Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/16 05:53:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6231829.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_SRR6231829 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6231829.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Sep 16 05:53:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6231829.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	5,675,645
Mapped reads	5,013,826 / 88.34%
Unmapped reads	661,819 / 11.66%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,087 / 0.46%
Read min/max/mean length	30 / 76 / 76.16
Duplicated reads (estimated)	491,465 / 8.66%
Duplication rate	7.85%
Clipped reads	2,751,748 / 48.48%

2.2. ACGT Content

Number/percentage of A's	80,754,564 / 25.31%
Number/percentage of C's	57,754,324 / 18.1%
Number/percentage of T's	103,787,520 / 32.53%
Number/percentage of G's	76,602,065 / 24.01%
Number/percentage of N's	120,609 / 0.04%
GC Percentage	42.12%

2.3. Coverage

Mean	0.1031

Standard Deviation	1.0418

2.4. Mapping Quality

Mean Mapping Quality	44.02

2.5. Mismatches and indels

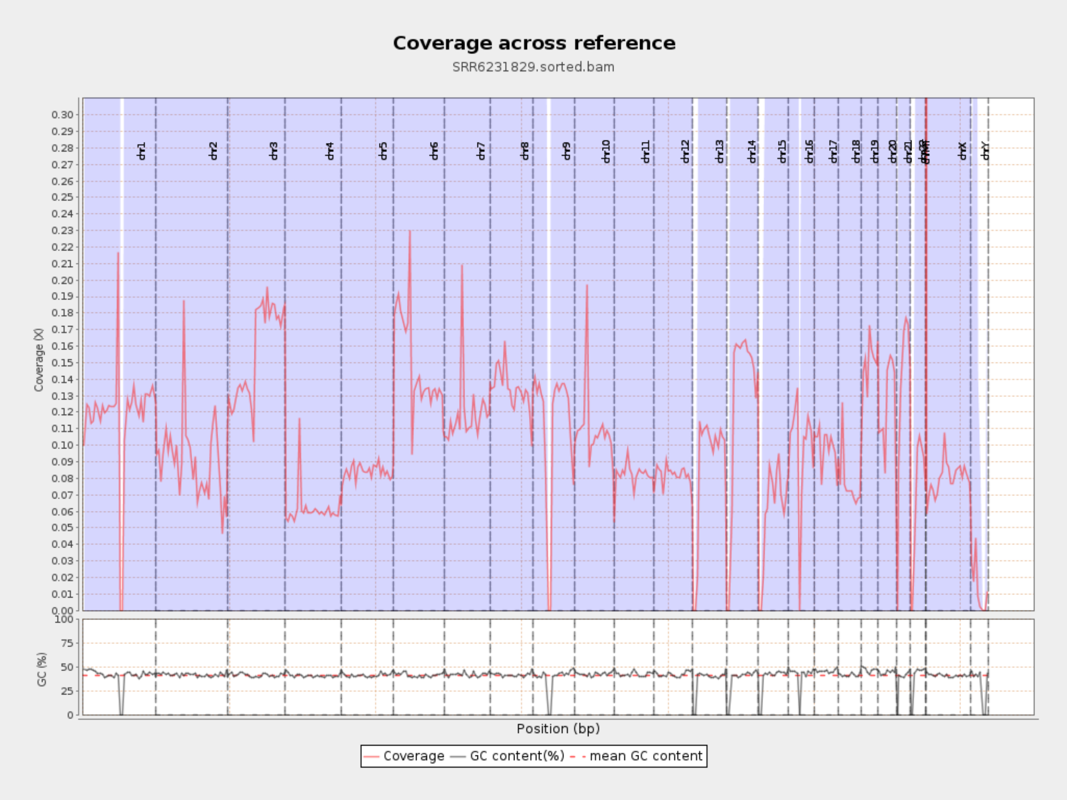
General error rate	0.63%
Mismatches	1,983,262
Insertions	20,612
Mapped reads with at least one insertion	0.41%
Deletions	72,039
Mapped reads with at least one deletion	1.42%
Homopolymer indels	44.23%

2.6. Chromosome stats

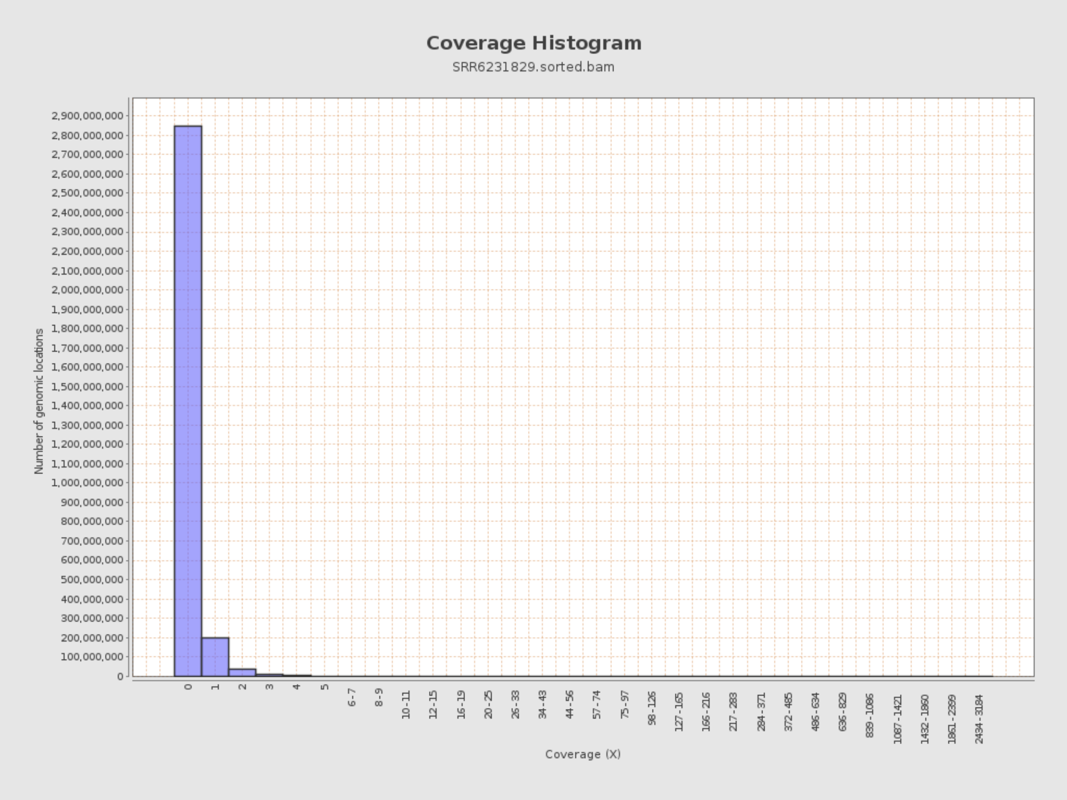
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	29389147	0.1179	2.3425
chr2	243199373	22119117	0.091	1.4826
chr3	198022430	30801362	0.1555	0.4922
chr4	191154276	11803227	0.0617	0.3774
chr5	180915260	15225403	0.0842	0.373
chr6	171115067	25533718	0.1492	0.874
chr7	159138663	18988822	0.1193	1.3926

chr8	146364022	19610521	0.134	0.9007
chr9	141213431	15733696	0.1114	0.7328
chr10	135534747	14909285	0.11	0.9704
chr11	135006516	11123759	0.0824	0.6325
chr12	133851895	11013245	0.0823	0.3905
chr13	115169878	10120267	0.0879	0.3996
chr14	107349540	13781312	0.1284	0.4992
chr15	102531392	6029144	0.0588	0.3613
chr16	90354753	8676483	0.096	0.5172
chr17	81195210	8084286	0.0996	0.4565
chr18	78077248	6048367	0.0775	1.7127
chr19	59128983	8820987	0.1492	1.3875
chr20	63025520	7865273	0.1248	0.4874
chr21	48129895	6468946	0.1344	0.4996
chr22	51304566	3492553	0.0681	0.3174
chrMT	16571	261232	15.7644	8.925
chrX	155270560	12449044	0.0802	0.4666
chrY	59373566	799010	0.0135	0.2865

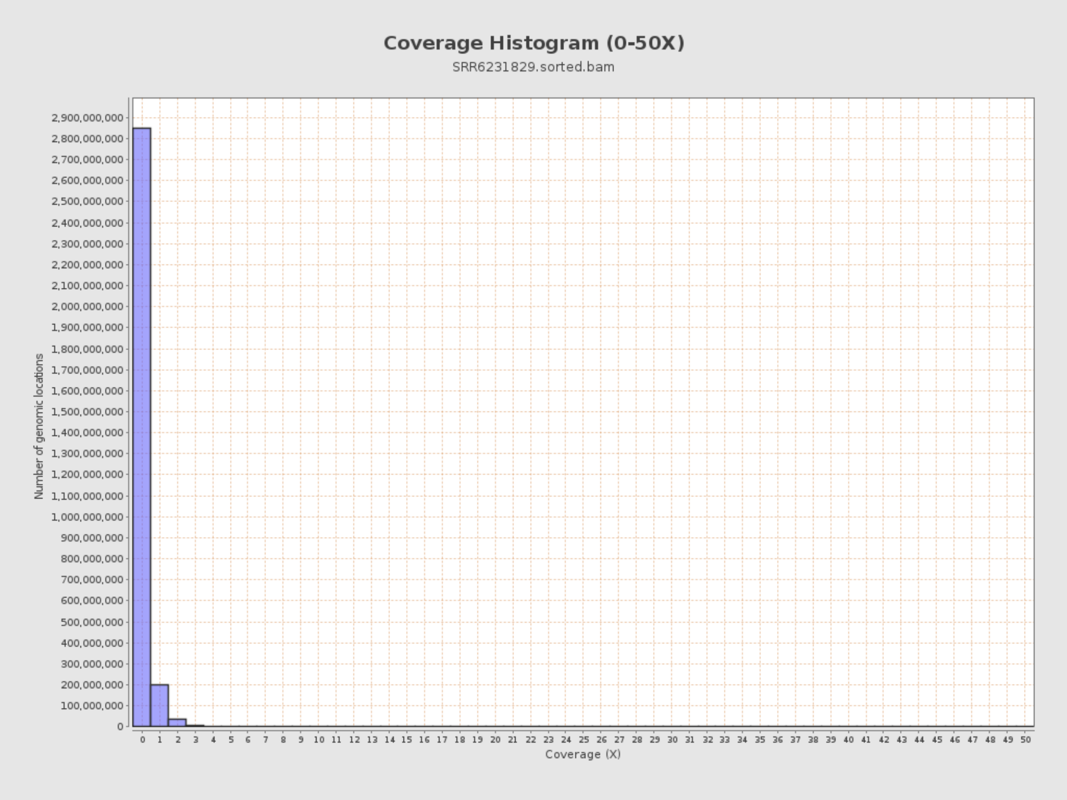
3. Results : Coverage across reference



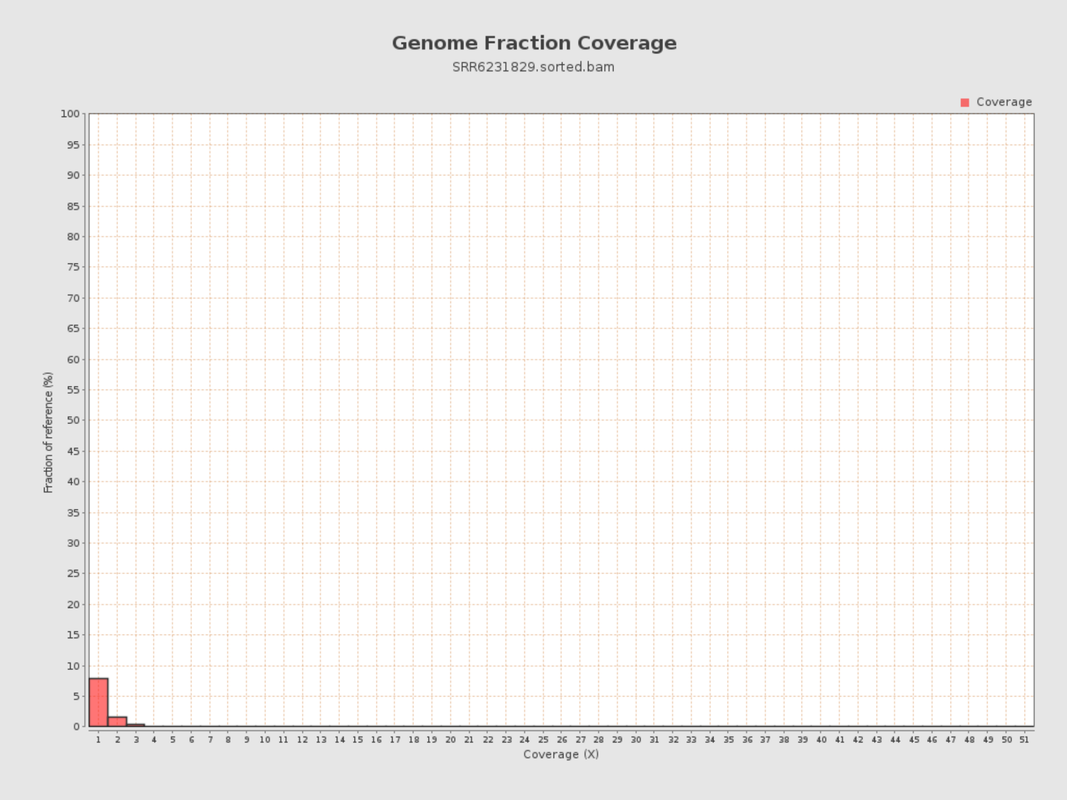
4. Results : Coverage Histogram



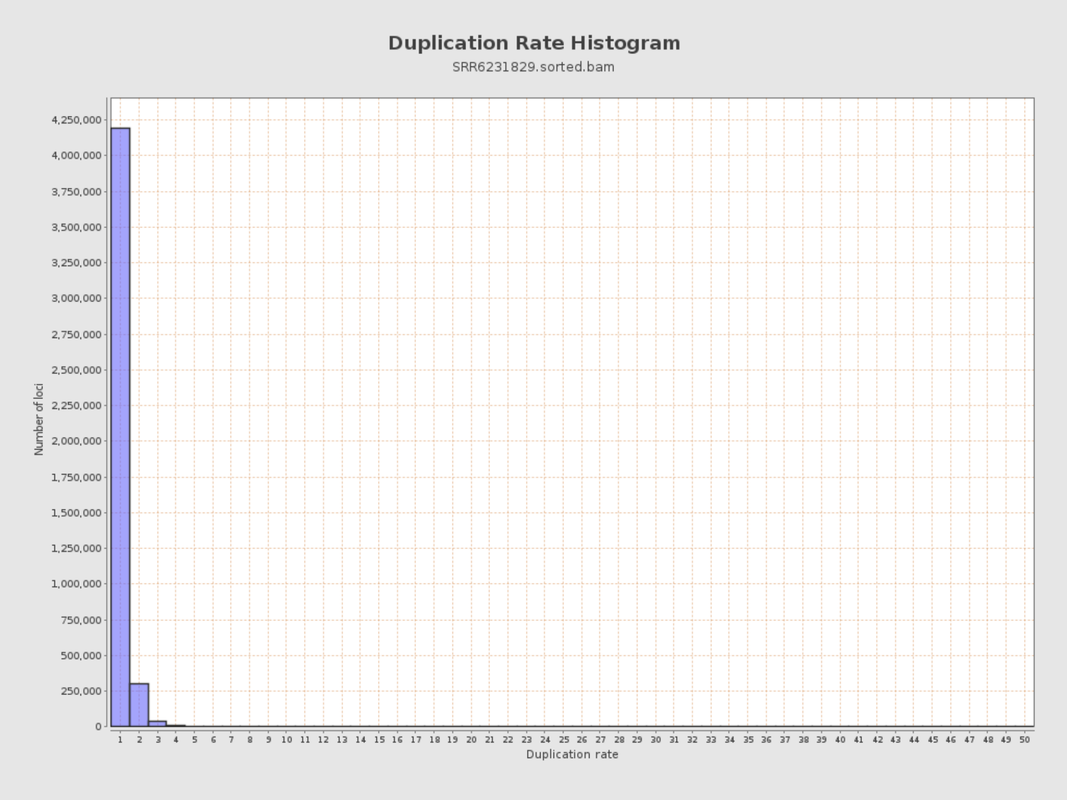
5. Results : Coverage Histogram (0-50X)



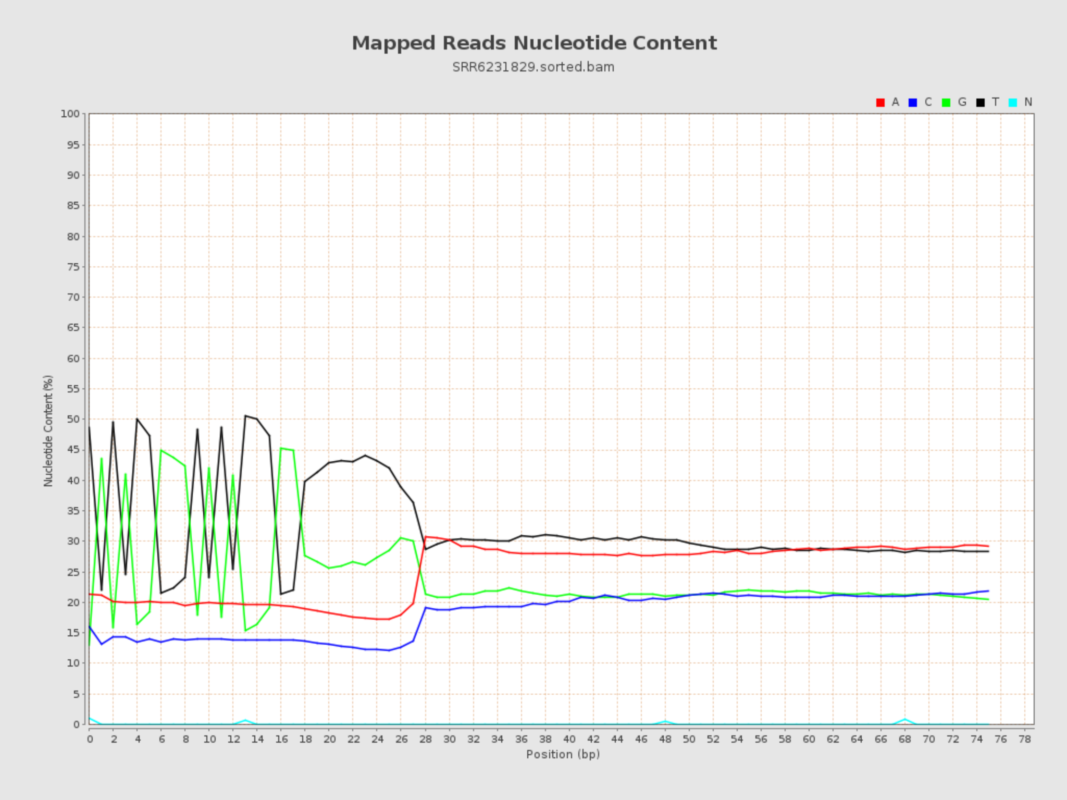
6. Results : Genome Fraction Coverage



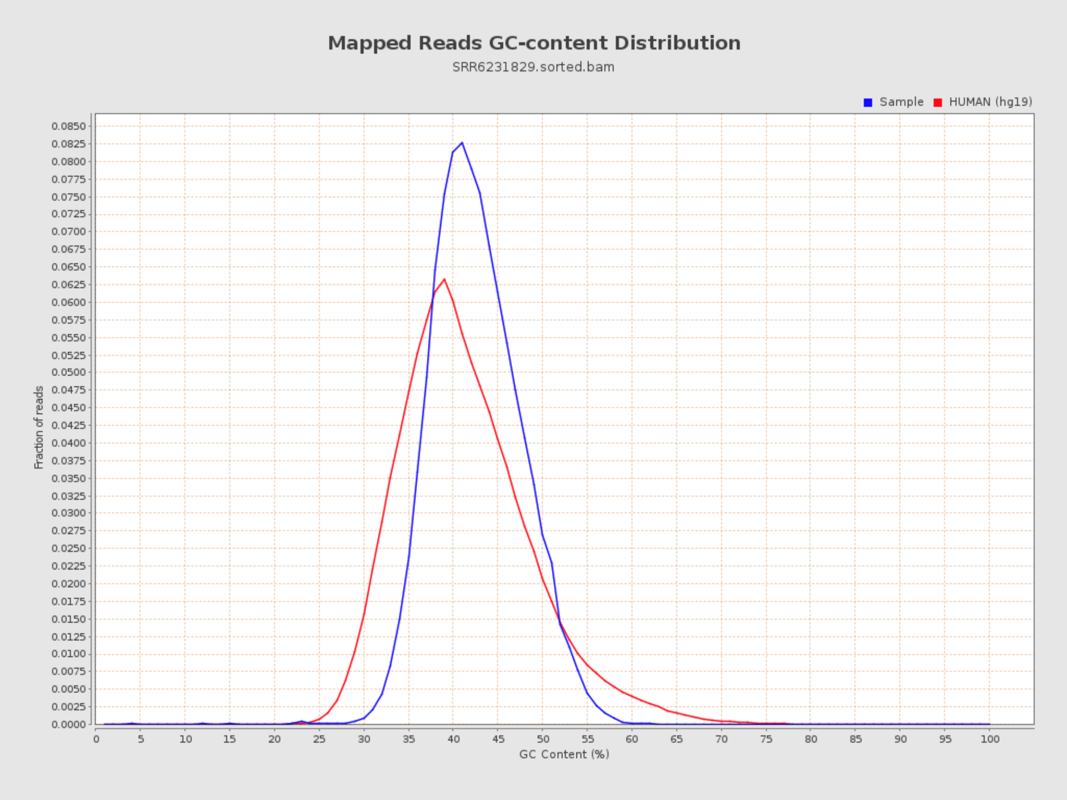
7. Results : Duplication Rate Histogram



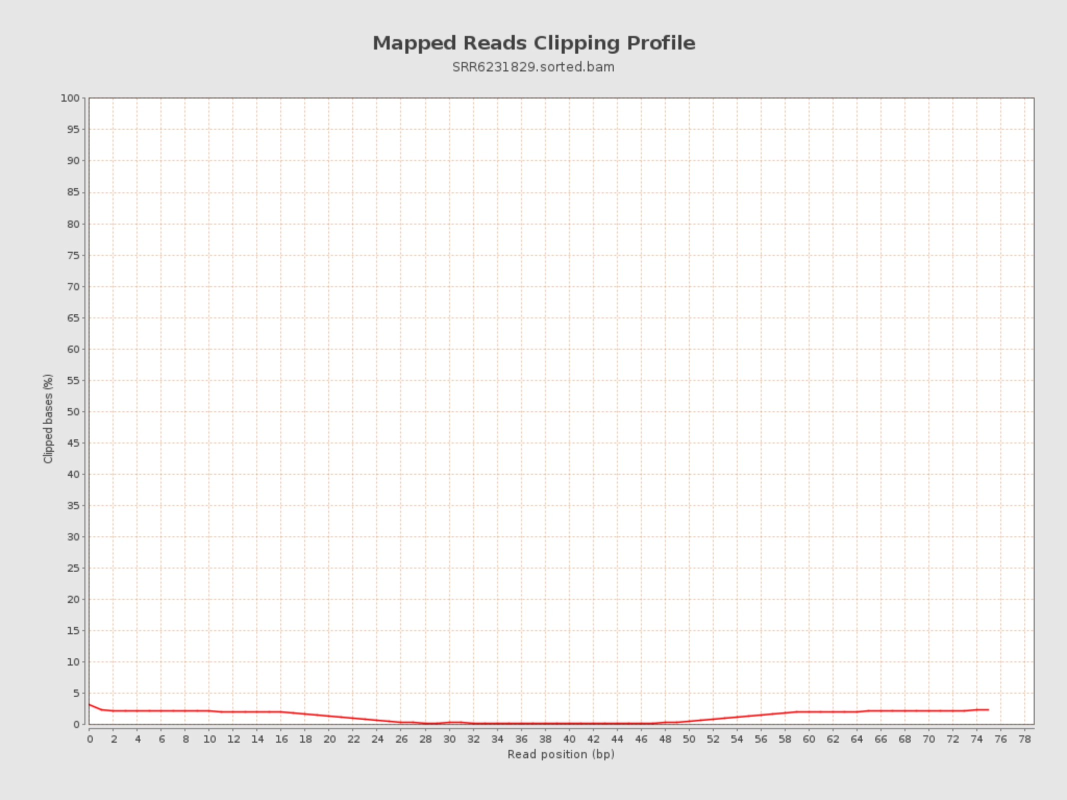
8. Results : Mapped Reads Nucleotide Content



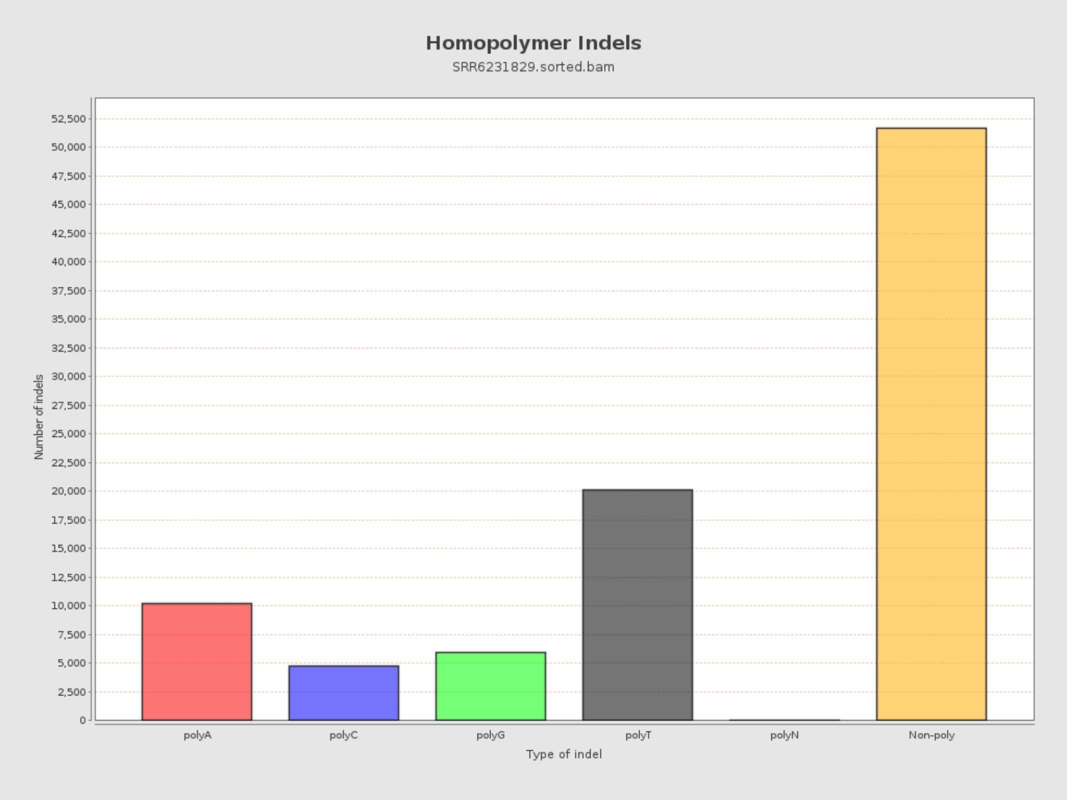
9. Results : Mapped Reads GC-content Distribution



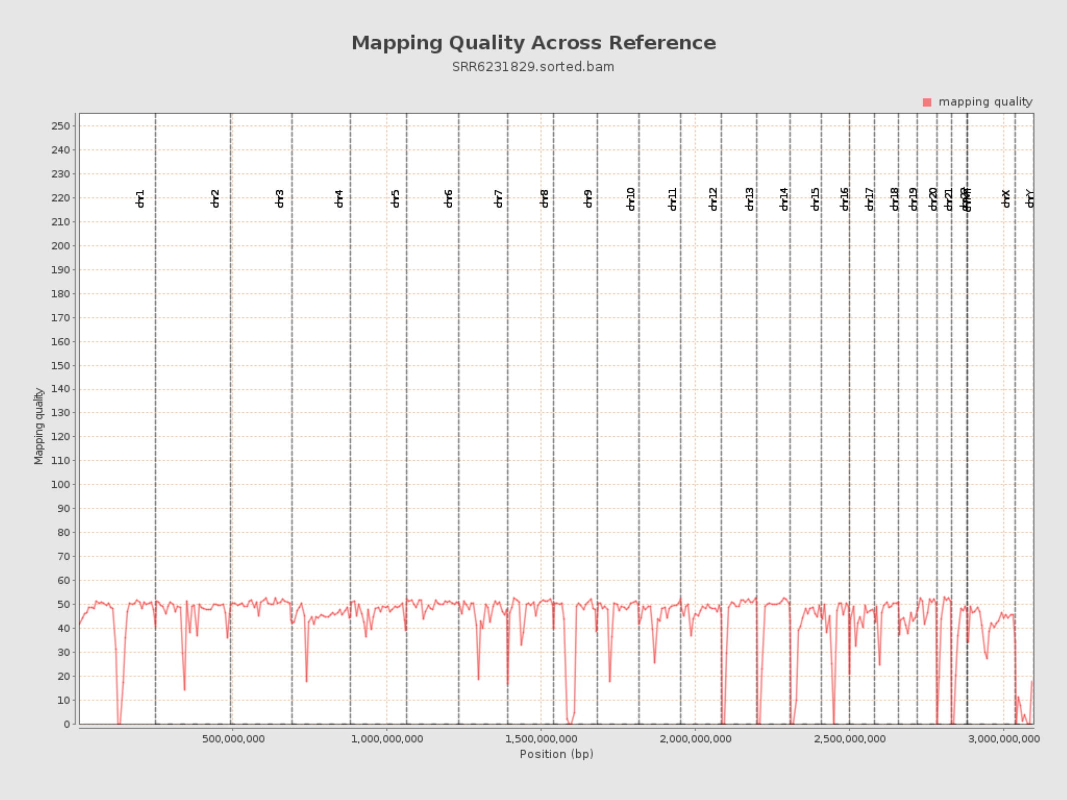
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram