Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 19:56:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716548.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_SRR9716548 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716548.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 19:56:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716548.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,351,227
Mapped reads	1,046,947 / 77.48%
Unmapped reads	304,280 / 22.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,648 / 0.12%
Read min/max/mean length	30 / 76 / 76.04
Duplicated reads (estimated)	50,566 / 3.74%
Duplication rate	4.18%
Clipped reads	1,046,034 / 77.41%

2.2. ACGT Content

Number/percentage of A's	12,997,191 / 23%
Number/percentage of C's	9,821,135 / 17.38%
Number/percentage of T's	18,027,623 / 31.9%
Number/percentage of G's	15,667,961 / 27.72%
Number/percentage of N's	965 / 0%
GC Percentage	45.1%

2.3. Coverage

Mean	0.0183

Standard Deviation	0.1757

2.4. Mapping Quality

Mean Mapping Quality	43.23

2.5. Mismatches and indels

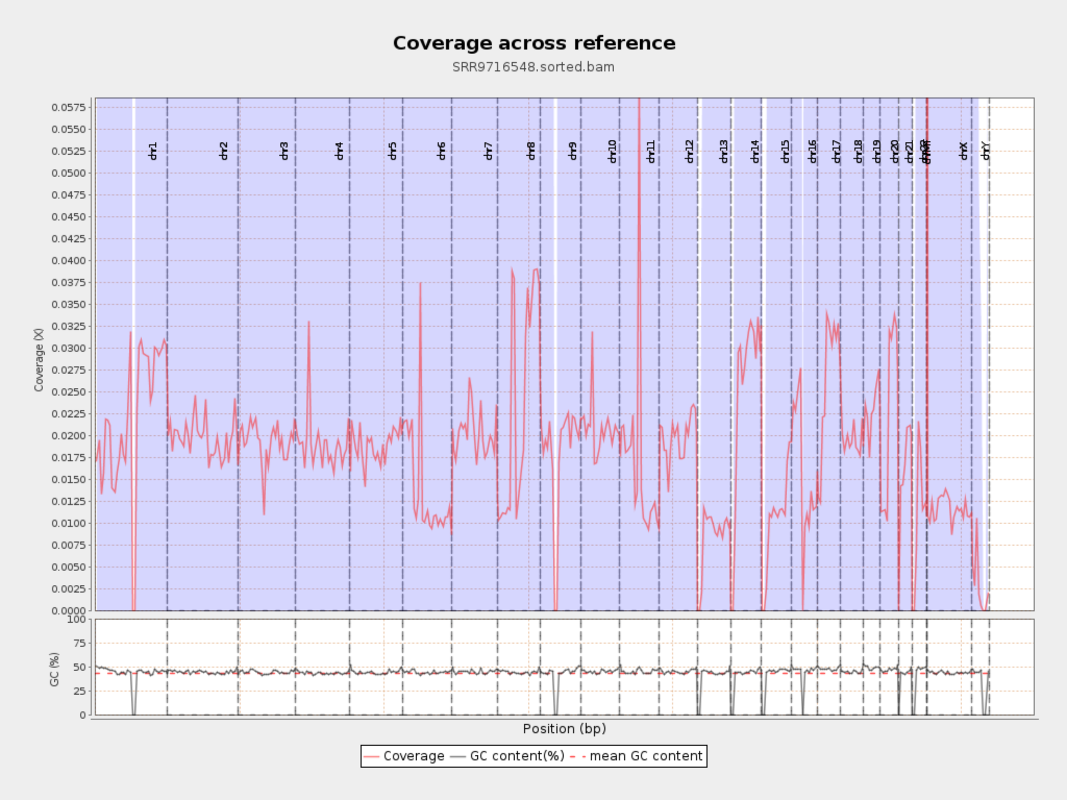
General error rate	0.7%
Mismatches	385,049
Insertions	4,192
Mapped reads with at least one insertion	0.4%
Deletions	9,037
Mapped reads with at least one deletion	0.86%
Homopolymer indels	38.88%

2.6. Chromosome stats

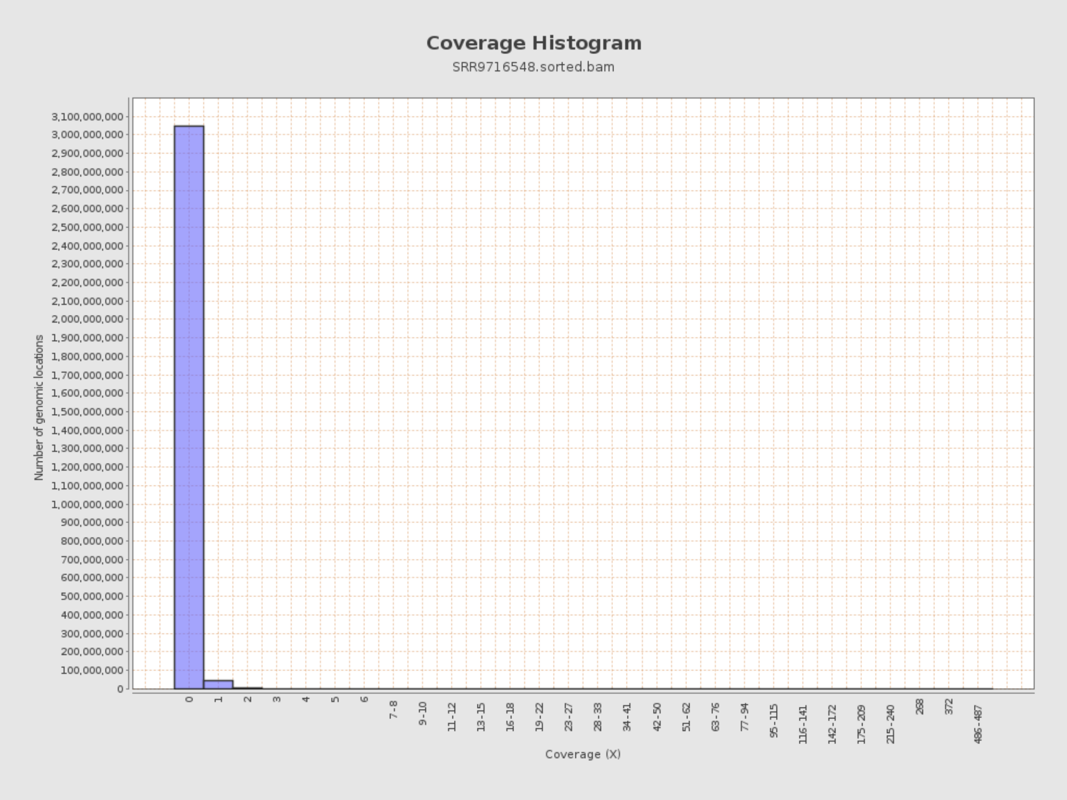
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5466006	0.0219	0.2285
chr2	243199373	4813002	0.0198	0.2518
chr3	198022430	3800593	0.0192	0.1522
chr4	191154276	3655762	0.0191	0.1626
chr5	180915260	3436730	0.019	0.1517
chr6	171115067	2410483	0.0141	0.1464
chr7	159138663	3235967	0.0203	0.1988

chr8	146364022	3470774	0.0237	0.1778
chr9	141213431	2527927	0.0179	0.161
chr10	135534747	2830916	0.0209	0.1919
chr11	135006516	2351730	0.0174	0.1663
chr12	133851895	2649719	0.0198	0.1553
chr13	115169878	958675	0.0083	0.1009
chr14	107349540	2679525	0.025	0.1753
chr15	102531392	1048144	0.0102	0.1114
chr16	90354753	1387600	0.0154	0.1464
chr17	81195210	2150760	0.0265	0.1871
chr18	78077248	1528162	0.0196	0.2076
chr19	59128983	1352899	0.0229	0.2028
chr20	63025520	1407517	0.0223	0.1705
chr21	48129895	774479	0.0161	0.1477
chr22	51304566	571427	0.0111	0.1163
chrMT	16571	53994	3.2583	2.8106
chrX	155270560	1800682	0.0116	0.1264
chrY	59373566	166662	0.0028	0.0827

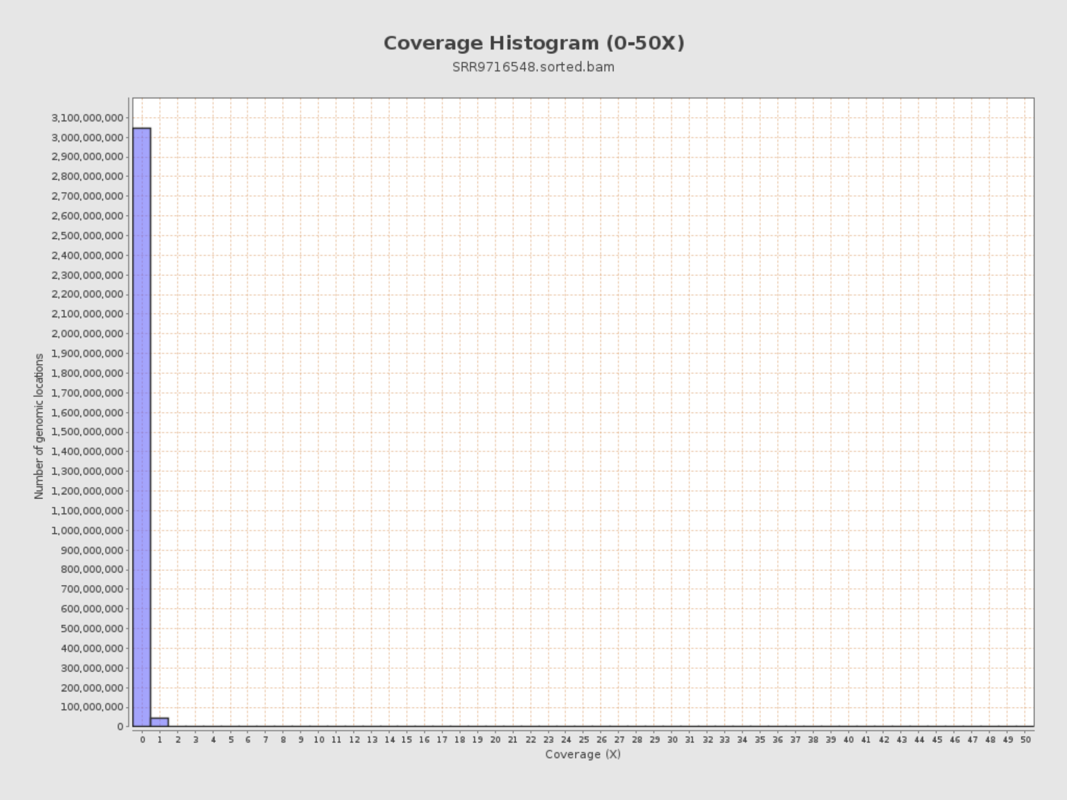
3. Results : Coverage across reference



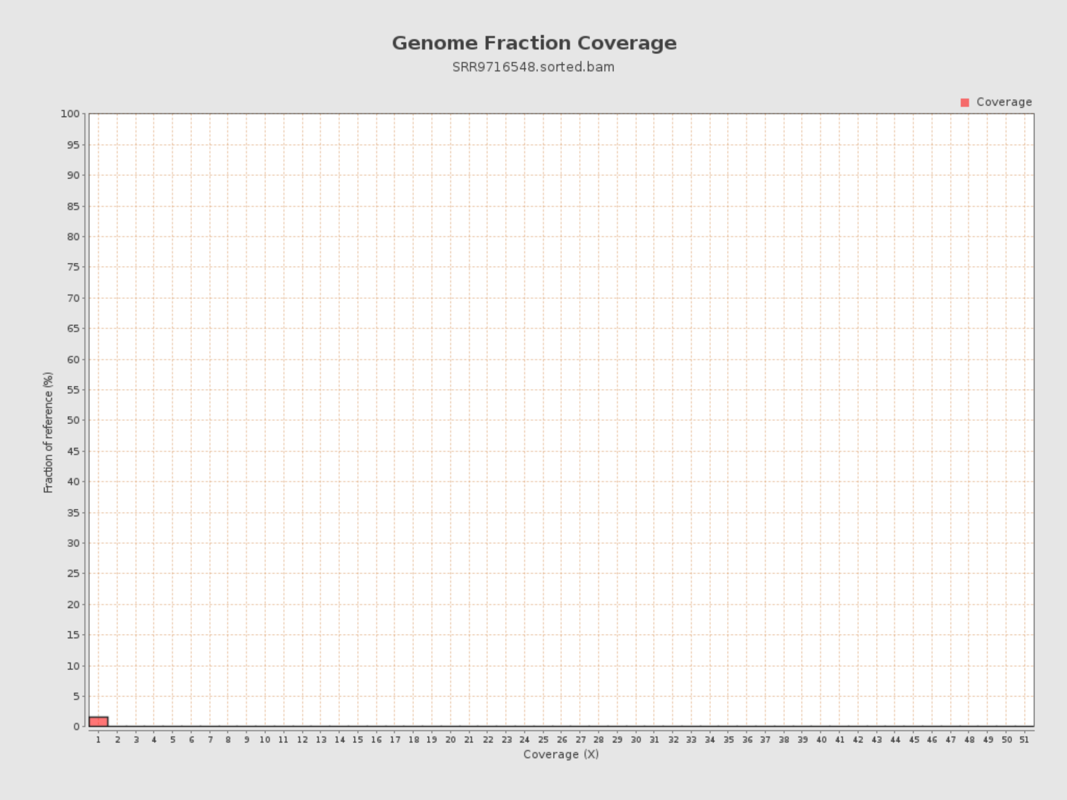
4. Results : Coverage Histogram



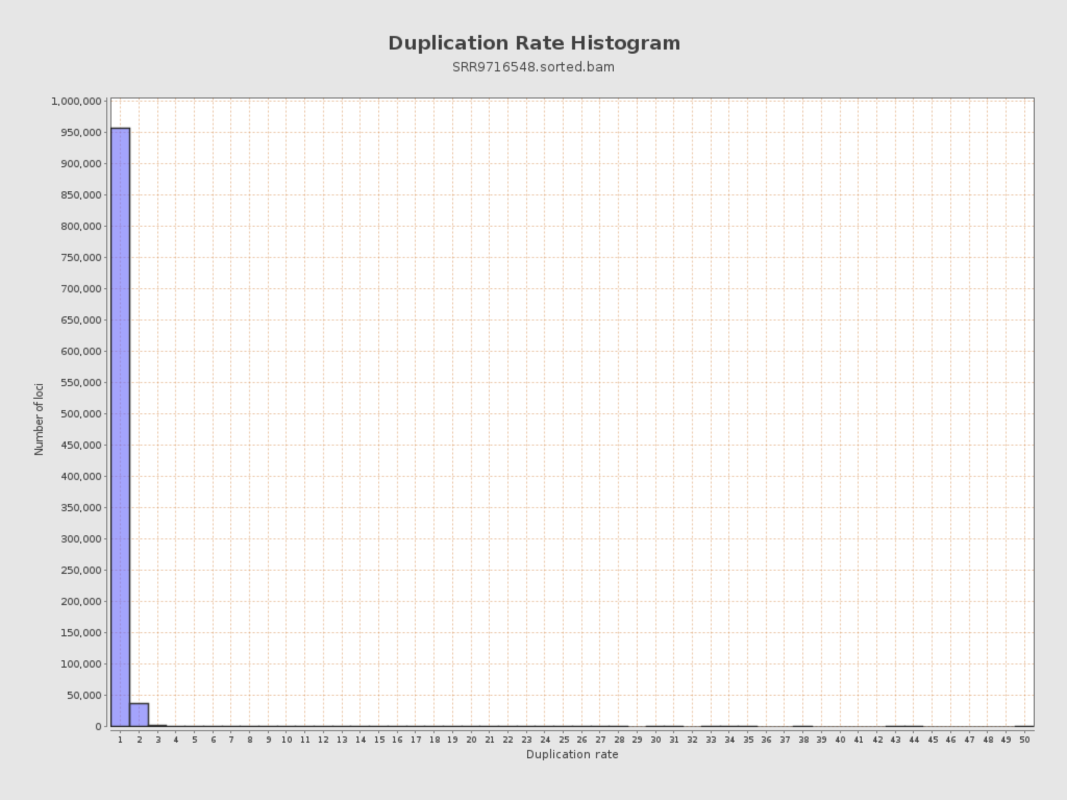
5. Results : Coverage Histogram (0-50X)



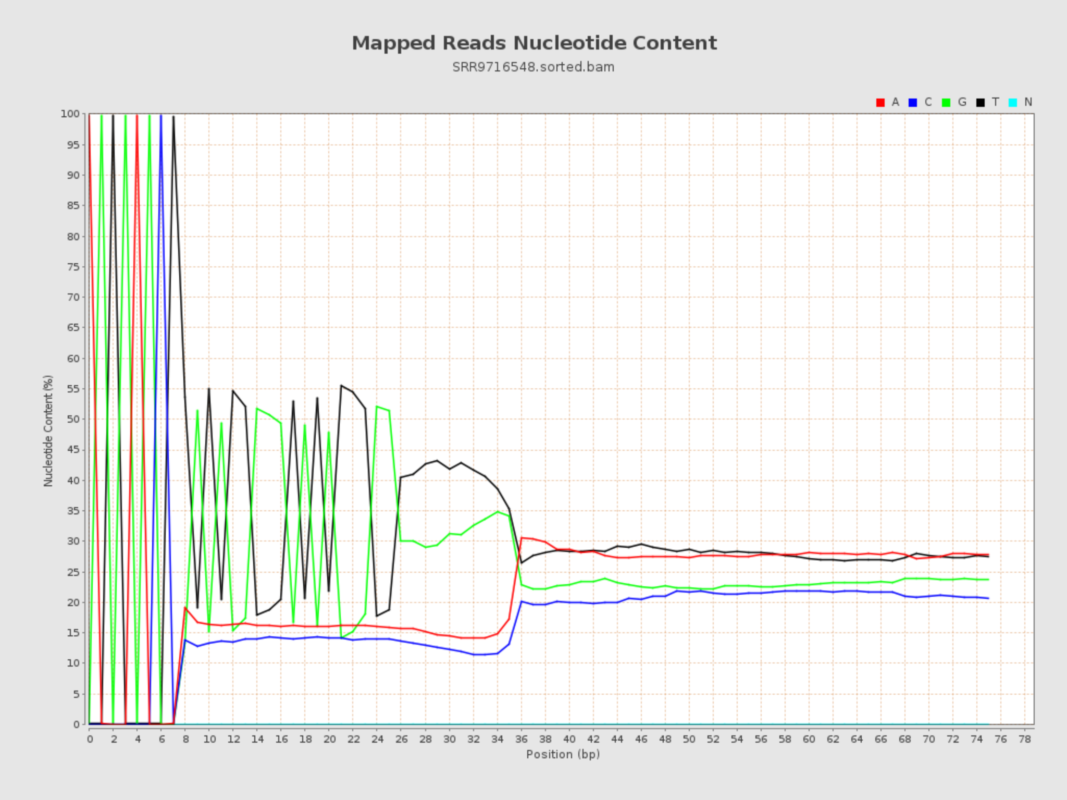
6. Results : Genome Fraction Coverage



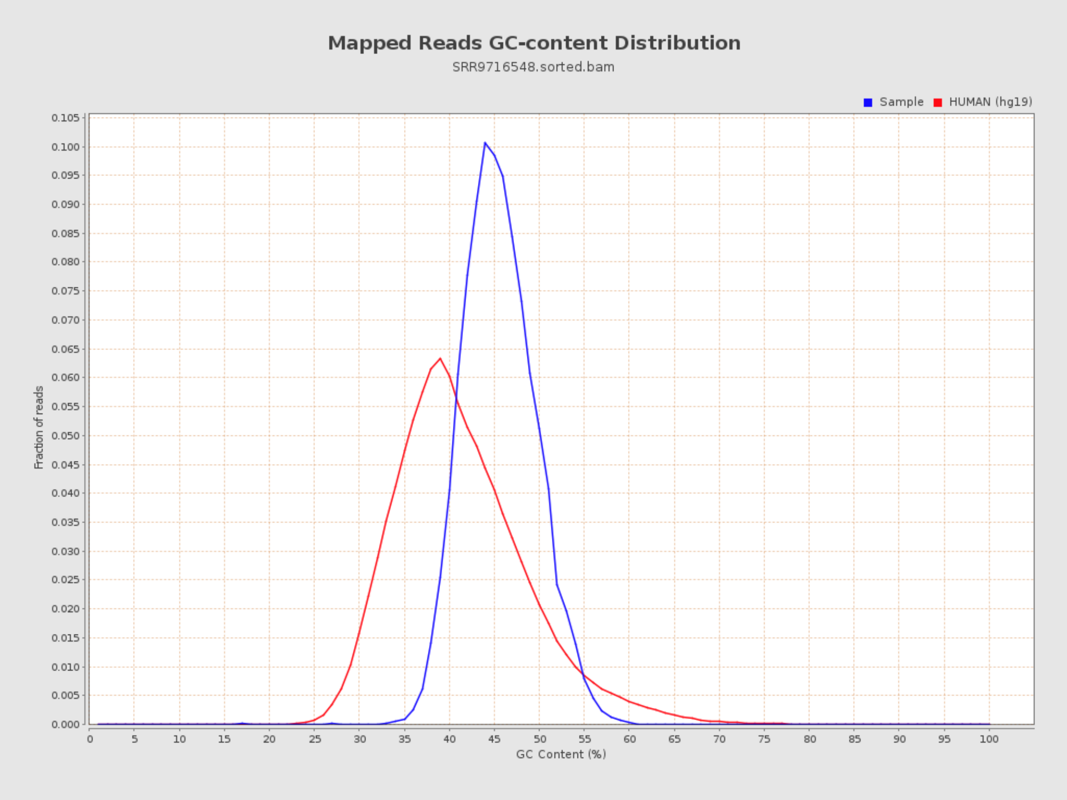
7. Results : Duplication Rate Histogram



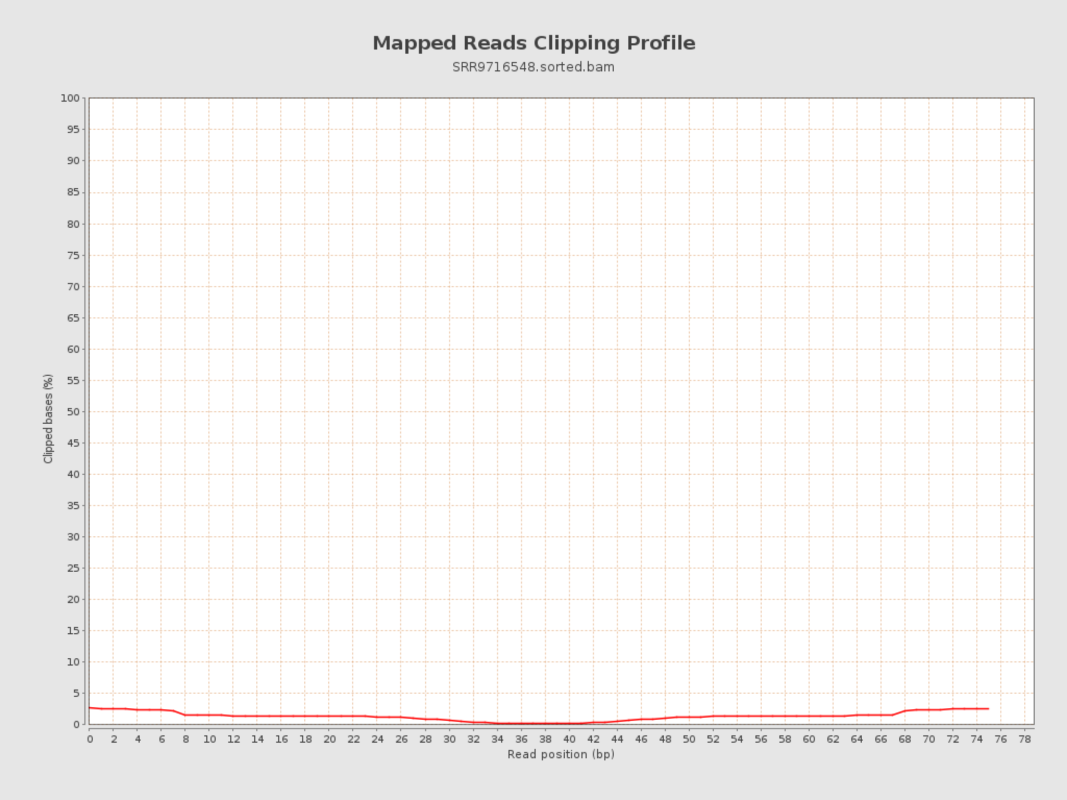
8. Results : Mapped Reads Nucleotide Content



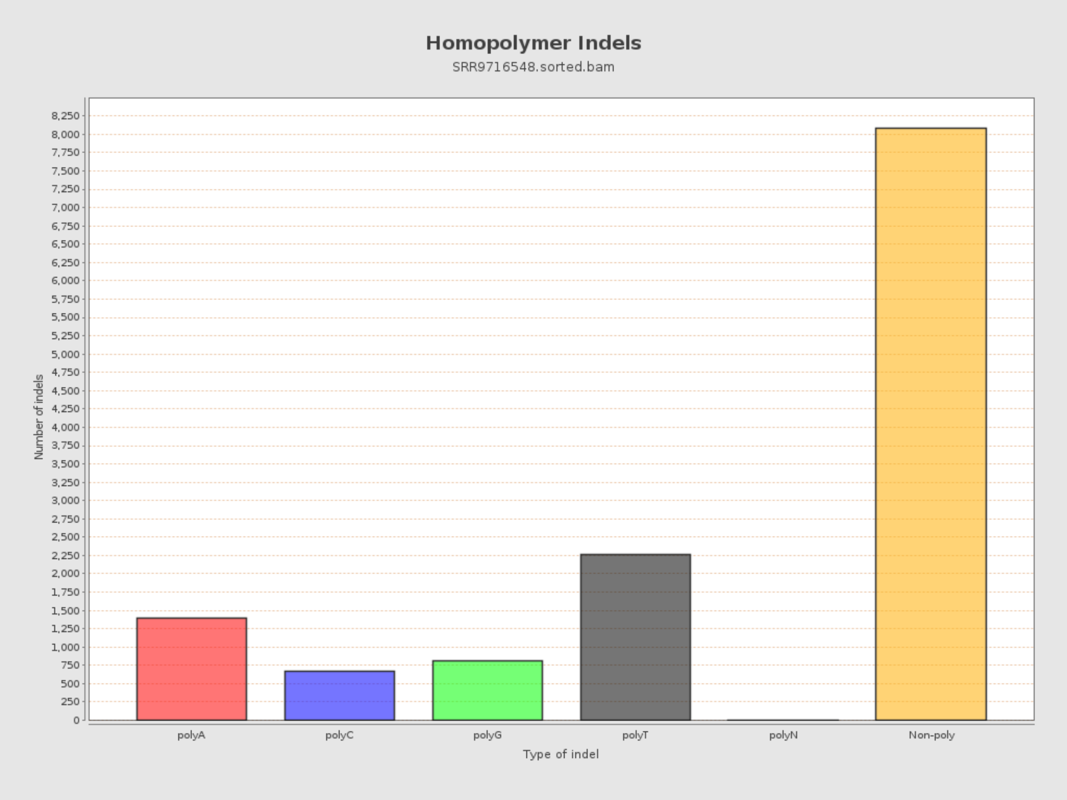
9. Results : Mapped Reads GC-content Distribution



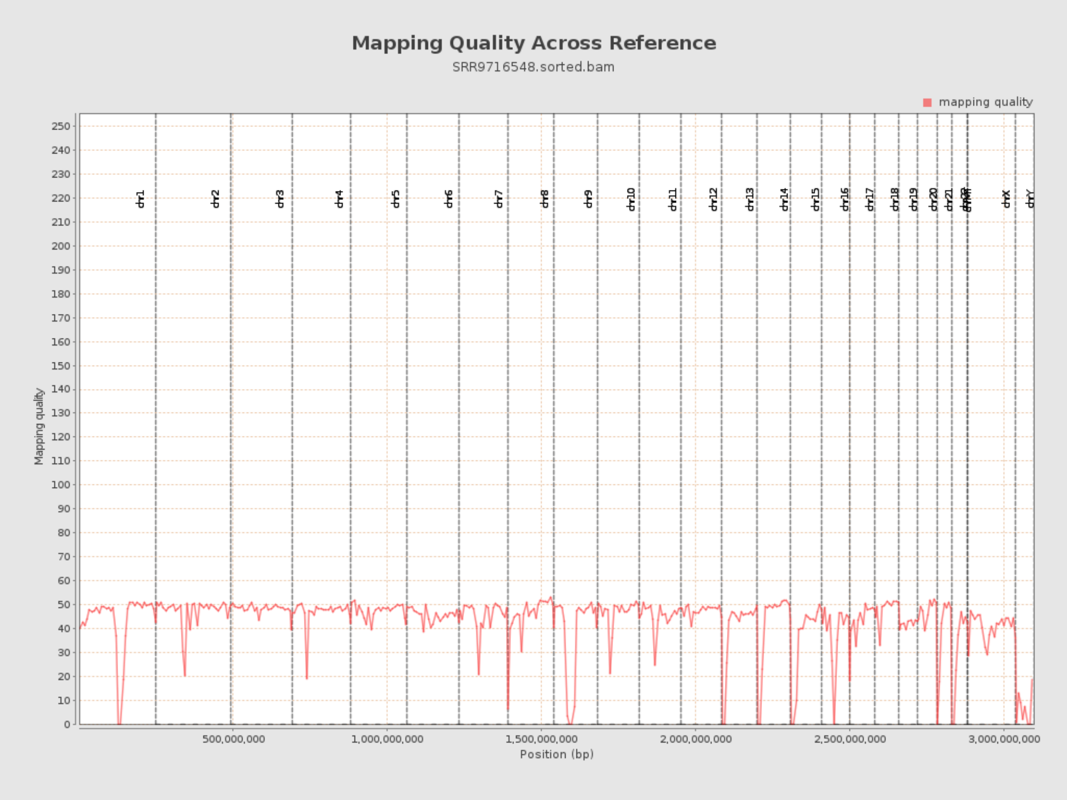
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram