Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 23:47:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617381.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_SRR617381 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617381_1.fastq.gz SRR617381_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 23:47:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617381.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,655,623 / 92.67%
Unmapped reads	2,344,377 / 7.33%
Mapped paired reads	29,655,623 / 92.67%
Mapped reads, first in pair	14,925,843 / 46.64%
Mapped reads, second in pair	14,729,780 / 46.03%
Mapped reads, both in pair	29,088,224 / 90.9%
Mapped reads, singletons	567,399 / 1.77%
Secondary alignments	0
Supplementary alignments	65,035 / 0.2%
Read min/max/mean length	30 / 100 / 100.08
Duplicated reads (estimated)	1,522,355 / 4.76%
Duplication rate	1.47%
Clipped reads	2,679,333 / 8.37%

2.2. ACGT Content

Number/percentage of A's	883,045,723 / 30.4%
Number/percentage of C's	574,600,904 / 19.78%
Number/percentage of T's	869,298,390 / 29.92%
Number/percentage of G's	576,961,833 / 19.86%
Number/percentage of N's	1,250,166 / 0.04%

GC Percentage	39.64%

2.3. Coverage

Mean	0.9387
Standard Deviation	9.6127

2.4. Mapping Quality

Mean Mapping Quality	53.4

2.5. Insert size

Mean	47,084.75
Standard Deviation	2,053,026.11
P25/Median/P75	169 / 207 / 266

2.6. Mismatches and indels

General error rate	1.37%
Mismatches	38,947,957
Insertions	292,145
Mapped reads with at least one insertion	0.95%
Deletions	352,544
Mapped reads with at least one deletion	1.15%
Homopolymer indels	40.89%

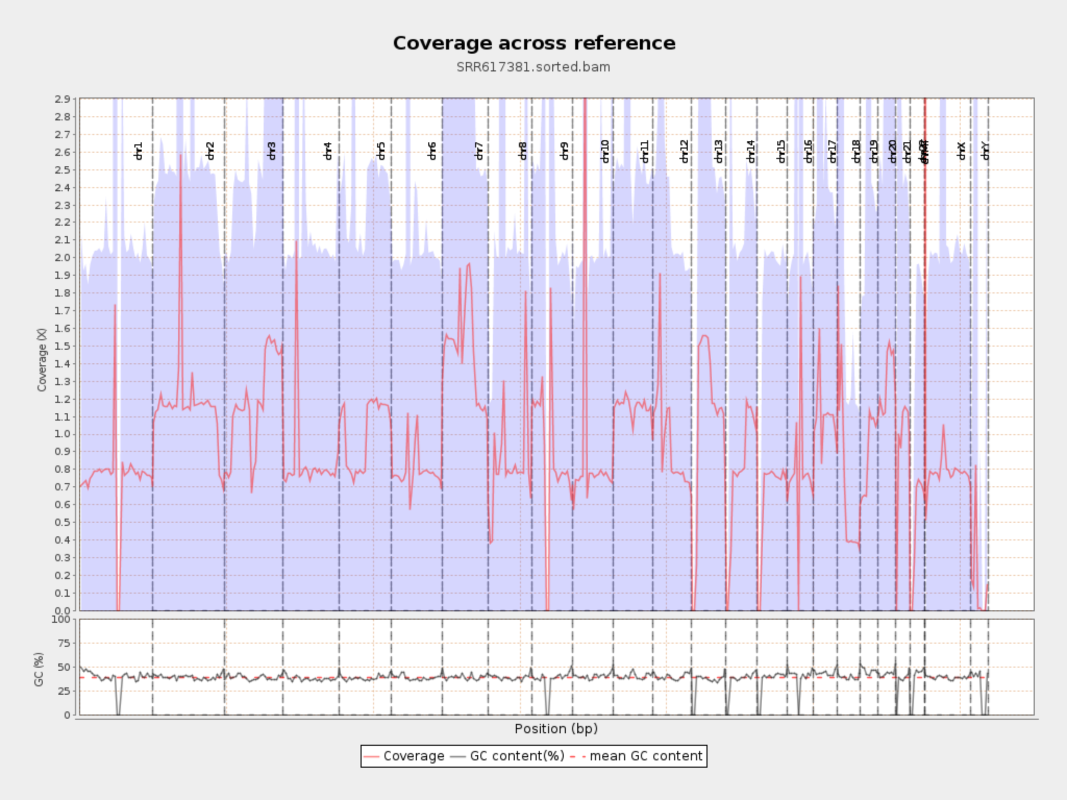
2.7. Chromosome stats

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

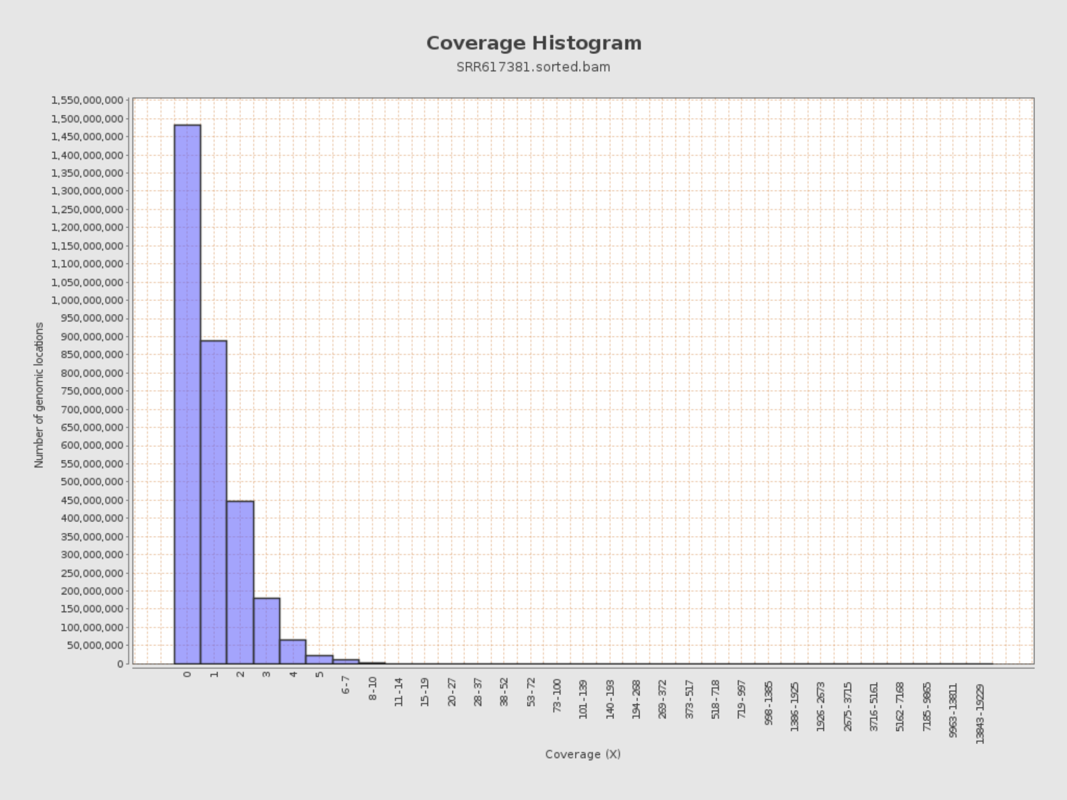
		bases	coverage	deviation
chr1	249250621	188508879	0.7563	19.7104
chr2	243199373	286903009	1.1797	8.6115
chr3	198022430	232047224	1.1718	1.4708
chr4	191154276	159870659	0.8363	8.8203
chr5	180915260	183370092	1.0136	1.4553
chr6	171115067	136763789	0.7993	3.6117
chr7	159138663	236360845	1.4853	10.8323
chr8	146364022	122501584	0.837	7.4296
chr9	141213431	122428857	0.867	14.3955
chr10	135534747	122292448	0.9023	20.0037
chr11	135006516	155833014	1.1543	5.3924
chr12	133851895	128203043	0.9578	1.3258
chr13	115169878	127390276	1.1061	1.2866
chr14	107349540	83967568	0.7822	1.3656
chr15	102531392	65145248	0.6354	0.9691
chr16	90354753	72477243	0.8021	7.9151
chr17	81195210	89435680	1.1015	6.8956
chr18	78077248	52437561	0.6716	14.7607
chr19	59128983	52794884	0.8929	9.65
chr20	63025520	82554972	1.3099	2.4659
chr21	48129895	46262724	0.9612	3.1777
chr22	51304566	25260512	0.4924	0.8982
chrMT	16571	1929005	116.4085	21.1188
chrX	155270560	121568243	0.7829	2.929

chrY	59373566	9694381	0.1633	7.8744

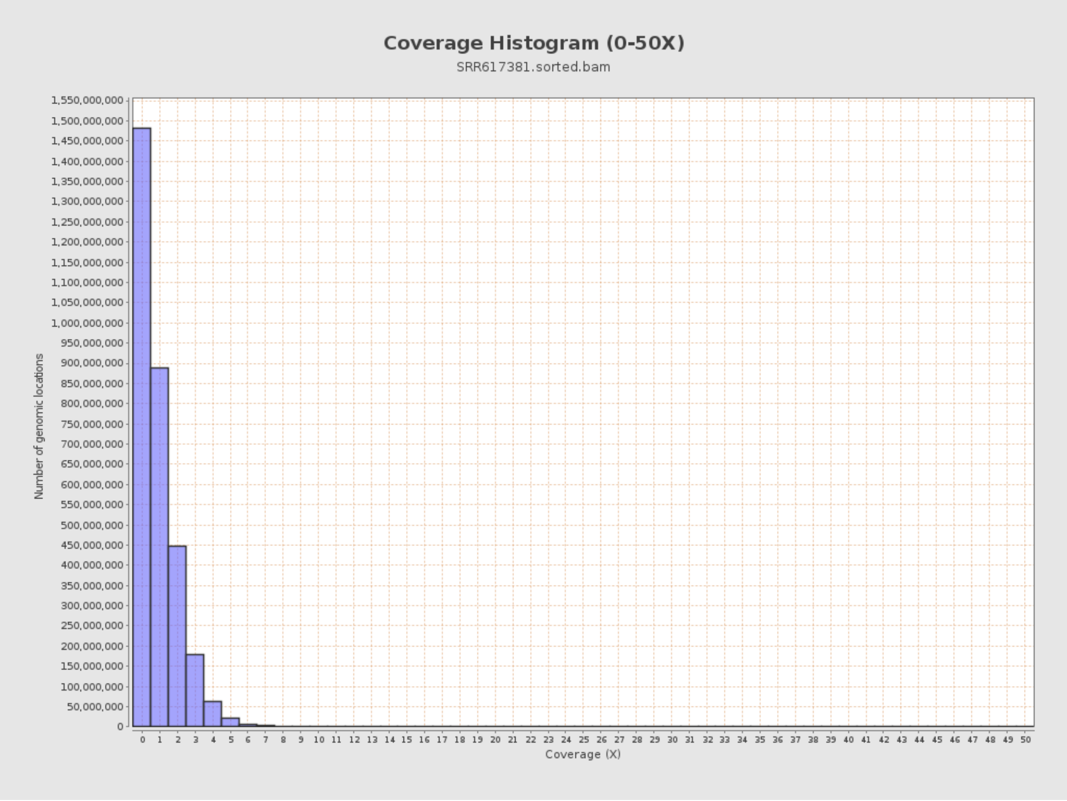
3. Results : Coverage across reference



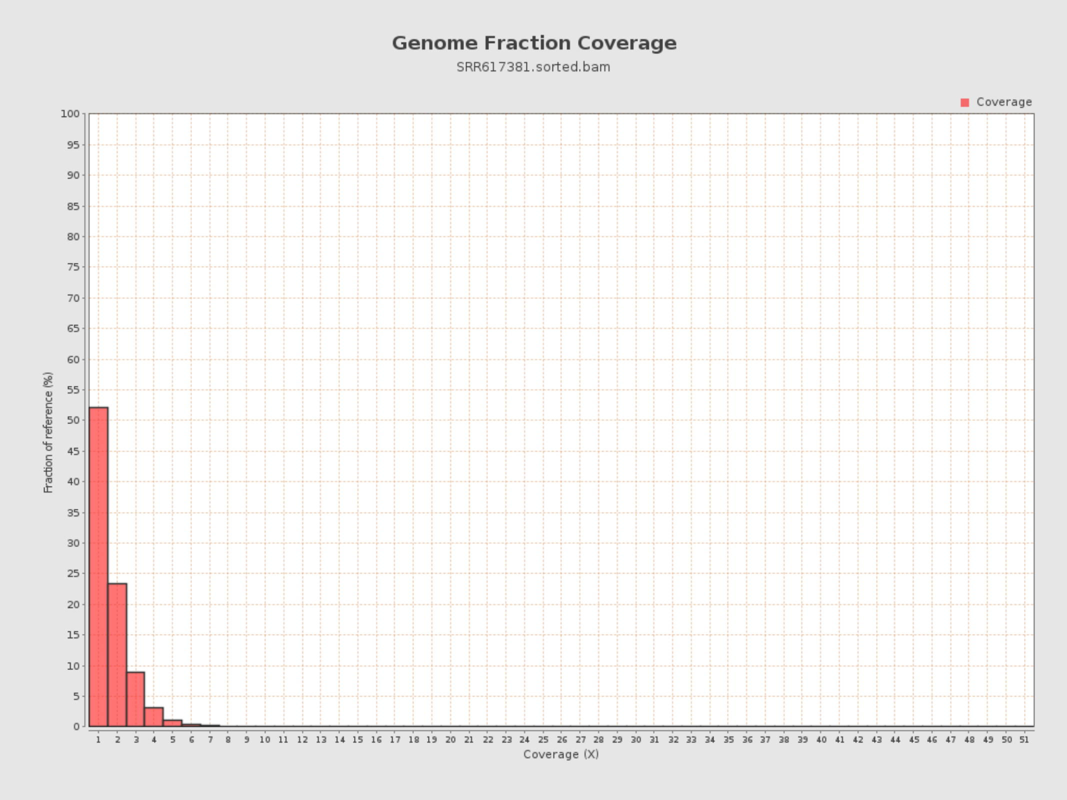
4. Results : Coverage Histogram



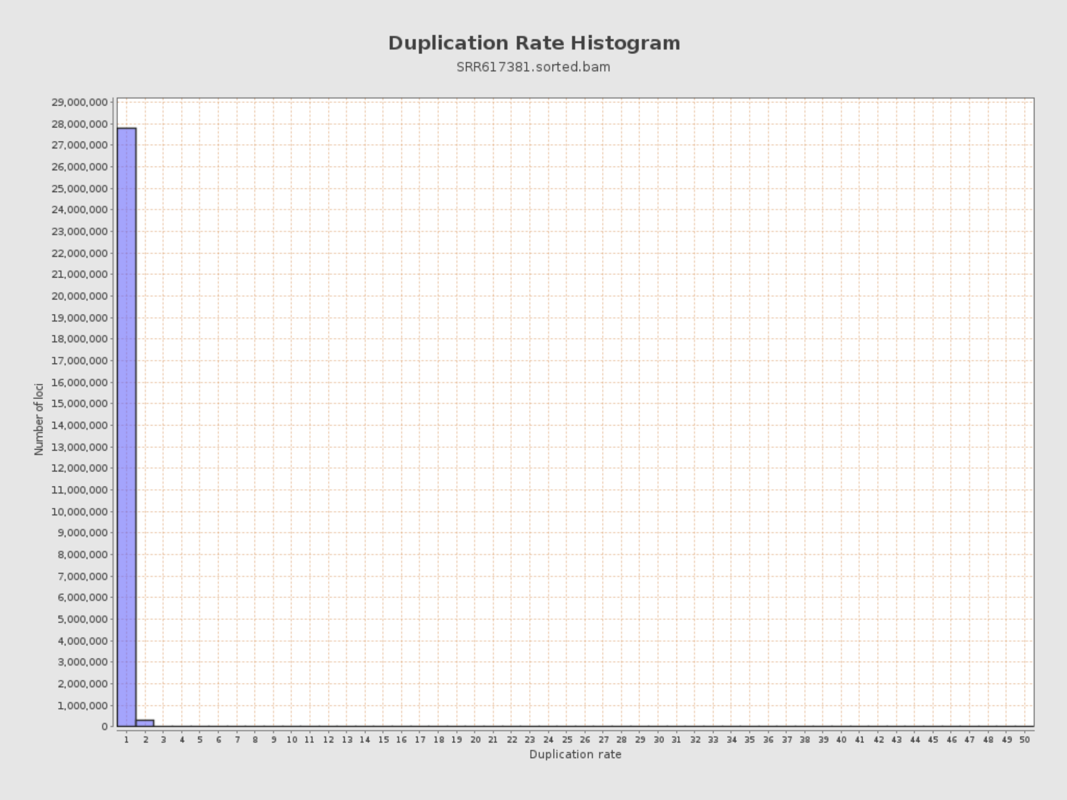
5. Results : Coverage Histogram (0-50X)



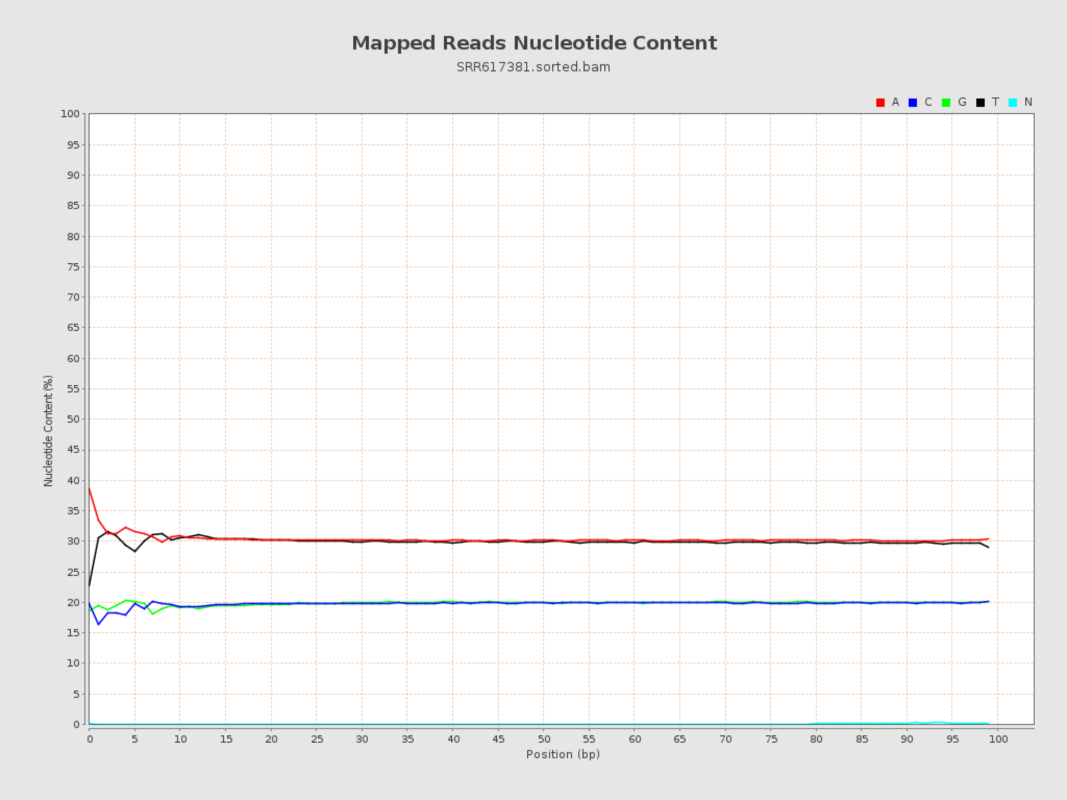
6. Results : Genome Fraction Coverage



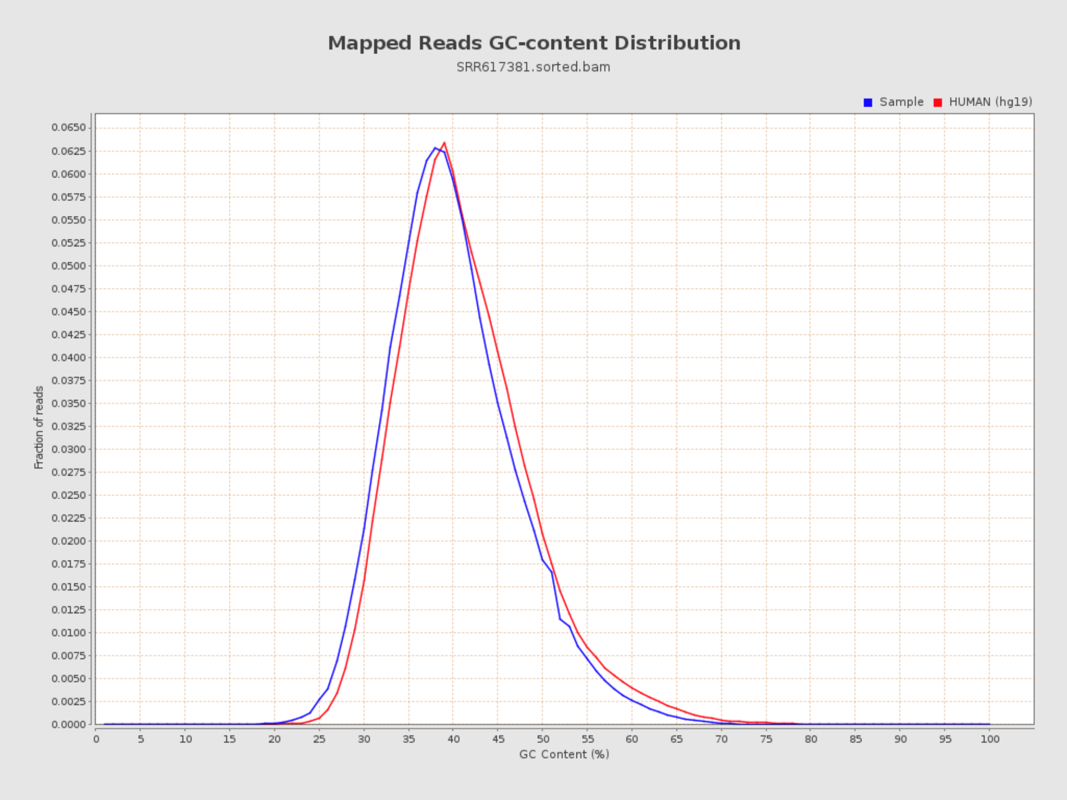
7. Results : Duplication Rate Histogram



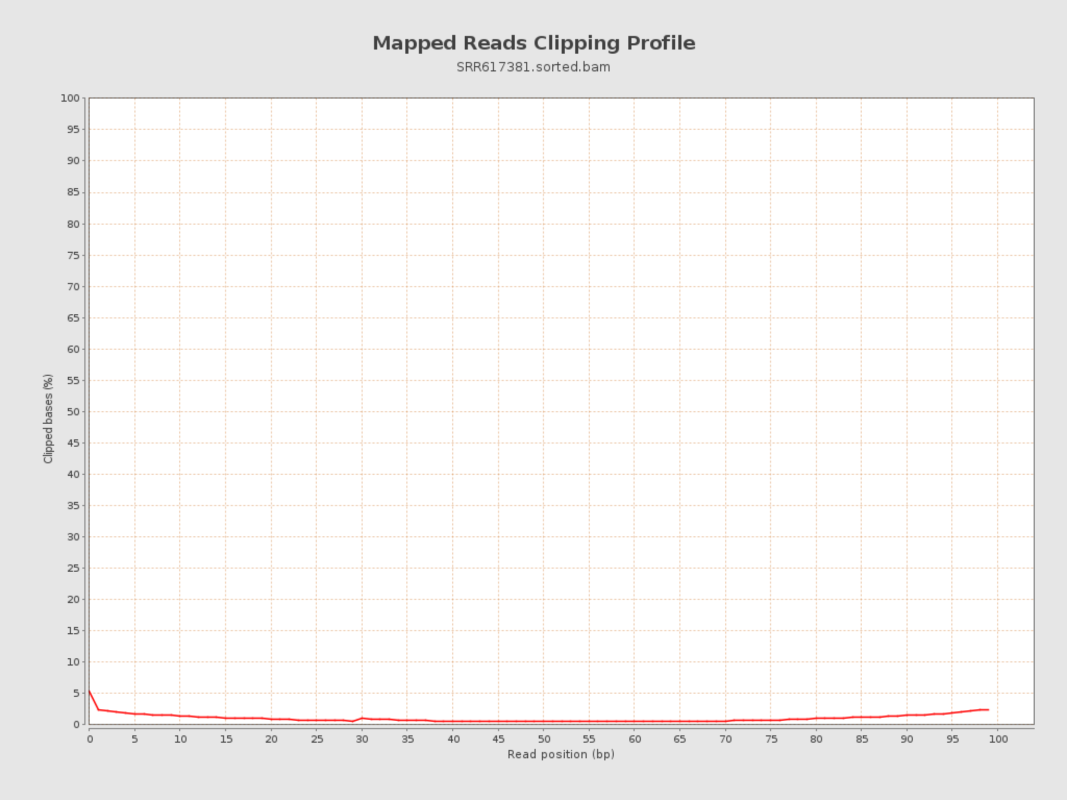
8. Results : Mapped Reads Nucleotide Content



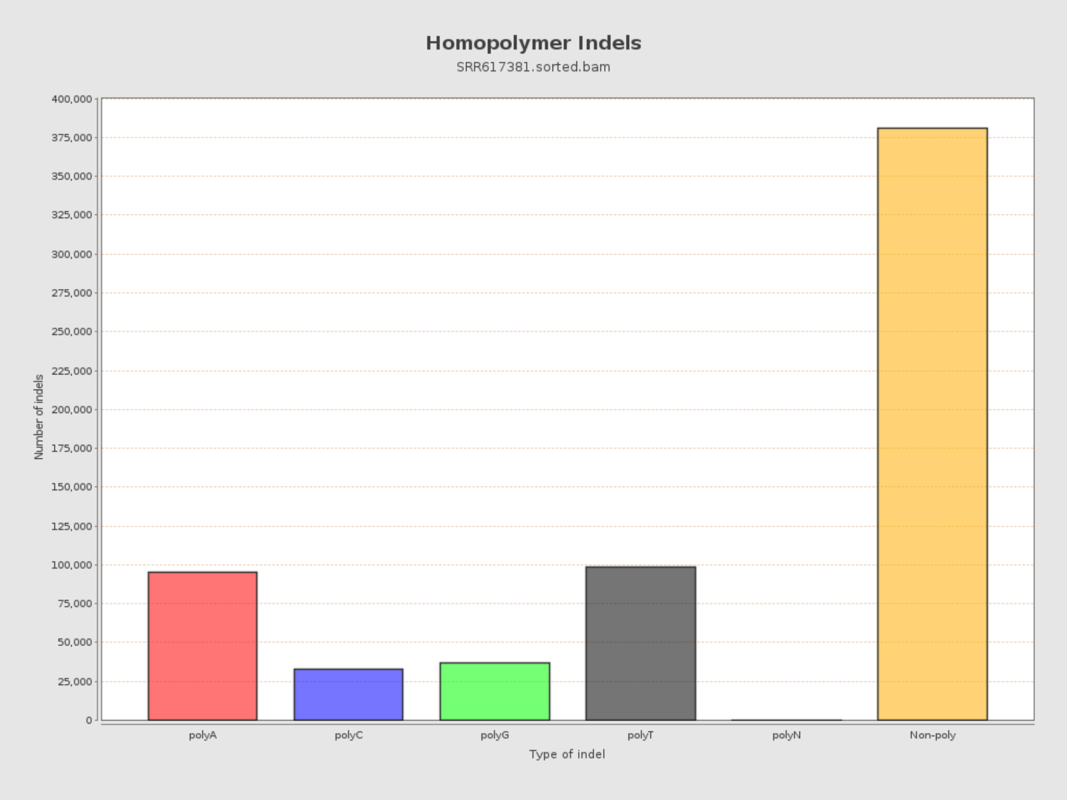
9. Results : Mapped Reads GC-content Distribution



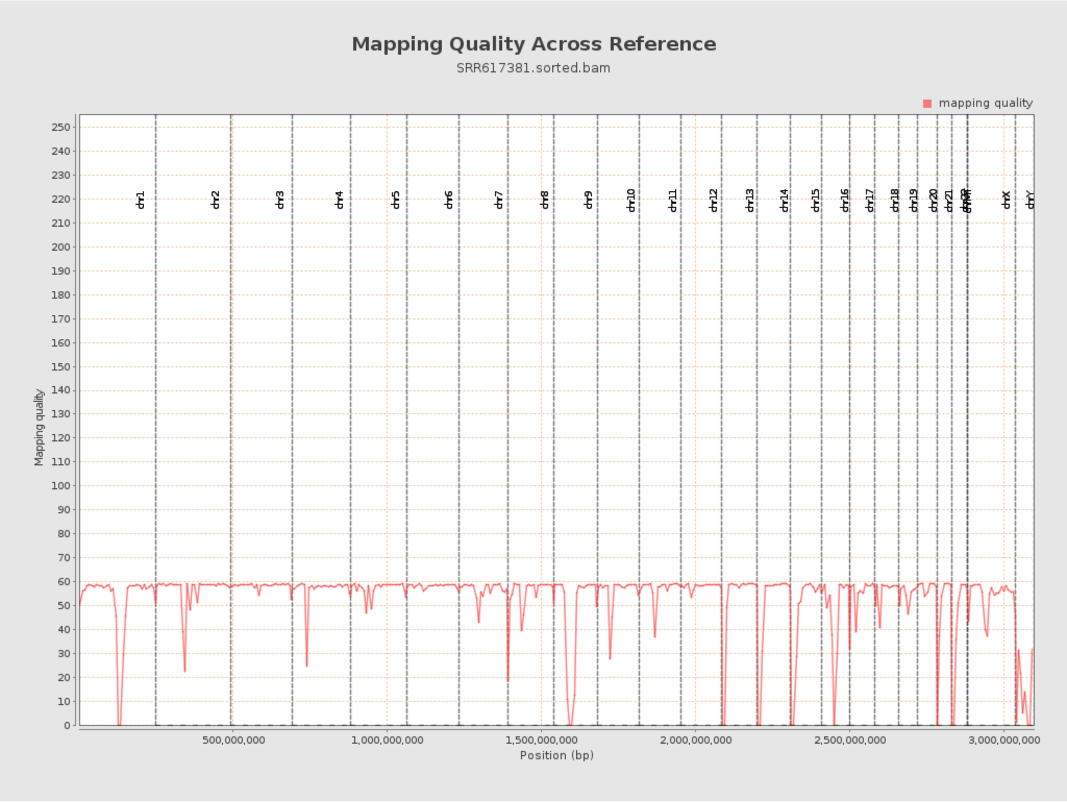
10. Results : Mapped Reads Clipping Profile



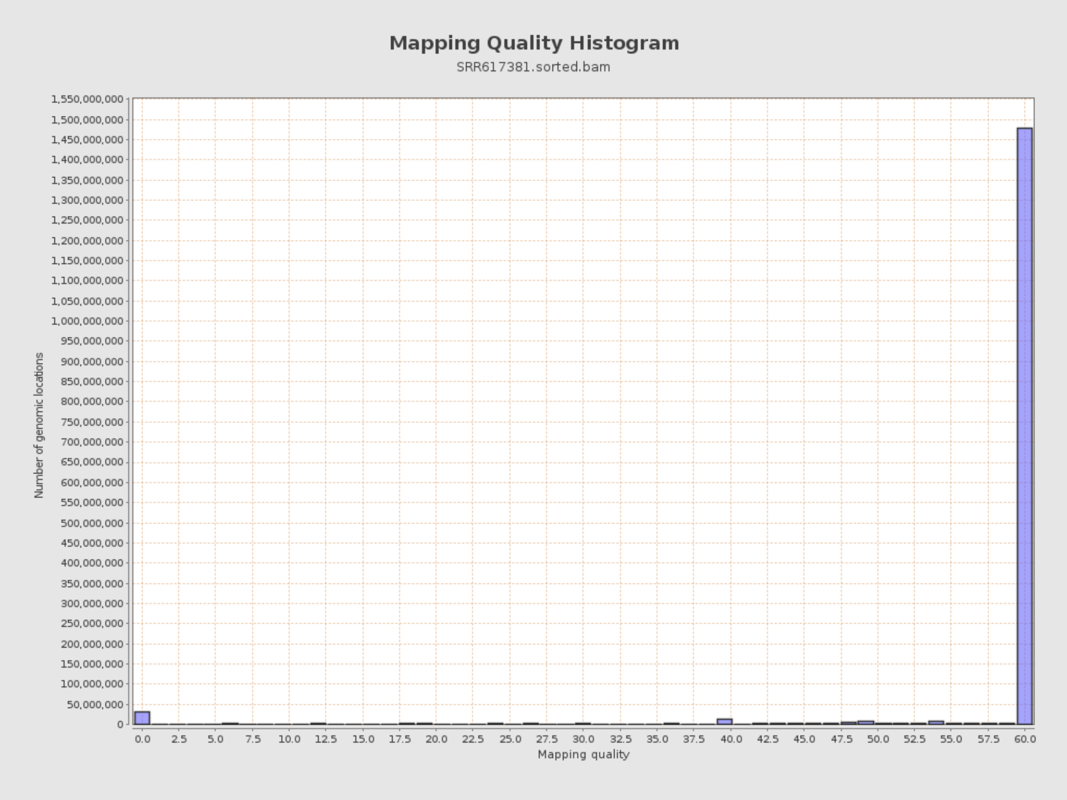
11. Results : Homopolymer Indels



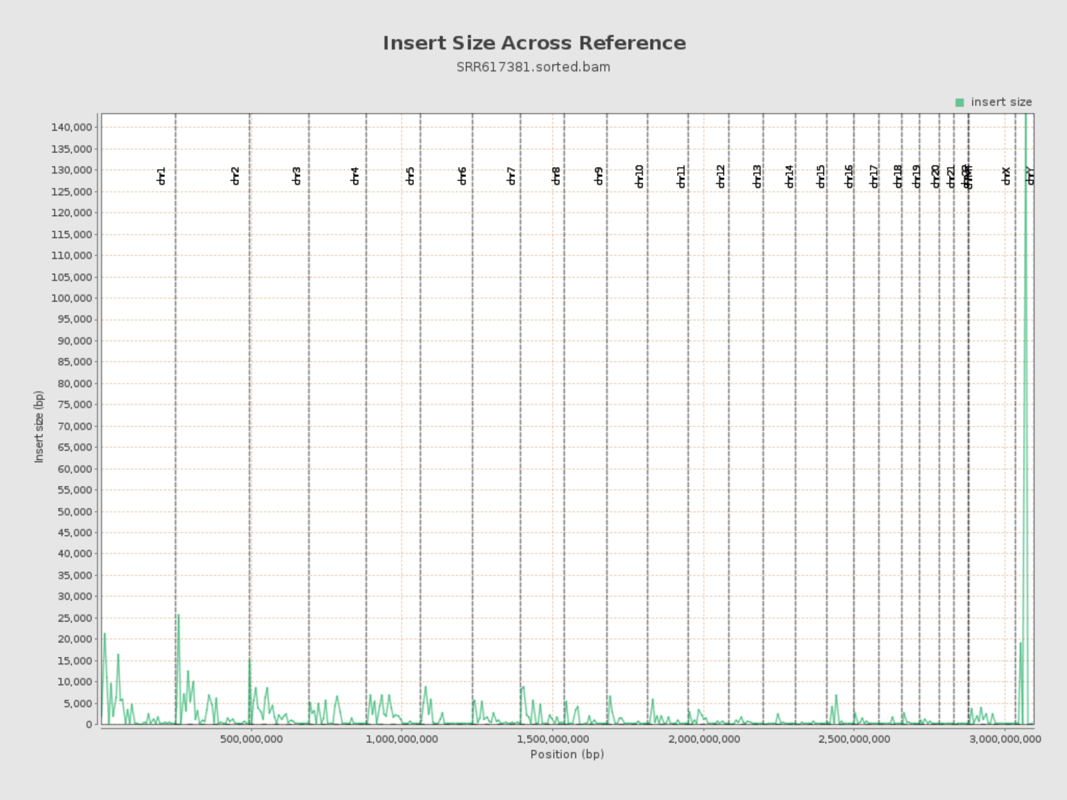
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram