, ECRG4, EHD1, GABRA2, NTF3, SYT10, LOC614124, ITPR3, ITPR1, SYNGR3, SLC17A7, SLC17A6, SLC18A2, ATP8A1	947	265	0.05611726
GOTERM_CC_FAT	GO:0031982~vesicle	53	2.06	0.006176	SYT1, SYT5, SYT7, CSPG5, AP1S3, SLC2A8, PACSIN1, AP1S1, SLC2A4, SMAGP, NECAP1, RAB6B, MT3, SCAMP5, SEC23A, SVOP, STX1A, ACTN1, STXBP2, RPH3A, CHGA, DOC2A, RHCG, CLIC5, NRSN2, VAMP1, CHGB, CALCR, HCRT, RAB3B, AP1M2, CLU, RHBG, POMC, SYPL2, GCH1, PCSK2, PCSK1, ECE2, CRISPLD2, ECRG4, EHD1, GABRA2, NTF3, SYT10, LOC614124, ITPR3, ITPR1, SYNGR3, SLC17A7, SLC17A6,	947	273	0.06068273

					SLC18A2, ATP8A1			
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	40	1.56	0.054814	CALCR, SYT1, HCRT, RAB3B, SYT5, CLU, CSPG5, SYT7, POMC, SYPL2, PCSK2, AP1S3, PCSK1, ECE2, AP1S1, PACSIN1, SLC2A4, CRISPLD2, ECRG4, NECAP1, RAB6B, EHD1, MT3, SEC23A, STX1A, GABRA2, NTF3, SYT10, LOC614124, ACTN1, STXBP2, RPH3A, ITPR1, SYNGR3, SLC17A7, CHGA, SLC17A6, DOC2A, CLIC5, NRSN2	947	223	0.34051525
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	39	1.52	0.059857	CALCR, SYT1, HCRT, RAB3B, SYT5, CLU, CSPG5, SYT7, POMC, SYPL2, PCSK2, AP1S3, PCSK1, ECE2, AP1S1, PACSIN1, SLC2A4, CRISPLD2, ECRG4, NECAP1, RAB6B, EHD1, MT3, SEC23A, STX1A, GABRA2, NTF3, SYT10, LOC614124, STXBP2, RPH3A, ITPR1, SYNGR3, SLC17A7, CHGA, SLC17A6, DOC2A, CLIC5, NRSN2	947	218	0.35010321
Annotation Cluster 50 **Enrichment Score: 1.7332749274686088**								
GOTERM_MF_FAT	GO:0019992~diacylglycerol binding	8	0.31	0.004189	PRKCA, PRKCZ, STAC, RASGRP4, RASGRP2, PRKCH, PRKCG, PRKCB	1232	17	0.08375019
INTERPRO	IPR002219:Protein kinase C-like, phorbol ester/diacylglycerol binding	8	0.31	0.027856	PRKCA, PRKCZ, STAC, RASGRP4, RASGRP2, PRKCH, PRKCG, PRKCB	1185	24	0.54006735
SMART	SM00109:C1	8	0.31	0.054096	PRKCA, PRKCZ, STAC, RASGRP4, RASGRP2, PRKCH, PRKCG, PRKCB	649	24	0.50953013
Annotation Cluster 51 **Enrichment Score: 1.6967001364469438**								
INTERPRO	IPR006028:Gamma-aminobutyric acid A receptor	7	0.27	0.008111	GABRD, GABRA2, GABRA4, GLRA1, GABRB1, GABRA5, GABRP	1185	15	0.2593353
GOTERM_MF_FAT	GO:0004890~GABA-A receptor activity	7	0.27	0.024597	GABRD, GABRA2, GABRA4, GABRB1, GABRA5, GABRQ, GABRP	1232	18	0.31936396
GOTERM_MF_FAT	GO:0016917~GABA receptor activity	7	0.27	0.040735	GABRD, GABRA2, GABRA4, GABRB1, GABRA5, GABRQ, GABRP	1232	20	0.44134881
Annotation Cluster 52 **Enrichment Score: 1.6428664369212744**								
GOTERM_BP_FAT	GO:0014032~neural crest cell development	6	0.23	0.011806	EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1230	11	0.16085654
GOTERM_BP_FAT	GO:0014033~neural crest cell differentiation	6	0.23	0.011806	EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1230	11	0.16085654
GOTERM_BP_FAT	GO:0048762~mesenchymal cell differentiation	7	0.27	0.02317	FGFR2, EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1230	17	0.26560973
GOTERM_BP_FAT	GO:0060485~mesenchyme development	7	0.27	0.030747	FGFR2, EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1230	18	0.32799498
GOTERM_BP_FAT	GO:0014031~mesenchymal cell development	6	0.23	0.061482	EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1230	16	0.50818194
Annotation Cluster 53 **Enrichment Score: 1.6384553272075517**								
PIR_SUPERFAMILY	PIRSF002504:cadherin	6	0.23	9.51E-04	CDH13, CDH18, CDH1, CDH2, CDH3, CDH6	556	7	0.15906683

UP_SEQ_FEATURE	domain:Cadherin 5	6	0.23	0.009407	CDH13, CDH18, CDH1, CDH2, CDH3, CDH6	677	12	0.67151376
UP_SEQ_FEATURE	domain:Cadherin 3	6	0.23	0.013802	CDH13, CDH18, CDH1, CDH2, CDH3, CDH6	677	13	0.76126924
UP_SEQ_FEATURE	domain:Cadherin 4	6	0.23	0.013802	CDH13, CDH18, CDH1, CDH2, CDH3, CDH6	677	13	0.76126924
INTERPRO	IPR000233:Cadherin cytoplasmic region	5	0.19	0.043159	CDH18, CDH1, CDH2, CDH3, CDH6	1185	11	0.67310252
INTERPRO	IPR002126:Cadherin	8	0.31	0.060465	CDH8, CDH13, PCDH1, CDH18, CDH1, CDH2, CDH3, CDH6	1185	28	0.76430086
UP_SEQ_FEATURE	domain:Cadherin 1	5	0.19	0.060578	CDH13, CDH18, CDH1, CDH2, CDH6	677	13	0.95595874
UP_SEQ_FEATURE	domain:Cadherin 2	5	0.19	0.060578	CDH13, CDH18, CDH1, CDH2, CDH6	677	13	0.95595874
SMART	SM00112:CA	8	0.31	0.109891	CDH8, CDH13, PCDH1, CDH18, CDH1, CDH2, CDH3, CDH6	649	28	0.67319112
Annotation Cluster 54 **Enrichment Score: 1.5804046649145007**								
INTERPRO	IPR001723:Steroid hormone receptor	10	0.39	0.013741	PGR, VDR, AR, NR1I3, RARG, ESR1, RXRG, NR2F2, NR2F1, NR5A1	1185	31	0.35599042
INTERPRO	IPR008946:Nuclear hormone receptor, ligand-binding	10	0.39	0.016985	PGR, VDR, AR, NR1I3, RARG, ESR1, RXRG, NR2F2, NR2F1, NR5A1	1185	32	0.40802158
INTERPRO	IPR000536:Nuclear hormone receptor, ligand-binding, core	10	0.39	0.020755	PGR, VDR, AR, NR1I3, RARG, ESR1, RXRG, NR2F2, NR2F1, NR5A1	1185	33	0.45528602
INTERPRO	IPR001628:Zinc finger, nuclear hormone receptor-type	9	0.35	0.026725	PGR, VDR, NR1I3, RARG, ESR1, RXRG, NR2F2, NR2F1, NR5A1	1185	29	0.53118346
SMART	SM00430:HOLI	10	0.39	0.046163	PGR, VDR, AR, NR1I3, RARG, ESR1, RXRG, NR2F2, NR2F1, NR5A1	649	33	0.4878492
SMART	SM00399:ZnF_C4	9	0.35	0.055098	PGR, VDR, NR1I3, RARG, ESR1, RXRG, NR2F2, NR2F1, NR5A1	649	29	0.49991422
Annotation Cluster 55 **Enrichment Score: 1.5651599525612845**								
INTERPRO	IPR000152:EGF-type aspartate/asparagine hydroxylation conserved site	12	0.47	0.010409	THBD, LTBP2, DLL4, EFEMP1, NELL2, PROZ, ACAN, VCAN, DLK2, DLK1, CLEC14A, VLDLR	1185	40	0.29781893
INTERPRO	IPR001881:EGF-like calcium-binding	11	0.43	0.01616	THBD, LTBP2, DLL4, EFEMP1, NELL2, ACAN, VCAN, DLK2, DLK1, VLDLR, THBS4	1185	37	0.39841002
SMART	SM00179:EGF_CA	11	0.43	0.038749	THBD, LTBP2, DLL4, EFEMP1, NELL2, ACAN, VCAN, DLK2, DLK1, VLDLR, THBS4	649	37	0.48543127
INTERPRO	IPR018097:EGF-like calcium-binding, conserved site	9	0.35	0.084193	THBD, LTBP2, EFEMP1, NELL2, ACAN, VCAN, DLK2, VLDLR, THBS4	1185	36	0.84317834

Annotation Cluster 56 **Enrichment Score: 1.5347710805187218**								
INTERPRO	IPR000867:Insulin-like growth factor-binding protein, IGFBP	6	0.23	0.018717	NOV, IGFBPL1, ESM1, IGFBP2, IGFBP3, IGFBP4	1185	13	0.4271994
SMART	SM00121:IB	6	0.23	0.03262	NOV, IGFBPL1, ESM1, IGFBP2, IGFBP3, IGFBP4	649	13	0.44829002
GOTERM_MF_FAT	GO:0005520~insulin-like growth factor binding	7	0.27	0.040735	NOV, IGFBPL1, KAZALD1, ESM1, IGFBP2, IGFBP3, IGFBP4	1232	20	0.44134881
Annotation Cluster 57 **Enrichment Score: 1.3580869019059556**								
GOTERM_BP_FAT	GO:0010941~regulation of cell death	54	2.1	0.03819	LOC789855, SNCB, MMP9, SNCA, GDNF, KCNIP3, APOE, TMEM102, TERT, KCNMA1, PRKCA, RARG, NOL3, NDUFA13, LOC786391, BCL2L11, CARD10, CARD11, INHBA, PROK2, ALOX15, MSX1, TNFSF13B, SCIN, RIPK3, RIPK2, NGFR, ALOX12, FGFR3, CDH1, ZBTB16, BDKRB2, MSX2, PYCARD, LHX4, TRAF5, NEFL, NKX2-5, BMP4, COL4A3, FOXL2, NTF3, IL7, EEF1A2, CIDEA, MAPK10, LOC783956, TRADD, CDH13, DLX1, SARM1, IGFBP3, CACNA1A, F2R	1230	299	0.3773715
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	53	2.06	0.043433	LOC789855, SNCB, MMP9, SNCA, GDNF, KCNIP3, APOE, TMEM102, TERT, KCNMA1, PRKCA, RARG, NOL3, NDUFA13, LOC786391, BCL2L11, CARD10, CARD11, INHBA, PROK2, ALOX15, MSX1, TNFSF13B, SCIN, RIPK3, RIPK2, NGFR, ALOX12, FGFR3, CDH1, ZBTB16, BDKRB2, MSX2, PYCARD, LHX4, TRAF5, NEFL, NKX2-5, COL4A3, FOXL2, NTF3, IL7, EEF1A2, CIDEA, MAPK10, LOC783956, TRADD, CDH13, DLX1, SARM1, IGFBP3, CACNA1A, F2R	1230	295	0.41001051
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	53	2.06	0.050812	LOC789855, SNCB, MMP9, SNCA, GDNF, KCNIP3, APOE, TMEM102, TERT, KCNMA1, PRKCA, RARG, NOL3, NDUFA13, LOC786391, BCL2L11, CARD10, CARD11, INHBA, PROK2, ALOX15, MSX1, TNFSF13B, SCIN, RIPK3, RIPK2, NGFR, ALOX12, FGFR3, CDH1, ZBTB16, BDKRB2, MSX2, PYCARD, LHX4, TRAF5, NEFL, NKX2-5, COL4A3, FOXL2, NTF3, IL7, EEF1A2, CIDEA, MAPK10, LOC783956, TRADD, CDH13, DLX1, SARM1, IGFBP3, CACNA1A, F2R	1230	298	0.45292875
Annotation Cluster 58 **Enrichment Score: 1.3196304719810805**								
GOTERM_MF_FAT	GO:0015294~solute:cation symporter activity	13	0.51	0.032521	SLC6A2, SLC6A20, SLC6A12, SLC6A3, SLC10A4, SLC17A7, SLC2A6, SLC1A3, SLC6A7, SLC6A5, SLC13A3, SLC5A7, SLC1A1	1232	51	0.38468374
GOTERM_MF_FAT	GO:0015370~solute:sodium symporter activity	11	0.43	0.033213	SLC1A3, SLC6A7, SLC6A20, SLC6A2, SLC6A3, SLC6A5, SLC6A12, SLC13A3, SLC10A4, SLC5A7, SLC1A1	1232	40	0.38622556
GOTERM_MF_FAT	GO:0015293~symporter activity	14	0.55	0.101776	SLC6A2, SLC6A20, SLC6A3, SLC6A12, SLC10A4, SLC17A7, SLC2A6, SLC1A3, SLC17A6, SLC6A7, SLC6A5, SLC13A3, SLC5A7, SLC1A1	1232	67	0.70399637

B. Lamb DAVID clusters

						List	Pop	Pop	Fold Enrich-	Benjamini

Category	Term	Count	%	P-value	Genes	Total	Hits	Total	ment	P-value
Annotation Cluster 1 (Enrichment Score: 18.34445733208664)										
SP_PIR_KEYWORDS	Homeobox	47	1.814	2.55E-21	IRX3, HNF1B, CDX2, ONECUT1, PAX6, PAX3, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, MEIS2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, NKX2-5, LHX9, PITX1, DBX1, PITX2, NKX2-3, NANOG, EMX2, ISL1, HOXB3, DLX3, HOXB4, HHEX, DLX1, ZFHX4, MSX1, HOXC11, MEOX2, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	985	78	7349	4.5	3.87E-19
INTERPRO	IPR001356:Homeobox	44	1.698	1.06E-19	IRX3, HNF1B, ONECUT1, PAX6, PAX3, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, NKX2-5, LHX9, PITX1, DBX1, NKX2-3, PITX2, NANOG, EMX2, ISL1, HOXB3, DLX3, HOXB4, HHEX, DLX1, HOXC11, MSX1, MEOX2, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	1200	75	9171	4.48	1.68E-16
INTERPRO	IPR017970:Homeobox, conserved site	39	1.505	5.85E-19	IRX3, HNF1B, PAX6, PAX3, HOXD10, OTP, CRX, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, LHX9, NKX2-5, PITX1, DBX1, NKX2-3, PITX2, NANOG, EMX2, ISL1, HOXB3, DLX3, HOXB4, HHEX, DLX1, MSX1, MEOX2, HOXB7, HOXC13, DLX5, HOXB6, SIX1, HOPX	1200	62	9171	4.81	4.63E-16
INTERPRO	IPR012287:Homeodomain-related	43	1.66	6.71E-18	IRX3, HNF1B, ONECUT1, PAX6, PAX3, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, MYB, NKX2-5, LHX9, PITX1, DBX1, NKX2-3, PITX2, NANOG, EMX2, HOXB3, DLX3, HOXB4, HHEX, HOXC11, MSX1, MEOX2, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	1200	78	9171	4.21	3.54E-15
SMART	SM00389:HOX	44	1.698	1.79E-17	IRX3, HNF1B, ONECUT1, PAX6, PAX3, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, NKX2-5, LHX9, PITX1, DBX1, NKX2-3, PITX2, NANOG, EMX2, ISL1, HOXB3, DLX3, HOXB4, HHEX, DLX1, HOXC11, MSX1, MEOX2, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	661	75	4364	3.87	4.86E-15
Annotation Cluster 2 (Enrichment Score: 15.307083113782918)										
GOTERM_MF_FAT	GO:0022836~gated channel activity	76	2.933	1.56E-17	KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, GRIK2, GABRB2, SCN3B, GRIK3, GABRB1, GRIN3B, KCNJ10, KCNJ12, KCNJ11, KCNIP3, SHKBP1, KCNQ3, MGC139528, GRIN2C, CHRNA5, CHRNA7, KCNQ2, KCNG3, FGF2, CHRNA3, CHRNA2, KCNMA1, KCND2, CACNG2, CNGA3, KCNT1, LOC100139857, KCNH2, KCNH5, KCNA2, KCNA1, KCNA4, KCNA6, CACNB4, KCNA5, KCNS2, KCNE1, HTR3A, SCN5A, SCNN1A, GABRP, GABRD, GABRA2, GLRB, CACNA2D1, GABRA4, LOC100138074, LOC783386,	1248	204	9249	2.76	3.48E-15

					ITPR3, KCNK1, KCNK2, KCNV1, KCTD8, ACCN1, KCNN4, KCNJ9, KCNN1, GRIA2, KCNJ8, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, CACNA1D, CACNA1A, CHRNG, KCTD12					
GOTERM_MF_FAT	GO:0005216~ion channel activity	88	3.396	3.96E-16	KCNK17, KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, SCN3B, GRIK2, GABRB2, GRIK3, GABRB1, GRIN3B, KCNJ10, KCNJ12, KCNJ11, KCNIP3, SHKBP1, MGC139528, KCNQ3, GRIN2C, CHRNA5, CHRNA7, ANO4, KCNQ2, KCNG3, FGF2, CHRNA3, CHRNA2, KCNMA1, TRPM6, KCND2, CFTR, CACNG2, CNGA3, CATSPER4, KCNT1, SLC26A8, LOC100139857, KCNH2, KCNH5, KCNA2, KCNA1, KCNA4, KCNA6, KCNA5, CACNB4, FXYD6, FXYD7, KCNS2, TTYH1, KCNE1, HTR3A, SCN5A, SCNN1A, GABRP, GABRD, GABRA2, GLRB, CACNA2D1, TRPC3, GABRA4, LOC100138074, LOC783386, ITPR3, KCNK1, KCNK2, KCNV1, KCNK4, KCTD8, ACCN1, KCNN4, KCNJ9, GRIA2, KCNN1, KCNJ8, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, LOC505697, CACNA1D, CACNA1A, CHRNG, KCTD12	1248	268	9249	2.43	7.92E-14
GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	88	3.396	8.27E-16	KCNK17, KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, SCN3B, GRIK2, GABRB2, GRIK3, GABRB1, GRIN3B, KCNJ10, KCNJ12, KCNJ11, KCNIP3, SHKBP1, MGC139528, KCNQ3, GRIN2C, CHRNA5, CHRNA7, ANO4, KCNQ2, KCNG3, FGF2, CHRNA3, CHRNA2, KCNMA1, TRPM6, KCND2, CFTR, CACNG2, CNGA3, CATSPER4, KCNT1, SLC26A8, LOC100139857, KCNH2, KCNH5, KCNA2, KCNA1, KCNA4, KCNA6, KCNA5, CACNB4, FXYD6, FXYD7, KCNS2, TTYH1, KCNE1, HTR3A, SCN5A, SCNN1A, GABRP, GABRD, GABRA2, GLRB, CACNA2D1, TRPC3, GABRA4, LOC100138074, LOC783386, ITPR3, KCNK1, KCNK2, KCNV1, KCNK4, KCTD8, ACCN1, KCNN4, KCNJ9, GRIA2, KCNN1, KCNJ8, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, LOC505697, CACNA1D, CACNA1A, CHRNG, KCTD12	1248	271	9249	2.41	1.15E-13
GOTERM_MF_FAT	GO:0015267~channel activity	88	3.396	2.39E-15	KCNK17, KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, SCN3B, GRIK2, GABRB2, GRIK3, GABRB1, GRIN3B, KCNJ10, KCNJ12, KCNJ11, KCNIP3, SHKBP1, MGC139528, KCNQ3, GRIN2C, CHRNA5, CHRNA7, ANO4, KCNQ2, KCNG3, FGF2, CHRNA3, CHRNA2, KCNMA1, TRPM6, KCND2, CFTR, CACNG2, CNGA3, CATSPER4, KCNT1, SLC26A8, LOC100139857, KCNH2, KCNH5, KCNA2, KCNA1, KCNA4, KCNA6, KCNA5, CACNB4, FXYD6, FXYD7, KCNS2, TTYH1, KCNE1, HTR3A, SCN5A, SCNN1A, GABRP, GABRD, GABRA2, GLRB, CACNA2D1, TRPC3, GABRA4, LOC100138074, LOC783386, ITPR3, KCNK1, KCNK2, KCNV1, KCNK4, KCTD8, ACCN1,	1248	275	9249	2.37	2.97E-13

					KCNN4, KCNJ9, GRIA2, KCNN1, KCNJ8, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, LOC505697, CACNA1D, CACNA1A, CHRNG, KCTD12					
GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	88	3.396	2.39E-15	KCNK17, KCNH1, KCNC1, GRIK1, GLRA1, KCNAB1, SCN3B, GRIK2, GABRB2, GRIK3, GABRB1, GRIN3B, KCNJ10, KCNJ12, KCNJ11, KCNIP3, SHKBP1, MGC139528, KCNQ3, GRIN2C, CHRNA5, CHRNA7, ANO4, KCNQ2, KCNG3, FGF2, CHRNA3, CHRNA2, KCNMA1, TRPM6, KCND2, CFTR, CACNG2, CNGA3, CATSPER4, KCNT1, SLC26A8, LOC100139857, KCNH2, KCNH5, KCNA2, KCNA1, KCNA4, KCNA6, KCNA5, CACNB4, FXYD6, FXYD7, KCNS2, TTYH1, KCNE1, HTR3A, SCN5A, SCNN1A, GABRP, GABRD, GABRA2, GLRB, CACNA2D1, TRPC3, GABRA4, LOC100138074, LOC783386, ITPR3, KCNK1, KCNK2, KCNV1, KCNK4, KCTD8, ACCN1, KCNN4, KCNJ9, GRIA2, KCNN1, KCNJ8, KCNN2, CHRNB4, CACNA1G, KCNF1, SCN4B, CHRNB2, CHRND, CACNA1E, LOC505697, CACNA1D, CACNA1A, CHRNG, KCTD12	1248	275	9249	2.37	2.97E-13
Annotation Cluster 3 (Enrichment Score: 11.642818517677654)										
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	185	7.14	2.58E-20	MYOD1, CDX2, ARNT2, RORC, RORB, NR2E1, LOC782183, HOXD10, TAF7L, HOXC6, PGR, ATOH1, OLIG3, GATA5, GATA3, FOXF1, HOXC4, GATA4, OLIG1, ATOH7, PITX1, TWIST2, PITX2, TWIST1, PHOX2A, SATB2, RARG, EMX1, LOC787396, BARHL2, EMX2, EOMES, RXRG, MLXIPL, HES6, AHR, ASCL2, ASCL1, HHEX, MSX1, HES5, SIX1, TFAP2A, TFAP2C, NFE2L3, ASCL4, UNCX, EID1, LOC527381, LOC781206, ONECUT1, SOX2, LOC783396, OTP, FOXH1, TCF21, DBX2, T, VDR, AHRR, MEIS3, MEIS2, HOXA7, LHX3, LHX4, HOXA10, LHX5, HOXA9, NKX2-5, LHX9, DBX1, NKX2-3, KLF5, DMBX1, GSX2, MAFB, FOXA1, ESRRG, NEUROG1, NEUROG3, SHOX2, HOXB3, DLX3, HOXB4, LOC784735, NR1I3, DLX1, ATF3, HOXB2, DMRTC2, HOXB7, LOC789959, DLX6, DLX5, EBF2, DLX4, HOXB6, HOPX, CRYM, KLF4, TCF15, HNF1B, FOXA2, ELF5, LOC783703, HR, PAX6, DMRTA2, PAX3, FEV, KCNIP3, GLI1, CRX, FERD3L, LBH, HEY1, LOC509704, POU5F1, MKX, SOX18, FOXB1, MYB, NR2F2, ALX4, ALX3, NR2F1, EGR1, SSBP4, AR, NANOG, TBX15, ZNF287, OTX2, ESR1, TLE4, MIXL1, HOXC11, NRL, HOXC13, FOXC2, LOC617563, CUX2, CUX1, ZNF483, LOC522736, IRX3, SBNO2, TRIB3, LOC618065, MSX2, STAT4, HAND1, LOC787194, POU2F3, BCL11A, NFATC4, POU3F2, POU3F1, TLX2, SIM1, LOC615643, CEBPA, MAF, MYF6, FOXL2, FOXL1, LMX1B, TBX5, MYF5, TBX4, VSX2, ISL1, ID2, IRF5, MEOX2, ID1, IRF6, IRF8, HEYL, NEUROD1, SP7, ID3, LOC654400, NR5A2, FOXE3, PBX4	1248	715	9249	1.92	7.65E-18

GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	187	7.217	4.13E-11	MYOD1, CDX2, ARNT2, FST, RORC, CBX2, RORB, GDNF, NR2E1, IL10, LOC782183, HOXD10, HOXC6, PGR, ATOH1, GATA5, GATA3, FOXF1, HOXC4, GATA4, ZNF180, PITX1, TWIST2, PITX2, PHOX2A, SATB2, RARG, EMX1, LOC787396, BARHL2, EMX2, EOMES, RXRG, HES6, AHR, HHEX, MSX1, HES5, SIX1, TFAP2A, ZNF383, TFAP2C, NFE2L3, UNCX, LOC527381, ONECUT1, SOX2, LOC783396, LIN28B, OTP, LIF, FOXH1, VDR, T, DBX2, AHRR, MEIS3, MEIS2, HOXA7, OVOL1, LHX3, LHX4, HOXA10, LHX5, LOC789268, NKX2-5, LHX9, DBX1, NKX2-3, KLF5, DMBX1, BMP4, BMP3, RFX4, GSX2, NTF3, MAFB, FOXA1, GSX1, ESRRG, SHOX2, HOXB3, DLX3, HOXB4, NR1I3, GCM2, DLX1, ATF3, HOXB2, DMRTC2, HOXB7, LOC789959, DLX6, DLX5, EBF2, DLX4, HOXB6, HOPX, CRYM, KLF4, KCNH1, HNF1B, FOXA2, ELF5, LOC783703, PAX6, DMRTA2, PAX3, FEV, KCNIP3, GLI1, CRX, LBH, HEY1, POU5F1, MKX, SOX18, FOXB1, MYB, ALX4, NR2F2, ALX3, FGF2, NR2F1, EGR1, AR, NANOG, TBX15, ZNF287, OTX2, ESR1, TLE4, NDUFA13, MIXL1, INHBA, HOXC11, NRL, HOXC13, FOXC2, CUX2, KCNH2, CUX1, ZNF483, KCNH5, LOC522736, IRX3, SBNO2, ABLIM3, LOC618065, MSX2, STAT4, HAND1, LOC787194, POU2F3, PER1, NFATC4, POU3F2, POU3F1, TLX2, SIM1, LOC615643, EPO, CEBPA, MAF, MYF6, FOXL2, FOXL1, LMX1B, TBX5, MYF5, TBX4, VSX2, ISL1, ID2, IRF5, MEOX2, ID1, IRF6, IRF8, HEYL, NEUROD1, SP7, ID3, LOC654400, NR5A2, FOXE3, PBX4, F2R	1242	845	8785	1.57	4.11E-08
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	188	7.256	1.06E-10	MYOD1, CDX2, ARNT2, FST, RORC, CBX2, RORB, GDNF, NR2E1, IL10, LOC782183, HOXD10, HOXC6, PGR, ATOH1, GATA5, GATA3, FOXF1, HOXC4, GATA4, ZNF180, PITX1, TWIST2, PITX2, PHOX2A, SATB2, RARG, EMX1, LOC787396, BARHL2, EMX2, EOMES, RXRG, HES6, AHR, HHEX, MSX1, HES5, SIX1, TFAP2A, ZNF383, TFAP2C, NFE2L3, UNCX, LOC527381, ONECUT1, SOX2, LOC783396, LIN28B, OTP, LIF, FOXH1, VDR, T, DBX2, AHRR, MEIS3, MEIS2, HOXA7, OVOL1, LHX3, LHX4, HOXA10, LHX5, LOC789268, NKX2-5, LHX9, DBX1, NKX2-3, KLF5, DMBX1, BMP4, BMP3, RFX4, GSX2, NTF3, MAFB, FOXA1, GSX1, ESRRG, SHOX2, HOXB3, DLX3, HOXB4, NR1I3, GCM2, DLX1, ATF3, HOXB2, DMRTC2, HOXB7, LOC789959, DLX6, DLX5, EBF2, DLX4, HOXB6, HOPX, CRYM, KLF4, KCNH1, HNF1B, FOXA2, ELF5, LOC783703, PAX6, DMRTA2, PAX3, FEV, KCNIP3, GLI1, CRX, LBH, HEY1, POU5F1, MKX, SOX18, FOXB1, MYB, ALX4, NR2F2, ALX3, FGF2, NR2F1, EGR1, AR, NANOG, TBX15, ZNF287, OTX2, ESR1, TLE4, NDUFA13, MIXL1, INHBA, HOXC11,	1242	860	8785	1.55	7.90E-08

					NRL, HOXC13, FOXC2, CUX2, KCNH2, CUX1, ZNF483, KCNH5, CALCR, LOC522736, IRX3, SBNO2, ABLIM3, LOC618065, MSX2, STAT4, HAND1, LOC787194, POU2F3, PER1, NFATC4, POU3F2, POU3F1, TLX2, SIM1, LOC615643, EPO, CEBPA, MAF, MYF6, FOXL2, FOXL1, LMX1B, TBX5, MYF5, TBX4, VSX2, ISL1, ID2, IRF5, MEOX2, ID1, IRF6, IRF8, HEYL, NEUROD1, SP7, ID3, LOC654400, NR5A2, FOXE3, PBX4, F2R					
GOTERM_BP_FAT	GO:0045449~regulation of transcription	224	8.645	2.38E-07	CDX2, GDF6, FST, RORC, RORB, HOXD10, PGR, FOXF1, PITX1, TWIST2, PITX2, TWIST1, PHOX2A, RARG, EMX1, EMX2, BARHL2, RXRG, EOMES, MSX1, HES5, ECOP, PRDM6, ZNF383, UNCX, LOC783396, OTP, FOXH1, LIF, T, TCF21, AHRR, LHX3, LHX4, HOXA10, LHX5, LOC789268, NKX2-5, LHX9, NKX2-3, KLF5, DMBX1, BMP4, BMP3, IKZF3, NTF3, ESRRG, SHOX2, DLX3, NR1I3, DLX1, DMRTC2, LOC789959, DLX6, DLX5, DLX4, HOPX, CRYM, KLF4, TCF15, KCNH1, HNF1B, FOXA2, ELF5, LOC783703, KCNIP3, GLI1, FERD3L, LOC789450, MKX, FOXB1, MYB, NR2F2, FGF2, NR2F1, AR, TBX15, ZNF287, TLE3, TLE4, NDUFA13, INHBA, FOXC2, KCNH2, ZNF483, KCNH5, LOC522736, SEC14L2, STAT4, LOC787194, PER1, ACTL6B, TLX2, SIM1, LOC615643, MYF6, LMX1B, TBX5, MYF5, TBX4, MEOX2, NEUROD1, LOC654400, NR5A2, FOXE3, PBX4, MYOD1, LMO3, ARNT2, CBX2, NR2E1, GDNF, IL10, LOC782183, HOXC6, ATOH1, OLIG3, GATA5, GATA3, HOXC4, GATA4, OLIG1, ATOH7, ZNF180, SATB2, LOC787396, MLXIPL, HES6, AHR, PTHLH, ASCL2, ASCL1, HHEX, SIX1, TFAP2A, TFAP2C, NFE2L3, ASCL4, LOC527381, ONECUT1, LOC781206, SOX2, LIN28B, DBX2, VDR, MEIS3, MEIS2, HOXA7, OVOL1, DBX1, GSX2, RFX4, MAFB, FOXA1, GSX1, NEUROG1, NEUROG3, HOXB3, FEZF2, HOXB4, GCM2, HOXB2, ATF3, HOXB7, EBF2, HOXB6, BMI1, HR, PAX6, PAX5, DMRTA2, PAX3, PAX1, FEV, CRX, LBH, HEY1, PAX9, LOC509704, POU5F1, PAX8, SOX18, ALX4, ALX3, EGR1, NANOG, EGR4, OTX2, ESR1, MIXL1, HOXC11, HOXC13, NRL, LOC617563, CUX2, CUX1, IRX3, SBNO2, ABLIM3, TRIB3, LOC618065, MSX2, HAND1, POU2F3, PYCARD, NFATC4, POU3F2, POU3F1, EPO, CEBPA, INSM1, MAF, FOXL2, FOXL1, ISL1, VSX2, ID2, IRF5, ID1, IRF6, IRF8, HEYL, SP7, ID3, F2R	1242	1166	8785	1.36	3.10E-05
Annotation Cluster 4 (Enrichment Score: 10.40242929598037)										
SP_PIR_KEYWORDS	g-protein coupled receptor	60	2.316	4.73E-12	F2RL2, GPR84, F2RL3, CASR, TACR3, F2RL1, LHCGR, VIPR1, GHRHR, EDNRA, EDNRB, S1PR3, S1PR1, LTB4R, GALR2, LOC781367, MC5R, EBI2, LPHN1, C5AR1, PTGER3, GPR92, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, CRHR1, SSTR2, GRM3, ADRB1, PTGDR, NK1R,	985	177	7349	2.53	1.80E-10

					TSHR, CALCR, DRD1, PRLHR, GPRC5C, ADORA2B, OPRK1, NPY2R, ADCYAP1R1, PTH1R, GPR6, OXTR, BDKRB2, GPR4, ADRB3, HCRTR1, ADRA2A, PTGFR, FZD6, FZD10, AVPR1B, ADRA1B, AVPR1A, UTS2R, GHSR, F2R, HTR2A					
INTERPRO	IPR000276:7TM GPCR, rhodopsin-like	54	2.084	1.01E-10	F2RL2, F2RL3, MCHR1, GPR84, GPR162, GPR85, TACR3, F2RL1, LHCGR, EDNRA, EDNRB, S1PR3, S1PR1, HTR1A, LTB4R, GALR2, LOC781367, MC5R, EBI2, PTGER3, C5AR1, GPR92, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, SSTR2, ADRB1, PTGDR, NK1R, TSHR, DRD1, PRLHR, ADORA2B, OPRK1, NPY2R, GPR6, OXTR, BDKRB2, GPR4, ADRB3, HCRTR1, ADRA2A, PTGFR, GPR37, AVPR1B, ADRA1B, AVPR1A, UTS2R, GHSR, HTR2A, F2R	1200	164	9171	2.52	3.99E-08
INTERPRO	IPR017452:GPCR, rhodopsin-like superfamily	54	2.084	1.30E-10	F2RL2, F2RL3, MCHR1, GPR84, GPR162, GPR85, TACR3, F2RL1, LHCGR, EDNRA, EDNRB, S1PR3, S1PR1, HTR1A, LTB4R, GALR2, LOC781367, MC5R, EBI2, PTGER3, C5AR1, GPR92, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, SSTR2, ADRB1, PTGDR, NK1R, TSHR, DRD1, PRLHR, ADORA2B, OPRK1, NPY2R, GPR6, OXTR, BDKRB2, GPR4, ADRB3, HCRTR1, ADRA2A, PTGFR, GPR37, AVPR1B, ADRA1B, AVPR1A, UTS2R, GHSR, HTR2A, F2R	1200	165	9171	2.5	4.12E-08
Annotation Cluster 5 (Enrichment Score: 8.146215146623781)										
GOTERM_MF_FAT	GO:0022843~voltage-gated cation channel activity	37	1.428	1.89E-09	KCNH1, KCNC1, KCNAB1, KCNA2, KCNA1, KCNA4, KCNJ10, KCNA6, CACNB4, KCNA5, KCNJ12, KCNJ11, SHKBP1, KCNS2, KCNQ3, KCNE1, KCNQ2, KCNG3, SCN5A, FGF2, KCNMA1, CACNA2D1, KCND2, CACNG2, KCNK2, KCNV1, KCTD8, KCNJ9, KCNJ8, CACNA1G, KCNF1, CACNA1E, KCNH2, CACNA1D, CACNA1A, KCTD12, KCNH5	1248	95	9249	2.89	1.41E-07
GOTERM_MF_FAT	GO:0022832~voltage-gated channel activity	41	1.582	1.39E-08	KCNH1, KCNC1, KCNAB1, SCN3B, KCNA2, KCNA1, KCNA4, KCNA6, KCNJ10, CACNB4, KCNA5, KCNJ12, KCNJ11, KCNIP3, SHKBP1, KCNS2, KCNQ3, KCNE1, KCNQ2, KCNG3, SCN5A, FGF2, KCNMA1, CACNA2D1, KCND2, CACNG2, KCNK1, KCNK2, KCNV1, KCTD8, KCNJ9, KCNJ8, CACNA1G, KCNF1, SCN4B, CACNA1E, KCNH2, CACNA1D, CACNA1A, KCNH5, KCTD12	1248	119	9249	2.55	8.83E-07
GOTERM_MF_FAT	GO:0005244~voltage-gated ion channel activity	41	1.582	1.39E-08	KCNH1, KCNC1, KCNAB1, SCN3B, KCNA2, KCNA1, KCNA4, KCNA6, KCNJ10, CACNB4, KCNA5, KCNJ12, KCNJ11, KCNIP3, SHKBP1, KCNS2, KCNQ3, KCNE1, KCNQ2, KCNG3, SCN5A, FGF2, KCNMA1, CACNA2D1, KCND2, CACNG2, KCNK1, KCNK2, KCNV1, KCTD8, KCNJ9, KCNJ8, CACNA1G, KCNF1, SCN4B, CACNA1E, KCNH2, CACNA1D, CACNA1A, KCNH5, KCTD12	1248	119	9249	2.55	8.83E-07
Annotation Cluster 6 (Enrichment Score: 7.458505989675213)										

GOTERM_MF_FAT	GO:0005267~potassium channel activity	36	1.389	2.81E-09	KCNK17, KCNH1, KCNC1, KCNAB1, KCNA2, KCNA1, KCNA4, KCNJ10, KCNA6, KCNA5, KCNJ12, KCNJ11, KCNIP3, SHKBP1, KCNS2, KCNQ3, KCNE1, KCNQ2, KCNG3, KCNMA1, KCND2, KCNK1, KCNK2, KCNV1, KCNK4, KCTD8, KCNN4, KCNT1, KCNN1, KCNJ9, KCNJ8, KCNN2, KCNF1, KCNH2, KCTD12, KCNH5	1248	92	9249	2.9	1.93E-07
GOTERM_BP_FAT	GO:0006813~potassium ion transport	37	1.428	5.83E-08	KCNK17, KCNH1, KCNC1, ATP1B1, KCNAB1, ATP1B2, KCNA2, KCNA1, KCNA4, KCNJ10, KCNA6, KCNA5, KCNJ12, KCNJ11, KCNIP3, SHKBP1, KCNS2, KCNQ3, KCNE1, KCNQ2, KCNG3, KCNMA1, KCND2, KCNK1, KCNK2, KCNV1, KCNK4, KCTD8, KCNT1, KCNN1, KCNJ9, KCNJ8, KCNN2, KCNF1, KCNH2, KCTD12, KCNH5	1242	102	8785	2.57	1.02E-05
GOTERM_MF_FAT	GO:0005249~voltage-gated potassium channel activity	28	1.081	2.57E-07	KCNH1, KCNC1, KCNAB1, KCNA2, KCNA1, KCNA4, KCNJ10, KCNA6, KCNA5, KCNJ12, KCNJ11, SHKBP1, KCNQ3, KCNS2, KCNE1, KCNG3, KCNQ2, KCNMA1, KCND2, KCNK2, KCNV1, KCTD8, KCNJ9, KCNJ8, KCNF1, KCNH2, KCTD12, KCNH5	1248	72	9249	2.88	1.20E-05
Annotation Cluster 7 (Enrichment Score: 6.738373191455444)										
GOTERM_MF_FAT	GO:0008528~peptide receptor activity, G-protein coupled	31	1.196	1.06E-07	GPR83, F2RL2, F2RL3, PRLHR, TACR3, NPY2R, OPRK1, F2RL1, OXTR, BDKRB2, EDNRA, HCRTR2, EDNRB, HCRTR1, GALR2, MC5R, C5AR1, CCKBR, PROKR2, NPR1, PROKR1, NPR3, NTSR1, SSTR5, SSTR2, NK1R, AVPR1B, AVPR1A, UTS2R, F2R, OPRD1	1248	82	9249	2.8	5.27E-06
GOTERM_MF_FAT	GO:0001653~peptide receptor activity	31	1.196	1.06E-07	GPR83, F2RL2, F2RL3, PRLHR, TACR3, NPY2R, OPRK1, F2RL1, OXTR, BDKRB2, EDNRA, HCRTR2, EDNRB, HCRTR1, GALR2, MC5R, C5AR1, CCKBR, PROKR2, NPR1, PROKR1, NPR3, NTSR1, SSTR5, SSTR2, NK1R, AVPR1B, AVPR1A, UTS2R, F2R, OPRD1	1248	82	9249	2.8	5.27E-06
GOTERM_MF_FAT	GO:0042277~peptide binding	34	1.312	5.38E-07	GPR83, F2RL2, CALCR, F2RL3, PRLHR, TACR3, NPY2R, CRHBP, OPRK1, F2RL1, OXTR, BDKRB2, EDNRA, HCRTR2, EDNRB, HCRTR1, GALR2, MC5R, KDELR1, C5AR1, CCKBR, PROKR2, NPR1, PROKR1, NPR3, NTSR1, SSTR5, SSTR2, NK1R, AVPR1B, AVPR1A, UTS2R, F2R, OPRD1	1248	101	9249	2.49	2.28E-05
Annotation Cluster 8 (Enrichment Score: 6.578741050689114)										
INTERPRO	IPR006201:Neurotransmitter-gated ion-channel	17	0.656	4.30E-08	GABRD, GABRA2, GLRB, GLRA1, GABRA4, LOC100138074, GABRB2, GABRB1, MGC139528, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRND, CHRNA3, CHRNG, GABRP	1200	28	9171	4.64	9.73E-06
INTERPRO	IPR006202:Neurotransmitter-gated ion-channel ligand-binding	17	0.656	4.30E-08	GABRD, GABRA2, GLRB, GLRA1, GABRA4, LOC100138074, GABRB2, GABRB1, MGC139528, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRND, CHRNA3, CHRNG, GABRP	1200	28	9171	4.64	9.73E-06
INTERPRO	IPR006029:Neurotransmitter-gated ion-channel	16	0.618	9.66E-08	GABRD, GABRA2, GLRB, GLRA1, GABRA4, GABRB2, GABRB1, MGC139528, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, CHRNG, GABRP	1200	26	9171	4.7	1.91E-05

	transmembrane region									
INTERPRO	IPR018000:Neurotransmitter-gated ion-channel, conserved site	16	0.618	9.66E-08	GABRD, GABRA2, GLRB, GLRA1, GABRA4, GABRB2, GABRB1, MGC139528, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, CHRNG, GABRP	1200	26	9171	4.7	1.91E-05
PIR_SUPERFAMILY	PIRSF002443:acetylcholine receptor	12	0.463	7.40E-05	GLRB, GABRA2, GABRA4, GLRA1, GABRB1, CHRNA5, CHRNB4, CHRND, CHRNA7, CHRNA3, GABRP, CHRNG	558	22	3890	3.8	0.0192872
Annotation Cluster 9 (Enrichment Score: 5.931891644140119)										
INTERPRO	IPR000742:EGF-like, type 3	32	1.235	1.29E-08	PTGS2, LTBP2, PTGS1, NELL2, BTC, BCAN, DLK2, DLK1, ACAN, TGFA, MRCL, NRG1, THBS1, THBS2, THBS4, TMEFF2, TNXB, EGFL7, ADAM23, EFEMP2, EFEMP1, NTNG2, FBLN1, THBD, EGFLAM, MGC139448, DLL4, FBLN5, VCAN, WIF1, ADAM12, VLDLR	1200	82	9171	2.98	3.39E-06
INTERPRO	IPR006210:EGF-like	29	1.119	2.92E-06	PTGS2, LTBP2, NELL2, BTC, BCAN, DLK2, DLK1, CSPG5, RSPO3, TGFA, MRCL, NRG1, THBS1, THBS2, THBS4, TMEFF2, TNXB, EGFL7, ADAM23, EFEMP2, NTNG2, FBLN1, THBD, EGFLAM, DLL4, MGC139448, VCAN, WIF1, VLDLR	1200	87	9171	2.55	3.85E-04
SMART	SM00181:EGF	29	1.119	4.27E-05	PTGS2, LTBP2, NELL2, BTC, BCAN, DLK2, DLK1, CSPG5, RSPO3, TGFA, MRCL, NRG1, THBS1, THBS2, THBS4, TMEFF2, TNXB, EGFL7, ADAM23, EFEMP2, NTNG2, FBLN1, THBD, EGFLAM, DLL4, MGC139448, VCAN, WIF1, VLDLR	661	87	4364	2.2	0.0038627
Annotation Cluster 10 (Enrichment Score: 5.481954390503736)										
GOTERM_BP_FAT	GO:0007517~muscle organ development	32	1.235	2.81E-07	MYOD1, RBP4, MYL2, ELN, PAX3, CACNB4, CXADR, HOXD10, LIF, LY6E, HAND1, PAK1, NR2F2, COL11A1, NKX2-5, PITX1, MYF6, FOXL2, ACTA1, CRYAB, MYF5, CACNG2, AFG3L2, TNNI3, HOMER1, MSX1, MEOX2, TAGLN, SIX1, PDGFRB, LOC654400, TCF15	1242	86	8785	2.63	3.23E-05
GOTERM_BP_FAT	GO:0060537~muscle tissue development	25	0.965	9.35E-06	MYOD1, RBP4, MYL2, ELN, CACNB4, CXADR, HOXD10, HAND1, LY6E, PAK1, NR2F2, COL11A1, NKX2-5, PITX1, FOXL2, ACTA1, MYF5, CACNG2, AFG3L2, TNNI3, HOMER1, MEOX2, SIX1, PDGFRB, LOC654400	1242	68	8785	2.6	6.07E-04
GOTERM_BP_FAT	GO:0014706~striated muscle tissue development	24	0.926	1.36E-05	RBP4, MYOD1, FOXL2, ACTA1, MYL2, MYF5, ELN, CACNG2, CACNB4, CXADR, AFG3L2, HOMER1, TNNI3, HOXD10, LY6E, MEOX2, HAND1, SIX1, PAK1, NR2F2, LOC654400, COL11A1, NKX2-5, PITX1	1242	65	8785	2.61	7.83E-04
Annotation Cluster 11 (Enrichment Score: 5.330322960380449)										
GOTERM_BP_FAT	GO:0050801~ion homeostasis	50	1.93	2.70E-07	CASR, JPH2, GLRA1, SLC9A3, EDN2, SNCA, EDN1, CKB, EDNRB, APOE, LTF, CHRNA7, MT3, KCNMA1, PRKCA, PTGER3, LOC786683, CCKBR, LOC783224, CACNG2, PRKCB, RHCG, LOC100139857, LOC525947, CALCR, PTH1R, GPR6, TAC1, CACNB4, CLDN11, KCNA5, ATP6V1B1, FKBP1B, CCL28, SYPL2, VDR, CD9, KCNE1,	1242	168	8785	2.11	3.37E-05

					GAL3ST1, GLRB, UPK3A, AFG3L2, TNNI3, KDR, CACNA1G, CHRNB4, CHRNB2, CACNA1A, CHRNG, F2R					
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	45	1.737	1.13E-06	CALCR, CASR, JPH2, GLRA1, EDN2, PTH1R, EDN1, SNCA, GPR6, TAC1, CACNB4, KCNA5, CLDN11, FKBP1B, CCL28, SYPL2, CKB, CD9, VDR, APOE, KCNE1, LTF, CHRNA7, GAL3ST1, MT3, PRKCA, KCNMA1, GLRB, PTGER3, LOC786683, CCKBR, LOC783224, CACNG2, TNNI3, AFG3L2, PRKCB, RHCG, LOC100139857, CHRNB4, CACNA1G, LOC525947, CHRNB2, CACNA1A, F2R, CHRNG	1242	151	8785	2.11	1.12E-04
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	45	1.737	1.67E-06	CALCR, CASR, JPH2, GLRA1, EDN2, PTH1R, EDN1, SNCA, GPR6, TAC1, CACNB4, KCNA5, CLDN11, FKBP1B, CCL28, SYPL2, CKB, CD9, VDR, APOE, KCNE1, LTF, CHRNA7, GAL3ST1, MT3, PRKCA, KCNMA1, GLRB, PTGER3, LOC786683, CCKBR, LOC783224, CACNG2, TNNI3, AFG3L2, PRKCB, RHCG, LOC100139857, CHRNB4, CACNA1G, LOC525947, CHRNB2, CACNA1A, F2R, CHRNG	1242	153	8785	2.08	1.51E-04
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	57	2.2	3.59E-06	CASR, JPH2, GLRA1, EDN2, SLC9A3, SNCA, EDN1, CKB, EDNRB, SLC2A4, APOE, LTF, CHRNA7, MT3, KCNMA1, PRKCA, AVP, PTGER3, LOC786683, CCKBR, LOC783224, CACNG2, PRKCB, PTHLH, RHCG, LOC100139857, LOC525947, CALCR, RBP4, PTH1R, GPR6, TAC1, CLDN11, KCNA5, CACNB4, ATP6V1B1, CCL28, SYPL2, FKBP1B, CD9, VDR, KCNE1, GAL3ST1, LPL, GLRB, FOXA1, UPK3A, AFG3L2, TNNI3, KDR, CHRNB4, CACNA1G, CHRNB2, CACNA1E, CACNA1A, F2R, CHRNG	1242	218	8785	1.85	2.82E-04
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	48	1.853	0.001223	CALCR, CASR, JPH2, GLRA1, EDN2, PTH1R, EDN1, SNCA, GPR6, TAC1, CACNB4, CLDN11, KCNA5, FKBP1B, CCL28, SYPL2, CKB, CD9, VDR, APOE, KCNE1, LTF, CHRNA7, GAL3ST1, MT3, PRKCA, KCNMA1, GLRB, PTGER3, LOC786683, AIFM3, CCKBR, LOC783224, CACNG2, TNNI3, AFG3L2, PRKCB, KCNN4, RHCG, LOC100139857, TXNDC6, CHRNB4, CACNA1G, LOC525947, CHRNB2, CACNA1A, F2R, CHRNG	1242	215	8785	1.58	0.0257706
Annotation Cluster 12 (Enrichment Score: 5.209817423404222)										
SP_PIR_KEYWORDS	potassium transport	18	0.695	5.28E-07	KCNMA1, KCNH1, KCNC1, KCNAB1, ATP1B2, KCNA2, KCNA4, KCNJ10, KCNA5, KCNK1, KCNJ12, KCNJ11, KCNV1, KCNIP3, KCNQ3, KCNJ8, KCNE1, KCNF1	985	35	7349	3.84	1.09E-05
GOTERM_MF_FAT	GO:0030955~potassium ion binding	19	0.733	1.82E-05	KCNMA1, KCNH1, KCNC1, KCNAB1, ATP1B2, KCNA2, KCNA4, KCNJ10, KCNA5, KCNK1, KCNJ12, KCNJ11, KCNV1, KCNIP3, KCNQ3, KCNJ8, PKLR, KCNE1, KCNF1	1248	47	9249	3	6.01E-04
SP_PIR_KEYWORDS	potassium	18	0.695	2.44E-05	KCNMA1, KCNH1, KCNC1, KCNAB1, ATP1B2, KCNA2, KCNA4, KCNJ10, KCNA5, KCNK1, KCNJ12, KCNJ11, KCNV1, KCNIP3, KCNQ3, KCNJ8, KCNE1, KCNF1	985	44	7349	3.05	3.96E-04
Annotation Cluster 13 (Enrichment Score: 5.015326164240715)										
GOTERM_BP_FAT	GO:0055065~metal ion homeostasis	28	1.081	1.69E-07	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, VDR, APOE, CHRNA7,	1242	68	8785	2.91	2.53E-05

					MT3, PRKCA, KCNMA1, LOC786683, PTGER3, CCKBR, UPK3A, TNNI3, KDR, PRKCB, LOC100139857, CACNA1A, F2R					
GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	26	1.003	9.85E-07	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, VDR, APOE, CHRNA7, MT3, PRKCA, KCNMA1, LOC786683, PTGER3, CCKBR, TNNI3, PRKCB, LOC100139857, CACNA1A, F2R	1242	65	8785	2.83	1.01E-04
GOTERM_BP_FAT	GO:0055074~calcium ion homeostasis	25	0.965	1.41E-06	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, VDR, APOE, CHRNA7, PRKCA, LOC786683, PTGER3, CCKBR, TNNI3, PRKCB, KDR, LOC100139857, CACNA1A, F2R	1242	62	8785	2.85	1.32E-04
GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	24	0.926	2.85E-06	PRKCA, CALCR, CASR, JPH2, LOC786683, PTGER3, CCKBR, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, TNNI3, SYPL2, CCL28, FKBP1B, PRKCB, VDR, APOE, LOC100139857, CHRNA7, CACNA1A, F2R	1242	60	8785	2.83	2.36E-04
GOTERM_BP_FAT	GO:0055080~cation homeostasis	35	1.351	1.30E-05	CALCR, CASR, JPH2, SLC9A3, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, ATP6V1B1, FKBP1B, SYPL2, CCL28, VDR, EDNRB, APOE, LTF, CHRNA7, MT3, PRKCA, KCNMA1, PTGER3, LOC786683, CCKBR, LOC783224, UPK3A, TNNI3, KDR, PRKCB, RHCG, LOC100139857, LOC525947, CACNA1A, F2R	1242	115	8785	2.15	7.62E-04
GOTERM_BP_FAT	GO:0030003~cellular cation homeostasis	29	1.119	1.73E-04	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, VDR, APOE, LTF, CHRNA7, MT3, PRKCA, KCNMA1, LOC786683, PTGER3, CCKBR, LOC783224, TNNI3, PRKCB, LOC100139857, LOC525947, CACNA1A, F2R	1242	99	8785	2.07	0.00565
GOTERM_BP_FAT	GO:0055066~di-, tri-valent inorganic cation homeostasis	28	1.081	2.05E-04	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, VDR, APOE, LTF, CHRNA7, PRKCA, LOC786683, PTGER3, CCKBR, LOC783224, TNNI3, KDR, PRKCB, LOC100139857, LOC525947, CACNA1A, F2R	1242	95	8785	2.08	0.0061701
GOTERM_BP_FAT	GO:0030005~cellular di-, tri-valent inorganic cation homeostasis	27	1.042	2.44E-04	CALCR, CASR, JPH2, EDN2, EDN1, PTH1R, GPR6, TAC1, CACNB4, SYPL2, CCL28, FKBP1B, VDR, APOE, LTF, CHRNA7, PRKCA, LOC786683, PTGER3, CCKBR, LOC783224, TNNI3, PRKCB, LOC100139857, LOC525947, CACNA1A, F2R	1242	91	8785	2.1	0.0067769
Annotation Cluster 14 (Enrichment Score: 4.993558707825291)										
GOTERM_MF_FAT	GO:0005539~glycosaminoglycan binding	24	0.926	2.92E-07	HAPLN2, BMP4, LPL, HAPLN1, HAPLN4, HAPLN3, TNXB, CXCL5, PGLYRP1, TLR2, BCAN, PF4, EGFLAM, CD44, APOE, CRISPLD2, RSPO3, ACAN, PTN, ADAMTS1, VCAN, THBS1, THBS2, FGF2	1248	56	9249	3.18	1.30E-05
GOTERM_MF_FAT	GO:0001871~pattern binding	25	0.965	4.14E-06	CXCL5, PGLYRP1, TLR2, BCAN, PF4, CD44, APOE, CRISPLD2, RSPO3, ACAN, PTN, PTX3, THBS1, THBS2, FGF2, BMP4, HAPLN2, LPL, HAPLN1, HAPLN4, TNXB, HAPLN3, EGFLAM, ADAMTS1, VCAN	1248	68	9249	2.72	1.47E-04
GOTERM_MF_FAT	GO:0030247~polysa	25	0.965	4.14E-	CXCL5, PGLYRP1, TLR2, BCAN, PF4, CD44, APOE,	1248	68	9249	2.72	1.47E-04

	ccharide binding			06	CRISPLD2, RSPO3, ACAN, PTN, PTX3, THBS1, THBS2, FGF2, BMP4, HAPLN2, LPL, HAPLN1, HAPLN4, TNXB, HAPLN3, EGFLAM, ADAMTS1, VCAN					
GOTERM_MF_FAT	GO:0030246~carbohydrate binding	34	1.312	0.002119	CXCL5, GALNT6, TLR2, PGLYRP1, BCAN, PF4, CD44, CRISPLD2, APOE, RSPO3, UPK1A, ACAN, PTN, THBS1, PTX3, THBS2, FGF2, GALNT13, LPHN1, BMP4, HAPLN2, HAPLN1, LPL, HAPLN4, HAPLN3, TNXB, LGALS12, COLEC12, EGFLAM, IGF2R, GFPT2, ADAMTS1, VCAN, LOC782210	1248	148	9249	1.7	0.0472992
Annotation Cluster 15 (Enrichment Score: 4.955433603646678)										
GOTERM_BP_FAT	GO:0001944~vasculature development	38	1.467	2.27E-06	FGFR2, FGF18, CDX2, PDGFA, EDN1, CDH2, GJA4, MMP2, SHH, T, TCF21, S1PR1, HEY1, HAND1, APOE, TGFA, SOX18, LOX, ADRA2B, THBS1, NR2F2, FGF2, ANGPT2, NKX2-5, BMP4, KLF5, PDPN, ITGA4, TNNI3, KDR, THY1, PROK2, CXCL17, MEOX2, DLL4, ECSCR, COL1A2, COL1A1	1242	121	8785	2.22	1.99E-04
GOTERM_BP_FAT	GO:0001568~blood vessel development	36	1.389	9.01E-06	FGFR2, FGF18, CDX2, PDGFA, EDN1, CDH2, GJA4, MMP2, SHH, T, S1PR1, HEY1, HAND1, APOE, TGFA, SOX18, LOX, ADRA2B, THBS1, NR2F2, ANGPT2, NKX2-5, FGF2, BMP4, KLF5, ITGA4, TNNI3, KDR, THY1, PROK2, CXCL17, MEOX2, DLL4, ECSCR, COL1A2, COL1A1	1242	118	8785	2.16	5.98E-04
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	30	1.158	6.67E-05	FGFR2, FGF18, PDGFA, EDN1, CDH2, SHH, T, S1PR1, HEY1, HAND1, APOE, TGFA, SOX18, ADRA2B, THBS1, NR2F2, ANGPT2, NKX2-5, FGF2, KLF5, BMP4, ITGA4, TNNI3, KDR, THY1, PROK2, CXCL17, MEOX2, DLL4, ECSCR	1242	99	8785	2.14	0.0026518
Annotation Cluster 16 (Enrichment Score: 4.829513614204084)										
GOTERM_BP_FAT	GO:0060284~regulation of cell development	24	0.926	3.97E-06	BMP4, IRX3, DTX1, EDN1, FOXA1, SOX2, PAX6, ISL1, THY1, METRN, DLX1, ATOH1, ITGB1BP3, HES5, LOC787355, SIX1, CHRNB2, SEMA4D, IGFBP3, NKX2-5, FGF2, NEFL, CACNA1A, MT3	1242	61	8785	2.78	2.96E-04
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	23	0.888	5.73E-06	IRX3, DTX1, FOXA1, SOX2, PAX6, ISL1, GLI1, THY1, METRN, DLX1, ATOH1, HES5, LOC787355, SIX1, LHX5, CHRNB2, SEMA4D, GHSR, NKX2-5, FGF2, NEFL, CACNA1A, MT3	1242	58	8785	2.8	4.07E-04
GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	17	0.656	2.35E-05	IRX3, DTX1, SOX2, FOXA1, PAX6, ISL1, THY1, ATOH1, METRN, HES5, LOC787355, SIX1, CHRNB2, SEMA4D, NKX2-5, NEFL, CACNA1A	1242	38	8785	3.16	0.0012328
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	19	0.733	8.99E-05	IRX3, DTX1, SOX2, FOXA1, PAX6, ISL1, THY1, DLX1, ATOH1, METRN, HES5, LOC787355, SIX1, CHRNB2, SEMA4D, NKX2-5, NEFL, CACNA1A, MT3	1242	50	8785	2.69	0.0034355
Annotation Cluster 17 (Enrichment Score: 3.974148908748379)										
GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	13	0.502	1.79E-05	CALCR, PTGER3, ADORA2B, PTH1R, ADRB3, GNAL, S1PR3, UCN3, SSTR2, S1PR1, ADRB1, APOE, TSHR	1242	23	8785	4	9.90E-04

GOTERM_BP_FAT	GO:0007188~G-protein signaling, coupled to cAMP nucleotide second messenger	12	0.463	3.86E-05	CALCR, ADRB3, S1PR3, GNAL, SSTR2, UCN3, PTGER3, ADRB1, S1PR1, ADORA2B, PTH1R, TSHR	1242	21	8785	4.04	0.0017197
GOTERM_BP_FAT	GO:0007187~G-protein signaling, coupled to cyclic nucleotide second messenger	12	0.463	3.86E-05	CALCR, ADRB3, S1PR3, GNAL, SSTR2, UCN3, PTGER3, ADRB1, S1PR1, ADORA2B, PTH1R, TSHR	1242	21	8785	4.04	0.0017197
GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	14	0.54	3.96E-05	CALCR, AVP, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB1, S1PR1, PDE2A, TSHR	1242	28	8785	3.54	0.0017392
GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	13	0.502	5.24E-05	CALCR, AVP, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, S1PR1, ADRB1, TSHR	1242	25	8785	3.68	0.0021696
GOTERM_BP_FAT	GO:0019933~cAMP-mediated signaling	12	0.463	6.74E-05	CALCR, ADRB3, S1PR3, GNAL, SSTR2, UCN3, PTGER3, ADRB1, S1PR1, ADORA2B, PTH1R, TSHR	1242	22	8785	3.86	0.0026452
GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	14	0.54	9.63E-05	CALCR, AVP, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, S1PR1, ADRB1, APOE, TSHR	1242	30	8785	3.3	0.0035886
GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	14	0.54	9.63E-05	CALCR, AVP, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, S1PR1, ADRB1, APOE, TSHR	1242	30	8785	3.3	0.0035886
GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	15	0.579	1.02E-04	CALCR, AVP, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB1, S1PR1, PDE2A, APOE, TSHR	1242	34	8785	3.12	0.00376
GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	15	0.579	1.48E-04	CALCR, AVP, ADORA2B, PTH1R, EDN1, ADRB3, GNAL, S1PR3, UCN3, SSTR2, ADRB1, S1PR1, PDE2A, APOE, TSHR	1242	35	8785	3.03	0.0049109
GOTERM_BP_FAT	GO:0045761~regulation of adenylate cyclase activity	11	0.425	2.44E-04	CALCR, ADRB3, S1PR3, GNAL, SSTR2, UCN3, ADRB1, S1PR1, ADORA2B, PTH1R, TSHR	1242	21	8785	3.71	0.0068402
GOTERM_BP_FAT	GO:0031279~regulation of cyclase activity	11	0.425	9.05E-04	CALCR, ADRB3, S1PR3, GNAL, SSTR2, UCN3, ADRB1, S1PR1, ADORA2B, PTH1R, TSHR	1242	24	8785	3.24	0.0202877
GOTERM_BP_FAT	GO:0051339~regulation of lyase activity	11	0.425	0.001877	CALCR, ADRB3, S1PR3, GNAL, SSTR2, UCN3, ADRB1, S1PR1, ADORA2B, PTH1R, TSHR	1242	26	8785	2.99	0.0377037
Annotation Cluster 18 (Enrichment Score: 3.8949901859251477)										
GOTERM_BP_FAT	GO:0060541~respiratory system development	19	0.733	6.61E-05	FGFR2, BMP4, FGF18, RBP4, FGFR4, PDPN, PDGFA, FOXA1, SOX2, GLI1, KDR, PTHLH, TCF21, PDGFRA, HOPX, LOX, CUX1, LOC654400, FGF2	1242	49	8785	2.74	0.0026662
GOTERM_BP_FAT	GO:0030324~lung development	18	0.695	1.77E-04	FGFR2, BMP4, FGF18, RBP4, FGFR4, PDPN, PDGFA, FOXA1, GLI1, KDR, PTHLH, TCF21, PDGFRA, HOPX, LOX,	1242	48	8785	2.65	0.0056604

					CUX1, LOC654400, FGF2					
GOTERM_BP_FAT	GO:0030323~respiratory tube development	18	0.695	1.77E-04	FGFR2, BMP4, FGF18, RBP4, FGFR4, PDPN, PDGFA, FOXA1, GLI1, KDR, PTHLH, TCF21, PDGFRA, HOPX, LOX, CUX1, LOC654400, FGF2	1242	48	8785	2.65	0.0056604
Annotation Cluster 19 (Enrichment Score: 3.839982027242997)										
GOTERM_BP_FAT	GO:0050880~regulation of blood vessel size	14	0.54	1.45E-04	CASR, AVP, ADORA2B, EDN2, EDN1, LOC784945, ADRB3, CALCB, EDNRB, ECE2, ADRB1, APOE, NPPC, NPPB	1242	31	8785	3.19	0.0048948
GOTERM_BP_FAT	GO:0003018~vascular process in circulatory system	14	0.54	1.45E-04	CASR, AVP, ADORA2B, EDN2, EDN1, LOC784945, ADRB3, CALCB, EDNRB, ECE2, ADRB1, APOE, NPPC, NPPB	1242	31	8785	3.19	0.0048948
GOTERM_BP_FAT	GO:0035150~regulation of tube size	14	0.54	1.45E-04	CASR, AVP, ADORA2B, EDN2, EDN1, LOC784945, ADRB3, CALCB, EDNRB, ECE2, ADRB1, APOE, NPPC, NPPB	1242	31	8785	3.19	0.0048948
Annotation Cluster 20 (Enrichment Score: 3.812964832939763)										
GOTERM_BP_FAT	GO:0031175~neuron projection development	27	1.042	3.30E-06	CCK, ATL1, UCHL1, PAX6, GDNF, EFHD1, ATOH1, GALR2, LHX4, PAK1, NEFL, LOC506110, STMN3, NTF3, KIF5C, NTNG2, AFG3L2, ISL1, EPHA4, FEZF2, DLX5, EFNA5, CHRNB2, NGFR, GAP43, CACNA1A, GFRA3	1242	73	8785	2.62	2.66E-04
GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron differentiation	23	0.888	2.65E-05	LOC506110, CCK, NTF3, ATL1, KIF5C, UCHL1, PAX6, NTNG2, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, DLX5, LHX4, CHRNB2, EFNA5, NGFR, NEFL, CACNA1A, GAP43, GRK1, GFRA3	1242	63	8785	2.58	0.001297
GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	22	0.849	2.90E-05	LOC506110, CCK, NTF3, ATL1, KIF5C, UCHL1, PAX6, NTNG2, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, DLX5, LHX4, CHRNB2, EFNA5, NGFR, NEFL, CACNA1A, GAP43, GFRA3	1242	59	8785	2.64	0.001394
GOTERM_BP_FAT	GO:0007409~axonogenesis	21	0.81	4.22E-05	LOC506110, CCK, NTF3, ATL1, KIF5C, UCHL1, PAX6, NTNG2, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, DLX5, LHX4, CHRNB2, EFNA5, NGFR, NEFL, GAP43, GFRA3	1242	56	8785	2.65	0.0018261
GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	22	0.849	1.46E-04	LOC506110, CCK, NTF3, ATL1, KIF5C, UCHL1, PAX6, NTNG2, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, DLX5, LHX4, CHRNB2, EFNA5, NGFR, NEFL, CACNA1A, GAP43, GFRA3	1242	65	8785	2.39	0.0048781
GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiation	24	0.926	2.17E-04	LOC506110, CCK, NTF3, ATL1, KIF5C, UCHL1, PAX6, NTNG2, ISL1, AFG3L2, CRYGB, EPHA4, FEZF2, ATOH1, DLX5, LHX4, CHRNB2, EFNA5, NGFR, NEFL, CACNA1A, GAP43, GRK1, GFRA3	1242	76	8785	2.23	0.0061493
GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	22	0.849	5.66E-04	LOC506110, CCK, NTF3, ATL1, KIF5C, UCHL1, PAX6, NTNG2, ISL1, AFG3L2, EPHA4, FEZF2, ATOH1, DLX5, LHX4, CHRNB2, EFNA5, NGFR, NEFL, CACNA1A, GAP43, GFRA3	1242	71	8785	2.19	0.013768
GOTERM_BP_FAT	GO:0000902~cell morphogenesis	27	1.042	0.002874	SHROOM1, CCK, ATL1, UCHL1, PAX6, CRYGB, ATOH1, LHX4, NEFL, LOC506110, NTF3, PDPN, KIF5C, NTNG2, UPK3A, ISL1, AFG3L2, EPHA4, FEZF2, DLX5, EFNA5, CHRNB2, NGFR, GAP43, CACNA1A, GFRA3, GRK1	1242	106	8785	1.8	0.0532913

GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	29	1.119	0.008786	SHROOM1, CCK, ATL1, UCHL1, PAX6, CRYGB, CD9, ATOH1, LHX4, NEFL, LOC506110, ACTA1, NTF3, PDPN, KIF5C, NTNG2, UPK3A, ISL1, AFG3L2, EPHA4, FEZF2, DLX5, EFNA5, CHRNB2, NGFR, GAP43, CACNA1A, GFRA3, GRK1	1242	126	8785	1.63	0.1314796
Annotation Cluster 21 (Enrichment Score: 3.7562939604877776)										
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	58	2.239	2.17E-05	MYOD1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, ATOH1, GATA5, APOE, GATA3, GATA4, FGF2, EGR1, AR, AVP, RARG, RXRG, PRKCG, CD40, AHR, INHBA, HES5, SIX1, ADORA2B, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, LOC510369, PTX3, NKX2-5, EPO, NKX2-3, MYF6, BMP4, MAF, KLF5, IL3, BMP3, FOXL2, NTF3, FOXA1, MYF5, GSX1, ISL1, IRF6, NEUROD1, LOC654400, KLF4, F2R	1242	236	8785	1.74	0.0011796
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	56	2.161	3.57E-05	MYOD1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, ATOH1, GATA5, APOE, GATA3, GATA4, FGF2, EGR1, AVP, AR, RARG, RXRG, PRKCG, CD40, AHR, INHBA, HES5, SIX1, ADORA2B, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, NKX2-5, EPO, NKX2-3, MYF6, BMP4, MAF, KLF5, IL3, BMP3, FOXL2, NTF3, FOXA1, MYF5, GSX1, ISL1, IRF6, NEUROD1, LOC654400, KLF4, F2R	1242	229	8785	1.73	0.0016394
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	40	1.544	4.92E-05	MYOD1, HNF1B, ABLIM3, SOX2, PAX6, PAX3, GDNF, HOXD10, GLI1, CRX, LIF, FOXH1, T, ATOH1, MEIS2, HAND1, GATA3, GATA4, NKX2-5, FGF2, NKX2-3, MAF, BMP4, BMP3, AR, FOXL2, RARG, NTF3, MYF5, FOXA1, GSX1, RXRG, ISL1, AHR, INHBA, HES5, SIX1, NEUROD1, LOC654400, KLF4	1242	147	8785	1.92	0.002068
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	51	1.968	1.88E-04	MYOD1, HNF1B, GDF6, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, ATOH1, GATA5, GATA3, GATA4, FGF2, EGR1, AR, RARG, RXRG, AHR, INHBA, TNFSF13B, HES5, SIX1, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, NKX2-5, EPO, NKX2-3, MYF6, BMP4, KLF5, MAF, BMP3, IL3, FOXL2, NTF3, MYF5, FOXA1, GSX1, ISL1, IRF6, NEUROD1, LOC654400, KLF4, F2R	1242	215	8785	1.68	0.0058298
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	43	1.66	1.98E-04	MYOD1, HNF1B, ABLIM3, SOX2, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, FOXH1, LIF, T, ATOH1, MEIS2, HAND1, GATA3, GATA4, NKX2-5, FGF2, NKX2-3, EPO, BMP4, MAF, BMP3, FOXL2, AR, RARG, NTF3, MYF5, FOXA1, GSX1, RXRG, ISL1, AHR, INHBA, HES5, SIX1, NEUROD1, LOC654400, KLF4, F2R	1242	172	8785	1.77	0.006012
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	43	1.66	1.98E-04	MYOD1, HNF1B, ABLIM3, SOX2, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, FOXH1, LIF, T, ATOH1, MEIS2, HAND1, GATA3, GATA4, NKX2-5, FGF2, NKX2-3, EPO, BMP4, MAF, BMP3, FOXL2, AR, RARG, NTF3, MYF5, FOXA1, GSX1, RXRG, ISL1, AHR, INHBA, HES5, SIX1,	1242	172	8785	1.77	0.006012

					NEUROD1, LOC654400, KLF4, F2R					
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	49	1.891	2.11E-04	MYOD1, HNF1B, GDF6, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, ATOH1, GATA5, GATA3, GATA4, FGF2, EGR1, AR, RARG, RXRG, AHR, INHBA, HES5, SIX1, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, NKX2-5, EPO, NKX2-3, BMP4, KLF5, MAF, MYF6, BMP3, FOXL2, NTF3, MYF5, FOXA1, GSX1, ISL1, IRF6, NEUROD1, LOC654400, KLF4, F2R	1242	205	8785	1.69	0.0061749
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	58	2.239	2.64E-04	MYOD1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, ATOH1, GATA5, APOE, GATA3, GATA4, FGF2, SYK, EGR1, AR, AVP, RARG, RXRG, AHR, CARD11, INHBA, HES5, SIX1, ADORA2B, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, THBS1, PTX3, NKX2-5, EPO, NKX2-3, MYF6, BMP4, MAF, KLF5, IL3, BMP3, FOXL2, NTF3, FOXA1, MYF5, GSX1, ISL1, IRF6, NEUROD1, LOC654400, KLF4, F2R	1242	257	8785	1.6	0.0071965
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	58	2.239	3.61E-04	MYOD1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, ATOH1, GATA5, APOE, GATA3, GATA4, FGF2, SYK, EGR1, AR, AVP, RARG, RXRG, AHR, CARD11, INHBA, HES5, SIX1, ADORA2B, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, THBS1, PTX3, NKX2-5, EPO, NKX2-3, MYF6, BMP4, MAF, KLF5, IL3, BMP3, FOXL2, NTF3, FOXA1, MYF5, GSX1, ISL1, IRF6, NEUROD1, LOC654400, KLF4, F2R	1242	260	8785	1.58	0.0094996
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	54	2.084	8.81E-04	MYOD1, HNF1B, PDGFA, GDF6, PAX6, PAX3, GDNF, HOXD10, IL10, GLI1, CRX, ATOH1, GATA5, GATA3, GATA4, FGF2, SYK, EGR1, AR, RARG, RXRG, AHR, CARD11, INHBA, HES5, SIX1, ABLIM3, SOX2, LIF, FOXH1, T, MEIS2, HAND1, THBS1, NKX2-5, EPO, NKX2-3, MYF6, BMP4, MAF, KLF5, IL3, BMP3, FOXL2, NTF3, FOXA1, MYF5, GSX1, ISL1, IRF6, NEUROD1, LOC654400, KLF4, F2R	1242	246	8785	1.55	0.0200386
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	64	2.47	9.64E-04	MYOD1, HNF1B, PDGFA, GDF6, SNCA, PAX6, PAX3, GDNF, HOXD10, IL10, CRX, GLI1, ATOH1, GATA5, APOE, GATA3, GATA4, FGF2, SYK, EGR1, PRKCA, AR, RARG, RXRG, PRKCG, CD40, AHR, CARD11, INHBA, CCND1, TNFSF13B, HES5, CCND2, SIX1, IL12A, FGFR3, ABLIM3, SOX2, FOXH1, LIF, T, MEIS2, HAND1, THBS1, NKX2-5, EPO, NKX2-3, MYF6, BMP4, MAF, KLF5, IL3, BMP3, FOXL2, NTF3, FOXA1, MYF5, GSX1, ISL1, IRF6, NEUROD1, LOC654400, KLF4, F2R	1242	305	8785	1.48	0.0214245
Annotation Cluster 22 (nrichment Score: 3.472267495762944)										
UP_SEQ_FEATURE	region of interest:Tail	14	0.54	5.94E-05	KRT6C, INA, VIM, BFSP1, KRT81, KRT73, DES, KRT80, KRT5, KRT7, KRT8, NEFL, KRT83, KRT71	682	33	5635	3.51	0.0108648
UP_SEQ_FEATURE	region of interest:Linker 1	13	0.502	6.47E-05	INA, VIM, BFSP1, KRT81, KRT73, DES, KRT80, KRT5, KRT7, KRT8, NEFL, KRT71, KRT83	682	29	5635	3.7	0.0096874

UP_SEQ_FEATURE	region of interest:Coil 1A	13	0.502	6.47E-05	INA, VIM, BFSP1, KRT81, KRT73, DES, KRT80, KRT5, KRT7, KRT8, NEFL, KRT71, KRT83	682	29	5635	3.7	0.0096874
UP_SEQ_FEATURE	region of interest:Coil 1B	13	0.502	6.47E-05	INA, VIM, BFSP1, KRT81, KRT73, DES, KRT80, KRT5, KRT7, KRT8, NEFL, KRT71, KRT83	682	29	5635	3.7	0.0096874
UP_SEQ_FEATURE	region of interest:Rod	14	0.54	8.56E-05	KRT6C, INA, VIM, BFSP1, KRT81, KRT73, DES, KRT80, KRT5, KRT7, KRT8, NEFL, KRT83, KRT71	682	34	5635	3.4	0.0117489
UP_SEQ_FEATURE	region of interest:Head	13	0.502	9.61E-05	INA, VIM, BFSP1, KRT81, KRT73, DES, KRT80, KRT5, KRT7, KRT8, NEFL, KRT71, KRT83	682	30	5635	3.58	0.0121635
UP_SEQ_FEATURE	region of interest:Linker 12	12	0.463	2.28E-04	KRT73, KRT81, DES, KRT80, KRT5, KRT7, VIM, KRT8, BFSP1, NEFL, KRT83, KRT71	682	28	5635	3.54	0.0265851
UP_SEQ_FEATURE	region of interest:Coil 2	12	0.463	2.28E-04	KRT73, INA, KRT81, KRT6C, KRT80, KRT5, KRT7, VIM, KRT8, BFSP1, KRT83, KRT71	682	28	5635	3.54	0.0265851
SP_PIR_KEYWORDS	Intermediate filament	16	0.618	0.00257	KRT6C, INA, VIM, BFSP1, KRT81, KRT73, KRT82, DES, KRT80, KRT5, LOC787355, KRT7, KRT8, NEFL, KRT83, KRT71	985	52	7349	2.3	0.0281508
INTERPRO	IPR016044:Filament	15	0.579	0.003841	KRT6C, INA, VIM, KRT81, KRT73, KRT82, DES, KRT80, KRT5, LOC787355, KRT7, KRT8, NEFL, KRT83, KRT71	1200	50	9171	2.29	0.144702
INTERPRO	IPR018039:Intermediate filament protein, conserved site	15	0.579	0.005641	KRT6C, INA, VIM, BFSP1, KRT81, KRT73, KRT82, DES, KRT80, KRT5, KRT7, KRT8, NEFL, KRT83, KRT71	1200	52	9171	2.2	0.1881158
INTERPRO	IPR001664:Intermediate filament protein	15	0.579	0.005641	KRT6C, INA, VIM, KRT81, KRT73, KRT82, DES, KRT80, KRT5, LOC787355, KRT7, KRT8, NEFL, KRT83, KRT71	1200	52	9171	2.2	0.1881158
Annotation Cluster 23 (nrichment Score: 3.430368409876335)										
GOTERM_CC_FAT	GO:0005923~tight junction	17	0.656	7.01E-05	PRKCZ, CLDN7, F11R, LOC526866, CLDN9, CLDN4, CLDN3, CLDN6, CLDN5, CLDN10, MPP7, CLDN11, CXADR, AMOTL2, CLDN23, CLDN1, LOC536606	984	41	6966	2.94	0.0012711
GOTERM_CC_FAT	GO:0070160~occluding junction	17	0.656	7.01E-05	PRKCZ, CLDN7, F11R, LOC526866, CLDN9, CLDN4, CLDN3, CLDN6, CLDN5, CLDN10, MPP7, CLDN11, CXADR, AMOTL2, CLDN23, CLDN1, LOC536606	984	41	6966	2.94	0.0012711
GOTERM_CC_FAT	GO:0016327~apicolateral plasma membrane	18	0.695	0.001316	PRKCZ, F11R, CLDN7, LOC526866, CLDN9, CLDN4, CLDN3, CLDN6, CLDN5, CLDN10, MPP7, CLDN11, CXADR, AMOTL2, CLDN23, FZD6, CLDN1, LOC536606	984	56	6966	2.28	0.0175488
GOTERM_CC_FAT	GO:0043296~apical junction complex	17	0.656	0.002939	PRKCZ, CLDN7, F11R, LOC526866, CLDN9, CLDN4, CLDN3, CLDN6, CLDN5, CLDN10, MPP7, CLDN11, CXADR, AMOTL2, CLDN23, CLDN1, LOC536606	984	55	6966	2.19	0.0309329
Annotation Cluster 24 (Enrichment Score: 3.4291217609225852)										
INTERPRO	IPR001839:Transforming growth factor beta	10	0.386	9.82E-05	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, BMP7, GDNF	1200	17	9171	4.5	0.0086069
SMART	SM00204:TGFB	10	0.386	3.04E-04	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, BMP7, GDNF	661	17	4364	3.88	0.0204796
INTERPRO	IPR015615:Transforming growth factor-beta-related	9	0.347	4.05E-04	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, BMP7	1200	16	9171	4.3	0.0264108
INTERPRO	IPR017948:Transfor	8	0.309	0.0015	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10	1200	15	9171	4.08	0.073327

	ming growth factor beta, conserved site			85						5
Annotation Cluster 25 (Enrichment Score: 3.219967997045056)										
INTERPRO	IPR001881:EGF-like calcium-binding	15	0.579	1.29E-04	LTBP2, EGFL7, EFEMP2, NELL2, EFEMP1, DLK2, DLK1, FBLN1, THBD, FBLN5, DLL4, ACAN, VCAN, VLDLR, THBS4	1200	37	9171	3.1	0.0096649
SMART	SM00179:EGF_CA	15	0.579	5.89E-04	LTBP2, EGFL7, EFEMP2, NELL2, EFEMP1, DLK2, DLK1, FBLN1, THBD, FBLN5, DLL4, ACAN, VCAN, VLDLR, THBS4	661	37	4364	2.68	0.0263648
INTERPRO	IPR000152:EGF-type aspartate/asparagine hydroxylation conserved site	14	0.54	0.001206	LTBP2, EGFL7, EFEMP2, NELL2, EFEMP1, DLK2, DLK1, FBLN1, THBD, FBLN5, DLL4, ACAN, VCAN, VLDLR	1200	40	9171	2.67	0.0659851
INTERPRO	IPR018097:EGF-like calcium-binding, conserved site	13	0.502	0.001441	LTBP2, EGFL7, EFEMP2, NELL2, EFEMP1, DLK2, FBLN1, THBD, FBLN5, ACAN, VCAN, THBS4, VLDLR	1200	36	9171	2.76	0.0710547
Annotation Cluster 26 (Enrichment Score: 3.1680872789756704)										
GOTERM_MF_FAT	GO:0005540~hyaluronic acid binding	8	0.309	3.39E-04	HAPLN2, HAPLN1, HAPLN4, HAPLN3, CD44, ACAN, BCAN, VCAN	1248	12	9249	4.94	0.0094092
INTERPRO	IPR000538:Link	7	0.27	6.47E-04	HAPLN2, HAPLN1, HAPLN3, CD44, ACAN, BCAN, VCAN	1200	10	9171	5.35	0.037285
SMART	SM00445:LINK	7	0.27	0.001425	HAPLN2, HAPLN1, HAPLN3, CD44, ACAN, BCAN, VCAN	661	10	4364	4.62	0.0473166
Annotation Cluster 27 (Enrichment Score: 2.9449835820864276)										
INTERPRO	IPR018933:Netrin module, non-TIMP type	7	0.27	6.47E-04	SFRP5, SFRP1, C3, SFRP2, SFRP4, NTN4, FRZB	1200	10	9171	5.35	0.037285
SMART	SM00643:C345C	7	0.27	0.001425	SFRP5, SFRP1, C3, SFRP2, SFRP4, NTN4, FRZB	661	10	4364	4.62	0.0473166
INTERPRO	IPR001134:Netrin domain	8	0.309	0.001585	SFRP5, SFRP1, C3, SFRP2, SFRP4, NTN4, TIMP4, FRZB	1200	15	9171	4.08	0.0733275
Annotation Cluster 28 (Enrichment Score: 2.792203888069219)										
GOTERM_BP_FAT	GO:0031128~developmental induction	7	0.27	9.90E-04	BMP4, FGFR4, HOXC11, SIX1, SOX2, FGF2, GDNF	1242	10	8785	4.95	0.0216789
GOTERM_BP_FAT	GO:0045168~cell-cell signaling involved in cell fate specification	7	0.27	9.90E-04	BMP4, FGFR4, HOXC11, SIX1, SOX2, FGF2, GDNF	1242	10	8785	4.95	0.0216789
GOTERM_BP_FAT	GO:0001759~induction of an organ	6	0.232	0.004286	BMP4, FGFR4, HOXC11, SIX1, FGF2, GDNF	1242	9	8785	4.72	0.0748089
Annotation Cluster 29 (Enrichment Score: 2.725693780645293)										
GOTERM_BP_FAT	GO:0010579~positive regulation of adenylate cyclase	8	0.309	8.68E-04	CALCR, ADRB3, GNAL, UCN3, ADRB1, ADORA2B, PTH1R, TSHR	1242	13	8785	4.35	0.0200546

	activity by G-protein signaling pathway									
GOTERM_BP_FAT	GO:0010578~regulation of adenylate cyclase activity involved in G-protein signaling	8	0.309	8.68E-04	CALCR, ADRB3, GNAL, UCN3, ADRB1, ADORA2B, PTH1R, TSHR	1242	13	8785	4.35	0.0200546
GOTERM_BP_FAT	GO:0007189~activation of adenylate cyclase activity by G-protein signaling pathway	8	0.309	8.68E-04	CALCR, ADRB3, GNAL, UCN3, ADRB1, ADORA2B, PTH1R, TSHR	1242	13	8785	4.35	0.0200546
GOTERM_BP_FAT	GO:0007190~activation of adenylate cyclase activity	8	0.309	0.001525	CALCR, ADRB3, GNAL, UCN3, ADRB1, ADORA2B, PTH1R, TSHR	1242	14	8785	4.04	0.0313741
GOTERM_BP_FAT	GO:0045762~positive regulation of adenylate cyclase activity	8	0.309	0.002513	CALCR, ADRB3, GNAL, UCN3, ADRB1, ADORA2B, PTH1R, TSHR	1242	15	8785	3.77	0.0479386
GOTERM_BP_FAT	GO:0031281~positive regulation of cyclase activity	8	0.309	0.003928	CALCR, ADRB3, GNAL, UCN3, ADRB1, ADORA2B, PTH1R, TSHR	1242	16	8785	3.54	0.0700058
GOTERM_BP_FAT	GO:0051349~positive regulation of lyase activity	8	0.309	0.008458	CALCR, ADRB3, GNAL, UCN3, ADRB1, ADORA2B, PTH1R, TSHR	1242	18	8785	3.14	0.1294646
Annotation Cluster 30 (Enrichment Score: 2.6733643244411827)										
GOTERM_MF_FAT	GO:0015370~solute:sodium symporter activity	14	0.54	0.001609	SLC6A2, SLC6A20, SLC6A12, SLC6A3, SLC6A13, SLC10A4, LOC529341, LOC785907, SLC6A7, SLC6A5, SLC6A6, SLC13A3, SLC5A7, SLC1A1	1248	40	9249	2.59	0.0380362
GOTERM_MF_FAT	GO:0015294~solute:cation symporter activity	16	0.618	0.002247	SLC6A2, SLC6A20, SLC6A3, SLC6A12, SLC6A13, SLC10A4, LOC529341, SLC17A7, LOC785907, SLC2A6, SLC6A7, SLC6A5, SLC6A6, SLC13A3, SLC5A7, SLC1A1	1248	51	9249	2.33	0.0477195
GOTERM_MF_FAT	GO:0015293~symporter activity	19	0.733	0.00264	SLC6A2, SLC6A20, SLC6A3, SLC6A12, SLC6A13, SLC10A4, LOC529341, SLC34A2, SLC17A7, LOC785907, SLC2A6, SLC17A6, SLC6A7, SLC6A5, SLC6A6, SLC13A3, SLC5A7, SLC1A1, SLC5A11	1248	67	9249	2.1	0.0533085
Annotation Cluster 31 (Enrichment Score: 2.5882128098656034)										
GOTERM_CC_FAT	GO:0005626~insoluble fraction	47	1.814	0.001522	ARHGDIG, GAL3ST4, JPH2, GLRA1, PTGS2, SNCB, ATL1, SNCA, PTGS1, ACSBG2, ATP6V1B1, PCDHGA2, APLP1, ADRB3, DES, SLC2A4, RASGRP4, PTGES, CHRNA7, NT5E, SNAP25, PRKCA, MOGAT1, GLRB, STX1A, CYP1A1, CCKBR, CRYAB, CPNE6, ITGA3, HOMER1, ITPR3, CAMK2N1, SLC17A7, CD38, SSTR2, ADRB1, SLC17A6, DGAT1, LYNX1, DGAT2, ITGA5, IGF2R, HSD11B2, SLC13A3, STEAP2, GRB14	984	212	6966	1.57	0.0195588
GOTERM_CC_FAT	GO:0005624~memb	45	1.737	0.0021	ARHGDIG, GAL3ST4, JPH2, GLRA1, PTGS2, SNCB, ATL1,	984	204	6966	1.56	0.024224

	rane fraction			59	SNCA, PTGS1, ACSBG2, ATP6V1B1, PCDHGA2, APLP1, ADRB3, SLC2A4, RASGRP4, PTGES, CHRNA7, NT5E, SNAP25, PRKCA, GLRB, STX1A, MOGAT1, CYP1A1, CCKBR, CPNE6, ITGA3, HOMER1, ITPR3, CAMK2N1, SLC17A7, CD38, SSTR2, ADRB1, SLC17A6, DGAT1, LYNX1, DGAT2, ITGA5, IGF2R, HSD11B2, SLC13A3, STEAP2, GRB14					6
GOTERM_CC_FAT	GO:0000267~cell fraction	49	1.891	0.00523	JPH2, GLRA1, PTGS2, SNCB, ATL1, SNCA, PTGS1, PCDHGA2, DES, SLC2A4, PTGES, CHRNA7, NT5E, PRKCA, STX1A, CCKBR, CYP1A1, CRYAB, CD38, SSTR2, ADRB1, DGAT1, LYNX1, DGAT2, IGF2R, HSD11B2, STEAP2, GRB14, CRYBA4, ARHGDIG, GAL3ST4, ACSBG2, ATP6V1B1, APLP1, PCSK2, ADRB3, RASGRP4, SNAP25, GLRB, MOGAT1, CPNE6, ITGA3, ITPR3, HOMER1, CAMK2N1, SLC17A7, SLC17A6, ITGA5, SLC13A3	984	237	6966	1.46	0.0501409
Annotation Cluster 32 (Enrichment Score: 2.4239382492006647)										
GOTERM_BP_FAT	GO:0000122~negative regulation of transcription from RNA polymerase II promoter	27	1.042	1.34E-04	CDX2, SOX2, FST, CBX2, PAX3, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, NR2F1, EGR1, NANOG, RARG, FOXA1, TLE4, DLX1, MSX1, ID2, HES5, ID1, HOPX, ID3, CUX1, CRYM	1242	88	8785	2.17	0.0046387
GOTERM_BP_FAT	GO:0045892~negative regulation of transcription, DNA-dependent	31	1.196	0.001029	SBNO2, CDX2, SOX2, FST, CBX2, PAX3, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, NANOG, RARG, FOXA1, NDUFA13, TLE4, DLX1, MSX1, ID2, HES5, ID1, HOPX, ID3, CUX1, CRYM	1242	120	8785	1.83	0.0223516
GOTERM_BP_FAT	GO:0051253~negative regulation of RNA metabolic process	31	1.196	0.001187	SBNO2, CDX2, SOX2, FST, CBX2, PAX3, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, NANOG, RARG, FOXA1, NDUFA13, TLE4, DLX1, MSX1, ID2, HES5, ID1, HOPX, ID3, CUX1, CRYM	1242	121	8785	1.81	0.0252073
GOTERM_BP_FAT	GO:0009890~negative regulation of biosynthetic process	42	1.621	0.005061	SBNO2, CDX2, PDGFA, SOX2, EDN1, FST, HR, CBX2, PAX3, ITGB3, IL10, KCNIP3, FOXH1, VDR, HAND1, APOE, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, MYF6, NANOG, RARG, FOXA1, NDUFA13, TLE4, INHBB, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, ID3, CUX1, CACNA1A, CRYM	1242	195	8785	1.52	0.0852951
GOTERM_BP_FAT	GO:0016481~negative regulation of transcription	35	1.351	0.005164	SBNO2, CDX2, SOX2, FST, HR, CBX2, PAX3, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, MYF6, NANOG, RARG, FOXA1, NDUFA13, TLE4, NR1I3, DLX1, MSX1, ID2, HES5, ID1, PRDM6, HOPX, ID3, CUX1, CRYM	1242	155	8785	1.6	0.0864671
GOTERM_BP_FAT	GO:0051172~negative regulation of nitrogen compound metabolic process	37	1.428	0.006065	SBNO2, CDX2, SOX2, EDN1, FST, HR, CBX2, PAX3, IL10, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, MYF6, NANOG, RARG, FOXA1, NDUFA13, TLE4, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, ID3, CUX1, CRYM	1242	168	8785	1.56	0.0980976
GOTERM_BP_FAT	GO:0010629~negati	37	1.428	0.0073	SBNO2, CDX2, SOX2, FST, HR, CBX2, PAX3, KCNIP3,	1242	170	8785	1.54	0.116088

	ve regulation of gene expression			68	FOXH1, VDR, HAND1, CLP1, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, MYF6, BMP4, NANOG, RARG, FOXA1, NDUFA13, TLE4, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, ID3, CUX1, CRYM					7
GOTERM_BP_FAT	GO:0031327~negative regulation of cellular biosynthetic process	40	1.544	0.008479	SBNO2, CDX2, PDGFA, SOX2, EDN1, FST, HR, CBX2, PAX3, IL10, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, MYF6, NANOG, RARG, FOXA1, NDUFA13, TLE4, INHBB, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, ID3, CUX1, CACNA1A, CRYM	1242	189	8785	1.5	0.1290984
GOTERM_BP_FAT	GO:0045934~negative regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	36	1.389	0.008738	SBNO2, CDX2, SOX2, EDN1, FST, HR, CBX2, PAX3, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, MYF6, NANOG, RARG, FOXA1, NDUFA13, TLE4, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, ID3, CUX1, CRYM	1242	166	8785	1.53	0.131456
GOTERM_BP_FAT	GO:0010558~negative regulation of macromolecule biosynthetic process	39	1.505	0.010911	SBNO2, CDX2, SOX2, EDN1, FST, HR, CBX2, PAX3, ITGB3, IL10, KCNIP3, FOXH1, VDR, HAND1, OVOL1, NR2F2, NKX2-5, FGF2, TWIST2, NR2F1, EGR1, MYF6, NANOG, RARG, FOXA1, NDUFA13, TLE4, INHBB, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, ID3, CUX1, CRYM	1242	186	8785	1.48	0.1561622
GOTERM_BP_FAT	GO:0010605~negative regulation of macromolecule metabolic process	46	1.775	0.014067	SBNO2, CDX2, SOX2, EDN1, SNCA, FST, HR, CBX2, PAX3, ITGB3, BDKRB2, IL10, KCNIP3, FOXH1, VDR, HAND1, CLP1, OVOL1, THBS1, NR2F2, FGF2, NKX2-5, TWIST2, NR2F1, PRKCA, EGR1, MYF6, BMP4, NANOG, RARG, FOXA1, NDUFA13, TLE4, PRKCG, INHBB, NR1I3, DLX1, MSX1, HES5, ID2, ID1, PRDM6, HOPX, ID3, CUX1, CRYM	1242	231	8785	1.41	0.1873273
Annotation Cluster 33 (Enrichment Score: 2.3897317034736862)										
GOTERM_MF_FAT	GO:0004955~prostaglandin receptor activity	6	0.232	0.001737	PTGER3, PTGER4, PTGDR, LOC781367, PTGFR, HPGD	1248	8	9249	5.56	0.039953
GOTERM_MF_FAT	GO:0004954~prostanoid receptor activity	6	0.232	0.003476	PTGER3, PTGER4, PTGDR, LOC781367, PTGFR, HPGD	1248	9	9249	4.94	0.063883
GOTERM_MF_FAT	GO:0004953~icosanoid receptor activity	6	0.232	0.003476	PTGER3, PTGER4, PTGDR, LOC781367, PTGFR, HPGD	1248	9	9249	4.94	0.063883
INTERPRO	IPR008365:Prostanoid receptor	5	0.193	0.013151	PTGER3, PTGER4, PTGDR, LOC781367, PTGFR	1200	8	9171	4.78	0.3371227
Annotation Cluster 34 (Enrichment Score: 2.3602060755250664)										
GOTERM_BP_FAT	GO:0060043~regulation of cardiac muscle cell proliferation	5	0.193	0.001759	FGFR2, RBP4, GATA4, CXADR, FGF2	1242	5	8785	7.07	0.0358677
GOTERM_BP_FAT	GO:0055024~regulation of cardiac muscle tissue	5	0.193	0.001759	FGFR2, RBP4, GATA4, CXADR, FGF2	1242	5	8785	7.07	0.0358677

	development									
GOTERM_BP_FAT	GO:0055021~regulation of cardiac muscle growth	5	0.193	0.001759	FGFR2, RBP4, GATA4, CXADR, FGF2	1242	5	8785	7.07	0.0358677
GOTERM_BP_FAT	GO:0060420~regulation of heart growth	5	0.193	0.001759	FGFR2, RBP4, GATA4, CXADR, FGF2	1242	5	8785	7.07	0.0358677
GOTERM_BP_FAT	GO:0046620~regulation of organ growth	6	0.232	0.165023	FGFR2, RBP4, IL7, GATA4, CXADR, FGF2	1242	21	8785	2.02	0.8152474
Annotation Cluster 35 (Enrichment Score: 2.3302773758897715)										
SP_PIR_KEYWORDS	chloride channel	10	0.386	5.60E-04	GLRB, GABRA2, GABRA4, GLRA1, GABRB2, GABRB1, TTYH1, CFTR, ANO4, GABRP	985	20	7349	3.73	0.0072589
GOTERM_CC_FAT	GO:0034707~chloride channel complex	10	0.386	8.30E-04	GLRB, GABRA2, GABRA4, GLRA1, GABRB2, GABRB1, TTYH1, CFTR, ANO4, GABRP	984	20	6966	3.54	0.0119863
SP_PIR_KEYWORDS	chloride	10	0.386	0.001873	GLRB, GABRA2, GABRA4, GLRA1, GABRB2, GABRB1, TTYH1, CFTR, ANO4, GABRP	985	23	7349	3.24	0.0211036
GOTERM_MF_FAT	GO:0031404~chloride ion binding	10	0.386	0.002788	GLRB, GABRA2, GABRA4, GLRA1, GABRB2, GABRB1, TTYH1, CFTR, ANO4, GABRP	1248	24	9249	3.09	0.0537797
GOTERM_MF_FAT	GO:0043168~anion binding	11	0.425	0.00579	GLRB, GABRA2, GABRA4, GLRA1, GABRB2, GABRB1, TTYH1, CFTR, ANO4, GABRP, SLC34A2	1248	31	9249	2.63	0.0964745
GOTERM_MF_FAT	GO:0005254~chloride channel activity	11	0.425	0.041983	GLRB, GABRA2, GABRA4, SLC26A8, GLRA1, GABRB2, GABRB1, TTYH1, CFTR, ANO4, GABRP	1248	41	9249	1.99	0.4206927
GOTERM_MF_FAT	GO:0005253~anion channel activity	11	0.425	0.082574	GLRB, GABRA2, GABRA4, SLC26A8, GLRA1, GABRB2, GABRB1, TTYH1, CFTR, ANO4, GABRP	1248	46	9249	1.77	0.5905327
Annotation Cluster 36 (Enrichment Score: 2.3069362445435933)										
GOTERM_CC_FAT	GO:0008021~synaptic vesicle	14	0.54	0.001878	SYT1, GABRA2, RAB3B, STX1A, SYT4, SYT10, SYT5, SYT7, SYPL2, SLC17A7, DOC2A, SLC17A6, SYT17, MT3	984	39	6966	2.54	0.0224833
GOTERM_CC_FAT	GO:0030136~clathrin-coated vesicle	17	0.656	0.00435	SYT1, GABRA2, RAB3B, STX1A, SYT4, SYT10, SYT5, SYT7, SYPL2, SLC17A7, DOC2A, SLC17A6, SLC2A4, IGF2R, STEAP2, SYT17, MT3	984	57	6966	2.11	0.043009
GOTERM_CC_FAT	GO:0030135~coated vesicle	19	0.733	0.014692	SEC23A, SYT1, GABRA2, RAB3B, STX1A, SYT4, SYT10, SYT5, SYT7, SYPL2, SLC17A7, PACSIN1, DOC2A, SLC17A6, SLC2A4, IGF2R, STEAP2, SYT17, MT3	984	75	6966	1.79	0.1256873
Annotation Cluster 37 (Enrichment Score: 2.2941644208137317)										
UP_SEQ_FEATURE	metal ion-binding site:Calcium 3	7	0.27	8.23E-04	PRKCA, SYT1, MMP9, PRKCG, COLEC12, MMP2, PRKCB	682	11	5635	5.26	0.0868779
UP_SEQ_FEATURE	metal ion-binding site:Calcium 3; via carbonyl oxygen	6	0.232	0.003798	PRKCA, SYT1, MMP9, PRKCG, MMP2, PRKCB	682	10	5635	4.96	0.2822968
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2; via carbonyl oxygen	8	0.309	0.004961	PRKCA, SYT1, MMP9, CABP1, PRKCG, COLEC12, MMP2, PRKCB	682	19	5635	3.48	0.3375233
UP_SEQ_FEATURE	metal ion-binding site:Calcium 1	8	0.309	0.004961	PRKCA, SYT1, MMP9, CABP1, PRKCG, COLEC12, MMP2, PRKCB	682	19	5635	3.48	0.3375233
UP_SEQ_FEATURE	metal ion-binding site:Calcium 1; via	6	0.232	0.014231	PRKCA, SYT1, CABP1, PRKCG, COLEC12, PRKCB	682	13	5635	3.81	0.5986362

	carbonyl oxygen									
UP_SEQ_FEATURE	metal ion-binding site:Calcium 2	8	0.309	0.015694	PRKCA, SYT1, MMP9, CABP1, PRKCG, COLEC12, MMP2, PRKCB	682	23	5635	2.87	0.5947731
Annotation Cluster 38 (Enrichment Score: 2.272973668053311)										
INTERPRO	IPR017981:GPCR, family 2-like	9	0.347	0.002449	CALCR, CRHR1, FZD10, GPR133, ADCYAP1R1, PTH1R, VIPR1, GHRHR, LPHN1, FZD6	1200	20	9171	3.44	0.1079541
INTERPRO	IPR017983:GPCR, family 2, secretin-like, conserved site	7	0.27	0.003729	CALCR, CRHR1, GPR133, ADCYAP1R1, PTH1R, VIPR1, GHRHR, LPHN1	1200	13	9171	4.12	0.1477939
INTERPRO	IPR001879:GPCR, family 2, extracellular region	6	0.232	0.005402	CALCR, CRHR1, ADCYAP1R1, PTH1R, VIPR1, GHRHR, LPHN1	1200	10	9171	4.59	0.1888285
INTERPRO	IPR000832:GPCR, family 2, secretin-like	7	0.27	0.008628	CALCR, CRHR1, GPR133, ADCYAP1R1, PTH1R, VIPR1, GHRHR, LPHN1	1200	15	9171	3.57	0.2443124
SMART	SM00008:HormR	6	0.232	0.010141	CALCR, CRHR1, ADCYAP1R1, PTH1R, VIPR1, GHRHR, LPHN1	661	10	4364	3.96	0.2421326
Annotation Cluster 39 (Enrichment Score: 2.100866112550209)										
GOTERM_BP_FAT	GO:0040012~regulation of locomotion	21	0.81	0.002556	PRKCA, ICAM1, HS3ST5, PDGFB, PDGFA, MMP9, EDN2, SNCA, F2RL1, PAX6, ITGB3, THY1, KDR, APOE, DLL4, CXCL16, THBS1, SST, FGF2, TSHR, F2R	1242	74	8785	2.01	0.0481203
GOTERM_BP_FAT	GO:0030334~regulation of cell migration	17	0.656	0.012345	ICAM1, PDGFB, PDGFA, EDN2, MMP9, F2RL1, PAX6, ITGB3, THY1, KDR, APOE, DLL4, CXCL16, THBS1, SST, FGF2, F2R	1242	63	8785	1.91	0.1716667
GOTERM_BP_FAT	GO:0051270~regulation of cell motion	18	0.695	0.01579	ICAM1, PDGFB, PDPN, PDGFA, MMP9, EDN2, F2RL1, PAX6, ITGB3, THY1, KDR, APOE, DLL4, CXCL16, THBS1, SST, FGF2, F2R	1242	70	8785	1.82	0.2069834
Annotation Cluster 40 (Enrichment Score: 2.0628037826401338)										
GOTERM_CC_FAT	GO:0005892~nicotinic acetylcholine-gated receptor-channel complex	6	0.232	0.002141	CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3, CHRNG	984	8	6966	5.31	0.0247862
GOTERM_BP_FAT	GO:0035095~behavioral response to nicotine	5	0.193	0.004686	CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1242	6	8785	5.89	0.0805857
GOTERM_BP_FAT	GO:0035094~response to nicotine	5	0.193	0.009716	CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1242	7	8785	5.05	0.1422862
GOTERM_MF_FAT	GO:0042166~acetylcholine binding	6	0.232	0.022311	CHRM1, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1248	13	9249	3.42	0.2660369
GOTERM_MF_FAT	GO:0015464~acetylcholine receptor activity	6	0.232	0.022311	CHRM1, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRNA3	1248	13	9249	3.42	0.2660369
Annotation Cluster 41 (Enrichment Score: 2.024283509815954)										
INTERPRO	IPR000008:C2 calcium-dependent	14	0.54	0.005884	PRKCA, CPNE9, SYT1, ABR, SYT4, SYT5, CPNE6, PRKCH, PRKCG, PRKCB, CADPS, DOC2A, CADPS2, SYT13	1200	47	9171	2.28	0.1913845

	membrane targeting									
INTERPRO	IPR018029:C2 membrane targeting protein	12	0.463	0.007584	PRKCA, CPNE9, SYT1, DOC2A, ABR, SYT4, SYT5, CPNE6, PRKCH, SYT13, PRKCG, PRKCB	1200	38	9171	2.41	0.2306128
SMART	SM00239:C2	14	0.54	0.018949	PRKCA, CPNE9, SYT1, ABR, SYT4, SYT5, CPNE6, PRKCH, PRKCG, PRKCB, CADPS, DOC2A, CADPS2, SYT13	661	47	4364	1.97	0.3518549
Annotation Cluster 42 (Enrichment Score: 1.955320557934815)										
GOTERM_BP_FAT	GO:0016477~cell migration	27	1.042	0.00802	CCK, CCL2, PDGFB, EDN2, PAX6, PF4, ITGB2, CDH2, PAX3, GDNF, EDNRB, ATOH1, NR2F2, NKX2-3, NR2F1, PRKCA, ICAM1, LOC786683, EMX2, ITGA3, ITGA4, ISL1, KDR, ITGA5, SIX1, IL12A, GFRA3	1242	114	8785	1.68	0.1237998
GOTERM_BP_FAT	GO:0048870~cell motility	28	1.081	0.013029	CCK, CCL2, PDGFB, EDN2, PAX6, PF4, ITGB2, CDH2, PAX3, GDNF, EDNRB, ATOH1, CHRNA7, NR2F2, NKX2-3, NR2F1, PRKCA, ICAM1, LOC786683, EMX2, ITGA3, ITGA4, ISL1, KDR, ITGA5, SIX1, IL12A, GFRA3	1242	124	8785	1.6	0.1786918
GOTERM_BP_FAT	GO:0051674~localization of cell	28	1.081	0.013029	CCK, CCL2, PDGFB, EDN2, PAX6, PF4, ITGB2, CDH2, PAX3, GDNF, EDNRB, ATOH1, CHRNA7, NR2F2, NKX2-3, NR2F1, PRKCA, ICAM1, LOC786683, EMX2, ITGA3, ITGA4, ISL1, KDR, ITGA5, SIX1, IL12A, GFRA3	1242	124	8785	1.6	0.1786918
Annotation Cluster 43 (Enrichment Score: 1.9481348860230916)										
SP_PIR_KEYWORDS	Sodium transport	13	0.502	0.003771	ATP1B2, SCN3B, SLC38A11, SLC34A2, SLC17A7, ACCN1, SLC17A6, SLC5A8, SCN4B, SLC5A7, SCNN1A, SCN5A, SLC5A11	985	39	7349	2.49	0.0366841
SP_PIR_KEYWORDS	Sodium	10	0.386	0.017176	SLC17A7, ACCN1, SLC17A6, ATP1B2, SCN3B, SCN4B, SLC38A11, SCNN1A, SLC5A11, SLC34A2	985	31	7349	2.41	0.1335285
GOTERM_MF_FAT	GO:0031402~sodium ion binding	10	0.386	0.022089	SLC17A7, ACCN1, SLC17A6, ATP1B2, SCN3B, SCN4B, SLC38A11, SCNN1A, SLC5A11, SLC34A2	1248	32	9249	2.32	0.2672648
Annotation Cluster 44 (Enrichment Score: 1.7882114924855212)										
INTERPRO	IPR016054:Ly-6 antigen / uPA receptor -like	6	0.232	0.005402	LYPD1, LYNX1, LYPD3, LY6E, LY6H, PLAUR	1200	10	9171	4.59	0.1888285
SMART	SM00134:LU	6	0.232	0.010141	LYPD1, LYNX1, LYPD3, LY6E, LY6H, PLAUR	661	10	4364	3.96	0.2421326
INTERPRO	IPR001526:CD59 antigen	5	0.193	0.078833	LYNX1, LYPD3, LY6E, LY6H, PLAUR	1200	13	9171	2.94	0.8316579
Annotation Cluster 45 (Enrichment Score: 1.764761298343279)										
GOTERM_MF_FAT	GO:0015269~calcium-activated potassium channel activity	5	0.193	0.014664	KCNMA1, KCNN4, KCNT1, KCNN1, KCNN2	1248	8	9249	4.63	0.2062011
GOTERM_MF_FAT	GO:0005227~calcium activated cation channel activity	5	0.193	0.014664	KCNMA1, KCNN4, KCNT1, KCNN1, KCNN2	1248	8	9249	4.63	0.2062011
GOTERM_MF_FAT	GO:0022839~ion gated channel	5	0.193	0.023615	KCNMA1, KCNN4, KCNT1, KCNN1, KCNN2	1248	9	9249	4.12	0.2757557

	activity									
Annotation Cluster 46 (Enrichment Score: 1.753544591040803)										
SP_PIR_KEYWORDS	mitogen	10	0.386	0.002646	IL3, PDGFB, PDGFA, BTC, PTN, TGFA, IGF2, PDGFD, FGF2, FGF4	985	24	7349	3.11	0.0282983
GOTERM_BP_FAT	GO:0051781~positive regulation of cell division	8	0.309	0.02728	PDGFB, PDGFA, BTC, PTN, IGF2, PDGFD, FGF2, FGF4	1242	22	8785	2.57	0.3061909
GOTERM_BP_FAT	GO:0051302~regulation of cell division	8	0.309	0.076013	PDGFB, PDGFA, BTC, PTN, IGF2, PDGFD, FGF2, FGF4	1242	27	8785	2.1	0.585687
Annotation Cluster 47 (Enrichment Score: 1.716403497626699)										
GOTERM_MF_FAT	GO:0008066~glutamate receptor activity	7	0.27	0.014248	GRM3, GRIK1, GRIA2, GRIN2C, GRIK2, GRIK3, GRIN3B	1248	16	9249	3.24	0.2041334
GOTERM_MF_FAT	GO:0005234~extracellular-glutamate-gated ion channel activity	6	0.232	0.022311	GRIK1, GRIA2, GRIN2C, GRIK2, GRIK3, GRIN3B	1248	13	9249	3.42	0.2660369
GOTERM_MF_FAT	GO:0004970~ionotropic glutamate receptor activity	6	0.232	0.022311	GRIK1, GRIA2, GRIN2C, GRIK2, GRIK3, GRIN3B	1248	13	9249	3.42	0.2660369
Annotation Cluster 48 (Enrichment Score: 1.701389683116179)										
GOTERM_MF_FAT	GO:0019992~diacylglycerol binding	8	0.309	0.00451	PRKCA, PRKCZ, STAC, RASGRP4, CHN1, PRKCH, PRKCG, PRKCB	1248	17	9249	3.49	0.0789049
INTERPRO	IPR002219:Protein kinase C-like, phorbol ester/diacylglycerol binding	8	0.309	0.029639	PRKCA, PRKCZ, STAC, RASGRP4, CHN1, PRKCH, PRKCG, PRKCB	1200	24	9171	2.55	0.5363778
SMART	SM00109:C1	8	0.309	0.058857	PRKCA, PRKCZ, STAC, RASGRP4, CHN1, PRKCH, PRKCG, PRKCB	661	24	4364	2.2	0.6211288
Annotation Cluster 49 (Enrichment Score: 1.6796217389327168)										
GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	11	0.425	0.016053	ICAM1, PDGFA, PDPN, EDN2, MMP9, CXCL16, F2RL1, THBS1, FGF2, KDR, F2R	1242	34	8785	2.29	0.2082649
GOTERM_BP_FAT	GO:0030335~positive regulation of cell migration	10	0.386	0.023796	ICAM1, PDGFA, EDN2, MMP9, CXCL16, F2RL1, THBS1, FGF2, KDR, F2R	1242	31	8785	2.28	0.2789064
GOTERM_BP_FAT	GO:0040017~positive regulation of locomotion	11	0.425	0.023937	PRKCA, ICAM1, PDGFA, EDN2, MMP9, CXCL16, F2RL1, THBS1, FGF2, KDR, F2R	1242	36	8785	2.16	0.2792515
Annotation Cluster 50 (Enrichment Score: 1.6250860261477884)										
GOTERM_BP_FAT	GO:0014032~neural crest cell development	6	0.232	0.012301	EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1242	11	8785	3.86	0.1719062
GOTERM_BP_FAT	GO:0014033~neural crest cell	6	0.232	0.012301	EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1242	11	8785	3.86	0.1719062

	differentiation									
GOTERM_BP_FAT	GO:0048762~mesenchymal cell differentiation	7	0.27	0.024219	FGFR2, EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1242	17	8785	2.91	0.2809924
GOTERM_BP_FAT	GO:0060485~mesenchyme development	7	0.27	0.0321	FGFR2, EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1242	18	8785	2.75	0.3429976
GOTERM_BP_FAT	GO:0014031~mesenchymal cell development	6	0.232	0.063681	EDNRB, EDN1, CYP26A1, PAX3, ISL1, GDNF	1242	16	8785	2.65	0.53317
Annotation Cluster 51 (Enrichment Score: 1.5966423782468115)										
INTERPRO	IPR006028:Gamma-aminobutyric acid A receptor	8	0.309	0.001585	GABRD, GABRA2, MGC139528, GABRA4, GLRA1, GABRB2, GABRB1, GABRP	1200	15	9171	4.08	0.0733275
GOTERM_MF_FAT	GO:0004890~GABA-A receptor activity	6	0.232	0.084089	GABRD, GABRA2, GABRA4, GABRB2, GABRB1, GABRP	1248	18	9249	2.47	0.5890752
GOTERM_MF_FAT	GO:0016917~GABA receptor activity	6	0.232	0.12168	GABRD, GABRA2, GABRA4, GABRB2, GABRB1, GABRP	1248	20	9249	2.22	0.7114917
Annotation Cluster 52 (Enrichment Score: 1.5695517976033782)										
GOTERM_BP_FAT	GO:0010975~regulation of neuron projection development	7	0.27	0.008543	METRN, LOC787355, CHRNB2, SEMA4D, NEFL, CACNA1A, THY1	1242	14	8785	3.54	0.1293668
GOTERM_BP_FAT	GO:0010769~regulation of cell morphogenesis involved in differentiation	7	0.27	0.024219	METRN, LOC787355, CHRNB2, SEMA4D, NEFL, CACNA1A, THY1	1242	17	8785	2.91	0.2809924
GOTERM_BP_FAT	GO:0050770~regulation of axonogenesis	6	0.232	0.026883	METRN, LOC787355, SEMA4D, NEFL, CACNA1A, THY1	1242	13	8785	3.26	0.3035598
GOTERM_BP_FAT	GO:0031344~regulation of cell projection organization	7	0.27	0.094736	METRN, LOC787355, CHRNB2, SEMA4D, NEFL, CACNA1A, THY1	1242	23	8785	2.15	0.6567843
Annotation Cluster 53 (Enrichment Score: 1.5628272430017303)										
UP_SEQ_FEATURE	domain:Ig-like C2-type 3	6	0.232	0.009706	NCAM1, ICAM1, OPCML, PTPRF, ICAM3, NTM	682	12	5635	4.13	0.5045429
UP_SEQ_FEATURE	domain:Ig-like C2-type 1	7	0.27	0.0416	NCAM1, ICAM1, OPCML, PTPRF, ICAM3, CXADR, NTM	682	22	5635	2.63	0.8737499
UP_SEQ_FEATURE	domain:Ig-like C2-type 2	7	0.27	0.050743	NCAM1, ICAM1, OPCML, PTPRF, ICAM3, CXADR, NTM	682	23	5635	2.51	0.9088691
Annotation Cluster 54 (Enrichment Score: 1.5469850867397477)										
GOTERM_BP_FAT	GO:0030888~regulation of B cell proliferation	7	0.27	0.012564	CARD11, CD38, TNFSF13B, IL7, CHRNB2, CD40, IL10	1242	15	8785	3.3	0.1736475
GOTERM_BP_FAT	GO:0030890~positive regulation of B cell	6	0.232	0.018672	CARD11, CD38, TNFSF13B, IL7, CHRNB2, CD40	1242	12	8785	3.54	0.2313301

	proliferation									
GOTERM_BP_FAT	GO:0050871~positive regulation of B cell activation	7	0.27	0.052405	CARD11, CD38, TNFSF13B, IL7, CHRNB2, CD40, SYK	1242	20	8785	2.48	0.4743577
GOTERM_BP_FAT	GO:0050864~regulation of B cell activation	8	0.309	0.052768	CARD11, CD38, TNFSF13B, IL7, CHRNB2, CD40, IL10, SYK	1242	25	8785	2.26	0.4754092
Annotation Cluster 55 (Enrichment Score: 1.5448623143153664)										
INTERPRO	IPR001723:Steroid hormone receptor	10	0.386	0.014861	PGR, VDR, AR, NR1I3, RARG, ESR1, RXRG, RORC, NR2F2, NR2F1	1200	31	9171	2.47	0.3607657
INTERPRO	IPR008946:Nuclear hormone receptor, ligand-binding	10	0.386	0.018342	PGR, VDR, AR, NR1I3, RARG, ESR1, RXRG, RORC, NR2F2, NR2F1	1200	32	9171	2.39	0.4132558
INTERPRO	IPR000536:Nuclear hormone receptor, ligand-binding, core	10	0.386	0.02238	PGR, VDR, AR, NR1I3, RARG, ESR1, RXRG, RORC, NR2F2, NR2F1	1200	33	9171	2.32	0.4553786
INTERPRO	IPR001628:Zinc finger, nuclear hormone receptor-type	9	0.347	0.028605	PGR, VDR, NR1I3, RARG, ESR1, RXRG, RORC, NR2F2, NR2F1	1200	29	9171	2.37	0.5293442
SMART	SM00430:HOLI	10	0.386	0.051068	PGR, VDR, AR, NR1I3, RARG, ESR1, RXRG, RORC, NR2F2, NR2F1	661	33	4364	2	0.6134568
SMART	SM00399:ZnF_C4	9	0.347	0.060377	PGR, VDR, NR1I3, RARG, ESR1, RXRG, RORC, NR2F2, NR2F1	661	29	4364	2.05	0.6097889
Annotation Cluster 56 (Enrichment Score: 1.509208226524016)										
GOTERM_BP_FAT	GO:0055008~cardiac muscle tissue morphogenesis	6	0.232	0.026883	LY6E, HAND1, MYL2, TNNI3, COL11A1, NKX2-5	1242	13	8785	3.26	0.3035598
GOTERM_BP_FAT	GO:0060415~muscle tissue morphogenesis	6	0.232	0.026883	LY6E, HAND1, MYL2, TNNI3, COL11A1, NKX2-5	1242	13	8785	3.26	0.3035598
GOTERM_BP_FAT	GO:0055010~ventricular cardiac muscle morphogenesis	5	0.193	0.04106	LY6E, HAND1, MYL2, TNNI3, COL11A1	1242	10	8785	3.54	0.4052682
Annotation Cluster 57 (Enrichment Score: 1.4625363071650401)										
GOTERM_CC_FAT	GO:0030173~integral to Golgi membrane	11	0.425	0.001853	ST6GALNAC5, ST6GAL2, ST8SIA6, ST8SIA4, ST8SIA1, ST8SIA3, ST8SIA2, STEAP2, CUX1, LFNG, B4GALNT1	984	26	6966	3	0.0229503
GOTERM_CC_FAT	GO:0031228~intrinsic to Golgi membrane	11	0.425	0.001853	ST6GALNAC5, ST6GAL2, ST8SIA6, ST8SIA4, ST8SIA1, ST8SIA3, ST8SIA2, STEAP2, CUX1, LFNG, B4GALNT1	984	26	6966	3	0.0229503
GOTERM_CC_FAT	GO:0031301~integral to organelle membrane	14	0.54	0.119241	GABRA2, ST6GAL2, ST8SIA1, ST8SIA3, ST8SIA2, ST6GALNAC5, ST8SIA6, ST8SIA4, ASPHD1, CUX1, STEAP2, LFNG, UPK2, B4GALNT1	984	65	6966	1.52	0.5545208
GOTERM_CC_FAT	GO:0031300~intrinsic to organelle	14	0.54	0.269814	GABRA2, ST6GAL2, ST8SIA1, ST8SIA3, ST8SIA2, ST6GALNAC5, ST8SIA6, ST8SIA4, ASPHD1, CUX1,	984	76	6966	1.3	0.8226285

	membrane				STEAP2, LFNG, UPK2, B4GALNT1					
GOTERM_CC_FAT	GO:0000139~Golgi membrane	14	0.54	0.440565	SEC23A, ST6GAL2, ST8SIA1, ST8SIA3, ST8SIA2, CSPG5, ST6GALNAC5, ST8SIA6, ST8SIA4, CUX1, STEAP2, LFNG, B4GALNT1, SCAMP5	984	86	6966	1.15	0.9398679
Annotation Cluster 58 (Enrichment Score: 1.452032896505212)										
GOTERM_BP_FAT	GO:0042327~positive regulation of phosphorylation	14	0.54	0.007609	PRKCA, BMP4, IL3, FGFR3, GDF6, LIF, CCND1, CCND2, IL12A, THBS1, FGF2, EPO, SYK, GRK1	1242	45	8785	2.2	0.1184309
GOTERM_BP_FAT	GO:0010562~positive regulation of phosphorus metabolic process	14	0.54	0.007609	PRKCA, BMP4, IL3, FGFR3, GDF6, LIF, CCND1, CCND2, IL12A, THBS1, FGF2, EPO, SYK, GRK1	1242	45	8785	2.2	0.1184309
GOTERM_BP_FAT	GO:0045937~positive regulation of phosphate metabolic process	14	0.54	0.007609	PRKCA, BMP4, IL3, FGFR3, GDF6, LIF, CCND1, CCND2, IL12A, THBS1, FGF2, EPO, SYK, GRK1	1242	45	8785	2.2	0.1184309
GOTERM_BP_FAT	GO:0001934~positive regulation of protein amino acid phosphorylation	12	0.463	0.023616	PRKCA, BMP4, LIF, IL3, CCND1, FGFR3, CCND2, GDF6, IL12A, FGF2, SYK, EPO	1242	41	8785	2.07	0.2781762
GOTERM_BP_FAT	GO:0031401~positive regulation of protein modification process	12	0.463	0.096424	PRKCA, BMP4, LIF, IL3, CCND1, FGFR3, CCND2, GDF6, IL12A, FGF2, SYK, EPO	1242	51	8785	1.66	0.6622812
GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic process	14	0.54	0.224624	PRKCA, BMP4, IL3, FGFR3, GDF6, LIF, CCND1, CCND2, APOE, IL12A, THBS1, FGF2, EPO, SYK	1242	73	8785	1.36	0.8958213
GOTERM_BP_FAT	GO:0051247~positive regulation of protein metabolic process	14	0.54	0.304027	PRKCA, BMP4, IL3, FGFR3, GDF6, LIF, CCND1, CCND2, APOE, IL12A, THBS1, FGF2, EPO, SYK	1242	78	8785	1.27	0.9501607
Annotation Cluster 59 (Enrichment Score: 1.4187896000374836)										
GOTERM_BP_FAT	GO:0030097~hemopoiesis	24	0.926	0.026563	EGR1, BMI1, CALCR, BMP4, CD3D, CD8A, IL7, RORC, OSTM1, KDR, HOXB3, CARD11, HOXB7, ID2, IRF8, BCL11A, IL12A, HOXA9, KLF1, TSHR, NKX2-5, NKX2-3, EPO, SYK	1242	108	8785	1.57	0.3016294
GOTERM_BP_FAT	GO:0048534~hemopoietic or lymphoid organ development	26	1.003	0.030247	BMI1, CALCR, CD8A, RORC, CACNB4, BCL11A, HOXA9, NKX2-5, NKX2-3, SYK, EPO, EGR1, BMP4, CD3D, IL7, OSTM1, KDR, HOXB3, CARD11, HOXB7, ID2, SIX1, IRF8, IL12A, TSHR, KLF1	1242	121	8785	1.52	0.3277696
GOTERM_BP_FAT	GO:0002520~immune system development	26	1.003	0.068971	BMI1, CALCR, CD8A, RORC, CACNB4, BCL11A, HOXA9, NKX2-5, NKX2-3, SYK, EPO, EGR1, BMP4, CD3D, IL7, OSTM1, KDR, HOXB3, CARD11, HOXB7, ID2, SIX1, IRF8, IL12A, TSHR, KLF1	1242	131	8785	1.4	0.5545108

Annotation Cluster 60 (Enrichment Score: 1.3532214068948132)										
INTERPRO	IPR003961:Fibronectin, type III	14	0.54	0.022563	PHYHIPL, PHYHIP, TNXB, PTPRF, PTPRZ1, NCAM1, FSD1, EPHB6, FNDC5, EGFLAM, MYOM2, TRIM9, EPOR, EBI3	1200	55	9171	1.95	0.452552
INTERPRO	IPR008957:Fibronectin, type III-like fold	13	0.502	0.061832	TNXB, PTPRF, PTPRZ1, NCAM1, FSD1, EPHB6, FNDC5, EGFLAM, MYOM2, TRIM9, TGM1, EPOR, EBI3	1200	57	9171	1.74	0.7689722
SMART	SM00060:FN3	14	0.54	0.062478	PHYHIPL, PHYHIP, TNXB, PTPRF, PTPRZ1, NCAM1, FSD1, EPHB6, FNDC5, EGFLAM, MYOM2, TRIM9, EPOR, EBI3	661	55	4364	1.68	0.5841396

C. Foetal Pfam

Term	Count	%	P-value	Genes	List Total	Pop Hits	Pop Total	Fold Enrich-ment	Benjamini P-value
PF00046:Homeobox	47	1.830218	9.58E-23	IRX3, CDX1, HNF1B, ONECUT1, PAX6, PAX3, MEIS1, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, NKX2-5, LHX9, PITX1, DBX1, NKX2-3, PITX2, SATB1, NANOG, EMX2, ISL1, DLX3, HOXB4, HHEX, DLX1, MSX1, HOXC11, MEOX2, LASS4, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	1168	75	8945	4.799258	1.41E-19
PF00046:Homeobox domain	38	1.479751	3.65E-20	CDX1, HNF1B, ONECUT1, MEIS1, HOXD10, CRX, OTP, MSX2, HOXC6, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, LHX9, NKX2-5, PITX1, DBX1, PITX2, NANOG, ISL1, HOXB4, HHEX, DLX1, HOXC11, MSX1, MEOX2, LASS4, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1	1168	56	8945	5.196765	2.68E-17
PF00001:7tm_1	52	2.024922	5.97E-10	MCHR1, GPR162, TACR3, F2RL1, LHCGR, S1PR2, AGTR1, EDNRB, S1PR3, HTR1A, CXCR4, LTB4R, CXCR7, GALR2, LOC781367, MC5R, PTGER3, C5AR1, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, ADRB2, SSTR2, ADRB1, PTGDR, NK1R, TSHR, DRD1, PRLHR, ADORA2B, FFAR2, NPY2R, GPR6, OXTR, BDKRB2, GPR4, HCRTR1, ADRB3, ADRA2A, PTGFR, GPR37, AVPR1B, ADRA1B, MC4R, AVPR1A, UTS2R, GHSR, HTR2A, F2R	1168	162	8945	2.458249	2.92E-07
PF00001:7 transmembrane receptor	44	1.713396	1.44E-09	MCHR1, DRD1, PRLHR, ADORA2B, TACR3, OPRK1, LHCGR, GPR6, OXTR, BDKRB2, GPR4, ADRB3, EDNRB, S1PR3, AGTR1, HCRTR1, PTGIR, HTR1A, LTB4R, CXCR4, CXCR7, GALR2, ADRA2A, MC5R, LOC781367, C5AR1, PTGER3, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, PTGFR, SSTR2, ADRB2, ADRB1, AVPR1B, NK1R, ADRA1B, MC4R, UTS2R, TSHR, HTR2A	1168	128	8945	2.632572	5.29E-07
PF02931:Neur_chan_LBD	15	0.584112	1.47E-06	GABRD, GABRA2, GLRB, GLRA1, GABRA4, LOC100138074, GABRB1, GABRA5, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	1168	27	8945	4.254661	4.31E-04
PF00520:Ion_trans	17	0.661994	2.26E-06	KCNH1, KCNMA1, KCNC1, KCNA2, KCNA4, KCNA5, CNGA3, ITPR3, ITPR1, KCNV1, KCNQ3, KCNF1, CACNA1E, KCNH2, CACNA1D, SCN5A, CACNA1A	1168	35	8945	3.71979	5.53E-04
PF02932:Neur_chan_memb	14	0.545171	3.38E-06	GABRD, GABRA2, GLRB, GLRA1, GABRA4, GABRB1, GABRA5, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	1168	25	8945	4.288699	7.07E-04
PF00010:HLH	19	0.739875	3.80E-06	MYOD1, EPAS1, MYF5, HES6, AHR, ASCL2, TCF21, AHRR, ATOH1, HEY1, ID2, HAND1, HES5, ID1, EBF2, HEYL, NEUROD1, BHLHE41, TCF15	1168	44	8945	3.307032	6.96E-04
PF00019:TGF_beta	11	0.428349	1.12E-05	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, BMP7, GDNF, TGFB1	1168	17	8945	4.955429	0.001826
PF00008:EGF	20	0.778816	2.00E-05	TMEFF2, PTGS2, LTBP2, NTNG2, BCAN, DLK2, DLK1, THBD, EGFLAM, DLL4, PROZ, ACAN, TGFA, VCAN, WIF1, AREG, NRG1, THBS2, VLDLR, THBS4	1168	53	8945	2.889959	0.002923

PF02932:Neurotransmitter-gated ion-channel transmembrane region	13	0.506231	2.32E-05	GABRA2, GLRB, GLRA1, GABRA4, GABRB1, GABRA5, CHRNB4, CHRNA5, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	1168	25	8945	3.982363	0.003096
PF02931:Neurotransmitter-gated ion-channel ligand binding domain	13	0.506231	3.81E-05	GABRA2, GLRB, GLRA1, GABRA4, GABRB1, GABRA5, CHRNB4, CHRNA5, CHRNB2, CHRND, CHRNA7, CHRNA3, GABRP	1168	26	8945	3.829195	0.004644
PF01391:Collagen	16	0.623053	4.86E-04	COL4A3, CTHRC1, COL21A1, COL13A1, COL2A1, COLEC12, C1QA, EMID1, COL27A1, COL1A2, COL12A1, COL1A1, COL11A2, COL8A1, SCARA5, COL8A2	1168	46	8945	2.663788	0.049631

D. Lamb Pfam

Term	Count	%	P-value	Genes	List Total	Pop Hits	Pop Total	Fold Enrich-ment	Benjamini P-value
PF00046:Homeobox	44	1.698186	1.43E-19	IRX3, HNF1B, ONECUT1, PAX6, PAX3, HOXD10, OTP, CRX, HOXC6, MSX2, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, NKX2-5, LHX9, PITX1, DBX1, NKX2-3, PITX2, NANOG, EMX2, ISL1, HOXB3, DLX3, HOXB4, HHEX, DLX1, HOXC11, MSX1, MEOX2, HOXB7, HOXC13, DLX5, DLX4, HOXB6, SIX1, HOPX, UNCX	1180	75	8945	4.447232	2.09E-16
PF00046:Homeobox domain	35	1.35083	8.16E-17	HNF1B, ONECUT1, HOXD10, CRX, OTP, MSX2, HOXC6, DBX2, POU5F1, HOXC4, LHX3, LHX4, HOXA10, LHX5, POU3F2, POU3F1, ALX4, LHX9, NKX2-5, PITX1, DBX1, PITX2, NANOG, ISL1, HOXB4, HHEX, DLX1, HOXC11, MSX1, MEOX2, HOXB7, HOXC13, DLX5, HOXB6, SIX1, DLX4	1180	56	8945	4.737818	8.08E-14
PF00001:7tm_1	53	2.045542	2.67E-10	F2RL2, F2RL3, MCHR1, GPR84, GPR162, GPR85, TACR3, F2RL1, LHCGR, EDNRA, EDNRB, S1PR3, S1PR1, HTR1A, LTB4R, GALR2, LOC781367, MC5R, EBI2, PTGER3, C5AR1, GPR92, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, SSTR2, ADRB1, PTGDR, NK1R, TSHR, DRD1, PRLHR, ADORA2B, NPY2R, GPR6, OXTR, BDKRB2, GPR4, ADRB3, HCRTR1, ADRA2A, PTGFR, GPR37, AVPR1B, ADRA1B, AVPR1A, UTS2R, GHSR, HTR2A, F2R	1180	162	8945	2.480043	1.30E-07
PF00001:7 transmembrane receptor	44	1.698186	1.99E-09	F2RL2, MCHR1, GPR84, DRD1, PRLHR, ADORA2B, TACR3, OPRK1, LHCGR, GPR6, OXTR, BDKRB2, GPR4, EDNRA, ADRB3, S1PR3, EDNRB, HCRTR1, HTR1A, S1PR1, LTB4R, GALR2, ADRA2A, MC5R, LOC781367, EBI2, C5AR1, PTGER3, GPR92, CCKBR, PTGER4, HTR4, PROKR2, PROKR1, MRGPRF, PTGFR, SSTR2, ADRB1, AVPR1B, NK1R, ADRA1B, UTS2R, TSHR, HTR2A	1180	128	8945	2.6058	7.23E-07
PF02931:Neur_chan_LBD	17	0.656117	2.36E-08	GABRD, GABRA2, GLRB, GLRA1, GABRA4, LOC100138074, GABRB2, GABRB1, MGC139528, CHRNA5, CHRNB4, CHRNA7, CHRNB2, CHRND, CHRNA3, CHRNG, GABRP	1180	27	8945	4.772913	6.86E-06

PF02932:Neur_chan_memb	16	0.617522	5.19E-08	GABRD, GABRA2, GLRB, GLRA1, GABRA4, GABRB2, GABRB1, MGC139528, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, CHRNG, GABRP	1180	25	8945	4.851525	1.26E-05
PF02932:Neurotransmitter-gated ion-channel transmembrane region	15	0.578927	4.79E-07	GABRA2, GLRB, GLRA1, GABRA4, GABRB2, GABRB1, MGC139528, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, CHRNG, GABRP	1180	25	8945	4.548305	9.97E-05
PF02931:Neurotransmitter-gated ion-channel ligand binding domain	15	0.578927	9.13E-07	GABRA2, GLRB, GLRA1, GABRA4, GABRB2, GABRB1, MGC139528, CHRNA5, CHRNB4, CHRNB2, CHRND, CHRNA7, CHRNA3, CHRNG, GABRP	1180	26	8945	4.37337	1.66E-04
PF00520:Ion_trans	17	0.656117	2.59E-06	KCNH1, KCNMA1, KCNC1, TRPC3, KCNA2, KCNA4, KCNA5, CNGA3, ITPR3, KCNV1, KCNQ3, KCNF1, CACNA1E, KCNH2, CACNA1D, SCN5A, CACNA1A	1180	35	8945	3.681961	4.20E-04
PF00010:HLH	19	0.733308	4.41E-06	MYF6, MYOD1, MYF5, HES6, AHR, ASCL2, TCF21, AHRR, ATOH1, HEY1, ID2, HAND1, HES5, ID1, EBF2, HEYL, NEUROD1, ID3, TCF15	1180	44	8945	3.273401	6.41E-04
PF00008:EGF	21	0.810498	5.75E-06	TMEFF2, LTBP2, PTGS2, PTGS1, BTC, NTNG2, BCAN, DLK2, DLK1, THBD, EGFLAM, DLL4, ACAN, TGFA, VCAN, WIF1, NRG1, THBS1, THBS2, VLDLR, THBS4	1180	53	8945	3.003598	7.61E-04
PF07686:V-set	27	1.042069	2.64E-05	CADM3, CD8A, CADM1, CD8B, SCN3B, LOC786246, BCAN, CXADR, PDCD1, LOC790208, ACAN, IGLL1, ESAM, LOC786219, KIRREL3, LRRC4, HAPLN2, F11R, LOC782991, HAPLN1, HAPLN3, MPZ, MXRA8, LOC529709, VSTM2L, SCN4B, MGC151567, VCAN, TREM1	1180	86	8945	2.379927	0.003204
PF01391:Collagen	18	0.694712	3.94E-05	COL4A3, CTHRC1, COL21A1, COL13A1, COL2A1, COLEC12, C1QC, C1QA, C1QTNF3, EMID1, COL27A1, COL1A2, COL12A1, COL1A1, COL11A2, COL8A1, COL11A1, COL8A2	1180	46	8945	2.966286	0.004406
PF07686:Immunoglobulin V-set domain	21	0.810498	4.78E-05	LRRC4, LOC782991, MPZ, CADM1, CD8A, SCN3B, CD8B, LOC786246, BCAN, CXADR, PDCD1, LOC790208, LOC529709, VSTM2L, ACAN, SCN4B, IGLL1, VCAN, ESAM, MGC151567, LOC786219, NTM, KIRREL3	1180	60	8945	2.653178	0.00496
PF00822:PMP-22/EMP/MP20/Claudin family	10	0.385951	5.58E-05	CLDN7, CLDN4, CLDN3, CLDN5, CLDN1, CLDN10, CACNG2, CLDN11, NKG7, LIM2	1180	16	8945	4.737818	0.005403
PF00019:TGF_beta	10	0.385951	1.05E-04	INHBB, BMP4, INHBA, BMP3, BMP2, FOXJ1, GDF6, GDF10, BMP7, GDNF	1180	17	8945	4.459123	0.009487
PF00520:Ion transport protein	12	0.463142	1.51E-04	KCNH1, KCNMA1, KCNC1, TRPC3, KCNA2, KCNA4, KCNF1, KCNA5, CNGA3, ITPR3, CACNA1D, CACNA1A	1180	25	8945	3.638644	0.012156
PF00010:Helix-loop-helix DNA-binding domain	12	0.463142	2.31E-04	MYF6, ASCL2, MYOD1, TCF21, ATOH1, HES5, HAND1, HEY1, ID1, NEUROD1, TWIST2, AHR	1180	26	8945	3.498696	0.017554
PF01391:Collagen triple helix repeat	15	0.578927	2.69E-04	COL4A3, COL21A1, COL13A1, COL2A1, COLEC12, C1QC, C1QA, EMID1, COL1A2, COL12A1, COL1A1, COL11A2, COL8A1, COL11A1, COL8A2	1180	39	8945	2.91558	0.01939

E. Foetal KEGG Pathway

Term	Count	%	P-value	Genes	List Total	Pop Hits	Pop Total	Fold Enrich-ment	Benjamini P-value
bta04080:Neuroactive ligand-receptor interaction	99	3.86	1.90E-25	GRIK1, GRIK2, LOC790124, GABRB1, GRIK3, LHCGR, F2RL1, GRIN3B, VIPR1, S1PR2, AGTR1, S1PR3, PTGIR, HTR1B, HTR1A, GALR1, LTB4R, GRIN2C, GALR3, GALR2, LOC781367, C5AR1, HTR4, NTSR1, NTSR2, CRHR1, CRHR2, SSTR2, SSTR1, HTR7, HTR6, GPR50, GLP1R, DRD1, PRLHR, ADORA2B, ADORA2A, ADCYAP1R1, PTH1R, BDKRB2, LOC541212, HCRTR2, ADRB3, HCRTR1, ADRA2A, ADRA2B, GABRQ, GABRP, GABRD, GABRA2, GABRA4, PTH2R, GABRA5, P2RX2, AVPR1B, AVPR1A, ADRA1B, UTS2R, GHSR, ADRA1D, MTNR1A, GPR83, MCHR1, TACR3, GLRA1, EDNRB, MC5R, HTR5A, PTGER3, CCKBR, PTGER4, GRM1, GRM3, ADRB2, LOC523484, ADRB1, CHRM1, GRM7, PTGDR, GIPR, GRM6, NK1R, TSHR, CALCR, PARD3, NPY2R, OPRK1, OXTR, GCGR, HRH3, GLRB, PTGFR, LEP, GRIA2, MC4R, NMBR, F2R, OPRD1, HTR2A	709	239	4940	2.886144	3.43E-23
bta04020:Calcium signaling pathway	62	2.41	1.12E-13	SLC8A3, ADCY3, ADCY4, GNA14, ADCY1, TACR3, ADCY8, LHCGR, LOC515280, ITPKA, AGTR1, ATP2B2, EDNRB, GRIN2C, CHRNA7, HTR5A, PRKCA, PTGER3, CCKBR, HTR4, PRKCG, NTSR1, GRM1, PRKCB, CD38, GNAL, ADRB2, LOC523484, ADRB1, HTR7, CHRM1, HTR6, NK1R, PDGFRA, PDGFRB, DRD1, ADORA2B, ERBB3, ADORA2A, OXTR, BDKRB2, ADRB3, PTK2B, CAMK2B, CALML5, SLC8A2, SPHK1, PTGFR, ITPR3, ITPR1, ATP2A3, AVPR1B, P2RX2, CACNA1G, AVPR1A, ADRA1B, CACNA1E, CACNA1D, ADRA1D, CACNA1A, F2R, HTR2A	709	164	4940	2.634078	1.01E-11
bta05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	26	1.01	1.19E-06	ITGB4, GJA1, ITGB5, CACNB3, CDH2, ITGB3, CACNB4, ITGB8, ITGB7, TCF7, CACNA2D1, CACNG8, CACNG6, LEF1, ACTN1, CACNG4, ITGA3, ITGA4, CACNG2, CACNA2D2, ITGA9, ITGA6, PKP2, ITGA7, DSP, CACNA1D	709	65	4940	2.787024	7.12E-05
bta04916:Melanogenesis	31	1.21	2.71E-06	WNT5A, ADCY3, ADCY4, ADCY1, ADCY8, ADCY5, POMC, WNT2, EDNRB, WNT1, WNT3, CREB3L1, CAMK2B, CALML5, CREB3L3, WNT6, PRKCA, TCF7, WNT10B, GNAO1, LEF1, PRKCG, FZD3, FZD5, WNT2B, PRKCB, FZD6, FZD10, WNT7B, WNT11, WNT7A	709	89	4940	2.426903	1.22E-04
bta05414:Dilated cardiomyopathy	28	1.09	3.65E-06	ADCY3, ADCY4, ADCY1, ADCY8, ADCY5, ITGB4, ITGB5, CACNB3, ITGB3, CACNB4, TGFB1, ITGB8, ITGB7, CACNA2D1, ACTC1, CACNG8, CACNG6, CACNG4, ITGA3, ITGA4, CACNG2, TNNI3, CACNA2D2, ITGA9, ADRB1, ITGA6, ITGA7, CACNA1D	709	77	4940	2.533658	1.32E-04

bta04514:Cell adhesion molecules (CAMs)	37	1.44	3.63E-05	CLDN7, CADM3, OCLN, CLDN9, CLDN4, CD8A, CADM1, CLDN3, CLDN6, CLDN5, CLDN10, CDH1, CDH2, CLDN11, CDH3, CDH4, LOC790208, ALCAM, ITGB8, ITGB7, ESAM, NEGR1, F11R, ICAM1, MPZ, PTPRM, PTPRF, NRXN2, CD40, ITGA4, CLDN23, ITGA9, ITGA6, CD34, CLDN1, VCAN, JAM2, JAM3	709	129	4940	1.998447	0.001088
bta05217:Basal cell carcinoma	20	0.78	7.19E-05	WNT5A, BMP4, TCF7, BMP2, WNT10B, LEF1, FZD3, FZD5, SHH, WNT2B, GLI1, FZD6, WNT2, WNT1, FZD10, WNT7B, WNT3, WNT11, WNT6, WNT7A	709	53	4940	2.629268	0.001848
bta04950:Maturity onset diabetes of the young	12	0.47	7.57E-05	HHEX, HNF1B, ONECUT1, FOXA2, PKLR, PAX6, NEUROD1, PDX1, NEUROG3, NR5A2, NKX2-2, NKX6-1	709	22	4940	3.800487	0.001701
bta05410:Hypertrophic cardiomyopathy (HCM)	23	0.9	2.97E-04	ACTC1, CACNA2D1, CACNG8, PRKAG2, CACNG6, ITGB4, CACNG4, ITGB5, CACNB3, ITGA3, CACNB4, ITGB3, ITGA4, CACNG2, TNNI3, CACNA2D2, TGFB1, ITGA9, ITGA6, ITGB8, ITGB7, ITGA7, CACNA1D	709	72	4940	2.225748	0.005933
bta05200:Pathways in cancer	66	2.57	3.41E-04	FGF18, PDGFB, PTGS2, PDGFA, MMP9, FGF11, FGF10, TGFB1, SHH, GLI1, ACVR1C, WNT2, WNT1, WNT3, CDKN2A, CDKN2B, PAX8, TGFA, WNT6, FGF4, PRKCA, WNT10B, AR, RXRG, FGF23, LEF1, PRKCG, FGF20, PRKCB, VEGFC, CCND1, LAMC3, PDGFRA, PDGFRB, WNT11, FGFR2, WNT5A, DCC, FGFR3, EGLN3, CDH1, ZBTB16, LOC100138788, STAT4, NKX3-1, LOC100138045, PIK3R3, TRAF5, BMP4, CEBPA, TCF7, BMP2, EPAS1, FZD3, ITGA3, MAPK10, FZD5, FZD6, WNT2B, CBLC, WNT7B, RASSF5, LAMA4, FZD10, ITGA6, WNT7A	709	303	4940	1.517686	0.006117
bta04310:Wnt signaling pathway	36	1.4	6.55E-04	WNT5A, NKD1, LOC515280, WNT2, WNT1, WNT3, CAMK2B, NFATC4, SOX17, WNT6, FOSL1, PRKCA, TCF7, WNT10B, VANGL1, LEF1, FZD3, PRKCG, MAPK10, FZD5, WNT2B, PRKCB, FZD6, DKK2, SFRP5, WNT7B, FZD10, CCND1, DKK1, SFRP1, CCND2, SFRP2, SFRP4, WIF1, WNT11, WNT7A	709	142	4940	1.766424	0.010668
bta04270:Vascular smooth muscle contraction	29	1.13	7.02E-04	ADCY3, ADCY4, KCNMB4, ADCY1, ADORA2B, ADCY8, ADORA2A, ADCY5, AGTR1, PTGIR, GUCY1A2, CALML5, RAMP1, PRKCA, KCNMA1, RAMP3, RAMP2, PLA2G10, PRKCH, NPR1, PRKCG, ITPR3, ITPR1, PRKCB, AVPR1B, AVPR1A, ADRA1B, CACNA1D, ADRA1D	709	106	4940	1.906219	0.010481
bta04540:Gap junction	23	0.9	0.00121279	PRKCA, ADCY3, ADCY4, ADCY1, DRD1, PDGFB, ADCY8, PDGFA, ADCY5, GJA1, PRKCG, ITPR3, GRM1, ITPR1, PRKCB, ADRB1, PDGFRA, GUCY1A2, TUBA4A, PDGFRB, TUBB3, TUBB4, HTR2A	709	79	4940	2.02853	0.016662
bta04512:ECM-receptor interaction	22	0.86	0.00144248	TNXB, ITGB4, ITGB5, ITGA3, COL2A1, ITGB3, ITGA4, COL5A3, ITGA9, LAMA4, GP5, ITGA6, ITGB8, LAMC3, ITGB7, ITGA7, COL1A2, LOC100138045, COL1A1, COL11A2, THBS2, THBS4	709	75	4940	2.043818	0.018388

bta04670:Leukocyte transendothelial migration	29	1.13	0.00176118	CLDN7, CLDN9, OCLN, CLDN4, CLDN3, MMP9, CLDN6, CLDN5, CLDN10, CLDN11, CXCR4, PTK2B, RAPGEF4, ESAM, PIK3R3, PRKCA, F11R, ICAM1, ACTN1, PRKCG, ITGA4, CLDN23, THY1, PRKCB, RASSF5, MAPK13, CLDN1, JAM2, JAM3	709	112	4940	1.8041	0.020931
bta04340:Hedgehog signaling pathway	16	0.62	0.00261339	WNT5A, BMP4, BMP2, WNT10B, SHH, WNT2B, GLI1, WNT2, WNT1, WNT7B, WNT3, WNT11, BMP7, WNT6, WNT7A, IHH	709	49	4940	2.275122	0.02901

F. Lamb KEGG Pathway

Term	Count	%	P-value	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Benjamini P-value
bta04080:Neuroactive ligand-receptor interaction	98	3.782323427	5.44E-26	F2RL2, F2RL3, GRIK1, GRIK2, LOC790124, GABRB2, GABRB1, GRIK3, LHCGR, F2RL1, GRIN3B, VIPR1, GHRHR, S1PR3, HTR1B, HTR1A, S1PR1, GALR1, LTB4R, GRIN2C, GALR3, GALR2, LOC781367, C5AR1, HTR4, NTSR1, NTSR2, CRHR1, SSTR5, CRHR2, SSTR2, SSTR1, HTR7, HTR6, GPR50, GLP1R, DRD1, PRLHR, ADORA2B, ADORA2A, ADCYAP1R1, PTH1R, LOC789065, BDKRB2, LOC541212, HCRTR2, ADRB3, HCRTR1, ADRA2A, ADRA2B, GABRP, GABRD, GABRA2, GABRA4, PTH2R, P2RX2, AVPR1B, AVPR1A, ADRA1B, UTS2R, GHSR, ADRA1D, MTNR1A, GPR83, MCHR1, TACR3, GLRA1, EDNRA, EDNRB, MC5R, HTR5A, PTGER3, CCKBR, PTGER4, GRM1, GRM3, LOC523484, ADRB1, CHRM1, GRM7, GIPR, PTGDR, GRM6, NK1R, TSHR, CALCR, NPY2R, OPRK1, OXTR, GCGR, HRH3, GLRB, PTGFR, LEP, GRIA2, NMBR, F2R, OPRD1, HTR2A	685	239	4940	2.957090065	9.42E-24
bta04020:Calcium signaling pathway	58	2.238517947	4.50E-12	SLC8A3, ADCY3, ADCY4, GNA14, ADCY1, TACR3, ADCY8, LHCGR, EDNRA, ATP2B2, EDNRB, GRIN2C, CHRNA7, HTR5A, PRKCA, PTGER3, CCKBR, HTR4, PRKCG, NTSR1, GRM1, PRKCB, CD38, GNAL, LOC523484, ADRB1, HTR7, CHRM1, NK1R, HTR6, PDGFRA, PDGFRB, DRD1, ADORA2B, ERBB3, ADORA2A, OXTR, BDKRB2, ADRB3, PTK2B, CAMK2B, CALML5, SLC8A2, SPHK1, PTGFR, ITPR3, ATP2A3, P2RX2, AVPR1B, AVPR1A, CACNA1G, ADRA1B, CACNA1E, CACNA1D, ADRA1D, CACNA1A, F2R, HTR2A	685	164	4940	2.550471782	3.89E-10
bta05414:Dilated cardiomyopathy	27	1.042068699	6.40E-06	ADCY3, ADCY4, ADCY1, MYL2, ADCY8, ADCY5, ITGB4, ITGB3, CACNB4, DES, ITGB8, ITGB7, CACNA2D1, ACTC1, CACNG8, CACNG6, CACNG4, ITGA3, ITGA4, CACNG2, TNNI3, CACNA2D2, ITGA9, ADRB1, ITGA5, ITGA7, CACNA1D	685	77	4940	2.5287705	3.69E-04
bta05412:Arrhythmogenic right ventricular cardiomyopathy (ARVC)	23	0.887688151	3.16E-05	TCF7, CACNA2D1, CACNG8, CACNG6, ITGB4, CACNG4, LEF1, ITGA3, CDH2, CACNB4, ITGB3, ITGA4, CACNG2, CACNA2D2, ITGA9, DES, ITGA5, ITGB8, PKP2, ITGB7, ITGA7, DSP, CACNA1D	685	65	4940	2.551824818	0.001366788

bta04916:Melanogenesis	28	1.080663836	3.91E-05	WNT5A, ADCY3, ADCY4, ADCY1, ADCY8, ADCY5, POMC, WNT2, EDNRB, WNT1, WNT3, CREB3L1, CAMK2B, CALML5, WNT6, PRKCA, TCF7, WNT10B, GNAO1, LEF1, PRKCG, FZD7, WNT2B, PRKCB, FZD6, FZD10, WNT7B, WNT7A	685	89	4940	2.268842779	0.001350337
bta04950:Maturity onset diabetes of the young	12	0.463141644	5.46E-05	HHEX, HNF1B, ONECUT1, FOXA2, PKLR, PAX6, NEUROD1, PDX1, NEUROG3, NR5A2, NKX2-2, NKX6-1	685	22	4940	3.933642999	0.001572474
bta04514:Cell adhesion molecules (CAMs)	35	1.350829795	1.03E-04	CLDN7, CADM3, CLDN9, CLDN4, CD8A, CADM1, CD8B, CLDN3, CLDN6, CLDN5, CLDN10, CDH1, ITGB2, CDH2, CLDN11, CDH3, CDH4, PDCD1, LOC790208, ITGB8, ITGB7, CNTNAP1, ESAM, NEGR1, F11R, ICAM1, MPZ, PTPRF, ICAM3, CD40, ITGA4, CLDN23, NCAM1, ITGA9, CLDN1, VCAN	685	129	4940	1.956657047	0.002532113
bta05217:Basal cell carcinoma	19	0.733307603	1.57E-04	WNT5A, BMP4, TCF7, BMP2, WNT10B, LEF1, FZD7, SHH, WNT2B, GLI1, FZD6, WNT2, WNT1, FZD10, WNT7B, WNT3, PTCH2, WNT6, WNT7A	685	53	4940	2.585318827	0.003387222
bta04360:Axon guidance	31	1.196449247	2.68E-04	DCC, PLXNC1, EFNA2, ABLIM3, EFNA3, LRRC4C, EPHB3, PAK6, EPHB6, ROBO1, SEMA3F, SEMA3D, SEMA3B, NFATC4, UNC5C, PAK1, NGEF, EFNB3, NTN4, DPYSL5, EPHA1, NTN1, SLIT2, EPHA3, EPHA4, SEMA4F, EPHA8, MGC139448, SRGAP3, EFNA5, SEMA4D	685	114	4940	1.96107056	0.005132783
bta04512:ECM-receptor interaction	23	0.887688151	3.43E-04	TNXB, ITGB4, ITGA3, COL2A1, ITGB3, ITGA4, COL5A3, ITGA9, GP5, CD44, ITGB8, LAMC3, ITGA5, ITGB7, ITGA7, COL1A2, LOC100138045, COL1A1, COL11A2, THBS1, COL11A1, THBS2, THBS4	685	75	4940	2.211581509	0.005923102
bta05410:Hypertrophic cardiomyopathy (HCM)	22	0.849093014	5.07E-04	CACNA2D1, ACTC1, MYL2, CACNG8, PRKAG2, CACNG6, ITGB4, CACNG4, ITGA3, CACNB4, ITGB3, ITGA4, CACNG2, TNNI3, CACNA2D2, ITGA9, DES, ITGA5, ITGB8, ITGB7, ITGA7, CACNA1D	685	72	4940	2.203568532	0.00794322
bta04270:Vascular smooth muscle contraction	28	1.080663836	9.27E-04	ADCY3, ADCY4, KCNMB4, ADCY1, ADORA2B, ADCY8, ADORA2A, ADCY5, MRVI1, EDNRA, GUCY1A2, CALML5, RAMP1, PRKCA, KCNMA1, RAMP3, RAMP2, PLA2G10, PRKCH, NPR1, PRKCG, ITPR3, PRKCB, AVPR1B, AVPR1A, ADRA1B, CACNA1D, ADRA1D	685	106	4940	1.904971767	0.013286223
bta05200:Pathways in cancer	62	2.392898495	0.001158814	FGF6, FGF18, PTGS2, PDGFB, PDGFA, MMP9, ARNT2, FGF11, FGF10, FGF12, MMP2, SHH, GLI1, ACVR1C, WNT2, WNT1, WNT3, CDKN2A, CDKN2B, PAX8, TGFA, WNT6, FGF2, FGF4, PRKCA, WNT10B, AR, RXRG, FGF23, LEF1, PRKCG, FGF20, PRKCB, DAPK1, CCND1, LAMC3, PDGFRA, PDGFRB, FGFR2, WNT5A, DCC, FGFR3, CDH1, STAT4, NKX3-1, LOC100138045, PIK3R3, BMP4, CEBPA, TCF7, BMP2, ITGA3, MAPK10, FZD7, FZD6, WNT2B, CBLC, WNT7B, RASSF5, FZD10, PTCH2, WNT7A	685	303	4940	1.475657055	0.015311645
bta04340:Hedgehog signaling pathway	16	0.617522192	0.001844064	WNT5A, BMP4, BMP2, WNT10B, SHH, WNT2B, GLI1, WNT2, WNT1, WNT7B, WNT3, PTCH2, BMP7, WNT6, WNT7A, IHH	685	49	4940	2.354833904	0.022550259
bta04540:Gap junction	22	0.849093014	0.001890374	PRKCA, ADCY3, ADCY4, ADCY1, DRD1, PDGFB, ADCY8, PDGFA, ADCY5, PRKCG, ITPR3, GRM1, PRKCB, ADRB1, PDGFRA, GUCY1A2, TUBA4A, PDGFRB, PDGFD, TUBB3, TUBB4, HTR2A	685	79	4940	2.008315624	0.021586548

bta04810:Regulation of actin cytoskeleton	41	1.582400618	0.003563494	FGF6, FGFR2, FGF18, FGFR4, FGFR3, MYL2, PDGFB, PDGFA, ITGB4, FGF11, FGF10, ITGB2, ITGB3, BDKRB2, FGF12, INSRR, PAK6, PFN3, GSN, ITGB8, ITGB7, PDGFD, PAK1, PIK3R3, FGF2, FGF4, ARHGEF4, FGF23, ITGA3, ITGA4, FGF20, ITGA9, ITGA5, CHRM1, SCIN, ITGA7, CYFIP2, PDGFRA, PDGFRB, CD14, F2R	685	190	4940	1.55620438	0.037863638
bta04350:TGF-beta signaling pathway	21	0.810497877	0.004439467	BMP4, NOG, BMP2, FOXJ1, GDF7, GDF6, NODAL, FST, ACVR1C, INHBB, INHBA, ID2, CDKN2B, INHBE, ID1, ID3, BMP7, THBS1, THBS2, THBS4, PITX2	685	79	4940	1.91702855	0.044268907
bta04670:Leukocyte transendothelial migration	27	1.042068699	0.004632428	CLDN7, CLDN9, MYL2, CLDN4, CLDN3, MMP9, CLDN6, CLDN5, CLDN10, ITGB2, CLDN11, MMP2, PTK2B, ESAM, PIK3R3, PRKCA, ICAM1, F11R, NCF1, PRKCG, ITGA4, CLDN23, THY1, PRKCB, RASSF5, MAPK13, CLDN1	685	112	4940	1.738529718	0.043645124
bta04310:Wnt signaling pathway	32	1.235044384	0.005616818	WNT5A, NKD1, WNT2, WNT1, WNT3, CAMK2B, NFATC4, SOX17, WNT6, FOSL1, PRKCA, TCF7, WNT10B, LEF1, PRKCG, MAPK10, FZD7, WNT2B, PRKCB, FZD6, SFRP5, DKK2, FZD10, CCND1, WNT7B, DKK1, SFRP1, SFRP2, CCND2, SFRP4, WIF1, WNT7A	685	142	4940	1.625167061	0.049993807