Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 01:49:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716640.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_SRR9716640 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716640.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 01:48:56 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716640.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	620,632
Mapped reads	571,444 / 92.07%
Unmapped reads	49,188 / 7.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,000 / 0.32%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	12,828 / 2.07%
Duplication rate	1.59%
Clipped reads	572,199 / 92.2%

2.2. ACGT Content

Number/percentage of A's	8,036,776 / 24.36%
Number/percentage of C's	6,403,117 / 19.41%
Number/percentage of T's	10,423,064 / 31.6%
Number/percentage of G's	8,123,143 / 24.63%
Number/percentage of N's	710 / 0%
GC Percentage	44.04%

2.3. Coverage

Mean	0.0107

Standard Deviation	0.1307

2.4. Mapping Quality

Mean Mapping Quality	44.38

2.5. Mismatches and indels

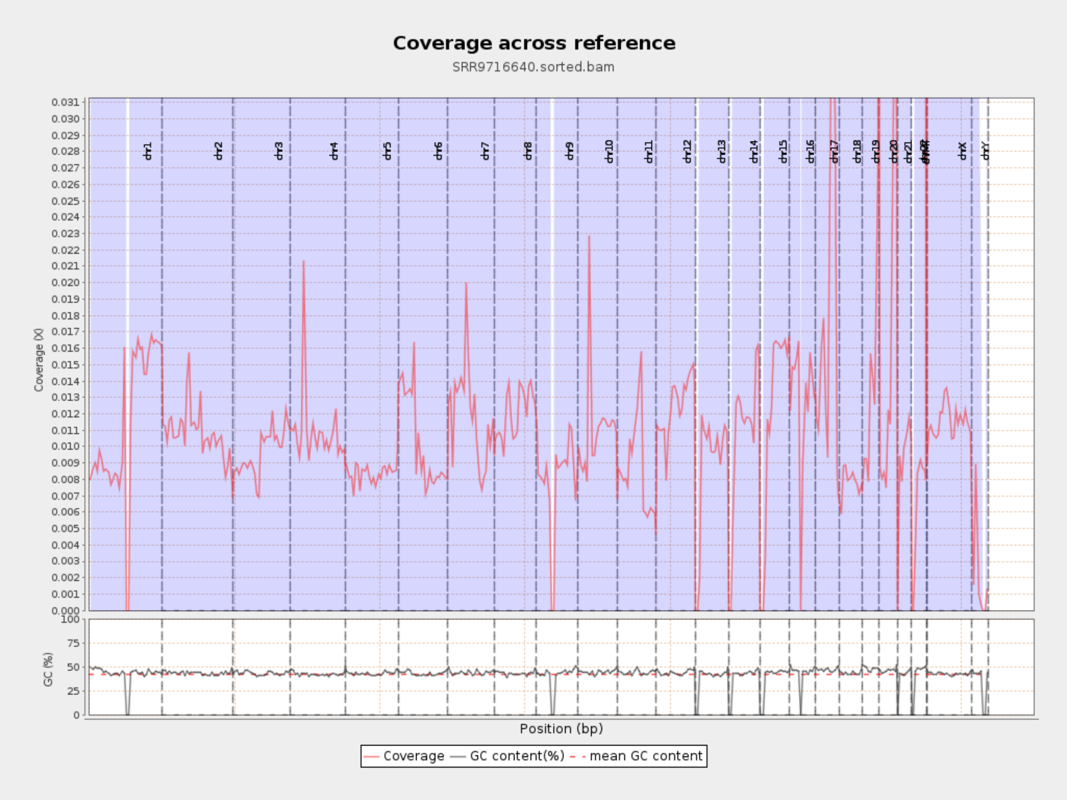
General error rate	0.52%
Mismatches	167,322
Insertions	2,381
Mapped reads with at least one insertion	0.41%
Deletions	6,243
Mapped reads with at least one deletion	1.09%
Homopolymer indels	42.16%

2.6. Chromosome stats

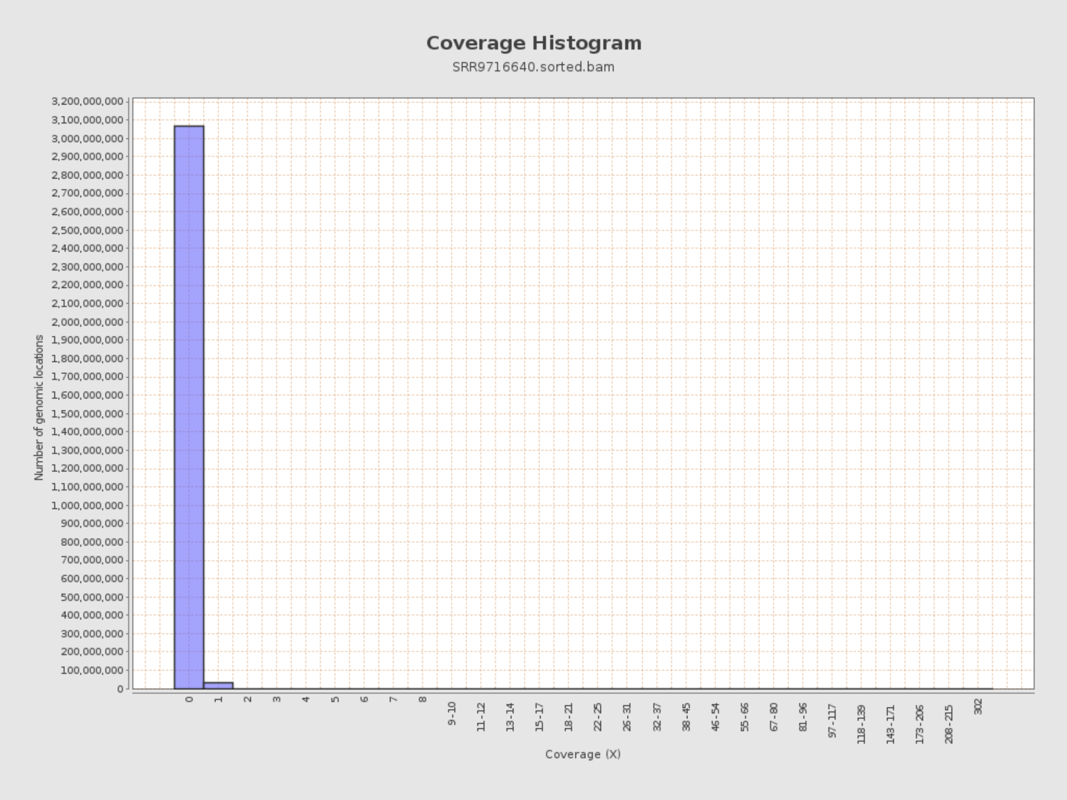
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2828602	0.0113	0.1728
chr2	243199373	2641910	0.0109	0.164
chr3	198022430	1910302	0.0096	0.1023
chr4	191154276	2080064	0.0109	0.1219
chr5	180915260	1510026	0.0083	0.0947
chr6	171115067	1768121	0.0103	0.1142
chr7	159138663	1905023	0.012	0.1582

chr8	146364022	1761606	0.012	0.1698
chr9	141213431	1103642	0.0078	0.1
chr10	135534747	1502699	0.0111	0.1434
chr11	135006516	1182941	0.0088	0.1082
chr12	133851895	1665047	0.0124	0.1156
chr13	115169878	1007799	0.0088	0.097
chr14	107349540	1132803	0.0106	0.1072
chr15	102531392	1219168	0.0119	0.1133
chr16	90354753	1146774	0.0127	0.1206
chr17	81195210	1447501	0.0178	0.1412
chr18	78077248	610106	0.0078	0.1408
chr19	59128983	856387	0.0145	0.1555
chr20	63025520	1048465	0.0166	0.1357
chr21	48129895	437633	0.0091	0.1124
chr22	51304566	315005	0.0061	0.0812
chrMT	16571	7000	0.4224	0.7175
chrX	155270560	1785061	0.0115	0.1144
chrY	59373566	123229	0.0021	0.1034

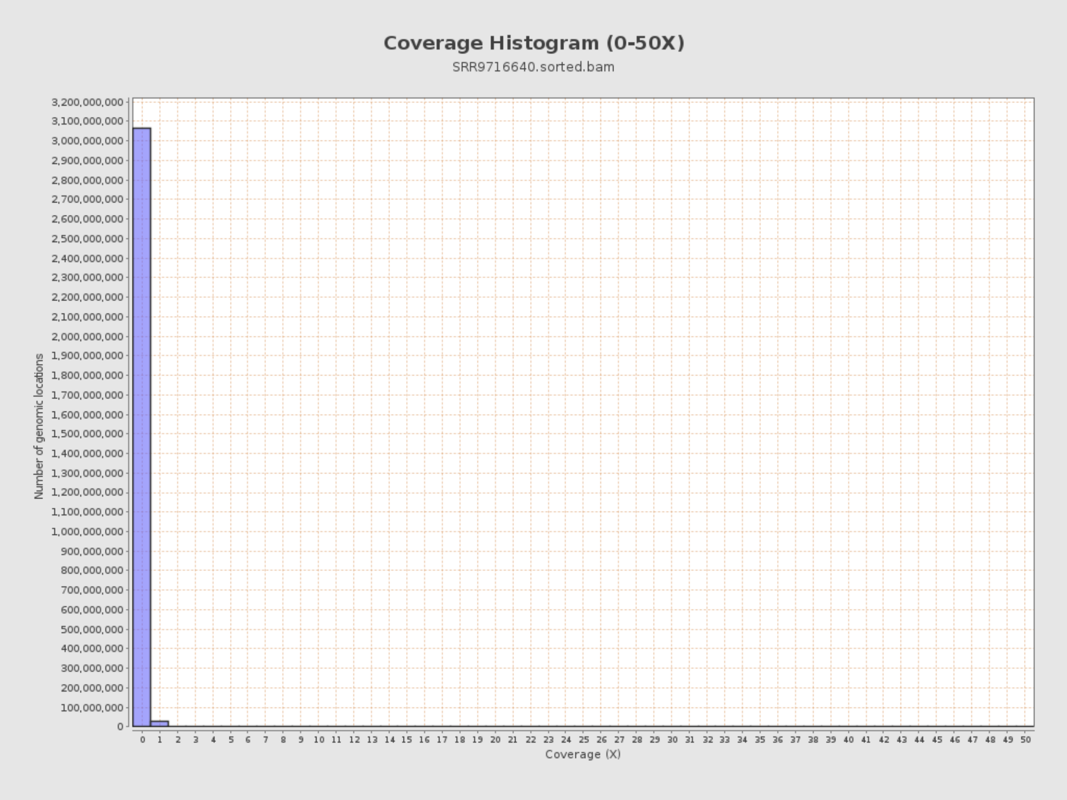
3. Results : Coverage across reference



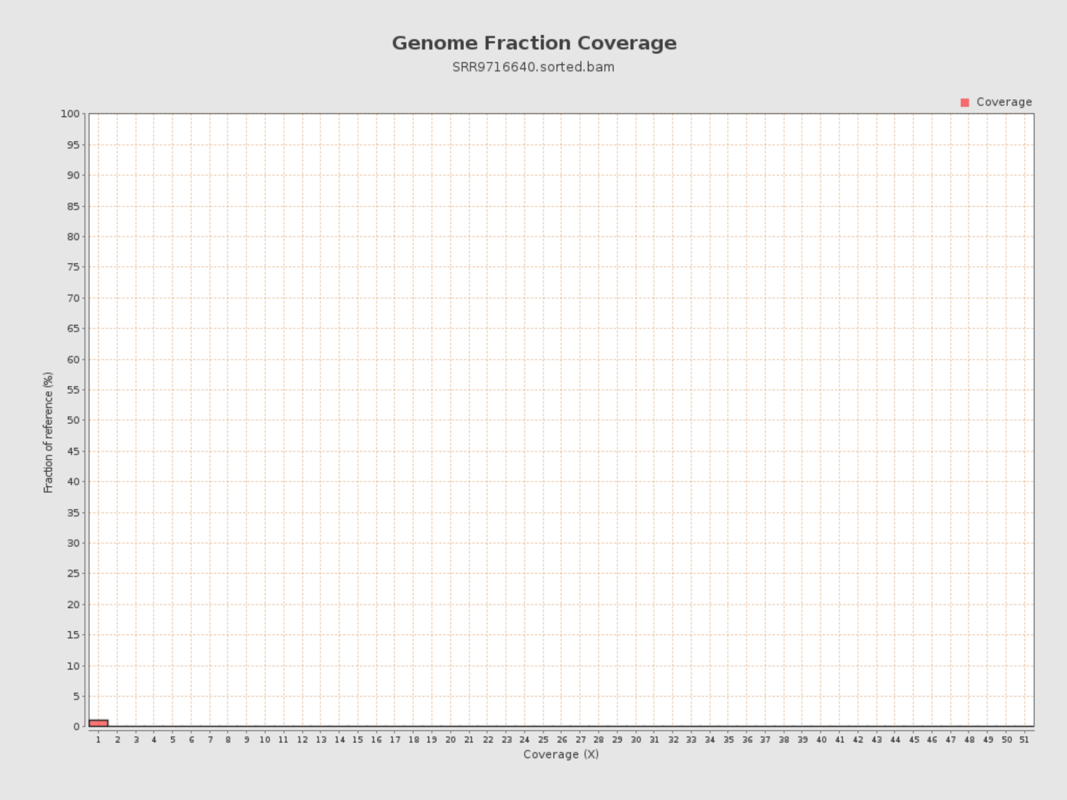
4. Results : Coverage Histogram



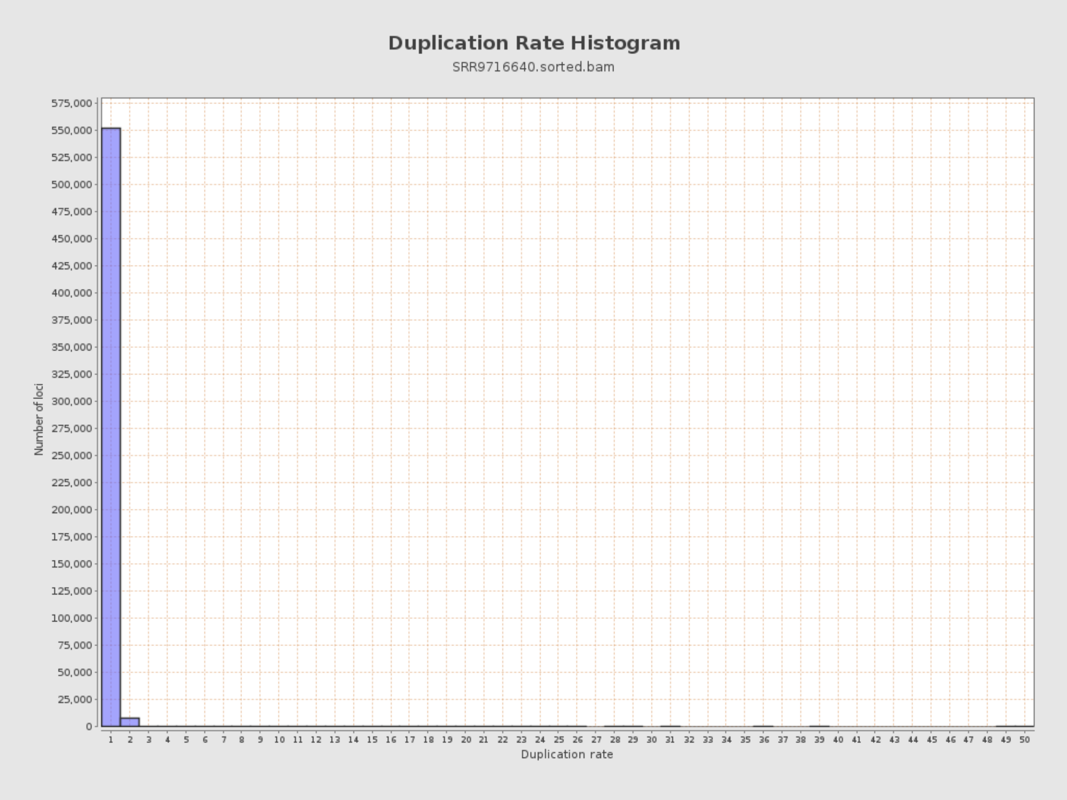
5. Results : Coverage Histogram (0-50X)



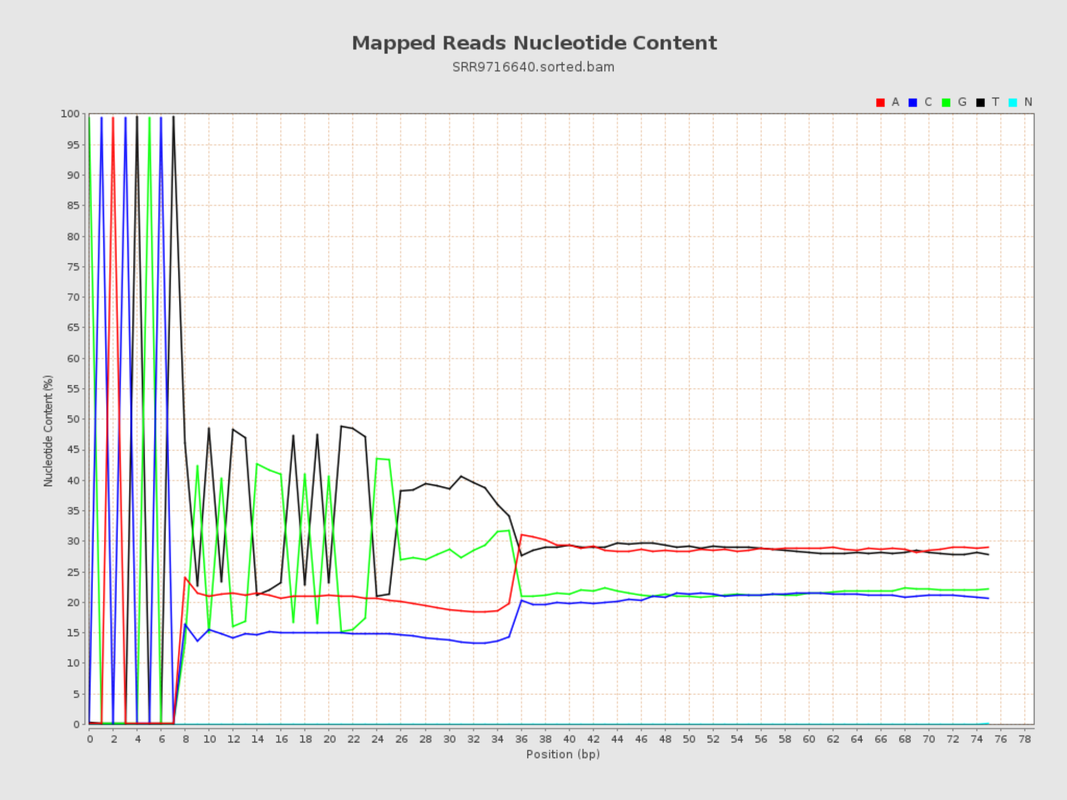
6. Results : Genome Fraction Coverage



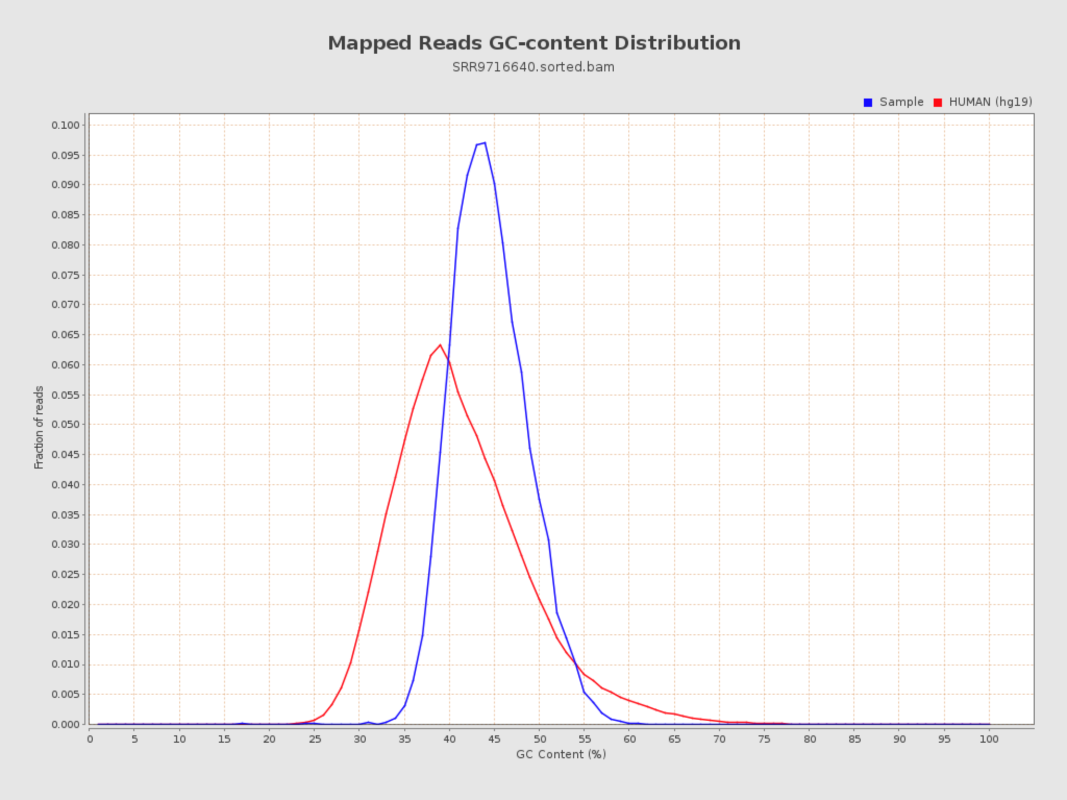
7. Results : Duplication Rate Histogram



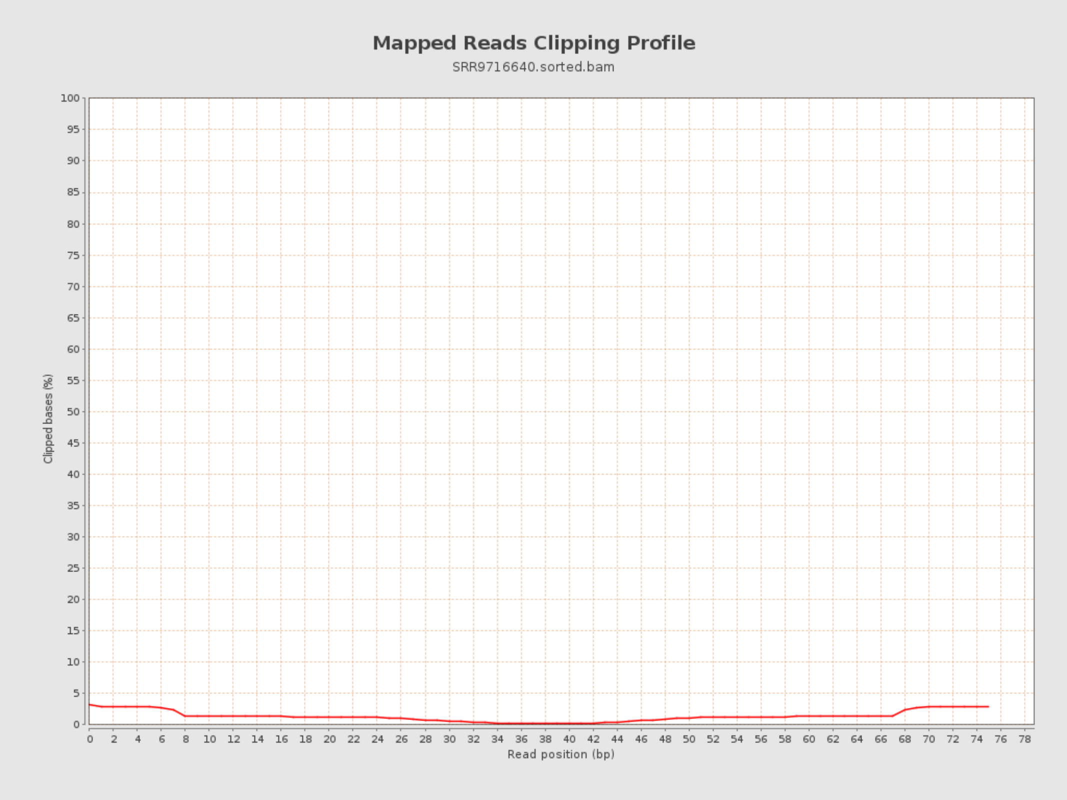
8. Results : Mapped Reads Nucleotide Content



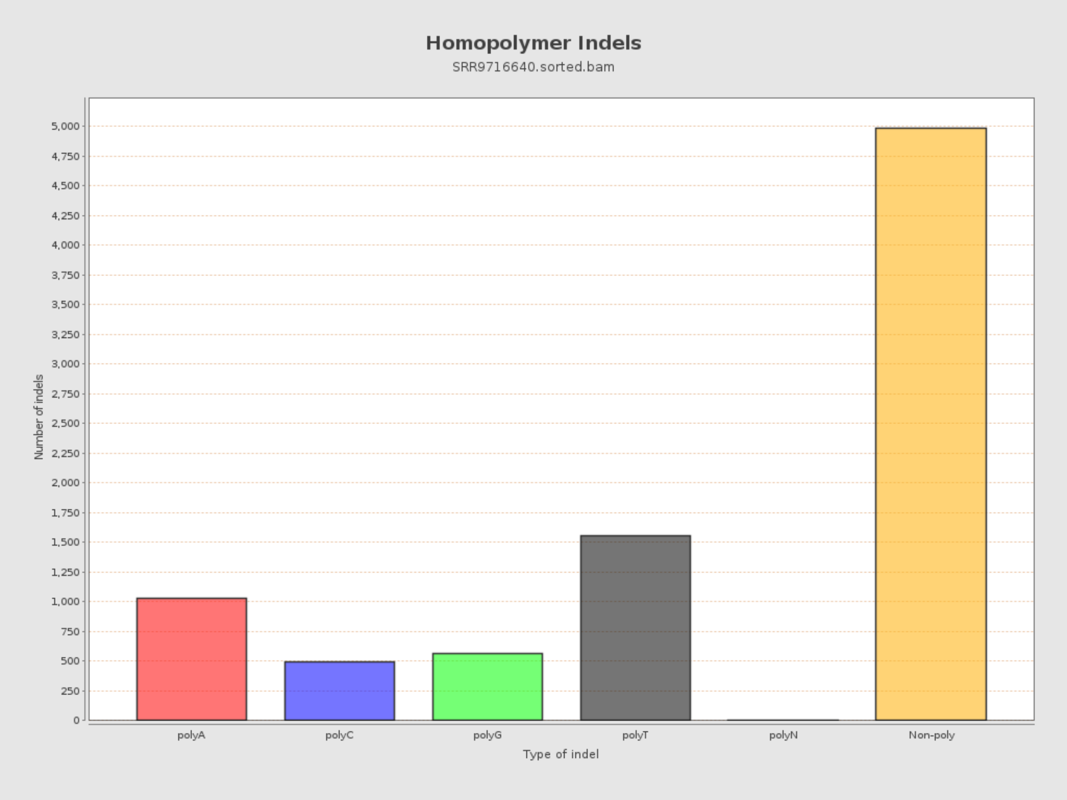
9. Results : Mapped Reads GC-content Distribution



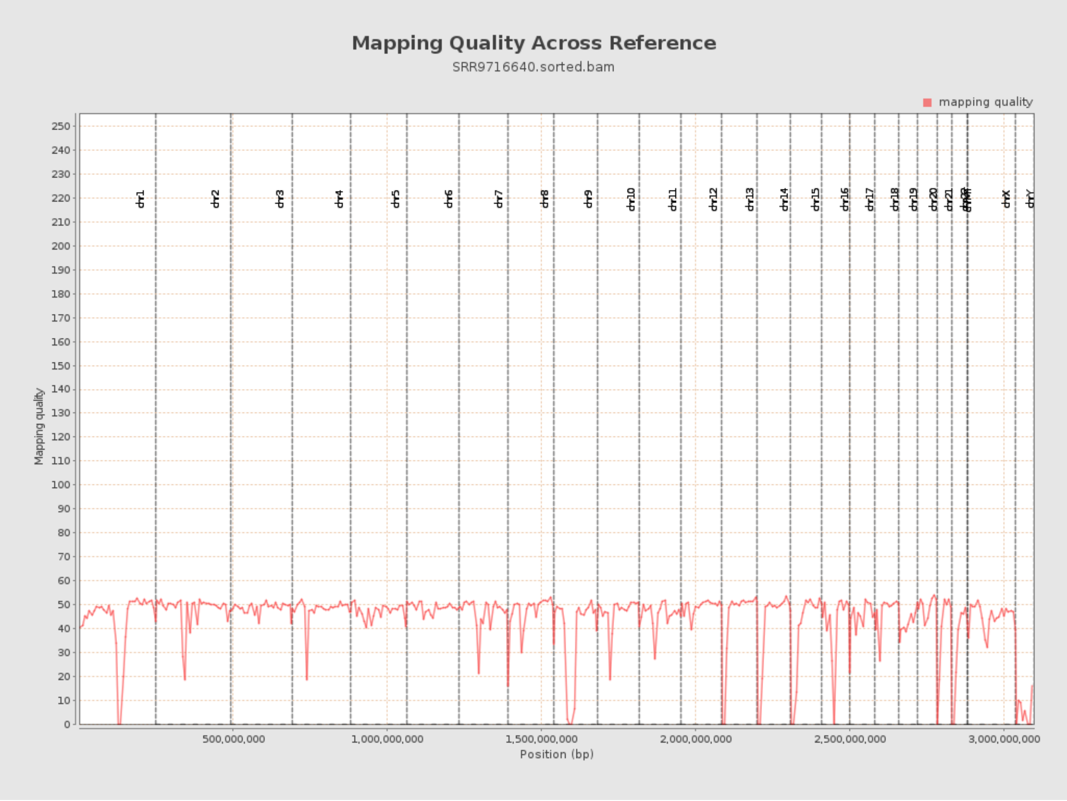
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram