Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:02:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083631.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_SRR3083631 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083631.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:02:38 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083631.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,720,751
Mapped reads	1,527,601 / 88.78%
Unmapped reads	193,150 / 11.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,573 / 0.96%
Read min/max/mean length	30 / 76 / 76.34
Duplicated reads (estimated)	74,324 / 4.32%
Duplication rate	4.27%
Clipped reads	722,908 / 42.01%

2.2. ACGT Content

Number/percentage of A's	26,994,364 / 26.8%
Number/percentage of C's	18,817,619 / 18.68%
Number/percentage of T's	31,690,814 / 31.46%
Number/percentage of G's	23,222,213 / 23.05%
Number/percentage of N's	4,959 / 0%
GC Percentage	41.74%

2.3. Coverage

Mean	0.0326

Standard Deviation	0.2508

2.4. Mapping Quality

Mean Mapping Quality	45.17

2.5. Mismatches and indels

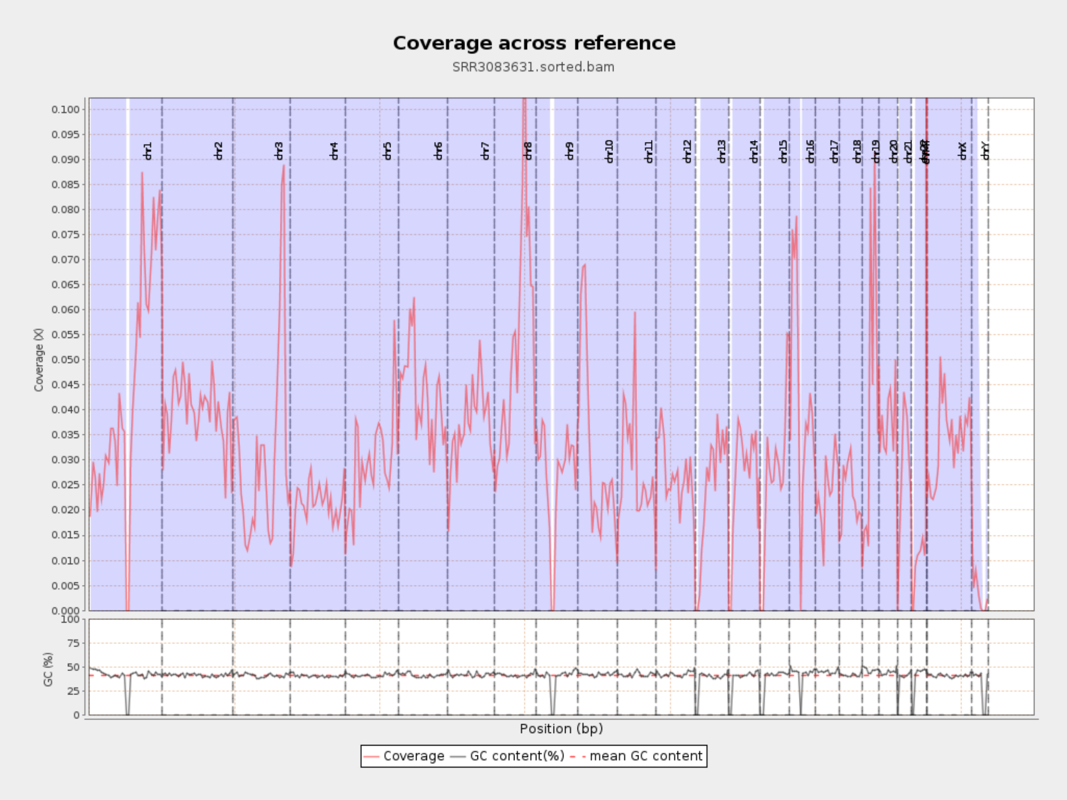
General error rate	0.69%
Mismatches	679,668
Insertions	7,379
Mapped reads with at least one insertion	0.48%
Deletions	22,418
Mapped reads with at least one deletion	1.46%
Homopolymer indels	48.56%

2.6. Chromosome stats

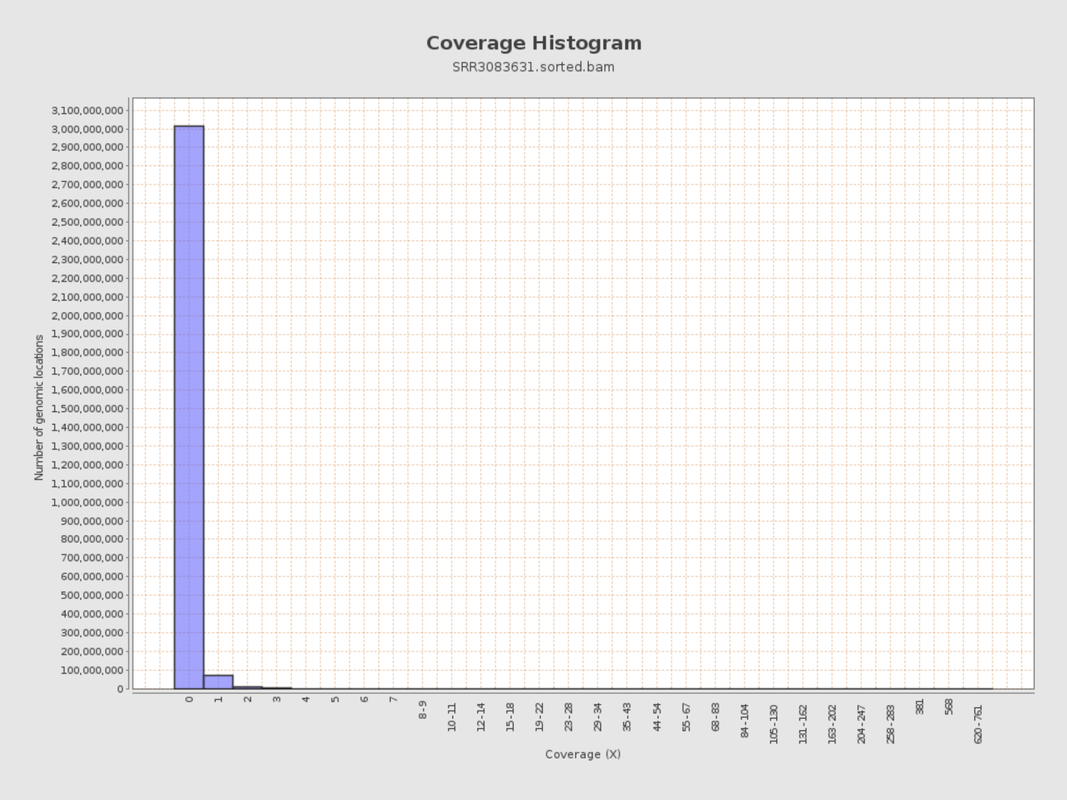
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10806282	0.0434	0.3374
chr2	243199373	9669134	0.0398	0.3969
chr3	198022430	6122704	0.0309	0.2085
chr4	191154276	4051276	0.0212	0.1731
chr5	180915260	5400445	0.0299	0.2029
chr6	171115067	7365388	0.043	0.2735
chr7	159138663	5932965	0.0373	0.2871

chr8	146364022	7861258	0.0537	0.2967
chr9	141213431	3721505	0.0264	0.2063
chr10	135534747	4335266	0.032	0.2225
chr11	135006516	3775335	0.028	0.2089
chr12	133851895	3629883	0.0271	0.1933
chr13	115169878	2749514	0.0239	0.1824
chr14	107349540	2808953	0.0262	0.1897
chr15	102531392	2749473	0.0268	0.1977
chr16	90354753	3883761	0.043	0.2488
chr17	81195210	1955263	0.0241	0.1838
chr18	78077248	1801317	0.0231	0.24
chr19	59128983	2461886	0.0416	0.2951
chr20	63025520	2381521	0.0378	0.2302
chr21	48129895	1314400	0.0273	0.1957
chr22	51304566	474426	0.0092	0.1105
chrMT	16571	5615	0.3388	0.6971
chrX	155270560	5313293	0.0342	0.2224
chrY	59373566	195659	0.0033	0.0743

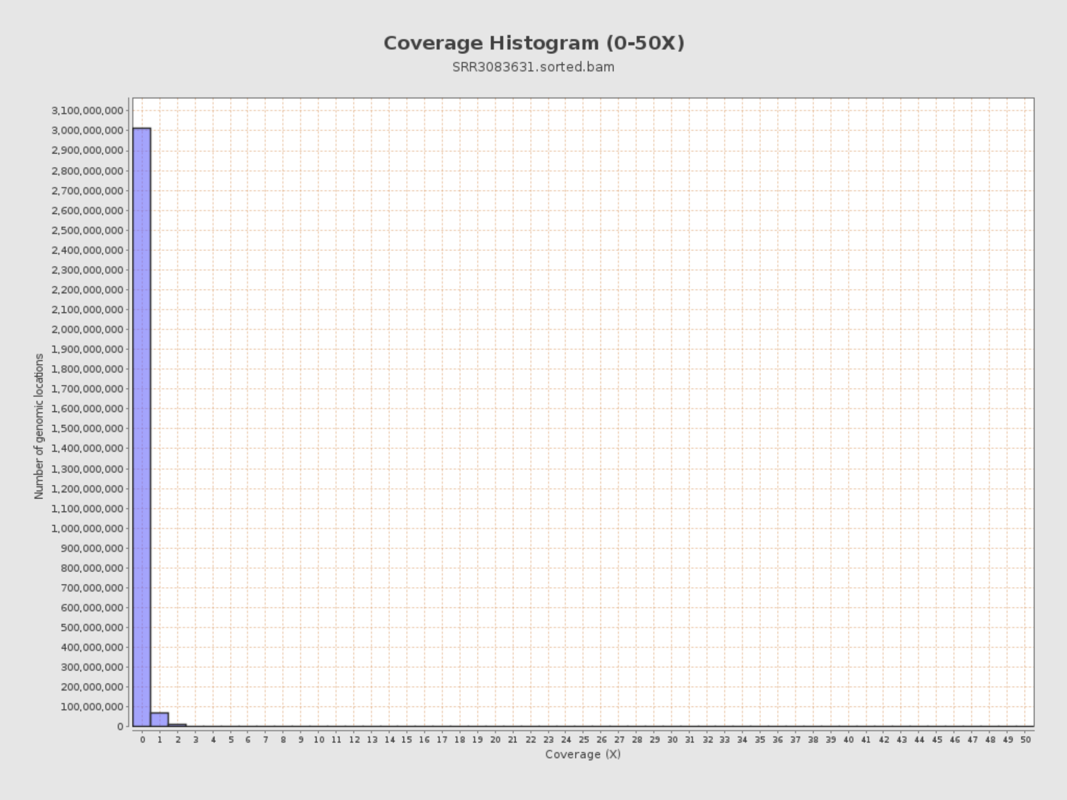
3. Results : Coverage across reference



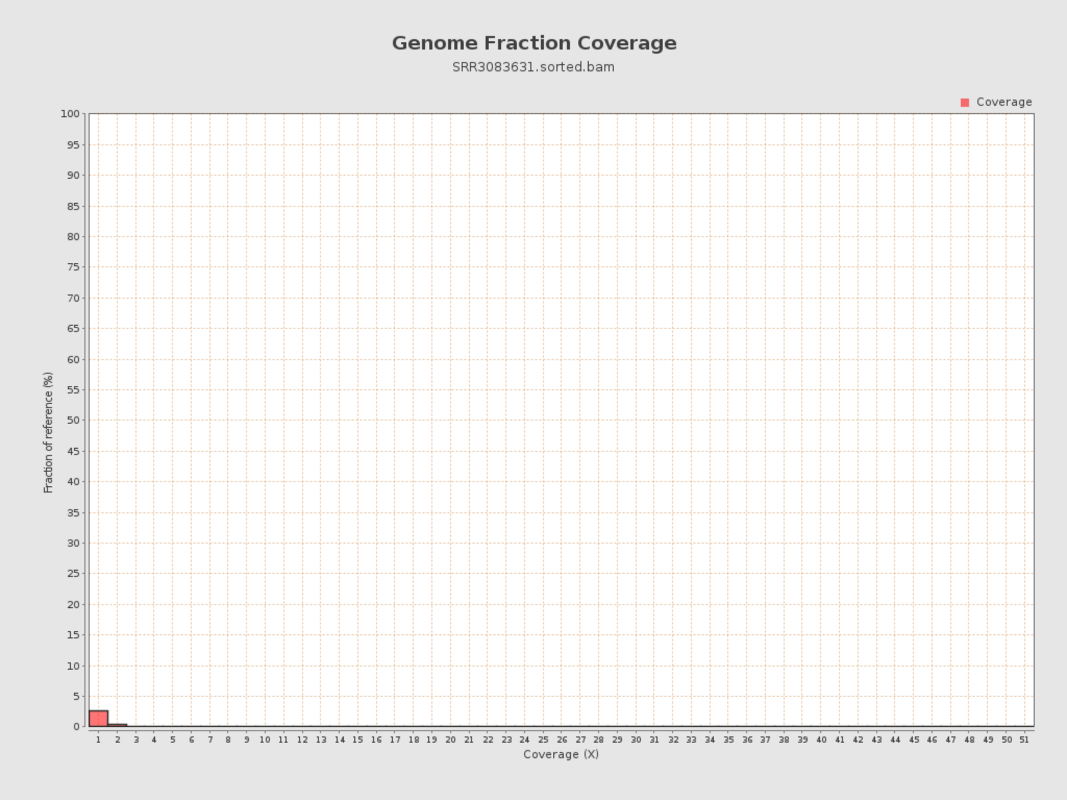
4. Results : Coverage Histogram



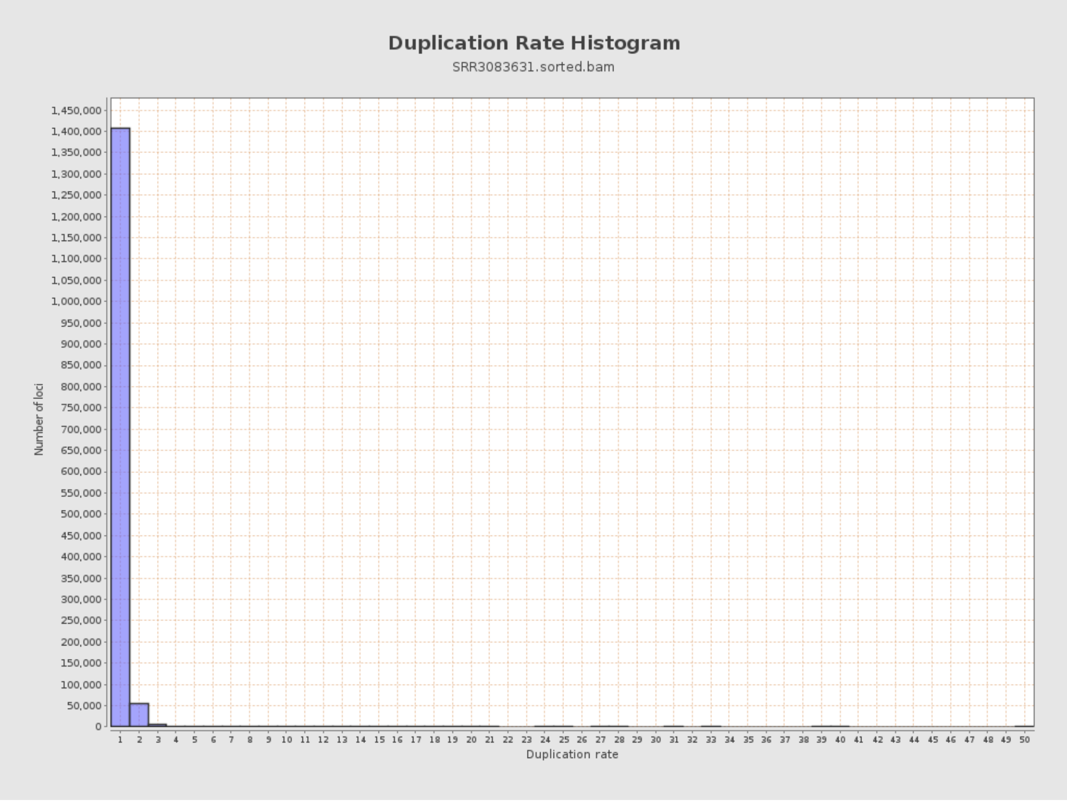
5. Results : Coverage Histogram (0-50X)



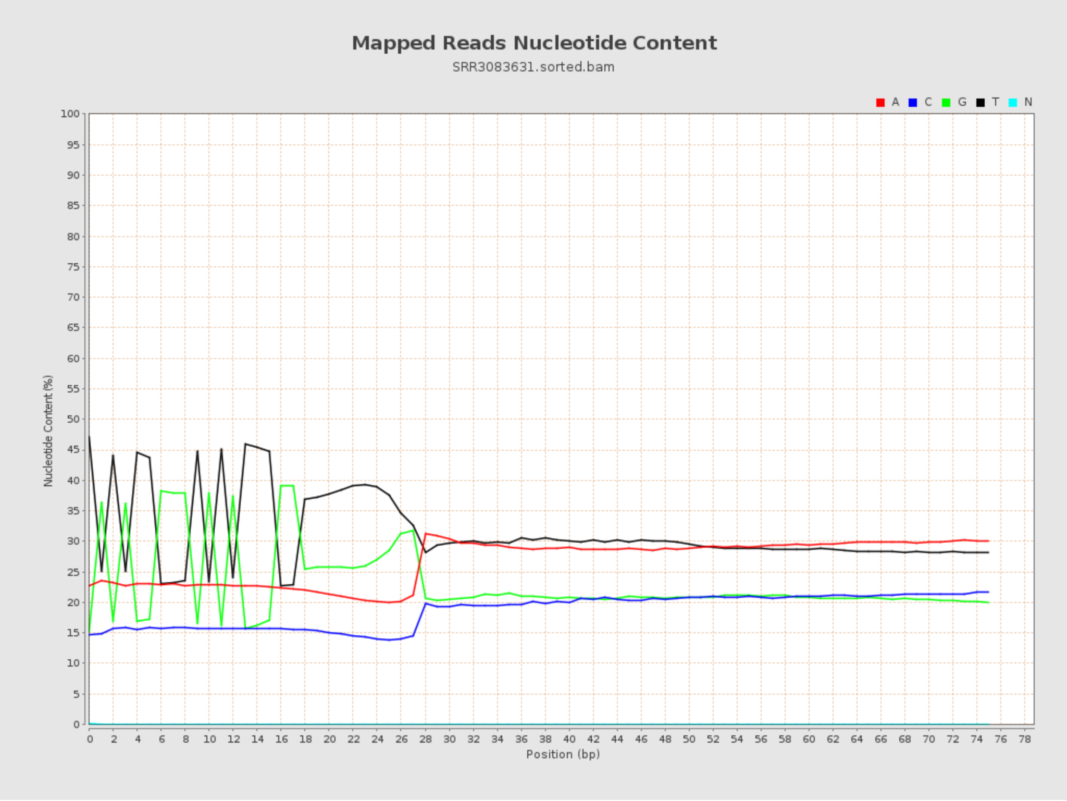
6. Results : Genome Fraction Coverage



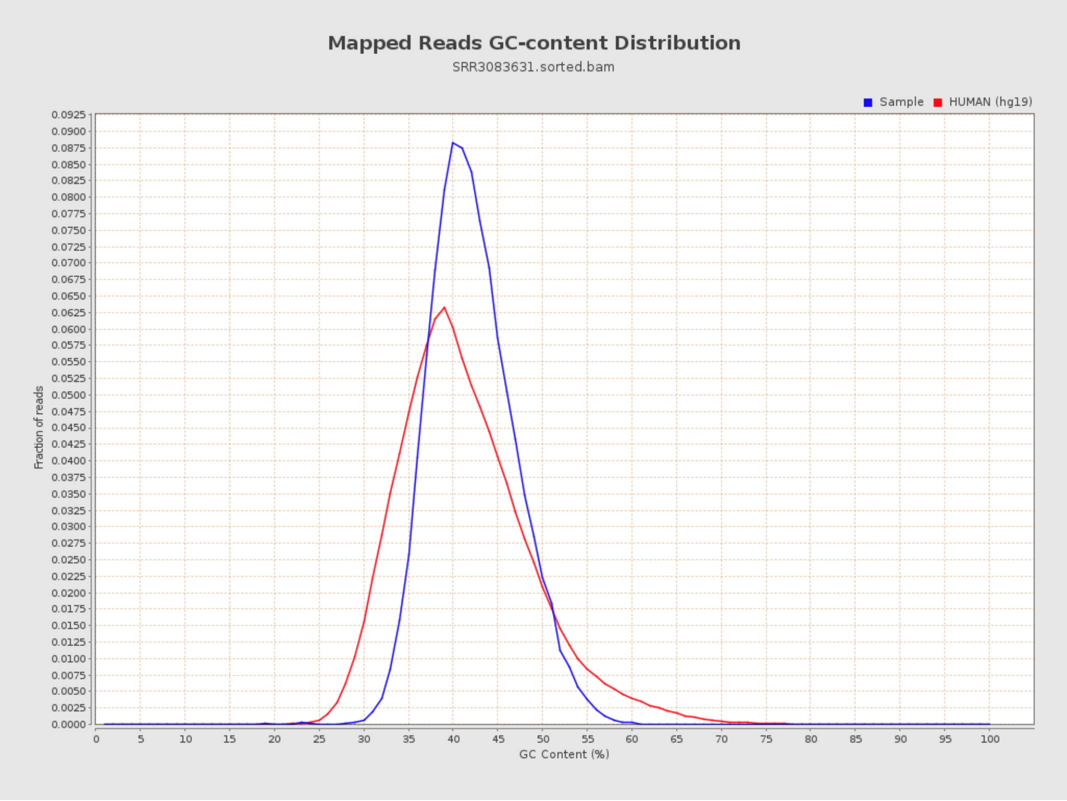
7. Results : Duplication Rate Histogram



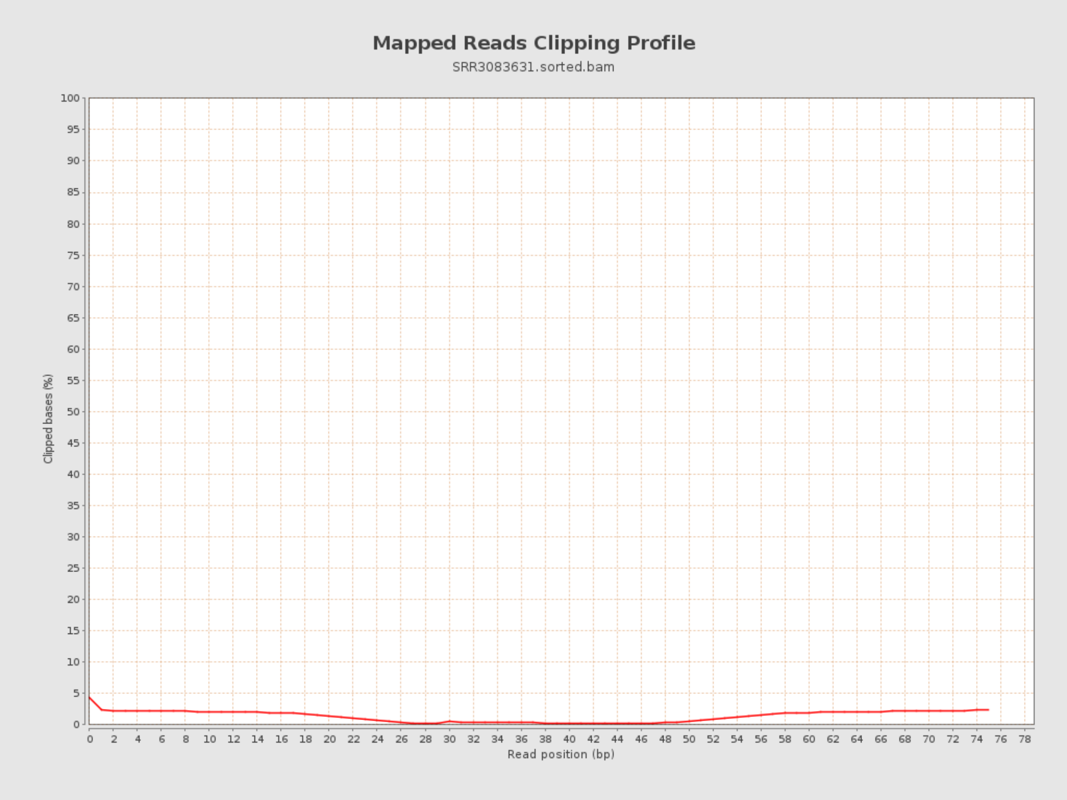
8. Results : Mapped Reads Nucleotide Content



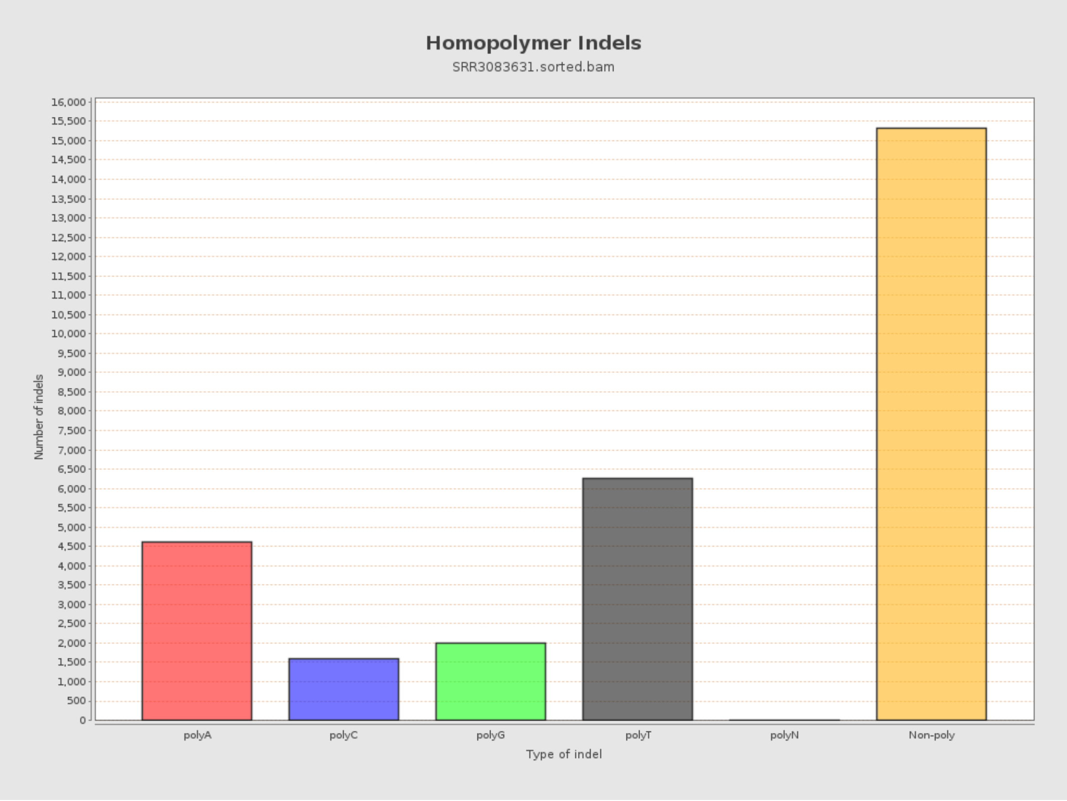
9. Results : Mapped Reads GC-content Distribution



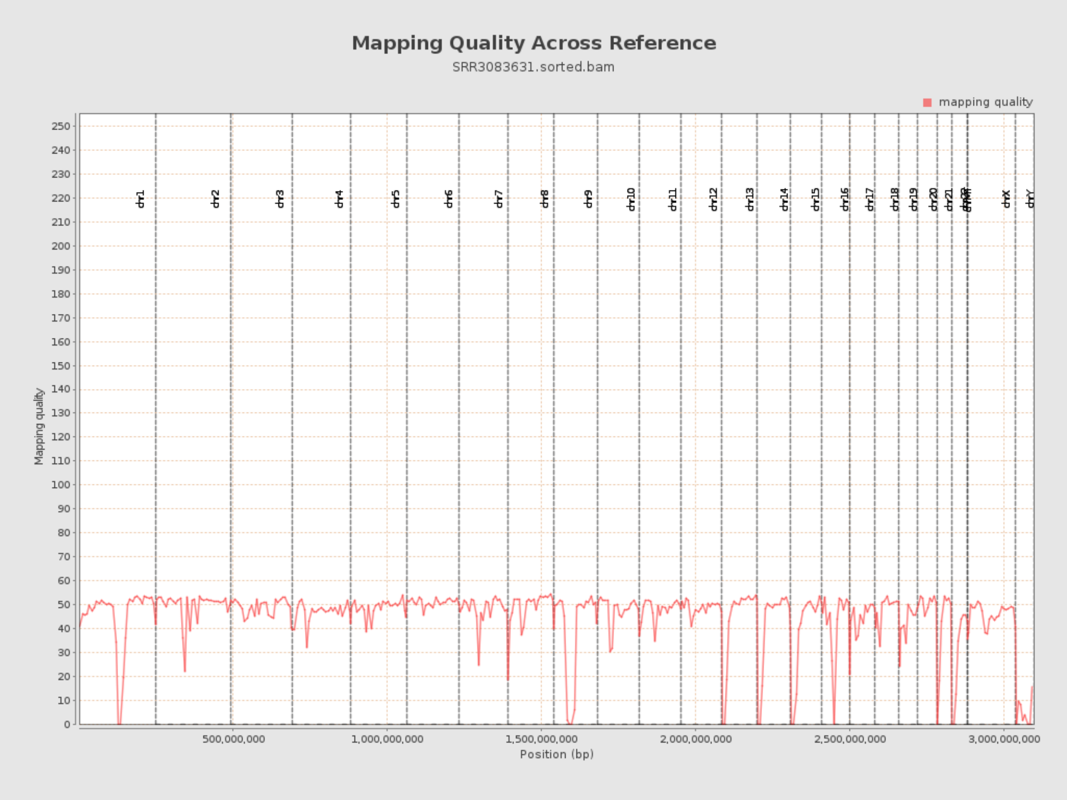
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram