Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 03:35:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3081225.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_SRR3081225 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3081225.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 03:35:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3081225.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,081,114
Mapped reads	2,678,437 / 86.93%
Unmapped reads	402,677 / 13.07%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	33,766 / 1.1%
Read min/max/mean length	30 / 76 / 76.38
Duplicated reads (estimated)	150,160 / 4.87%
Duplication rate	4.64%
Clipped reads	1,521,114 / 49.37%

2.2. ACGT Content

Number/percentage of A's	49,615,084 / 28.86%
Number/percentage of C's	33,369,262 / 19.41%
Number/percentage of T's	52,340,295 / 30.45%
Number/percentage of G's	36,551,878 / 21.26%
Number/percentage of N's	11,535 / 0.01%
GC Percentage	40.68%

2.3. Coverage

Mean	0.0555

Standard Deviation	0.3872

2.4. Mapping Quality

Mean Mapping Quality	45.02

2.5. Mismatches and indels

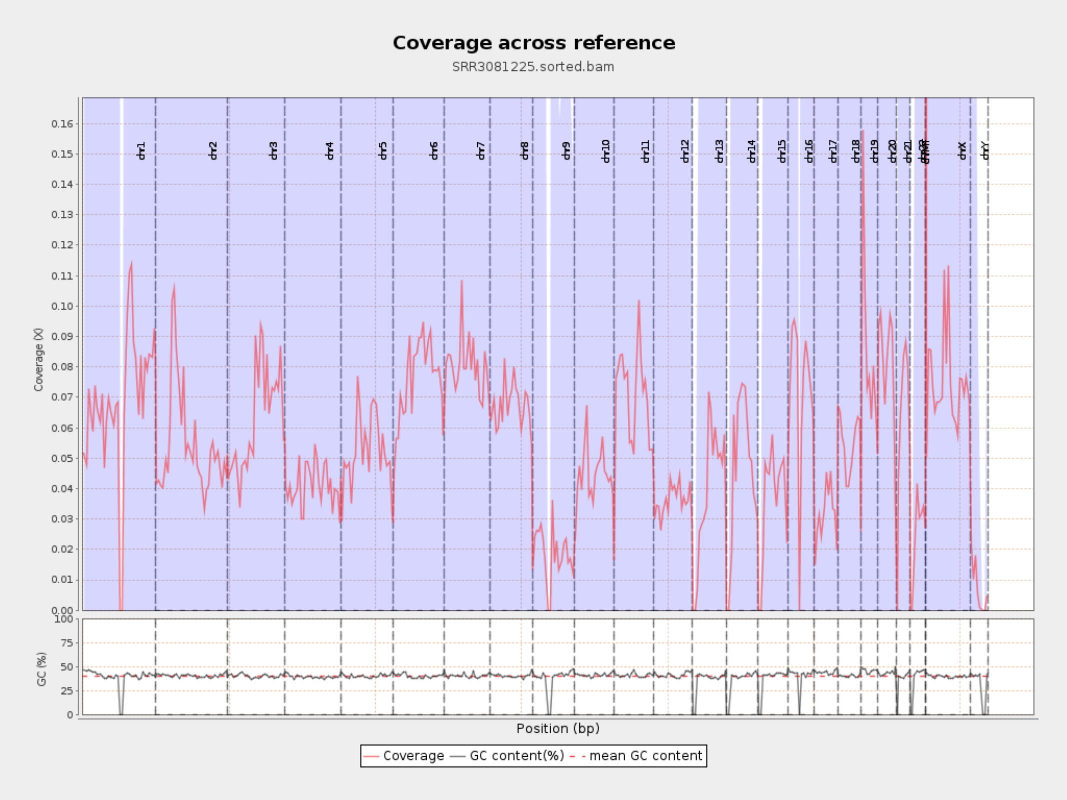
General error rate	0.9%
Mismatches	1,530,573
Insertions	12,590
Mapped reads with at least one insertion	0.47%
Deletions	38,622
Mapped reads with at least one deletion	1.43%
Homopolymer indels	47.68%

2.6. Chromosome stats

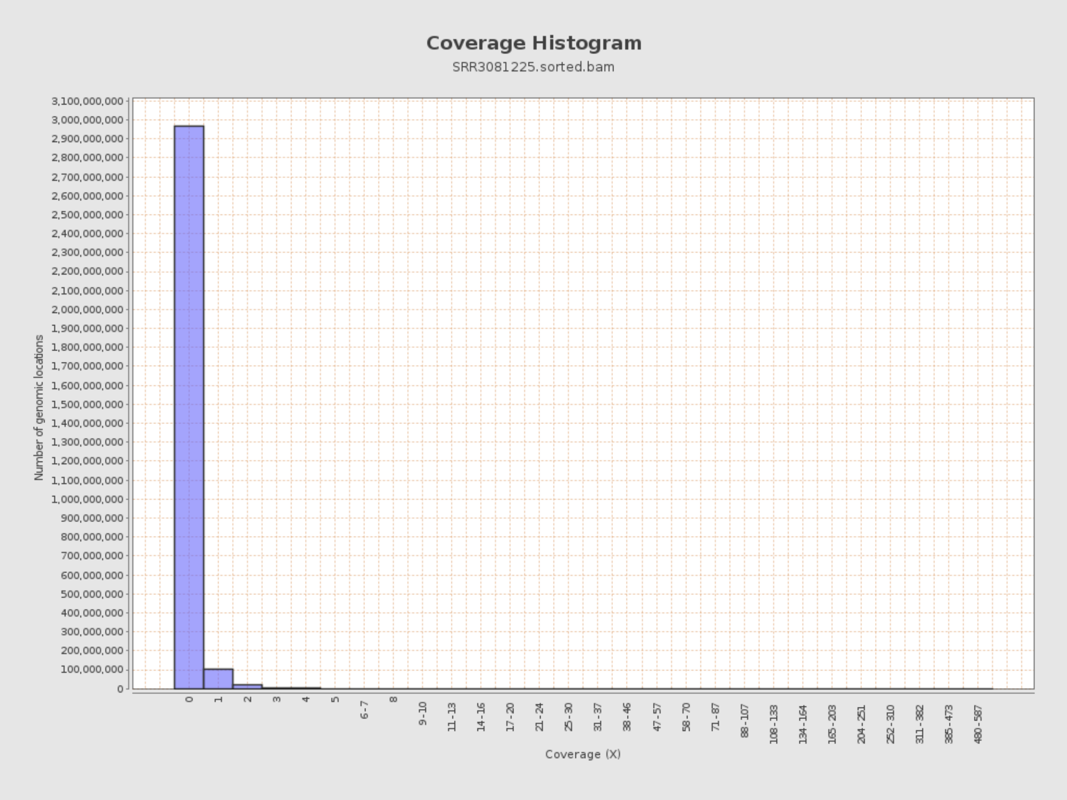
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	17172132	0.0689	0.5461
chr2	243199373	13270720	0.0546	0.4495
chr3	198022430	12386047	0.0625	0.3154
chr4	191154276	7816296	0.0409	0.264
chr5	180915260	9435405	0.0522	0.2891
chr6	171115067	13120462	0.0767	0.3872
chr7	159138663	12785984	0.0803	0.632

chr8	146364022	9870594	0.0674	0.481
chr9	141213431	2648786	0.0188	0.2477
chr10	135534747	6029608	0.0445	0.3711
chr11	135006516	9525331	0.0706	0.436
chr12	133851895	4839909	0.0362	0.2426
chr13	115169878	4575758	0.0397	0.2505
chr14	107349540	5043105	0.047	0.2781
chr15	102531392	3657051	0.0357	0.3321
chr16	90354753	6437811	0.0713	0.3423
chr17	81195210	2602281	0.032	0.2546
chr18	78077248	4287196	0.0549	0.4219
chr19	59128983	4926178	0.0833	0.4779
chr20	63025520	5151636	0.0817	0.3668
chr21	48129895	3047823	0.0633	0.3259
chr22	51304566	1241369	0.0242	0.1916
chrMT	16571	61707	3.7238	3.0173
chrX	155270560	11603681	0.0747	0.3656
chrY	59373566	413856	0.007	0.1194

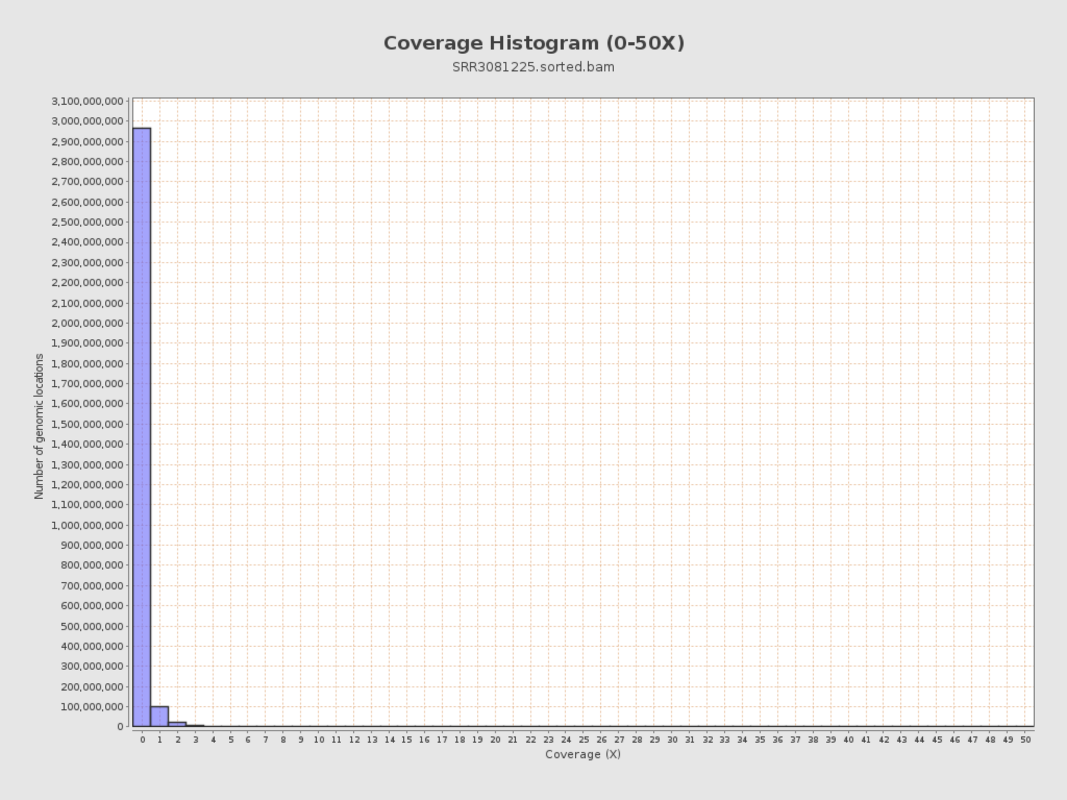
3. Results : Coverage across reference



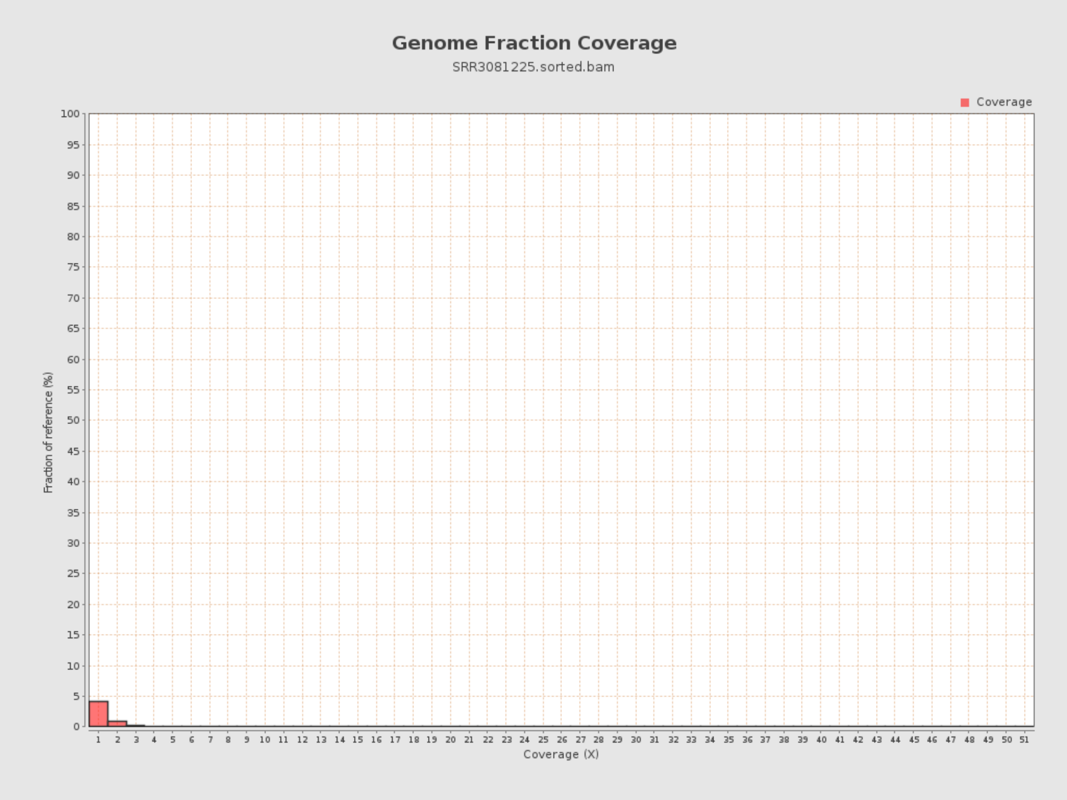
4. Results : Coverage Histogram



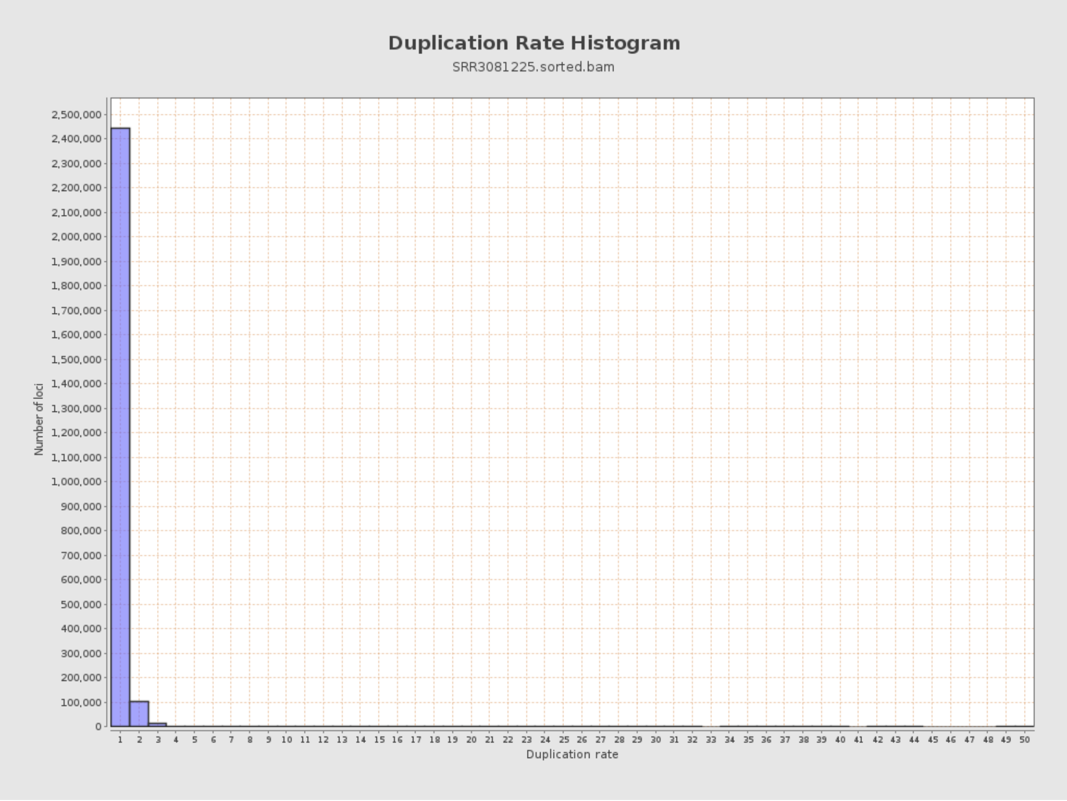
5. Results : Coverage Histogram (0-50X)



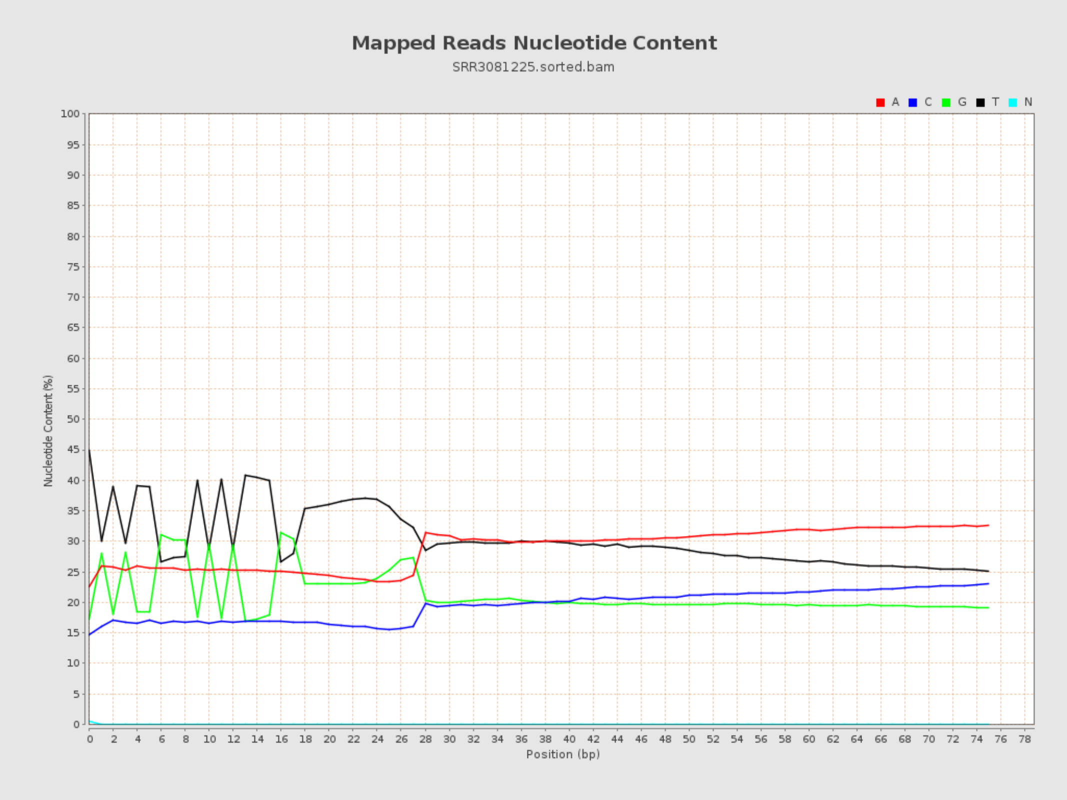
6. Results : Genome Fraction Coverage



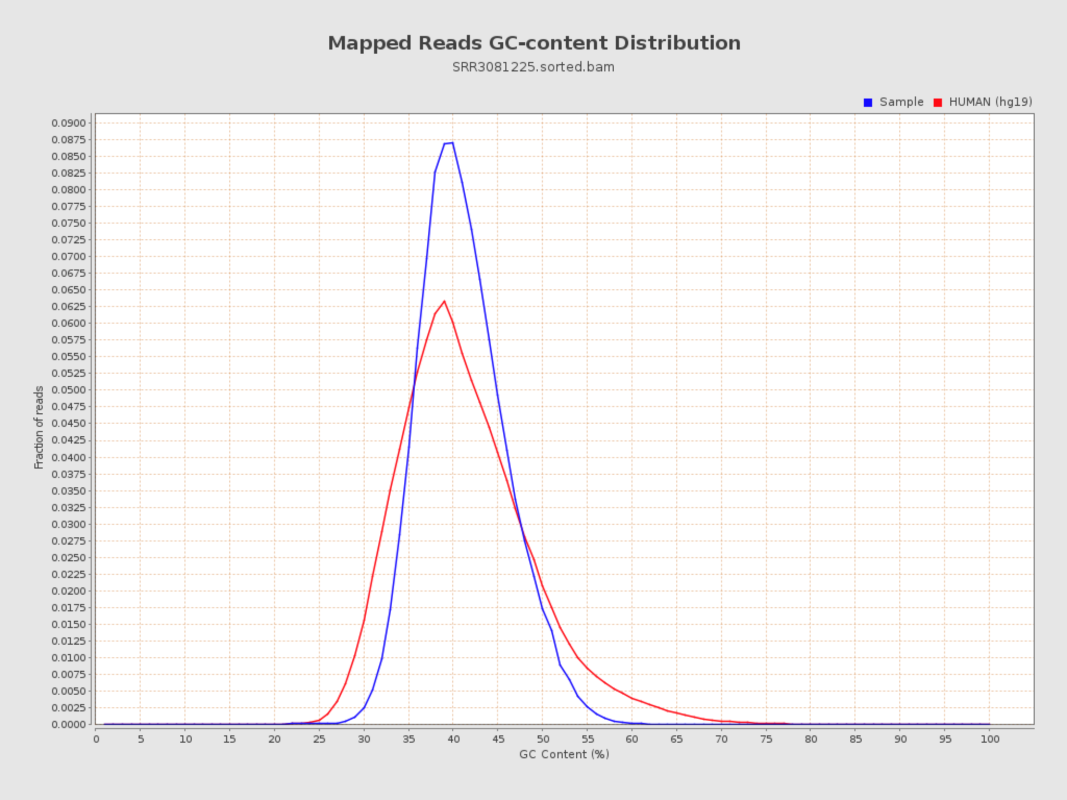
7. Results : Duplication Rate Histogram



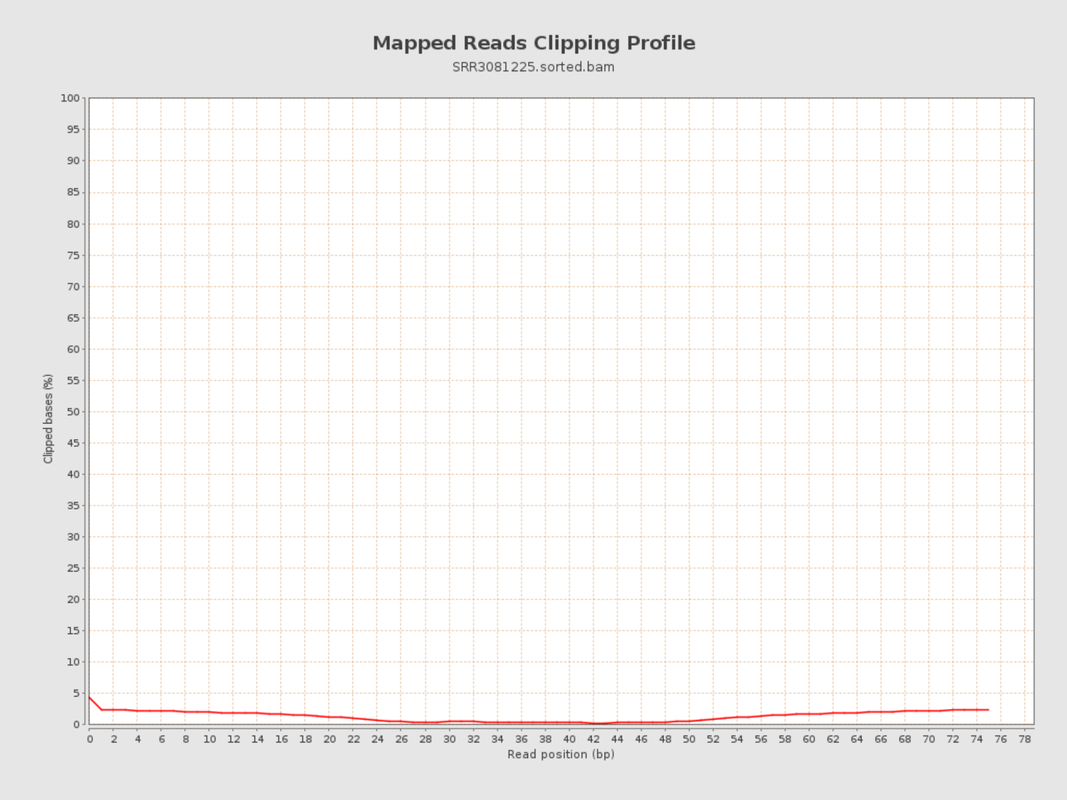
8. Results : Mapped Reads Nucleotide Content



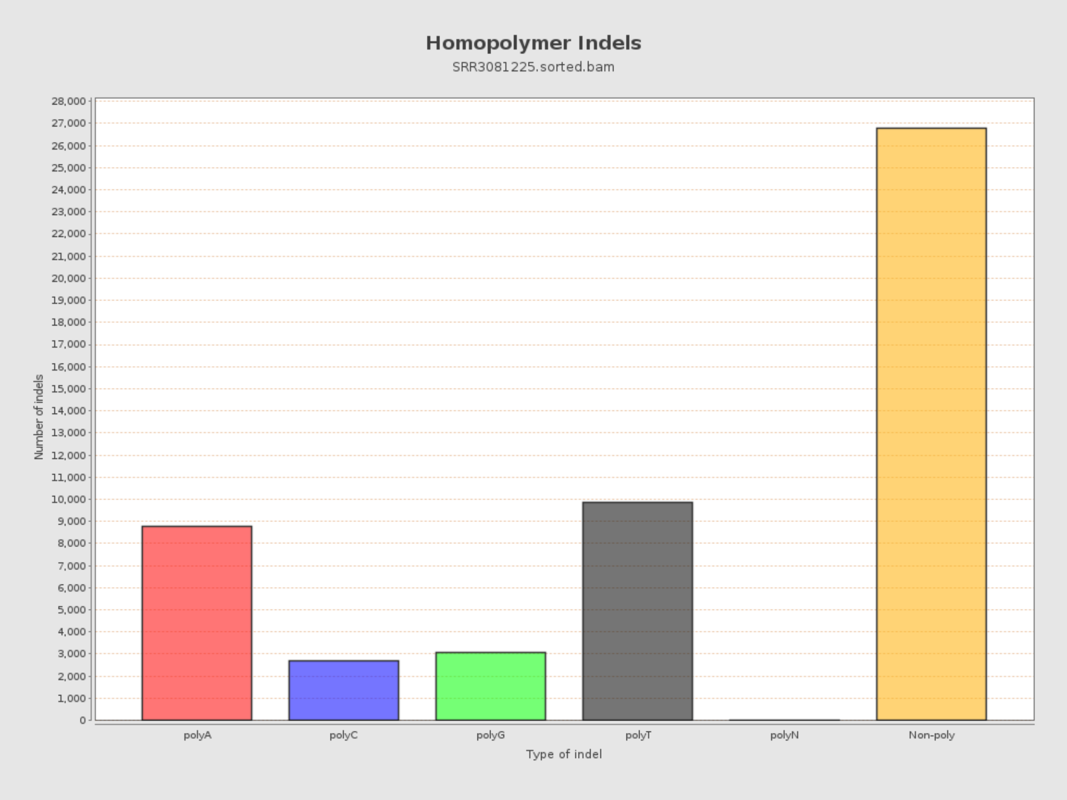
9. Results : Mapped Reads GC-content Distribution



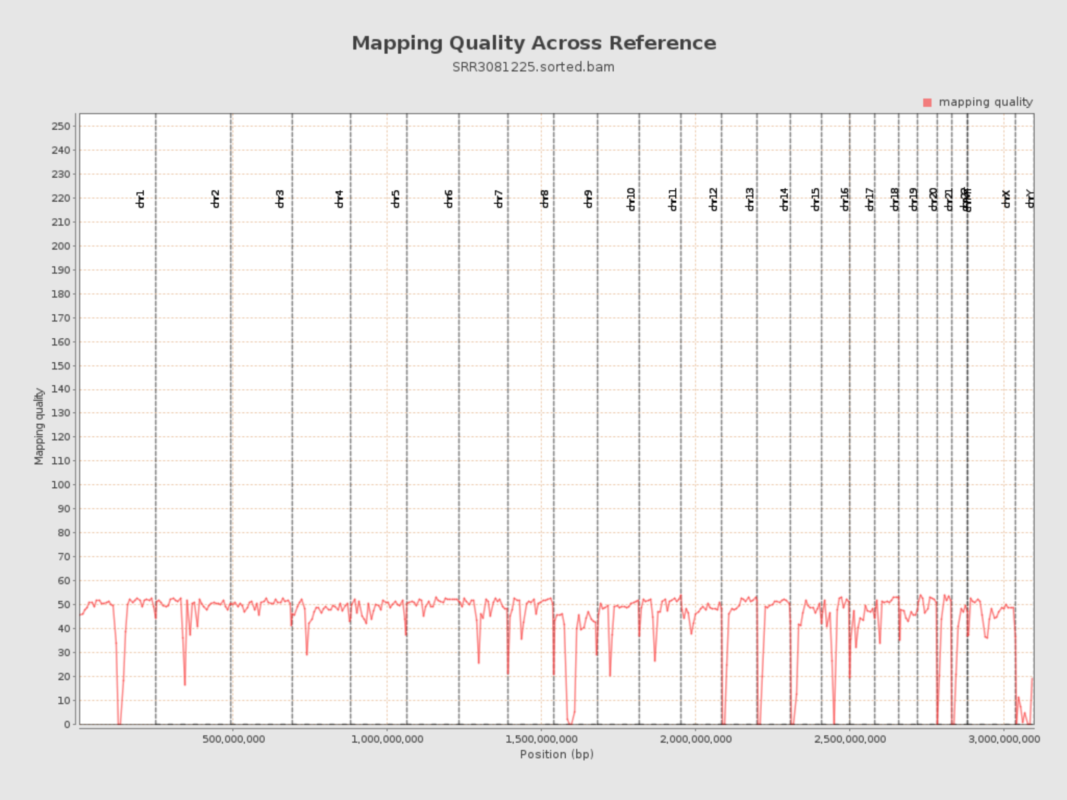
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram