Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 04:14:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081236.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_SRR3081236 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081236.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 04:14:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081236.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,013,671
Mapped reads	2,650,067 / 87.93%
Unmapped reads	363,604 / 12.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,736 / 1.12%
Read min/max/mean length	30 / 76 / 76.39
Duplicated reads (estimated)	166,058 / 5.51%
Duplication rate	5.12%
Clipped reads	1,557,063 / 51.67%

2.2. ACGT Content

Number/percentage of A's	49,187,153 / 29.08%
Number/percentage of C's	32,820,366 / 19.4%
Number/percentage of T's	51,533,587 / 30.47%
Number/percentage of G's	35,591,944 / 21.04%
Number/percentage of N's	21,056 / 0.01%
GC Percentage	40.44%

2.3. Coverage

Mean	0.0547

Standard Deviation	0.4273

2.4. Mapping Quality

Mean Mapping Quality	45.11

2.5. Mismatches and indels

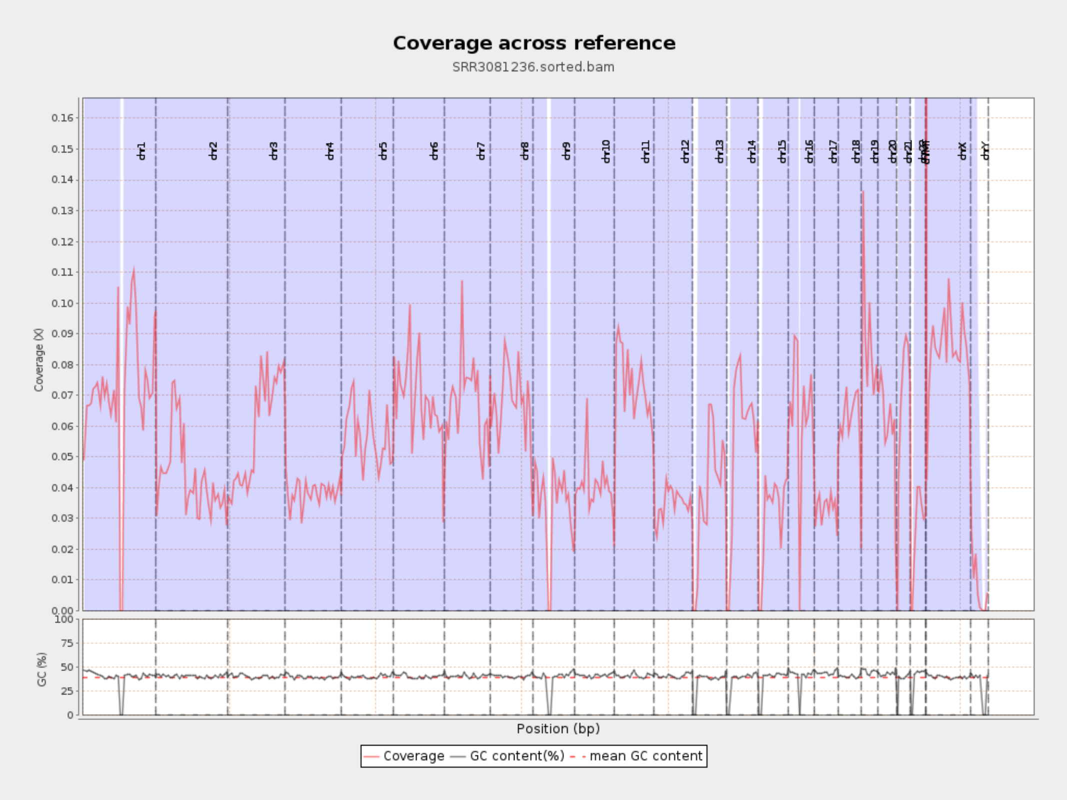
General error rate	0.92%
Mismatches	1,532,914
Insertions	12,544
Mapped reads with at least one insertion	0.47%
Deletions	38,316
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.97%

