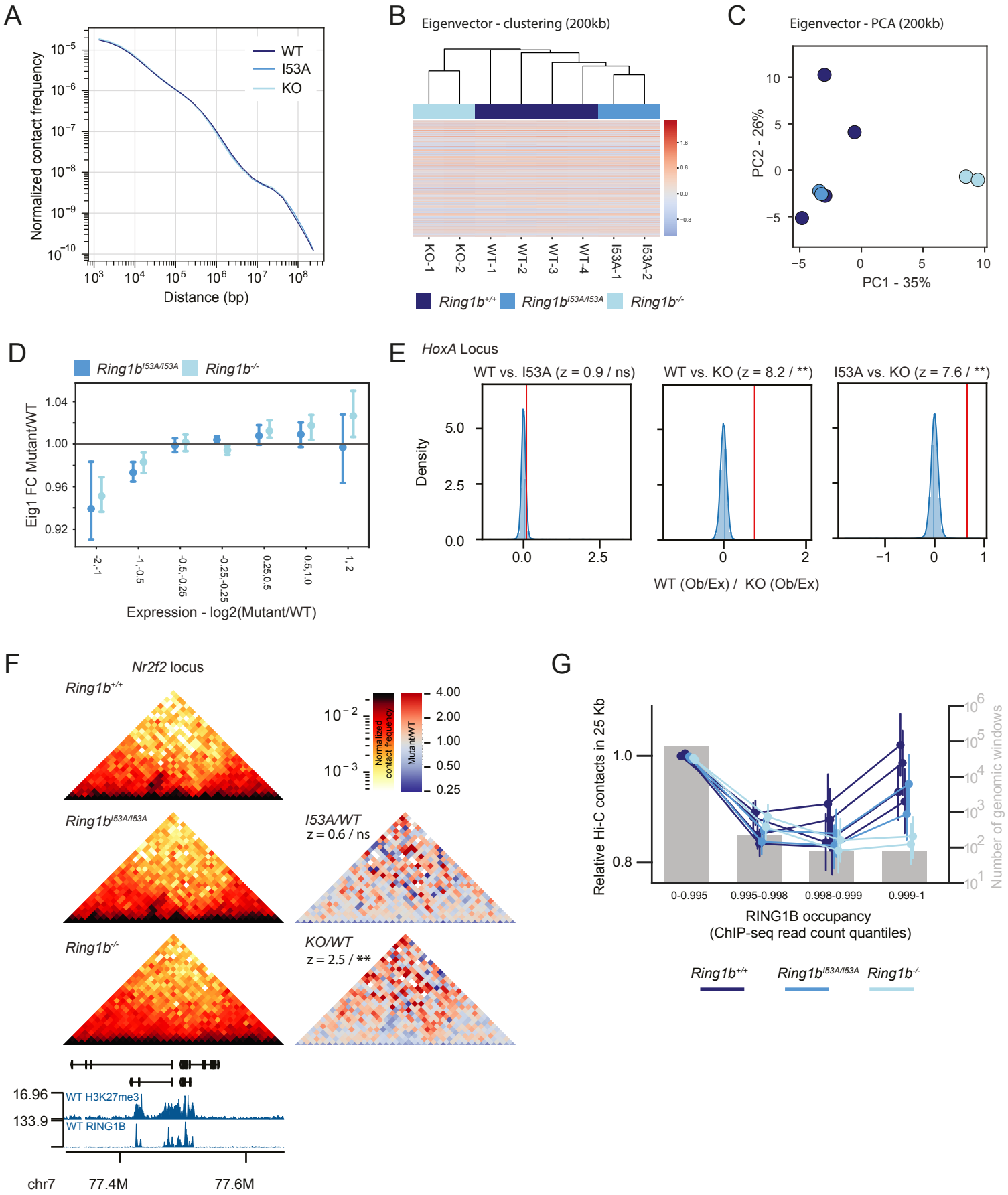

Supplemental Fig. 3. Validation of Hi-C analysis. (A) Curves of probability of contact at different distance separations for *Ring1b*$^{+/+}$, *Ring1b*$^{I53A/I53A}$ and *Ring1b*$^{-/-}$ cells. **(B)** Clustering of first eigenvectors (200 kb resolution) for replicates of Hi-C data for *Ring1b*$^{+/+}$, *Ring1b*$^{I53A/I53A}$ and *Ring1b*$^{-/-}$ mESCs. **(C)** PCA analysis of eigenvectors from **(B)**. **(D)** Median fold-change of first eigenvectors from Hi-C data from *Ring1b*$^{I53A/I53A}$ and *Ring1b*$^{-/-}$ mESCs relative to *Ring1b*$^{+/+}$ mESCs (error bars show 95% confidence interval obtained by bootstrapping), for all 50 kb bins grouped by average log2 fold change in gene expression relative to *Ring1b*$^{+/+}$ within the bin. **(E)** Statistical estimation of contact frequency changes within the *HoxA* cluster for all pairwise comparisons between *Ring1b*$^{+/+}$, *Ring1b*$^{I53A/I53A}$ and *Ring1b*$^{-/-}$ cells. Shown are histograms of ratios of observed/expected signal for 10,000 random regions on the same chromosome (bars) and its associated kernel-density estimate (curve). The red vertical line represents the value for the *HoxA* region. Z-value and level of significance shown. **(F)** Same as **Fig. 3A**, but for the *Nr2f2* region (statistical estimation performed on chr7 77.43 – 77.52 Mb; mm9 genome build). **(G)** Same as **Fig. 3E**, but for individual replicates.