Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 12:23:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6008807.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_SRR6008807 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6008807.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 12:23:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6008807.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,354,947
Mapped reads	860,484 / 63.51%
Unmapped reads	494,463 / 36.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,137 / 0.67%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	39,372 / 2.91%
Duplication rate	3.74%
Clipped reads	362,919 / 26.78%

2.2. ACGT Content

Number/percentage of A's	15,780,246 / 27.31%
Number/percentage of C's	11,146,736 / 19.29%
Number/percentage of T's	17,825,435 / 30.85%
Number/percentage of G's	12,944,347 / 22.4%
Number/percentage of N's	87,667 / 0.15%
GC Percentage	41.69%

2.3. Coverage

Mean	0.0187

Standard Deviation	0.2118

2.4. Mapping Quality

Mean Mapping Quality	45.49

2.5. Mismatches and indels

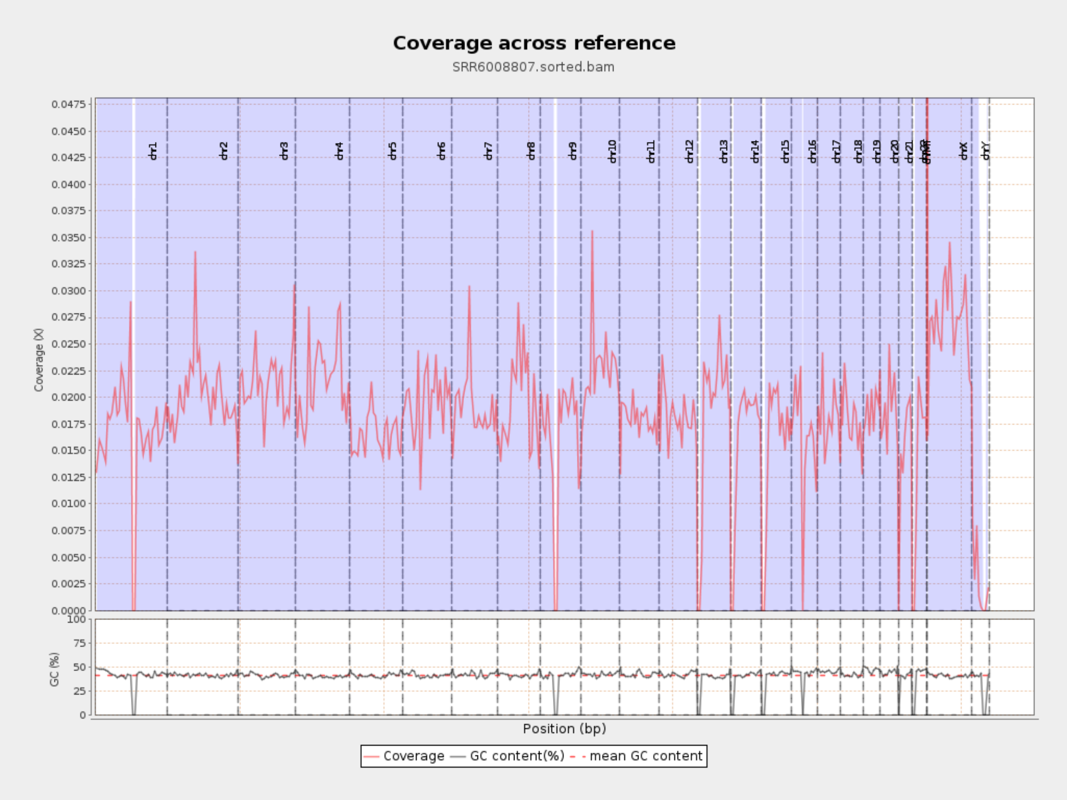
General error rate	0.86%
Mismatches	488,328
Insertions	4,220
Mapped reads with at least one insertion	0.49%
Deletions	15,325
Mapped reads with at least one deletion	1.76%
Homopolymer indels	46.31%

2.6. Chromosome stats

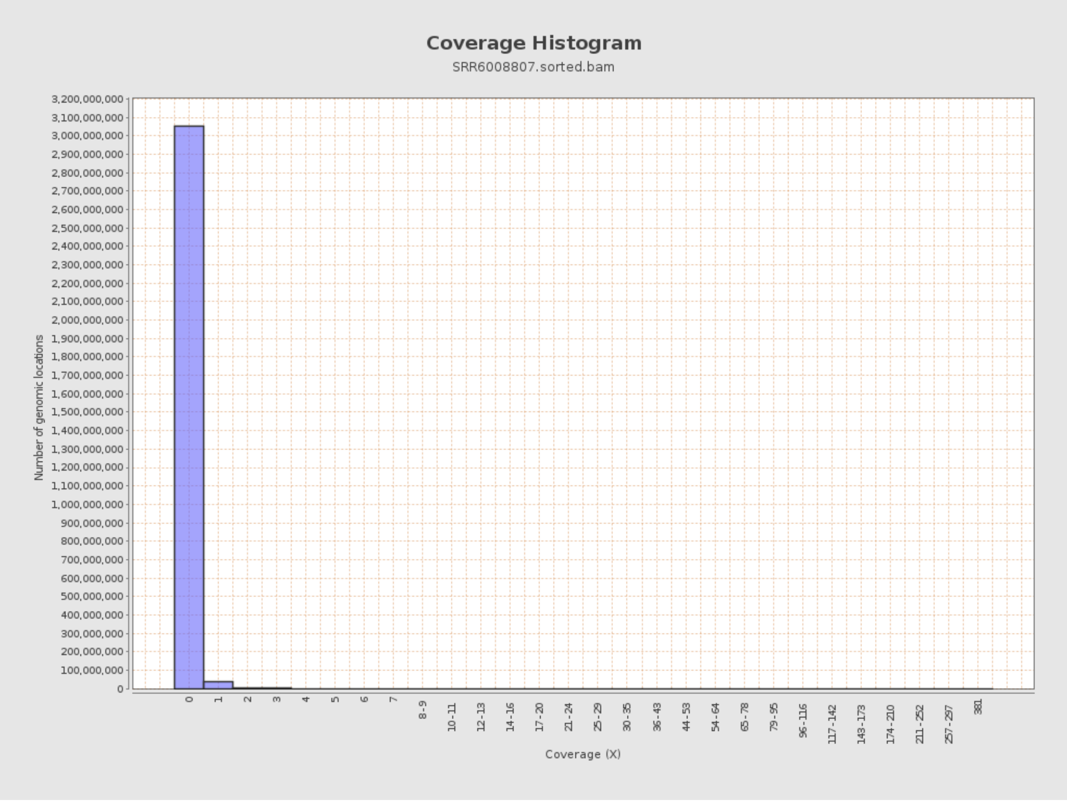
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4157520	0.0167	0.2858
chr2	243199373	4946203	0.0203	0.2588
chr3	198022430	4181057	0.0211	0.1799
chr4	191154276	4130376	0.0216	0.1849
chr5	180915260	2984933	0.0165	0.1585
chr6	171115067	3334420	0.0195	0.1896
chr7	159138663	3053150	0.0192	0.2537

chr8	146364022	2850633	0.0195	0.2374
chr9	141213431	2299932	0.0163	0.1978
chr10	135534747	3073396	0.0227	0.2474
chr11	135006516	2429419	0.018	0.1978
chr12	133851895	2442077	0.0182	0.1682
chr13	115169878	2108283	0.0183	0.1659
chr14	107349540	1707452	0.0159	0.1666
chr15	102531392	1566144	0.0153	0.152
chr16	90354753	1427746	0.0158	0.1669
chr17	81195210	1474906	0.0182	0.1747
chr18	78077248	1392806	0.0178	0.3301
chr19	59128983	1115908	0.0189	0.2222
chr20	63025520	1184416	0.0188	0.1742
chr21	48129895	729275	0.0152	0.1604
chr22	51304566	709426	0.0138	0.145
chrMT	16571	102583	6.1905	4.2541
chrX	155270560	4252604	0.0274	0.2087
chrY	59373566	157135	0.0026	0.0764

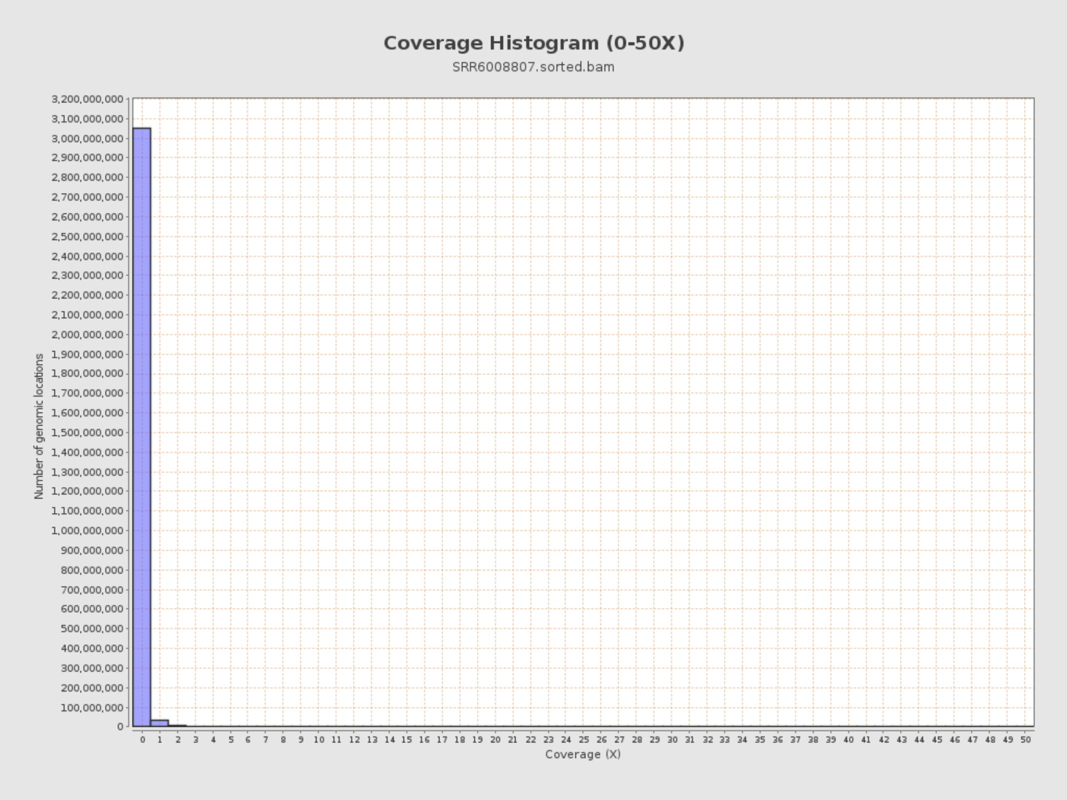
3. Results : Coverage across reference



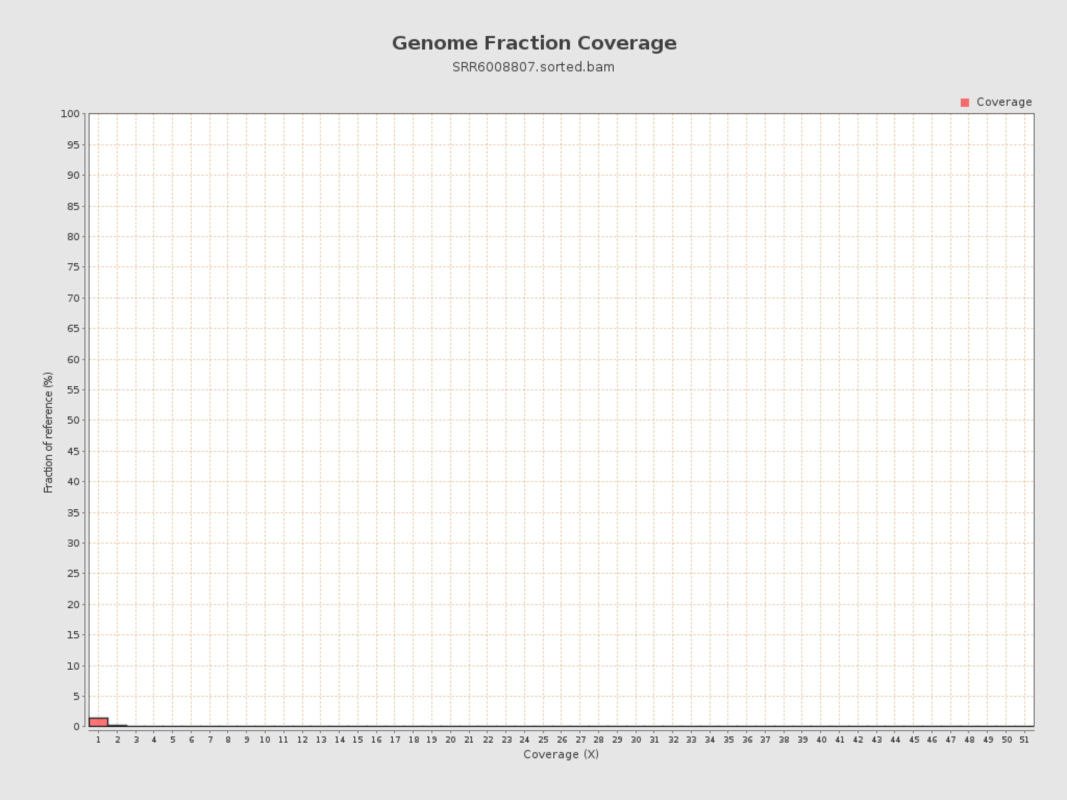
4. Results : Coverage Histogram



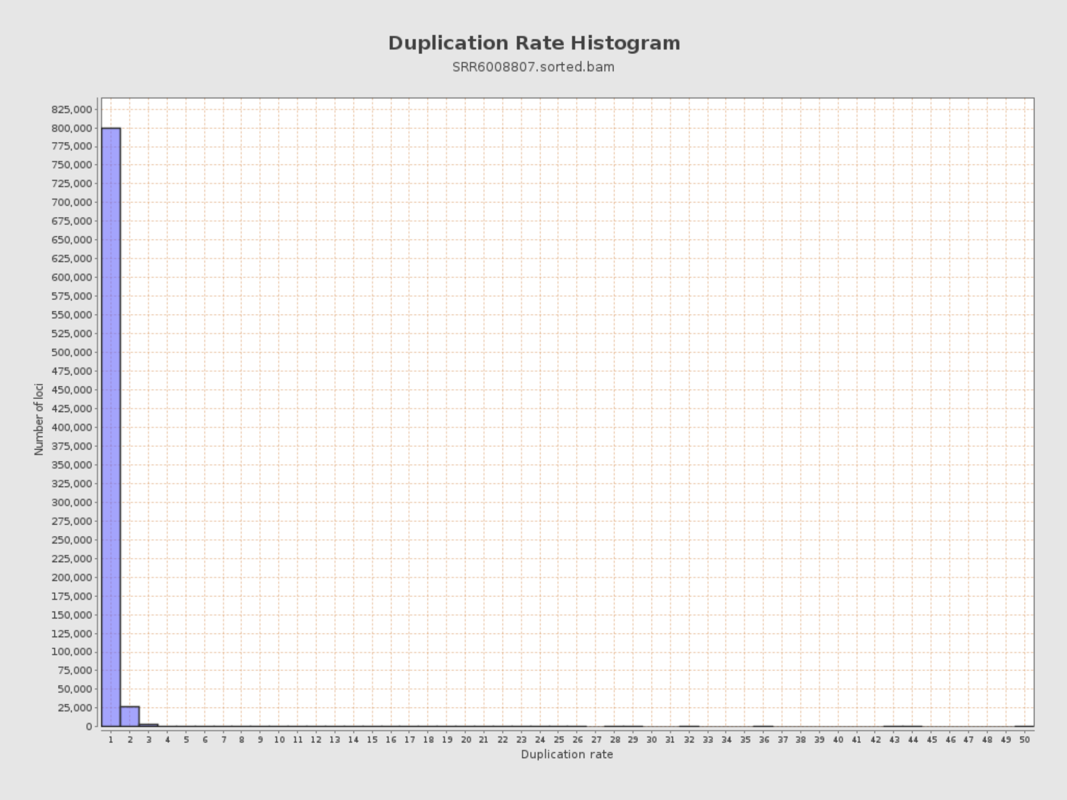
5. Results : Coverage Histogram (0-50X)



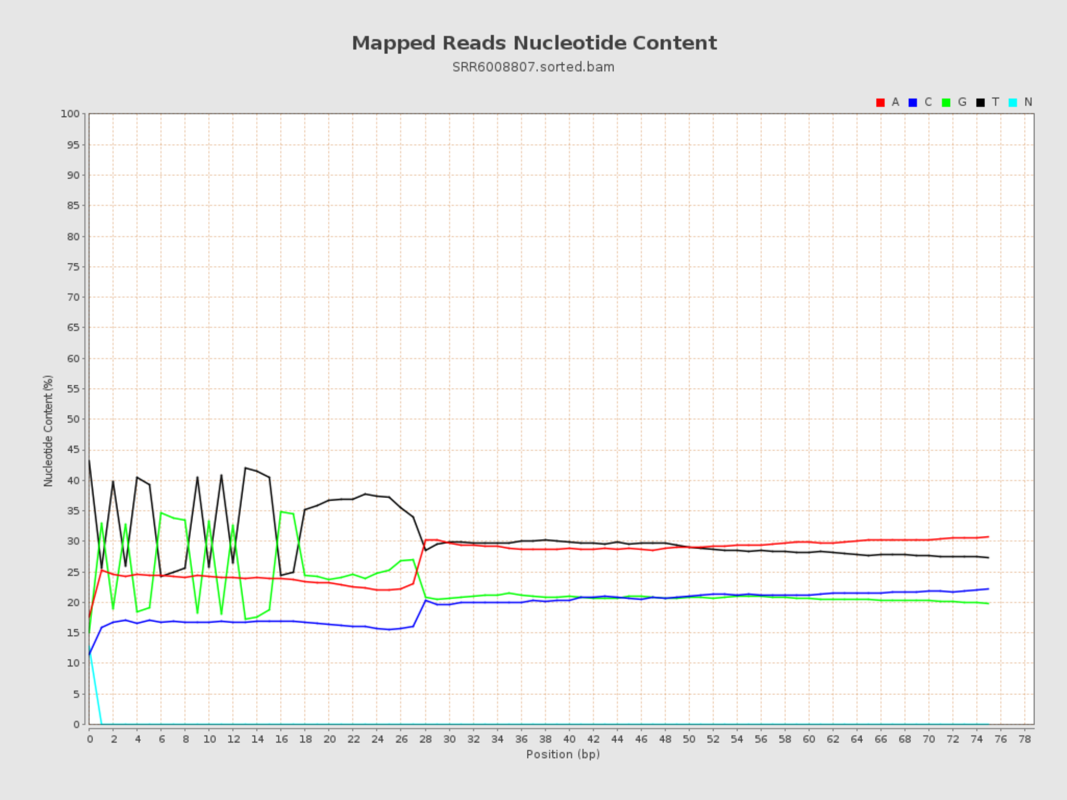
6. Results : Genome Fraction Coverage



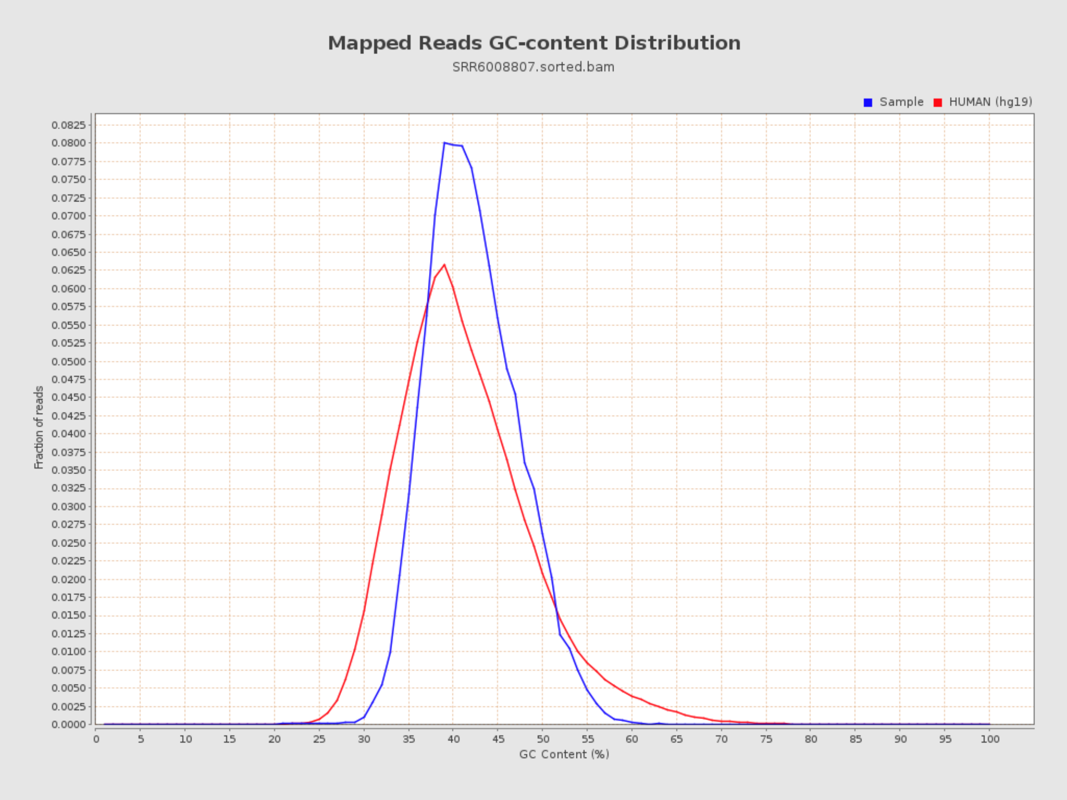
7. Results : Duplication Rate Histogram



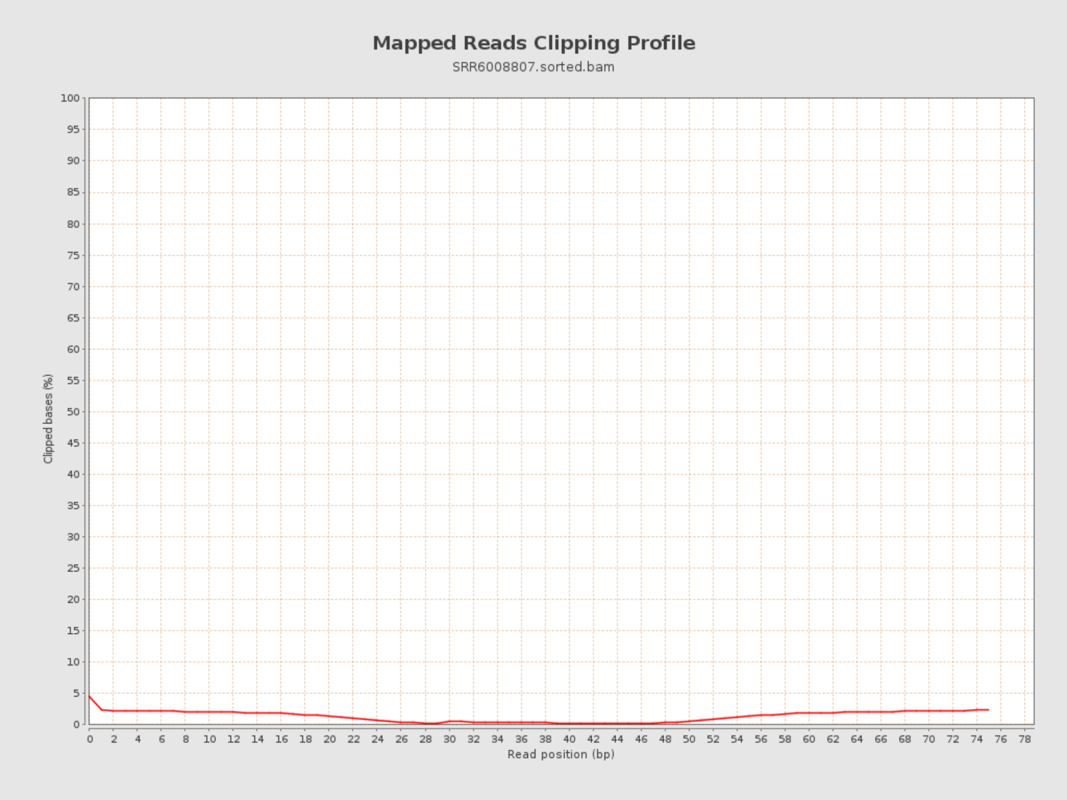
8. Results : Mapped Reads Nucleotide Content



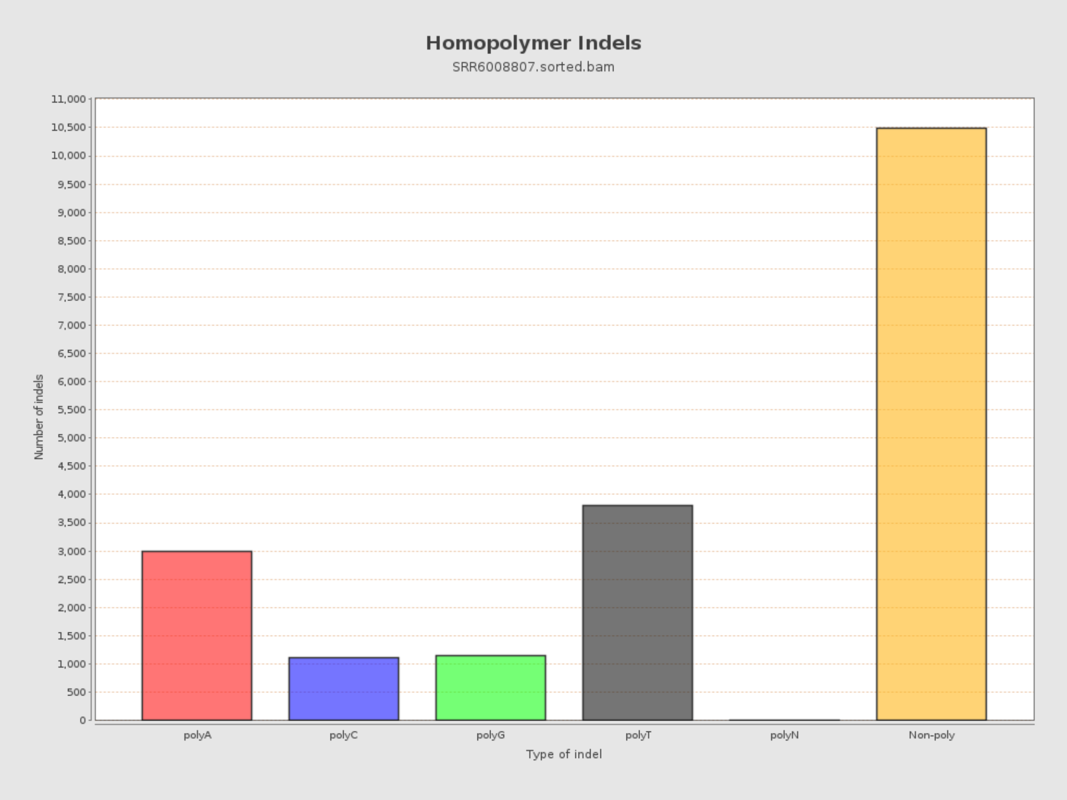
9. Results : Mapped Reads GC-content Distribution



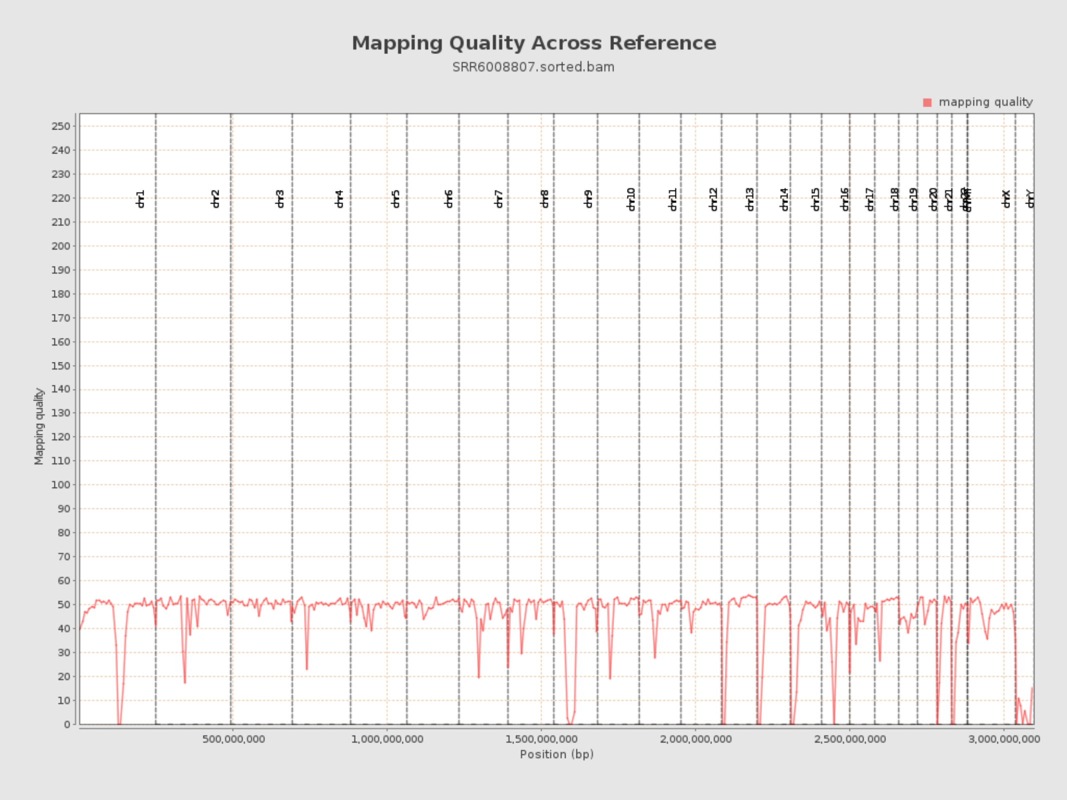
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram