Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/10 00:40:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617500.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_SRR617500 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617500_1.fastq.gz SRR617500_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Oct 10 00:40:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617500.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,490,417 / 95.28%
Unmapped reads	1,509,583 / 4.72%
Mapped paired reads	30,490,417 / 95.28%
Mapped reads, first in pair	15,351,919 / 47.97%
Mapped reads, second in pair	15,138,498 / 47.31%
Mapped reads, both in pair	29,944,362 / 93.58%
Mapped reads, singletons	546,055 / 1.71%
Secondary alignments	0
Supplementary alignments	158,233 / 0.49%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	6,280,109 / 19.63%
Duplication rate	9.95%
Clipped reads	6,003,408 / 18.76%

2.2. ACGT Content

Number/percentage of A's	876,174,711 / 29.5%
Number/percentage of C's	600,499,530 / 20.22%
Number/percentage of T's	875,810,450 / 29.49%
Number/percentage of G's	614,924,216 / 20.7%
Number/percentage of N's	2,677,247 / 0.09%

GC Percentage	40.92%

2.3. Coverage

Mean	0.96
Standard Deviation	9.6506

2.4. Mapping Quality

Mean Mapping Quality	52.72

2.5. Insert size

Mean	40,432.42
Standard Deviation	1,883,357
P25/Median/P75	174 / 220 / 291

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	36,727,182
Insertions	441,859
Mapped reads with at least one insertion	1.42%
Deletions	1,034,945
Mapped reads with at least one deletion	3.32%
Homopolymer indels	47.43%

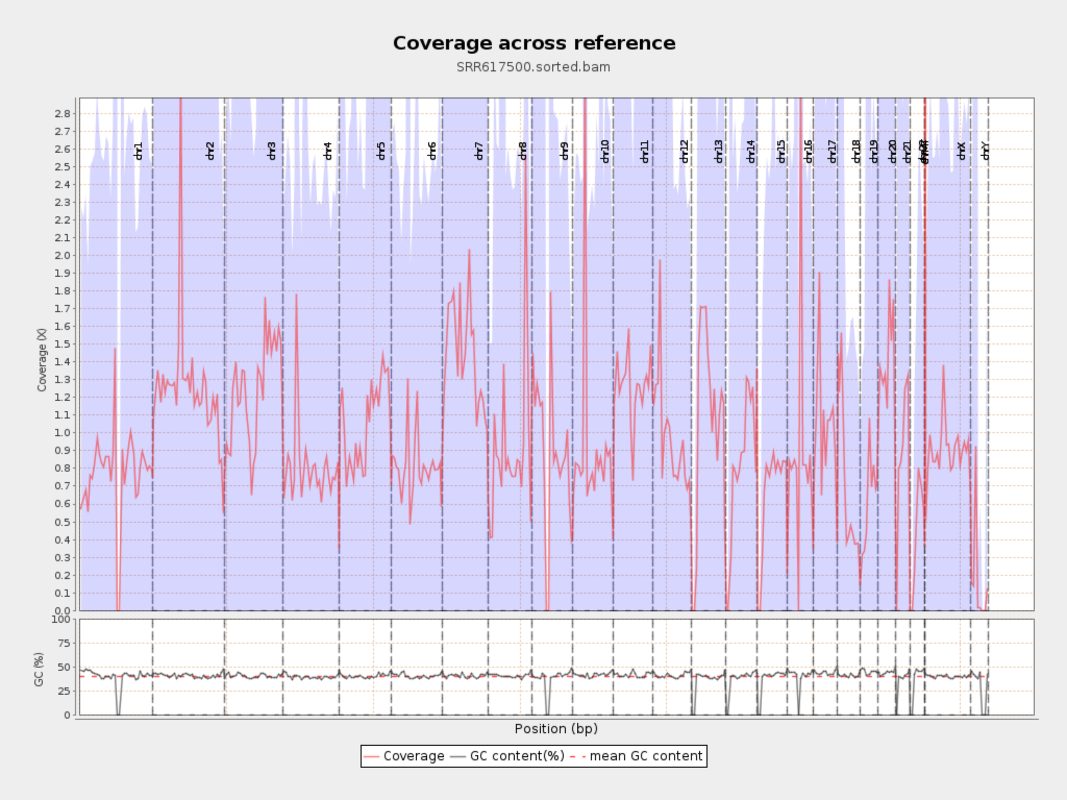
2.7. Chromosome stats

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

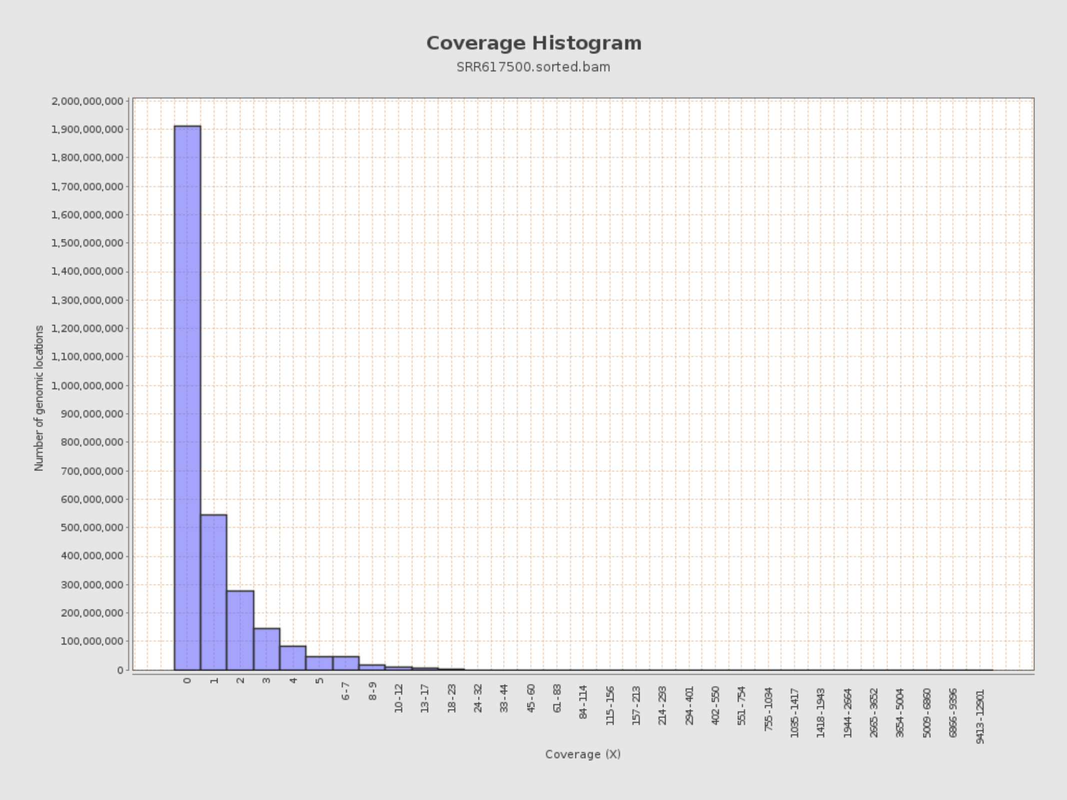
		bases	**coverage**	**deviation**
chr1	249250621	191569432	0.7686	9.3805
chr2	243199373	307164506	1.263	11.3396
chr3	198022430	245319993	1.2388	2.2527
chr4	191154276	153579965	0.8034	6.1019
chr5	180915260	190430848	1.0526	2.0867
chr6	171115067	140152601	0.8191	5.4387
chr7	159138663	229047809	1.4393	13.1941
chr8	146364022	132083894	0.9024	3.8369
chr9	141213431	123361246	0.8736	18.1801
chr10	135534747	125718233	0.9276	18.6223
chr11	135006516	167279724	1.239	12.5028
chr12	133851895	129899954	0.9705	2.0146
chr13	115169878	125958069	1.0937	2.132
chr14	107349540	86657202	0.8072	2.2303
chr15	102531392	66985792	0.6533	1.521
chr16	90354753	79967401	0.885	14.8547
chr17	81195210	83085151	1.0233	13.5494
chr18	78077248	53274744	0.6823	16.9778
chr19	59128983	35657086	0.603	5.7885
chr20	63025520	87757677	1.3924	2.8031
chr21	48129895	42785138	0.889	3.8052
chr22	51304566	22245343	0.4336	1.253
chrMT	16571	2087333	125.963	95.627
chrX	155270560	139551467	0.8988	4.0726

chrY	59373566	10229377	0.1723	13.5346

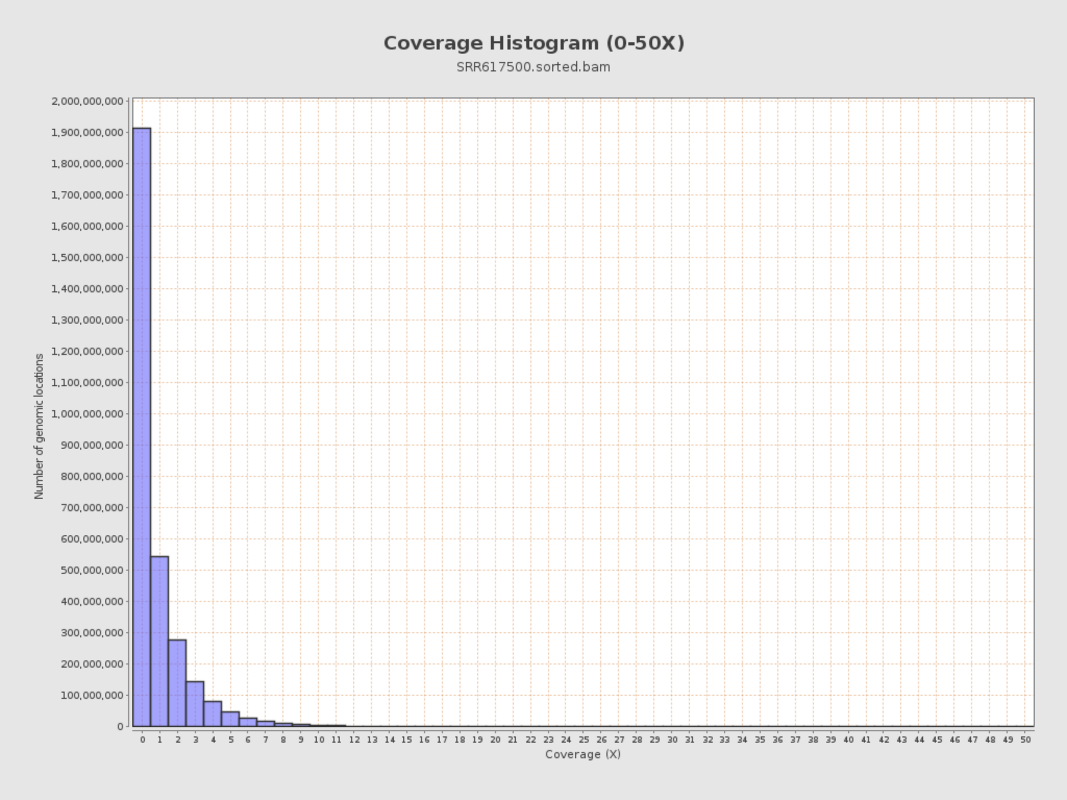
3. Results : Coverage across reference



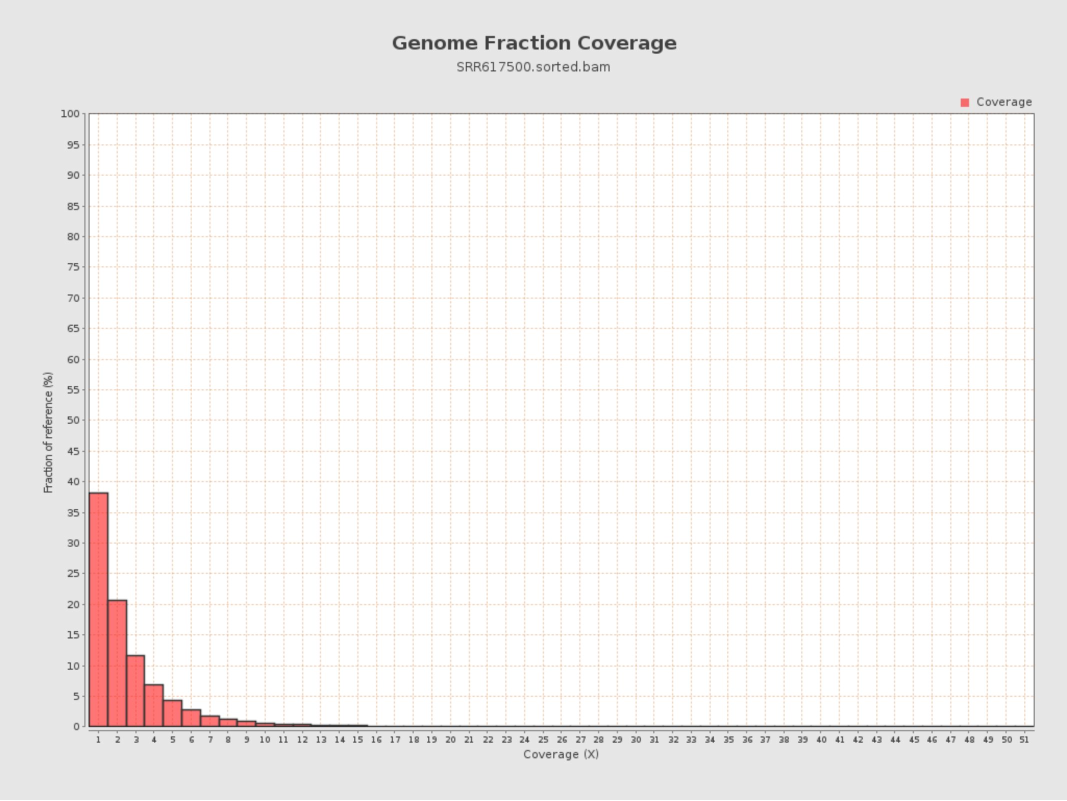
4. Results : Coverage Histogram



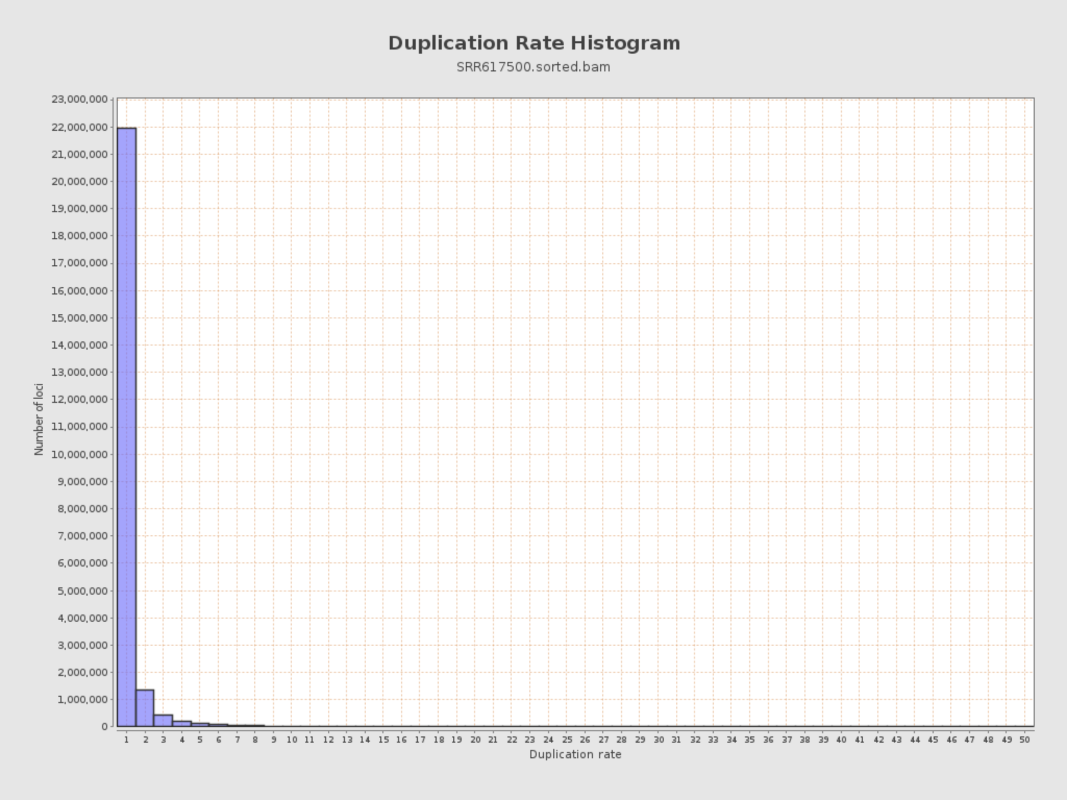
5. Results : Coverage Histogram (0-50X)



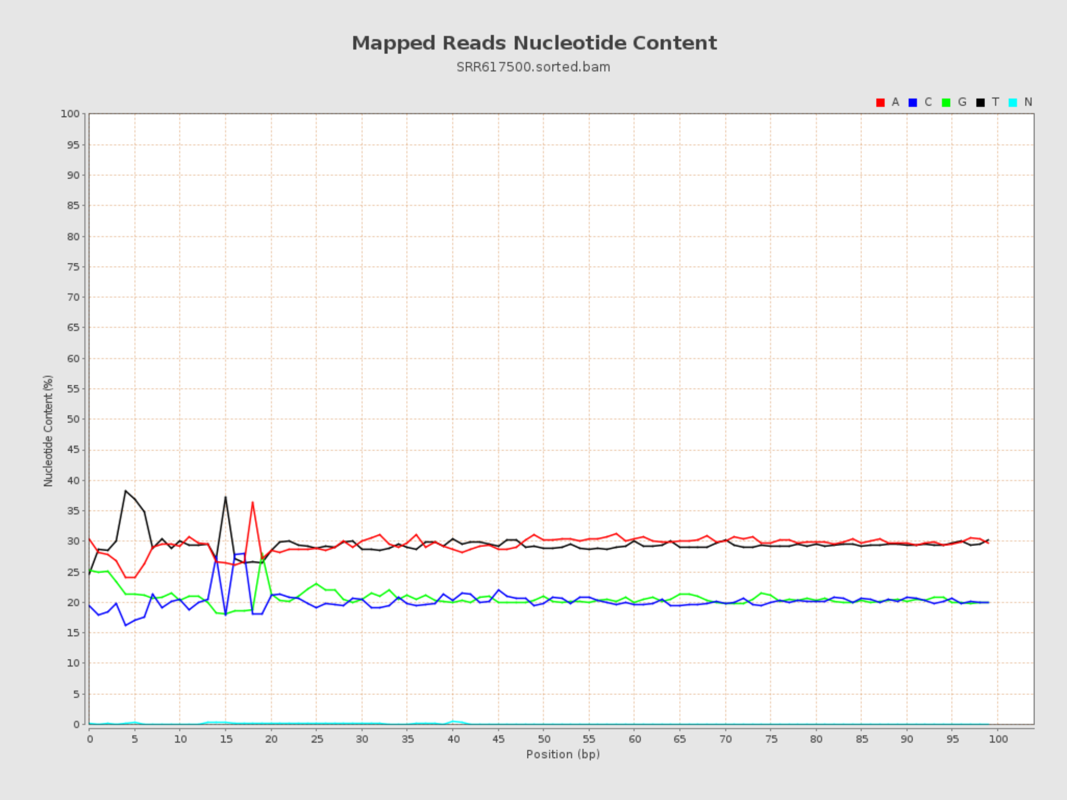
6. Results : Genome Fraction Coverage



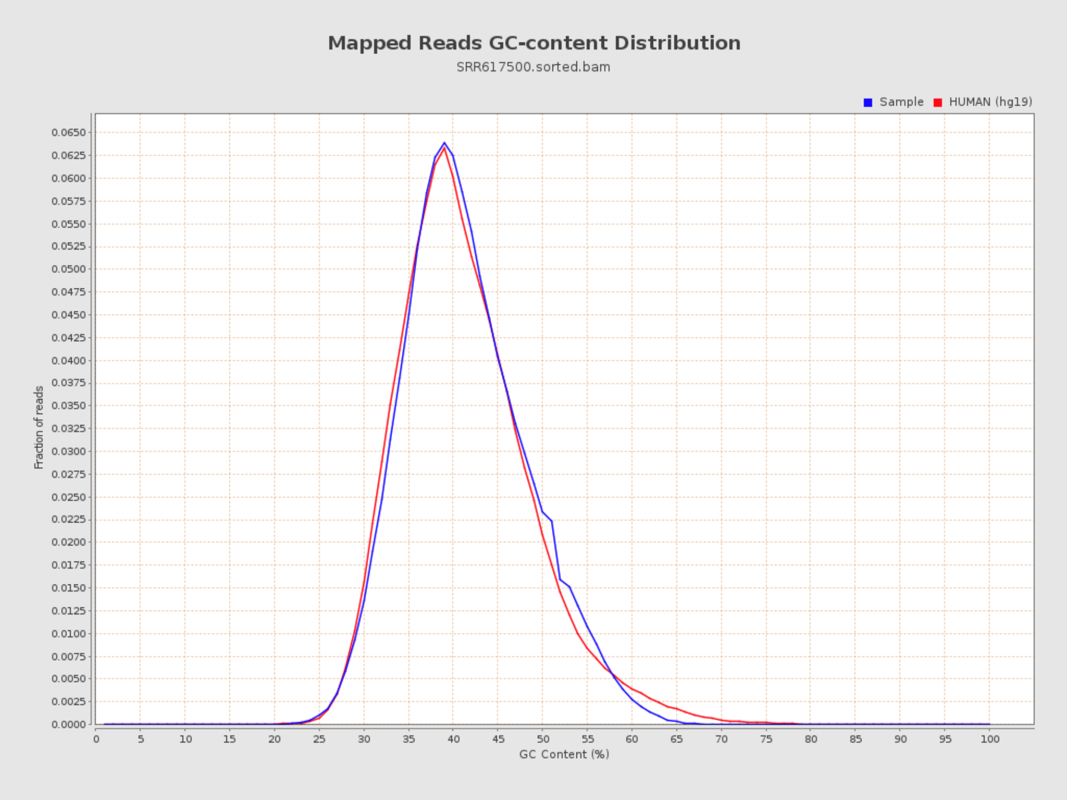
7. Results : Duplication Rate Histogram



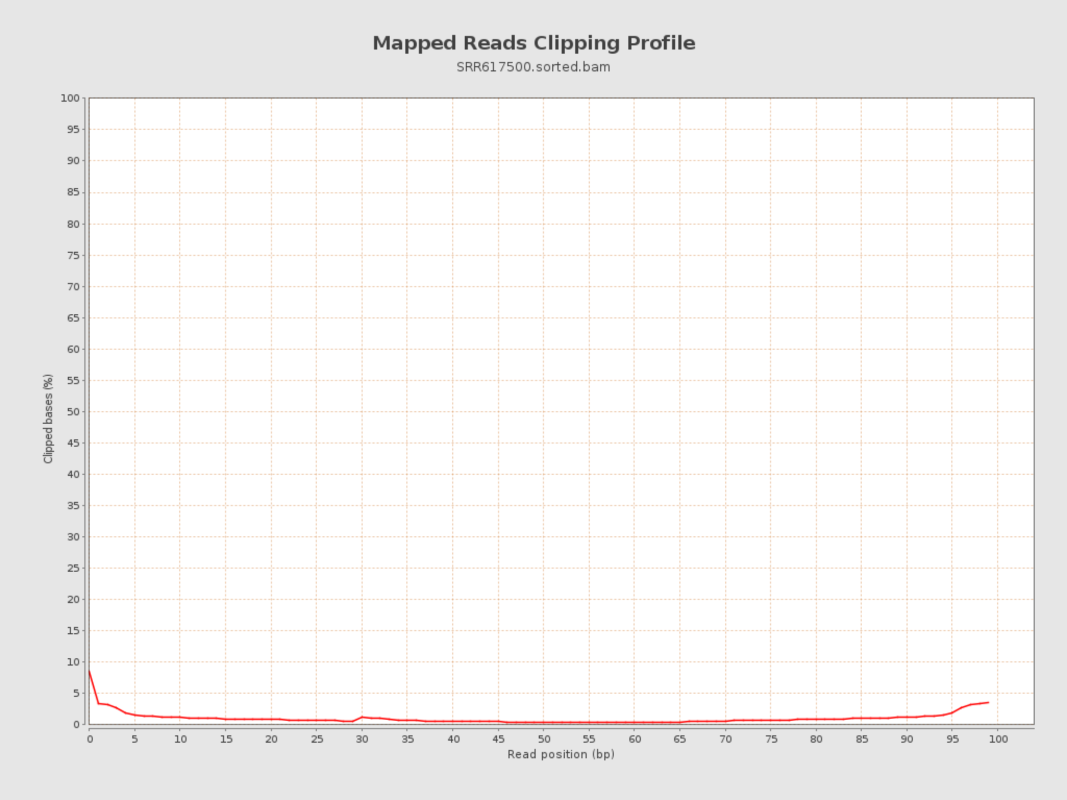
8. Results : Mapped Reads Nucleotide Content



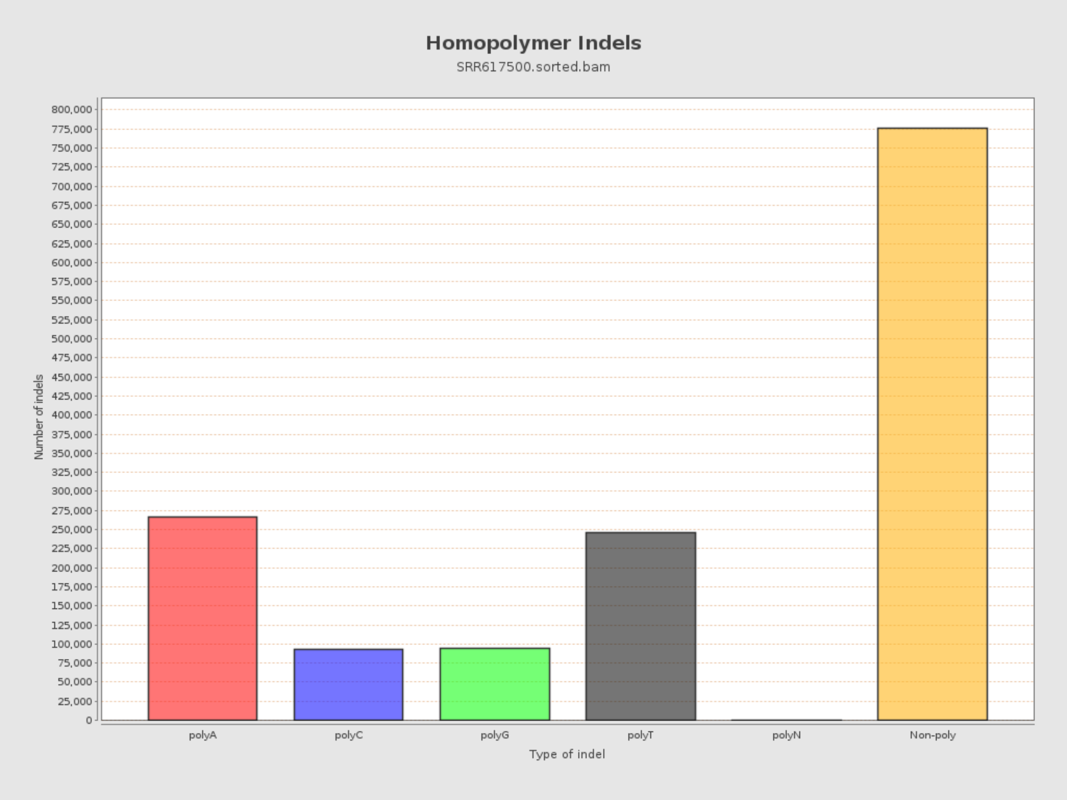
9. Results : Mapped Reads GC-content Distribution



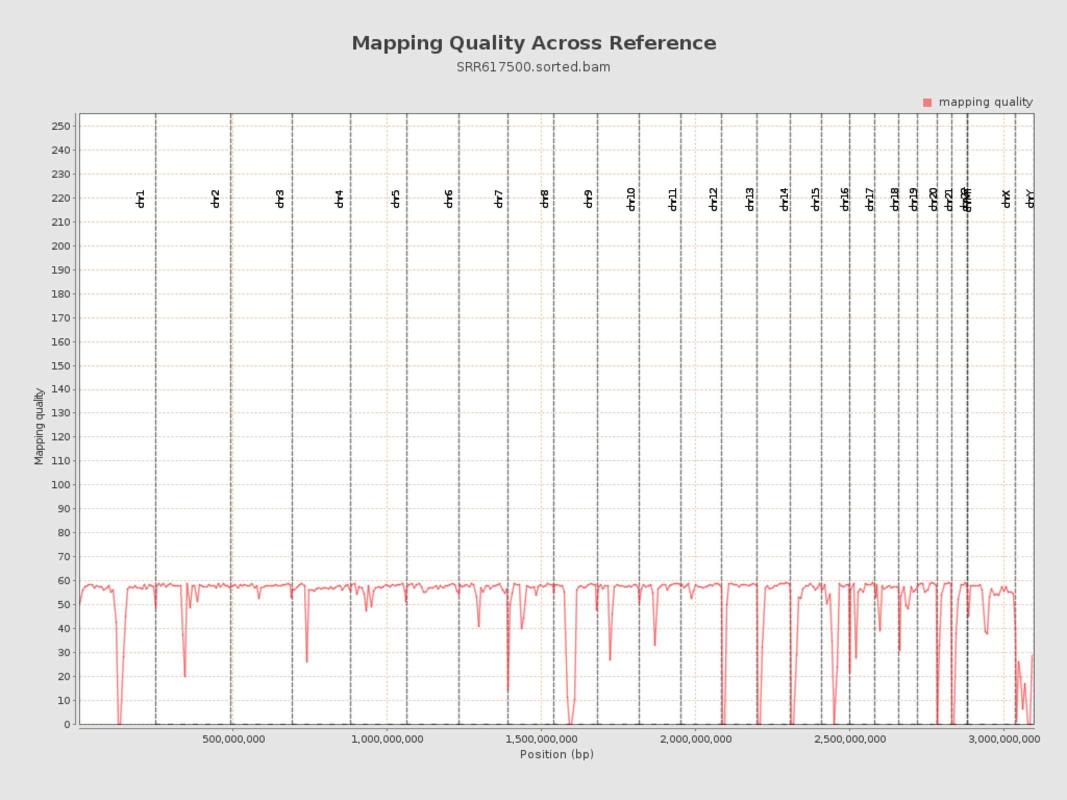
10. Results : Mapped Reads Clipping Profile



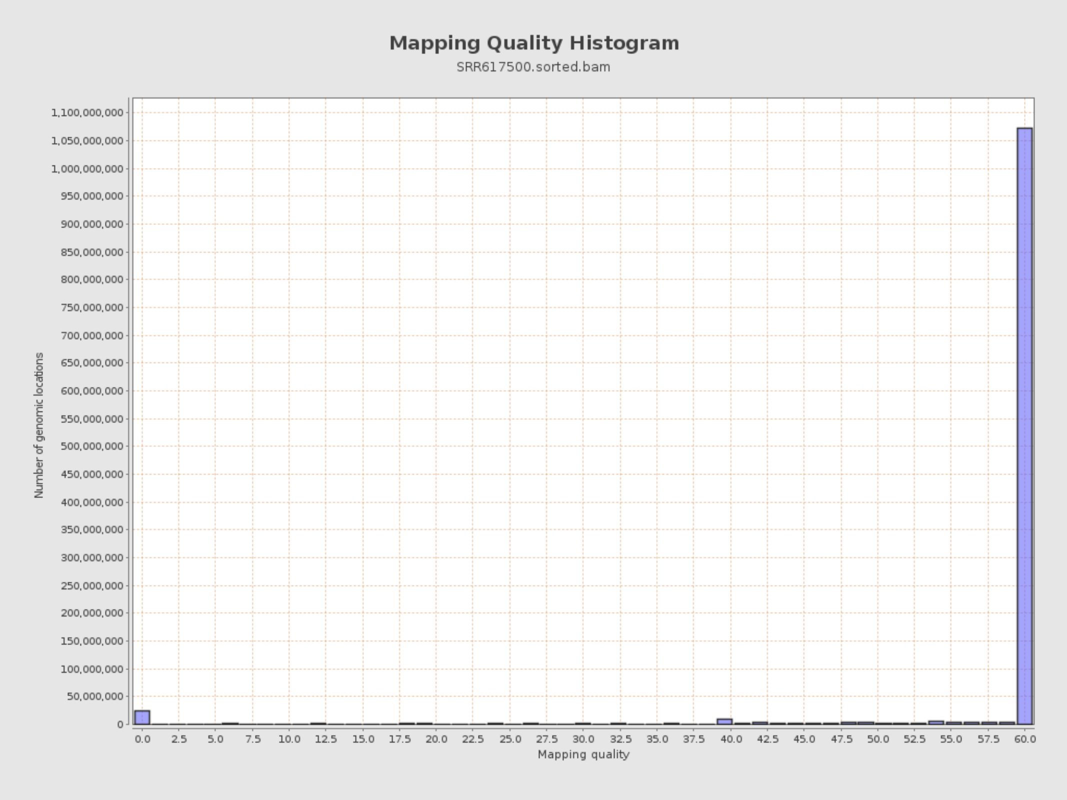
11. Results : Homopolymer Indels



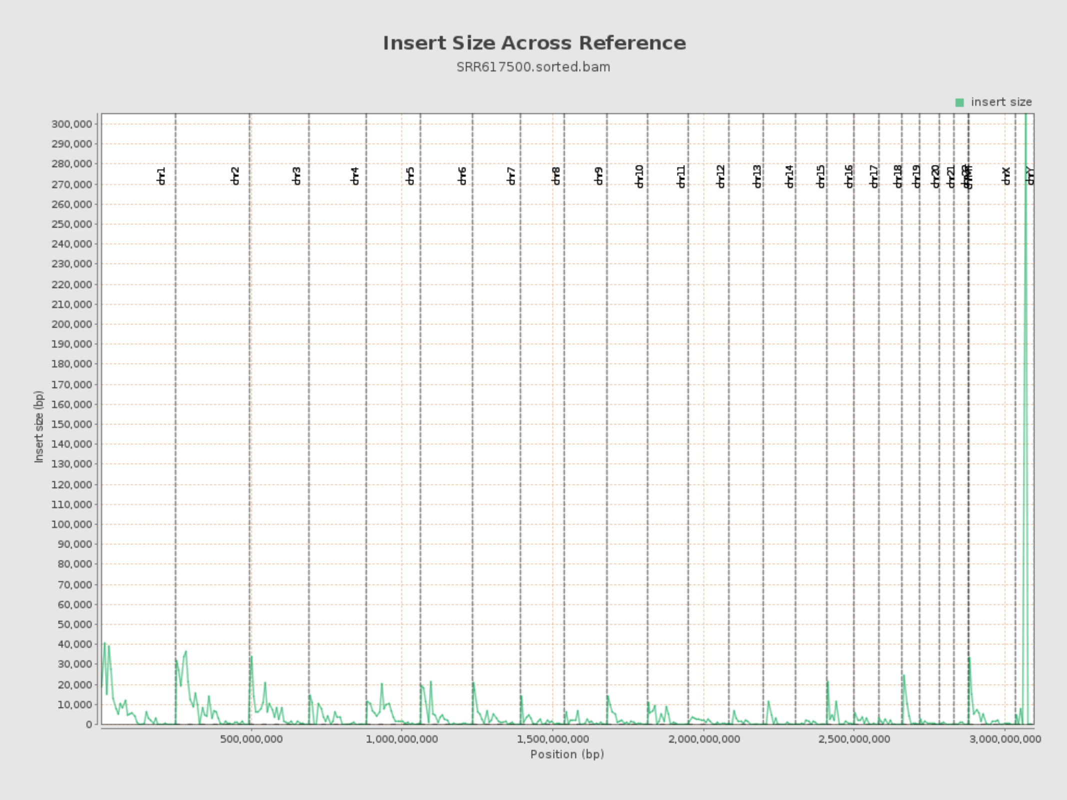
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram