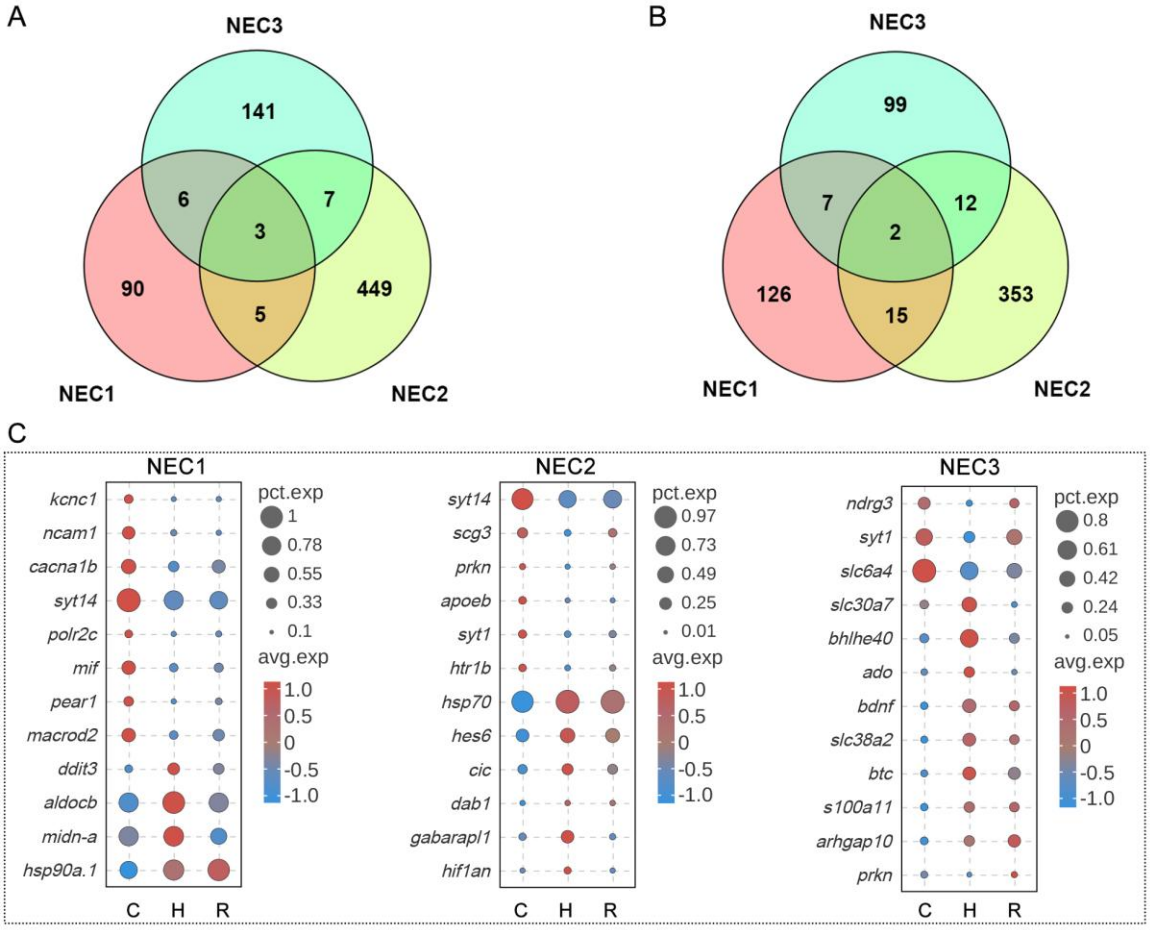
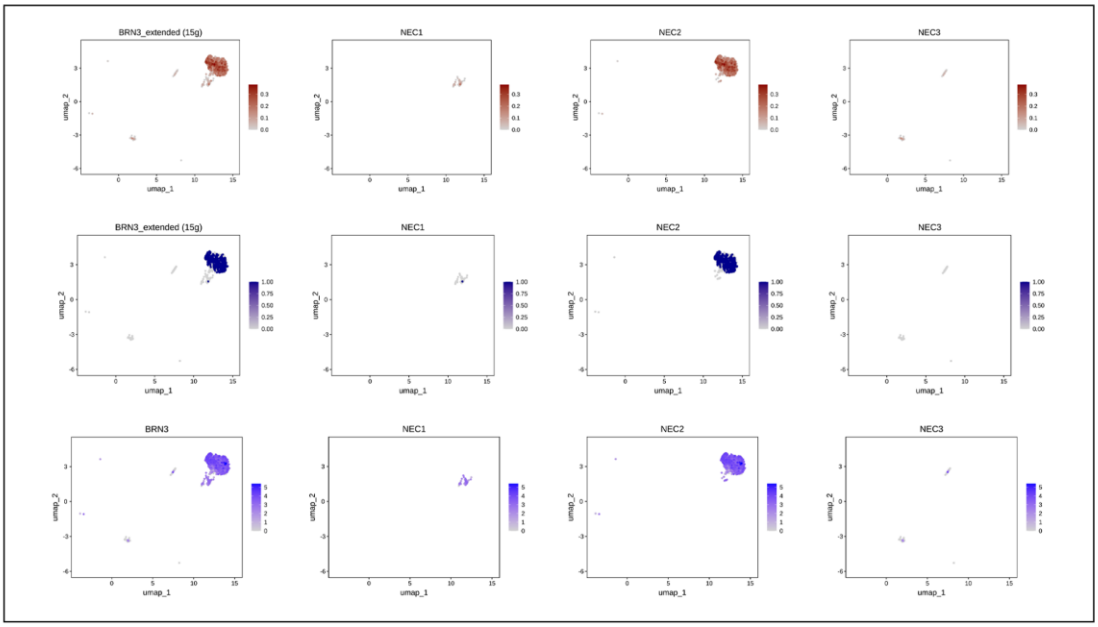
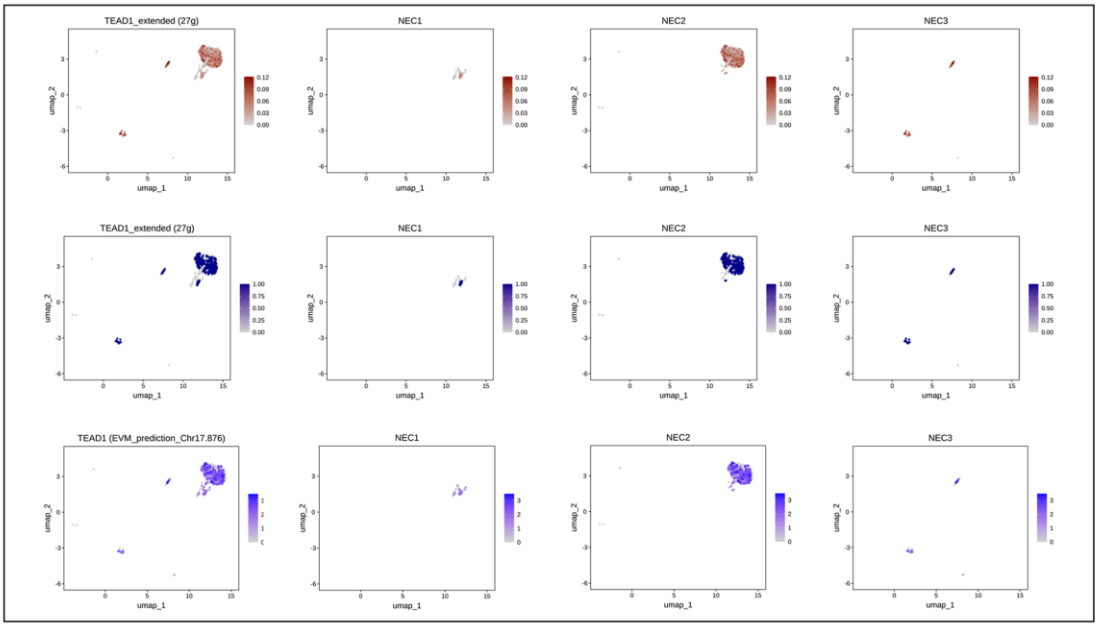


Figure S1. Analysis of DEGs among NECs. A: the Venn diagram of DEGs among NECs RvsC; B: the Venn diagram of DEGs among NECs RvsH; C: the bubble chart of partial DEGs among NECs.


BRN3_extended (15g)
NEC1
NEC2
NEC3
BRN3_extended (15g)
NEC1
NEC2
NEC3
BRN3
NEC1
NEC2
NEC3
umap_1
umap_2


TEAD1_extended (27g)
NEC1
NEC2
NEC3
TEAD1_extended (27g)
NEC1
NEC2
NEC3
TEAD1 (EVM_prediction_Chr17.876)
NEC1
NEC2
NEC3
umap_1
umap_2

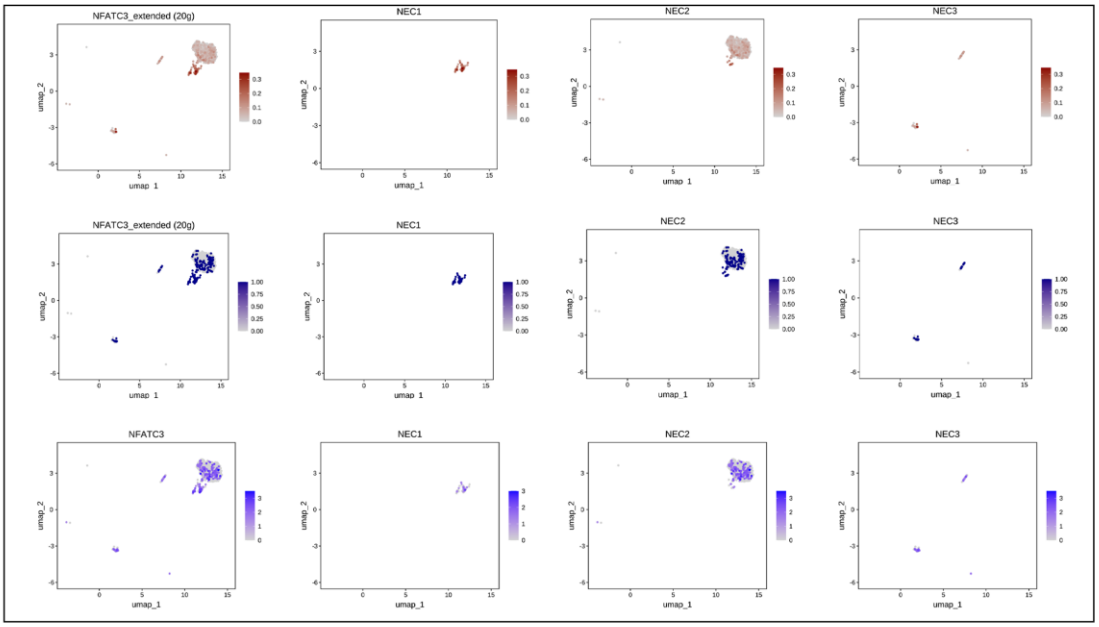

NFATC3_extended (20g)
NEC1
NEC2
NEC3
NFATC3_extended (20g)
NEC1
NEC2
NEC3
NFATC3
NEC1
NEC2
NEC3
umap_1
umap_2

Figure S2. UMAP prediction of average regulator activity, binary activity, and gene expression of *brn3* extended(15g), *tead1* extended(27g), and *nfatc3* extended(20g) in NECs.

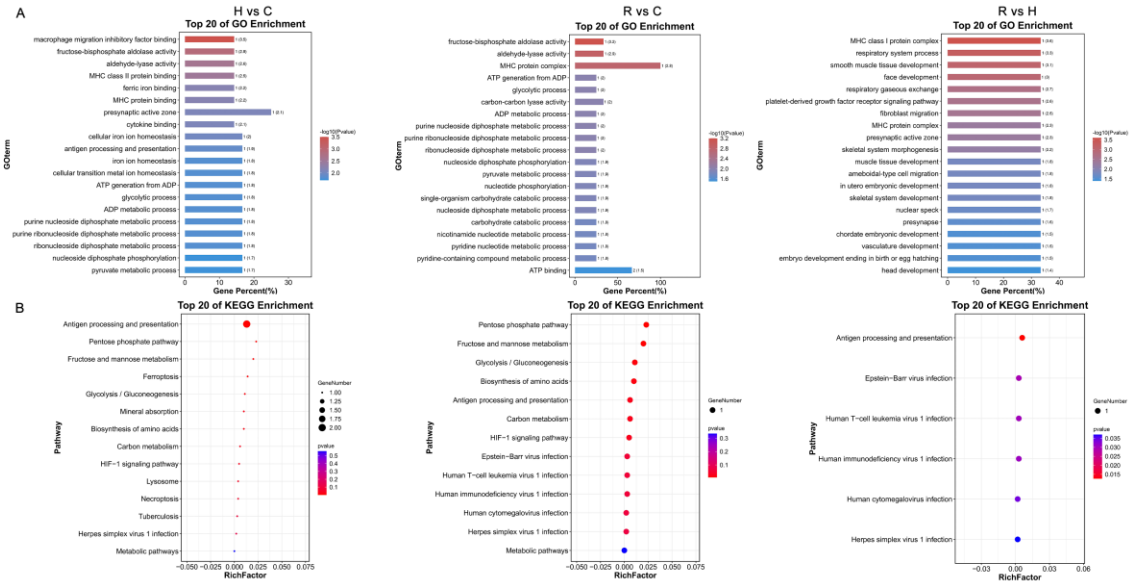


Figure S3. Analysis of DEGs in gill erythrocytes of *T. vachellii*. A: GO enrichment histogram of DEGs among groups; B: KEGG enrichment bubble plot of DEGs between groups.

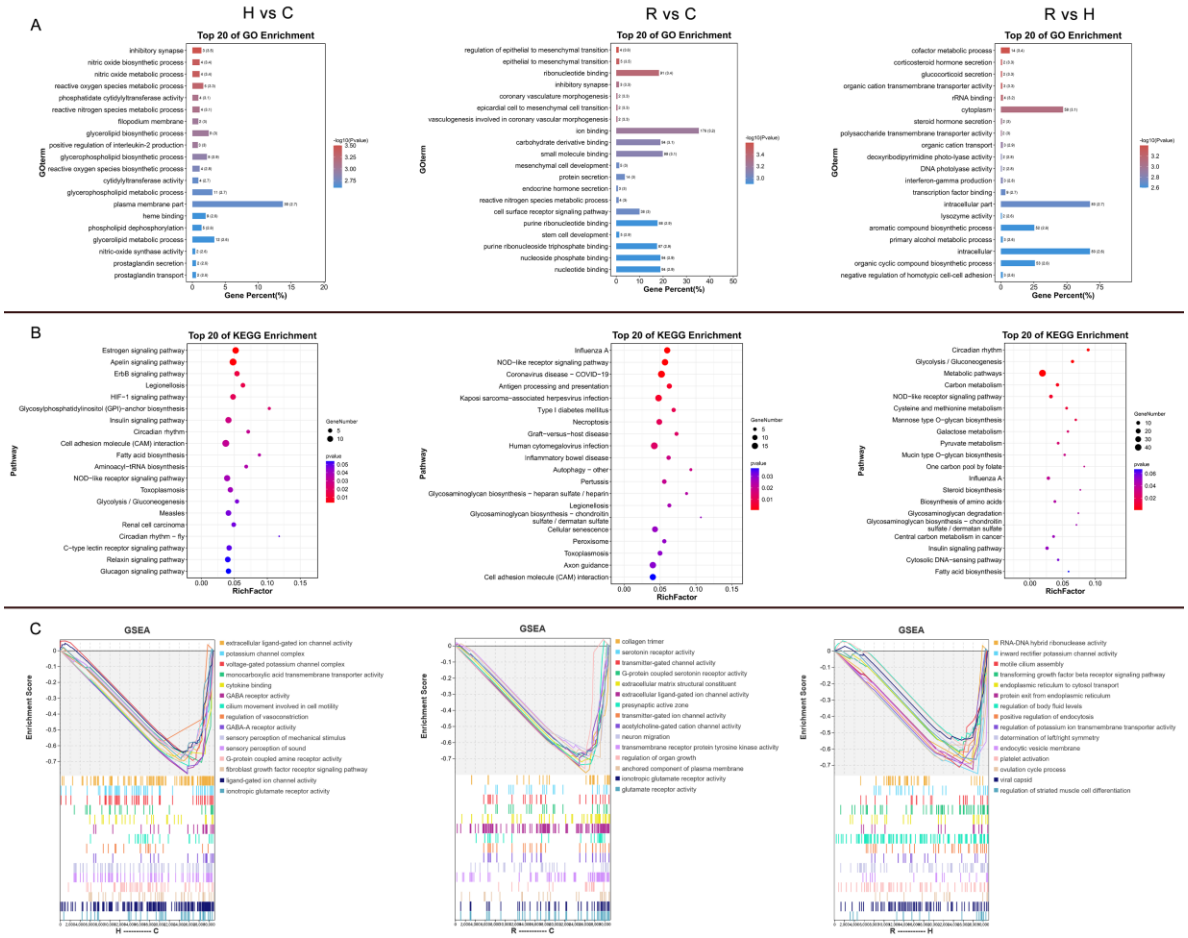


Figure S4. Analysis of DEGs in gill MCs of *T. vachellii*. A: GO enrichment histogram of DEGs among groups; B: KEGG enrichment bubble plot of DEGs between groups; C: GSEA analysis chart of DEGs between groups.

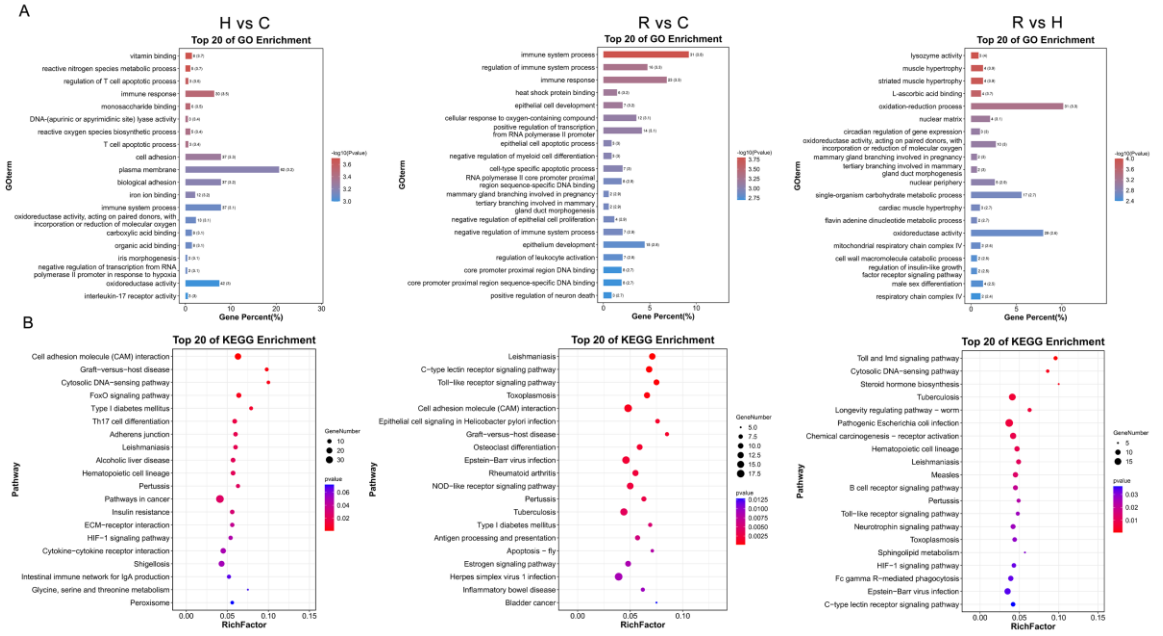


Figure S5. Analysis of DEGs in gill PVCs of *T. vachellii.* A: GO enrichment histogram of DEGs among groups; B: KEGG enrichment bubble plot of DEGs between groups.

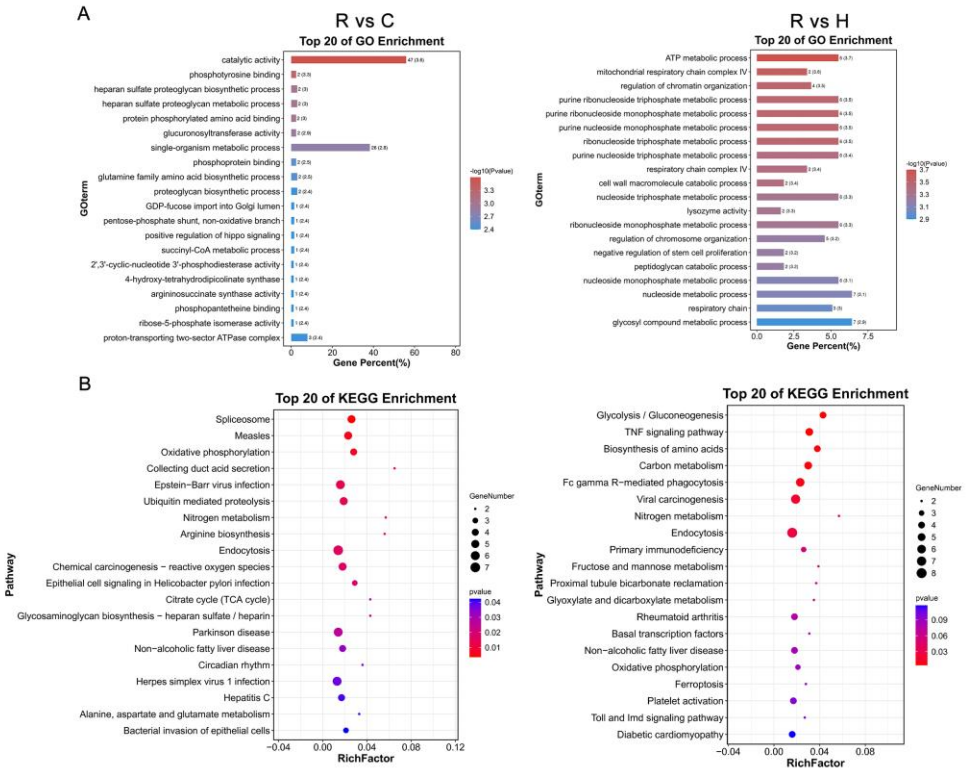


Figure S6. Analysis of DEGs in gill tuft cells of *T. vachelli*. A: GO enrichment histogram of DEGs among groups; B: KEGG enrichment bubble plot of DEGs between groups