Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:36:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716635.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_SRR9716635 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716635.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:36:44 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716635.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	610,429
Mapped reads	559,305 / 91.62%
Unmapped reads	51,124 / 8.38%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,743 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	14,237 / 2.33%
Duplication rate	1.83%
Clipped reads	559,180 / 91.6%

2.2. ACGT Content

Number/percentage of A's	7,863,422 / 24.41%
Number/percentage of C's	6,466,340 / 20.07%
Number/percentage of T's	10,498,969 / 32.59%
Number/percentage of G's	7,384,870 / 22.92%
Number/percentage of N's	622 / 0%
GC Percentage	43%

2.3. Coverage

Mean	0.0104

Standard Deviation	0.1326

2.4. Mapping Quality

Mean Mapping Quality	44.5

2.5. Mismatches and indels

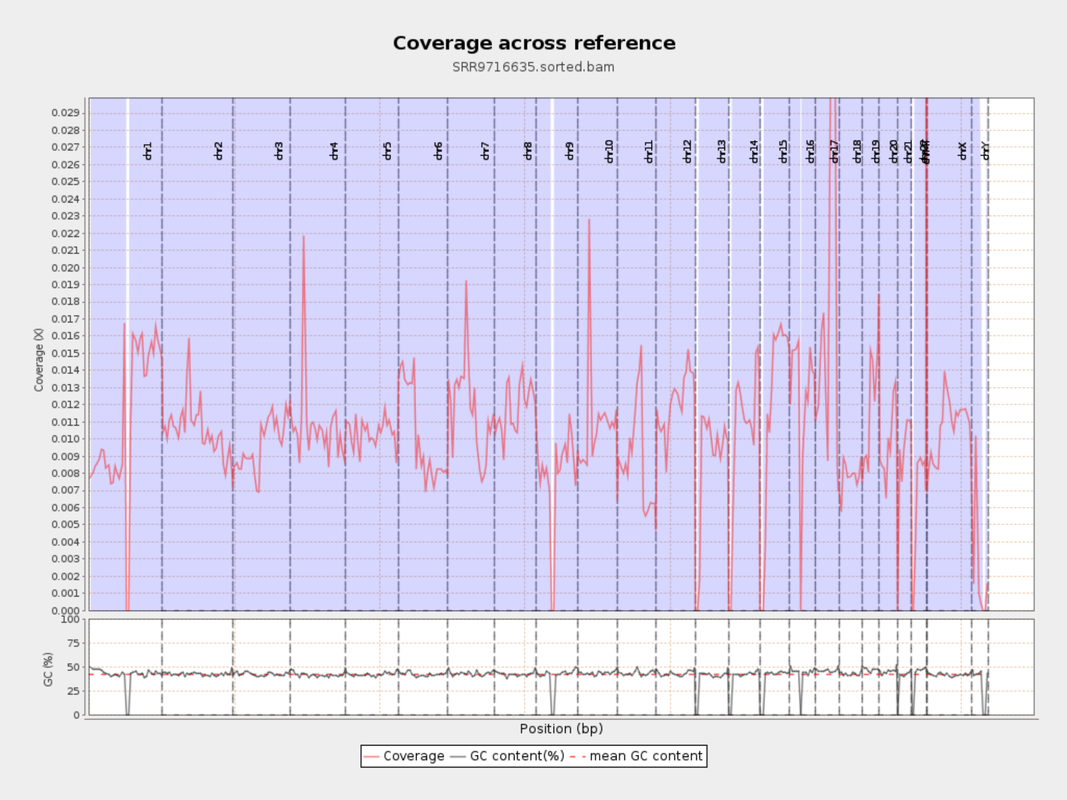
General error rate	0.53%
Mismatches	165,139
Insertions	2,688
Mapped reads with at least one insertion	0.48%
Deletions	6,597
Mapped reads with at least one deletion	1.17%
Homopolymer indels	42.64%

2.6. Chromosome stats

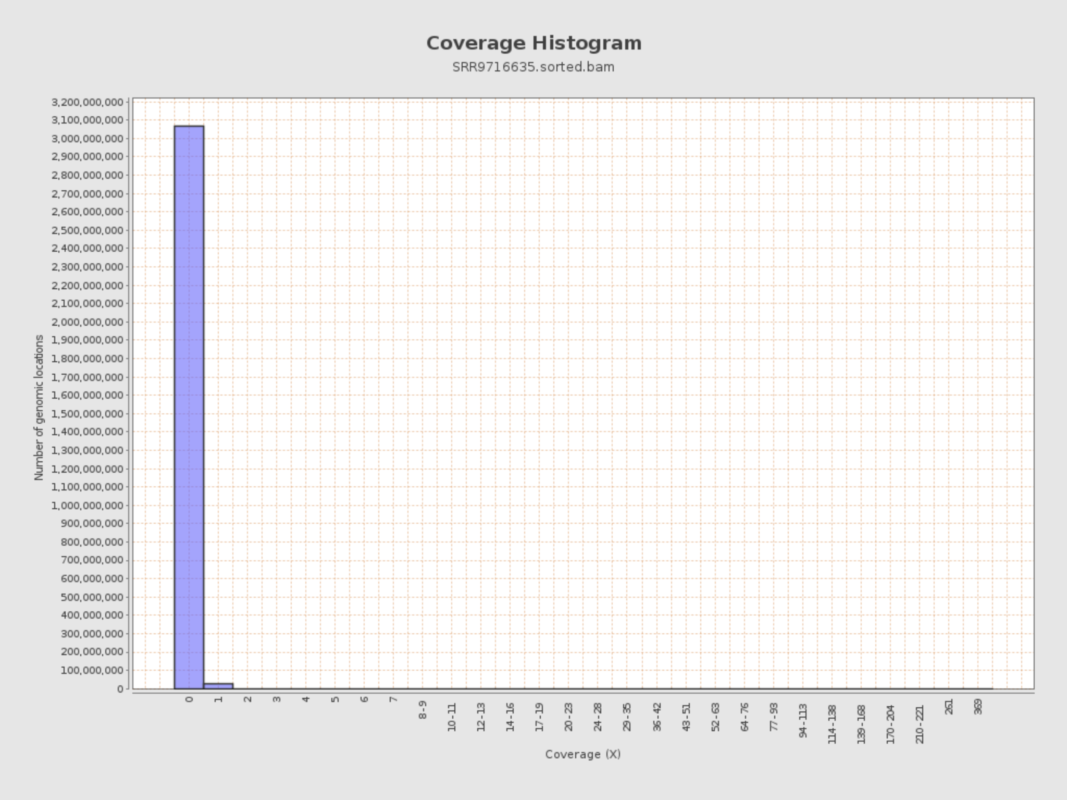
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2749669	0.011	0.1771
chr2	243199373	2577993	0.0106	0.1833
chr3	198022430	1913424	0.0097	0.1024
chr4	191154276	2046756	0.0107	0.1223
chr5	180915260	1868008	0.0103	0.1056
chr6	171115067	1741863	0.0102	0.1125
chr7	159138663	1862684	0.0117	0.1545

chr8	146364022	1727726	0.0118	0.1703
chr9	141213431	1094209	0.0077	0.0995
chr10	135534747	1473536	0.0109	0.1476
chr11	135006516	1189230	0.0088	0.1097
chr12	133851895	1629408	0.0122	0.1153
chr13	115169878	979456	0.0085	0.0957
chr14	107349540	1098536	0.0102	0.1061
chr15	102531392	1213643	0.0118	0.1135
chr16	90354753	1135877	0.0126	0.1186
chr17	81195210	1460679	0.018	0.1425
chr18	78077248	609625	0.0078	0.1346
chr19	59128983	704864	0.0119	0.1502
chr20	63025520	617283	0.0098	0.1048
chr21	48129895	428300	0.0089	0.1125
chr22	51304566	309665	0.006	0.0809
chrMT	16571	1707	0.103	0.3213
chrX	155270560	1654584	0.0107	0.111
chrY	59373566	136046	0.0023	0.1077

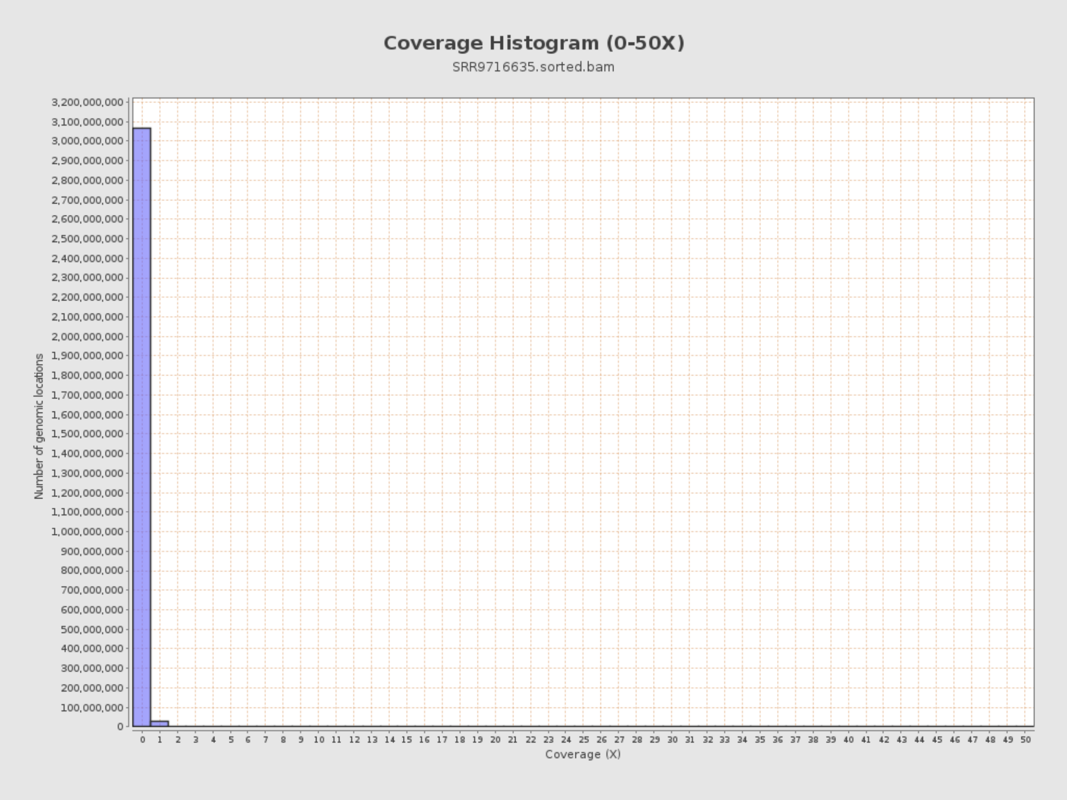
3. Results : Coverage across reference



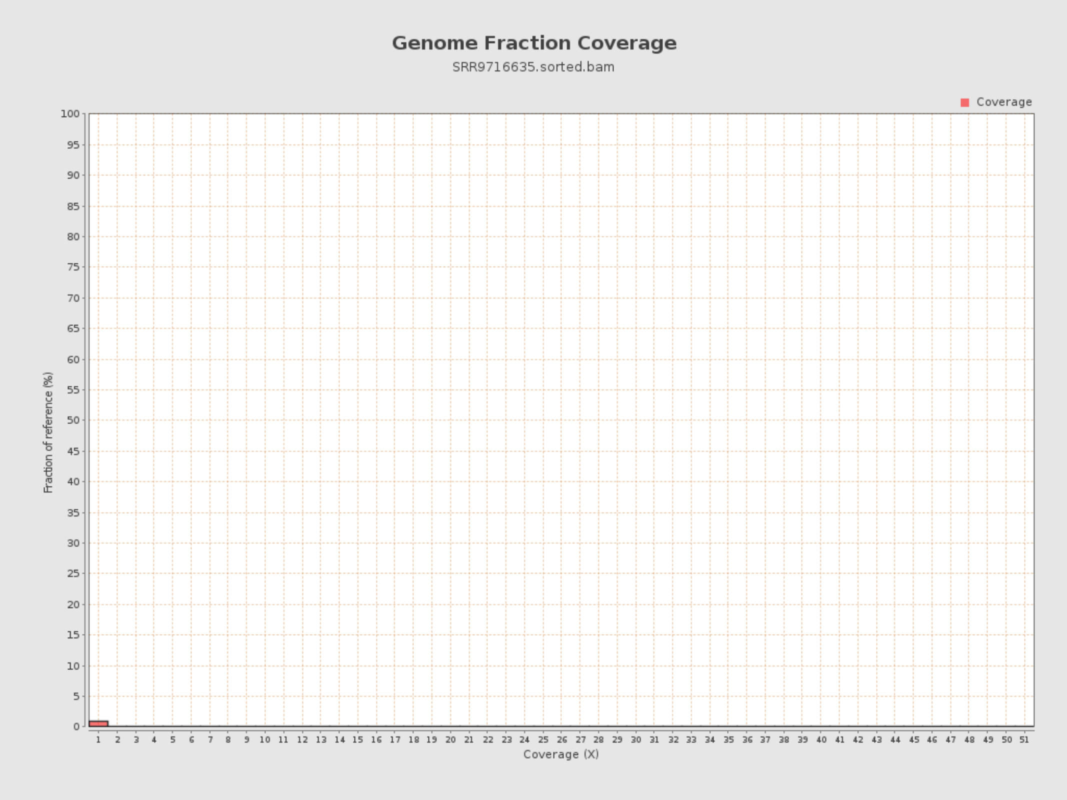
4. Results : Coverage Histogram



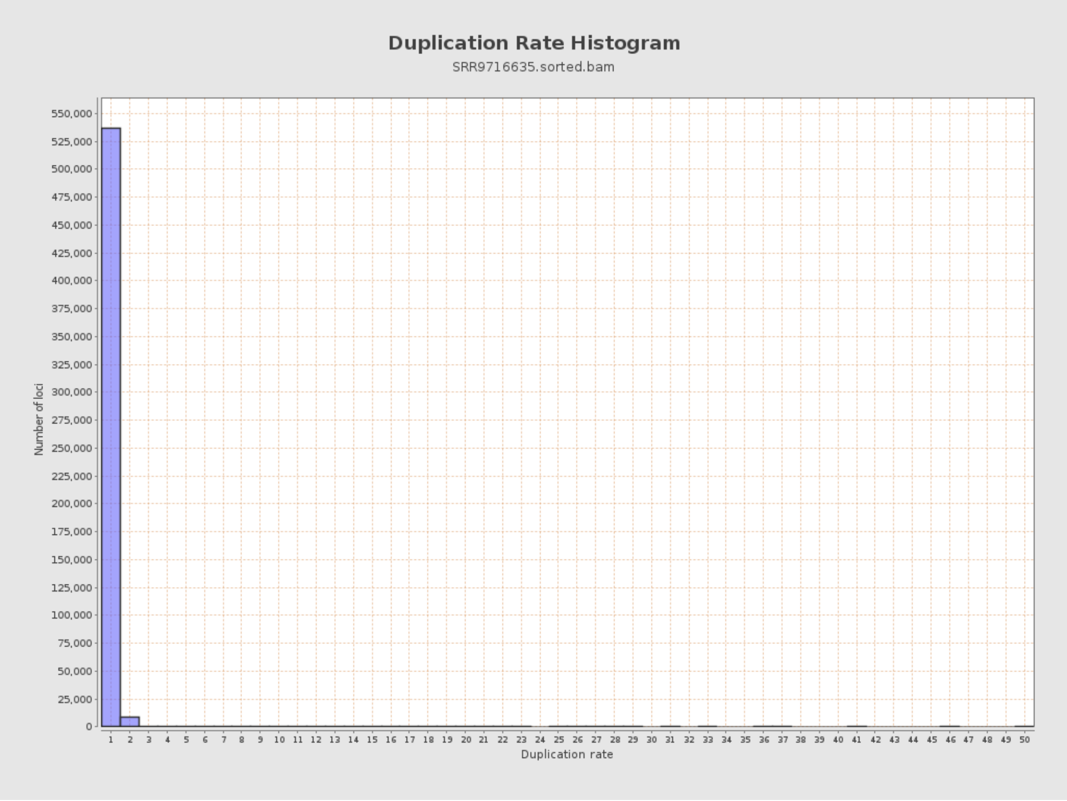
5. Results : Coverage Histogram (0-50X)



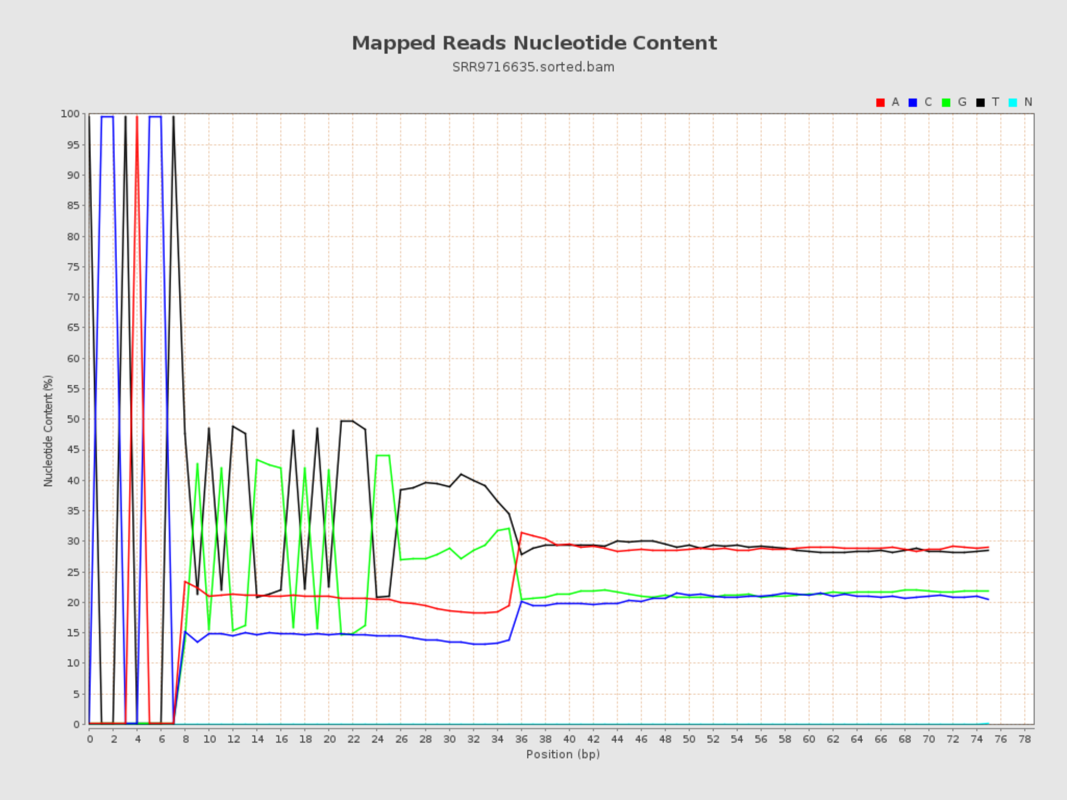
6. Results : Genome Fraction Coverage



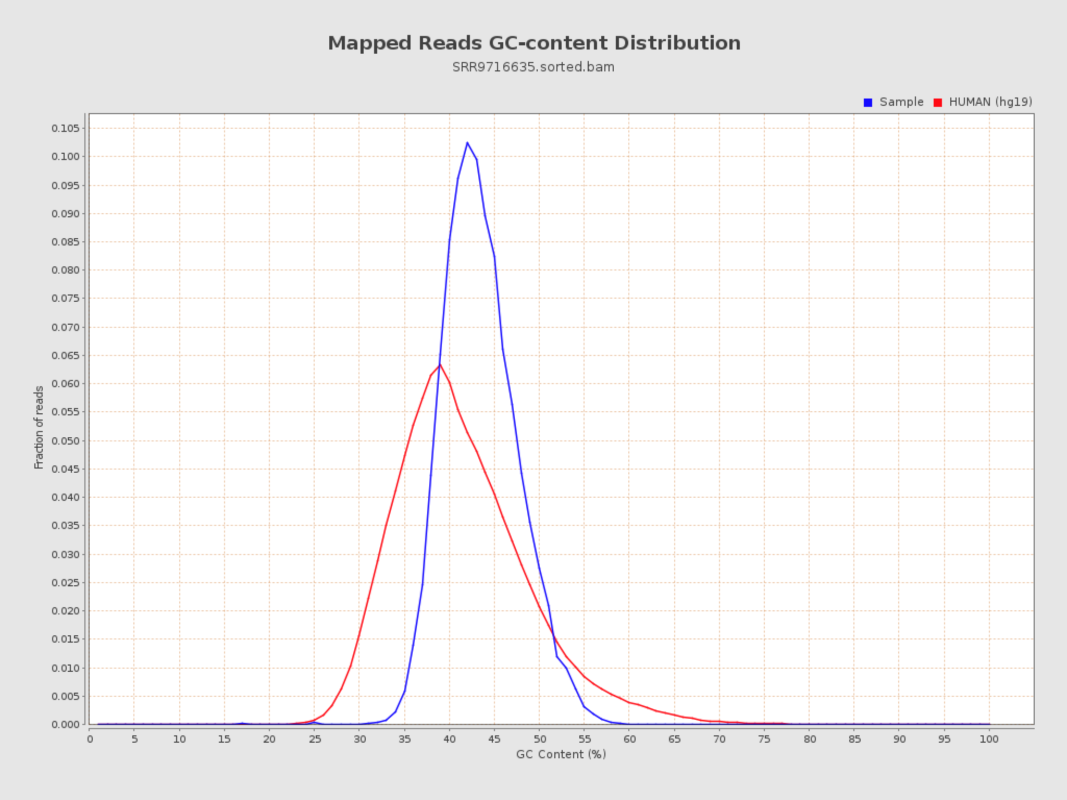
7. Results : Duplication Rate Histogram



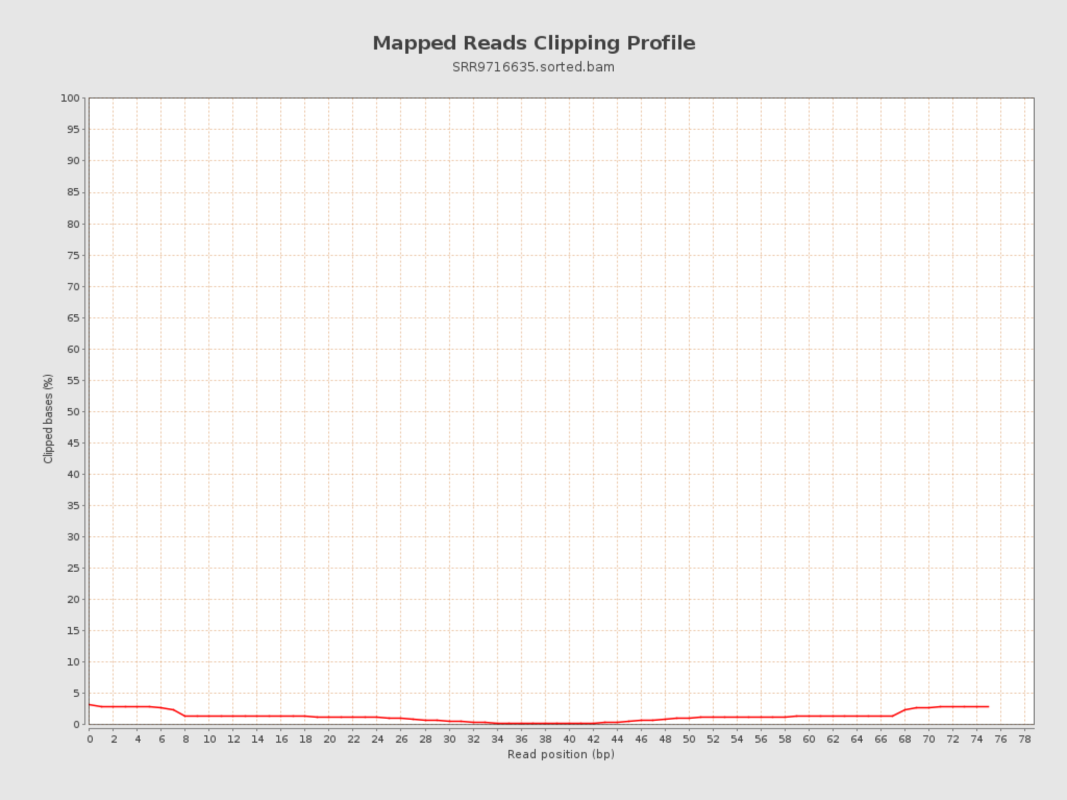
8. Results : Mapped Reads Nucleotide Content



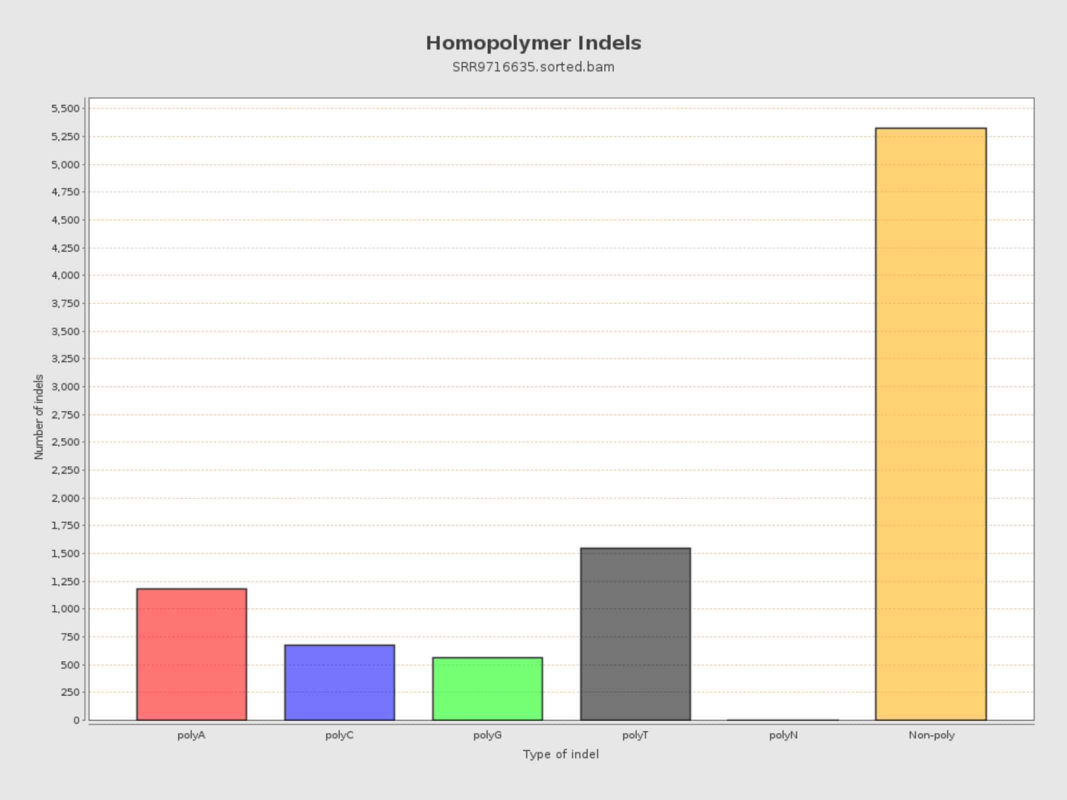
9. Results : Mapped Reads GC-content Distribution



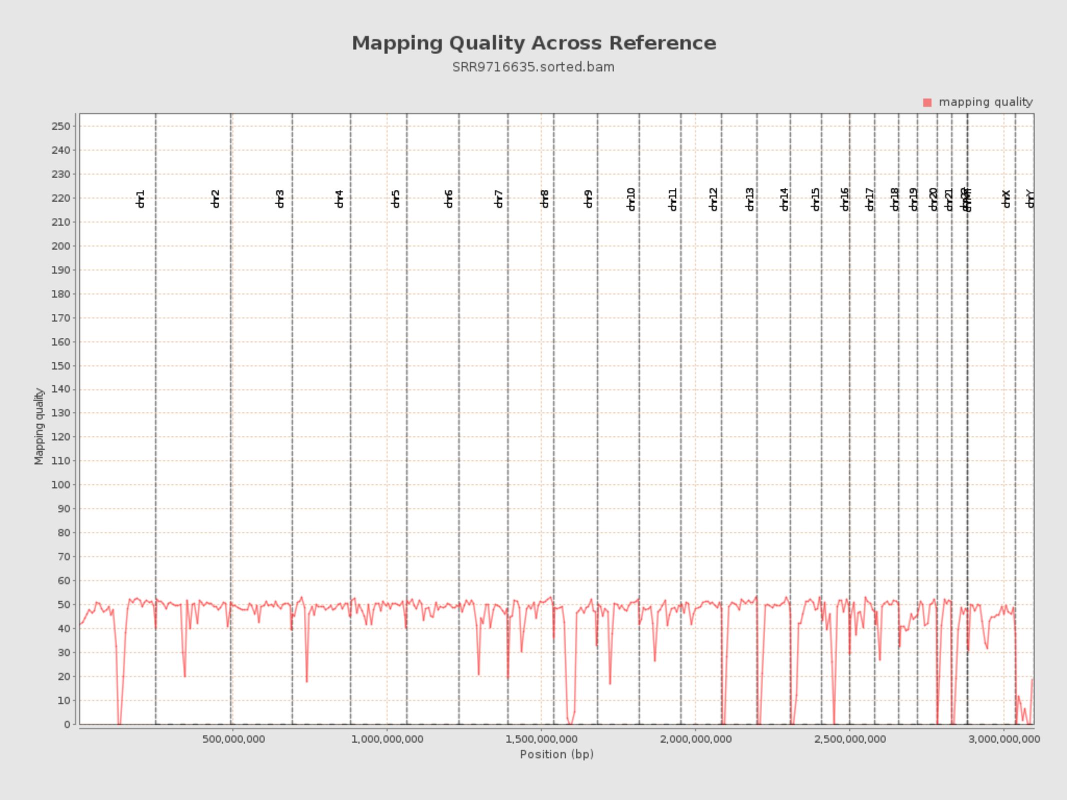
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram