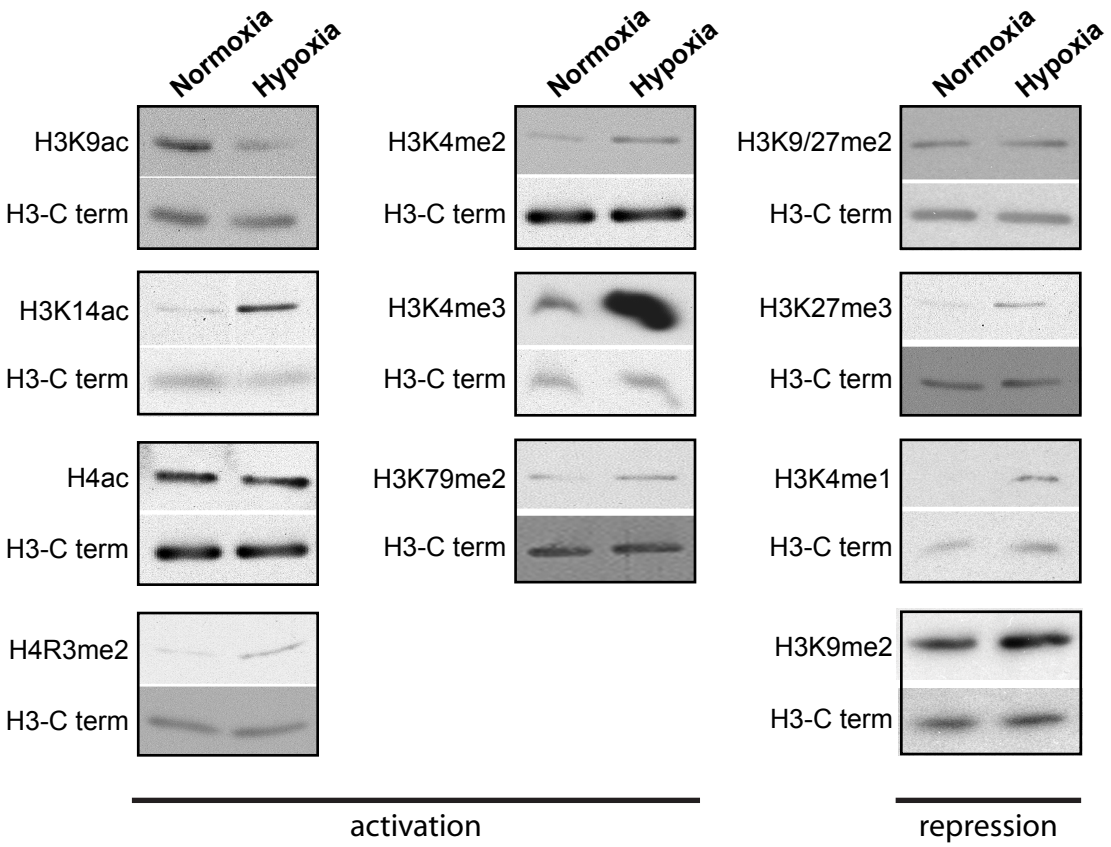
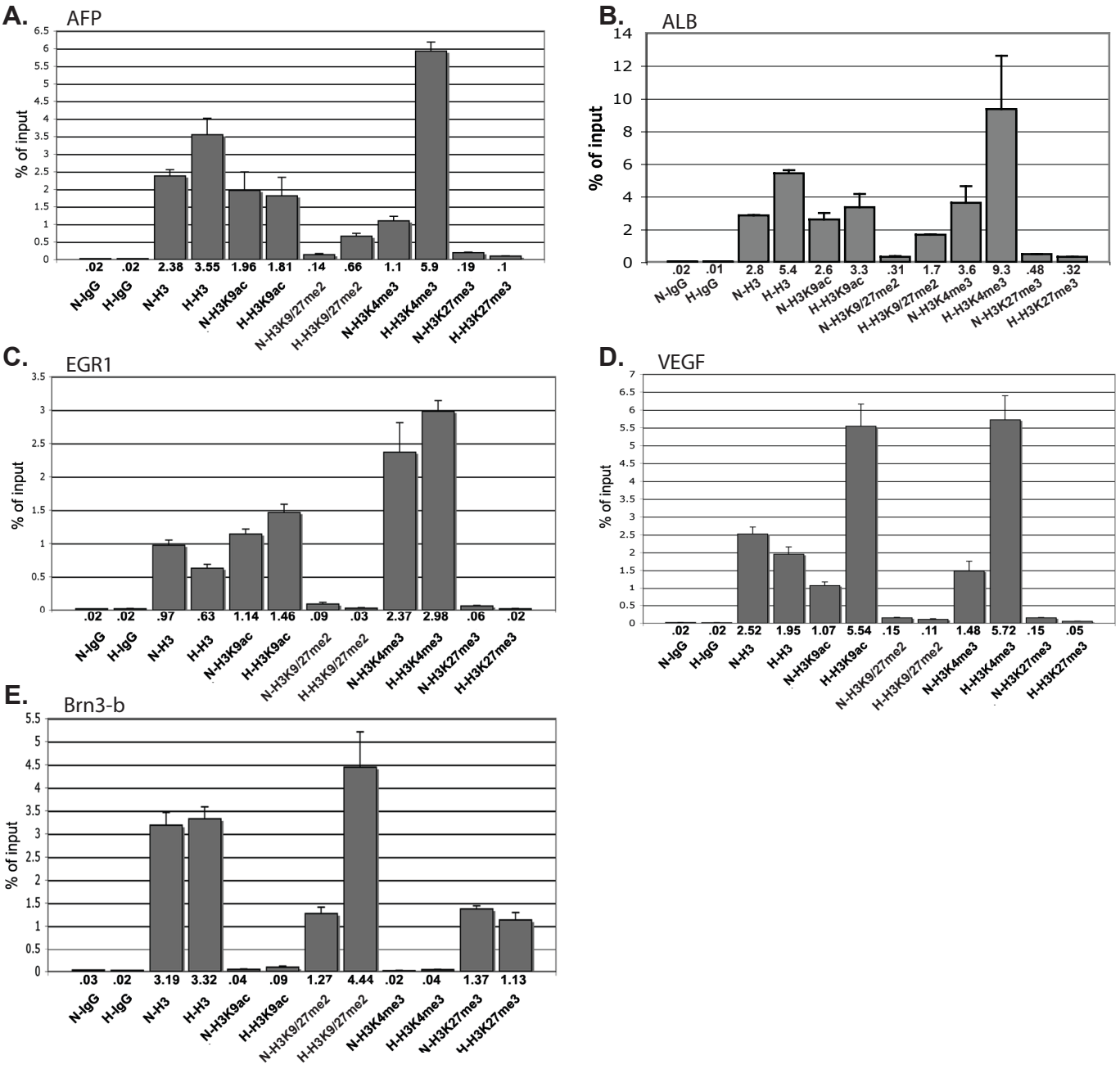



**Suppl. Fig. 1 Hypoxia induces altered post-translational modifications of total histone populations.** Representative immunoblot analysis of histone modifications associated with transcriptional activation (left and middle) and transcriptional repression (right) within extracts of Hepa 1-6 cells under normoxia or 48 hrs at 0.2% oxygen (Hypoxia).



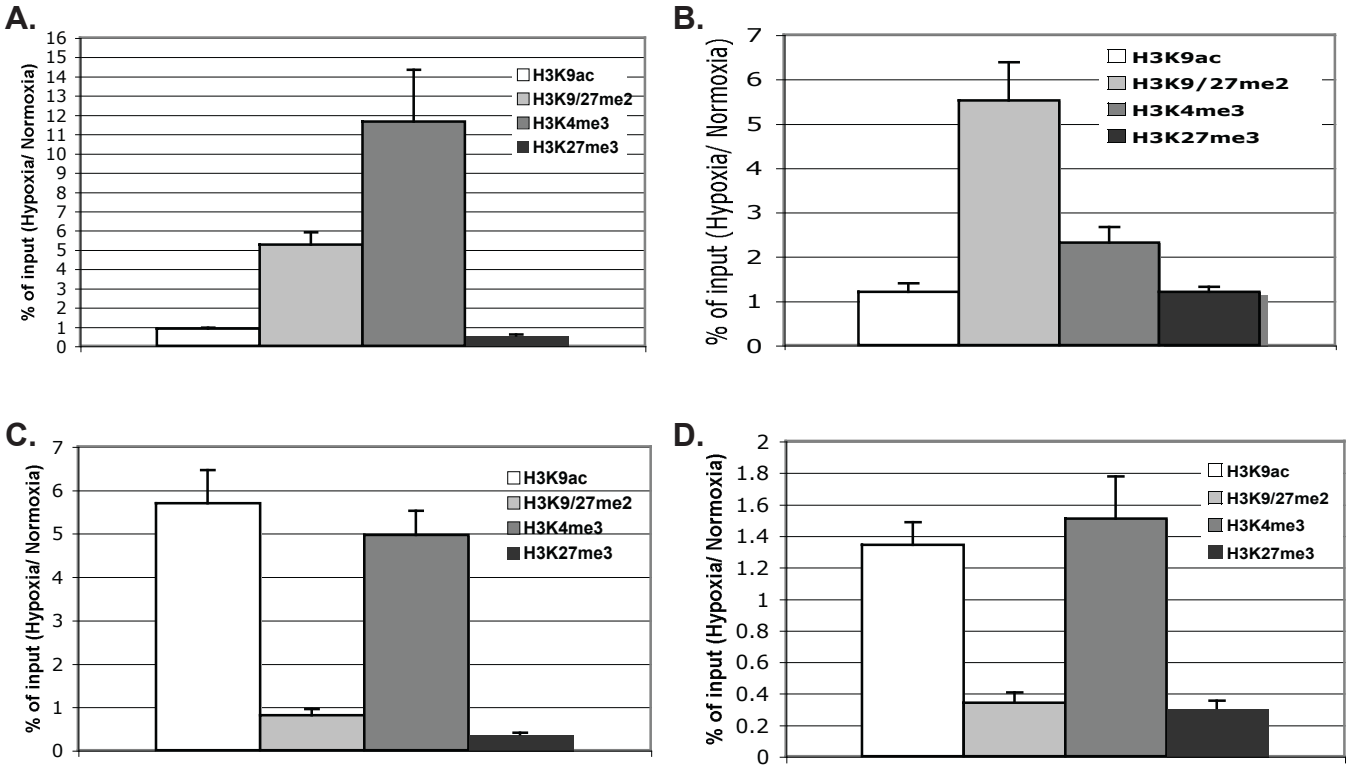

**Supplemental Figure 2. Hypoxia induces changes in total amounts of bound modified histones at core promoters of hypoxia-repressed and –activated genes**

ChIP for the indicated modified histones was conducted in Hepa 1-6 cells after 48 hrs at normoxia or 0.2% oxygen followed by quantitative PCR for the core promoters of AFP (A), ALB (B), EGR1 (C), and VEGF (D), as well as the 3'-UTR of silenced Brn3-b (E).

As a negative control, normoxic and hypoxic sample were also immunoprecipitated with anti-sheep IgG.

The % of input bound by the modified histones, minus background, in hypoxia relative to normoxia is shown.

An average of at least three experiments is shown, and error bars denote the standard error of the mean.




**Hypoxia induces changes in total amounts of bound modified histones at core promoters of hypoxia-repressed and –activated genes.** ChIP for the indicated modified histones was conducted in Hepa 1-6 cells after 48 hrs at normoxia or 0.2% oxygen followed by quantitative PCR for the core promoters of AFP (A), Albumin (B), VEGF (C), and EGR1 (D). As a negative control, normoxic and hypoxic sample were also immunoprecipitated with anti-sheep IgG. The % of input bound by the modified histones, minus background, in hypoxia relative to normoxia is shown. An average of two to three independent experiments is shown in each graph, each experiment quantified in duplicate. Error bars denote the SEM.