

Combined Gene Expression and RNAi Screening to Identify Alkylation Damage Survival Pathways from Fly to Human

Fig. S1 Time course of MMS-induced gene expression alterations in Kc167 cells.

(A) Description of MMS upregulated genes over 8, 24 and 72 h treatments in fly Kc167 cells. (B) Distribution of the 52 MMS survival hits with upregulated gene expressions over 8, 24 and 72 h treatments in fly Kc167 cells. In A and B, genes are annotated to their respective time points of upregulation. (C) Fold changes of MMS survival hits with concomitant up (52 genes) and downregulated (26 genes) expressions over 8, 24 and 72 h MMS treatment. (D) Representative pathways associated with MMS upregulated genes in 8 h compared to combined 8, 24 and 72 h gene lists shows better enrichments in combined analysis.

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(TIF)

Fig. S2 Venn Diagrams of pathways associated with MMS survival hits and microarray changes.

Detailed Venn diagrams of Pathway terms associated with MMS induced genes (microarray), RNAi survival hits (RNAi screening) and fusion (microarray+RNAi screening). In the bottom-right graph, the antilog p-values of pathway enrichments in each part of Venn diagram are shown. Pathway terms overlapping between two platforms show more significant p-values than orphan terms.

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(TIF)

Table S1 Differentially expressed genes in MMS-treated Kc167 cells.

MMS-induced changes in gene expression of fly Kc167 cells (8, 24 and 72 h) as determined by microarray. Essentiality of each gene for MMS survival is also annotated as previously determined by Ravi *et al.* 2009 [1].

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(XLSX)

Table S2 Detailed Pathway Enrichment Analysis (PEA) of MMS-treated Kc167 cells.

Pathway Enrichment Analysis (PEA) of MMS-induced genes (microarray), RNAi screening survival hits (from [1]), and fusion of microarray/RNAi screening gene lists in Kc167 *D. melanogaster* cell line treated with MMS.

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(XLSX)

Table S3 Alkylation-induced changes in NRF2 and UPR genes in fruitfly cells.

NRF2-GSH and UPR/ER stress pathway gene expression changes in Kc167 cells treated with 40 µg/mL MMS for 8 and 24 h as determined by microarray. Essentiality of each gene for MMS survival is annotated as previously determined by Ravi *et al.* 2009 [1]

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(XLSX)

Table S4 MMS-induced pathways in mouse and human cells.

Pathway Enrichment Analysis (PEA; Ingenuity) of alkylation-induced gene expressions in MDA-MB231 and MEF cells treated with 40 µg/mL MMS for 8 h as determined by RNA sequencing and microarray, respectively.

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(XLSX)