# Supplemental informations

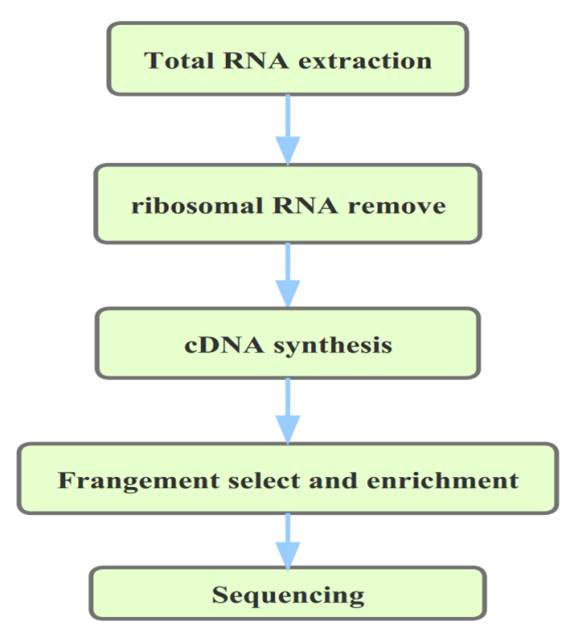
Supplemental table 1. The expression of selected circRNA (RPM) in three groups

and independent sample t-test between ACLF and HC

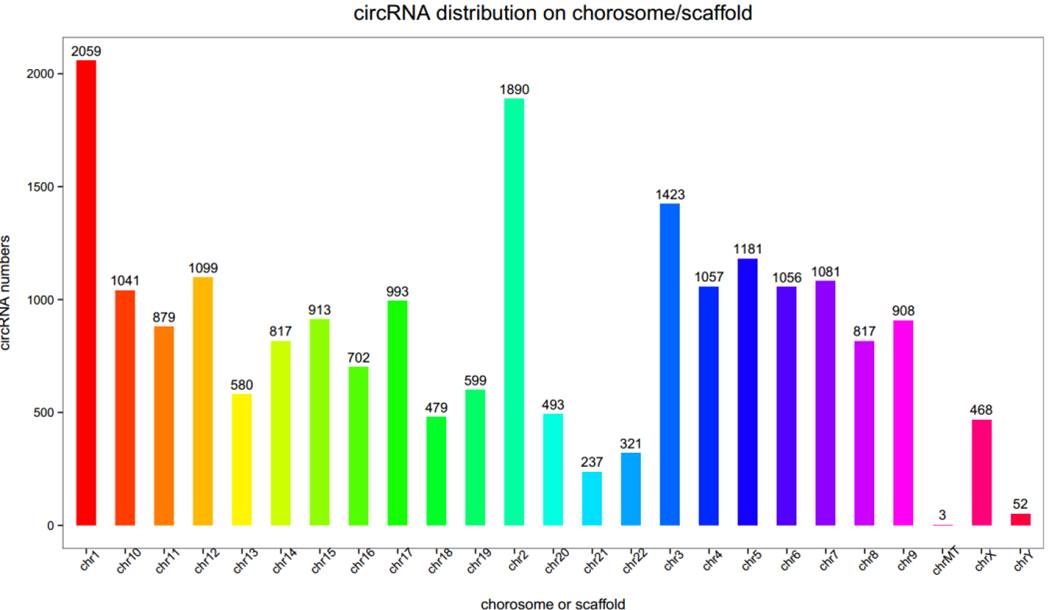
|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| CircRNA | HC (n=3) | CHB (n=3) | ACLF (n=3) | ACLFvsHC |
| mean±SD | mean±SD | mean±SD | P‑value |
| circRNA\_00389 | 0.2392±0.1132 | 0.0815±0.0156 | 0.0322±0.0188 | 0.035 |
| circRNA\_02808 | 0.0962±0.0453 | 0.0634±0.0613 | 0.0201±0.0142 | 0.053 |
| circRNA\_03646 | 0.1444±0.0115 | 0.1170±0.0564 | 0.0219±0.0158 | 0.001 |
| circRNA\_04205 | 0.1088±0.0308 | 0.0691±0.0046 | 0.0264±0.0127 | 0.014 |
| circRNA\_06400 | 0.6958±0.2890 | 0.4577±0.2799 | 0.1713±0.0272 | 0.035 |
| circRNA\_09331 | 0.1297±0.0703 | 0.0830±0.0271 | 0.0146±0.0119 | 0.050 |
| circRNA\_17523 | 0.1603±0.0940 | 0.0933±0.0321 | 0.0356±0.0153 | 0.087 |
| circRNA\_19214 | 0.1930±0.1023 | 0.1093±0.0632 | 0.0224±0.0160 | 0.047 |
| circRNA\_05781 | 0.1519±0.0839 | 0.0924±0.0419 | 0.0409±0.0186 | 0.091 |
| circRNA\_07485 | 0.1124±0.0333 | 0.0659±0.0440 | 0.0318±0.0152 | 0.021 |
| circRNA\_07734 | 0.1823±0.0611 | 0.1156±0.0991 | 0.0565±0.0275 | 0.035 |
| circRNA\_08533 | 0.3798±0.2071 | 0.1382±0.1155 | 0.0243±0.0209 | 0.042 |
| circRNA\_16562 | 0.2216±0.11947 | 0.0569±0.04378 | 0.0651±0.08233 | 0.135 |
| circRNA\_17526 | 0.2214±0.1506 | 0.0888±0.0191 | 0.0321±0.0268 | 0.100 |
| circRNA\_04487 | 0.0345±0.0098 | 0.0635±0.0281 | 0.1354±0.0342 | 0.015 |
| circRNA\_15699 | 0.0426±0.0093 | 0.0702±0.0211 | 0.1370±0.0607 | 0.095 |
| circRNA\_16083 | 0.2046±0.0971 | 0.2923±0.1392 | 1.0133±0.2018 | 0.006 |
| circRNA\_16987 | 0.0495±0.0243 | 0.0567±0.0244 | 0.3220±0.0788 | 0.009 |

Supplemental table 2. The expression of selected mRNA (fpkm) in three groups and ANOVA test

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| mRNA-id | HC (n=3) | CHB (n=3) | ACLF (n=3) | P‑value |
| mean±SD | mean±SD | mean±SD |
| NM\_000361.2 | 1.526±0.576 | 3.254±1.201 | 13.978±4.360 | 0.002 |
| NM\_001005862.2 | 1.609±0.639 | 0.668± 0.183 | 0.041±0.039 | 0.007 |
| NM\_001199139.1 | 0.047±0.043 | 0.510±0.422 | 4.591±0.785 | <0.001 |
| NM\_004633.3 | 0.216±0.225 | 1.479±0.931 | 159.220±98.032 | 0.021 |
| NM\_005204.3 | 0.834±0.178 | 2.902±0.716 | 7.480±3.148 | 0.012 |
| NM\_006720.3 | 3.090±0.990 | 1.228±0.739 | 0.342±0.278 | 0.010 |
| NM\_014790.4 | 1.688±0.255 | 0.724±0.133 | 0.178±0.111 | <0.001 |
| NM\_080913.3 | 1.649±1.325 | 6.342±3.601 | 17.297±4.355 | 0.003 |
| XM\_005257807.2 | 1.942±0.722 | 0.764±0.212 | 0.164±0.223 | 0.008 |
| XM\_011511061.1 | 0.143±0.032 | 0.574±0.251 | 1.531±0.537 | 0.007 |
| XM\_011520156.1 | 2.850±1.863 | 0.730±0.262 | 6.377±1.656 | 0.009 |
| XM\_011520271.1 | 3.739±1.129 | 1.711±0.603 | 0.580±0.503 | 0.008 |
| XM\_011524254.1 | 4.112±1.333 | 1.550±1.396 | 0.138±0.225 | 0.013 |
| XM\_011524699.1 | 9.874±3.598 | 2.428±2.342 | 0.085±0.080 | 0.007 |
| XM\_011531698.1 | 2.835±0.633 | 5.713±2.783 | 11.122±1.922 | 0.006 |
| XM\_011537524.1 | 3.118±1.143 | 1.148±0.745 | 0.263±0.450 | 0.014 |
| NM\_080913.3 | 1.649±1.325 | 6.342±3.601 | 17.297±4.355 | 0.003 |
| XM\_005257807.2 | 1.942±0.722 | 0.764±0.212 | 0.164±0.223 | 0.008 |
| XM\_011511061.1 | 0.143±0.032 | 0.574±0.251 | 1.531±0.537 | 0.007 |



Supplemental Figure 1. rRNA-depleted RNA-Seq experimental process.

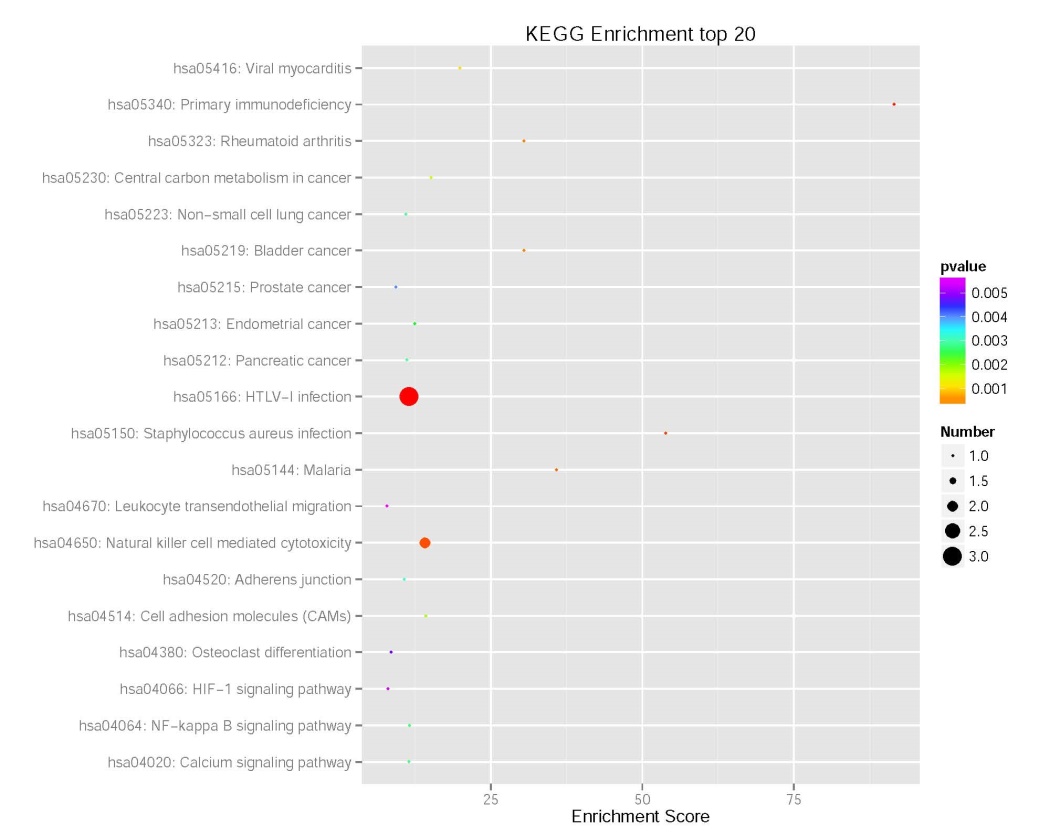


Supplemental Figure 2. Distribution of circRNAs on each chromosome.

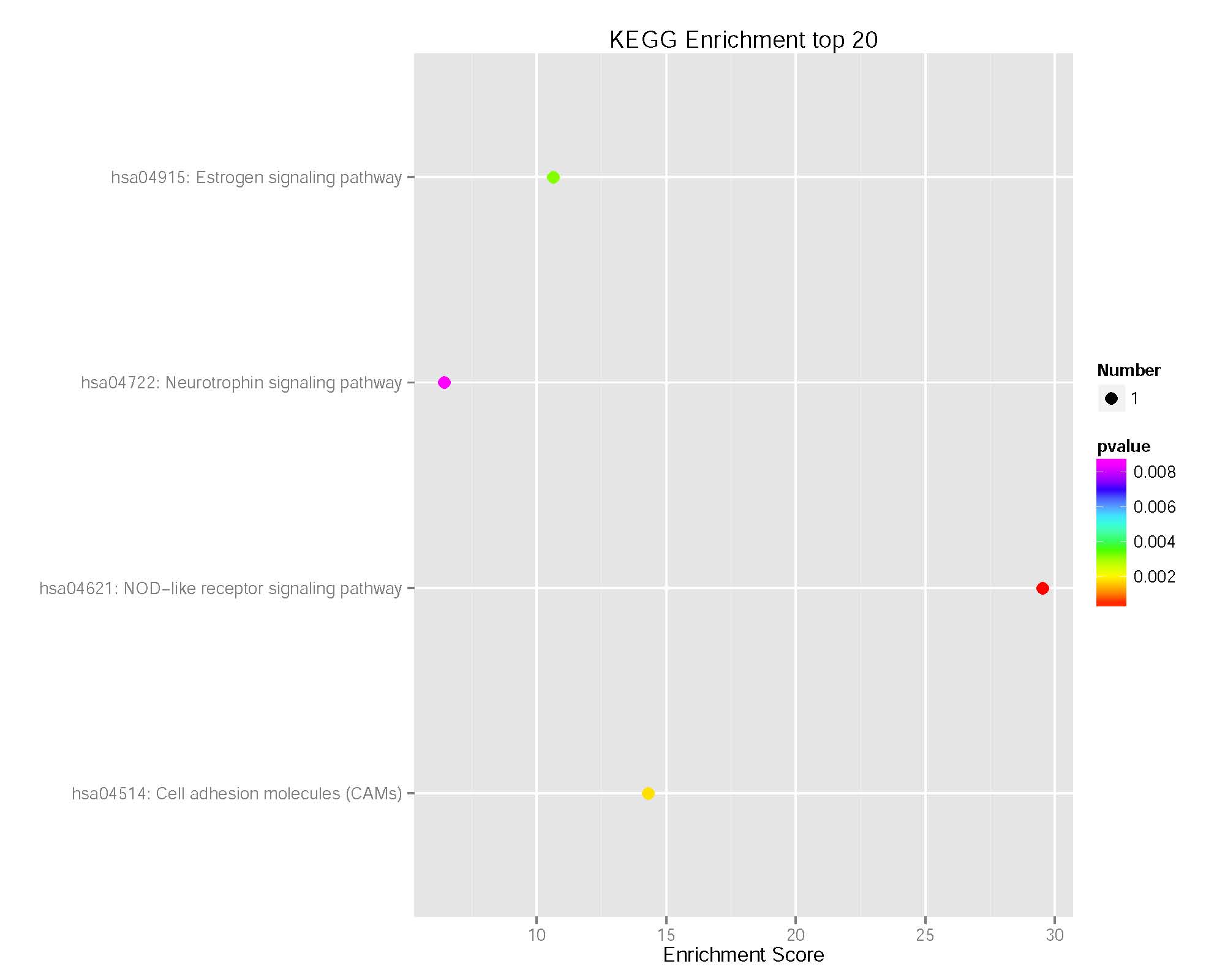




Supplemental Figure 3. Gene Oncology (GO) analysis of ACLF risk status according to the down (A) and up (B)-regulated circRNAs.

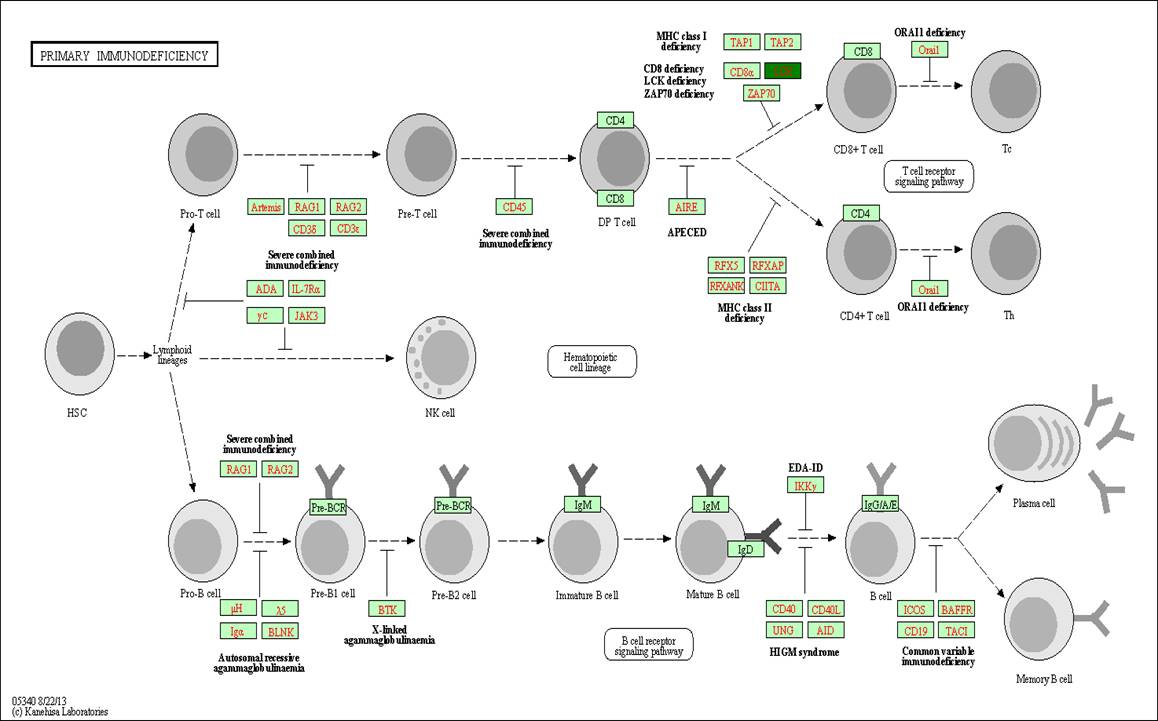


A

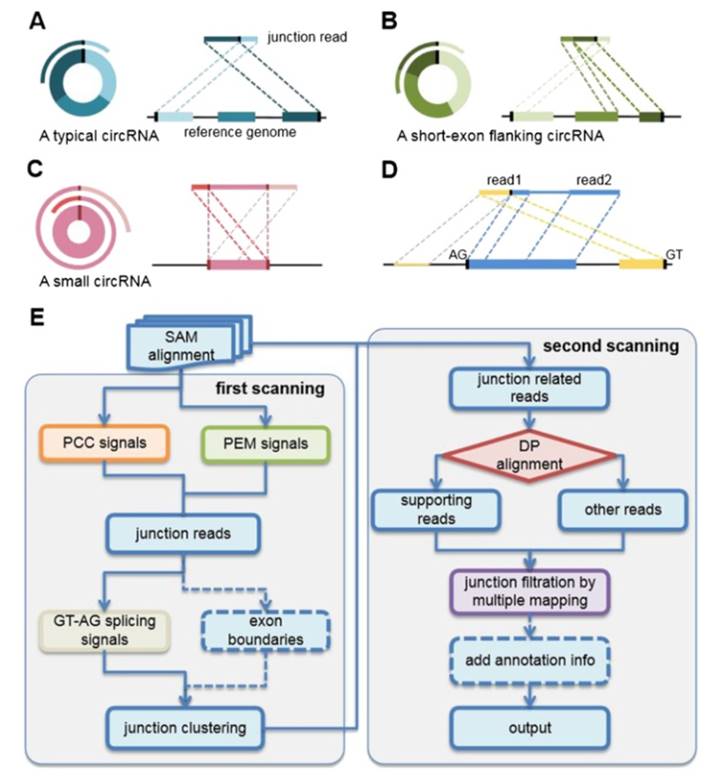


B

Supplemental Figure 4. KEGG enrichment analysis, A Down-regulated circRNAs, B Up-regulated circRNAs



Supplemental Figure 5. The hsa05340 map according to KEGG enrichment; red indicates up-regulated circRNAs, green indicates down-regulated circRNAs.



Supplemental Figure 6. Predictive flow diagram generated by CIRI software.