Supplementary Fig. 1

Enrichment analyses of differentially expressed genes identified in patients with ARDS compared with healthy controls

(A) Gene Ontology enrichment analysis of molecular function terms associated with upregulated differentially expressed genes identified in patients with ARDS compared with healthy controls

(B) Gene Ontology enrichment analysis of molecular function terms associated with downregulated differentially expressed genes identified in patients with ARDS

(C) KEGG pathway enrichment analysis of upregulated differentially expressed genes identified in patients with ARDS

(D) KEGG pathway enrichment analysis of downregulated differentially expressed genes identified in patients with ARDS