**Supplemental Methods**

**3’ RNA sequencing**

Systematic transcriptome analysis was performed by 3' RNA Sequencing using the 3' QuantSeq kit (Lexogen, Vienna, Austria). 500 ng of total RNA was used as input for the proctocol which was subsequently performed according to the standard protocol provided by the manufacturer. Upon quantity and quality assessment using TapeStation high sensitvity DNA assay (Agilent), sequencing was performed on a HiSeq 2500 (Illumina) in Rapid Mode and on-board clustering, with 50 bp single reads and an index of 6 bp. Raw sequencing reads were converted and demultiplexed using the bcl2fastq tool (v.1.8.4, Illumina). Alignment of sequencing reads to the human hg38 reference genome was performed using STAR aligner (v2.5.2) (1) and expression was quantified as counts per gene with RSEM (v1.2.31) (2). Differential gene expression and log2 gene expression fold-changes between DMSO controls and treated cells were calculated from count level data using DESeq2 (3). Resulting p-values were adjusted using Benjamini-Hochberg correction(4) (for visualization minimal adj. p-values were set to 10-12). To investigate the overrepresentation of biological functions among differentially expressed genes we performed a gene ontology (GO) enrichment analysis of up- or downregulated genes significant at an adjusted p-value < 0.01 with the online tool DAVID (david.ncifcrf.gov, 07/2016) including GO terms for biological process or molecular function and KEGG pathways(5,6). RNA-seq data was uploaded to the European Molecular Biology Lab’s ArrayExpress (www.ebi.ac.uk/arrayexpress, E-MTAB-5150).

1. Dobin A, Davis CA, Schlesinger F, Drenkow J, Zaleski C, Jha S, et al. STAR: ultrafast universal RNA-seq aligner. Bioinformatics. 2013;29:15–21.

2. Li B, Dewey CN. 1471-2105-12-323. BMC Bioinformatics. BioMed Central Ltd; 2011;12:323.

3. Love MI, Huber W, Anders S. Moderated estimation of fold change and dispersion for RNA-seq data with DESeq2. Genome Biol. 2014;15:31.

4. Benjamini Y, Hochberg Y. On the adaptive control of the false discovery rate in multiple testing with …. Journal of Educational and …. 2000.

5. Huang DW, Sherman BT, Lempicki RA. Systematic and integrative analysis of large gene lists using DAVID bioinformatics resources. Nat Protoc. 2009;4:44–57.

6. Huang DW, Sherman BT, Lempicki RA. Bioinformatics enrichment tools: paths toward the comprehensive functional analysis of large gene lists. Nucleic Acids Res. 2009;37:1–13.