Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 14:02:36

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082330.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_SRR3082330 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082330.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 14:02:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082330.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,367,430
Mapped reads	2,140,068 / 90.4%
Unmapped reads	227,362 / 9.6%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,238 / 0.73%
Read min/max/mean length	30 / 76 / 76.25
Duplicated reads (estimated)	75,852 / 3.2%
Duplication rate	2.65%
Clipped reads	871,289 / 36.8%

2.2. ACGT Content

Number/percentage of A's	41,488,276 / 28.51%
Number/percentage of C's	27,301,007 / 18.76%
Number/percentage of T's	44,911,967 / 30.86%
Number/percentage of G's	31,810,951 / 21.86%
Number/percentage of N's	2,897 / 0%
GC Percentage	40.62%

2.3. Coverage

Mean	0.047

Standard Deviation	0.4088

2.4. Mapping Quality

Mean Mapping Quality	46.12

2.5. Mismatches and indels

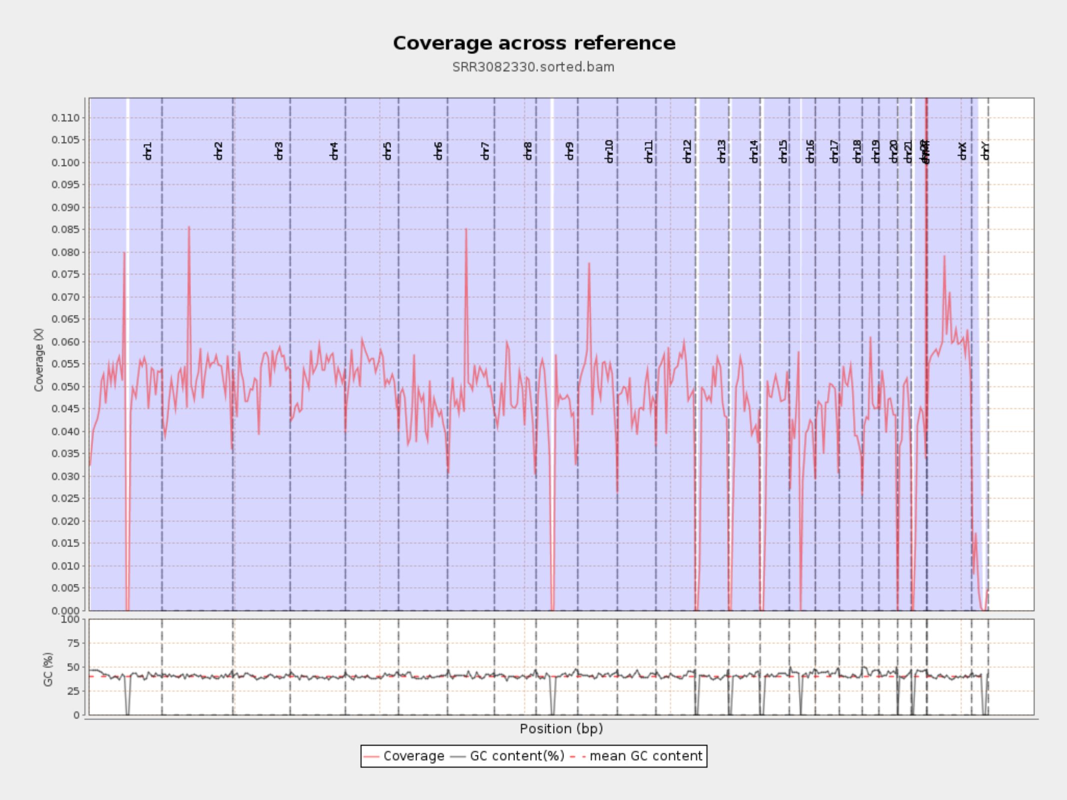
General error rate	0.85%
Mismatches	1,221,760
Insertions	11,948
Mapped reads with at least one insertion	0.55%
Deletions	33,416
Mapped reads with at least one deletion	1.55%
Homopolymer indels	46.66%

2.6. Chromosome stats

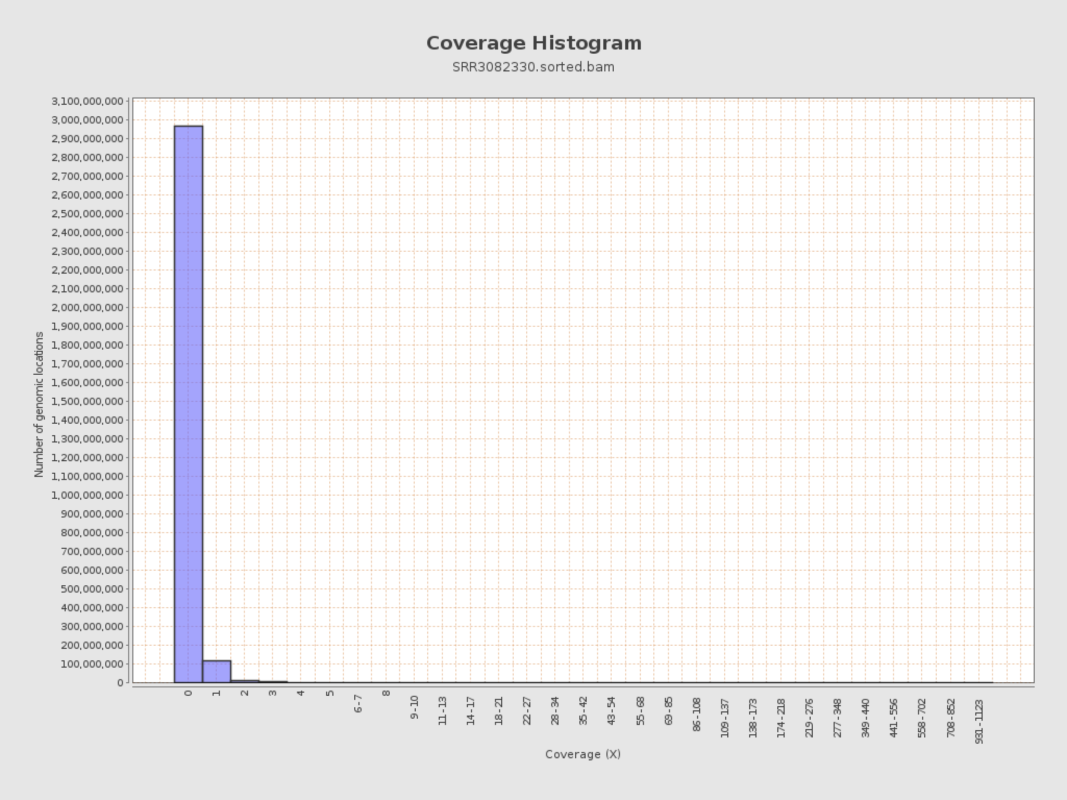
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11918838	0.0478	0.6881
chr2	243199373	12602051	0.0518	0.4957
chr3	198022430	10427070	0.0527	0.2549
chr4	191154276	9929291	0.0519	0.262
chr5	180915260	9677562	0.0535	0.2567
chr6	171115067	7572390	0.0443	0.2694
chr7	159138663	8103302	0.0509	0.5582

chr8	146364022	6887587	0.0471	0.7233
chr9	141213431	5914639	0.0419	0.3603
chr10	135534747	7208212	0.0532	0.3853
chr11	135006516	6272573	0.0465	0.3337
chr12	133851895	6998819	0.0523	0.2574
chr13	115169878	4685306	0.0407	0.2222
chr14	107349540	4160508	0.0388	0.2356
chr15	102531392	4090297	0.0399	0.2239
chr16	90354753	3327513	0.0368	0.2454
chr17	81195210	3629967	0.0447	0.2545
chr18	78077248	3589453	0.046	0.6516
chr19	59128983	2695504	0.0456	0.524
chr20	63025520	2836791	0.045	0.2416
chr21	48129895	1878716	0.039	0.2355
chr22	51304566	1501743	0.0293	0.1878
chrMT	16571	15484	0.9344	0.9994
chrX	155270560	9287689	0.0598	0.3059
chrY	59373566	358346	0.006	0.1282

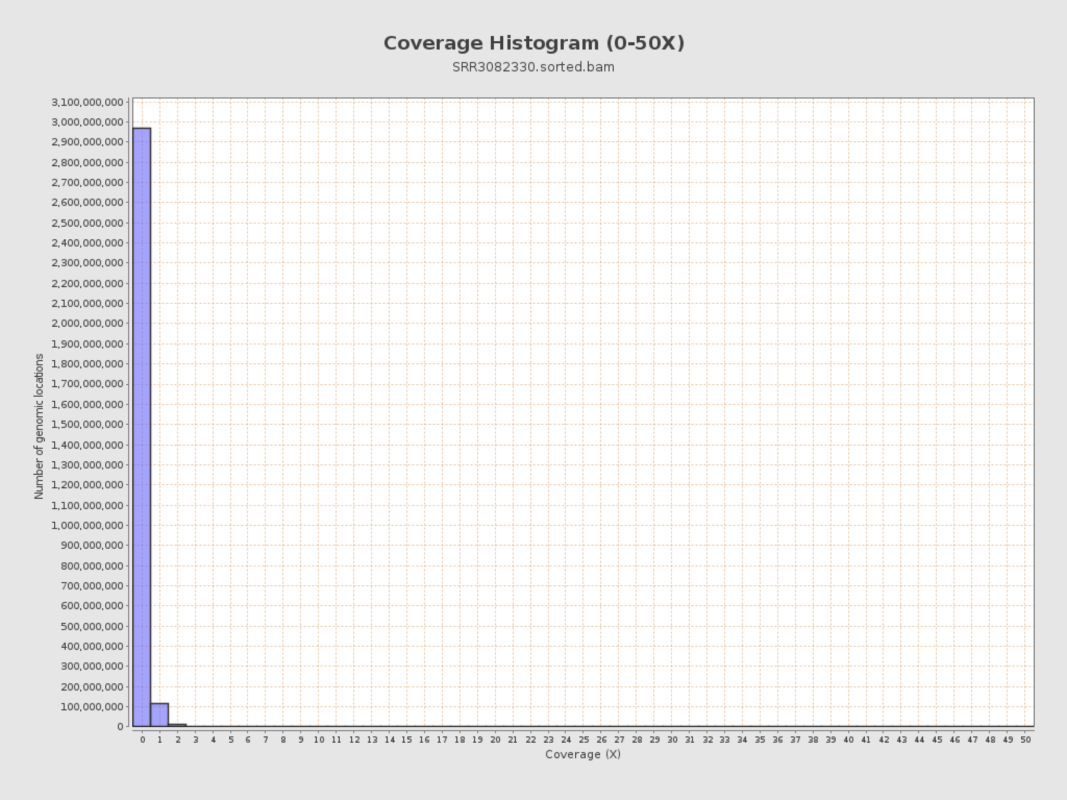
3. Results : Coverage across reference



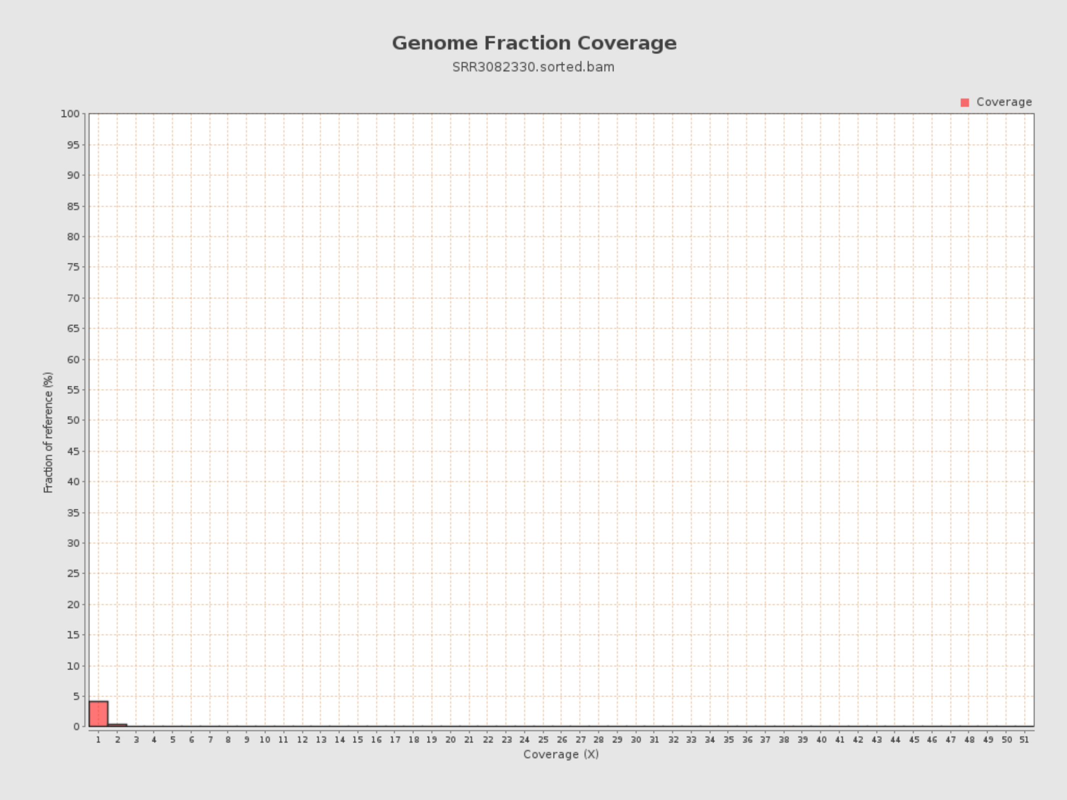
4. Results : Coverage Histogram



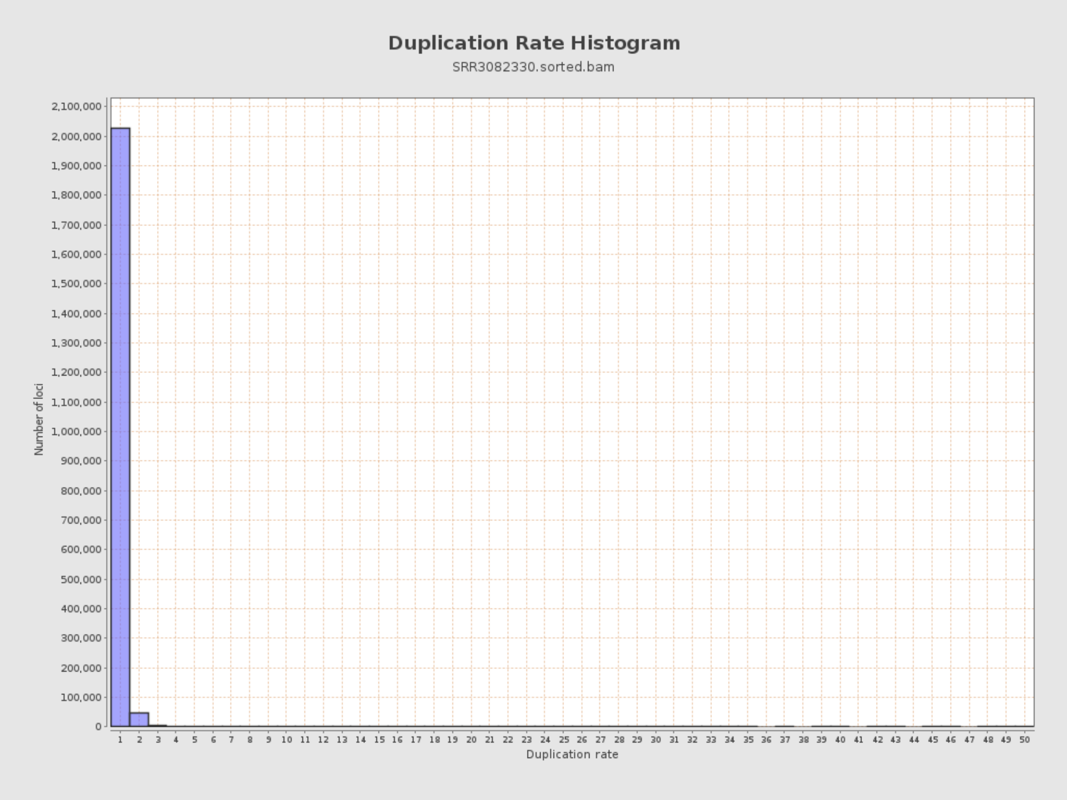
5. Results : Coverage Histogram (0-50X)



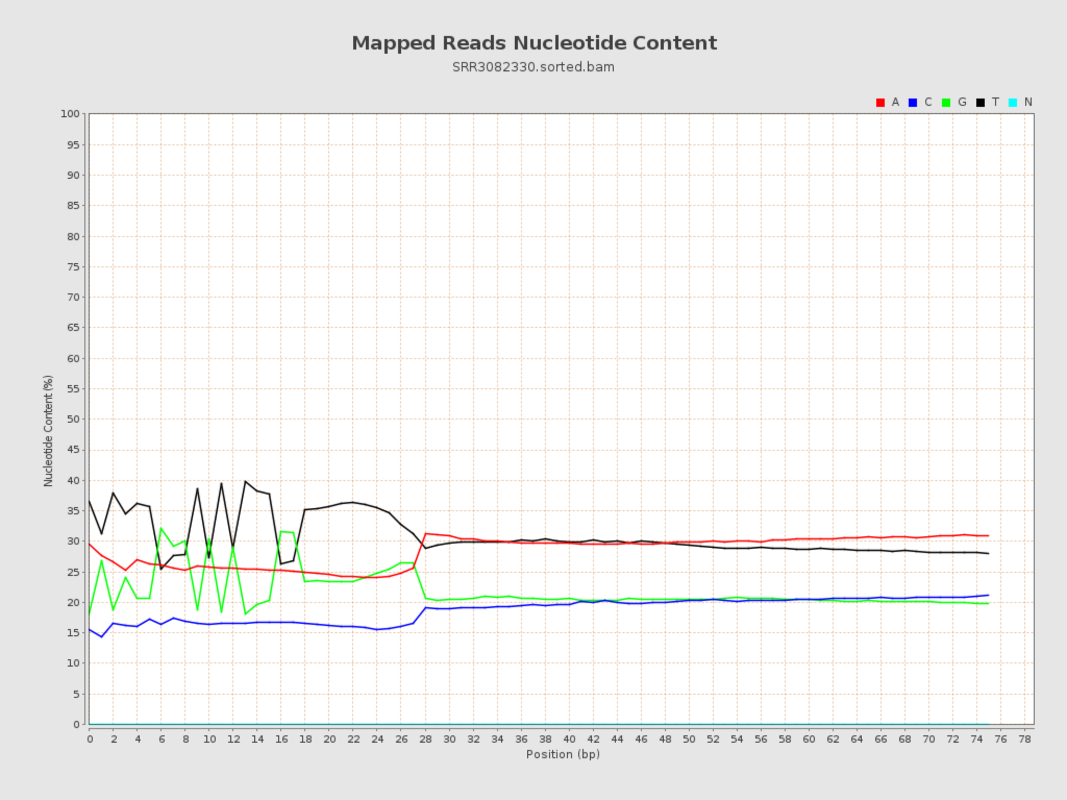
6. Results : Genome Fraction Coverage



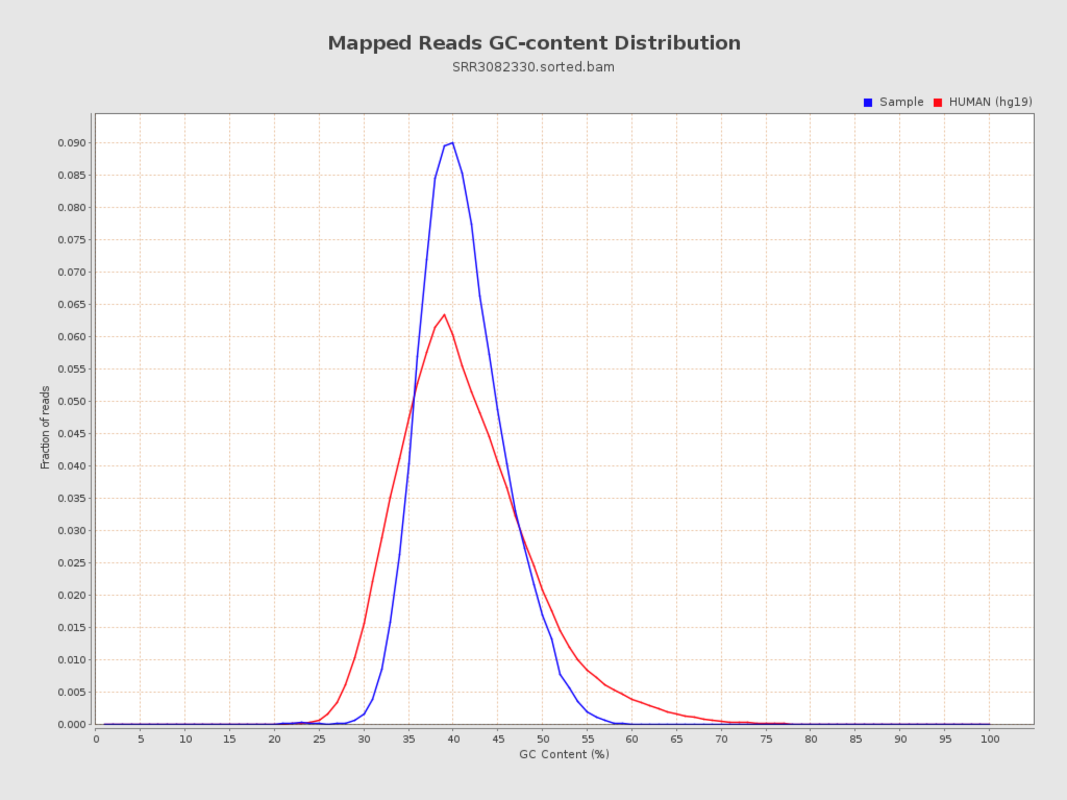
7. Results : Duplication Rate Histogram



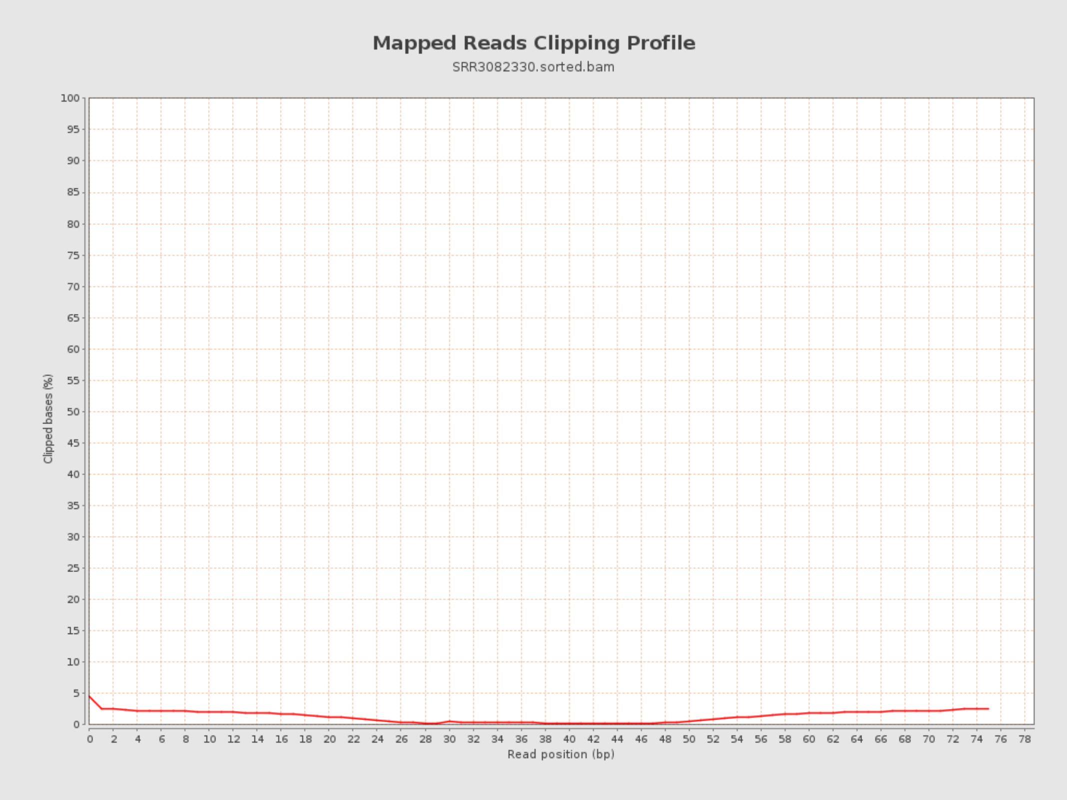
8. Results : Mapped Reads Nucleotide Content



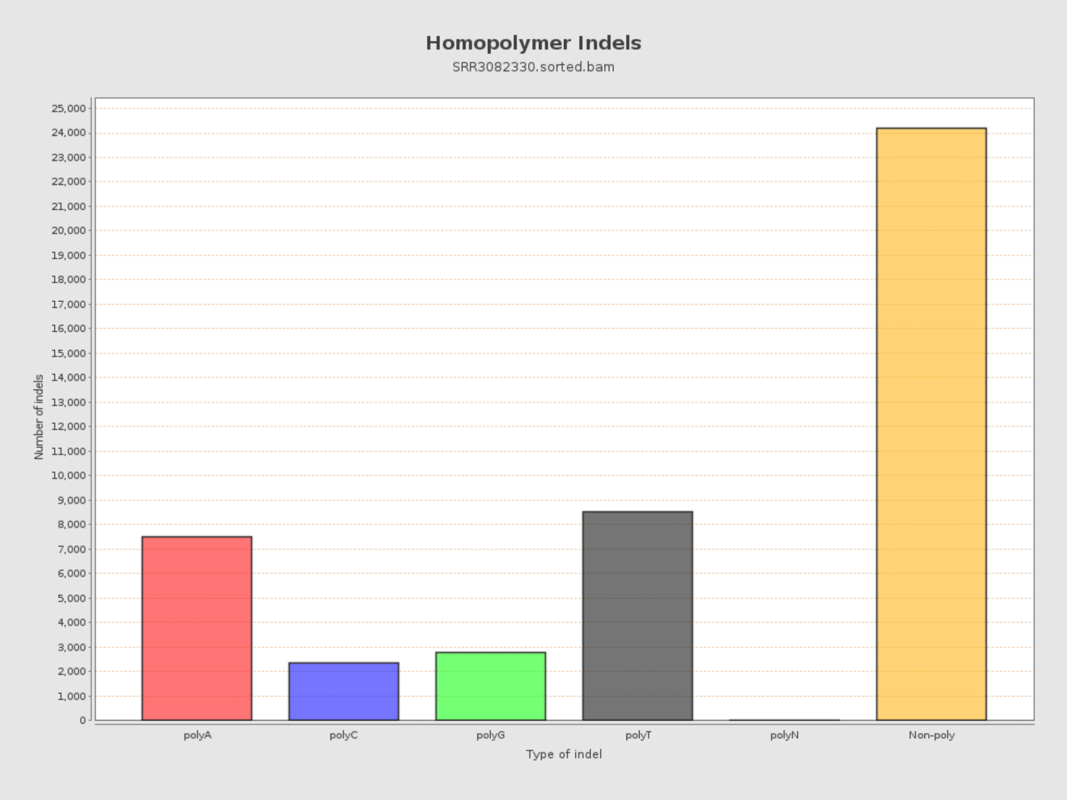
9. Results : Mapped Reads GC-content Distribution



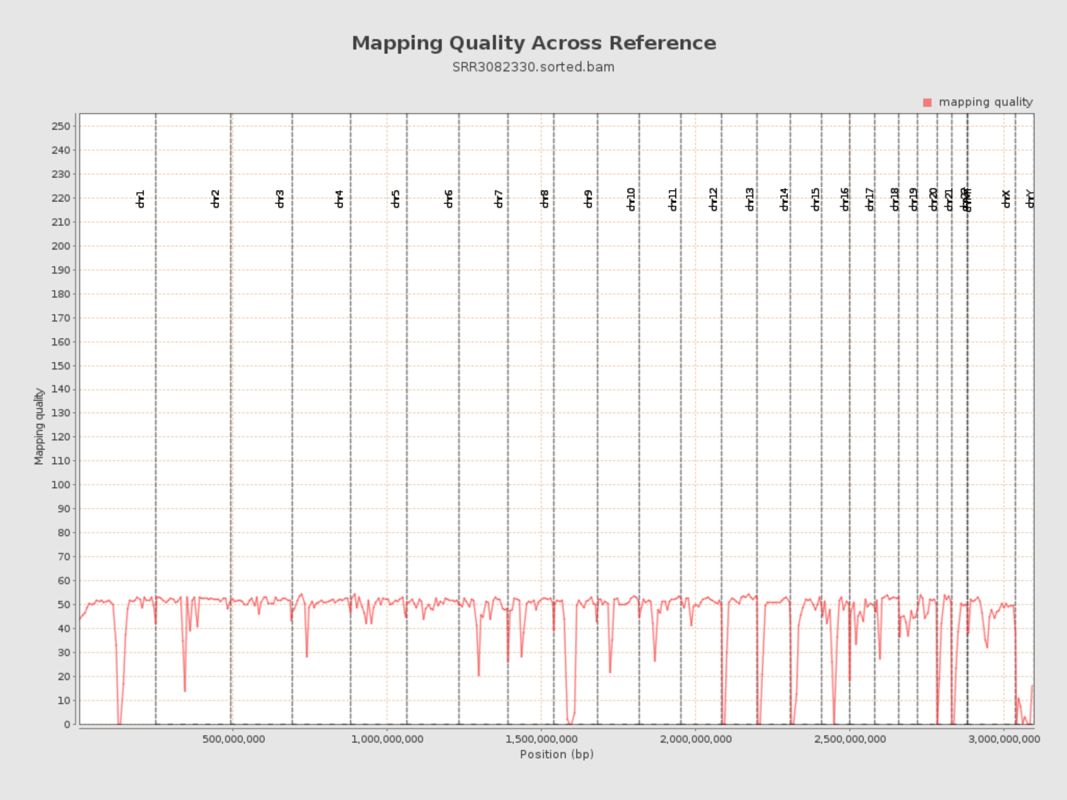
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram