Supplementary

ARDS patients were divided into different subphenotypes.

Severe ARDS group and non-severe group were divided according to the severity of lung injury.

Compared with non-severe group, LIB was lower in severe ARDS group [1,911.17 (1,870.37–1,944.03) *vs.* 1,855.11 (1,823.79–1,878.54), P=0.000], with the ROC of predictive value of 0.727 (P<0.0001). GO analysis showed that 25 functions were correlated with ARDS severity (P<0.01) (*Figure S1*), and KEGG enrichment analysis showed that these SNP/InDel were in 4 pathways, such as PI3K-Akt signaling pathway, ECM-receptor interaction (P<0.05) (*Figure S2*).

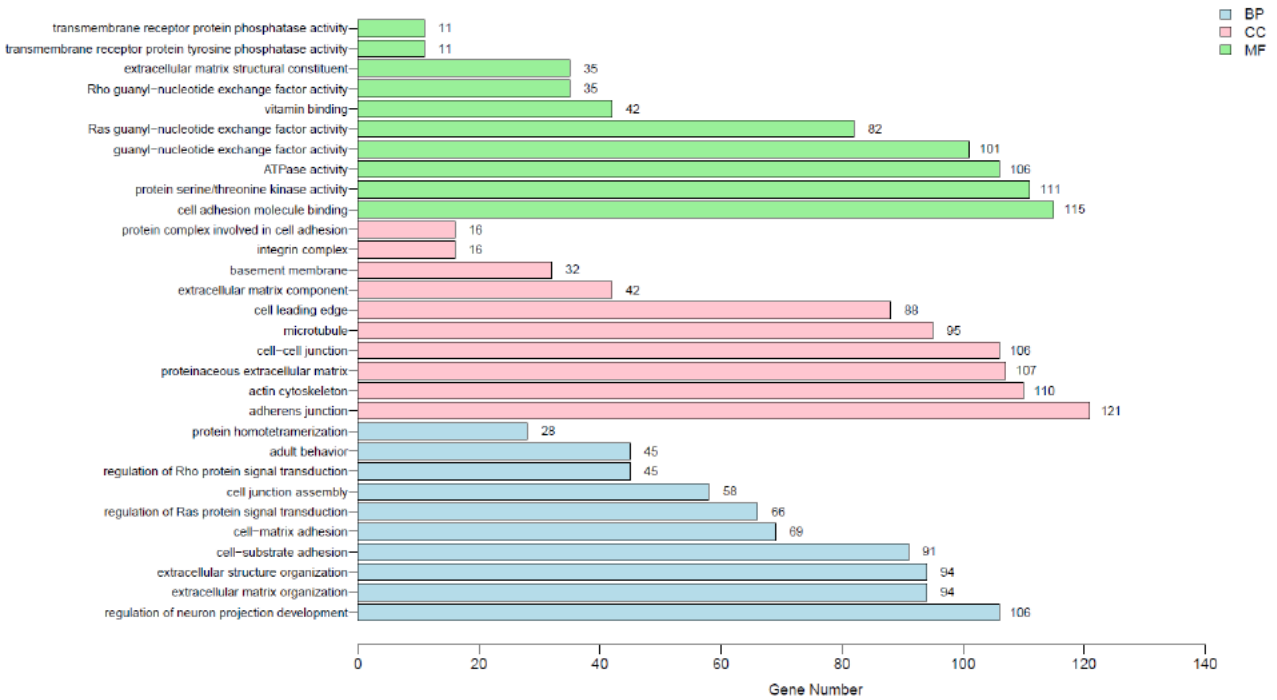

Figure S1 GO analysis showed that the Top 30 of the 60 functions were correlated with ARDS severity. BP, Biological process; CC, Cellular component; MF, Molecular function.

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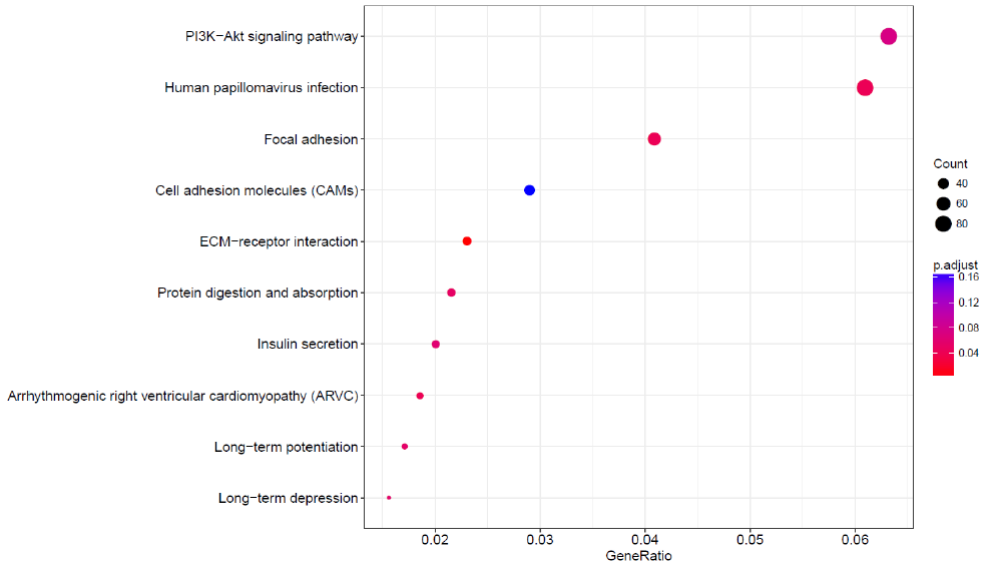

Figure S2 KEGG enrichment pathway analysis showed pathways correlated with ARDS severity. ARDS patients were divided into pulmonary ARDS and extrapulmonary ARDS group. LIB was not significantly altered between the pulmonary and extrapulmonary ARDS [1,877.49 (1,846.03–1,933.11) *vs.* 1,880.49 (1,835.22–1,919.92), P=0.717]. GO analysis showed that 19 functions were correlated with pulmonary and extrapulmonary ARDS (P<0.01) (*Figure S3*), and KEGG enrichment analysis showed that these SNP/InDel were in 8 pathways, such as ECM-receptor interaction (P<0.05) (*Figure S4*).

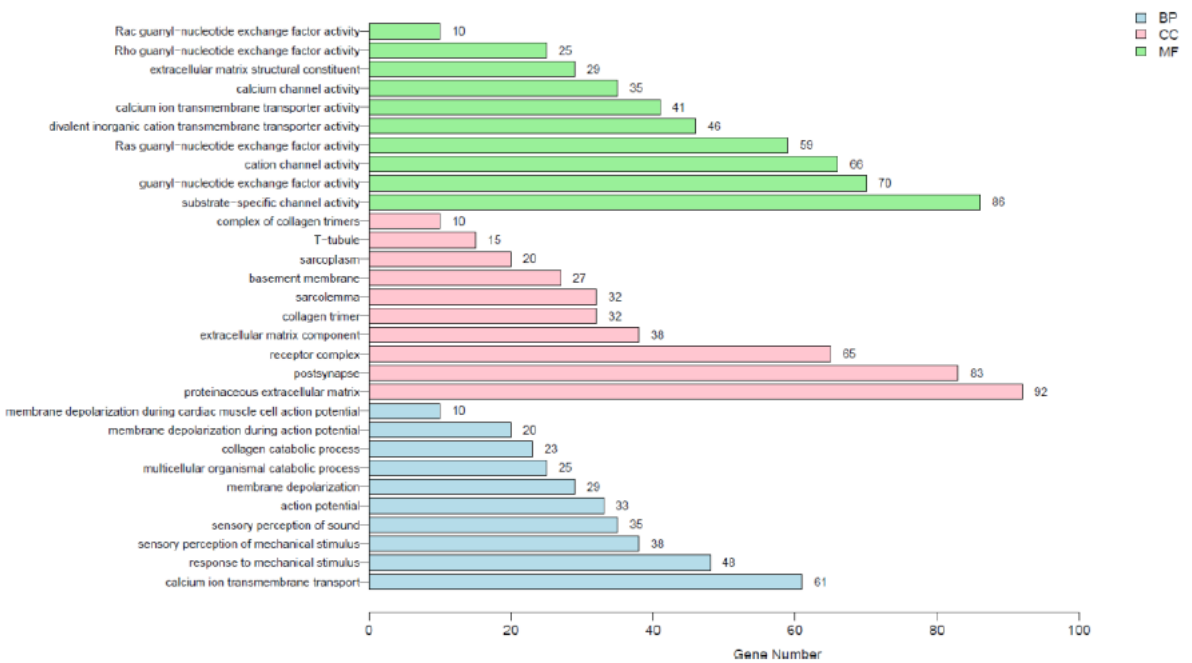

Figure S3 GO analysis showed that the Top 30 of the 60 functions were correlated with pulmonary and extrapulmonary ARDS. BP, Biological process; CC, Cellular component; MF, Molecular function.

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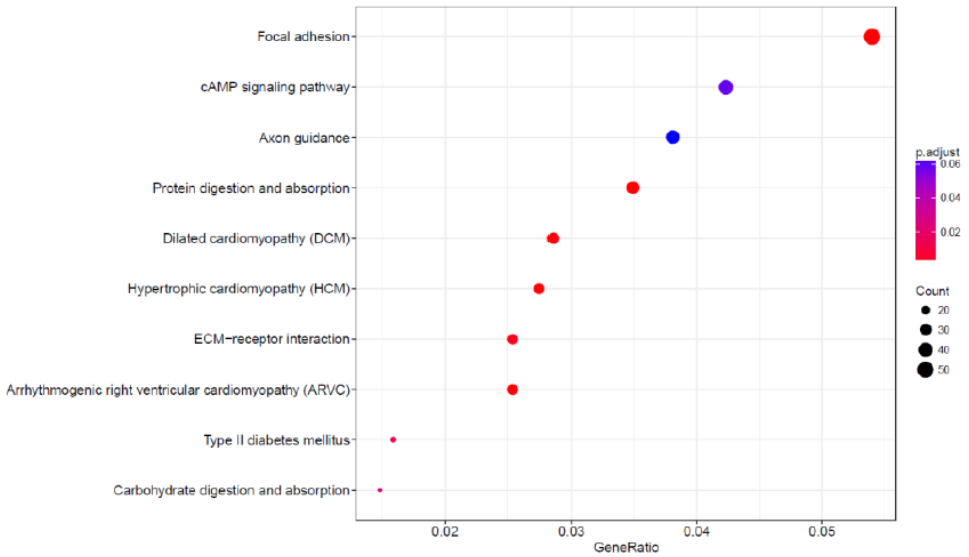

Figure S4 KEGG enrichment pathway analysis showed pathways correlated with pulmonary and extrapulmonary ARDS. ARDS patients were divided into ARDS combined with sepsis and ARDS without sepsis on enrollment. Compared with patients without sepsis, the LIB was lower in ARDS combined with sepsis [1911.82 (1880.22–1944.17) *vs.* 1870.13 (1833.88–1928.44), P=0.044], with the ROC of predictive value of 0.6803 (P=0.0084). GO analysis showed that 24 functions were correlated with ARDS combined with sepsis (P<0.01) (*Figure S5*), and KEGG enrichment analysis showed that these SNP/InDel were in 3 pathways, such as ECM-receptor interaction, Focal adhesion (P<0.05) (*Figure S6*).

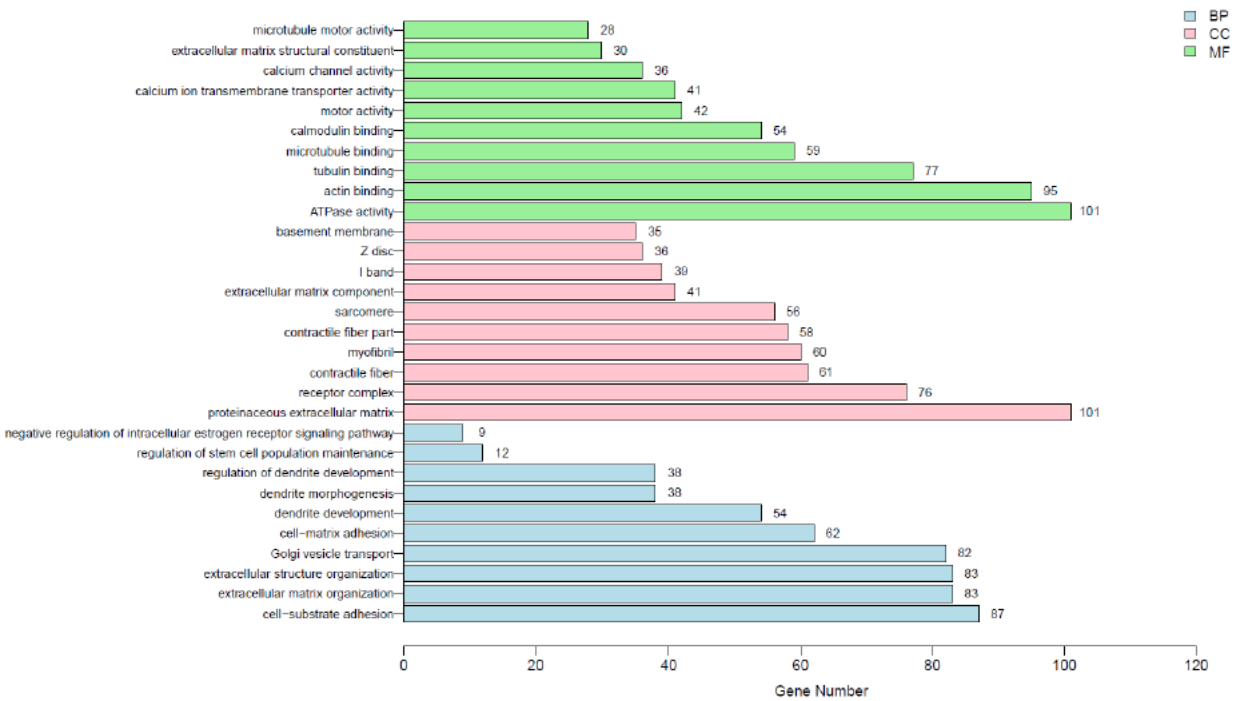

Figure S5 GO analysis showed that the Top 30 of the 60 functions were correlated with ARDS and sepsis. BP, Biological process; CC, Cellular component; MF, Molecular function.

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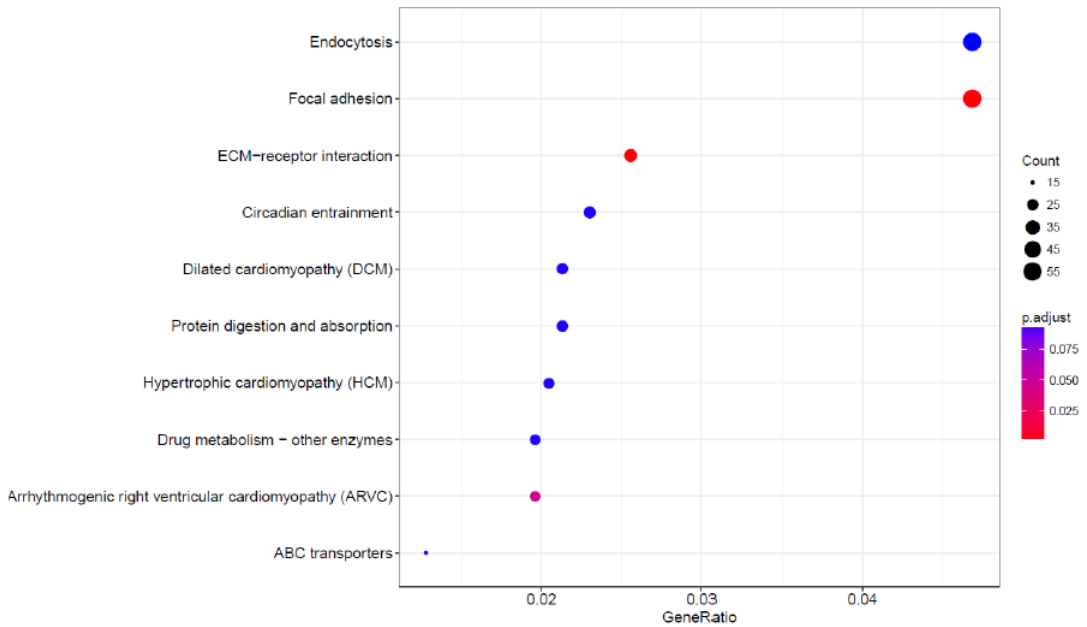

Figure S6 KEGG enrichment pathway analysis showed pathways correlated with ARDS and sepsis. ARDS patients were divided into ARDS combined with shock and ARDS without shock on enrollment. Compared with patients without shock, the LIB was lower in ARDS combined with shock [1,911.05 (1,874.18–1,940.98) *vs.* 1,858.70 (1,825.16–1,908.99), P=0.004], with the ROC of predictive value of 0.6915 (P=0.0008). GO analysis showed that 46 functions were correlated with ARDS combined with shock (P<0.01) (*Figure S7*), and KEGG enrichment analysis showed that these SNP/InDel were in 10 pathways, such as cAMP signaling pathway, ECM-receptor interaction (P<0.05) (*Figure S8*).

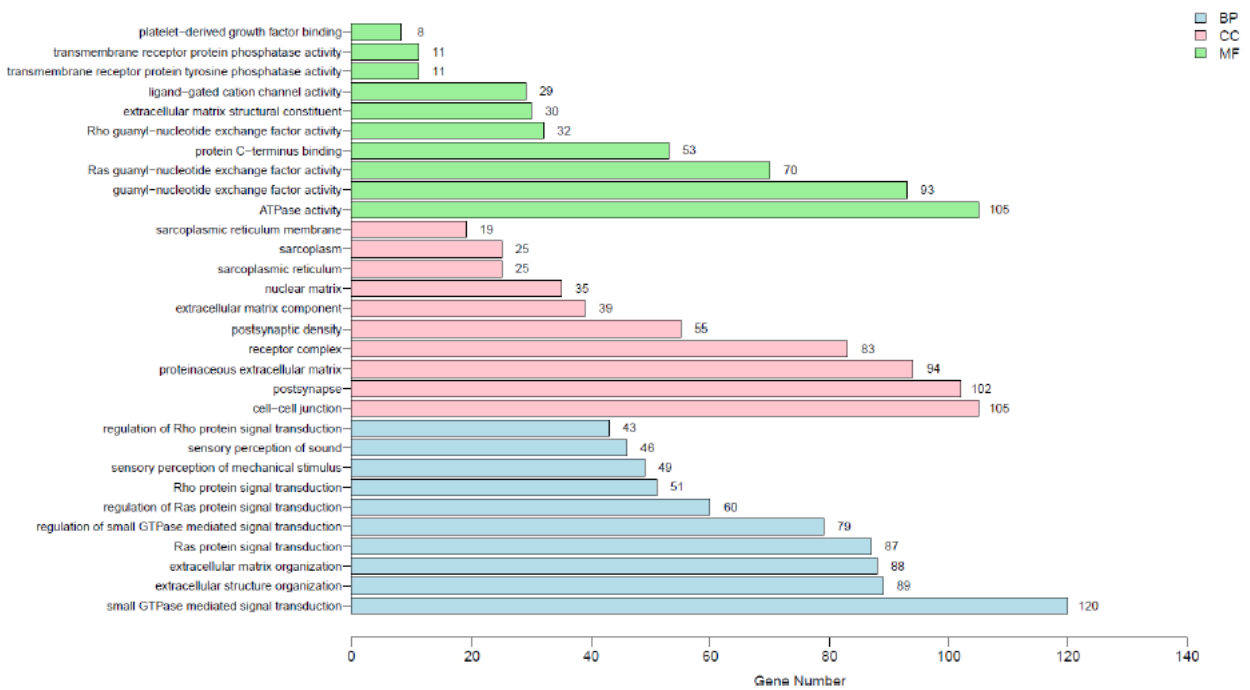

Figure S7 GO analysis showed that the Top 30 of the 60 functions were correlated with ARDS and shock. BP, Biological process; CC, Cellular component; MF, Molecular function.

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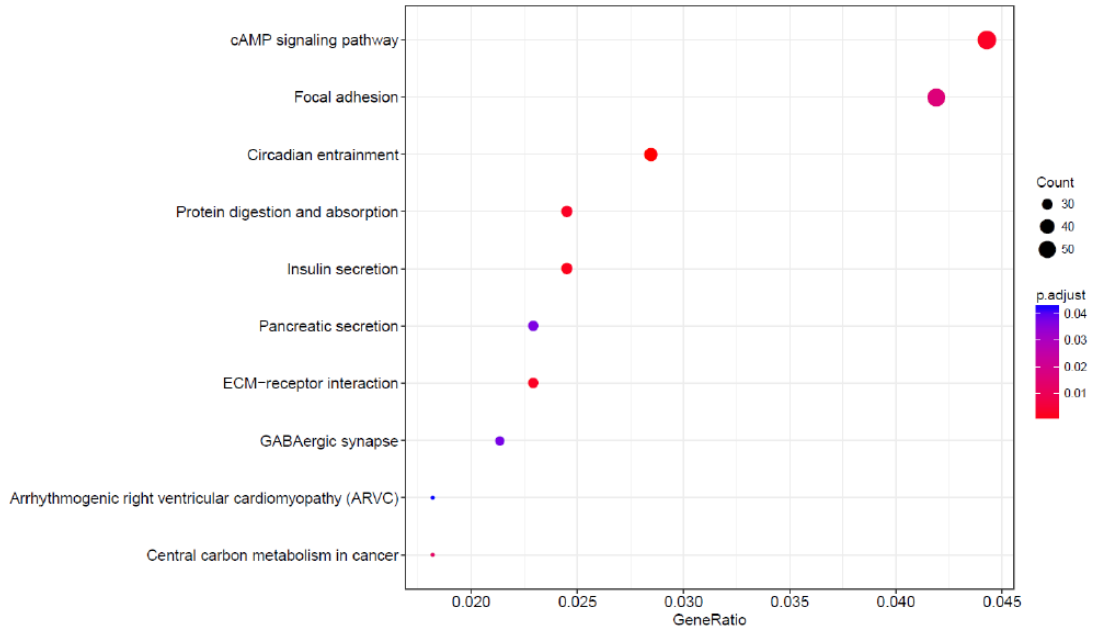

Figure S8 KEGG enrichment pathway analysis showed pathways correlated with ARDS and shock.

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