- SUPPLEMENTARY INFORMATION -

Endogenous retroviruses function as species-specific enhancer elements in the placenta

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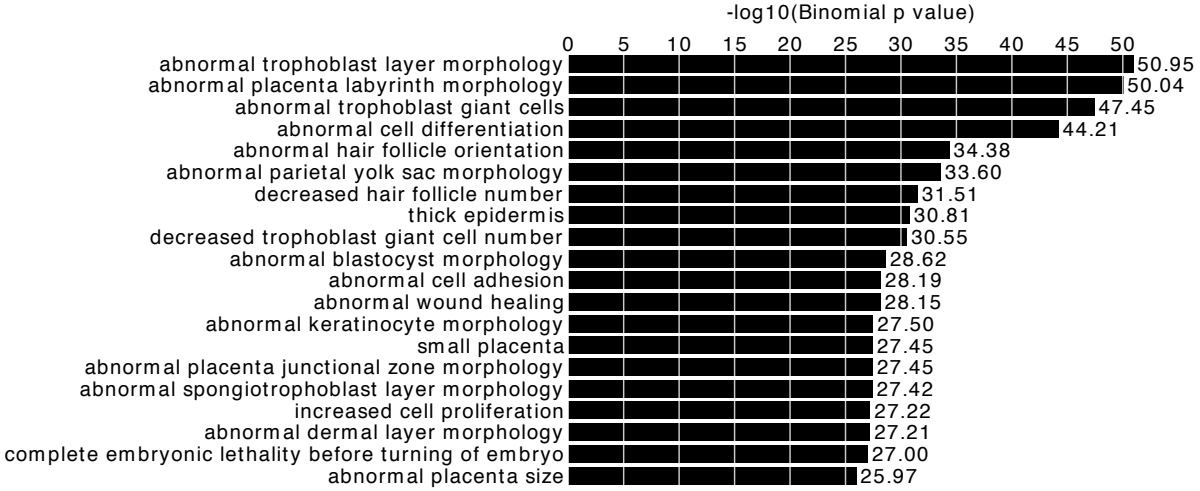
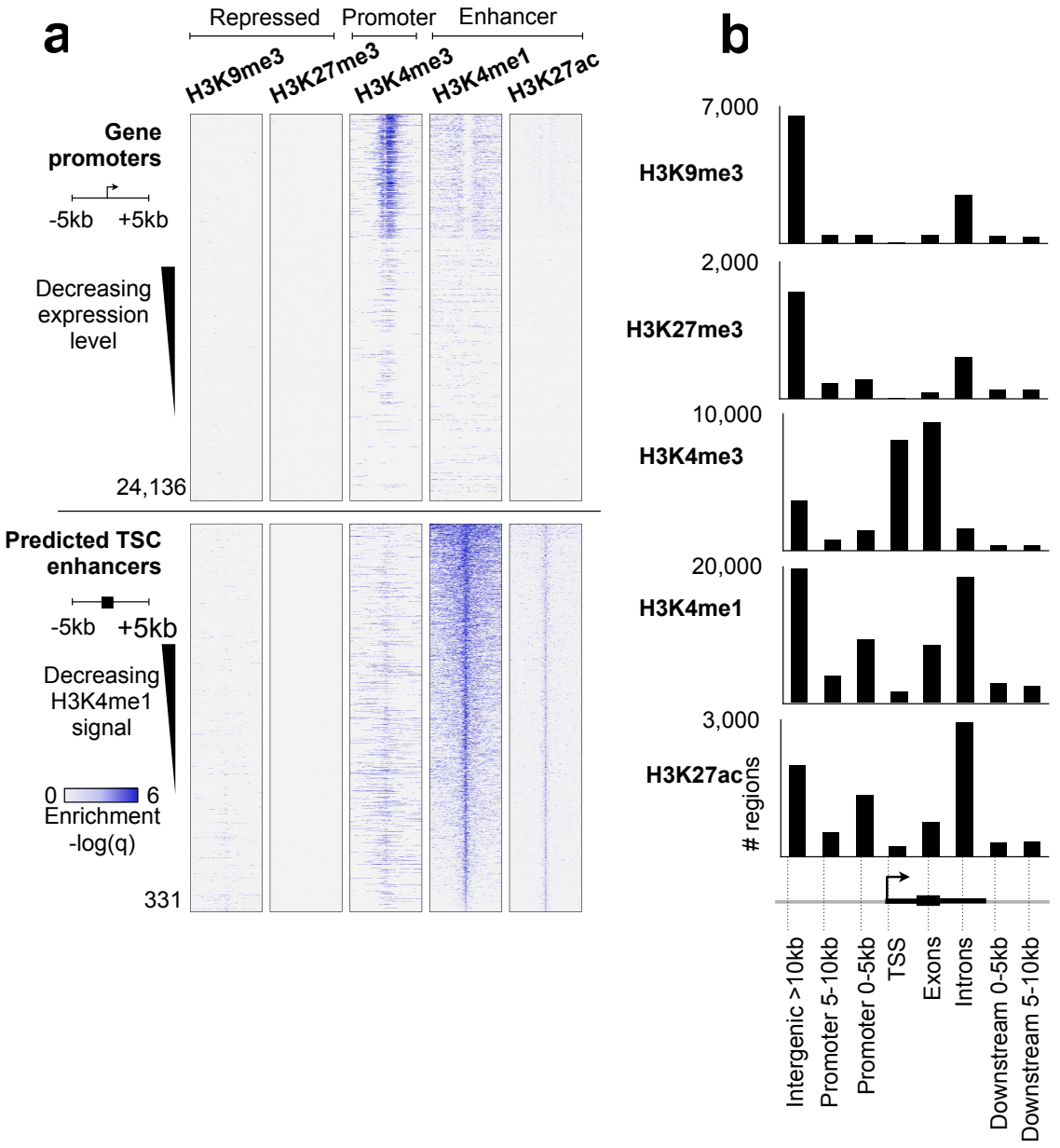
Supplementary Tables 1-13. Transposable elements (TEs) enriched within a set of ChIP-Seq defined regulatory regions against a randomized background. TEs are unfiltered and sorted by significance (Bonferroni corrected binomial *P* value).

Supplementary Table 1. Putative regulatory TEs in mouse TSCs, H3K9me3
Supplementary Table 2. Putative regulatory TEs in mouse TSCs, H3K27me3
Supplementary Table 3. Putative regulatory TEs in mouse TSCs, H3K4me3/TSS
Supplementary Table 4. Putative regulatory TEs in mouse TSCs, H3K4me1/distal
Supplementary Table 5. Putative regulatory TEs in mouse TSCs, H3K27ac/distal
Supplementary Table 6. Putative regulatory TEs in mouse TSCs, Eomes
Supplementary Table 7. Putative regulatory TEs in mouse TSCs, Cdx2
Supplementary Table 8. Putative regulatory TEs in mouse TSCs, Elf5
Supplementary Table 9. Putative regulatory TEs in rat TSCs, H3K9me3
Supplementary Table 10. Putative regulatory TEs in rat TSCs, H3K27me3
Supplementary Table 11. Putative regulatory TEs in rat TSCs, H3K4me3/TSS
Supplementary Table 12. Putative regulatory TEs in rat TSCs, H3K4me1/distal
Supplementary Table 13. Putative regulatory TEs in rat TSCs, H3K27ac/distal

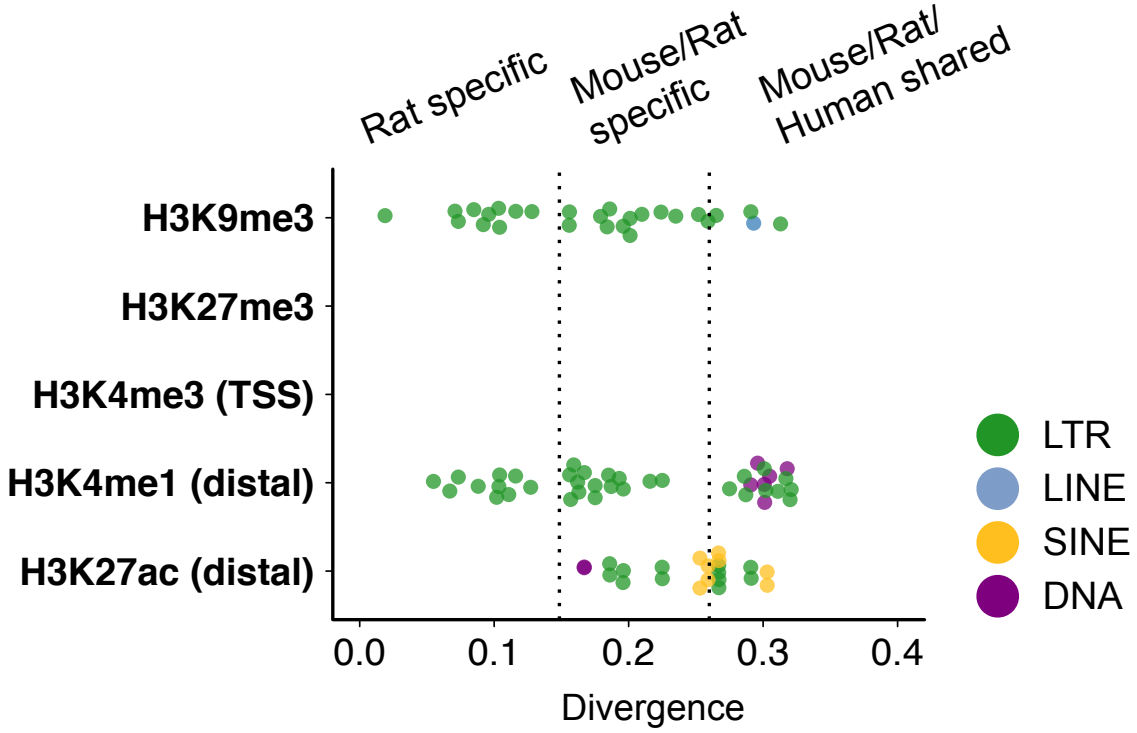
Supplementary Figures



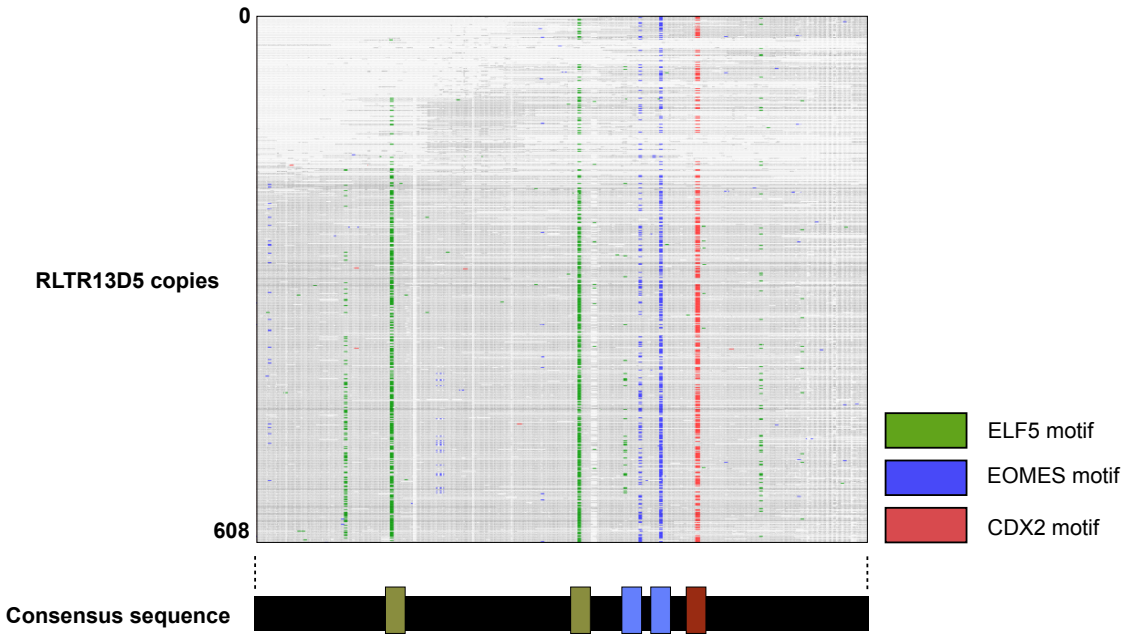
Supplemental Figure 1. TSC enhancers predicted by histone ChIP-Seq associate with known placental developmental genes. GREAT analysis of enhancers (those shown in Fig. 1a lower panel), showing the top 20 mouse phenotypes significantly associated with genes near distal H3K27ac+H3K4me1-defined enhancers in mouse.



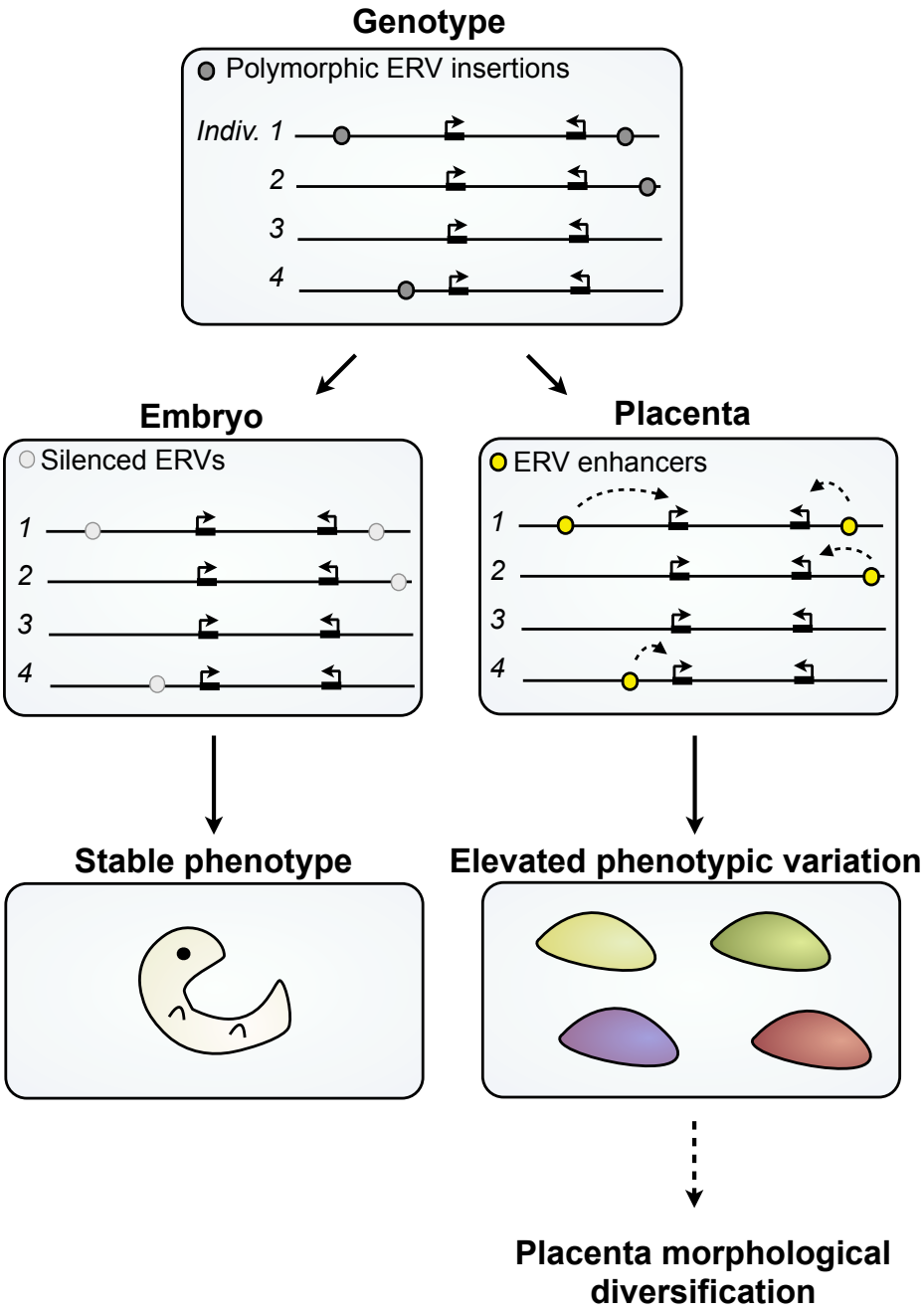
Supplemental Figure 2. The epigenetic landscape of rat TSCs using histone ChIP-Seq. (a) Heatmap of rat ChIP-Seq signals over gene promoters and predicted enhancers. (b) Genomic distribution of histone enrichment. For details see Fig. 1 in the main text.



Supplemental Figure 3. Species-specific ERVs are enriched in repressed regions and enhancers in rat. Significantly overrepresented TE families from Figure 2b are plot against their divergence time, for rat. The absence of rat-specific LTR elements enriched in H3K27ac may be due to low coverage of the rat H3K27ac ChIP-Seq experiment (4,471 peaks). For figure details see Fig. 2c in the main text.



Supplemental Figure 4. Most individual RLTR13D5 copies harbor predicted TSC TF binding motifs. Graphical overview of a multiple alignment of all 608 RLTR13D5 copies, sorted by increasing pairwise identity. Individual predictions of TSC transcription factor motifs are highlighted in color. Diagram overview of motif locations in the RLTR13D5 consensus sequence (from Fig. 3d) displayed for reference.



Supplemental Figure 5. Model illustrating how placental ERV activity may contribute to the evolutionary diversification of placental morphology. Recently integrated, polymorphic ERVs are typically silenced in the embryo. In the placenta, ERVs are epigenetically exposed and effectively increase the developmental evolvability of the fetal placenta. Recurrent cooption of ERVs, due to parent-offspring conflict, may drive placental morphological diversification across lineages.