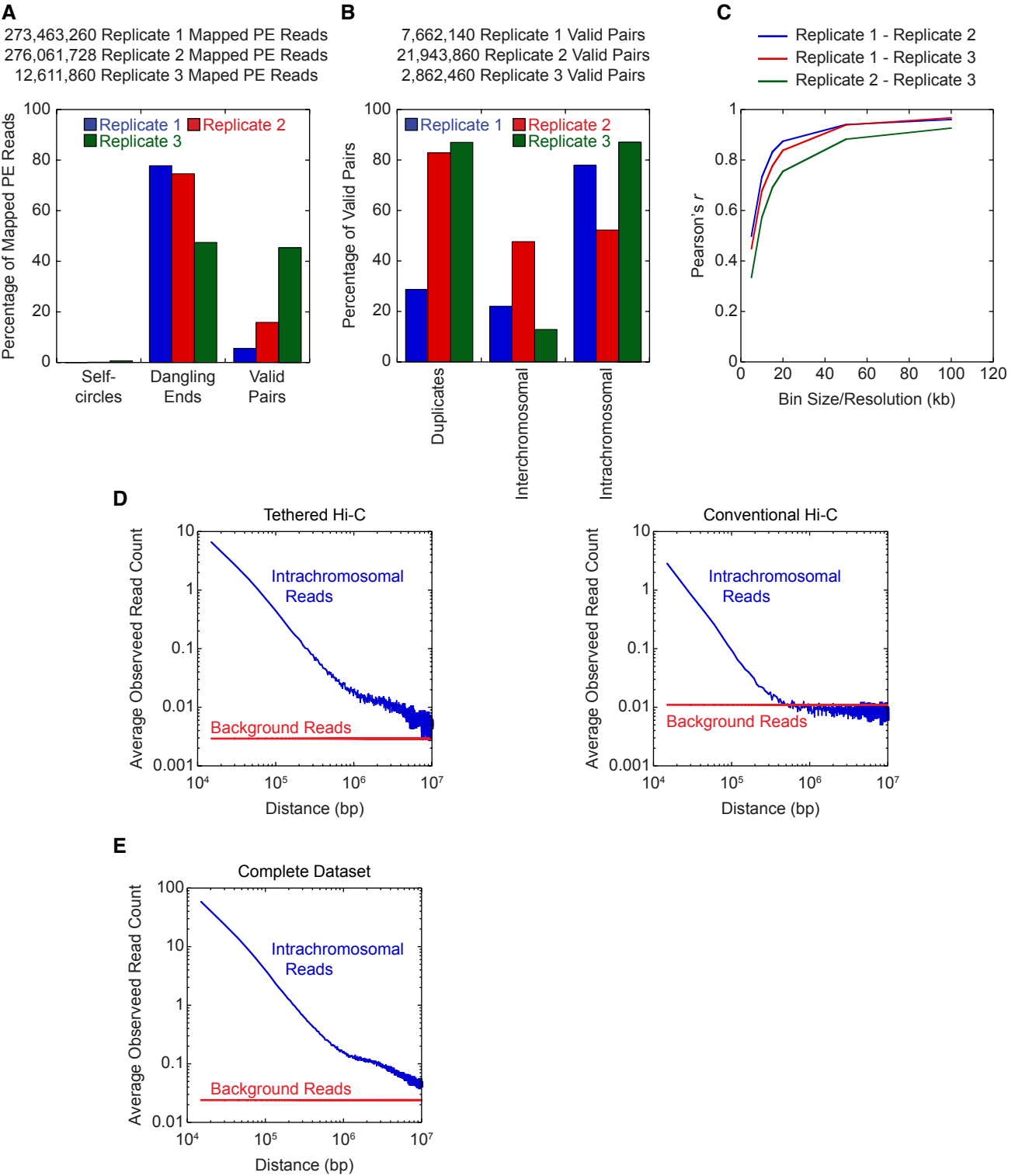
Figure S2


A
273,463,260 Replicate 1 Mapped PE Reads
276,061,728 Replicate 2 Mapped PE Reads
12,611,860 Replicate 3 Maped PE Reads
Percentage of Mapped PE Reads
Replicate 1
Replicate 2
Replicate 3
Self-circles
Dangling Ends
Valid Pairs
B
7,662,140 Replicate 1 Valid Pairs
21,943,860 Replicate 2 Valid Pairs
2,862,460 Replicate 3 Valid Pairs
Percentage of Valid Pairs
Duplicates
Interchromosomal
Intrachromosomal
C
Replicate 1 - Replicate 2
Replicate 1 - Replicate 3
Replicate 2 - Replicate 3
Pearson's r
Bin Size/Resolution (kb)
D
Tethered Hi-C
Conventional Hi-C
Average Observed Read Count
Intrachromosomal Reads
Background Reads
Distance (bp)
E
Complete Dataset