**SUPPLEMENTARY TABLES**

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

| Gene      |
|-----------|
| 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     |
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  | P 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  |
| CBS      | 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  |
| Id                                      | Log FC | Ave Expr | T     | P Value | adj.P.Val | B     |
|-----------------------------------------|--------|----------|-------|---------|-----------|-------|
| HALLMARK.REACTIVE.OXYGEN_SPECIES.PATHWAY | -0.1249| -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 | 0.00136 | 3.143607 |

Supplementary Table 3. The GSVA results in two clusters (cluster1/2) in TCGA dataset.
| Hallmark                  | Coefficient | Standard Error | t Value | p Value | Odds Ratio |
|--------------------------|-------------|----------------|---------|---------|------------|
| HALLMARK_SPERMATOGENESIS | -0.0423     | -0.01905       | -4.6555 | 4.14E-06 | 0.000141   | 3.08229   |
| HALLMARK_PROTEIN_SECRETION | -0.05754    | -0.05715       | -3.9619 | 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       | -4.0461 | 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 | -0.04666    | -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.**