Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:57:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082982.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_SRR3082982 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082982.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:57:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082982.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,284,571
Mapped reads	2,389,887 / 72.76%
Unmapped reads	894,684 / 27.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,676 / 0.63%
Read min/max/mean length	30 / 76 / 76.22
Duplicated reads (estimated)	95,938 / 2.92%
Duplication rate	2.65%
Clipped reads	1,035,103 / 31.51%

2.2. ACGT Content

Number/percentage of A's	45,418,067 / 28.2%
Number/percentage of C's	29,448,832 / 18.29%
Number/percentage of T's	51,047,876 / 31.7%
Number/percentage of G's	35,120,506 / 21.81%
Number/percentage of N's	15,311 / 0.01%
GC Percentage	40.09%

2.3. Coverage

Mean	0.052

Standard Deviation	0.5097

2.4. Mapping Quality

Mean Mapping Quality	44.96

2.5. Mismatches and indels

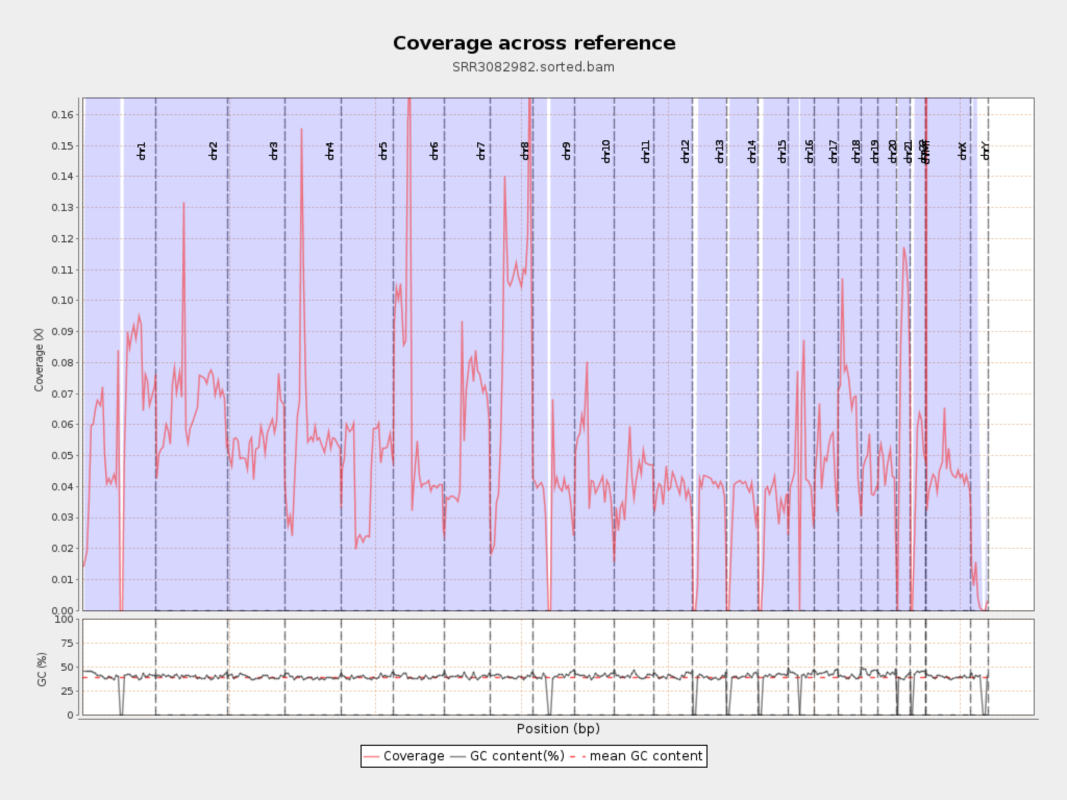
General error rate	1.05%
Mismatches	1,660,548
Insertions	15,513
Mapped reads with at least one insertion	0.64%
Deletions	40,578
Mapped reads with at least one deletion	1.68%
Homopolymer indels	47.37%

2.6. Chromosome stats

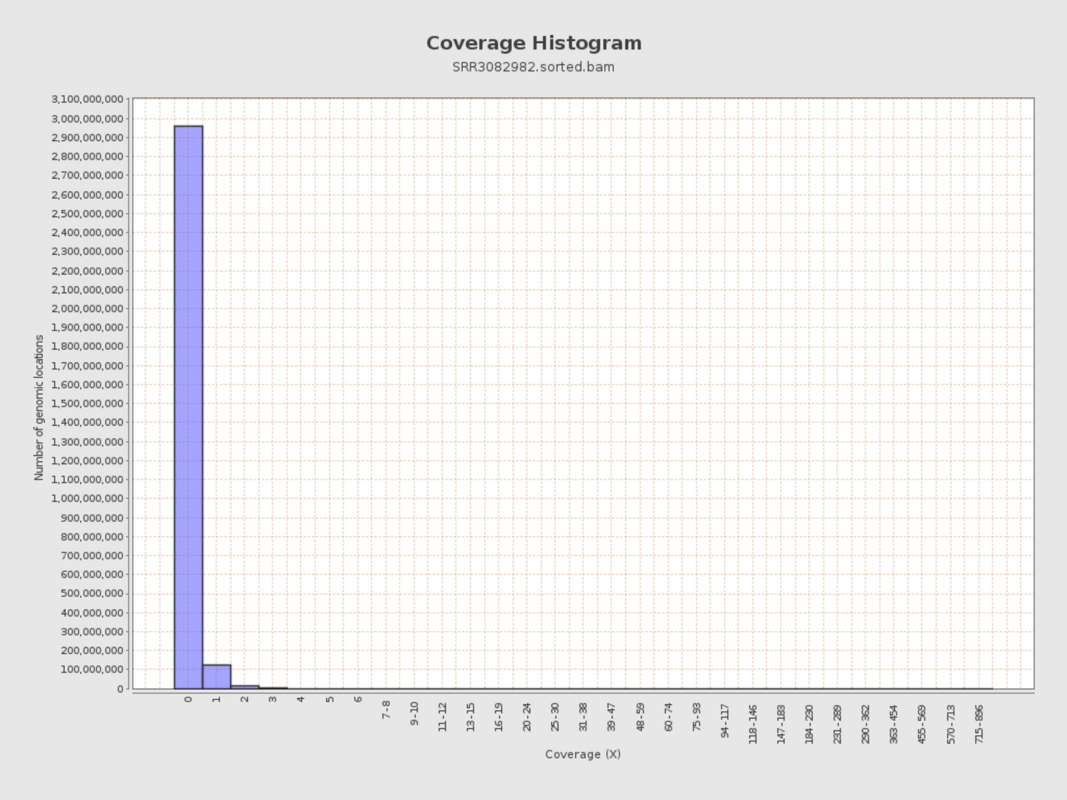
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	14895660	0.0598	0.8118
chr2	243199373	16534816	0.068	0.7058
chr3	198022430	10964178	0.0554	0.2658
chr4	191154276	11086921	0.058	0.2836
chr5	180915260	8094404	0.0447	0.2429
chr6	171115067	11394105	0.0666	0.4878
chr7	159138663	9559830	0.0601	0.6619

chr8	146364022	13472950	0.0921	0.595
chr9	141213431	5070511	0.0359	0.5089
chr10	135534747	6240070	0.046	0.381
chr11	135006516	5608672	0.0415	0.4051
chr12	133851895	5272118	0.0394	0.2428
chr13	115169878	3946455	0.0343	0.2056
chr14	107349540	3562015	0.0332	0.3153
chr15	102531392	3057230	0.0298	0.1936
chr16	90354753	4107950	0.0455	0.3483
chr17	81195210	4071083	0.0501	0.3435
chr18	78077248	5506157	0.0705	1.3274
chr19	59128983	2621334	0.0443	0.5695
chr20	63025520	2900221	0.046	0.2897
chr21	48129895	3865507	0.0803	0.3426
chr22	51304566	2075674	0.0405	0.225
chrMT	16571	50874	3.0701	3.1925
chrX	155270560	6840965	0.0441	0.3398
chrY	59373566	321400	0.0054	0.1218

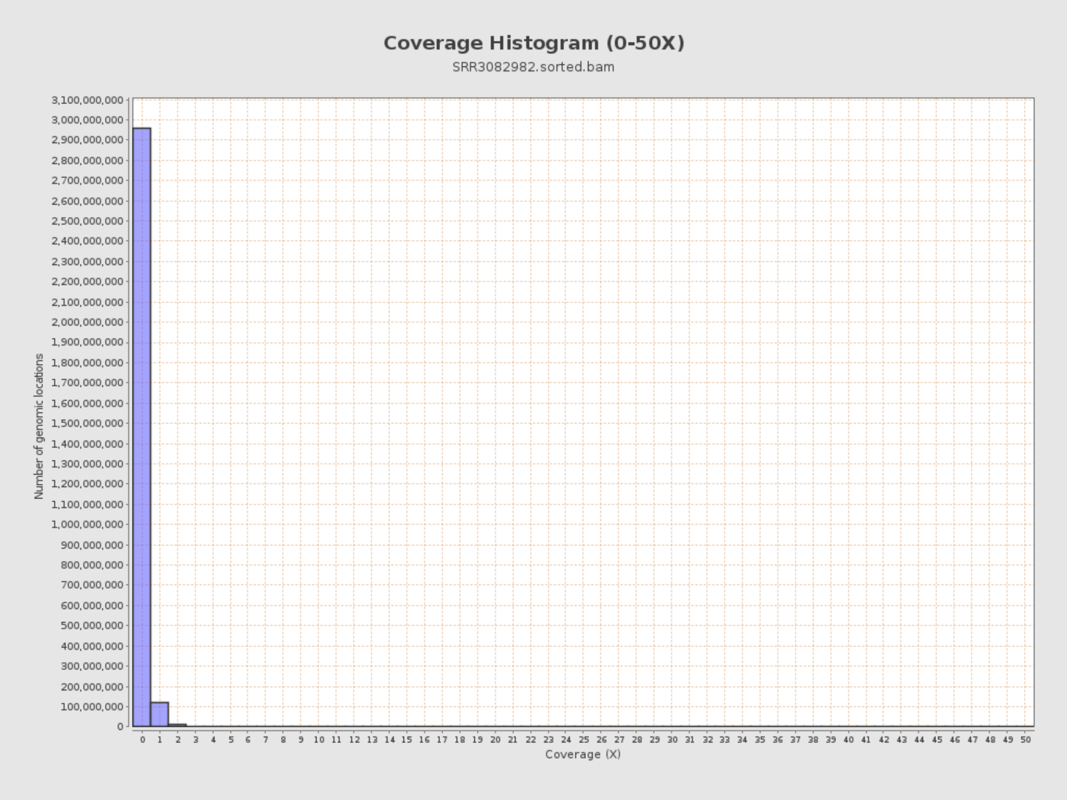
3. Results : Coverage across reference



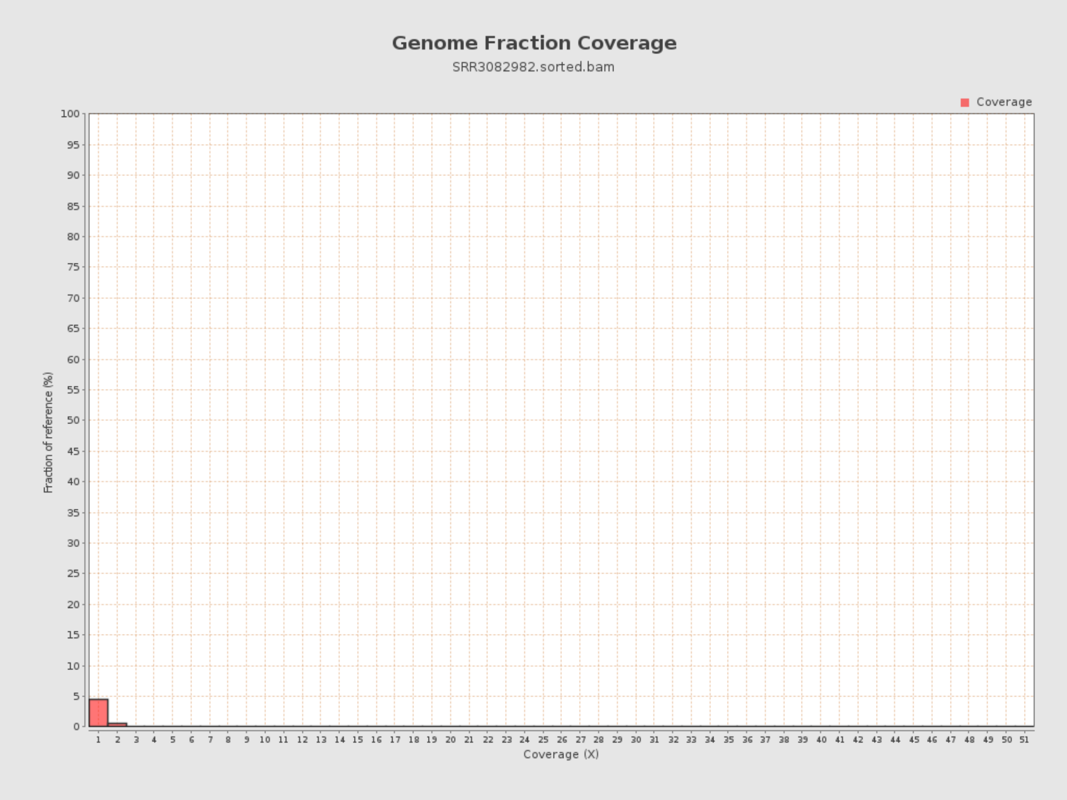
4. Results : Coverage Histogram



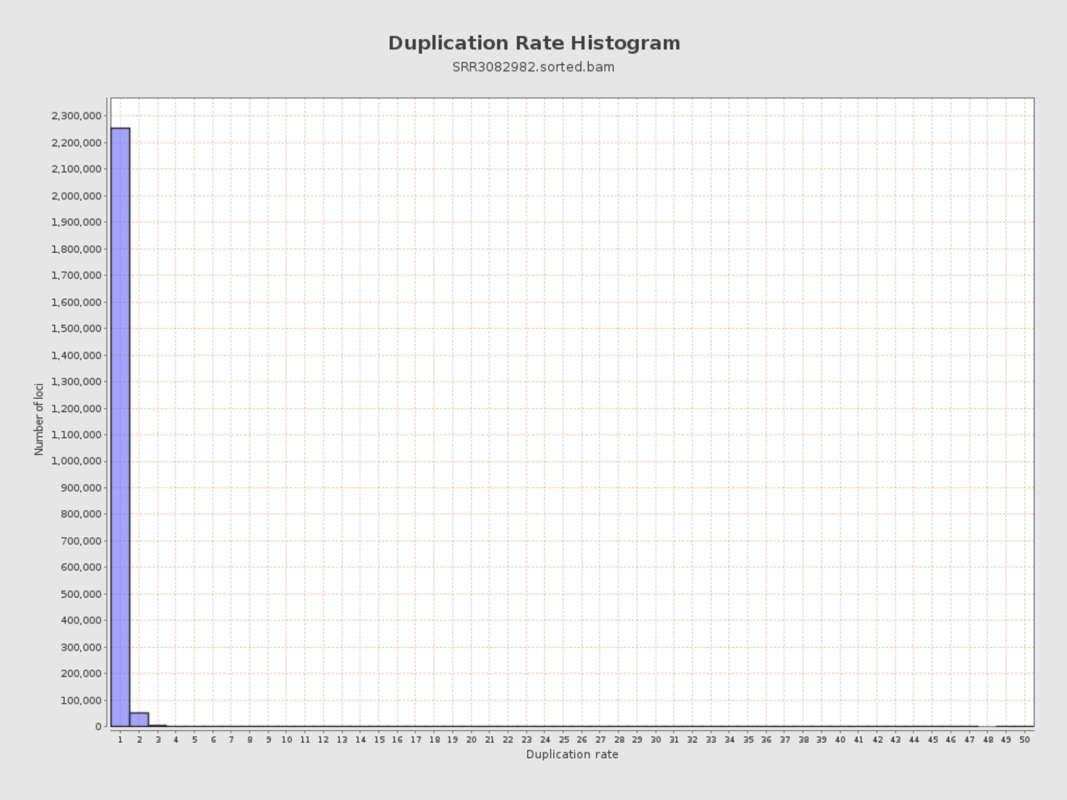
5. Results : Coverage Histogram (0-50X)



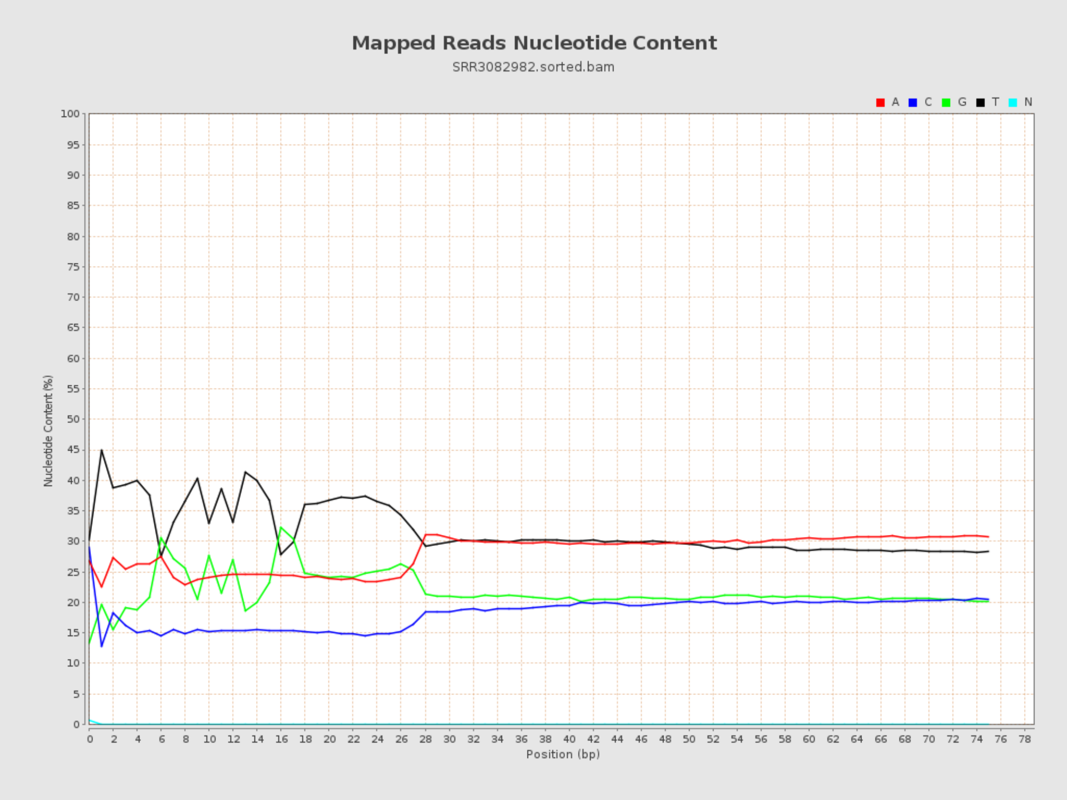
6. Results : Genome Fraction Coverage



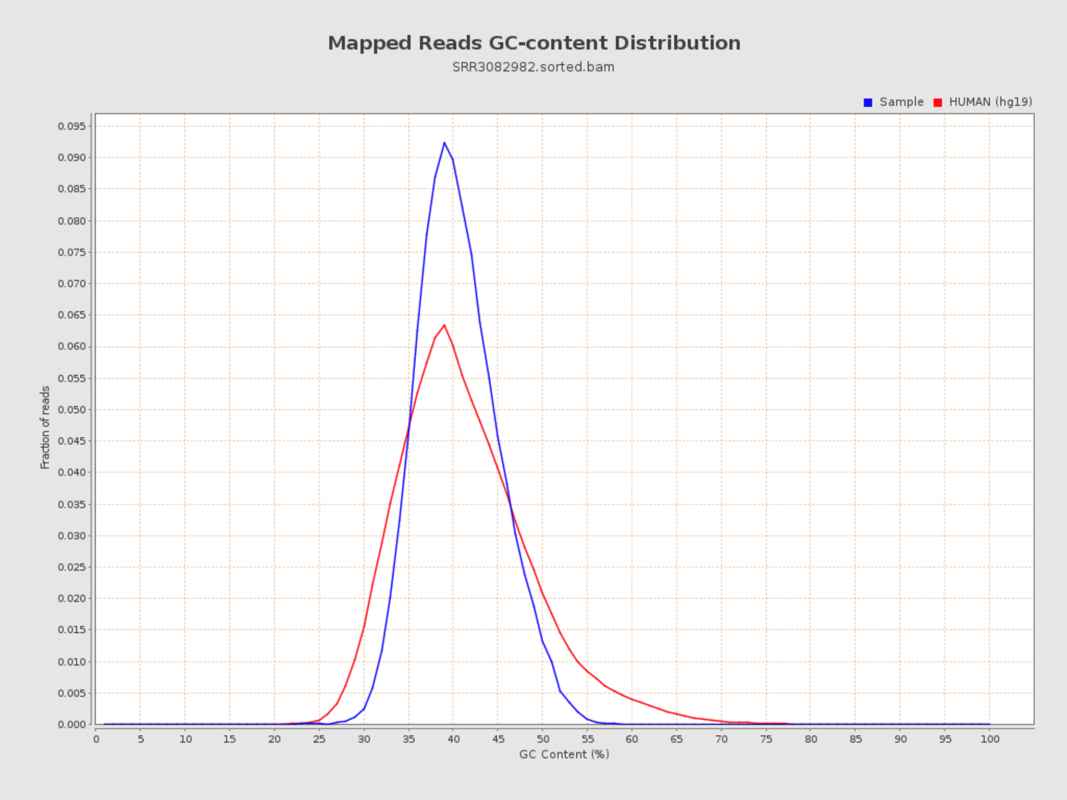
7. Results : Duplication Rate Histogram



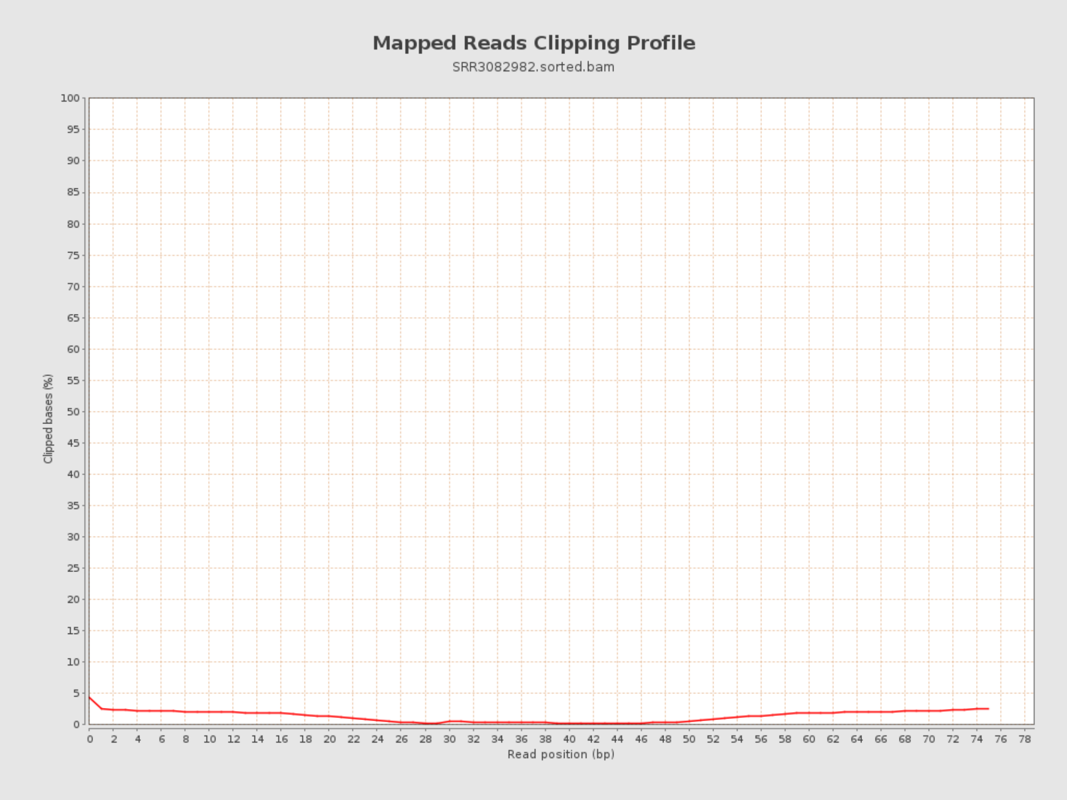
8. Results : Mapped Reads Nucleotide Content



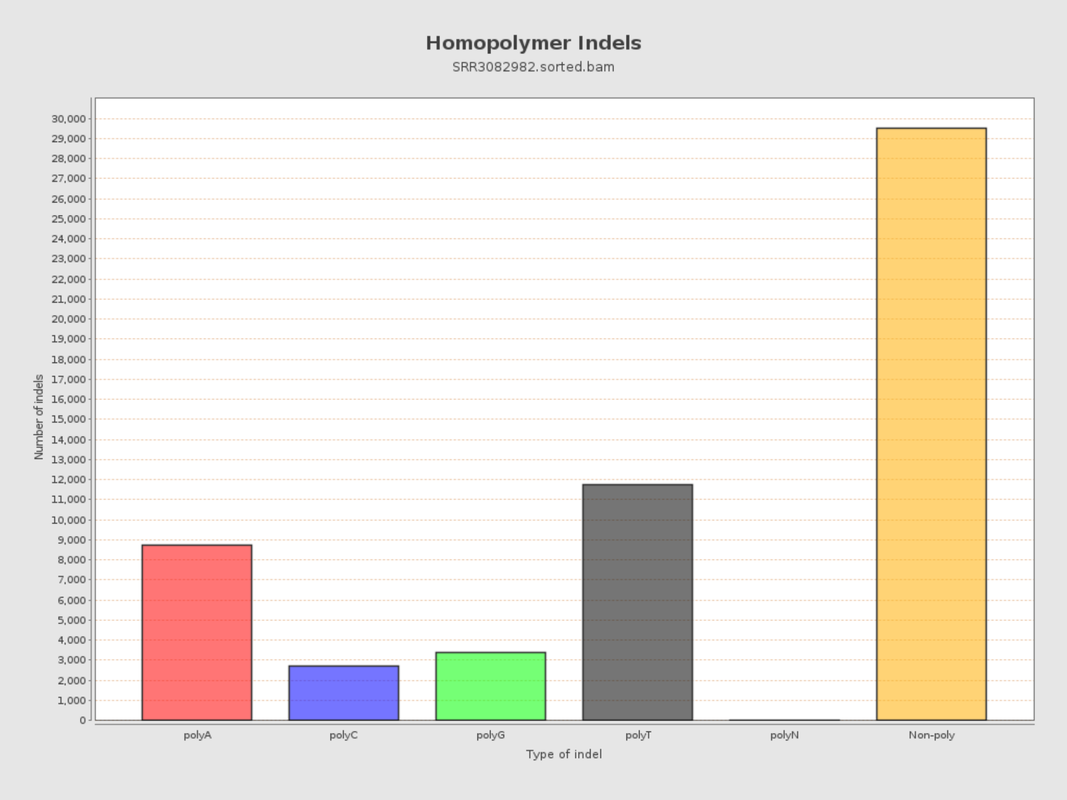
9. Results : Mapped Reads GC-content Distribution



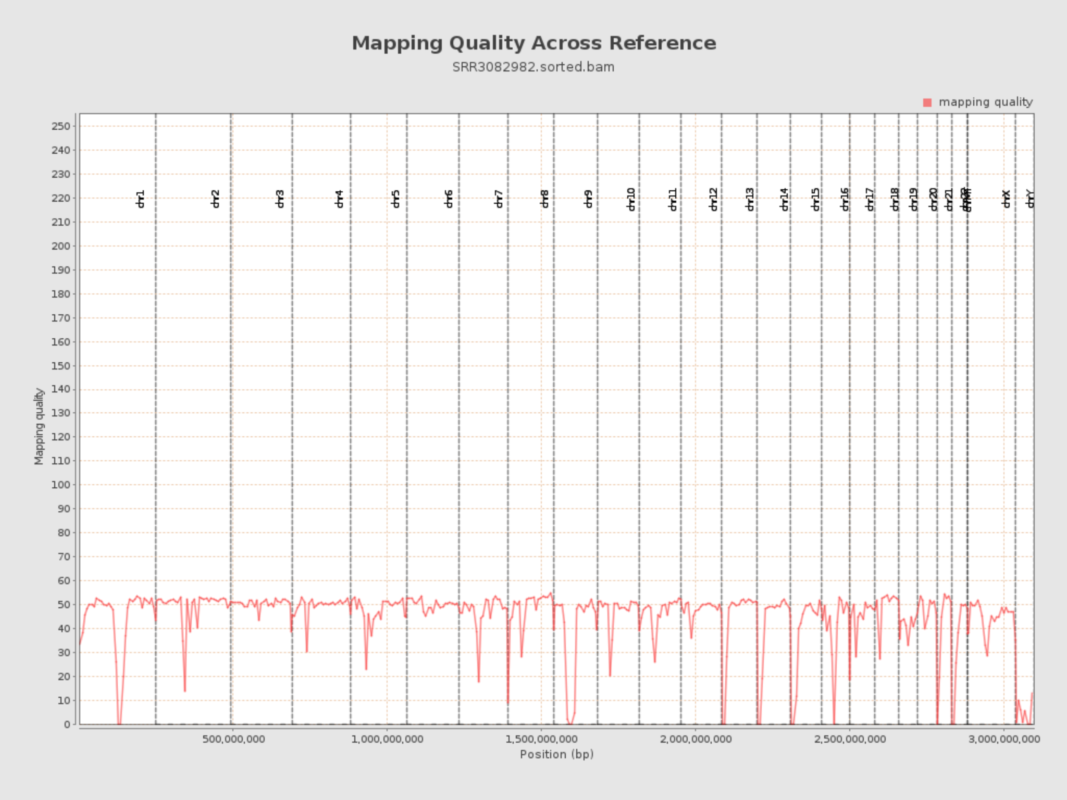
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram