Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:11:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716277.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_SRR9716277 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716277.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:11:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716277.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	32,419,461
Mapped reads	31,644,682 / 97.61%
Unmapped reads	774,779 / 2.39%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,078 / 0.06%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	1,720,831 / 5.31%
Duplication rate	1.68%
Clipped reads	31,528,872 / 97.25%

2.2. ACGT Content

Number/percentage of A's	595,518,737 / 27.8%
Number/percentage of C's	467,796,119 / 21.84%
Number/percentage of T's	621,014,070 / 28.99%
Number/percentage of G's	457,418,833 / 21.35%
Number/percentage of N's	358,528 / 0.02%
GC Percentage	43.19%

2.3. Coverage

Mean	0.6921

Standard Deviation	7.1777

2.4. Mapping Quality

Mean Mapping Quality	48.78

2.5. Mismatches and indels

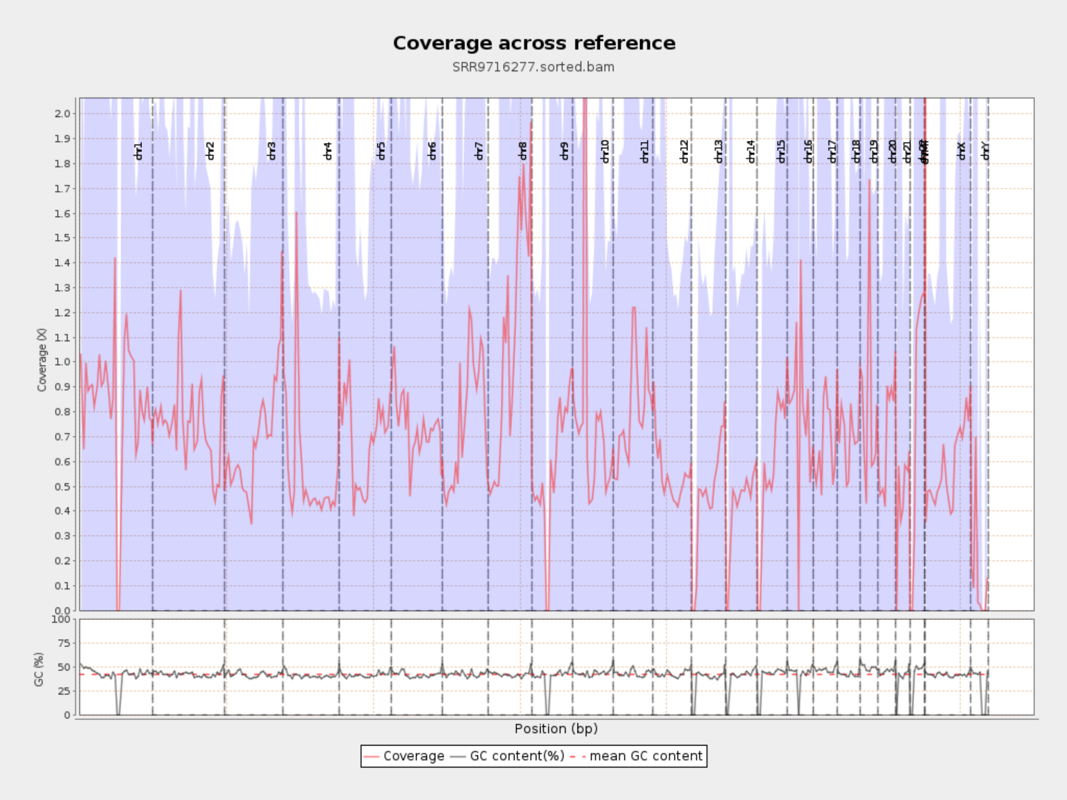
General error rate	0.38%
Mismatches	7,625,950
Insertions	182,351
Mapped reads with at least one insertion	0.57%
Deletions	187,509
Mapped reads with at least one deletion	0.59%
Homopolymer indels	36.72%

2.6. Chromosome stats

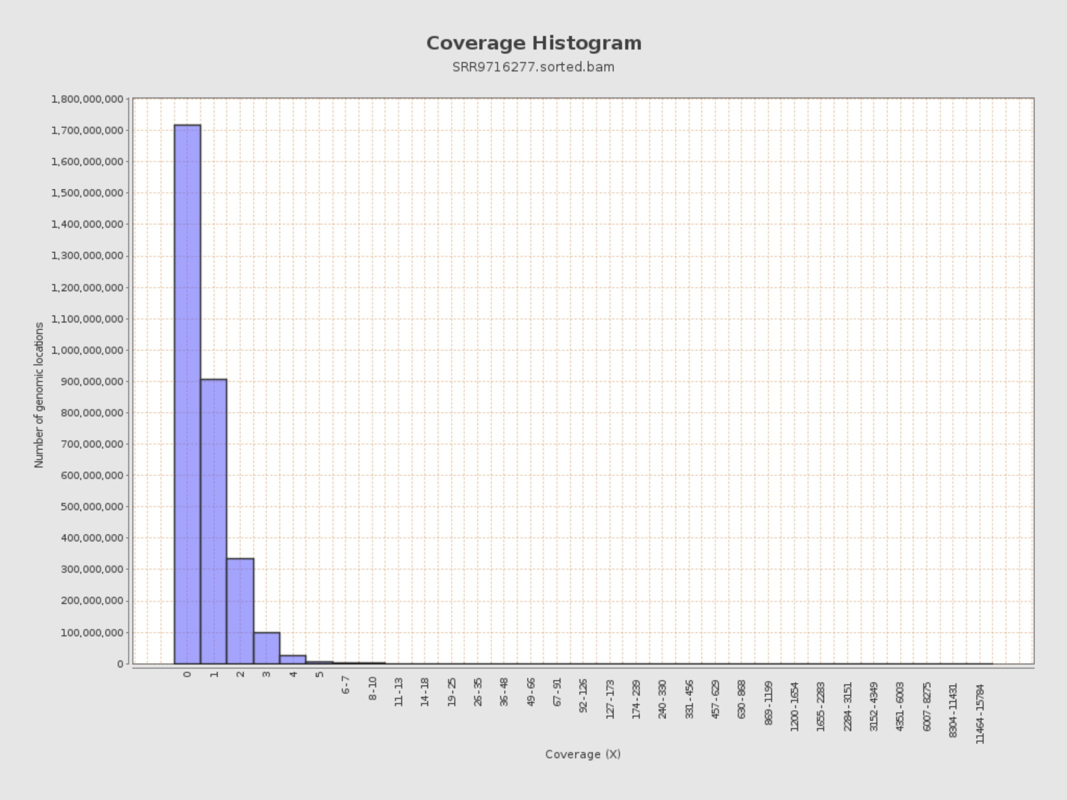
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	211065425	0.8468	14.0537
chr2	243199373	183185572	0.7532	5.7198
chr3	198022430	133861753	0.676	3.7797
chr4	191154276	105413240	0.5515	4.9611
chr5	180915260	125095059	0.6915	1.0844
chr6	171115067	128287071	0.7497	2.2706
chr7	159138663	122486697	0.7697	5.0887

chr8	146364022	161547659	1.1037	4.1413
chr9	141213431	80910026	0.573	2.9749
chr10	135534747	111005317	0.819	22.0551
chr11	135006516	110378147	0.8176	2.6619
chr12	133851895	73523392	0.5493	1.1969
chr13	115169878	52348472	0.4545	0.768
chr14	107349540	44711999	0.4165	1.2868
chr15	102531392	56907529	0.555	0.8748
chr16	90354753	72574279	0.8032	5.4487
chr17	81195210	55905663	0.6885	2.0922
chr18	78077248	54533490	0.6985	6.3289
chr19	59128983	47449606	0.8025	9.931
chr20	63025520	44080222	0.6994	1.927
chr21	48129895	22473552	0.4669	4.6587
chr22	51304566	42377682	0.826	1.411
chrMT	16571	4894745	295.3802	80.5168
chrX	155270560	89007153	0.5732	1.7768
chrY	59373566	8454481	0.1424	6.9801

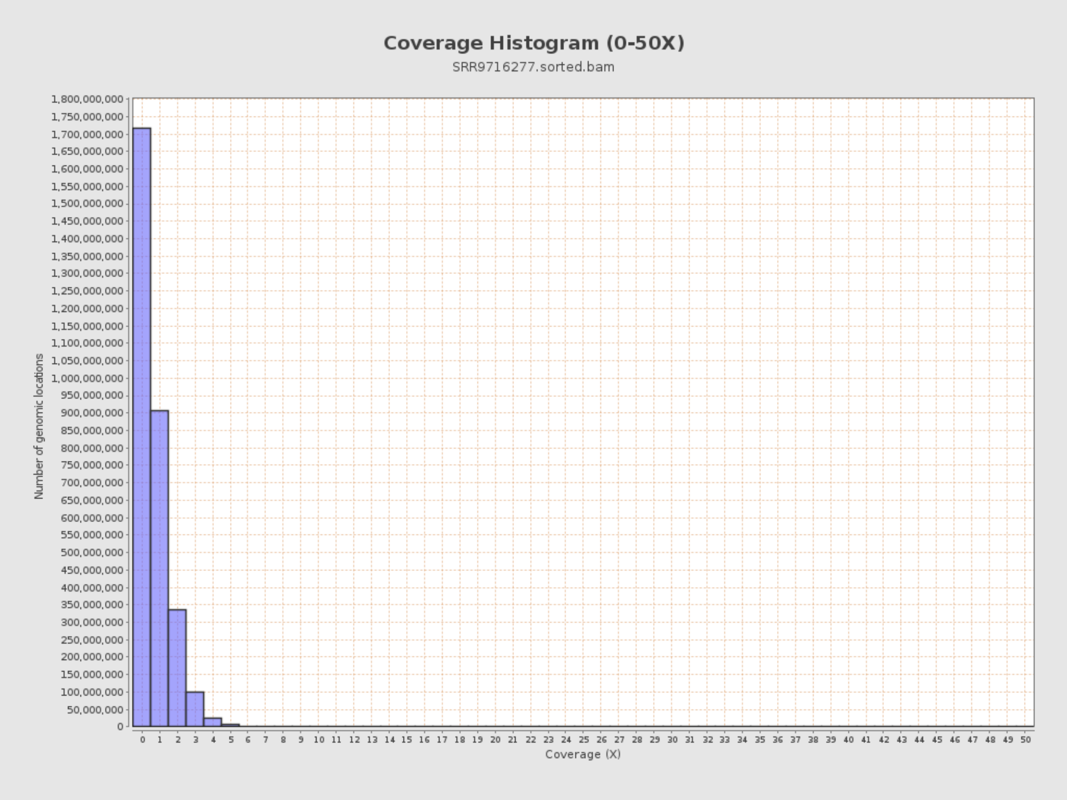
3. Results : Coverage across reference



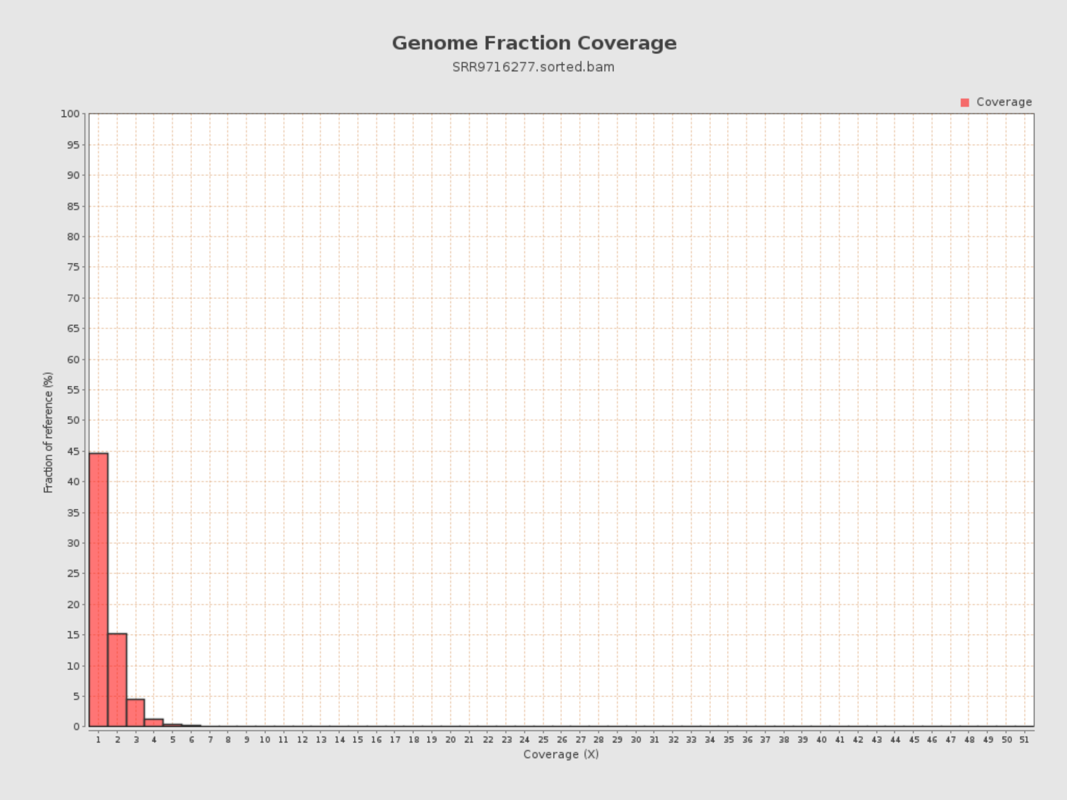
4. Results : Coverage Histogram



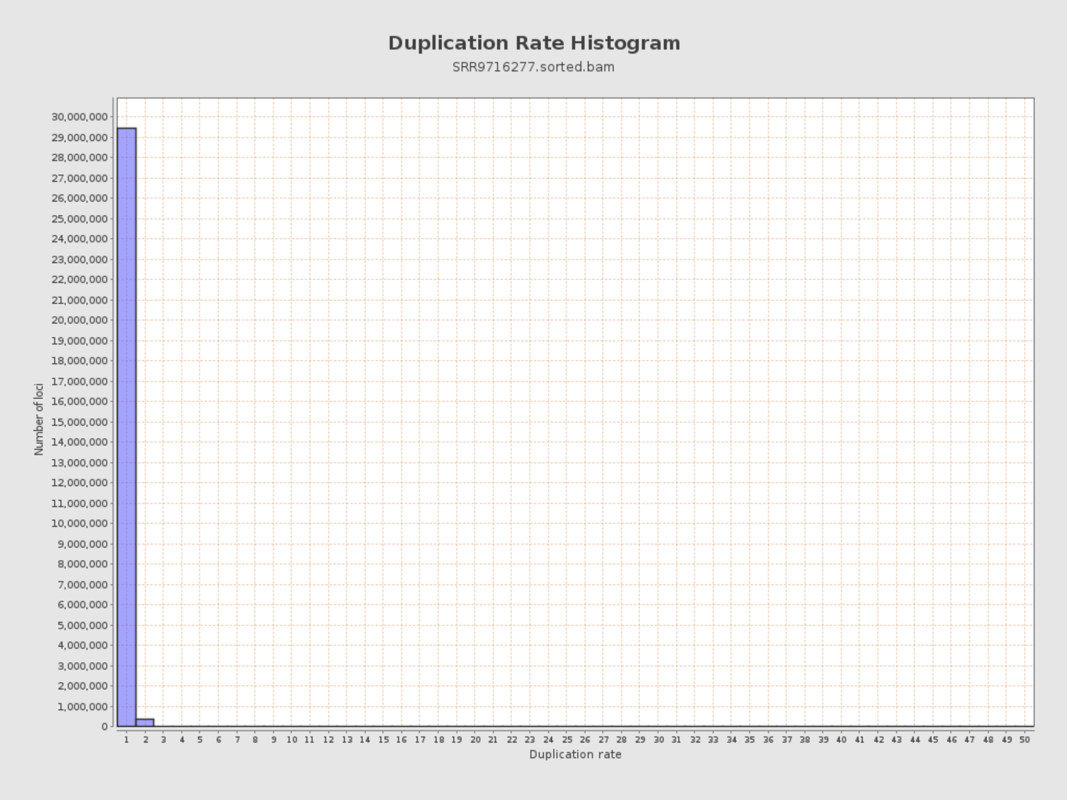
5. Results : Coverage Histogram (0-50X)



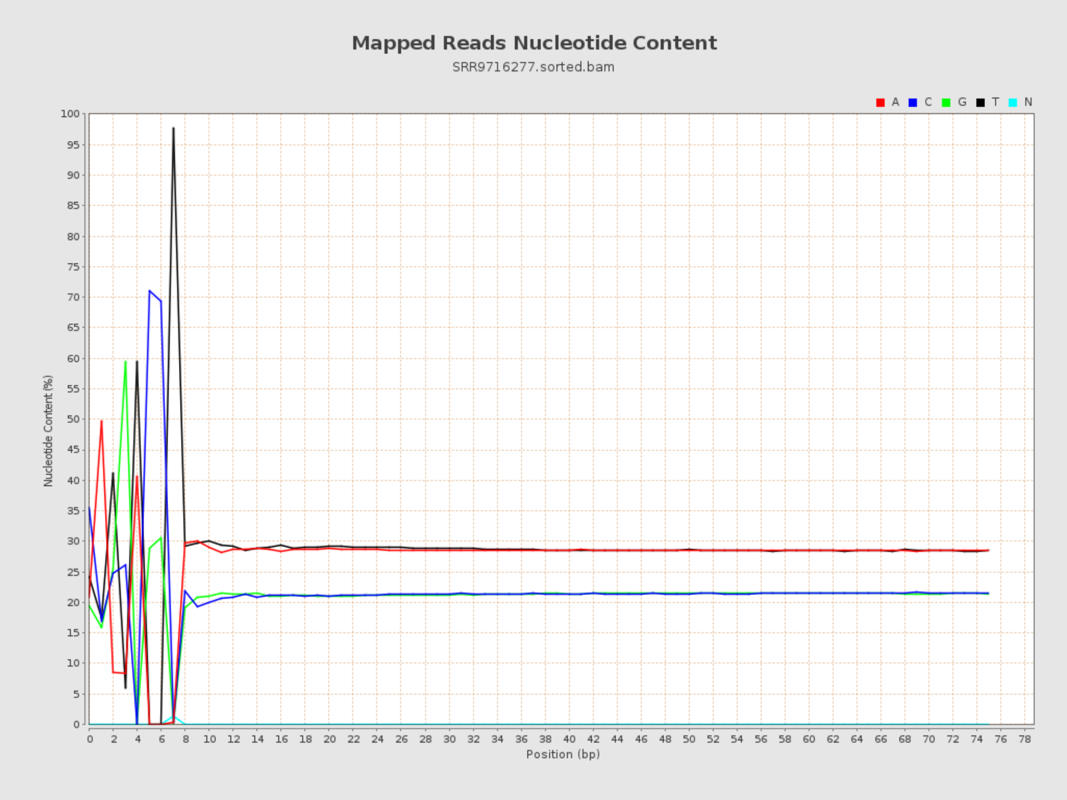
6. Results : Genome Fraction Coverage



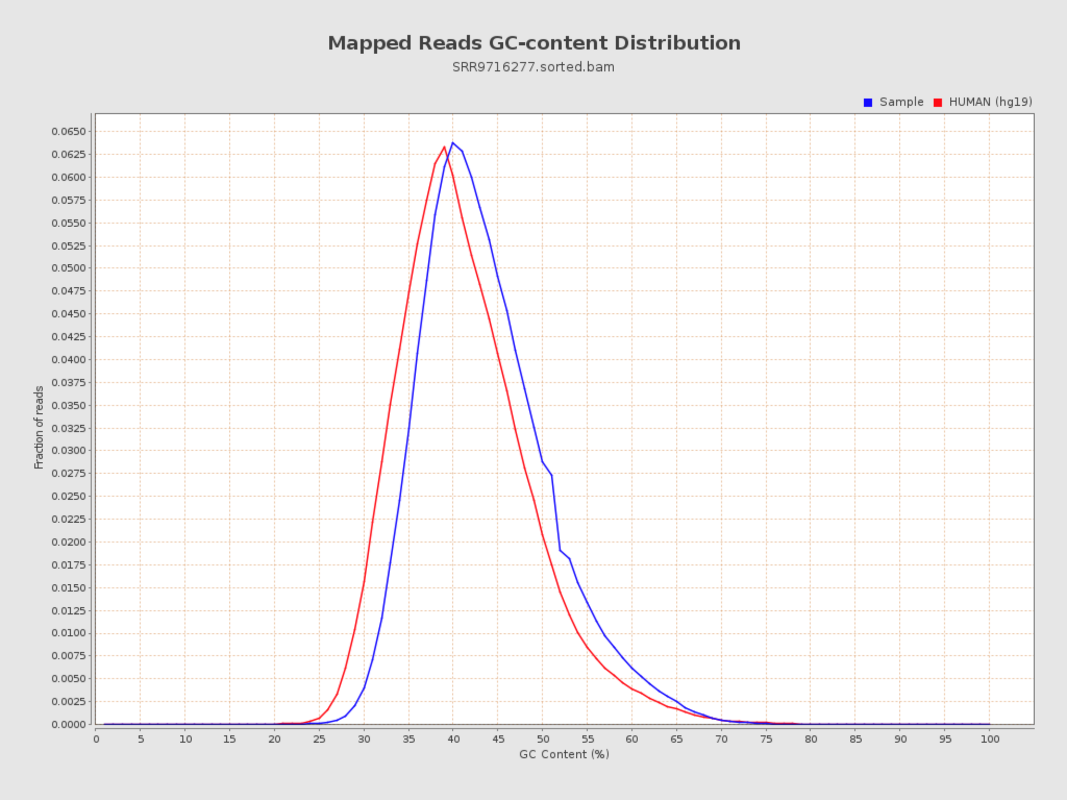
7. Results : Duplication Rate Histogram



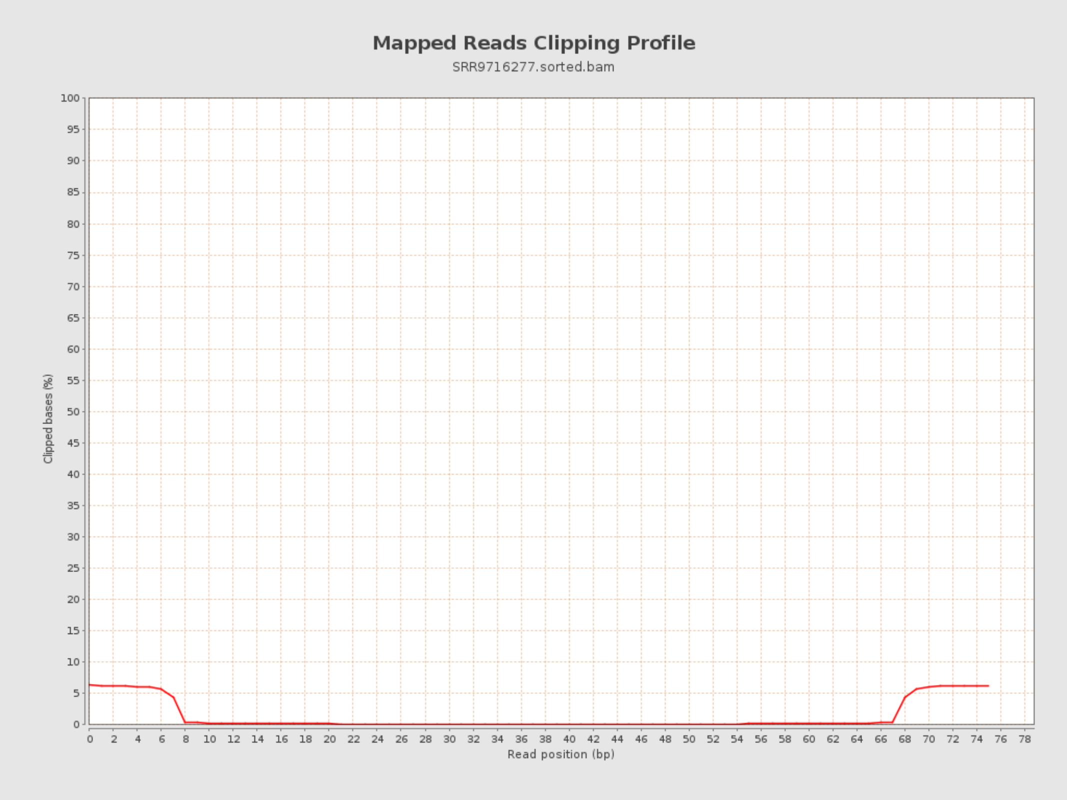
8. Results : Mapped Reads Nucleotide Content



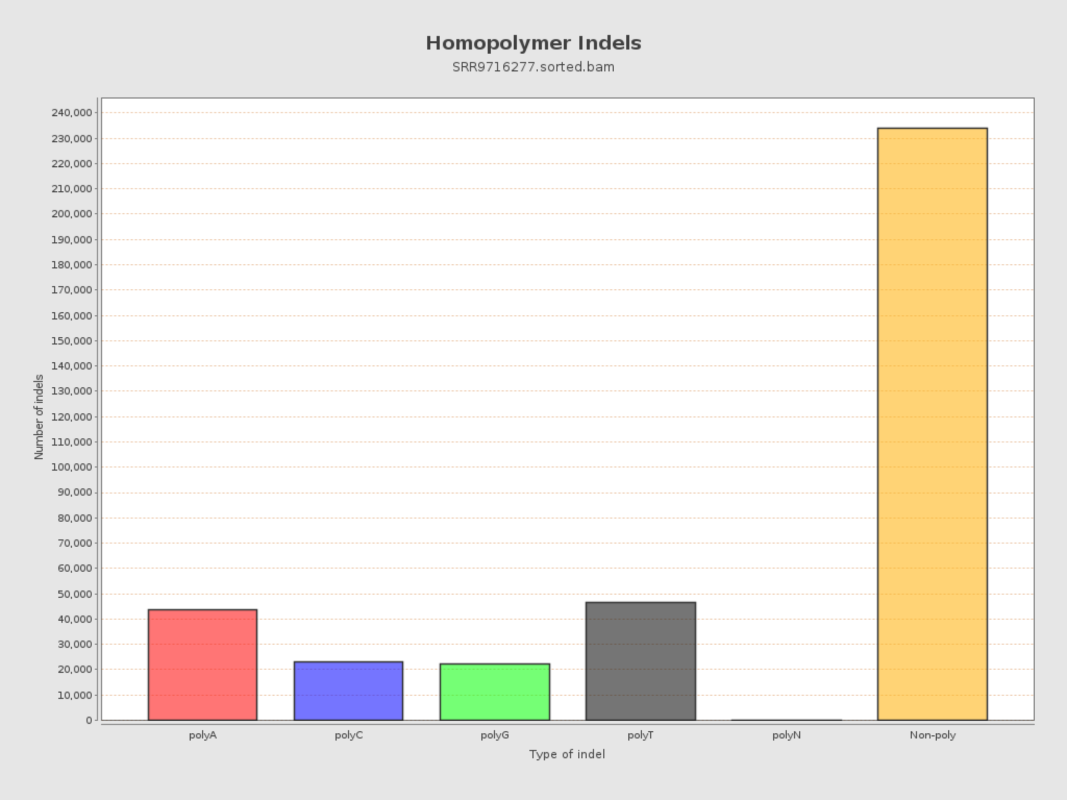
9. Results : Mapped Reads GC-content Distribution



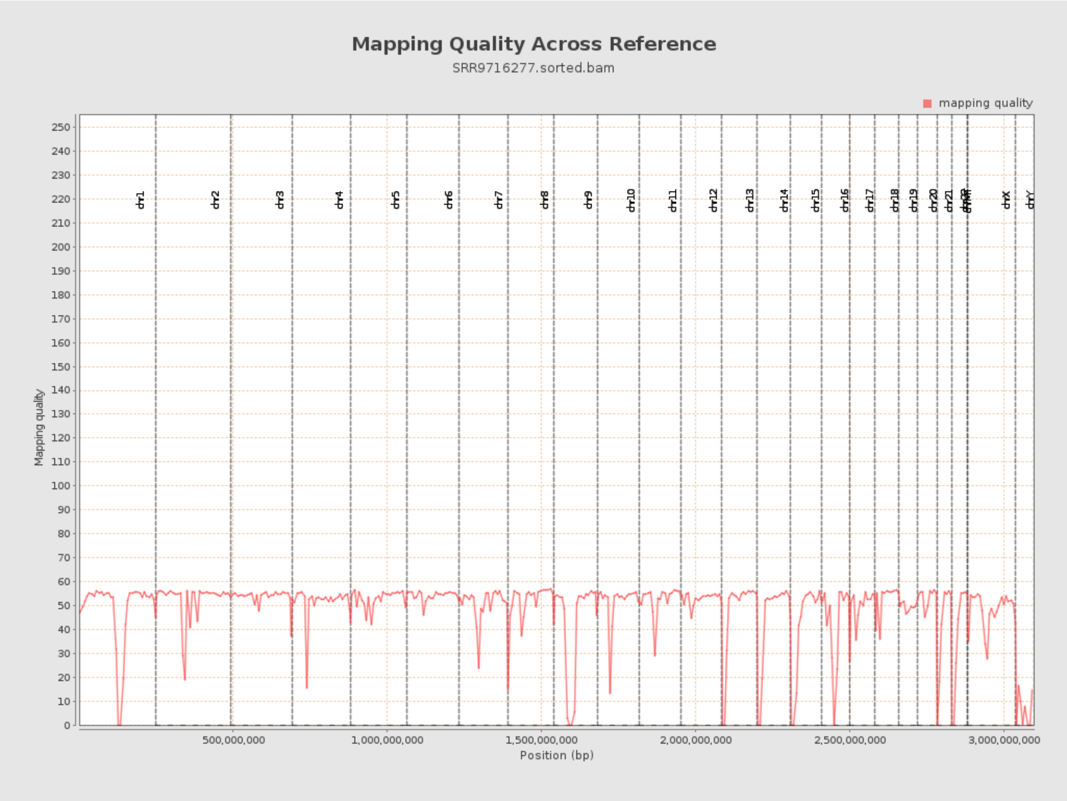
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram