Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 11:40:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524978.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_SRR10524978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524978.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 11:40:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,823,313
Mapped reads	1,697,039 / 93.07%
Unmapped reads	126,274 / 6.93%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,341 / 0.4%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	120,045 / 6.58%
Duplication rate	5.41%
Clipped reads	1,699,093 / 93.19%

2.2. ACGT Content

Number/percentage of A's	26,639,450 / 26.22%
Number/percentage of C's	20,343,164 / 20.02%
Number/percentage of T's	31,097,081 / 30.61%
Number/percentage of G's	23,510,857 / 23.14%
Number/percentage of N's	3,111 / 0%
GC Percentage	43.17%

2.3. Coverage

Mean	0.0328

Standard Deviation	0.355

2.4. Mapping Quality

Mean Mapping Quality	46.6

2.5. Mismatches and indels

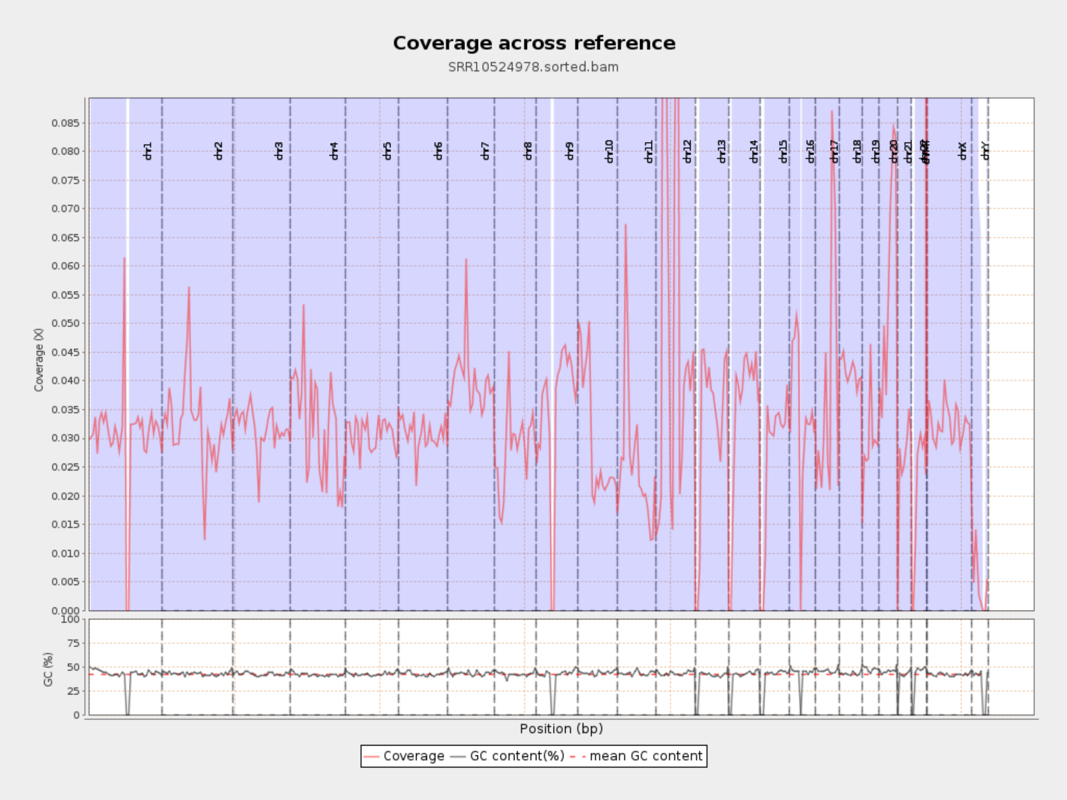
General error rate	0.48%
Mismatches	473,969
Insertions	7,606
Mapped reads with at least one insertion	0.45%
Deletions	15,738
Mapped reads with at least one deletion	0.92%
Homopolymer indels	41.85%

2.6. Chromosome stats

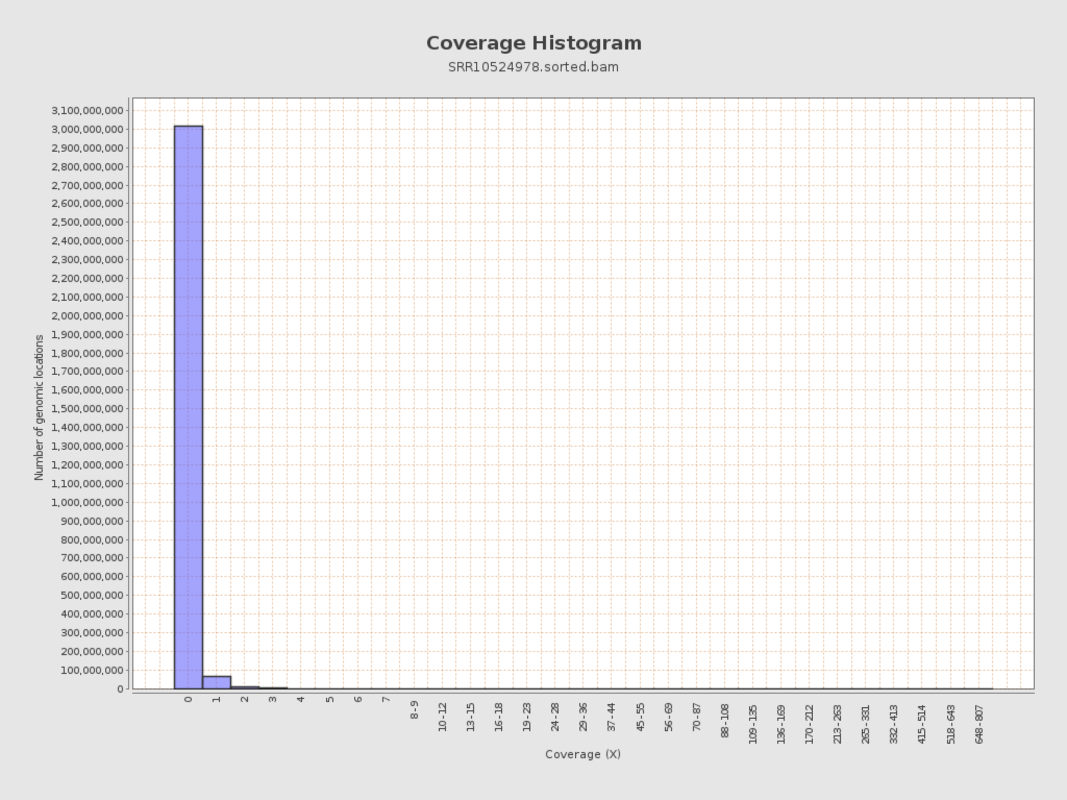
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7572854	0.0304	0.7283
chr2	243199373	7962240	0.0327	0.3144
chr3	198022430	6296630	0.0318	0.2105
chr4	191154276	6190669	0.0324	0.2307
chr5	180915260	5542602	0.0306	0.2121
chr6	171115067	5288497	0.0309	0.2263
chr7	159138663	6415516	0.0403	0.4313

chr8	146364022	4150427	0.0284	0.5023
chr9	141213431	4906859	0.0347	0.2959
chr10	135534747	4055743	0.0299	0.3761
chr11	135006516	3545408	0.0263	0.2432
chr12	133851895	7098247	0.053	0.3088
chr13	115169878	3722545	0.0323	0.2148
chr14	107349540	3663733	0.0341	0.2353
chr15	102531392	2740668	0.0267	0.1925
chr16	90354753	3121719	0.0345	0.2398
chr17	81195210	3068795	0.0378	0.2409
chr18	78077248	3263439	0.0418	0.5111
chr19	59128983	1764522	0.0298	0.4925
chr20	63025520	3604127	0.0572	0.298
chr21	48129895	1248622	0.0259	0.2124
chr22	51304566	1035256	0.0202	0.1685
chrMT	16571	50292	3.0349	3.2811
chrX	155270560	5032689	0.0324	0.2432
chrY	59373566	277326	0.0047	0.1091

