Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 18:06:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716516.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_SRR9716516 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716516.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 18:06:02 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716516.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	534,909
Mapped reads	451,967 / 84.49%
Unmapped reads	82,942 / 15.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,997 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	8,684 / 1.62%
Duplication rate	1.46%
Clipped reads	452,474 / 84.59%

2.2. ACGT Content

Number/percentage of A's	6,836,427 / 26.43%
Number/percentage of C's	4,778,593 / 18.47%
Number/percentage of T's	7,953,252 / 30.74%
Number/percentage of G's	6,300,868 / 24.36%
Number/percentage of N's	768 / 0%
GC Percentage	42.83%

2.3. Coverage

Mean	0.0084

Standard Deviation	0.1121

2.4. Mapping Quality

Mean Mapping Quality	44.39

2.5. Mismatches and indels

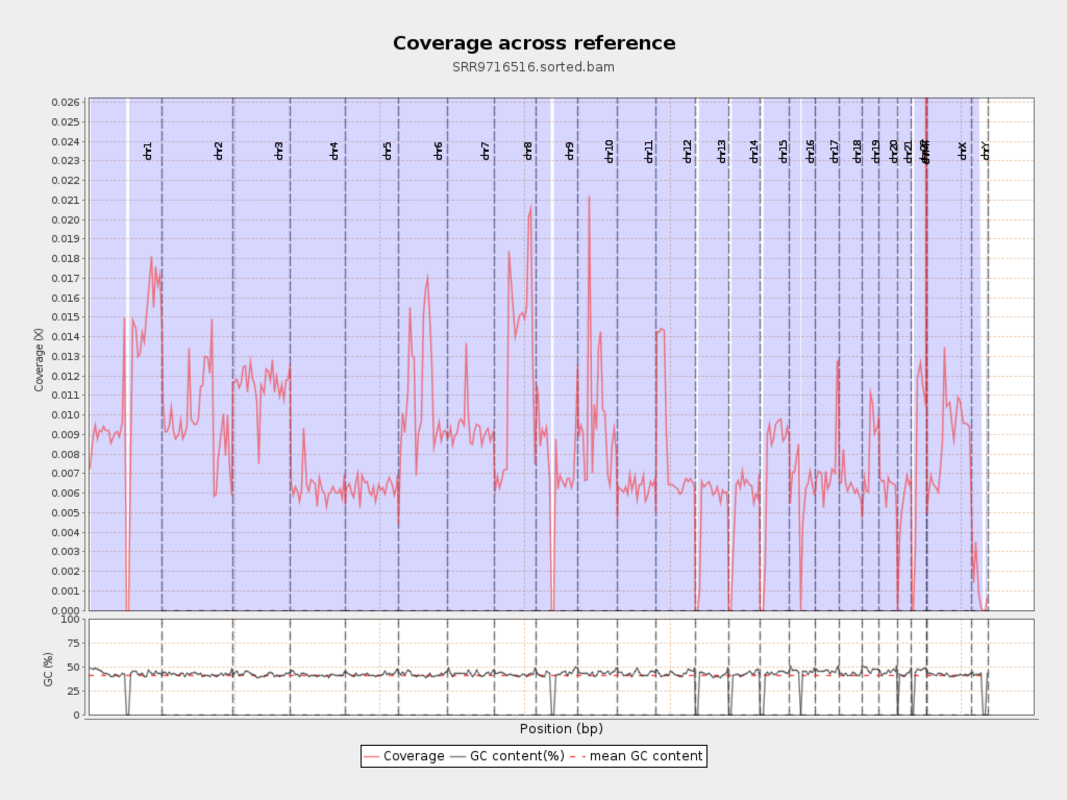
General error rate	0.52%
Mismatches	130,907
Insertions	2,129
Mapped reads with at least one insertion	0.47%
Deletions	4,702
Mapped reads with at least one deletion	1.03%
Homopolymer indels	42.91%

2.6. Chromosome stats

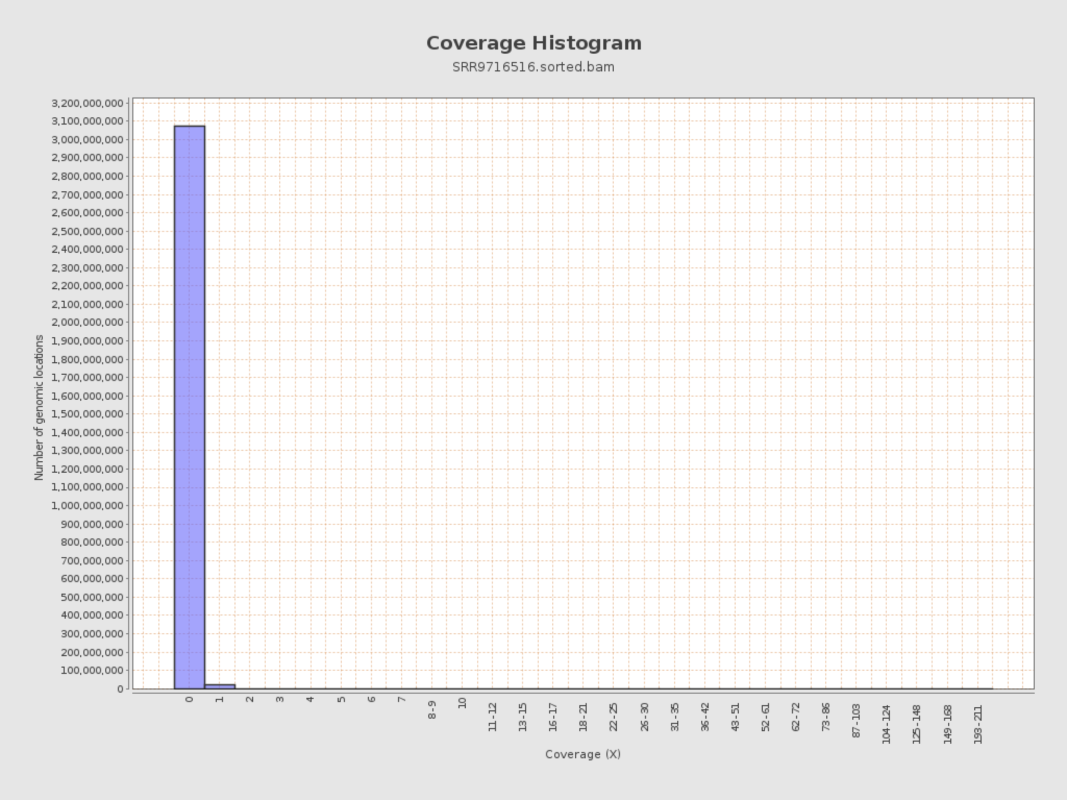
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2791415	0.0112	0.1782
chr2	243199373	2371455	0.0098	0.1333
chr3	198022430	2291258	0.0116	0.1111
chr4	191154276	1200533	0.0063	0.0832
chr5	180915260	1134920	0.0063	0.0819
chr6	171115067	1879204	0.011	0.1172
chr7	159138663	1488464	0.0094	0.1256

chr8	146364022	1860961	0.0127	0.1201
chr9	141213431	985873	0.007	0.0984
chr10	135534747	1332532	0.0098	0.1251
chr11	135006516	848159	0.0063	0.0916
chr12	133851895	1120281	0.0084	0.0953
chr13	115169878	595446	0.0052	0.0743
chr14	107349540	566861	0.0053	0.0777
chr15	102531392	754737	0.0074	0.0886
chr16	90354753	549611	0.0061	0.084
chr17	81195210	615301	0.0076	0.091
chr18	78077248	503177	0.0064	0.1419
chr19	59128983	492630	0.0083	0.133
chr20	63025520	400745	0.0064	0.0824
chr21	48129895	249697	0.0052	0.0759
chr22	51304566	408988	0.008	0.0924
chrMT	16571	6446	0.389	0.6838
chrX	155270560	1363882	0.0088	0.1019
chrY	59373566	64699	0.0011	0.0399

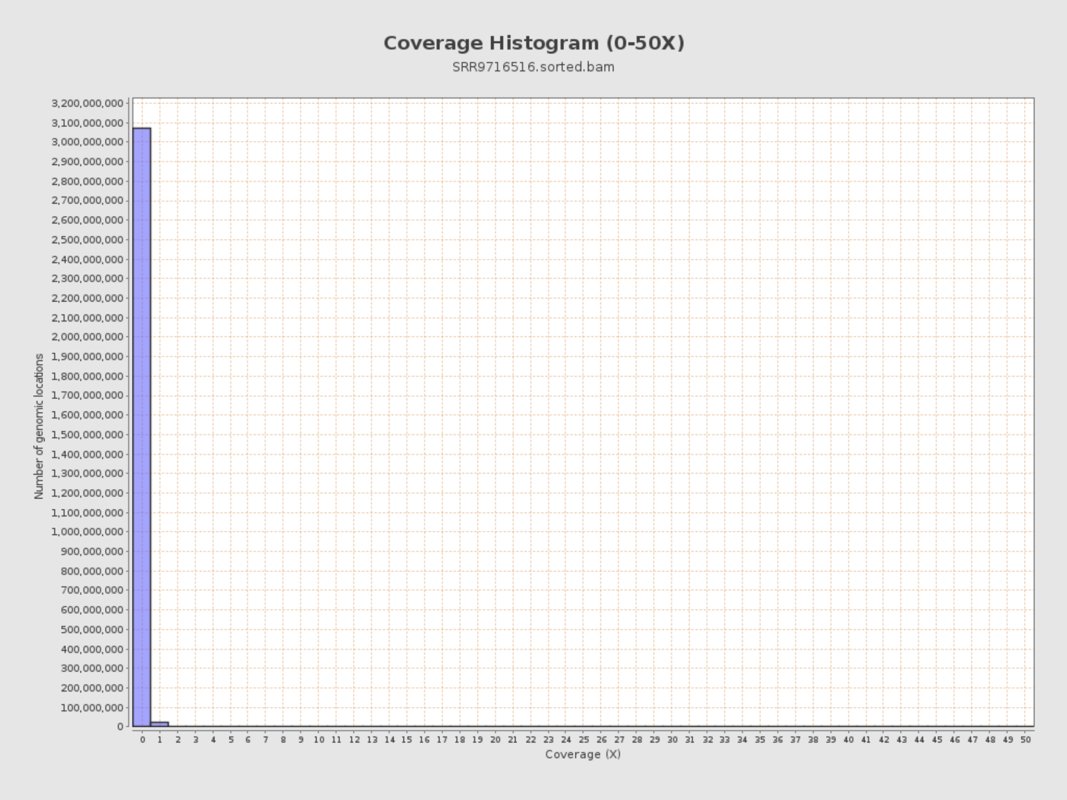
3. Results : Coverage across reference



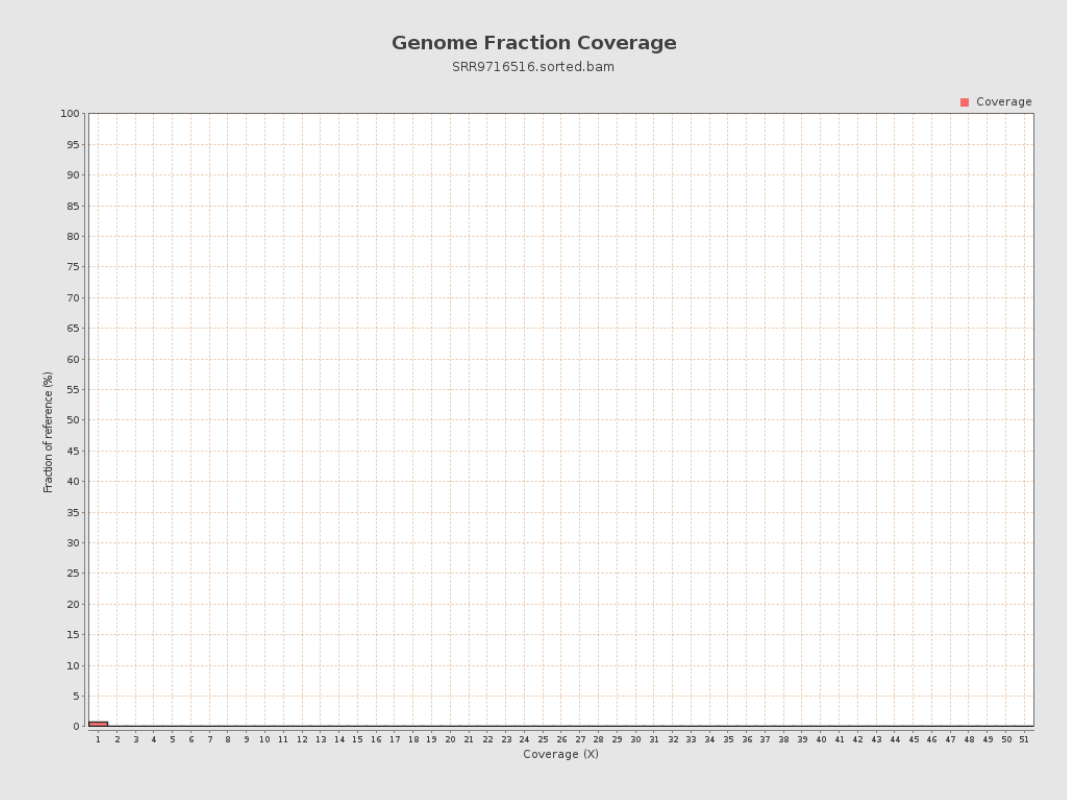
4. Results : Coverage Histogram



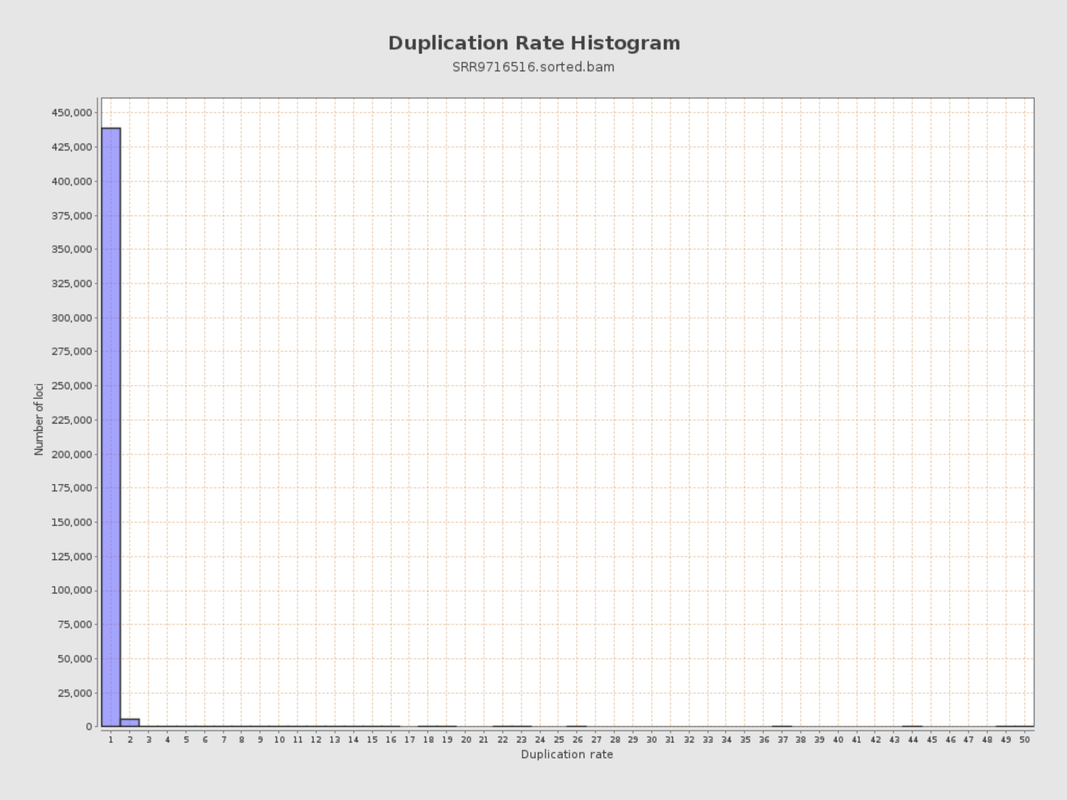
5. Results : Coverage Histogram (0-50X)



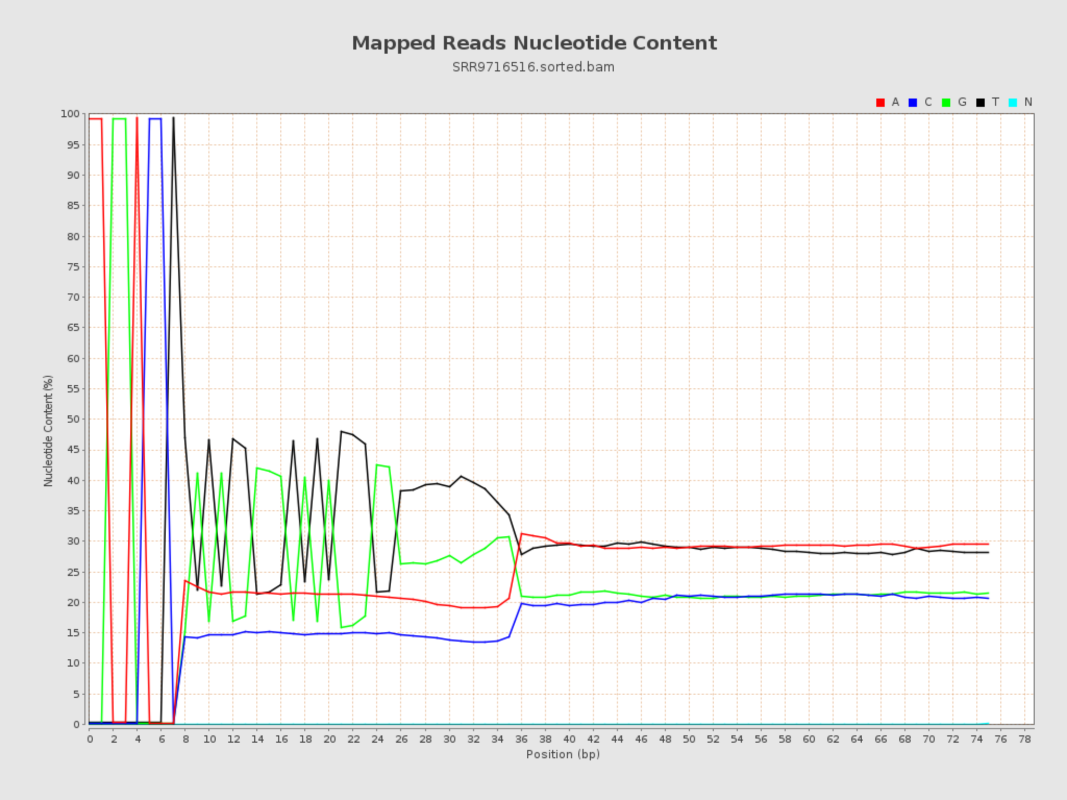
6. Results : Genome Fraction Coverage



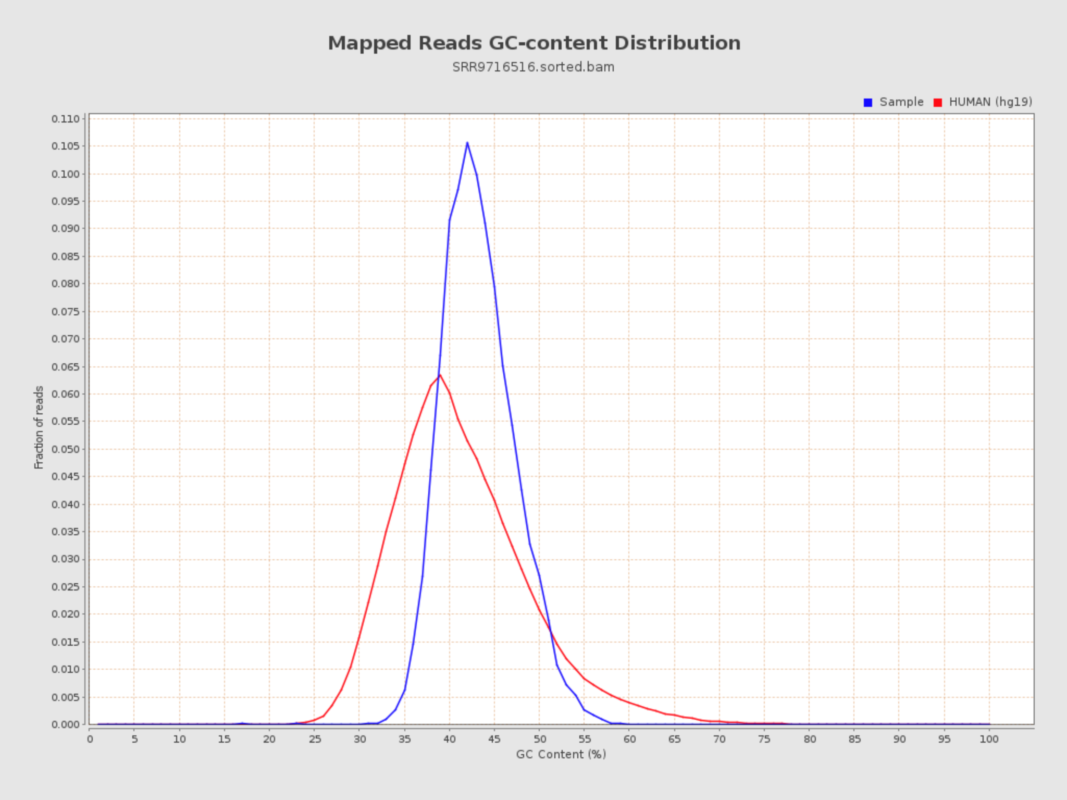
7. Results : Duplication Rate Histogram



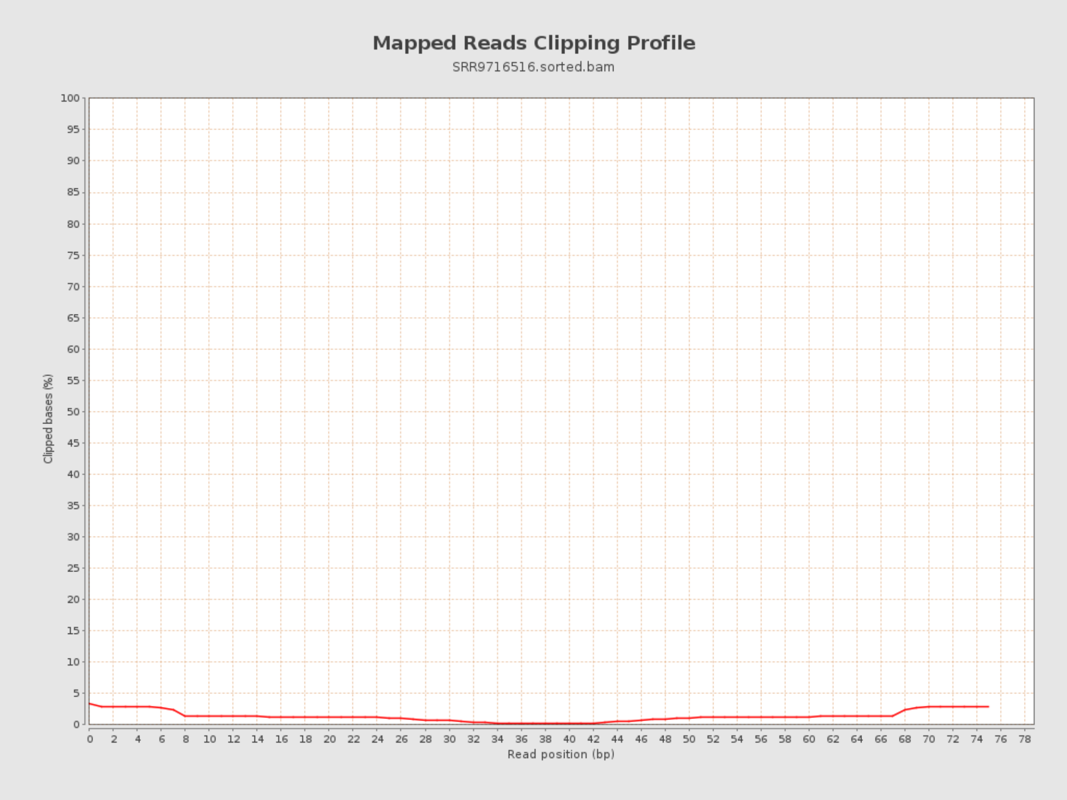
8. Results : Mapped Reads Nucleotide Content



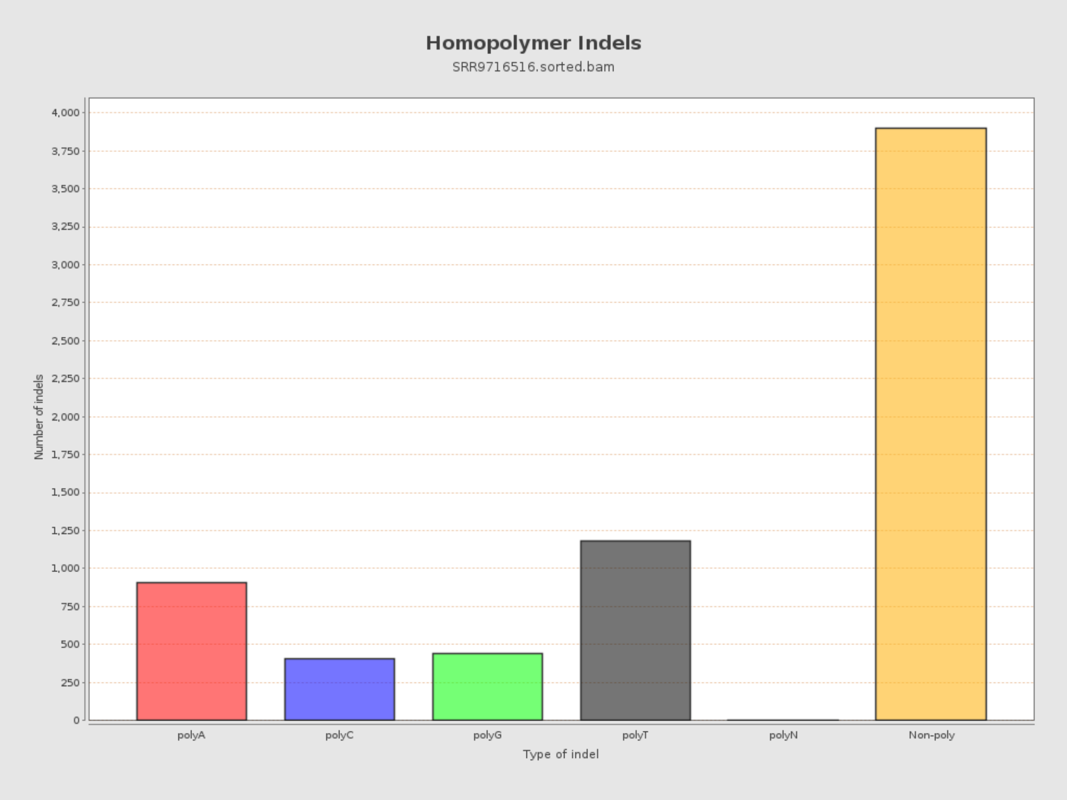
9. Results : Mapped Reads GC-content Distribution



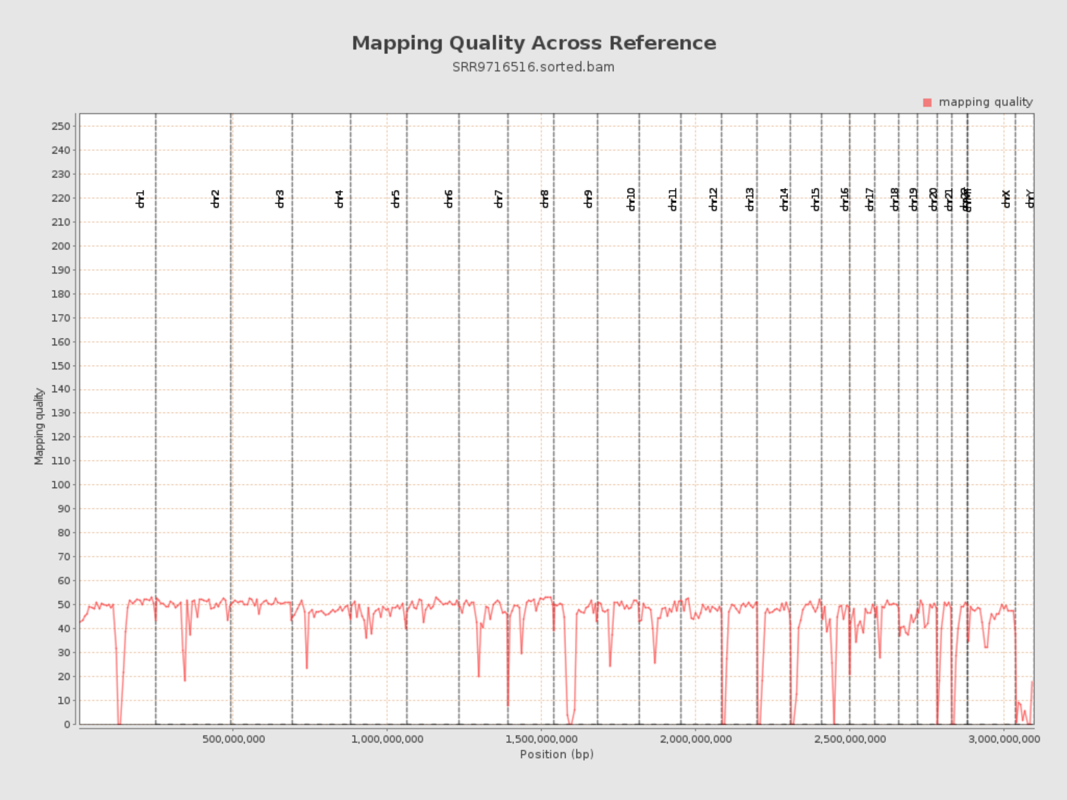
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram