Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 17:38:03

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524714.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_SRR10524714 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524714.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 17:38:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524714.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	265,721
Mapped reads	240,643 / 90.56%
Unmapped reads	25,078 / 9.44%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	825 / 0.31%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	3,285 / 1.24%
Duplication rate	1.05%
Clipped reads	240,838 / 90.64%

2.2. ACGT Content

Number/percentage of A's	3,566,792 / 25.2%
Number/percentage of C's	2,510,364 / 17.74%
Number/percentage of T's	4,670,031 / 33%
Number/percentage of G's	3,402,725 / 24.04%
Number/percentage of N's	2,250 / 0.02%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0046

Standard Deviation	0.0767

2.4. Mapping Quality

Mean Mapping Quality	45.72

2.5. Mismatches and indels

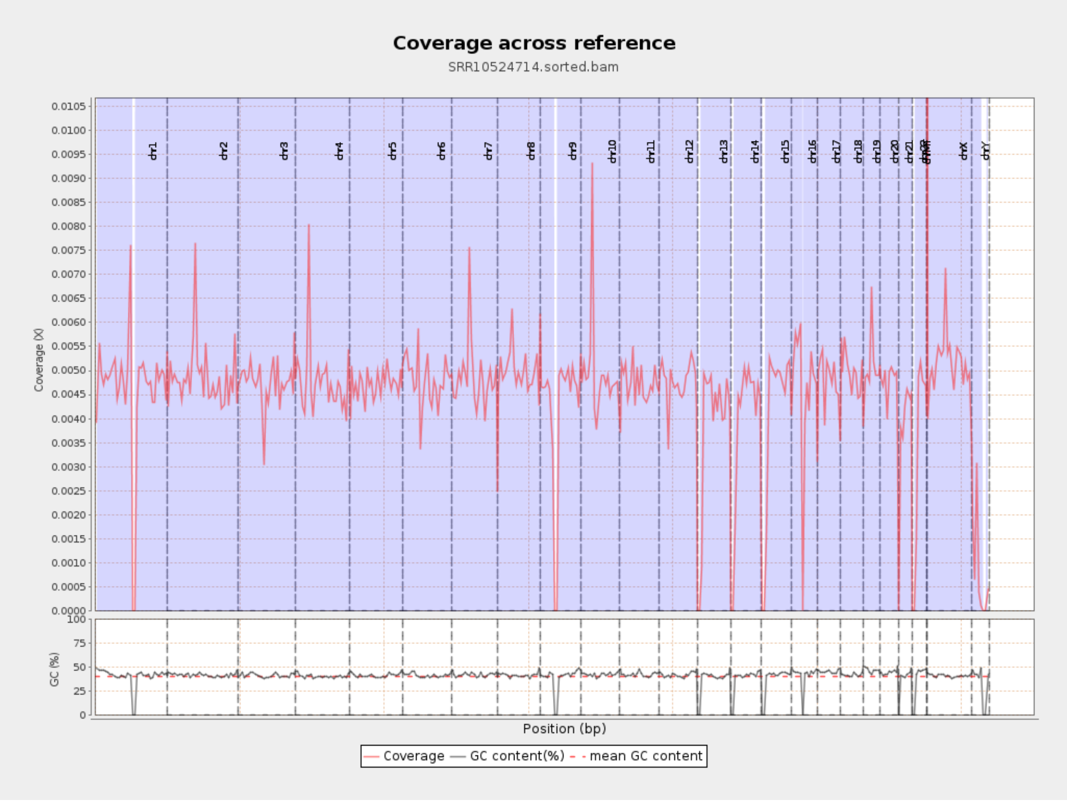
General error rate	0.52%
Mismatches	71,957
Insertions	1,004
Mapped reads with at least one insertion	0.42%
Deletions	2,756
Mapped reads with at least one deletion	1.13%
Homopolymer indels	43.38%

2.6. Chromosome stats

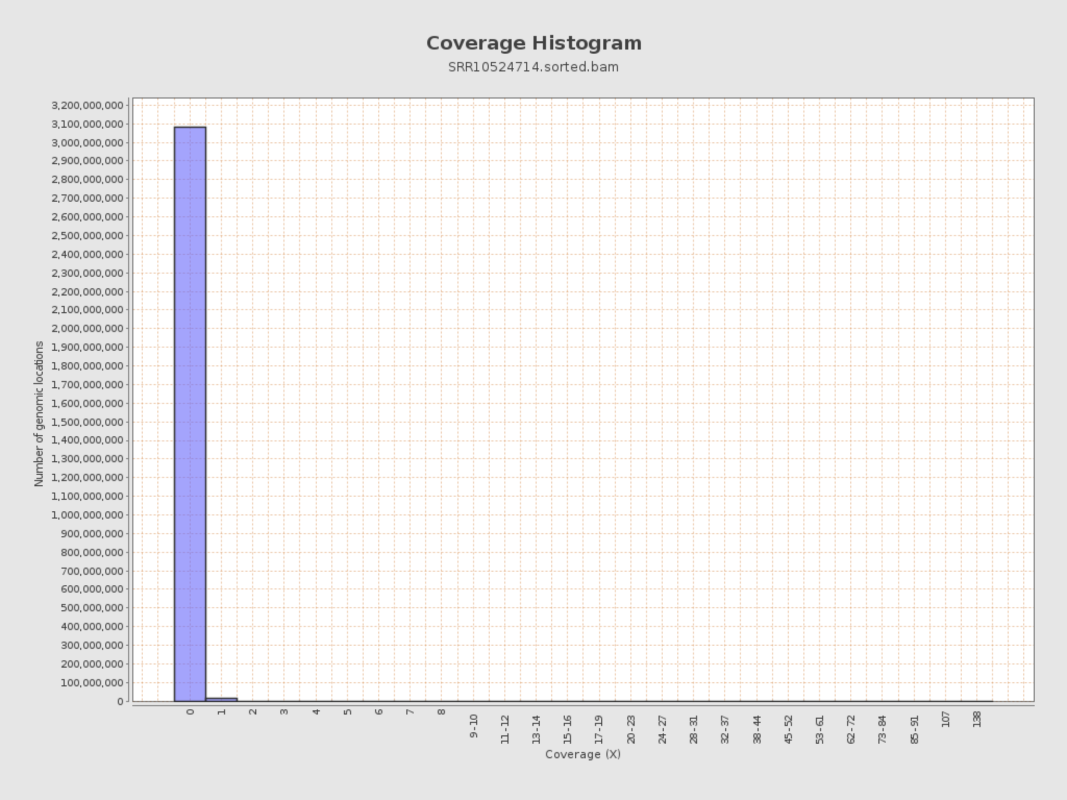
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1143723	0.0046	0.0987
chr2	243199373	1184841	0.0049	0.0925
chr3	198022430	935974	0.0047	0.0699
chr4	191154276	916209	0.0048	0.0723
chr5	180915260	857060	0.0047	0.0701
chr6	171115067	819778	0.0048	0.0726
chr7	159138663	776142	0.0049	0.0805

chr8	146364022	730942	0.005	0.0828
chr9	141213431	589832	0.0042	0.0696
chr10	135534747	672176	0.005	0.081
chr11	135006516	642056	0.0048	0.0738
chr12	133851895	639410	0.0048	0.0705
chr13	115169878	433403	0.0038	0.0625
chr14	107349540	409699	0.0038	0.0633
chr15	102531392	411857	0.004	0.0646
chr16	90354753	411230	0.0046	0.0698
chr17	81195210	390540	0.0048	0.0713
chr18	78077248	386760	0.005	0.0911
chr19	59128983	302407	0.0051	0.092
chr20	63025520	298285	0.0047	0.0705
chr21	48129895	182498	0.0038	0.0648
chr22	51304566	170664	0.0033	0.0586
chrMT	16571	4116	0.2484	0.5241
chrX	155270560	800798	0.0052	0.0746
chrY	59373566	46084	0.0008	0.0371

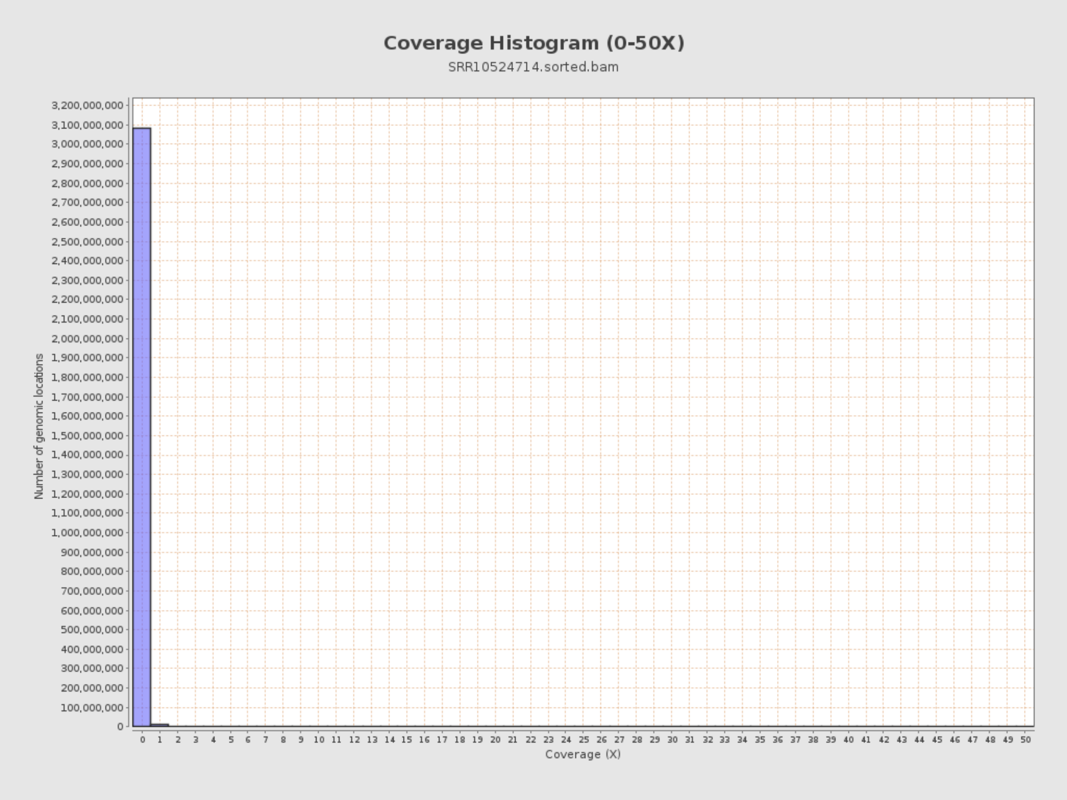
3. Results : Coverage across reference



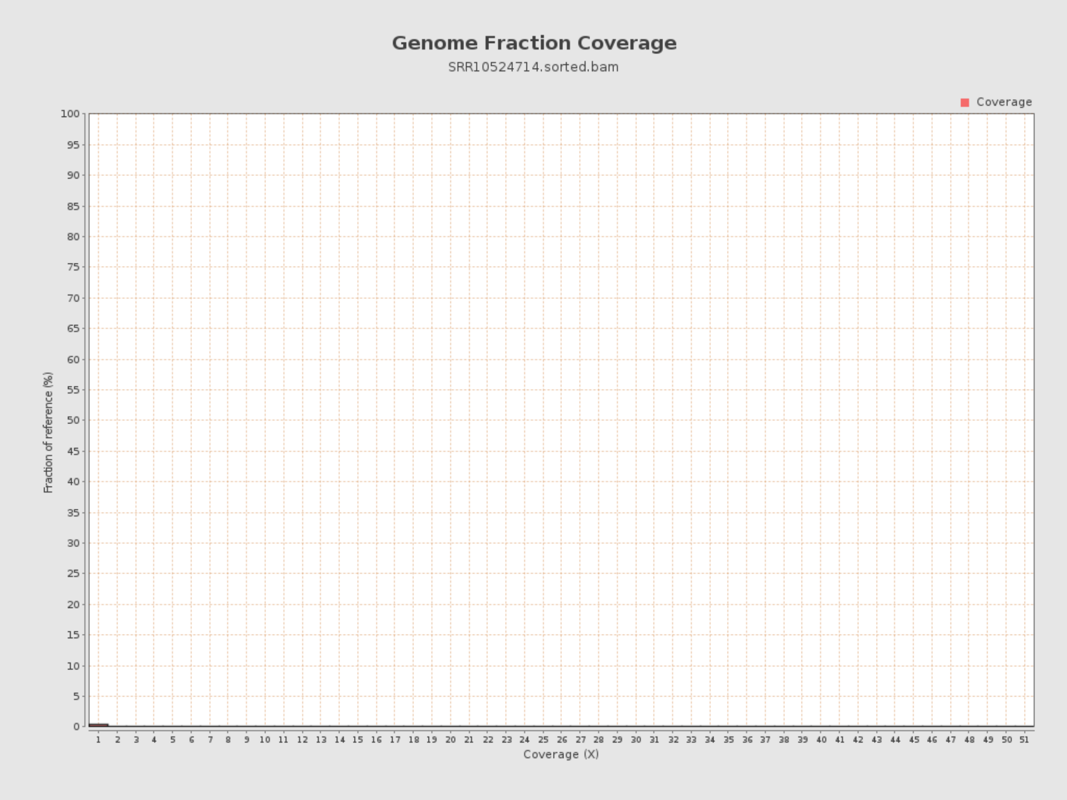
4. Results : Coverage Histogram



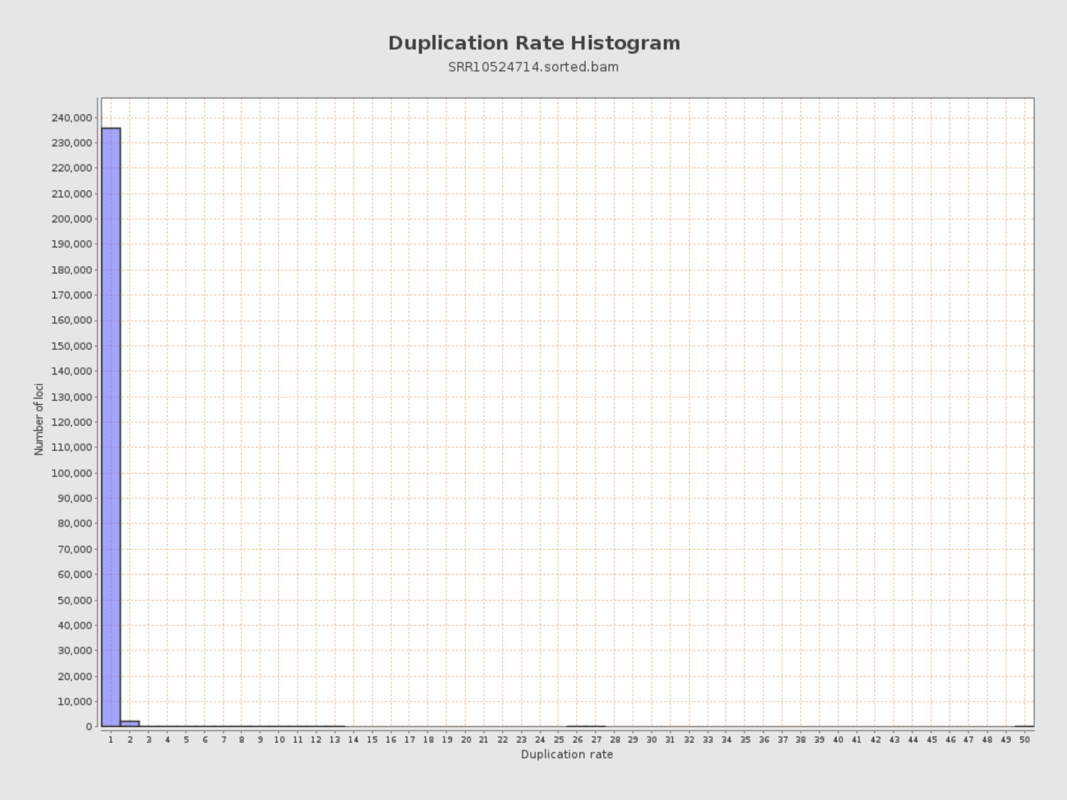
5. Results : Coverage Histogram (0-50X)



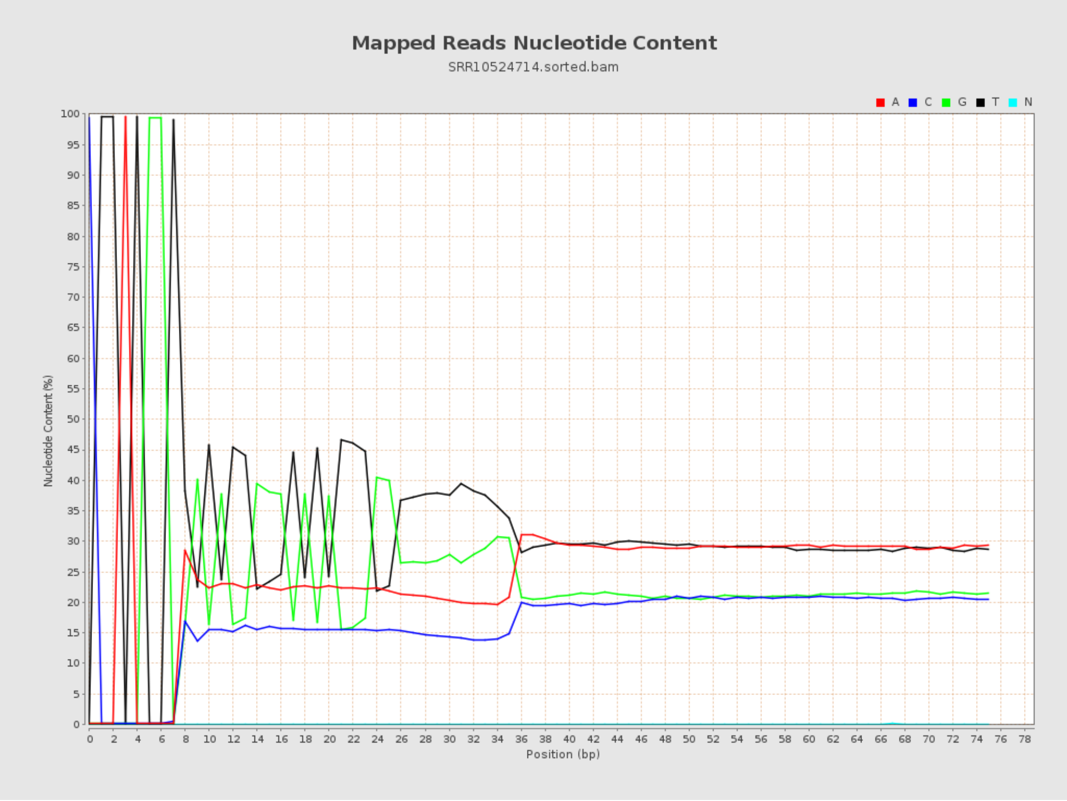
6. Results : Genome Fraction Coverage



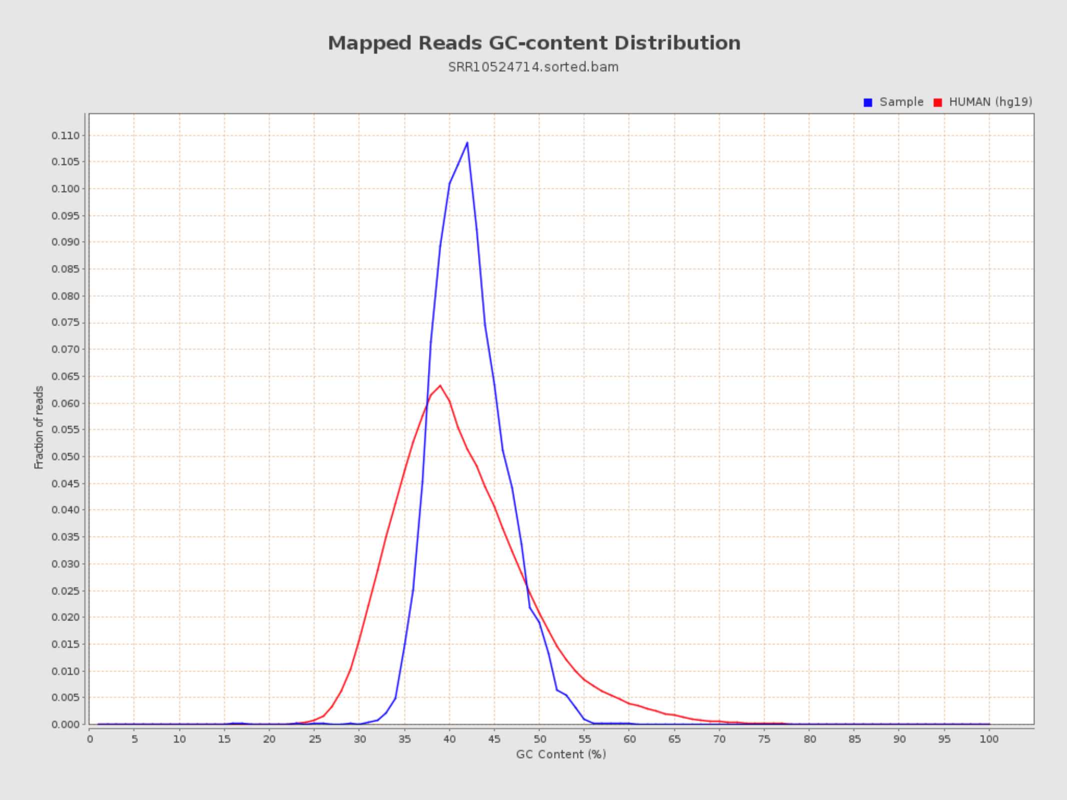
7. Results : Duplication Rate Histogram



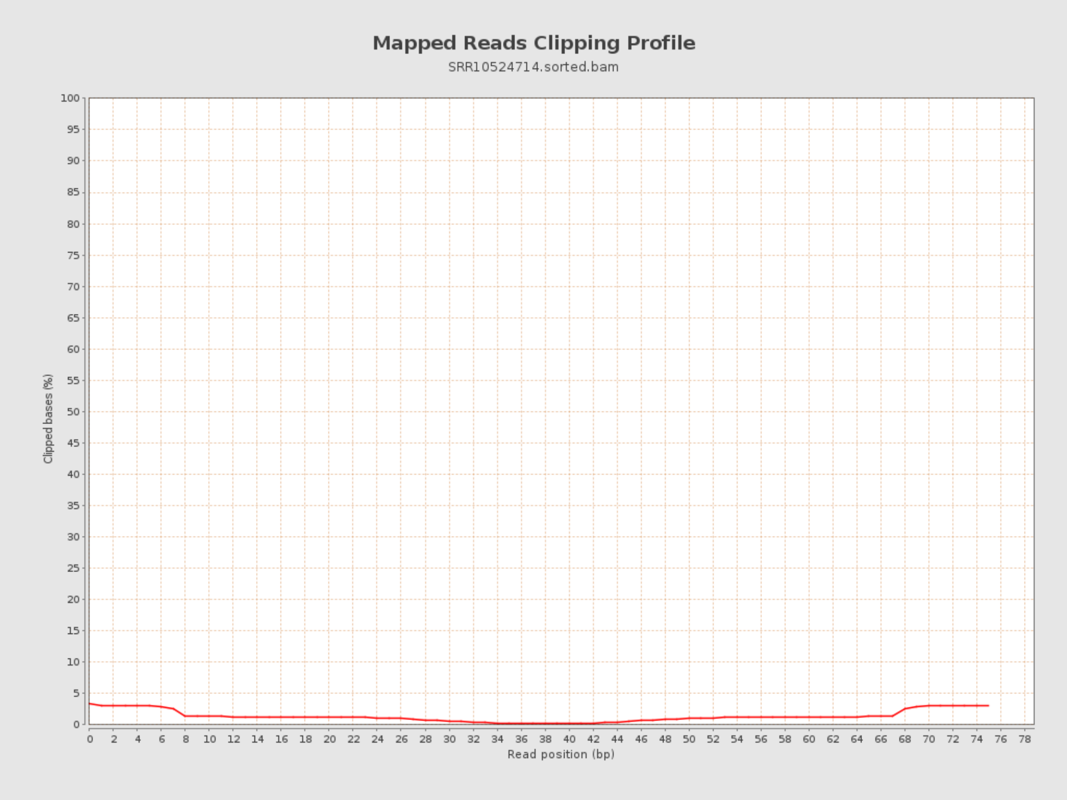
8. Results : Mapped Reads Nucleotide Content



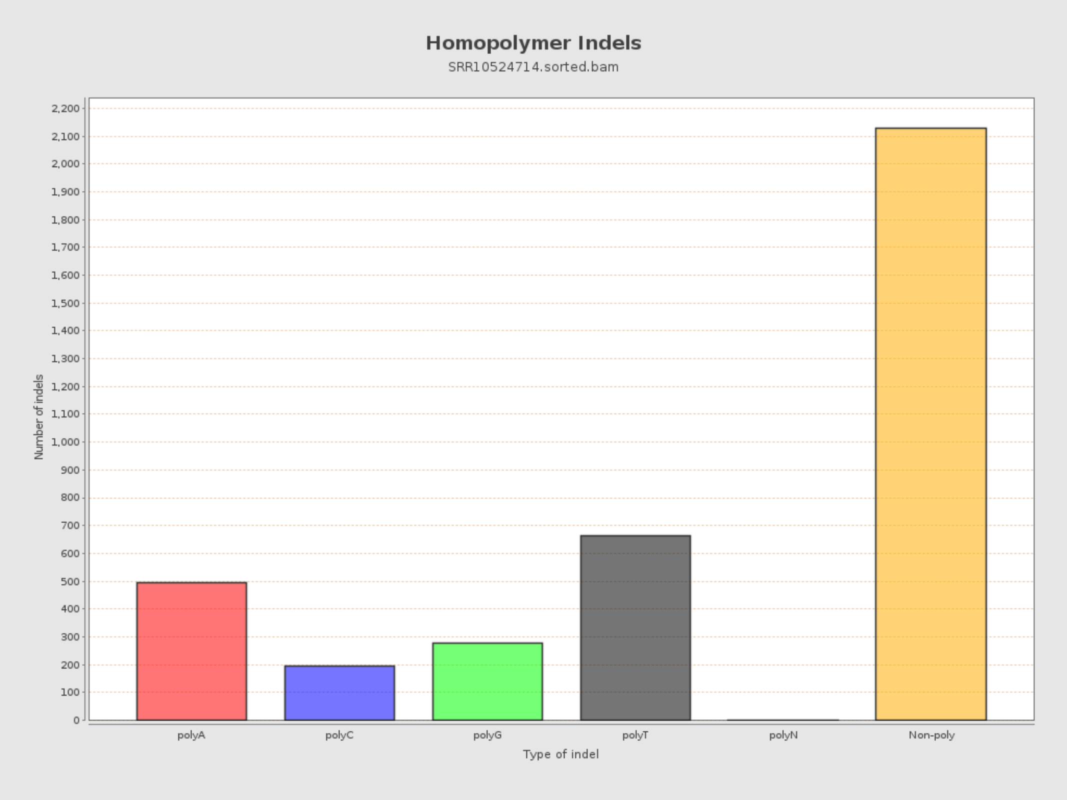
9. Results : Mapped Reads GC-content Distribution



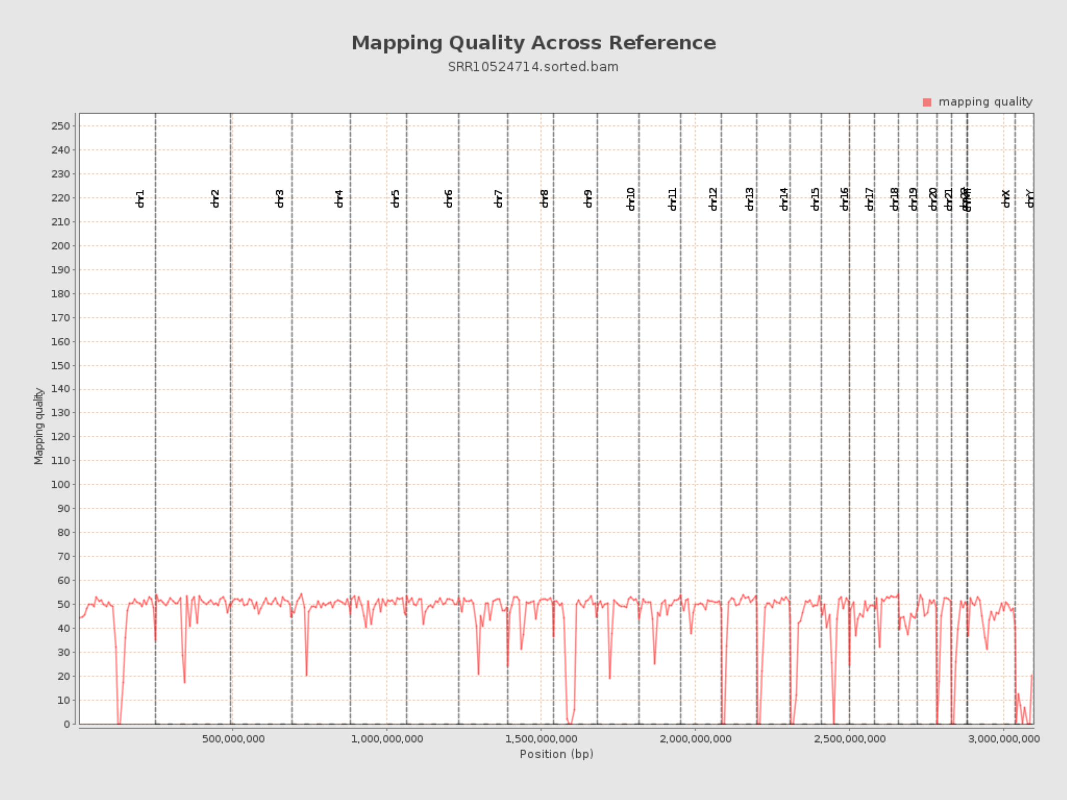
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram