Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 13:58:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716831.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_SRR9716831 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716831.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 13:58:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716831.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	763,583
Mapped reads	530,914 / 69.53%
Unmapped reads	232,669 / 30.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	484 / 0.06%
Read min/max/mean length	30 / 76 / 76.02
Duplicated reads (estimated)	32,793 / 4.29%
Duplication rate	5.47%
Clipped reads	530,912 / 69.53%

2.2. ACGT Content

Number/percentage of A's	5,781,973 / 21.07%
Number/percentage of C's	4,656,951 / 16.97%
Number/percentage of T's	9,324,853 / 33.98%
Number/percentage of G's	7,674,683 / 27.97%
Number/percentage of N's	480 / 0%
GC Percentage	44.94%

2.3. Coverage

Mean	0.0089

Standard Deviation	0.1155

2.4. Mapping Quality

Mean Mapping Quality	42.08

2.5. Mismatches and indels

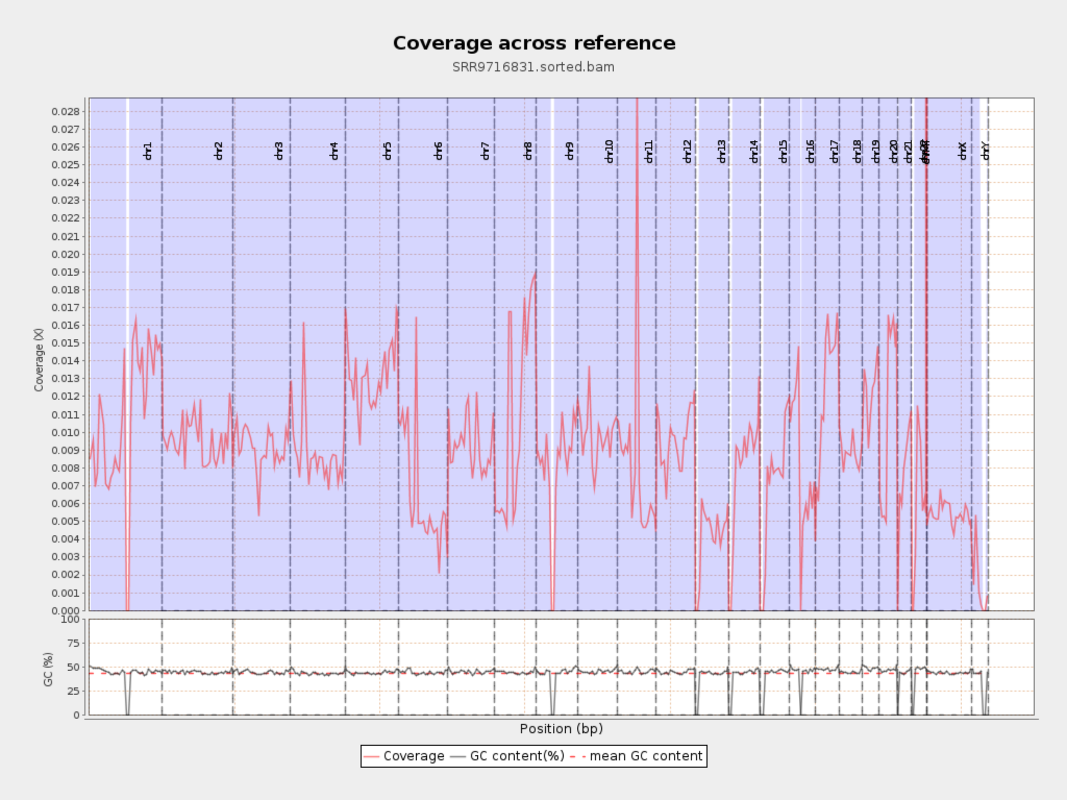
General error rate	0.73%
Mismatches	198,787
Insertions	1,537
Mapped reads with at least one insertion	0.29%
Deletions	4,115
Mapped reads with at least one deletion	0.77%
Homopolymer indels	40.04%

2.6. Chromosome stats

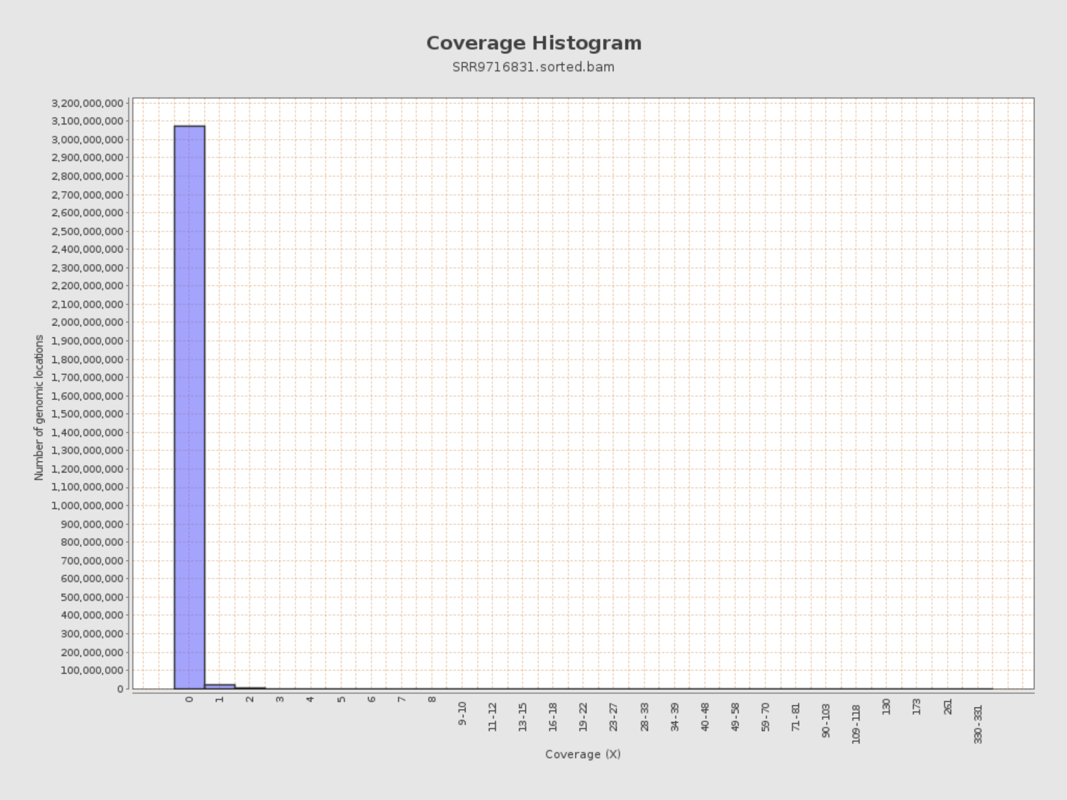
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2666437	0.0107	0.1288
chr2	243199373	2334666	0.0096	0.1711
chr3	198022430	1807389	0.0091	0.1048
chr4	191154276	1686405	0.0088	0.1074
chr5	180915260	2375448	0.0131	0.1264
chr6	171115067	1121042	0.0066	0.111
chr7	159138663	1468303	0.0092	0.1169

chr8	146364022	1630777	0.0111	0.1199
chr9	141213431	1117765	0.0079	0.1036
chr10	135534747	1324109	0.0098	0.118
chr11	135006516	1145897	0.0085	0.1081
chr12	133851895	1282685	0.0096	0.1085
chr13	115169878	468630	0.0041	0.0702
chr14	107349540	832835	0.0078	0.0977
chr15	102531392	709833	0.0069	0.092
chr16	90354753	728143	0.0081	0.1039
chr17	81195210	1046687	0.0129	0.1282
chr18	78077248	689859	0.0088	0.1123
chr19	59128983	724084	0.0122	0.1362
chr20	63025520	696723	0.0111	0.1203
chr21	48129895	367195	0.0076	0.1015
chr22	51304566	288723	0.0056	0.0838
chrMT	16571	4653	0.2808	0.5927
chrX	155270560	843852	0.0054	0.0826
chrY	59373566	83803	0.0014	0.0514

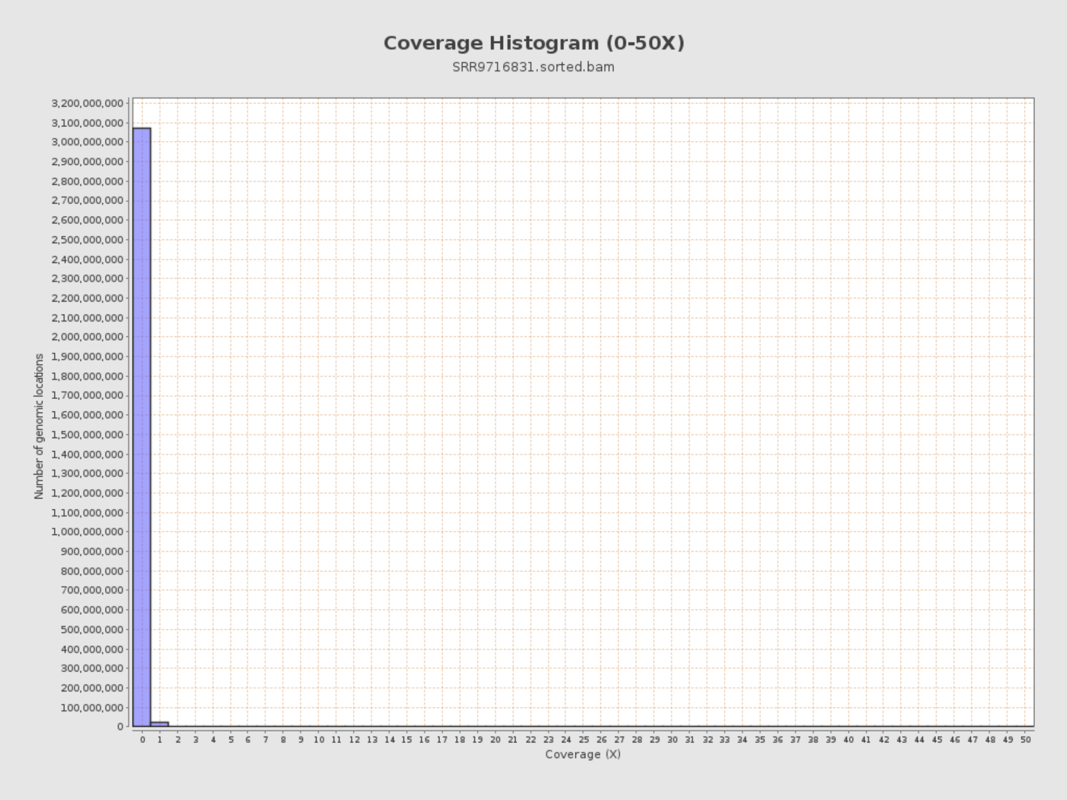
3. Results : Coverage across reference



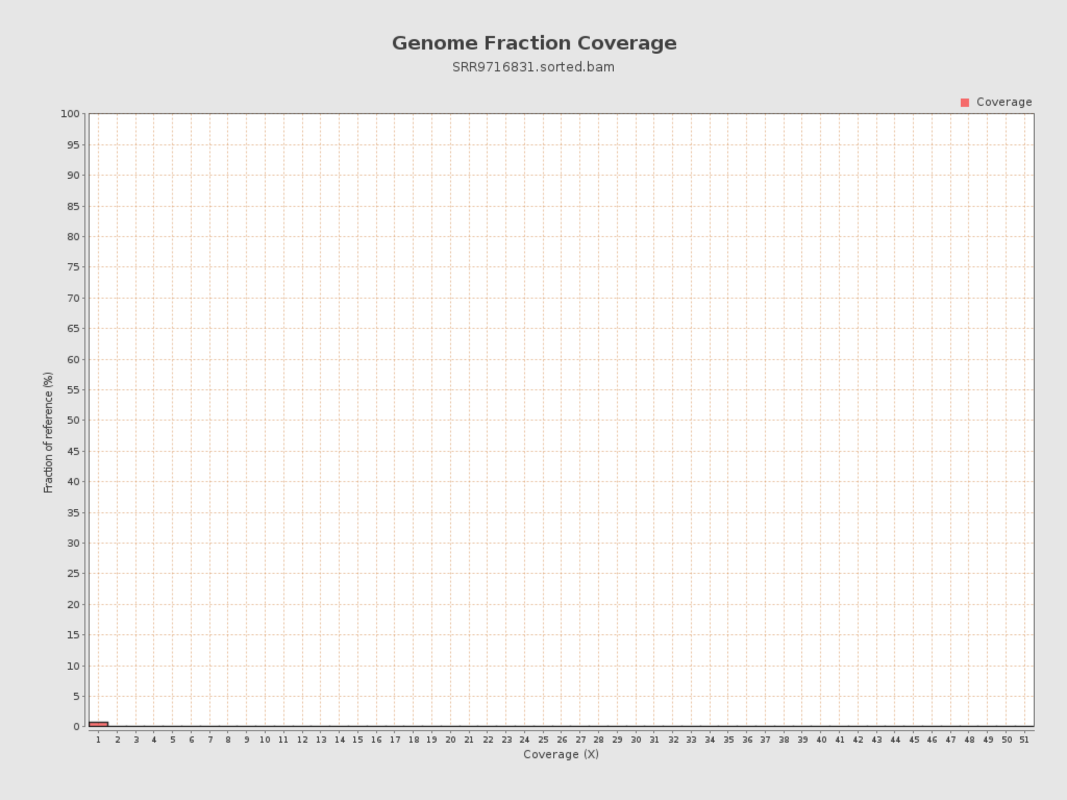
4. Results : Coverage Histogram



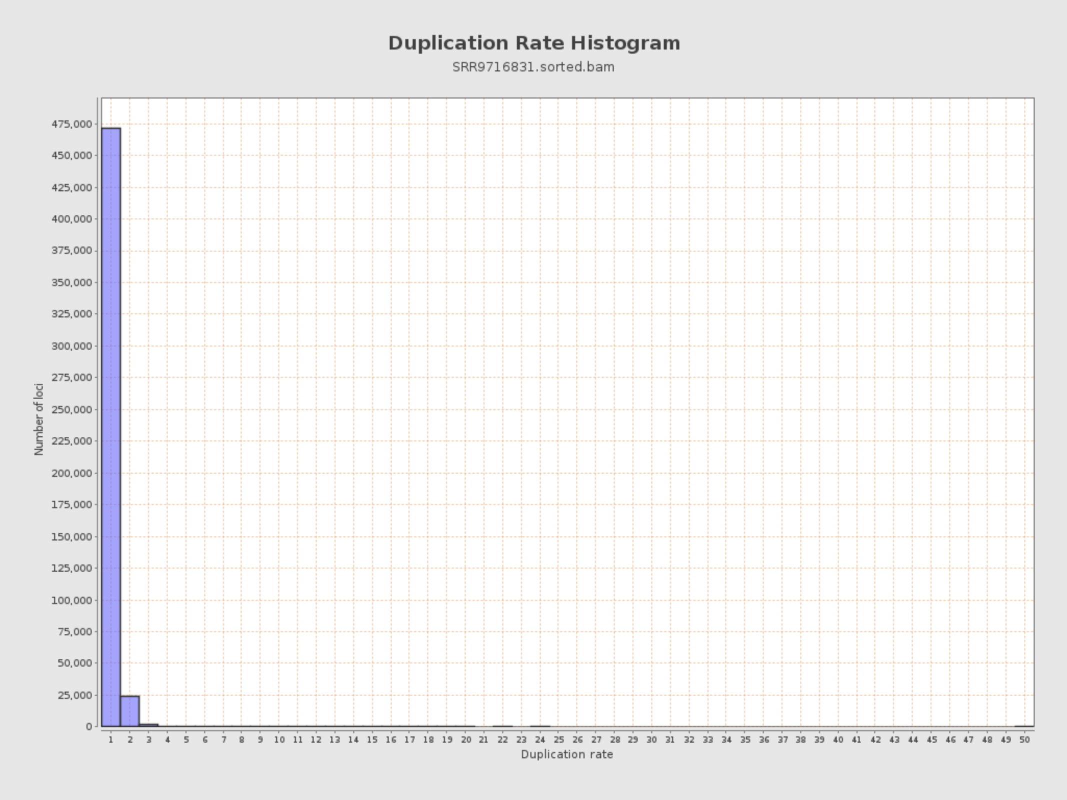
5. Results : Coverage Histogram (0-50X)



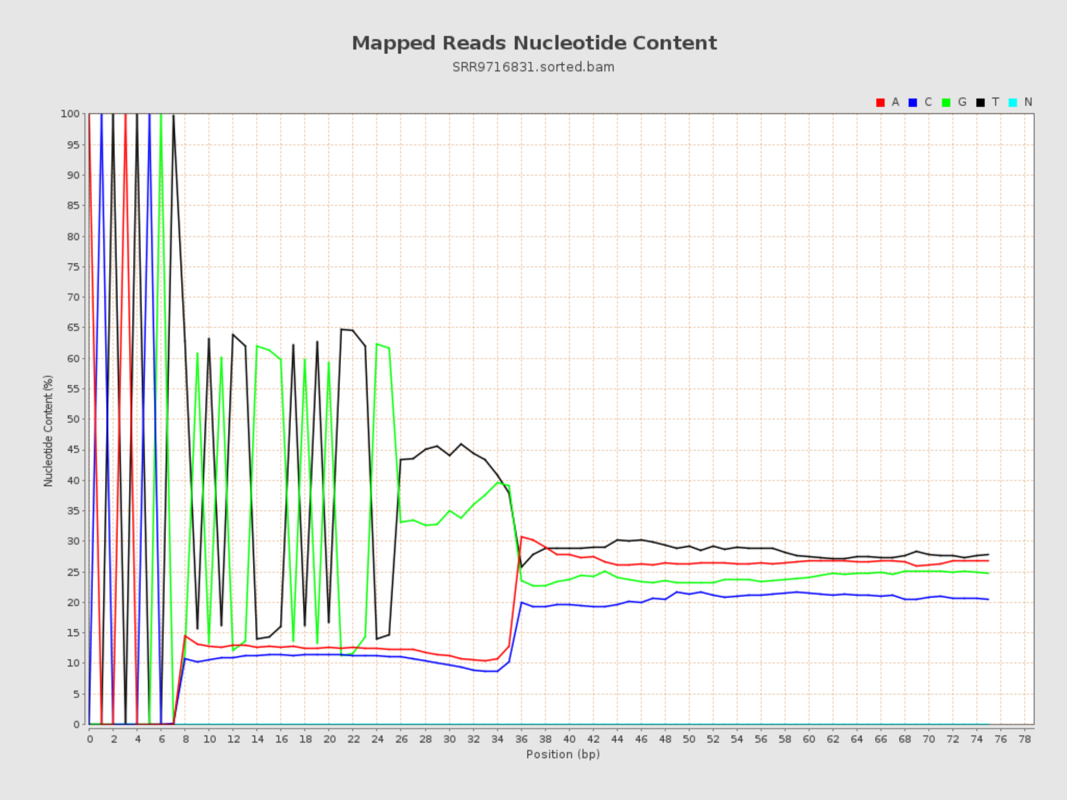
6. Results : Genome Fraction Coverage



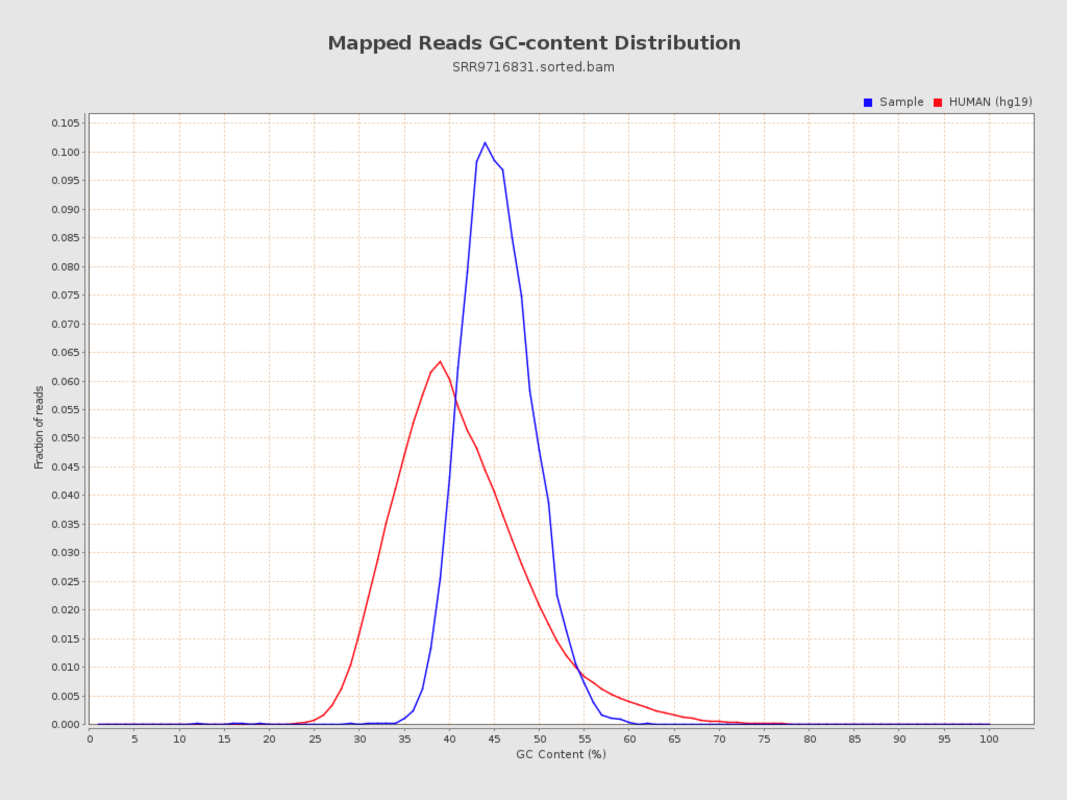
7. Results : Duplication Rate Histogram



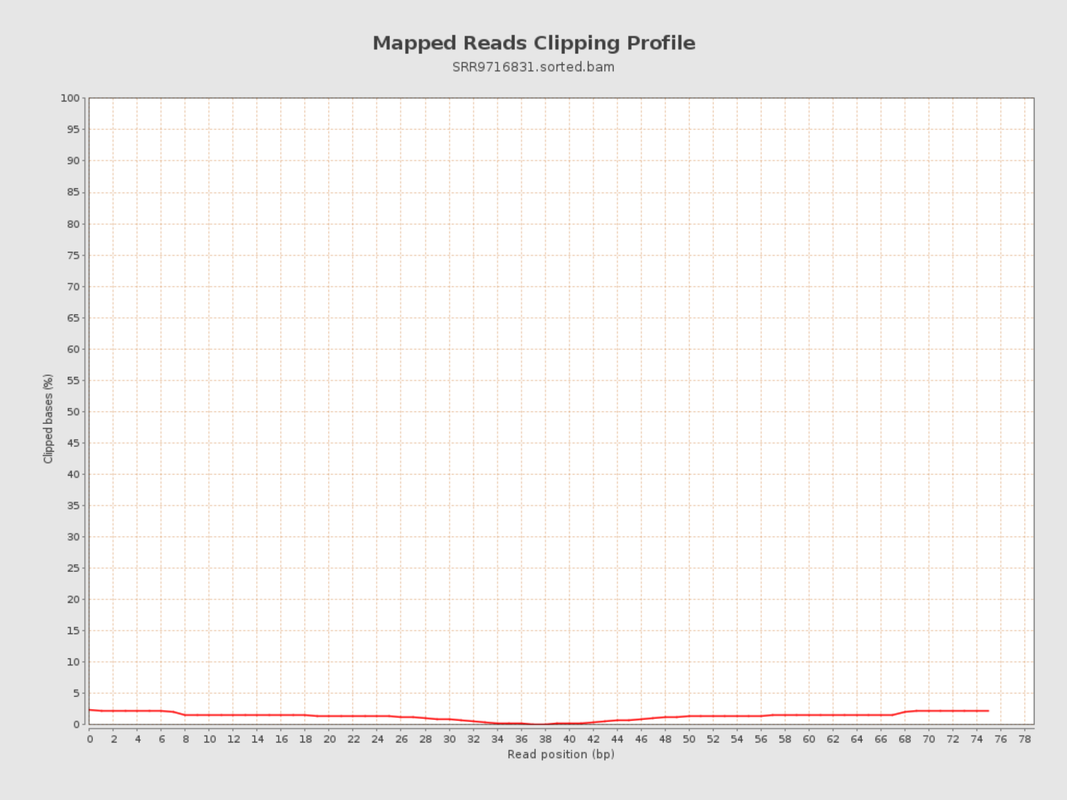
8. Results : Mapped Reads Nucleotide Content



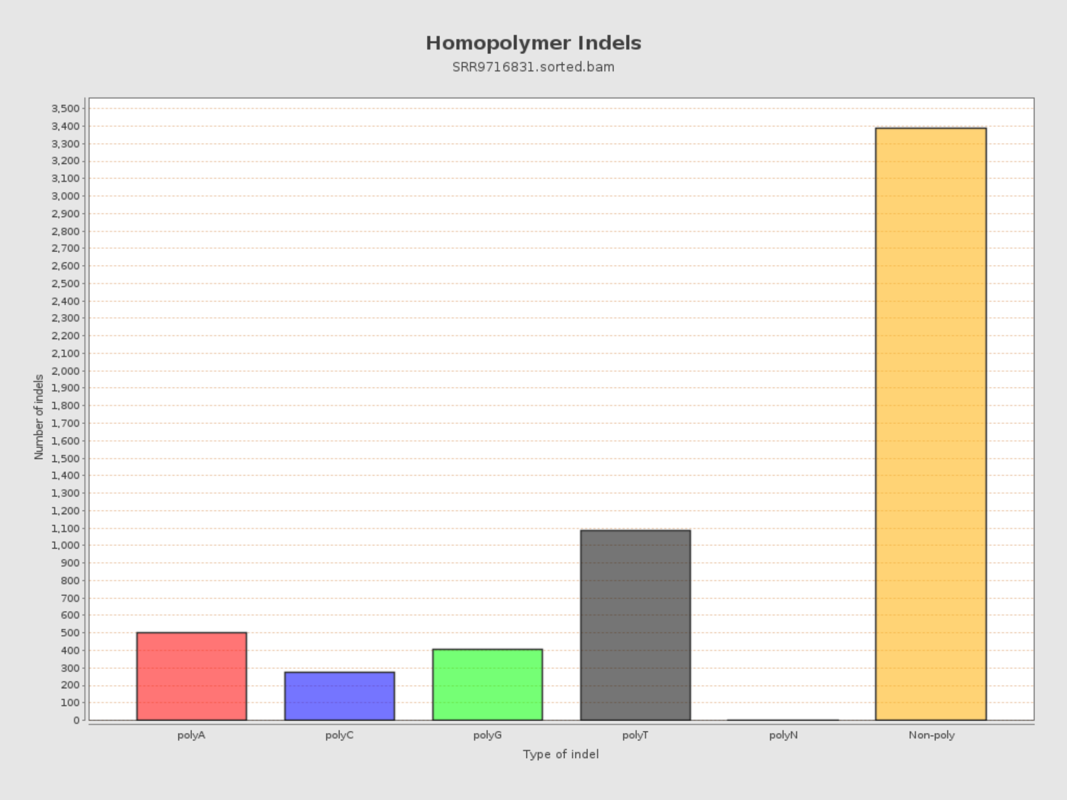
9. Results : Mapped Reads GC-content Distribution



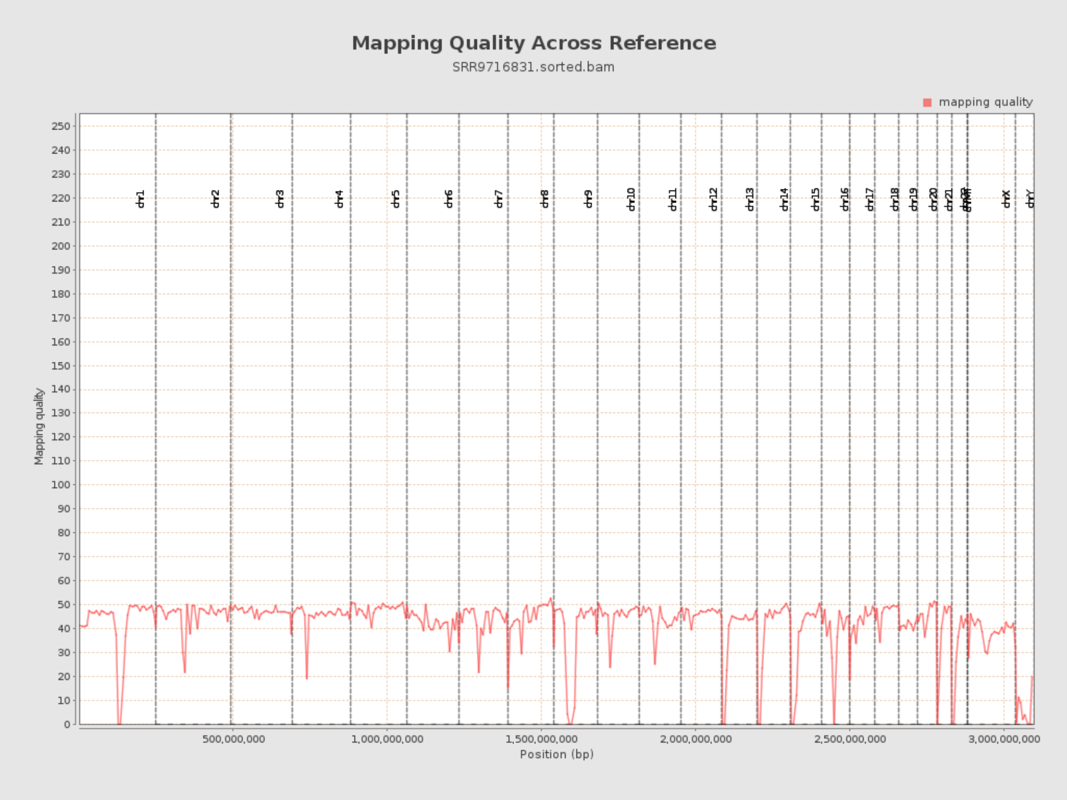
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram