Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:43:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524840.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_SRR10524840 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524840.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:43:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524840.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	860,964
Mapped reads	795,660 / 92.42%
Unmapped reads	65,304 / 7.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,126 / 0.48%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	16,762 / 1.95%
Duplication rate	1.42%
Clipped reads	797,459 / 92.62%

2.2. ACGT Content

Number/percentage of A's	12,194,998 / 25.97%
Number/percentage of C's	7,860,538 / 16.74%
Number/percentage of T's	15,141,359 / 32.24%
Number/percentage of G's	11,759,275 / 25.04%
Number/percentage of N's	6,405 / 0.01%
GC Percentage	41.78%

2.3. Coverage

Mean	0.0152

Standard Deviation	0.1795

2.4. Mapping Quality

Mean Mapping Quality	45.18

2.5. Mismatches and indels

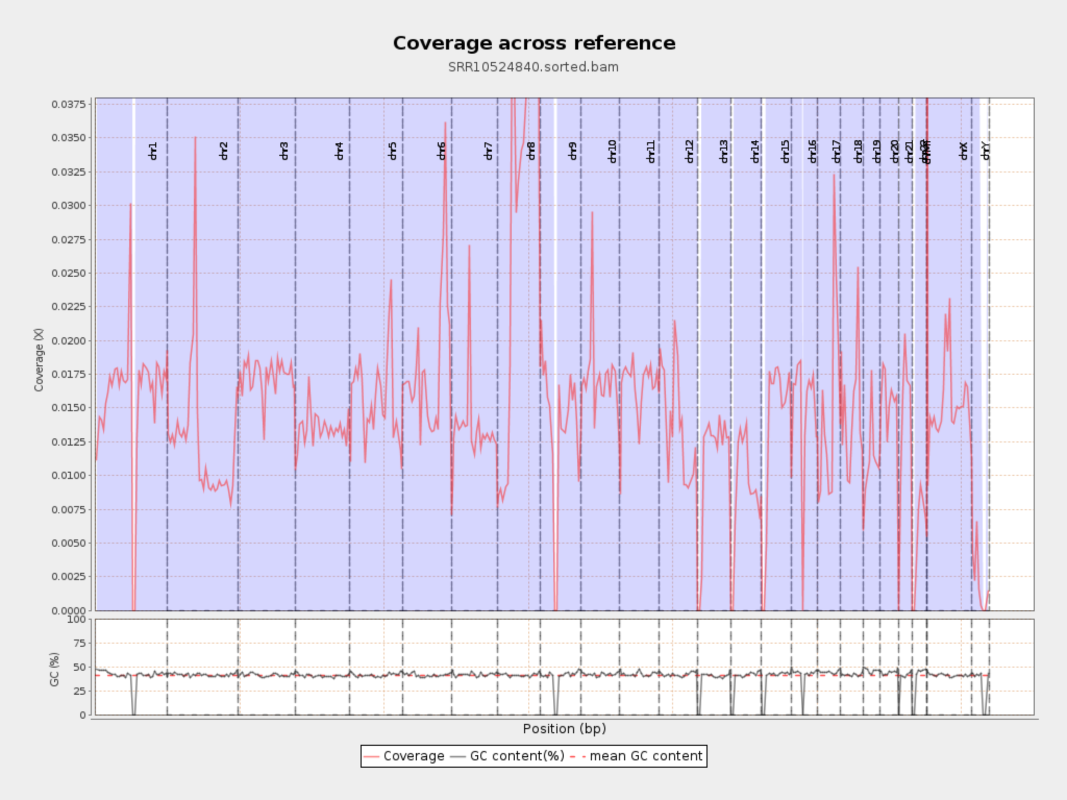
General error rate	0.49%
Mismatches	222,042
Insertions	3,315
Mapped reads with at least one insertion	0.41%
Deletions	8,844
Mapped reads with at least one deletion	1.1%
Homopolymer indels	44.54%

2.6. Chromosome stats

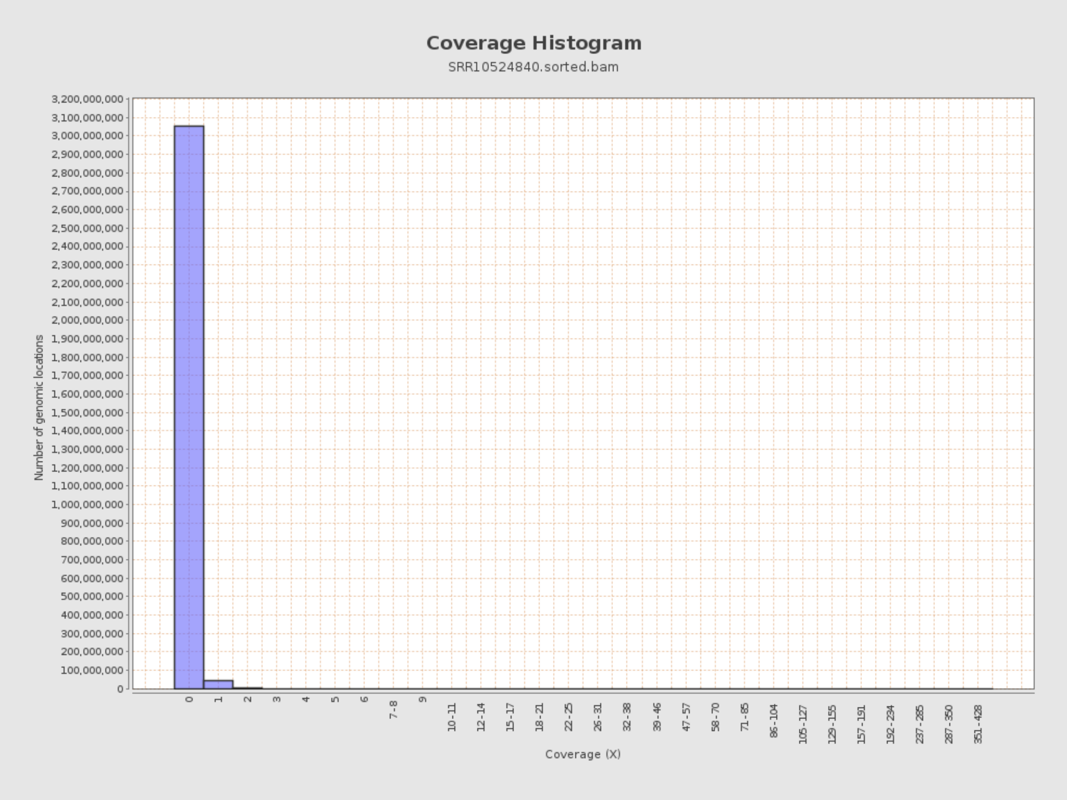
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3946748	0.0158	0.3413
chr2	243199373	3006056	0.0124	0.1664
chr3	198022430	3442918	0.0174	0.1366
chr4	191154276	2573919	0.0135	0.1246
chr5	180915260	2886966	0.016	0.1313
chr6	171115067	3067186	0.0179	0.1488
chr7	159138663	2175733	0.0137	0.2287

chr8	146364022	5071111	0.0346	0.2447
chr9	141213431	1928879	0.0137	0.1537
chr10	135534747	2350333	0.0173	0.1778
chr11	135006516	2259262	0.0167	0.1637
chr12	133851895	1826148	0.0136	0.1224
chr13	115169878	1252738	0.0109	0.1081
chr14	107349540	953901	0.0089	0.1024
chr15	102531392	1391399	0.0136	0.1207
chr16	90354753	1317730	0.0146	0.1331
chr17	81195210	1236492	0.0152	0.1362
chr18	78077248	1158293	0.0148	0.245
chr19	59128983	666939	0.0113	0.2202
chr20	63025520	977054	0.0155	0.1301
chr21	48129895	679545	0.0141	0.1278
chr22	51304566	285436	0.0056	0.077
chrMT	16571	3167	0.1911	0.436
chrX	155270560	2401390	0.0155	0.1395
chrY	59373566	117122	0.002	0.0613

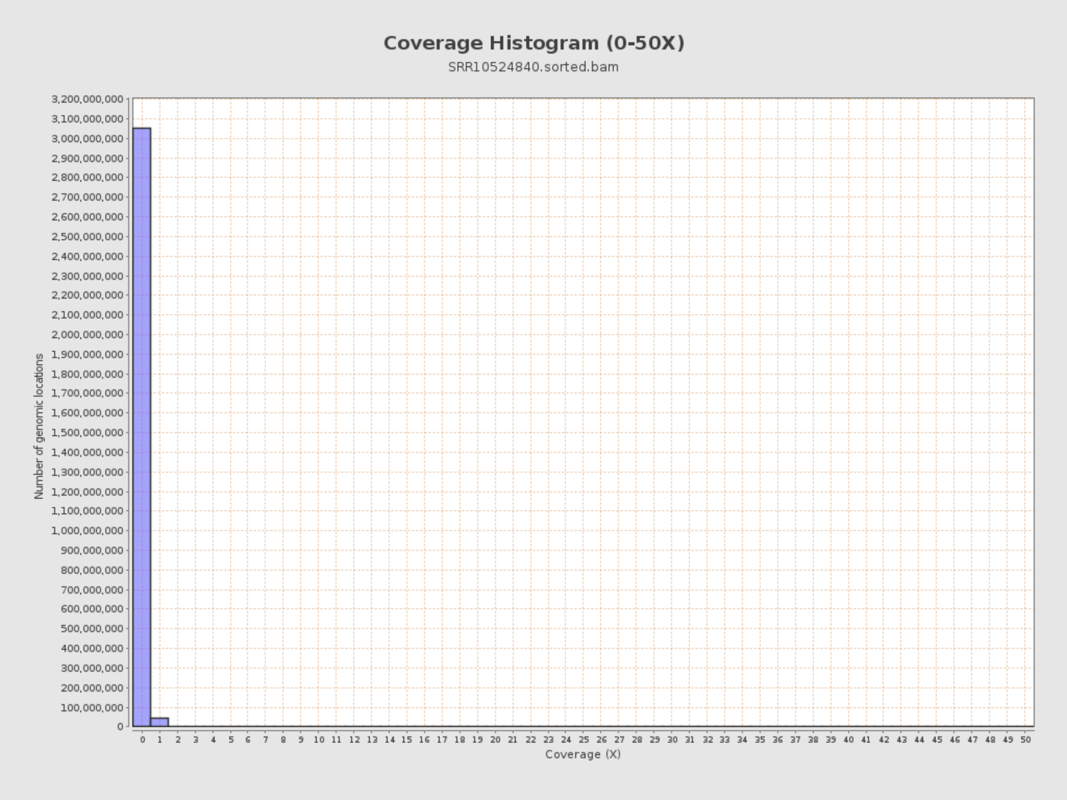
3. Results : Coverage across reference



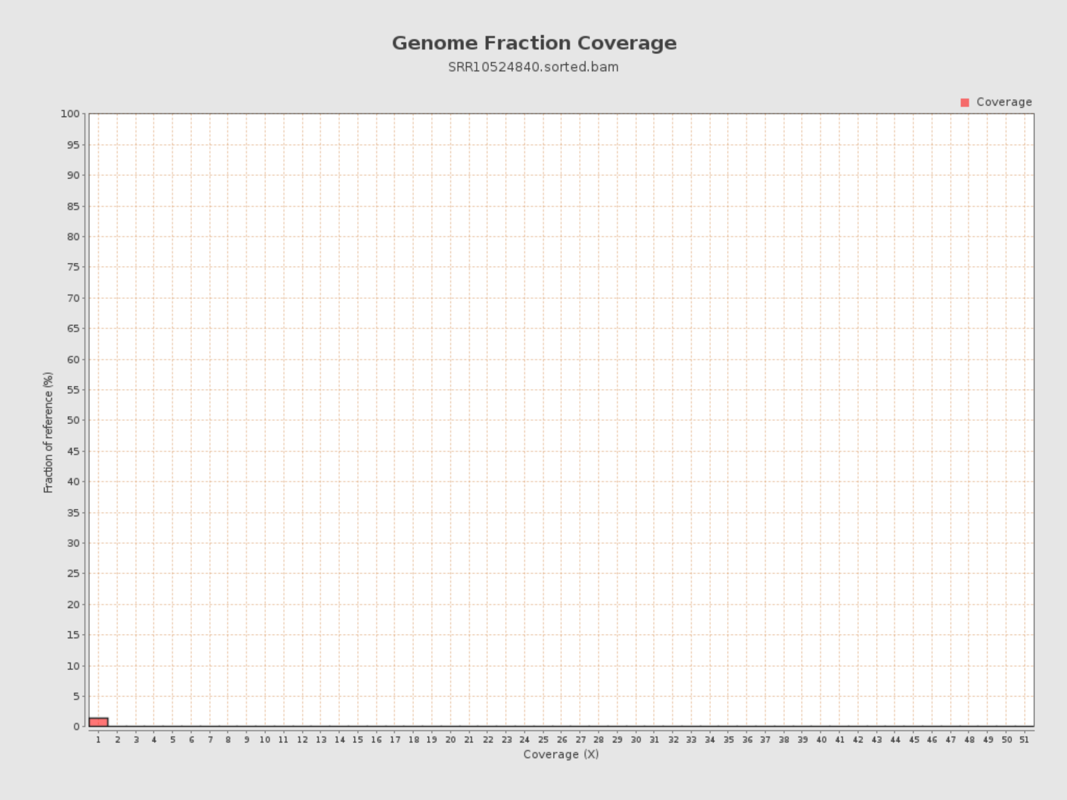
4. Results : Coverage Histogram



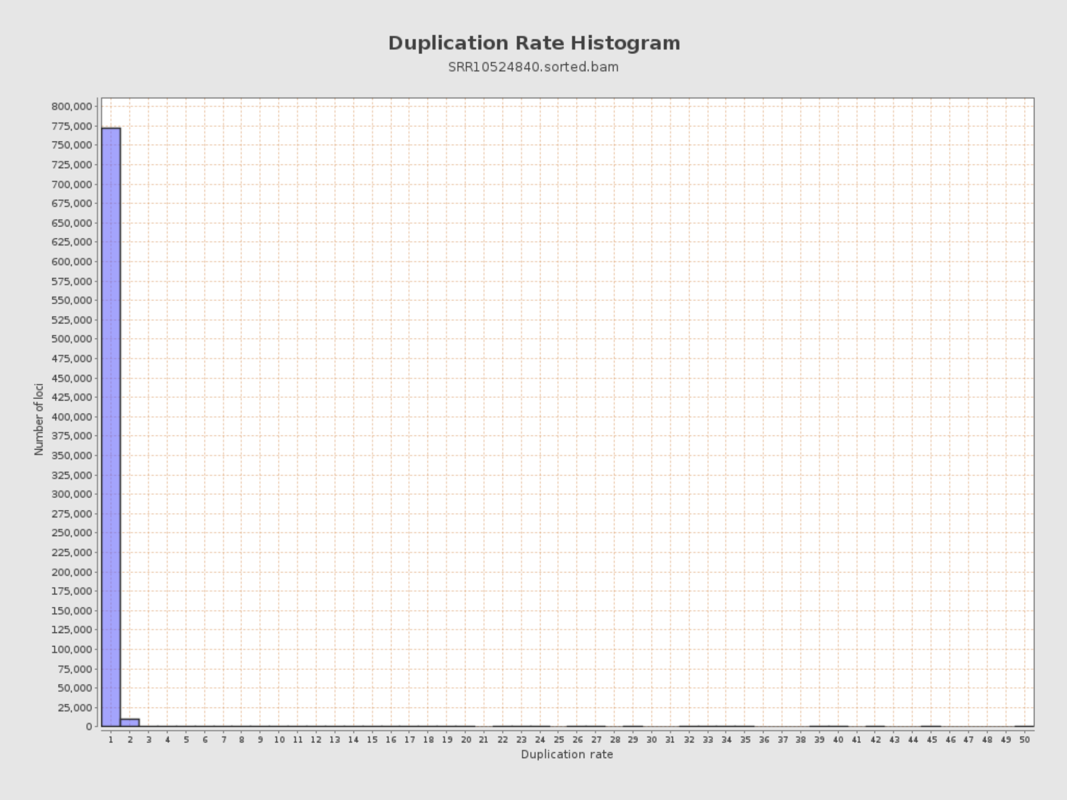
5. Results : Coverage Histogram (0-50X)



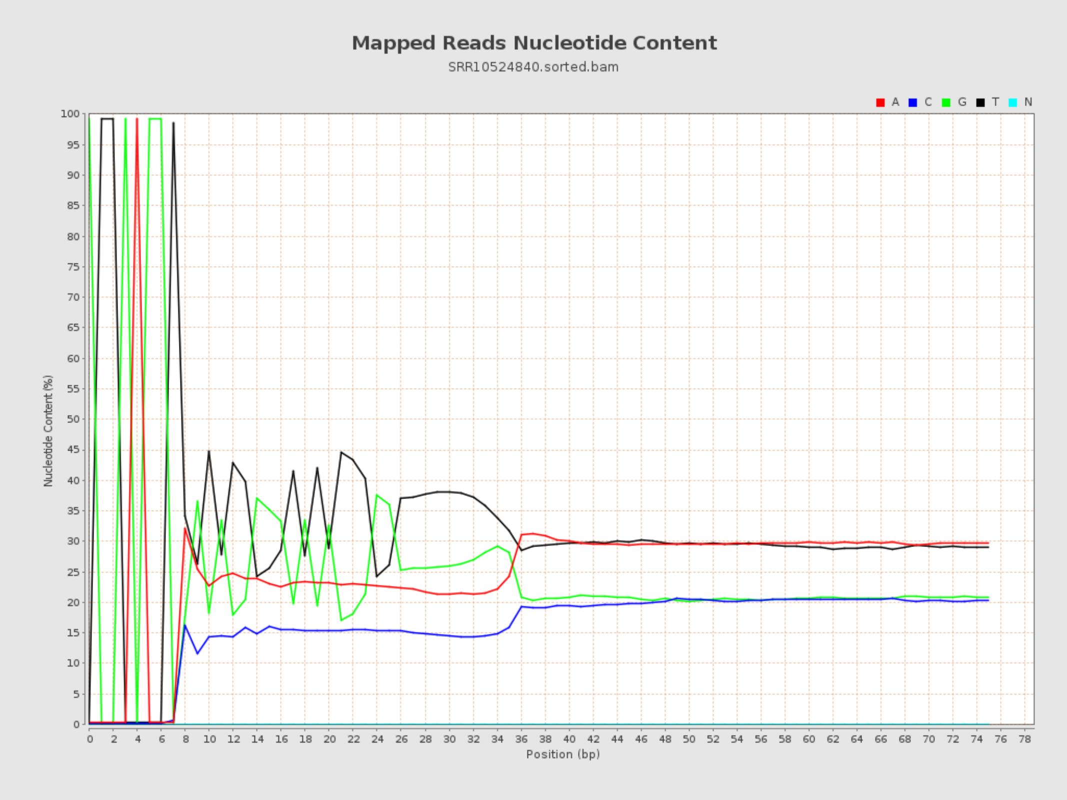
6. Results : Genome Fraction Coverage



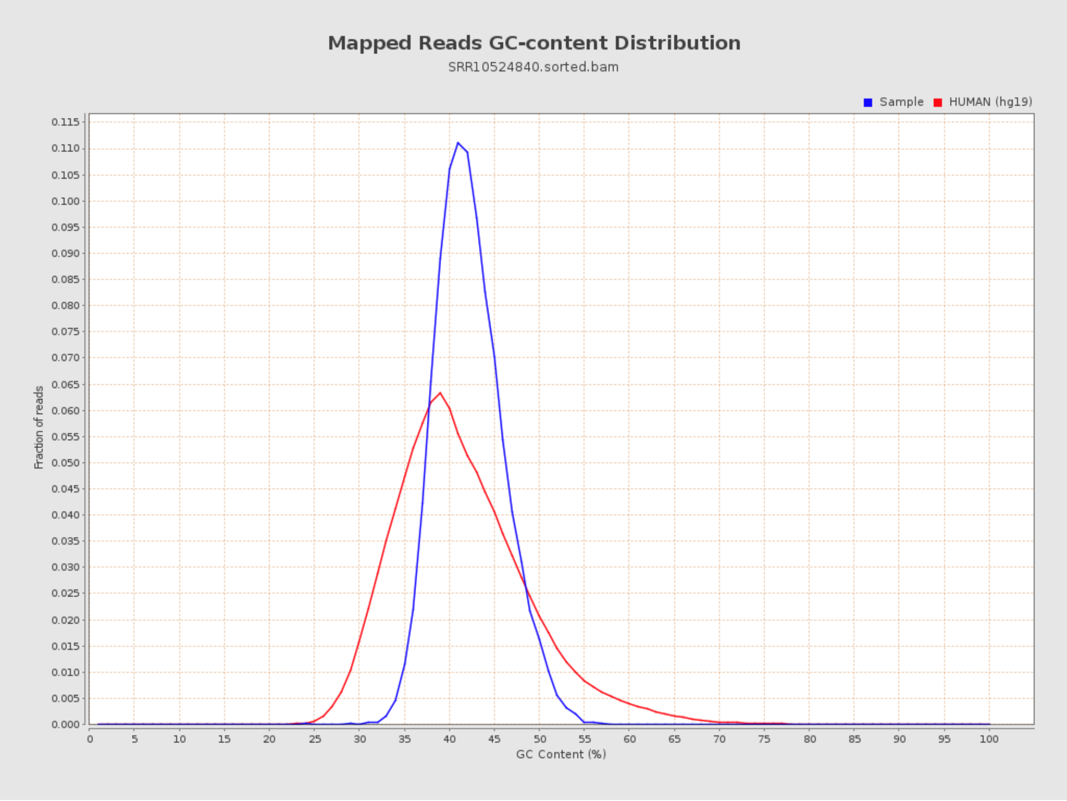
7. Results : Duplication Rate Histogram



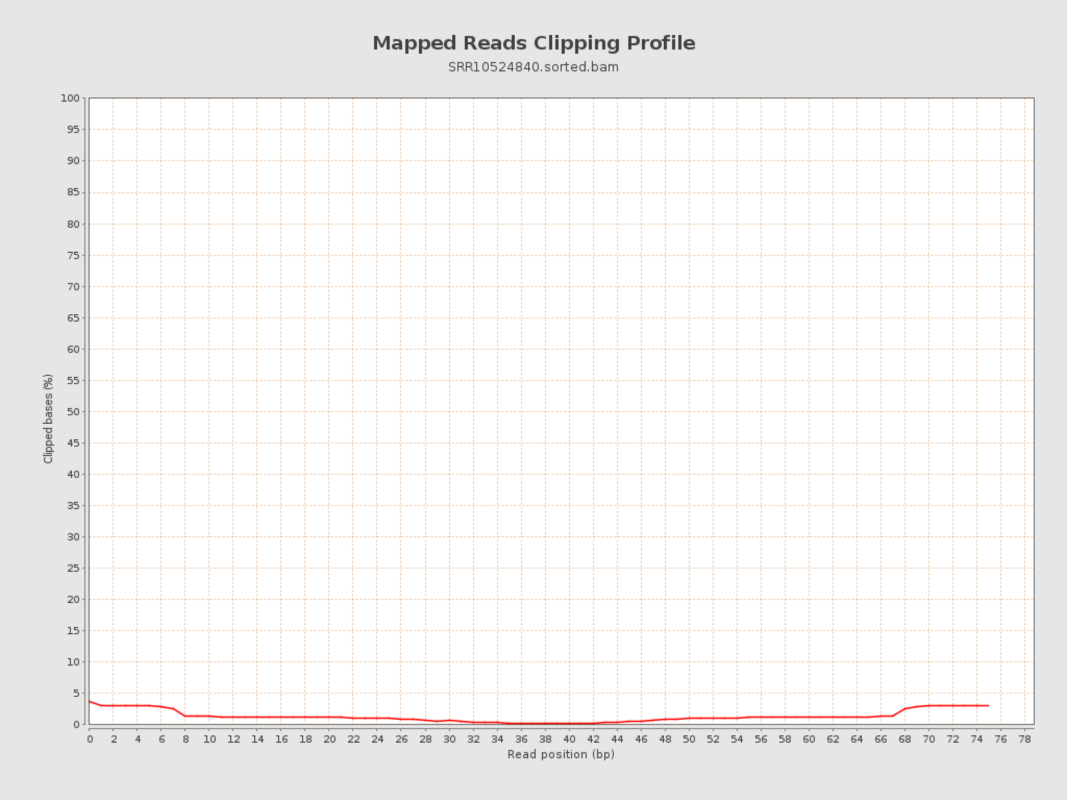
8. Results : Mapped Reads Nucleotide Content



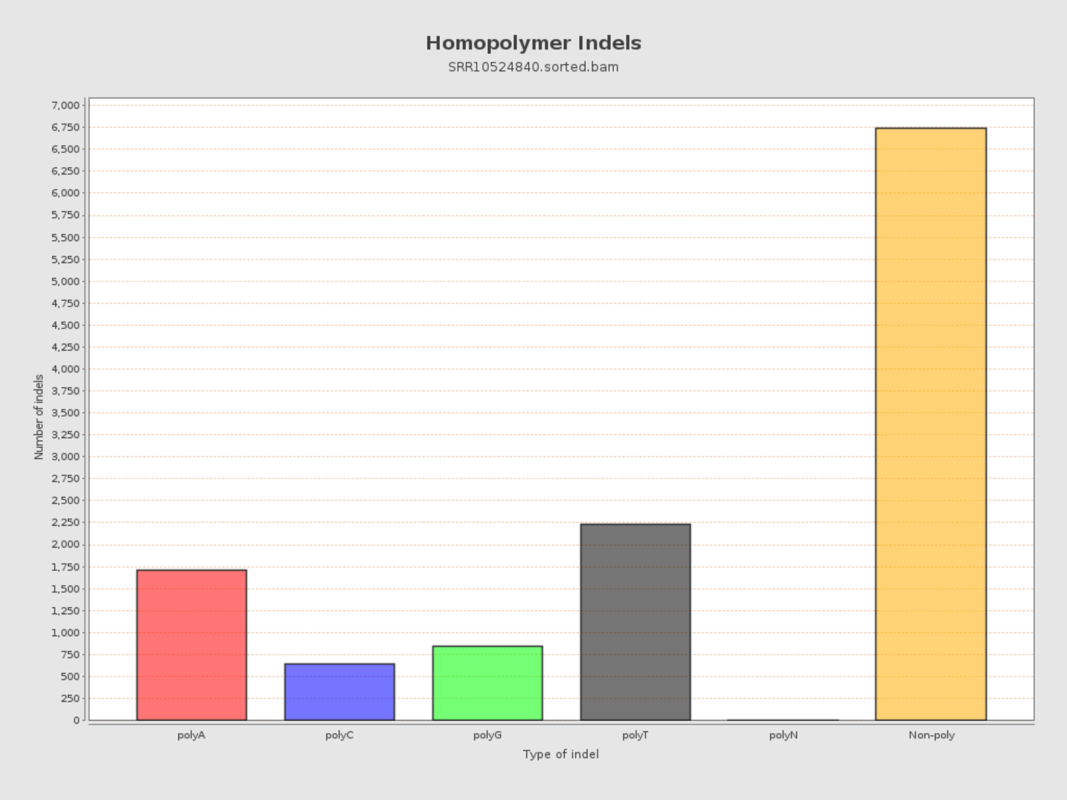
9. Results : Mapped Reads GC-content Distribution



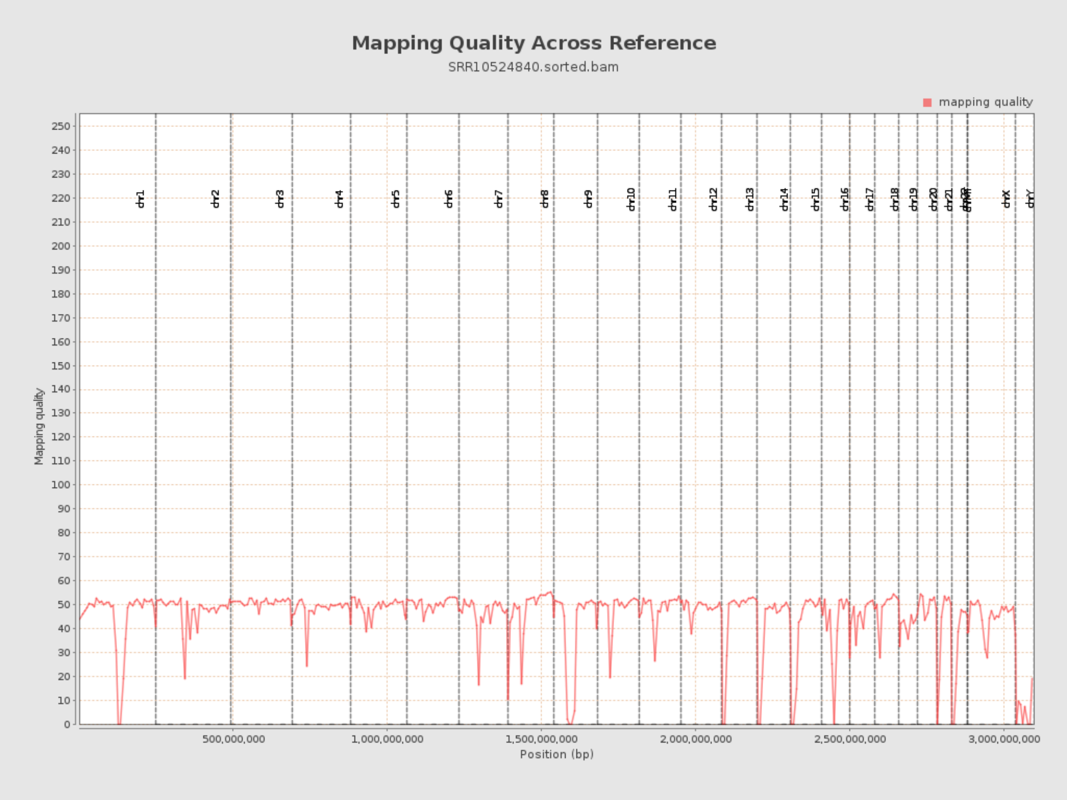
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram