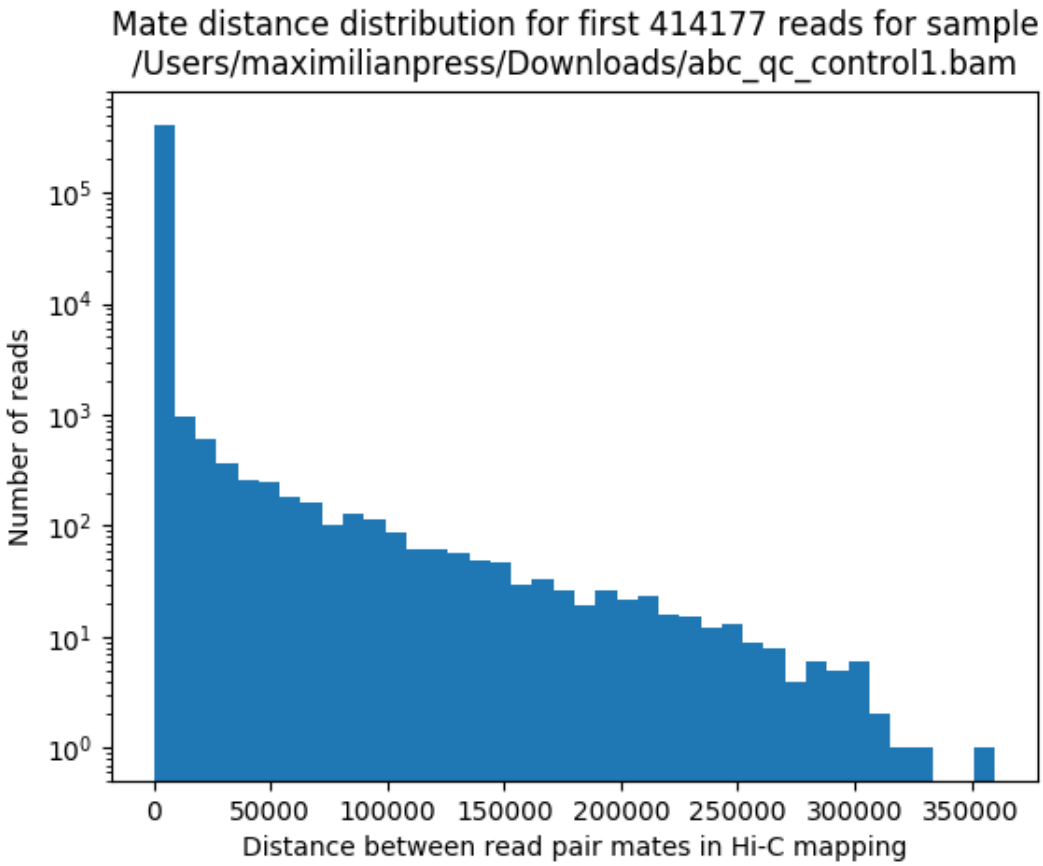
Hi-C library QC report

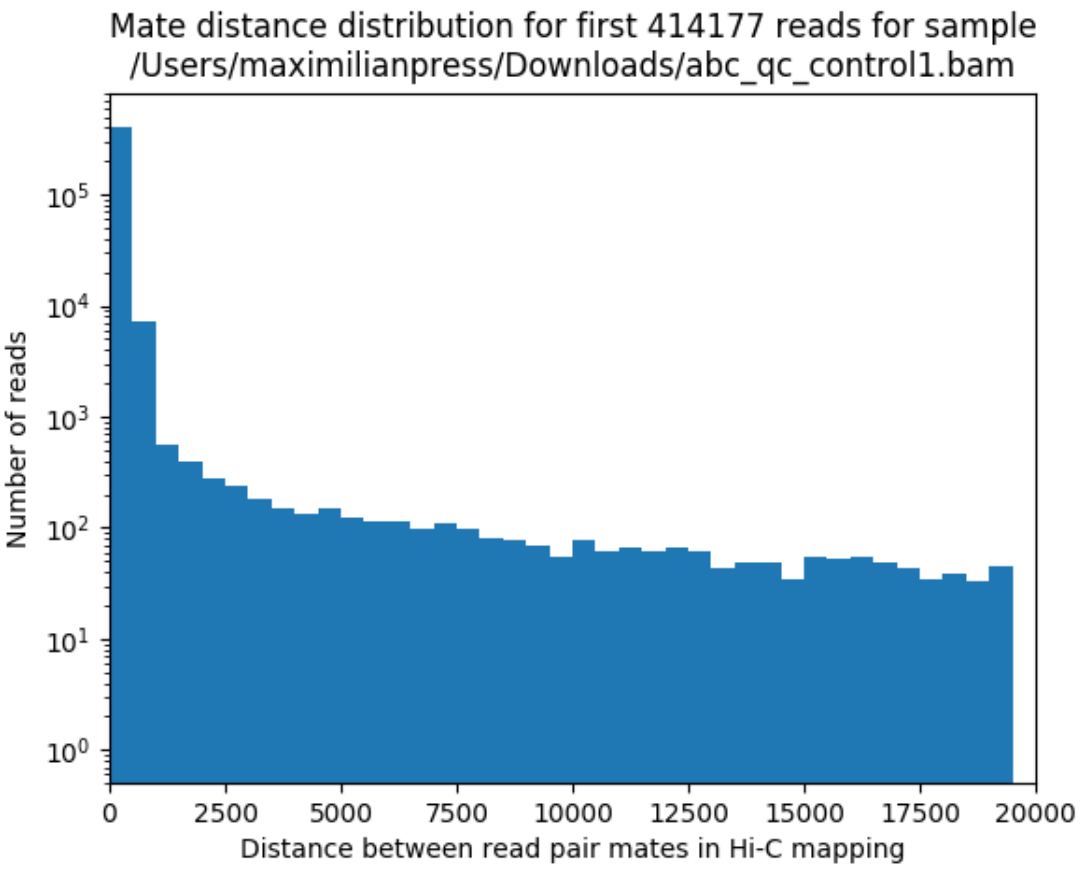
Library statistics

Label	Your library	Expected values
BAM file	abc_qc_control1.bam	N/A
Number of read pairs	414177	N/A
Fraction of read pairs >10KB apart	0.009	0.005-0.05
Fraction of read pairs mapping to different contigs/chromosomes	0.236	0.1-0.5 (contigs) 0.01-0.1 (chromosomes)
Fraction of split reads	0.267	0.1-0.4 (PG libraries) 0.3+ (other libraries)
Fraction of zero-distance pairs	0.257	0-0.15

See below for information on differences between Phase Genomics Hi-C libraries and traditional Hi-C libraries.

Aligned mate distance histograms





Alignment distance statistics and plots

We briefly describe some of the statistics we compute below to aid interpretation of this report.

Fraction of read pairs > 10KB apart

Fraction of read pairs mapping to different contigs or chromosomes

Fraction of zero-distance pairs

Split reads

Traditionally, split reads have been a favored measure of Hi-C library quality. This is because traditional Hi-C library preparations are expected to produce many reads reading through junctions.

Phase Genomics libraries, whether produced in our laboratory or by means of ProxiMeta ©, Animal, Plant, or Human kits, will have a generally lower fraction of split reads. This is because we have optimized our Hi-C protocol to