Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 16:07:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6234103.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_SRR6234103 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6234103.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 16:07:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6234103.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,284,526
Mapped reads	5,009,240 / 94.79%
Unmapped reads	275,286 / 5.21%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	35,052 / 0.66%
Read min/max/mean length	30 / 76 / 76.23
Duplicated reads (estimated)	554,446 / 10.49%
Duplication rate	9.23%
Clipped reads	2,602,700 / 49.25%

2.2. ACGT Content

Number/percentage of A's	83,447,968 / 25.82%
Number/percentage of C's	58,885,939 / 18.22%
Number/percentage of T's	104,464,273 / 32.32%
Number/percentage of G's	76,346,328 / 23.62%
Number/percentage of N's	30,813 / 0.01%
GC Percentage	41.84%

2.3. Coverage

Mean	0.1044

Standard Deviation	1.0035

2.4. Mapping Quality

Mean Mapping Quality	44.27

2.5. Mismatches and indels

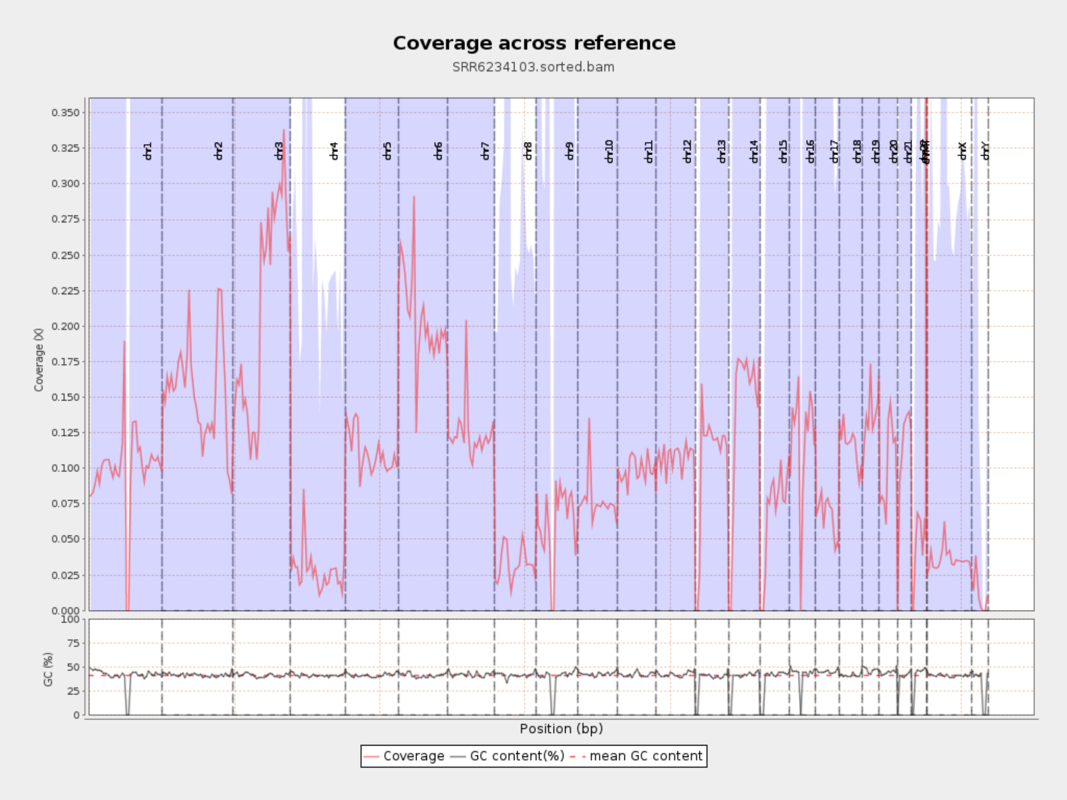
General error rate	0.55%
Mismatches	1,738,762
Insertions	20,254
Mapped reads with at least one insertion	0.4%
Deletions	73,694
Mapped reads with at least one deletion	1.46%
Homopolymer indels	44.48%

2.6. Chromosome stats

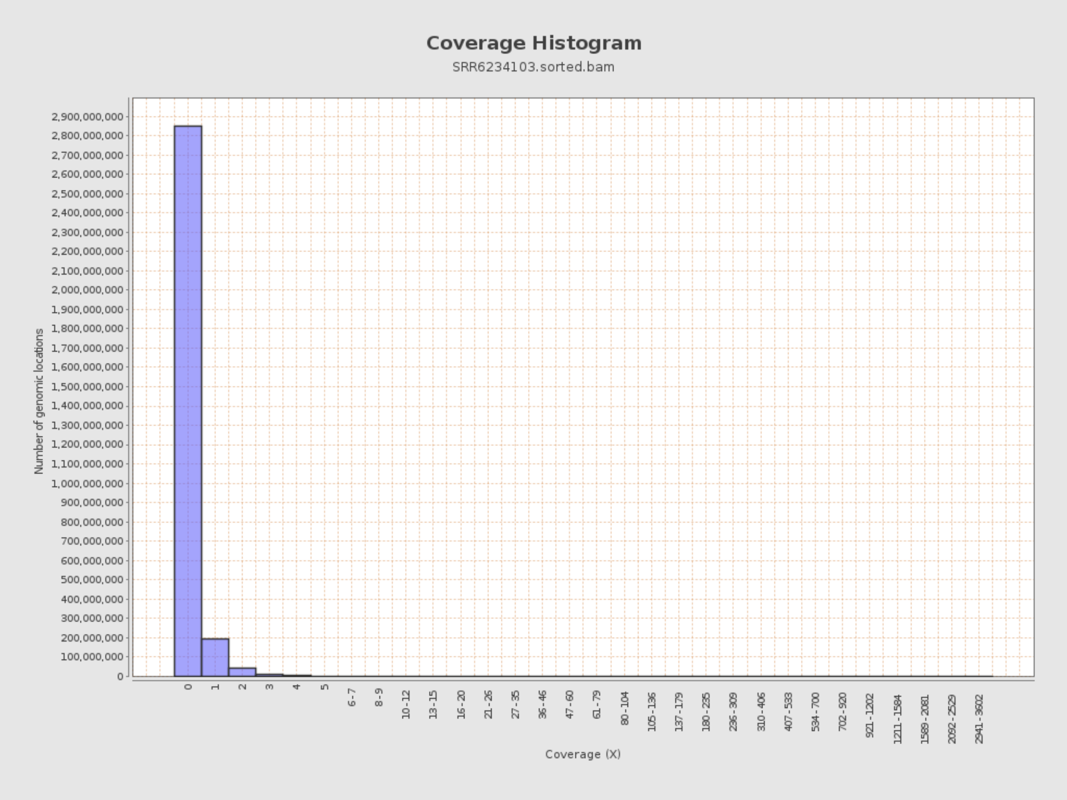
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	24647194	0.0989	2.0281
chr2	243199373	37326798	0.1535	1.7279
chr3	198022430	41623766	0.2102	0.5825
chr4	191154276	5245569	0.0274	0.2917
chr5	180915260	20045823	0.1108	0.424
chr6	171115067	35278070	0.2062	0.9634
chr7	159138663	19796006	0.1244	1.4011

chr8	146364022	4752822	0.0325	0.7952
chr9	141213431	8544292	0.0605	0.5587
chr10	135534747	10426178	0.0769	0.7453
chr11	135006516	13246379	0.0981	0.753
chr12	133851895	14419712	0.1077	0.4164
chr13	115169878	11959082	0.1038	0.4489
chr14	107349540	14835765	0.1382	0.4945
chr15	102531392	7041430	0.0687	0.3738
chr16	90354753	10929454	0.121	0.525
chr17	81195210	5357270	0.066	0.4205
chr18	78077248	9110690	0.1167	1.5974
chr19	59128983	8053419	0.1362	1.2519
chr20	63025520	6443820	0.1022	0.4339
chr21	48129895	5309769	0.1103	0.4419
chr22	51304566	2246057	0.0438	0.2539
chrMT	16571	419394	25.3089	13.3395
chrX	155270560	5586058	0.036	0.3756
chrY	59373566	658485	0.0111	0.24

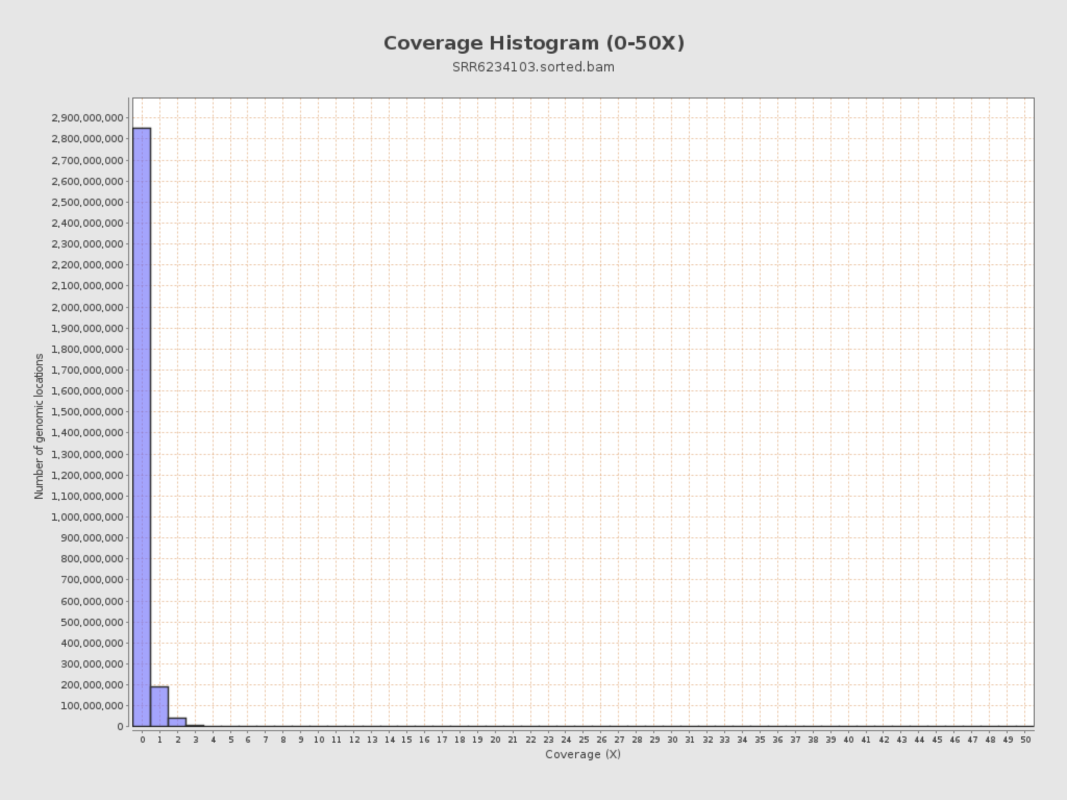
3. Results : Coverage across reference



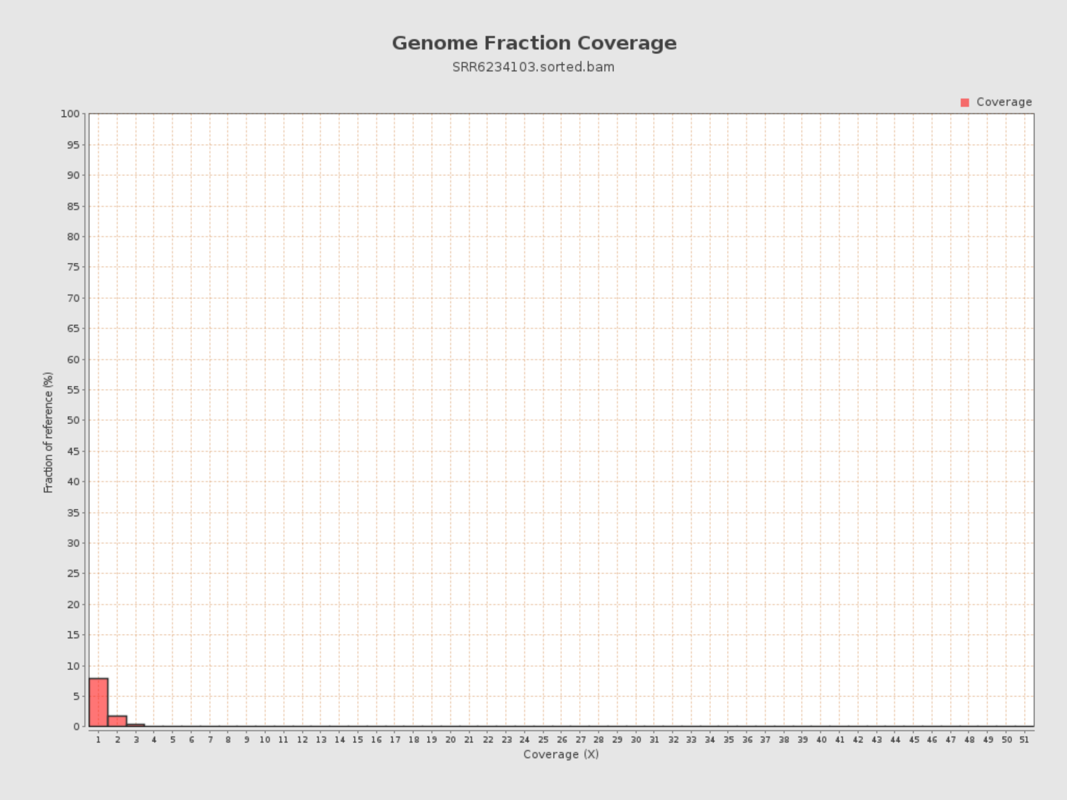
4. Results : Coverage Histogram



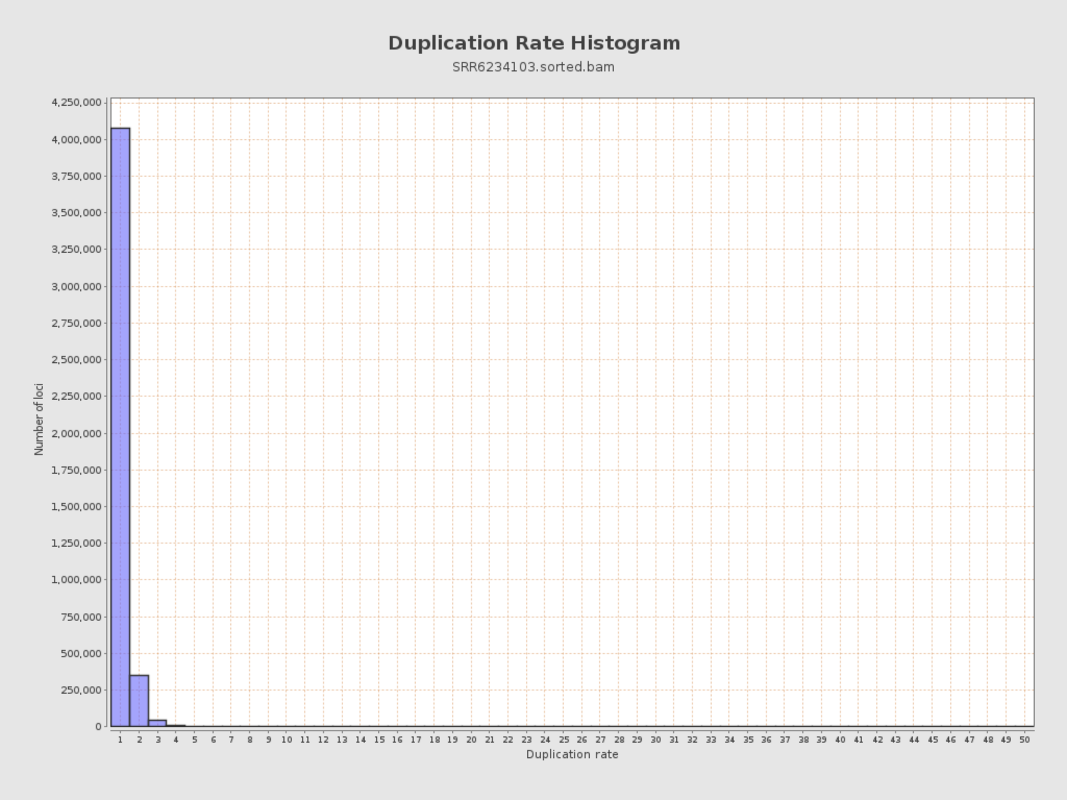
5. Results : Coverage Histogram (0-50X)



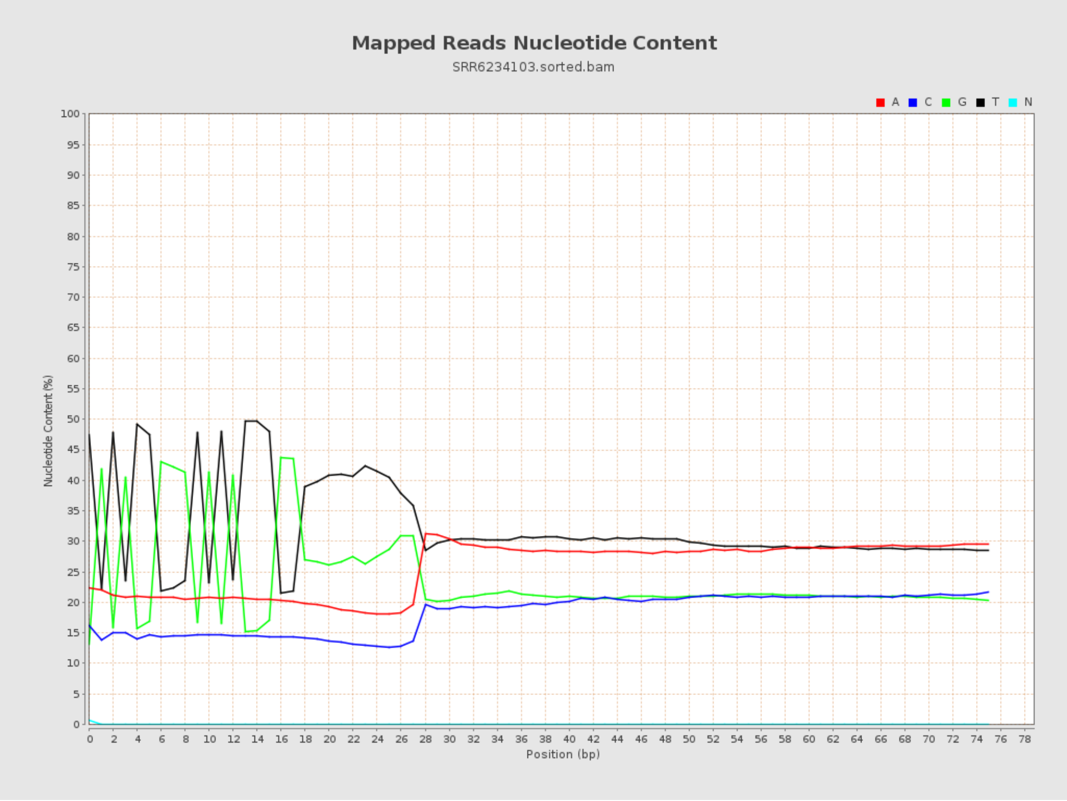
6. Results : Genome Fraction Coverage



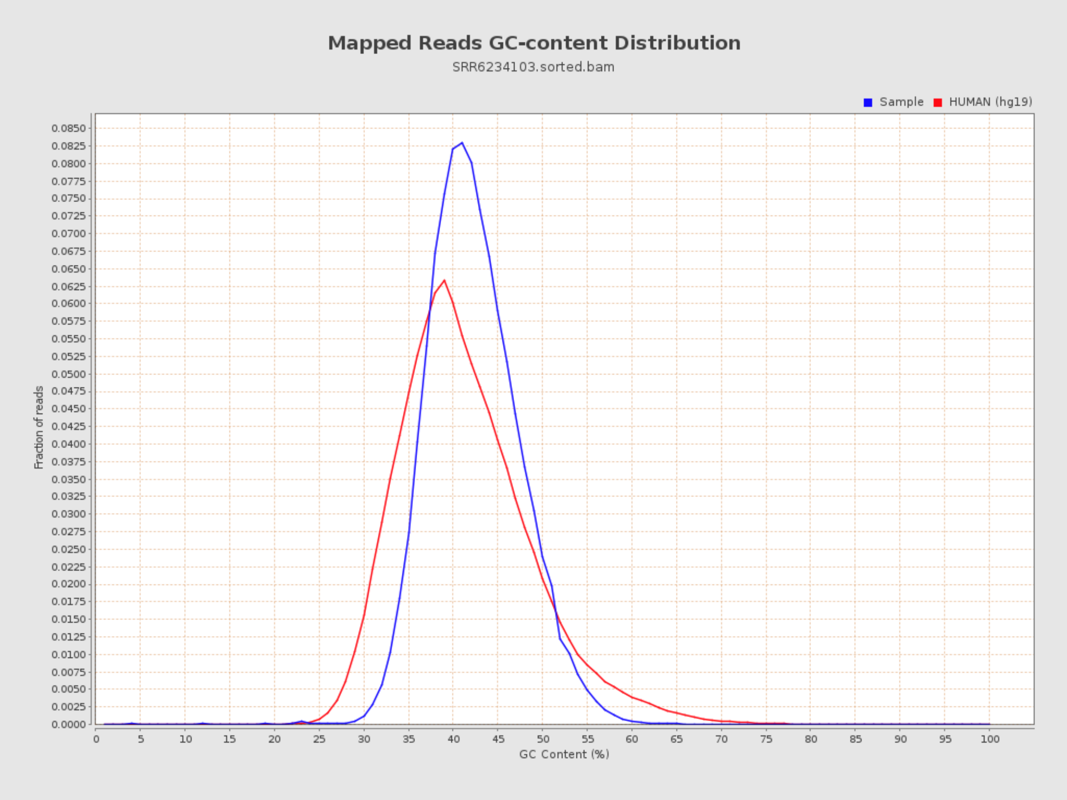
7. Results : Duplication Rate Histogram



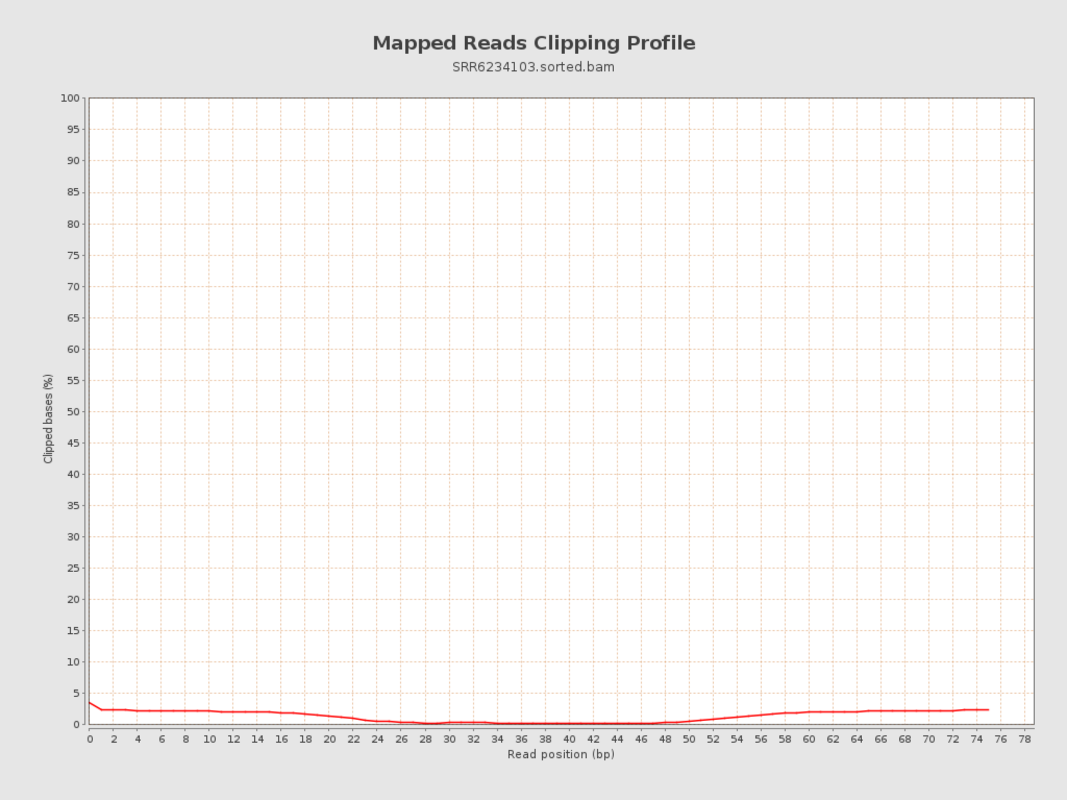
8. Results : Mapped Reads Nucleotide Content



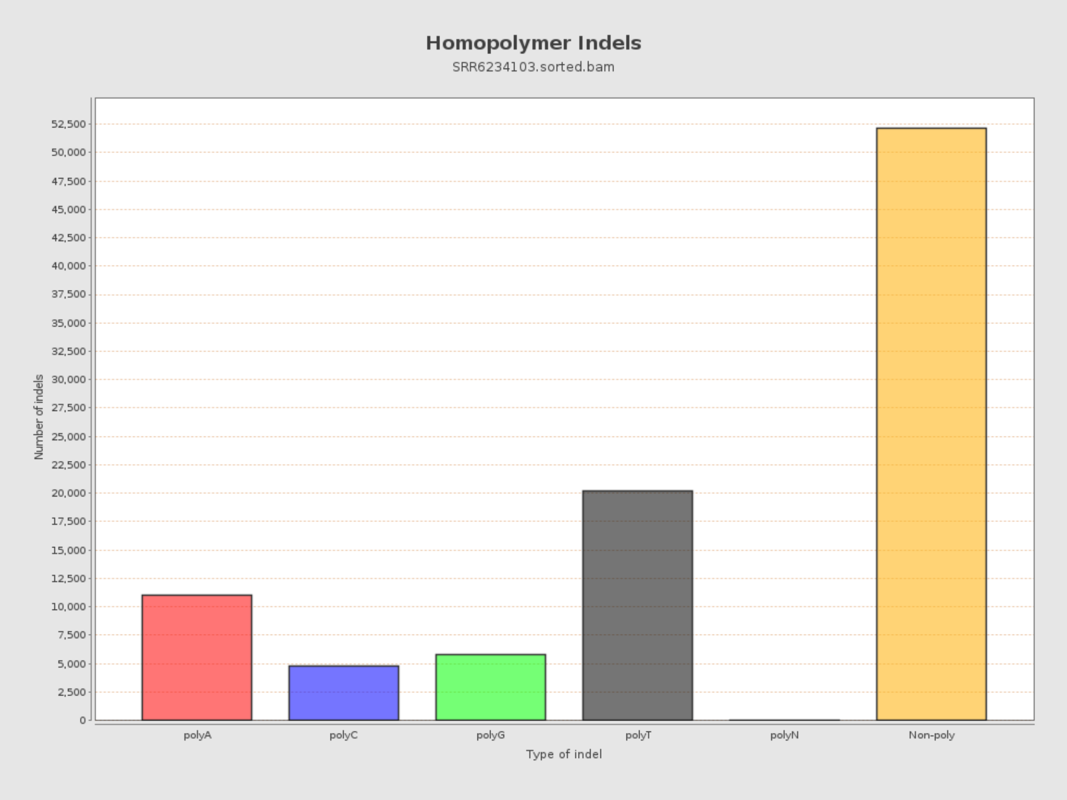
9. Results : Mapped Reads GC-content Distribution



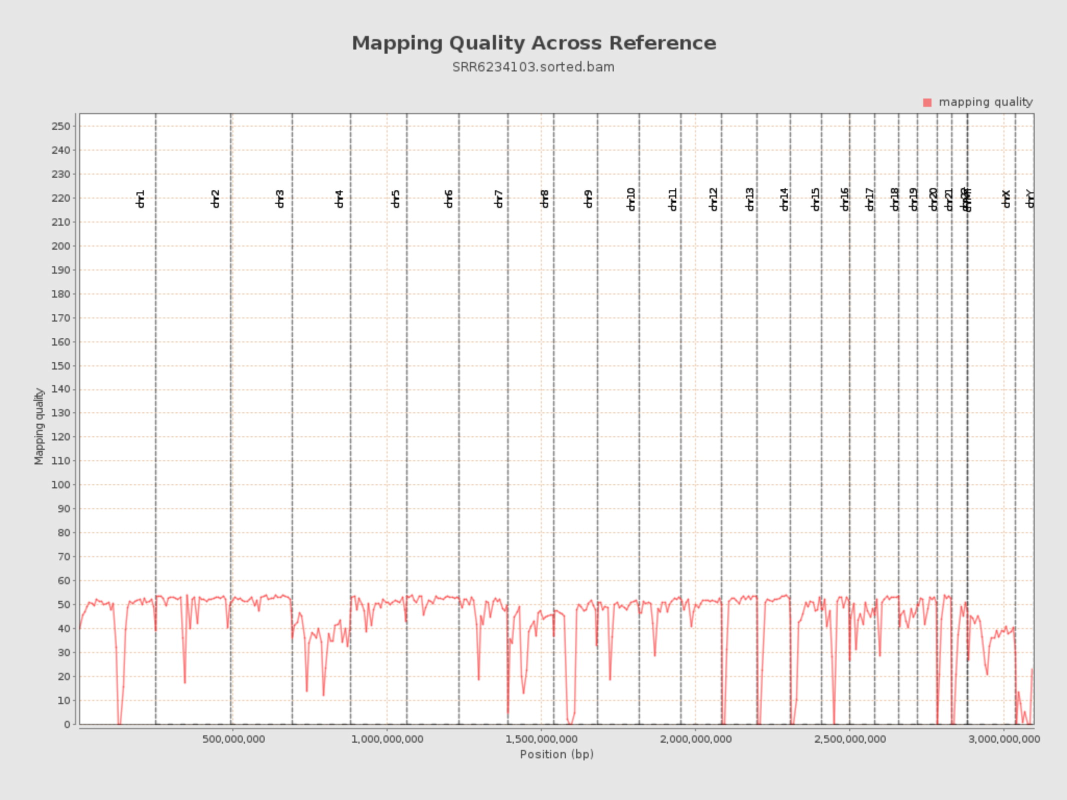
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram