Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 22:31:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716572.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_SRR9716572 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716572.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 22:31:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716572.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,436,102
Mapped reads	1,350,567 / 94.04%
Unmapped reads	85,535 / 5.96%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,252 / 2.45%
Read min/max/mean length	30 / 101 / 101.9
Duplicated reads (estimated)	47,143 / 3.28%
Duplication rate	2.73%
Clipped reads	1,382,714 / 96.28%

2.2. ACGT Content

Number/percentage of A's	26,827,868 / 25.71%
Number/percentage of C's	21,726,374 / 20.82%
Number/percentage of T's	29,819,539 / 28.58%
Number/percentage of G's	25,960,481 / 24.88%
Number/percentage of N's	4,187 / 0%
GC Percentage	45.7%

2.3. Coverage

Mean	0.0337

Standard Deviation	0.2765

2.4. Mapping Quality

Mean Mapping Quality	46.04

2.5. Mismatches and indels

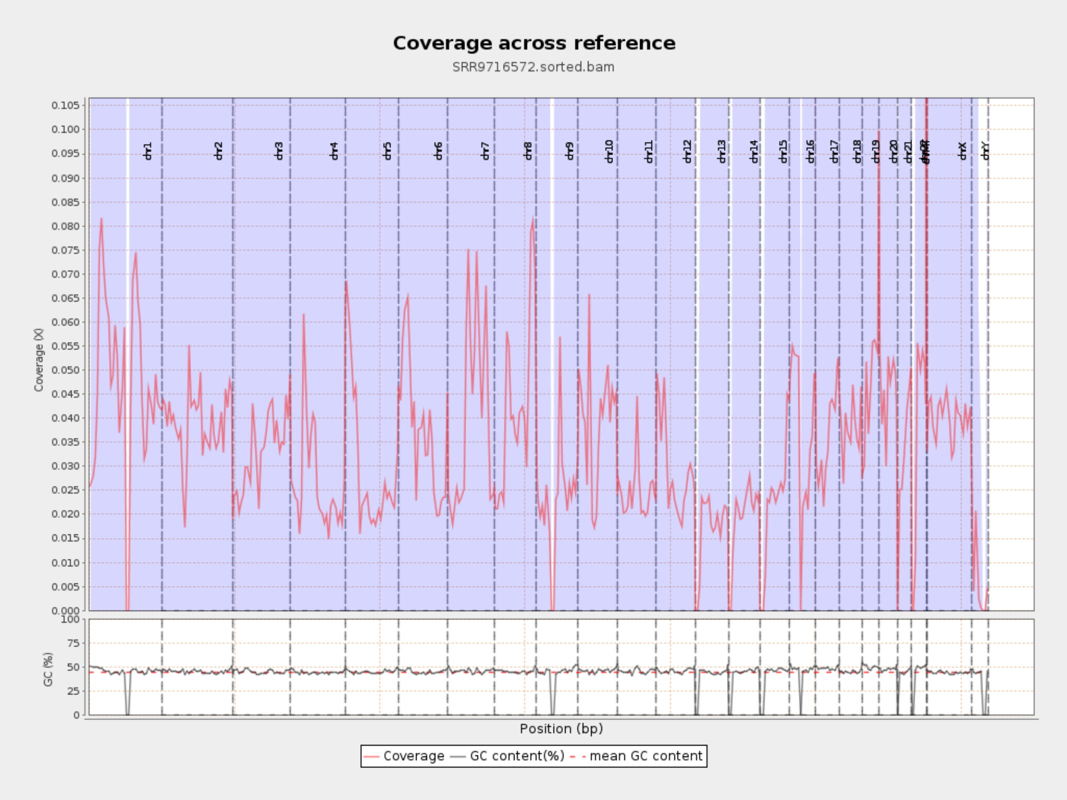
General error rate	0.65%
Mismatches	658,112
Insertions	9,494
Mapped reads with at least one insertion	0.69%
Deletions	19,199
Mapped reads with at least one deletion	1.4%
Homopolymer indels	38.54%

