Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 10:11:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524955.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_SRR10524955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524955.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 10:11:15 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	912,946
Mapped reads	850,499 / 93.16%
Unmapped reads	62,447 / 6.84%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	2,346 / 0.26%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	17,465 / 1.91%
Duplication rate	1.41%
Clipped reads	850,150 / 93.12%

2.2. ACGT Content

Number/percentage of A's	12,335,118 / 24.53%
Number/percentage of C's	9,434,270 / 18.76%
Number/percentage of T's	15,877,433 / 31.57%
Number/percentage of G's	12,638,046 / 25.13%
Number/percentage of N's	634 / 0%
GC Percentage	43.89%

2.3. Coverage

Mean	0.0162

Standard Deviation	0.1744

2.4. Mapping Quality

Mean Mapping Quality	44.56

2.5. Mismatches and indels

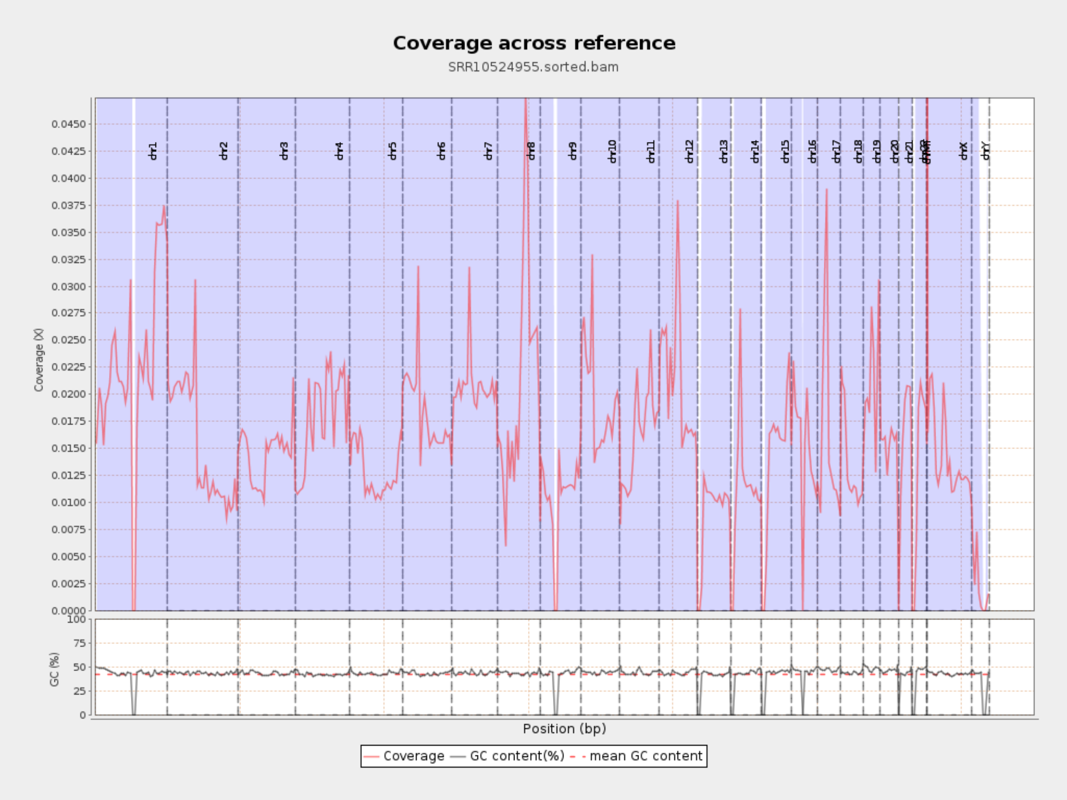
General error rate	0.5%
Mismatches	246,985
Insertions	3,365
Mapped reads with at least one insertion	0.39%
Deletions	9,993
Mapped reads with at least one deletion	1.17%
Homopolymer indels	43.52%

2.6. Chromosome stats

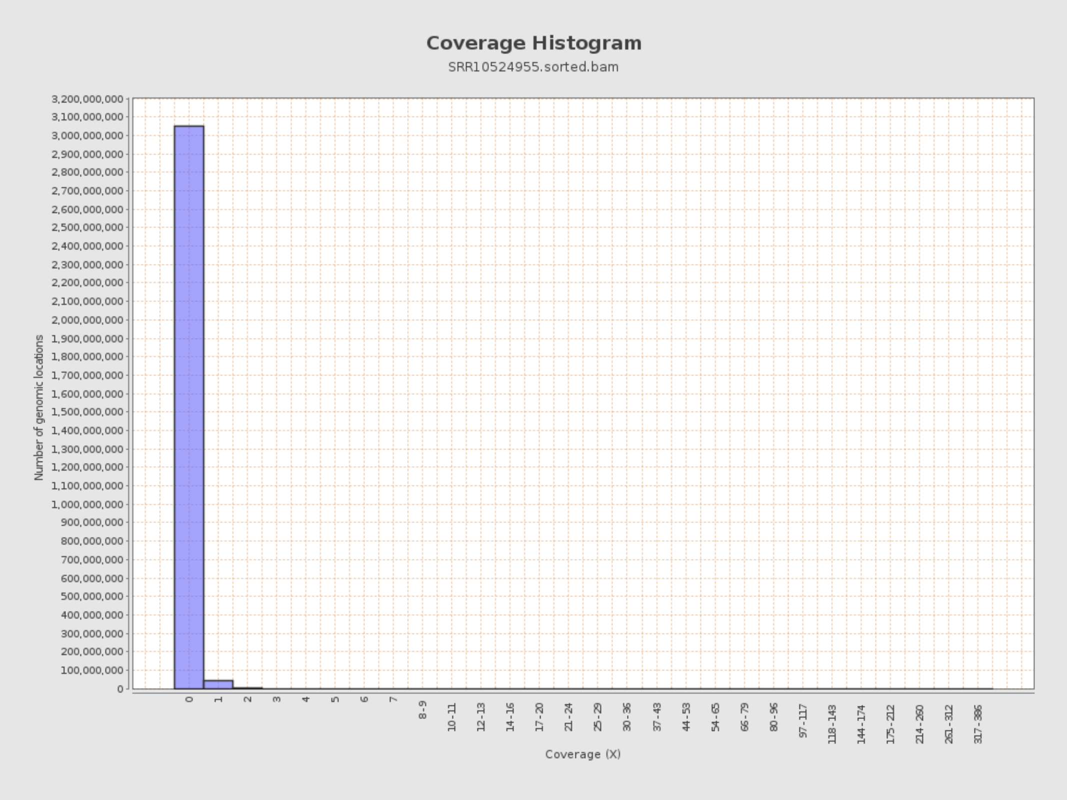
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	5621261	0.0226	0.3046
chr2	243199373	3697552	0.0152	0.1845
chr3	198022430	2883170	0.0146	0.126
chr4	191154276	3445999	0.018	0.1451
chr5	180915260	2326909	0.0129	0.1195
chr6	171115067	3139141	0.0183	0.179
chr7	159138663	3321872	0.0209	0.2362

chr8	146364022	3153531	0.0215	0.1844
chr9	141213431	1469313	0.0104	0.1343
chr10	135534747	2670771	0.0197	0.1829
chr11	135006516	2213225	0.0164	0.1553
chr12	133851895	2871384	0.0215	0.1539
chr13	115169878	1025745	0.0089	0.1011
chr14	107349540	1200521	0.0112	0.1122
chr15	102531392	1455502	0.0142	0.1319
chr16	90354753	1354855	0.015	0.1333
chr17	81195210	1342645	0.0165	0.1681
chr18	78077248	1053872	0.0135	0.2083
chr19	59128983	1268246	0.0214	0.2129
chr20	63025520	964238	0.0153	0.1308
chr21	48129895	764835	0.0159	0.1356
chr22	51304566	687606	0.0134	0.1198
chrMT	16571	3862	0.2331	0.5114
chrX	155270560	2230356	0.0144	0.1357
chrY	59373566	136275	0.0023	0.066

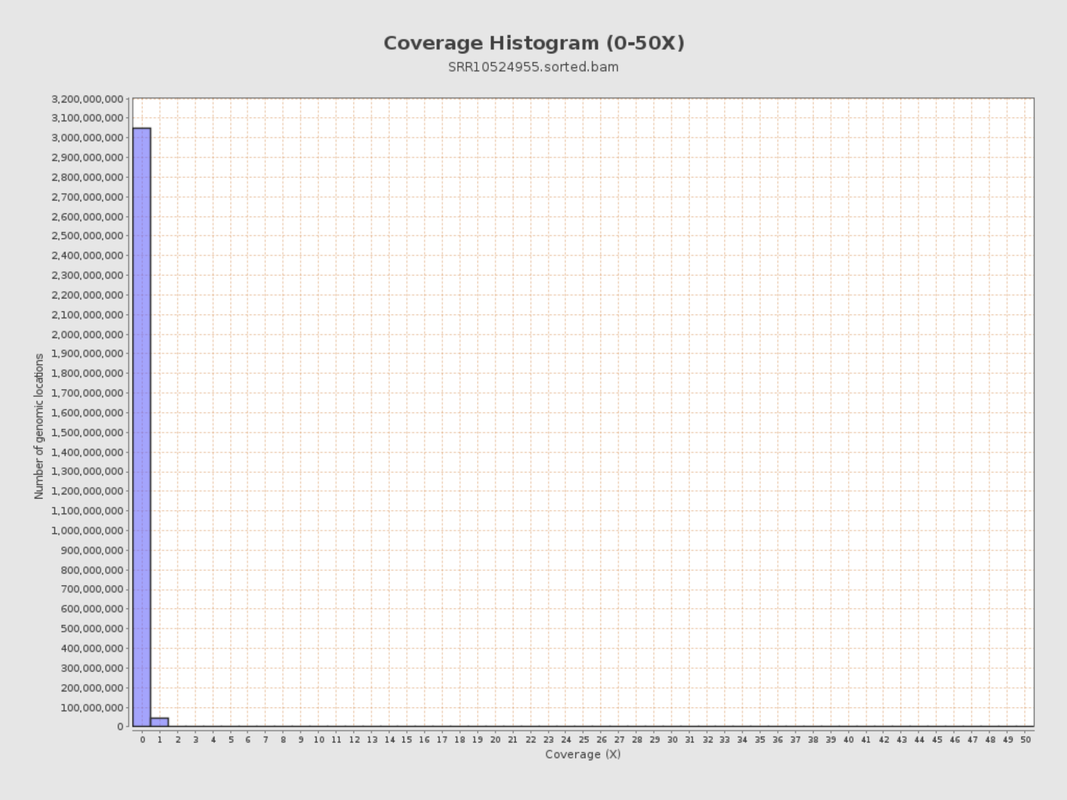
3. Results : Coverage across reference



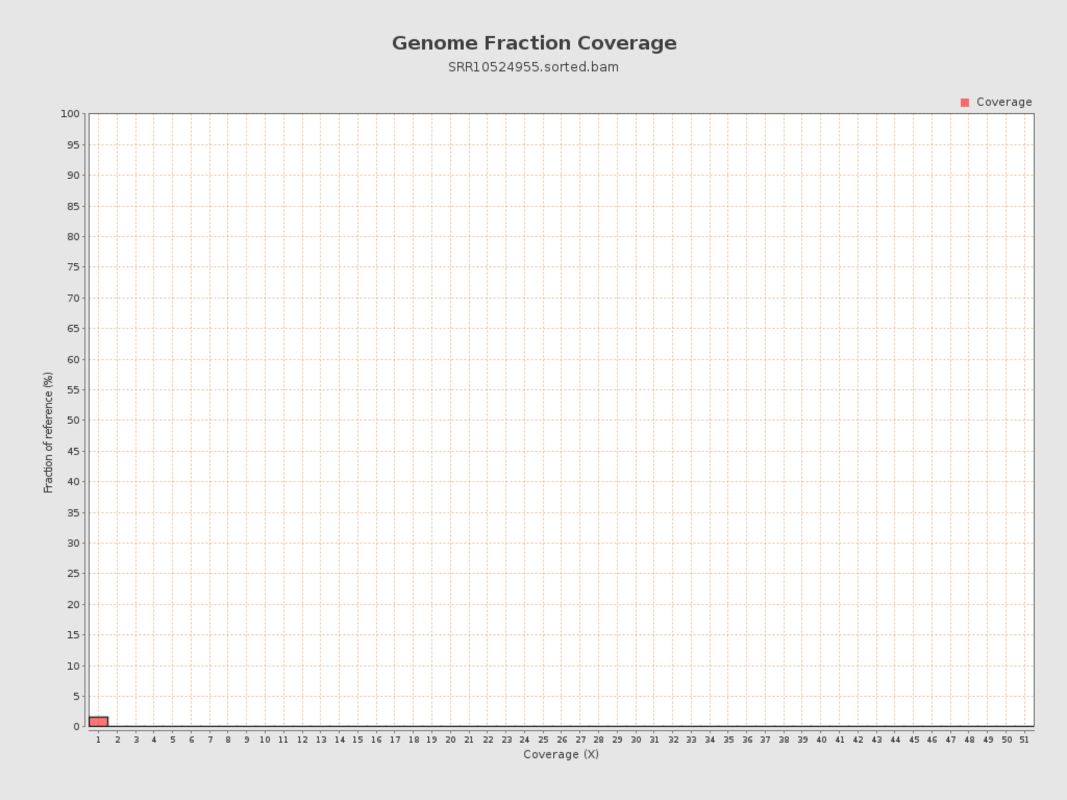
4. Results : Coverage Histogram



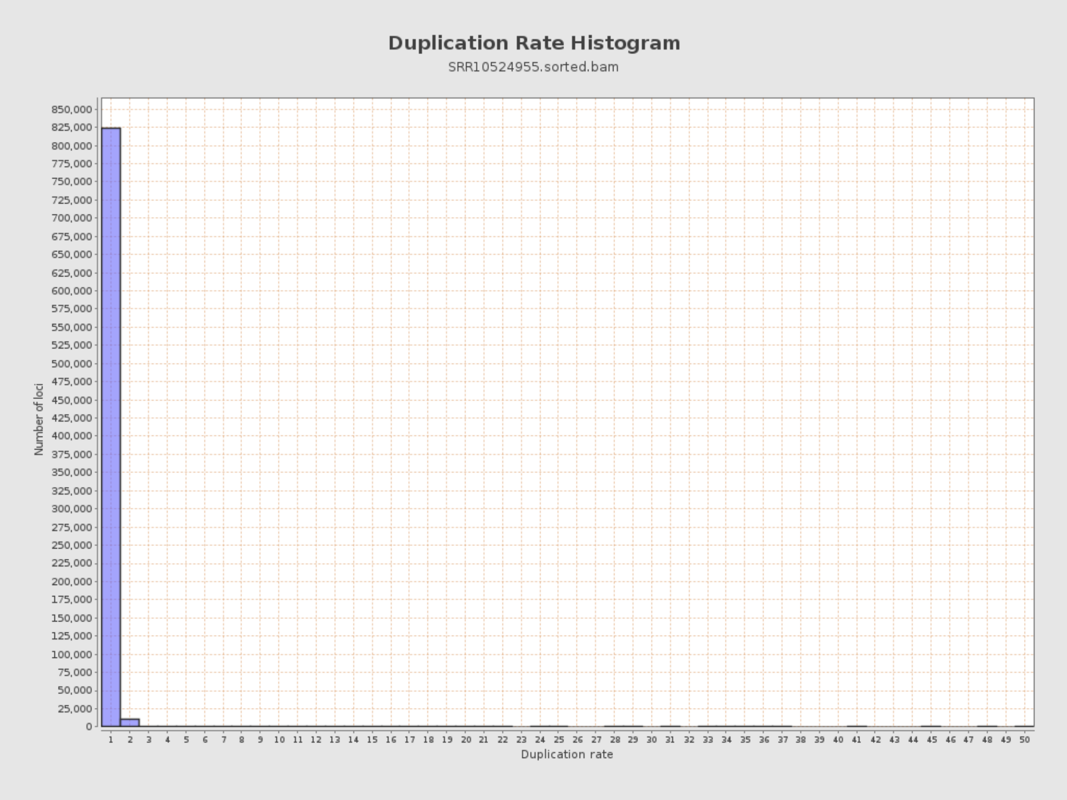
5. Results : Coverage Histogram (0-50X)



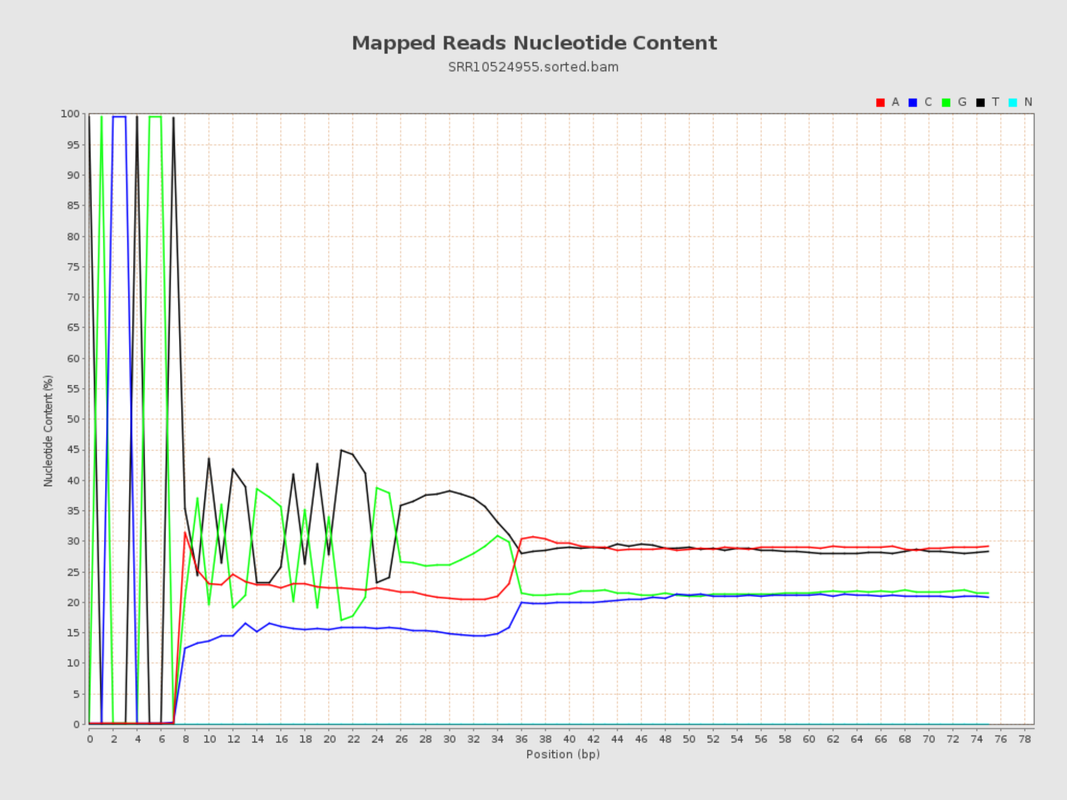
6. Results : Genome Fraction Coverage



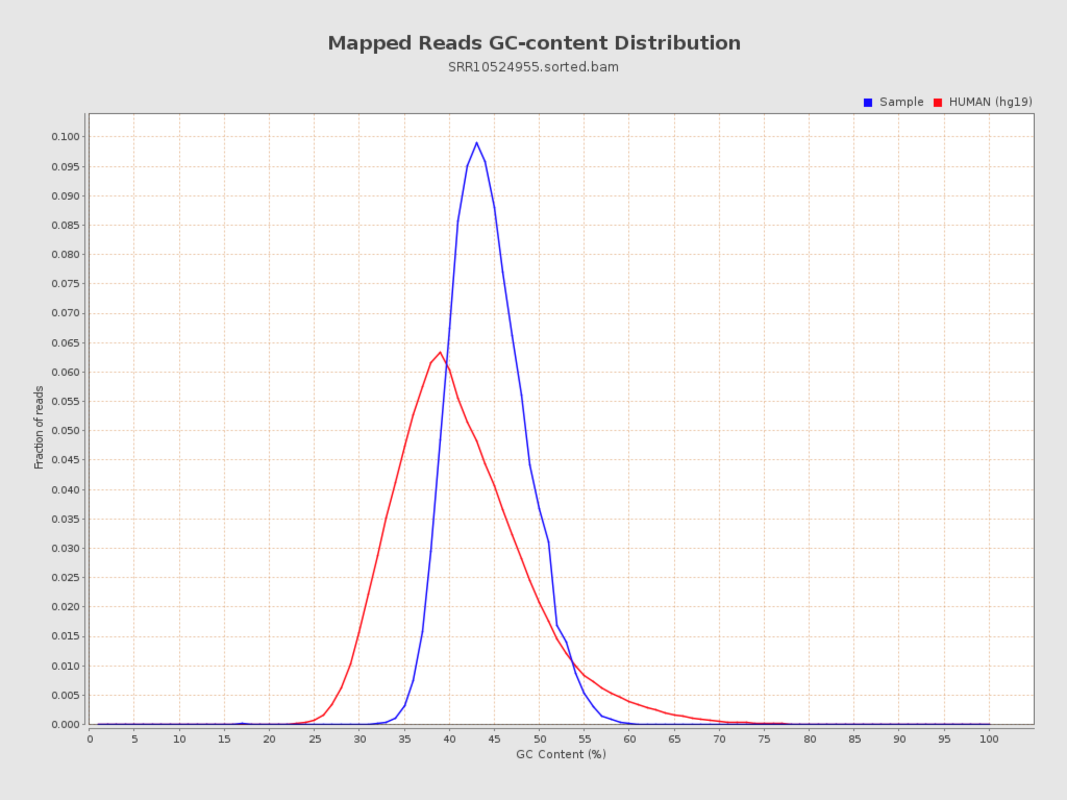
7. Results : Duplication Rate Histogram



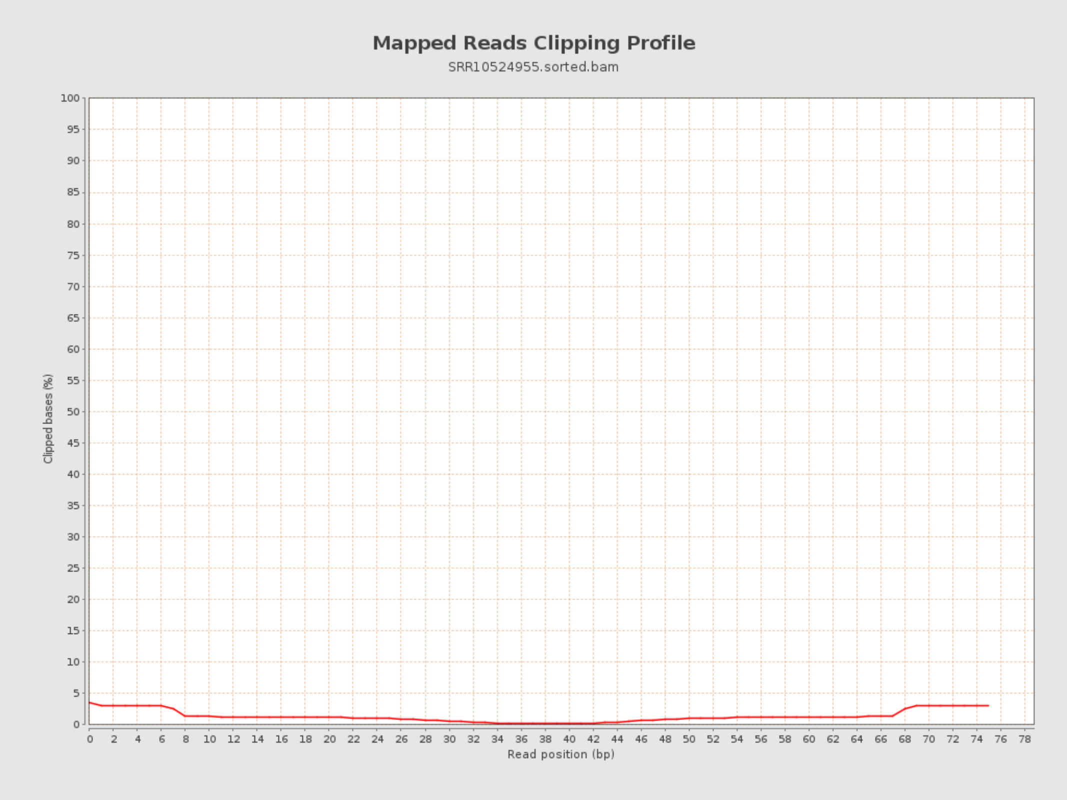
8. Results : Mapped Reads Nucleotide Content



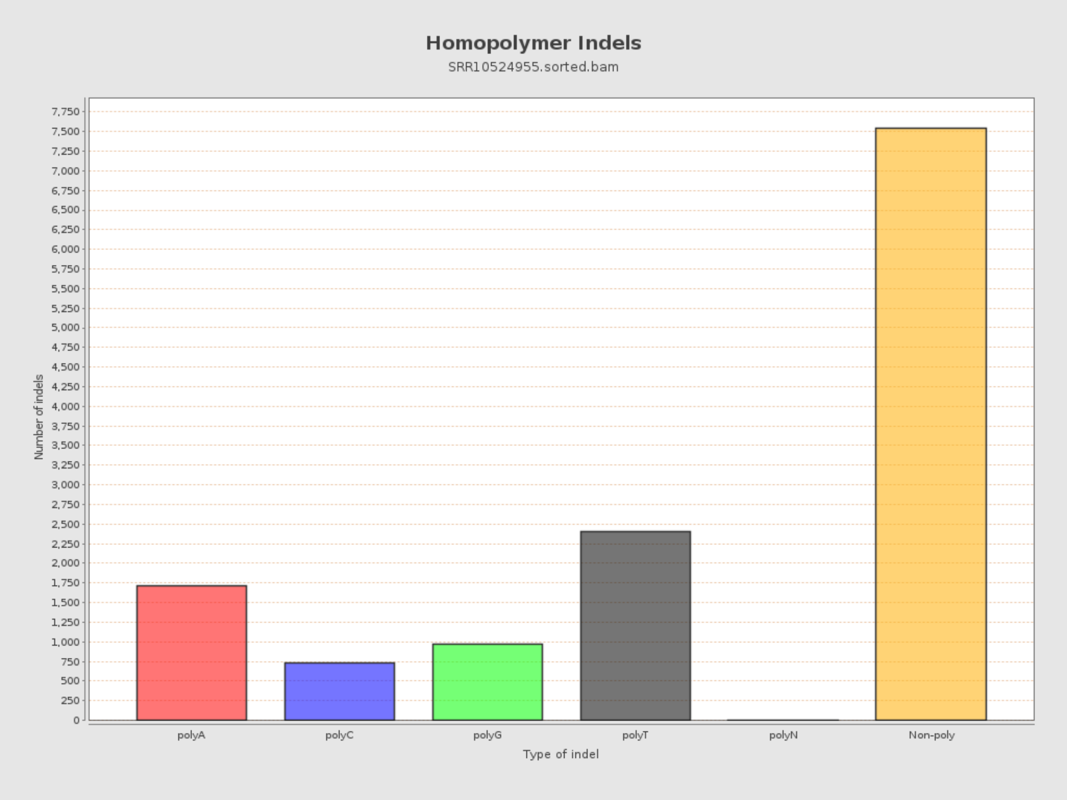
9. Results : Mapped Reads GC-content Distribution



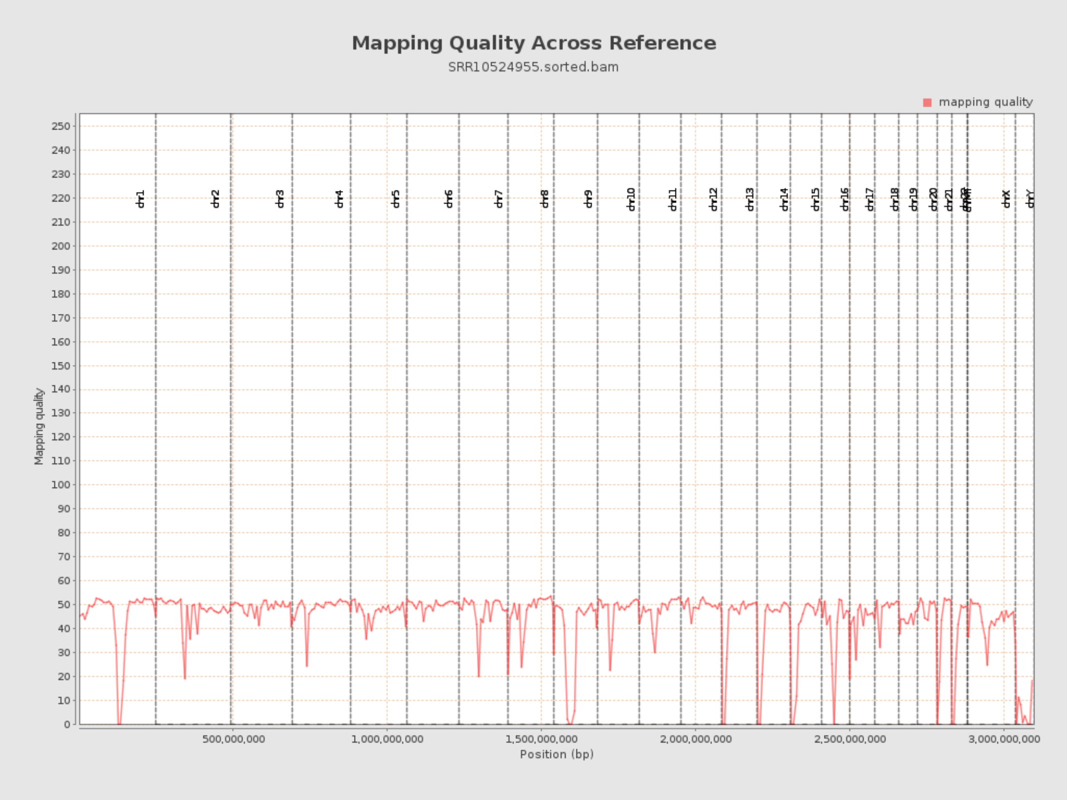
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram