Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 18:10:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716906.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_SRR9716906 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716906.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 18:10:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716906.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	788,172
Mapped reads	656,805 / 83.33%
Unmapped reads	131,367 / 16.67%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,823 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	13,076 / 1.66%
Duplication rate	1.4%
Clipped reads	657,225 / 83.39%

2.2. ACGT Content

Number/percentage of A's	8,121,966 / 22.41%
Number/percentage of C's	7,247,606 / 20%
Number/percentage of T's	11,324,146 / 31.25%
Number/percentage of G's	9,546,625 / 26.34%
Number/percentage of N's	1,084 / 0%
GC Percentage	46.34%

2.3. Coverage

Mean	0.0117

Standard Deviation	0.1307

2.4. Mapping Quality

Mean Mapping Quality	39.28

2.5. Mismatches and indels

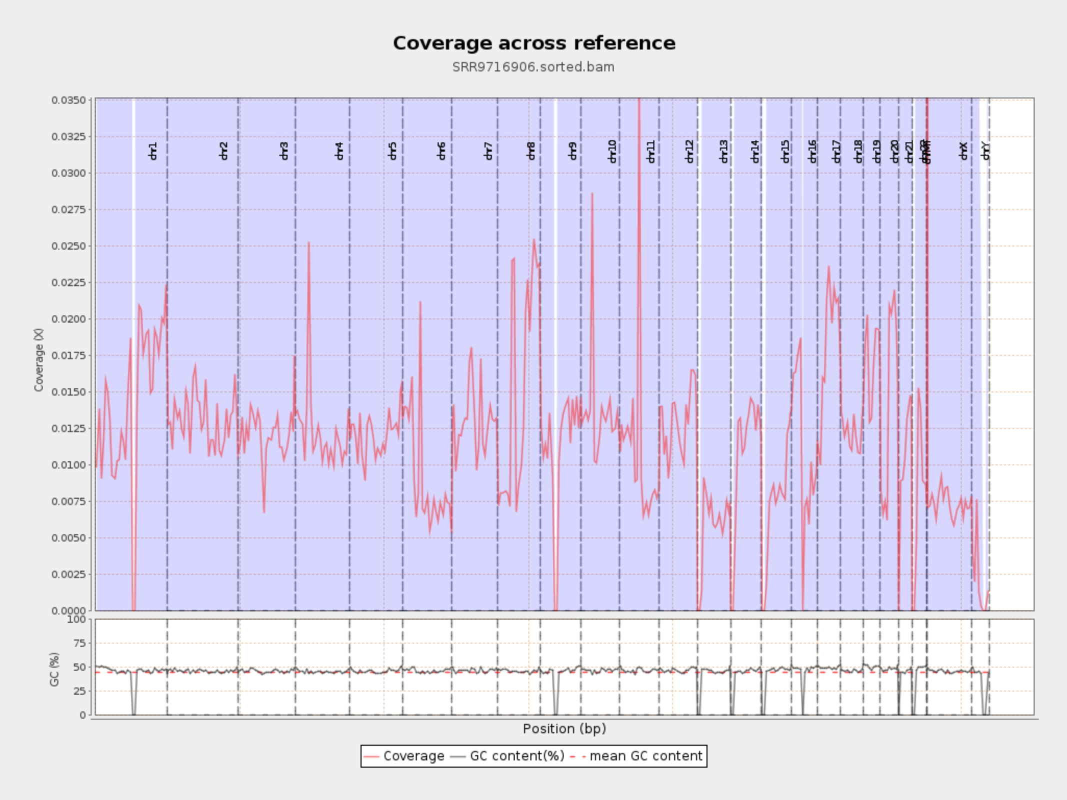
General error rate	0.56%
Mismatches	196,337
Insertions	2,635
Mapped reads with at least one insertion	0.4%
Deletions	6,531
Mapped reads with at least one deletion	0.98%
Homopolymer indels	36.32%

2.6. Chromosome stats

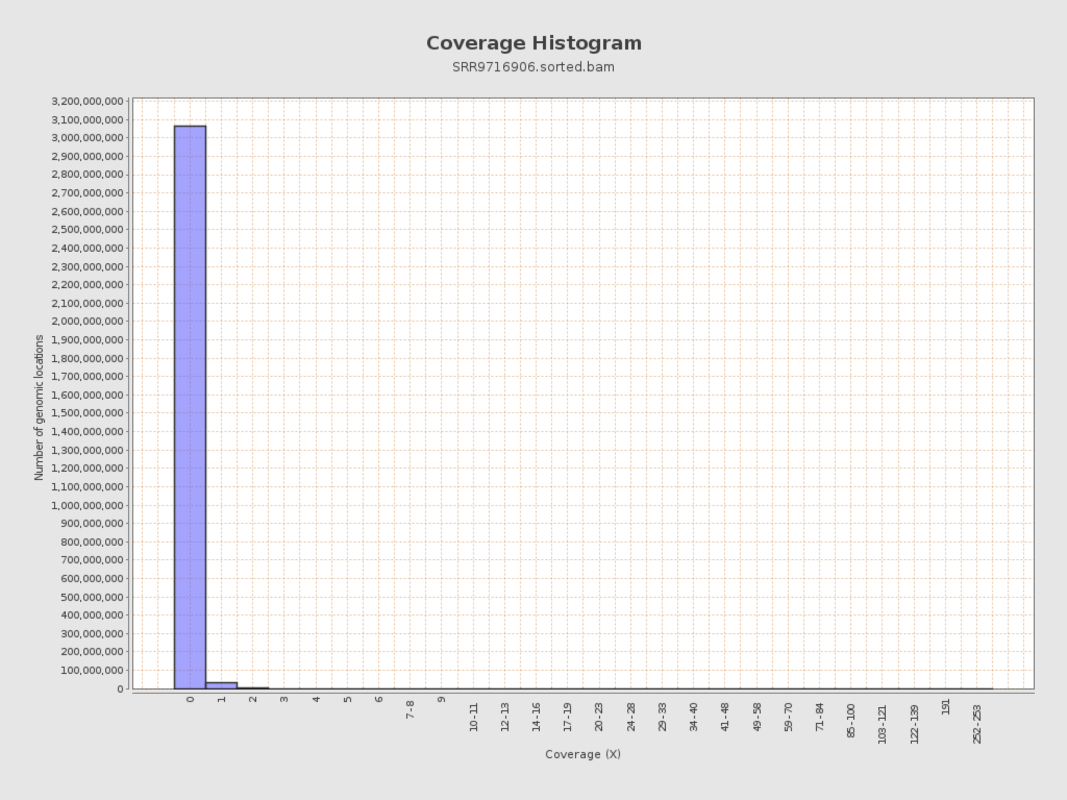
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3539138	0.0142	0.1544
chr2	243199373	3190370	0.0131	0.167
chr3	198022430	2374404	0.012	0.1206
chr4	191154276	2358780	0.0123	0.1283
chr5	180915260	2188960	0.0121	0.1165
chr6	171115067	1575723	0.0092	0.1045
chr7	159138663	2079482	0.0131	0.1408

chr8	146364022	2230743	0.0152	0.1364
chr9	141213431	1565781	0.0111	0.1189
chr10	135534747	1861312	0.0137	0.1824
chr11	135006516	1516562	0.0112	0.1315
chr12	133851895	1733938	0.013	0.1211
chr13	115169878	653785	0.0057	0.0815
chr14	107349540	1151308	0.0107	0.112
chr15	102531392	739015	0.0072	0.0923
chr16	90354753	977164	0.0108	0.1183
chr17	81195210	1481675	0.0182	0.1497
chr18	78077248	944685	0.0121	0.1392
chr19	59128983	1008598	0.0171	0.1596
chr20	63025520	891827	0.0142	0.1288
chr21	48129895	506662	0.0105	0.1171
chr22	51304566	411415	0.008	0.0968
chrMT	16571	14318	0.864	1.1331
chrX	155270560	1138656	0.0073	0.0996
chrY	59373566	118039	0.002	0.0693

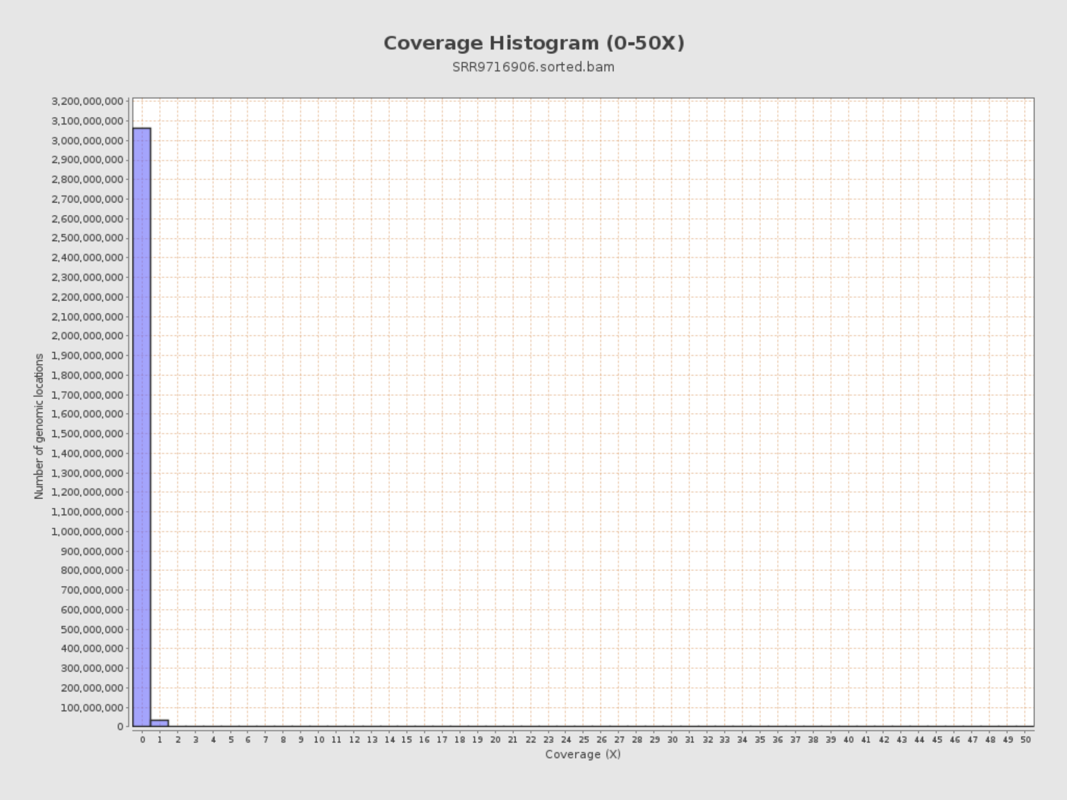
3. Results : Coverage across reference



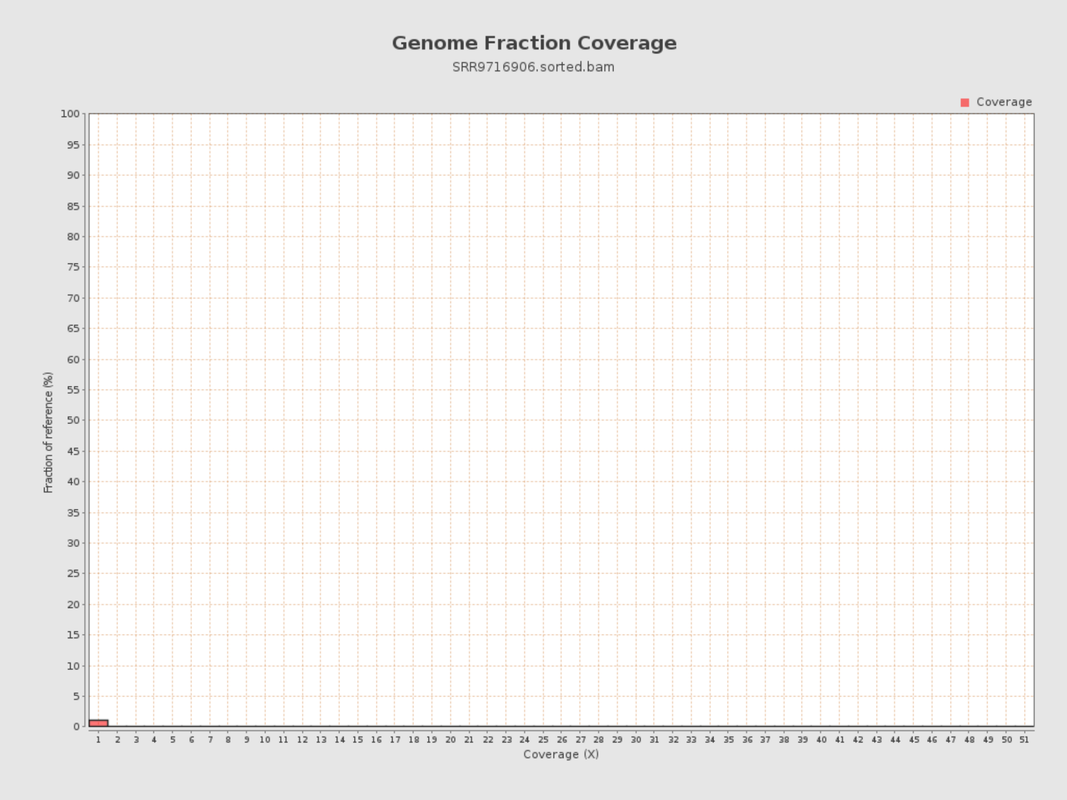
4. Results : Coverage Histogram



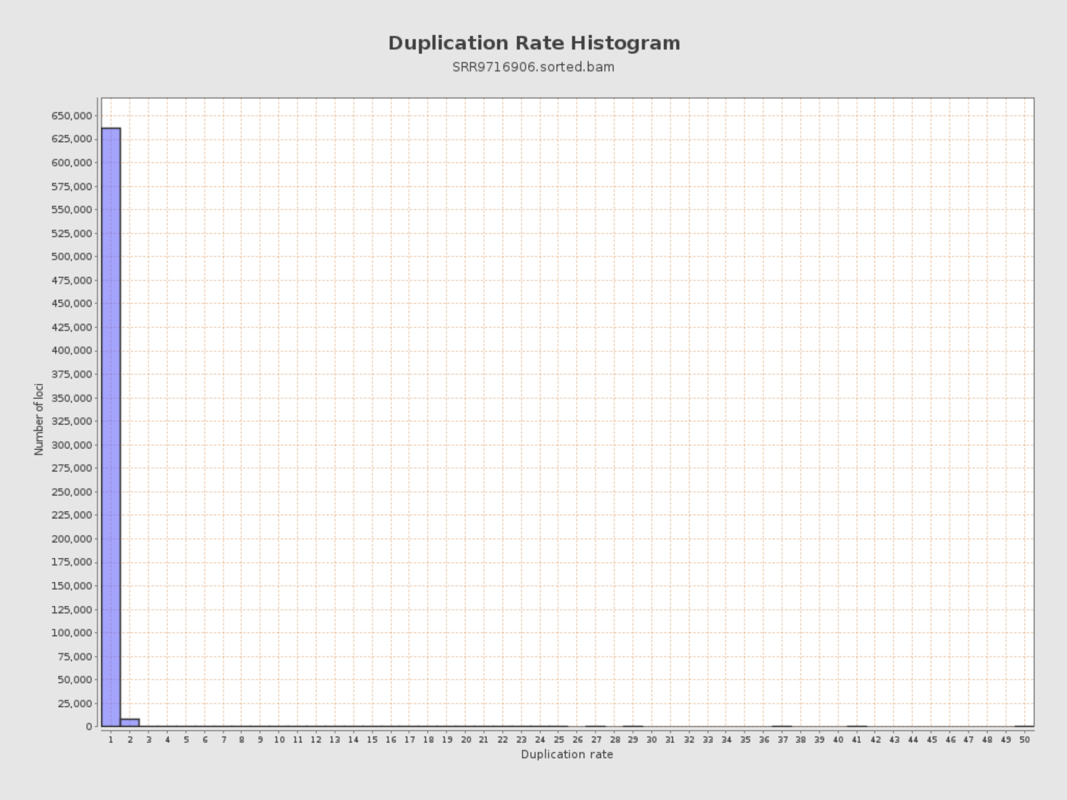
5. Results : Coverage Histogram (0-50X)



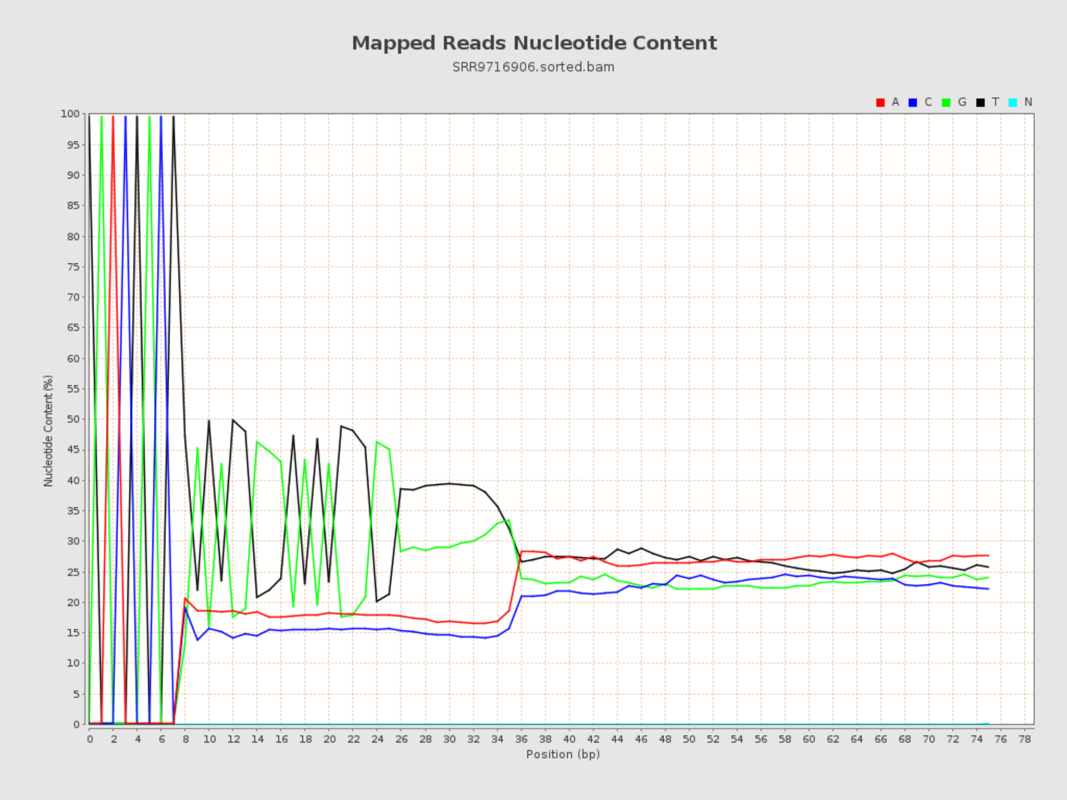
6. Results : Genome Fraction Coverage



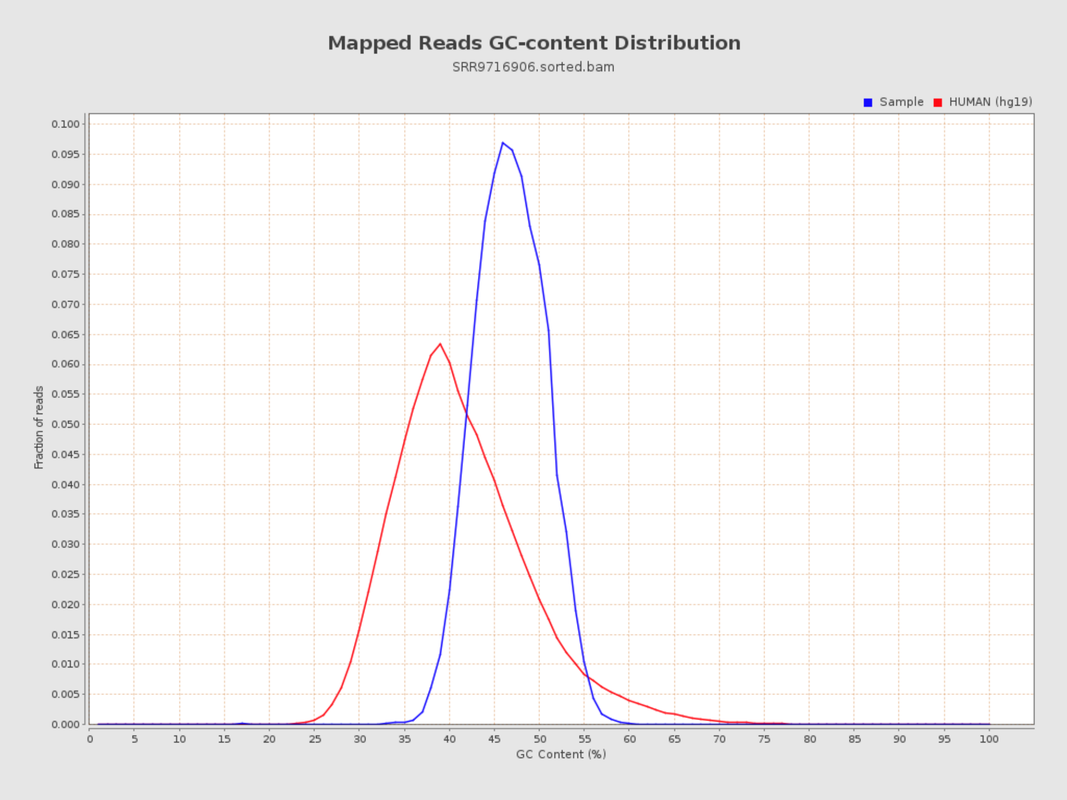
7. Results : Duplication Rate Histogram



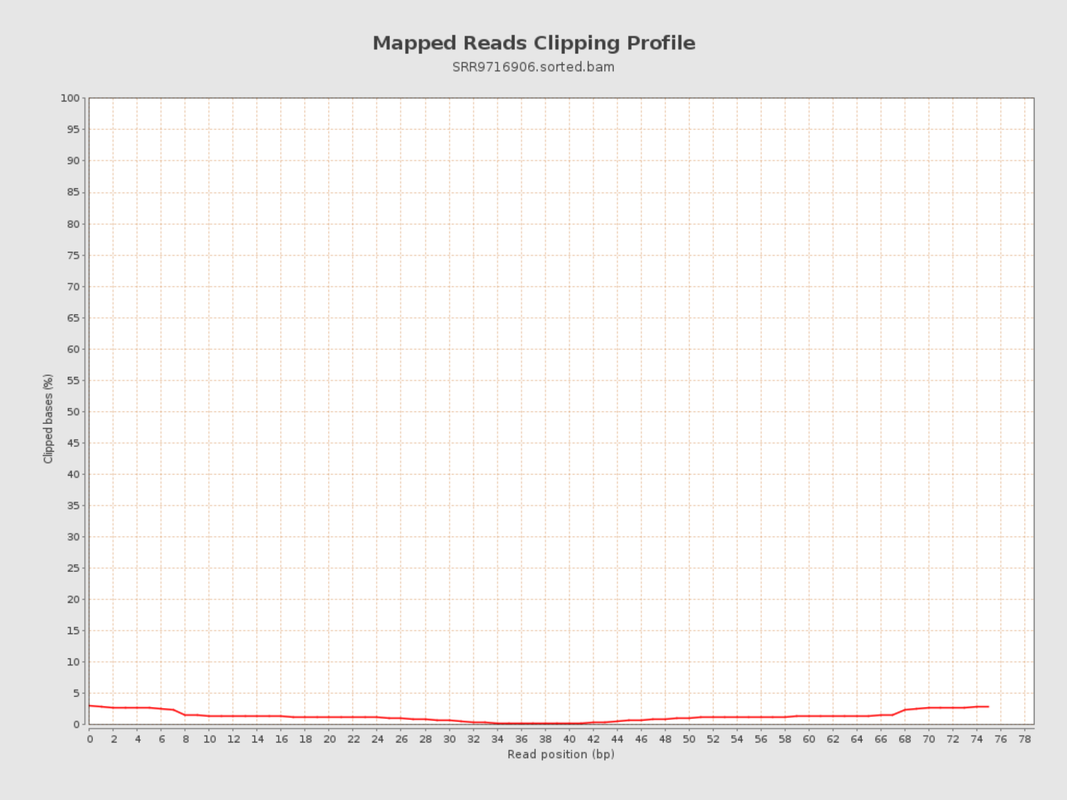
8. Results : Mapped Reads Nucleotide Content



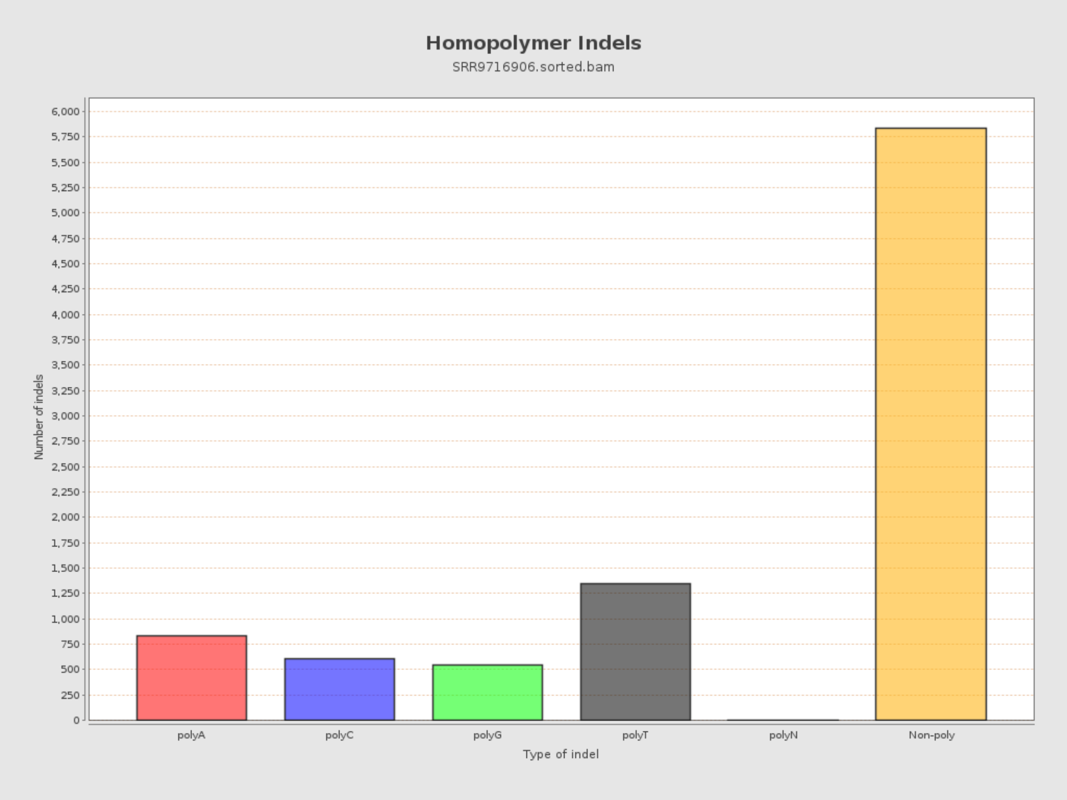
9. Results : Mapped Reads GC-content Distribution



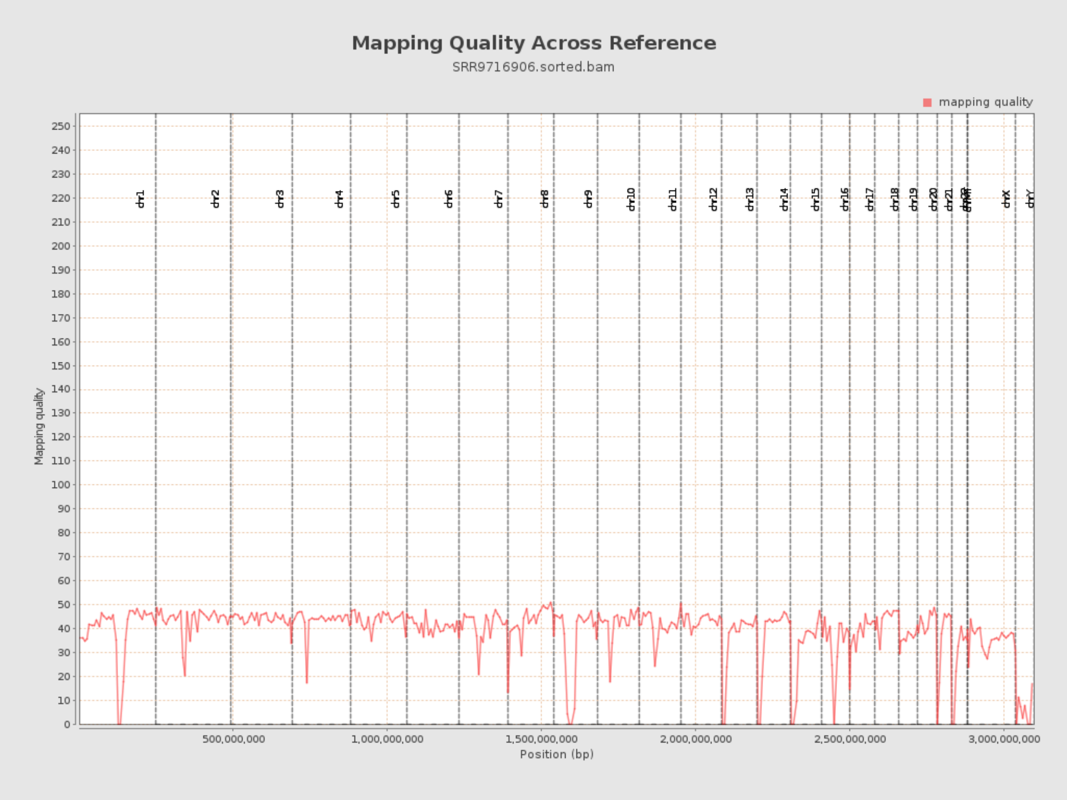
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram