Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:14:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716755.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_SRR9716755 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716755.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:14:07 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716755.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	504,028
Mapped reads	459,584 / 91.18%
Unmapped reads	44,444 / 8.82%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,954 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	8,293 / 1.65%
Duplication rate	1.36%
Clipped reads	460,270 / 91.32%

2.2. ACGT Content

Number/percentage of A's	6,643,636 / 24.92%
Number/percentage of C's	5,001,761 / 18.76%
Number/percentage of T's	8,542,075 / 32.04%
Number/percentage of G's	6,469,734 / 24.27%
Number/percentage of N's	727 / 0%
GC Percentage	43.03%

2.3. Coverage

Mean	0.0086

Standard Deviation	0.1137

2.4. Mapping Quality

Mean Mapping Quality	44.75

2.5. Mismatches and indels

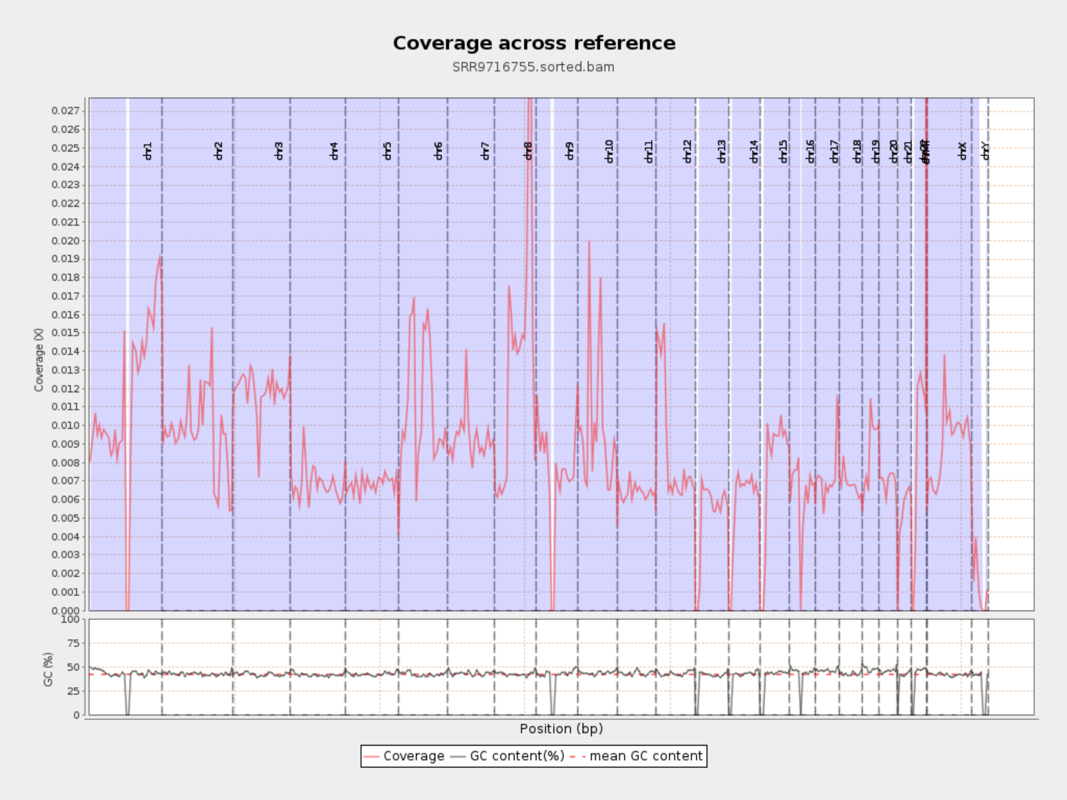
General error rate	0.5%
Mismatches	130,444
Insertions	1,811
Mapped reads with at least one insertion	0.39%
Deletions	4,803
Mapped reads with at least one deletion	1.04%
Homopolymer indels	42.92%

2.6. Chromosome stats

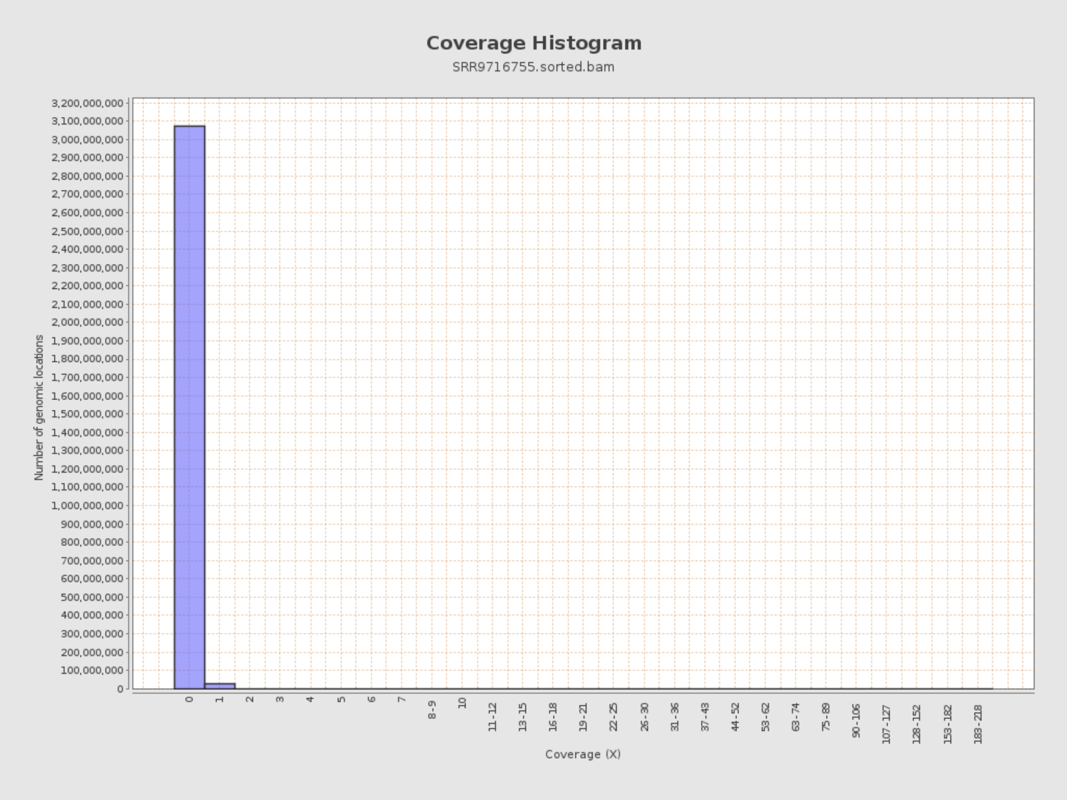
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2840243	0.0114	0.1803
chr2	243199373	2357171	0.0097	0.1365
chr3	198022430	2346575	0.0119	0.1126
chr4	191154276	1300172	0.0068	0.0875
chr5	180915260	1240764	0.0069	0.0858
chr6	171115067	1905405	0.0111	0.127
chr7	159138663	1490837	0.0094	0.1255

chr8	146364022	2000422	0.0137	0.1265
chr9	141213431	1016771	0.0072	0.0993
chr10	135534747	1352054	0.01	0.1196
chr11	135006516	860532	0.0064	0.0908
chr12	133851895	1173065	0.0088	0.0974
chr13	115169878	587965	0.0051	0.0742
chr14	107349540	612597	0.0057	0.0793
chr15	102531392	779572	0.0076	0.0906
chr16	90354753	563692	0.0062	0.0856
chr17	81195210	600752	0.0074	0.0897
chr18	78077248	535370	0.0069	0.1355
chr19	59128983	511794	0.0087	0.1213
chr20	63025520	439139	0.007	0.0863
chr21	48129895	248637	0.0052	0.0784
chr22	51304566	422352	0.0082	0.0935
chrMT	16571	3205	0.1934	0.4664
chrX	155270560	1397287	0.009	0.1016
chrY	59373566	79247	0.0013	0.0437

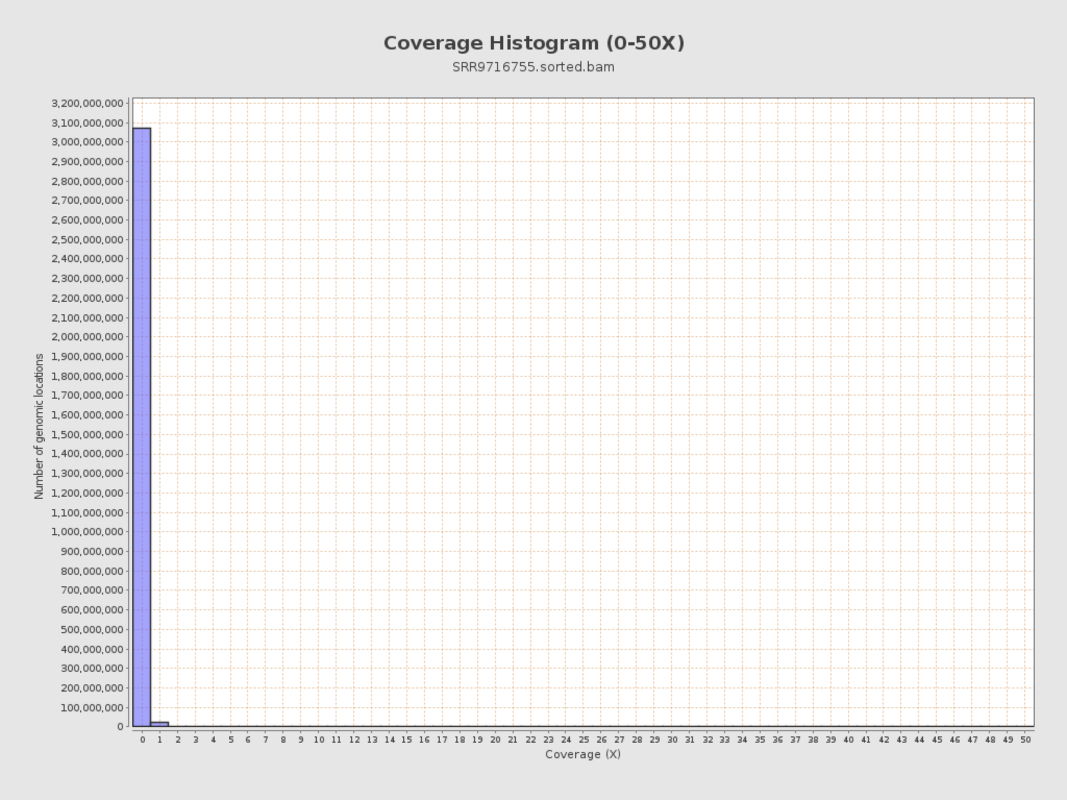
3. Results : Coverage across reference



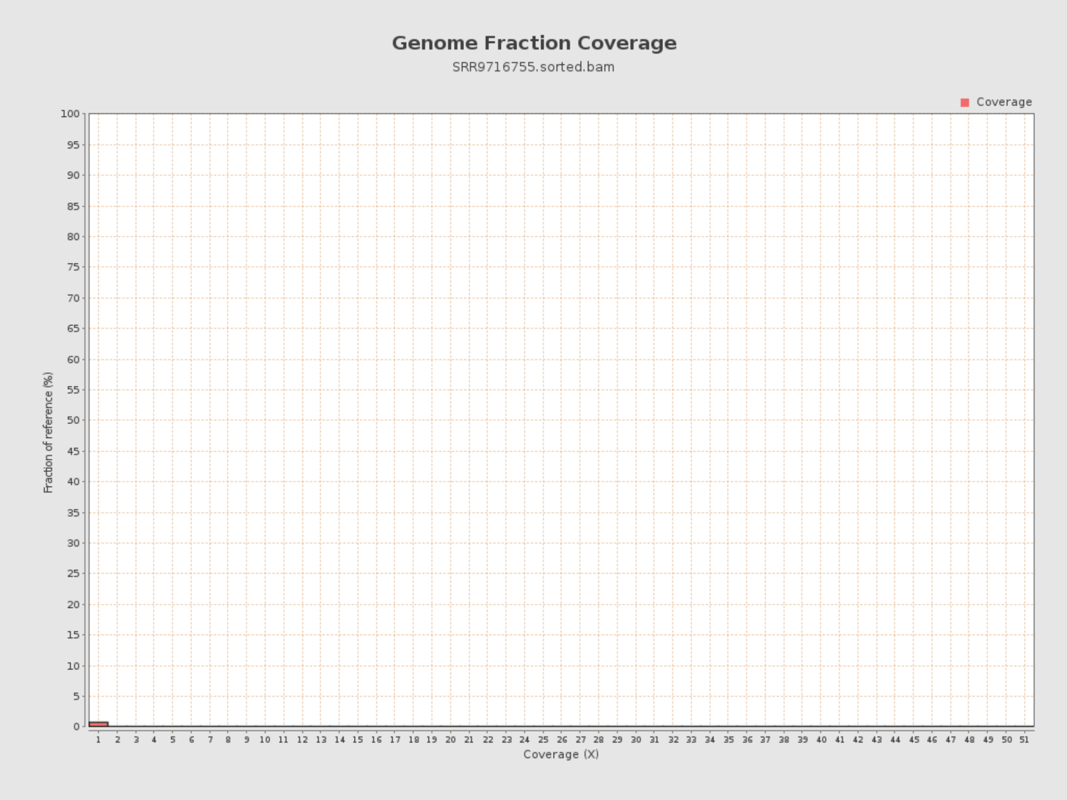
4. Results : Coverage Histogram



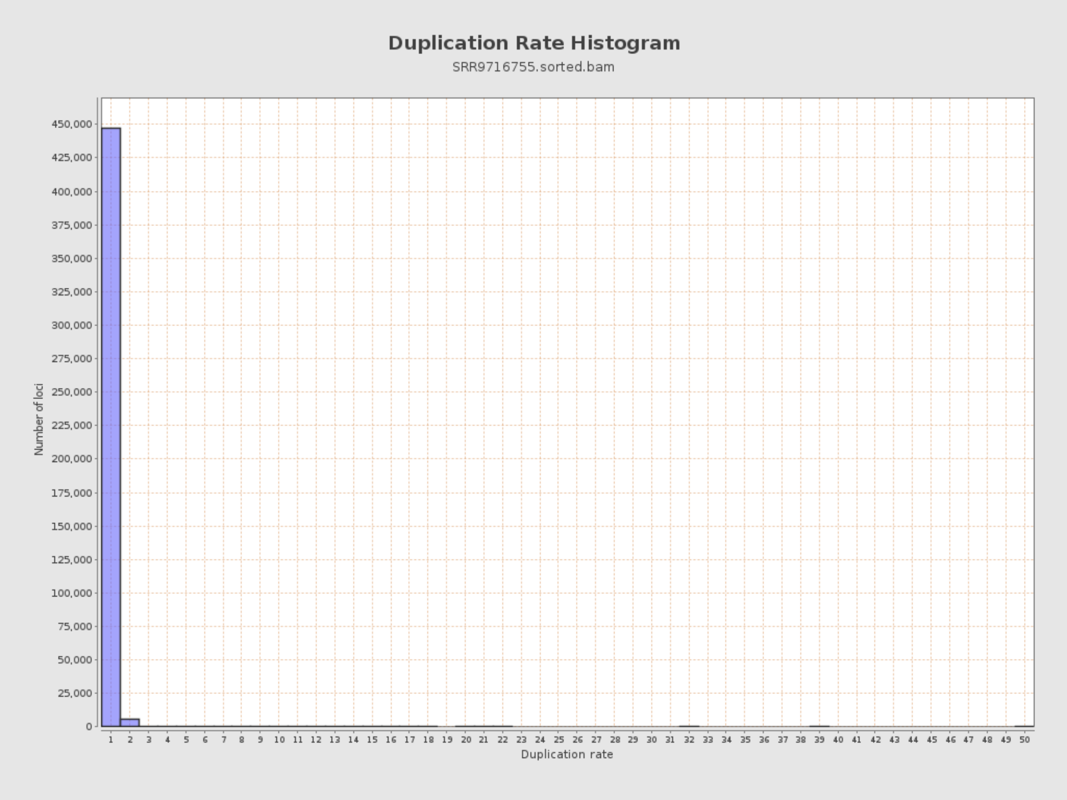
5. Results : Coverage Histogram (0-50X)



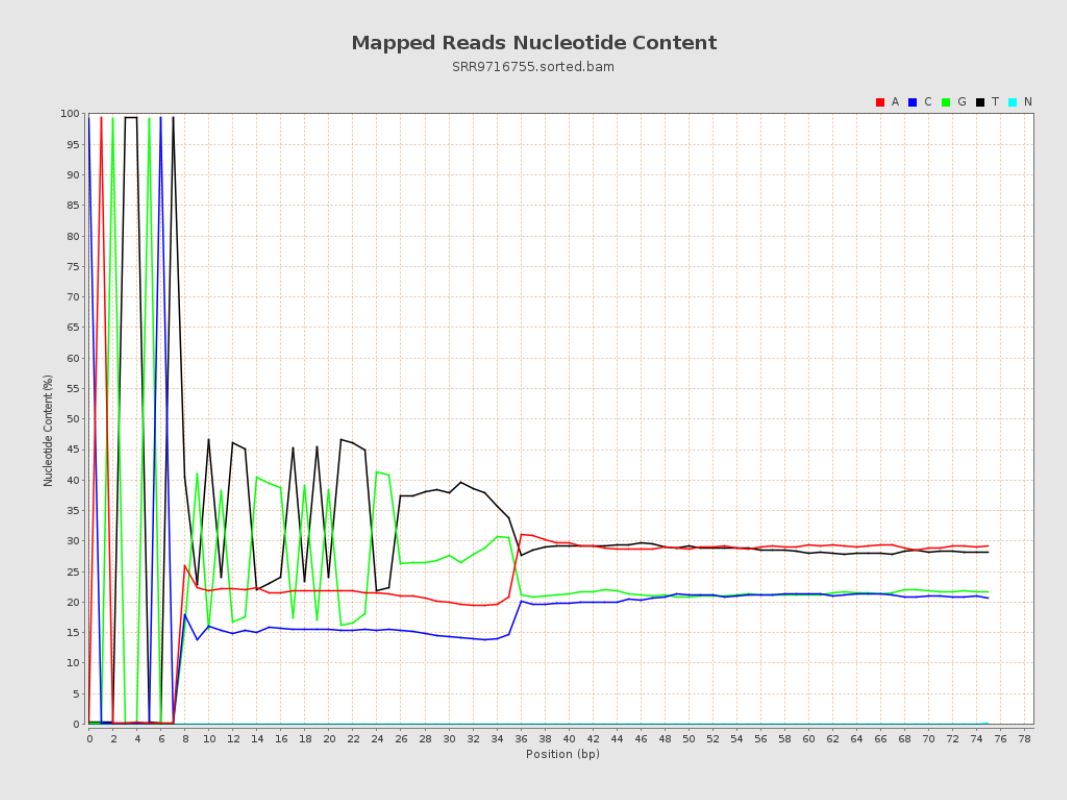
6. Results : Genome Fraction Coverage



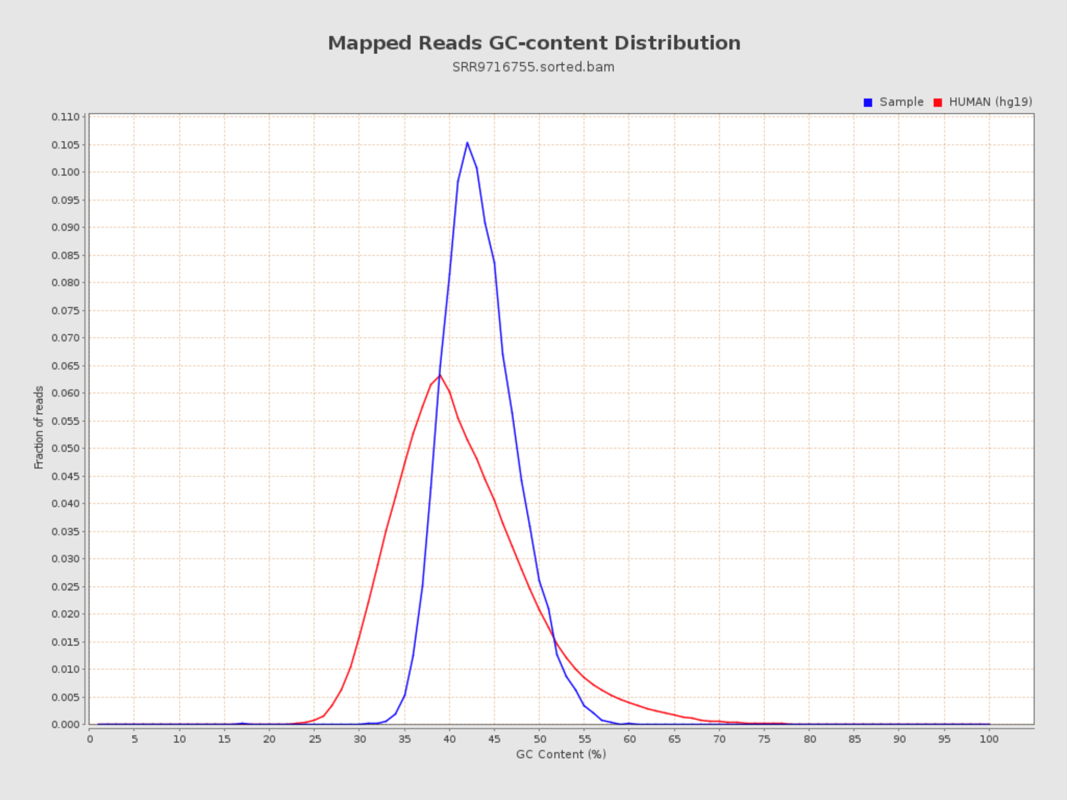
7. Results : Duplication Rate Histogram



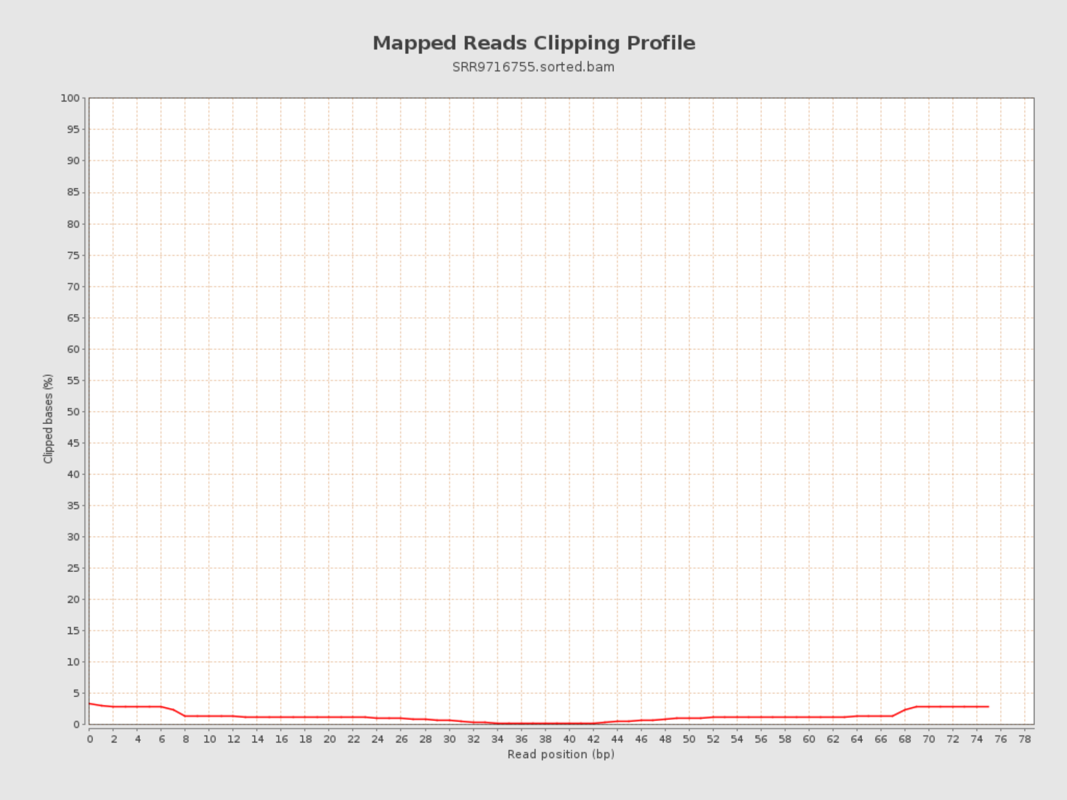
8. Results : Mapped Reads Nucleotide Content



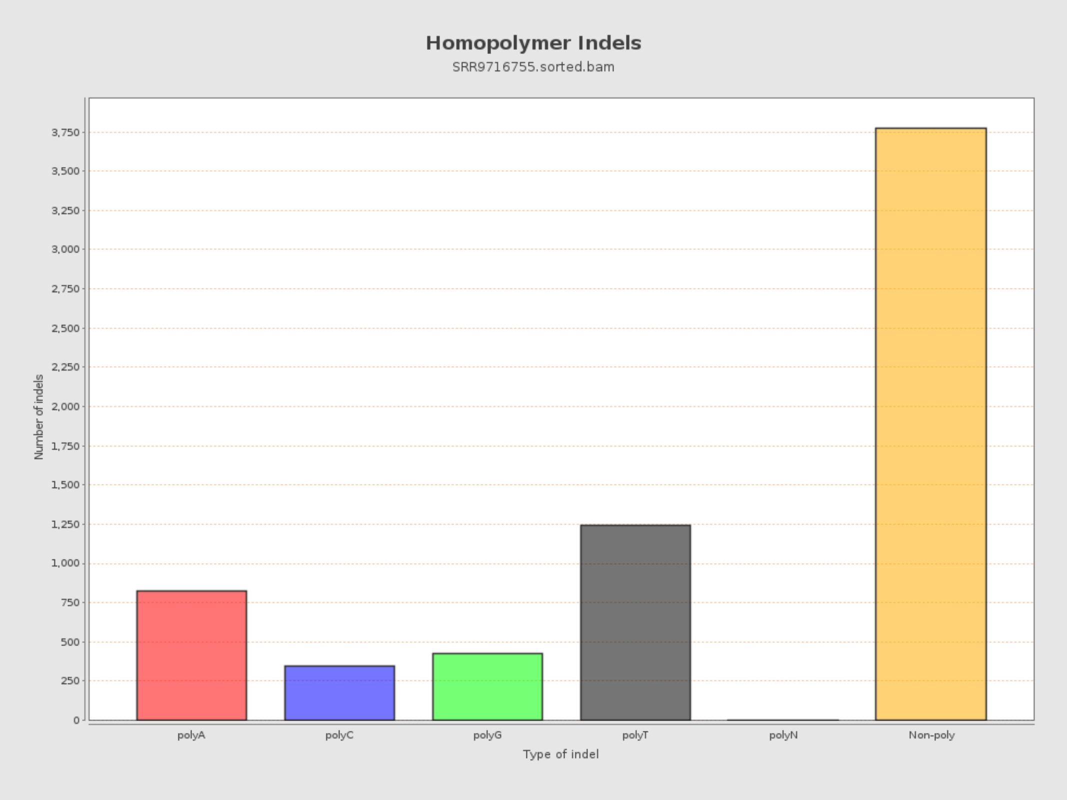
9. Results : Mapped Reads GC-content Distribution



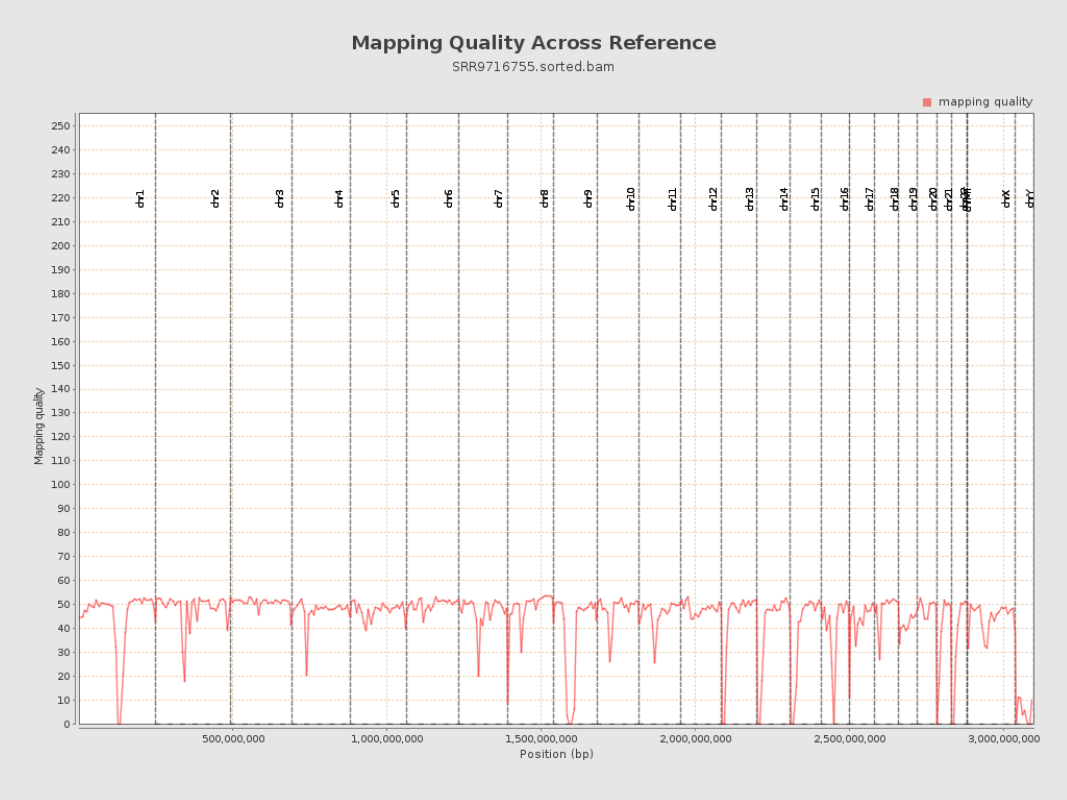
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram