Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:34:08

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234097.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_SRR6234097 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234097.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:34:08 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234097.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,412,854
Mapped reads	4,137,120 / 93.75%
Unmapped reads	275,734 / 6.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	36,406 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	737,216 / 16.71%
Duplication rate	14.51%
Clipped reads	2,451,632 / 55.56%

2.2. ACGT Content

Number/percentage of A's	65,964,827 / 25.35%
Number/percentage of C's	47,073,447 / 18.09%
Number/percentage of T's	85,242,546 / 32.76%
Number/percentage of G's	61,893,646 / 23.79%
Number/percentage of N's	24,935 / 0.01%
GC Percentage	41.88%

2.3. Coverage

Mean	0.0841

Standard Deviation	0.8832

2.4. Mapping Quality

Mean Mapping Quality	44.73

2.5. Mismatches and indels

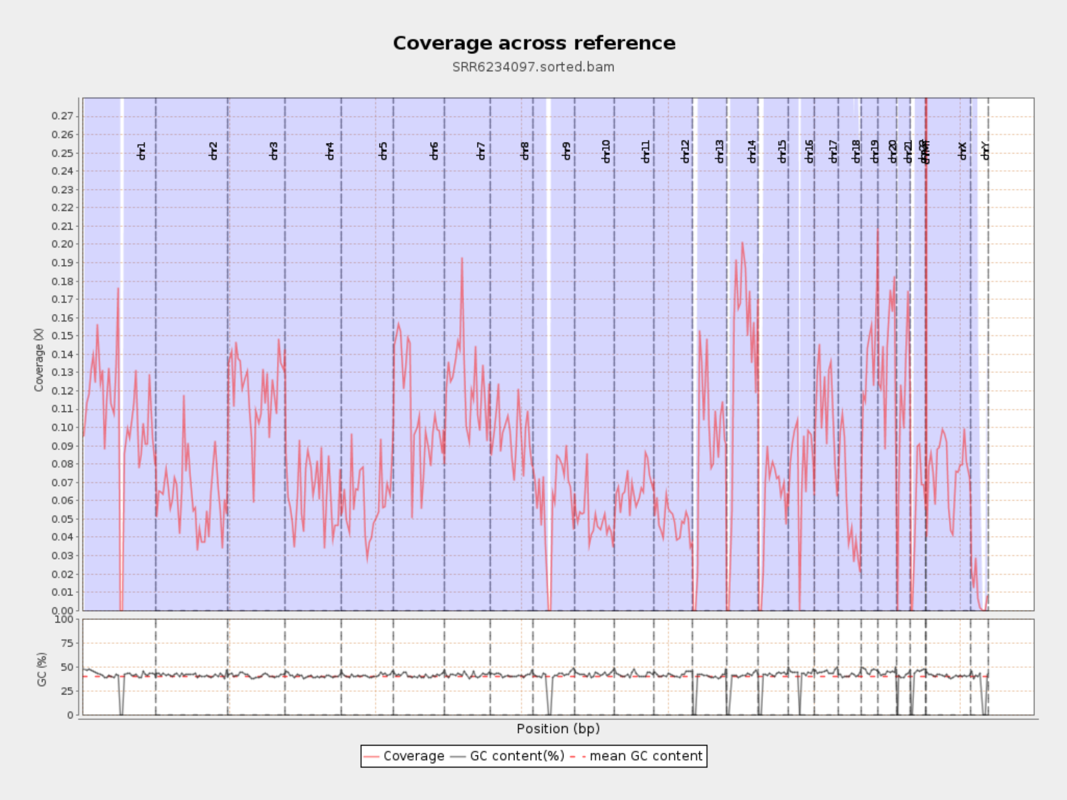
General error rate	0.55%
Mismatches	1,408,971
Insertions	16,113
Mapped reads with at least one insertion	0.39%
Deletions	54,506
Mapped reads with at least one deletion	1.31%
Homopolymer indels	43.72%

2.6. Chromosome stats

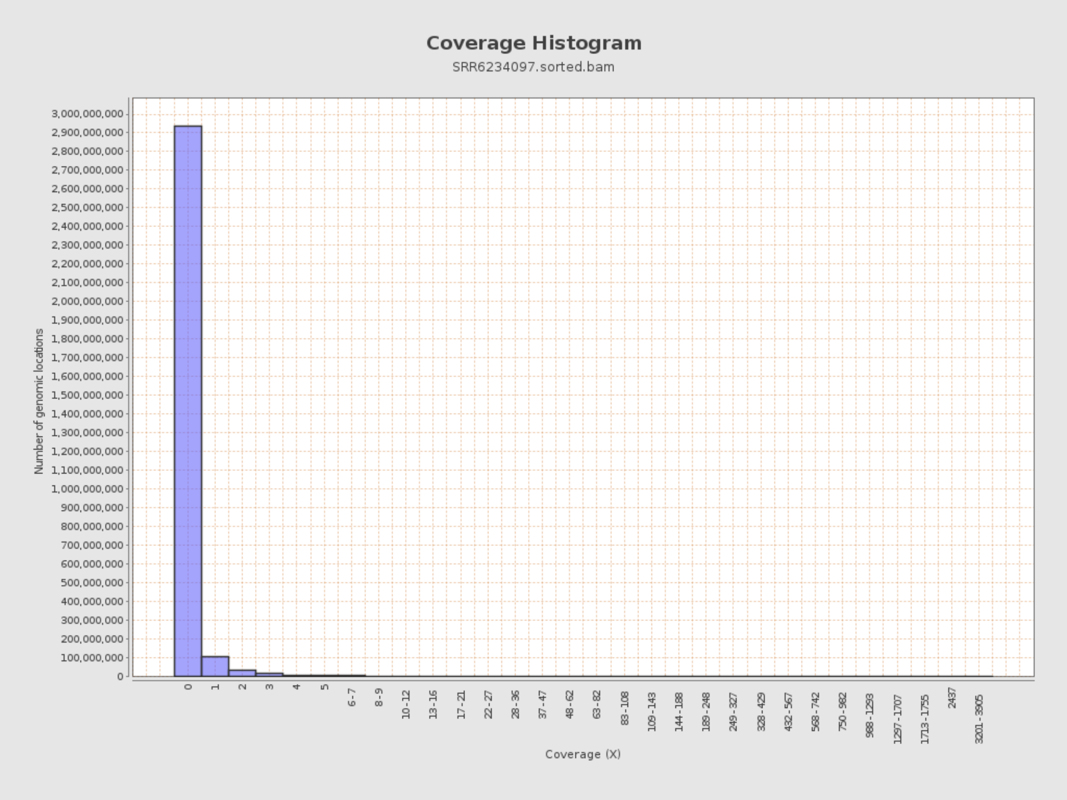
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	26307009	0.1055	1.4824
chr2	243199373	15058109	0.0619	1.7819
chr3	198022430	23715731	0.1198	0.5289
chr4	191154276	12188785	0.0638	0.3946
chr5	180915260	10928096	0.0604	0.383
chr6	171115067	18457778	0.1079	0.7588
chr7	159138663	19778846	0.1243	1.2083

chr8	146364022	14015996	0.0958	0.7171
chr9	141213431	8432928	0.0597	0.4951
chr10	135534747	6662593	0.0492	0.4915
chr11	135006516	8964511	0.0664	0.4993
chr12	133851895	6509222	0.0486	0.3474
chr13	115169878	10442684	0.0907	0.529
chr14	107349540	14587677	0.1359	0.5898
chr15	102531392	5897348	0.0575	0.4324
chr16	90354753	7057061	0.0781	0.4708
chr17	81195210	9101702	0.1121	0.5477
chr18	78077248	4495514	0.0576	1.5266
chr19	59128983	8213612	0.1389	0.999
chr20	63025520	8916612	0.1415	0.5955
chr21	48129895	5224322	0.1085	0.5171
chr22	51304566	2801593	0.0546	0.3445
chrMT	16571	218357	13.1771	11.7142
chrX	155270560	11759198	0.0757	0.4607
chrY	59373566	558162	0.0094	0.2516

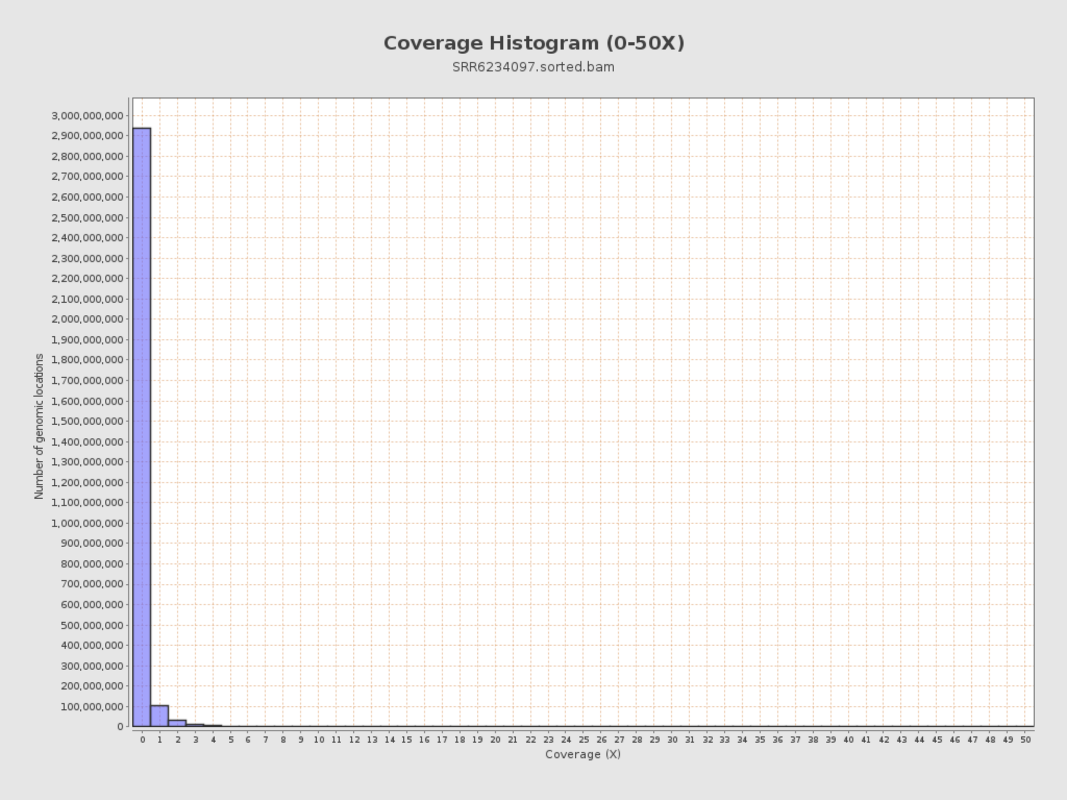
3. Results : Coverage across reference



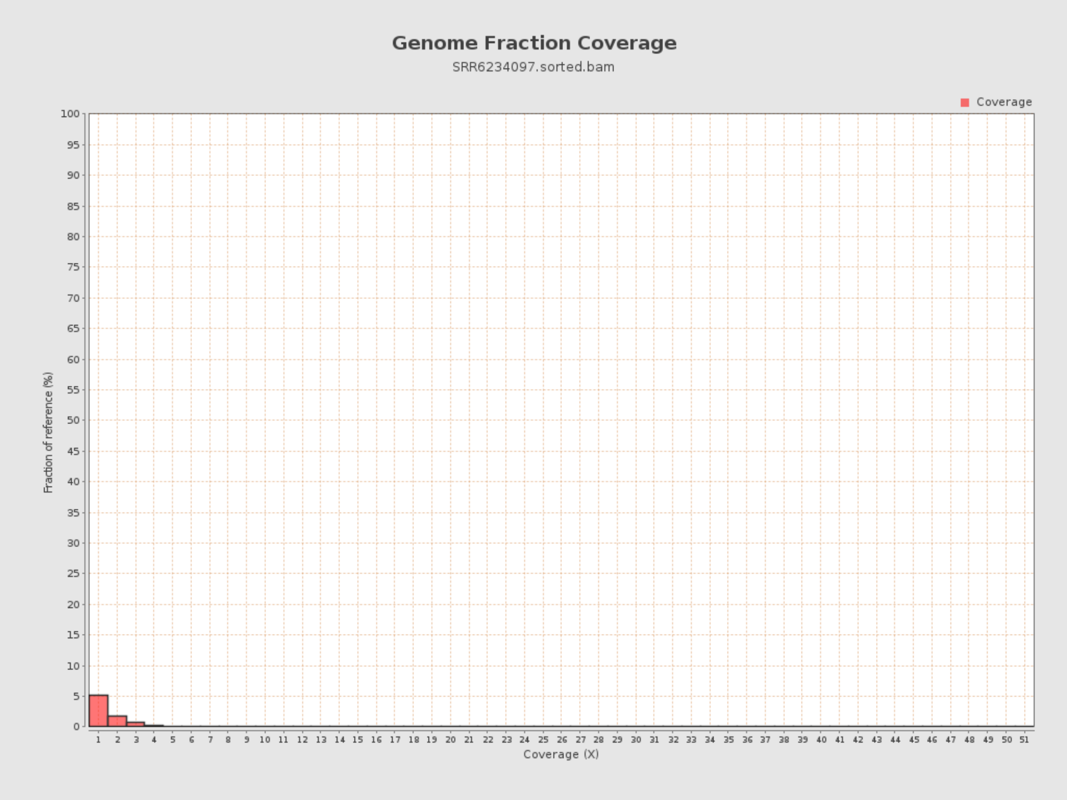
4. Results : Coverage Histogram



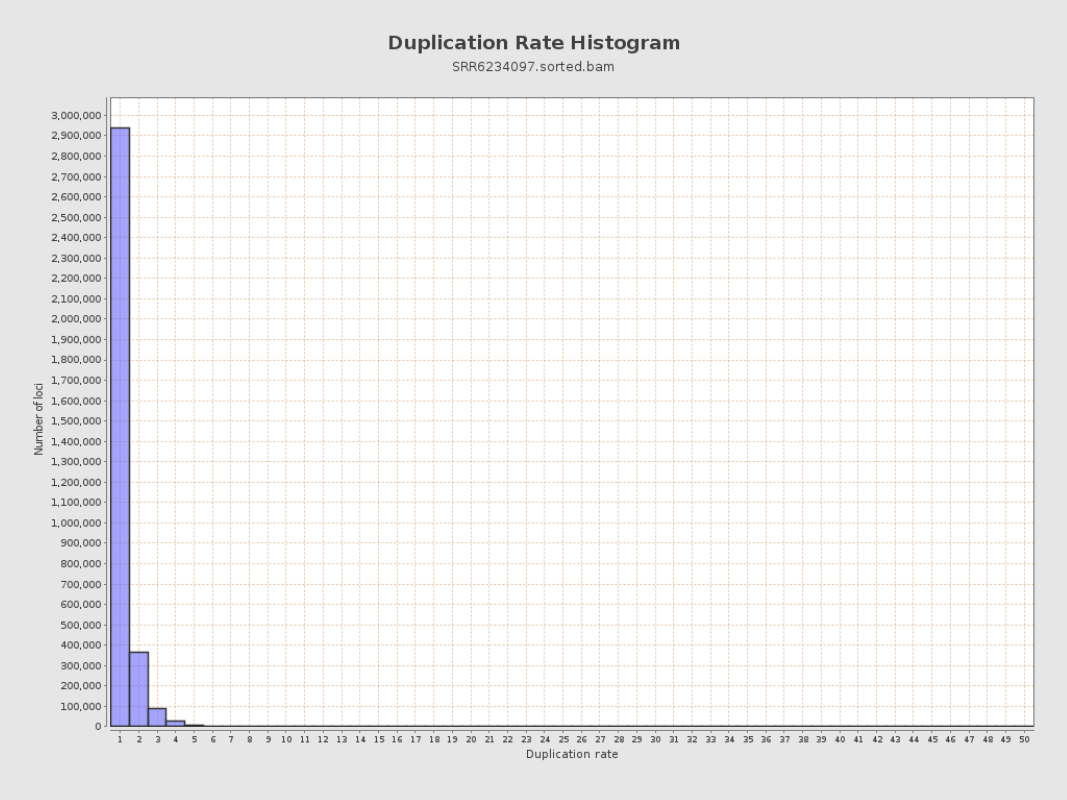
5. Results : Coverage Histogram (0-50X)



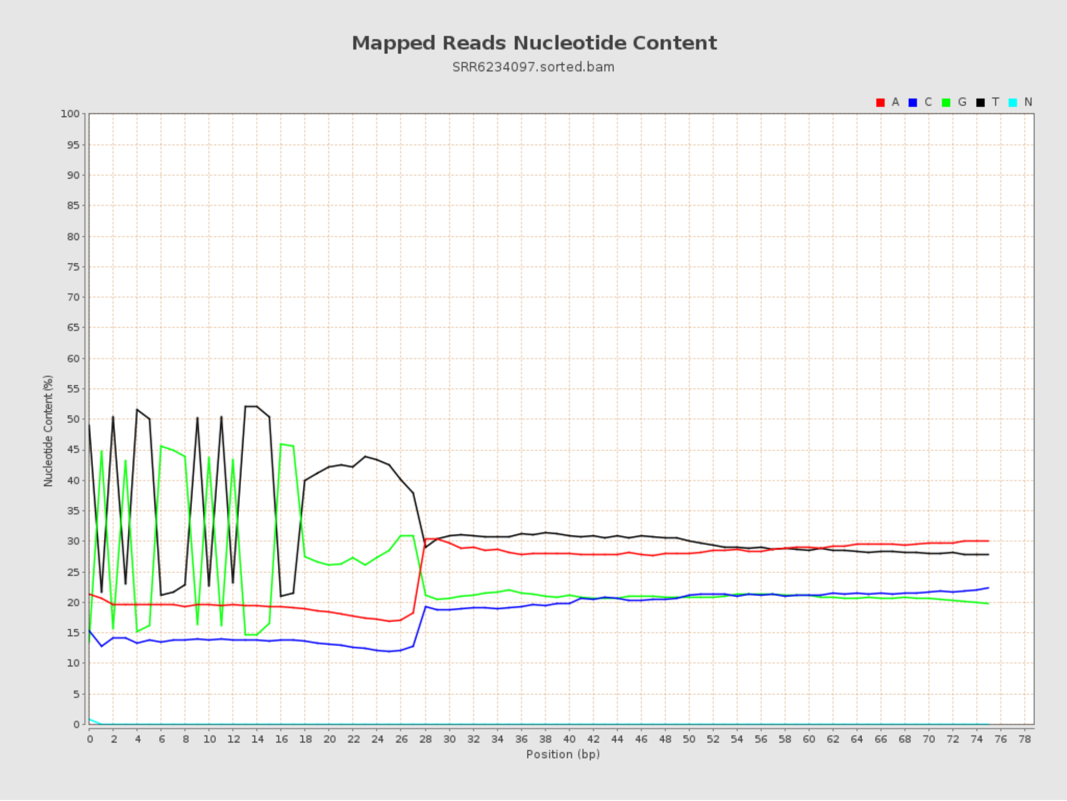
6. Results : Genome Fraction Coverage



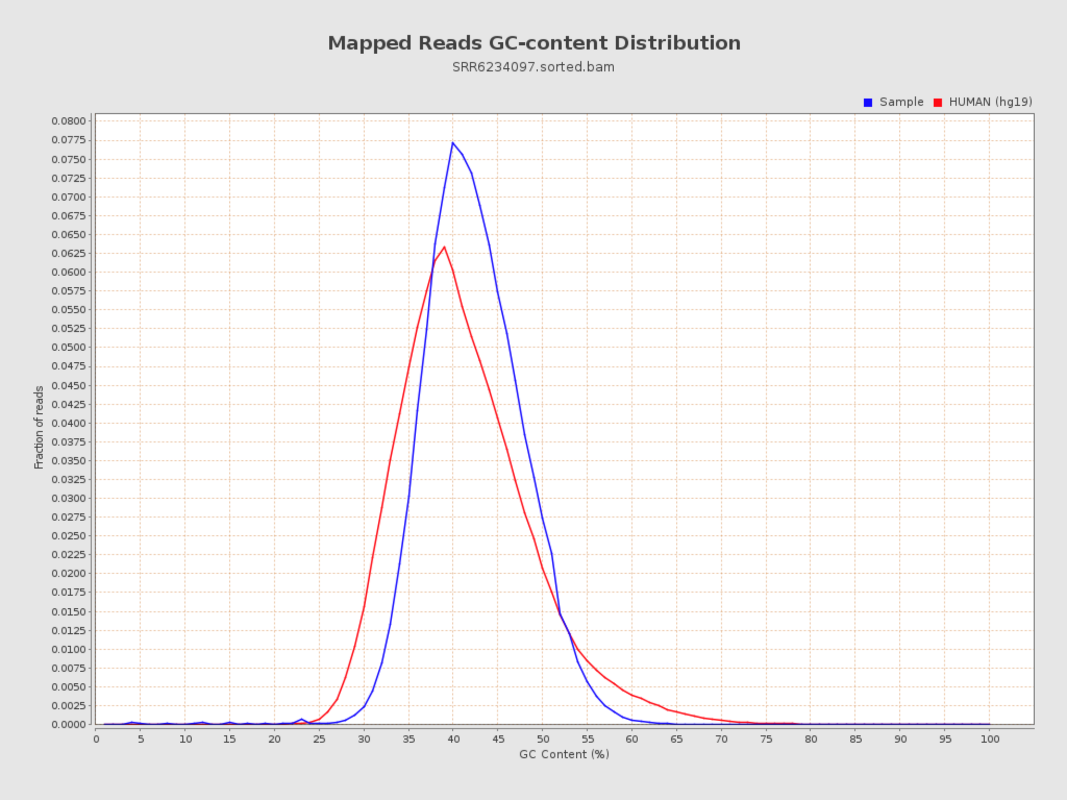
7. Results : Duplication Rate Histogram



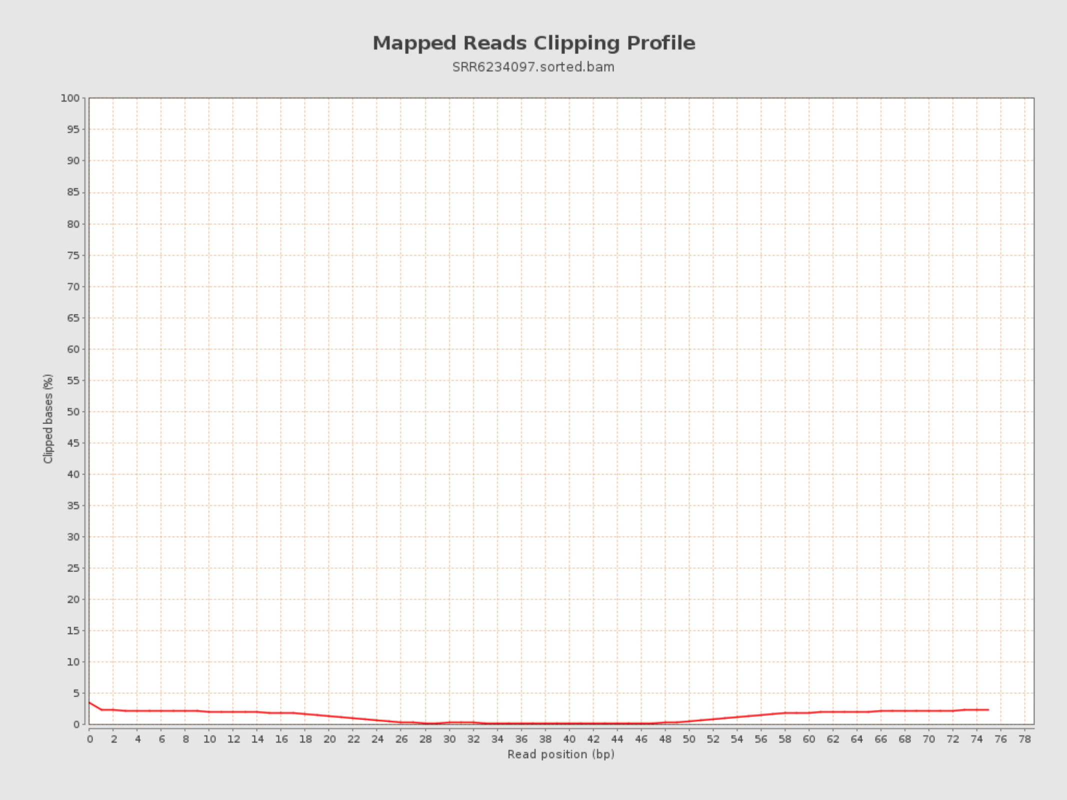
8. Results : Mapped Reads Nucleotide Content



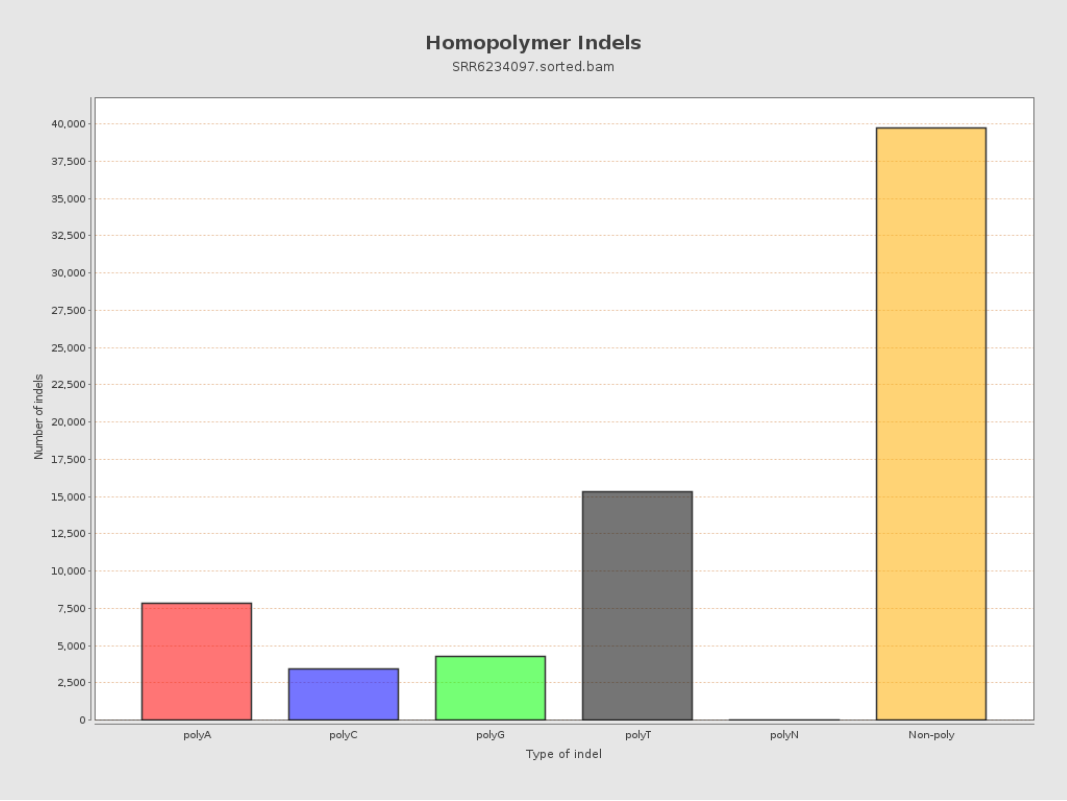
9. Results : Mapped Reads GC-content Distribution



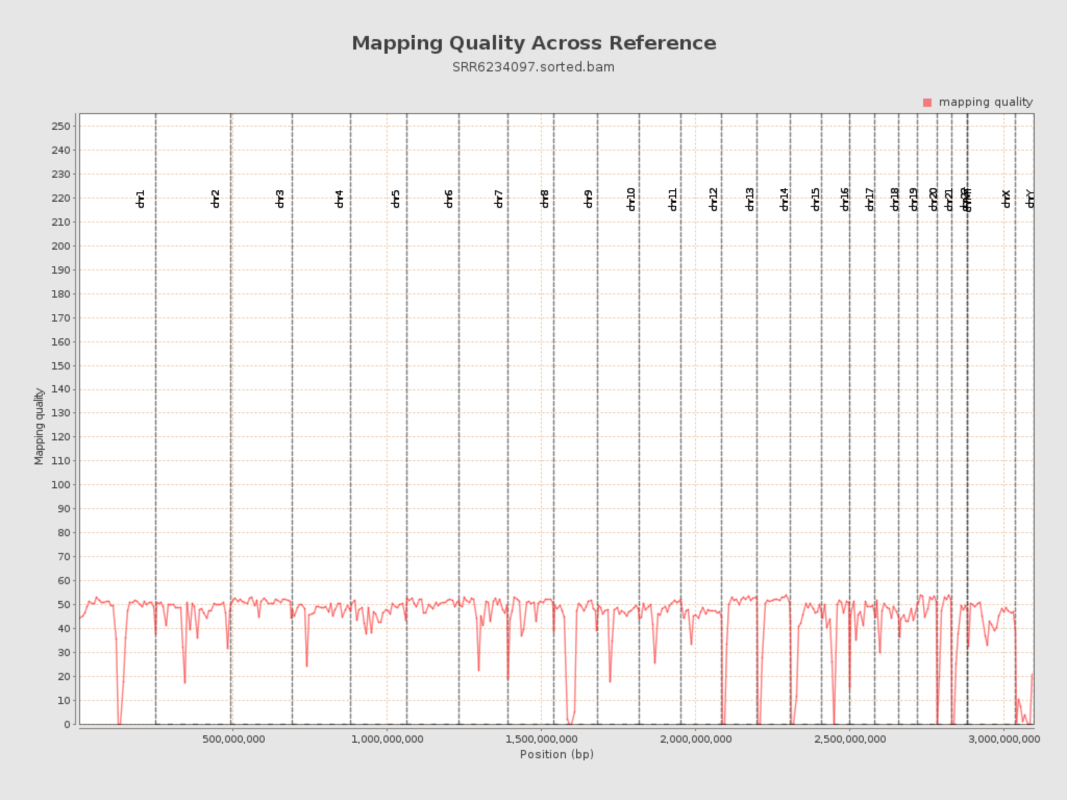
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram