

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 13:24:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046407.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR2046407 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046407_1.fastq.gz SRR2046407_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 13:24:37 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046407.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	10,433,928
Mapped reads	10,326,509 / 98.97%
Unmapped reads	107,419 / 1.03%
Mapped paired reads	10,326,509 / 98.97%
Mapped reads, first in pair	5,194,394 / 49.78%
Mapped reads, second in pair	5,132,115 / 49.19%
Mapped reads, both in pair	10,249,610 / 98.23%
Mapped reads, singletons	76,899 / 0.74%
Secondary alignments	0
Supplementary alignments	18,308 / 0.18%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	6,940,135 / 66.52%
Duplication rate	45.69%
Clipped reads	2,946,134 / 28.24%

2.2. ACGT Content

Number/percentage of A's	280,248,460 / 28.73%
Number/percentage of C's	207,965,776 / 21.32%
Number/percentage of T's	276,960,014 / 28.39%
Number/percentage of G's	210,316,116 / 21.56%
Number/percentage of N's	91,776 / 0.01%

GC Percentage	42.88%
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2.3. Coverage

Mean	0.3152
Standard Deviation	13.0434

2.4. Mapping Quality

Mean Mapping Quality	53.38
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2.5. Insert size

Mean	18,255.5
Standard Deviation	1,362,900.4
P25/Median/P75	96 / 120 / 150

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	3,310,661
Insertions	64,074
Mapped reads with at least one insertion	0.61%
Deletions	90,769
Mapped reads with at least one deletion	0.85%
Homopolymer indels	46.73%

