Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 01:33:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716228.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_SRR9716228 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716228.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 01:33:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716228.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,703,674
Mapped reads	1,535,019 / 90.1%
Unmapped reads	168,655 / 9.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,371 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	57,071 / 3.35%
Duplication rate	2.8%
Clipped reads	1,539,076 / 90.34%

2.2. ACGT Content

Number/percentage of A's	22,355,825 / 25.58%
Number/percentage of C's	16,835,734 / 19.26%
Number/percentage of T's	27,461,012 / 31.42%
Number/percentage of G's	20,756,858 / 23.75%
Number/percentage of N's	1,304 / 0%
GC Percentage	43.01%

2.3. Coverage

Mean	0.0282

Standard Deviation	0.2611

2.4. Mapping Quality

Mean Mapping Quality	45.09

2.5. Mismatches and indels

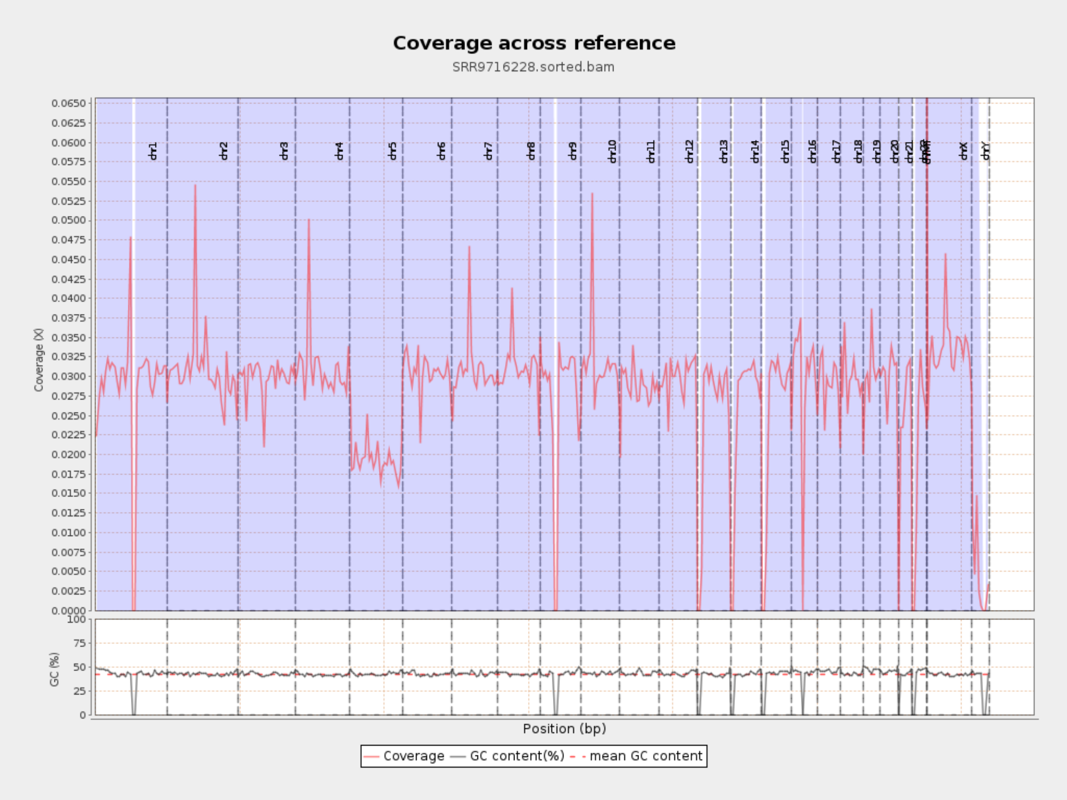
General error rate	0.56%
Mismatches	484,876
Insertions	4,848
Mapped reads with at least one insertion	0.31%
Deletions	14,941
Mapped reads with at least one deletion	0.97%
Homopolymer indels	44.43%

2.6. Chromosome stats

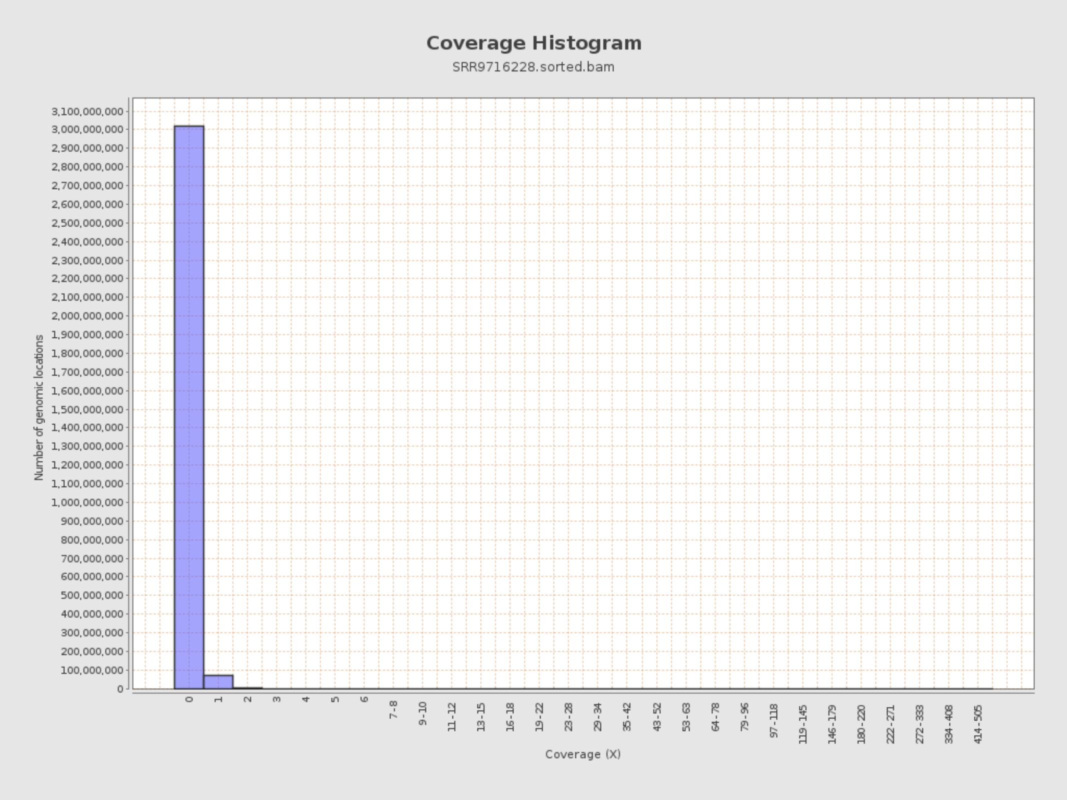
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7158009	0.0287	0.4278
chr2	243199373	7527337	0.031	0.2924
chr3	198022430	5910610	0.0298	0.1874
chr4	191154276	5936678	0.0311	0.2102
chr5	180915260	3475084	0.0192	0.1527
chr6	171115067	5219378	0.0305	0.2086
chr7	159138663	4917055	0.0309	0.3173

chr8	146364022	4553446	0.0311	0.2725
chr9	141213431	3776933	0.0267	0.271
chr10	135534747	4311854	0.0318	0.2679
chr11	135006516	3907608	0.0289	0.2525
chr12	133851895	4009046	0.03	0.1954
chr13	115169878	2782592	0.0242	0.1677
chr14	107349540	2712455	0.0253	0.1877
chr15	102531392	2528709	0.0247	0.171
chr16	90354753	2623231	0.029	0.2008
chr17	81195210	2368599	0.0292	0.2032
chr18	78077248	2339670	0.03	0.4789
chr19	59128983	1802996	0.0305	0.3457
chr20	63025520	1884740	0.0299	0.1943
chr21	48129895	1188145	0.0247	0.1944
chr22	51304566	1023377	0.0199	0.1524
chrMT	16571	1376	0.083	0.295
chrX	155270560	5219070	0.0336	0.2351
chrY	59373566	257489	0.0043	0.1142

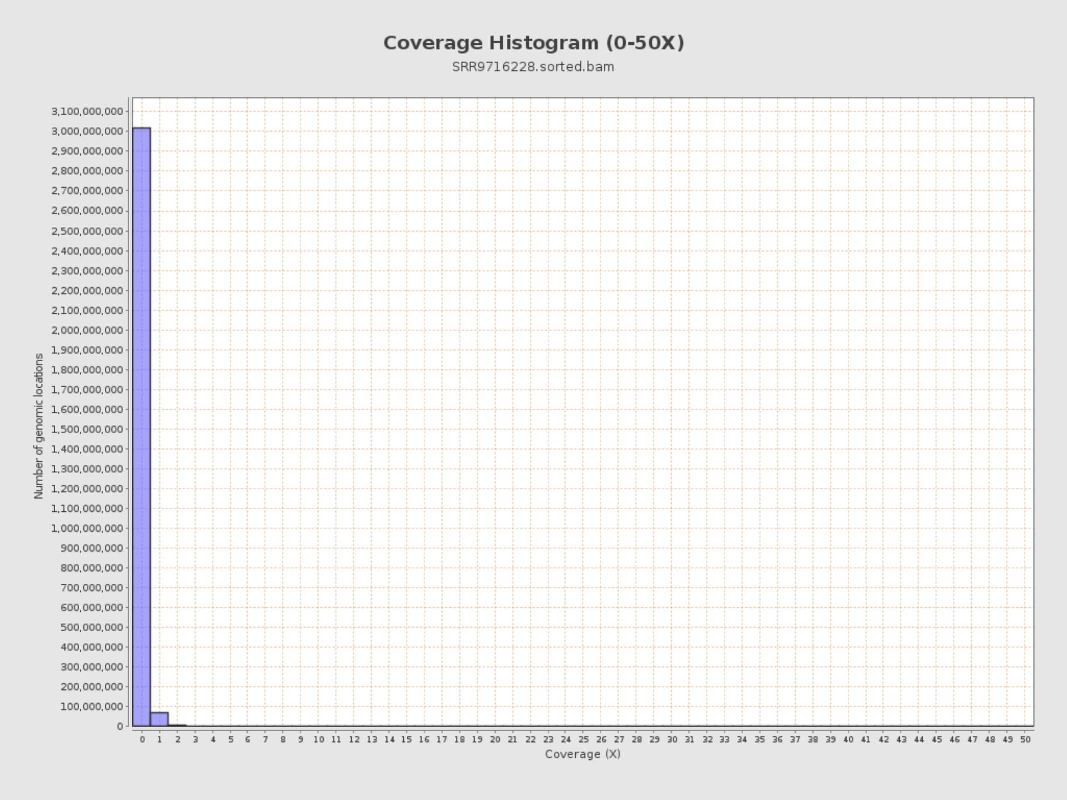
3. Results : Coverage across reference



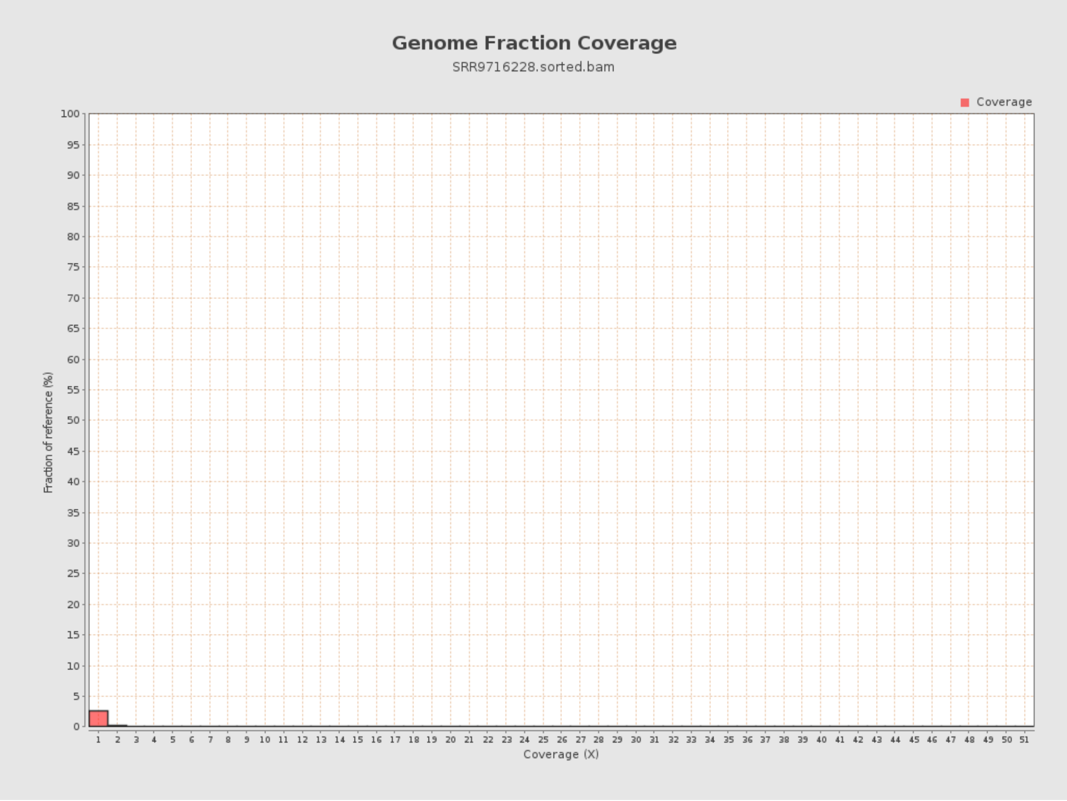
4. Results : Coverage Histogram



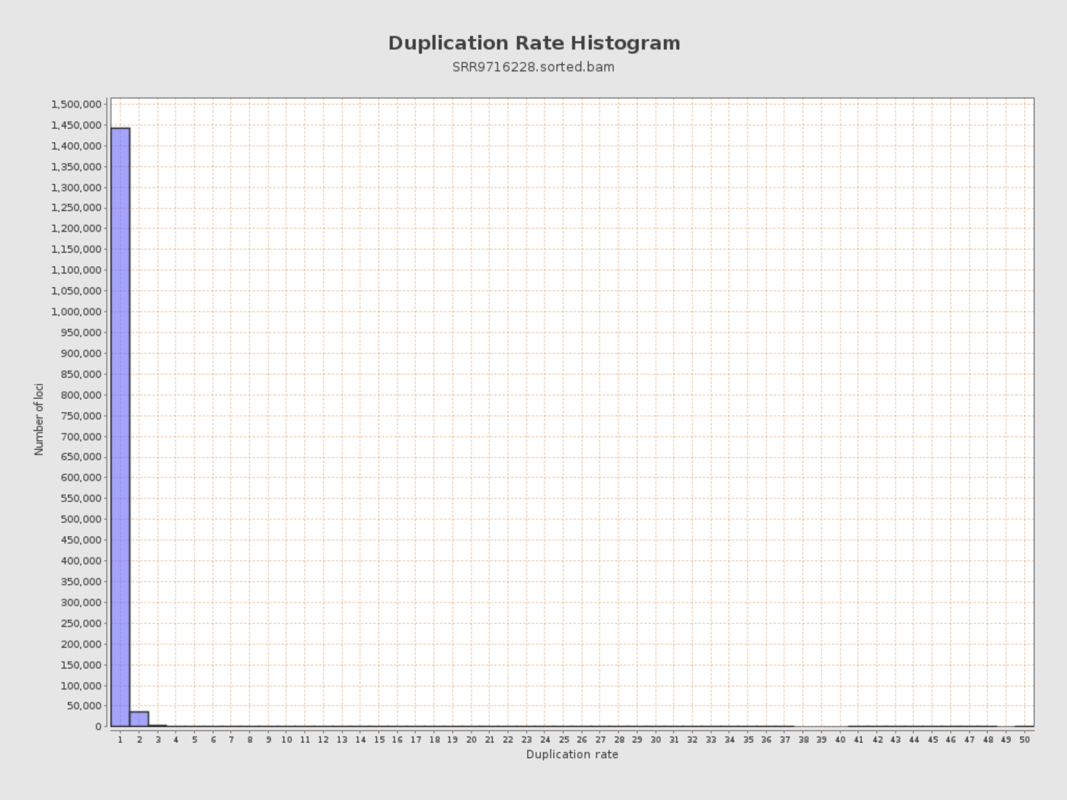
5. Results : Coverage Histogram (0-50X)



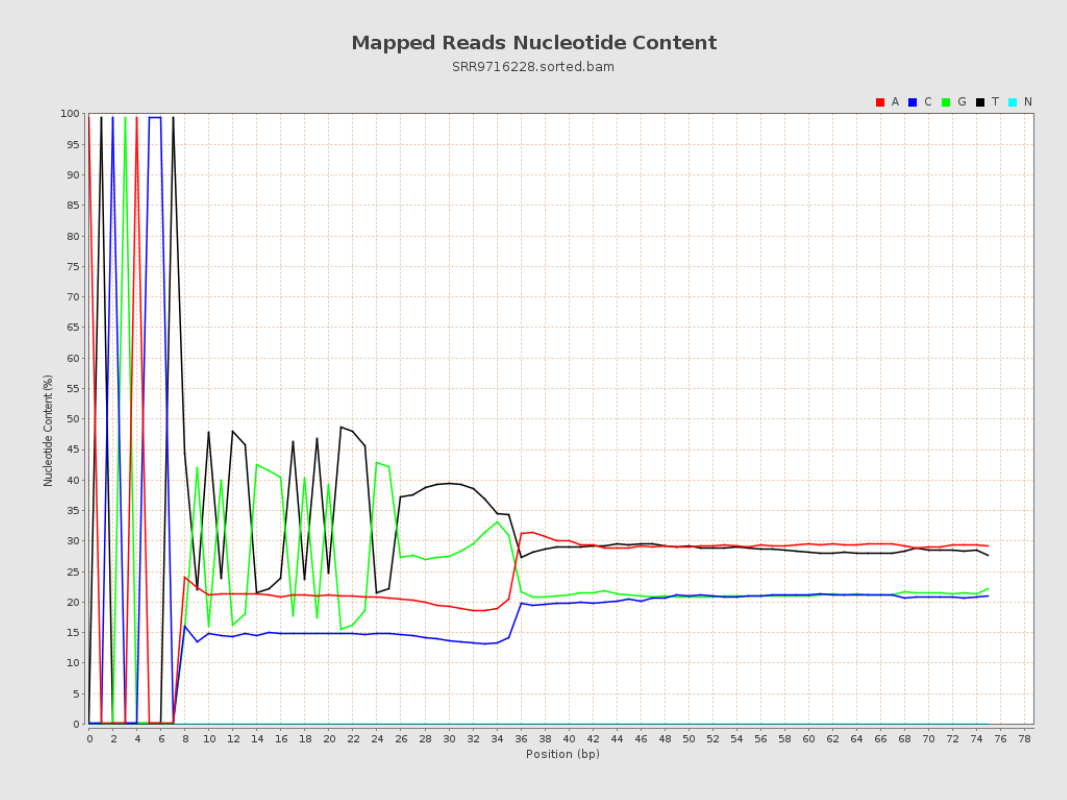
6. Results : Genome Fraction Coverage



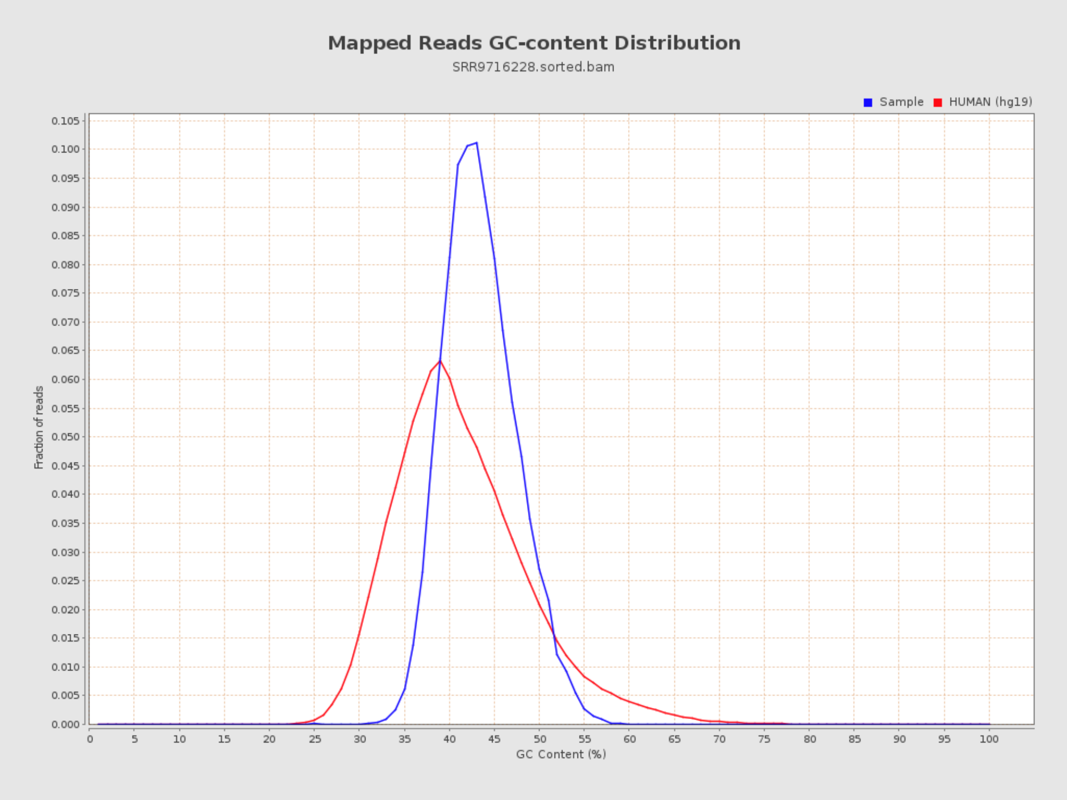
7. Results : Duplication Rate Histogram



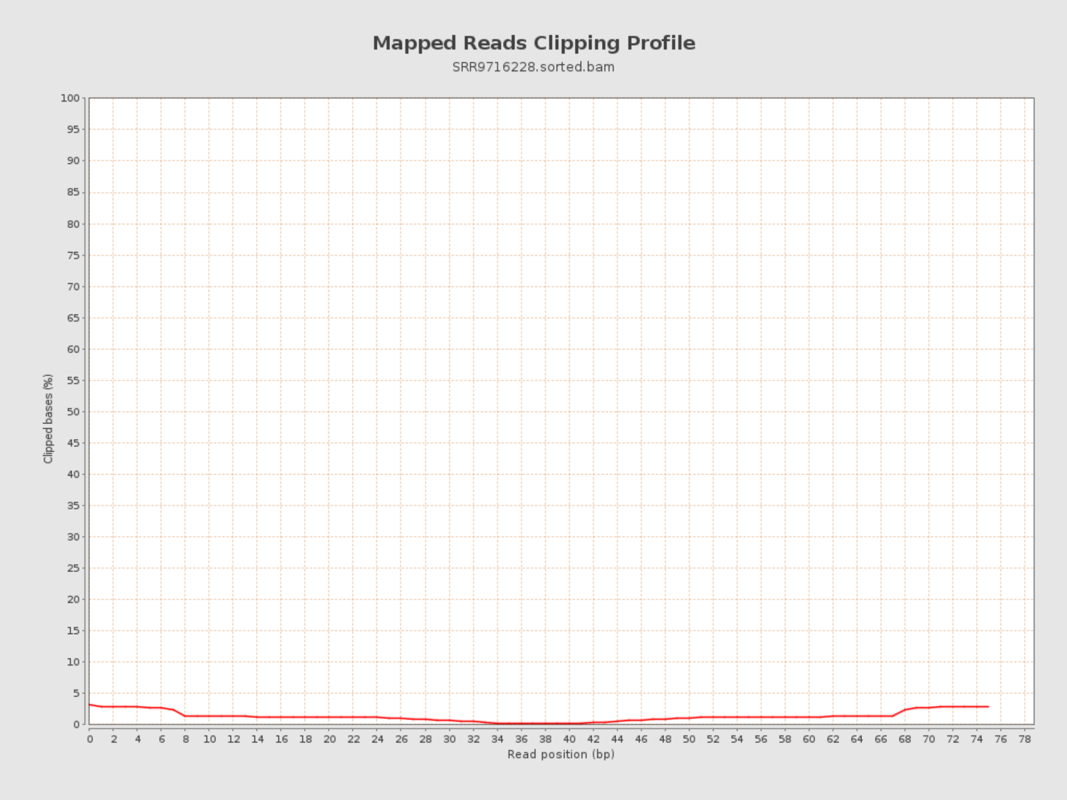
8. Results : Mapped Reads Nucleotide Content



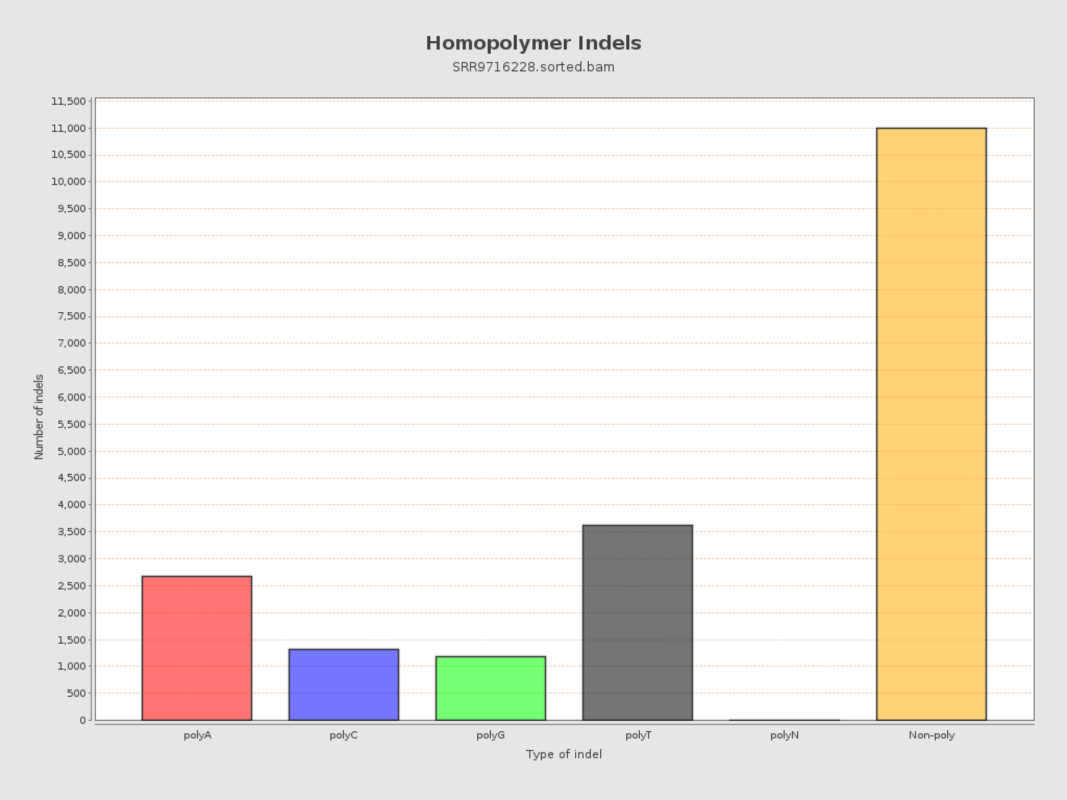
9. Results : Mapped Reads GC-content Distribution



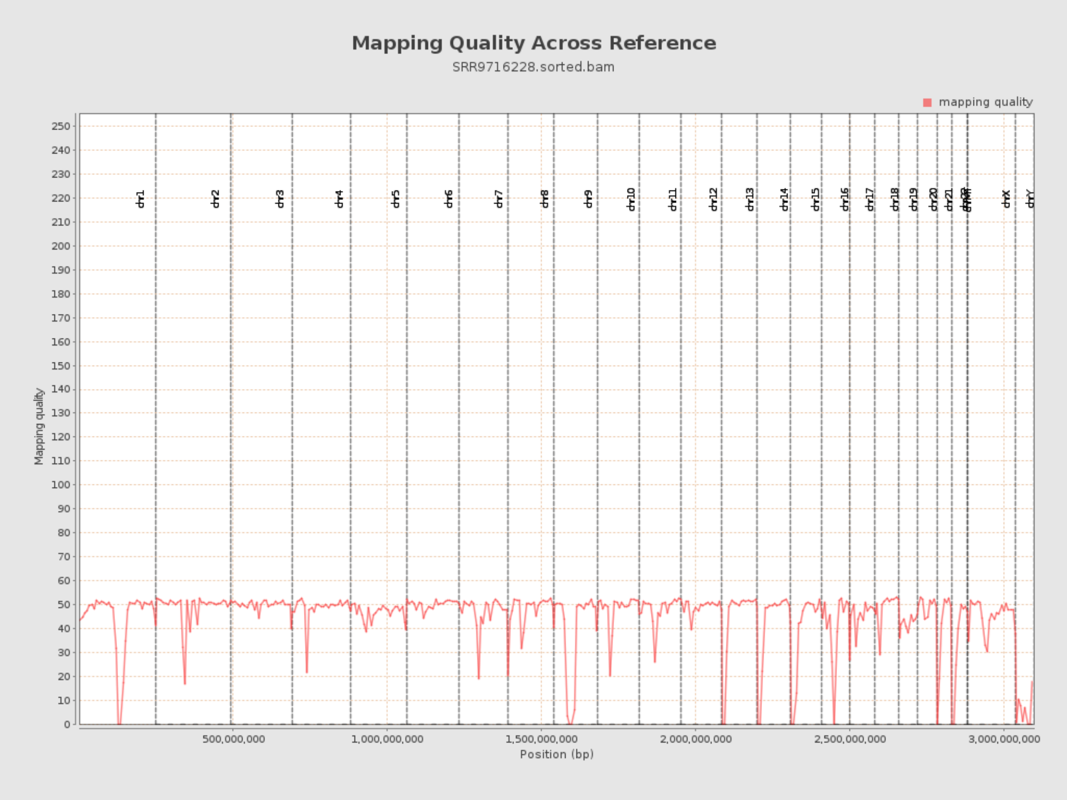
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram