

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Proteome data for all normally transcribed genes (transcript fold change <1.5 and >-1.5) and codon usage for Lys, Gln, and Glu.

File Name: Supplementary Data 2

Description: Numerical data for Fig. 3b-e.

File Name: Supplementary Data 3

Description: List of genes within the mouse ORFeome that meet stringent indicators of Elongator dependence (≥ 1755 codons with AA:AG >1.3 or ≤ 150 codons with AA:AG <0.3).

File Name: Supplementary Data 4

Description: List of genes within the human ORFeome that meet less stringent indicators of Elongator dependence (≥ 1005 codons with AA:AG >1.3 or ≤ 150 codons with AA:AG <0.3).

File Name: Supplementary Data 5

Description: Potential Elongator targets: genes that were transcribed normally (transcript fold change < 1.5 and > -1.5) and consist of ≥ 1755 total codons with an AA:AG ratio > 1.3 .

File Name: Supplementary Data 6

Description: Misregulated double-strand break repair genes (protein fold change ≤ -2.0 , or ≥ 2.0).

File Name: Supplementary Data 7

Description: Codon usage of genes involved in double-strand break repair via nonhomologous end joining (NHEJ).

File Name: Supplementary Data 8

Description: Potential Elongator targets: genes that were transcribed normally (transcript fold change < 1.5 and > -1.5) and consist of ≤ 150 total codons with an AA:AG ratio < 0.2 .

File Name: Supplementary Data 9

Description: List of upregulated genes that were used to determine GO biological processes: genes encoding proteins with a fold change ≥ 2 and an AA:AG ratio < 0.3 and transcript size ≤ 300 codons.