Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:27:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008809.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_SRR6008809 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008809.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:27:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008809.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	797,542
Mapped reads	689,472 / 86.45%
Unmapped reads	108,070 / 13.55%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,365 / 0.8%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	41,599 / 5.22%
Duplication rate	5.04%
Clipped reads	350,720 / 43.98%

2.2. ACGT Content

Number/percentage of A's	12,196,179 / 27.17%
Number/percentage of C's	8,665,415 / 19.31%
Number/percentage of T's	13,825,877 / 30.8%
Number/percentage of G's	10,143,389 / 22.6%
Number/percentage of N's	55,362 / 0.12%
GC Percentage	41.9%

2.3. Coverage

Mean	0.0145

Standard Deviation	0.1909

2.4. Mapping Quality

Mean Mapping Quality	44.91

2.5. Mismatches and indels

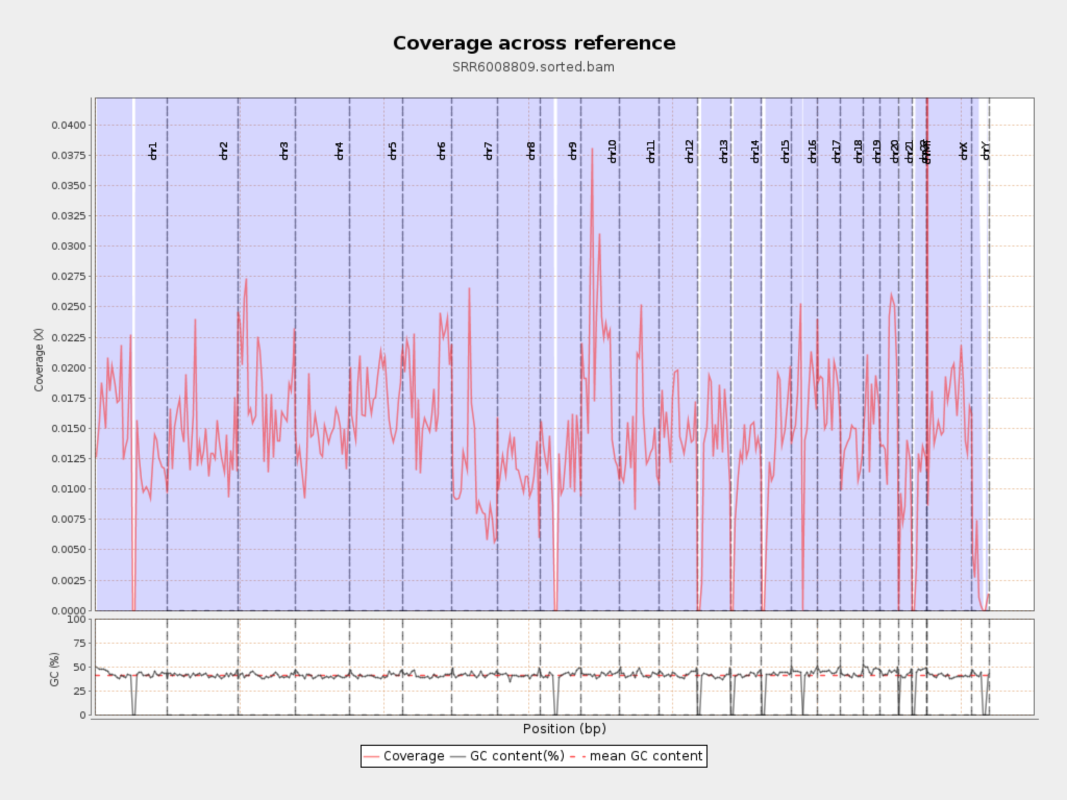
General error rate	0.87%
Mismatches	382,869
Insertions	3,303
Mapped reads with at least one insertion	0.48%
Deletions	13,985
Mapped reads with at least one deletion	2.01%
Homopolymer indels	44.43%

2.6. Chromosome stats

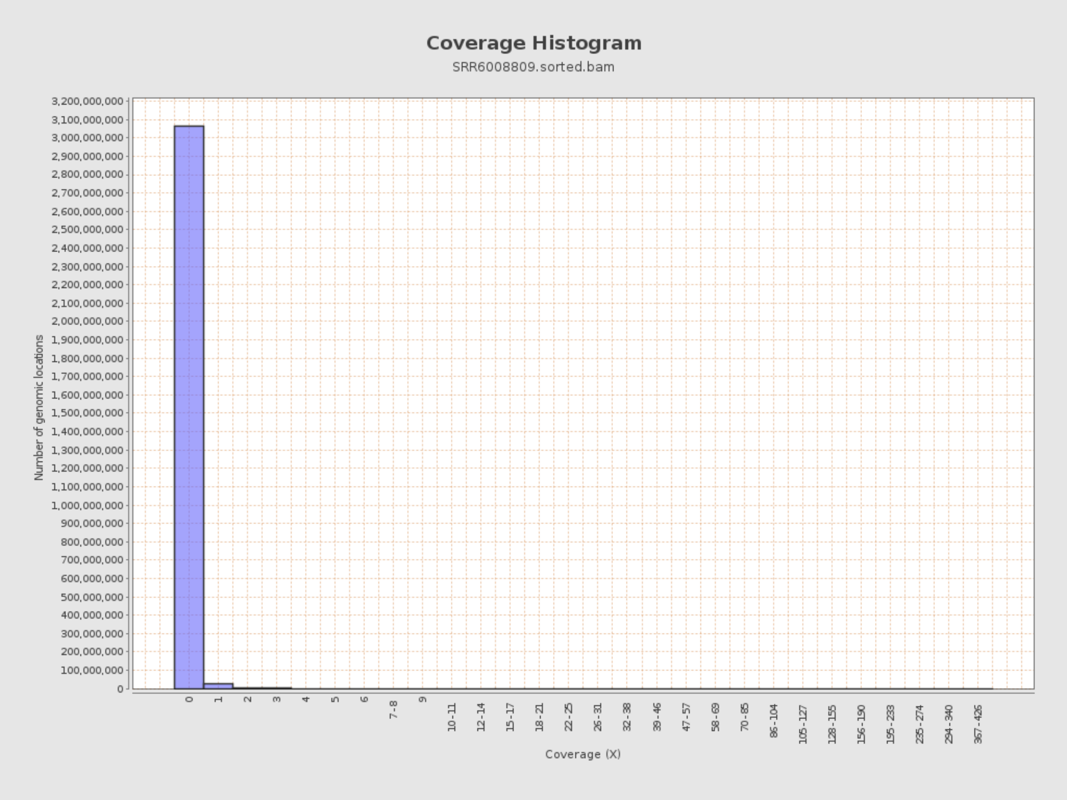
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3429651	0.0138	0.245
chr2	243199373	3432091	0.0141	0.229
chr3	198022430	3558859	0.018	0.1725
chr4	191154276	2704058	0.0141	0.1546
chr5	180915260	3162301	0.0175	0.1686
chr6	171115067	3146127	0.0184	0.1821
chr7	159138663	1666598	0.0105	0.237

chr8	146364022	1669416	0.0114	0.2796
chr9	141213431	1591918	0.0113	0.1508
chr10	135534747	2873550	0.0212	0.2362
chr11	135006516	1943017	0.0144	0.1588
chr12	133851895	2062580	0.0154	0.1595
chr13	115169878	1477840	0.0128	0.1441
chr14	107349540	1221956	0.0114	0.1391
chr15	102531392	1270533	0.0124	0.1407
chr16	90354753	1454068	0.0161	0.1793
chr17	81195210	1465174	0.018	0.1752
chr18	78077248	1028078	0.0132	0.1874
chr19	59128983	1000426	0.0169	0.2275
chr20	63025520	1158627	0.0184	0.175
chr21	48129895	443821	0.0092	0.1252
chr22	51304566	441459	0.0086	0.1178
chrMT	16571	13357	0.806	1.2881
chrX	155270560	2570799	0.0166	0.1667
chrY	59373566	124583	0.0021	0.0789

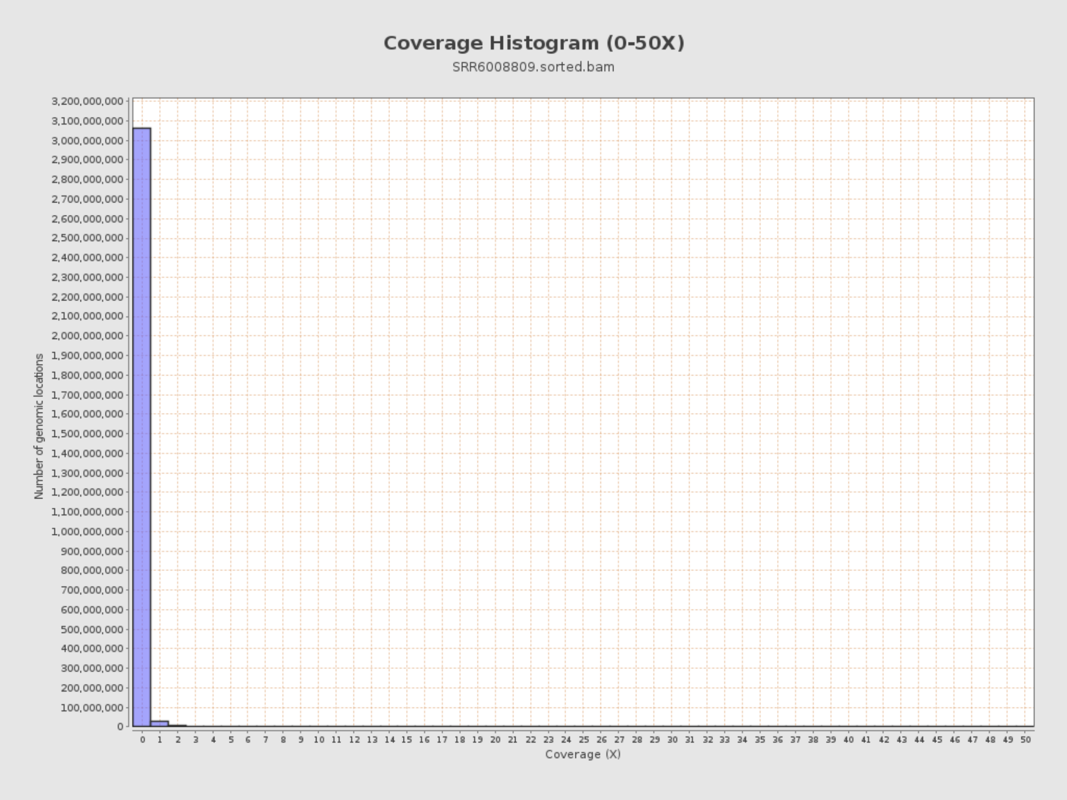
3. Results : Coverage across reference



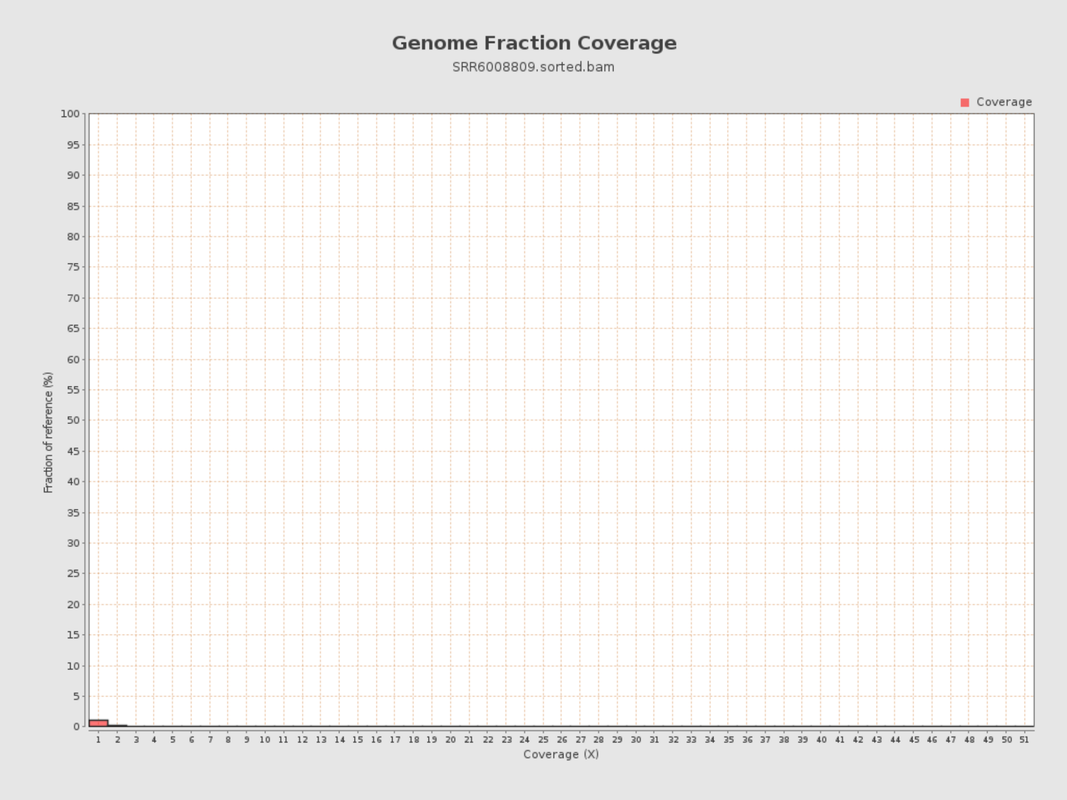
4. Results : Coverage Histogram



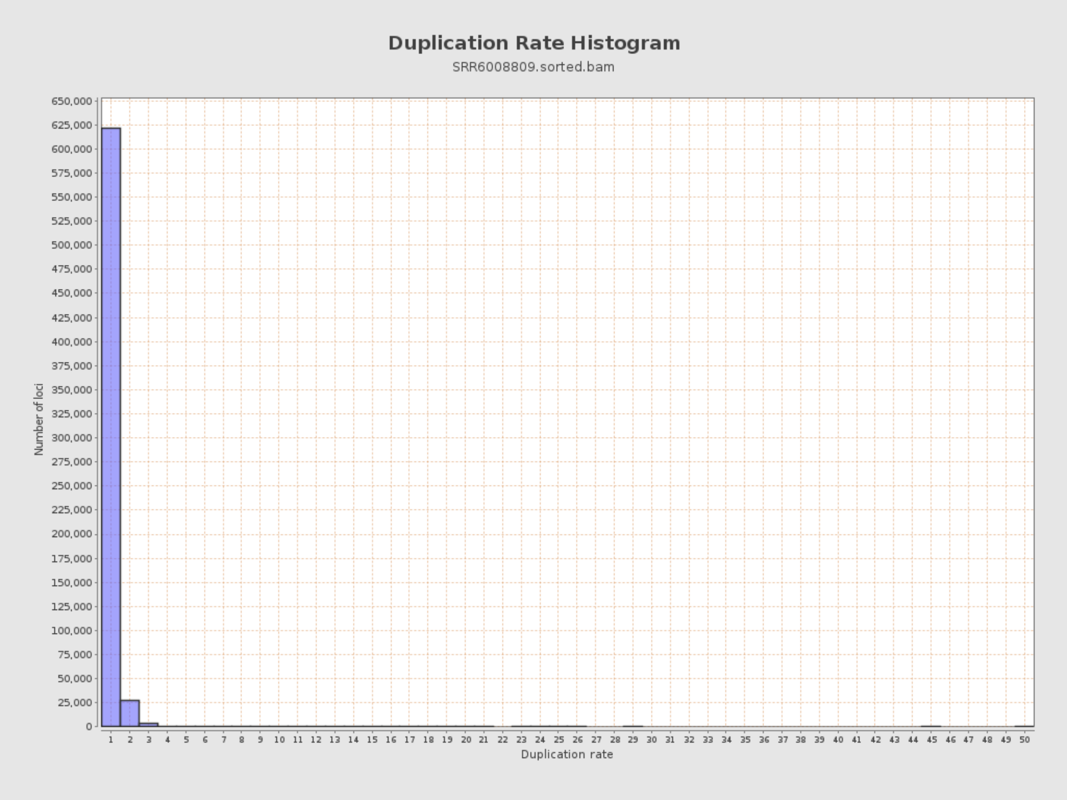
5. Results : Coverage Histogram (0-50X)



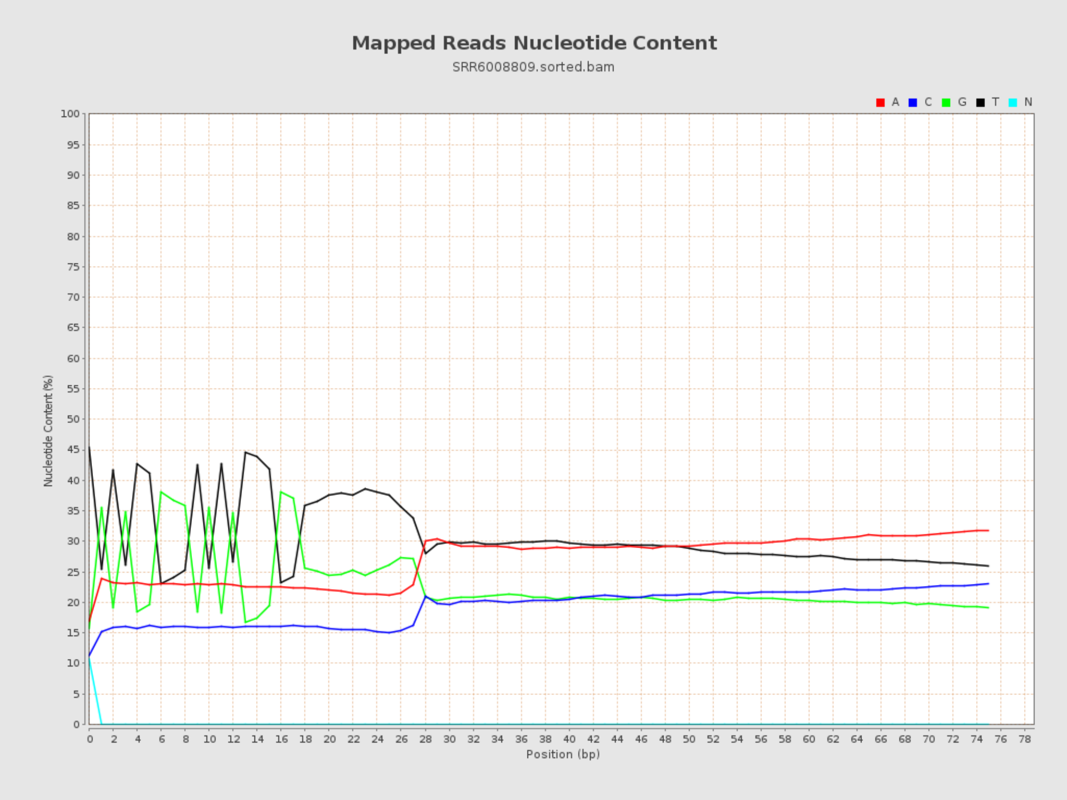
6. Results : Genome Fraction Coverage



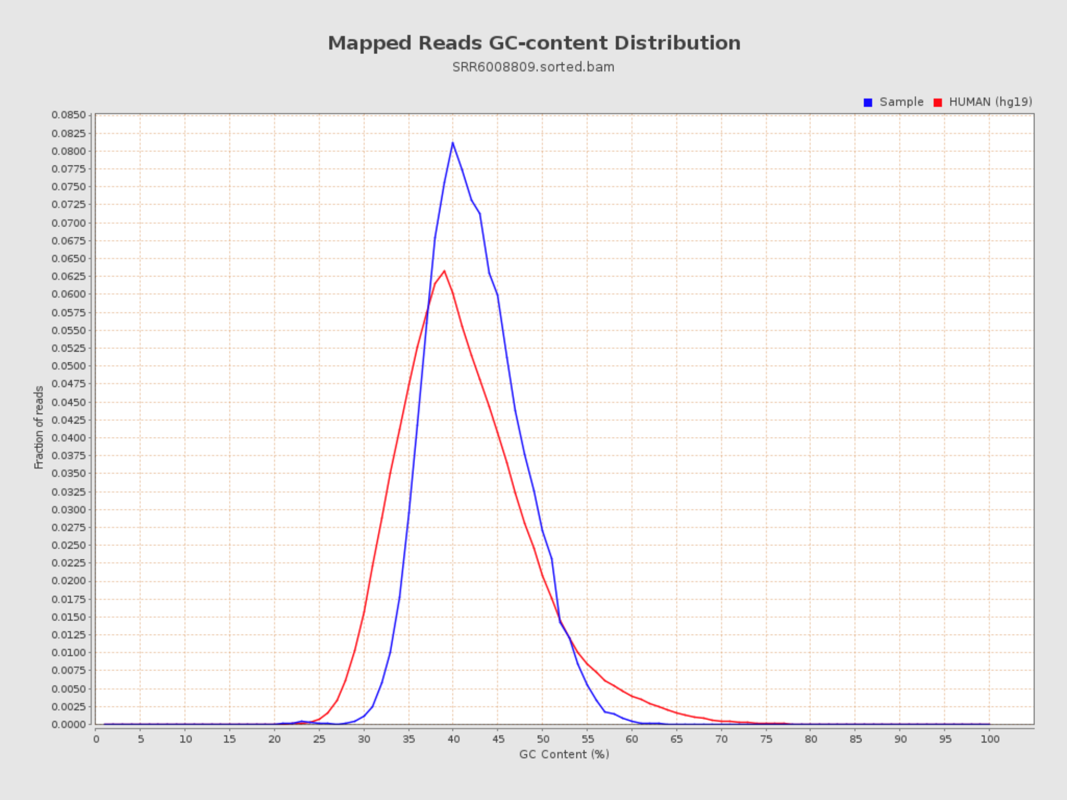
7. Results : Duplication Rate Histogram



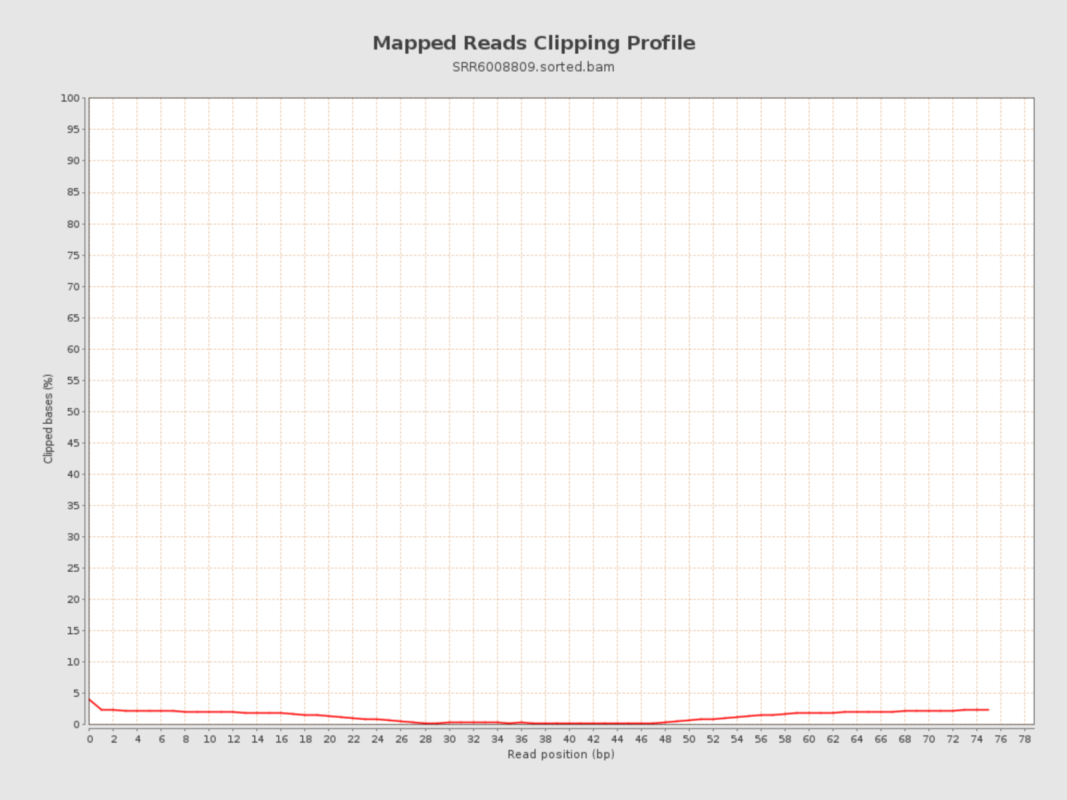
8. Results : Mapped Reads Nucleotide Content



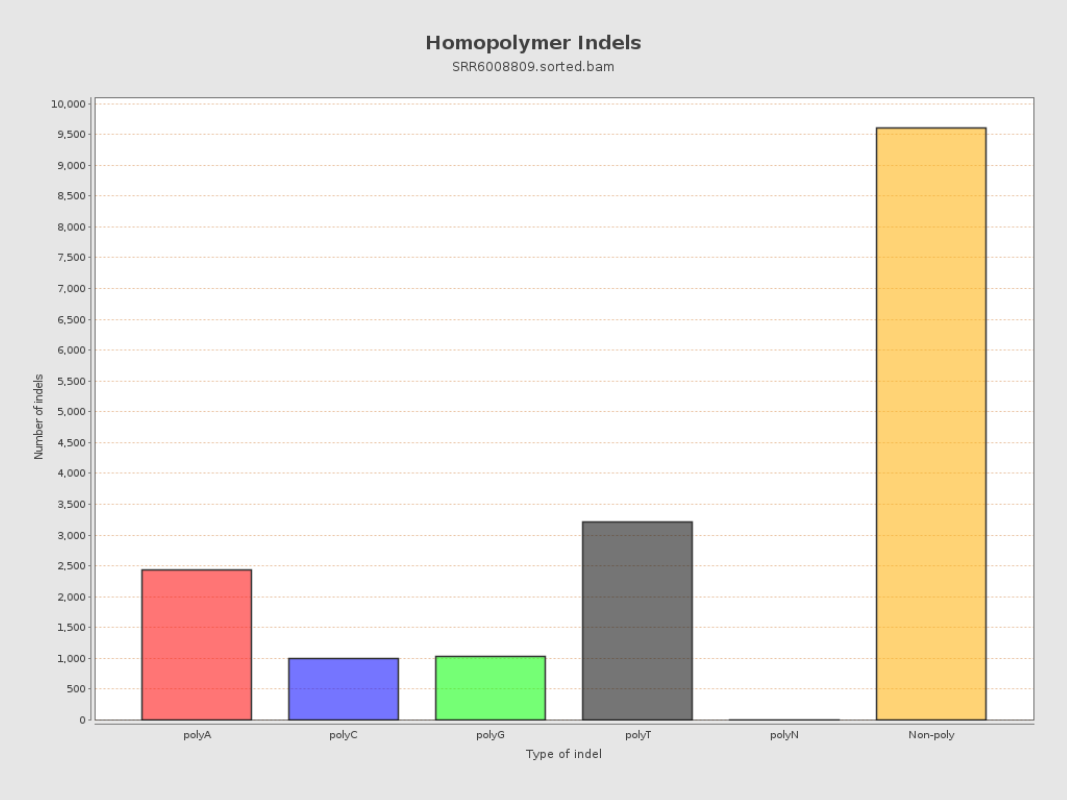
9. Results : Mapped Reads GC-content Distribution



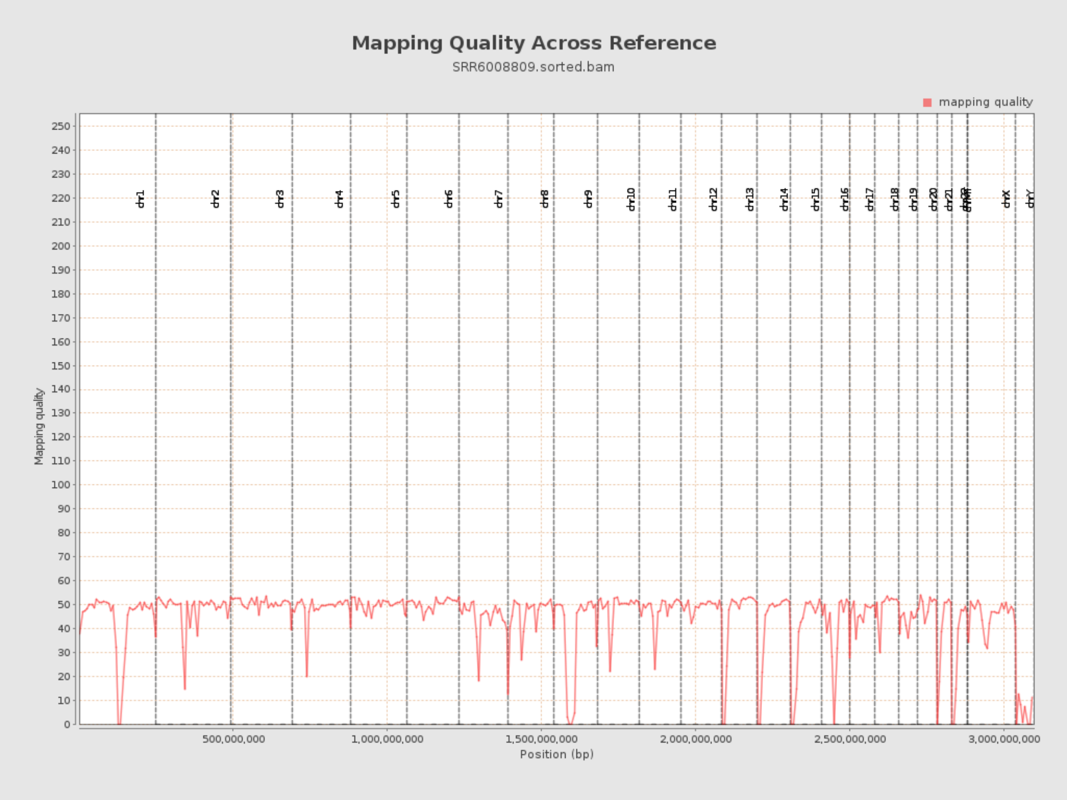
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram