Table S2

Category	Term	Enrichment	Sensitivity	p-value	FDR	pos	neg	genes
GOTERM_BP_FAT	GO:0045785: positive regulation of cell adhesion	14.4	8/60 (13%)	1.18E-06	1.92E-05	4	4	CCDC80 (-7.90), CITED2 (8.10), ECM2 (-37.90), FGF1 (-7.70), SAA1 (18.90), SAA2 (21.30), SRC (-4.80), TNF (4.80)
GOTERM_BP_FAT	GO:0030155: regulation of cell adhesion	7.1	9/137 (6%)	3.70E-05	0.00059904	5	4	CCDC80 (-7.90), CITED2 (8.10), ECM2 (-37.90), FGF1 (-7.70), SAA1 (18.90), SAA2 (21.30), SERPINI1 (7.60), SRC (-4.80), TNF (4.80)
GOTERM_BP_FAT	GO:0006334: nucleosome assembly	9.0	7/84 (8%)	1.19E-04	0.00192731	4	3	HIST1H2AB (-10.60), HIST1H2AC (14.20), HIST1H2AJ (-4.70), HIST1H2AL (-27.90), HIST1H2BK (4.20), HIST2H2BE (12.20), HIST2H4A (5.70)
GOTERM_BP_FAT	GO:0031497: chromatin assembly	8.7	7/87 (8%)	1.45E-04	0.00234099	4	3	HIST1H2AB (-10.60), HIST1H2AC (14.20), HIST1H2AJ (-4.70), HIST1H2AL (-27.90), HIST1H2BK (4.20), HIST2H2BE (12.20), HIST2H4A (5.70)
GOTERM_BP_FAT	GO:0065004: protein-DNA complex assembly	8.3	7/91 (7%)	1.85E-04	0.00299848	4	3	HIST1H2AB (-10.60), HIST1H2AC (14.20), HIST1H2AJ (-4.70), HIST1H2AL (-27.90), HIST1H2BK (4.20), HIST2H2BE (12.20), HIST2H4A (5.70)
GOTERM_BP_FAT	GO:0034728: nucleosome organization	8.1	7/93 (7%)	2.09E-04	0.00337764	4	3	HIST1H2AB (-10.60), HIST1H2AC (14.20), HIST1H2AJ (-4.70), HIST1H2AL (-27.90), HIST1H2BK (4.20), HIST2H2BE (12.20), HIST2H4A (5.70)
GOTERM_BP_FAT	GO:0014912: negative regulation of smooth muscle cell migration	81.2	3/4 (75%)	4.94E-04	0.00797181	0	3	IGFBP3 (-4.70), IGFBP5 (-10.00), TRIB1 (-102.70)
GOTERM_BP_FAT	GO:0006323: DNA packaging	6.5	7/117 (5%)	7.17E-04	0.01155096	4	3	HIST1H2AB (-10.60), HIST1H2AC (14.20), HIST1H2AJ (-4.70), HIST1H2AL (-27.90), HIST1H2BK (4.20), HIST2H2BE (12.20), HIST2H4A (5.70)
GOTERM_BP_FAT	GO:0006333: chromatin assembly or disassembly	6.0	7/127 (5%)	0.00110061	0.0176761	4	3	HIST1H2AB (-10.60), HIST1H2AC (14.20), HIST1H2AJ (-4.70), HIST1H2AL (-27.90), HIST1H2BK (4.20), HIST2H2BE (12.20), HIST2H4A (5.70)
GOTERM_BP_FAT	GO:0006928: cell motion	3.0	13/475 (2%)	0.00138108	0.02213336	9	4	CTGF (17.30), DNAH1 (34.10), DOCK2 (-40.00), EPHB1 (10.40), ETV4 (-5.20), KAL1 (4.60), MYLIP (4.20), S100A2 (-6.90), SAA1 (18.90), SAA2 (21.30), SRC (-4.80), TNF (4.80), UNC5B (10.00)
GOTERM_BP_FAT	GO:0048247: lymphocyte chemotaxis	46.4	3/7 (42%)	0.00169837	0.02715302	2	1	DOCK2 (-40.00), SAA1 (18.90), SAA2 (21.30)
GOTERM_BP_FAT	GO:0009617: response to bacterium	4.5	8/193 (4%)	0.00199406	0.03180912	5	3	BDKRB1 (-7.00), DEFB4A (-55.60), FOS (10.80), HIST1H2BK (4.20), HIST2H2BE (12.20), PLCG2 (5.50), TNF (4.80), TRIB1 (-102.70)
GOTERM_BP_FAT	GO:0006952: defense response	2.5	14/615 (2%)	0.00417596	0.06552569	10	4	ADORA2B (-5.00), ALOX5 (10.30), ANKRD1 (9.70), BDKRB1 (-7.00), CLU (15.50), DEFB4A (-55.60), FOS (10.80), GAL (-4.20), HIST1H2BK (4.20), HIST2H2BE (12.20), SAA1 (18.90), SAA2 (21.30), SAA4 (34.70), TNF (4.80)
GOTERM_BP_FAT	GO:0014910: regulation of smooth muscle cell migration	27.1	3/12 (25%)	0.00517995	0.08066729	0	3	IGFBP3 (-4.70), IGFBP5 (-10.00), TRIB1 (-102.70)
GOTERM_BP_FAT	GO:0048662: negative regulation of smooth muscle cell proliferation	23.2	3/14 (21%)	0.00705705	0.10836102	0	3	IGFBP3 (-4.70), IGFBP5 (-10.00), TRIB1 (-102.70)
GOTERM_BP_FAT	GO:0048660: regulation of smooth muscle cell proliferation	9.4	4/46 (8%)	0.00856435	0.13003019	1	3	IGFBP3 (-4.70), IGFBP5 (-10.00), TNF (4.80), TRIB1 (-102.70)
GOTERM_BP_FAT	GO:0007160: cell-matrix adhesion	6.1	5/89 (5%)	0.00902037	0.13648806	2	3	CTGF (17.30), ECM2 (-37.90), ITGB8 (6.50), ITGBL1 (-4.20), NID2 (-9.60)
GOTERM_BP_FAT	GO:0009611: response to wounding	2.5	12/530 (2%)	0.00942085	0.1421223	9	3	ALOX5 (10.30), BDKRB1 (-7.00), CLU (15.50), CTGF (17.30), FOS (10.80), GAL (-4.20), SAA1 (18.90), SAA2 (21.30), SAA4 (34.70), SDC1 (-5.50), TFPI2 (4.70), TNF (4.80)
GOTERM_BP_FAT	GO:0006954: inflammatory response	3.0	9/325 (2%)	0.01009226	0.1514907	7	2	ALOX5 (10.30), BDKRB1 (-7.00), CLU (15.50), FOS (10.80), GAL (-4.20), SAA1 (18.90), SAA2 (21.30), SAA4 (34.70), TNF (4.80)
GOTERM_BP_FAT	GO:0007155: cell adhesion	2.2	14/700 (2%)	0.01185628	0.17564956	9	5	CLSTN2 (201.80), CTGF (17.30), ECM2 (-37.90), ISLR (-89.90), ITGB8 (6.50), ITGBL1 (-4.20), KAL1 (4.60), NID2 (-9.60), NLGN1 (31.50), PCDH17 (71.10), PCDH19 (4.30), PCDHGA7 (32.50), SRC (-4.80), TNF (4.80)
GOTERM_BP_FAT	GO:0022610: biological adhesion	2.2	14/701 (1%)	0.01198764	0.17742258	9	5	CLSTN2 (201.80), CTGF (17.30), ECM2 (-37.90), ISLR (-89.90), ITGB8 (6.50), ITGBL1 (-4.20), KAL1 (4.60), NID2 (-9.60), NLGN1 (31.50), PCDH17 (71.10), PCDH19 (4.30), PCDHGA7 (32.50), SRC (-4.80), TNF (4.80)
GOTERM_BP_FAT	GO:0031589: cell-substrate adhesion	5.5	5/98 (5%)	0.0125352	0.18477447	2	3	CTGF (17.30), ECM2 (-37.90), ITGB8 (6.50), ITGBL1 (-4.20), NID2 (-9.60)
GOTERM_BP_FAT	GO:0016337: cell-cell adhesion	3.1	8/276 (2%)	0.01357538	0.1985711	7	1	CLSTN2 (201.80), CTGF (17.30), NLGN1 (31.50), PCDH17 (71.10), PCDH19 (4.30), PCDHGA7 (32.50), SRC (-4.80), TNF (4.80)