Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 13:54:05

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3082328.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_SRR3082328 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3082328.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 13:54:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3082328.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,313,527
Mapped reads	2,997,332 / 90.46%
Unmapped reads	316,195 / 9.54%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	29,870 / 0.9%
Read min/max/mean length	30 / 76 / 76.32
Duplicated reads (estimated)	121,385 / 3.66%
Duplication rate	3.03%
Clipped reads	1,280,045 / 38.63%

2.2. ACGT Content

Number/percentage of A's	57,739,088 / 28.46%
Number/percentage of C's	38,178,721 / 18.82%
Number/percentage of T's	62,876,048 / 30.99%
Number/percentage of G's	44,115,129 / 21.74%
Number/percentage of N's	4,140 / 0%
GC Percentage	40.56%

2.3. Coverage

Mean	0.0656

Standard Deviation	0.5312

2.4. Mapping Quality

Mean Mapping Quality	46.21

2.5. Mismatches and indels

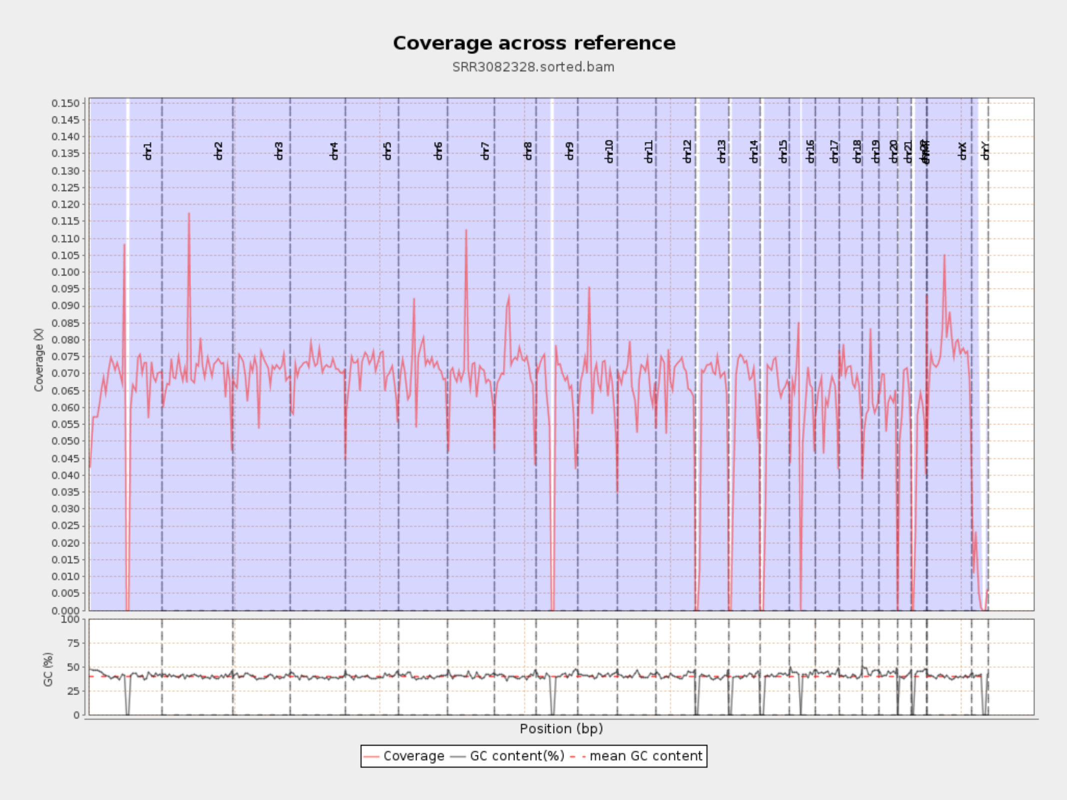
General error rate	0.85%
Mismatches	1,691,654
Insertions	16,331
Mapped reads with at least one insertion	0.54%
Deletions	44,547
Mapped reads with at least one deletion	1.47%
Homopolymer indels	47.09%

