

Supplementary Table S4. Top 10 terms of KEGG analysis for differentially expressed genes in glomeruli from diabetic mGPDH KO mice compared with WT mice.

Down-regulated pathway:

ID	Term	Ratio_in_study	Ratio_in_pop	P value_corrected
map00071	Fatty acid degradation	20/621	67/24050	3.81E-09
map04146	Peroxisome	32/621	116/24050	4.34E-09
map00380	Tryptophan metabolism	15/621	59/24050	4.49E-09
map00280	Valine, leucine and isoleucine degradation	21/621	67/24050	4.57E-09
map00410	beta-Alanine metabolism	15/621	51/24050	5.34E-09
map00650	Butanoate metabolism	14/621	34/24050	5.48E-09
map03320	PPAR signaling pathway	22/621	130/24050	5.6E-09
map00830	Retinol metabolism	20/621	144/24050	4.13E-08
map00983	Drug metabolism - other enzymes	21/621	178/24050	2.44E-07
map00140	Steroid hormone biosynthesis	19/621	145/24050	2.48E-07

Up-regulated pathway:

ID	Term	Ratio_in_study	Ratio_in_pop	P value_corrected
map04933	AGE-RAGE signaling pathway in diabetic complications	52/2665	138/24050	<0.001
map04668	TNF signaling pathway	56/2665	146/24050	1.80789E-11
map05165	Human papillomavirus infection	126/2665	551/24050	1.15375E-09
map04062	Chemokine signaling pathway	79/2665	257/24050	1.18971E-09
map04926	Relaxin signaling pathway	53/2665	161/24050	1.2209E-09
map05200	Pathways in cancer	166/2665	851/24050	1.31326E-09
map05145	Toxoplasmosis	54/2665	186/24050	1.31872E-09
map04512	ECM-receptor interaction	44/2665	99/24050	1.36314E-09
map04060	Cytokine-cytokine receptor interaction	95/2665	344/24050	1.36865E-09
map04380	Osteoclast differentiation	67/2665	160/24050	1.39373E-09