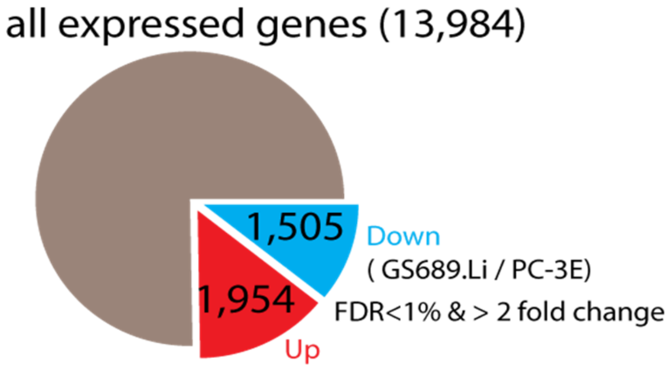
Table S5: Enriched GO in differentially expressed genes



Downregulated gene list 1505 vs. all 13984 genes

Category	Term	Count	%	P-Value	Benjamini-Hochberg FDR
GOTERM_BP_FAT	epidermis development	29	2.2	0.00000056	0.00094
GOTERM_BP_FAT	ectoderm development	31	2.3	0.00000048	0.0016
GOTERM_BP_FAT	response to wounding	54	4.1	0.0000049	0.0054
GOTERM_BP_FAT	defense response	47	3.5	0.000011	0.0094
GOTERM_BP_FAT	immune response	55	4.1	0.00002	0.013
GOTERM_BP_FAT	inflammatory response	32	2.4	0.000024	0.013
GOTERM_BP_FAT	epithelium development	32	2.4	0.000028	0.013
GOTERM_BP_FAT	embryonic organ development	25	1.9	0.000051	0.019
GOTERM_BP_FAT	leukocyte chemotaxis	10	0.8	0.000046	0.019
GOTERM_BP_FAT	cell chemotaxis	10	0.8	0.000079	0.026
GOTERM_BP_FAT	response to steroid hormone stimulus	28	2.1	0.000089	0.027
GOTERM_BP_FAT	positive regulation of response to external stimulus	13	1	0.00017	0.046
GOTERM_CC_FAT	extracellular region	140	10.6	1.9E-10	0.000000091
GOTERM_CC_FAT	plasma membrane	271	20.4	0.00000007	0.000016
GOTERM_CC_FAT	extracellular region part	78	5.9	0.00000068	0.000081
GOTERM_CC_FAT	plasma membrane part	188	14.2	0.00000057	0.00009
GOTERM_CC_FAT	extracellular space	56	4.2	0.0000038	0.00036
GOTERM_CC_FAT	apical junction complex	22	1.7	0.000054	0.0042
GOTERM_CC_FAT	intrinsic to plasma membrane	92	6.9	0.000086	0.0051
GOTERM_CC_FAT	apicolateral plasma membrane	22	1.7	0.000083	0.0056
GOTERM_CC_FAT	cell-cell junction	32	2.4	0.00013	0.0061
GOTERM_CC_FAT	integral to plasma membrane	89	6.7	0.00013	0.0067
GOTERM_CC_FAT	integral to membrane	351	26.5	0.00044	0.019
GOTERM_CC_FAT	intrinsic to membrane	361	27.2	0.00079	0.031

Upregulated gene list 1954 vs. all 13984 genes

Category	Term	Count	%	P-Value	Benjamini-Hochberg FDR
GOTERM_BP_FAT	biological adhesion	99	6.4	6.3E-16	1.1E-12
GOTERM_BP_FAT	cell adhesion	99	6.4	5.6E-16	1.9E-12
GOTERM_BP_FAT	cell surface receptor linked signal transduction	151	9.8	1.1E-12	1.3E-09
GOTERM_BP_FAT	G-protein coupled receptor protein signaling pathway	64	4.2	1.3E-10	0.000000089
GOTERM_BP_FAT	response to wounding	70	4.5	1.3E-10	0.00000011
GOTERM_BP_FAT	cell-cell signaling	66	4.3	2.3E-09	0.0000013
GOTERM_BP_FAT	regulation of adenylate cyclase activity	17	1.1	0.000000066	0.000032
GOTERM_BP_FAT	regulation of cyclase activity	17	1.1	0.00000012	0.000051
GOTERM_BP_FAT	regulation of cyclic nucleotide biosynthetic process	18	1.2	0.00000015	0.000058
GOTERM_BP_FAT	regulation of nucleotide biosynthetic process	18	1.2	0.00000015	0.000058
GOTERM_BP_FAT	regulation of cAMP biosynthetic process	17	1.1	0.00000022	0.000073
GOTERM_BP_FAT	regulation of lyase activity	17	1.1	0.00000022	0.000073
GOTERM_BP_FAT	G-protein signaling, coupled to cAMP nucleotide second messenger	16	1	0.00000029	0.00009
GOTERM_BP_FAT	neurological system process	79	5.1	0.00000038	0.000092
GOTERM_BP_FAT	regulation of cell proliferation	102	6.6	0.00000046	0.000092
GOTERM_BP_FAT	regulation of cell migration	36	2.3	0.00000044	0.000092
GOTERM_BP_FAT	regulation of cyclic nucleotide metabolic process	18	1.2	0.00000042	0.000095
GOTERM_BP_FAT	regulation of cell motion	40	2.6	0.00000038	0.000099
GOTERM_BP_FAT	wound healing	35	2.3	0.00000035	0.000099
GOTERM_BP_FAT	cell-cell adhesion	36	2.3	0.00000068	0.00011
GOTERM_BP_FAT	regulation of cAMP metabolic process	17	1.1	0.00000062	0.00012
GOTERM_BP_FAT	regulation of locomotion	37	2.4	0.00000066	0.00012
GOTERM_BP_FAT	regulation of nucleotide metabolic process	18	1.2	0.0000016	0.00025
GOTERM_BP_FAT	cAMP-mediated signaling	17	1.1	0.0000016	0.00026
GOTERM_BP_FAT	homophilic cell adhesion	19	1.2	0.0000034	0.0005
GOTERM_BP_FAT	extracellular structure organization	28	1.8	0.0000047	0.00066

GOTERM_BP_FAT	positive regulation of cell proliferation	58	3.8	0.0000055	0.00074
GOTERM_BP_FAT	defense response	51	3.3	0.000008	0.001
GOTERM_BP_FAT	G-protein signaling, coupled to cyclic nucleotide second messenger	16	1	0.0000091	0.0011
GOTERM_BP_FAT	cyclic-nucleotide-mediated signaling	18	1.2	0.000011	0.0013
GOTERM_BP_FAT	metal ion homeostasis	26	1.7	0.000012	0.0014
GOTERM_BP_FAT	response to hormone stimulus	53	3.4	0.000015	0.0017
GOTERM_BP_FAT	vasculature development	43	2.8	0.000018	0.0019
GOTERM_BP_FAT	transmission of nerve impulse	39	2.5	0.000018	0.002
GOTERM_BP_FAT	behavior	48	3.1	0.000023	0.0023
GOTERM_BP_FAT	blood vessel development	42	2.7	0.000027	0.0027
GOTERM_BP_FAT	cellular metal ion homeostasis	24	1.6	0.000031	0.0029
GOTERM_BP_FAT	regulation of body fluid levels	22	1.4	0.000031	0.003
GOTERM_BP_FAT	lung development	22	1.4	0.00004	0.0036
GOTERM_BP_FAT	morphogenesis of a branching structure	18	1.2	0.000041	0.0036
GOTERM_BP_FAT	hemostasis	19	1.2	0.000045	0.0037
GOTERM_BP_FAT	negative regulation of lyase activity	11	0.7	0.000044	0.0038
GOTERM_BP_FAT	negative regulation of adenylate cyclase activity	11	0.7	0.000044	0.0038
GOTERM_BP_FAT	negative regulation of cyclase activity	11	0.7	0.000044	0.0038
GOTERM_BP_FAT	neuron differentiation	53	3.4	0.000045	0.0038
GOTERM_BP_FAT	immune response	58	3.8	0.00005	0.004
GOTERM_BP_FAT	blood coagulation	18	1.2	0.000055	0.0041
GOTERM_BP_FAT	coagulation	18	1.2	0.000055	0.0041
GOTERM_BP_FAT	cell morphogenesis involved in differentiation	36	2.3	0.000054	0.0041
GOTERM_BP_FAT	response to endogenous stimulus	55	3.6	0.000054	0.0042
GOTERM_BP_FAT	regulation of cell adhesion	25	1.6	0.000058	0.0043
GOTERM_BP_FAT	respiratory tube development	22	1.4	0.000064	0.0045
GOTERM_BP_FAT	blood vessel morphogenesis	37	2.4	0.000065	0.0046
GOTERM_BP_FAT	second-messenger-mediated signaling	28	1.8	0.000071	0.0049
GOTERM_BP_FAT	tube development	36	2.3	0.000073	0.0049
GOTERM_BP_FAT	inflammatory response	33	2.1	0.000075	0.0049

GOTERM_BP_FAT	positive regulation of cell migration	21	1.4	0.000081	0.0052
GOTERM_BP_FAT	response to steroid hormone stimulus	30	1.9	0.000086	0.0054
GOTERM_BP_FAT	positive regulation of cell motion	22	1.4	0.0001	0.0062
GOTERM_BP_FAT	cell motion	59	3.8	0.00011	0.0065
GOTERM_BP_FAT	synaptic transmission	31	2	0.00011	0.0066
GOTERM_BP_FAT	response to oxygen levels	27	1.8	0.00013	0.0078
GOTERM_BP_FAT	skeletal system development	43	2.8	0.00015	0.0086
GOTERM_BP_FAT	locomotory behavior	31	2	0.00015	0.0086
GOTERM_BP_FAT	positive regulation of locomotion	21	1.4	0.00016	0.0089
GOTERM_BP_FAT	extracellular matrix organization	19	1.2	0.00017	0.0091
GOTERM_BP_FAT	response to organic substance	84	5.4	0.00018	0.01
GOTERM_BP_FAT	respiratory system development	22	1.4	0.00019	0.01
GOTERM_BP_FAT	calcium ion homeostasis	22	1.4	0.00019	0.01
GOTERM_BP_FAT	response to estrogen stimulus	21	1.4	0.0002	0.01
GOTERM_BP_FAT	cellular calcium ion homeostasis	21	1.4	0.00025	0.013
GOTERM_BP_FAT	intracellular signaling cascade	142	9.2	0.00026	0.013
GOTERM_BP_FAT	response to virus	19	1.2	0.00026	0.013
GOTERM_BP_FAT	axon guidance	19	1.2	0.00026	0.013
GOTERM_BP_FAT	response to cytokine stimulus	18	1.2	0.00034	0.017
GOTERM_BP_FAT	enzyme linked receptor protein signaling pathway	48	3.1	0.00036	0.017
GOTERM_BP_FAT	cell morphogenesis	47	3	0.00037	0.018
GOTERM_BP_FAT	metal ion transport	46	3	0.00039	0.018
GOTERM_BP_FAT	cellular component morphogenesis	51	3.3	0.00039	0.018
GOTERM_BP_FAT	muscle organ development	30	1.9	0.00041	0.019
GOTERM_BP_FAT	neuron projection morphogenesis	30	1.9	0.00047	0.021
GOTERM_BP_FAT	calcium ion transport	20	1.3	0.00048	0.021
GOTERM_BP_FAT	epithelial cell differentiation	20	1.3	0.00048	0.021
GOTERM_BP_FAT	negative regulation of cell proliferation	49	3.2	0.00047	0.021
GOTERM_BP_FAT	branching morphogenesis of a tube	15	1	0.00054	0.023

GOTERM_BP_FAT	heart morphogenesis	16	1	0.00055	0.023
GOTERM_BP_FAT	positive regulation of DNA replication	10	0.6	0.00069	0.029
GOTERM_BP_FAT	di-, tri-valent inorganic cation transport	24	1.6	0.00069	0.029
GOTERM_BP_FAT	axonogenesis	27	1.8	0.00078	0.032
GOTERM_BP_FAT	neuron projection development	34	2.2	0.0008	0.032
GOTERM_BP_FAT	cellular cation homeostasis	28	1.8	0.00079	0.032
GOTERM_BP_FAT	neuron development	41	2.7	0.00085	0.033
GOTERM_BP_FAT	response to estradiol stimulus	13	0.8	0.0011	0.043
GOTERM_BP_FAT	cell morphogenesis involved in neuron differentiation	28	1.8	0.0012	0.046
GOTERM_BP_FAT	bone development	21	1.4	0.0013	0.049
GOTERM_BP_FAT	cell projection morphogenesis	33	2.1	0.0013	0.049
GOTERM_CC_FAT	extracellular region	205	13.3	2.3E-31	1.1E-28
GOTERM_CC_FAT	extracellular region part	124	8	9E-24	2.1E-21
GOTERM_CC_FAT	plasma membrane	342	22.2	1.7E-18	2.6E-16
GOTERM_CC_FAT	intrinsic to membrane	467	30.3	2.7E-15	3.1E-13
GOTERM_CC_FAT	extracellular matrix	61	4	3.5E-15	3.2E-13
GOTERM_CC_FAT	extracellular space	79	5.1	8.2E-14	6.4E-12
GOTERM_CC_FAT	intrinsic to plasma membrane	131	8.5	1E-13	7E-12
GOTERM_CC_FAT	integral to membrane	445	28.9	1.9E-13	1.1E-11
GOTERM_CC_FAT	integral to plasma membrane	127	8.2	2.8E-13	1.3E-11
GOTERM_CC_FAT	proteinaceous extracellular matrix	54	3.5	2.8E-13	1.5E-11
GOTERM_CC_FAT	plasma membrane part	224	14.5	6.4E-11	2.8E-09
GOTERM_CC_FAT	extracellular matrix part	27	1.8	0.000000028	0.0000011
GOTERM_CC_FAT	basement membrane	19	1.2	0.000015	0.00053
GOTERM_CC_FAT	cell projection	88	5.7	0.000019	0.00065
GOTERM_CC_FAT	neuron projection	50	3.2	0.000037	0.0012
GOTERM_CC_FAT	external side of plasma membrane	22	1.4	0.00058	0.017
GOTERM_CC_FAT	synapse part	29	1.9	0.00069	0.019
GOTERM_CC_FAT	cell surface	39	2.5	0.0014	0.036
GOTERM_MF_FAT	calcium ion binding	121	7.8	8.6E-18	9.2E-15
GOTERM_MF_FAT	growth factor binding	26	1.7	0.00000022	0.00012
GOTERM_MF_FAT	ion channel activity	36	2.3	0.000035	0.0041
GOTERM_MF_FAT	endopeptidase inhibitor activity	20	1.3	0.000024	0.0042
GOTERM_MF_FAT	channel activity	38	2.5	0.000033	0.0044

GOTERM_MF_FAT	passive transmembrane transporter activity	38	2.5	0.000033	0.0044
GOTERM_MF_FAT	peptidase inhibitor activity	20	1.3	0.000032	0.0048
GOTERM_MF_FAT	gated channel activity	30	1.9	0.000024	0.005
GOTERM_MF_FAT	neurotransmitter binding	11	0.7	0.000047	0.005
GOTERM_MF_FAT	peptide binding	25	1.6	0.000068	0.006
GOTERM_MF_FAT	substrate specific channel activity	37	2.4	0.000023	0.0061
GOTERM_MF_FAT	neurotransmitter receptor activity	10	0.6	0.000065	0.0063
GOTERM_MF_FAT	peptide receptor activity	12	0.8	0.00002	0.0069
GOTERM_MF_FAT	peptide receptor activity, G-protein coupled	12	0.8	0.00002	0.0069
GOTERM_MF_FAT	calcium channel activity	13	0.8	0.000086	0.007
GOTERM_MF_FAT	cation channel activity	27	1.8	0.00022	0.016
GOTERM_MF_FAT	glycosaminoglycan binding	19	1.2	0.00023	0.017
GOTERM_MF_FAT	serine-type endopeptidase inhibitor activity	13	0.8	0.00037	0.024
GOTERM_MF_FAT	integrin binding	13	0.8	0.00037	0.024
GOTERM_MF_FAT	lipid binding	56	3.6	0.00062	0.038
GOTERM_MF_FAT	growth factor activity	21	1.4	0.00073	0.042
GOTERM_MF_FAT	polysaccharide binding	19	1.2	0.00084	0.046
GOTERM_MF_FAT	pattern binding	19	1.2	0.00084	0.046