

## Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Membrane-to-cytosol enrichment as determined by RNA-seq including the determined localization category (membrane or cytosol), expression level (tpm\_wt), enrichment (log2 fold change) and DESeq2-derived P values adjusted for multiple comparisons. Wald test was used for comparisons.

File Name: Supplementary Data 2

Description: HDLBP PAR-CLIP signal per transcript including number of T-C transitions, uniquely mapping reads or number of clusters per compartment (5'UTR, CDS, 3'UTR or whole transcript)

File Name: Supplementary Data 3

Description: HDLBP PAR-CLIP clusters per replicate (1, 2) including chromosome coordinates (hg19) per cluster, number of T-C transitions, number of uniquely mapping reads per cluster, number of overlapping nucleotides between clusters, and the corresponding transcript region (5'UTR, CDS, 3'UTR).

File Name: Supplementary Data 4

Description: BioID results table including LFQ values and calculated enrichment per replicate (1-3), as well as mean enrichment and mean LFQ values.

File Name: Supplementary Data 5

Description: Differences in translation efficiency (TE - log2 fold change ribo rna) between wild-type (293) and knockout conditions (guide 1 or 2), as well as mean wild-type vs. knockout TE and DESeq2-derived P values adjusted for multiple comparisons. Likelihood ratio test was used for comparisons.

File Name: Supplementary Data 6

Description: pSILAC results table including iBAQ values normalized SILAC heavy-to-medium (H/M) ratios per replicate (1, 2), mean H/M and per protein information with respect to the corresponding mRNA localization, targeting signal presence and HDLBP target category

File Name: Supplementary Data 7

Description: HDLBP PAR-CLIP tRNA enrichment table including T-C transitions in tRNA coordinates (tc\_start, tc\_stop), number of T-C transitions and total read coverage for every position in both replicates (TCnumber\_hdlbp2 TCnumber\_hdlbp3, allReadsPerPos\_hdlbp2 allReadsPerPos\_hdlbp3), sequence of the crosslink-centred 7-mer (seq\_tc\_middle\_t), normalized number of T-C transitions, mean fraction of T-C transitions over total coverage, standard deviation of fraction of T-C transitions over total coverage, T-C transition signal in whole tRNA normalized to the total tRNA abundance

File Name: Supplementary Data 8

Description: Xenograft tumor RNA-seq results table with upregulated and downregulated mRNAs in the HDLBP KO condition including mean of normalized read counts (baseMean), log2 fold changes, DESeq2-derived Padj values and TPM values for replicate experiments.