



Supplementary Figure 6. The uridylation activity of TUT4/7 is required for mRNA downregulation. **a**, qPCR analysis of different transcripts in *Tut4/7^{CTL}* (white) vs *Tut4/7^{cKO}* (black) pachytene spermatocytes is shown. The height of the bars represents the mean fold change, and the error bars the range. Each dot represents a biological replicate. Transcripts upregulated or unchanged in the array profiling are indicated. mRNAs that significantly change more than two-fold ($P < 0.01$) are indicated with a star. **b**, Ternary plot of mRNA expression levels from *Tut4/7^{CTL}*, *Tut4/7^{cKO}* and *Tut4/7^{cAAD}* pachytene cells. Upregulated transcripts in *Tut4/7^{cKO}* and *Tut4/7^{cAAD}* samples are highlighted in red ($P < 0.05$ and fold-change > 2 , moderated t-statistic adjusted; *Tut4/7^{CTL}*, $n=4$; *Tut4/7^{cKO}*, $n=3$; *Tut4/7^{cAAD}*, $n=4$). **c**, Gene ontology analysis of upregulated transcripts in TUT4/7-deficient pachytene cells. The enrichment for each term is shown. **d**, Number of histone transcripts with 3' end terminal additions in *Tut4/7^{CTL}* and *Tut4/7^{cKO}* pachytene spermatocytes. **e**, Scatter plot of mRNA vs protein expression fold change between *Tut4/7^{CTL}* and *TUT4/7^{cKO}* pachytene spermatocytes. Genes with proteins and transcript simultaneously changing (adjusted $P < 0.01$) more than two-fold are highlighted in red. The sensitivity of our mass spectrometry analysis allowed us to identify a total of 3604 proteins.

177 out of the 732 genes upregulated at the transcript level were detected. While only 1 in 40 genes with not upregulated transcripts show upregulation at the protein level, the ratio increases to 1 in 6 for genes with upregulated transcripts. The significance of the protein and transcript upregulation dependency evaluated using a Pearson's Chi-squared test is indicated at the panel top.