

## Supplementary figures

**Figure S1: Proteins-protein interactions (PPIs) map.** PPIs between *A. fumigatus* proteins coded by positively selected genes (PSGs) and human proteins. Orange - *A. fumigatus* proteins and blue - human proteins.

**Figure S2: Gene Ontology (GO) overrepresentation analysis.** Biological process (GO) significantly overrepresented in human proteins targeted by *A. fumigatus* virulence related proteins coded by multi-copy category positively selected genes (PSGs).

**Figure S3: *A. fumigatus* and *A. fischeri* genome synteny map.** Image was generated using the Mauve genome alignment tool. Upper and lower lines of the genomes correspond to *A. fumigatus* and *A. fischeri* respectively. Red vertical bars indicate concatenated chromosomal boundaries. Color-coded syntenic blocks indicate conserved segments (LCBs; Locally Collinear Blocks) identified by Mauve (minimum LCB weight = 999). Plots of sequence similarity are shown within each syntenic block. Regions with no color indicate no detectable homology between the two genomes with the settings used in Mauve. Unmatched regions (white area) within an LCBs indicate the presence of strain-specific sequence. The connecting lines between blocks indicate the location of each block in two genomes. Homologous regions with possible rearrangements are shown in first row.

### Figure S1

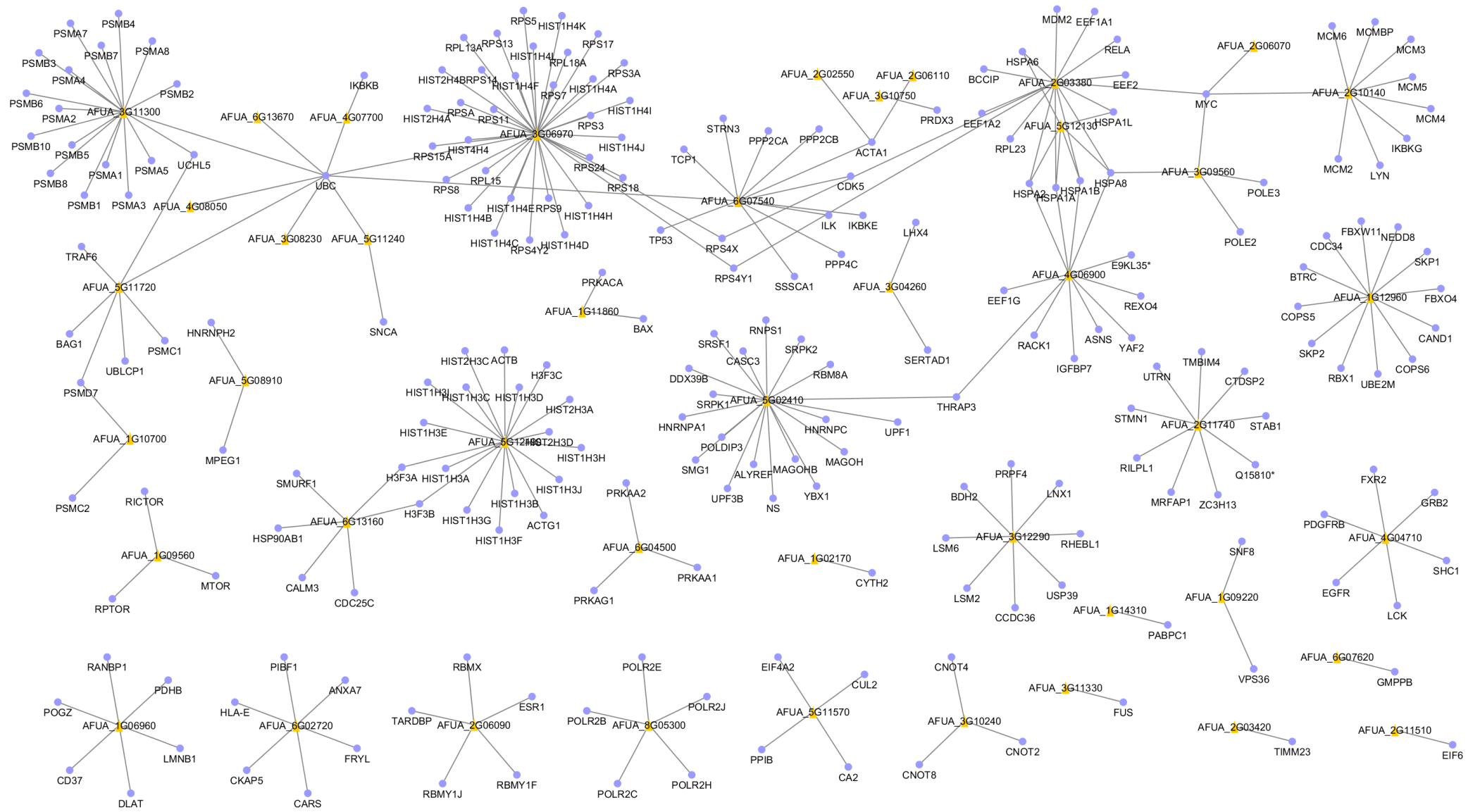


Figure S2

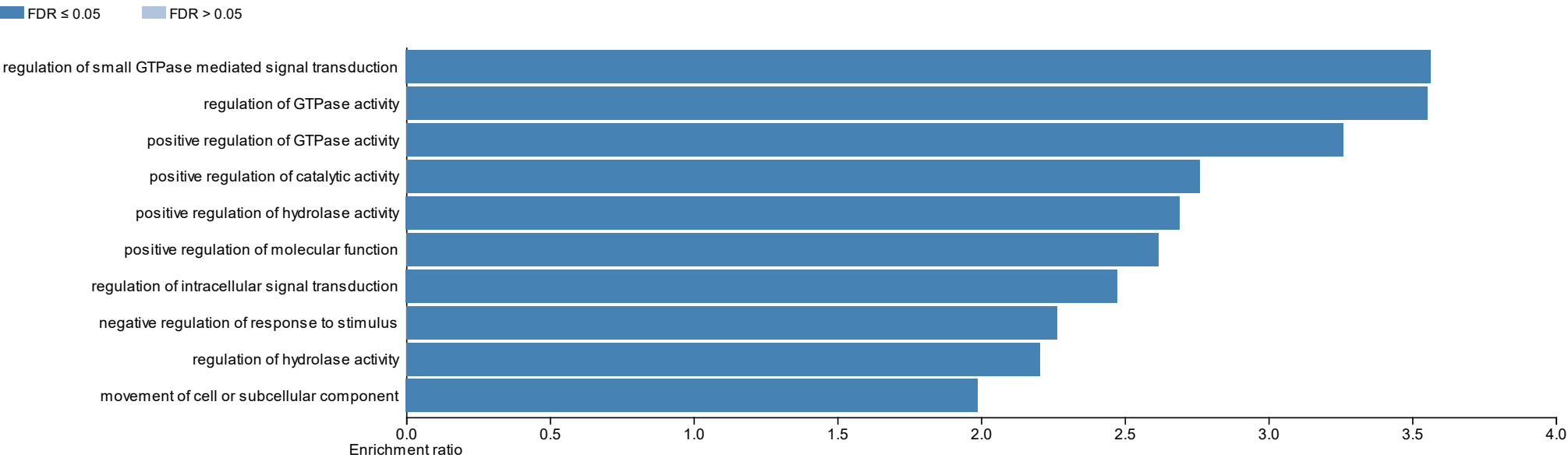


Figure S3

