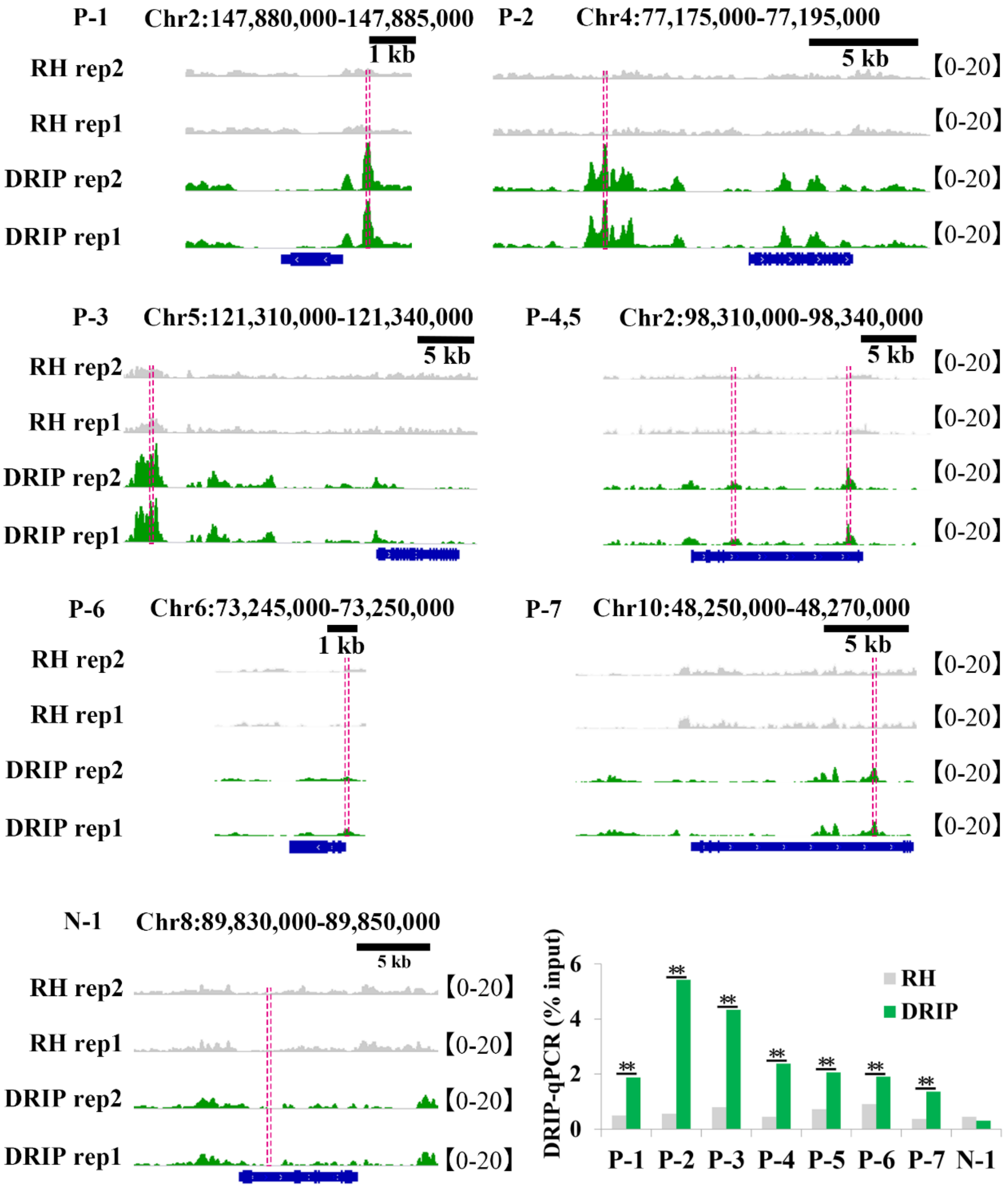

Supplemental_Fig_S3. Validating of the R-loops by DRIP-qPCR.

The snapshots of Integrative Genomics Viewer (IGV) spanning eight regions for DRIP-qPCR assay. The red dash lines indicated the regions for DRIP-qPCR primer design. Of the 9 positive loci examined, 7 (78%, P-1, P-2, P-3, P-4, P-5, P-6 and P-7) exhibited a significantly higher value (relative to the percent input) than RNase H-treated sample, while one negative control (N-1) lacking R-loops showed no significantly difference between DRIP sample and RNase H-treated sample. Primer sequences were listed in Supplemental Table S3.