

Supplementary Figures S1-S5

Proteomic Analysis of the Mediator Complex Interactome in *Saccharomyces cerevisiae*

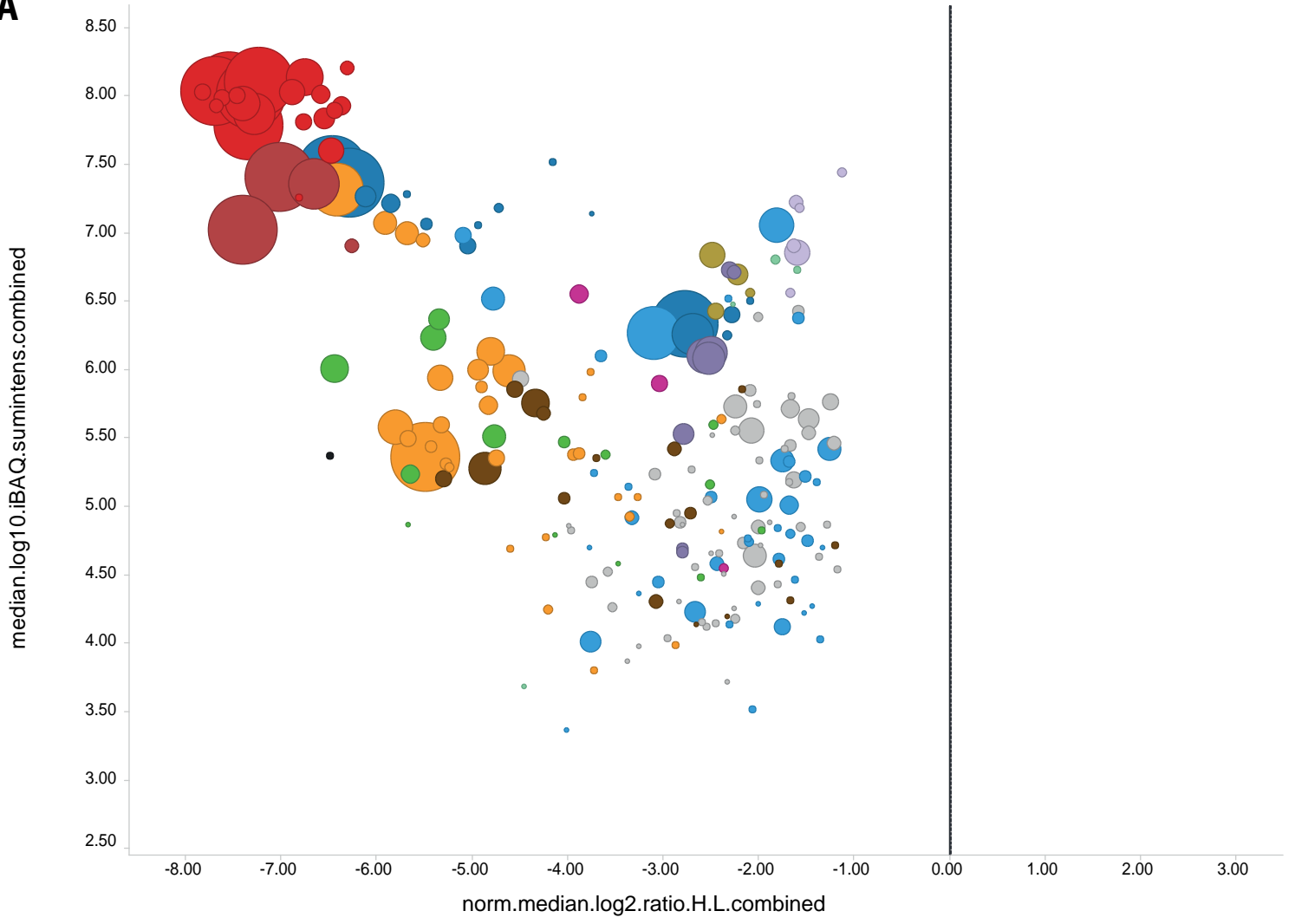
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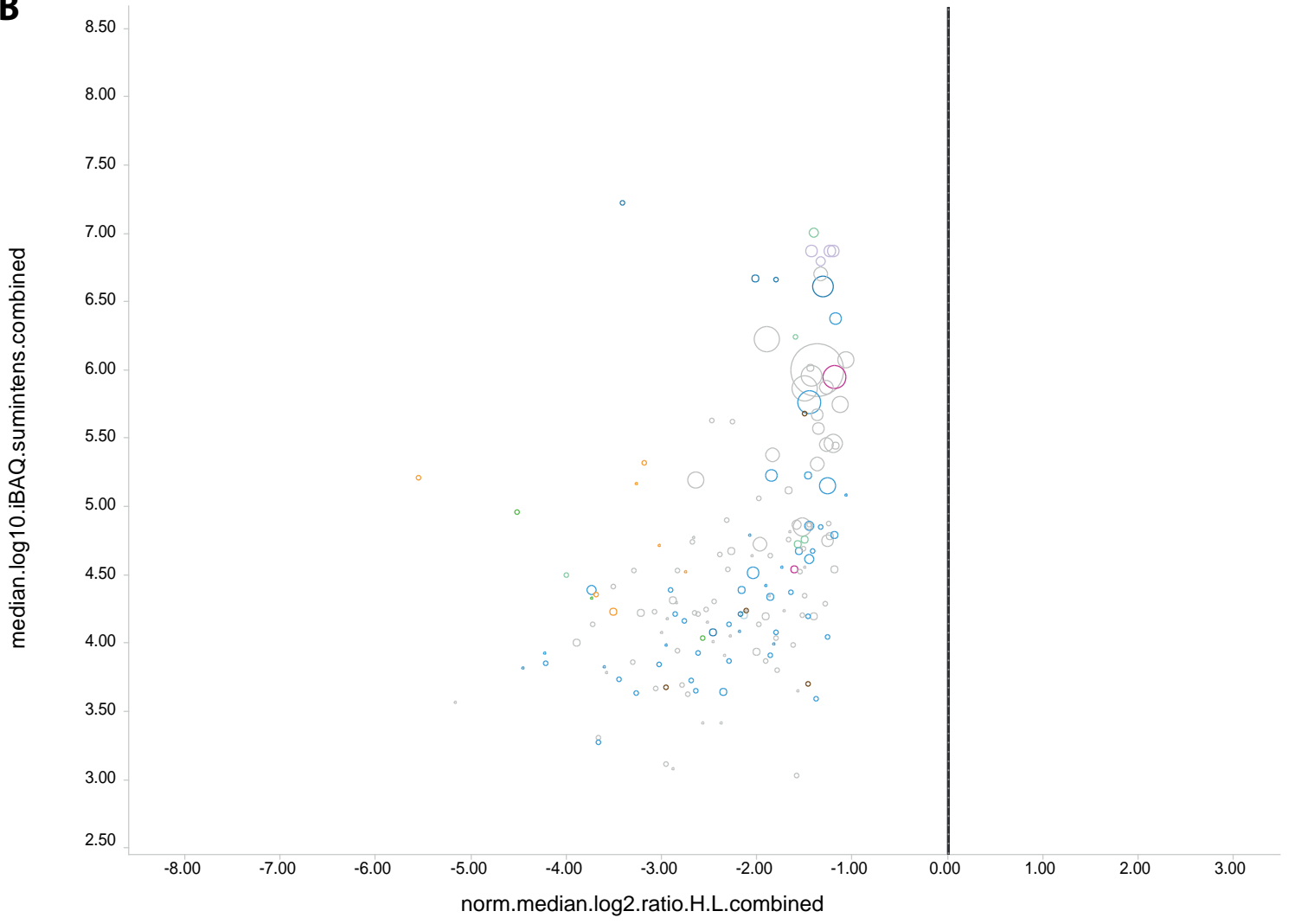
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A



B



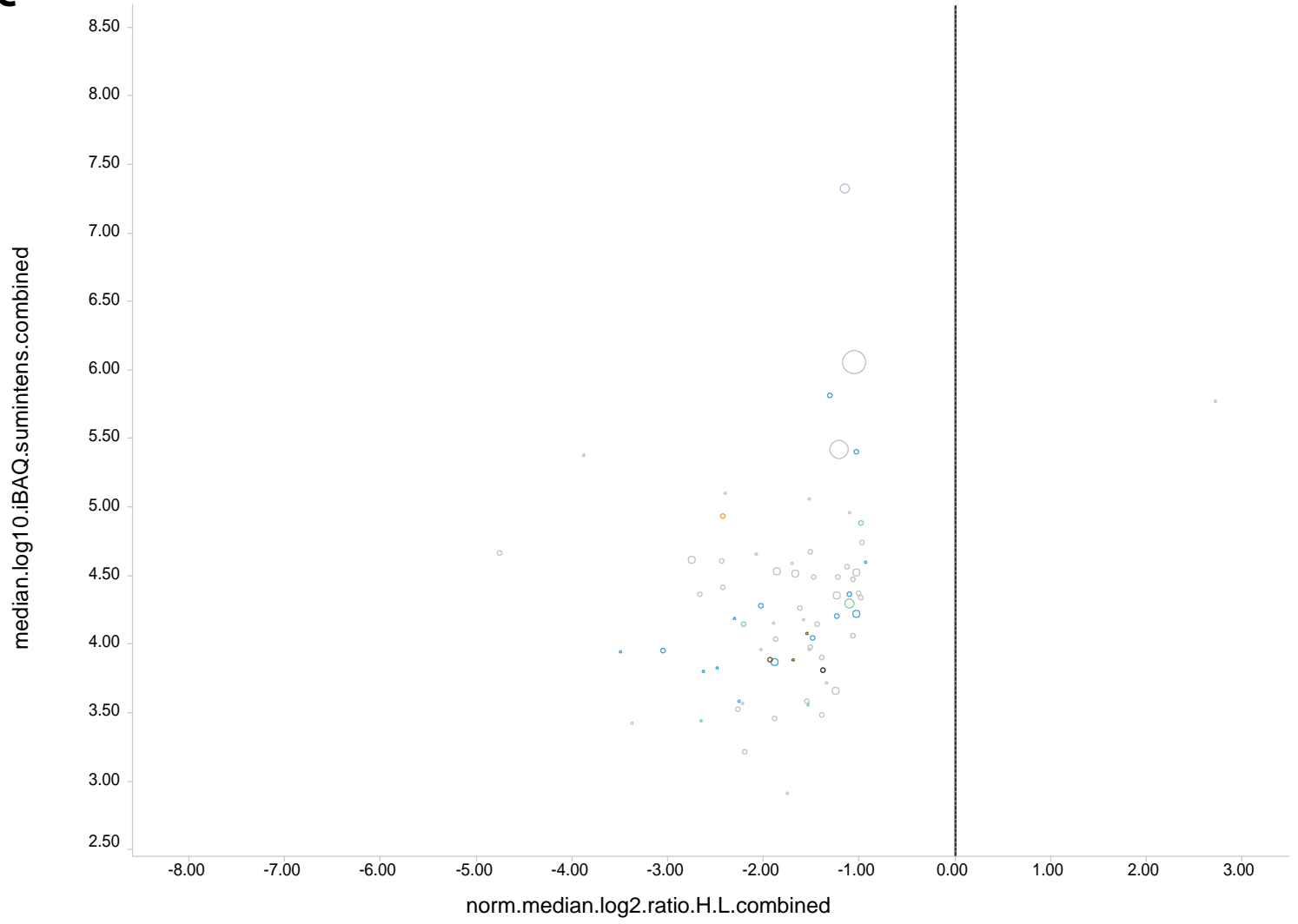
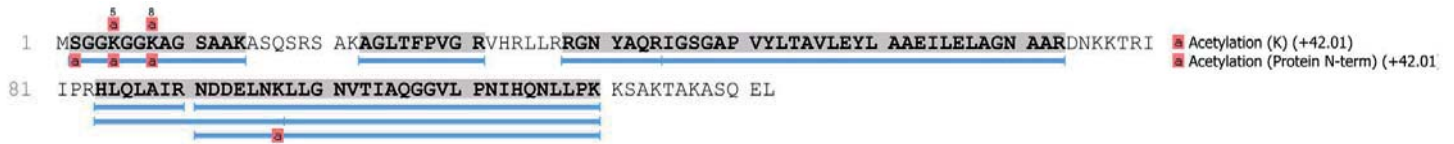
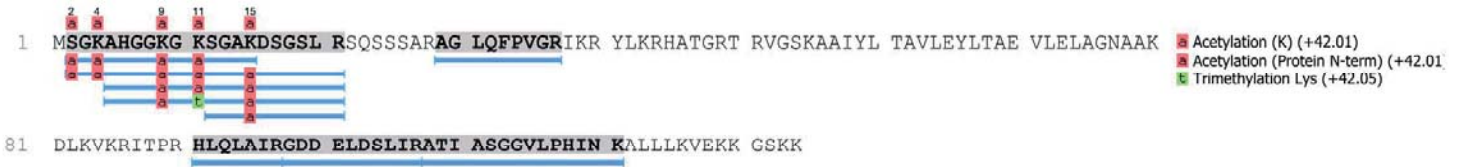
C

Figure S1: The 467 identified interaction partners of the yeast Mediator complex as shown in Figure 1, but separated by the three different categories. **A.** 228 interactors of category I. **B.** 167 interactors of category II. **C.** 72 interactors of category III (see also Table S1 for details).

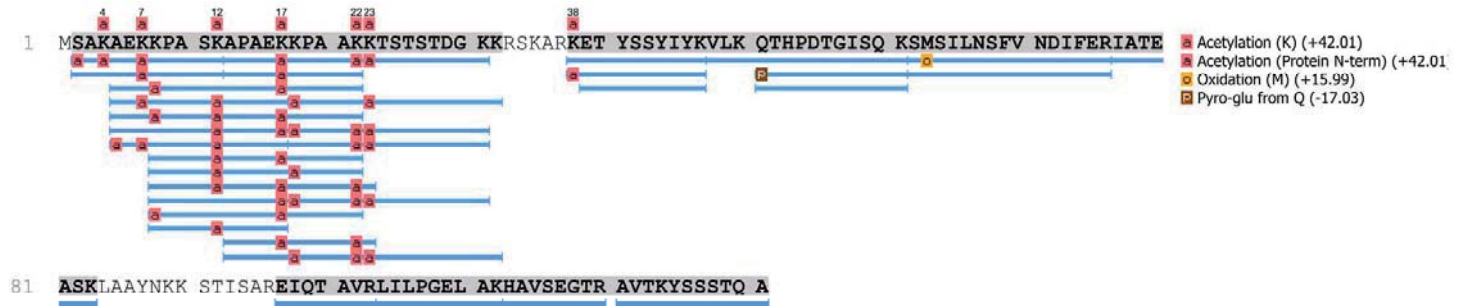
Histone H2A1



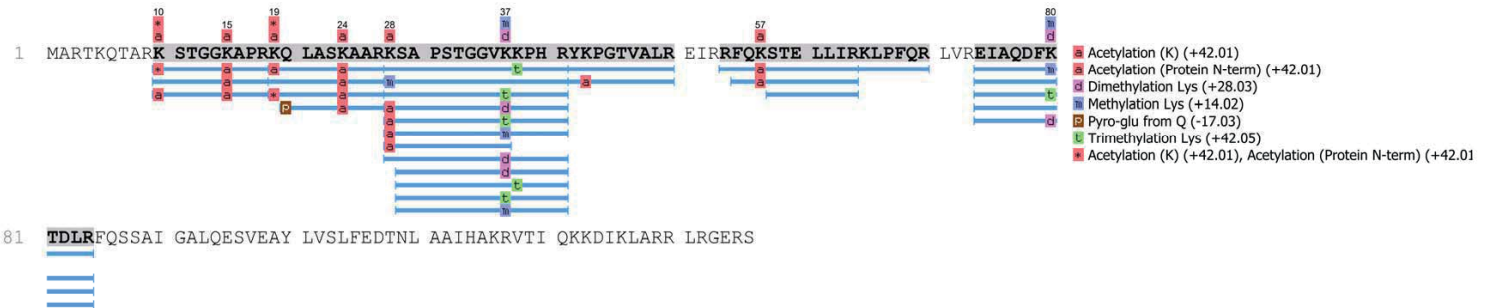
Histone H2A.Z



Histone H2B1



Histone H3



Histone H4

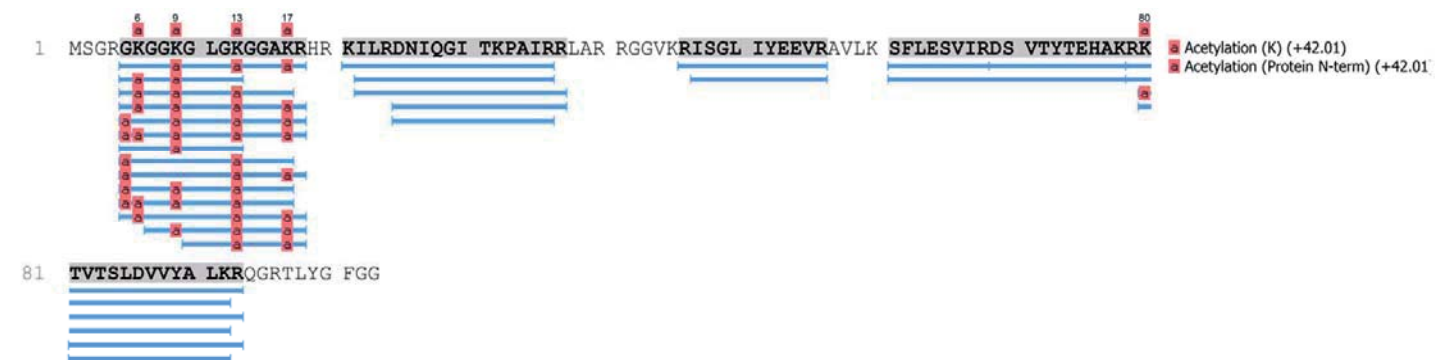


Figure S3: Sequence coverage of histones H2A, H2A.Z, H2B, H3 and H4, which have been identified as specific interactors of the Mediator complex (see Figure 1). All histones are highly acetylated at their N-termini. Database search was performed with PEAKS 7.5, and peptides were filtered with 1 % FDR.

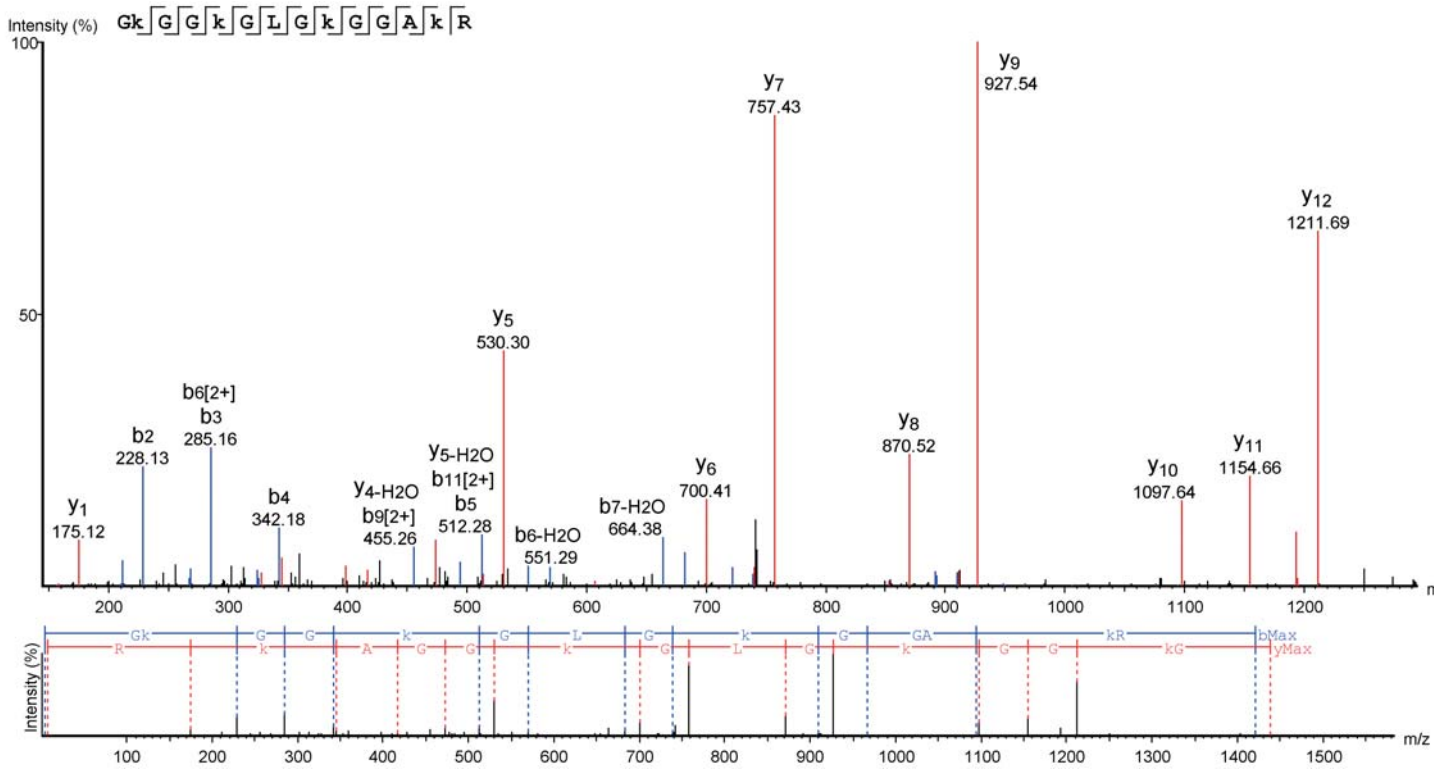


Figure S4: Annotated fragment ion spectrum (HCD spectrum) of the tryptic peptide GKGKGLGKGGAKR of the histone H4 indicating acetylation of all four lysine residues.

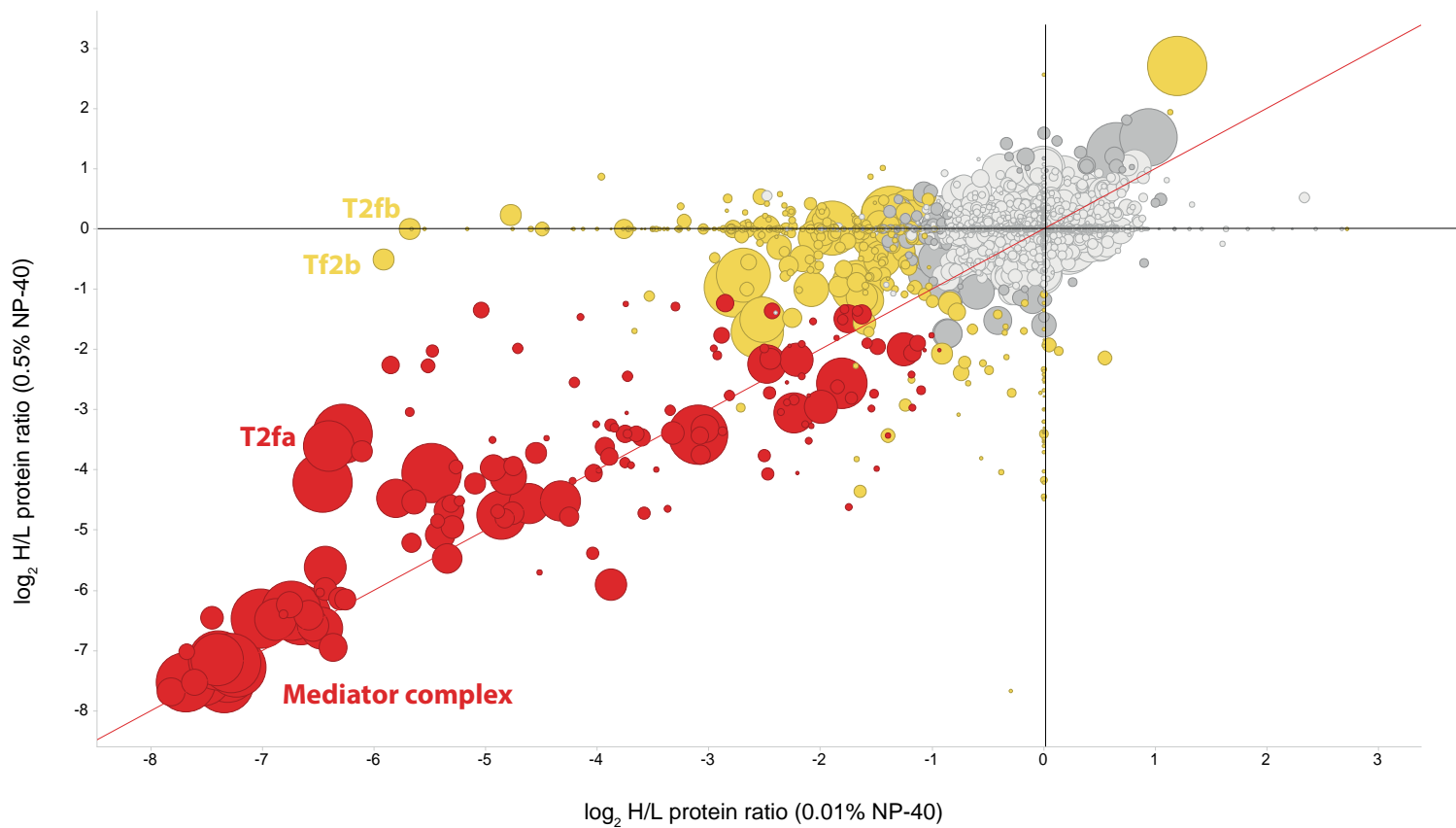


Figure S5: Triplicate Med17-HA CoIP experiments performed with 0.01% NP-40 and with 0.5% NP-40. The log₂ H/L protein ratios from the two experiments are plotted against each other. Significantly less interactors are identified with 0.5% NP-40. Colors: red: identified as specific interactor in both experiments; yellow: identified as specific interactor in only one experiment; grey: unspecific binder in both experiments.