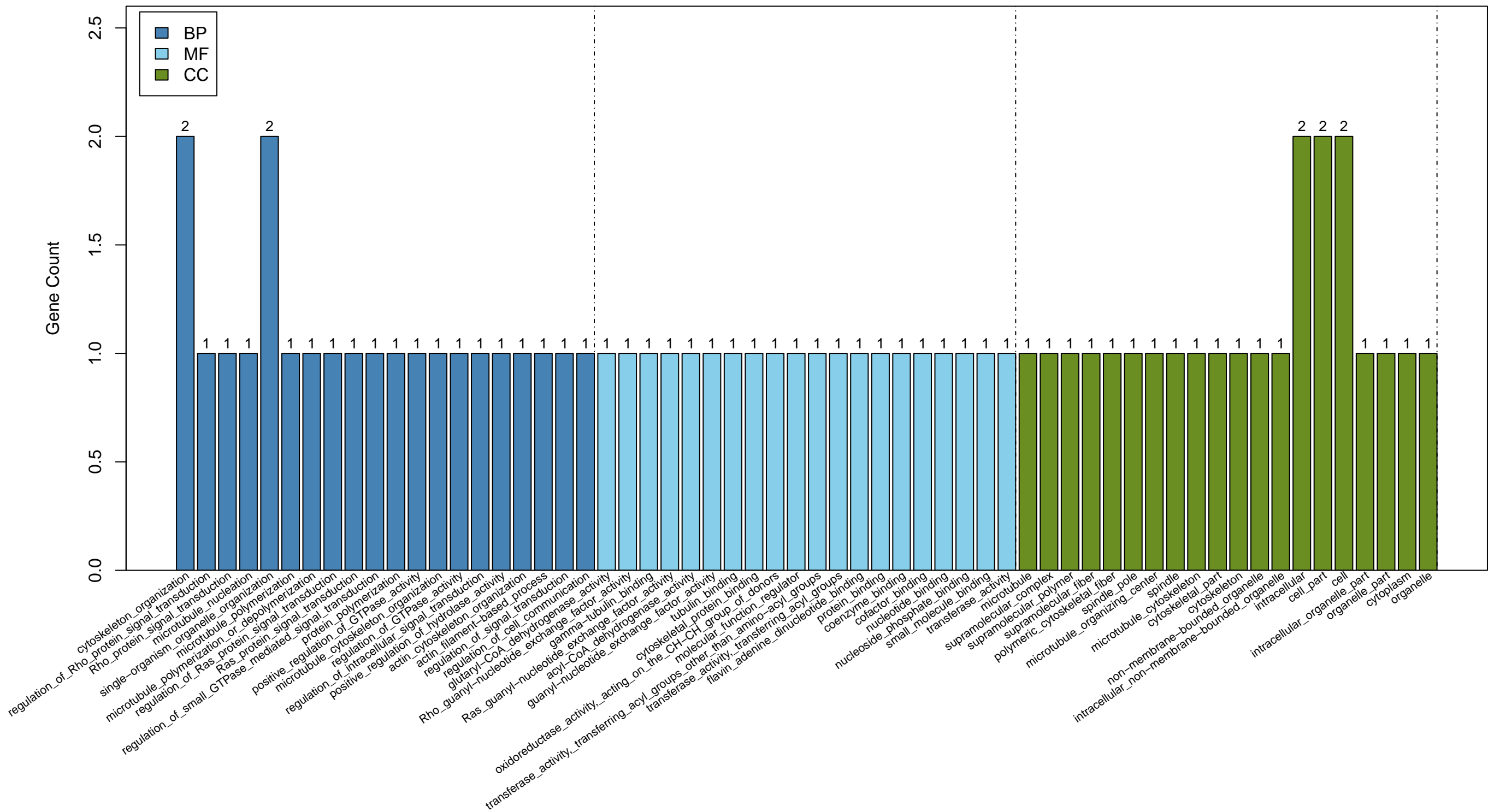


A

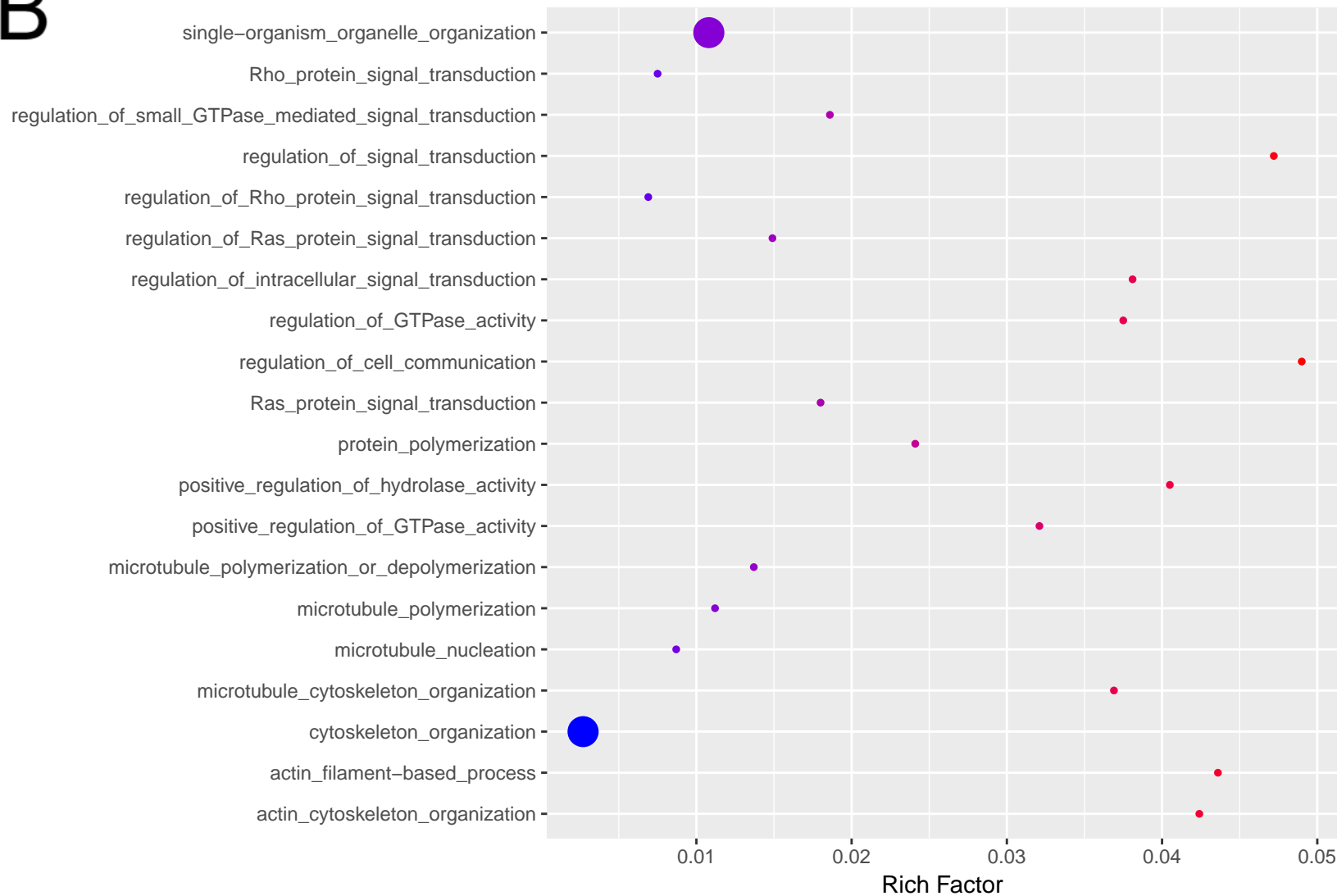
Gene Ontology Analysis



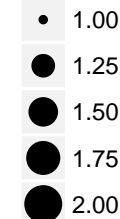
B

## Statistics of GO Enrichment

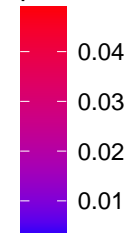
GO Term



GeneNumber



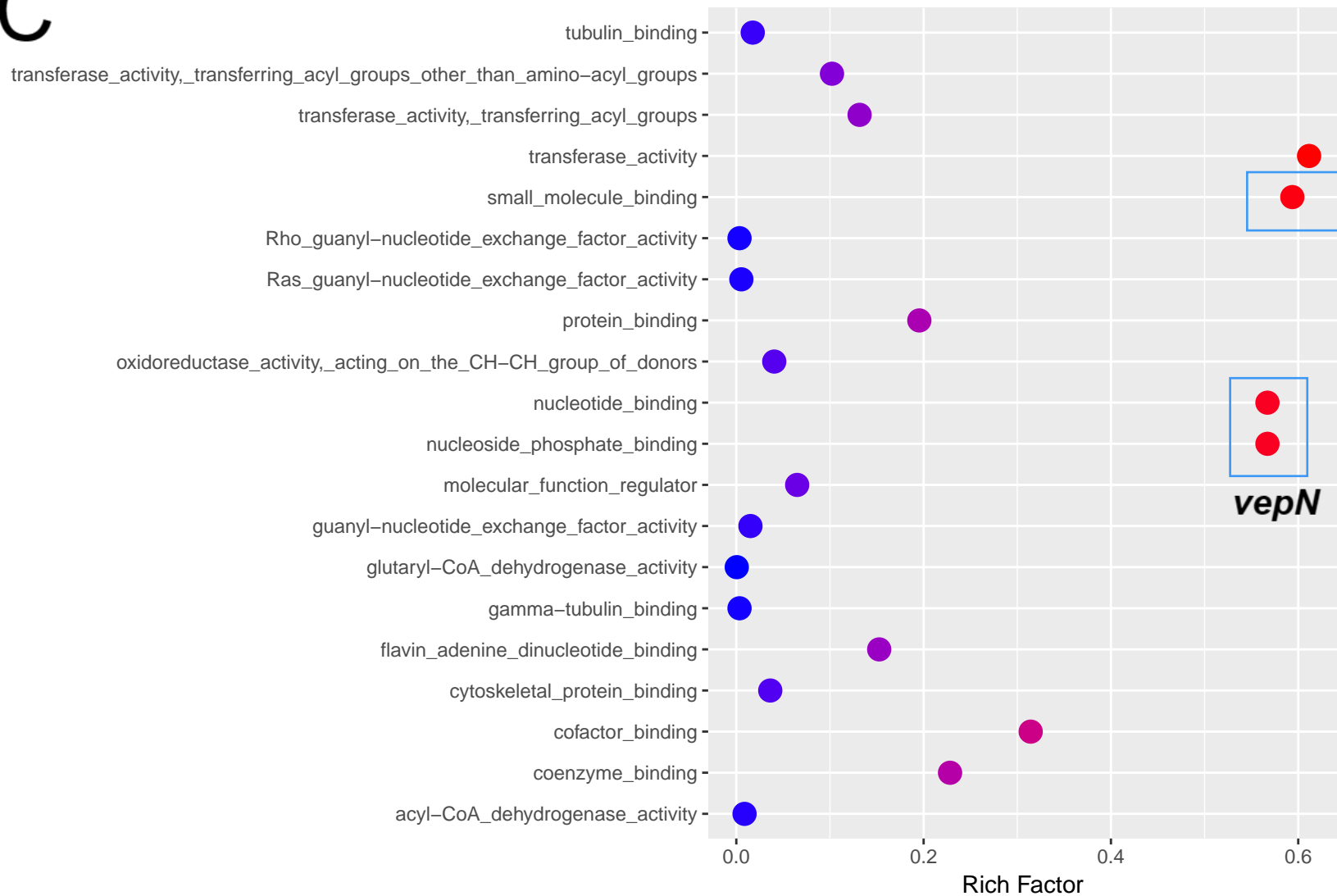
pvalue



C

## Statistics of GO Enrichment

GO Term

*vepN*

pvalue

0.6

0.4

0.2

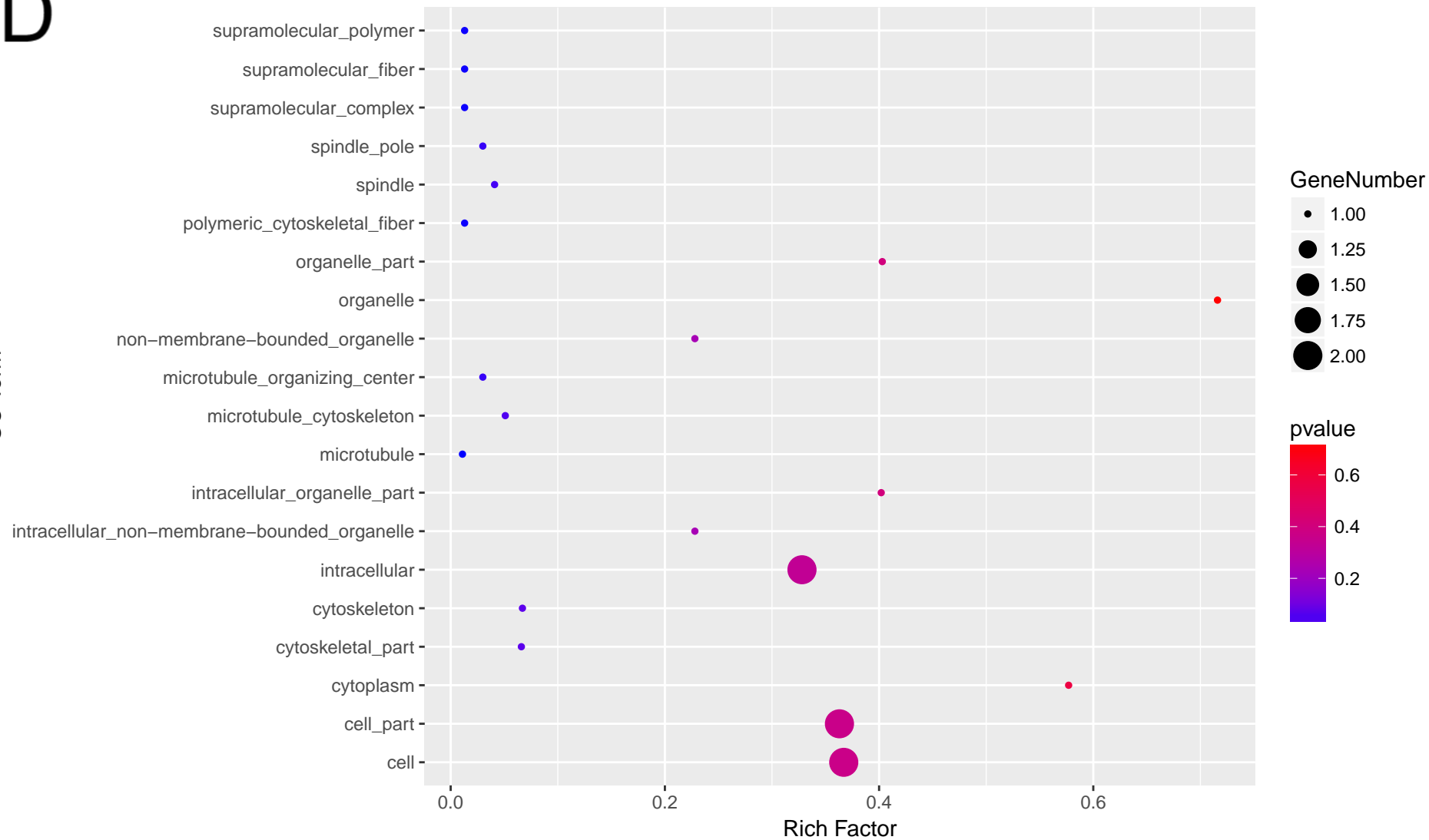
GeneNumber

● 1

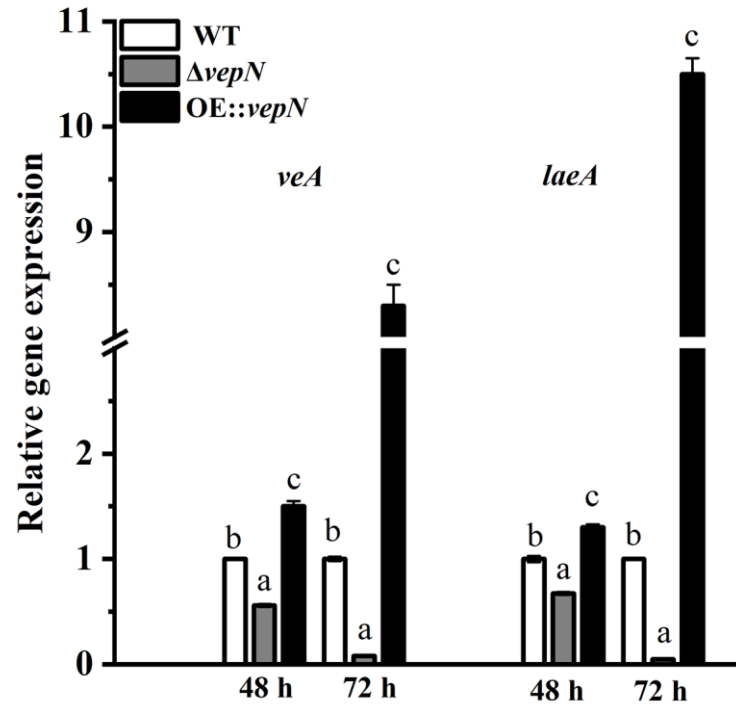
D

## Statistics of GO Enrichment

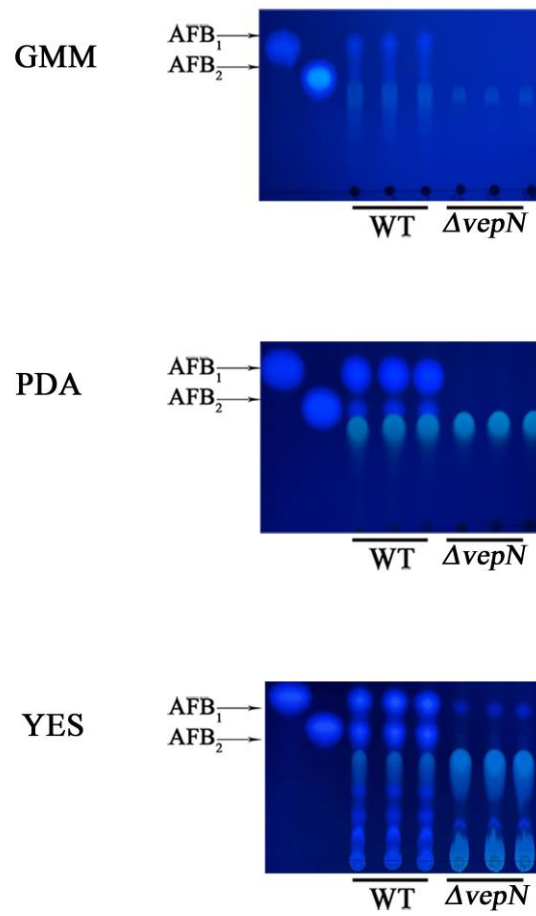
GO Term



**Figure S1.** GO analysis and statistics of GO enrichment. **(A)** GO analysis. BP: biological process; MF: molecular function; CC: cellular component. **(B)** Statistics of GO enrichment in BP. **(C)** Statistics of GO enrichment in MF. **(D)** Statistics of GO enrichment in CC. The experimental results of the CHIP-seq performed with the VeA antibody are displayed by the results of the GO analysis. The *vepN* gene is enriched in MF, exhibiting binding activity, specifically in nucleotide binding, small molecule binding, nucleoside phosphate binding (It has been marked with a blue border in Figure S1C.)



**Figure S2** The q-PCR analysis of *veA* and *laeA* genes for conidiation. The strains were cultivated on PDA at 30°C for 7 days and then transferred to PDB, cultured for 12 hours. The relative expression was calculated using the method of  $2^{-\Delta\Delta C_t}$ . The expression of 18S rRNA was used as an internal reference. Values were normalized to the expression levels in the wild-type, considered as one. Error bars represent the standard errors. Error bars represent the standard errors and different letters above the bars represent significantly different values ( $p < 0.05$ ).



**Figure S3** AFB production examined by TLC cultured on GMM, PDA and YES media for 5 days at 30°C.