Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:19:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082320.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_SRR3082320 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082320.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:19:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082320.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,650,089
Mapped reads	2,359,821 / 89.05%
Unmapped reads	290,268 / 10.95%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	17,921 / 0.68%
Read min/max/mean length	30 / 76 / 76.24
Duplicated reads (estimated)	96,888 / 3.66%
Duplication rate	3.14%
Clipped reads	1,058,510 / 39.94%

2.2. ACGT Content

Number/percentage of A's	43,771,948 / 27.75%
Number/percentage of C's	29,130,857 / 18.47%
Number/percentage of T's	49,494,513 / 31.38%
Number/percentage of G's	35,346,563 / 22.41%
Number/percentage of N's	3,344 / 0%
GC Percentage	40.87%

2.3. Coverage

Mean	0.051

Standard Deviation	0.4316

2.4. Mapping Quality

Mean Mapping Quality	45.76

2.5. Mismatches and indels

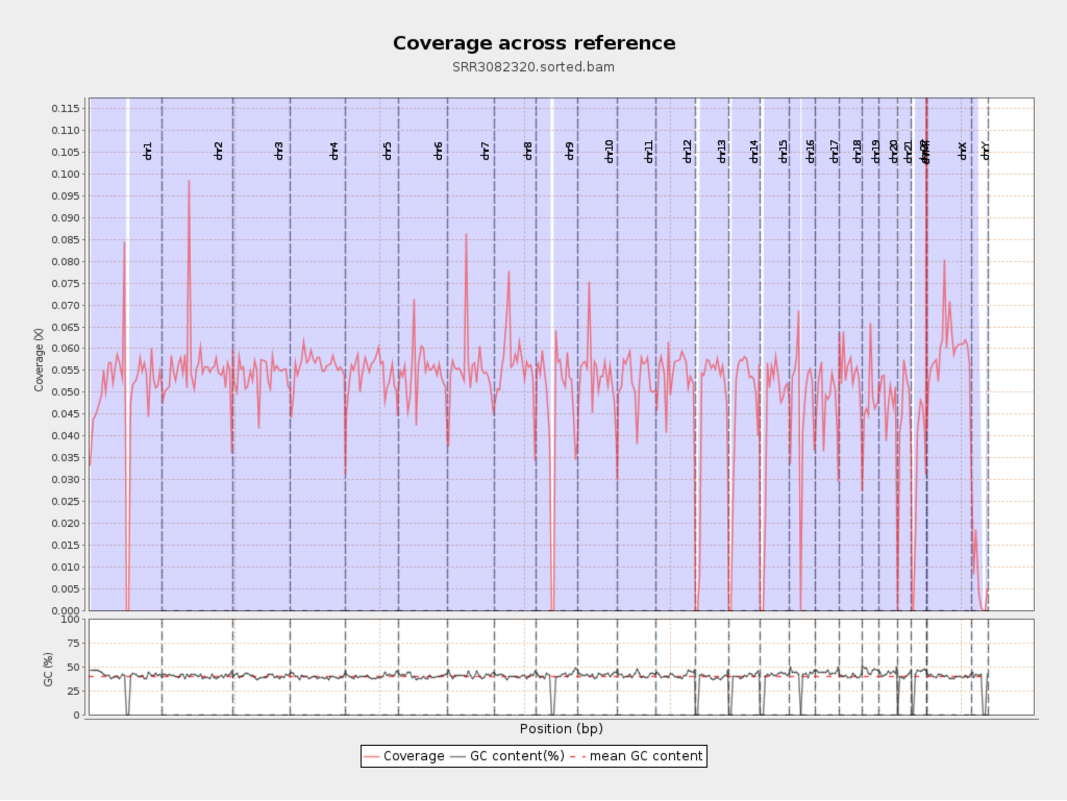
General error rate	0.84%
Mismatches	1,307,601
Insertions	12,509
Mapped reads with at least one insertion	0.53%
Deletions	34,356
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.52%

2.6. Chromosome stats

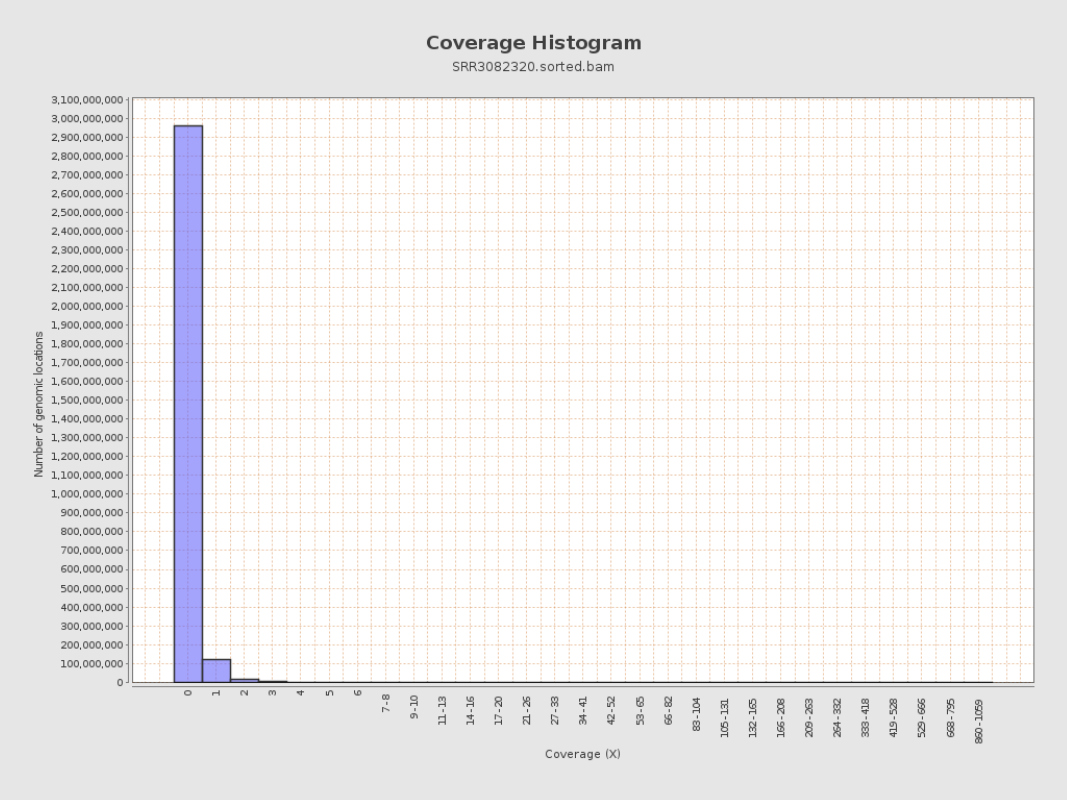
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	12385654	0.0497	0.7359
chr2	243199373	13553964	0.0557	0.5829
chr3	198022430	10724909	0.0542	0.2604
chr4	191154276	10690208	0.0559	0.2759
chr5	180915260	9814317	0.0542	0.2632
chr6	171115067	9316855	0.0544	0.3248
chr7	159138663	8839445	0.0555	0.5424

chr8	146364022	8223860	0.0562	0.6975
chr9	141213431	6622821	0.0469	0.3997
chr10	135534747	7335518	0.0541	0.3763
chr11	135006516	7112767	0.0527	0.3594
chr12	133851895	7216798	0.0539	0.2656
chr13	115169878	5216875	0.0453	0.2377
chr14	107349540	4810027	0.0448	0.2548
chr15	102531392	4378611	0.0427	0.237
chr16	90354753	4256053	0.0471	0.2745
chr17	81195210	3855897	0.0475	0.2702
chr18	78077248	4288492	0.0549	0.7081
chr19	59128983	2858040	0.0483	0.5454
chr20	63025520	3020704	0.0479	0.2529
chr21	48129895	2078879	0.0432	0.2513
chr22	51304566	1553844	0.0303	0.1934
chrMT	16571	4180	0.2522	0.5257
chrX	155270560	9259778	0.0596	0.3087
chrY	59373566	383706	0.0065	0.1325

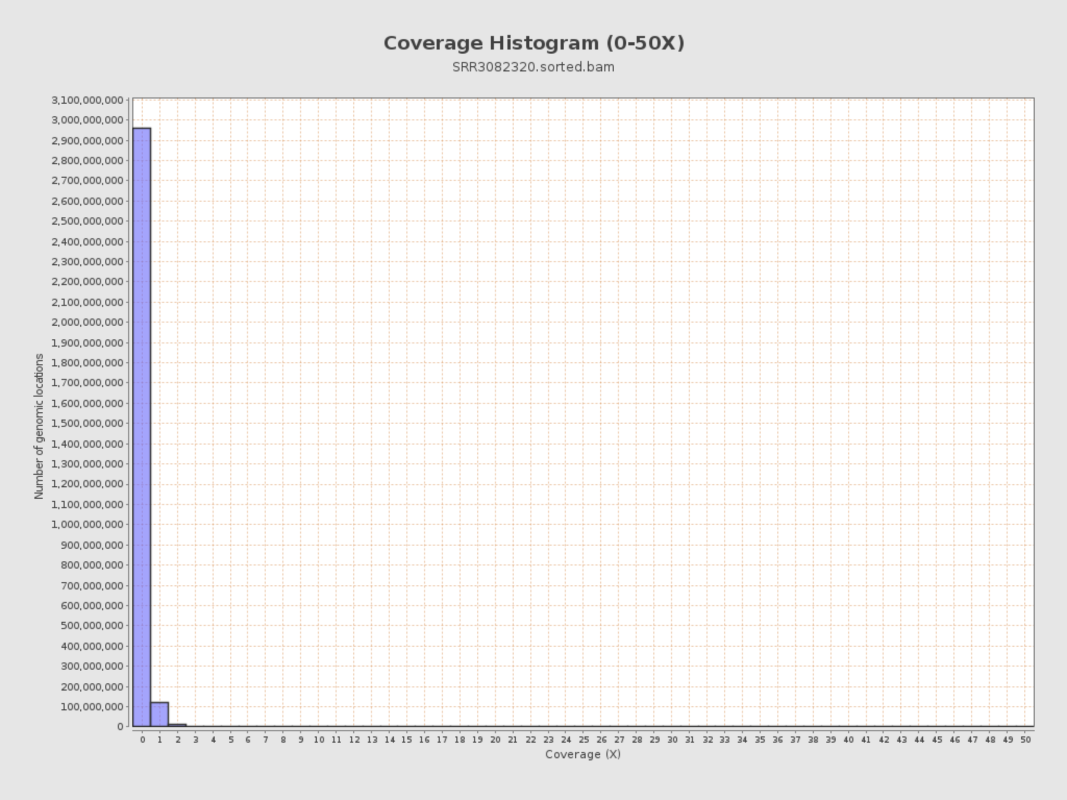
3. Results : Coverage across reference



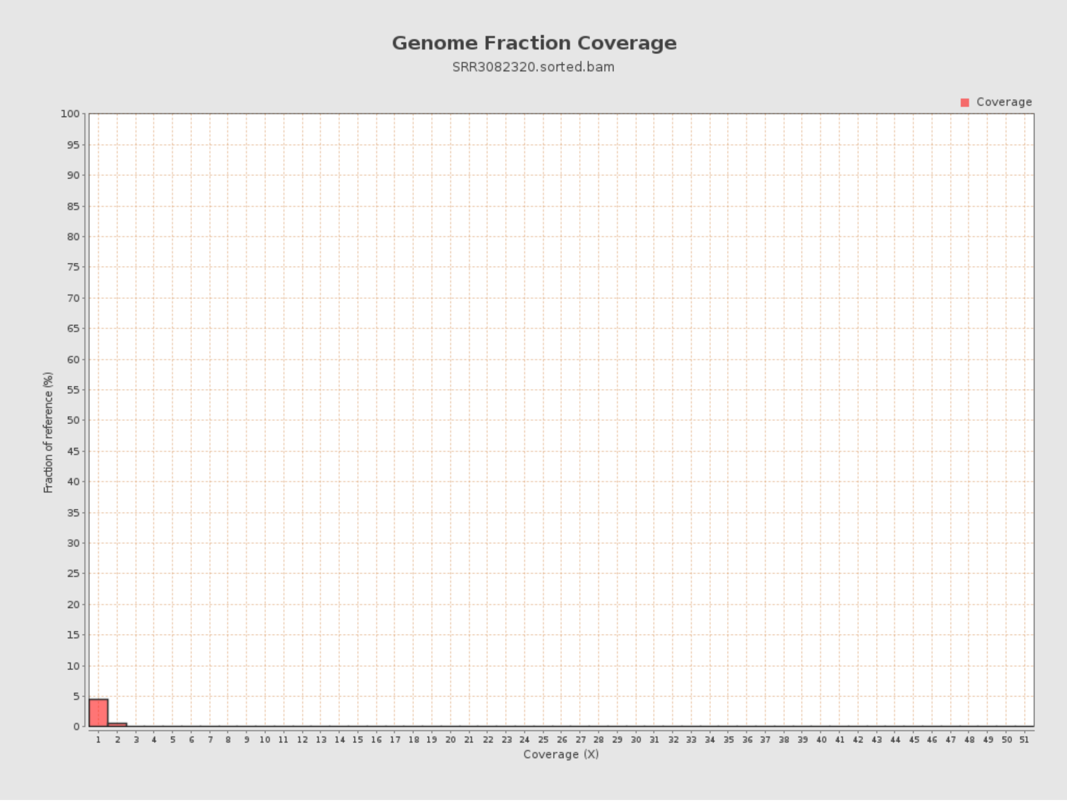
4. Results : Coverage Histogram



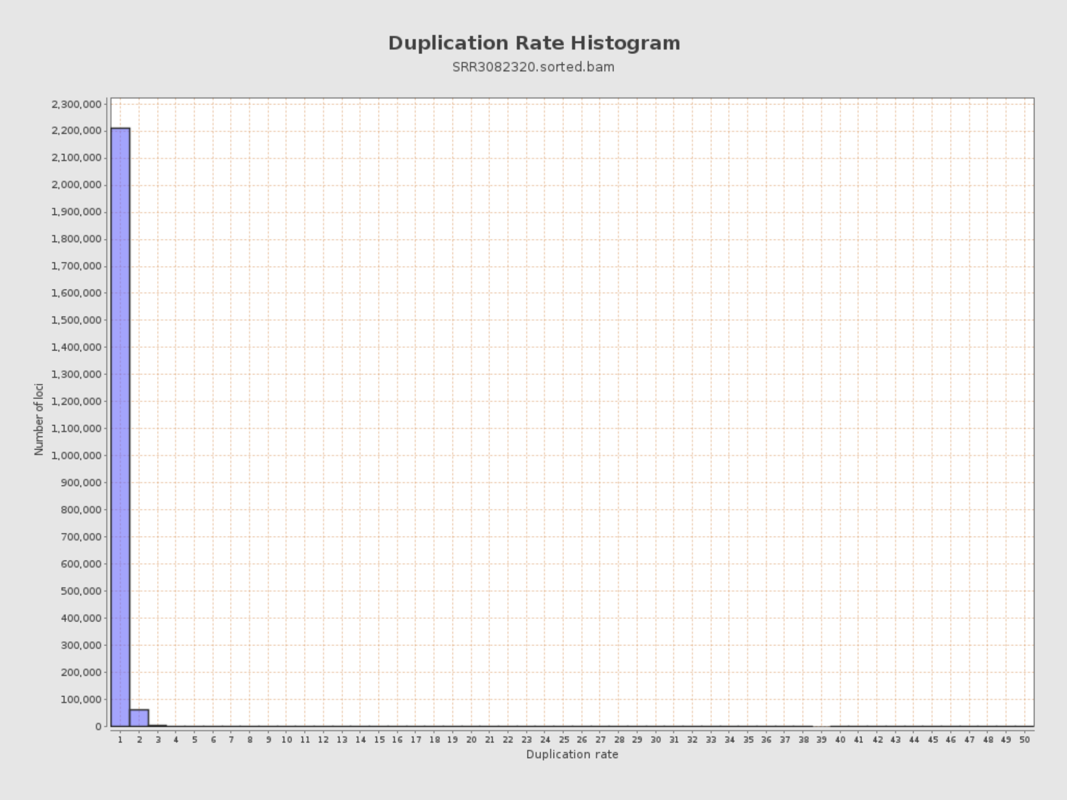
5. Results : Coverage Histogram (0-50X)



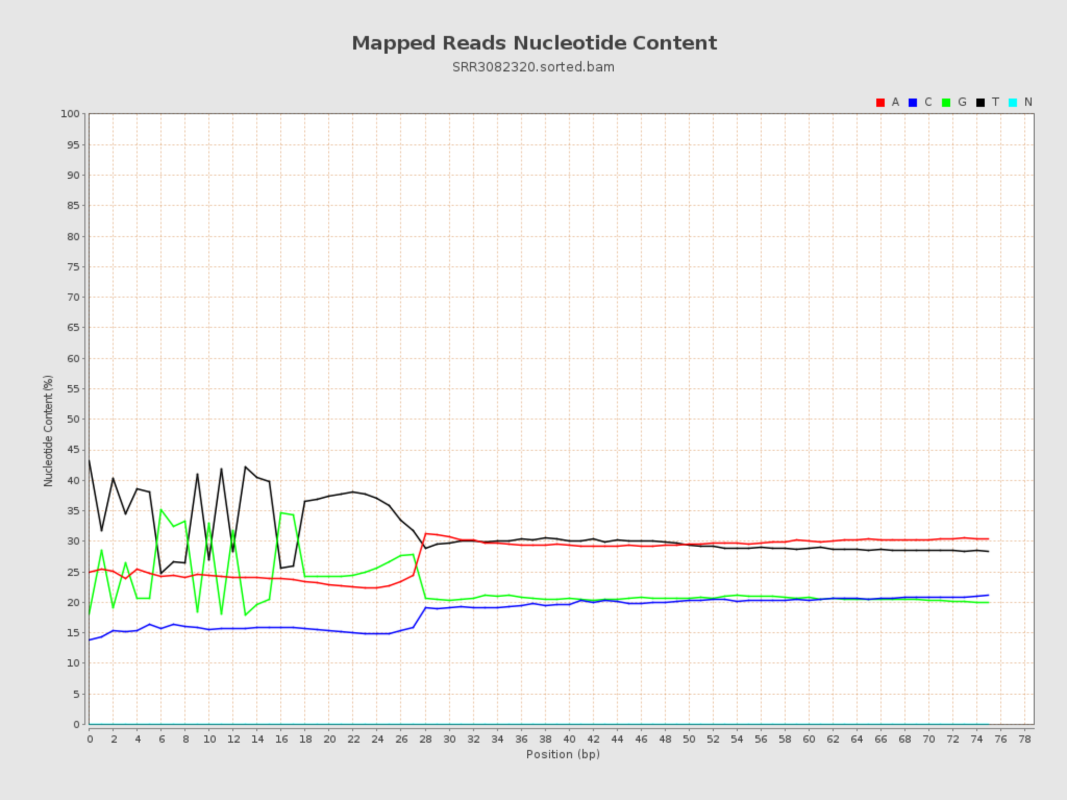
6. Results : Genome Fraction Coverage



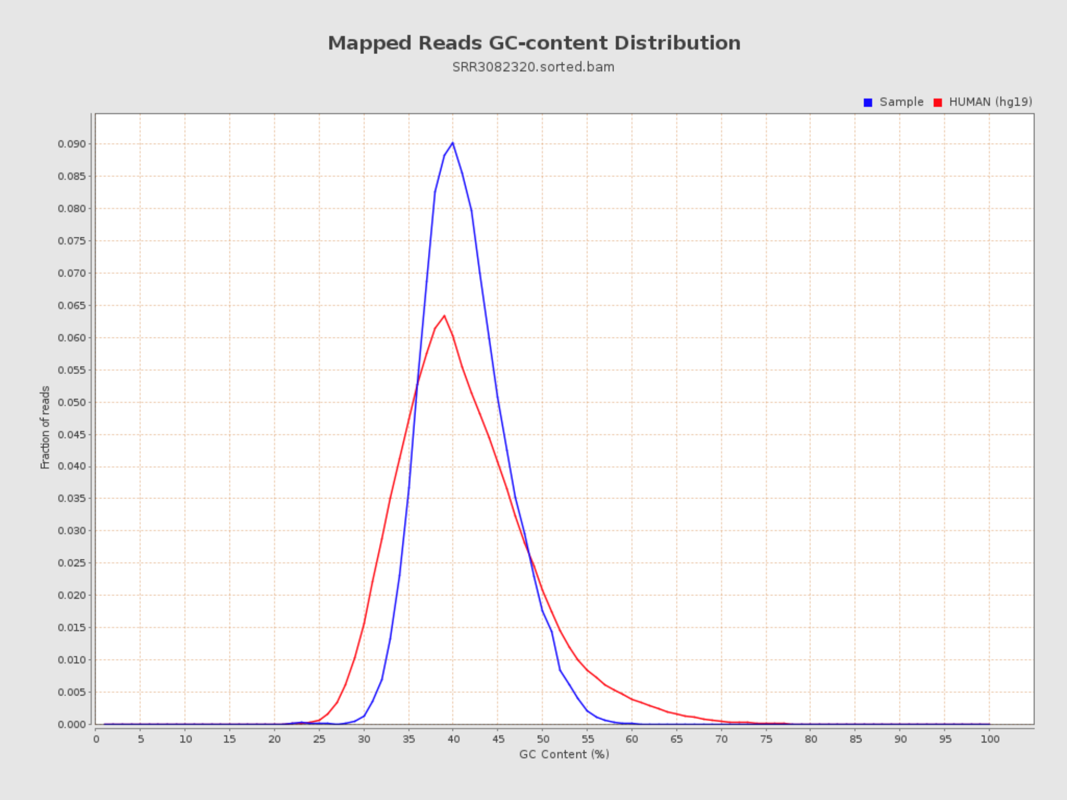
7. Results : Duplication Rate Histogram



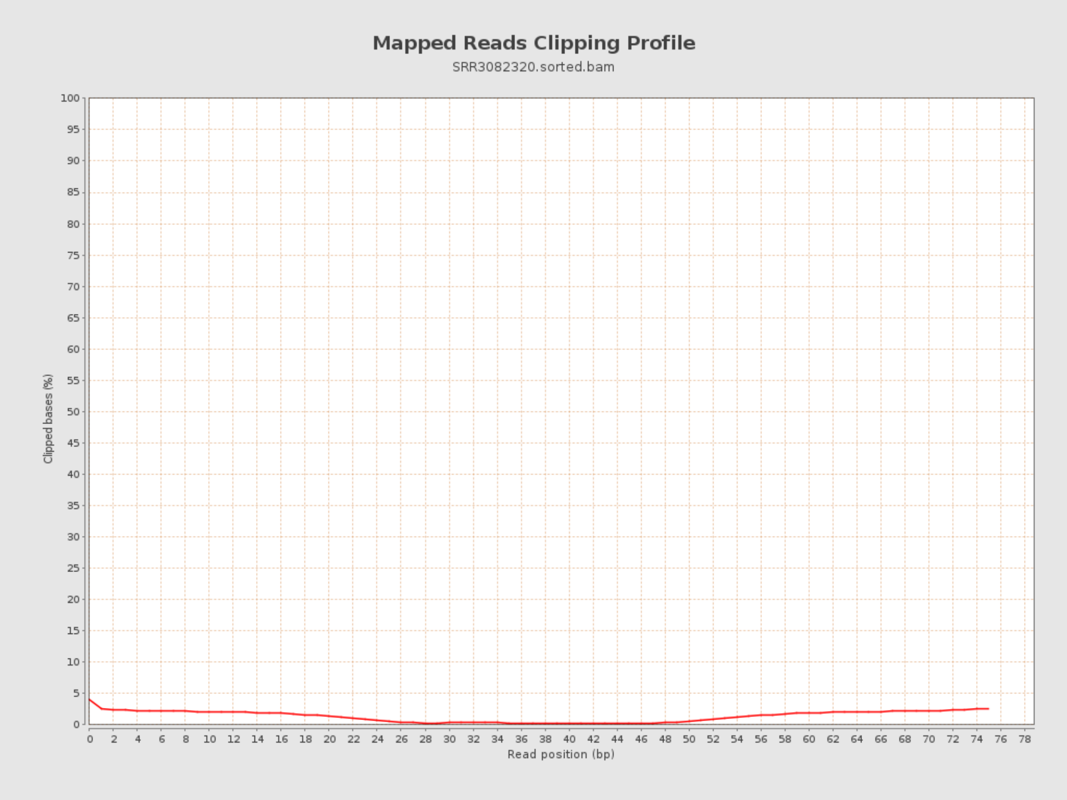
8. Results : Mapped Reads Nucleotide Content



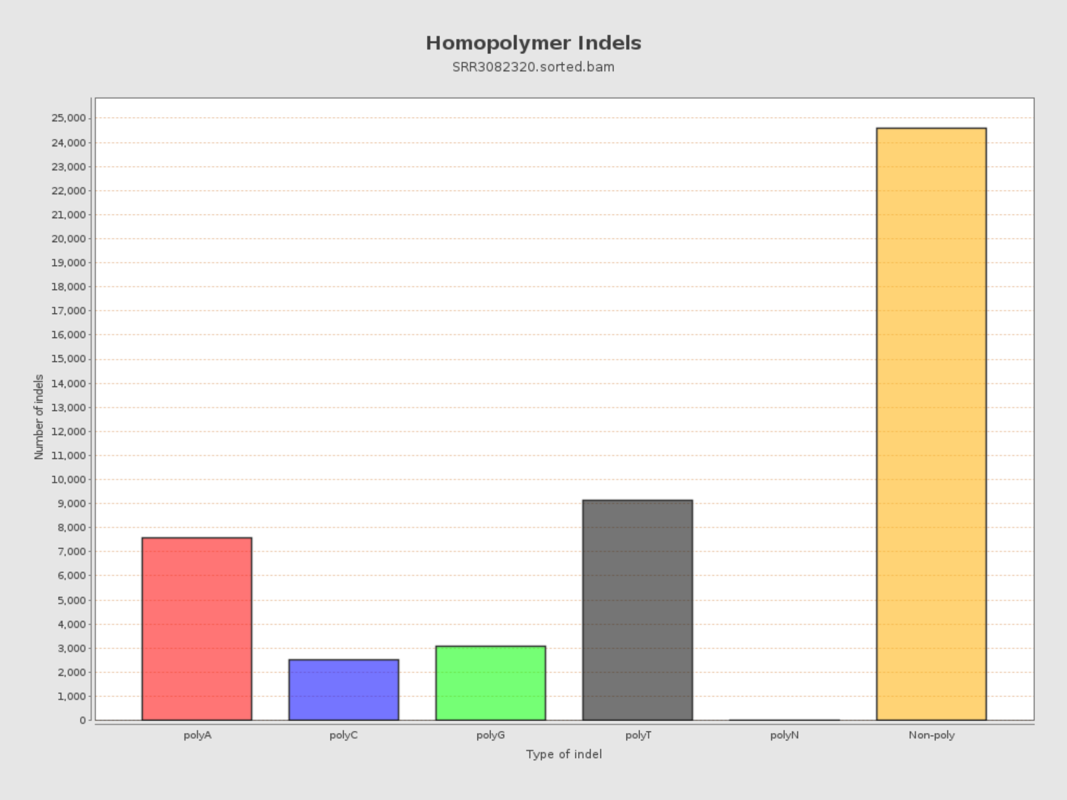
9. Results : Mapped Reads GC-content Distribution



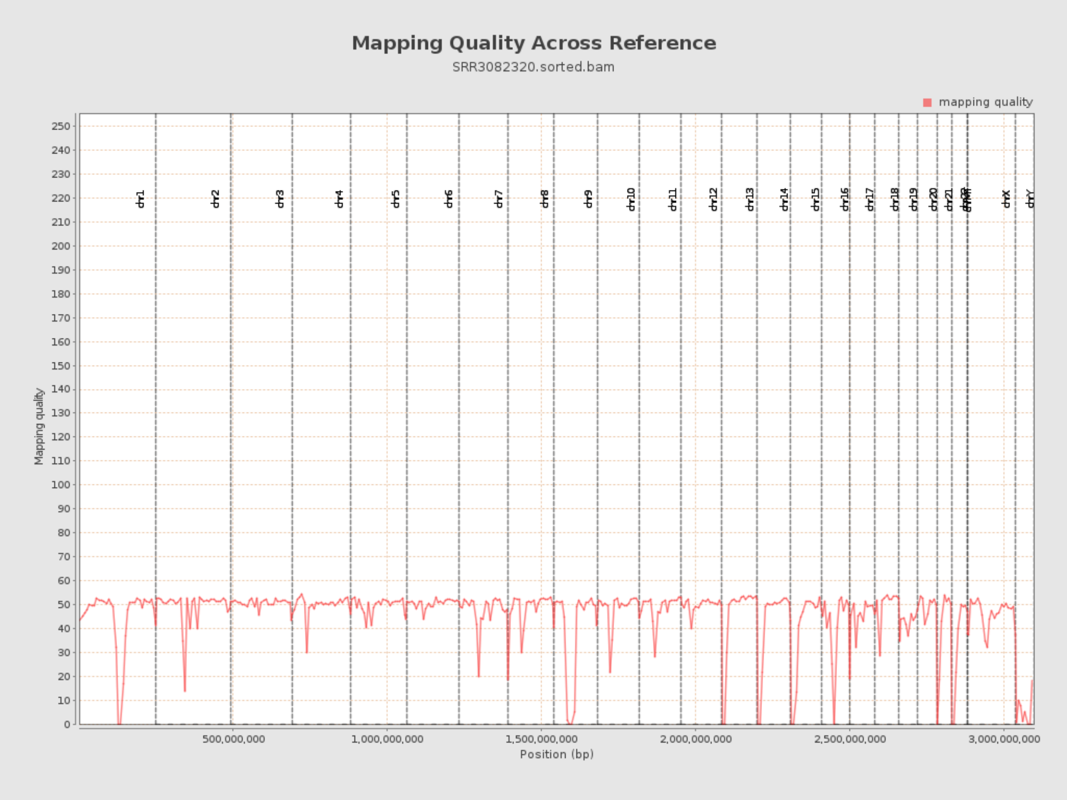
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram