Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 16:17:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082682.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_SRR3082682 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082682.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 16:17:18 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082682.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,365,891
Mapped reads	3,142,624 / 93.37%
Unmapped reads	223,267 / 6.63%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,086 / 0.45%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	121,587 / 3.61%
Duplication rate	2.9%
Clipped reads	1,464,116 / 43.5%

2.2. ACGT Content

Number/percentage of A's	57,744,265 / 27.62%
Number/percentage of C's	36,148,119 / 17.29%
Number/percentage of T's	69,393,711 / 33.19%
Number/percentage of G's	45,721,971 / 21.87%
Number/percentage of N's	56,869 / 0.03%
GC Percentage	39.16%

2.3. Coverage

Mean	0.0676

Standard Deviation	0.515

2.4. Mapping Quality

Mean Mapping Quality	46.84

2.5. Mismatches and indels

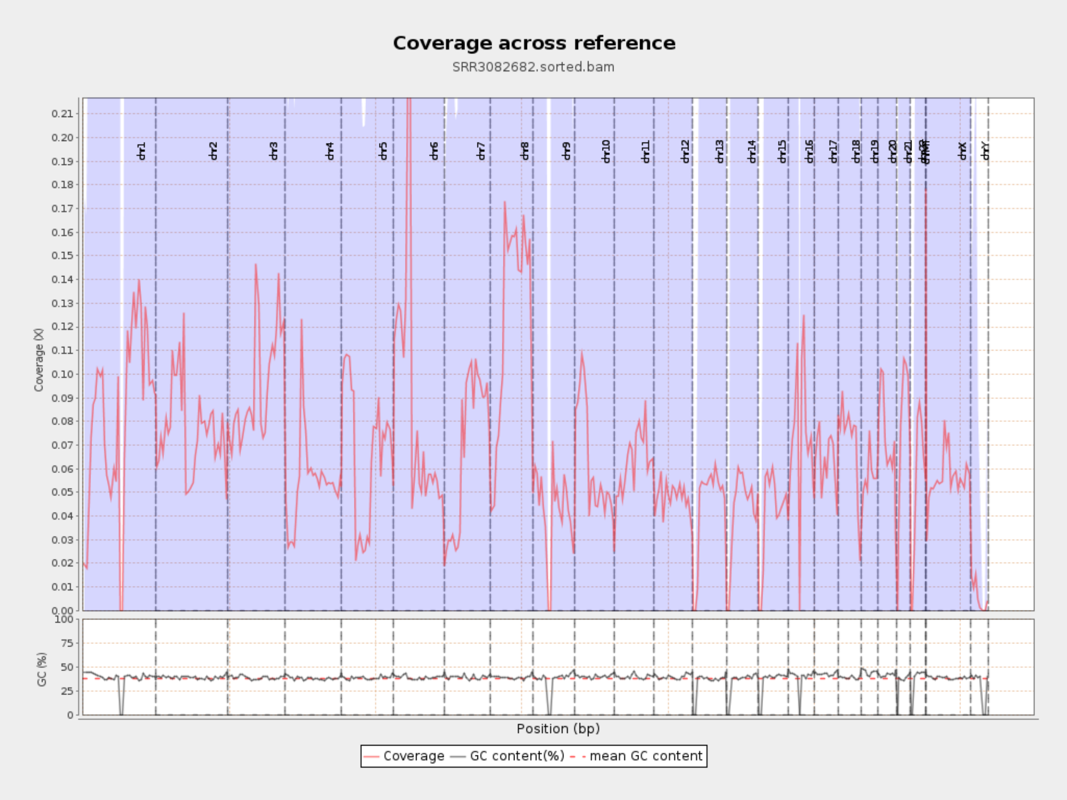
General error rate	0.91%
Mismatches	1,872,936
Insertions	18,420
Mapped reads with at least one insertion	0.58%
Deletions	49,371
Mapped reads with at least one deletion	1.56%
Homopolymer indels	49.15%

2.6. Chromosome stats

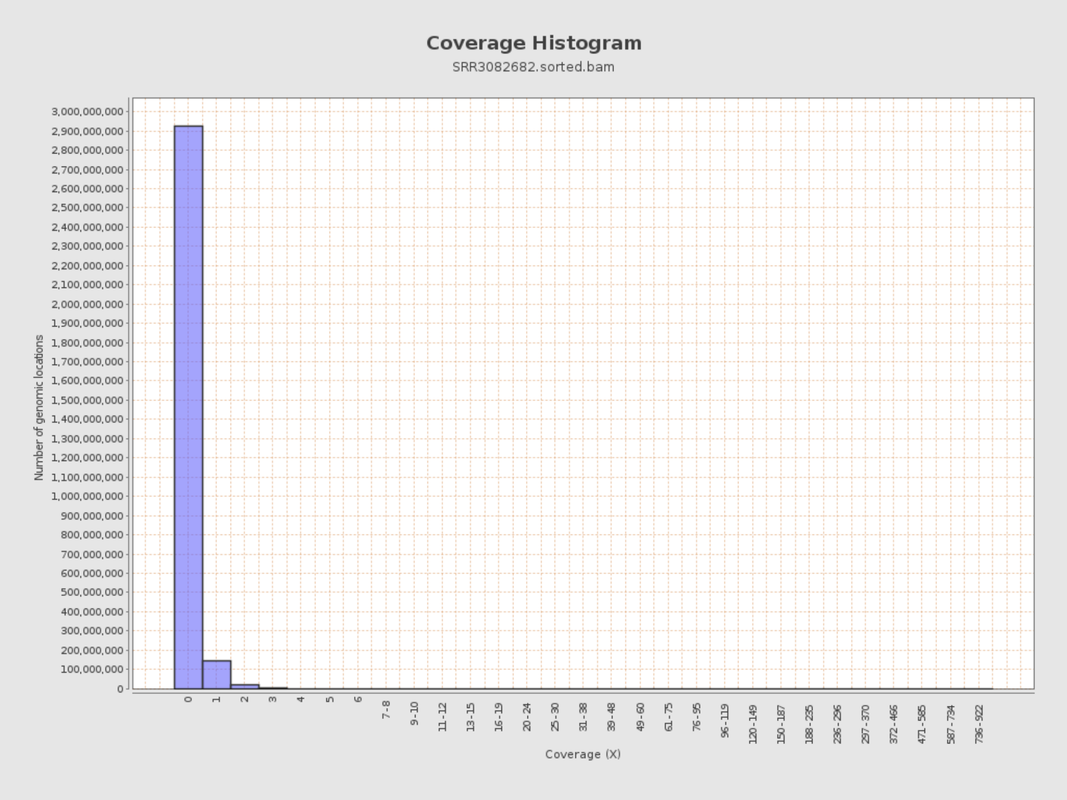
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	20514985	0.0823	0.8946
chr2	243199373	18687462	0.0768	0.6332
chr3	198022430	18630884	0.0941	0.3591
chr4	191154276	10546002	0.0552	0.277
chr5	180915260	11976002	0.0662	0.3003
chr6	171115067	15261837	0.0892	0.6271
chr7	159138663	10925068	0.0687	0.6522

chr8	146364022	18340440	0.1253	0.572
chr9	141213431	5990854	0.0424	0.4957
chr10	135534747	8575047	0.0633	0.4282
chr11	135006516	8487911	0.0629	0.4382
chr12	133851895	6427171	0.048	0.2575
chr13	115169878	5133492	0.0446	0.2399
chr14	107349540	4547654	0.0424	0.2754
chr15	102531392	4140114	0.0404	0.2292
chr16	90354753	6580823	0.0728	0.3535
chr17	81195210	5255655	0.0647	0.3718
chr18	78077248	5640926	0.0722	1.089
chr19	59128983	3359791	0.0568	0.5798
chr20	63025520	4700858	0.0746	0.3347
chr21	48129895	3614117	0.0751	0.3326
chr22	51304566	2742004	0.0534	0.2666
chrMT	16571	2954	0.1783	0.4352
chrX	155270560	8721370	0.0562	0.3292
chrY	59373566	341175	0.0057	0.1159

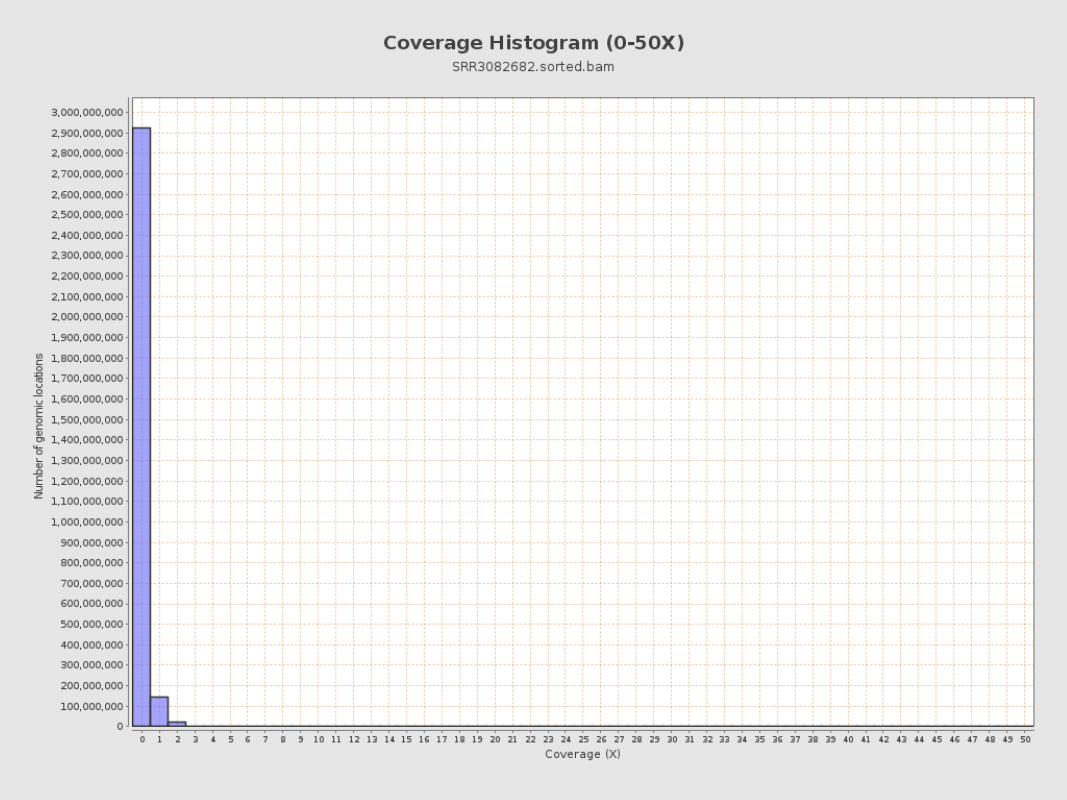
3. Results : Coverage across reference



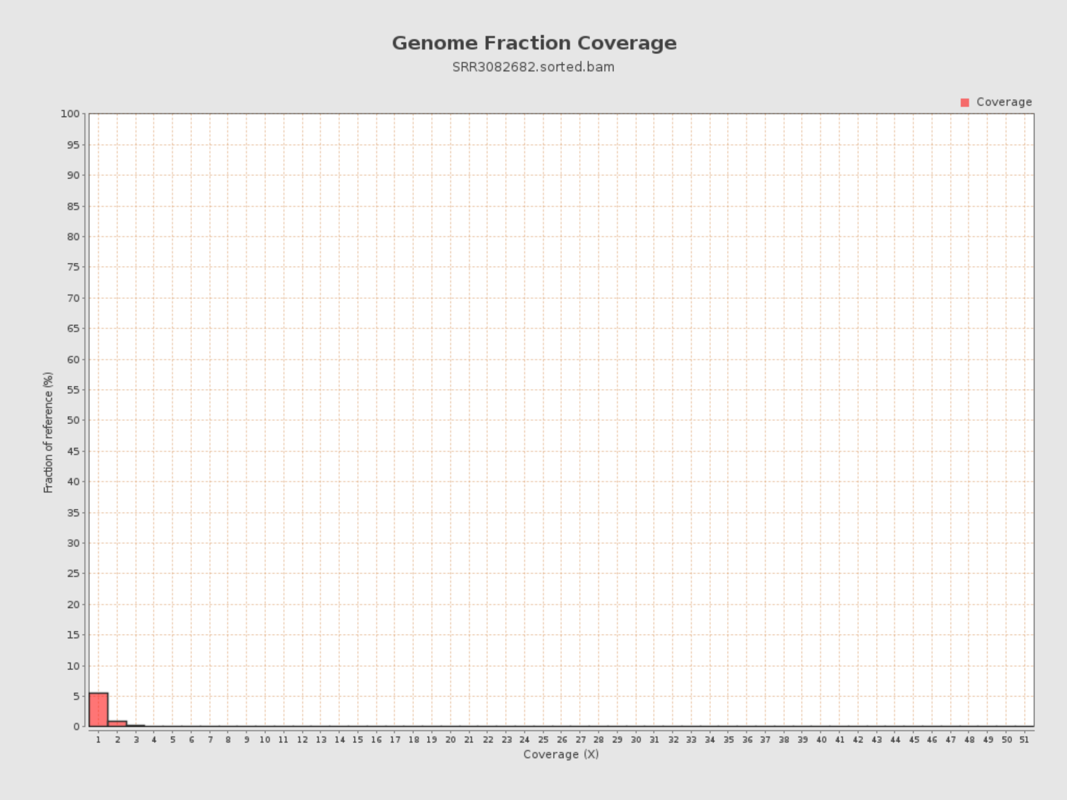
4. Results : Coverage Histogram



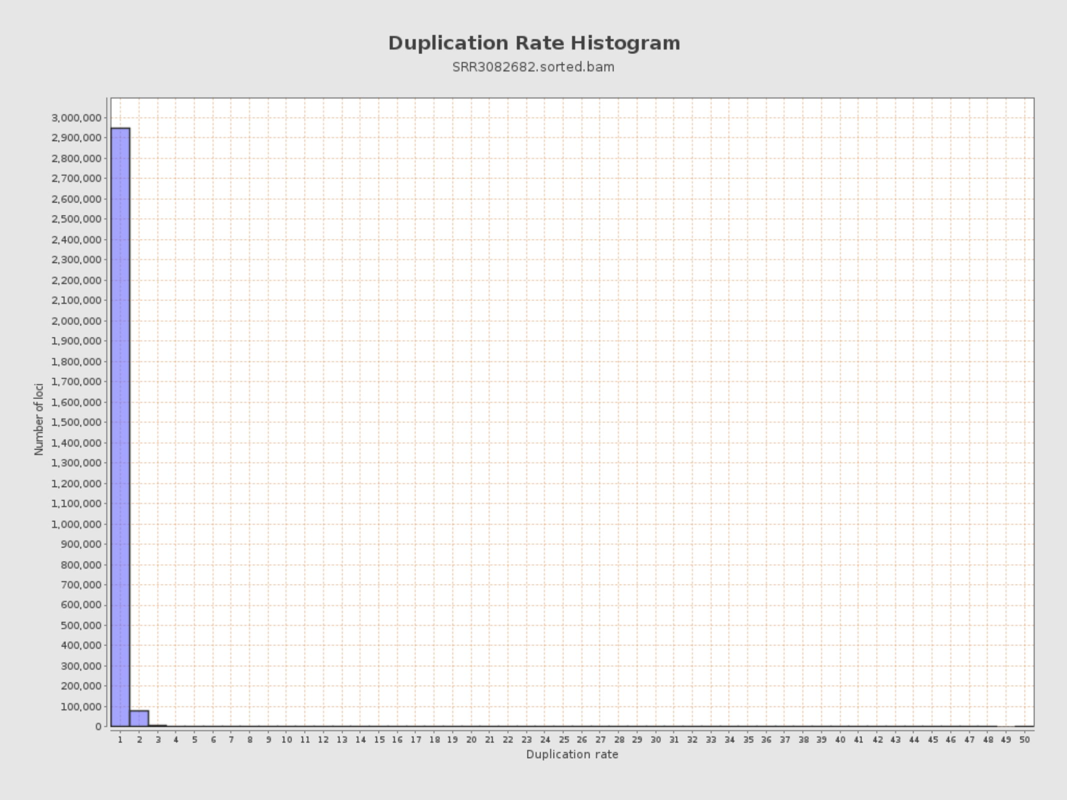
5. Results : Coverage Histogram (0-50X)



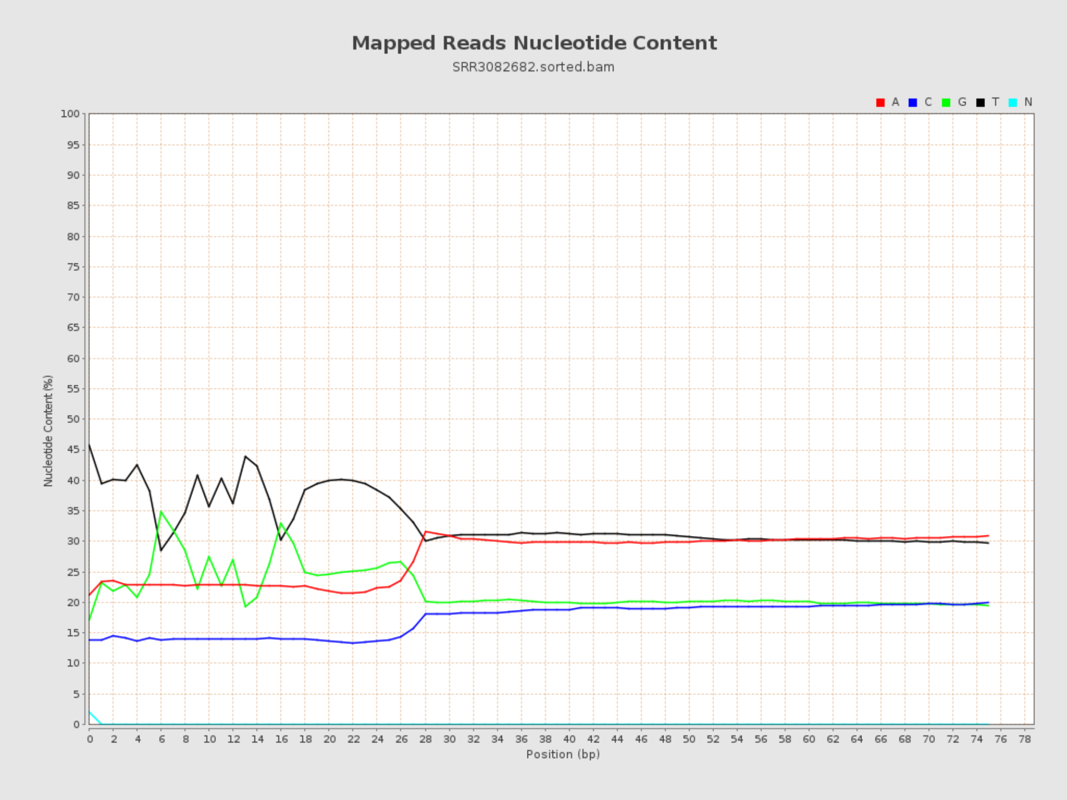
6. Results : Genome Fraction Coverage



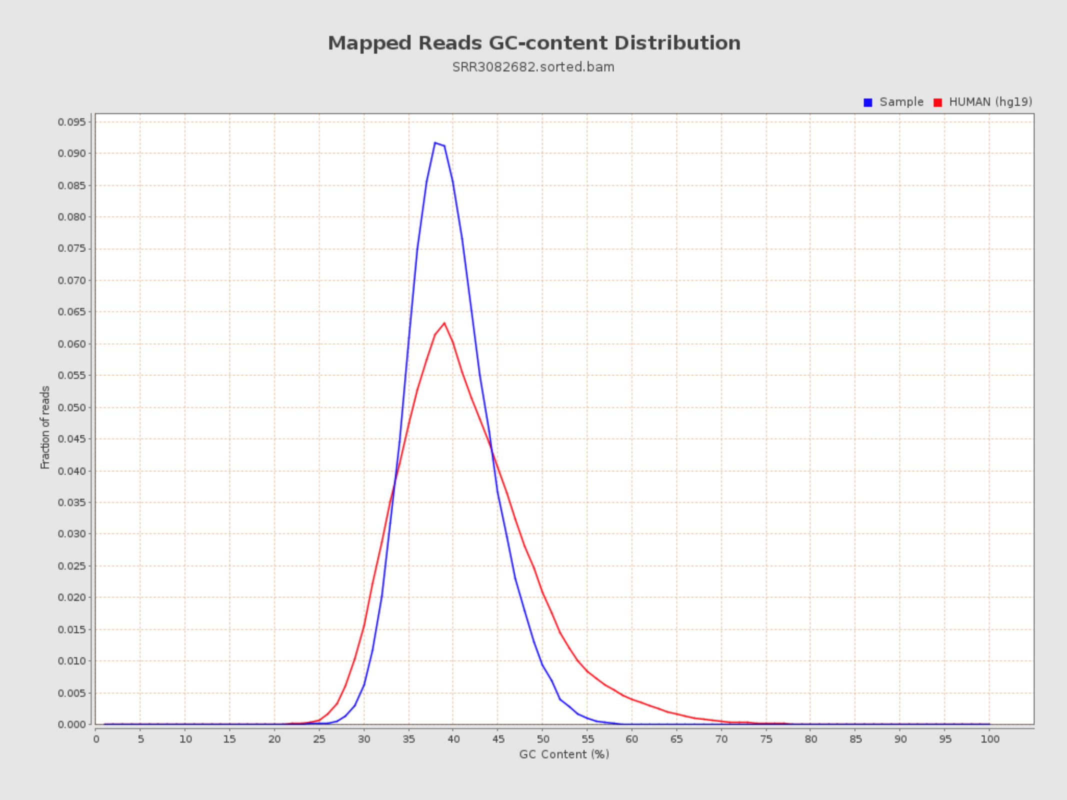
7. Results : Duplication Rate Histogram



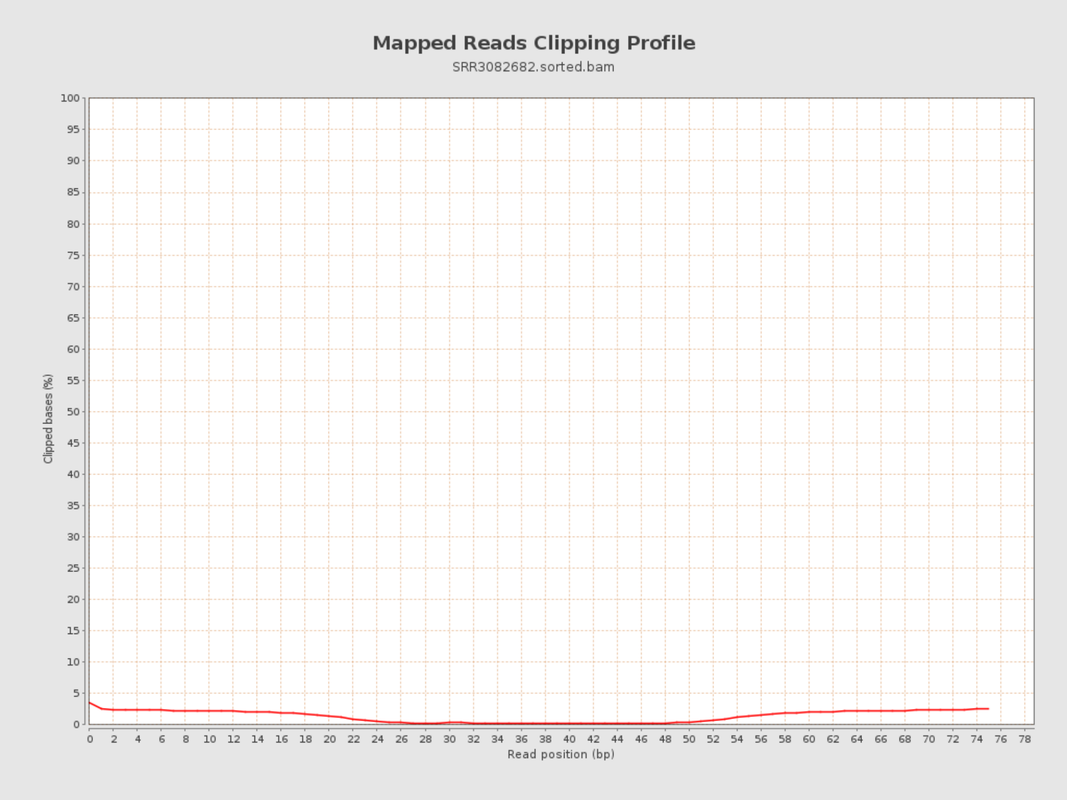
8. Results : Mapped Reads Nucleotide Content



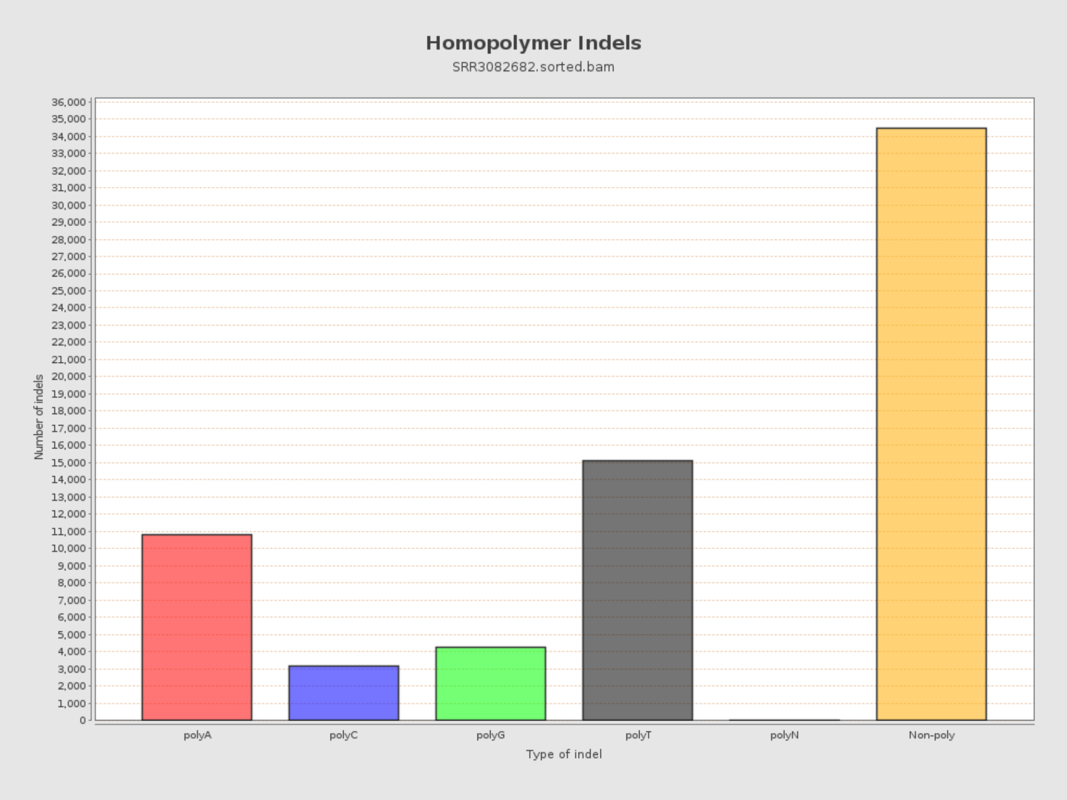
9. Results : Mapped Reads GC-content Distribution



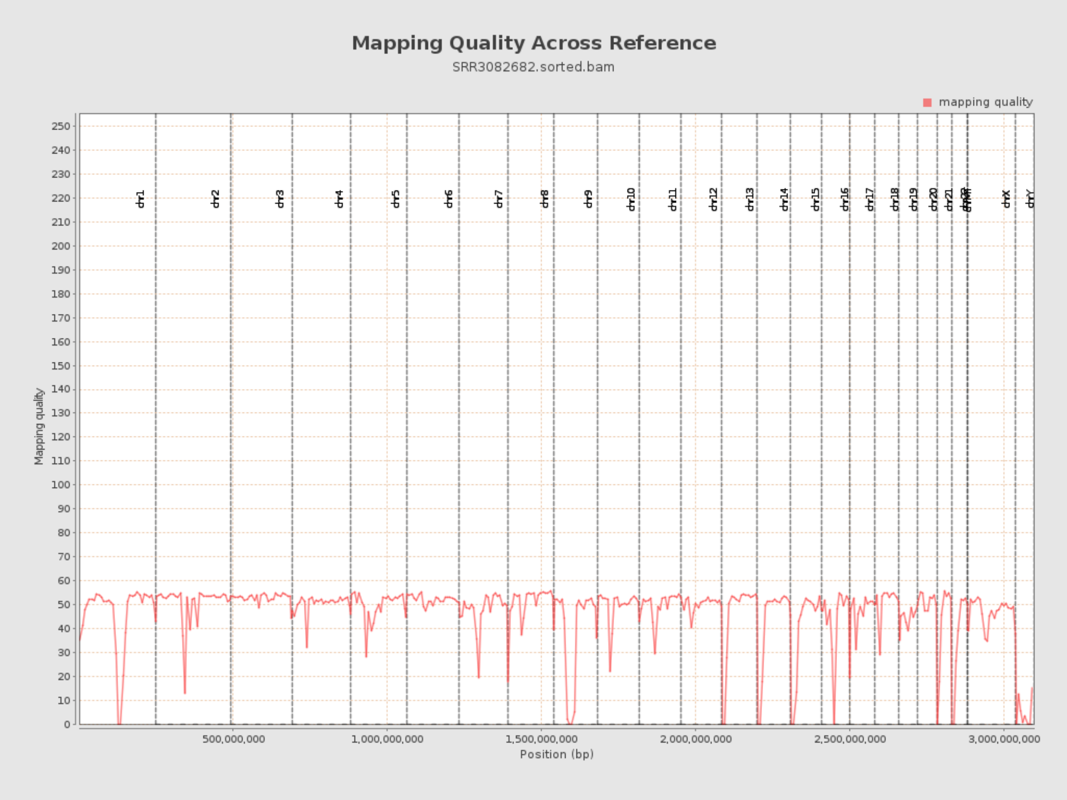
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram