Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 05:46:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716681.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_SRR9716681 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716681.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 05:46:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716681.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	588,811
Mapped reads	491,558 / 83.48%
Unmapped reads	97,253 / 16.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,848 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	6,940 / 1.18%
Duplication rate	0.98%
Clipped reads	491,978 / 83.55%

2.2. ACGT Content

Number/percentage of A's	6,934,545 / 24.94%
Number/percentage of C's	5,117,226 / 18.41%
Number/percentage of T's	8,644,060 / 31.09%
Number/percentage of G's	7,106,730 / 25.56%
Number/percentage of N's	202 / 0%
GC Percentage	43.97%

2.3. Coverage

Mean	0.009

Standard Deviation	0.1114

2.4. Mapping Quality

Mean Mapping Quality	41.67

2.5. Mismatches and indels

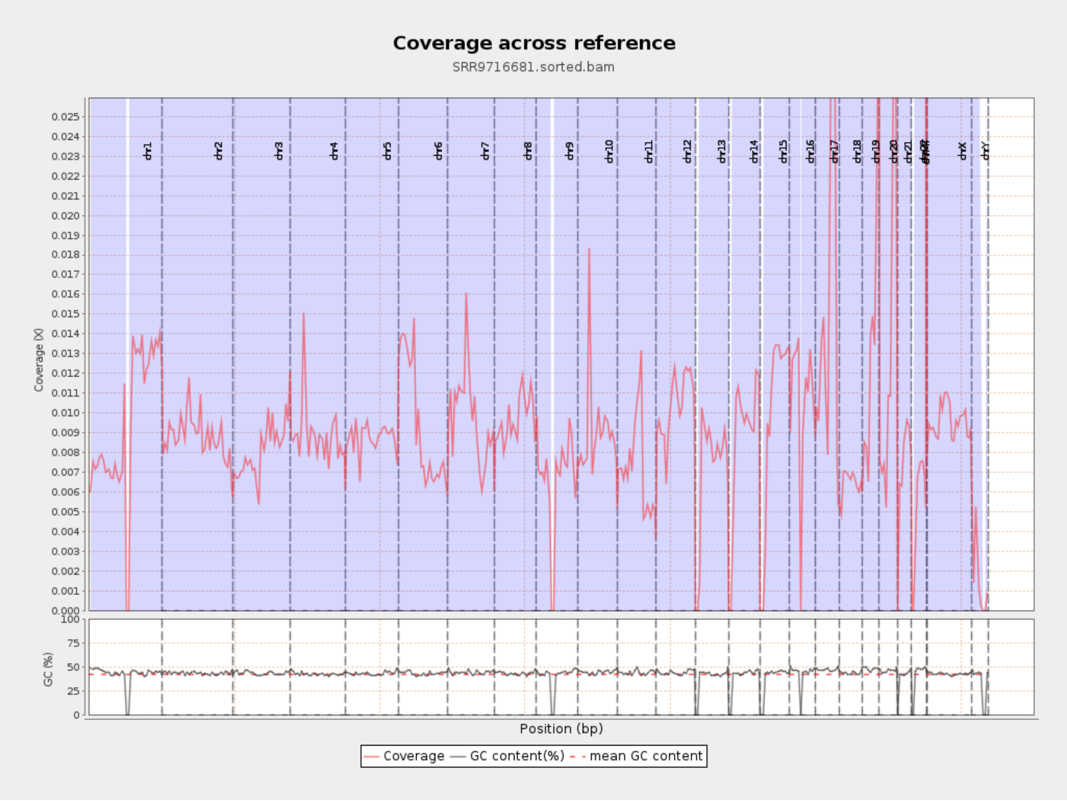
General error rate	0.54%
Mismatches	146,855
Insertions	2,381
Mapped reads with at least one insertion	0.48%
Deletions	5,682
Mapped reads with at least one deletion	1.14%
Homopolymer indels	38.39%

2.6. Chromosome stats

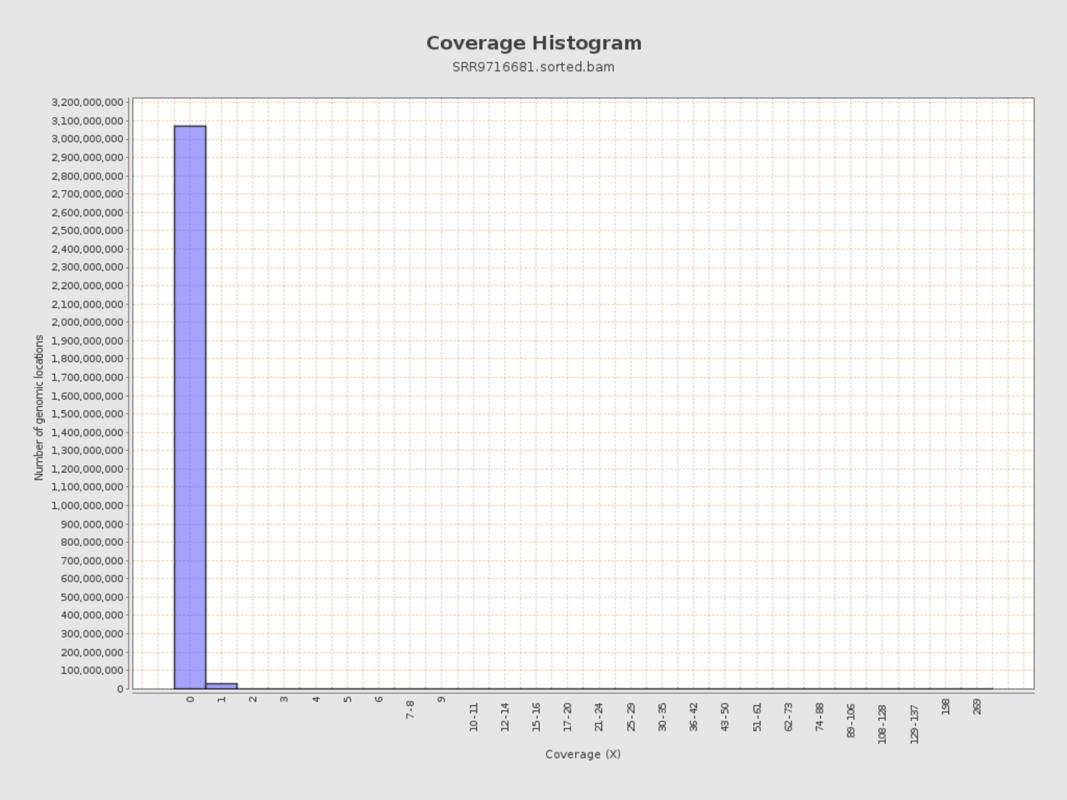
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2326225	0.0093	0.1305
chr2	243199373	2149577	0.0088	0.1451
chr3	198022430	1595050	0.0081	0.0937
chr4	191154276	1690915	0.0088	0.1008
chr5	180915260	1580175	0.0087	0.0958
chr6	171115067	1609787	0.0094	0.1081
chr7	159138663	1568885	0.0099	0.1364

chr8	146364022	1419547	0.0097	0.1092
chr9	141213431	922158	0.0065	0.0882
chr10	135534747	1223404	0.009	0.1229
chr11	135006516	984356	0.0073	0.0966
chr12	133851895	1394034	0.0104	0.1054
chr13	115169878	823322	0.0071	0.087
chr14	107349540	925735	0.0086	0.0972
chr15	102531392	1000807	0.0098	0.1029
chr16	90354753	969316	0.0107	0.1104
chr17	81195210	1231268	0.0152	0.1295
chr18	78077248	503728	0.0065	0.1117
chr19	59128983	813522	0.0138	0.1405
chr20	63025520	876140	0.0139	0.1234
chr21	48129895	350089	0.0073	0.091
chr22	51304566	256377	0.005	0.073
chrMT	16571	26386	1.5923	1.6387
chrX	155270560	1481025	0.0095	0.1032
chrY	59373566	90195	0.0015	0.0549

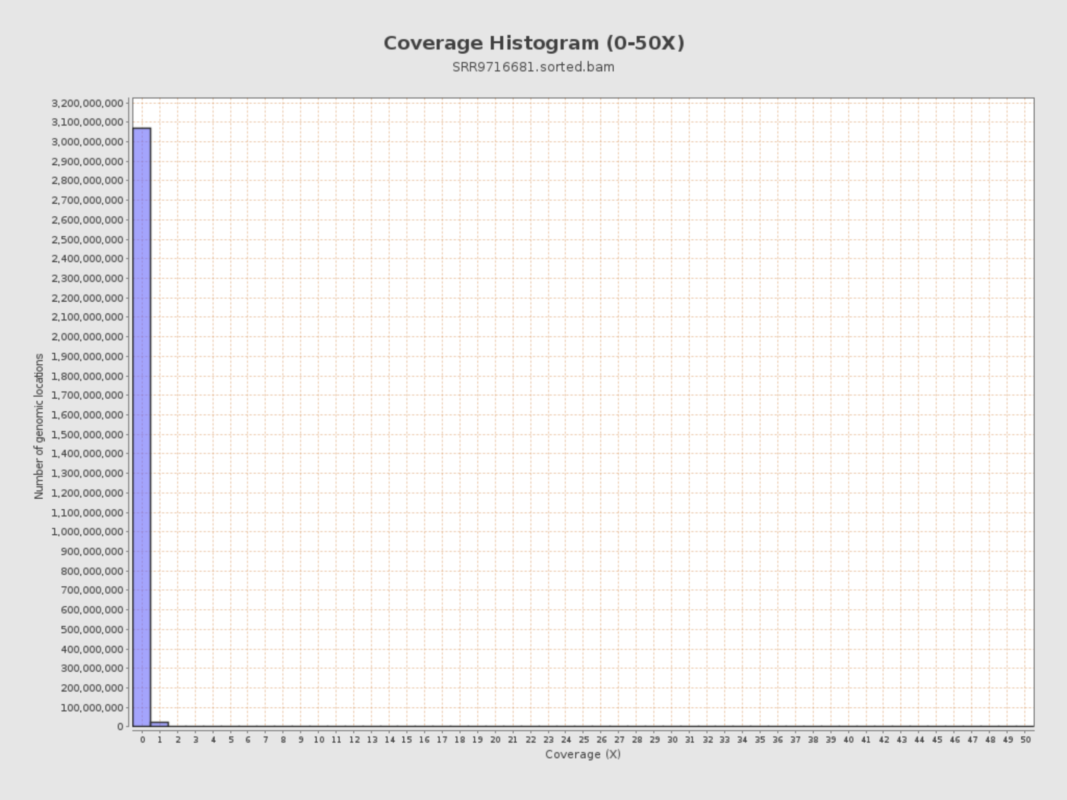
3. Results : Coverage across reference



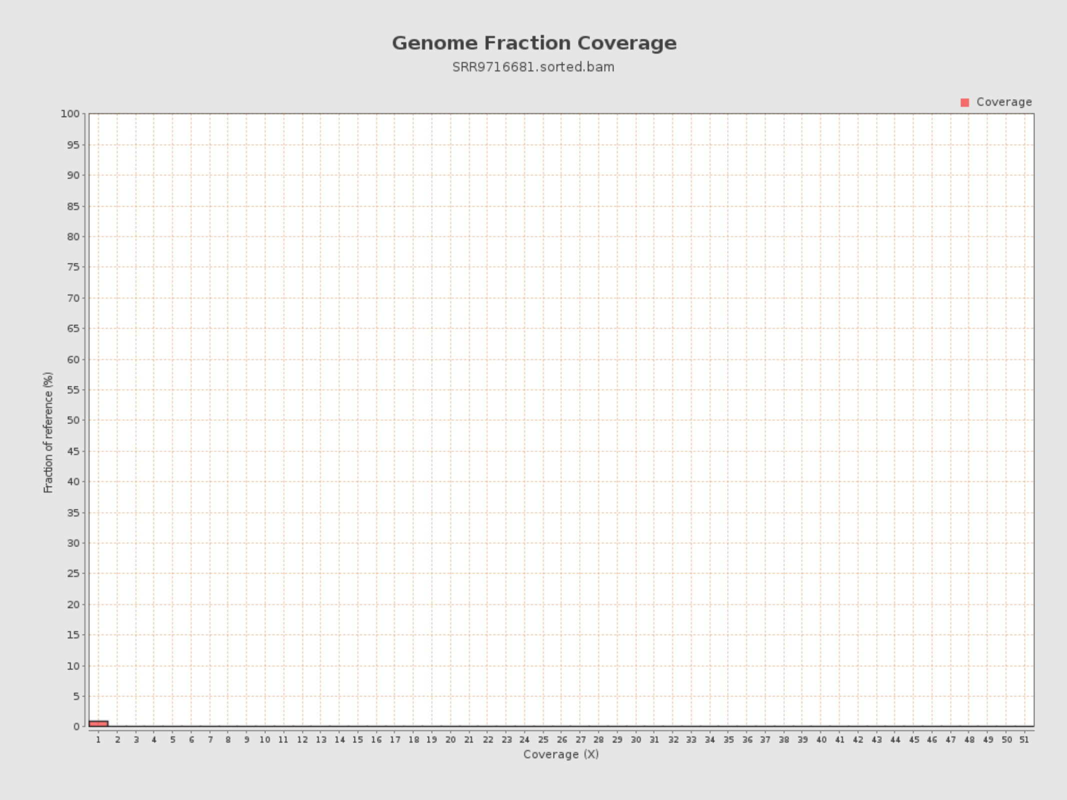
4. Results : Coverage Histogram



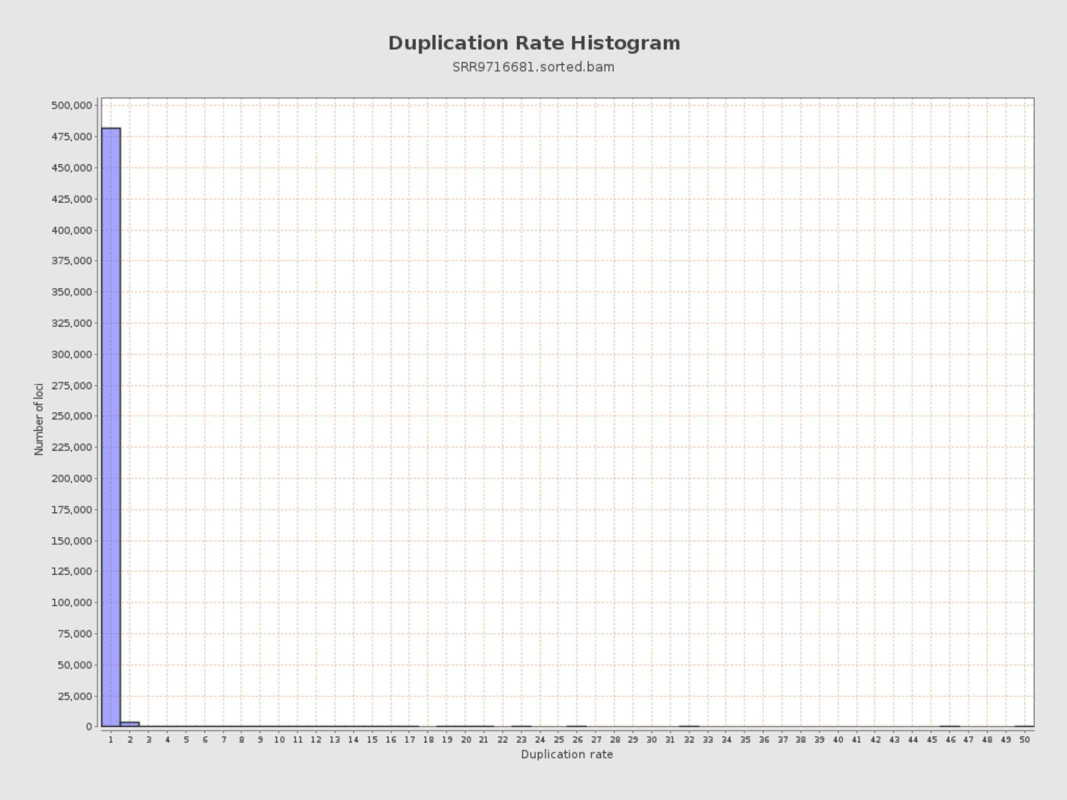
5. Results : Coverage Histogram (0-50X)



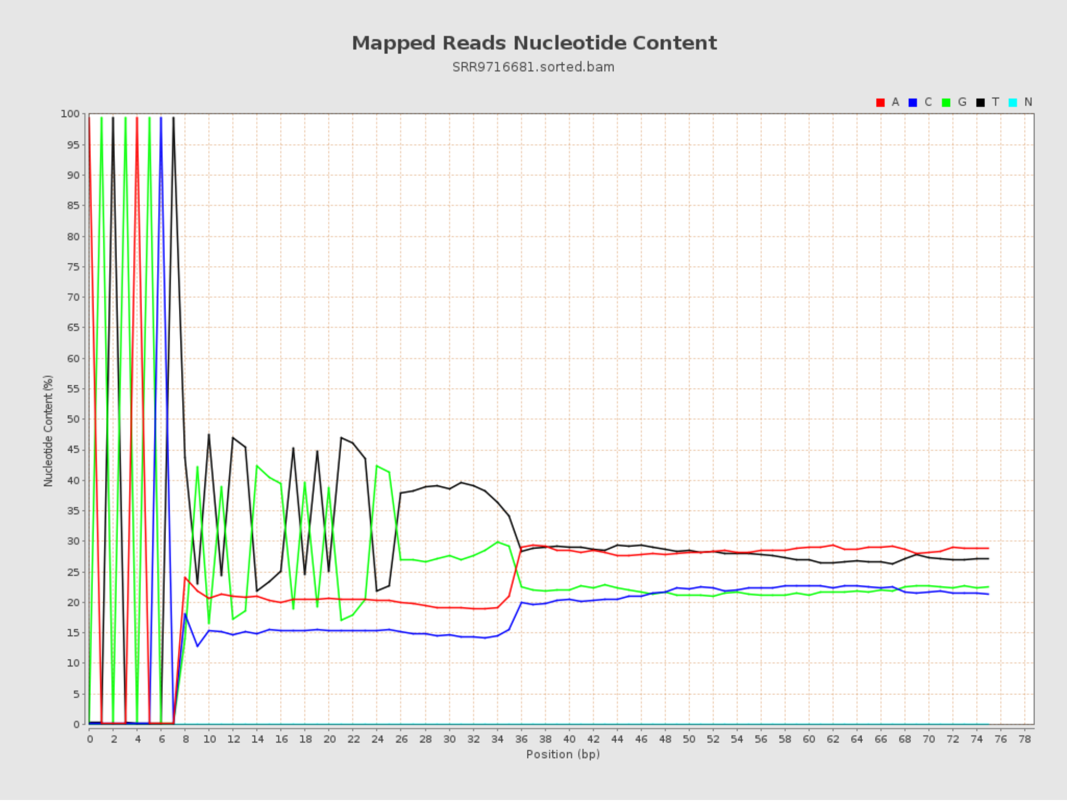
6. Results : Genome Fraction Coverage



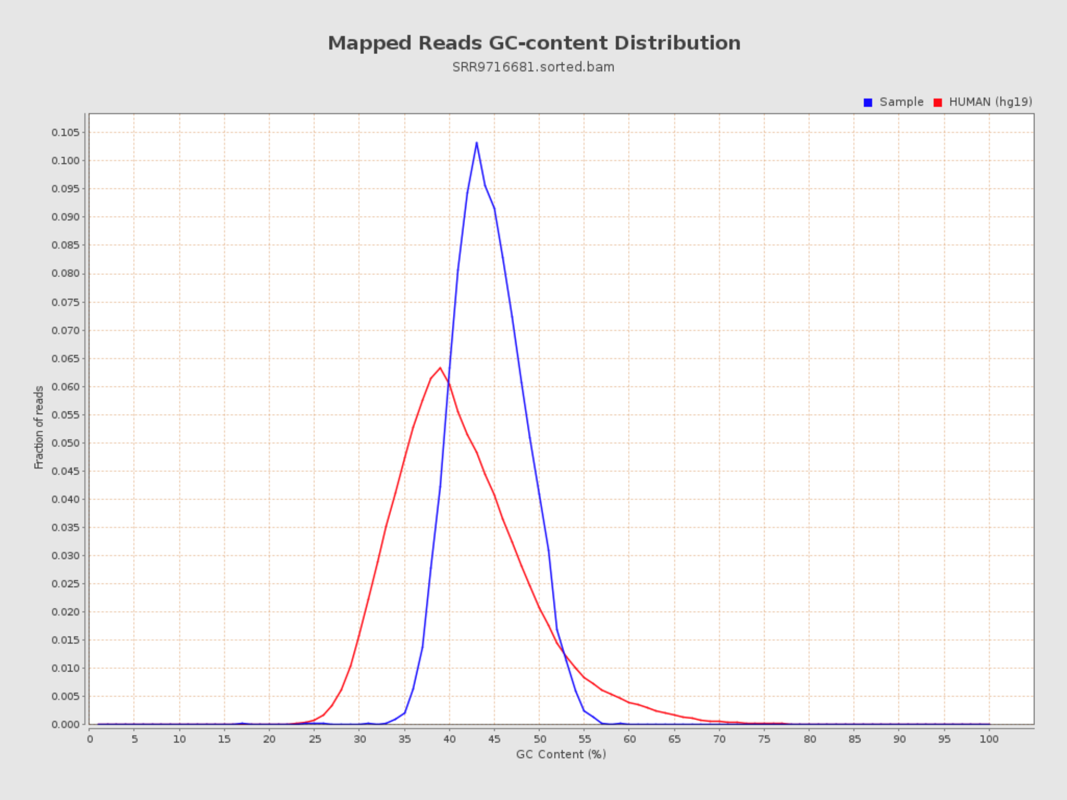
7. Results : Duplication Rate Histogram



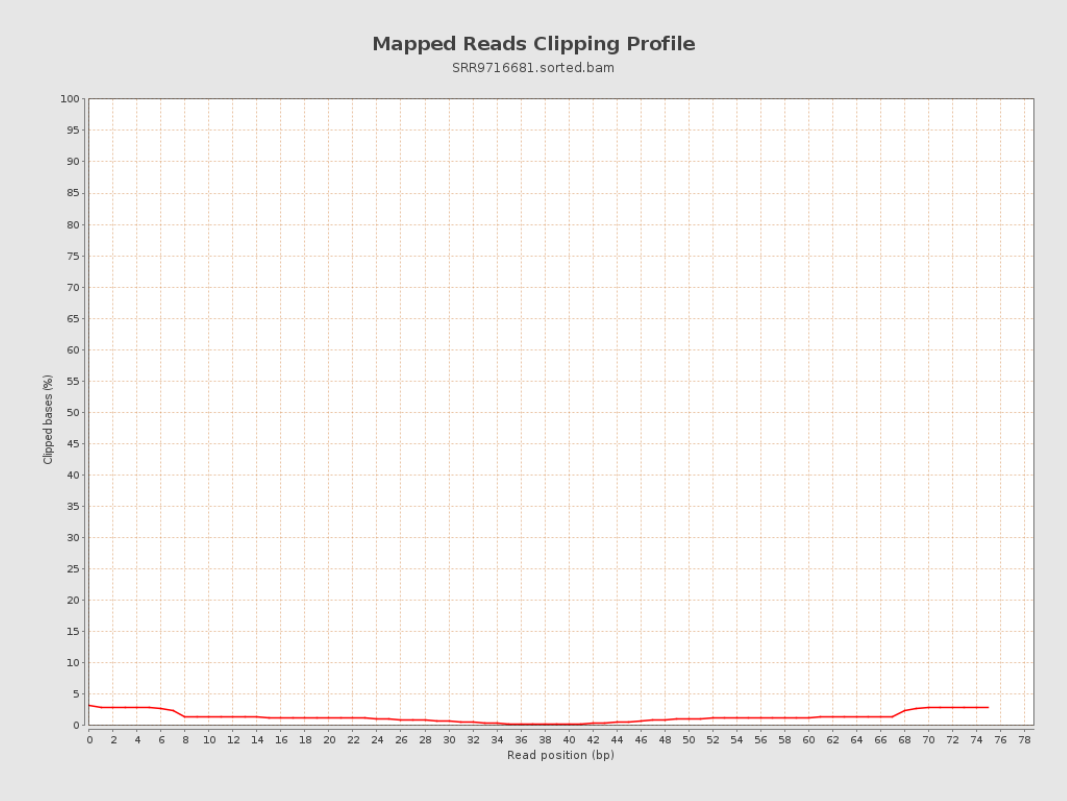
8. Results : Mapped Reads Nucleotide Content



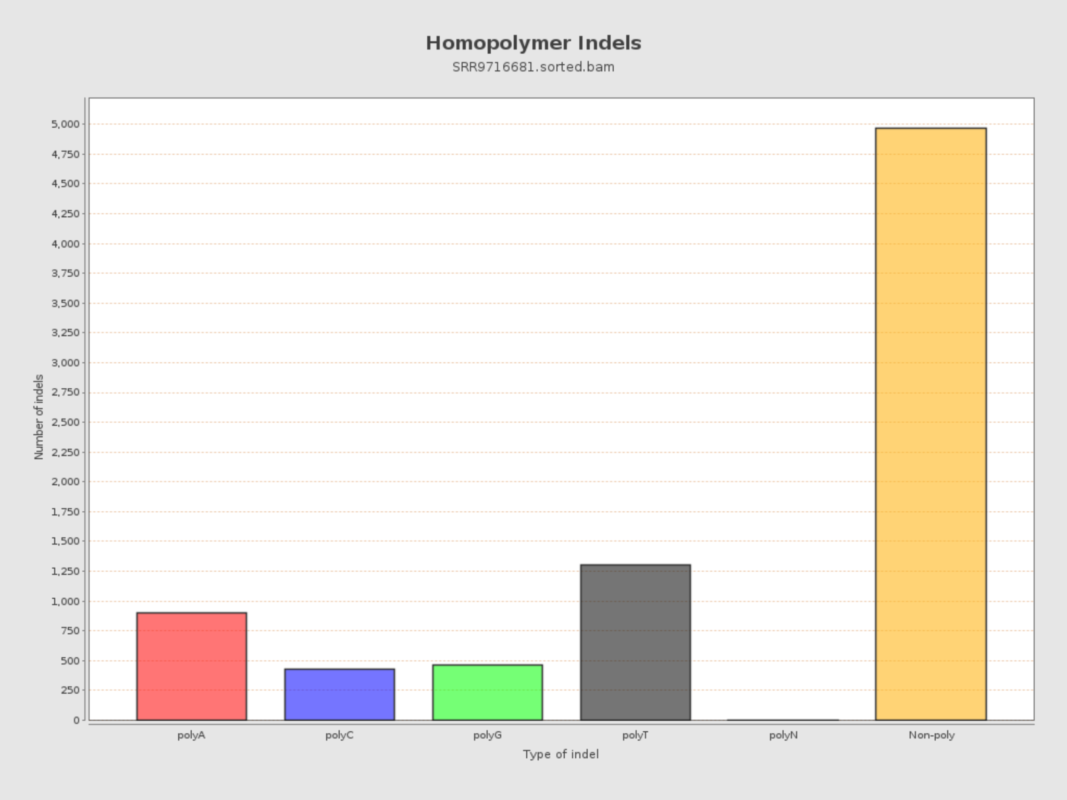
9. Results : Mapped Reads GC-content Distribution



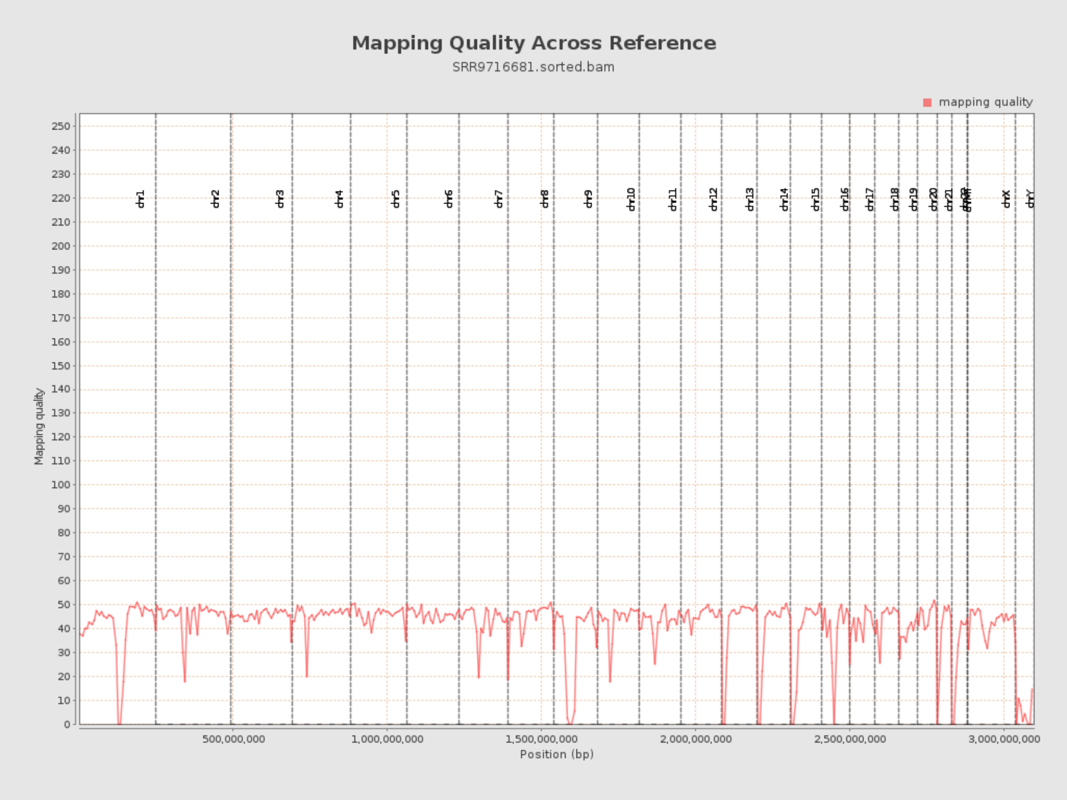
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram