Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/02 06:16:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716299.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_SRR9716299 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716299.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 02 06:16:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716299.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,451,960
Mapped reads	1,264,434 / 87.08%
Unmapped reads	187,526 / 12.92%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,784 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	31,105 / 2.14%
Duplication rate	1.81%
Clipped reads	1,267,480 / 87.29%

2.2. ACGT Content

Number/percentage of A's	17,927,603 / 25.08%
Number/percentage of C's	13,747,552 / 19.23%
Number/percentage of T's	22,465,023 / 31.42%
Number/percentage of G's	17,349,146 / 24.27%
Number/percentage of N's	1,378 / 0%
GC Percentage	43.5%

2.3. Coverage

Mean	0.0231

Standard Deviation	0.2011

2.4. Mapping Quality

Mean Mapping Quality	43.79

2.5. Mismatches and indels

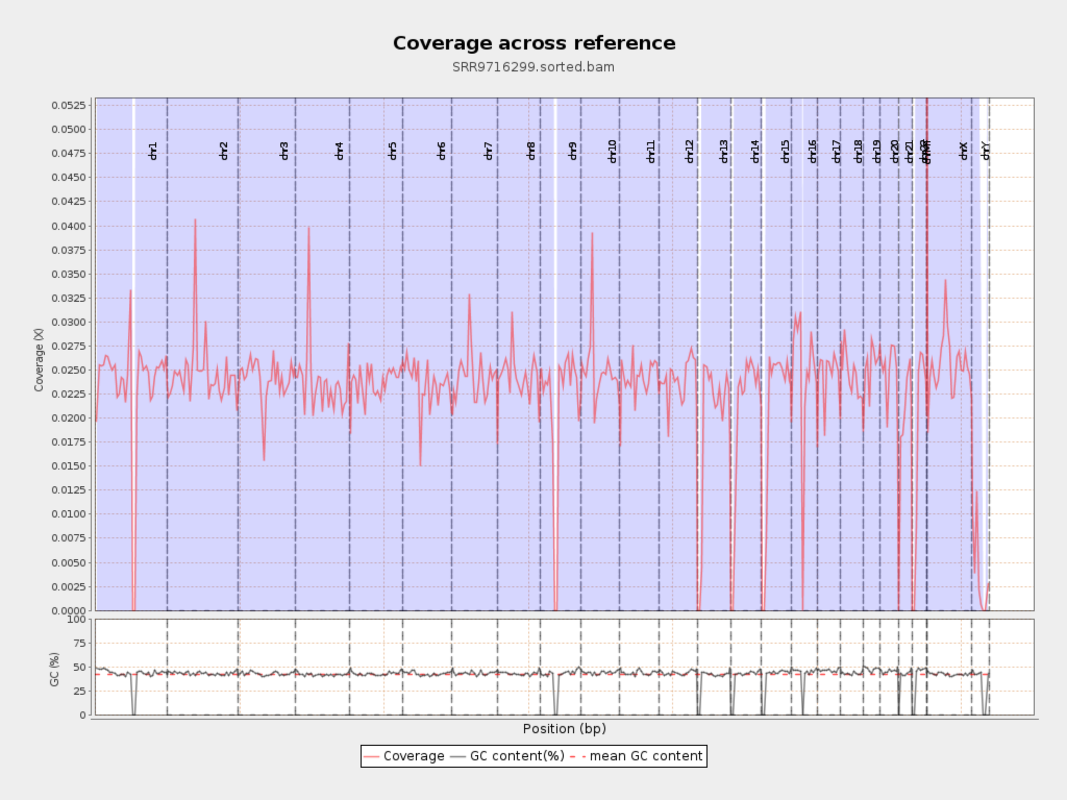
General error rate	0.52%
Mismatches	361,674
Insertions	4,540
Mapped reads with at least one insertion	0.36%
Deletions	11,237
Mapped reads with at least one deletion	0.88%
Homopolymer indels	40.06%

2.6. Chromosome stats

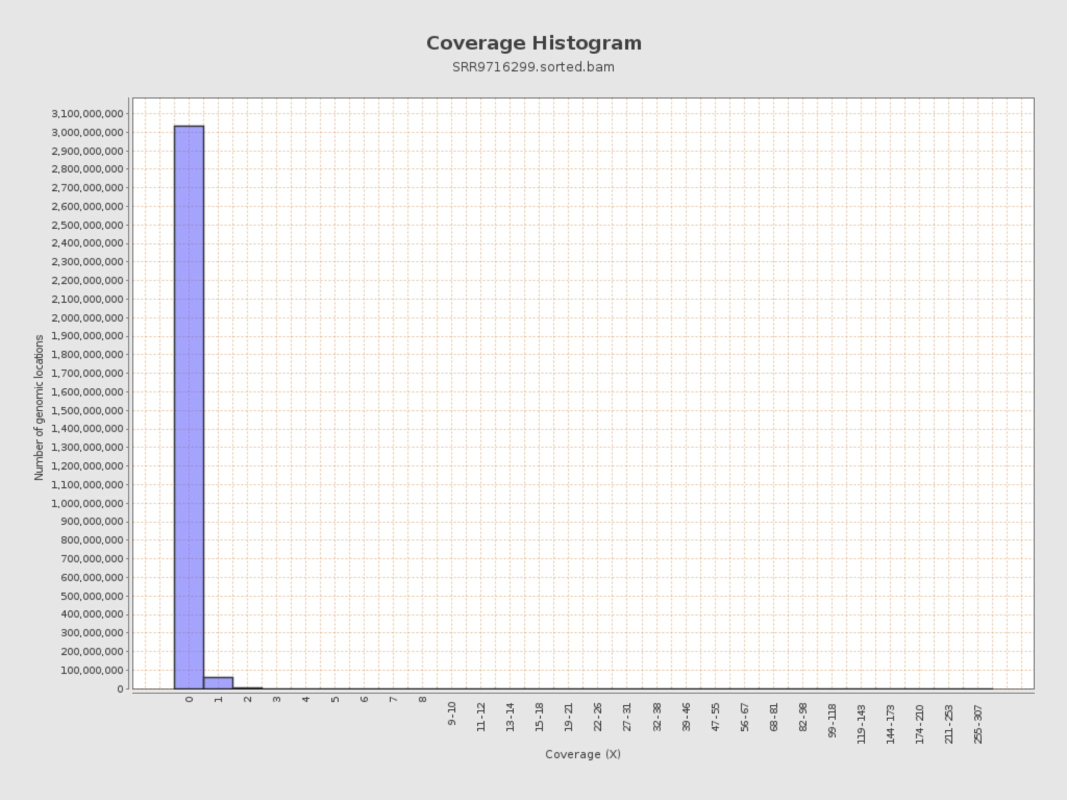
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5805697	0.0233	0.281
chr2	243199373	6007674	0.0247	0.2313
chr3	198022430	4761897	0.024	0.1662
chr4	191154276	4556159	0.0238	0.1794
chr5	180915260	4312968	0.0238	0.1666
chr6	171115067	4030381	0.0236	0.172
chr7	159138663	3883770	0.0244	0.2227

chr8	146364022	3570838	0.0244	0.1886
chr9	141213431	3006531	0.0213	0.2053
chr10	135534747	3412312	0.0252	0.2092
chr11	135006516	3289293	0.0244	0.2021
chr12	133851895	3212761	0.024	0.1679
chr13	115169878	2217377	0.0193	0.1476
chr14	107349540	2157465	0.0201	0.1576
chr15	102531392	2085038	0.0203	0.1527
chr16	90354753	2177545	0.0241	0.1784
chr17	81195210	1997906	0.0246	0.1743
chr18	78077248	1915937	0.0245	0.3509
chr19	59128983	1505353	0.0255	0.2382
chr20	63025520	1562251	0.0248	0.176
chr21	48129895	939393	0.0195	0.1657
chr22	51304566	898942	0.0175	0.1418
chrMT	16571	1325	0.08	0.2969
chrX	155270560	3978655	0.0256	0.193
chrY	59373566	222449	0.0037	0.0955

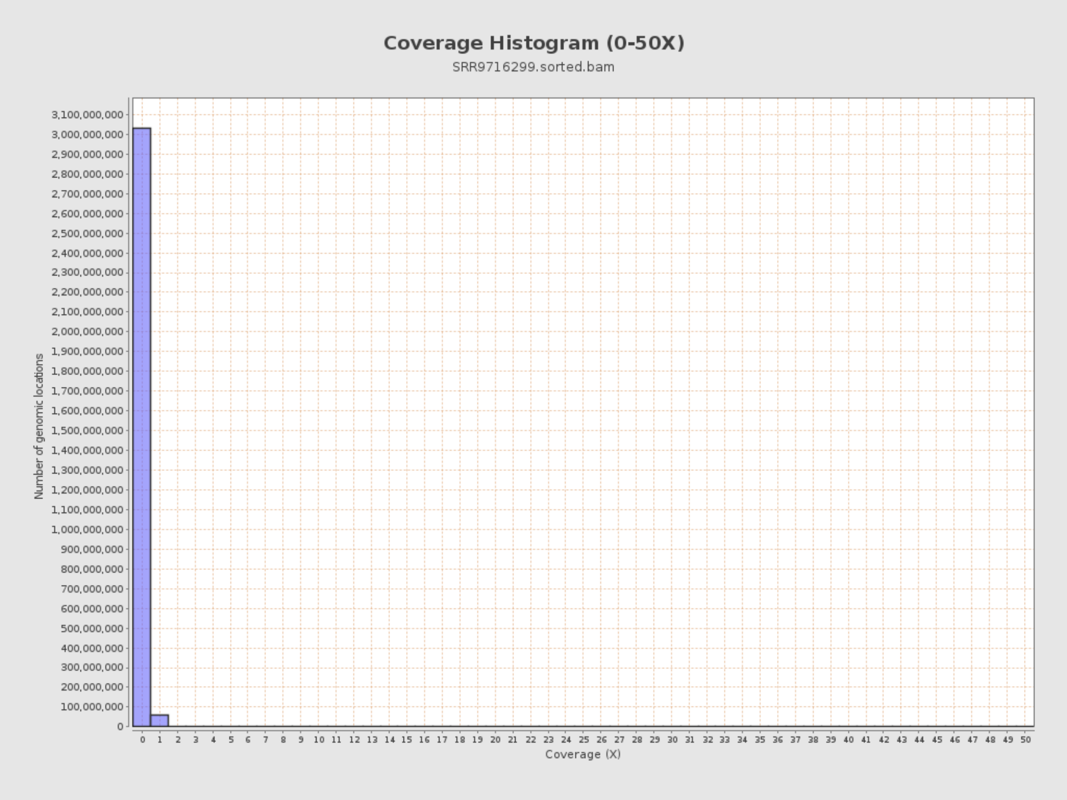
3. Results : Coverage across reference



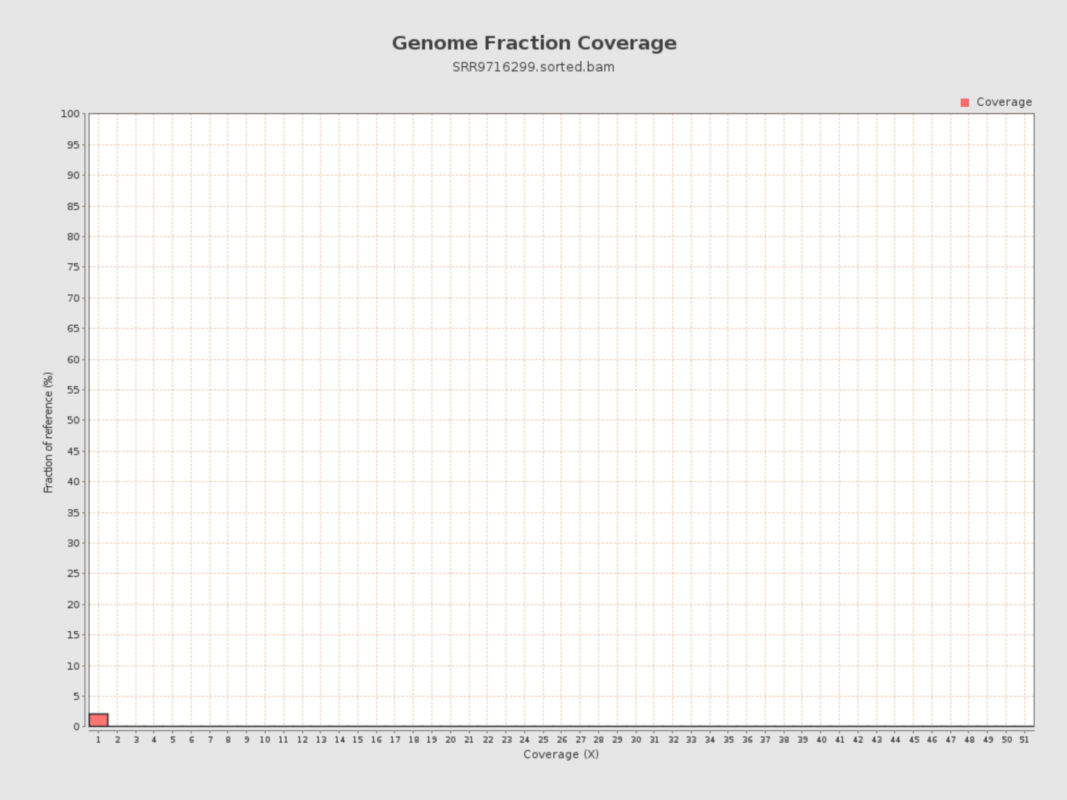
4. Results : Coverage Histogram



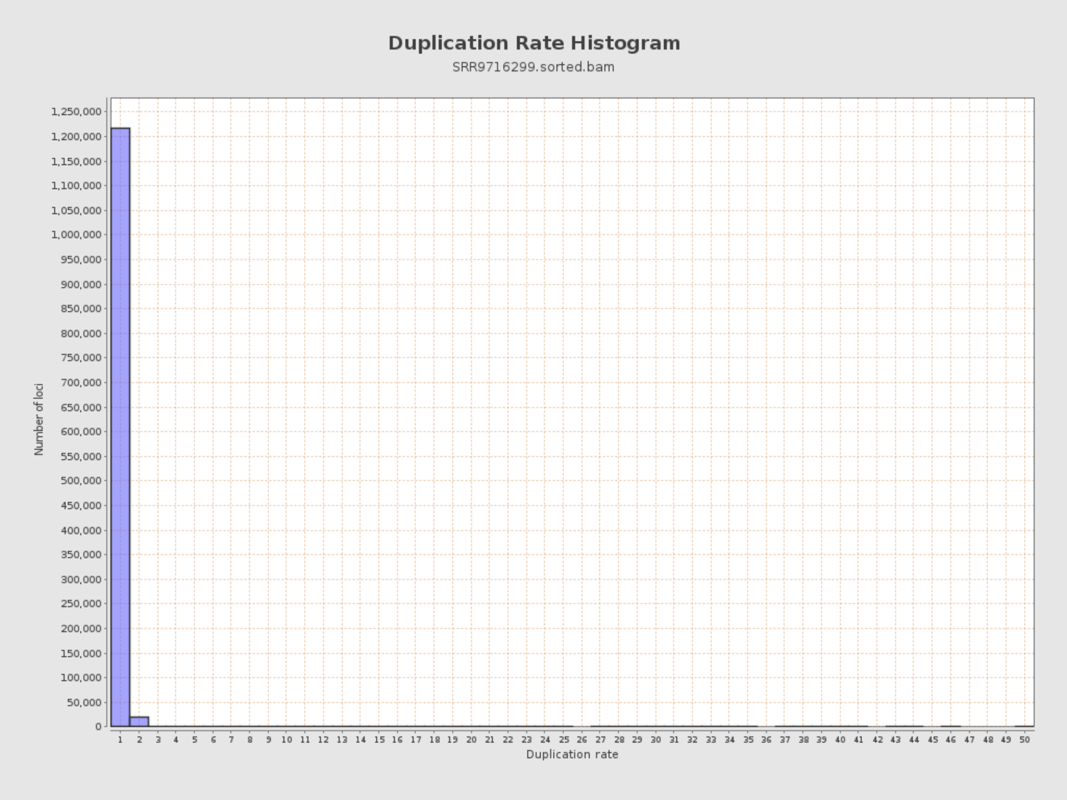
5. Results : Coverage Histogram (0-50X)



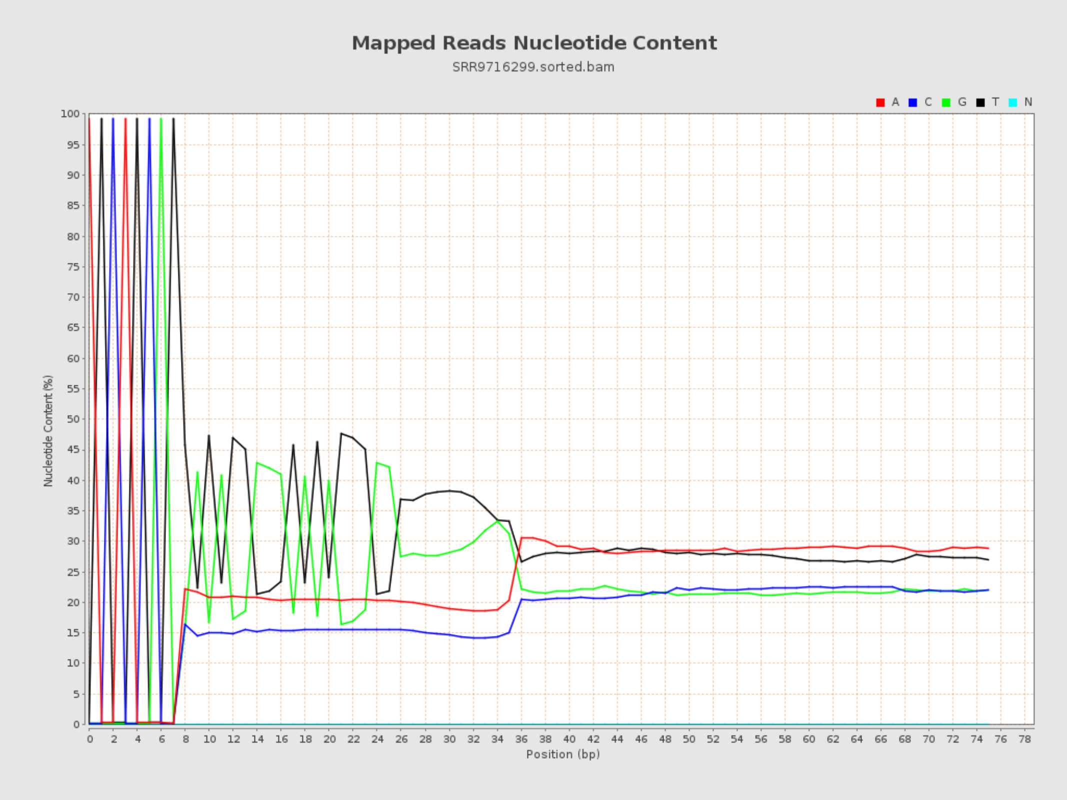
6. Results : Genome Fraction Coverage



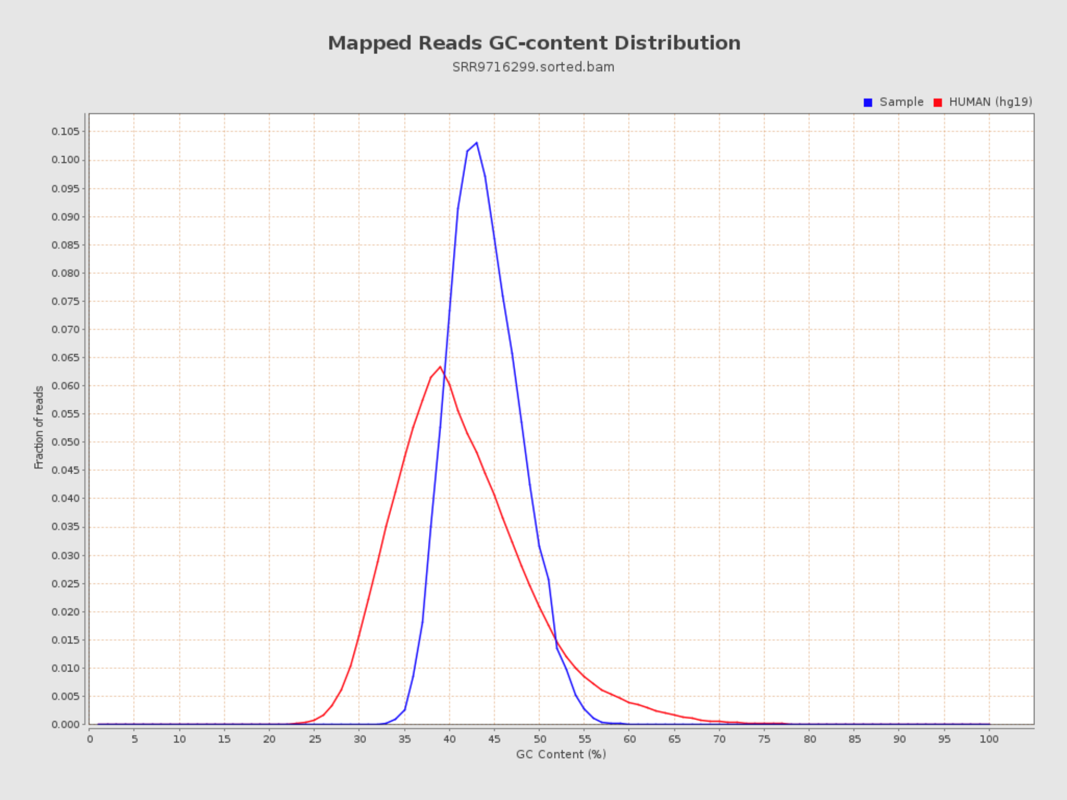
7. Results : Duplication Rate Histogram



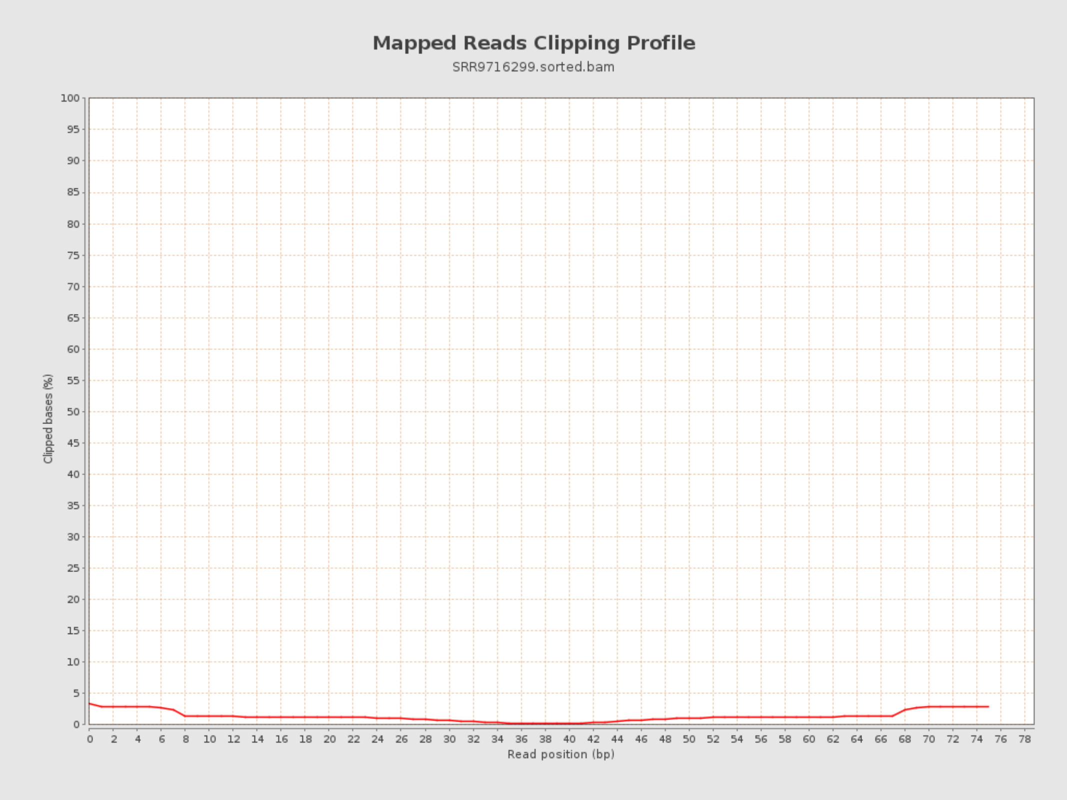
8. Results : Mapped Reads Nucleotide Content



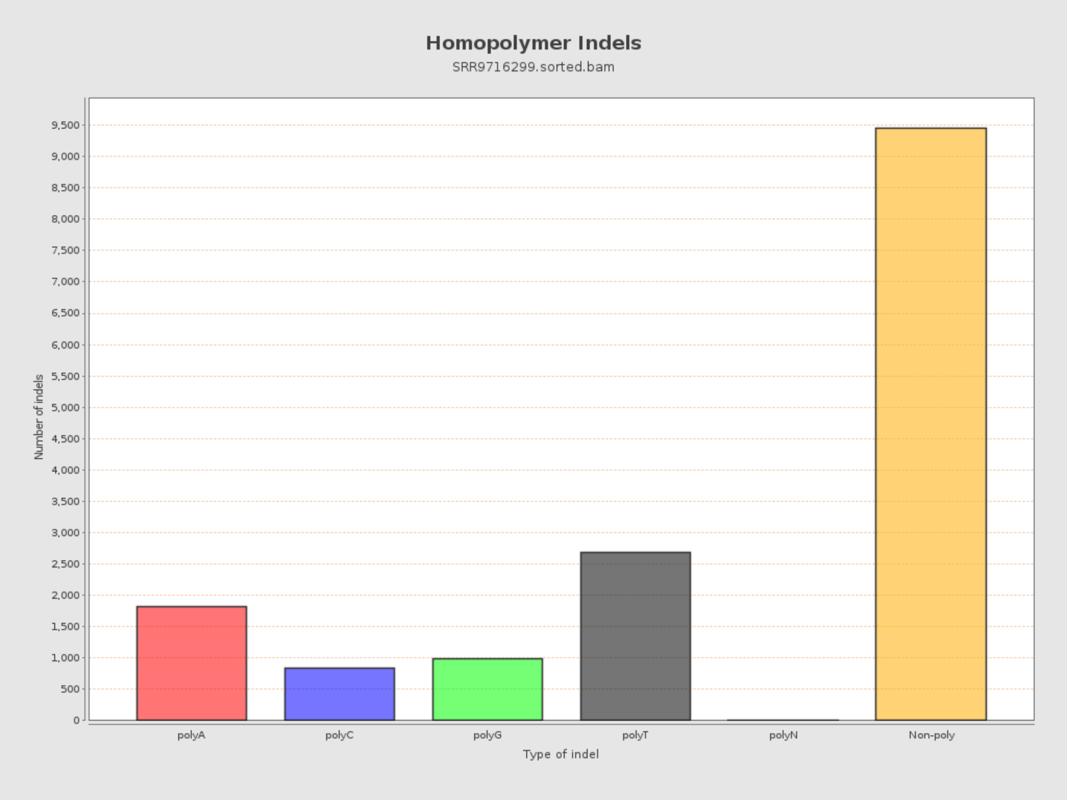
9. Results : Mapped Reads GC-content Distribution



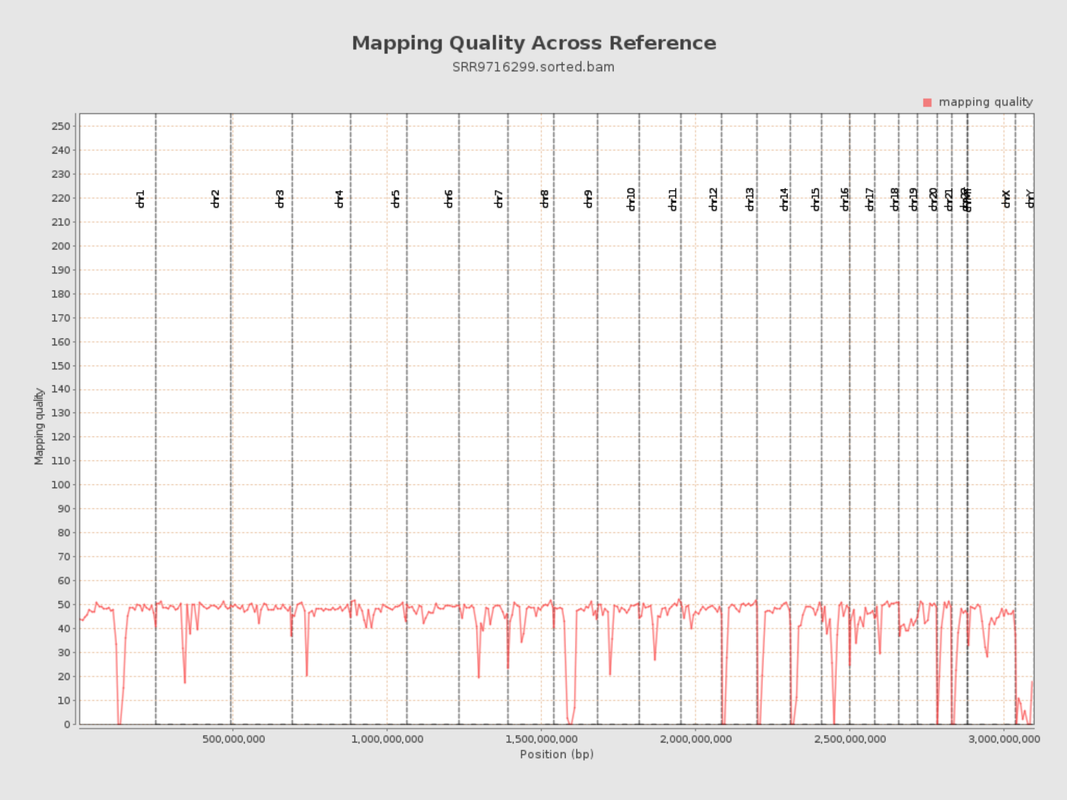
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram