



**Fig. S2** Replication domain maps of the 46C mouse ES cell (chromosome 16) from sequencing by Ion Proton and Illumina HiSeq.

A publicly available Illumina Hiseq data set (GSE95091) was used for comparison. Loess-smoothed plots of  $\log_2$  (early/late) ratio determined at each 5-Kb genomic bin are shown. Data sets were quantile-normalized for comparison. Remarkable conservation between two data sets seen in a merged plot (bottom,  $R=0.96$ ) suggests that amplification bias from WGA is negligible if it exists.