Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 03:02:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716658.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_SRR9716658 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716658.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 03:02:33 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716658.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	465,399
Mapped reads	427,260 / 91.81%
Unmapped reads	38,139 / 8.19%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,706 / 0.37%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	7,947 / 1.71%
Duplication rate	1.31%
Clipped reads	427,960 / 91.96%

2.2. ACGT Content

Number/percentage of A's	6,409,971 / 25.66%
Number/percentage of C's	4,917,531 / 19.68%
Number/percentage of T's	7,805,053 / 31.24%
Number/percentage of G's	5,851,018 / 23.42%
Number/percentage of N's	514 / 0%
GC Percentage	43.1%

2.3. Coverage

Mean	0.0081

Standard Deviation	0.1104

2.4. Mapping Quality

Mean Mapping Quality	44.82

2.5. Mismatches and indels

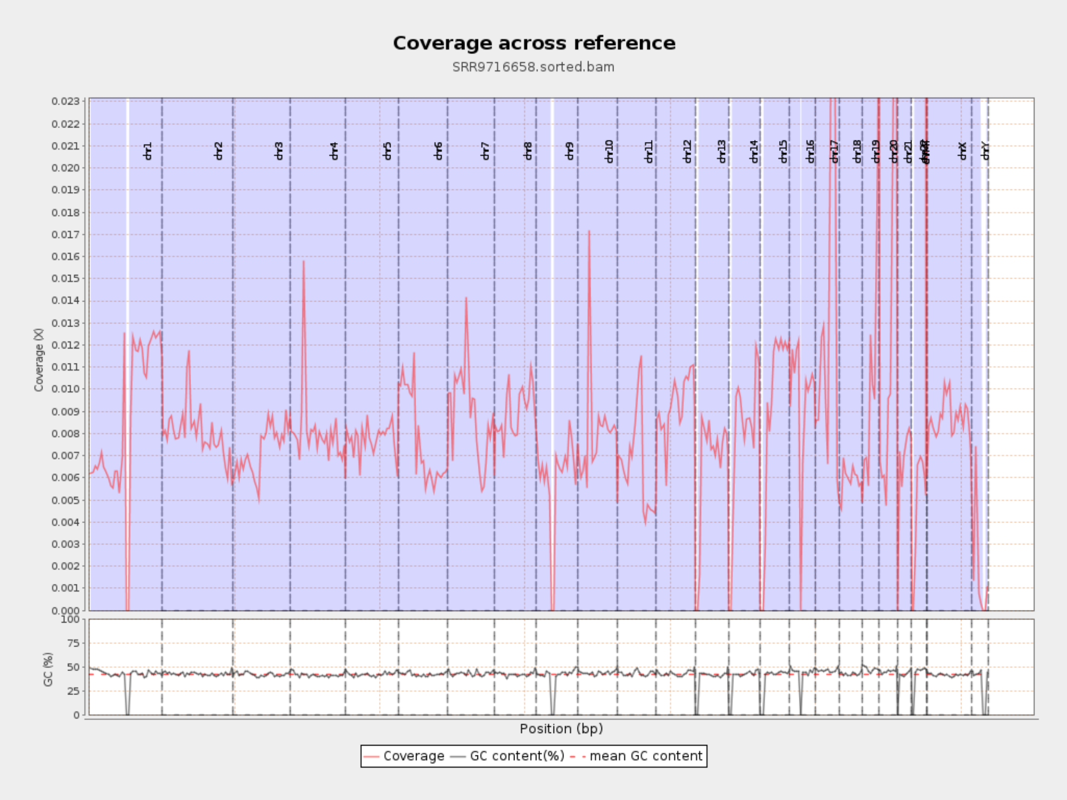
General error rate	0.52%
Mismatches	125,022
Insertions	1,949
Mapped reads with at least one insertion	0.45%
Deletions	4,953
Mapped reads with at least one deletion	1.15%
Homopolymer indels	42.05%

2.6. Chromosome stats

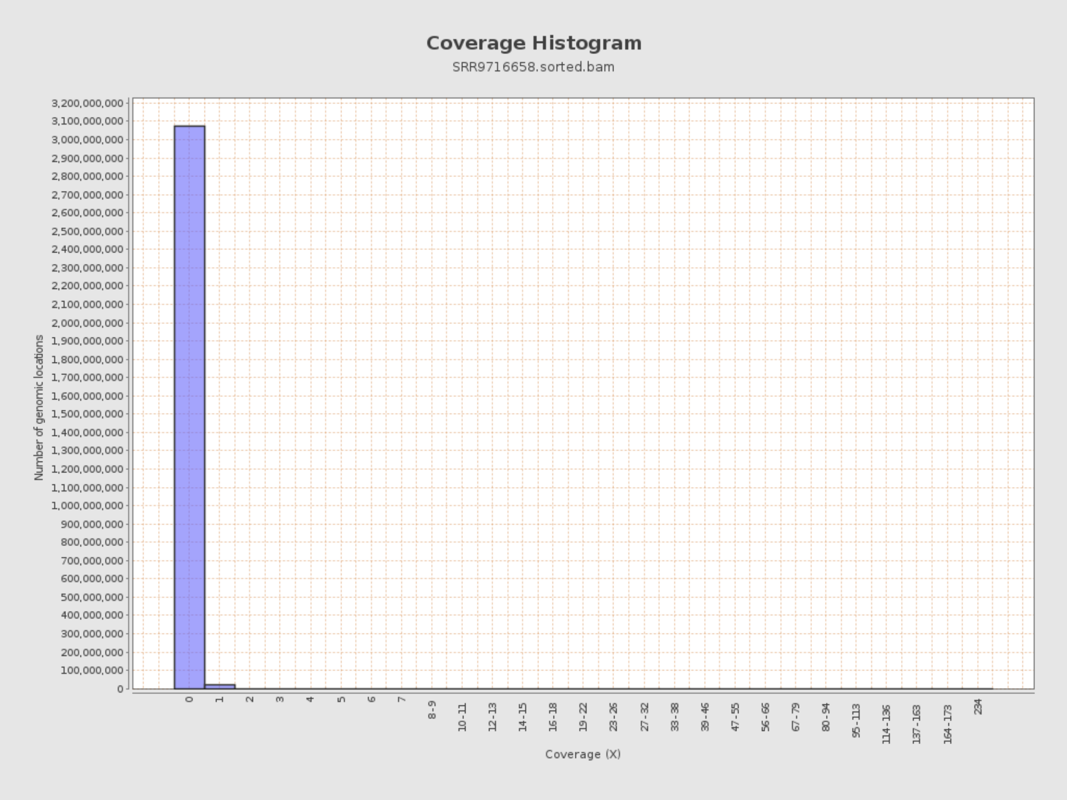
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2116002	0.0085	0.1485
chr2	243199373	1958626	0.0081	0.1349
chr3	198022430	1430061	0.0072	0.0876
chr4	191154276	1542794	0.0081	0.1006
chr5	180915260	1400471	0.0077	0.0904
chr6	171115067	1319188	0.0077	0.0951
chr7	159138663	1428475	0.009	0.1256

chr8	146364022	1314467	0.009	0.1377
chr9	141213431	831934	0.0059	0.0847
chr10	135534747	1091758	0.0081	0.1169
chr11	135006516	895635	0.0066	0.0911
chr12	133851895	1247033	0.0093	0.0993
chr13	115169878	747005	0.0065	0.0827
chr14	107349540	833749	0.0078	0.0905
chr15	102531392	914831	0.0089	0.0967
chr16	90354753	858850	0.0095	0.1013
chr17	81195210	1086512	0.0134	0.121
chr18	78077248	462428	0.0059	0.1168
chr19	59128983	644413	0.0109	0.1348
chr20	63025520	810492	0.0129	0.1177
chr21	48129895	315823	0.0066	0.0941
chr22	51304566	234231	0.0046	0.07
chrMT	16571	62693	3.7833	2.8612
chrX	155270560	1342272	0.0086	0.0974
chrY	59373566	102407	0.0017	0.0905

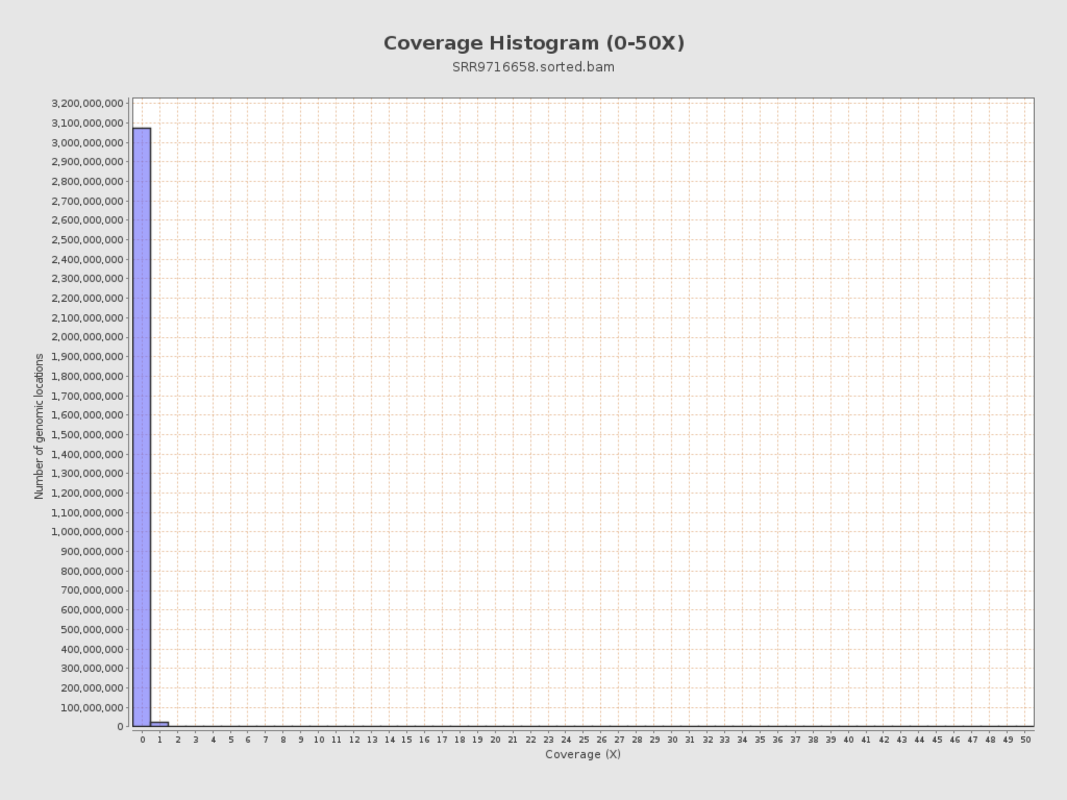
3. Results : Coverage across reference



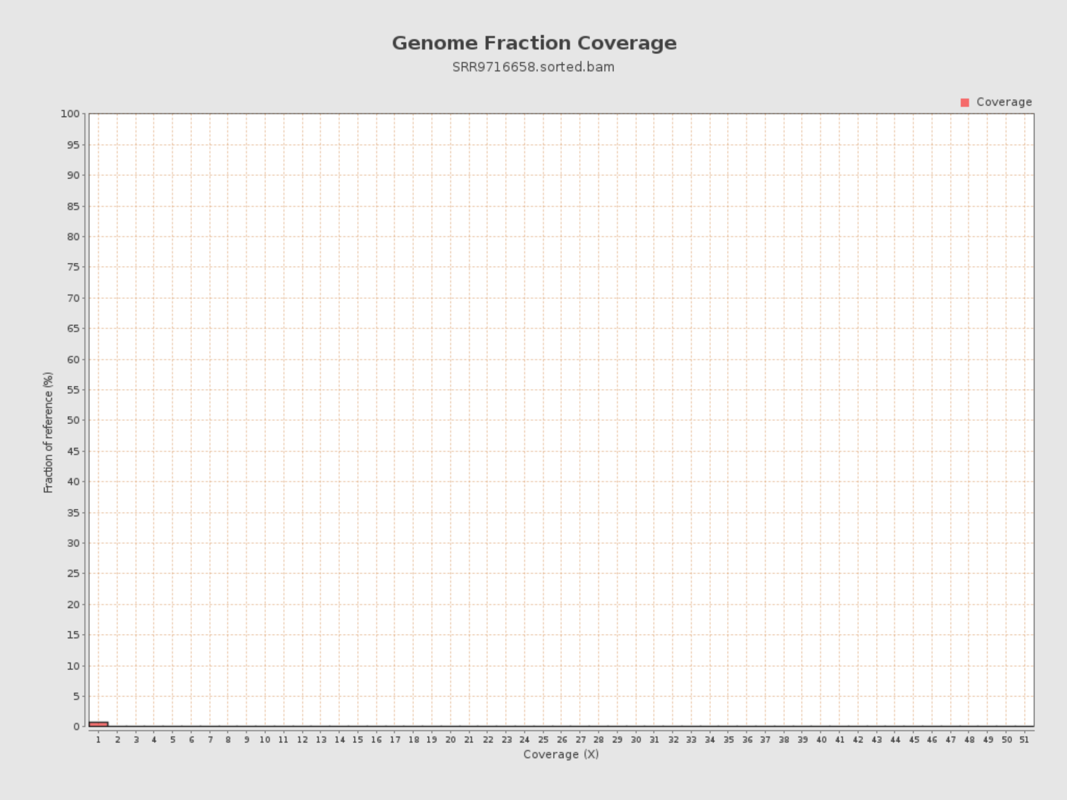
4. Results : Coverage Histogram



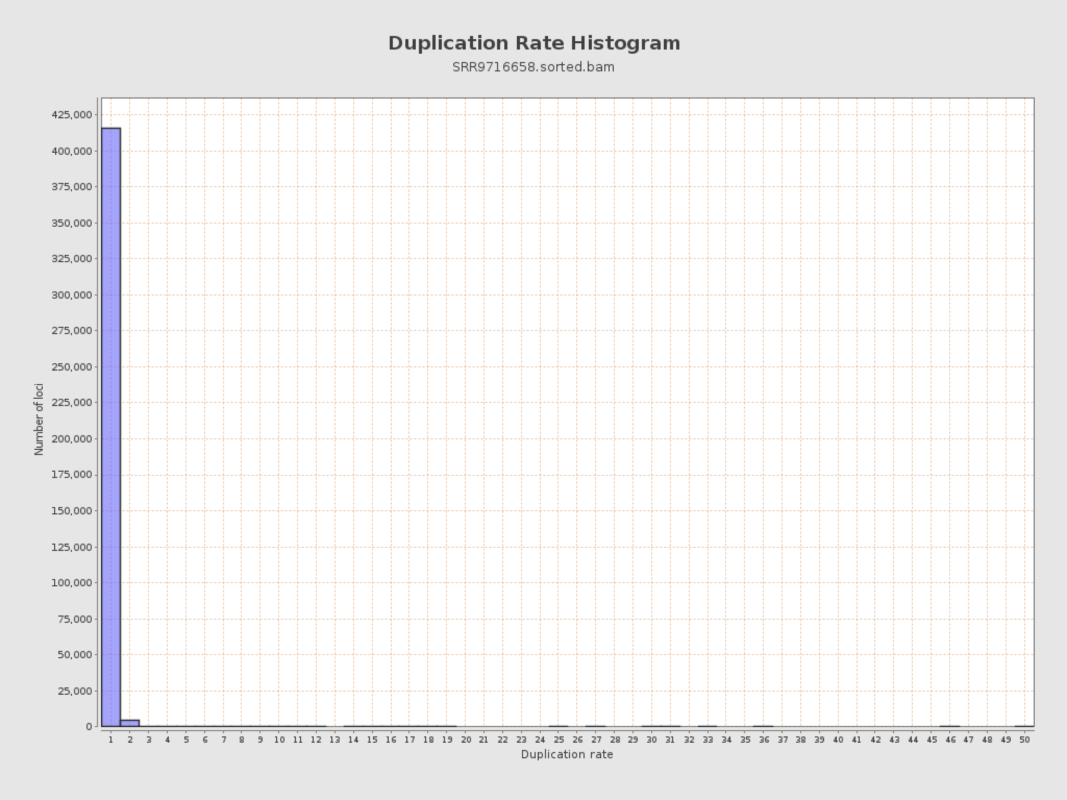
5. Results : Coverage Histogram (0-50X)



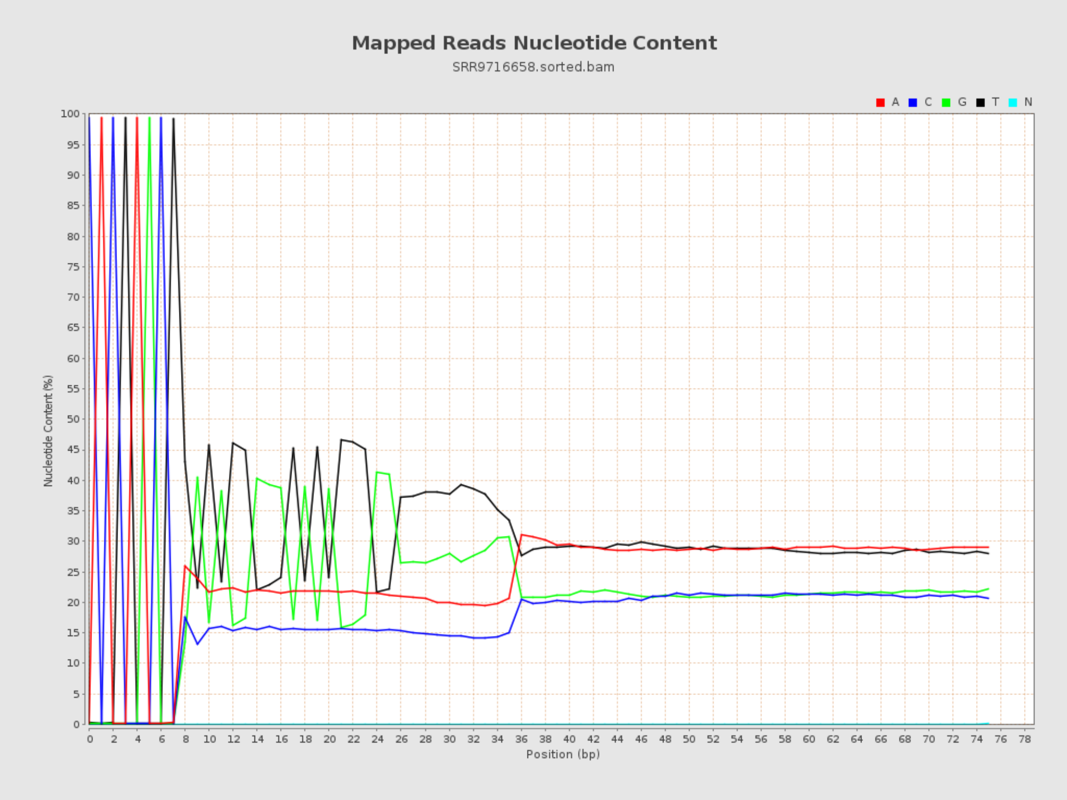
6. Results : Genome Fraction Coverage



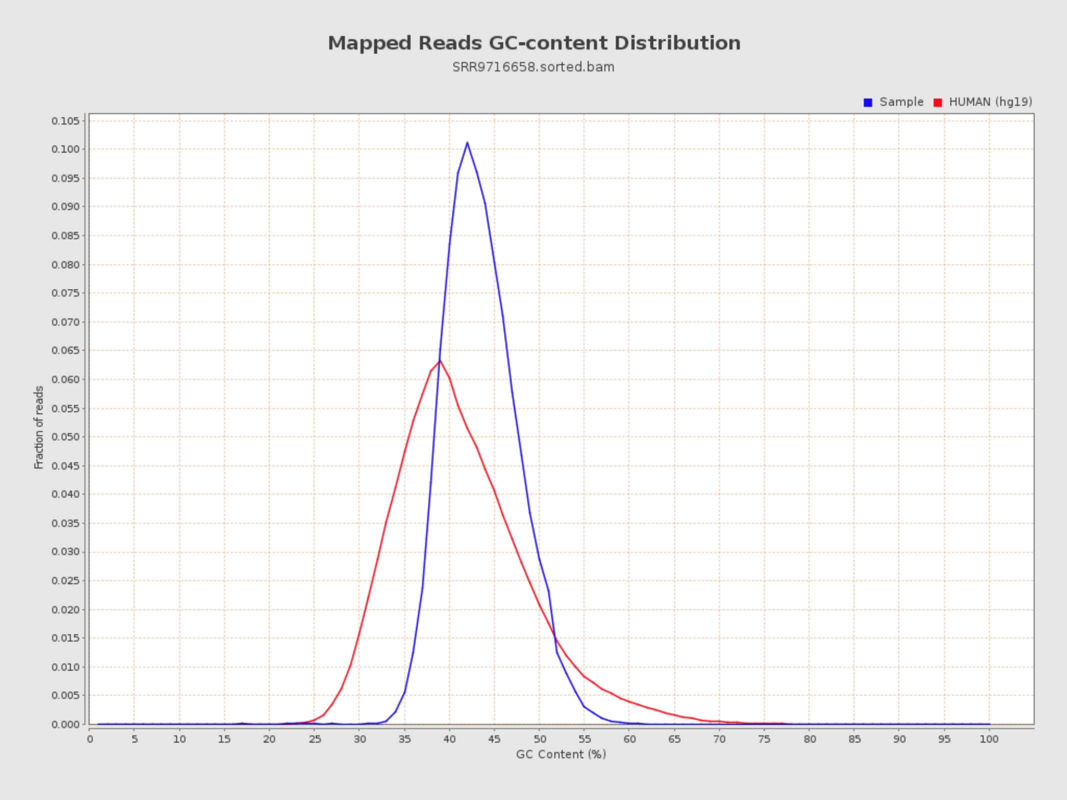
7. Results : Duplication Rate Histogram



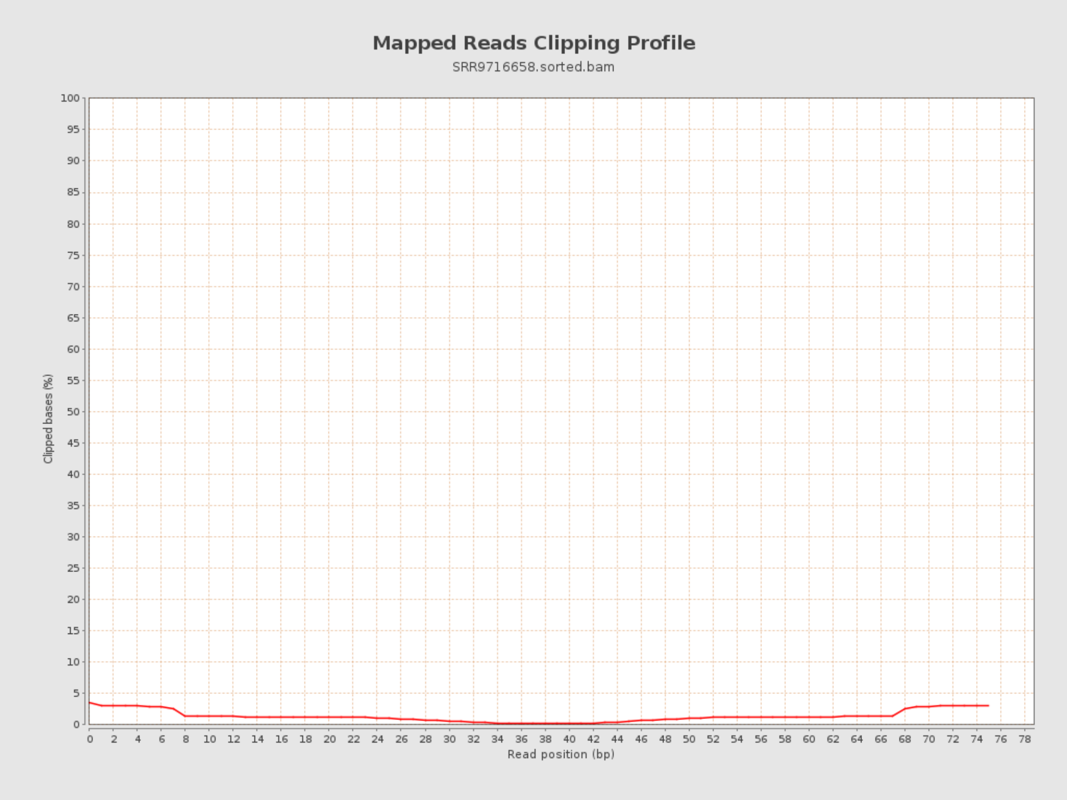
8. Results : Mapped Reads Nucleotide Content



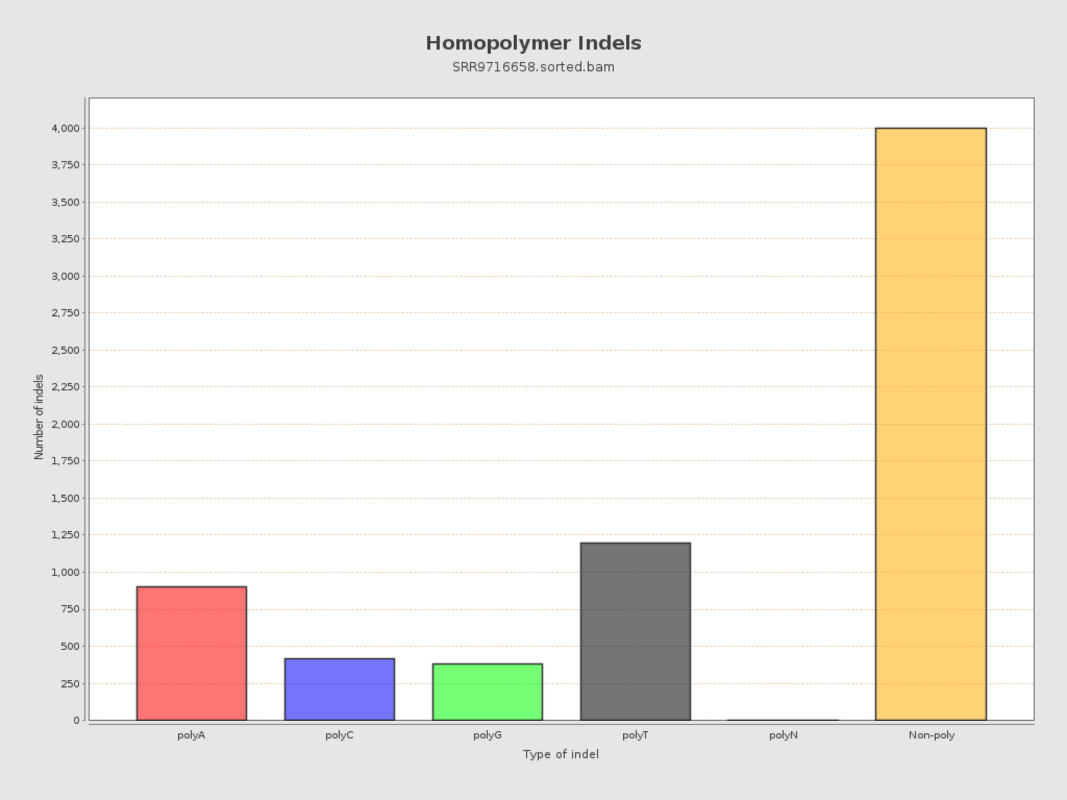
9. Results : Mapped Reads GC-content Distribution



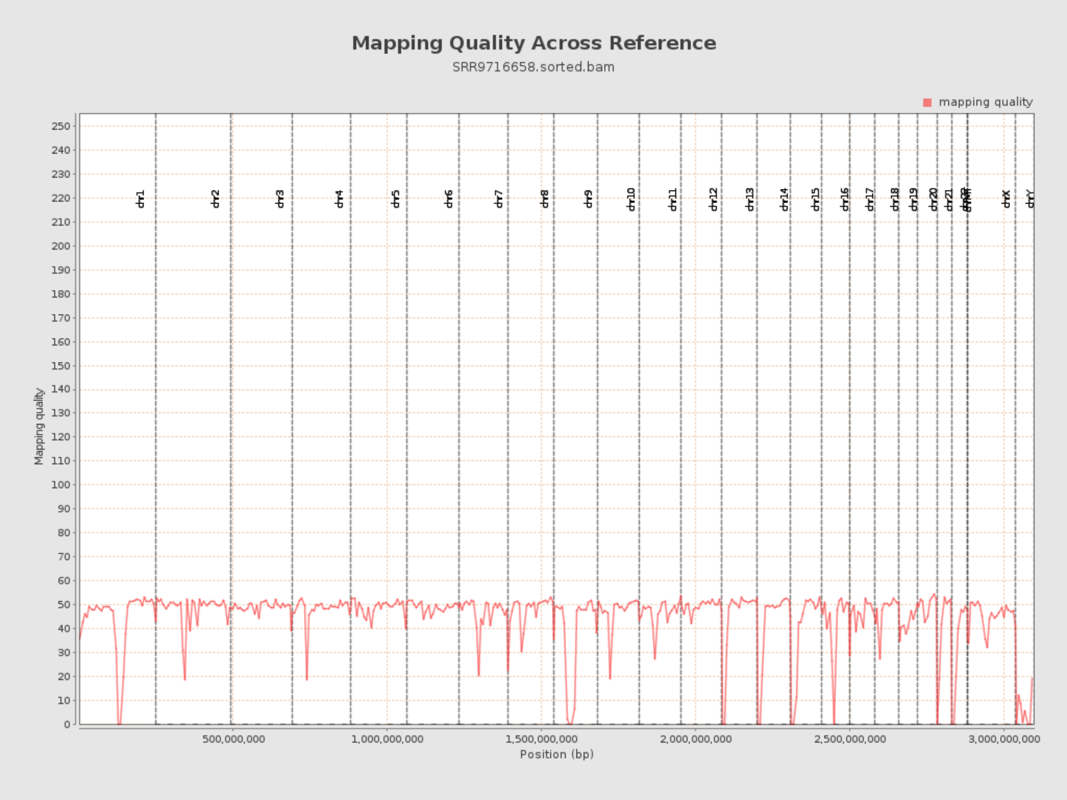
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram