Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 14:13:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234074.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_SRR6234074 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234074.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 14:13:50 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234074.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,063,502
Mapped reads	2,903,109 / 94.76%
Unmapped reads	160,393 / 5.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,795 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	226,000 / 7.38%
Duplication rate	5.89%
Clipped reads	1,182,538 / 38.6%

2.2. ACGT Content

Number/percentage of A's	54,412,053 / 27.78%
Number/percentage of C's	36,231,249 / 18.5%
Number/percentage of T's	62,255,309 / 31.79%
Number/percentage of G's	42,937,874 / 21.92%
Number/percentage of N's	19,276 / 0.01%
GC Percentage	40.42%

2.3. Coverage

Mean	0.0633

Standard Deviation	0.9403

2.4. Mapping Quality

Mean Mapping Quality	44.64

2.5. Mismatches and indels

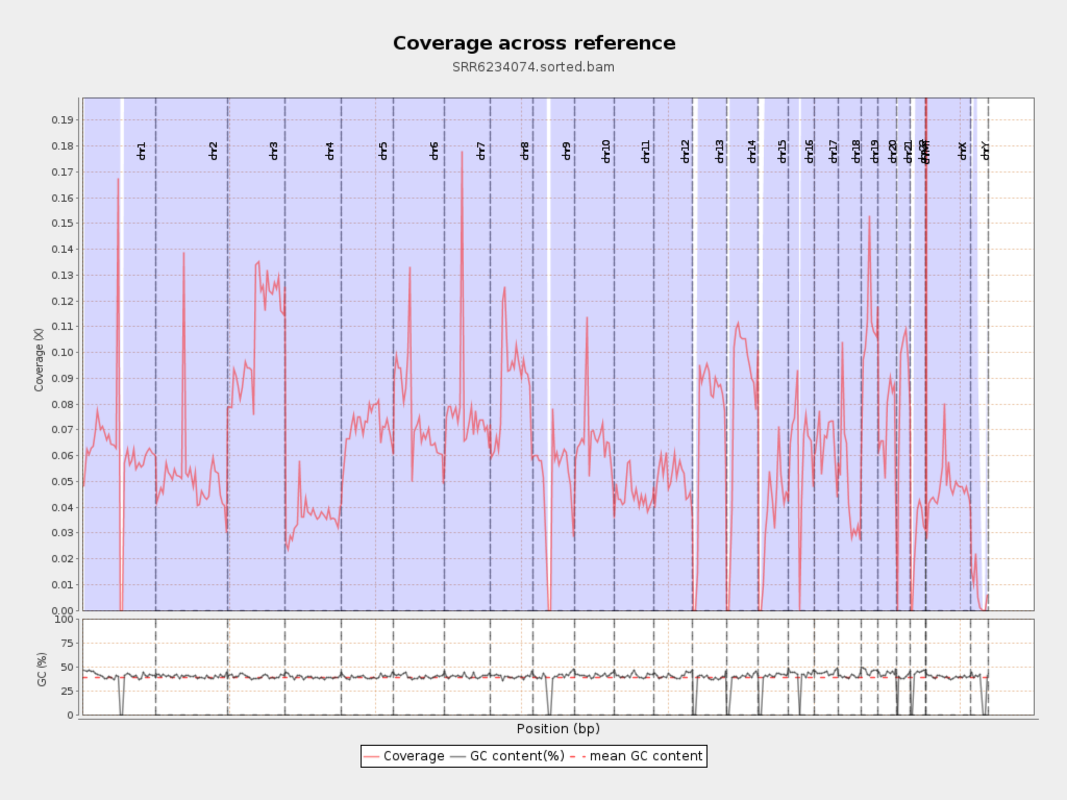
General error rate	0.63%
Mismatches	1,208,553
Insertions	14,157
Mapped reads with at least one insertion	0.48%
Deletions	47,726
Mapped reads with at least one deletion	1.63%
Homopolymer indels	45.4%

2.6. Chromosome stats

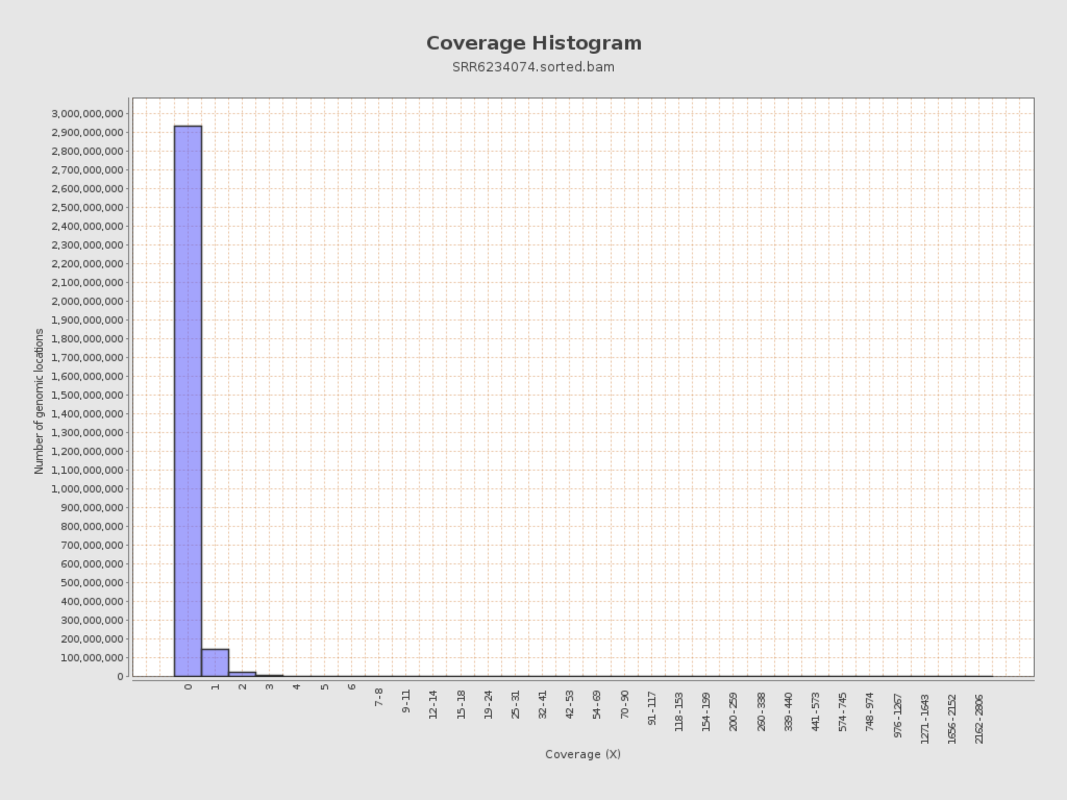
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15381583	0.0617	2.3813
chr2	243199373	12557753	0.0516	0.7878
chr3	198022430	21152568	0.1068	0.3741
chr4	191154276	6877210	0.036	0.2447
chr5	180915260	12801496	0.0708	0.3236
chr6	171115067	13033926	0.0762	0.5222
chr7	159138663	12366763	0.0777	1.4056

chr8	146364022	12821094	0.0876	1.3055
chr9	141213431	6968972	0.0494	0.5874
chr10	135534747	9013222	0.0665	0.7109
chr11	135006516	6029542	0.0447	0.4594
chr12	133851895	6898138	0.0515	0.2877
chr13	115169878	8392143	0.0729	0.3168
chr14	107349540	8837363	0.0823	0.3949
chr15	102531392	3731260	0.0364	0.235
chr16	90354753	5444694	0.0603	0.3982
chr17	81195210	5360841	0.066	0.3423
chr18	78077248	3843436	0.0492	1.434
chr19	59128983	6529941	0.1104	1.2348
chr20	63025520	4575491	0.0726	0.372
chr21	48129895	4008034	0.0833	0.3527
chr22	51304566	1404816	0.0274	0.1848
chrMT	16571	84010	5.0697	3.3832
chrX	155270560	7403005	0.0477	0.3522
chrY	59373566	423074	0.0071	0.1387

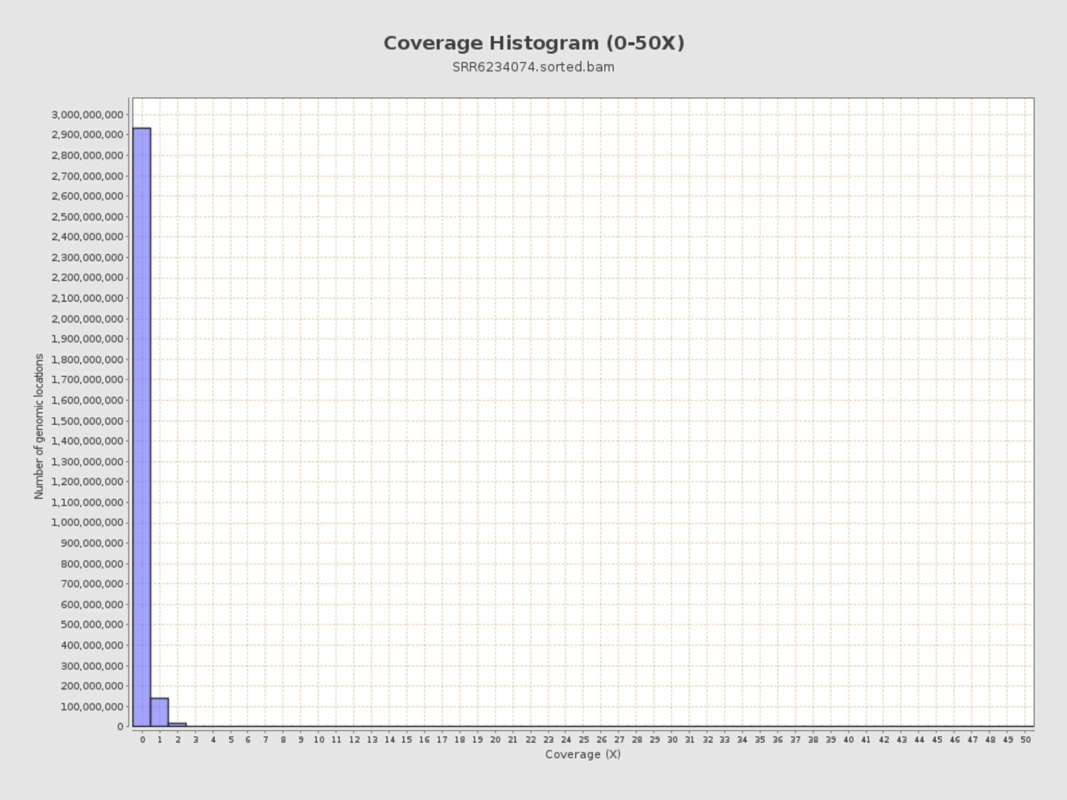
3. Results : Coverage across reference



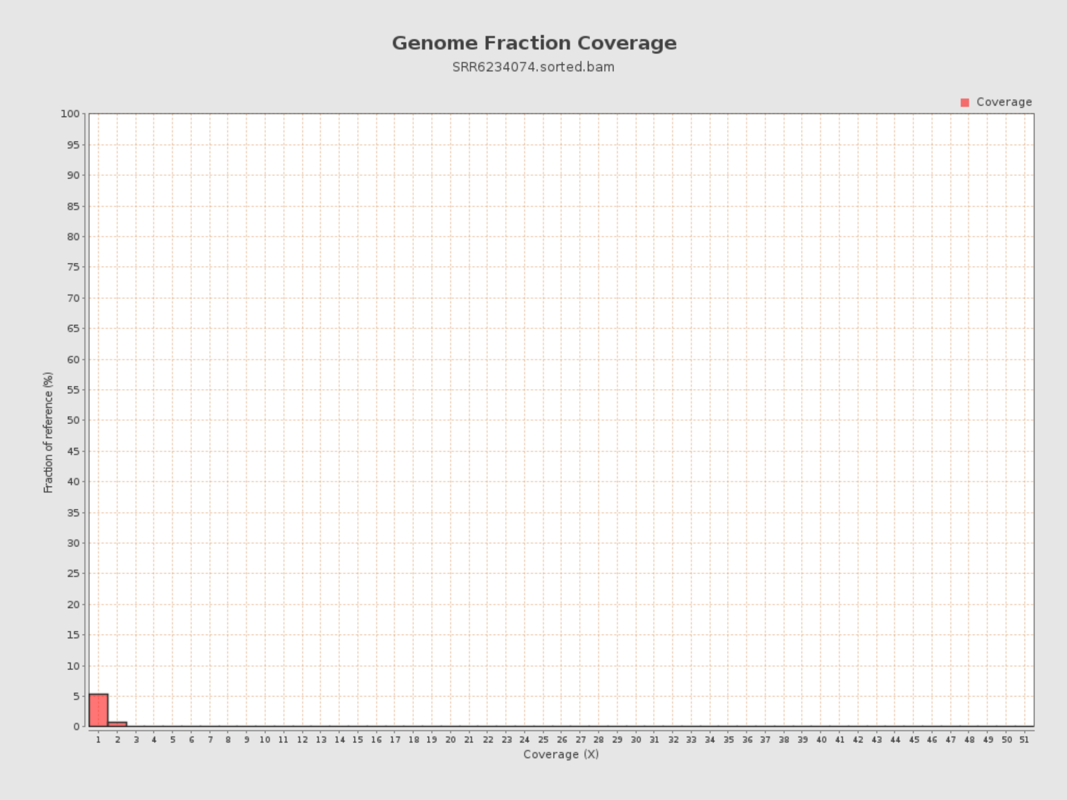
4. Results : Coverage Histogram



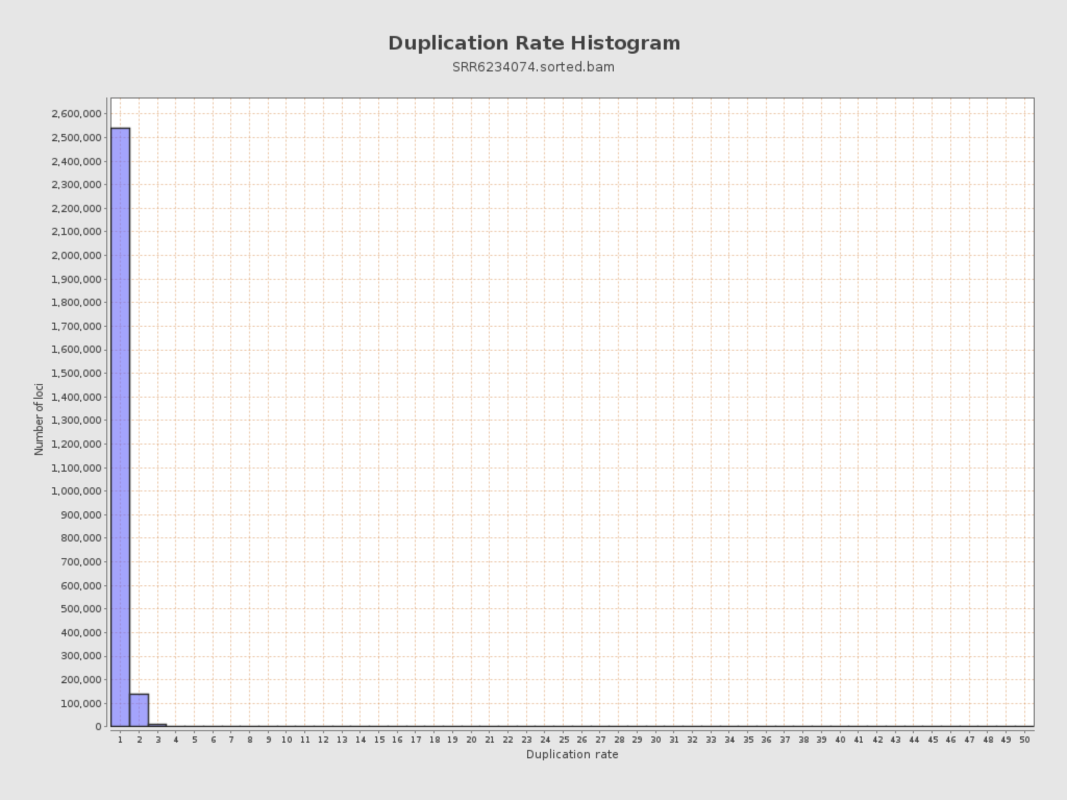
5. Results : Coverage Histogram (0-50X)



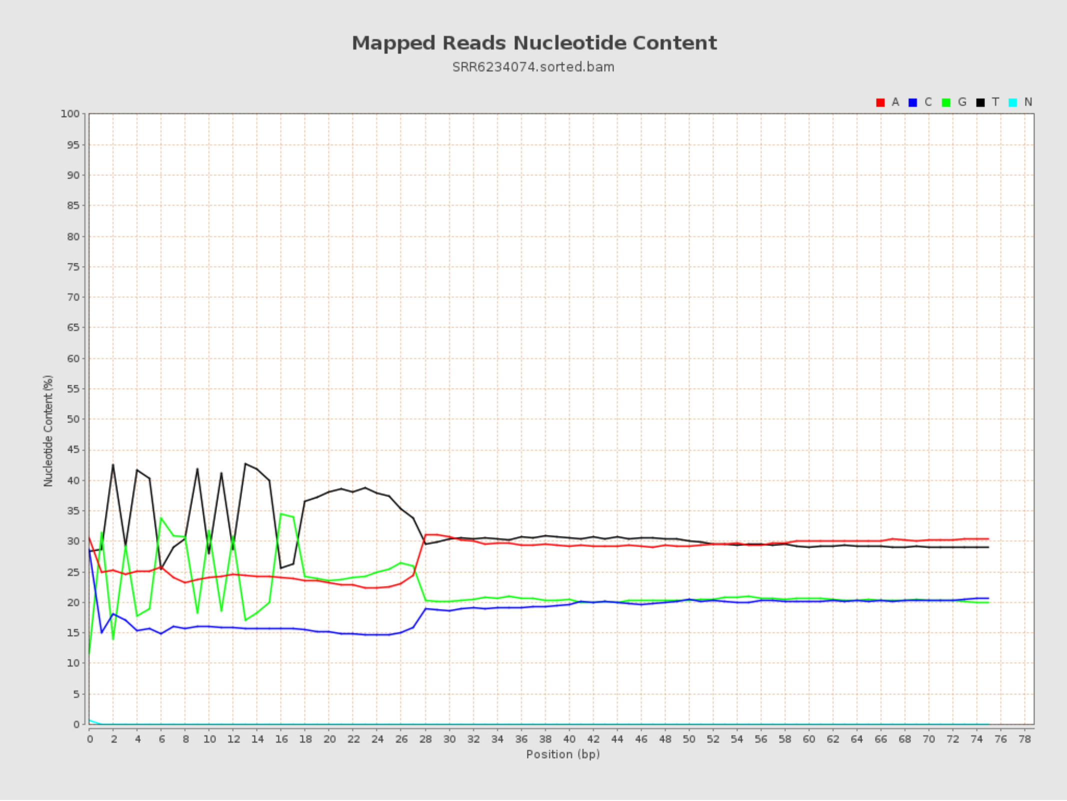
6. Results : Genome Fraction Coverage



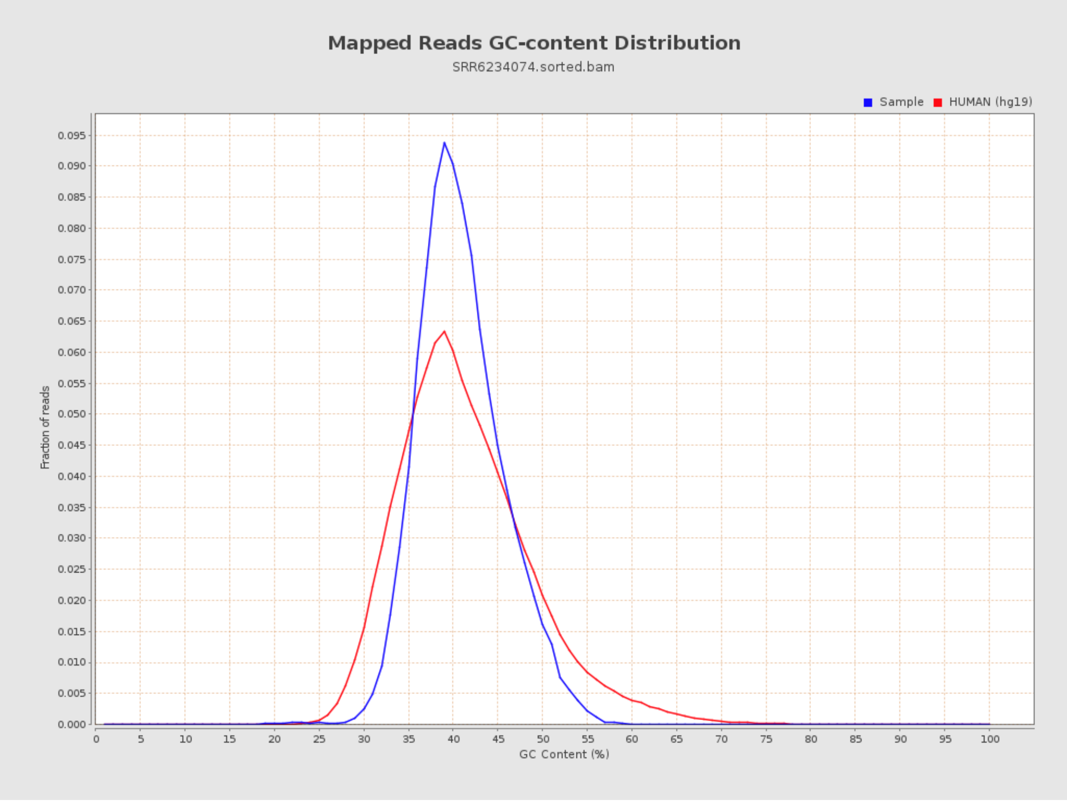
7. Results : Duplication Rate Histogram



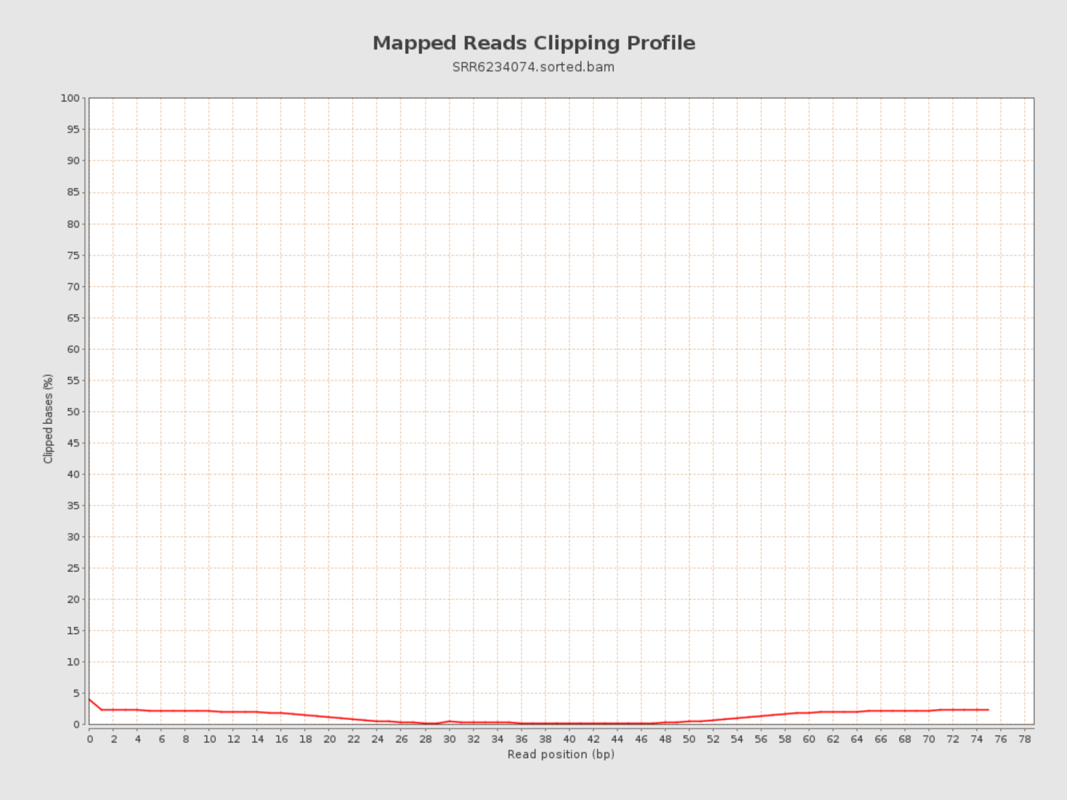
8. Results : Mapped Reads Nucleotide Content



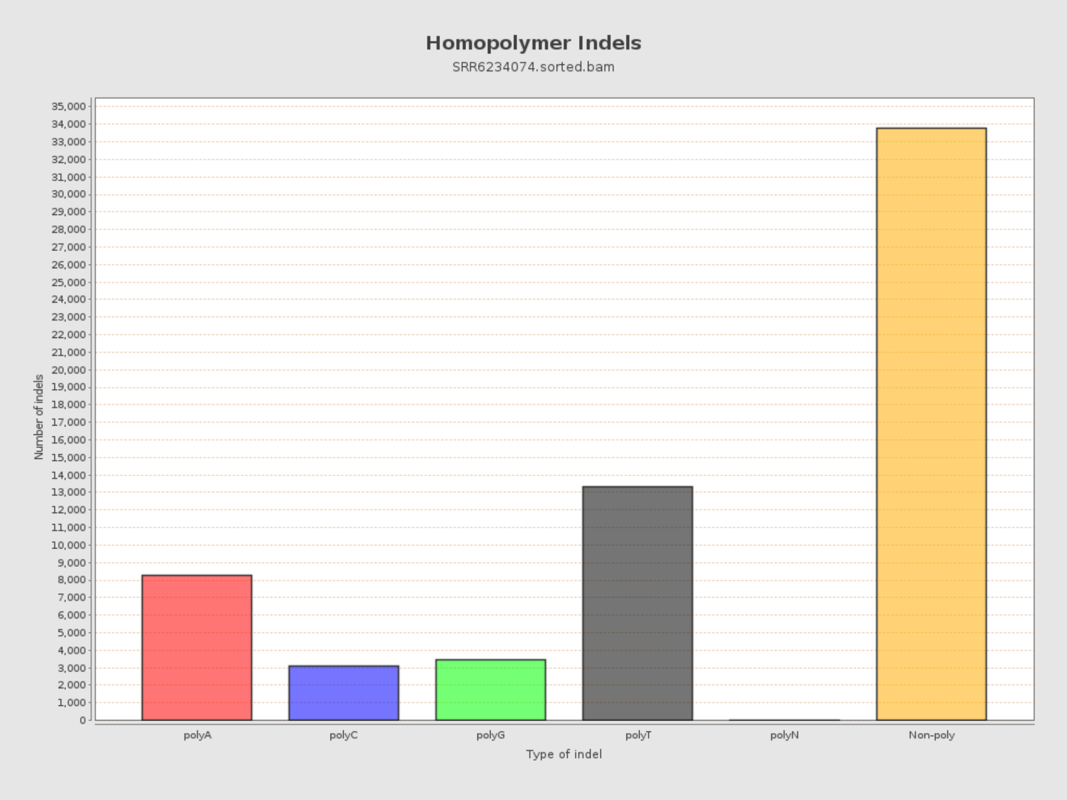
9. Results : Mapped Reads GC-content Distribution



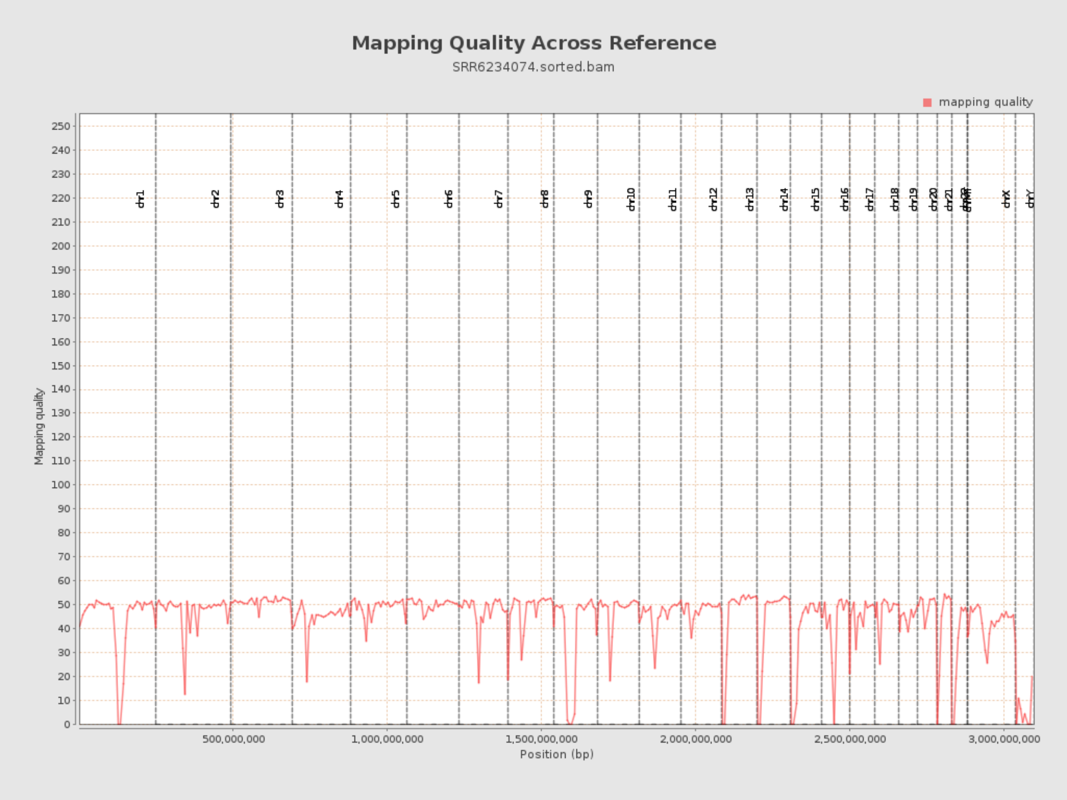
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram