Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 22:29:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524834.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_SRR10524834 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524834.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 22:29:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524834.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	900,620
Mapped reads	834,396 / 92.65%
Unmapped reads	66,224 / 7.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	4,258 / 0.47%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	19,072 / 2.12%
Duplication rate	1.61%
Clipped reads	836,485 / 92.88%

2.2. ACGT Content

Number/percentage of A's	12,087,094 / 24.83%
Number/percentage of C's	8,729,162 / 17.93%
Number/percentage of T's	15,976,349 / 32.82%
Number/percentage of G's	11,883,305 / 24.41%
Number/percentage of N's	6,456 / 0.01%
GC Percentage	42.34%

2.3. Coverage

Mean	0.0157

Standard Deviation	0.1776

2.4. Mapping Quality

Mean Mapping Quality	45.51

2.5. Mismatches and indels

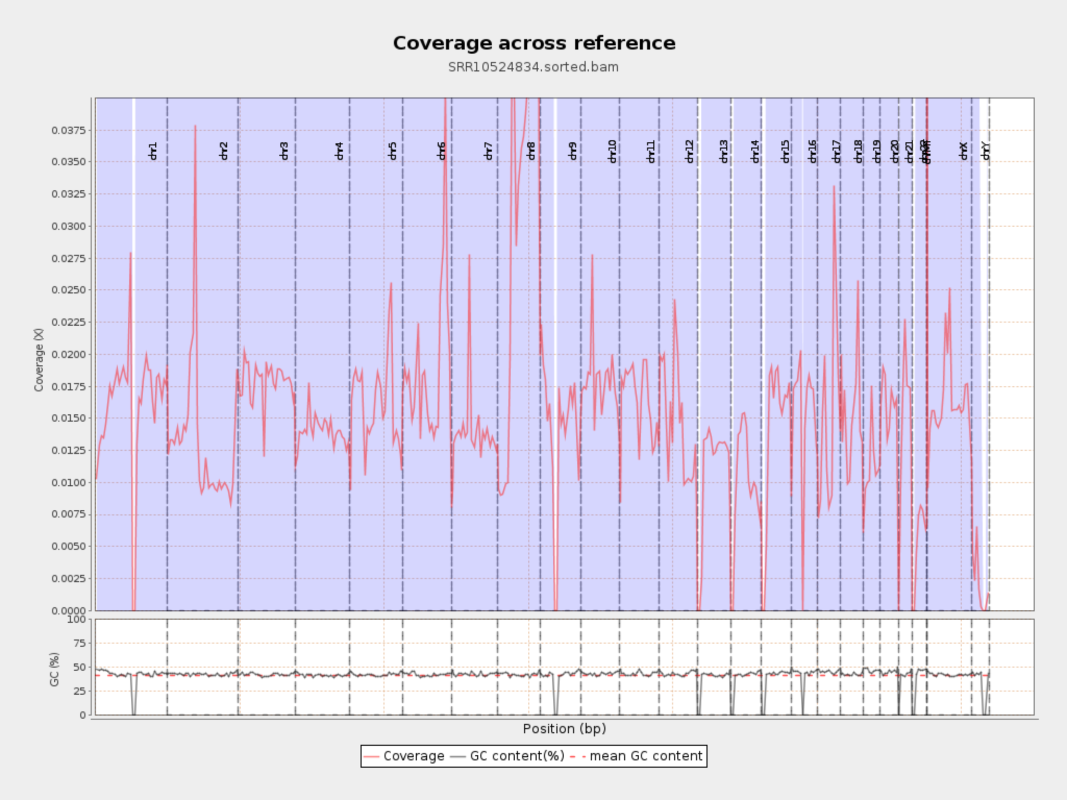
General error rate	0.49%
Mismatches	231,098
Insertions	3,053
Mapped reads with at least one insertion	0.36%
Deletions	8,962
Mapped reads with at least one deletion	1.07%
Homopolymer indels	44.04%

2.6. Chromosome stats

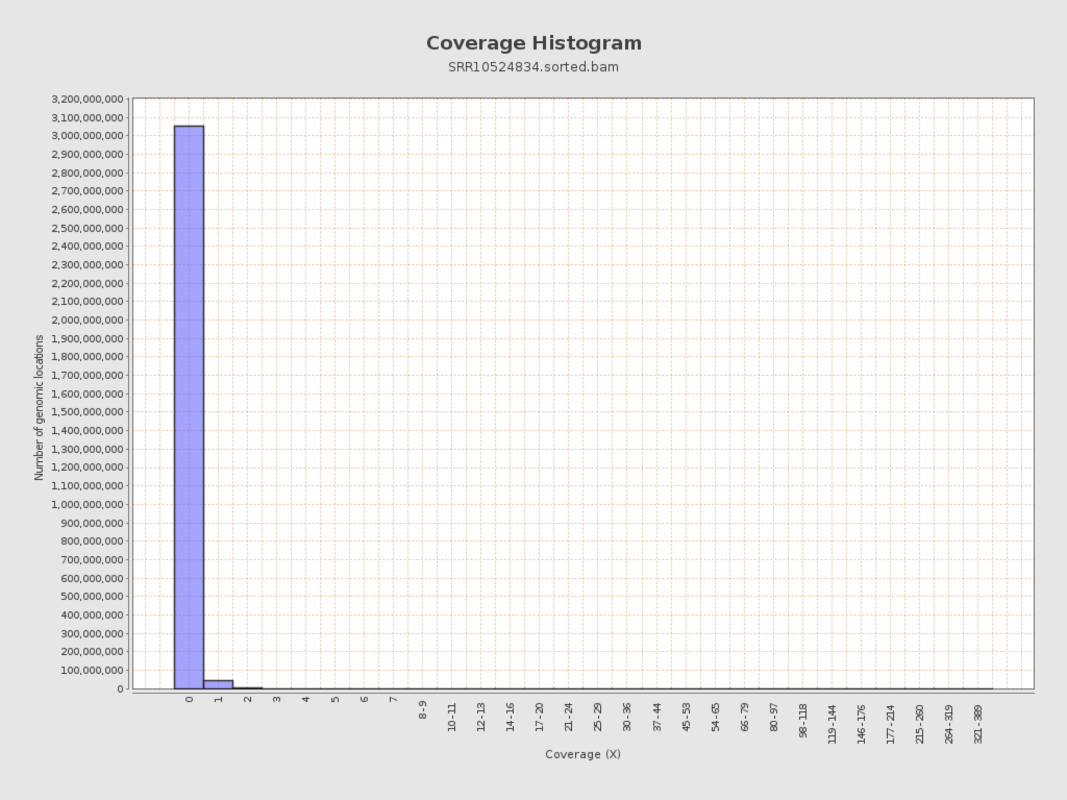
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3995082	0.016	0.3114
chr2	243199373	3169329	0.013	0.1673
chr3	198022430	3545523	0.0179	0.1397
chr4	191154276	2670770	0.014	0.1296
chr5	180915260	2976380	0.0165	0.1344
chr6	171115067	3231611	0.0189	0.1518
chr7	159138663	2246422	0.0141	0.2414

chr8	146364022	5320881	0.0364	0.2532
chr9	141213431	1999935	0.0142	0.1573
chr10	135534747	2430548	0.0179	0.1679
chr11	135006516	2221171	0.0165	0.1635
chr12	133851895	1967545	0.0147	0.1273
chr13	115169878	1247387	0.0108	0.1103
chr14	107349540	1048506	0.0098	0.1108
chr15	102531392	1435096	0.014	0.1254
chr16	90354753	1370520	0.0152	0.1347
chr17	81195210	1268177	0.0156	0.1411
chr18	78077248	1206066	0.0154	0.2506
chr19	59128983	669777	0.0113	0.1983
chr20	63025520	1004927	0.0159	0.1337
chr21	48129895	719864	0.015	0.1323
chr22	51304566	278040	0.0054	0.0765
chrMT	16571	1315	0.0794	0.2872
chrX	155270560	2553354	0.0164	0.1443
chrY	59373566	118165	0.002	0.0597

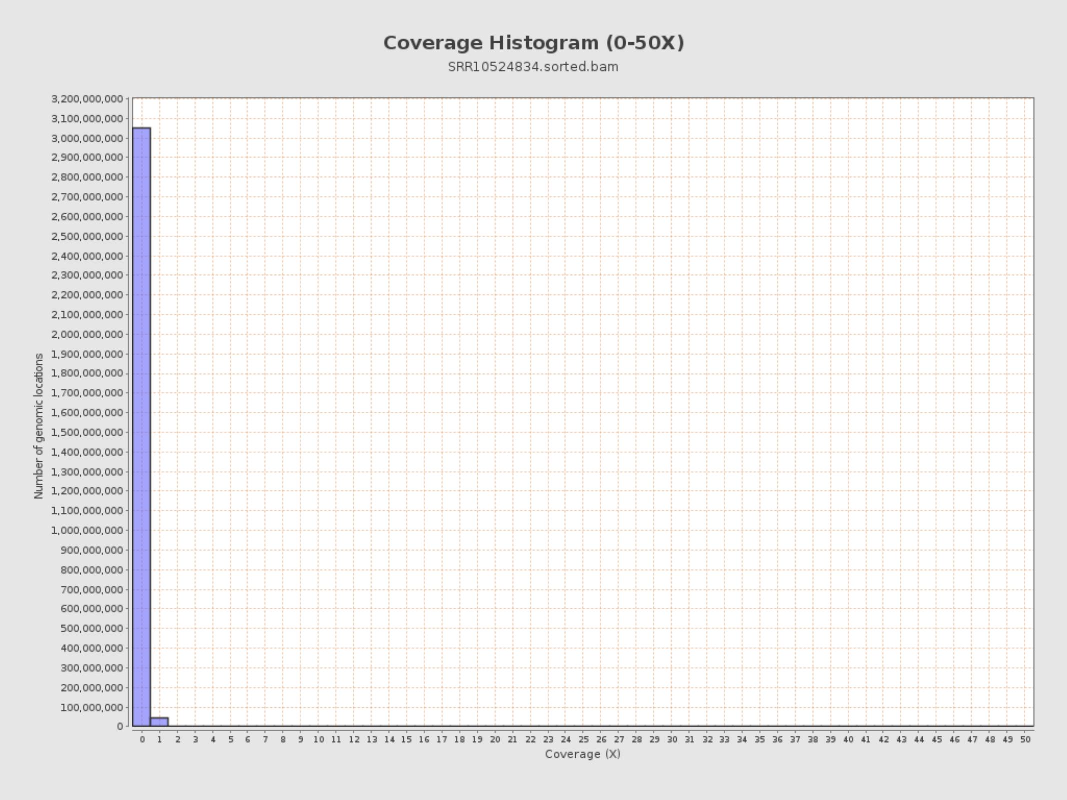
3. Results : Coverage across reference



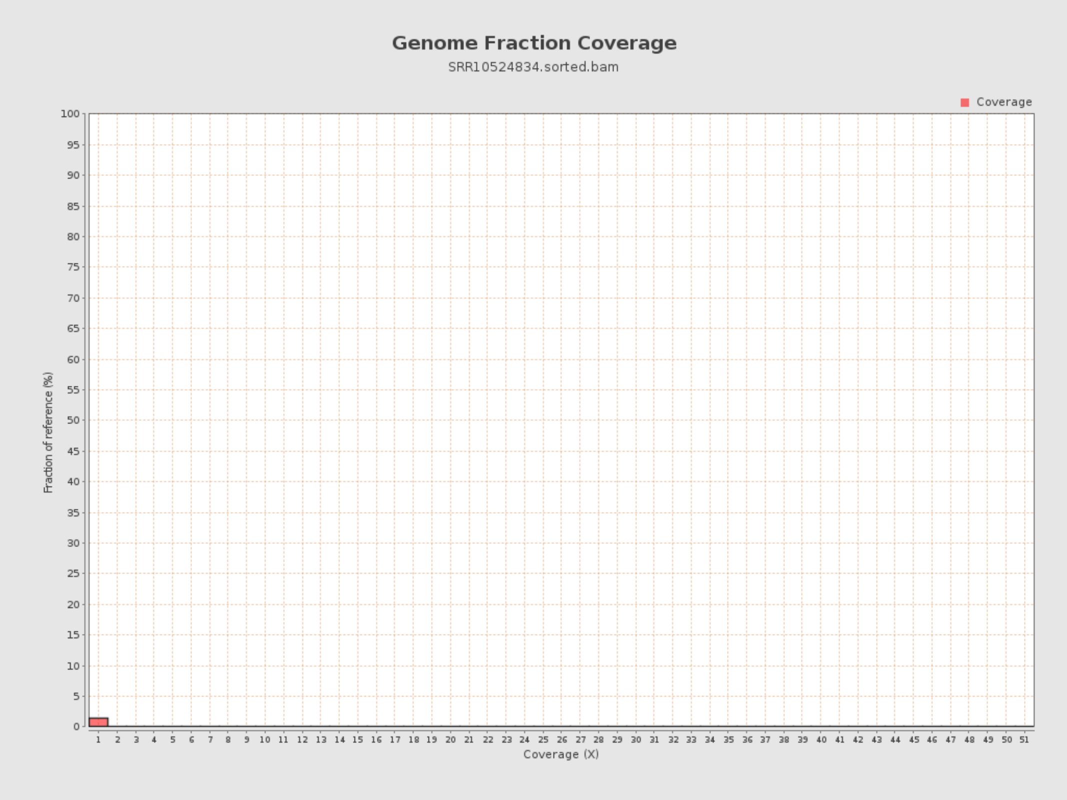
4. Results : Coverage Histogram



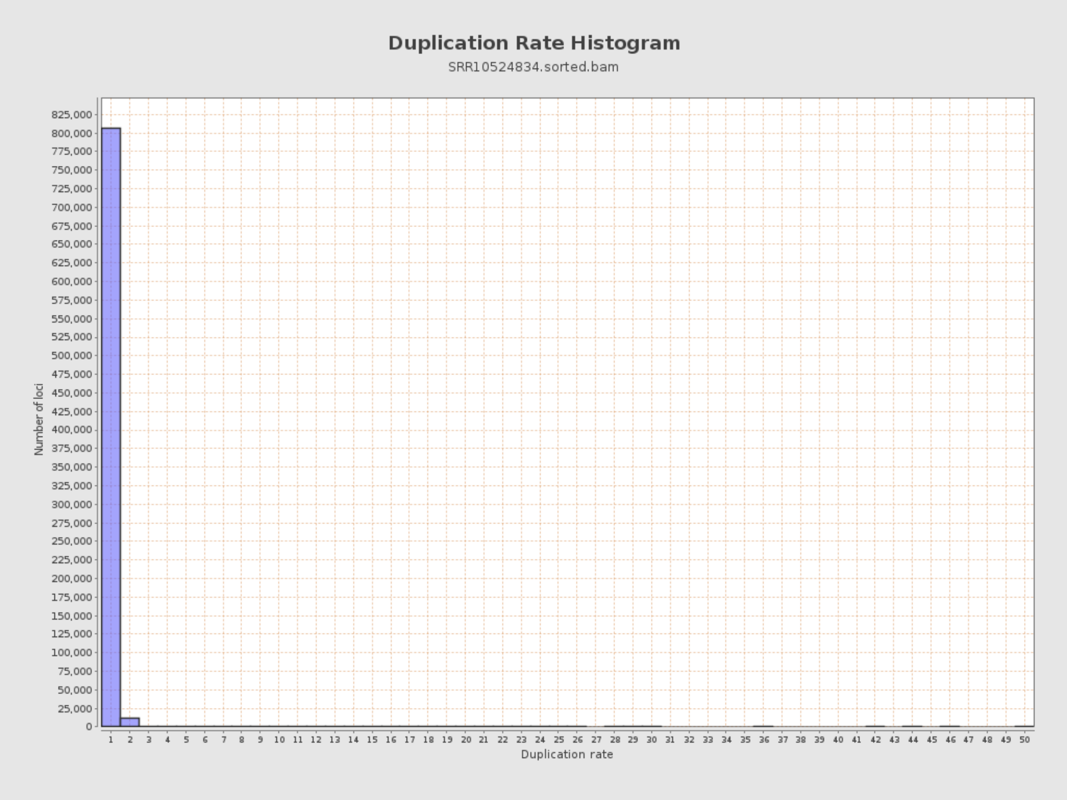
5. Results : Coverage Histogram (0-50X)



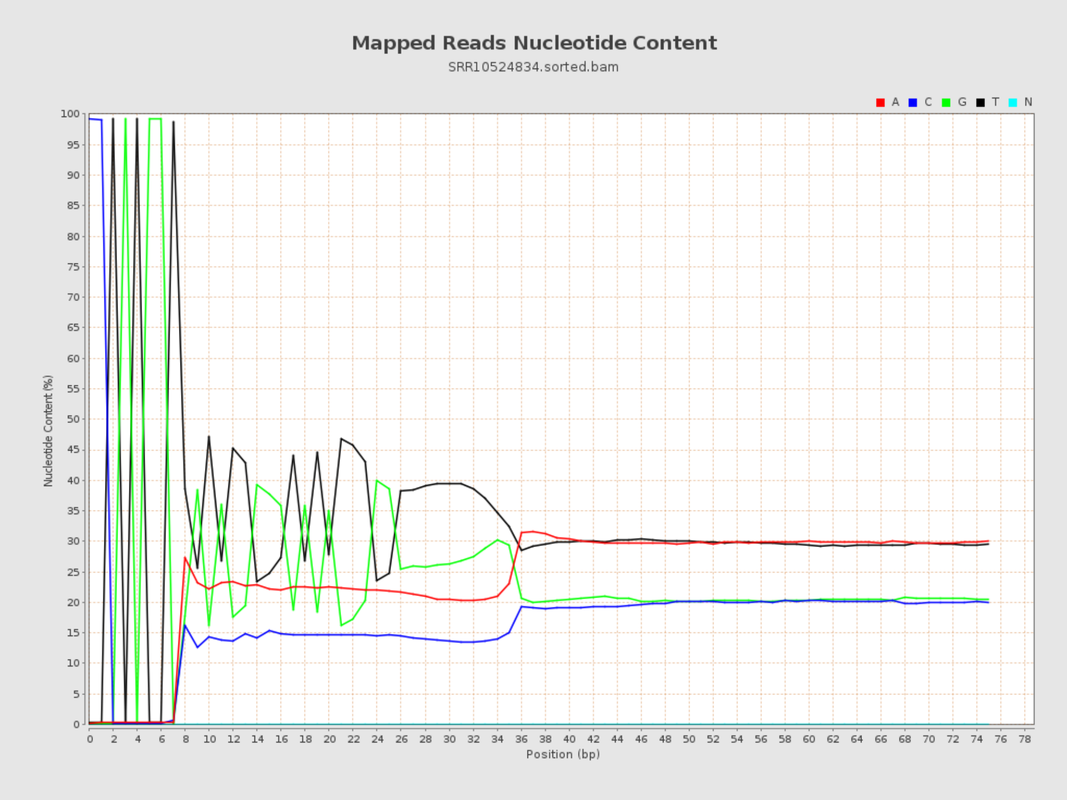
6. Results : Genome Fraction Coverage



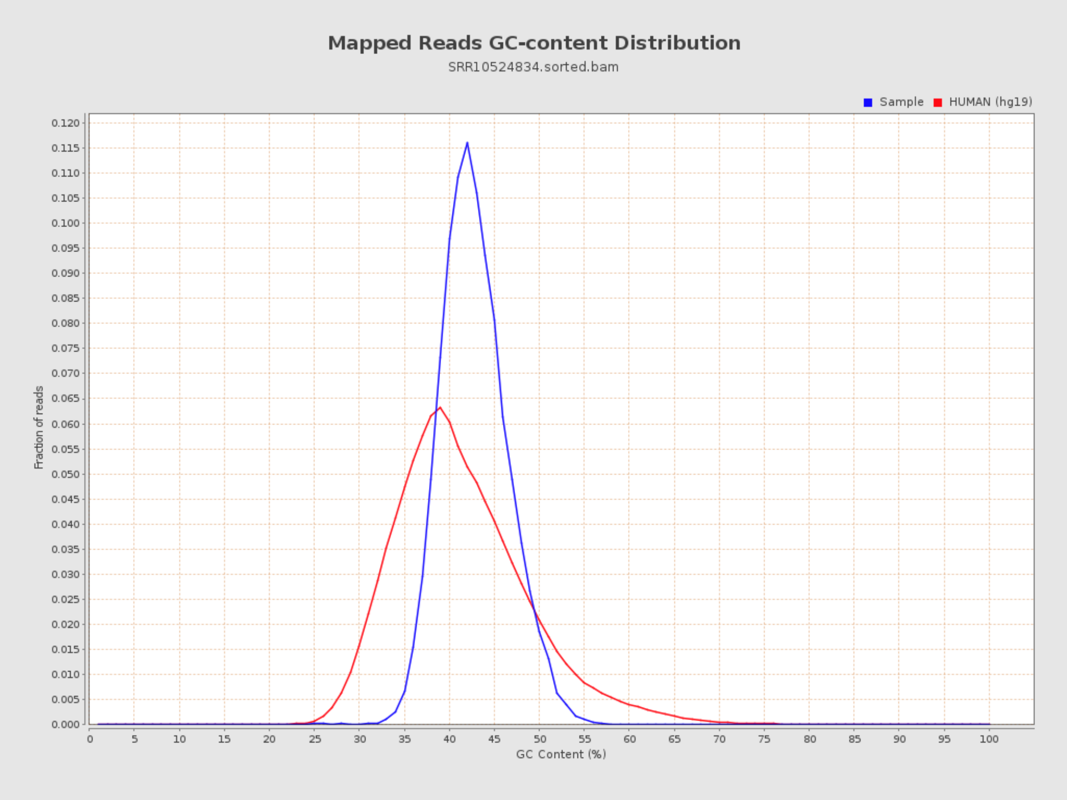
7. Results : Duplication Rate Histogram



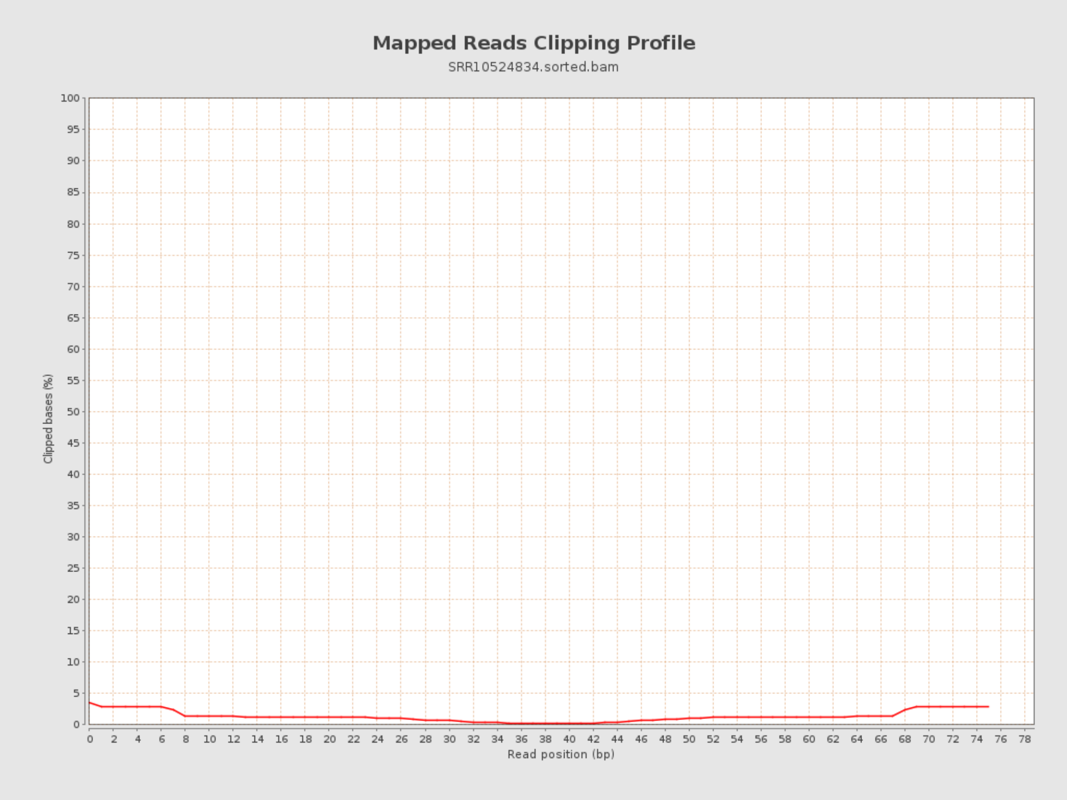
8. Results : Mapped Reads Nucleotide Content



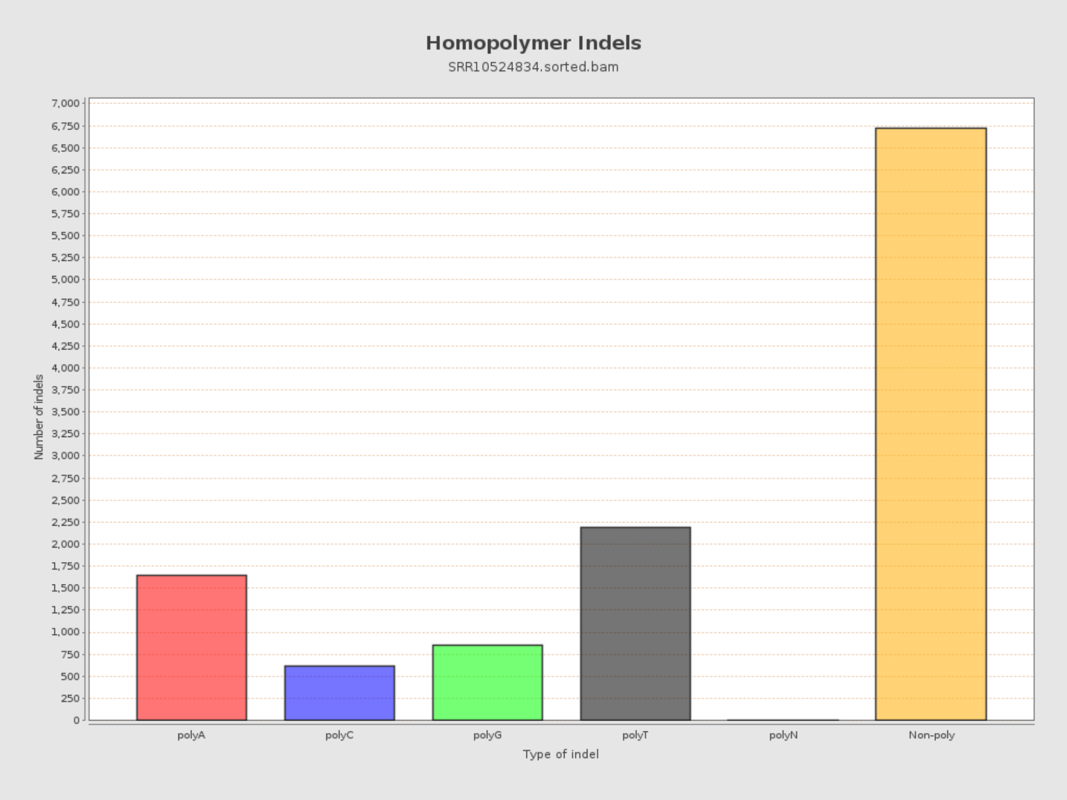
9. Results : Mapped Reads GC-content Distribution



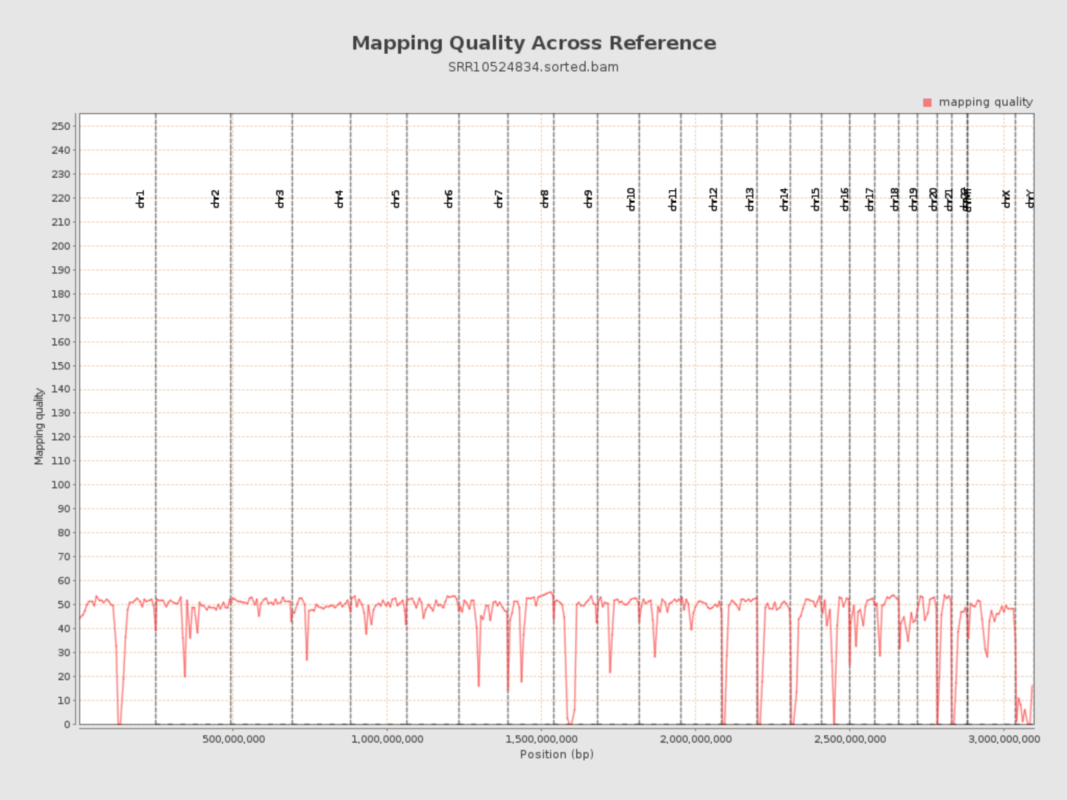
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram