

A high-resolution map of the three-dimensional chromatin interactome in human cells

Jim F. et al. *Nature* 503, 290-294, 2013

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Overview

- 1 Progress and rotation goal
- 2 The Hi-C technique
- 3 Results
- 4 Conclusions
- 5 Preliminary analysis

Progress and rotation goal



- ① Get familiar with Hi-C
- ② Reproduce published data
- ① Become an expert in Hi-C data analysis
- ② Combine Hi-C with ChIP-Seq data

The Hi-C technique

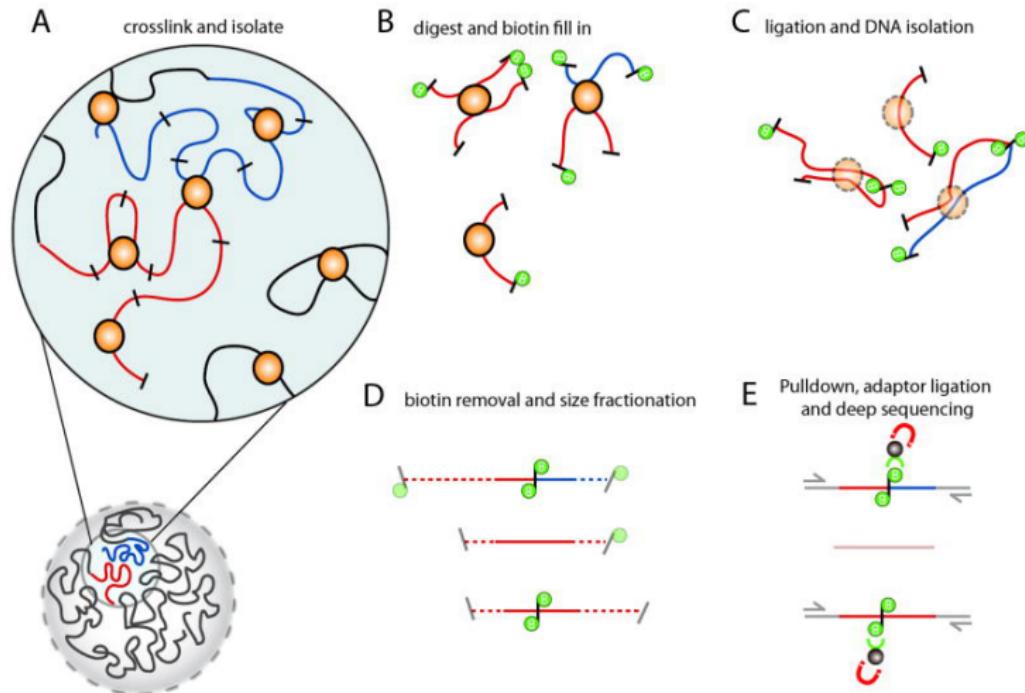
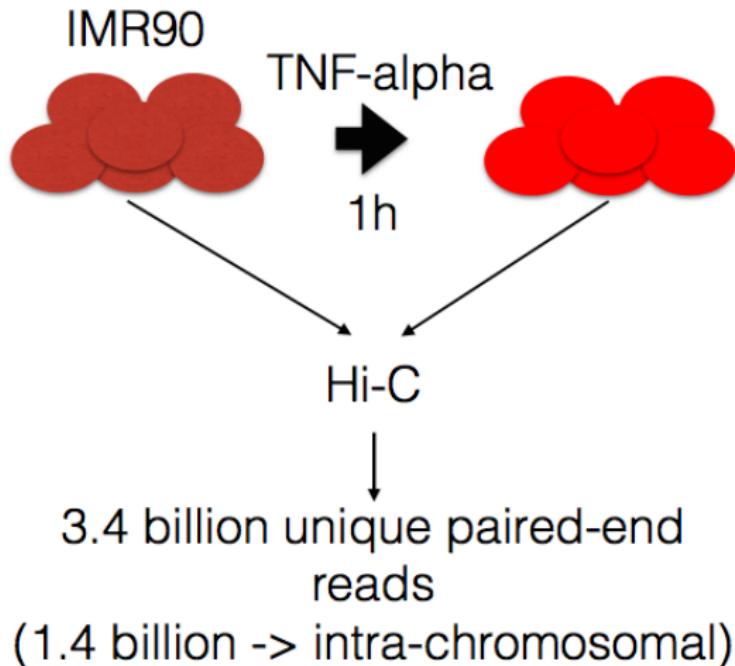
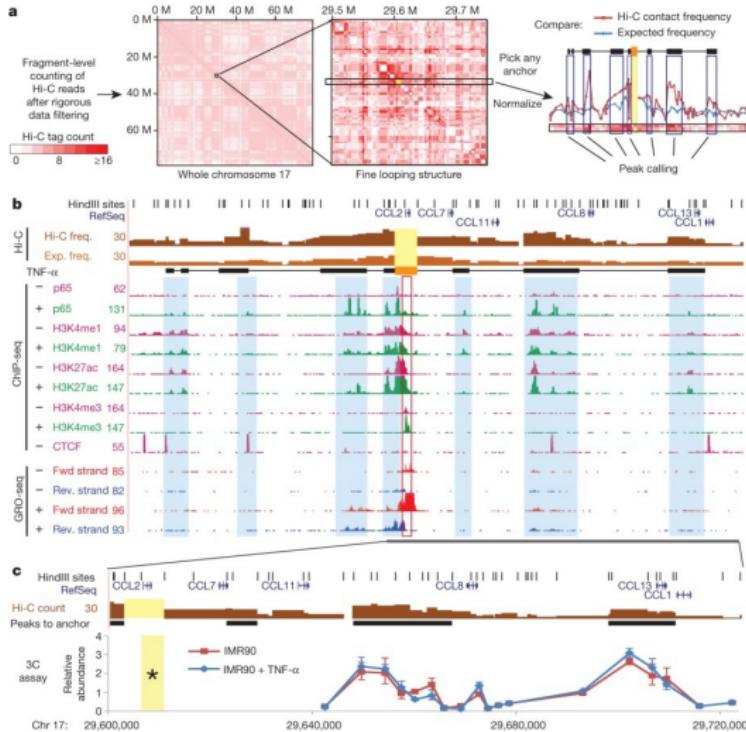


