Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 15:18:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234094.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_SRR6234094 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234094.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 15:18:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234094.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,136,279
Mapped reads	1,943,100 / 90.96%
Unmapped reads	193,179 / 9.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	14,678 / 0.69%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	126,463 / 5.92%
Duplication rate	4.63%
Clipped reads	685,102 / 32.07%

2.2. ACGT Content

Number/percentage of A's	38,608,748 / 28.83%
Number/percentage of C's	24,944,015 / 18.63%
Number/percentage of T's	41,990,934 / 31.35%
Number/percentage of G's	28,368,722 / 21.18%
Number/percentage of N's	12,637 / 0.01%
GC Percentage	39.81%

2.3. Coverage

Mean	0.0433

Standard Deviation	0.7071

2.4. Mapping Quality

Mean Mapping Quality	44.92

2.5. Mismatches and indels

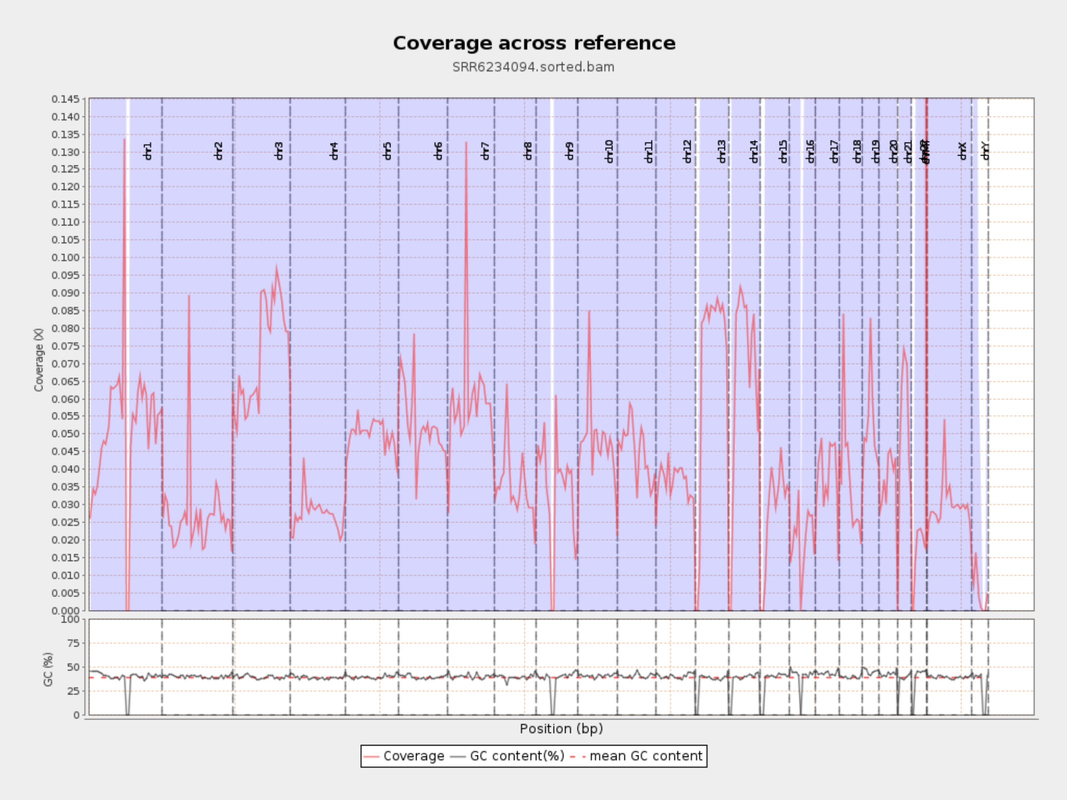
General error rate	0.75%
Mismatches	989,187
Insertions	10,559
Mapped reads with at least one insertion	0.54%
Deletions	33,419
Mapped reads with at least one deletion	1.7%
Homopolymer indels	44.79%

2.6. Chromosome stats

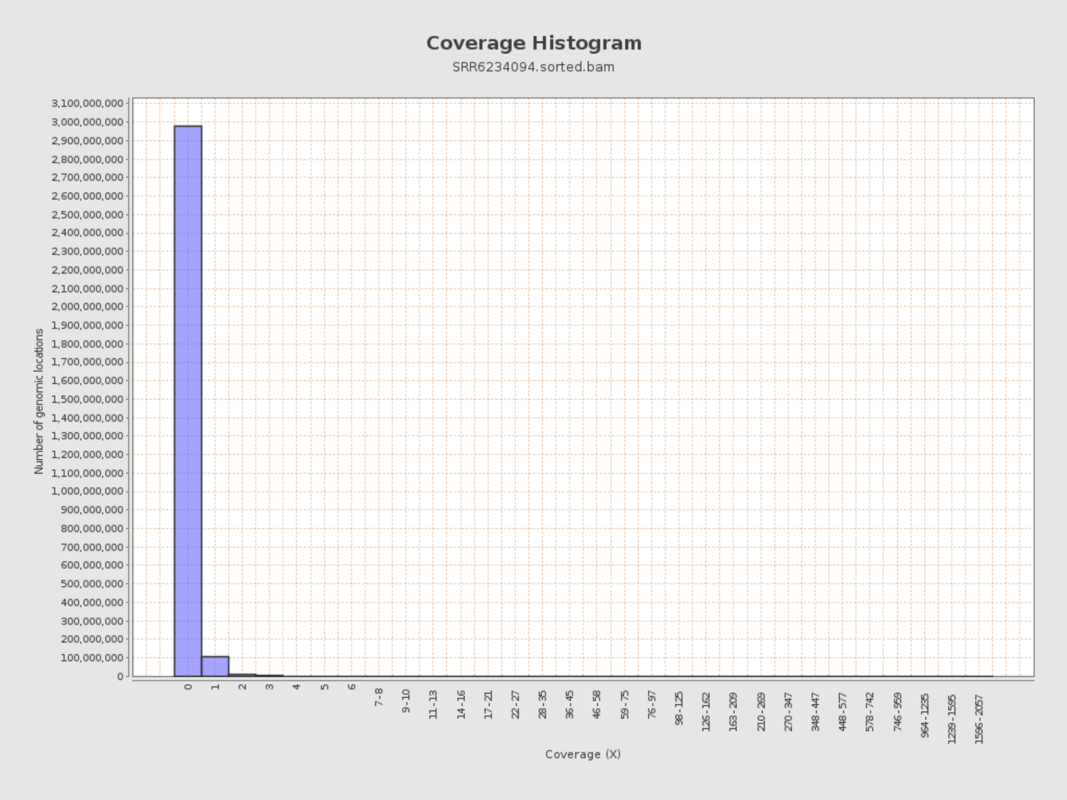
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12999277	0.0522	1.692
chr2	243199373	6622865	0.0272	0.5732
chr3	198022430	14486875	0.0732	0.2991
chr4	191154276	5210550	0.0273	0.1977
chr5	180915260	9028455	0.0499	0.2582
chr6	171115067	9064663	0.053	0.3523
chr7	159138663	9652868	0.0607	1.0219

chr8	146364022	5127443	0.035	1.1641
chr9	141213431	4856551	0.0344	0.4607
chr10	135534747	6538157	0.0482	0.5147
chr11	135006516	6037339	0.0447	0.4474
chr12	133851895	4893573	0.0366	0.2273
chr13	115169878	7976046	0.0693	0.2907
chr14	107349540	7021645	0.0654	0.3428
chr15	102531392	2888307	0.0282	0.1918
chr16	90354753	1821653	0.0202	0.3173
chr17	81195210	3075882	0.0379	0.2718
chr18	78077248	2934542	0.0376	1.2615
chr19	59128983	3151891	0.0533	0.8432
chr20	63025520	2332838	0.037	0.2745
chr21	48129895	2431537	0.0505	0.2676
chr22	51304566	809346	0.0158	0.1358
chrMT	16571	77390	4.6702	3.4013
chrX	155270560	4642288	0.0299	0.2866
chrY	59373566	302235	0.0051	0.1123

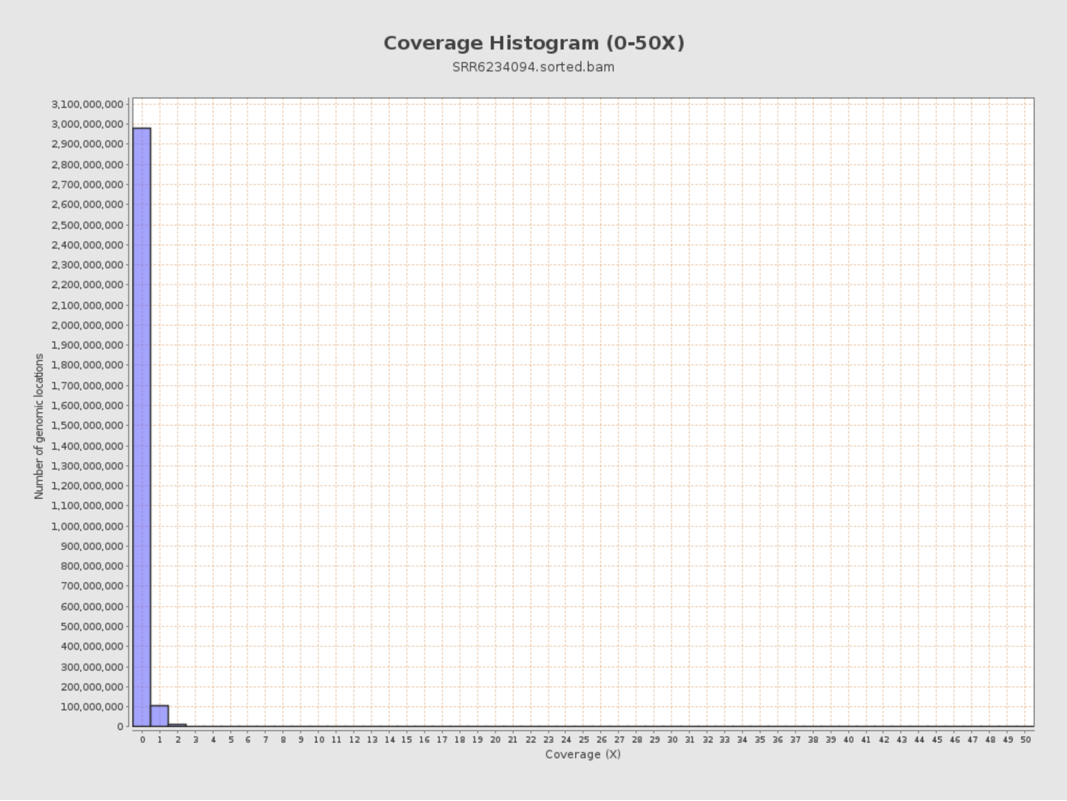
3. Results : Coverage across reference



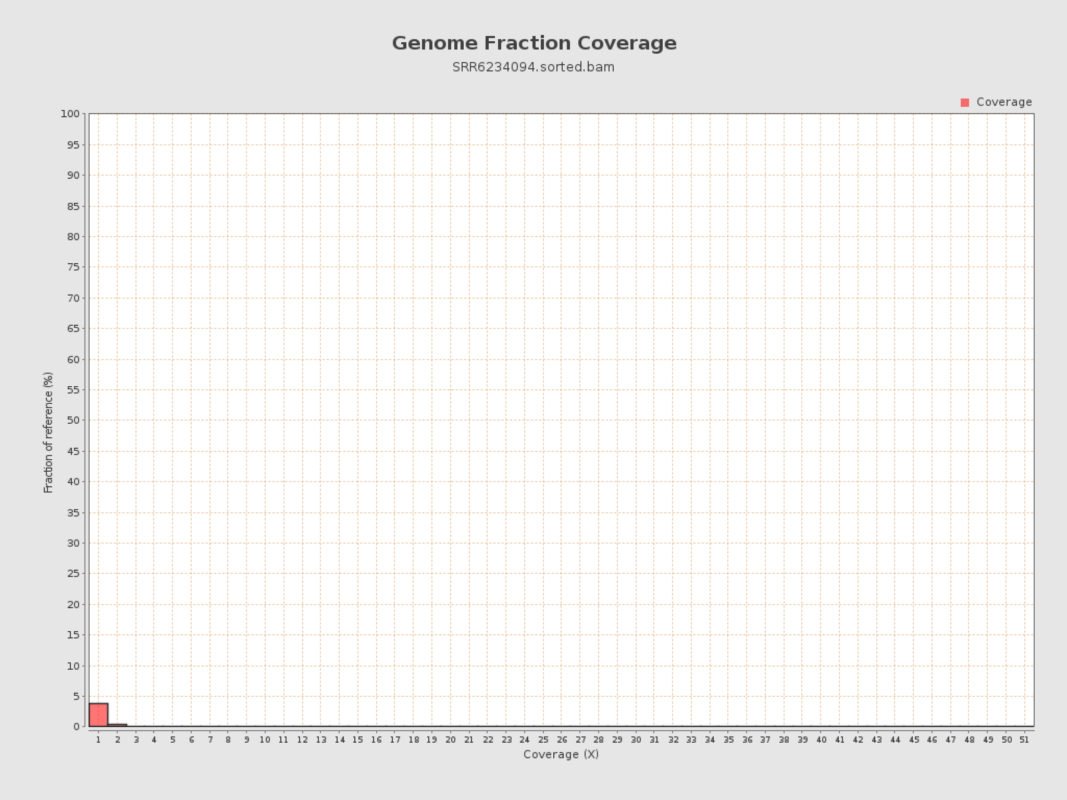
4. Results : Coverage Histogram



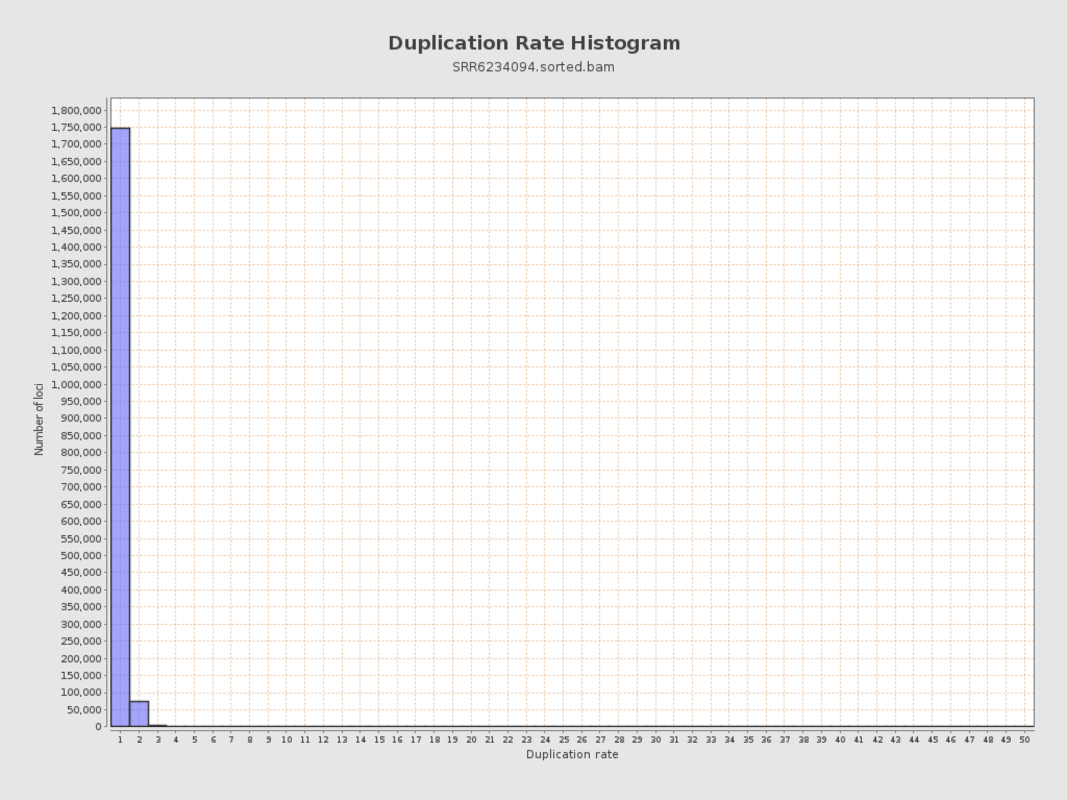
5. Results : Coverage Histogram (0-50X)



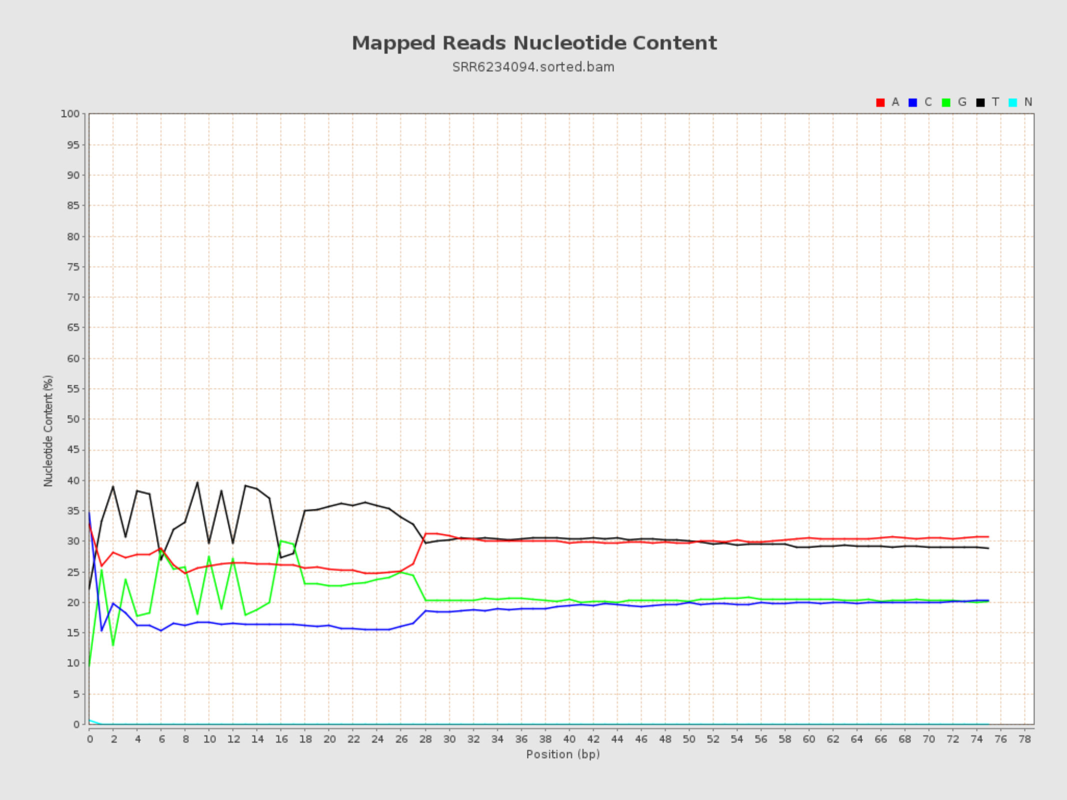
6. Results : Genome Fraction Coverage



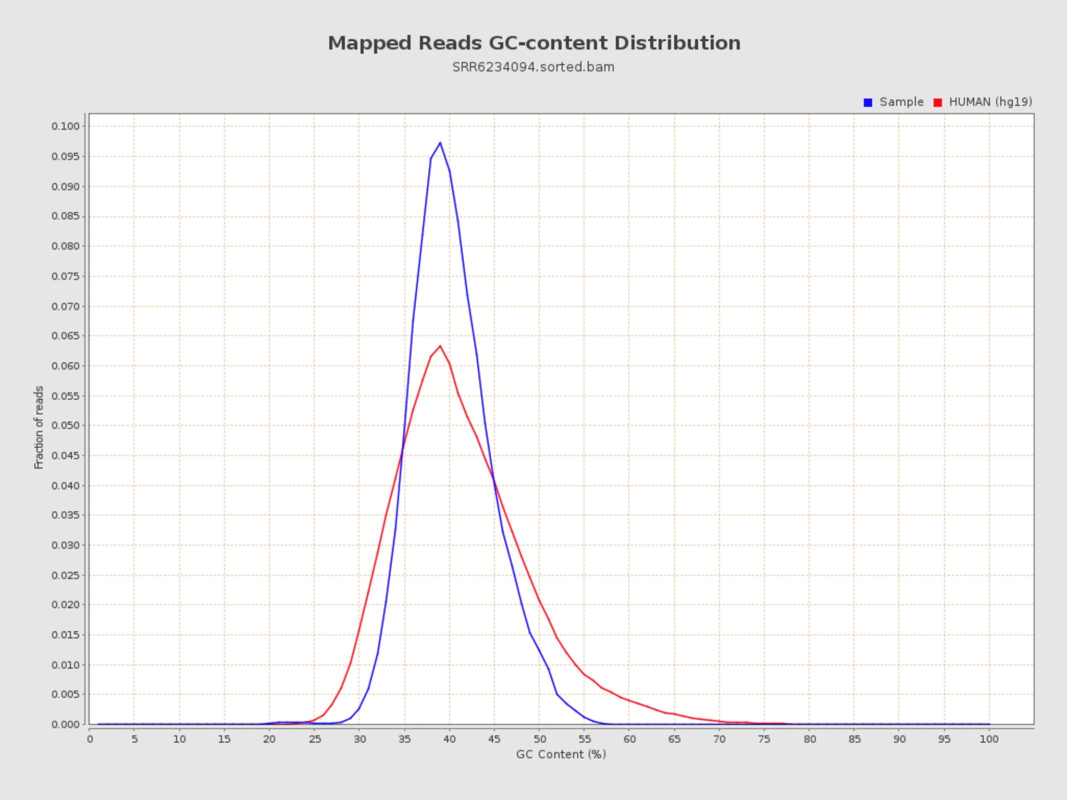
7. Results : Duplication Rate Histogram



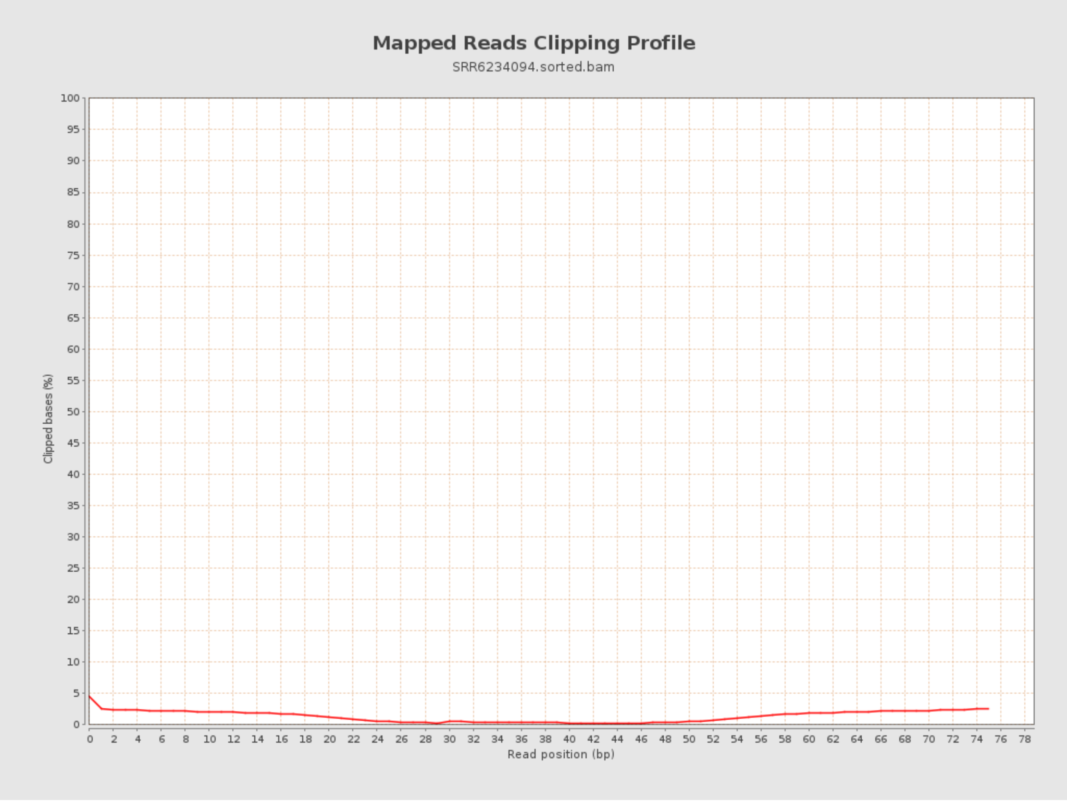
8. Results : Mapped Reads Nucleotide Content



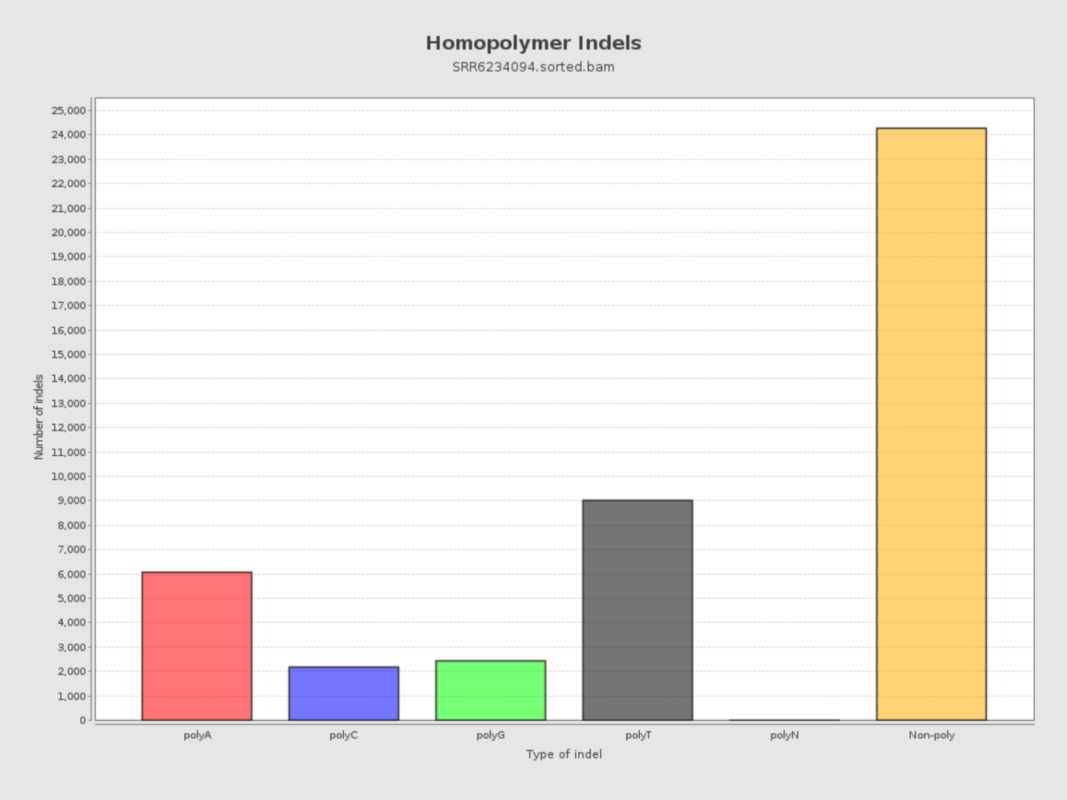
9. Results : Mapped Reads GC-content Distribution



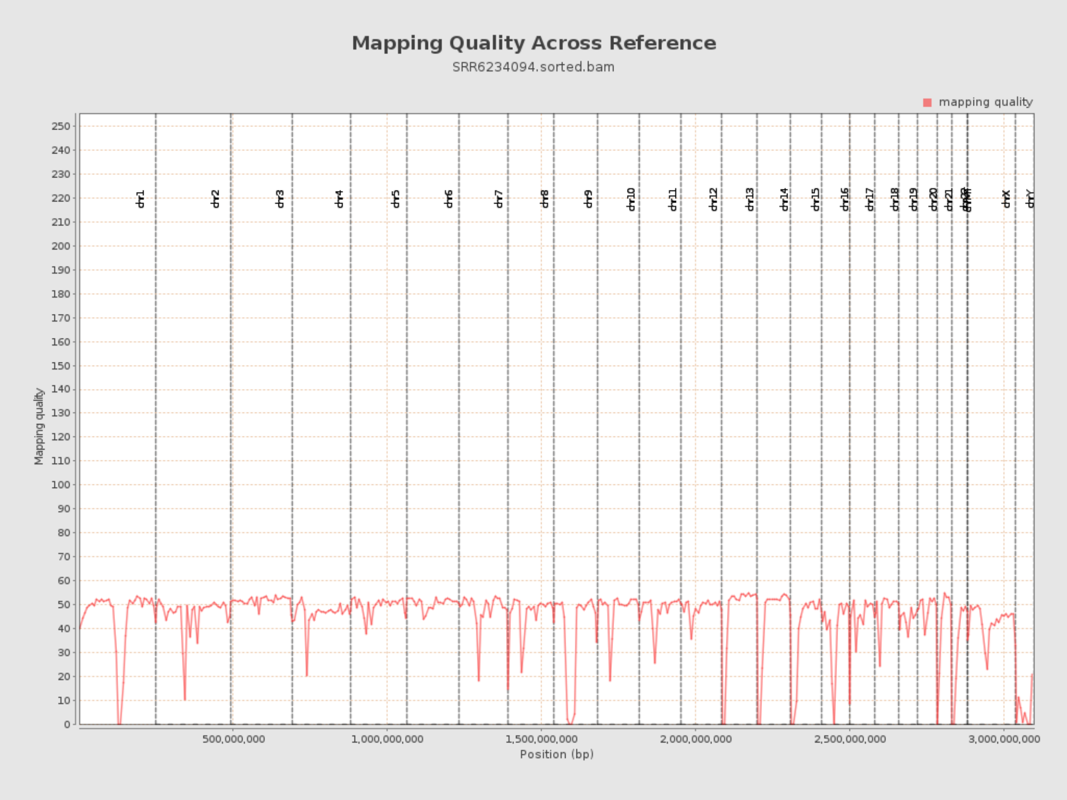
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram