List of Supplementary Figures and Tables

Figure S1. Experimental Flow Chart
Figure S2. Synchronization of 3T3 cells
Figure S3. POU5F1 (Oct4) Western blot
Figure S4. PCR confirmation of amplicons
Figure S5. Pie charts indicating relative usage of the 4 different repression mechanisms for the MEGs categories.
Figure S6A. Top gene ontology categories bound by H3me3K27 in the LEGs set for all 12 cell lines.
Figure S6B. Top gene ontology categories bound by PolR2A in the LEGs set for all 12 cell lines.
Figure S6C. Top gene ontology categories bound by H3me3K9 in the LEGs set for all 12 cell lines.
Figure S6D. Top gene ontology categories bound by 5-meC in the LEGs set for all 12 cell lines.
Figure S6E. Top gene ontology categories not bound by the 4 tested marks in the LEGs set for all 12 cell lines.
Table S1. Summary of arrays
Table S2. Mechanisms of repression used in low and middle expressed categories of genes.
Table S3. Fold enrichment (Log2) of the promoters (from the top 2000 targets of the indicated ChIP-chip experiment) that fell into the HEGs, MEGs, or LEGs category.
Table S4. Transition RNAs
Table S5. Mouse and human common HEGs
Table S6. Max4 enrichment values for all marks in all human cell lines.
Table S7. Max4 enrichment values for all marks in all mouse cell lines.
Table S8. Illumina RNA expression array data for 12 mouse and human cell populations
Table S9. Max4 values (log2) for the HOXD3 promoter.