Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 22:30:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082978.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_SRR3082978 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082978.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 22:30:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082978.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,701,438
Mapped reads	3,044,426 / 82.25%
Unmapped reads	657,012 / 17.75%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	20,332 / 0.55%
Read min/max/mean length	30 / 76 / 76.19
Duplicated reads (estimated)	116,573 / 3.15%
Duplication rate	3.08%
Clipped reads	1,166,983 / 31.53%

2.2. ACGT Content

Number/percentage of A's	60,361,402 / 28.95%
Number/percentage of C's	38,099,935 / 18.27%
Number/percentage of T's	66,597,627 / 31.94%
Number/percentage of G's	43,429,194 / 20.83%
Number/percentage of N's	21,223 / 0.01%
GC Percentage	39.1%

2.3. Coverage

Mean	0.0674

Standard Deviation	0.4555

2.4. Mapping Quality

Mean Mapping Quality	46.5

2.5. Mismatches and indels

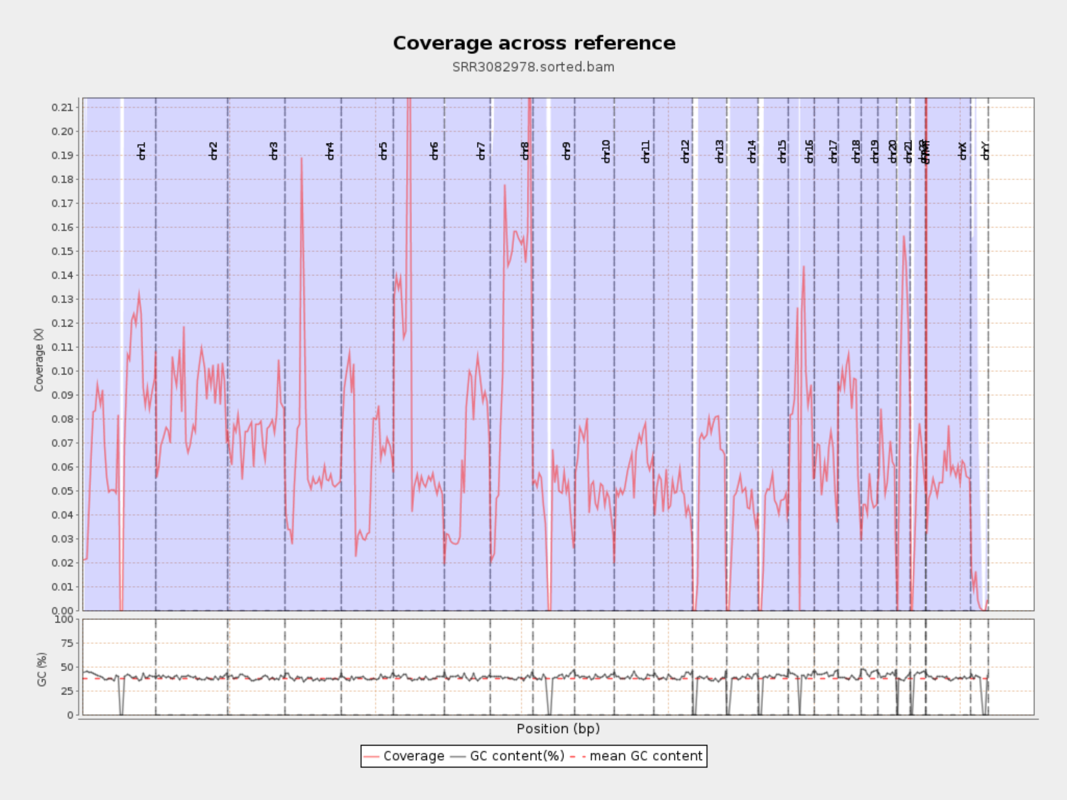
General error rate	0.94%
Mismatches	1,919,868
Insertions	17,738
Mapped reads with at least one insertion	0.58%
Deletions	48,129
Mapped reads with at least one deletion	1.56%
Homopolymer indels	47.99%

2.6. Chromosome stats

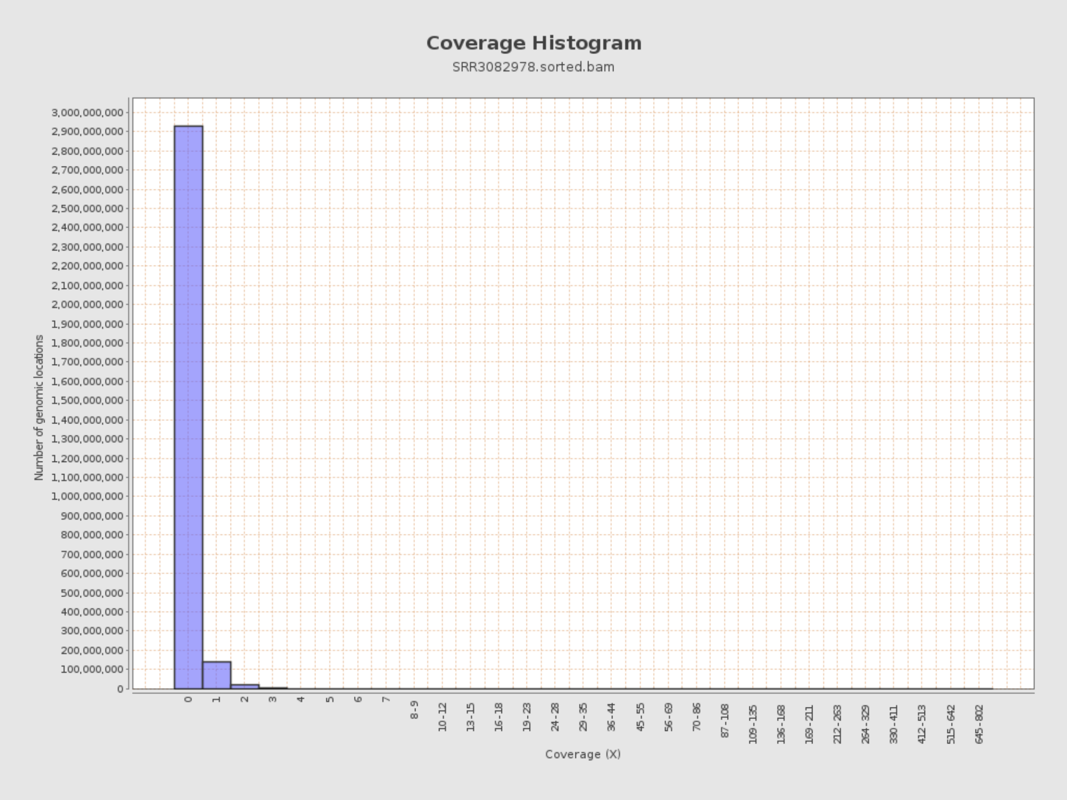
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	19060887	0.0765	0.7034
chr2	243199373	21255712	0.0874	0.5887
chr3	198022430	14906569	0.0753	0.3228
chr4	191154276	12035369	0.063	0.3032
chr5	180915260	11667776	0.0645	0.3012
chr6	171115067	14990015	0.0876	0.5141
chr7	159138663	10297620	0.0647	0.421

chr8	146364022	18363242	0.1255	0.6858
chr9	141213431	6326996	0.0448	0.432
chr10	135534747	7397947	0.0546	0.3672
chr11	135006516	8057027	0.0597	0.3462
chr12	133851895	6417887	0.0479	0.2645
chr13	115169878	6969130	0.0605	0.2904
chr14	107349540	4255511	0.0396	0.277
chr15	102531392	3940371	0.0384	0.2308
chr16	90354753	7826143	0.0866	0.398
chr17	81195210	4951136	0.061	0.3325
chr18	78077248	6929193	0.0887	0.9371
chr19	59128983	2673106	0.0452	0.5039
chr20	63025520	3854831	0.0612	0.3074
chr21	48129895	4830377	0.1004	0.389
chr22	51304566	2369402	0.0462	0.2519
chrMT	16571	207452	12.519	8.3895
chrX	155270560	8656888	0.0558	0.3096
chrY	59373566	352244	0.0059	0.1141

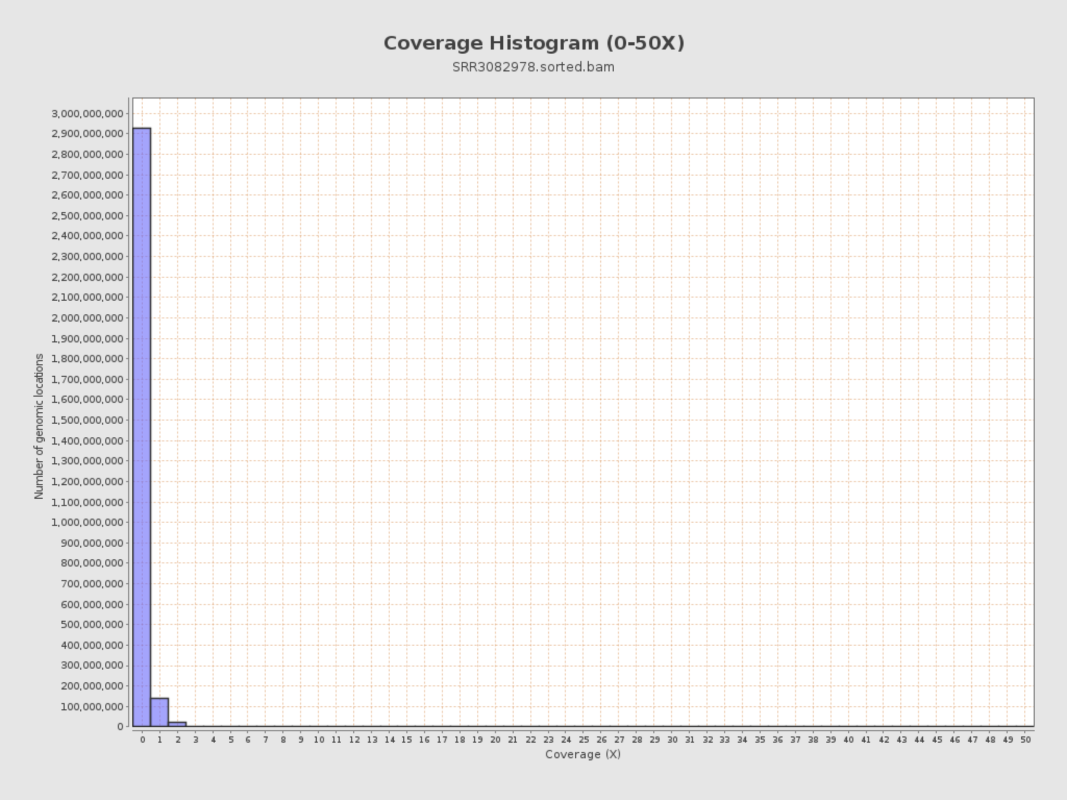
3. Results : Coverage across reference



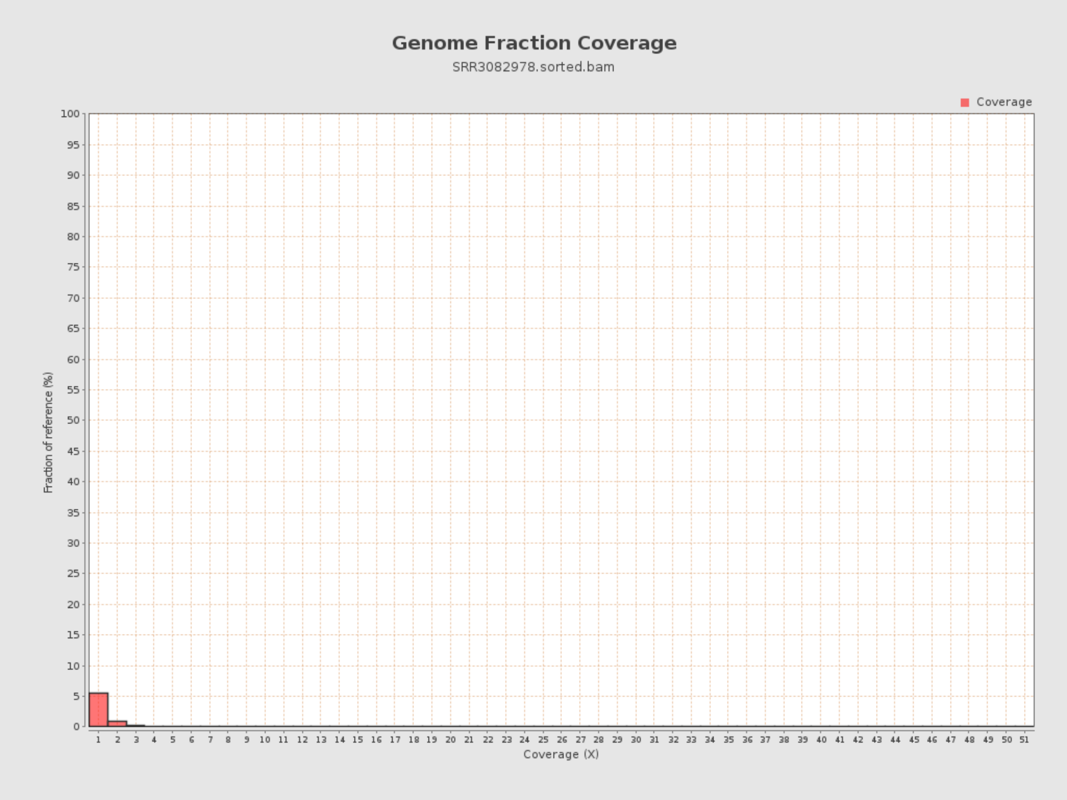
4. Results : Coverage Histogram



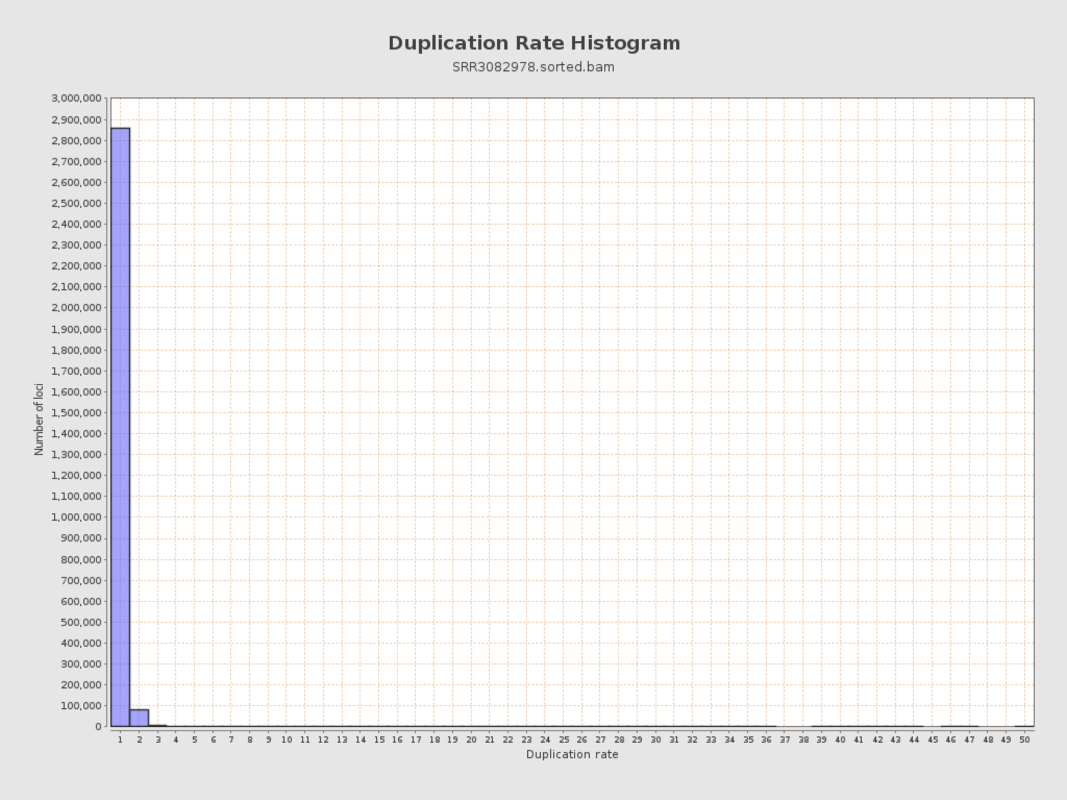
5. Results : Coverage Histogram (0-50X)



