Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 15:57:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716870.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_SRR9716870 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716870.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 15:57:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716870.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,981,805
Mapped reads	1,790,437 / 90.34%
Unmapped reads	191,368 / 9.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,276 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	54,950 / 2.77%
Duplication rate	2.35%
Clipped reads	1,793,194 / 90.48%

2.2. ACGT Content

Number/percentage of A's	25,731,044 / 25.21%
Number/percentage of C's	18,890,782 / 18.51%
Number/percentage of T's	31,314,353 / 30.68%
Number/percentage of G's	26,144,641 / 25.61%
Number/percentage of N's	2,223 / 0%
GC Percentage	44.12%

2.3. Coverage

Mean	0.033

Standard Deviation	0.2515

2.4. Mapping Quality

Mean Mapping Quality	44.21

2.5. Mismatches and indels

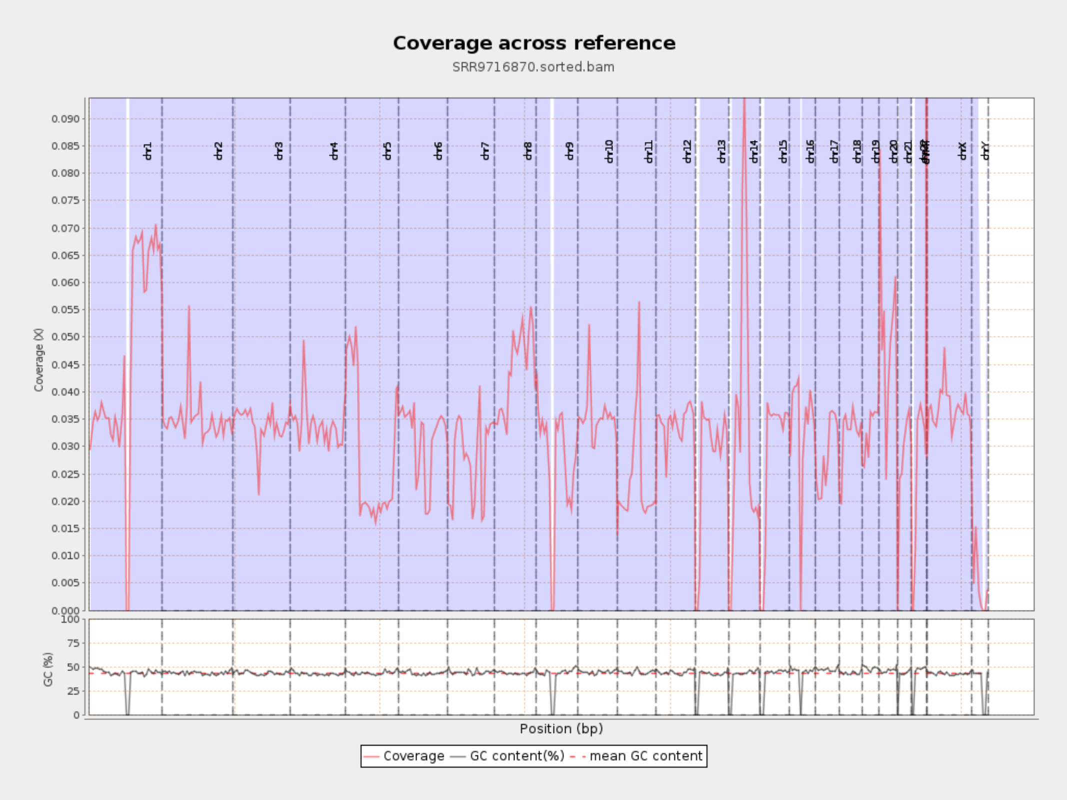
General error rate	0.49%
Mismatches	493,485
Insertions	6,298
Mapped reads with at least one insertion	0.35%
Deletions	16,339
Mapped reads with at least one deletion	0.91%
Homopolymer indels	40.61%

2.6. Chromosome stats

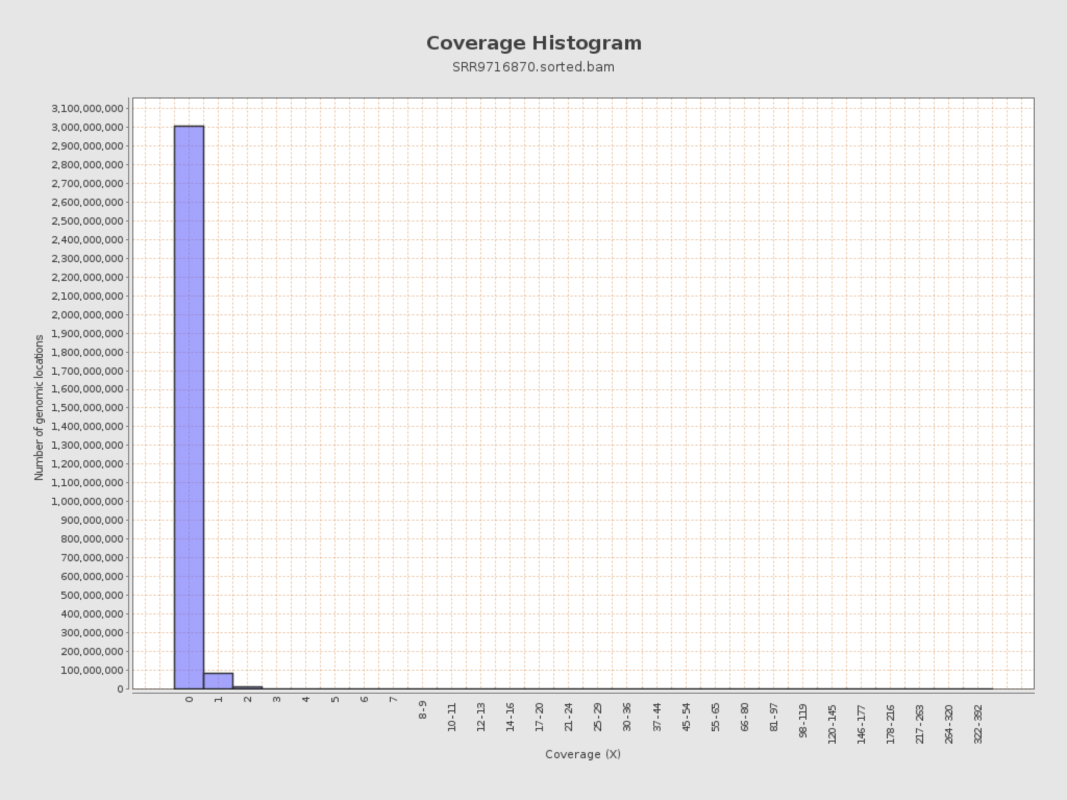
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11411469	0.0458	0.3795
chr2	243199373	8538938	0.0351	0.2861
chr3	198022430	6709084	0.0339	0.2023
chr4	191154276	6463528	0.0338	0.2163
chr5	180915260	5081038	0.0281	0.1871
chr6	171115067	5392107	0.0315	0.209
chr7	159138663	4390691	0.0276	0.2227

chr8	146364022	6453802	0.0441	0.2669
chr9	141213431	3724961	0.0264	0.2603
chr10	135534747	4821492	0.0356	0.2621
chr11	135006516	3225439	0.0239	0.2293
chr12	133851895	4581823	0.0342	0.2063
chr13	115169878	3157497	0.0274	0.1796
chr14	107349540	3584772	0.0334	0.213
chr15	102531392	2950374	0.0288	0.1871
chr16	90354753	3050297	0.0338	0.22
chr17	81195210	2328299	0.0287	0.1928
chr18	78077248	2512498	0.0322	0.4698
chr19	59128983	1950441	0.033	0.2929
chr20	63025520	3183418	0.0505	0.2545
chr21	48129895	1324572	0.0275	0.2014
chr22	51304566	1234336	0.0241	0.1696
chrMT	16571	5445	0.3286	0.6395
chrX	155270560	5742119	0.037	0.2393
chrY	59373566	292148	0.0049	0.1098

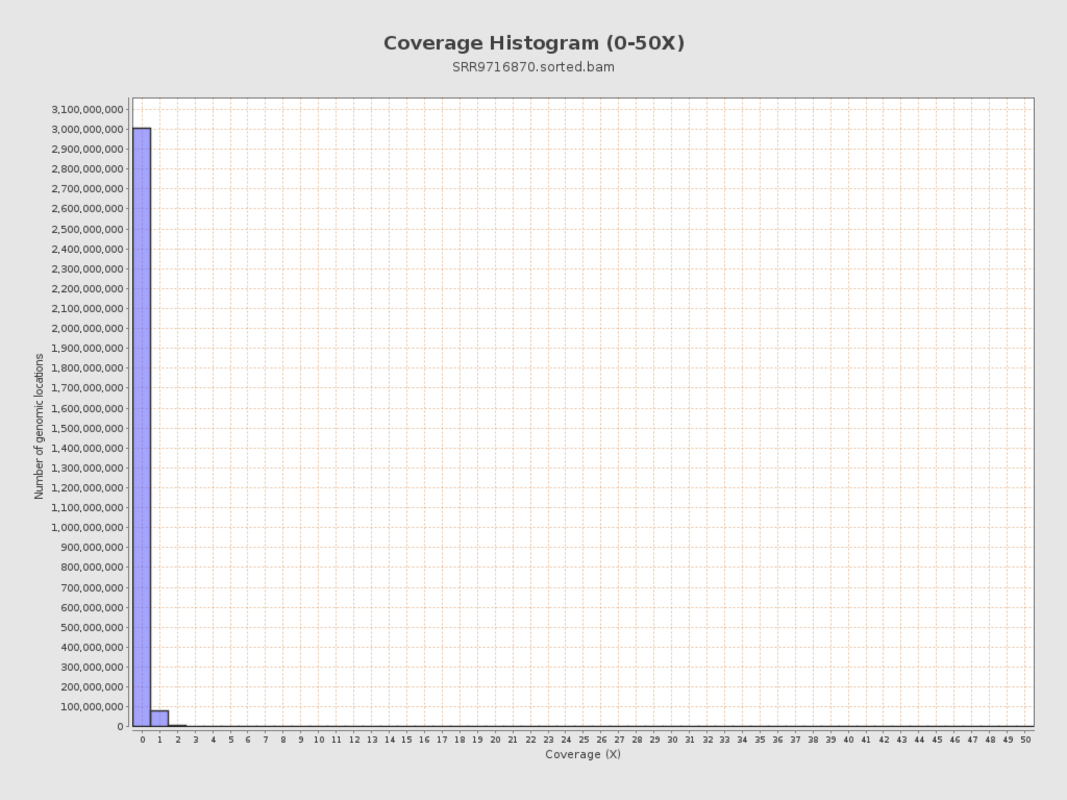
3. Results : Coverage across reference



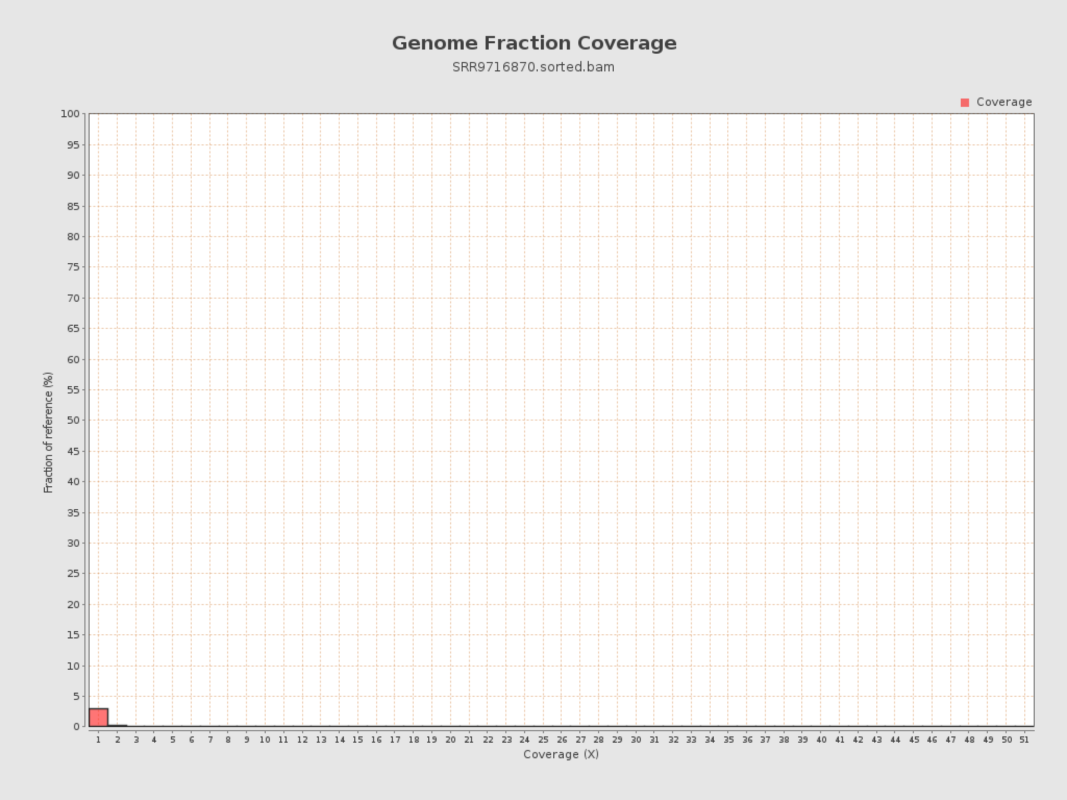
4. Results : Coverage Histogram



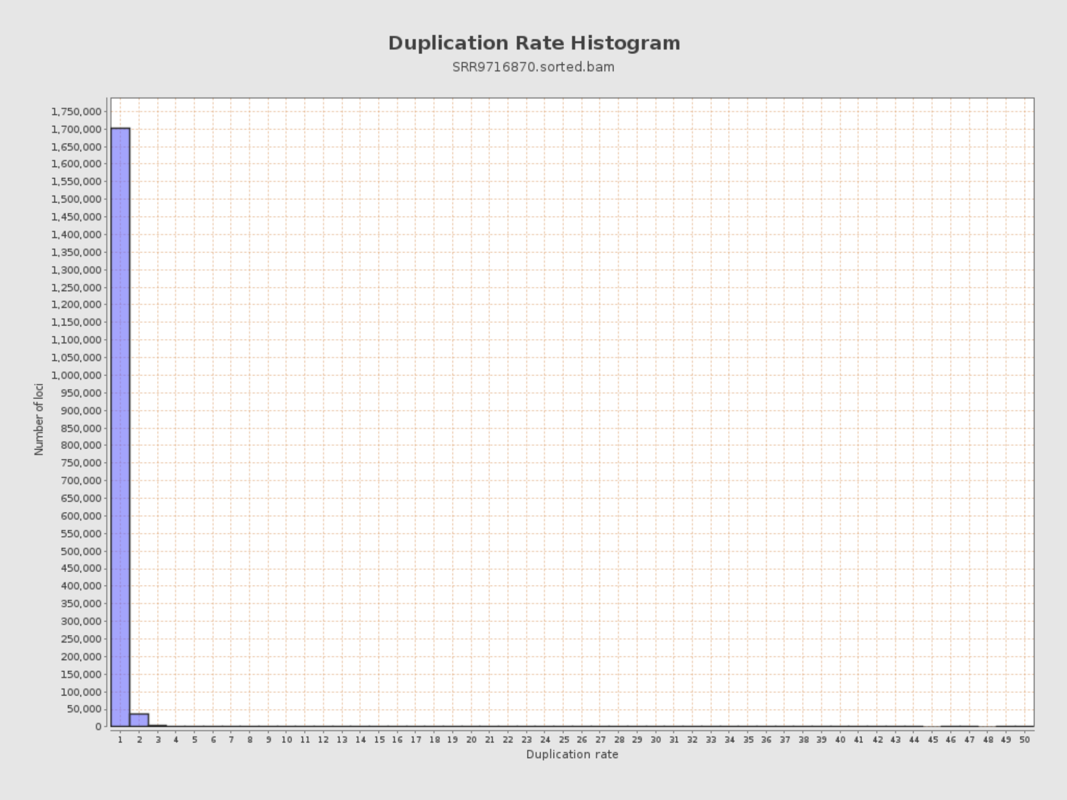
5. Results : Coverage Histogram (0-50X)



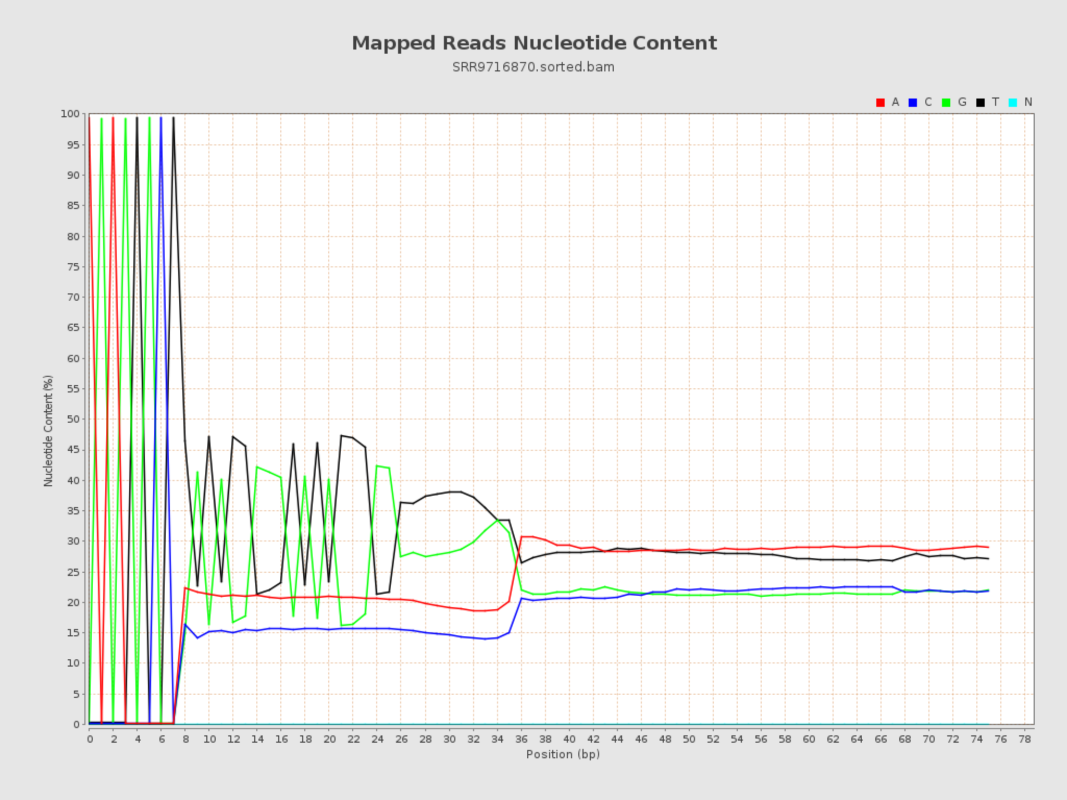
6. Results : Genome Fraction Coverage



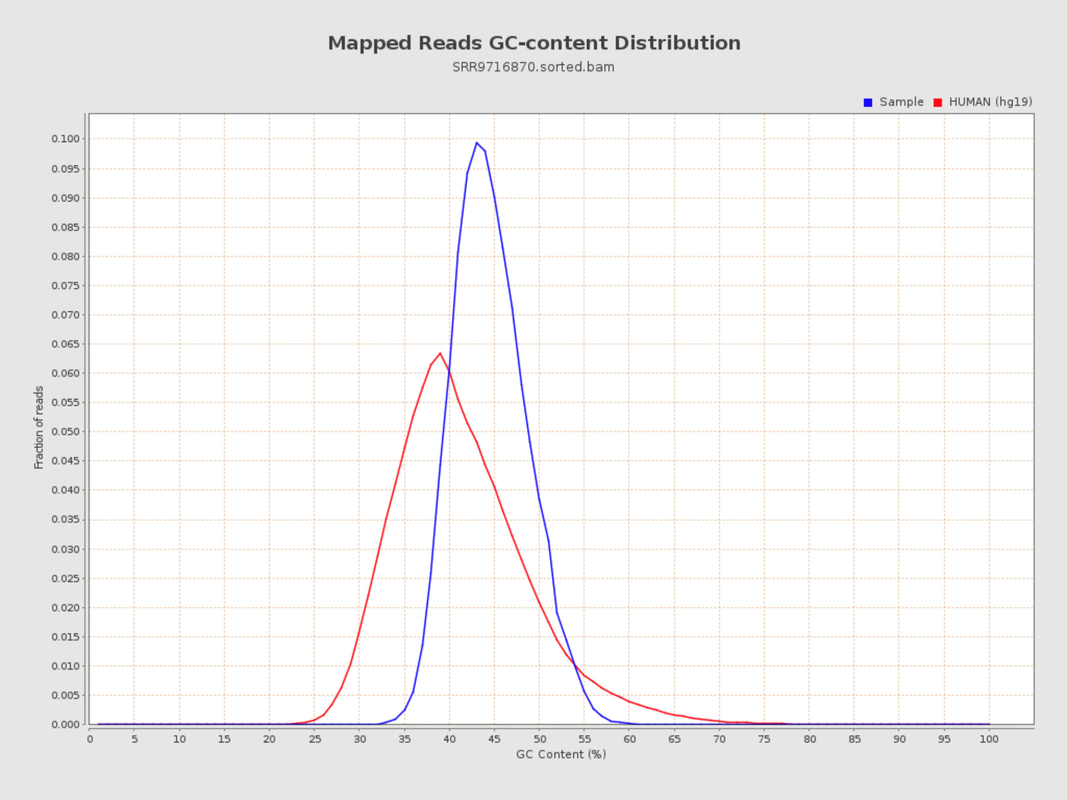
7. Results : Duplication Rate Histogram



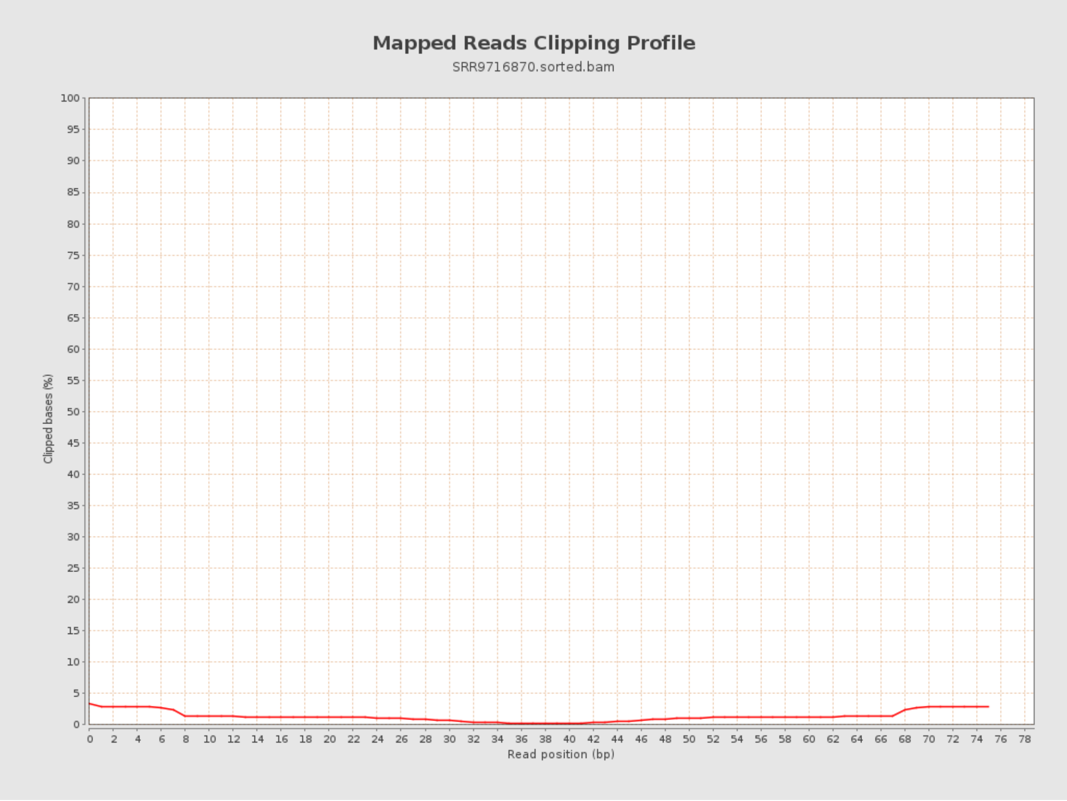
8. Results : Mapped Reads Nucleotide Content



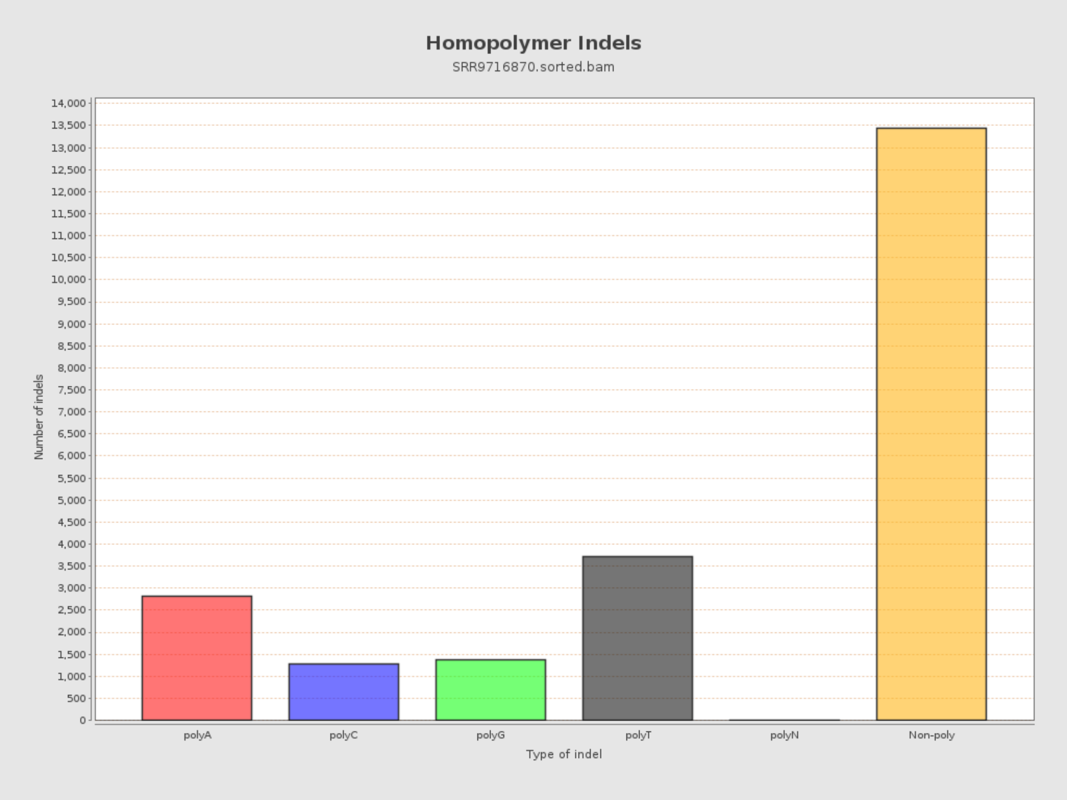
9. Results : Mapped Reads GC-content Distribution



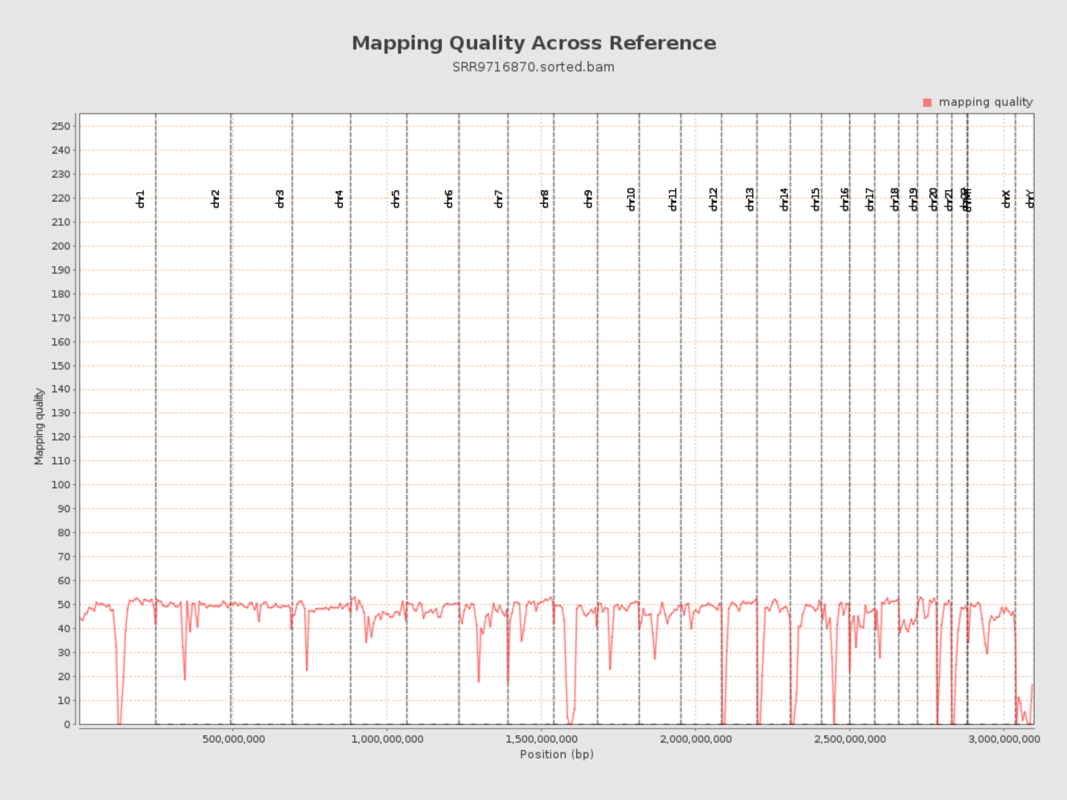
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram