Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:50:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716682.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_SRR9716682 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716682.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:50:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716682.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	727,339
Mapped reads	632,566 / 86.97%
Unmapped reads	94,773 / 13.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,039 / 0.28%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	9,822 / 1.35%
Duplication rate	1.08%
Clipped reads	632,903 / 87.02%

2.2. ACGT Content

Number/percentage of A's	8,386,203 / 23.48%
Number/percentage of C's	6,510,392 / 18.23%
Number/percentage of T's	11,720,165 / 32.82%
Number/percentage of G's	9,093,099 / 25.46%
Number/percentage of N's	293 / 0%
GC Percentage	43.69%

2.3. Coverage

Mean	0.0115

Standard Deviation	0.1296

2.4. Mapping Quality

Mean Mapping Quality	42.45

2.5. Mismatches and indels

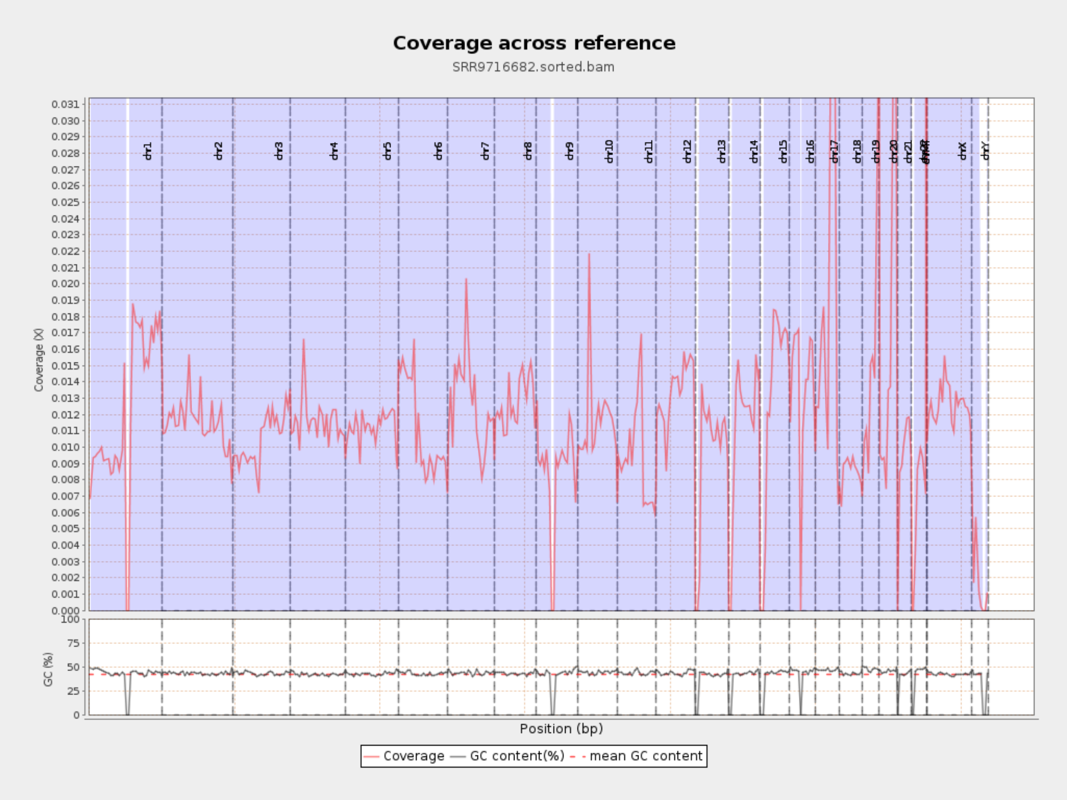
General error rate	0.53%
Mismatches	185,011
Insertions	2,599
Mapped reads with at least one insertion	0.41%
Deletions	6,851
Mapped reads with at least one deletion	1.07%
Homopolymer indels	42.57%

2.6. Chromosome stats

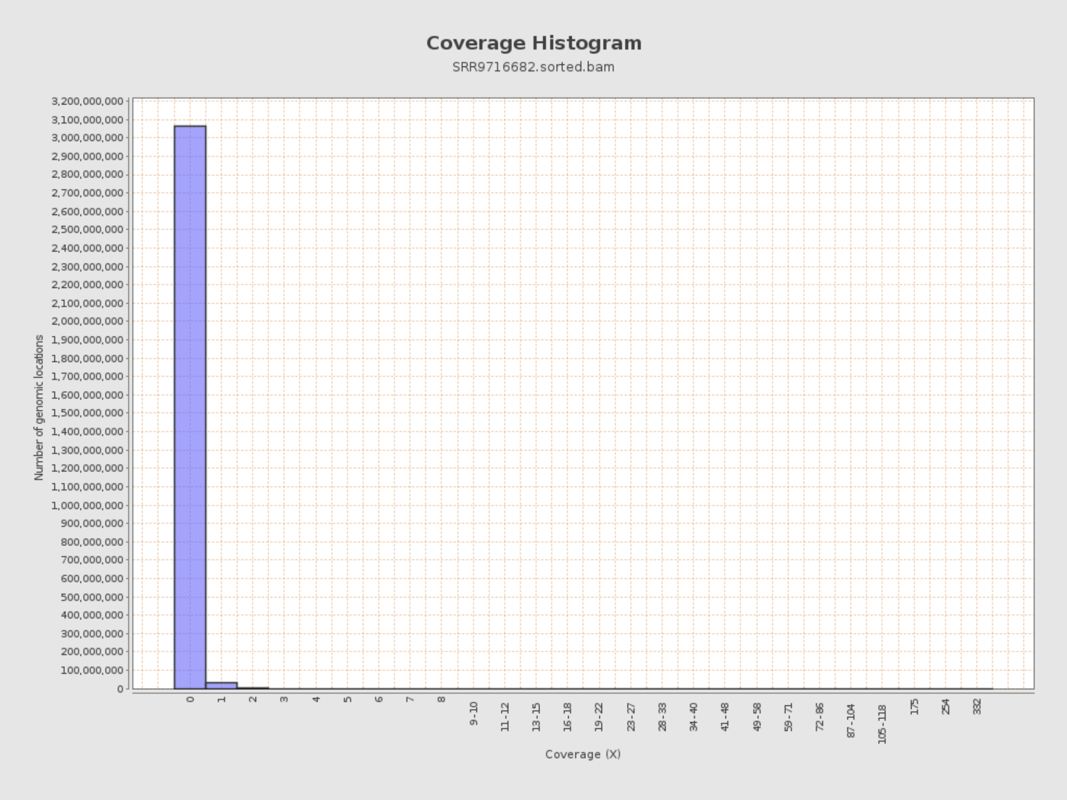
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3006269	0.0121	0.1508
chr2	243199373	2808629	0.0115	0.1757
chr3	198022430	2072390	0.0105	0.1078
chr4	191154276	2216528	0.0116	0.1145
chr5	180915260	2029753	0.0112	0.1094
chr6	171115067	1907247	0.0111	0.1189
chr7	159138663	2040090	0.0128	0.1661

chr8	146364022	1869841	0.0128	0.1294
chr9	141213431	1170327	0.0083	0.101
chr10	135534747	1588598	0.0117	0.1463
chr11	135006516	1269492	0.0094	0.1124
chr12	133851895	1792267	0.0134	0.1201
chr13	115169878	1095065	0.0095	0.1011
chr14	107349540	1190388	0.0111	0.1114
chr15	102531392	1310397	0.0128	0.1186
chr16	90354753	1230772	0.0136	0.1253
chr17	81195210	1560873	0.0192	0.147
chr18	78077248	666624	0.0085	0.1381
chr19	59128983	933870	0.0158	0.1506
chr20	63025520	1131001	0.0179	0.1414
chr21	48129895	442667	0.0092	0.1026
chr22	51304566	320512	0.0062	0.0821
chrMT	16571	3405	0.2055	0.4382
chrX	155270560	1959362	0.0126	0.1212
chrY	59373566	104586	0.0018	0.0604

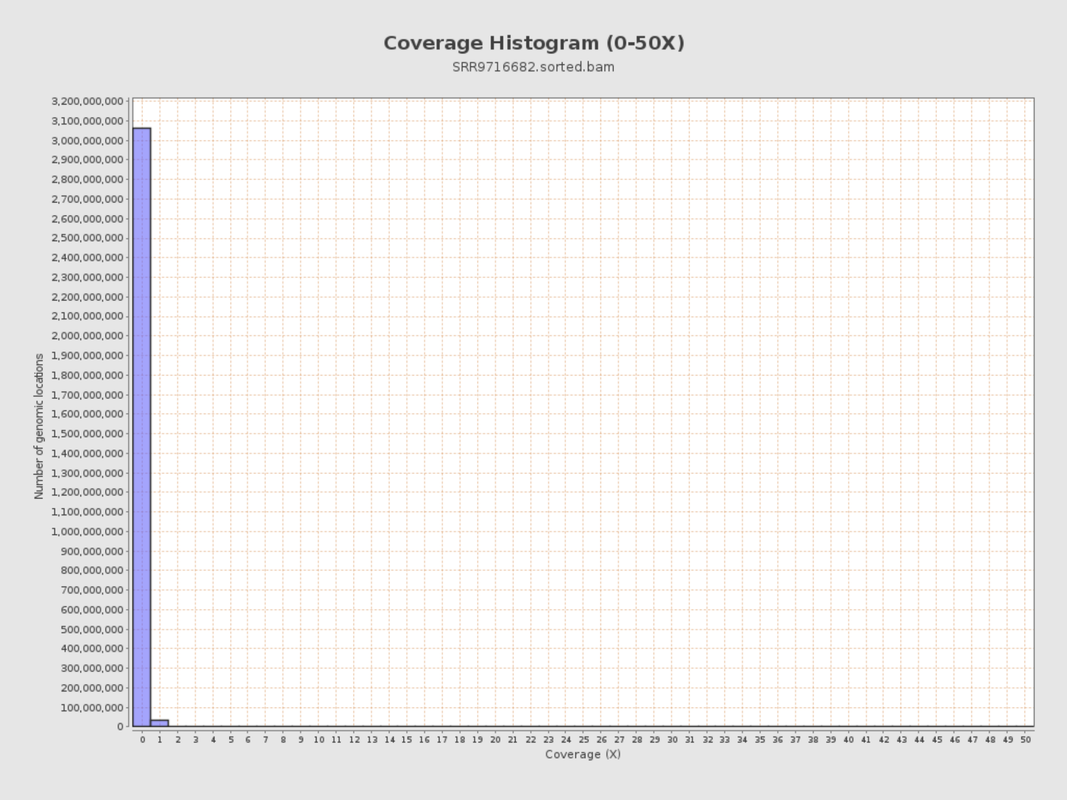
3. Results : Coverage across reference



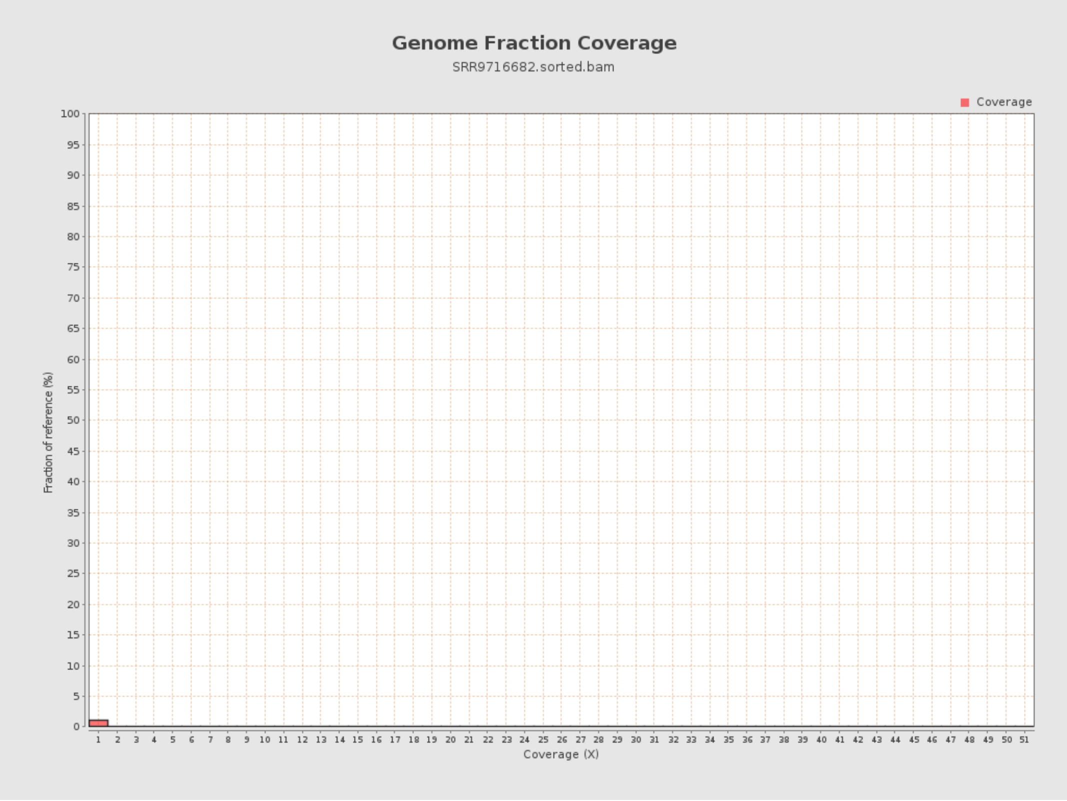
4. Results : Coverage Histogram



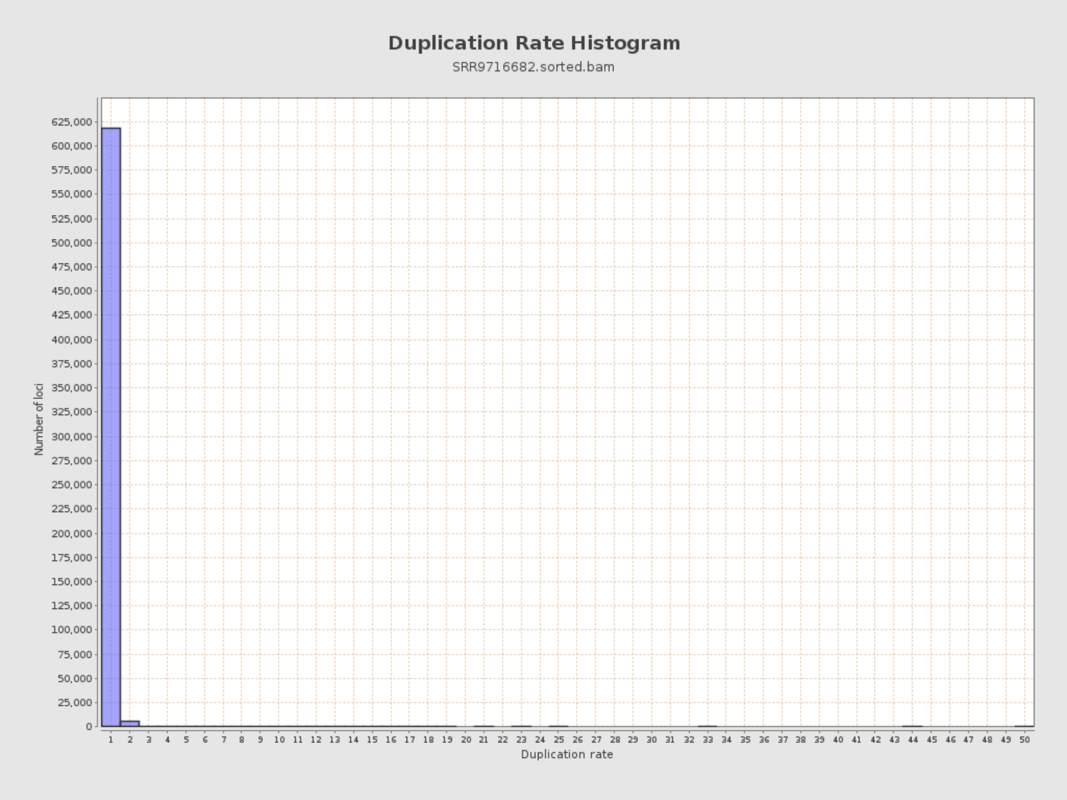
5. Results : Coverage Histogram (0-50X)



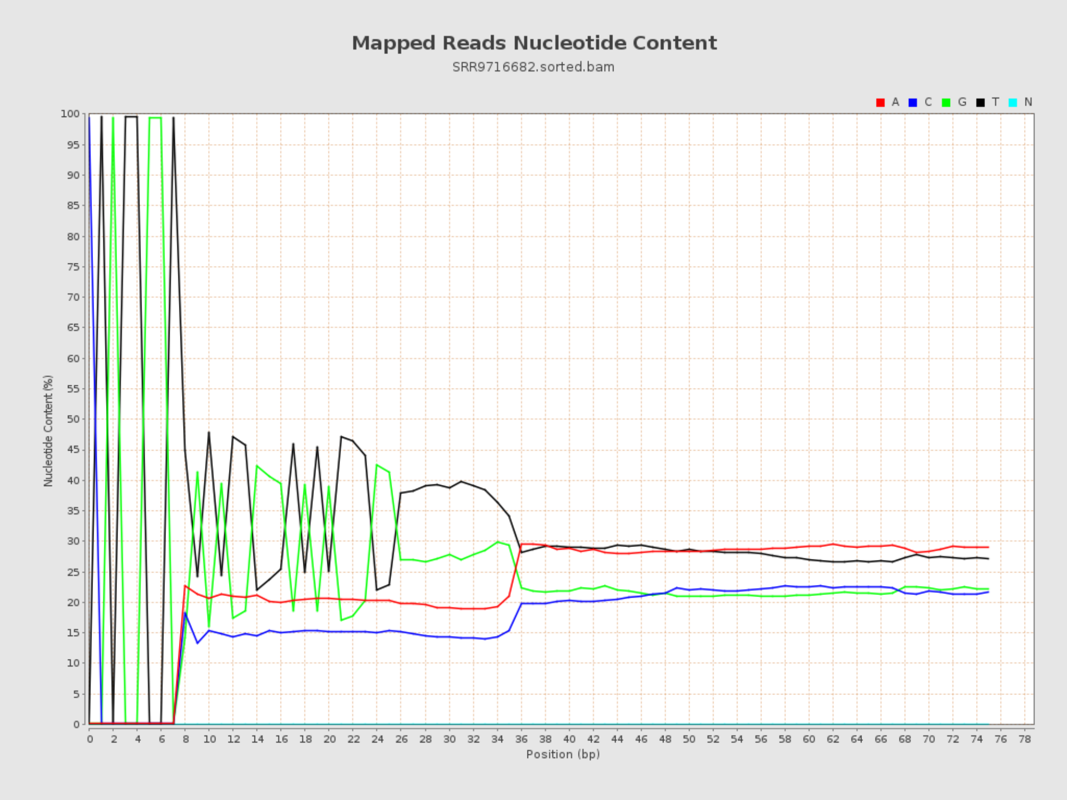
6. Results : Genome Fraction Coverage



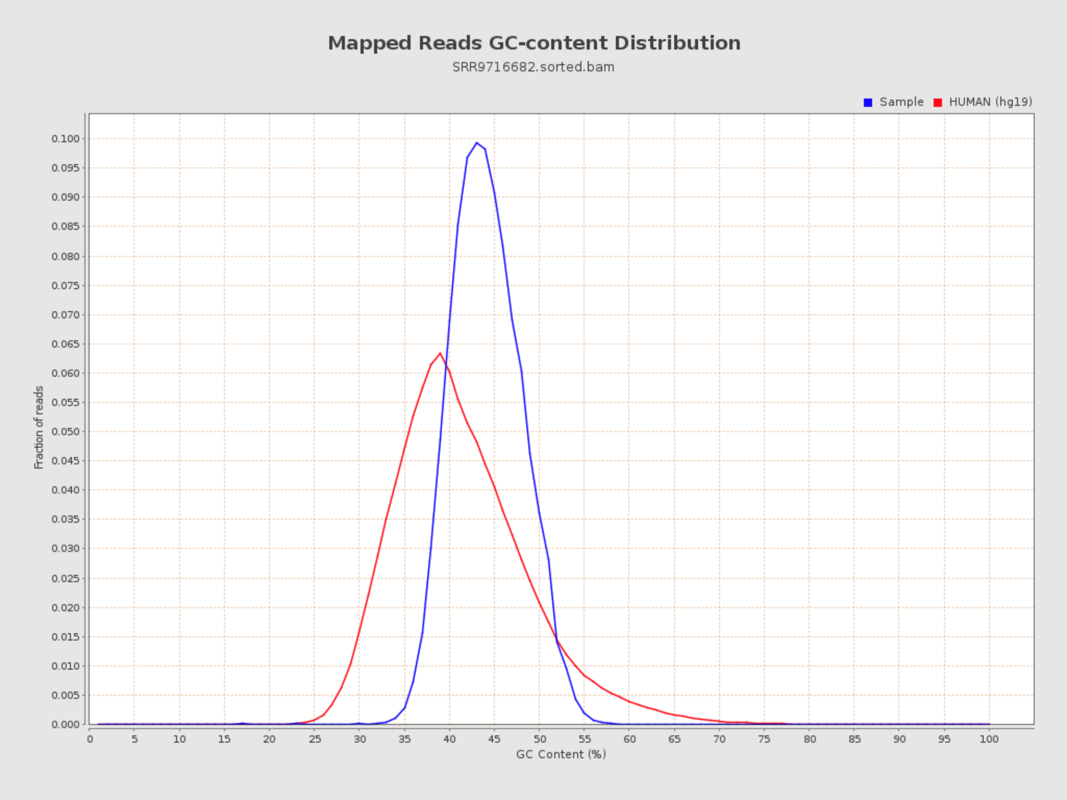
7. Results : Duplication Rate Histogram



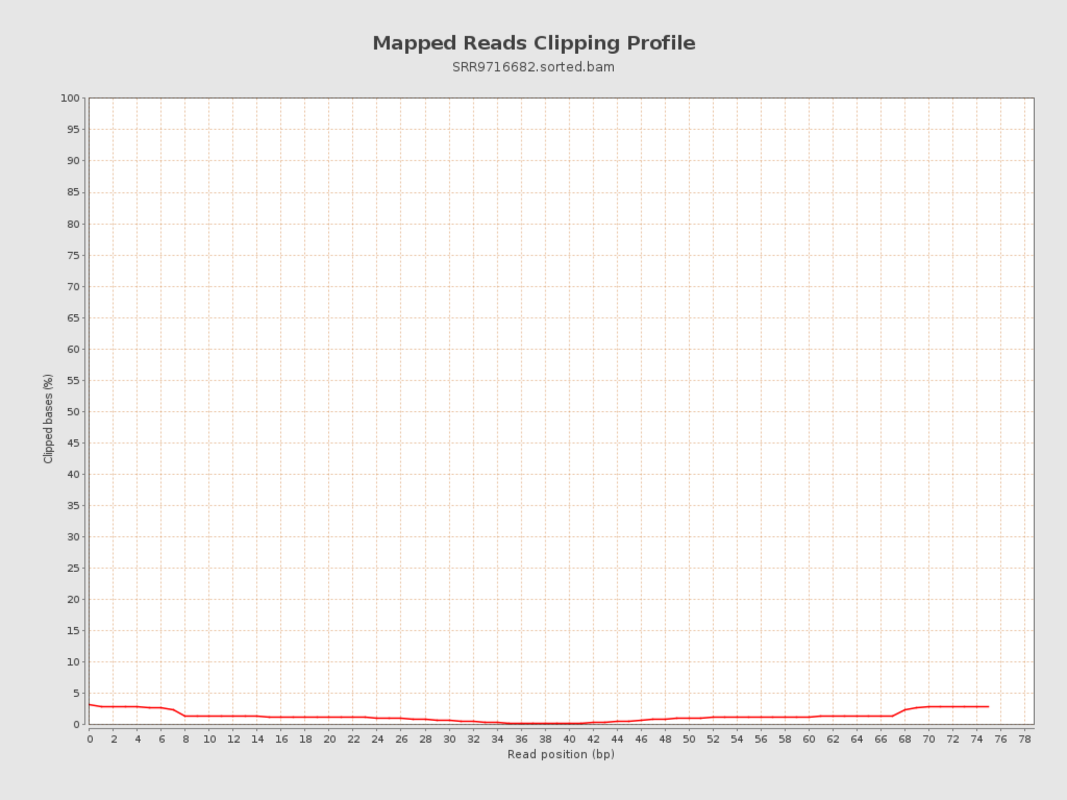
8. Results : Mapped Reads Nucleotide Content



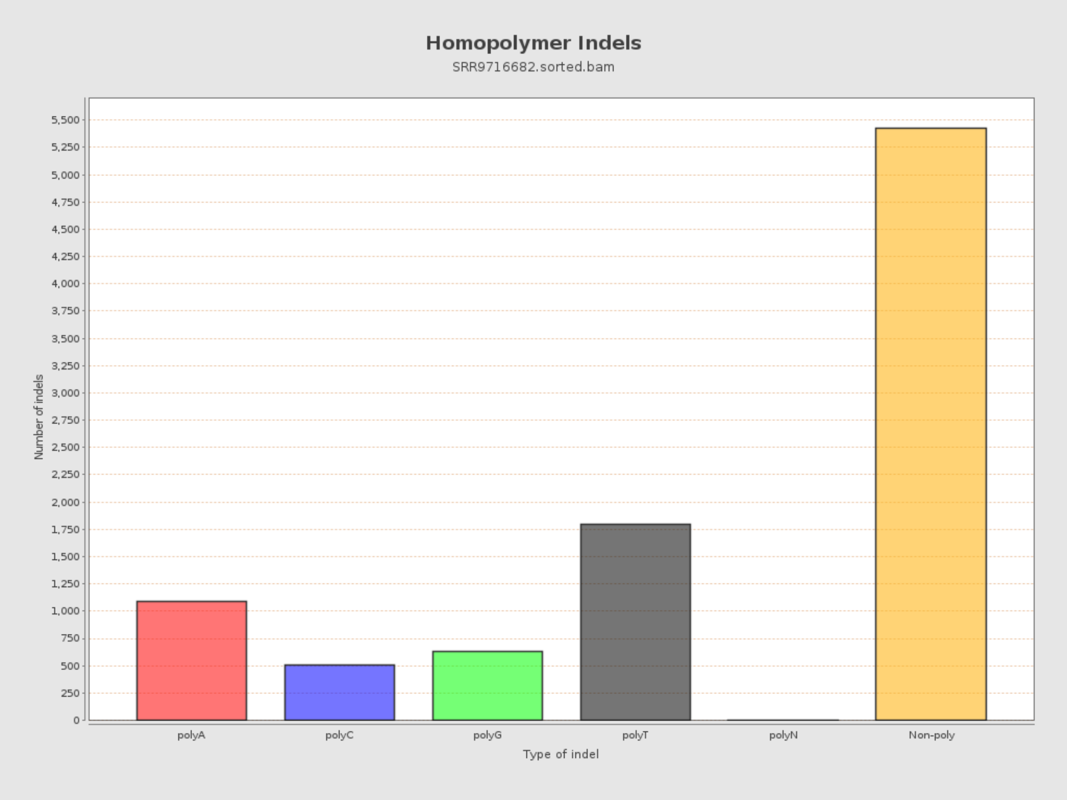
9. Results : Mapped Reads GC-content Distribution



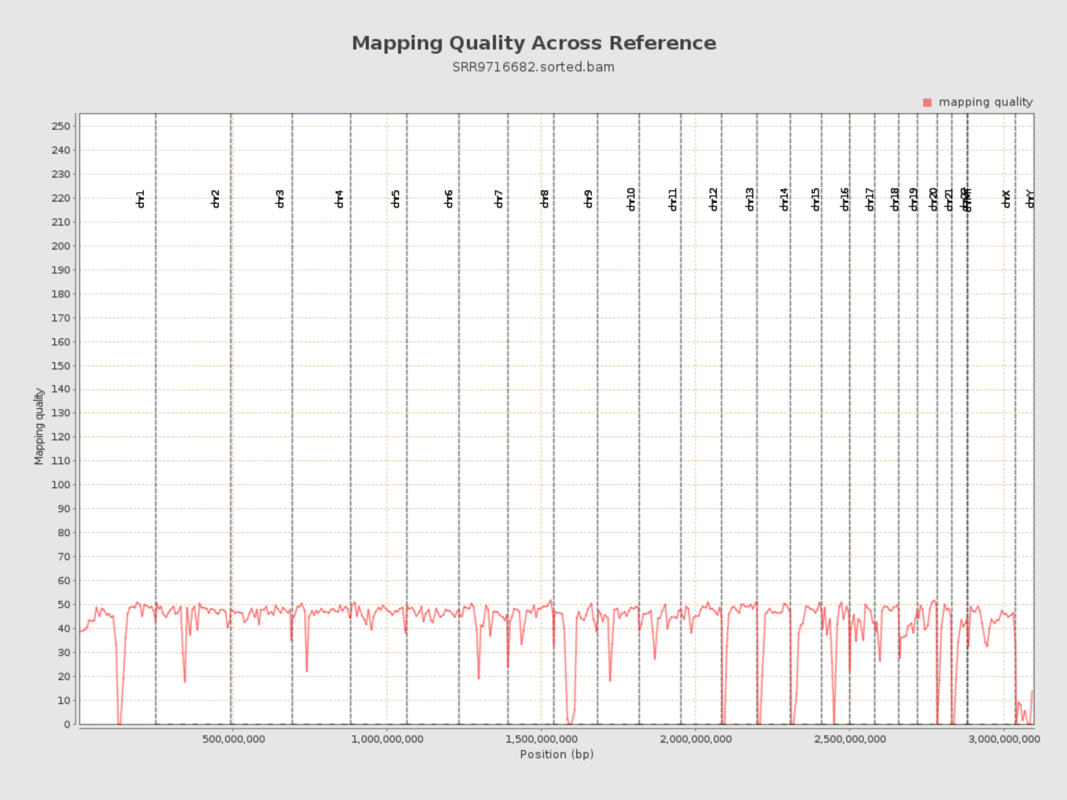
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram