Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:05:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524954.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_SRR10524954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524954.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:05:09 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,959,464
Mapped reads	1,818,195 / 92.79%
Unmapped reads	141,269 / 7.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,595 / 0.23%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	59,906 / 3.06%
Duplication rate	2.29%
Clipped reads	1,818,130 / 92.79%

2.2. ACGT Content

Number/percentage of A's	27,514,004 / 25.84%
Number/percentage of C's	20,728,985 / 19.46%
Number/percentage of T's	32,966,003 / 30.96%
Number/percentage of G's	25,284,970 / 23.74%
Number/percentage of N's	1,259 / 0%
GC Percentage	43.21%

2.3. Coverage

Mean	0.0344

Standard Deviation	0.3105

2.4. Mapping Quality

Mean Mapping Quality	44.42

2.5. Mismatches and indels

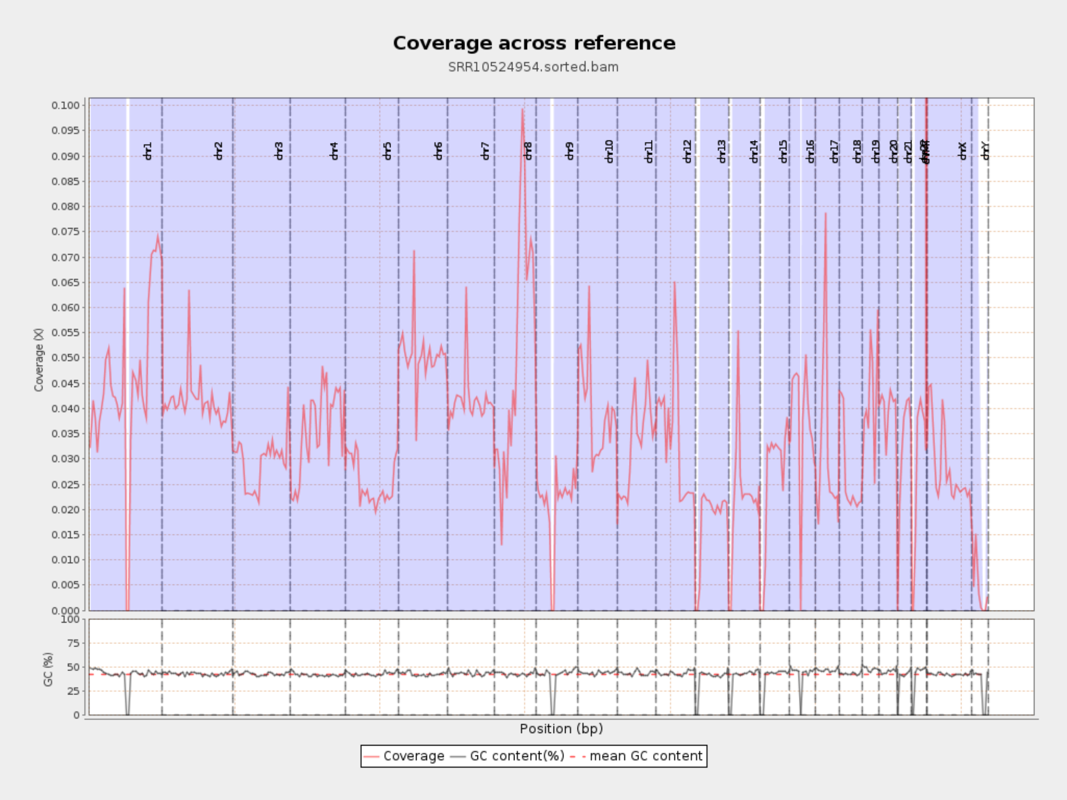
General error rate	0.5%
Mismatches	523,412
Insertions	6,390
Mapped reads with at least one insertion	0.35%
Deletions	20,919
Mapped reads with at least one deletion	1.14%
Homopolymer indels	44.64%

2.6. Chromosome stats

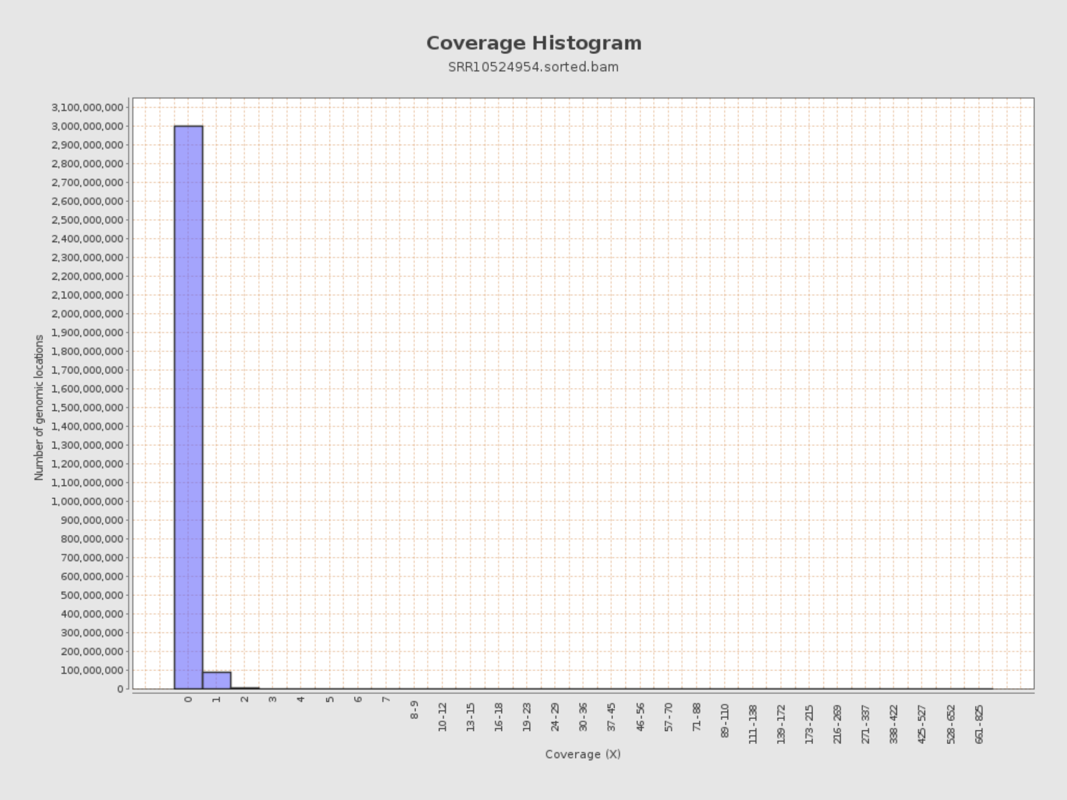
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11239169	0.0451	0.6128
chr2	243199373	10095371	0.0415	0.3526
chr3	198022430	5825203	0.0294	0.1889
chr4	191154276	6850088	0.0358	0.2231
chr5	180915260	4600095	0.0254	0.177
chr6	171115067	8673597	0.0507	0.3454
chr7	159138663	6661897	0.0419	0.4302

chr8	146364022	7482820	0.0511	0.3043
chr9	141213431	2959334	0.021	0.2397
chr10	135534747	5359166	0.0395	0.2943
chr11	135006516	4433432	0.0328	0.2659
chr12	133851895	4500029	0.0336	0.2026
chr13	115169878	2029379	0.0176	0.1476
chr14	107349540	2407157	0.0224	0.1696
chr15	102531392	2660077	0.0259	0.1922
chr16	90354753	3379810	0.0374	0.2257
chr17	81195210	2618445	0.0322	0.2636
chr18	78077248	2096898	0.0269	0.3812
chr19	59128983	2506813	0.0424	0.3707
chr20	63025520	2499288	0.0397	0.2165
chr21	48129895	1523462	0.0317	0.2018
chr22	51304566	1382764	0.027	0.178
chrMT	16571	24381	1.4713	1.4831
chrX	155270560	4446959	0.0286	0.217
chrY	59373566	275395	0.0046	0.1096

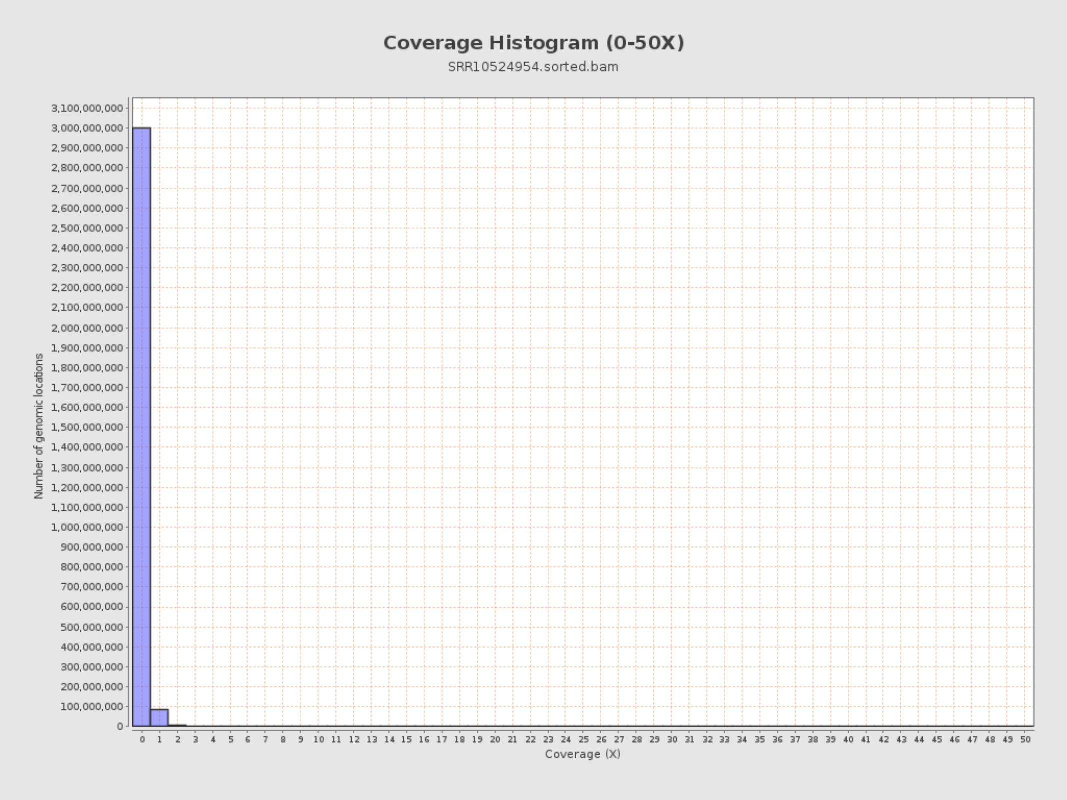
3. Results : Coverage across reference



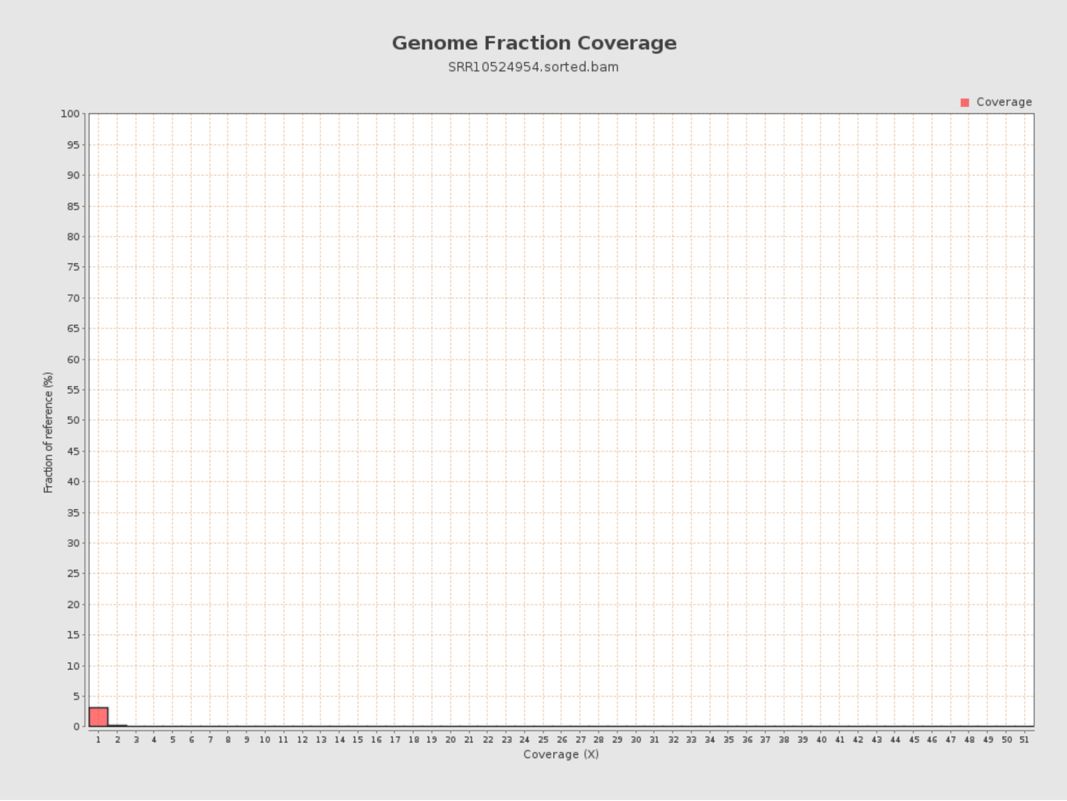
4. Results : Coverage Histogram



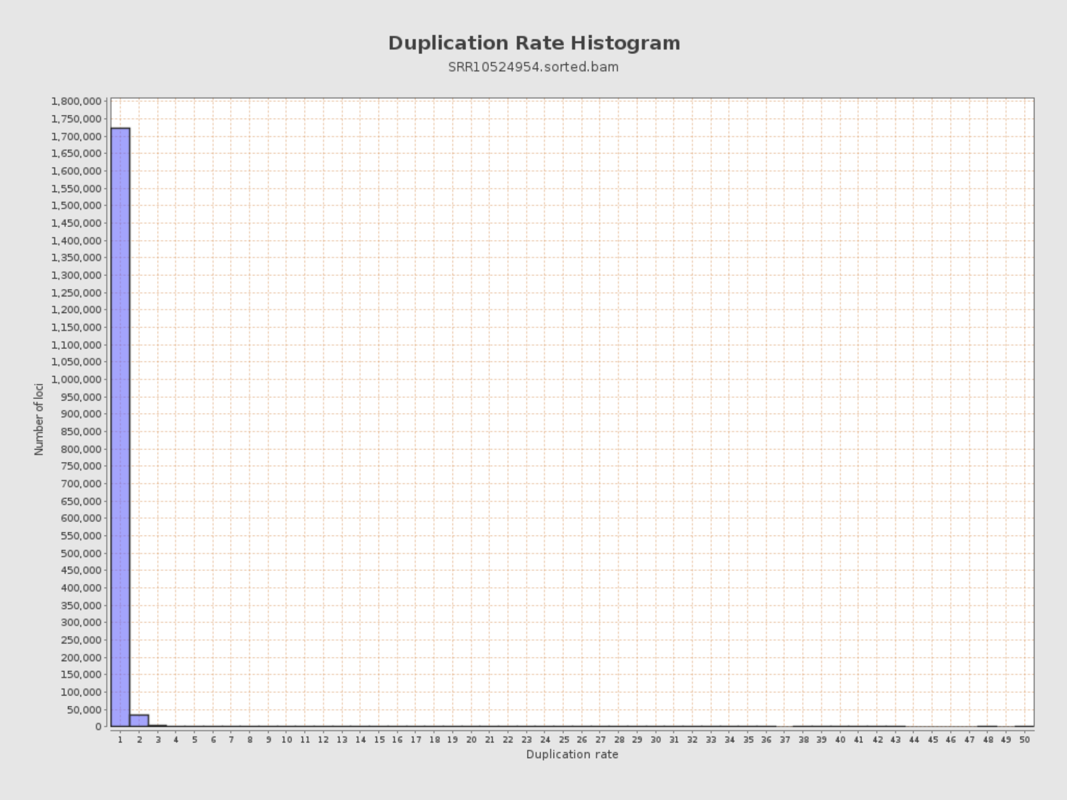
5. Results : Coverage Histogram (0-50X)



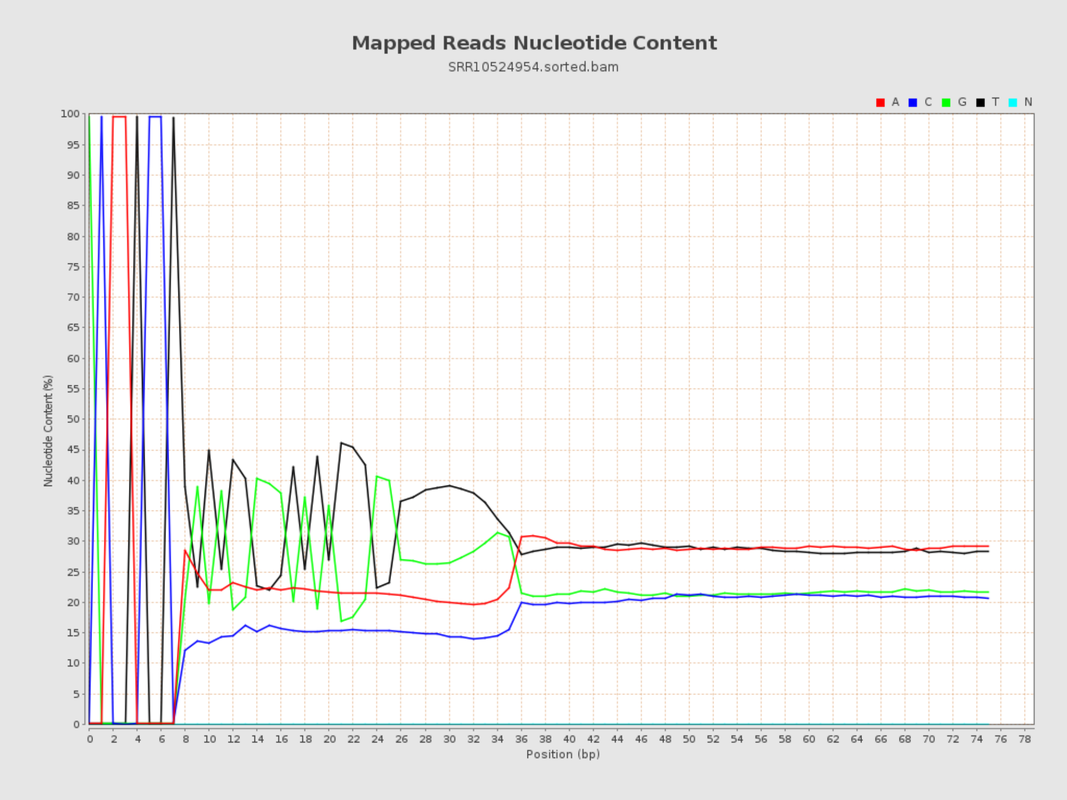
6. Results : Genome Fraction Coverage



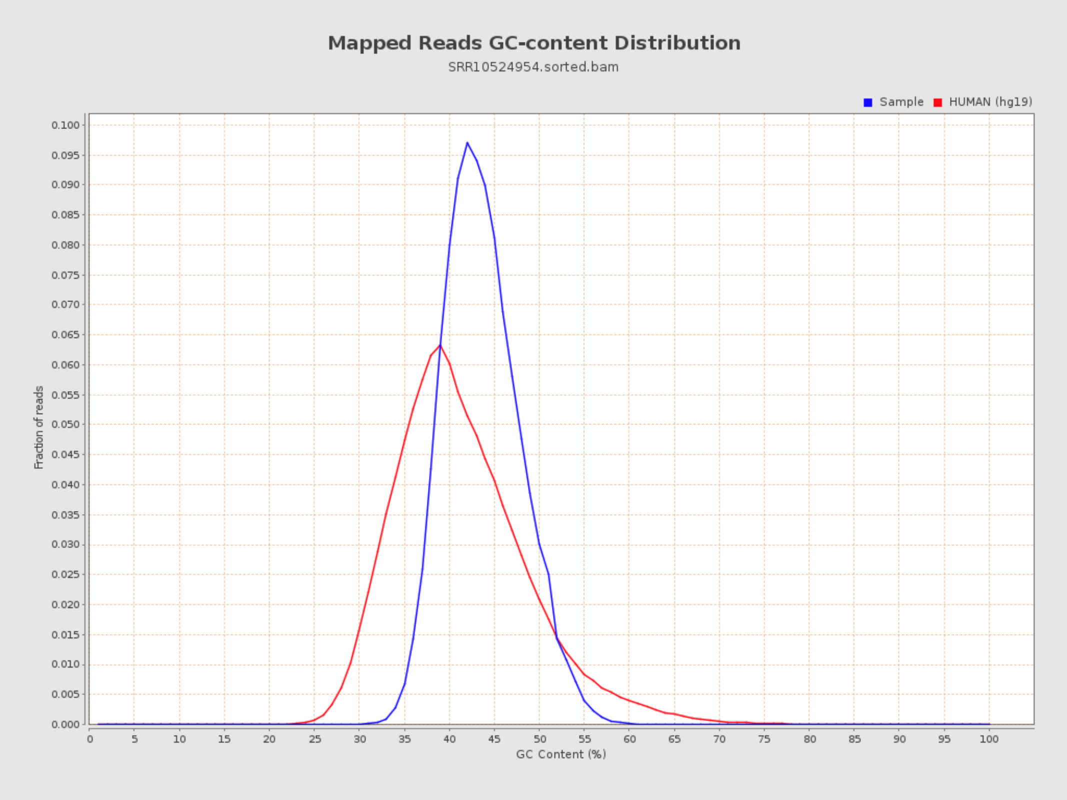
7. Results : Duplication Rate Histogram



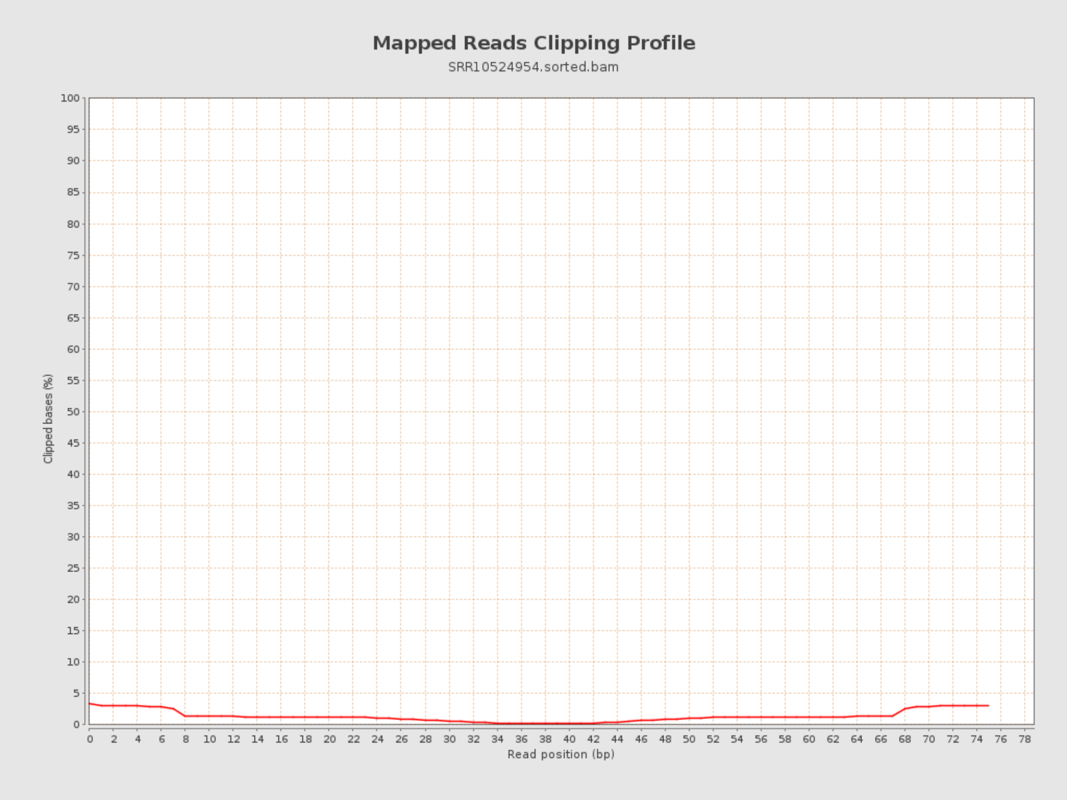
8. Results : Mapped Reads Nucleotide Content



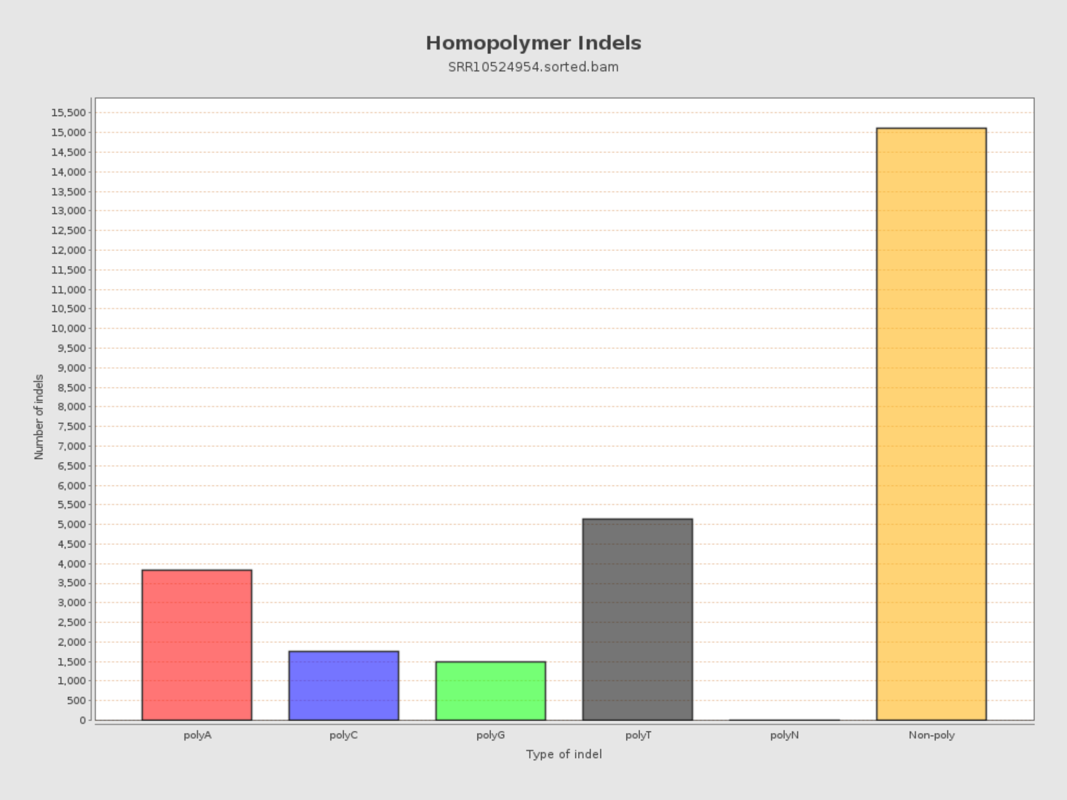
9. Results : Mapped Reads GC-content Distribution



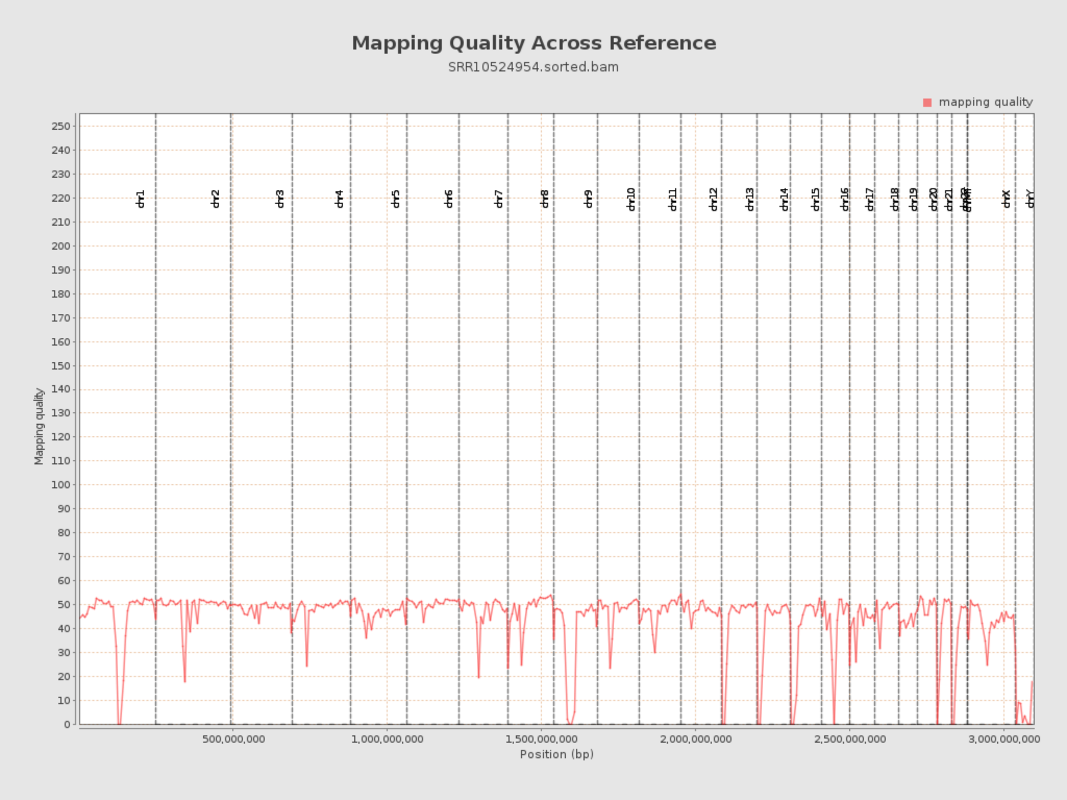
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram