A

Sample Name	shCtrl rep1	shCtrl rep2	shU rep1	shU rep2
Total Reads	613265393	557713946	612445541	558876278
Side 1 Aligned	580035777	528966928	579619289	530266033
Side 2 Aligned	565954266	510182434	566416018	514095963
Unique Pairs	426574977	393546155	425336683	397836834
Dangling Ends Pairs	3489347	3864660	2814643	3313922
Self circles Pairs	240585	232561	224611	226006
Dumped Pairs	45655886	46179542	44258953	43937556
Duplicate Pairs	87057010	115947527	78769563	104330191
Unique Valid Pairs	290132149	227321865	299268913	246029159
Unique Valid Pairs %	47.31%	40.76%	48.86%	44.02%
cis interaction	232549213	183327610	246532290	204529499
trans interaction	57582936	43994255	52736623	41499660

B

Cis Genome
200kb resolution

C

D

Chr19 (200kb resolution)

Supplemental Figure S3. Mapping statistics and the repeatability of Hi-C experiments. (A) Mapping statistics of Hi-C deep sequencing data of two replicates in the control and *Hnrnpu* knockdown samples. (B) Pearson correlation coefficients from 200 kb binned Hi-C cis contact matrices between replicates. (C) Contact matrices in shCtrl (left) and shU (right) treated cells: all chromosomes at 1MB resolution (top); Chr13 at 500 kb resolution (middle); Chr13:72–92 Mb at 40 kb resolution (bottom). (D) Hi-C contact matrices and their changes with *Hnrnpu* knockdown are highly consistent between replicates.