Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:35:57

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082324.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_SRR3082324 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082324.fastq.gz`
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:35:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082324.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,007,558
Mapped reads	3,629,665 / 90.57%
Unmapped reads	377,893 / 9.43%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	34,515 / 0.86%
Read min/max/mean length	30 / 76 / 76.3
Duplicated reads (estimated)	167,615 / 4.18%
Duplication rate	3.5%
Clipped reads	1,481,996 / 36.98%

2.2. ACGT Content

Number/percentage of A's	70,560,098 / 28.58%
Number/percentage of C's	45,874,810 / 18.58%
Number/percentage of T's	77,600,620 / 31.43%
Number/percentage of G's	52,834,631 / 21.4%
Number/percentage of N's	5,119 / 0%
GC Percentage	39.98%

2.3. Coverage

Mean	0.0798

Standard Deviation	0.6242

2.4. Mapping Quality

Mean Mapping Quality	47.11

2.5. Mismatches and indels

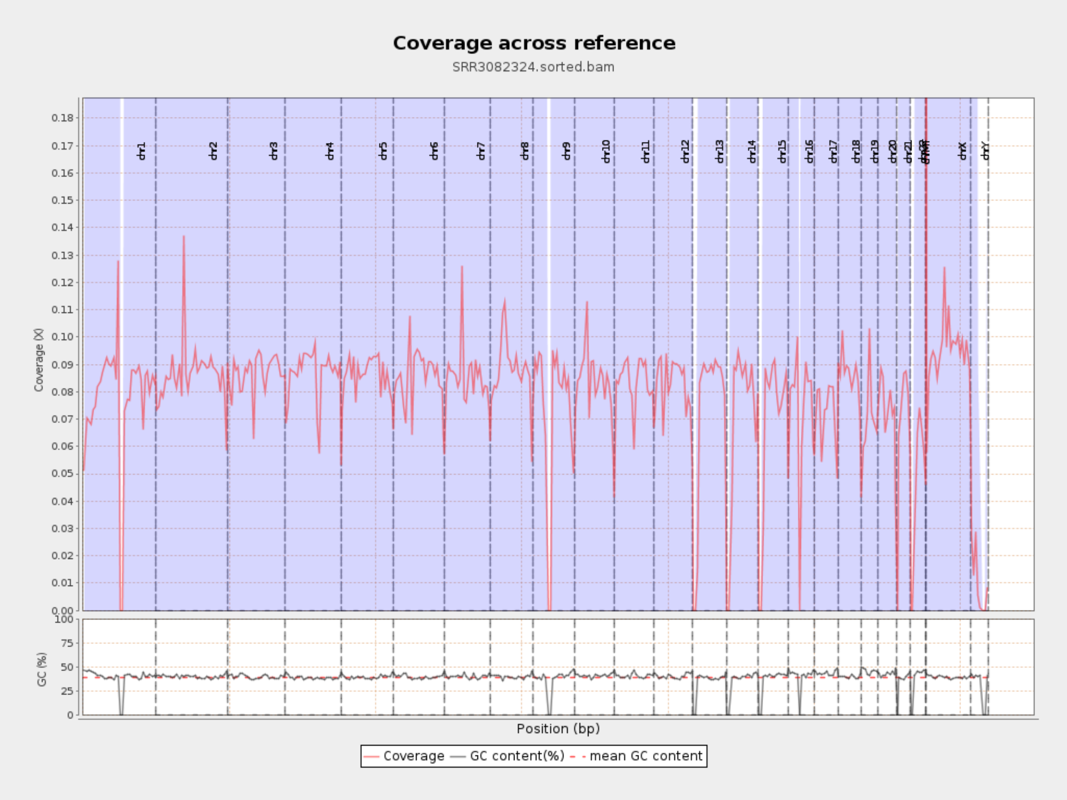
General error rate	0.84%
Mismatches	2,030,504
Insertions	19,357
Mapped reads with at least one insertion	0.53%
Deletions	54,715
Mapped reads with at least one deletion	1.49%
Homopolymer indels	48.01%

2.6. Chromosome stats

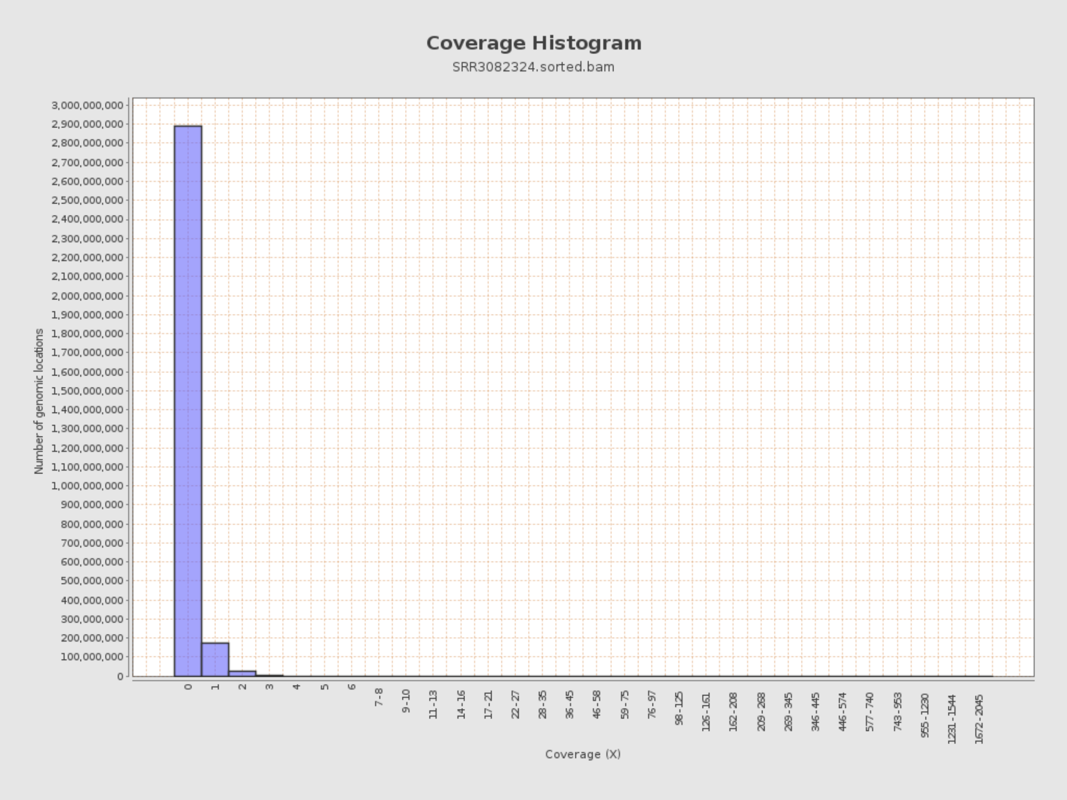
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19333231	0.0776	1.0904
chr2	243199373	21129645	0.0869	0.7139
chr3	198022430	17213609	0.0869	0.3401
chr4	191154276	16617888	0.0869	0.3584
chr5	180915260	15563001	0.086	0.3427
chr6	171115067	14732524	0.0861	0.4109
chr7	159138663	13573199	0.0853	0.758

chr8	146364022	12899489	0.0881	1.2632
chr9	141213431	10382531	0.0735	0.5551
chr10	135534747	11420926	0.0843	0.5245
chr11	135006516	11214850	0.0831	0.5097
chr12	133851895	11097771	0.0829	0.3434
chr13	115169878	8300819	0.0721	0.3101
chr14	107349540	7583894	0.0706	0.3406
chr15	102531392	6886419	0.0672	0.3083
chr16	90354753	6458725	0.0715	0.3596
chr17	81195210	5912414	0.0728	0.3577
chr18	78077248	6800046	0.0871	1.0713
chr19	59128983	4174501	0.0706	0.8335
chr20	63025520	4710983	0.0747	0.3319
chr21	48129895	3301024	0.0686	0.3277
chr22	51304566	2352984	0.0459	0.2444
chrMT	16571	16745	1.0105	1.0917
chrX	155270560	14707428	0.0947	0.4185
chrY	59373566	578114	0.0097	0.205

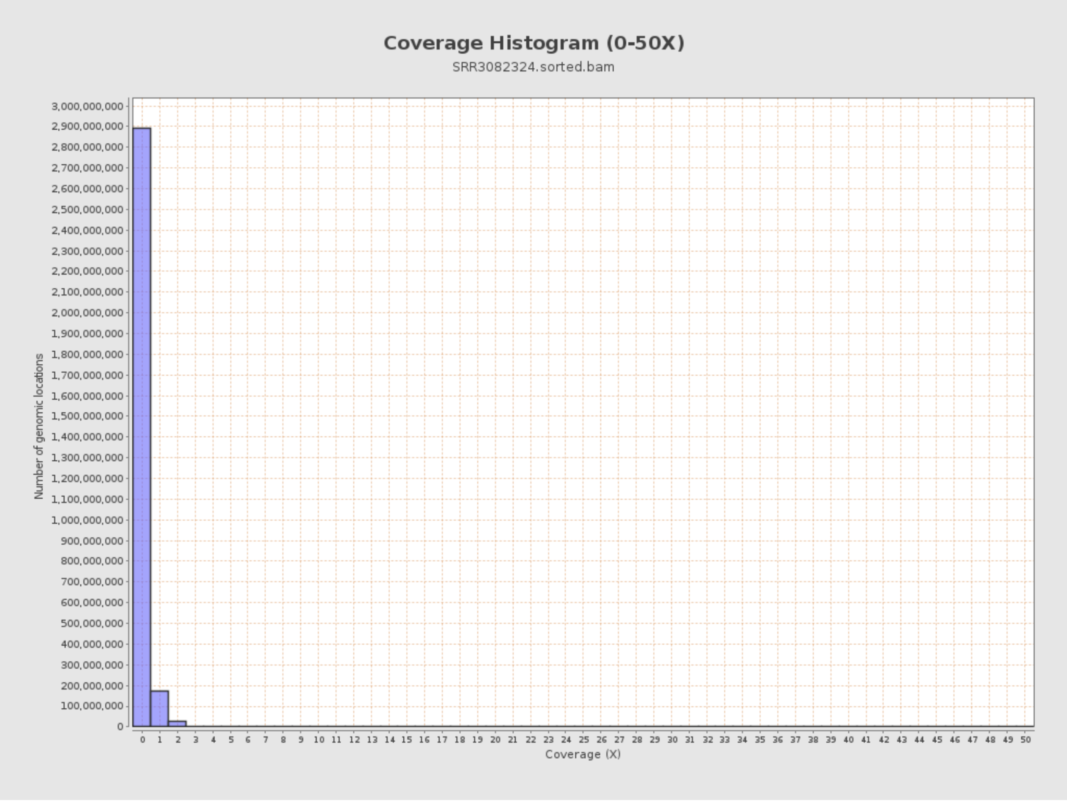
3. Results : Coverage across reference



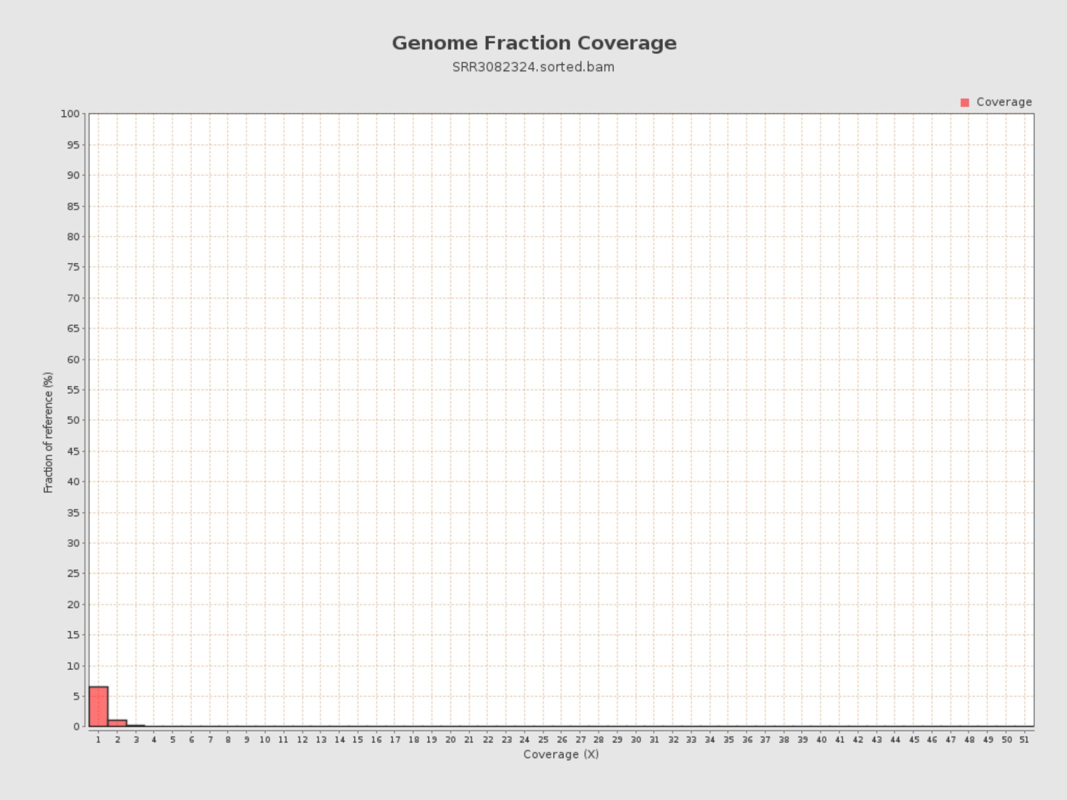
4. Results : Coverage Histogram



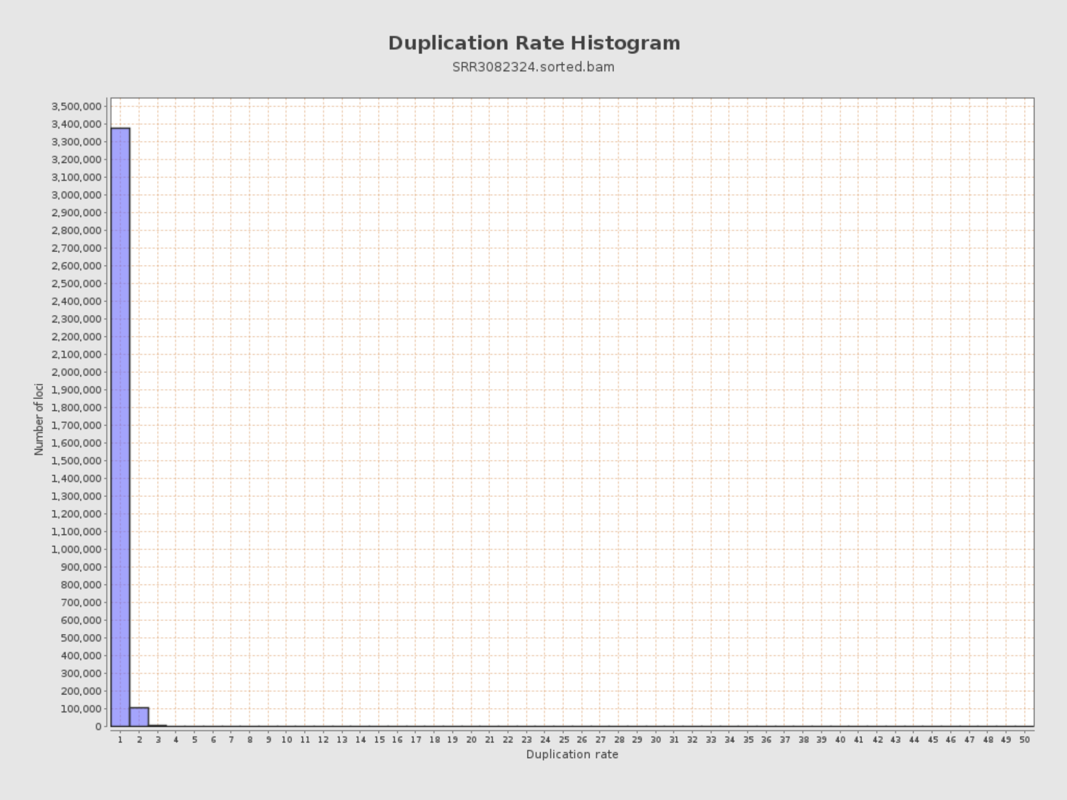
5. Results : Coverage Histogram (0-50X)



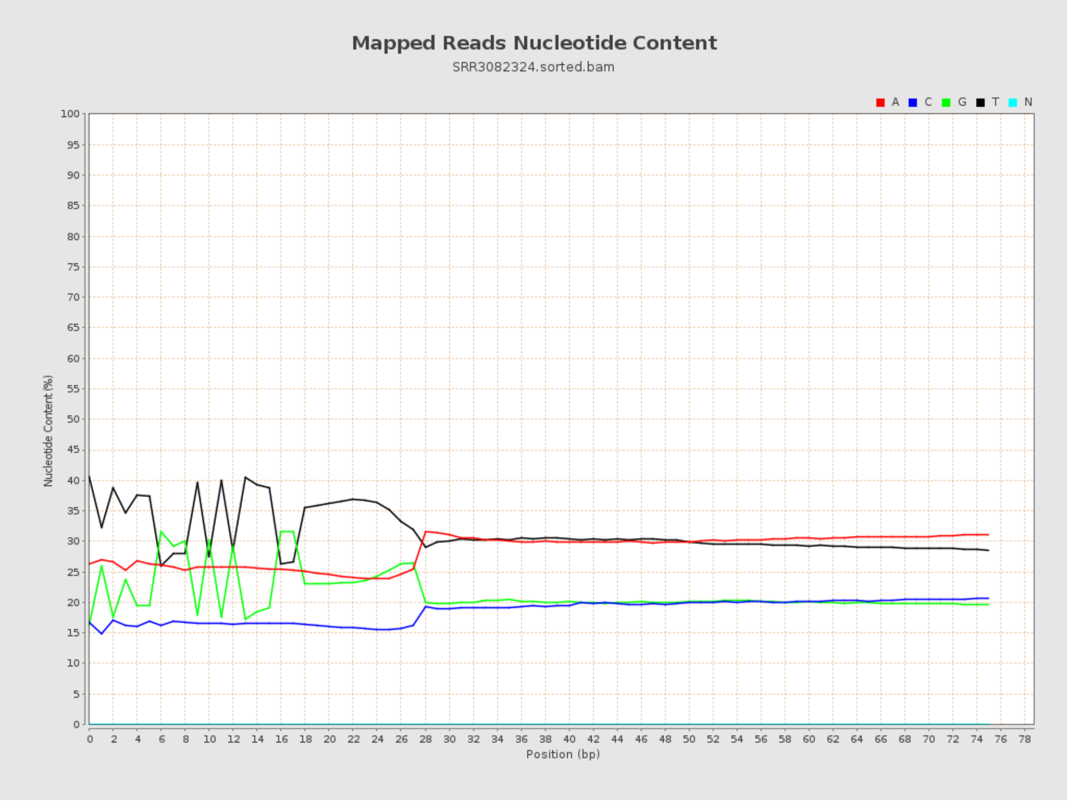
6. Results : Genome Fraction Coverage



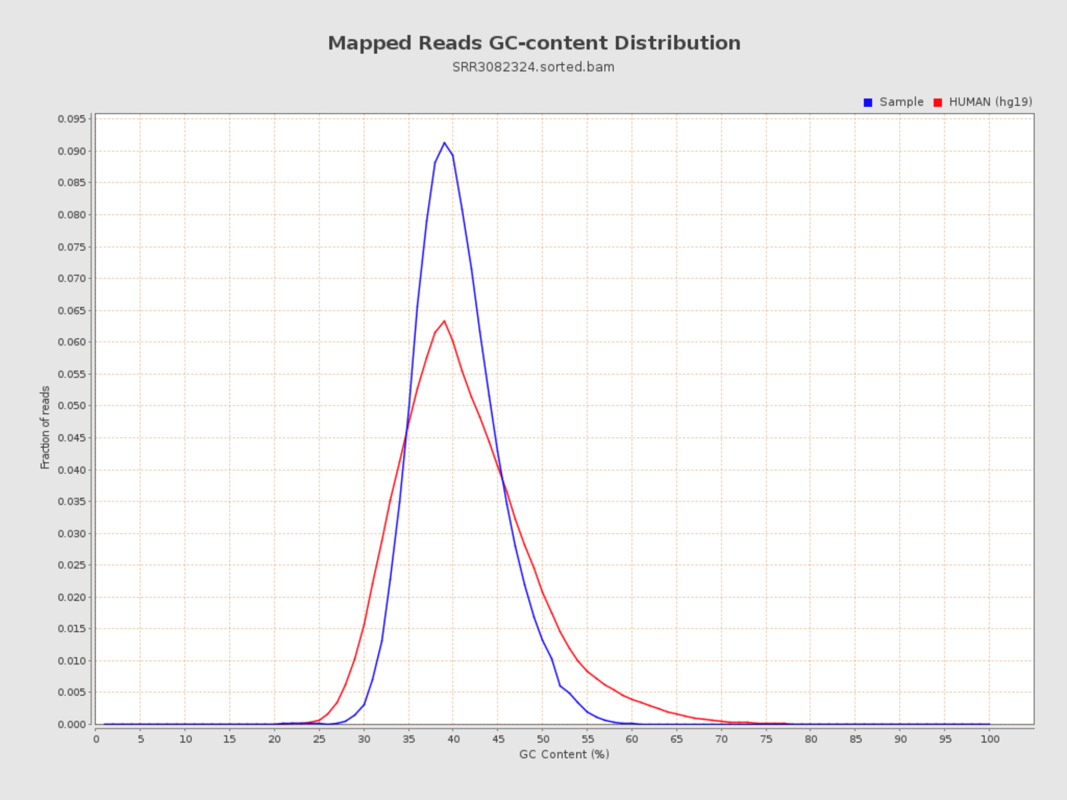
7. Results : Duplication Rate Histogram



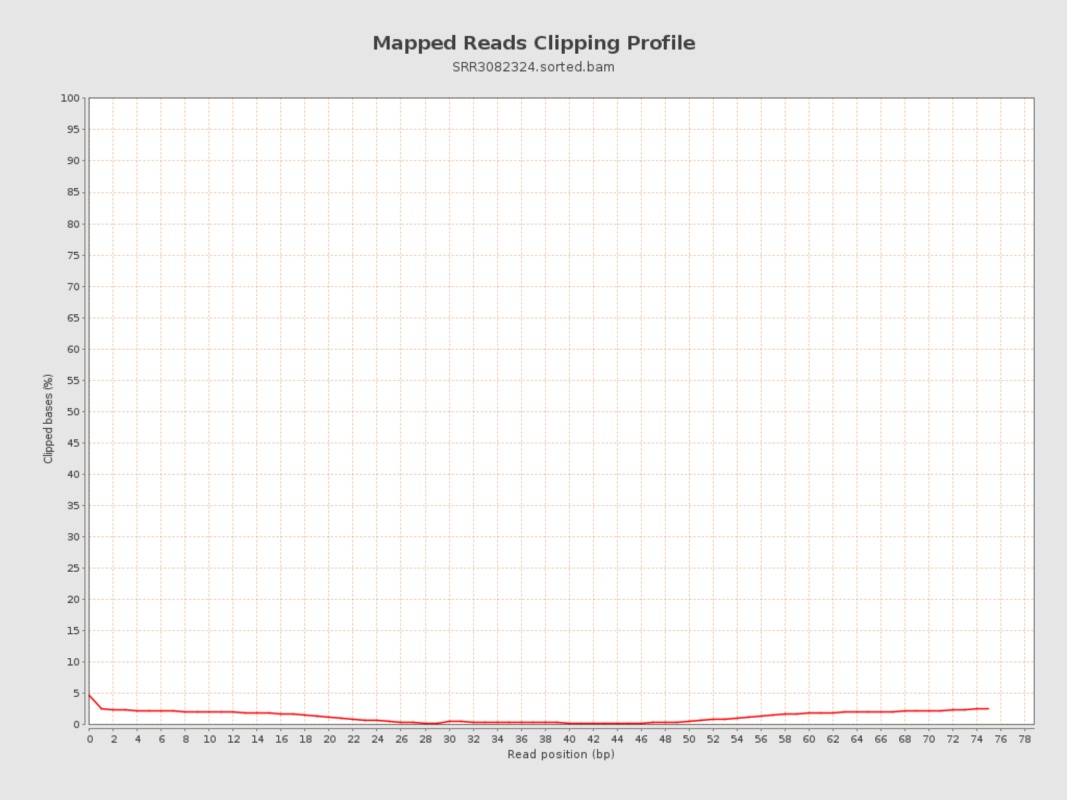
8. Results : Mapped Reads Nucleotide Content



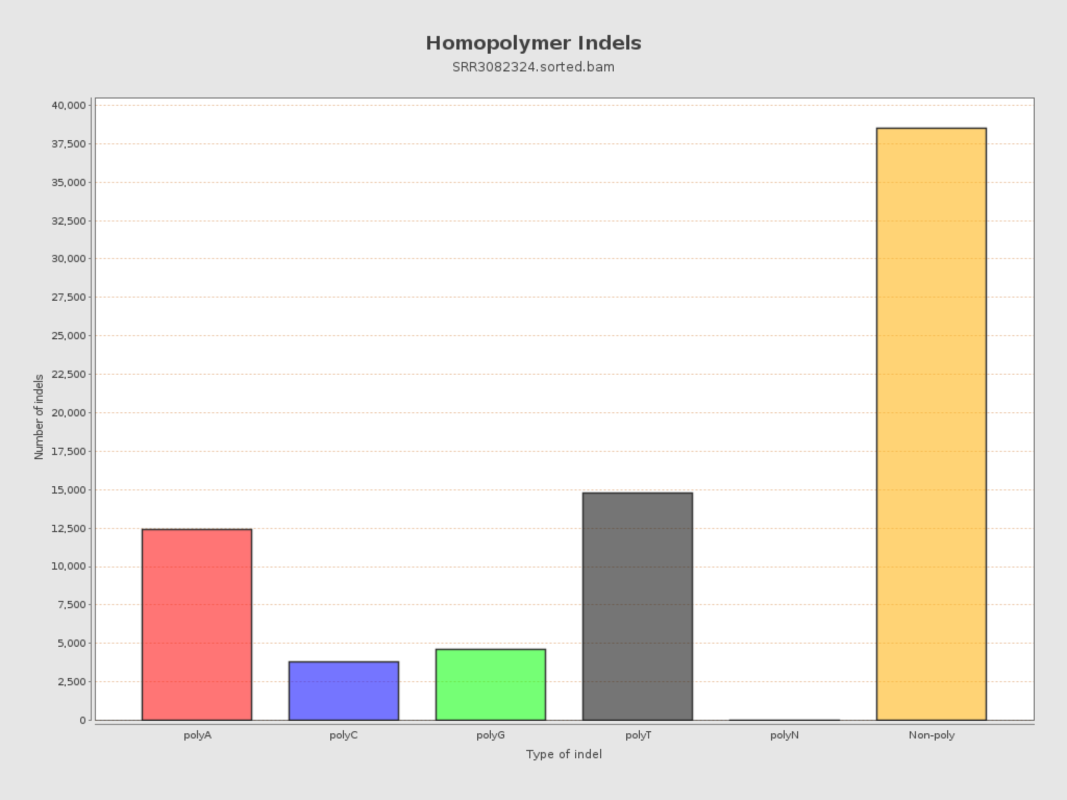
9. Results : Mapped Reads GC-content Distribution



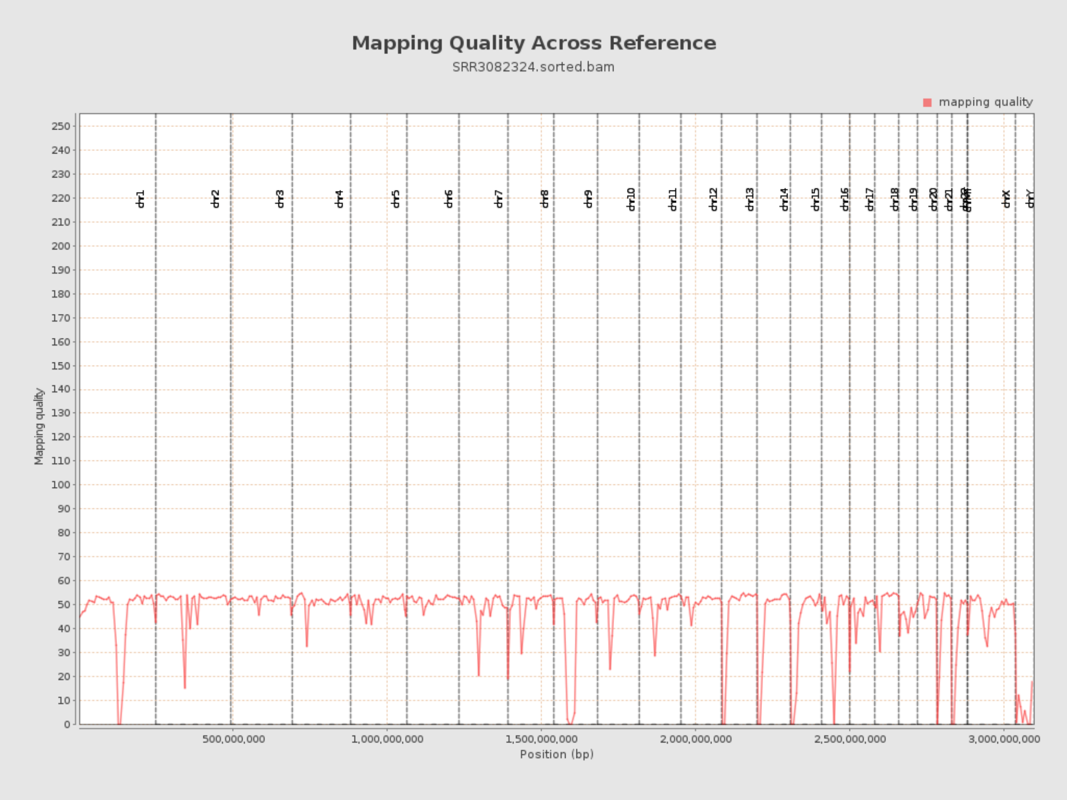
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram