10.10.2016 :

Hi-C experiments used to define TADs (Rao et al, 2014) are subject to biases caused by chromatine accessibility, nucleosome occupancy, restriction site-density and alignability. These bias have been corrected by coverage normalization. (and other algorithms, see supplemental data)

11.10.2016

Because of the large number of overlaps between TADs, I merged the overlapping TADs together to consider only the large ones. (used merge from BEDtools)