Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 02:12:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083651.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_SRR3083651 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083651.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 02:12:29 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083651.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,858,633
Mapped reads	1,482,273 / 79.75%
Unmapped reads	376,360 / 20.25%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,534 / 0.51%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	37,157 / 2%
Duplication rate	2.04%
Clipped reads	979,356 / 52.69%

2.2. ACGT Content

Number/percentage of A's	27,024,785 / 29.81%
Number/percentage of C's	17,415,140 / 19.21%
Number/percentage of T's	26,604,698 / 29.35%
Number/percentage of G's	19,609,592 / 21.63%
Number/percentage of N's	5,336 / 0.01%
GC Percentage	40.84%

2.3. Coverage

Mean	0.0293

Standard Deviation	0.257

2.4. Mapping Quality

Mean Mapping Quality	45.13

2.5. Mismatches and indels

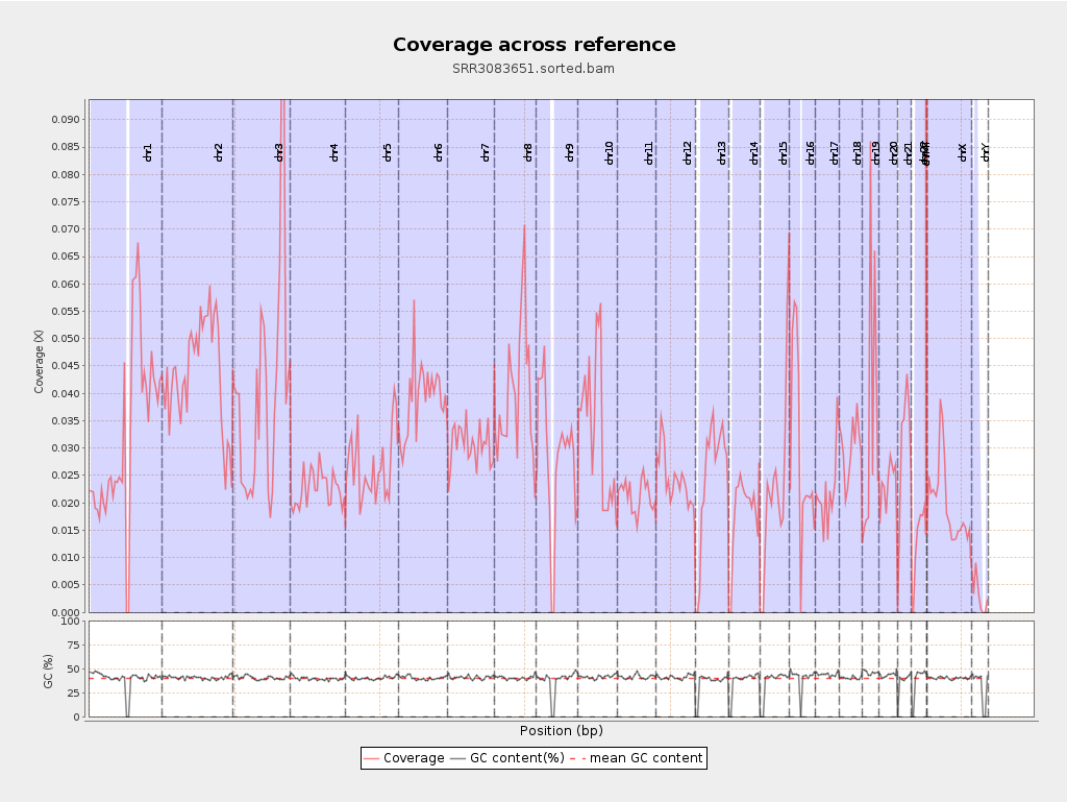
General error rate	0.85%
Mismatches	761,115
Insertions	6,249
Mapped reads with at least one insertion	0.42%
Deletions	18,340
Mapped reads with at least one deletion	1.23%
Homopolymer indels	45.95%

2.6. Chromosome stats

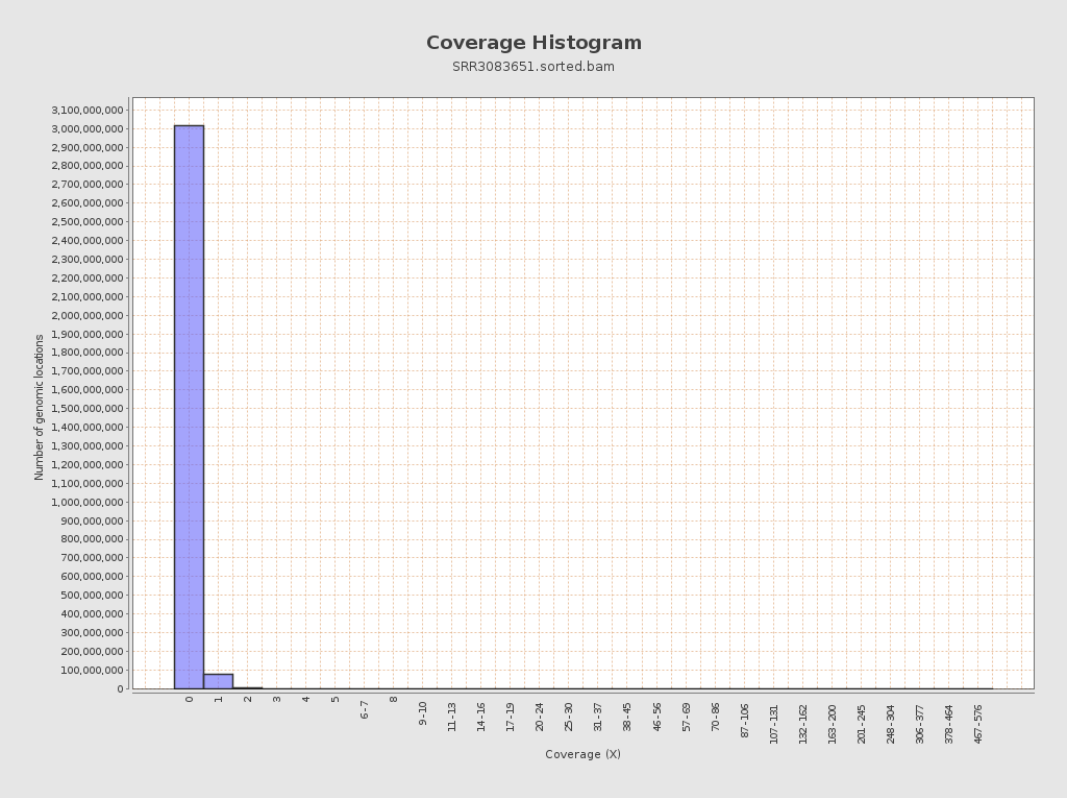
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	8025776	0.0322	0.5204
chr2	243199373	10580961	0.0435	0.2655
chr3	198022430	7948613	0.0401	0.2162
chr4	191154276	4298638	0.0225	0.1616
chr5	180915260	4850345	0.0268	0.175
chr6	171115067	6672749	0.039	0.2555
chr7	159138663	4885305	0.0307	0.2567

chr8	146364022	5846695	0.0399	0.3413
chr9	141213431	4076105	0.0289	0.2043
chr10	135534747	4584900	0.0338	0.262
chr11	135006516	2870788	0.0213	0.1709
chr12	133851895	3241233	0.0242	0.1667
chr13	115169878	2827293	0.0245	0.1665
chr14	107349540	1912630	0.0178	0.1436
chr15	102531392	2289738	0.0223	0.1601
chr16	90354753	2656298	0.0294	0.1888
chr17	81195210	1819243	0.0224	0.1629
chr18	78077248	2353550	0.0301	0.3008
chr19	59128983	2030255	0.0343	0.3696
chr20	63025520	1468097	0.0233	0.1643
chr21	48129895	1425495	0.0296	0.1862
chr22	51304566	649418	0.0127	0.1193
chrMT	16571	136634	8.2454	4.6687
chrX	155270560	3064213	0.0197	0.157
chrY	59373566	173610	0.0029	0.069

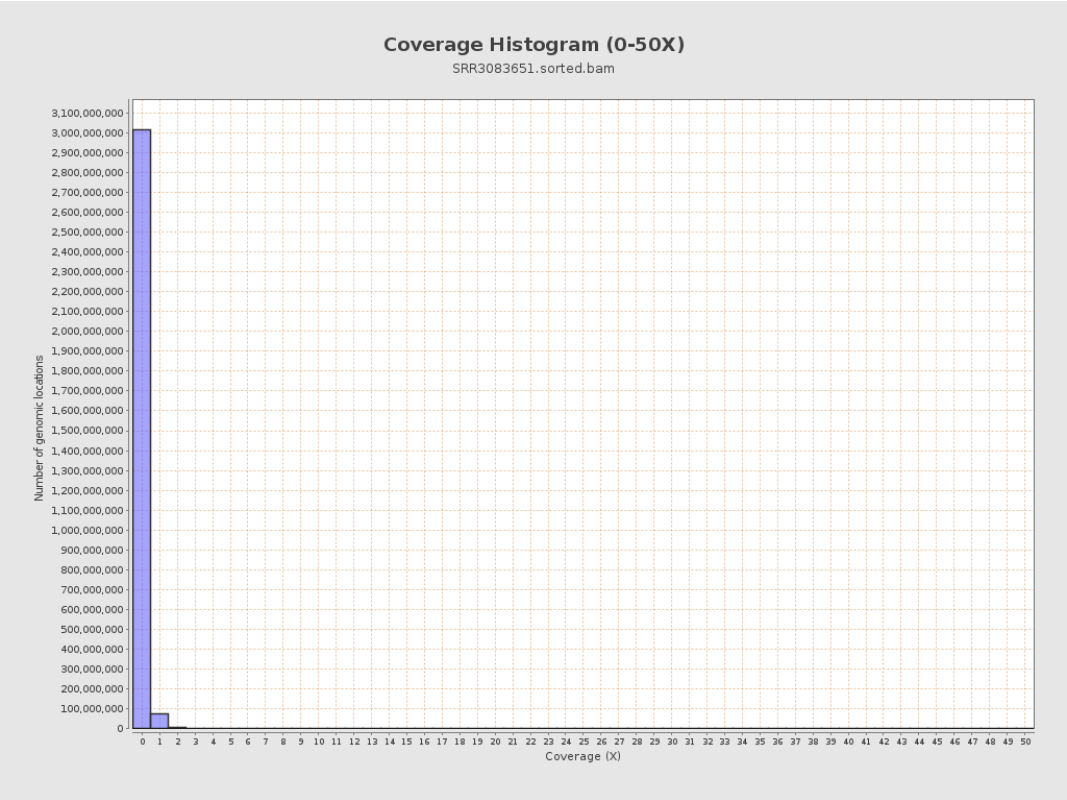
3. Results : Coverage across reference



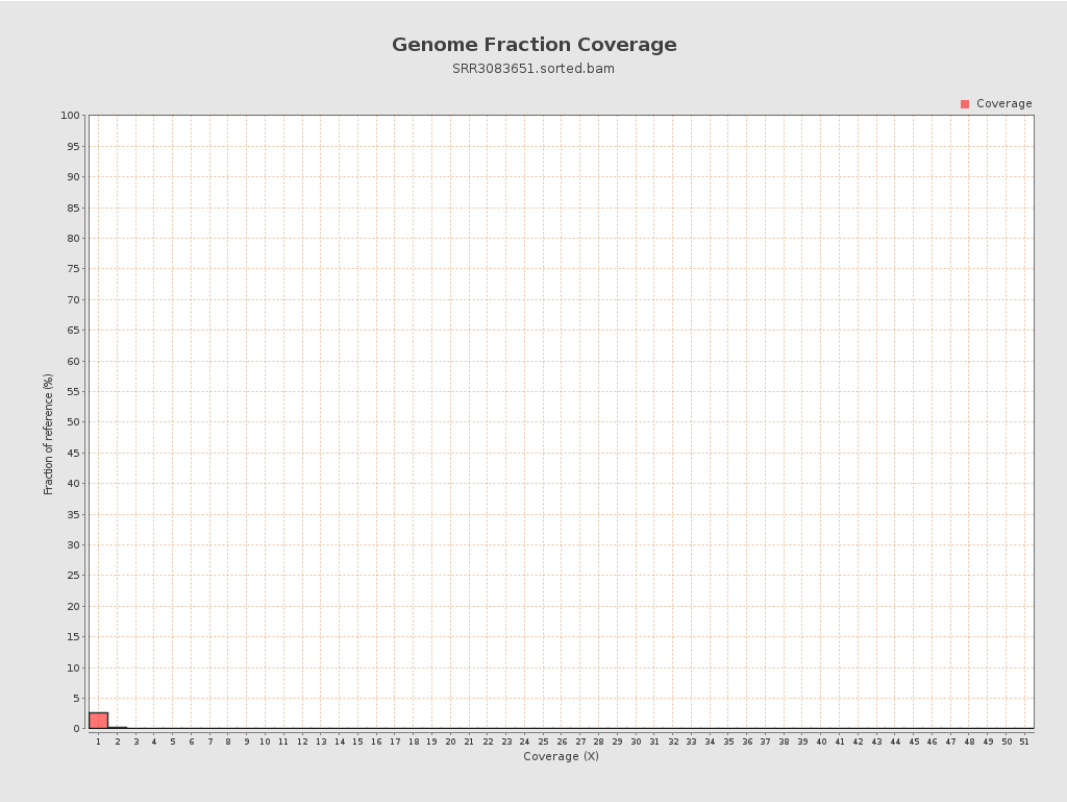
4. Results : Coverage Histogram



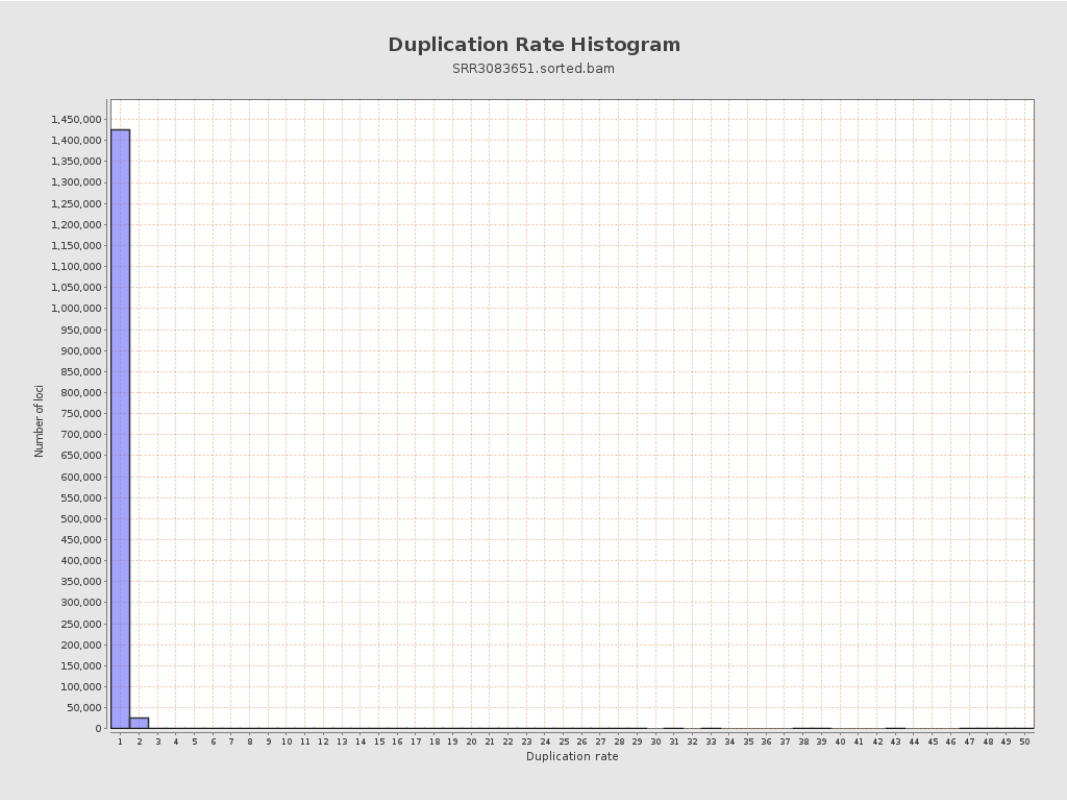
5. Results : Coverage Histogram (0-50X)



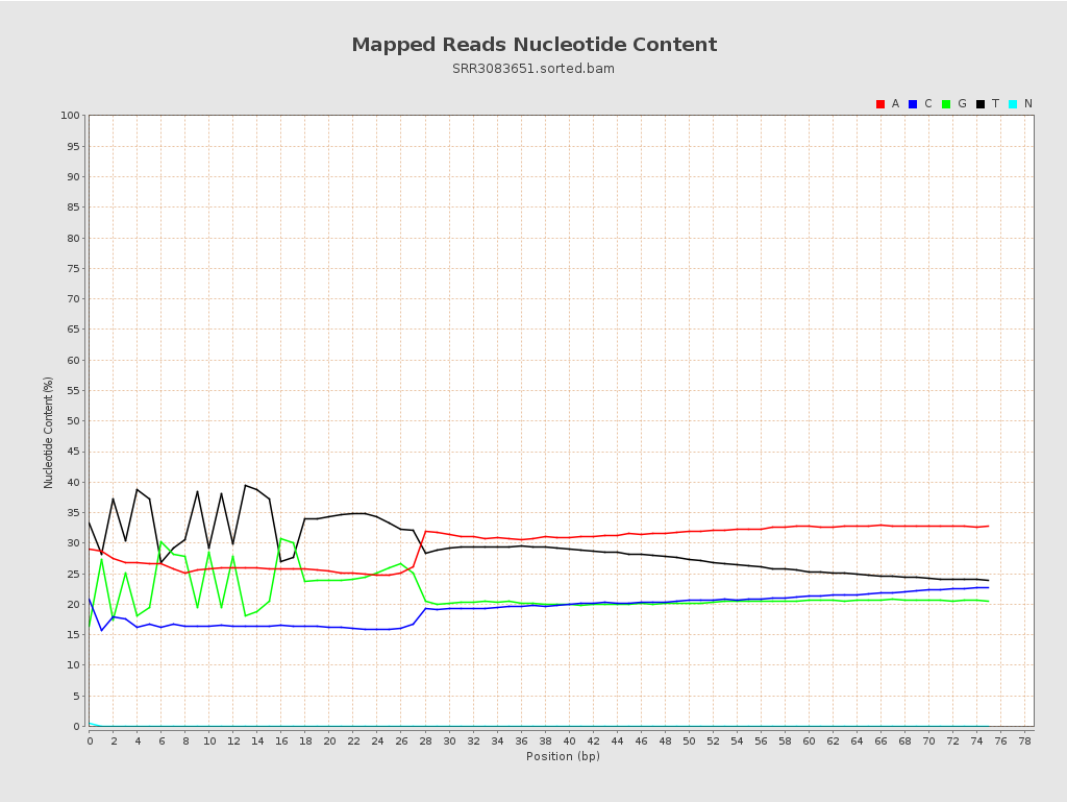
6. Results : Genome Fraction Coverage



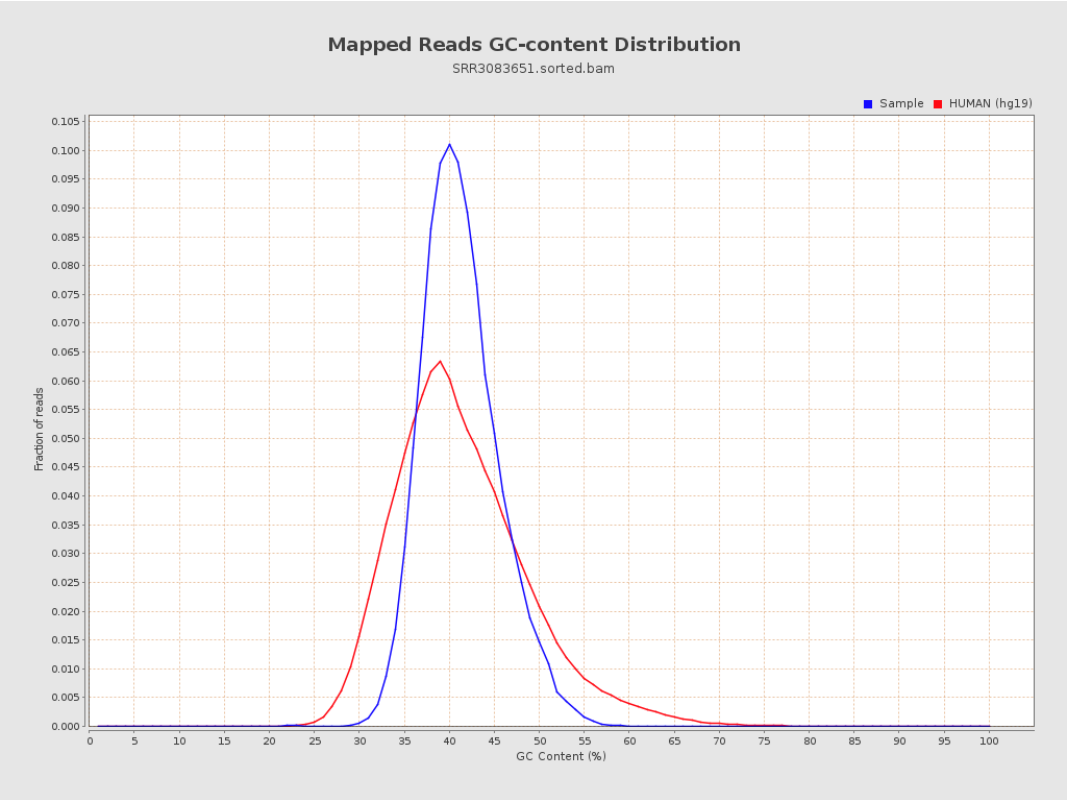
7. Results : Duplication Rate Histogram



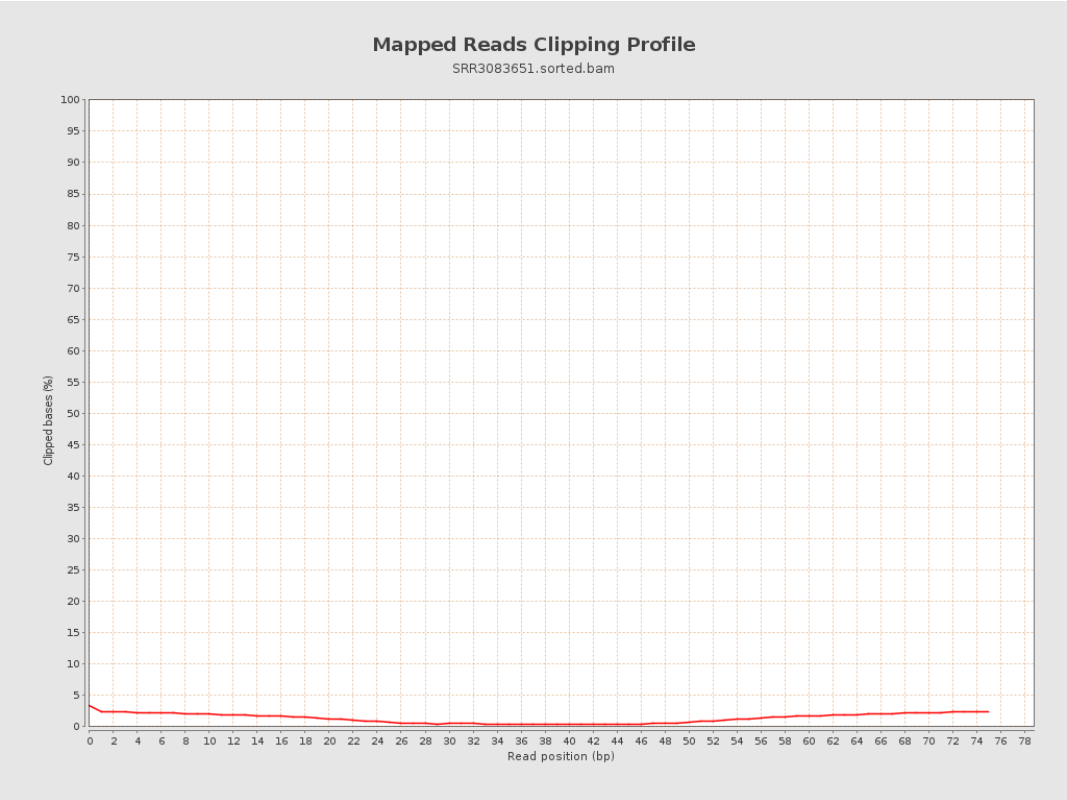
8. Results : Mapped Reads Nucleotide Content



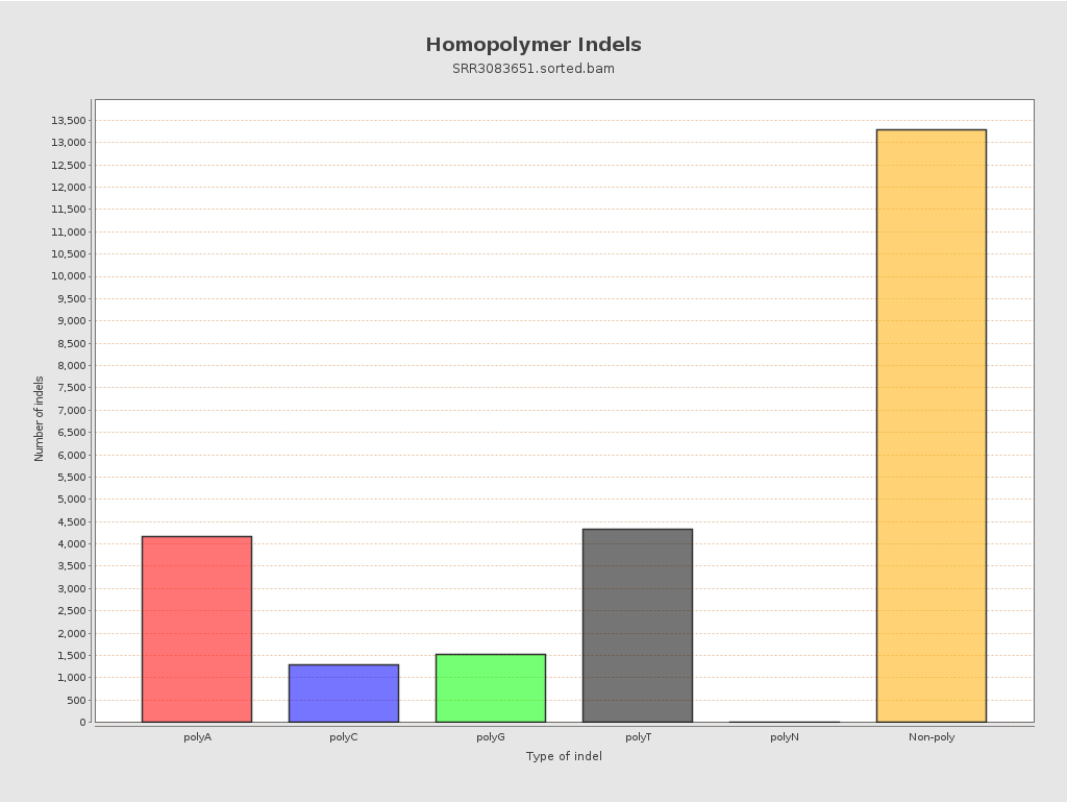
9. Results : Mapped Reads GC-content Distribution



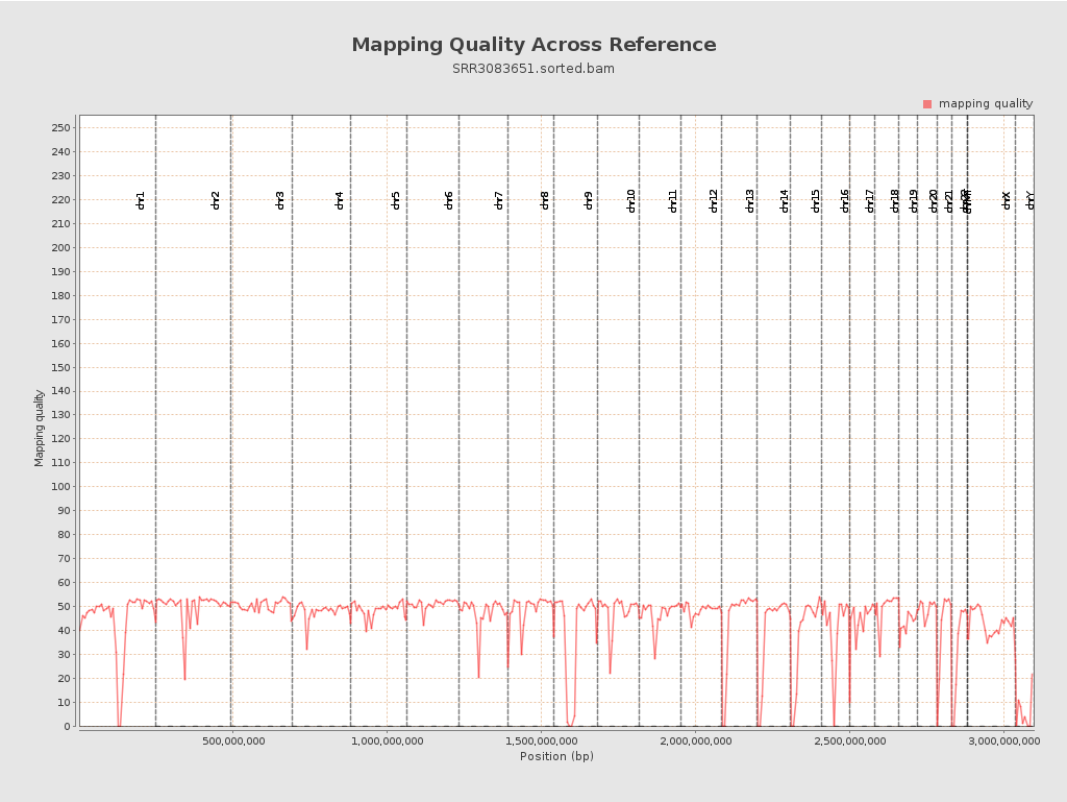
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram