Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 21:17:06

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082955.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_SRR3082955 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082955.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 21:17:06 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082955.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,333,604
Mapped reads	3,594,592 / 82.95%
Unmapped reads	739,012 / 17.05%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	23,449 / 0.54%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	155,902 / 3.6%
Duplication rate	3.42%
Clipped reads	1,324,121 / 30.55%

2.2. ACGT Content

Number/percentage of A's	72,078,111 / 29.1%
Number/percentage of C's	45,910,286 / 18.53%
Number/percentage of T's	79,158,913 / 31.96%
Number/percentage of G's	50,525,943 / 20.4%
Number/percentage of N's	25,437 / 0.01%
GC Percentage	38.93%

2.3. Coverage

Mean	0.08

Standard Deviation	0.5817

2.4. Mapping Quality

Mean Mapping Quality	47.55

2.5. Mismatches and indels

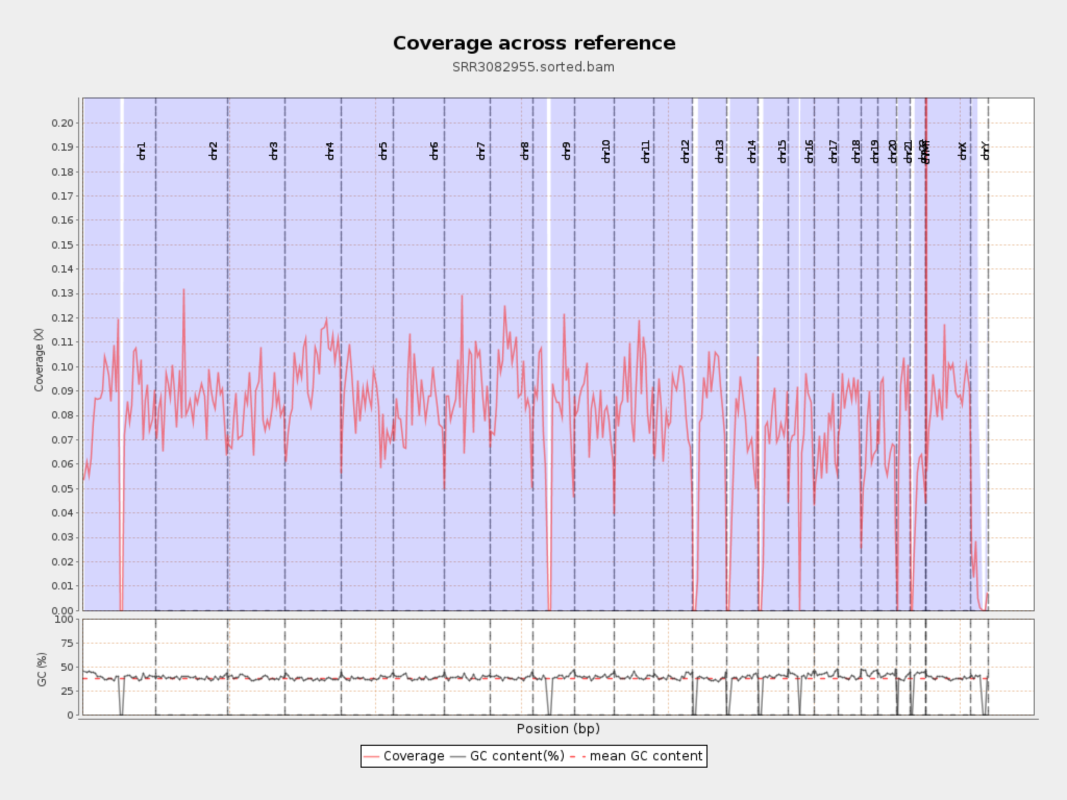
General error rate	0.93%
Mismatches	2,258,652
Insertions	21,178
Mapped reads with at least one insertion	0.58%
Deletions	56,685
Mapped reads with at least one deletion	1.56%
Homopolymer indels	47.5%

2.6. Chromosome stats

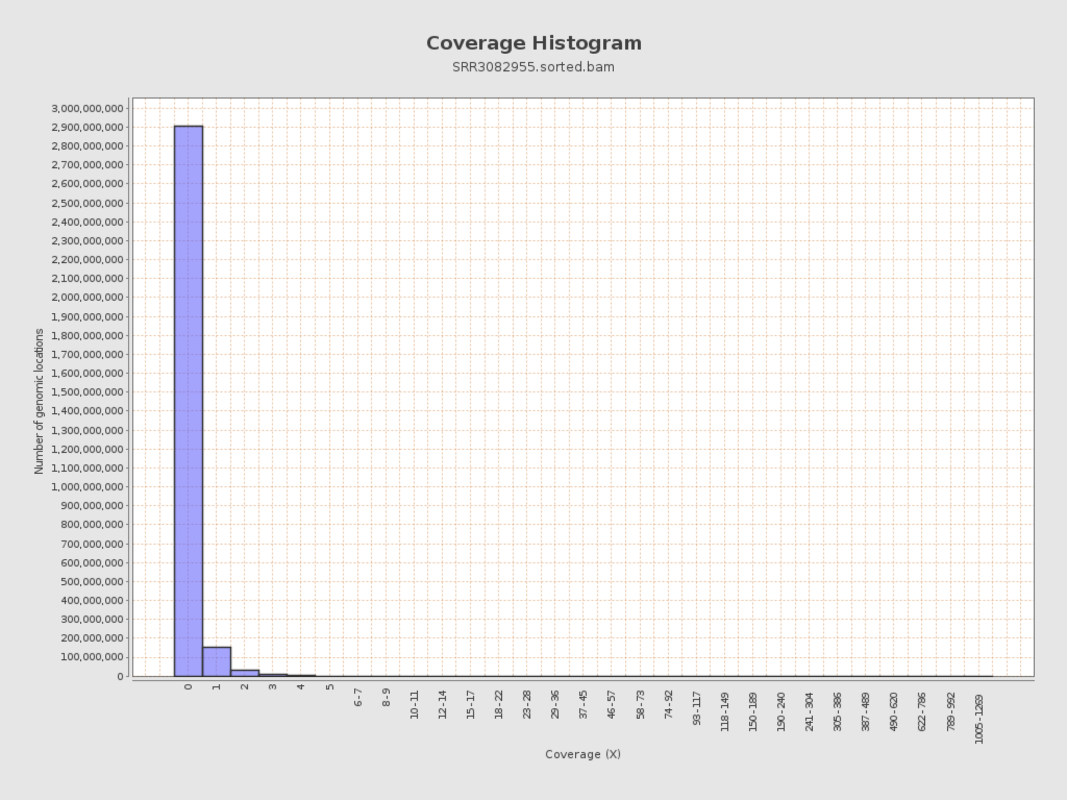
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20123447	0.0807	1.0583
chr2	243199373	21181922	0.0871	0.6114
chr3	198022430	16174395	0.0817	0.3566
chr4	191154276	19006500	0.0994	0.4054
chr5	180915260	15120822	0.0836	0.3632
chr6	171115067	14533708	0.0849	0.4289
chr7	159138663	14371906	0.0903	0.7565

chr8	146364022	13789688	0.0942	0.8951
chr9	141213431	10920746	0.0773	0.5332
chr10	135534747	11029117	0.0814	0.4759
chr11	135006516	12083731	0.0895	0.6218
chr12	133851895	10960599	0.0819	0.3659
chr13	115169878	8617482	0.0748	0.345
chr14	107349540	6683421	0.0623	0.3533
chr15	102531392	6326750	0.0617	0.3069
chr16	90354753	6186788	0.0685	0.3885
chr17	81195210	5417864	0.0667	0.3891
chr18	78077248	6746683	0.0864	0.9885
chr19	59128983	3851807	0.0651	0.7116
chr20	63025520	4380092	0.0695	0.3371
chr21	48129895	3685943	0.0766	0.3801
chr22	51304566	2124086	0.0414	0.2486
chrMT	16571	65603	3.9589	3.2808
chrX	155270560	13863149	0.0893	0.411
chrY	59373566	551160	0.0093	0.2187

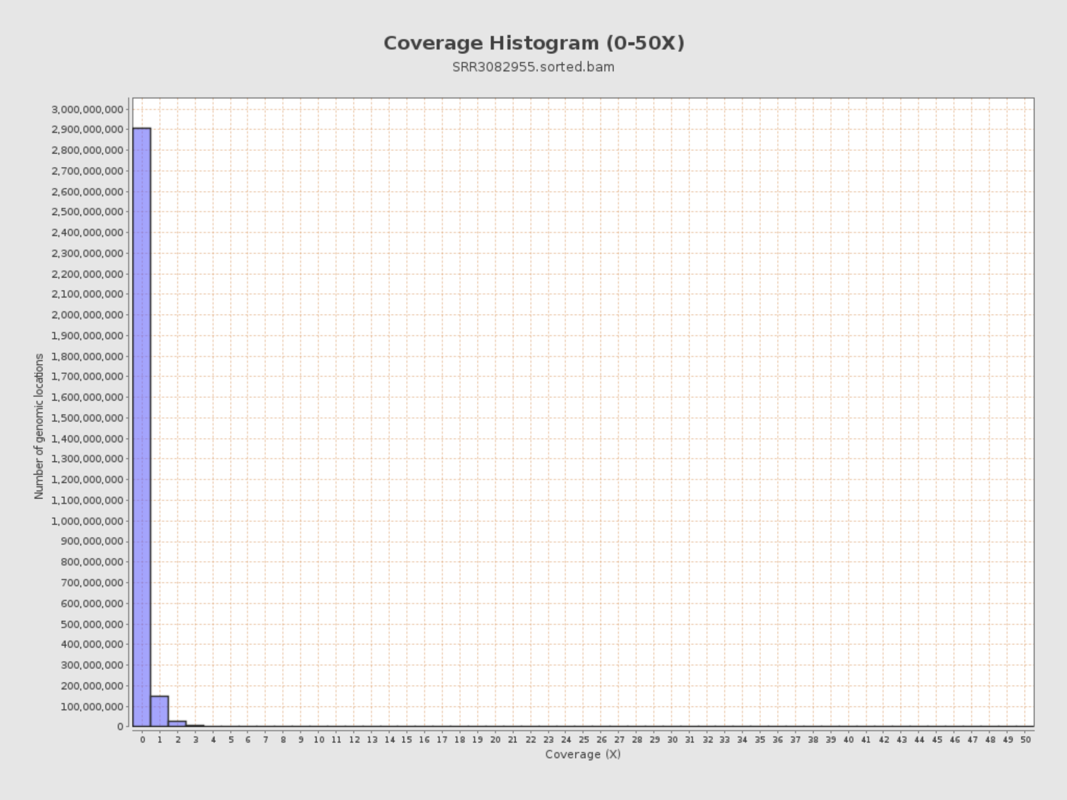
3. Results : Coverage across reference



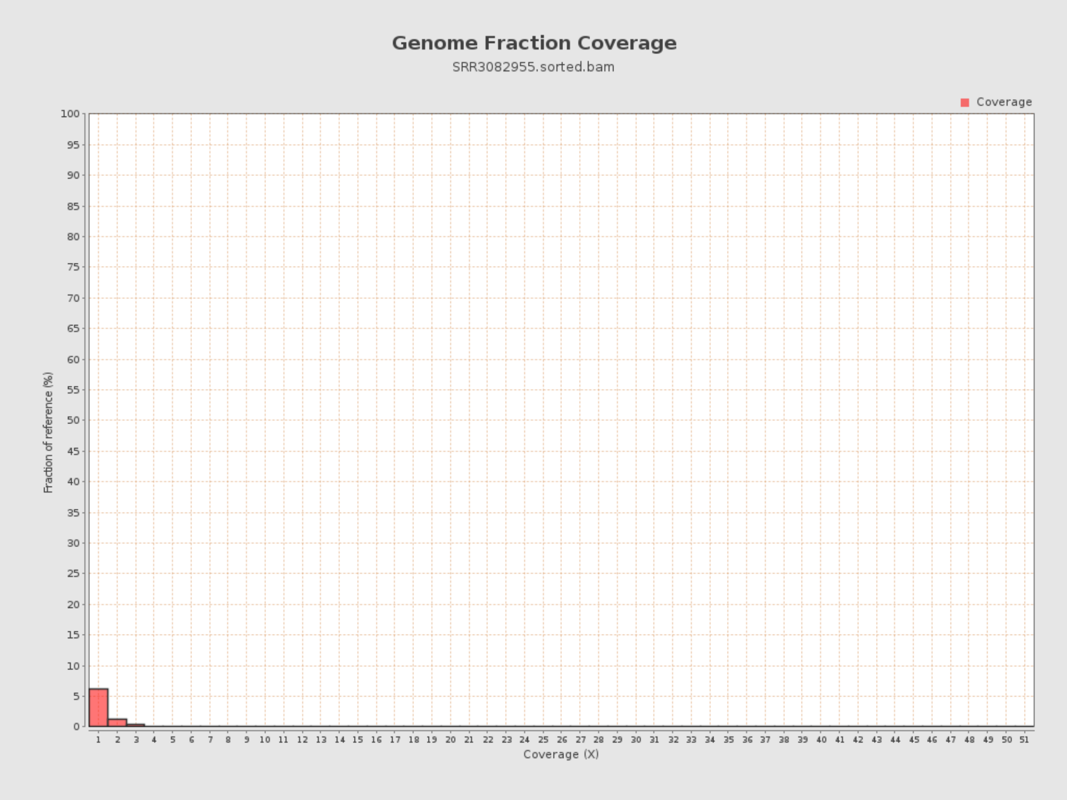
4. Results : Coverage Histogram



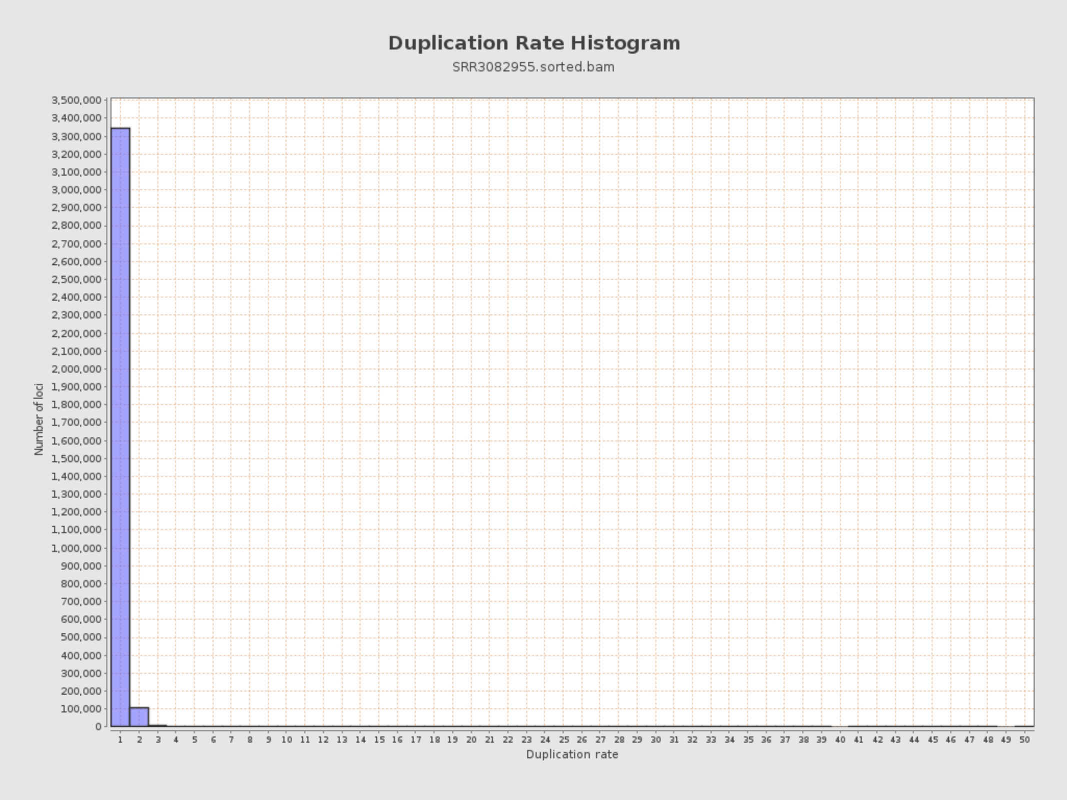
5. Results : Coverage Histogram (0-50X)



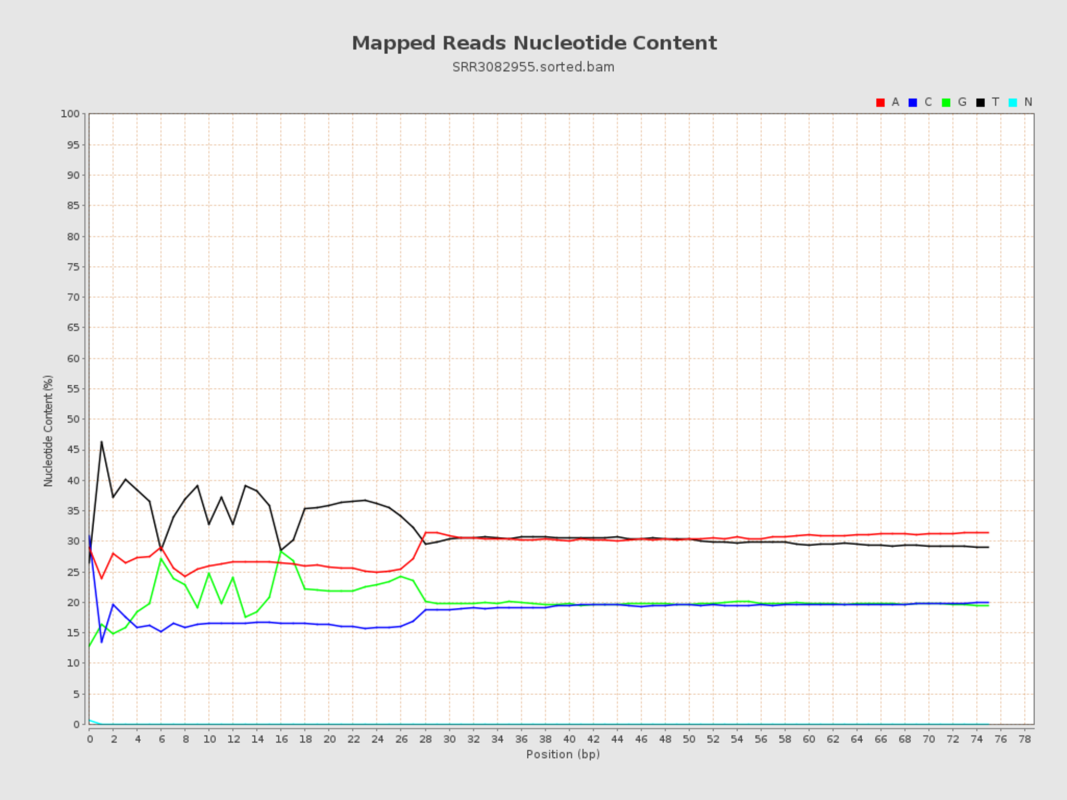
6. Results : Genome Fraction Coverage



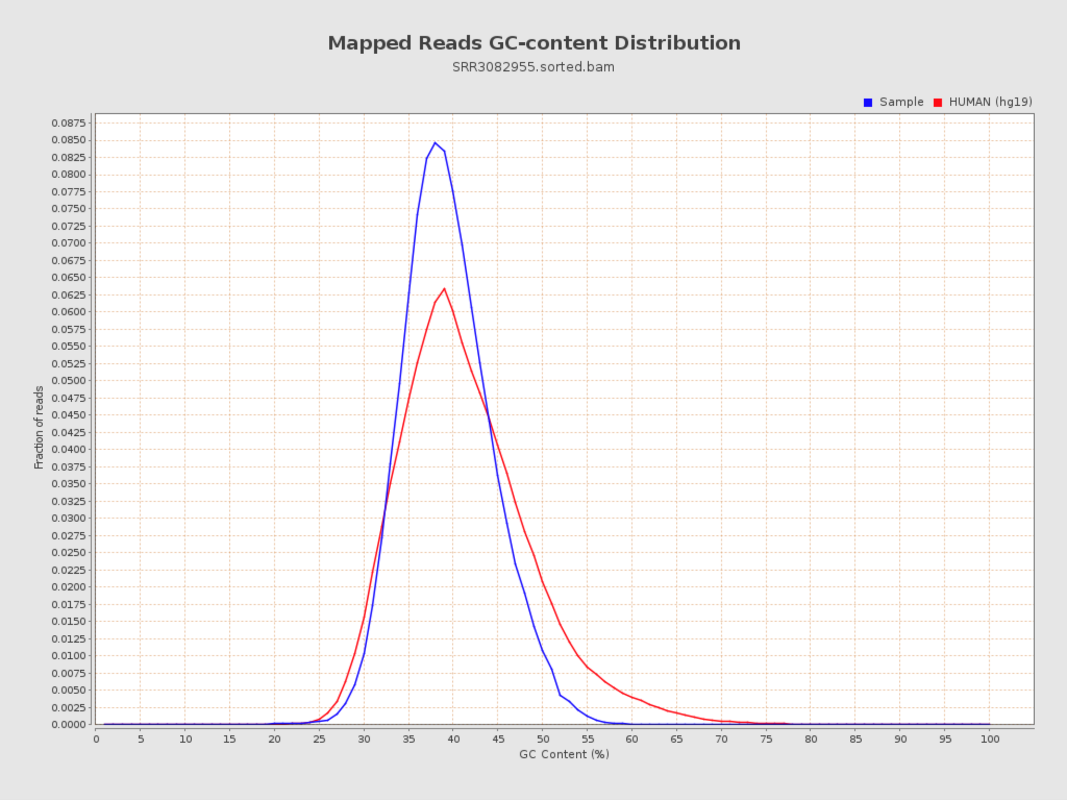
7. Results : Duplication Rate Histogram



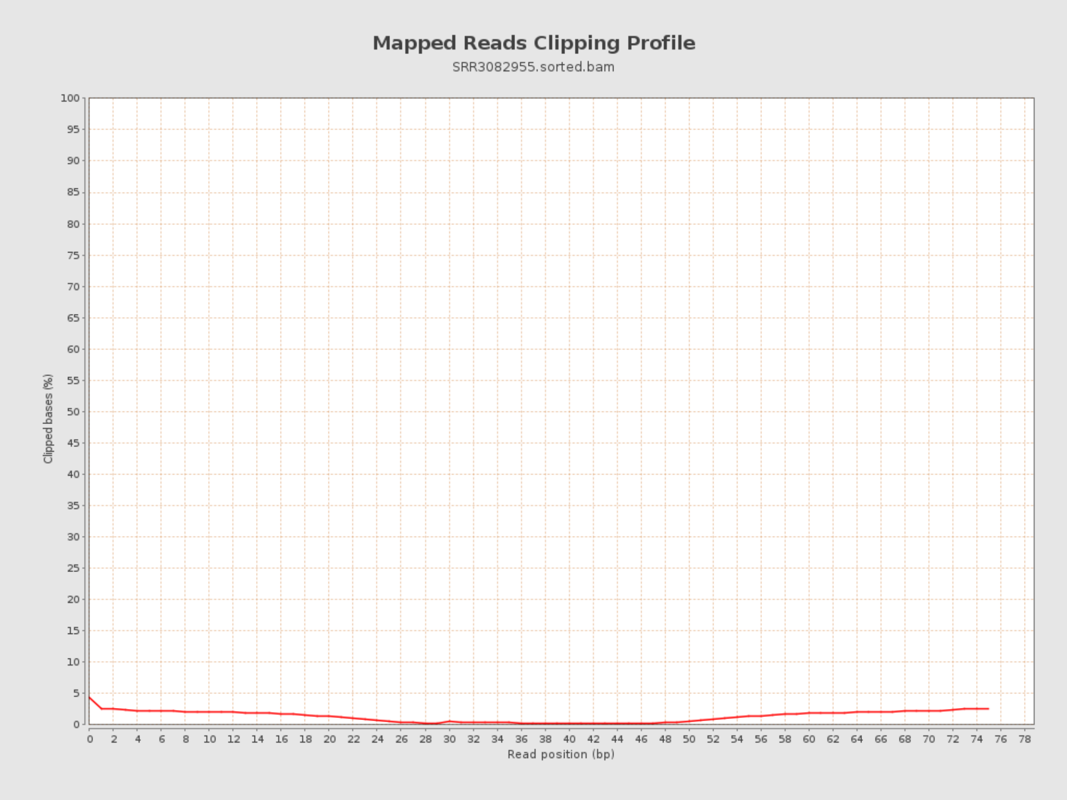
8. Results : Mapped Reads Nucleotide Content



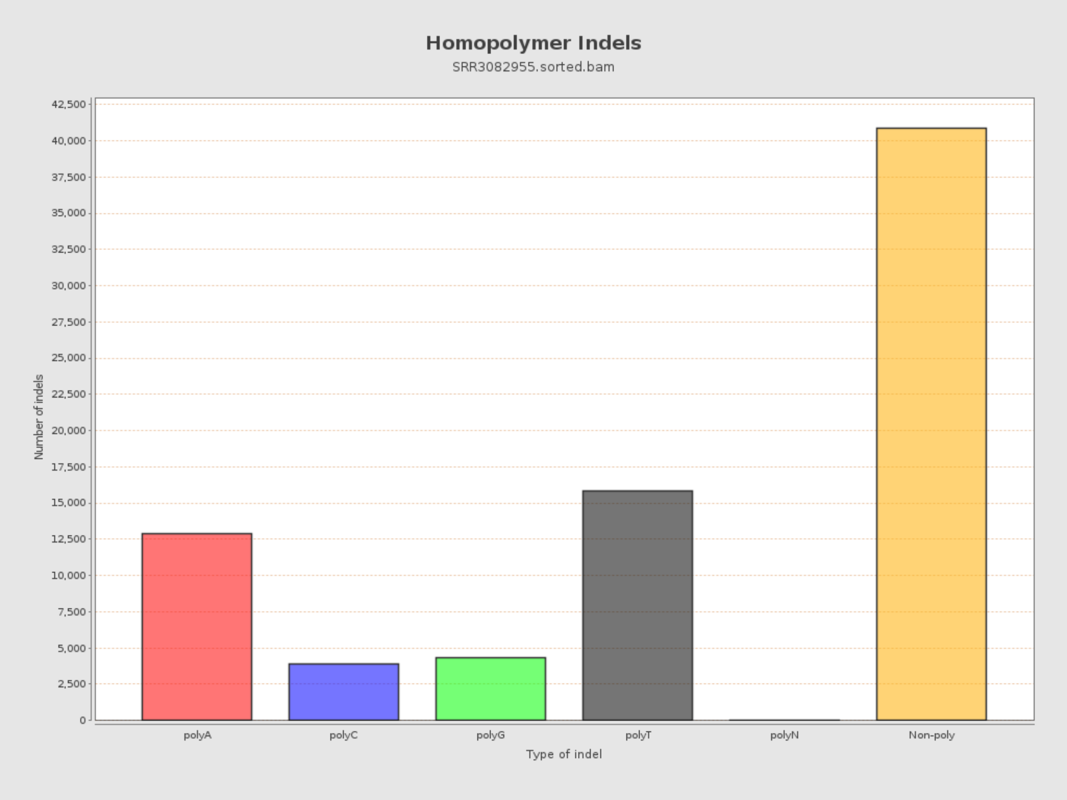
9. Results : Mapped Reads GC-content Distribution



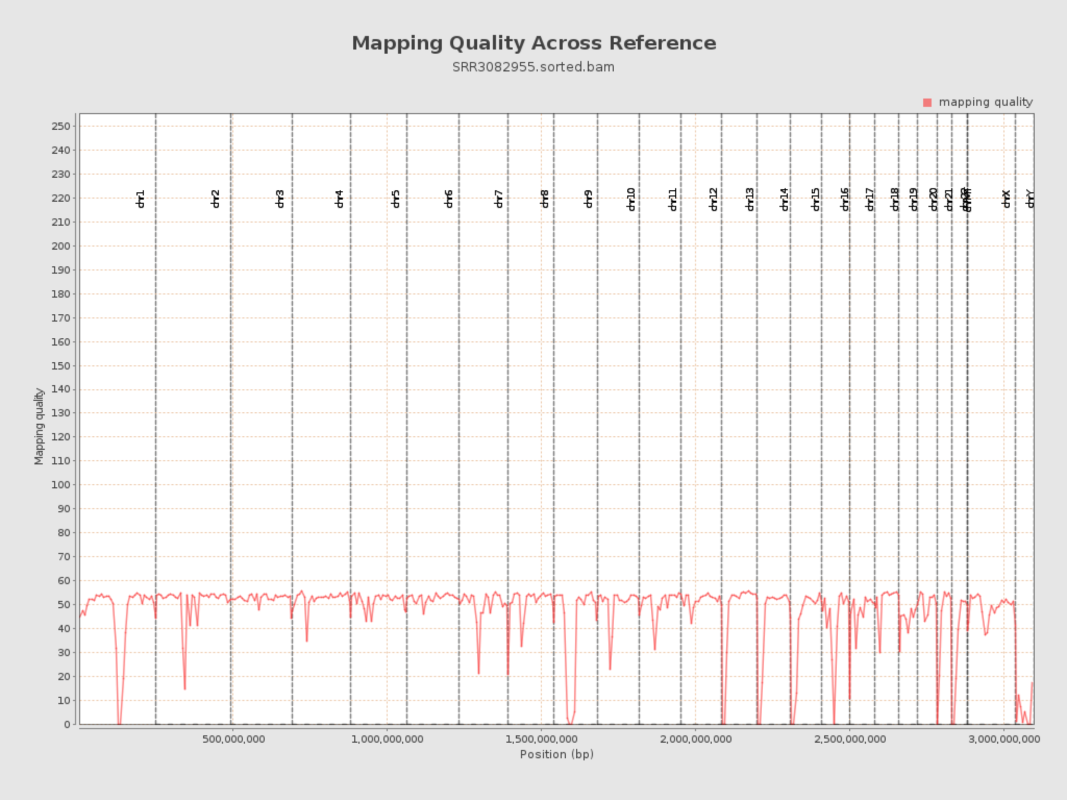
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram