Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:34:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716634.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_SRR9716634 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716634.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:34:36 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716634.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,192,006
Mapped reads	1,031,511 / 86.54%
Unmapped reads	160,495 / 13.46%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,166 / 0.43%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	29,466 / 2.47%
Duplication rate	2.06%
Clipped reads	1,034,001 / 86.74%

2.2. ACGT Content

Number/percentage of A's	14,350,323 / 24.09%
Number/percentage of C's	11,410,837 / 19.15%
Number/percentage of T's	18,847,872 / 31.63%
Number/percentage of G's	14,971,707 / 25.13%
Number/percentage of N's	763 / 0%
GC Percentage	44.28%

2.3. Coverage

Mean	0.0193

Standard Deviation	0.2167

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

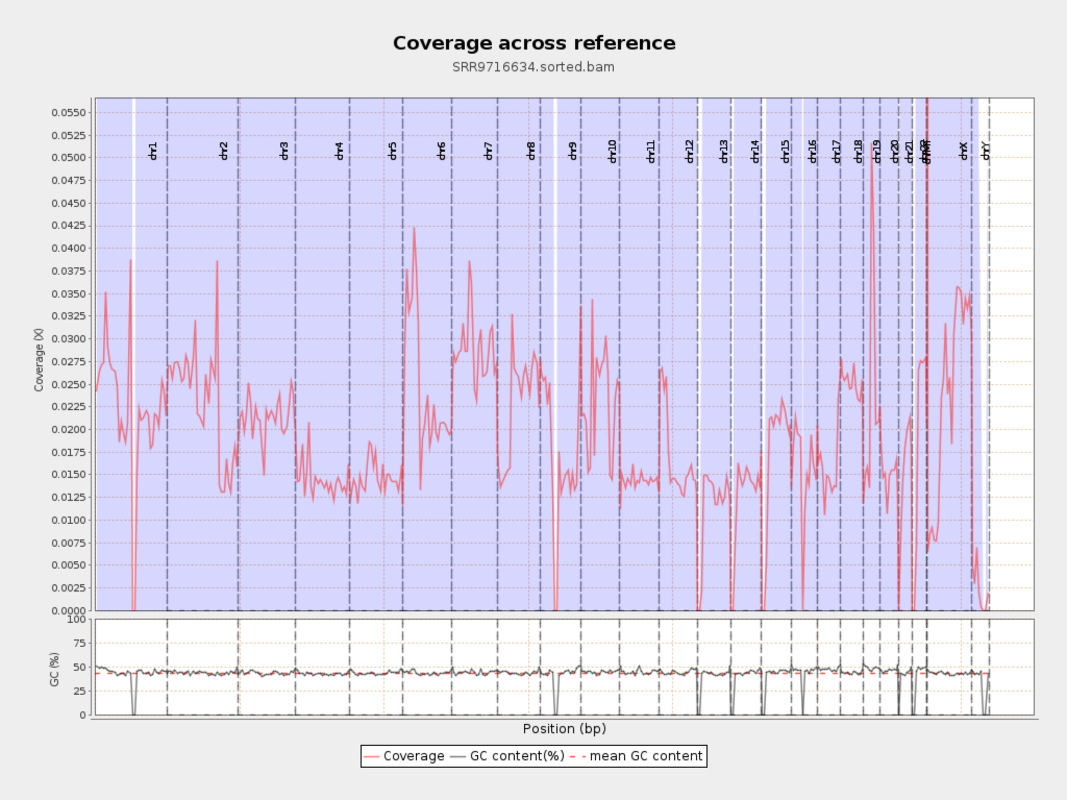
General error rate	0.5%
Mismatches	293,482
Insertions	3,778
Mapped reads with at least one insertion	0.36%
Deletions	10,327
Mapped reads with at least one deletion	1%
Homopolymer indels	42.88%

2.6. Chromosome stats

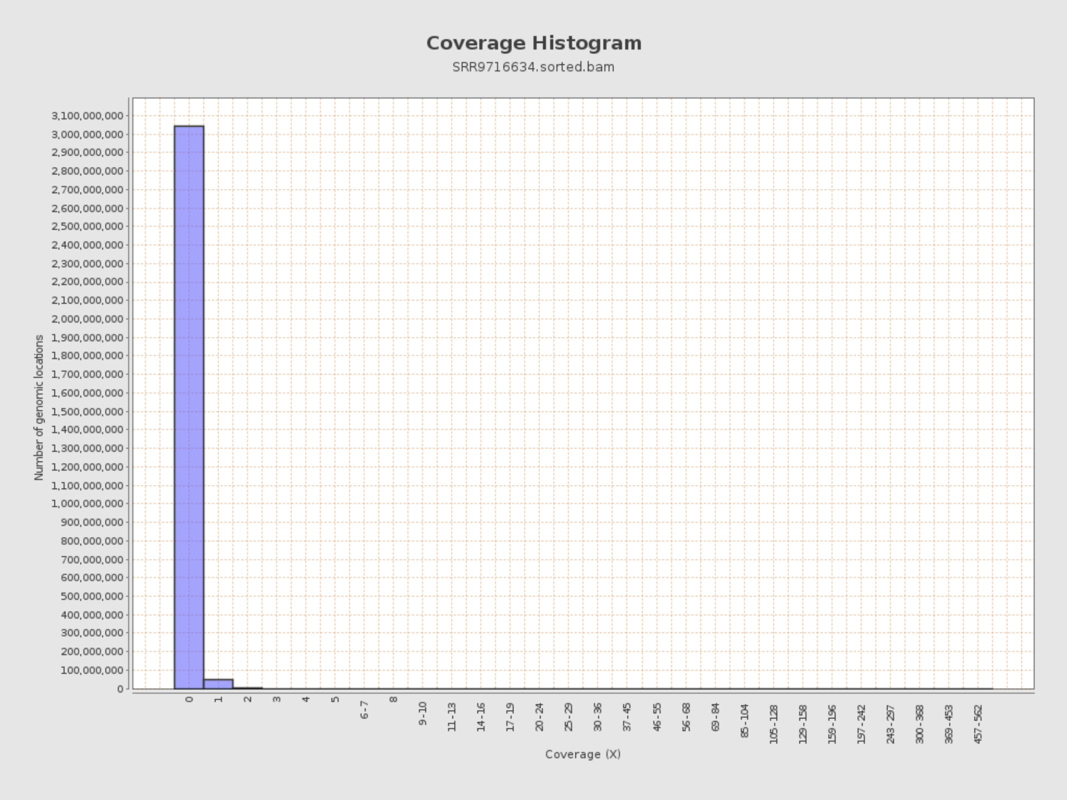
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5507112	0.0221	0.4454
chr2	243199373	5627984	0.0231	0.2549
chr3	198022430	4236365	0.0214	0.1554
chr4	191154276	2779324	0.0145	0.1337
chr5	180915260	2671361	0.0148	0.1306
chr6	171115067	4175819	0.0244	0.1917
chr7	159138663	4595481	0.0289	0.29

chr8	146364022	3329726	0.0227	0.1783
chr9	141213431	2318059	0.0164	0.1653
chr10	135534747	3121006	0.023	0.1903
chr11	135006516	1943229	0.0144	0.158
chr12	133851895	2283881	0.0171	0.1406
chr13	115169878	1293007	0.0112	0.113
chr14	107349540	1312947	0.0122	0.1231
chr15	102531392	1740382	0.017	0.1408
chr16	90354753	1379870	0.0153	0.1383
chr17	81195210	1292276	0.0159	0.1364
chr18	78077248	1964862	0.0252	0.2824
chr19	59128983	1472354	0.0249	0.3077
chr20	63025520	943515	0.015	0.1312
chr21	48129895	719540	0.0149	0.1353
chr22	51304566	942788	0.0184	0.1445
chrMT	16571	112137	6.7671	4.4409
chrX	155270560	3698459	0.0238	0.1804
chrY	59373566	136164	0.0023	0.062

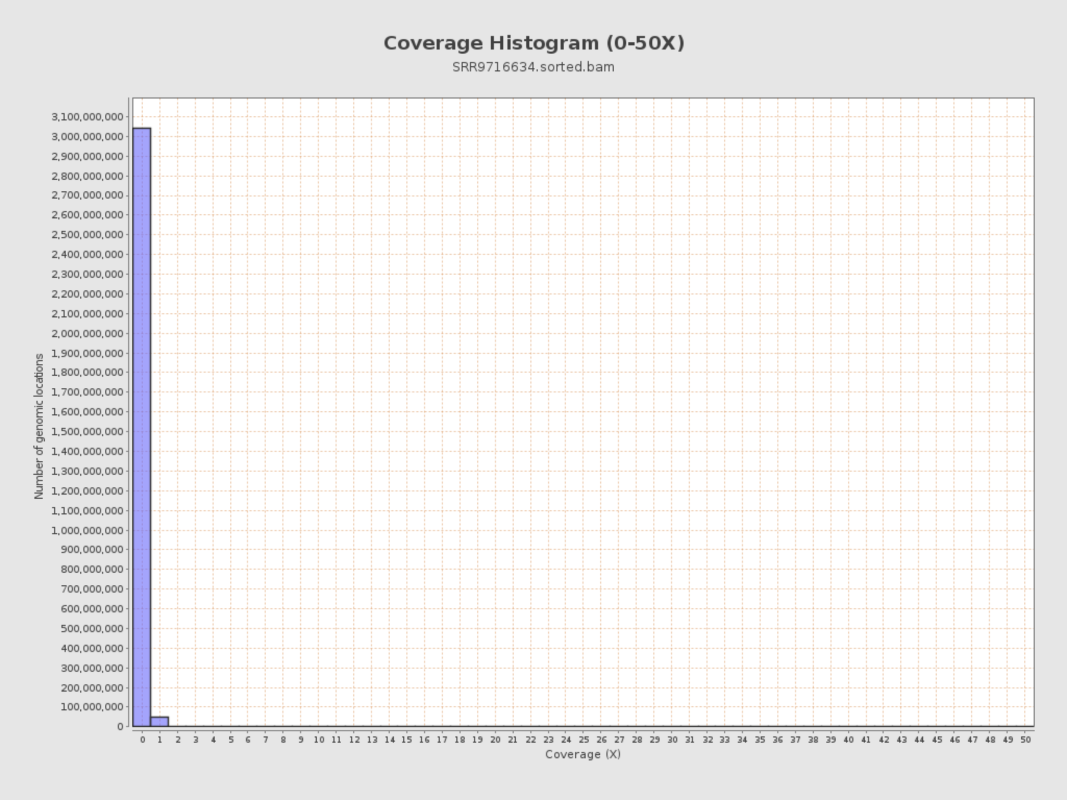
3. Results : Coverage across reference



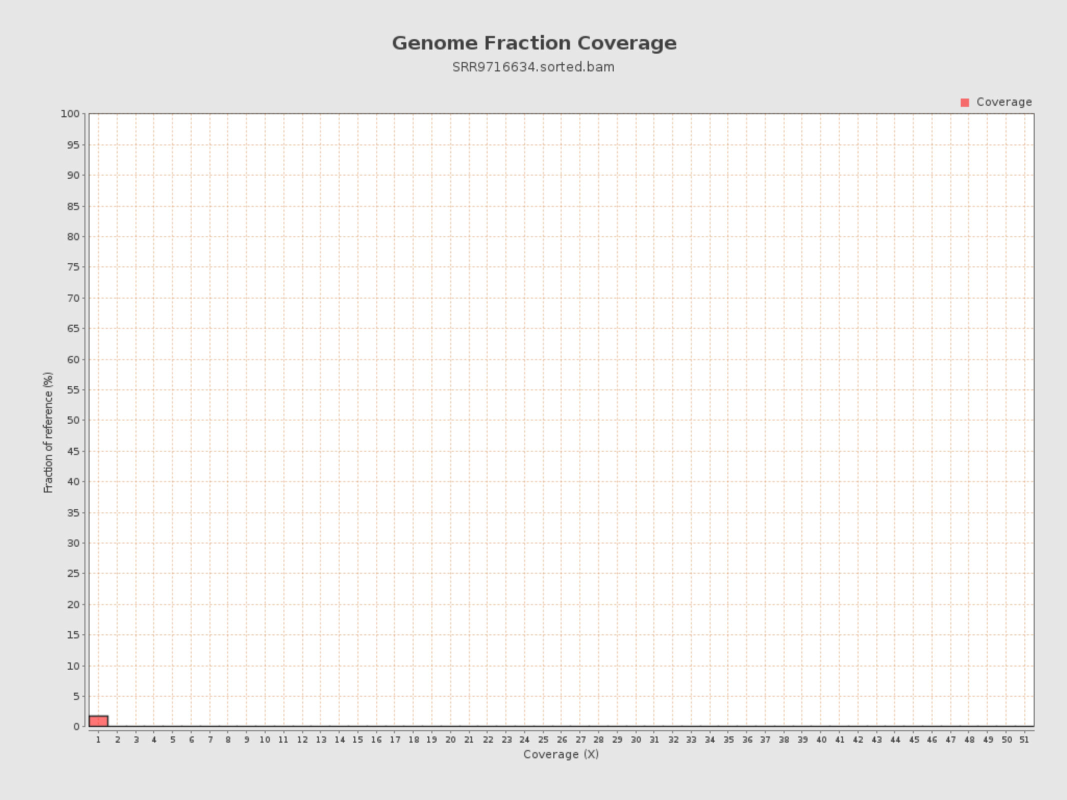
4. Results : Coverage Histogram



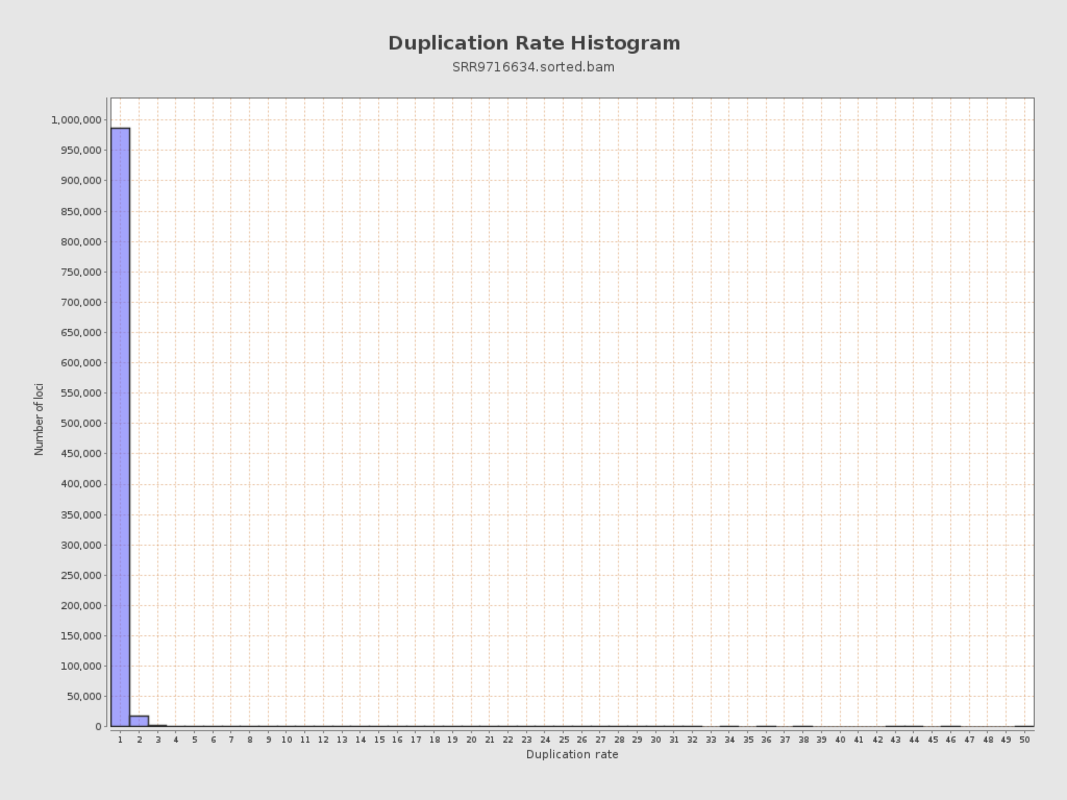
5. Results : Coverage Histogram (0-50X)



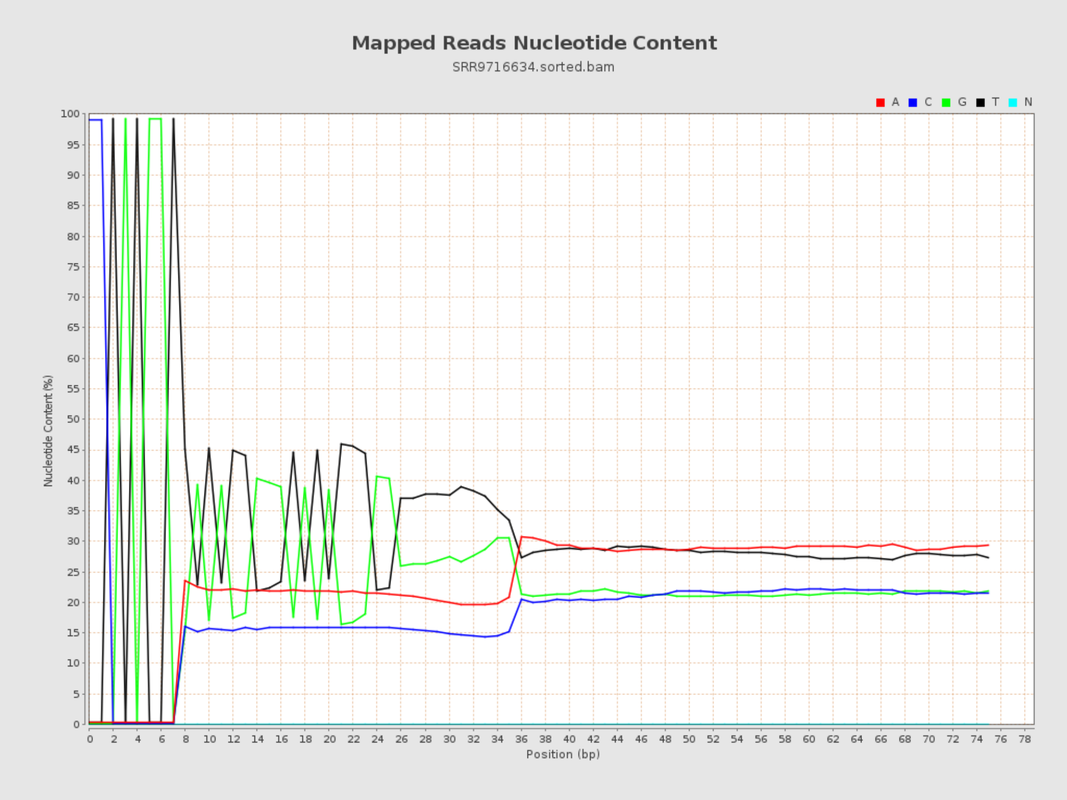
6. Results : Genome Fraction Coverage



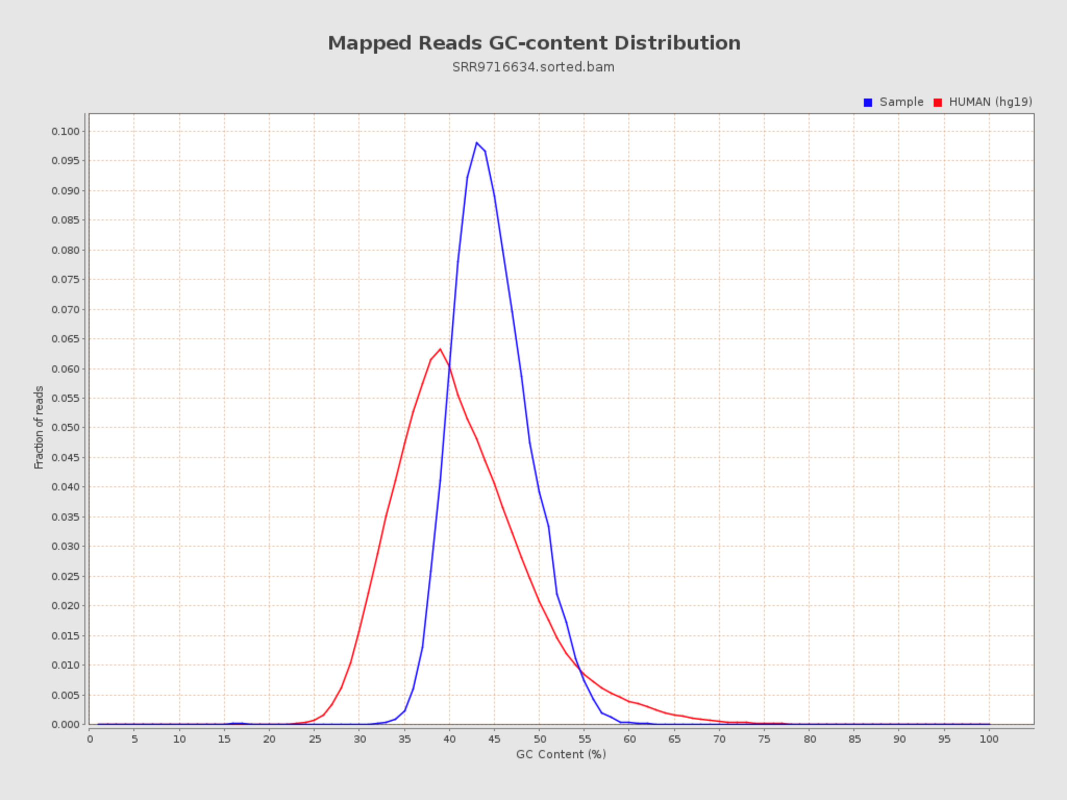
7. Results : Duplication Rate Histogram



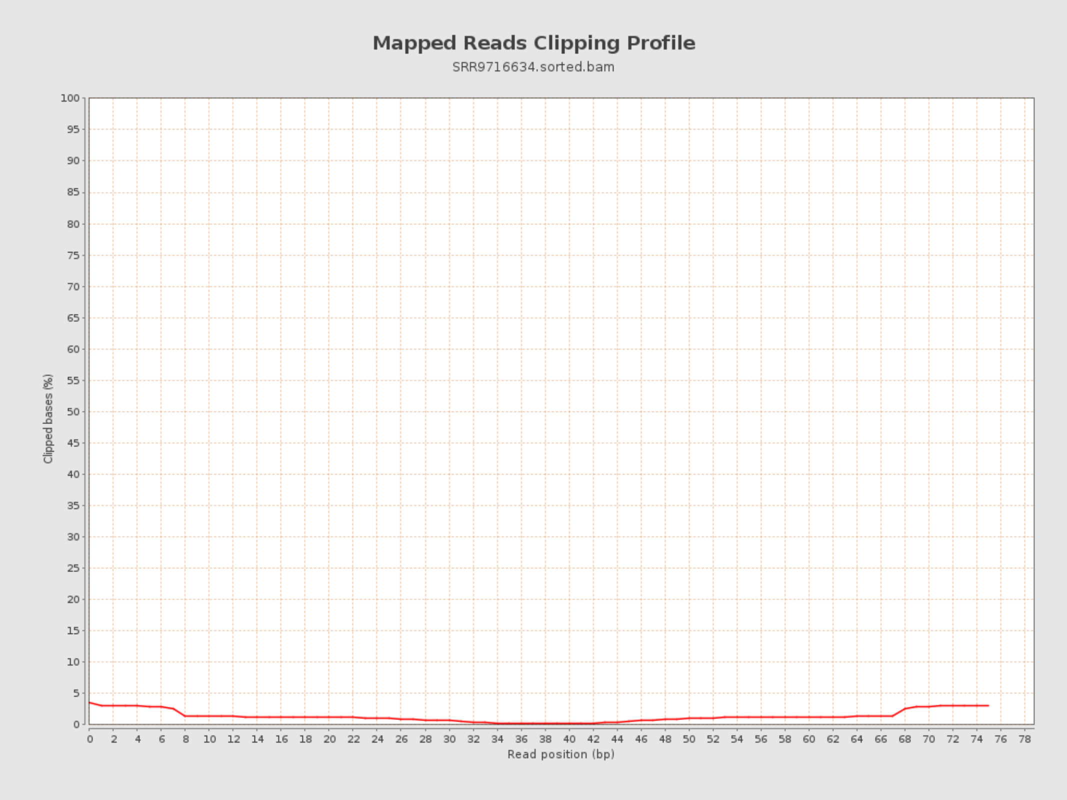
8. Results : Mapped Reads Nucleotide Content



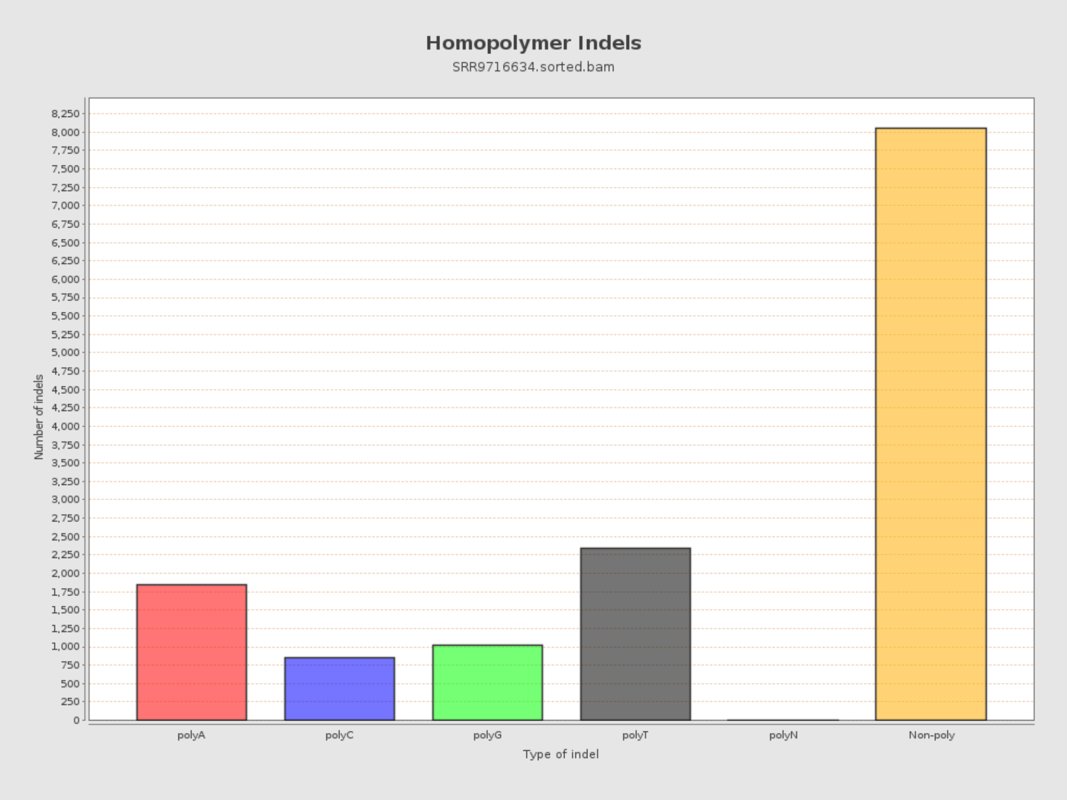
9. Results : Mapped Reads GC-content Distribution



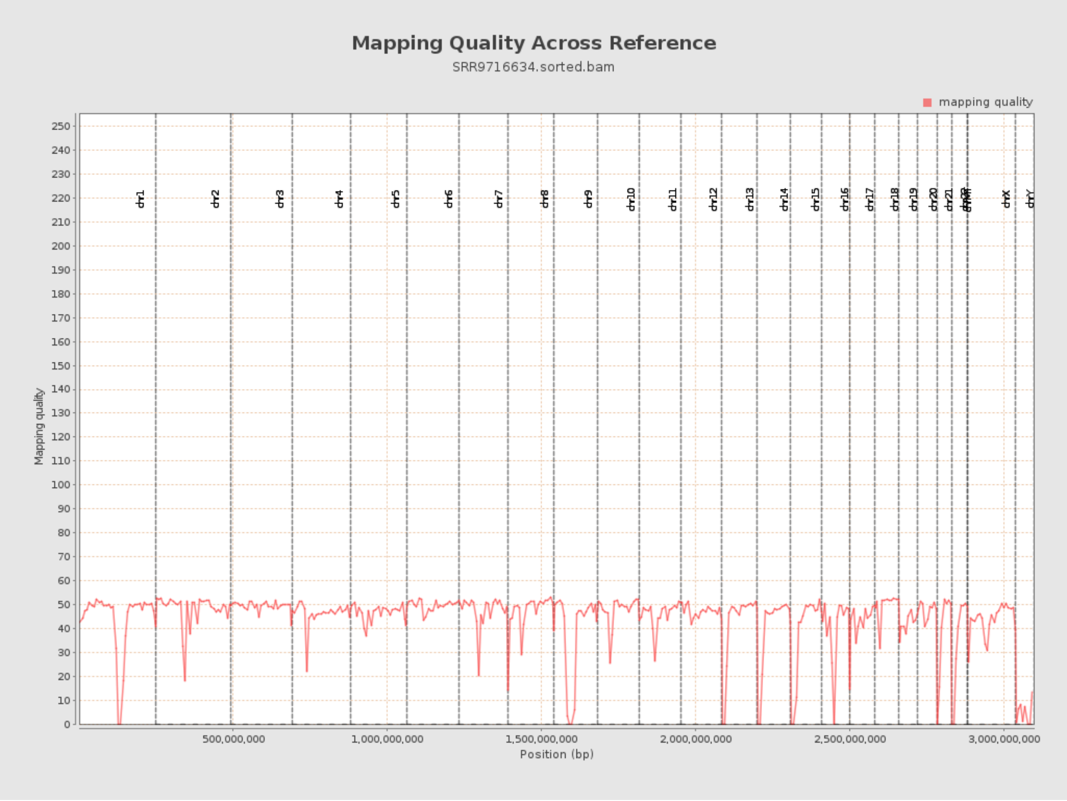
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram