Supplemental material: Figure legends

Supplemental Figure S1. Histone H1 variant gene expression in the course of ES[2] cells differentiation. ES[4] cells were cultured in differentiation media for 4, 8, 15 or 20 days. At the indicated time points, cells were processed for RNA extraction and H1 variant gene expression was analyzed by RT-qPCR as in Figure 1B and normalized by gDNA amplification with the same set of specific oligonucleotides and GAPDH expression. Mean and SD of a representative experiment quantified in triplicate is shown.

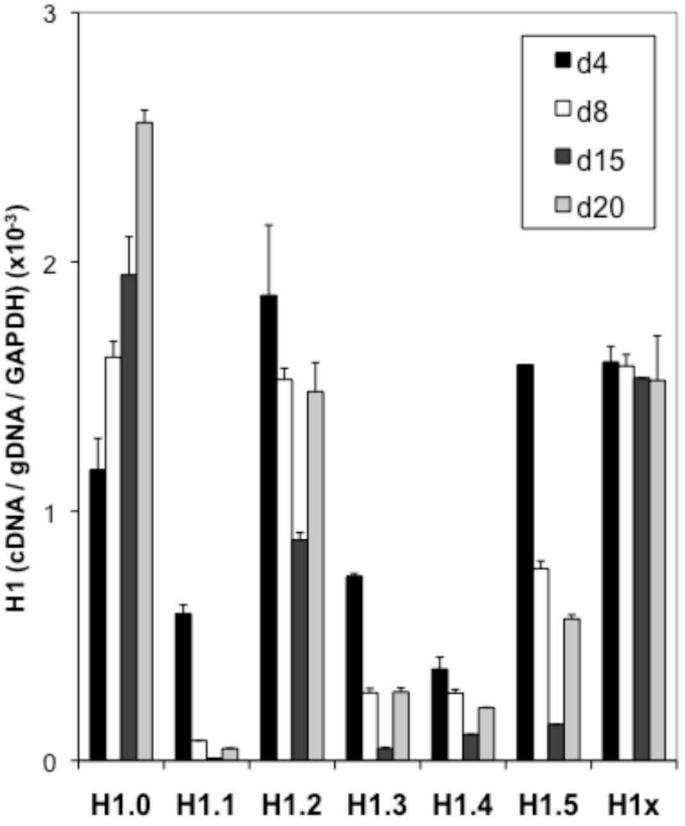
Supplemental Figure S2. Histone H1 variant gene expression in normal and reprogrammed keratinocytes, compared to *FOXA2* and *SOX2* gene expression. The RNA samples of fibroblasts (HF), keratinocytes (K1 and K2), and iPS cells (KiPS4F1 and KiPS4F4), were used to measure histone H1 and *FOXA2* and *SOX2* gene expression by RT-qPCR with specific oligonucleotide pairs. cDNA amplification was normalized with the values of HF or K1-derived genomic DNA amplified with the same primers set and *GAPDH* expression. This is a different representation of data shown in Figure 3B.

Supplemental Figure S3. Comparison of histone H1 variant content in differentiated and pluripotent cells. **(A)** Comparison of histone H1 variants content in several differentiated and pluripotent cell lines. Histone H1 was extracted from hES cells (ES[2] and ES[4]), iPS cells (KiPS4F1 and KiPS4F4), keratinocytes (K1 and K3), and fibroblasts (HF), and analyzed by immunoblot with H1 variant specific antibodies as in Figure 4A. H1.2 was expected to serve as loading control for normalization. (**B**) The immunoblot in (A) was quantified and data is shown as relative light intensity units (RU) for each tested H1 variant. Notice that the data has been organized to present the following order: differentiated cells (HF, K1 and K3), iPS cells (KiPS4F1 and KiPS4F4), and hES cells (ES[2] and ES[4]). The right panels represent the mean and SD of the pooled values for the differentiated (HF, K1 and K2) or pluripotent (KiPS4F1, KiPS4F4, ES[2] and ES[4]) samples. Differences were interrogated with the Student's *t* test for statistical significance when possible. *, $P<0.1$; **, $P<0.05$.

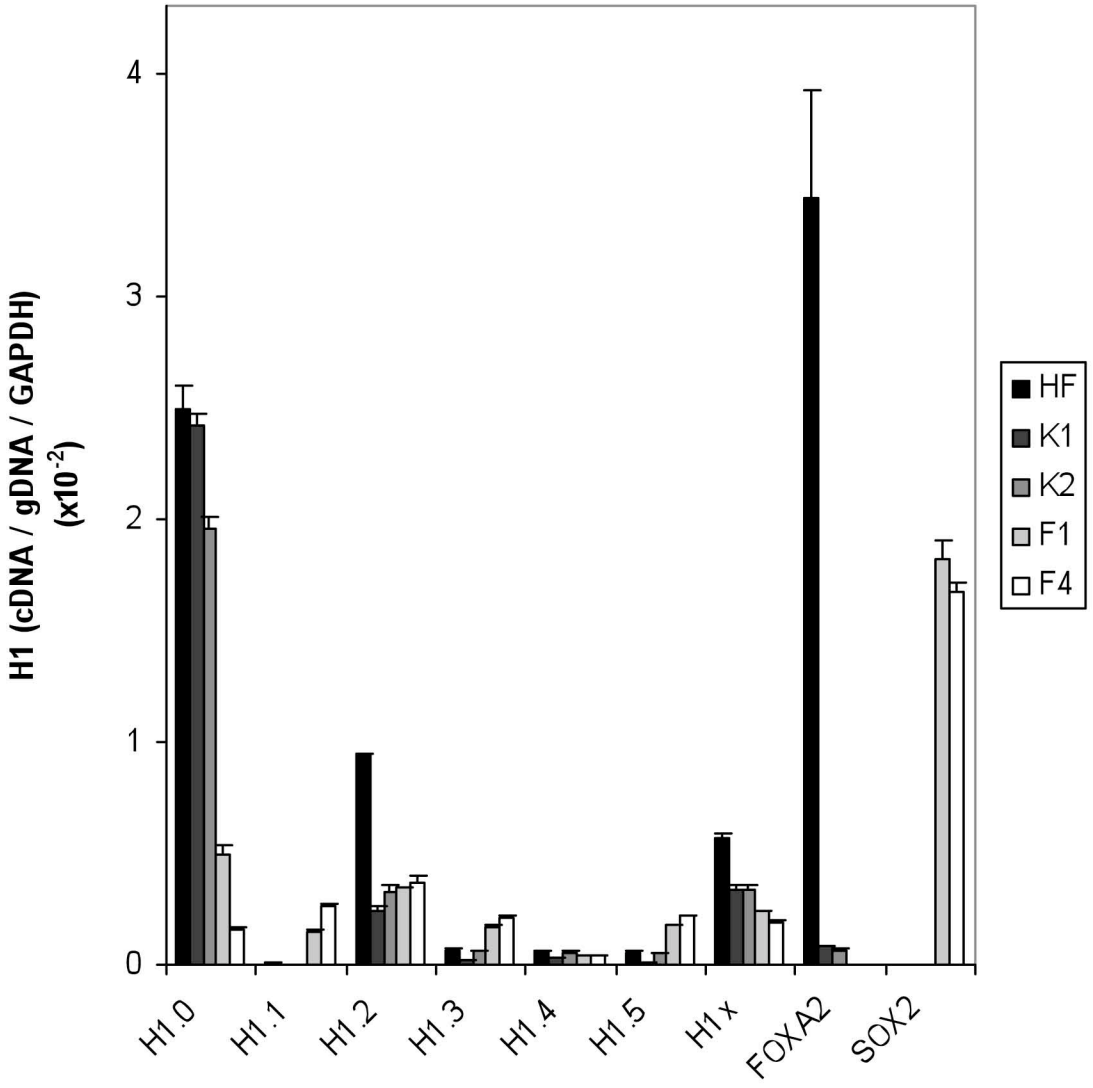
Supplemental Figure S4. Interference of H1.3, H1.5 and H1.0 expression in hES cells. ES[4] H1.3 KD (**A**), H1.5 KD (**B**), H1.0 KD (**C**), or control (shRandom) cells were processed for RNA extraction. Expression of several pluripotency (NANOG, OCT4, SOX2), differentiation (HNF4, FOXA2, SOX17, PAX6) and H1 genes was determined by RT-qPCR with specific oligonucleotide pairs. *GAPDH* expression was measured for normalization. Mean and SD of a representative experiment quantified in triplicate is shown.

Supplemental Figure S5. Expression of H1 variant genes in the course of ES[4] H1.0 KD or control cell differentiation. ES[4] H1.0 KD or control (shRandom) cells were cultured in differentiation media for the indicated days, and cells were processed for RNA extraction. Expression of H1 genes not shown in Figure 6 was determined by RT-qPCR with specific oligonucleotide pairs. *GAPDH* expression was measured for normalization. Mean and SD of a representative experiment quantified in triplicate is shown.

Supplemental Figure S1.



Supplemental Figure S2.



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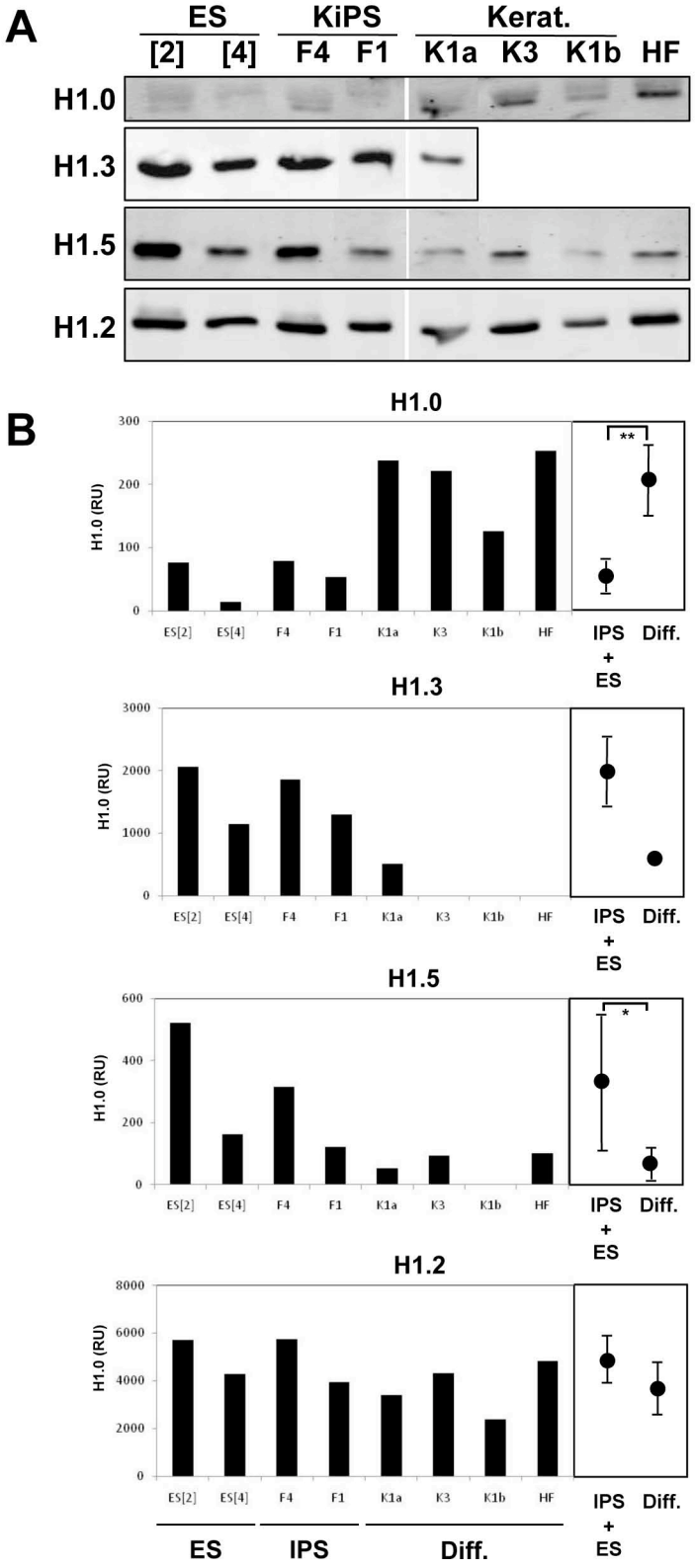
Supplemental Figure S3.



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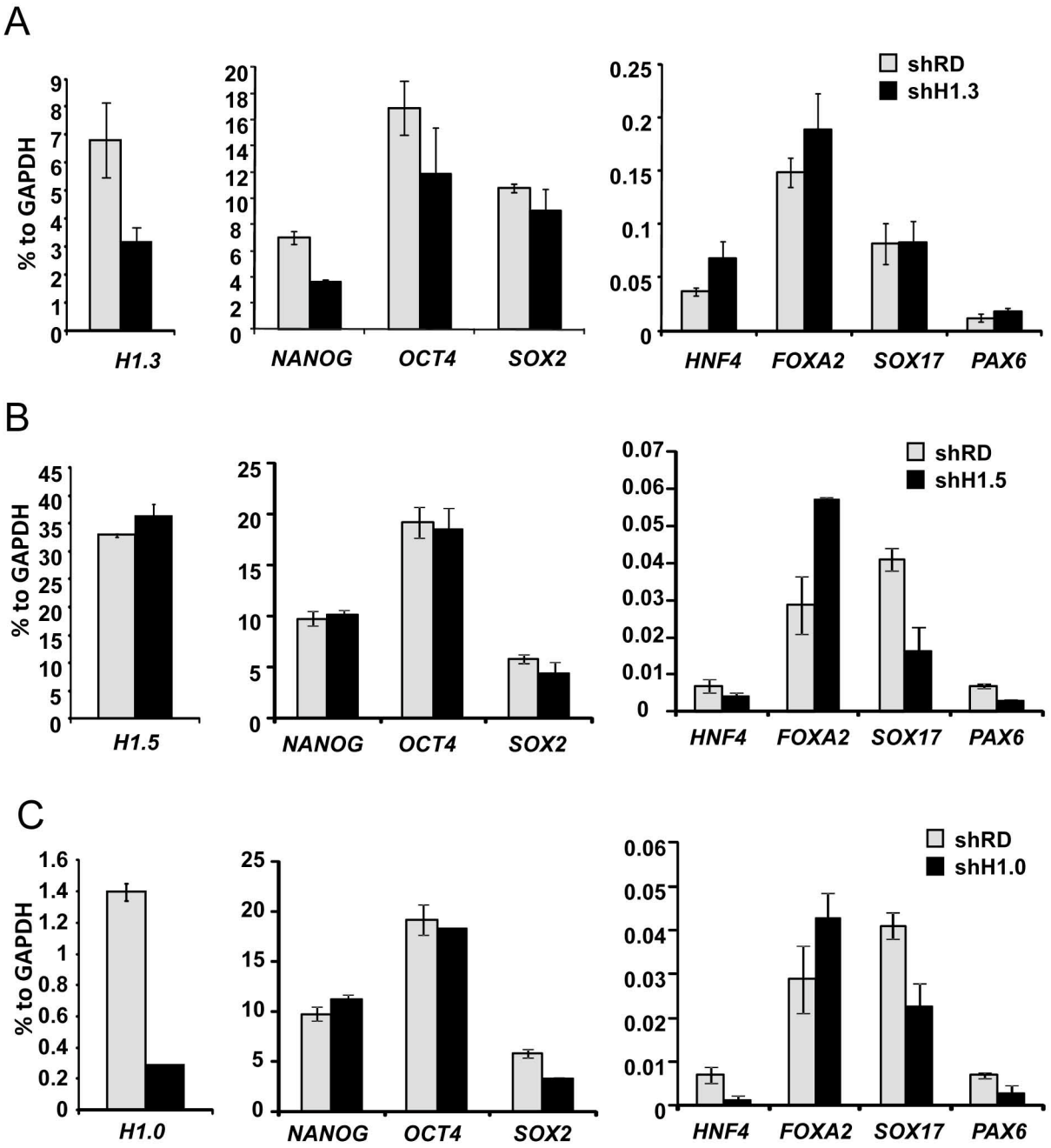
Supplemental Figure S4.



Supplemental Figure S5.