

Genes involved in *response to oxidative stress* and *cellular response to stress* contribute to the relatively low mean CpG_{O/E} for the *stress response* Gene Ontology term.

The figure illustrates the variation in CpG_{O/E} of Gene Ontology (GO) terms nested within stress response. Each bar represents mean CpG_{O/E} for the indicated GO term and its standard error. Asterisks indicate significance of enrichment in the low- or high-CpG components (* < 0.05, ** < 0.01, *** < 0.001; Fisher's test). The bar labeled 'stress response reduced' represents the *stress response* GO term with genes from *response to oxidative stress* and *cellular response to stress* removed. GO terms with fewer than 20 representative genes were not plotted.

