

Table S3 Clustering results on bootstrapped Hi-C link datasets

M-Y (total sequence length = 135206617)				
	Sequence clustered	% clustered	Seq misclustered	% misclustered
Main result	111112059	82.18%	922932	0.83%
Bootstrap 1	111136126	82.20%	4146798	3.73%
Bootstrap 2	111102736	82.17%	4500167	4.05%
Bootstrap 3	111106339	82.18%	4655083	4.19%
Bootstrap 4	111101816	82.17%	4389061	3.95%
Bootstrap 5	111106542	82.18%	4425448	3.98%
Bootstrap 6	111158559	82.21%	4356095	3.92%
Bootstrap 7	111089140	82.16%	4173561	3.76%
Bootstrap 8	110777343	81.93%	1294345	1.17%
M-PE (total sequence length = 133169811)				
	Sequence clustered	% clustered	Seq misclustered	% misclustered
Main result	118841530	89.24%	461626	0.39%
Bootstrap 1	117677687	88.37%	1748183	1.49%
Bootstrap 2	117818421	88.47%	737953	0.63%
Bootstrap 3	117636660	88.34%	1834184	1.56%
Bootstrap 4	117604654	88.31%	497732	0.42%
Bootstrap 5	117695244	88.38%	509778	0.43%
Bootstrap 6	117566728	88.28%	1600895	1.36%
Bootstrap 7	117679867	88.37%	1870031	1.59%
Bootstrap 8	117760573	88.43%	1748183	1.48%

We ran the MetaPhase clustering algorithm on the M-Y and M-PE datasets, producing the results given in the main Results section. We also re-ran the clustering algorithm in each of these cases and applied randomized bootstrapping (that is, re-sampling with replacement of N data points) to the Hi-C link data. Shown are the results of eight bootstrapping runs for each sample.