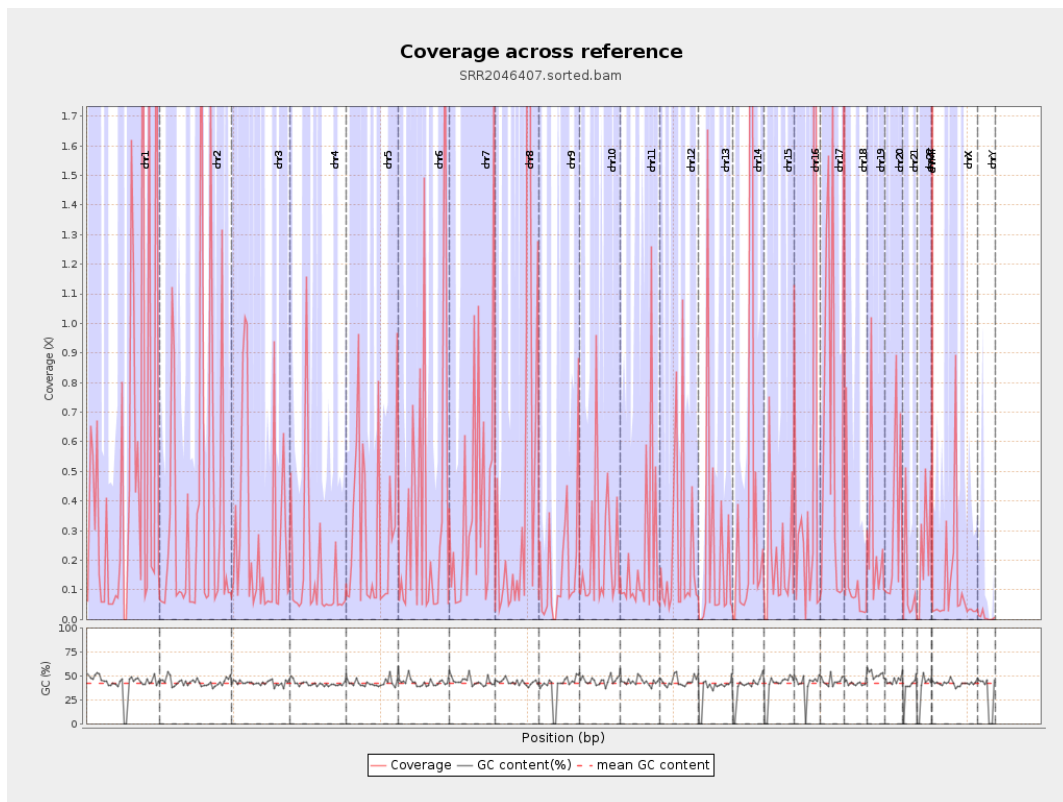
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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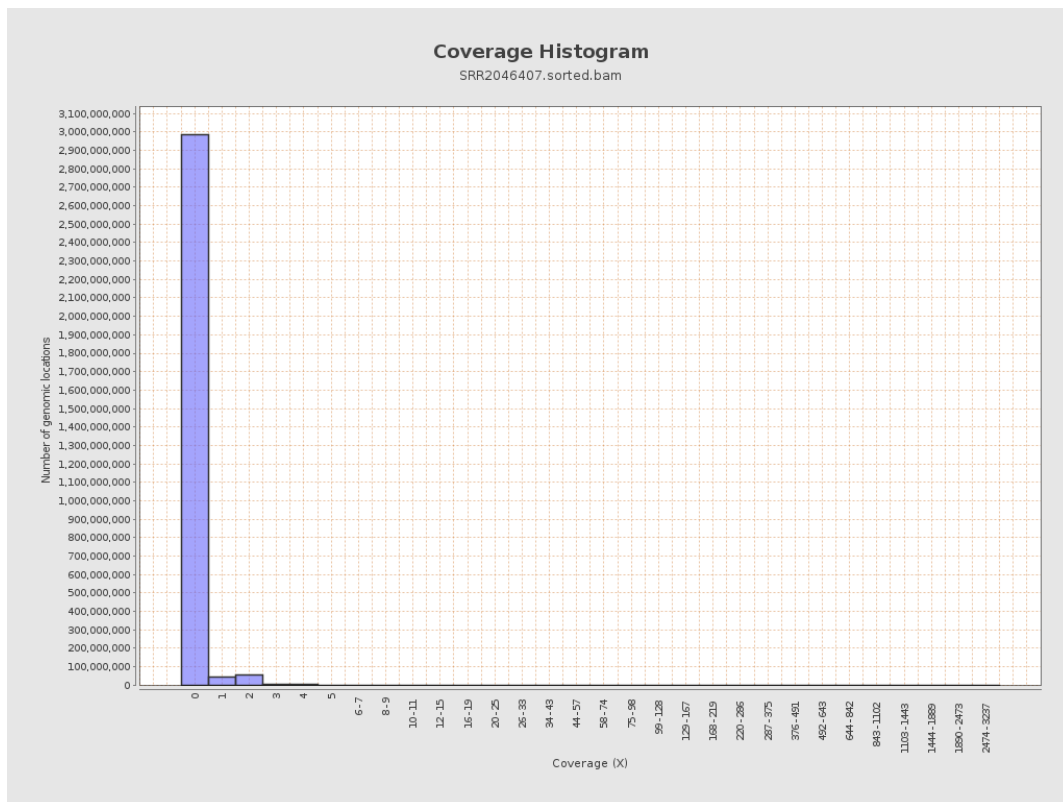
		bases	coverage	deviation
chr1	249250621	129716001	0.5204	17.5553
chr2	243199373	91457320	0.3761	14.6262
chr3	198022430	57213802	0.2889	12.1748
chr4	191154276	29476527	0.1542	6.7088
chr5	180915260	55885637	0.3089	12.1689
chr6	171115067	63158879	0.3691	12.211
chr7	159138663	65687981	0.4128	13.9931
chr8	146364022	83821091	0.5727	21.2596
chr9	141213431	25572649	0.1811	8.1517
chr10	135534747	30045503	0.2217	9.2248
chr11	135006516	28870165	0.2138	8.4293
chr12	133851895	31213214	0.2332	9.0655
chr13	115169878	25958729	0.2254	9.6553
chr14	107349540	46075654	0.4292	18.1546
chr15	102531392	20976093	0.2046	9.5353
chr16	90354753	48190340	0.5333	21.6275
chr17	81195210	58841588	0.7247	21.2499
chr18	78077248	10680108	0.1368	5.7695
chr19	59128983	16283635	0.2754	7.807
chr20	63025520	20610121	0.327	14.9532
chr21	48129895	5530061	0.1149	8.4934
chr22	51304566	12607844	0.2457	9.979
chrMT	16571	658035	39.71	11.2782
chrX	155270560	16826845	0.1084	5.8925

chrY	59373566	468528	0.0079	0.3805
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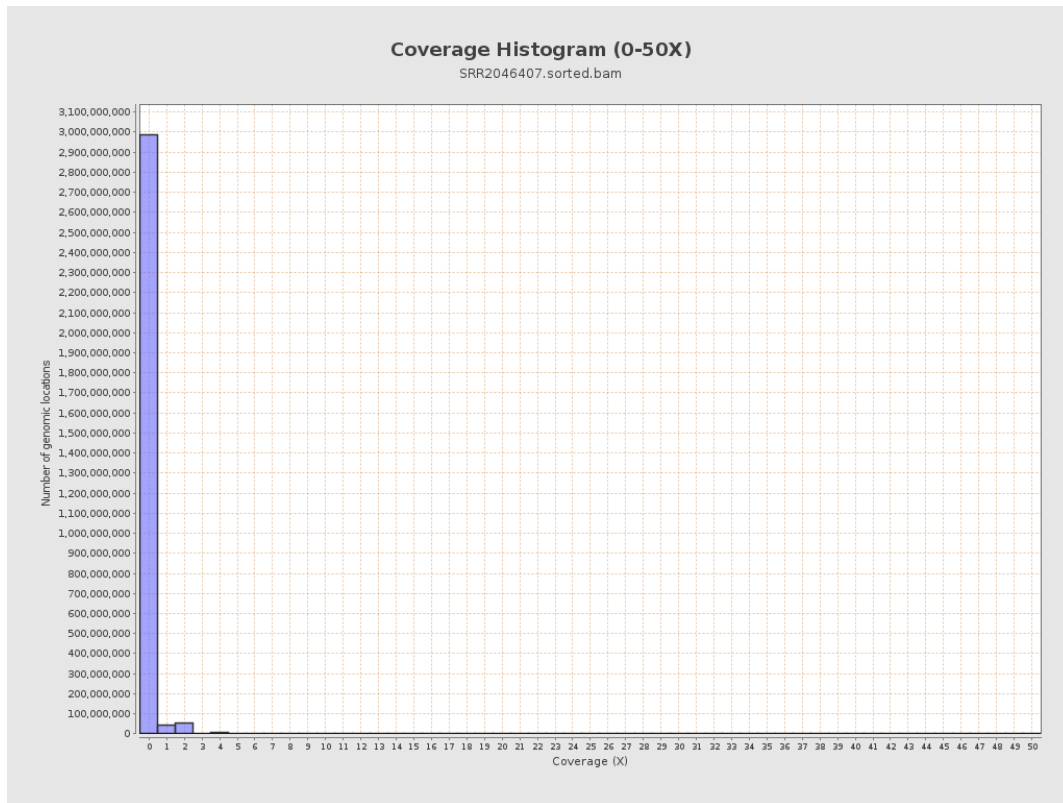
3. Results : Coverage across reference



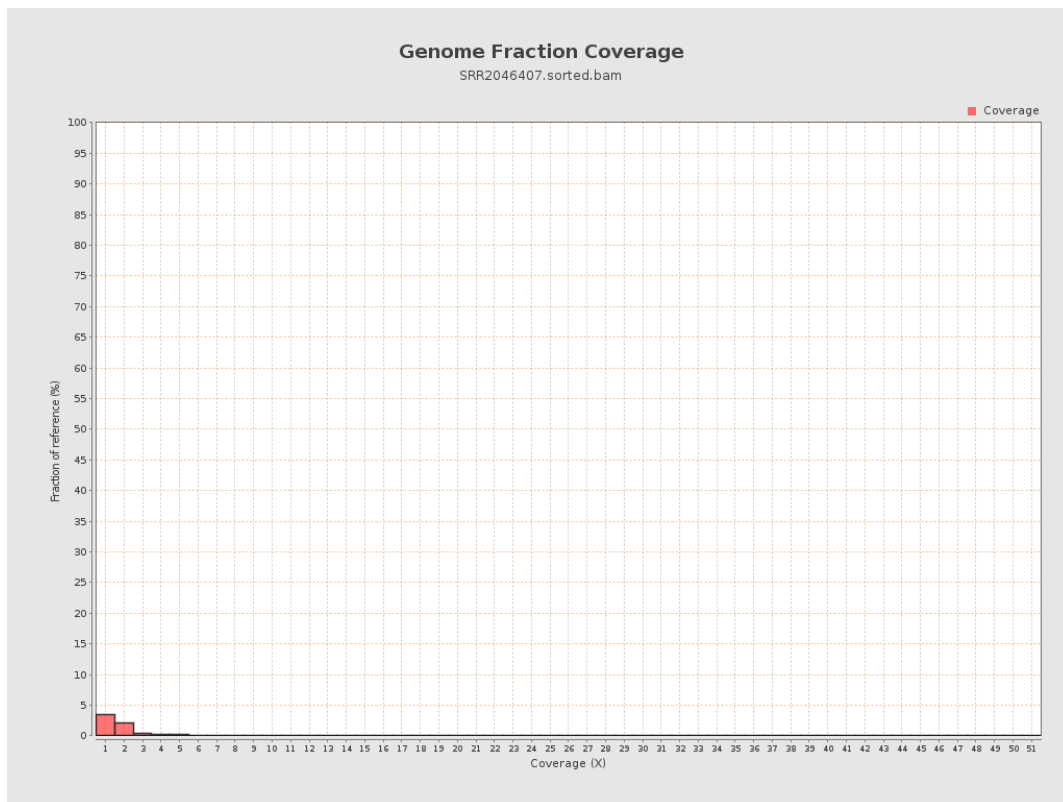
4. Results : Coverage Histogram



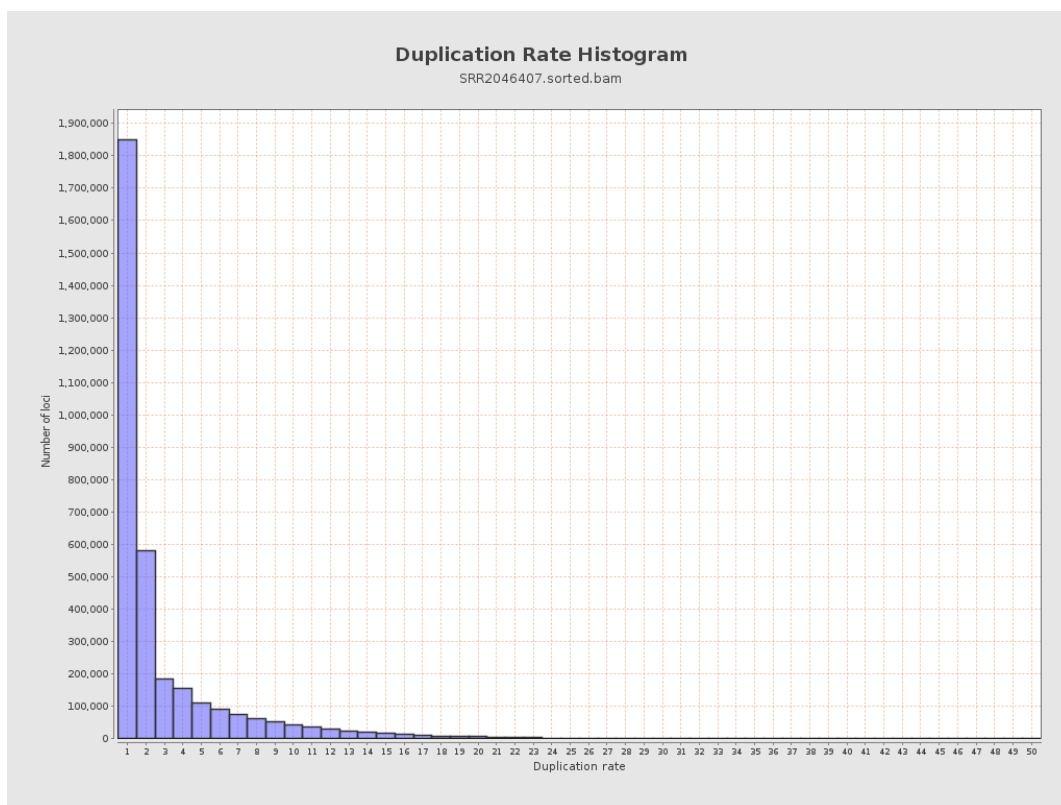
5. Results : Coverage Histogram (0-50X)



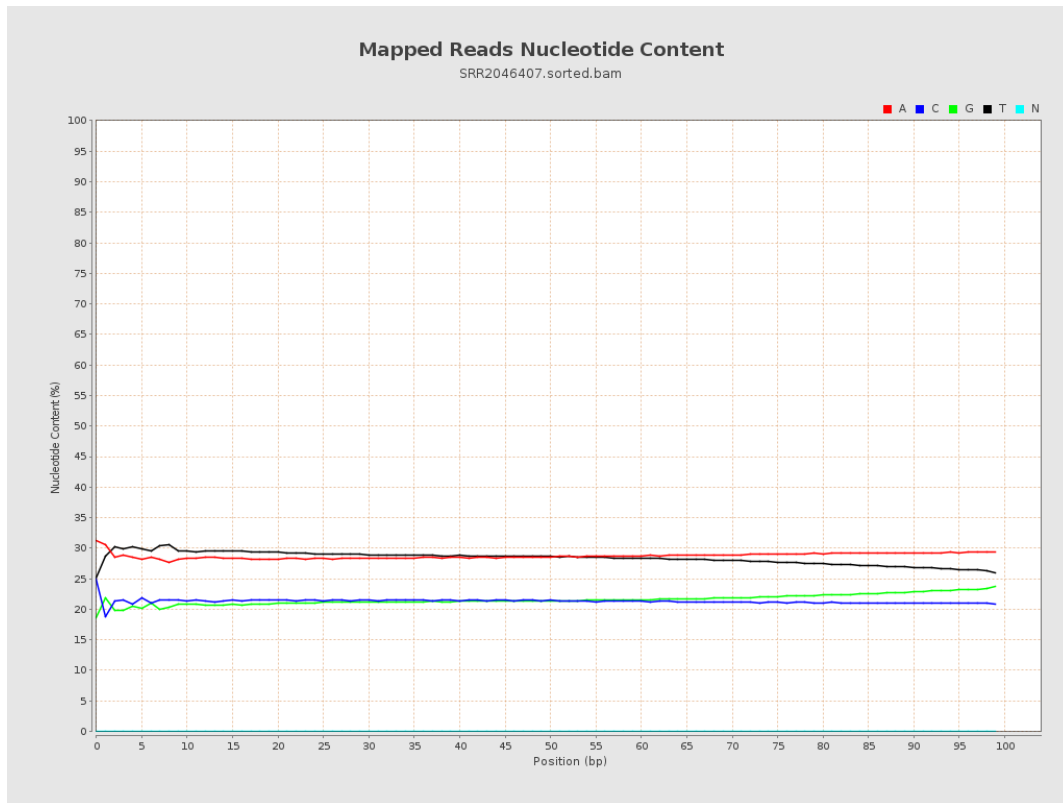
6. Results : Genome Fraction Coverage



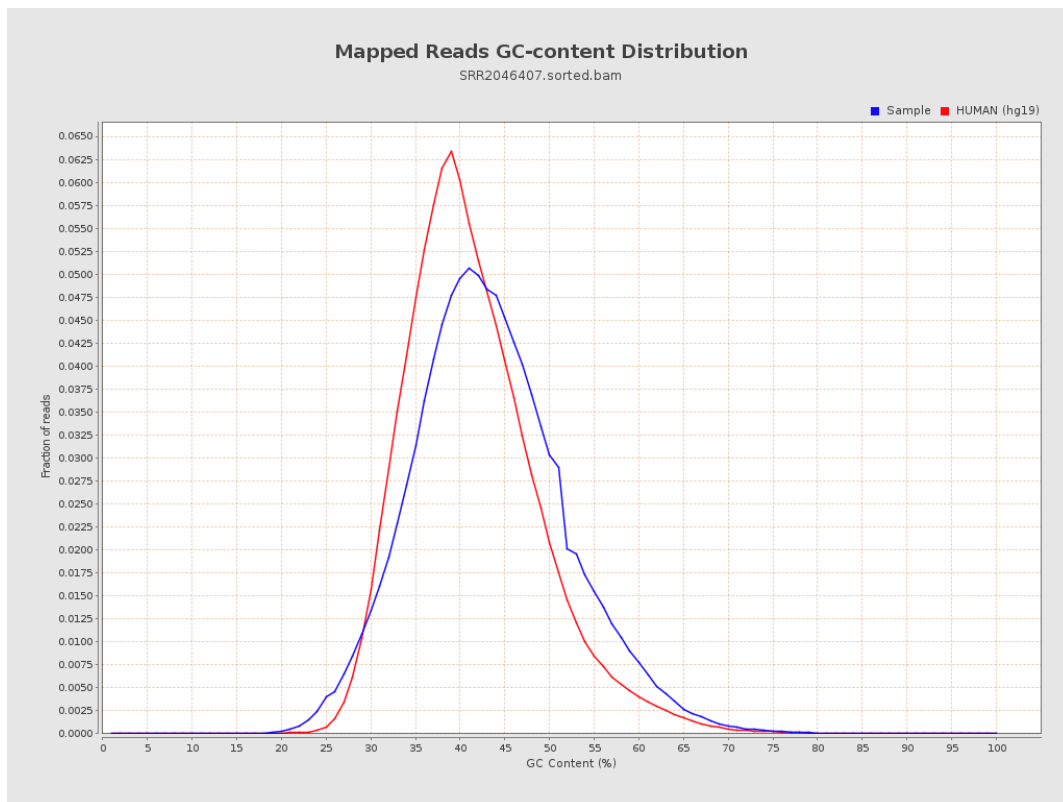
7. Results : Duplication Rate Histogram



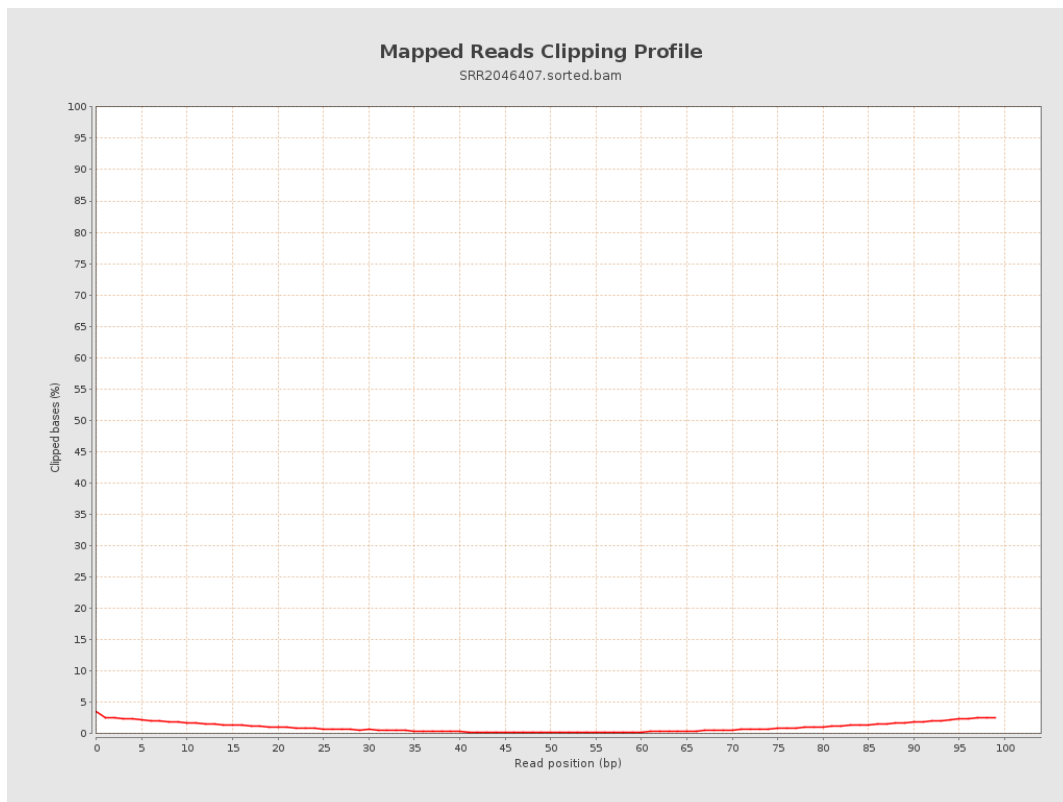
8. Results : Mapped Reads Nucleotide Content



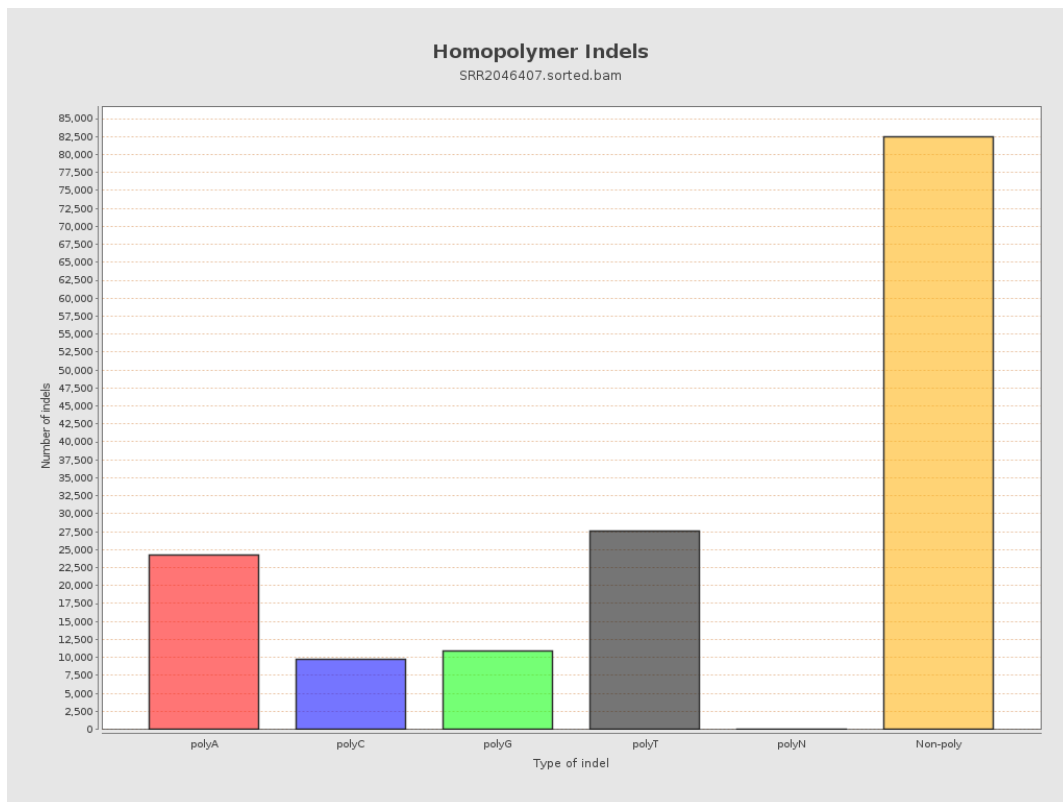
9. Results : Mapped Reads GC-content Distribution



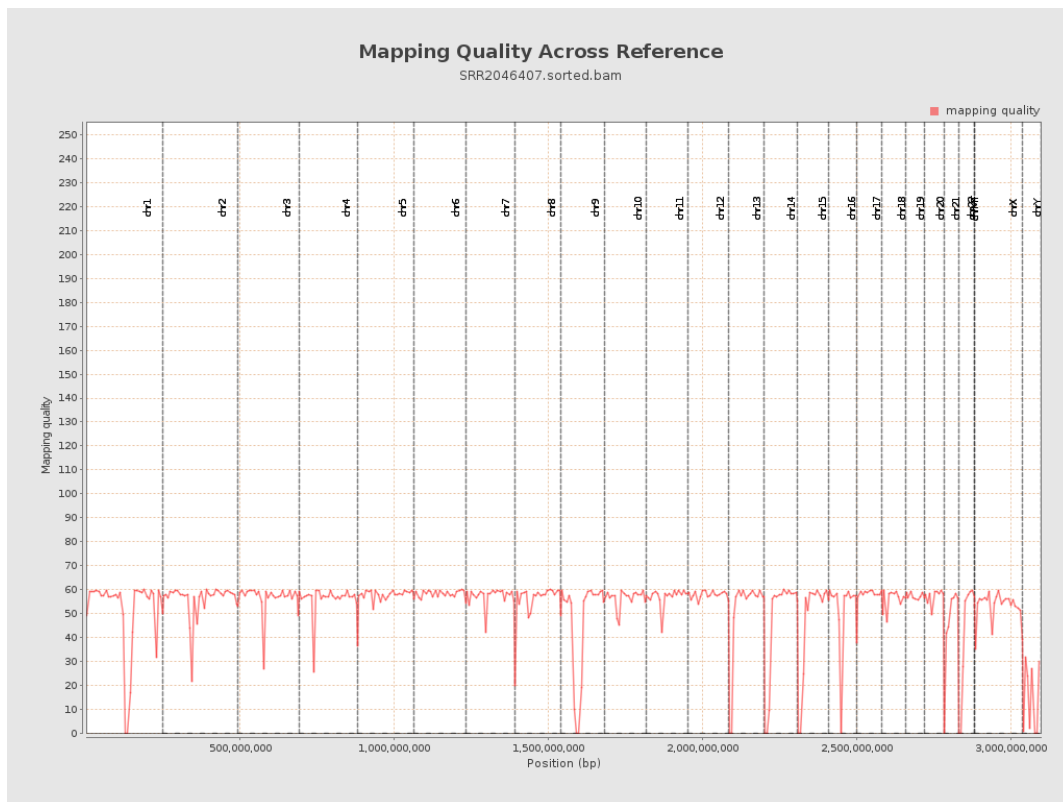
10. Results : Mapped Reads Clipping Profile



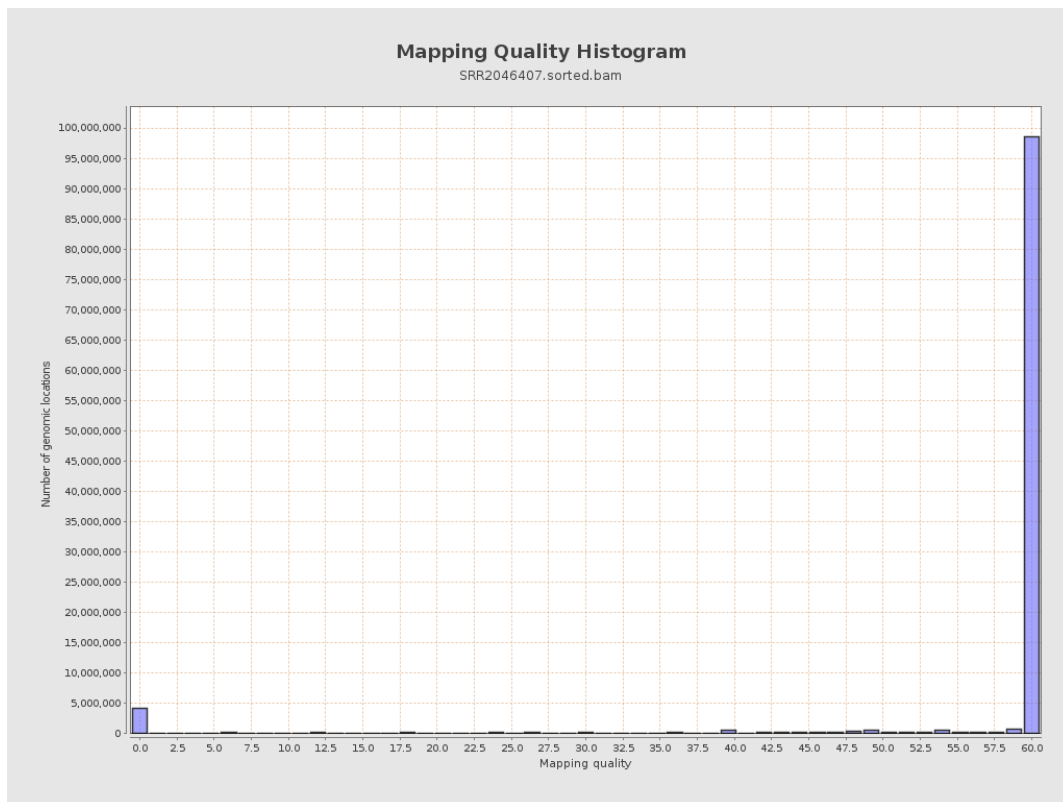
11. Results : Homopolymer Indels



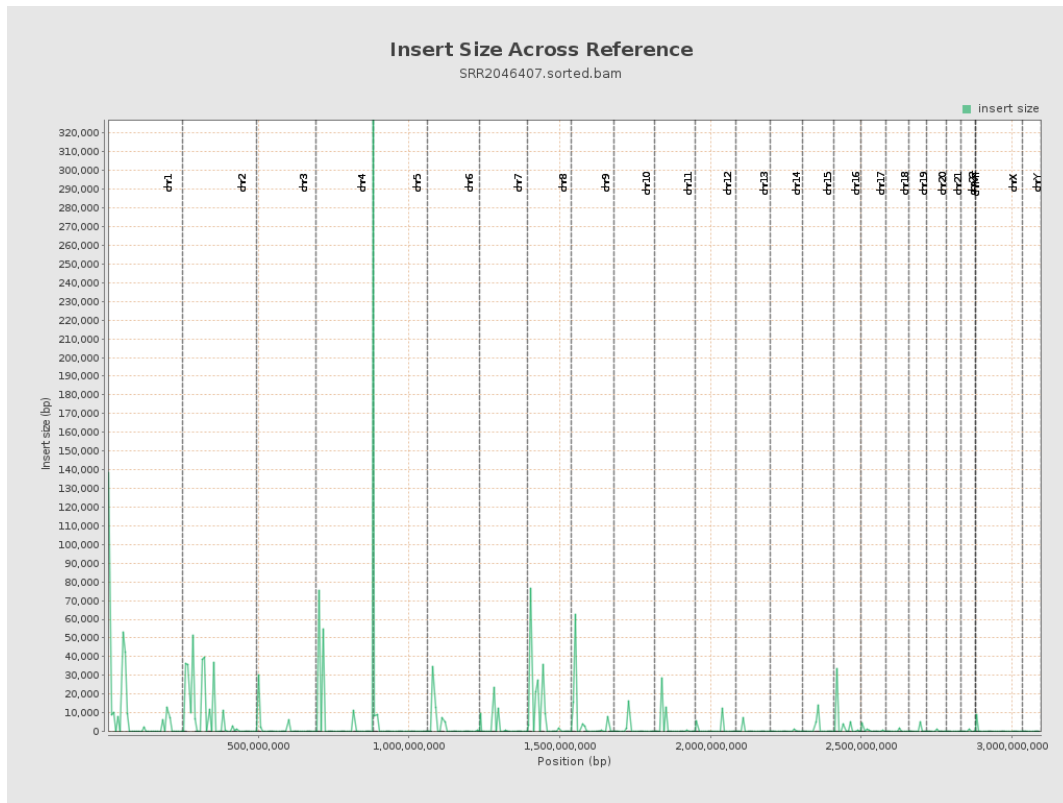
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

