Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:36:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716283.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_SRR9716283 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716283.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:36:43 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716283.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,352,877
Mapped reads	1,237,849 / 91.5%
Unmapped reads	115,028 / 8.5%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,083 / 0.38%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	27,459 / 2.03%
Duplication rate	1.68%
Clipped reads	1,242,238 / 91.82%

2.2. ACGT Content

Number/percentage of A's	17,480,482 / 24.52%
Number/percentage of C's	14,423,672 / 20.23%
Number/percentage of T's	21,734,670 / 30.49%
Number/percentage of G's	17,655,747 / 24.76%
Number/percentage of N's	1,531 / 0%
GC Percentage	44.99%

2.3. Coverage

Mean	0.023

Standard Deviation	0.1944

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

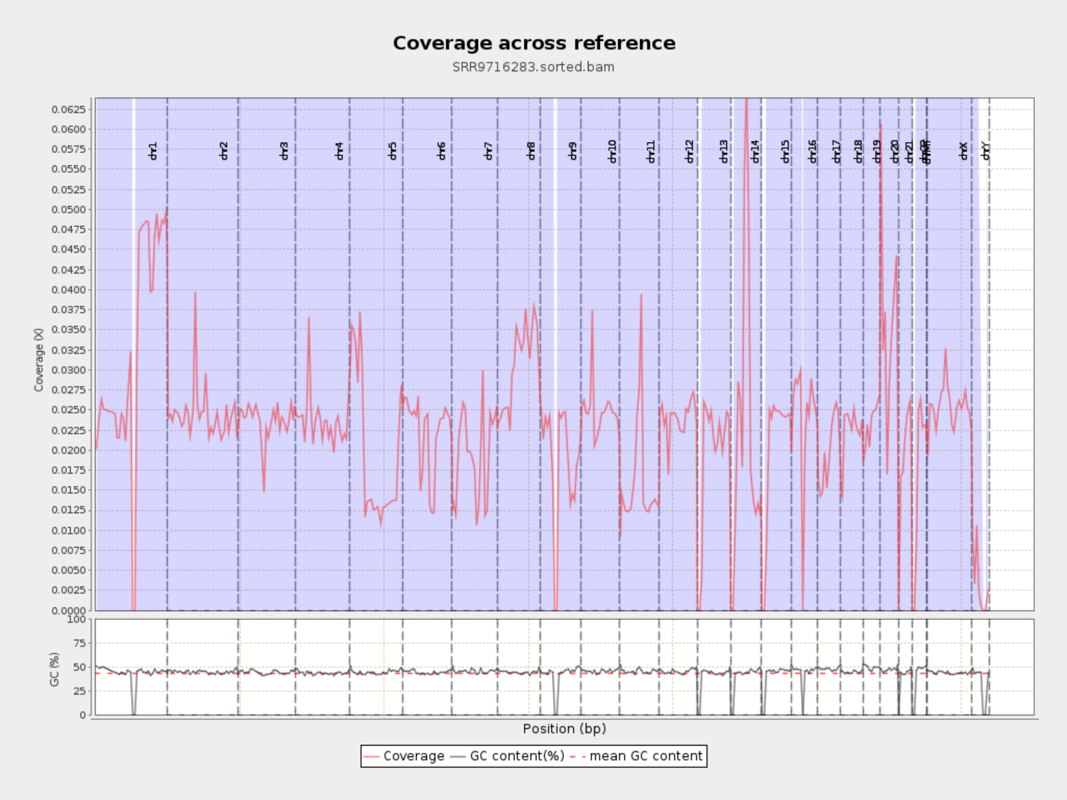
General error rate	0.5%
Mismatches	347,950
Insertions	3,533
Mapped reads with at least one insertion	0.28%
Deletions	11,123
Mapped reads with at least one deletion	0.89%
Homopolymer indels	42.36%

2.6. Chromosome stats

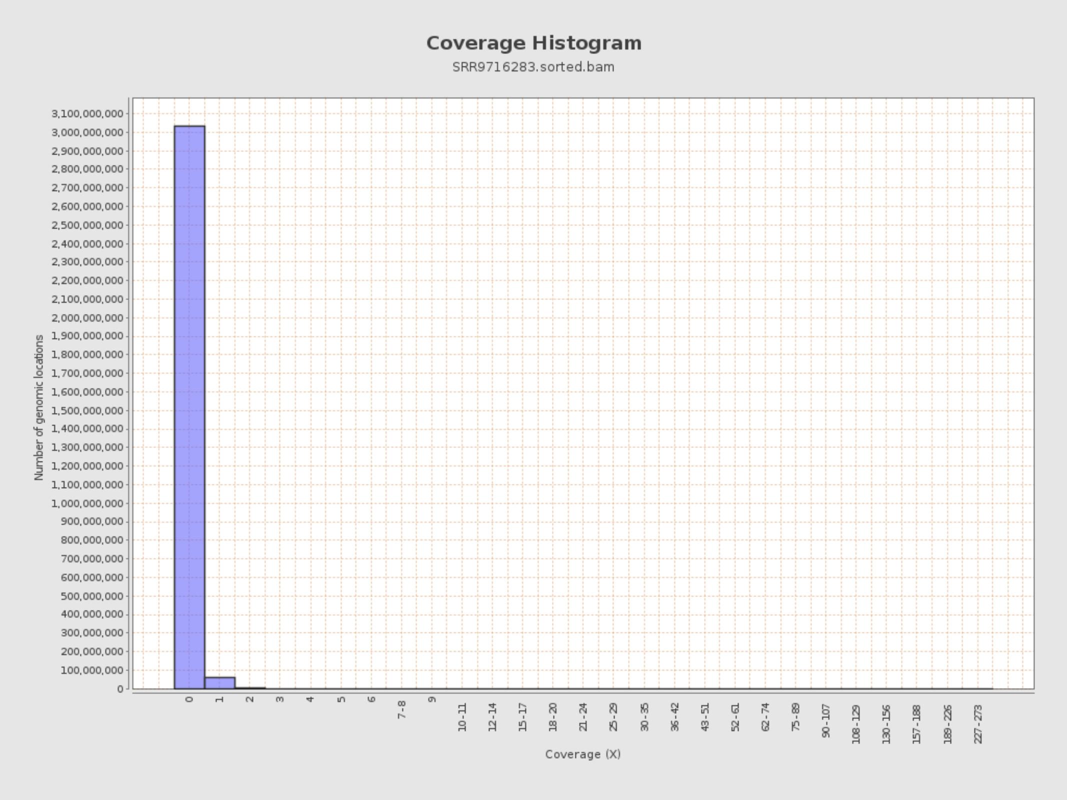
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8054569	0.0323	0.2821
chr2	243199373	5960099	0.0245	0.2252
chr3	198022430	4673910	0.0236	0.1642
chr4	191154276	4529600	0.0237	0.173
chr5	180915260	3523162	0.0195	0.15
chr6	171115067	3782883	0.0221	0.1675
chr7	159138663	3101788	0.0195	0.1752

chr8	146364022	4486717	0.0307	0.2079
chr9	141213431	2597468	0.0184	0.1919
chr10	135534747	3396191	0.0251	0.2079
chr11	135006516	2211116	0.0164	0.172
chr12	133851895	3212290	0.024	0.1669
chr13	115169878	2206935	0.0192	0.1467
chr14	107349540	2500930	0.0233	0.1707
chr15	102531392	2033363	0.0198	0.1503
chr16	90354753	2149437	0.0238	0.1762
chr17	81195210	1601073	0.0197	0.1541
chr18	78077248	1730237	0.0222	0.3329
chr19	59128983	1381703	0.0234	0.2203
chr20	63025520	2238274	0.0355	0.2078
chr21	48129895	920804	0.0191	0.1581
chr22	51304566	855670	0.0167	0.1375
chrMT	16571	384	0.0232	0.1571
chrX	155270560	3967871	0.0256	0.185
chrY	59373566	198870	0.0033	0.0803

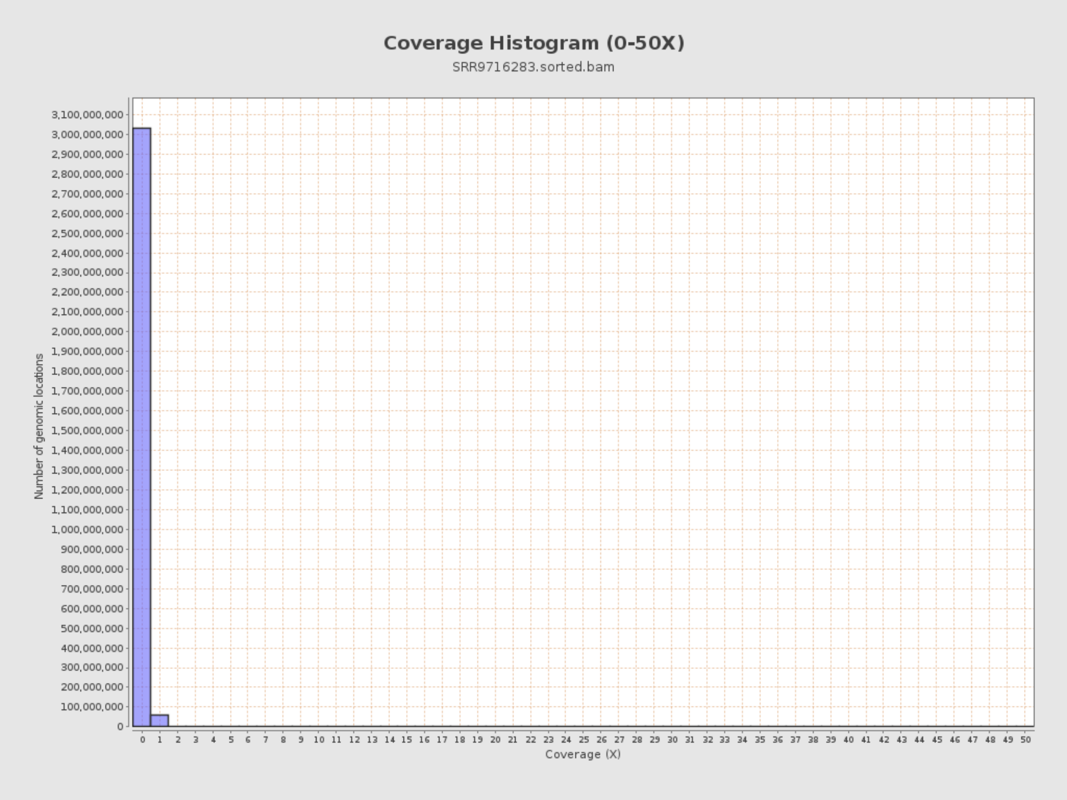
3. Results : Coverage across reference



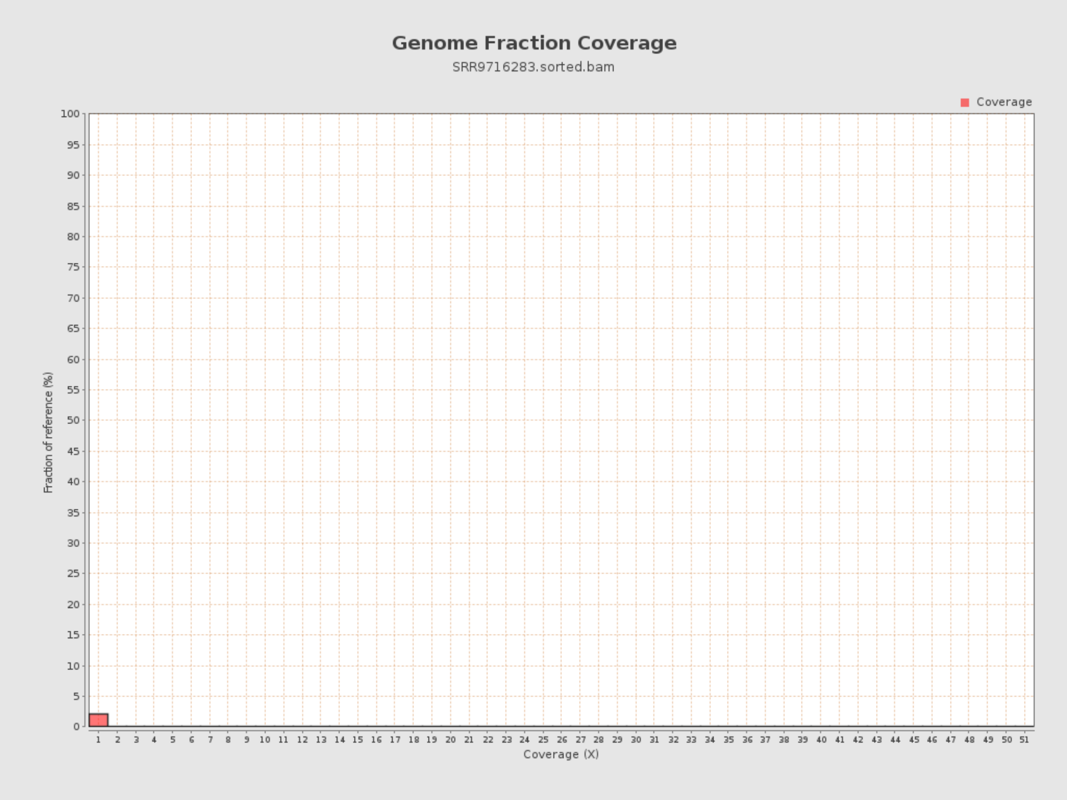
4. Results : Coverage Histogram



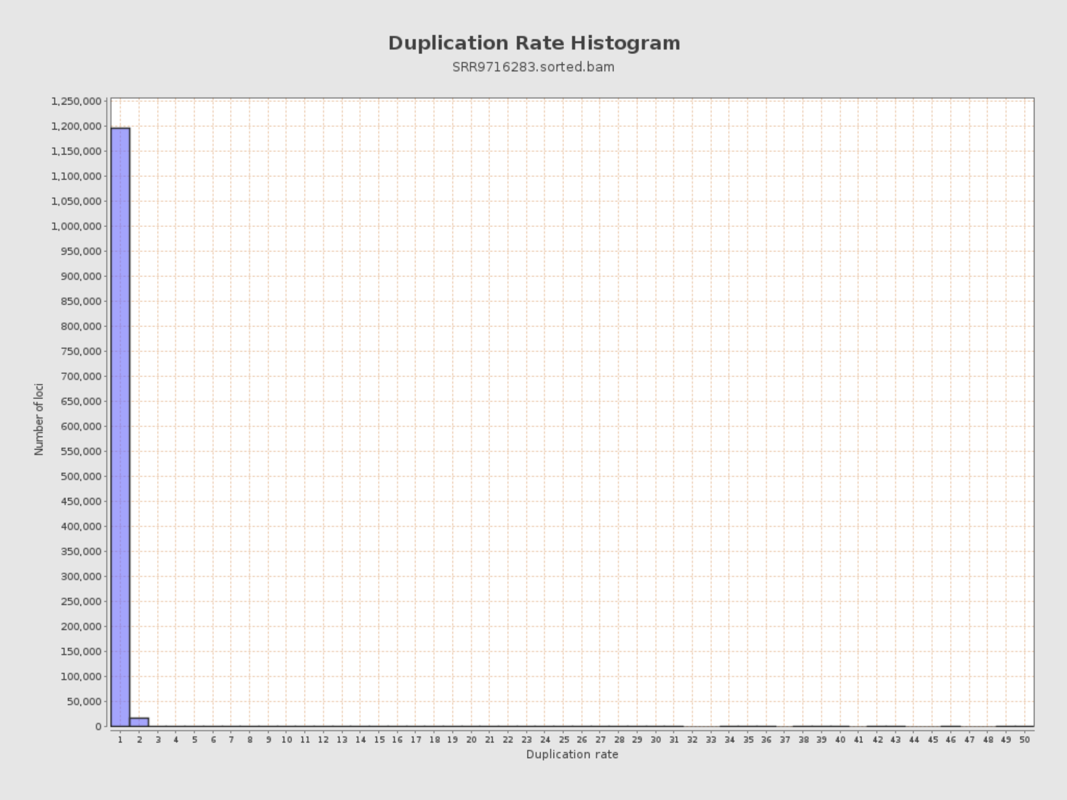
5. Results : Coverage Histogram (0-50X)



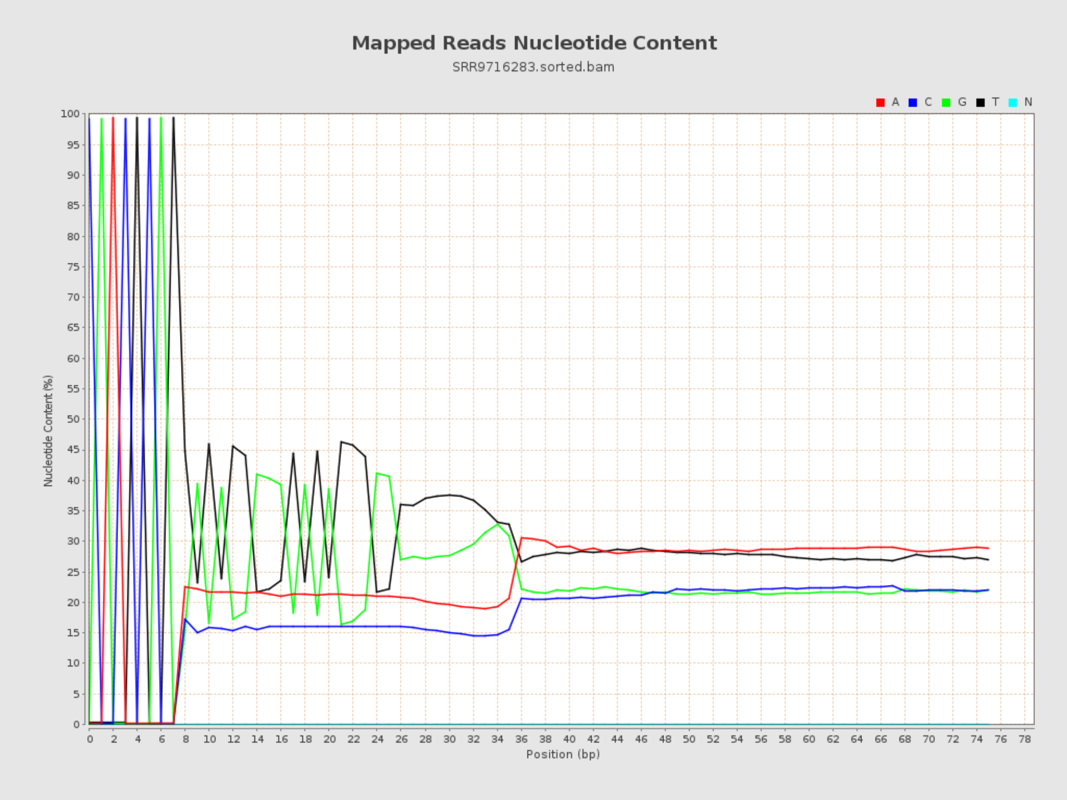
6. Results : Genome Fraction Coverage



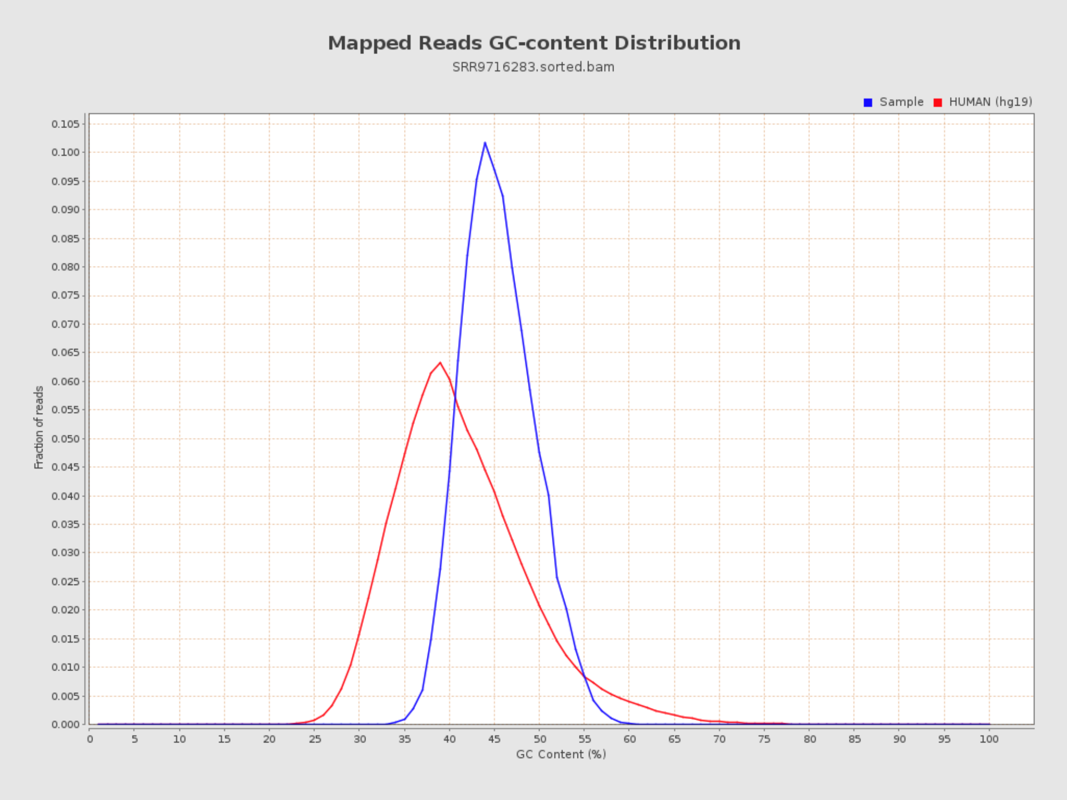
7. Results : Duplication Rate Histogram



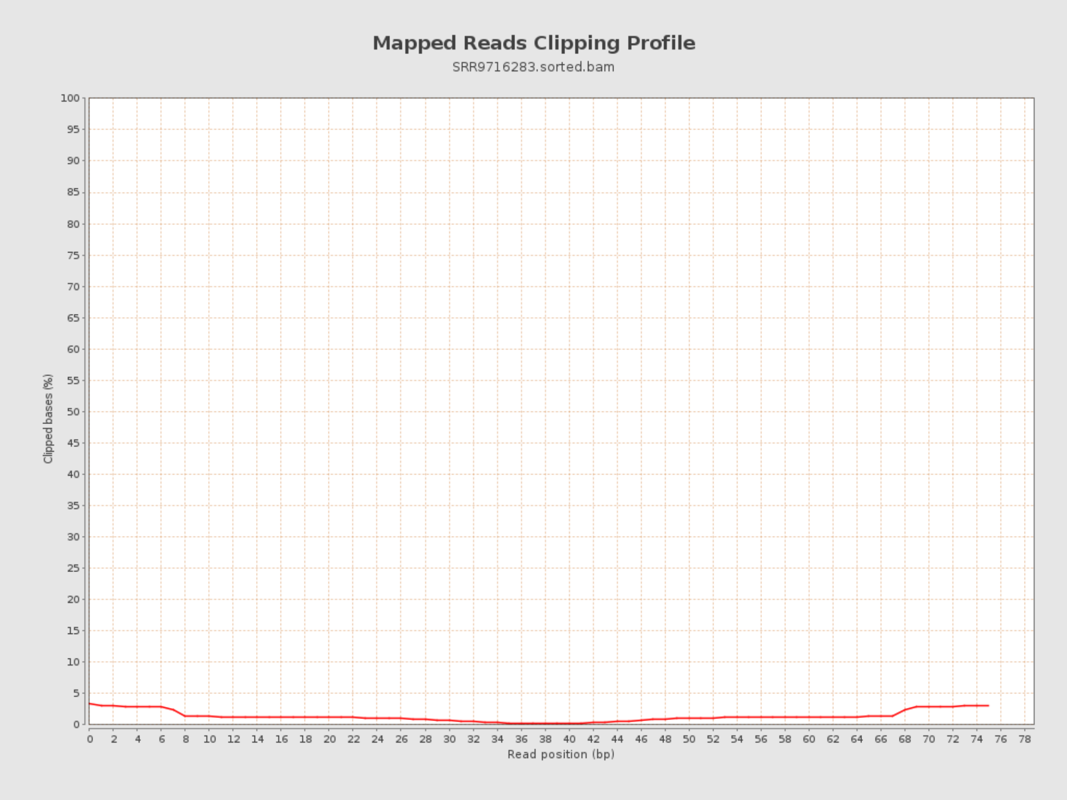
8. Results : Mapped Reads Nucleotide Content



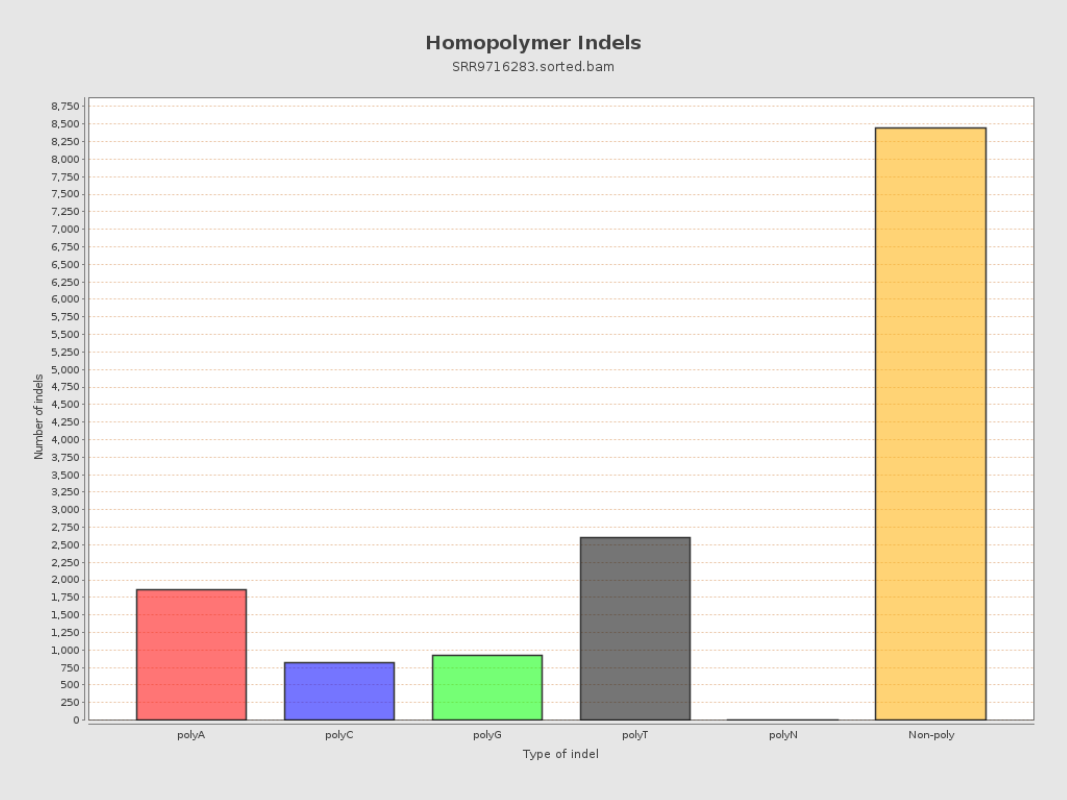
9. Results : Mapped Reads GC-content Distribution



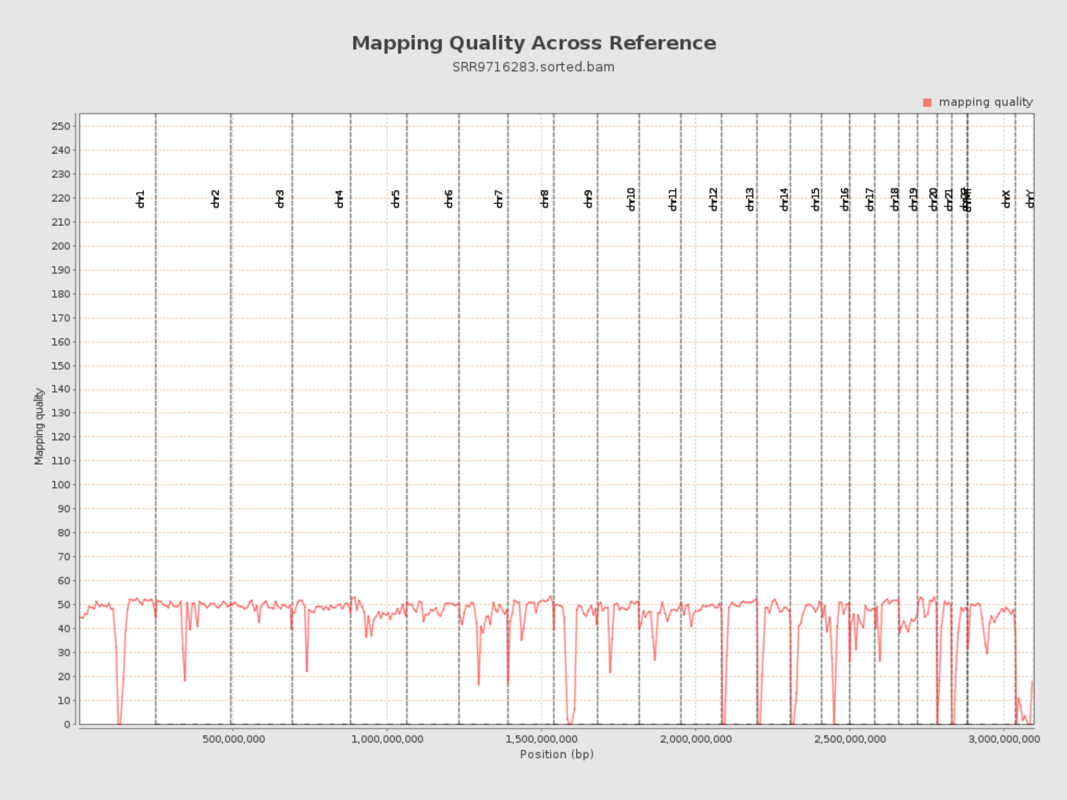
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram