

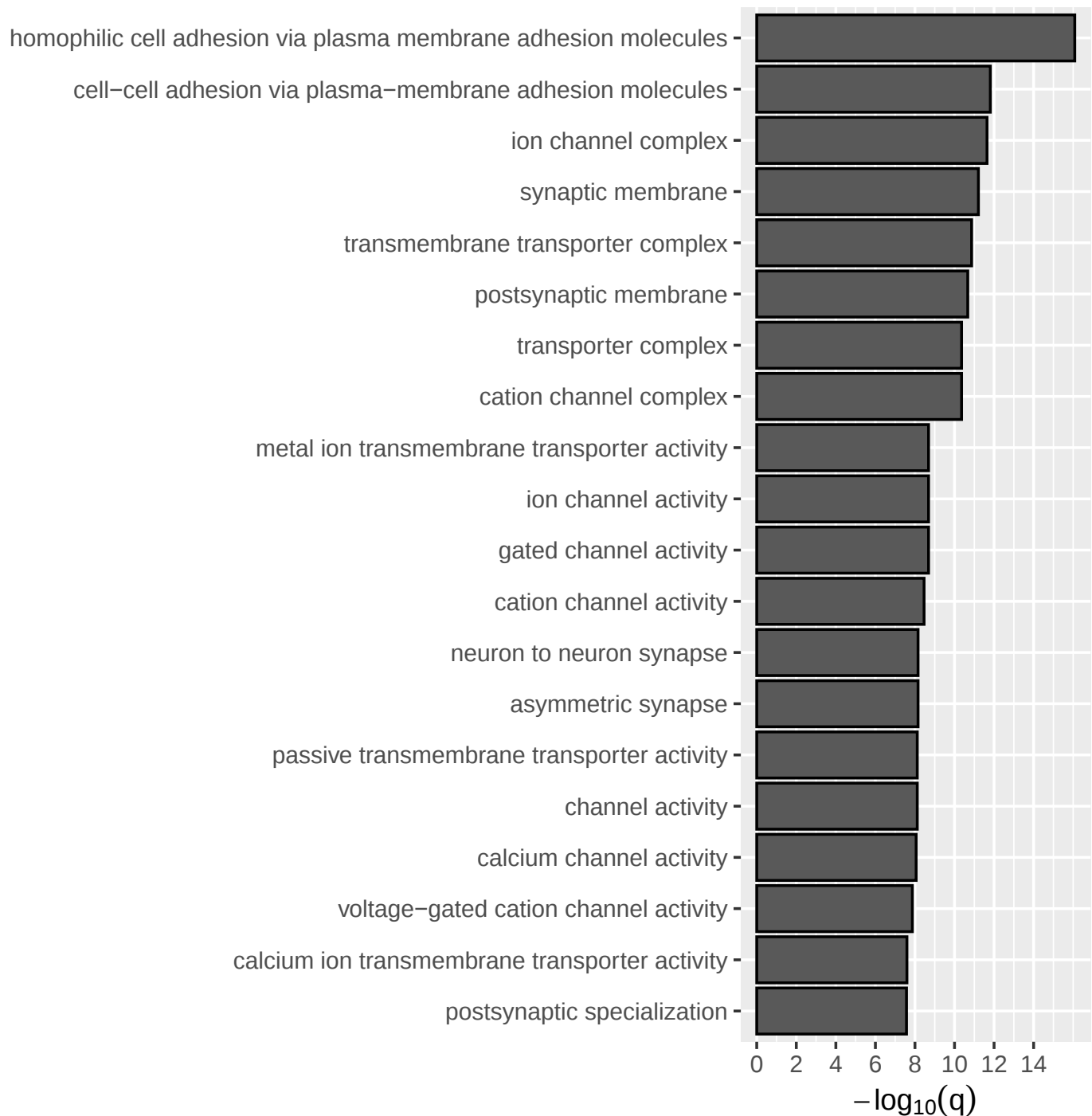


Figure S4: Enrichment of gene ontology (GO) terms for candidate genes that showed either decreased methylation (1,151 genes) or increased methylation (71 genes) of at least one CpG in at least 7 of 14 patients. The x-axis represents the $-\log_{10}(q)$ of the obtained q-value and the y-axis shows the corresponding significantly enriched GO terms.