2.6. Chromosome stats

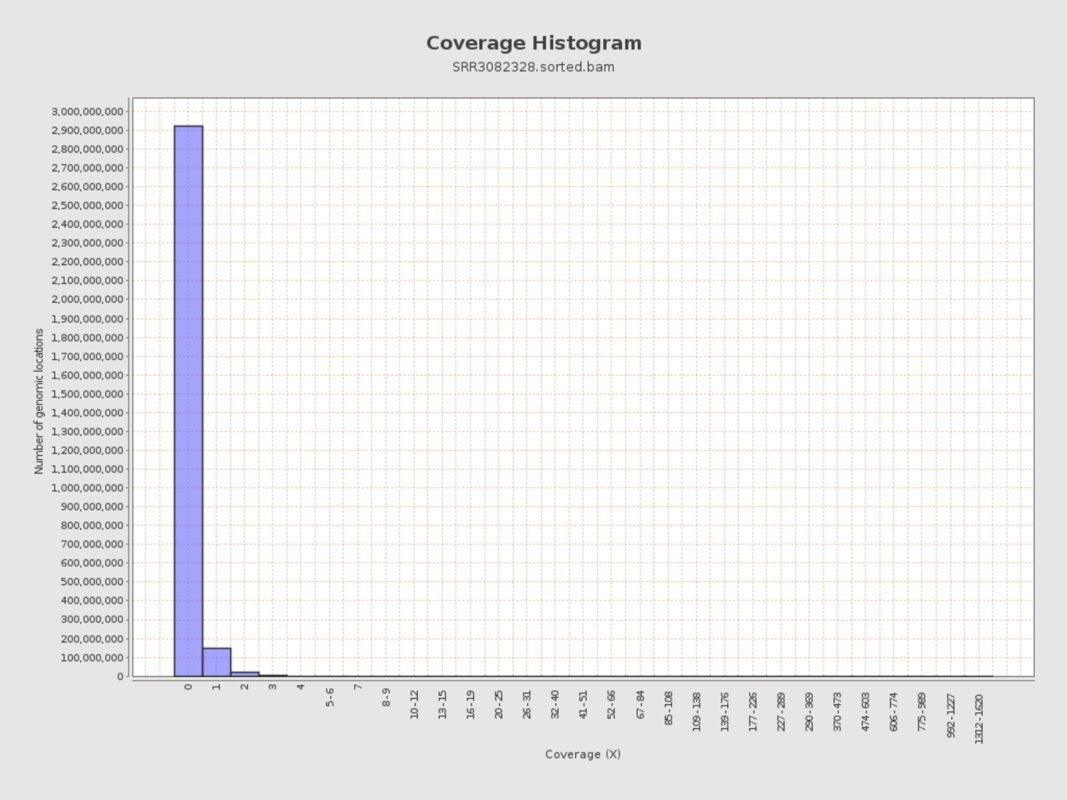
Name	**Length**	**Mapped bases**	**Mean coverage**	**Standard deviation**
chr1	249250621	15974095	0.0641	0.928
chr2	243199373	17387172	0.0715	0.6284
chr3	198022430	13990438	0.0707	0.3
chr4	191154276	13681813	0.0716	0.3149
chr5	180915260	12850883	0.071	0.3052
chr6	171115067	12225180	0.0714	0.3882
chr7	159138663	11229298	0.0706	0.6789

chr8	146364022	10553653	0.0721	1.0198
chr9	141213431	8452130	0.0599	0.4521
chr10	135534747	9335178	0.0689	0.463
chr11	135006516	9121926	0.0676	0.432
chr12	133851895	9145633	0.0683	0.3034
chr13	115169878	6741563	0.0585	0.2722
chr14	107349540	6214165	0.0579	0.2949
chr15	102531392	5751718	0.0561	0.272
chr16	90354753	5295189	0.0586	0.3123
chr17	81195210	4940711	0.0608	0.3171
chr18	78077248	5431248	0.0696	0.8432
chr19	59128983	3613207	0.0611	0.713
chr20	63025520	3910356	0.062	0.2901
chr21	48129895	2679415	0.0557	0.2864
chr22	51304566	2092345	0.0408	0.2258
chrMT	16571	1546	0.0933	0.3332
chrX	155270560	11876353	0.0765	0.3652
chrY	59373566	489628	0.0082	0.1574