Figure : An overview of the Hi-C technique. Source: Belton, J.-M. et al. Methods 58, 268–276 (2012).

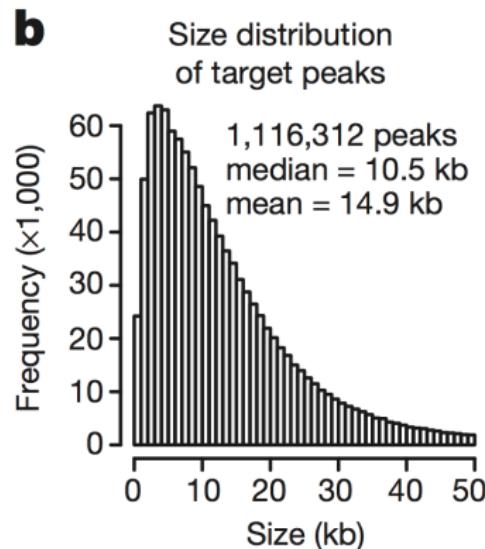
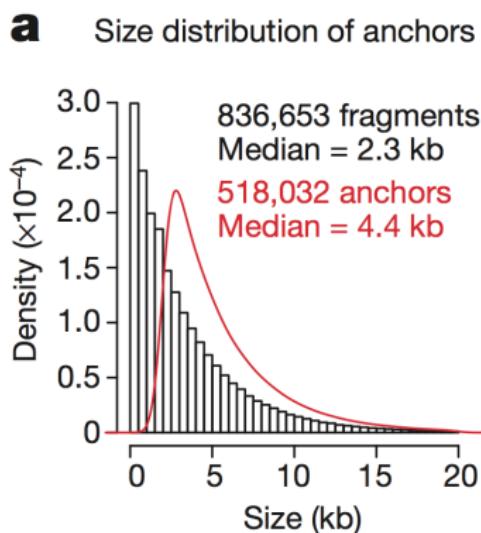
The experimental procedure



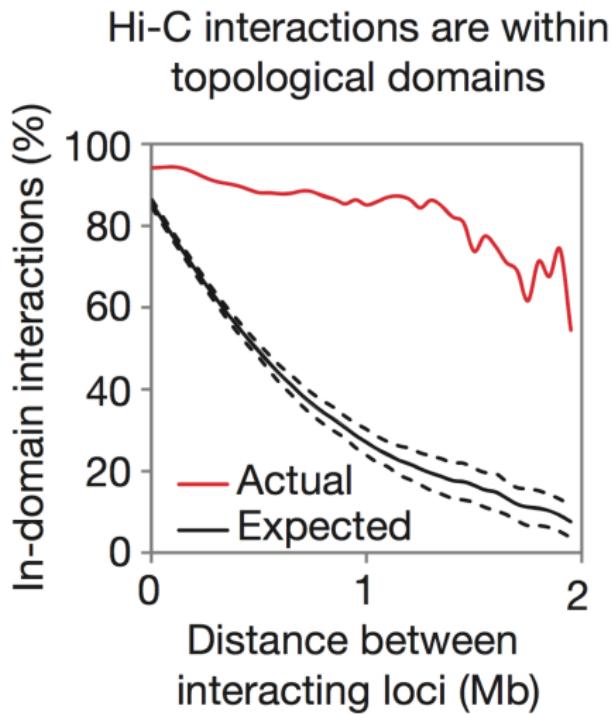
The *CCL2* interactome in IMR90 cells



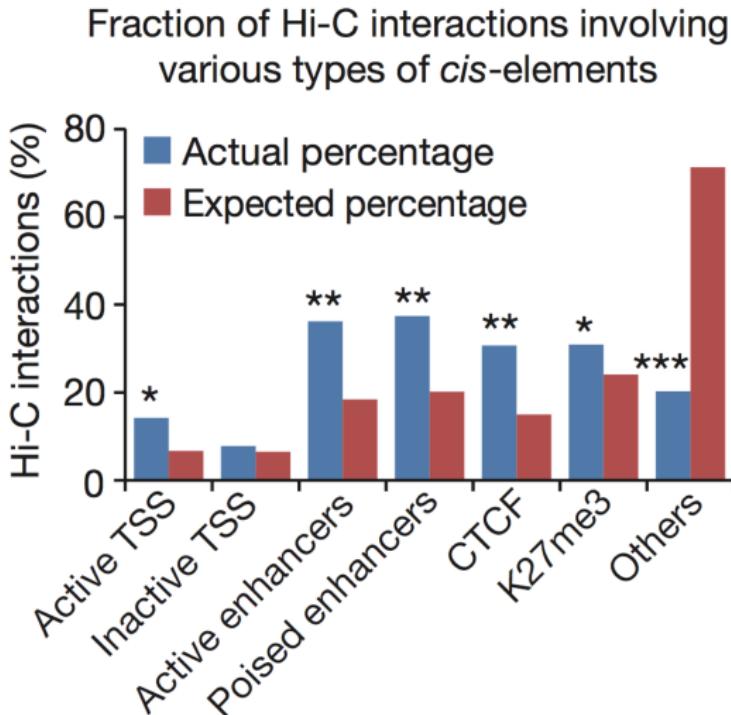
Size distribution of anchors and target peaks



Hi-C interactions are within topological domains

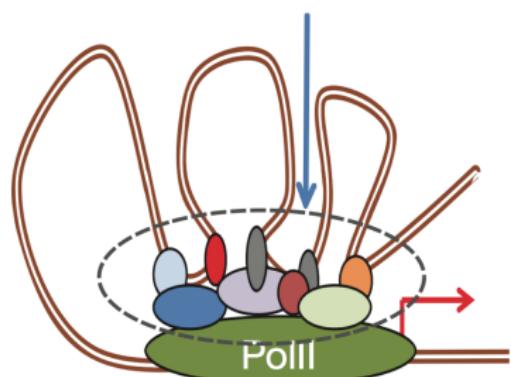


cis interactions in IMR90

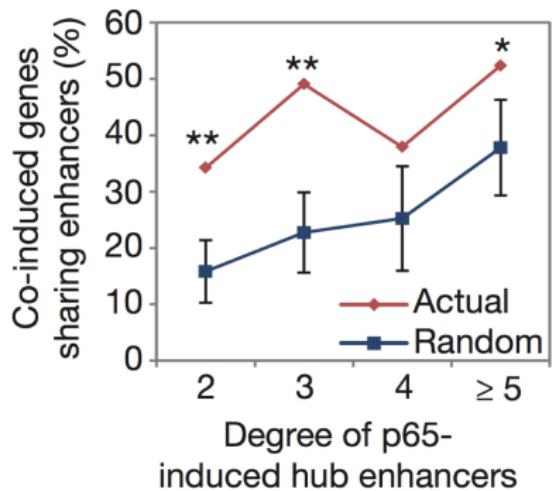


Increased promoter-enhancer interaction in active genes

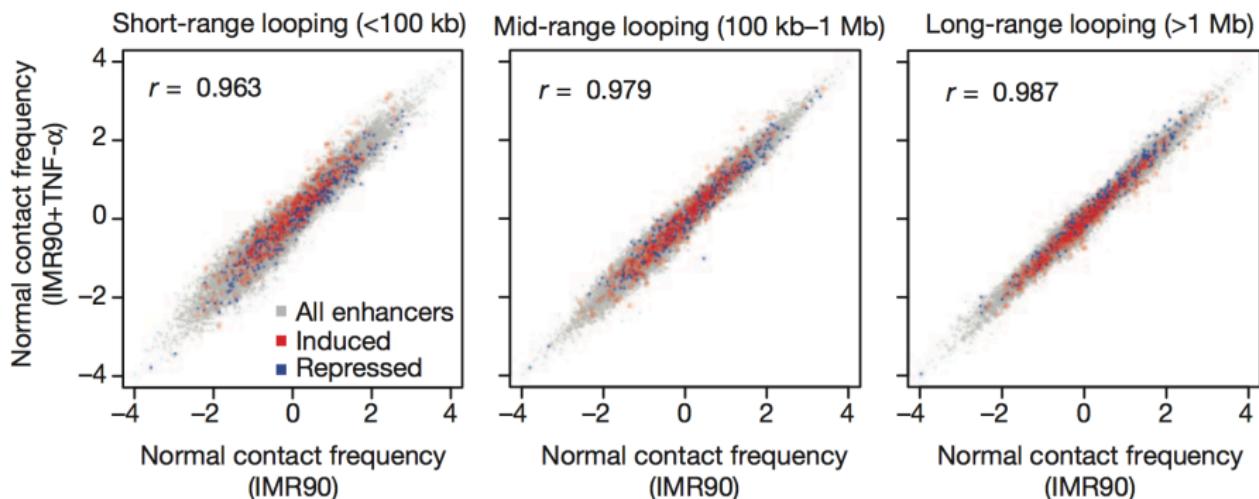
Promoter tethered regions



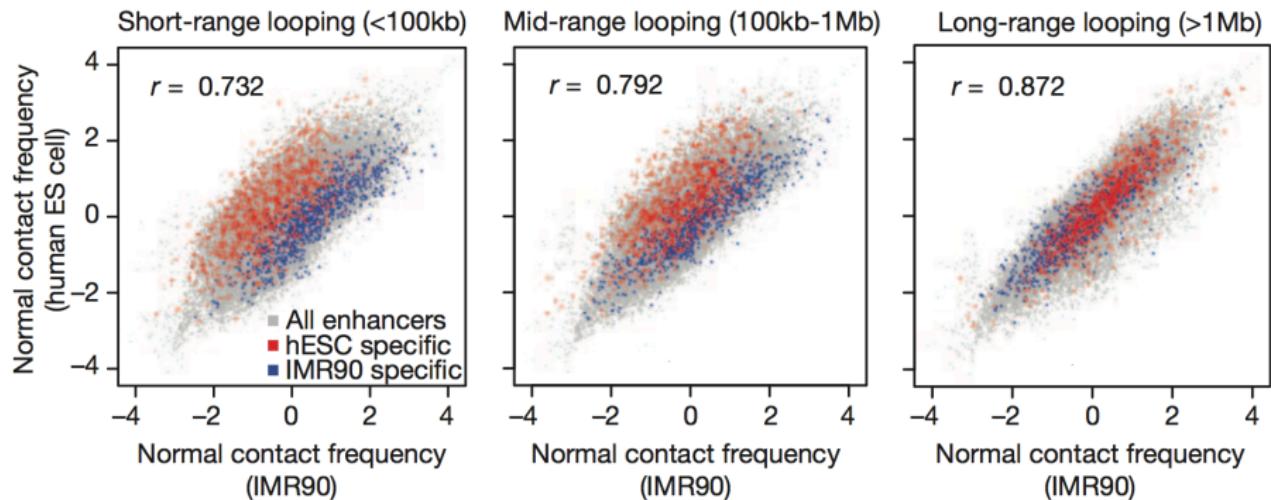
Target genes of hub enhancers
are co-induced by TNF- α



Higher-order chromatin structure is stable during transient TNF- α signaling (IMR90)



This is not the case in embryonic stem cells

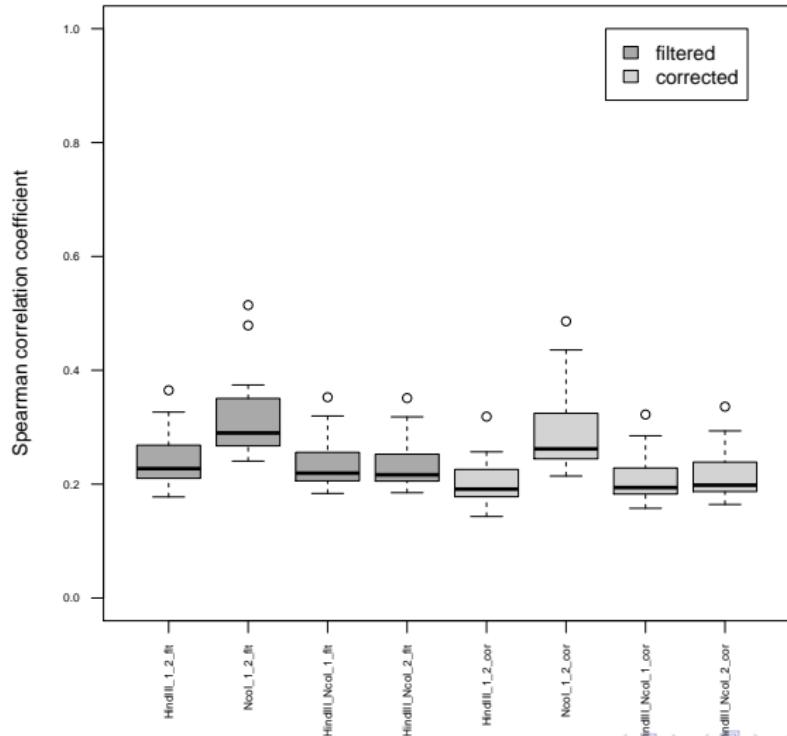


Results

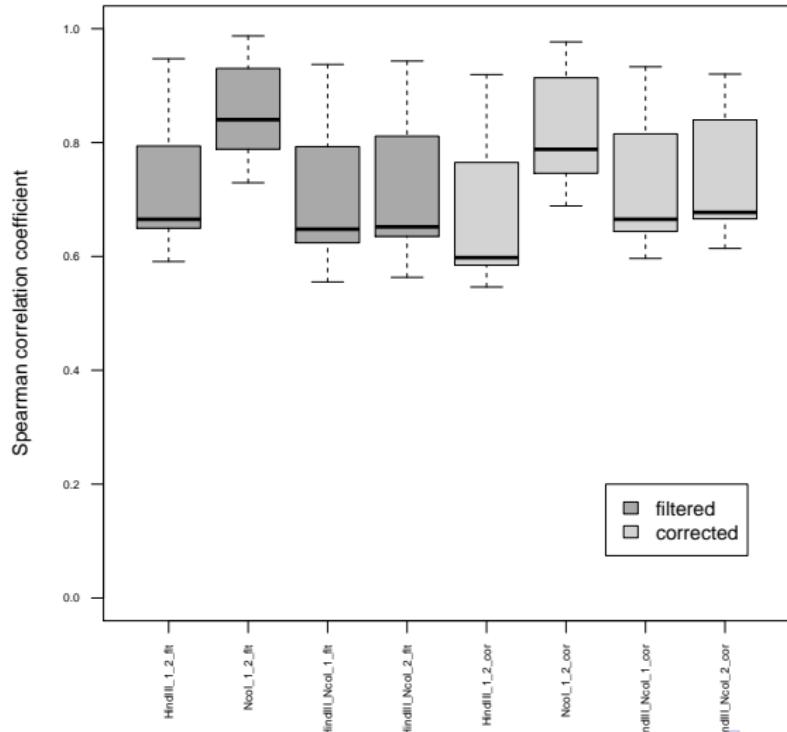
- ① A comprehensive map of genomic interactions in fibroblasts
- ② Over one million interactions identified
- ③ Unprecedented resolution of 5-10Kb
- ④ Asymmetric distribution of *cis*-contacts between highly expressed promoters and the downstream genes (even when transcription is blocked).
- ⑤ TNF- α enhancers in contact with target genes before signaling (experiment to show that TNF- α is really absent?)

Preliminary results

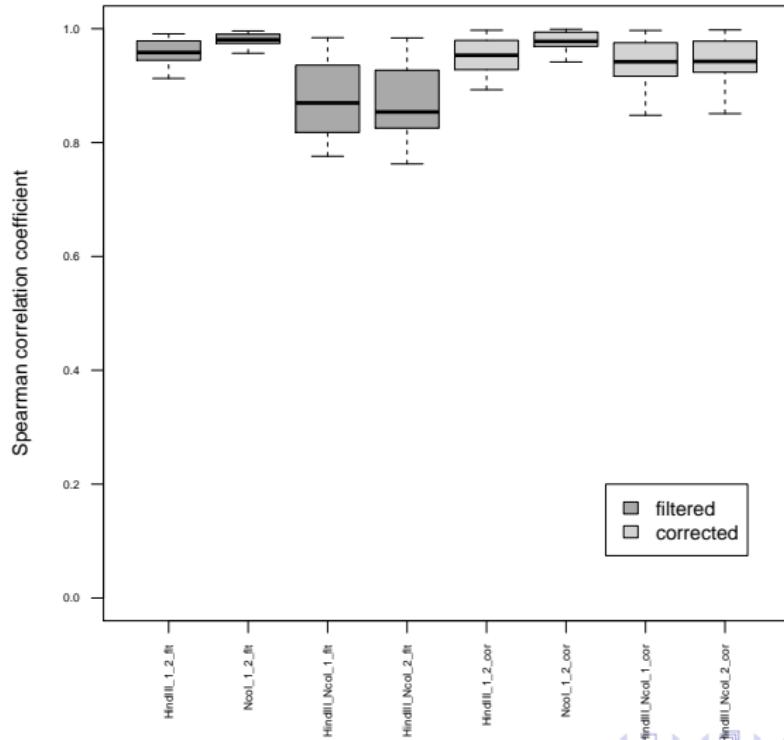
Correlation of Hi-C results between replicates (128kb)



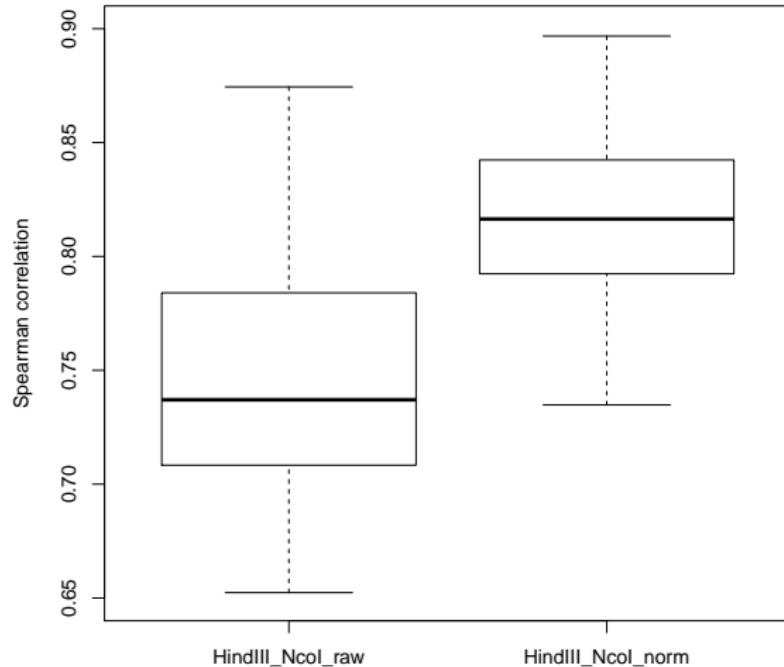
Correlation of Hi-C results between replicates (1024kb)



Correlation of Hi-C results between replicates (4096kb)



Correlation of Hi-C results (HindIII–Ncol) (1MB)



Q & A