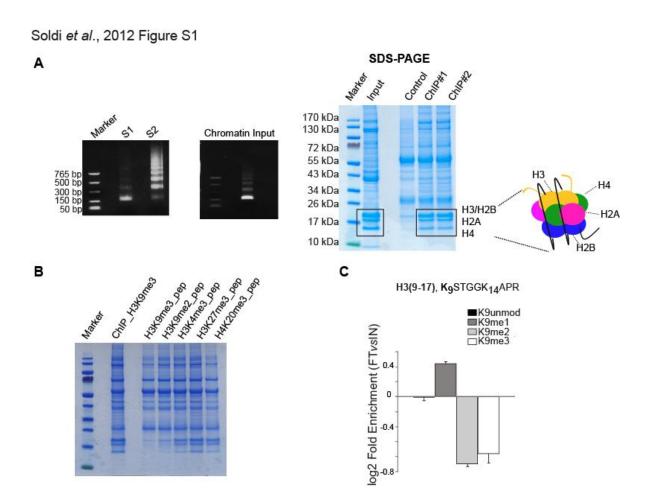
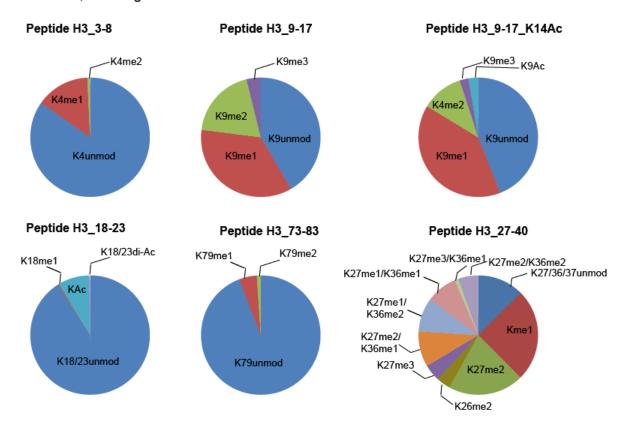
# The proteomic investigation of chromatin functional domains reveals novel synergisms among distinct heterochromatin components

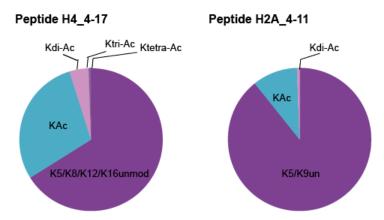
Monica Soldi and Tiziana Bonaldi

### SUPPLEMENTAL FIGURES

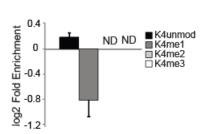


## Soldi et al., 2012 Figure S2





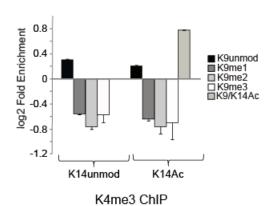
A H3 (3-8), TK<sub>4</sub>QTAR



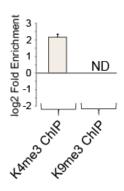
K9me3 ChIP

H3 (9-17), K9STGGK<sub>14</sub>APR

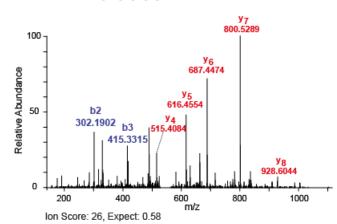
В



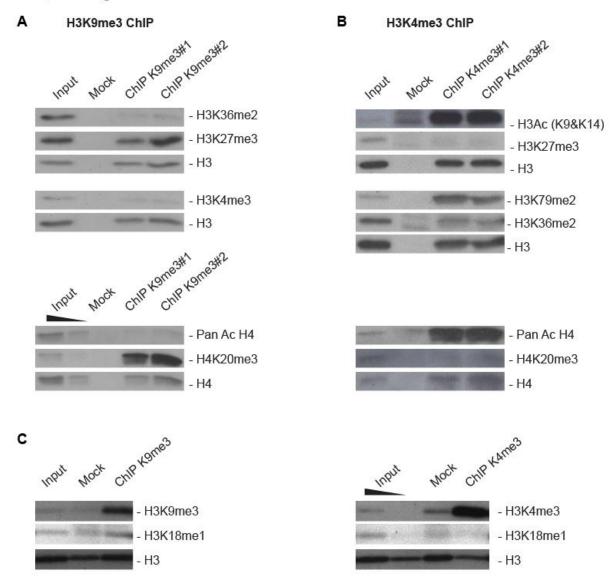
C H3 (18-26), KQLATK(Ac)AAR(me2)

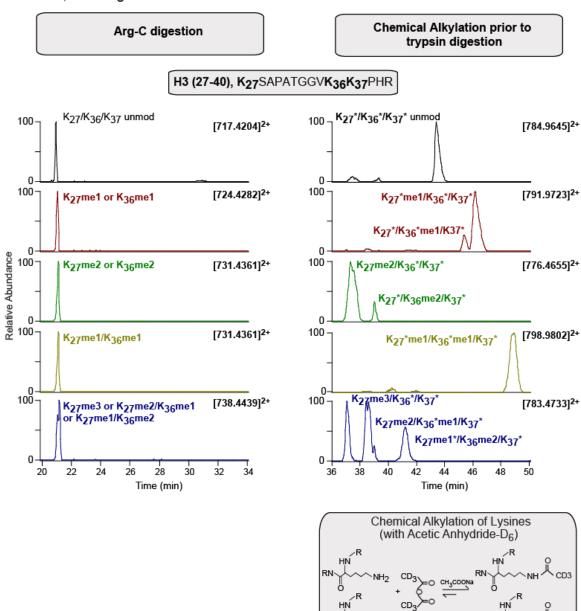






# Soldi et al., 2012 Figure S4

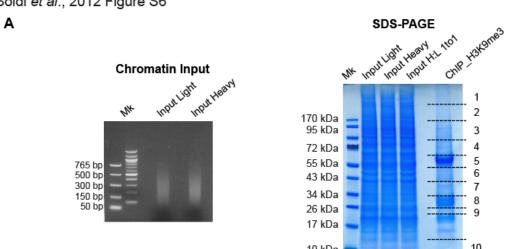


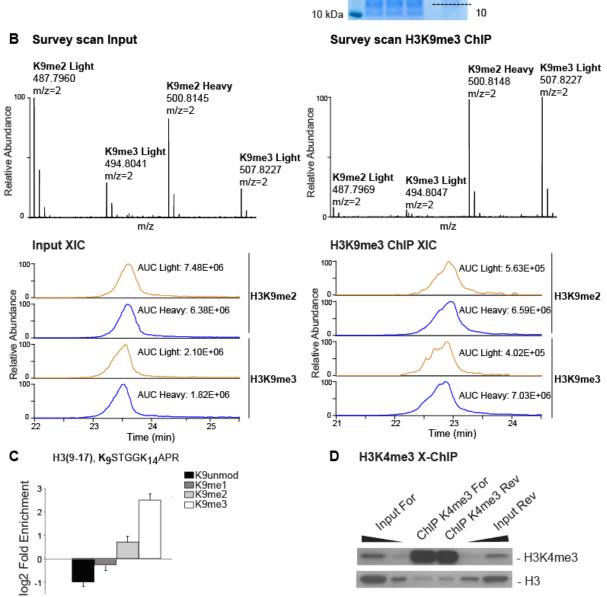


СН3

Trypsin digestion

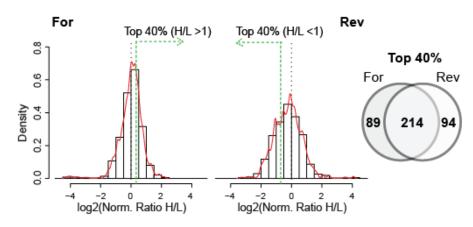
\*= D3-Acetyl=45.0294 Da





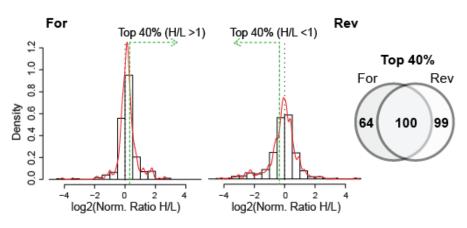
Α

#### Proteins ratio distribution: H3K9me3



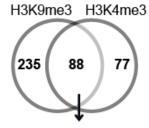
В

### Proteins ratio distribution: H3K4me3



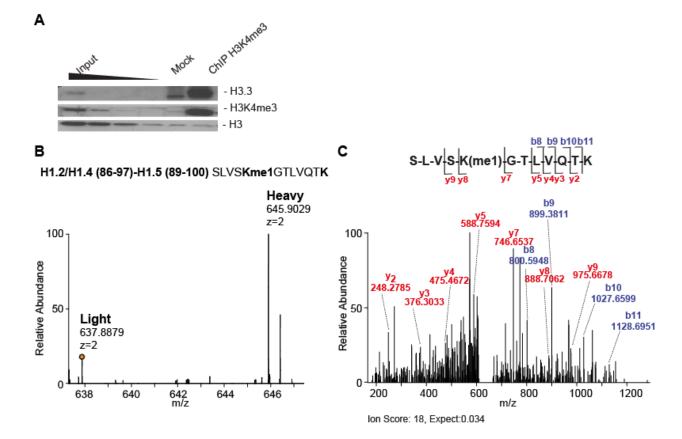
С

X-ChIP Match Common protein, Ratio ≥ 1



Enriched proteins (Top 40%)





A) B)

