Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:06:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716752.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_SRR9716752 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716752.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:06:01 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716752.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,665,886
Mapped reads	1,517,148 / 91.07%
Unmapped reads	148,738 / 8.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,620 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	50,672 / 3.04%
Duplication rate	2.66%
Clipped reads	1,520,598 / 91.28%

2.2. ACGT Content

Number/percentage of A's	22,537,872 / 25.63%
Number/percentage of C's	16,843,532 / 19.16%
Number/percentage of T's	27,768,885 / 31.58%
Number/percentage of G's	20,776,704 / 23.63%
Number/percentage of N's	2,062 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0284

Standard Deviation	0.2319

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

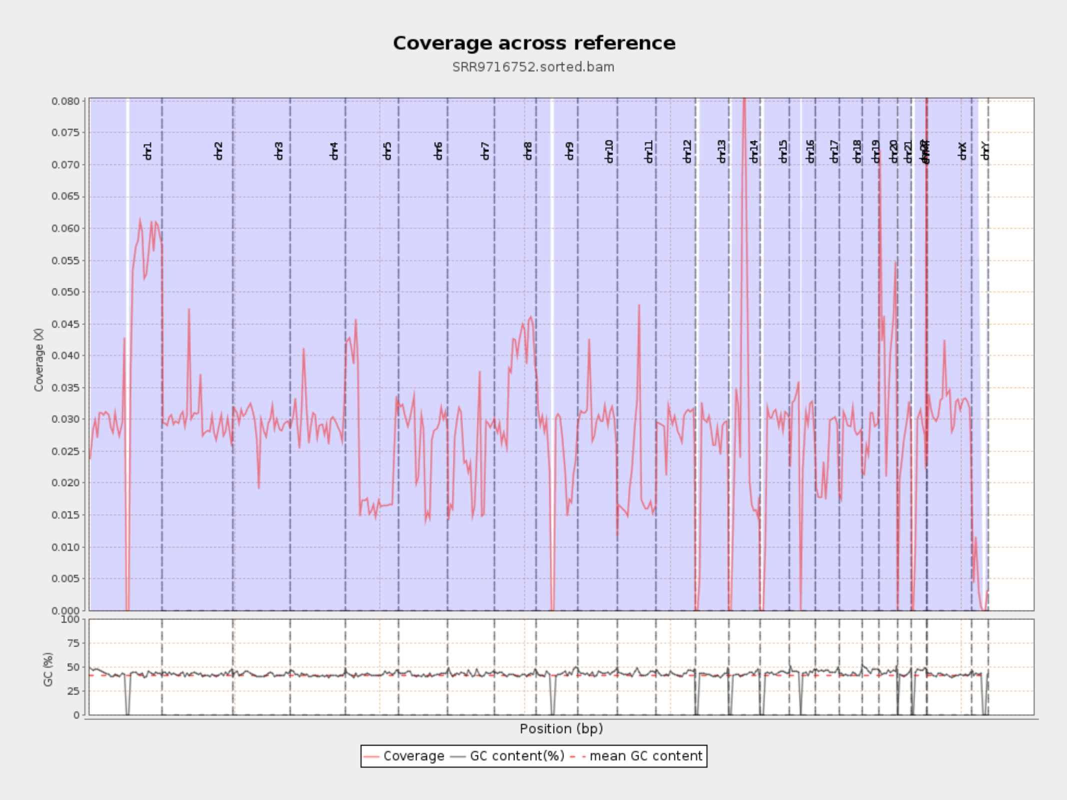
General error rate	0.49%
Mismatches	416,649
Insertions	5,592
Mapped reads with at least one insertion	0.37%
Deletions	12,997
Mapped reads with at least one deletion	0.85%
Homopolymer indels	40.66%

2.6. Chromosome stats

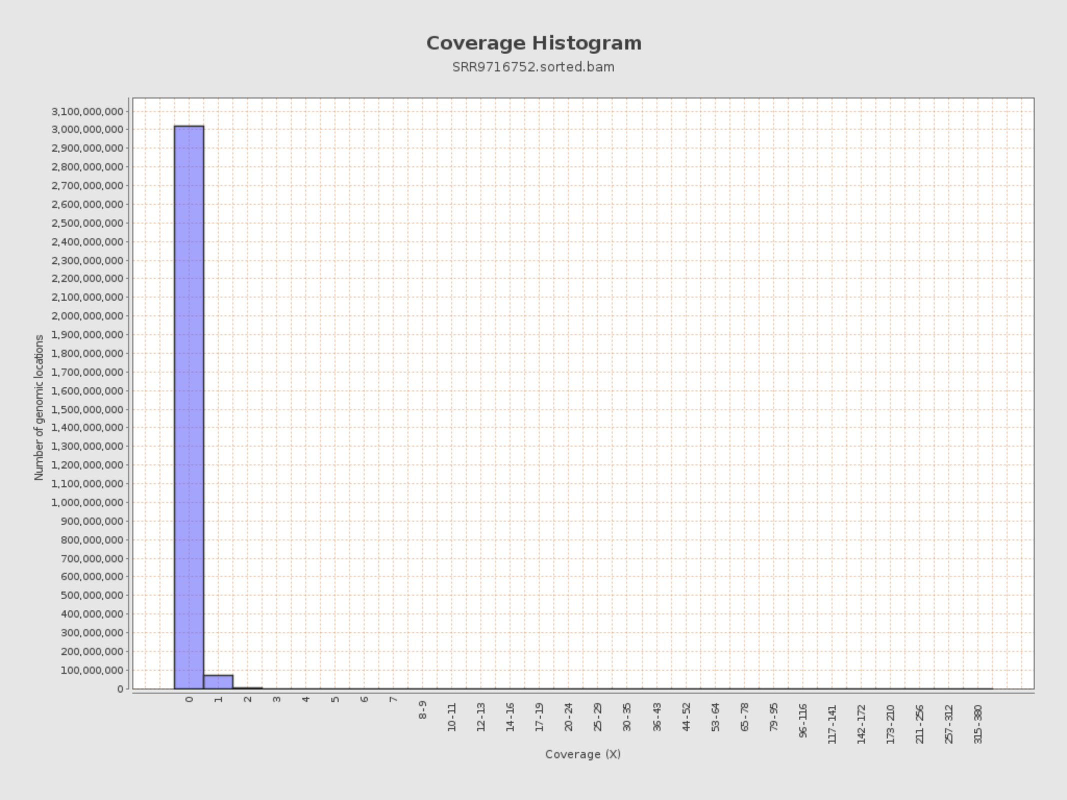
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9900494	0.0397	0.3684
chr2	243199373	7326506	0.0301	0.2587
chr3	198022430	5845943	0.0295	0.1879
chr4	191154276	5681385	0.0297	0.2013
chr5	180915260	4392299	0.0243	0.1725
chr6	171115067	4679464	0.0273	0.1947
chr7	159138663	3806697	0.0239	0.2075

chr8	146364022	5487920	0.0375	0.2488
chr9	141213431	3207881	0.0227	0.2243
chr10	135534747	4170264	0.0308	0.2295
chr11	135006516	2717895	0.0201	0.2077
chr12	133851895	3920454	0.0293	0.1897
chr13	115169878	2755975	0.0239	0.1681
chr14	107349540	3141382	0.0293	0.1993
chr15	102531392	2525549	0.0246	0.1719
chr16	90354753	2530559	0.028	0.193
chr17	81195210	1928106	0.0237	0.1737
chr18	78077248	2160353	0.0277	0.4249
chr19	59128983	1619027	0.0274	0.2646
chr20	63025520	2712925	0.043	0.2318
chr21	48129895	1174857	0.0244	0.1846
chr22	51304566	1033794	0.0202	0.1548
chrMT	16571	2509	0.1514	0.4109
chrX	155270560	4996165	0.0322	0.2193
chrY	59373566	232598	0.0039	0.0898

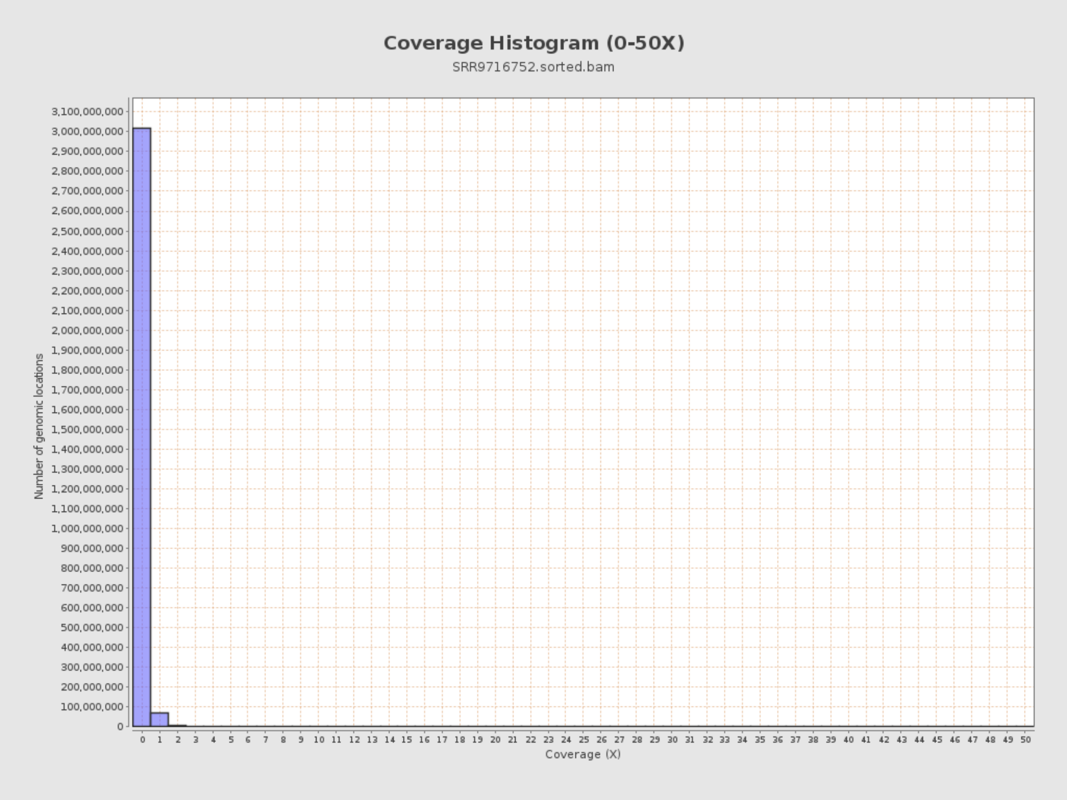
3. Results : Coverage across reference



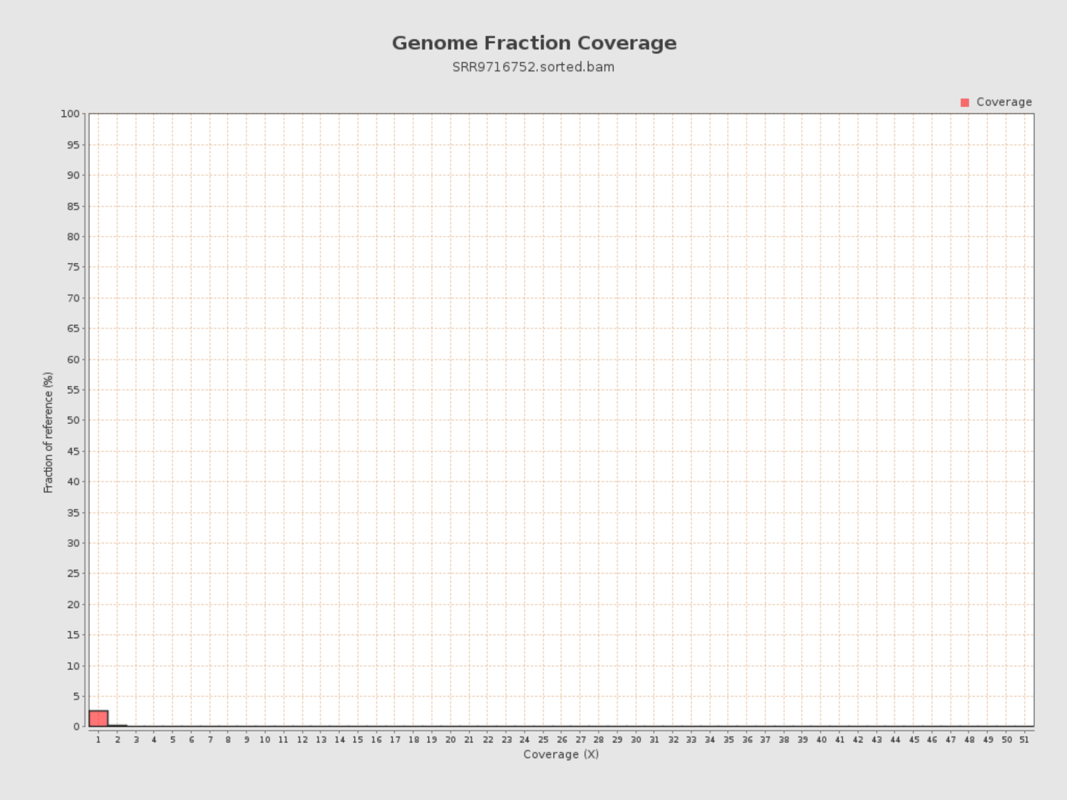
4. Results : Coverage Histogram



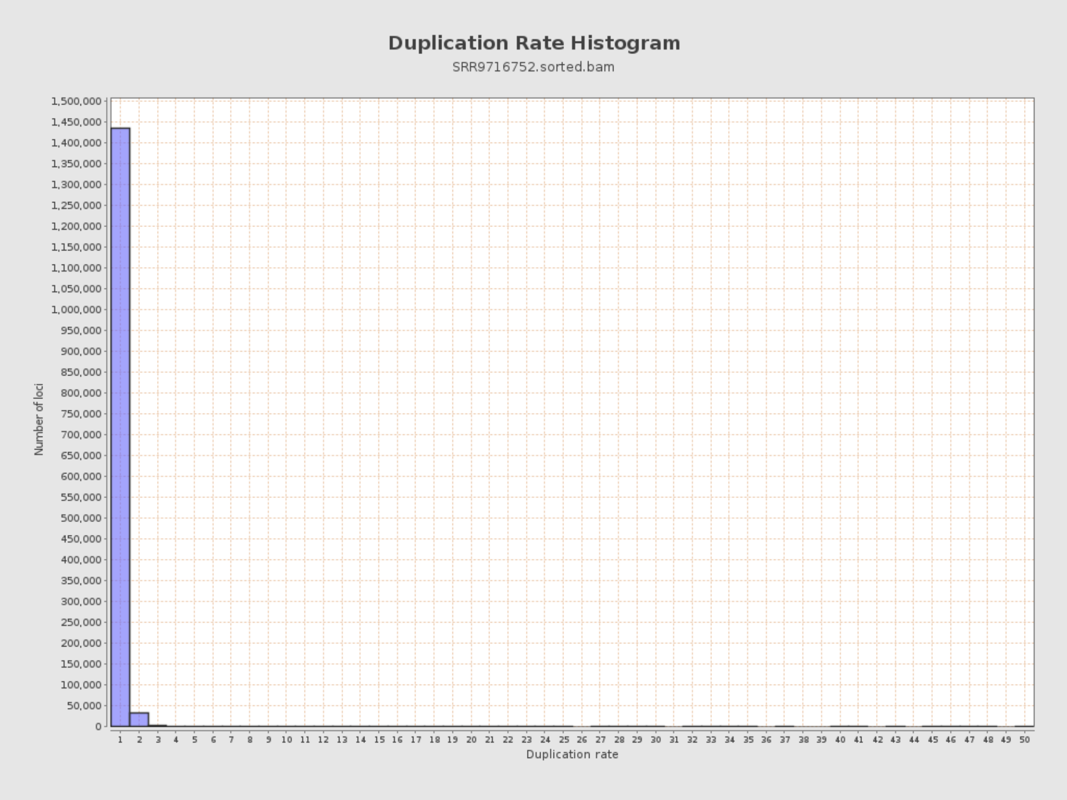
5. Results : Coverage Histogram (0-50X)



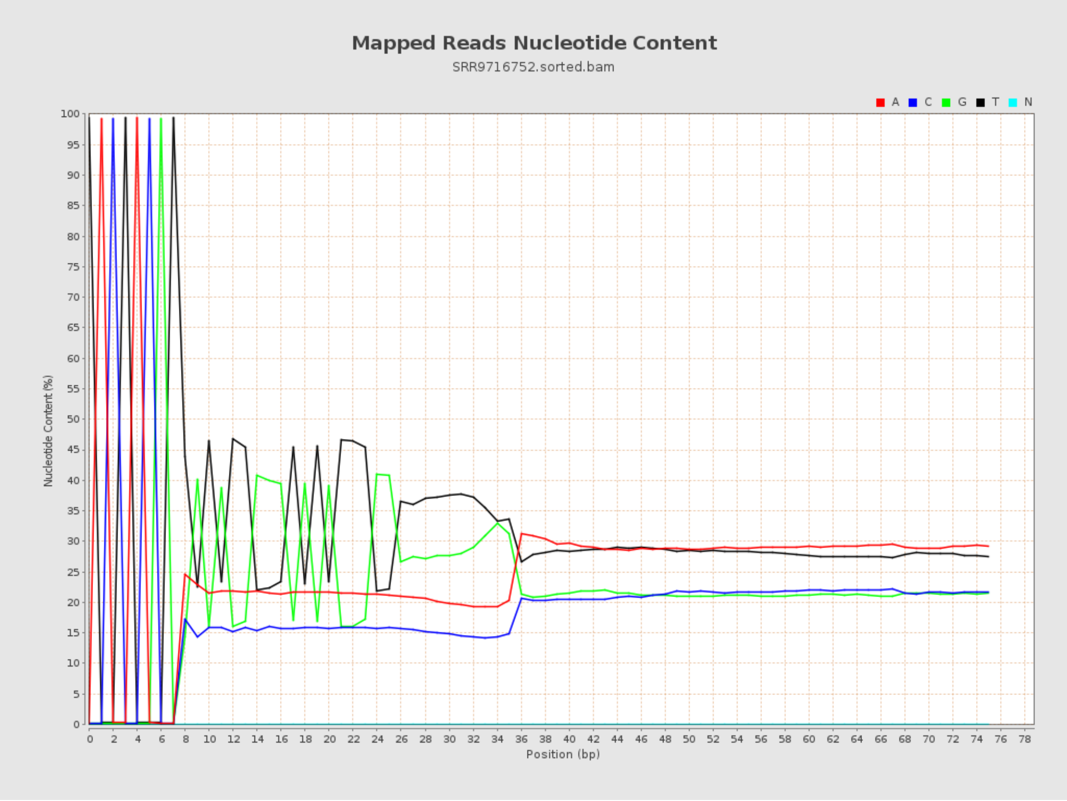
6. Results : Genome Fraction Coverage



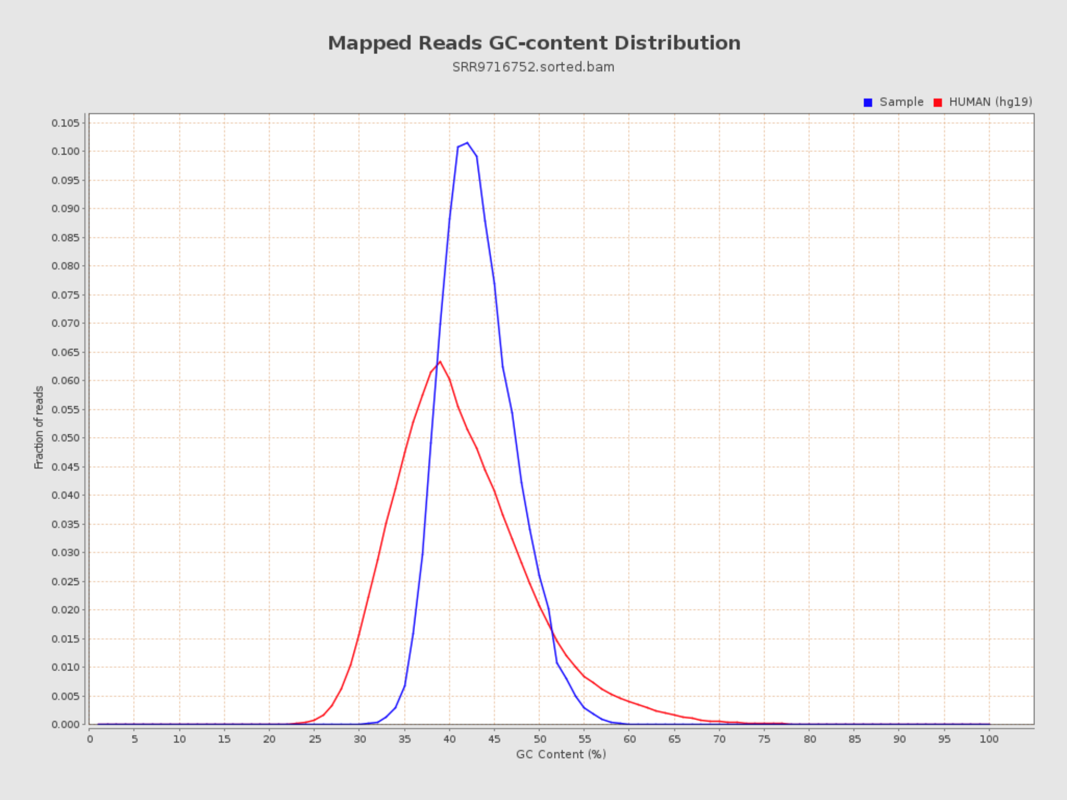
7. Results : Duplication Rate Histogram



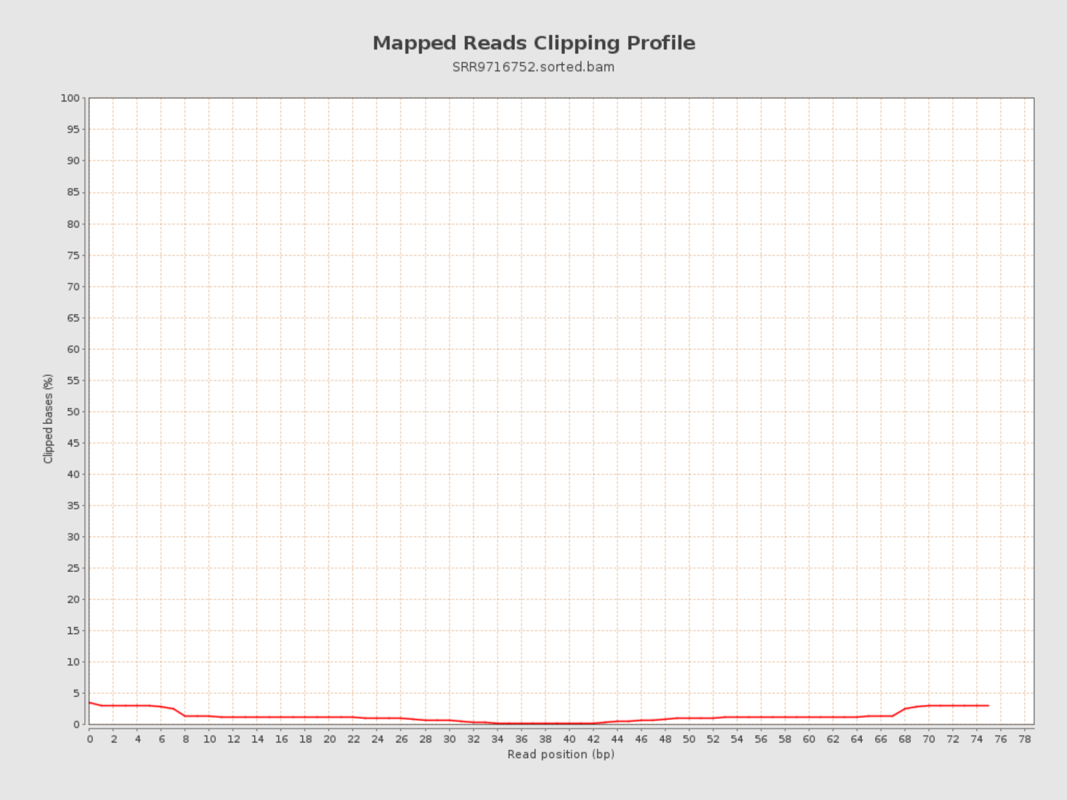
8. Results : Mapped Reads Nucleotide Content



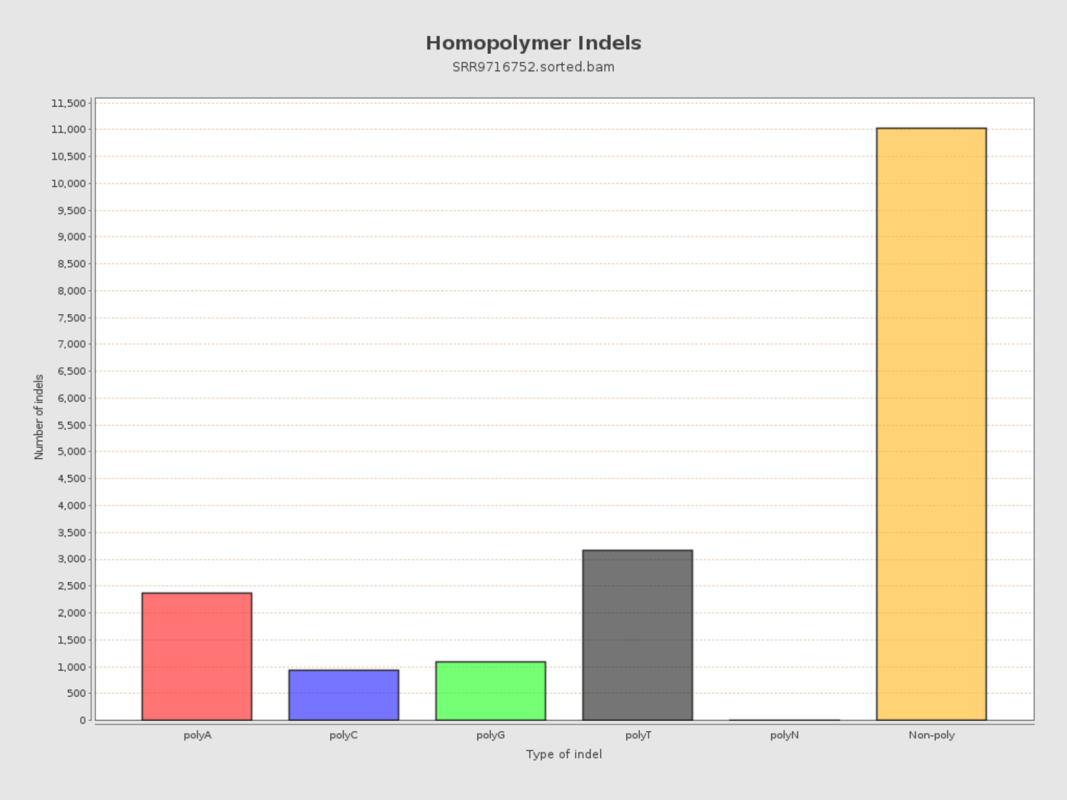
9. Results : Mapped Reads GC-content Distribution



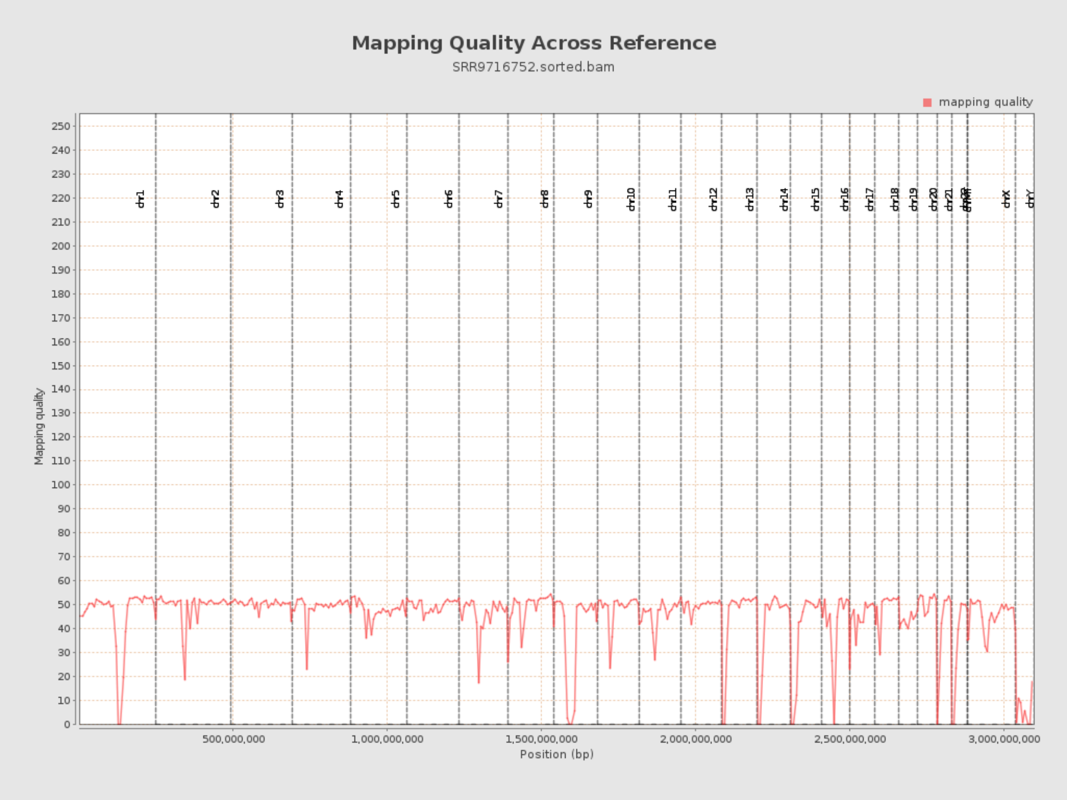
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram