Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/15 17:27:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6068959.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_SRR6068959 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6068959.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 15 17:27:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6068959.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,120,864
Mapped reads	1,589,896 / 74.96%
Unmapped reads	530,968 / 25.04%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,270 / 0.44%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	49,451 / 2.33%
Duplication rate	1.95%
Clipped reads	864,417 / 40.76%

2.2. ACGT Content

Number/percentage of A's	26,799,227 / 26.13%
Number/percentage of C's	17,929,809 / 17.48%
Number/percentage of T's	33,447,970 / 32.61%
Number/percentage of G's	24,143,308 / 23.54%
Number/percentage of N's	239,798 / 0.23%
GC Percentage	41.02%

2.3. Coverage

Mean	0.0331

Standard Deviation	0.3506

2.4. Mapping Quality

Mean Mapping Quality	42.85

2.5. Mismatches and indels

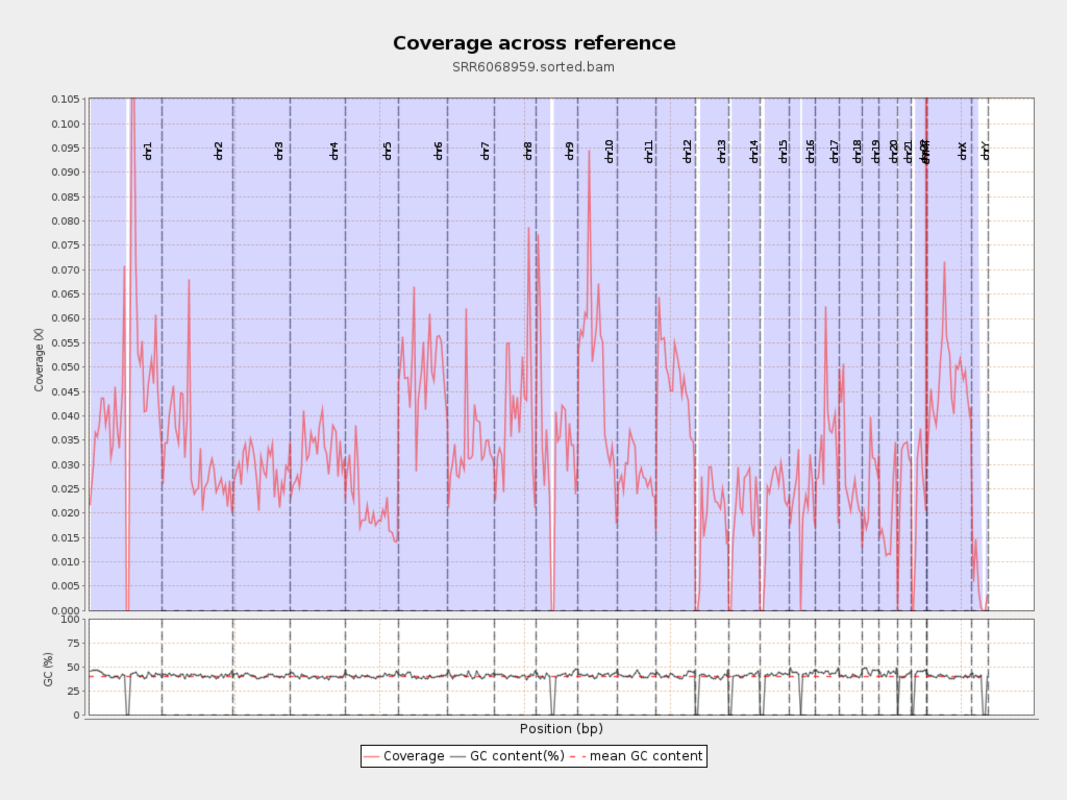
General error rate	1%
Mismatches	1,009,666
Insertions	10,144
Mapped reads with at least one insertion	0.63%
Deletions	30,533
Mapped reads with at least one deletion	1.9%
Homopolymer indels	48.18%

2.6. Chromosome stats

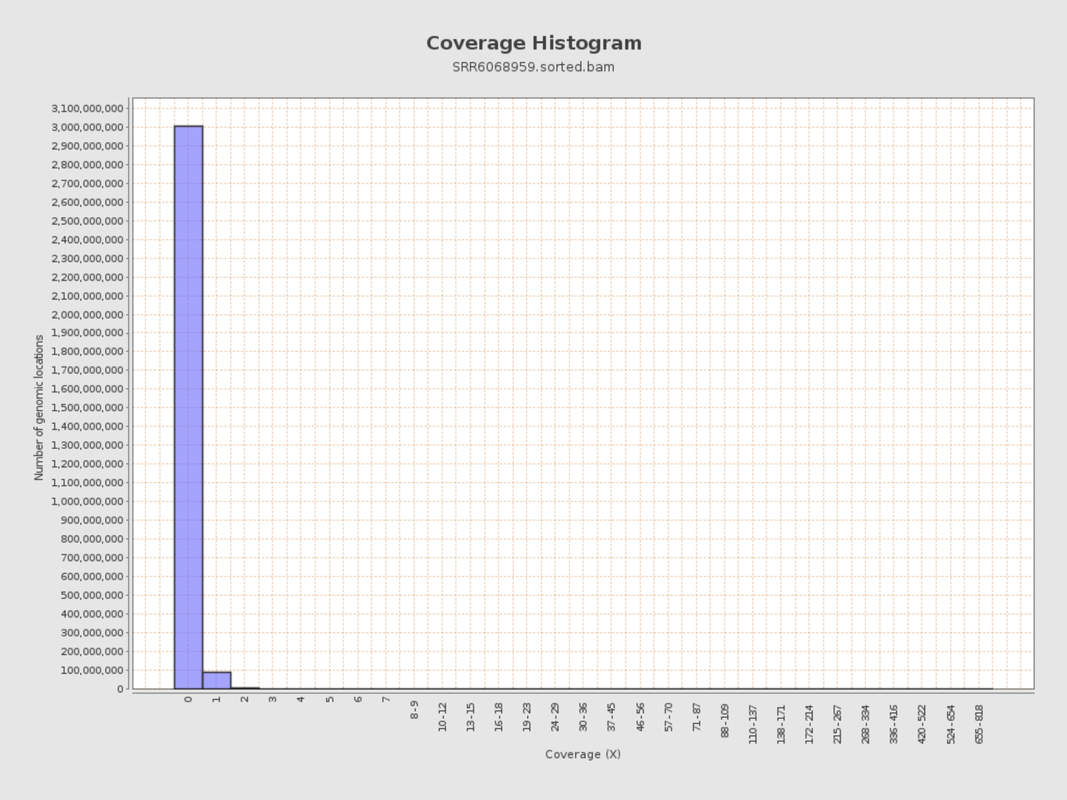
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	11138055	0.0447	0.6519
chr2	243199373	7754724	0.0319	0.338
chr3	198022430	5729146	0.0289	0.1967
chr4	191154276	6160922	0.0322	0.2126
chr5	180915260	3805661	0.021	0.161
chr6	171115067	8497094	0.0497	0.3156
chr7	159138663	5355410	0.0337	0.4798

chr8	146364022	5973217	0.0408	0.4649
chr9	141213431	4819474	0.0341	0.3562
chr10	135534747	6916056	0.051	0.4847
chr11	135006516	3774870	0.028	0.3093
chr12	133851895	6334360	0.0473	0.2381
chr13	115169878	2174005	0.0189	0.1468
chr14	107349540	2128406	0.0198	0.1843
chr15	102531392	2169909	0.0212	0.157
chr16	90354753	2008613	0.0222	0.192
chr17	81195210	2870224	0.0353	0.2247
chr18	78077248	2267208	0.029	0.5752
chr19	59128983	1541452	0.0261	0.4171
chr20	63025520	1147483	0.0182	0.1605
chr21	48129895	1332947	0.0277	0.1961
chr22	51304566	1055575	0.0206	0.1537
chrMT	16571	47422	2.8617	2.3576
chrX	155270560	7316162	0.0471	0.2794
chrY	59373566	292539	0.0049	0.1129

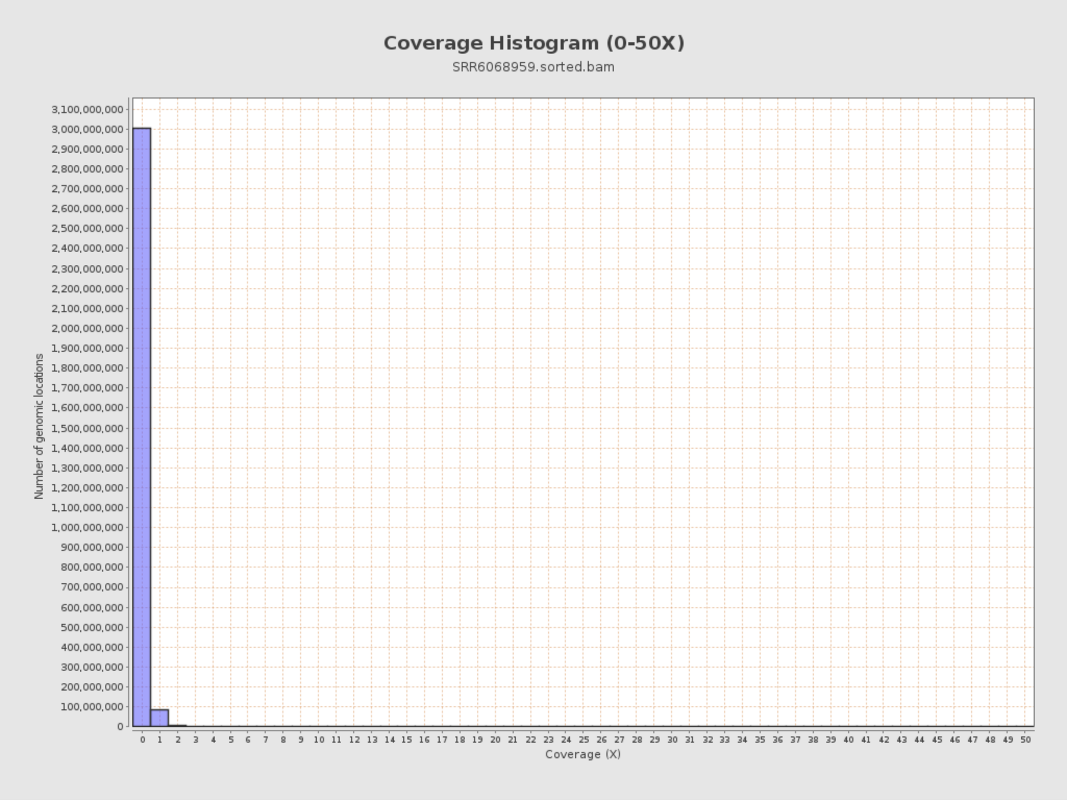
3. Results : Coverage across reference



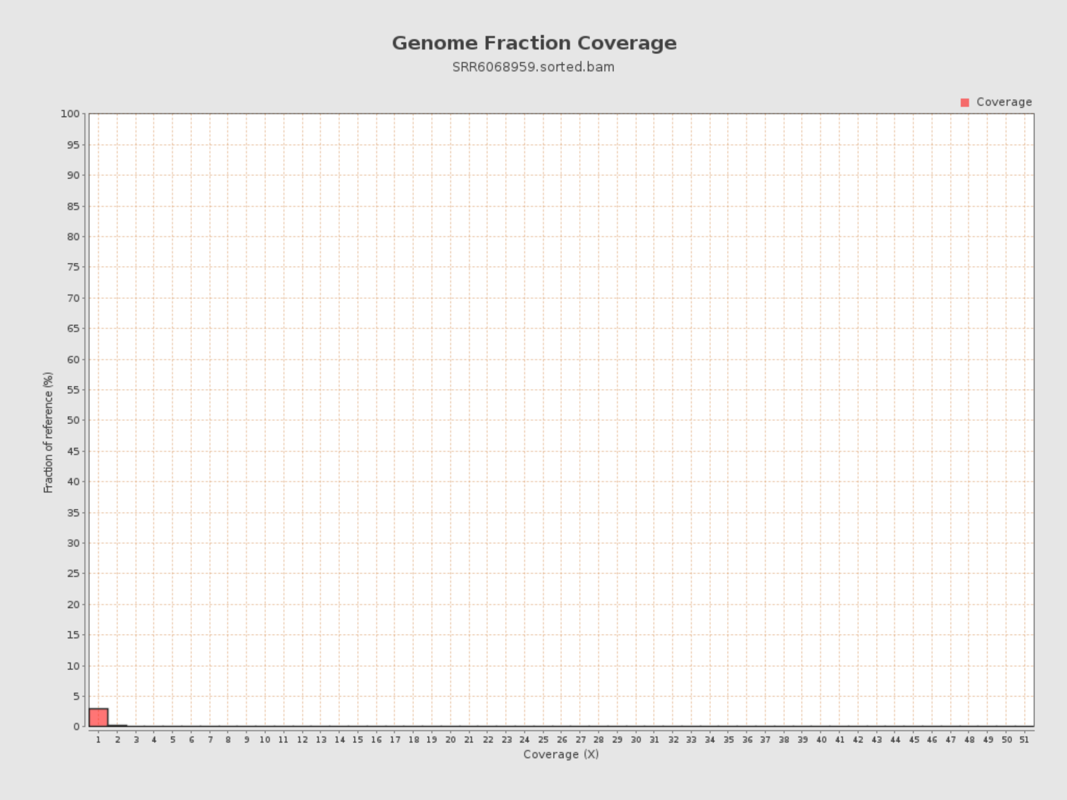
4. Results : Coverage Histogram



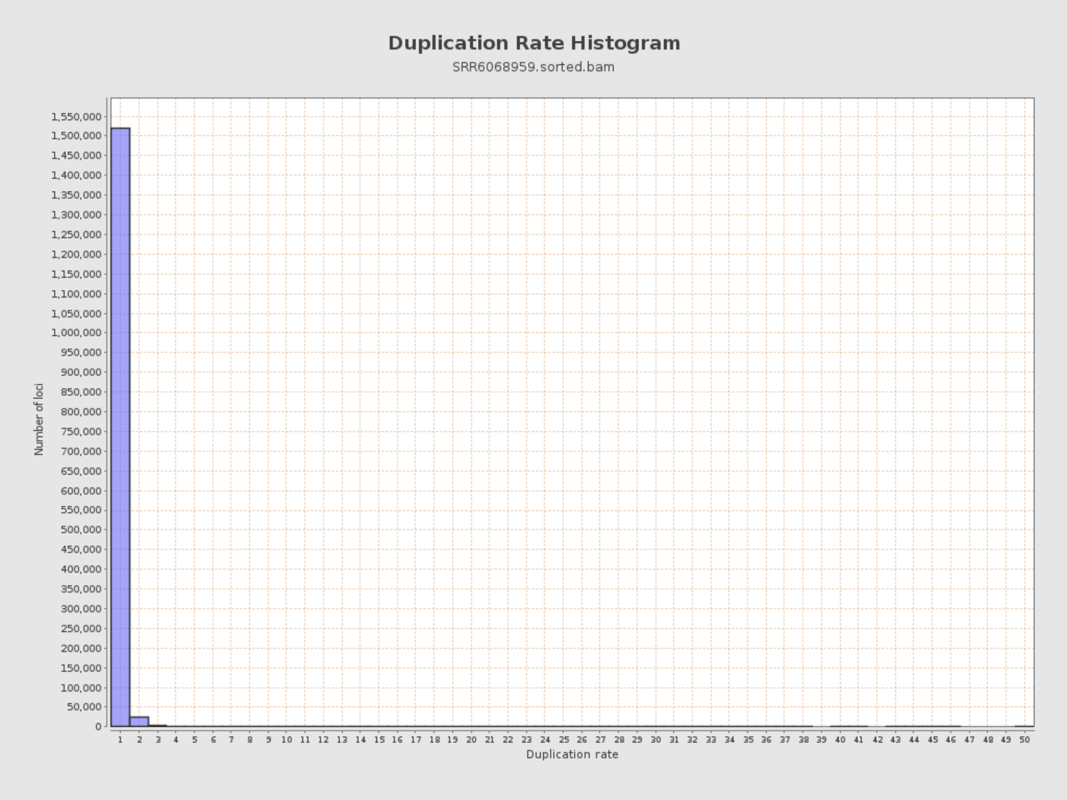
5. Results : Coverage Histogram (0-50X)



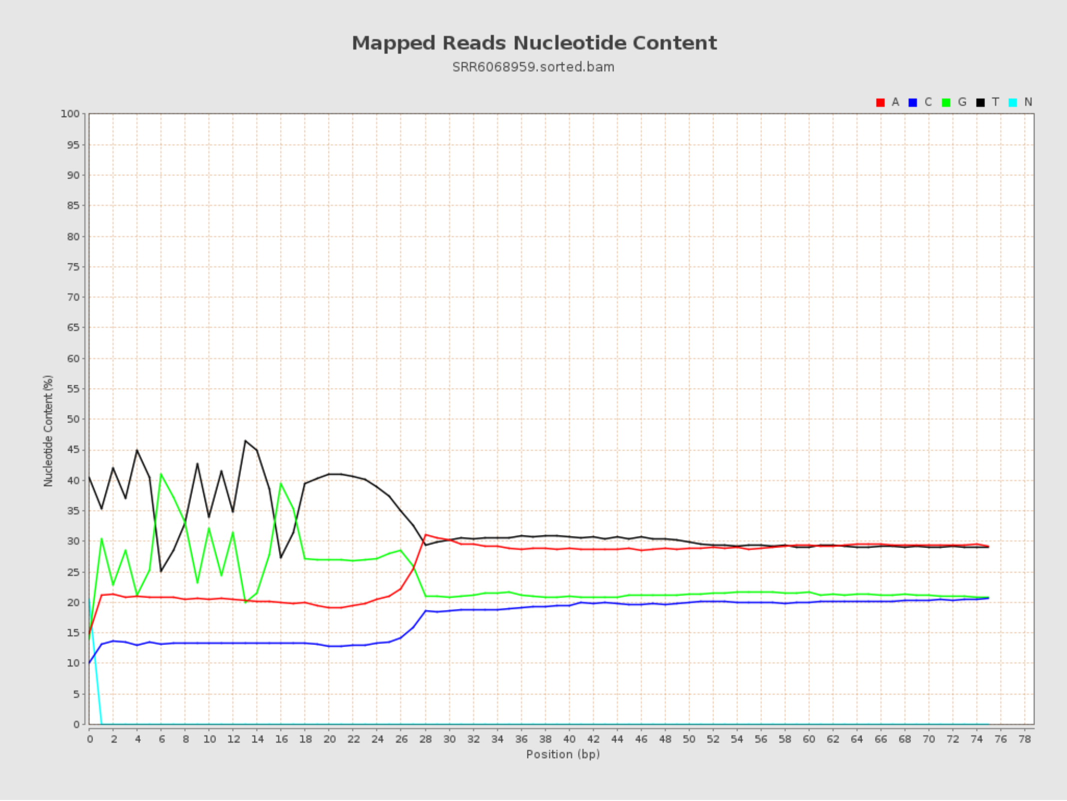
6. Results : Genome Fraction Coverage



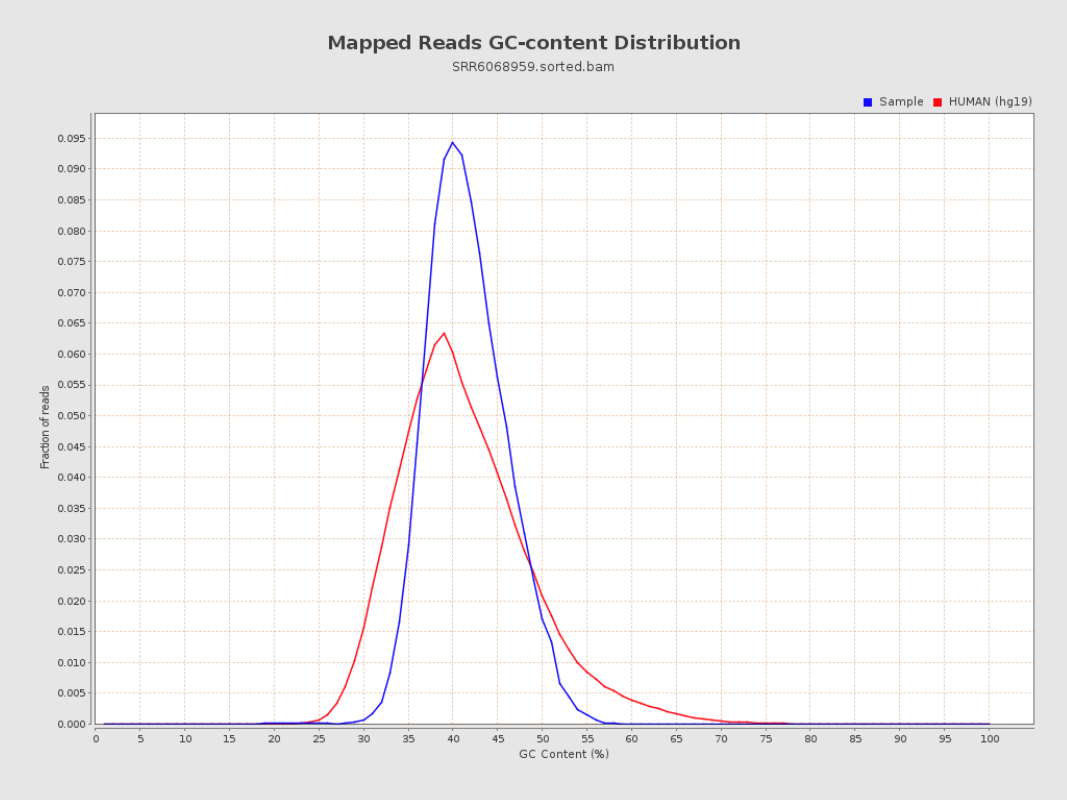
7. Results : Duplication Rate Histogram



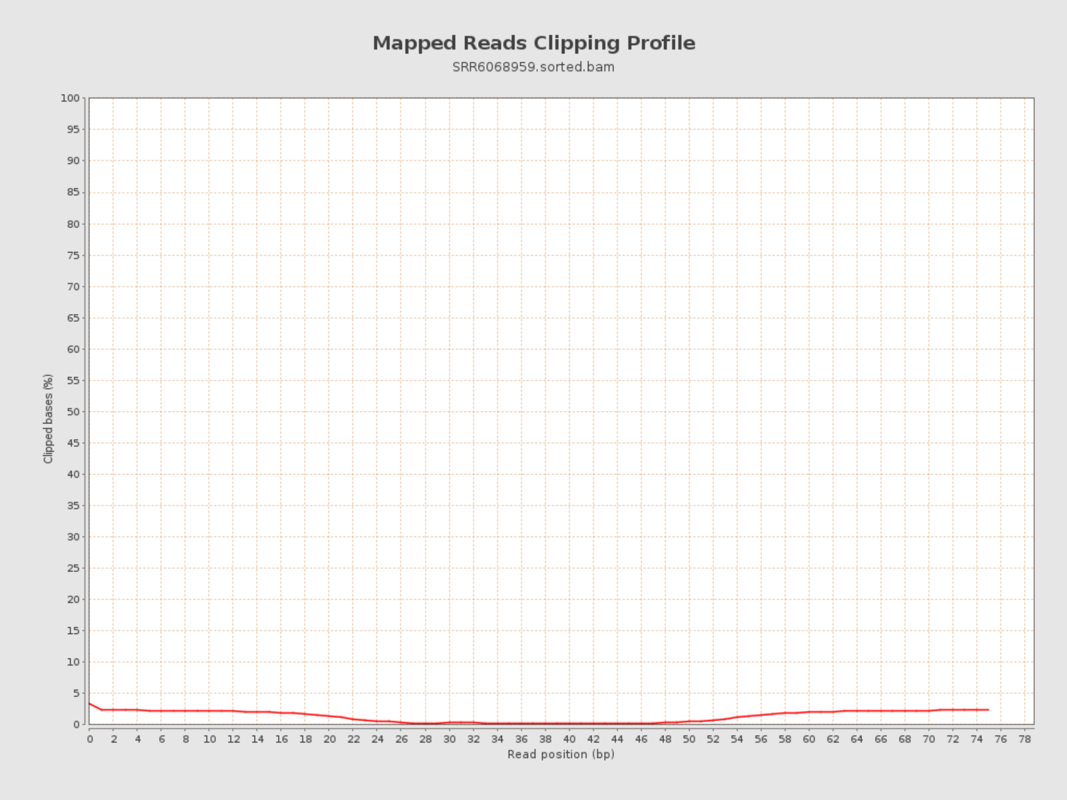
8. Results : Mapped Reads Nucleotide Content



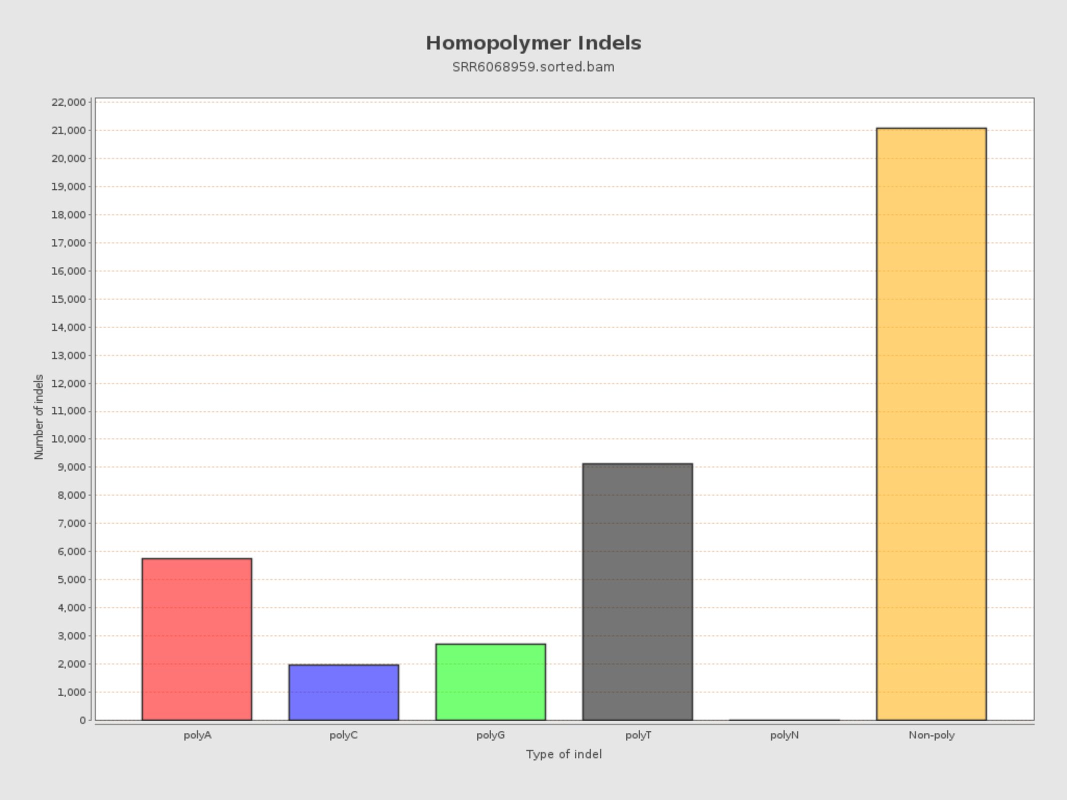
9. Results : Mapped Reads GC-content Distribution



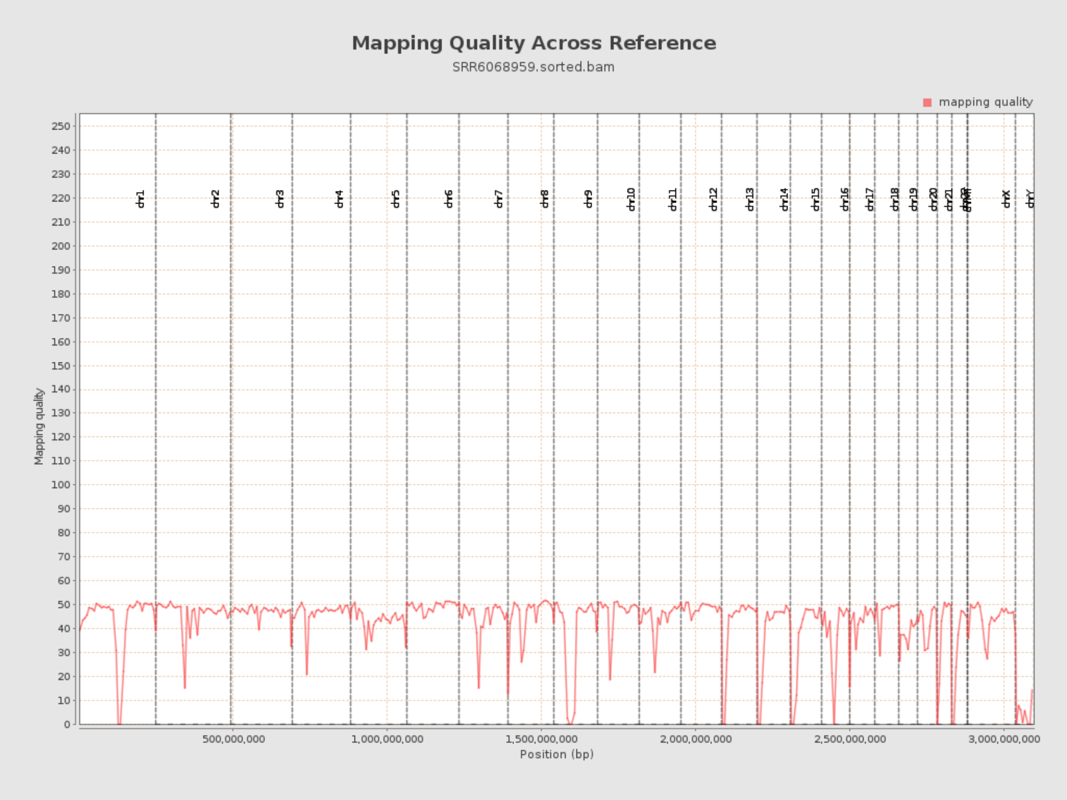
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram