Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/30 19:20:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716135.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_SRR9716135 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716135.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 30 19:20:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716135.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,055,289
Mapped reads	975,942 / 92.48%
Unmapped reads	79,347 / 7.52%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,013 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	25,136 / 2.38%
Duplication rate	1.94%
Clipped reads	977,909 / 92.67%

2.2. ACGT Content

Number/percentage of A's	14,365,456 / 25.35%
Number/percentage of C's	10,603,397 / 18.71%
Number/percentage of T's	17,323,272 / 30.57%
Number/percentage of G's	14,367,024 / 25.36%
Number/percentage of N's	544 / 0%
GC Percentage	44.07%

2.3. Coverage

Mean	0.0183

Standard Deviation	0.1828

2.4. Mapping Quality

Mean Mapping Quality	44.12

2.5. Mismatches and indels

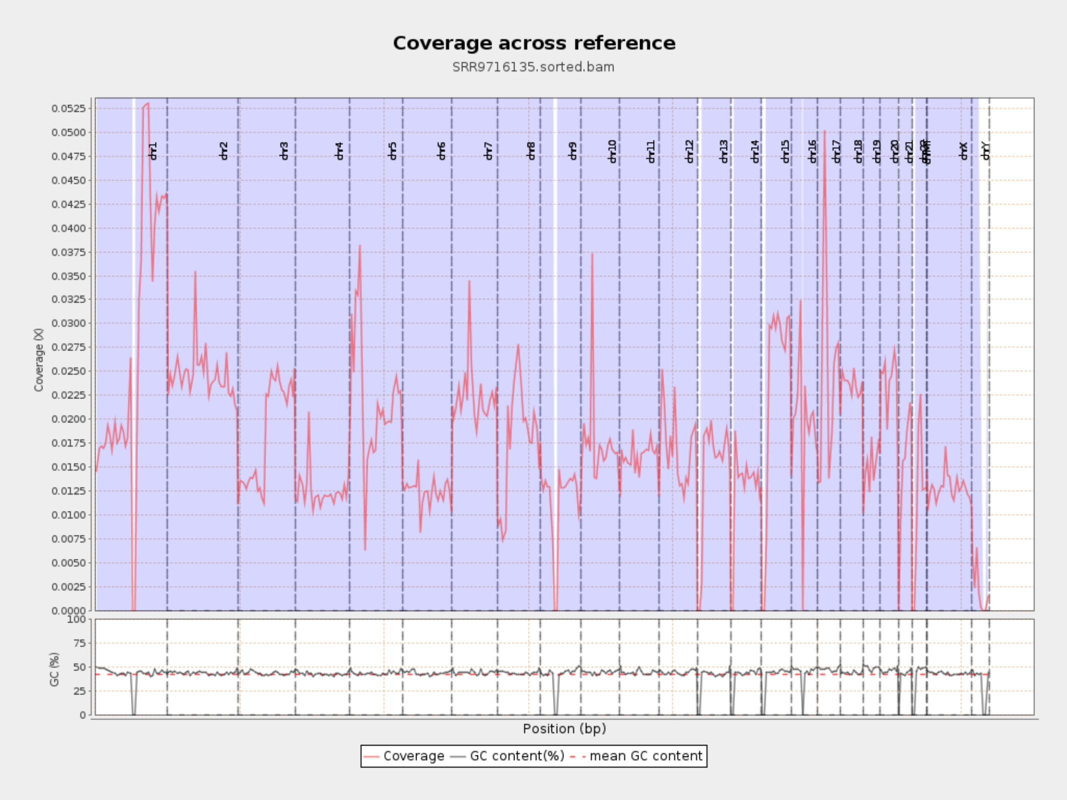
General error rate	0.5%
Mismatches	274,358
Insertions	3,394
Mapped reads with at least one insertion	0.35%
Deletions	11,206
Mapped reads with at least one deletion	1.14%
Homopolymer indels	42.68%

2.6. Chromosome stats

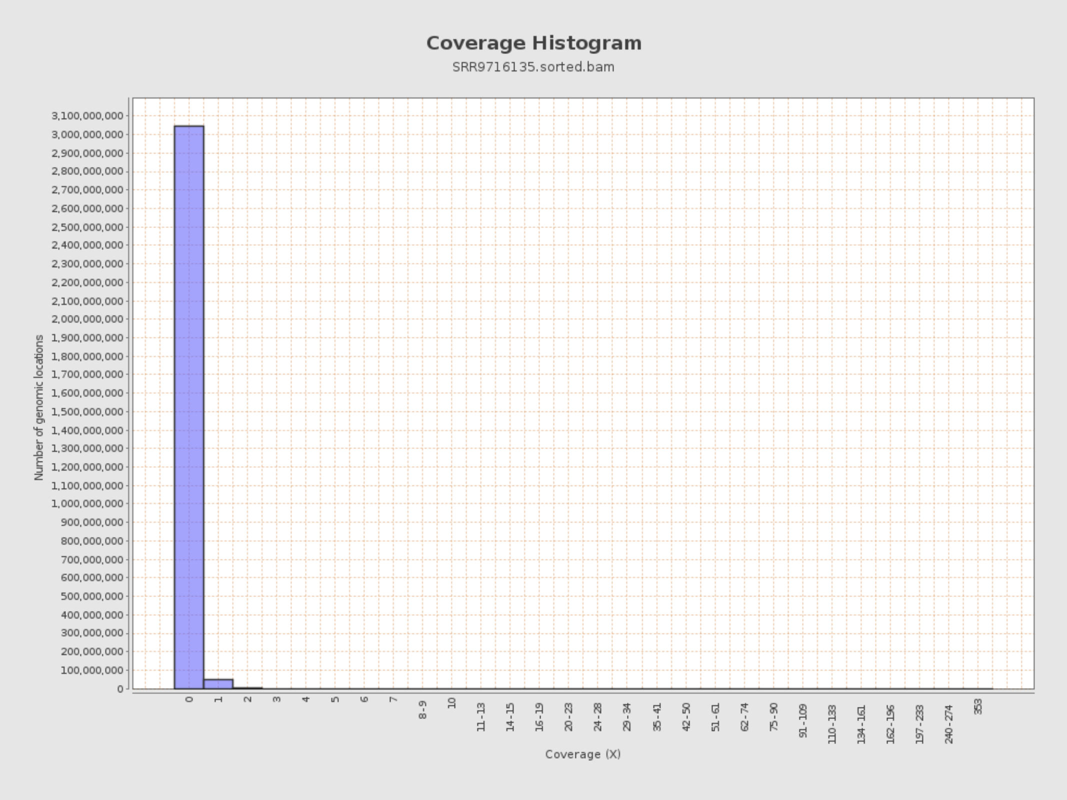
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6805455	0.0273	0.2668
chr2	243199373	5996310	0.0247	0.2443
chr3	198022430	3654047	0.0185	0.1464
chr4	191154276	2388456	0.0125	0.124
chr5	180915260	4013392	0.0222	0.1579
chr6	171115067	2129987	0.0124	0.1289
chr7	159138663	3582653	0.0225	0.2594

chr8	146364022	2650527	0.0181	0.1627
chr9	141213431	1614326	0.0114	0.1395
chr10	135534747	2396171	0.0177	0.2242
chr11	135006516	2195234	0.0163	0.1691
chr12	133851895	2274382	0.017	0.1385
chr13	115169878	1677210	0.0146	0.1285
chr14	107349540	1332698	0.0124	0.1221
chr15	102531392	2440326	0.0238	0.1636
chr16	90354753	1742612	0.0193	0.1617
chr17	81195210	2070346	0.0255	0.1794
chr18	78077248	1849142	0.0237	0.2762
chr19	59128983	896211	0.0152	0.2091
chr20	63025520	1511416	0.024	0.1647
chr21	48129895	732804	0.0152	0.1333
chr22	51304566	605632	0.0118	0.115
chrMT	16571	243	0.0147	0.1202
chrX	155270560	1991137	0.0128	0.1322
chrY	59373566	126679	0.0021	0.0604

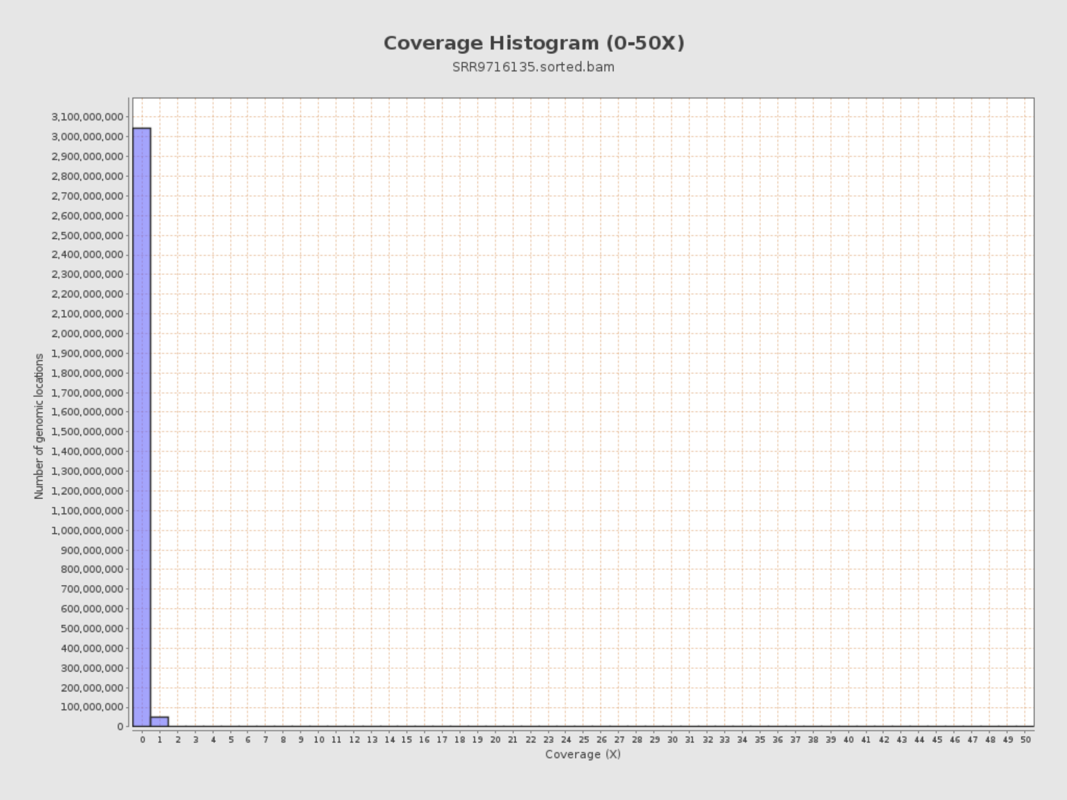
3. Results : Coverage across reference



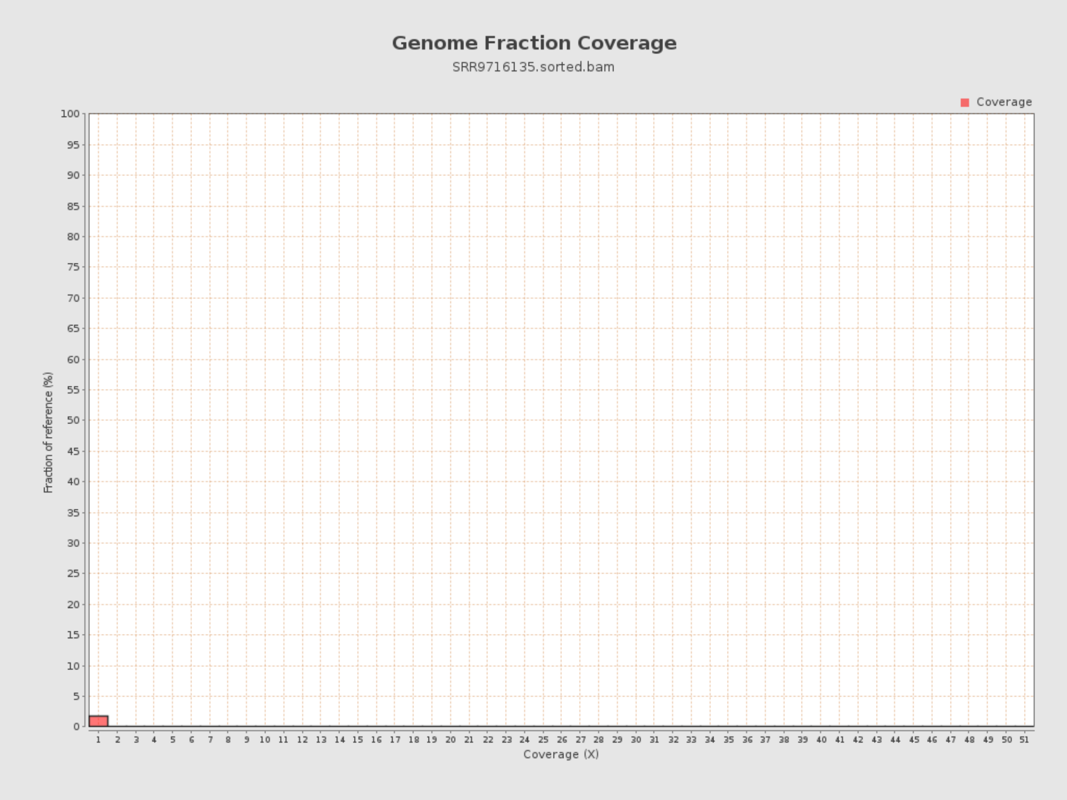
4. Results : Coverage Histogram



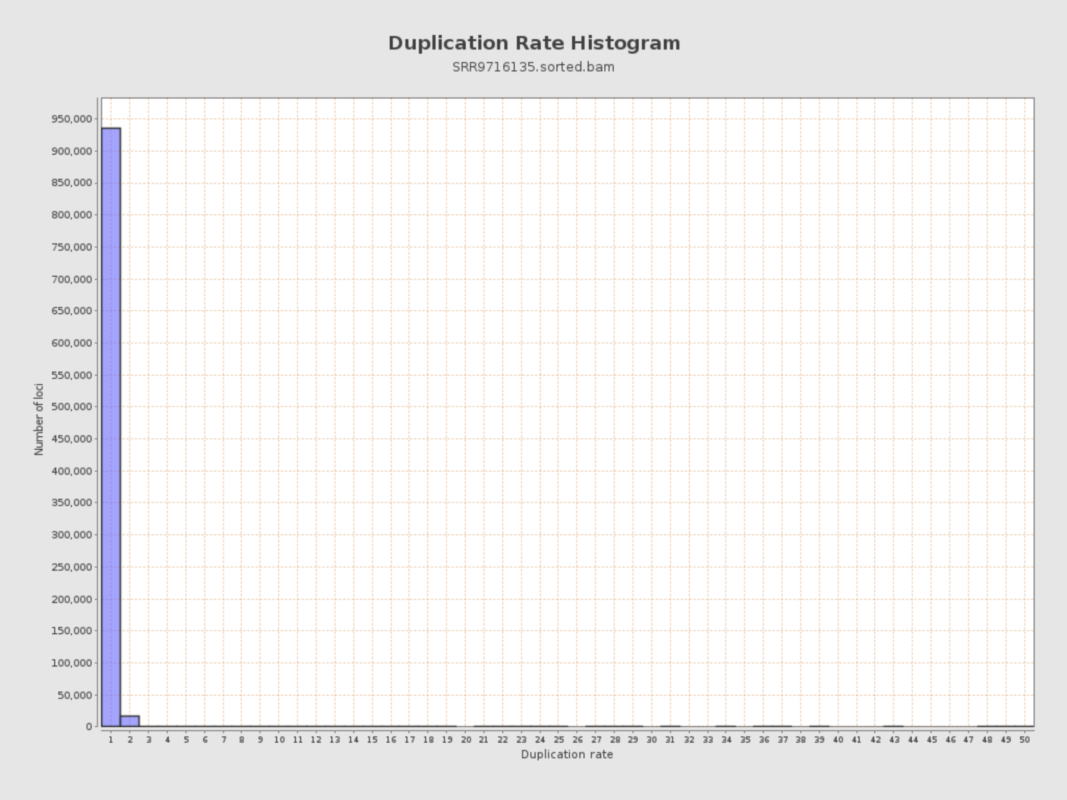
5. Results : Coverage Histogram (0-50X)



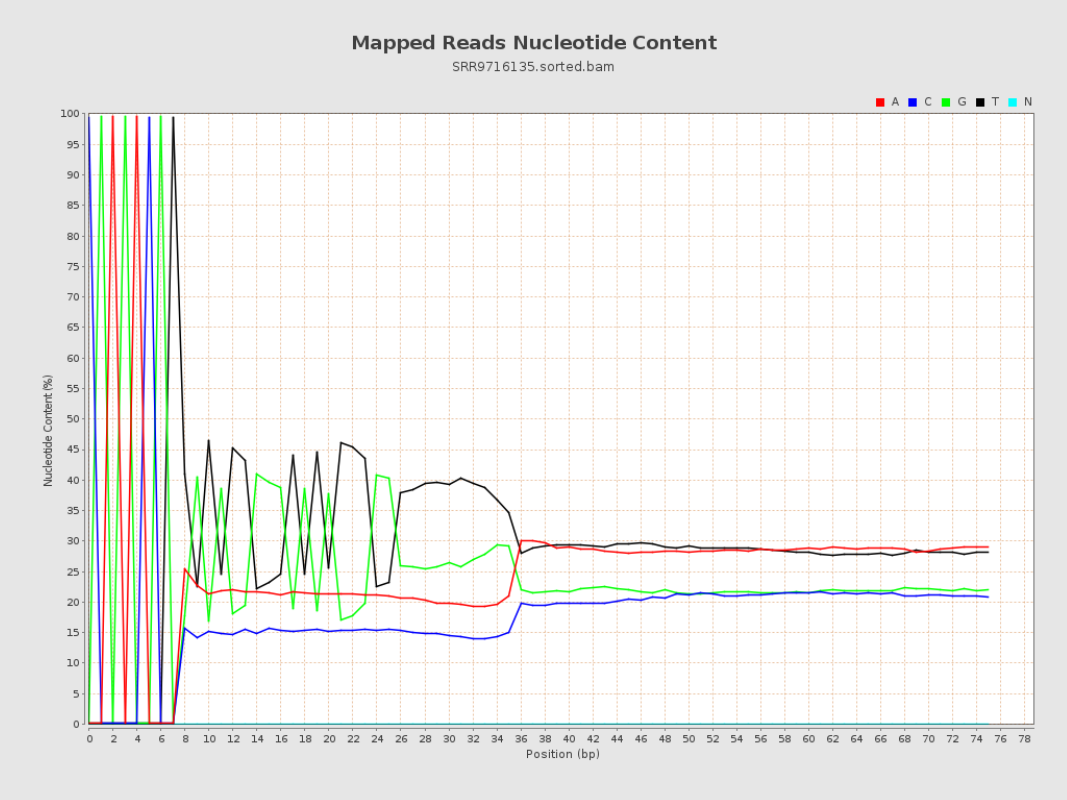
6. Results : Genome Fraction Coverage



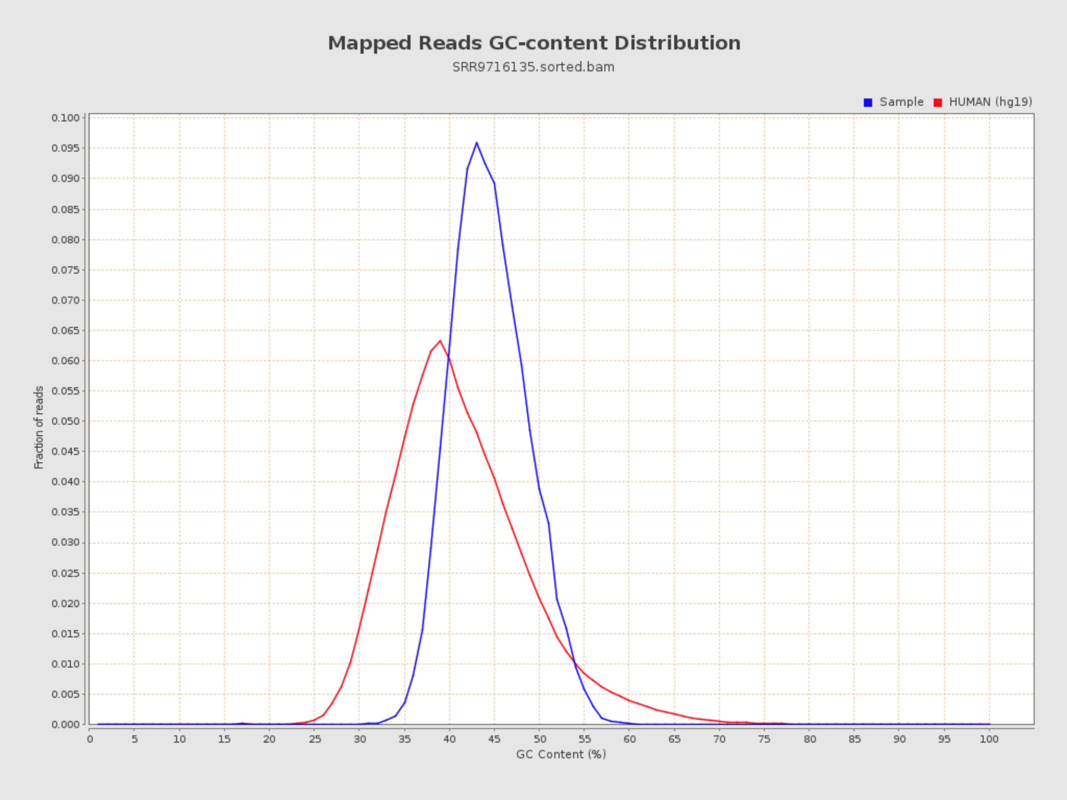
7. Results : Duplication Rate Histogram



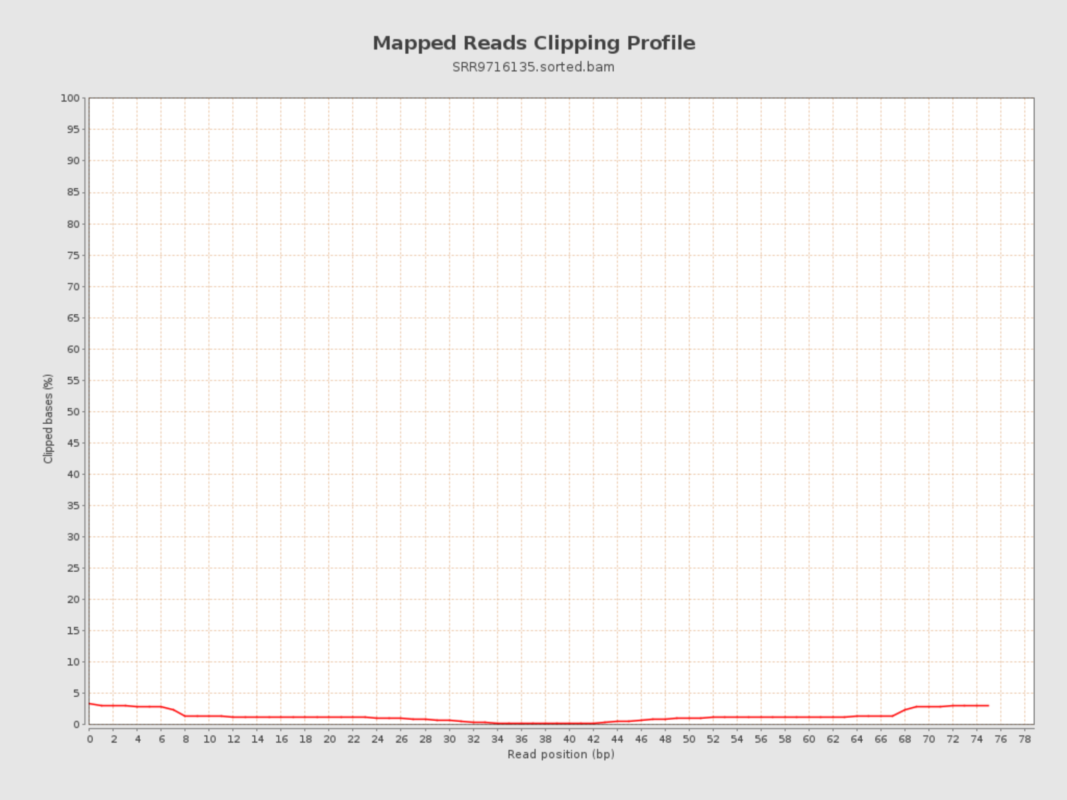
8. Results : Mapped Reads Nucleotide Content



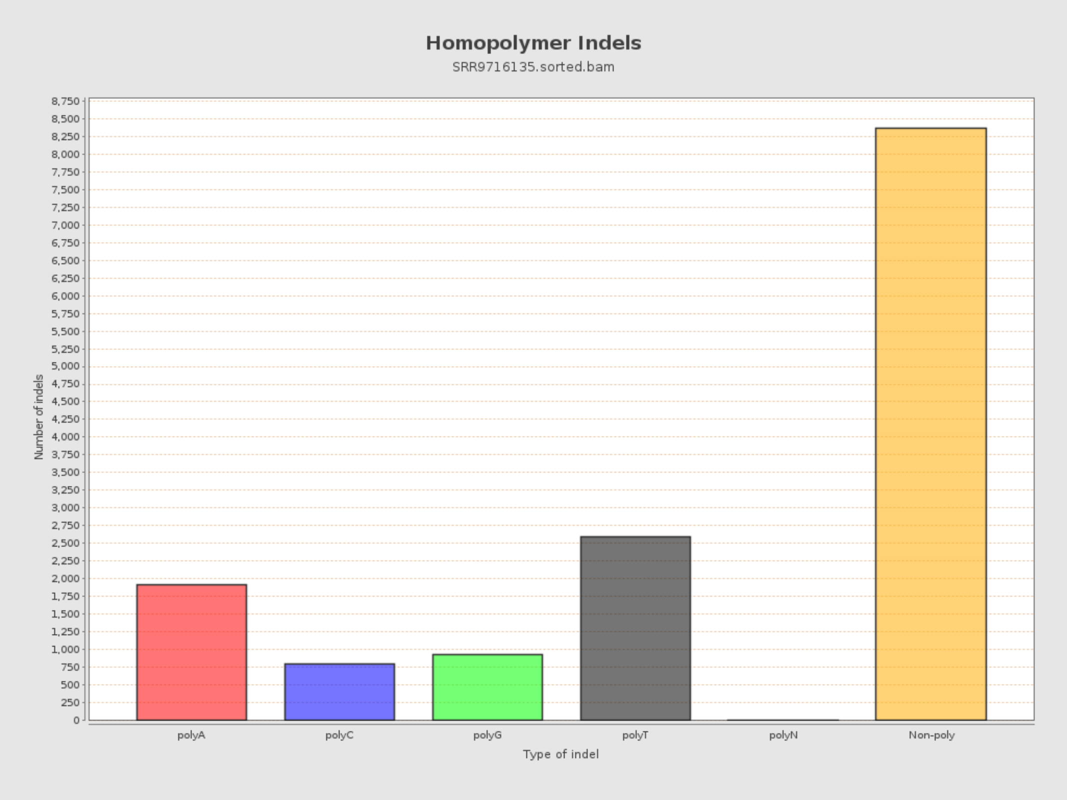
9. Results : Mapped Reads GC-content Distribution



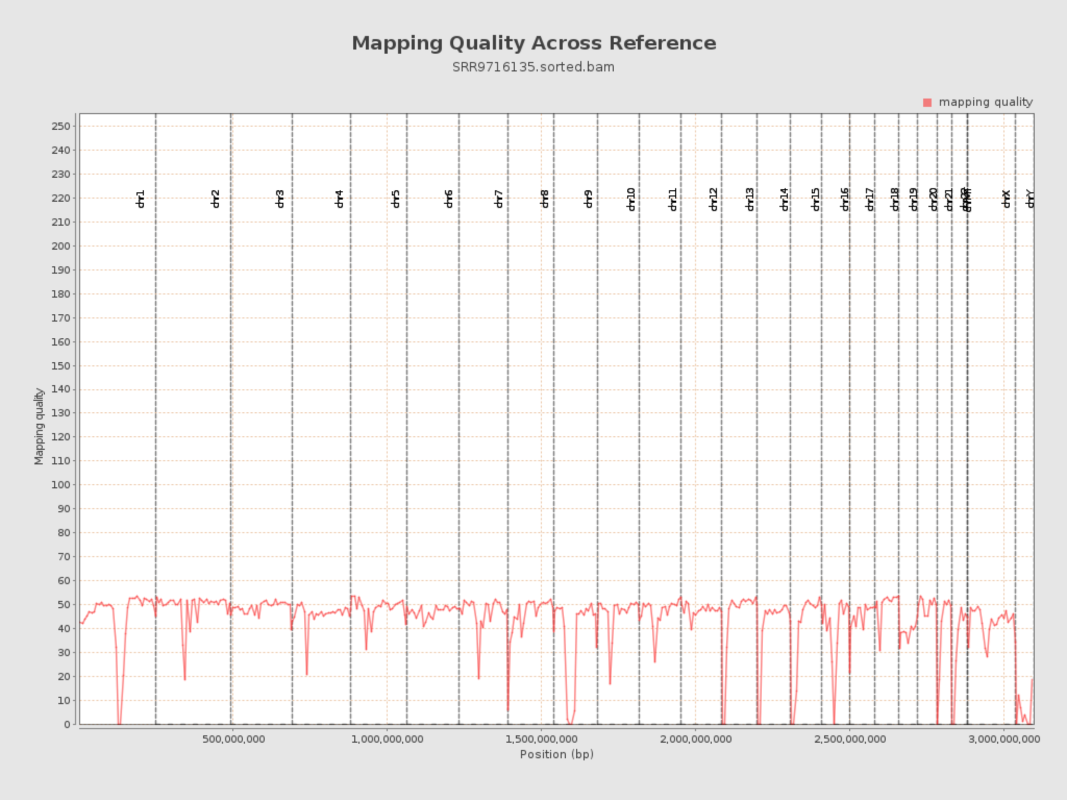
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram