Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:45:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082326.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_SRR3082326 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082326.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:45:05 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082326.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,228,269
Mapped reads	1,996,253 / 89.59%
Unmapped reads	232,016 / 10.41%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	18,360 / 0.82%
Read min/max/mean length	30 / 76 / 76.29
Duplicated reads (estimated)	66,270 / 2.97%
Duplication rate	2.67%
Clipped reads	881,984 / 39.58%

2.2. ACGT Content

Number/percentage of A's	37,774,675 / 28.15%
Number/percentage of C's	24,934,588 / 18.58%
Number/percentage of T's	41,941,736 / 31.26%
Number/percentage of G's	29,529,679 / 22.01%
Number/percentage of N's	2,732 / 0%
GC Percentage	40.59%

2.3. Coverage

Mean	0.0434

Standard Deviation	0.3298

2.4. Mapping Quality

Mean Mapping Quality	46.34

2.5. Mismatches and indels

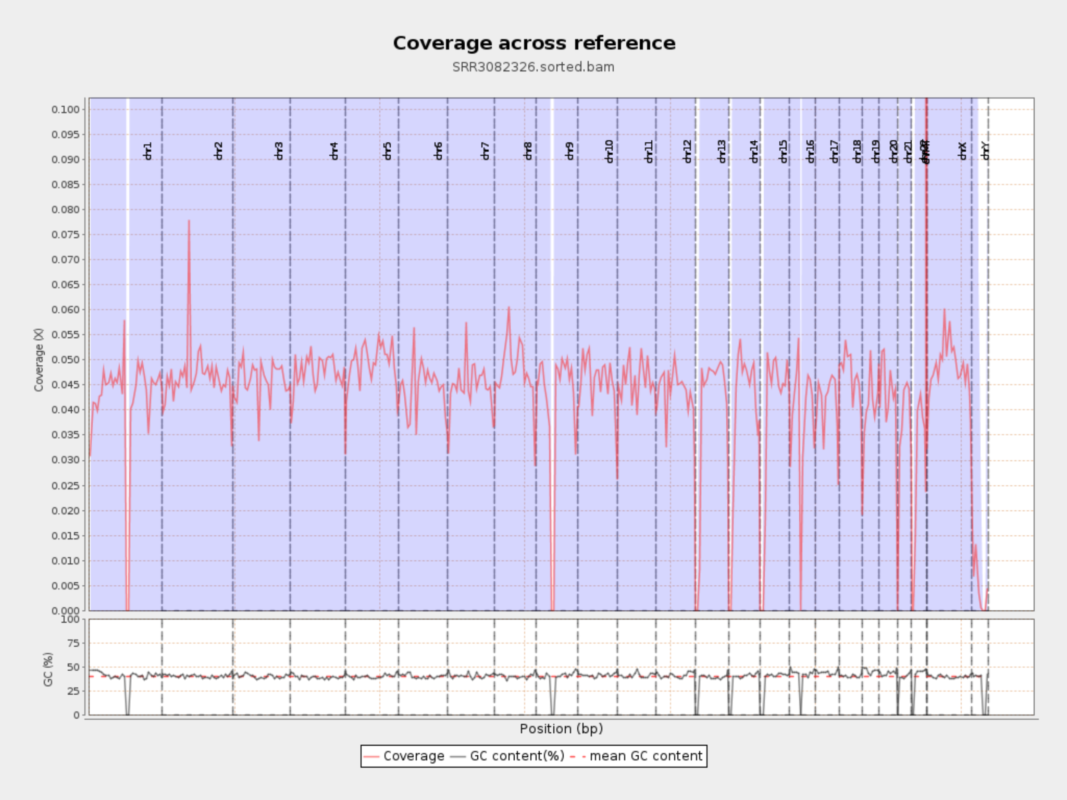
General error rate	0.84%
Mismatches	1,104,345
Insertions	10,517
Mapped reads with at least one insertion	0.52%
Deletions	29,062
Mapped reads with at least one deletion	1.44%
Homopolymer indels	47.87%

2.6. Chromosome stats

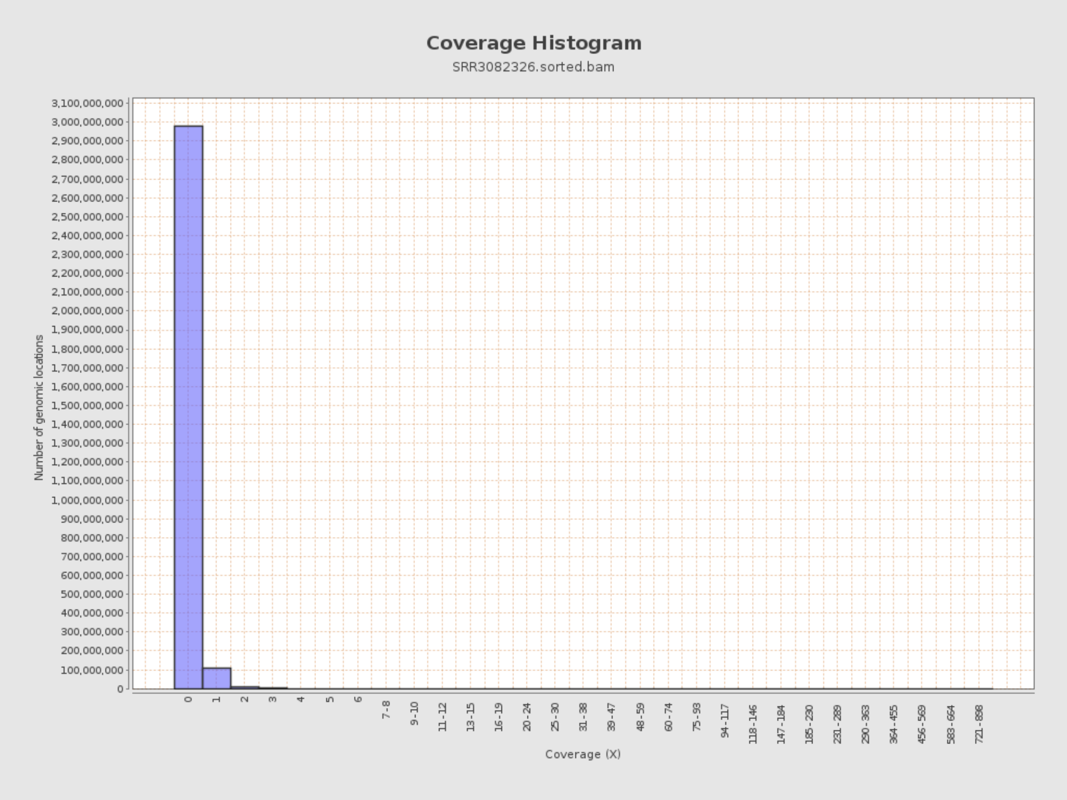
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	10457342	0.042	0.4845
chr2	243199373	11445132	0.0471	0.4469
chr3	198022430	9134138	0.0461	0.2365
chr4	191154276	9107964	0.0476	0.2446
chr5	180915260	8978801	0.0496	0.2455
chr6	171115067	7622650	0.0445	0.2651
chr7	159138663	7186228	0.0452	0.3503

chr8	146364022	7004094	0.0479	0.5909
chr9	141213431	5733518	0.0406	0.3016
chr10	135534747	6277357	0.0463	0.2849
chr11	135006516	6186985	0.0458	0.2902
chr12	133851895	5872162	0.0439	0.2328
chr13	115169878	4494485	0.039	0.2187
chr14	107349540	4152429	0.0387	0.225
chr15	102531392	3931608	0.0383	0.2191
chr16	90354753	3450422	0.0382	0.2292
chr17	81195210	3349604	0.0413	0.2337
chr18	78077248	3709809	0.0475	0.4885
chr19	59128983	2419835	0.0409	0.3791
chr20	63025520	2751208	0.0437	0.2342
chr21	48129895	1724065	0.0358	0.2163
chr22	51304566	1384846	0.027	0.18
chrMT	16571	37269	2.249	1.849
chrX	155270560	7523286	0.0485	0.2612
chrY	59373566	294865	0.005	0.1007

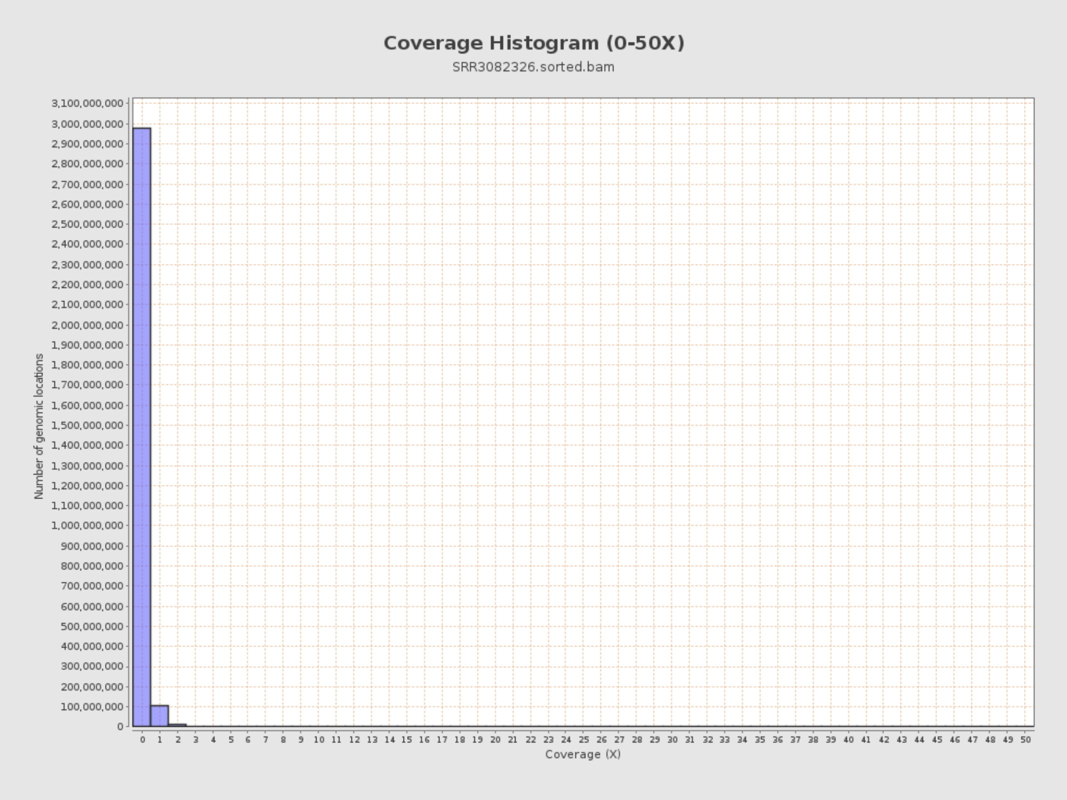
3. Results : Coverage across reference



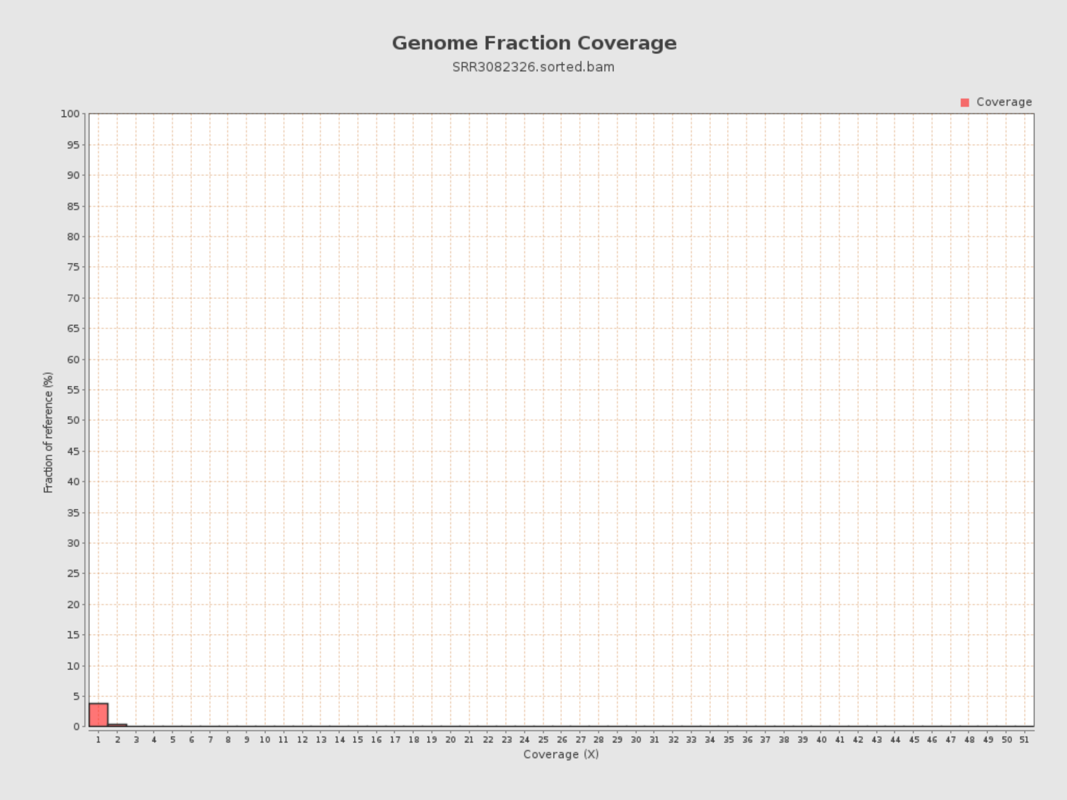
4. Results : Coverage Histogram



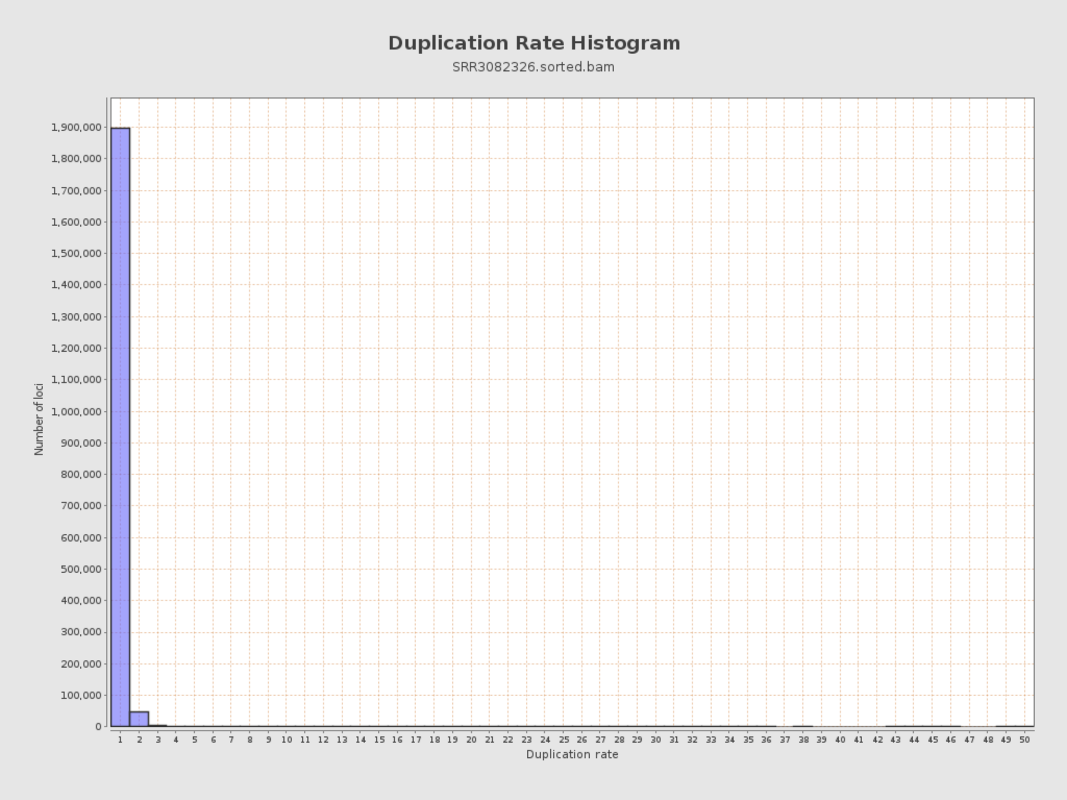
5. Results : Coverage Histogram (0-50X)



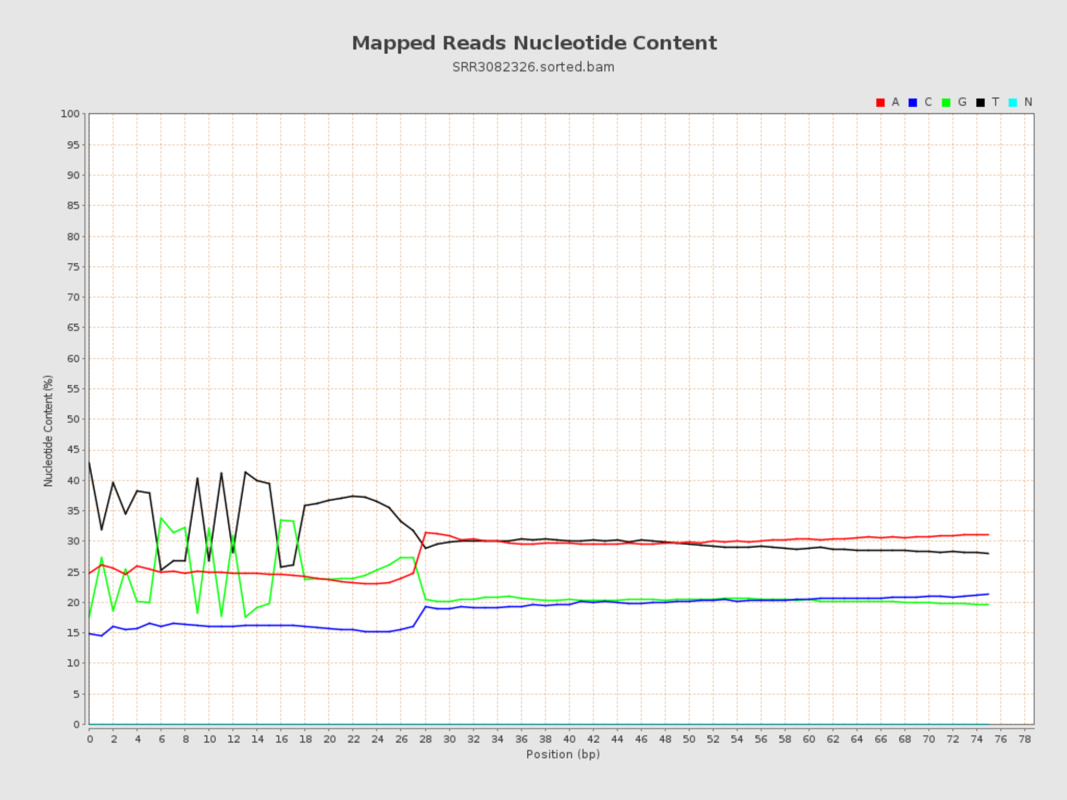
6. Results : Genome Fraction Coverage



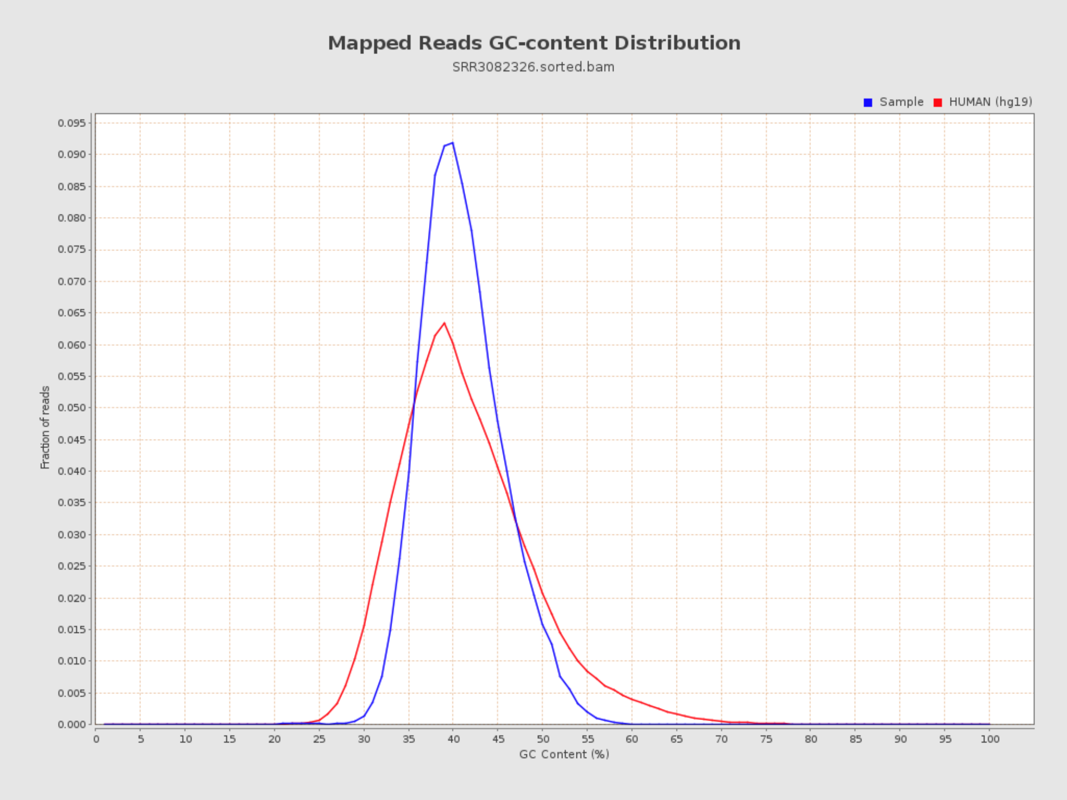
7. Results : Duplication Rate Histogram



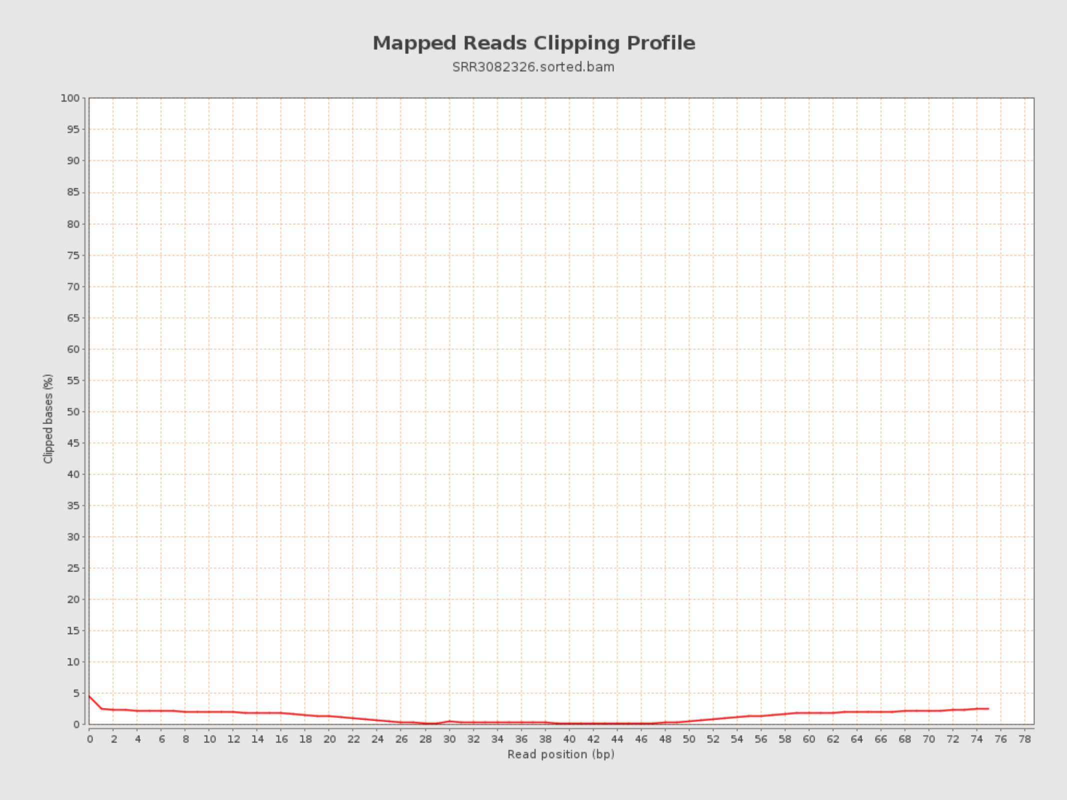
8. Results : Mapped Reads Nucleotide Content



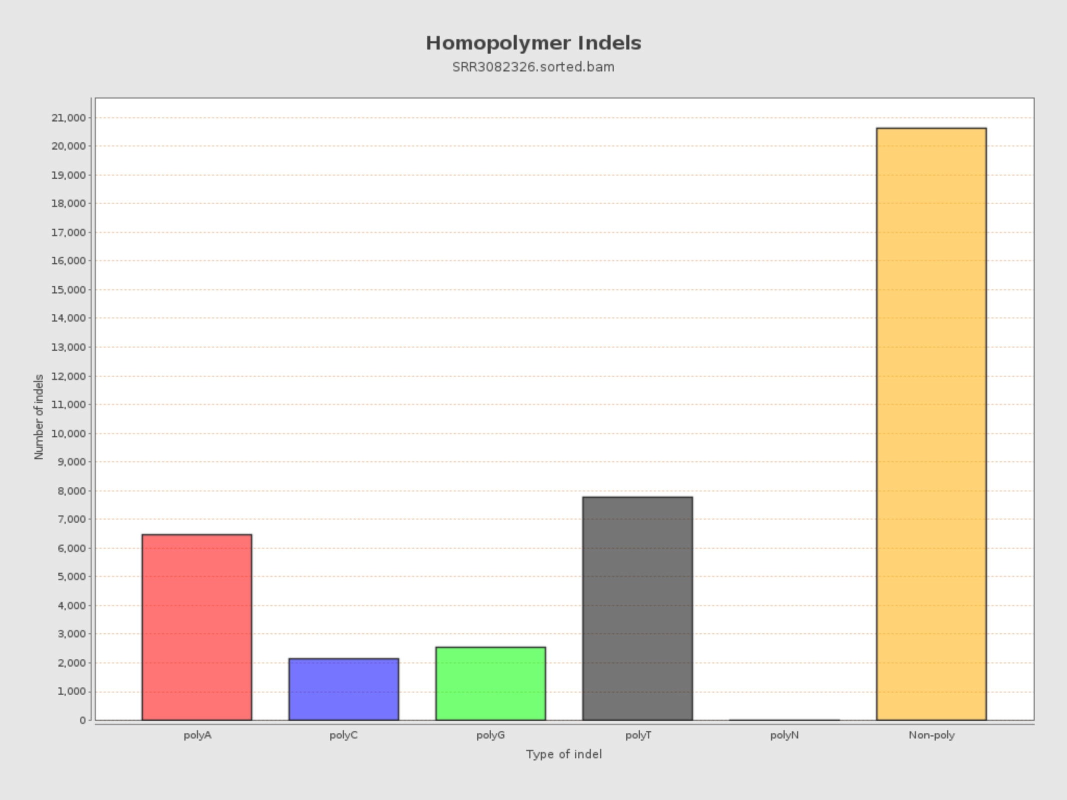
9. Results : Mapped Reads GC-content Distribution



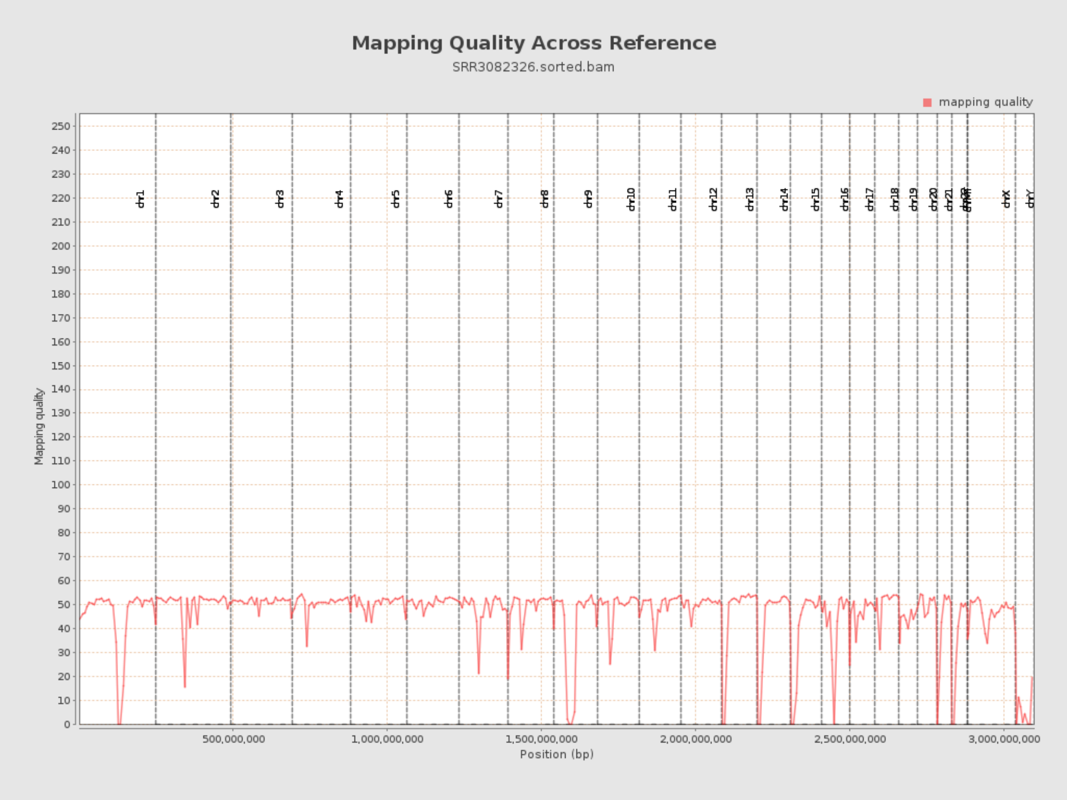
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram