Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 07:56:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008709.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_SRR6008709 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008709.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 07:56:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008709.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,907,306
Mapped reads	1,402,846 / 73.55%
Unmapped reads	504,460 / 26.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,251 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	31,871 / 1.67%
Duplication rate	1.69%
Clipped reads	563,208 / 29.53%

2.2. ACGT Content

Number/percentage of A's	28,730,501 / 30.4%
Number/percentage of C's	16,421,502 / 17.38%
Number/percentage of T's	28,308,230 / 29.95%
Number/percentage of G's	21,028,625 / 22.25%
Number/percentage of N's	21,778 / 0.02%
GC Percentage	39.63%

2.3. Coverage

Mean	0.0305

Standard Deviation	0.2388

2.4. Mapping Quality

Mean Mapping Quality	48.04

2.5. Mismatches and indels

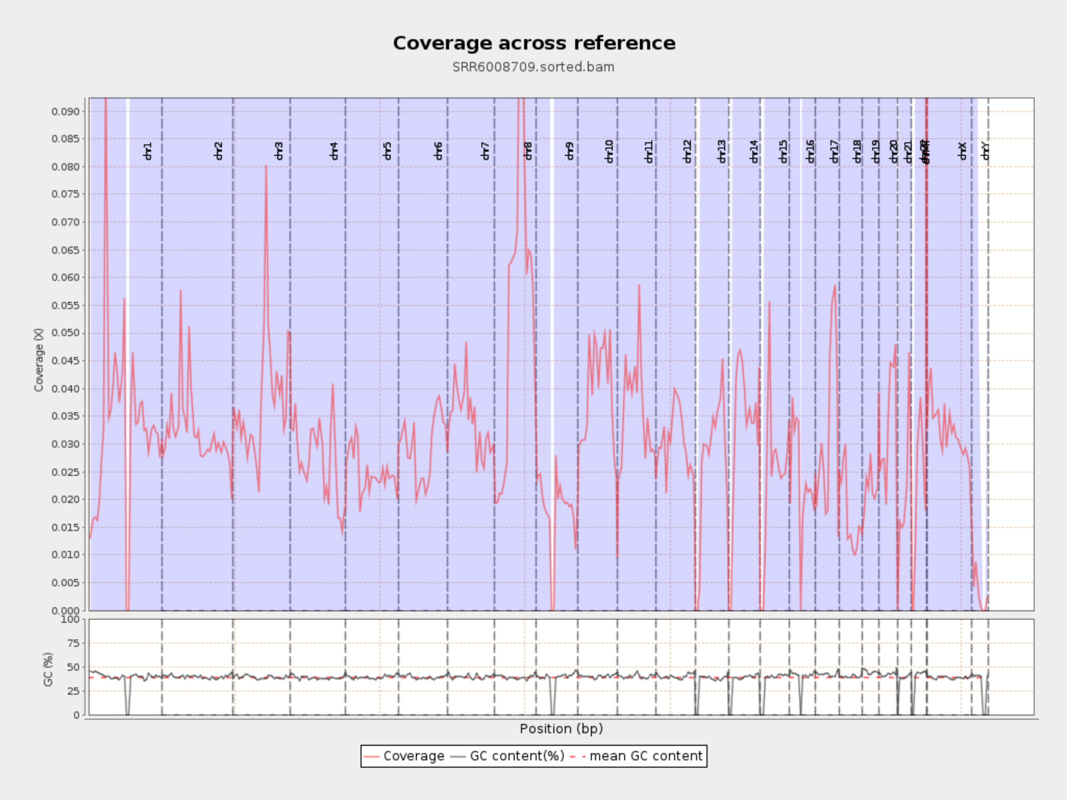
General error rate	0.92%
Mismatches	861,665
Insertions	6,787
Mapped reads with at least one insertion	0.48%
Deletions	27,589
Mapped reads with at least one deletion	1.94%
Homopolymer indels	47.76%

2.6. Chromosome stats

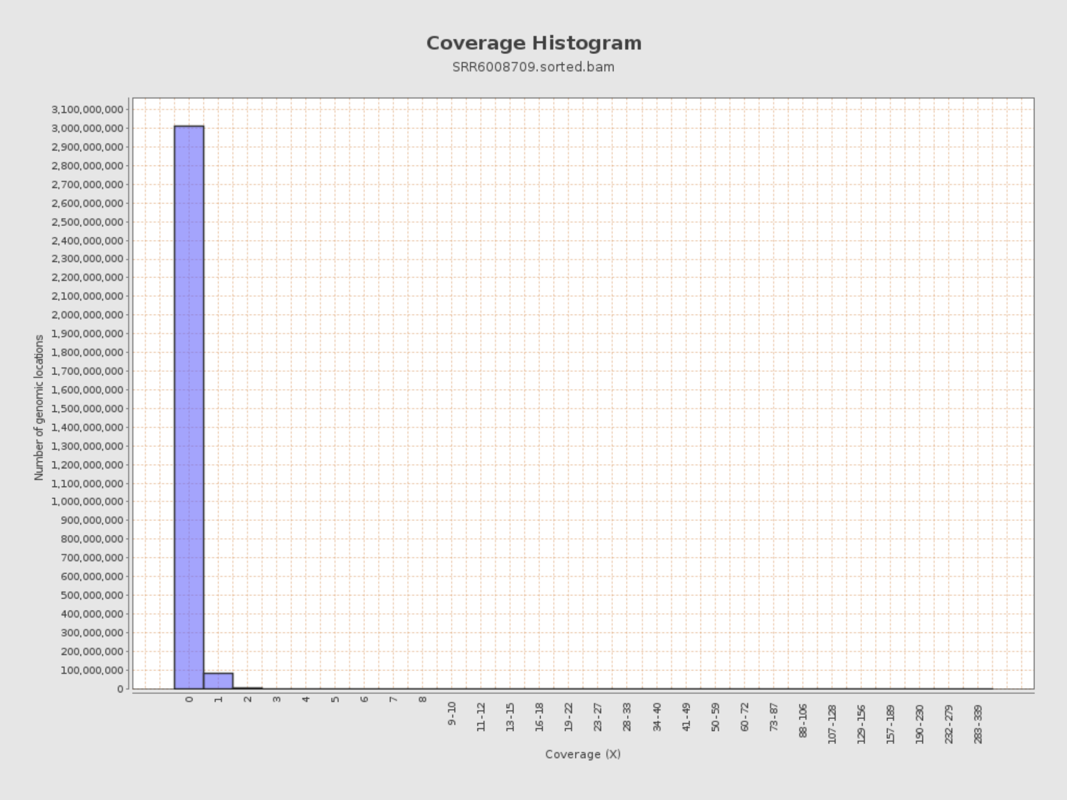
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8206149	0.0329	0.3495
chr2	243199373	7880489	0.0324	0.2697
chr3	198022430	7549256	0.0381	0.2123
chr4	191154276	5175178	0.0271	0.1791
chr5	180915260	4507773	0.0249	0.1699
chr6	171115067	5053426	0.0295	0.1971
chr7	159138663	5502061	0.0346	0.3182

chr8	146364022	7976734	0.0545	0.3332
chr9	141213431	2500415	0.0177	0.1887
chr10	135534747	5358911	0.0395	0.2697
chr11	135006516	4838718	0.0358	0.2539
chr12	133851895	4065821	0.0304	0.1887
chr13	115169878	3063083	0.0266	0.1762
chr14	107349540	3469687	0.0323	0.1953
chr15	102531392	2484558	0.0242	0.1689
chr16	90354753	2133025	0.0236	0.1798
chr17	81195210	2652670	0.0327	0.2131
chr18	78077248	1354440	0.0173	0.3314
chr19	59128983	1327526	0.0225	0.2154
chr20	63025520	2112030	0.0335	0.1991
chr21	48129895	1021340	0.0212	0.1608
chr22	51304566	1049865	0.0205	0.1533
chrMT	16571	29961	1.808	1.9371
chrX	155270560	5043014	0.0325	0.2063
chrY	59373566	197826	0.0033	0.0754

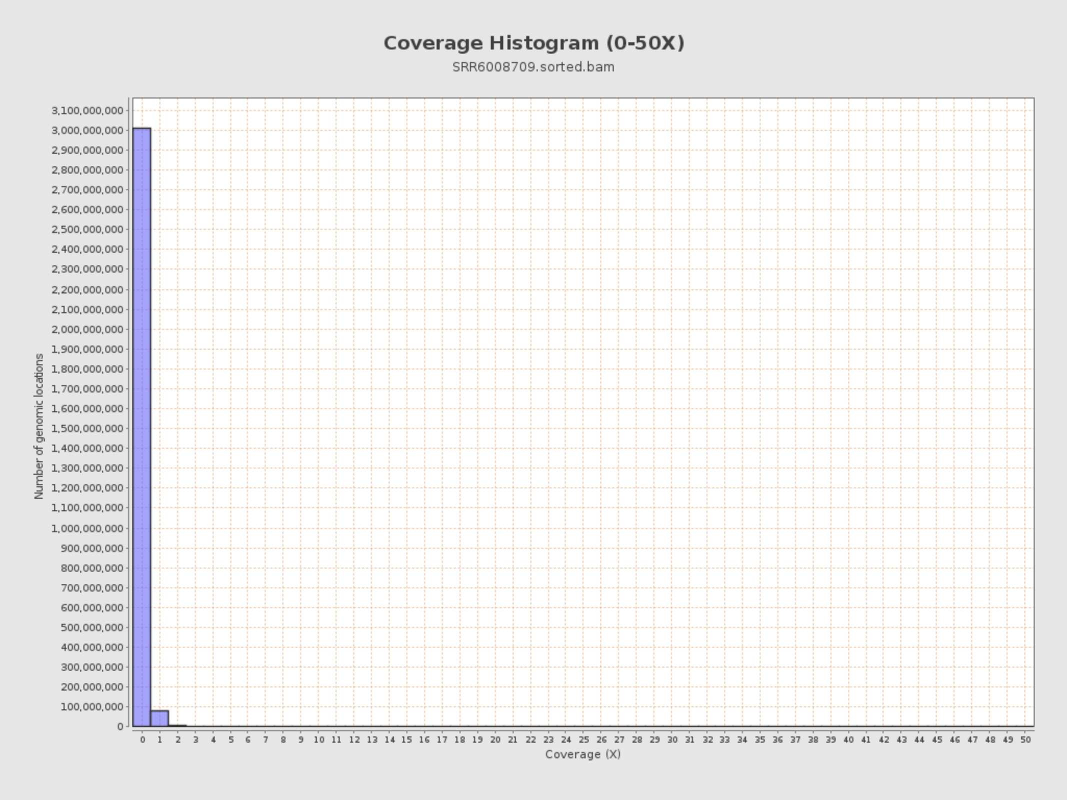
3. Results : Coverage across reference



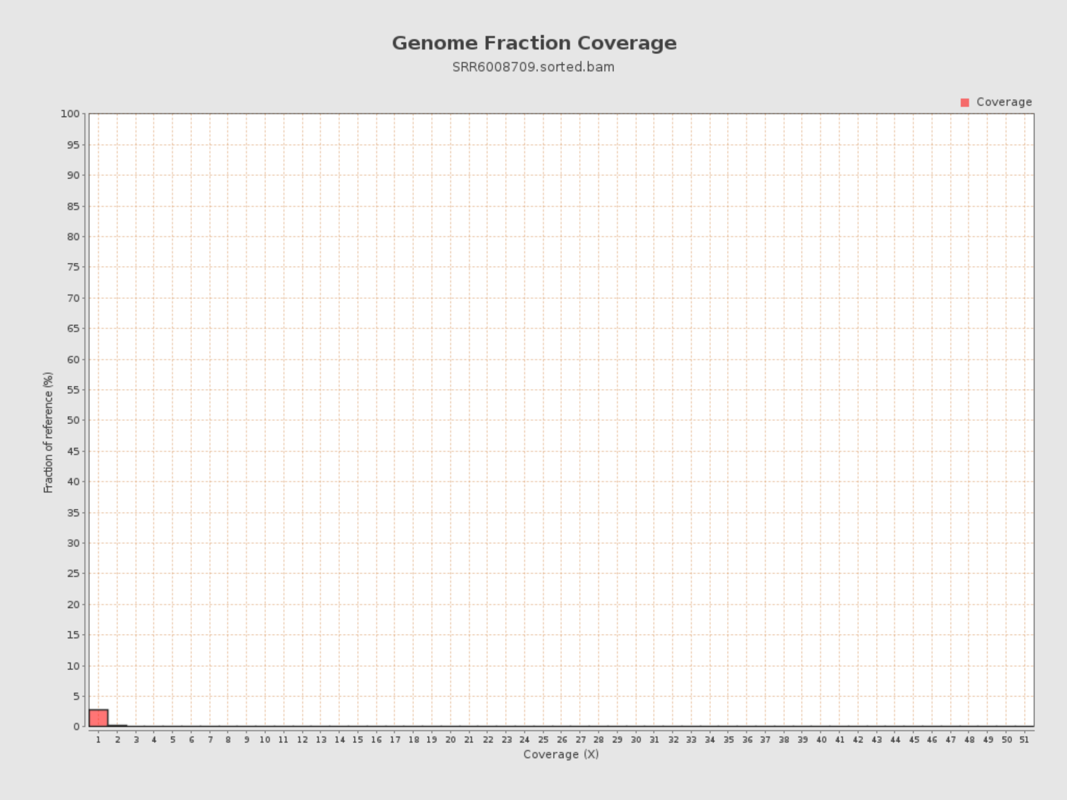
4. Results : Coverage Histogram



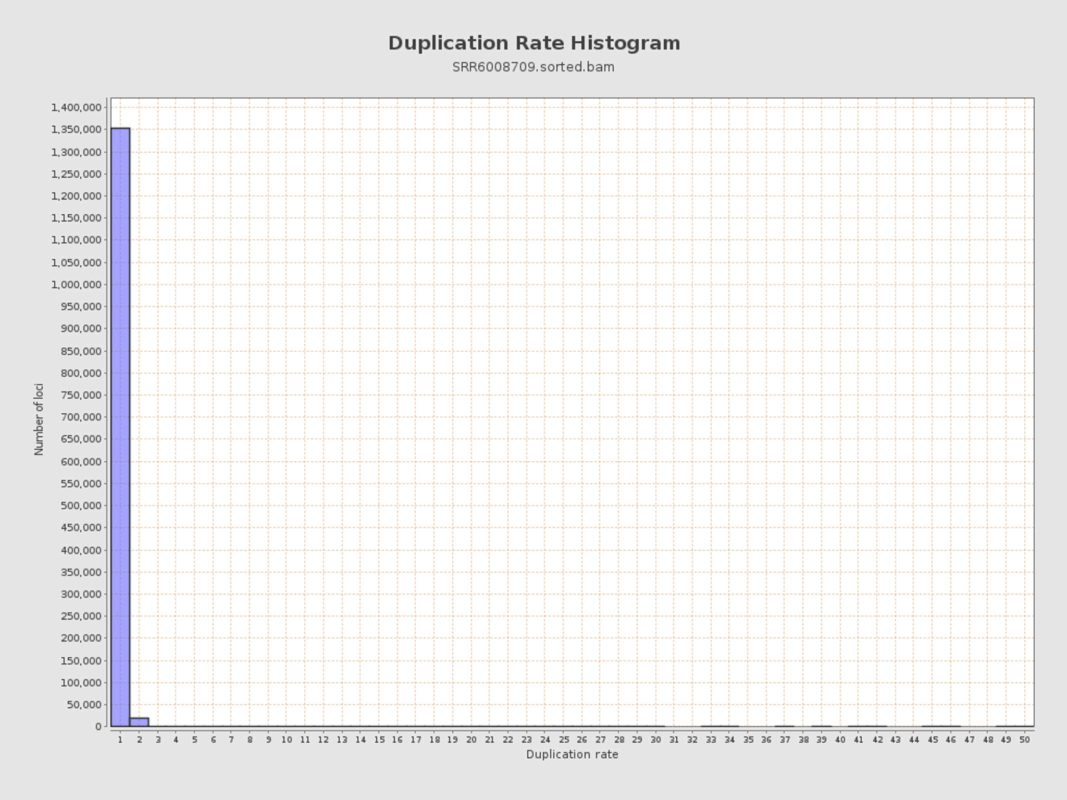
5. Results : Coverage Histogram (0-50X)



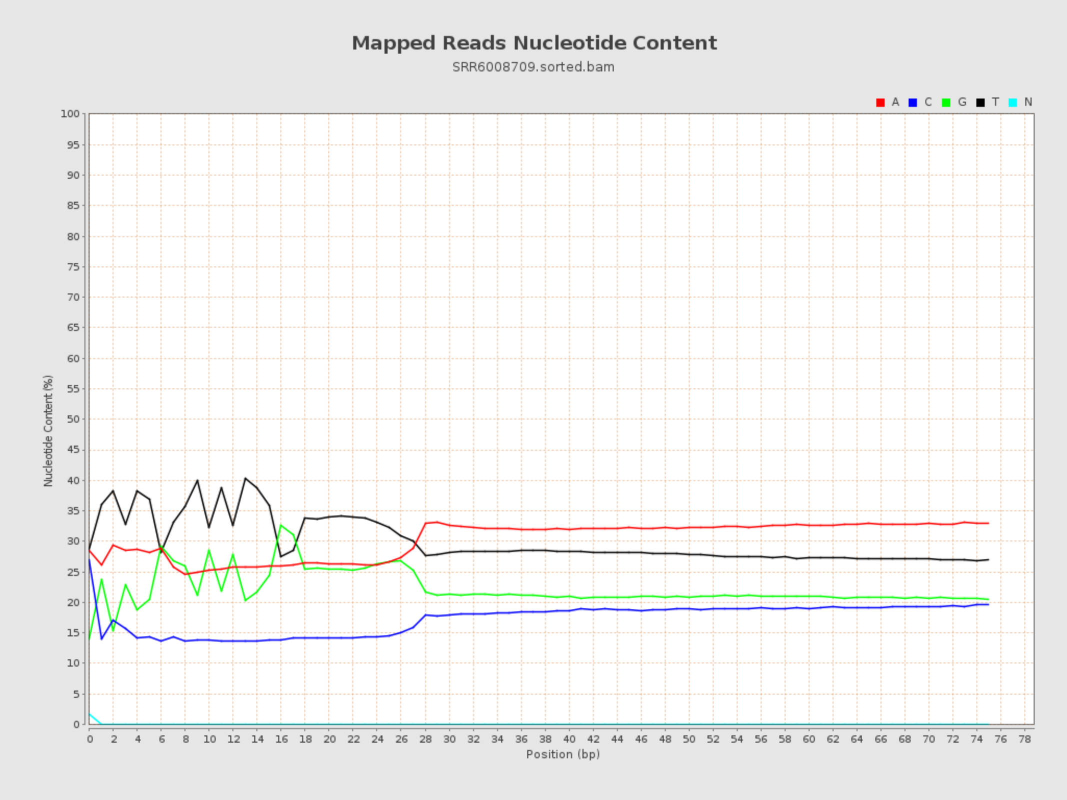
6. Results : Genome Fraction Coverage



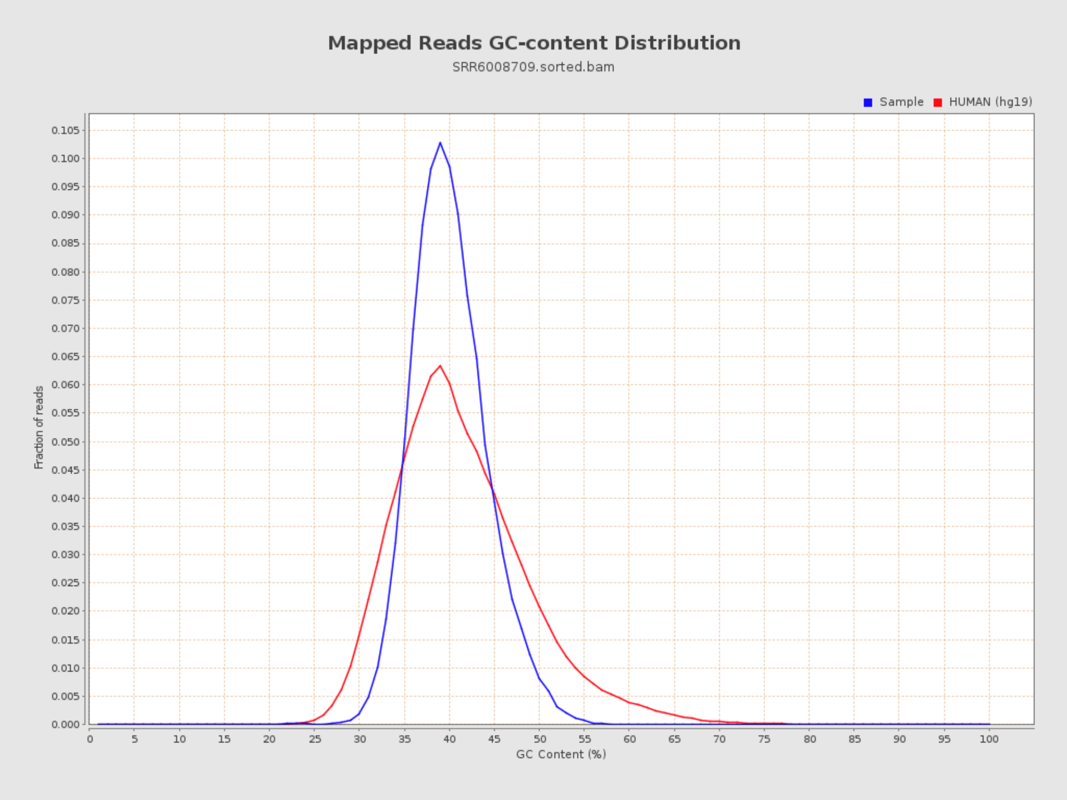
7. Results : Duplication Rate Histogram



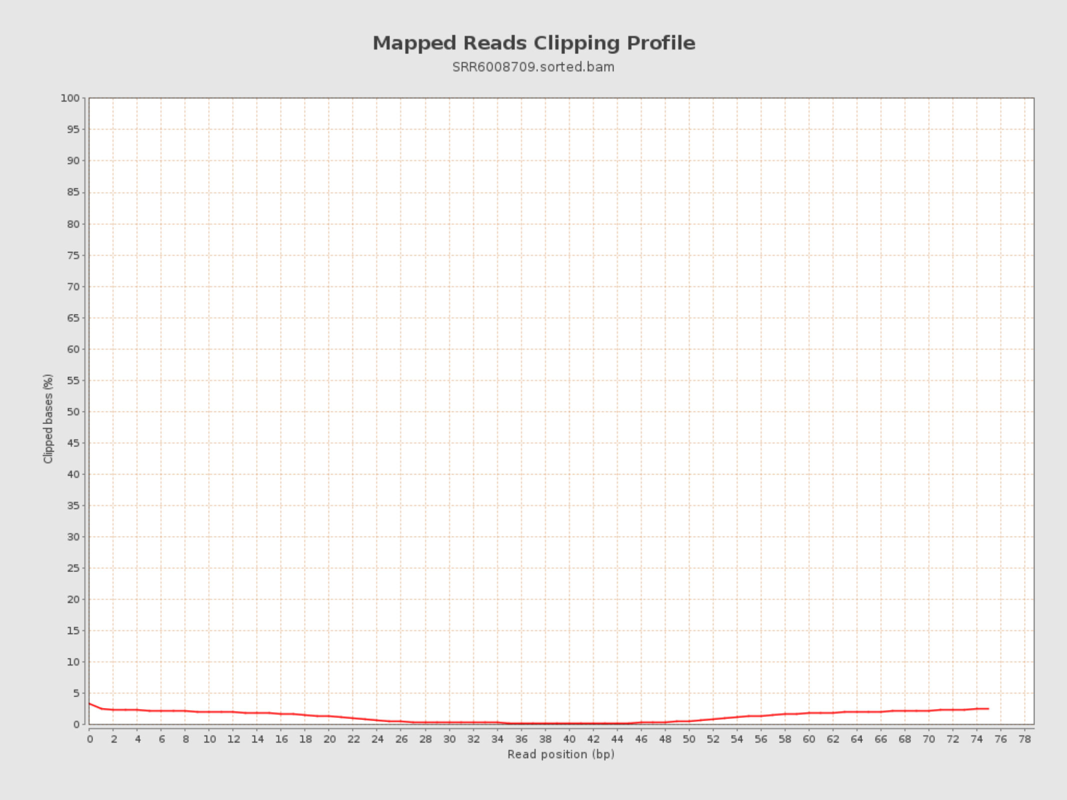
8. Results : Mapped Reads Nucleotide Content



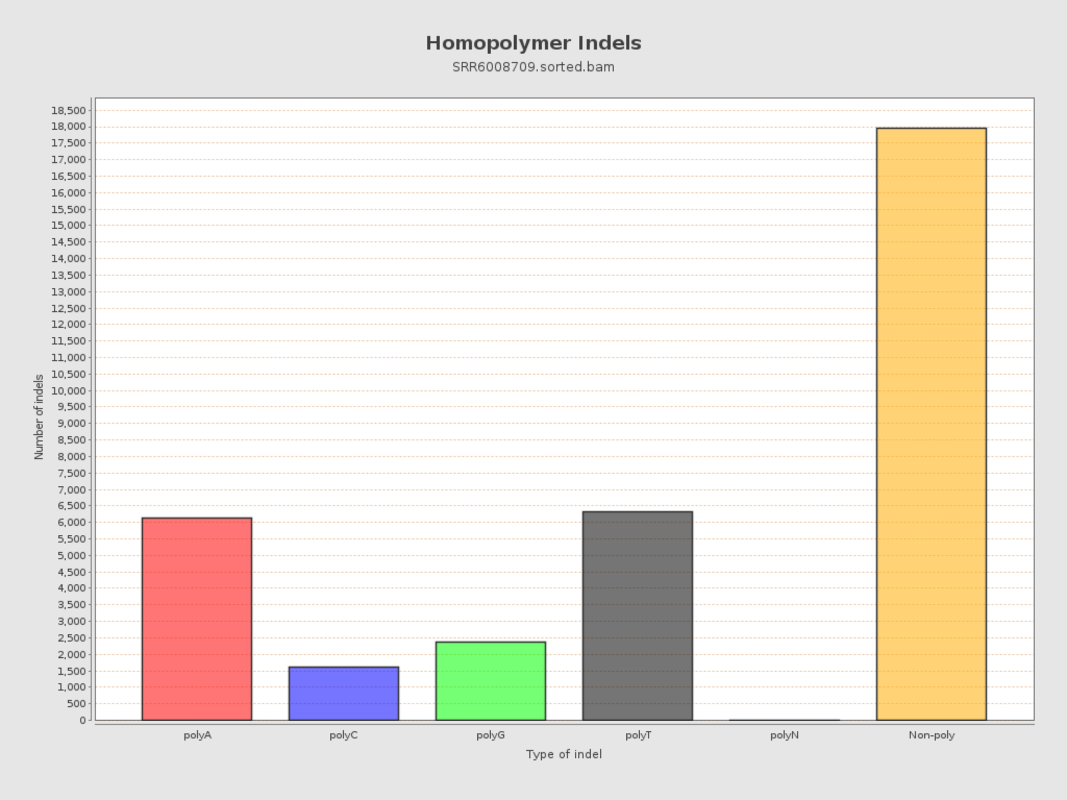
9. Results : Mapped Reads GC-content Distribution



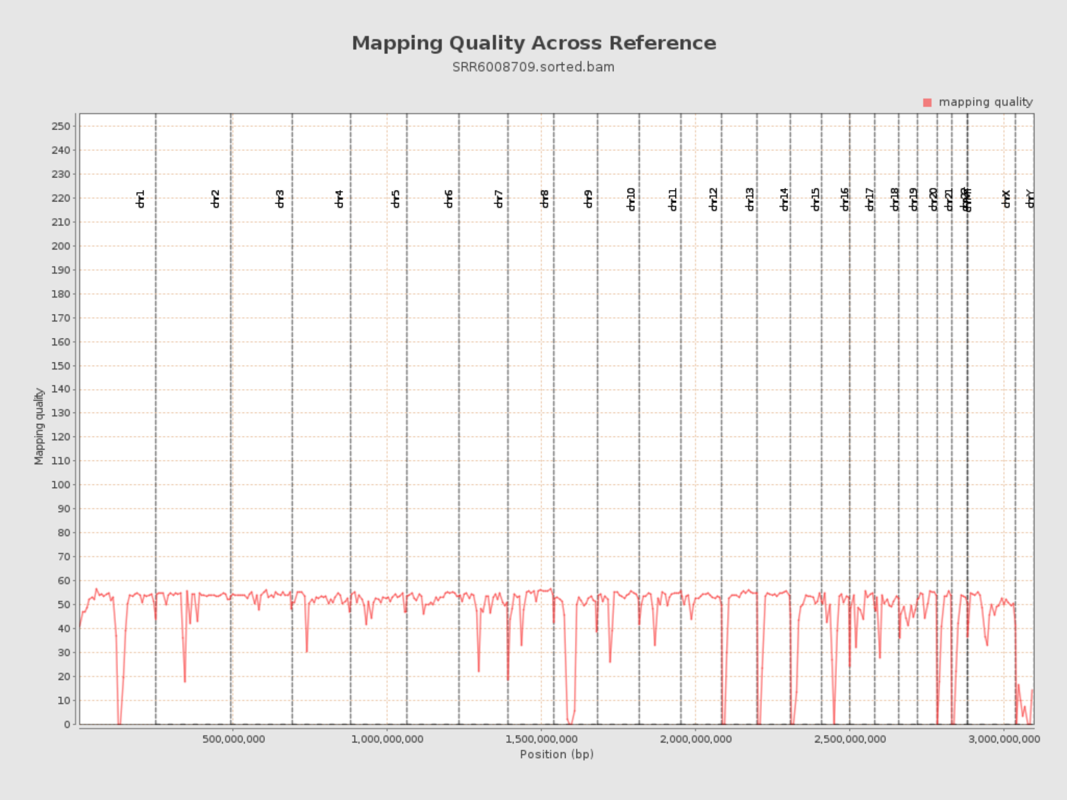
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram