Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 21:53:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716976.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_SRR9716976 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716976.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 21:53:16 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716976.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,602,714
Mapped reads	2,274,636 / 87.39%
Unmapped reads	328,078 / 12.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,210 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	72,334 / 2.78%
Duplication rate	2.2%
Clipped reads	2,282,171 / 87.68%

2.2. ACGT Content

Number/percentage of A's	30,648,403 / 23.66%
Number/percentage of C's	25,896,036 / 19.99%
Number/percentage of T's	39,786,690 / 30.72%
Number/percentage of G's	33,193,548 / 25.63%
Number/percentage of N's	1,874 / 0%
GC Percentage	45.62%

2.3. Coverage

Mean	0.0419

Standard Deviation	0.341

2.4. Mapping Quality

Mean Mapping Quality	42.34

2.5. Mismatches and indels

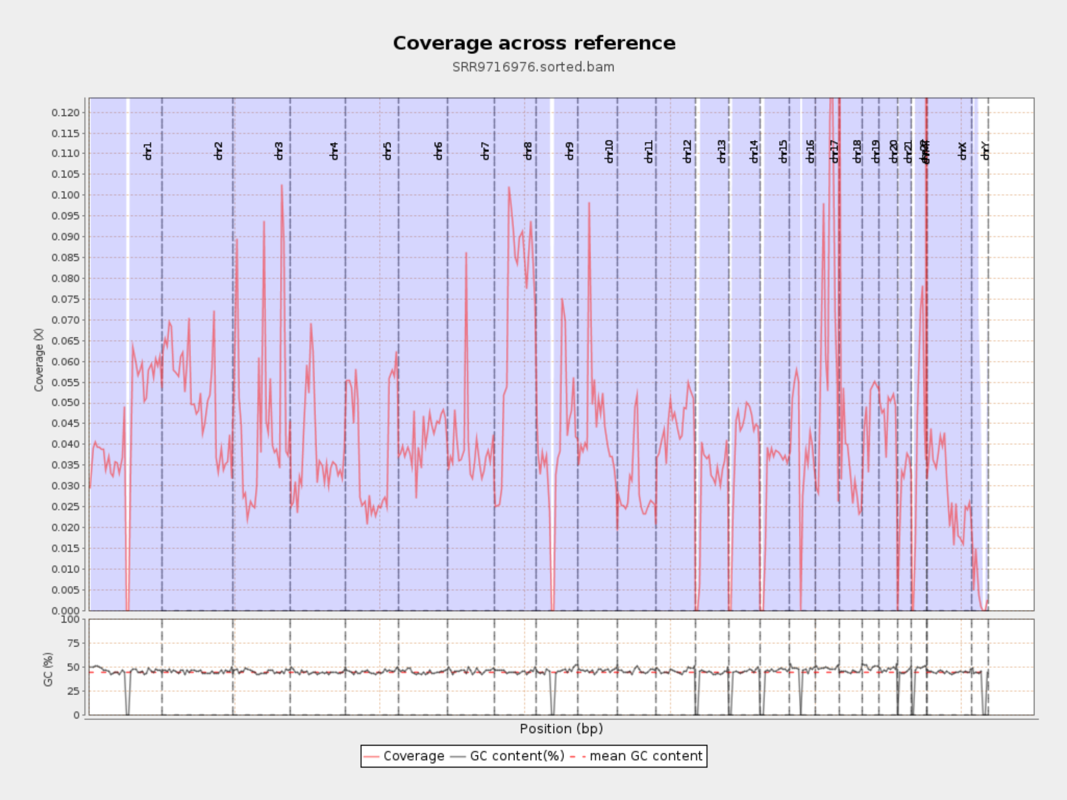
General error rate	0.52%
Mismatches	656,434
Insertions	7,523
Mapped reads with at least one insertion	0.33%
Deletions	23,775
Mapped reads with at least one deletion	1.04%
Homopolymer indels	41.47%

2.6. Chromosome stats

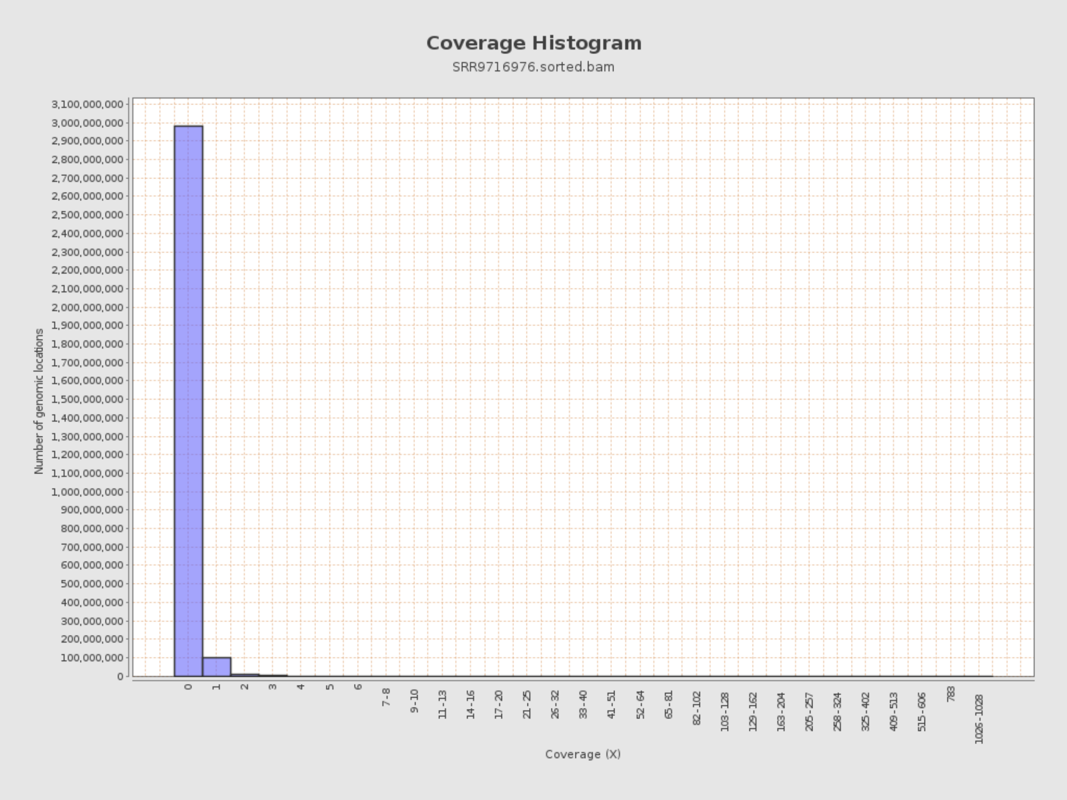
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10763757	0.0432	0.415
chr2	243199373	12675890	0.0521	0.5045
chr3	198022430	9303517	0.047	0.2576
chr4	191154276	7218663	0.0378	0.2322
chr5	180915260	6954527	0.0384	0.2193
chr6	171115067	7083318	0.0414	0.2662
chr7	159138663	6305849	0.0396	0.6947

chr8	146364022	10411024	0.0711	0.3621
chr9	141213431	5437301	0.0385	0.26
chr10	135534747	6175489	0.0456	0.4038
chr11	135006516	3901219	0.0289	0.2501
chr12	133851895	6038033	0.0451	0.2464
chr13	115169878	3384159	0.0294	0.1919
chr14	107349540	4144578	0.0386	0.2258
chr15	102531392	3125007	0.0305	0.2032
chr16	90354753	3589590	0.0397	0.2365
chr17	81195210	5692112	0.0701	0.3169
chr18	78077248	3086052	0.0395	0.3977
chr19	59128983	2850544	0.0482	0.3818
chr20	63025520	2991386	0.0475	0.2486
chr21	48129895	1397432	0.029	0.2001
chr22	51304566	2063738	0.0402	0.23
chrMT	16571	108693	6.5592	4.2889
chrX	155270560	4571767	0.0294	0.2252
chrY	59373566	290896	0.0049	0.1164

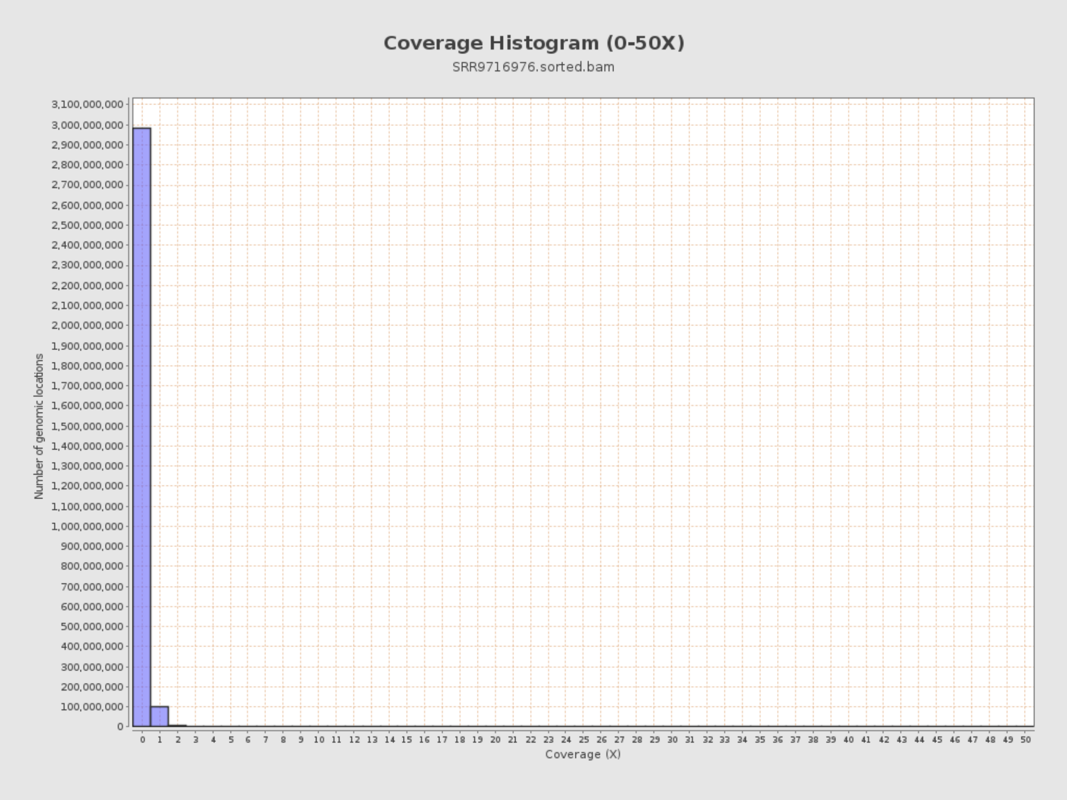
3. Results : Coverage across reference



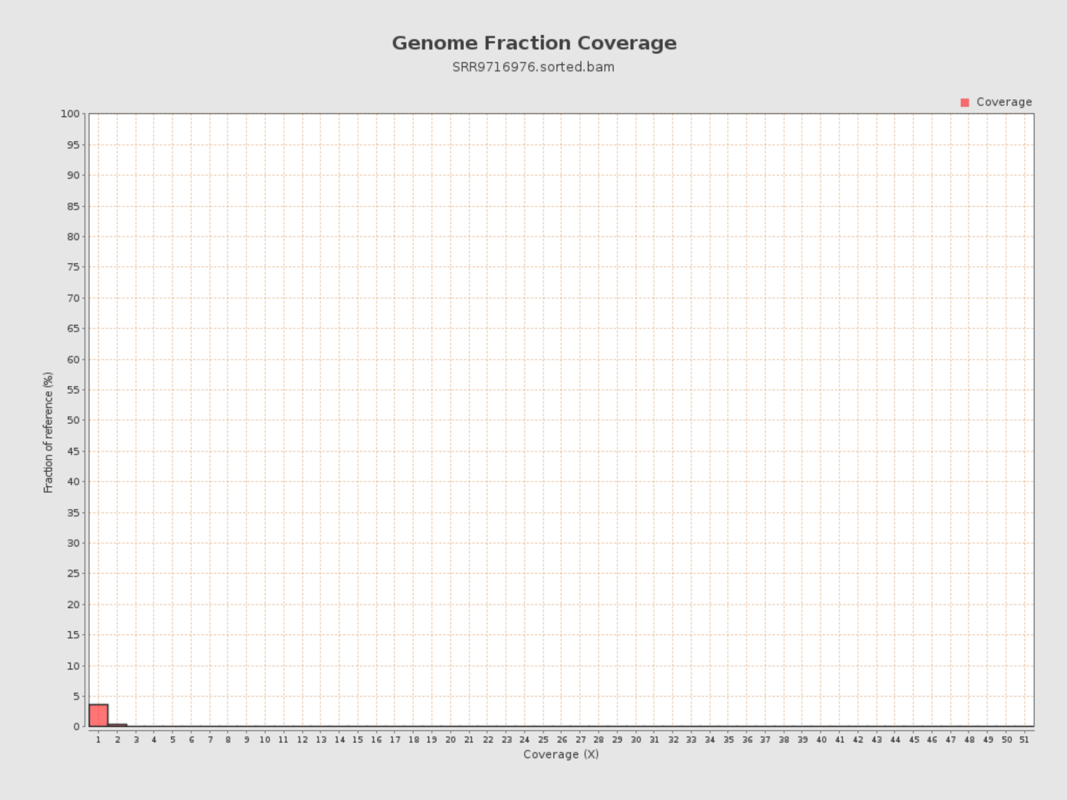
4. Results : Coverage Histogram



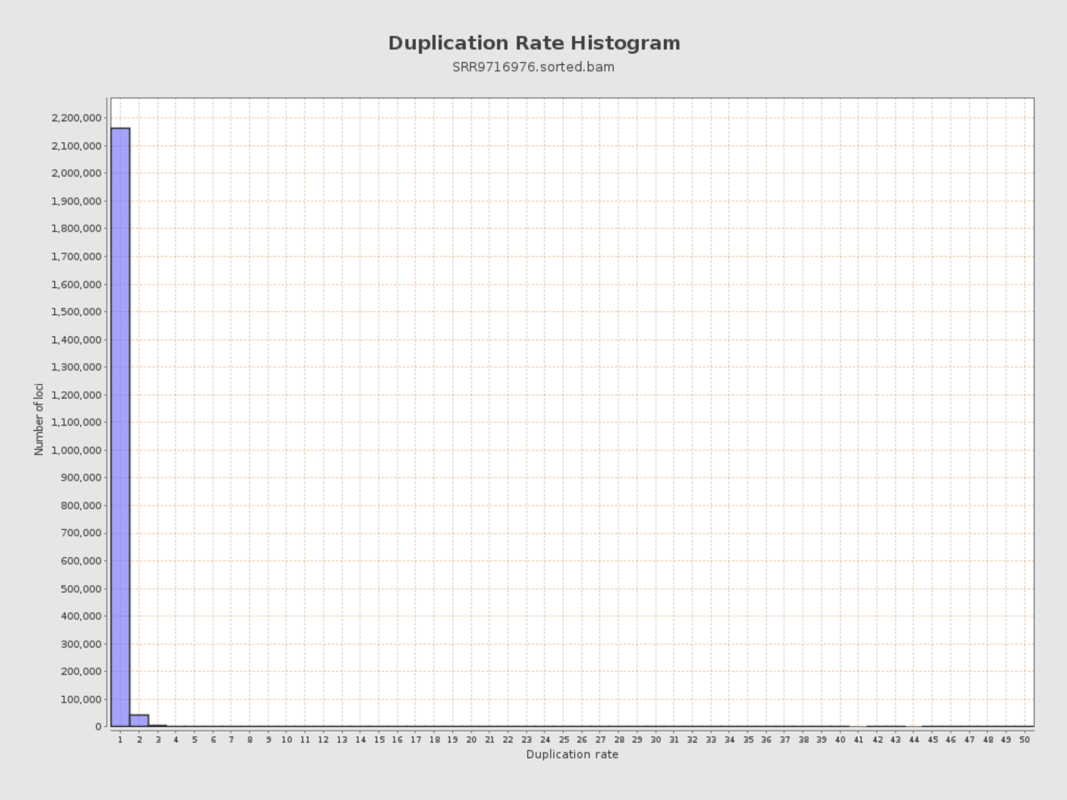
5. Results : Coverage Histogram (0-50X)



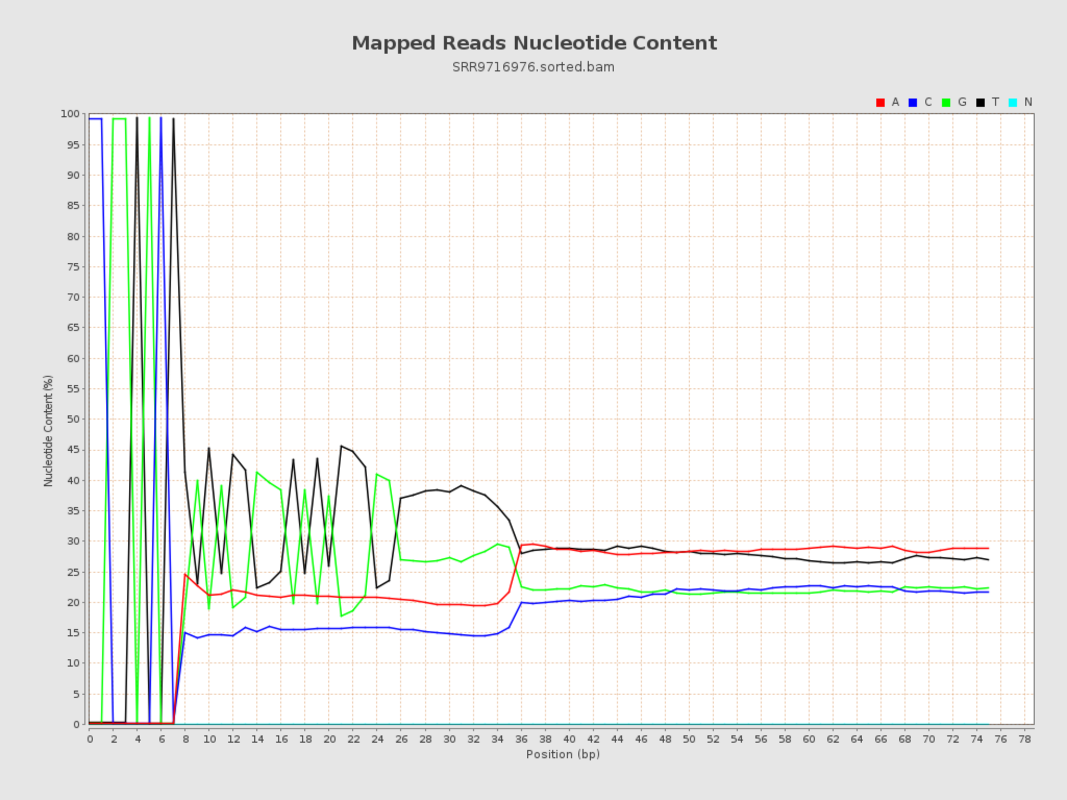
6. Results : Genome Fraction Coverage



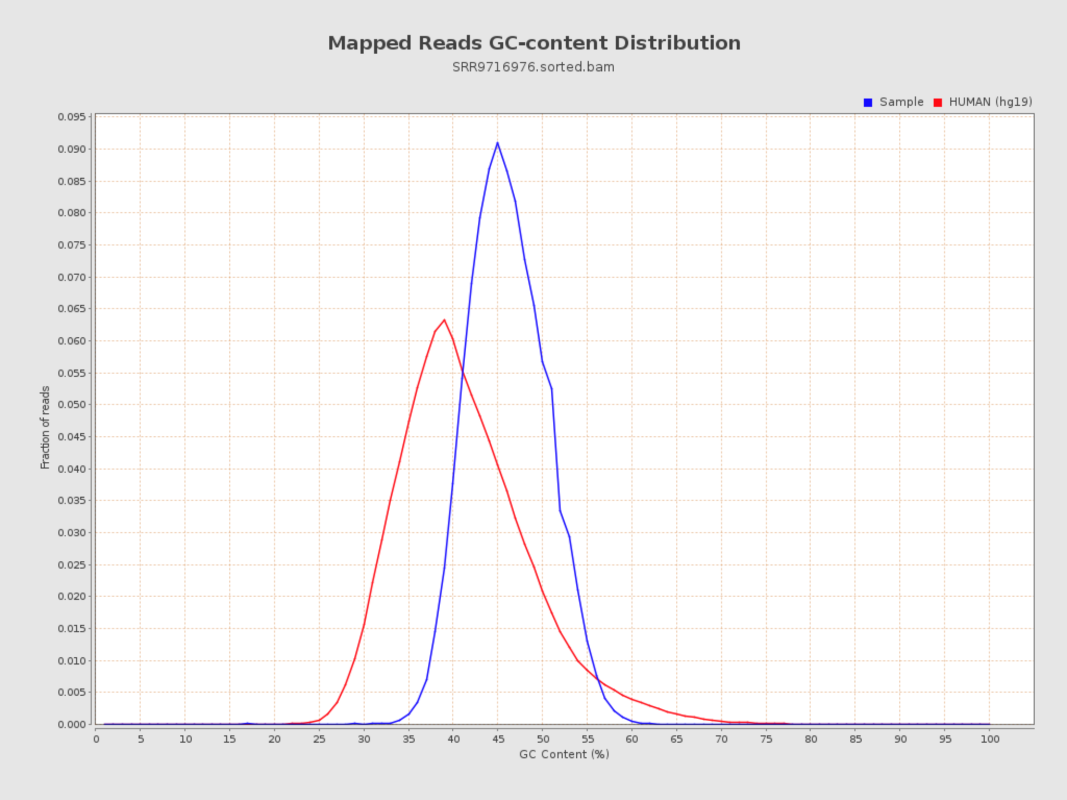
7. Results : Duplication Rate Histogram



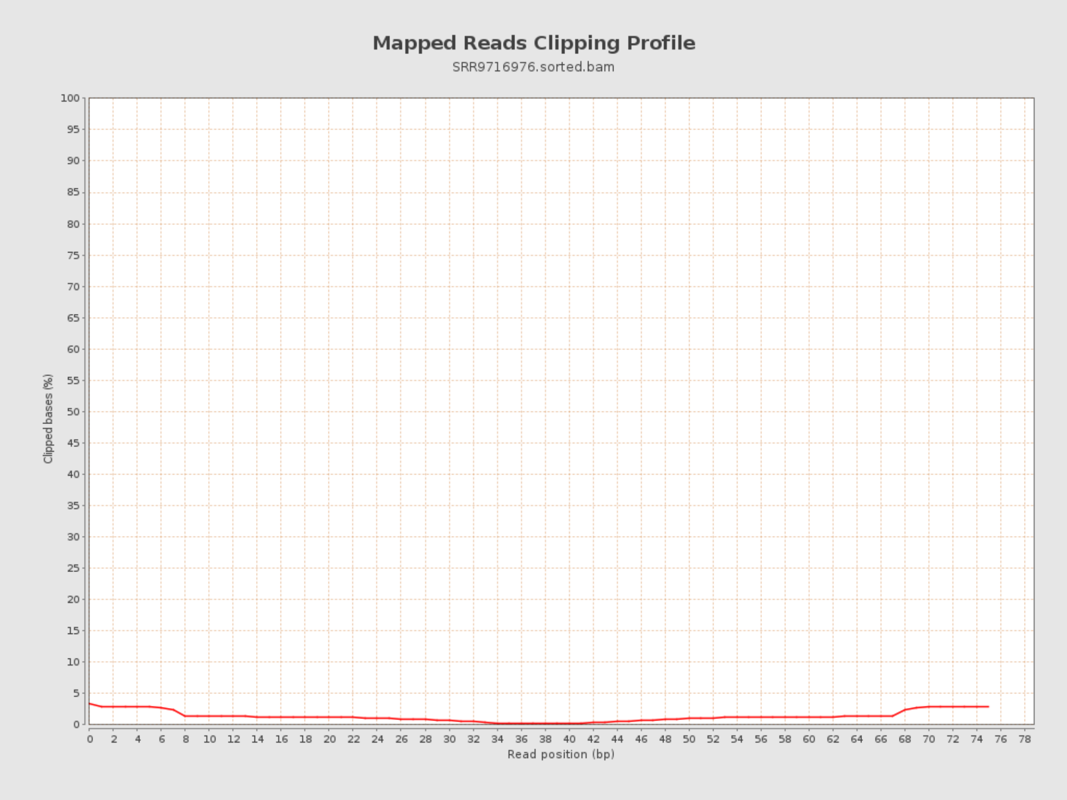
8. Results : Mapped Reads Nucleotide Content



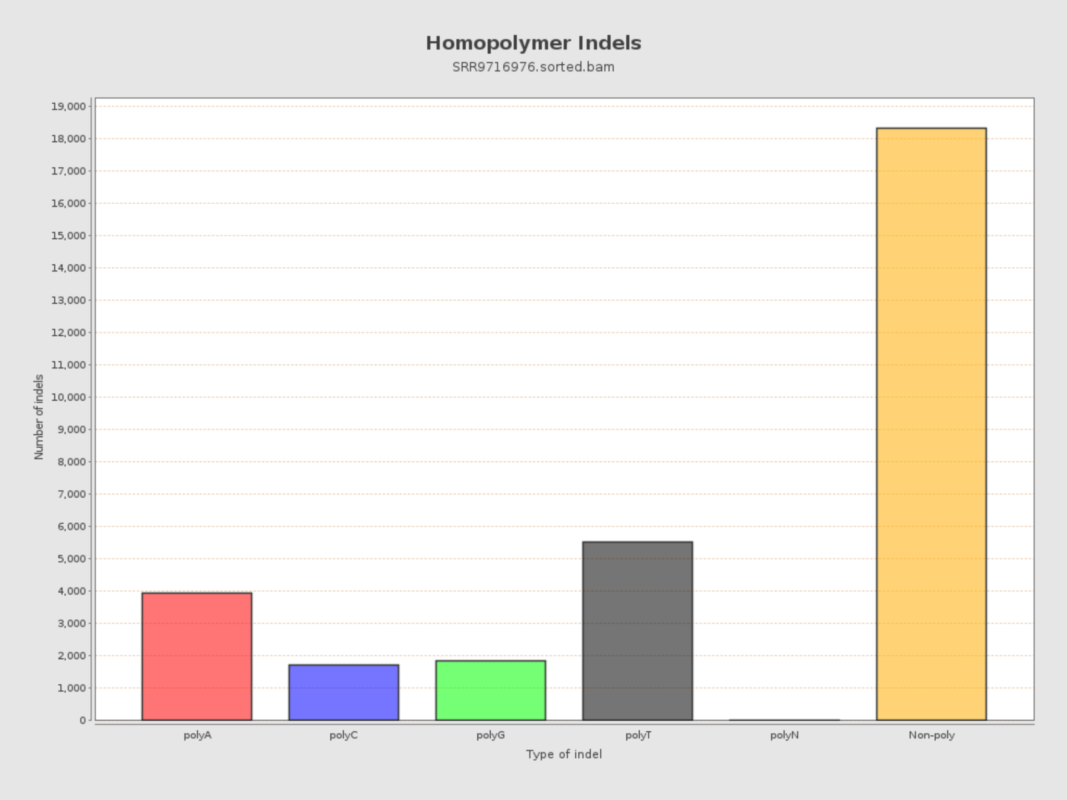
9. Results : Mapped Reads GC-content Distribution



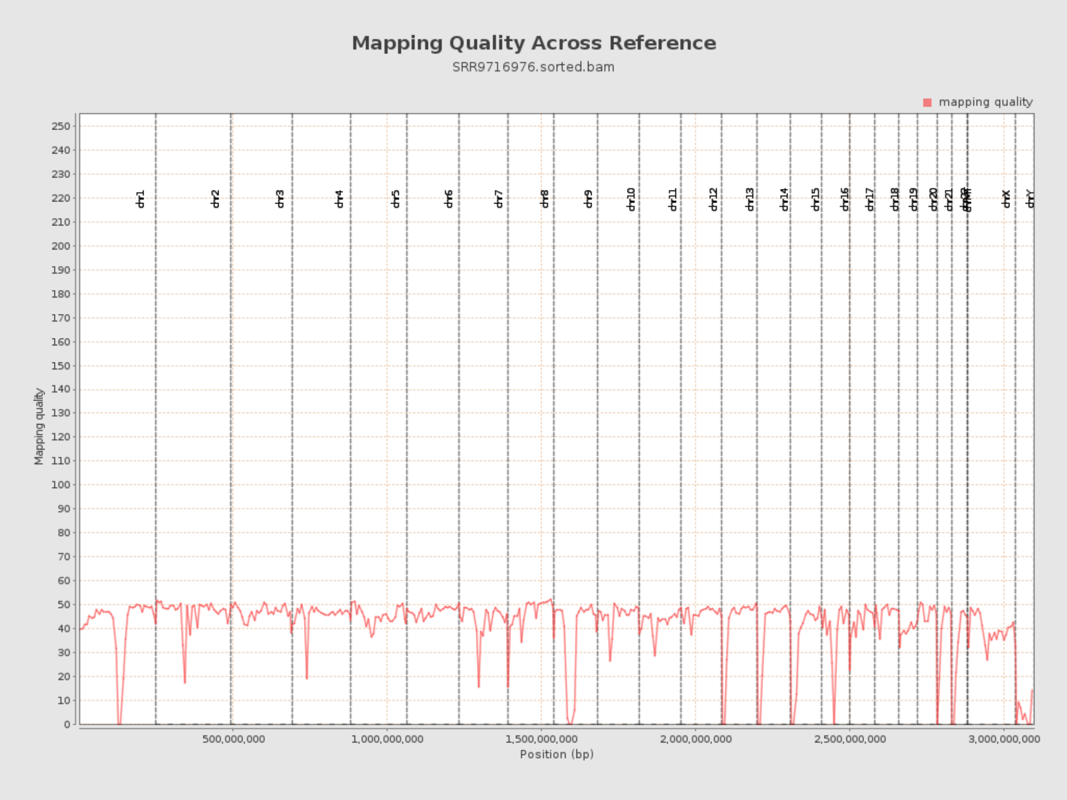
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram