Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 02:43:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716250.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_SRR9716250 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716250.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 02:43:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716250.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,666,519
Mapped reads	1,504,425 / 90.27%
Unmapped reads	162,094 / 9.73%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,950 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	40,213 / 2.41%
Duplication rate	2.08%
Clipped reads	1,510,168 / 90.62%

2.2. ACGT Content

Number/percentage of A's	21,499,320 / 25.22%
Number/percentage of C's	17,295,553 / 20.29%
Number/percentage of T's	25,943,065 / 30.43%
Number/percentage of G's	20,521,884 / 24.07%
Number/percentage of N's	2,004 / 0%
GC Percentage	44.35%

2.3. Coverage

Mean	0.0275

Standard Deviation	0.2187

2.4. Mapping Quality

Mean Mapping Quality	44.22

2.5. Mismatches and indels

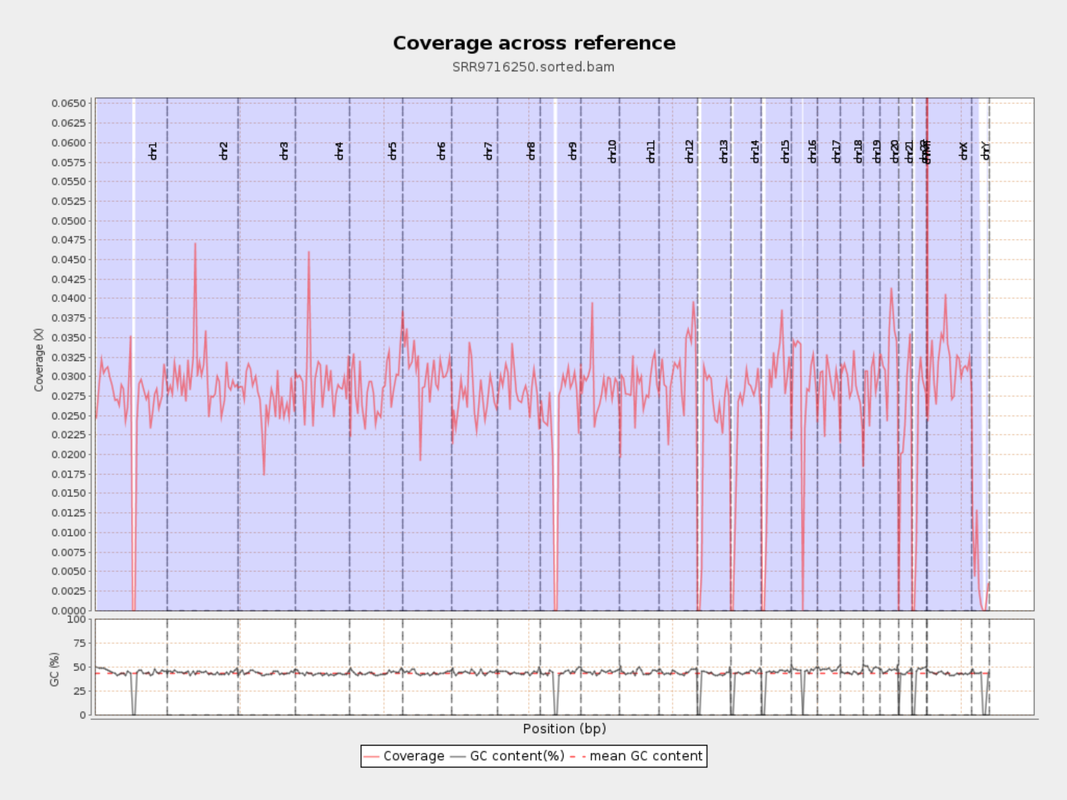
General error rate	0.5%
Mismatches	419,774
Insertions	4,498
Mapped reads with at least one insertion	0.3%
Deletions	12,504
Mapped reads with at least one deletion	0.83%
Homopolymer indels	41.67%

2.6. Chromosome stats

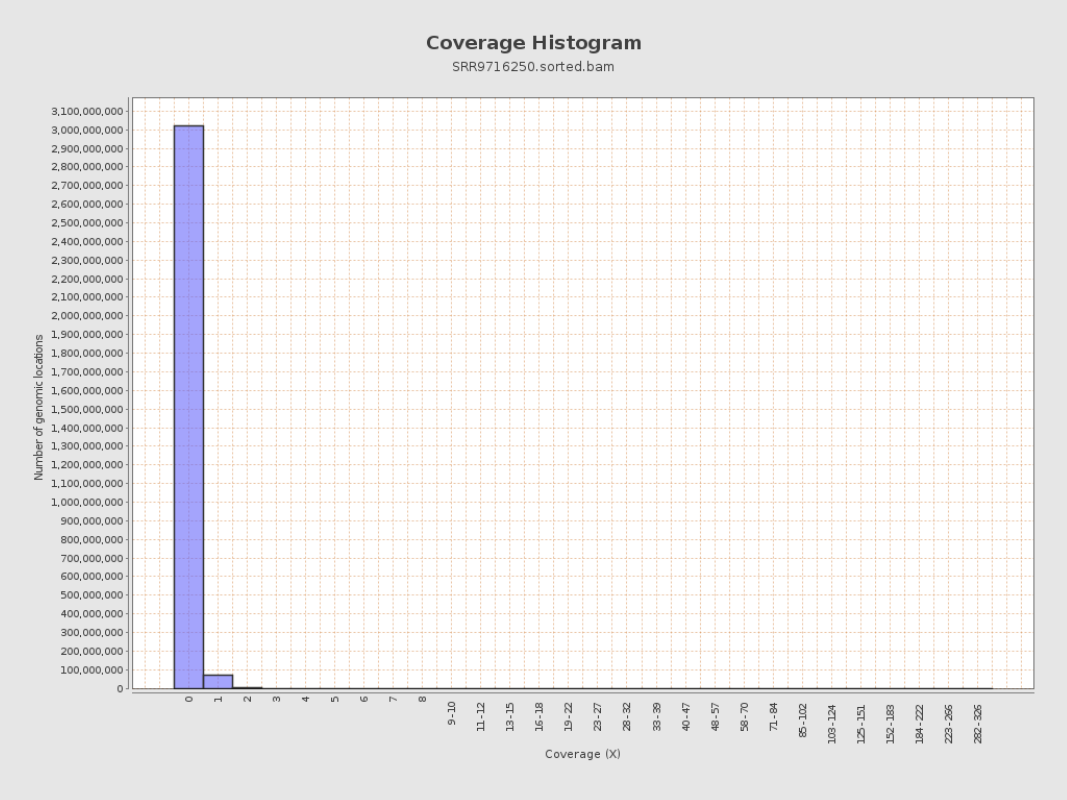
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6604396	0.0265	0.3039
chr2	243199373	7263338	0.0299	0.2584
chr3	198022430	5385690	0.0272	0.1781
chr4	191154276	5664469	0.0296	0.1988
chr5	180915260	5193336	0.0287	0.185
chr6	171115067	5262419	0.0308	0.2021
chr7	159138663	4330720	0.0272	0.2216

chr8	146364022	4180800	0.0286	0.2117
chr9	141213431	3403182	0.0241	0.2118
chr10	135534747	3921546	0.0289	0.2172
chr11	135006516	3899446	0.0289	0.2244
chr12	133851895	4141381	0.0309	0.1921
chr13	115169878	2634427	0.0229	0.1627
chr14	107349540	2521986	0.0235	0.1721
chr15	102531392	2624413	0.0256	0.1734
chr16	90354753	2509957	0.0278	0.1938
chr17	81195210	2325111	0.0286	0.1917
chr18	78077248	2274828	0.0291	0.3658
chr19	59128983	1726890	0.0292	0.2529
chr20	63025520	2091921	0.0332	0.2017
chr21	48129895	1131785	0.0235	0.1772
chr22	51304566	1040522	0.0203	0.1542
chrMT	16571	5107	0.3082	0.61
chrX	155270560	4897204	0.0315	0.2149
chrY	59373566	248445	0.0042	0.0962

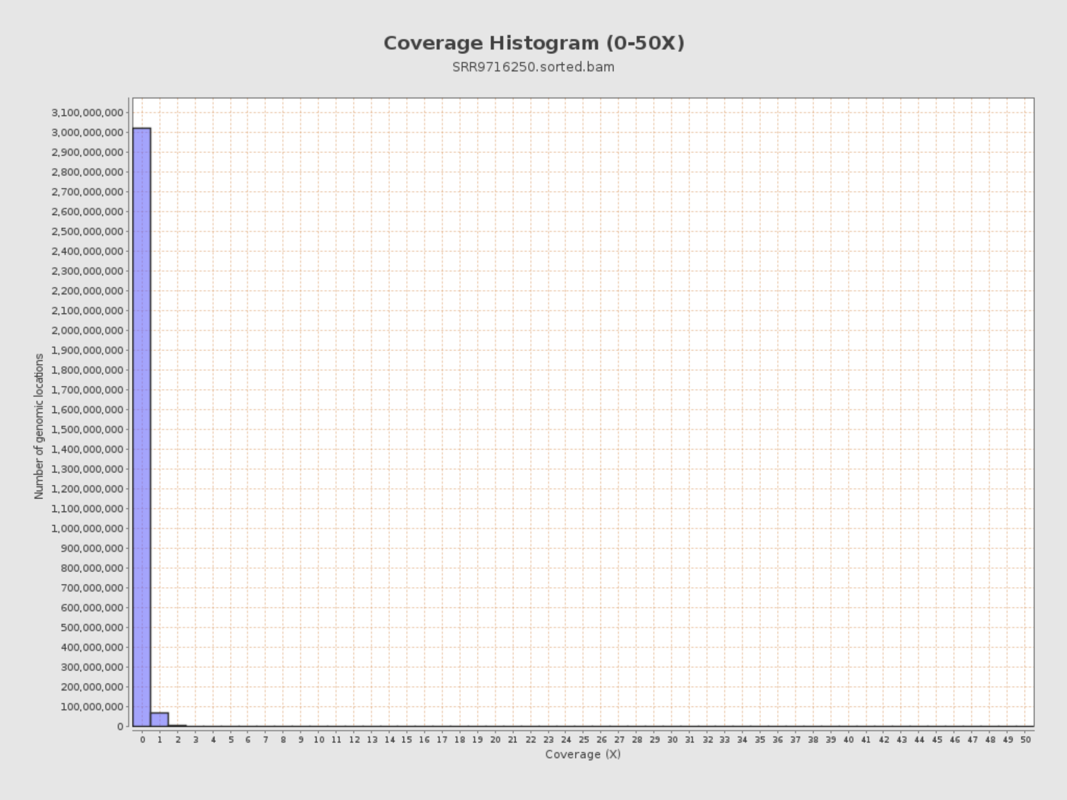
3. Results : Coverage across reference



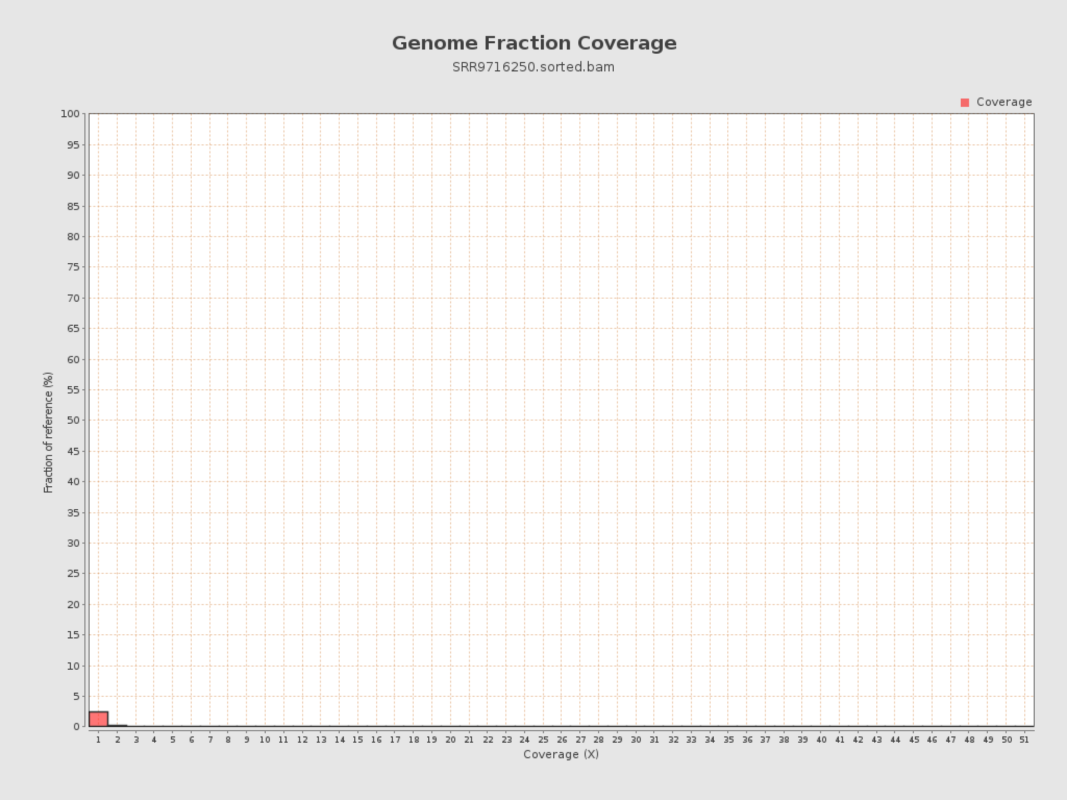
4. Results : Coverage Histogram



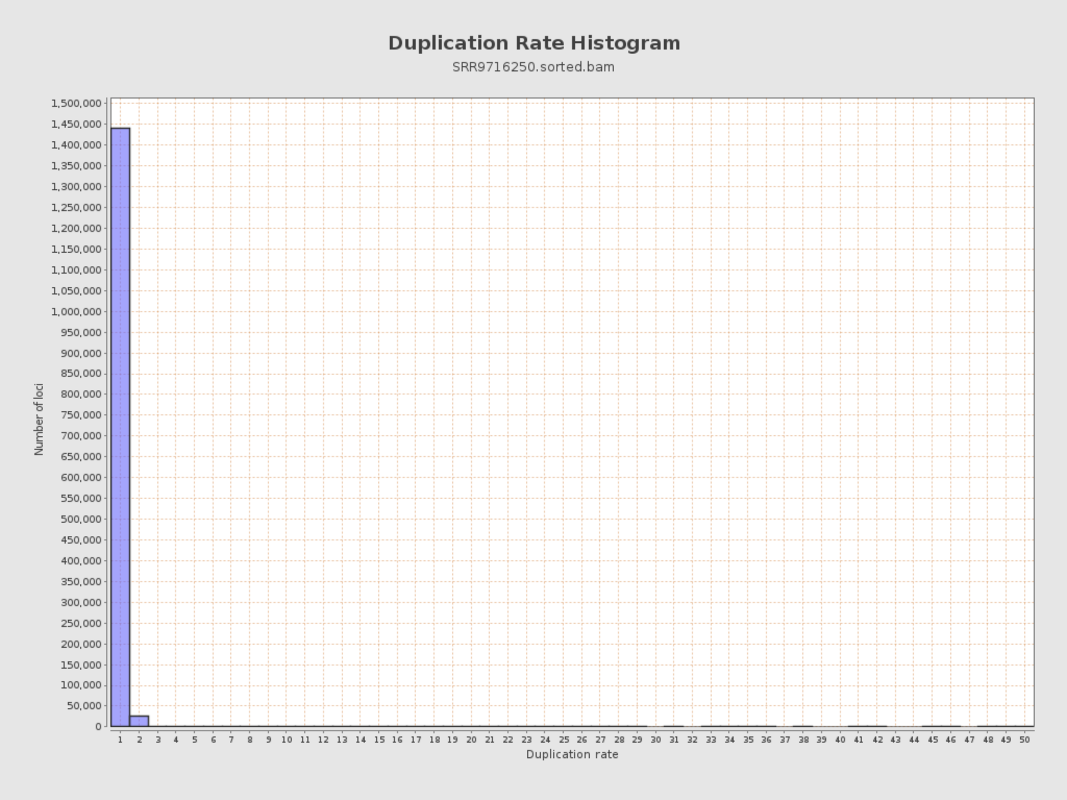
5. Results : Coverage Histogram (0-50X)



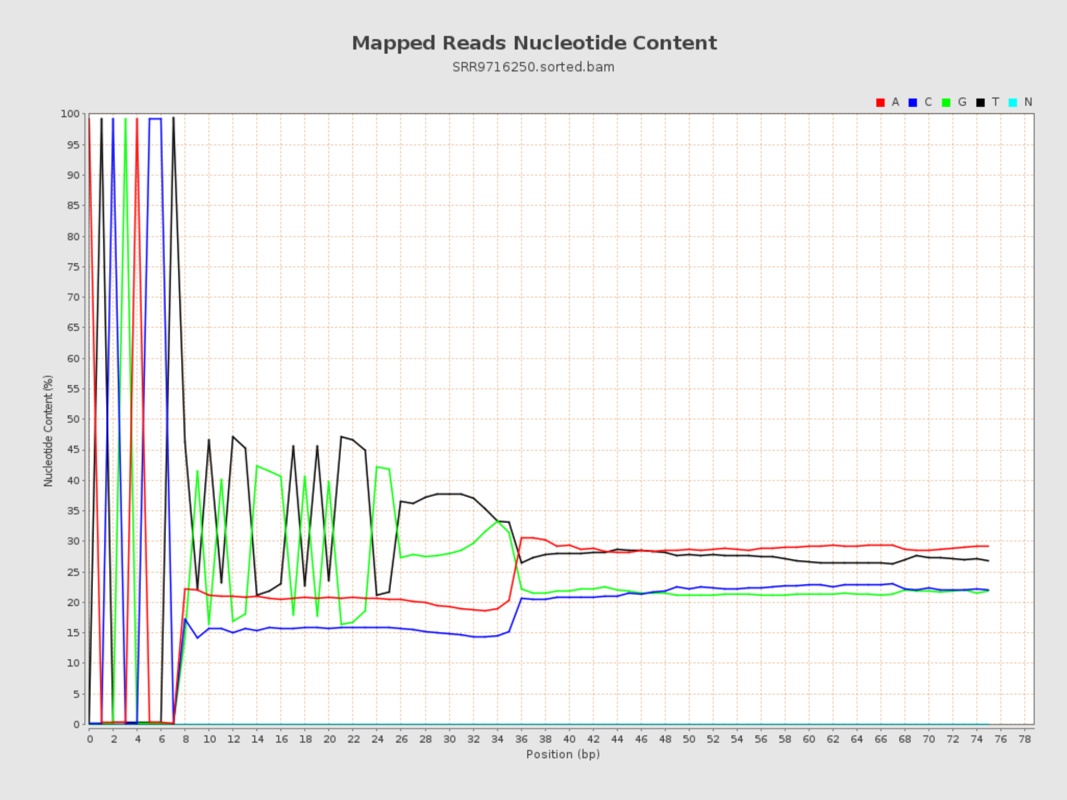
6. Results : Genome Fraction Coverage



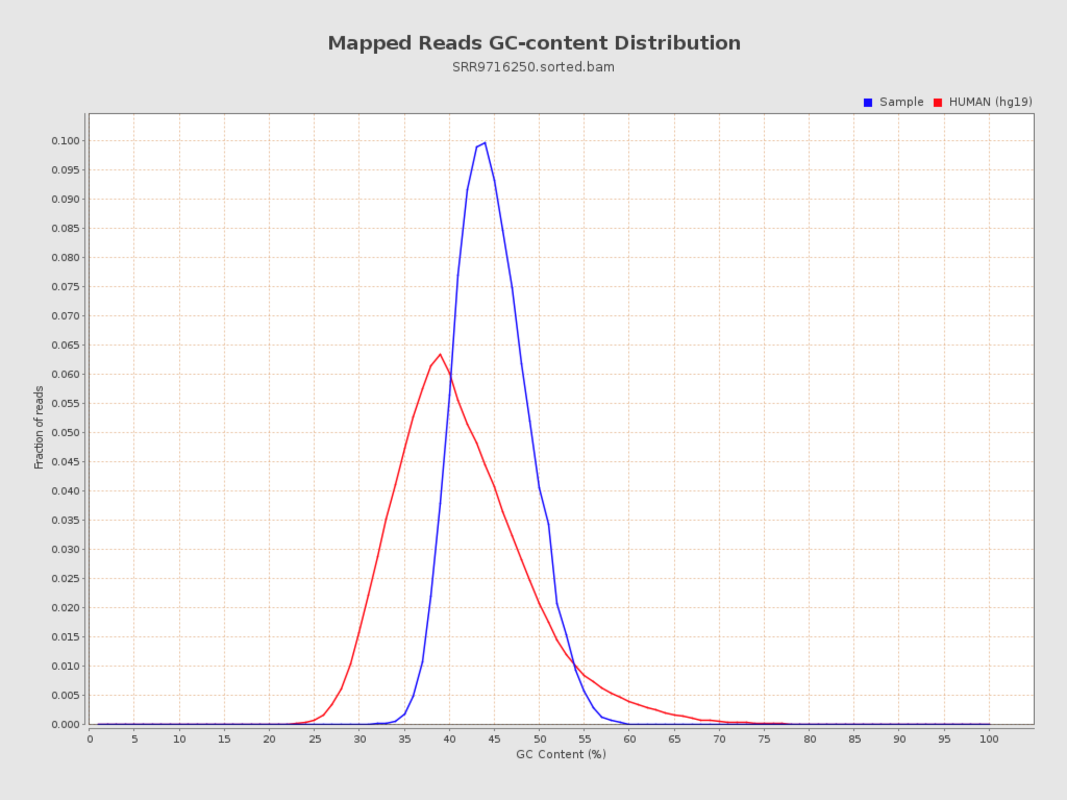
7. Results : Duplication Rate Histogram



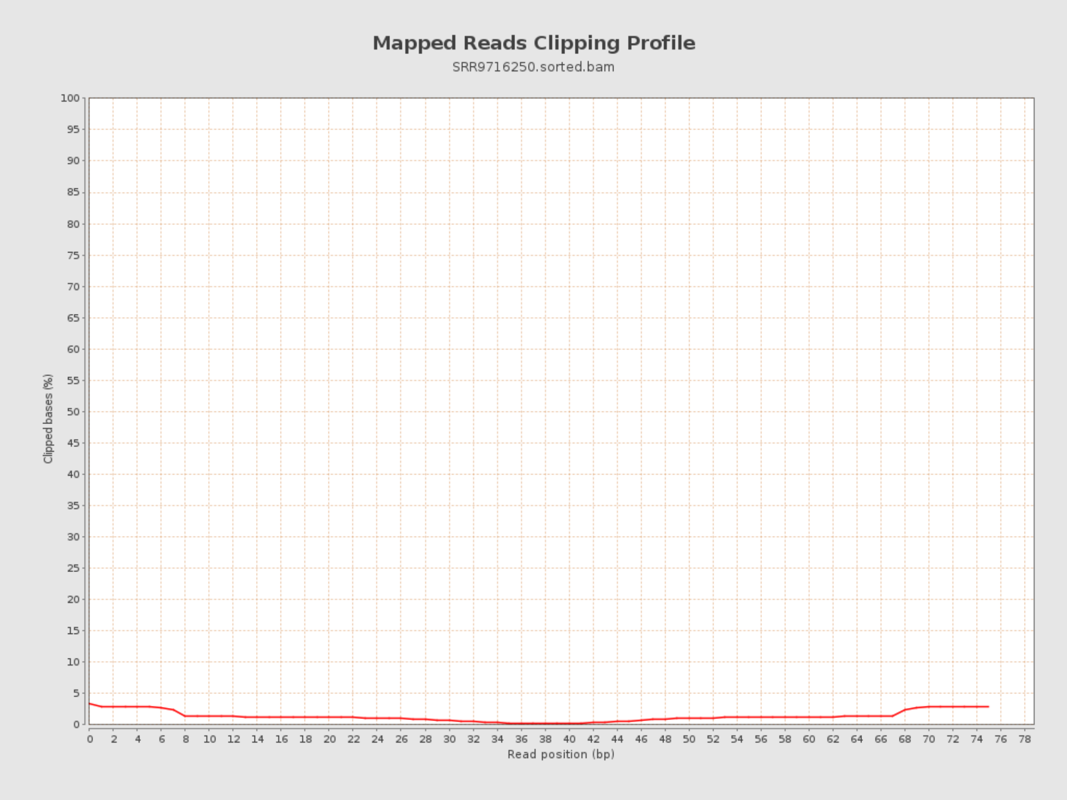
8. Results : Mapped Reads Nucleotide Content



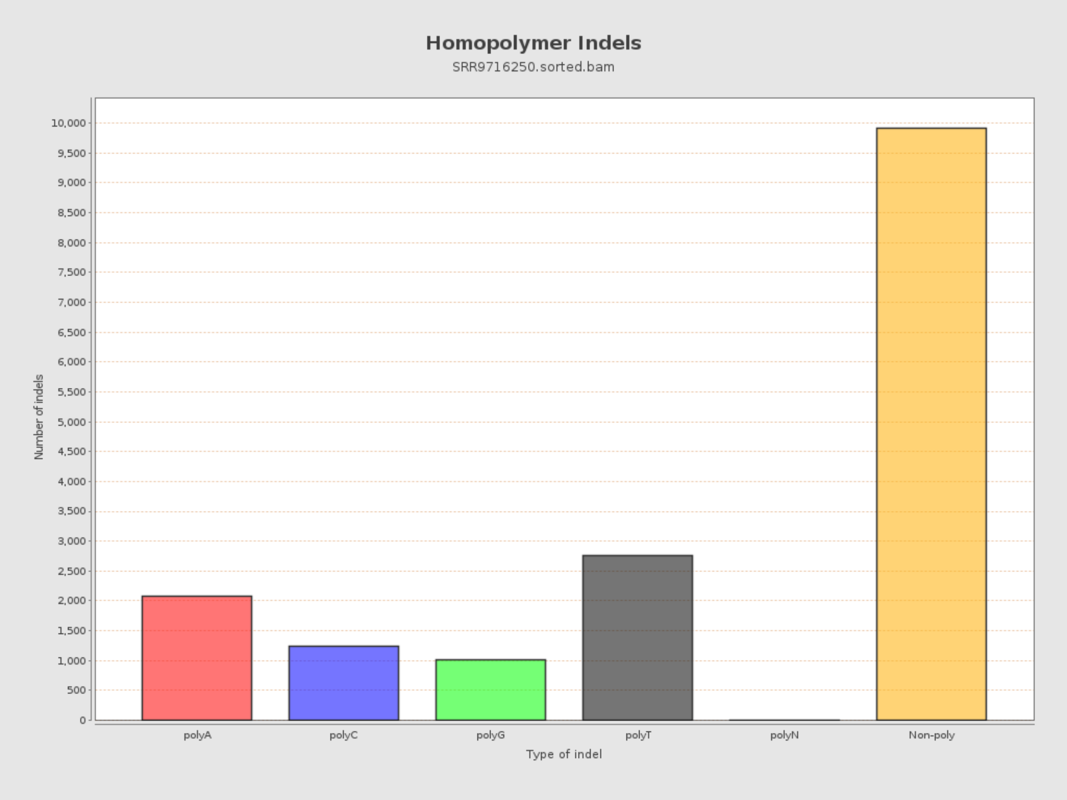
9. Results : Mapped Reads GC-content Distribution



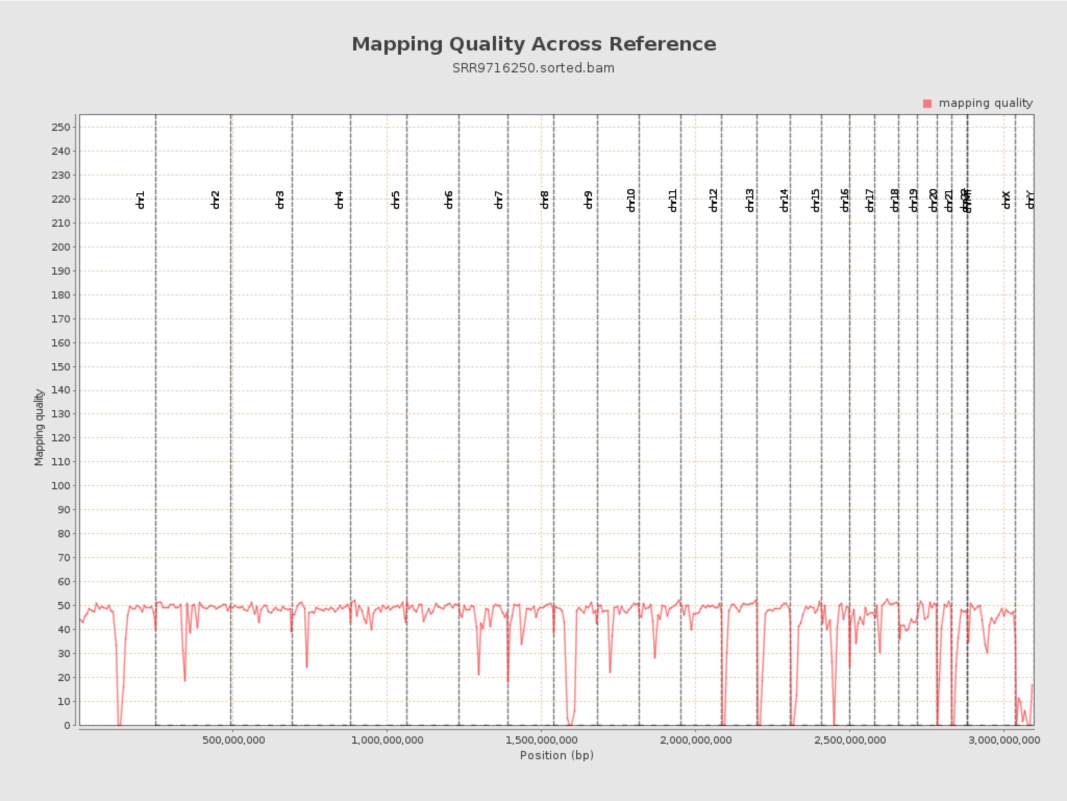
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram