Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 21:16:23

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1819086.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_SRR1819086 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1819086.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 21:16:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1819086.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	880,322
Mapped reads	811,355 / 92.17%
Unmapped reads	68,967 / 7.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,248 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	18,931 / 2.15%
Duplication rate	1.73%
Clipped reads	811,594 / 92.19%

2.2. ACGT Content

Number/percentage of A's	12,856,730 / 26.8%
Number/percentage of C's	9,148,891 / 19.07%
Number/percentage of T's	14,459,655 / 30.15%
Number/percentage of G's	11,498,471 / 23.97%
Number/percentage of N's	761 / 0%
GC Percentage	43.05%

2.3. Coverage

Mean	0.0155

Standard Deviation	0.1675

2.4. Mapping Quality

Mean Mapping Quality	45.07

2.5. Mismatches and indels

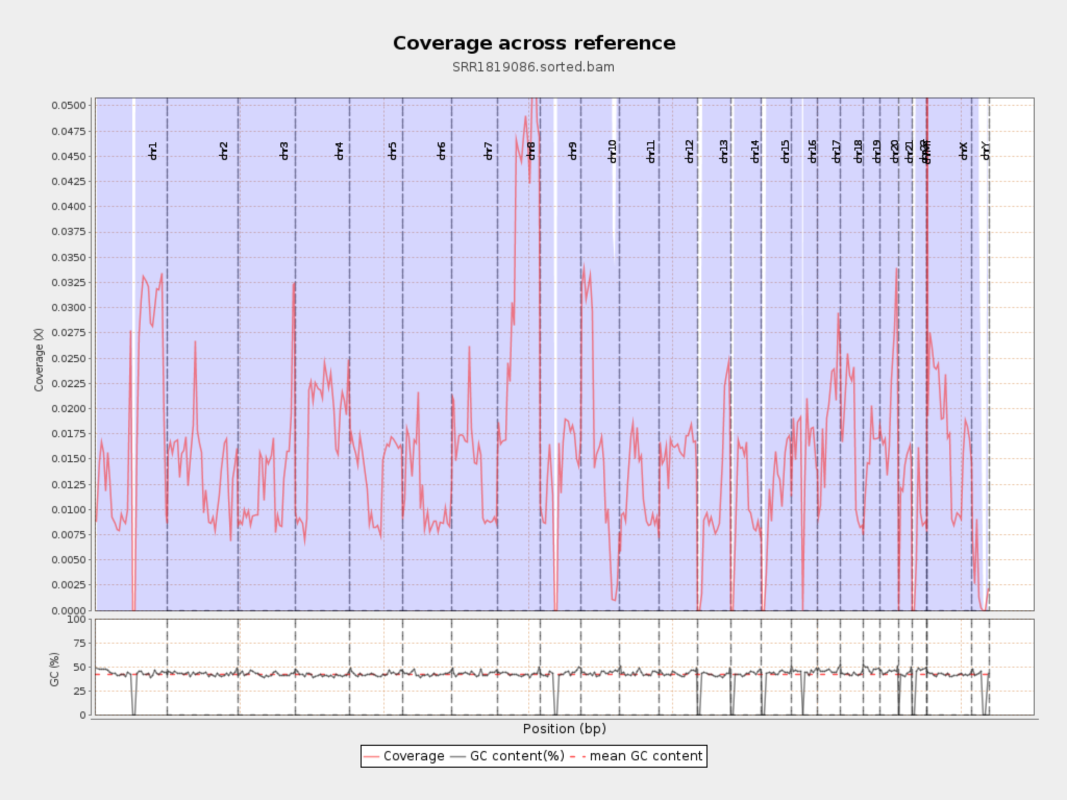
General error rate	0.52%
Mismatches	240,889
Insertions	3,823
Mapped reads with at least one insertion	0.47%
Deletions	9,228
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.65%

2.6. Chromosome stats

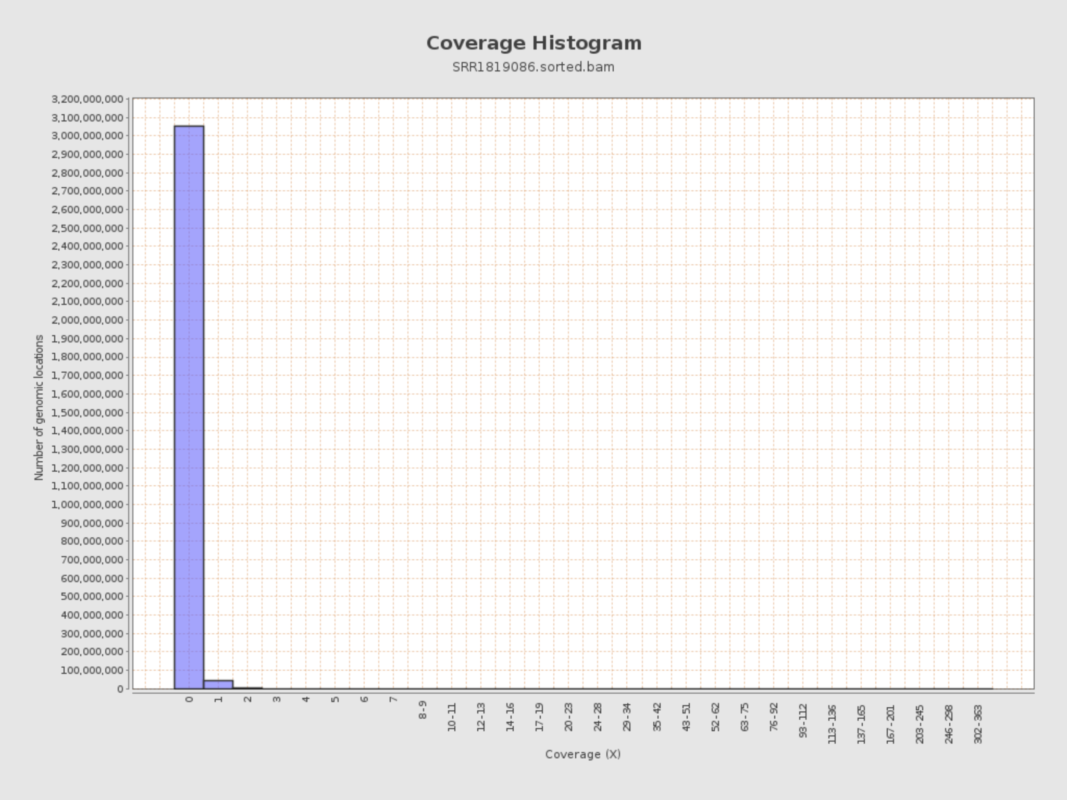
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4495687	0.018	0.2862
chr2	243199373	3431947	0.0141	0.1693
chr3	198022430	2534494	0.0128	0.1188
chr4	191154276	3497585	0.0183	0.1507
chr5	180915260	2521032	0.0139	0.1237
chr6	171115067	1956373	0.0114	0.1264
chr7	159138663	2329992	0.0146	0.1994

chr8	146364022	5384963	0.0368	0.2205
chr9	141213431	1837225	0.013	0.1448
chr10	135534747	2318277	0.0171	0.1735
chr11	135006516	1600344	0.0119	0.1437
chr12	133851895	2148048	0.016	0.1337
chr13	115169878	1248892	0.0108	0.1087
chr14	107349540	1090099	0.0102	0.1071
chr15	102531392	1133576	0.0111	0.1108
chr16	90354753	1394590	0.0154	0.1363
chr17	81195210	1551566	0.0191	0.15
chr18	78077248	1338374	0.0171	0.2503
chr19	59128983	927221	0.0157	0.2022
chr20	63025520	1320123	0.0209	0.1523
chr21	48129895	616080	0.0128	0.1268
chr22	51304566	387226	0.0075	0.0908
chrMT	16571	2335	0.1409	0.373
chrX	155270560	2758764	0.0178	0.147
chrY	59373566	155055	0.0026	0.0837

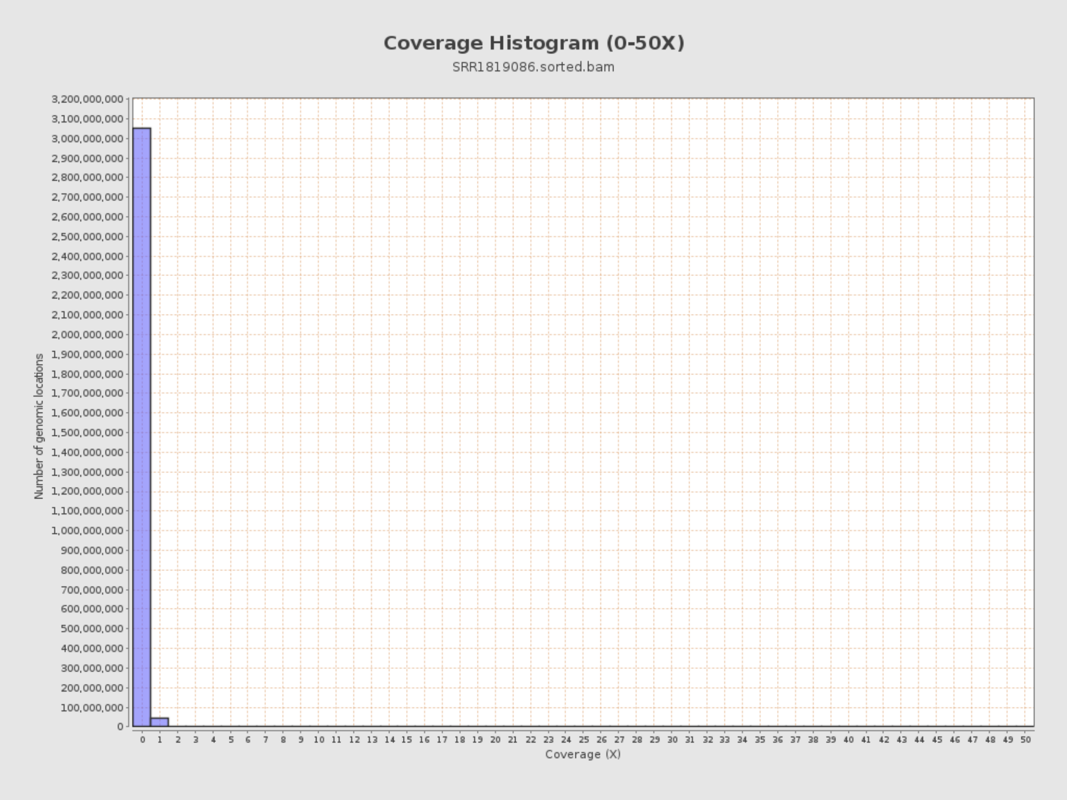
3. Results : Coverage across reference



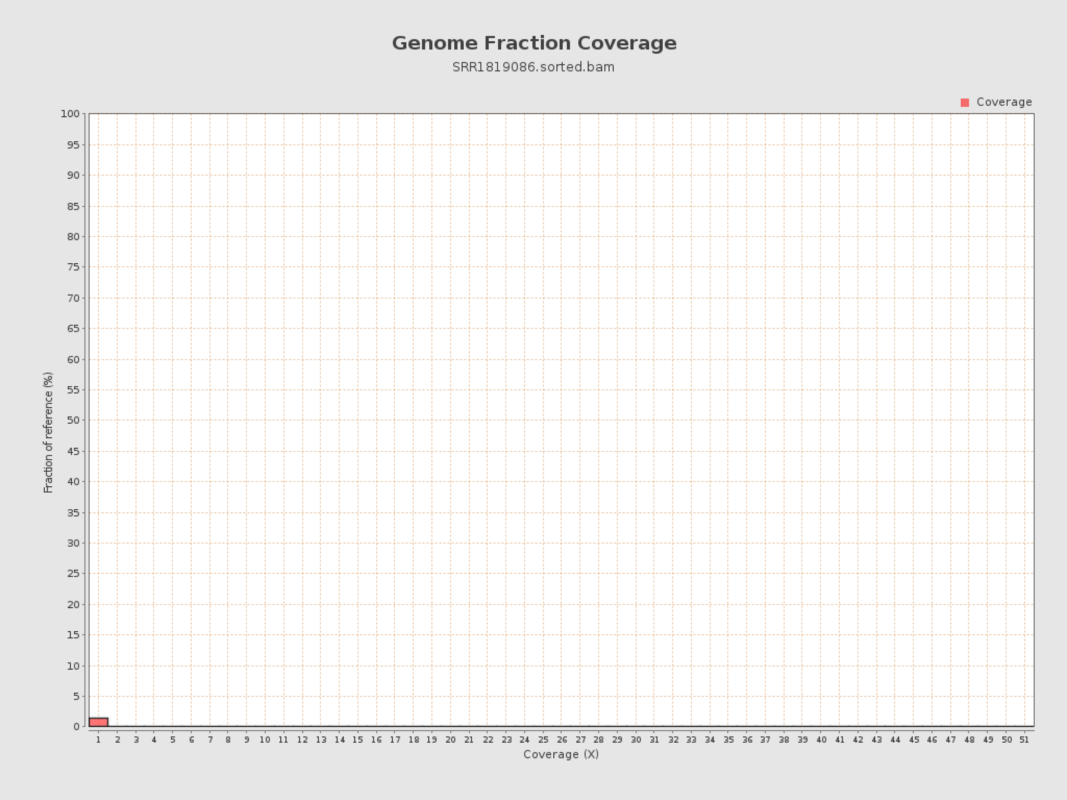
4. Results : Coverage Histogram



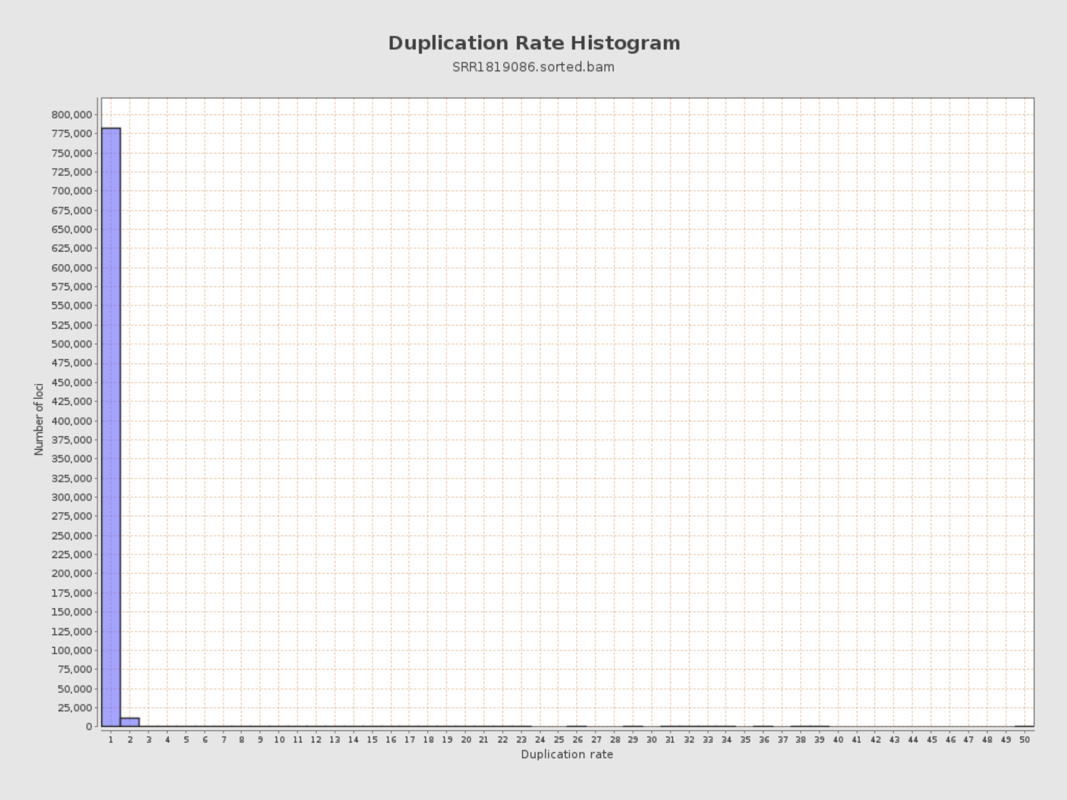
5. Results : Coverage Histogram (0-50X)



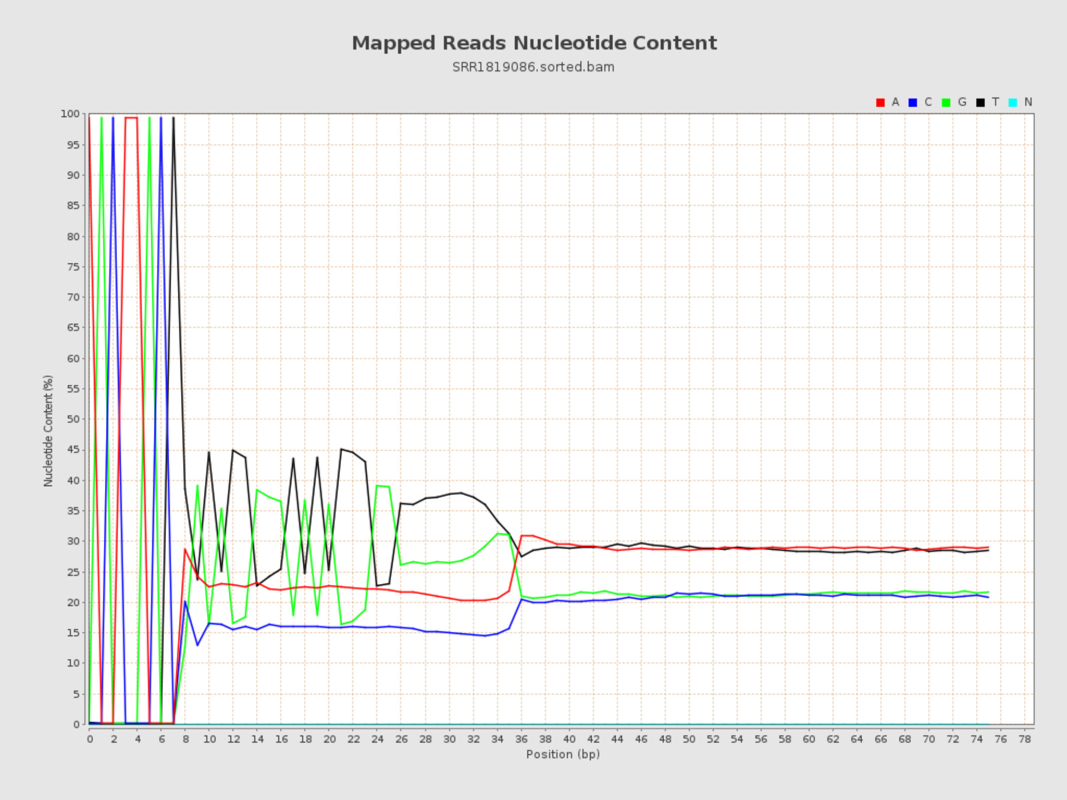
6. Results : Genome Fraction Coverage



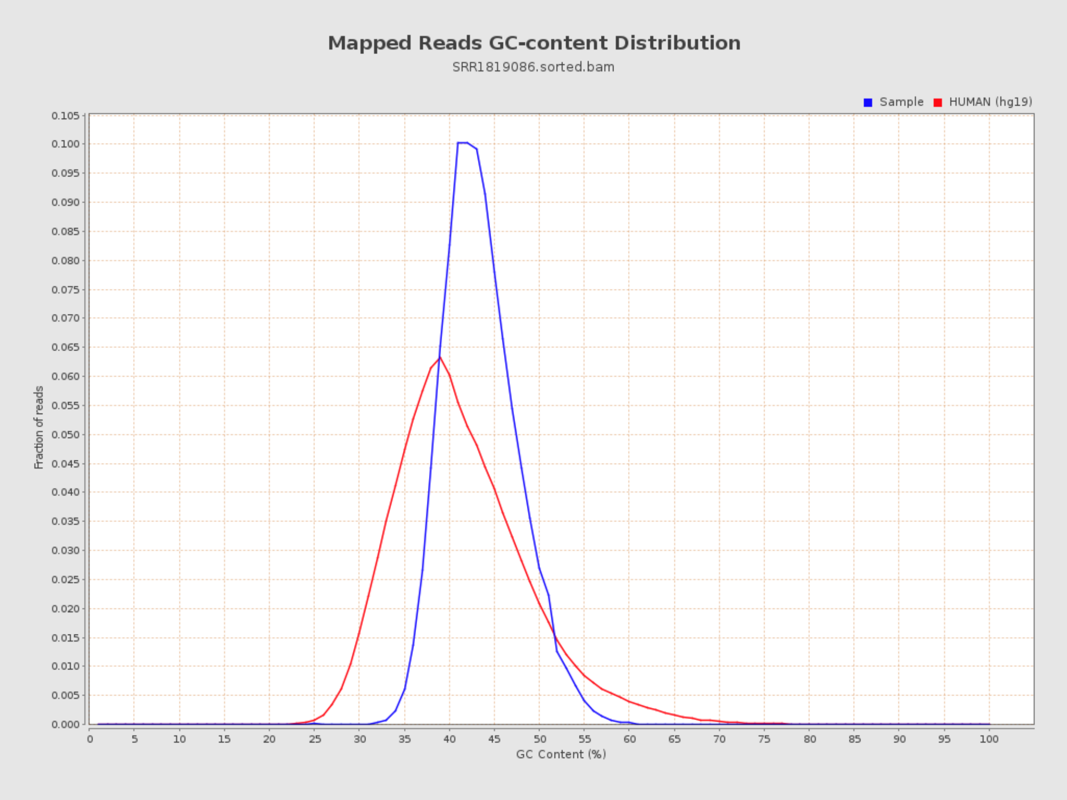
7. Results : Duplication Rate Histogram



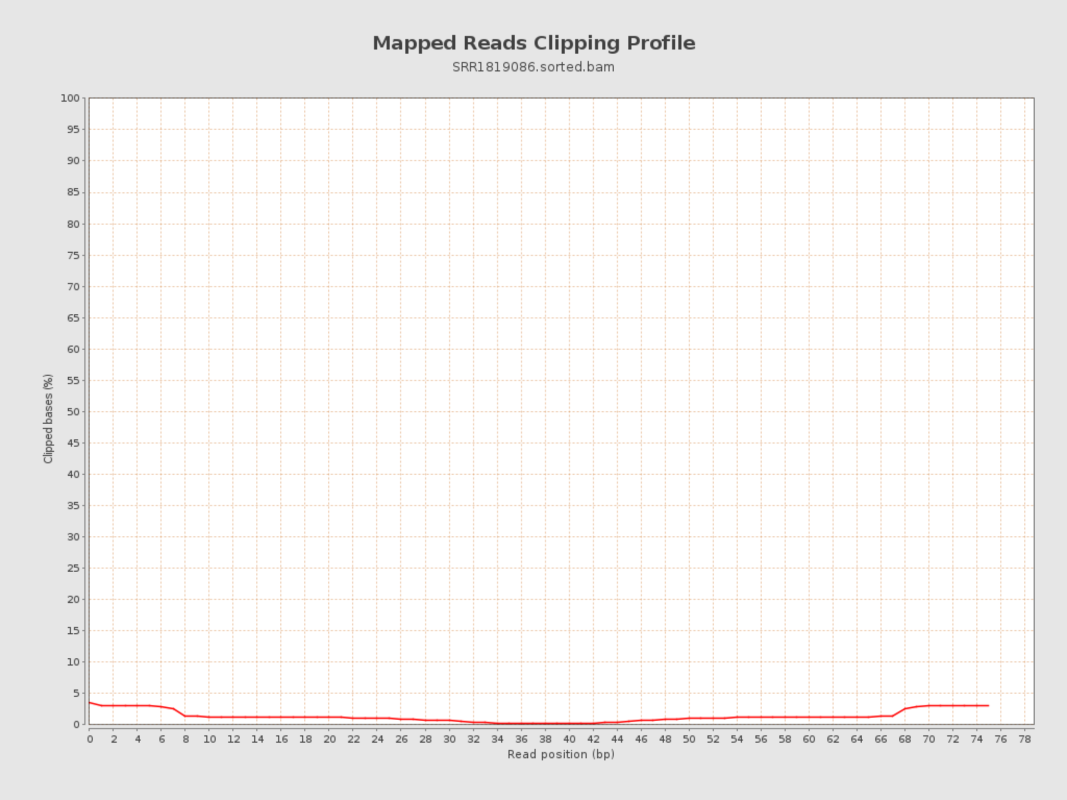
8. Results : Mapped Reads Nucleotide Content



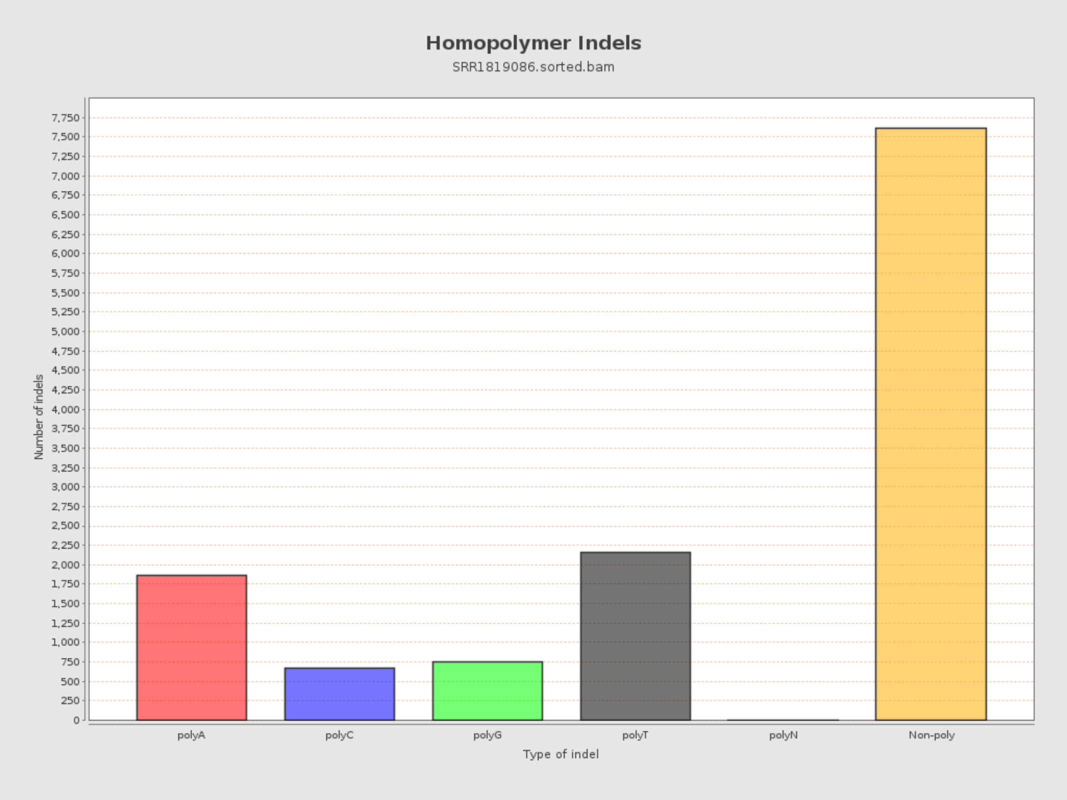
9. Results : Mapped Reads GC-content Distribution



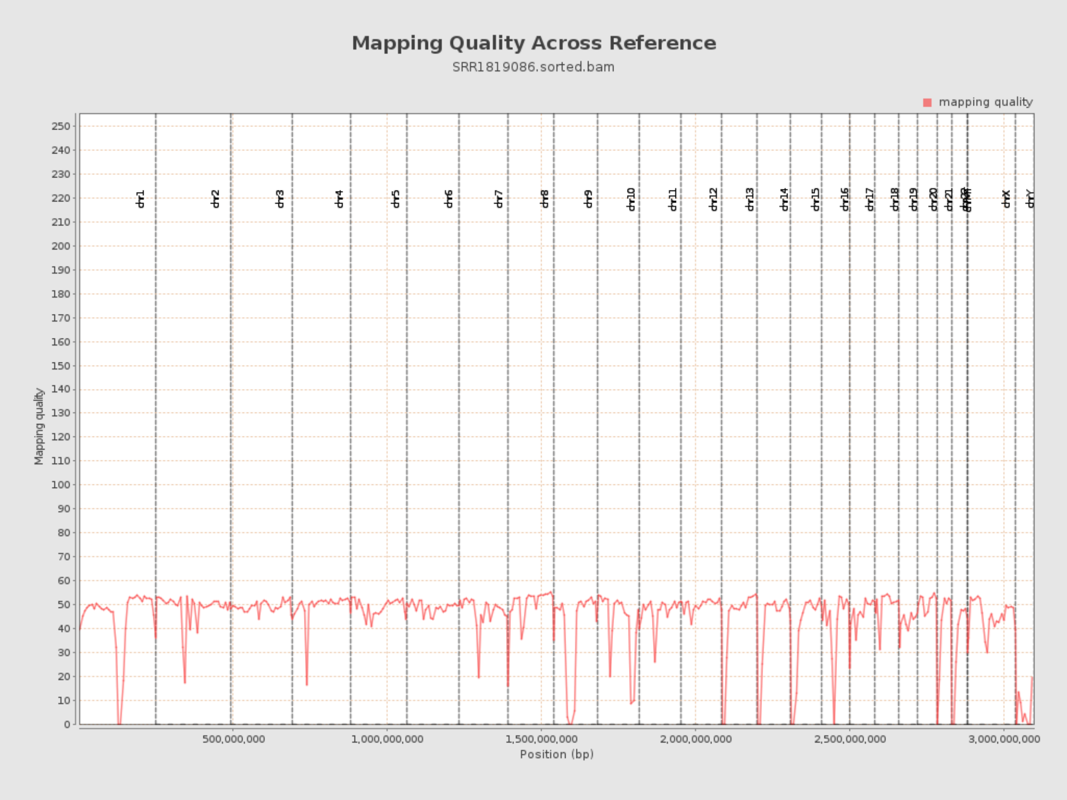
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram