

Supplementary figure legends:

Supplementary Figure 1. The expression profile of the seven datasets after combined. (A) The PCA (principal components analysis) plot grouped by batch before batch correction. (B) The PCA plot grouped by batch after batch correction. (C) The boxplot of the combined data before batch correction. (D) The boxplot of the combined data after batch correction. (E) The PCA plot grouped by normal and tumor after batch correction. (F) The PCA plot grouped by tumor and normal after removing three outliers (tumor and paired normal samples) (sample size = 282).

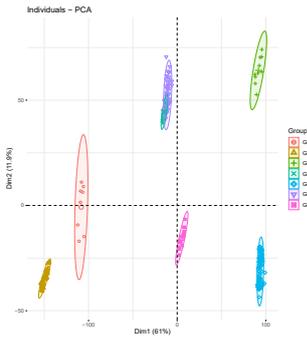
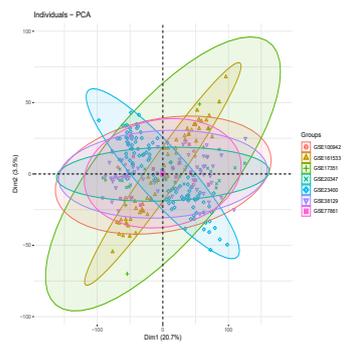
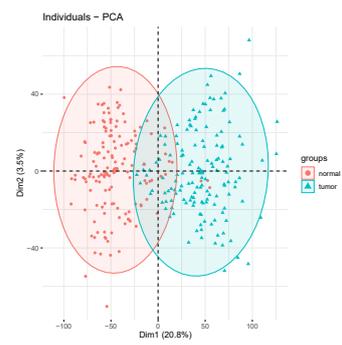
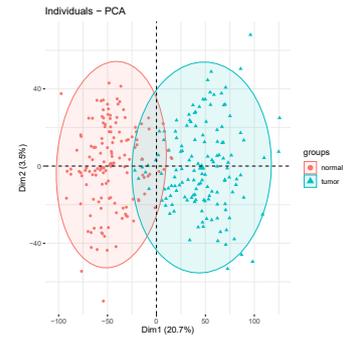
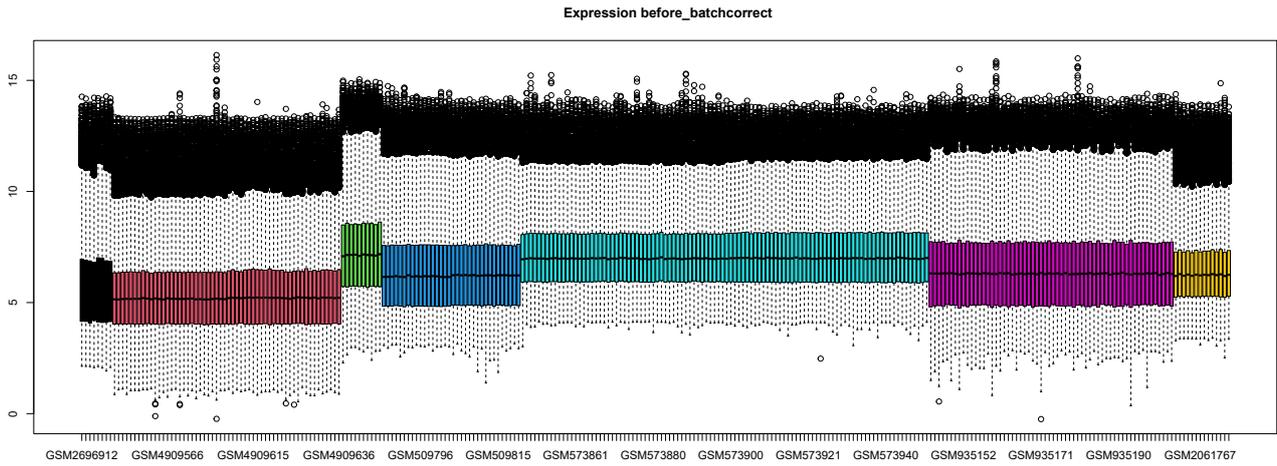
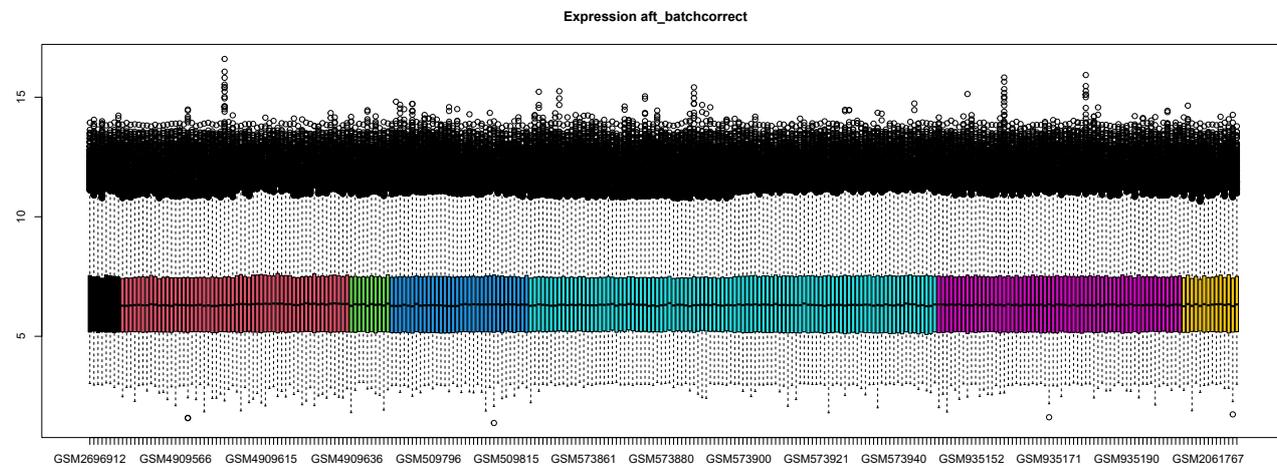
Supplementary Figure 2. The hierarchical clustering tree of 141 ESCC samples that labeled by different groups. (A) The hierarchical clustering of the 141 ESCC samples labeled by batch. (B) The hierarchical clustering of the 141 ESCC samples labeled by K-means_Subtype.

Supplementary Figure 3. The volcano plots of differential expressed genes (DEGs) in three subtypes. Subtypes 1, 2, and 3 had 83, 376, and 743 total DEGs, respectively.

Supplementary Figure 4. The profiles of 18 DEGs that were specific to Subtype 1 or 2 rather than Subtype 3. (A) The log₂FC of 18 genes in three subtypes. (B) The 16 upregulated DEGs among these 18 genes are enriched in the immune-related pathways.

Supplementary Figure 5. Immune cell infiltration scores in tumor tissues of three ESCC subtypes. There are fewer infiltrating T cells in Subtype 1 and less neutrophil infiltration in Subtype 3 tumor tissues.

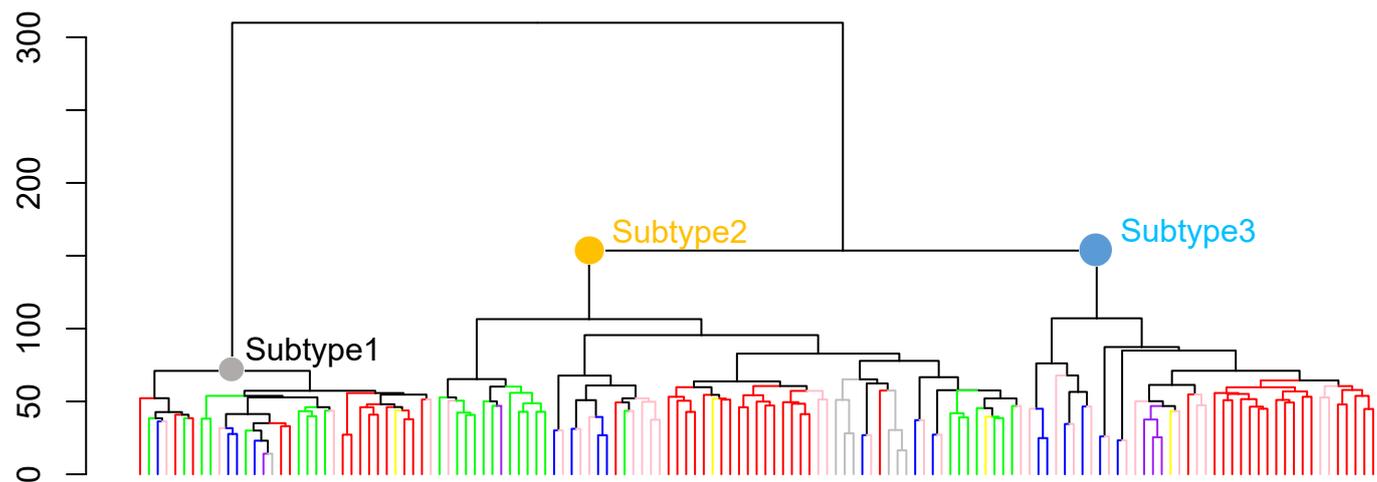
Supplementary Figure 6. Enrichment of biological pathways in module 2.

A**B****E****F****C****D**

Supplementary Figure 1

A

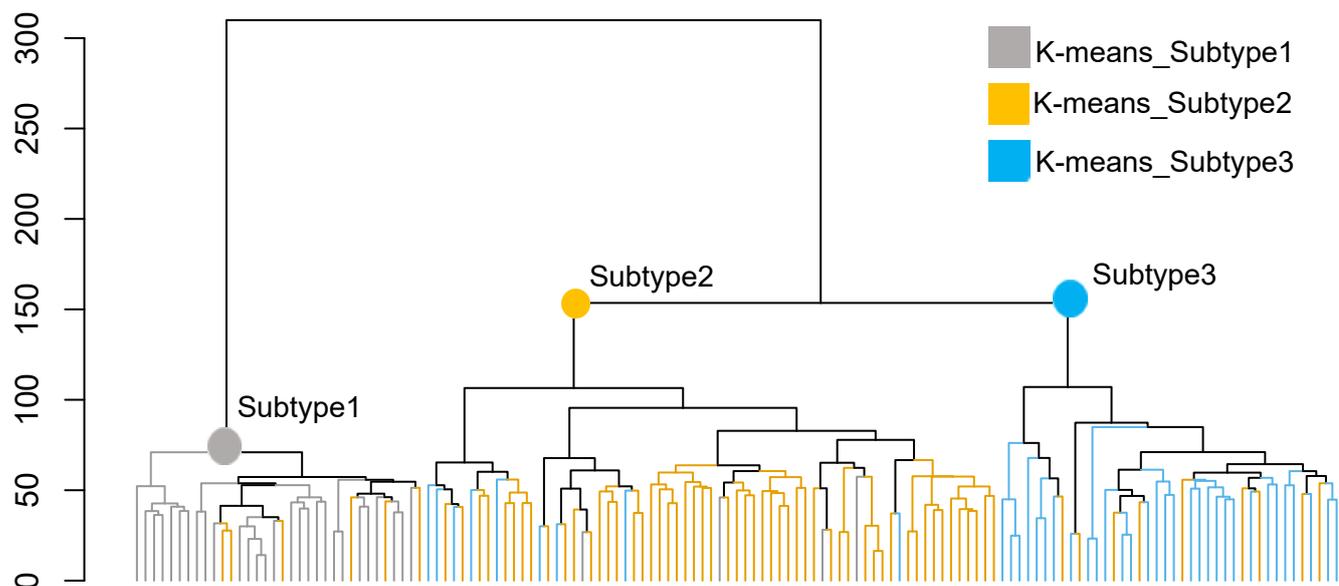
Clustering of 141 ESCC samples colored by batches



color labels:GSE23400;GSE161533;GSE20347;GSE38129;GSE17351;GSE100942;GSE77861

B

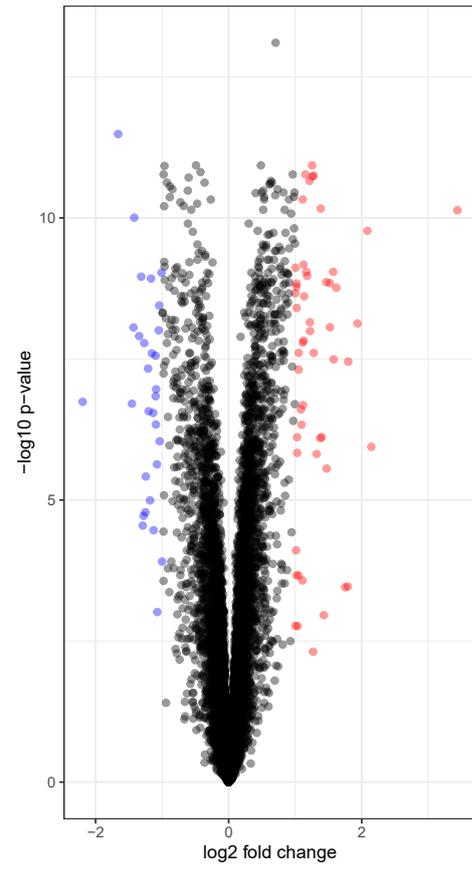
Clustering of 141 ESCC samples colored by K-means_Subtypes



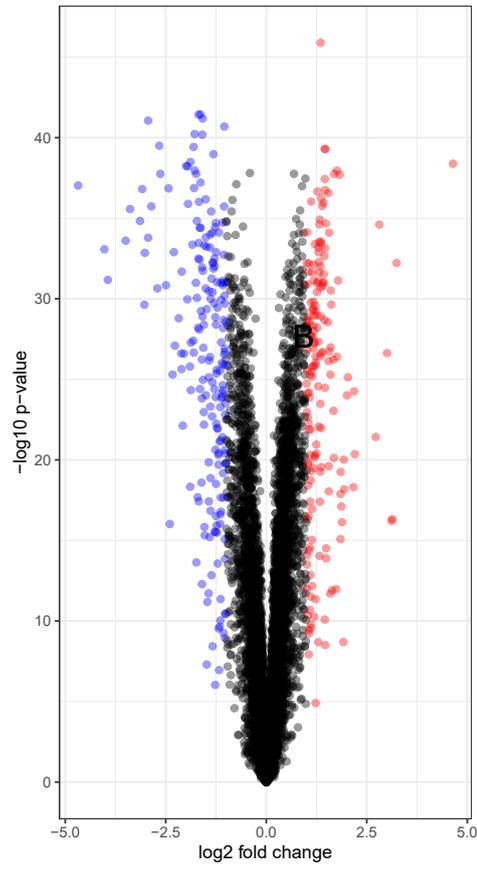
Supplementary Figure 2

A

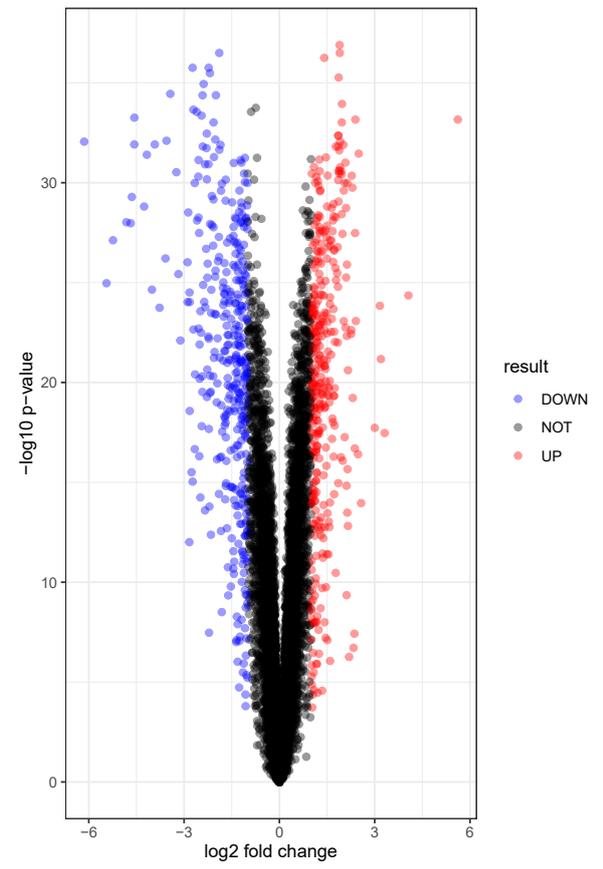
Subtype1
 The number of up gene is 53
 The number of down gene is 30

**B**

Subtype2
 The number of up gene is 178
 The number of down gene is 198

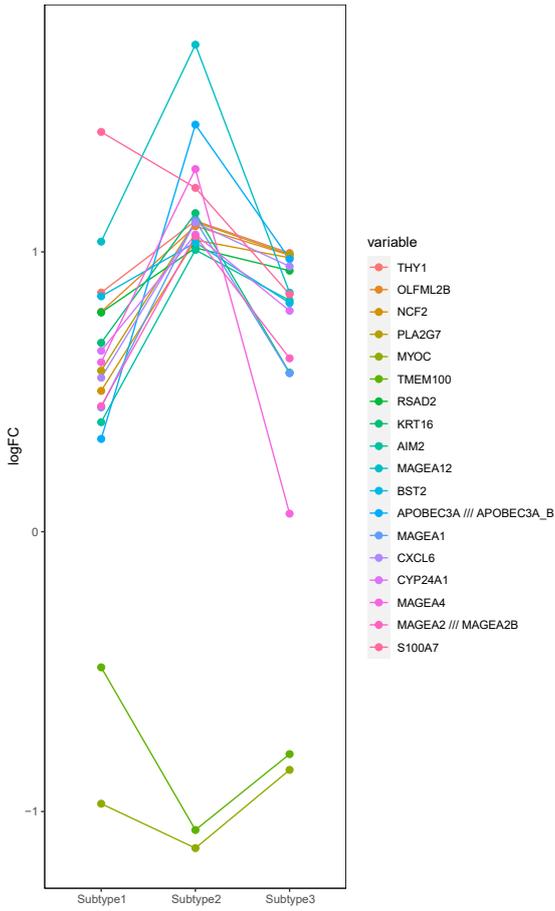
**C**

Subtype3
 The number of up gene is 363
 The number of down gene is 380

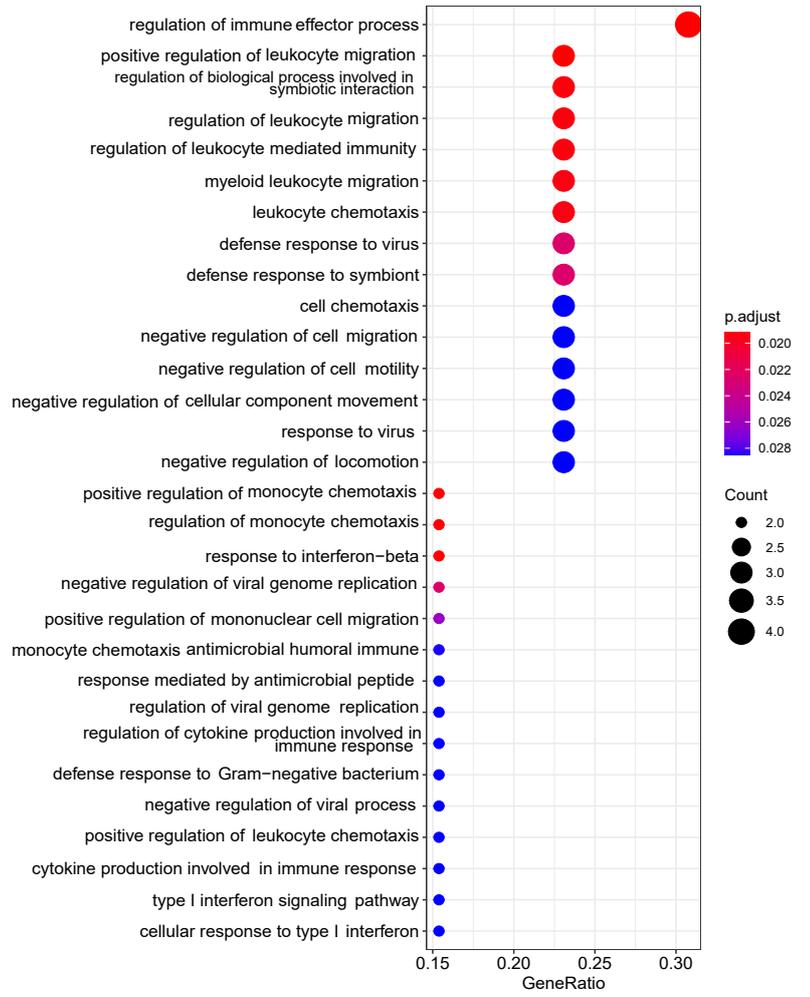


Supplementary Figure 3

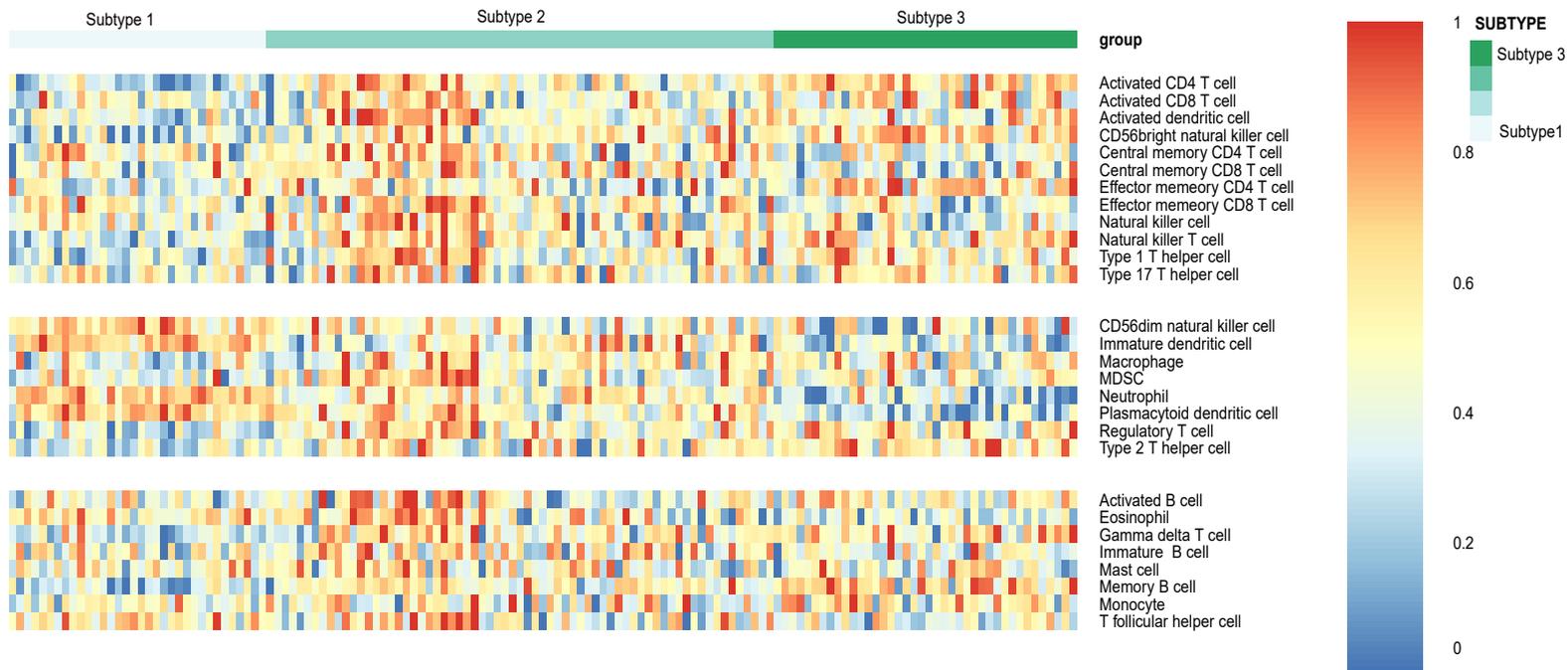
A



B

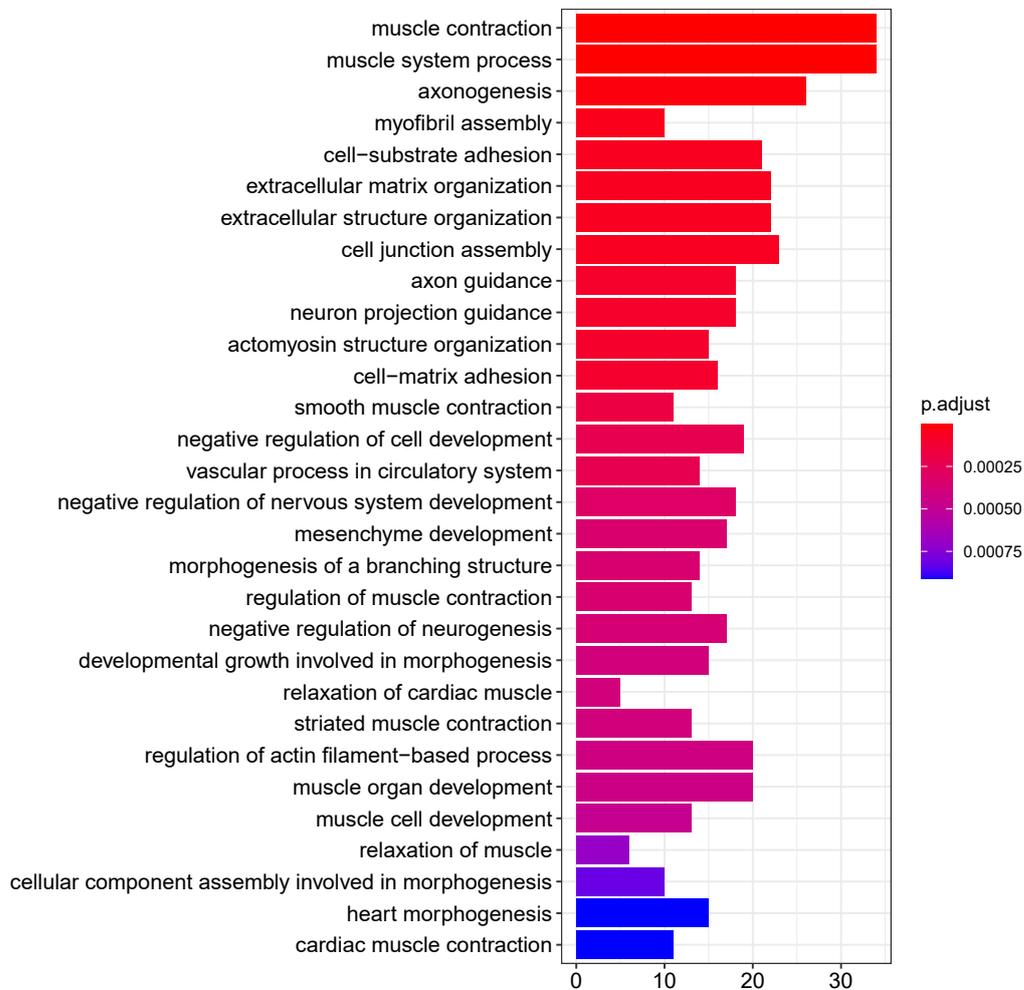


Supplementary Figure 4



Supplementary Figure 5

module 2



Supplementary Figure 6