Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 17:57:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716100.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_SRR9716100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 17:57:13 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	633,843
Mapped reads	563,899 / 88.97%
Unmapped reads	69,944 / 11.03%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,460 / 0.39%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	11,765 / 1.86%
Duplication rate	1.6%
Clipped reads	565,746 / 89.26%

2.2. ACGT Content

Number/percentage of A's	7,814,116 / 24.11%
Number/percentage of C's	5,908,840 / 18.23%
Number/percentage of T's	10,545,037 / 32.53%
Number/percentage of G's	8,144,343 / 25.13%
Number/percentage of N's	456 / 0%
GC Percentage	43.36%

2.3. Coverage

Mean	0.0105

Standard Deviation	0.1267

2.4. Mapping Quality

Mean Mapping Quality	44.59

2.5. Mismatches and indels

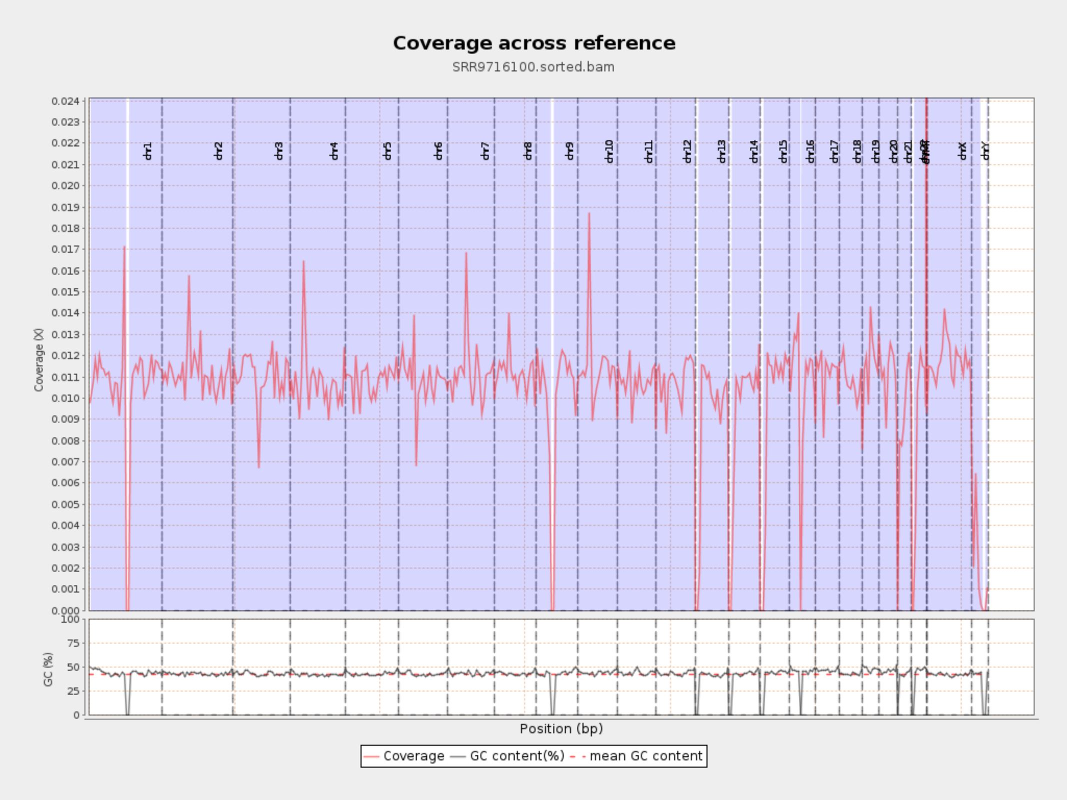
General error rate	0.52%
Mismatches	164,681
Insertions	1,858
Mapped reads with at least one insertion	0.33%
Deletions	6,014
Mapped reads with at least one deletion	1.06%
Homopolymer indels	44.22%

2.6. Chromosome stats

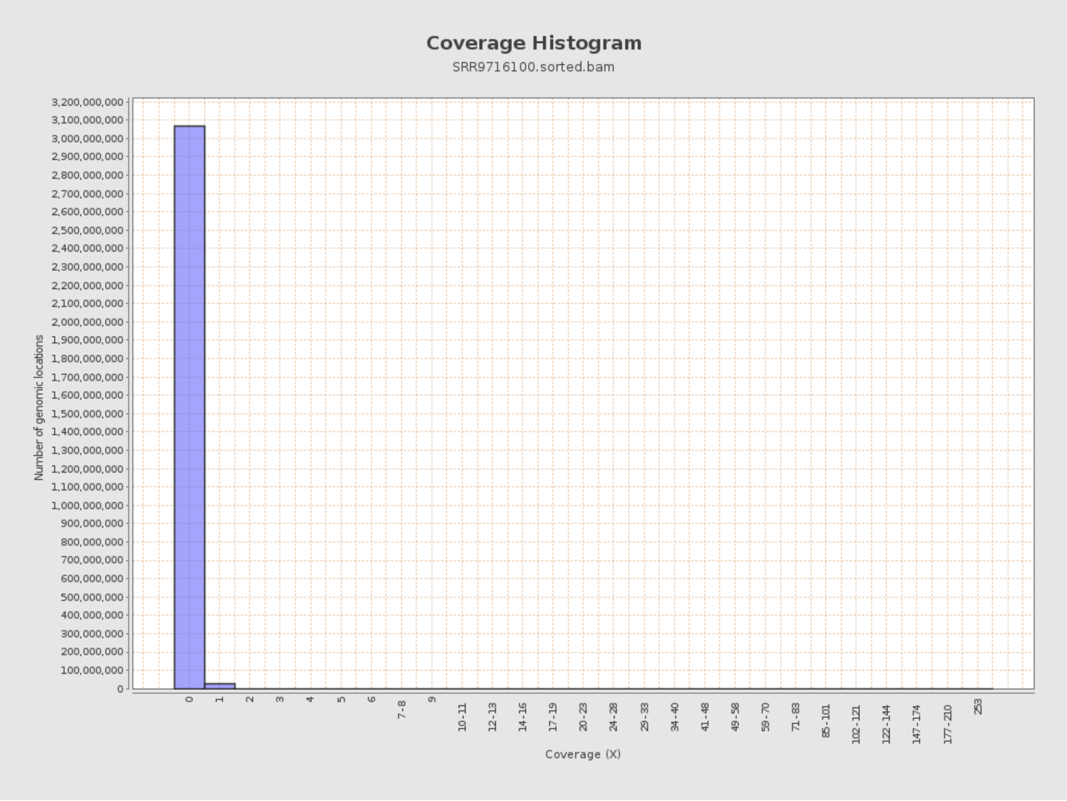
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	2618779	0.0105	0.1945
chr2	243199373	2723729	0.0112	0.1538
chr3	198022430	2182874	0.011	0.1091
chr4	191154276	2051418	0.0107	0.1111
chr5	180915260	1965598	0.0109	0.1088
chr6	171115067	1863523	0.0109	0.1152
chr7	159138663	1787345	0.0112	0.1423

chr8	146364022	1634034	0.0112	0.1218
chr9	141213431	1363090	0.0097	0.1126
chr10	135534747	1554186	0.0115	0.129
chr11	135006516	1452112	0.0108	0.1176
chr12	133851895	1453057	0.0109	0.1088
chr13	115169878	1003178	0.0087	0.0967
chr14	107349540	961294	0.009	0.0997
chr15	102531392	952259	0.0093	0.1013
chr16	90354753	953503	0.0106	0.1089
chr17	81195210	905871	0.0112	0.1122
chr18	78077248	850957	0.0109	0.1525
chr19	59128983	692681	0.0117	0.1507
chr20	63025520	701720	0.0111	0.1102
chr21	48129895	422562	0.0088	0.1022
chr22	51304566	399318	0.0078	0.0917
chrMT	16571	1659	0.1001	0.32
chrX	155270560	1819831	0.0117	0.1166
chrY	59373566	107668	0.0018	0.061

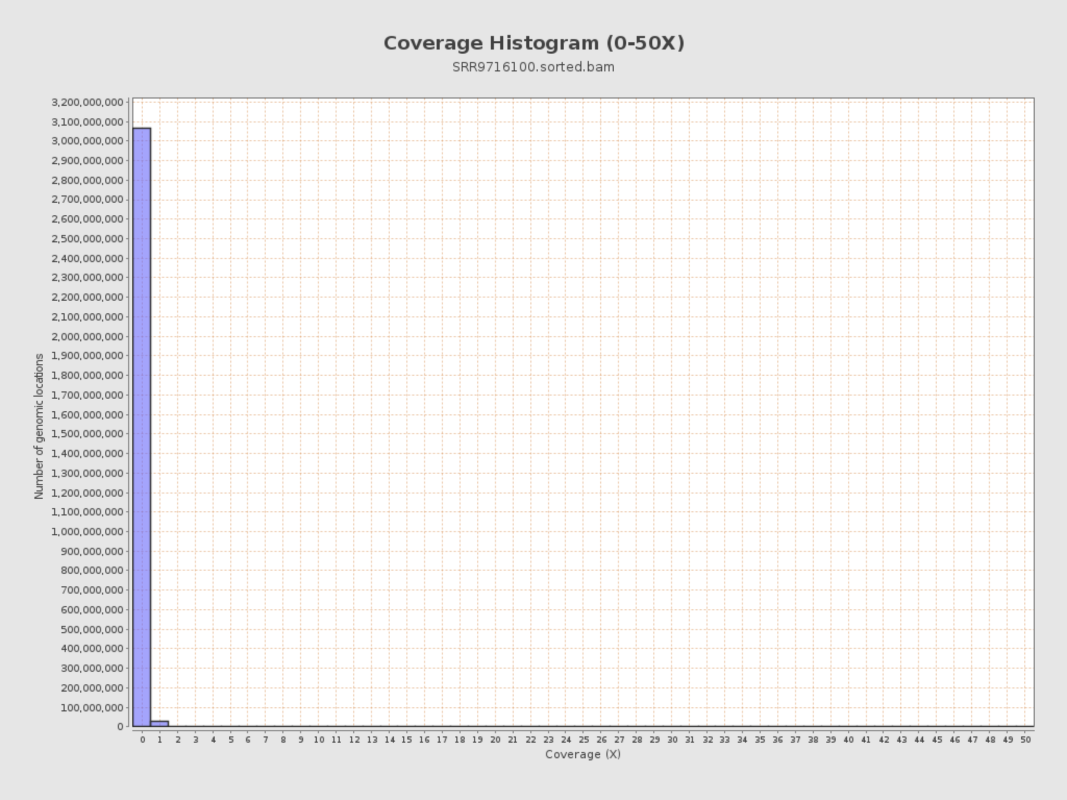
3. Results : Coverage across reference



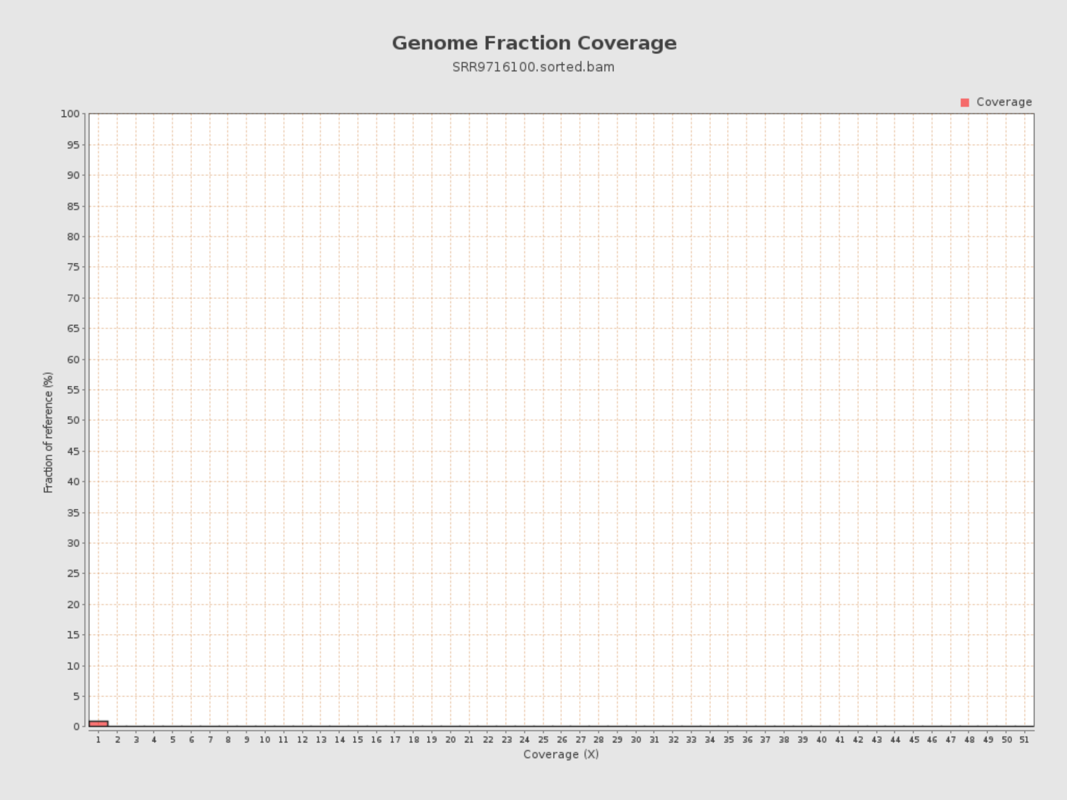
4. Results : Coverage Histogram



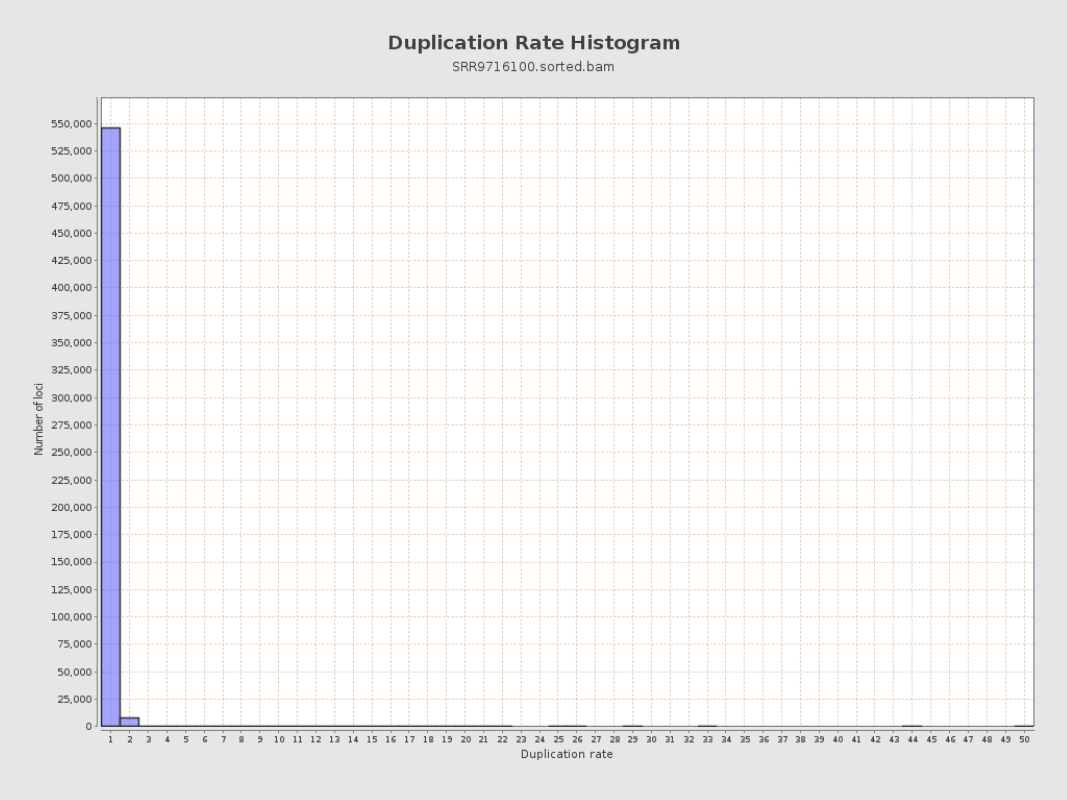
5. Results : Coverage Histogram (0-50X)



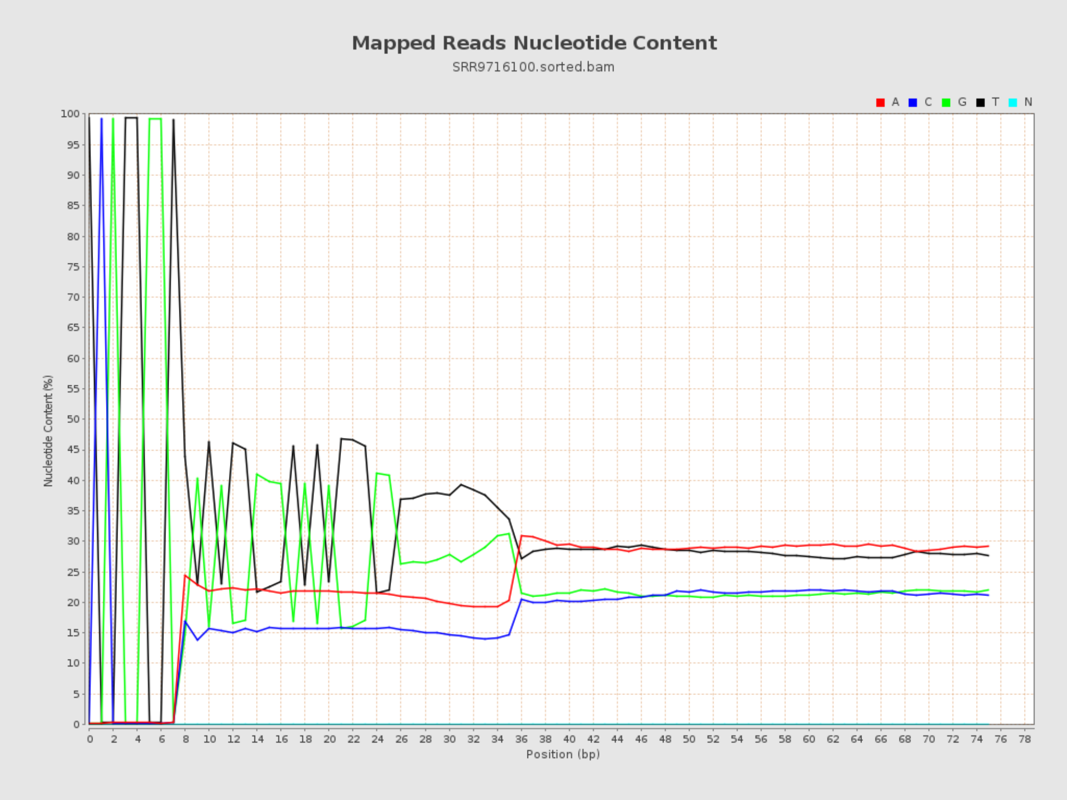
6. Results : Genome Fraction Coverage



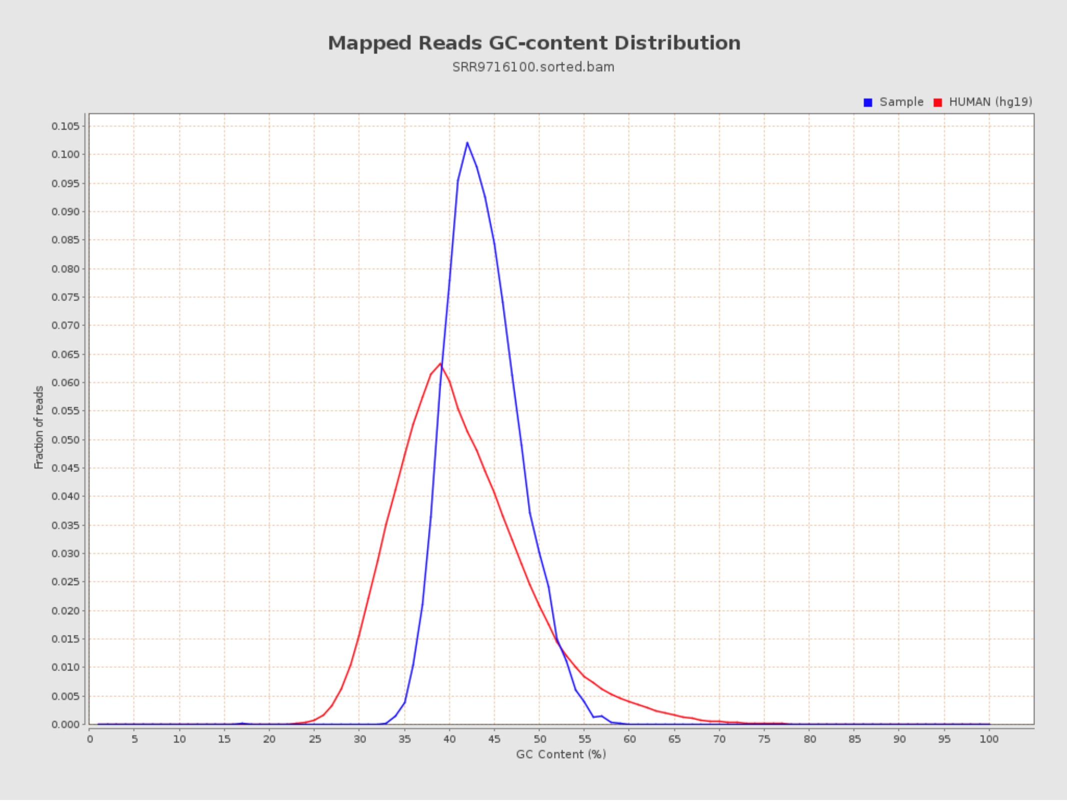
7. Results : Duplication Rate Histogram



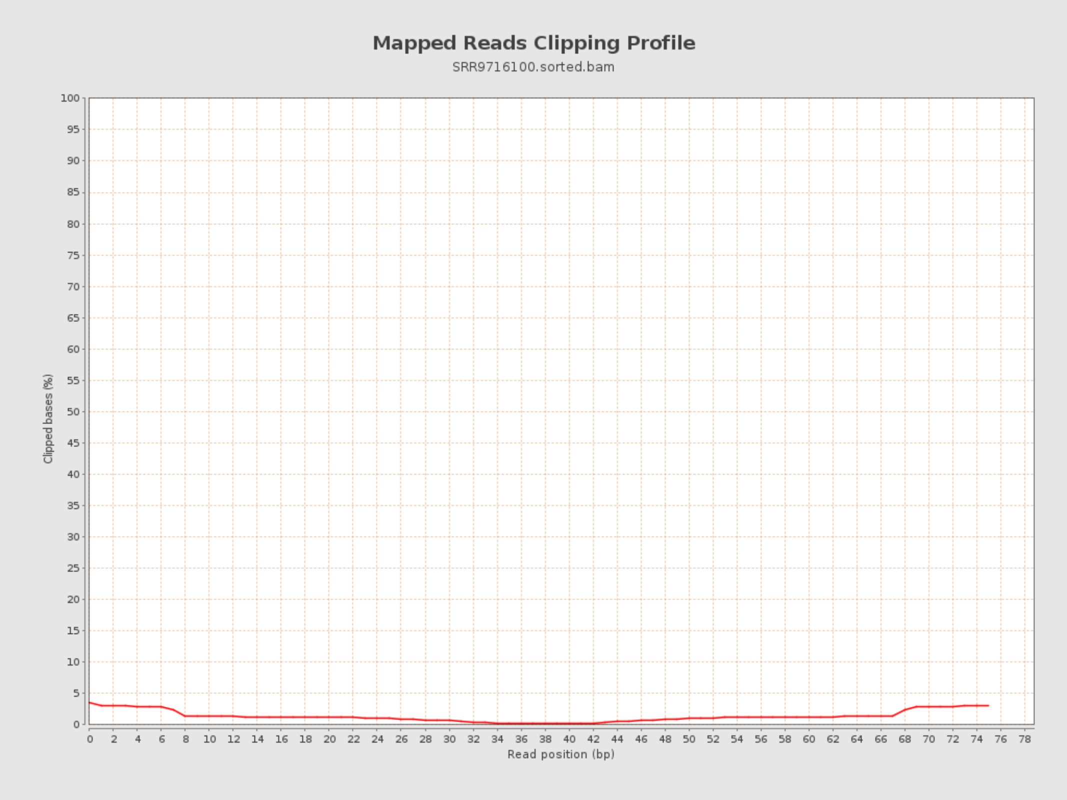
8. Results : Mapped Reads Nucleotide Content



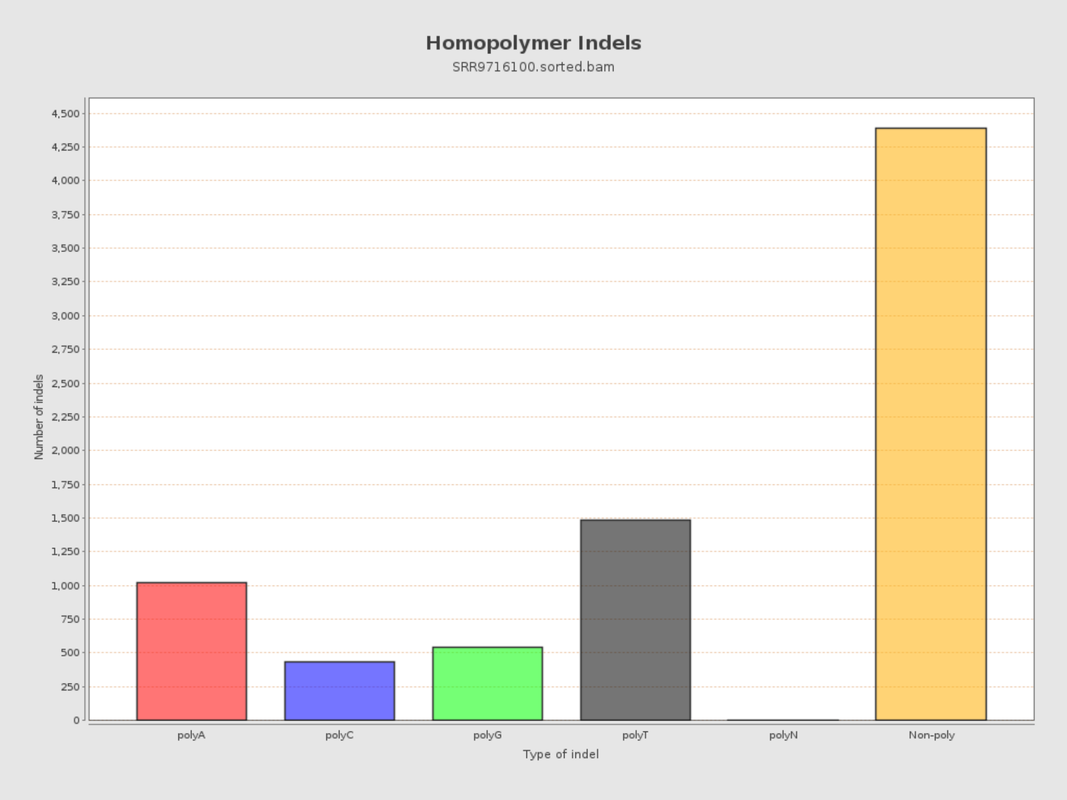
9. Results : Mapped Reads GC-content Distribution



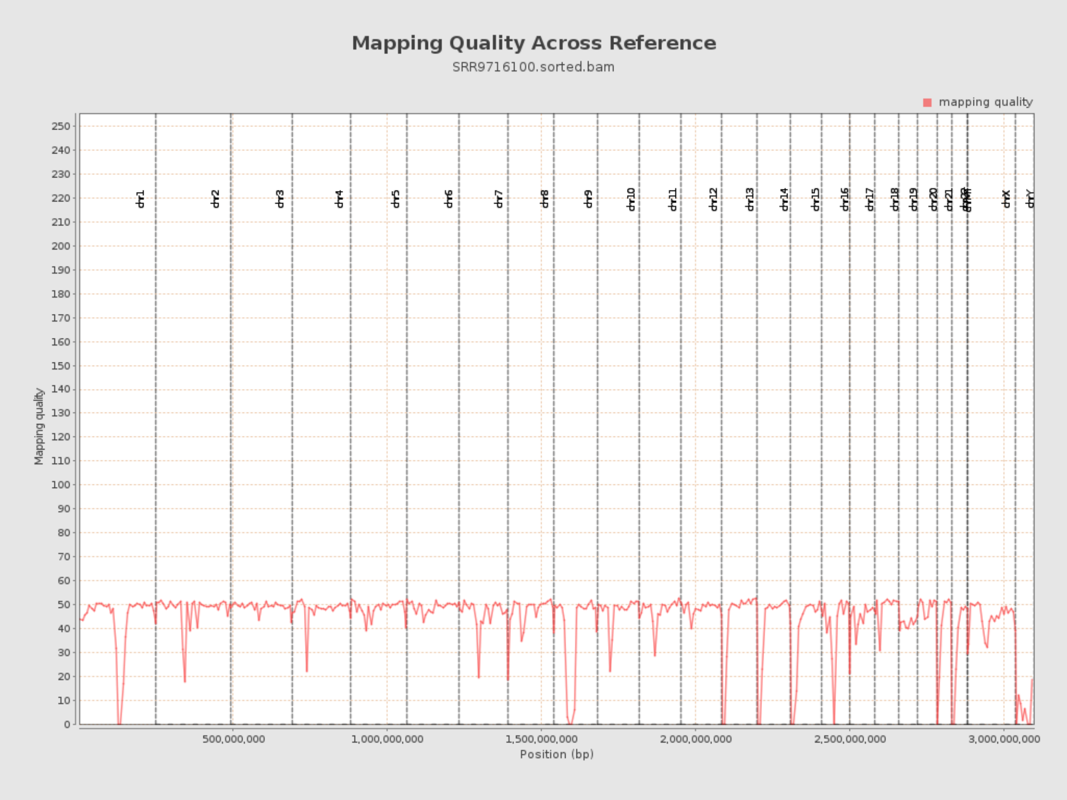
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram