Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 10:32:19

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716763.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_SRR9716763 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716763.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 10:32:19 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716763.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,150,474
Mapped reads	982,661 / 85.41%
Unmapped reads	167,813 / 14.59%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,660 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	18,481 / 1.61%
Duplication rate	1.37%
Clipped reads	983,171 / 85.46%

2.2. ACGT Content

Number/percentage of A's	13,288,938 / 24.12%
Number/percentage of C's	12,030,764 / 21.83%
Number/percentage of T's	16,023,760 / 29.08%
Number/percentage of G's	13,755,056 / 24.96%
Number/percentage of N's	1,648 / 0%
GC Percentage	46.8%

2.3. Coverage

Mean	0.0178

Standard Deviation	0.1627

2.4. Mapping Quality

Mean Mapping Quality	40.09

2.5. Mismatches and indels

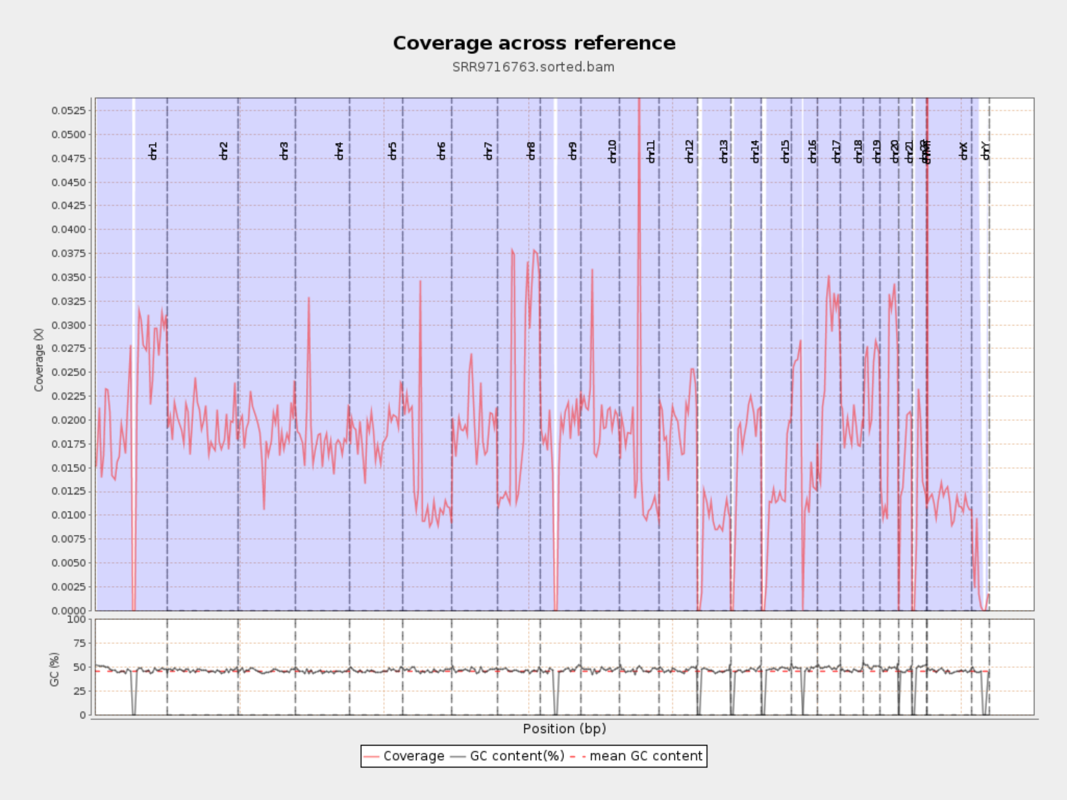
General error rate	0.53%
Mismatches	286,098
Insertions	4,011
Mapped reads with at least one insertion	0.41%
Deletions	8,859
Mapped reads with at least one deletion	0.89%
Homopolymer indels	36.56%

2.6. Chromosome stats

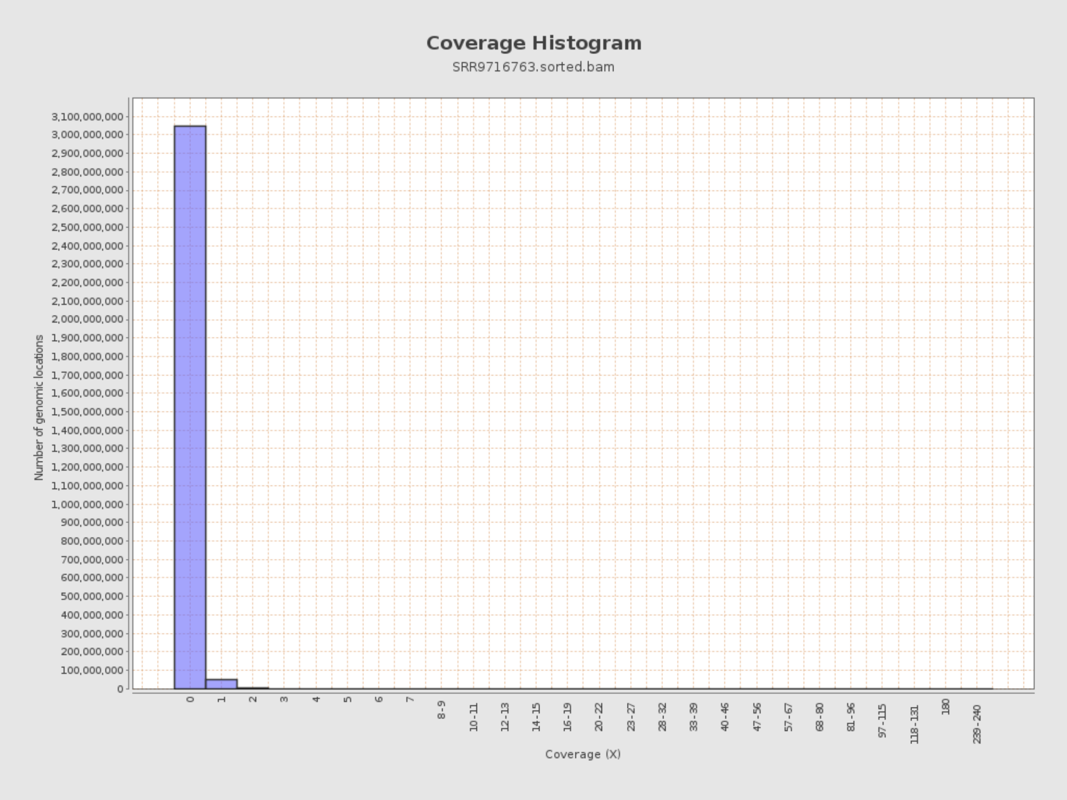
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5389384	0.0216	0.1916
chr2	243199373	4755681	0.0196	0.1981
chr3	198022430	3730340	0.0188	0.1521
chr4	191154276	3515981	0.0184	0.1586
chr5	180915260	3406038	0.0188	0.148
chr6	171115067	2383718	0.0139	0.1303
chr7	159138663	3129870	0.0197	0.1865

chr8	146364022	3417077	0.0233	0.1735
chr9	141213431	2397368	0.017	0.1511
chr10	135534747	2846717	0.021	0.2207
chr11	135006516	2288927	0.017	0.1628
chr12	133851895	2690284	0.0201	0.1534
chr13	115169878	972395	0.0084	0.0999
chr14	107349540	1768416	0.0165	0.1435
chr15	102531392	1107309	0.0108	0.1128
chr16	90354753	1501476	0.0166	0.1483
chr17	81195210	2182744	0.0269	0.1836
chr18	78077248	1491984	0.0191	0.1821
chr19	59128983	1455687	0.0246	0.1926
chr20	63025520	1393800	0.0221	0.1661
chr21	48129895	741972	0.0154	0.145
chr22	51304566	608970	0.0119	0.119
chrMT	16571	25405	1.5331	1.7895
chrX	155270560	1757818	0.0113	0.1209
chrY	59373566	155124	0.0026	0.082

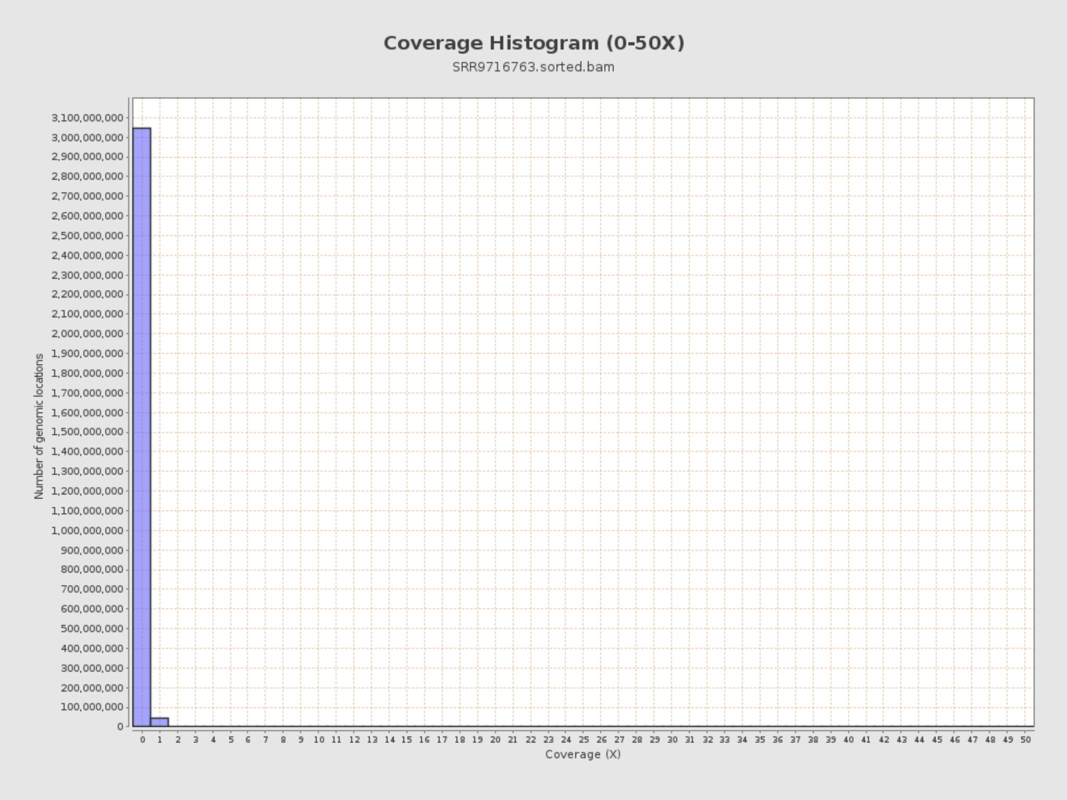
3. Results : Coverage across reference



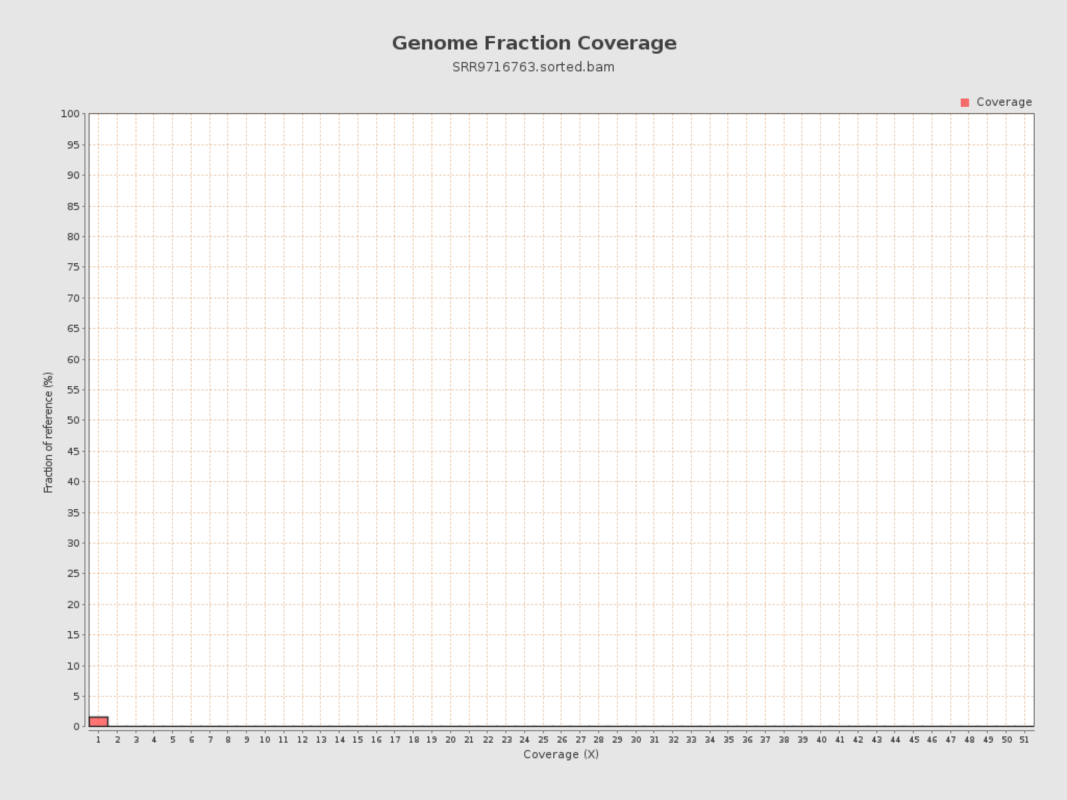
4. Results : Coverage Histogram



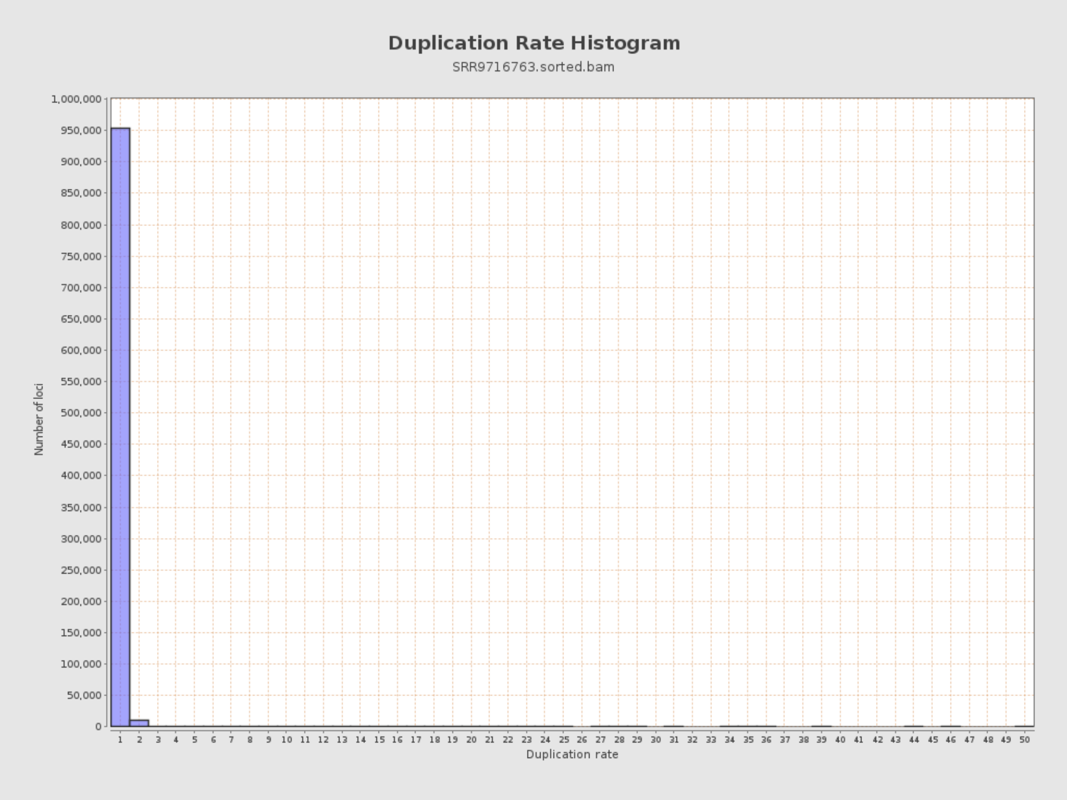
5. Results : Coverage Histogram (0-50X)



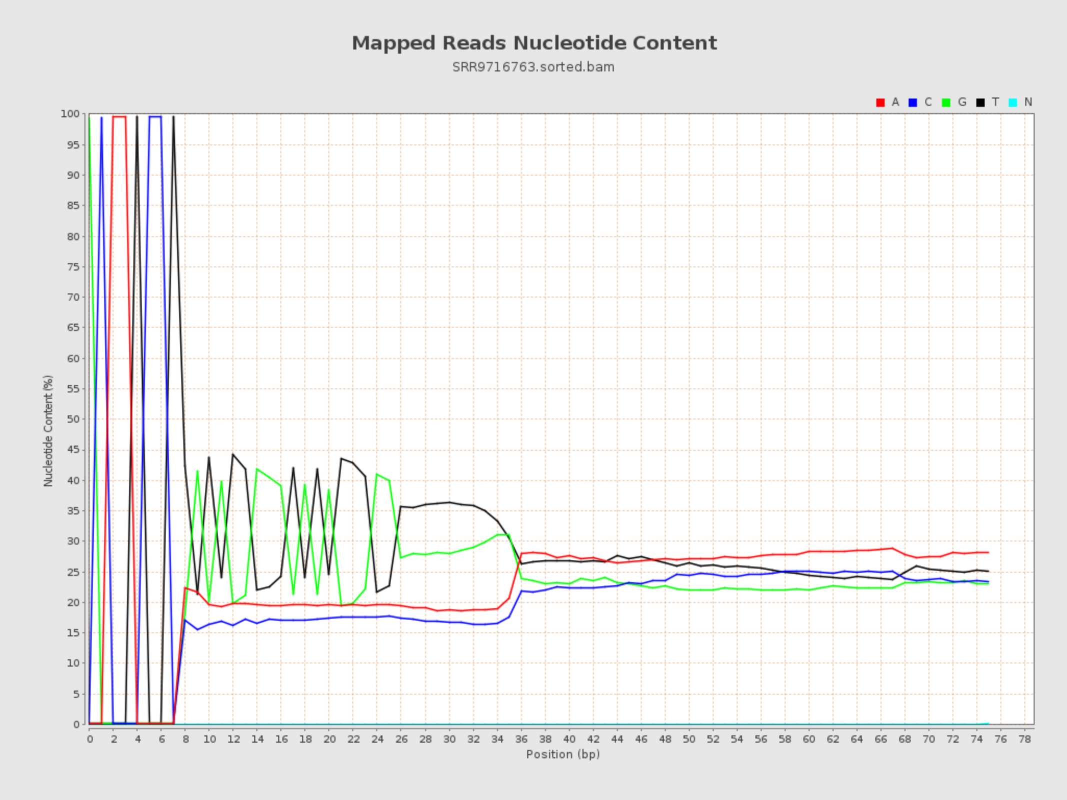
6. Results : Genome Fraction Coverage



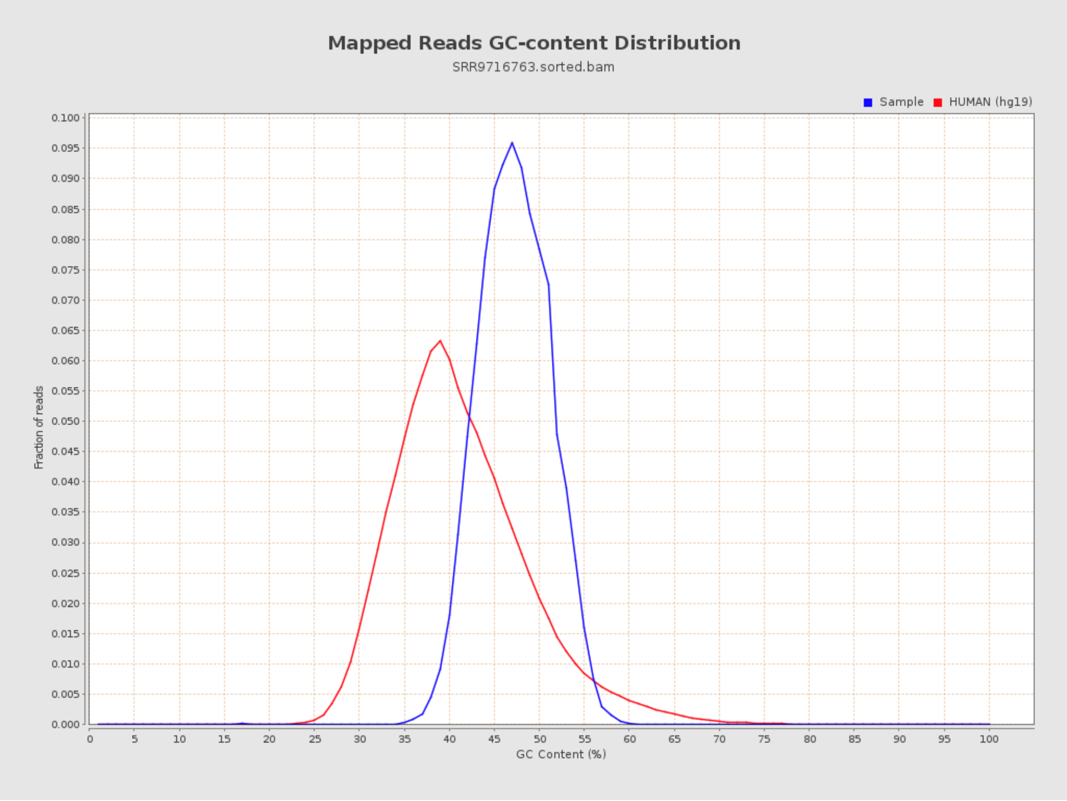
7. Results : Duplication Rate Histogram



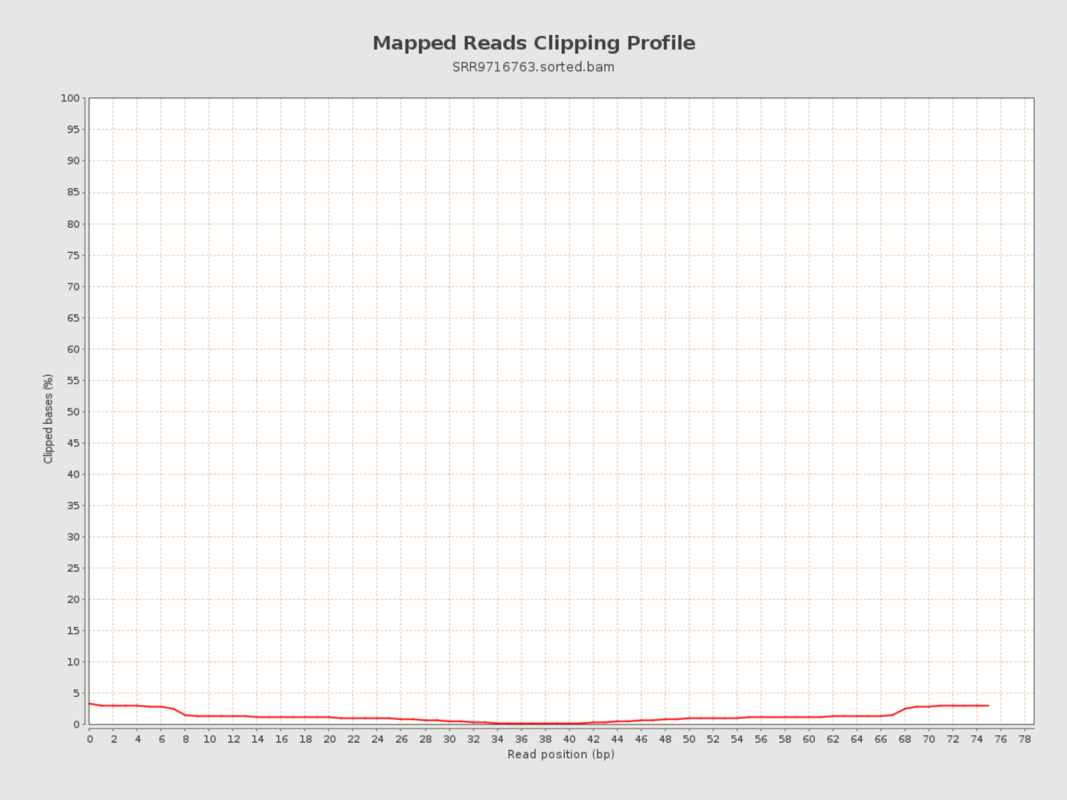
8. Results : Mapped Reads Nucleotide Content



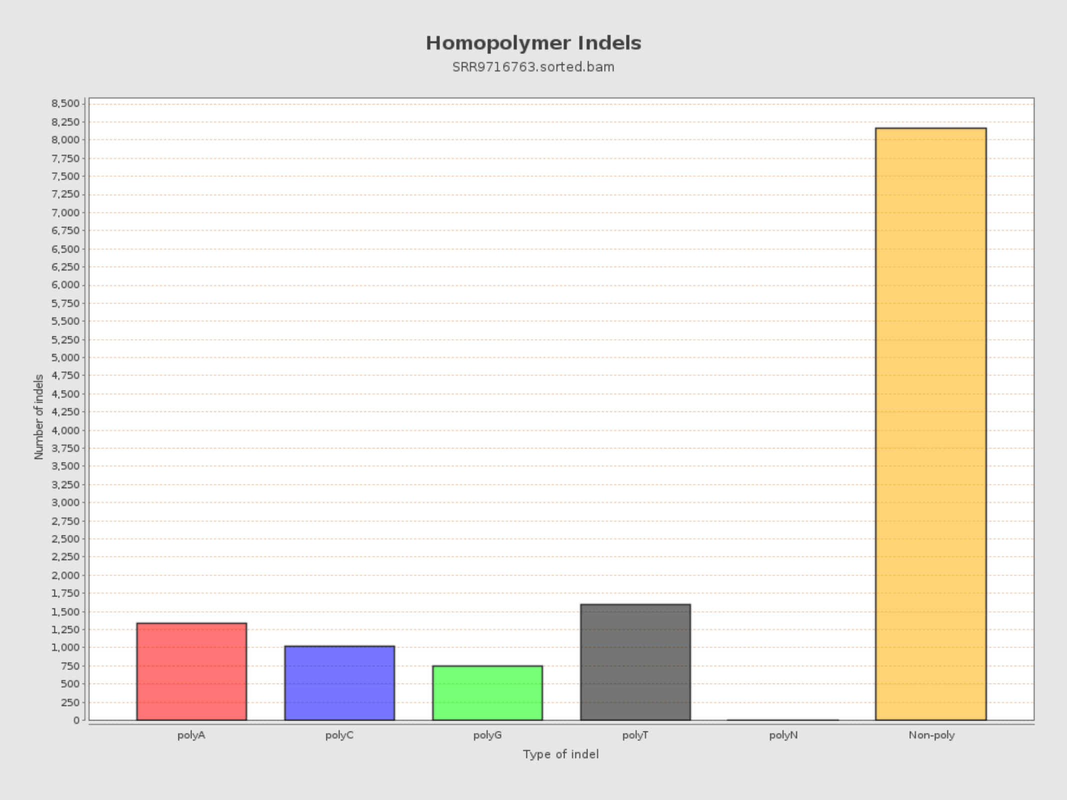
9. Results : Mapped Reads GC-content Distribution



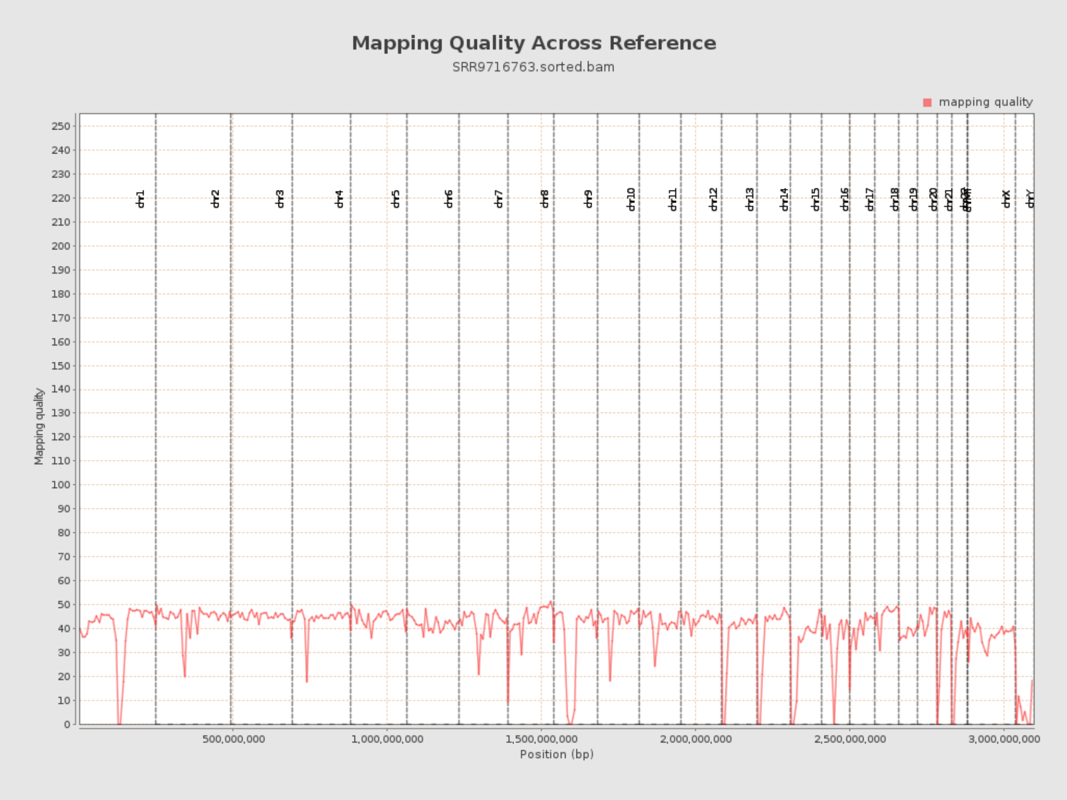
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram