Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 14:59:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716852.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_SRR9716852 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716852.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 14:59:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716852.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	627,240
Mapped reads	576,774 / 91.95%
Unmapped reads	50,466 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,926 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	14,825 / 2.36%
Duplication rate	2.06%
Clipped reads	577,926 / 92.14%

2.2. ACGT Content

Number/percentage of A's	8,625,251 / 25.59%
Number/percentage of C's	7,027,073 / 20.85%
Number/percentage of T's	10,087,831 / 29.93%
Number/percentage of G's	7,970,006 / 23.64%
Number/percentage of N's	195 / 0%
GC Percentage	44.49%

2.3. Coverage

Mean	0.0109

Standard Deviation	0.1289

2.4. Mapping Quality

Mean Mapping Quality	44.93

2.5. Mismatches and indels

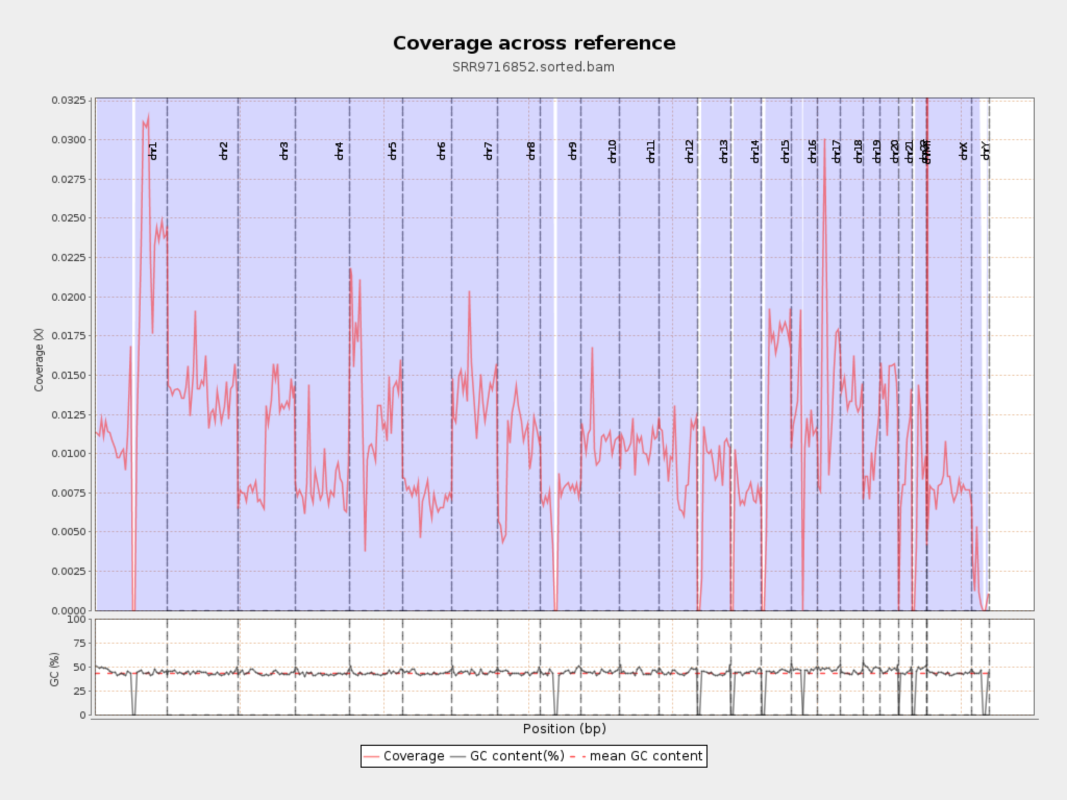
General error rate	0.51%
Mismatches	165,942
Insertions	2,590
Mapped reads with at least one insertion	0.45%
Deletions	6,063
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.84%

2.6. Chromosome stats

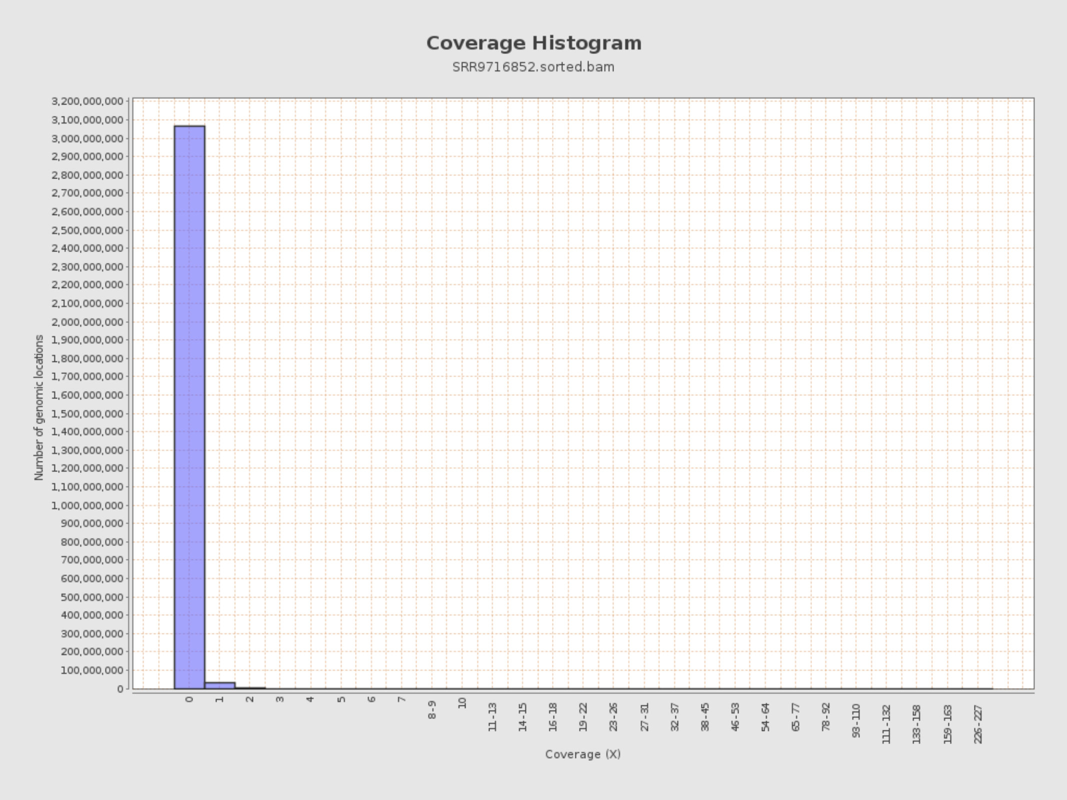
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3969716	0.0159	0.1847
chr2	243199373	3400598	0.014	0.1651
chr3	198022430	2103428	0.0106	0.1081
chr4	191154276	1537745	0.008	0.1027
chr5	180915260	2420689	0.0134	0.1216
chr6	171115067	1230531	0.0072	0.092
chr7	159138663	2249764	0.0141	0.1754

chr8	146364022	1510162	0.0103	0.1207
chr9	141213431	934241	0.0066	0.1011
chr10	135534747	1508250	0.0111	0.1285
chr11	135006516	1428750	0.0106	0.1226
chr12	133851895	1278027	0.0095	0.1027
chr13	115169878	957558	0.0083	0.0955
chr14	107349540	713002	0.0066	0.0879
chr15	102531392	1462742	0.0143	0.1251
chr16	90354753	1025690	0.0114	0.1143
chr17	81195210	1292431	0.0159	0.1383
chr18	78077248	1076413	0.0138	0.1881
chr19	59128983	555547	0.0094	0.1275
chr20	63025520	907619	0.0144	0.1264
chr21	48129895	424904	0.0088	0.1017
chr22	51304566	390832	0.0076	0.0916
chrMT	16571	35607	2.1488	1.9409
chrX	155270560	1217930	0.0078	0.0967
chrY	59373566	87847	0.0015	0.053

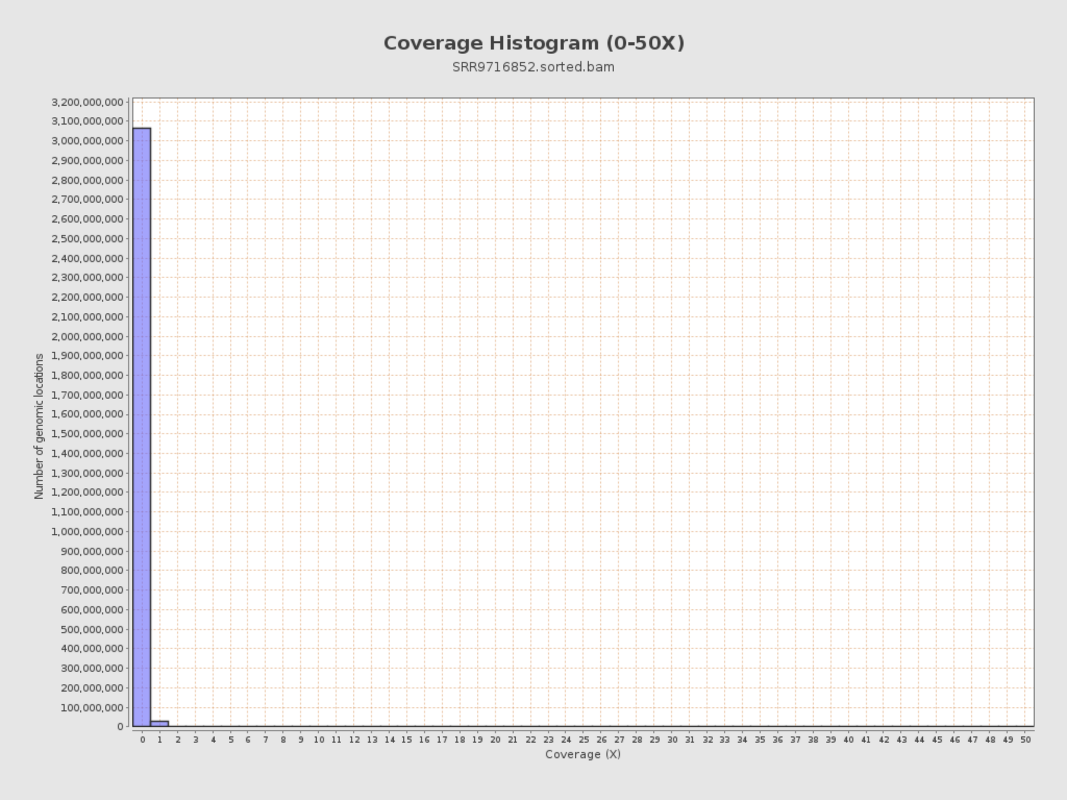
3. Results : Coverage across reference



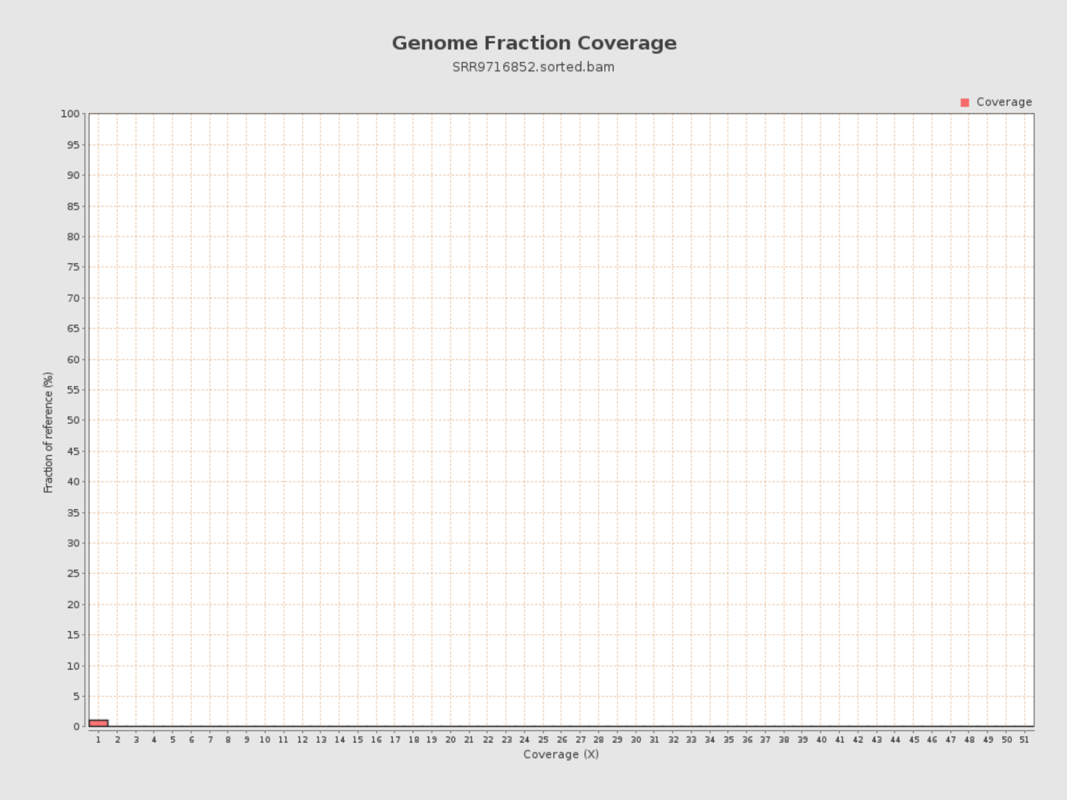
4. Results : Coverage Histogram



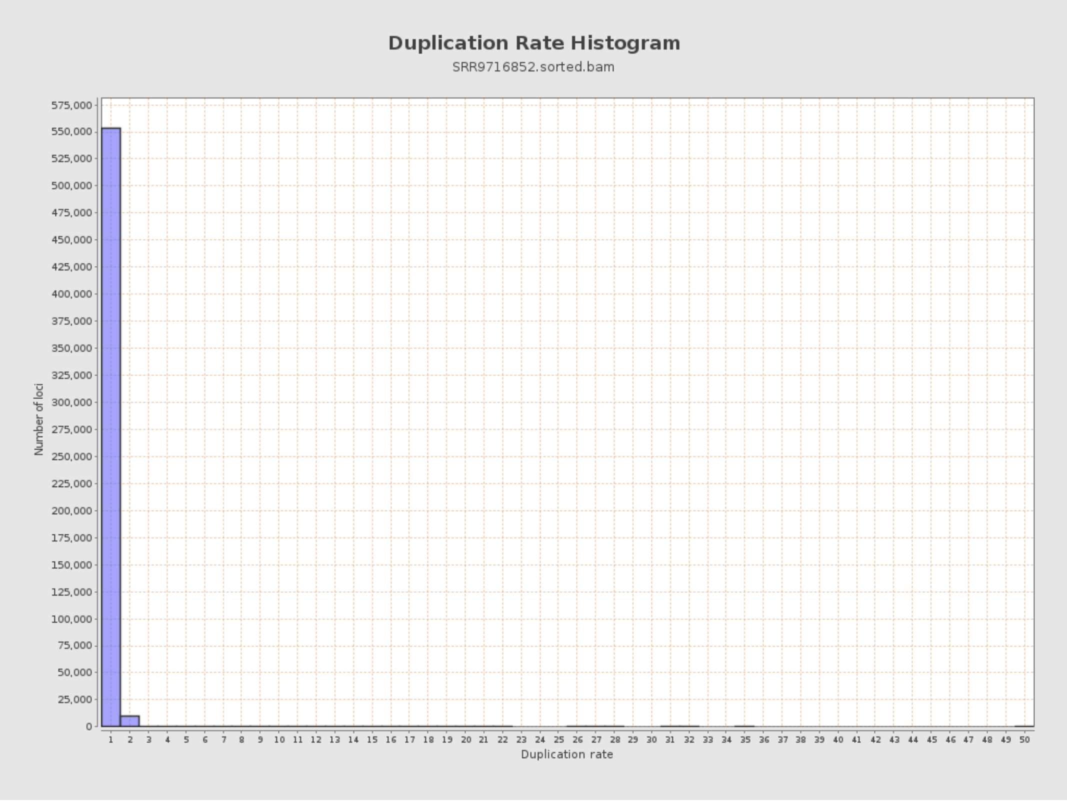
5. Results : Coverage Histogram (0-50X)



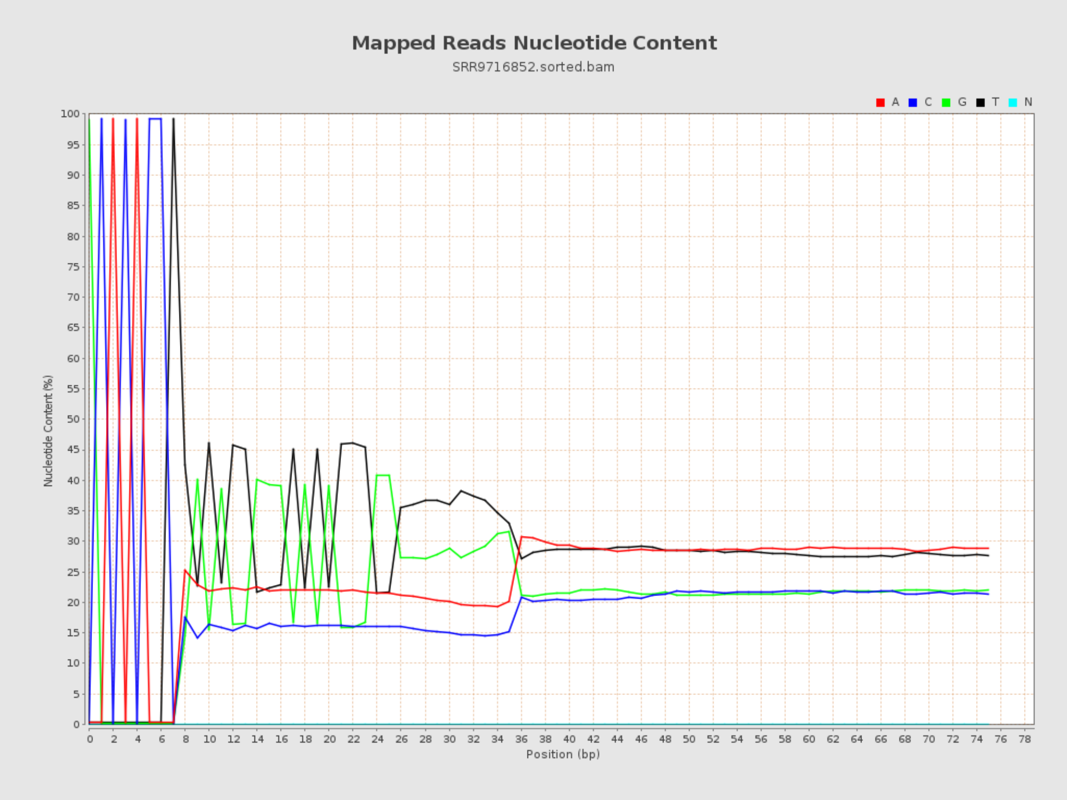
6. Results : Genome Fraction Coverage



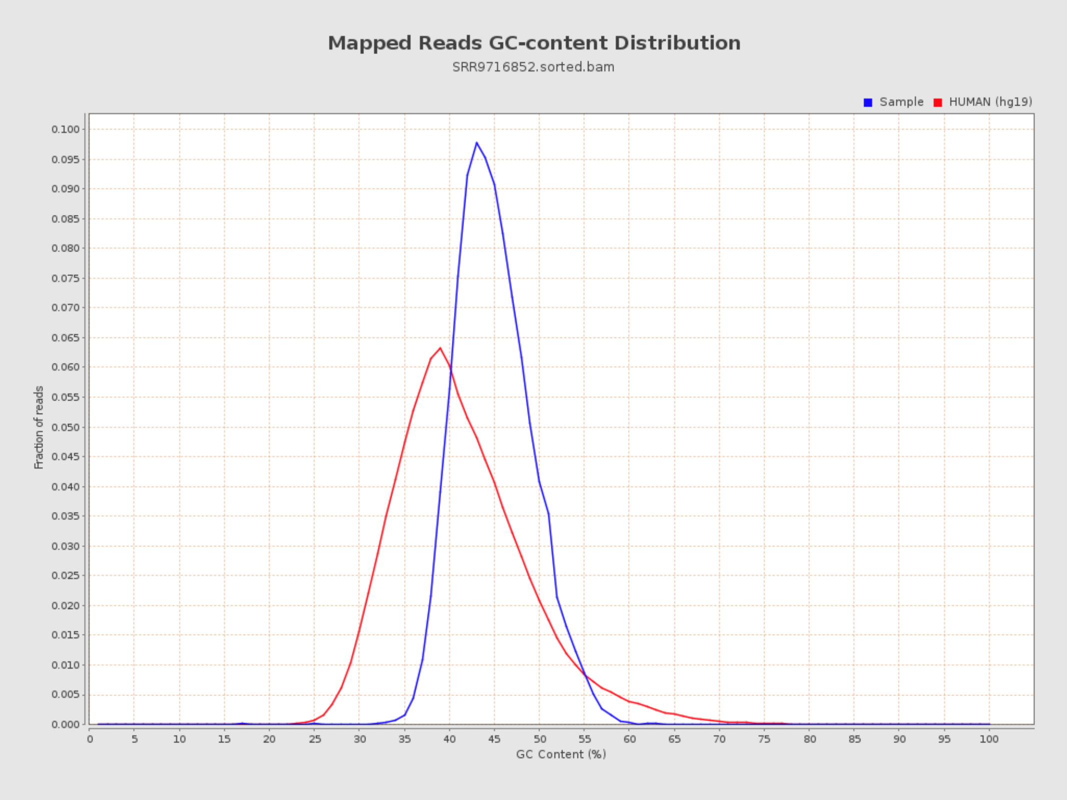
7. Results : Duplication Rate Histogram



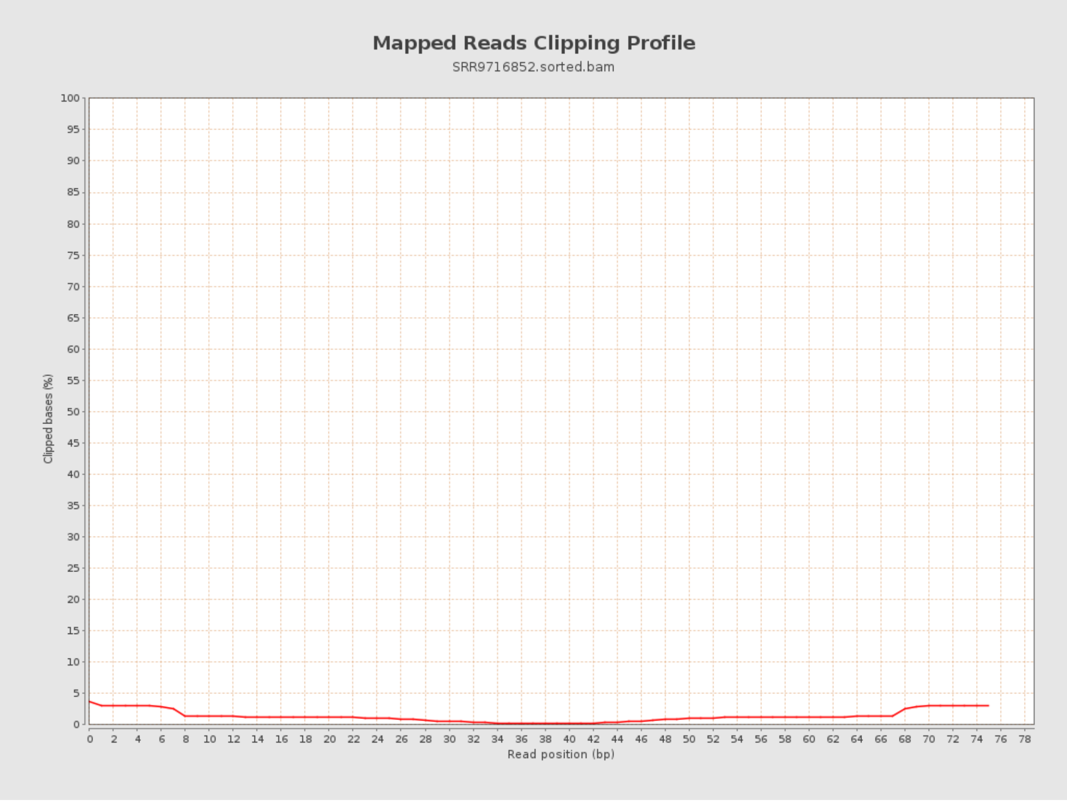
8. Results : Mapped Reads Nucleotide Content



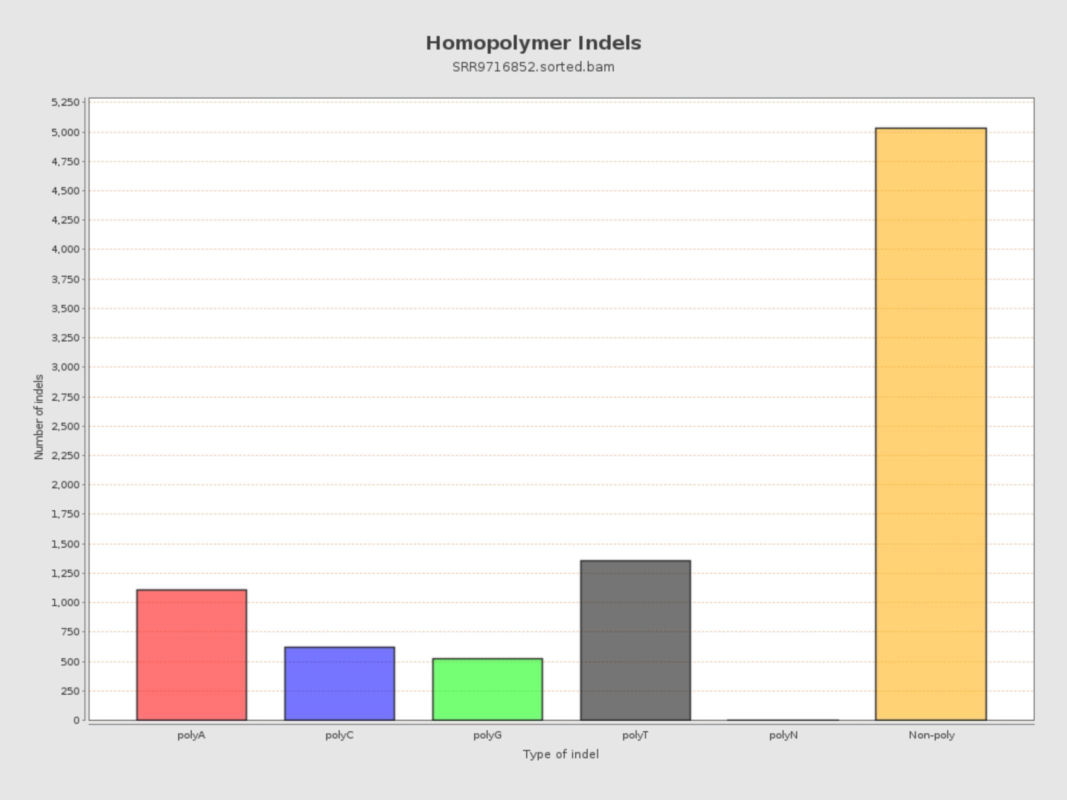
9. Results : Mapped Reads GC-content Distribution



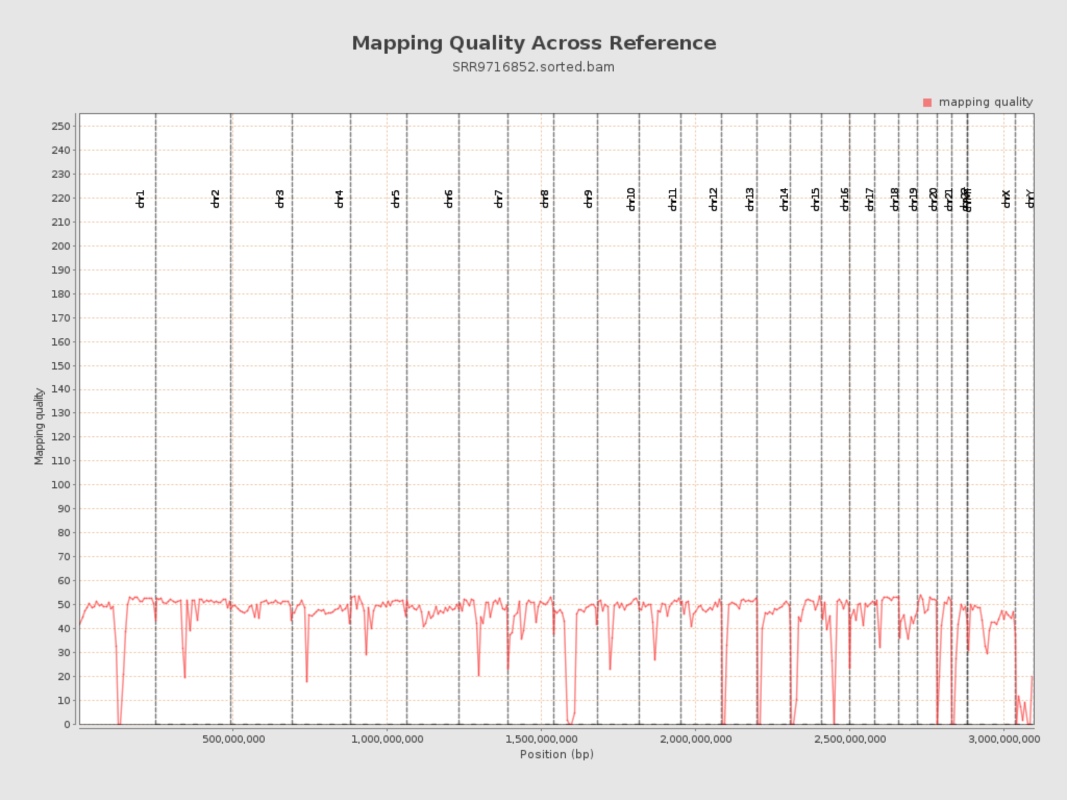
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram