Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 19:11:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716932.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_SRR9716932 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716932.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 19:11:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716932.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,039,982
Mapped reads	948,709 / 91.22%
Unmapped reads	91,273 / 8.78%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,201 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	35,012 / 3.37%
Duplication rate	2.73%
Clipped reads	949,018 / 91.25%

2.2. ACGT Content

Number/percentage of A's	12,864,435 / 23.42%
Number/percentage of C's	10,707,537 / 19.5%
Number/percentage of T's	18,207,828 / 33.15%
Number/percentage of G's	13,141,018 / 23.93%
Number/percentage of N's	1,058 / 0%
GC Percentage	43.42%

2.3. Coverage

Mean	0.0177

Standard Deviation	0.1924

2.4. Mapping Quality

Mean Mapping Quality	44.54

2.5. Mismatches and indels

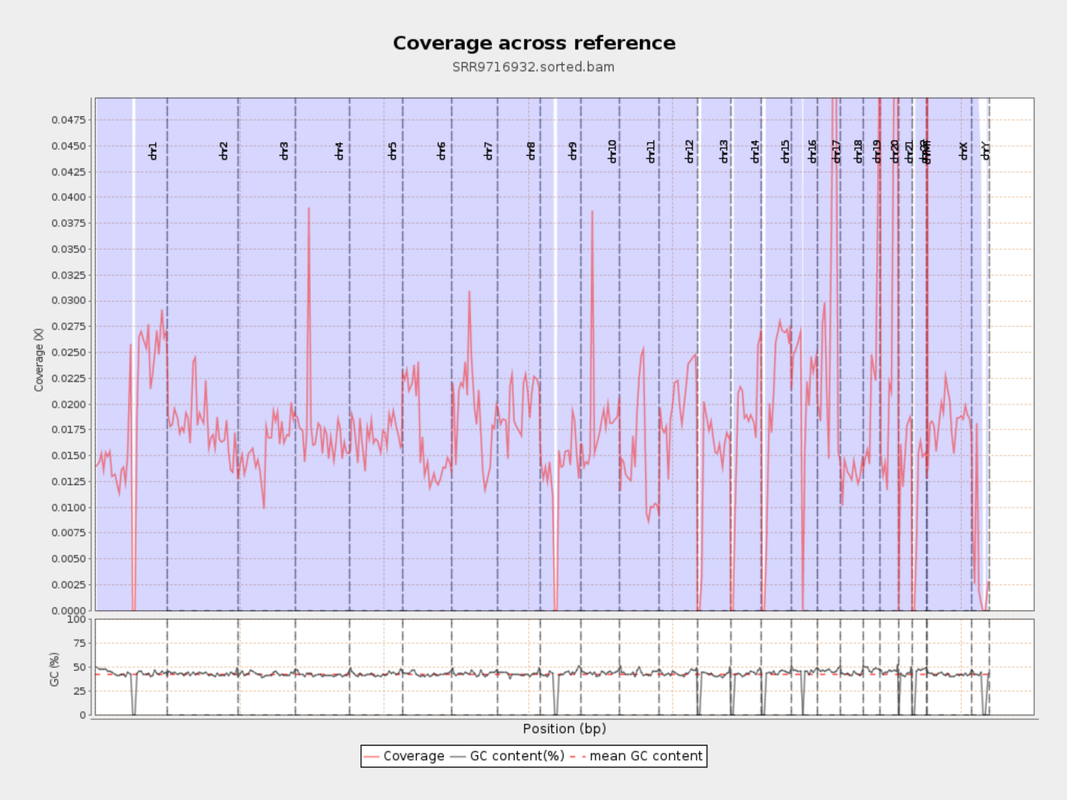
General error rate	0.53%
Mismatches	279,972
Insertions	4,268
Mapped reads with at least one insertion	0.45%
Deletions	11,058
Mapped reads with at least one deletion	1.15%
Homopolymer indels	43.02%

2.6. Chromosome stats

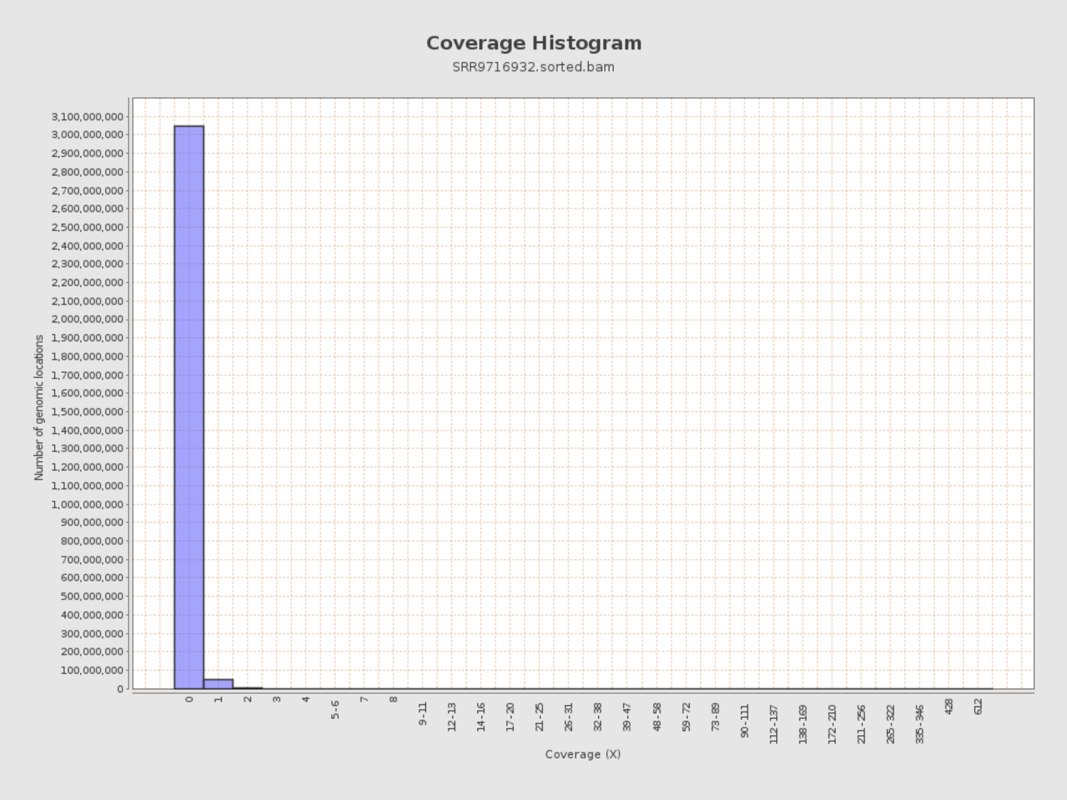
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4597337	0.0184	0.2542
chr2	243199373	4335518	0.0178	0.2871
chr3	198022430	3150469	0.0159	0.1358
chr4	191154276	3358012	0.0176	0.1775
chr5	180915260	3073289	0.017	0.139
chr6	171115067	2862396	0.0167	0.1509
chr7	159138663	3070952	0.0193	0.2203

chr8	146364022	2903369	0.0198	0.255
chr9	141213431	1834473	0.013	0.1391
chr10	135534747	2486596	0.0183	0.2259
chr11	135006516	1968100	0.0146	0.1515
chr12	133851895	2720853	0.0203	0.153
chr13	115169878	1622301	0.0141	0.1276
chr14	107349540	1849130	0.0172	0.1419
chr15	102531392	2030462	0.0198	0.1522
chr16	90354753	1913893	0.0212	0.1604
chr17	81195210	2428922	0.0299	0.1925
chr18	78077248	1022877	0.0131	0.2022
chr19	59128983	1464836	0.0248	0.2281
chr20	63025520	1870656	0.0297	0.1909
chr21	48129895	705196	0.0147	0.1625
chr22	51304566	551061	0.0107	0.1111
chrMT	16571	3557	0.2147	0.4802
chrX	155270560	2871499	0.0185	0.1518
chrY	59373566	243997	0.0041	0.201

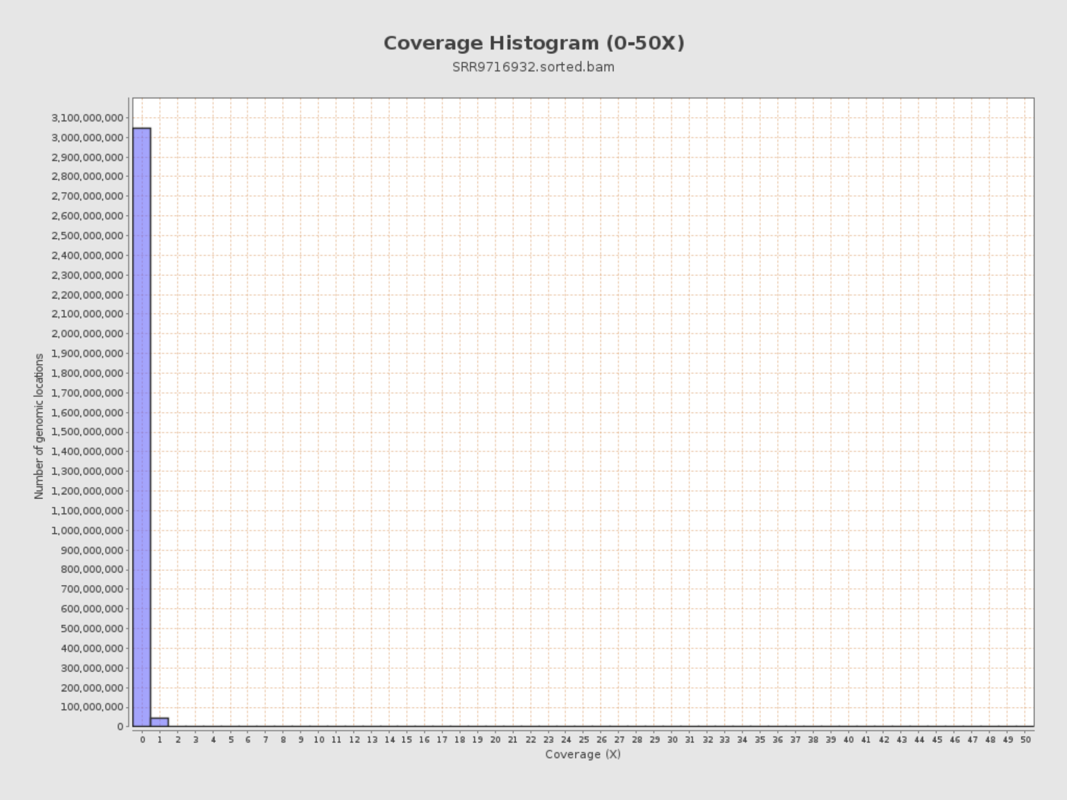
3. Results : Coverage across reference



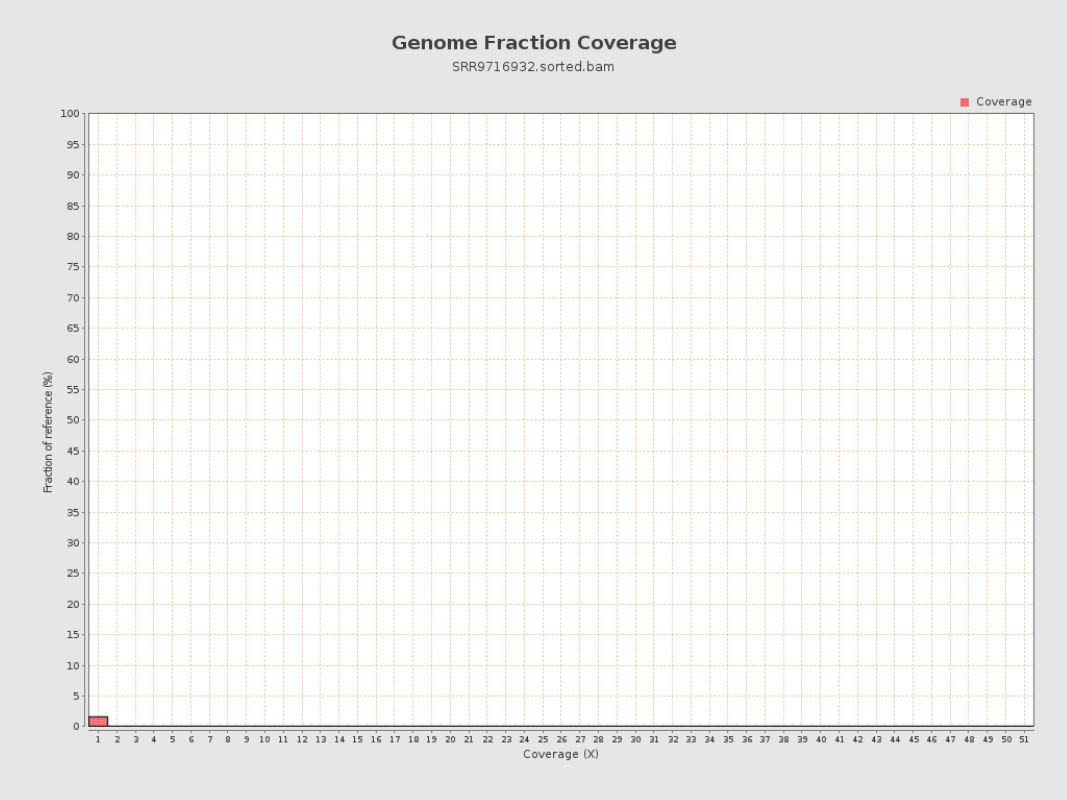
4. Results : Coverage Histogram



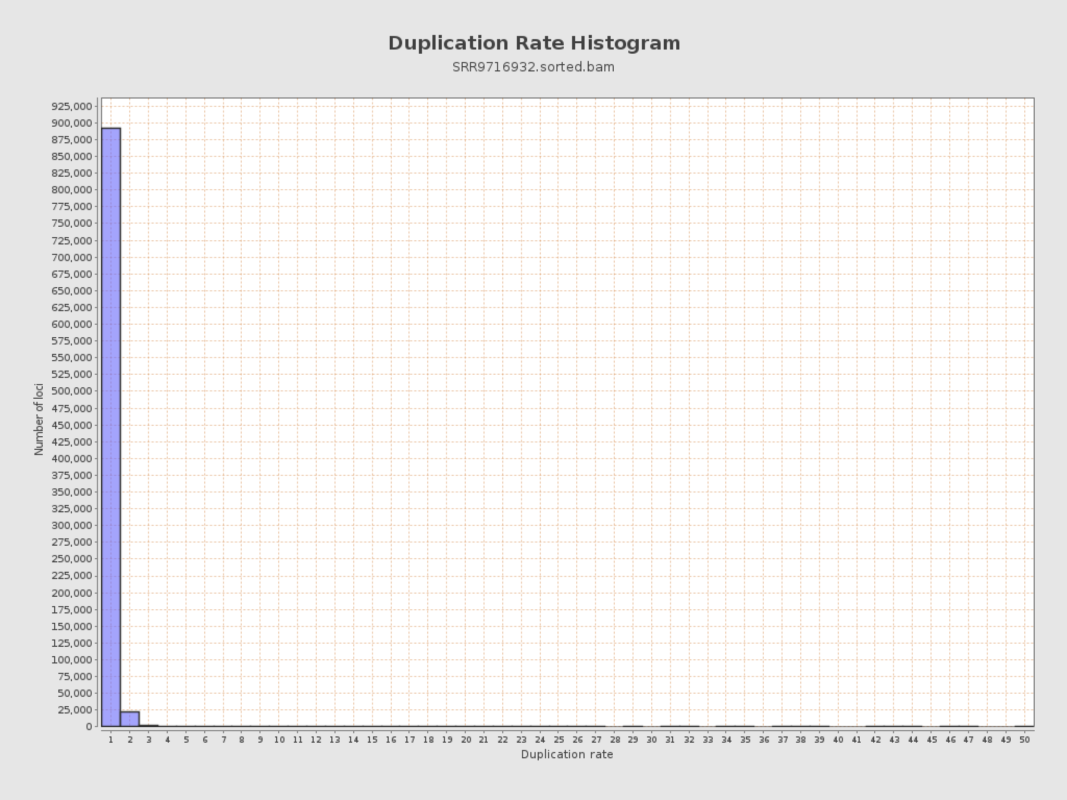
5. Results : Coverage Histogram (0-50X)



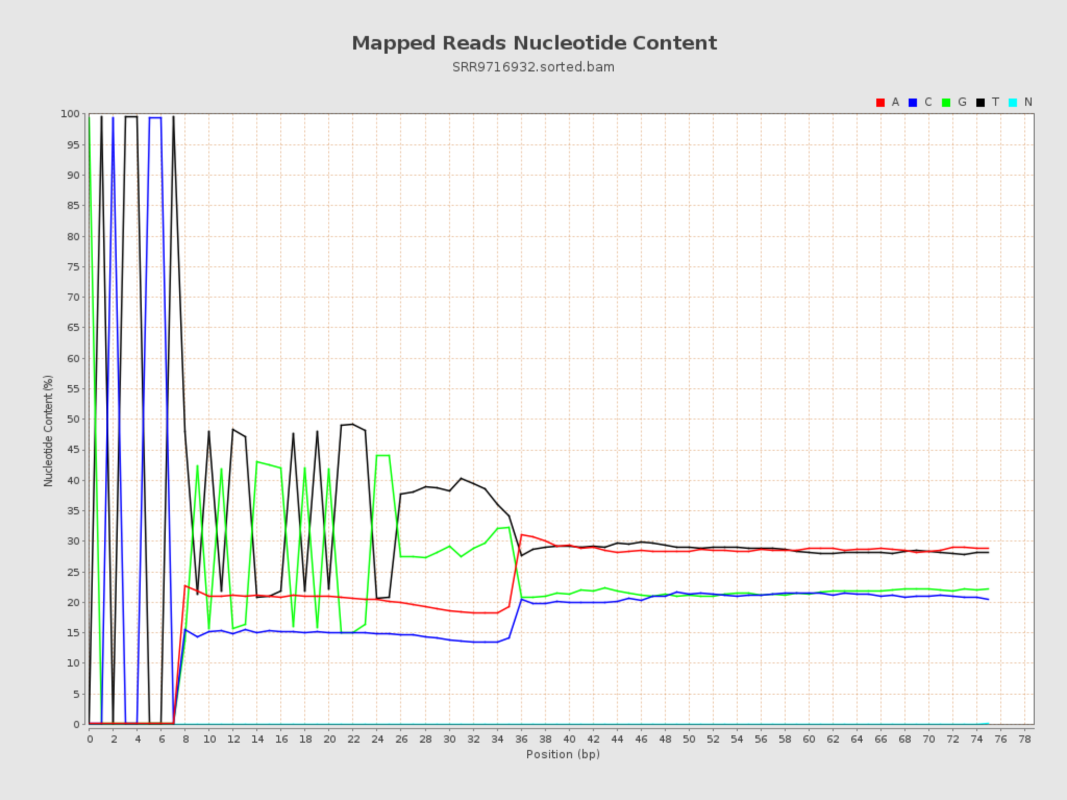
6. Results : Genome Fraction Coverage



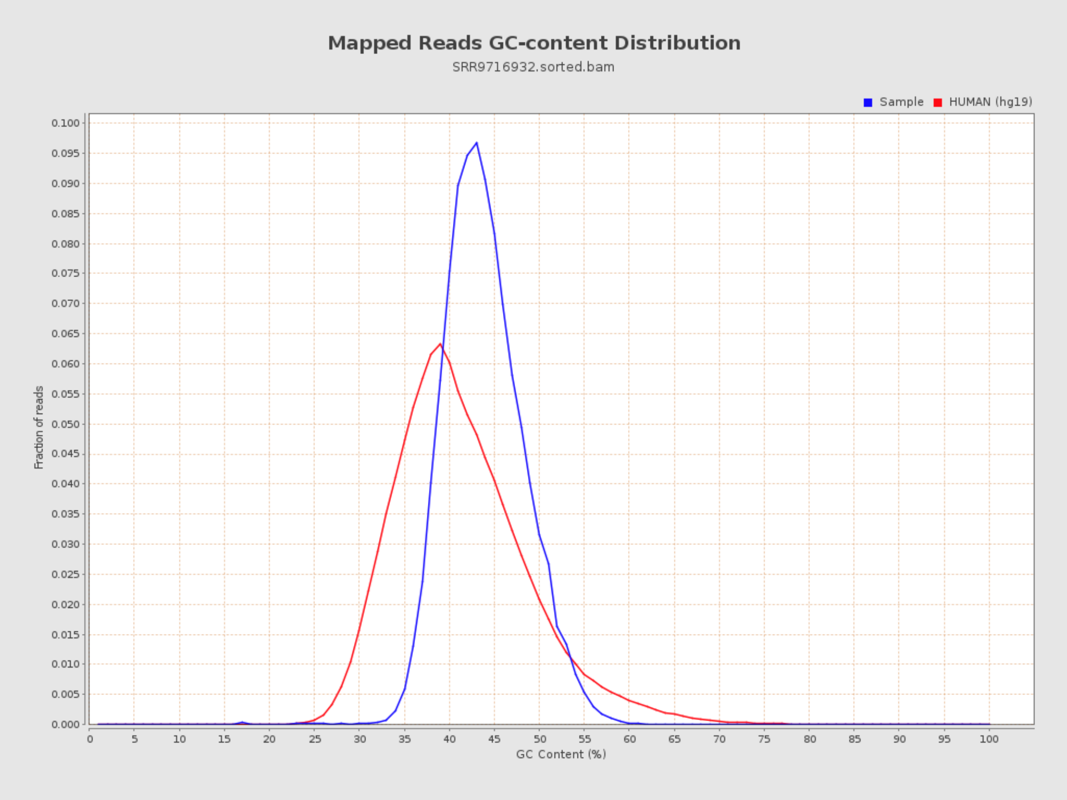
7. Results : Duplication Rate Histogram



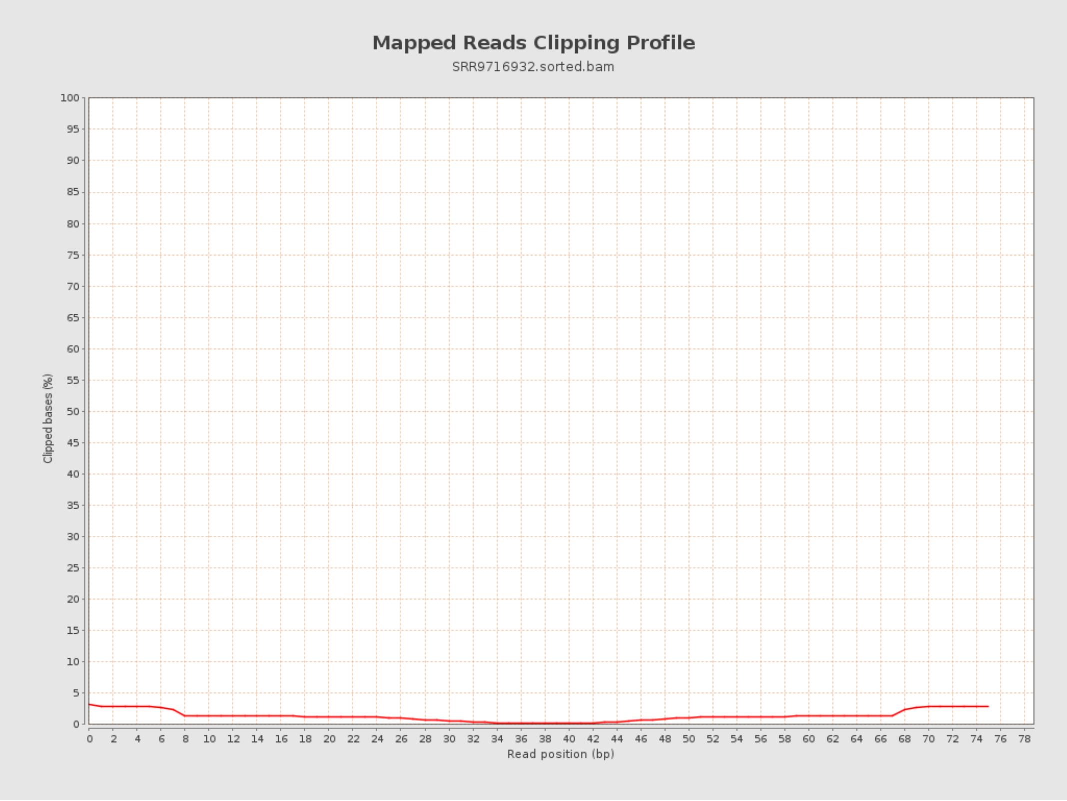
8. Results : Mapped Reads Nucleotide Content



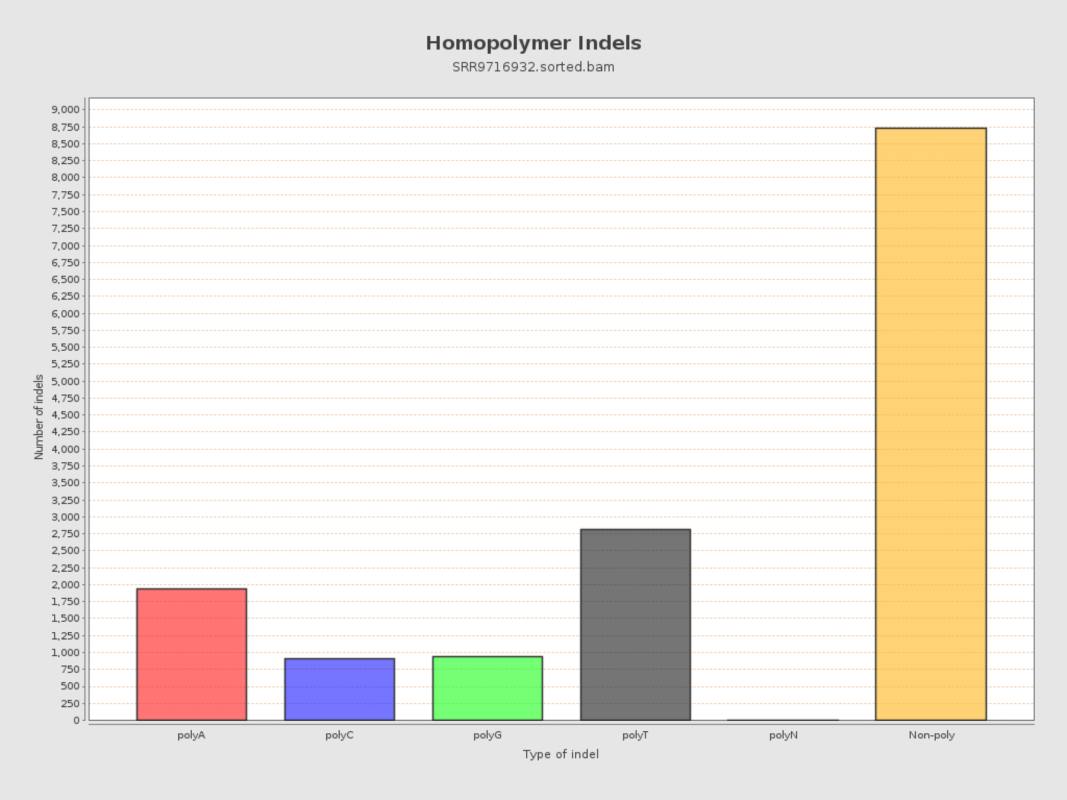
9. Results : Mapped Reads GC-content Distribution



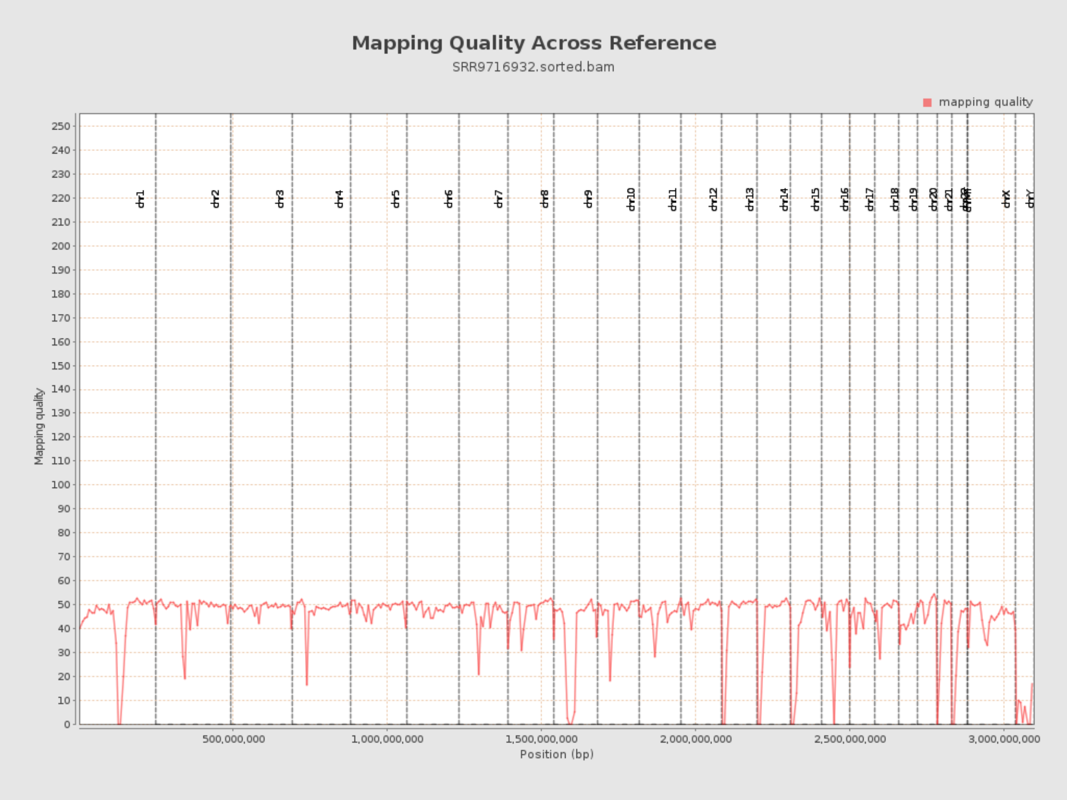
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram