

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 15:08:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046447.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_SRR2046447 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046447_1.fastq.gz SRR2046447_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 15:08:03 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046447.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,482,322
Mapped reads	8,442,942 / 99.54%
Unmapped reads	39,380 / 0.46%
Mapped paired reads	8,442,942 / 99.54%
Mapped reads, first in pair	4,225,599 / 49.82%
Mapped reads, second in pair	4,217,343 / 49.72%
Mapped reads, both in pair	8,414,976 / 99.21%
Mapped reads, singletons	27,966 / 0.33%
Secondary alignments	0
Supplementary alignments	49,202 / 0.58%
Read min/max/mean length	30 / 100 / 100.24
Duplicated reads (estimated)	7,036,251 / 82.95%
Duplication rate	28.21%
Clipped reads	1,142,556 / 13.47%

2.2. ACGT Content

Number/percentage of A's	245,084,032 / 29.69%
Number/percentage of C's	167,677,228 / 20.32%
Number/percentage of T's	245,655,985 / 29.76%
Number/percentage of G's	166,878,494 / 20.22%
Number/percentage of N's	77,878 / 0.01%

GC Percentage	40.53%
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2.3. Coverage

Mean	0.2667
Standard Deviation	51.0224

2.4. Mapping Quality

Mean Mapping Quality	44.2
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2.5. Insert size

Mean	20,503.36
Standard Deviation	1,536,173.22
P25/Median/P75	128 / 169 / 213

2.6. Mismatches and indels

General error rate	0.35%
Mismatches	2,724,564
Insertions	67,194
Mapped reads with at least one insertion	0.78%
Deletions	78,679
Mapped reads with at least one deletion	0.91%
Homopolymer indels	50.63%

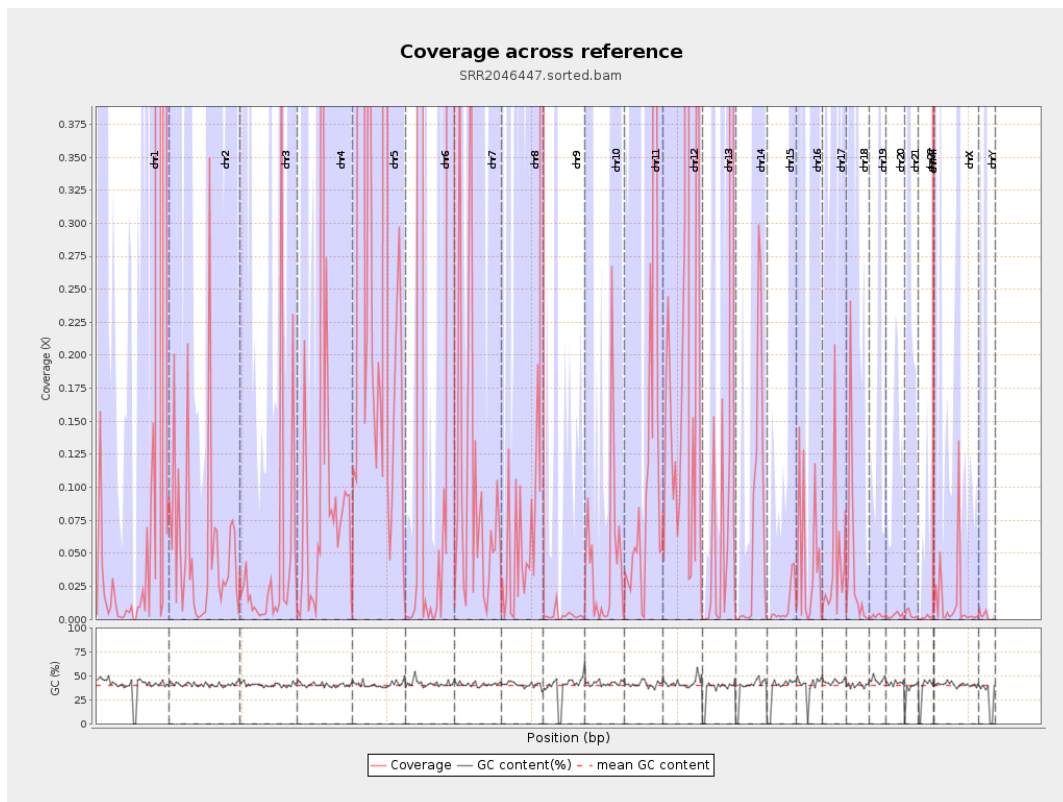
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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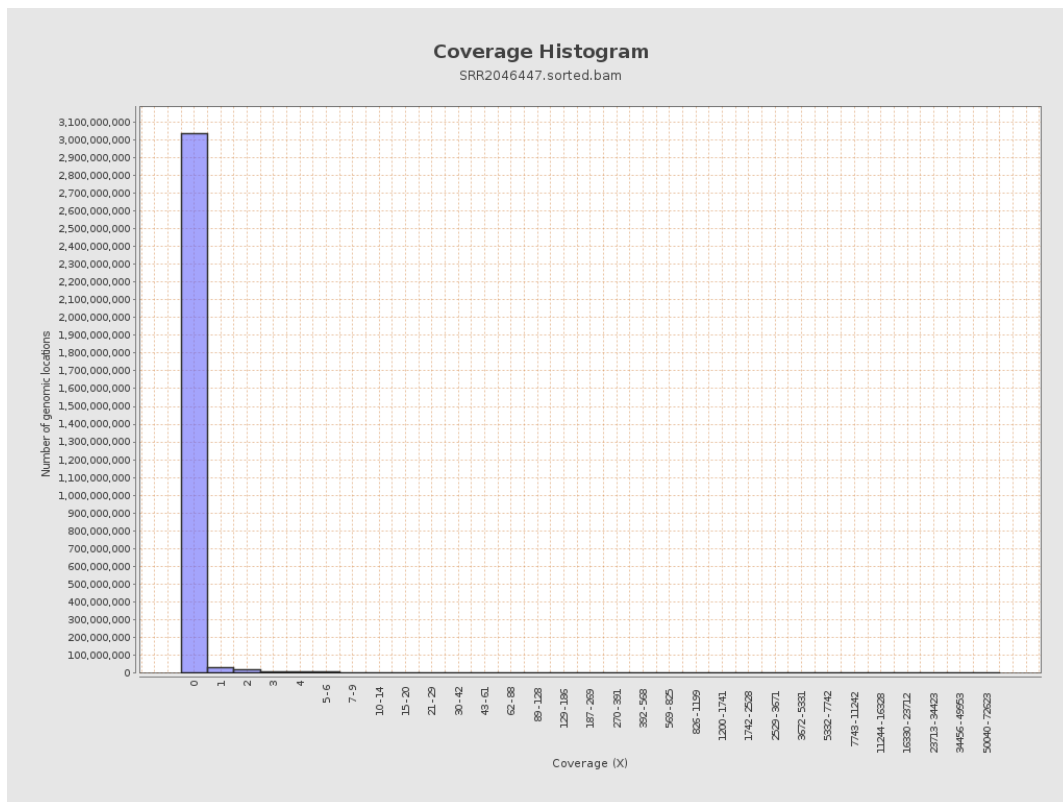
		bases	coverage	deviation
chr1	249250621	138081968	0.554	95.1803
chr2	243199373	13761993	0.0566	2.9852
chr3	198022430	8542579	0.0431	5.3096
chr4	191154276	21695574	0.1135	16.2906
chr5	180915260	103788802	0.5737	43.9527
chr6	171115067	340966867	1.9926	160.4339
chr7	159138663	16445046	0.1033	14.3128
chr8	146364022	30143309	0.2059	40.0617
chr9	141213431	413655	0.0029	0.3085
chr10	135534747	5888900	0.0434	4.8803
chr11	135006516	18183719	0.1347	10.2251
chr12	133851895	81987984	0.6125	68.4268
chr13	115169878	23477509	0.2039	24.4234
chr14	107349540	7260726	0.0676	6.2418
chr15	102531392	1018023	0.0099	0.4324
chr16	90354753	4143510	0.0459	1.188
chr17	81195210	3640520	0.0448	3.6706
chr18	78077248	3261722	0.0418	5.3199
chr19	59128983	151584	0.0026	0.2608
chr20	63025520	186021	0.003	0.14
chr21	48129895	168607	0.0035	0.3604
chr22	51304566	70158	0.0014	0.0921
chrMT	16571	128211	7.7371	4.309
chrX	155270560	2038584	0.0131	0.4253

chrY	59373566	130204	0.0022	0.4227
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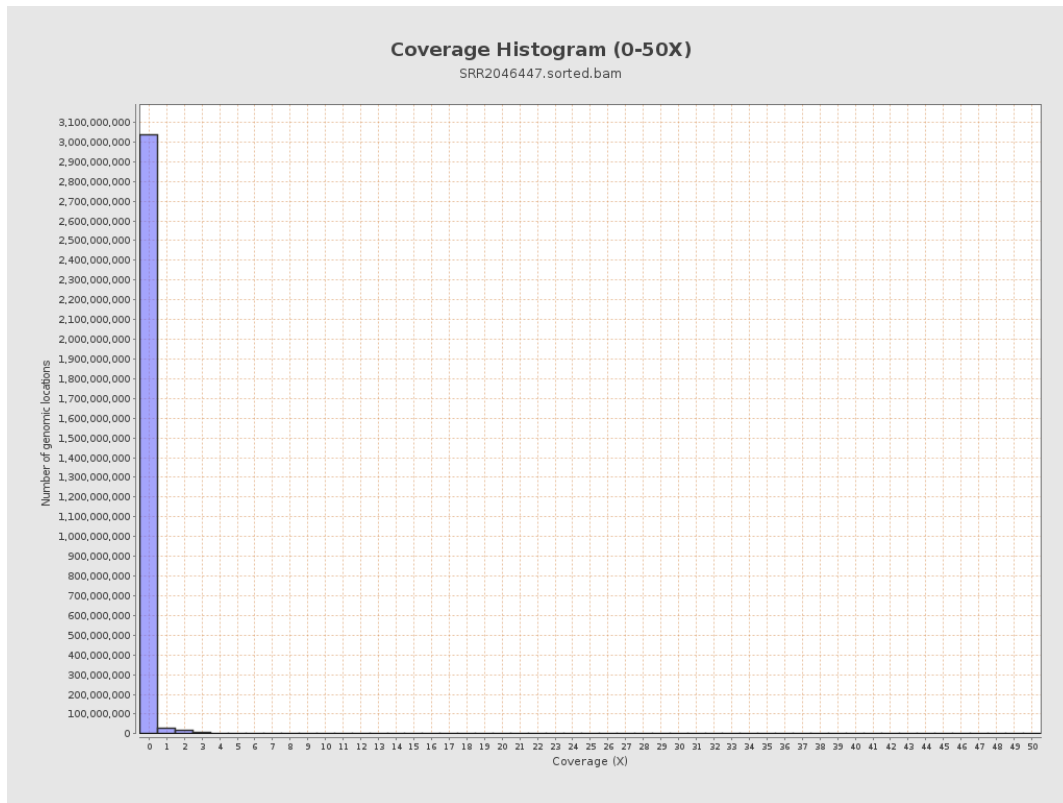
3. Results : Coverage across reference



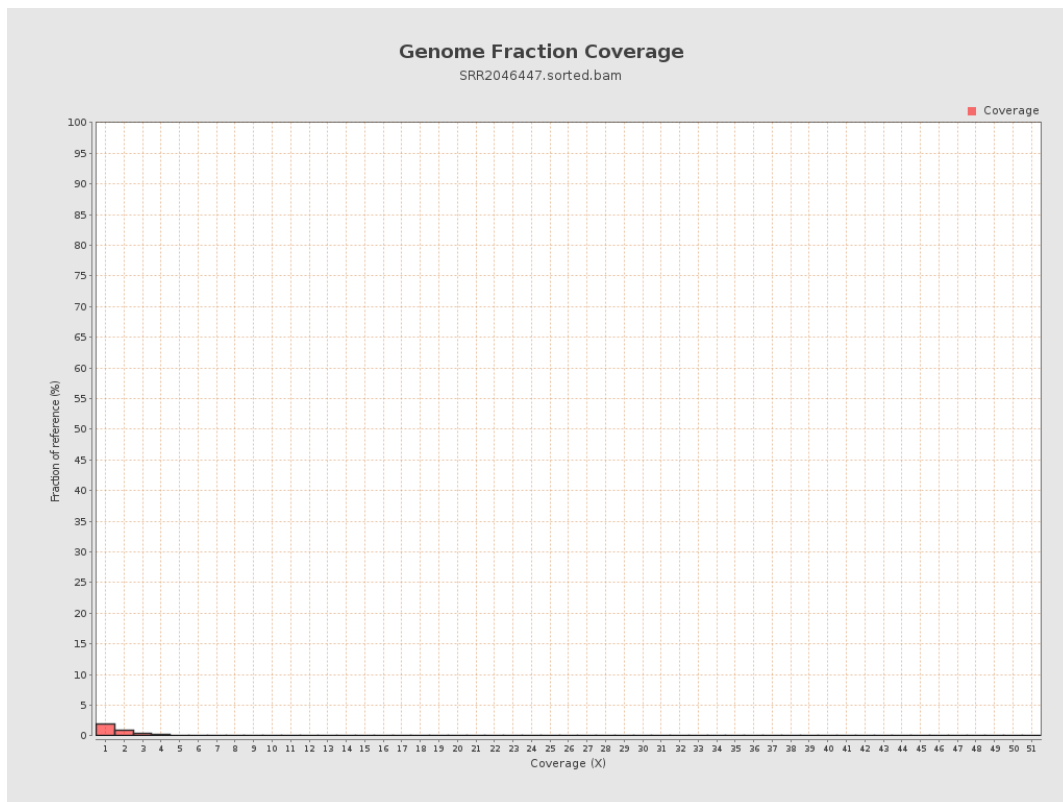
4. Results : Coverage Histogram



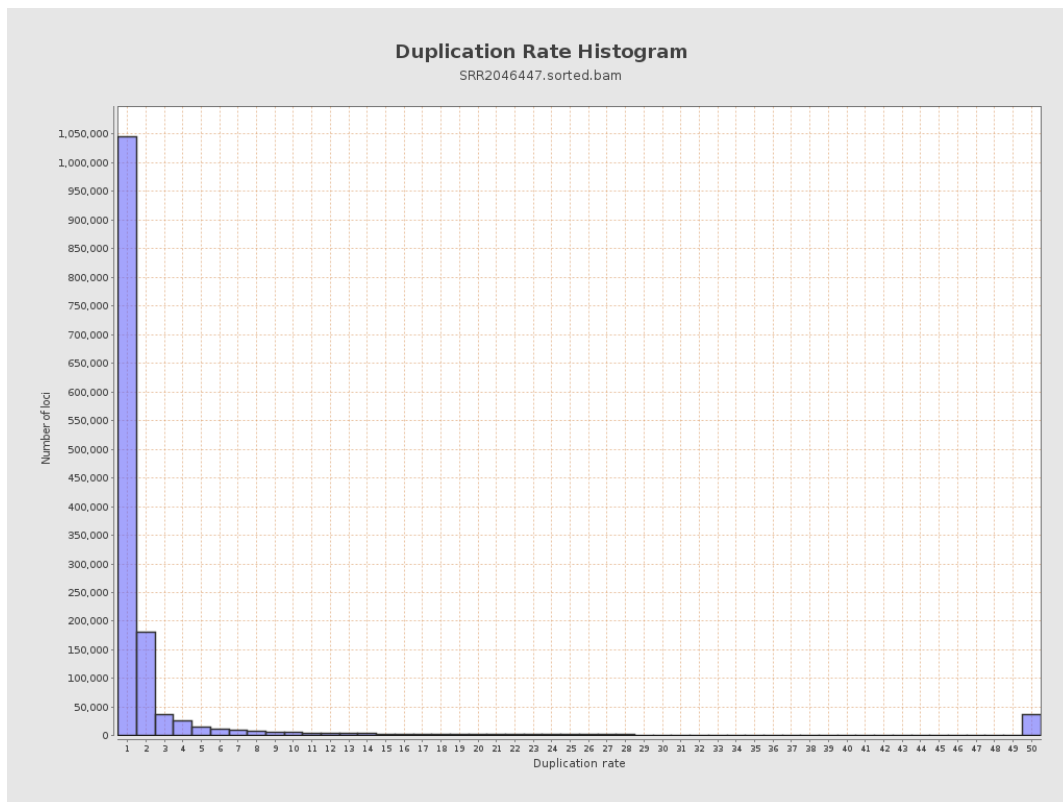
5. Results : Coverage Histogram (0-50X)



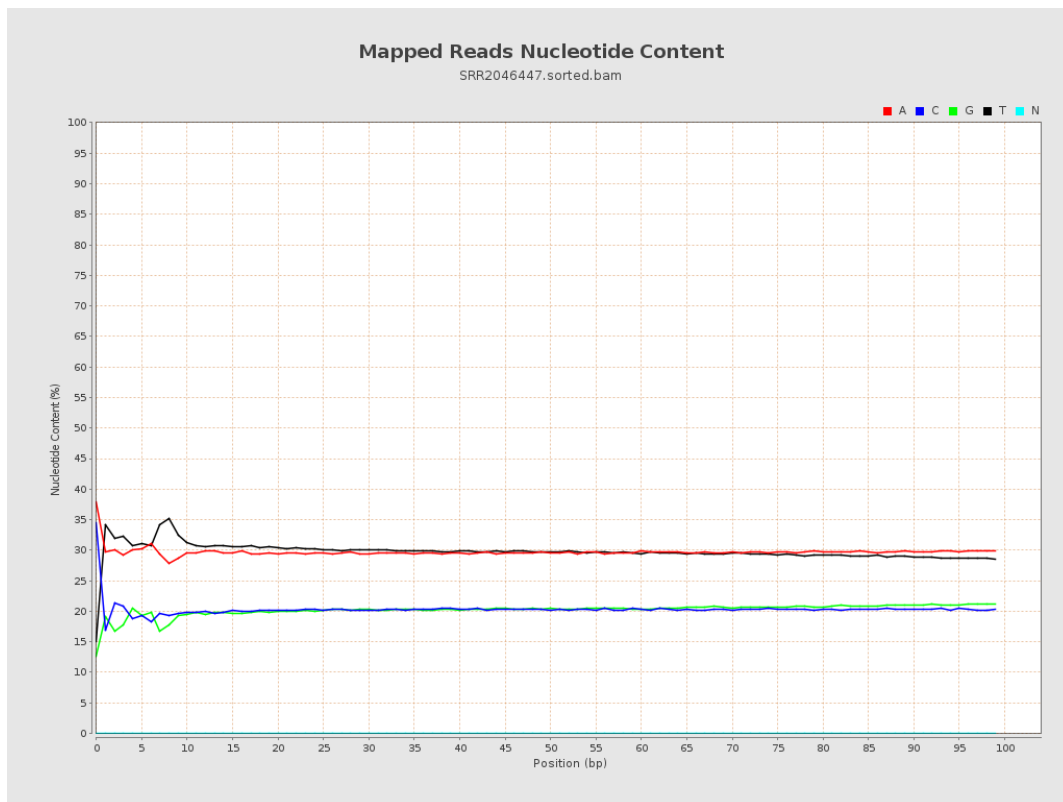
6. Results : Genome Fraction Coverage



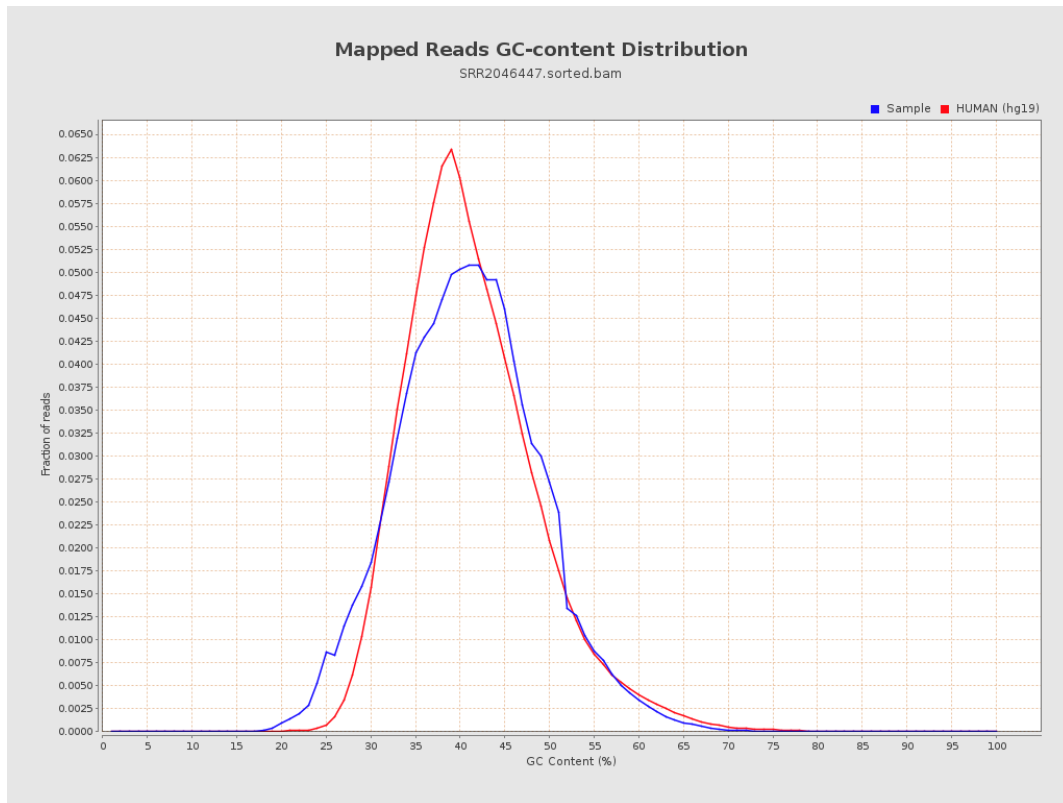
7. Results : Duplication Rate Histogram



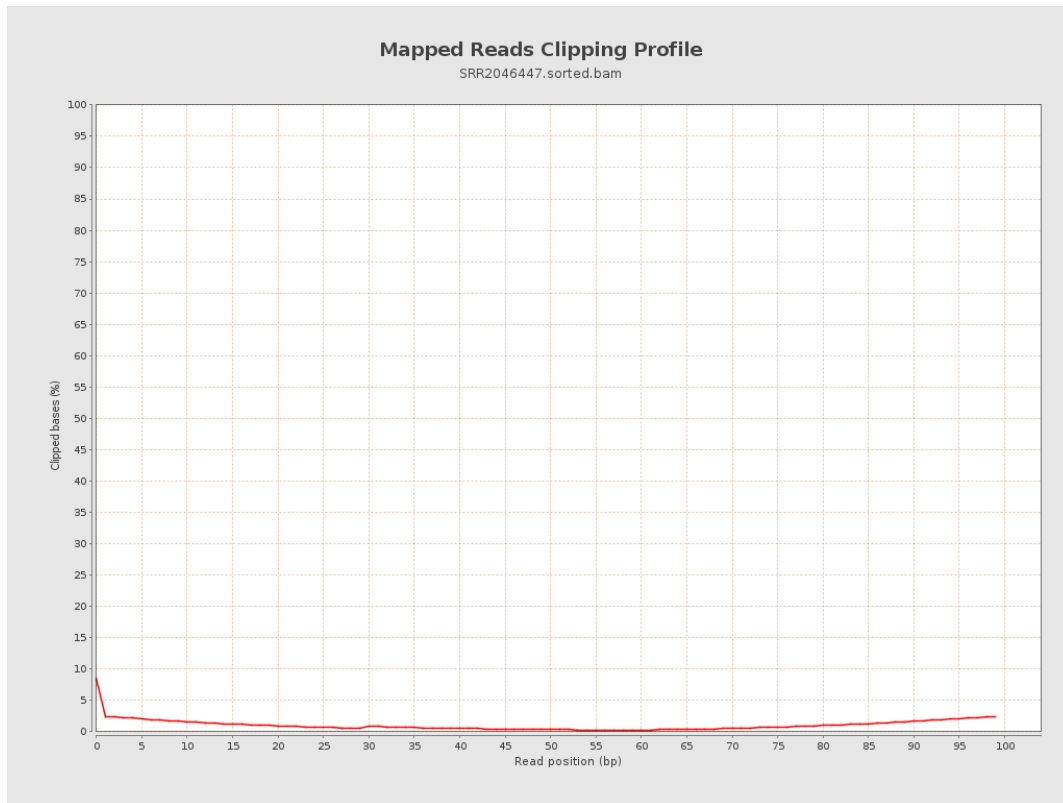
8. Results : Mapped Reads Nucleotide Content



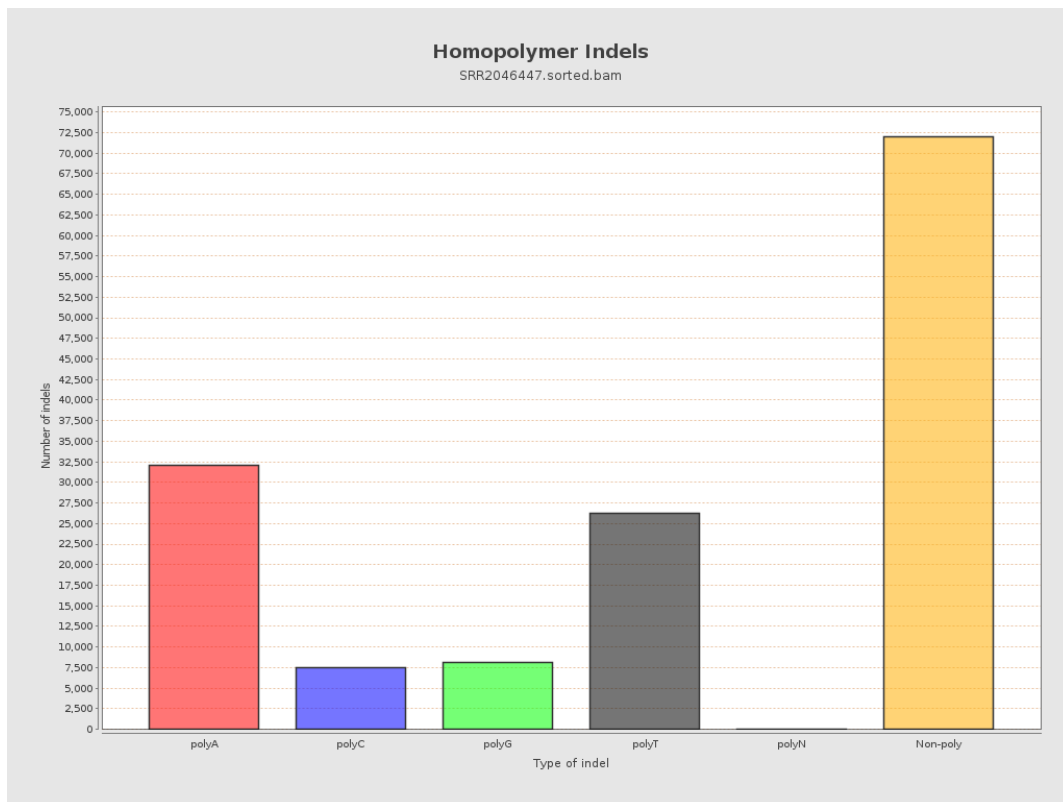
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



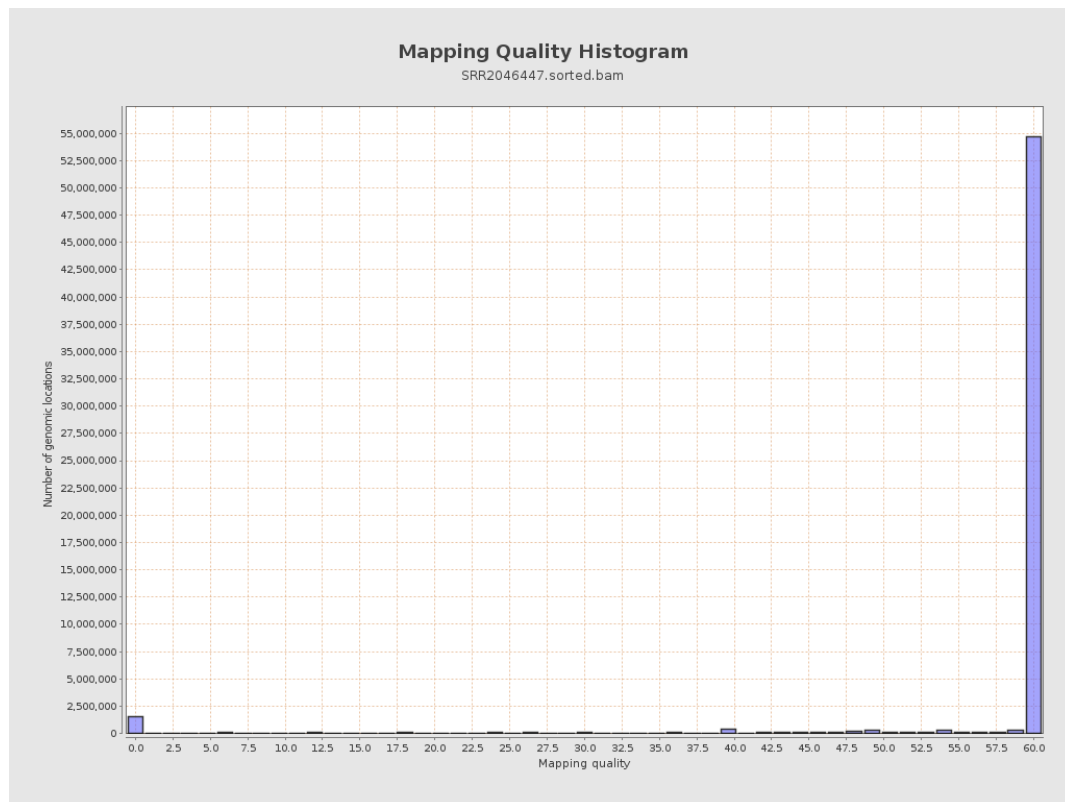
11. Results : Homopolymer Indels



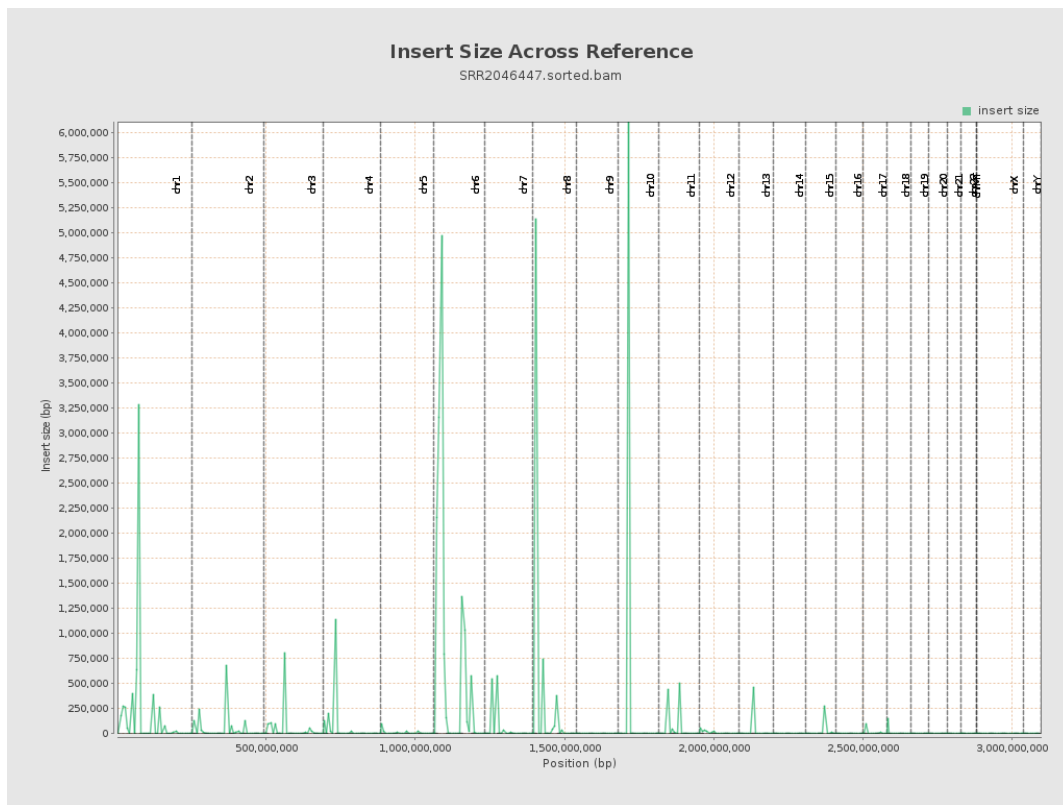
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

