

Placenta

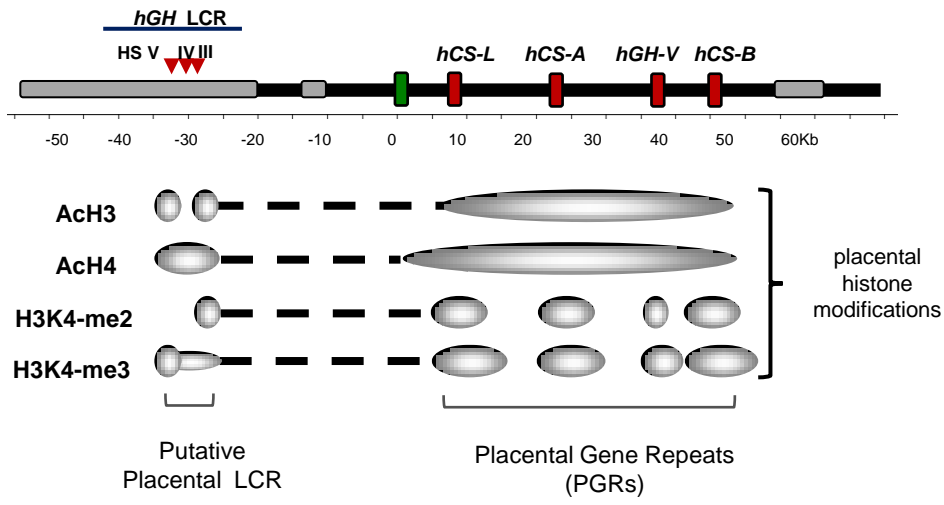


Fig. S1. Histone modifications at the placental *hGH* locus. The active histone marks are located at placental LCR (HSIII-V) and the PGR units during the activation of placental genes. This diagram summarize our previously published studies (20).

Figure S2

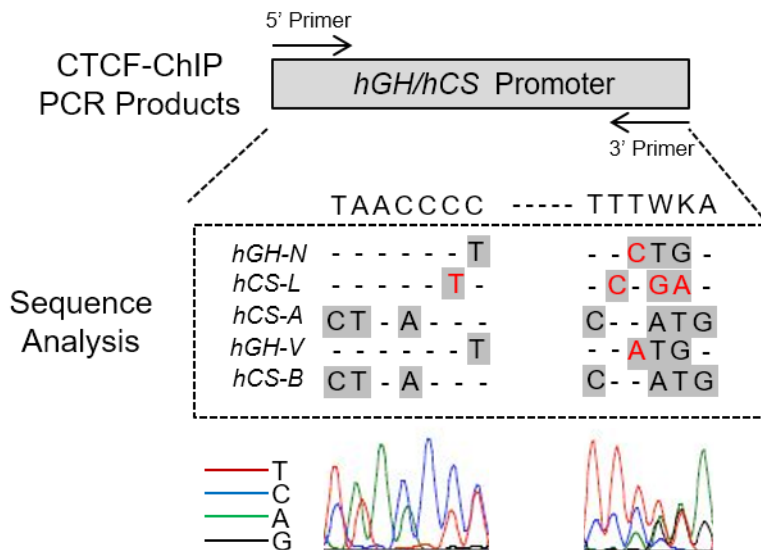


Fig. S2. CTCF is recruited to all five of the promoters in the *hGH* cluster in the human STB chromatin. CTCF occupancy at the *hGH/hCS* gene promoters was mapped by sequencing PCR-amplified ChIP'ed DNA (as in **Fig. 4B**). The sequence divergences that were used to assign each occupancy at each specific promoter are shown (dashed box). The sequence tracing demonstrates that all five promoter regions are enriched for the CTCF.

Figure S3

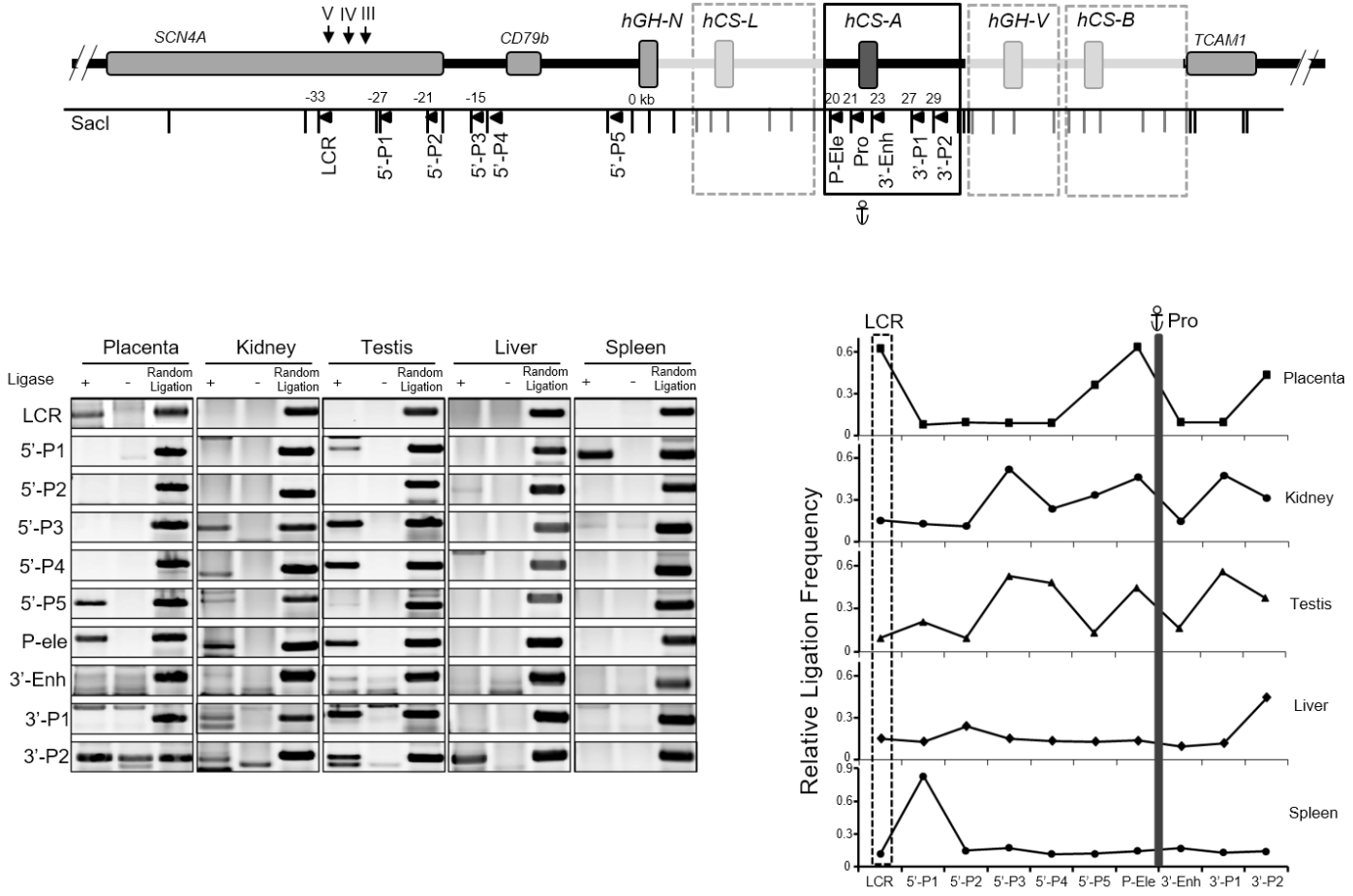


Fig. S3. 3C analysis of *hGH/BAC* transgene locus in placenta and in non-placental tissues. 3C analysis of placenta, kidney, testis, liver, and spleen chromatin from *hGH/BAC* transgenic mouse was performed to investigate the chromatin conformation of *hGH* locus in different tissues. These PCR analyses used the promoter primer ('Pro') as anchor. These studies demonstrate that the looping of the placental LCR (HSIII-V) to the gene promoters is specific to the placenta. In the kidney, testis, and spleen, the promoter was involved in interactions at sites in the region between the LCR and the gene cluster that were not observed in the placental tissue.

Figure S4

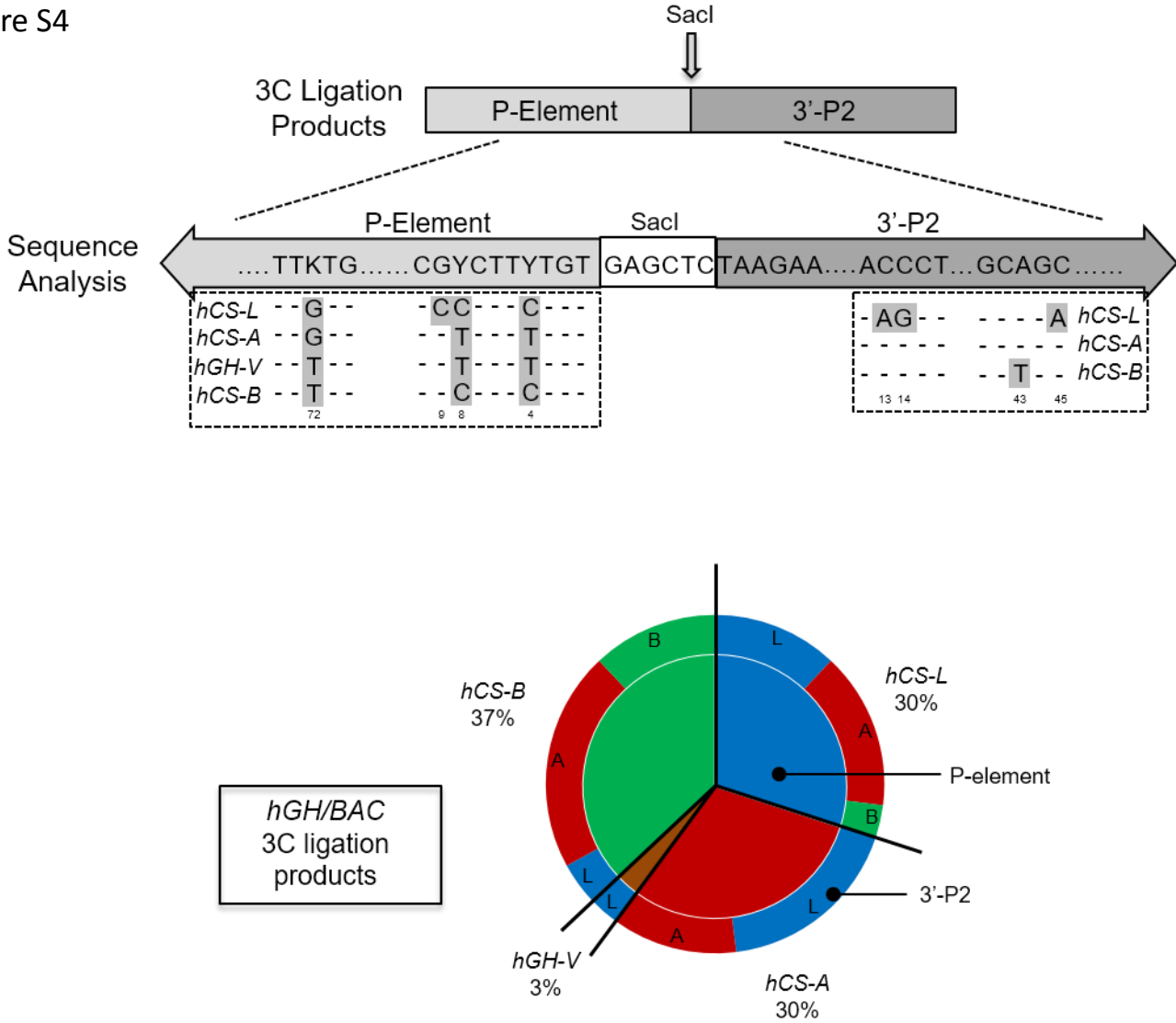


Fig. S4. The native chromatin organization within *hGH* cluster in STB cells is recapitulated in the *hGH/BAC* transgenic mouse. The 3'-P2/P-element ligation products were subcloned and each sequenced to determine the higher-order chromatin structure within the *hGH* gene cluster (as described in **Fig. 3D**). The displayed ligation frequencies, based on the analysis of 106 clones, demonstrate that the chromatin structure established in the placenta of *hGH/BAC* transgenic mouse is consistent with the structure in the native locus.

Figure S5

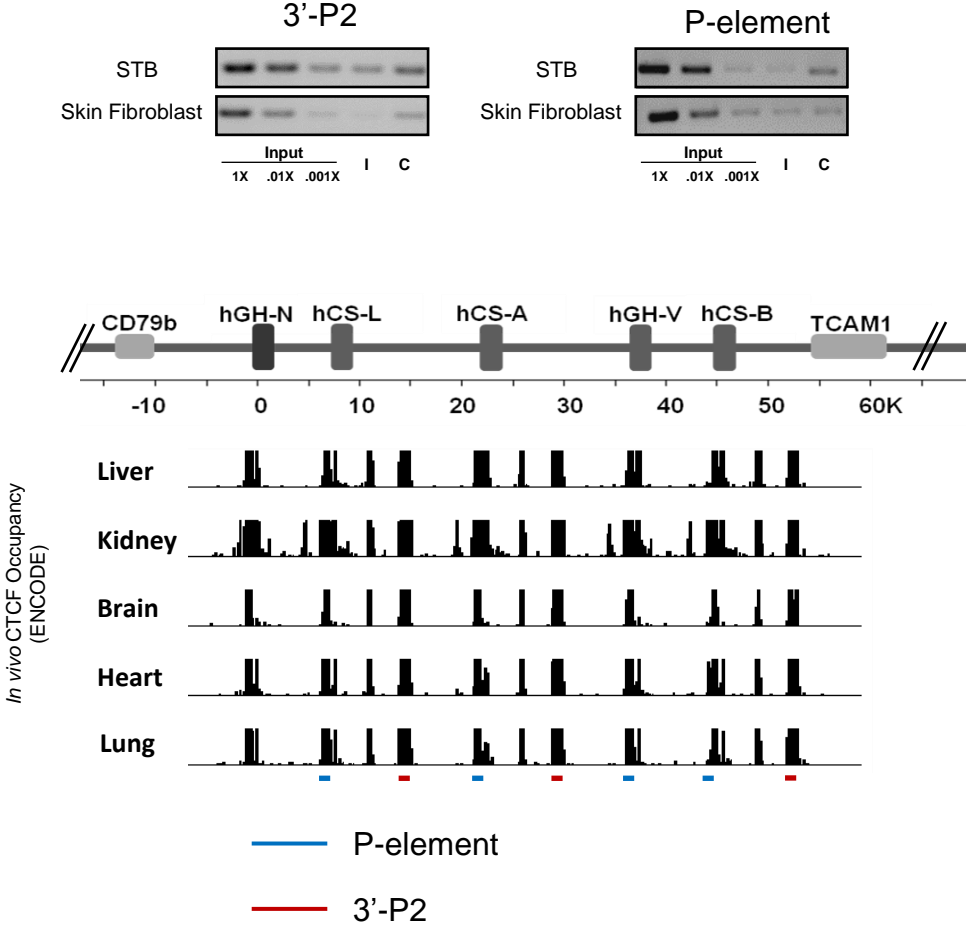


Fig. S5. CTCF recruitment within *hGH* Cluster. CTCF proteins are enriched at 3'-P2 (red) and p-elements (blue) constitutively in different human tissues based on our ChIP-PCR (top) and the ChIP-seq data from ENCODE project (bottom) (24).

Table S1

Primer	Sequence
LCR	5'-TCAGCCTCCCCGAGGCTGAGCAT-3'
5'-P1	5'-GGTGCTGGGTTTCTCTGGAAG-3'
5'-P2	5'-CCAGAGGAGGTCAGAGCAACTTG-3'
5'-P3	5'-CATTACGGCAACCTTGCCA-3'
5'-P4	5'-GGGCTTCACATTCTGACTTCTGACG-3'
5'-P5	5'-ACCTCCTTTTGGCTTCTAATGTCCTTT-3'
P-Ele	5'-GAGTTTAAGAGCATCTAGCACTTGA-3'
Pro	5'-GCTCTCCCCTTTCCCTGAACC-3'
3'-Enh	5'-GGAGGTCTGGGAGTCATGCAG-3'
3'-P1	5'-GGAAGGGGTCAGTTCTGCTCTC-3'
3'-P2	5'-CAGATGGTCCCACACAGTACCCTCA-3'