2.6. Chromosome stats

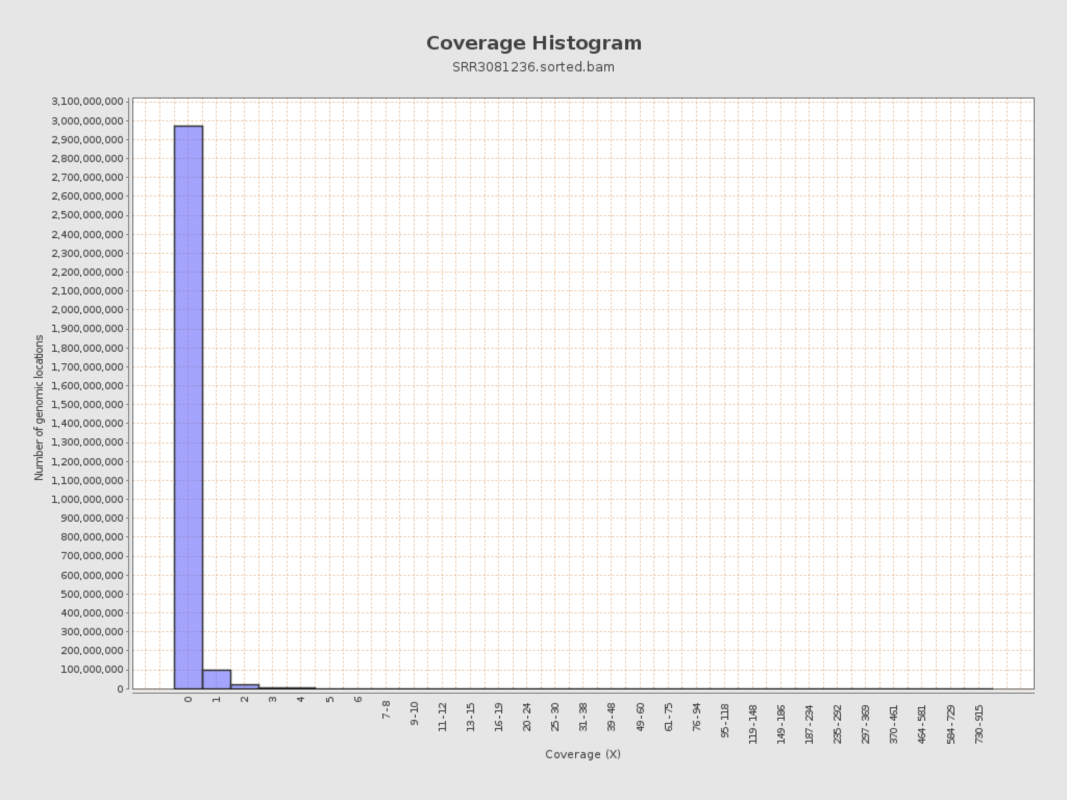
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17856877	0.0716	0.7981
chr2	243199373	10597085	0.0436	0.4194
chr3	198022430	11570673	0.0584	0.3092
chr4	191154276	7310277	0.0382	0.2549
chr5	180915260	10201120	0.0564	0.3034
chr6	171115067	11882750	0.0694	0.3936
chr7	159138663	10692552	0.0672	0.5969

chr8	146364022	9877757	0.0675	0.4949
chr9	141213431	4847599	0.0343	0.308
chr10	135534747	5557625	0.041	0.3972
chr11	135006516	9905963	0.0734	0.4958
chr12	133851895	4634898	0.0346	0.2404
chr13	115169878	4520608	0.0393	0.255
chr14	107349540	6059488	0.0564	0.313
chr15	102531392	3138957	0.0306	0.2278
chr16	90354753	5638541	0.0624	0.3265
chr17	81195210	2715324	0.0334	0.2709
chr18	78077248	4984407	0.0638	0.4801
chr19	59128983	5088557	0.0861	0.6249
chr20	63025520	3925276	0.0623	0.3206
chr21	48129895	3239004	0.0673	0.34
chr22	51304566	1315894	0.0256	0.1967
chrMT	16571	51450	3.1048	3.0979
chrX	155270560	13158900	0.0847	0.3985
chrY	59373566	444946	0.0075	0.1252

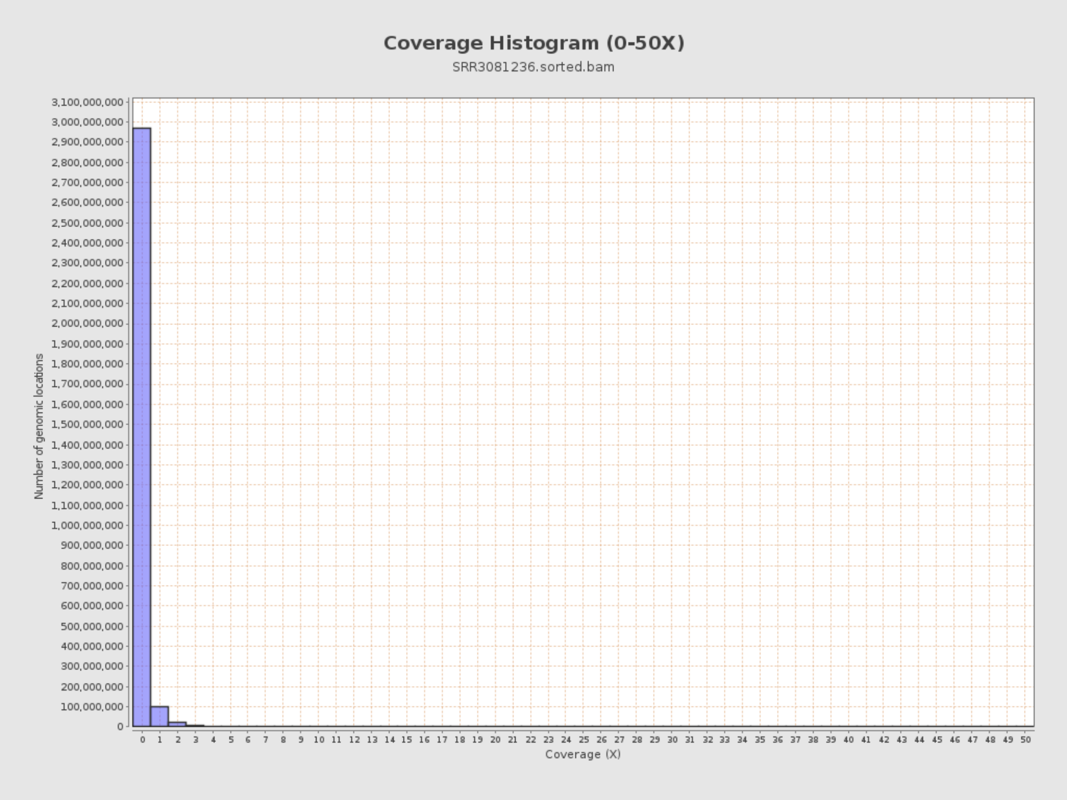
3. Results : Coverage across reference



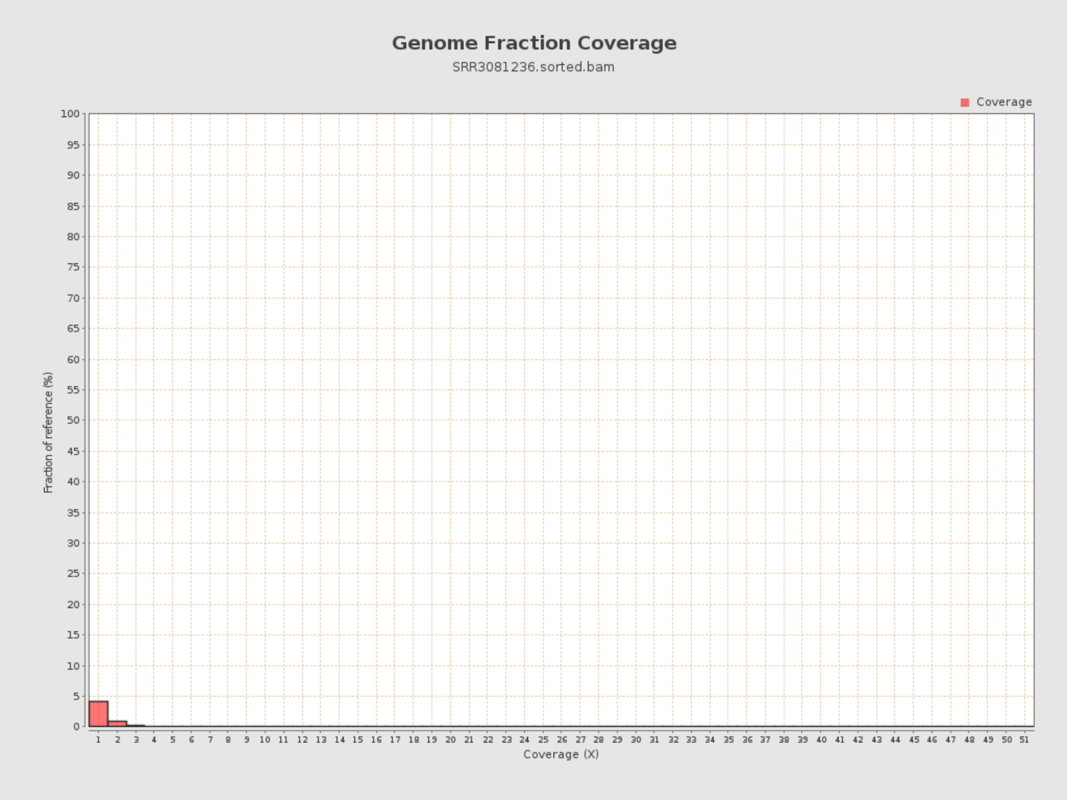
4. Results : Coverage Histogram



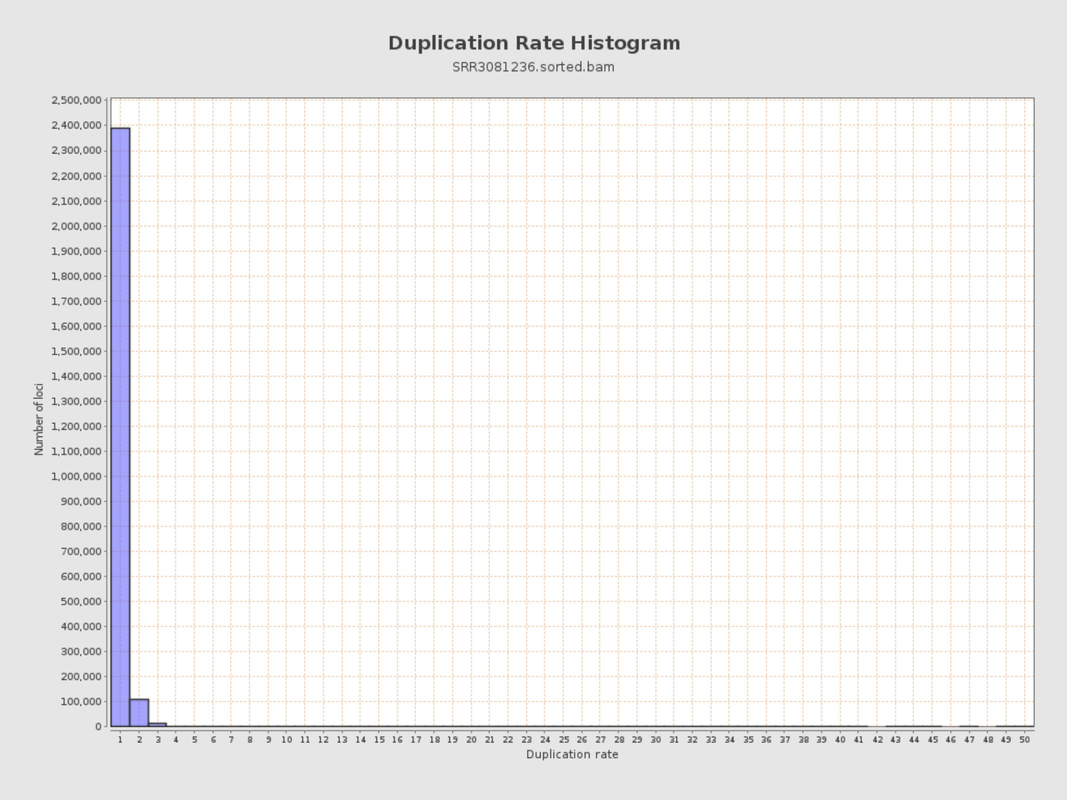
5. Results : Coverage Histogram (0-50X)



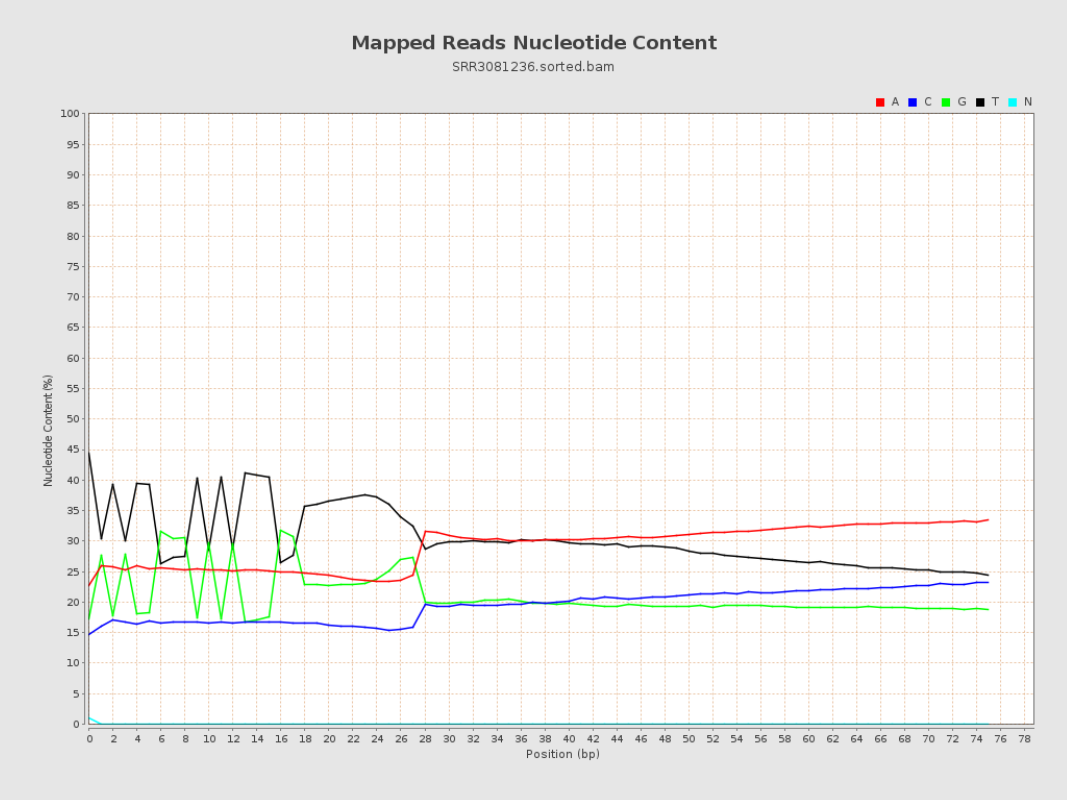
6. Results : Genome Fraction Coverage



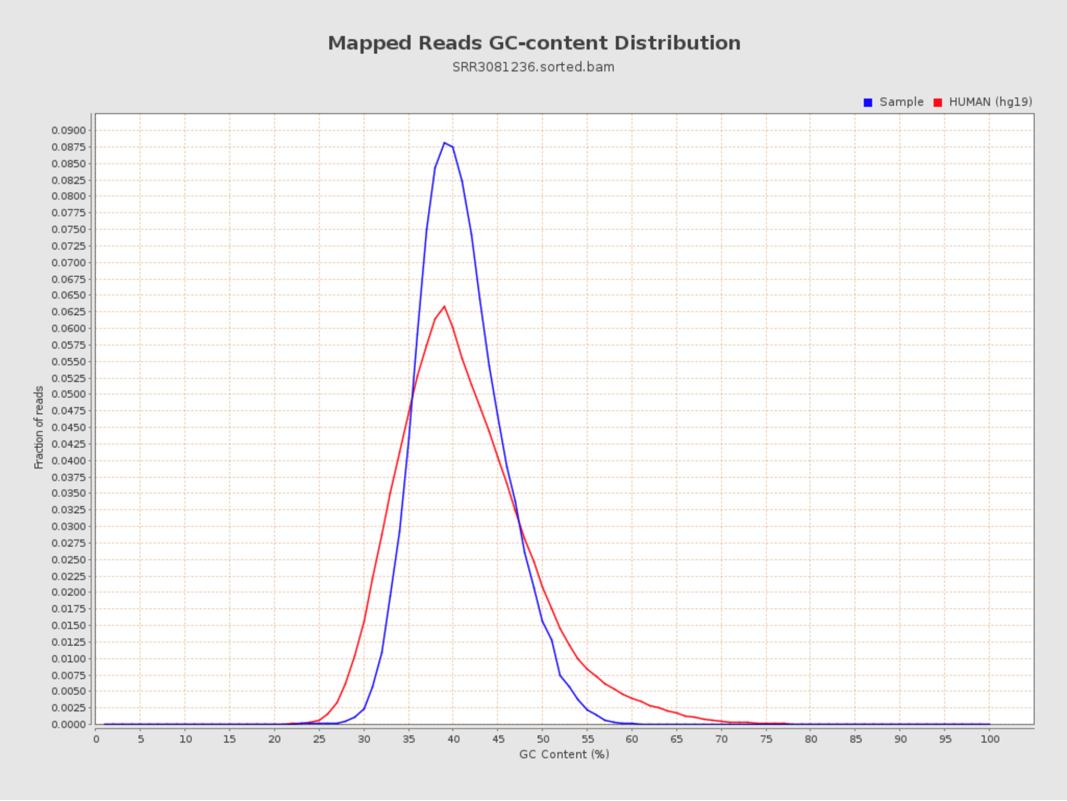
7. Results : Duplication Rate Histogram



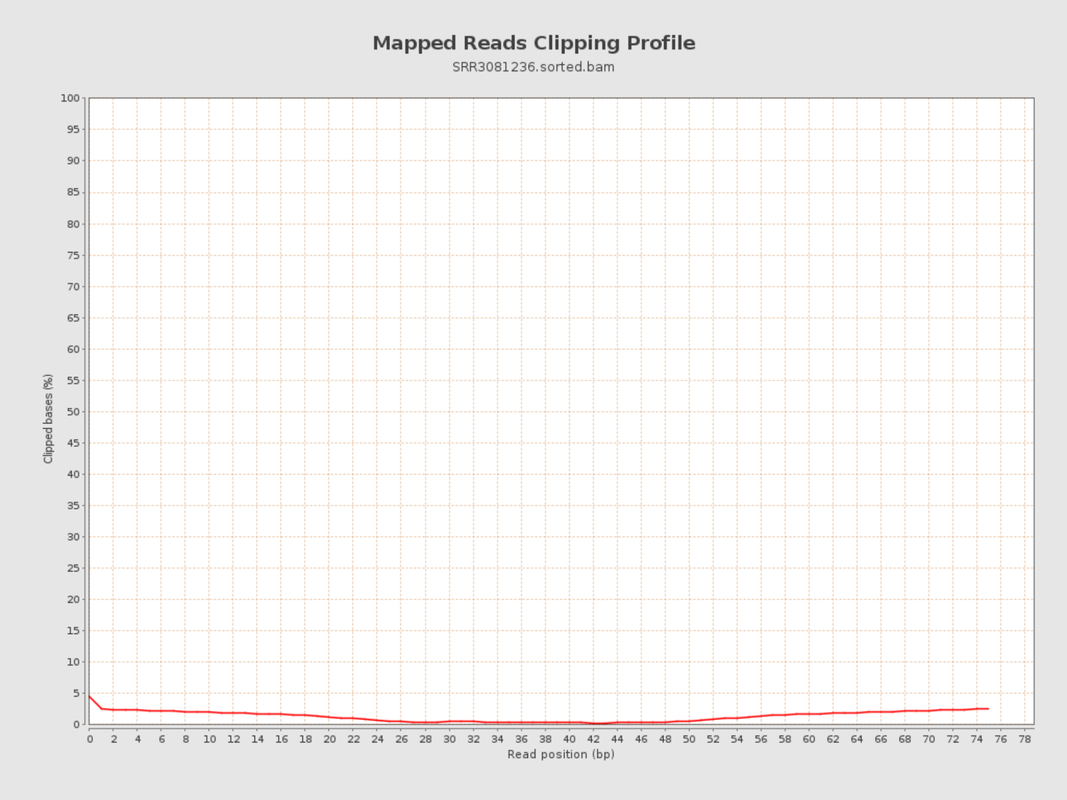
8. Results : Mapped Reads Nucleotide Content



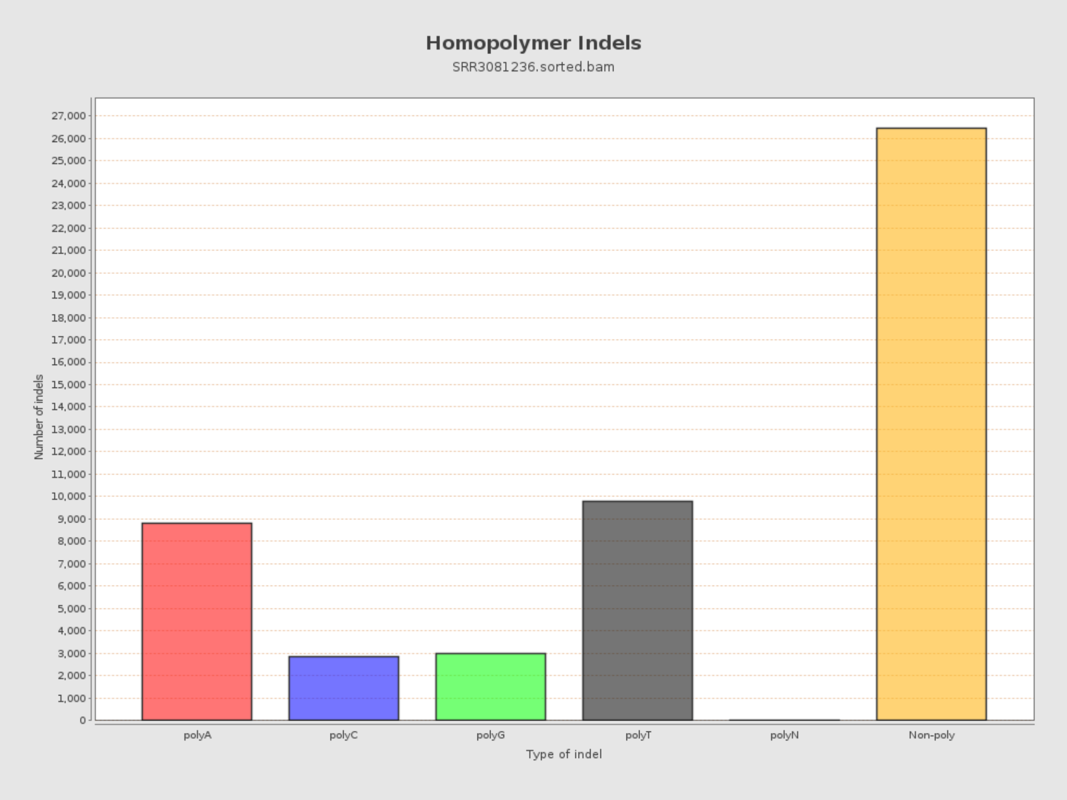
9. Results : Mapped Reads GC-content Distribution



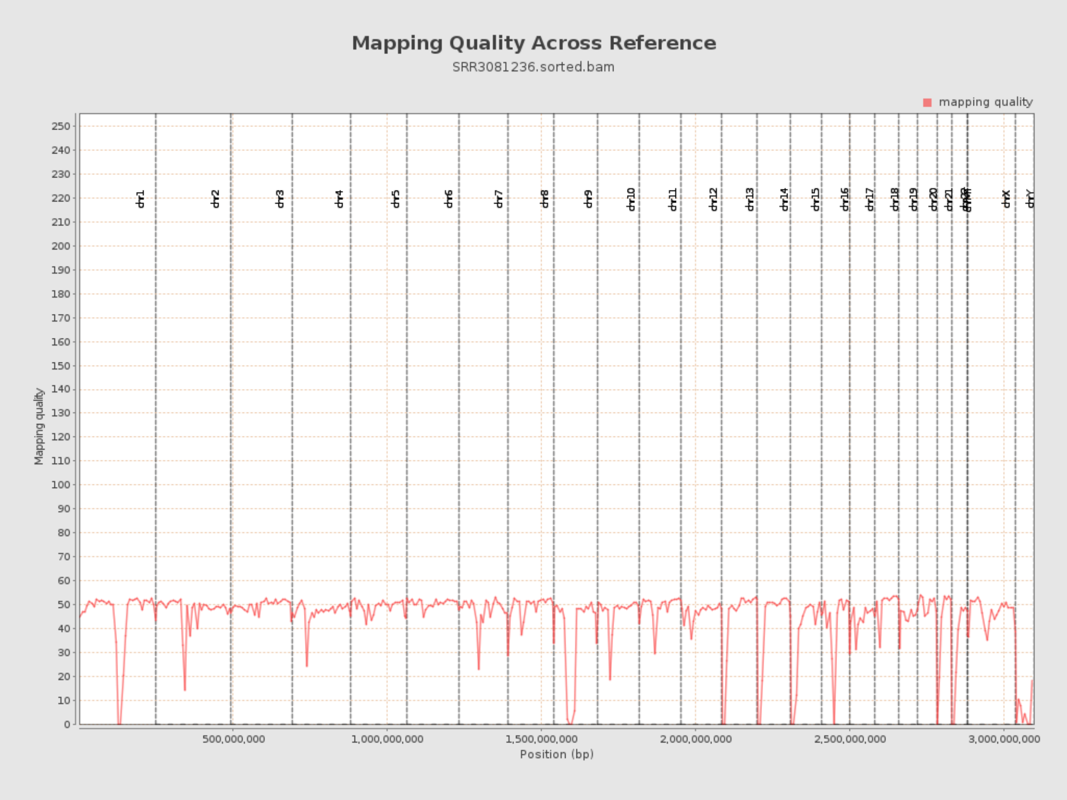
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram