Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/08 03:50:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617385.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_SRR617385 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617385_1.fastq.gz SRR617385_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 08 03:50:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617385.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	29,967,218 / 93.65%
Unmapped reads	2,032,782 / 6.35%
Mapped paired reads	29,967,218 / 93.65%
Mapped reads, first in pair	15,127,986 / 47.27%
Mapped reads, second in pair	14,839,232 / 46.37%
Mapped reads, both in pair	29,297,022 / 91.55%
Mapped reads, singletons	670,196 / 2.09%
Secondary alignments	0
Supplementary alignments	98,637 / 0.31%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	1,578,442 / 4.93%
Duplication rate	1.52%
Clipped reads	2,614,650 / 8.17%

2.2. ACGT Content

Number/percentage of A's	888,051,045 / 30.29%
Number/percentage of C's	581,655,248 / 19.84%
Number/percentage of T's	876,247,647 / 29.89%
Number/percentage of G's	584,531,239 / 19.94%
Number/percentage of N's	901,091 / 0.03%

GC Percentage	39.78%

2.3. Coverage

Mean	0.9472
Standard Deviation	9.5916

2.4. Mapping Quality

Mean Mapping Quality	53.35

2.5. Insert size

Mean	70,398.52
Standard Deviation	2,543,943.26
P25/Median/P75	173 / 215 / 279

2.6. Mismatches and indels

General error rate	1.11%
Mismatches	31,719,529
Insertions	301,793
Mapped reads with at least one insertion	0.98%
Deletions	360,346
Mapped reads with at least one deletion	1.17%
Homopolymer indels	41.2%

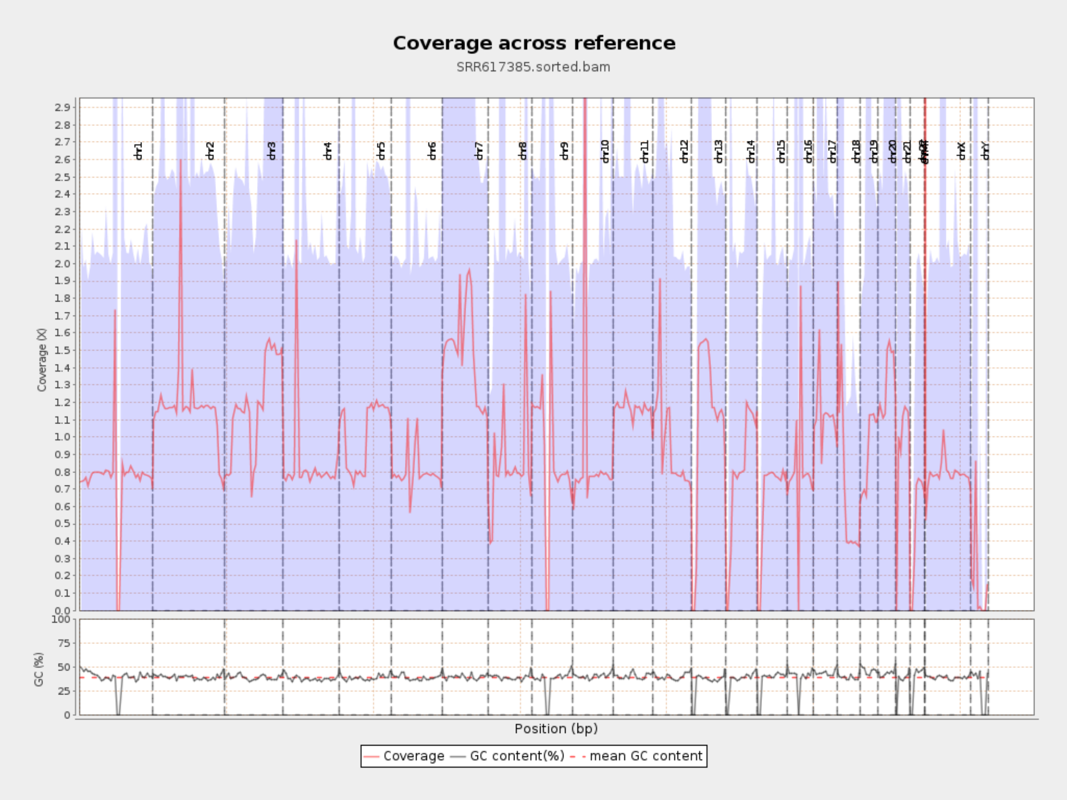
2.7. Chromosome stats

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

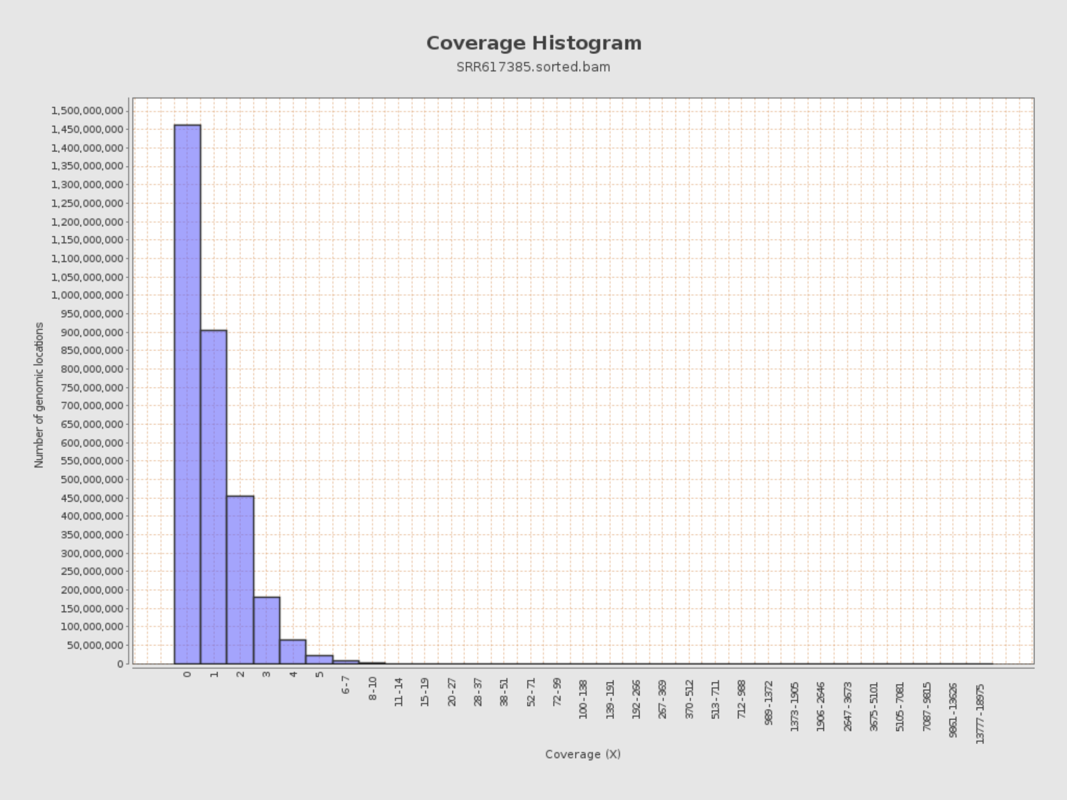
		bases	coverage	deviation
chr1	249250621	190475983	0.7642	19.536
chr2	243199373	289540004	1.1905	8.6555
chr3	198022430	233614336	1.1797	1.481
chr4	191154276	160584462	0.8401	9.2332
chr5	180915260	184090785	1.0176	1.4425
chr6	171115067	137568686	0.804	3.6037
chr7	159138663	238274858	1.4973	10.7762
chr8	146364022	123397176	0.8431	7.5641
chr9	141213431	123559017	0.875	14.4532
chr10	135534747	123352297	0.9101	19.575
chr11	135006516	157417162	1.166	5.4578
chr12	133851895	129376903	0.9666	1.393
chr13	115169878	127633556	1.1082	1.331
chr14	107349540	84708825	0.7891	1.359
chr15	102531392	65885687	0.6426	1.1285
chr16	90354753	73799053	0.8168	7.7358
chr17	81195210	91253076	1.1239	7.0213
chr18	78077248	52898427	0.6775	15.0964
chr19	59128983	54384380	0.9198	9.2975
chr20	63025520	83799518	1.3296	2.4108
chr21	48129895	46595167	0.9681	3.1823
chr22	51304566	26063677	0.508	0.9256
chrMT	16571	1993252	120.2856	20.9115
chrX	155270560	121917716	0.7852	2.9623

chrY	59373566	10072417	0.1696	8.2324

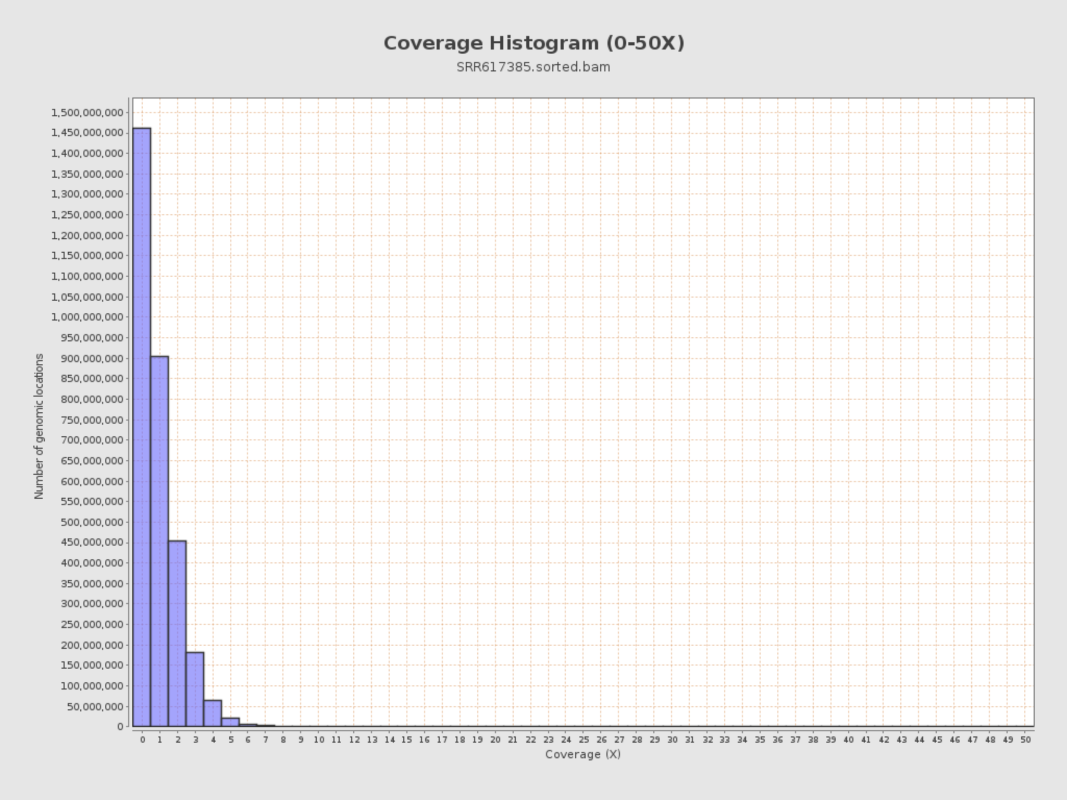
3. Results : Coverage across reference



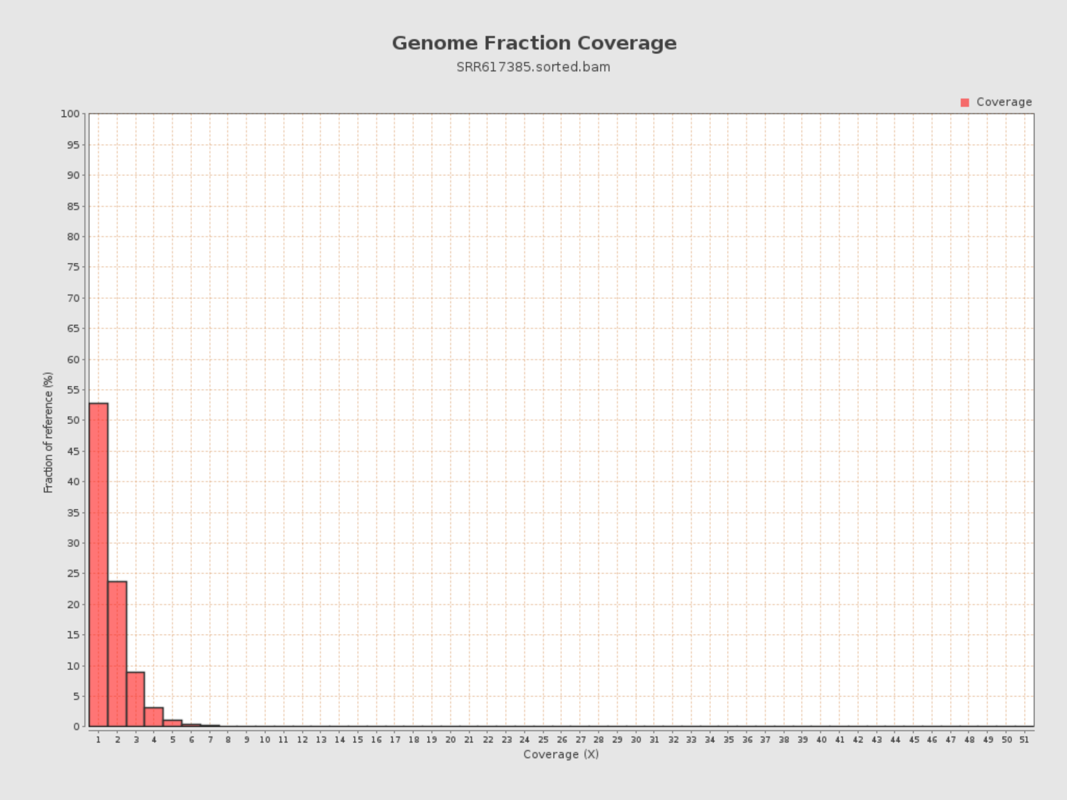
4. Results : Coverage Histogram



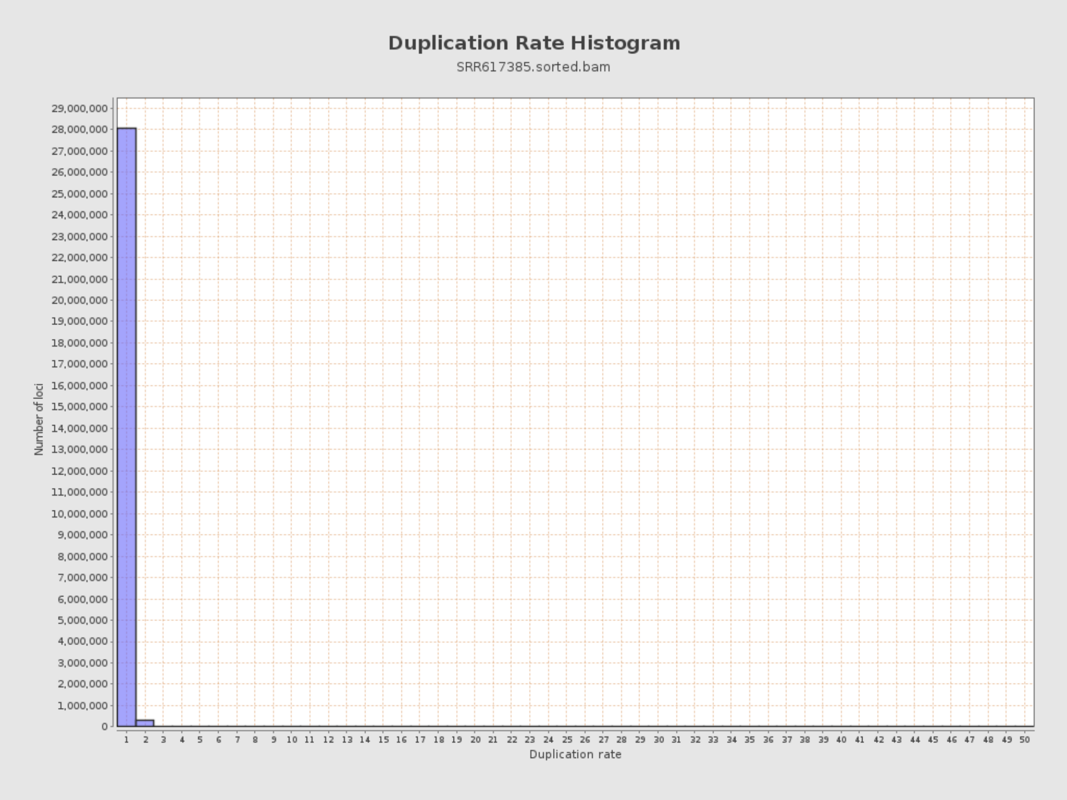
5. Results : Coverage Histogram (0-50X)



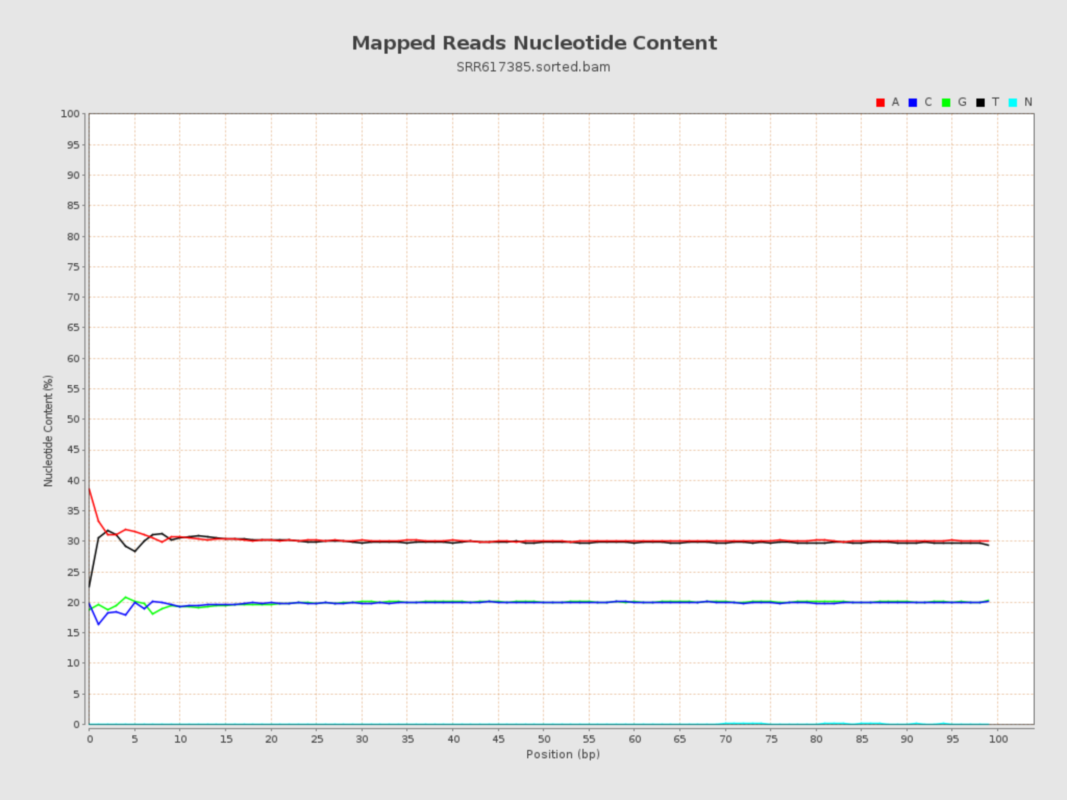
6. Results : Genome Fraction Coverage



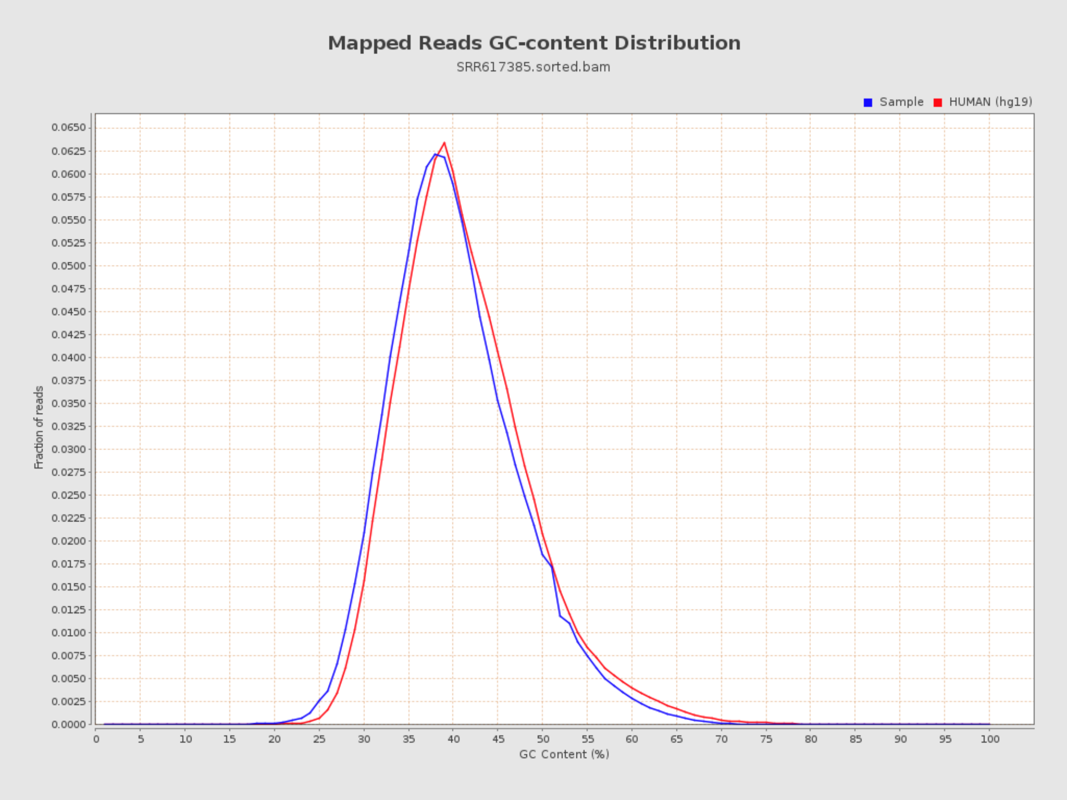
7. Results : Duplication Rate Histogram



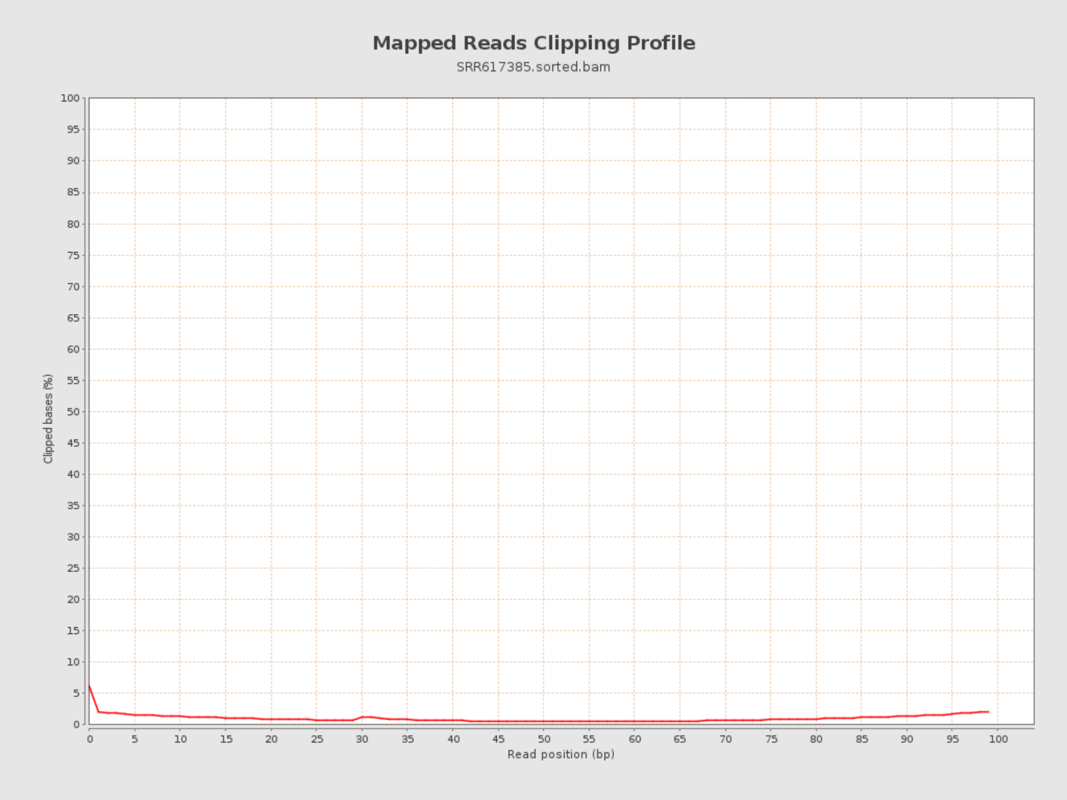
8. Results : Mapped Reads Nucleotide Content



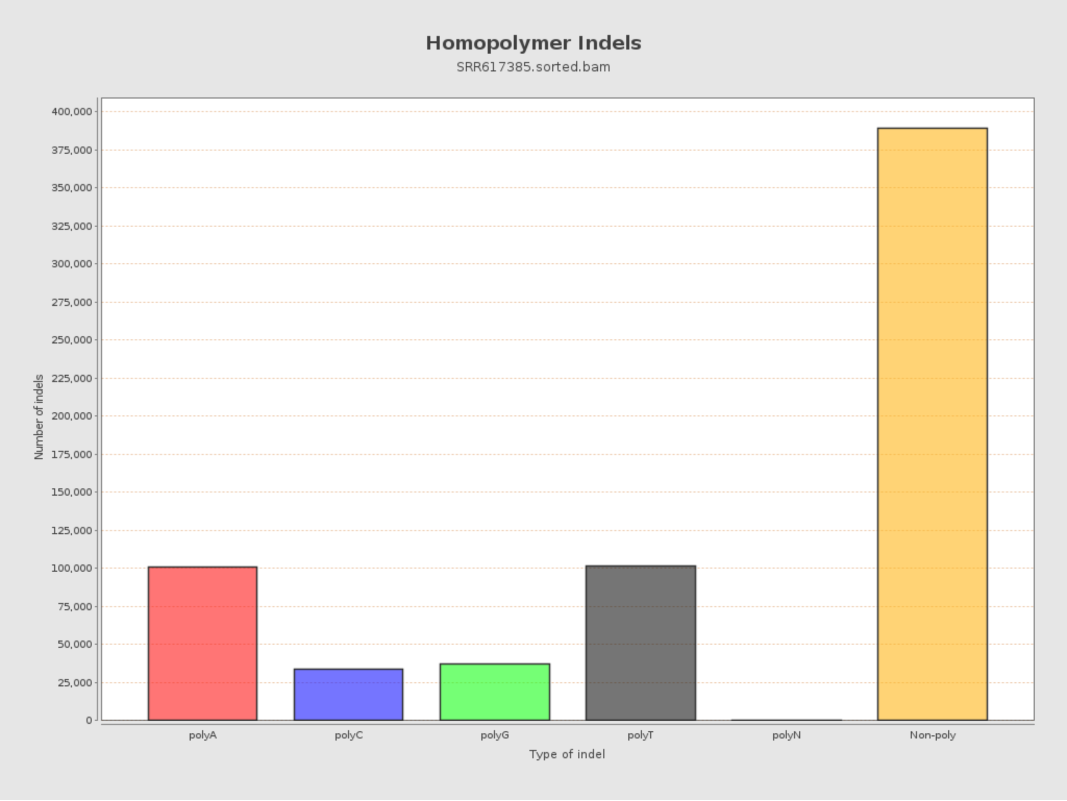
9. Results : Mapped Reads GC-content Distribution



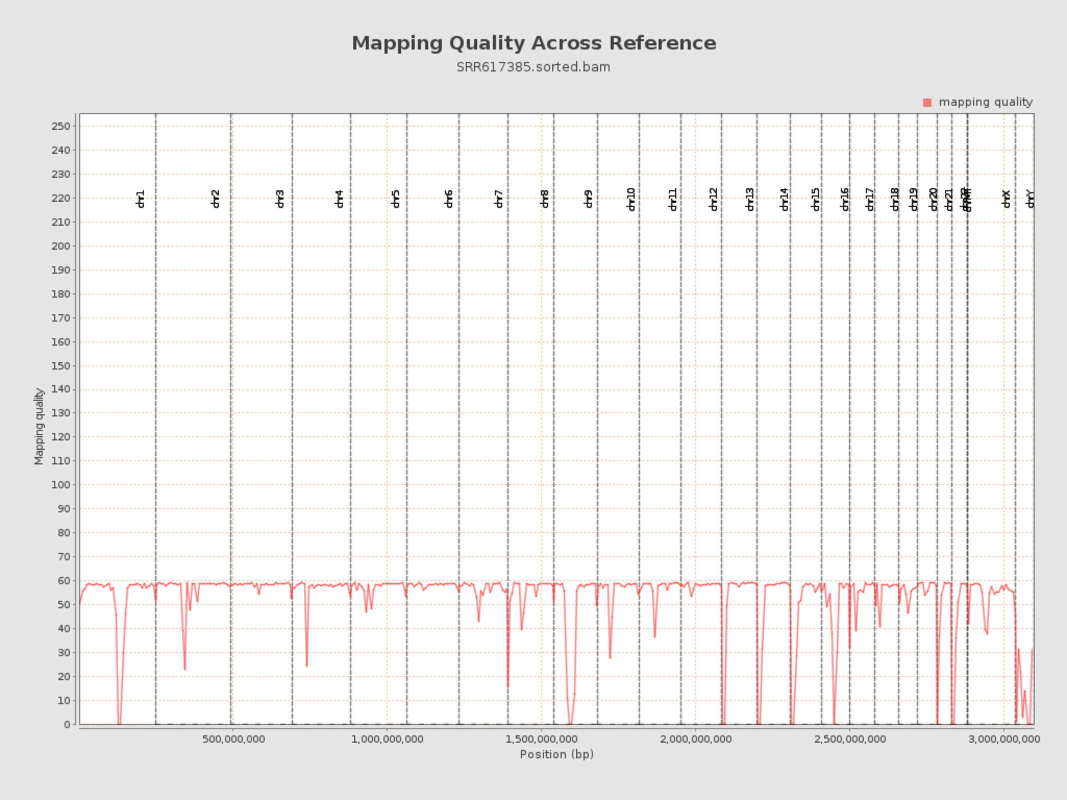
10. Results : Mapped Reads Clipping Profile



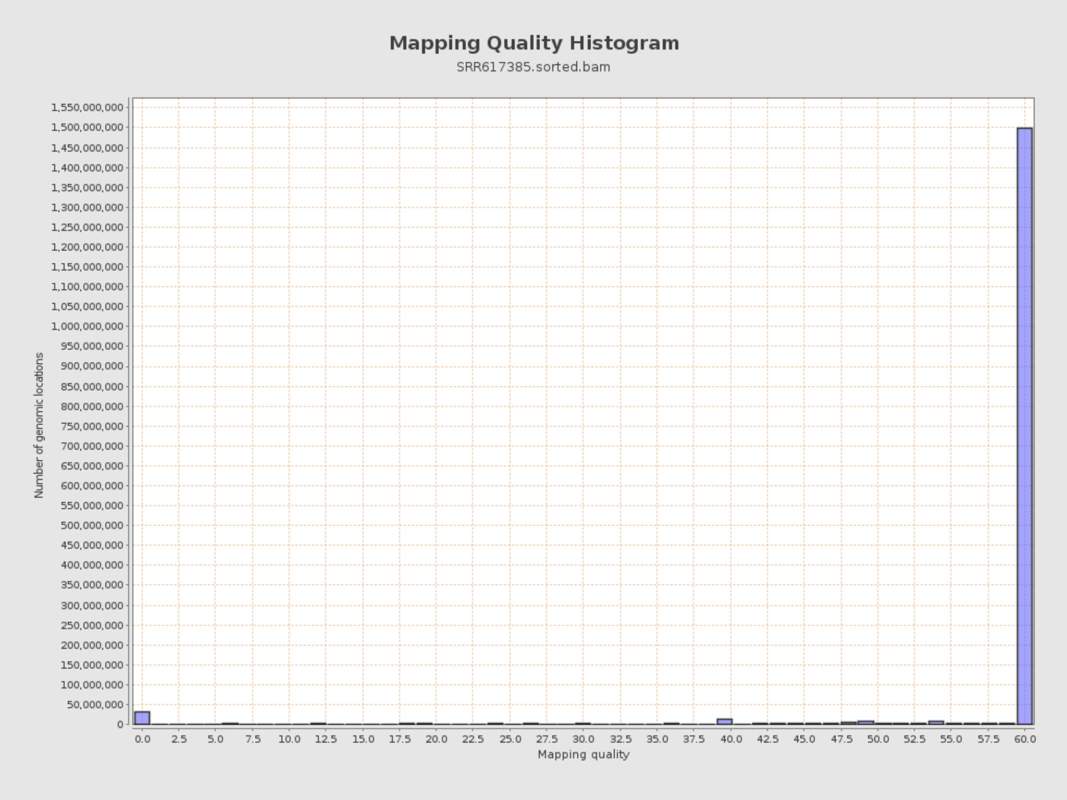
11. Results : Homopolymer Indels



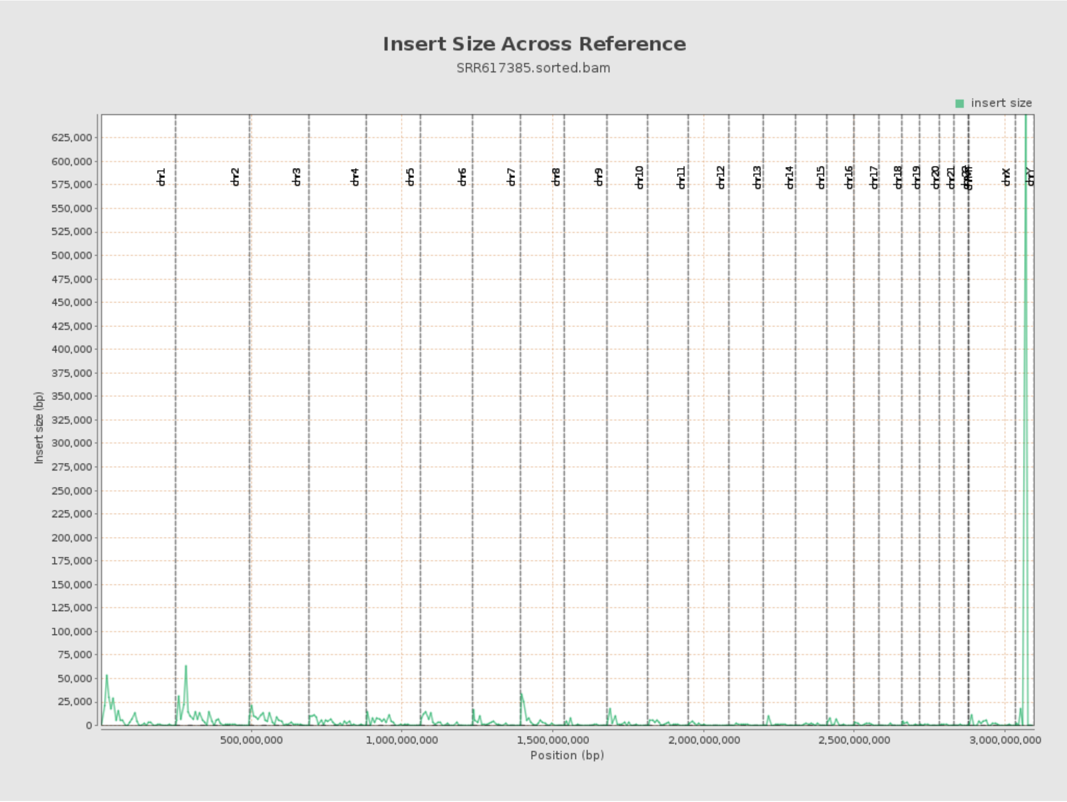
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram