Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:42:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234082.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_SRR6234082 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234082.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:42:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234082.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,076,777
Mapped reads	618,317 / 57.42%
Unmapped reads	458,460 / 42.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	3,069 / 0.29%
Read min/max/mean length	30 / 76 / 76.1
Duplicated reads (estimated)	20,347 / 1.89%
Duplication rate	2.6%
Clipped reads	330,825 / 30.72%

2.2. ACGT Content

Number/percentage of A's	11,144,898 / 28.18%
Number/percentage of C's	6,564,111 / 16.6%
Number/percentage of T's	12,892,179 / 32.6%
Number/percentage of G's	8,941,177 / 22.61%
Number/percentage of N's	9,805 / 0.02%
GC Percentage	39.2%

2.3. Coverage

Mean	0.0128

Standard Deviation	0.1661

2.4. Mapping Quality

Mean Mapping Quality	45.79

2.5. Mismatches and indels

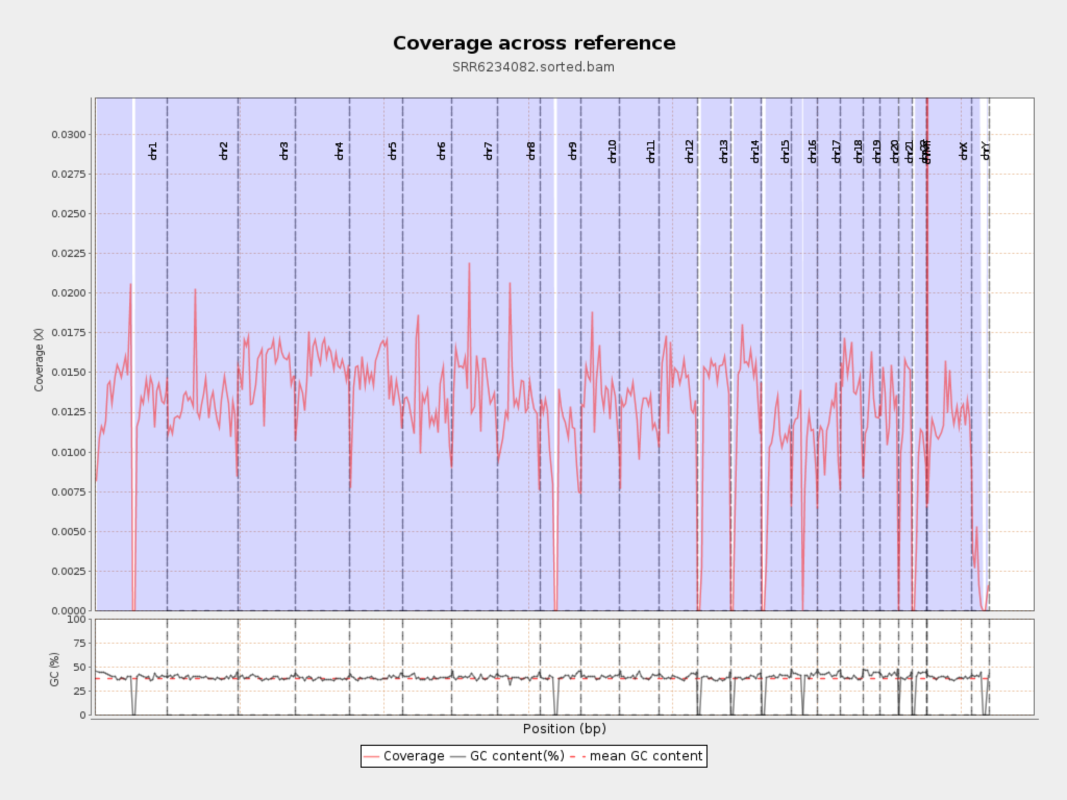
General error rate	1.08%
Mismatches	422,844
Insertions	3,465
Mapped reads with at least one insertion	0.55%
Deletions	13,697
Mapped reads with at least one deletion	2.18%
Homopolymer indels	45.8%

2.6. Chromosome stats

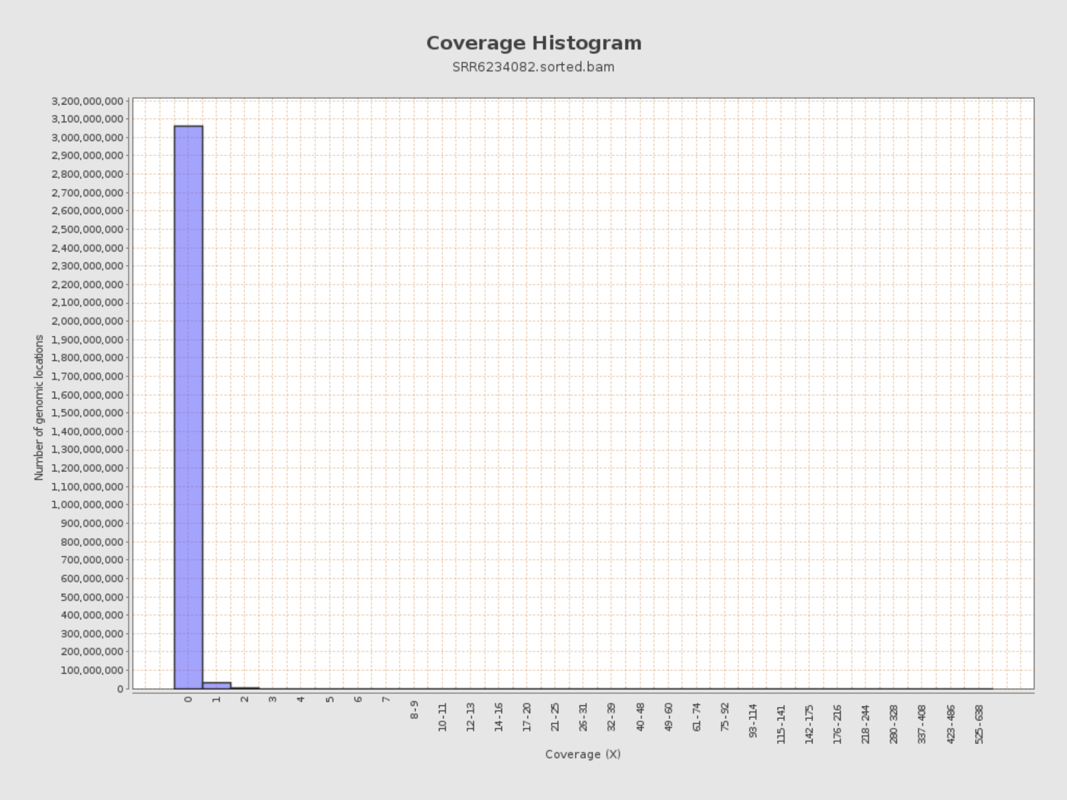
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	3191837	0.0128	0.2181
chr2	243199373	3143918	0.0129	0.1582
chr3	198022430	3075263	0.0155	0.1353
chr4	191154276	2926638	0.0153	0.1345
chr5	180915260	2661231	0.0147	0.13
chr6	171115067	2215981	0.013	0.1312
chr7	159138663	2321356	0.0146	0.1862

chr8	146364022	1892480	0.0129	0.3886
chr9	141213431	1444572	0.0102	0.1306
chr10	135534747	1880368	0.0139	0.1418
chr11	135006516	1702546	0.0126	0.1399
chr12	133851895	1931407	0.0144	0.1292
chr13	115169878	1441937	0.0125	0.1214
chr14	107349540	1348853	0.0126	0.1241
chr15	102531392	931057	0.0091	0.1036
chr16	90354753	902474	0.01	0.1104
chr17	81195210	919332	0.0113	0.117
chr18	78077248	1150774	0.0147	0.2293
chr19	59128983	752395	0.0127	0.1526
chr20	63025520	808553	0.0128	0.1247
chr21	48129895	574980	0.0119	0.1191
chr22	51304566	363526	0.0071	0.0897
chrMT	16571	15259	0.9208	1.2279
chrX	155270560	1870201	0.012	0.1209
chrY	59373566	108905	0.0018	0.0522

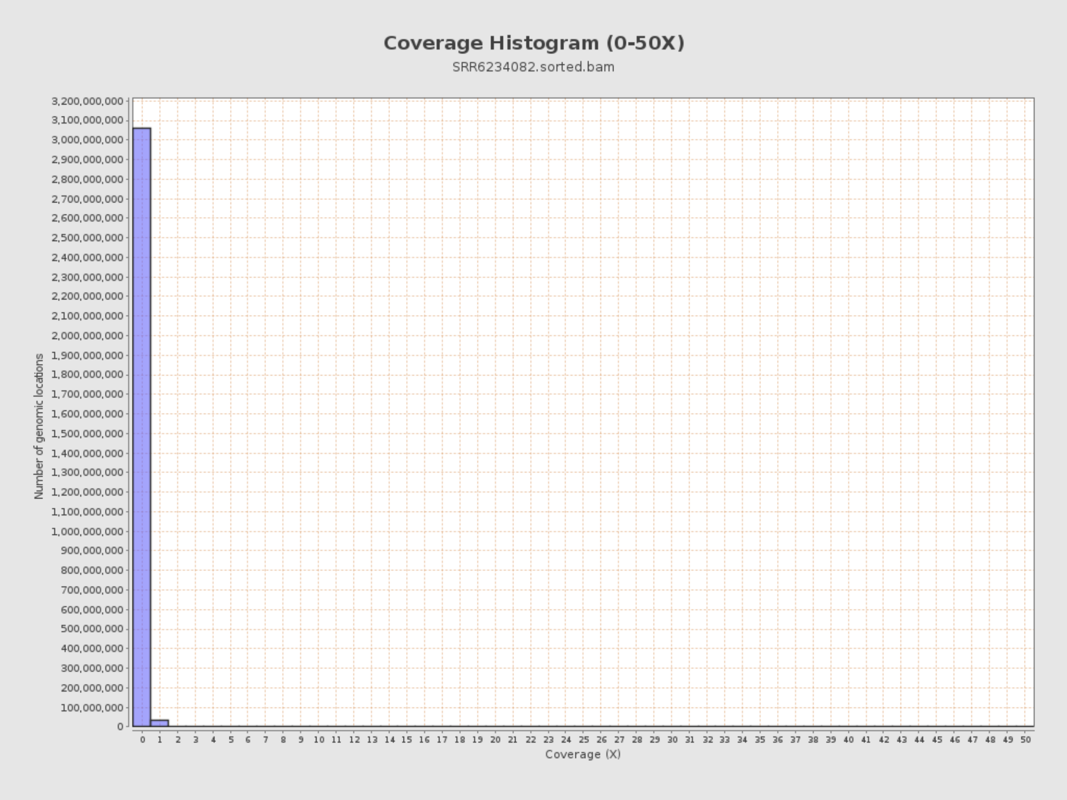
3. Results : Coverage across reference



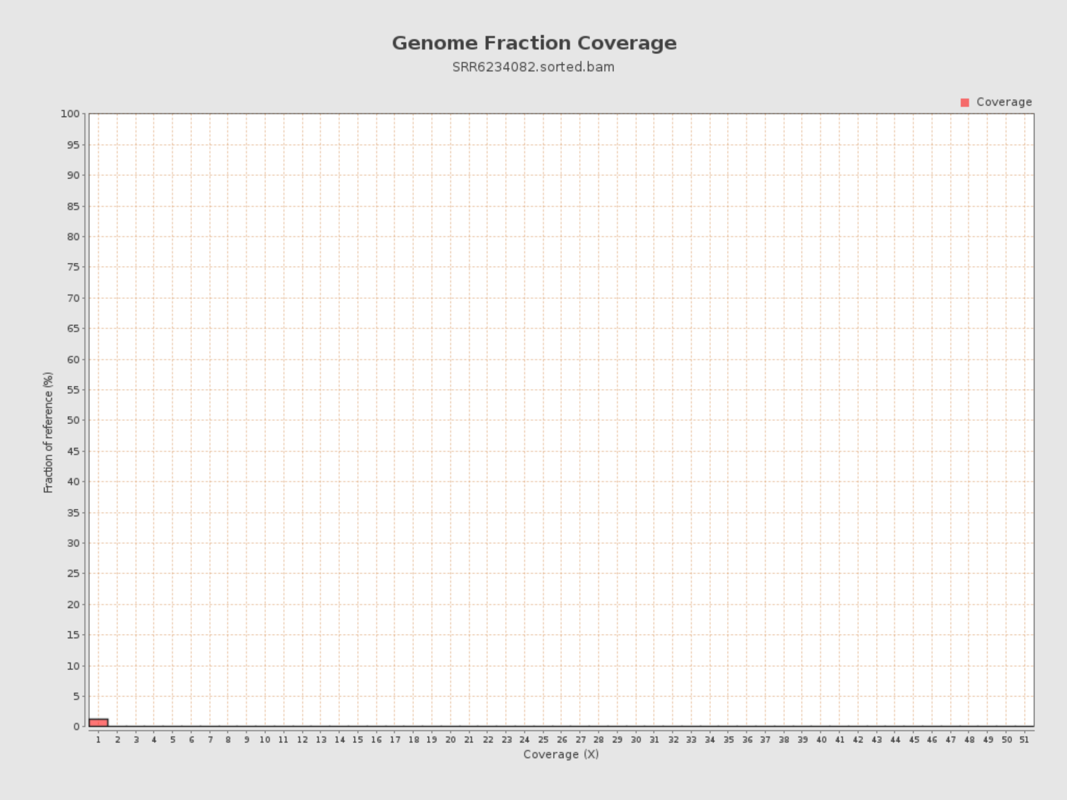
4. Results : Coverage Histogram



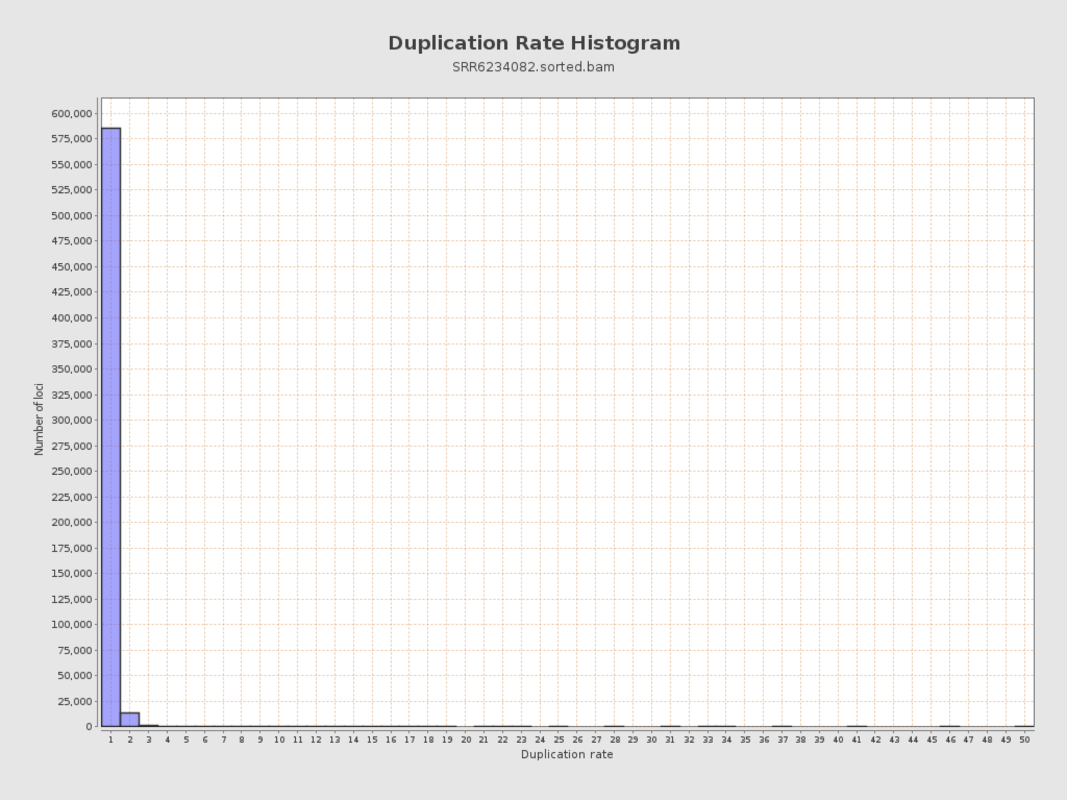
5. Results : Coverage Histogram (0-50X)



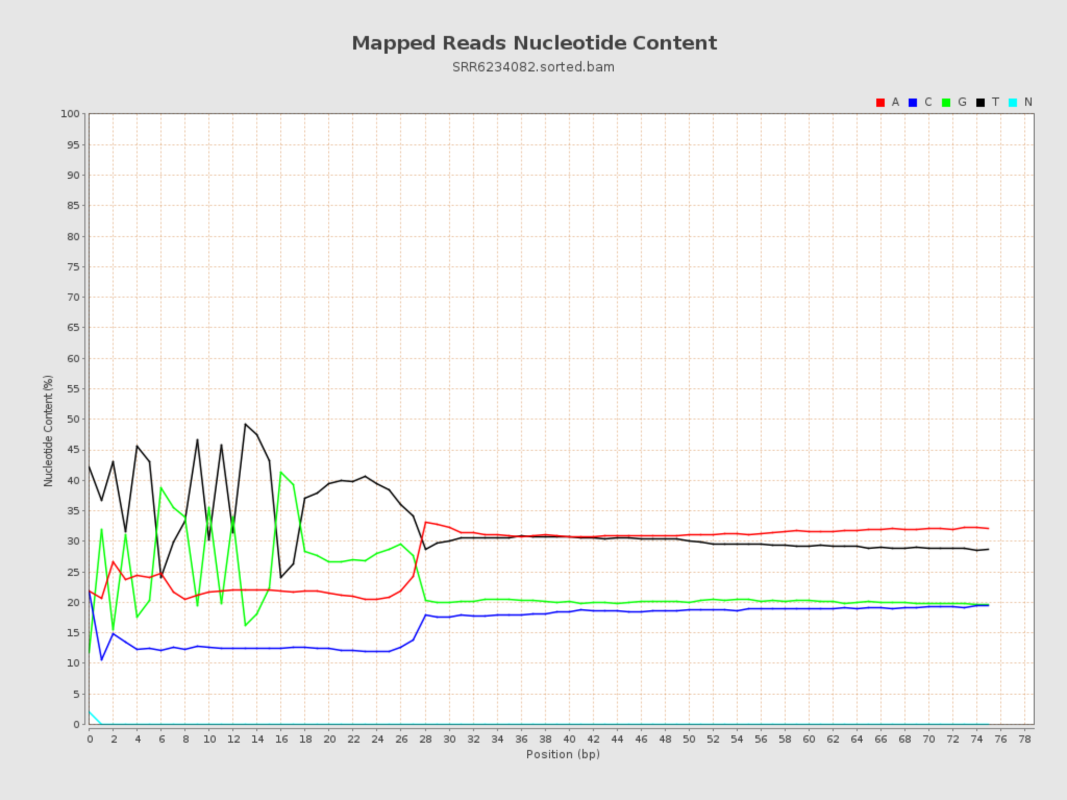
6. Results : Genome Fraction Coverage



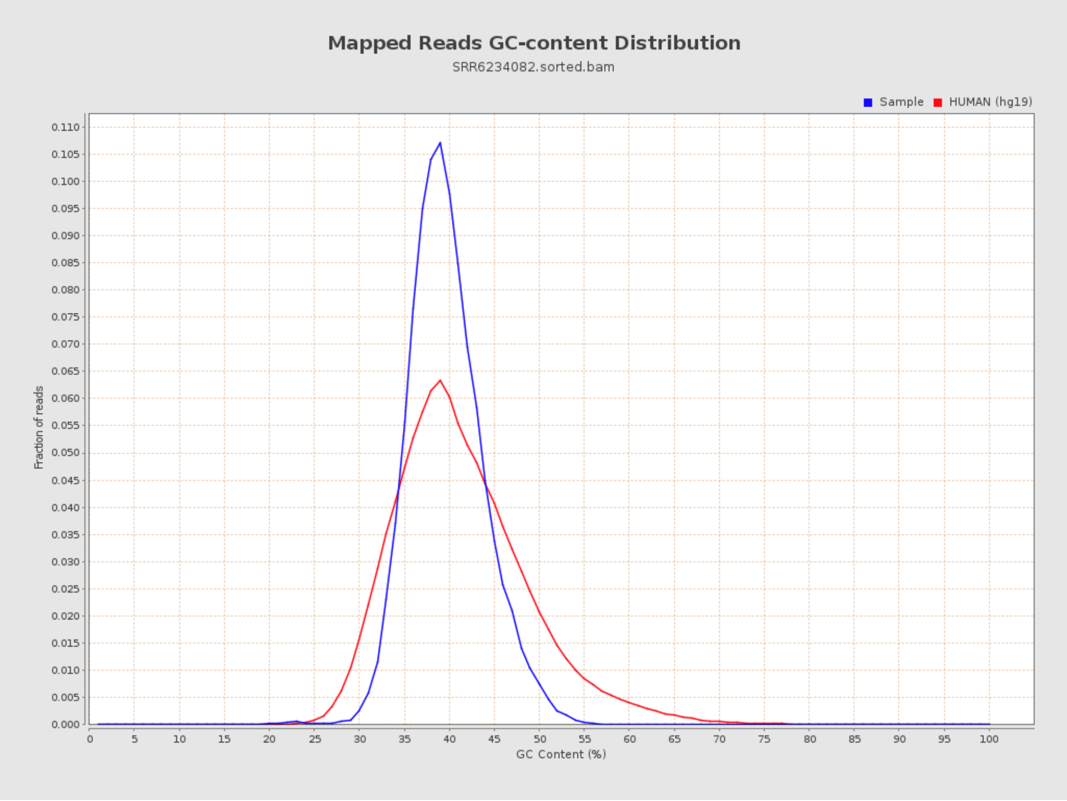
7. Results : Duplication Rate Histogram



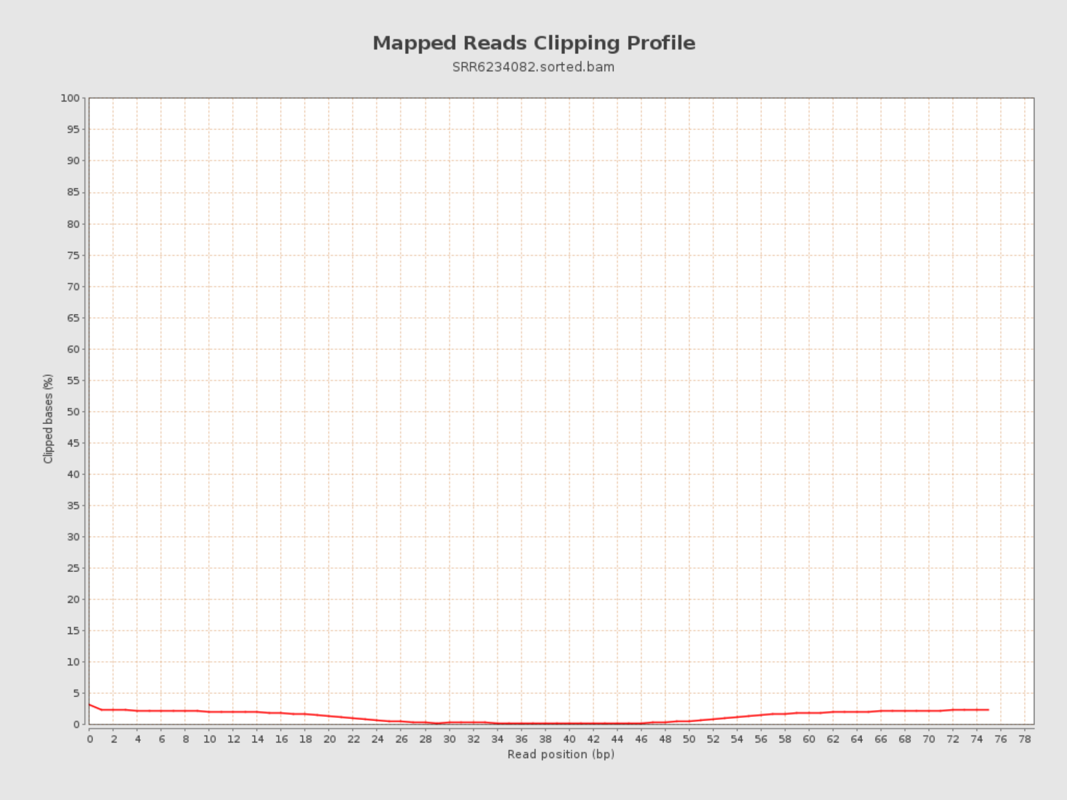
8. Results : Mapped Reads Nucleotide Content



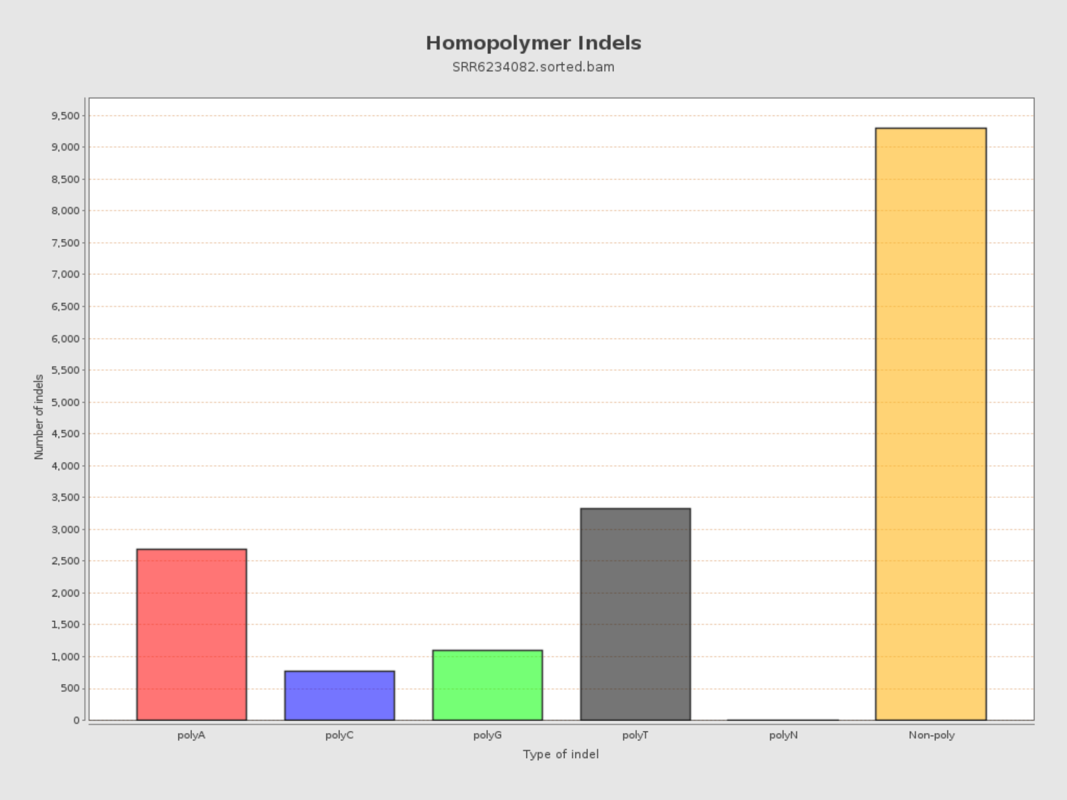
9. Results : Mapped Reads GC-content Distribution



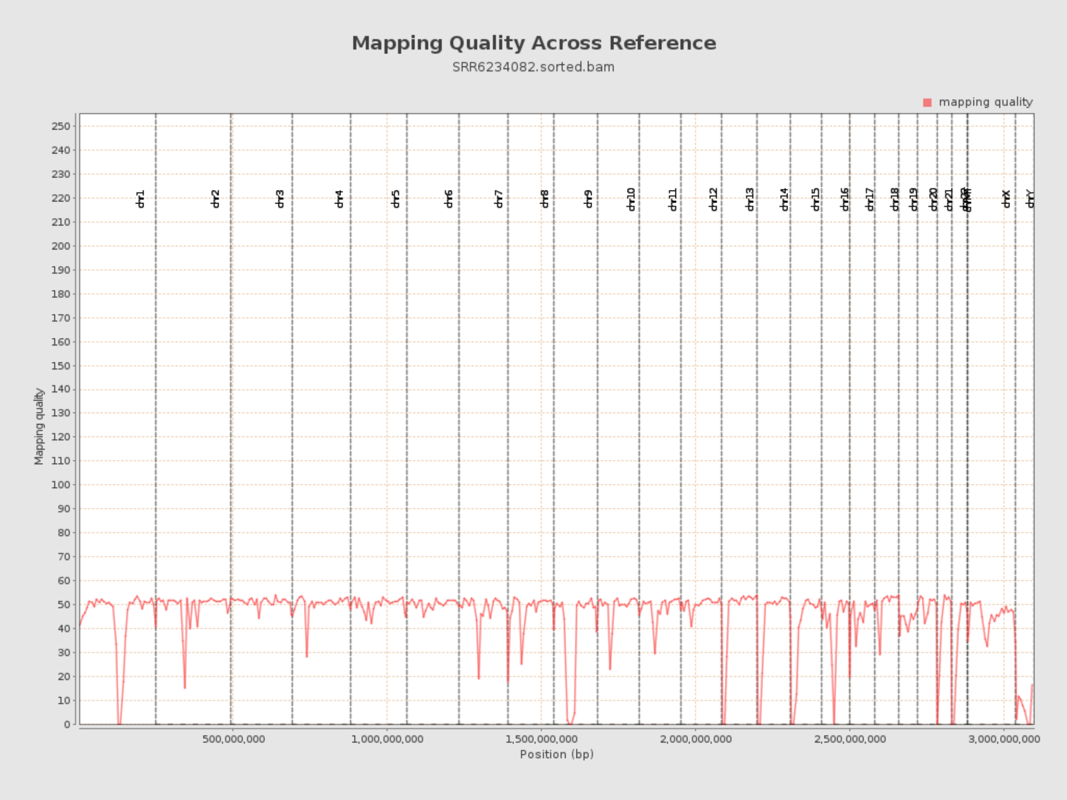
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram