

Supplementary Table 1 GEO Microarray Chip Information

	GSE27276	GSE138125	GSE4316
Platform	GPL2507	GPL21827	GPL570
Species	Homo sapiens	Homo sapiens	Homo sapiens
Tissue	Trabecular meshwork	Trabecular meshwork	Trabecular meshwork
Samples in POAG group	17	4	2
Samples in Control group	19	4	3
Reference	PMID: 24003086 PMID: 37037464	PMID: 34244823	PMID: 16862071

GEO, Gene Expression Omnibus; POAG, Primary Open-Angle Glaucoma.

Supplementary Table 2 Result of GO and KEGG Enrichment Analysis for MRDEGs

ONTOL	ID	Description	Gene	BgRa	pvalue	p.adjust	qvalue
OGY			Ratio	tio			

BP	GO:00229	electron transport chain	6/25	176/1	9.24026	5.11911	3.29731
	00			8870	E-08	E-05	E-05
BP	GO:00091	purine ribonucleotide metabolic process	7/25	365/1	3.40575	6.3602E	4.09673
	50			8870	E-07	-05	E-05
BP	GO:00092	ribonucleotide metabolic process	7/25	385/1	4.87927	6.3602E	4.09673
	59			8870	E-07	-05	E-05
BP	GO:00196	ribose phosphate metabolic process	7/25	393/1	5.60307	6.3602E	4.09673
	93			8870	E-07	-05	E-05
BP	GO:00061	mitochondrial electron transport, NADH	4/25	51/18	5.74025	6.3602E	4.09673
	20	to ubiquinone		870	E-07	-05	E-05
CC	GO:00057	mitochondrial inner membrane	12/25	497/1	2.016E-	8.87041	4.03201
	43			9886	13	E-12	E-12
CC	GO:00057	mitochondrial matrix	9/25	487/1	4.24382	9.33641	4.24382
	59			9886	E-09	E-08	E-08
CC	GO:00987	mitochondrial protein-containing complex	6/25	300/1	1.55988	2.28782	1.03992
	98			9886	E-06	E-05	E-05

CC	GO:00057	mitochondrial outer membrane	5/25	217/1	6.57047	7.22752	3.28524
	41			9886	E-06	E-05	E-05
CC	GO:00319	organelle outer membrane	5/25	246/1	1.20714	9.20564	4.18438
	68			9886	E-05	E-05	E-05
MF	GO:00090	electron transfer activity	5/25	117/1	4.46272	3.21316	1.69113
	55			8496	E-07	E-05	E-05
MF	GO:00081	NADH dehydrogenase (ubiquinone)	3/25	41/18	2.24774	0.00042	0.00022
	37	activity		496	E-05	9323	596
MF	GO:00501	NADH dehydrogenase (quinone) activity	3/25	42/18	2.41849	0.00042	0.00022
	36			496	E-05	9323	596
MF	GO:00039	NADH dehydrogenase activity	3/25	44/18	2.78514	0.00042	0.00022
	54			496	E-05	9323	596
MF	GO:00039	NAD(P)H dehydrogenase (quinone)	3/25	45/18	2.98141	0.00042	0.00022
	55	activity		496	E-05	9323	596
KEGG	hsa05012	Parkinson disease	7/19	271/8	8.64066	3.73991	1.92978
				842	E-07	E-05	E-05

KEGG	hsa00260	Glycine, serine and threonine metabolism	4/19	41/88	1.46663	3.73991	1.92978
				42	E-06	E-05	E-05
KEGG	hsa00330	Arginine and proline metabolism	4/19	50/88	3.2947E	5.60098	2.89009
				42	-06	E-05	E-05
KEGG	hsa00340	Histidine metabolism	3/19	22/88	1.26265	0.00016	8.30688
				42	E-05	0987	E-05
KEGG	hsa05415	Diabetic cardiomyopathy	5/19	205/8	5.69188	0.00058	0.00029
				842	E-05	0571	9572

GO, Gene Ontology; BP, Biological Process; CC, Cellular Component; MF, Molecular Function; KEGG, Kyoto Encyclopedia of Genes and Genomes; MRDEGs, Mitochondrial-Related Differentially Expressed Genes.

Supplementary Table 3 Results of GSEA for GSE27276

ID	Set Size	Enrichment Score	NES	p value	p.adjust	q value
REACTOME_FORMATION_OF_THE_C	114	-0.791214014	-	1E-10	1.247E-07	1.15053E-

ORNIFIED_ENVELOPE			2.590348012			07
REACTOME_THE_CITRIC_ACID_TCA			2.06728872	1.92986E-	1.60436E-	1.48024E-
_CYCLE_AND_RESPIRATORY_ELECTRO	164	0.625966029	3	08	05	05
N_TRANSPORT						
REACTOME_COLLAGEN_BIOSYNTH			2.04730980	6.24249E-	0.00038921	0.0003591
ESIS_AND_MODIFYING_ENZYMES	64	0.71421111	8	07	9	07
REACTOME_ERYTHROCYTES_TAKE			1.99218435	8.40591E-		0.0003717
_UP_CARBON_DIOXIDE_AND_RELEASE_	12	0.941920038	9	07	0.00040297	94
OXYGEN						
REACTOME_CYTOPROTECTION_BY			2.08803216	1.34845E-		0.0003717
_HMOX1	59	0.736699492	9	06	0.00040297	94
REACTOME_ECM_PROTEOGLYCANS			2.04723058	1.60134E-		0.0003717
	71	0.699493875	4	06	0.00040297	94
KEGG_ALLOGRAFT_REJECTION			2.11271371	1.6124E-		0.0003717
	37	0.795218209	5	06	0.00040297	94
REACTOME_RESPIRATORY_ELECTR			2.06532255	1.61576E-		0.0003717
ON_TRANSPORT_ATP_SYNTHESIS_BY_C	113	0.652829319	1	06	0.00040297	94

HEMIOSMOTIC_COUPLING_AND_HEAT_
PRODUCTION_BY_UNCOUPLING_PROTE

INS

KEGG_TYPE_I_DIABETES_MELLITU	43	0.777074569	2.08348341	2.40654E-	0.00054562	0.0005034
S			9	06	8	16
PID_TAP63_PATHWAY	53	-0.743623241	-	2.98684E-	0.00061818	0.0005703
			2.151027945	06	1	56
KEGG_ANTIGEN_PROCESSING_AND	87	0.667347909	2.02234051	3.22227E-	0.00061818	0.0005703
_PRESENTATION			1	06	1	56
PID_P53_DOWNSTREAM_PATHWAY	136	-0.59210366	-	6.56808E-	0.00096357	0.0008890
			1.972057545	06	6	3
REACTOME_INTEGRIN_CELL_SURF	81	0.657421812	1.96255772	7.13198E-	0.00098817	0.0009117
ACE_INTERACTIONS			4	06	5	25
WP_ELECTRON_TRANSPORT_CHAIN	90	0.654770176	1.99928546	1.18841E-	0.00155995	0.0014392
_OXPHOS_SYSTEM_IN_MITOCHONDRIA			6	05	1	66
PID_DELTA_NP63_PATHWAY	46	-0.725876512	-	1.99826E-	0.00238201	0.0021977
			2.061527167	05	6	33

NABA_CORE_MATRISOME	250	0.497732012	1.72766575	2.65034E-	0.00300452	0.0027720
			8	05	7	83
REACTOME_RESPIRATORY_ELECTR	91	0.637084029	1.94644832	2.90883E-	0.00315418	0.0029101
ON_TRANSPORT			7	05	7	64
KEGG_OXIDATIVE_PHOSPHORYLATI	114	0.604311269	1.91418253	3.1239E-	0.00324625	0.0029951
ON			8	05	3	08
REACTOME_SIGNALING_BY_INTER	461	-0.408016859	-	5.11E-05	0.00490013	0.0045210
LEUKINS			1.559333874		5	38
REACTOME_CROSSLINKING_OF_CO	17	0.817799924	1.85914735	0.0008197	0.04259119	0.0392961
LLAGEN_FIBRILS			7	18	3	41

GSEA, Gene Set Enrichment Analysis.

Supplementary Table 4 Results of GSEA for Risk Group

ID	Set Size	Enrichment Score	NES	p value	p.adjust	q value
HSIAO_HOUSEKEEPING_G	388	0.457282742	2.06952	1.00E-10	6.67E-08	5.62E-08

ENES			6235			
JOHNSTONE_PARVB_TARG	402	0.446899869	2.03308	1.00E-10	6.67E-08	5.62E-08
ETS_3_UP			3748			
DELYS_THYROID_CANCER	429	0.420441884	1.92875	1.00E-10	6.67E-08	5.62E-08
_UP			8244			
RODWELL_AGING_KIDNE	438	0.419514441	1.92207	1.00E-10	6.67E-08	5.62E-08
Y_UP			7461			
VERHAAK_GLIOBLASTOM	125	-0.594841544	-	6.34E-10	3.81E-07	3.21E-07
A_NEURAL			2.282359919			
REACTOME_NEURONAL_S	391	-0.430302853	-	1.49E-09	8.15E-07	6.86E-07
YSTEM			1.881775854			
BOQUEST_STEM_CELL_UP	248	0.463362267	1.99670	2.24E-09	1.12E-06	9.43E-07
			8637			
NAKAYAMA_SOFT_TISSUE	75	0.624976833	2.25569	1.37E-08	5.47E-06	4.60E-06
_TUMORS_PCA1_UP			8465			
REACTOME_NEUTROPHIL	455	0.38504298	1.77069	1.29E-08	5.47E-06	4.60E-06
_DEGRANULATION			8616			

WP_CALCIIUM_REGULATIO N_IN_CARDIAC_CELLS	150	-0.538895871	- 2.123366075	3.23E-08	1.21E-05	1.02E-05
STEIN_ESRRA_TARGETS_U P	369	-0.412953692	- 1.79031552	4.88E-08	1.63E-05	1.37E-05
COLINA_TARGETS_OF_4E BP1_AND_4EBP2	346	0.403807688	1.79950 6966	7.55E-08	2.39E-05	2.01E-05
REACTOME_REGULATION _OF_INSULIN_LIKE_GROWTH_ FACTOR_IGF_TRANSPORT_AN D_UPTAKE_BY_INSULIN_LIKE _GROWTH_FACTOR_BINDING_ PROTEINS_IGFBPS	121	0.534956163	2.10372 6085	1.10E-07	3.15E-05	2.66E-05
REACTOME_TRANSMISSIO N_ACROSS_CHEMICAL_SYNAP SES	256	-0.455689128	- 1.90612286	1.33E-07	3.63E-05	3.06E-05
VERHAAK_GLIOMASTOM A_PRONEURAL	171	-0.503494769	- 1.997088323	1.43E-07	3.74E-05	3.15E-05

NABA_CORE_MATRISOME	250	0.436759171	1.88530 0128	1.57E-07	3.93E-05	3.31E-05
KAAB_HEART_ATRIUM_VS _VENTRICLE_DN	252	-0.454997837	- 1.899710506	1.72E-07	4.14E-05	3.48E-05
REACTOME_PYRUVATE_M ETABOLISM_AND_CITRIC_ACI D_TCA_CYCLE	55	-0.555051781	- 1.861481645	0.000373933	0.0113388 52	0.0095441 34
KEGG_OXIDATIVE_PHOSP HORYLATION	114	-0.460182259	- 1.739888242	0.000373832	0.0113388 52	0.0095441 34
KEGG_WNT_SIGNALING_P ATHWAY	147	-0.3931508	- 1.533366544	0.002803272	0.0425021 34	0.0357748 78

GSEA, Gene Set Enrichment Analysis

Supplementary Table 5 Basic Information of the Subjects

	All Subjects (n=10)	POAG (n=5)	Control (n=5)
Age (median (range)), years	71(62-74)	71(62-74)	70(67-74)
Female (percentage)	5(50%)	3(60%)	2(40%)
Male (percentage)	5(50%)	2(40%)	3(60%)

POAG, Primary Open-Angle Glaucoma.

Supplementary Table 6 Primer Sequences for Real-Time PCR

Gene	GenBank accession number	Sequences
ALAS2	NM_000032.5	Forward Primer: 5'-ACAGATCTGCCTAGCTCCCT-3' Reverse Primer: 5'-ACTGAAGACATAGTTTCCAGGCA-3'
MAOA	NM_000240.4	Forward Primer: 5'-CTGATCGACTTGCTAAGCTAC-3' Reverse Primer: 5'-ATGCACTGGATGTAAAGCTTC-3'

GSR	NM_000637.5	Forward Primer: 5'-GTGCCAGCTTAGGAATAACCAG-3'
		Reverse Primer: 5'-GTGAGTCCCAGTGTCCCAATAG-3'
MGARP	NM_032623.4	Forward Primer: 5'-TCGGAAAGGACGCATCTCTG-3'
		Reverse Primer: 5'-GACTGTGACGCCTACAACCA-3'
MPC2	NM_001143674.4	Forward Primer: 5'-AGTCAGATGAGTCAGCAAAGCA-3'
		Reverse Primer: 5'-AGAACCTCTTCATTGTGGCCTA-3'
NDUFV2	NM_021074.5	Forward Primer: 5'-TTTAGGGGCCTGTGTGAACG-3'
		Reverse Primer: 5'-GAGAAGCGTCCACTCCTTGG-3'
MFN2	NM_001127660.2	Forward Primer: 5'-ACATAGAGGAAGGACTGGGT-3'
		Reverse Primer: 5'-TAGTTGAGGGAGAAGCACTG-3'
GLS	NM_001256310.2	Forward Primer: 5'-TGCATTCCTGTGGCATGTAT-3'
		Reverse Primer: 5'-TTGCCCATCTTATCCAGAGG-3'
GAPDH	NM_001256799.3	Forward Primer: 5'-ACAACCTTGGTATCGTGGAAGG-3'
		Reverse Primer: 5'-CCATCACGCCACAGTTTC-3'
