Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:23:07

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234141.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_SRR6234141 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234141.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:23:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234141.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,742,365
Mapped reads	309,762 / 17.78%
Unmapped reads	1,432,603 / 82.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,844 / 0.22%
Read min/max/mean length	30 / 76 / 76.08
Duplicated reads (estimated)	48,710 / 2.8%
Duplication rate	11.36%
Clipped reads	194,641 / 11.17%

2.2. ACGT Content

Number/percentage of A's	4,988,017 / 26.5%
Number/percentage of C's	3,520,070 / 18.7%
Number/percentage of T's	5,918,754 / 31.44%
Number/percentage of G's	4,392,158 / 23.33%
Number/percentage of N's	4,205 / 0.02%
GC Percentage	42.03%

2.3. Coverage

Mean	0.0061

Standard Deviation	0.1461

2.4. Mapping Quality

Mean Mapping Quality	40.13

2.5. Mismatches and indels

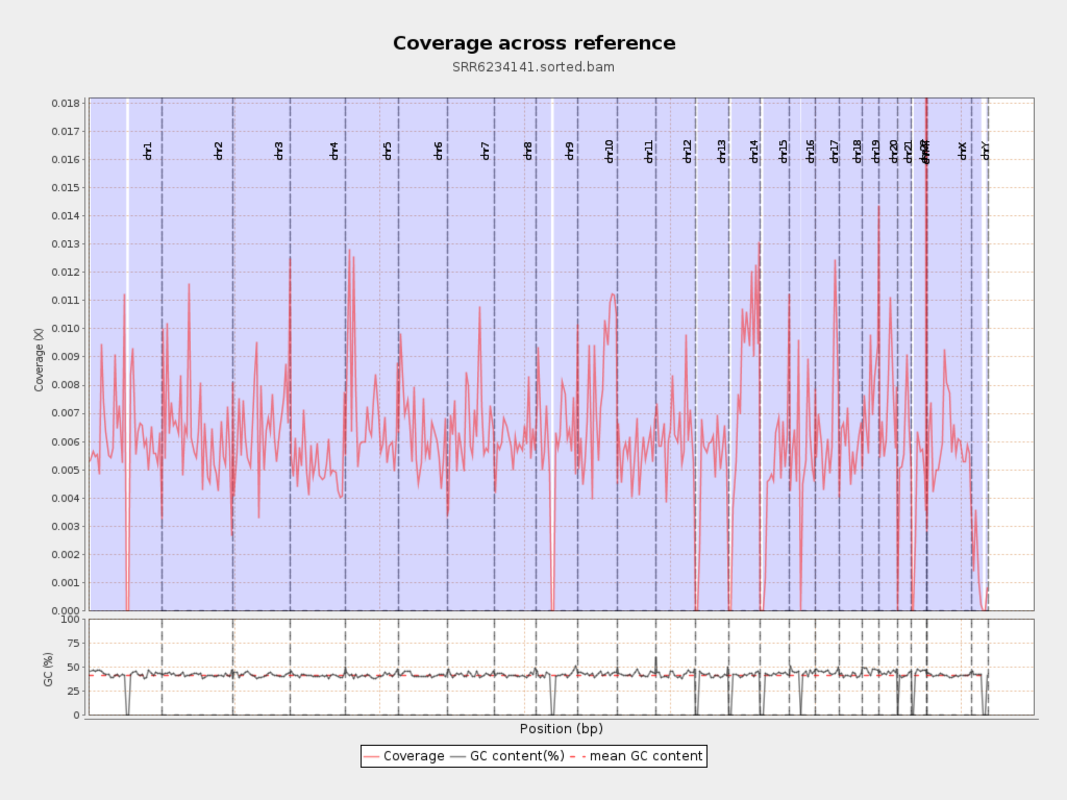
General error rate	0.96%
Mismatches	174,205
Insertions	2,485
Mapped reads with at least one insertion	0.78%
Deletions	5,911
Mapped reads with at least one deletion	1.88%
Homopolymer indels	39.42%

2.6. Chromosome stats

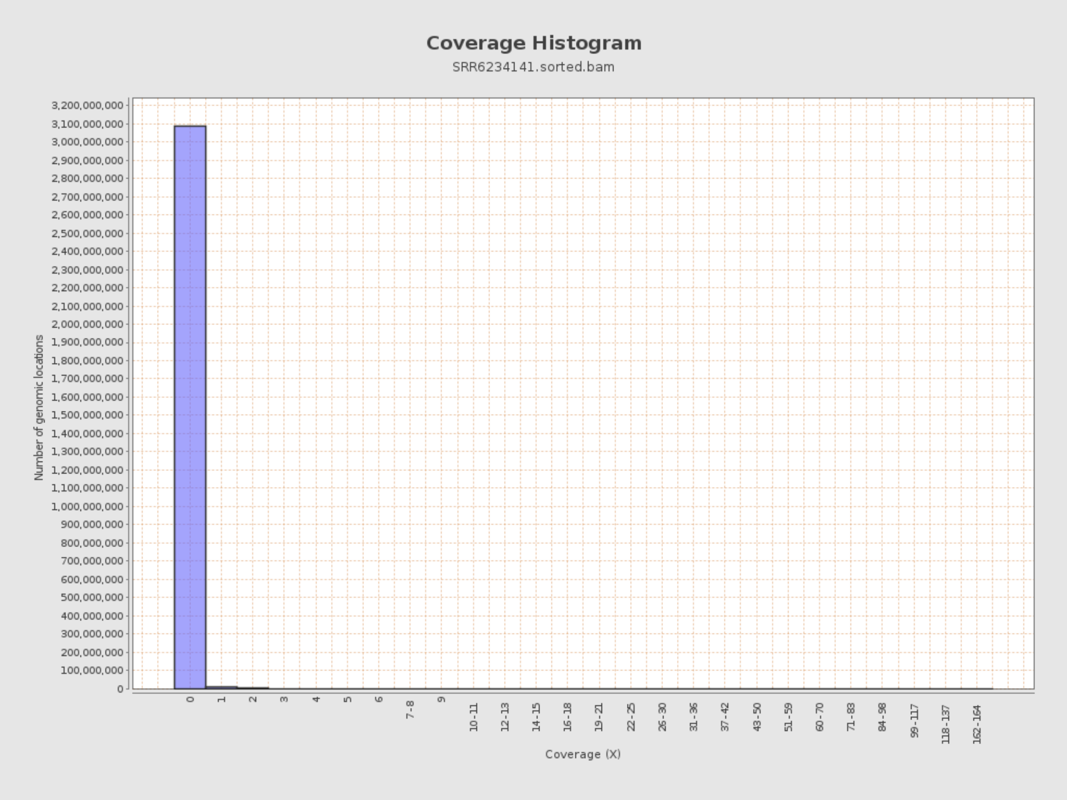
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	1514279	0.0061	0.1747
chr2	243199373	1538541	0.0063	0.1596
chr3	198022430	1302628	0.0066	0.1471
chr4	191154276	990775	0.0052	0.1262
chr5	180915260	1258948	0.007	0.1463
chr6	171115067	1072313	0.0063	0.1361
chr7	159138663	1039251	0.0065	0.14

chr8	146364022	876735	0.006	0.1463
chr9	141213431	820804	0.0058	0.1365
chr10	135534747	1059556	0.0078	0.1598
chr11	135006516	760550	0.0056	0.1348
chr12	133851895	846025	0.0063	0.1398
chr13	115169878	566520	0.0049	0.1671
chr14	107349540	838287	0.0078	0.1666
chr15	102531392	463418	0.0045	0.1308
chr16	90354753	495346	0.0055	0.1374
chr17	81195210	546646	0.0067	0.141
chr18	78077248	456758	0.0059	0.1446
chr19	59128983	463662	0.0078	0.1642
chr20	63025520	450186	0.0071	0.1496
chr21	48129895	267097	0.0055	0.133
chr22	51304566	200072	0.0039	0.1007
chrMT	16571	11639	0.7024	1.3182
chrX	155270560	926432	0.006	0.1394
chrY	59373566	67134	0.0011	0.0511

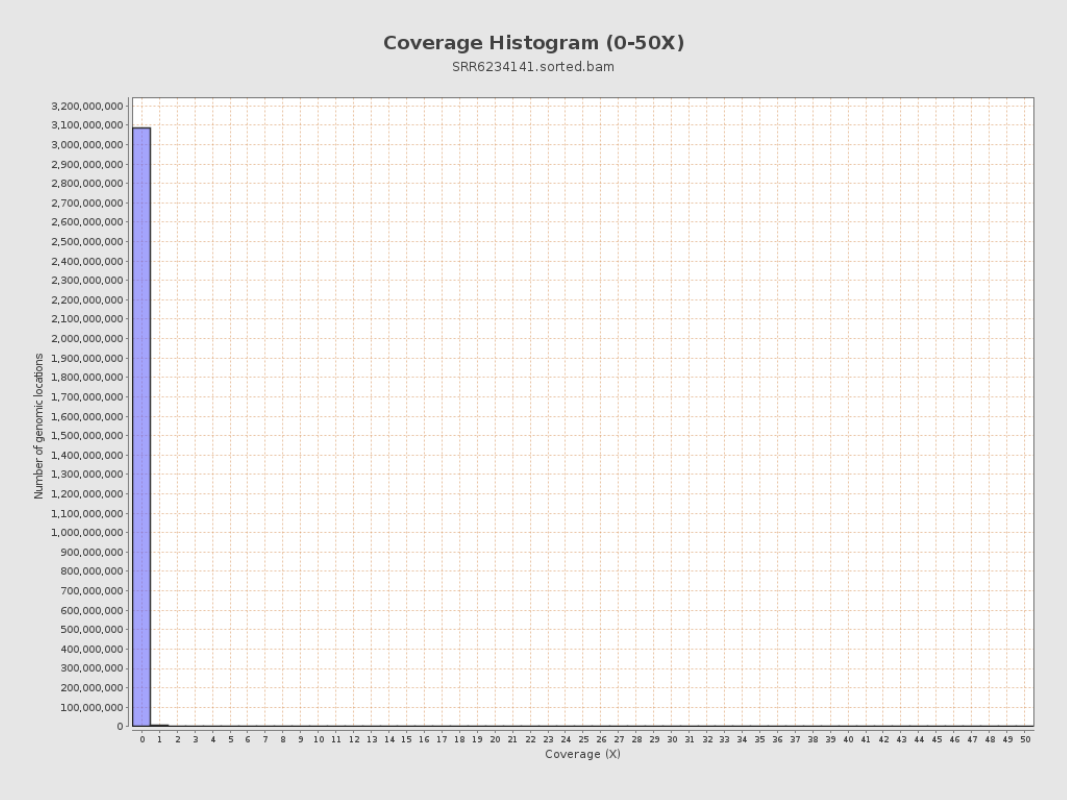
3. Results : Coverage across reference



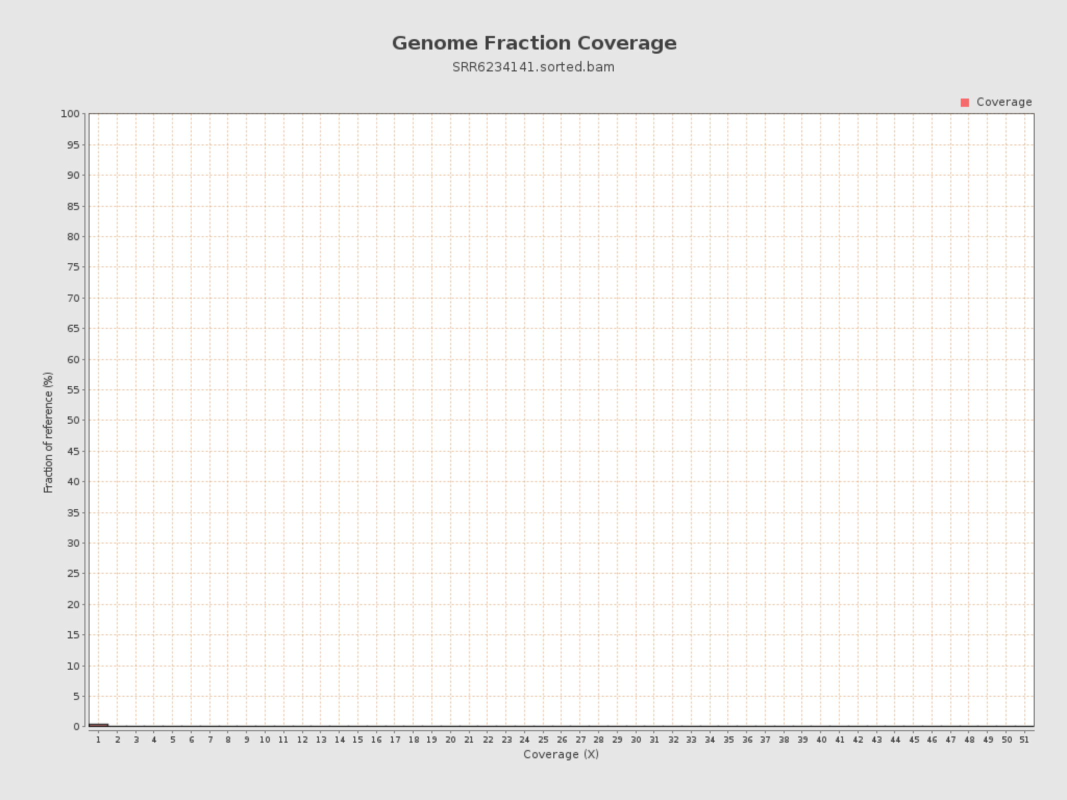
4. Results : Coverage Histogram



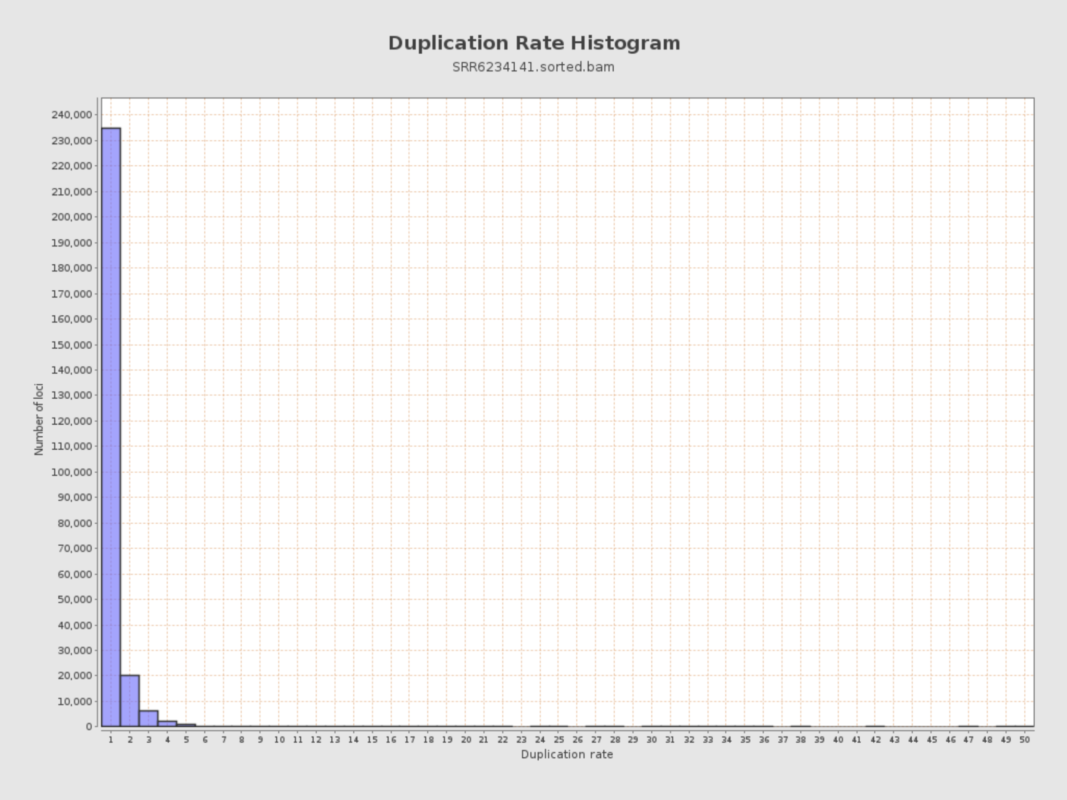
5. Results : Coverage Histogram (0-50X)



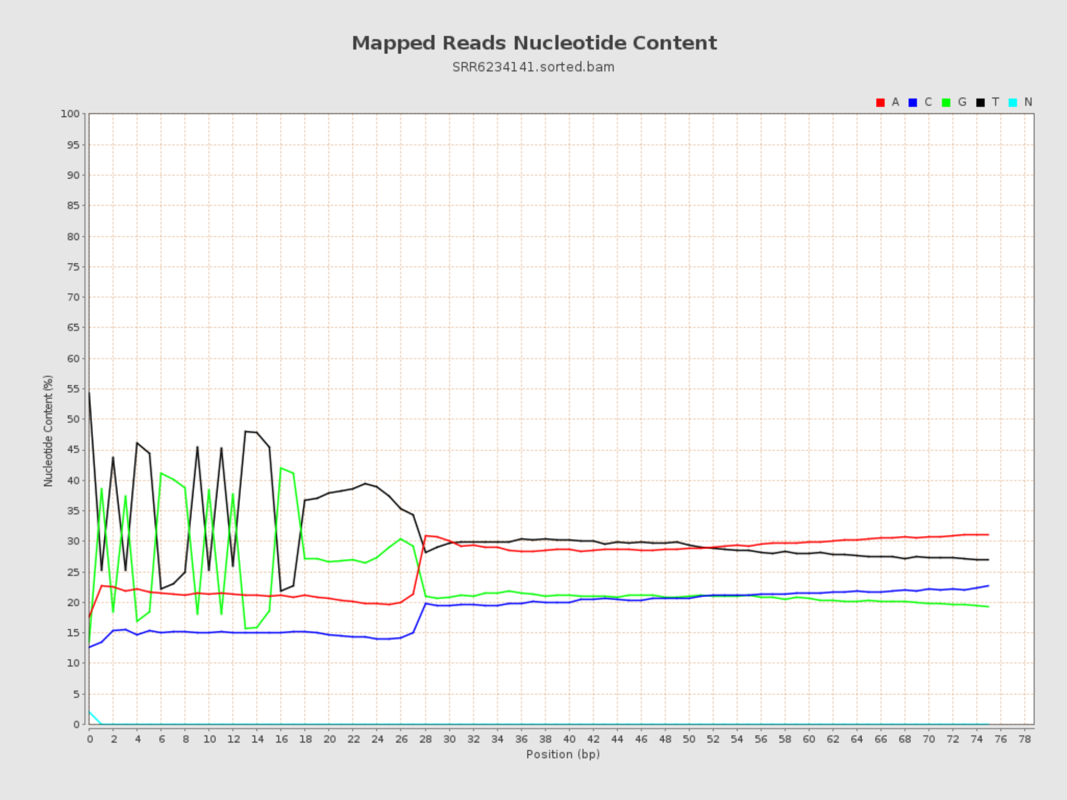
6. Results : Genome Fraction Coverage



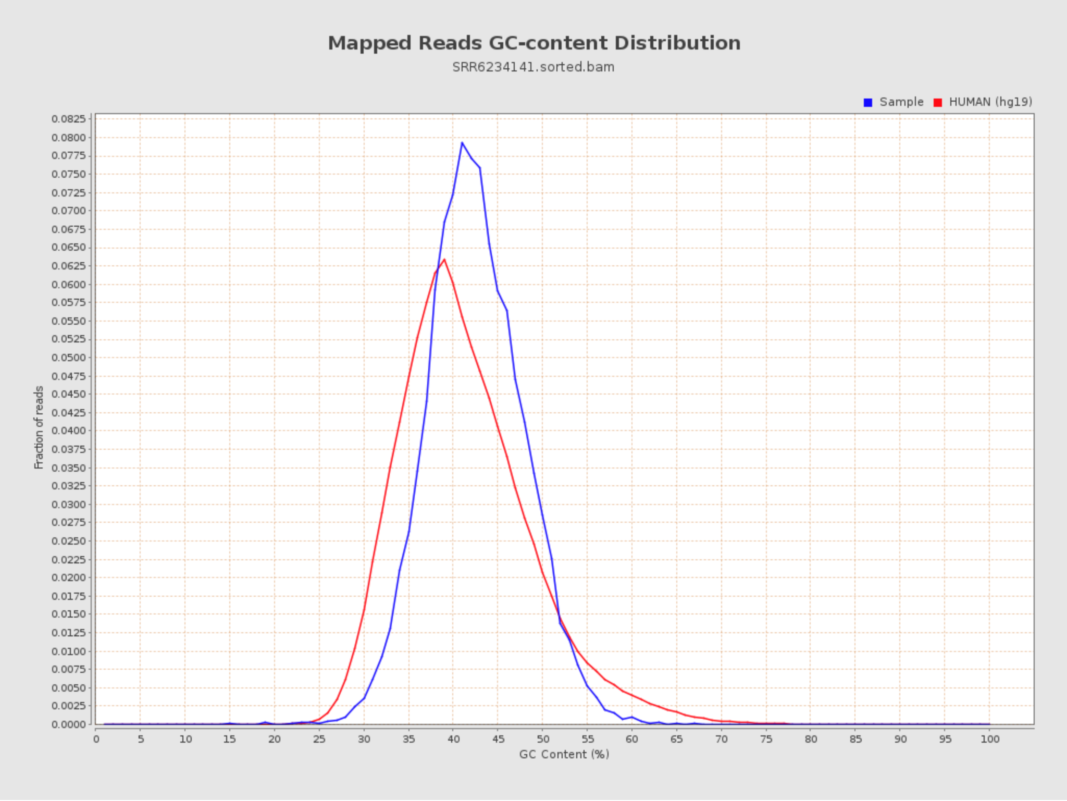
7. Results : Duplication Rate Histogram



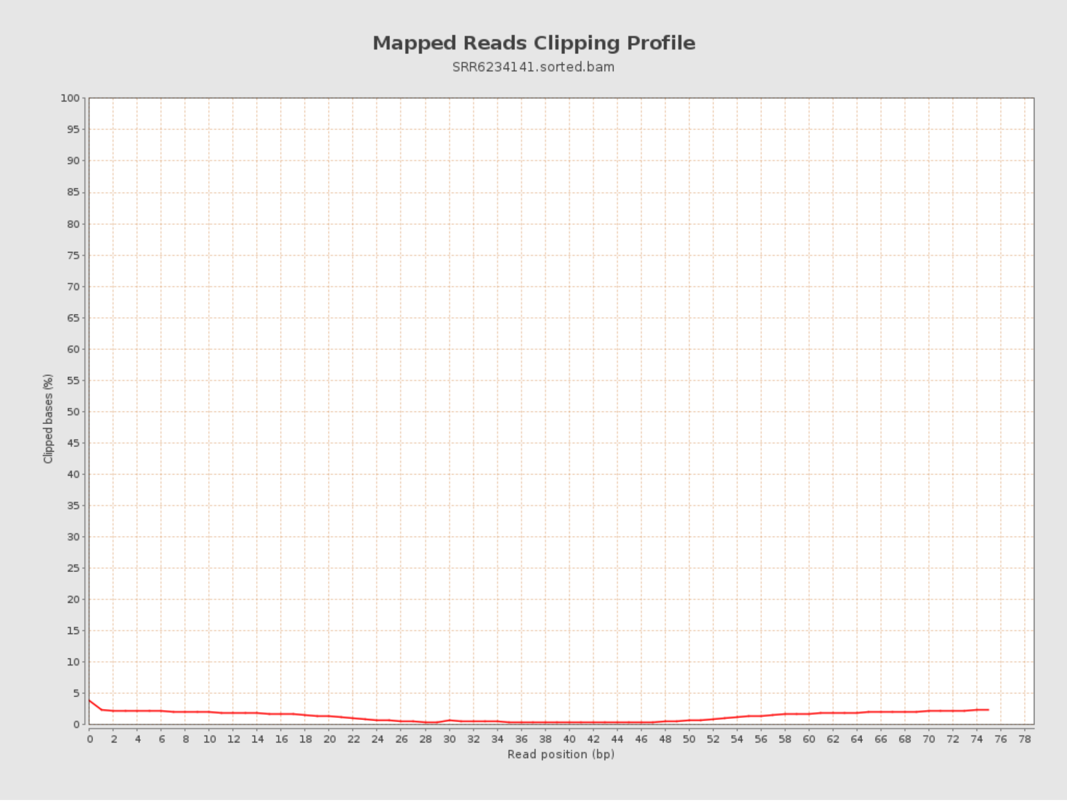
8. Results : Mapped Reads Nucleotide Content



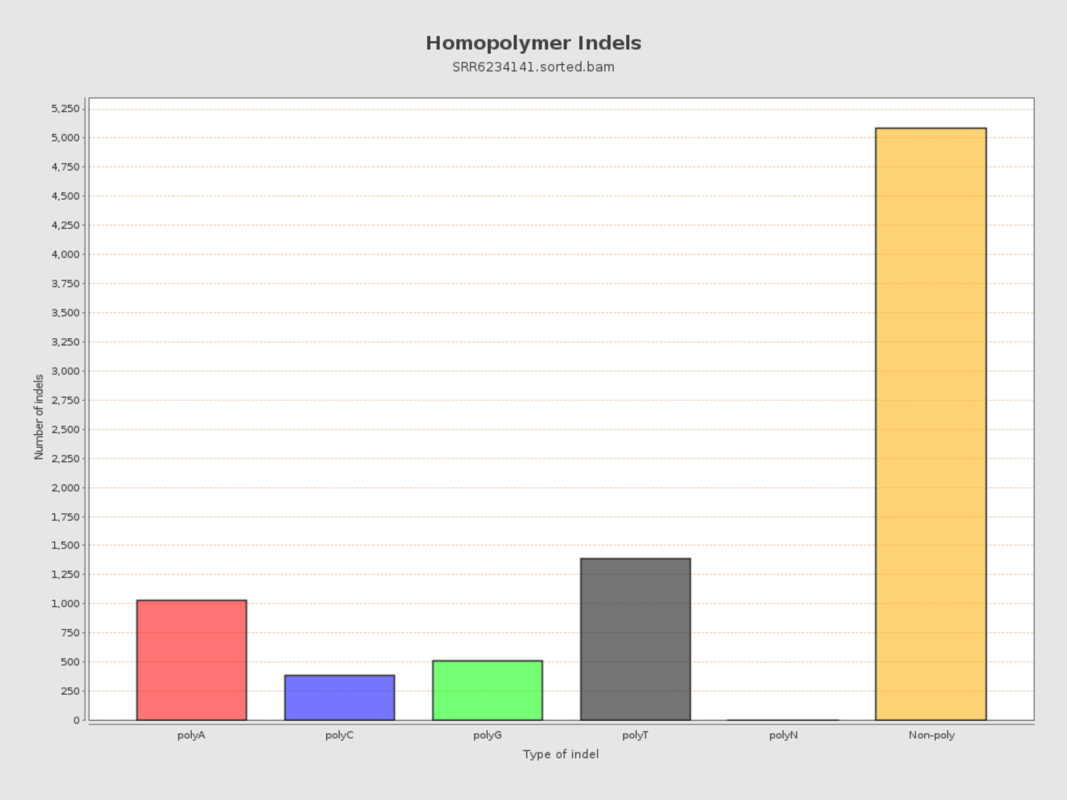
9. Results : Mapped Reads GC-content Distribution



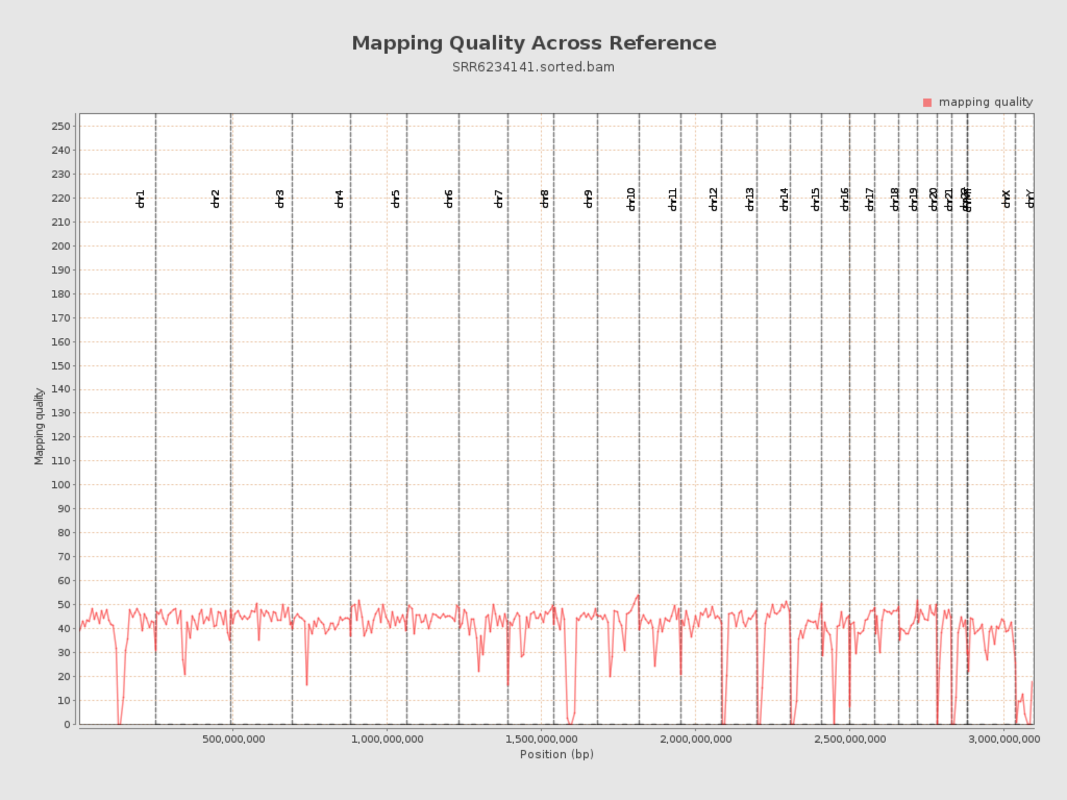
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram