Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:59:38

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083669.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_SRR3083669 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083669.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:59:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083669.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,432,631
Mapped reads	1,068,350 / 74.57%
Unmapped reads	364,281 / 25.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,969 / 0.42%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	24,722 / 1.73%
Duplication rate	1.92%
Clipped reads	639,175 / 44.62%

2.2. ACGT Content

Number/percentage of A's	19,609,118 / 29.4%
Number/percentage of C's	12,502,358 / 18.75%
Number/percentage of T's	19,782,079 / 29.66%
Number/percentage of G's	14,799,030 / 22.19%
Number/percentage of N's	4,188 / 0.01%
GC Percentage	40.93%

2.3. Coverage

Mean	0.0216

Standard Deviation	0.2115

2.4. Mapping Quality

Mean Mapping Quality	45.47

2.5. Mismatches and indels

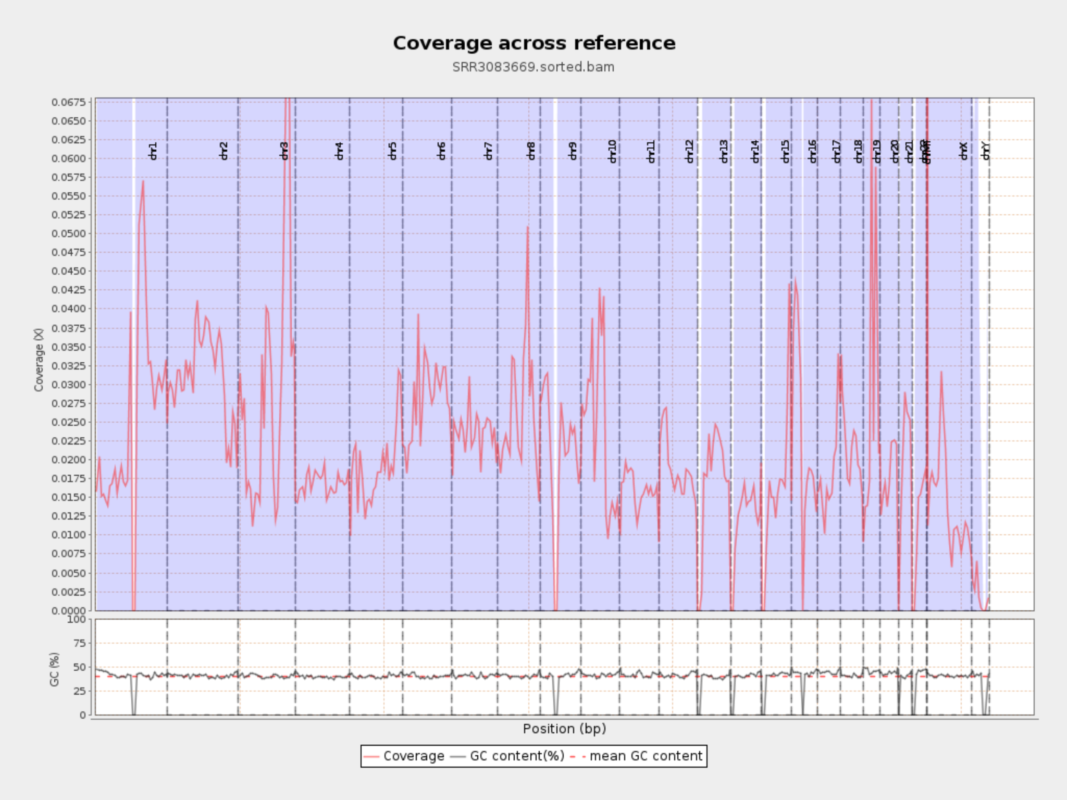
General error rate	0.9%
Mismatches	591,171
Insertions	4,804
Mapped reads with at least one insertion	0.45%
Deletions	13,365
Mapped reads with at least one deletion	1.24%
Homopolymer indels	46.52%

2.6. Chromosome stats

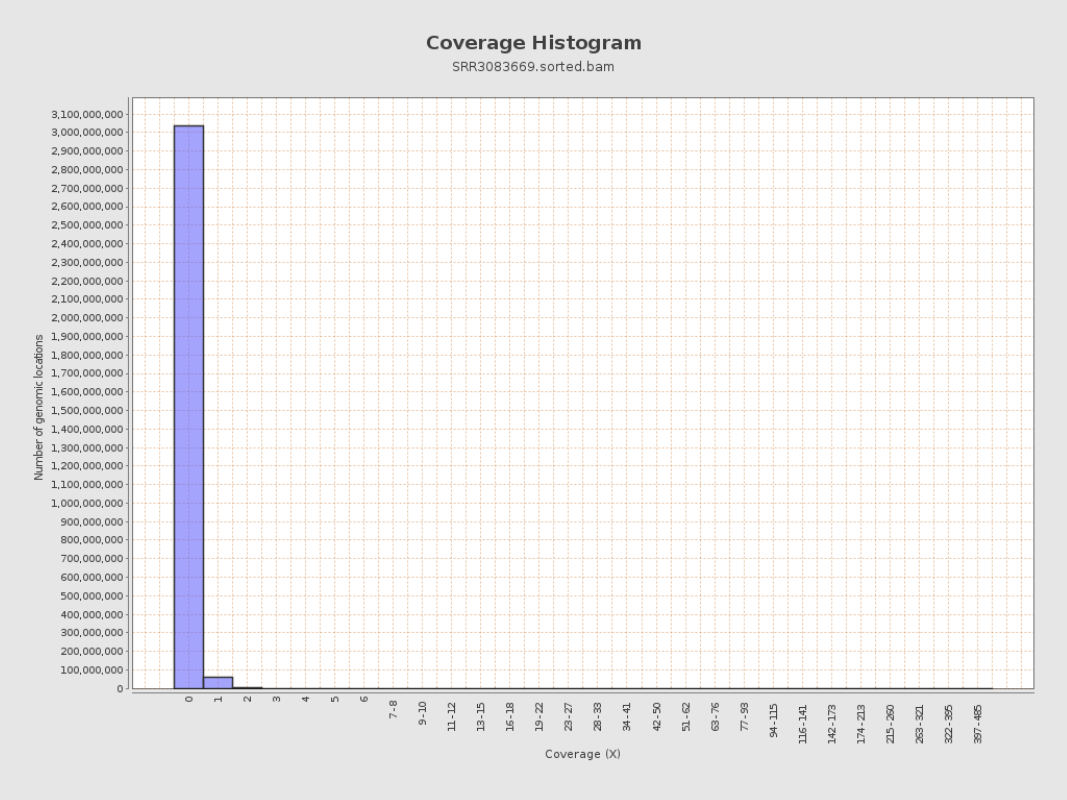
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	6237112	0.025	0.4537
chr2	243199373	7614199	0.0313	0.2073
chr3	198022430	5823193	0.0294	0.1831
chr4	191154276	3219955	0.0168	0.1382
chr5	180915260	3488576	0.0193	0.1469
chr6	171115067	4773495	0.0279	0.1928
chr7	159138663	3772151	0.0237	0.2294

chr8	146364022	3894104	0.0266	0.2367
chr9	141213431	2980370	0.0211	0.1641
chr10	135534747	3269999	0.0241	0.207
chr11	135006516	2162724	0.016	0.1421
chr12	133851895	2535311	0.0189	0.1462
chr13	115169878	1934709	0.0168	0.1364
chr14	107349540	1289326	0.012	0.1164
chr15	102531392	1700474	0.0166	0.1358
chr16	90354753	2029433	0.0225	0.1616
chr17	81195210	1503157	0.0185	0.1468
chr18	78077248	1706362	0.0219	0.2162
chr19	59128983	1736632	0.0294	0.2926
chr20	63025520	1109237	0.0176	0.1412
chr21	48129895	972557	0.0202	0.1518
chr22	51304566	597962	0.0117	0.1132
chrMT	16571	37557	2.2664	2.0613
chrX	155270560	2208629	0.0142	0.1287
chrY	59373566	120989	0.002	0.0543

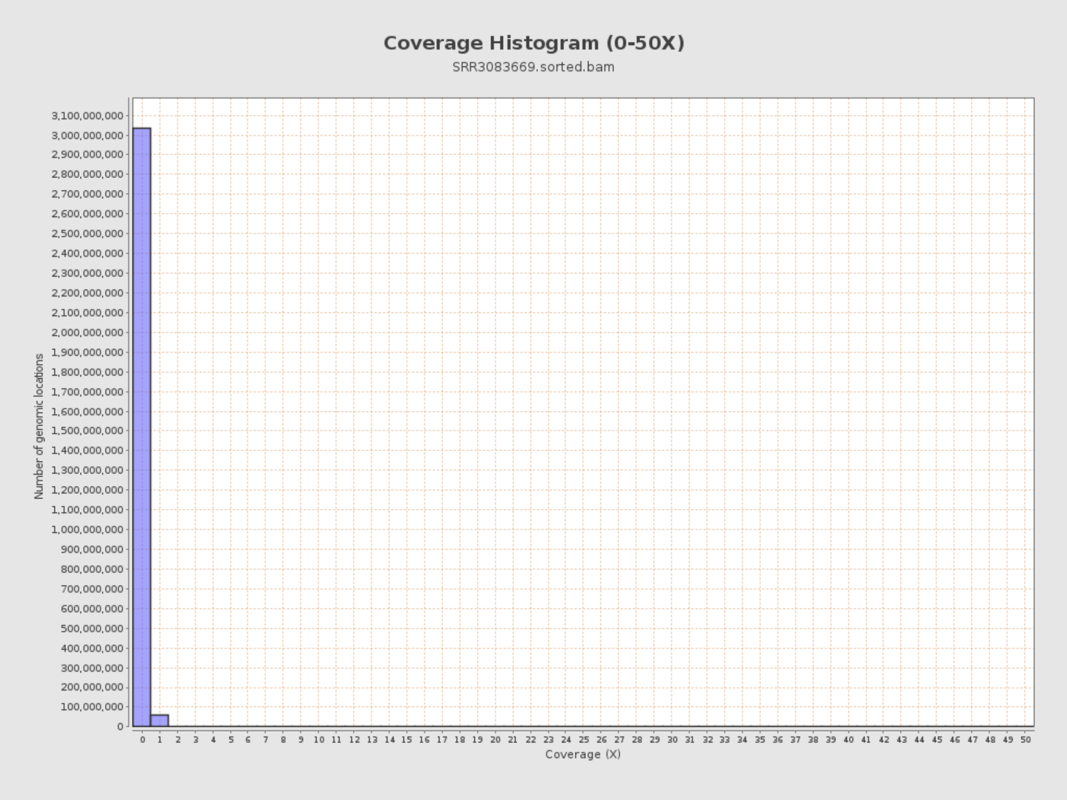
3. Results : Coverage across reference



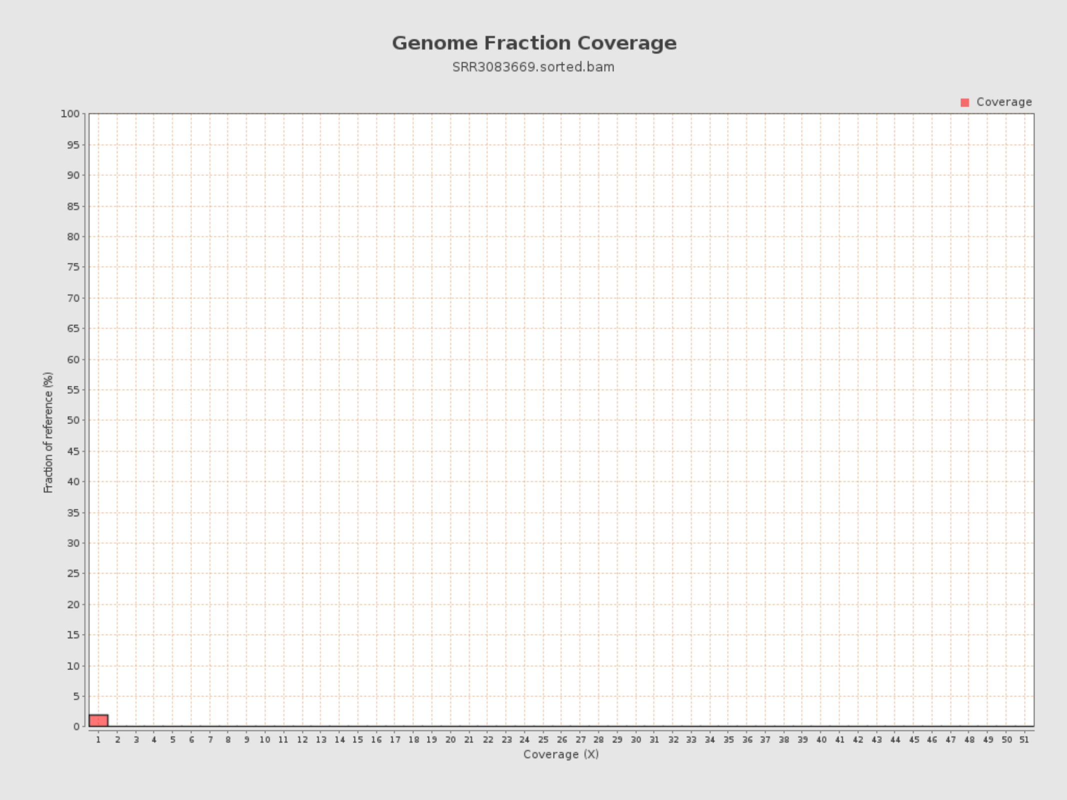
4. Results : Coverage Histogram



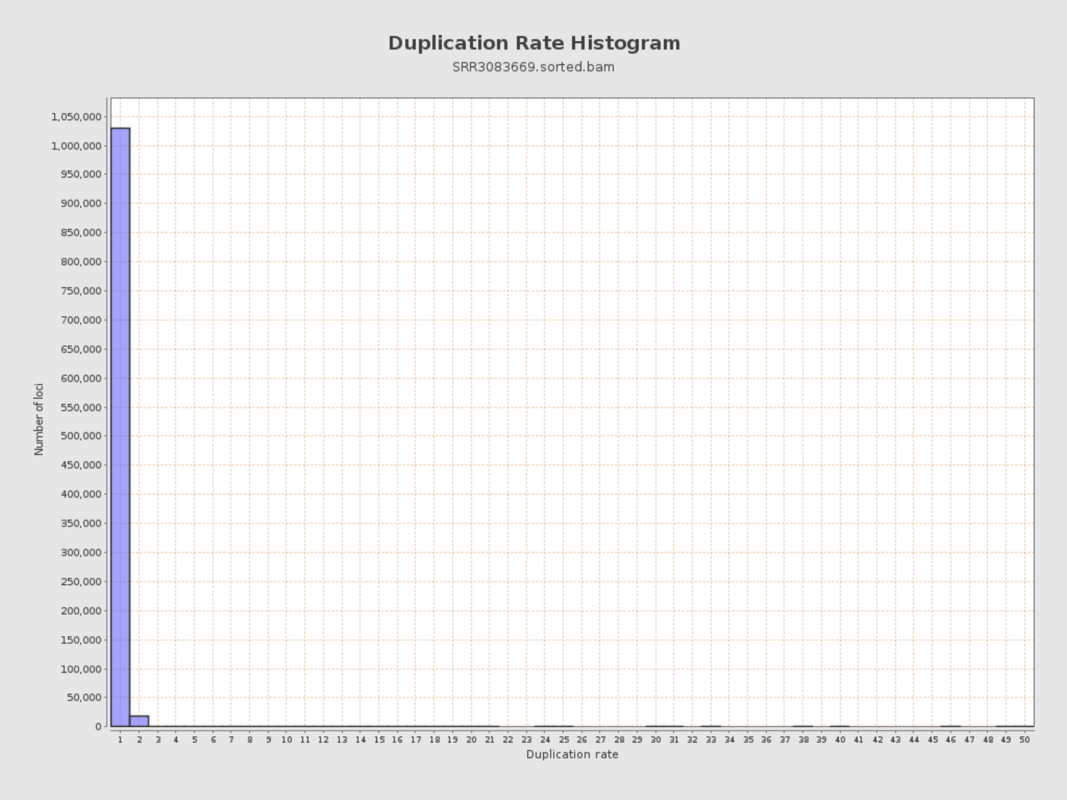
5. Results : Coverage Histogram (0-50X)



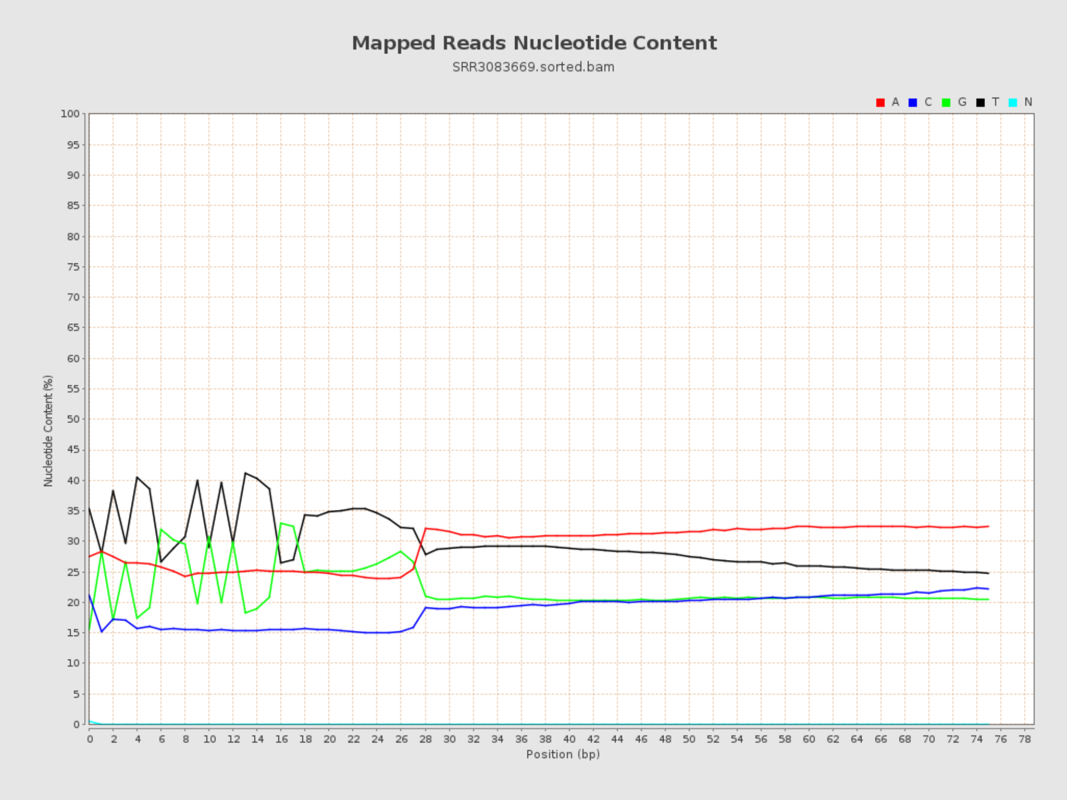
6. Results : Genome Fraction Coverage



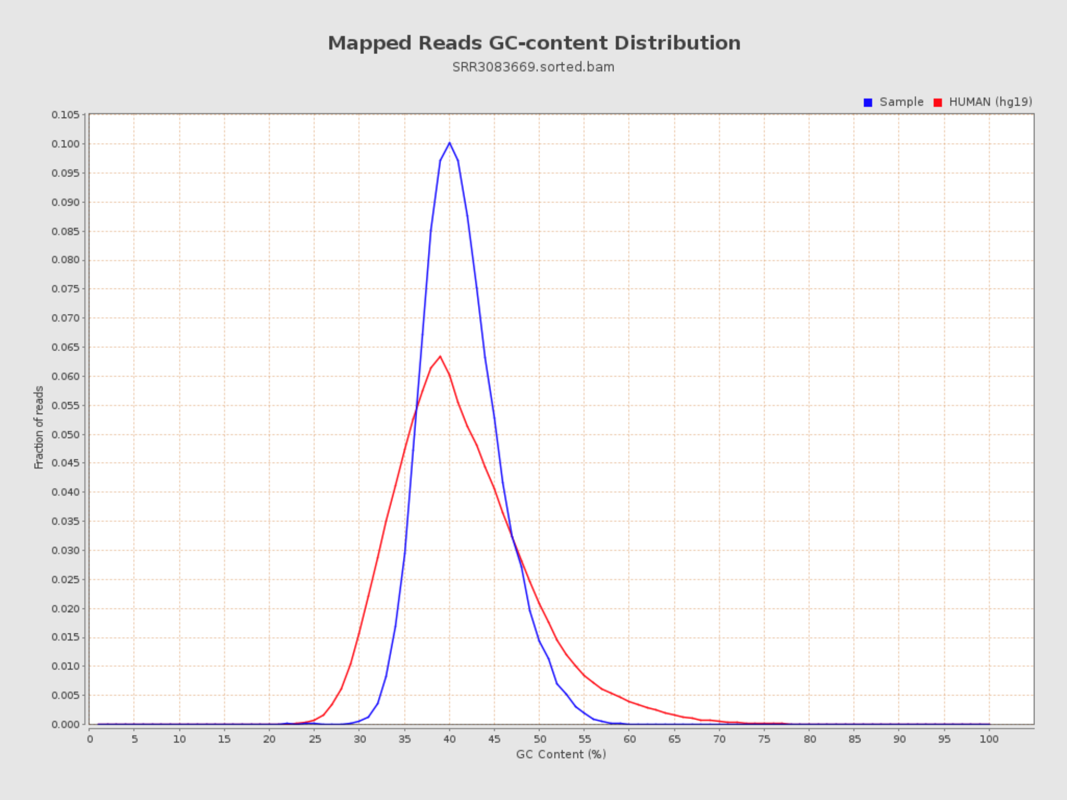
7. Results : Duplication Rate Histogram



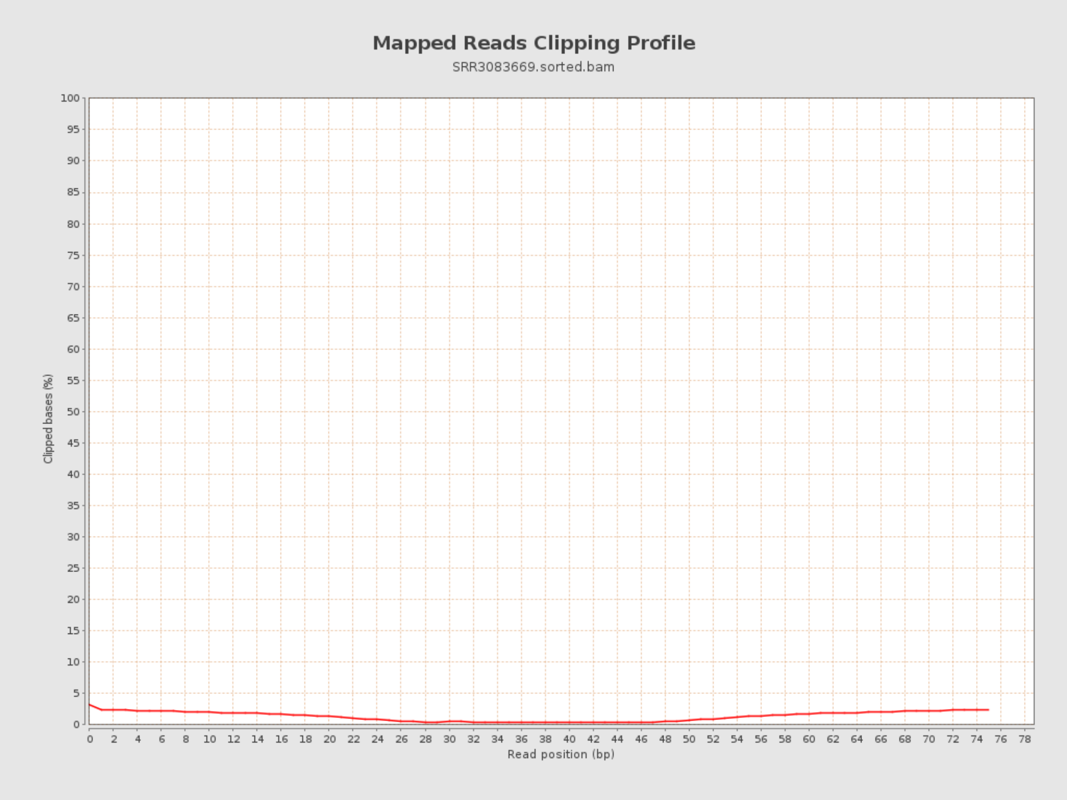
8. Results : Mapped Reads Nucleotide Content



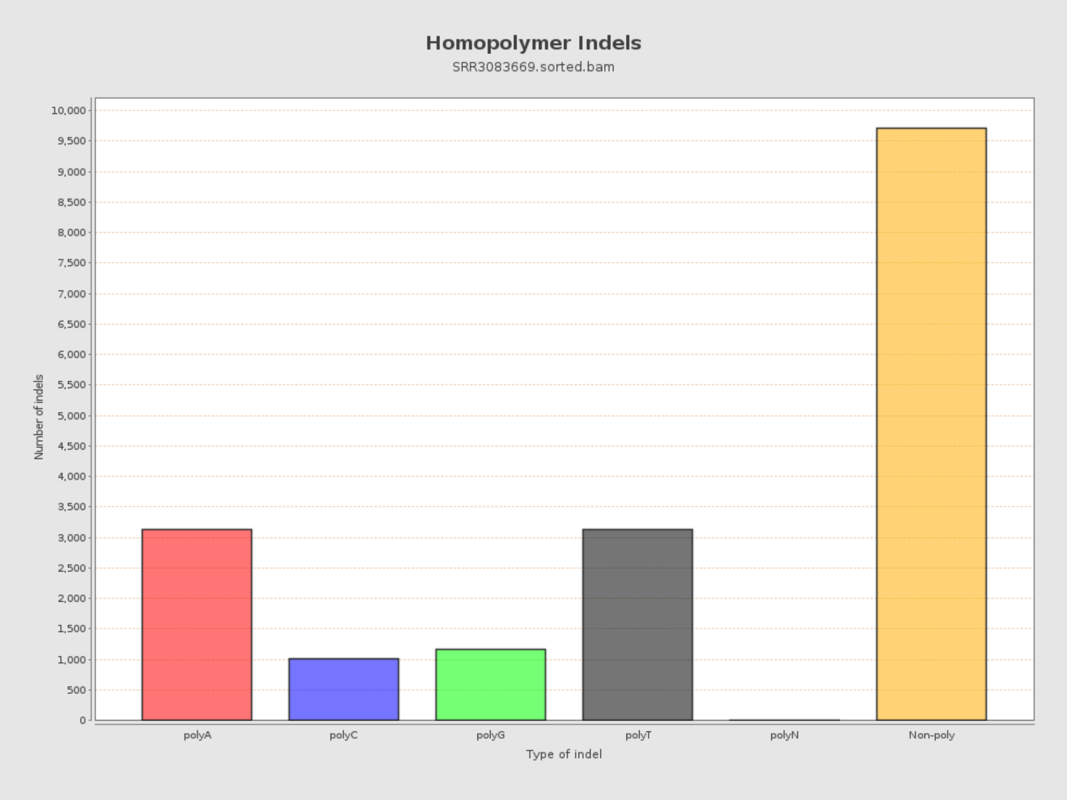
9. Results : Mapped Reads GC-content Distribution



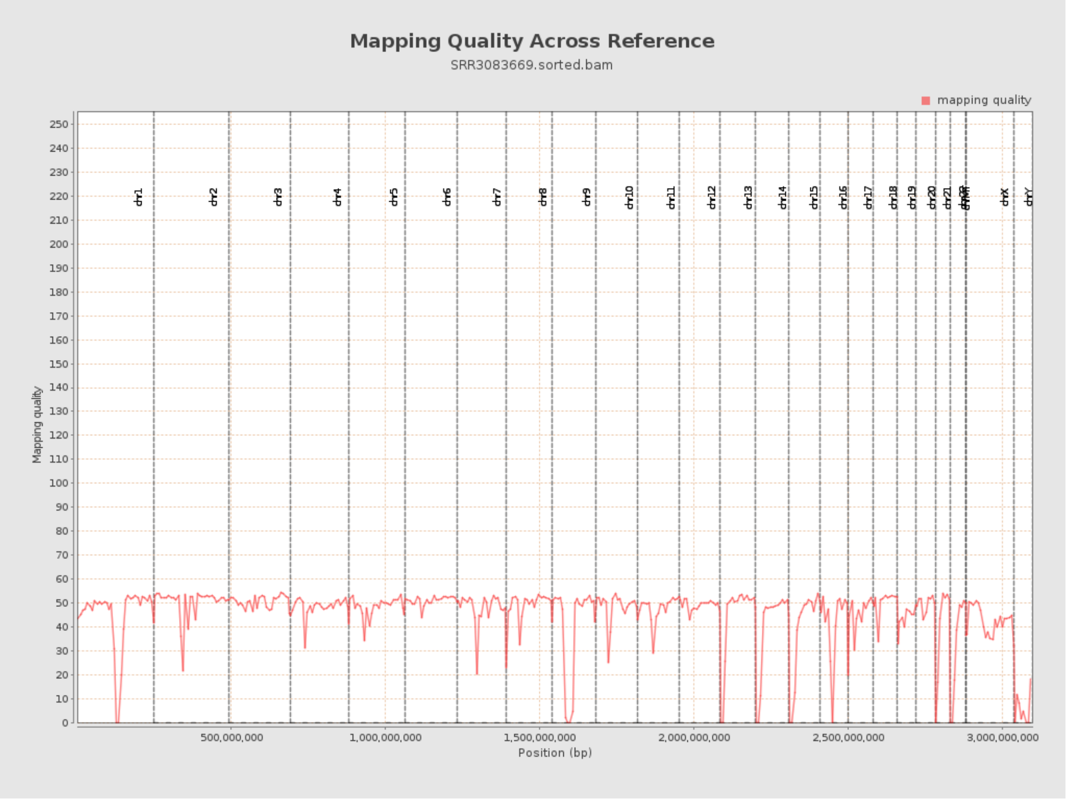
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram