Sup. Table 11: DAVID analysis to determine GO term enrichment for genes whose DNA methylation level was correlated with maternal stress during infancy in the full sample. All CpG sites with FDR<20% from Sup. Table 2 were used for DAVID analysis.

Annotation Cluster 1	Enrichment Score: 1.4468517847164948				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	6	4.444	0.003	4.39
GOTERM_BP_FAT	GO:0019319~hexose biosynthetic process	4	2.963	0.003	5.01
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	4	2.963	0.005	7.48
GOTERM_BP_FAT	GO:0046165~alcohol biosynthetic process	4	2.963	0.008	11.34
GOTERM_BP_FAT	GO:0006094~gluconeogenesis	3	2.222	0.024	32.27
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	4	2.963	0.028	36.46
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	5	3.704	0.042	49.32
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	3	2.222	0.058	61.79
GOTERM_CC_FAT	GO:0005625~soluble fraction	7	5.185	0.070	58.80
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	5	3.704	0.082	74.49
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	6	4.444	0.093	78.93
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	5	3.704	0.124	87.87
GOTERM_BP_FAT	GO:0046164~alcohol catabolic process	3	2.222	0.145	91.75
GOTERM_BP_FAT	GO:0044275~cellular carbohydrate catabolic process	3	2.222	0.157	93.43
GOTERM_BP_FAT	GO:0016052~carbohydrate catabolic process	3	2.222	0.245	98.88

Annotation Cluster 2	Enrichment Score: 0.987105723000385				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0051674~localization of cell	7	5.185	0.057	61.03
GOTERM_BP_FAT	GO:0048870~cell motility	7	5.185	0.057	61.03
GOTERM_BP_FAT	GO:0006928~cell motion	8	5.926	0.140	91.02

GOTERM_BP_FAT	GO:0016477~cell migration	5	3.704	0.245	98.87

Annotation Cluster 3 Enrichment Score: 0.6934863934063452

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0001568~blood vessel development	5	3.704	0.166	94.50
GOTERM_BP_FAT	GO:0001944~vasculature development	5	3.704	0.177	95.58
GOTERM_BP_FAT	GO:0048514~blood vessel morphogenesis	4	2.963	0.282	99.50

Annotation Cluster 4 Enrichment Score: 0.6431480091803988

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0006006~glucose metabolic process	5	3.704	0.042	49.32
GOTERM_BP_FAT	GO:0019318~hexose metabolic process	5	3.704	0.082	74.49
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	6	4.444	0.093	78.93
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	5	3.704	0.124	87.87
GOTERM_BP_FAT	GO:0032868~response to insulin stimulus	3	2.222	0.219	98.08
GOTERM_BP_FAT	GO:0043434~response to peptide hormone stimulus	3	2.222	0.410	99.98
GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	4	2.963	0.684	100.00
GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	4	2.963	0.748	100.00
GOTERM_BP_FAT	GO:0010033~response to organic substance	5	3.704	0.902	100.00

Annotation Cluster 5 Enrichment Score: 0.6190408676219872

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	7	5.185	0.179	95.70
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	7	5.185	0.179	95.70
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	9	6.667	0.189	96.47

GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	7	5.185	0.209	97.64
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	7	5.185	0.213	97.80
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	8	5.926	0.234	98.59
GOTERM_BP_FAT	GO:0030163~protein catabolic process	7	5.185	0.239	98.72
GOTERM_BP_FAT	GO:0006508~proteolysis	10	7.407	0.372	99.94
GOTERM_BP_FAT	GO:0006511~ubiquitin-dependent protein catabolic process	3	2.222	0.480	100.00

Annotation Cluster 6 Enrichment Score: 0.606012642460105

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	6	4.444	0.152	92.80
GOTERM_BP_FAT	GO:0015031~protein transport	9	6.667	0.187	96.37
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	9	6.667	0.193	96.77
GOTERM_BP_FAT	GO:0034613~cellular protein localization	6	4.444	0.202	97.29
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	6	4.444	0.206	97.51
GOTERM_BP_FAT	GO:0008104~protein localization	9	6.667	0.314	99.75
GOTERM_BP_FAT	GO:0046907~intracellular transport	7	5.185	0.398	99.97
GOTERM_BP_FAT	GO:0006605~protein targeting	3	2.222	0.495	100.00

Annotation Cluster 7 Enrichment Score: 0.5888884587220655

Category	Term	Count	%	p value	FDR
GOTERM_MF_FAT	GO:0048037~cofactor binding	5	3.704	0.164	90.67
GOTERM_MF_FAT	GO:0050662~coenzyme binding	4	2.963	0.181	93.00
GOTERM_BP_FAT	GO:0055114~oxidation reduction	6	4.444	0.577	100.00

Annotation Cluster 8 Enrichment Score: 0.5084786439026264

Category	Term	Count	%	p value	FDR

GOTERM_CC_FAT	GO:0034702~ion channel complex	5	3.704	0.106	74.37
GOTERM_MF_FAT	GO:0015276~ligand-gated ion channel activity	4	2.963	0.136	85.62
GOTERM_MF_FAT	GO:0022834~ligand-gated channel activity	4	2.963	0.136	85.62
GOTERM_MF_FAT	GO:0022836~gated channel activity	6	4.444	0.166	91.08
GOTERM_BP_FAT	GO:0030001~metal ion transport	7	5.185	0.216	97.96
GOTERM_MF_FAT	GO:0005261~cation channel activity	5	3.704	0.275	98.61
GOTERM_MF_FAT	GO:0005216~ion channel activity	6	4.444	0.283	98.80
GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	6	4.444	0.311	99.28
GOTERM_BP_FAT	GO:0006811~ion transport	9	6.667	0.312	99.74
GOTERM_BP_FAT	GO:0006812~cation transport	7	5.185	0.331	99.84
GOTERM_MF_FAT	GO:0015267~channel activity	6	4.444	0.341	99.60
GOTERM_CC_FAT	GO:0034703~cation channel complex	3	2.222	0.343	99.40
GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	6	4.444	0.343	99.62
GOTERM_MF_FAT	GO:0046873~metal ion transmembrane transporter activity	5	3.704	0.385	99.84
GOTERM_BP_FAT	GO:0050877~neurological system process	9	6.667	0.485	100.00
GOTERM_CC_FAT	GO:0044459~plasma membrane part	20	14.815	0.644	100.00
GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	9	6.667	0.908	100.00
GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	9	6.667	0.918	100.00

Annotation Cluster 9 Enrichment Score: 0.49905155844646204

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0000187~activation of MAPK activity	4	2.963	0.027	35.13
GOTERM_BP_FAT	GO:0043406~positive regulation of MAP kinase activity	4	2.963	0.047	53.71
GOTERM_BP_FAT	GO:0043405~regulation of MAP kinase activity	4	2.963	0.109	84.20
GOTERM_BP_FAT	GO:0000165~MAPKKK cascade	4	2.963	0.173	95.18
GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	8	5.926	0.275	99.41

GOTERM_BP_FAT	GO:0045860~positive regulation of protein kinase activity	4	2.963	0.289	99.56
GOTERM_BP_FAT	GO:0033674~positive regulation of kinase activity	4	2.963	0.304	99.70
GOTERM_BP_FAT	GO:0051347~positive regulation of transferase activity	4	2.963	0.320	99.79
GOTERM_BP_FAT	GO:0045859~regulation of protein kinase activity	5	3.704	0.333	99.85
GOTERM_BP_FAT	GO:0043549~regulation of kinase activity	5	3.704	0.349	99.89
GOTERM_BP_FAT	GO:0042325~regulation of phosphorylation	6	4.444	0.362	99.92
GOTERM_BP_FAT	GO:0051338~regulation of transferase activity	5	3.704	0.367	99.93
GOTERM_BP_FAT	GO:0051174~regulation of phosphorus metabolic process	6	4.444	0.385	99.96
GOTERM_BP_FAT	GO:0019220~regulation of phosphate metabolic process	6	4.444	0.385	99.96
GOTERM_BP_FAT	GO:0016310~phosphorylation	8	5.926	0.415	99.98
GOTERM_BP_FAT	GO:0006796~phosphate metabolic process	9	6.667	0.481	100.00
GOTERM_BP_FAT	GO:0006793~phosphorus metabolic process	9	6.667	0.481	100.00
GOTERM_BP_FAT	GO:0007243~protein kinase cascade	4	2.963	0.588	100.00
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	10	7.407	0.707	100.00
GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	5	3.704	0.765	100.00
GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	4	2.963	0.842	100.00
GOTERM_MF_FAT	GO:0004672~protein kinase activity	3	2.222	0.969	100.00

Annotation Cluster 10	Enrichment Score: 0.47736470491945077				
Category	Term	Count	%	p value	FDR
GOTERM_CC_FAT	GO:0030017~sarcomere	3	2.222	0.288	98.42
GOTERM_CC_FAT	GO:0030016~myofibril	3	2.222	0.329	99.23
GOTERM_CC_FAT	GO:0044449~contractile fiber part	3	2.222	0.347	99.45
GOTERM_CC_FAT	GO:0043292~contractile fiber	3	2.222	0.374	99.67

Annotation Cluster 11	Enrichment Score: 0.46215666450248655				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0009100~glycoprotein metabolic process	5	3.704	0.085	75.91
GOTERM_BP_FAT	GO:0009101~glycoprotein biosynthetic process	4	2.963	0.140	90.97
GOTERM_BP_FAT	GO:0006486~protein amino acid glycosylation	3	2.222	0.284	99.51
GOTERM_BP_FAT	GO:0043413~biopolymer glycosylation	3	2.222	0.284	99.51
GOTERM_BP_FAT	GO:0070085~glycosylation	3	2.222	0.284	99.51
GOTERM_CC_FAT	GO:0005794~Golgi apparatus	9	6.667	0.404	99.82
GOTERM_CC_FAT	GO:0000139~Golgi membrane	3	2.222	0.479	99.96
GOTERM_CC_FAT	GO:0012505~endomembrane system	7	5.185	0.663	100.00
GOTERM_CC_FAT	GO:0044431~Golgi apparatus part	3	2.222	0.715	100.00
GOTERM_CC_FAT	GO:0031090~organelle membrane	6	4.444	0.958	100.00

Annotation Cluster 12	Enrichment Score: 0.4329072021759315				
Category	Term	Count	%	p value	FDR
GOTERM_CC_FAT	GO:0005576~extracellular region	22	16.296	0.244	96.68
GOTERM_CC_FAT	GO:0005615~extracellular space	9	6.667	0.415	99.85
GOTERM_CC_FAT	GO:0044421~extracellular region part	11	8.148	0.497	99.98

Annotation Cluster 13	Enrichment Score: 0.4050936612964293				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0003007~heart morphogenesis	3	2.222	0.121	87.29
GOTERM_BP_FAT	GO:0035270~endocrine system development	3	2.222	0.137	90.44
GOTERM_BP_FAT	GO:0045165~cell fate commitment	4	2.963	0.153	92.99
GOTERM_BP_FAT	GO:0045944~positive regulation of transcription from RNA polymerase II promoter	6	4.444	0.229	98.44
GOTERM_BP_FAT	GO:0007507~heart development	4	2.963	0.285	99.53
GOTERM_BP_FAT	GO:0030182~neuron differentiation	6	4.444	0.298	99.65

GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	8	5.926	0.336	99.86
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	7	5.185	0.354	99.91
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	7	5.185	0.383	99.96
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	8	5.926	0.386	99.96
GOTERM_BP_FAT	GO:0045893~positive regulation of transcription, DNA-dependent	6	4.444	0.399	99.97
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	8	5.926	0.400	99.97
GOTERM_BP_FAT	GO:0051254~positive regulation of RNA metabolic process	6	4.444	0.404	99.97
GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polymerase II promoter	8	5.926	0.417	99.98
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	7	5.185	0.448	99.99
GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	7	5.185	0.450	99.96
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	9	6.667	0.451	99.99
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	7	5.185	0.477	100.00
GOTERM_MF_FAT	GO:0003700~transcription factor activity	10	7.407	0.498	99.99
GOTERM_MF_FAT	GO:0016563~transcription activator activity	5	3.704	0.519	99.99
GOTERM_MF_FAT	GO:0030528~transcription regulator activity	14	10.370	0.536	100.00
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	14	10.370	0.565	100.00
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	13	9.630	0.642	100.00
GOTERM_BP_FAT	GO:0045449~regulation of transcription	17	12.593	0.781	100.00
GOTERM_MF_FAT	GO:0003677~DNA binding	16	11.852	0.832	100.00
GOTERM_BP_FAT	GO:0006350~transcription	12	8.889	0.887	100.00

Annotation Cluster 14	Enrichment Score: 0.3814899036994951				
Category	Term	Count	%	p value	FDR
GOTERM_CC_FAT	GO:0030054~cell junction	7	5.185	0.335	99.30
GOTERM_CC_FAT	GO:0045211~postsynaptic membrane	3	2.222	0.369	99.64
GOTERM_CC_FAT	GO:0044456~synapse part	4	2.963	0.393	99.77
GOTERM_CC_FAT	GO:0045202~synapse	4	2.963	0.614	100.00

Annotation Cluster 15	Enrichment Score: 0.37723503483387205				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0007268~synaptic transmission	5	3.704	0.304	99.69
GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	5	3.704	0.402	99.97
GOTERM_BP_FAT	GO:0050877~neurological system process	9	6.667	0.485	100.00
GOTERM_BP_FAT	GO:0007267~cell-cell signaling	7	5.185	0.523	100.00

Annotation Cluster 16	Enrichment Score: 0.3751858189340333				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0030001~metal ion transport	7	5.185	0.216	97.96
GOTERM_BP_FAT	GO:0006812~cation transport	7	5.185	0.331	99.84
GOTERM_BP_FAT	GO:0006816~calcium ion transport	3	2.222	0.339	99.87
GOTERM_BP_FAT	GO:0015674~di-, tri-valent inorganic cation transport	3	2.222	0.442	99.99
GOTERM_MF_FAT	GO:0031420~alkali metal ion binding	3	2.222	0.684	100.00
GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	3	2.222	0.765	100.00

Annotation Cluster 17	Enrichment Score: 0.3735251918508316				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0051046~regulation of secretion	4	2.963	0.311	99.74

GOTERM_BP_FAT	GO:0007610~behavior	6	4.444	0.427	99.99
GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	4	2.963	0.427	99.99
GOTERM_BP_FAT	GO:0007626~locomotory behavior	4	2.963	0.461	99.99
GOTERM_BP_FAT	GO:0006935~chemotaxis	3	2.222	0.469	100.00
GOTERM_BP_FAT	GO:0042330~taxis	3	2.222	0.469	100.00

Annotation Cluster 18 Enrichment Score: 0.35440431602242245

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0001775~cell activation	5	3.704	0.263	99.23
GOTERM_BP_FAT	GO:0046649~lymphocyte activation	3	2.222	0.521	100.00
GOTERM_BP_FAT	GO:0045321~leukocyte activation	3	2.222	0.632	100.00

Annotation Cluster 19 Enrichment Score: 0.344009405486796

Category	Term	Count	%	p value	FDR
GOTERM_CC_FAT	GO:0019717~synaptosome	3	2.222	0.193	92.71
GOTERM_CC_FAT	GO:0000267~cell fraction	12	8.889	0.420	99.87
GOTERM_CC_FAT	GO:0005626~insoluble fraction	8	5.926	0.671	100.00
GOTERM_CC_FAT	GO:0005624~membrane fraction	7	5.185	0.772	100.00

Annotation Cluster 20 Enrichment Score: 0.2869411201436296

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	3	2.222	0.461	99.99
GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	3	2.222	0.531	100.00
GOTERM_BP_FAT	GO:0060284~regulation of cell development	3	2.222	0.562	100.00

Annotation Cluster 21 Enrichment Score: 0.2755636424922422

Category	Term	Count	%	p value	FDR

GOTERM_BP_FAT	GO:0008380~RNA splicing	4	2.963	0.317	99.77
GOTERM_MF_FAT	GO:0003723~RNA binding	7	5.185	0.446	99.96
GOTERM_BP_FAT	GO:0016071~mRNA metabolic process	4	2.963	0.502	100.00
GOTERM_BP_FAT	GO:0006396~RNA processing	5	3.704	0.519	100.00
GOTERM_BP_FAT	GO:0006397~mRNA processing	3	2.222	0.669	100.00
GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	3	2.222	0.900	100.00

Annotation Cluster 22 Enrichment Score: 0.2742875941180644

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0007276~gamete generation	5	3.704	0.349	99.89
GOTERM_BP_FAT	GO:0019953~sexual reproduction	5	3.704	0.472	100.00
GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	5	3.704	0.539	100.00
GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular organism	5	3.704	0.539	100.00
GOTERM_BP_FAT	GO:0007283~spermatogenesis	3	2.222	0.688	100.00
GOTERM_BP_FAT	GO:0048232~male gamete generation	3	2.222	0.688	100.00

Annotation Cluster 23 Enrichment Score: 0.2583863578081032

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0007178~transmembrane receptor protein serine/threonine kinase signaling pathway	3	2.222	0.211	97.72
GOTERM_BP_FAT	GO:0007167~enzyme linked receptor protein signaling pathway	3	2.222	0.803	100.00
GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduction	7	5.185	0.992	100.00

Annotation Cluster 24 Enrichment Score: 0.23477071937104096

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	5	3.704	0.524	100.00

GOTERM_BP_FAT	GO:0032270~positive regulation of cellular protein metabolic process	3	2.222	0.605	100.00
GOTERM_BP_FAT	GO:0051247~positive regulation of protein metabolic process	3	2.222	0.623	100.00

Annotation Cluster 25 Enrichment Score: 0.20968335675558622

Category	Term	Count	%	p value	FDR
GOTERM_MF_FAT	GO:0008270~zinc ion binding	19	14.074	0.404	99.90
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	22	16.296	0.527	100.00
GOTERM_MF_FAT	GO:0043167~ion binding	32	23.704	0.734	100.00
GOTERM_MF_FAT	GO:0046872~metal ion binding	31	22.963	0.746	100.00
GOTERM_MF_FAT	GO:0043169~cation binding	31	22.963	0.768	100.00

Annotation Cluster 26 Enrichment Score: 0.20836007234614076

Category	Term	Count	%	p value	FDR
GOTERM_MF_FAT	GO:0008092~cytoskeletal protein binding	6	4.444	0.422	99.93
GOTERM_CC_FAT	GO:0044430~cytoskeletal part	9	6.667	0.476	99.96
GOTERM_CC_FAT	GO:0015630~microtubule cytoskeleton	5	3.704	0.594	100.00
GOTERM_CC_FAT	GO:0005856~cytoskeleton	11	8.148	0.639	100.00
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	17	12.593	0.859	100.00
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	17	12.593	0.859	100.00

Annotation Cluster 27 Enrichment Score: 0.19709029864617553

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0050877~neurological system process	9	6.667	0.485	100.00
GOTERM_BP_FAT	GO:0050890~cognition	5	3.704	0.707	100.00
GOTERM_BP_FAT	GO:0007600~sensory perception	4	2.963	0.748	100.00

Annotation Cluster 28	Enrichment Score: 0.19438566956152456				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0006461~protein complex assembly	5	3.704	0.570	100.00
GOTERM_BP_FAT	GO:0070271~protein complex biogenesis	5	3.704	0.570	100.00
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	6	4.444	0.597	100.00
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	6	4.444	0.660	100.00
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	3	2.222	0.703	100.00
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	3	2.222	0.758	100.00

Annotation Cluster 29	Enrichment Score: 0.18739516622803057				
Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0006508~proteolysis	10	7.407	0.372	99.94
GOTERM_MF_FAT	GO:0004175~endopeptidase activity	4	2.963	0.657	100.00
GOTERM_MF_FAT	GO:0070011~peptidase activity, acting on L-amino acid peptides	4	2.963	0.843	100.00
GOTERM_MF_FAT	GO:0008233~peptidase activity	4	2.963	0.863	100.00

Annotation Cluster 30	Enrichment Score: 0.13659216707106298				
Category	Term	Count	%	p value	FDR
GOTERM_CC_FAT	GO:0030141~secretory granule	3	2.222	0.537	99.99
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	5	3.704	0.733	100.00
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	5	3.704	0.757	100.00
GOTERM_CC_FAT	GO:0031410~cytoplasmic vesicle	5	3.704	0.820	100.00
GOTERM_CC_FAT	GO:0031982~vesicle	5	3.704	0.850	100.00

Annotation Cluster 31	Enrichment Score: 0.10172376949180104

Category	Term	Count	%	p value	FDR
GOTERM_MF_FAT	GO:0005525~GTP binding	3	2.222	0.779	100.00
GOTERM_MF_FAT	GO:0019001~guanyl nucleotide binding	3	2.222	0.797	100.00
GOTERM_MF_FAT	GO:0032561~guanyl ribonucleotide binding	3	2.222	0.797	100.00

Annotation Cluster 32 Enrichment Score: 0.10033844682052483

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0042981~regulation of apoptosis	8	5.926	0.572	100.00
GOTERM_BP_FAT	GO:0043067~regulation of programmed cell death	8	5.926	0.581	100.00
GOTERM_BP_FAT	GO:0010941~regulation of cell death	8	5.926	0.586	100.00
GOTERM_BP_FAT	GO:0043066~negative regulation of apoptosis	3	2.222	0.846	100.00
GOTERM_BP_FAT	GO:0043069~negative regulation of programmed cell death	3	2.222	0.850	100.00
GOTERM_BP_FAT	GO:0060548~negative regulation of cell death	3	2.222	0.851	100.00
GOTERM_BP_FAT	GO:0043065~positive regulation of apoptosis	3	2.222	0.891	100.00
GOTERM_BP_FAT	GO:0043068~positive regulation of programmed cell death	3	2.222	0.893	100.00
GOTERM_BP_FAT	GO:0010942~positive regulation of cell death	3	2.222	0.895	100.00
GOTERM_BP_FAT	GO:0022402~cell cycle process	3	2.222	0.943	100.00
GOTERM_BP_FAT	GO:0007049~cell cycle	3	2.222	0.985	100.00

Annotation Cluster 33 Enrichment Score: 0.08969046576078288

Category	Term	Count	%	p value	FDR
GOTERM_CC_FAT	GO:0005730~nucleolus	7	5.185	0.441	99.92
GOTERM_CC_FAT	GO:0031981~nuclear lumen	10	7.407	0.815	100.00
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	17	12.593	0.859	100.00
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	17	12.593	0.859	100.00
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	10	7.407	0.952	100.00

GOTERM_CC_FAT	GO:0043233~organelle lumen	10	7.407	0.963	100.00
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	10	7.407	0.969	100.00

Annotation Cluster 34 Enrichment Score: 0.0796247136988019

Category	Term	Count	%	p value	FDR
GOTERM_MF_FAT	GO:0000166~nucleotide binding	17	12.593	0.724	100.00
GOTERM_MF_FAT	GO:0001882~nucleoside binding	12	8.889	0.783	100.00
GOTERM_MF_FAT	GO:0032553~ribonucleotide binding	13	9.630	0.820	100.00
GOTERM_MF_FAT	GO:0032555~purine ribonucleotide binding	13	9.630	0.820	100.00
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	11	8.148	0.856	100.00
GOTERM_MF_FAT	GO:0005524~ATP binding	10	7.407	0.862	100.00
GOTERM_MF_FAT	GO:0017076~purine nucleotide binding	13	9.630	0.863	100.00
GOTERM_MF_FAT	GO:0032559~adenyl ribonucleotide binding	10	7.407	0.873	100.00
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	10	7.407	0.908	100.00

Annotation Cluster 35 Enrichment Score: 0.07931744355330472

Category	Term	Count	%	p value	FDR
GOTERM_BP_FAT	GO:0048878~chemical homeostasis	5	3.704	0.686	100.00
GOTERM_BP_FAT	GO:0042592~homeostatic process	6	4.444	0.796	100.00
GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	3	2.222	0.862	100.00
GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	3	2.222	0.869	100.00
GOTERM_BP_FAT	GO:0050801~ion homeostasis	3	2.222	0.888	100.00
GOTERM_BP_FAT	GO:0019725~cellular homeostasis	3	2.222	0.920	100.00

Note. FDR = False Discovery Rate