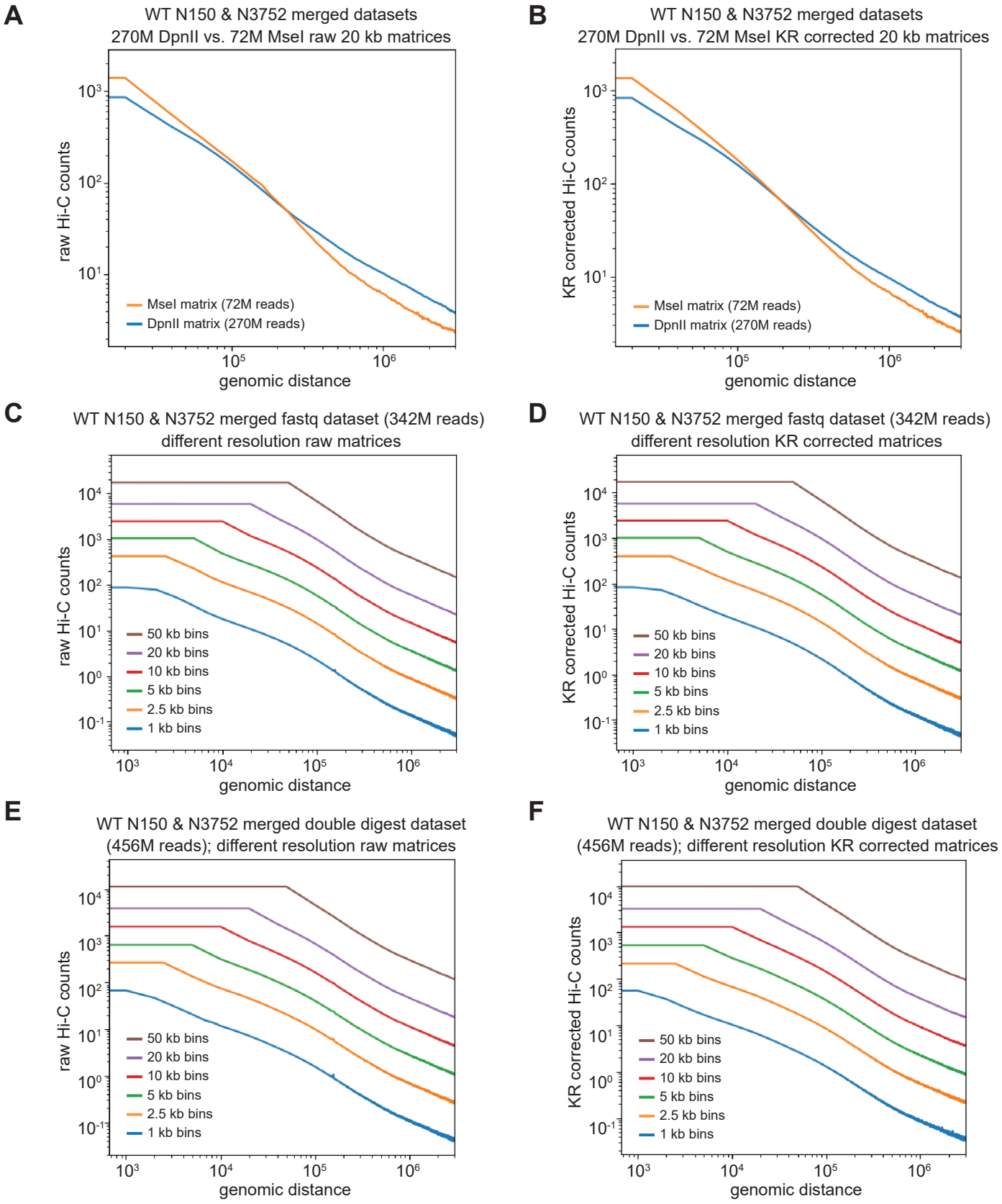

Figure S9. The contact strength of interacting regions is inversely related to genomic distance in *in situ* Hi-C datasets. (A-B). Genomic distance vs. contact strength plots of the merged DpnII Hi-C dataset (in which all four DpnII replicates were merged into a single matrix accounting for 270M total reads, 89.2M of which were valid) or the merged MseI Hi-C dataset (in which three MseI replicates were merged into a single matrix accounting for 72M total reads, 16.7M of which were valid; 21.4M reads, or 3.8M valid reads, were excluded from the MseI merged dataset to appropriate represent the heterochromatic [15.76%] reads in the single matrix combined dataset - see Materials and Methods for details). Plots were generated using the raw (A) or KR-corrected (B) contact matrices at 20 kb bin resolution using the hicExplorer command hicPlotDistVsCounts. (C-D). Genomic distance vs. contact strength plots of the 342M total read (106M valid read) combined DpnII+MseI dataset, in which replicate fastq files were merged into a single fastq file prior to generating individual raw (C) or KR-corrected (D) Hi-C contact matrices at six different resolutions. (E-F). Genomic distance vs. contact strength plots of the raw (E) or KR-corrected (F) Hi-C contact matrices of the 456M total read (76.5M valid read) DpnII+MseI double digest dataset at six different resolutions.