Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 22:40:10

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524321.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_SRR10524321 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524321.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 22:40:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524321.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,626,706
Mapped reads	1,478,442 / 90.89%
Unmapped reads	148,264 / 9.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,980 / 0.49%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	45,189 / 2.78%
Duplication rate	2.16%
Clipped reads	1,485,068 / 91.29%

2.2. ACGT Content

Number/percentage of A's	21,304,018 / 24.95%
Number/percentage of C's	16,888,202 / 19.78%
Number/percentage of T's	26,580,132 / 31.13%
Number/percentage of G's	20,594,954 / 24.12%
Number/percentage of N's	11,844 / 0.01%
GC Percentage	43.9%

2.3. Coverage

Mean	0.0276

Standard Deviation	0.2616

2.4. Mapping Quality

Mean Mapping Quality	43.87

2.5. Mismatches and indels

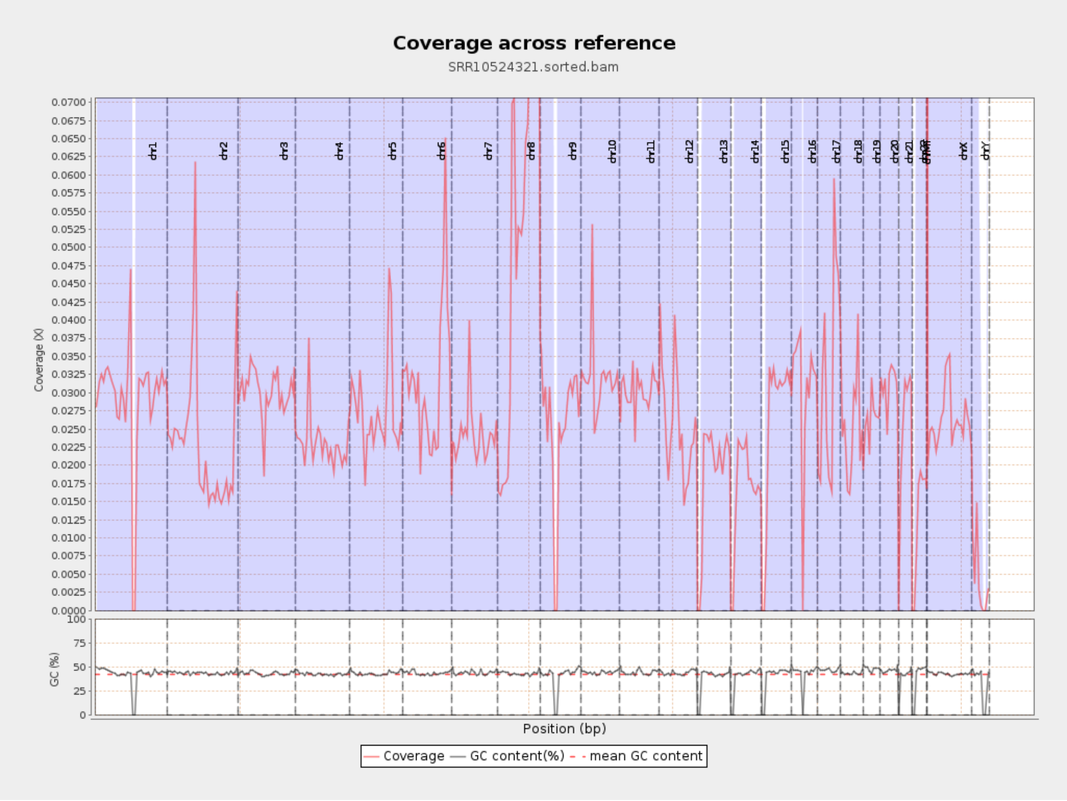
General error rate	0.52%
Mismatches	438,135
Insertions	4,663
Mapped reads with at least one insertion	0.31%
Deletions	13,761
Mapped reads with at least one deletion	0.92%
Homopolymer indels	43.9%

2.6. Chromosome stats

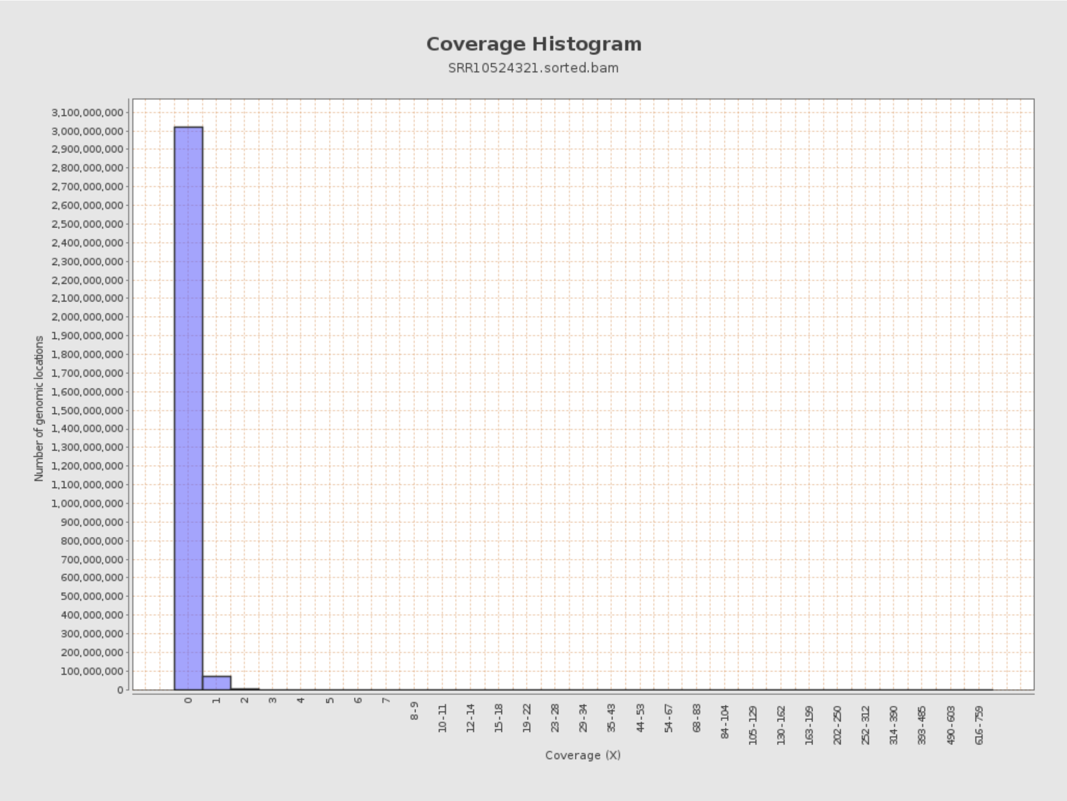
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7240032	0.029	0.4835
chr2	243199373	5572664	0.0229	0.3515
chr3	198022430	5962582	0.0301	0.1869
chr4	191154276	4415160	0.0231	0.1834
chr5	180915260	5015565	0.0277	0.1798
chr6	171115067	5377644	0.0314	0.2061
chr7	159138663	3883288	0.0244	0.305

chr8	146364022	8813716	0.0602	0.3271
chr9	141213431	3558743	0.0252	0.2041
chr10	135534747	4366552	0.0322	0.2564
chr11	135006516	4086942	0.0303	0.2199
chr12	133851895	3415946	0.0255	0.1754
chr13	115169878	2146454	0.0186	0.1465
chr14	107349540	1781134	0.0166	0.144
chr15	102531392	2633747	0.0257	0.1765
chr16	90354753	2736240	0.0303	0.1965
chr17	81195210	2668729	0.0329	0.2086
chr18	78077248	1974933	0.0253	0.3282
chr19	59128983	1562009	0.0264	0.3239
chr20	63025520	1951129	0.031	0.1931
chr21	48129895	1217770	0.0253	0.1829
chr22	51304566	654240	0.0128	0.1225
chrMT	16571	11827	0.7137	0.971
chrX	155270560	4105750	0.0264	0.1942
chrY	59373566	248749	0.0042	0.1221

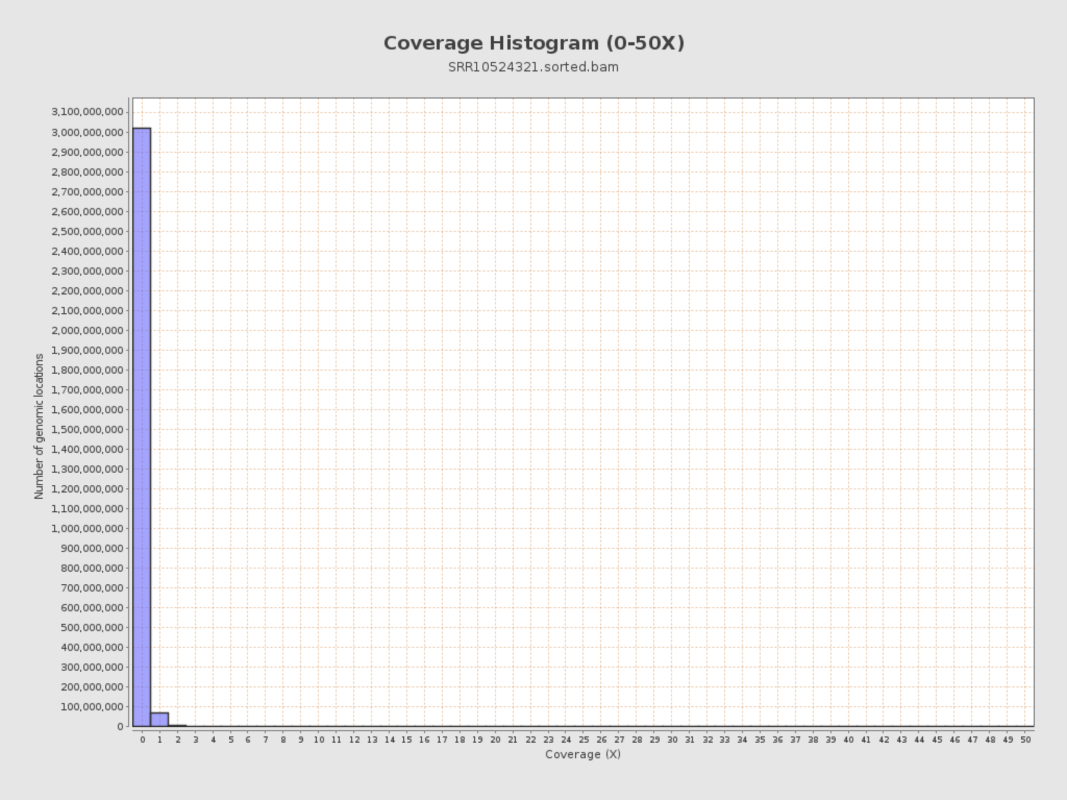
3. Results : Coverage across reference



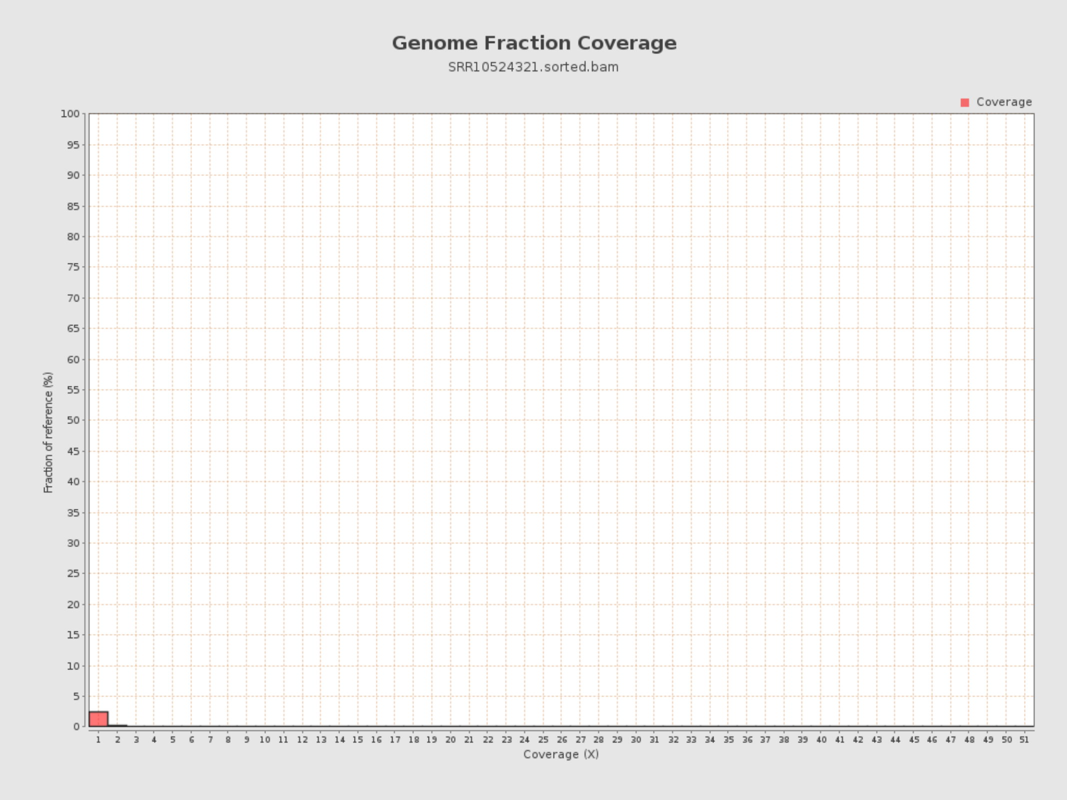
4. Results : Coverage Histogram



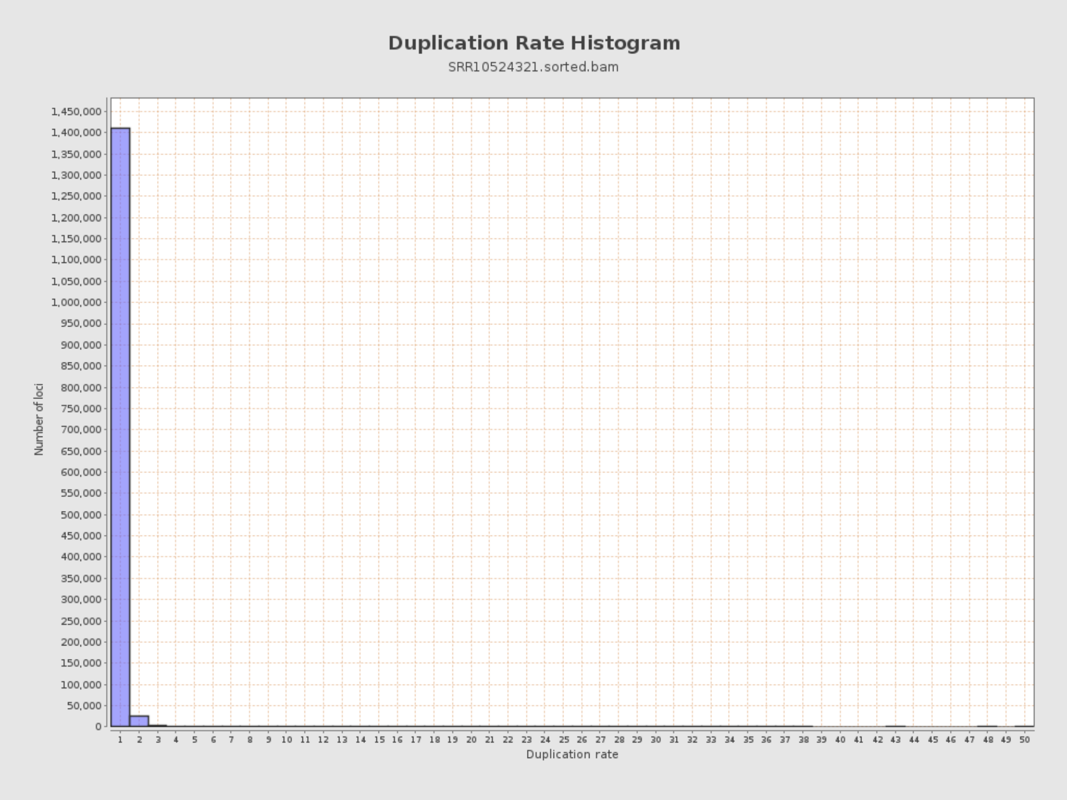
5. Results : Coverage Histogram (0-50X)



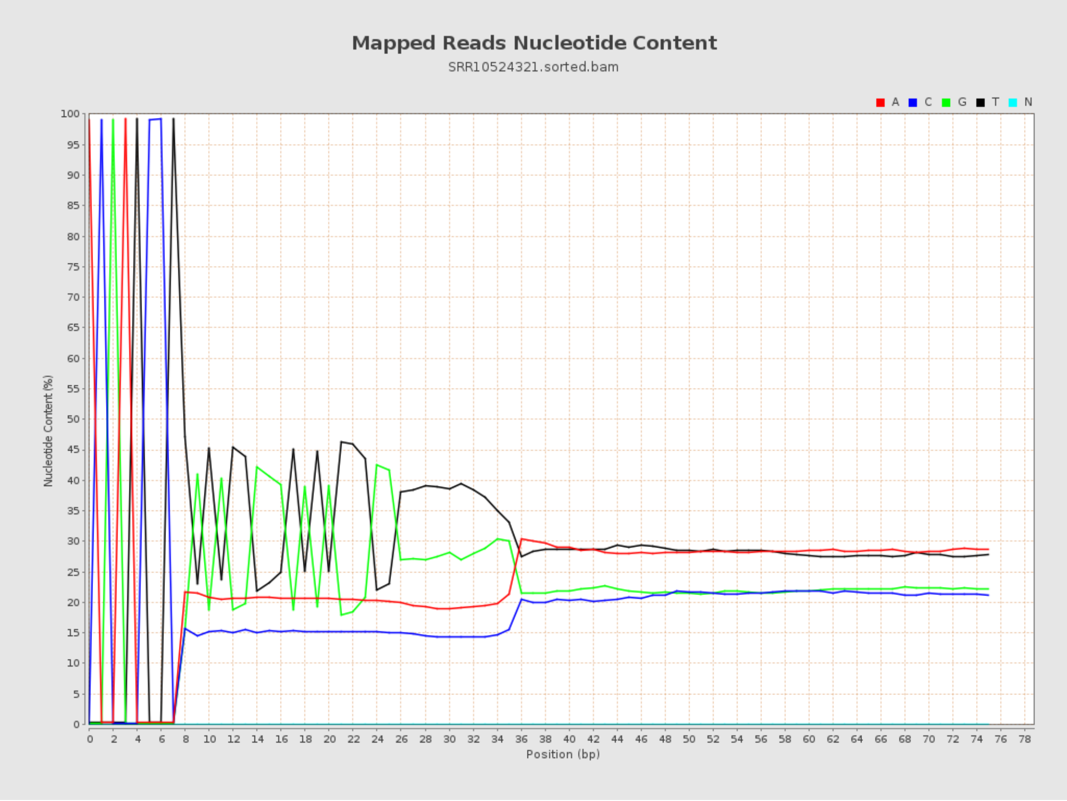
6. Results : Genome Fraction Coverage



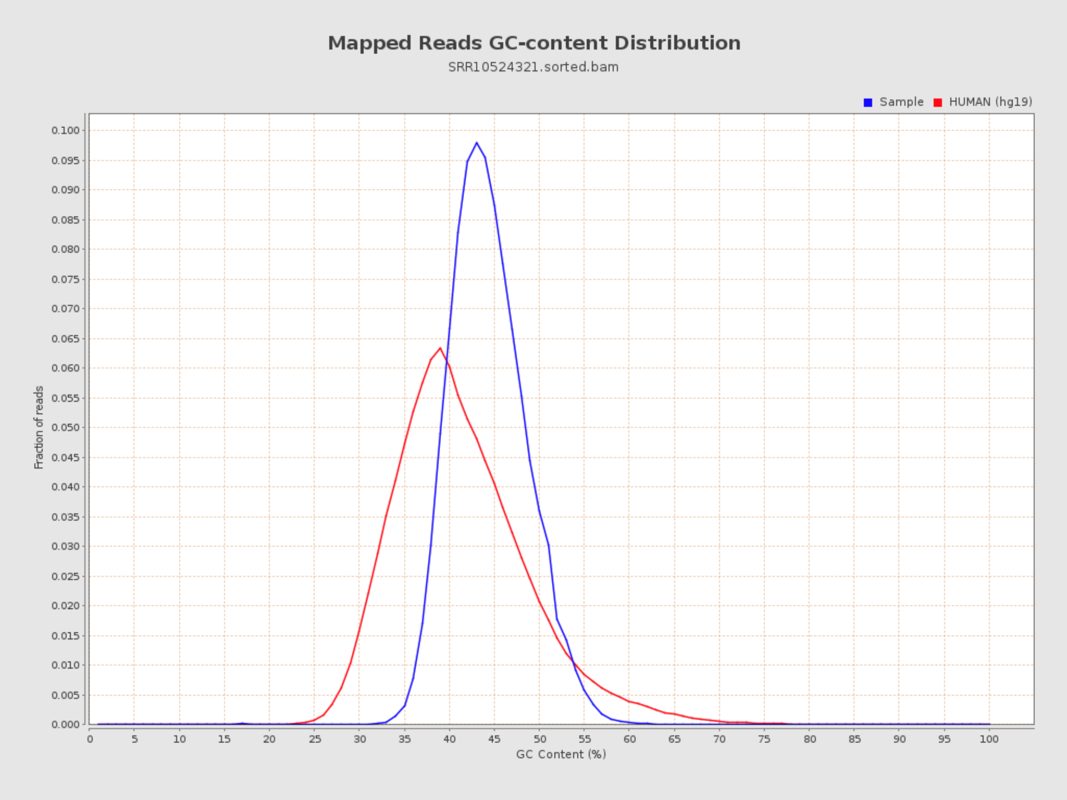
7. Results : Duplication Rate Histogram



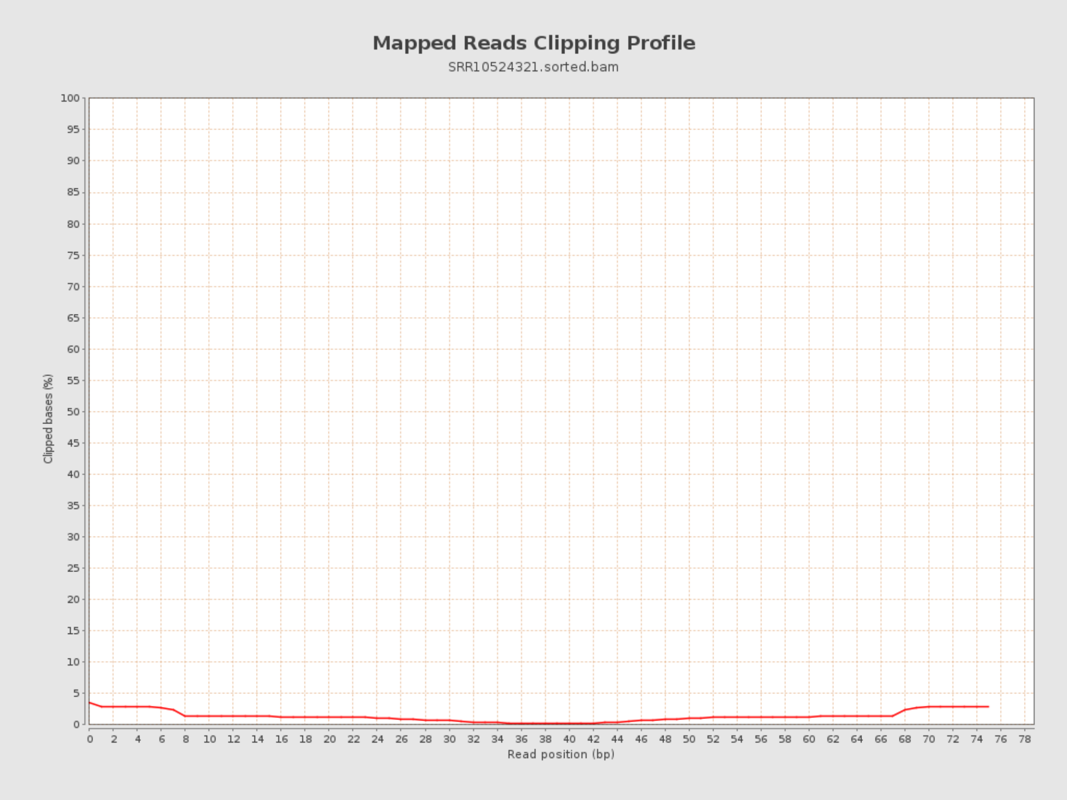
8. Results : Mapped Reads Nucleotide Content



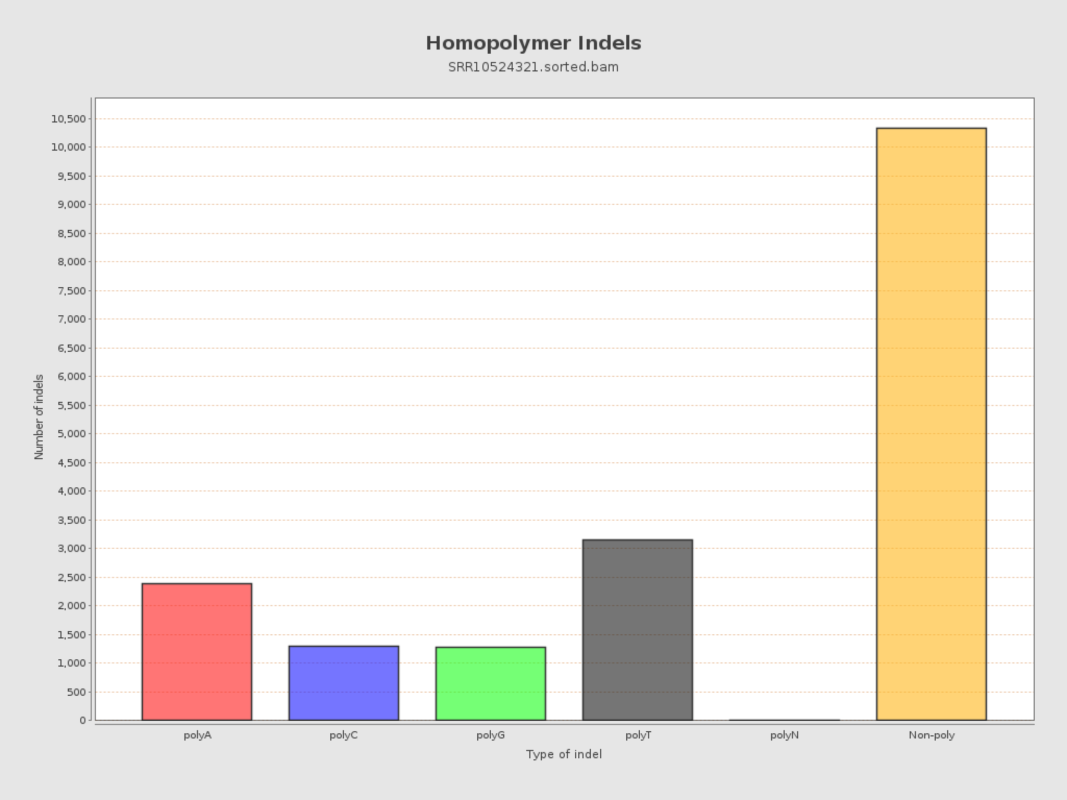
9. Results : Mapped Reads GC-content Distribution



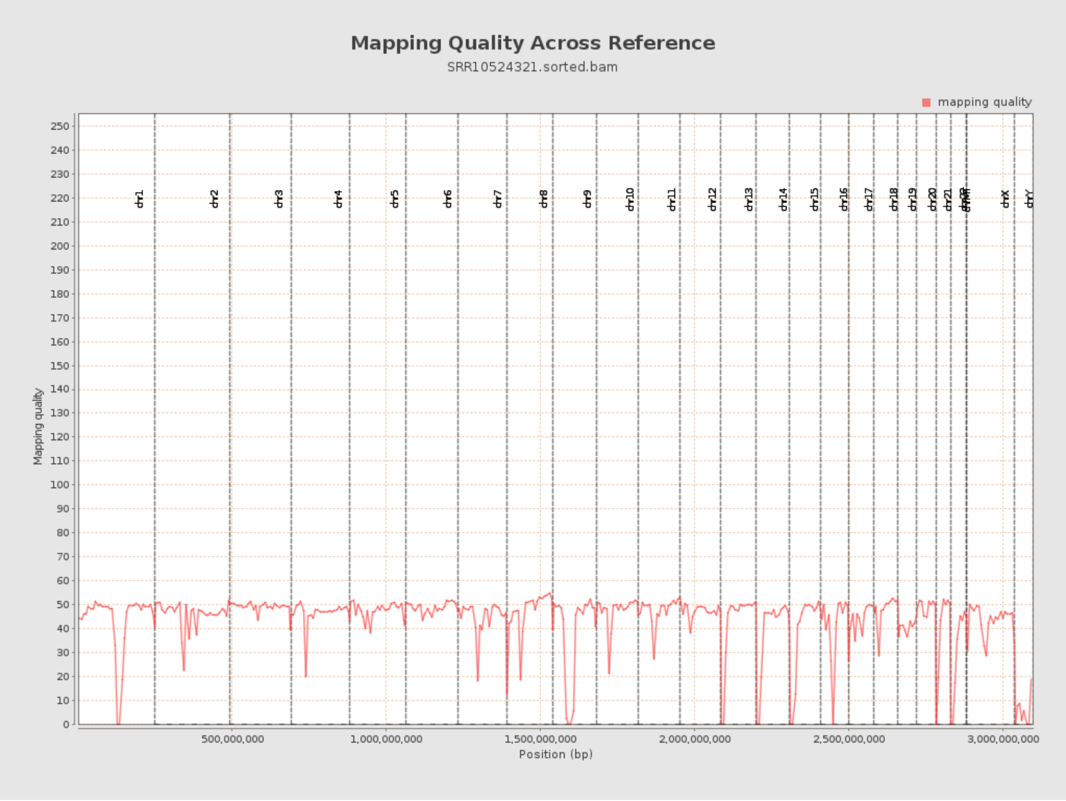
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram