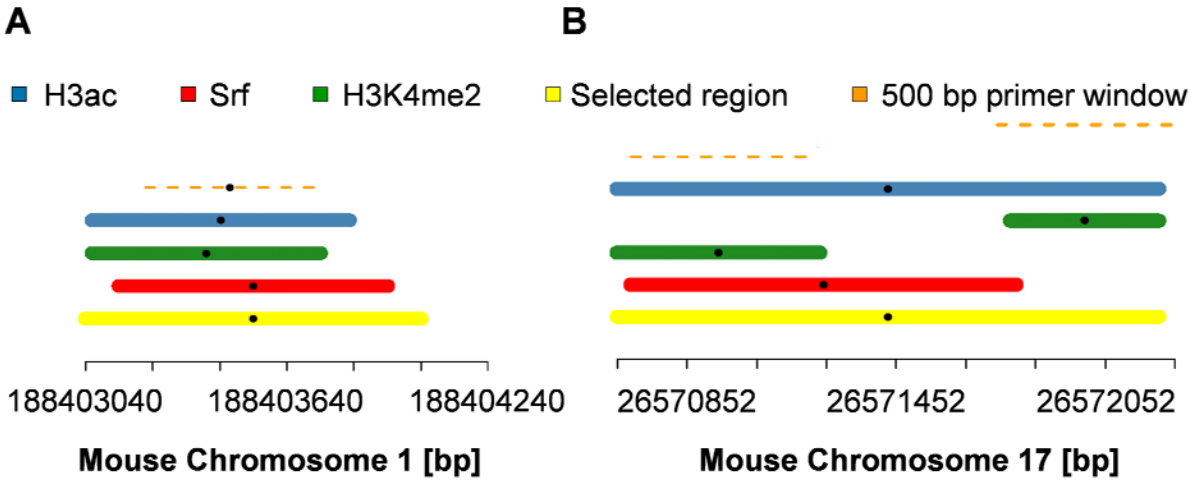

Supplemental Fig. S1: Two examples of selected regions based on ChIP peaks gathered in HL-1 cells. The selected region (yellow) spans all overlapping individual ChIP peaks (blue, green and red for H3ac, H3K4me2 and Srf, respectively). Fixed windows of 500bp length (orange dashed line) were positioned in the middle of the ChIP peaks for primer design. (A) A single 500bp primer window was associated with this selected region on chromosome 1. (B) Two primer windows were used to span all interesting ChIP peaks associated to this selected region on chromosome 17.

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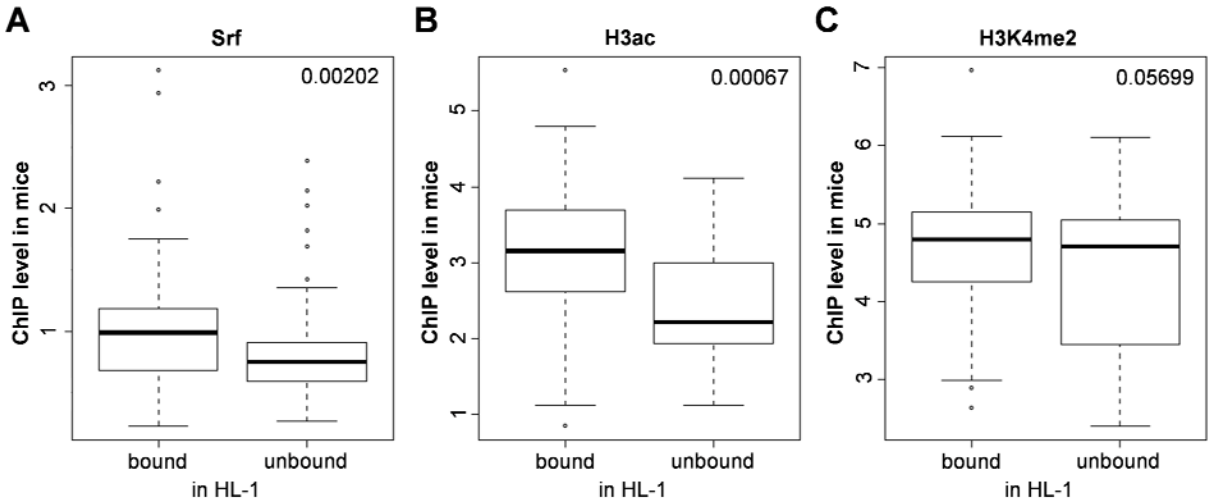

Supplemental Fig. S2: Boxplots comparing ChIP-qPCR enrichment in mouse hearts with regions showing enrichment of Srf, H3ac or H3K4me2 using ChIP-chip/seq in HL-1 cells. For each factor the regions that are bound in HL-1 cells also have a higher average enrichment in our analysis. T-test p-values for the difference in mean are indicated in the upper right corner.

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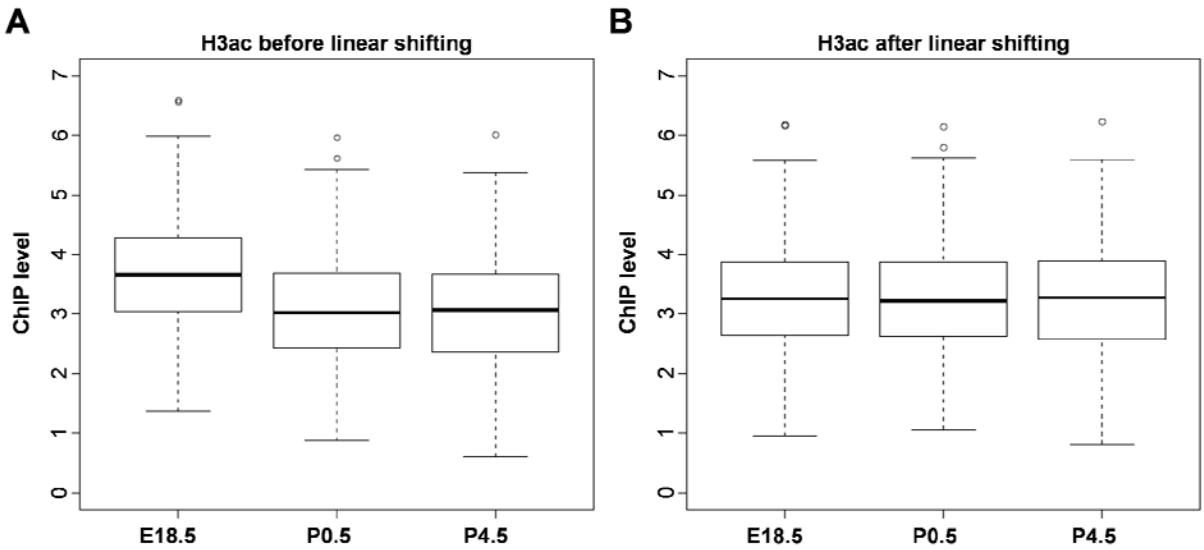

Supplemental Fig. S3: Boxplots of average enrichment over all regions for H3ac in every stage. (A) Measurements after ΔCP normalization showing a distinct trend between the individual stages. (B) Measurements after additional linear shifting which removes the trends.

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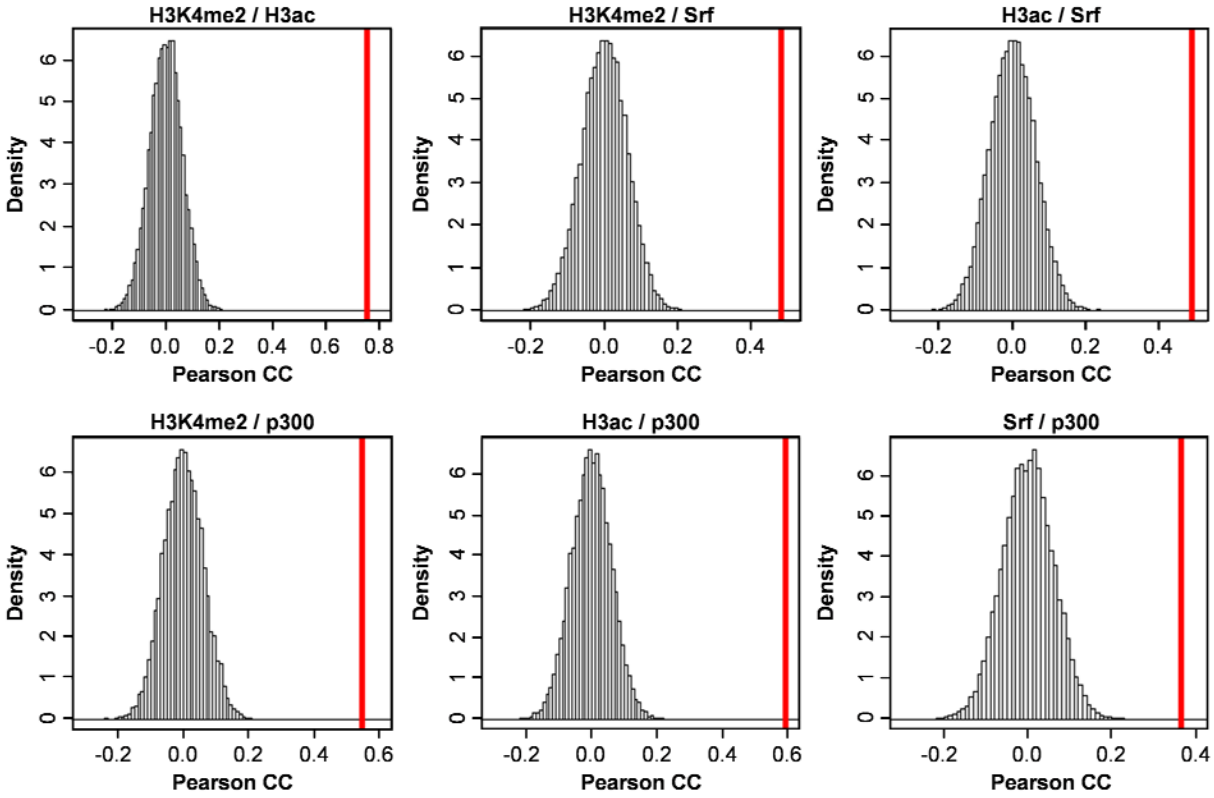
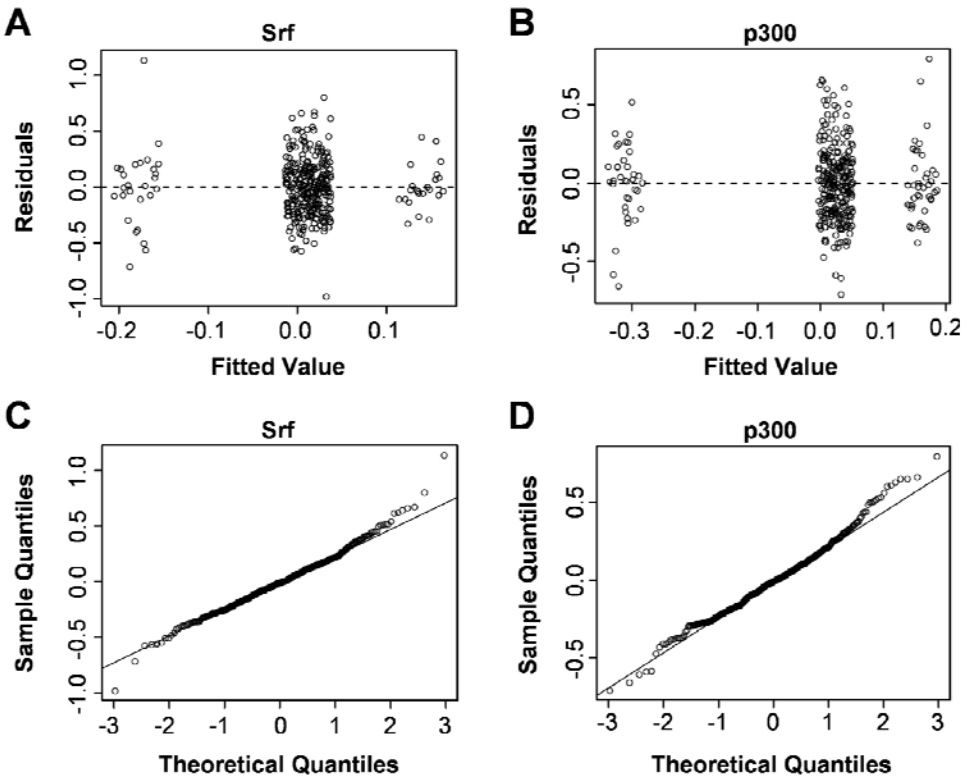


Supplemental Fig. S4: Distribution of Pearson correlation coefficients resulting from the random experiments. The correlation coefficients observed in the real data are indicated by a red vertical line. Data shown for combined time points.



Supplemental Fig. S5: Quality check of single-factor ANOVAs (combined time points). Residuals against fitted values for (A) Srf and (B) p300. Q-Q normal plot for (C) Srf and (D) p300.

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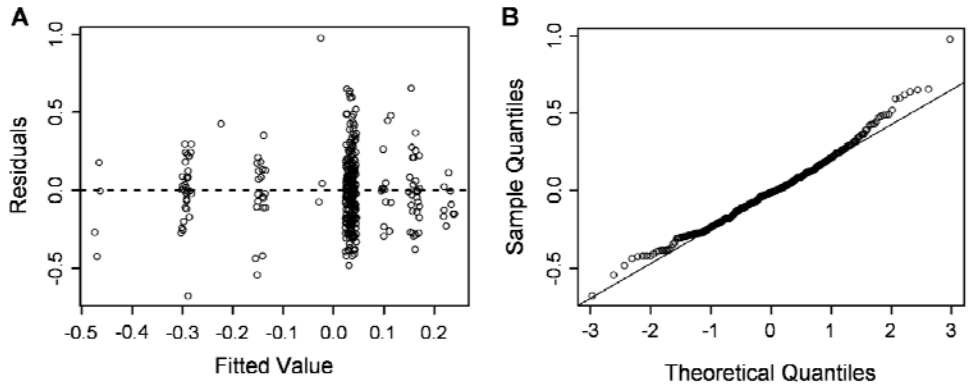
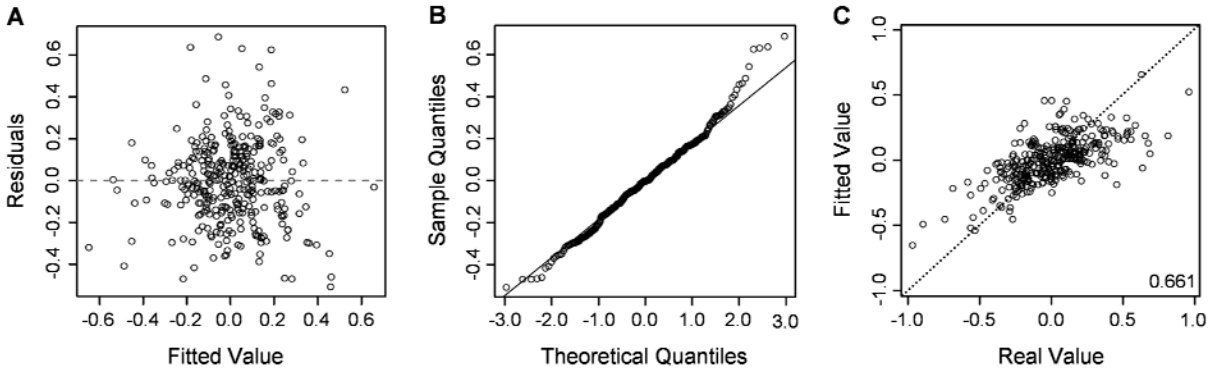


Supplemental Fig. S6: Quality check of two-factor ANOVAs (combined time points). (A) Residuals against fitted values. (B) Q-Q normal plots.



Supplemental Fig. S7: Quality check of quantitative linear regression model (combined time points). (A) Residuals against fitted values for the linear model. (B) Q-Q normal plot for the linear model. (C) Model fit against measured values for the linear model. Pearson correlation coefficients are indicated in the lower right corner.