Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 17:27:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081033.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_SRR3081033 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081033.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 17:27:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081033.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,764,002
Mapped reads	2,366,095 / 62.86%
Unmapped reads	1,397,907 / 37.14%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	10,150 / 0.27%
Read min/max/mean length	30 / 76 / 76.09
Duplicated reads (estimated)	98,544 / 2.62%
Duplication rate	3.28%
Clipped reads	1,397,505 / 37.13%

2.2. ACGT Content

Number/percentage of A's	41,058,088 / 27.98%
Number/percentage of C's	29,691,302 / 20.23%
Number/percentage of T's	42,962,846 / 29.28%
Number/percentage of G's	33,029,341 / 22.51%
Number/percentage of N's	1,755 / 0%
GC Percentage	42.74%

2.3. Coverage

Mean	0.0474

Standard Deviation	0.3731

2.4. Mapping Quality

Mean Mapping Quality	45.61

2.5. Mismatches and indels

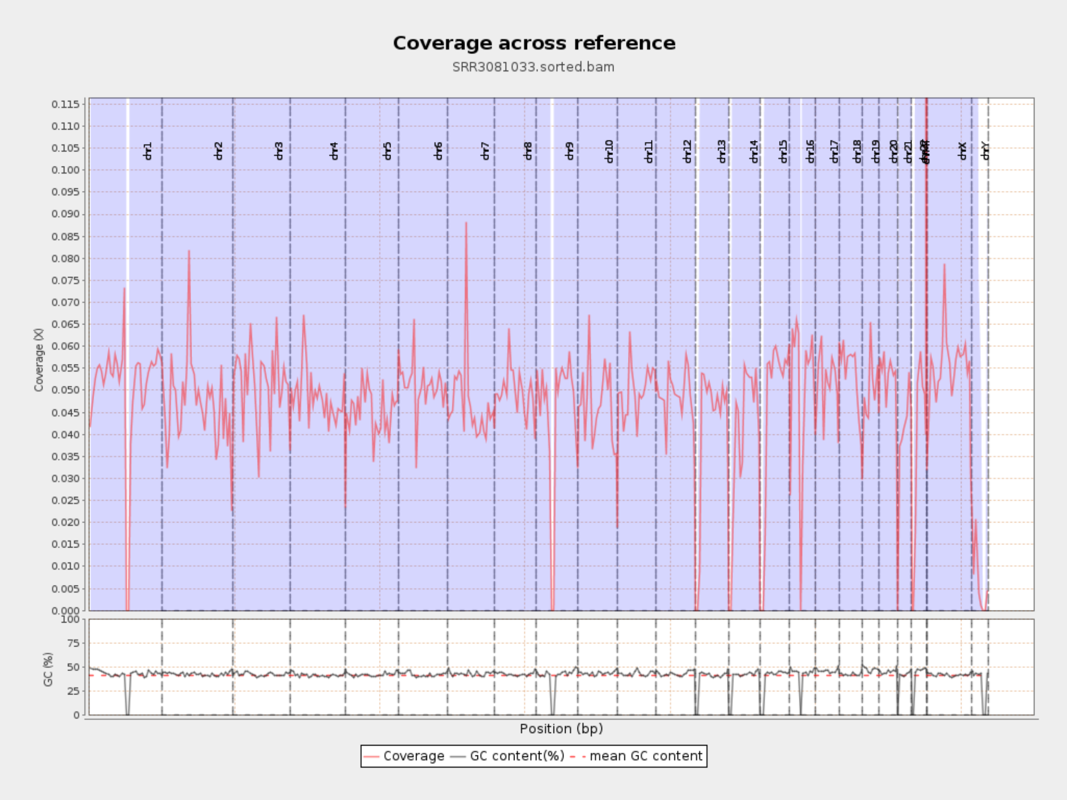
General error rate	0.74%
Mismatches	1,061,932
Insertions	9,655
Mapped reads with at least one insertion	0.4%
Deletions	27,108
Mapped reads with at least one deletion	1.13%
Homopolymer indels	45.22%

2.6. Chromosome stats

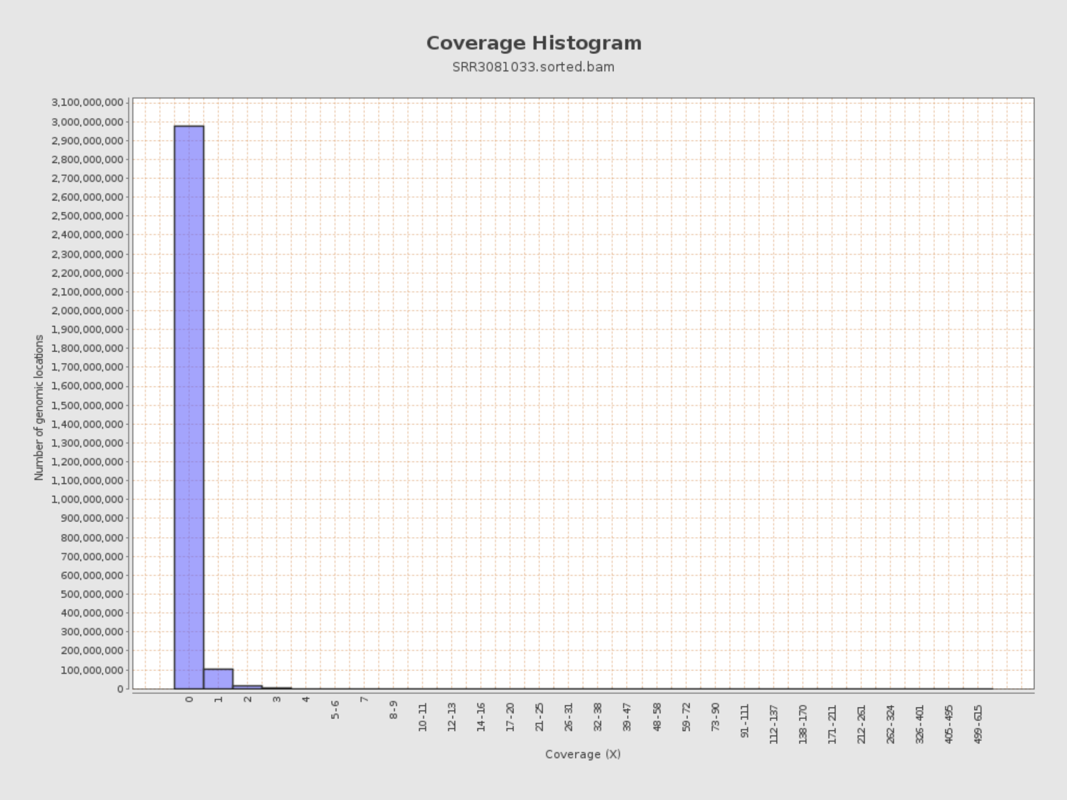
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12576400	0.0505	0.5619
chr2	243199373	11446394	0.0471	0.4138
chr3	198022430	10194641	0.0515	0.2635
chr4	191154276	9296625	0.0486	0.2833
chr5	180915260	8217814	0.0454	0.2497
chr6	171115067	8770462	0.0513	0.3235
chr7	159138663	7563725	0.0475	0.6175

chr8	146364022	7274415	0.0497	0.3441
chr9	141213431	6316188	0.0447	0.3641
chr10	135534747	6347422	0.0468	0.3489
chr11	135006516	6658379	0.0493	0.4009
chr12	133851895	6557290	0.049	0.2606
chr13	115169878	4714665	0.0409	0.2338
chr14	107349540	4215329	0.0393	0.245
chr15	102531392	4662528	0.0455	0.2599
chr16	90354753	4553858	0.0504	0.2849
chr17	81195210	4166022	0.0513	0.3134
chr18	78077248	4233506	0.0542	0.6639
chr19	59128983	2955122	0.05	0.4296
chr20	63025520	3365380	0.0534	0.2802
chr21	48129895	1893966	0.0394	0.2592
chr22	51304566	1845219	0.036	0.2212
chrMT	16571	36133	2.1805	2.1548
chrX	155270560	8538118	0.055	0.3171
chrY	59373566	390682	0.0066	0.1511

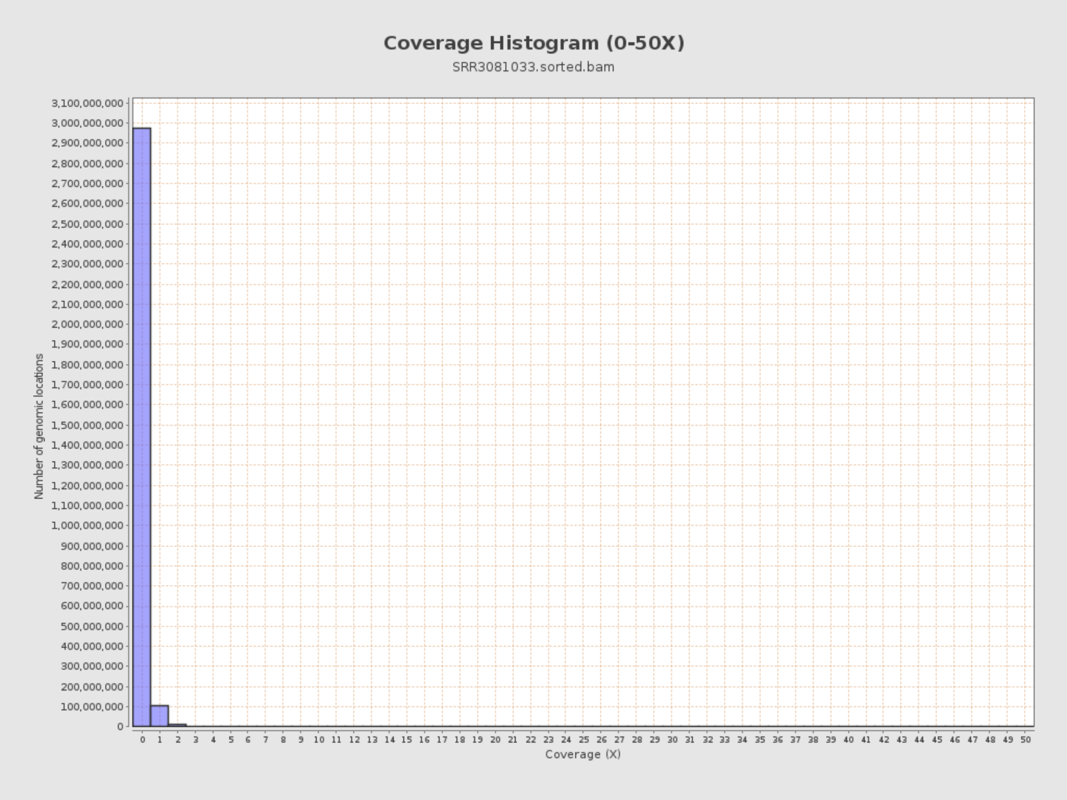
3. Results : Coverage across reference



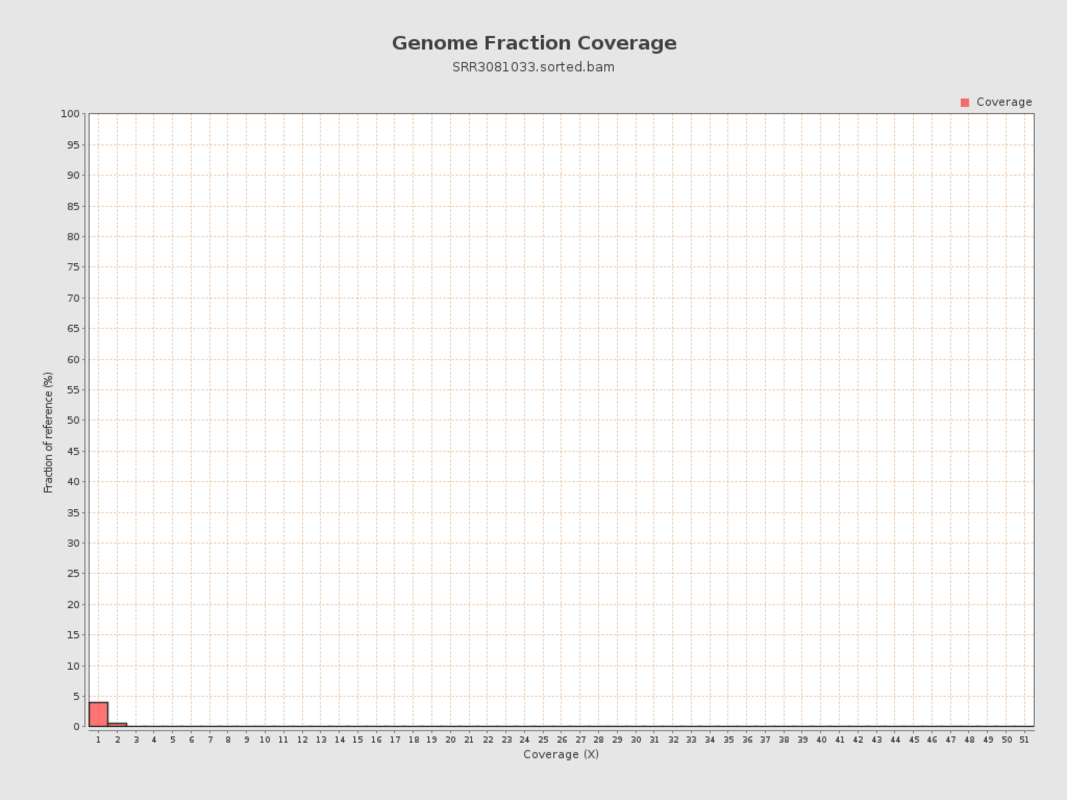
4. Results : Coverage Histogram



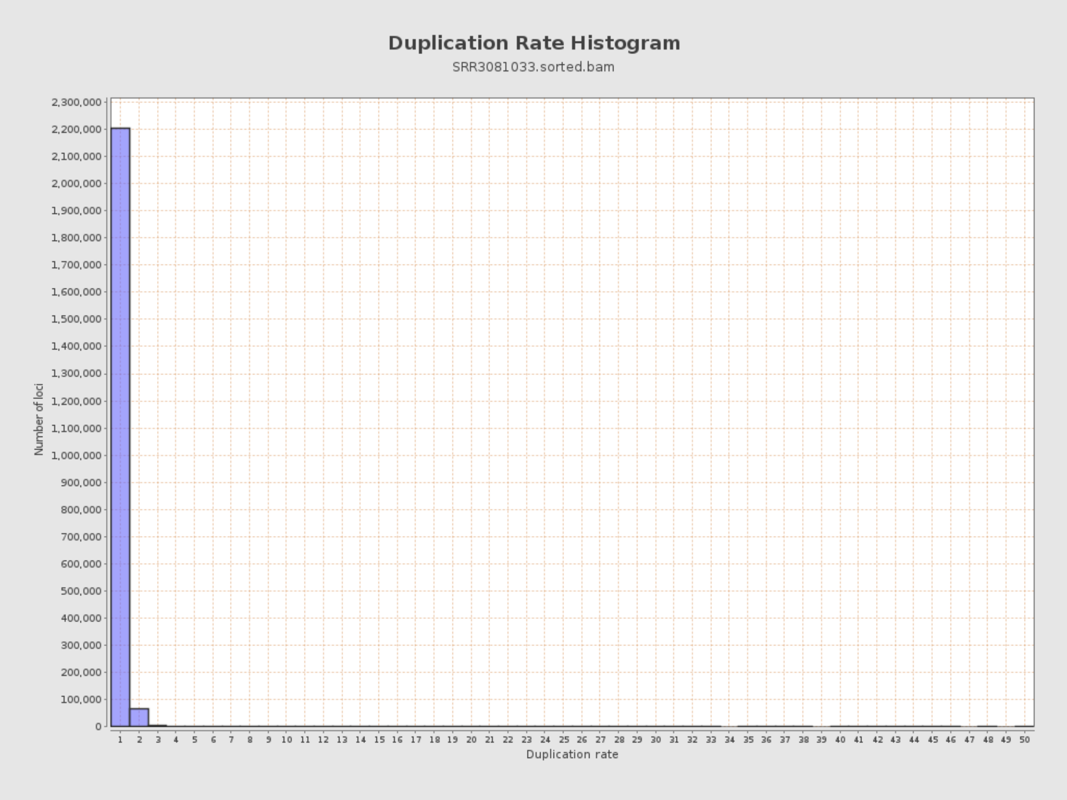
5. Results : Coverage Histogram (0-50X)



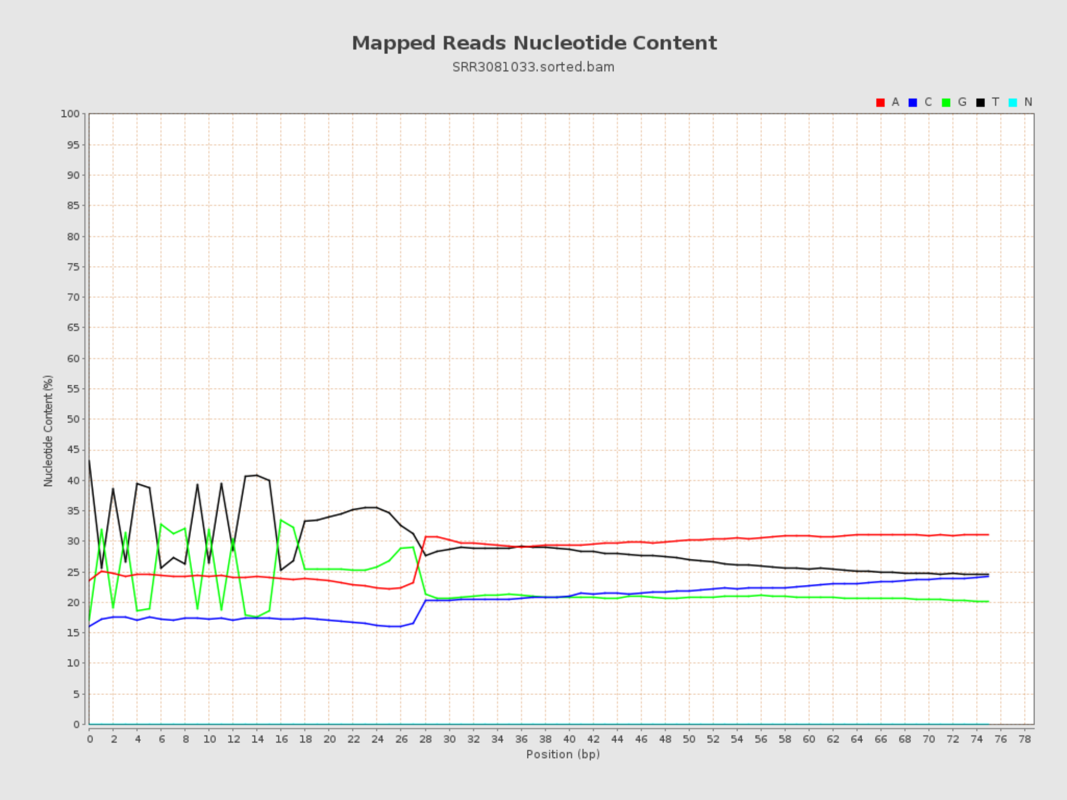
6. Results : Genome Fraction Coverage



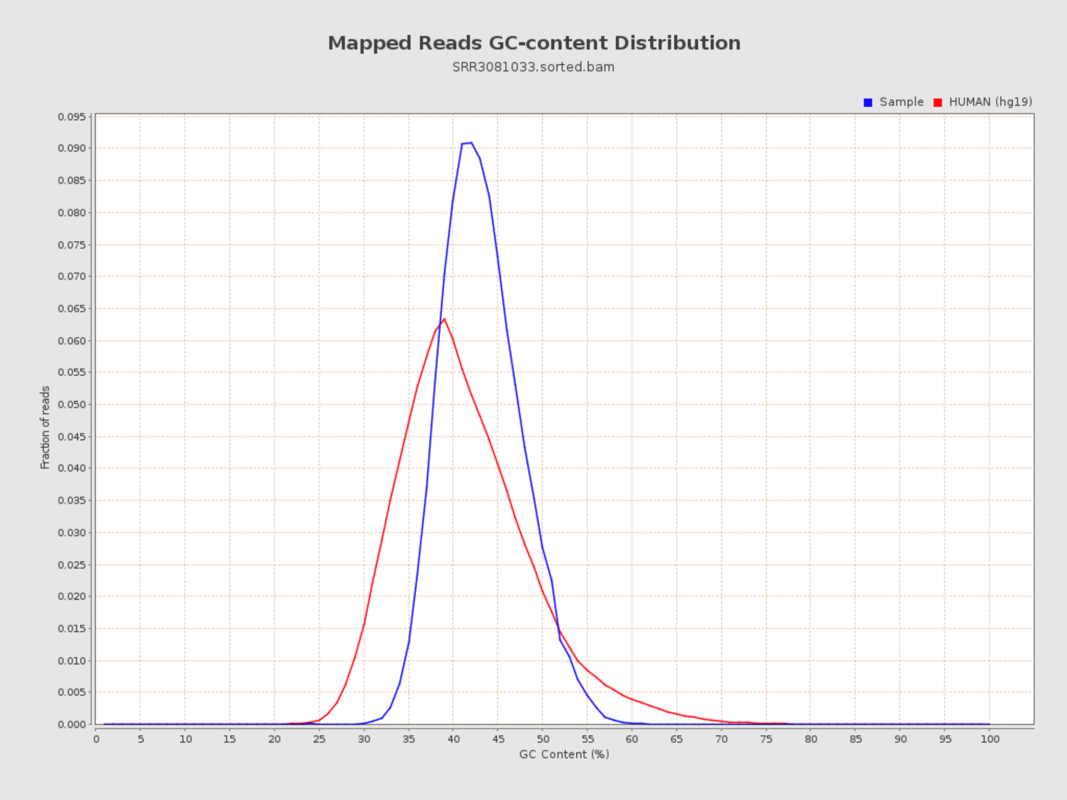
7. Results : Duplication Rate Histogram



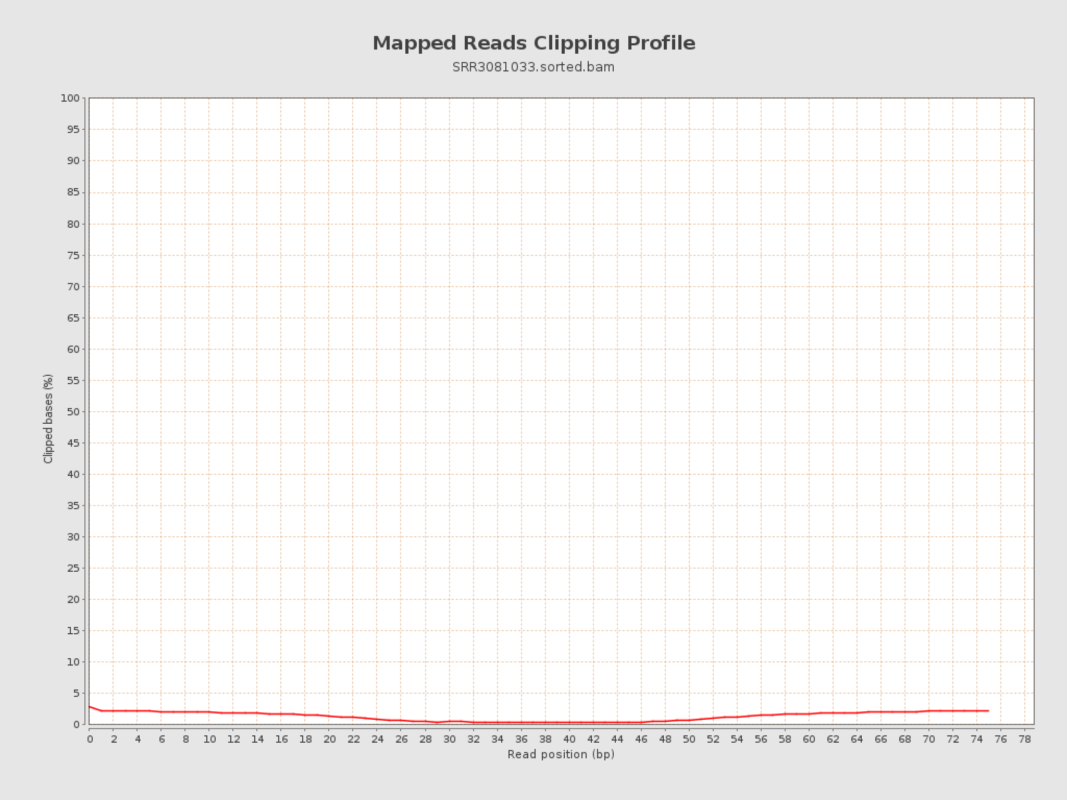
8. Results : Mapped Reads Nucleotide Content



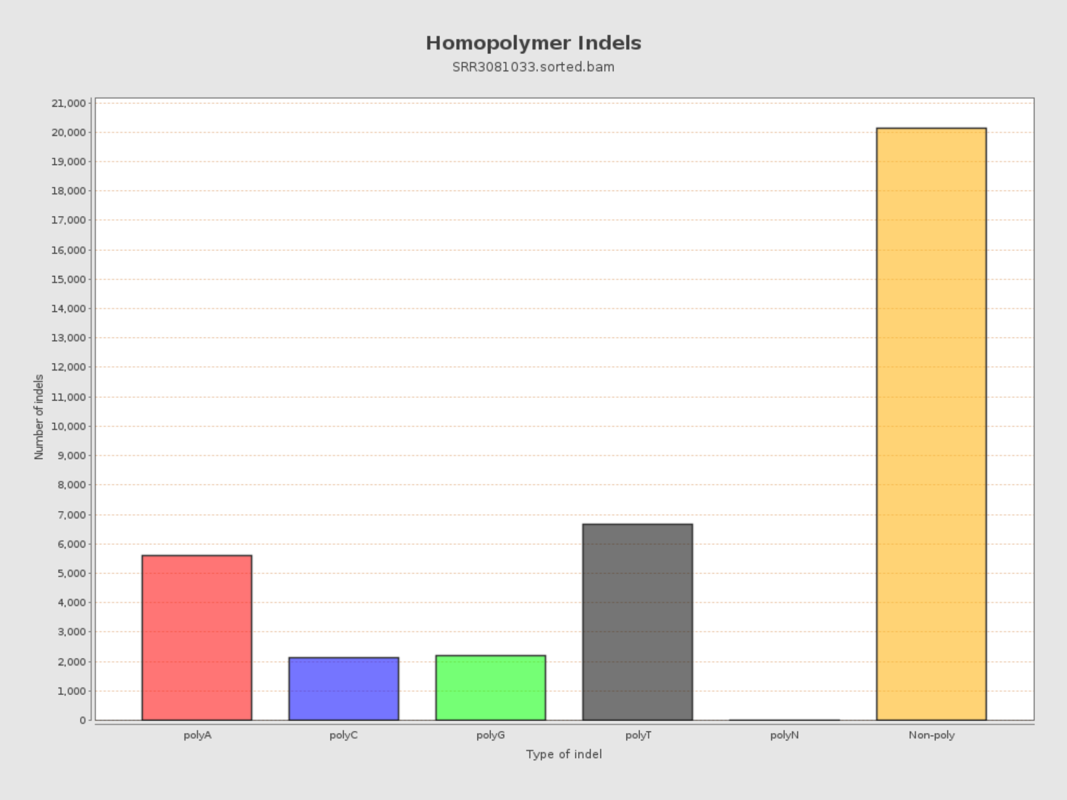
9. Results : Mapped Reads GC-content Distribution



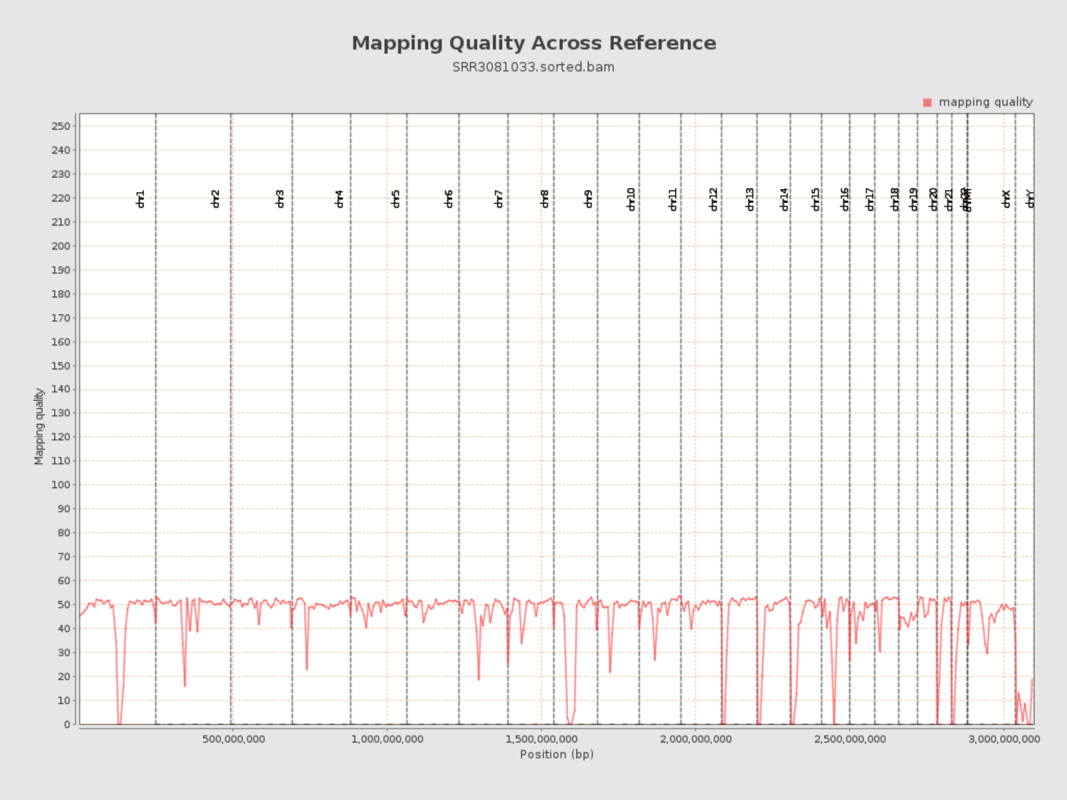
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram