LEGEND TO SUPPLEMENTAL TABLES

Supplemental Table S1.

Forty-eight hours after transfection of either Ctrl siRNA or miR-519, total protein was prepared as explained in the Materials and Methods section. Red, proteins showing higher abundance in miR-519-transfected cells (using 2.18 as cut-off); green, proteins showing lower abundance in miR-519-expressing cells (using 0.5 as cut-off). Protein showing intermediate changes were excluded from the table.

Supplemental Table S2.

Forty-eight hours after transfection of either Ctrl siRNA or miR-519, total RNA was extracted and differences in mRNA levels were identified by microarray analysis (Materials and Methods). After three independent microarray analyses, for each mRNA showing significantly different Z-ratios and Fold differences, the gene Symbols, Accession numbers, and definitions are listed. Analysis was performed as previously described (3).

Supplemental Table S3.

Forty-eight hours after transfection of either biot-Ctrl-miR or biot-miR-519, lysates were prepared and the associated RNA was pulled down using streptavidine beads and identified by microarray analysis as described [(31) and Materials and Methods]. Listed are mRNAs displaying significantly different Z-ratios and Fold differences (indicating their gene Symbols, Accession numbers, and definitions) in three independent pulldown and microarray analyses.

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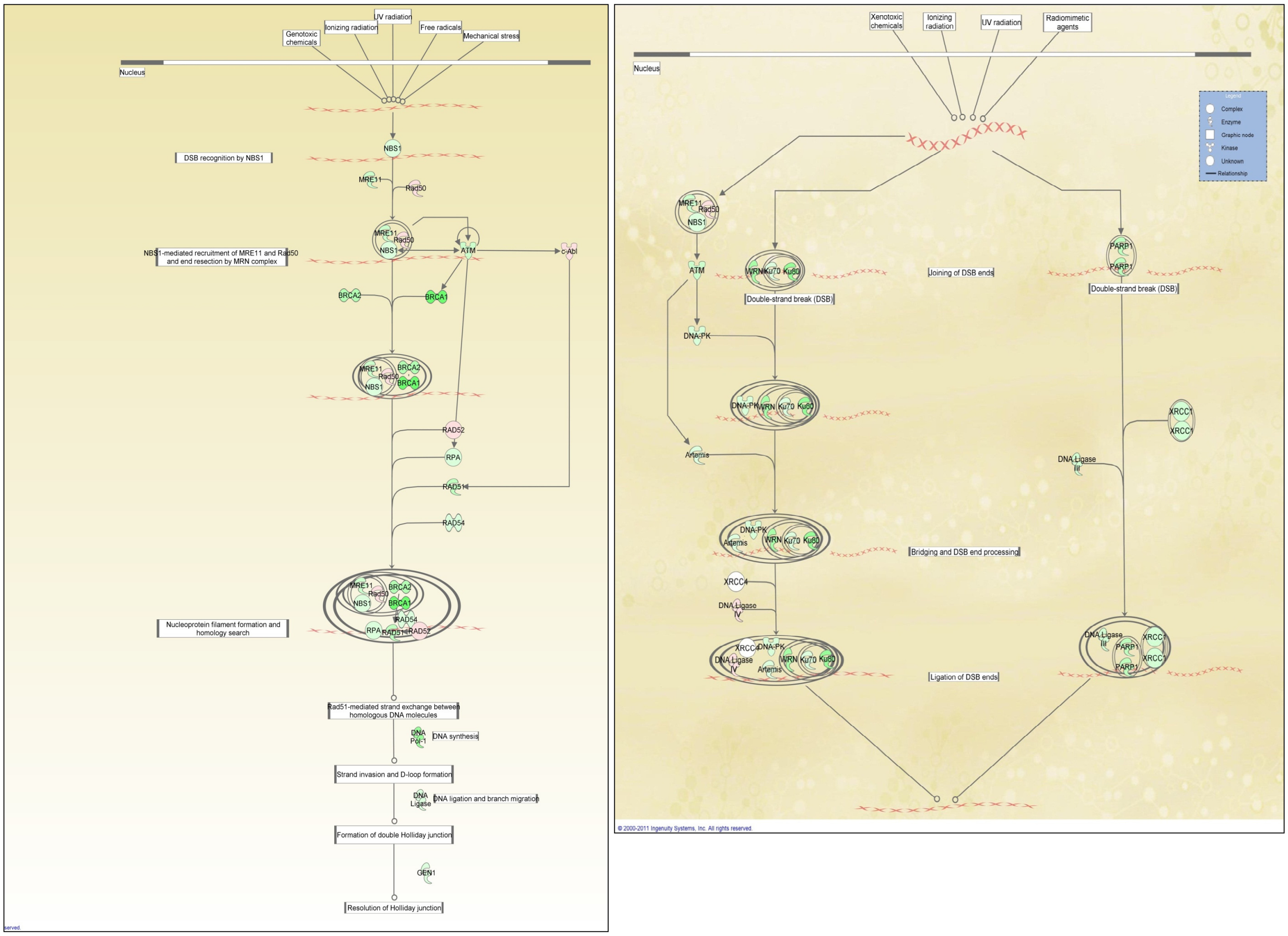
Path Designer DNA Double Strand Break Repair by Homologous Recombination

Path Designer DNA Double Strand Break Repair by Non-Homologous End Joining

Supplemental Figure S1. Ingenuity analysis of the pathways in which proteins affected by miR-519 (green: upregulated; red: downregulated) are known to participate.