Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:09:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524679.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_SRR10524679 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524679.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:09:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524679.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,307,326
Mapped reads	1,213,002 / 92.78%
Unmapped reads	94,324 / 7.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,205 / 0.4%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	38,557 / 2.95%
Duplication rate	2.28%
Clipped reads	1,215,135 / 92.95%

2.2. ACGT Content

Number/percentage of A's	18,439,985 / 25.55%
Number/percentage of C's	14,170,417 / 19.64%
Number/percentage of T's	22,459,512 / 31.12%
Number/percentage of G's	17,081,922 / 23.67%
Number/percentage of N's	9,581 / 0.01%
GC Percentage	43.31%

2.3. Coverage

Mean	0.0233

Standard Deviation	0.2343

2.4. Mapping Quality

Mean Mapping Quality	46.01

2.5. Mismatches and indels

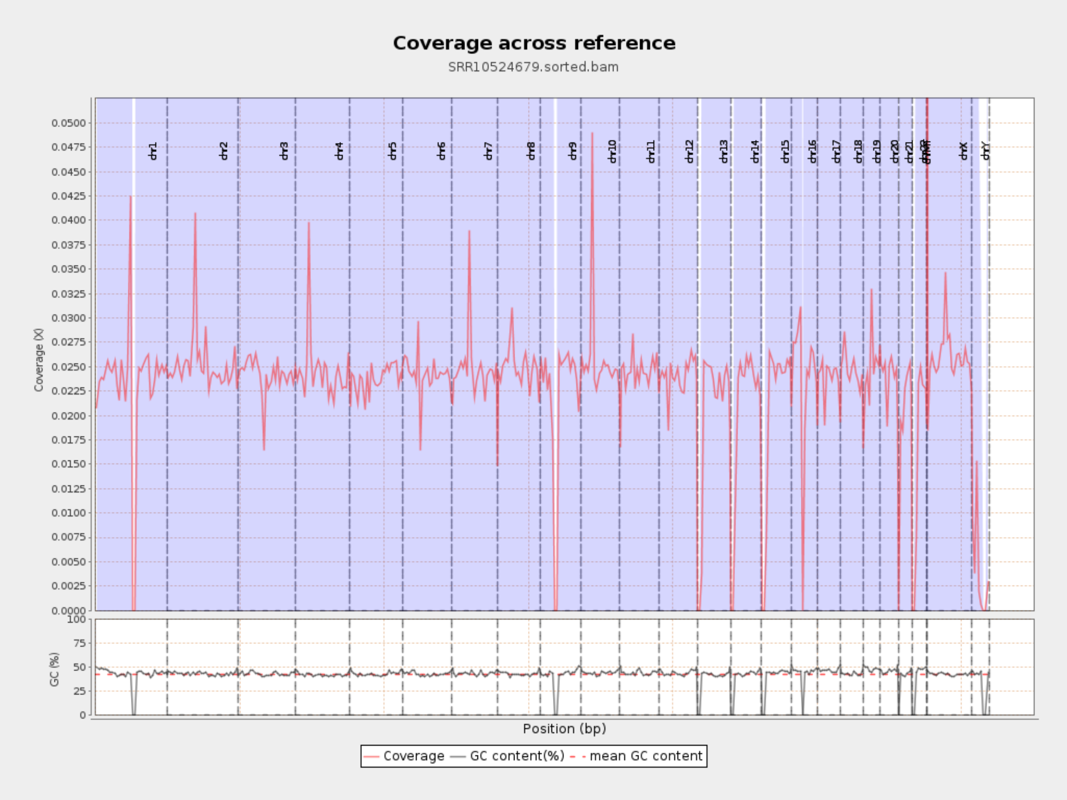
General error rate	0.51%
Mismatches	357,282
Insertions	5,029
Mapped reads with at least one insertion	0.41%
Deletions	13,648
Mapped reads with at least one deletion	1.12%
Homopolymer indels	42.01%

2.6. Chromosome stats

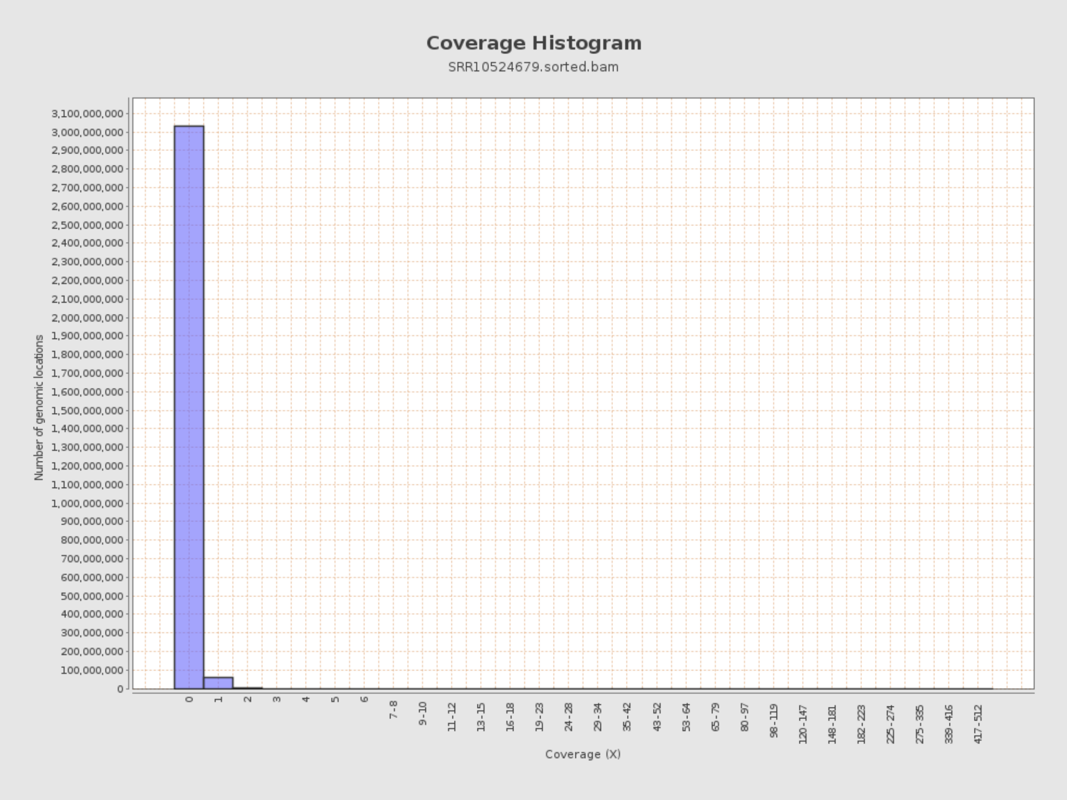
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5771358	0.0232	0.4156
chr2	243199373	6154086	0.0253	0.2894
chr3	198022430	4780460	0.0241	0.1653
chr4	191154276	4707705	0.0246	0.1866
chr5	180915260	4306289	0.0238	0.1646
chr6	171115067	4140529	0.0242	0.1816
chr7	159138663	3967970	0.0249	0.2699

chr8	146364022	3667111	0.0251	0.2597
chr9	141213431	3053973	0.0216	0.1957
chr10	135534747	3525027	0.026	0.2478
chr11	135006516	3311143	0.0245	0.2013
chr12	133851895	3224097	0.0241	0.168
chr13	115169878	2287128	0.0199	0.1503
chr14	107349540	2162435	0.0201	0.1565
chr15	102531392	2082272	0.0203	0.1523
chr16	90354753	2112181	0.0234	0.1737
chr17	81195210	1933826	0.0238	0.1732
chr18	78077248	1934344	0.0248	0.3527
chr19	59128983	1472071	0.0249	0.323
chr20	63025520	1509485	0.024	0.168
chr21	48129895	961446	0.02	0.1712
chr22	51304566	826762	0.0161	0.1356
chrMT	16571	16972	1.0242	1.2034
chrX	155270560	4035579	0.026	0.1856
chrY	59373566	238808	0.004	0.1496

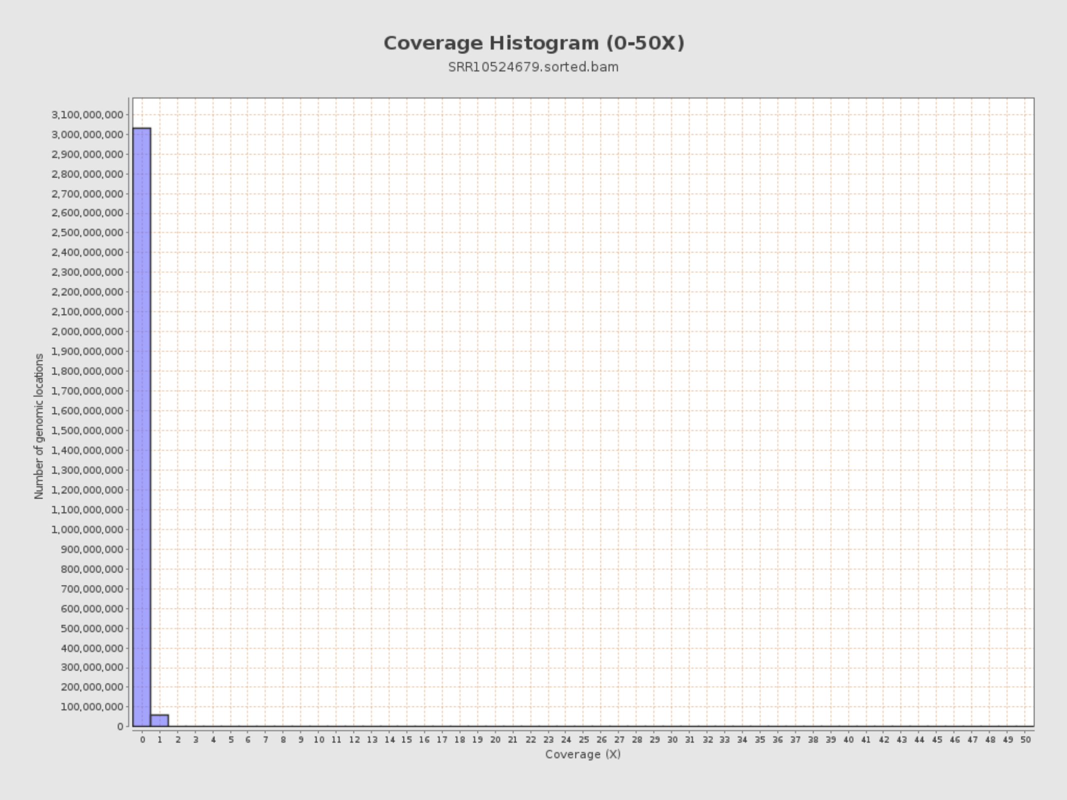
3. Results : Coverage across reference



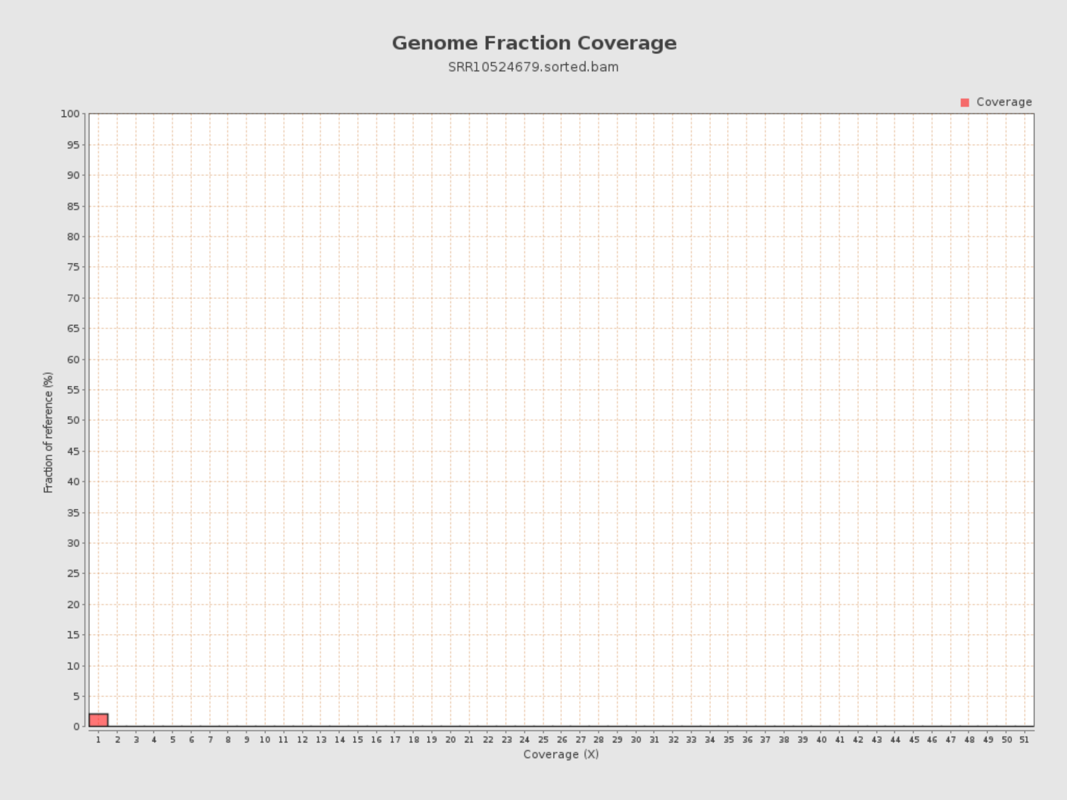
4. Results : Coverage Histogram



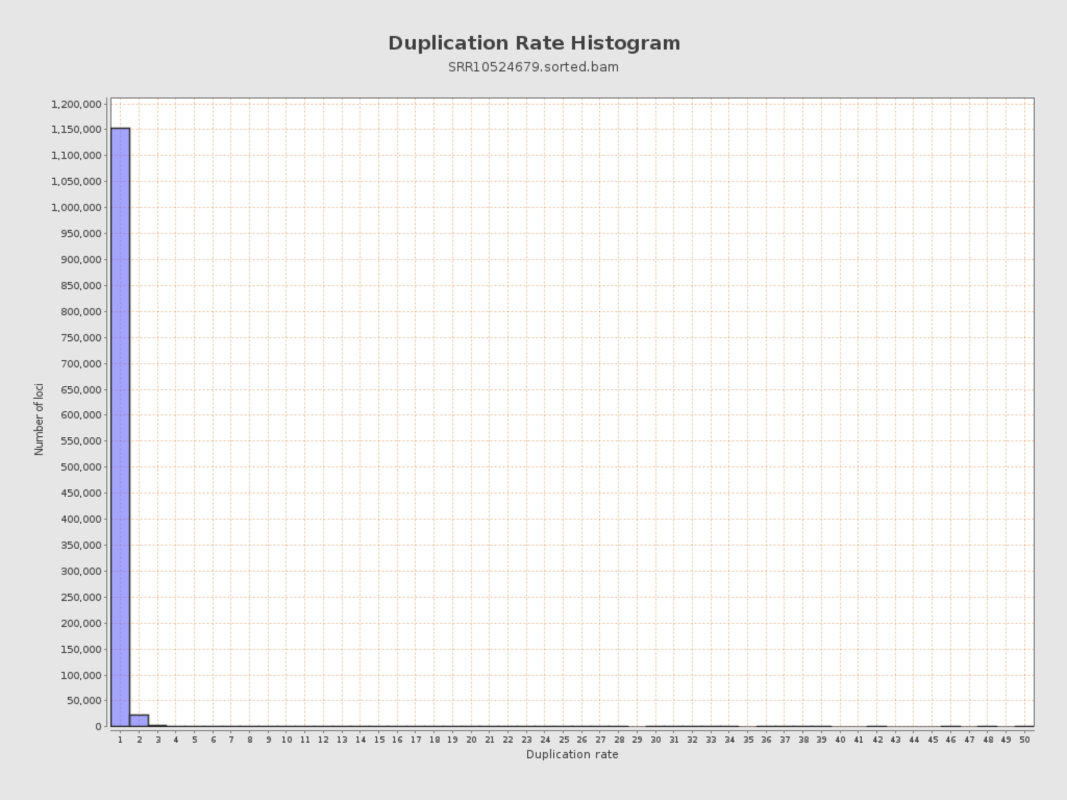
5. Results : Coverage Histogram (0-50X)



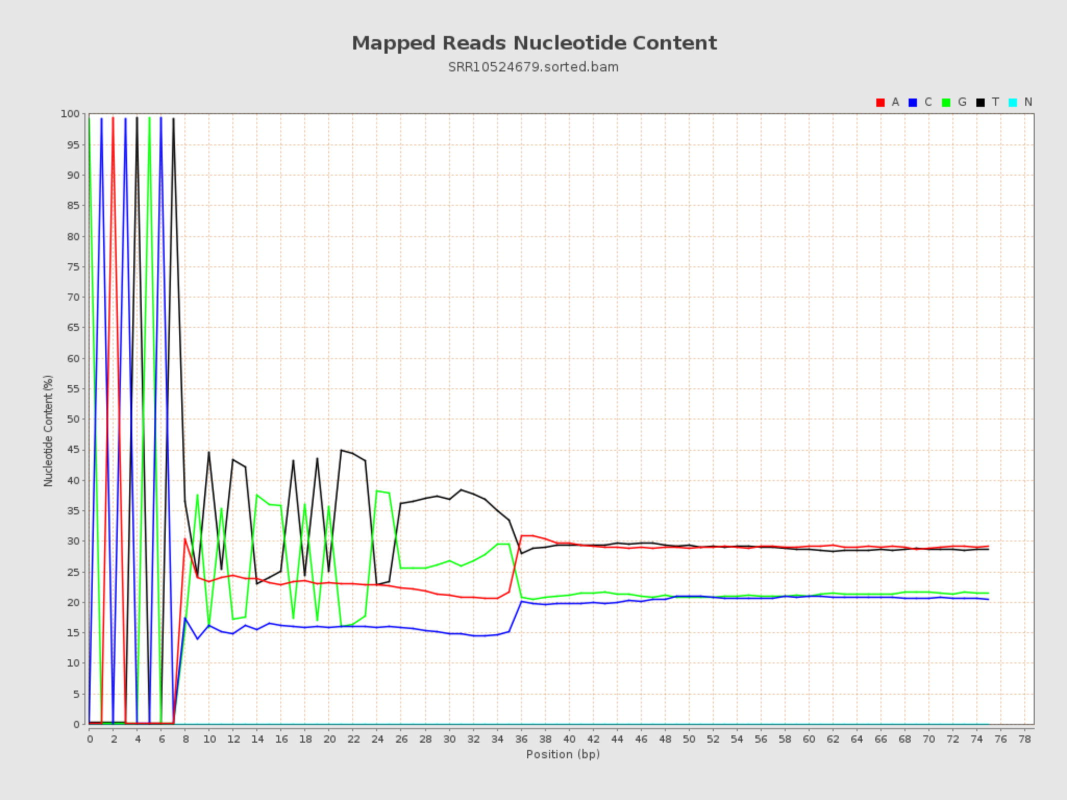
6. Results : Genome Fraction Coverage



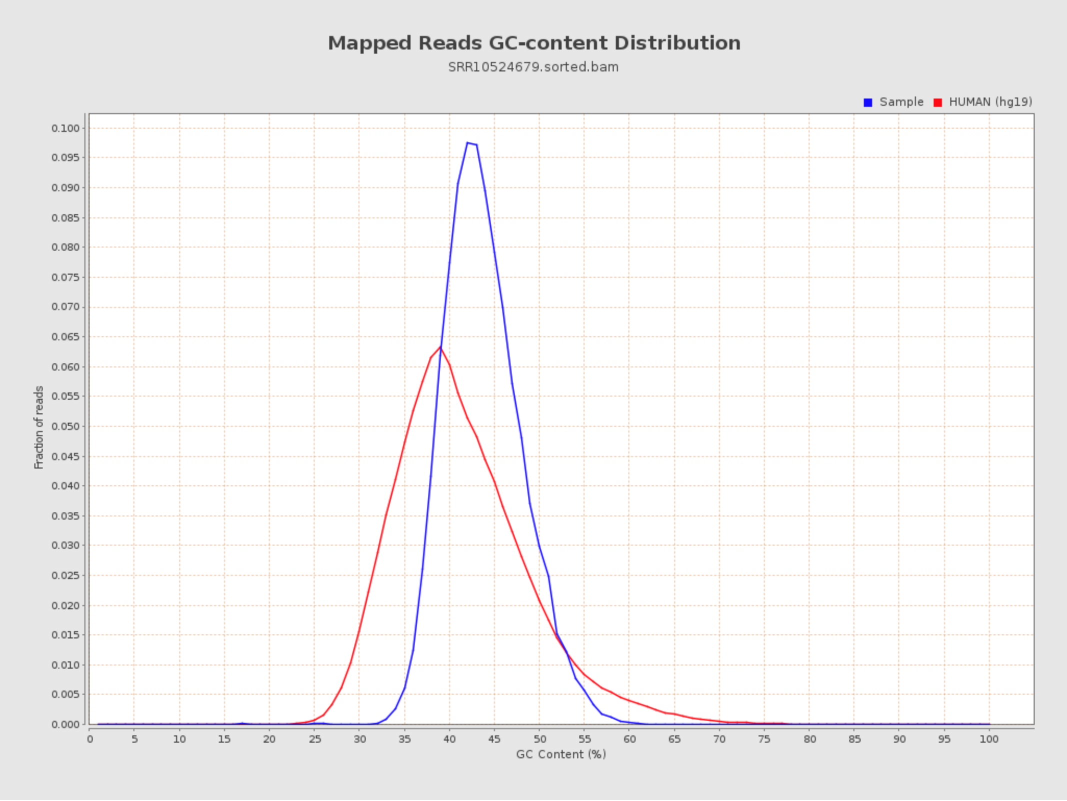
7. Results : Duplication Rate Histogram



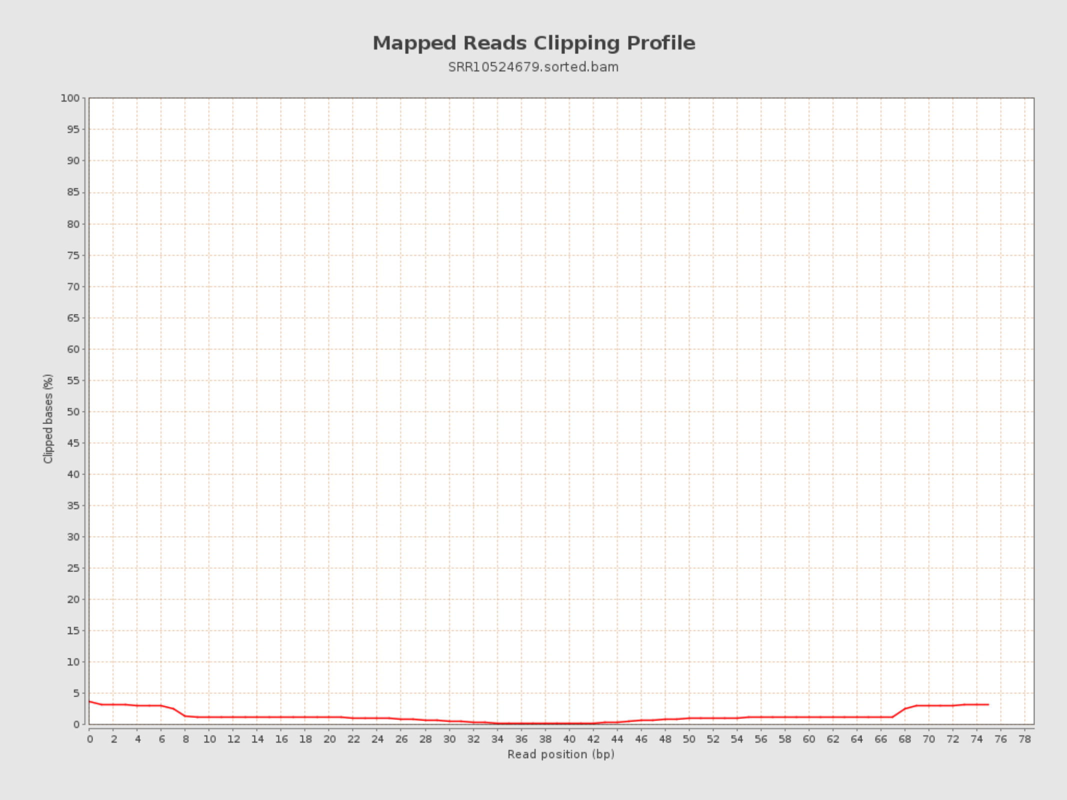
8. Results : Mapped Reads Nucleotide Content



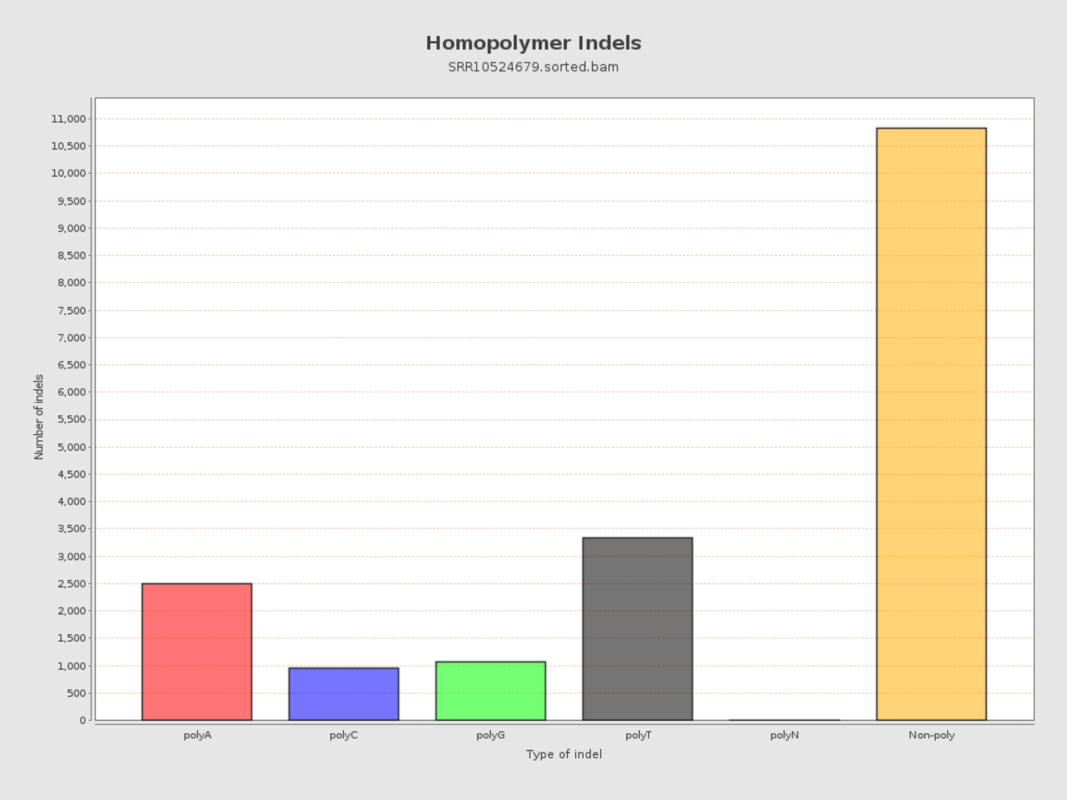
9. Results : Mapped Reads GC-content Distribution



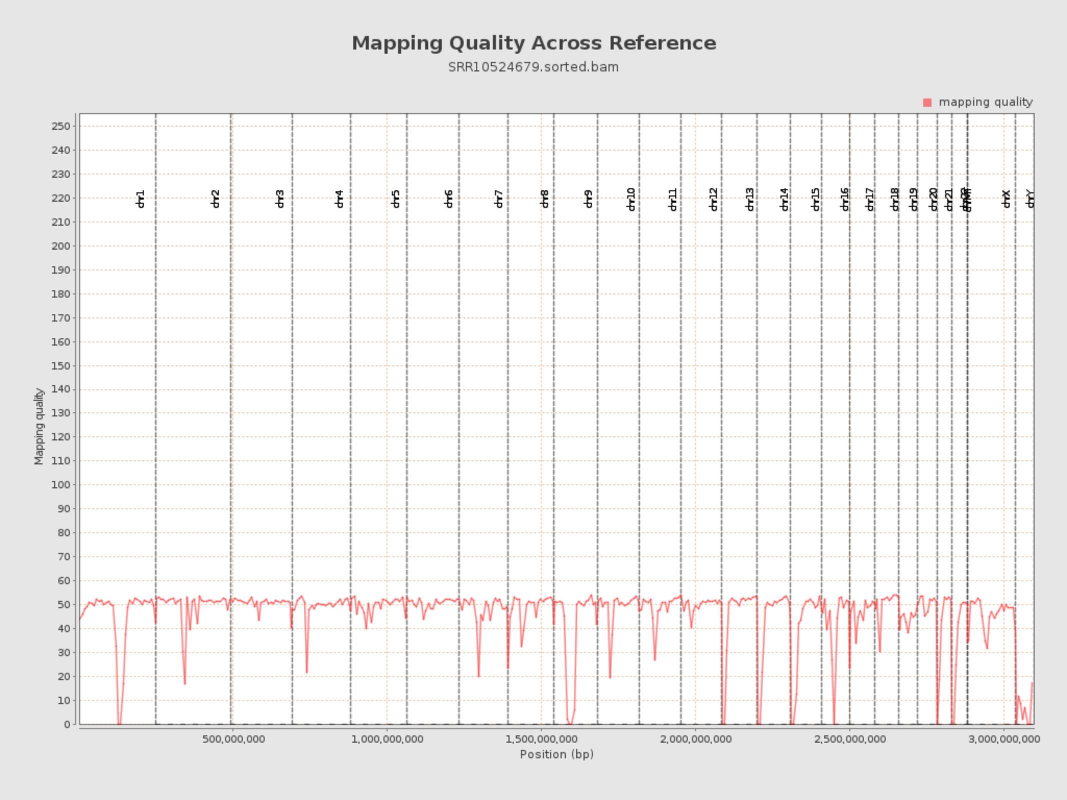
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram