Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 16:15:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716879.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_SRR9716879 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716879.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 16:15:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716879.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	463,645
Mapped reads	363,100 / 78.31%
Unmapped reads	100,545 / 21.69%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	883 / 0.19%
Read min/max/mean length	30 / 76 / 76.06
Duplicated reads (estimated)	5,324 / 1.15%
Duplication rate	1.17%
Clipped reads	363,190 / 78.33%

2.2. ACGT Content

Number/percentage of A's	5,395,808 / 25.5%
Number/percentage of C's	3,967,452 / 18.75%
Number/percentage of T's	6,775,847 / 32.02%
Number/percentage of G's	5,024,486 / 23.74%
Number/percentage of N's	194 / 0%
GC Percentage	42.49%

2.3. Coverage

Mean	0.0068

Standard Deviation	0.0931

2.4. Mapping Quality

Mean Mapping Quality	44.1

2.5. Mismatches and indels

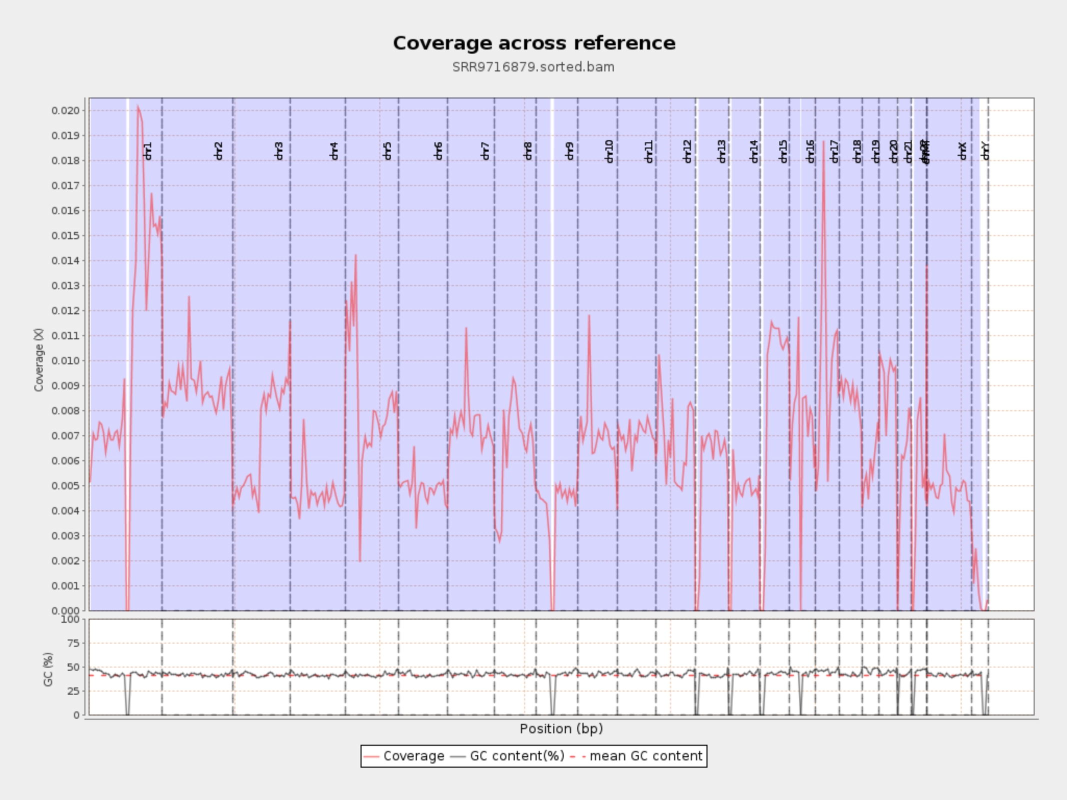
General error rate	0.49%
Mismatches	101,055
Insertions	1,298
Mapped reads with at least one insertion	0.36%
Deletions	4,174
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.12%

2.6. Chromosome stats

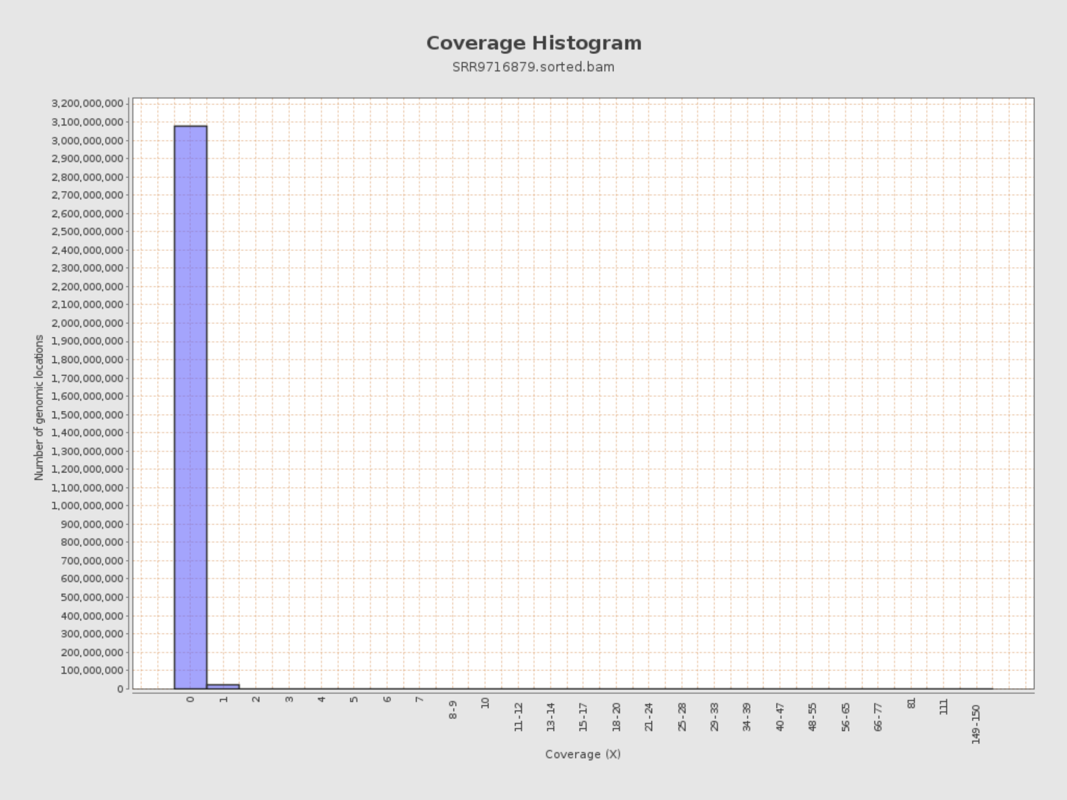
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2544963	0.0102	0.1205
chr2	243199373	2165343	0.0089	0.1192
chr3	198022430	1348173	0.0068	0.0851
chr4	191154276	886595	0.0046	0.0711
chr5	180915260	1509099	0.0083	0.0937
chr6	171115067	834744	0.0049	0.0743
chr7	159138663	1191373	0.0075	0.1157

chr8	146364022	943443	0.0064	0.087
chr9	141213431	567837	0.004	0.0714
chr10	135534747	964921	0.0071	0.0979
chr11	135006516	938449	0.007	0.0916
chr12	133851895	901865	0.0067	0.0846
chr13	115169878	642305	0.0056	0.0765
chr14	107349540	465588	0.0043	0.0684
chr15	102531392	892684	0.0087	0.0963
chr16	90354753	659767	0.0073	0.0902
chr17	81195210	803307	0.0099	0.1039
chr18	78077248	674132	0.0086	0.1156
chr19	59128983	336631	0.0057	0.096
chr20	63025520	579264	0.0092	0.0986
chr21	48129895	273866	0.0057	0.0779
chr22	51304566	234678	0.0046	0.0695
chrMT	16571	229	0.0138	0.1304
chrX	155270560	761021	0.0049	0.0763
chrY	59373566	50009	0.0008	0.0324

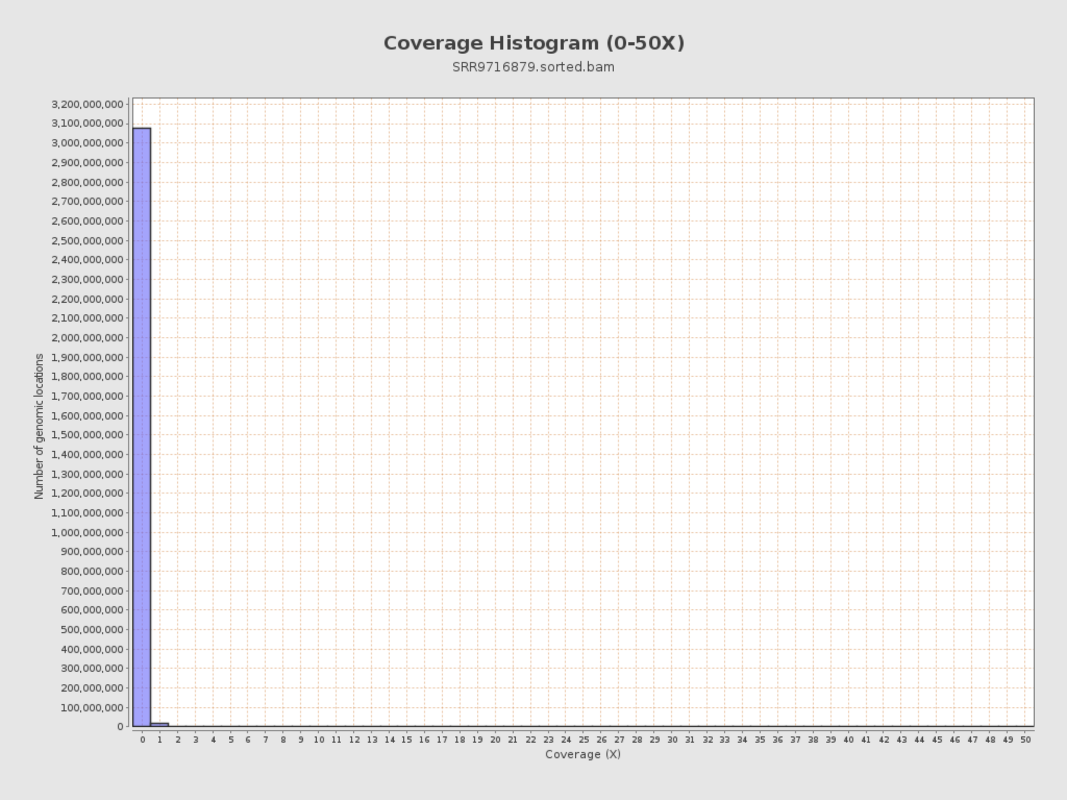
3. Results : Coverage across reference



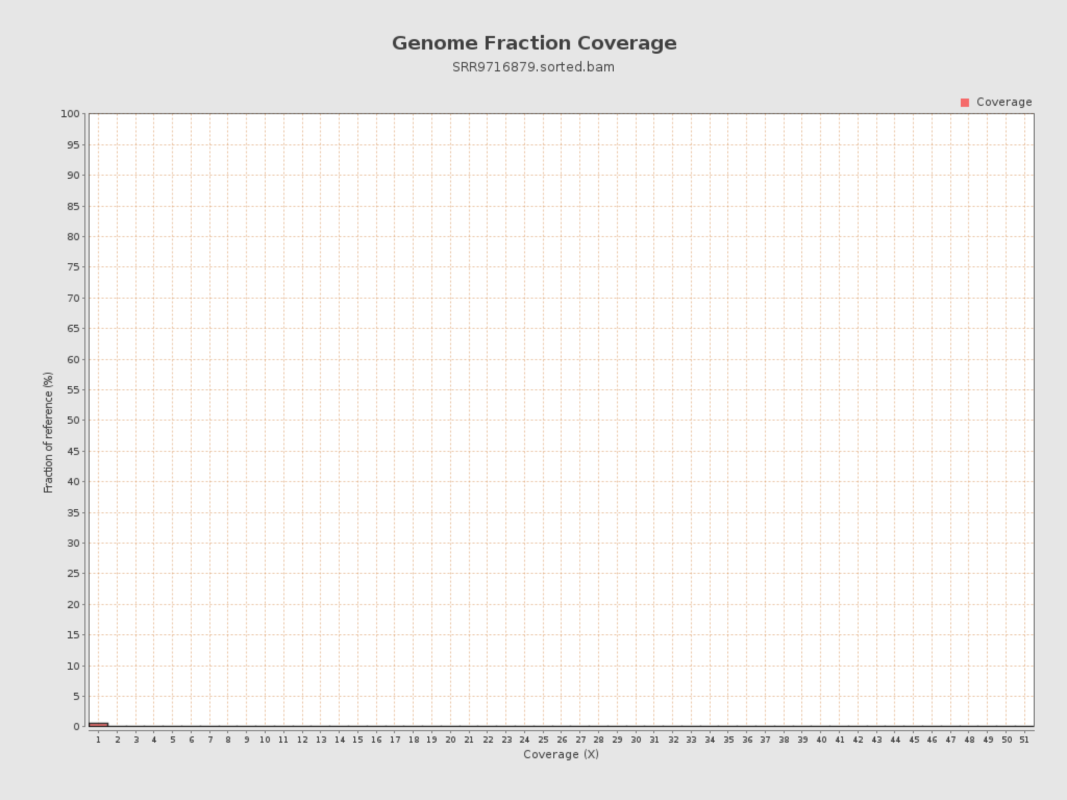
4. Results : Coverage Histogram



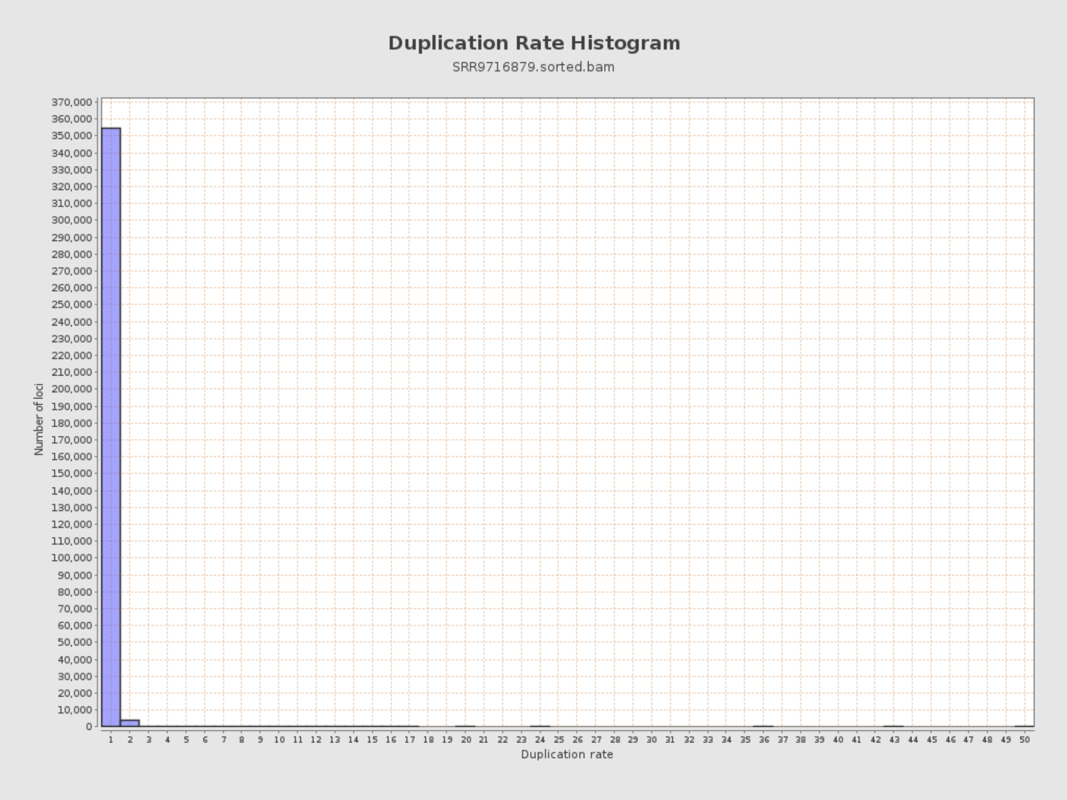
5. Results : Coverage Histogram (0-50X)



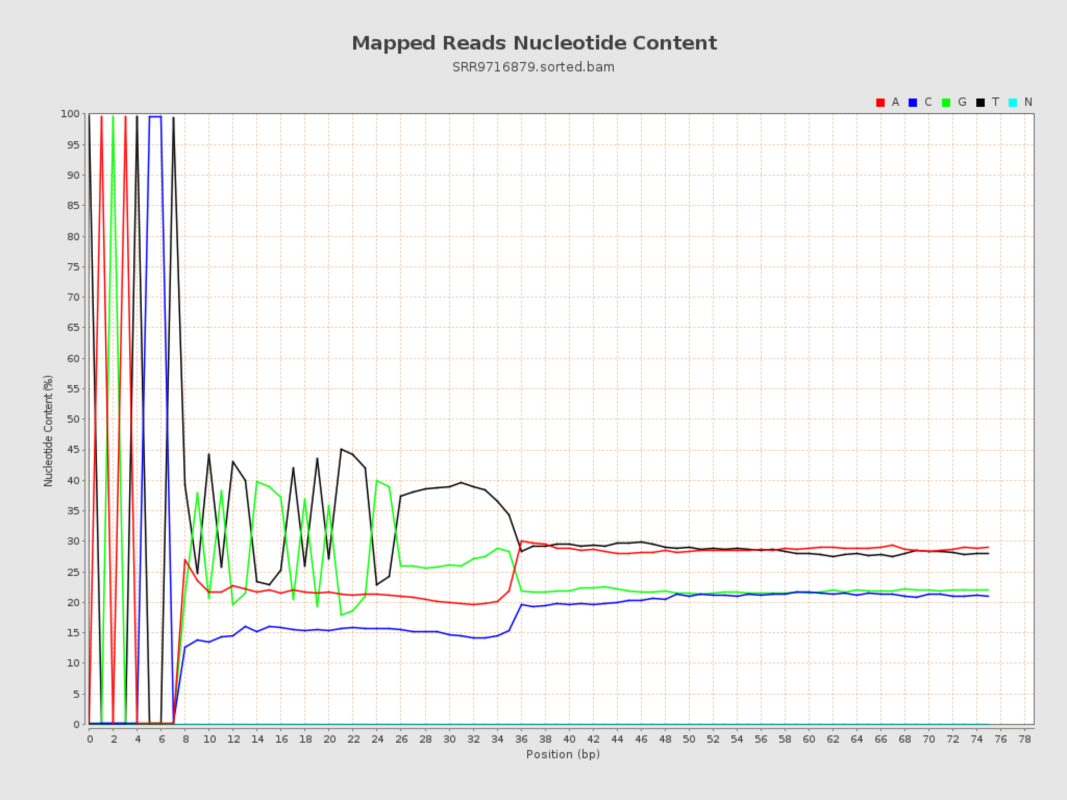
6. Results : Genome Fraction Coverage



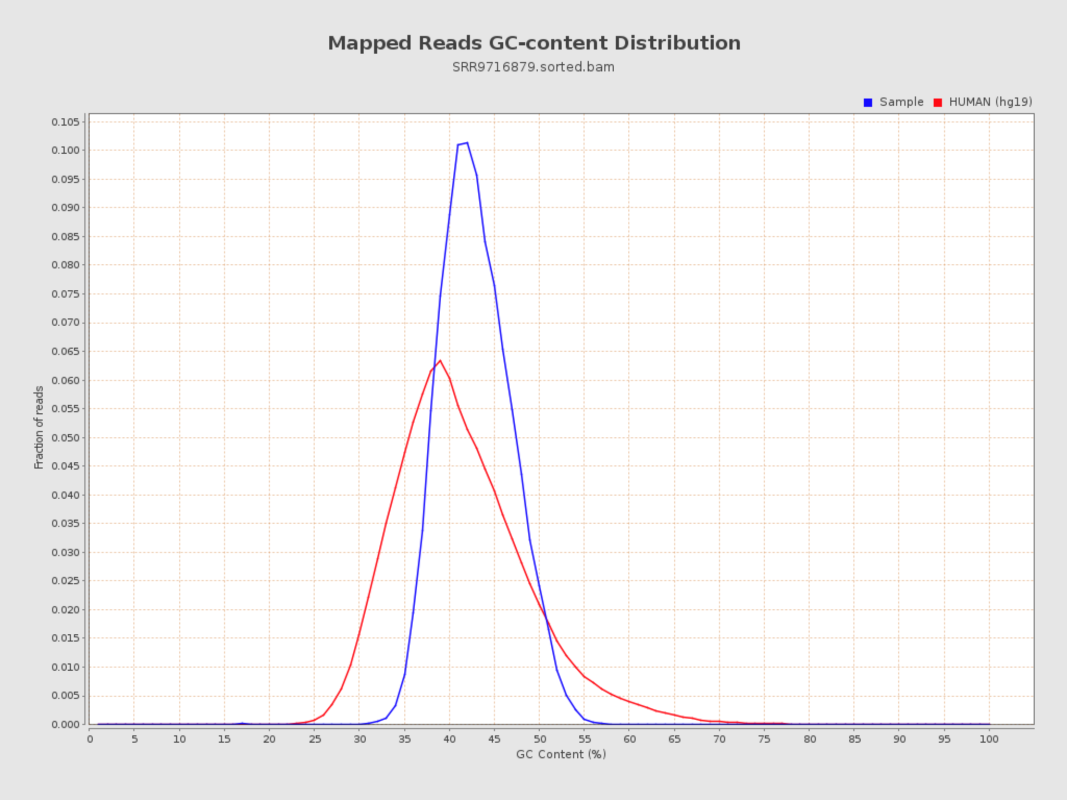
7. Results : Duplication Rate Histogram



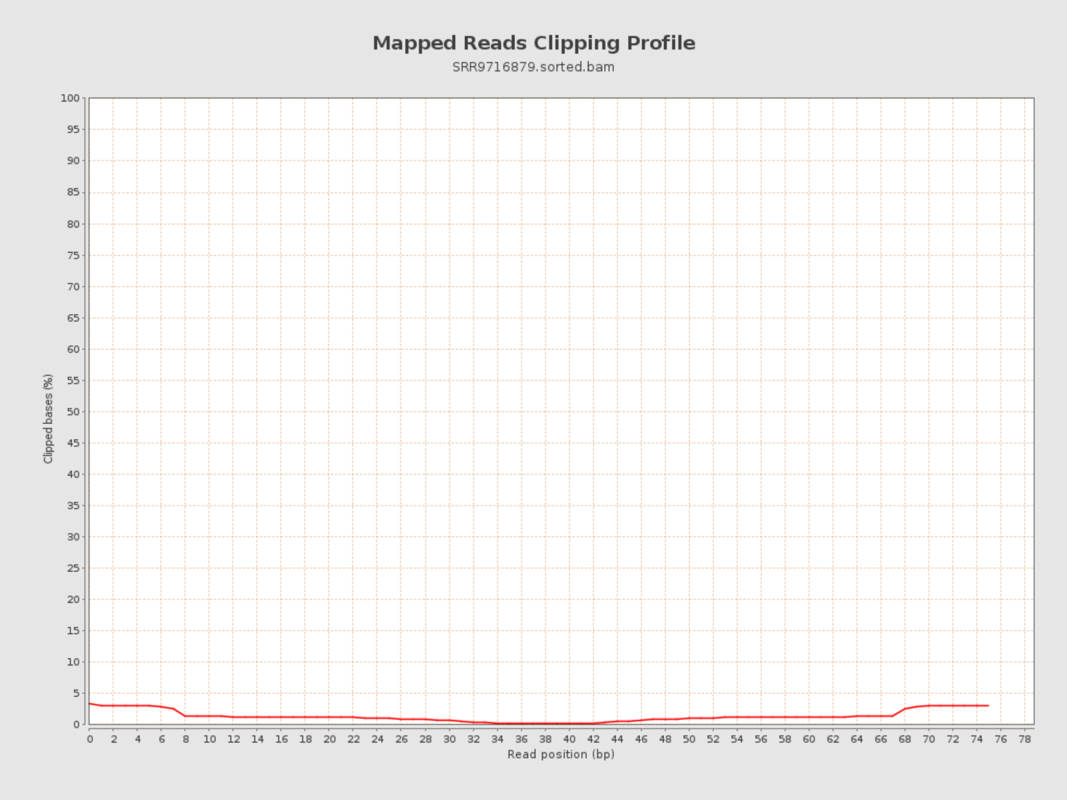
8. Results : Mapped Reads Nucleotide Content



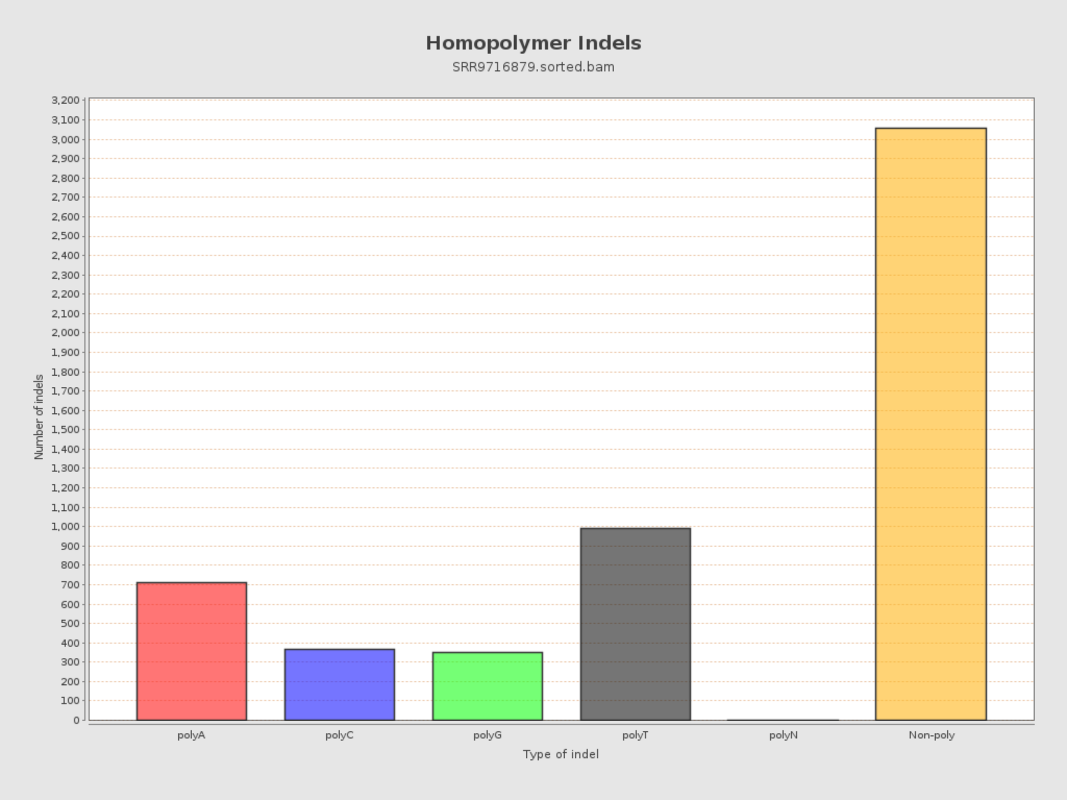
9. Results : Mapped Reads GC-content Distribution



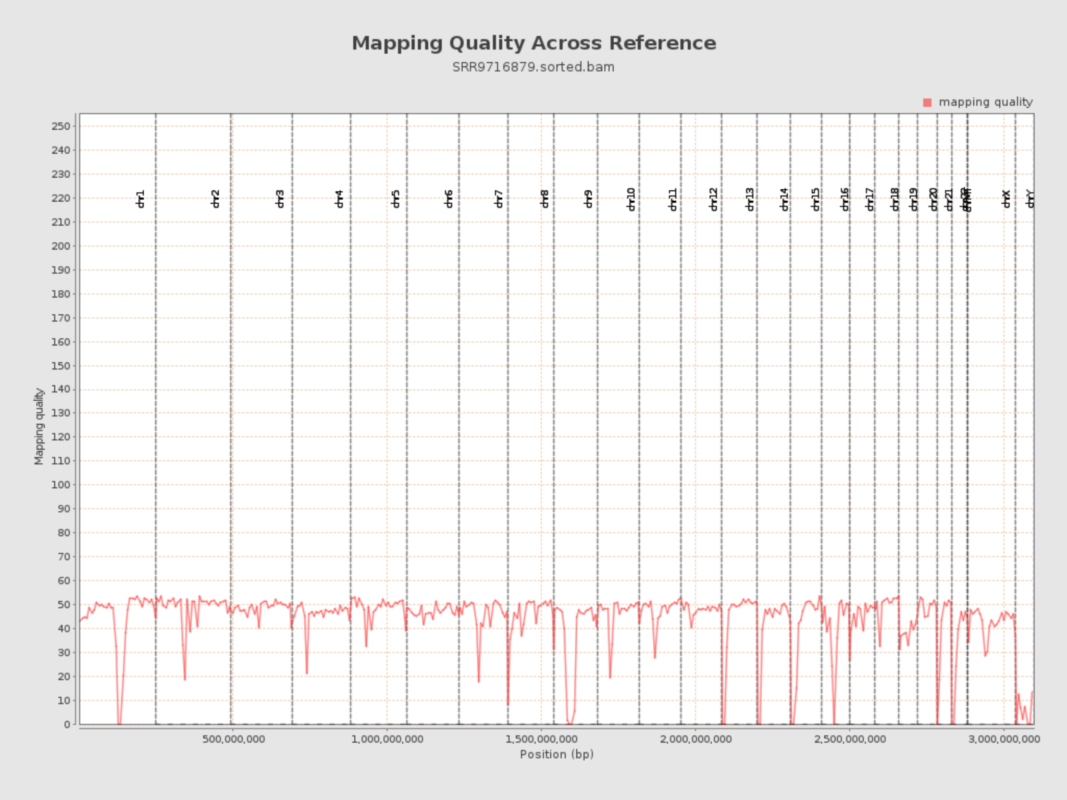
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram