

SUPPLEMENTARY FIGURE LEGENDS:

Figure S1: Temporal expression of histone H4 and Hinfp expression during murine development. Total RNA of embryos at different stages of pre-natal development was analyzed by qRT-PCR for histone H4 and Hinfp expression. The graphs show expression levels of individual histone H4 mRNAs relative to Hprt1 on E5.5, E6.5, E12.5 and E15.5 as indicated. Data for E10.5 are presented in Figure 3.

Figure S2: Post-natal expression of the mouse histone H4 multi-gene family. Expression levels of distinct histone H4 genes mRNAs were determined by qRT-PCR using samples harvested from post-natal mice on Day 1, 14 or 60 as indicated in, respectively, the top, middle and bottom graphs. Histone H4 genes are detectable in all tissues examined, including brain, heart, lung, stomach, intestine, thymus, liver, spleen and kidney (abbreviated by the first three letters in each graph). The graph shows the expression profile for the entire set of H4 genes and the data are grouped per tissue. Among the tissues examined, the highest levels of histone H4 gene expression were observed in spleen in newborn (Day 1) mice, as well as in thymus in young mice (Day 14) mice mouse and in the intestine of the adult mouse (Day 60). Thymus data are not included in the Day 60 graph, because this tissue was too small for routine expression analysis. Expression levels were normalized relative to Hprt1. Error bars indicate standard deviations of triplicate experiments.

Figure S3: Contribution of individual histone H4 genes to the total H4 mRNA pool during post-natal development. The column charts depict the percentage that each histone H4 gene contributes to the total histone H4 mRNA pool. To obtain this percentage, qRT-PCR data for all H4 mRNAs (see Fig. S2) were added for each tissue, and values for each mRNA were then divided by this total to obtain a fraction that was multiplied by 100%. The third panel contains a reference column in which the relative sizes of each mRNA were scaled as if they were to contribute equally to the total (i.e, 12 genes generate 100% of the total H4 mRNAs, and each gene theoretically contributes ~8.3 %; the Hist1h4k/Hist1h4j mRNAs, which are detected by the same primer pair, are represented here as a single gene copy).

Highly expressed histone H4 genes are Hist1h4d, Histh41f, Hist1h4m, Hist2h4 and Hist4h4, which typically contribute >90% to the total H4 mRNA pools in each tissue. Minimally expressed histone H4 genes are Hist1h4a, Hist1h4k/Hist1h4j, Hist1h4c, Hist1h4h, Hist1h4b and Hist1h4i, which typically contribute <10%.