Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 20:22:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716958.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_SRR9716958 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716958.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 20:22:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716958.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	976,518
Mapped reads	897,956 / 91.95%
Unmapped reads	78,562 / 8.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,930 / 0.3%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	23,094 / 2.36%
Duplication rate	1.78%
Clipped reads	897,638 / 91.92%

2.2. ACGT Content

Number/percentage of A's	13,283,348 / 25.52%
Number/percentage of C's	10,032,031 / 19.27%
Number/percentage of T's	16,523,978 / 31.74%
Number/percentage of G's	12,214,544 / 23.46%
Number/percentage of N's	1,022 / 0%
GC Percentage	42.74%

2.3. Coverage

Mean	0.0168

Standard Deviation	0.1844

2.4. Mapping Quality

Mean Mapping Quality	44.43

2.5. Mismatches and indels

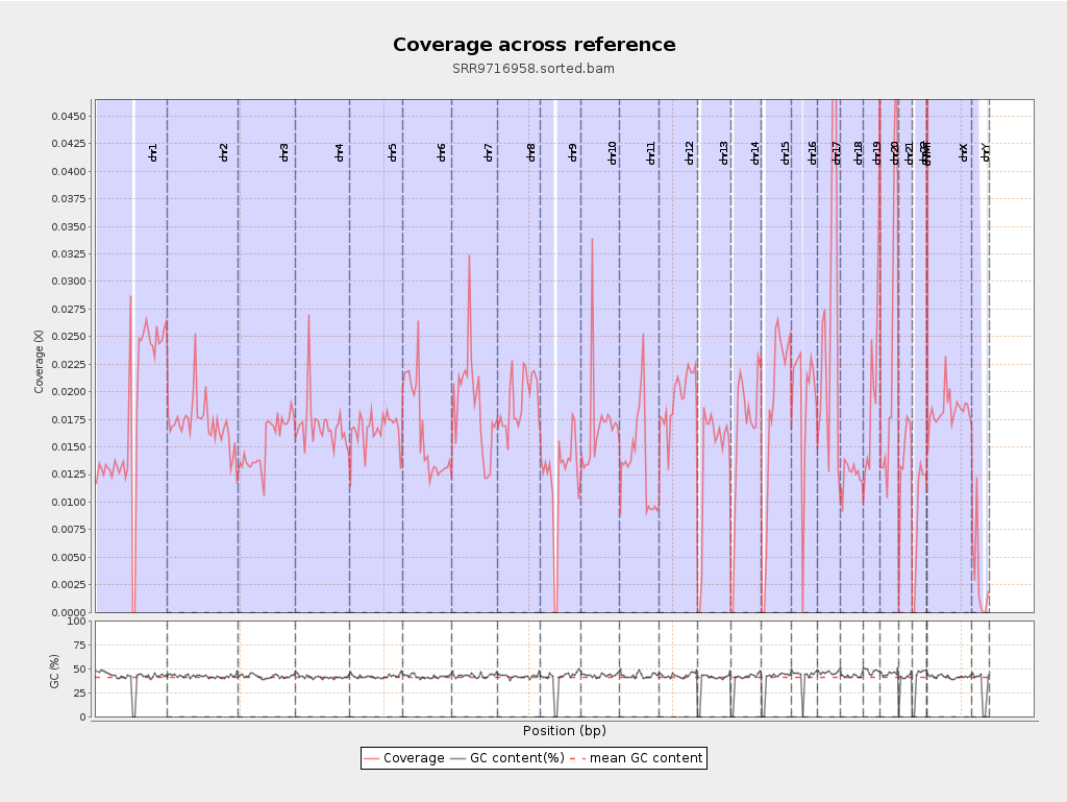
General error rate	0.51%
Mismatches	258,790
Insertions	4,324
Mapped reads with at least one insertion	0.48%
Deletions	9,743
Mapped reads with at least one deletion	1.08%
Homopolymer indels	42.58%

2.6. Chromosome stats

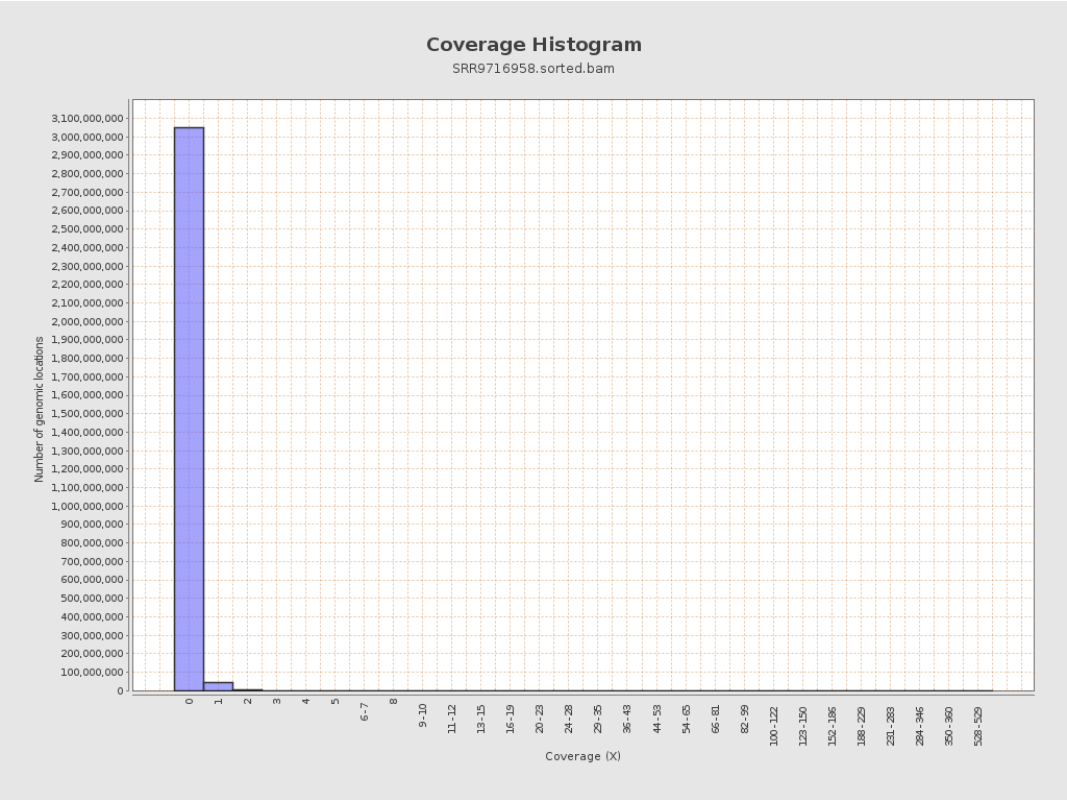
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4423388	0.0177	0.2862
chr2	243199373	4151126	0.0171	0.2527
chr3	198022430	3040245	0.0154	0.131
chr4	191154276	3237726	0.0169	0.1485
chr5	180915260	3010434	0.0166	0.1357
chr6	171115067	2793185	0.0163	0.1508
chr7	159138663	2997543	0.0188	0.234

chr8	146364022	2805438	0.0192	0.2308
chr9	141213431	1730101	0.0123	0.1361
chr10	135534747	2286521	0.0169	0.1902
chr11	135006516	1863590	0.0138	0.1425
chr12	133851895	2597244	0.0194	0.1477
chr13	115169878	1594418	0.0138	0.1233
chr14	107349540	1756600	0.0164	0.136
chr15	102531392	1875572	0.0183	0.1422
chr16	90354753	1730857	0.0192	0.1498
chr17	81195210	2229037	0.0275	0.1781
chr18	78077248	970249	0.0124	0.205
chr19	59128983	1241156	0.021	0.2223
chr20	63025520	1504298	0.0239	0.1652
chr21	48129895	670525	0.0139	0.1353
chr22	51304566	454780	0.0089	0.0986
chrMT	16571	76343	4.607	3.3835
chrX	155270560	2849359	0.0184	0.1499
chrY	59373566	180699	0.003	0.1297

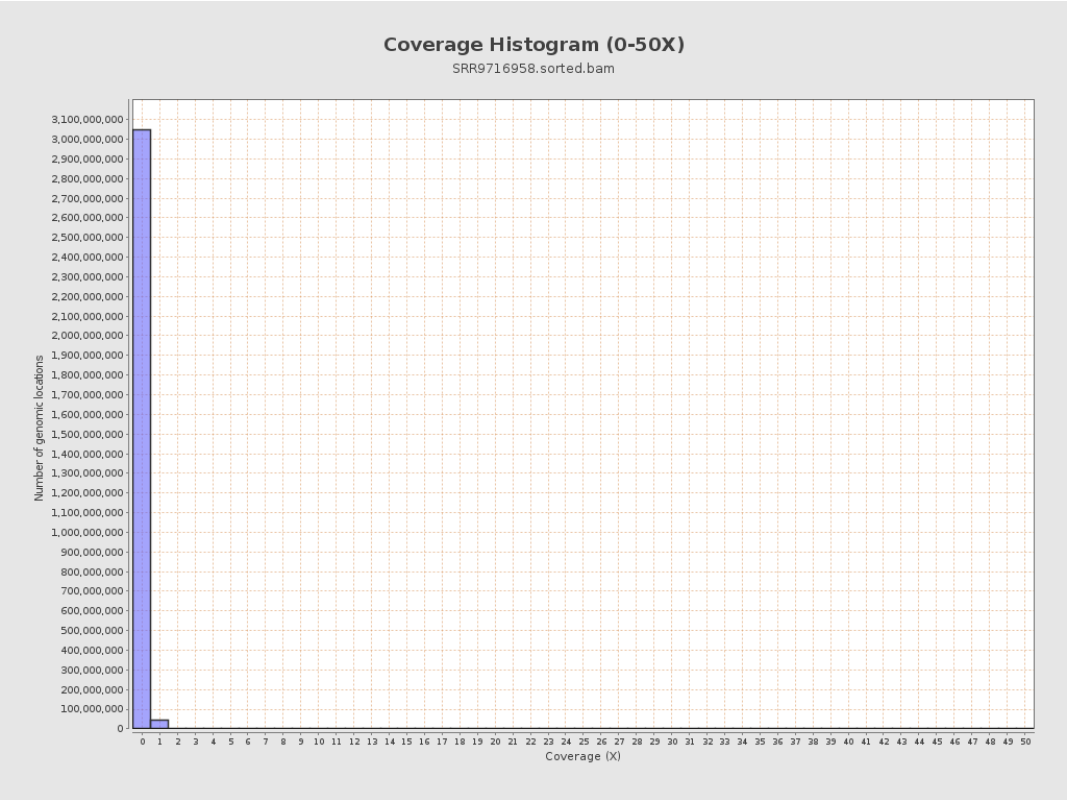
3. Results : Coverage across reference



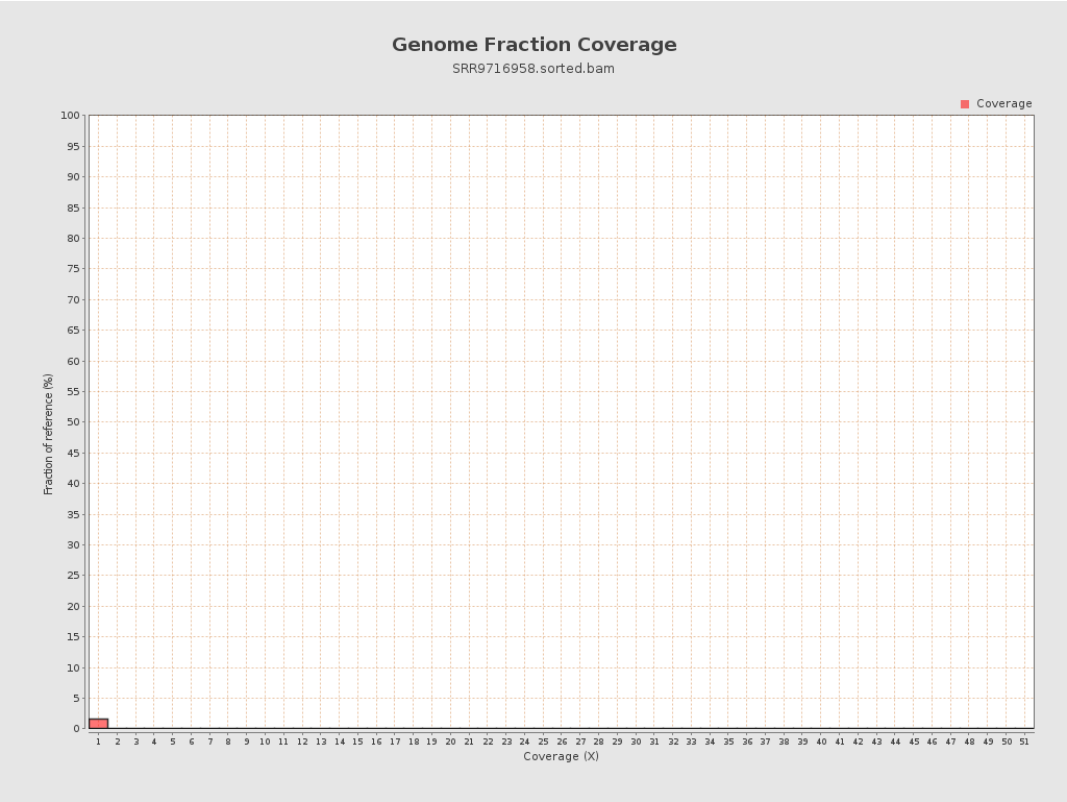
4. Results : Coverage Histogram



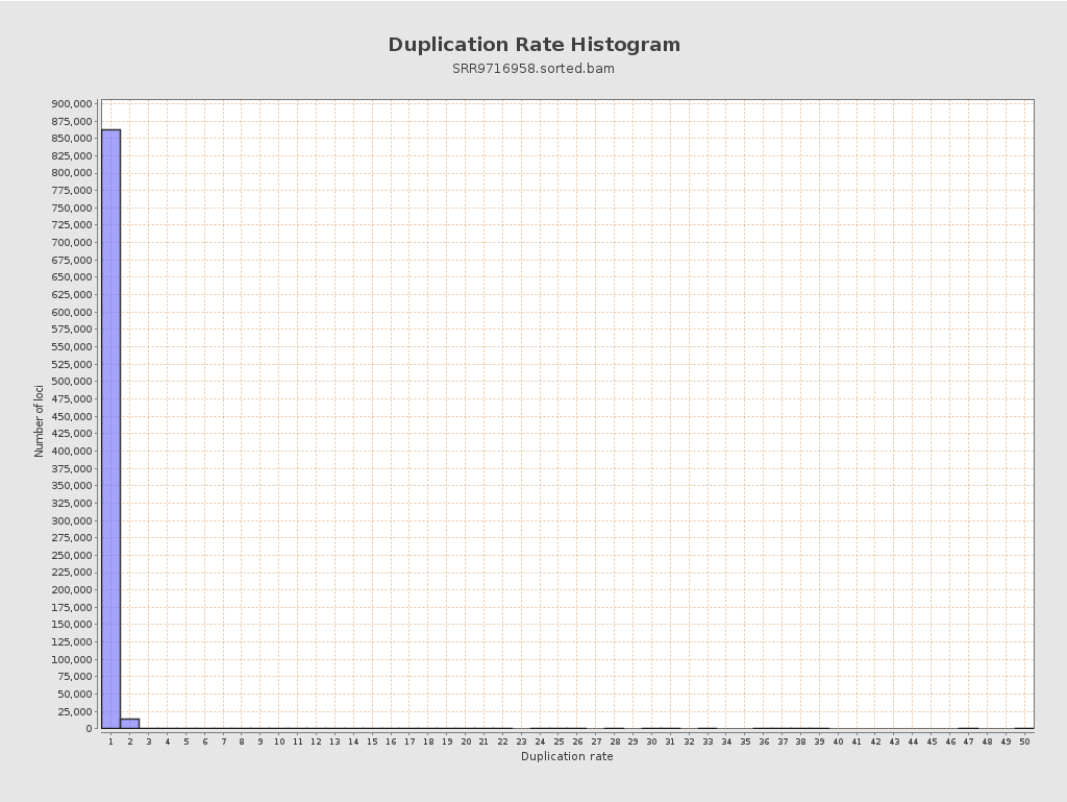
5. Results : Coverage Histogram (0-50X)



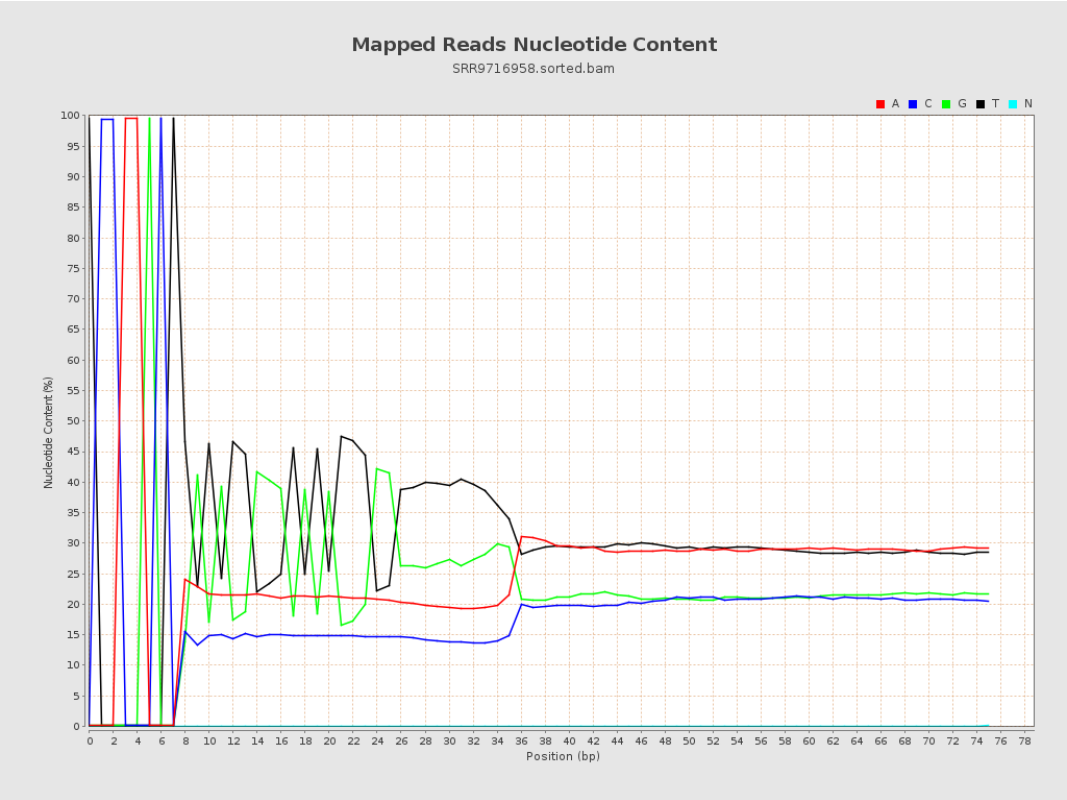
6. Results : Genome Fraction Coverage



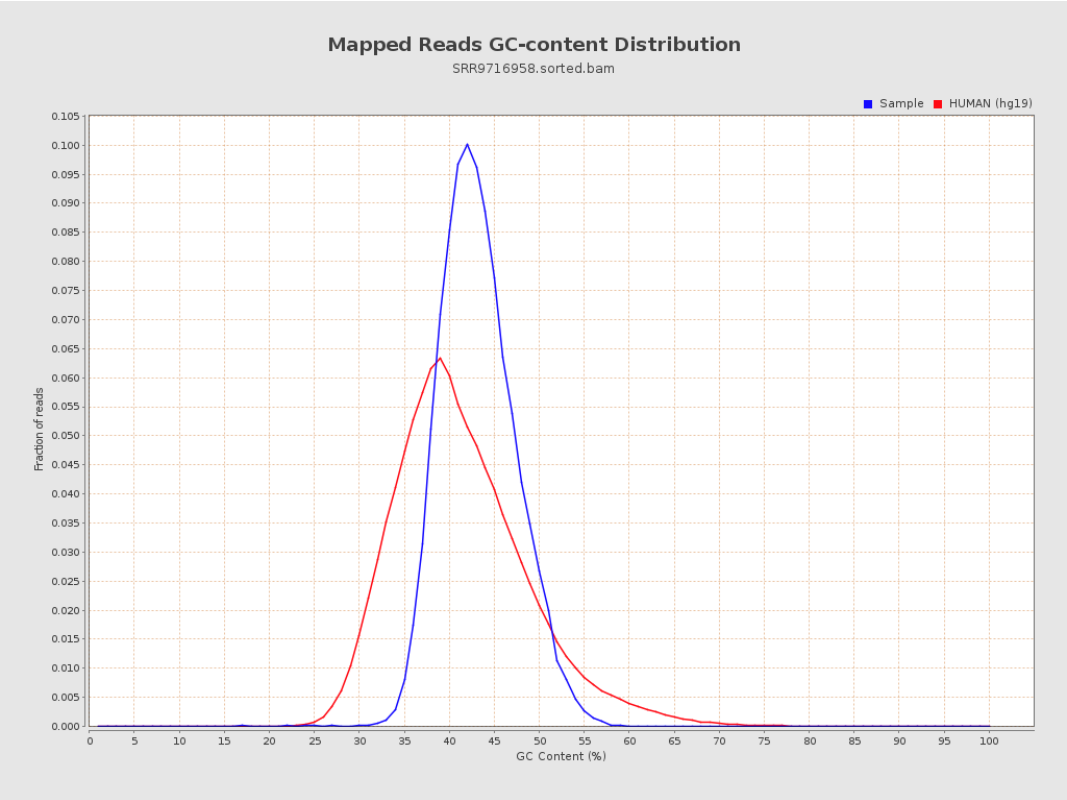
7. Results : Duplication Rate Histogram



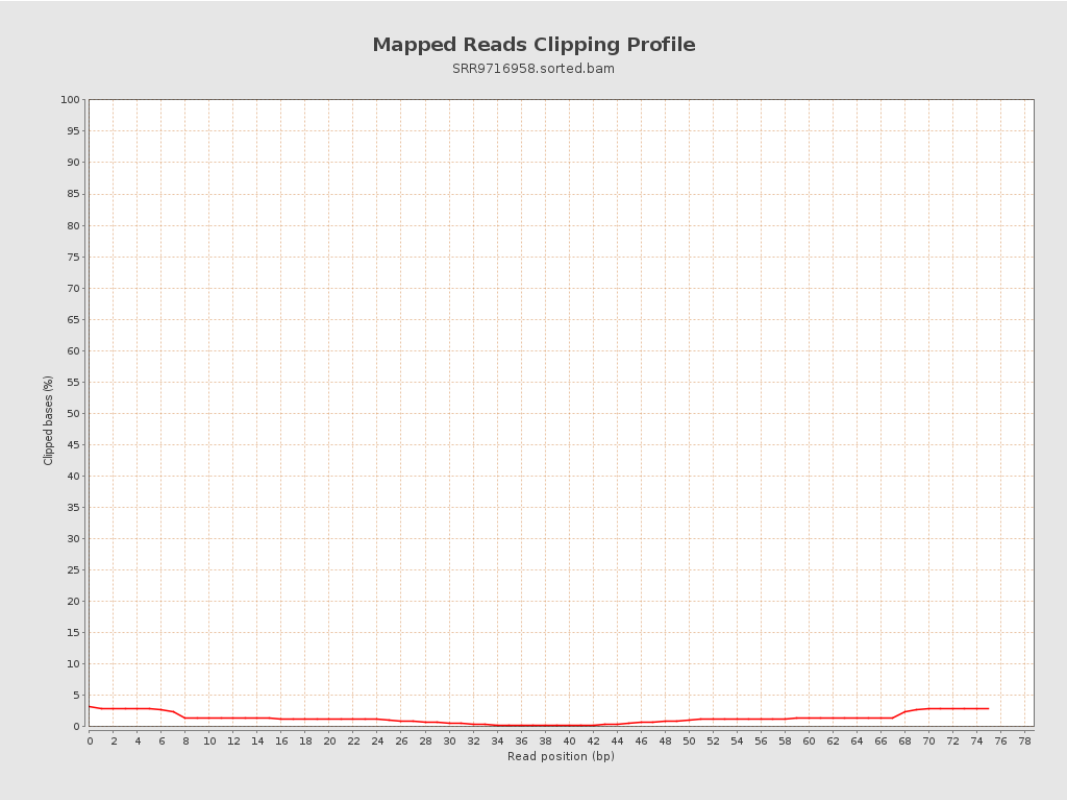
8. Results : Mapped Reads Nucleotide Content



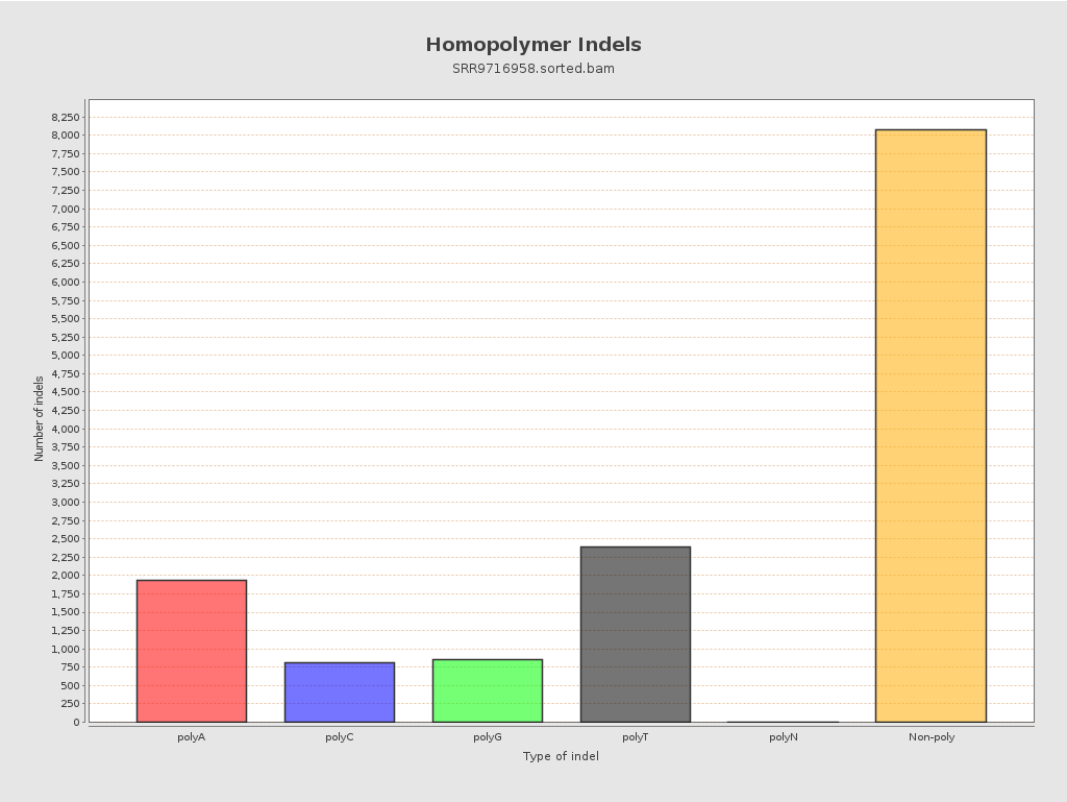
9. Results : Mapped Reads GC-content Distribution



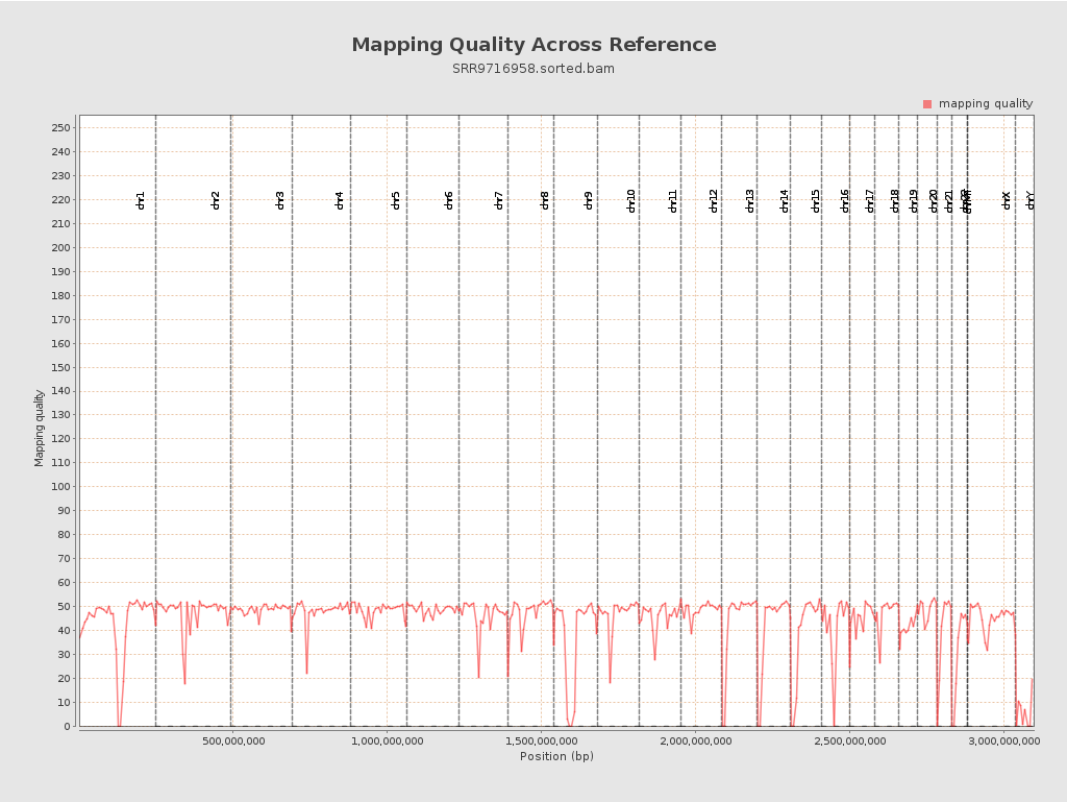
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram