

## SUPPLEMENTARY TABLES

Supplementary Table 1. There were 60 FRGs identified from previous literature.

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ACSL4  
AKR1C1  
AKR1C2  
AKR1C3  
ALOX15  
ALOX5  
ALOX12  
ATP5MC3  
CARS  
CBS  
CD44  
CHAC1  
CISD1  
CS  
DPP4  
FANCD2  
GCLC  
GCLM  
GLS2  
GPX4  
GSS  
HMGCR  
HSPB1  
CRYAB  
LPCAT3  
MT1G  
NCOA4  
PTGS2  
RPL8  
SAT1  
SLC7A11  
FDFT1  
TFRC  
TP53  
EMC2  
AIFM2  
PHKG2  
HSBP1  
ACO1  
FTH1  
STEAP3  
NFS1  
ACSL3  
ACACA  
PEBP1

ZEB1  
 SQLE  
 FADS2  
 NFE2L2  
 KEAP1  
 NQO1  
 NOX1  
 ABCC1  
 SLC1A5  
 GOT1  
 G6PD  
 PGD  
 IREB2  
 HMOX1  
 ACSF2

**Supplementary Table 2. A total of 46 differentially expressed FRGs identified between the 510 LUAD tissues and 58 normal adjacent tissues with adj *P* value < 0.05.**

Gene	Con Mean	Treat Mean	Log FC	<i>P</i> Value	Fdr
LPCAT3	3.159412	2.3466	-0.81281	5.02E-27	4.77E-26
GPX4	6.544112	6.888866	0.344754	1.23E-06	2.06E-06
G6PD	4.257216	5.075513	0.818296	2.09E-06	3.40E-06
CBS	0.092336	0.223733	0.131396	0.00029	0.000394
PEBP1	7.485216	6.98014	-0.50508	1.77E-14	4.38E-14
ACSL3	3.739216	3.959468	0.220251	0.006011	0.007614
DPP4	3.488111	4.058837	0.570726	0.001083	0.001435
CD44	6.034208	4.905438	-1.12877	1.81E-22	9.36E-22
GSS	4.147503	4.954165	0.806662	9.01E-28	1.28E-26
ALOX15	2.358251	0.957525	-1.40073	3.43E-12	6.74E-12
GLS2	0.207865	0.322023	0.114158	0.005949	0.007614
RPL8	8.804998	9.509746	0.704748	5.57E-14	1.22E-13
PGD	5.81347	6.212381	0.398911	0.010224	0.012669
TFRC	5.22247	4.080503	-1.14197	4.60E-18	1.87E-17
CHAC1	1.018744	1.721919	0.703175	6.37E-16	1.82E-15
FDFT1	4.921858	4.564213	-0.35765	4.53E-06	6.80E-06
FANCD2	0.702023	1.504381	0.802358	1.53E-29	8.74E-28
EMC2	3.38608	3.656837	0.270758	2.52E-06	4.00E-06
ZEB1	2.862145	1.767656	-1.09449	3.60E-25	2.94E-24
ACSL4	4.86119	3.849839	-1.01135	9.01E-20	3.95E-19
ALOX5	5.421907	3.605919	-1.81599	2.39E-28	6.67E-27
SLC7A11	0.538602	1.839077	1.300475	6.91E-18	2.62E-17
AIFM2	2.175042	2.791287	0.616244	5.04E-16	1.51E-15
KEAP1	4.090052	4.257769	0.167717	4.89E-05	6.96E-05

HMGCR	3.841814	3.205199	-0.63662	1.57E-17	5.59E-17
CRYAB	3.704674	1.928149	-1.77652	3.51E-28	6.67E-27
NCOA4	6.144397	5.644094	-0.5003	2.02E-14	4.79E-14
HMOX1	5.277925	4.590963	-0.68696	2.69E-06	4.14E-06
STEAP3	3.333276	4.064916	0.73164	4.13E-13	8.42E-13
NQO1	3.429814	5.714839	2.285025	2.38E-23	1.36E-22
GCLC	1.880546	3.063667	1.183121	7.79E-12	1.48E-11
NFS1	1.777912	2.386447	0.608535	1.21E-27	1.38E-26
FTH1	8.465463	8.137851	-0.32761	8.08E-06	1.18E-05
PTGS2	4.179196	3.367837	-0.81136	5.98E-05	8.31E-05
TP53	3.562903	4.018418	0.455515	6.00E-10	1.07E-09
NOX1	0.374526	0.776181	0.401655	2.56E-17	8.57E-17
SLC1A5	4.795671	5.466592	0.670922	2.12E-16	6.70E-16
GOT1	3.664455	4.52046	0.856006	2.28E-23	1.36E-22
CS	4.339807	4.722226	0.382419	3.50E-11	6.44E-11
HSPB1	7.181479	7.930812	0.749333	5.05E-14	1.15E-13
PHKG2	1.850388	2.547034	0.696646	3.47E-24	2.47E-23
CISD1	2.683009	3.149152	0.466143	6.42E-14	1.35E-13
NFE2L2	4.857844	4.427938	-0.42991	1.21E-14	3.27E-14
ATP5MC3	3.952662	4.4678	0.515138	1.36E-14	3.52E-14
CARS	2.234765	2.709365	0.4746	3.62E-22	1.72E-21
GCLM	2.483958	3.155553	0.671595	2.59E-09	4.47E-09

**Supplementary Table 3. The GSEA results in two clusters (cluster1/2) in TCGA dataset.**

Id	Log FC	Ave Expr	T	P Value	adj.P.Val	B
HALLMARK_REACTIVE_OXYGEN_SPECIES_PATHWAY	-0.12439	-0.04013	-12.5544	1.17E-31	5.85E-30	60.98507
HALLMARK_ADIPOGENESIS	-0.09228	-0.06732	-11.1868	4.15E-26	2.03E-24	48.31816
HALLMARK_FATTY_ACID_METABOLISM	-0.0992	-0.05793	-10.4683	2.41E-23	1.16E-21	42.0136
HALLMARK_XENOBIOTIC_METABOLISM	-0.07355	-0.0452	-8.61505	8.97E-17	4.22E-15	27.06837
HALLMARK_CHOLESTEROL_HOMEOSTASIS	-0.08923	-0.0809	-8.59963	1.01E-16	4.64E-15	26.95273
HALLMARK_HEME_METABOLISM	-0.06282	-0.07123	-8.35957	6.14E-16	2.76E-14	25.17307
HALLMARK_PEROXISOME	-0.06174	-0.04912	-8.14164	3.06E-15	1.35E-13	23.59048
HALLMARK_PI3K_AKT_MTOR_SIGNALING	-0.06342	-0.06412	-7.57823	1.68E-13	7.25E-12	19.64987
HALLMARK_UV_RESPONSE_UP	-0.05034	-0.04669	-7.55563	1.97E-13	8.27E-12	19.49645
HALLMARK_ESTROGEN_RESPONSE_LATE	-0.05688	-0.05315	-7.42486	4.83E-13	1.98E-11	18.61592
HALLMARK_BILE_ACID_METABOLISM	-0.07118	-0.06607	-7.4066	5.47E-13	2.19E-11	18.49392
HALLMARK_ANDROGEN_RESPONSE	-0.07252	-0.08439	-6.71009	5.23E-11	2.04E-09	14.02504
HALLMARK_OXIDATIVE_PHOSPHORYLATION	-0.0925	-0.02326	-6.29895	6.52E-10	2.48E-08	11.56034
HALLMARK_ESTROGEN_RESPONSE_EARLY	-0.05285	-0.05997	-5.70771	1.95E-08	7.23E-07	8.251375
HALLMARK_MTORC1_SIGNALING	-0.06535	-0.01653	-5.27857	1.94E-07	6.97E-06	6.029441
HALLMARK_P53_PATHWAY	-0.041	-0.05822	-4.66923	3.88E-06	0.000136	3.143607

HALLMARK_SPERMATOGENESIS	-0.0423	-0.01905	-4.6555	4.14E-06	0.000141	3.08229
HALLMARK_PROTEIN_SECRETION	-0.05754	-0.05715	-4.39619	1.34E-05	0.000443	1.95559
HALLMARK_DNA_REPAIR	-0.03859	-0.00917	-4.11694	4.48E-05	0.001435	0.809281
HALLMARK_UV_RESPONSE_DN	-0.0528	-0.09663	-4.04061	6.16E-05	0.00191	0.508204
HALLMARK_HYPOXIA	-0.03702	-0.05444	-3.3353	0.000915	0.027441	-2.02172
HALLMARK_TGF_BETA_SIGNALING	-0.04466	-0.08957	-3.20737	0.001424	0.041309	-2.43114
HALLMARK_KRAS_SIGNALING_DN	-0.02526	-0.03956	-3.16511	0.001644	0.046023	-2.56298
HALLMARK_WNT_BETA_CATENIN_SIGNALING	-0.03848	-0.04962	-3.14145	0.00178	0.04805	-2.63608

Please browse Full Text version to see the data of Supplementary Table 4.

**Supplementary Table 4. The results of the univariate Cox regression analysis.**