Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:13:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082954.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_SRR3082954 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082954.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:13:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082954.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,424,376
Mapped reads	1,262,700 / 88.65%
Unmapped reads	161,676 / 11.35%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	11,952 / 0.84%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	37,677 / 2.65%
Duplication rate	2.12%
Clipped reads	648,369 / 45.52%

2.2. ACGT Content

Number/percentage of A's	22,761,443 / 27.76%
Number/percentage of C's	15,785,545 / 19.25%
Number/percentage of T's	24,311,381 / 29.65%
Number/percentage of G's	19,120,687 / 23.32%
Number/percentage of N's	3,455 / 0%
GC Percentage	42.58%

2.3. Coverage

Mean	0.0265

Standard Deviation	0.2807

2.4. Mapping Quality

Mean Mapping Quality	43.94

2.5. Mismatches and indels

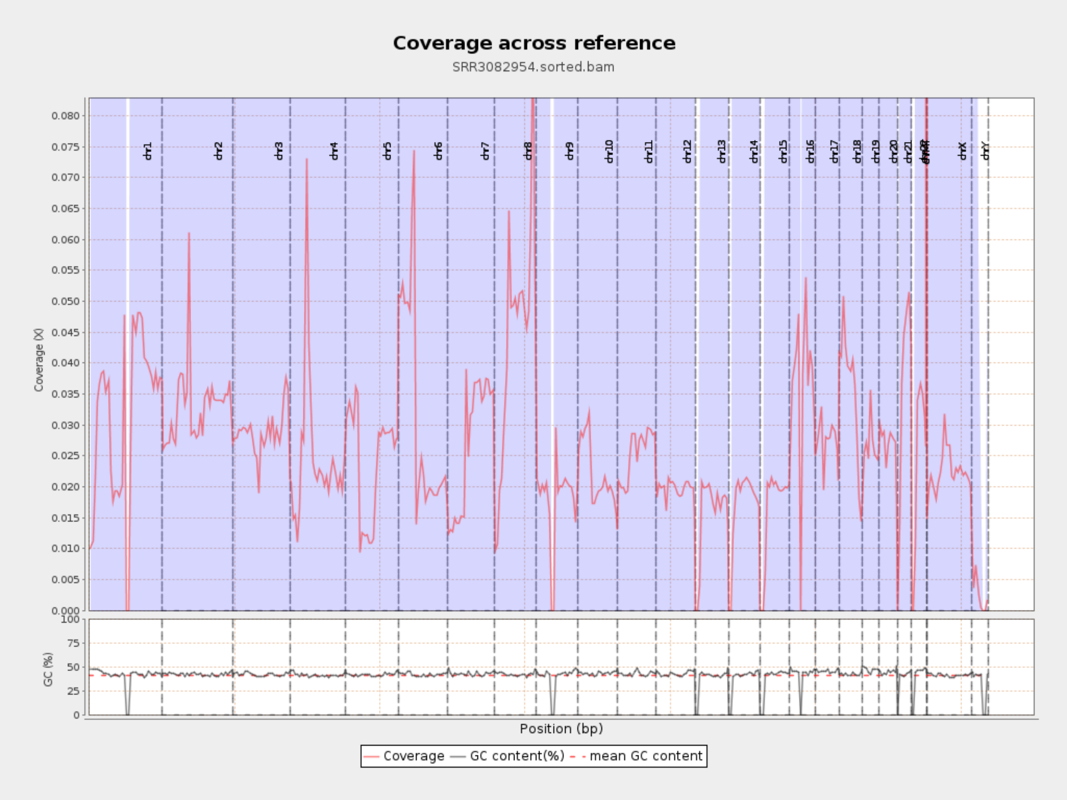
General error rate	0.81%
Mismatches	654,868
Insertions	6,660
Mapped reads with at least one insertion	0.52%
Deletions	17,124
Mapped reads with at least one deletion	1.34%
Homopolymer indels	45.37%

2.6. Chromosome stats

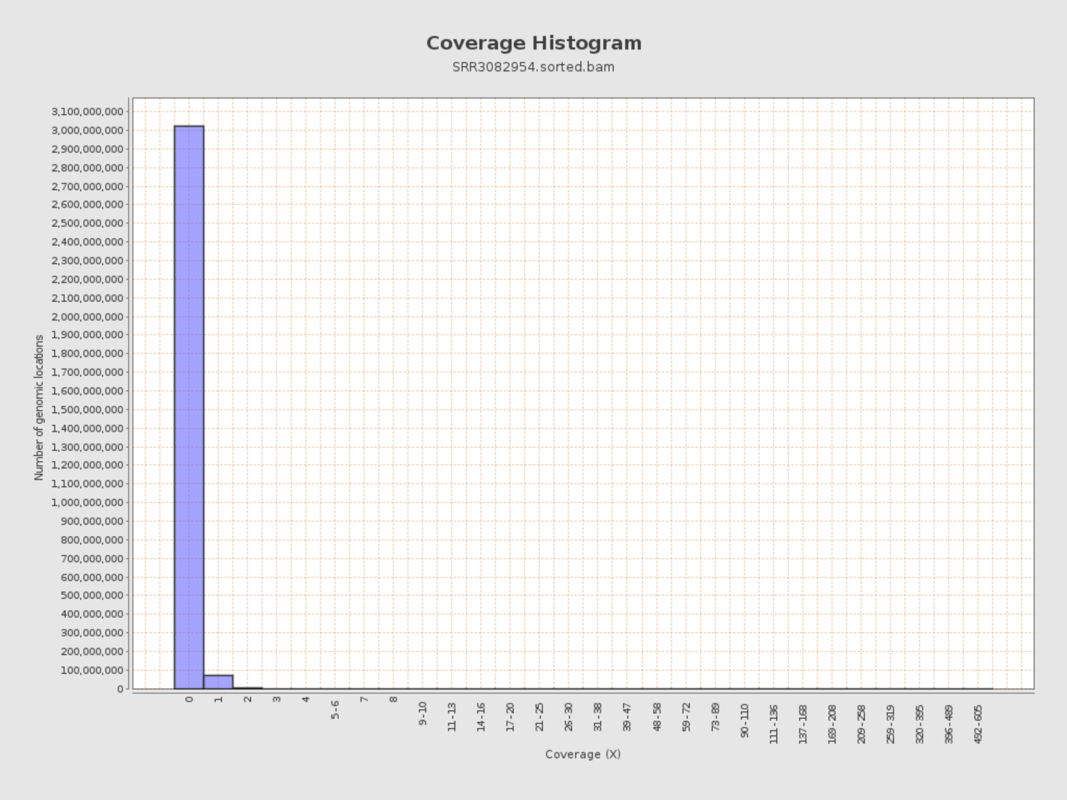
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	7789436	0.0313	0.5417
chr2	243199373	8051116	0.0331	0.3518
chr3	198022430	5718462	0.0289	0.1788
chr4	191154276	4670496	0.0244	0.1749
chr5	180915260	4368915	0.0241	0.1663
chr6	171115067	5492532	0.0321	0.2532
chr7	159138663	4325038	0.0272	0.3129

chr8	146364022	6528311	0.0446	0.2949
chr9	141213431	2507145	0.0178	0.2395
chr10	135534747	3034662	0.0224	0.1891
chr11	135006516	3387968	0.0251	0.281
chr12	133851895	2634468	0.0197	0.1542
chr13	115169878	1789235	0.0155	0.1303
chr14	107349540	1804606	0.0168	0.1569
chr15	102531392	1668007	0.0163	0.1421
chr16	90354753	3300663	0.0365	0.2186
chr17	81195210	2211766	0.0272	0.205
chr18	78077248	2822030	0.0361	0.5469
chr19	59128983	1575043	0.0266	0.3656
chr20	63025520	1704130	0.027	0.1868
chr21	48129895	1728715	0.0359	0.2053
chr22	51304566	1194571	0.0233	0.1605
chrMT	16571	72513	4.3759	3.2824
chrX	155270560	3471406	0.0224	0.1836
chrY	59373566	160068	0.0027	0.0651

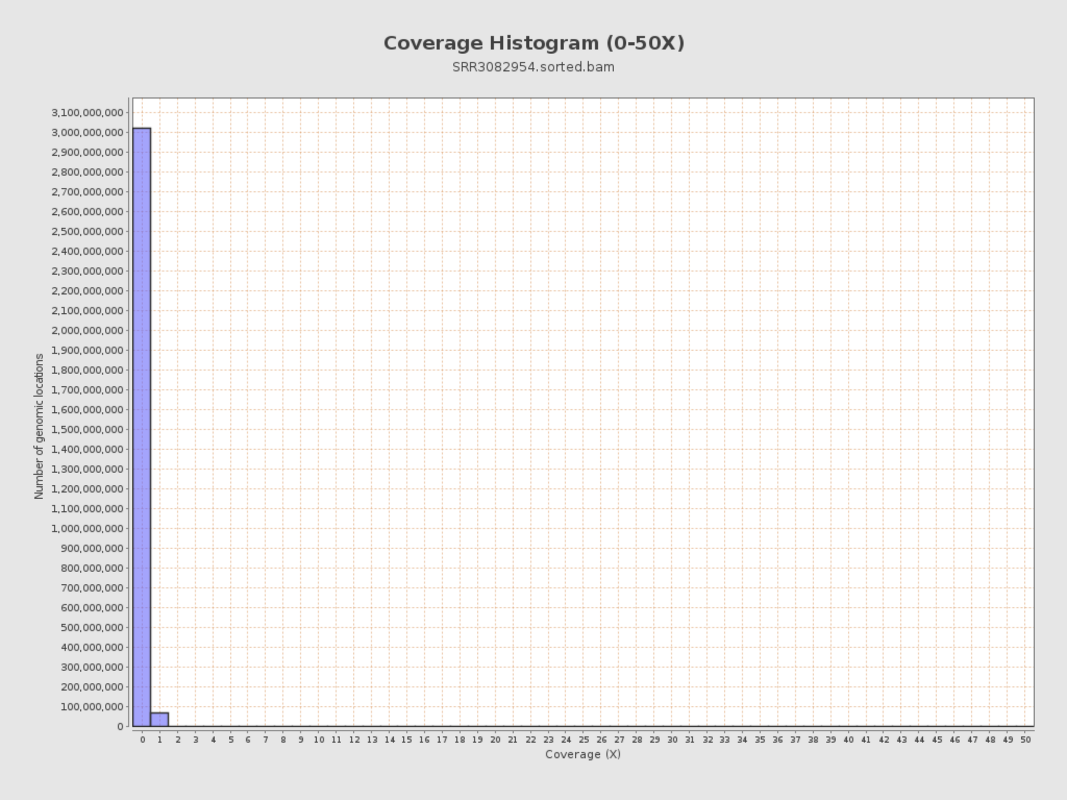
3. Results : Coverage across reference



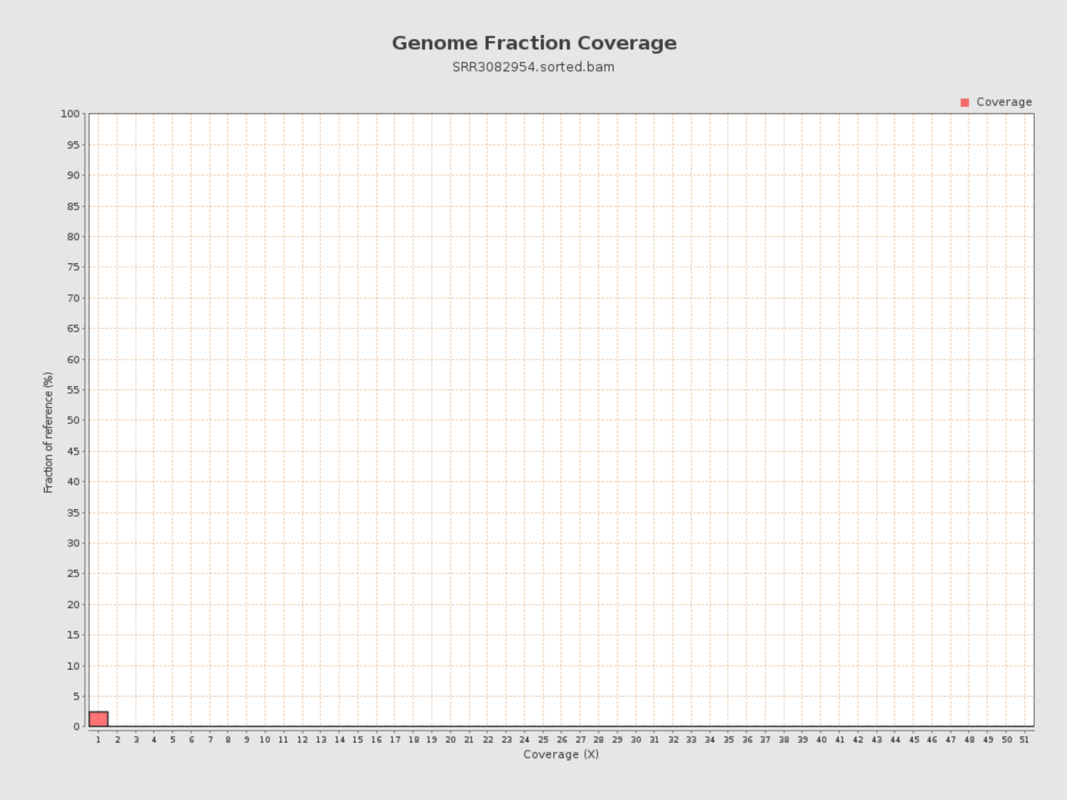
4. Results : Coverage Histogram



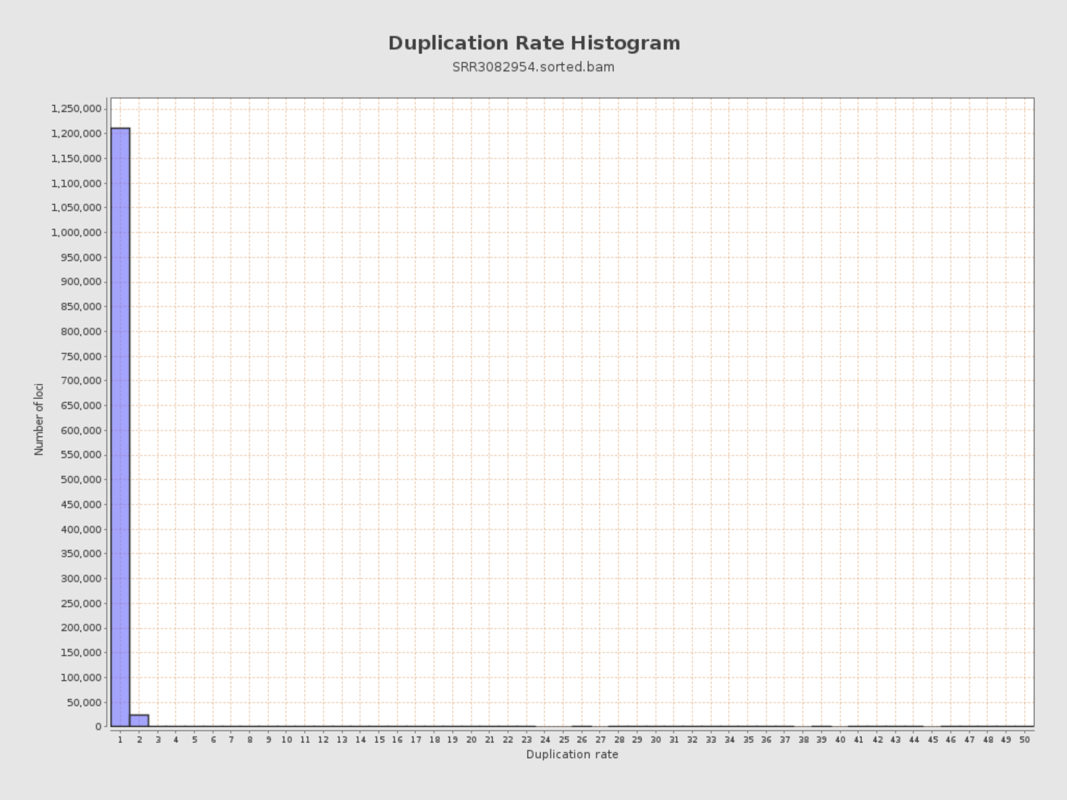
5. Results : Coverage Histogram (0-50X)



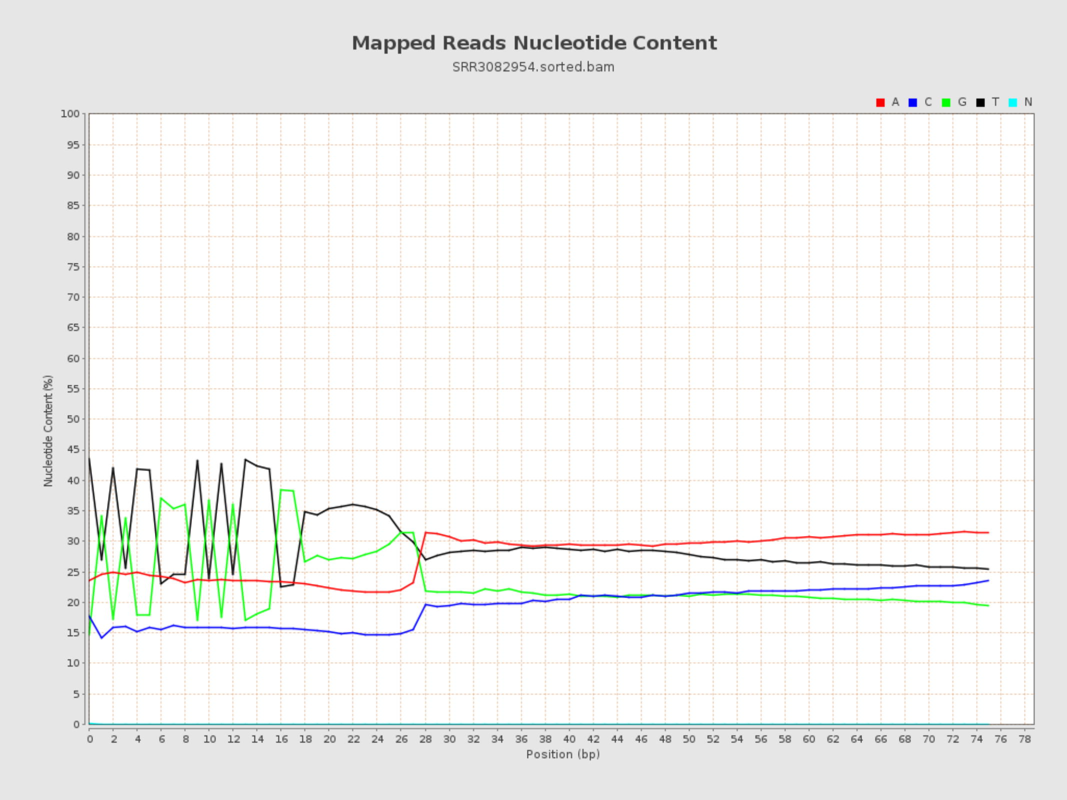
6. Results : Genome Fraction Coverage



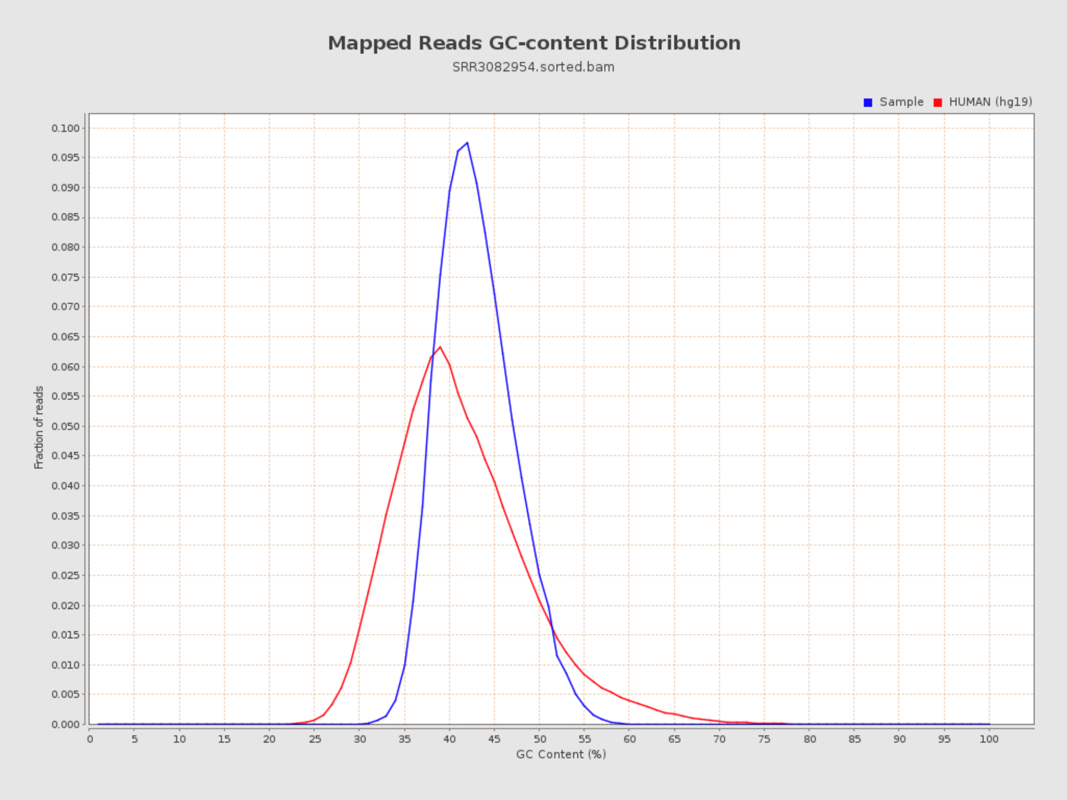
7. Results : Duplication Rate Histogram



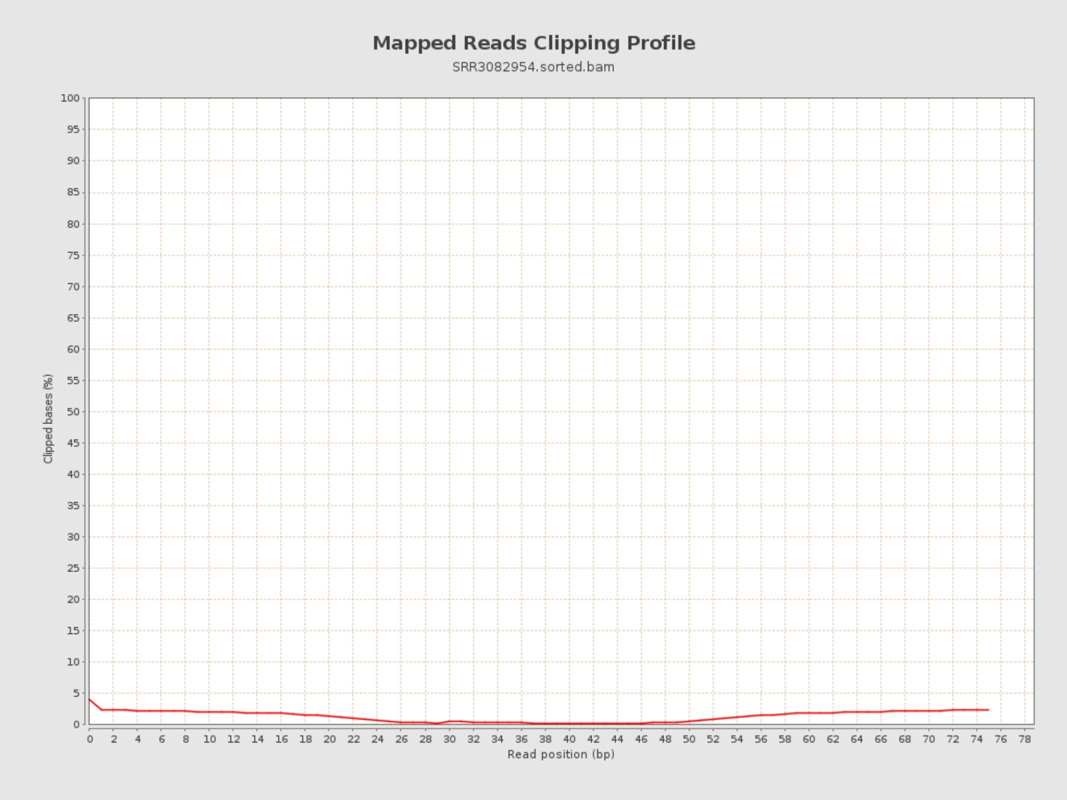
8. Results : Mapped Reads Nucleotide Content



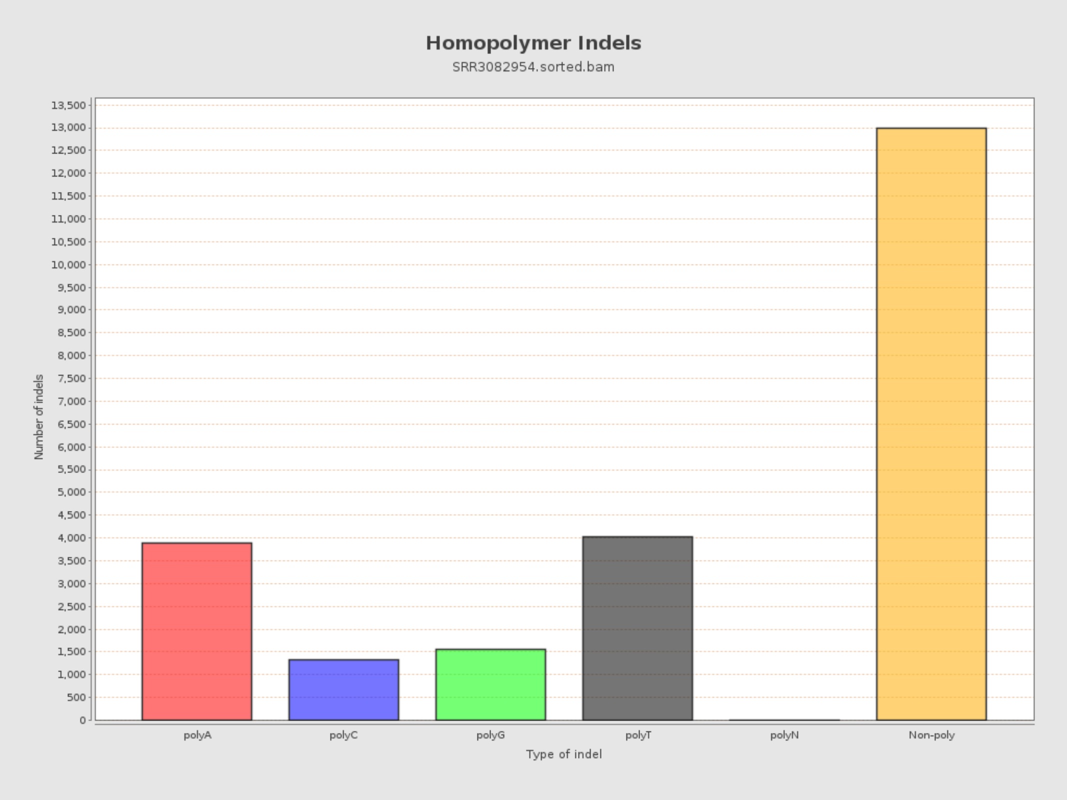
9. Results : Mapped Reads GC-content Distribution



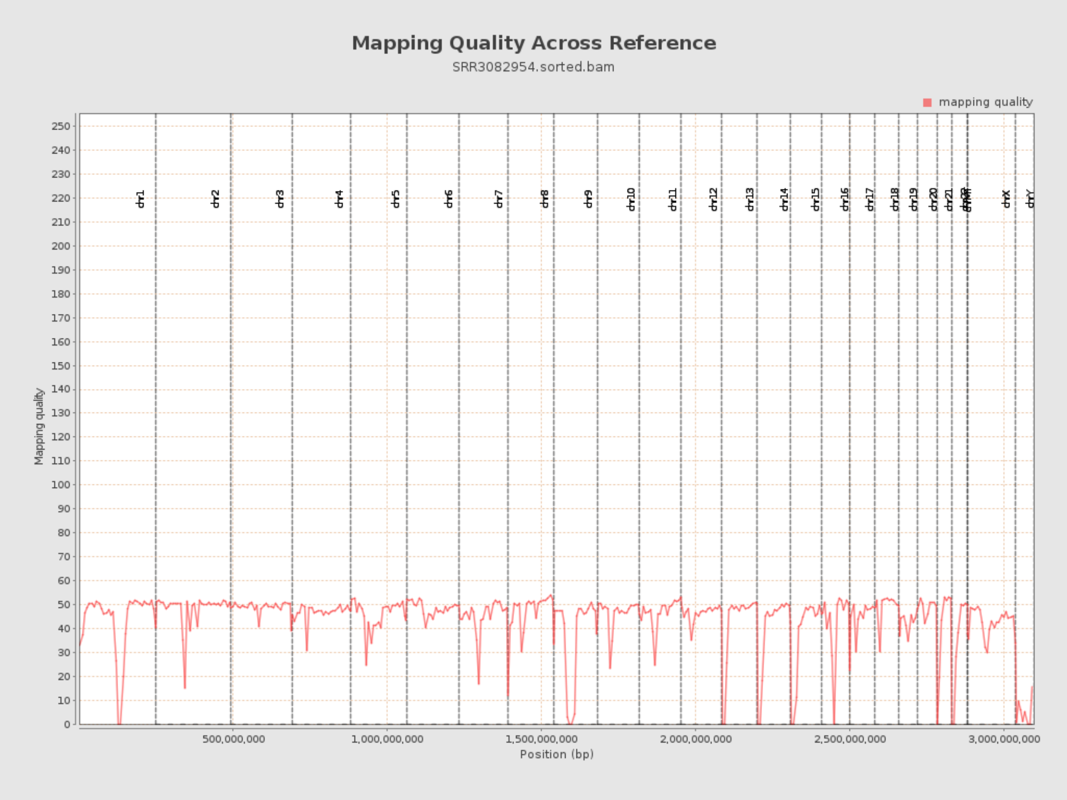
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram