



**Figure S4. The MMS-inducible proteins (in abundance) are enriched in the functional categories of oxidation-reduction processes and metabolism processes.** Gene ontology enrichment analysis was conducted on the 56 MMS-induced proteins ( $\geq 2\sigma$  or 1.5-fold) using the Funspec software package (<http://funspec.med.utoronto.ca/>). After inputting the 56 gene names and setting the p-value cut-off as  $10^{-6}$ , the following processes were found to be enriched: oxidation and reduction ( $p < 10^{-14}$ ), deoxynucleotide biosynthesis ( $p = 1.3 \times 10^{-10}$ ), metabolism ( $p = 9.7 \times 10^{-10}$ ).