Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 12:00:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234045.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_SRR6234045 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234045.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 12:00:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234045.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,113,463
Mapped reads	3,852,847 / 93.66%
Unmapped reads	260,616 / 6.34%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	30,573 / 0.74%
Read min/max/mean length	30 / 76 / 76.26
Duplicated reads (estimated)	595,837 / 14.49%
Duplication rate	12.99%
Clipped reads	2,105,433 / 51.18%

2.2. ACGT Content

Number/percentage of A's	63,185,045 / 25.76%
Number/percentage of C's	43,646,116 / 17.79%
Number/percentage of T's	81,194,769 / 33.1%
Number/percentage of G's	57,260,328 / 23.34%
Number/percentage of N's	23,840 / 0.01%
GC Percentage	41.13%

2.3. Coverage

Mean	0.0793

Standard Deviation	0.9266

2.4. Mapping Quality

Mean Mapping Quality	40.05

2.5. Mismatches and indels

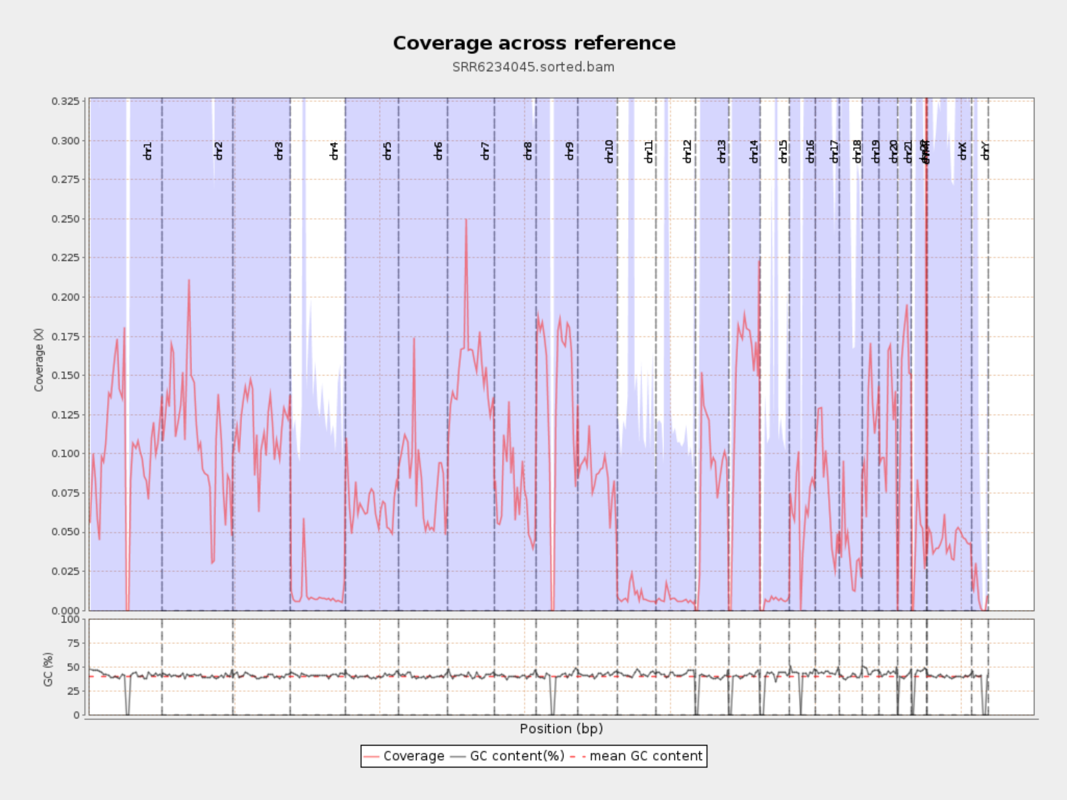
General error rate	0.56%
Mismatches	1,336,503
Insertions	16,425
Mapped reads with at least one insertion	0.42%
Deletions	54,256
Mapped reads with at least one deletion	1.4%
Homopolymer indels	44.1%

2.6. Chromosome stats

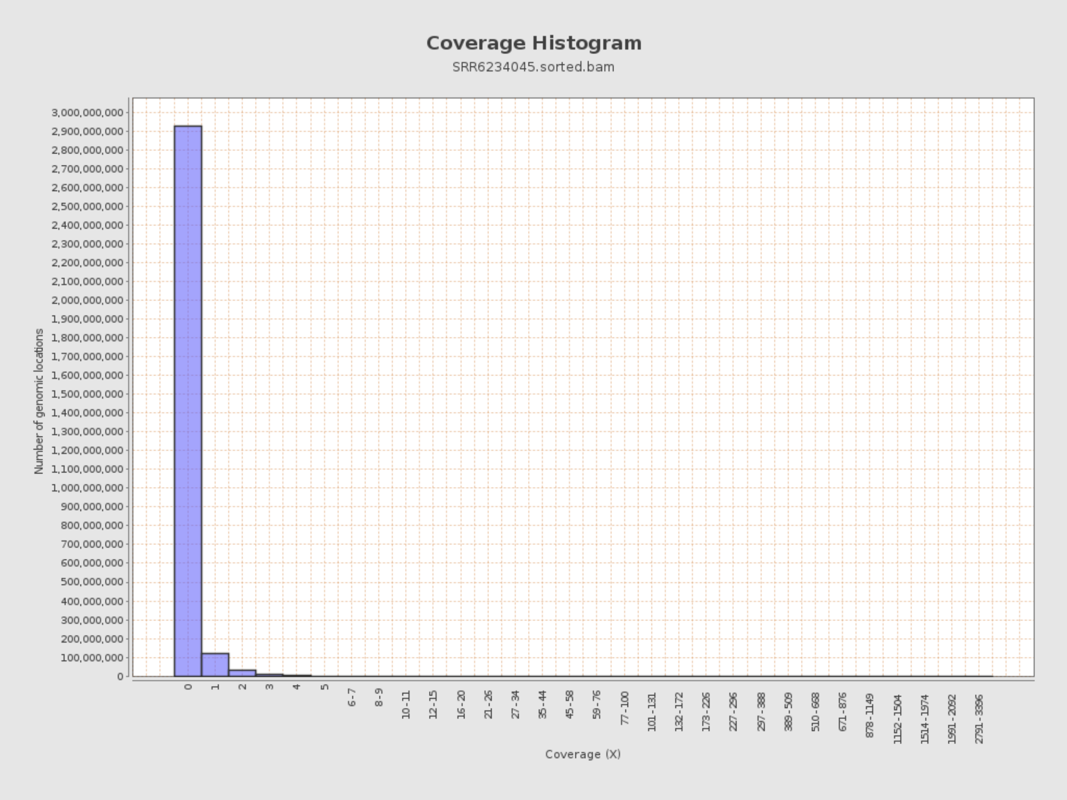
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	25460719	0.1021	1.659
chr2	243199373	27294354	0.1122	1.6269
chr3	198022430	22973315	0.116	0.4637
chr4	191154276	1875671	0.0098	0.179
chr5	180915260	12162376	0.0672	0.3689
chr6	171115067	14329585	0.0837	0.7919
chr7	159138663	24619817	0.1547	1.6498

chr8	146364022	10846512	0.0741	0.7811
chr9	141213431	19872940	0.1407	0.7679
chr10	135534747	11655266	0.086	0.5437
chr11	135006516	1239082	0.0092	0.3765
chr12	133851895	1001449	0.0075	0.2367
chr13	115169878	10097829	0.0877	0.4677
chr14	107349540	15306772	0.1426	0.5661
chr15	102531392	616520	0.006	0.2035
chr16	90354753	5930211	0.0656	0.4507
chr17	81195210	6413058	0.079	0.4483
chr18	78077248	2905581	0.0372	1.8176
chr19	59128983	7090328	0.1199	0.9257
chr20	63025520	7449928	0.1182	0.5044
chr21	48129895	6693920	0.1391	0.5551
chr22	51304566	2035977	0.0397	0.2621
chrMT	16571	155245	9.3685	6.228
chrX	155270560	6842006	0.0441	0.3731
chrY	59373566	537204	0.009	0.2393

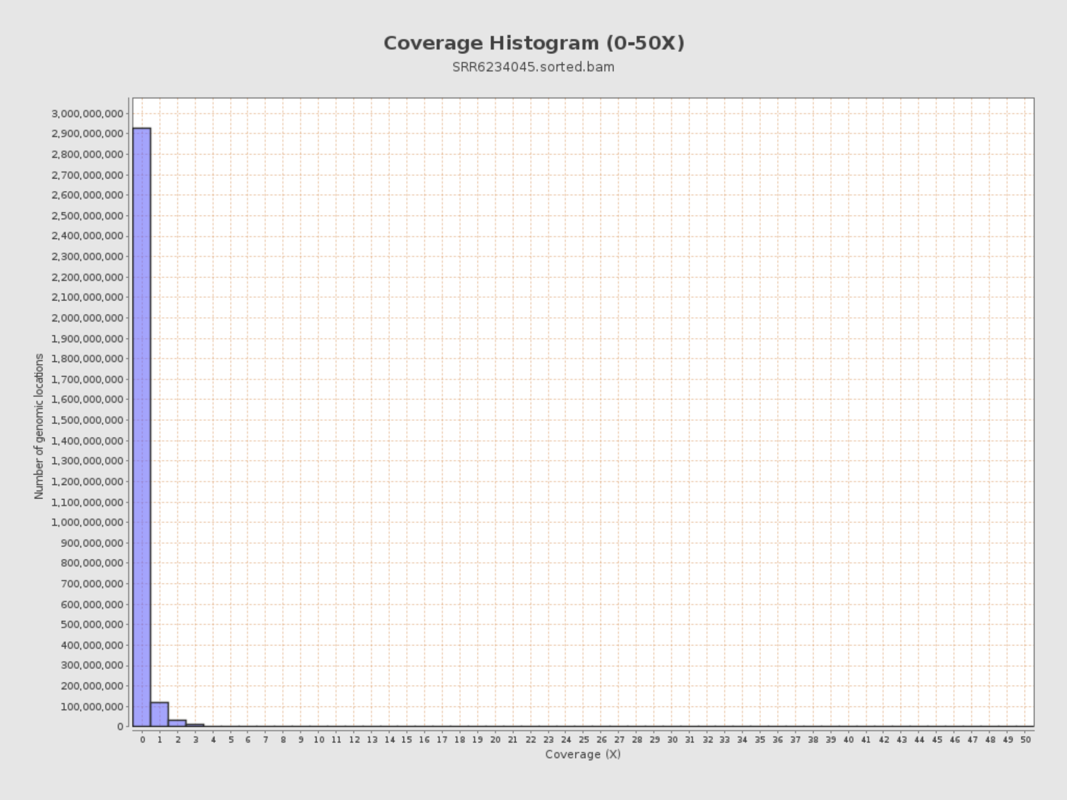
3. Results : Coverage across reference



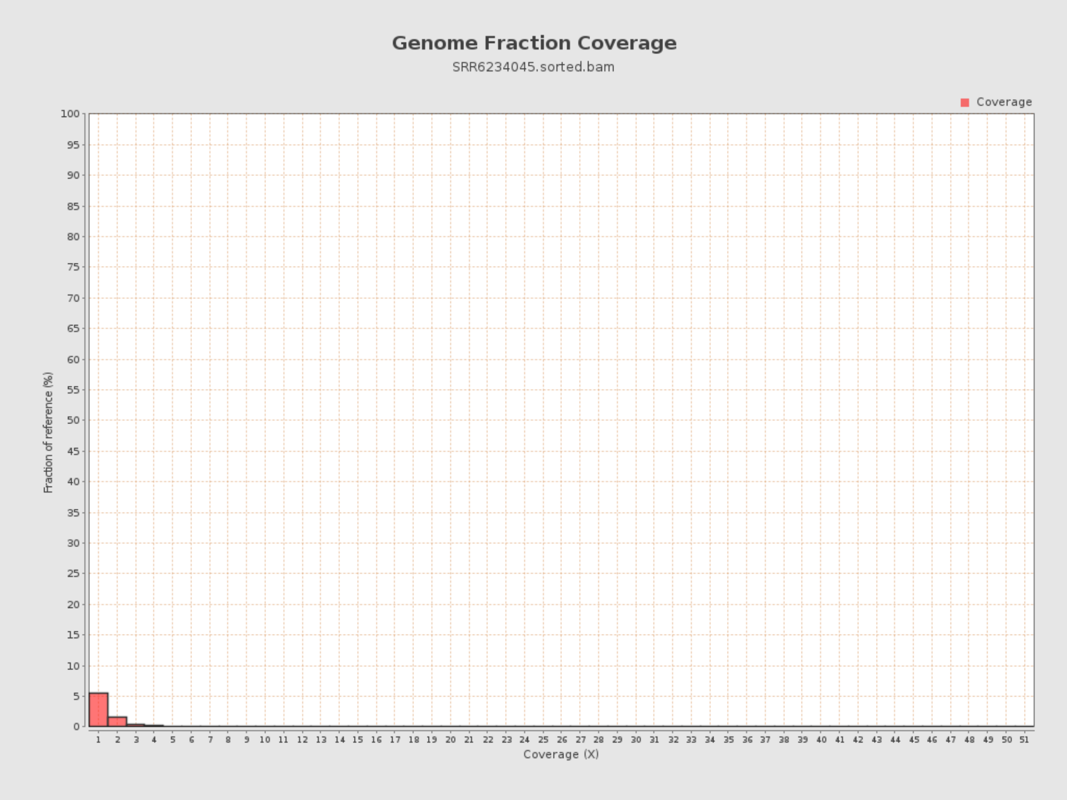
4. Results : Coverage Histogram



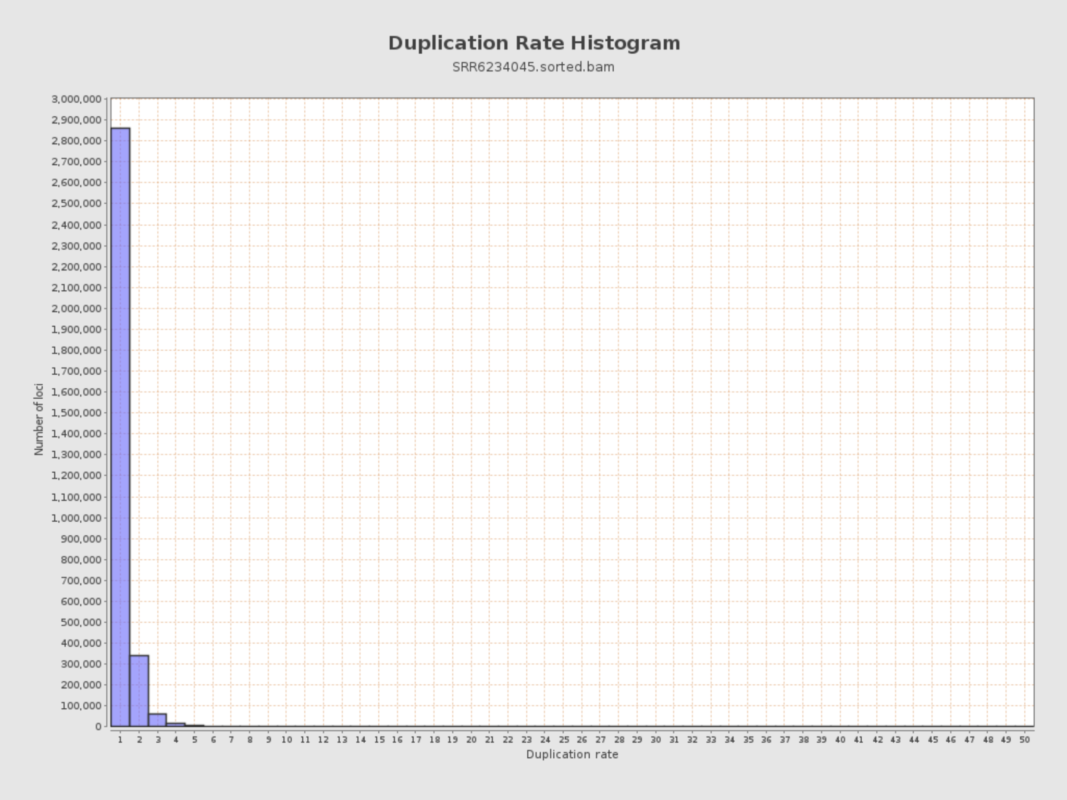
5. Results : Coverage Histogram (0-50X)



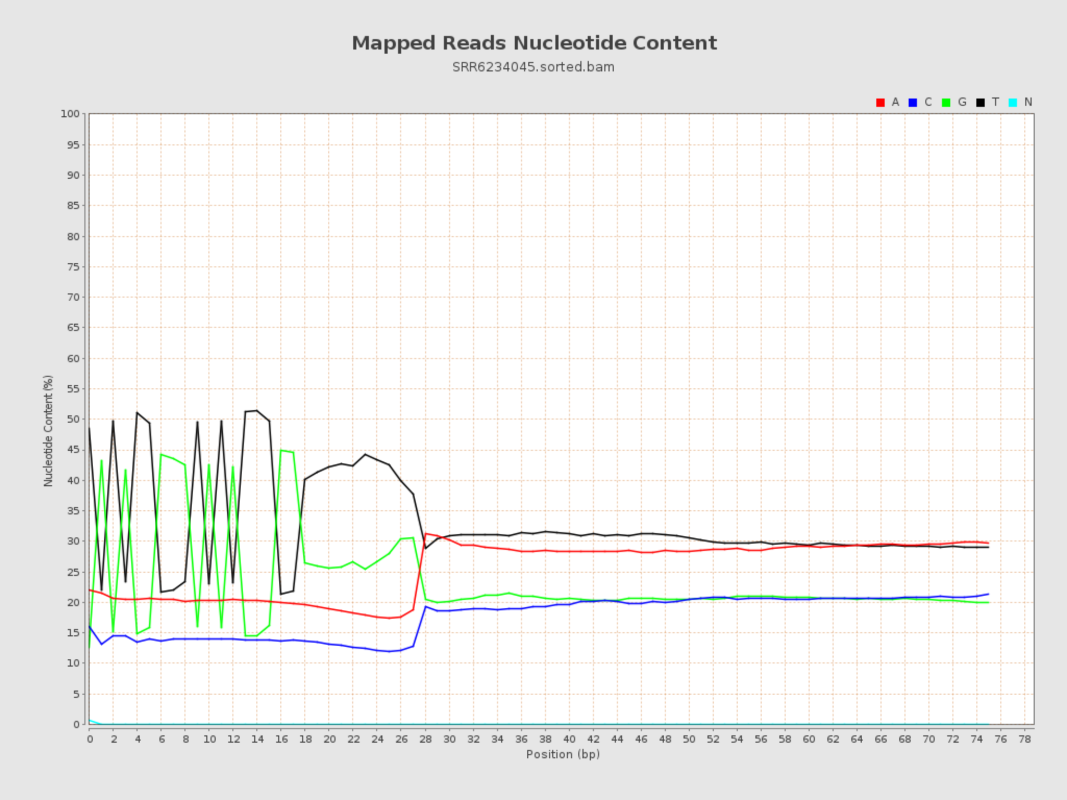
6. Results : Genome Fraction Coverage



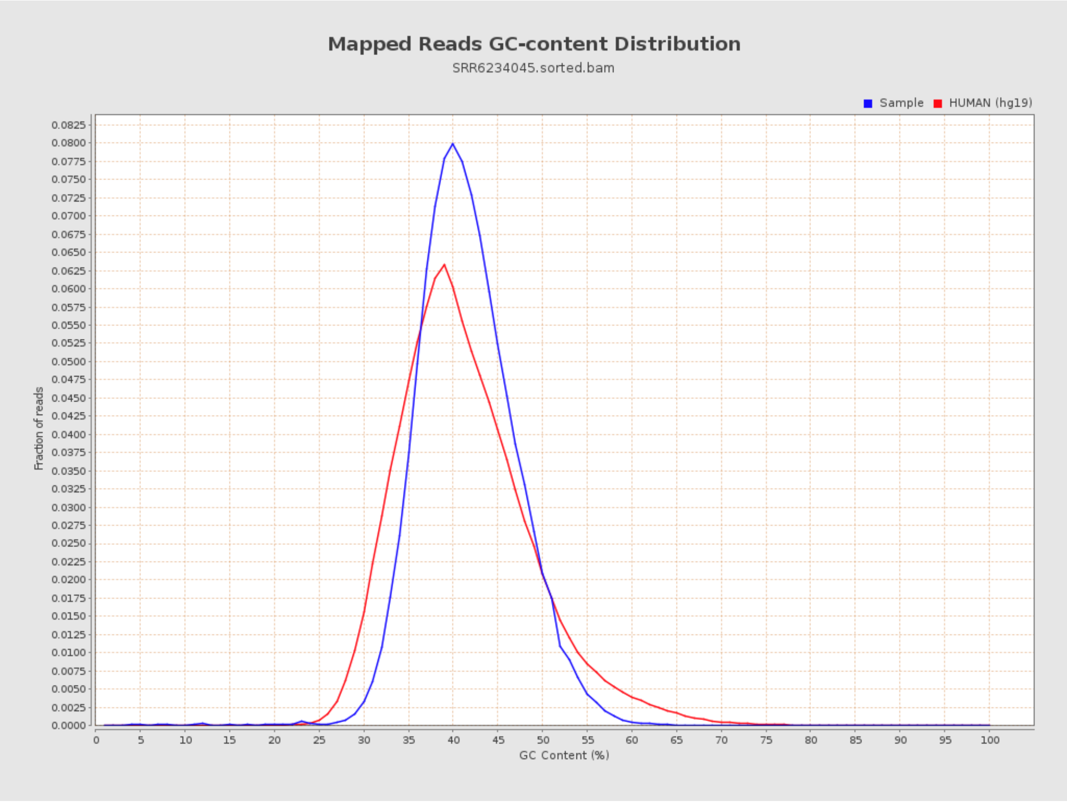
7. Results : Duplication Rate Histogram



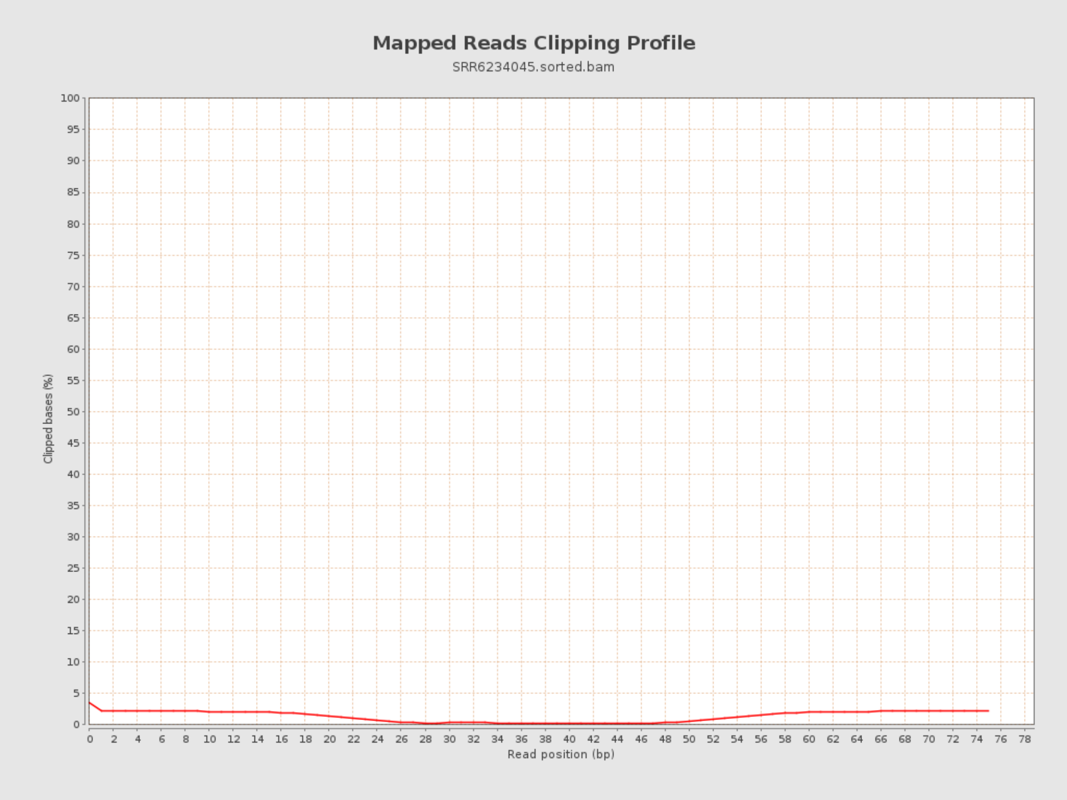
8. Results : Mapped Reads Nucleotide Content



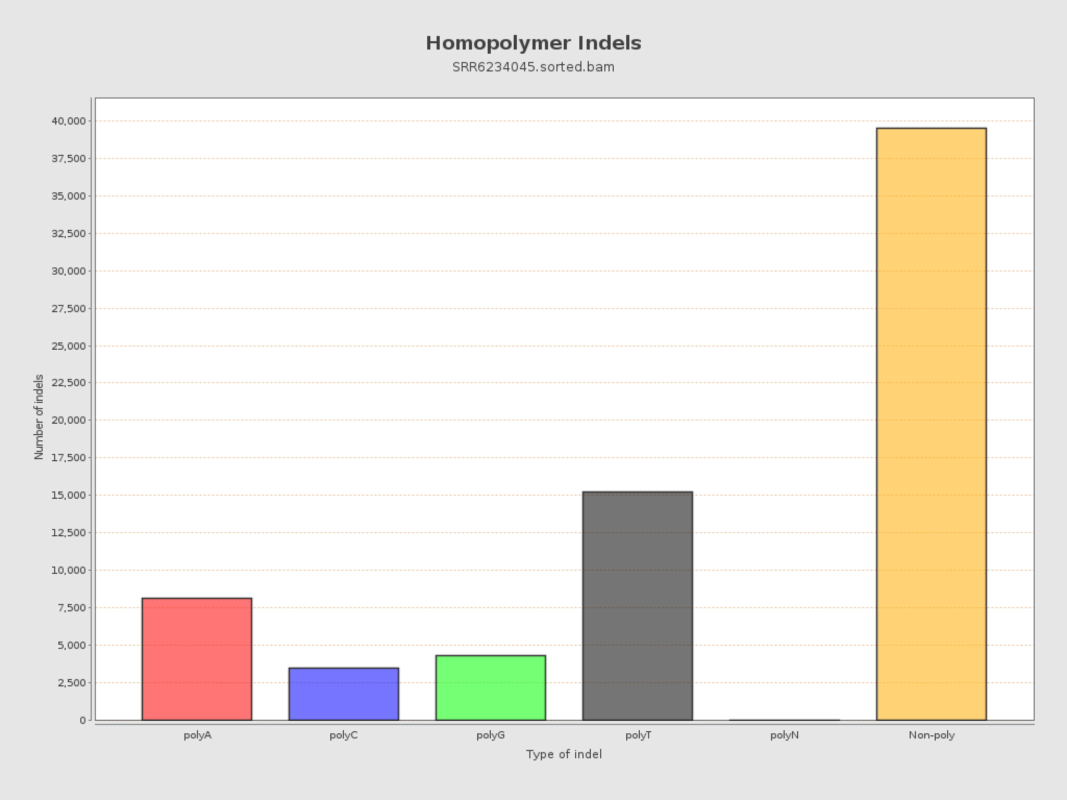
9. Results : Mapped Reads GC-content Distribution



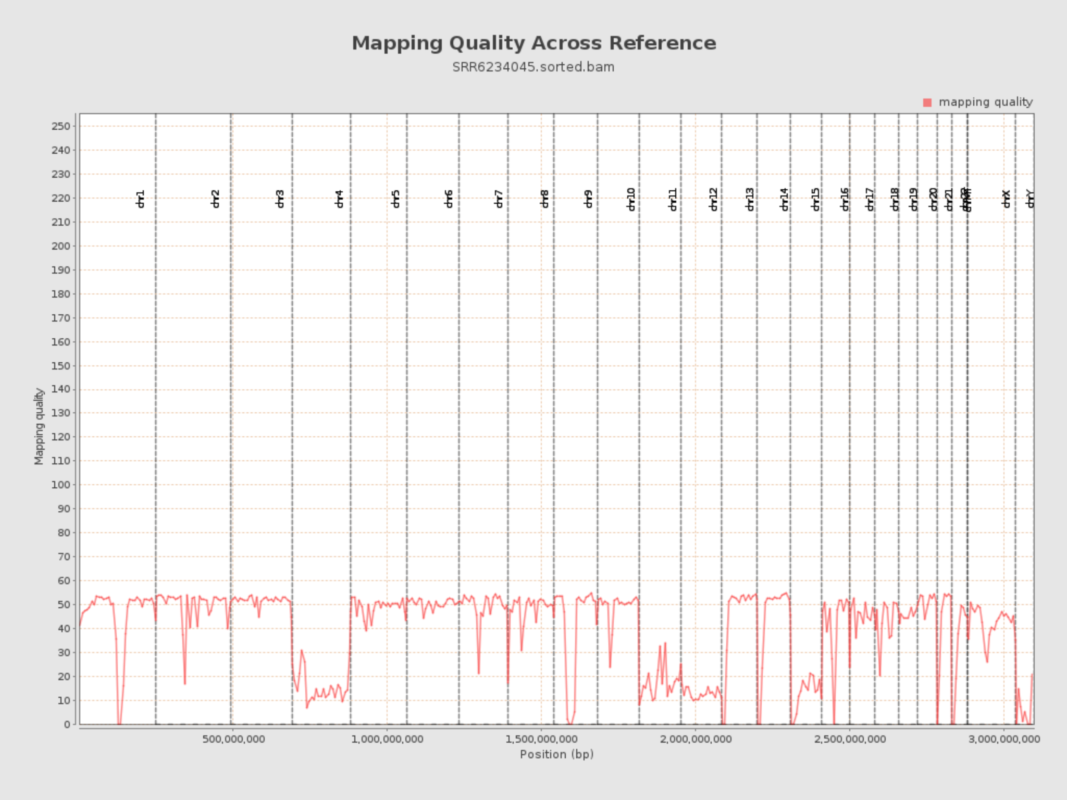
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram