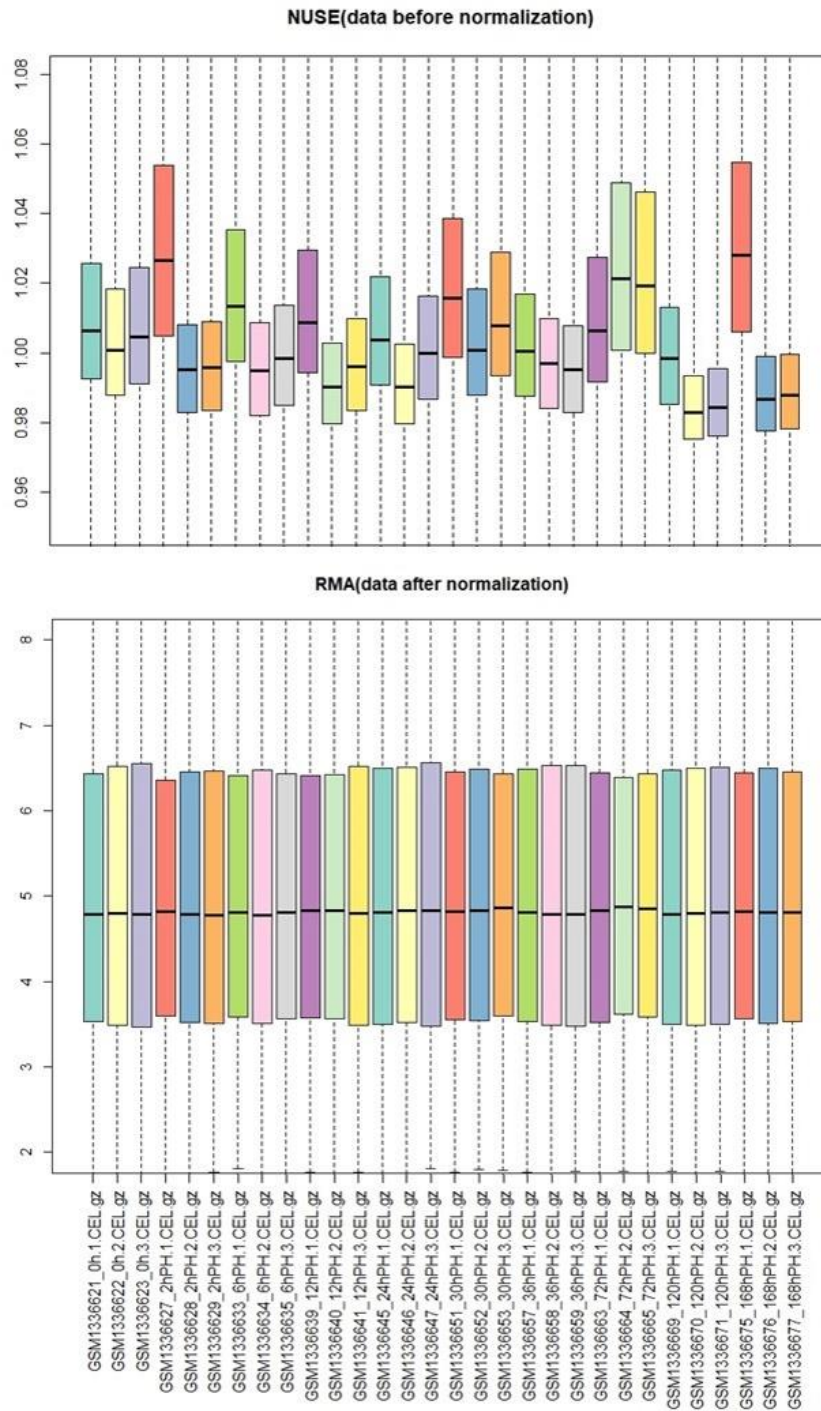
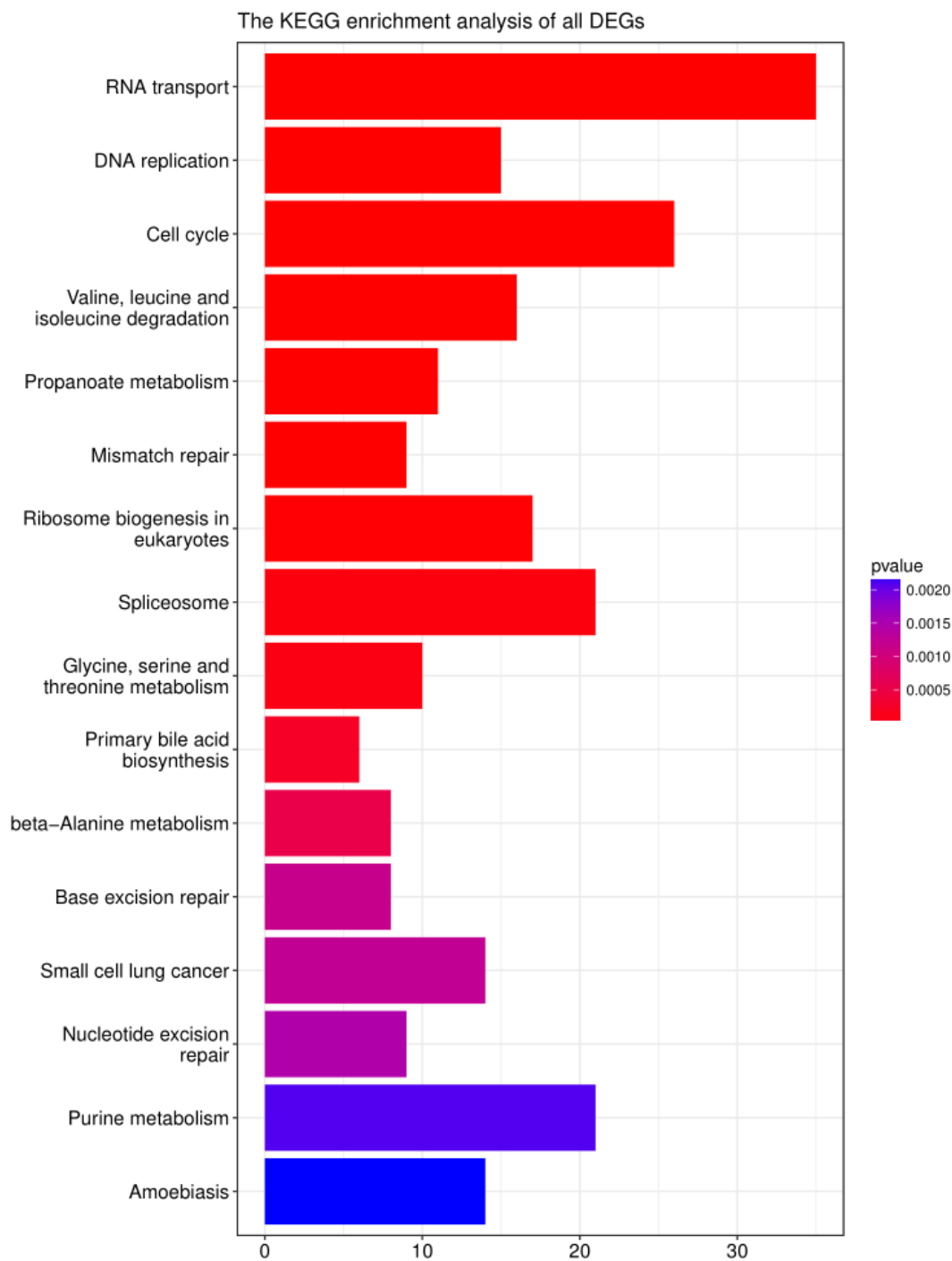


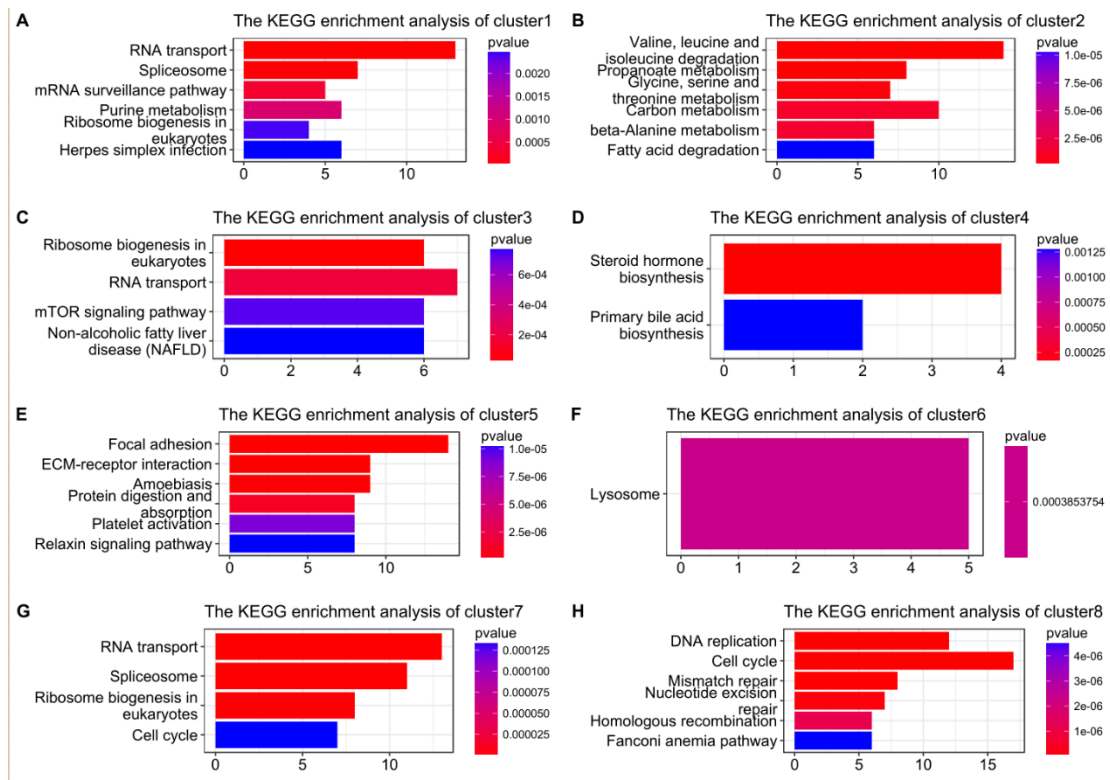
Supplementary Figure1 The QC plot for all the raw data in LR.



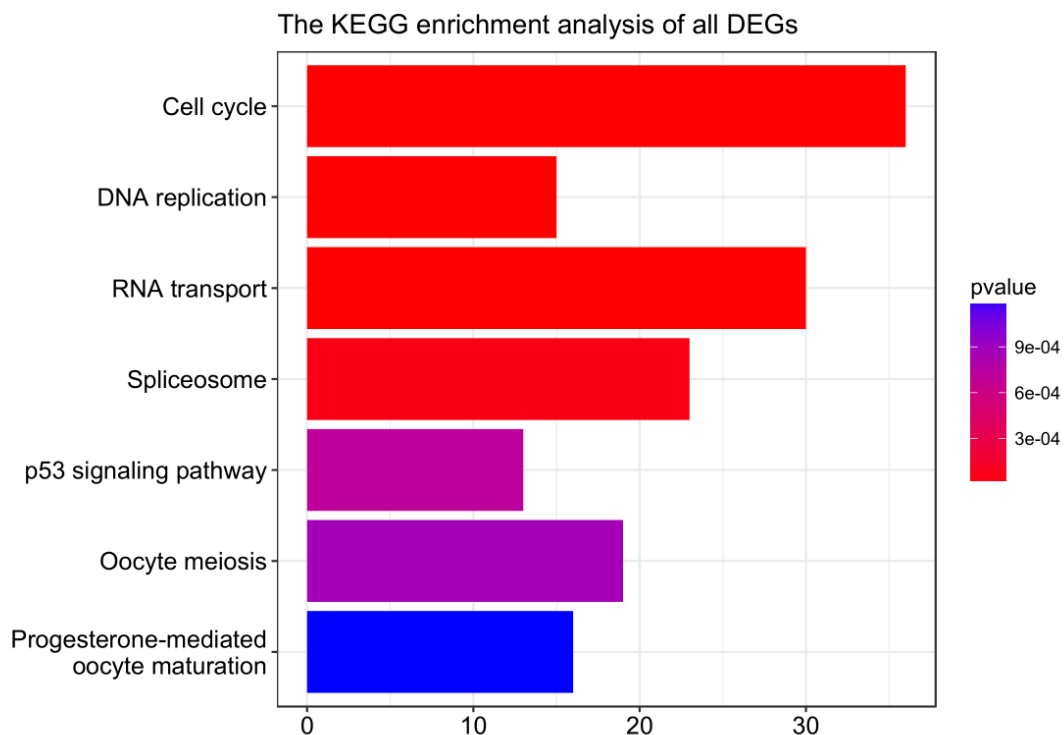
Supplementary Figure2 The box plot for the data before and after normalization in LR.



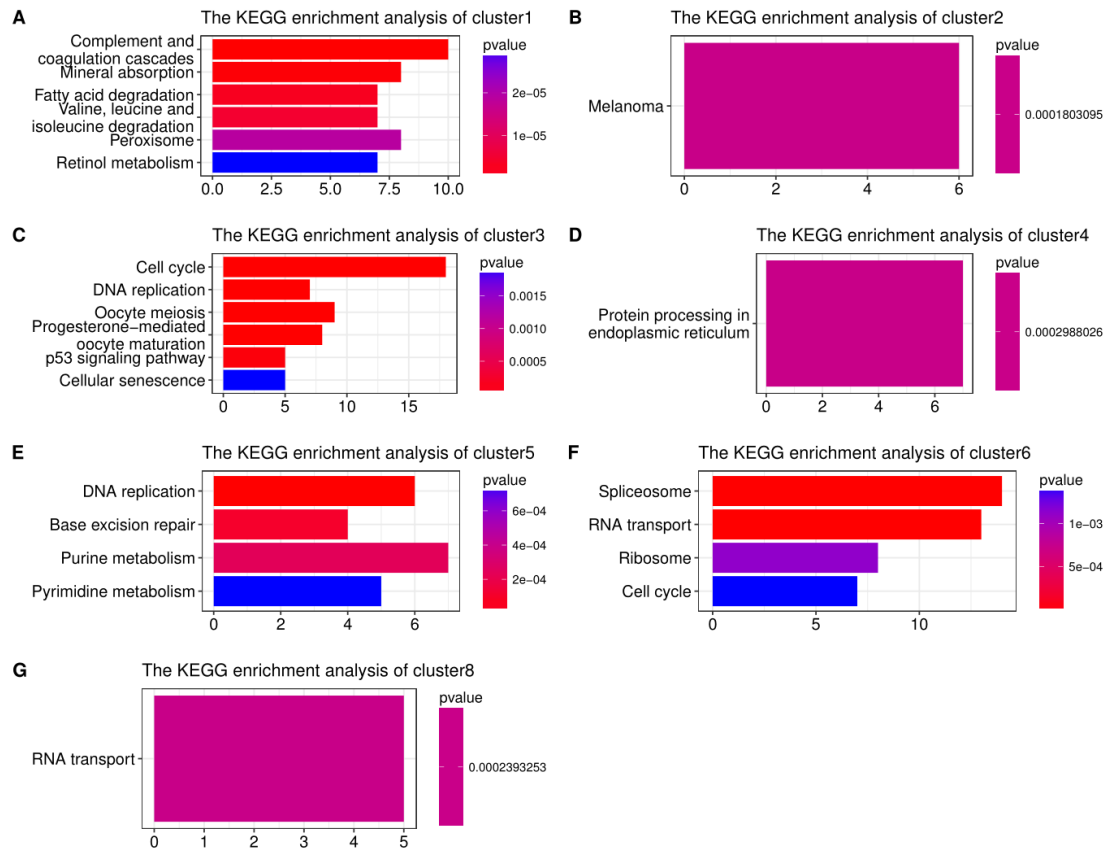
Supplementary Figure3 The KEGG enrichment analysis of all DEGs identified by masigPro in LR.



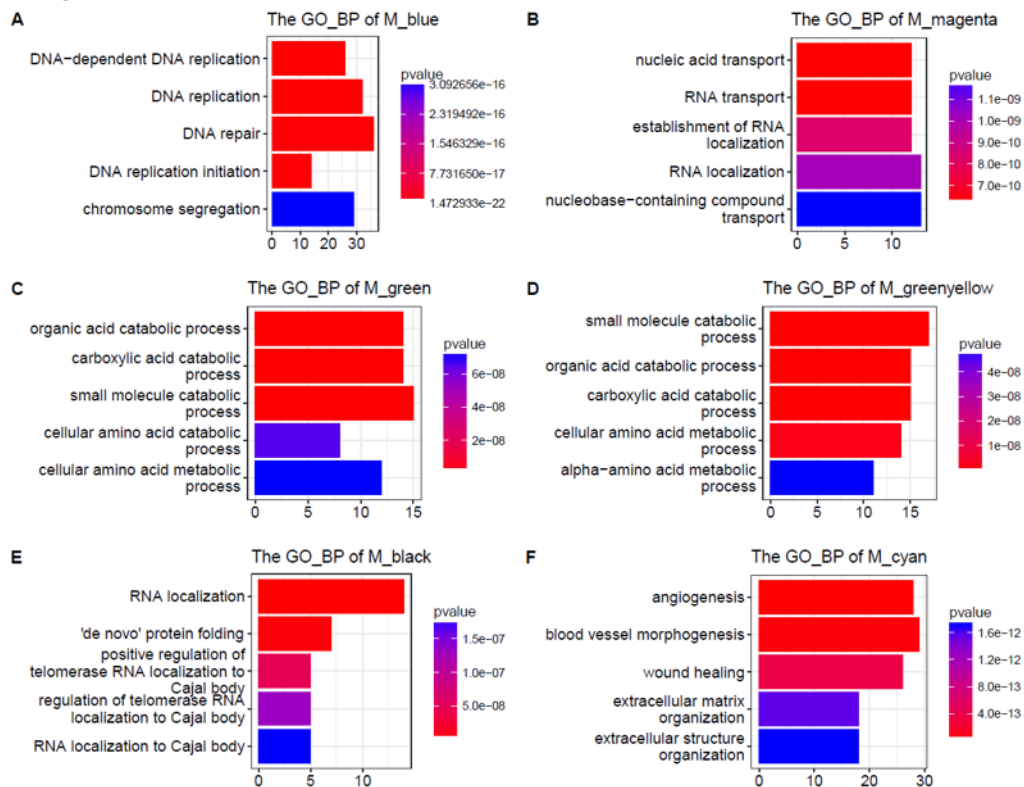
Supplementary Figure4 The KEGG enrichment analysis of all DEGs in every cluster identified by masigPro in LR.



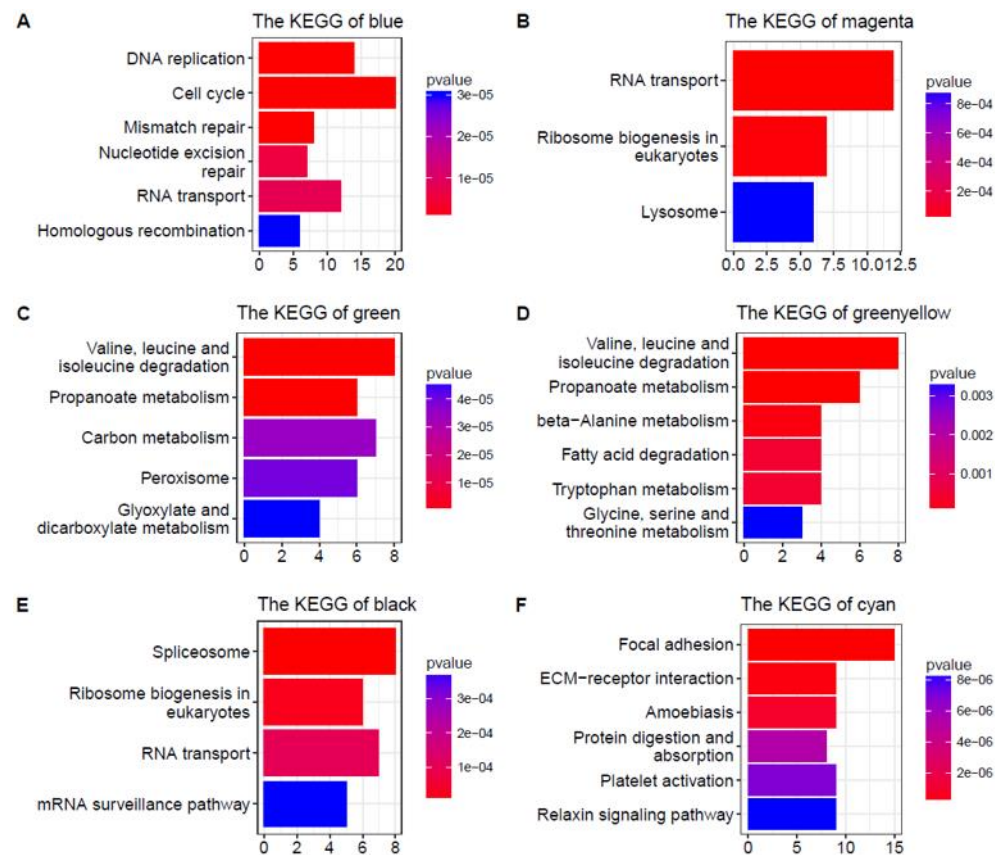
Supplementary Figure5 The KEGG enrichment analysis of all DEGs identified by masigPro in HCC.



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



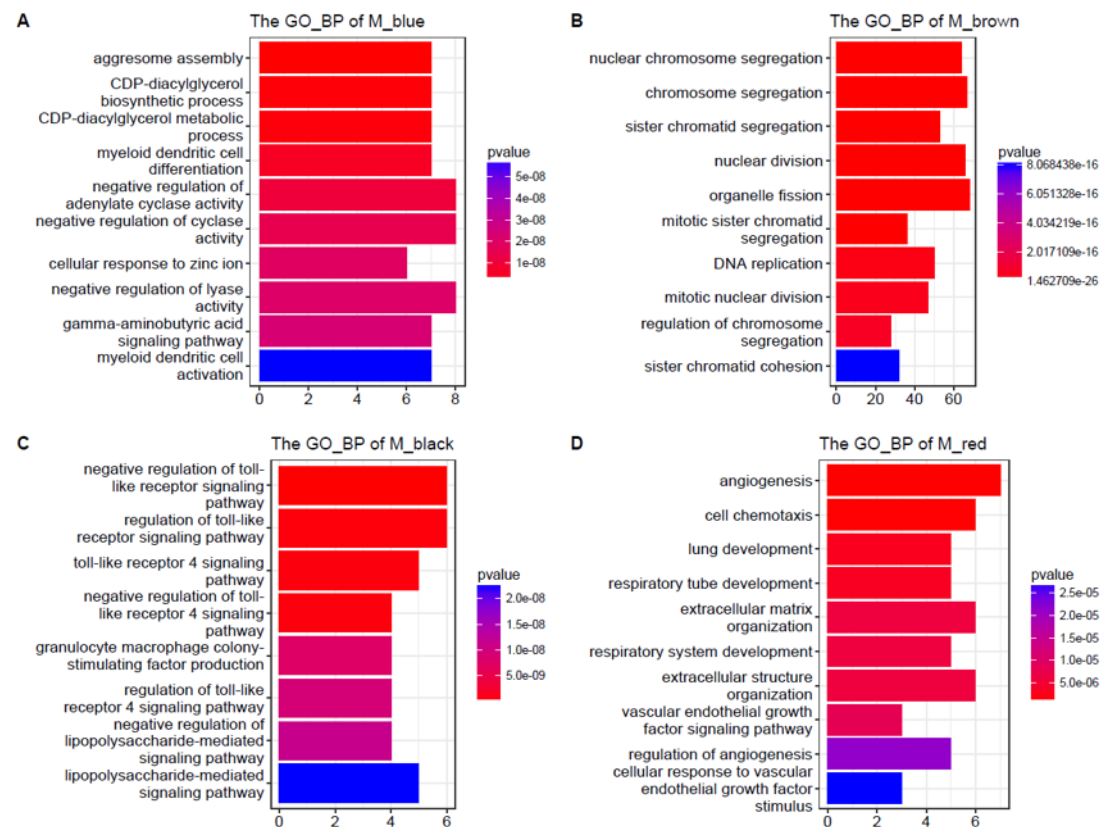
Supplementary Figure7 The GO:BP enrichment analysis of all DEGs in every module identified by WGCNA in LR.



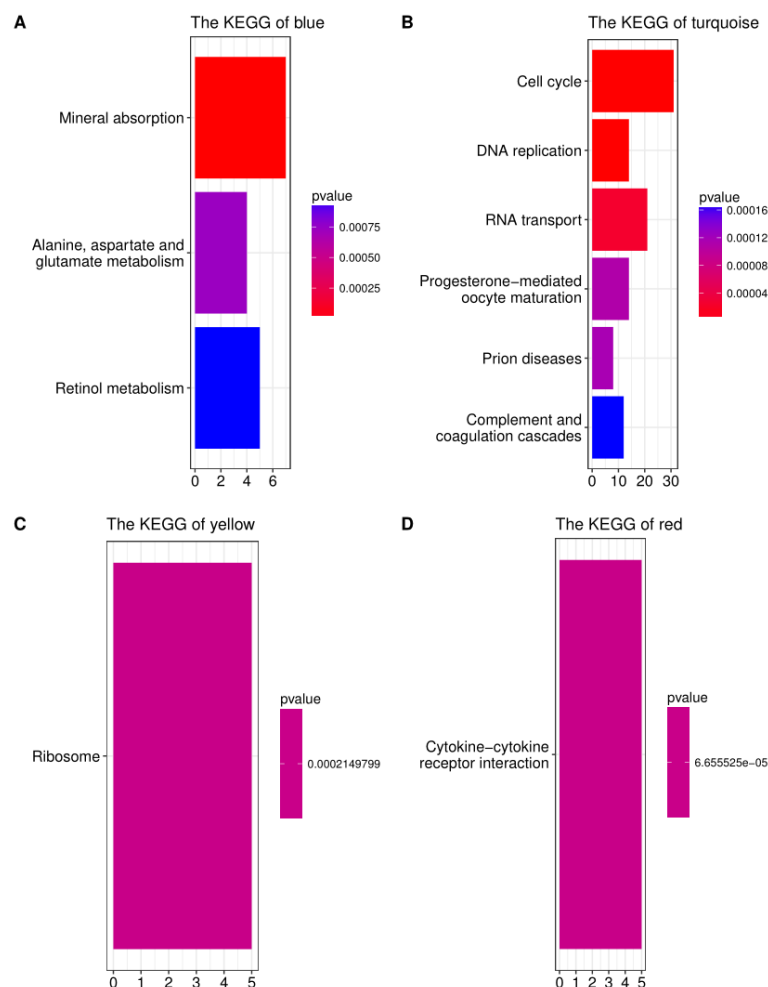
Supplementary Figure8 The KEGG enrichment analysis of all DEGs in every module identified by WGCNA in LR.

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%)
	c1(104)	c2(225)	c3(154)	c4(102)	c5(211)	c6(130)	c7(171)	c8(217)	c9(48)

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



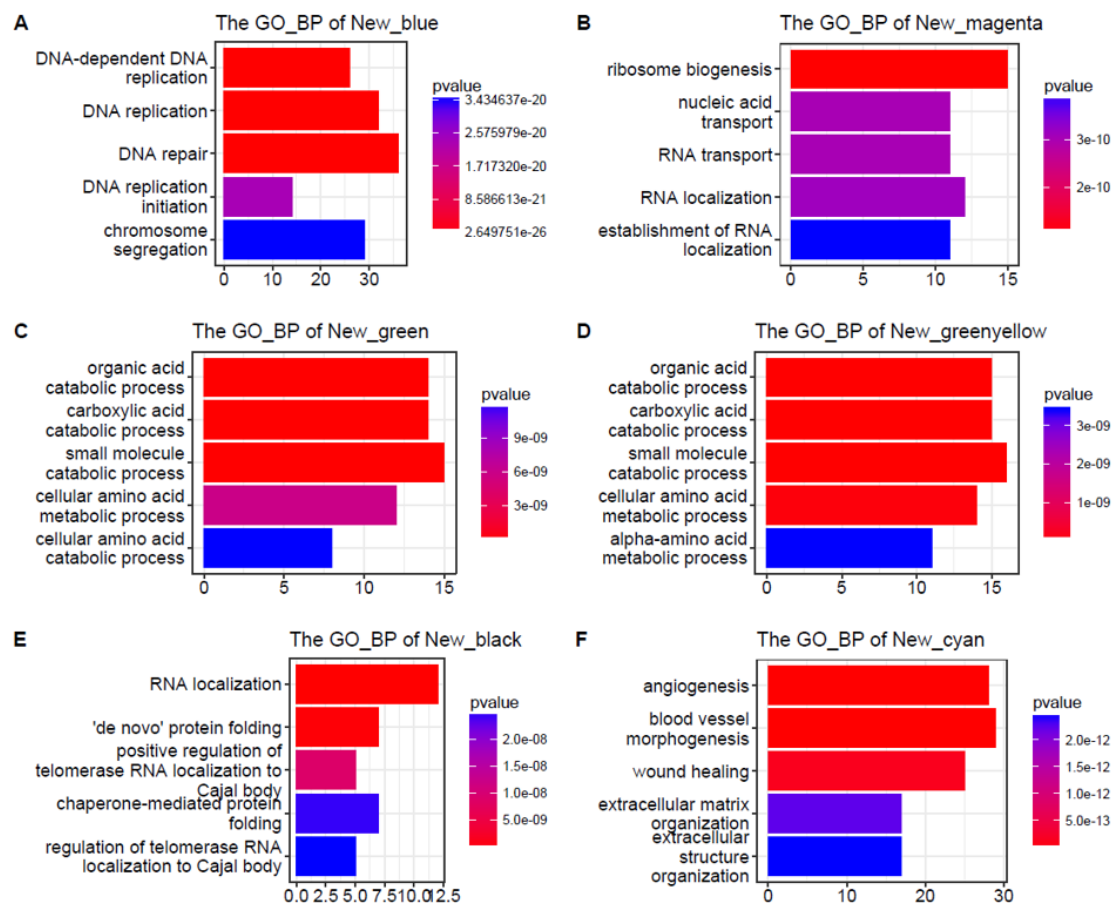
Supplementary Figure10 The GO:BP enrichment analysis of all DEGs in every module identified by WGCNA in HCC.



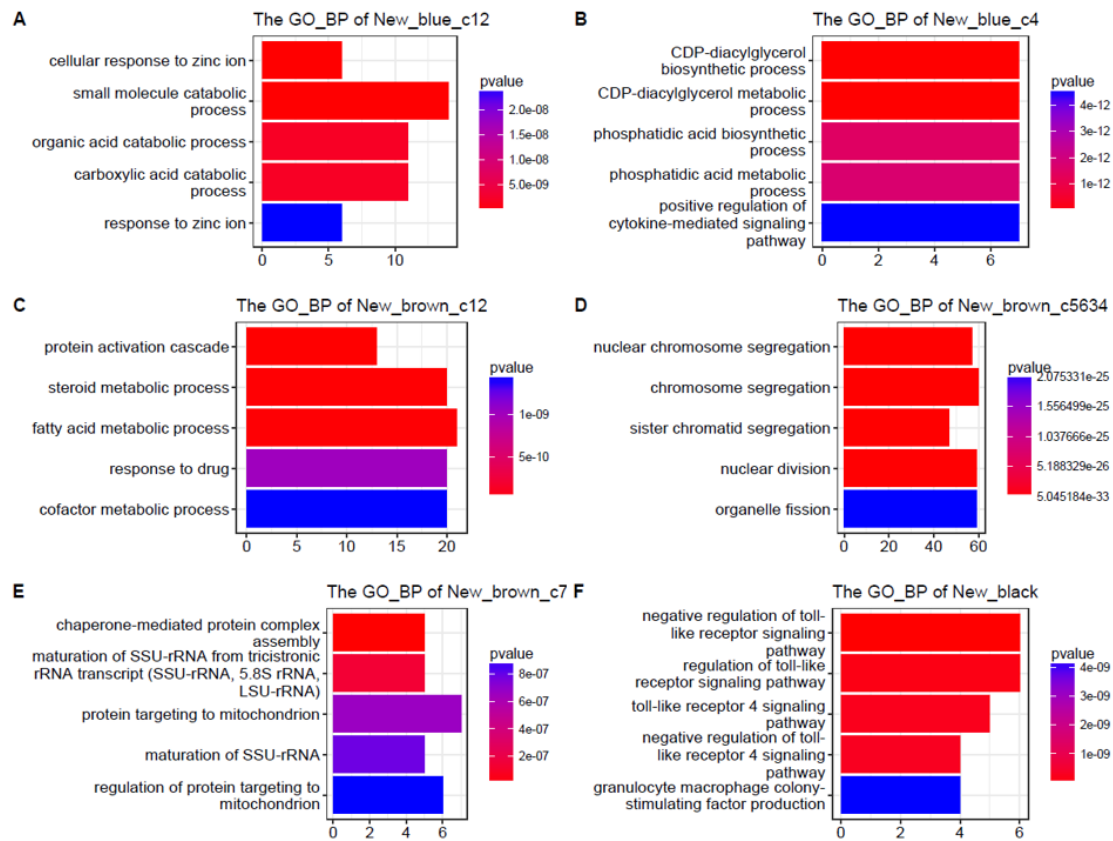
Supplementary Figure11 The KEGG enrichment analysis of all DEGs in every module identified by WGCNA in HCC.

	c1(268)	c2(247)	c3(129)	c4(193)	c5(156)	c6(273)	c7(89)	c8(92)	c9(110)
w.black(31)	0 (0.0%)	20 (7.8%)	0 (0.0%)	7 (3.2%)	1 (0.5%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	3 (2.2%)
w.blue(256)	123 (30.7%)	57 (12.8%)	0 (0.0%)	52 (13.1%)	3 (0.7%)	2 (0.4%)	11 (3.3%)	0 (0.0%)	8 (2.2%)
w.brown(1222)	144 (10.7%)	124 (9.2%)	129 (10.6%)	133 (10.4%)	152 (12.4%)	271 (22.1%)	78 (6.3%)	92 (7.5%)	99 (8.0%)
w.red(45)	0 (0.0%)	45 (18.2%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)	0 (0.0%)

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