Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/07 15:03:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617371.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_SRR617371 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617371_1.fastq.gz SRR617371_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Oct 07 15:03:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617371.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,000,000
Mapped reads	30,477,767 / 95.24%
Unmapped reads	1,522,233 / 4.76%
Mapped paired reads	30,477,767 / 95.24%
Mapped reads, first in pair	15,337,019 / 47.93%
Mapped reads, second in pair	15,140,748 / 47.31%
Mapped reads, both in pair	29,922,596 / 93.51%
Mapped reads, singletons	555,171 / 1.73%
Secondary alignments	0
Supplementary alignments	91,279 / 0.29%
Read min/max/mean length	30 / 100 / 100.11
Duplicated reads (estimated)	1,611,748 / 5.04%
Duplication rate	1.52%
Clipped reads	2,436,341 / 7.61%

2.2. ACGT Content

Number/percentage of A's	904,080,163 / 30.25%
Number/percentage of C's	594,390,467 / 19.89%
Number/percentage of T's	893,131,135 / 29.88%
Number/percentage of G's	596,527,048 / 19.96%
Number/percentage of N's	738,714 / 0.02%

GC Percentage	39.85%

2.3. Coverage

Mean	0.9658
Standard Deviation	9.852

2.4. Mapping Quality

Mean Mapping Quality	53.44

2.5. Insert size

Mean	63,907.53
Standard Deviation	2,409,916.02
P25/Median/P75	172 / 213 / 276

2.6. Mismatches and indels

General error rate	0.99%
Mismatches	28,821,282
Insertions	305,414
Mapped reads with at least one insertion	0.97%
Deletions	369,574
Mapped reads with at least one deletion	1.18%
Homopolymer indels	41.33%

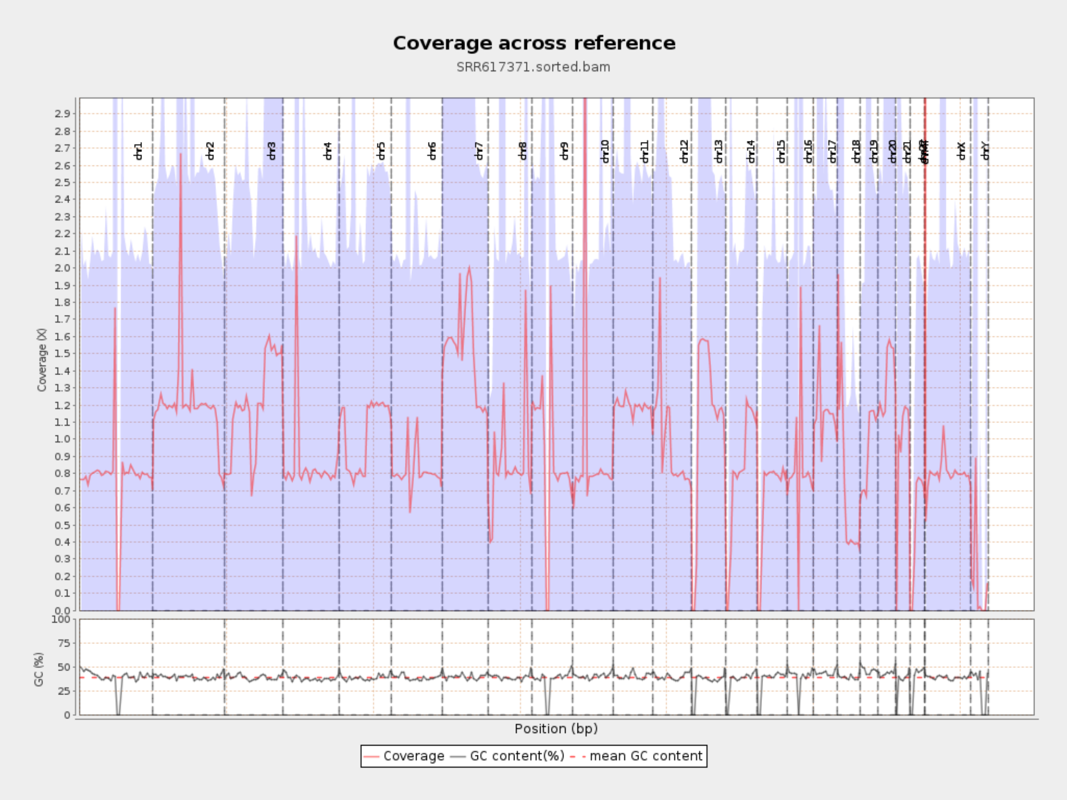
2.7. Chromosome stats

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

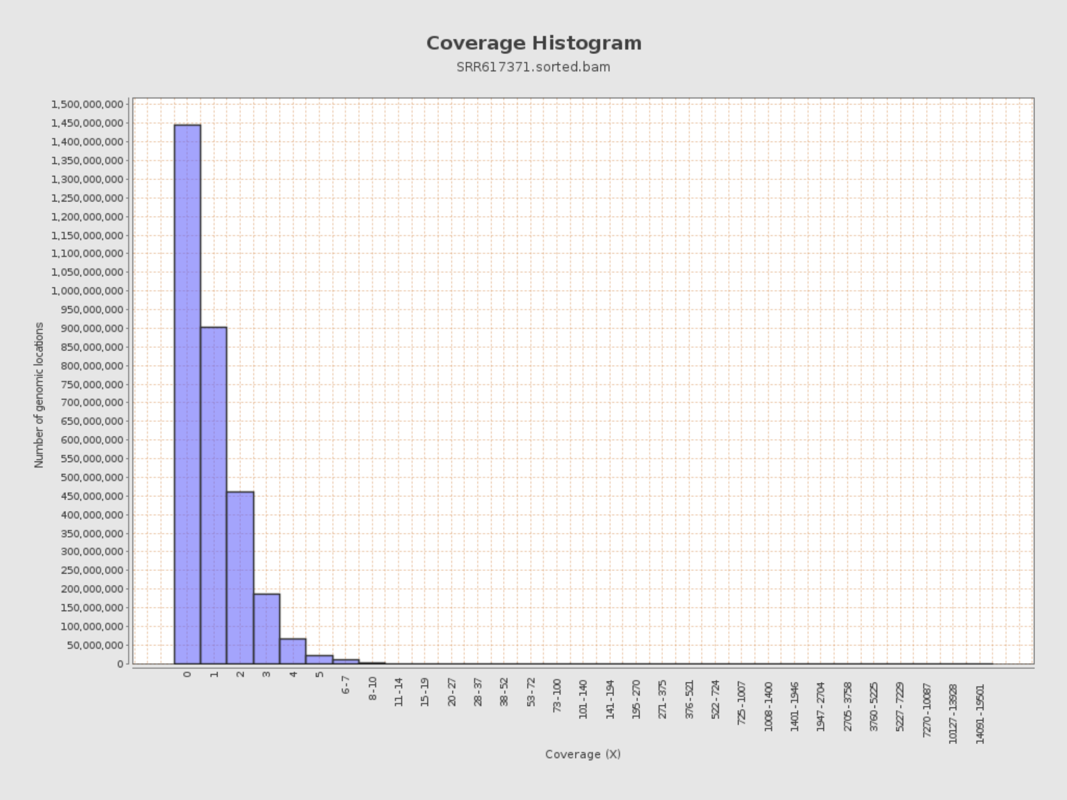
		bases	coverage	deviation
chr1	249250621	194025903	0.7784	19.9473
chr2	243199373	295016801	1.2131	8.9114
chr3	198022430	237510413	1.1994	1.4842
chr4	191154276	163245012	0.854	9.5138
chr5	180915260	187521812	1.0365	1.4754
chr6	171115067	139860839	0.8173	3.6128
chr7	159138663	242636896	1.5247	10.9526
chr8	146364022	125734296	0.8591	7.6977
chr9	141213431	125788852	0.8908	15.1461
chr10	135534747	125963375	0.9294	20.186
chr11	135006516	160854134	1.1915	5.6884
chr12	133851895	131792998	0.9846	1.3942
chr13	115169878	130116878	1.1298	1.3229
chr14	107349540	86681993	0.8075	1.3855
chr15	102531392	67329009	0.6567	1.0746
chr16	90354753	75133779	0.8315	7.824
chr17	81195210	93730350	1.1544	7.1732
chr18	78077248	54105223	0.693	15.5189
chr19	59128983	55892269	0.9453	9.5293
chr20	63025520	85826042	1.3618	2.4755
chr21	48129895	47557406	0.9881	3.2831
chr22	51304566	26754206	0.5215	0.9305
chrMT	16571	2043112	123.2944	22.1712
chrX	155270560	124272935	0.8004	3.059

chrY	59373566	10364681	0.1746	8.5615

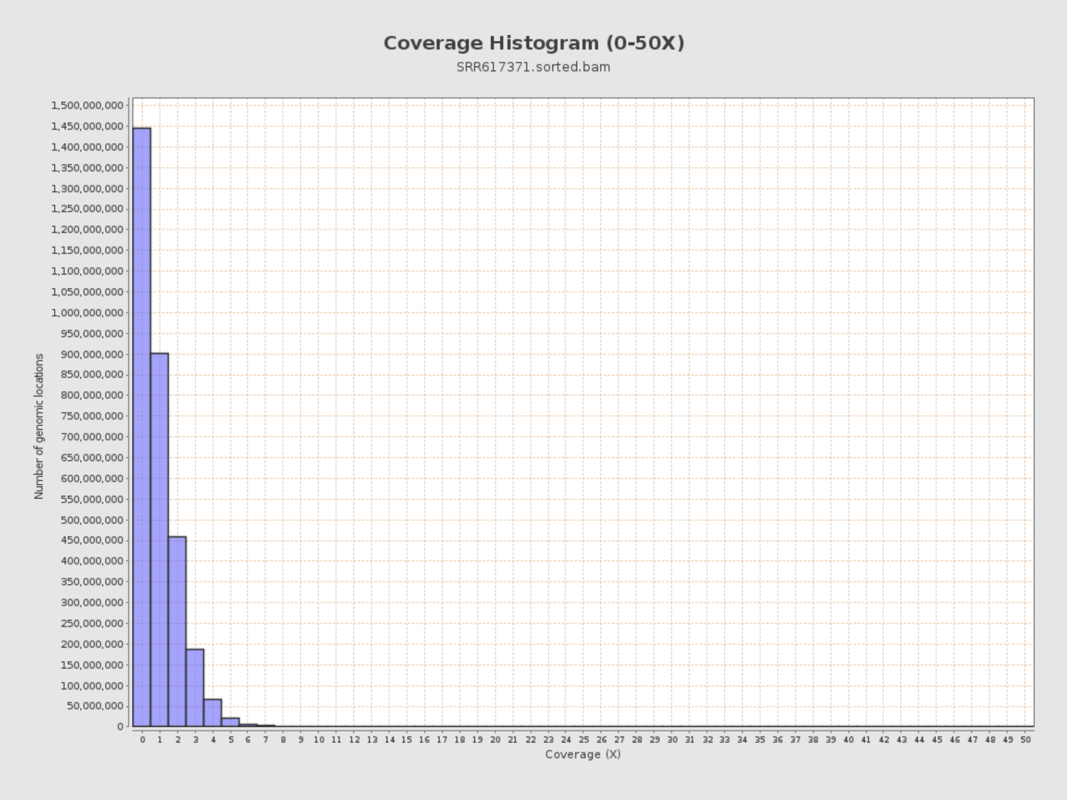
3. Results : Coverage across reference



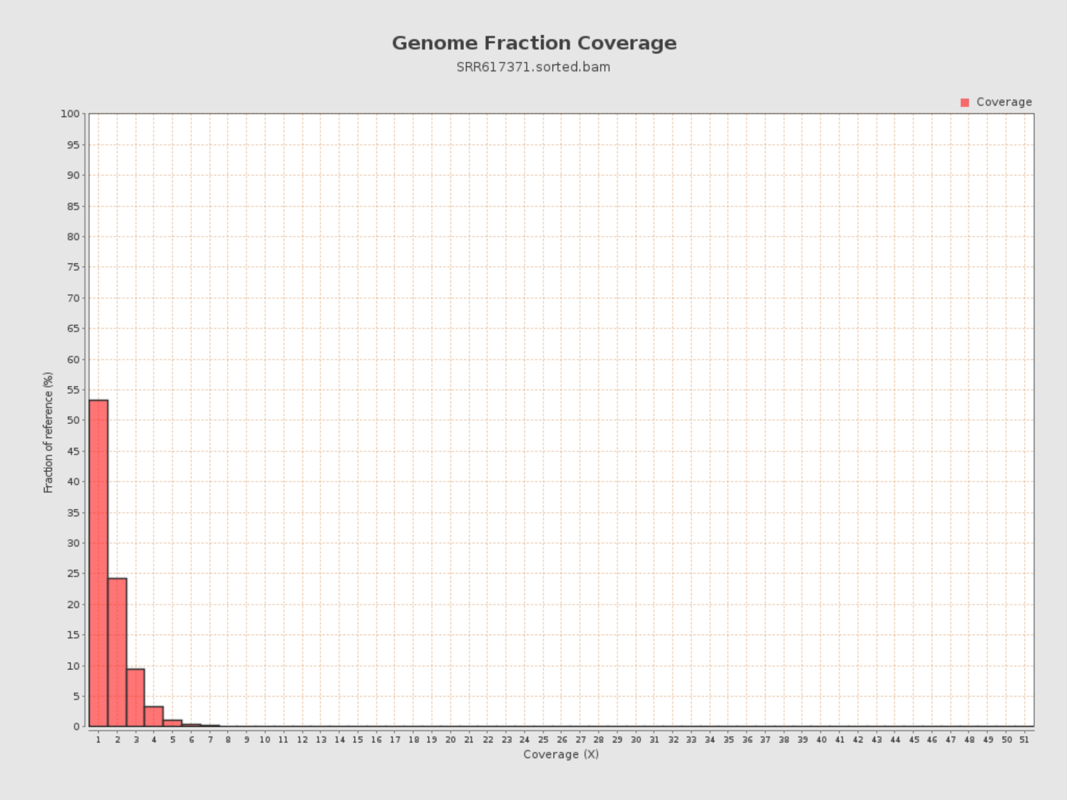
4. Results : Coverage Histogram



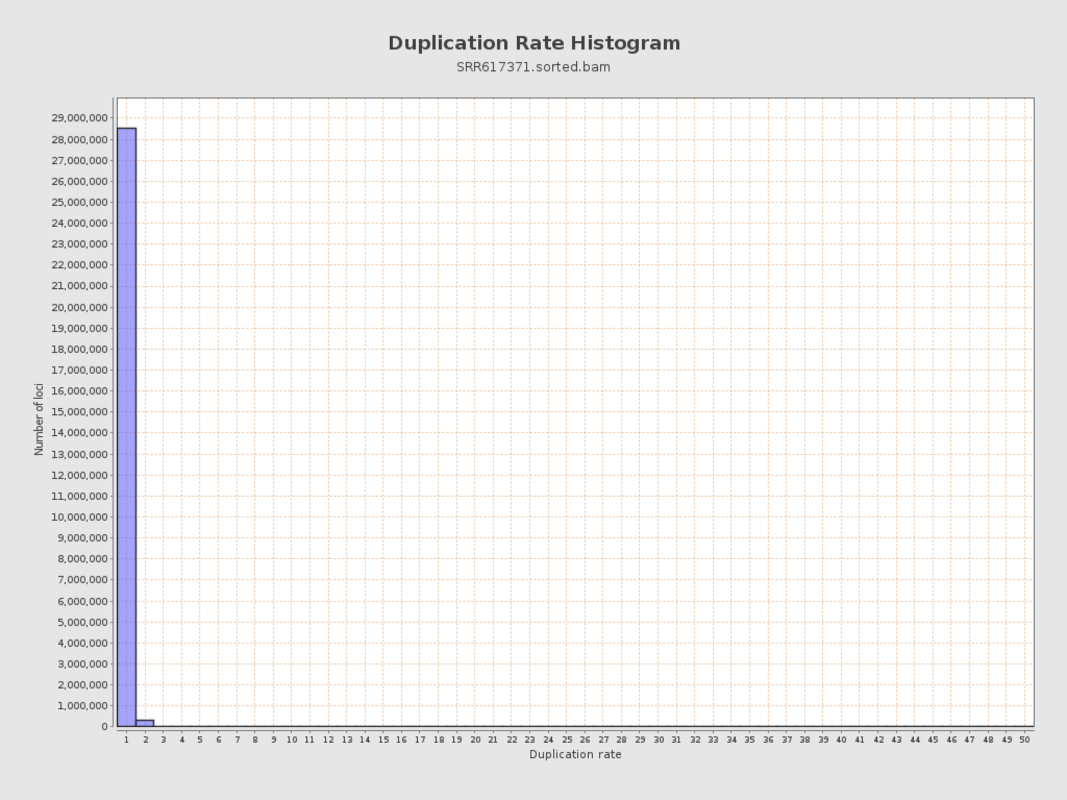
5. Results : Coverage Histogram (0-50X)



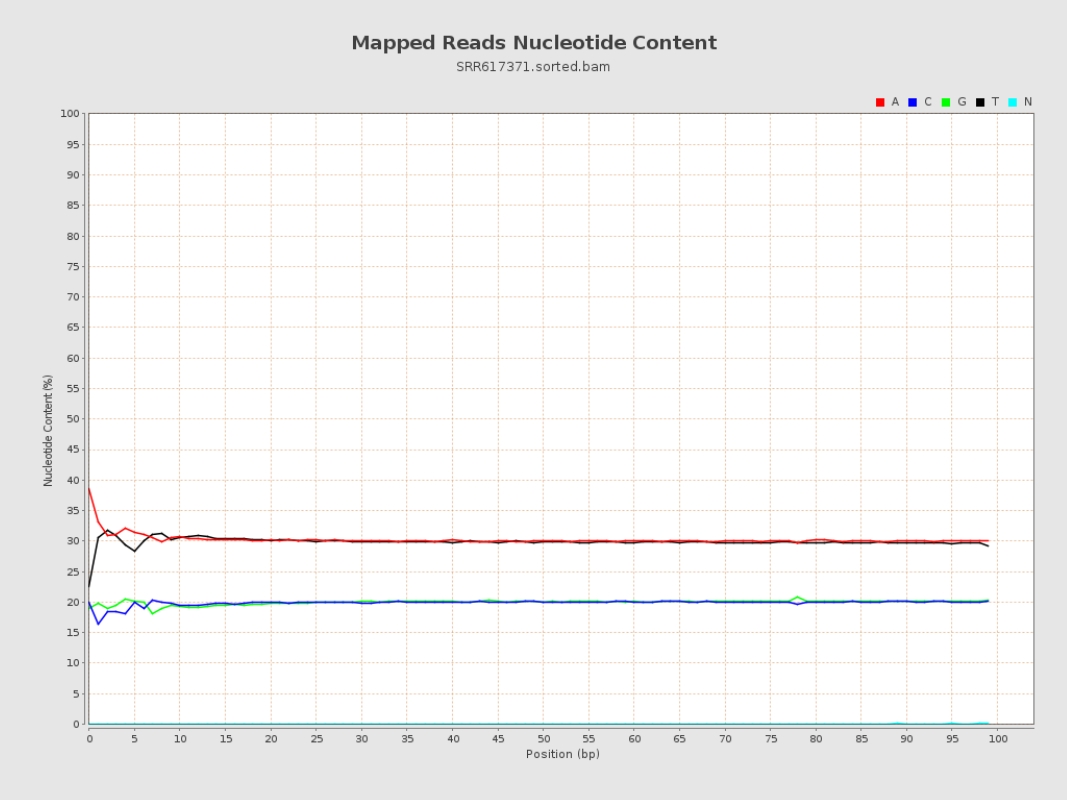
6. Results : Genome Fraction Coverage



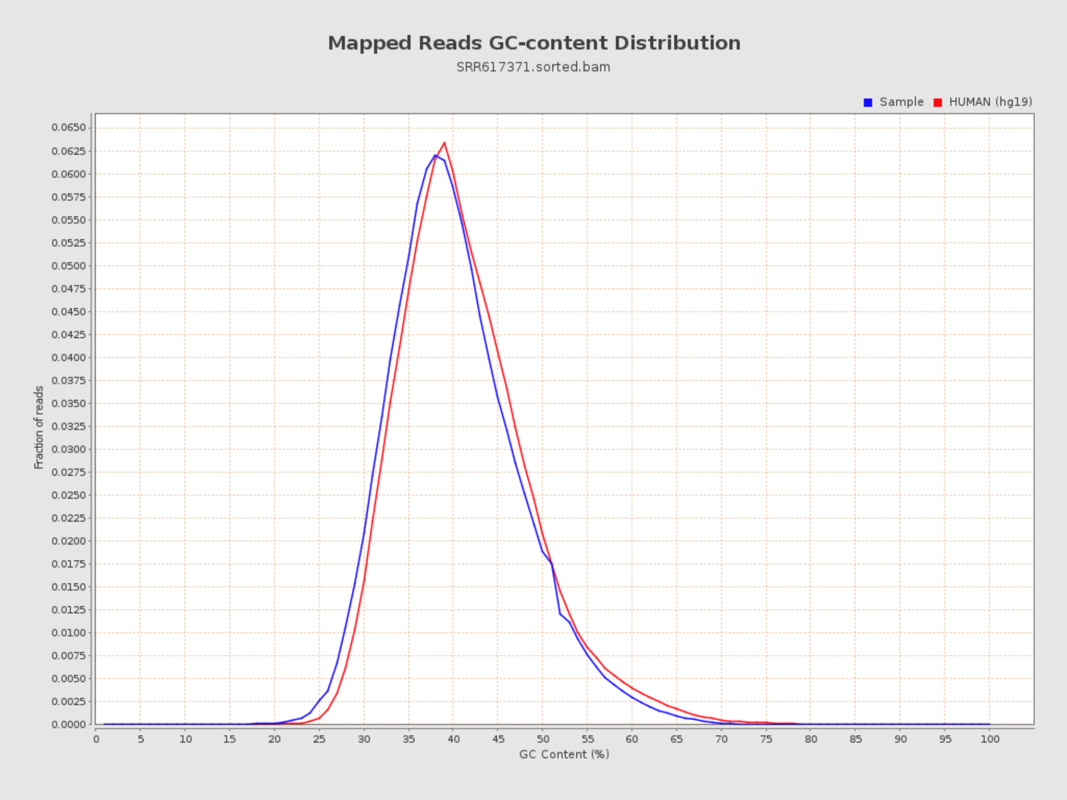
7. Results : Duplication Rate Histogram



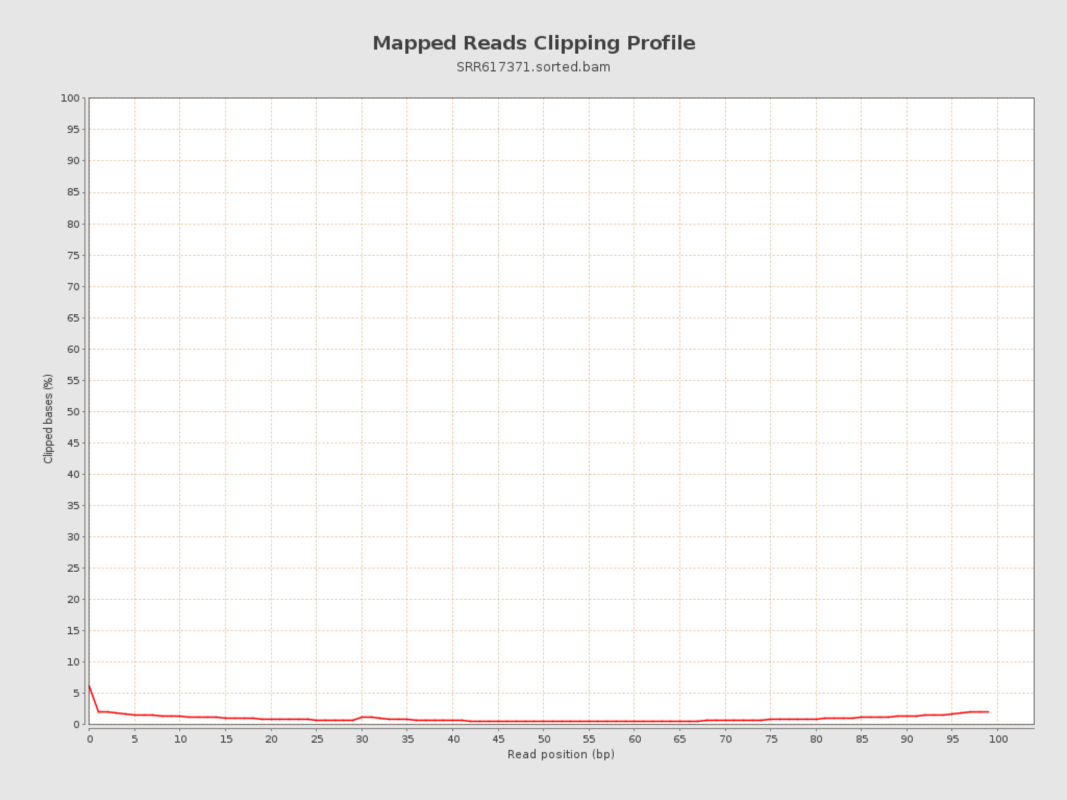
8. Results : Mapped Reads Nucleotide Content



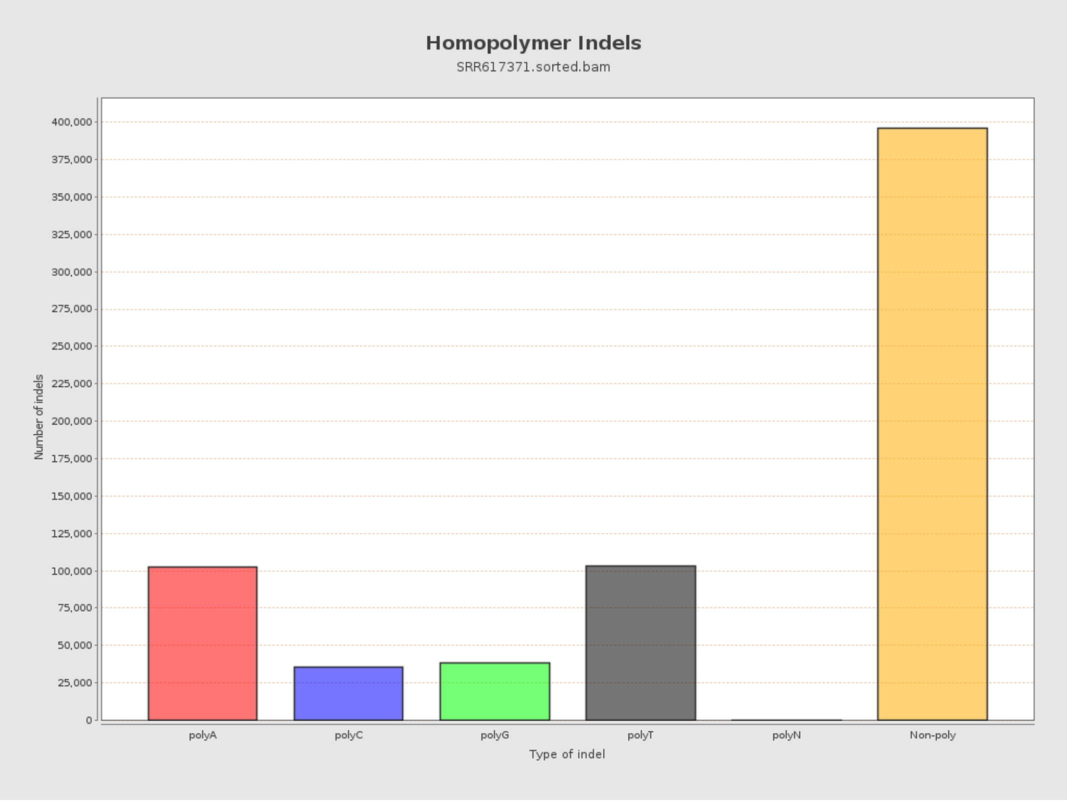
9. Results : Mapped Reads GC-content Distribution



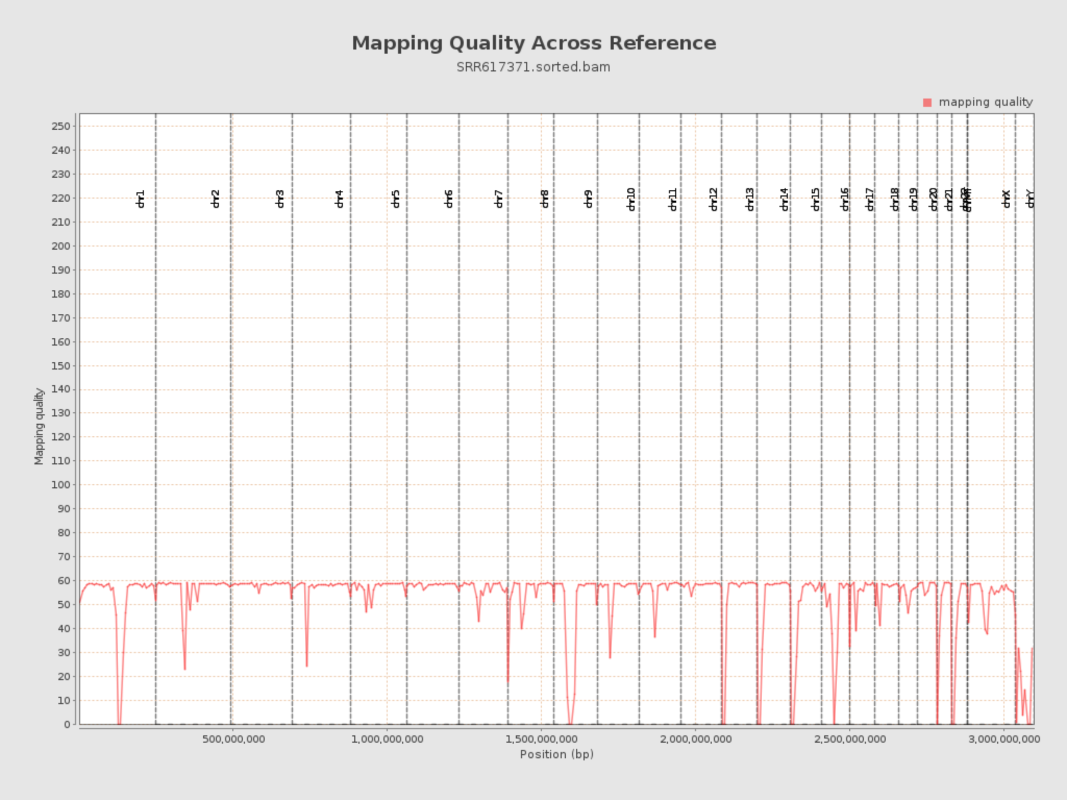
10. Results : Mapped Reads Clipping Profile



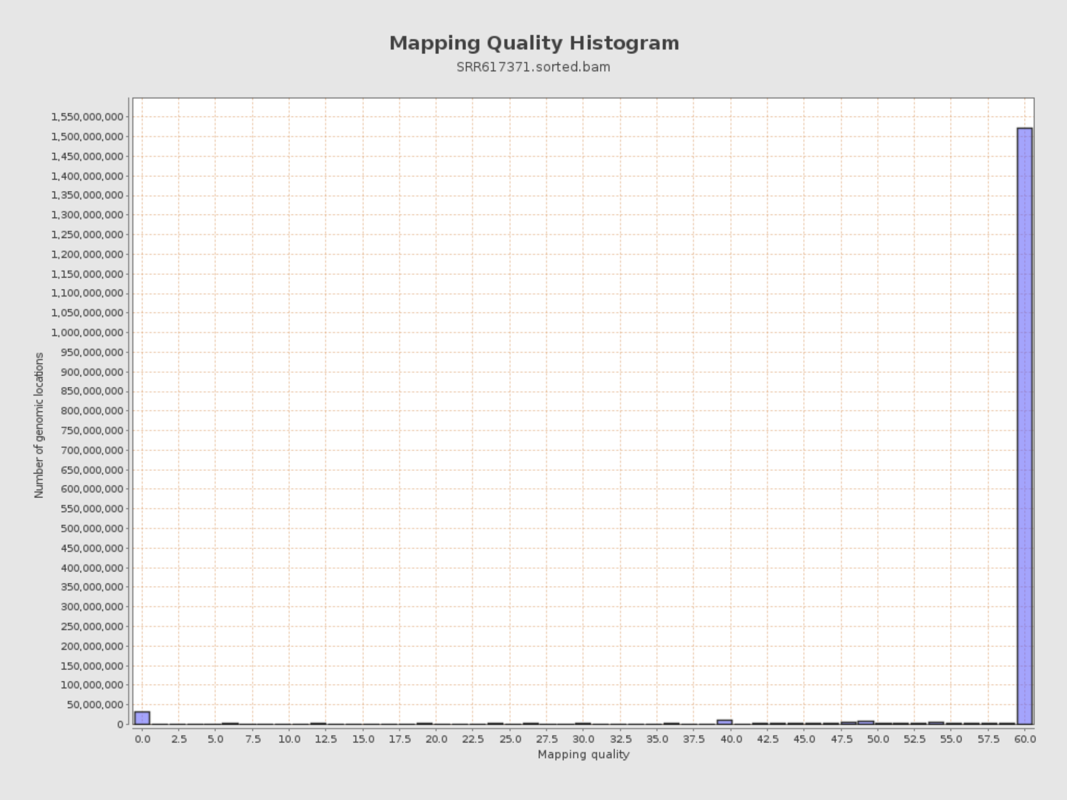
11. Results : Homopolymer Indels



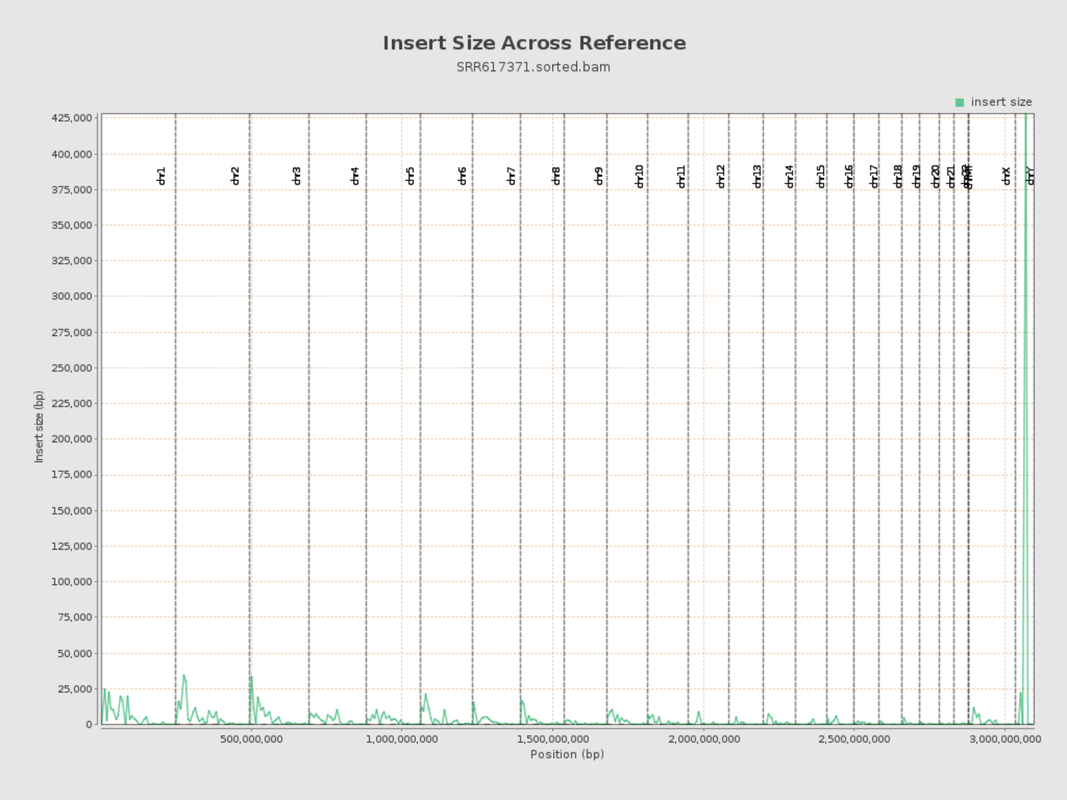
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram