

Description of Additional Supplementary Files

File Name: Supplementary Data 1

Description: Analysis of nascent RNA-seq and total RNA-seq upon acute NANOG degradation. This dataset contains differential expression analyses of nascent RNA-seq and total RNA-seq in NANOG-AID cells following IAA-induced NANOG degradation. For nascent RNA-seq, changes at 2 h, 4 h, 8 h, and 24 h relative to 0 h are provided, including normalized read counts, log₂ fold changes, and adjusted p values; these data correspond to Figure 1. For total RNA-seq, changes at 2 h, 4 h, and 48 h relative to 0 h are summarized and correspond to Supplementary Figure 1. The final sheet (Fig 1D dataset) integrates nascent and total RNA results and lists co-regulated gene clusters (I-V) based on their expression dynamics.

File Name: Supplementary Data 2

Description: Mass Spectrometry analysis of RICK identified RBPs and UTP15 Co-IP. The first sheet (RICK) lists RNA-binding proteins captured by RNA Interactome using Click Chemistry (RICK) in NANOG-AID cells labeled with 5-ethynyluridine (EU) for 2 h and 6 h after IAA-induced NANOG degradation, compared with 0 h. It reports UniProt IDs, protein names, log₂ fold changes, calculated isoelectric points (pI), and regulation categories, corresponding to Figure 2 and Supplementary Figure 2. The second sheet (UTP15 Co-IP) summarizes proteins enriched by FLAG-tagged UTP15 co-immunoprecipitation in UTP15-AID cells, including protein names, UniProt IDs, p values, log₂ enrichment ratios, and normalized LFQ intensities.

File Name: Supplementary Data 3

Description: Analysis of total RNA-seq in UTP15-AID and summary of UTP15 ChIP-seq and UTP15 CLIP-seq peaks. This dataset compiles the peak information from UTP15 ChIP-seq and CLIP-seq experiments, alongside the normalized read counts and Fold Change data from UTP15 total RNA-seq under three conditions (IAA 0h, 24h, and 48h), including differential expression statistics for the comparisons of IAA 24h vs. 0h and IAA 48h vs. 0h.

File Name: Supplementary Data 4

Description: Summary of 685 UTP15 target genes. This dataset compiles the list of genes identified as direct targets of UTP15, providing their gene names, assigned chromosomes, and precise genomic locations

File Name: Supplementary Data 5

Description: List of primers and target sequences. This dataset compiles the essential nucleic acid sequences utilized throughout the manuscript, including the primer sets for quantitative PCR, the target guide RNA sequences designed for CRISPR-Cas9 mediated genome editing and shRNA mediated gene knock down, as well as the specific sequence of the spike-in RNA employed for normalization in nascent RNA-seq.