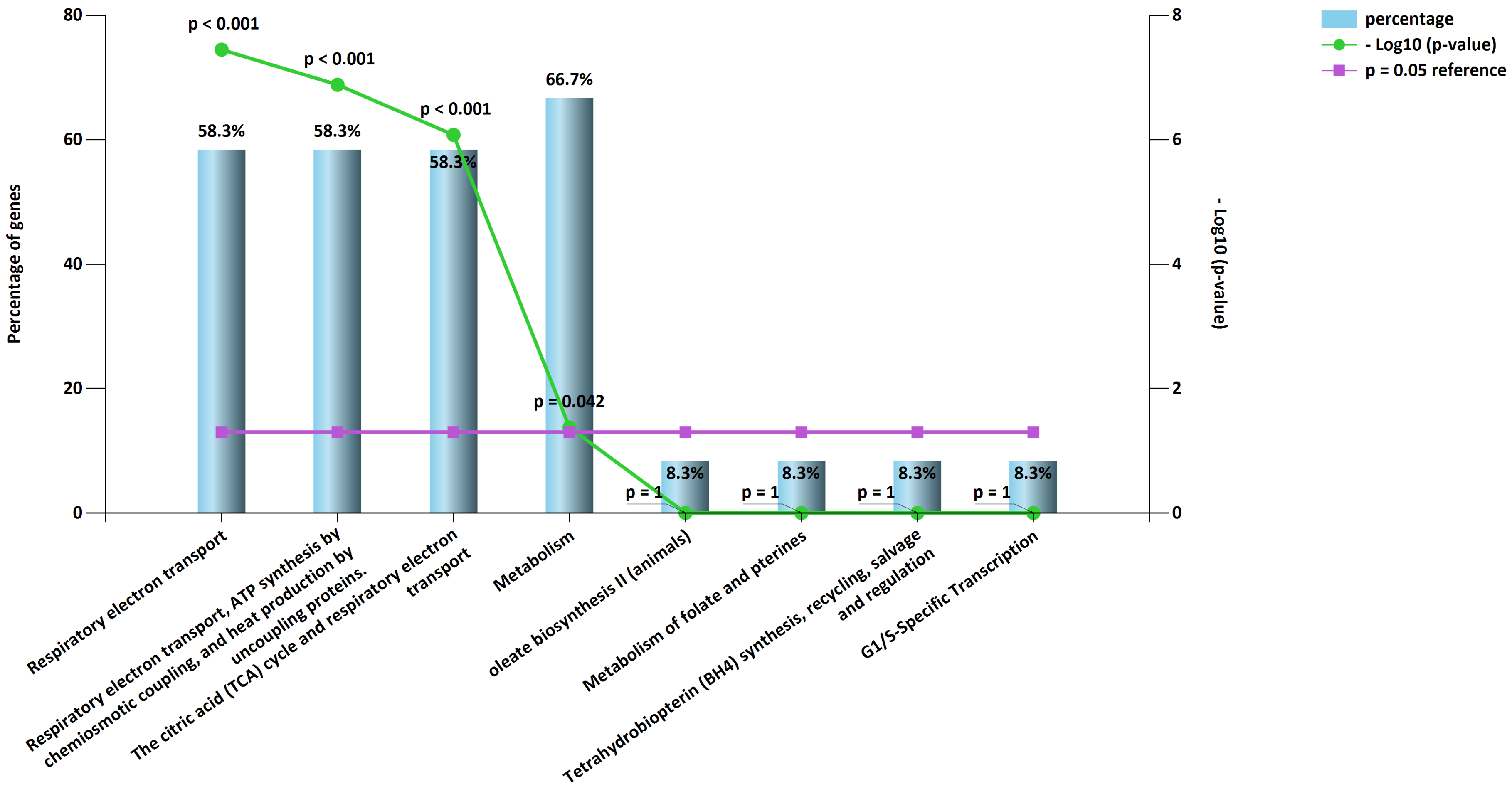

Supplementary figure 3. Functional enrichment based on the biological process GO category of differentially expressed mitochondrial proteins identified by TMT-based quantitative proteomic analysis of MC2494-treated *versus* untreated U937 cells. Enrichment analysis was performed using FunRich software. Percentages of mapped proteins/genes and p-values based on a hypergeometric test are reported in bar graphs along with reference p-value (p = 0.05).

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