

Table S1 Biological process of gene ontology analysis results.

#term ID	term description	observed gene count	background gene count	false discovery rate	matching proteins in network
GO:0051289	protein homotetramerization	4	78	0.00035	ACACB,CAT,GPX3,TK1
GO:0051260	protein homooligomerization	5	312	0.0011	ACACB,CAT,GBP1,GPX3,TK1
GO:0055114	oxidation-reduction process	7	923	0.0011	AGPS,ALDH6A1,CAT,ENO1,GPD1L,GPX3,NCF2
GO:0055086	nucleobase-containing small molecule metabolic process	6	662	0.0013	ACACB,ALDH6A1,ENO1,GPD1L,PDE2A,TK1
GO:0044281	small molecule metabolic process	8	1779	0.0026	ACACB,AGPS,ALDH6A1,CAT,ENO1,GPD1L,PDE2A,TK1
GO:0051186	cofactor metabolic process	5	467	0.0026	ACACB,CAT,ENO1,GPD1L,GPX3
GO:0009117	nucleotide metabolic process	5	576	0.0054	ACACB,ENO1,GPD1L,PDE2A,TK1
GO:0072593	reactive oxygen species metabolic process	3	103	0.0056	CAT,GPX3,NCF2
GO:0042744	hydrogen peroxide catabolic process	2	20	0.0096	CAT,GPX3
GO:0034404	nucleobase-containing small molecule biosynthetic process	3	149	0.0138	ENO1,PDE2A,TK1
GO:0046434	organophosphate catabolic process	3	152	0.0138	ENO1,GPD1L,PDE2A
GO:0009056	catabolic process	7	1859	0.014	ALDH6A1,CAT,ENO1,GPD1L,GPX3,PDE2A,RNASEH2A
GO:0042743	hydrogen peroxide metabolic process	2	31	0.0164	CAT,GPX3
GO:0044270	cellular nitrogen compound catabolic process	4	441	0.0164	ALDH6A1,ENO1,PDE2A,RNASEH2A
GO:0046700	heterocycle catabolic process	4	440	0.0164	ALDH6A1,ENO1,PDE2A,RNASEH2A
GO:0006734	NADH metabolic process	2	34	0.0165	ENO1,GPD1L
GO:1901361	organic cyclic compound catabolic process	4	484	0.0193	ALDH6A1,ENO1,PDE2A,RNASEH2A
GO:0044283	small molecule biosynthetic process	4	569	0.0307	ACACB,ENO1,PDE2A,TK1
GO:0090407	organophosphate biosynthetic process	4	577	0.0307	ACACB,ENO1,GPD1L,TK1

GO:0044248	cellular catabolic process	6	1646	0.0325	ALDH6A1,CAT,ENO1,GPX3,PDE2A,RNASEH2A
GO:1901135	carbohydrate derivative metabolic process	5	1083	0.0336	ACACB,ENO1,GPD1L,PDE2A,TK1
GO:0006625	protein targeting to peroxisome	2	68	0.0408	AGPS,CAT
GO:0006732	coenzyme metabolic process	3	297	0.0408	ACACB,ENO1,GPD1L
GO:0009165	nucleotide biosynthetic process	3	291	0.0408	ACACB,ENO1,TK1

Table S2 Cellular component of gene ontology analysis results.

#term ID	term description	observed gene count	background gene count	false discovery rate	matching proteins in network
GO:0005829	cytosol	13	4958	0.00013	ACACB,AGPS,CAT,ENO1,GBP1,GPD1L,MAP3K3,NCF2,PDE2A,RNASEH2A,TAGLN2,TDRD3,TK1
GO:0044444	cytoplasmic part	14	9377	0.0171	ACACB,AGPS,ALDH6A1,CAT,ENO1,GBP1,GPD1L,MAP3K3,NCF2,PDE2A,RNASEH2A,TAGLN2,TDRD3,TK1
GO:0005778	peroxisomal membrane	2	51	0.03	AGPS,CAT
GO:0005782	peroxisomal matrix	2	53	0.03	AGPS,CAT
GO:1990204	oxidoreductase complex	2	103	0.0435	GPD1L,NCF2

Table S3 Molecular functionality of gene ontology analysis results.

#term ID	term description	observed gene count	background gene count	false discovery rate	matching proteins in network
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GO:0050662	coenzyme binding	5	274	0.00027	ACACB,AGPS,ALDH6A1,CAT,GPD1L
GO:0000166	nucleotide binding	9	2097	0.00044	ACACB,AGPS,ALDH6A1,CAT,GBP1,GPD1L,MAP3K3,PDE2A,TK1
GO:0003824	catalytic activity	13	5592	0.00044	ACACB,AGPS,ALDH6A1,CAT,ENO1,GBP1,GPD1L,GPX3,MAP3K3,NCF2,PDE2A,RNASEH2A,TK1
GO:0016491	oxidoreductase activity	6	716	0.00044	AGPS,ALDH6A1,CAT,GPD1L,GPX3,NCF2
GO:0042802	identical protein binding	7	1754	0.0035	ACACB,CAT,ENO1,GBP1,GPD1L,PDE2A,TK1
GO:1901363	heterocyclic compound binding	11	5305	0.0051	ACACB,AGPS,ALDH6A1,CAT,ENO1,GBP1,GPD1L,MAP3K3,PDE2A,RNASEH2A,TK1
GO:0042803	protein homodimerization activity	5	830	0.0052	CAT,ENO1,GBP1,GPD1L,PDE2A
GO:0097159	organic cyclic compound binding	11	5382	0.0052	ACACB,AGPS,ALDH6A1,CAT,ENO1,GBP1,GPD1L,MAP3K3,PDE2A,RNASEH2A,TK1
GO:0004601	peroxidase activity	2	40	0.0069	CAT,GPX3
GO:0032555	purine ribonucleotide binding	6	1853	0.0218	ACACB,ALDH6A1,GBP1,MAP3K3,PDE2A,TK1
GO:0043168	anion binding	7	2696	0.0219	ACACB,AGPS,ALDH6A1,GBP1,MAP3K3,PDE2A,TK1

GO:0032559	adenyl ribonucleotide binding	5	1514	0.0369	ACACB,ALDH6A1,MAP3K3,PDE2A,TK1
GO:0016614	oxidoreductase activity, acting on CH-OH group of donors	2	135	0.0373	AGPS,GPD1L
GO:0043167	ion binding	10	6066	0.0373	ACACB,AGPS,ALDH6A1,CAT,ENO1,GBP1,MAP3K3,PDE2A,RNASEH2A,TK1
GO:0005488	binding	14	11878	0.0431	ACACB,AGPS,ALDH6A1,CAT,ENO1,GBP1,GPD1L,GPX3,MAP3K3,NCF2,PDE2A,RNASEH2A,TD RD3,TK1

Table S4 Kyoto encyclopedia of genes and genomes analysis results.

#term ID	term description	observed gene count	background gene count	false discovery rate	matching proteins in network
hsa01200	Carbon metabolism	3	116	0.0044	ALDH6A1,CAT,ENO1
hsa00640	Propanoate metabolism	2	32	0.0071	ACACB,ALDH6A1
hsa01100	Metabolic pathways	5	1250	0.0282	ACACB,AGPS,ALDH6A1,ENO1,TK1
hsa04146	Peroxisome	2	81	0.0282	AGPS,CAT

Figure S1 Pearson correlation coefficients for hub gene expression levels.

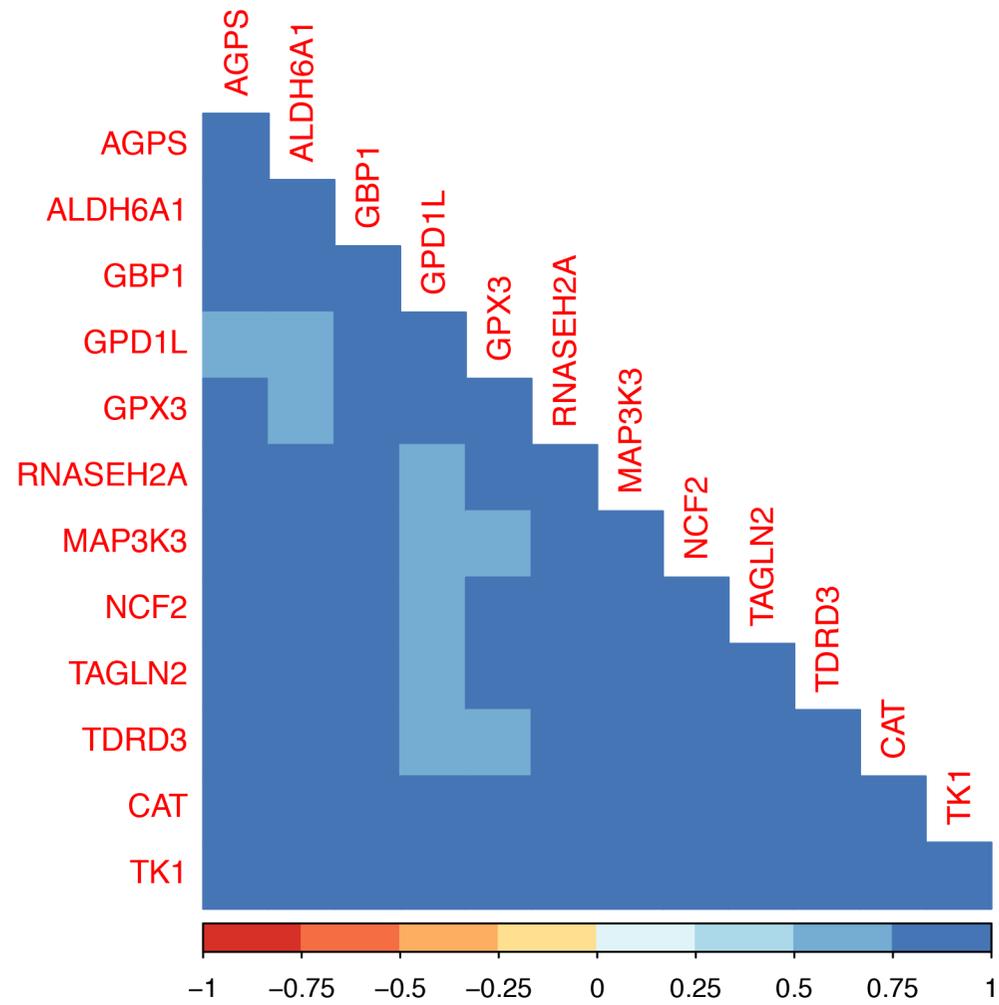


Figure S2 Survival plots for hub genes.

