Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/03 22:12:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR9716979.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_SRR9716979 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR9716979.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 03 22:12:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR9716979.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,093,315
Mapped reads	3,470,381 / 84.78%
Unmapped reads	622,934 / 15.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	12,831 / 0.31%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	155,631 / 3.8%
Duplication rate	3.05%
Clipped reads	3,474,315 / 84.88%

2.2. ACGT Content

Number/percentage of A's	49,805,870 / 25.39%
Number/percentage of C's	35,861,910 / 18.28%
Number/percentage of T's	60,634,555 / 30.91%
Number/percentage of G's	49,884,501 / 25.43%
Number/percentage of N's	3,078 / 0%
GC Percentage	43.71%

2.3. Coverage

Mean	0.0634

Standard Deviation	0.5466

2.4. Mapping Quality

Mean Mapping Quality	42.2

2.5. Mismatches and indels

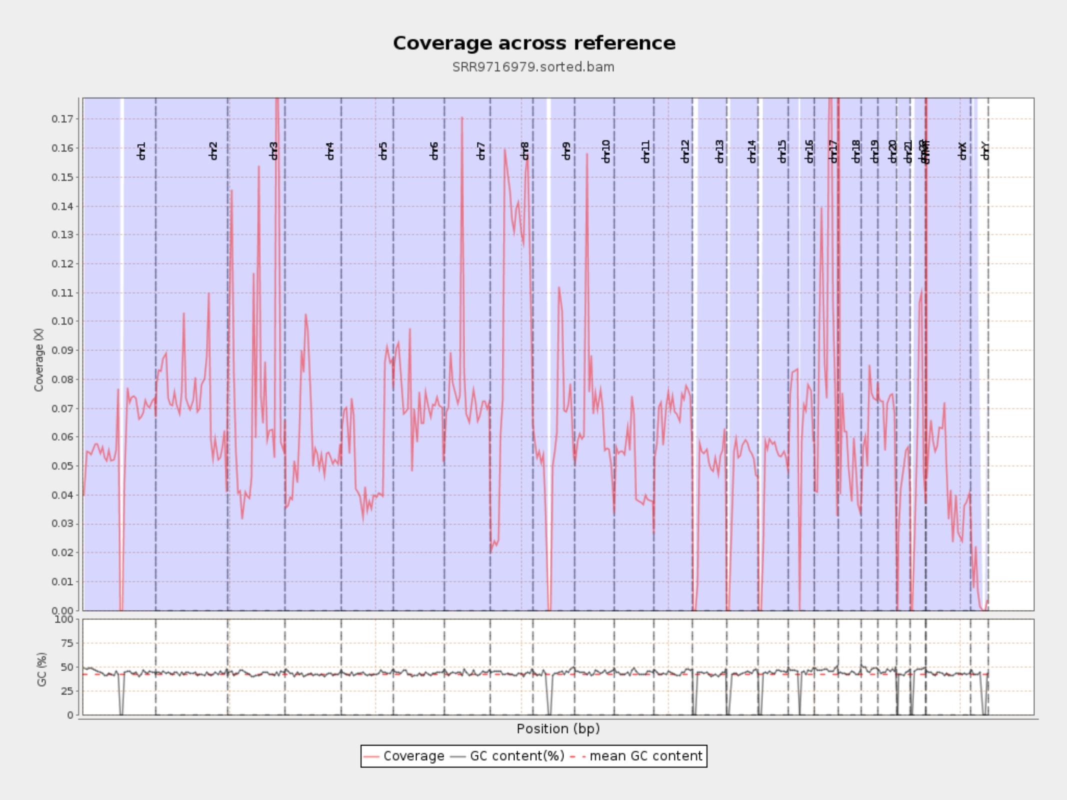
General error rate	0.53%
Mismatches	1,016,560
Insertions	13,484
Mapped reads with at least one insertion	0.39%
Deletions	35,905
Mapped reads with at least one deletion	1.03%
Homopolymer indels	40.83%

2.6. Chromosome stats

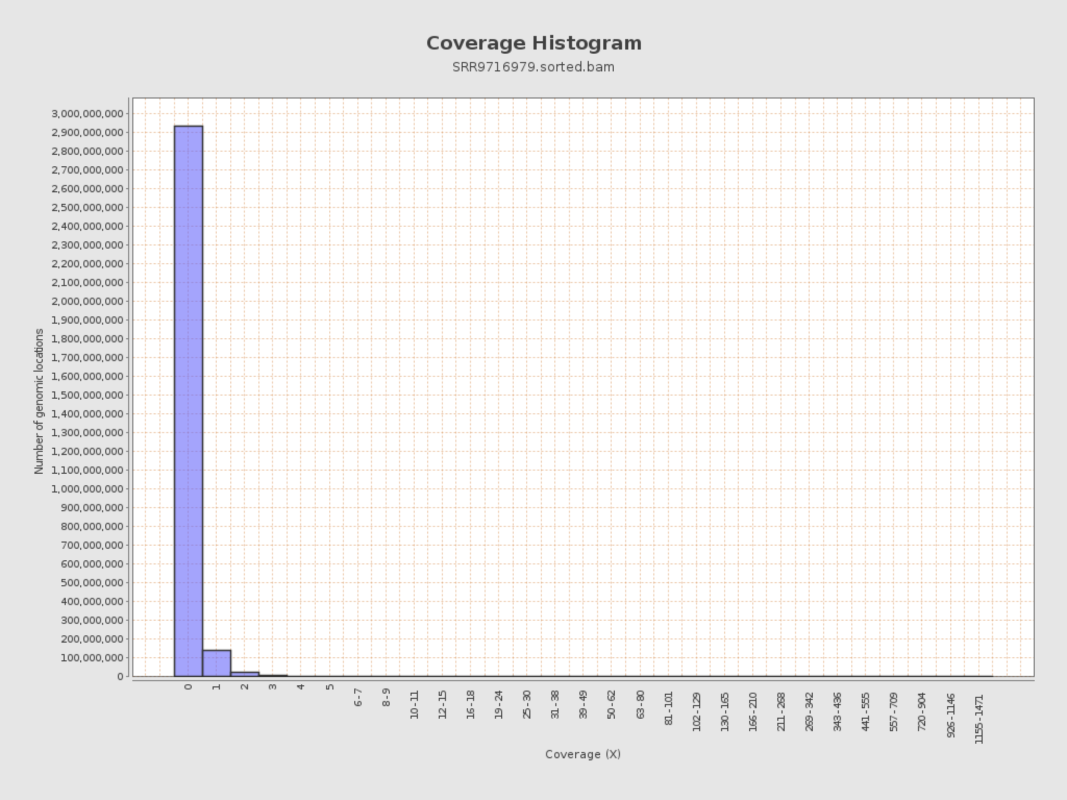
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14493621	0.0581	0.6303
chr2	243199373	17785486	0.0731	0.7123
chr3	198022430	15227237	0.0769	0.376
chr4	191154276	11028072	0.0577	0.3092
chr5	180915260	9912463	0.0548	0.2759
chr6	171115067	12415018	0.0726	0.388
chr7	159138663	12263592	0.0771	1.4235

chr8	146364022	15477284	0.1057	0.4996
chr9	141213431	8096569	0.0573	0.3601
chr10	135534747	9369163	0.0691	0.7213
chr11	135006516	6615650	0.049	0.3635
chr12	133851895	9258709	0.0692	0.3468
chr13	115169878	5142863	0.0447	0.2471
chr14	107349540	4972625	0.0463	0.2728
chr15	102531392	4649214	0.0453	0.2642
chr16	90354753	5952718	0.0659	0.3351
chr17	81195210	8158463	0.1005	0.409
chr18	78077248	4751676	0.0609	0.6105
chr19	59128983	3933246	0.0665	0.659
chr20	63025520	4346792	0.069	0.3251
chr21	48129895	1996677	0.0415	0.2565
chr22	51304566	2759649	0.0538	0.278
chrMT	16571	129051	7.7878	5.8407
chrX	155270560	7070621	0.0455	0.3258
chrY	59373566	439947	0.0074	0.1668

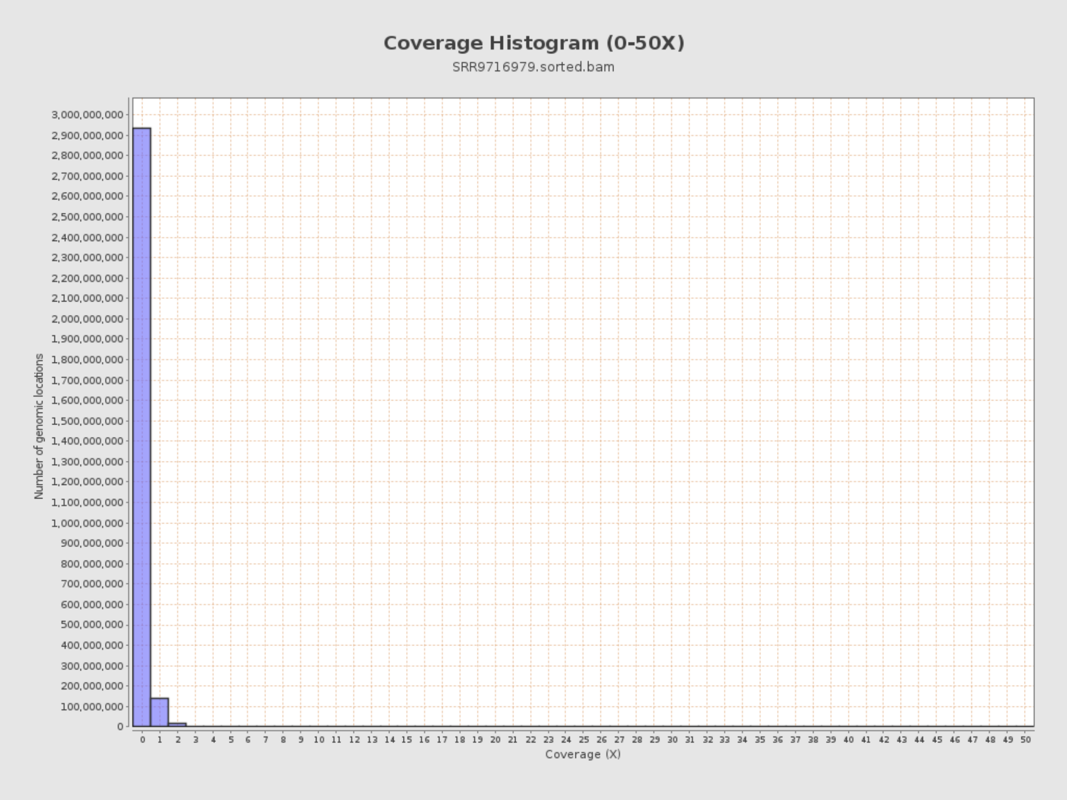
3. Results : Coverage across reference



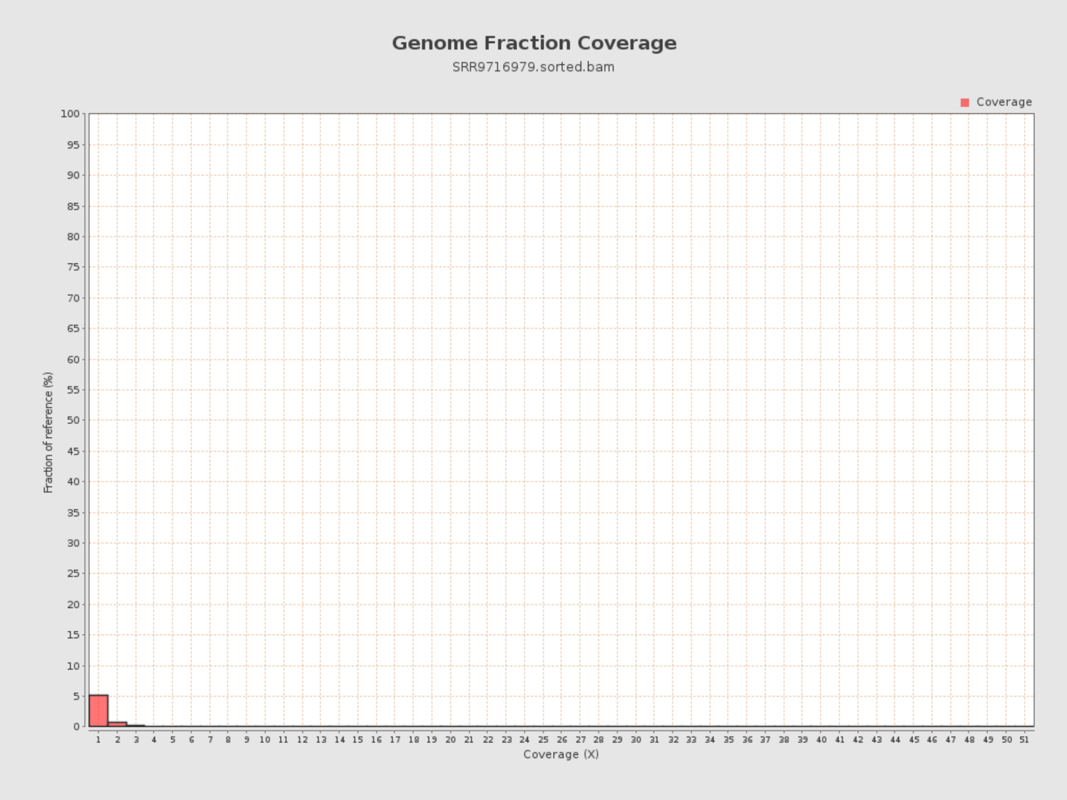
4. Results : Coverage Histogram



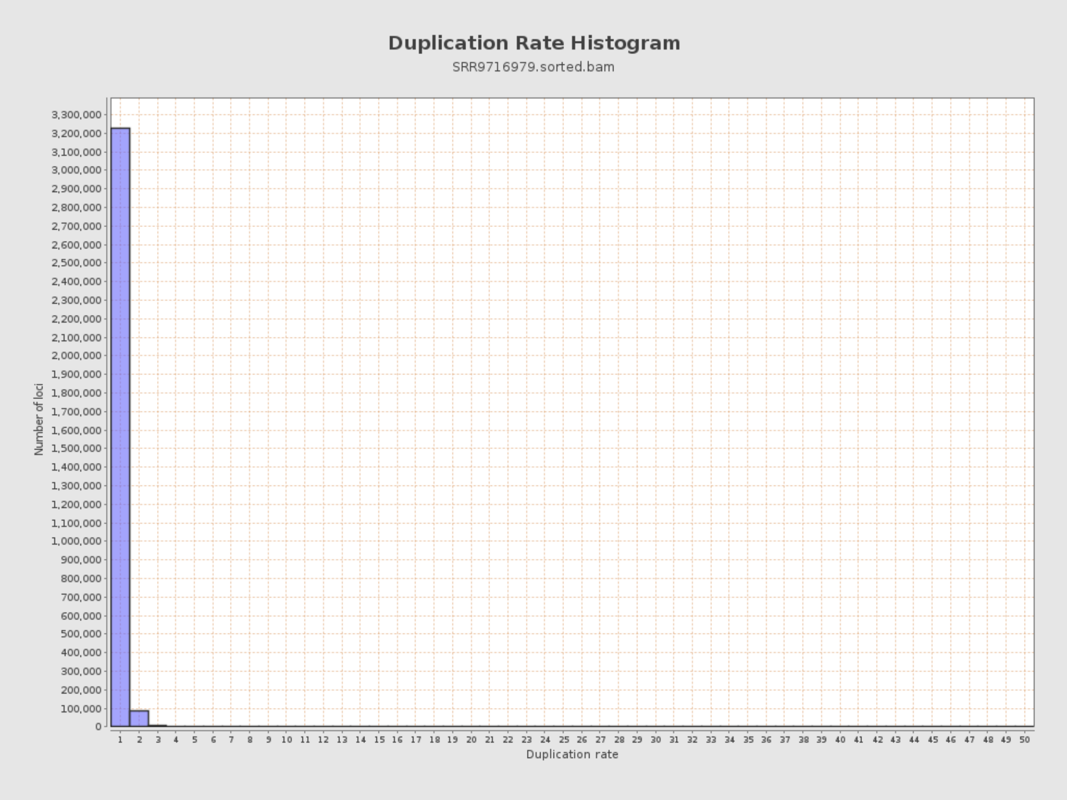
5. Results : Coverage Histogram (0-50X)



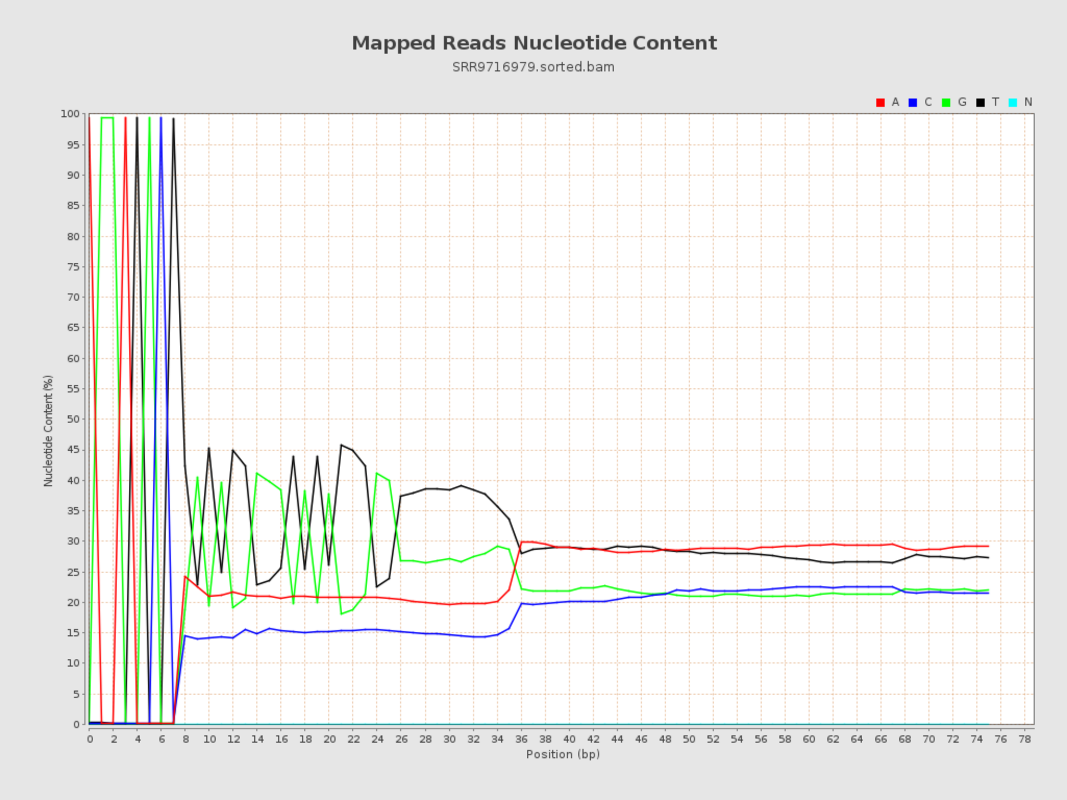
6. Results : Genome Fraction Coverage



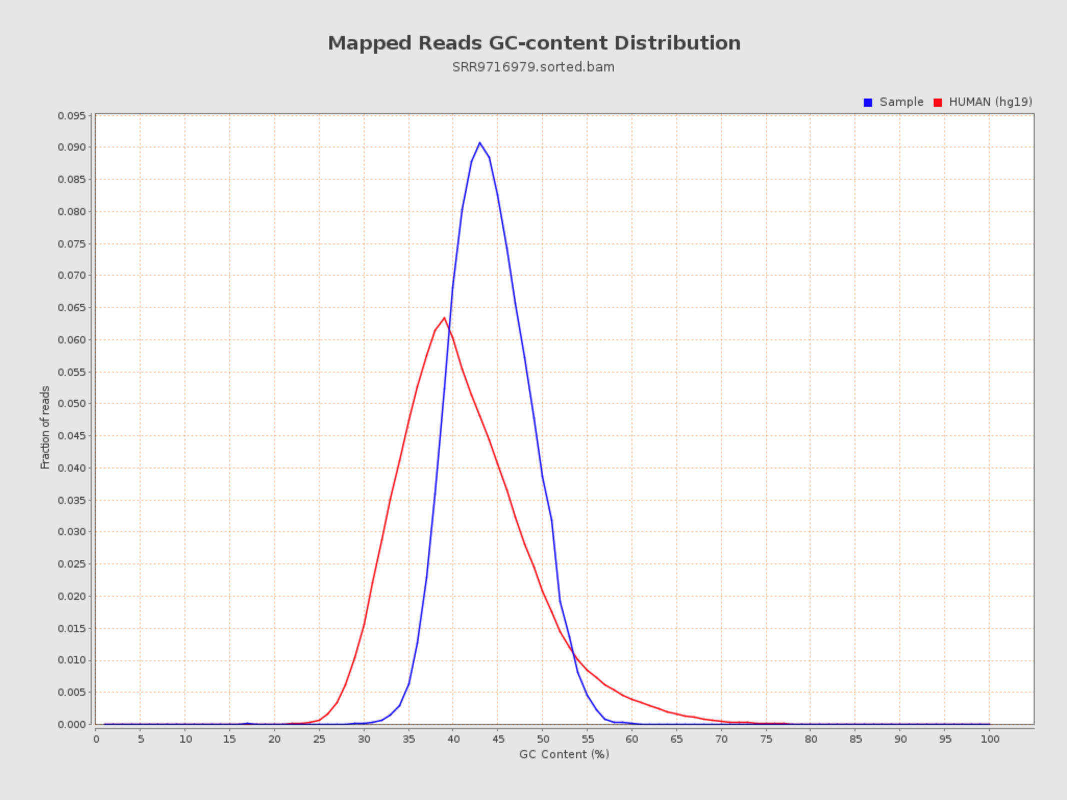
7. Results : Duplication Rate Histogram



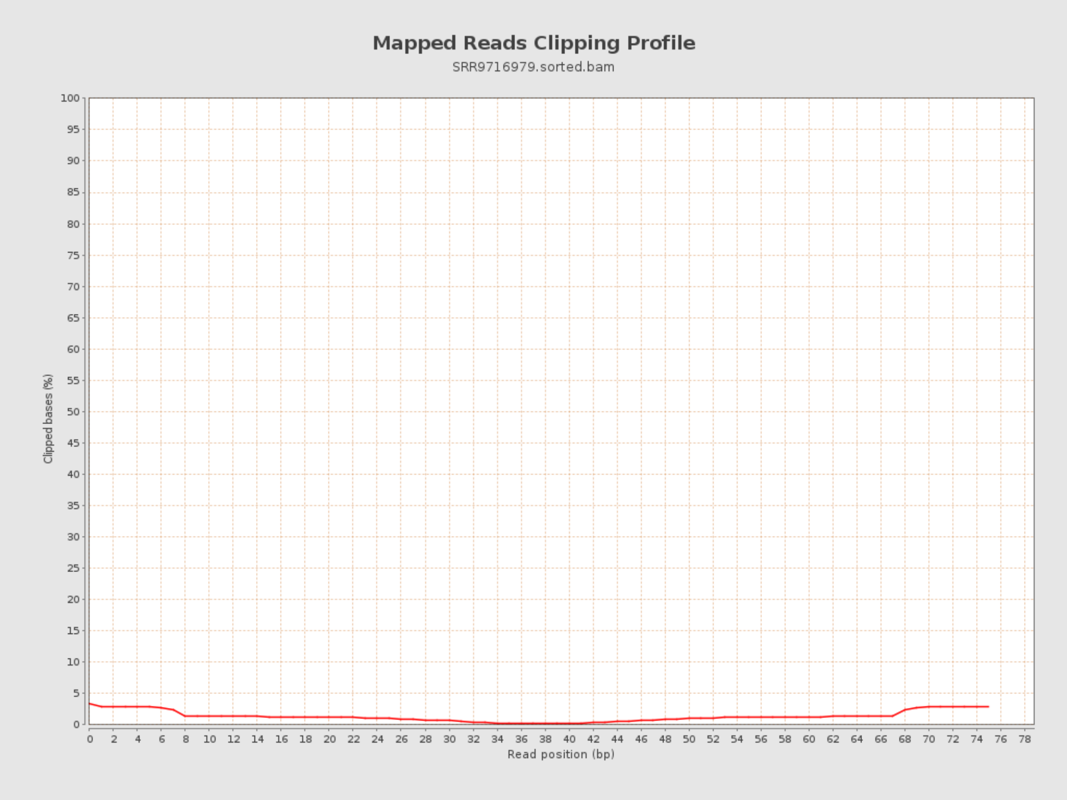
8. Results : Mapped Reads Nucleotide Content



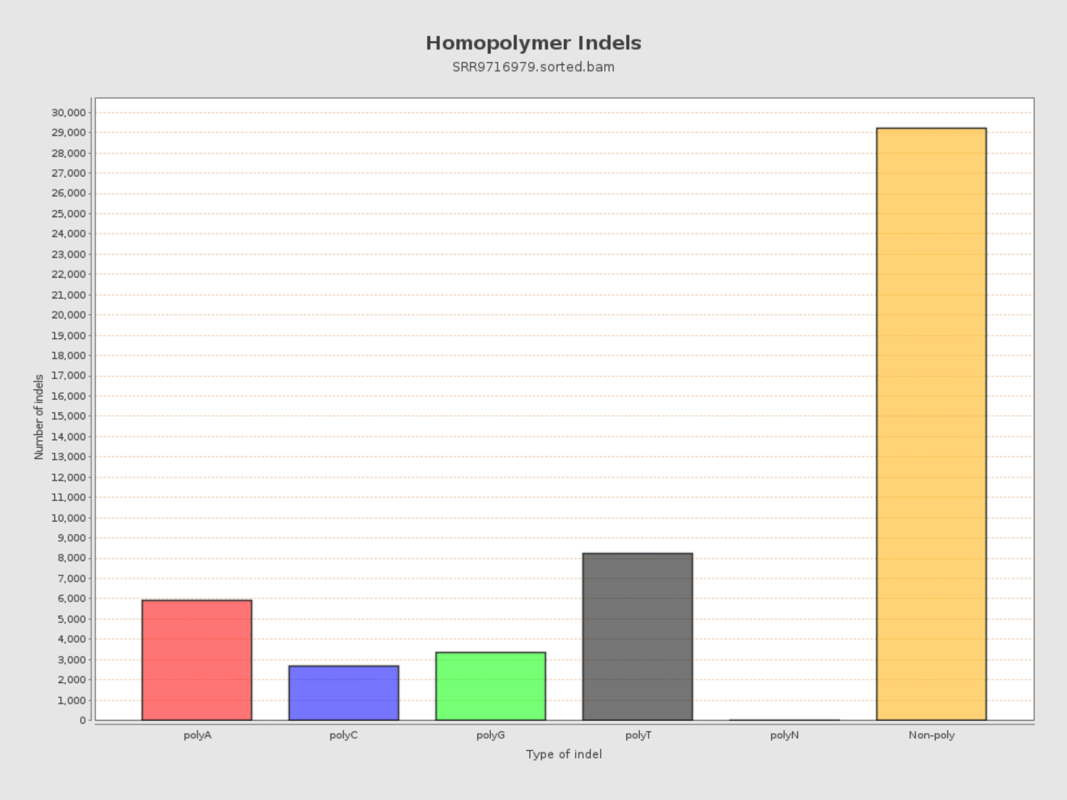
9. Results : Mapped Reads GC-content Distribution



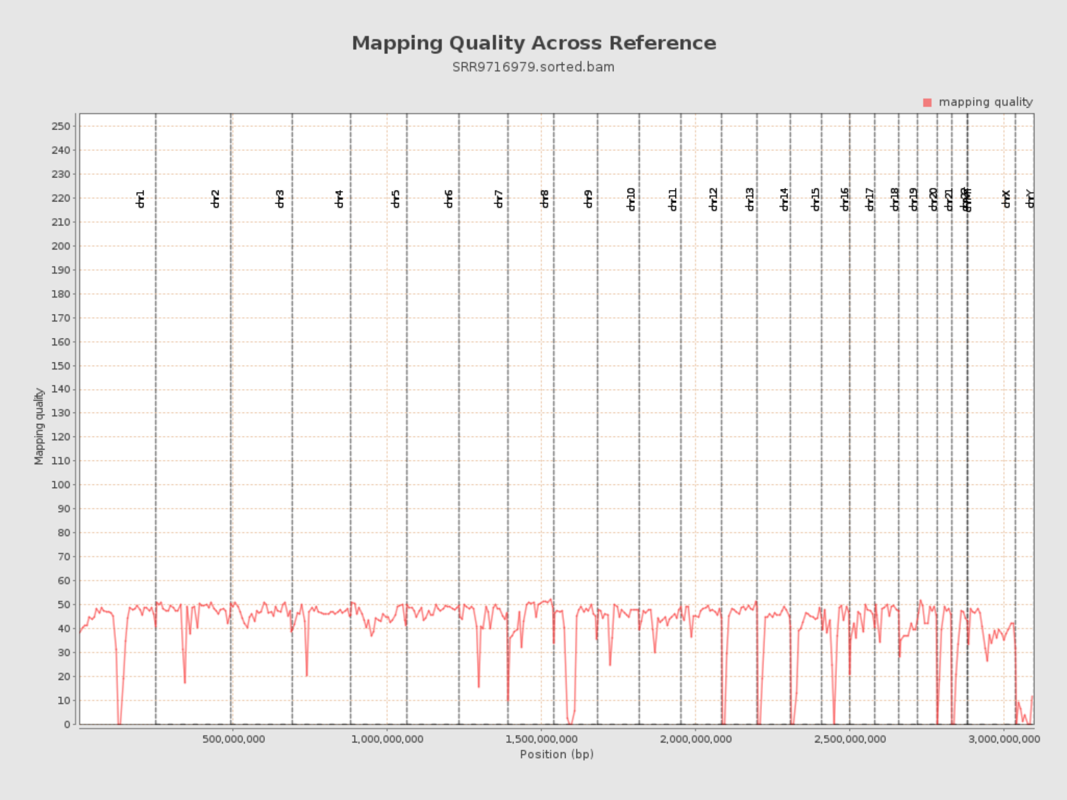
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram