Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 00:06:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524351.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_SRR10524351 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524351.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 00:06:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524351.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,441,246
Mapped reads	1,328,745 / 92.19%
Unmapped reads	112,501 / 7.81%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,618 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	61,736 / 4.28%
Duplication rate	3.39%
Clipped reads	1,333,765 / 92.54%

2.2. ACGT Content

Number/percentage of A's	18,802,250 / 23.99%
Number/percentage of C's	14,443,327 / 18.42%
Number/percentage of T's	25,440,287 / 32.45%
Number/percentage of G's	19,694,494 / 25.12%
Number/percentage of N's	10,537 / 0.01%
GC Percentage	43.55%

2.3. Coverage

Mean	0.0253

Standard Deviation	0.2771

2.4. Mapping Quality

Mean Mapping Quality	45.27

2.5. Mismatches and indels

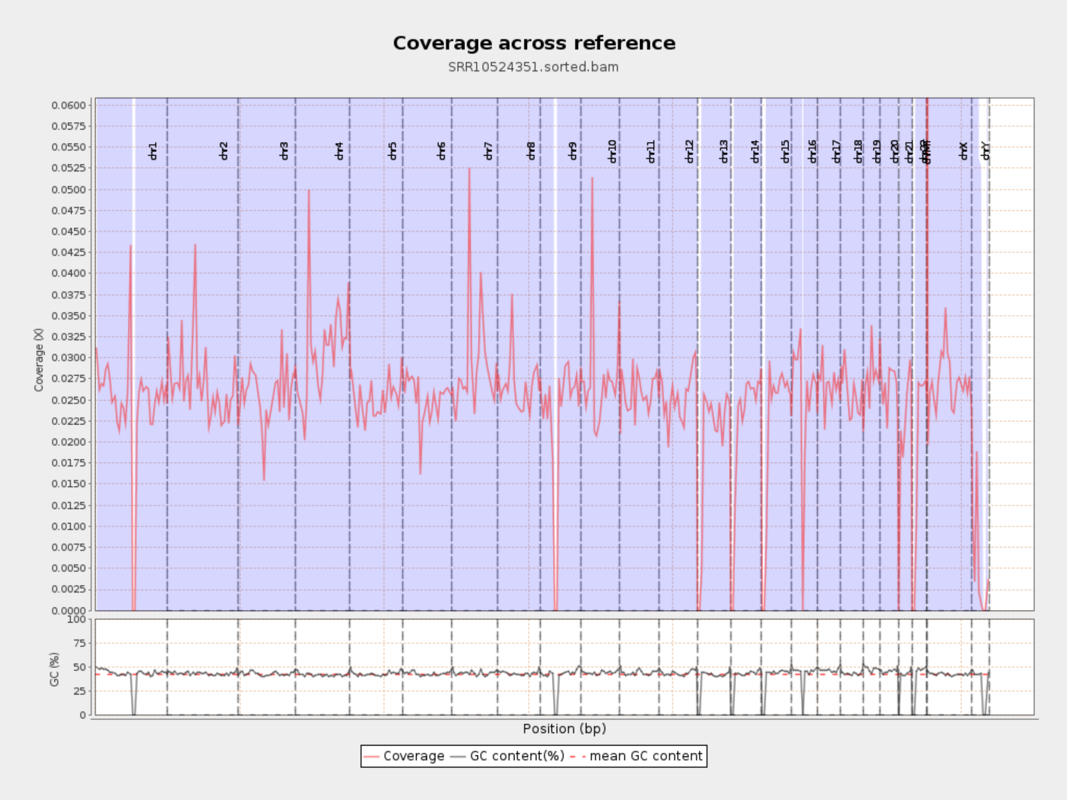
General error rate	0.53%
Mismatches	403,353
Insertions	4,795
Mapped reads with at least one insertion	0.36%
Deletions	13,801
Mapped reads with at least one deletion	1.03%
Homopolymer indels	43.81%

2.6. Chromosome stats

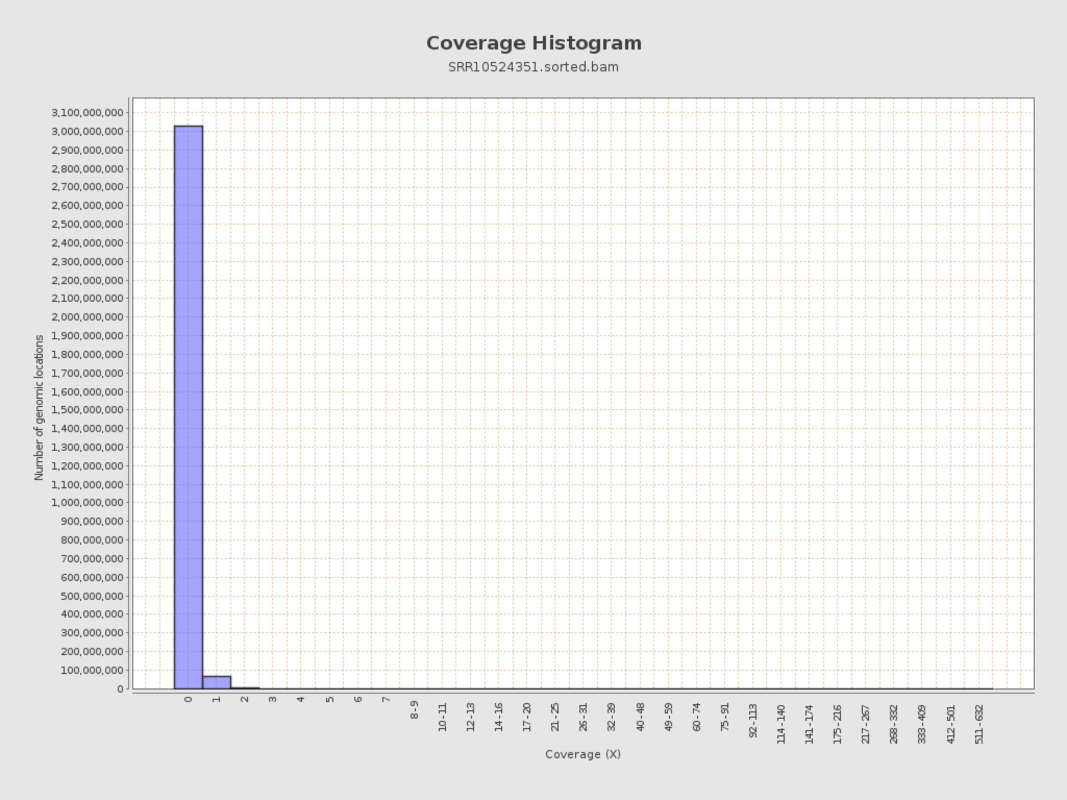
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6103137	0.0245	0.4925
chr2	243199373	6567976	0.027	0.3273
chr3	198022430	5070742	0.0256	0.1755
chr4	191154276	5898799	0.0309	0.2264
chr5	180915260	4541437	0.0251	0.1762
chr6	171115067	4304884	0.0252	0.1844
chr7	159138663	4662956	0.0293	0.3868

chr8	146364022	3918507	0.0268	0.2388
chr9	141213431	3216419	0.0228	0.2177
chr10	135534747	3732614	0.0275	0.2701
chr11	135006516	3512720	0.026	0.229
chr12	133851895	3409709	0.0255	0.178
chr13	115169878	2273220	0.0197	0.1546
chr14	107349540	2305983	0.0215	0.1675
chr15	102531392	2214849	0.0216	0.1599
chr16	90354753	2246806	0.0249	0.1841
chr17	81195210	2178143	0.0268	0.1909
chr18	78077248	2005686	0.0257	0.4272
chr19	59128983	1644978	0.0278	0.3404
chr20	63025520	1675052	0.0266	0.1839
chr21	48129895	1039006	0.0216	0.1926
chr22	51304566	962067	0.0188	0.1509
chrMT	16571	434625	26.228	15.7265
chrX	155270560	4211189	0.0271	0.1992
chrY	59373566	281723	0.0047	0.157

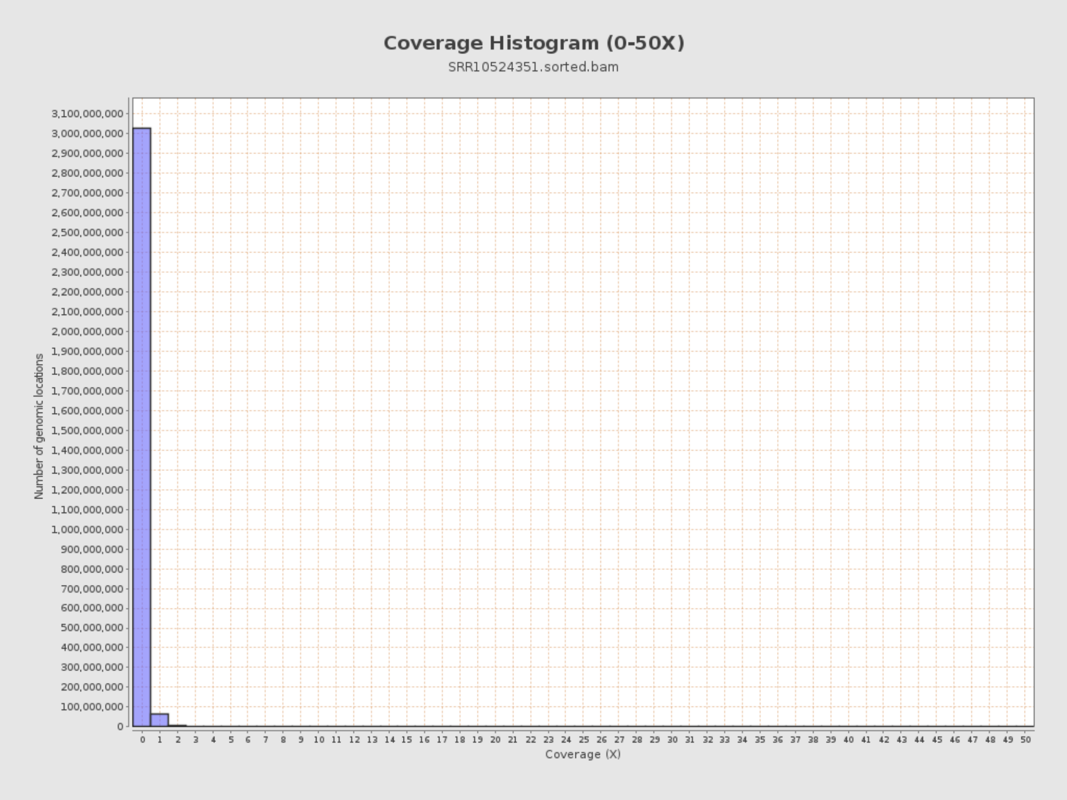
3. Results : Coverage across reference



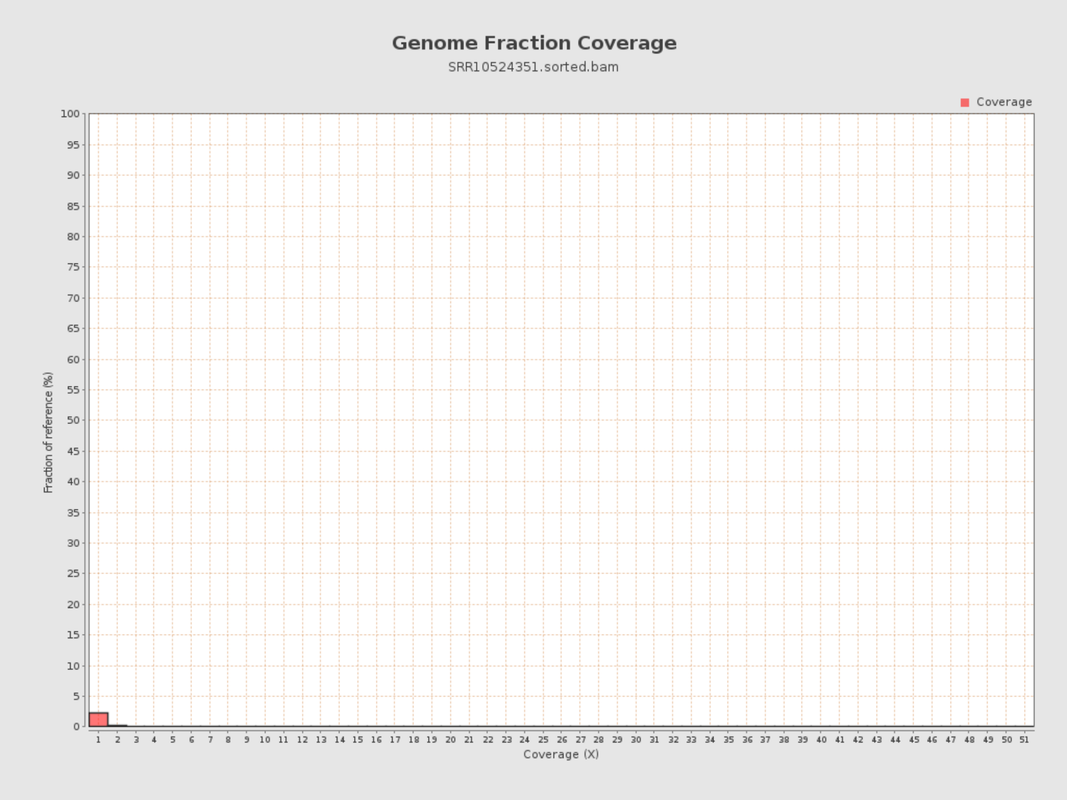
4. Results : Coverage Histogram



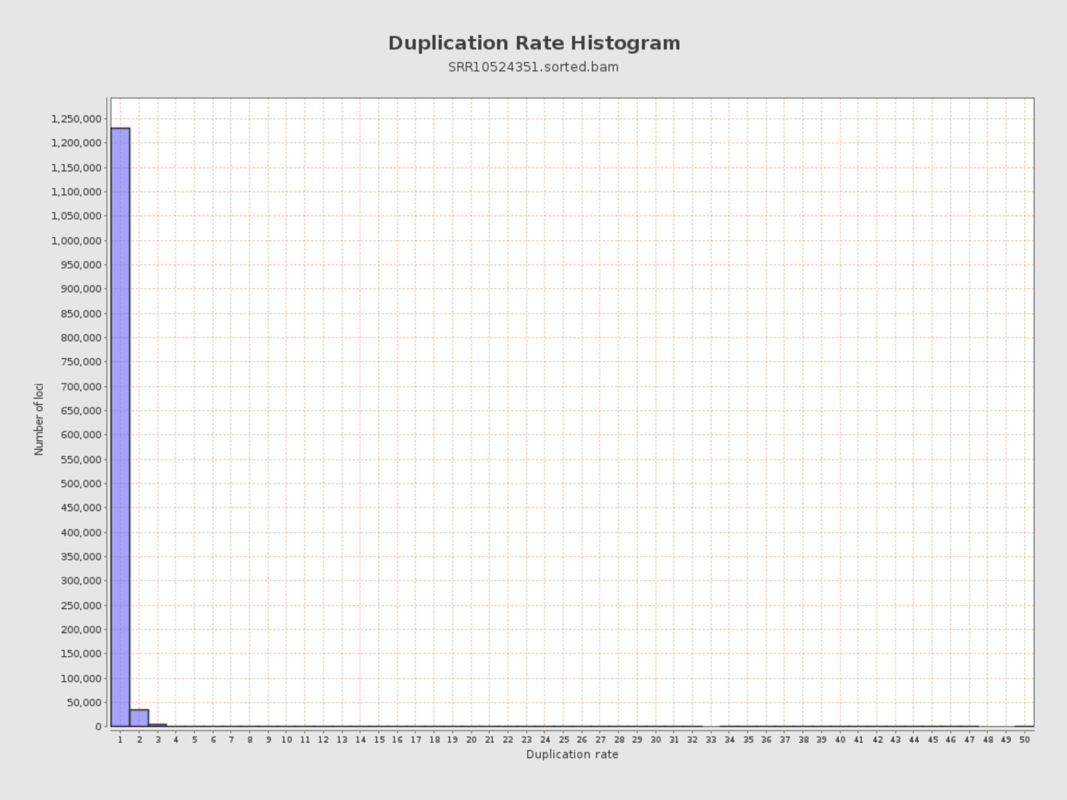
5. Results : Coverage Histogram (0-50X)



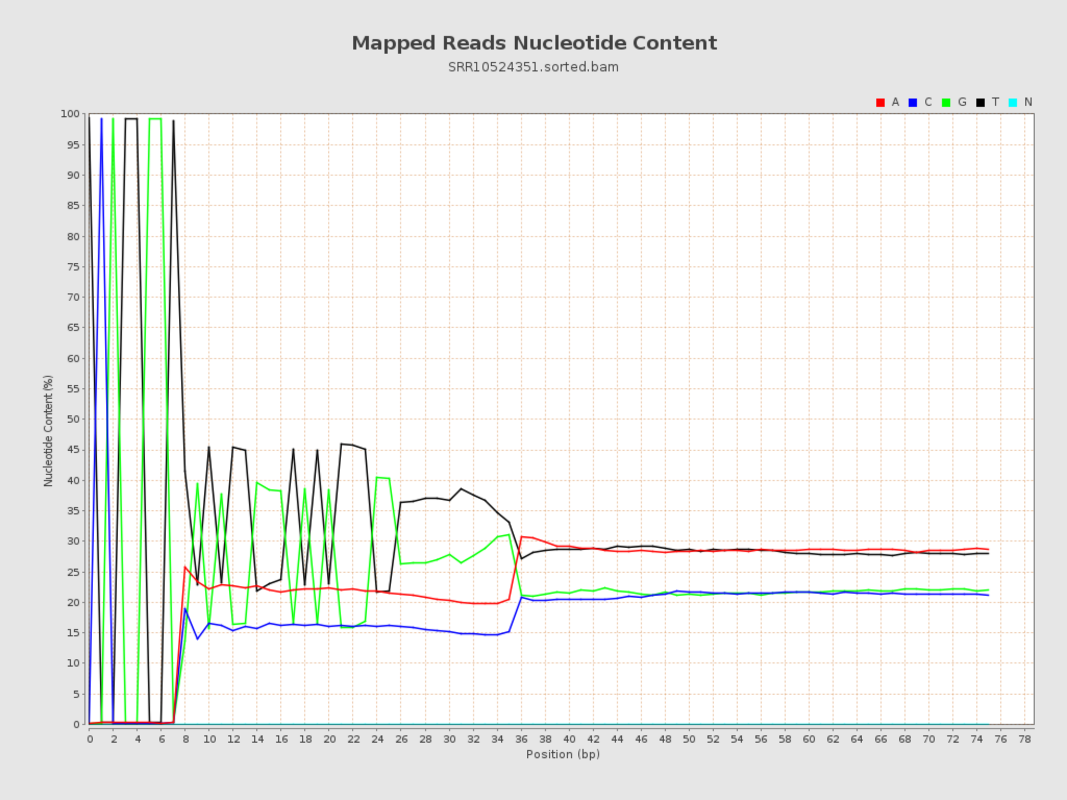
6. Results : Genome Fraction Coverage



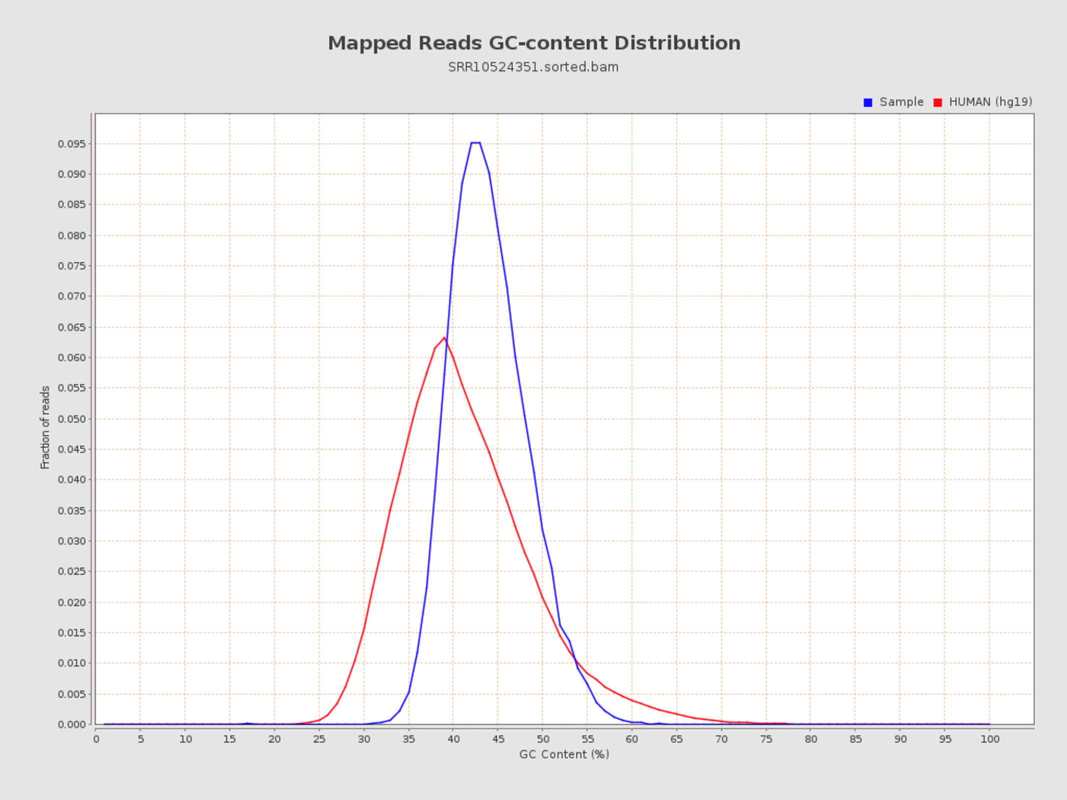
7. Results : Duplication Rate Histogram



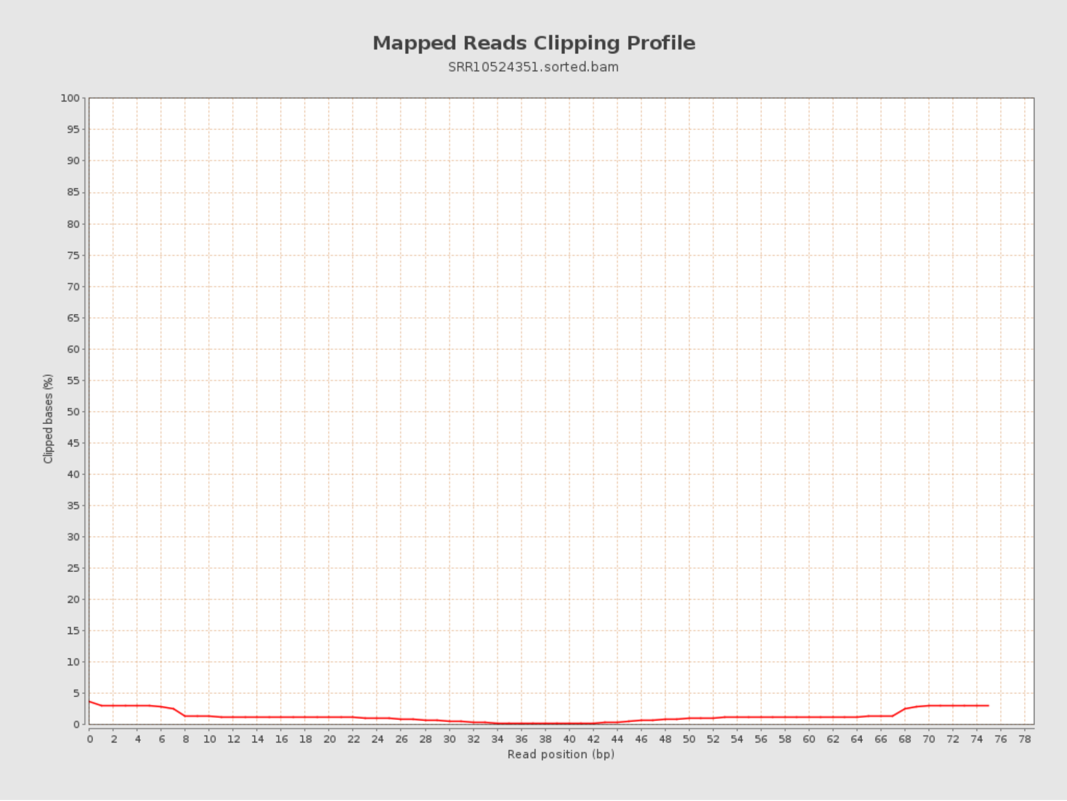
8. Results : Mapped Reads Nucleotide Content



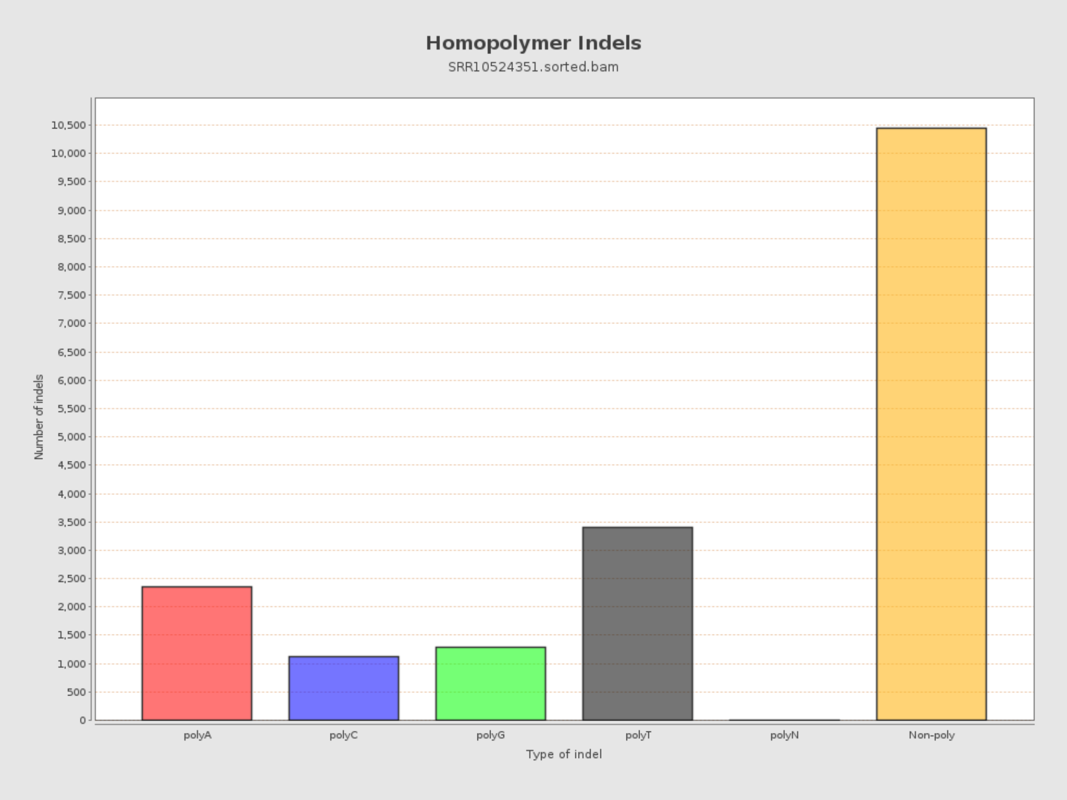
9. Results : Mapped Reads GC-content Distribution



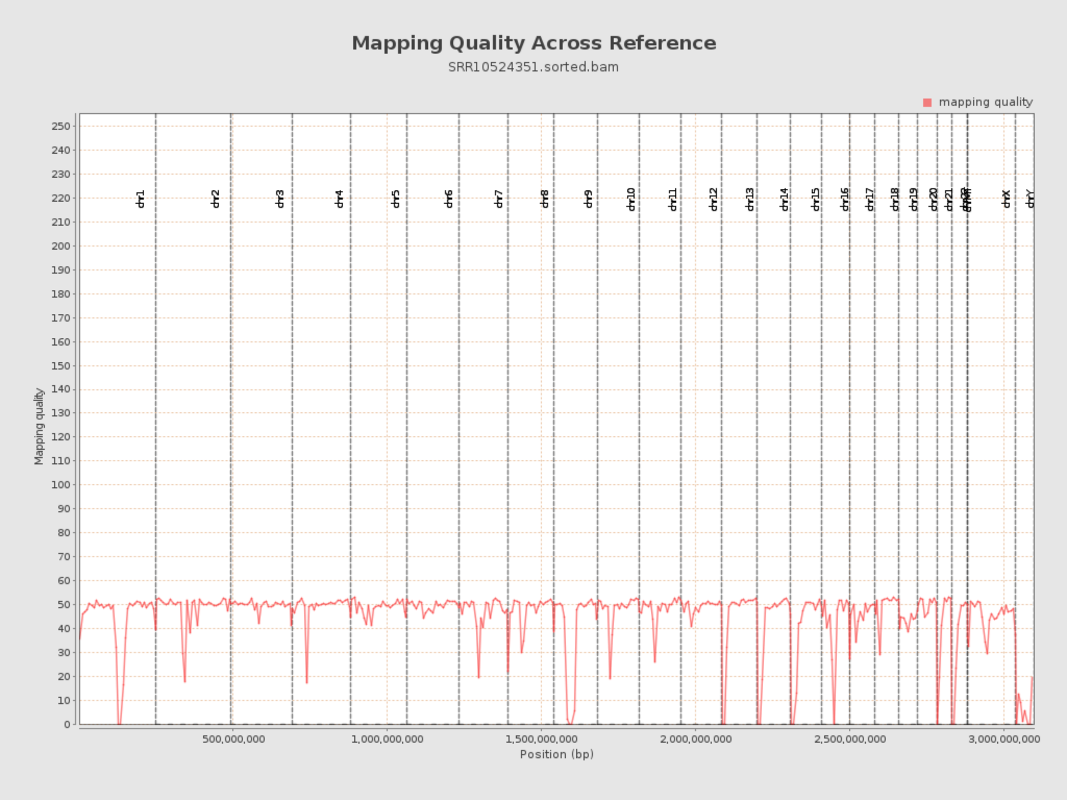
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram