# Supporting Information

## SILAC-MS profiling of reconstituted human chromatin platforms for the study of transcription and RNA regulation

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**List of Supporting Information Tables (separate spreadsheet files)**

**Supplementary Table S1.** Gene Ontology analysis of all proteins enriched >1.5-fold in each of the Gal4-VP16 experiments. File contains three tabs. Tabs 1 and 2 contain GO analysis for the two label swap experiments, analyzing the Gal4-VP16 enriched protein ID list, list of proteins appears on the right. Green shading indicates transcription-related functions and gray shading indicates generic biological processes. Tab 3 represents a GO analysis of the proteins that had a ratio between 0.95-1.05 in the Light experiment, representing background proteins. All GO results with FDR <0.05 listed.

**Supplementary Table S2.** Gene Ontology analysis of the combined list of proteins enriched >1.5-fold in the two RepA-containing experiments (see Table 1). All GO results with FDR <0.05 listed.

**Supplementary Table S3.** Primer list for RNA Immunoprecipitation Reverse Transcription-qPCR analysis.

**Supplementary Table S4.** Full Protein ID list from Gal4-VP16 SILAC experiments with reproducible protein IDs and enrichments, light recombinant and contaminant proteins removed.

**Supplementary Table S5.** Full Protein ID list from RepA SILAC experiments with reproducible protein IDs and enrichments, light recombinant and contaminant proteins removed.