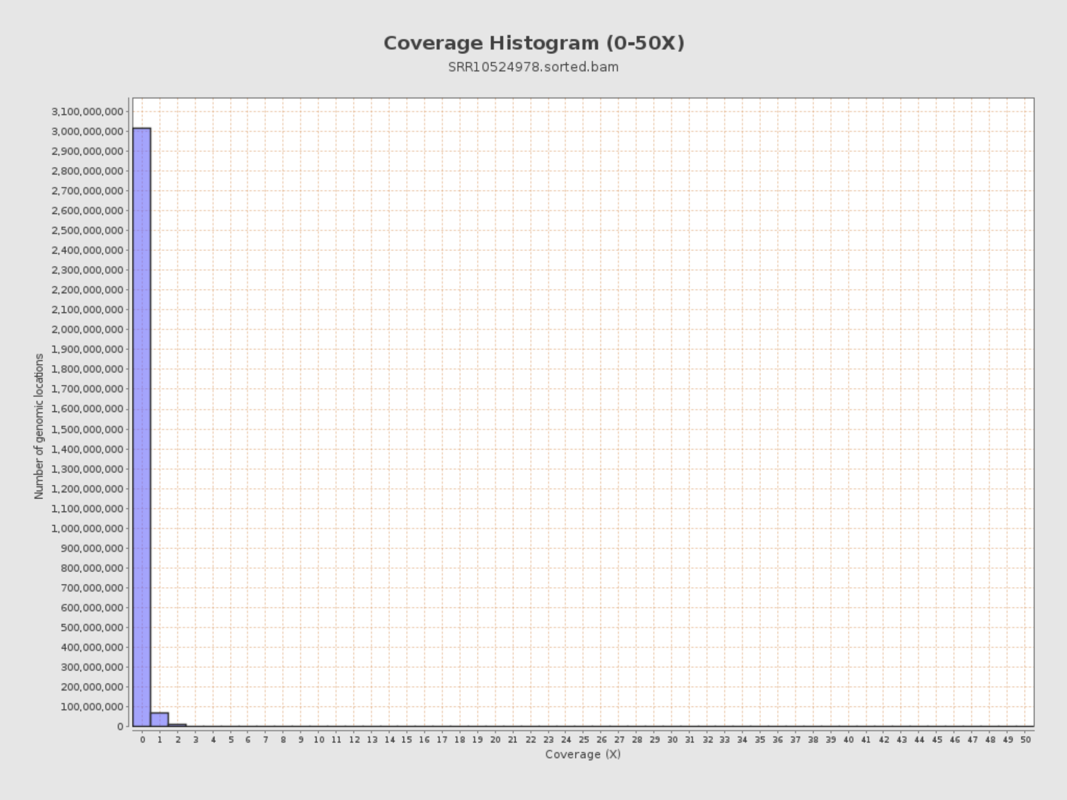
3. Results : Coverage across reference



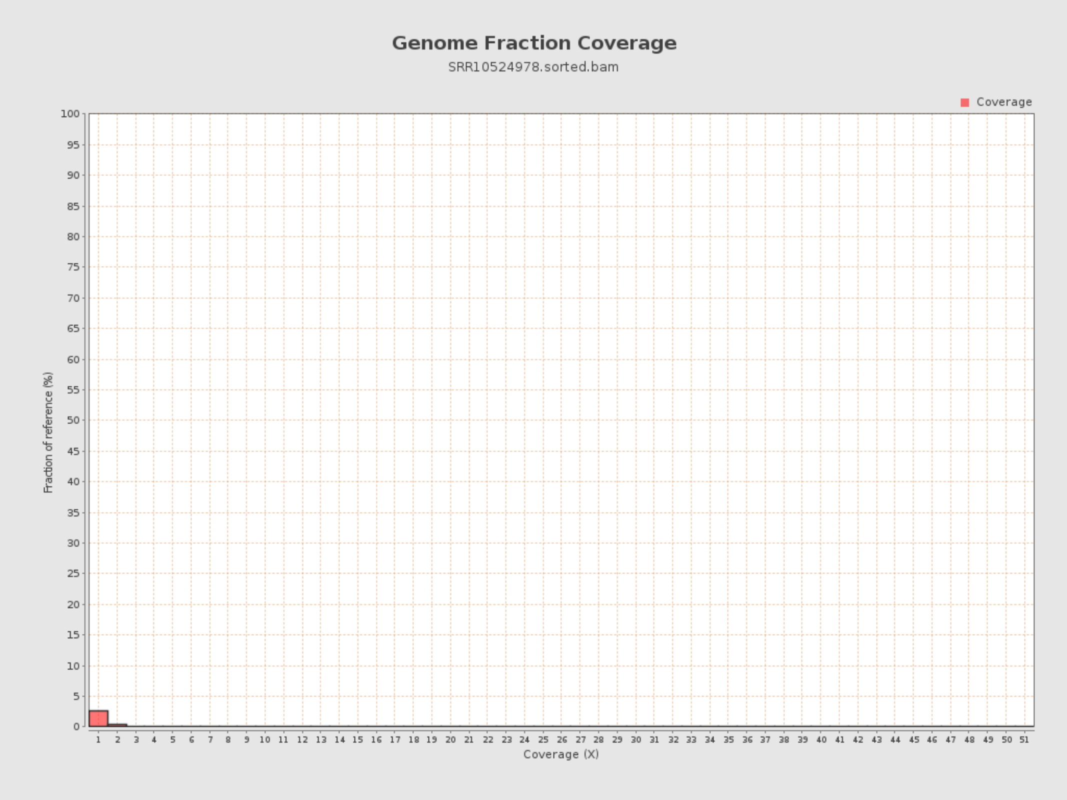
4. Results : Coverage Histogram



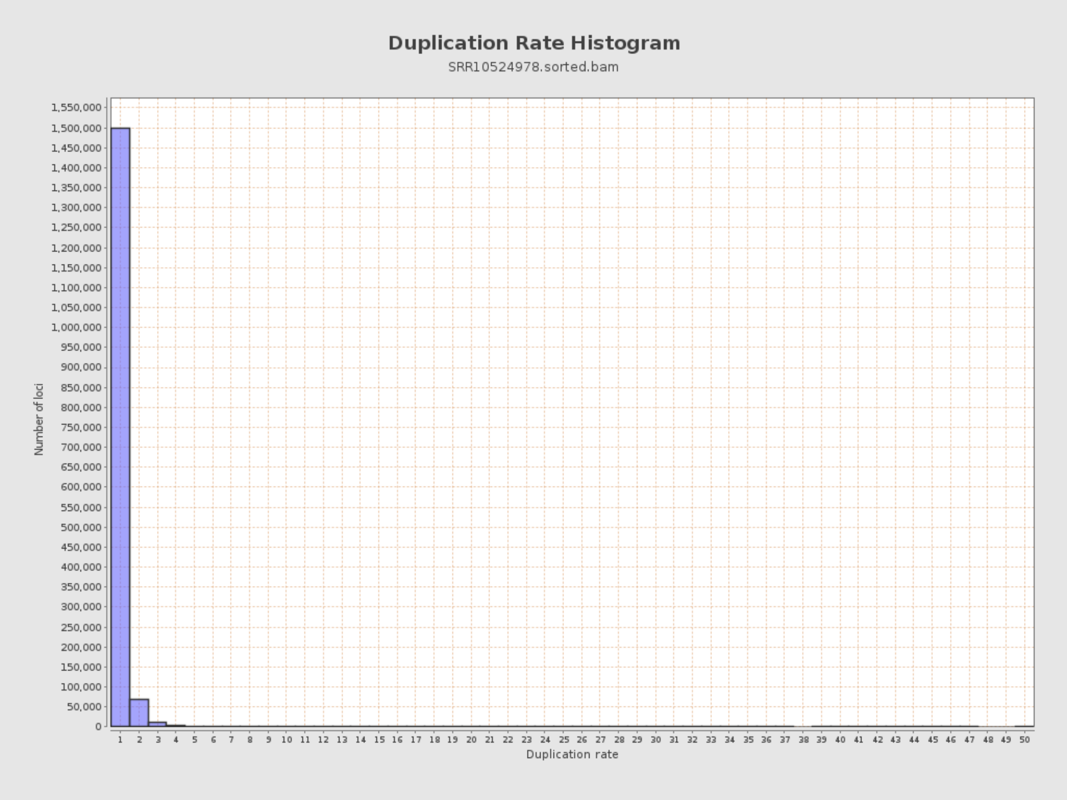
5. Results : Coverage Histogram (0-50X)



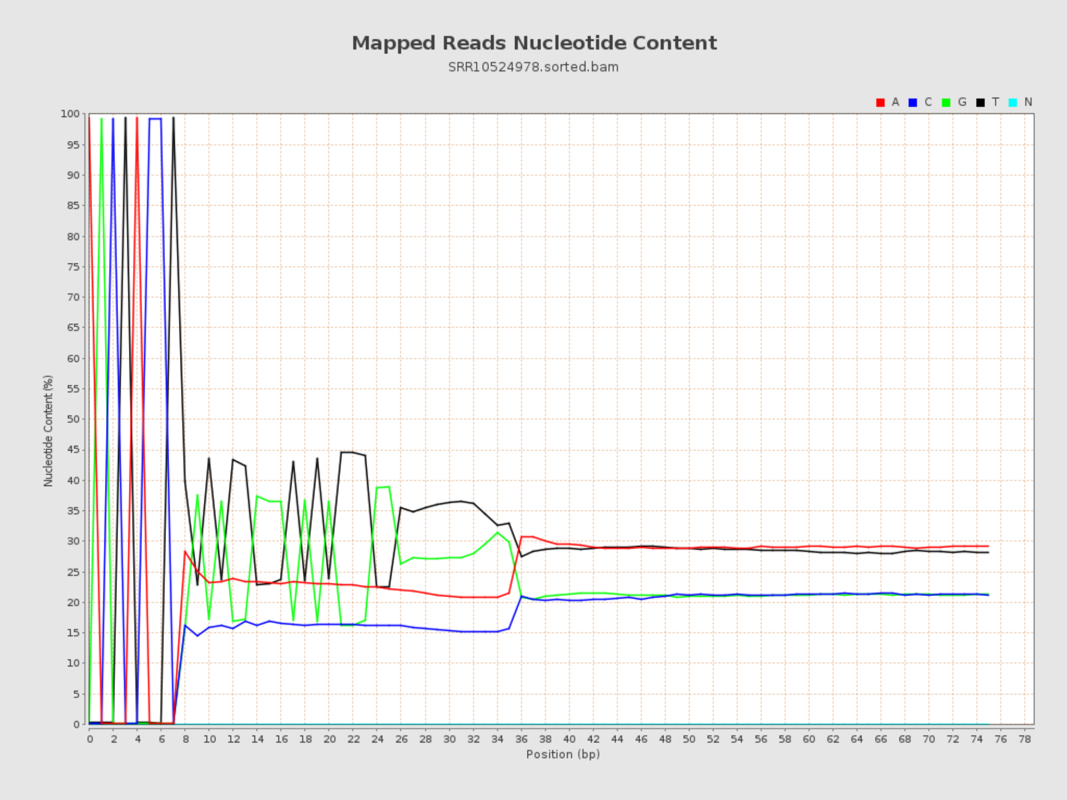
6. Results : Genome Fraction Coverage



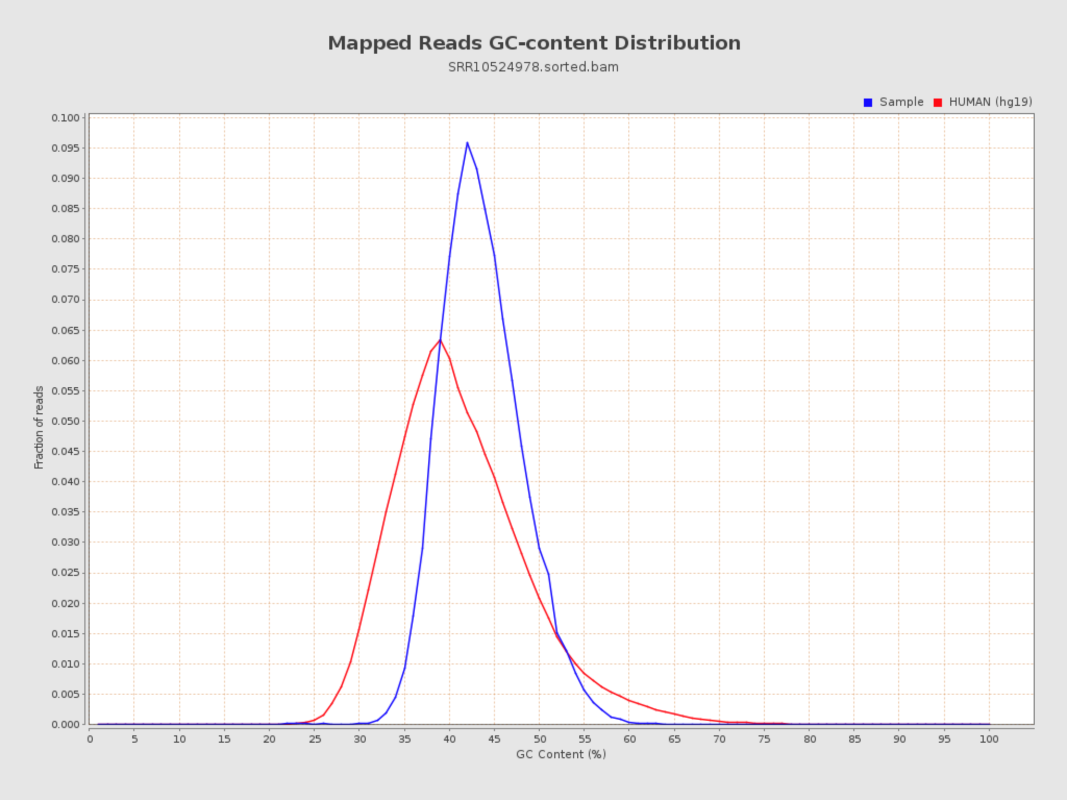
7. Results : Duplication Rate Histogram



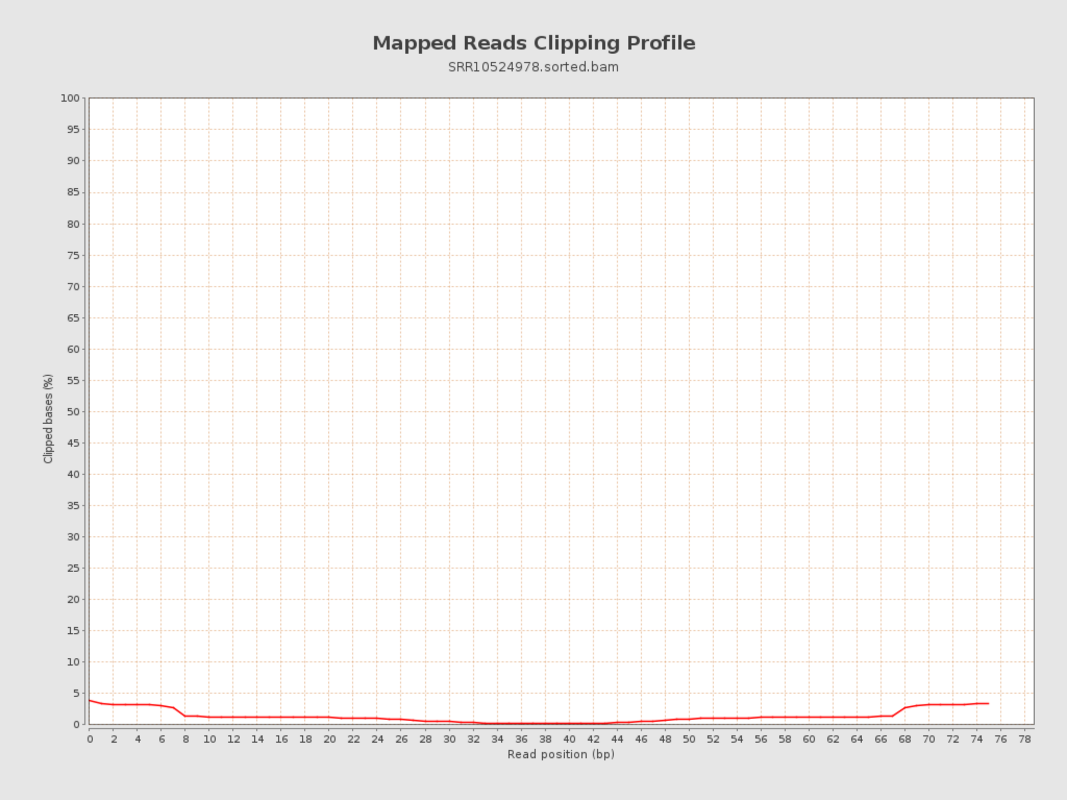
8. Results : Mapped Reads Nucleotide Content



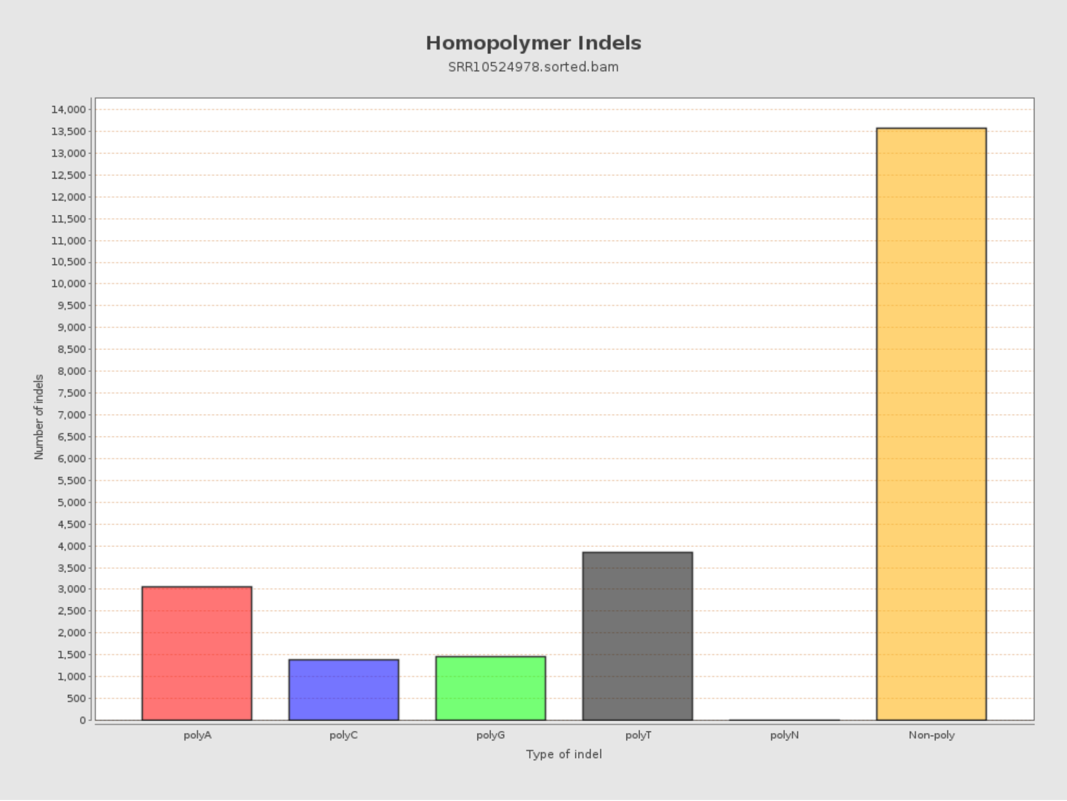
9. Results : Mapped Reads GC-content Distribution



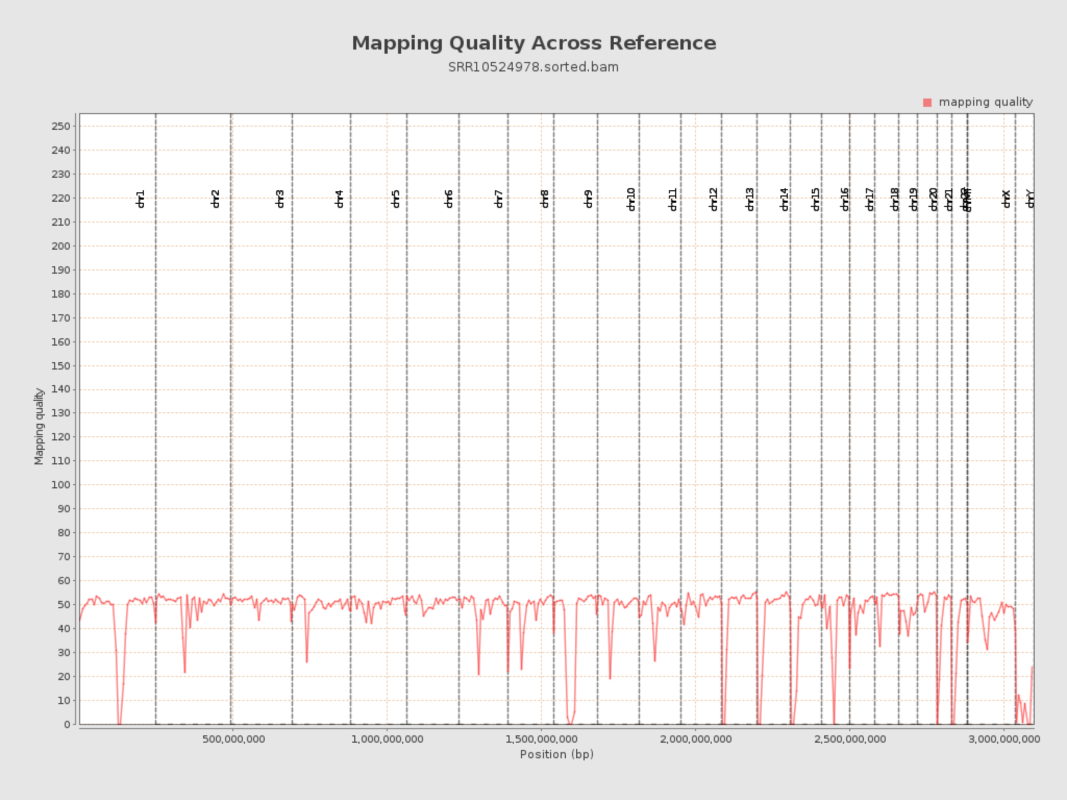
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram