Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 06:16:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716689.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_SRR9716689 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716689.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 06:16:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716689.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	927,384
Mapped reads	853,426 / 92.03%
Unmapped reads	73,958 / 7.97%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,519 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	32,431 / 3.5%
Duplication rate	2.85%
Clipped reads	854,237 / 92.11%

2.2. ACGT Content

Number/percentage of A's	11,592,097 / 23.54%
Number/percentage of C's	9,993,433 / 20.29%
Number/percentage of T's	15,932,110 / 32.35%
Number/percentage of G's	11,734,769 / 23.83%
Number/percentage of N's	972 / 0%
GC Percentage	44.12%

2.3. Coverage

Mean	0.0159

Standard Deviation	0.1791

2.4. Mapping Quality

Mean Mapping Quality	44.76

2.5. Mismatches and indels

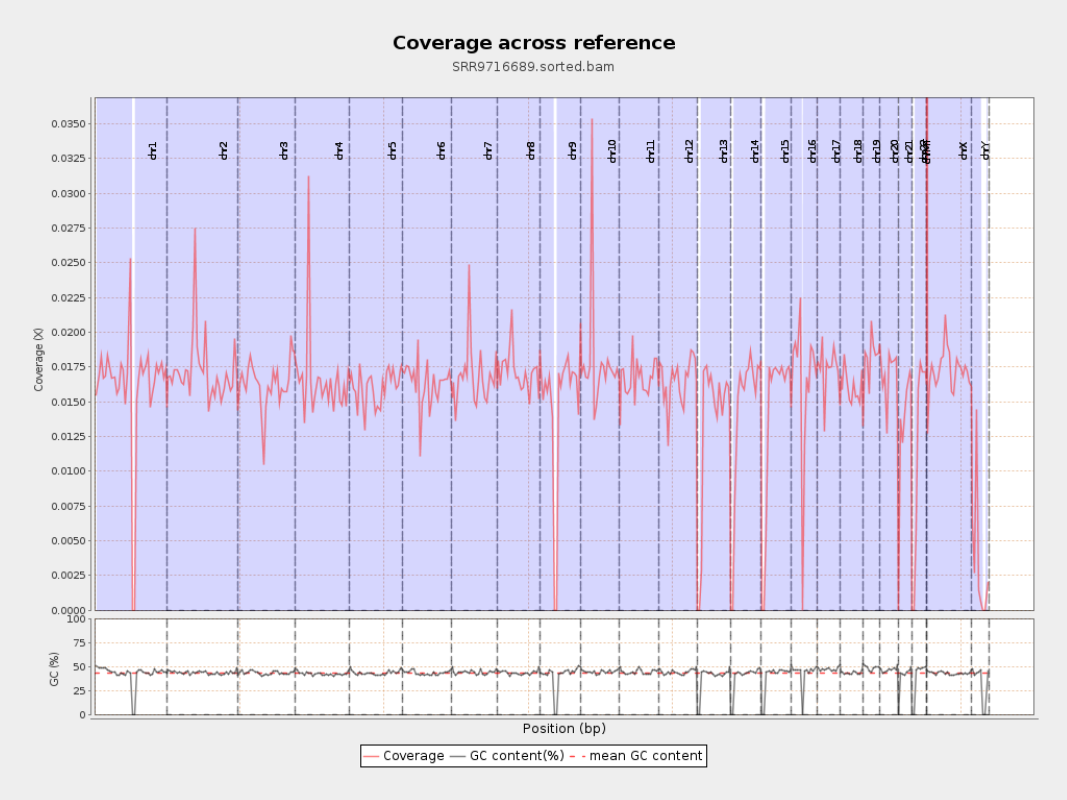
General error rate	0.53%
Mismatches	252,195
Insertions	3,818
Mapped reads with at least one insertion	0.44%
Deletions	9,679
Mapped reads with at least one deletion	1.13%
Homopolymer indels	41.16%

2.6. Chromosome stats

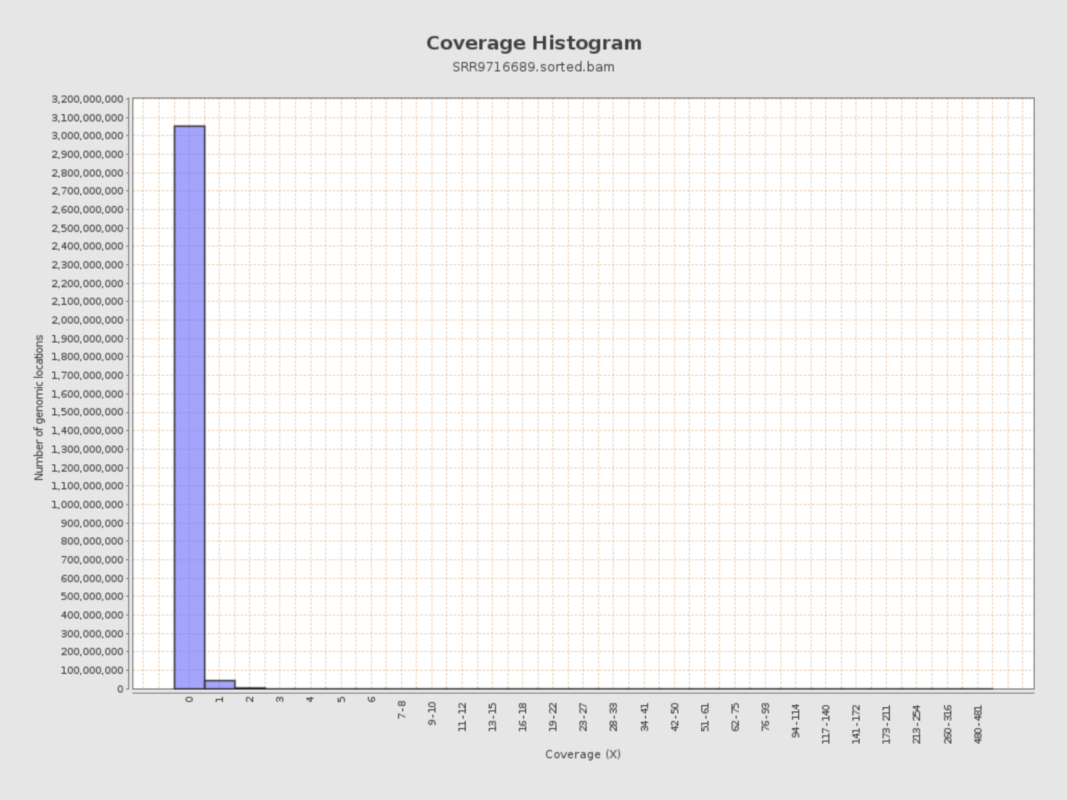
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3997893	0.016	0.2614
chr2	243199373	4185556	0.0172	0.2523
chr3	198022430	3221974	0.0163	0.1368
chr4	191154276	3170093	0.0166	0.1591
chr5	180915260	2902908	0.016	0.1356
chr6	171115067	2784449	0.0163	0.1462
chr7	159138663	2685127	0.0169	0.1929

chr8	146364022	2513326	0.0172	0.2212
chr9	141213431	2071093	0.0147	0.1504
chr10	135534747	2427559	0.0179	0.2048
chr11	135006516	2258535	0.0167	0.1601
chr12	133851895	2206517	0.0165	0.1387
chr13	115169878	1526133	0.0133	0.1227
chr14	107349540	1511462	0.0141	0.1282
chr15	102531392	1422742	0.0139	0.1263
chr16	90354753	1450966	0.0161	0.1438
chr17	81195210	1408023	0.0173	0.147
chr18	78077248	1248000	0.016	0.2211
chr19	59128983	1076655	0.0182	0.2166
chr20	63025520	1062055	0.0169	0.1435
chr21	48129895	647439	0.0135	0.1482
chr22	51304566	603884	0.0118	0.1163
chrMT	16571	7971	0.481	0.734
chrX	155270560	2681183	0.0173	0.1461
chrY	59373566	197520	0.0033	0.1602

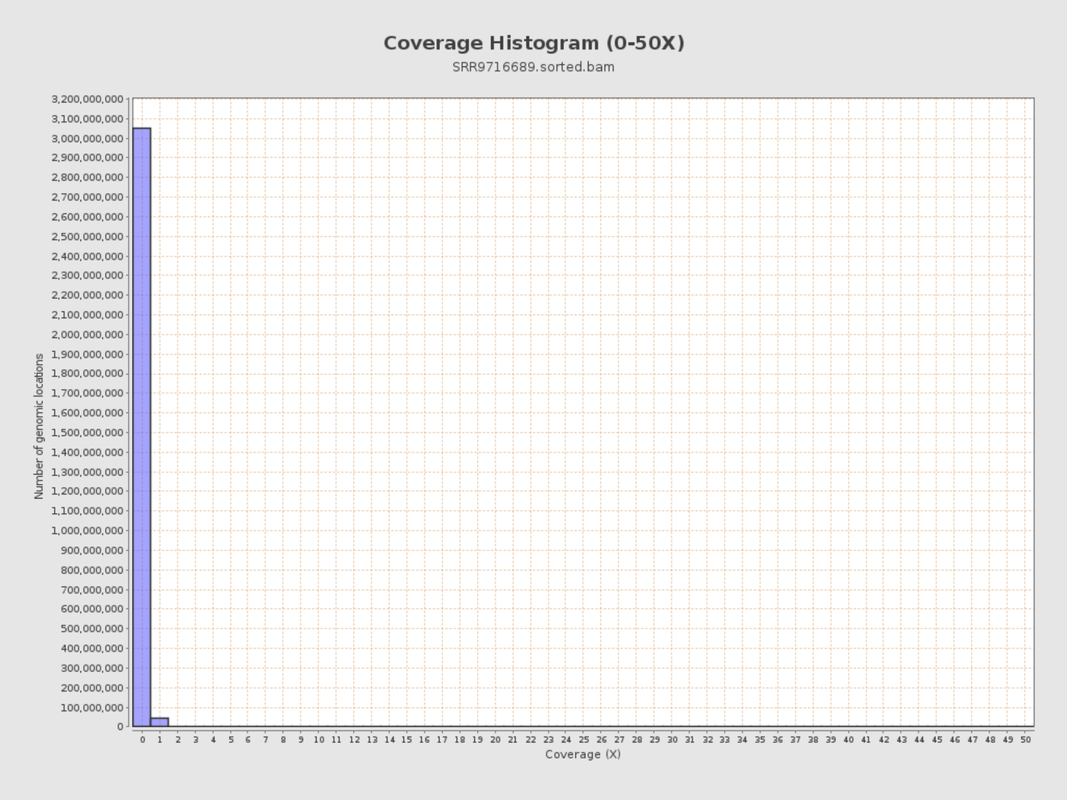
3. Results : Coverage across reference



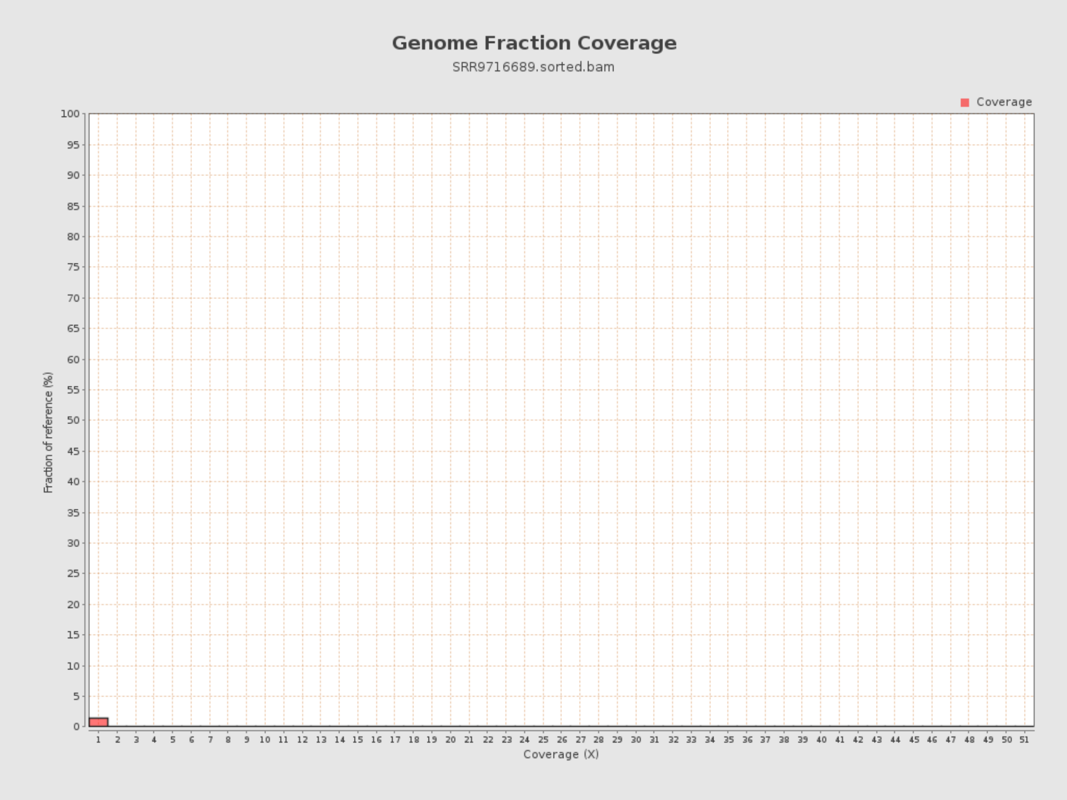
4. Results : Coverage Histogram



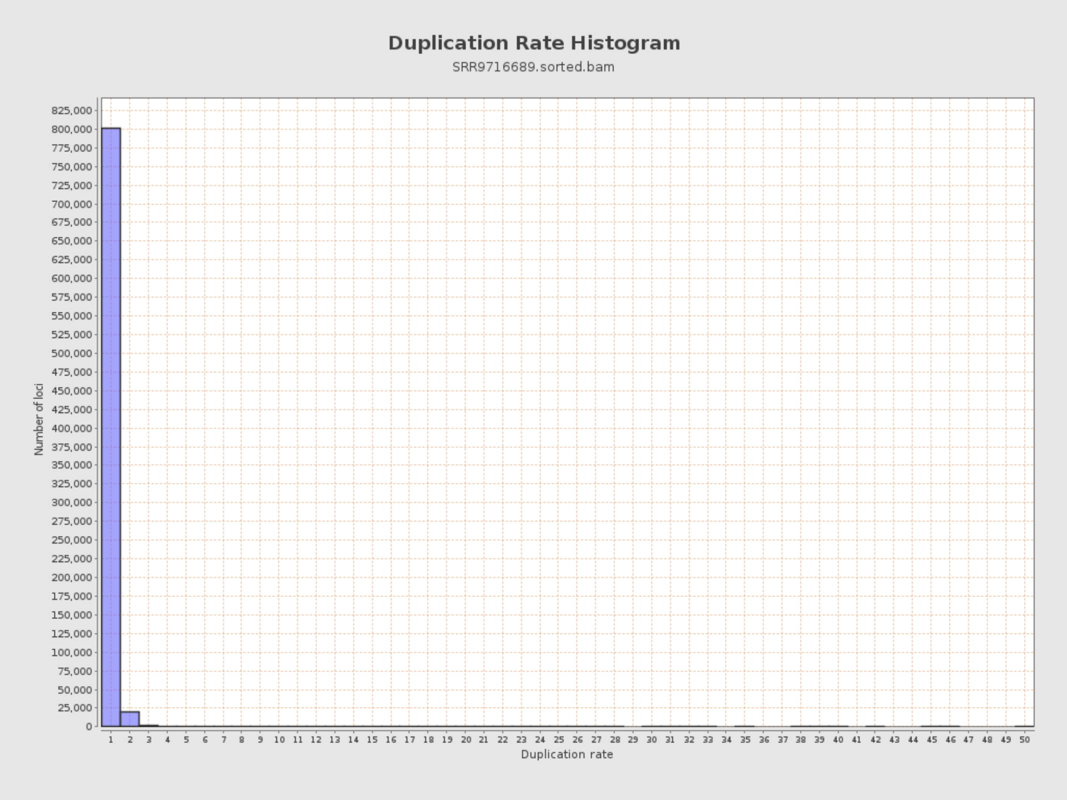
5. Results : Coverage Histogram (0-50X)



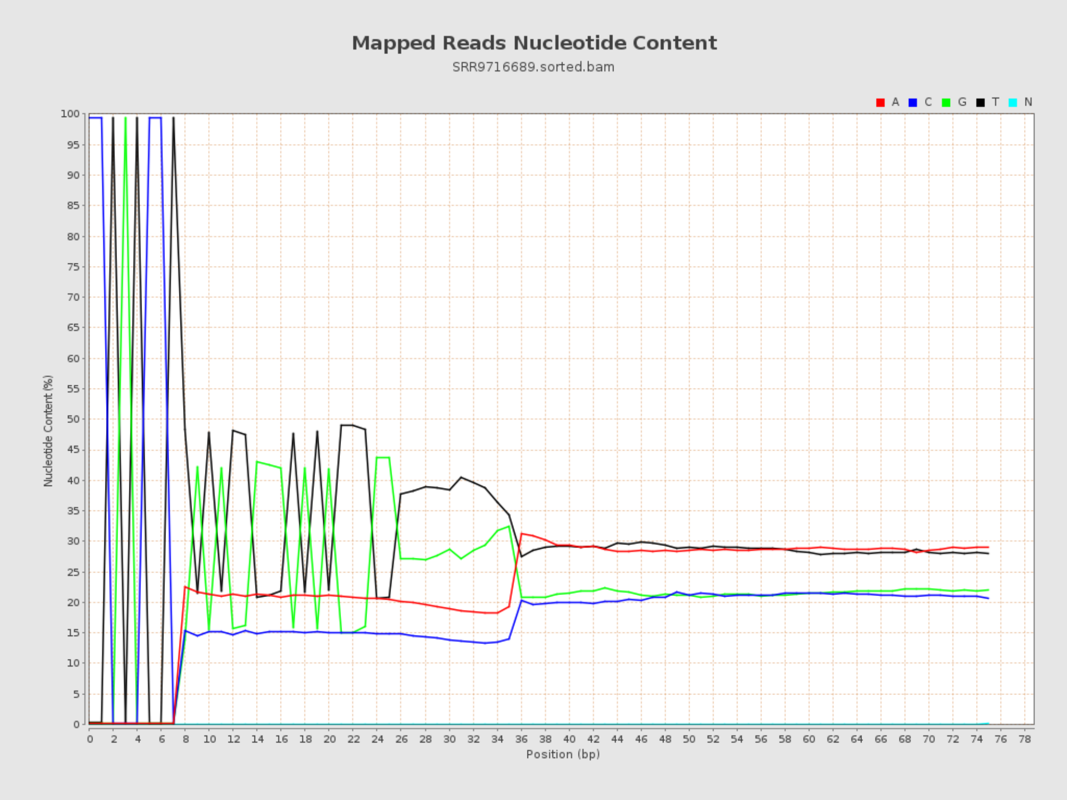
6. Results : Genome Fraction Coverage



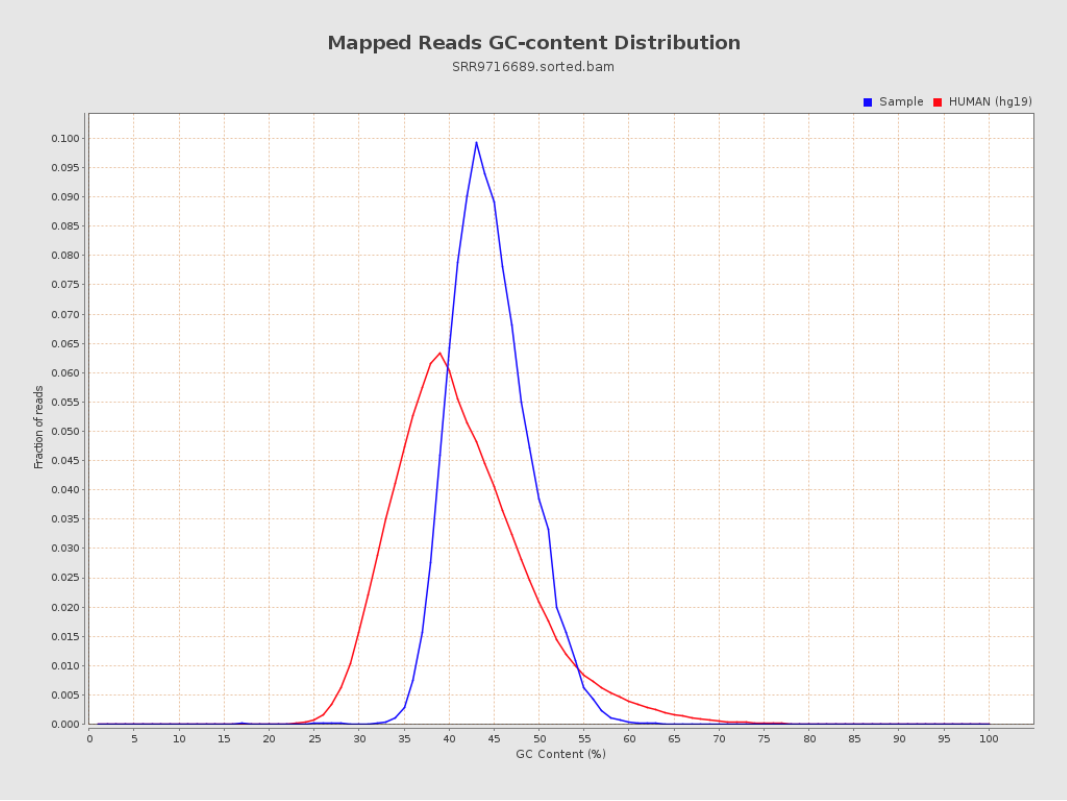
7. Results : Duplication Rate Histogram



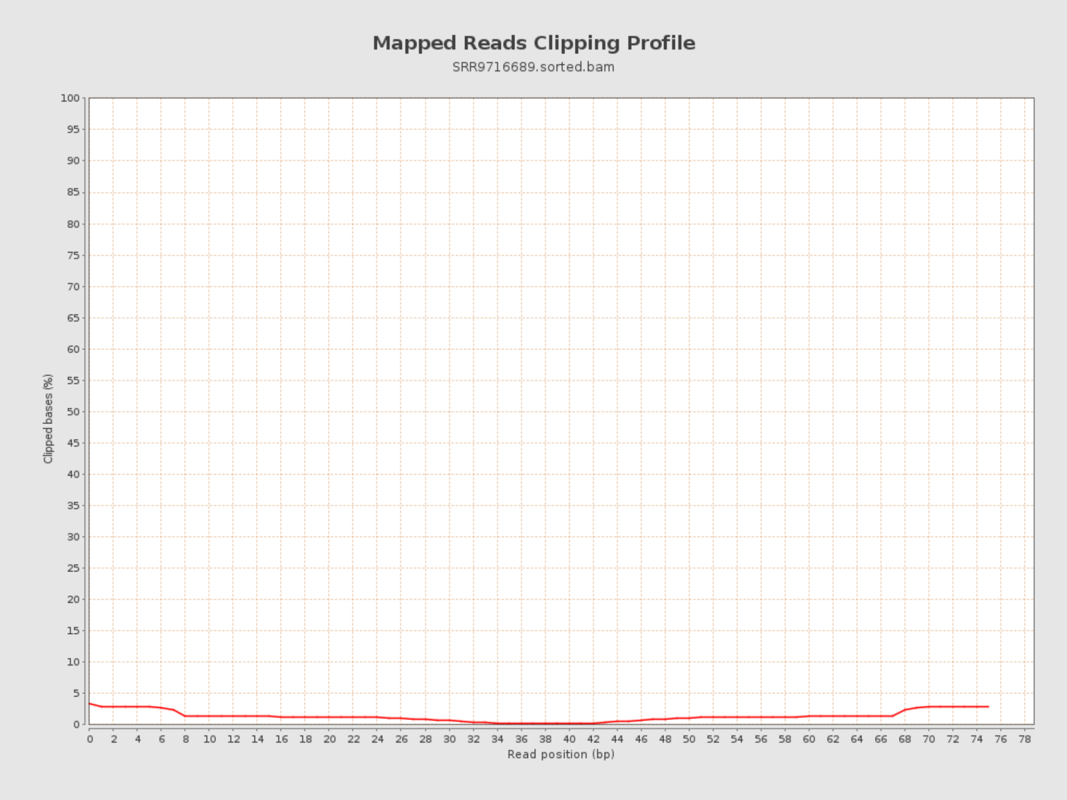
8. Results : Mapped Reads Nucleotide Content



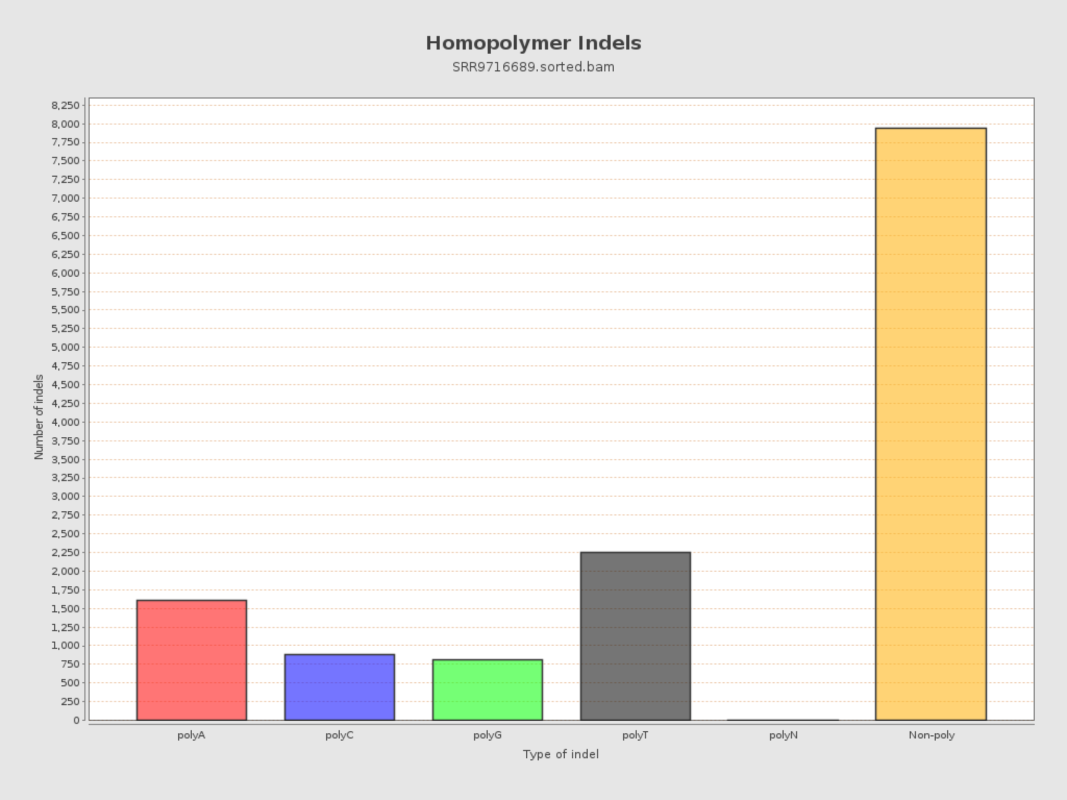
9. Results : Mapped Reads GC-content Distribution



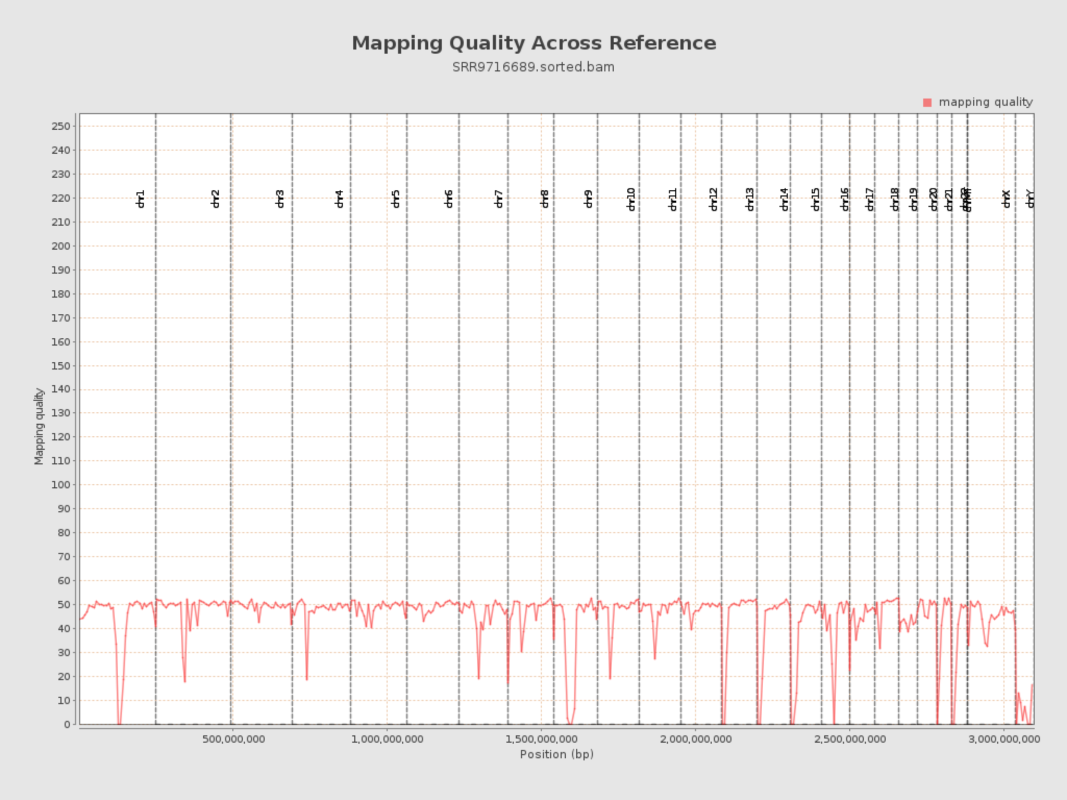
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram