Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:17:13

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234049.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_SRR6234049 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234049.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:17:12 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234049.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,100,630
Mapped reads	1,965,563 / 93.57%
Unmapped reads	135,067 / 6.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,560 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	141,106 / 6.72%
Duplication rate	5.51%
Clipped reads	826,836 / 39.36%

2.2. ACGT Content

Number/percentage of A's	36,235,945 / 27.33%
Number/percentage of C's	25,111,995 / 18.94%
Number/percentage of T's	41,224,456 / 31.09%
Number/percentage of G's	30,012,965 / 22.63%
Number/percentage of N's	11,795 / 0.01%
GC Percentage	41.57%

2.3. Coverage

Mean	0.0429

Standard Deviation	0.5862

2.4. Mapping Quality

Mean Mapping Quality	42.97

2.5. Mismatches and indels

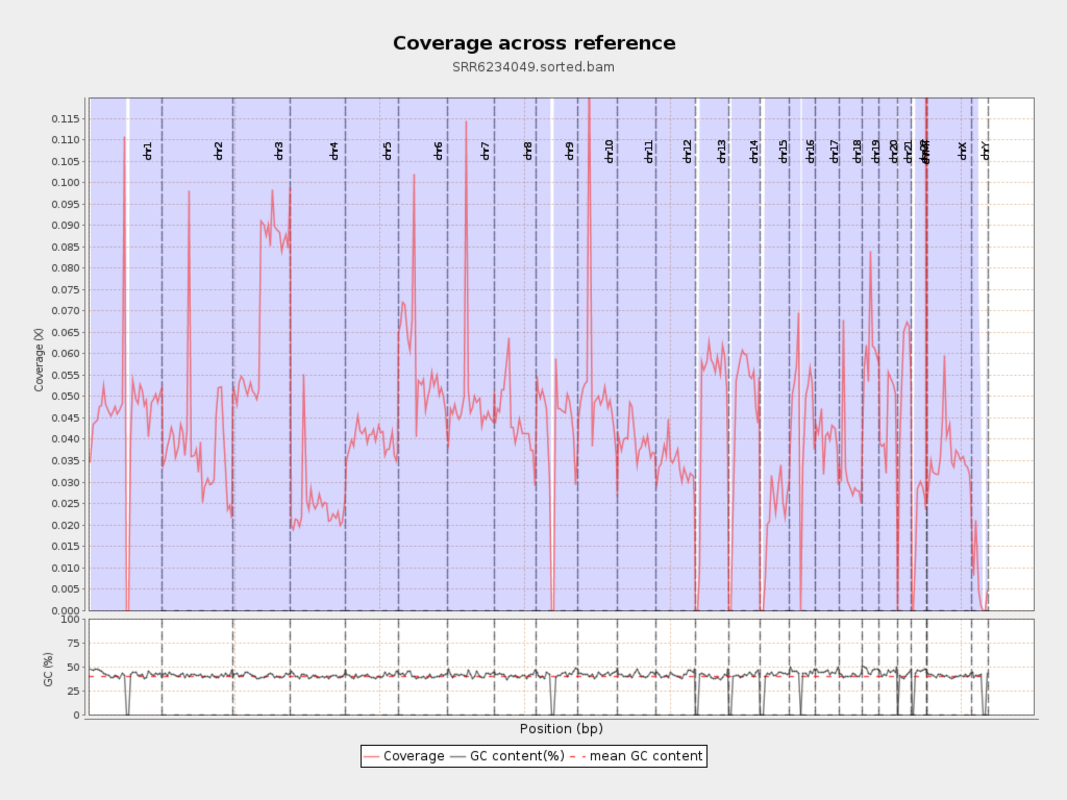
General error rate	0.81%
Mismatches	1,054,784
Insertions	12,031
Mapped reads with at least one insertion	0.61%
Deletions	39,824
Mapped reads with at least one deletion	2%
Homopolymer indels	44.14%

2.6. Chromosome stats

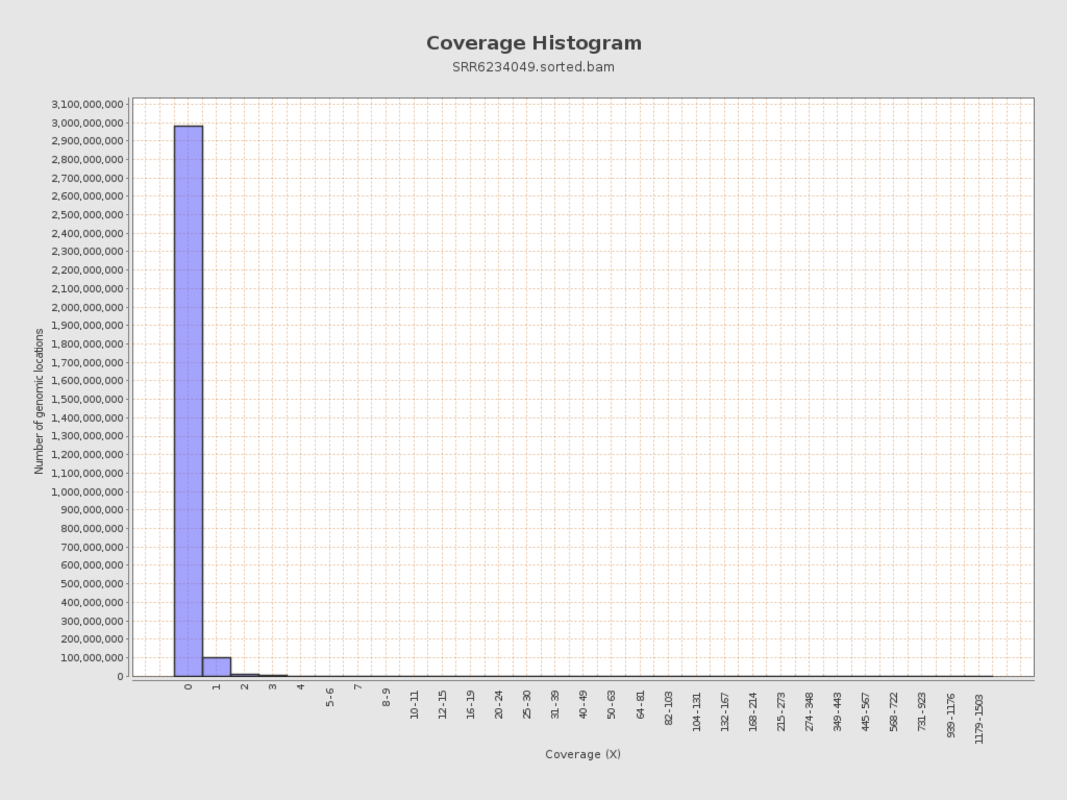
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11562723	0.0464	1.3174
chr2	243199373	9315180	0.0383	0.5833
chr3	198022430	14033506	0.0709	0.3127
chr4	191154276	4635970	0.0243	0.2118
chr5	180915260	7222439	0.0399	0.2286
chr6	171115067	9890406	0.0578	0.4609
chr7	159138663	7939773	0.0499	0.8454

chr8	146364022	6511533	0.0445	0.6188
chr9	141213431	5832359	0.0413	0.4327
chr10	135534747	7134774	0.0526	0.7292
chr11	135006516	5308841	0.0393	0.3818
chr12	133851895	4559683	0.0341	0.2186
chr13	115169878	5523315	0.048	0.2479
chr14	107349540	4920012	0.0458	0.2889
chr15	102531392	2167877	0.0211	0.1747
chr16	90354753	4190873	0.0464	0.3177
chr17	81195210	3274812	0.0403	0.2737
chr18	78077248	2572382	0.0329	1.0253
chr19	59128983	3624865	0.0613	0.8173
chr20	63025520	2824549	0.0448	0.2652
chr21	48129895	2504975	0.052	0.2825
chr22	51304566	1021307	0.0199	0.1537
chrMT	16571	112984	6.8182	5.1091
chrX	155270560	5610919	0.0361	0.2777
chrY	59373566	370397	0.0062	0.1545

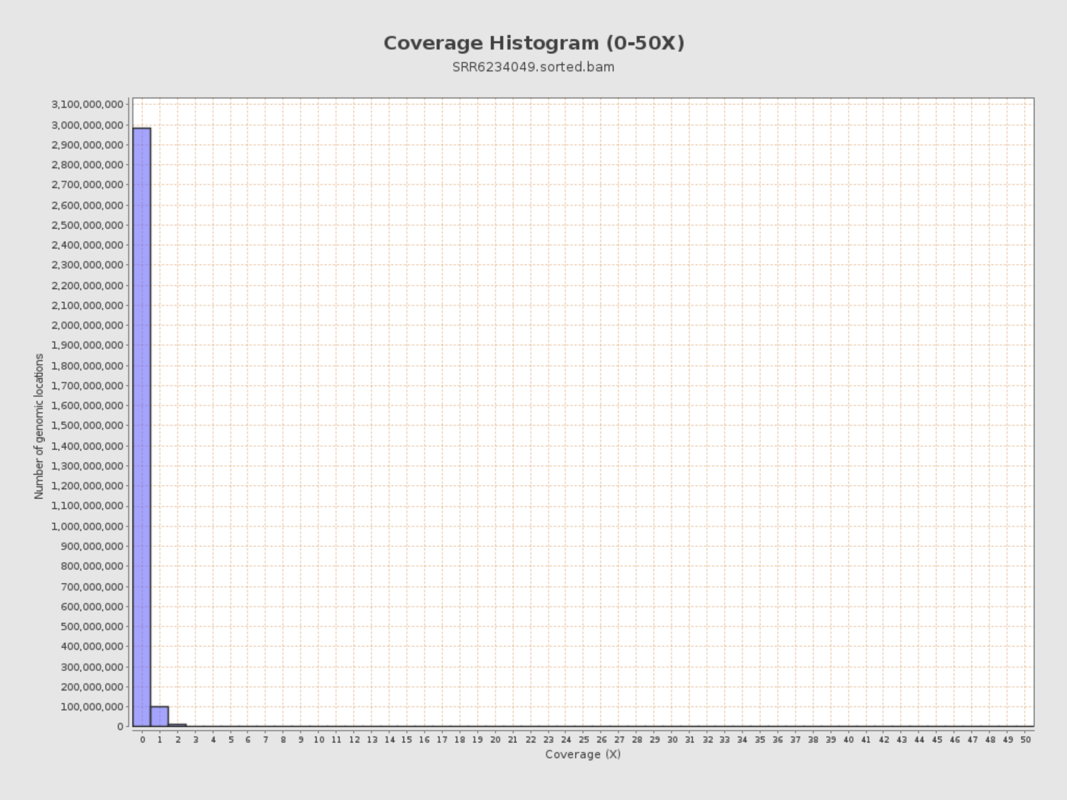
3. Results : Coverage across reference



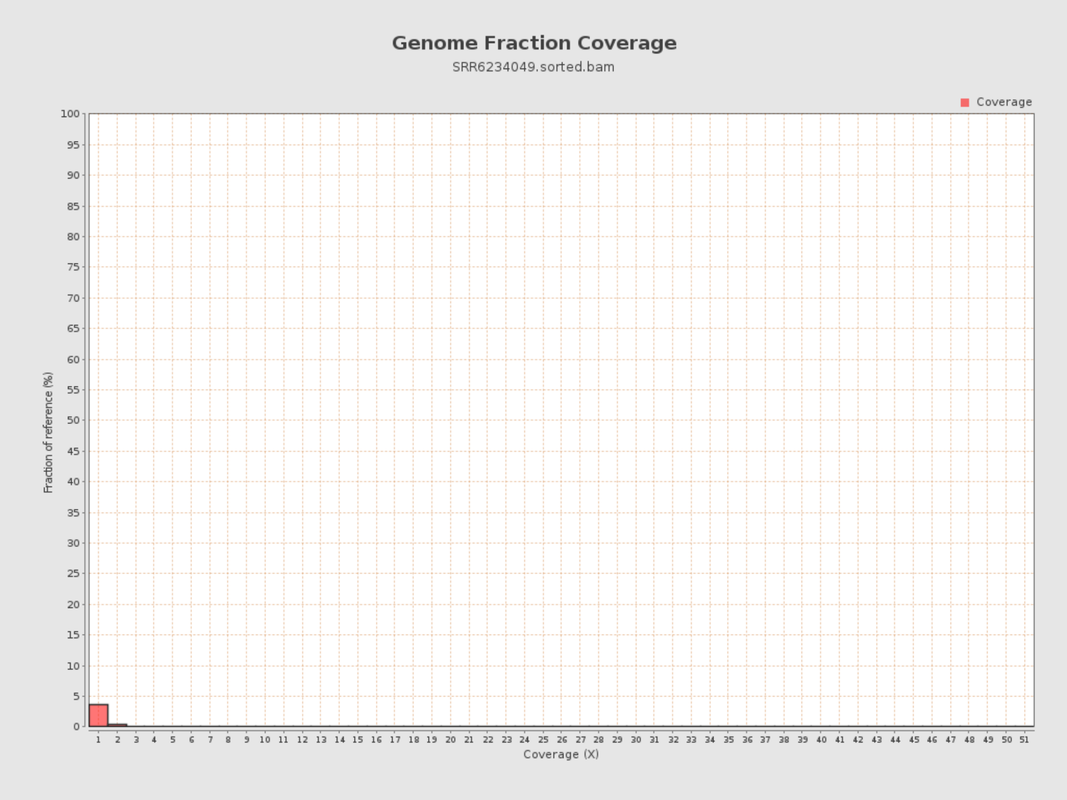
4. Results : Coverage Histogram



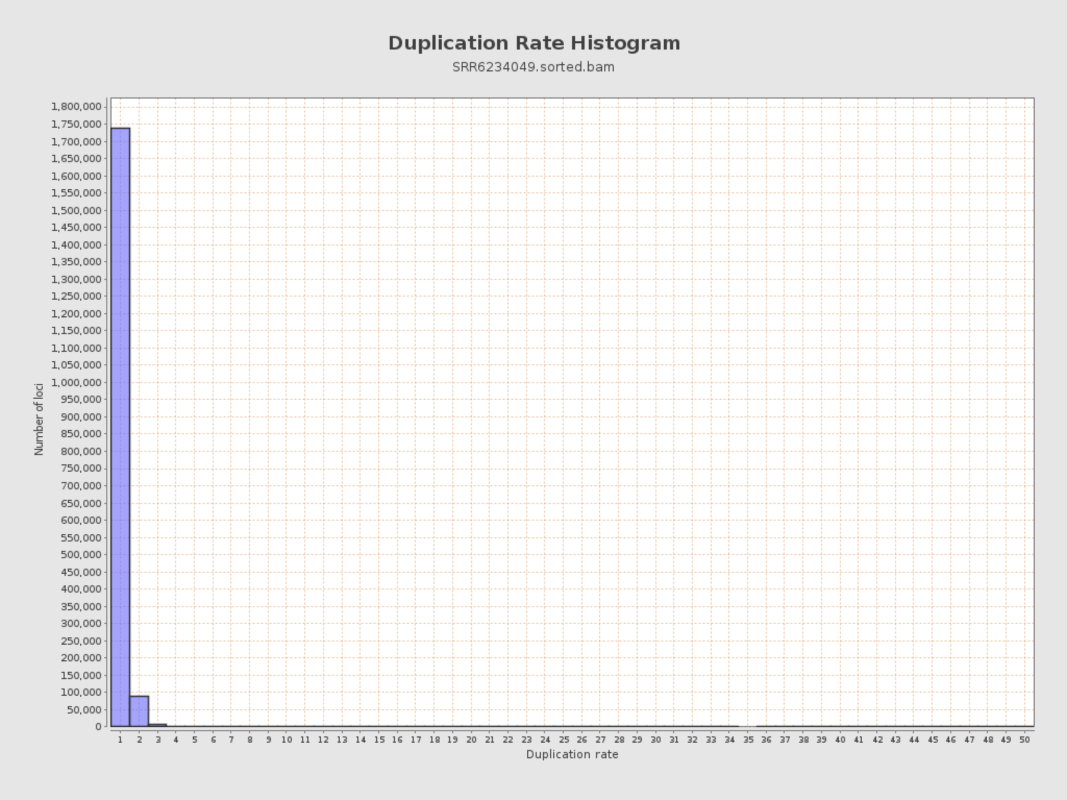
5. Results : Coverage Histogram (0-50X)



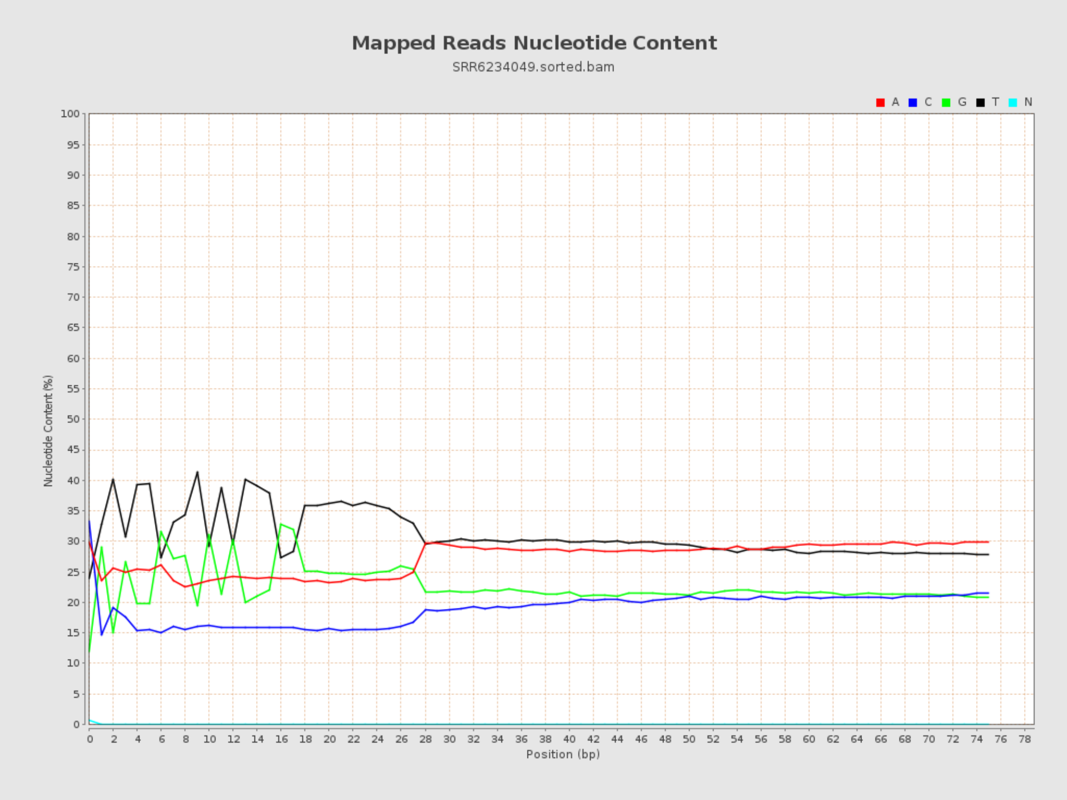
6. Results : Genome Fraction Coverage



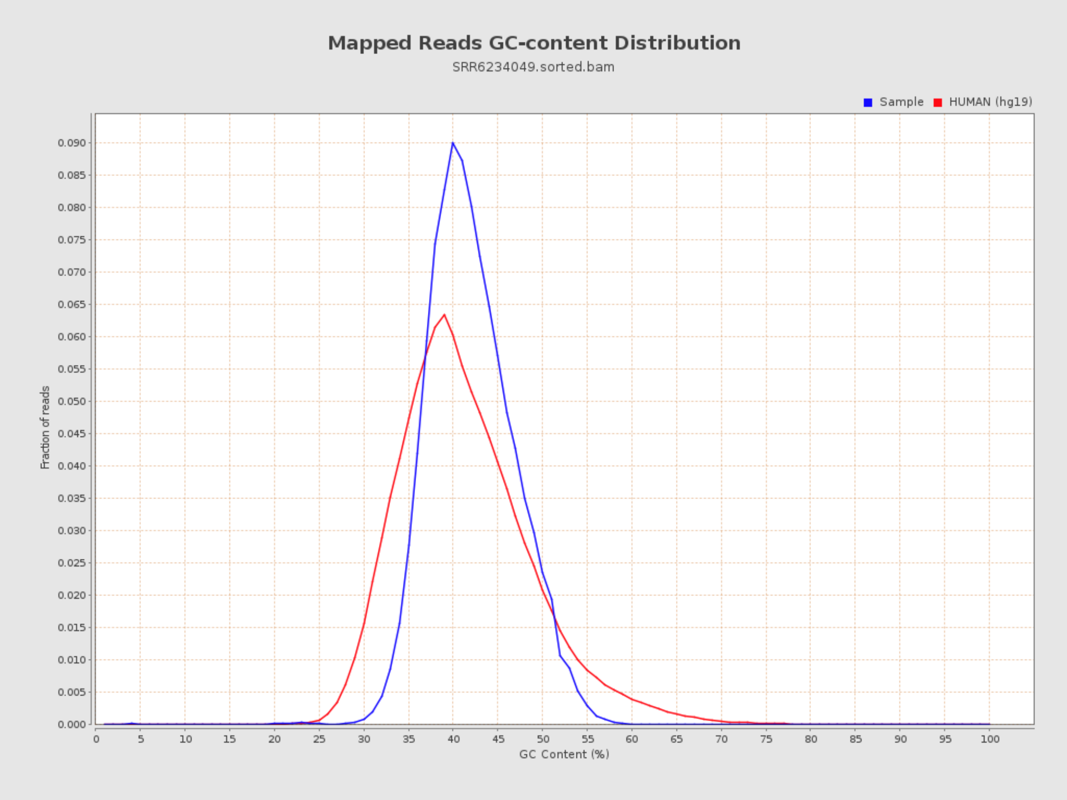
7. Results : Duplication Rate Histogram



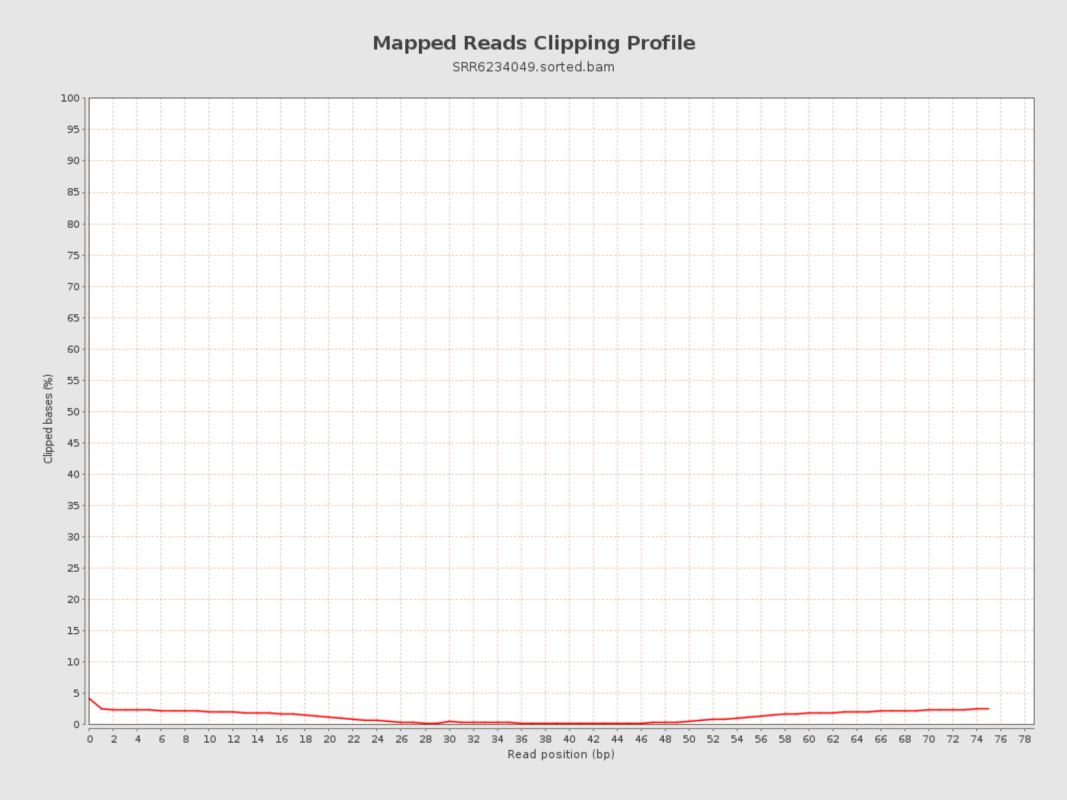
8. Results : Mapped Reads Nucleotide Content



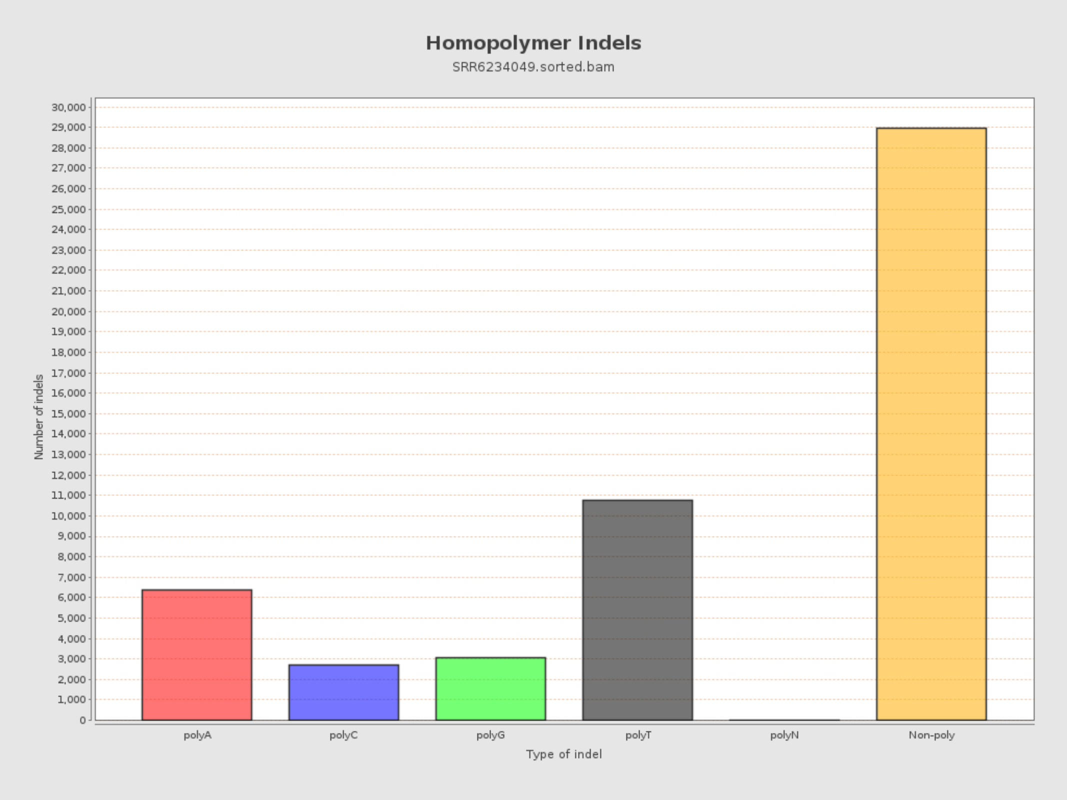
9. Results : Mapped Reads GC-content Distribution



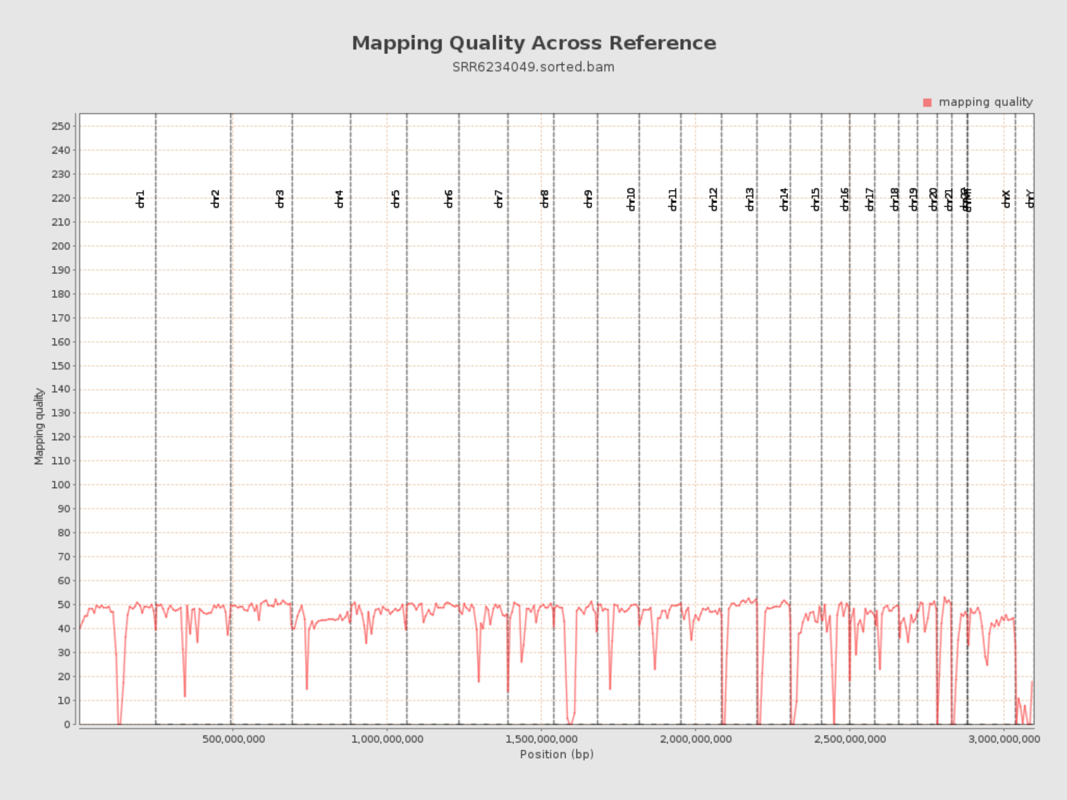
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram