Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:11:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716566.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_SRR9716566 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716566.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:11:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716566.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,445,754
Mapped reads	2,306,100 / 94.29%
Unmapped reads	139,654 / 5.71%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	64,952 / 2.66%
Read min/max/mean length	30 / 101 / 101.97
Duplicated reads (estimated)	121,132 / 4.95%
Duplication rate	3.95%
Clipped reads	2,369,054 / 96.86%

2.2. ACGT Content

Number/percentage of A's	43,724,173 / 24.75%
Number/percentage of C's	37,510,883 / 21.23%
Number/percentage of T's	51,407,184 / 29.1%
Number/percentage of G's	44,008,612 / 24.91%
Number/percentage of N's	6,892 / 0%
GC Percentage	46.15%

2.3. Coverage

Mean	0.0571

Standard Deviation	0.4157

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

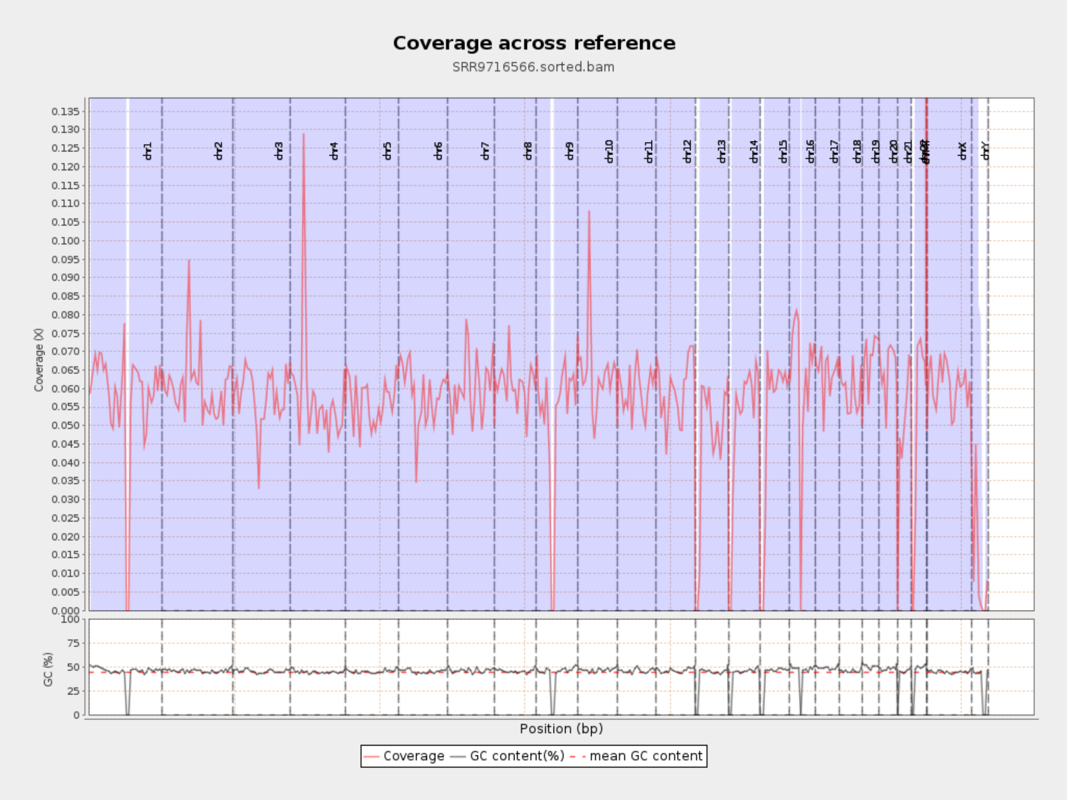
General error rate	0.66%
Mismatches	1,124,772
Insertions	15,006
Mapped reads with at least one insertion	0.64%
Deletions	34,447
Mapped reads with at least one deletion	1.47%
Homopolymer indels	39.5%

2.6. Chromosome stats

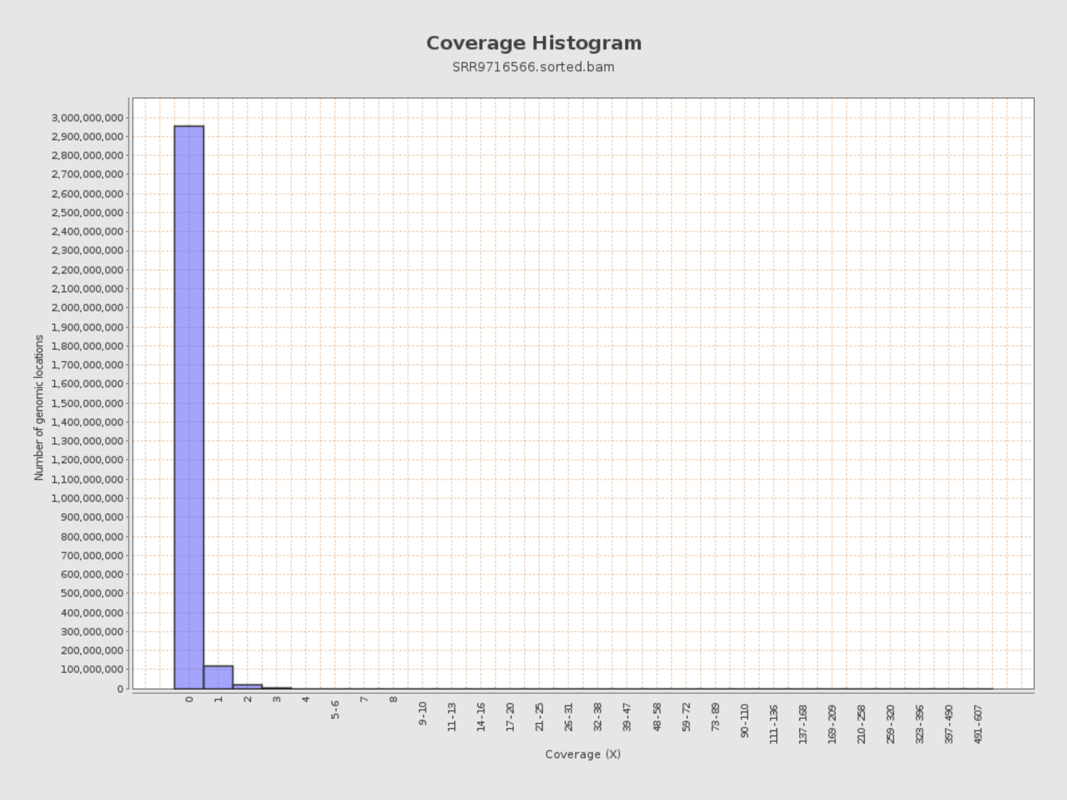
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14267229	0.0572	0.5846
chr2	243199373	14796049	0.0608	0.498
chr3	198022430	11450663	0.0578	0.2837
chr4	191154276	11014686	0.0576	0.4506
chr5	180915260	10192616	0.0563	0.282
chr6	171115067	10047857	0.0587	0.3066
chr7	159138663	9611915	0.0604	0.5259

chr8	146364022	8959626	0.0612	0.4193
chr9	141213431	7274573	0.0515	0.3688
chr10	135534747	8696272	0.0642	0.5893
chr11	135006516	8036102	0.0595	0.4096
chr12	133851895	7980950	0.0596	0.295
chr13	115169878	5107541	0.0443	0.2493
chr14	107349540	5371883	0.05	0.3044
chr15	102531392	5250986	0.0512	0.2699
chr16	90354753	5700911	0.0631	0.342
chr17	81195210	5199761	0.064	0.3443
chr18	78077248	4641889	0.0595	0.6145
chr19	59128983	4038469	0.0683	0.4744
chr20	63025520	4114808	0.0653	0.3364
chr21	48129895	2363551	0.0491	0.3687
chr22	51304566	2484392	0.0484	0.2712
chrMT	16571	38304	2.3115	2.2383
chrX	155270560	9460326	0.0609	0.3252
chrY	59373566	628141	0.0106	0.4533

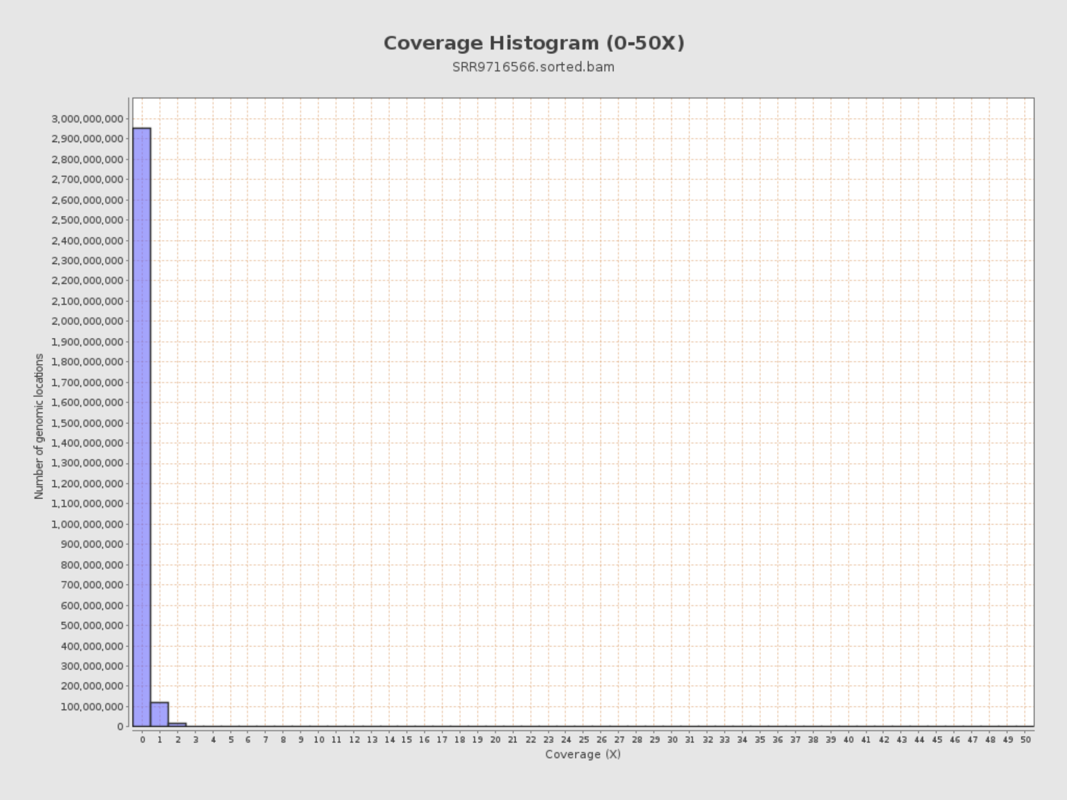
3. Results : Coverage across reference



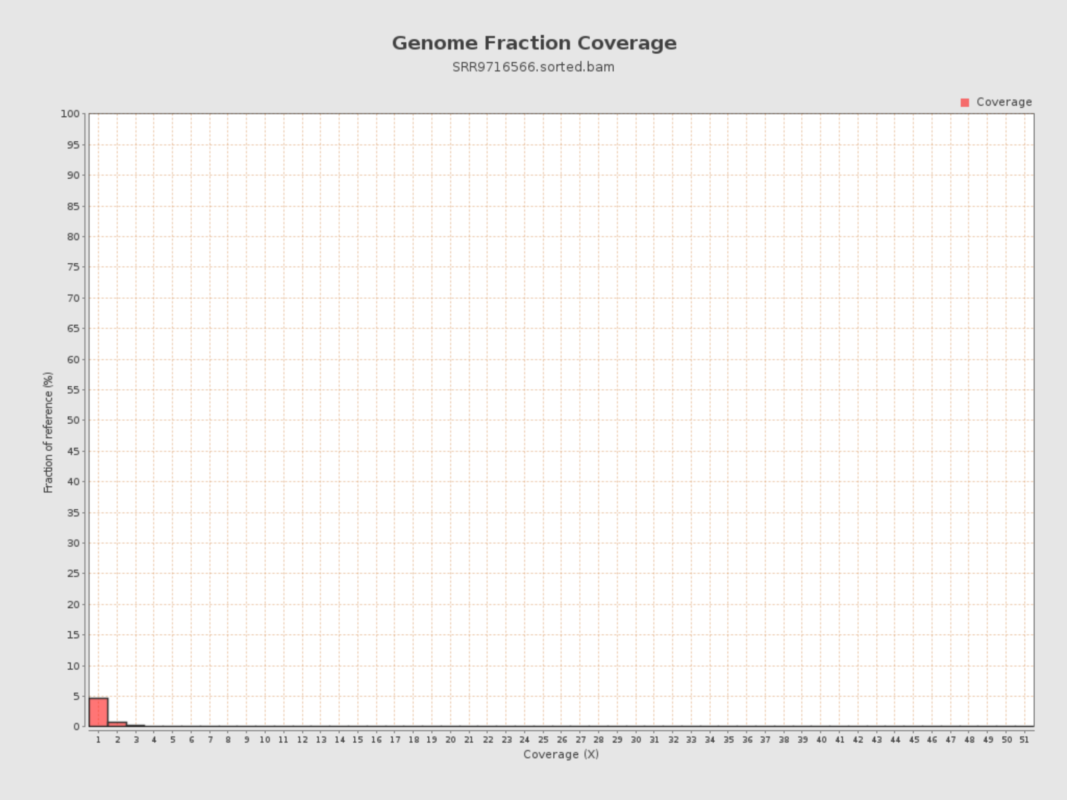
4. Results : Coverage Histogram



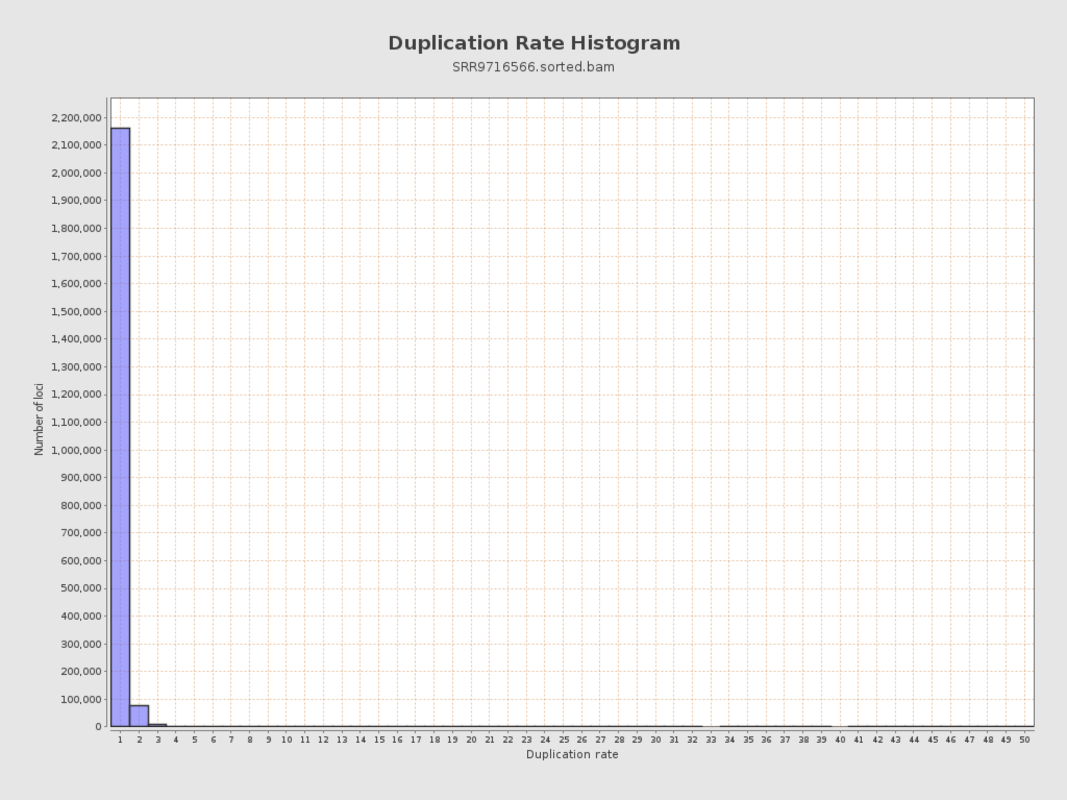
5. Results : Coverage Histogram (0-50X)



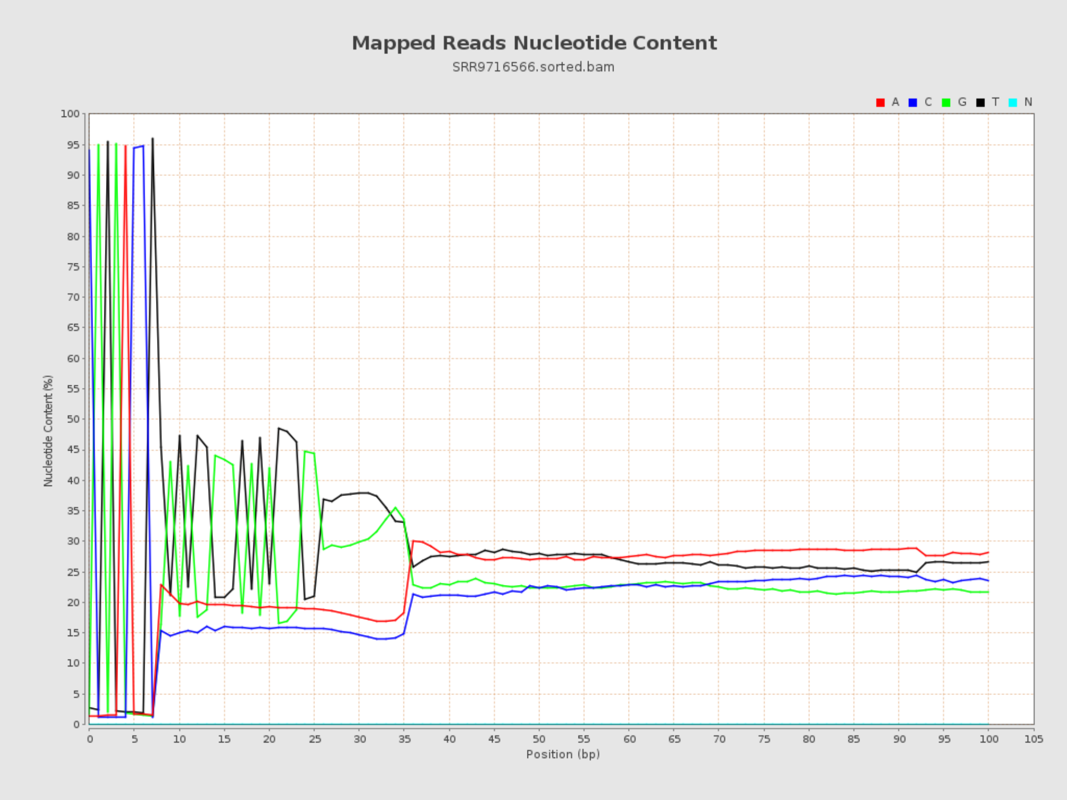
6. Results : Genome Fraction Coverage



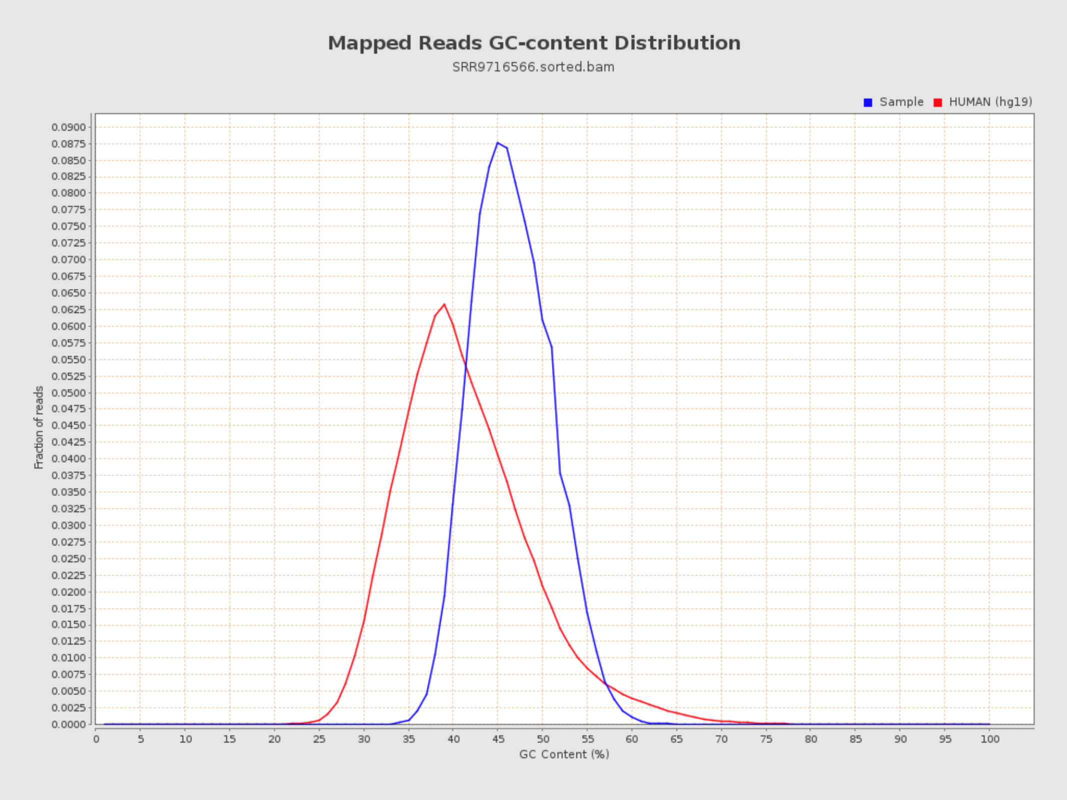
7. Results : Duplication Rate Histogram



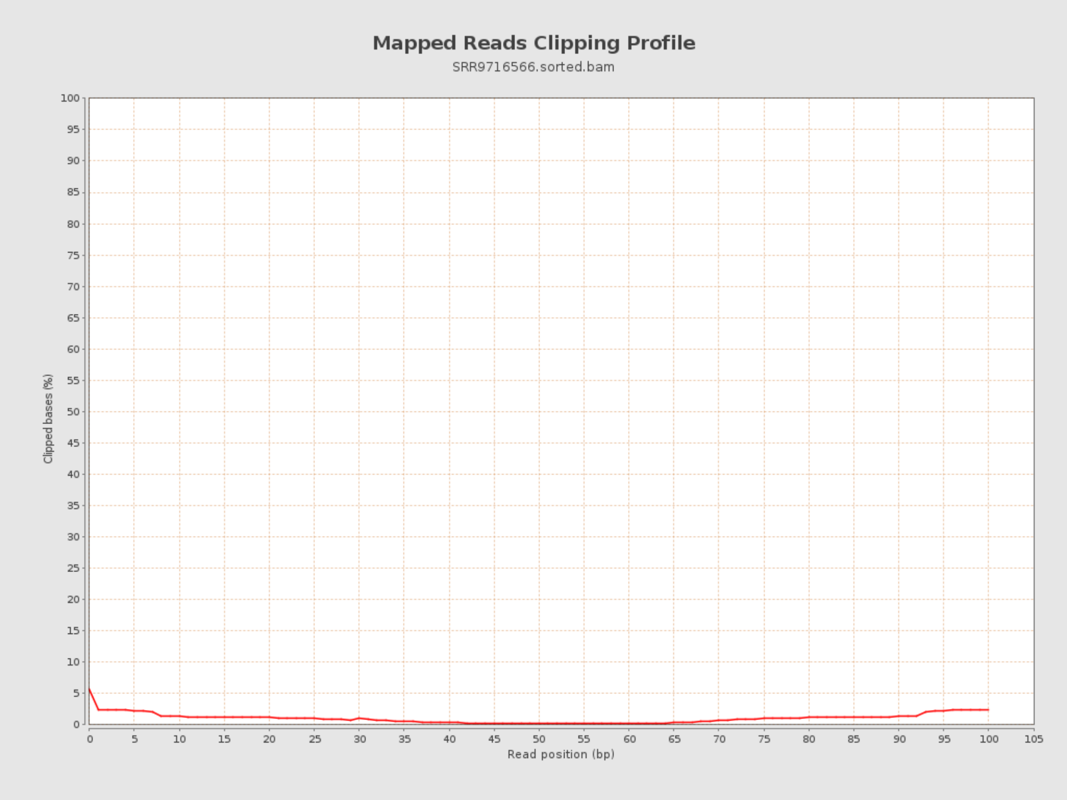
8. Results : Mapped Reads Nucleotide Content



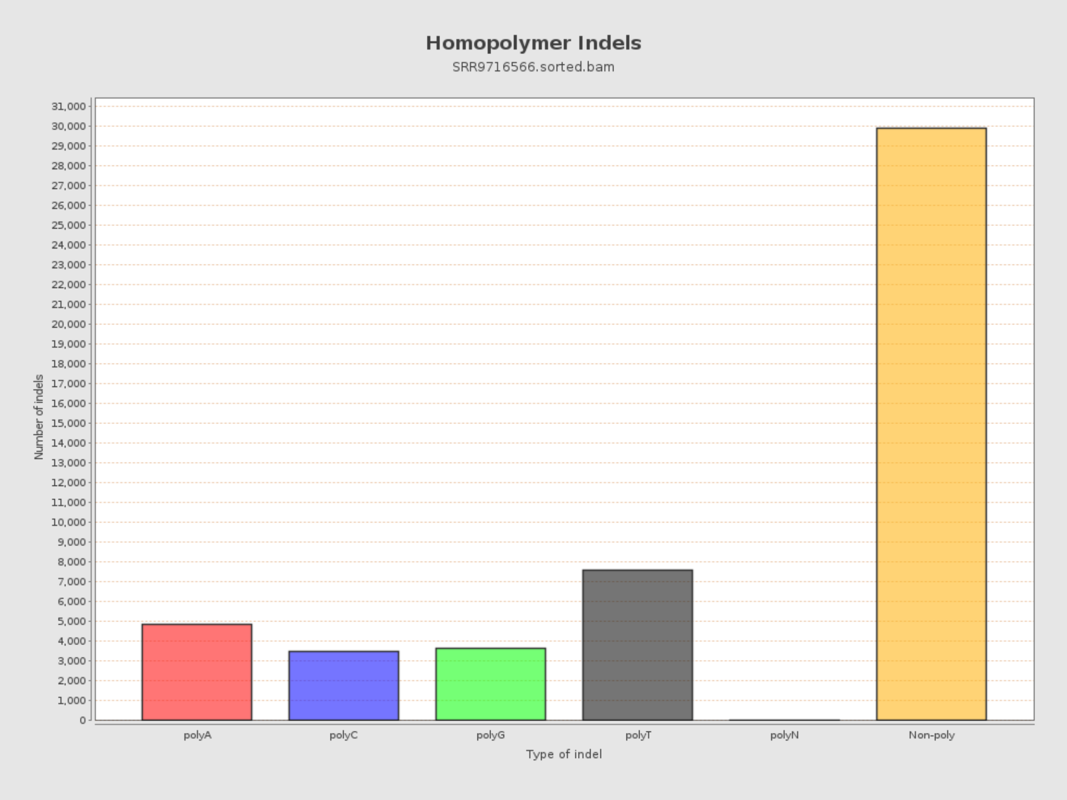
9. Results : Mapped Reads GC-content Distribution



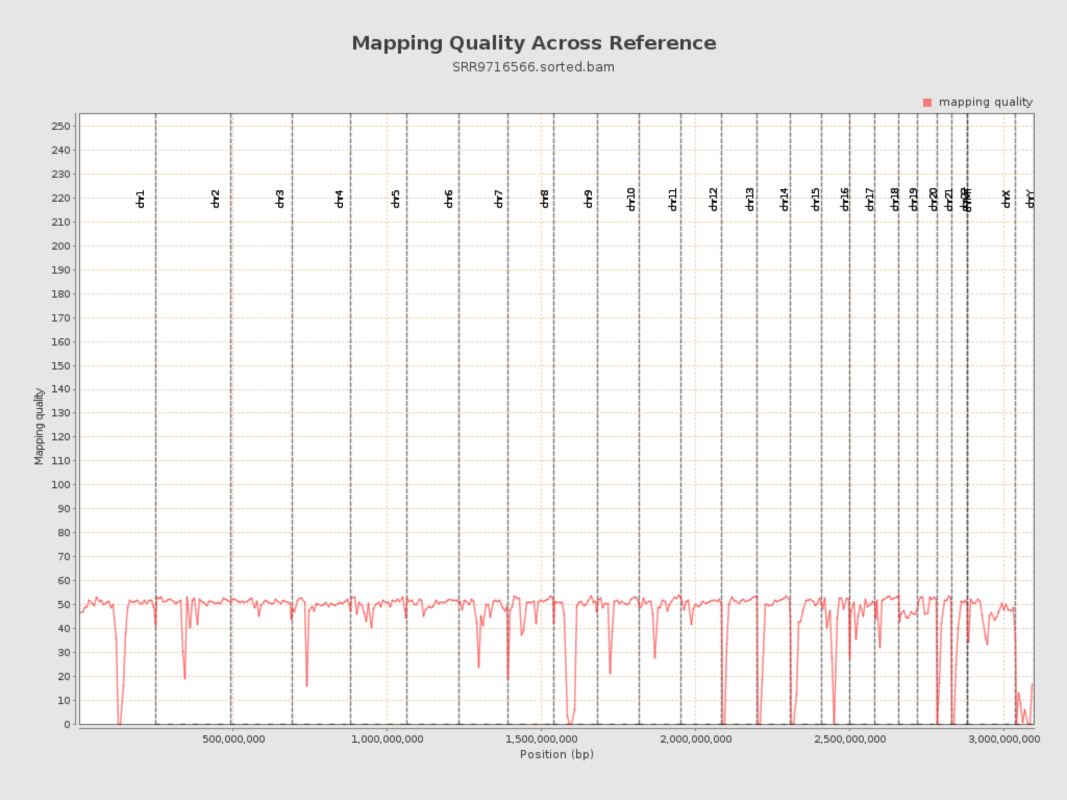
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram