Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:41:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716285.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_SRR9716285 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716285.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:41:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716285.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,049,841
Mapped reads	960,814 / 91.52%
Unmapped reads	89,027 / 8.48%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,330 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	19,179 / 1.83%
Duplication rate	1.55%
Clipped reads	961,681 / 91.6%

2.2. ACGT Content

Number/percentage of A's	14,304,585 / 25.77%
Number/percentage of C's	11,330,241 / 20.41%
Number/percentage of T's	16,833,313 / 30.33%
Number/percentage of G's	13,032,781 / 23.48%
Number/percentage of N's	1,218 / 0%
GC Percentage	43.9%

2.3. Coverage

Mean	0.0179

Standard Deviation	0.1655

2.4. Mapping Quality

Mean Mapping Quality	45.06

2.5. Mismatches and indels

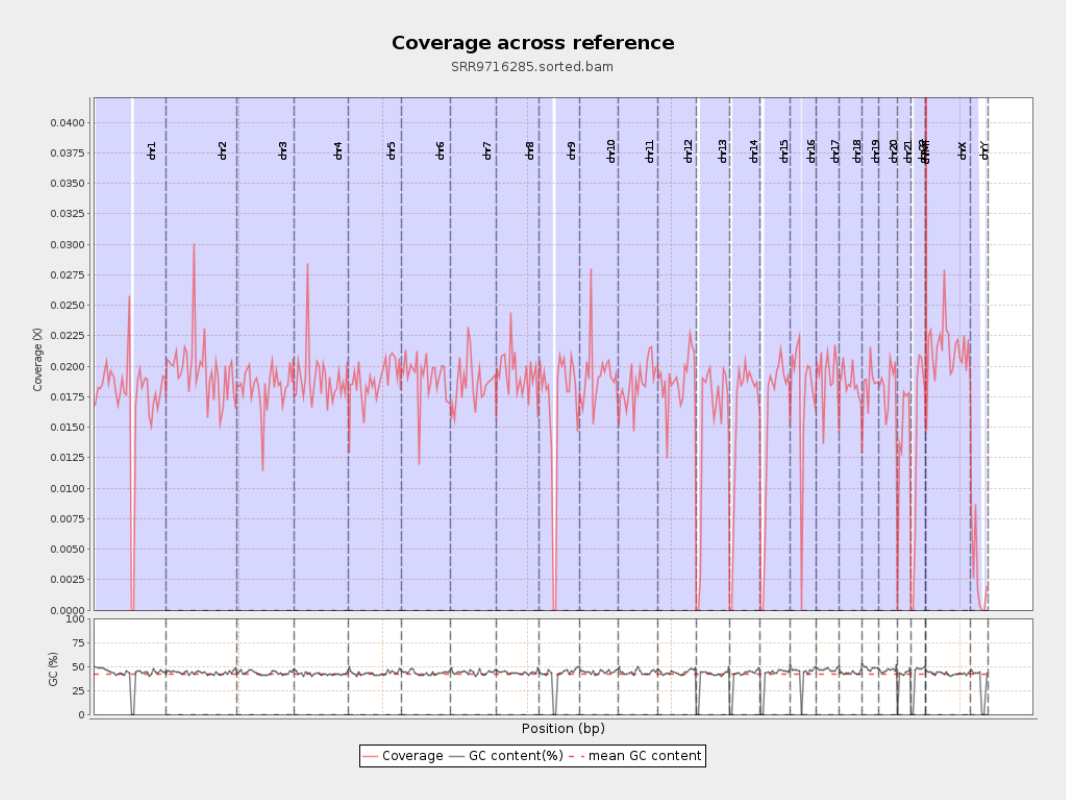
General error rate	0.49%
Mismatches	264,979
Insertions	4,141
Mapped reads with at least one insertion	0.43%
Deletions	8,452
Mapped reads with at least one deletion	0.87%
Homopolymer indels	39.34%

2.6. Chromosome stats

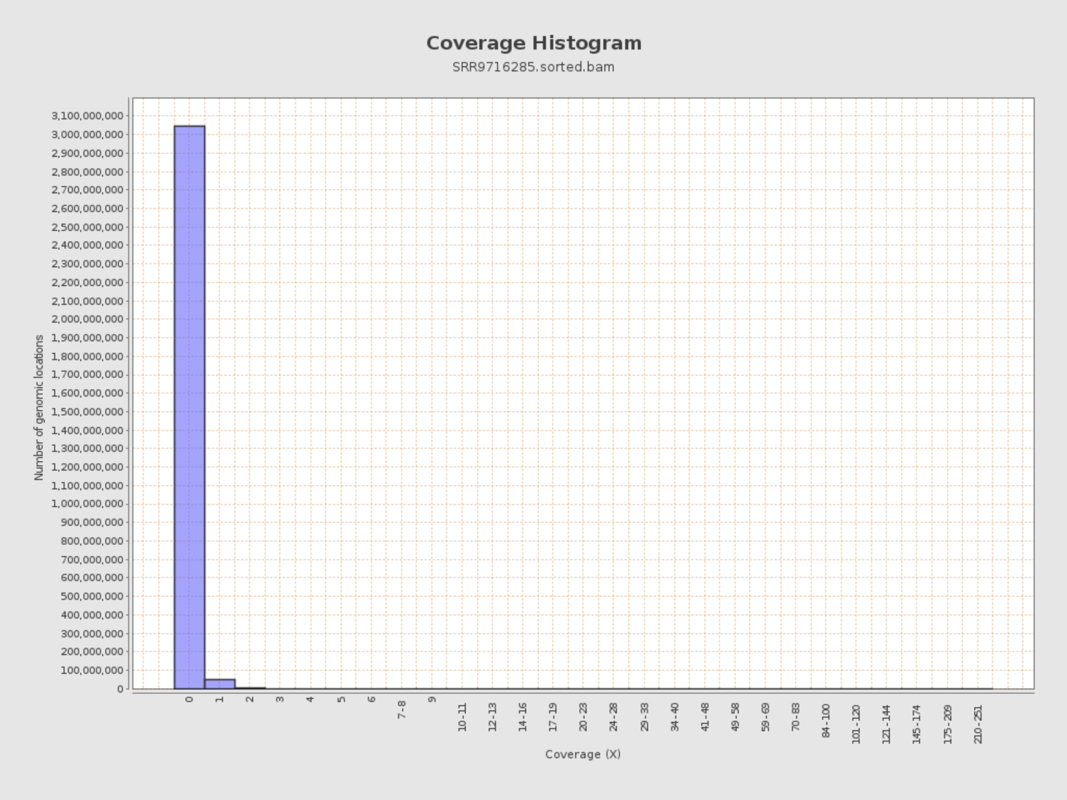
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4298516	0.0172	0.2344
chr2	243199373	4788753	0.0197	0.1818
chr3	198022430	3631398	0.0183	0.1429
chr4	191154276	3623940	0.019	0.1526
chr5	180915260	3440841	0.019	0.1463
chr6	171115067	3259484	0.019	0.1513
chr7	159138663	2965036	0.0186	0.1743

chr8	146364022	2833851	0.0194	0.1586
chr9	141213431	2348974	0.0166	0.1648
chr10	135534747	2597310	0.0192	0.1707
chr11	135006516	2519749	0.0187	0.162
chr12	133851895	2511453	0.0188	0.1455
chr13	115169878	1737042	0.0151	0.1291
chr14	107349540	1672975	0.0156	0.1366
chr15	102531392	1587581	0.0155	0.1309
chr16	90354753	1583067	0.0175	0.147
chr17	81195210	1554871	0.0191	0.1512
chr18	78077248	1461872	0.0187	0.2524
chr19	59128983	1097270	0.0186	0.1849
chr20	63025520	1148135	0.0182	0.1465
chr21	48129895	679066	0.0141	0.1329
chr22	51304566	688449	0.0134	0.1219
chrMT	16571	2853	0.1722	0.4193
chrX	155270560	3322448	0.0214	0.166
chrY	59373566	161313	0.0027	0.0728

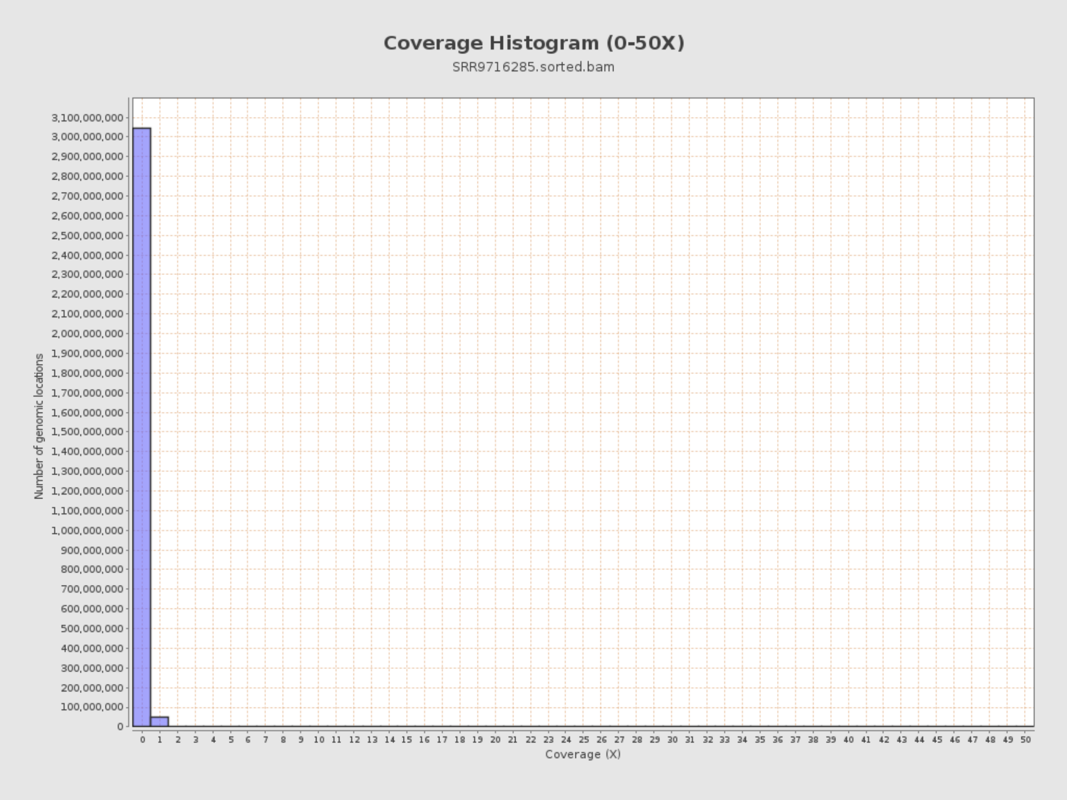
3. Results : Coverage across reference



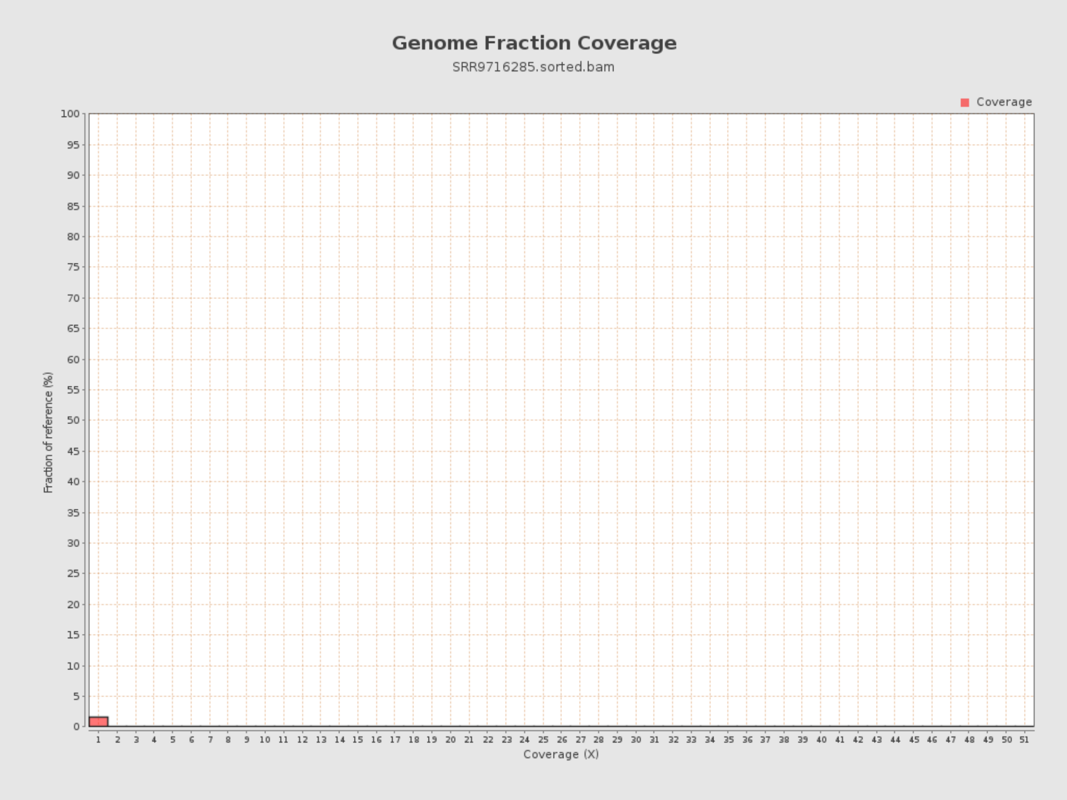
4. Results : Coverage Histogram



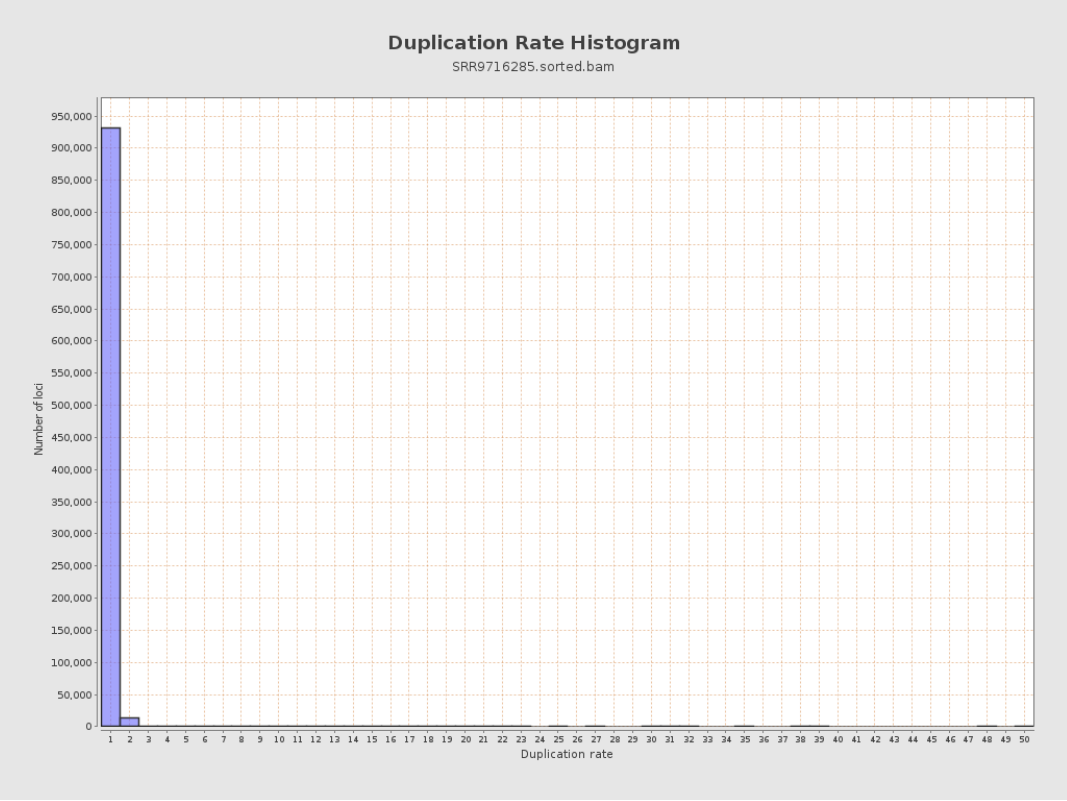
5. Results : Coverage Histogram (0-50X)



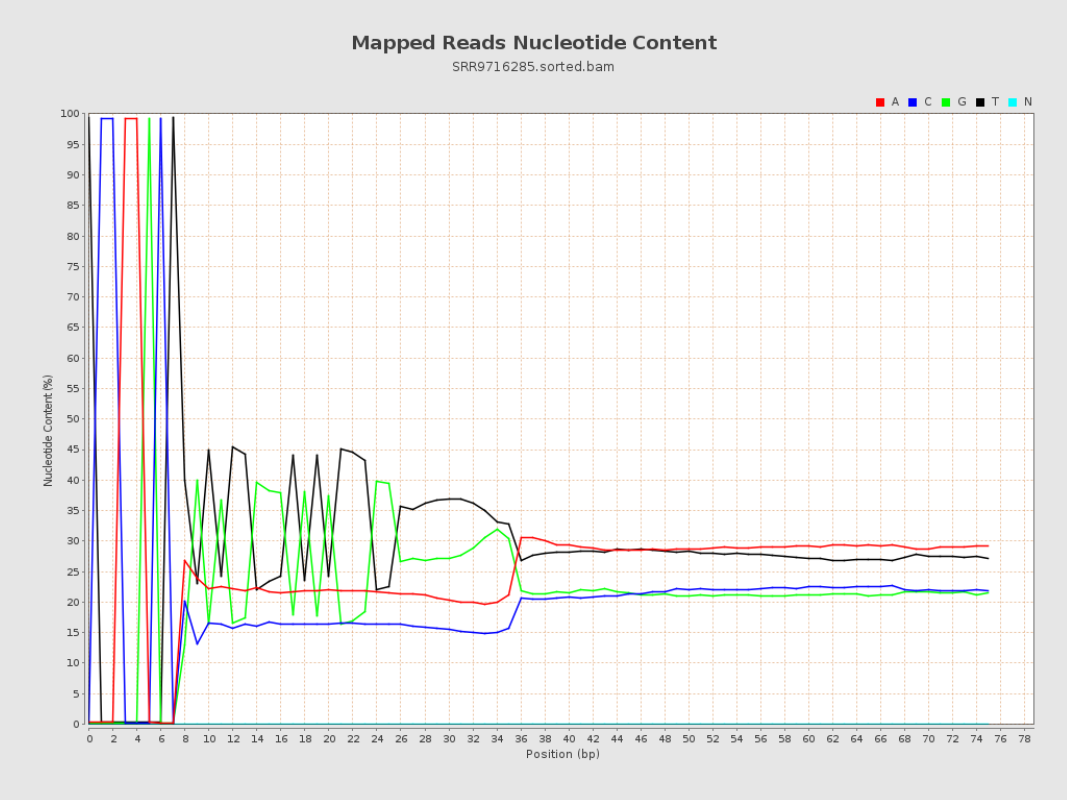
6. Results : Genome Fraction Coverage



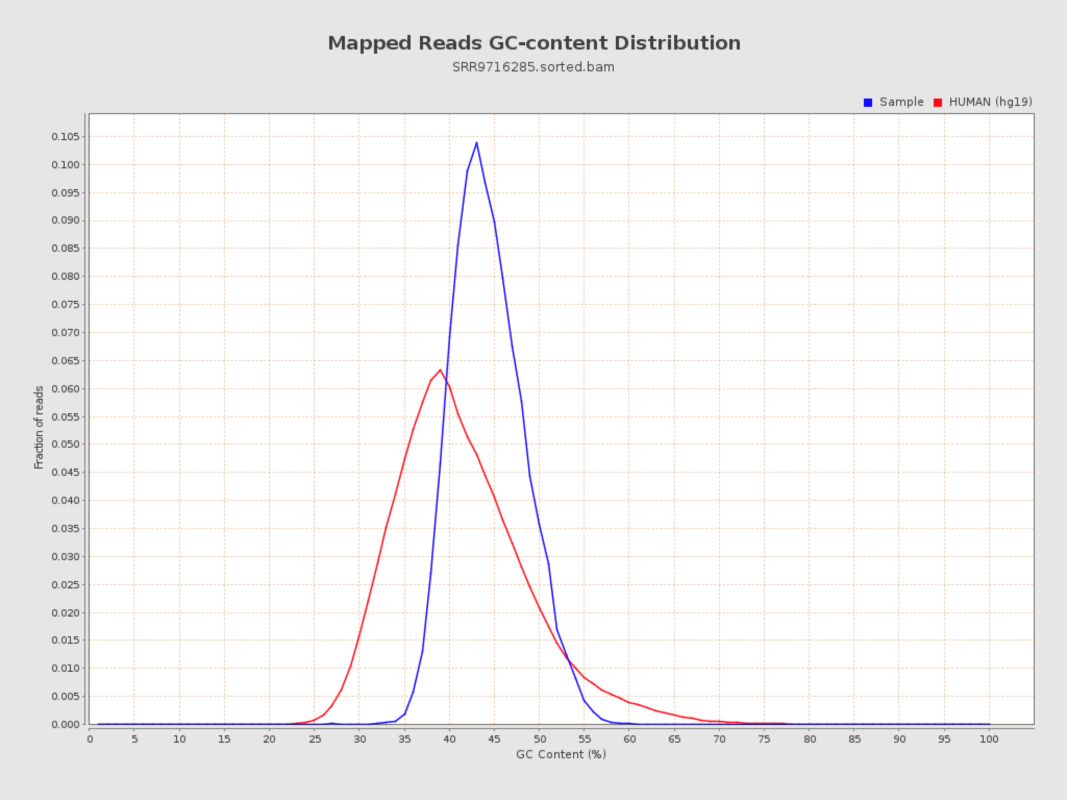
7. Results : Duplication Rate Histogram



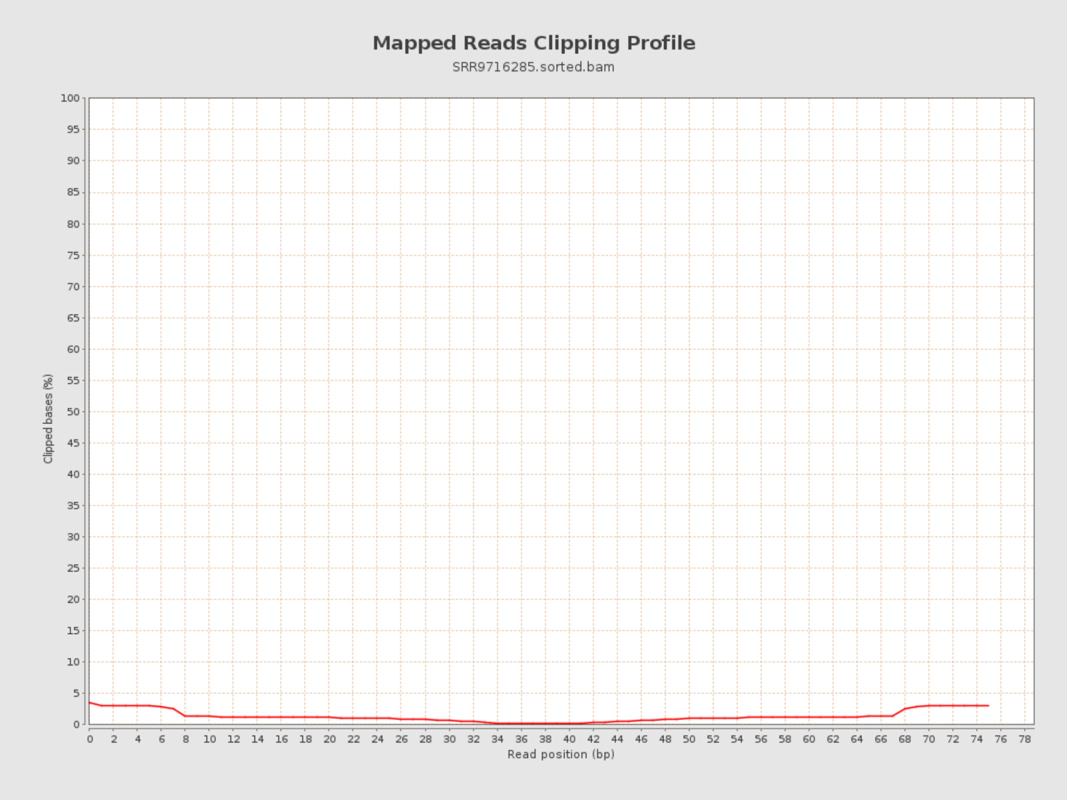
8. Results : Mapped Reads Nucleotide Content



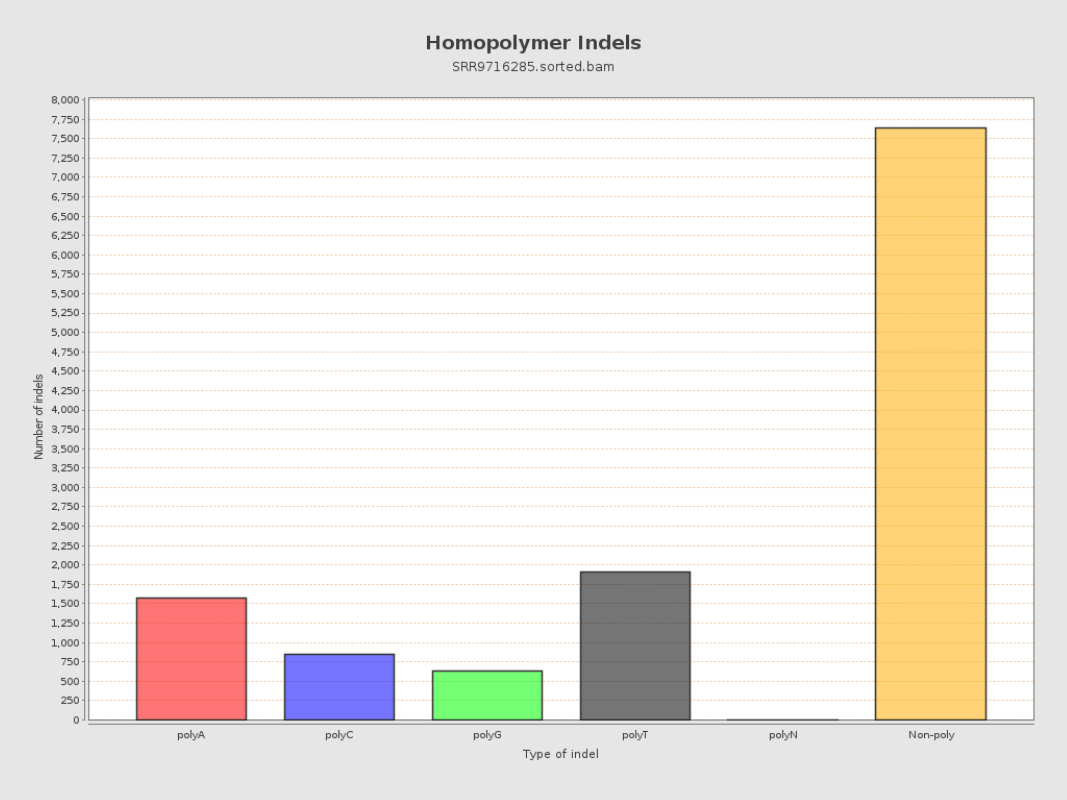
9. Results : Mapped Reads GC-content Distribution



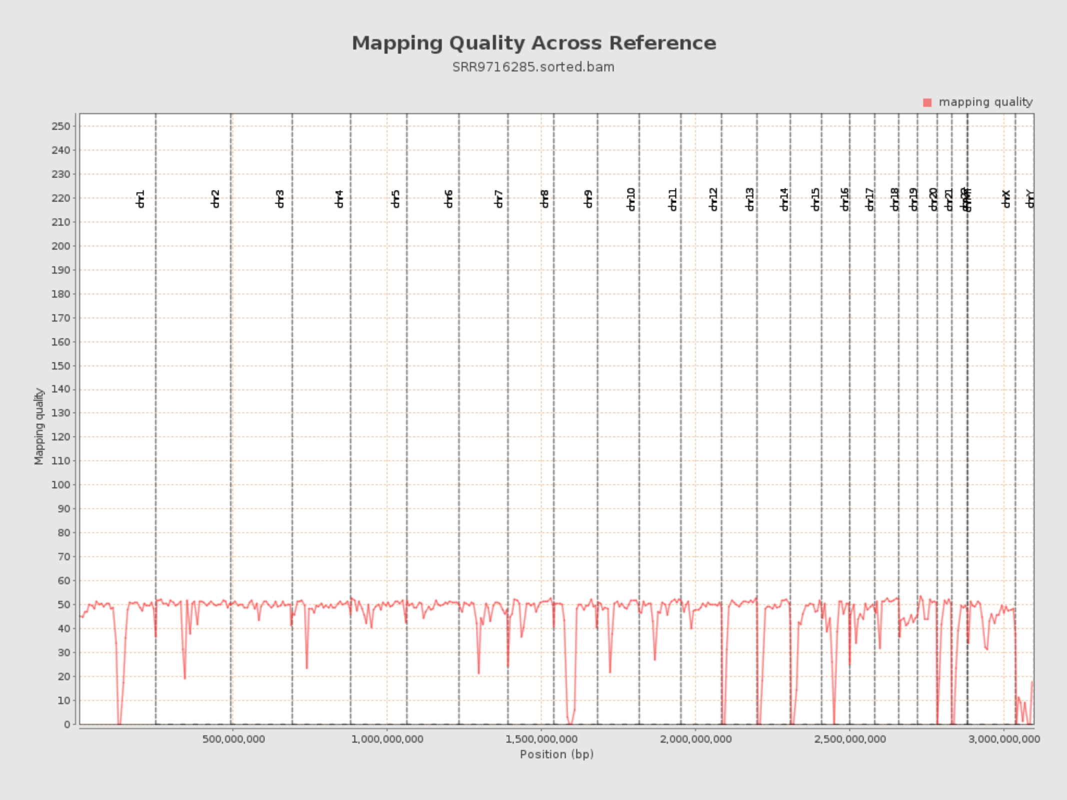
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram