

Table S10. Gene set enrichment analysis of differentially expressed mRNAs in GAS of *db/db* vs. *db/m* mice

KEGG pathway term	KEGG Pathway Term	Count	Enrichment score(ES)	Normalized enrichment score(NES)	p-value	q-value
Path: 00190	Oxidative phosphorylation	127	-0.5526848	-2.0429156	0	0.00222351
Path: 00330	Arginine and proline metabolism	54	-0.5889819	-1.8983037	0	0.01518323
Path: 04621	NOD-like receptor signaling pathway	165	-0.49058524	-1.8674083	0	0.01310986
Path: 04260	Cardiac muscle contraction	73	-0.53326494	-1.8339995	0	0.01554834
Path: 03040	Spliceosome	145	-0.48090827	-1.7948809	0	0.01919736
Path: 04668	TNF signaling pathway	121	-0.47786793	-1.7660106	0	0.02615792
Path: 04714	Thermogenesis	224	-0.44887698	-1.760888	0	0.02452575
Path: 04215	Apoptosis - multiple species	32	-0.58779675	-1.7351348	0.001472754	0.03038663
Path: 04612	Antigen processing and presentation	92	-0.48597893	-1.7295831	0	0.02789833
Path: 00970	Aminoacyl-tRNA biosynthesis	44	-0.55156153	-1.7230982	0.00270636	0.02693685
Path: 00520	Amino sugar and nucleotide sugar metabolism	52	-0.5233406	-1.7163136	0.001347709	0.02562705
Path: 03008	Ribosome biogenesis in eukaryotes	78	-0.49748105	-1.710581	0	0.0262608
Path: 00620	Pyruvate metabolism	38	-0.55128986	-1.7048439	0	0.02579342
Path: 00270	Cysteine and methionine metabolism	45	-0.5256719	-1.674743	0.002688172	0.03695324
Path: 04622	RIG-I-like receptor signaling pathway	56	-0.5064118	-1.6657387	0.009383378	0.03925965
Path: 01110	Biosynthesis of secondary metabolites	408	-0.4016611	-1.64127	0	0.04969784
Path: 00020	Citrate cycle (TCA cycle)	33	-0.5588199	-1.6380706	0.007062147	0.04857261
Path: 00760	Nicotinate and nicotinamide metabolism	37	-0.52634275	-1.6229776	0.009873061	0.05352934
Path: 00240	Pyrimidine metabolism	103	-0.44775844	-1.622756	0.00239521	0.05083772
Path: 01120	Microbial metabolism in diverse environments	197	-0.41644928	-1.6215492	0	0.04891422
Path: 00052	Galactose metabolism	34	-0.5362767	-1.6123178	0.015602837	0.05217607
Path: 04141	Protein processing in endoplasmic reticulum	175	-0.4203752	-1.6065907	0	0.05313872
Path: 03020	RNA polymerase	30	-0.54538834	-1.6059985	0.008275862	0.05111904
Path: 04210	Apoptosis	139	-0.43250751	-1.6047664	0	0.04955835
Path: 03030	DNA replication	35	-0.52853376	-1.603016	0.016574586	0.04829614
Path: 00790	Folate biosynthesis	25	-0.5647241	-1.5977005	0.018284107	0.04892057
Path: 04217	Necroptosis	168	-0.41426623	-1.5951003	0.001132503	0.04857654
Path: 00630	Glyoxylate and dicarboxylate metabolism	31	-0.53893936	-1.5940472	0.008720931	0.04759575
Path: 01230	Biosynthesis of amino acids	88	-0.4495537	-1.5777572	0	0.05520424
Path: 01130	Biosynthesis of antibiotics	237	-0.4020137	-1.57719	0	0.05358679
Path: 01200	Carbon metabolism	138	-0.4250244	-1.5748466	0.001187649	0.05277475
Path: 00120	Primary bile acid biosynthesis	15	-0.63615996	-1.5686022	0.020833334	0.05487995
Path: 04216	Ferroptosis	44	-0.4959733	-1.5655997	0.012096774	0.05520907
Path: 00561	Glycerolipid metabolism	67	-0.46571037	-1.5636723	0.00794702	0.05472251
Path: 04623	Cytosolic DNA-sensing pathway	52	-0.483717	-1.5538176	0.01321004	0.05908325
Path: 03050	Proteasome	49	-0.4789619	-1.5368923	0.010596027	0.06931855
Path: 00670	One carbon pool by folate	20	-0.57616717	-1.529518	0.030837005	0.07297418
Path: 00600	Sphingolipid metabolism	47	-0.47145516	-1.5163796	0.013175231	0.07978042
Path: 04144	Endocytosis	277	-0.37838146	-1.4988393	0	0.09153216
Path: 00983	Drug metabolism - other enzymes	80	-0.4240861	-1.4832975	0.014084507	0.10244641
Path: 00720	Carbon fixation pathways in prokaryotes	16	-0.58658737	-1.4786525	0.042682927	0.10412729
Path: 00230	Purine metabolism	176	-0.38347492	-1.4747382	0.003409091	0.10543973
Path: 04380	Osteoclast differentiation	129	-0.39830652	-1.4646047	0.012048192	0.11283693
Path: 04212	Longevity regulating pathway - worm	73	-0.42626804	-1.4621549	0.013871375	0.11319479
Path: 00564	Glycerophospholipid metabolism	105	-0.40026918	-1.4492073	0.019680196	0.1236824
Path: 04066	HIF-1 signaling pathway	108	-0.39681992	-1.4367079	0.017199017	0.1322489
Path: 04620	Toll-like receptor signaling pathway	90	-0.40204182	-1.4335115	0.030150754	0.13308004
Path: 04630	Jak-STAT signaling pathway	139	-0.38611218	-1.4329159	0.014285714	0.13118261
Path: 04514	Cell adhesion molecules (CAMs)	165	-0.3714898	-1.4254291	0.009174312	0.13814448
Path: 00280	Valine, leucine and isoleucine degradation	56	-0.4284441	-1.4168553	0.04953146	0.14301506
Path: 04137	Mitophagy - animal	67	-0.40939978	-1.389222	0.030534351	0.17517814
Path: 00480	Glutathione metabolism	67	-0.41029608	-1.3777372	0.03529412	0.18587226
Path: 00010	Glycolysis / Gluconeogenesis	75	-0.40324086	-1.3750738	0.04865557	0.18318556
Path: 04625	C-type lectin receptor signaling pathway	109	-0.3726755	-1.361083	0.043156598	0.1979647
Path: 04071	Sphingolipid signaling pathway	128	-0.36472544	-1.3609551	0.030805686	0.19488622
Path: 04145	Phagosome	174	-0.35446945	-1.3420619	0.023809524	0.21662267
Path: 03013	RNA transport	176	-0.3414098	-1.302725	0.03686636	0.25030002
Path: 03010	Ribosome	175	-0.33895674	-1.2990037	0.04084014	0.24999419
Path: 04924	Renin secretion	70	0.34984162	1.4207784	0.026548672	0.55237496
Path: 04080	Neuroactive ligand-receptor interaction	237	0.30620188	1.4746653	0.012987013	0.7719984