Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 10:28:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524551.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_SRR10524551 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524551.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 10:28:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524551.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,633,288
Mapped reads	1,495,026 / 91.53%
Unmapped reads	138,262 / 8.47%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,677 / 0.35%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	63,750 / 3.9%
Duplication rate	3.22%
Clipped reads	1,495,934 / 91.59%

2.2. ACGT Content

Number/percentage of A's	20,575,066 / 23.71%
Number/percentage of C's	17,002,150 / 19.59%
Number/percentage of T's	28,522,810 / 32.87%
Number/percentage of G's	20,671,022 / 23.82%
Number/percentage of N's	1,275 / 0%
GC Percentage	43.42%

2.3. Coverage

Mean	0.028

Standard Deviation	0.2661

2.4. Mapping Quality

Mean Mapping Quality	44.89

2.5. Mismatches and indels

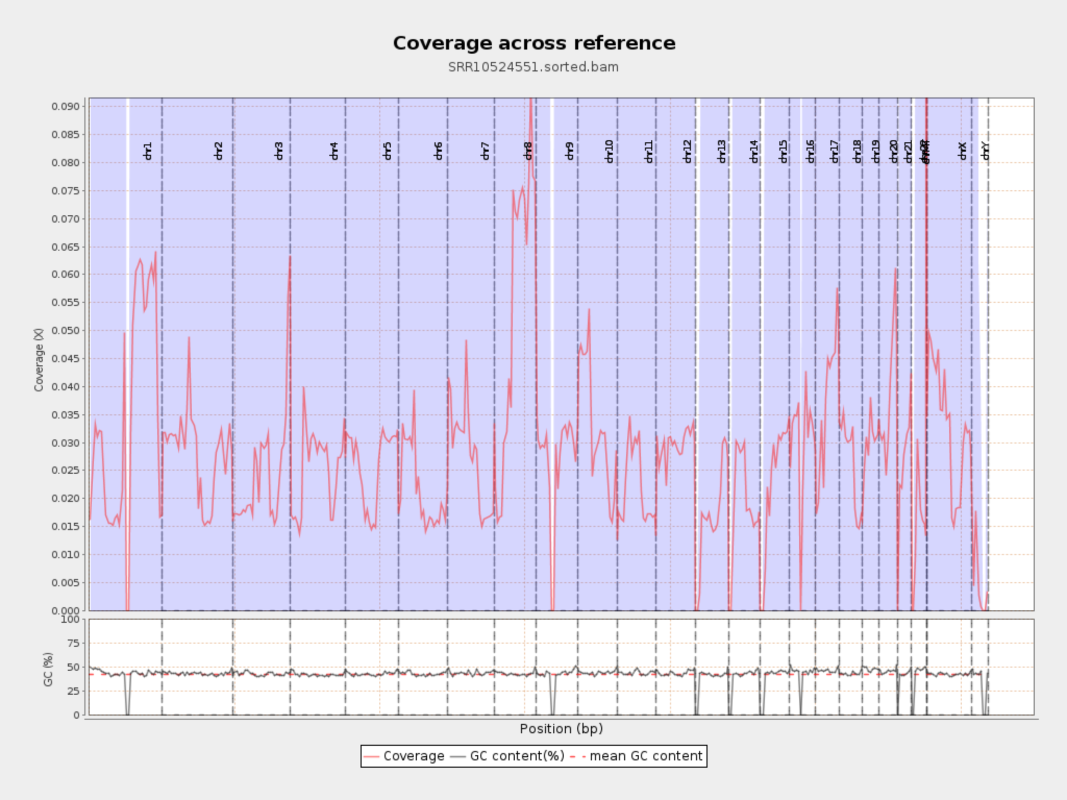
General error rate	0.52%
Mismatches	442,359
Insertions	5,657
Mapped reads with at least one insertion	0.38%
Deletions	16,636
Mapped reads with at least one deletion	1.1%
Homopolymer indels	43.21%

2.6. Chromosome stats

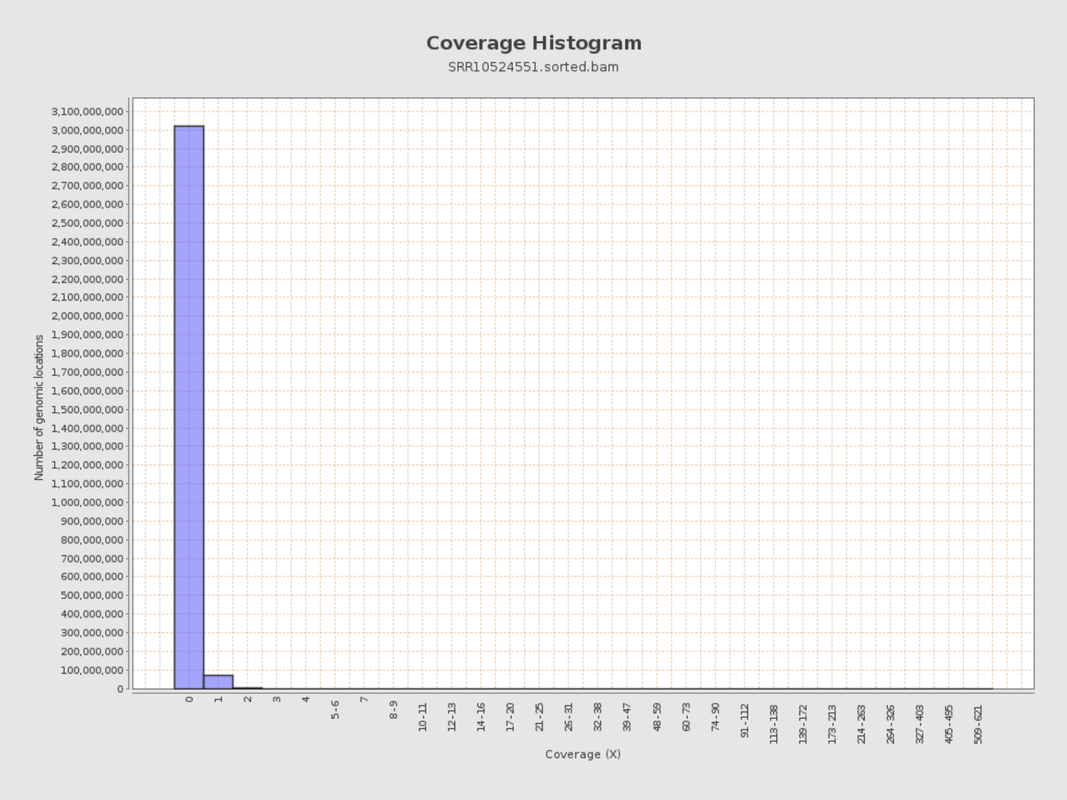
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	8643184	0.0347	0.4873
chr2	243199373	6877924	0.0283	0.3071
chr3	198022430	4761846	0.024	0.1718
chr4	191154276	4816766	0.0252	0.1973
chr5	180915260	4702241	0.026	0.1791
chr6	171115067	3687682	0.0216	0.2004
chr7	159138663	4396605	0.0276	0.3296

chr8	146364022	7981440	0.0545	0.2995
chr9	141213431	3705429	0.0262	0.2281
chr10	135534747	4482556	0.0331	0.2711
chr11	135006516	2993370	0.0222	0.2426
chr12	133851895	3975831	0.0297	0.1902
chr13	115169878	1923880	0.0167	0.1416
chr14	107349540	2021560	0.0188	0.1524
chr15	102531392	2301018	0.0224	0.1685
chr16	90354753	2734023	0.0303	0.2043
chr17	81195210	3064494	0.0377	0.2263
chr18	78077248	2061197	0.0264	0.4084
chr19	59128983	1788695	0.0303	0.3419
chr20	63025520	2447595	0.0388	0.2188
chr21	48129895	1264575	0.0263	0.193
chr22	51304566	718812	0.014	0.13
chrMT	16571	5802	0.3501	0.6097
chrX	155270560	5148642	0.0332	0.2236
chrY	59373566	294467	0.005	0.1506

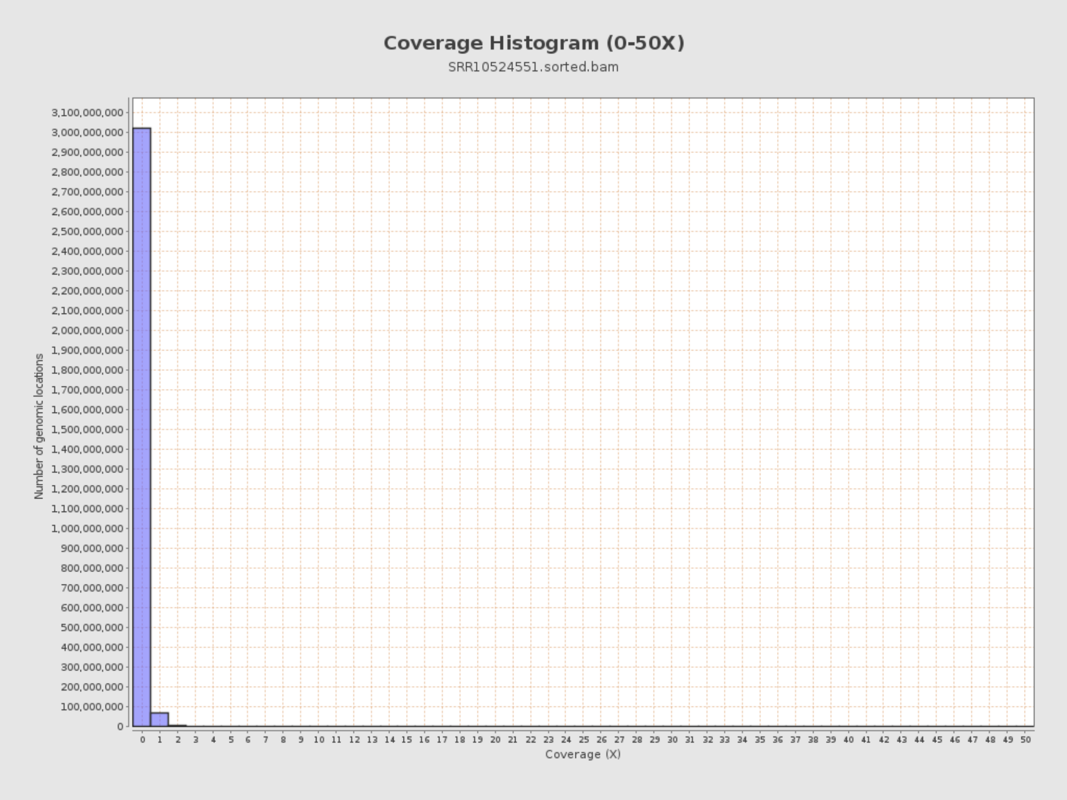
3. Results : Coverage across reference



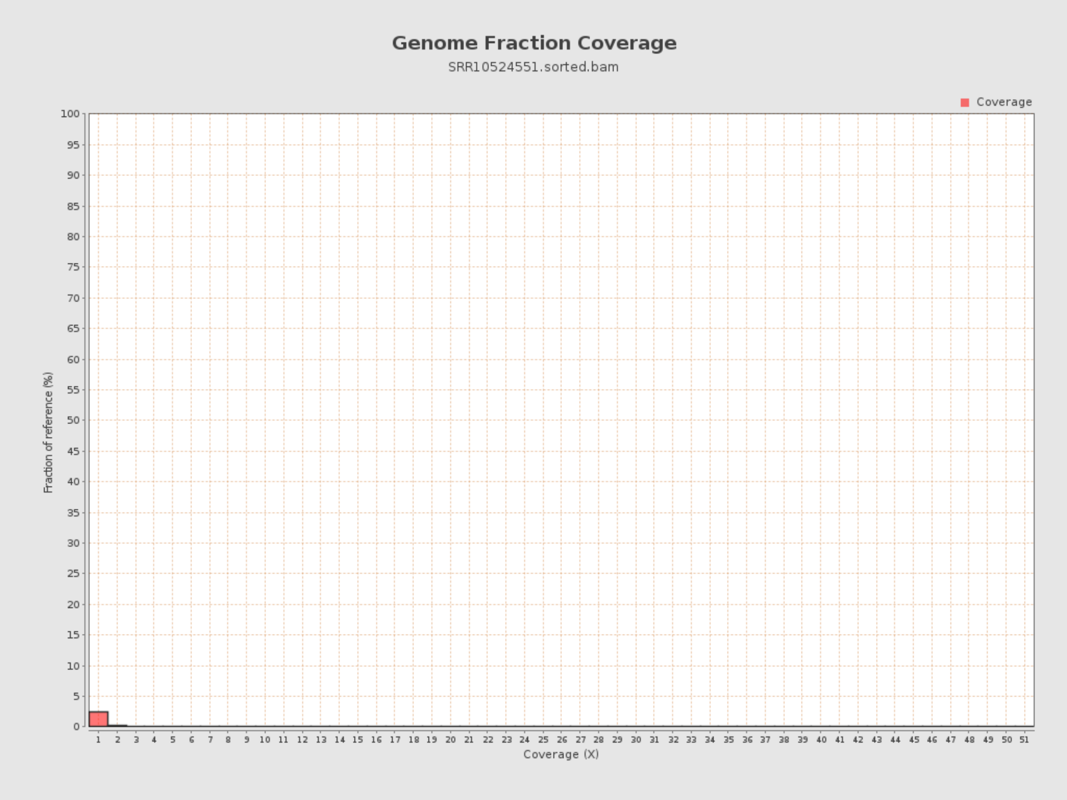
4. Results : Coverage Histogram



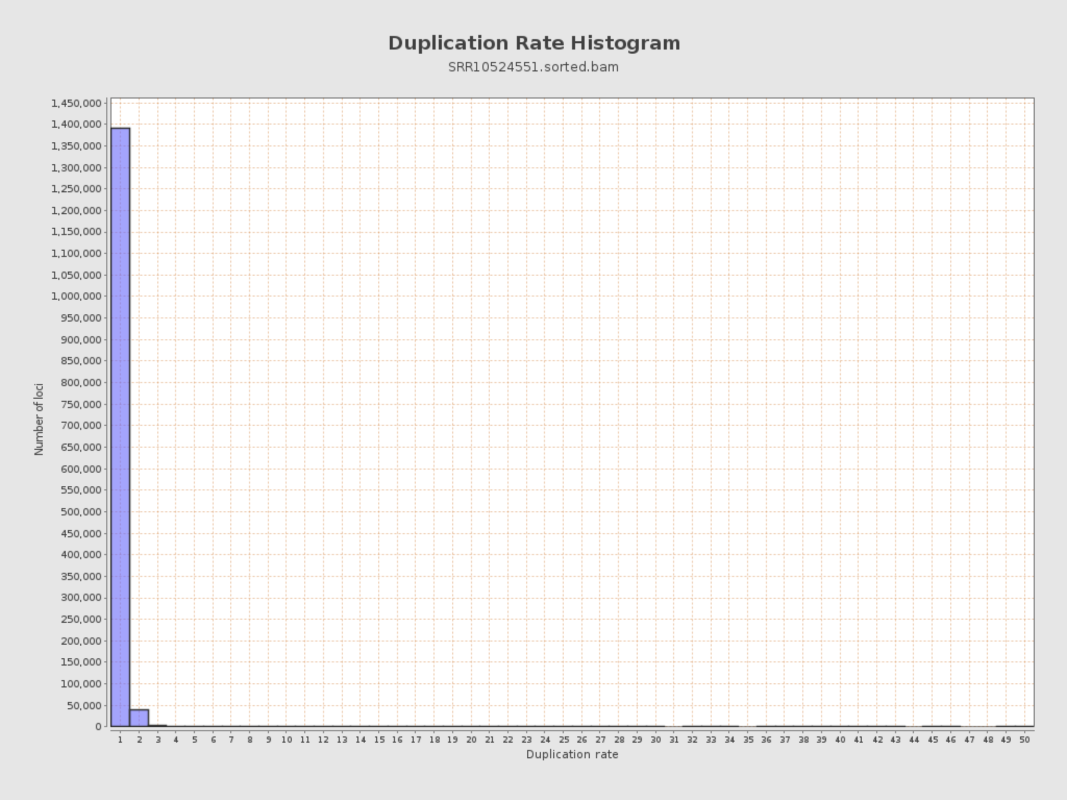
5. Results : Coverage Histogram (0-50X)



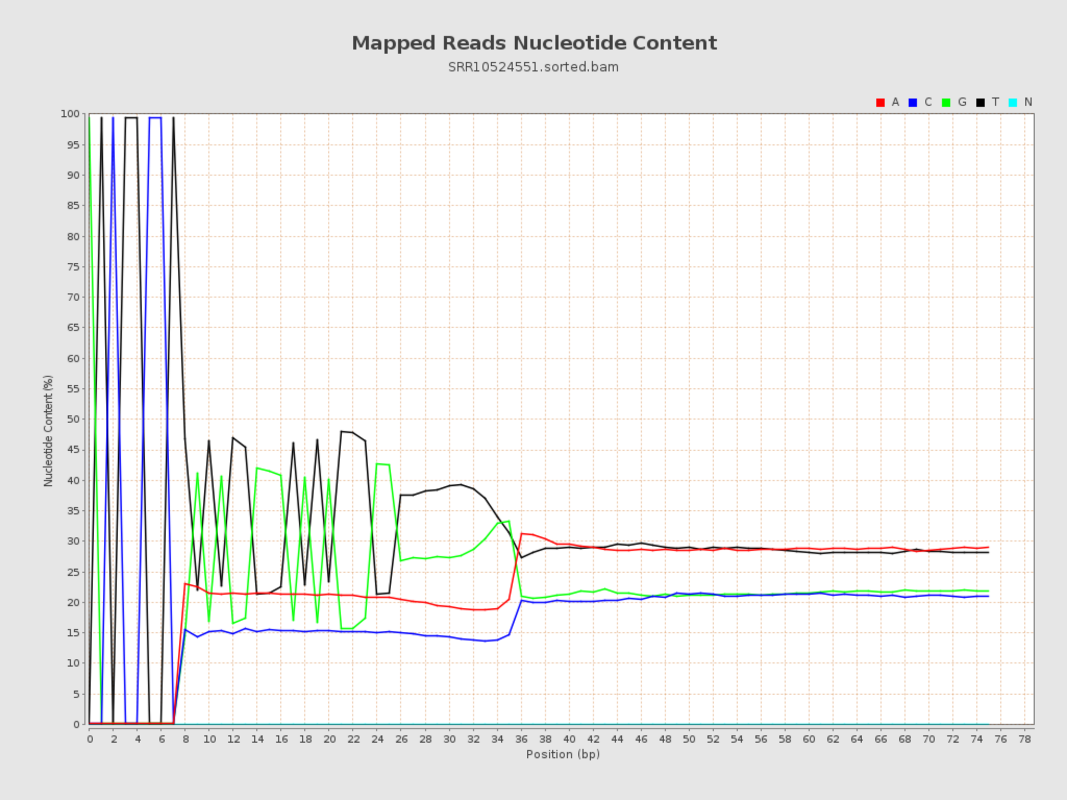
6. Results : Genome Fraction Coverage



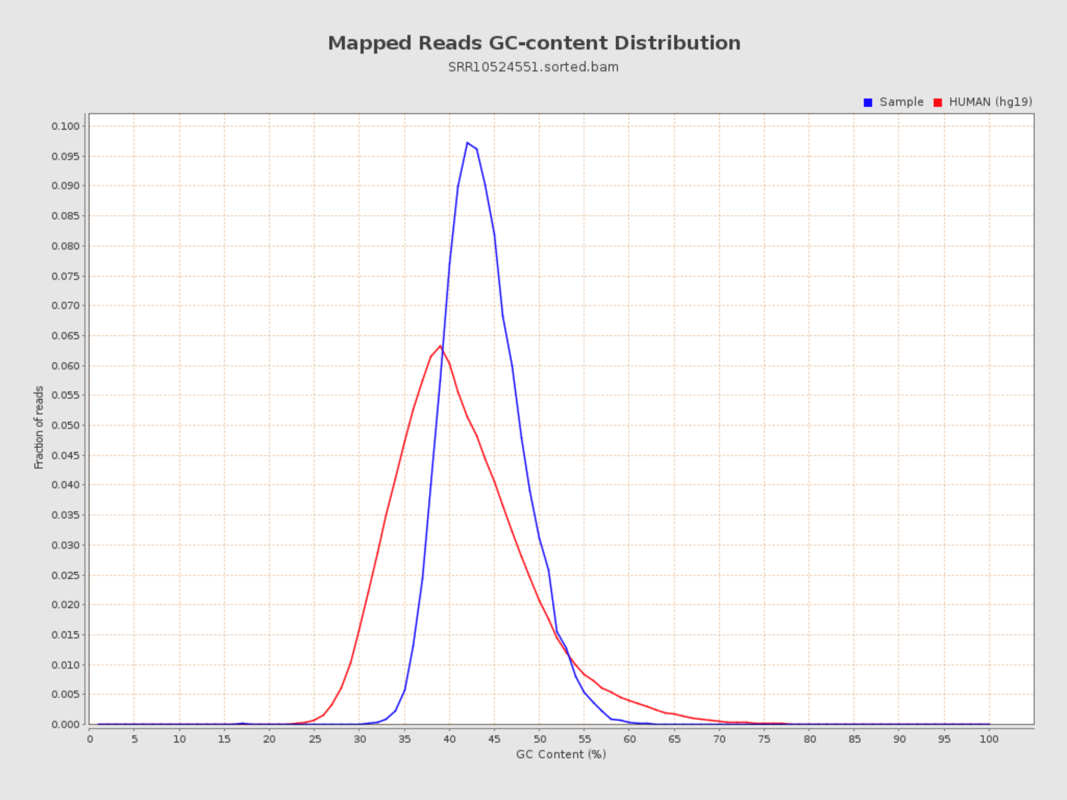
7. Results : Duplication Rate Histogram



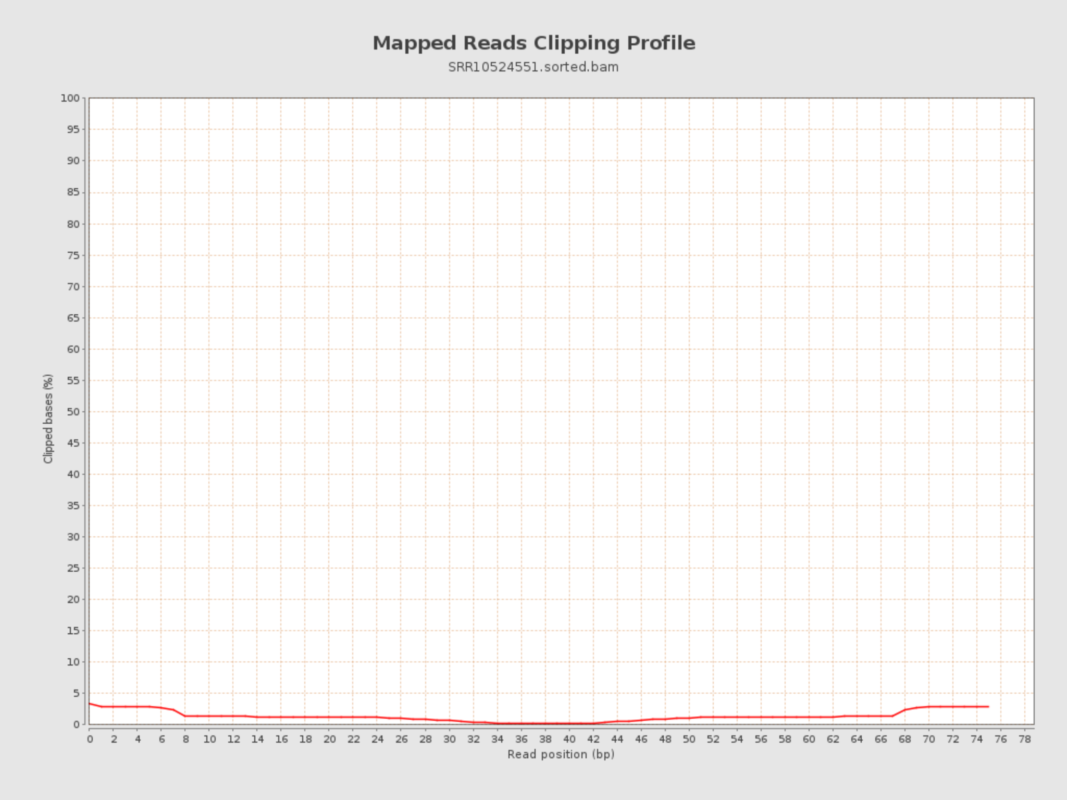
8. Results : Mapped Reads Nucleotide Content



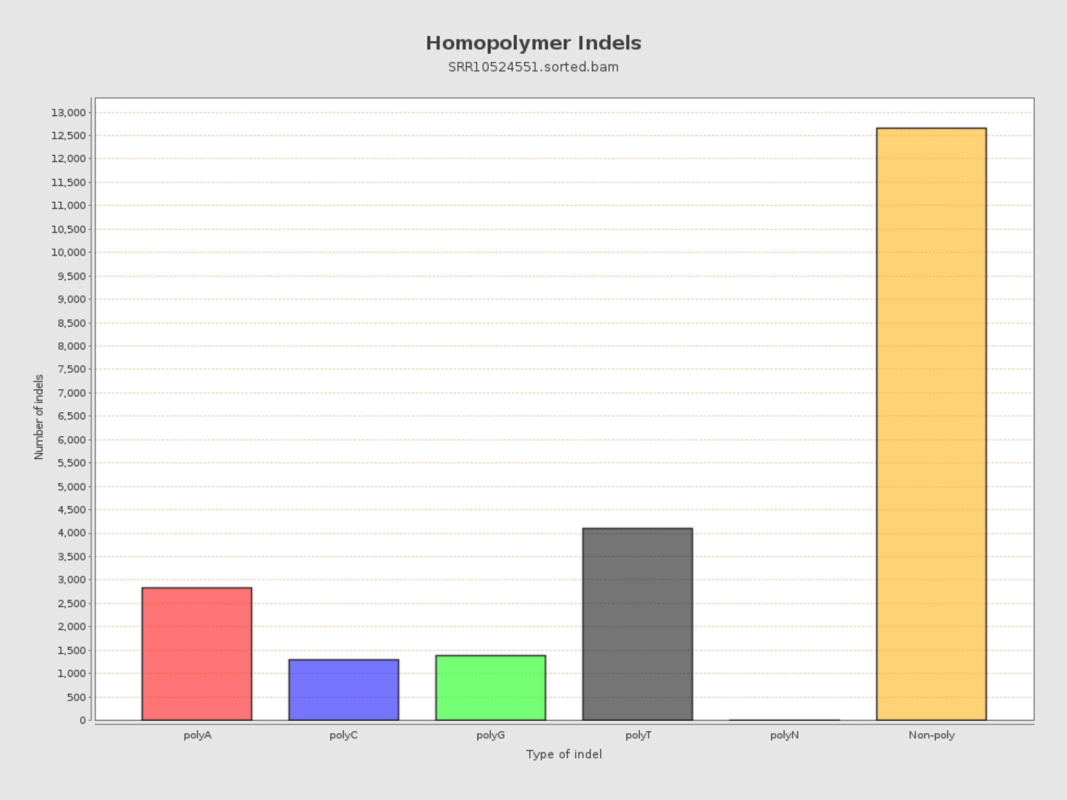
9. Results : Mapped Reads GC-content Distribution



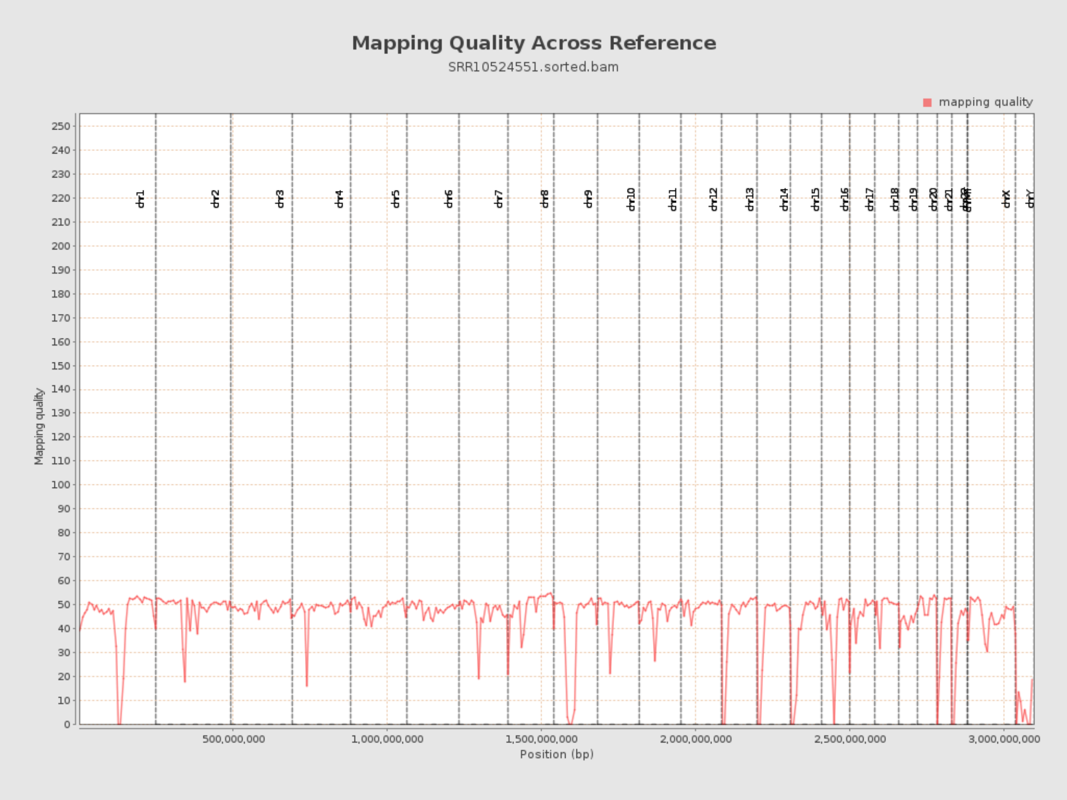
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram