Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 13:30:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524630.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_SRR10524630 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524630.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 13:30:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524630.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	780,146
Mapped reads	724,884 / 92.92%
Unmapped reads	55,262 / 7.08%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	1,623 / 0.21%
Read min/max/mean length	30 / 76 / 76.07
Duplicated reads (estimated)	18,958 / 2.43%
Duplication rate	2.01%
Clipped reads	724,468 / 92.86%

2.2. ACGT Content

Number/percentage of A's	9,986,404 / 23.78%
Number/percentage of C's	7,342,594 / 17.48%
Number/percentage of T's	13,936,724 / 33.19%
Number/percentage of G's	10,731,051 / 25.55%
Number/percentage of N's	282 / 0%
GC Percentage	43.04%

2.3. Coverage

Mean	0.0136

Standard Deviation	0.1495

2.4. Mapping Quality

Mean Mapping Quality	45.14

2.5. Mismatches and indels

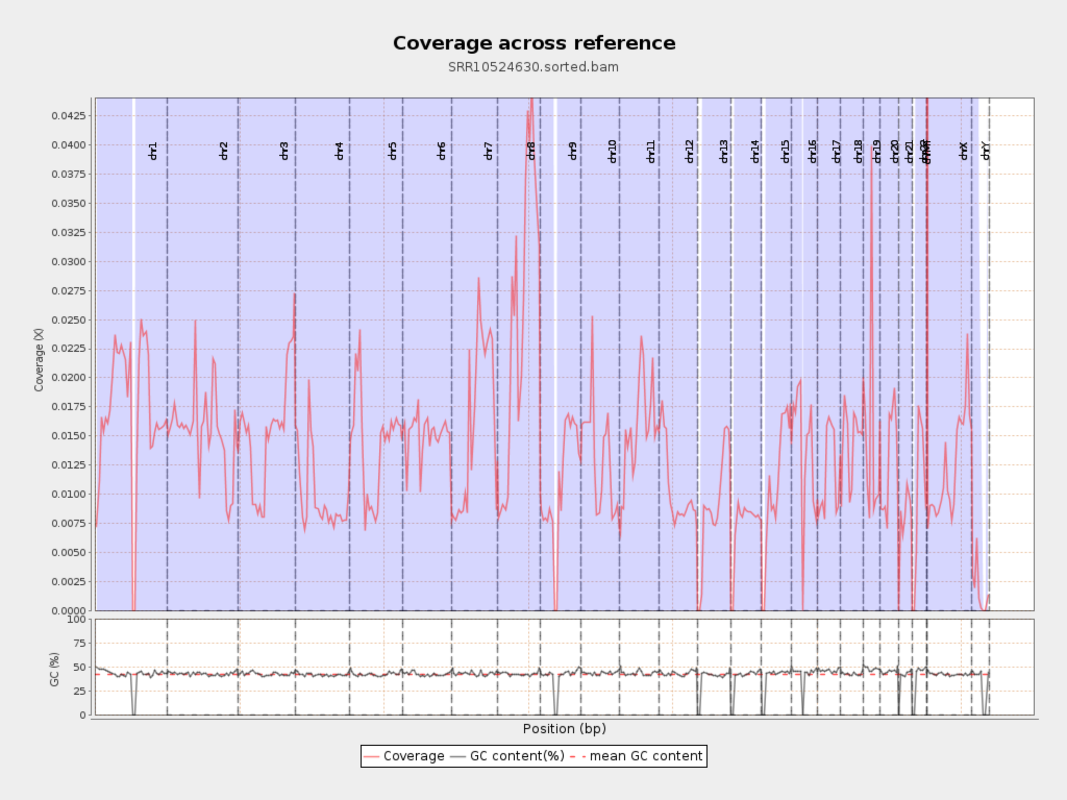
General error rate	0.47%
Mismatches	193,014
Insertions	2,611
Mapped reads with at least one insertion	0.36%
Deletions	7,671
Mapped reads with at least one deletion	1.05%
Homopolymer indels	43.94%

2.6. Chromosome stats

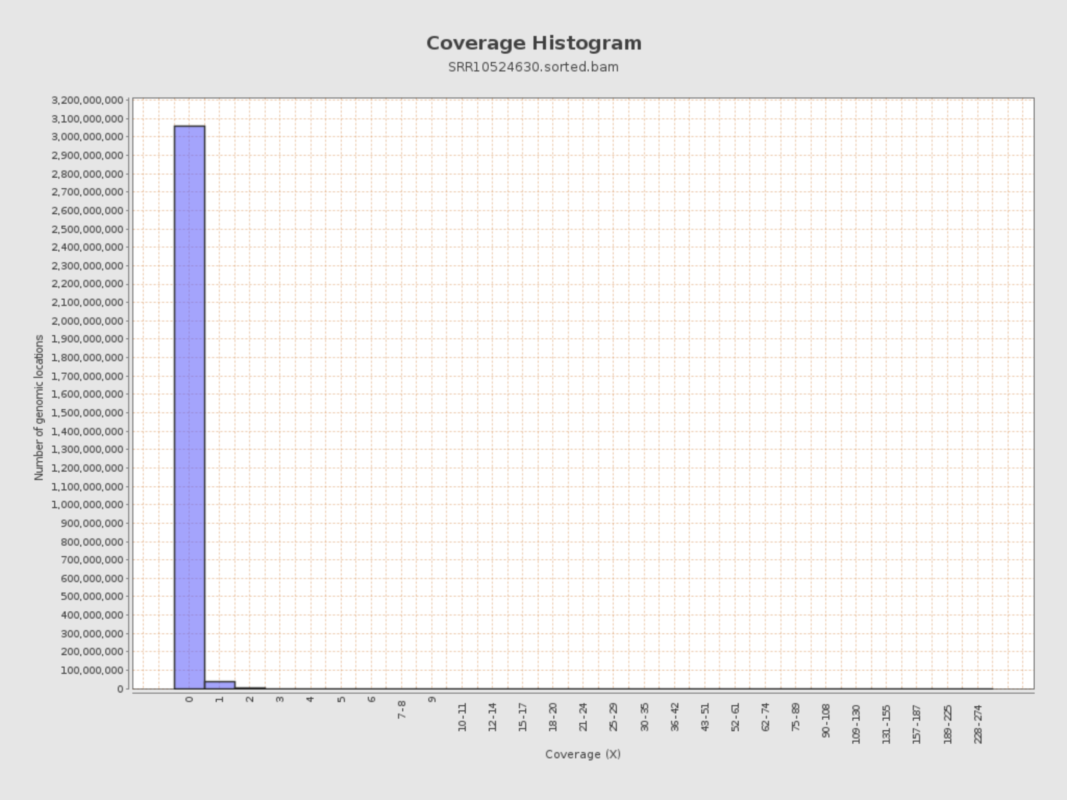
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4270389	0.0171	0.2333
chr2	243199373	3729109	0.0153	0.168
chr3	198022430	3036010	0.0153	0.1311
chr4	191154276	1884556	0.0099	0.1137
chr5	180915260	2585681	0.0143	0.1262
chr6	171115067	2567110	0.015	0.1336
chr7	159138663	2577054	0.0162	0.1872

chr8	146364022	3707430	0.0253	0.1995
chr9	141213431	1518357	0.0108	0.1283
chr10	135534747	1806312	0.0133	0.1492
chr11	135006516	2117376	0.0157	0.1519
chr12	133851895	1398346	0.0104	0.1088
chr13	115169878	1024124	0.0089	0.1
chr14	107349540	771977	0.0072	0.0909
chr15	102531392	1093408	0.0107	0.1106
chr16	90354753	1235164	0.0137	0.1271
chr17	81195210	949133	0.0117	0.1158
chr18	78077248	1126718	0.0144	0.1996
chr19	59128983	893509	0.0151	0.1756
chr20	63025520	801691	0.0127	0.12
chr21	48129895	377610	0.0078	0.1005
chr22	51304566	514167	0.01	0.1057
chrMT	16571	9334	0.5633	0.8505
chrX	155270560	1915756	0.0123	0.1259
chrY	59373566	99981	0.0017	0.0586

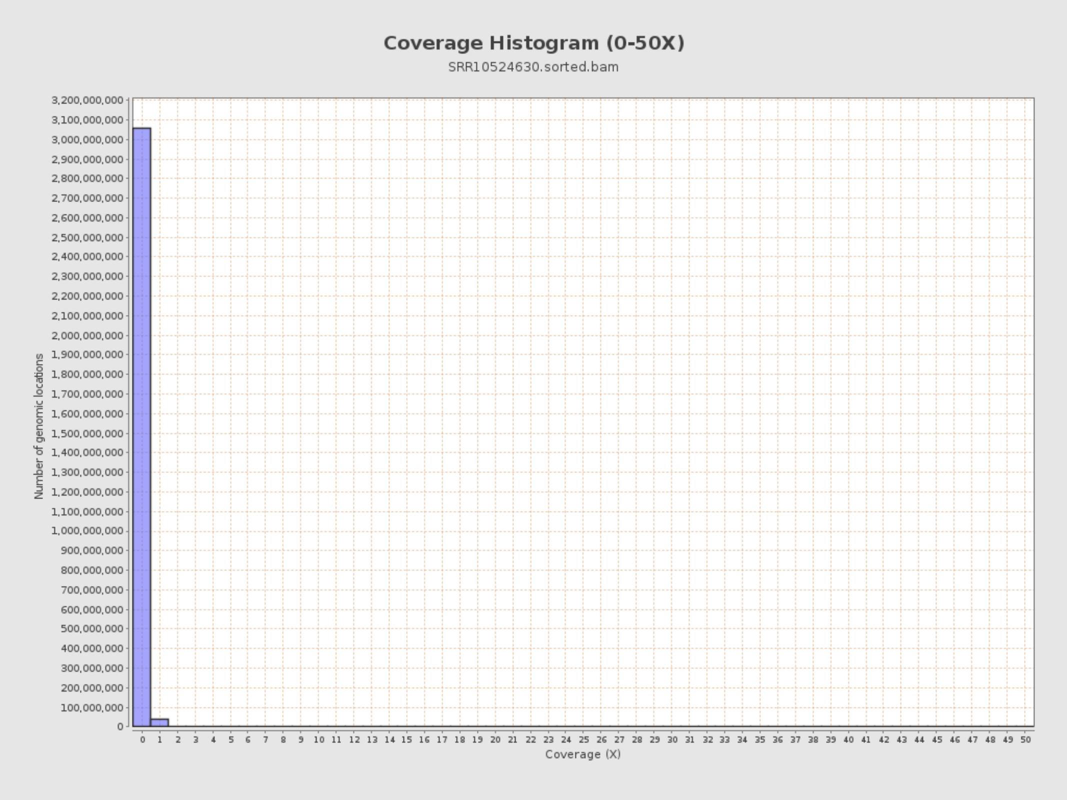
3. Results : Coverage across reference



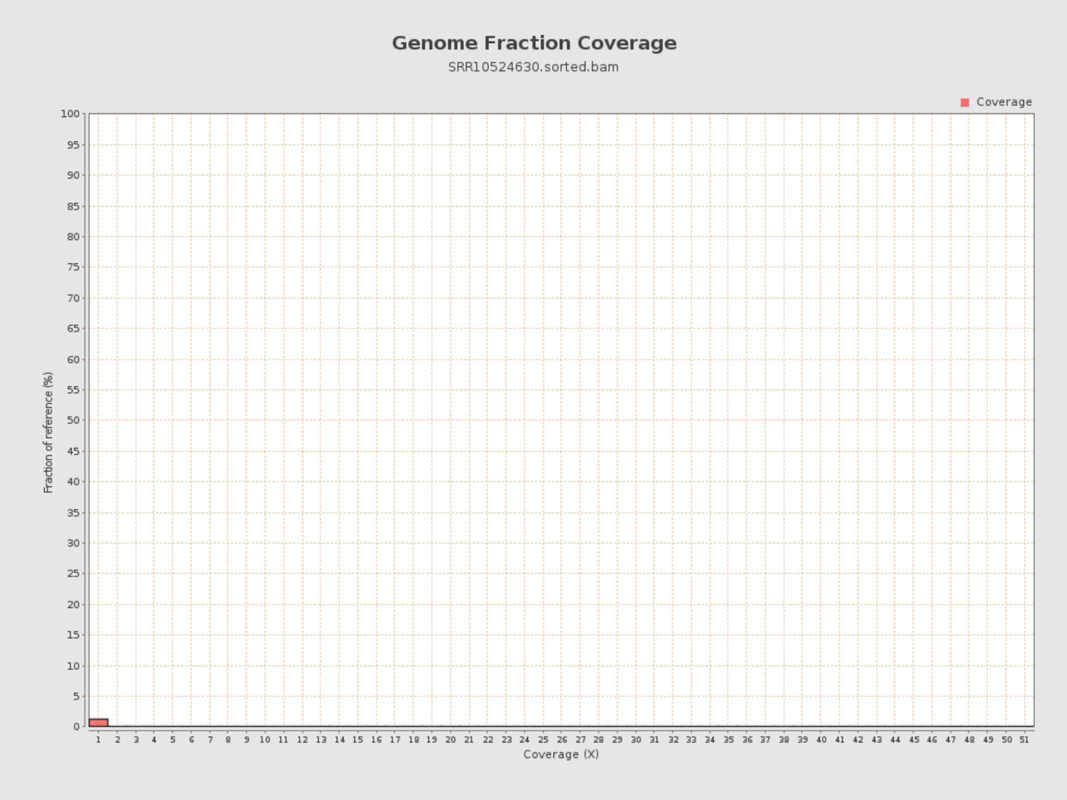
4. Results : Coverage Histogram



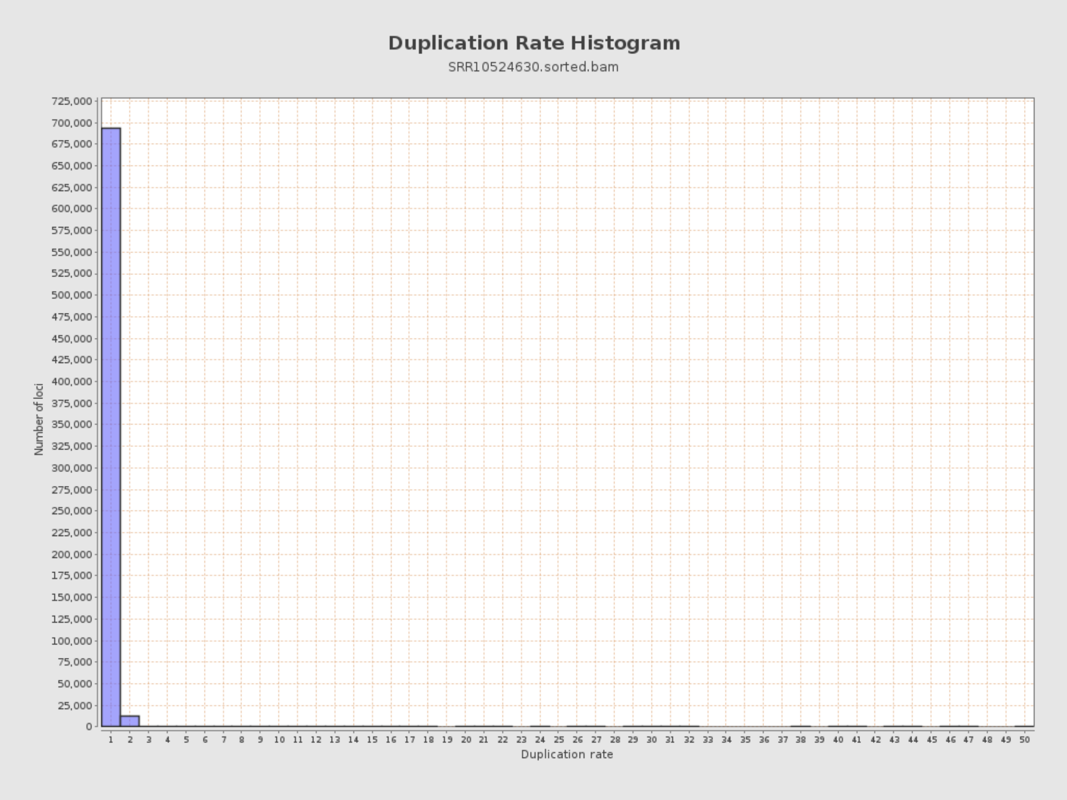
5. Results : Coverage Histogram (0-50X)



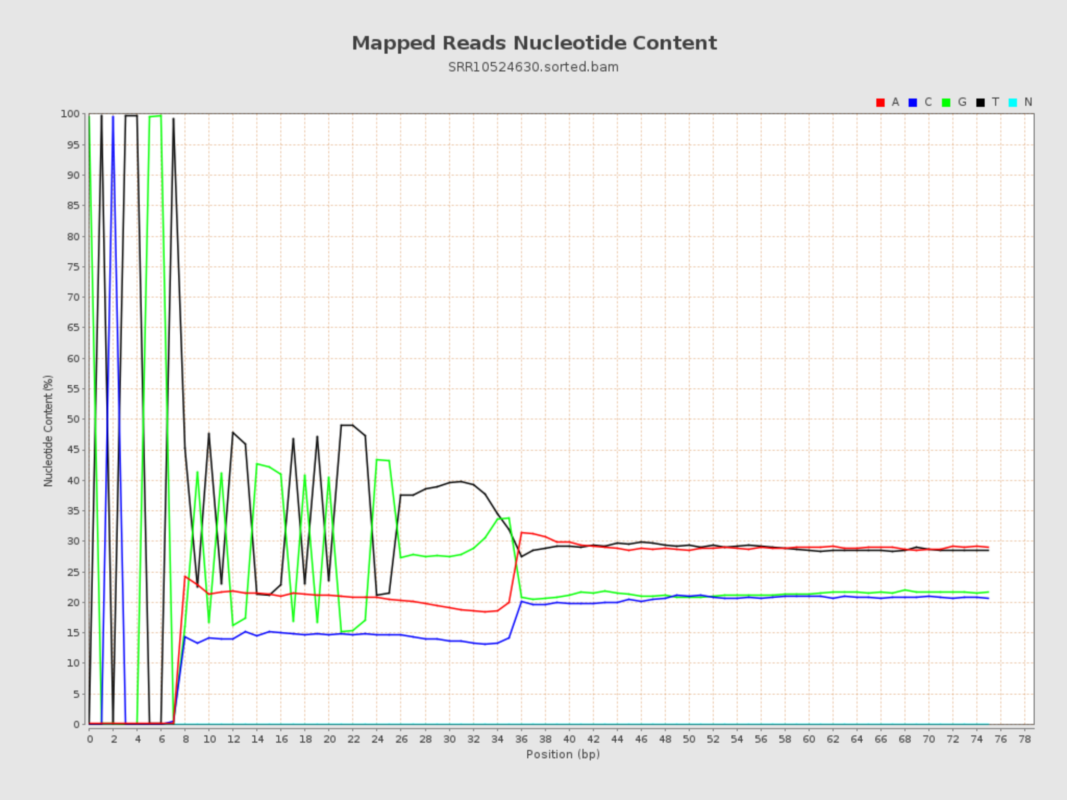
6. Results : Genome Fraction Coverage



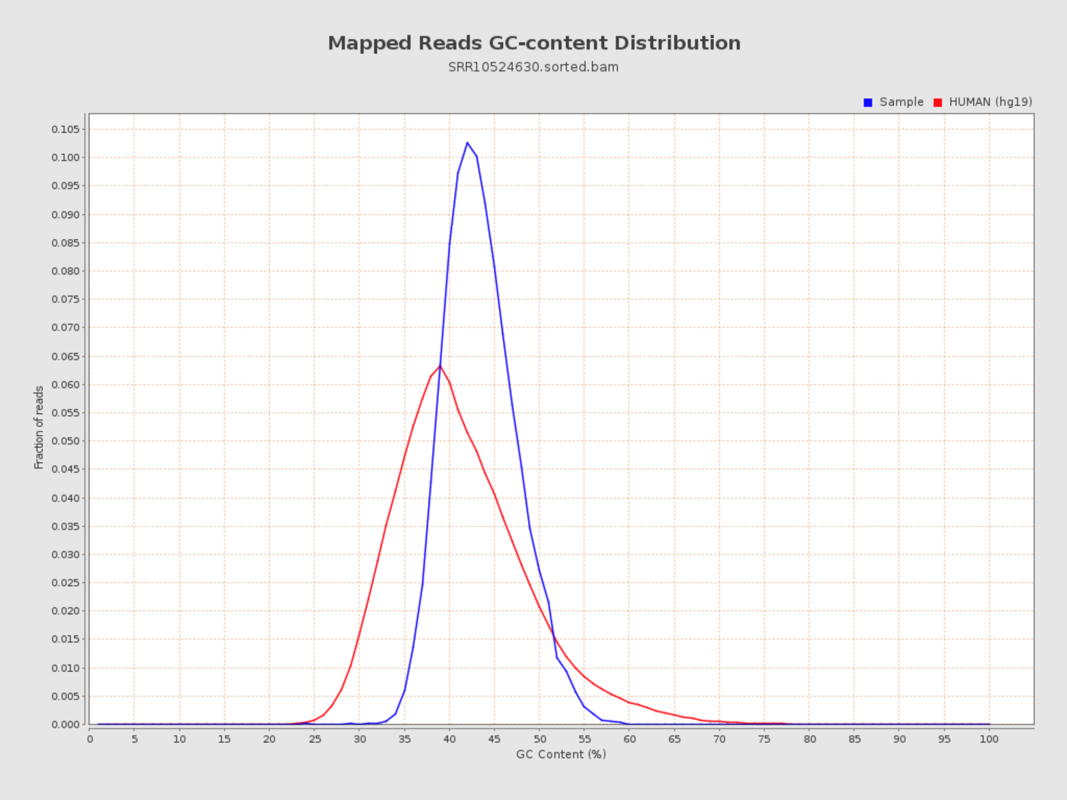
7. Results : Duplication Rate Histogram



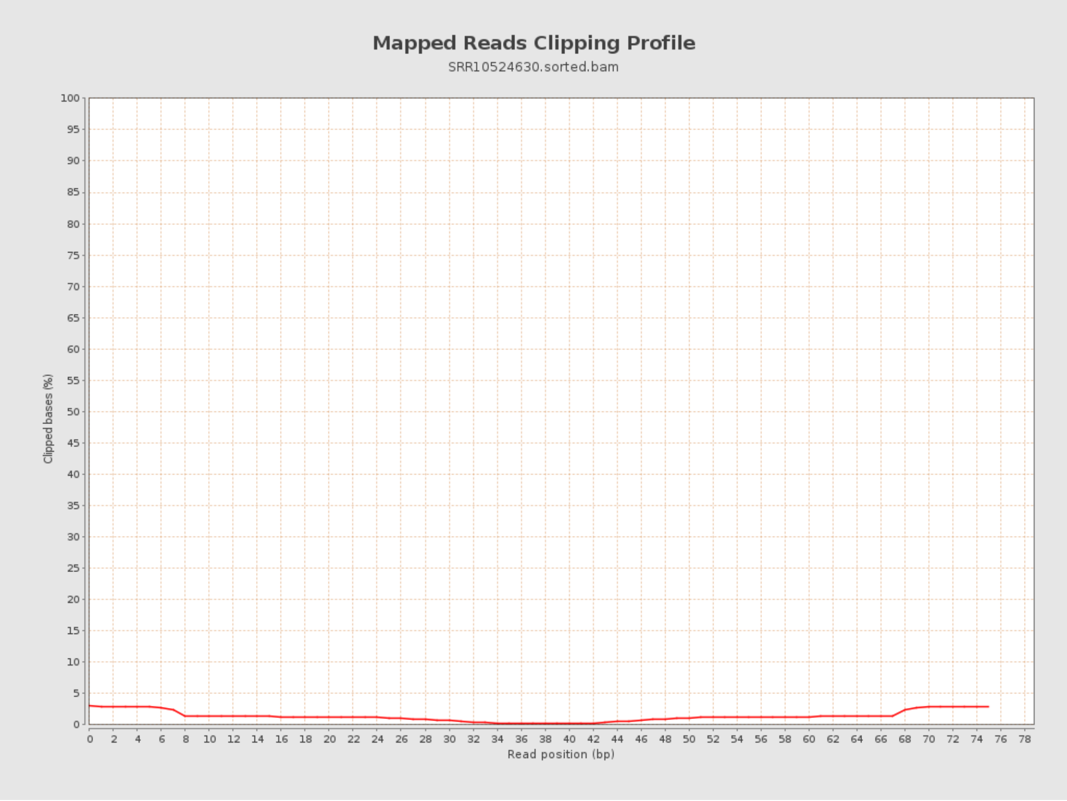
8. Results : Mapped Reads Nucleotide Content



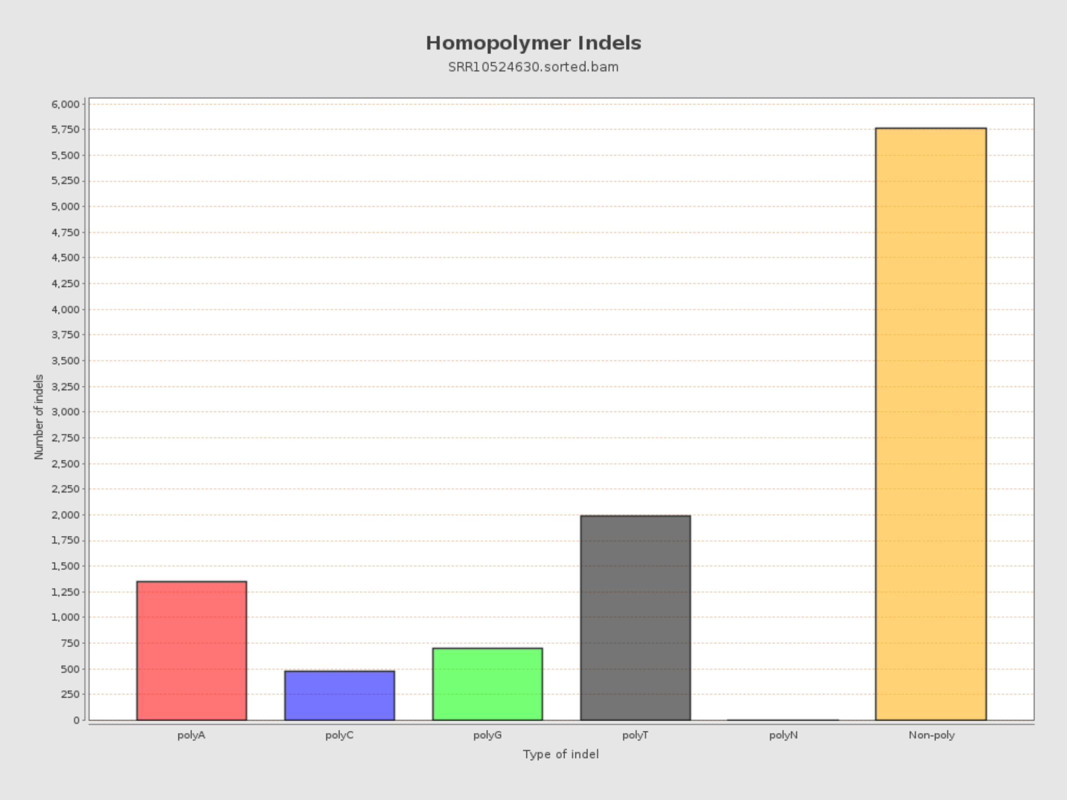
9. Results : Mapped Reads GC-content Distribution



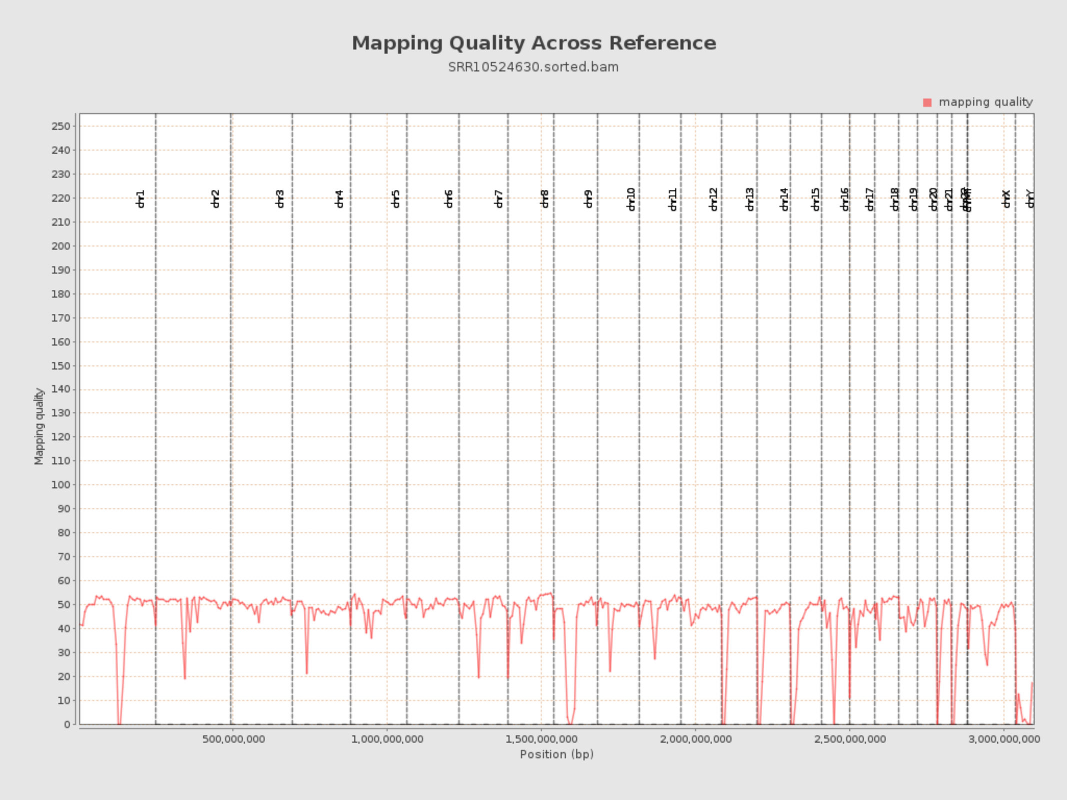
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram