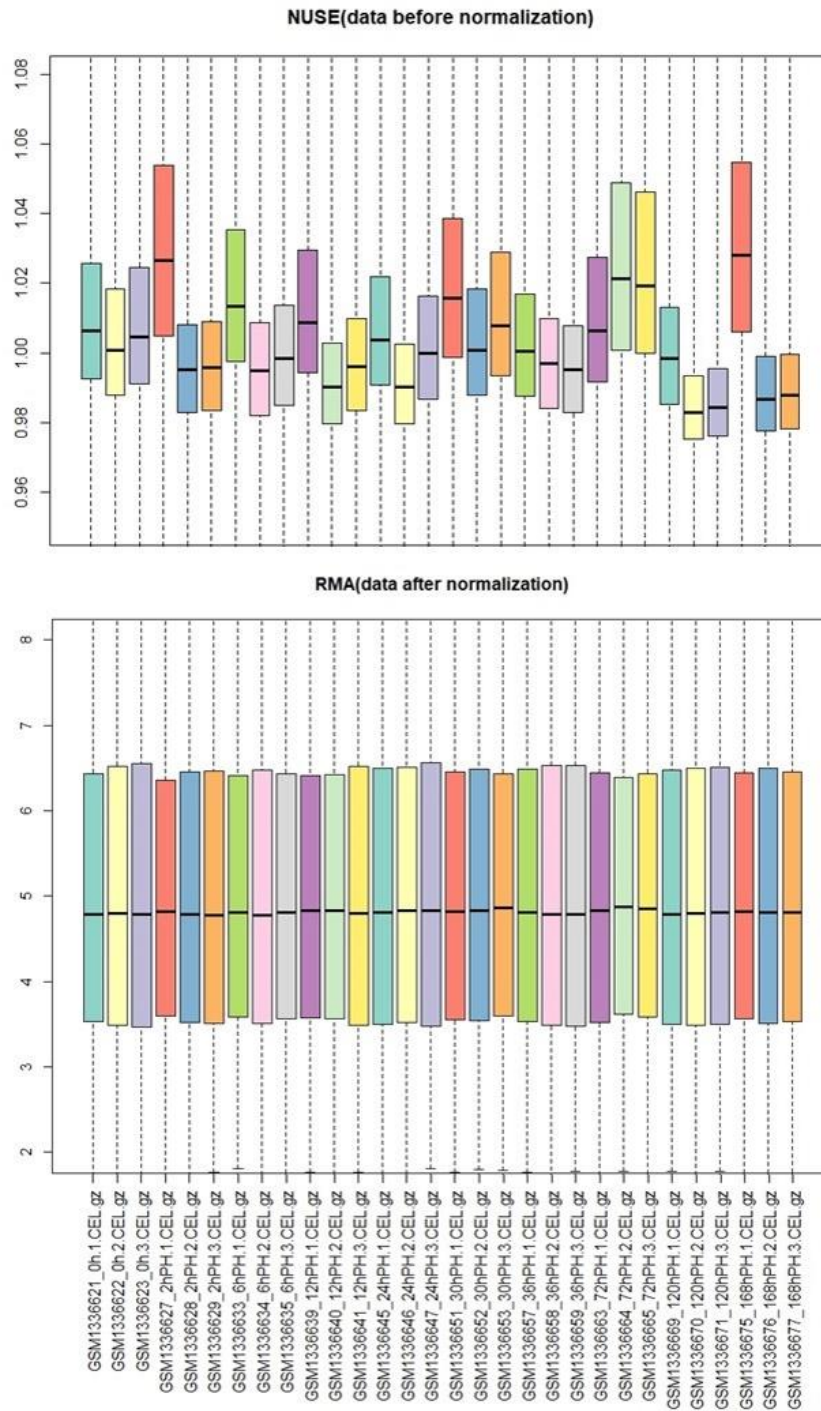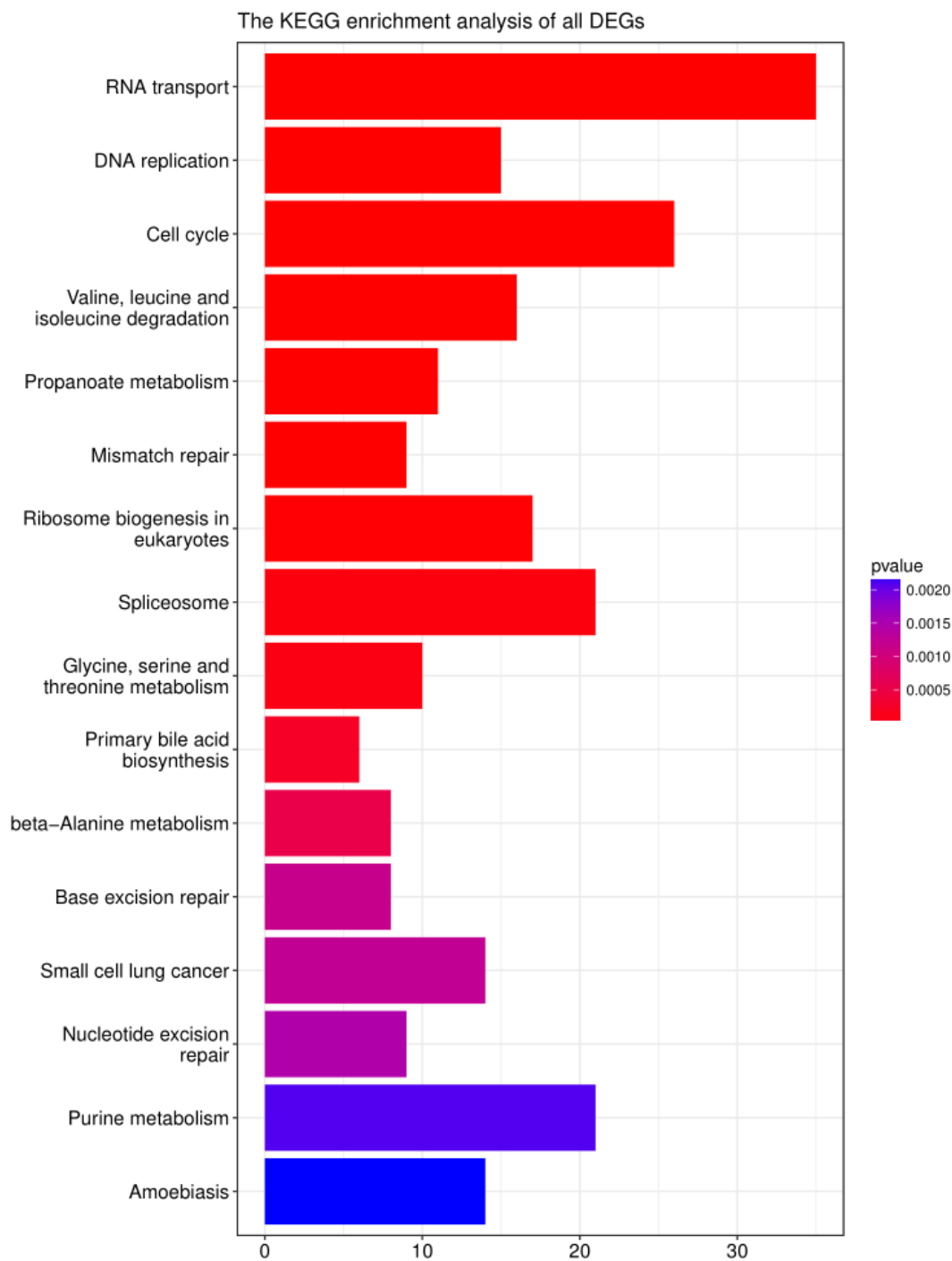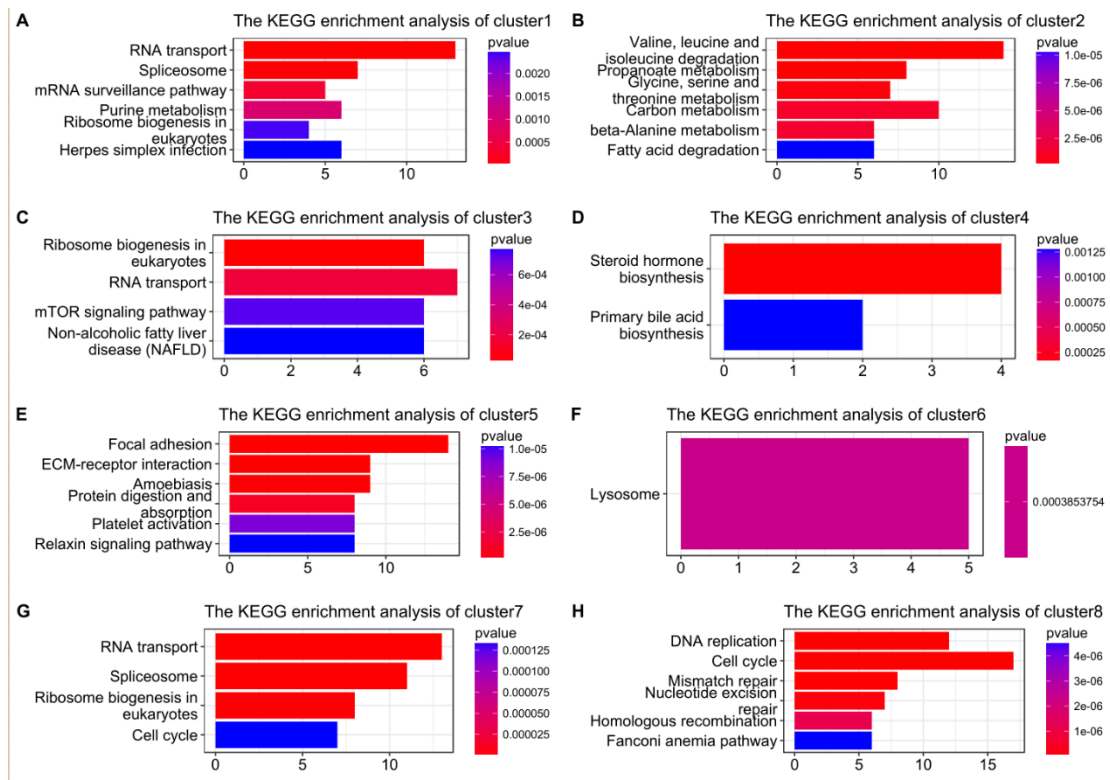**Supplementary Figure1** The QC plot for all the raw data in LR.
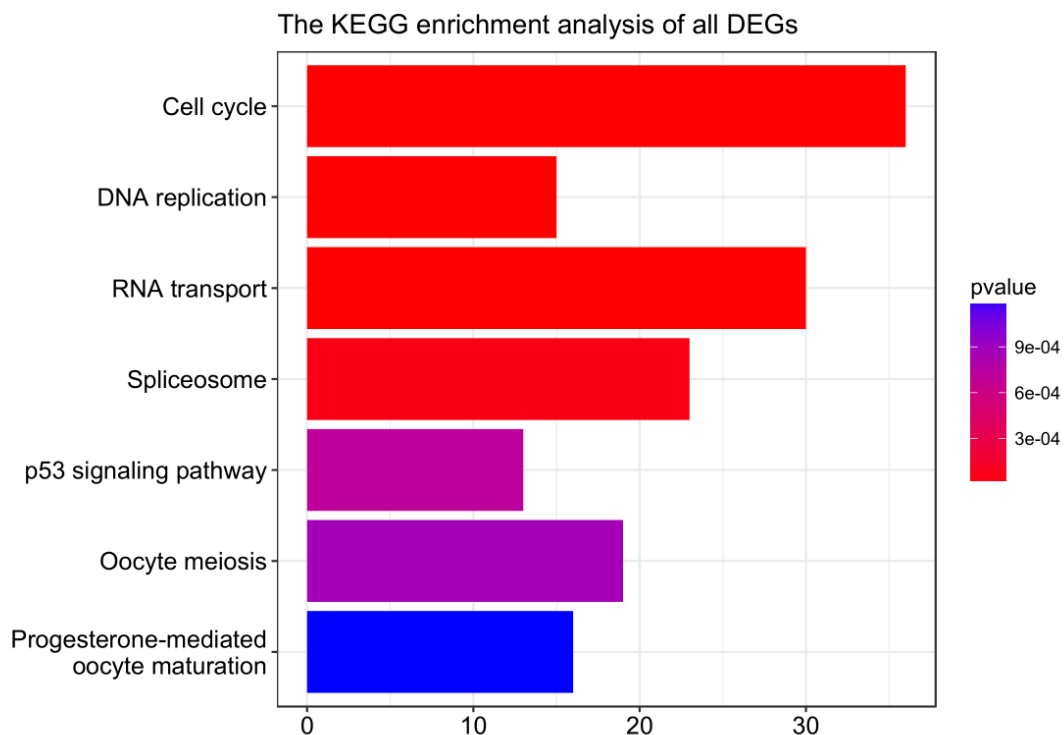
**Supplementary Figure2** The box plot for the data before and after normalization in LR.
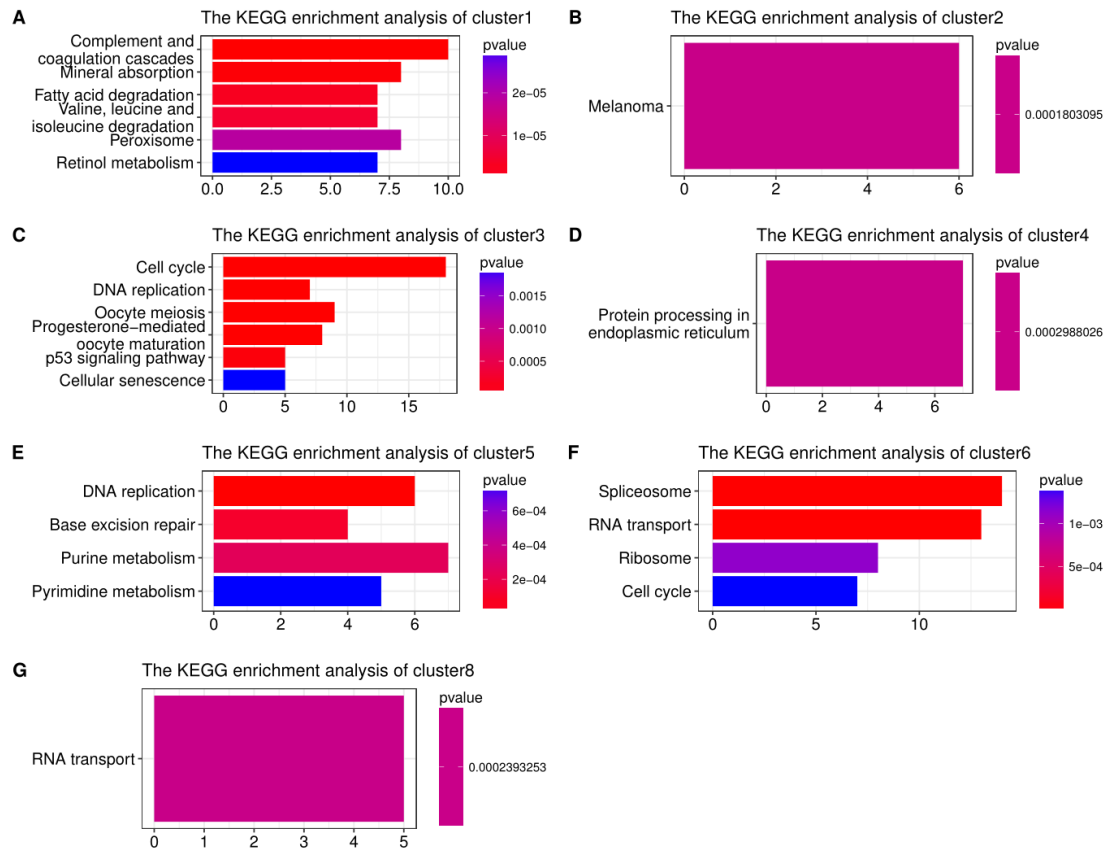
**Supplementary Figure3** The KEGG enrichment analysis of all DEGs identified by masigPro in LR.
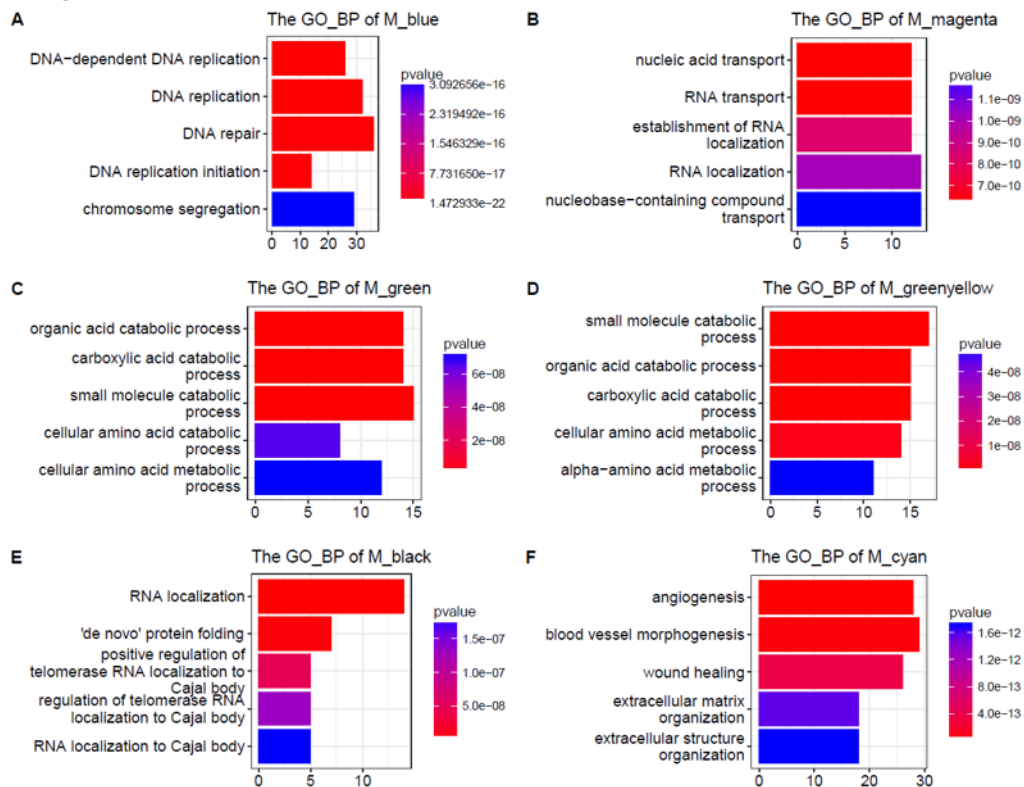
**Supplementary Figure4** The KEGG enrichment analysis of all DEGs in every cluster identified by masigPro in LR.
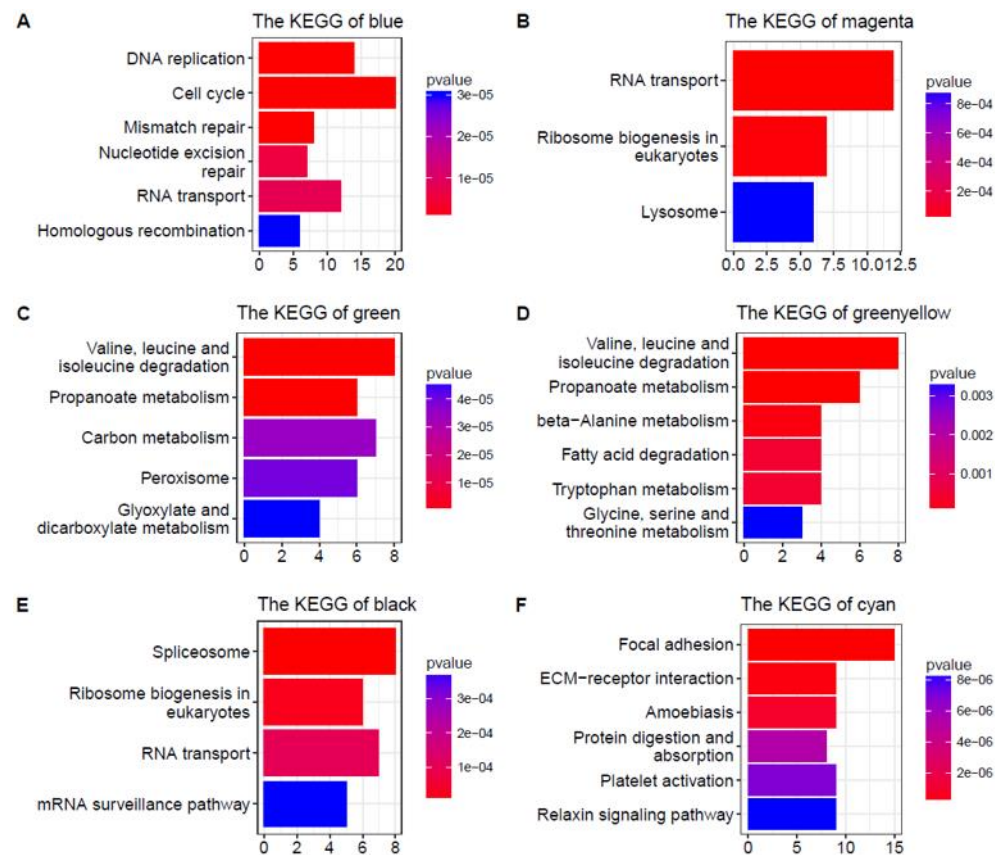


**Supplementary Figure5** The KEGG enrichment analysis of all DEGs identified by masigPro in HCC.

**Supplementary Figure6** The KEGG enrichment analysis of all DEGs in every cluster identified by masigPro in HCC.
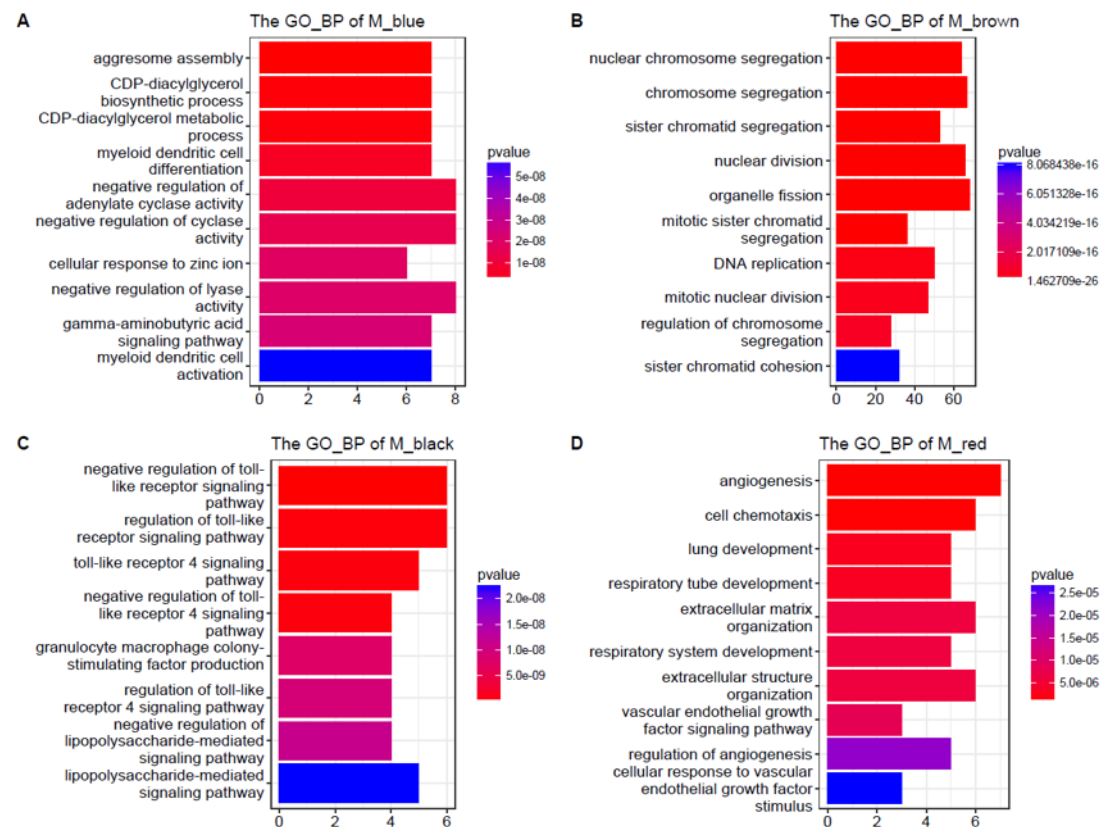


**Supplementary Figure7** The GO:BP enrichment analysis of all DEGs in every module identified by WGCNA in LR.
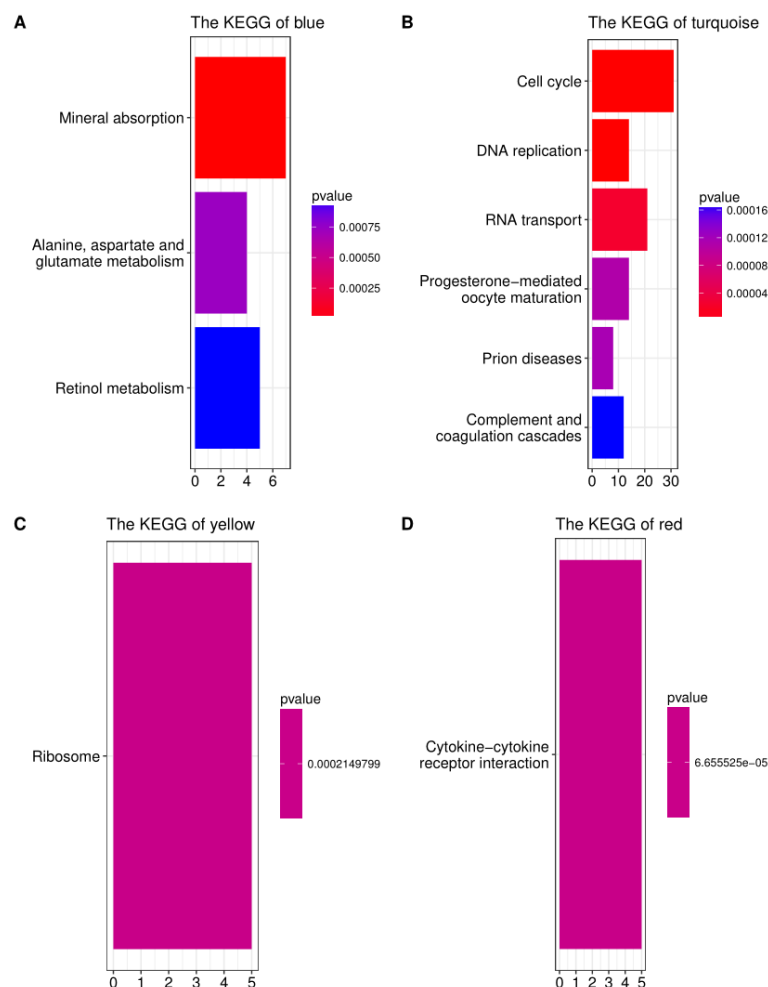
**Supplementary Figure8** The KEGG enrichment analysis of all DEGs in every module identified by WGCNA in LR.

| | c1(104) | c2(225) | c3(154) | c4(102) | c5(211) | c6(130) | c7(171) | c8(217) | c9(48) |
|---|---|---|---|---|---|---|---|---|---|
| w.black(166) | 35 (14.9%) | 0 (0.0%) | 0 (0.0%) | 41 (18.1%) | 0 (0.0%) | 11 (3.9%) | 79 (30.6%) | 0 (0.0%) | 0 (0.0%) |
| w.blue(384) | 0 (0.0%) | 78 (14.7%) | 8 (1.5%) | 10 (2.1%) | 0 (0.0%) | 3 (0.6%) | 75 (15.6%) | 191 (46.6%) | 19 (4.6%) |
| w.green(156) | 0 (0.0%) | 70 (22.5%) | 54 (21.1%) | 0 (0.0%) | 6 (1.7%) | 0 (0.0%) | 0 (0.0%) | 8 (2.2%) | 18 (9.7%) |
| w.grey(7) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 0 (0.0%) | 6 (4.6%) | 1 (0.6%) | 0 (0.0%) | 0 (0.0%) |
| w.cyan(293) | 0 (0.0%) | 0 (0.0%) | 23 (5.4%) | 0 (0.0%) | 204 (68.0%) | 60 (16.5%) | 0 (0.0%) | 0 (0.0%) | 6 (1.8%) |
| w.greenyellow(163) | 0 (0.0%) | 77 (24.8%) | 0 (0.0%) | 51 (23.8%) | 0 (0.0%) | 0 (0.0%) | 15 (4.7%) | 18 (5.0%) | 2 (1.0%) |
| w.magenta(193) | 69 (30.3%) | 0 (0.0%) | 69 (24.8%) | 0 (0.0%) | 1 (0.2%) | 50 (18.3%) | 1 (0.3%) | 0 (0.0%) | 3 (1.3%) |

**Supplementary Figure9** The overlapping analysis for the genes in 9 clusters from maSigPro and 7 modules from WGCNA.
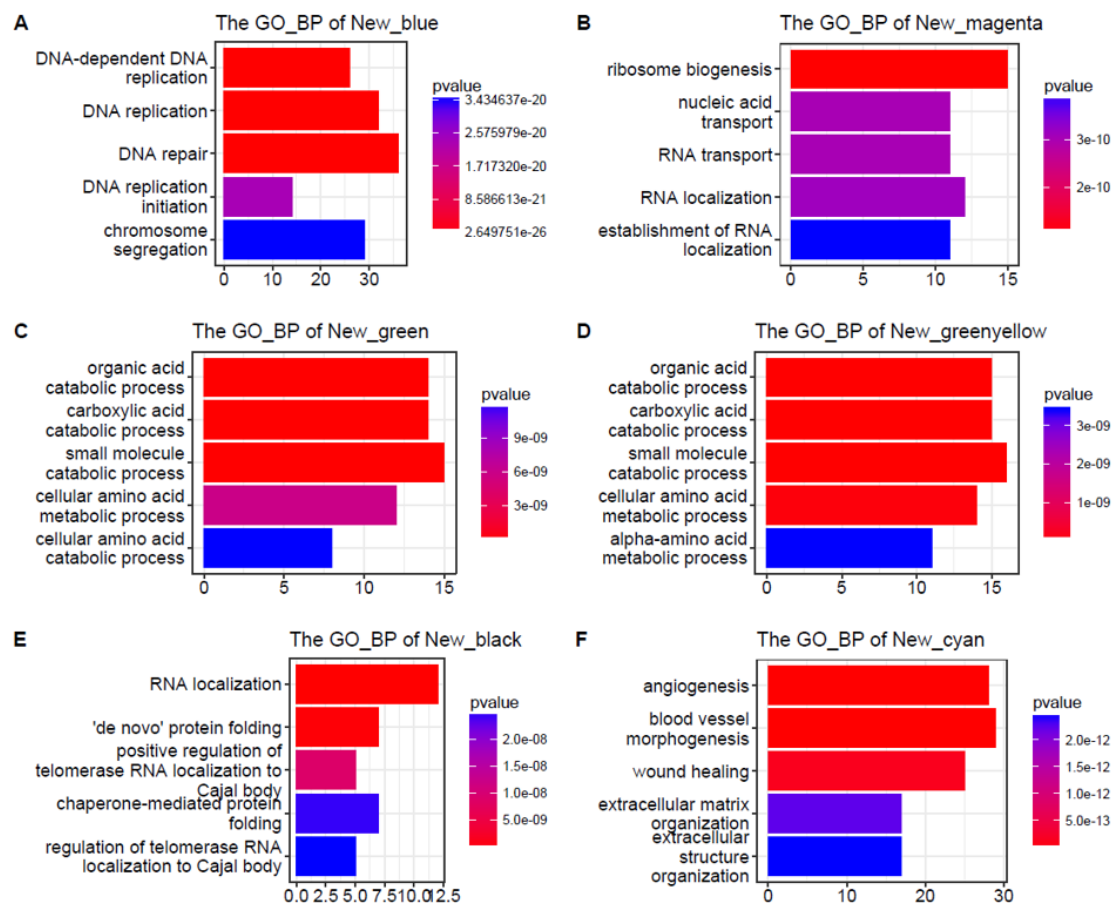


**Supplementary Figure10** The GO:BP enrichment analysis of all DEGs in every module identified by WGCNA in HCC.
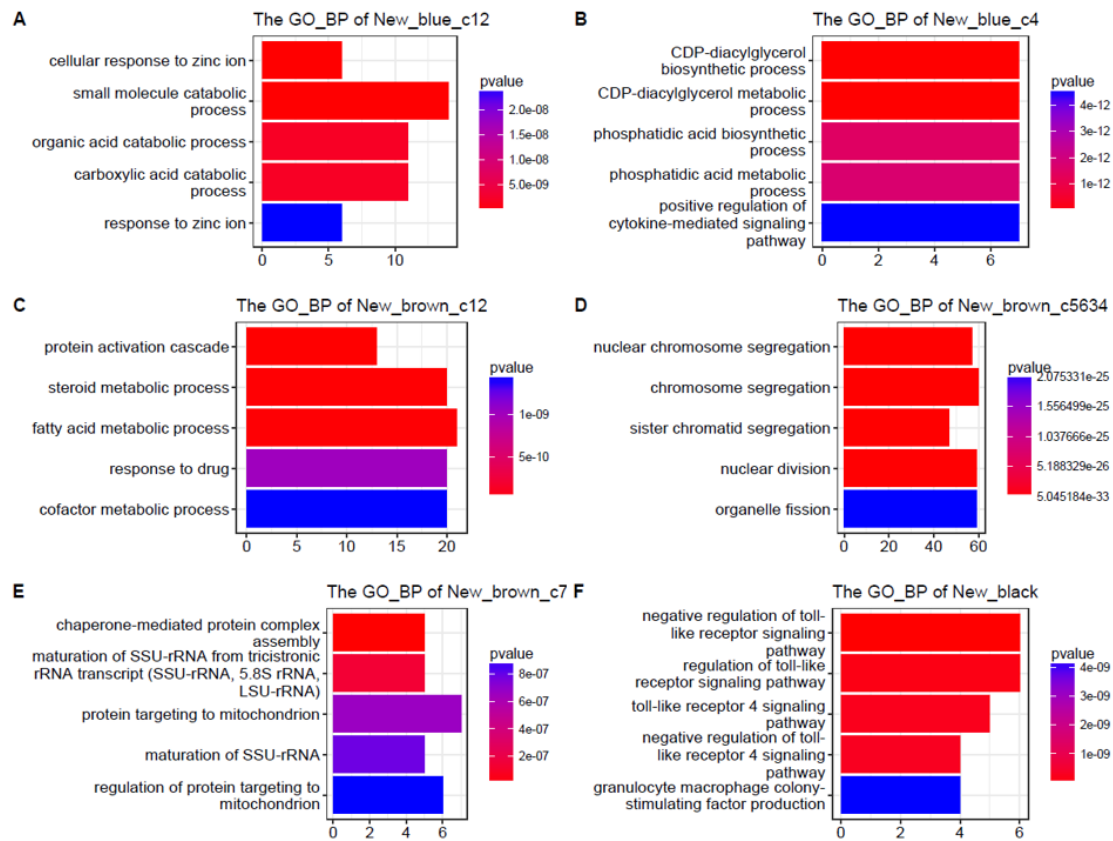
**Supplementary Figure11** The KEGG enrichment analysis of all DEGs in every module identified by WGCNA in HCC.



**Supplementary Figure12** The overlapping analysis for the genes in 9 clusters from maSigPro and 4 modules from WGCNA.

Supplementary Figure13 The GO:BP enrichment analysis for new modules in LR

**Supplementary Figure14 The GO:BP enrichment analysis for new modules in HCC**