Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/23 06:42:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR8617669.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_SRR8617669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR8617669_1.fastq.gz SRR8617669_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Dec 23 06:42:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR8617669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,995,320
Mapped reads	4,940,674 / 98.91%
Unmapped reads	54,646 / 1.09%
Mapped paired reads	4,940,674 / 98.91%
Mapped reads, first in pair	2,469,047 / 49.43%
Mapped reads, second in pair	2,471,627 / 49.48%
Mapped reads, both in pair	4,915,770 / 98.41%
Mapped reads, singletons	24,904 / 0.5%
Secondary alignments	0
Supplementary alignments	31,549 / 0.63%
Read min/max/mean length	30 / 101 / 101.25
Duplicated reads (estimated)	390,880 / 7.82%
Duplication rate	3.55%
Clipped reads	3,016,609 / 60.39%

2.2. ACGT Content

Number/percentage of A's	135,736,286 / 29.75%
Number/percentage of C's	86,960,081 / 19.06%
Number/percentage of T's	137,907,362 / 30.23%
Number/percentage of G's	95,621,277 / 20.96%
Number/percentage of N's	12,175 / 0%

GC Percentage	40.02%

2.3. Coverage

Mean	0.1475
Standard Deviation	2.2573

2.4. Mapping Quality

Mean Mapping Quality	52.76

2.5. Insert size

Mean	99,411.85
Standard Deviation	2,960,749.82
P25/Median/P75	142 / 175 / 223

2.6. Mismatches and indels

General error rate	0.9%
Mismatches	3,940,794
Insertions	76,109
Mapped reads with at least one insertion	1.5%
Deletions	157,223
Mapped reads with at least one deletion	3.1%
Homopolymer indels	45.75%

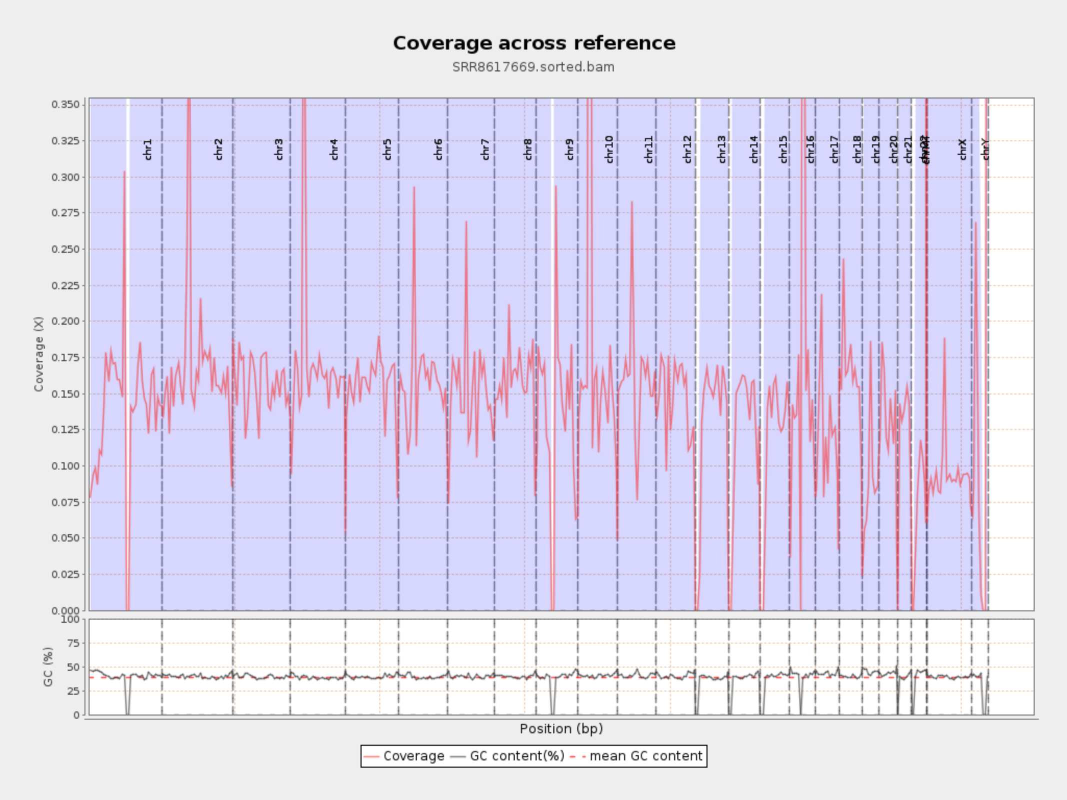
2.7. Chromosome stats

Name	**Length**	**Mapped**	**Mean**	**Standard**

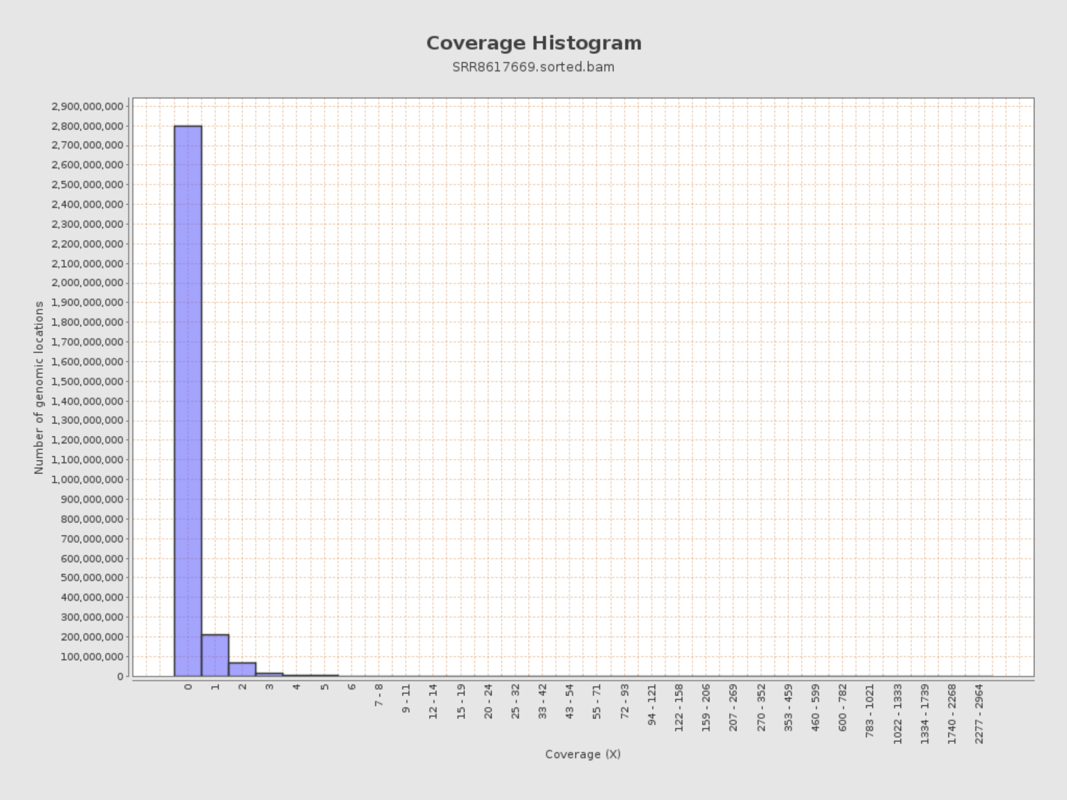
		bases	coverage	deviation
chr1	249250621	34573287	0.1387	2.4451
chr2	243199373	41527379	0.1708	1.9516
chr3	198022430	31246514	0.1578	0.6336
chr4	191154276	32866375	0.1719	1.9277
chr5	180915260	28294349	0.1564	0.5284
chr6	171115067	27178049	0.1588	1.5644
chr7	159138663	24342332	0.153	2.0896
chr8	146364022	23291307	0.1591	0.77
chr9	141213431	19320206	0.1368	2.961
chr10	135534747	26768354	0.1975	6.4508
chr11	135006516	21299646	0.1578	2.2461
chr12	133851895	19546413	0.146	0.5116
chr13	115169878	14538512	0.1262	0.459
chr14	107349540	12966508	0.1208	0.5546
chr15	102531392	11918262	0.1162	0.4465
chr16	90354753	16046965	0.1776	3.7416
chr17	81195210	9541752	0.1175	1.7023
chr18	78077248	13064511	0.1673	2.9263
chr19	59128983	5333134	0.0902	1.4689
chr20	63025520	8555859	0.1358	0.6489
chr21	48129895	5801702	0.1205	0.8518
chr22	51304566	3462948	0.0675	0.3545
chrMT	16571	84236	5.0833	5.8143
chrX	155270560	14654583	0.0944	0.9597

chrY	59373566	10305828	0.1736	4.3708

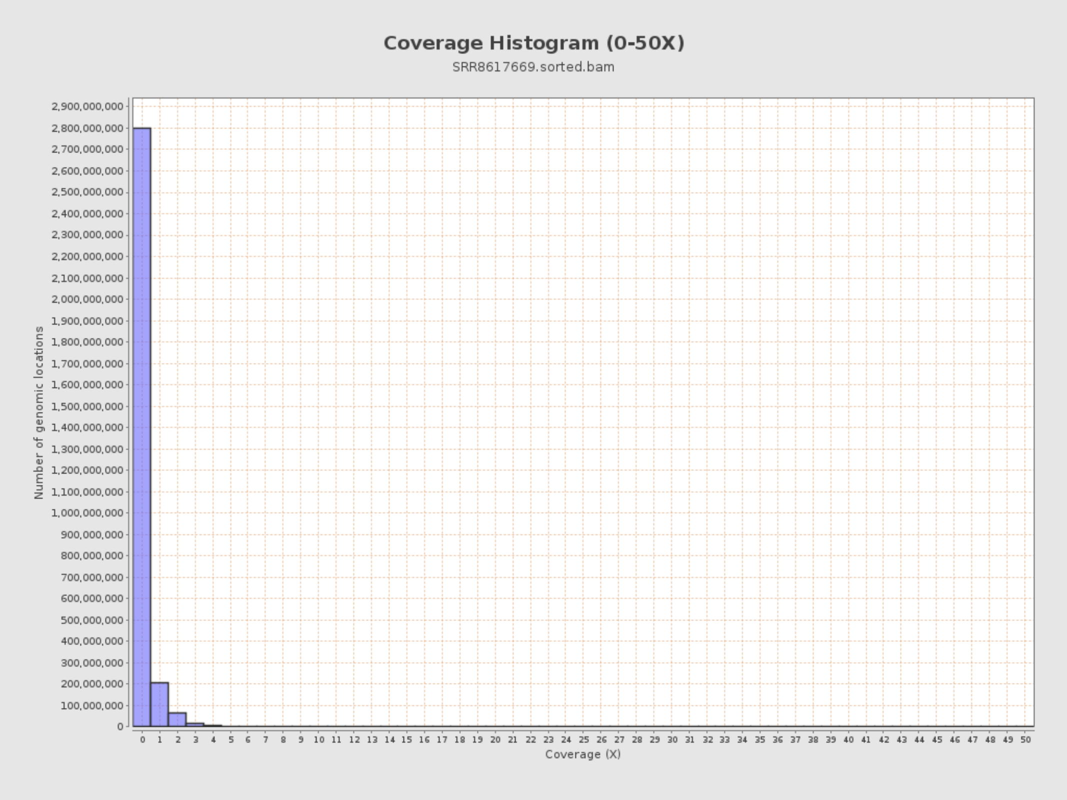
3. Results : Coverage across reference



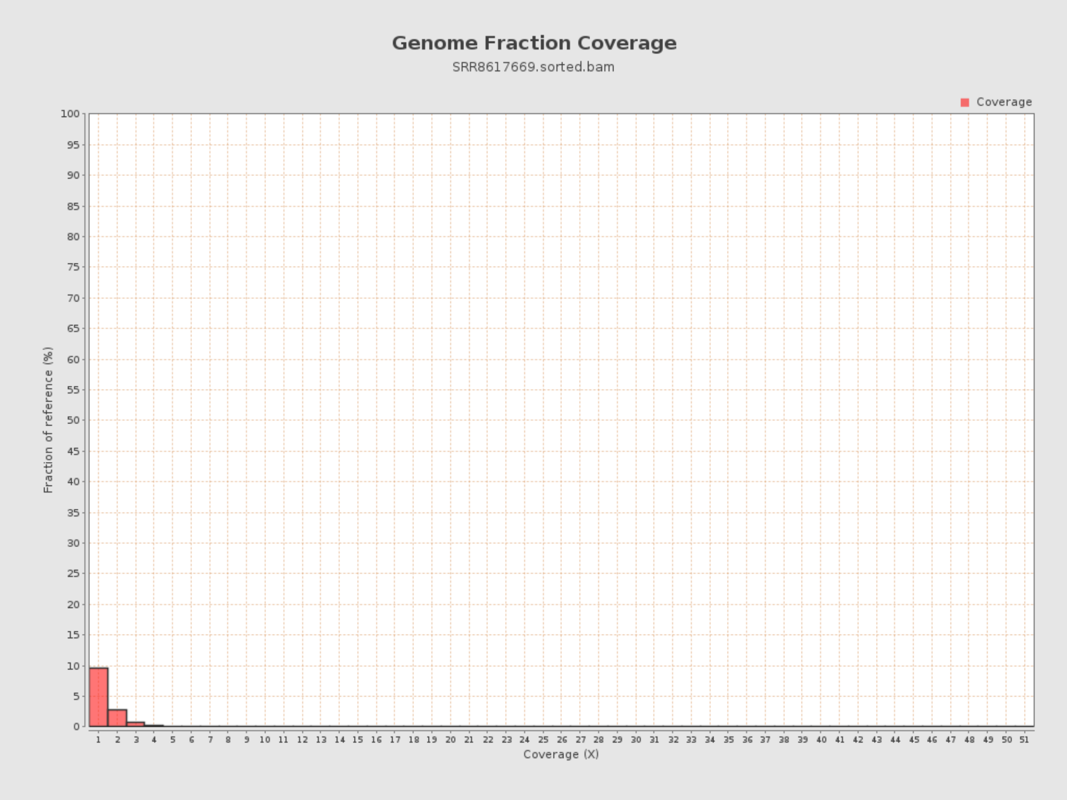
4. Results : Coverage Histogram



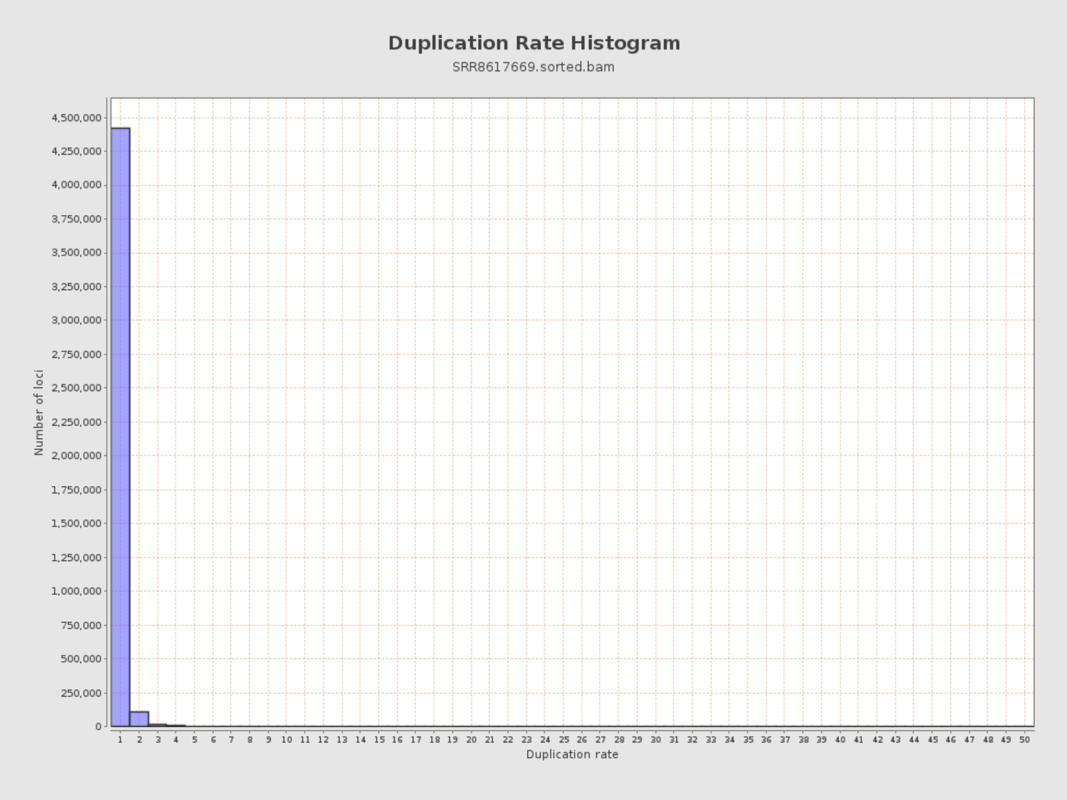
5. Results : Coverage Histogram (0-50X)



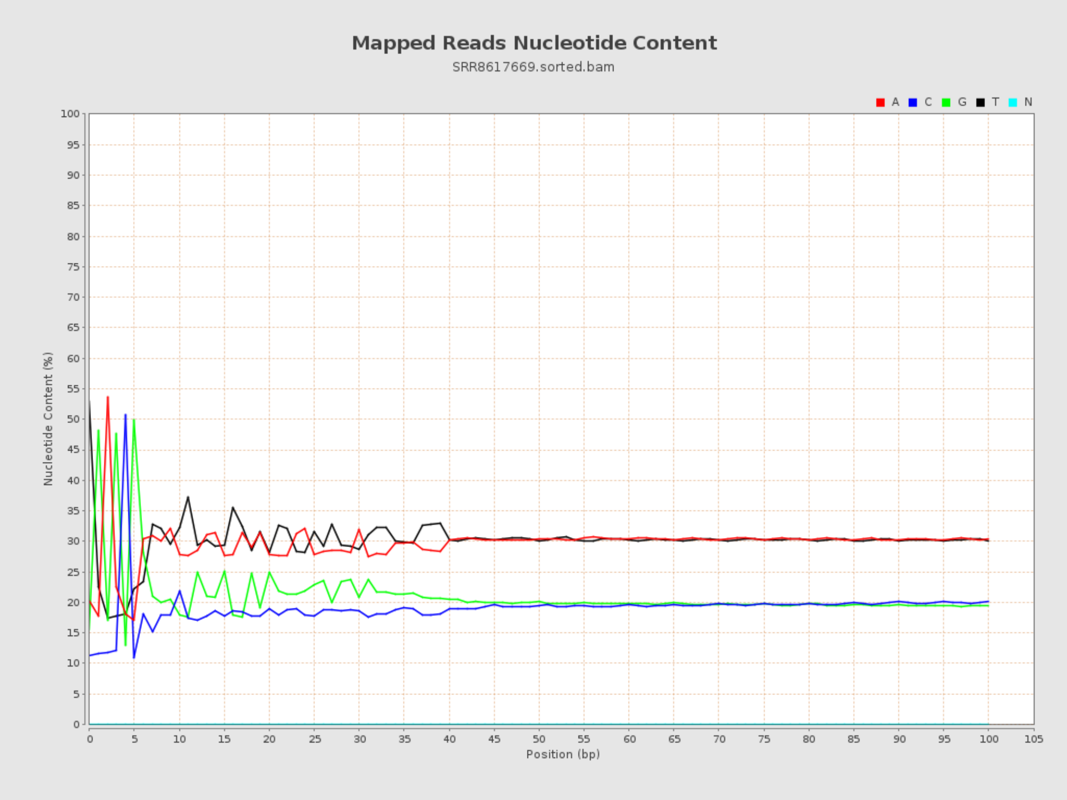
6. Results : Genome Fraction Coverage



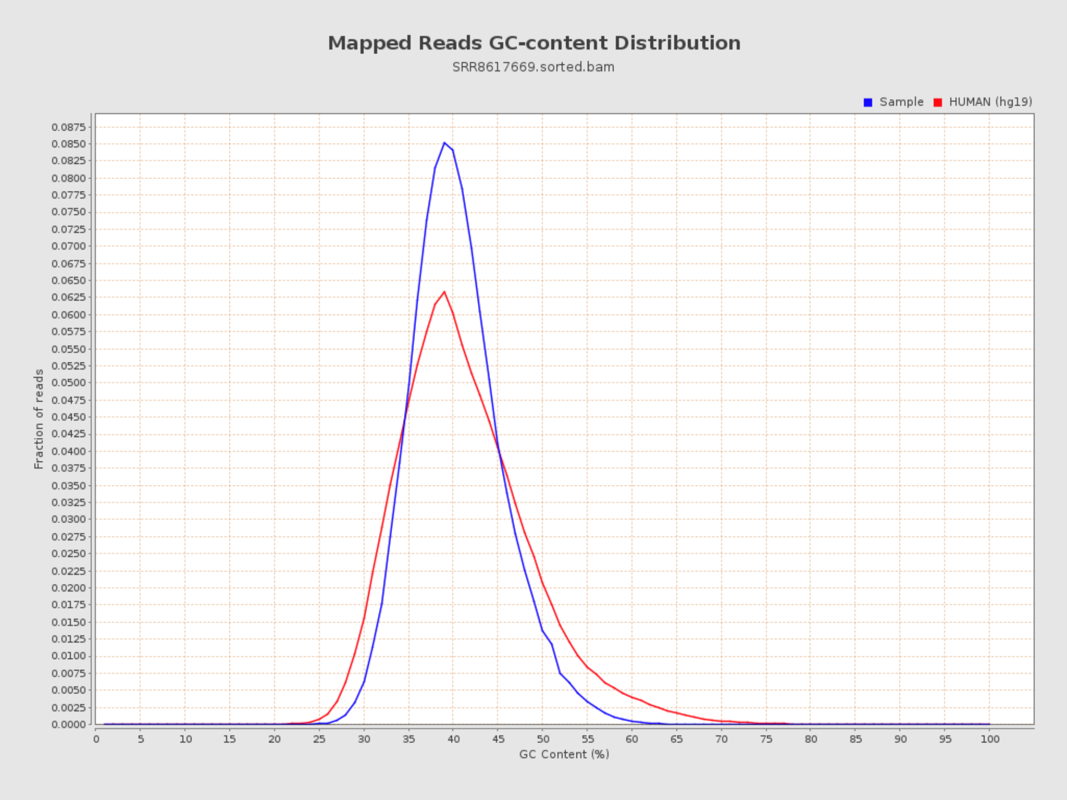
7. Results : Duplication Rate Histogram



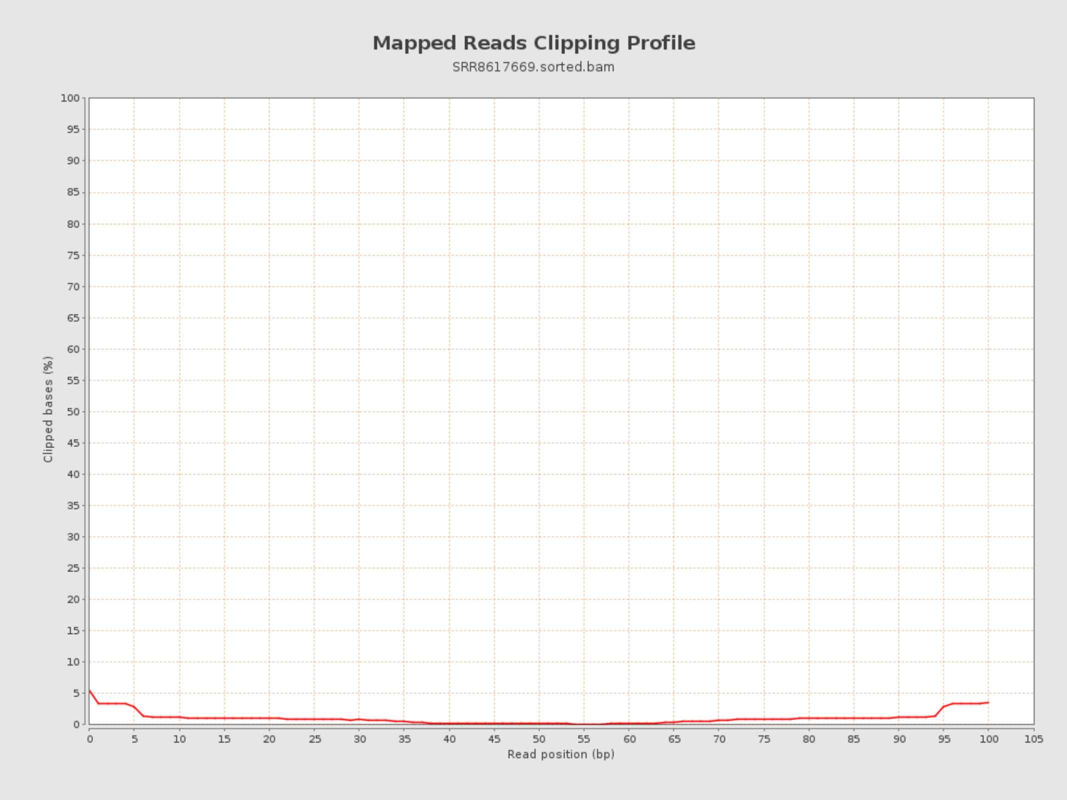
8. Results : Mapped Reads Nucleotide Content



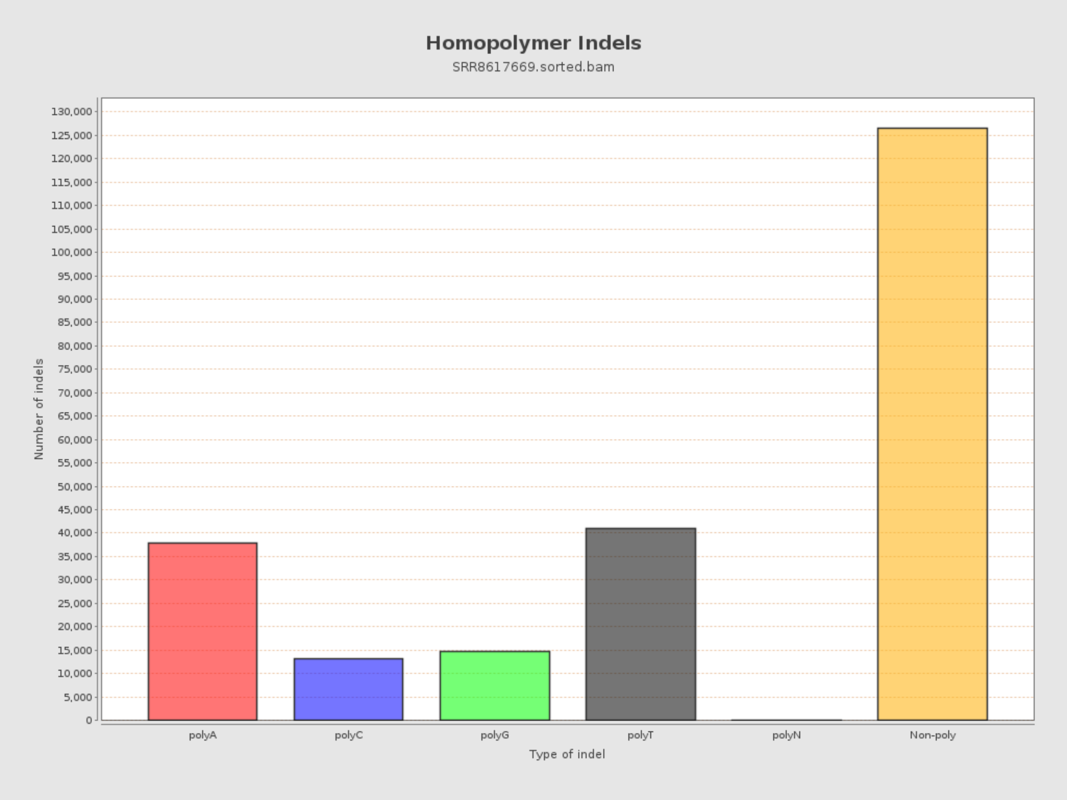
9. Results : Mapped Reads GC-content Distribution



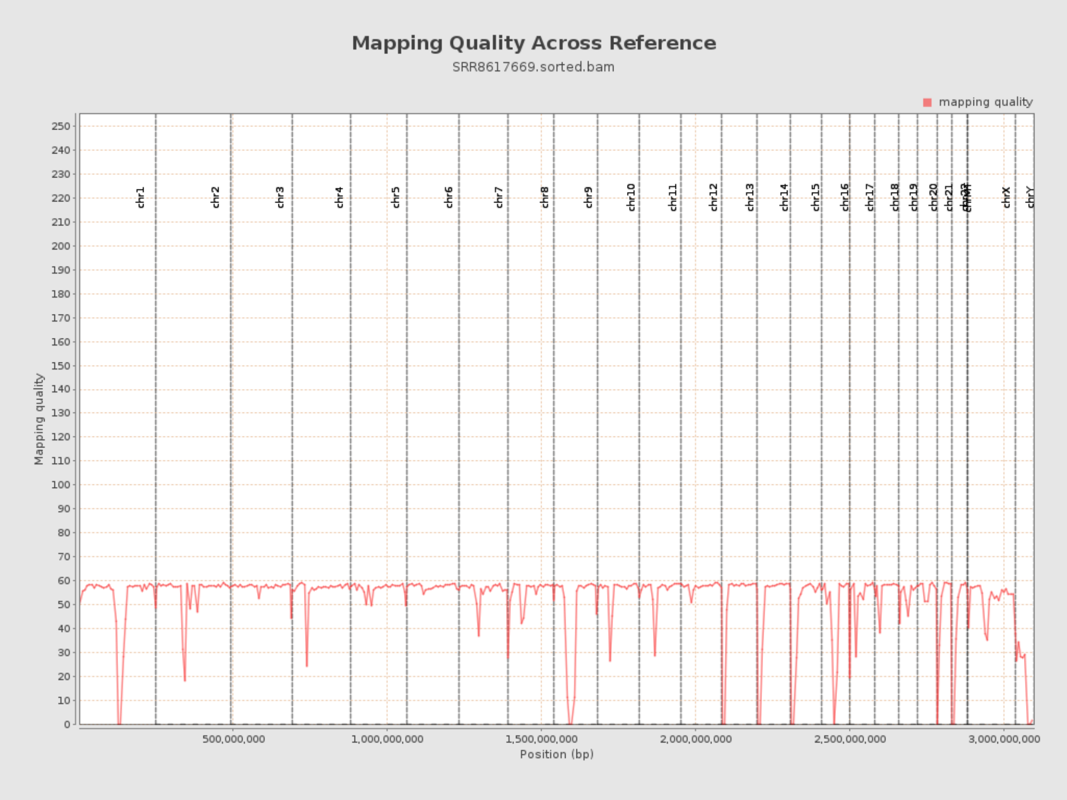
10. Results : Mapped Reads Clipping Profile



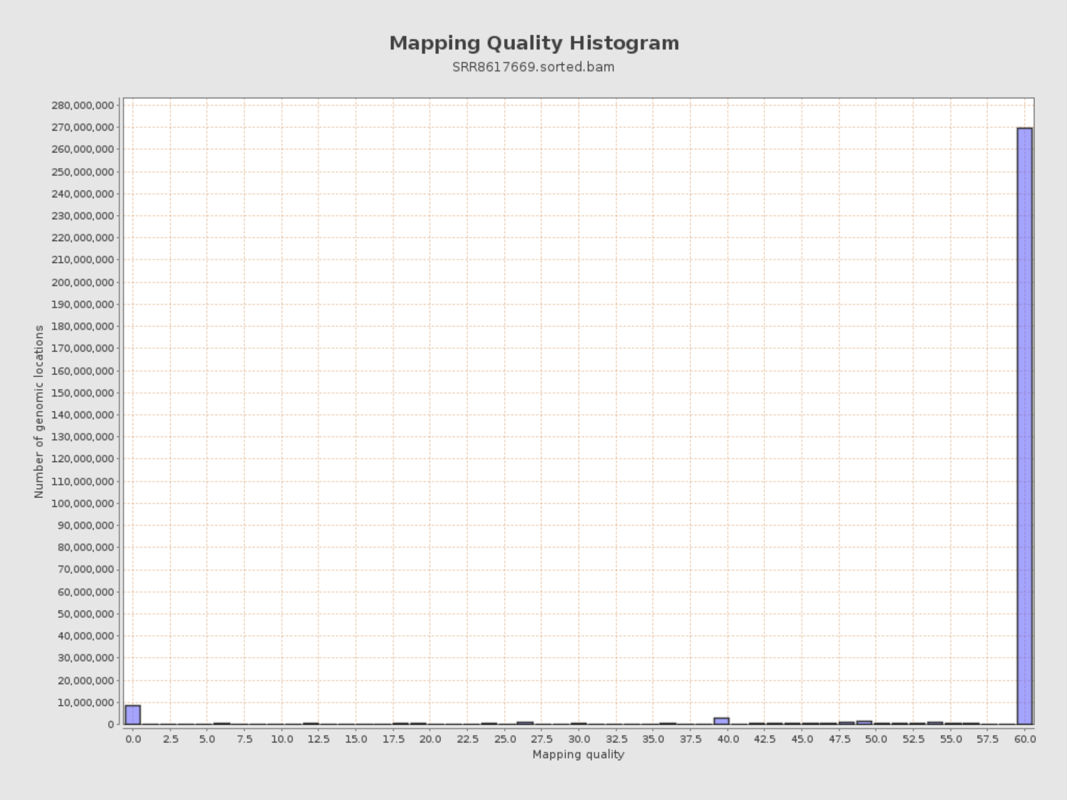
11. Results : Homopolymer Indels



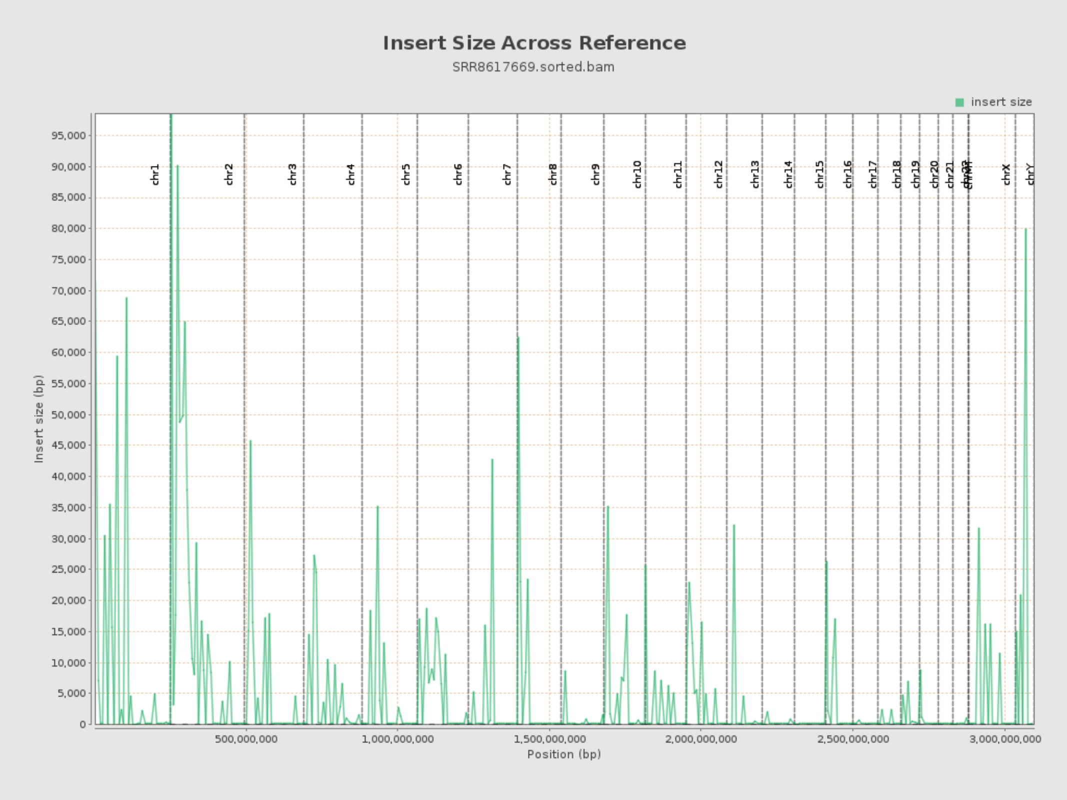
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram