Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:40:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082325.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_SRR3082325 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082325.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:40:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082325.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,849,002
Mapped reads	2,559,364 / 89.83%
Unmapped reads	289,638 / 10.17%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,625 / 0.93%
Read min/max/mean length	30 / 76 / 76.33
Duplicated reads (estimated)	111,739 / 3.92%
Duplication rate	3.31%
Clipped reads	1,075,796 / 37.76%

2.2. ACGT Content

Number/percentage of A's	48,928,310 / 28.21%
Number/percentage of C's	32,469,780 / 18.72%
Number/percentage of T's	54,262,450 / 31.29%
Number/percentage of G's	37,772,329 / 21.78%
Number/percentage of N's	3,410 / 0%
GC Percentage	40.5%

2.3. Coverage

Mean	0.056

Standard Deviation	0.4846

2.4. Mapping Quality

Mean Mapping Quality	46.96

2.5. Mismatches and indels

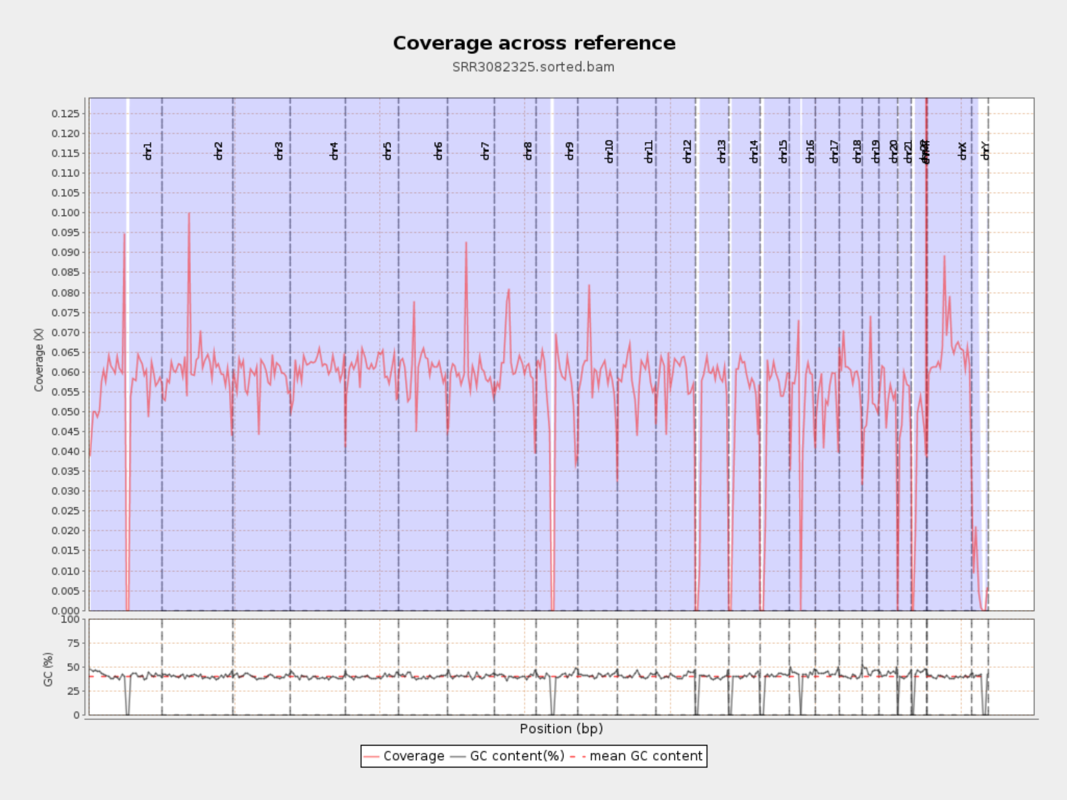
General error rate	0.84%
Mismatches	1,438,119
Insertions	13,370
Mapped reads with at least one insertion	0.52%
Deletions	37,500
Mapped reads with at least one deletion	1.45%
Homopolymer indels	47.42%

2.6. Chromosome stats

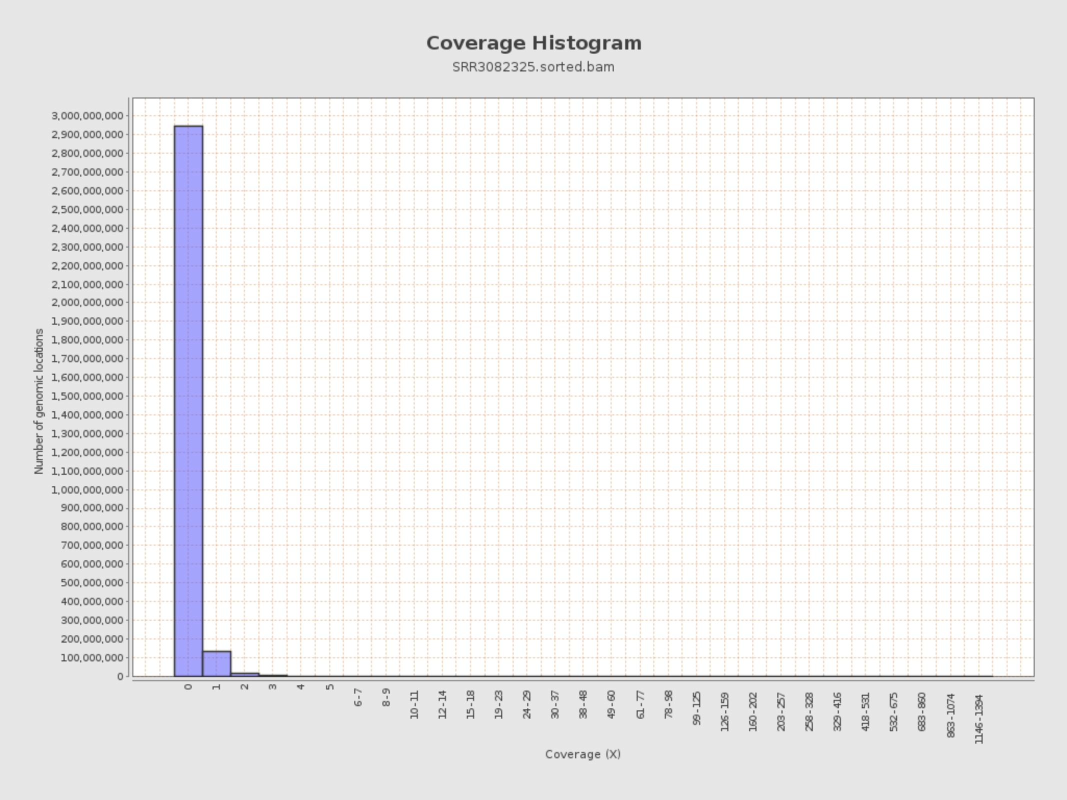
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	13733989	0.0551	0.8878
chr2	243199373	14917983	0.0613	0.5524
chr3	198022430	11691135	0.059	0.2737
chr4	191154276	11647614	0.0609	0.2895
chr5	180915260	11023310	0.0609	0.2811
chr6	171115067	10370953	0.0606	0.3349
chr7	159138663	9606311	0.0604	0.5964

chr8	146364022	8958733	0.0612	0.8891
chr9	141213431	7333482	0.0519	0.434
chr10	135534747	8126998	0.06	0.4181
chr11	135006516	7862108	0.0582	0.4028
chr12	133851895	7864960	0.0588	0.2808
chr13	115169878	5664562	0.0492	0.249
chr14	107349540	5220948	0.0486	0.2753
chr15	102531392	4856058	0.0474	0.25
chr16	90354753	4626186	0.0512	0.2821
chr17	81195210	4270324	0.0526	0.2911
chr18	78077248	4728484	0.0606	0.7797
chr19	59128983	3090053	0.0523	0.6521
chr20	63025520	3420583	0.0543	0.2706
chr21	48129895	2238347	0.0465	0.2614
chr22	51304566	1752830	0.0342	0.2058
chrMT	16571	7474	0.451	0.8117
chrX	155270560	10060520	0.0648	0.3303
chrY	59373566	422983	0.0071	0.1519

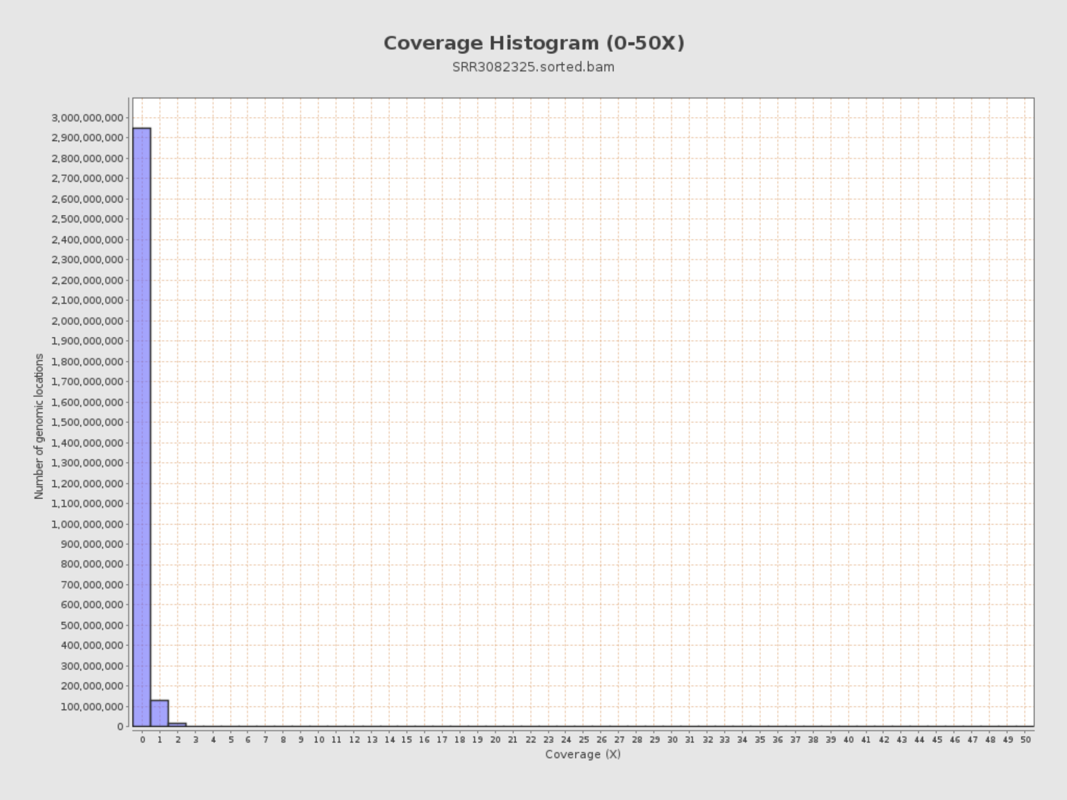
3. Results : Coverage across reference



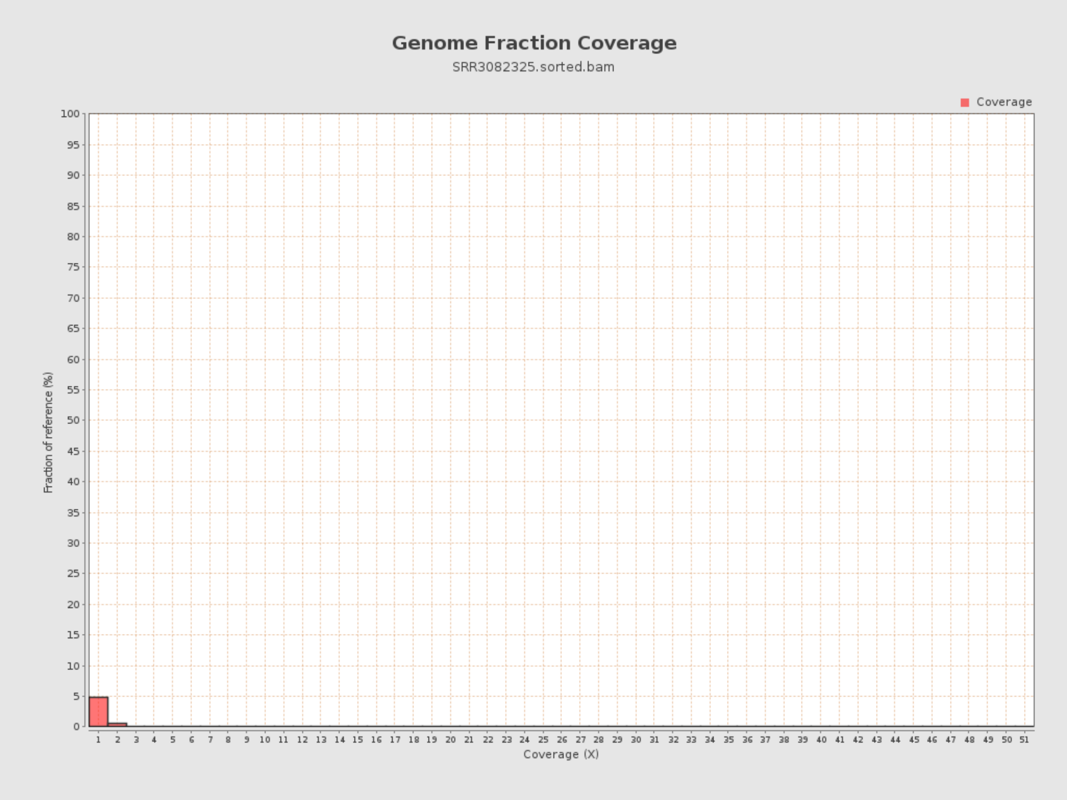
4. Results : Coverage Histogram



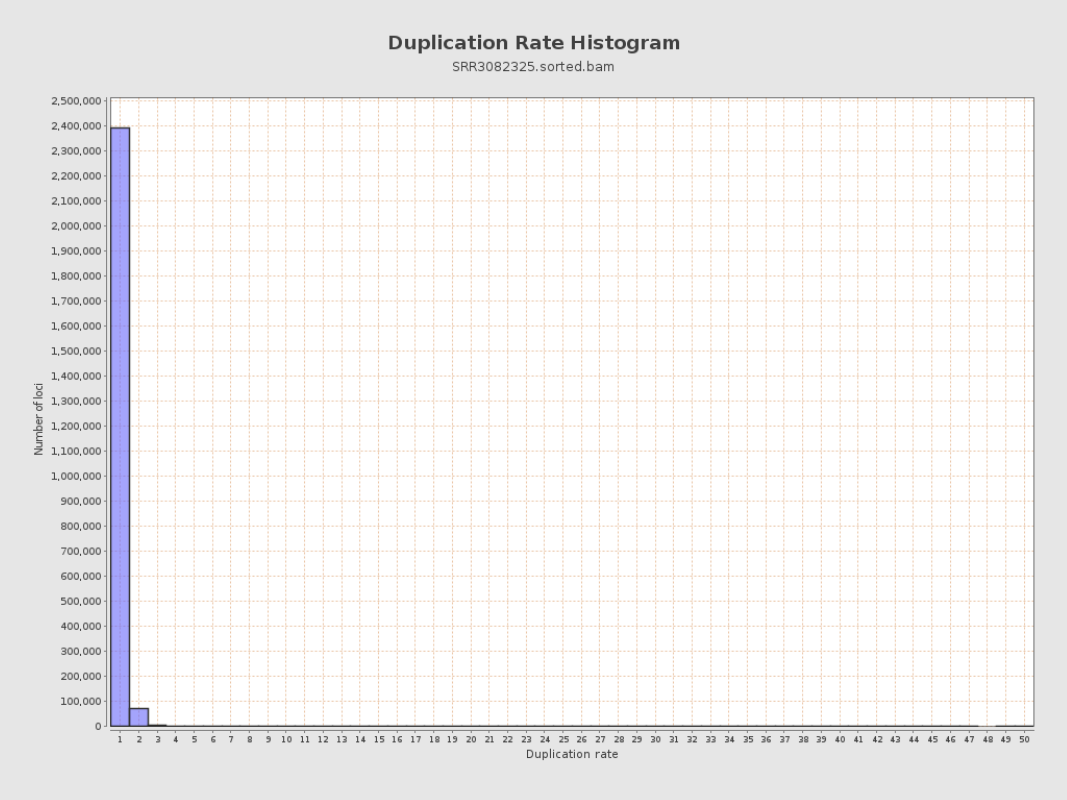
5. Results : Coverage Histogram (0-50X)



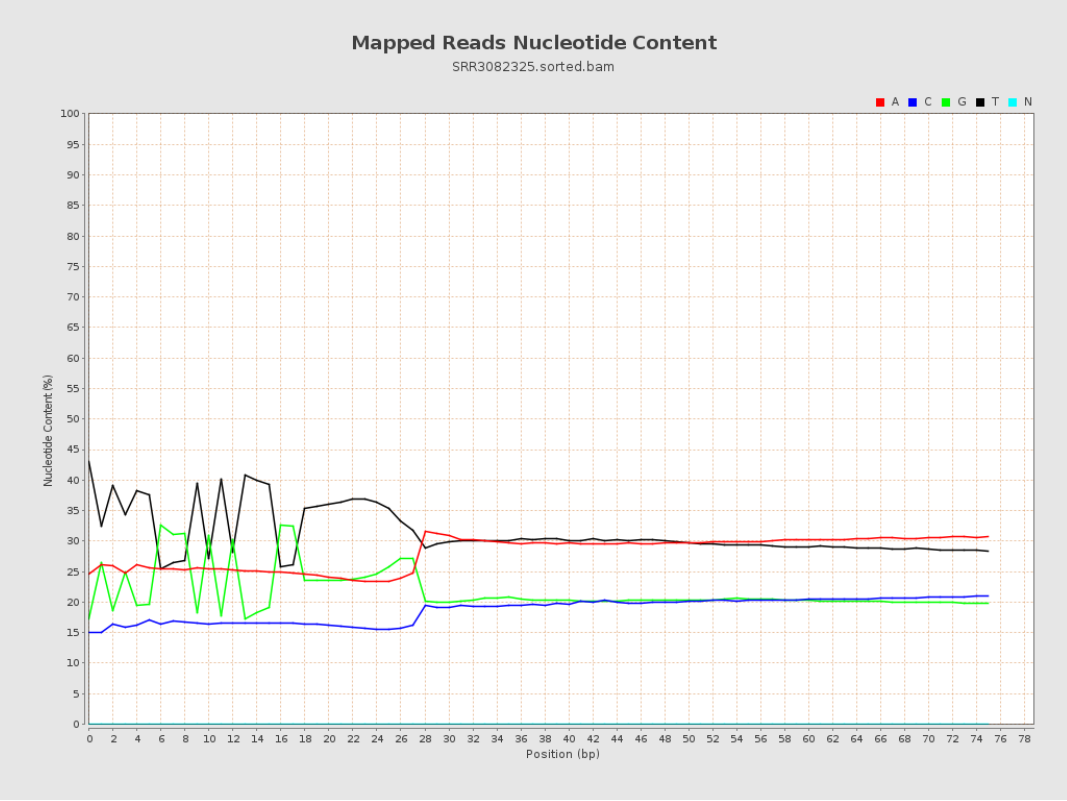
6. Results : Genome Fraction Coverage



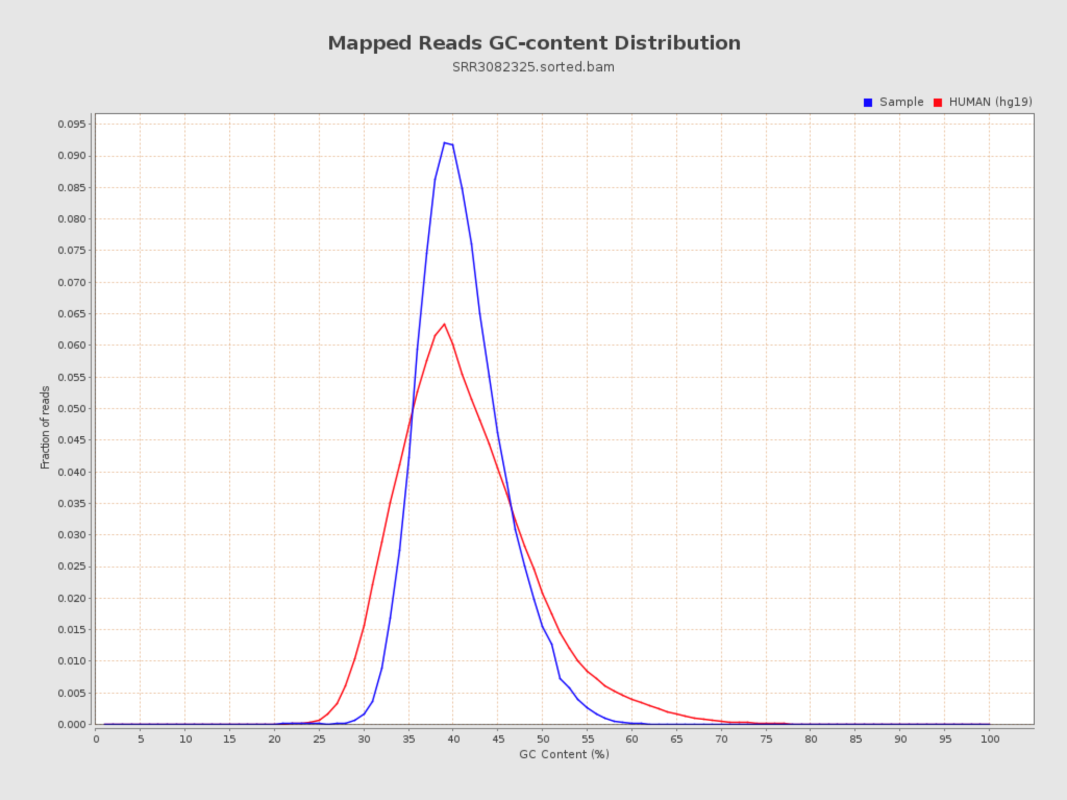
7. Results : Duplication Rate Histogram



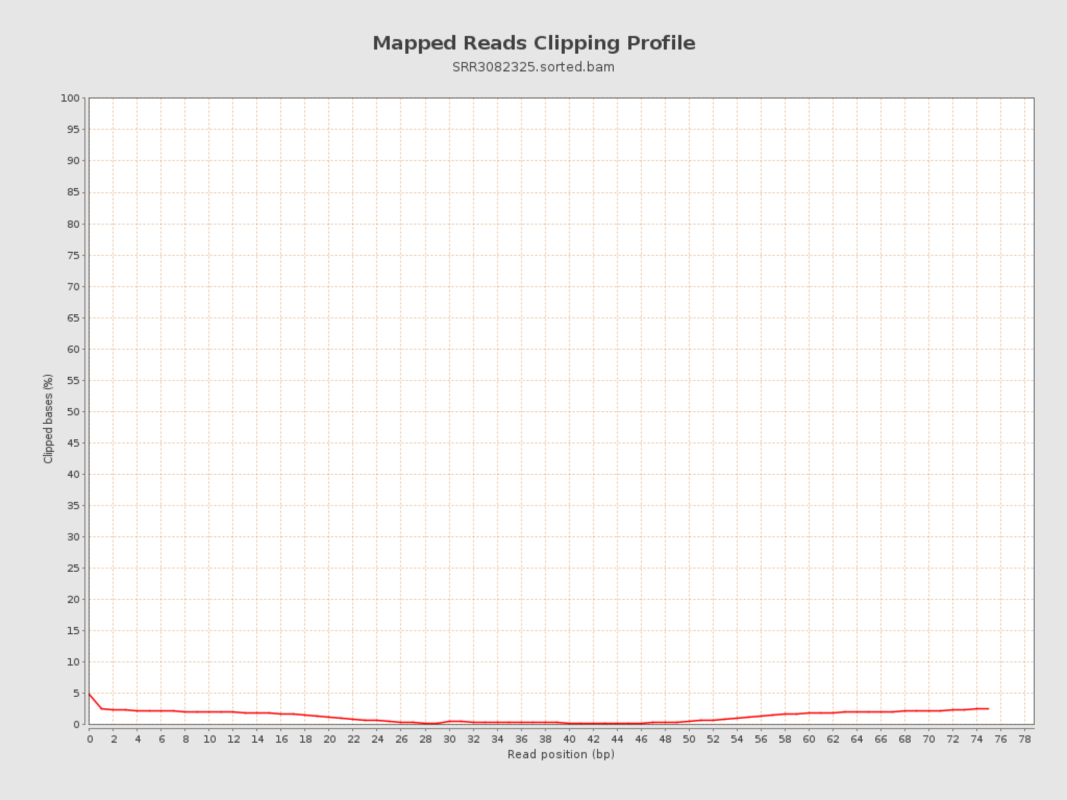
8. Results : Mapped Reads Nucleotide Content



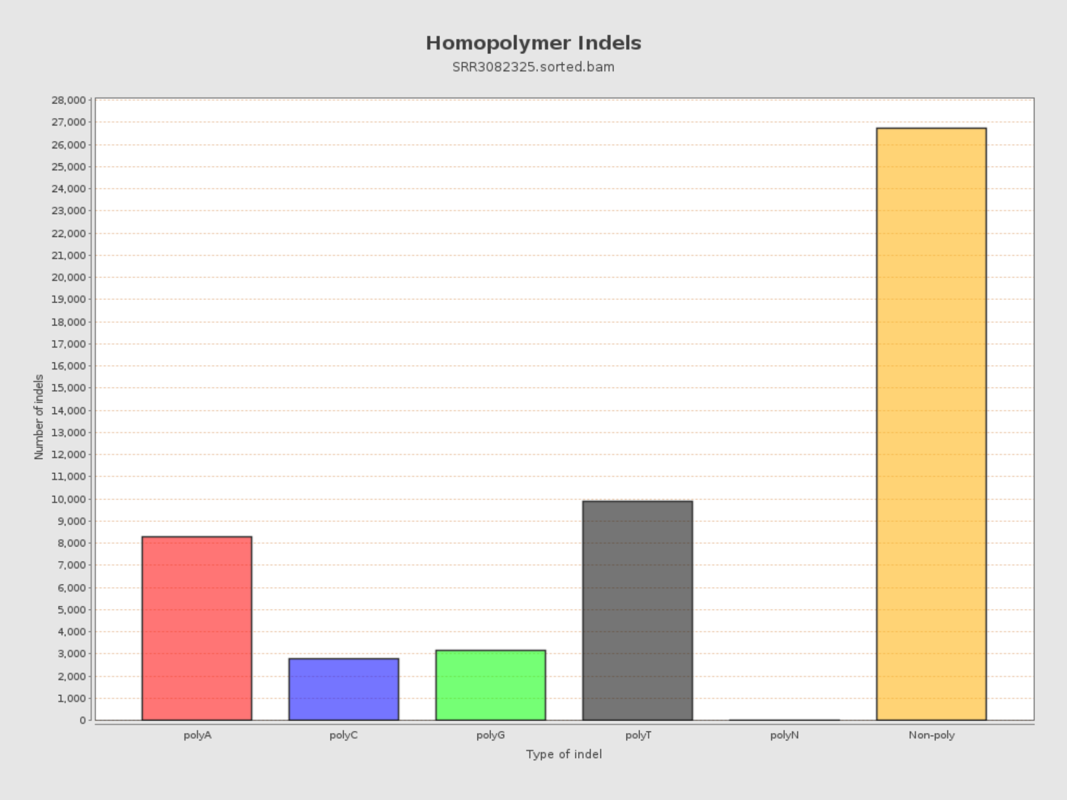
9. Results : Mapped Reads GC-content Distribution



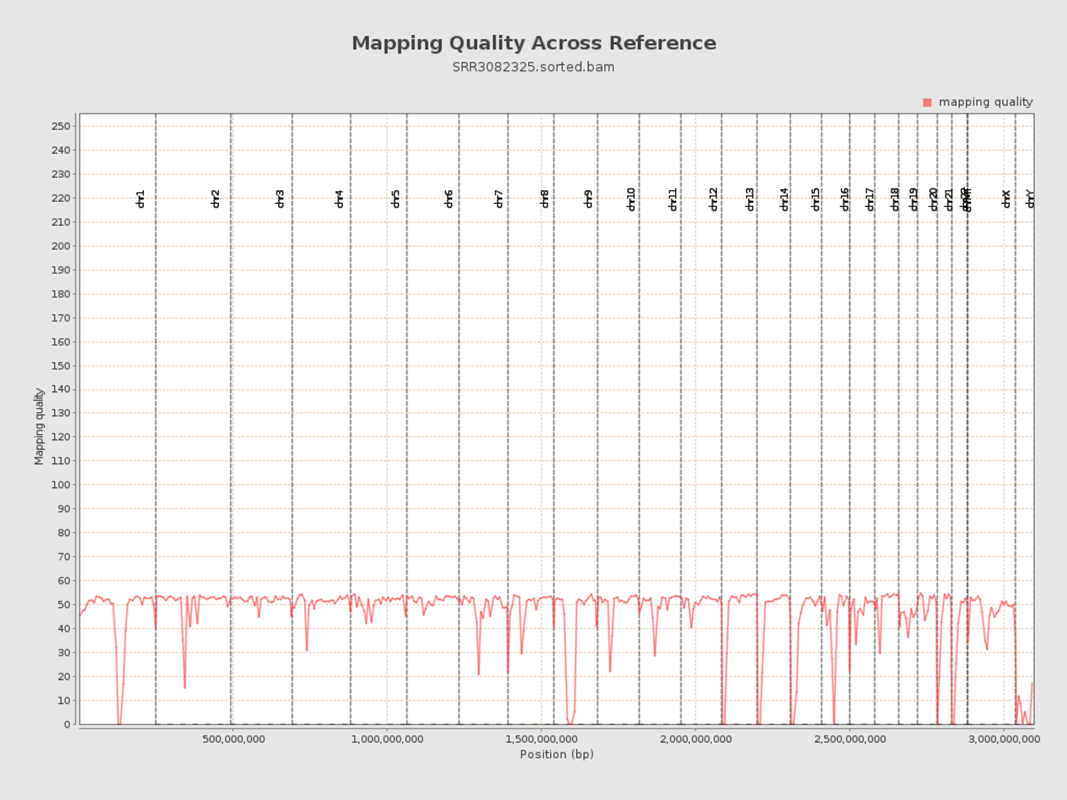
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram