Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:05:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082952.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_SRR3082952 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082952.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:05:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082952.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,641,430
Mapped reads	1,502,077 / 91.51%
Unmapped reads	139,353 / 8.49%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	16,409 / 1%
Read min/max/mean length	30 / 76 / 76.35
Duplicated reads (estimated)	63,841 / 3.89%
Duplication rate	3.57%
Clipped reads	626,583 / 38.17%

2.2. ACGT Content

Number/percentage of A's	28,301,751 / 27.98%
Number/percentage of C's	18,390,074 / 18.18%
Number/percentage of T's	32,549,805 / 32.18%
Number/percentage of G's	21,912,224 / 21.66%
Number/percentage of N's	5,350 / 0.01%
GC Percentage	39.84%

2.3. Coverage

Mean	0.0327

Standard Deviation	0.2724

2.4. Mapping Quality

Mean Mapping Quality	46.08

2.5. Mismatches and indels

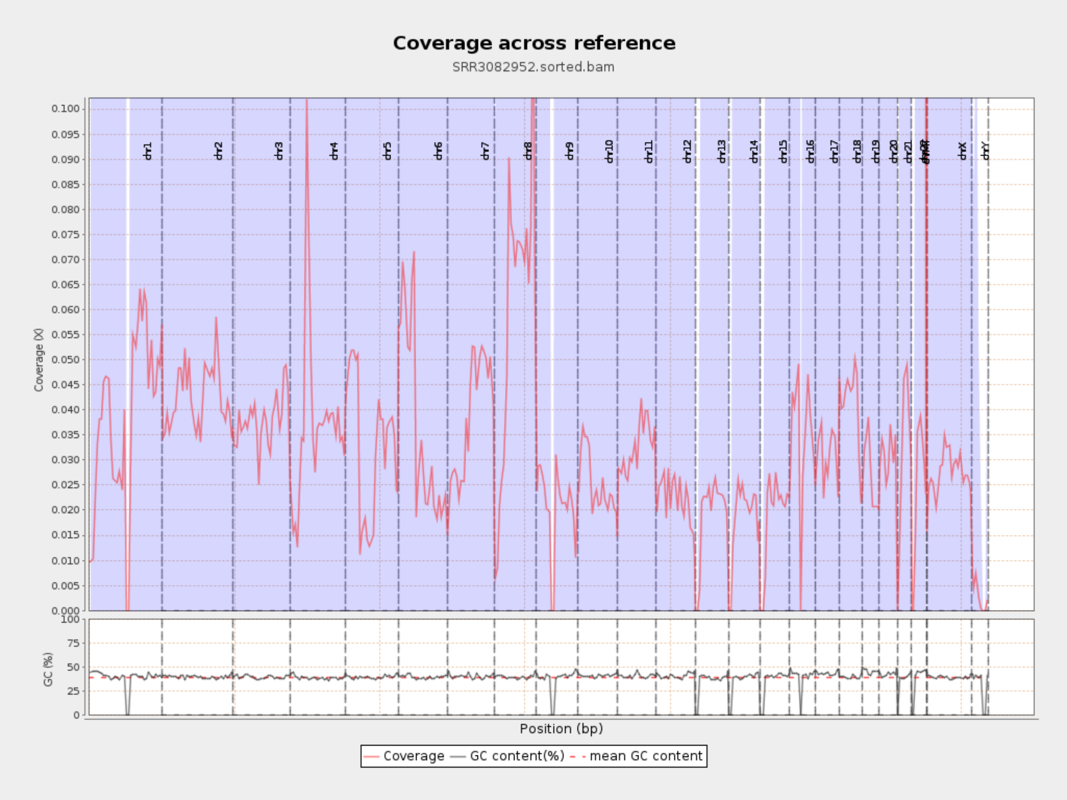
General error rate	0.72%
Mismatches	709,182
Insertions	8,633
Mapped reads with at least one insertion	0.57%
Deletions	23,957
Mapped reads with at least one deletion	1.58%
Homopolymer indels	49.14%

2.6. Chromosome stats

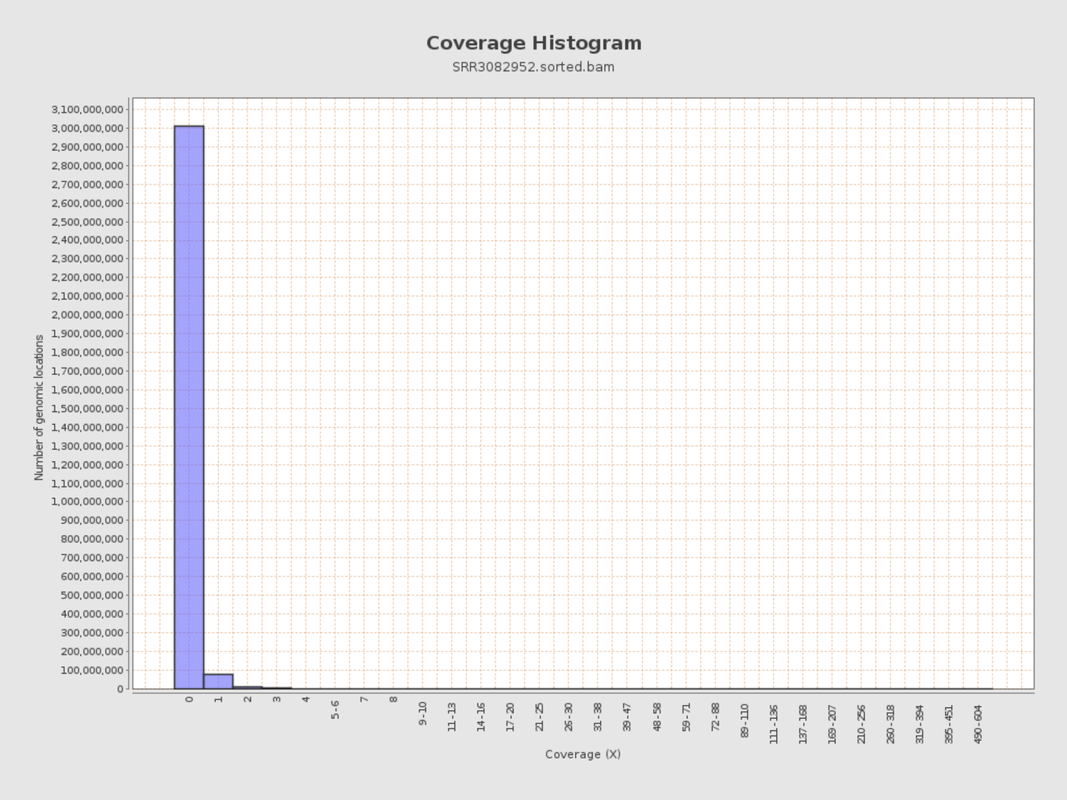
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	9537820	0.0383	0.4103
chr2	243199373	10345256	0.0425	0.3686
chr3	198022430	7507055	0.0379	0.2198
chr4	191154276	7116770	0.0372	0.2247
chr5	180915260	5883654	0.0325	0.2098
chr6	171115067	6247330	0.0365	0.2476
chr7	159138663	6191843	0.0389	0.2813

chr8	146364022	8812615	0.0602	0.4054
chr9	141213431	2908205	0.0206	0.2454
chr10	135534747	3465000	0.0256	0.2077
chr11	135006516	4373140	0.0324	0.2386
chr12	133851895	2985761	0.0223	0.2298
chr13	115169878	2176286	0.0189	0.1557
chr14	107349540	1979752	0.0184	0.1645
chr15	102531392	1905908	0.0186	0.1595
chr16	90354753	3189215	0.0353	0.2221
chr17	81195210	2469865	0.0304	0.2135
chr18	78077248	3267346	0.0418	0.4514
chr19	59128983	1631387	0.0276	0.2828
chr20	63025520	1913713	0.0304	0.2022
chr21	48129895	1529406	0.0318	0.204
chr22	51304566	1209078	0.0236	0.1705
chrMT	16571	125219	7.5565	5.1751
chrX	155270560	4256741	0.0274	0.1974
chrY	59373566	169545	0.0029	0.0664

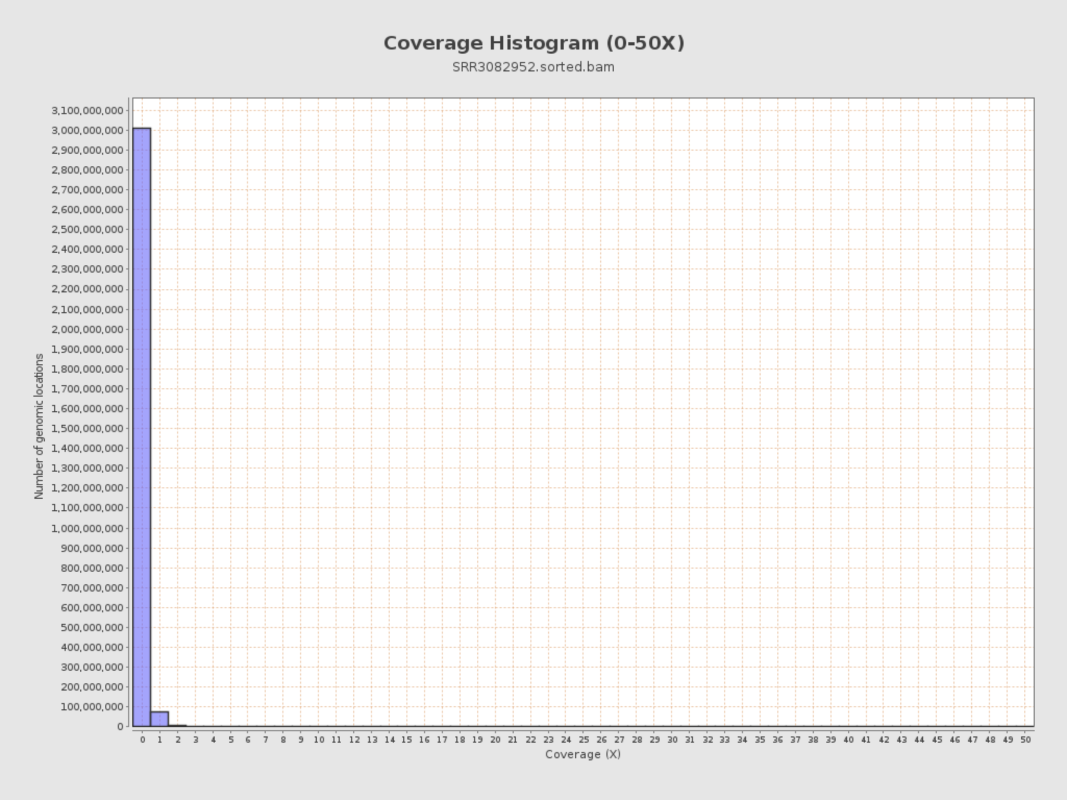
3. Results : Coverage across reference



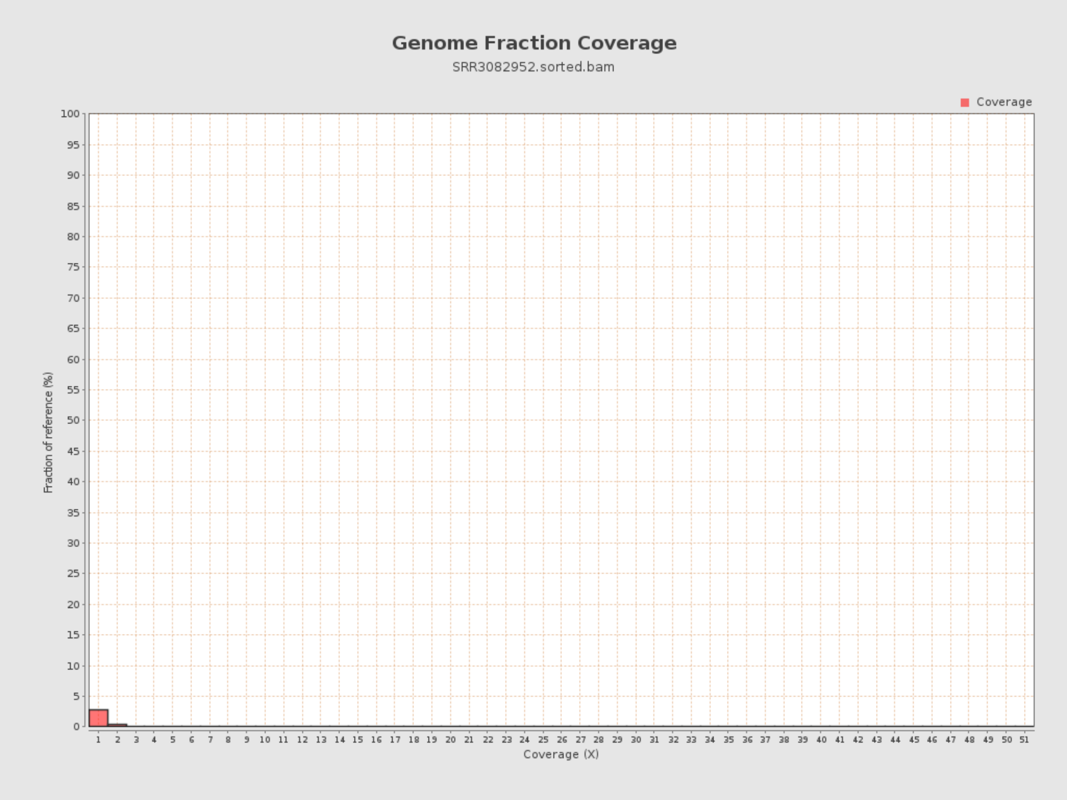
4. Results : Coverage Histogram



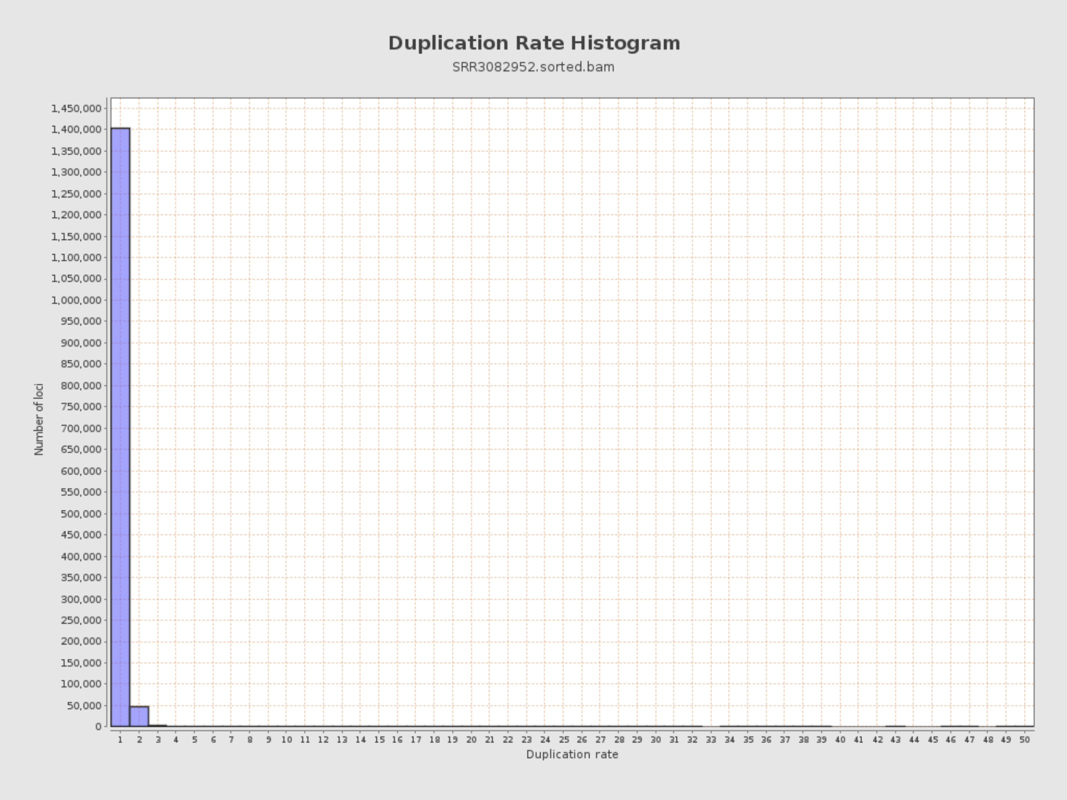
5. Results : Coverage Histogram (0-50X)



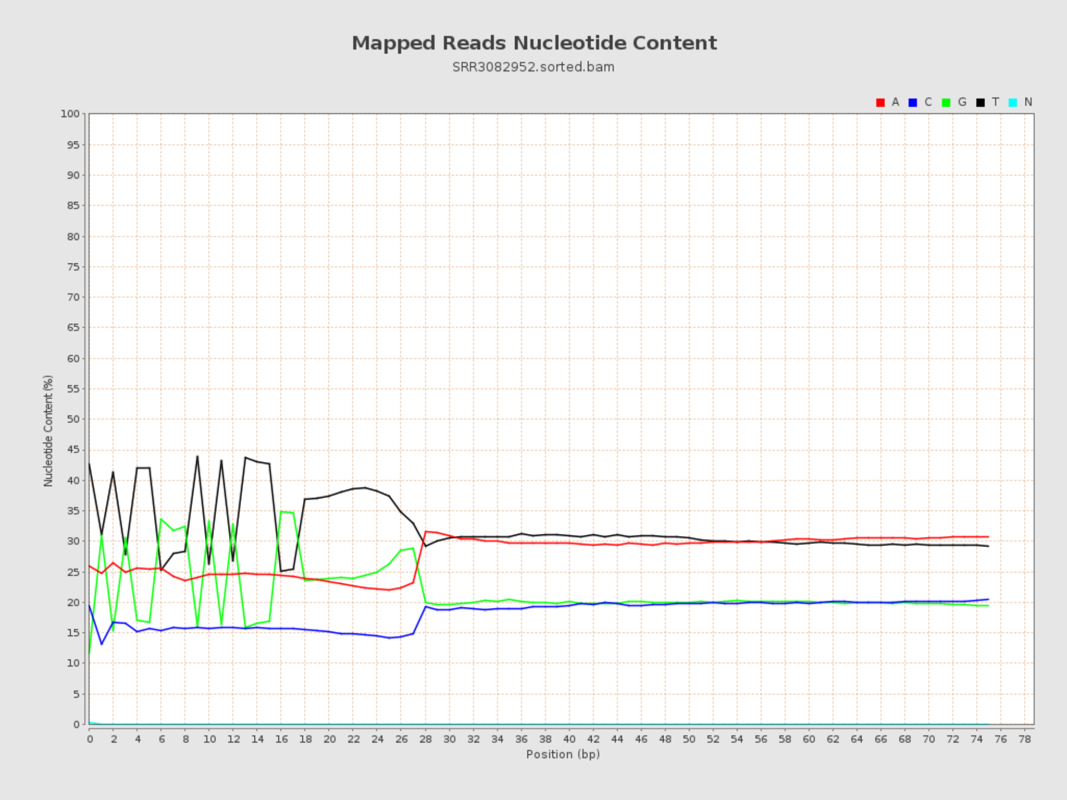
6. Results : Genome Fraction Coverage



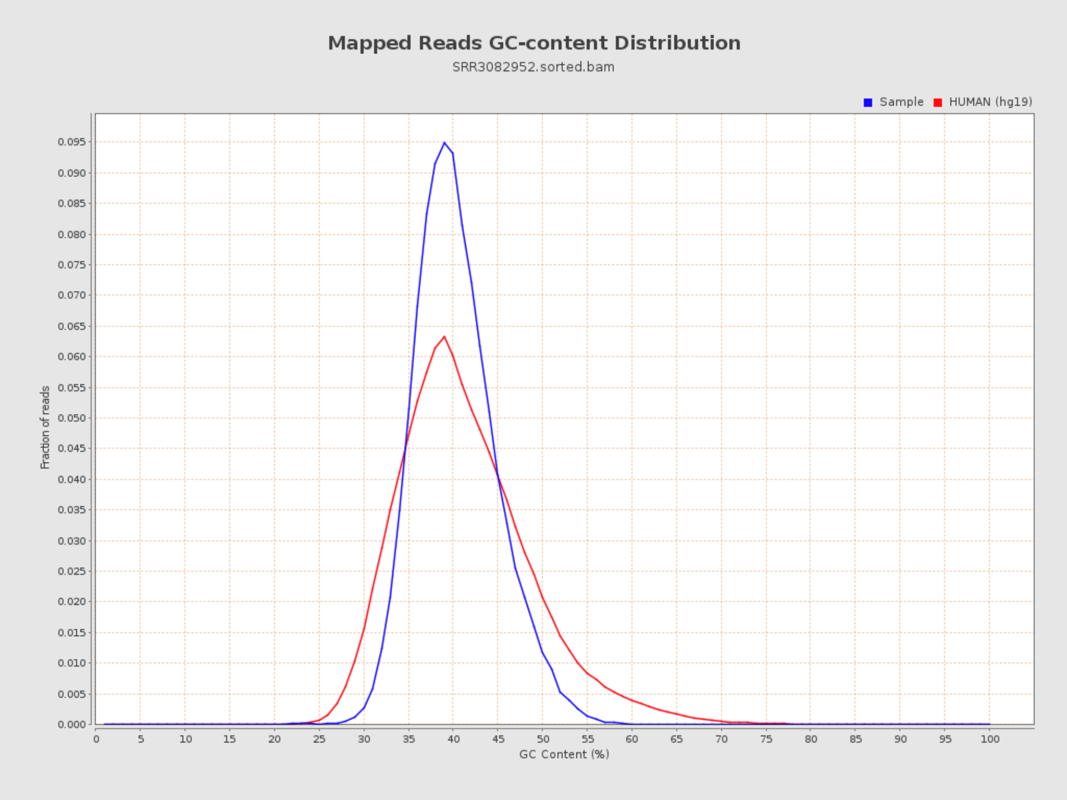
7. Results : Duplication Rate Histogram



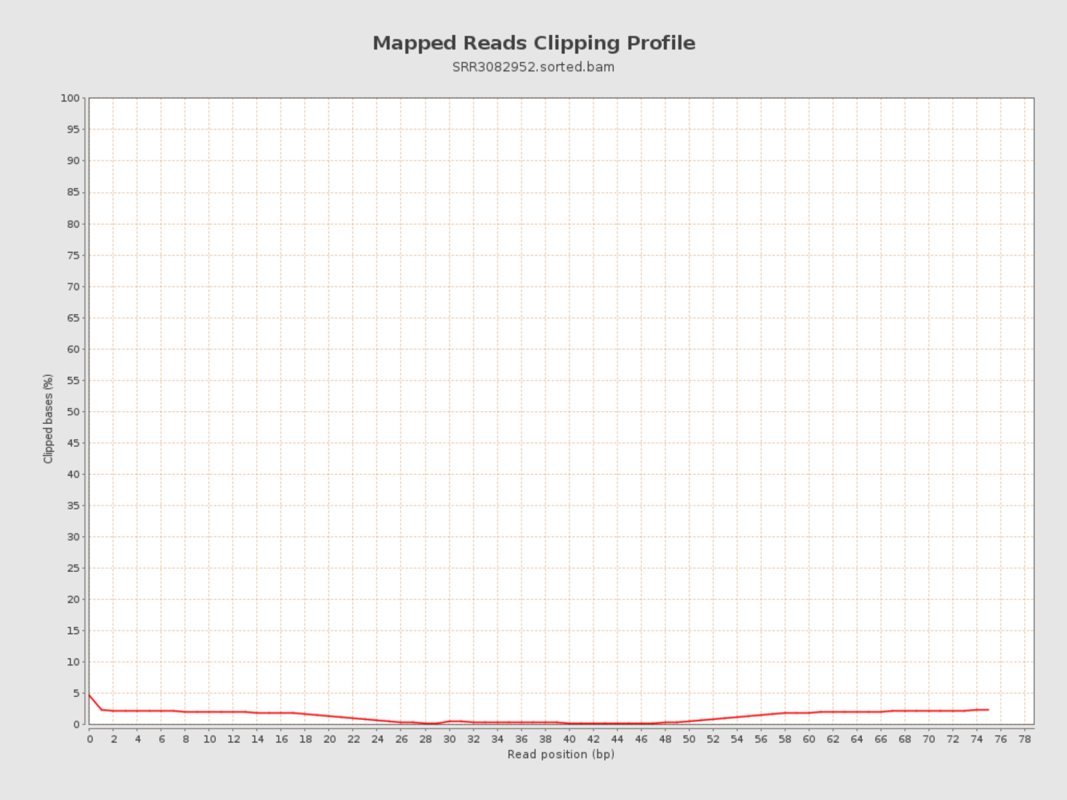
8. Results : Mapped Reads Nucleotide Content



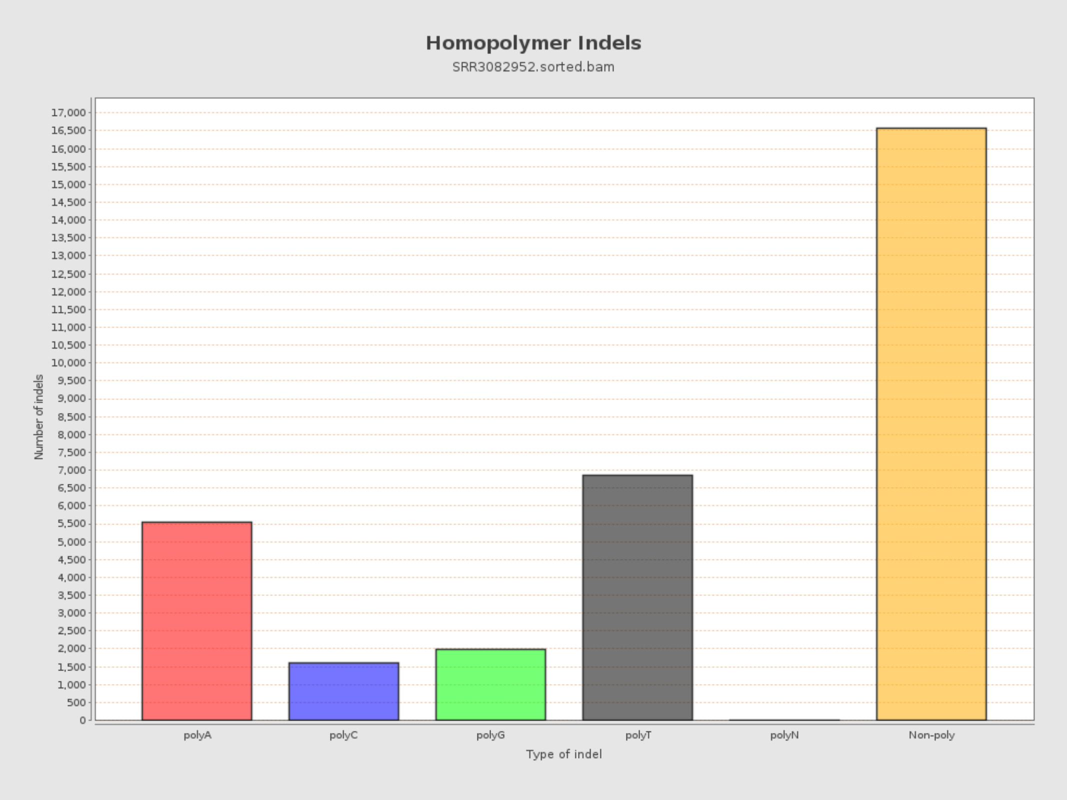
9. Results : Mapped Reads GC-content Distribution



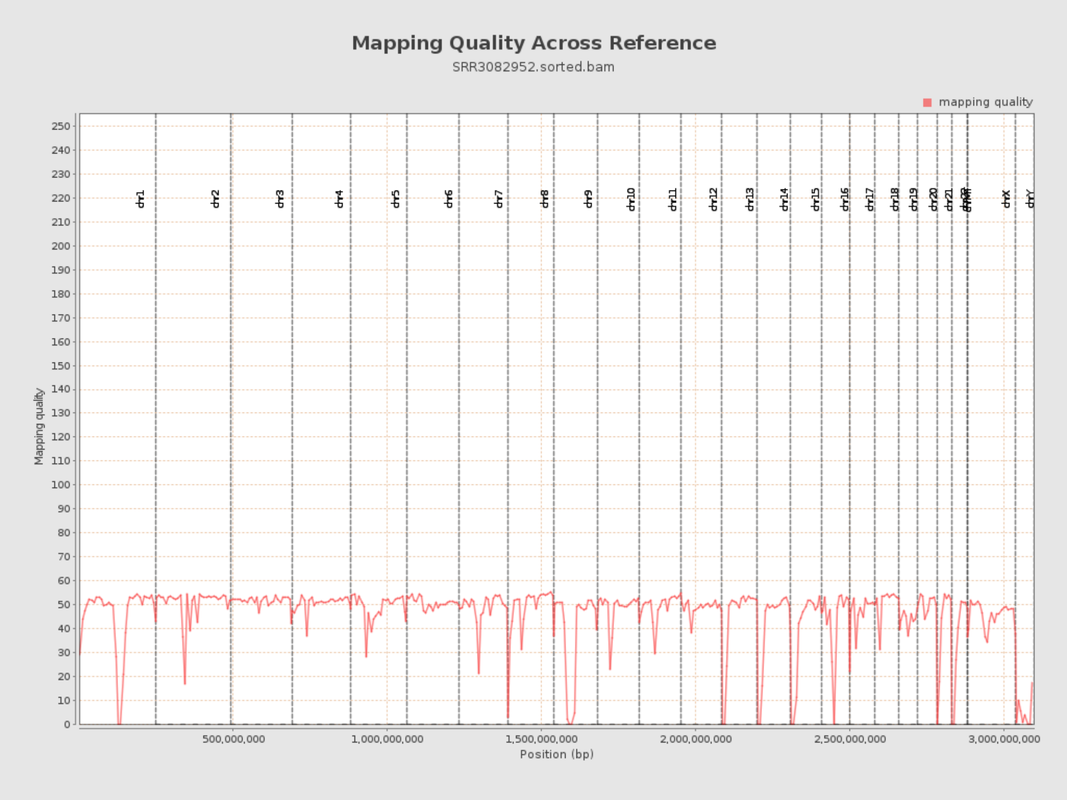
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram