Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 23:36:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716595.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_SRR9716595 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716595.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 23:36:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716595.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,245,154
Mapped reads	2,026,787 / 90.27%
Unmapped reads	218,367 / 9.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,701 / 0.43%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	96,157 / 4.28%
Duplication rate	3.48%
Clipped reads	2,031,737 / 90.49%

2.2. ACGT Content

Number/percentage of A's	28,657,933 / 24.68%
Number/percentage of C's	21,965,628 / 18.92%
Number/percentage of T's	37,154,325 / 32%
Number/percentage of G's	28,336,695 / 24.4%
Number/percentage of N's	1,828 / 0%
GC Percentage	43.32%

2.3. Coverage

Mean	0.0375

Standard Deviation	0.3626

2.4. Mapping Quality

Mean Mapping Quality	43.36

2.5. Mismatches and indels

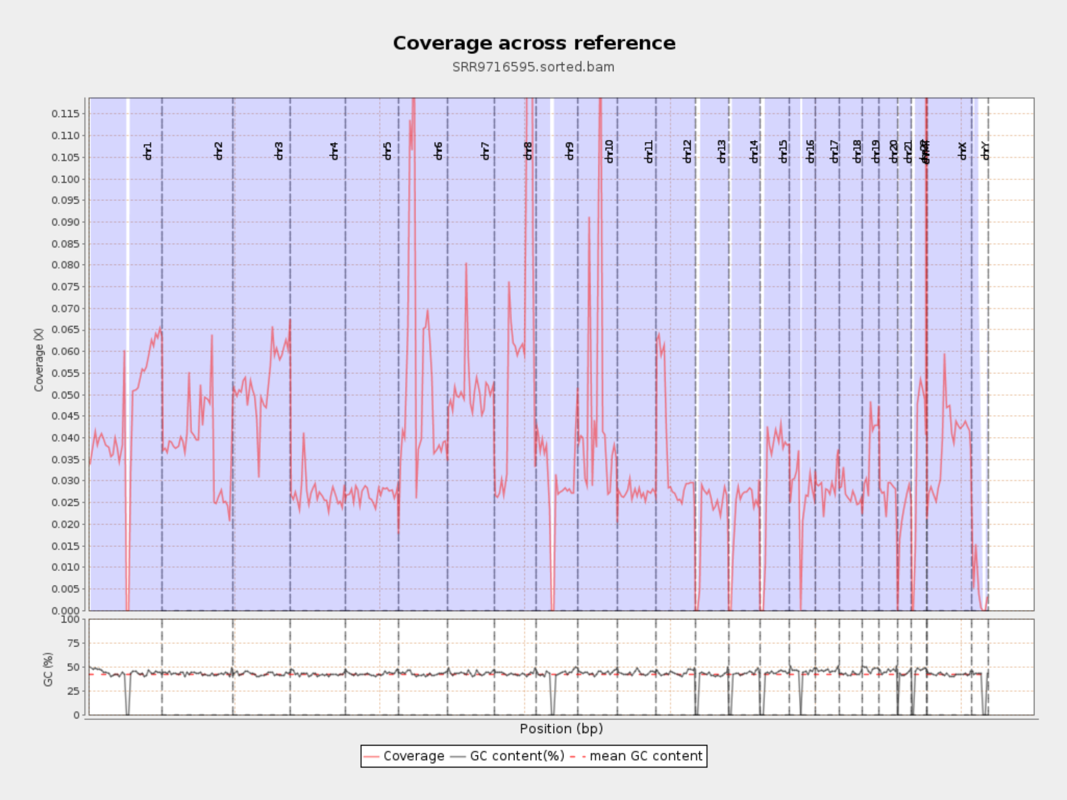
General error rate	0.51%
Mismatches	576,555
Insertions	7,485
Mapped reads with at least one insertion	0.37%
Deletions	18,951
Mapped reads with at least one deletion	0.93%
Homopolymer indels	41.06%

2.6. Chromosome stats

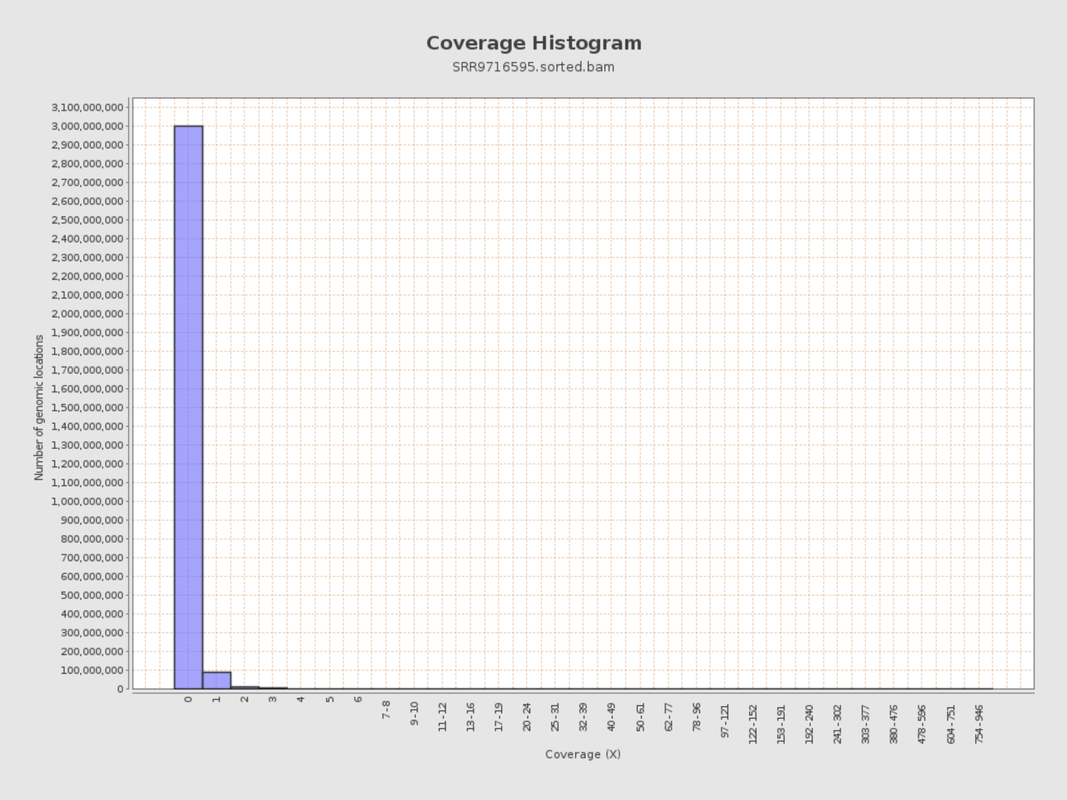
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11055233	0.0444	0.5868
chr2	243199373	9277225	0.0381	0.4433
chr3	198022430	10512546	0.0531	0.2625
chr4	191154276	5164155	0.027	0.2031
chr5	180915260	4898640	0.0271	0.1884
chr6	171115067	9409940	0.055	0.6406
chr7	159138663	8195331	0.0515	0.5556

chr8	146364022	10501120	0.0717	0.3498
chr9	141213431	4038936	0.0286	0.2483
chr10	135534747	6530924	0.0482	0.3766
chr11	135006516	3664878	0.0271	0.268
chr12	133851895	4850866	0.0362	0.2206
chr13	115169878	2508130	0.0218	0.1682
chr14	107349540	2390893	0.0223	0.1927
chr15	102531392	3252493	0.0317	0.2081
chr16	90354753	2382731	0.0264	0.2095
chr17	81195210	2351957	0.029	0.2044
chr18	78077248	2115727	0.0271	0.4552
chr19	59128983	2193021	0.0371	0.4156
chr20	63025520	1711881	0.0272	0.1898
chr21	48129895	1031813	0.0214	0.1887
chr22	51304566	1757223	0.0343	0.2103
chrMT	16571	108903	6.5719	4.0026
chrX	155270560	5953030	0.0383	0.2551
chrY	59373566	288481	0.0049	0.1176

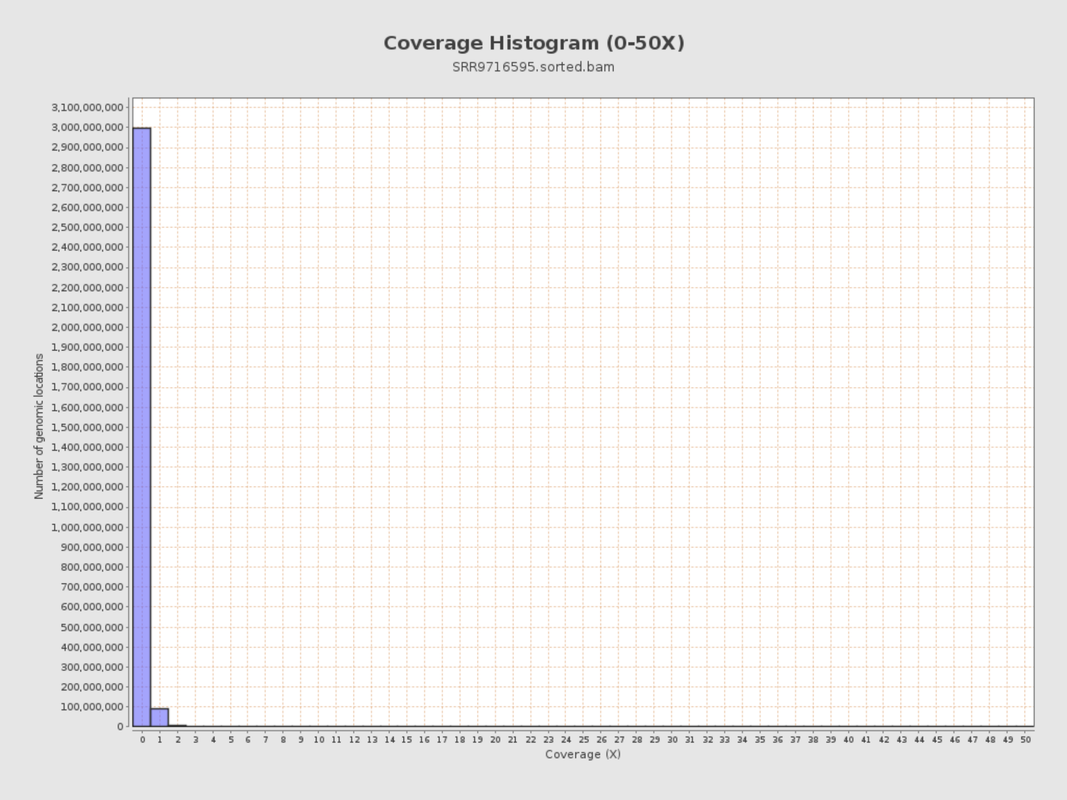
3. Results : Coverage across reference



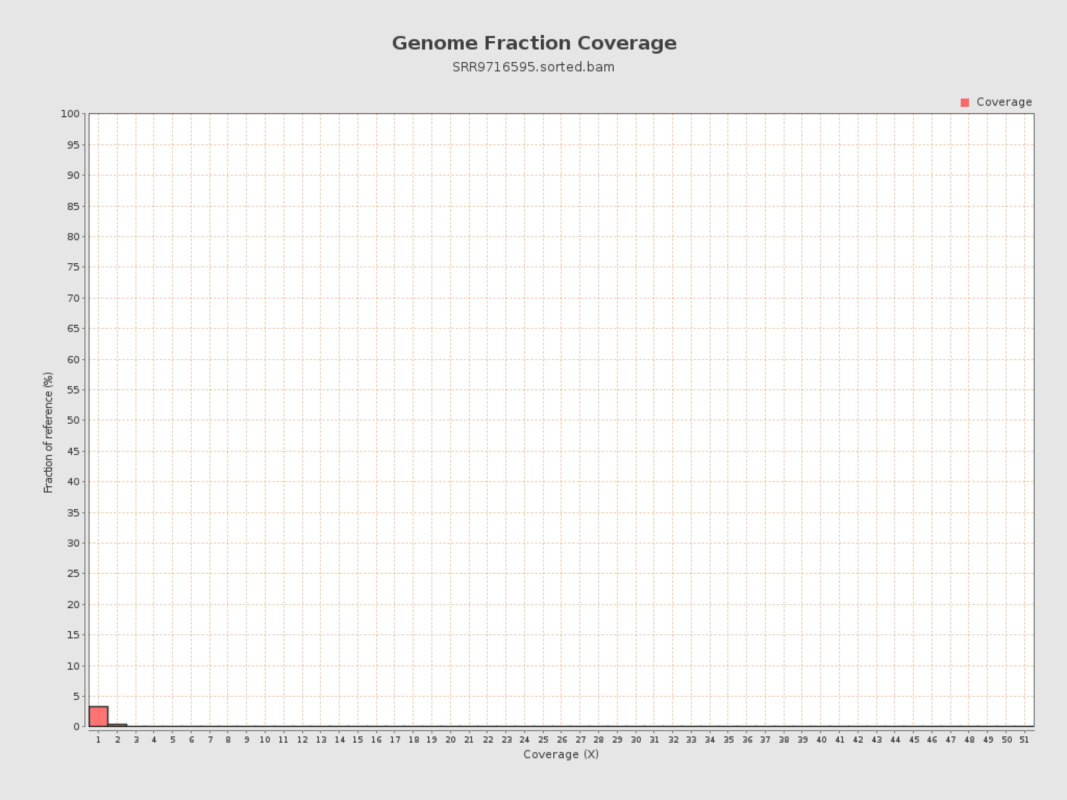
4. Results : Coverage Histogram



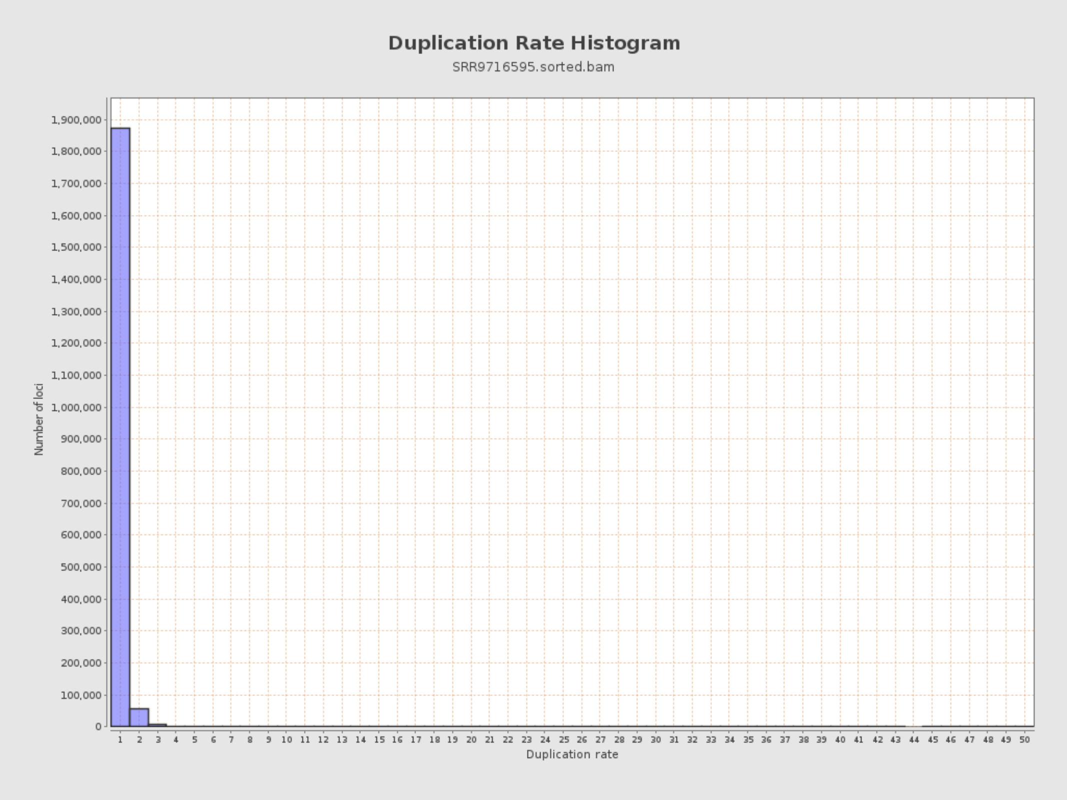
5. Results : Coverage Histogram (0-50X)



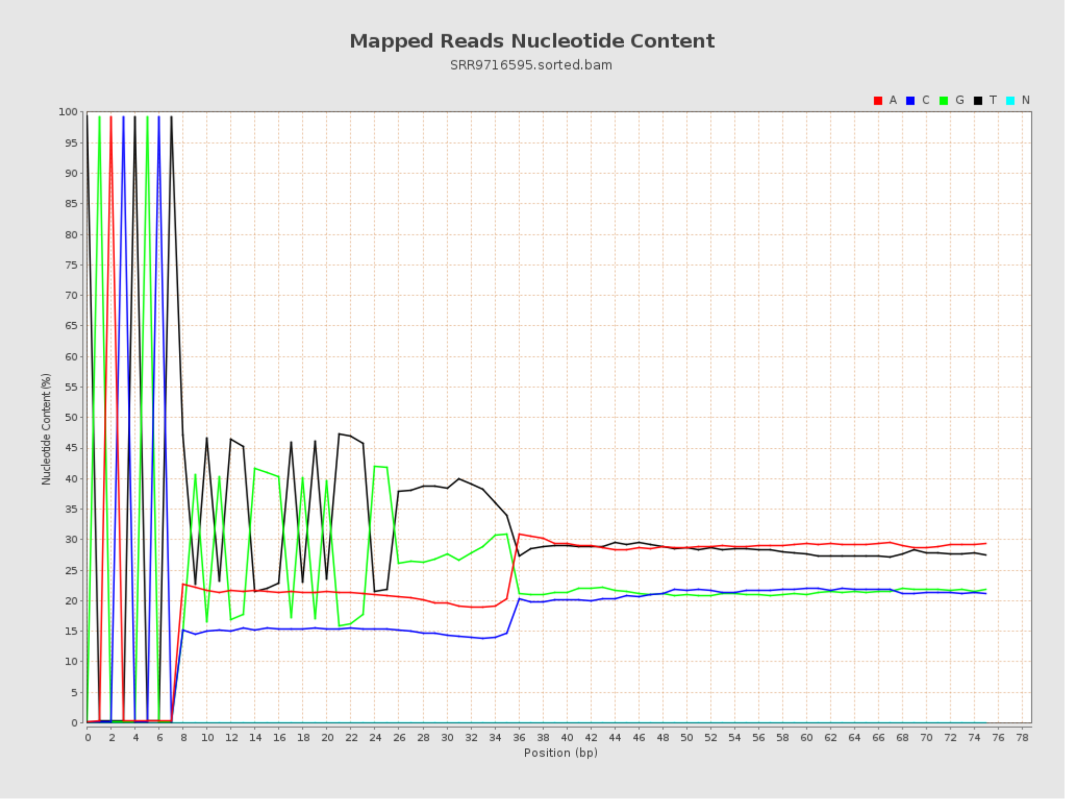
6. Results : Genome Fraction Coverage



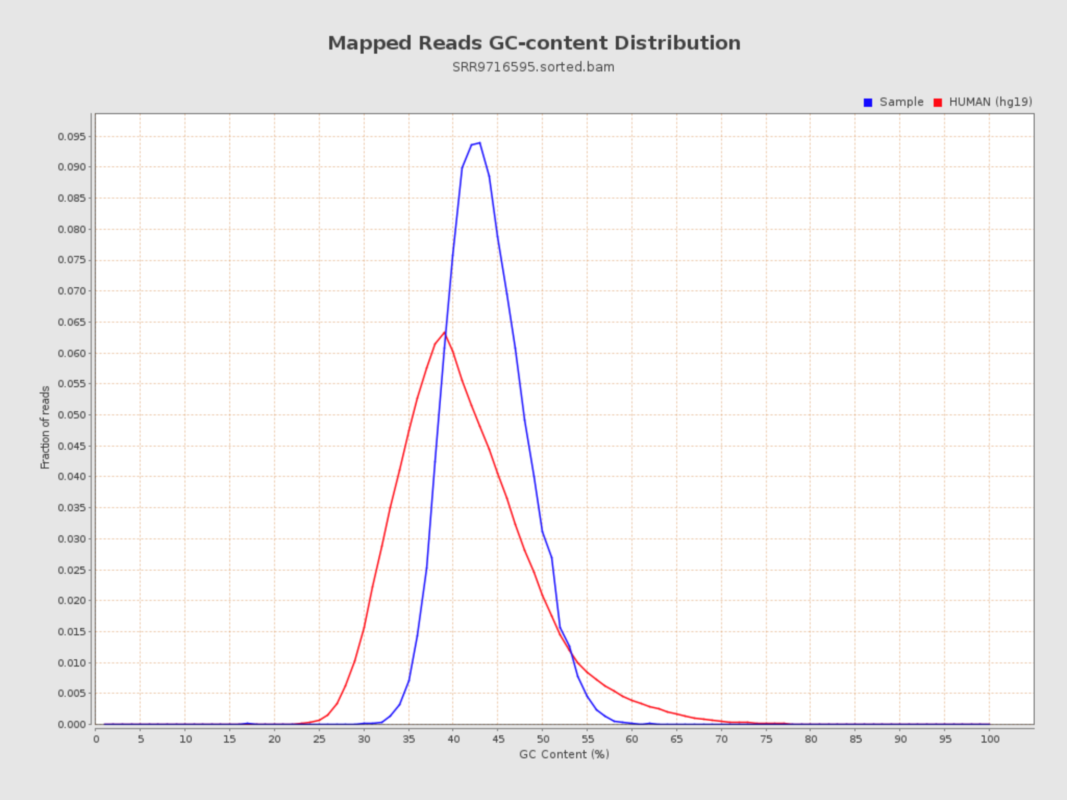
7. Results : Duplication Rate Histogram



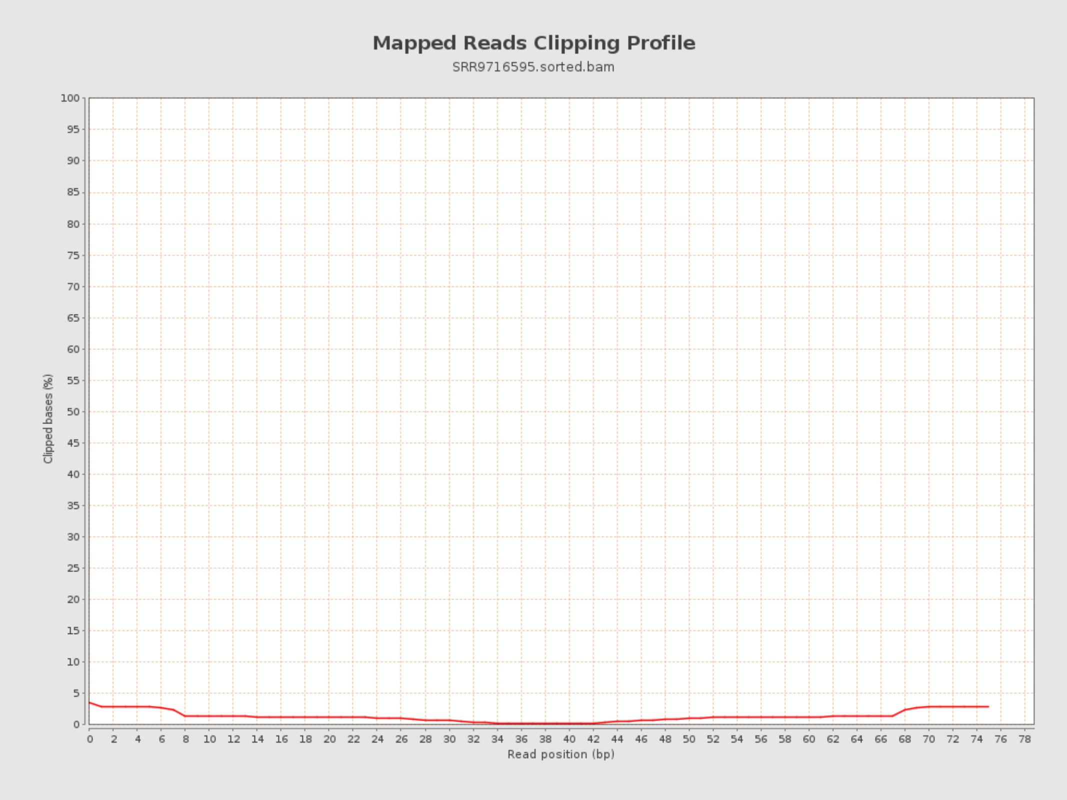
8. Results : Mapped Reads Nucleotide Content



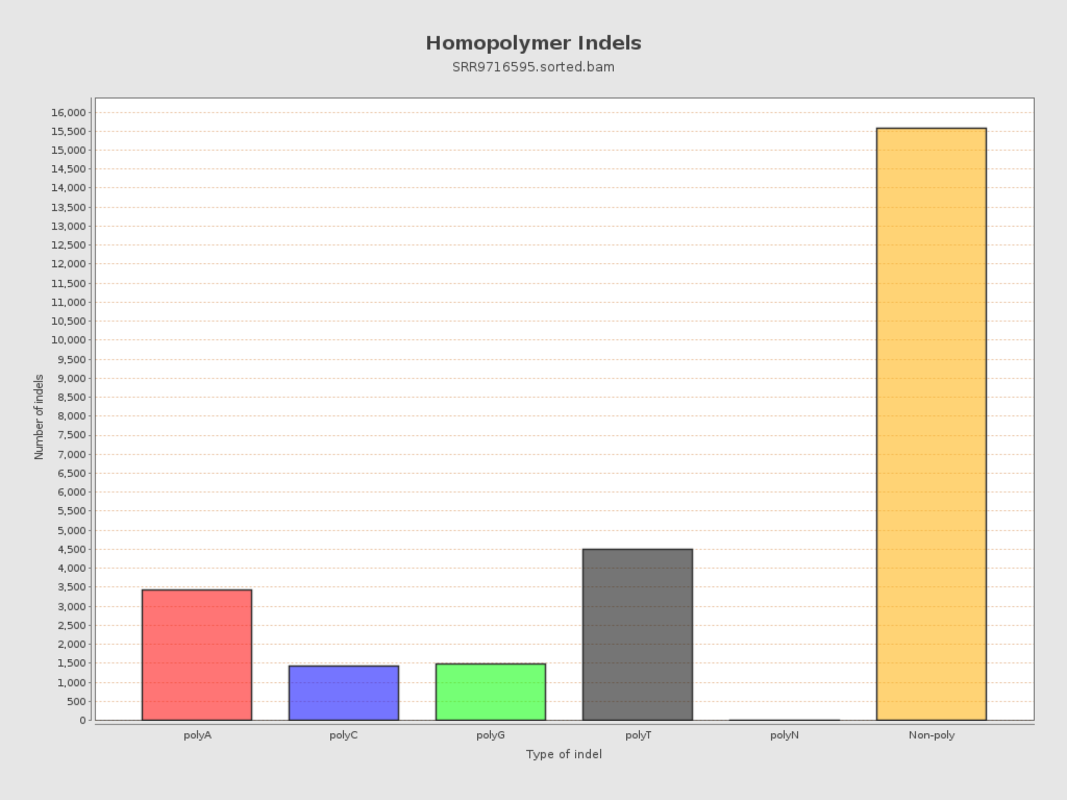
9. Results : Mapped Reads GC-content Distribution



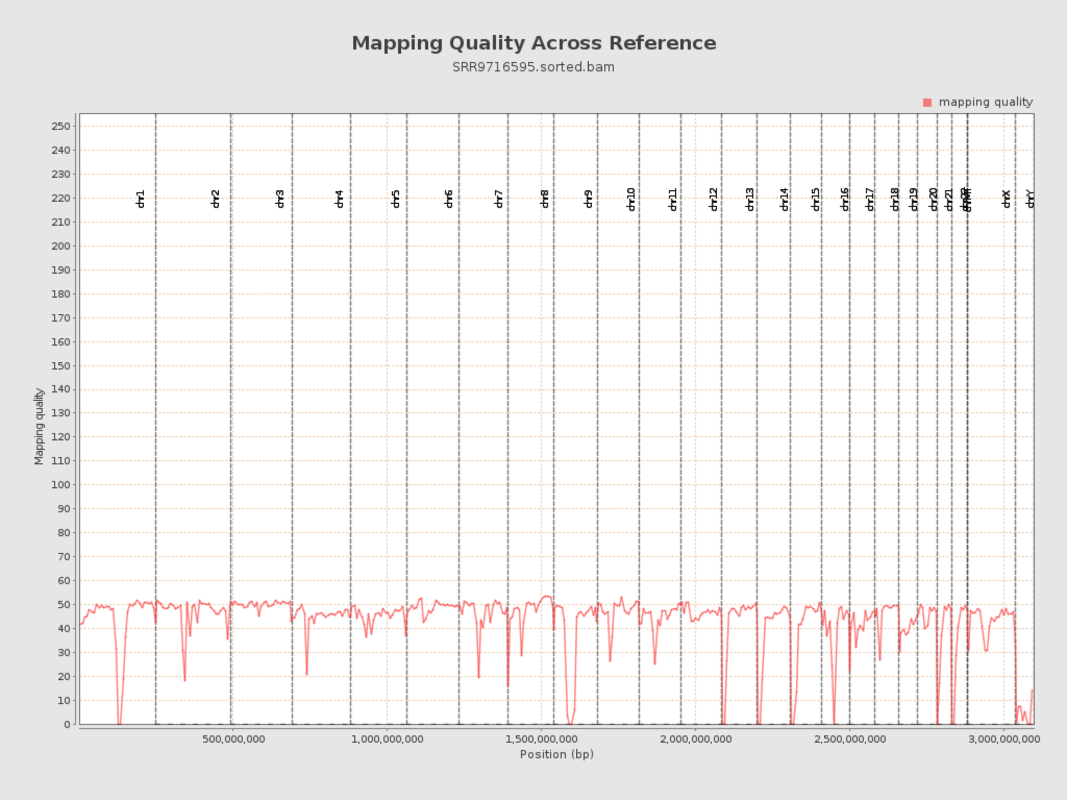
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram