Description of Additional Supplementary Files

Supplementary Data Legends

Supplementary Data 1. Sequence of oligos used in this study.

Supplementary Data 2. Antibodies used in this study.

Supplementary Data 3. Differentially expressed genes MAD-MSCs vs WT-MSCs. Passage 9 of WT-MSCs and MAD-MSCs were subjected for RNA-seq and summary of differentially expressed genes (log2|Fold change|≥1, FDR<0.05). All p-values were determined by edgeR with default parameters, and adjusted for multiple testing using the Benjamini-Hochberg method.

Supplementary Data 4. Differentially expressed genes associated with LADs reorganization. Integration of differentially expressed genes with LADs reorganization, including gained A-LADs, gained B-LADs, lost A-LADs and lost B-LADs (log2|Fold change|≥1, FDR<0.05). All p-values were determined by edgeR with default parameters, and adjusted for multiple testing using the Benjamini-Hochberg method.

Supplementary Data 5. Differentially expressed genes associated with non-LADs peaks reposition. Integration of differentially expressed genes with non-LADs peaks reposition, including gained A-LADs, gained B-LADs, lost A-LADs and lost B-LADs (log2|Fold change|≥1, FDR<0.05). All p-values were determined by edgeR with default parameters, and adjusted for multiple testing using the Benjamini-Hochberg method.

Supplementary Data 6. Summary of differential genes caused by A and B-type altered lamin-chromatin interaction (log2|Fold change|≥1, FDR<0.05). All p-values were determined using the two-sided Wilcoxon rank-sum test.

Supplementary Data 7. Statistical analysis of the HiC dataset quality. All p-values were determined using the two-sided Wilcoxon rank-sum test.

Supplementary Data 8. Differentially expressed genes associated with shortened TADs and altered lamin-chromatin interaction. Integration of differentially expressed genes with shortened TADs and altered lamin-chromatin interaction (log2|Fold change|≥1, FDR<0.05). All p-values were determined by edgeR with default parameters, and adjusted for multiple testing using the Benjamini-Hochberg method.

Supplementary Data 9. Summary of annotated chromatin loops, E-P loop and differentially expressed genes. Integration of differentially expressed genes with chromatin loop level alterations (log2|Fold change|≥1, FDR<0.05). All p-values were determined by edgeR with default parameters, and adjusted for multiple testing using the Benjamini-Hochberg method.