Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:27:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082423.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_SRR3082423 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082423.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:27:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082423.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,568,525
Mapped reads	2,347,369 / 91.39%
Unmapped reads	221,156 / 8.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	21,379 / 0.83%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	83,415 / 3.25%
Duplication rate	2.7%
Clipped reads	913,332 / 35.56%

2.2. ACGT Content

Number/percentage of A's	46,141,285 / 28.73%
Number/percentage of C's	29,843,744 / 18.58%
Number/percentage of T's	50,482,878 / 31.44%
Number/percentage of G's	34,113,360 / 21.24%
Number/percentage of N's	3,513 / 0%
GC Percentage	39.83%

2.3. Coverage

Mean	0.0519

Standard Deviation	0.4313

2.4. Mapping Quality

Mean Mapping Quality	46.94

2.5. Mismatches and indels

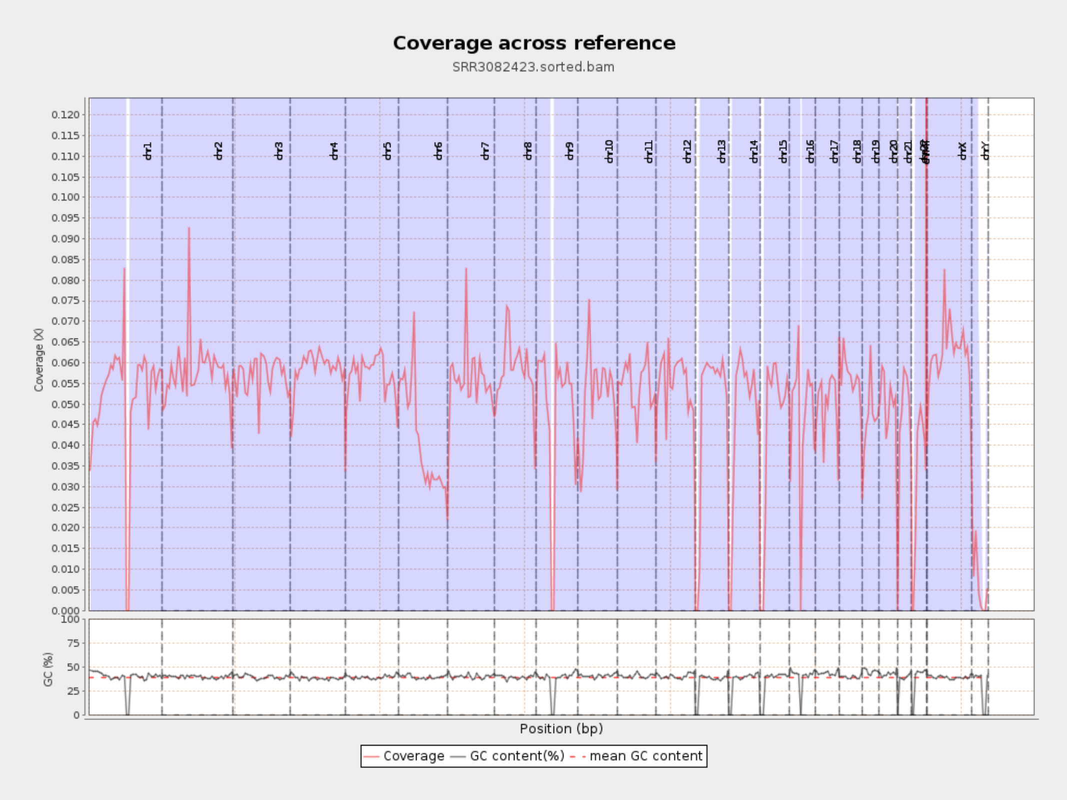
General error rate	0.83%
Mismatches	1,314,848
Insertions	13,310
Mapped reads with at least one insertion	0.56%
Deletions	36,397
Mapped reads with at least one deletion	1.54%
Homopolymer indels	48.23%

2.6. Chromosome stats

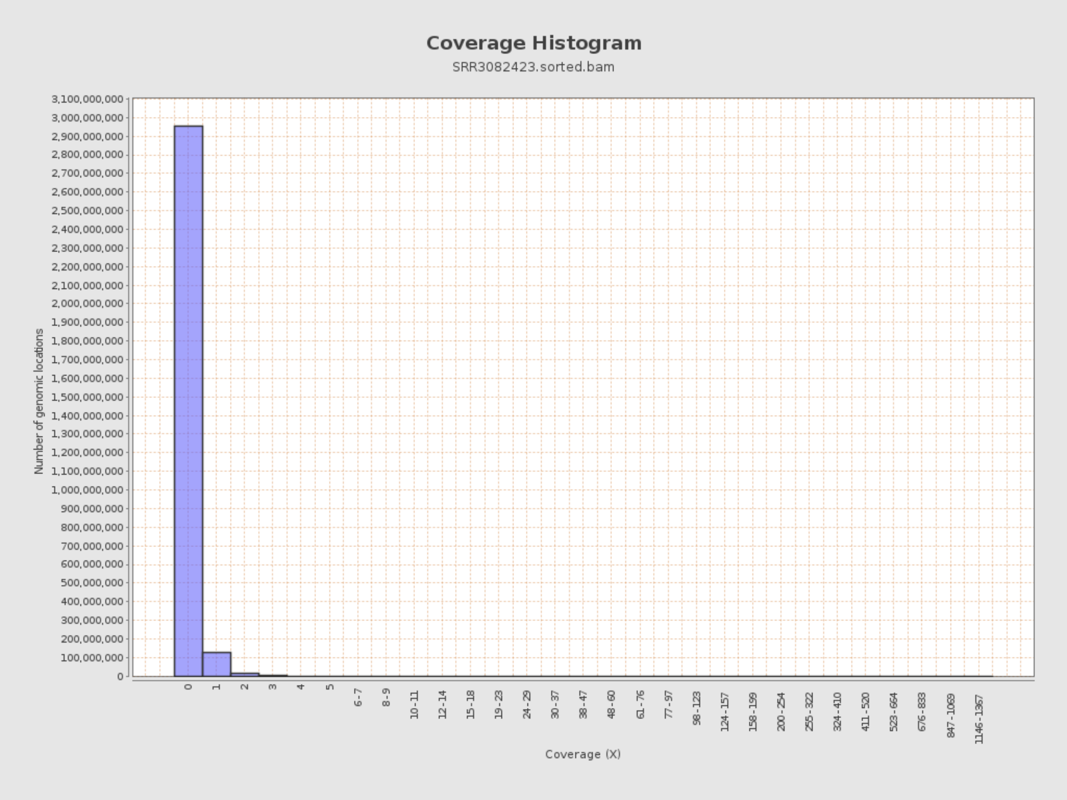
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12914483	0.0518	0.7273
chr2	243199373	14121764	0.0581	0.4953
chr3	198022430	11298764	0.0571	0.2632
chr4	191154276	11223335	0.0587	0.2763
chr5	180915260	10335735	0.0571	0.2651
chr6	171115067	7111052	0.0416	0.2746
chr7	159138663	8965654	0.0563	0.5152

chr8	146364022	8468086	0.0579	0.8677
chr9	141213431	6851688	0.0485	0.3804
chr10	135534747	7065769	0.0521	0.3699
chr11	135006516	7312170	0.0542	0.3425
chr12	133851895	7392322	0.0552	0.2652
chr13	115169878	5507493	0.0478	0.2407
chr14	107349540	4996350	0.0465	0.2561
chr15	102531392	4565213	0.0445	0.2376
chr16	90354753	4270296	0.0473	0.274
chr17	81195210	4002869	0.0493	0.2699
chr18	78077248	4460723	0.0571	0.7129
chr19	59128983	2778255	0.047	0.535
chr20	63025520	3162151	0.0502	0.2524
chr21	48129895	2183965	0.0454	0.2521
chr22	51304566	1579032	0.0308	0.1914
chrMT	16571	5767	0.348	0.6225
chrX	155270560	9679113	0.0623	0.3056
chrY	59373566	391857	0.0066	0.142

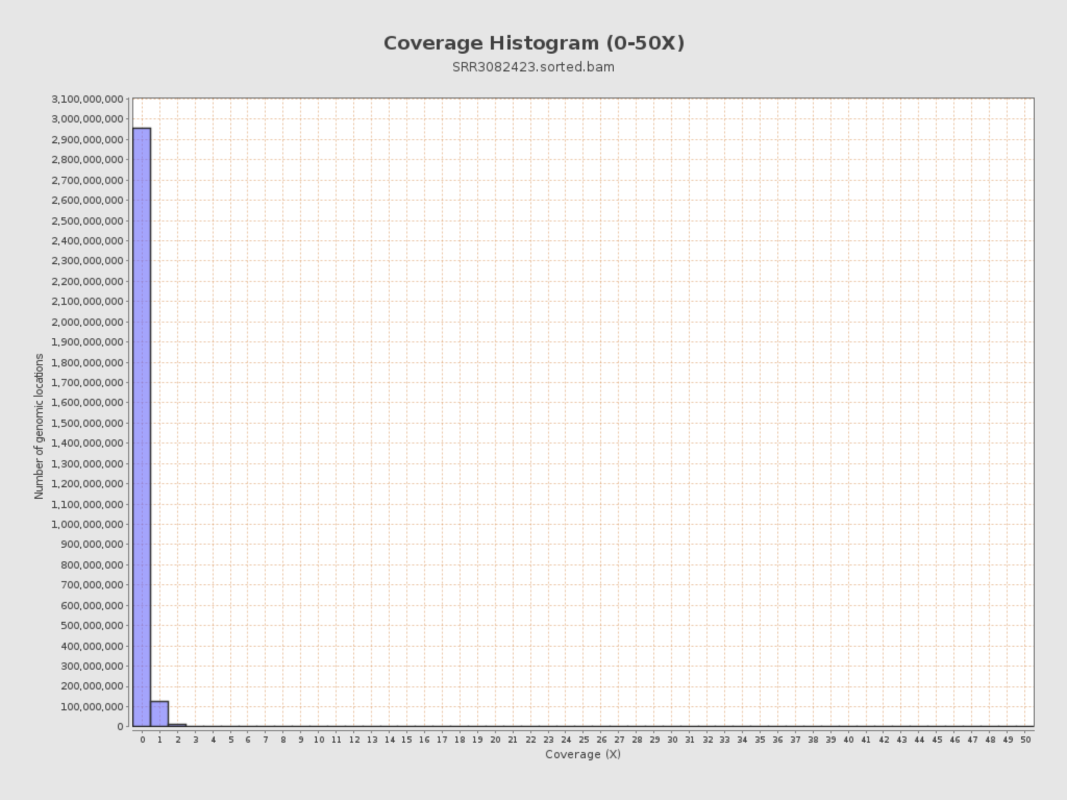
3. Results : Coverage across reference



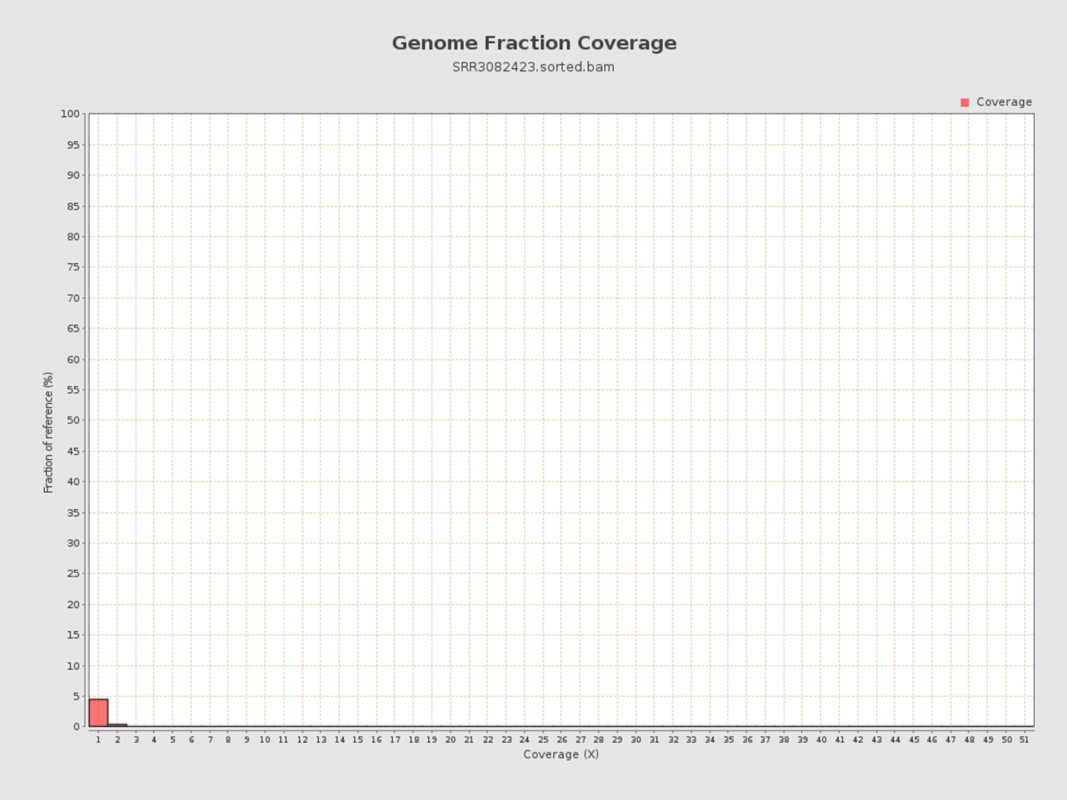
4. Results : Coverage Histogram



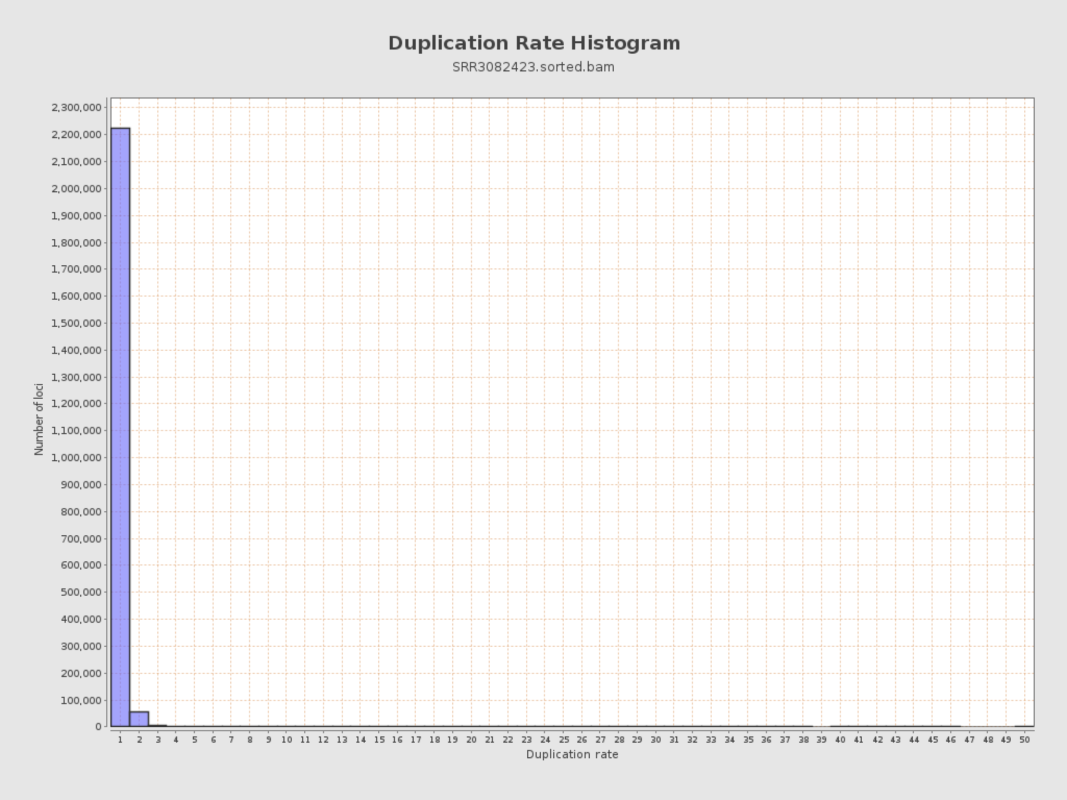
5. Results : Coverage Histogram (0-50X)



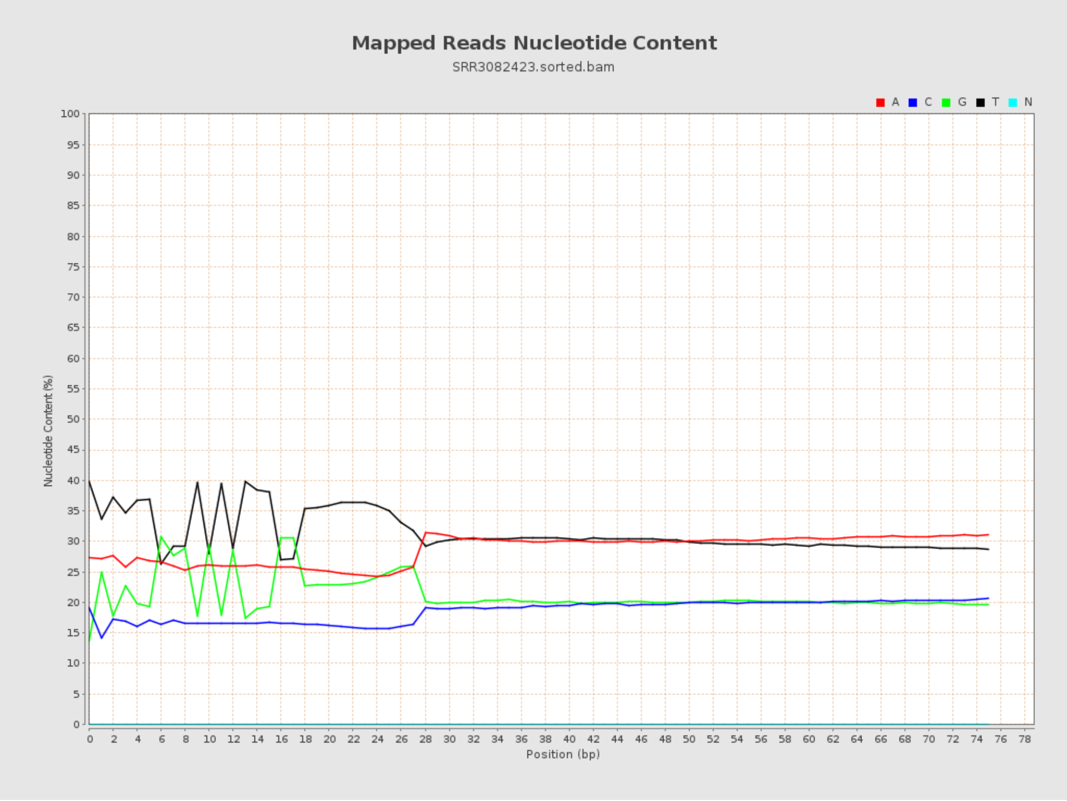
6. Results : Genome Fraction Coverage



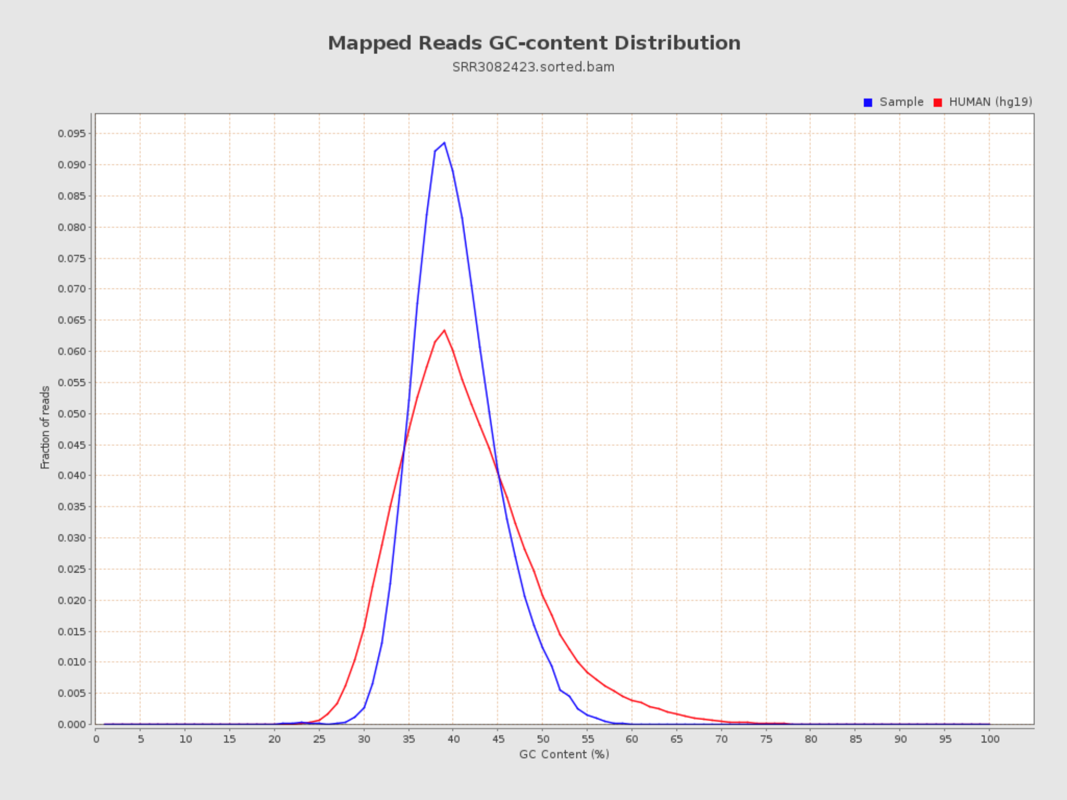
7. Results : Duplication Rate Histogram



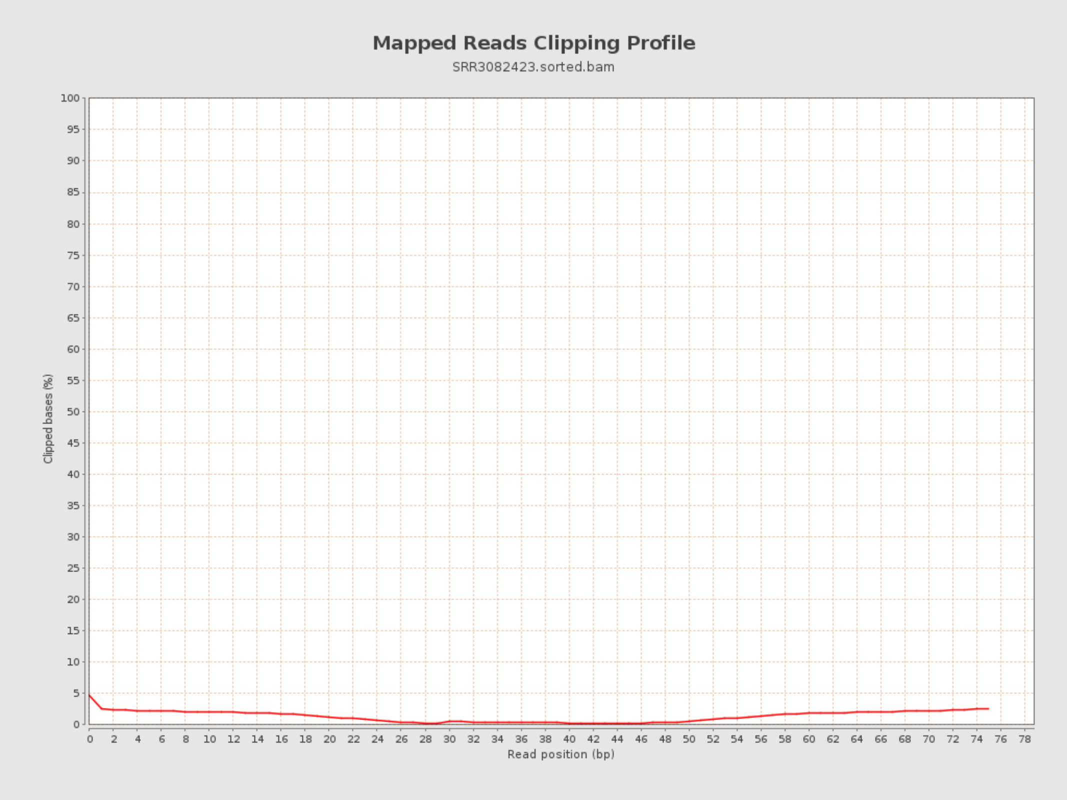
8. Results : Mapped Reads Nucleotide Content



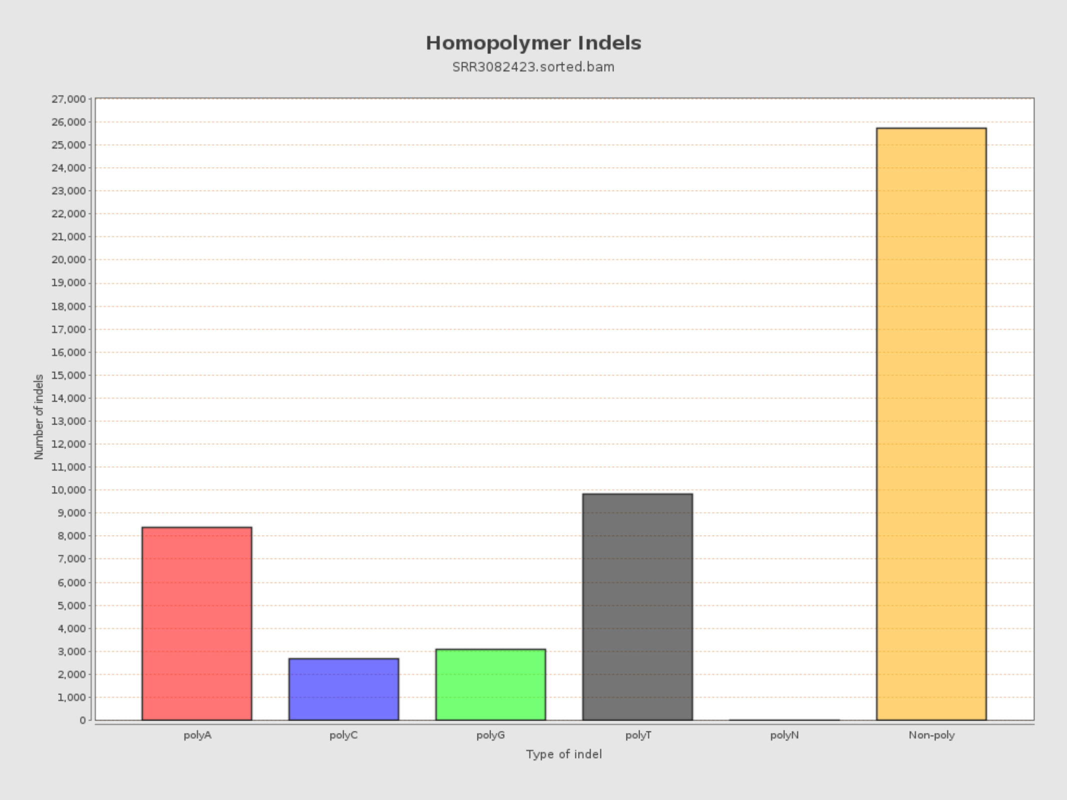
9. Results : Mapped Reads GC-content Distribution



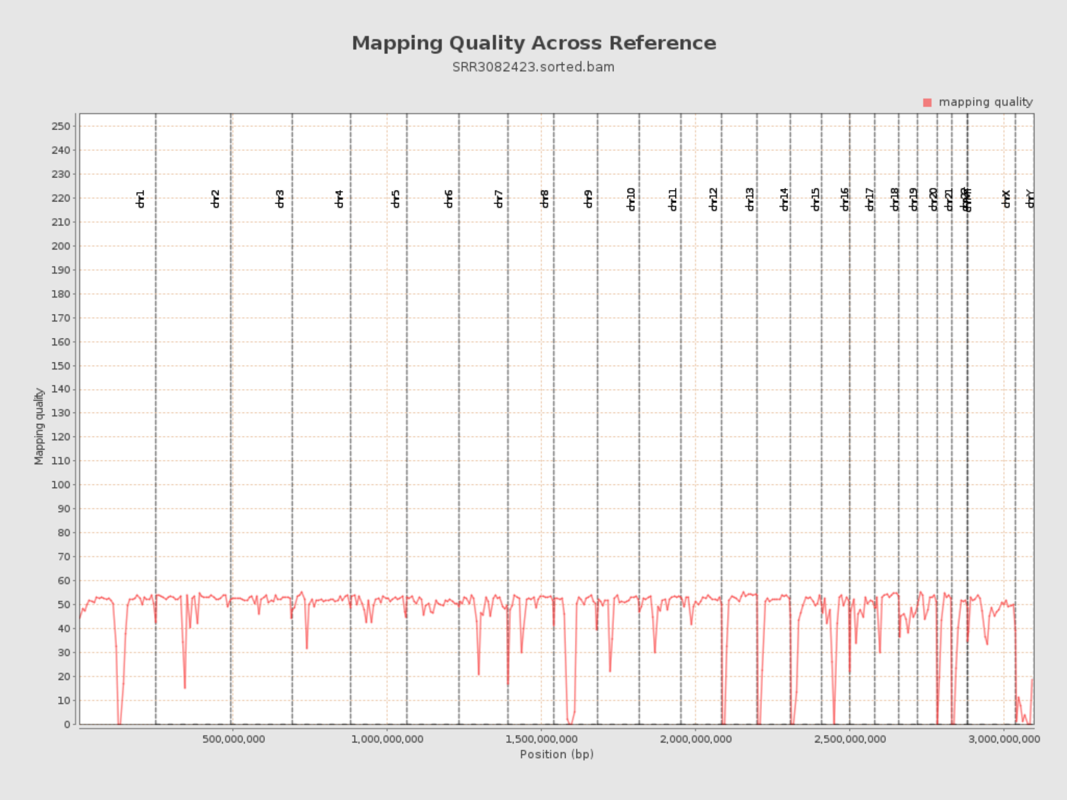
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram