Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 01:52:01

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3083643.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_SRR3083643 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3083643.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 01:52:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3083643.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,892,861
Mapped reads	1,705,359 / 90.09%
Unmapped reads	187,502 / 9.91%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,269 / 0.91%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	82,680 / 4.37%
Duplication rate	4.03%
Clipped reads	797,744 / 42.14%

2.2. ACGT Content

Number/percentage of A's	30,083,129 / 26.7%
Number/percentage of C's	21,124,225 / 18.75%
Number/percentage of T's	35,393,069 / 31.41%
Number/percentage of G's	26,081,822 / 23.15%
Number/percentage of N's	5,703 / 0.01%
GC Percentage	41.89%

2.3. Coverage

Mean	0.0364

Standard Deviation	0.3237

2.4. Mapping Quality

Mean Mapping Quality	45.35

2.5. Mismatches and indels

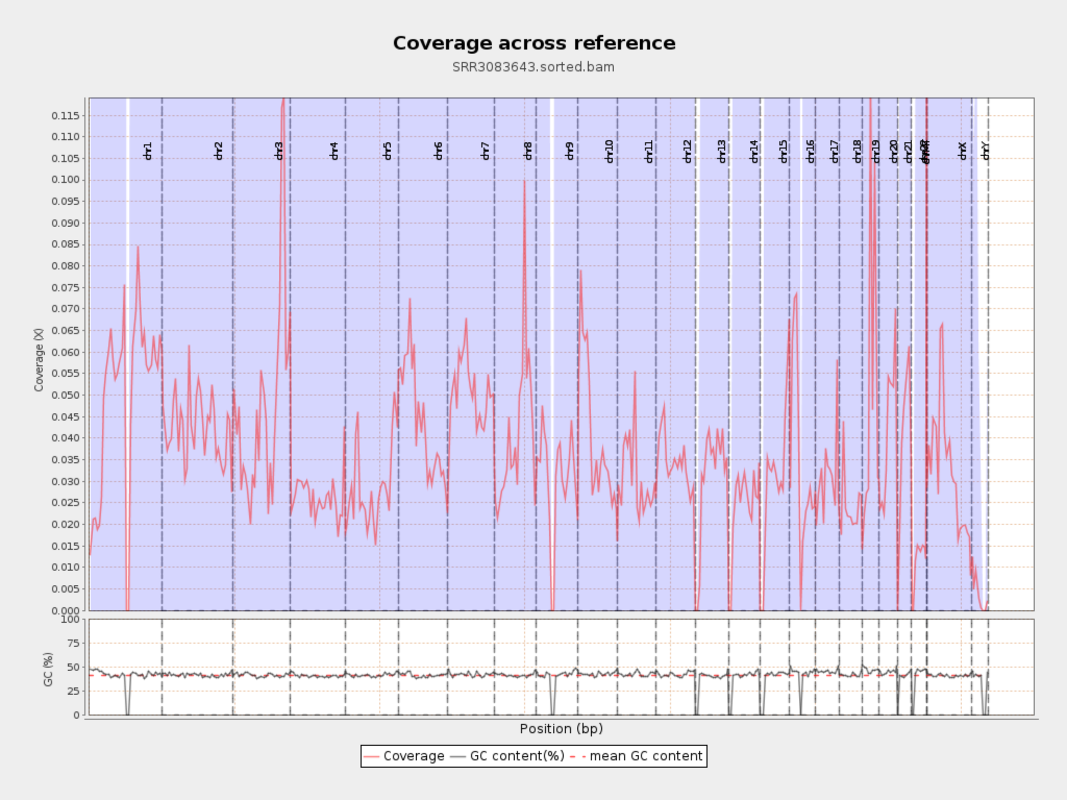
General error rate	0.71%
Mismatches	784,328
Insertions	8,464
Mapped reads with at least one insertion	0.49%
Deletions	26,223
Mapped reads with at least one deletion	1.52%
Homopolymer indels	47.75%

2.6. Chromosome stats

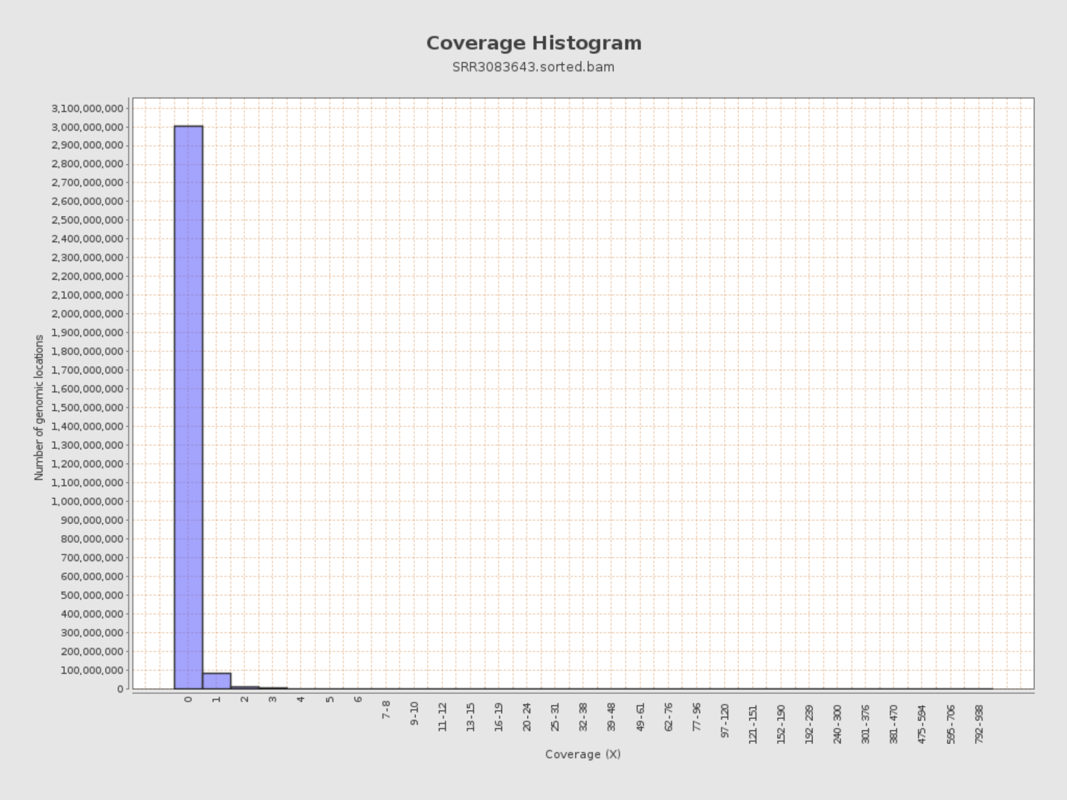
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12330483	0.0495	0.6223
chr2	243199373	10330291	0.0425	0.478
chr3	198022430	9287904	0.0469	0.2532
chr4	191154276	5014799	0.0262	0.1949
chr5	180915260	5222358	0.0289	0.1957
chr6	171115067	7511577	0.0439	0.296
chr7	159138663	8116413	0.051	0.4128

chr8	146364022	6012150	0.0411	0.2771
chr9	141213431	4359053	0.0309	0.241
chr10	135534747	5602039	0.0413	0.2803
chr11	135006516	4136999	0.0306	0.2403
chr12	133851895	4540740	0.0339	0.2134
chr13	115169878	3484240	0.0303	0.2018
chr14	107349540	2539102	0.0237	0.1794
chr15	102531392	3084481	0.0301	0.21
chr16	90354753	3177310	0.0352	0.2235
chr17	81195210	2567357	0.0316	0.2136
chr18	78077248	1888353	0.0242	0.3853
chr19	59128983	3098048	0.0524	0.4444
chr20	63025520	2647528	0.042	0.2411
chr21	48129895	1895051	0.0394	0.2328
chr22	51304566	569976	0.0111	0.1186
chrMT	16571	2705	0.1632	0.4919
chrX	155270560	5091132	0.0328	0.2201
chrY	59373566	220099	0.0037	0.0792

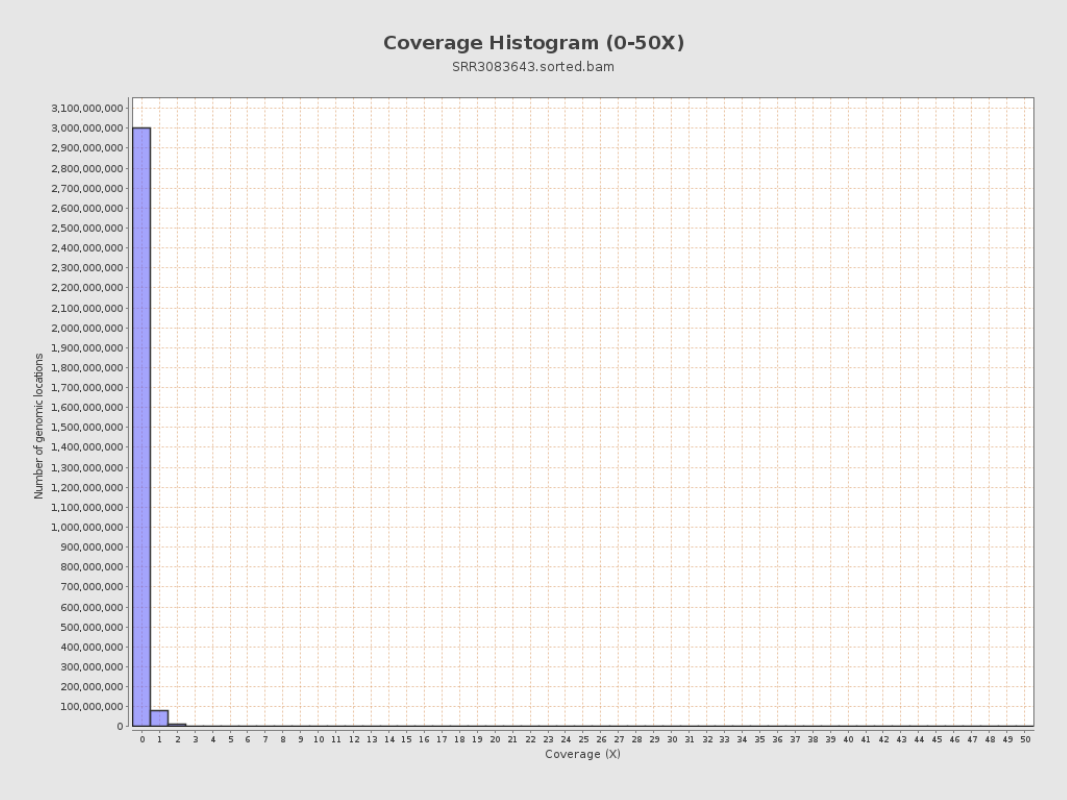
3. Results : Coverage across reference



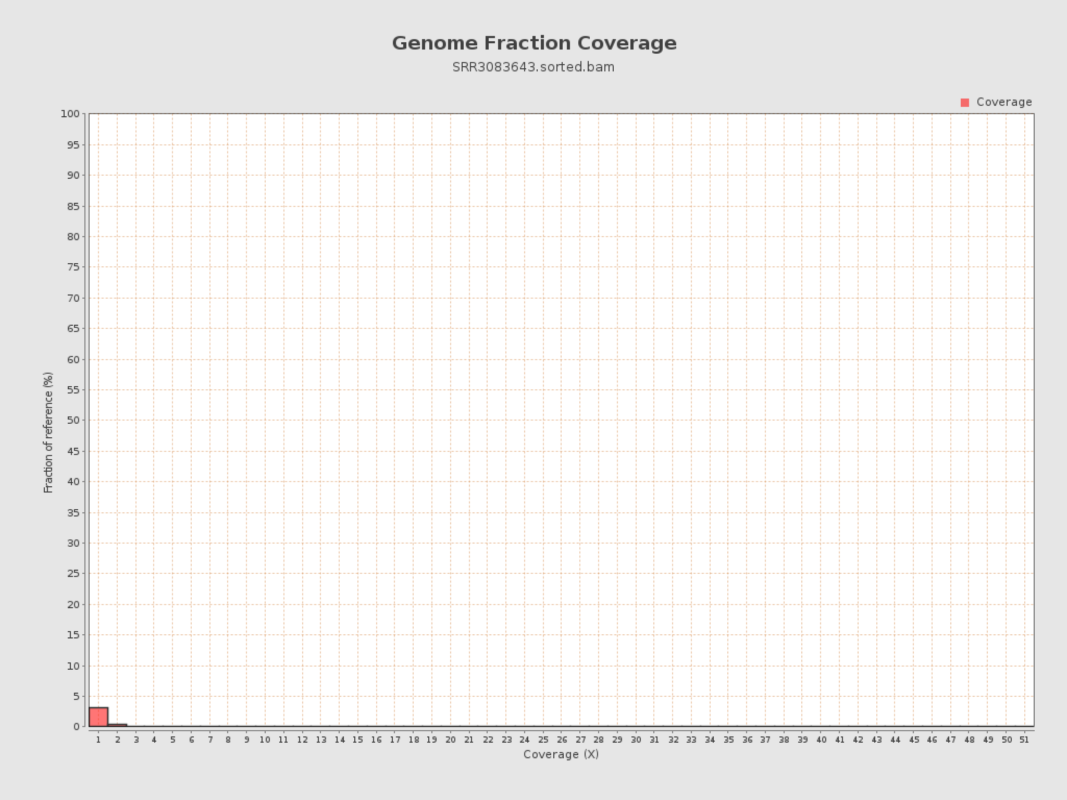
4. Results : Coverage Histogram



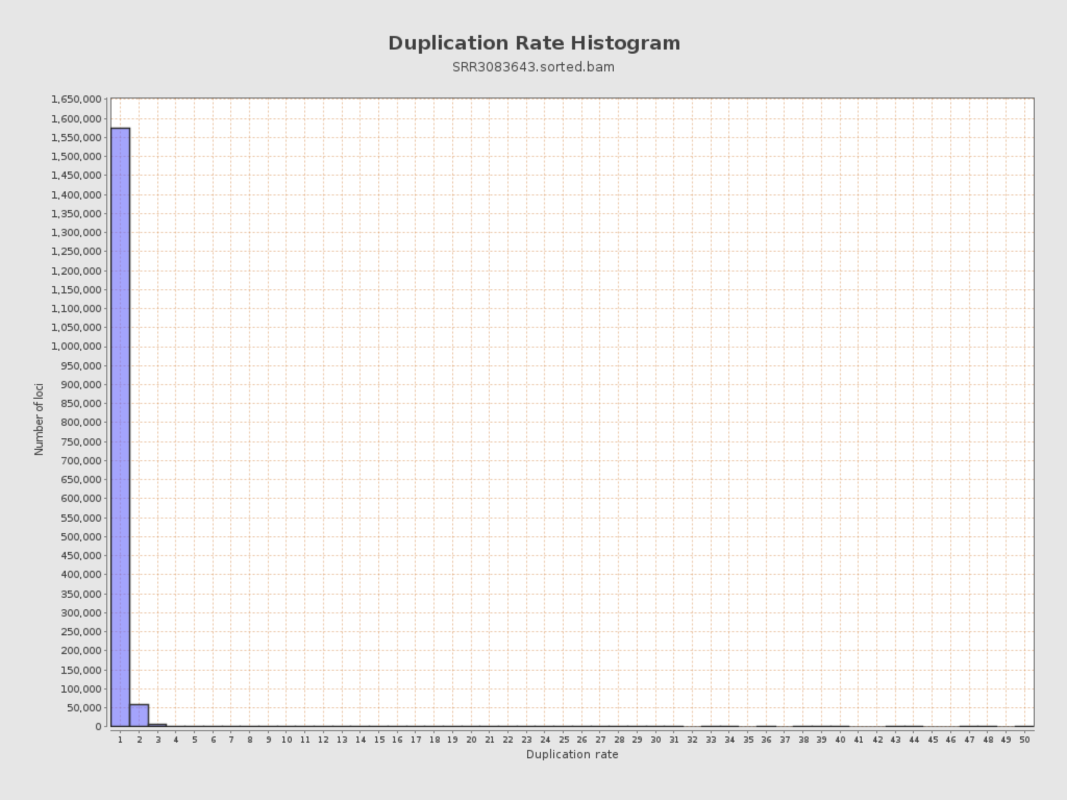
5. Results : Coverage Histogram (0-50X)



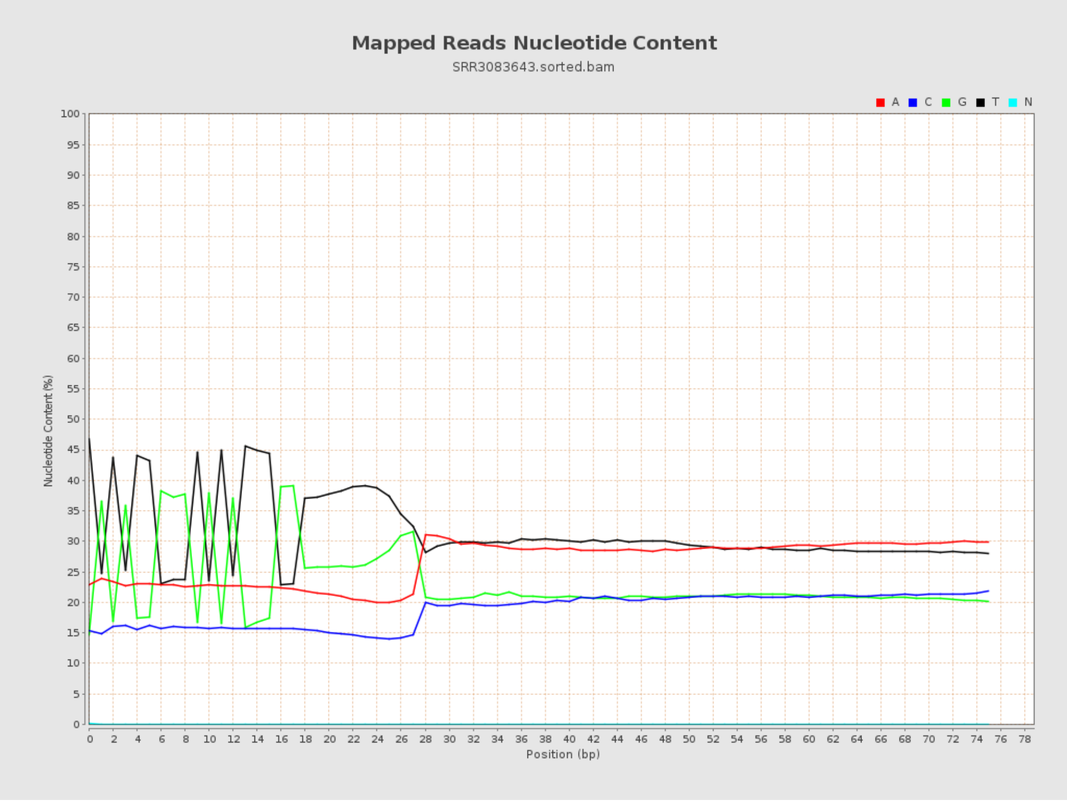
6. Results : Genome Fraction Coverage



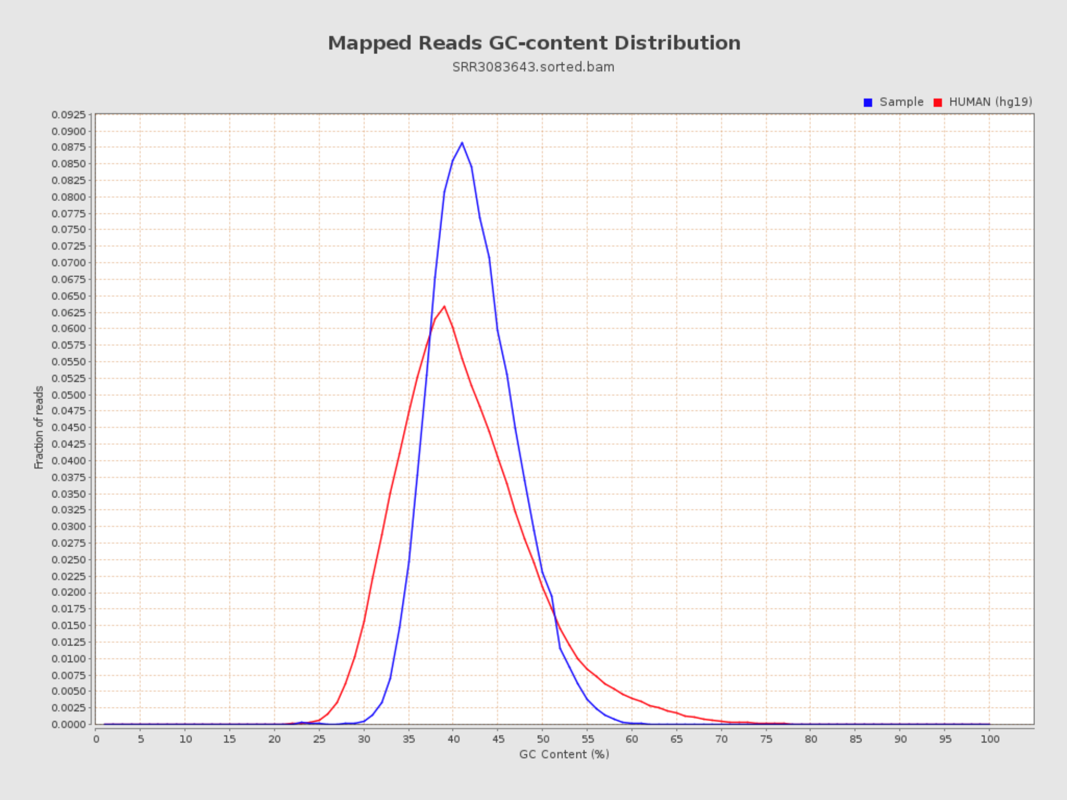
7. Results : Duplication Rate Histogram



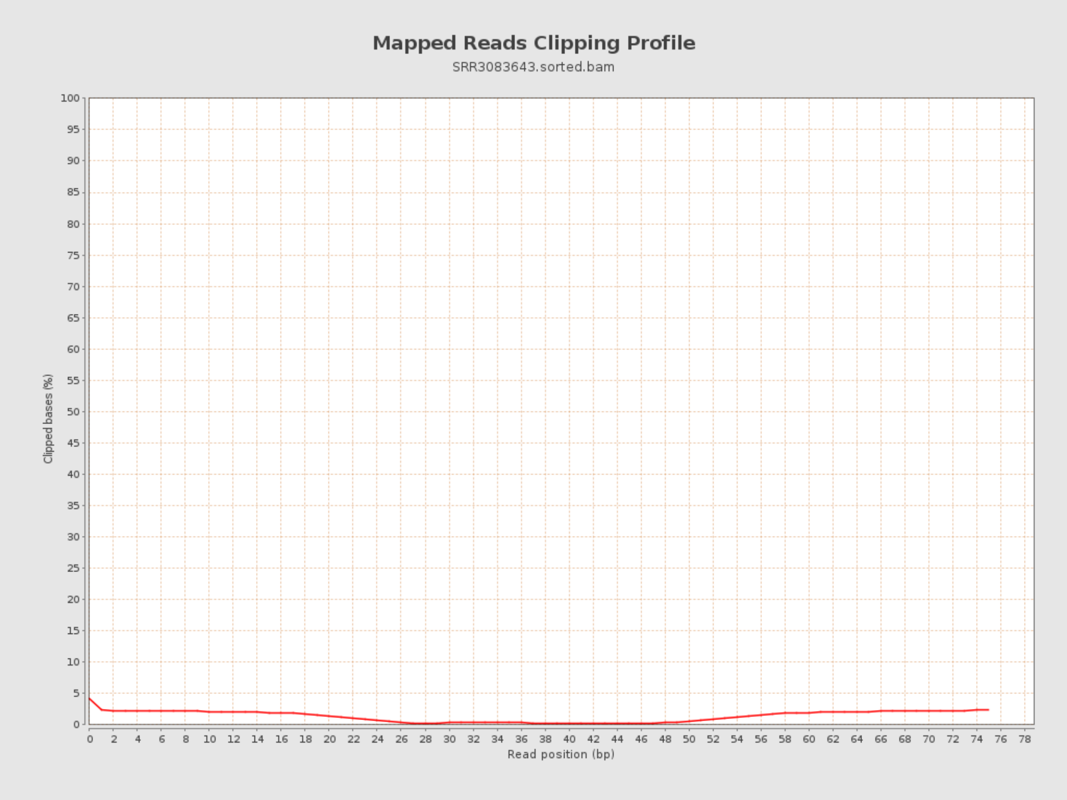
8. Results : Mapped Reads Nucleotide Content



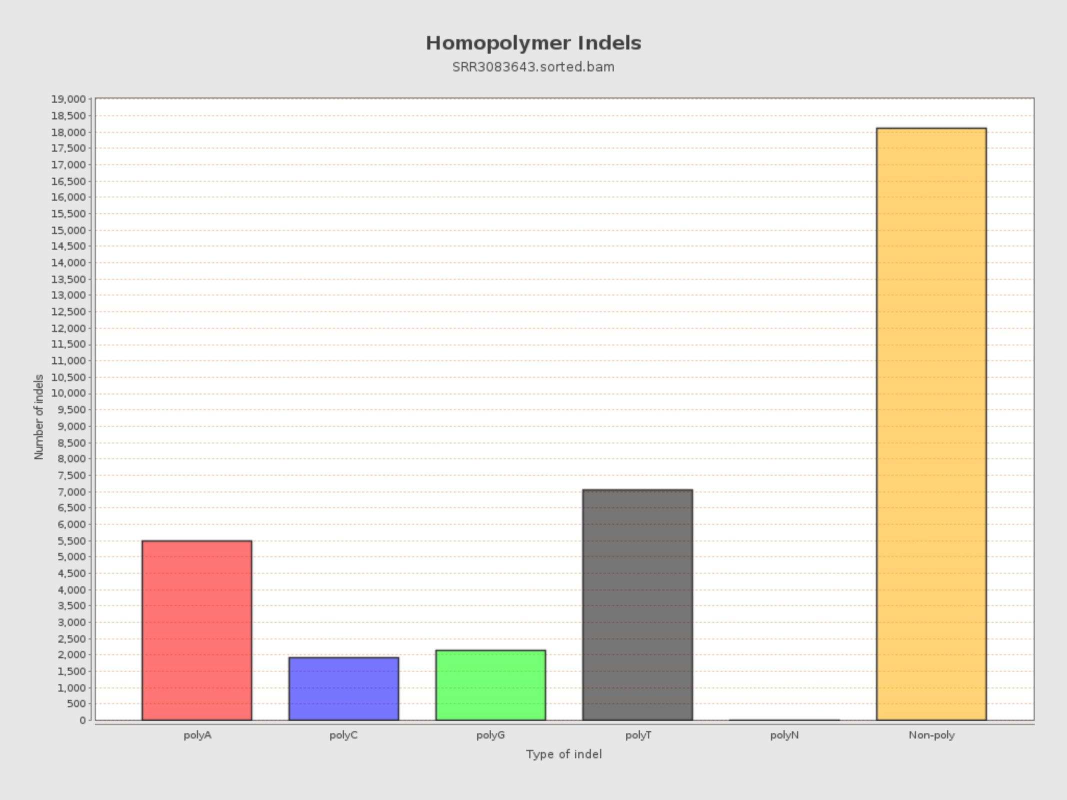
9. Results : Mapped Reads GC-content Distribution



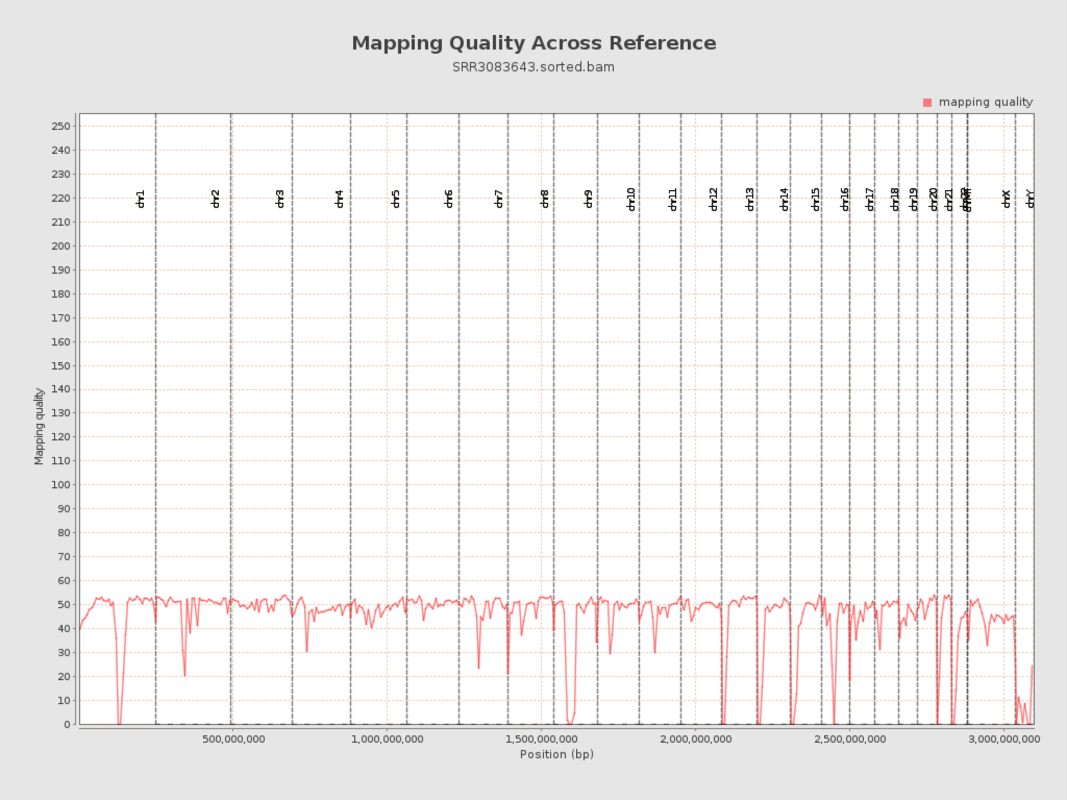
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram