Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 05:47:47

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716287.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_SRR9716287 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716287.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 05:47:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716287.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,037,369
Mapped reads	855,162 / 82.44%
Unmapped reads	182,207 / 17.56%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,498 / 0.24%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	19,289 / 1.86%
Duplication rate	1.55%
Clipped reads	856,234 / 82.54%

2.2. ACGT Content

Number/percentage of A's	10,336,540 / 21.82%
Number/percentage of C's	9,777,733 / 20.64%
Number/percentage of T's	14,345,450 / 30.28%
Number/percentage of G's	12,920,284 / 27.27%
Number/percentage of N's	1,230 / 0%
GC Percentage	47.91%

2.3. Coverage

Mean	0.0153

Standard Deviation	0.1555

2.4. Mapping Quality

Mean Mapping Quality	37.83

2.5. Mismatches and indels

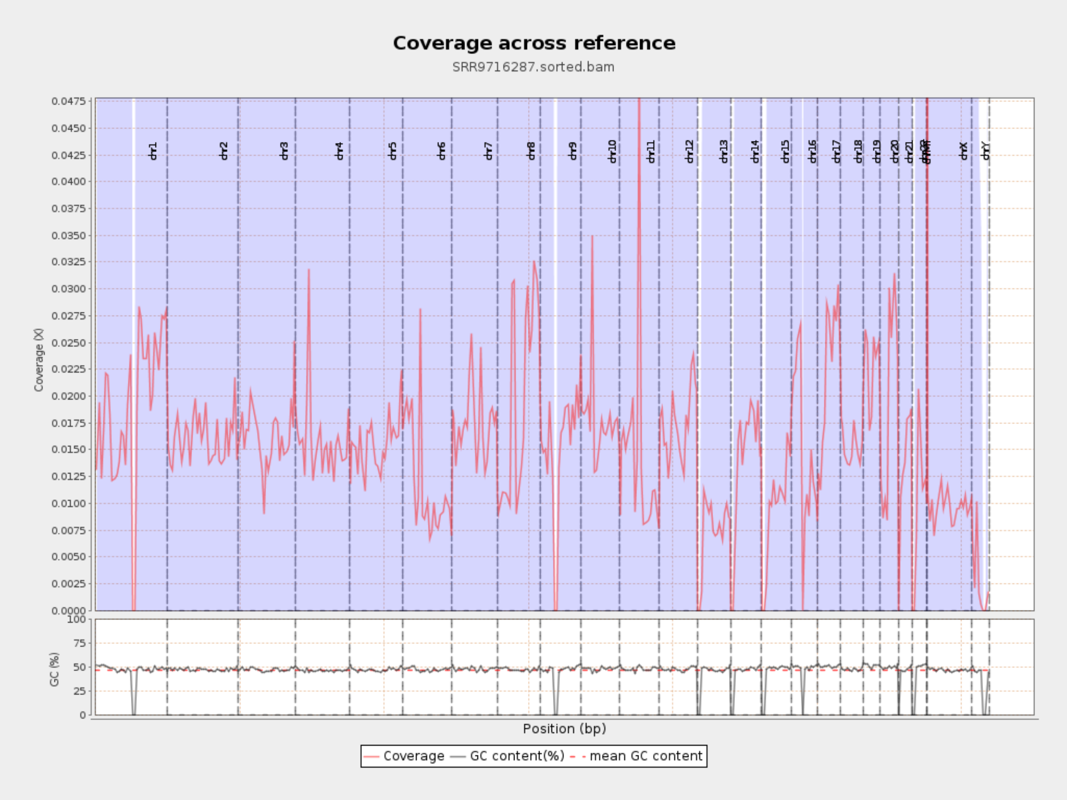
General error rate	0.56%
Mismatches	256,351
Insertions	3,507
Mapped reads with at least one insertion	0.41%
Deletions	8,114
Mapped reads with at least one deletion	0.94%
Homopolymer indels	36.61%

2.6. Chromosome stats

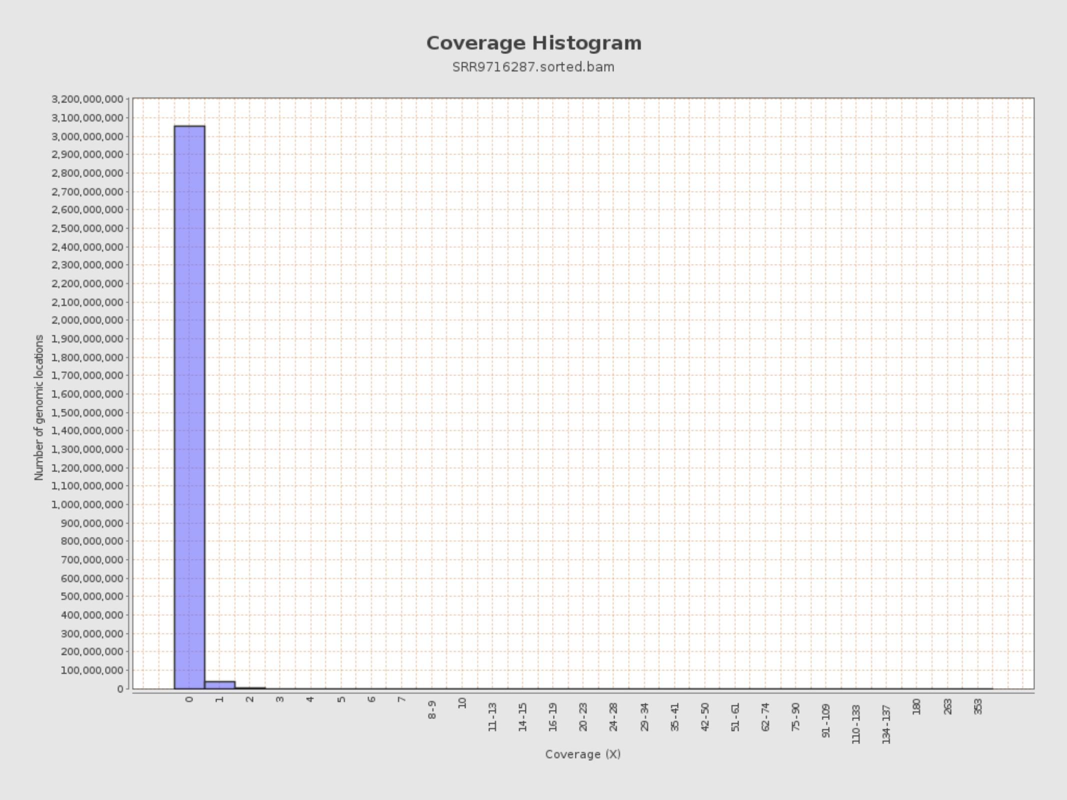
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4723916	0.019	0.1767
chr2	243199373	3909207	0.0161	0.21
chr3	198022430	3199649	0.0162	0.1471
chr4	191154276	3045609	0.0159	0.1533
chr5	180915260	2832155	0.0157	0.136
chr6	171115067	2049799	0.012	0.1228
chr7	159138663	2803341	0.0176	0.174

chr8	146364022	2846009	0.0194	0.1628
chr9	141213431	2101767	0.0149	0.1419
chr10	135534747	2431552	0.0179	0.2118
chr11	135006516	2009742	0.0149	0.153
chr12	133851895	2329233	0.0174	0.1425
chr13	115169878	838354	0.0073	0.0933
chr14	107349540	1501013	0.014	0.1332
chr15	102531392	965766	0.0094	0.1073
chr16	90354753	1345618	0.0149	0.1413
chr17	81195210	1817736	0.0224	0.1704
chr18	78077248	1188188	0.0152	0.1591
chr19	59128983	1344099	0.0227	0.1897
chr20	63025520	1238065	0.0196	0.1571
chr21	48129895	659539	0.0137	0.1364
chr22	51304566	542968	0.0106	0.1142
chrMT	16571	13226	0.7981	1.122
chrX	155270560	1499363	0.0097	0.1179
chrY	59373566	158944	0.0027	0.0894

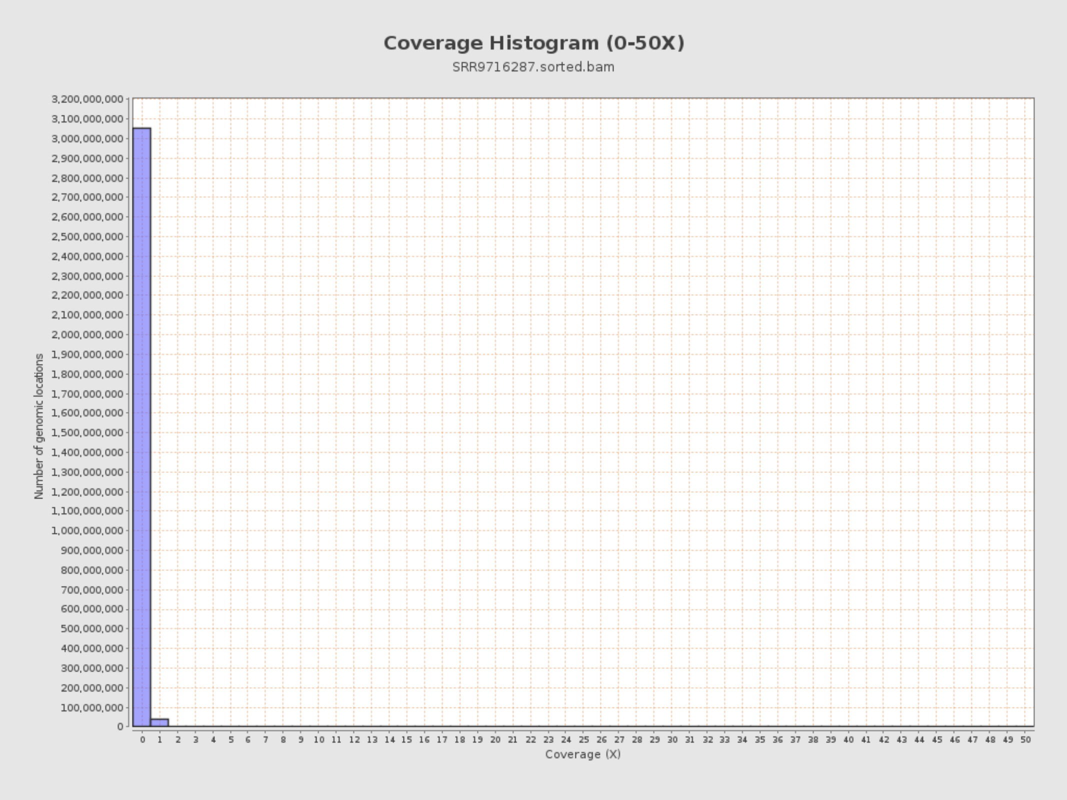
3. Results : Coverage across reference



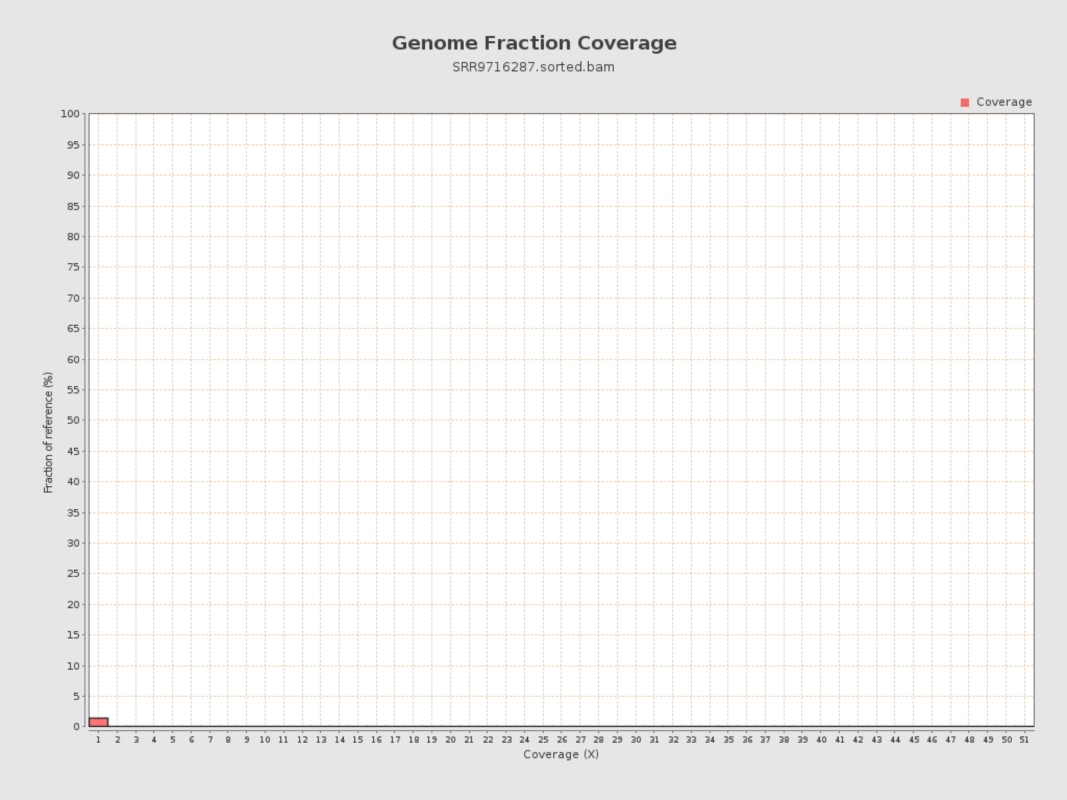
4. Results : Coverage Histogram



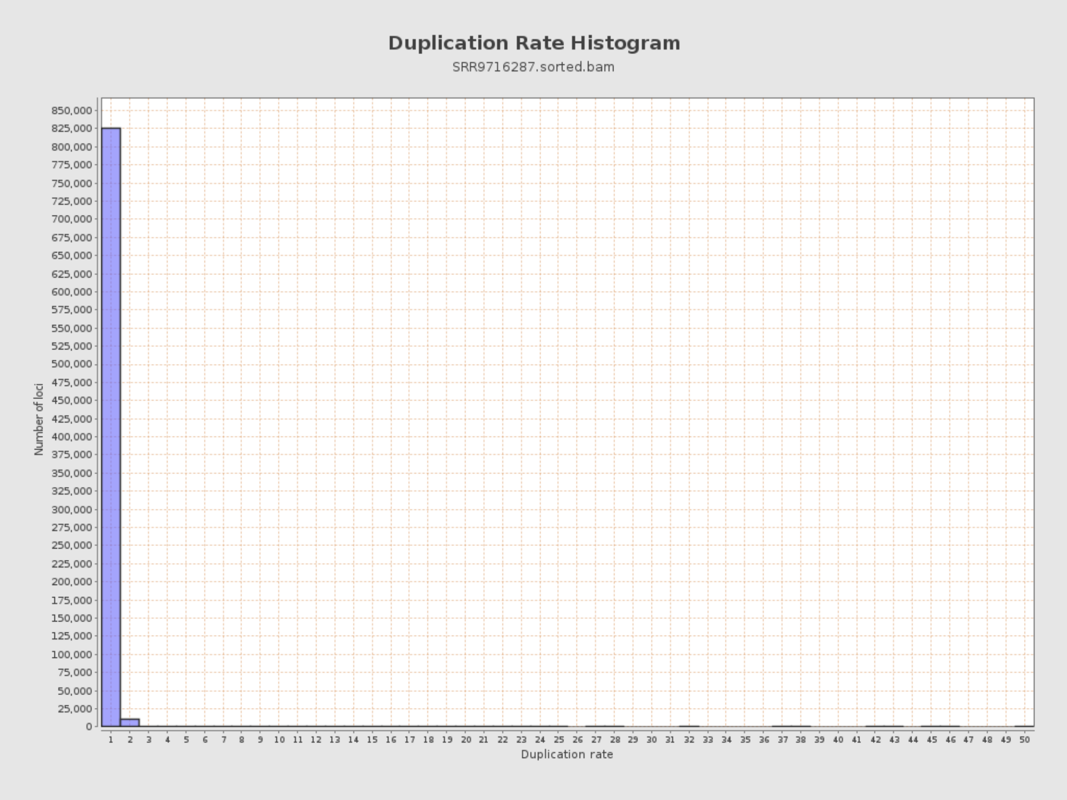
5. Results : Coverage Histogram (0-50X)



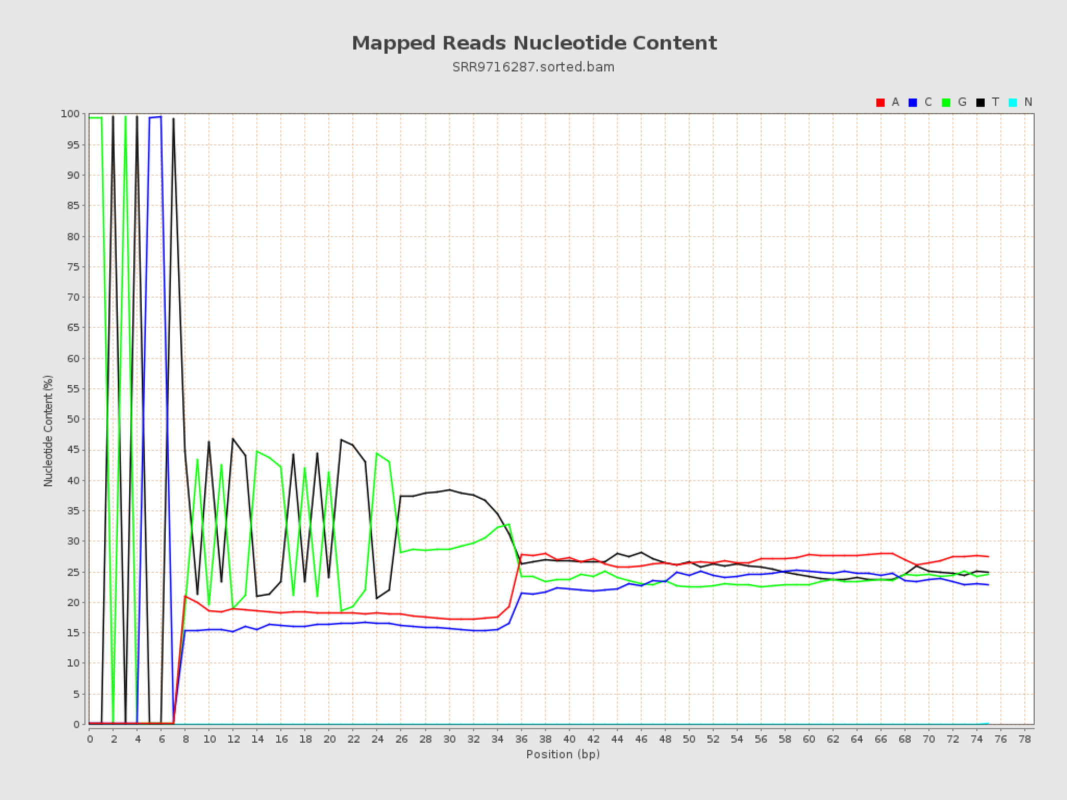
6. Results : Genome Fraction Coverage



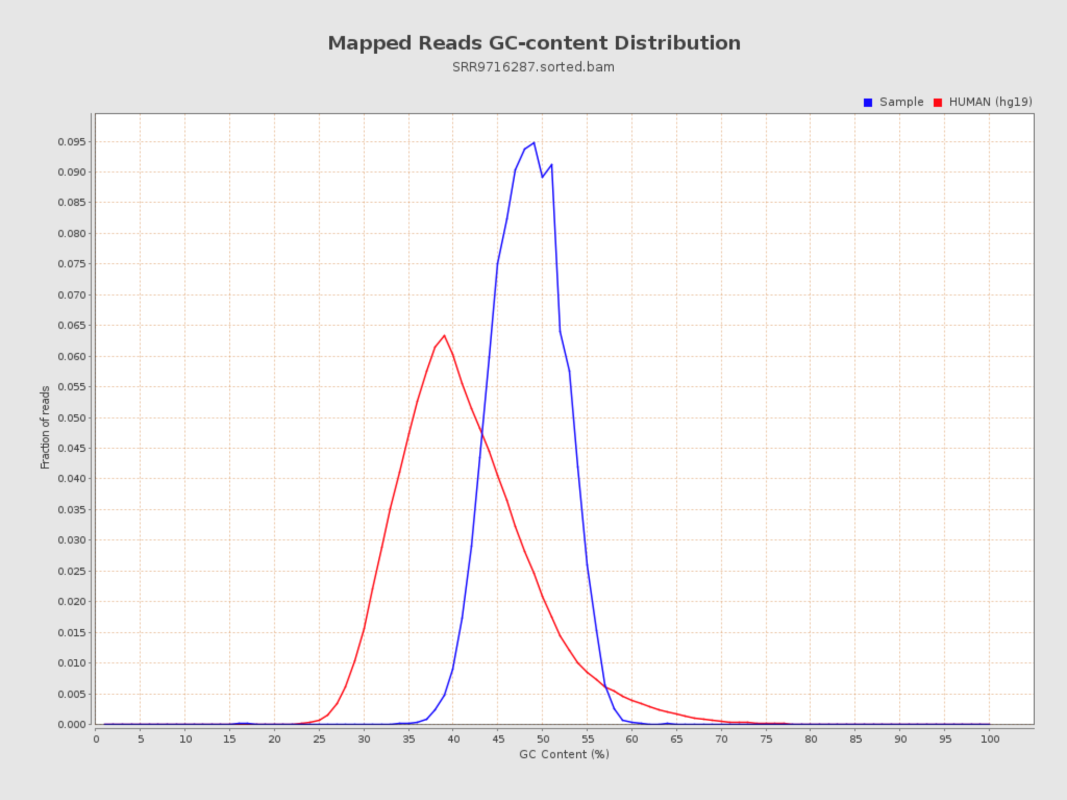
7. Results : Duplication Rate Histogram



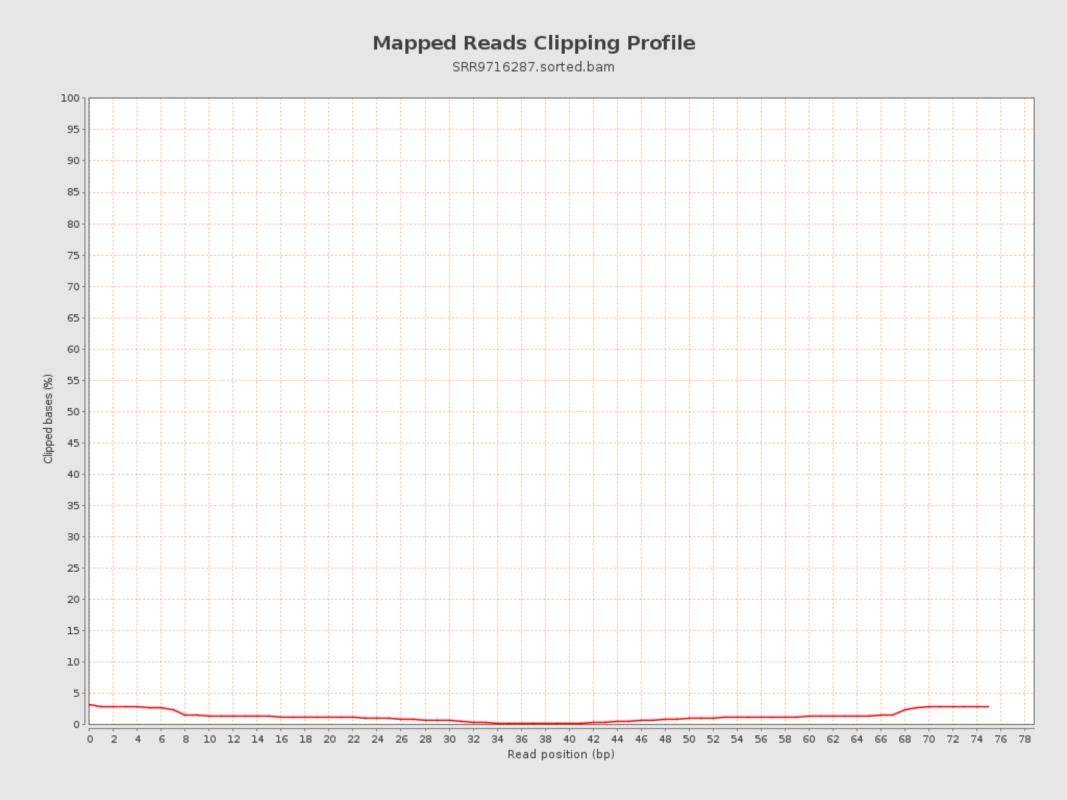
8. Results : Mapped Reads Nucleotide Content



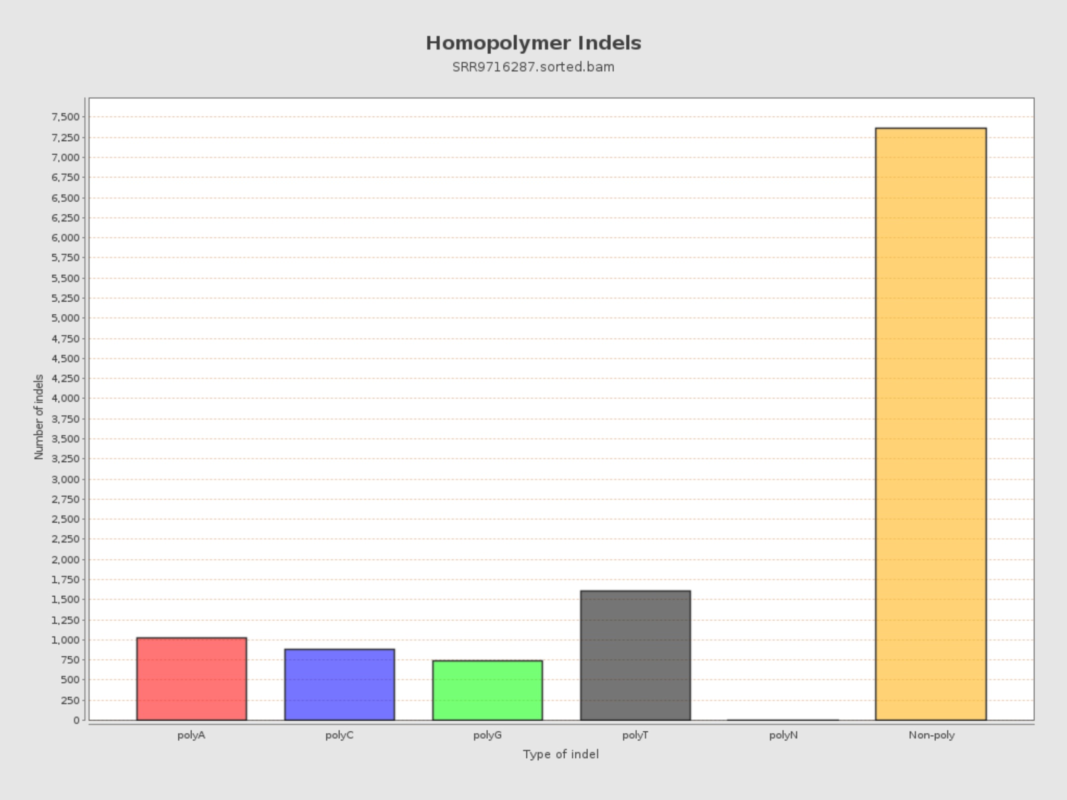
9. Results : Mapped Reads GC-content Distribution



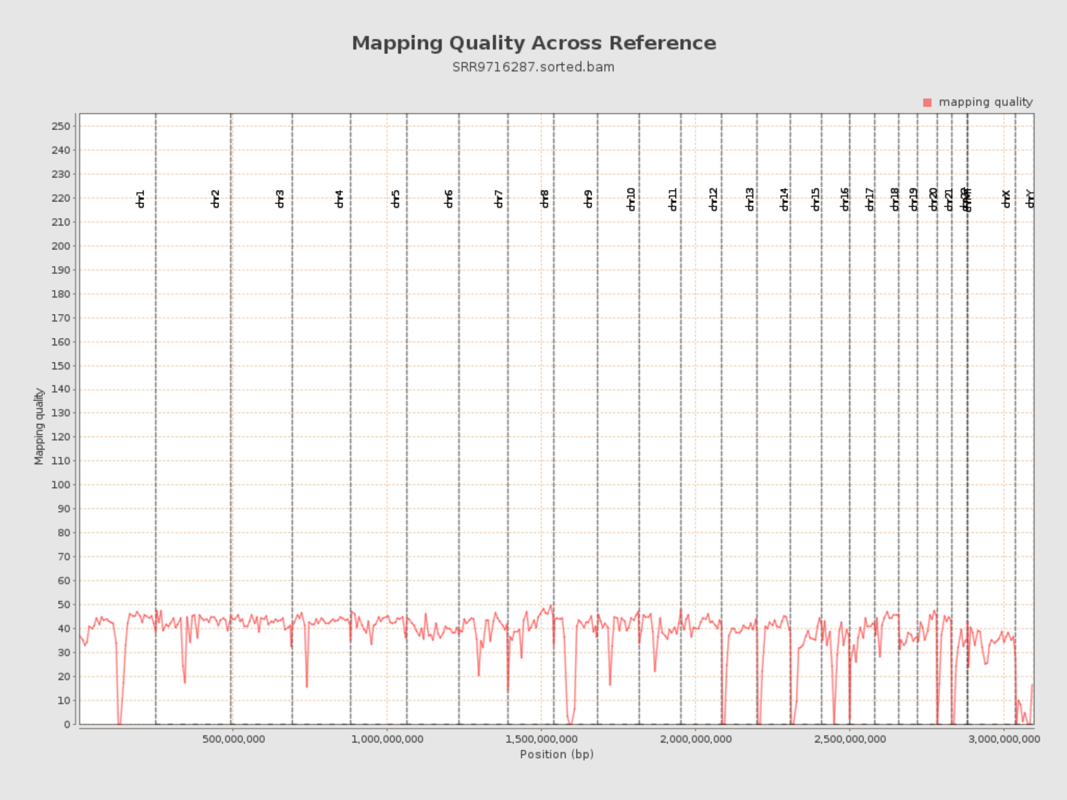
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram