Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 17:55:11

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716899.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_SRR9716899 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716899.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 17:55:10 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716899.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	888,199
Mapped reads	724,466 / 81.57%
Unmapped reads	163,733 / 18.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,169 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	13,360 / 1.5%
Duplication rate	1.33%
Clipped reads	726,695 / 81.82%

2.2. ACGT Content

Number/percentage of A's	9,348,394 / 23.04%
Number/percentage of C's	8,415,259 / 20.74%
Number/percentage of T's	12,209,910 / 30.1%
Number/percentage of G's	10,595,272 / 26.12%
Number/percentage of N's	1,125 / 0%
GC Percentage	46.86%

2.3. Coverage

Mean	0.0131

Standard Deviation	0.1379

2.4. Mapping Quality

Mean Mapping Quality	39.42

2.5. Mismatches and indels

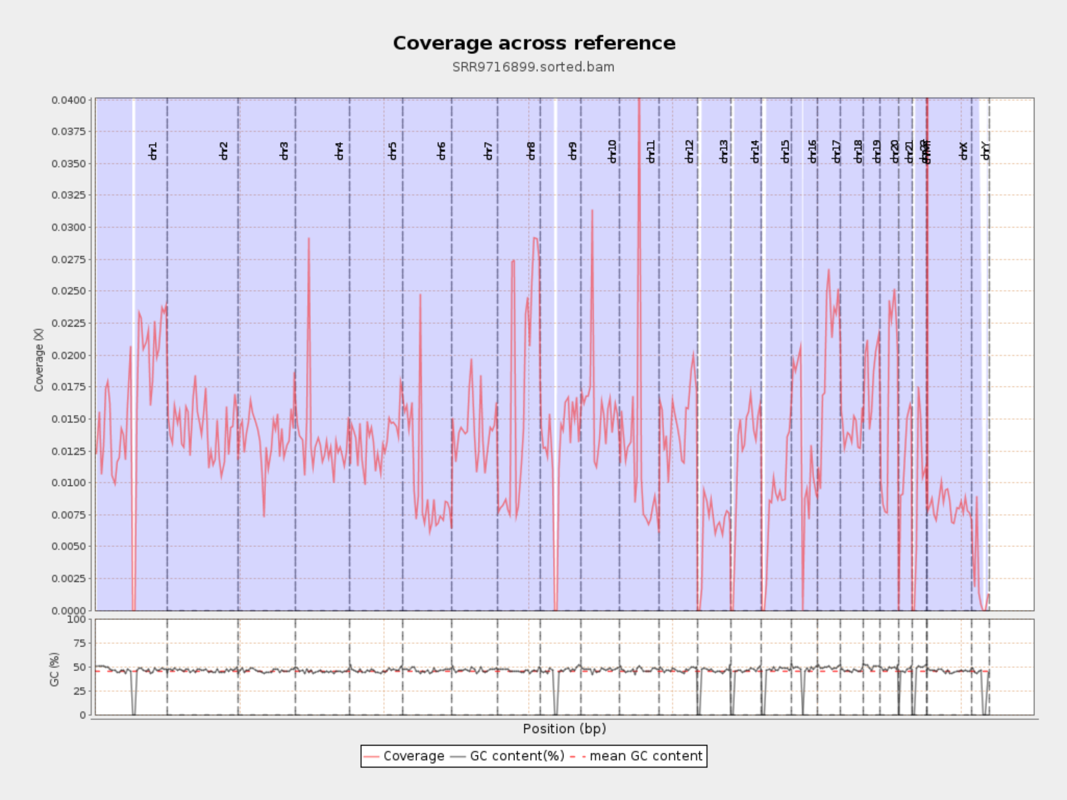
General error rate	0.55%
Mismatches	215,634
Insertions	2,954
Mapped reads with at least one insertion	0.41%
Deletions	7,066
Mapped reads with at least one deletion	0.97%
Homopolymer indels	34.05%

2.6. Chromosome stats

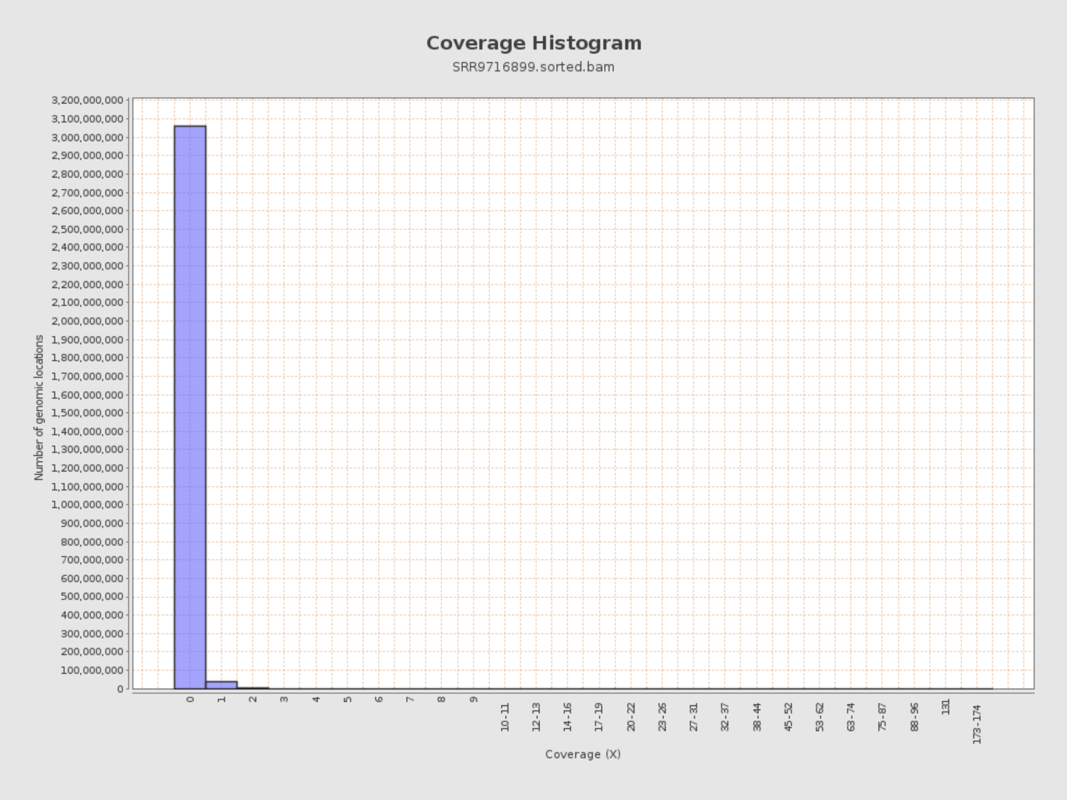
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4031101	0.0162	0.159
chr2	243199373	3453988	0.0142	0.1601
chr3	198022430	2680698	0.0135	0.1279
chr4	191154276	2574021	0.0135	0.1384
chr5	180915260	2438009	0.0135	0.1231
chr6	171115067	1739185	0.0102	0.11
chr7	159138663	2263999	0.0142	0.15

chr8	146364022	2485336	0.017	0.1445
chr9	141213431	1779230	0.0126	0.1299
chr10	135534747	2177280	0.0161	0.1996
chr11	135006516	1675877	0.0124	0.1406
chr12	133851895	1999005	0.0149	0.131
chr13	115169878	720575	0.0063	0.0854
chr14	107349540	1297406	0.0121	0.1196
chr15	102531392	830962	0.0081	0.0968
chr16	90354753	1137899	0.0126	0.1269
chr17	81195210	1630013	0.0201	0.1588
chr18	78077248	1093220	0.014	0.1559
chr19	59128983	1099039	0.0186	0.1737
chr20	63025520	1036344	0.0164	0.1413
chr21	48129895	553433	0.0115	0.1215
chr22	51304566	474478	0.0092	0.1122
chrMT	16571	6072	0.3664	0.6904
chrX	155270560	1272358	0.0082	0.1028
chrY	59373566	132672	0.0022	0.0834

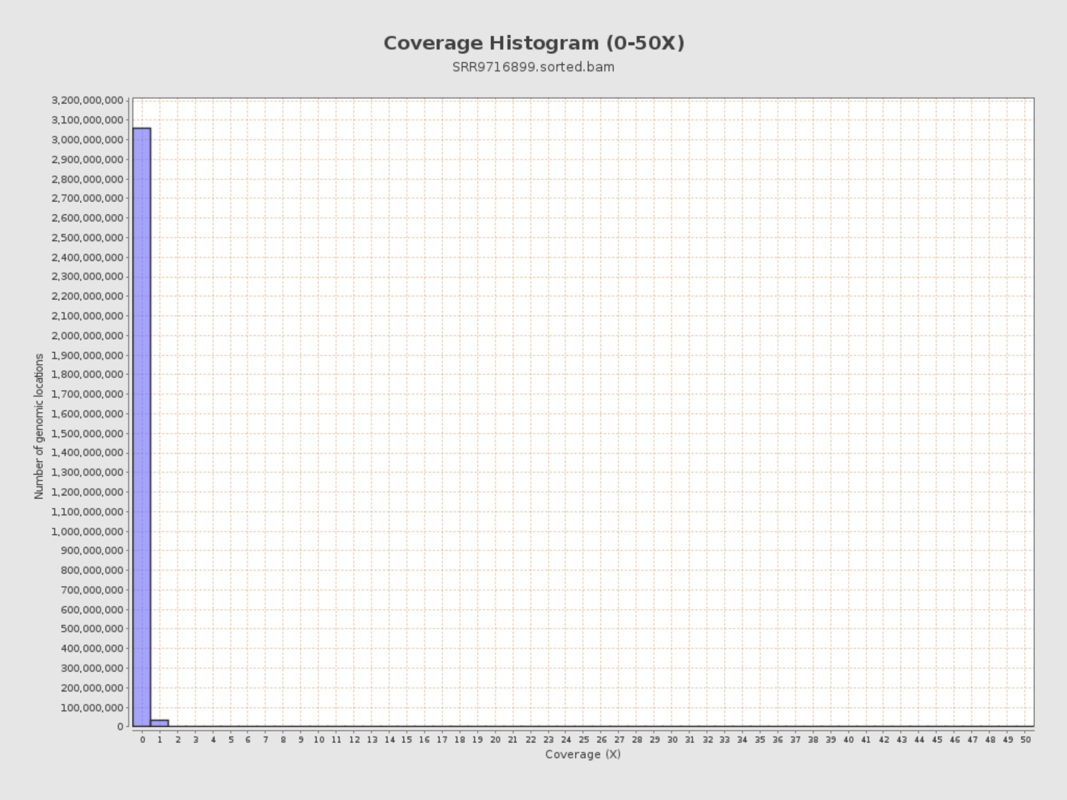
3. Results : Coverage across reference



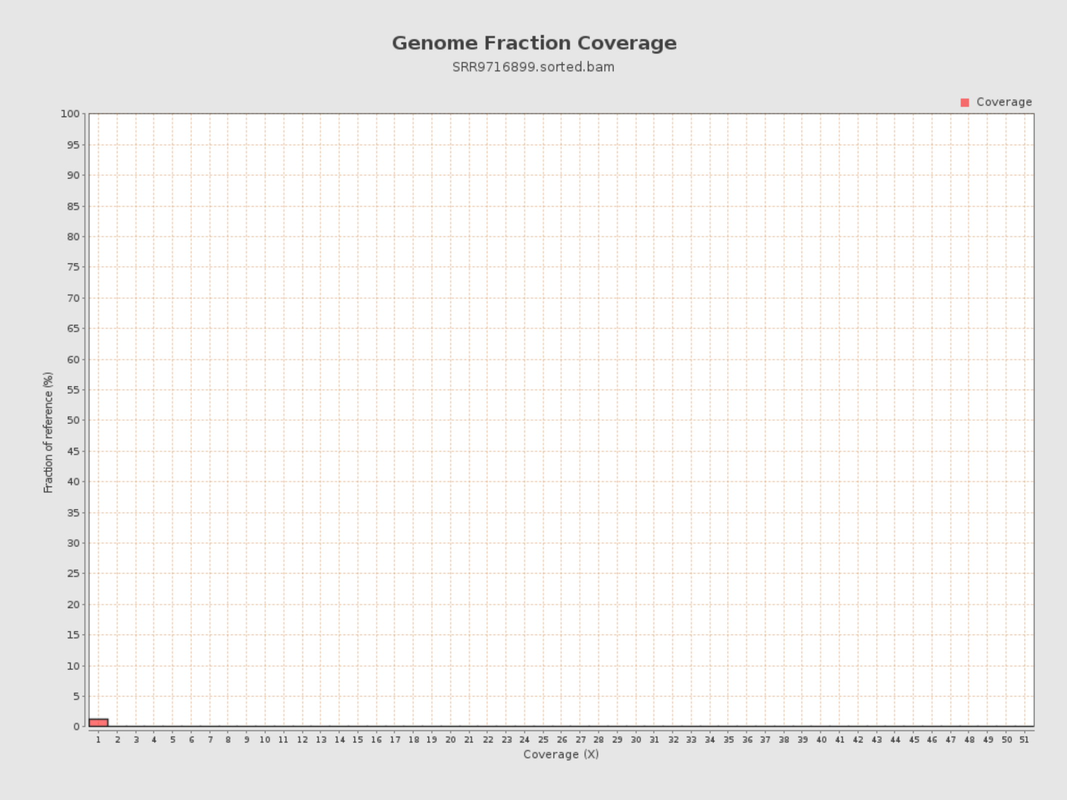
4. Results : Coverage Histogram



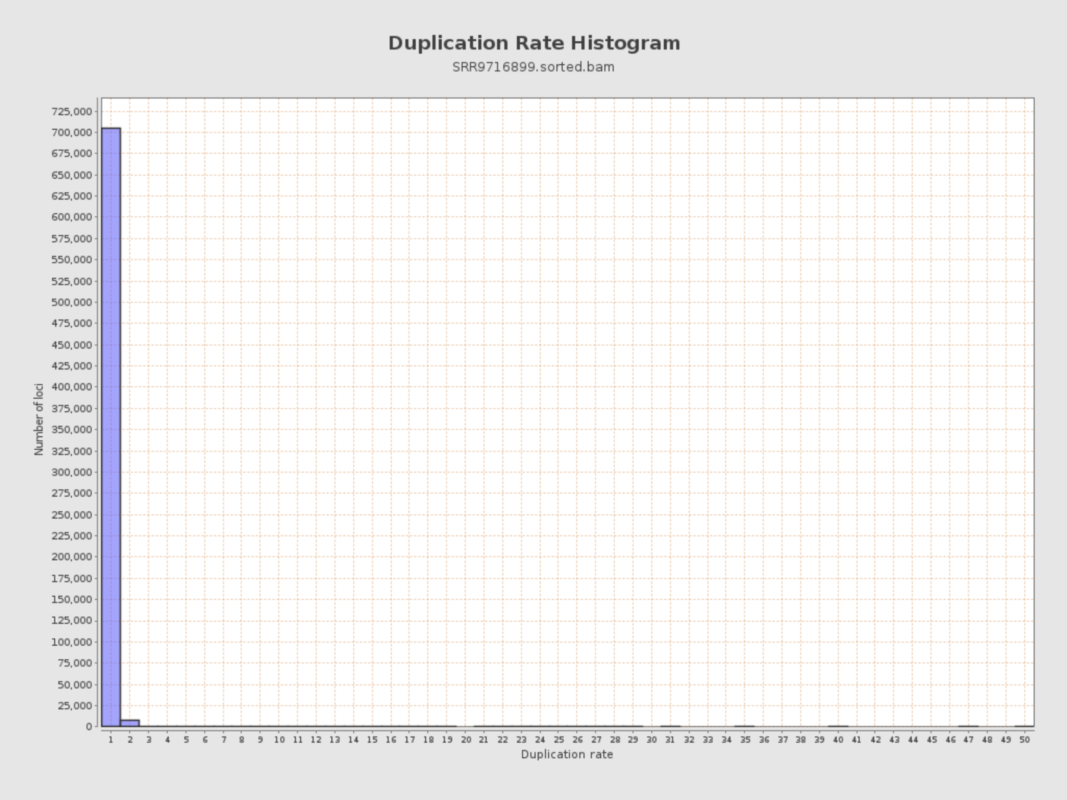
5. Results : Coverage Histogram (0-50X)



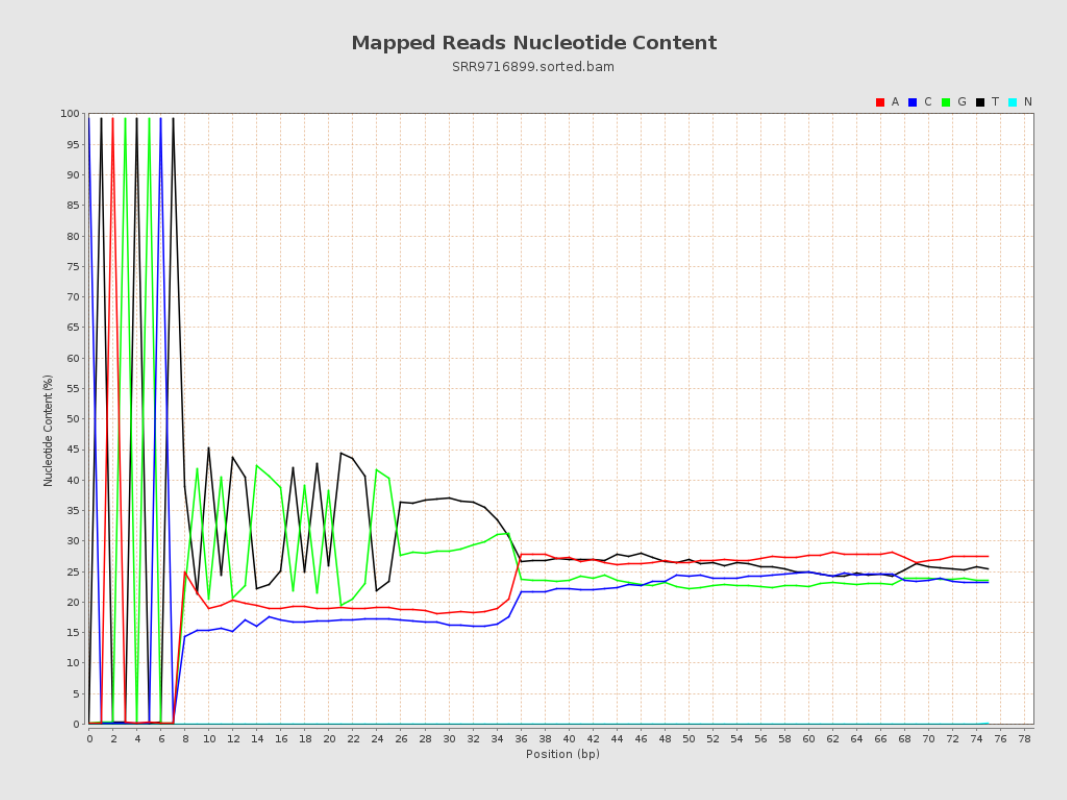
6. Results : Genome Fraction Coverage



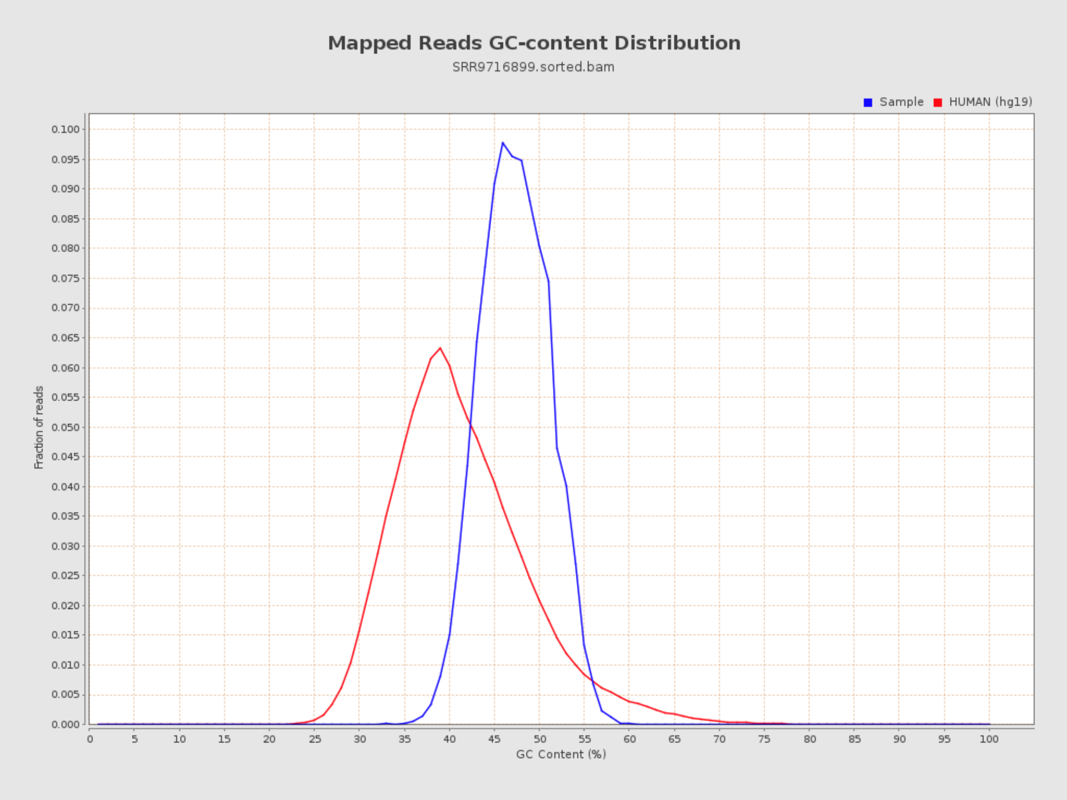
7. Results : Duplication Rate Histogram



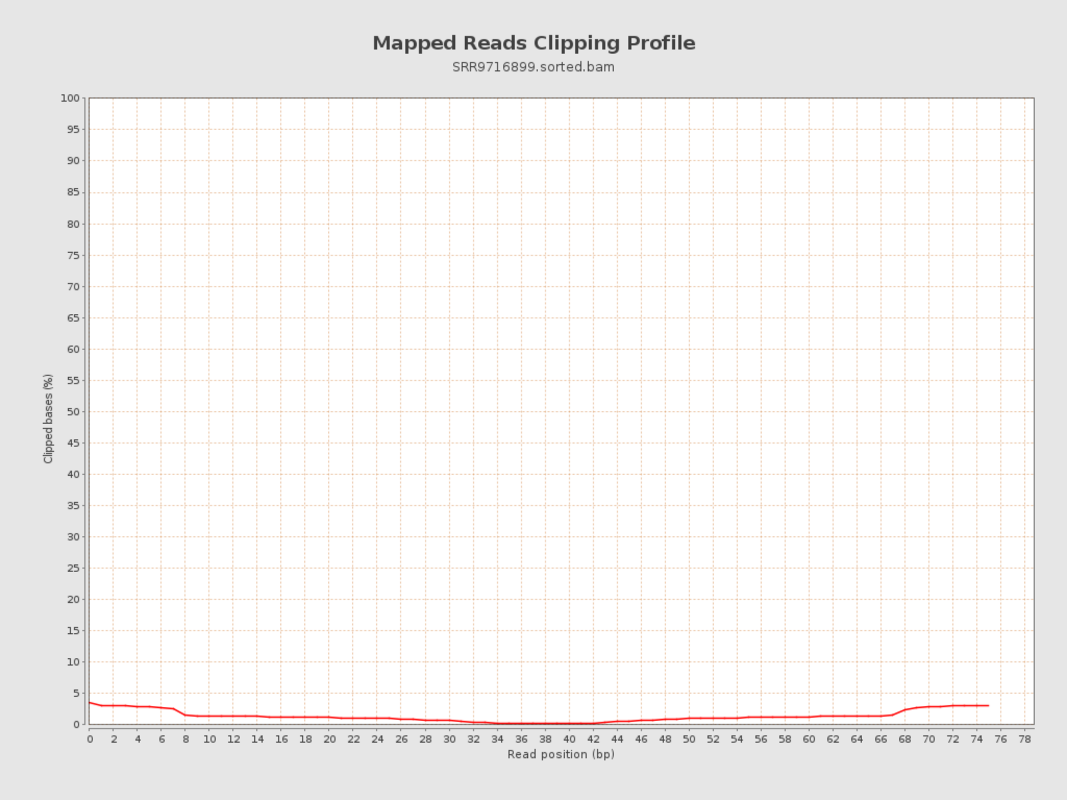
8. Results : Mapped Reads Nucleotide Content



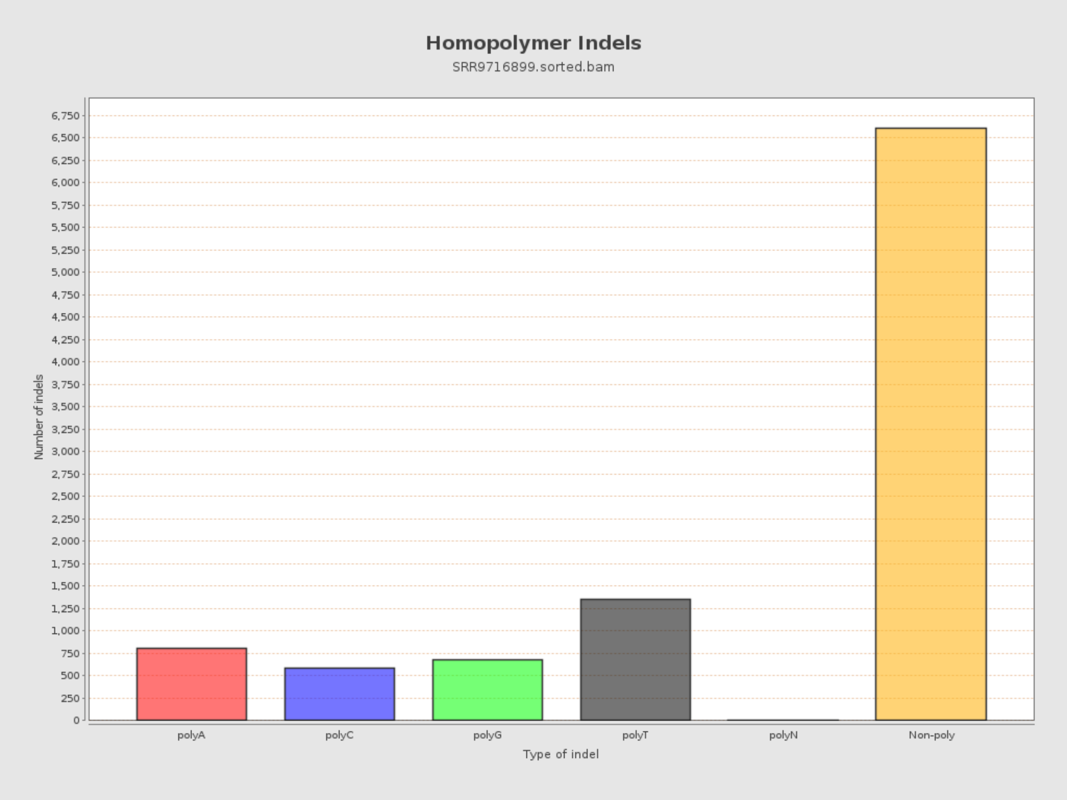
9. Results : Mapped Reads GC-content Distribution



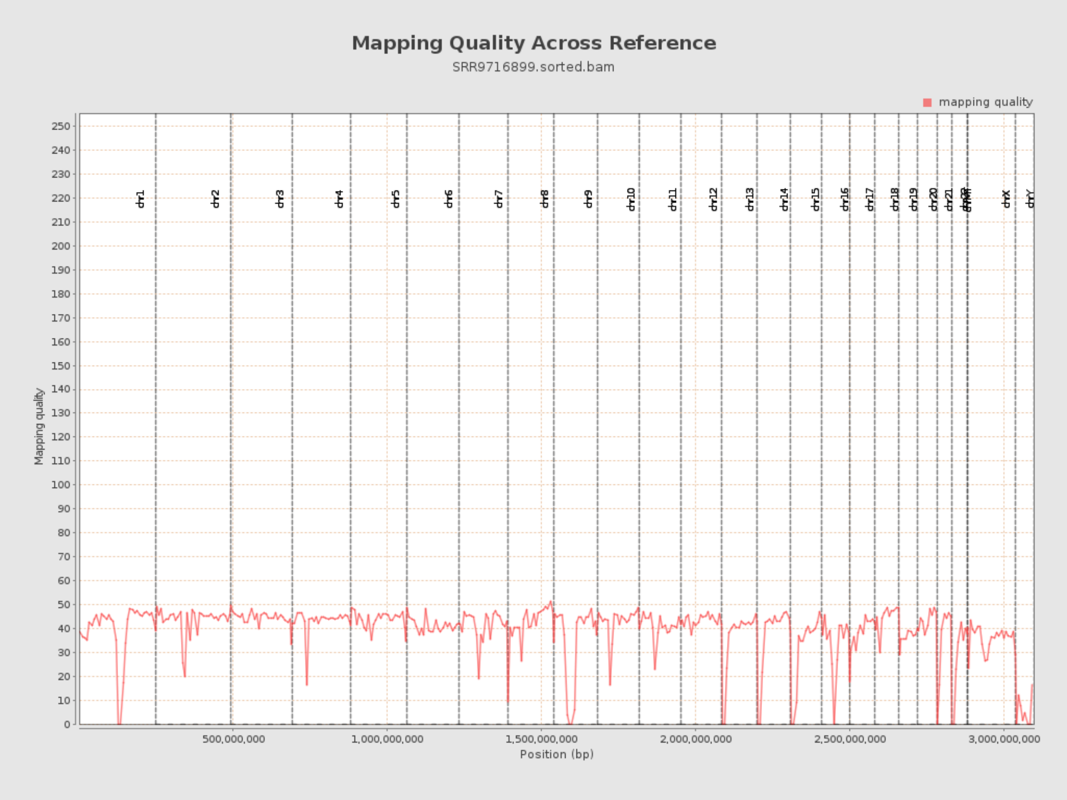
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram