5. Complete DAVID and ConceptGen results

5.1. DAVID terms in up-regulated 8-week DEGs

This is the complete list of significantly enriched annotation terms from DAVID in the 8-week up-regulated DEGs.

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_BP_FAT	GO:0009411~response to UV	4	8.95E-04	20.71	4.63E-01
GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	5	1.31E-03	10.29	1.76E-01
GOTERM_CC_FAT	GO:0000228~nuclear chromosome	5	2.37E-03	8.76	1.61E-01
GOTERM_CC_FAT	GO:0044427~chromosomal part	7	3.44E-03	4.67	1.56E-01
GOTERM_CC_FAT	GO:0034702~ion channel complex	5	6.13E-03	6.71	2.04E-01
GOTERM_CC_FAT	GO:0000785~chromatin	5	7.13E-03	6.42	1.91E-01
GOTERM_CC_FAT	GO:0005694~chromosome	7	7.89E-03	3.92	1.78E-01
GOTERM_BP_FAT	GO:0031032~actomyosin structure organization	3	8.09E-03	21.74	9.40E-01
GOTERM_BP_FAT	GO:0009416~response to light stimulus	4	1.63E-02	7.39	9.78E-01
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	6	2.00E-02	3.79	9.70E-01
GOTERM_MF_FAT	GO:0015459~potassium channel regulator activity	2	2.42E-02	80.53	9.92E-01
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	16	2.60E-02	1.77	4.27E-01
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	16	2.60E-02	1.77	4.27E-01
GOTERM_MF_FAT	GO:0043167~ion binding	28	2.65E-02	1.43	9.27E-01
GOTERM_CC_FAT	GO:0000790~nuclear chromatin	3	2.68E-02	11.56	3.95E-01
GOTERM_CC_FAT	GO:0008076~voltage-gated potassium channel complex	3	4.07E-02	9.21	4.95E-01
GOTERM_CC_FAT	GO:0034705~potassium channel complex	3	4.07E-02	9.21	4.95E-01
GOTERM_BP_FAT	GO:0009314~response to radiation	4	4.31E-02	5.07	9.98E-01
GOTERM_MF_FAT	GO:0008253~5'-nucleotidase activity	2	4.32E-02	44.74	9.43E-01
KEGG_PATHWAY	mmu04115:p53 signaling pathway	3	4.70E-02	8.32	9.36E-01
GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	5	4.79E-02	3.61	9.97E-01
GOTERM_MF_FAT	GO:0022836~gated channel activity	5	4.86E-02	3.58	9.12E-01

5.2. DAVID terms in down-regulated 8-week DEGs

This is the complete list of significantly enriched annotation terms from DAVID in the 8-week down-regulated DEGs.

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_MF_FAT	GO:0008270~zinc ion binding	26	1.08E-04	2.19	1.93E-02
GOTERM_MF_FAT	GO:0046914~transition metal ion binding	28	5.25E-04	1.90	4.64E-02
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	15	1.07E-03	2.63	1.43E-01
GOTERM_CC_FAT	GO:0043233~organelle lumen	15	1.10E-03	2.62	7.62E-02
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	15	1.51E-03	2.54	7.00E-02
GOTERM_BP_FAT	GO:0006350~transcription	19	5.03E-03	1.97	9.68E-01
GOTERM_MF_FAT	GO:0003697~single-stranded DNA binding	3	1.44E-02	16.11	5.84E-01
GOTERM_MF_FAT	GO:0003702~RNA polymerase II transcription factor activity	4	1.92E-02	6.95	5.84E-01
GOTERM_MF_FAT	GO:0046872~metal ion binding	31	2.15E-02	1.43	5.44E-01
GOTERM_BP_FAT	GO:0045449~regulation of transcription	20	2.38E-02	1.65	1.00E+00
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	8	2.43E-02	2.75	9.96E-01
GOTERM_MF_FAT	GO:0043169~cation binding	31	2.43E-02	1.41	5.23E-01
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	8	2.49E-02	2.74	9.86E-01
GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	15	2.56E-02	1.85	9.71E-01
GOTERM_CC_FAT	GO:0044432~endoplasmic reticulum part	5	2.75E-02	4.30	6.33E-01
GOTERM_CC_FAT	GO:0005654~nucleoplasm	8	2.81E-02	2.65	5.60E-01
GOTERM_MF_FAT	GO:0043167~ion binding	31	2.87E-02	1.40	5.29E-01
GOTERM_BP_FAT	GO:0030163~protein catabolic process	8	2.94E-02	2.64	9.66E-01
GOTERM_BP_FAT	GO:0032731~positive regulation of interleukin-1 beta production	2	3.70E-02	52.46	9.75E-01
GOTERM_BP_FAT	GO:0050718~positive regulation of interleukin-1 beta secretion	2	3.70E-02	52.46	9.75E-01
GOTERM_BP_FAT	GO:0032732~positive regulation of interleukin-1 production	2	3.70E-02	52.46	9.75E-01
GOTERM_BP_FAT	GO:0050704~regulation of interleukin-1 secretion	2	3.70E-02	52.46	9.75E-01
GOTERM_BP_FAT	GO:0050706~regulation of interleukin-1 beta secretion	2	3.70E-02	52.46	9.75E-01
GOTERM_BP_FAT	GO:0050716~positive regulation of interleukin-1 secretion	2	3.70E-02	52.46	9.75E-01
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	8	4.46E-02	2.41	9.80E-01
GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	14	4.70E-02	1.75	9.74E-01
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	4	4.70E-02	4.87	6.85E-01
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	4	4.70E-02	4.87	6.85E-01
GOTERM_MF_FAT	GO:0008234~cysteine-type peptidase activity	4	4.79E-02	4.85	6.70E-01

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_BP_FAT	GO:0006508~proteolysis	11	4.90E-02	1.95	9.67E-01
GOTERM_MF_FAT	GO:0016861~intramolecular oxidoreductase activity, interconverting aldoses and ketoses	2	4.90E-02	39.37	6.36E-01

5.3. DAVID terms in up-regulated 24-week DEGs

This is the complete list of significantly enriched annotation terms from DAVID in the 24-week up-regulated DEGs.

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_BP_FAT	GO:0019941~modification-dependent protein catabolic process	20	2.08E-04	2.64	2.20E-01
GOTERM_BP_FAT	GO:0043632~modification-dependent macromolecule catabolic process	20	2.08E-04	2.64	2.20E-01
GOTERM_BP_FAT	GO:0044265~cellular macromolecule catabolic process	22	2.92E-04	2.42	1.60E-01
GOTERM_BP_FAT	GO:0009057~macromolecule catabolic process	23	2.94E-04	2.35	1.10E-01
GOTERM_MF_FAT	GO:0019899~enzyme binding	13	3.00E-04	3.56	1.07E-01
GOTERM_BP_FAT	GO:0051603~proteolysis involved in cellular protein catabolic process	20	3.89E-04	2.51	1.10E-01
GOTERM_MF_FAT	GO:0019900~kinase binding	8	3.99E-04	5.90	7.26E-02
GOTERM_BP_FAT	GO:0044257~cellular protein catabolic process	20	4.17E-04	2.49	9.48E-02
GOTERM_BP_FAT	GO:0030163~protein catabolic process	20	6.37E-04	2.41	1.19E-01
GOTERM_BP_FAT	GO:0015031~protein transport	21	1.69E-03	2.16	2.50E-01
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	21	1.85E-03	2.14	2.41E-01
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	46	2.19E-03	1.55	4.37E-01
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	46	2.19E-03	1.55	4.37E-01
GOTERM_CC_FAT	GO:0005694~chromosome	15	2.20E-03	2.56	2.51E-01
GOTERM_BP_FAT	GO:0022402~cell cycle process	15	2.25E-03	2.55	2.59E-01
GOTERM_BP_FAT	GO:0006413~translational initiation	5	2.36E-03	8.81	2.45E-01
GOTERM_BP_FAT	GO:0051276~chromosome organization	15	2.91E-03	2.49	2.71E-01
GOTERM_MF_FAT	GO:0003743~translation initiation factor activity	6	2.99E-03	6.07	3.14E-01
GOTERM_CC_FAT	GO:0019717~synaptosome	6	3.47E-03	5.86	2.62E-01
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	11	3.55E-03	3.02	2.98E-01
GOTERM_BP_FAT	GO:0022403~cell cycle phase	13	3.70E-03	2.65	2.88E-01

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_BP_FAT	GO:0008104~protein localization	22	4.11E-03	1.96	2.96E-01
GOTERM_MF_FAT	GO:0019901~protein kinase binding	6	5.36E-03	5.30	3.98E-01
GOTERM_BP_FAT	GO:0010604~positive regulation of macromolecule metabolic process	19	6.37E-03	2.01	3.99E-01
GOTERM_BP_FAT	GO:0006325~chromatin organization	12	7.49E-03	2.55	4.29E-01
GOTERM_MF_FAT	GO:0008080~N-acetyltransferase activity	5	8.62E-03	6.15	4.80E-01
GOTERM_CC_FAT	GO:0048471~perinuclear region of cytoplasm	9	9.05E-03	3.07	4.49E-01
GOTERM_BP_FAT	GO:0045935~positive regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process	16	9.27E-03	2.10	4.80E-01
GOTERM_BP_FAT	GO:0007049~cell cycle	18	9.74E-03	1.97	4.78E-01
GOTERM_BP_FAT	GO:0016192~vesicle-mediated transport	15	9.90E-03	2.15	4.65E-01
GOTERM_CC_FAT	GO:0044427~chromosomal part	12	1.03E-02	2.43	4.20E-01
GOTERM_MF_FAT	GO:0019894~kinesin binding	3	1.04E-02	18.80	4.82E-01
GOTERM_MF_FAT	GO:0003723~RNA binding	20	1.07E-02	1.87	4.40E-01
GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound metabolic process	16	1.21E-02	2.04	5.15E-01
GOTERM_BP_FAT	GO:0046907~intracellular transport	14	1.24E-02	2.17	5.08E-01
GOTERM_CC_FAT	GO:0005624~membrane fraction	16	1.26E-02	2.02	4.26E-01
GOTERM_CC_FAT	GO:0000785~chromatin	8	1.41E-02	3.13	4.12E-01
GOTERM_CC_FAT	GO:0000786~nucleosome	5	1.53E-02	5.20	3.97E-01
GOTERM_MF_FAT	GO:0000166~nucleotide binding	48	1.58E-02	1.38	5.29E-01
GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	6	1.67E-02	4.02	5.99E-01
GOTERM_CC_FAT	GO:0005626~insoluble fraction	16	1.68E-02	1.95	3.90E-01
GOTERM_BP_FAT	GO:0006323~DNA packaging	6	1.73E-02	3.98	5.97E-01
GOTERM_BP_FAT	GO:0007242~intracellular signaling cascade	23	1.74E-02	1.68	5.83E-01
GOTERM_MF_FAT	GO:0016407~acetyltransferase activity	5	1.78E-02	4.97	5.29E-01
GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic process	16	1.79E-02	1.94	5.79E-01
GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	16	1.93E-02	1.92	5.91E-01
GOTERM_MF_FAT	GO:0008135~translation factor activity, nucleic acid binding	6	1.99E-02	3.84	5.32E-01
GOTERM_BP_FAT	GO:0051969~regulation of transmission of nerve impulse	6	2.17E-02	3.75	6.21E-01
GOTERM_MF_FAT	GO:0016410~N-acyltransferase activity	5	2.18E-02	4.68	5.30E-01
GOTERM_CC_FAT	GO:0000267~cell fraction	17	2.22E-02	1.84	4.45E-01
GOTERM_CC_FAT	GO:0005829~cytosol	16	2.30E-02	1.88	4.26E-01

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_BP_FAT	GO:0006334~nucleosome assembly	5	2.33E-02	4.58	6.34E-01
GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	6	2.33E-02	3.68	6.21E-01
GOTERM_BP_FAT	GO:0007067~mitosis	8	2.35E-02	2.82	6.12E-01
GOTERM_BP_FAT	GO:0000280~nuclear division	8	2.35E-02	2.82	6.12E-01
GOTERM_BP_FAT	GO:0051301~cell division	10	2.46E-02	2.38	6.17E-01
GOTERM_CC_FAT	GO:0030658~transport vesicle membrane	3	2.47E-02	12.09	4.20E-01
GOTERM_BP_FAT	GO:0045941~positive regulation of transcription	14	2.53E-02	1.97	6.16E-01
GOTERM_BP_FAT	GO:0031497~chromatin assembly	5	2.54E-02	4.46	6.06E-01
KEGG_PATHWAY	mmu04110:Cell cycle	6	2.54E-02	3.54	9.33E-01
GOTERM_BP_FAT	GO:0000279~M phase	10	2.59E-02	2.37	6.02E-01
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	8	2.60E-02	2.76	5.93E-01
GOTERM_BP_FAT	GO:0034728~nucleosome organization	5	2.65E-02	4.40	5.90E-01
GOTERM_BP_FAT	GO:0065004~protein-DNA complex assembly	5	2.65E-02	4.40	5.90E-01
GOTERM_BP_FAT	GO:0031644~regulation of neurological system process	6	2.67E-02	3.55	5.82E-01
GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthetic process	15	2.70E-02	1.89	5.77E-01
GOTERM_BP_FAT	GO:0006974~response to DNA damage stimulus	10	2.79E-02	2.33	5.79E-01
GOTERM_BP_FAT	GO:0048285~organelle fission	8	2.79E-02	2.72	5.71E-01
GOTERM_CC_FAT	GO:0032993~protein-DNA complex	5	2.86E-02	4.30	4.43E-01
GOTERM_BP_FAT	GO:0000070~mitotic sister chromatid segregation	3	2.88E-02	11.16	5.73E-01
GOTERM_BP_FAT	GO:0046619~optic placode formation involved in camera-type eye	2	2.95E-02	66.94	5.73E-01
GOTERM_BP_FAT	GO:0001743~optic placode formation	2	2.95E-02	66.94	5.73E-01
GOTERM_CC_FAT	GO:0030054~cell junction	14	3.04E-02	1.92	4.39E-01
GOTERM_BP_FAT	GO:0010628~positive regulation of gene expression	14	3.06E-02	1.92	5.78E-01
GOTERM_MF_FAT	GO:0003913~DNA photolyase activity	2	3.15E-02	62.68	6.35E-01
GOTERM_BP_FAT	GO:0000819~sister chromatid segregation	3	3.19E-02	10.57	5.85E-01
GOTERM_CC_FAT	GO:0005794~Golgi apparatus	18	3.48E-02	1.70	4.62E-01
GOTERM_BP_FAT	GO:0051726~regulation of cell cycle	8	4.07E-02	2.50	6.68E-01
GOTERM_BP_FAT	GO:0019585~glucuronate metabolic process	2	4.39E-02	44.62	6.89E-01
GOTERM_BP_FAT	GO:0006063~uronic acid metabolic process	2	4.39E-02	44.62	6.89E-01
GOTERM_CC_FAT	GO:0030659~cytoplasmic vesicle membrane	5	4.55E-02	3.70	5.34E-01
GOTERM_MF_FAT	GO:0003727~single-stranded RNA binding	3	4.71E-02	8.55	7.54E-01
GOTERM_CC_FAT	GO:0030662~coated vesicle membrane	4	4.83E-02	4.86	5.34E-01

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_MF_FAT	GO:0043167~ion binding	75	4.84E-02	1.19	7.38E-01
GOTERM_MF_FAT	GO:0019787~small conjugating protein ligase activity	6	4.90E-02	3.01	7.18E-01
GOTERM_MF_FAT	GO:0016881~acid-amino acid ligase activity	7	4.92E-02	2.64	6.96E-01

5.4. DAVID terms in down-regulated 24-week DEGs

This is the complete list of significantly enriched annotation terms from DAVID in the 24-week down-regulated DEGs.

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_CC_FAT	GO:0005739~mitochondrion	80	4.74E-15	2.52	1.31E-12
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	59	6.12E-08	2.09	8.38E-06
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	19	6.70E-08	4.86	6.12E-06
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	19	6.70E-08	4.86	6.12E-06
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	57	1.08E-07	2.10	7.39E-06
GOTERM_CC_FAT	GO:0043233~organelle lumen	57	1.18E-07	2.09	6.45E-06
GOTERM_CC_FAT	GO:0005788~endoplasmic reticulum lumen	11	7.60E-06	6.37	3.47E-04
GOTERM_CC_FAT	GO:0044429~mitochondrial part	31	8.49E-06	2.47	3.32E-04
GOTERM_CC_FAT	GO:0005783~endoplasmic reticulum	42	9.10E-06	2.09	3.12E-04
GOTERM_BP_FAT	GO:0055114~oxidation reduction	33	3.05E-05	2.23	4.41E-02
GOTERM_CC_FAT	GO:0044432~endoplasmic reticulum part	18	4.04E-05	3.25	1.23E-03
GOTERM_MF_FAT	GO:0016646~oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	5	2.61E-04	15.07	1.33E-01
GOTERM_BP_FAT	GO:0016126~sterol biosynthetic process	6	4.46E-04	9.09	2.80E-01
KEGG_PATHWAY	mmu00100:Steroid biosynthesis	5	4.62E-04	12.98	6.01E-02
KEGG_PATHWAY	mmu00640:Propanoate metabolism	6	4.82E-04	8.83	3.18E-02
KEGG_PATHWAY	mmu00280:Valine, leucine and isoleucine degradation	7	5.15E-04	6.72	2.27E-02
GOTERM_BP_FAT	GO:0006695~cholesterol biosynthetic process	5	1.44E-03	9.88	5.09E-01
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	8	1.47E-03	4.72	4.20E-01
GOTERM_MF_FAT	GO:0016645~oxidoreductase activity, acting on the CH-NH group of donors	5	2.03E-03	9.04	4.26E-01
KEGG_PATHWAY	mmu00620:Pyruvate metabolism	6	2.08E-03	6.46	6.74E-02
GOTERM_CC_FAT	GO:0005840~ribosome	13	2.25E-03	2.82	5.99E-02

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_BP_FAT	GO:0009064~glutamine family amino acid metabolic process	6	2.39E-03	6.34	5.06E-01
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	6	2.65E-03	6.20	4.79E-01
GOTERM_CC_FAT	GO:0000313~organellar ribosome	6	2.80E-03	6.10	6.74E-02
GOTERM_CC_FAT	GO:0005761~mitochondrial ribosome	6	2.80E-03	6.10	6.74E-02
GOTERM_MF_FAT	GO:0008568~microtubule-severing ATPase activity	3	2.82E-03	33.90	4.02E-01
GOTERM_BP_FAT	GO:0006886~intracellular protein transport	15	3.19E-03	2.47	4.91E-01
GOTERM_CC_FAT	GO:0033279~ribosomal subunit	7	4.85E-03	4.42	1.05E-01
GOTERM_BP_FAT	GO:0007033~vacuole organization	5	6.26E-03	6.68	6.86E-01
GOTERM_MF_FAT	GO:0003735~structural constituent of ribosome	10	6.29E-03	2.99	5.78E-01
GOTERM_BP_FAT	GO:0034613~cellular protein localization	15	6.42E-03	2.28	6.53E-01
KEGG_PATHWAY	mmu00330:Arginine and proline metabolism	6	6.43E-03	5.00	1.59E-01
GOTERM_BP_FAT	GO:0070727~cellular macromolecule localization	15	6.73E-03	2.26	6.31E-01
GOTERM_BP_FAT	GO:0006658~phosphatidylserine metabolic process	3	6.78E-03	22.72	5.99E-01
GOTERM_BP_FAT	GO:0006561~proline biosynthetic process	3	6.78E-03	22.72	5.99E-01
GOTERM_BP_FAT	GO:0006457~protein folding	9	6.88E-03	3.22	5.72E-01
GOTERM_BP_FAT	GO:0008104~protein localization	28	8.24E-03	1.69	6.10E-01
GOTERM_BP_FAT	GO:0015031~protein transport	25	9.05E-03	1.75	6.17E-01
GOTERM_BP_FAT	GO:0045184~establishment of protein localization	25	9.84E-03	1.73	6.22E-01
GOTERM_BP_FAT	GO:0008610~lipid biosynthetic process	14	1.05E-02	2.23	6.21E-01
GOTERM_BP_FAT	GO:0006560~proline metabolic process	3	1.23E-02	17.04	6.59E-01
GOTERM_CC_FAT	GO:0030117~membrane coat	6	1.23E-02	4.31	2.30E-01
GOTERM_CC_FAT	GO:0048475~coated membrane	6	1.23E-02	4.31	2.30E-01
GOTERM_MF_FAT	GO:0004017~adenylate kinase activity	3	1.24E-02	16.95	7.45E-01
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	9	1.25E-02	2.90	6.44E-01
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	9	1.25E-02	2.90	6.44E-01
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	13	1.27E-02	2.26	6.30E-01
KEGG_PATHWAY	mmu00310:Lysine degradation	5	1.30E-02	5.38	2.53E-01
GOTERM_BP_FAT	GO:0046907~intracellular transport	18	1.45E-02	1.90	6.59E-01
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	14	1.60E-02	2.11	6.79E-01
KEGG_PATHWAY	mmu04142:Lysosome	8	1.72E-02	2.97	2.83E-01
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	6	1.86E-02	3.90	7.17E-01
GOTERM_BP_FAT	GO:0006694~steroid biosynthetic process	6	1.97E-02	3.84	7.21E-01
GOTERM_MF_FAT	GO:0016776~phosphotransferase activity, phosphate group as acceptor	4	2.10E-02	6.70	8.55E-01

Category	Term	Count	PValue	Fold Enrichment	Benjamini
GOTERM_CC_FAT	GO:0016023~cytoplasmic membrane-bounded vesicle	18	2.15E-02	1.81	3.46E-01
GOTERM_BP_FAT	GO:0009309~amine biosynthetic process	6	2.19E-02	3.74	7.45E-01
GOTERM_CC_FAT	GO:0005763~mitochondrial small ribosomal subunit	3	2.26E-02	12.50	3.41E-01
GOTERM_CC_FAT	GO:0000314~organellar small ribosomal subunit	3	2.26E-02	12.50	3.41E-01
GOTERM_MF_FAT	GO:0010861~thyroid hormone receptor activator activity	3	2.34E-02	12.33	8.42E-01
GOTERM_MF_FAT	GO:0030375~thyroid hormone receptor coactivator activity	3	2.34E-02	12.33	8.42E-01
GOTERM_CC_FAT	GO:0031988~membrane-bounded vesicle	18	2.42E-02	1.79	3.43E-01
GOTERM_BP_FAT	GO:0006412~translation	14	2.43E-02	1.99	7.66E-01
GOTERM_BP_FAT	GO:0018130~heterocycle biosynthetic process	5	2.53E-02	4.46	7.67E-01
GOTERM_MF_FAT	GO:0016620~oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	4	2.54E-02	6.23	8.27E-01
GOTERM_MF_FAT	GO:0030546~receptor activator activity	3	2.76E-02	11.30	8.17E-01
GOTERM_BP_FAT	GO:0006914~autophagy	4	2.98E-02	5.86	8.09E-01
GOTERM_CC_FAT	GO:0015935~small ribosomal subunit	4	3.13E-02	5.75	4.01E-01
GOTERM_BP_FAT	GO:0009116~nucleoside metabolic process	5	3.42E-02	4.06	8.40E-01
GOTERM_MF_FAT	GO:0019201~nucleotide kinase activity	3	3.70E-02	9.69	8.73E-01
GOTERM_MF_FAT	GO:0031072~heat shock protein binding	5	4.09E-02	3.83	8.74E-01
GOTERM_BP_FAT	GO:0009084~glutamine family amino acid biosynthetic process	3	4.17E-02	9.09	8.86E-01
GOTERM_BP_FAT	GO:0006659~phosphatidylserine biosynthetic process	2	4.34E-02	45.44	8.87E-01
KEGG_PATHWAY	mmu00903:Limonene and pinene degradation	3	4.35E-02	8.83	5.25E-01
GOTERM_MF_FAT	GO:0047750~cholestenol delta-isomerase activity	2	4.36E-02	45.20	8.69E-01
GOTERM_BP_FAT	GO:0006730~one-carbon metabolic process	7	4.39E-02	2.72	8.82E-01
GOTERM_BP_FAT	GO:0045444~fat cell differentiation	5	4.46E-02	3.72	8.79E-01
GOTERM_BP_FAT	GO:0043193~positive regulation of gene-specific transcription	4	4.69E-02	4.91	8.84E-01
KEGG_PATHWAY	mmu00650:Butanoate metabolism	4	4.95E-02	4.77	5.31E-01

5.5. ConceptGen terms in up-regulated 24-week DEGs

This is the complete list of significantly enriched annotation terms from ConceptGen in the 24-week up-regulated DEGs.

ConceptId	Concept Name	Concept Type Name	Gene List Size	Overlap	P-Value	Q-Value
743177	Mass Spectrometry	MeSH	529	24	5.84763E-10	3.04895E-06
738083	Animals	MeSH	472	20	6.33738E-08	0.000165216
739540	Hela Cells	MeSH	621	22	2.39452E-07	0.000416167
738669	Proteome	MeSH	931	26	1.25106E-06	0.001630755
742752	Nuclear Proteins	MeSH	558	19	3.37837E-06	0.003522969
743375	Acetyltransferases	MeSH	153	10	9.91976E-06	0.008364454
742310	Protein Binding	MeSH	494	17	1.12296E-05	8.36E-03
747193	Two-Hybrid System Techniques	MeSH	387	14	5.12097E-05	0.033375948

5.6. ConceptGen terms in down-regulated 24-week DEGs

This is the complete list of significantly enriched annotation terms from ConceptGen in the 24-week up-regulated DEGs.

ConceptId	Concept Name	Concept Type Name	Gene List Size	Overlap	P-Value	Q-Value
743753	Ribosomal Proteins	MeSH	170	14	2.02535E-07	0.00105602
744804	Endoplasmic Reticulum	MeSH	141	12	1.42279E-06	0.003709217
746260	HSP90 Heat-Shock Proteins	MeSH	37	7	4.79491E-06	0.008333546
743995	Heat-Shock Proteins	MeSH	84	9	8.72359E-06	0.011371202
739129	Phenotype	MeSH	96	9	2.36435E-05	0.022175634
744513	Molecular Chaperones	MeSH	97	9	2.55186E-05	0.022175634
738668	Proteins	MeSH	722	24	3.80472E-05	2.83E-02