2.6. Chromosome stats

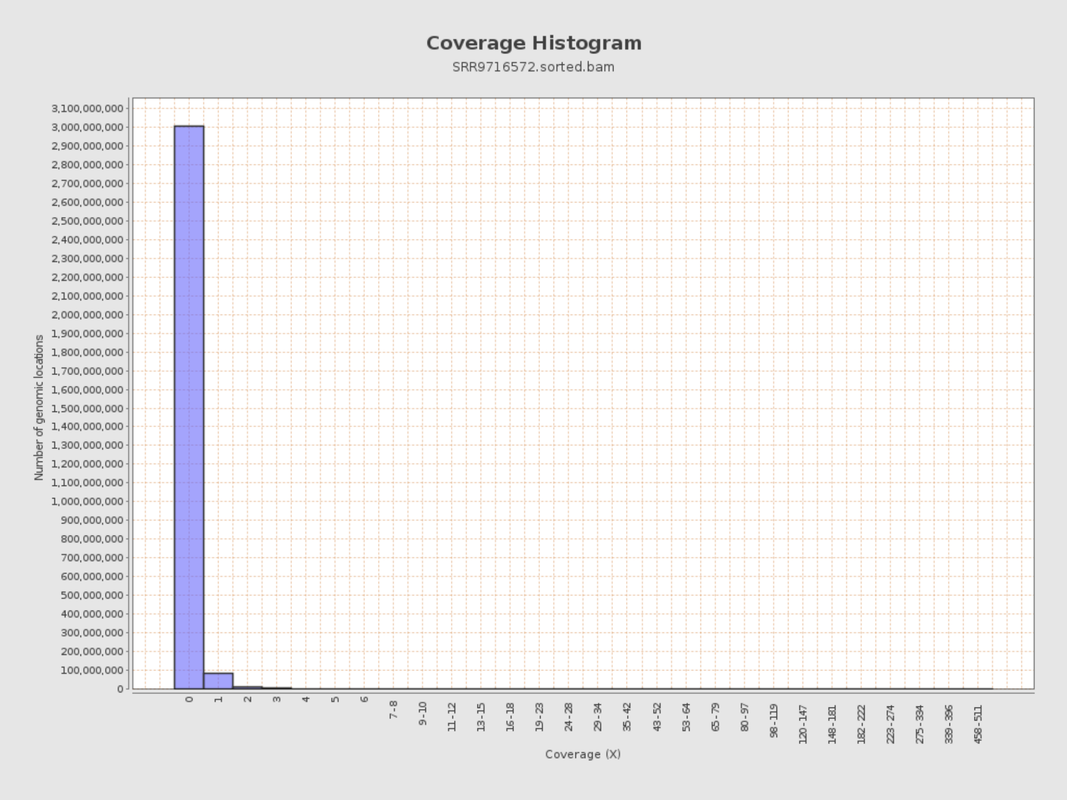
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11808947	0.0474	0.4932
chr2	243199373	9473381	0.039	0.2957
chr3	198022430	6540828	0.033	0.2038
chr4	191154276	5001697	0.0262	0.232
chr5	180915260	5352437	0.0296	0.1943
chr6	171115067	6413018	0.0375	0.2277
chr7	159138663	6513537	0.0409	0.3459

chr8	146364022	6242953	0.0427	0.2999
chr9	141213431	3211069	0.0227	0.2021
chr10	135534747	5350383	0.0395	0.3579
chr11	135006516	3346429	0.0248	0.2238
chr12	133851895	3929863	0.0294	0.1924
chr13	115169878	1945231	0.0169	0.1434
chr14	107349540	2038035	0.019	0.1585
chr15	102531392	2248924	0.0219	0.1659
chr16	90354753	3355474	0.0371	0.2273
chr17	81195210	2926868	0.036	0.2301
chr18	78077248	2971830	0.0381	0.3077
chr19	59128983	2843134	0.0481	0.3856
chr20	63025520	2886763	0.0458	0.2521
chr21	48129895	1562559	0.0325	0.2378
chr22	51304566	1796044	0.035	0.2177
chrMT	16571	61698	3.7233	3.4114
chrX	155270560	6227832	0.0401	0.2331
chrY	59373566	329178	0.0055	0.1891

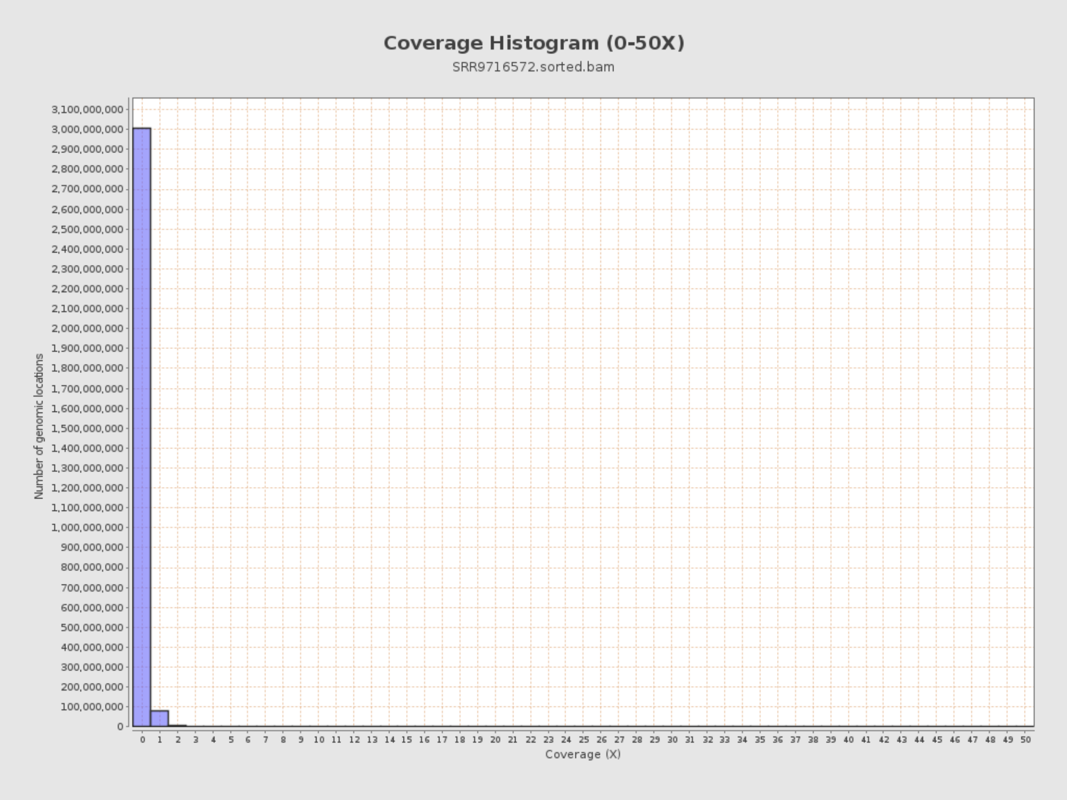
3. Results : Coverage across reference



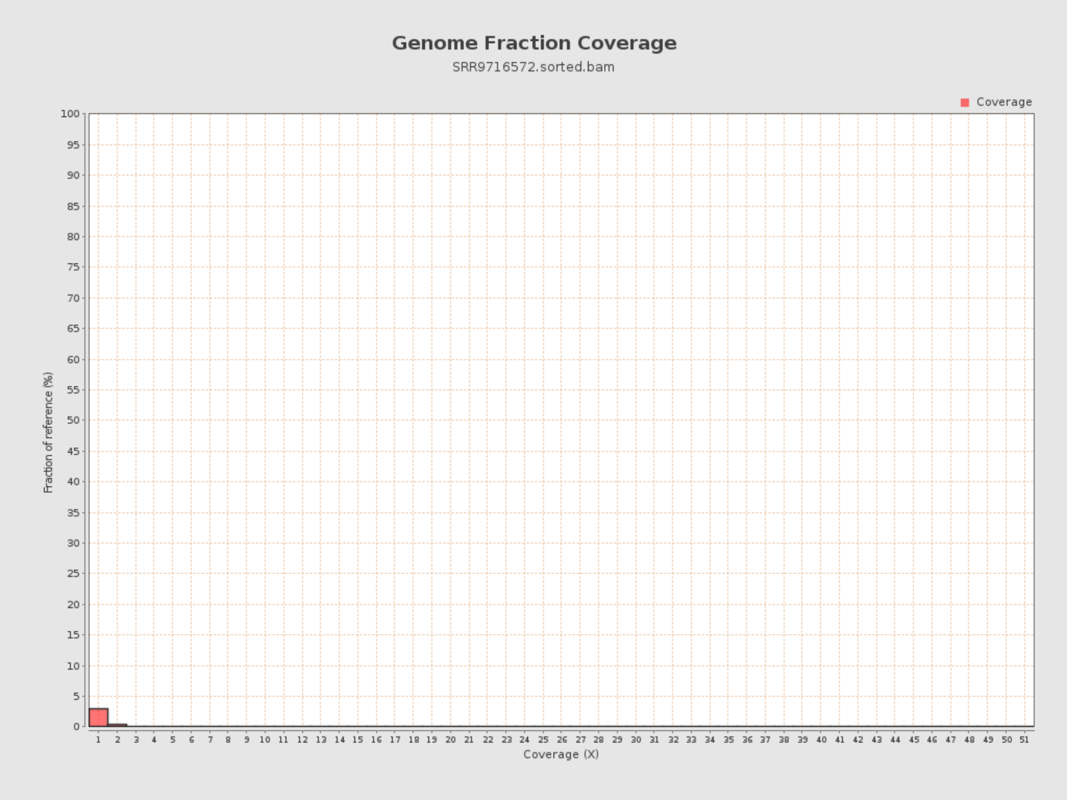
4. Results : Coverage Histogram



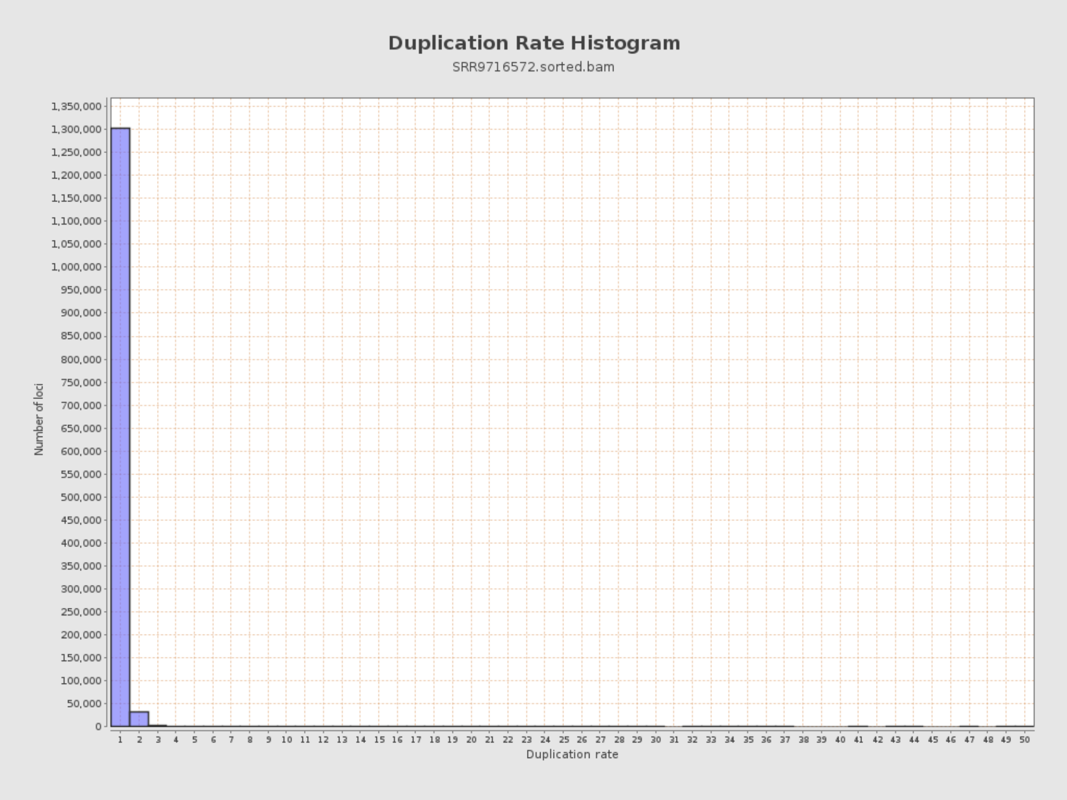
5. Results : Coverage Histogram (0-50X)



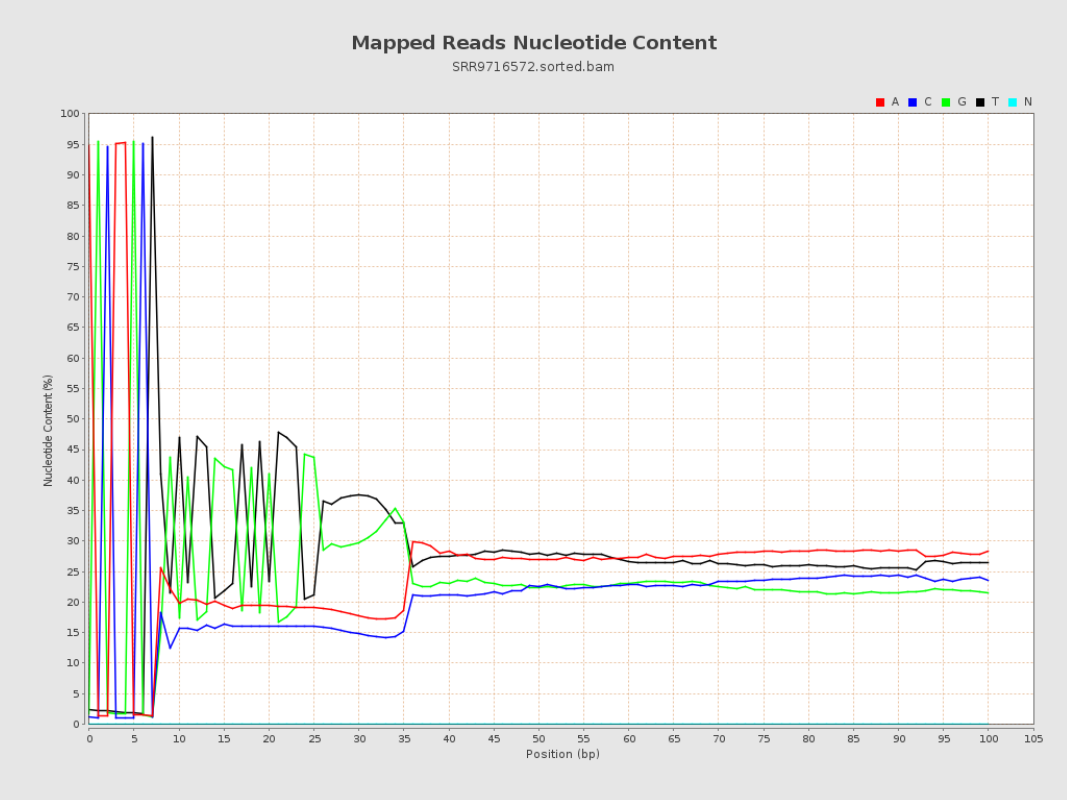
6. Results : Genome Fraction Coverage



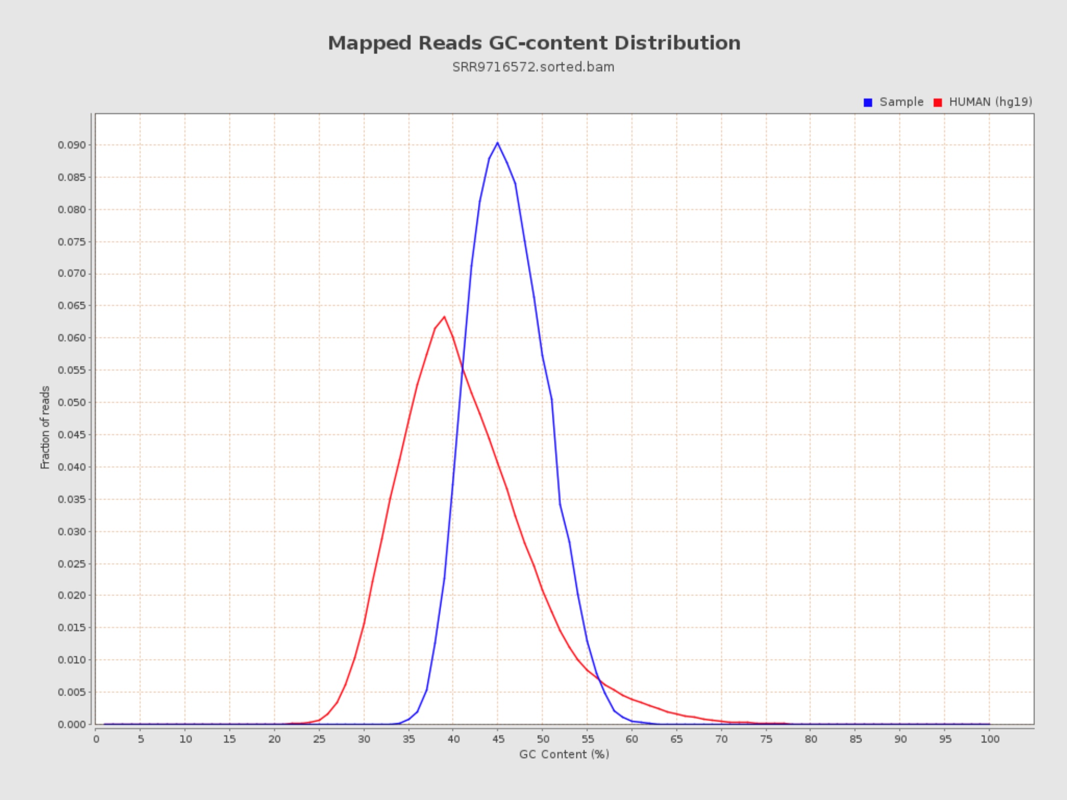
7. Results : Duplication Rate Histogram



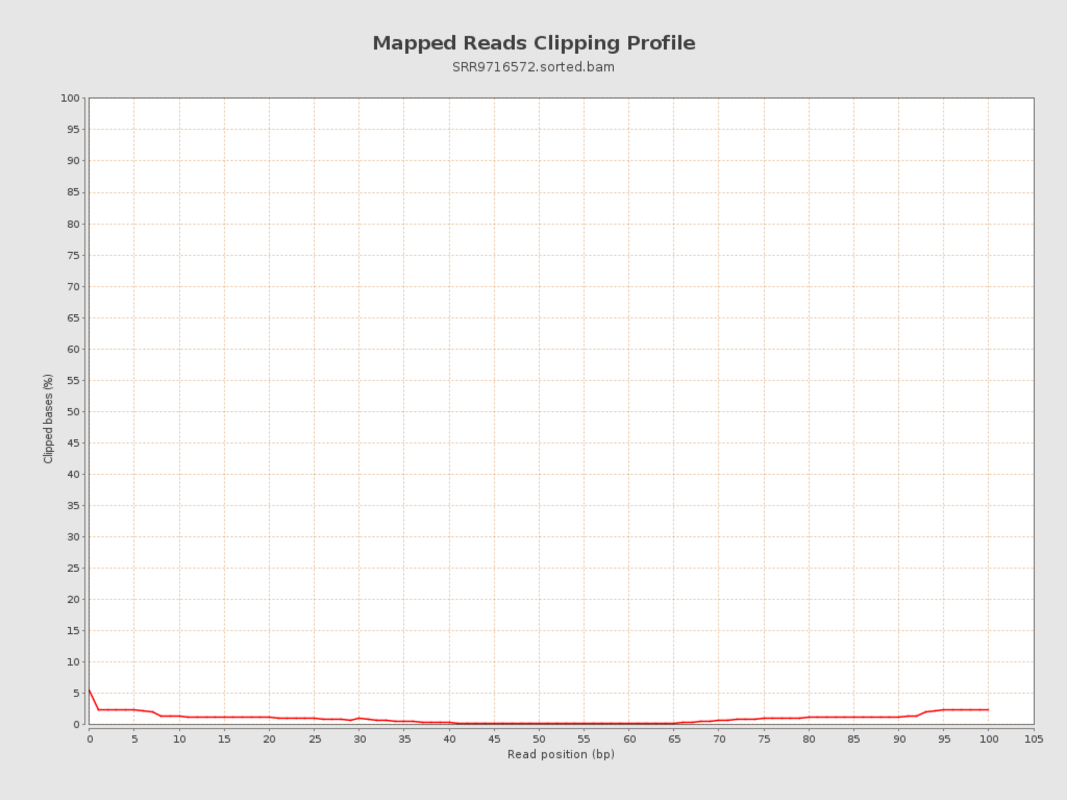
8. Results : Mapped Reads Nucleotide Content



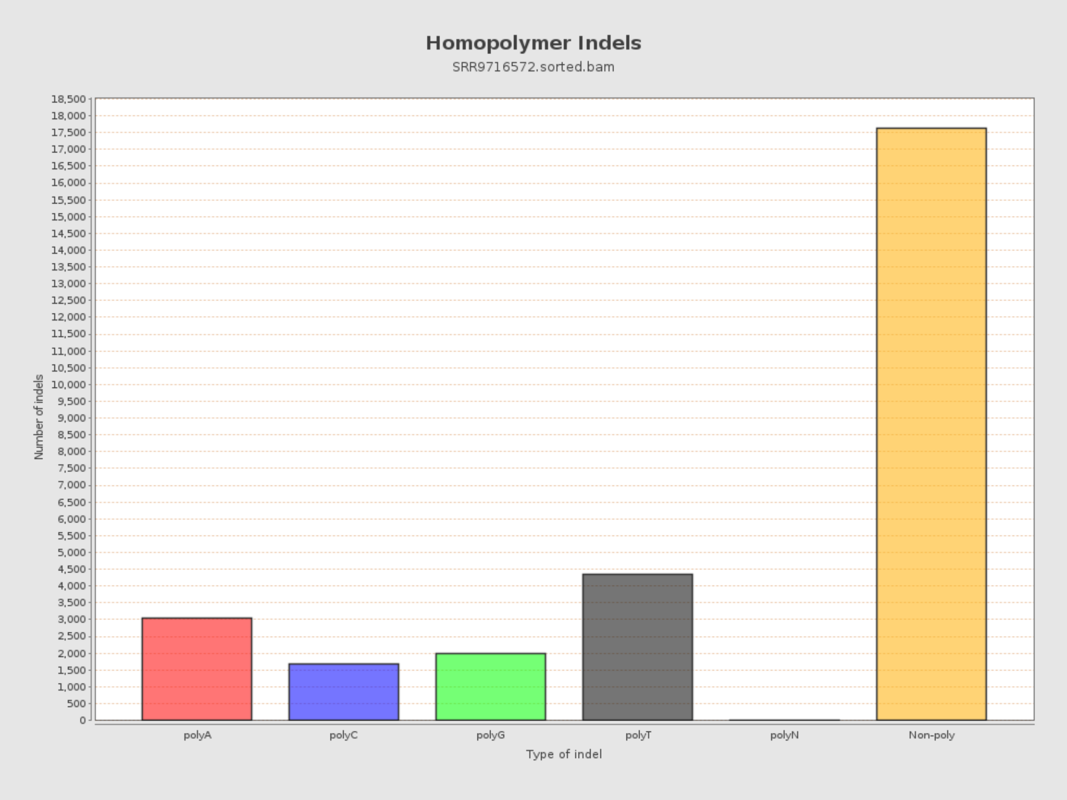
9. Results : Mapped Reads GC-content Distribution



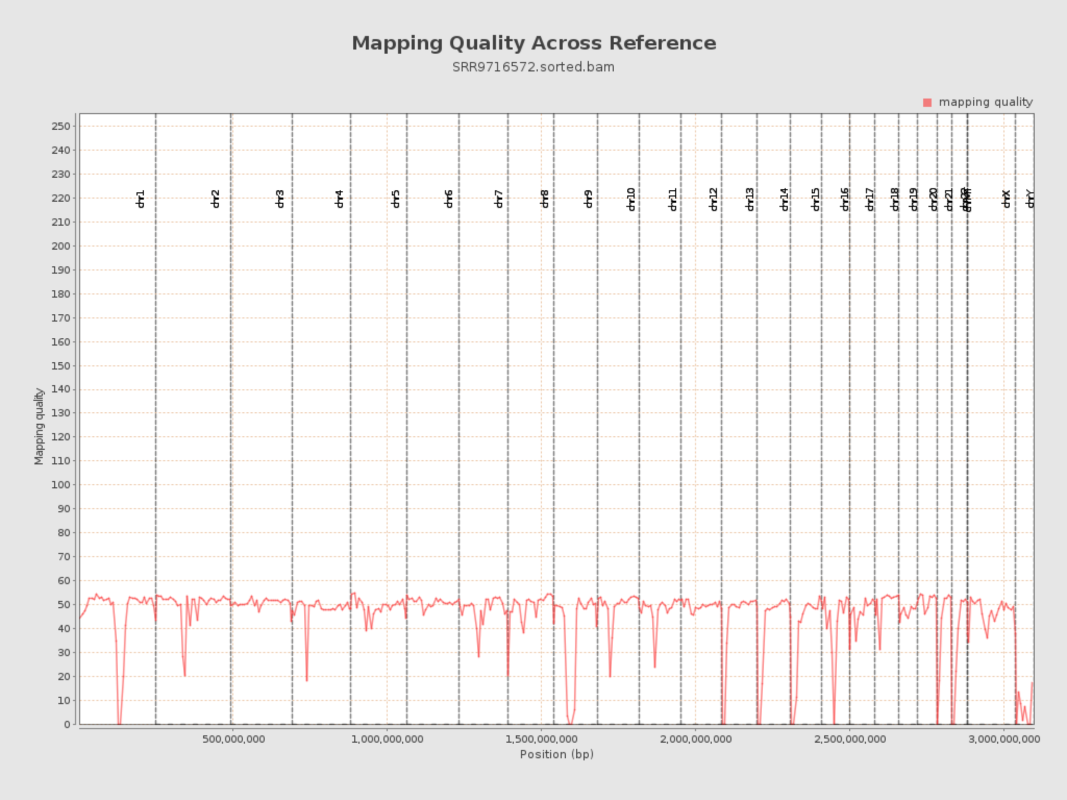
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram