Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 19:33:58

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524554.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_SRR10524554 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524554.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 19:33:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524554.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,008,236
Mapped reads	2,739,121 / 91.05%
Unmapped reads	269,115 / 8.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,772 / 0.36%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	162,321 / 5.4%
Duplication rate	4.43%
Clipped reads	2,743,008 / 91.18%

2.2. ACGT Content

Number/percentage of A's	40,075,131 / 25.26%
Number/percentage of C's	30,979,330 / 19.53%
Number/percentage of T's	49,693,013 / 31.33%
Number/percentage of G's	37,879,589 / 23.88%
Number/percentage of N's	2,219 / 0%
GC Percentage	43.41%

2.3. Coverage

Mean	0.0513

Standard Deviation	0.4347

2.4. Mapping Quality

Mean Mapping Quality	44.7

2.5. Mismatches and indels

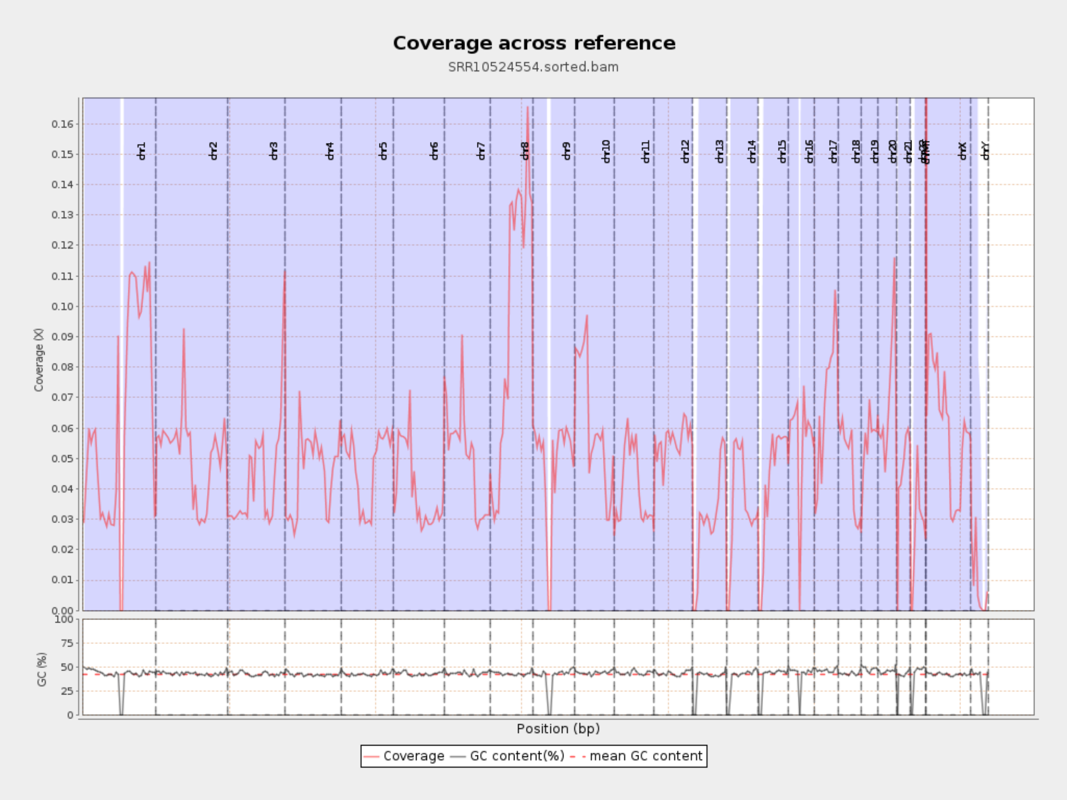
General error rate	0.53%
Mismatches	815,939
Insertions	9,511
Mapped reads with at least one insertion	0.35%
Deletions	30,197
Mapped reads with at least one deletion	1.09%
Homopolymer indels	43.89%

2.6. Chromosome stats

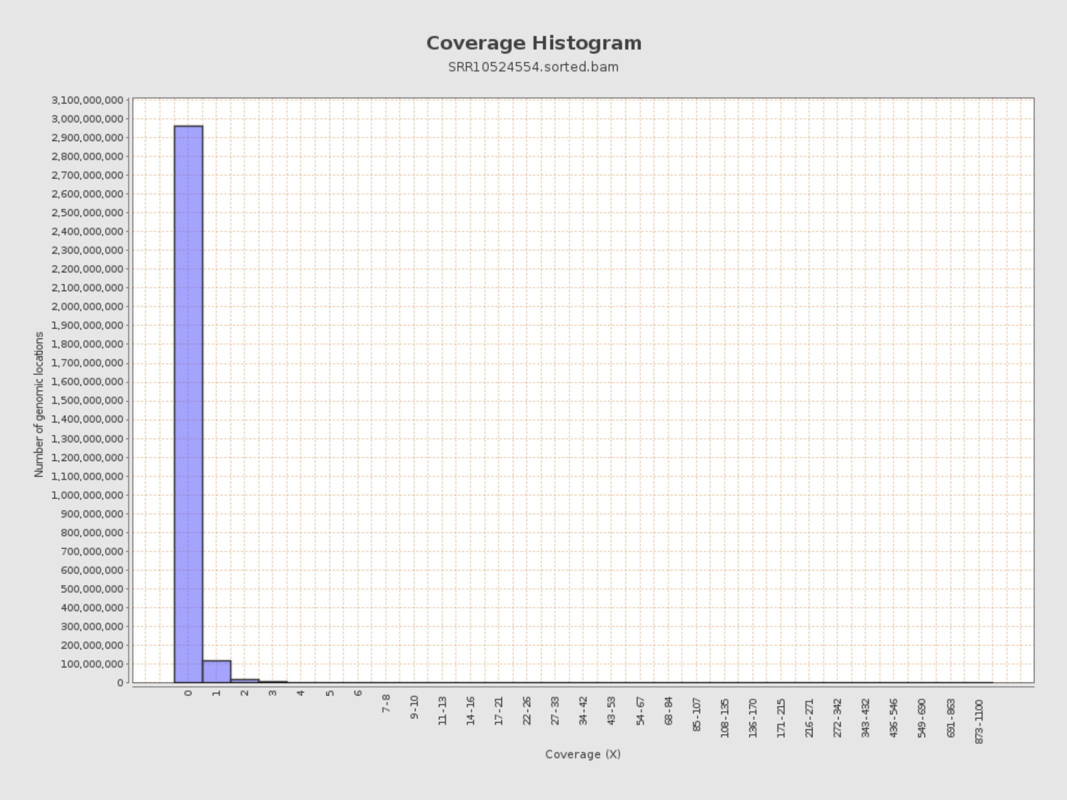
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15632119	0.0627	0.8336
chr2	243199373	12526600	0.0515	0.5295
chr3	198022430	8676316	0.0438	0.2483
chr4	191154276	8768963	0.0459	0.3004
chr5	180915260	8677612	0.048	0.2552
chr6	171115067	6791339	0.0397	0.3106
chr7	159138663	7980664	0.0501	0.5798

chr8	146364022	14474777	0.0989	0.4599
chr9	141213431	6757926	0.0479	0.3643
chr10	135534747	8284184	0.0611	0.4403
chr11	135006516	5453384	0.0404	0.3903
chr12	133851895	7510601	0.0561	0.2772
chr13	115169878	3510886	0.0305	0.2033
chr14	107349540	3750708	0.0349	0.2259
chr15	102531392	4196317	0.0409	0.247
chr16	90354753	4967315	0.055	0.3032
chr17	81195210	5591964	0.0689	0.3343
chr18	78077248	3725085	0.0477	0.7079
chr19	59128983	3320193	0.0562	0.5603
chr20	63025520	4535744	0.072	0.3179
chr21	48129895	2192971	0.0456	0.2782
chr22	51304566	1336134	0.026	0.1864
chrMT	16571	39362	2.3754	2.1199
chrX	155270560	9453917	0.0609	0.3369
chrY	59373566	523862	0.0088	0.2427

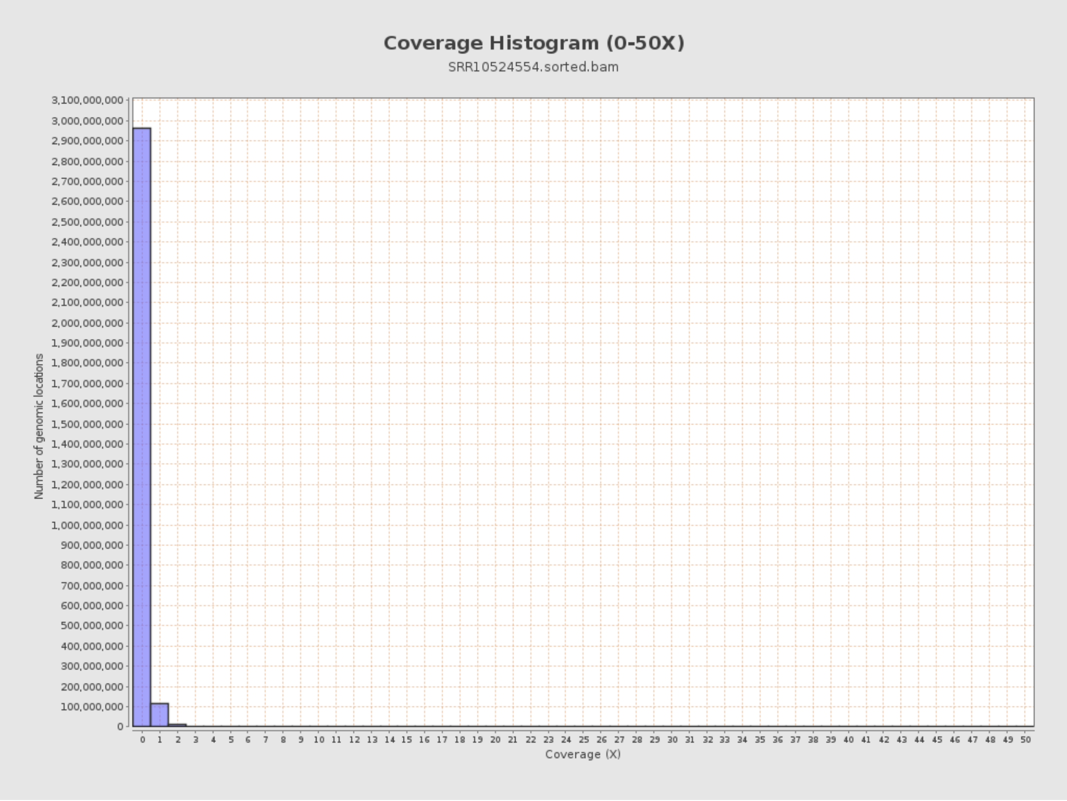
3. Results : Coverage across reference



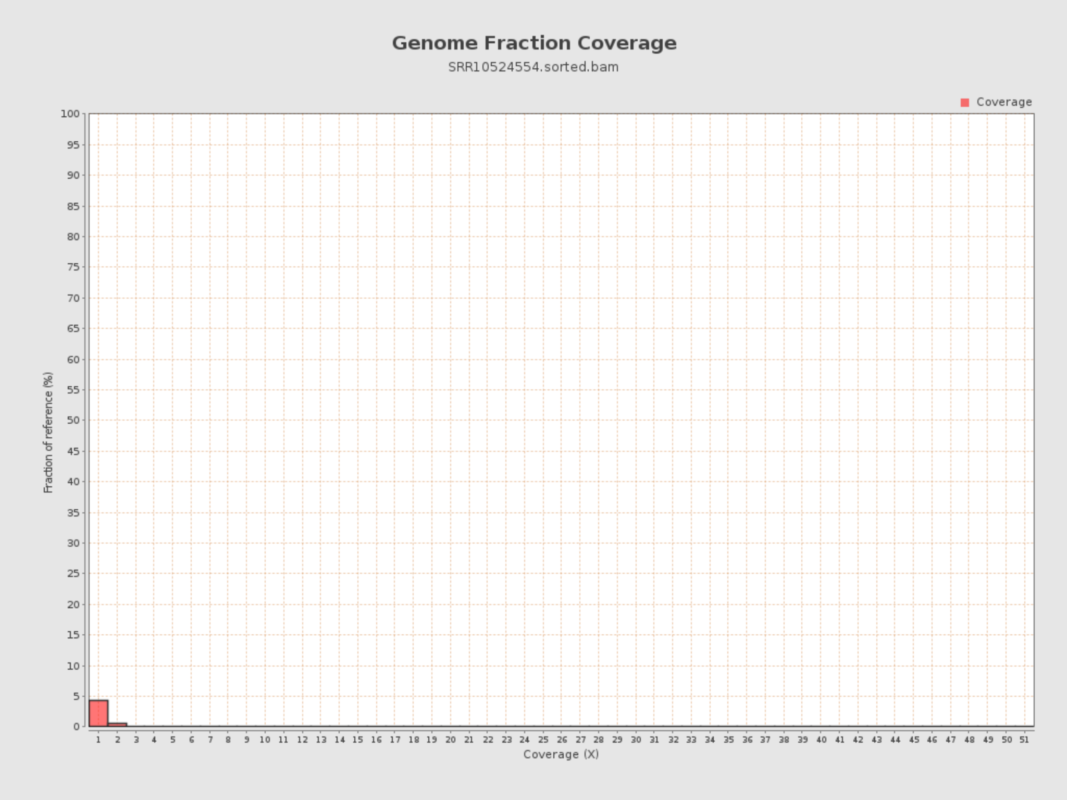
4. Results : Coverage Histogram



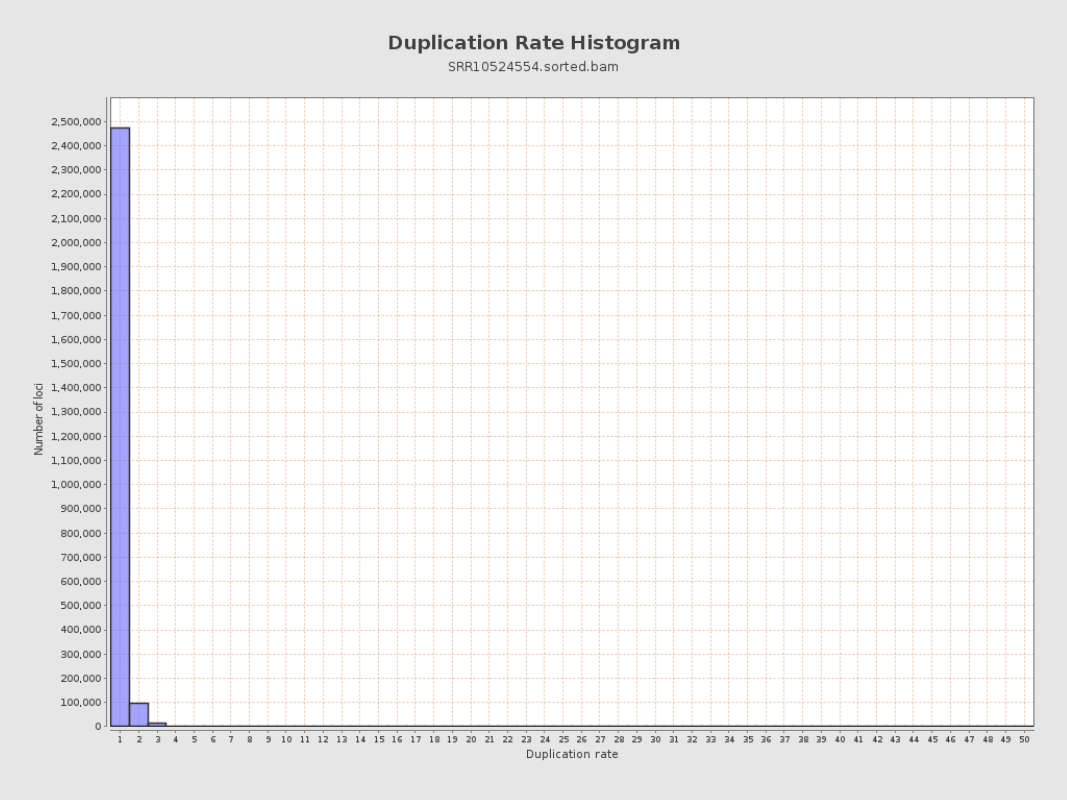
5. Results : Coverage Histogram (0-50X)



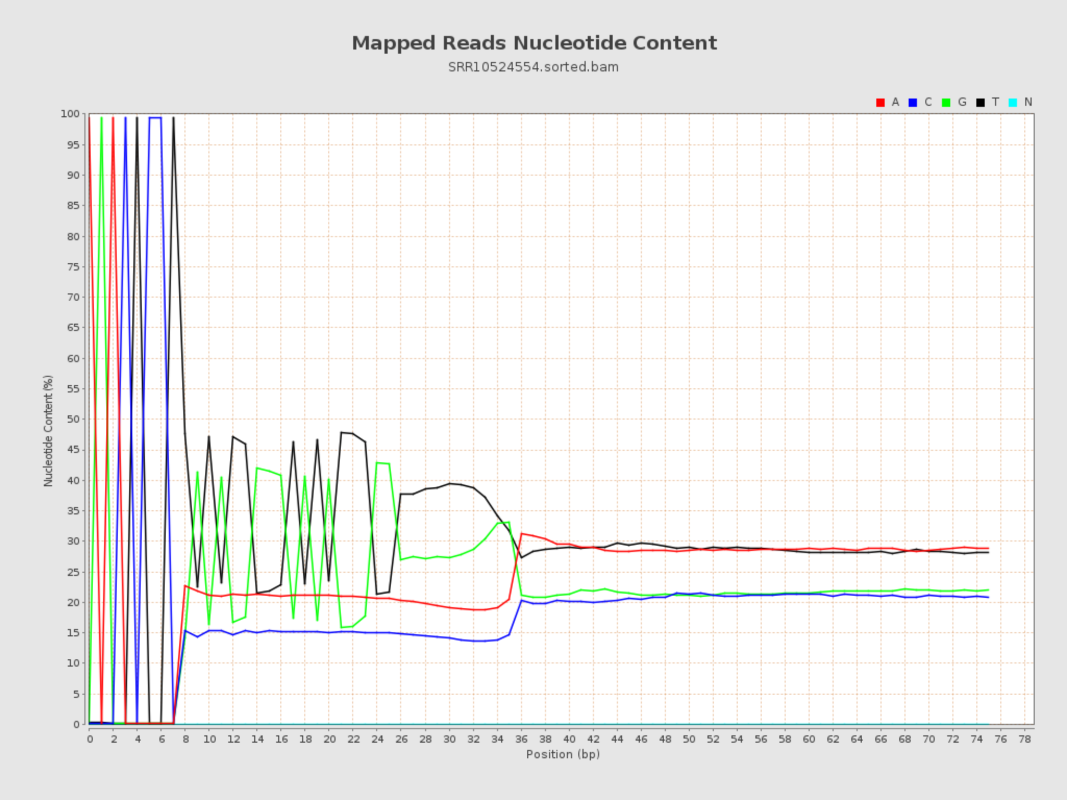
6. Results : Genome Fraction Coverage



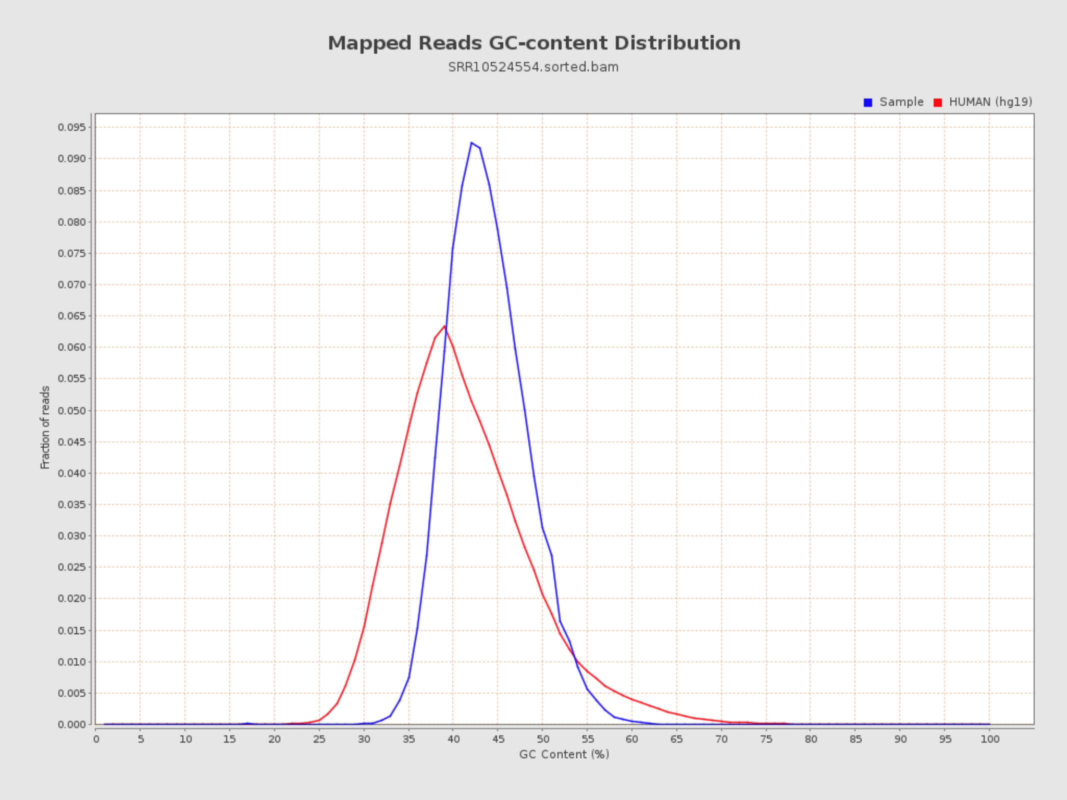
7. Results : Duplication Rate Histogram



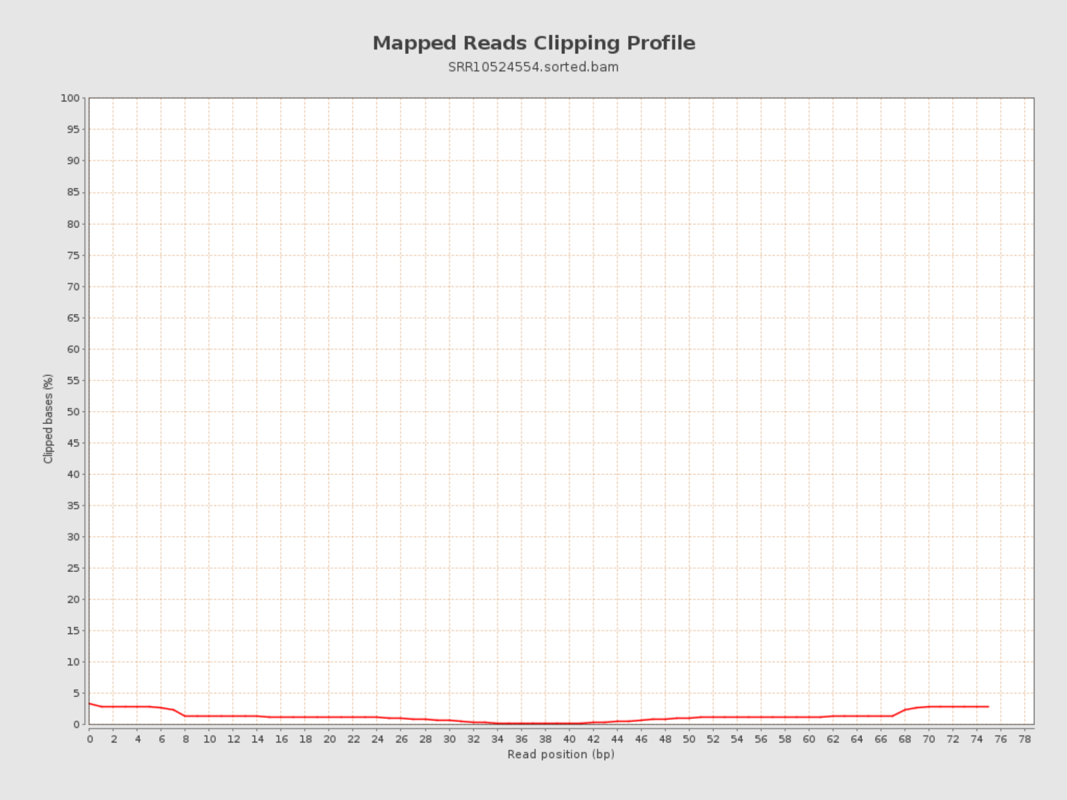
8. Results : Mapped Reads Nucleotide Content



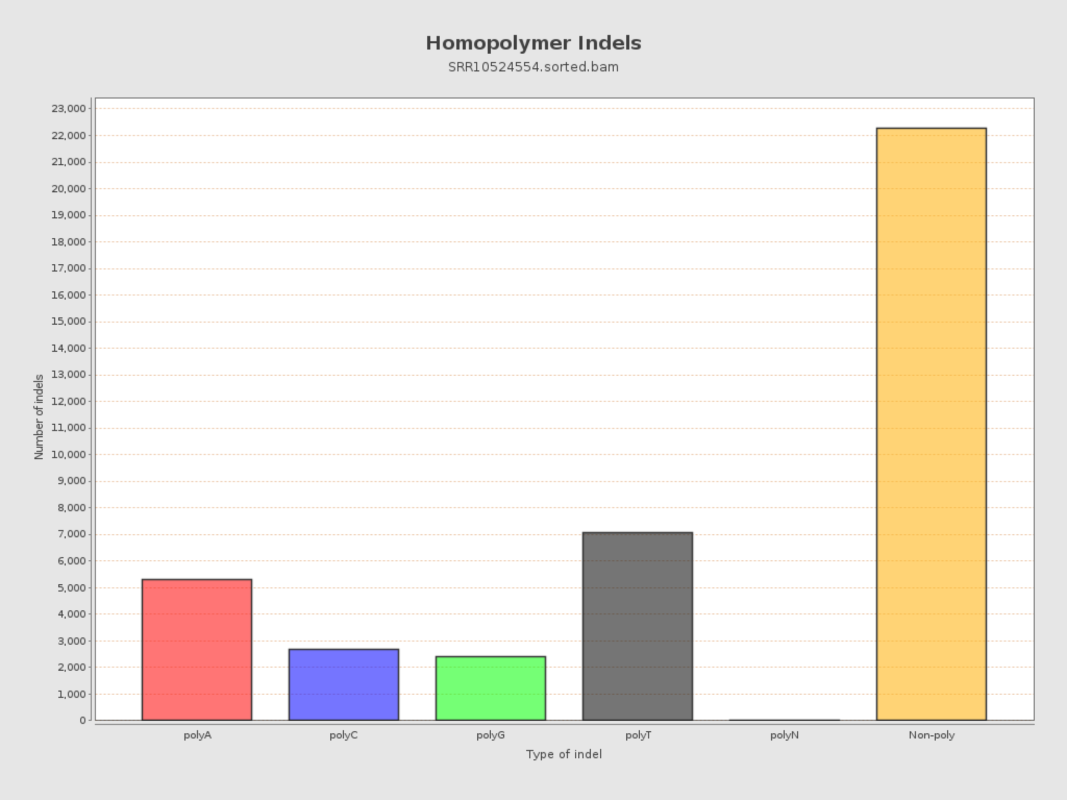
9. Results : Mapped Reads GC-content Distribution



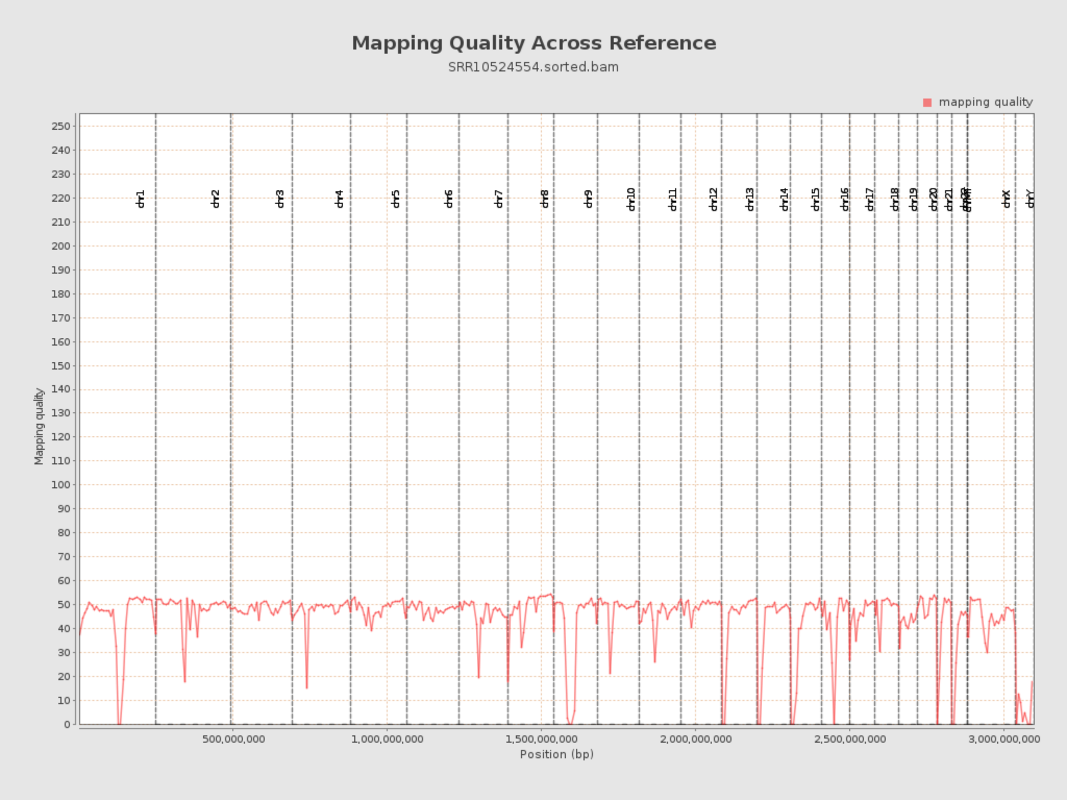
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram