Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 09:42:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716741.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_SRR9716741 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716741.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 09:42:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716741.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	868,173
Mapped reads	682,898 / 78.66%
Unmapped reads	185,275 / 21.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	772 / 0.09%
Read min/max/mean length	30 / 76 / 76.03
Duplicated reads (estimated)	48,009 / 5.53%
Duplication rate	6.28%
Clipped reads	682,255 / 78.59%

2.2. ACGT Content

Number/percentage of A's	6,938,554 / 19.37%
Number/percentage of C's	6,244,914 / 17.43%
Number/percentage of T's	11,960,638 / 33.39%
Number/percentage of G's	10,676,107 / 29.8%
Number/percentage of N's	690 / 0%
GC Percentage	47.24%

2.3. Coverage

Mean	0.0116

Standard Deviation	0.1296

2.4. Mapping Quality

Mean Mapping Quality	43.2

2.5. Mismatches and indels

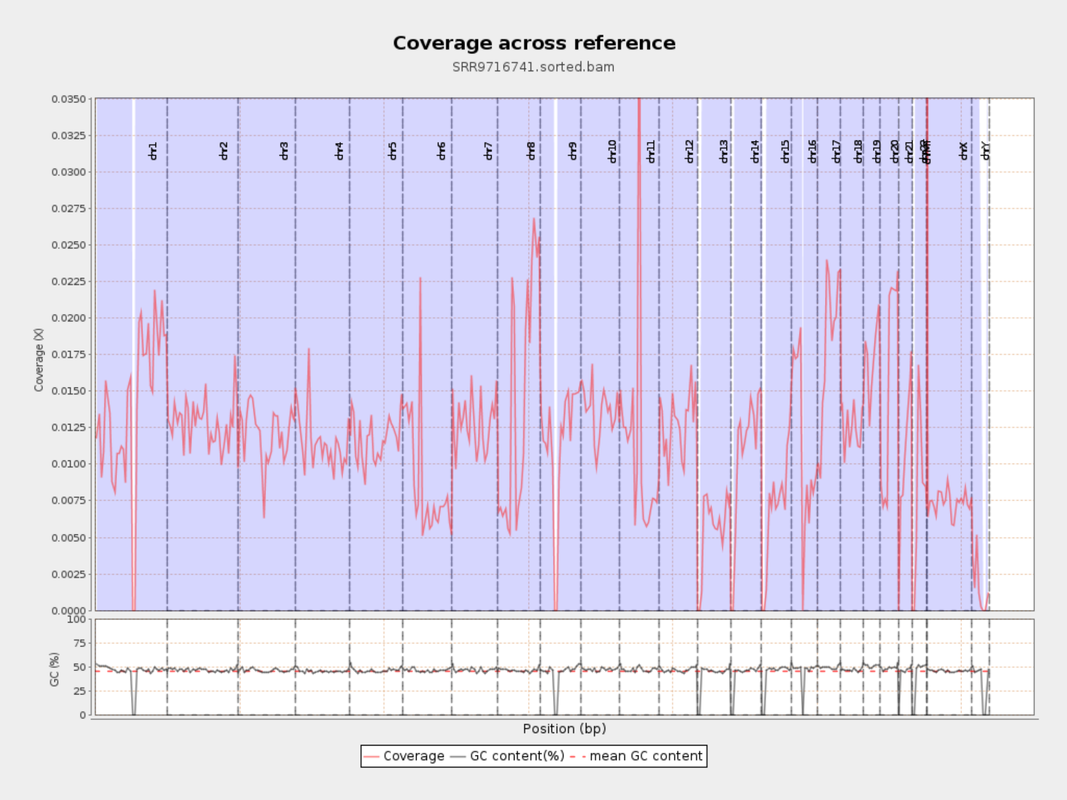
General error rate	0.65%
Mismatches	230,272
Insertions	2,098
Mapped reads with at least one insertion	0.31%
Deletions	4,810
Mapped reads with at least one deletion	0.7%
Homopolymer indels	39.74%

2.6. Chromosome stats

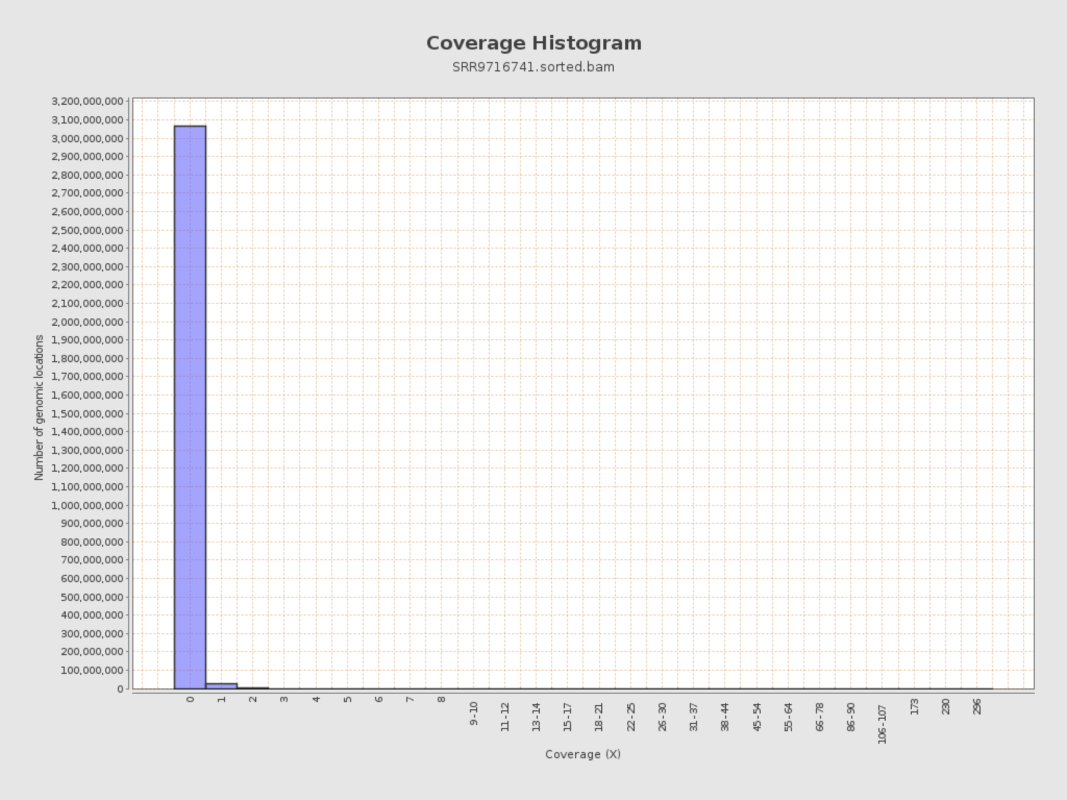
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3480103	0.014	0.1414
chr2	243199373	3123344	0.0128	0.1721
chr3	198022430	2392439	0.0121	0.1242
chr4	191154276	2212224	0.0116	0.123
chr5	180915260	2129838	0.0118	0.1221
chr6	171115067	1522072	0.0089	0.1171
chr7	159138663	2034778	0.0128	0.1324

chr8	146364022	2100667	0.0144	0.1384
chr9	141213431	1617401	0.0115	0.1237
chr10	135534747	1857128	0.0137	0.14
chr11	135006516	1573294	0.0117	0.1312
chr12	133851895	1708032	0.0128	0.1277
chr13	115169878	636540	0.0055	0.0853
chr14	107349540	1141235	0.0106	0.1171
chr15	102531392	711684	0.0069	0.094
chr16	90354753	995934	0.011	0.1218
chr17	81195210	1465812	0.0181	0.1576
chr18	78077248	973177	0.0125	0.1341
chr19	59128983	1013117	0.0171	0.1645
chr20	63025520	968181	0.0154	0.1467
chr21	48129895	512370	0.0106	0.1235
chr22	51304566	418455	0.0082	0.104
chrMT	16571	3123	0.1885	0.5014
chrX	155270560	1145897	0.0074	0.0979
chrY	59373566	92128	0.0016	0.0491

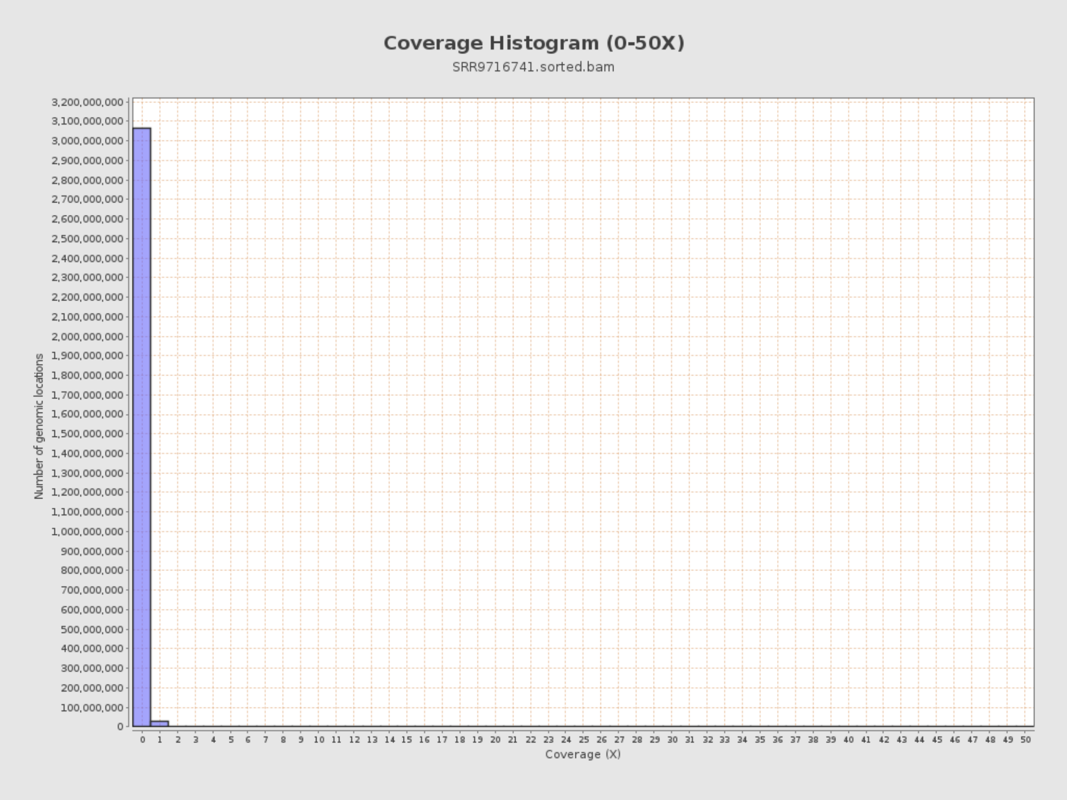
3. Results : Coverage across reference



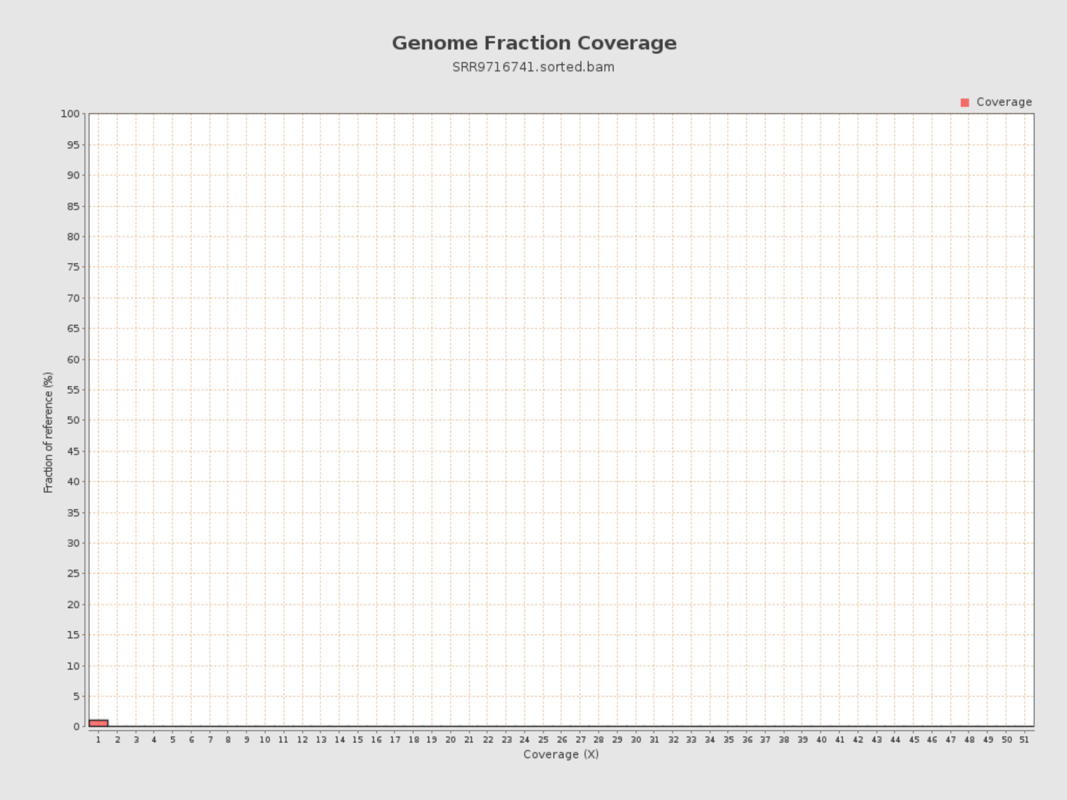
4. Results : Coverage Histogram



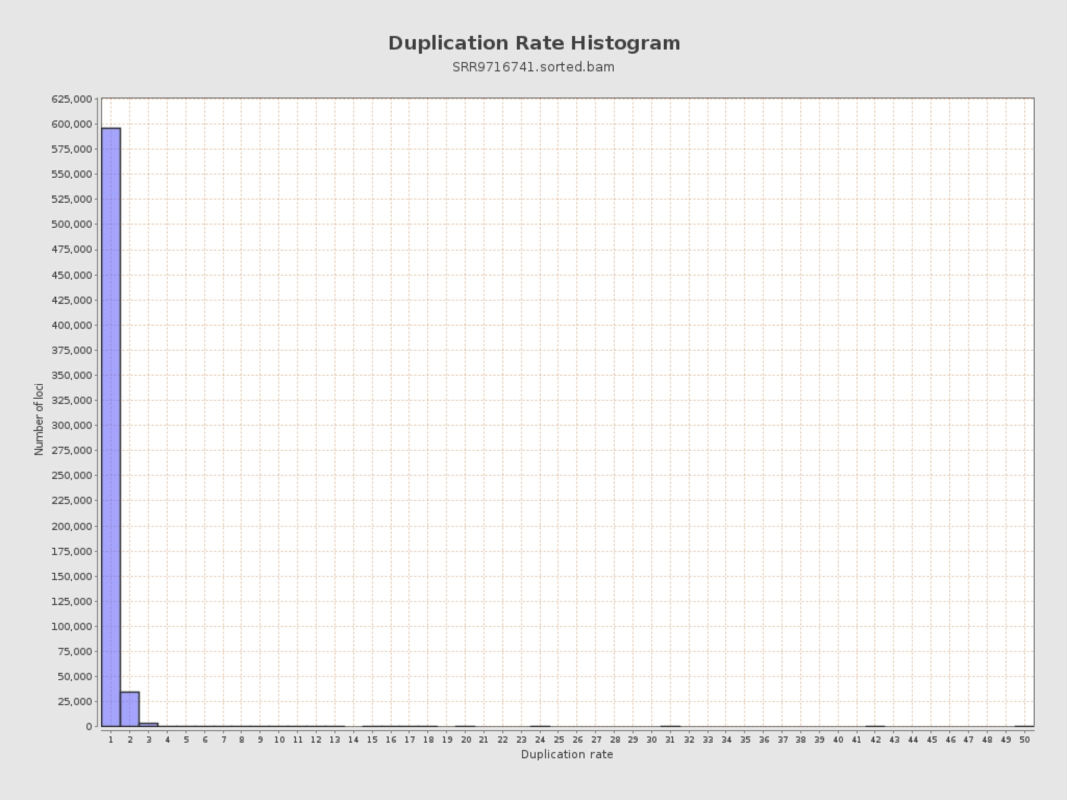
5. Results : Coverage Histogram (0-50X)



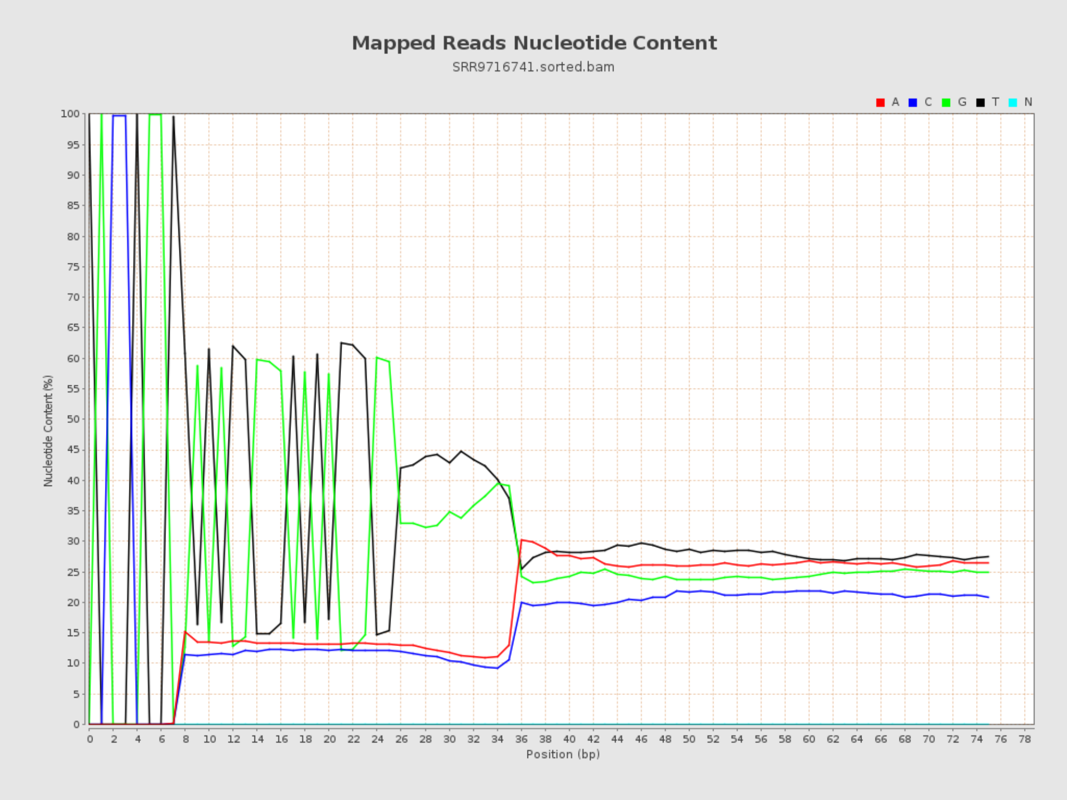
6. Results : Genome Fraction Coverage



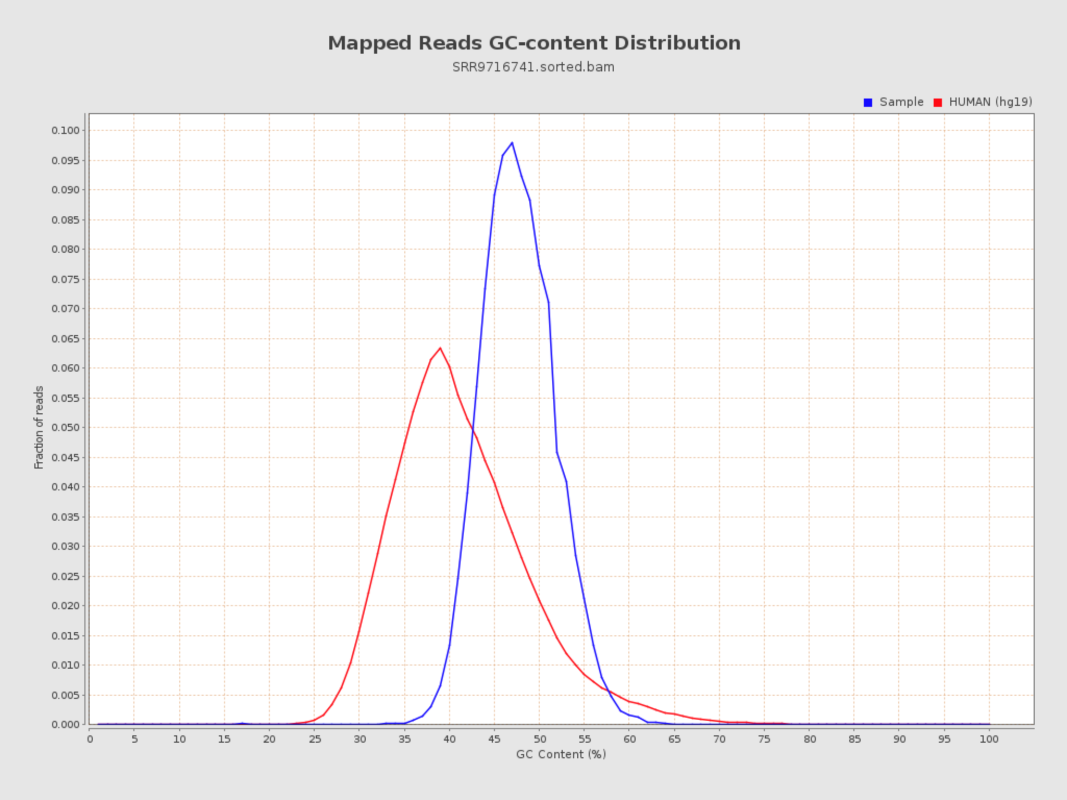
7. Results : Duplication Rate Histogram



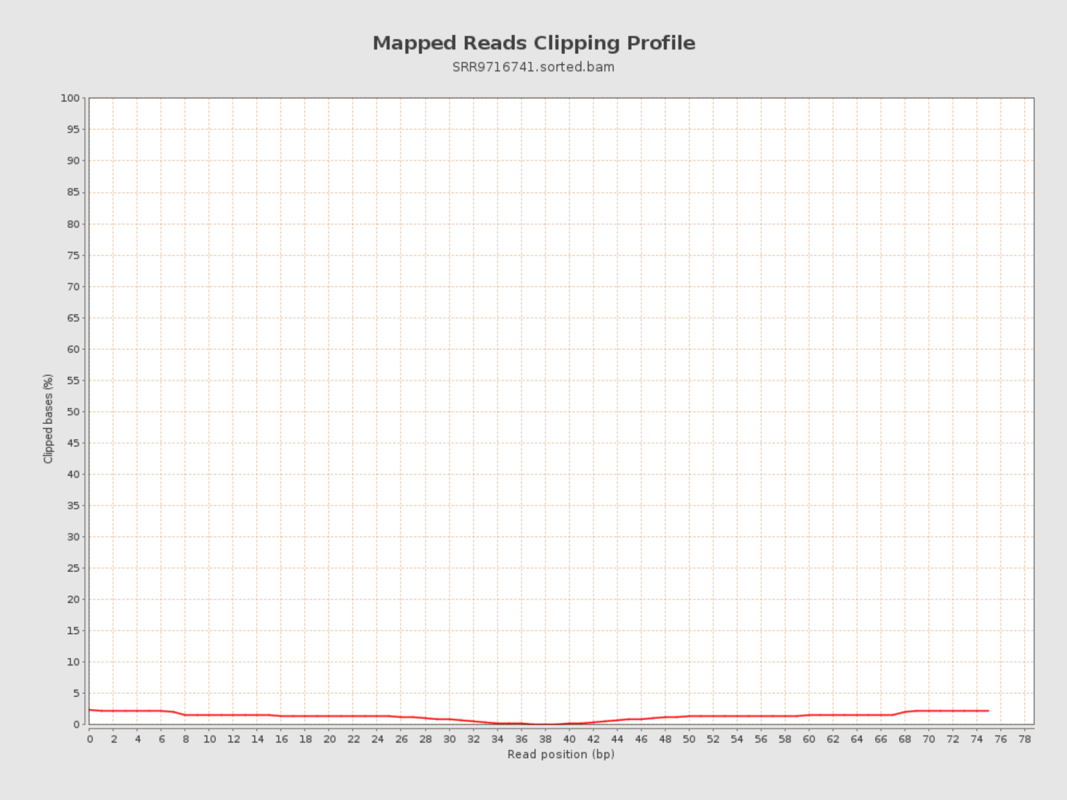
8. Results : Mapped Reads Nucleotide Content



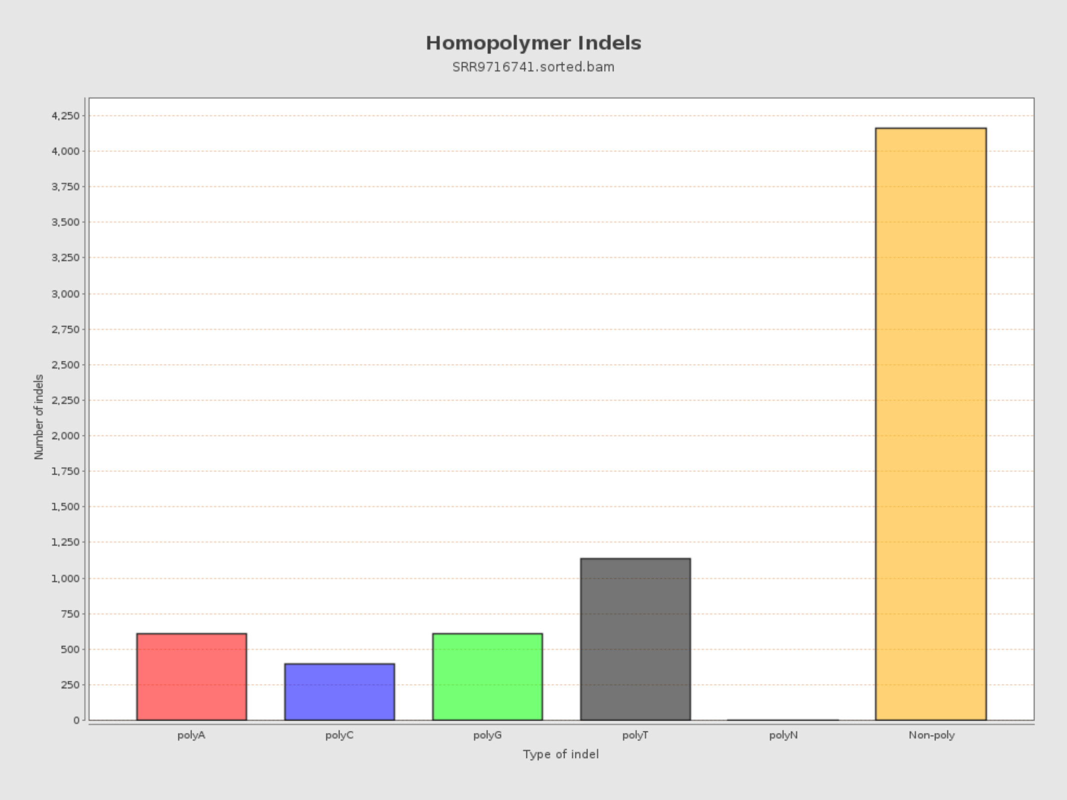
9. Results : Mapped Reads GC-content Distribution



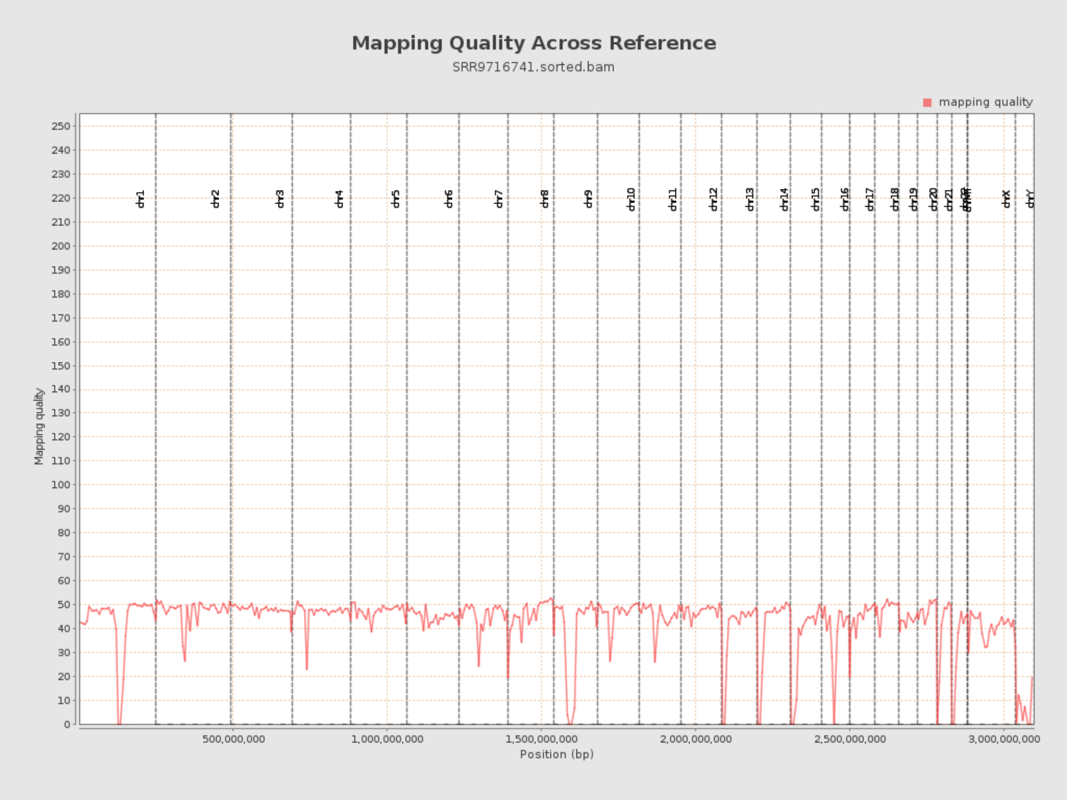
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram