Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:11:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716754.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_SRR9716754 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716754.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:11:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716754.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,228,001
Mapped reads	1,585,167 / 71.15%
Unmapped reads	642,834 / 28.85%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,523 / 0.2%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	44,056 / 1.98%
Duplication rate	2.08%
Clipped reads	1,586,431 / 71.2%

2.2. ACGT Content

Number/percentage of A's	20,254,220 / 23.68%
Number/percentage of C's	17,454,381 / 20.41%
Number/percentage of T's	24,922,832 / 29.14%
Number/percentage of G's	22,893,279 / 26.77%
Number/percentage of N's	2,394 / 0%
GC Percentage	47.18%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.2206

2.4. Mapping Quality

Mean Mapping Quality	38.99

2.5. Mismatches and indels

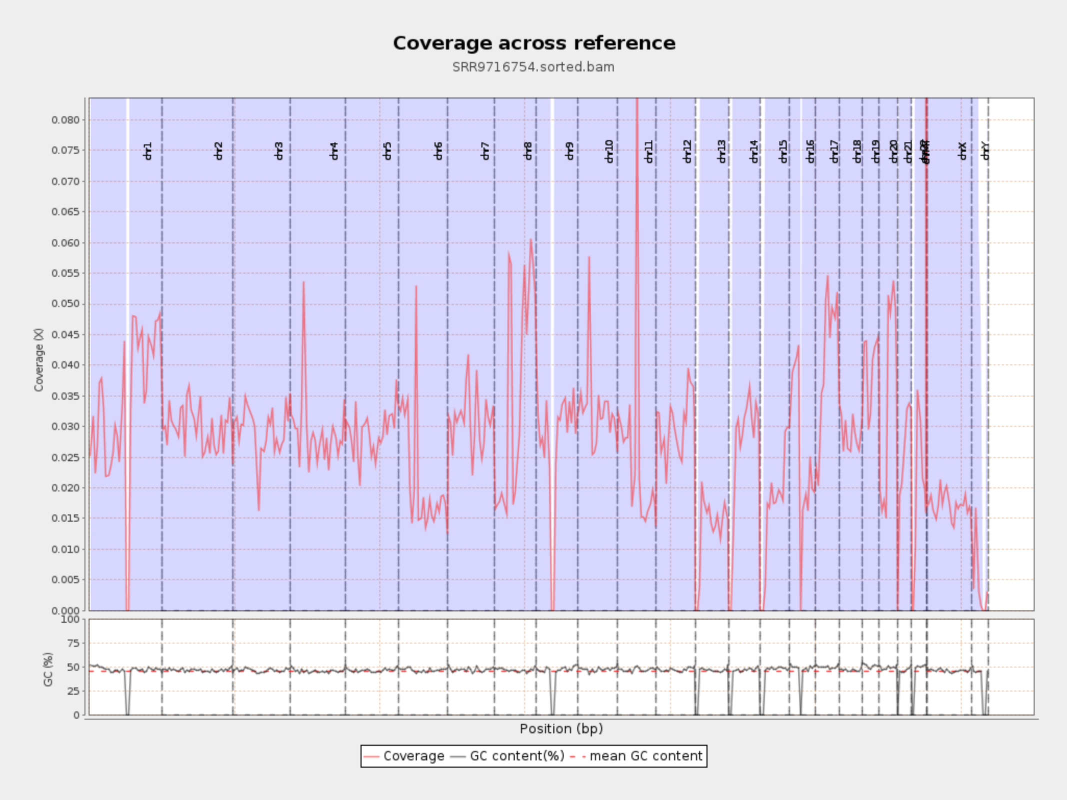
General error rate	0.54%
Mismatches	445,415
Insertions	6,239
Mapped reads with at least one insertion	0.39%
Deletions	13,428
Mapped reads with at least one deletion	0.84%
Homopolymer indels	36.03%

2.6. Chromosome stats

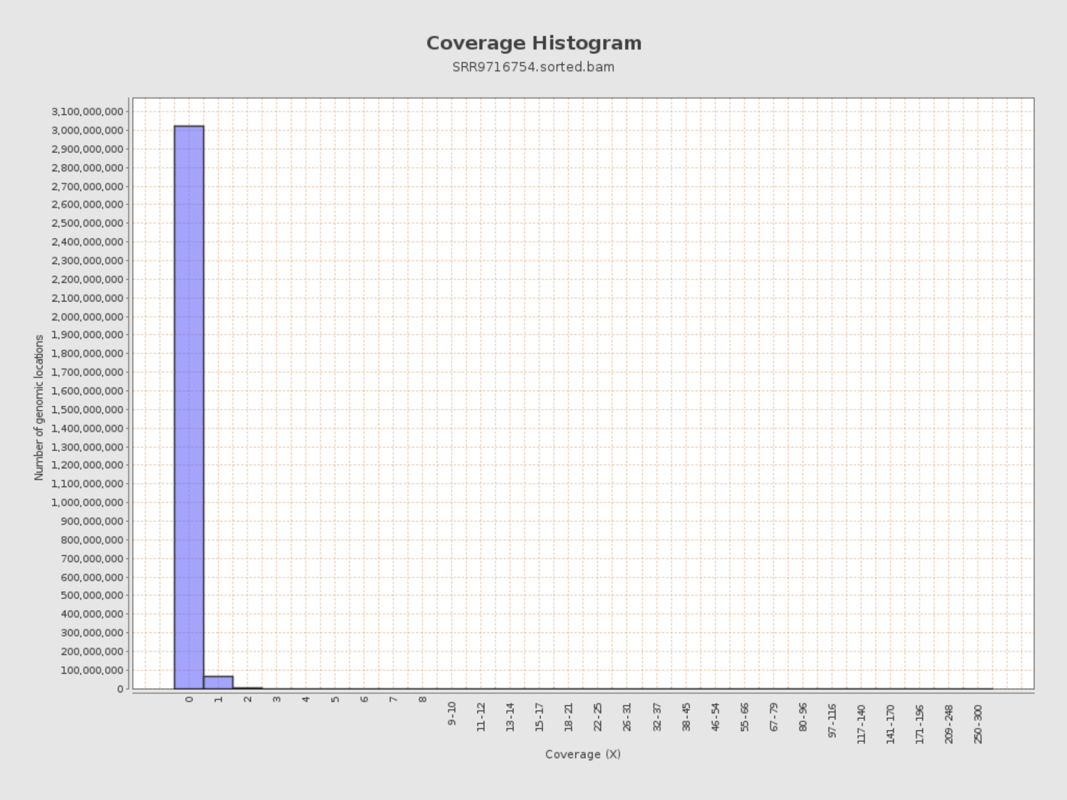
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8357305	0.0335	0.2892
chr2	243199373	7308139	0.03	0.2599
chr3	198022430	5758211	0.0291	0.1951
chr4	191154276	5537407	0.029	0.2199
chr5	180915260	5245266	0.029	0.1908
chr6	171115067	3730545	0.0218	0.1701
chr7	159138663	4954475	0.0311	0.2567

chr8	146364022	5223284	0.0357	0.2272
chr9	141213431	3805504	0.0269	0.2007
chr10	135534747	4460375	0.0329	0.311
chr11	135006516	3553377	0.0263	0.2241
chr12	133851895	4052694	0.0303	0.1953
chr13	115169878	1518285	0.0132	0.1308
chr14	107349540	2764230	0.0257	0.1831
chr15	102531392	1712636	0.0167	0.1517
chr16	90354753	2328174	0.0258	0.1959
chr17	81195210	3378235	0.0416	0.2403
chr18	78077248	2243002	0.0287	0.2387
chr19	59128983	2322388	0.0393	0.2717
chr20	63025520	2189202	0.0347	0.2153
chr21	48129895	1176514	0.0244	0.1957
chr22	51304566	950081	0.0185	0.1545
chrMT	16571	42759	2.5804	2.4988
chrX	155270560	2678232	0.0172	0.1614
chrY	59373566	258873	0.0044	0.1309

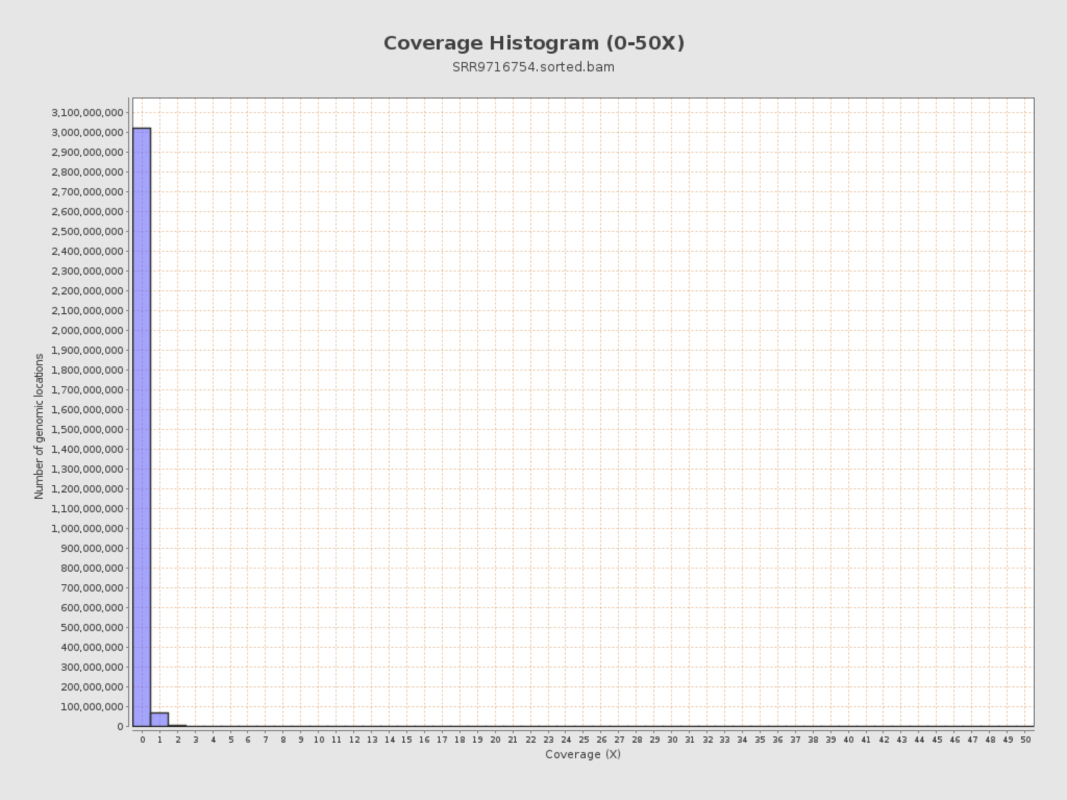
3. Results : Coverage across reference



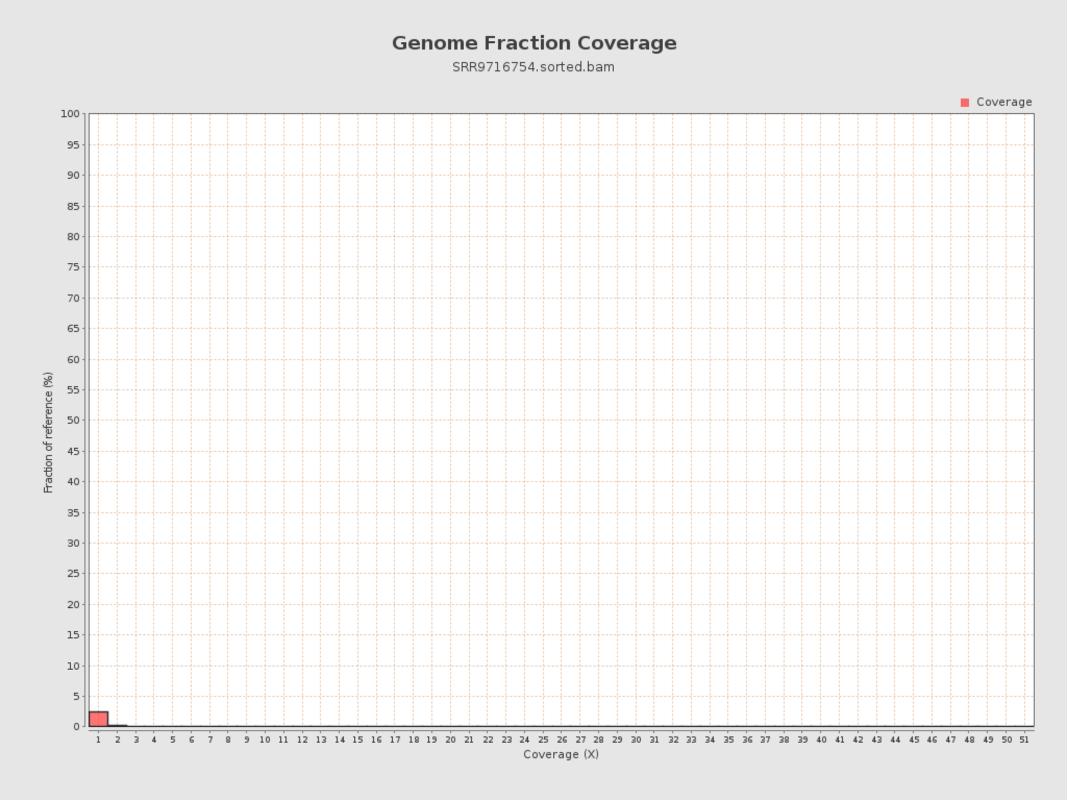
4. Results : Coverage Histogram



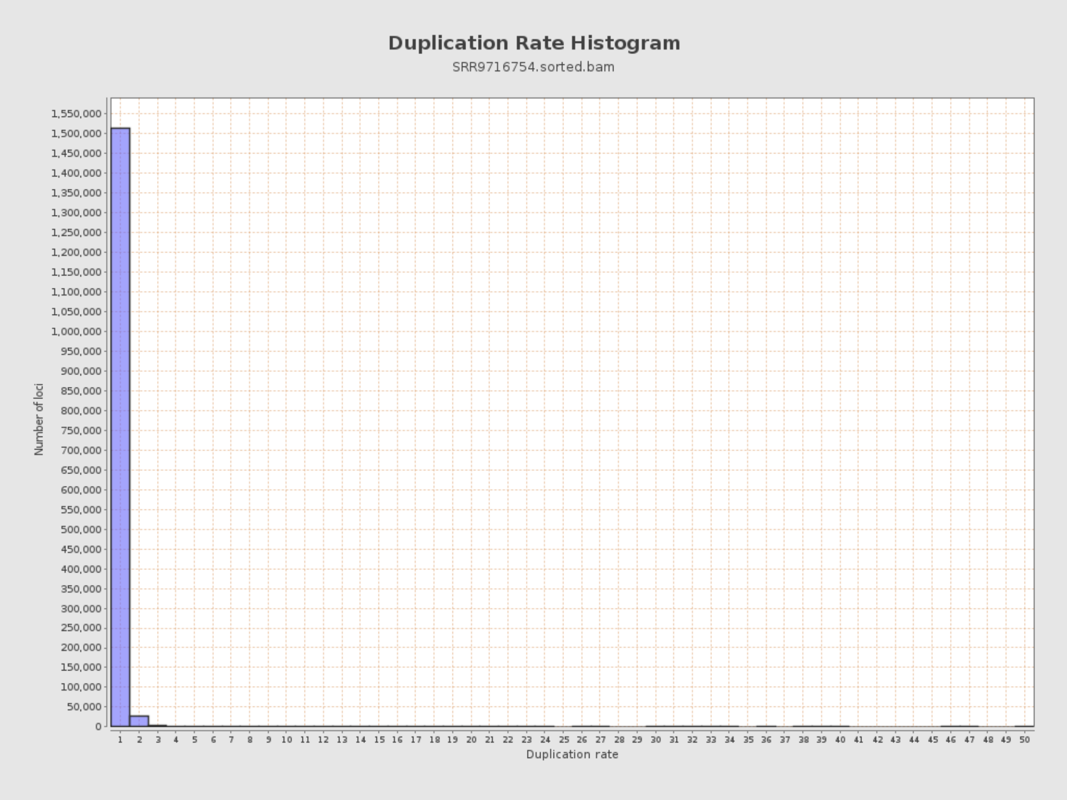
5. Results : Coverage Histogram (0-50X)



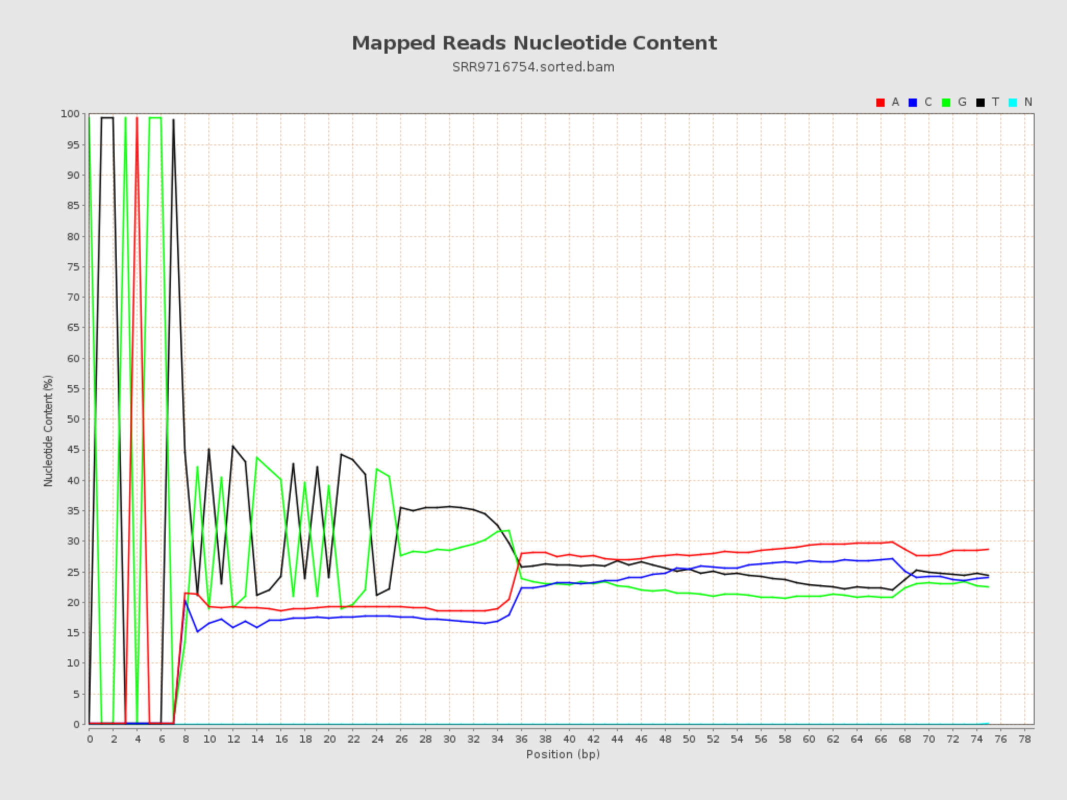
6. Results : Genome Fraction Coverage



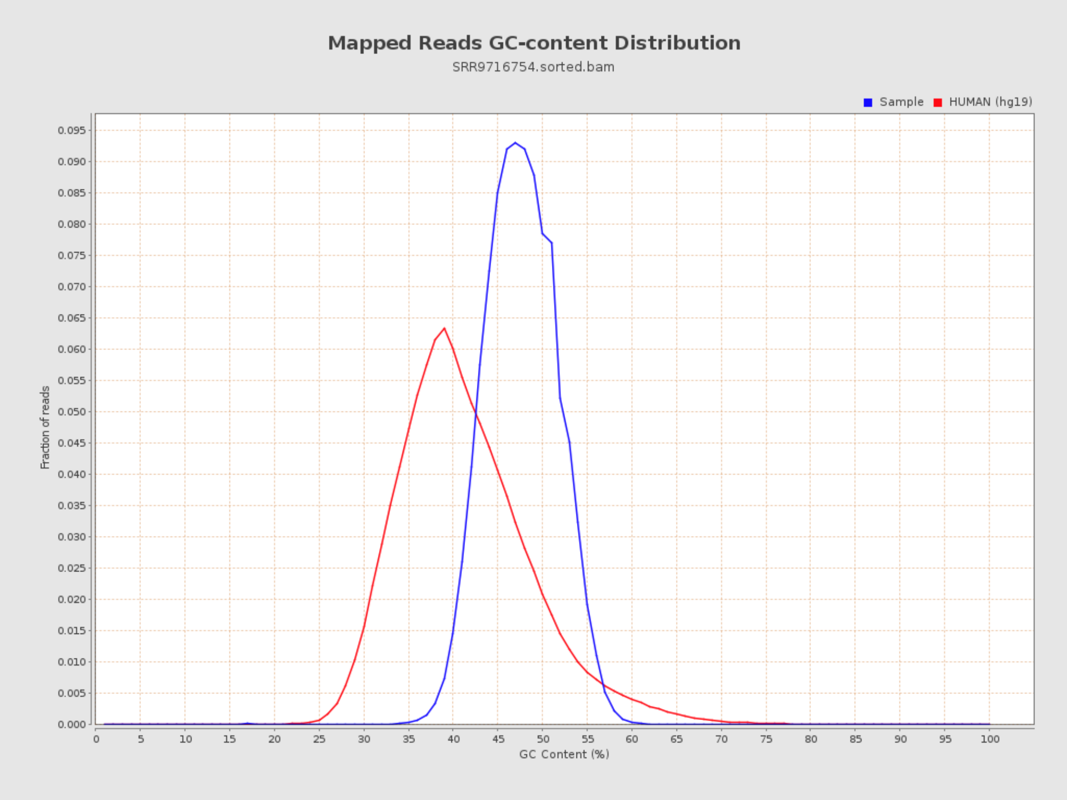
7. Results : Duplication Rate Histogram



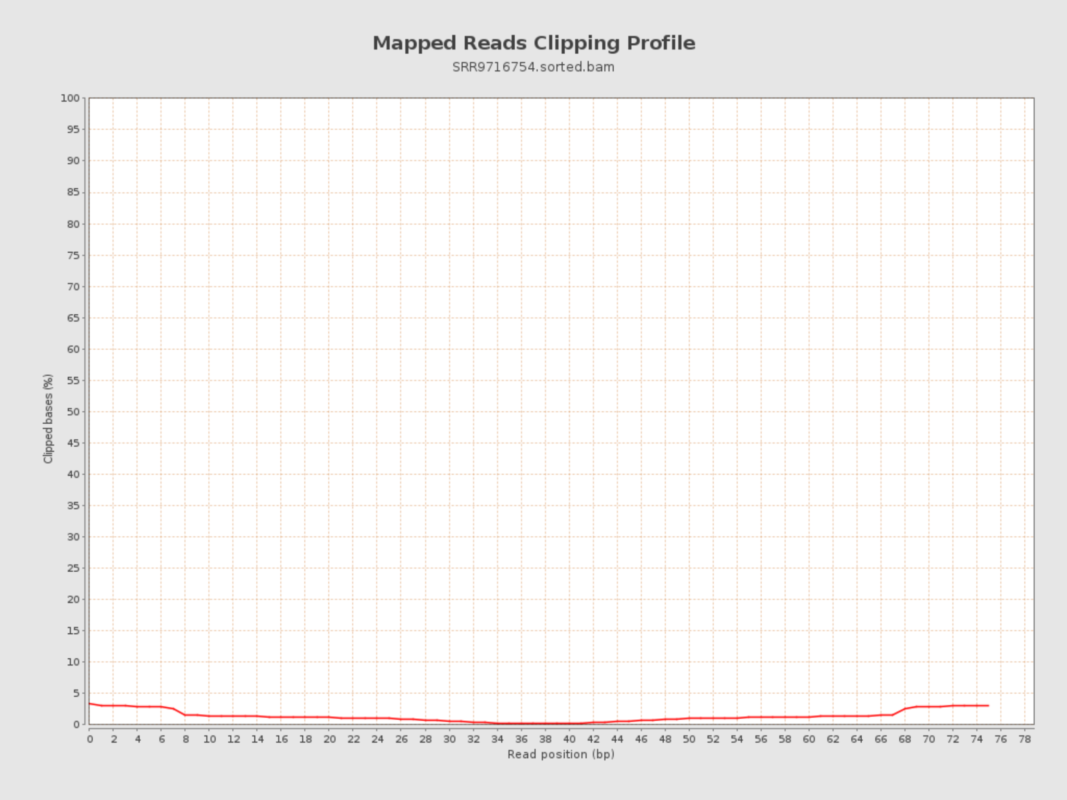
8. Results : Mapped Reads Nucleotide Content



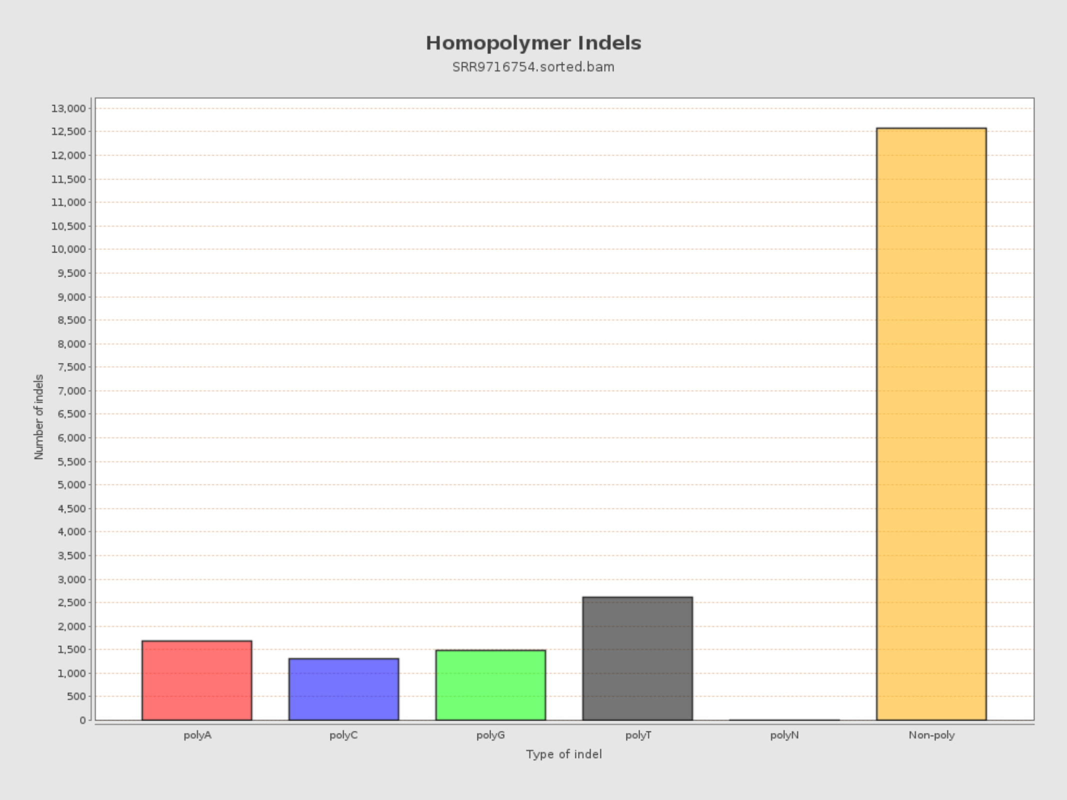
9. Results : Mapped Reads GC-content Distribution



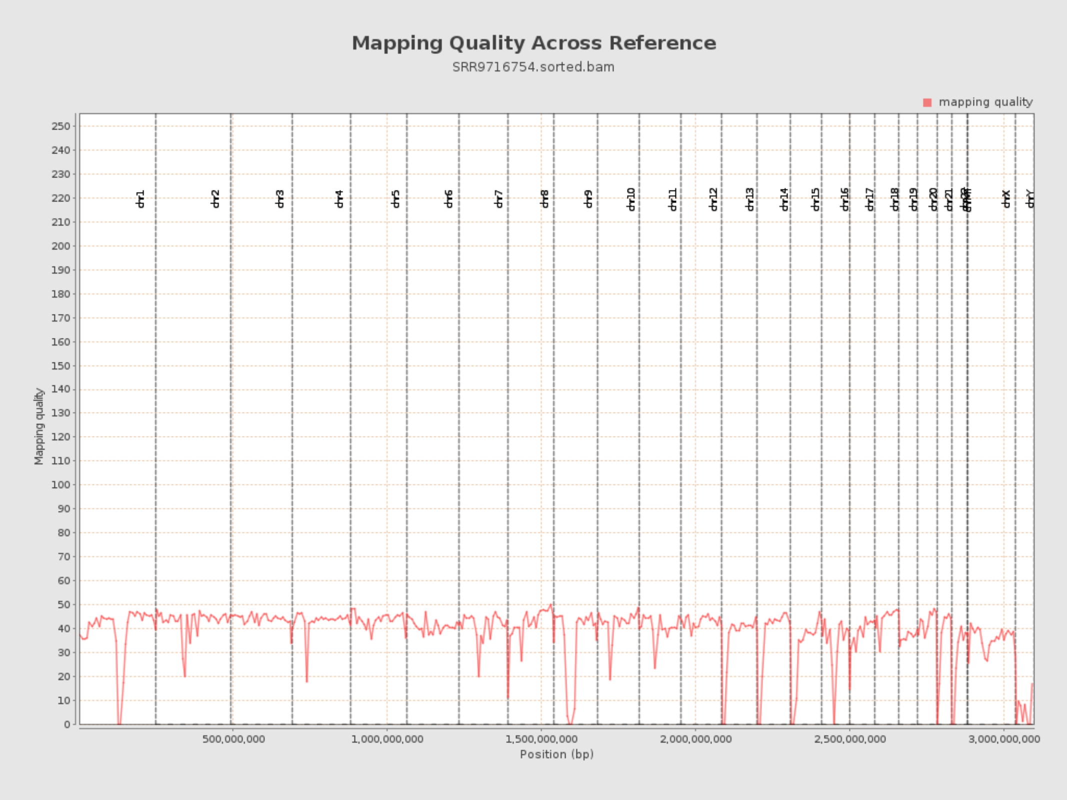
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram