Supplementary Text T4

1 Megabase (Mb) Contact maps of GM06990 HindIII and NcoI [1], after fragment filtration [2], were downloaded from http://compgenomics.weizmann.ac.il/tanay/?page_id=283. Since the number of 1Mb regions was different between the NcoI and HindIII replicates, we have removed several regions so that the contact maps will match (i.e. so that row i in the 2 matrices represents the same region) before computing their correlation (2 bins in NcoI and 5 bins for HindIII were removed from consideration). The spearman correlation was then calculated for each pairwise contact map (considering All chromosome pairs), for the observed and corrected maps. We have next downloaded the contact maps of the HindIII and NcoI replicates, that were corrected with YT (http://compgenomics.weizmann.ac.il/tanay/?page_id=283) and HiCNorm (http://www.people.fas.harvard.edu/~junliu/HiCNorm/Lieberman-Aiden.rar).   Since corrected contact maps were not available for ICE and as its current software implementation required complicated pre-processing, we have implemented ICE [4], as described in [4], and applied it to the contact maps used as input for our correction. Here, 2 additional regions were removed before correction as ICE cannot handle uncovered regions (i.e. regions with zero column and row sums). Finally, we have calculated the spearman correlation for each correction method as described above and compared it with the results of our correction (Table 1).

References

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