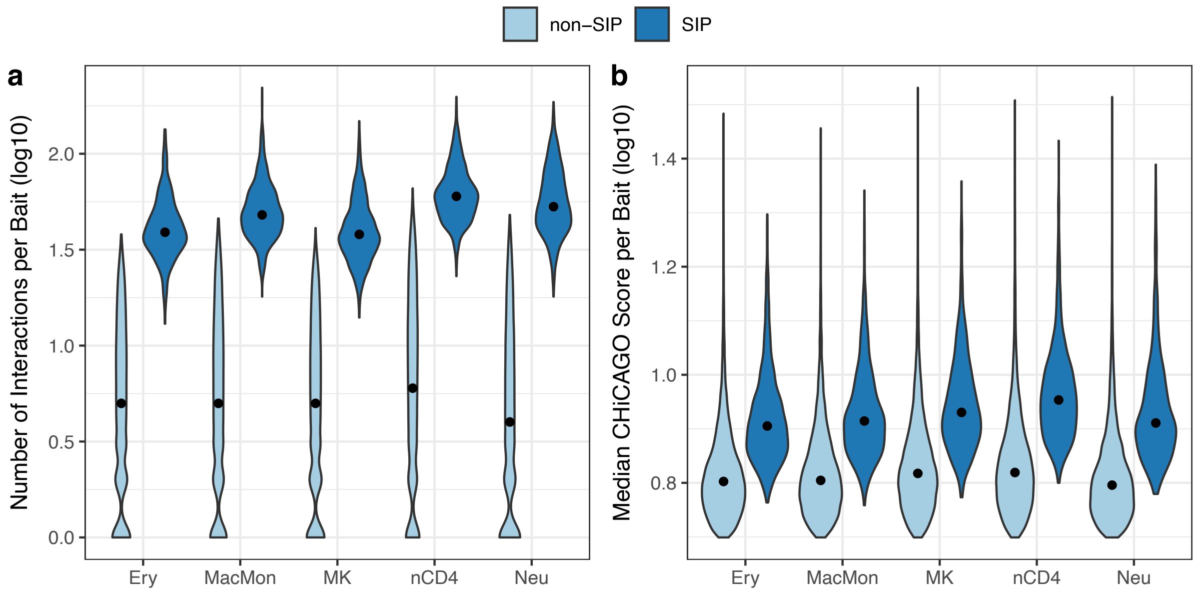

S22 Fig. SIP patterns when detected using a maximum 1D genomic distance of 1Mb (Javierre et al pcHi-C data) (A) The distribution of the number of significant interactions (log10 scale) for SIPs and non-SIPs**; (B)**. The distribution of the median CHiCAGO (log10 scale) of significant interactions per promoter bait for SIPs and non-SIPs.