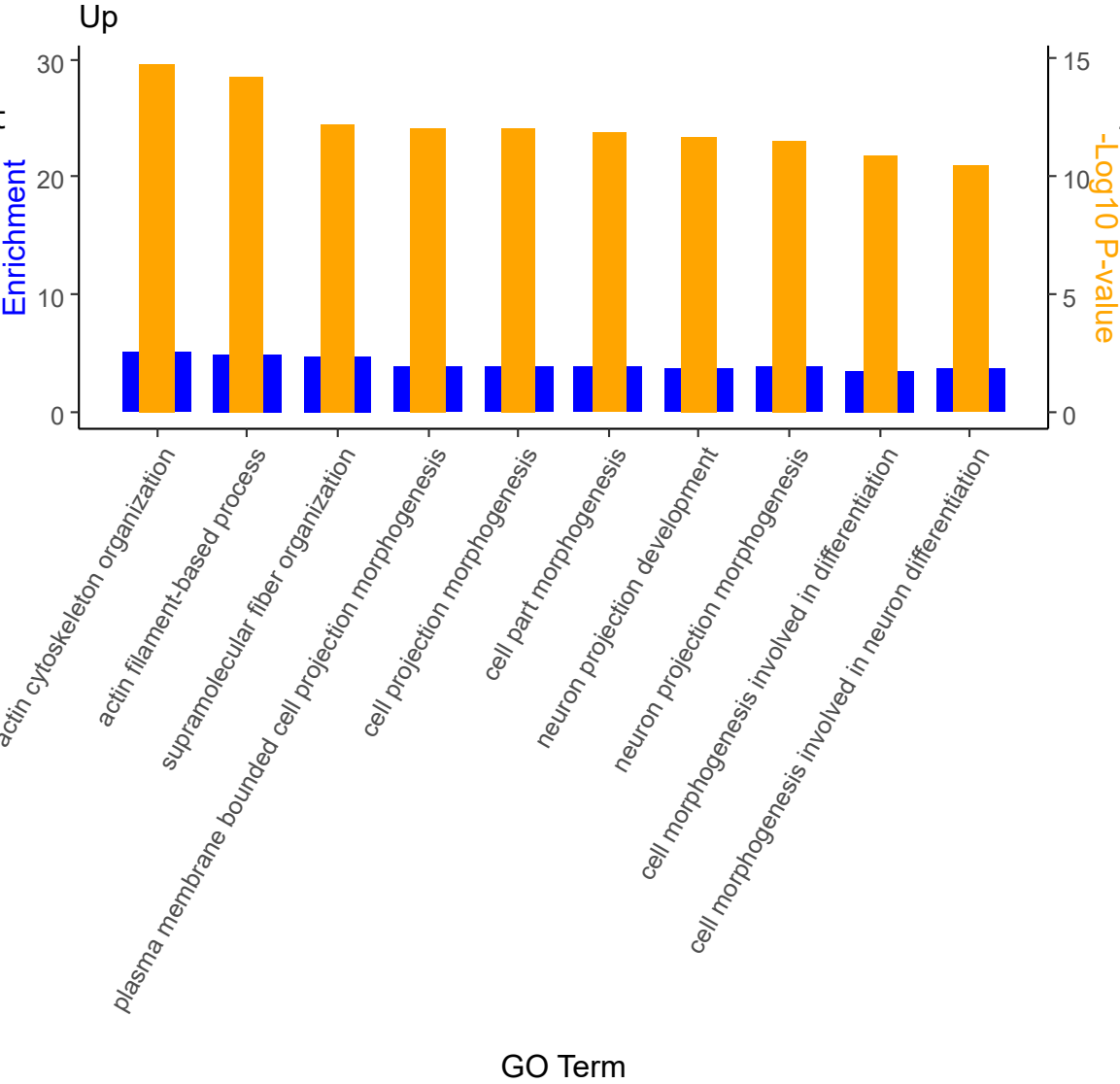# GO Bar Plot

Title will describe which subset of terms are represented in plot
Top Ten Significant terms (<500genes/term**)
Up

Left axis and blue bars represent term enrichment (See below)

Right axis and orange bars represent term significance (See below)

GO Term

Gene Ontology enrichment analysis is a hypergeometric test that examines what proportion genes belonging to a gene ontology group (e.g. pathway) are found in a query (e.g. differentially expressed genes) and compares it to the proportion of genes belonging to the GO group from the background (i.e. all genes analyzed). An enrichment value is calculated using the following equation:

$$Enrichment = \frac{{}^{\#Genes\ from\ query\ found\ in\ GO\ term}\big/_{\#Genes\ in\ query}}{{}^{\#Genes\ from\ background\ found\ in\ GO\ term}\big/_{\#Genes\ in\ background}}$$

This equation is also used to determine the probability (significance) that the number of genes from the GO term will be found in a random selection of genes the same size as the query using a hypergeometric distribution.

*Occasionally this figure will be shown with both up/down regulated pathways in one pathway
** Note that the subset will identify the maximum/minimum number of genes/term ('#Genes in query'). This subsetting helps to ensure more relevant pathways will be featured - all enriched pathways will be provided in the raw results files.