

Table S1 The oligonucleotide sequences of primers used in quantitative real-time PCR

Gene	Primer type	Sequence/target sequence
ALDOC	Forward	5'-TCTACTATCCCAACGTGCTTCAG-3'
	Reverse	5'-CTGAAGTTGGGCTGAGAGATAGA-3'
ANGPTL4	Forward	5'-CAGACAAGGGAGCTGAGGTTAAA-3'
	Reverse	5'-ACATCATGCTCCTGACCATTGTA-3'
CITED2	Forward	5'-CTCCTGTGAACCTTCTGCCAGTA-3'
	Reverse	5'-ACTTTGCCTGCCAGTCATATCTT-3'
β-actin	Forward	5'-GGAGCGAGATCCCTCCAAAAT-3'
	Reverse	5'-GGCTGTTGTCATACTTCTCATGG-3'

Table S2 GO enrichment results of significant GRGs

ID	Description	P value	q value
GO:0016758	hexosyltransferase activity	1.53E-05	0.001808
GO:0016616	oxidoreductase activity, acting on the CH-OH group of donors, NAD or NADP as acceptor	3.80E-05	0.001808
GO:0051287	NAD binding	4.98E-05	0.001808
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	5.52E-05	0.001808
GO:0030246	carbohydrate binding	9.15E-05	0.001808
GO:0016757	glycosyltransferase activity	9.34E-05	0.001808
GO:0048029	monosaccharide binding	9.54E-05	0.001808
GO:0008375	acetylglucosaminyltransferase activity	0.000224	0.003714
GO:0050308	sugar-phosphatase activity	0.000422	0.00622
GO:0019203	carbohydrate phosphatase activity	0.000506	0.006705
GO:0031994	insulin-like growth factor I binding	0.000596	0.007191
GO:0008194	UDP-glycosyltransferase activity	0.000736	0.008134
GO:0004029	aldehyde dehydrogenase (NAD+) activity	0.000913	0.009311
GO:0004030	Aldehyde dehydrogenase [NAD(P)+] activity	0.001159	0.010984
GO:0019200	carbohydrate kinase activity	0.001583	0.013995
GO:0005540	hyaluronic acid binding	0.002069	0.017151
GO:0035035	histone acetyltransferase binding	0.002813	0.020753
GO:0005520	insulin-like growth factor binding	0.003016	0.020753
GO:0008378	galactosyltransferase activity	0.003442	0.020753
GO:0015020	glucuronosyltransferase activity	0.003442	0.020753
GO:0071813	lipoprotein particle binding	0.003442	0.020753
GO:0071814	protein-lipid complex binding	0.003442	0.020753
GO:0043548	phosphatidylinositol 3-kinase binding	0.005407	0.031182
GO:0016620	oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	0.006542	0.036156

GO, Gene Ontology; GRGs, glycolysis-related genes.

Table S3 KEGG enrichment results of significant GRGs

ID	Description	P value	q value
rno00010	Glycolysis / Gluconeogenesis	5.00E-13	4.10E-11
rno01200	Carbon metabolism	3.65E-09	1.50E-07
rno00051	Fructose and mannose metabolism	6.75E-07	1.62E-05
rno05230	Central carbon metabolism in cancer	8.13E-07	1.62E-05
rno04066	HIF-1 signaling pathway	9.88E-07	1.62E-05
rno00620	Pyruvate metabolism	2.37E-06	3.24E-05
rno04922	Glucagon signaling pathway	9.09E-06	0.000106577
rno00052	Galactose metabolism	1.50E-05	0.000153726
rno04910	Insulin signaling pathway	4.75E-05	0.000433159
rno04152	AMPK signaling pathway	0.00030662	0.002517506
rno00030	Pentose phosphate pathway	0.00038155	0.002847963
rno01250	Biosynthesis of nucleotide sugars	0.00071334	0.004880759
rno00514	Other types of O-glycan biosynthesis	0.00111053	0.007013903
rno04930	Type II diabetes mellitus	0.00162509	0.009410216
rno00520	Amino sugar and nucleotide sugar metabolism	0.00182468	0.009410216
rno04931	Insulin resistance	0.00183379	0.009410216
rno00533	Glycosaminoglycan biosynthesis - keratan sulfate	0.00197245	0.009526391
rno04213	Longevity regulating pathway - multiple species	0.003496	0.015946661
rno04068	FoxO signaling pathway	0.00375343	0.016219826
rno00515	Mannose type O-glycan biosynthesis	0.00533584	0.021397881
rno04140	Autophagy - animal	0.00547292	0.021397881
rno00534	Glycosaminoglycan biosynthesis - heparan sulfate / heparin	0.00580327	0.021658141
rno01230	Biosynthesis of amino acids	0.00609346	0.021752387
rno04932	Non-alcoholic fatty liver disease	0.00717958	0.024561719
rno00601	Glycosphingolipid biosynthesis - lacto and neolacto series	0.00840823	0.027614391
rno04211	Longevity regulating pathway	0.00904286	0.02855639
rno00640	Propanoate metabolism	0.00957194	0.029107665
rno00500	Starch and sucrose metabolism	0.0101792	0.029848795

KEGG, Kyoto Encyclopedia of Genes and Genomes; GRGs, glycolysis-related genes.

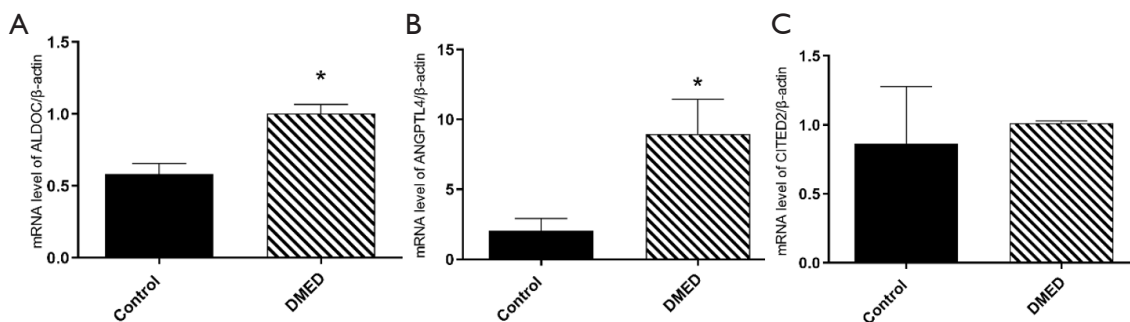


Figure S1 The mRNA levels of hub GRGs in control and DMED groups. *, P<0.05. GRGs, glycolysis-related genes; DMED = diabetes mellitus-related erectile dysfunction.