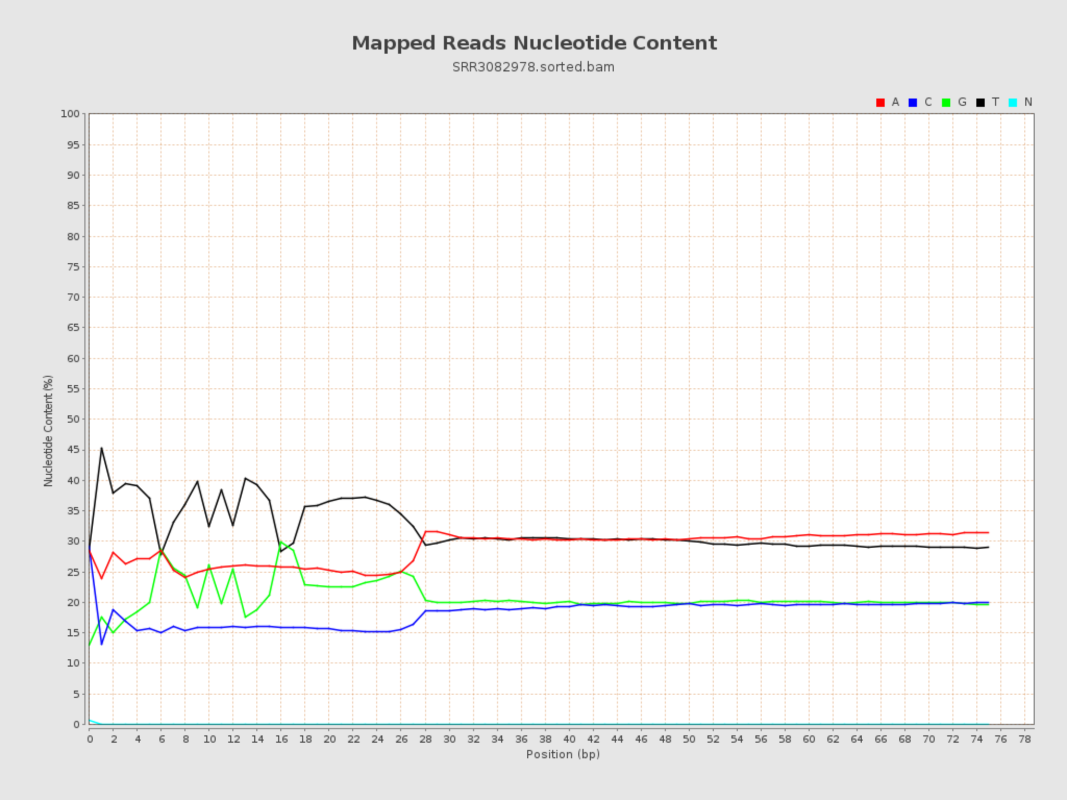
6. Results : Genome Fraction Coverage



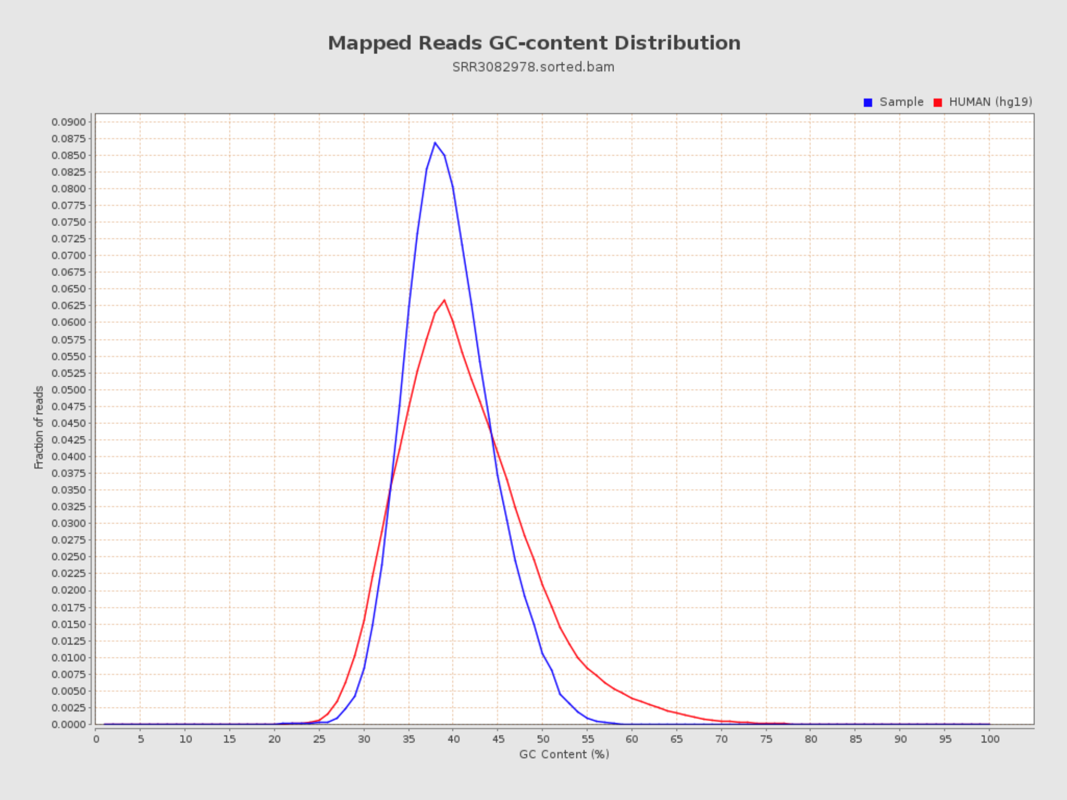
7. Results : Duplication Rate Histogram



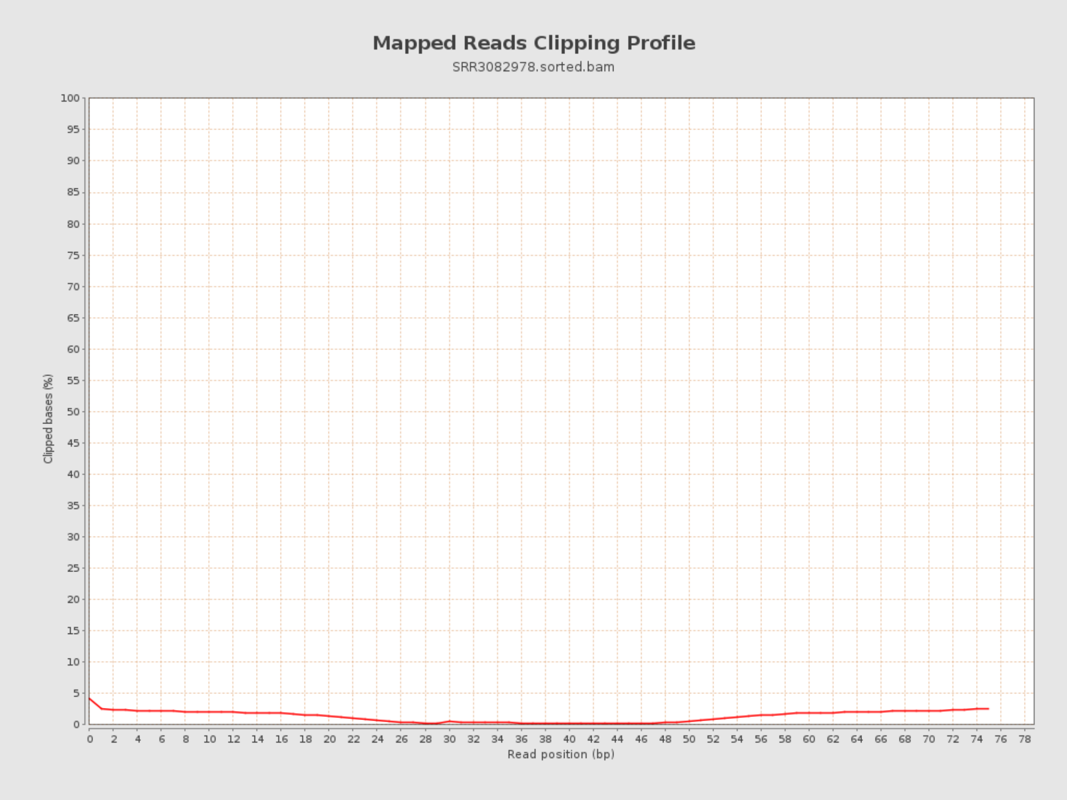
8. Results : Mapped Reads Nucleotide Content



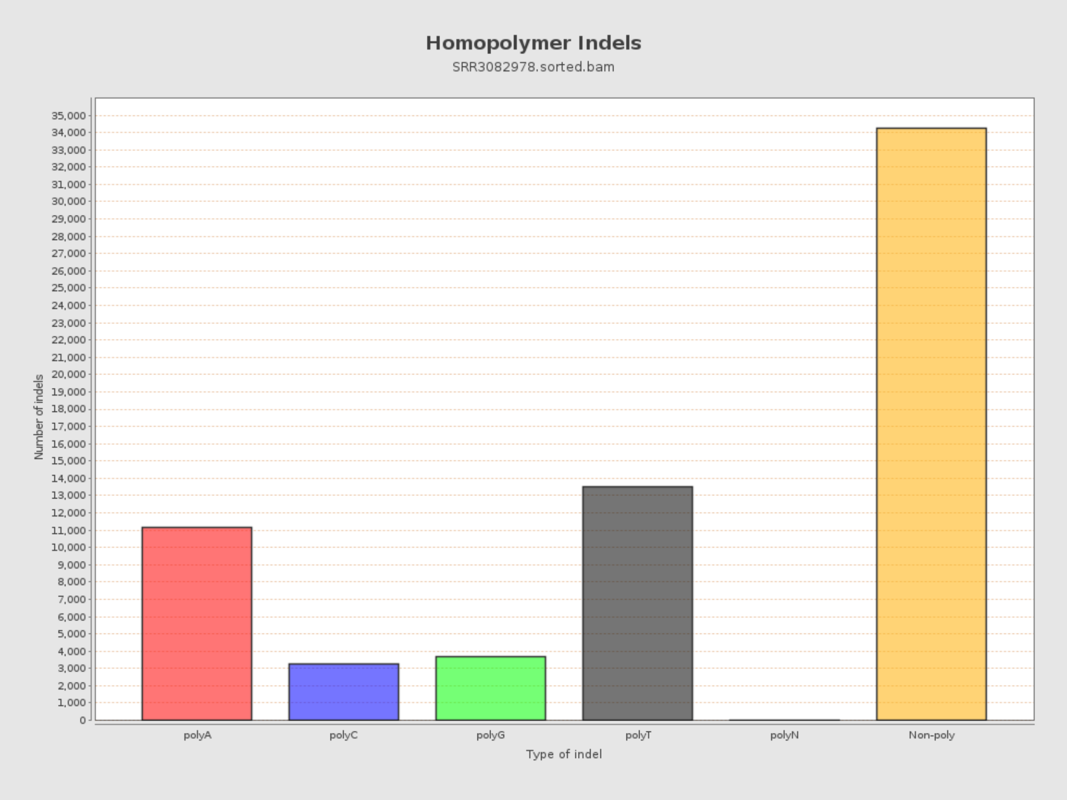
9. Results : Mapped Reads GC-content Distribution



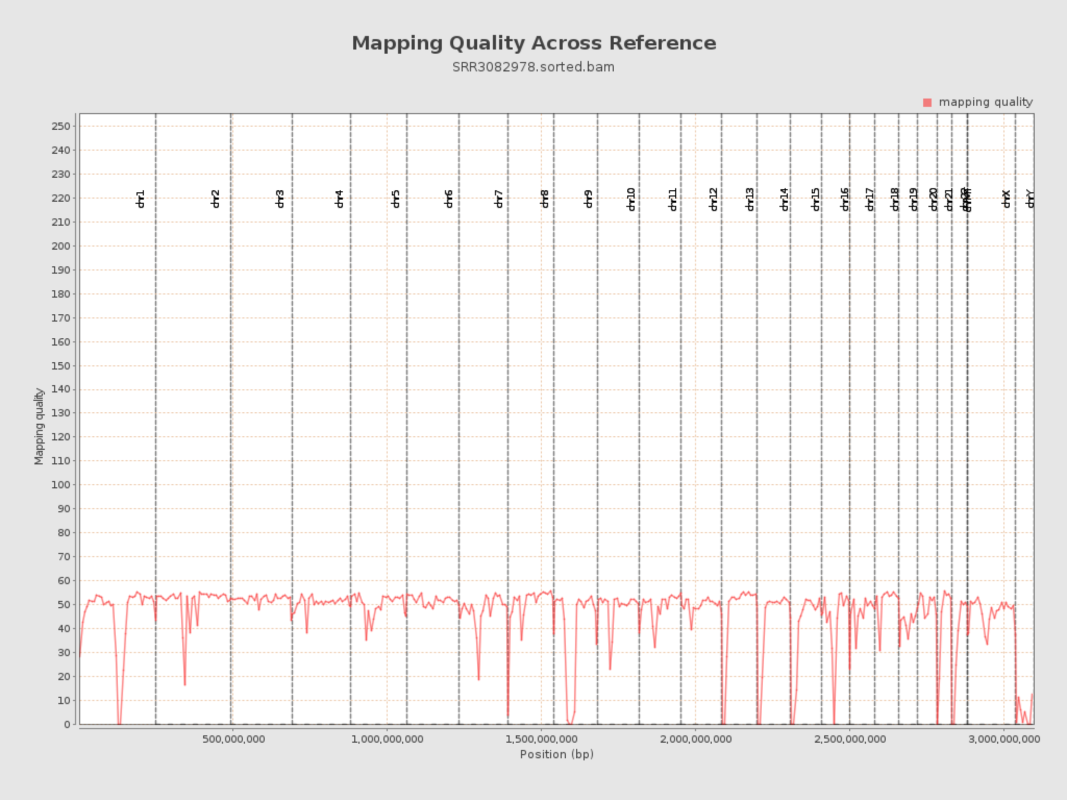
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram