Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 18:31:12

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234145.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_SRR6234145 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234145.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 18:31:11 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234145.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,165,844
Mapped reads	817,784 / 37.76%
Unmapped reads	1,348,060 / 62.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,054 / 0.37%
Read min/max/mean length	30 / 76 / 76.13
Duplicated reads (estimated)	115,579 / 5.34%
Duplication rate	10.31%
Clipped reads	384,378 / 17.75%

2.2. ACGT Content

Number/percentage of A's	15,182,563 / 28.43%
Number/percentage of C's	9,393,705 / 17.59%
Number/percentage of T's	17,495,357 / 32.76%
Number/percentage of G's	11,322,121 / 21.2%
Number/percentage of N's	8,440 / 0.02%
GC Percentage	38.79%

2.3. Coverage

Mean	0.0173

Standard Deviation	0.2811

2.4. Mapping Quality

Mean Mapping Quality	45.74

2.5. Mismatches and indels

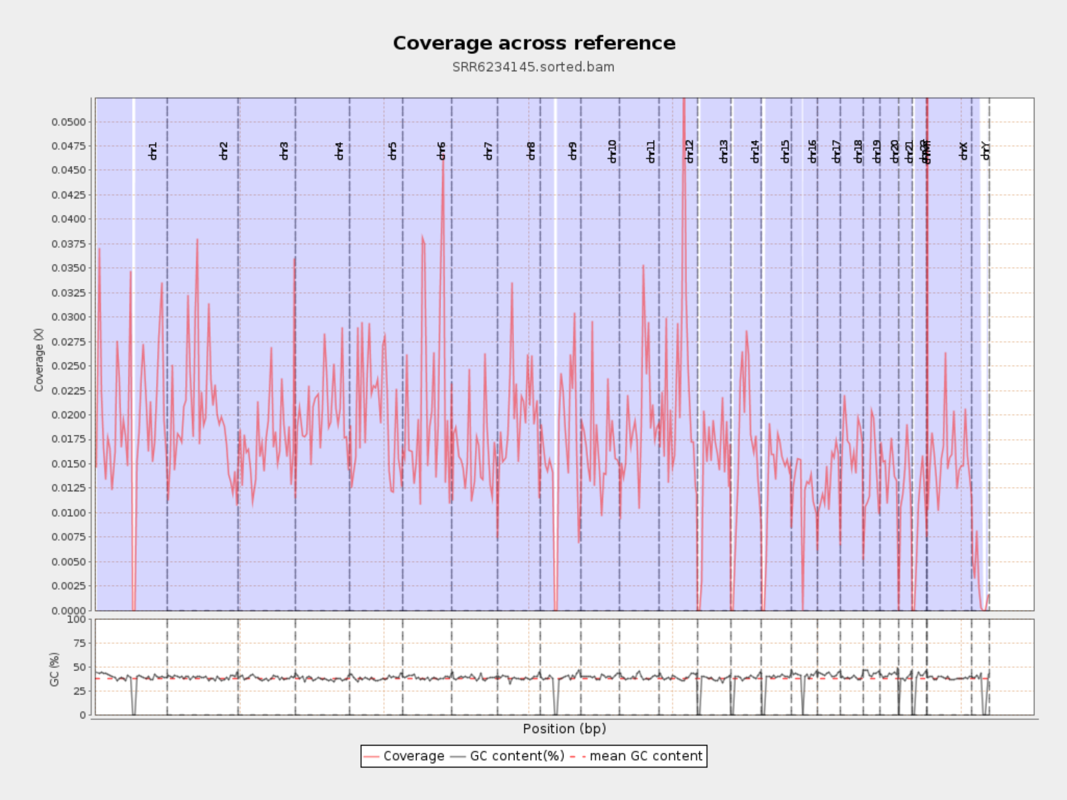
General error rate	0.79%
Mismatches	412,163
Insertions	5,221
Mapped reads with at least one insertion	0.63%
Deletions	13,539
Mapped reads with at least one deletion	1.63%
Homopolymer indels	44.62%

2.6. Chromosome stats

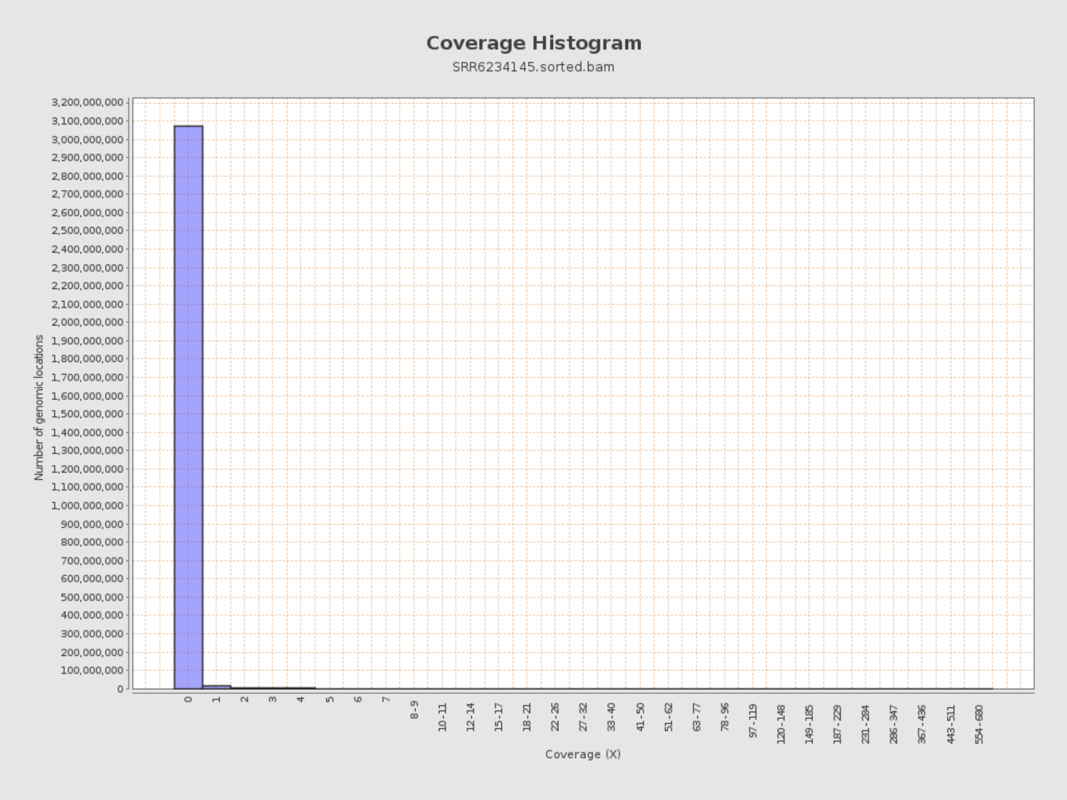
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	4791559	0.0192	0.3666
chr2	243199373	4911824	0.0202	0.2922
chr3	198022430	3401978	0.0172	0.2434
chr4	191154276	3837870	0.0201	0.2693
chr5	180915260	3658386	0.0202	0.2725
chr6	171115067	3600128	0.021	0.2766
chr7	159138663	2543013	0.016	0.2714

chr8	146364022	2953082	0.0202	0.4742
chr9	141213431	2312875	0.0164	0.2548
chr10	135534747	2268226	0.0167	0.265
chr11	135006516	2604733	0.0193	0.2703
chr12	133851895	3051047	0.0228	0.2905
chr13	115169878	1643796	0.0143	0.2426
chr14	107349540	1714054	0.016	0.2441
chr15	102531392	1322812	0.0129	0.2076
chr16	90354753	1060560	0.0117	0.1951
chr17	81195210	1063678	0.0131	0.2085
chr18	78077248	1343438	0.0172	0.349
chr19	59128983	806448	0.0136	0.2725
chr20	63025520	899635	0.0143	0.2122
chr21	48129895	580635	0.0121	0.202
chr22	51304566	441541	0.0086	0.1681
chrMT	16571	20402	1.2312	1.933
chrX	155270560	2446488	0.0158	0.2349
chrY	59373566	147930	0.0025	0.0836

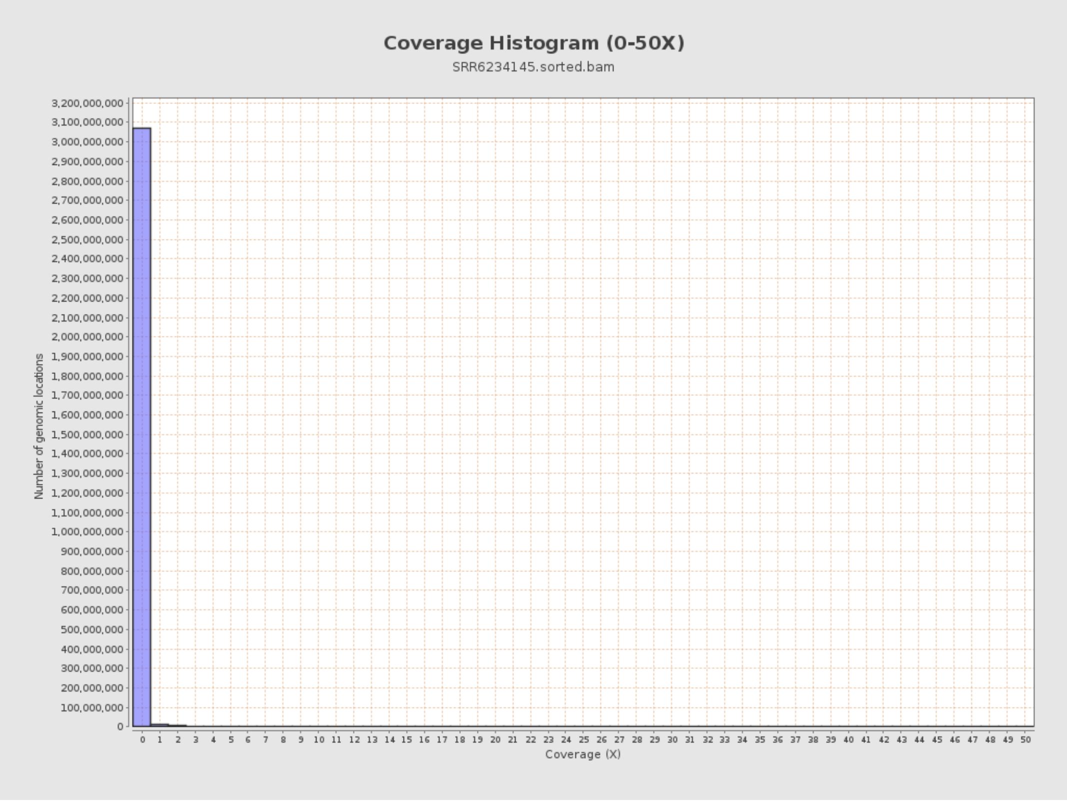
3. Results : Coverage across reference



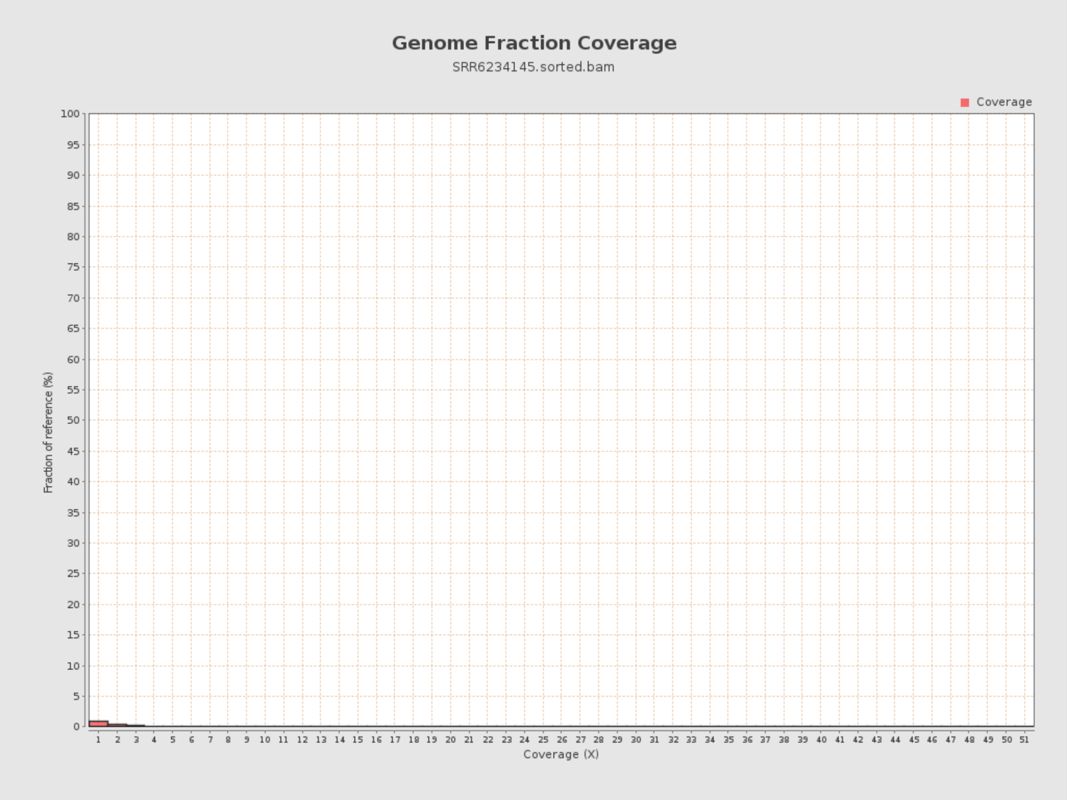
4. Results : Coverage Histogram



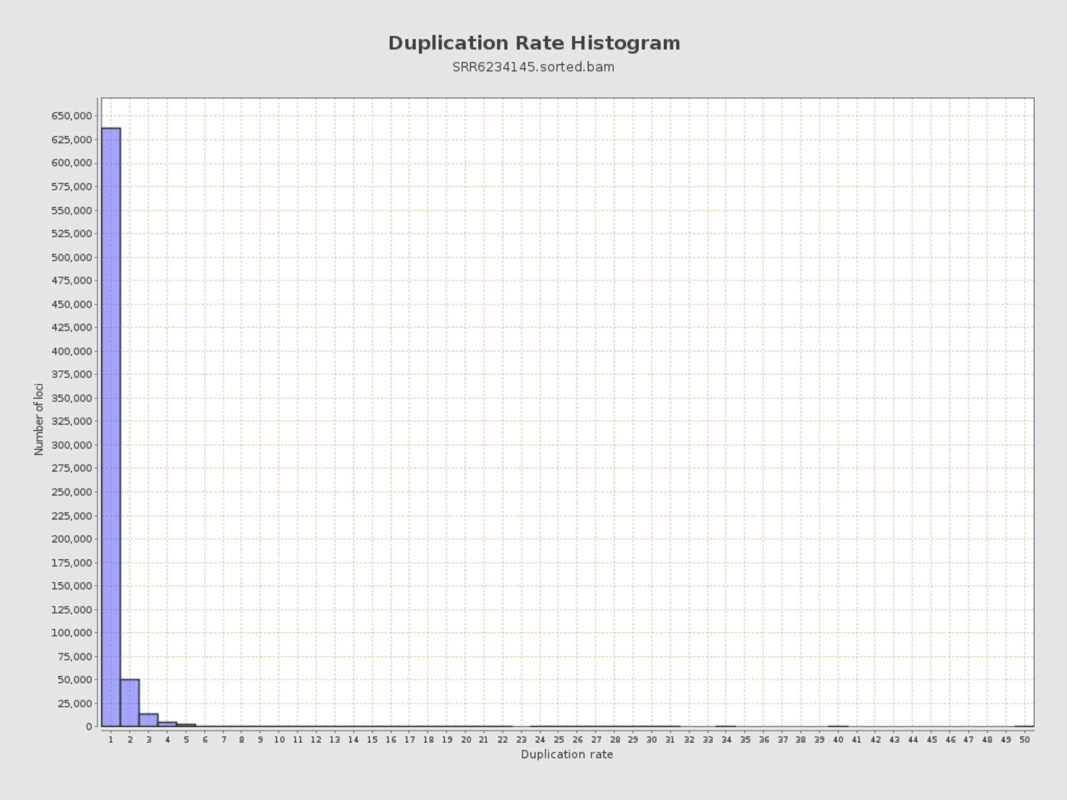
5. Results : Coverage Histogram (0-50X)



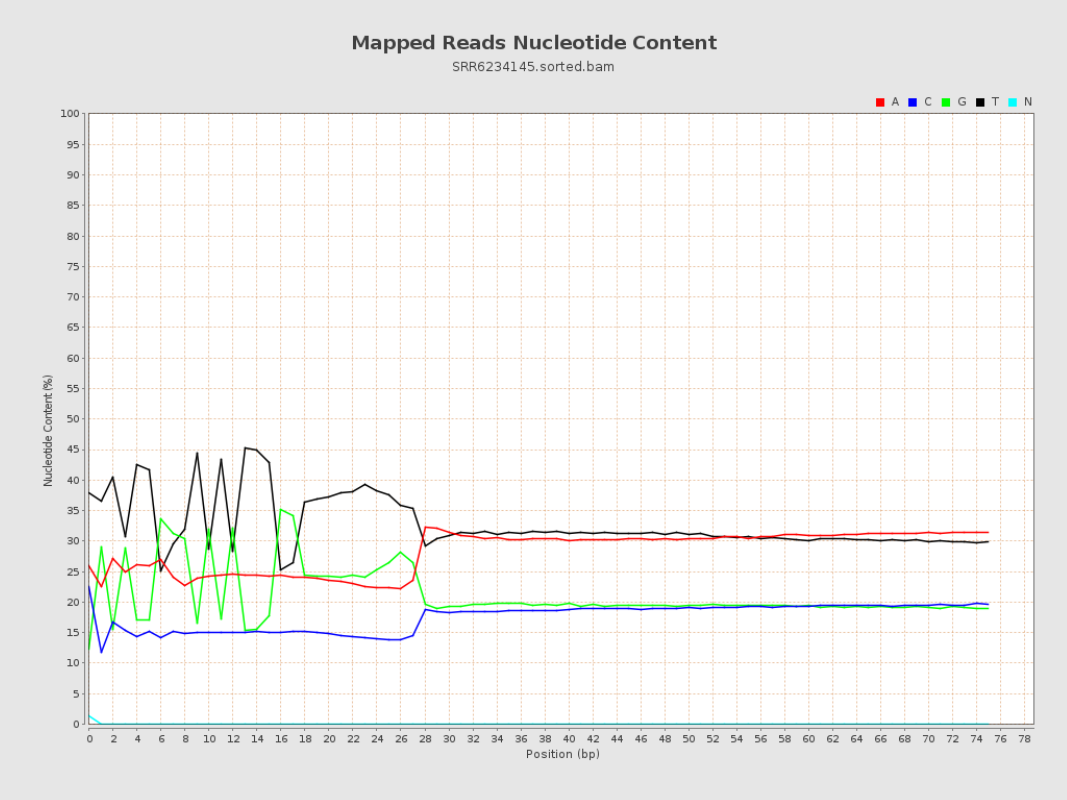
6. Results : Genome Fraction Coverage



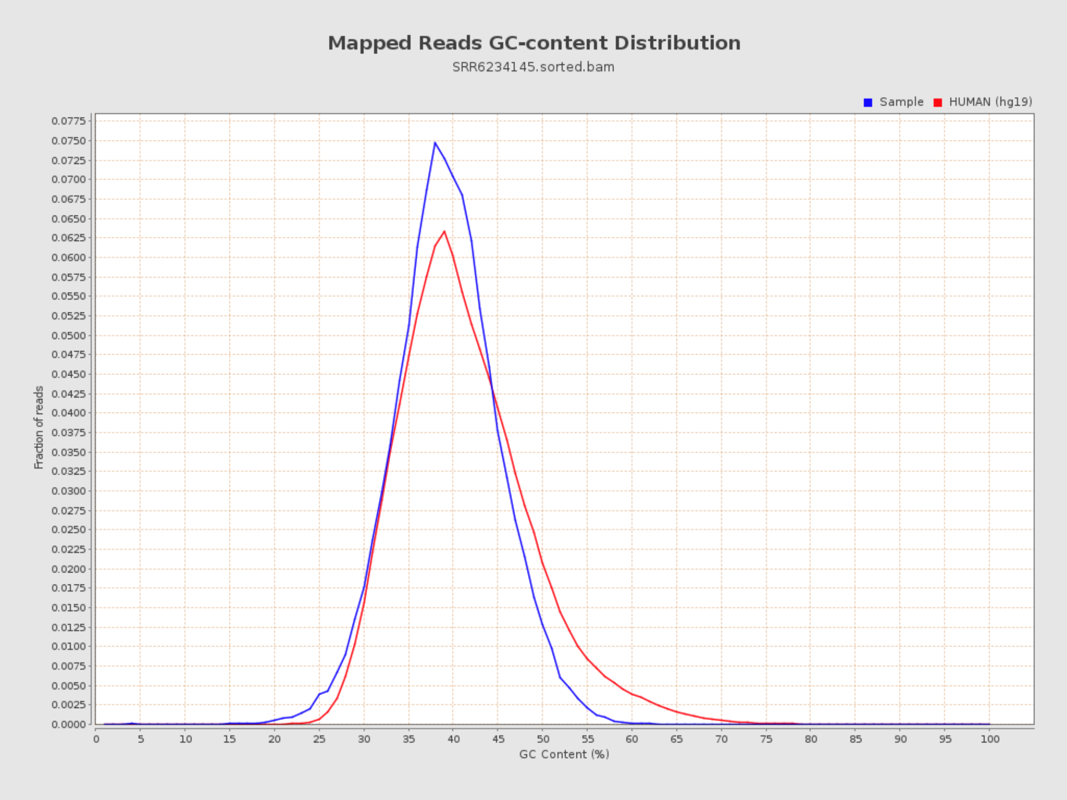
7. Results : Duplication Rate Histogram



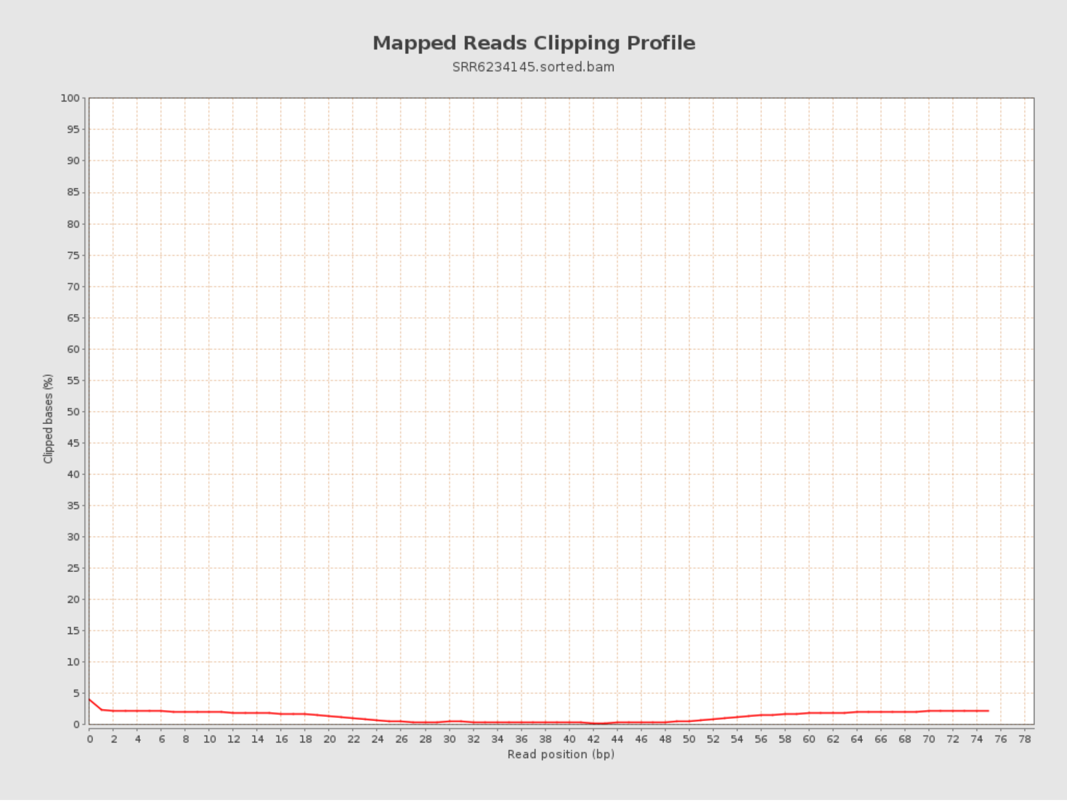
8. Results : Mapped Reads Nucleotide Content



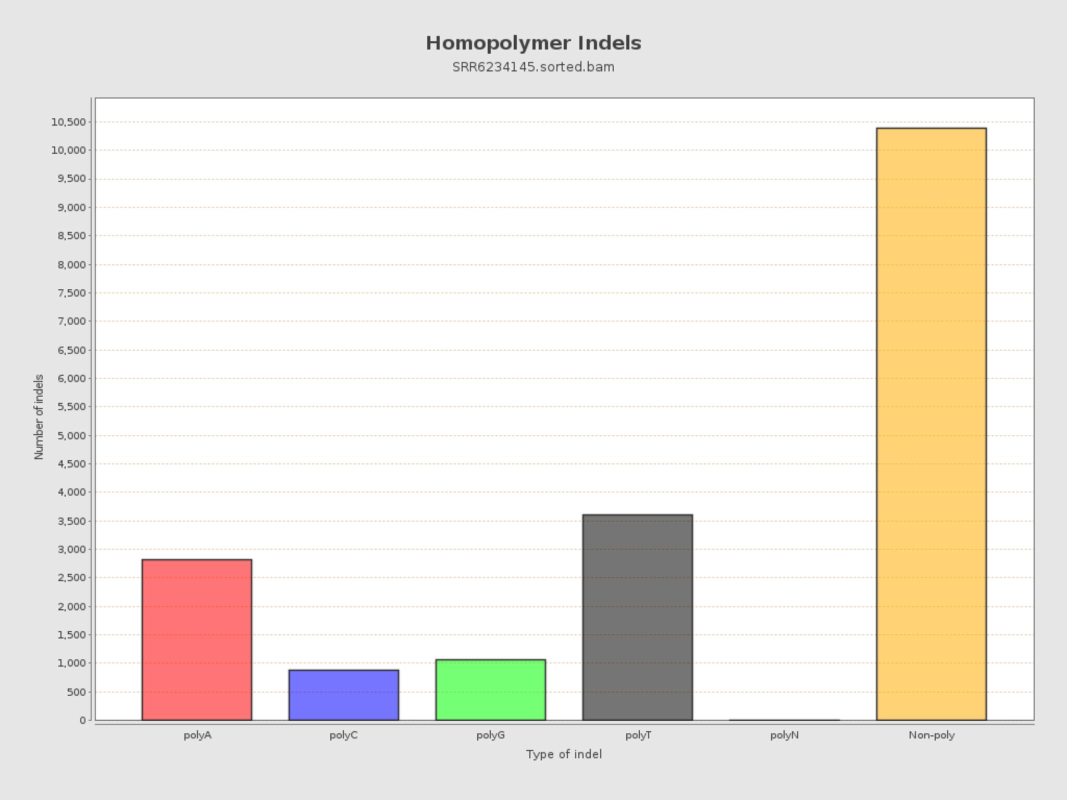
9. Results : Mapped Reads GC-content Distribution



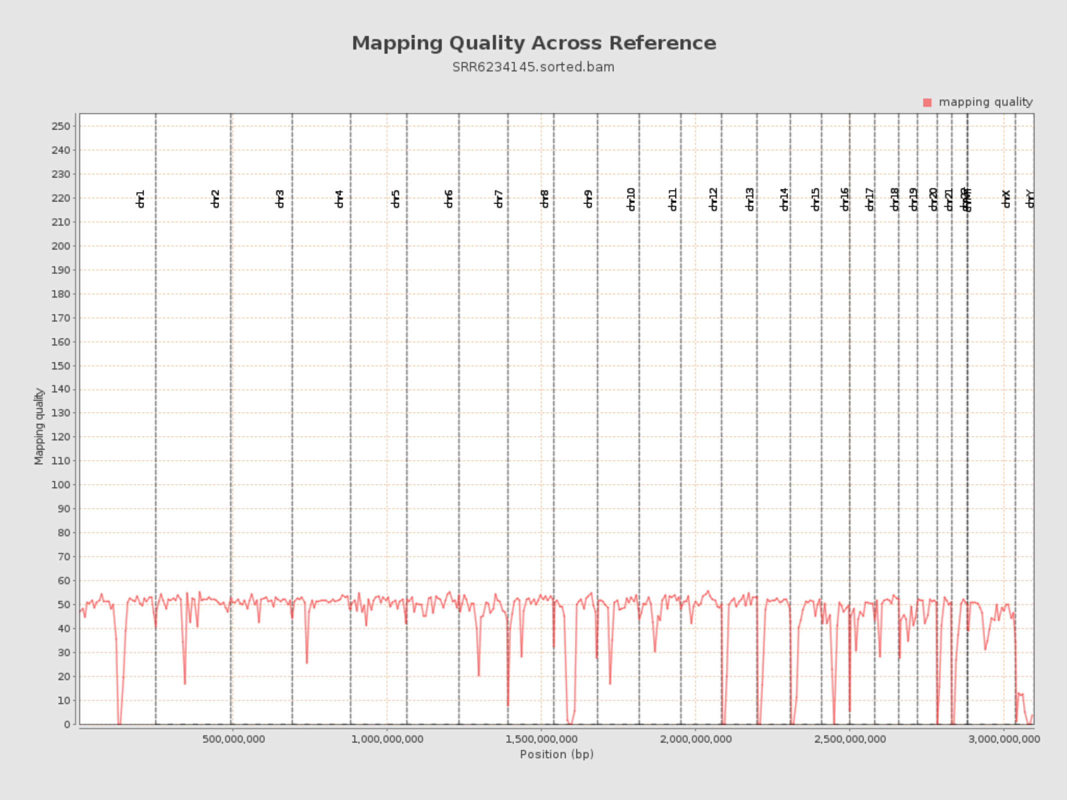
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram