Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap 2014/01/30 09:26:33

1. Summary

1.1. Globals

Reference size	4,639,675
Number of reads	5,967,350
Mapped reads	5,967,350 / 100%
Unmapped reads	0 / 0%
Paired reads	5,967,350 / 100%
Mapped reads, only first in pair	2,983,675 / 50%
Mapped reads, only second in pair	2,983,675 / 50%
Mapped reads, both in pair	5,967,350 / 100%
Mapped reads, singletons	0 / 0%
Read min/max/mean length	14 / 90 / 89.93
Clipped reads	101,633 / 1.7%
Duplication rate	52.19%

1.2. ACGT Content

Number/percentage of A's	132,309,516 / 24.66%
Number/percentage of C's	136,204,914 / 25.38%
Number/percentage of T's	132,261,383 / 24.65%
Number/percentage of G's	135,833,734 / 25.31%
Number/percentage of N's	0 / 0%
GC Percentage	50.7%

1.3. Coverage

Mean	115.66
Standard Deviation	25.98

1.4. Mapping Quality

Mean Mapping Quality	87.05

1.5. Indels

Total reads with indels	6,600
Insertions	2,275
Deletions	4,325
Homopolymer indels	49.44%

1.6. Insert size

Mean	483.47
Median	484

1.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation
gi|49175990|ref|NC_000913.2|	4639675	536622630	115.66	25.96

2. Input data & parameters

## 2.1. Alignment

|	
BAM file:	13YFP_paired_ssaha2.bam
Size of a homopolymer:	3
Number of windows:	400
Analysis date:	Thu Jan 30 09:26:33 WET 2014
Draw chromosome limits:	no

3. Coverage across reference
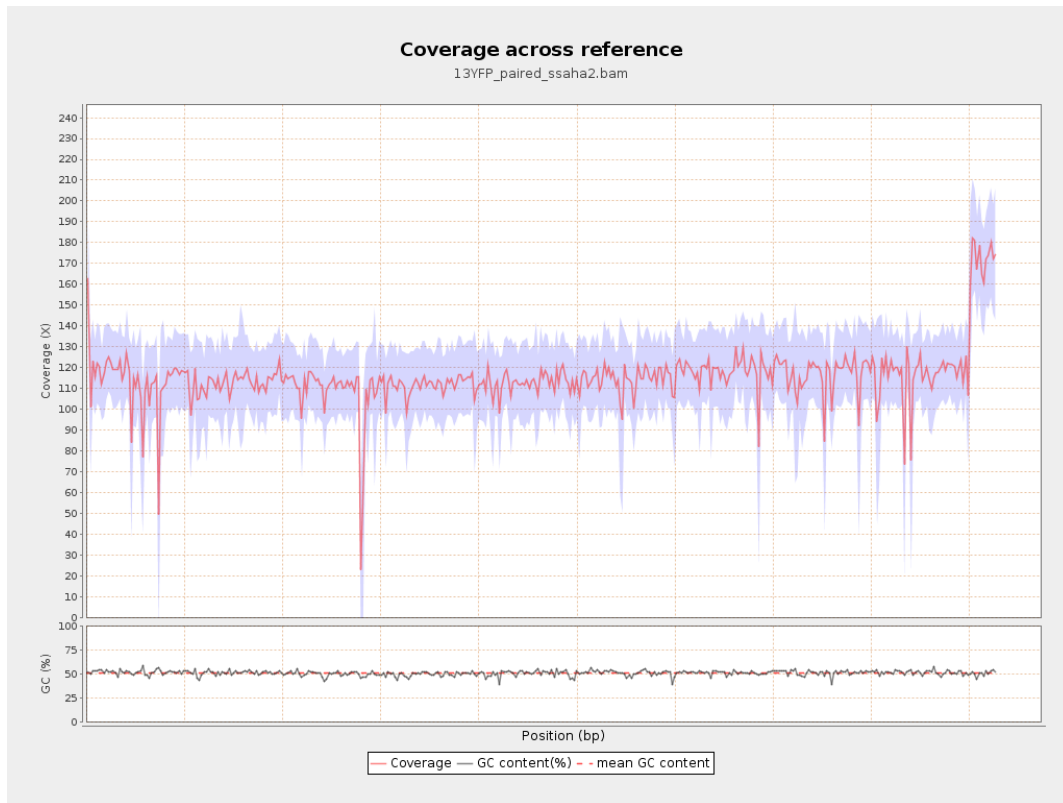
Coverage across reference

13YFP_paired_ssaha2.bam

4. Coverage Histogram

Coverage Histogram
13YFP_paired_ssaha2.bam

5. Coverage Histogram (0-50X)

Coverage Histogram (0-50X)
13YFP_paired_ssaha2.bam

6. Duplication Rate Histogram
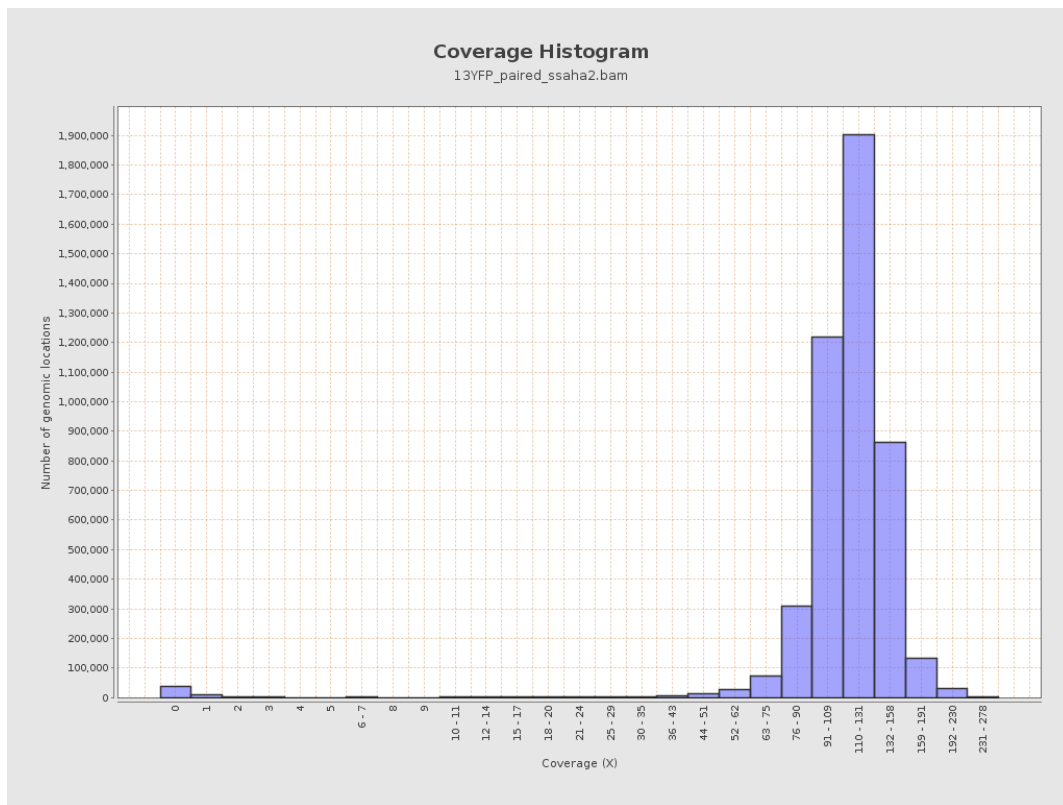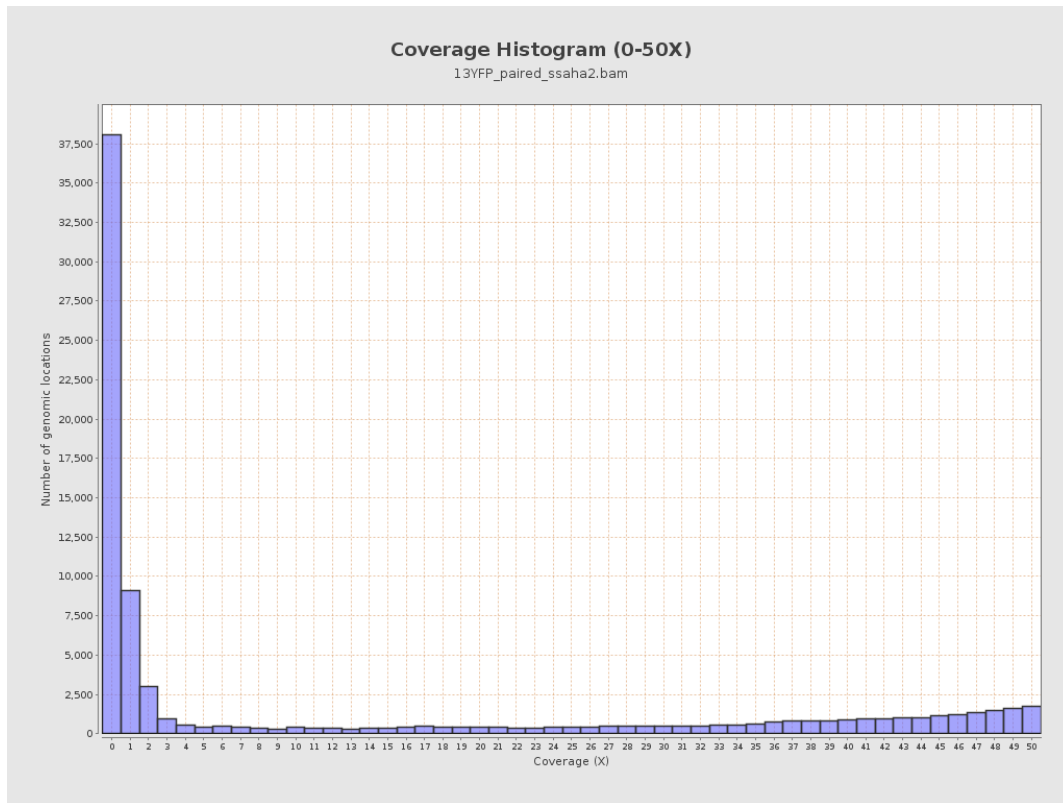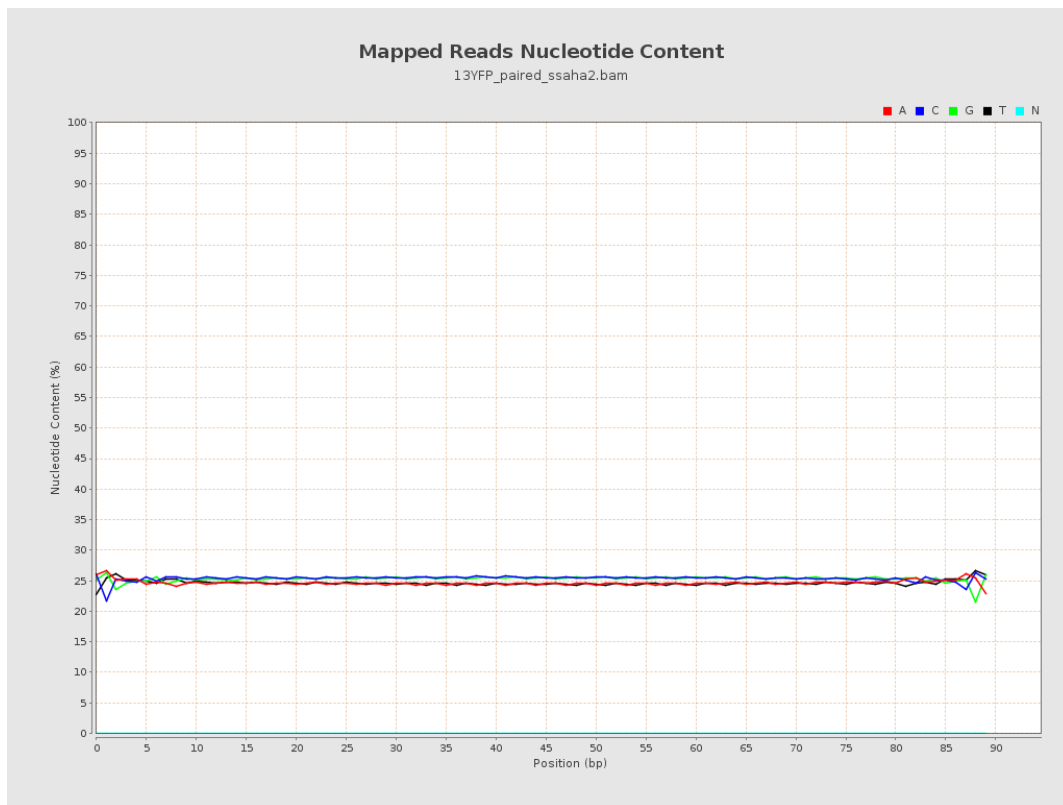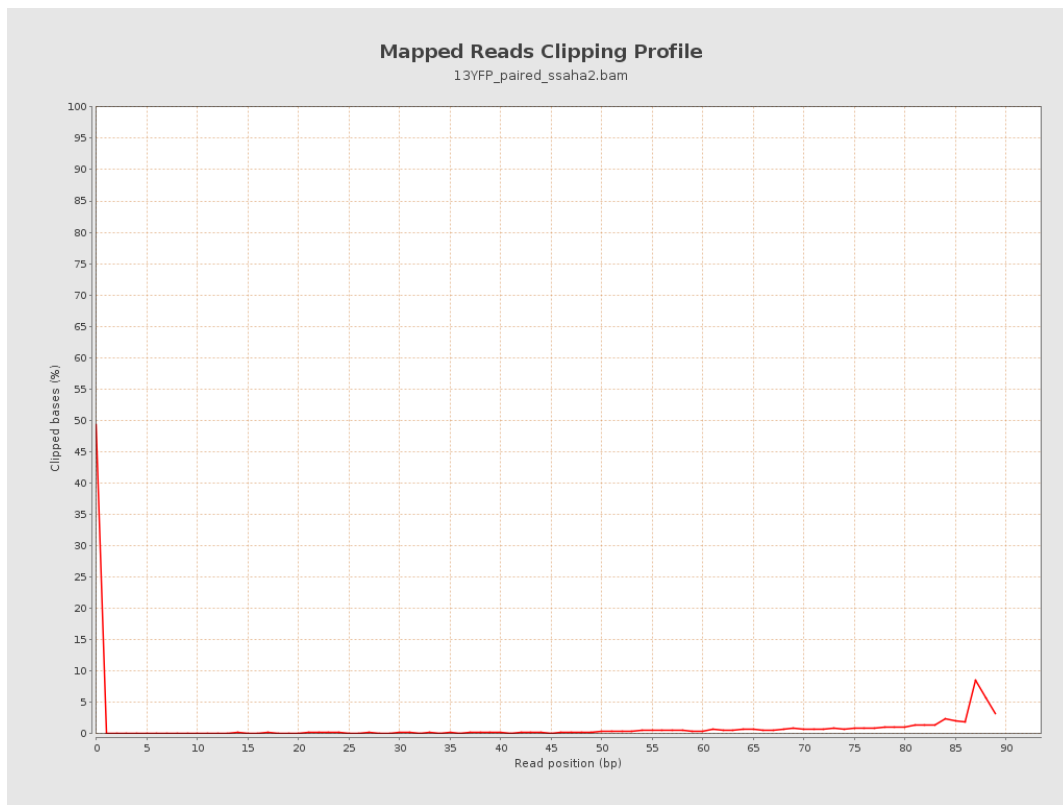

Duplication Rate Histogram
13YFP_paired_ssaha2.bam
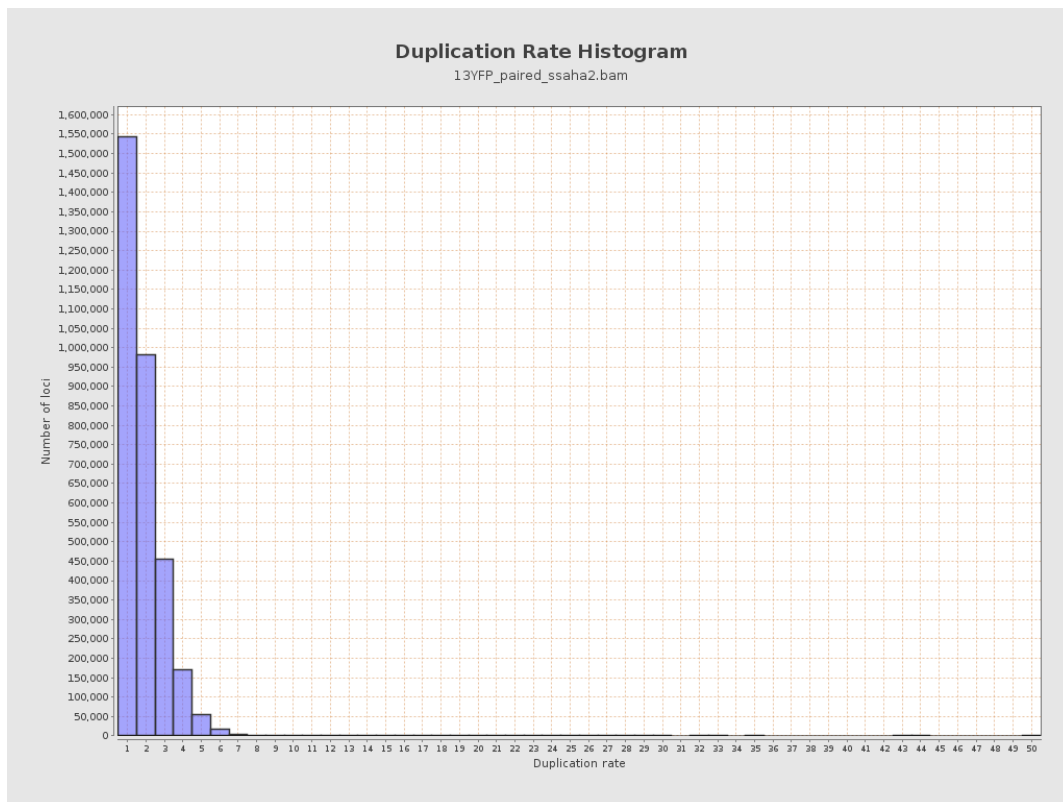
7. Genome Fraction Coverage

8. Mapped Reads Nucleotide Content

Mapped Reads Nucleotide Content
13YFP_paired_ssaha2.bam
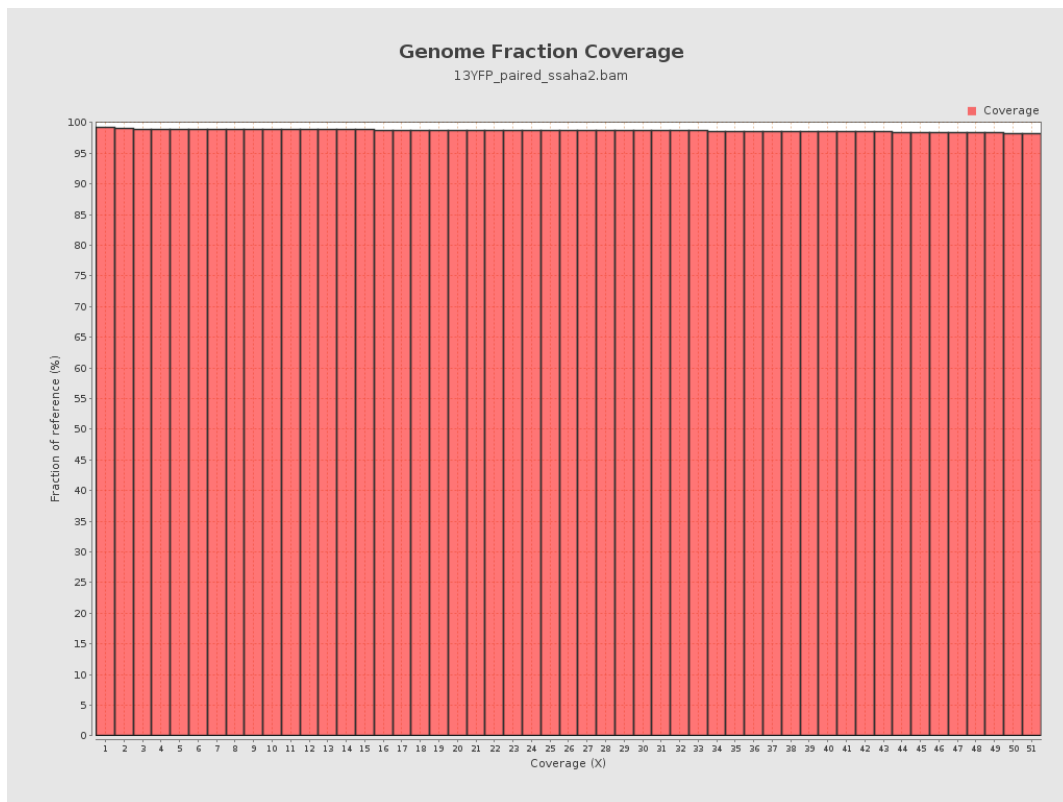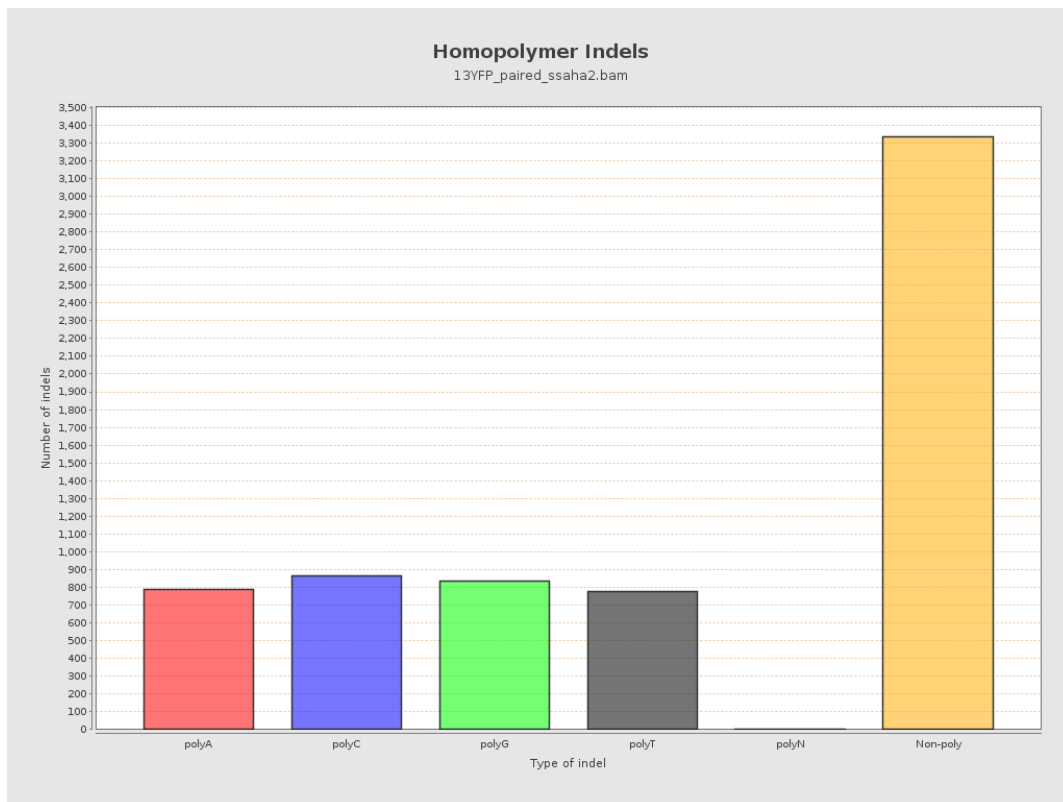
9. Mapped Reads Clipping Profile

10. Mapped Reads GC-content Distribution

Mapped Reads GC-content Distribution
13YFP_paired_ssaha2.bam

11. Homopolymer Indels
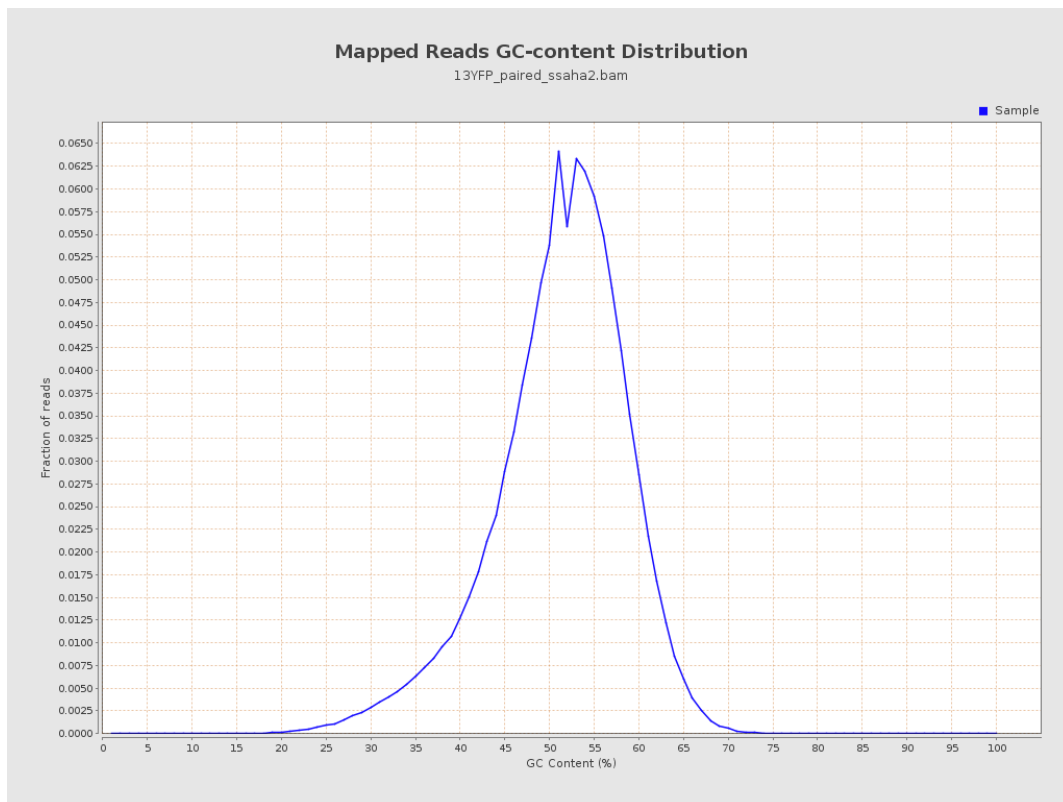
Homopolymer Indels
13YFP_paired_ssaha2.bam

12. Mapping Quality Across Reference

13. Mapping Quality Histogram
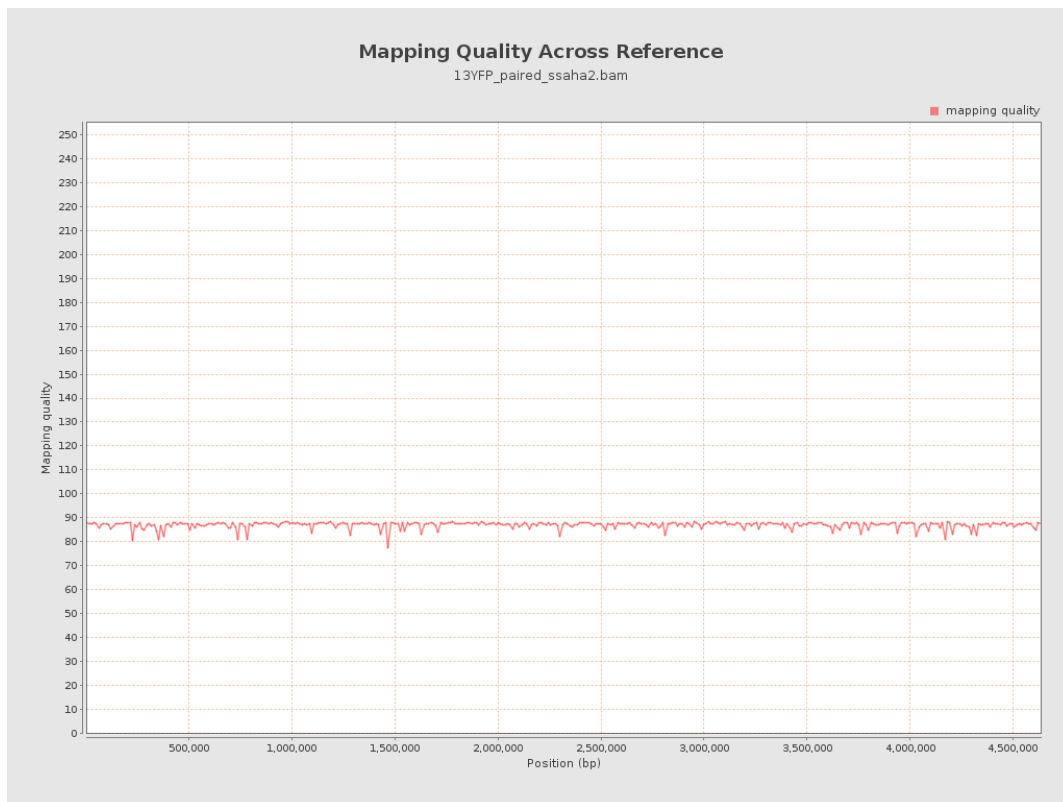
Mapping Quality Histogram
13YFP_paired_ssaha2.bam
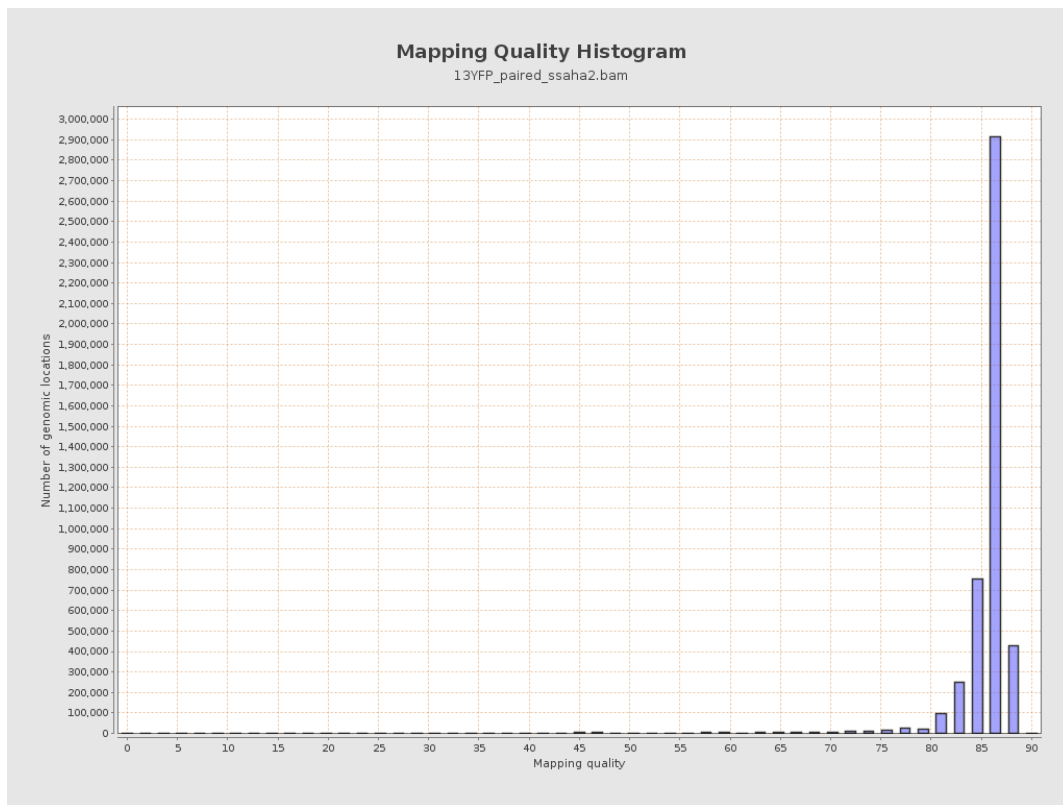
14. Insert Size Across Reference

15. Insert Size Histogram