

Table S6 GO analysis of down-regulated mRNAs in GAS of *dh/db* vs. *dh/m* mice. Top 10 significantly changed terms are shown.

GO_C Term ID	GO_C Term Desc	GO_C Term Level1	GO_C Term Level2	Term Candidate Gene	Total Candidate Gene Num	Term Gene Num	Total Gene Num	Rich Ratio	p-value	q-value
GO:0030018	Z disc	cellular_component	cell	27	1298	157	22482	0.171974522	3.23E-07	2.15E-04
GO:0043218	compact myelin	cellular_component	cell	5	1298	5	22482	1	6.37E-07	2.15E-04
GO:0009986	cell surface	cellular_component	cell	76	1298	745	22482	0.102013423	1.00E-06	2.25E-04
GO:0005737	cytoplasm	cellular_component	cell part	489	1298	7142	22482	0.068468216	1.95E-06	3.30E-04
GO:0005896	cytoskeleton	cellular_component	organelle	113	1298	1272	22482	0.088836478	2.84E-06	3.83E-04
GO:0014704	intercalated disc	cellular_component	cell junction	14	1298	60	22482	0.233333333	6.05E-06	6.07E-04
GO:0020005	symblont-containing vacuole membrane	cellular_component	extracellular region part	6	1298	10	22482	0.6	6.29E-06	6.07E-04
GO:0030016	myofibril	cellular_component	organelle	12	1298	48	22482	0.25	1.31E-05	8.89E-04
GO:0031430	M band	cellular_component	organelle	10	1298	33	22482	0.303030303	1.08E-05	8.89E-04
GO:0097512	cardiac myofibril	cellular_component	organelle	6	1298	11	22482	0.545454545	1.32E-05	8.89E-04
GO:0003779	actin binding	molecular_function	binding	51	1280	392	21691	0.130102041	9.62E-08	1.22E-04
GO:0000166	nucleotide binding	molecular_function	binding	154	1280	1749	21691	0.088050314	2.50E-07	1.58E-04
GO:0003924	GTPase activity	molecular_function	catalytic activity	43	1280	342	21691	0.125730994	2.38E-06	8.33E-04
GO:0042803	protein homodimerization activity	molecular_function	binding	98	1280	1039	21691	0.094321463	2.64E-06	8.33E-04
GO:0003774	motor activity	molecular_function	catalytic activity	21	1280	123	21691	0.170731707	1.00E-05	0.00253456
GO:0001730	2'-5'-oligoadenylate synthetase activity	molecular_function	catalytic activity	6	1280	11	21691	0.545454545	1.49E-05	0.00314103
GO:0005525	GTP binding	molecular_function	binding	48	1280	439	21691	0.109339408	2.92E-05	0.00409576
GO:0015293	symporter activity	molecular_function	transporter activity	19	1280	112	21691	0.169642857	2.87E-05	0.00409576
GO:0019911	structural constituent of myelin sheath	molecular_function	structural molecule activity	6	1280	12	21691	0.5	2.83E-05	0.00409576
GO:0003785	actin monomer binding	molecular_function	binding	9	1280	30	21691	0.3	3.90E-05	0.00492762
GO:0002376	immune system process	biological_process	immune system process	66	1285	457	22257	0.144420131	5.43E-12	1.16E-08
GO:0009615	response to virus	biological_process	response to stimulus	26	1285	90	22257	0.288888889	3.98E-12	1.16E-08
GO:0009617	response to bacterium	biological_process	response to stimulus	35	1285	209	22257	0.167464115	1.24E-08	1.70E-05
GO:0051607	defense response to virus	biological_process	multi-organism process	35	1285	211	22257	0.165876777	1.59E-08	1.70E-05
GO:0035458	cellular response to interferon-beta	biological_process	response to stimulus	18	1285	66	22257	0.272727273	2.19E-08	1.87E-05
GO:0006936	muscle contraction	biological_process	multicellular organismal process	15	1285	55	22257	0.272727273	3.25E-07	2.31E-04
GO:0045071	negative regulation of viral genome replication	biological_process	regulation of biological process	13	1285	46	22257	0.282608696	1.27E-06	7.73E-04
GO:0042832	defense response to protozoan	biological_process	response to stimulus	11	1285	34	22257	0.323529412	1.90E-06	0.00101293
GO:0003009	skeletal muscle contraction	biological_process	multicellular organismal process	10	1285	30	22257	0.333333333	4.12E-06	0.00195473
GO:0042552	myelination	biological_process	developmental process	14	1285	59	22257	0.237288136	4.89E-06	0.00208798