Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:46:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716233.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_SRR9716233 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716233.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:46:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716233.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,677,627
Mapped reads	3,234,431 / 87.95%
Unmapped reads	443,196 / 12.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,499 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	124,844 / 3.39%
Duplication rate	2.77%
Clipped reads	3,240,268 / 88.11%

2.2. ACGT Content

Number/percentage of A's	44,812,607 / 24.47%
Number/percentage of C's	36,088,943 / 19.71%
Number/percentage of T's	57,119,791 / 31.19%
Number/percentage of G's	45,118,236 / 24.64%
Number/percentage of N's	1,420 / 0%
GC Percentage	44.34%

2.3. Coverage

Mean	0.0592

Standard Deviation	0.4197

2.4. Mapping Quality

Mean Mapping Quality	42.06

2.5. Mismatches and indels

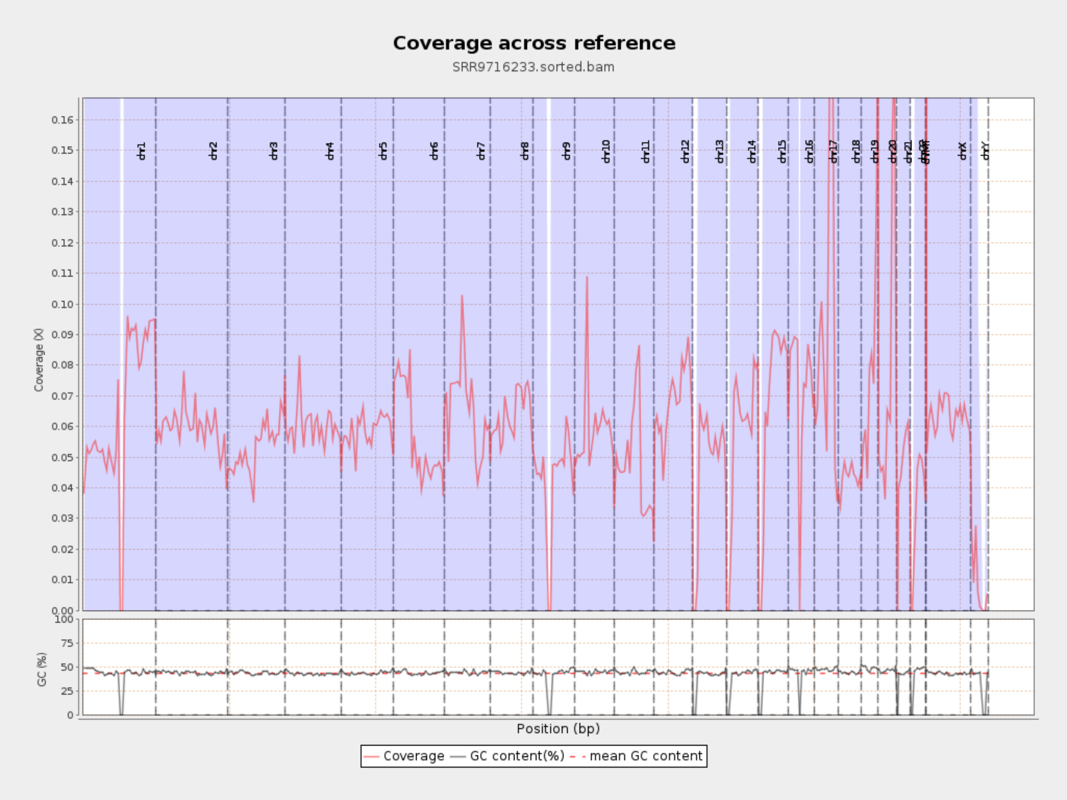
General error rate	0.54%
Mismatches	961,864
Insertions	12,059
Mapped reads with at least one insertion	0.37%
Deletions	32,694
Mapped reads with at least one deletion	1%
Homopolymer indels	41.04%

2.6. Chromosome stats

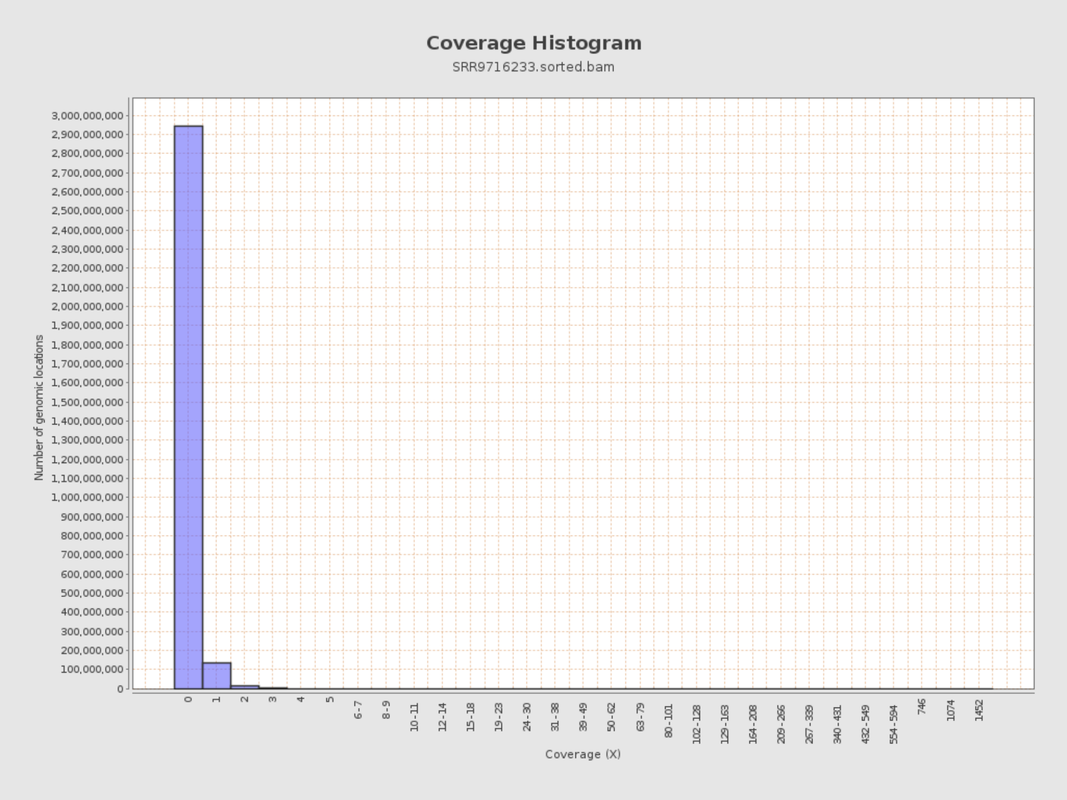
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	16117545	0.0647	0.5333
chr2	243199373	14531419	0.0598	0.6587
chr3	198022430	10507377	0.0531	0.2796
chr4	191154276	11525788	0.0603	0.3154
chr5	180915260	10612311	0.0587	0.2795
chr6	171115067	9790651	0.0572	0.3611
chr7	159138663	10572079	0.0664	0.6695

chr8	146364022	9350065	0.0639	0.383
chr9	141213431	6030331	0.0427	0.3023
chr10	135534747	8020731	0.0592	0.5413
chr11	135006516	6452875	0.0478	0.3585
chr12	133851895	9237165	0.069	0.3112
chr13	115169878	5466151	0.0475	0.2537
chr14	107349540	6104458	0.0569	0.301
chr15	102531392	6713558	0.0655	0.3121
chr16	90354753	6393306	0.0708	0.34
chr17	81195210	8116964	0.1	0.404
chr18	78077248	3379153	0.0433	0.5066
chr19	59128983	4693093	0.0794	0.5344
chr20	63025520	5247415	0.0833	0.3618
chr21	48129895	2236363	0.0465	0.2755
chr22	51304566	1697553	0.0331	0.2126
chrMT	16571	24952	1.5058	1.6252
chrX	155270560	9856817	0.0635	0.3299
chrY	59373566	514788	0.0087	0.2109

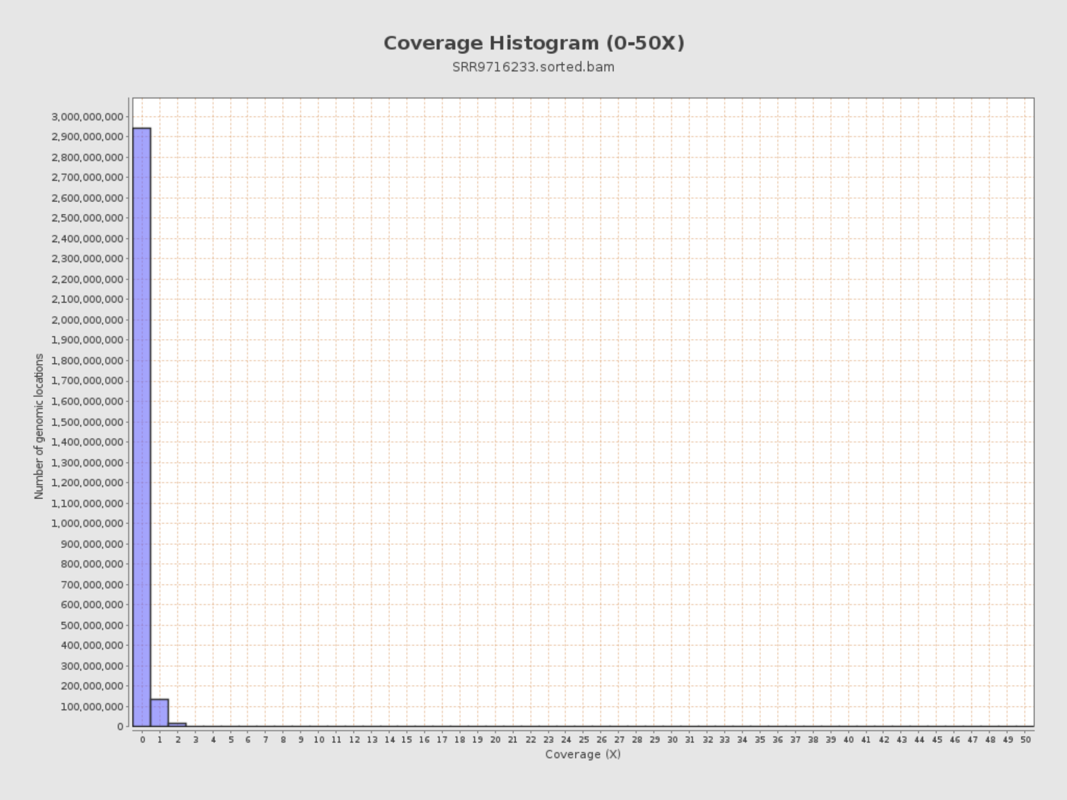
3. Results : Coverage across reference



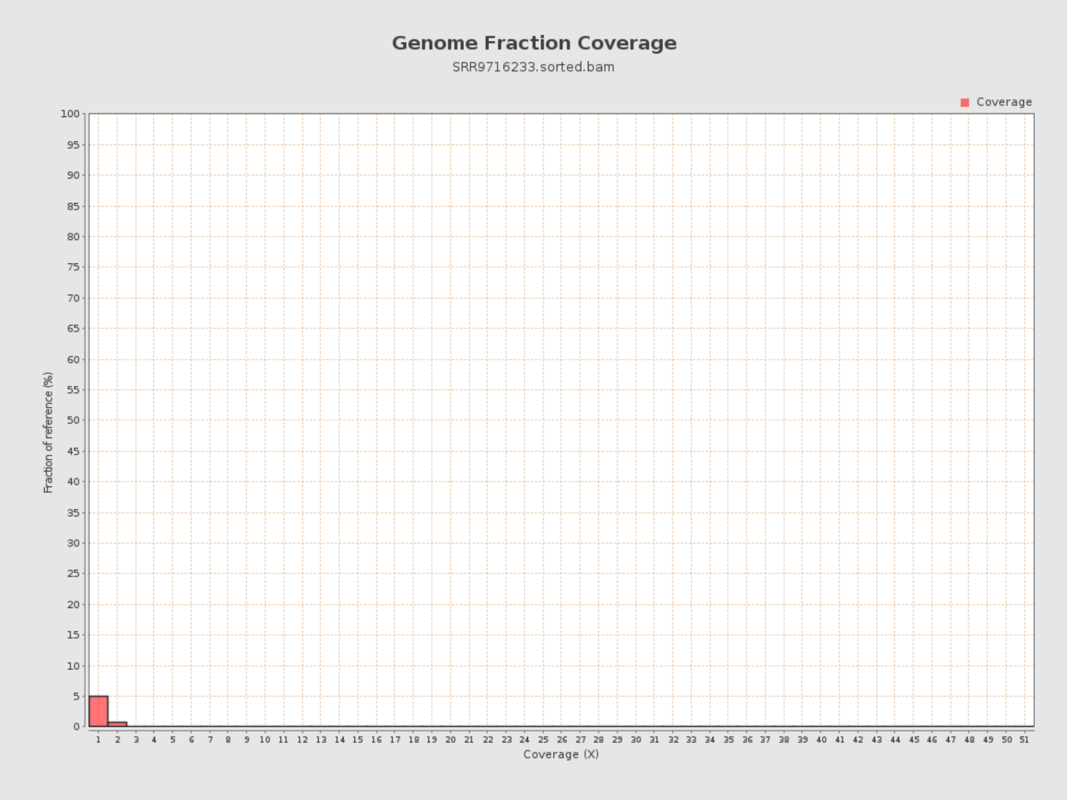
4. Results : Coverage Histogram



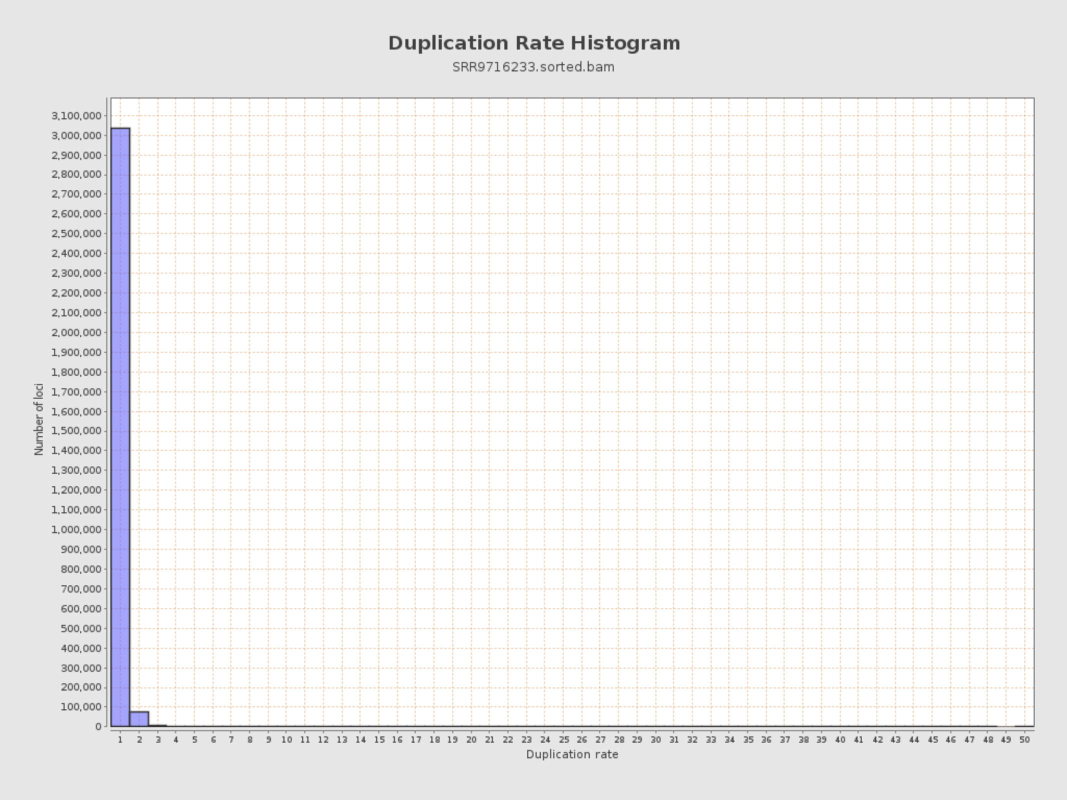
5. Results : Coverage Histogram (0-50X)



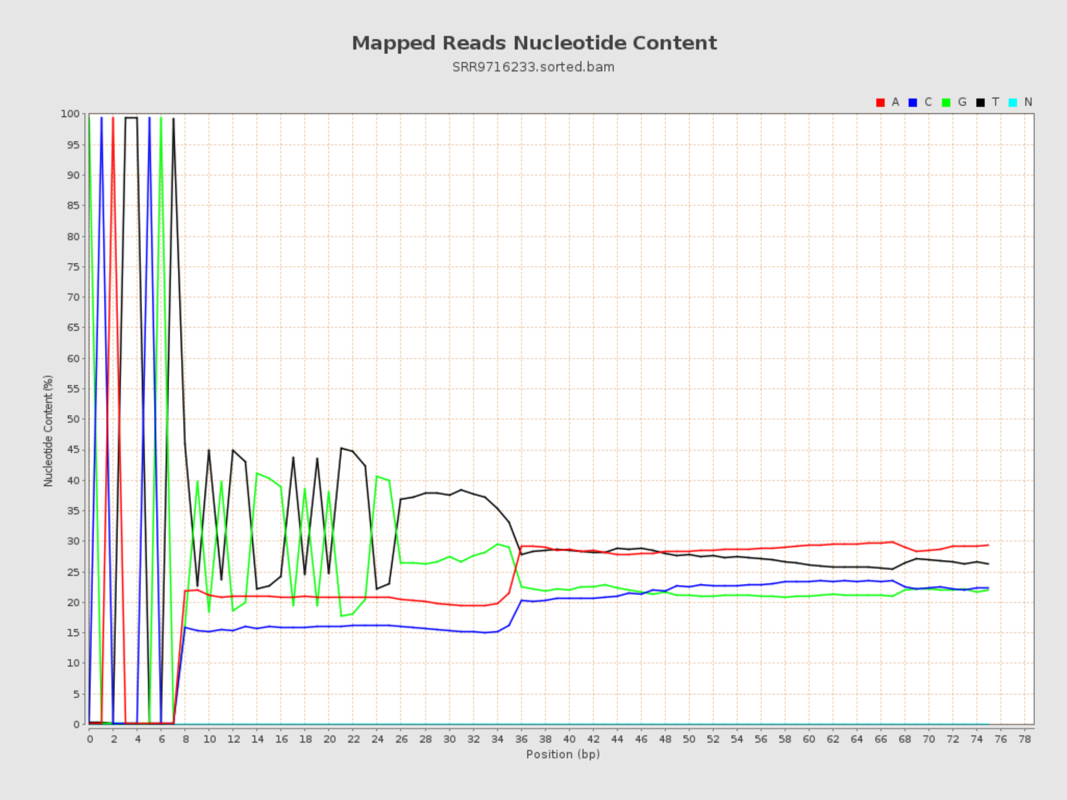
6. Results : Genome Fraction Coverage



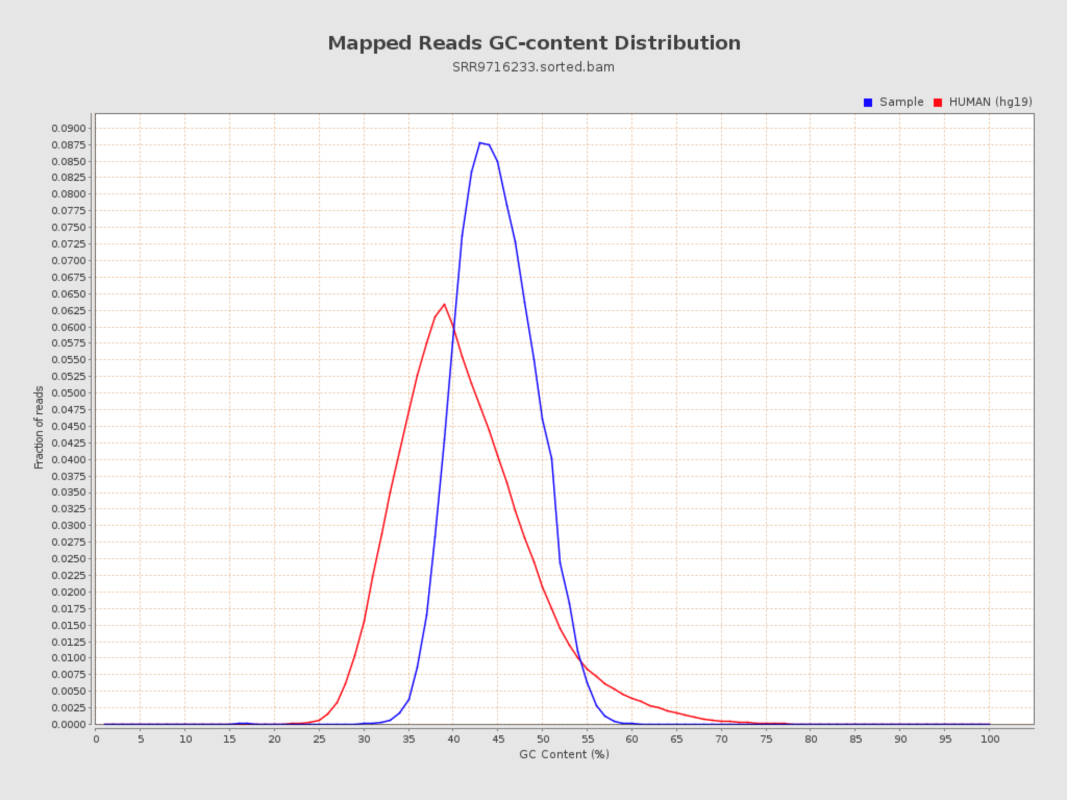
7. Results : Duplication Rate Histogram



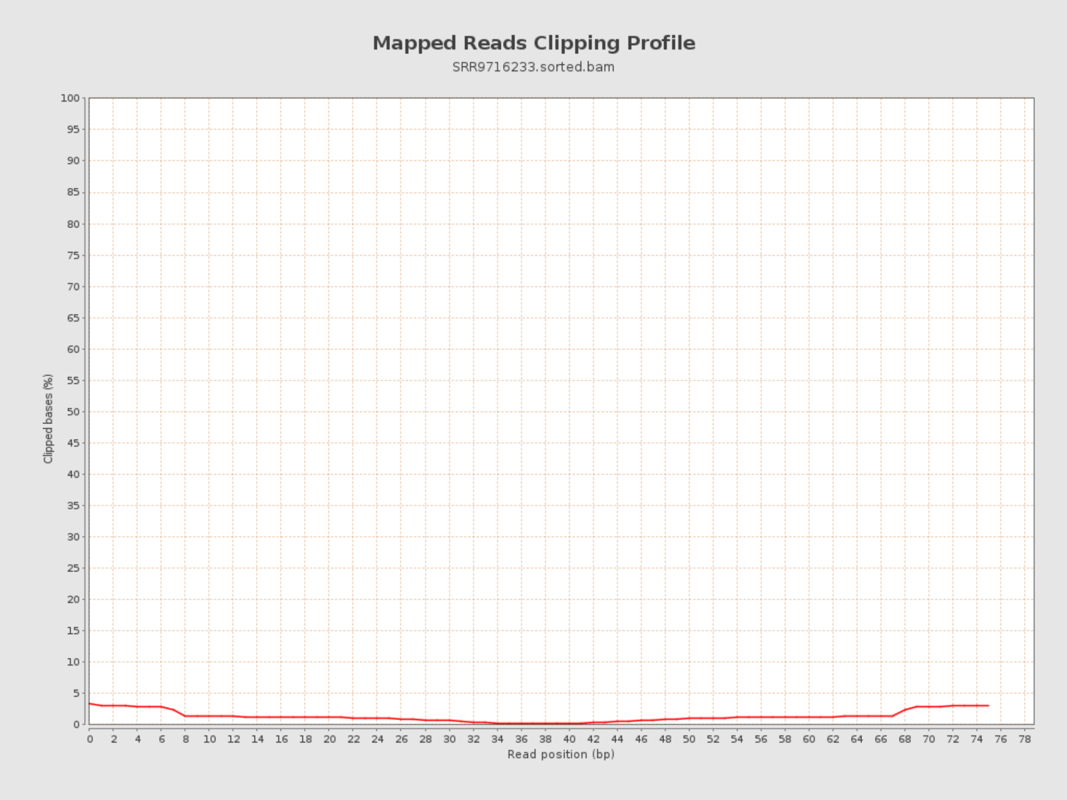
8. Results : Mapped Reads Nucleotide Content



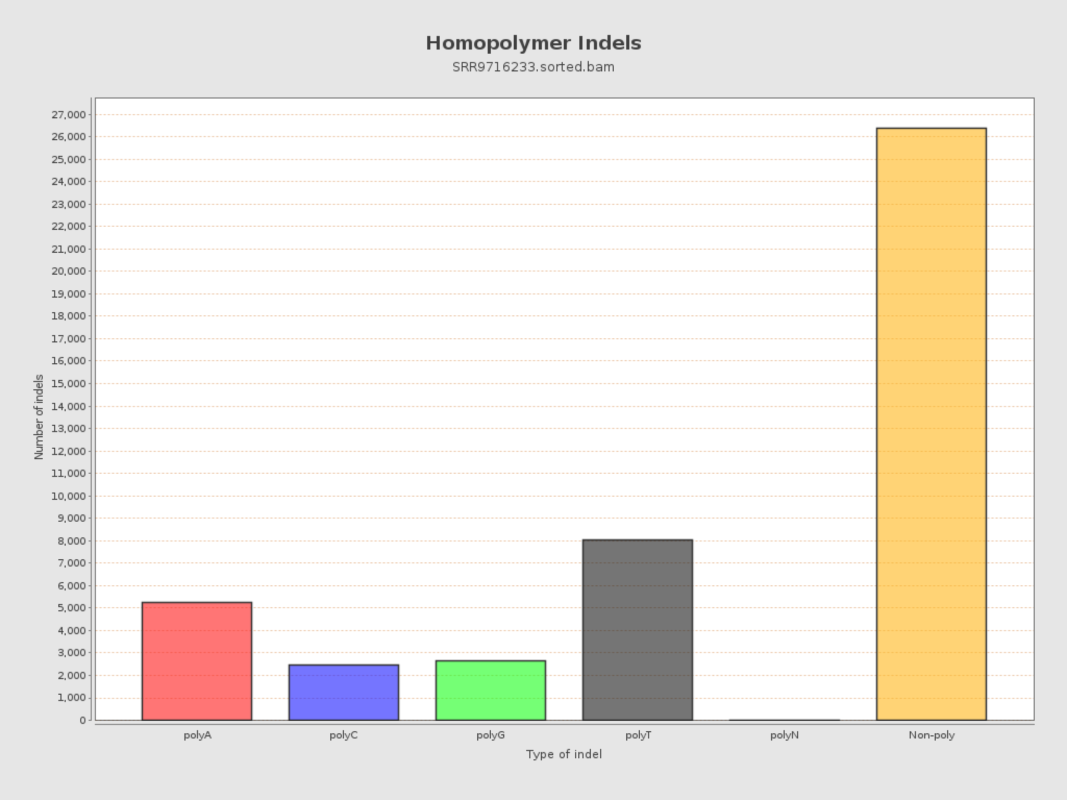
9. Results : Mapped Reads GC-content Distribution



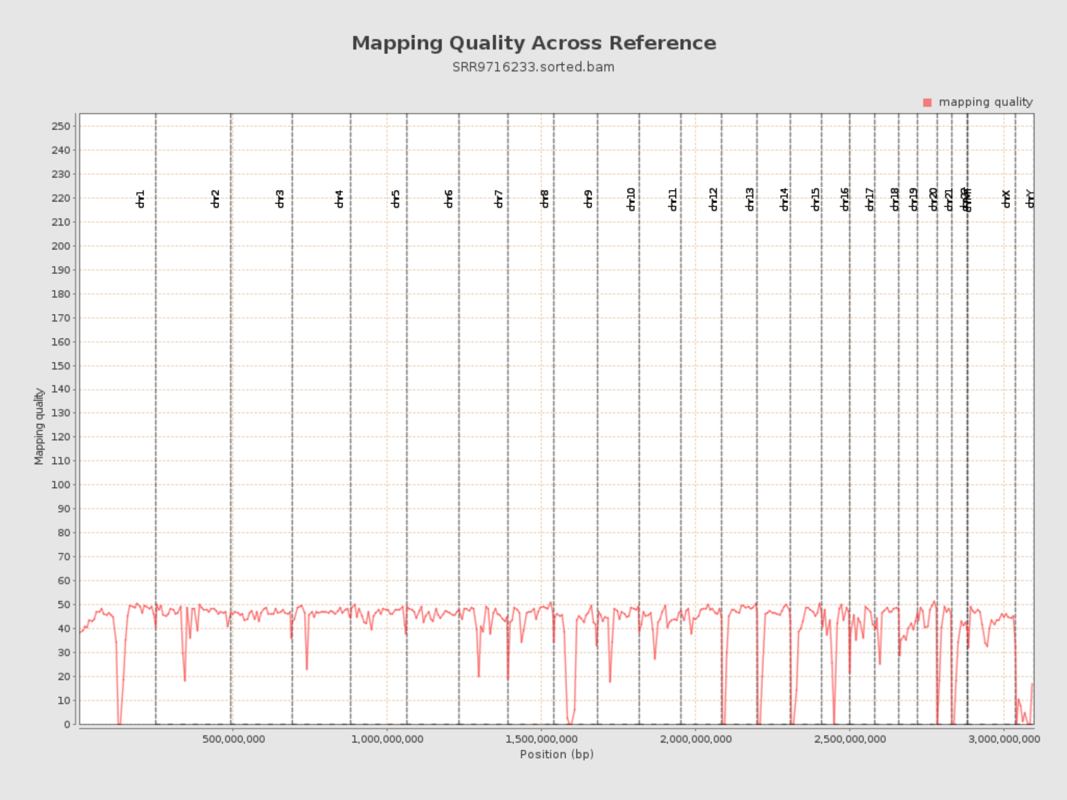
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram