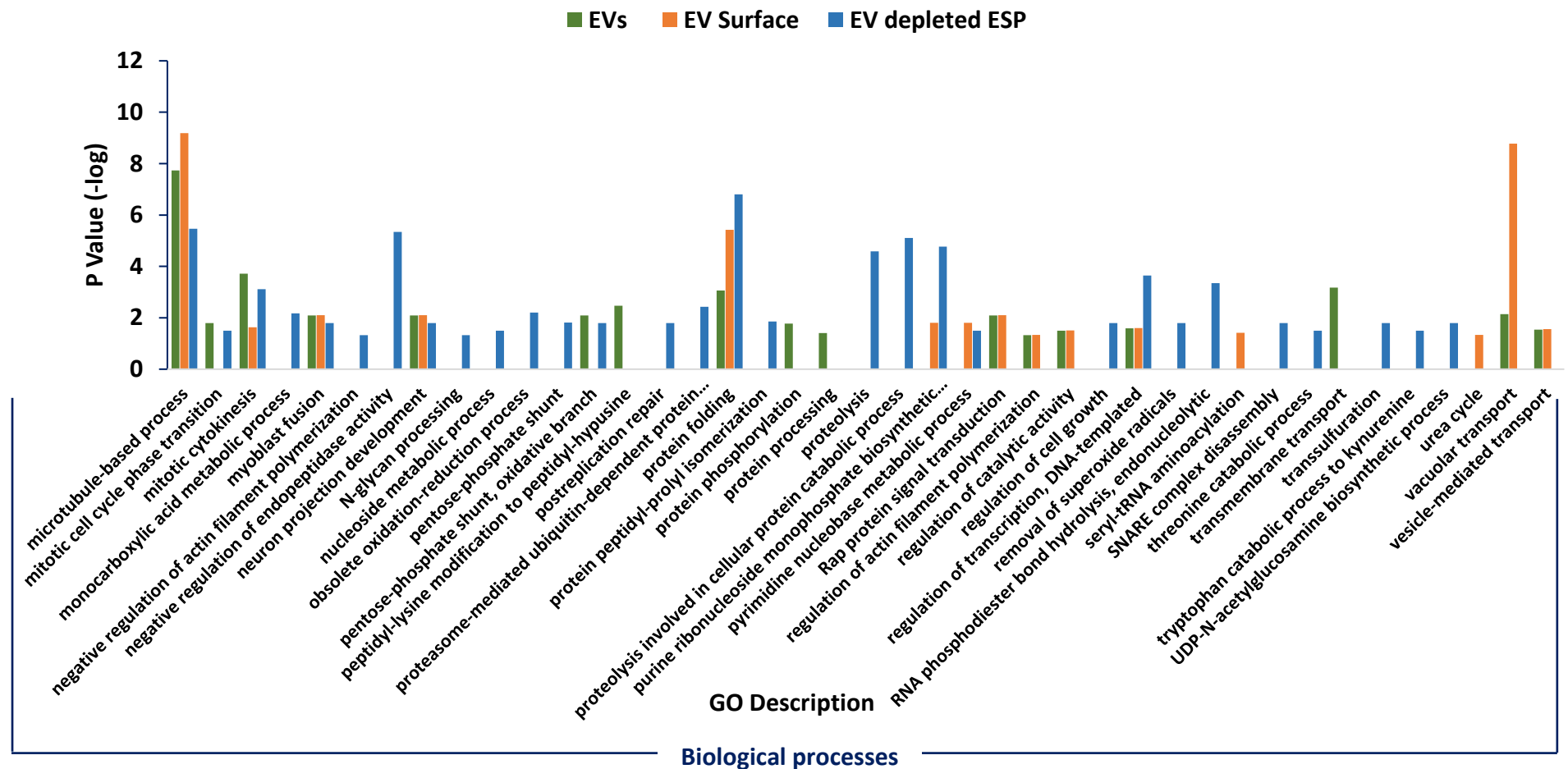
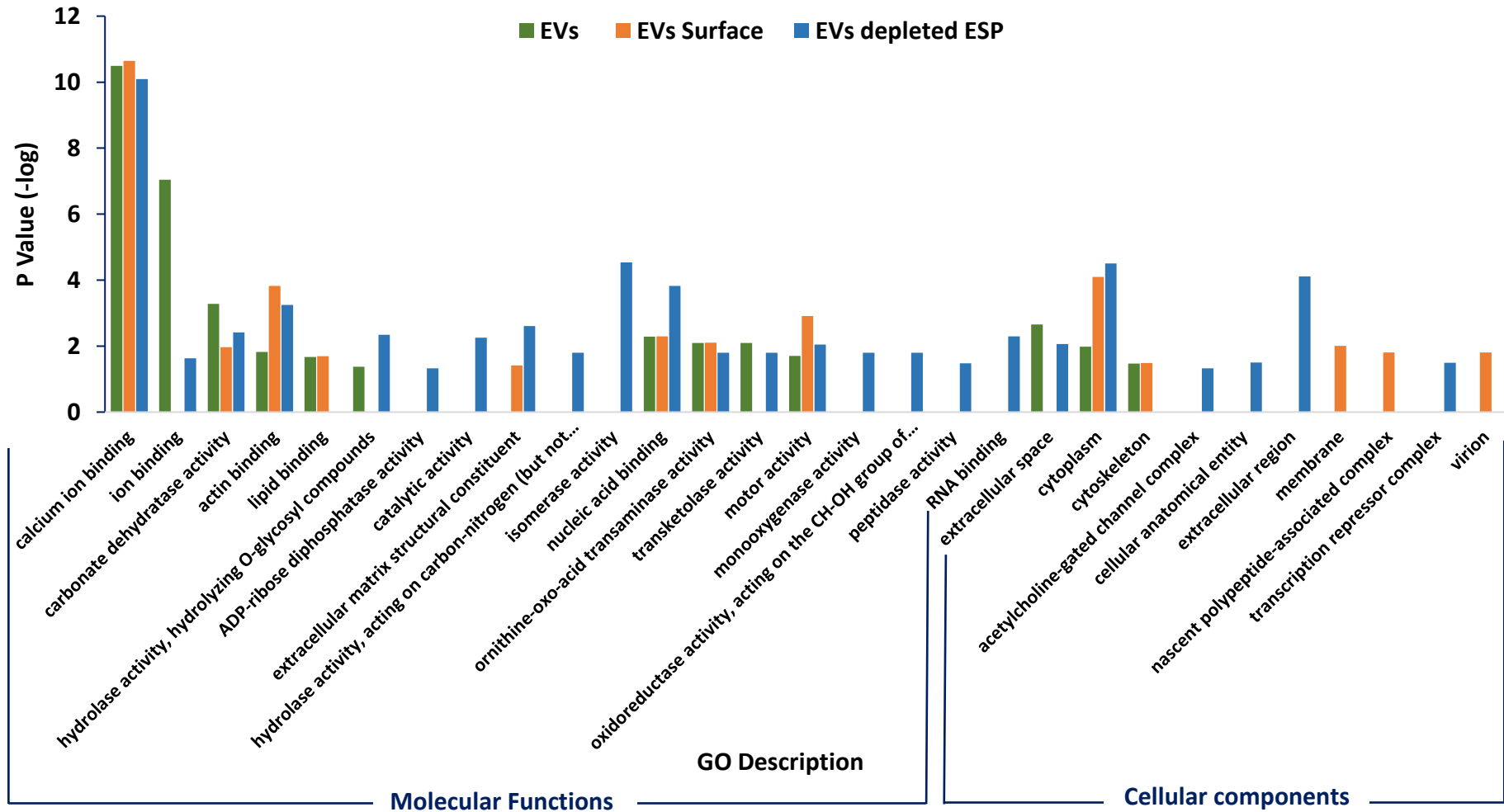


**Supplementary Figure S6.** Gene ontology enrichment analysis using GOATOOLS in python comparing all 3 proteomic datasets from the *A. perfoliata* secretome compared to the whole *A. perfoliata* transcriptome for the Biological process functional category. GO terms were not propagated up the hierarchy (nop) ( $p < 0.05$  identified significance) and where enriched in all or any of the 3 proteomic datasets were presented using -log transformation of  $p_{\text{uncorrected}}$  value and GO description.



**Supplementary Figure S6-continued 2.** Gene ontology enrichment analysis using GOATOOLS in python comparing all 3 proteomic datasets from the *A. perfoliata* secretome compared to the whole *A. perfoliata* transcriptome for the Biological process functional category. GO terms were not propagated up the hierarchy (nop) ( $p < 0.05$  identified significance) and where enriched in all or any of the 3 proteomic datasets were presented using -log transformation of  $p_{\text{uncorrected}}$  value and GO description.



**Supplementary Figure S6-continued 3.** Gene ontology enrichment analysis using GOATOOLS in python comparing all 3 proteomic datasets from the *A. perfoliata* secretome compared to the whole *A. perfoliata* transcriptome for the Molecular functions and Cellular components functional categories. GO terms were not propagated up the hierarchy (nop) ( $p < 0.05$  identified significance) and where enriched in all or any of the 3 proteomic datasets were presented using  $-\log$  transformation of  $p_{\text{uncorrected}}$  value and GO description.