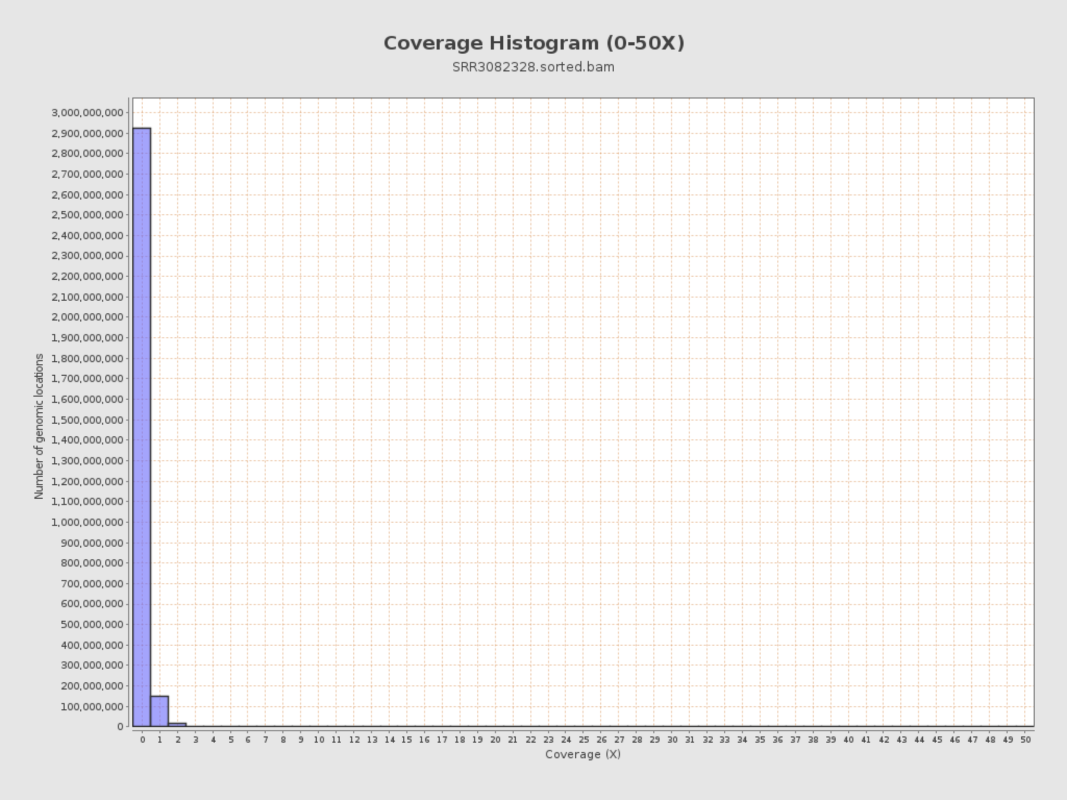
3. Results : Coverage across reference



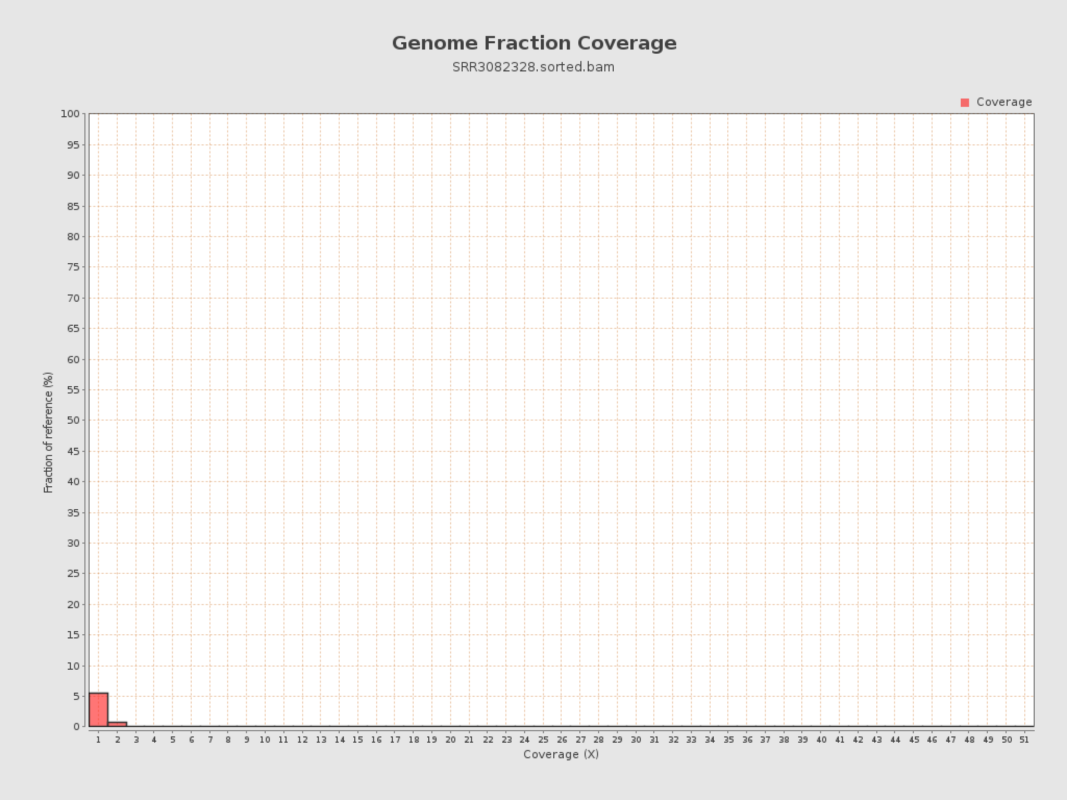
4. Results : Coverage Histogram



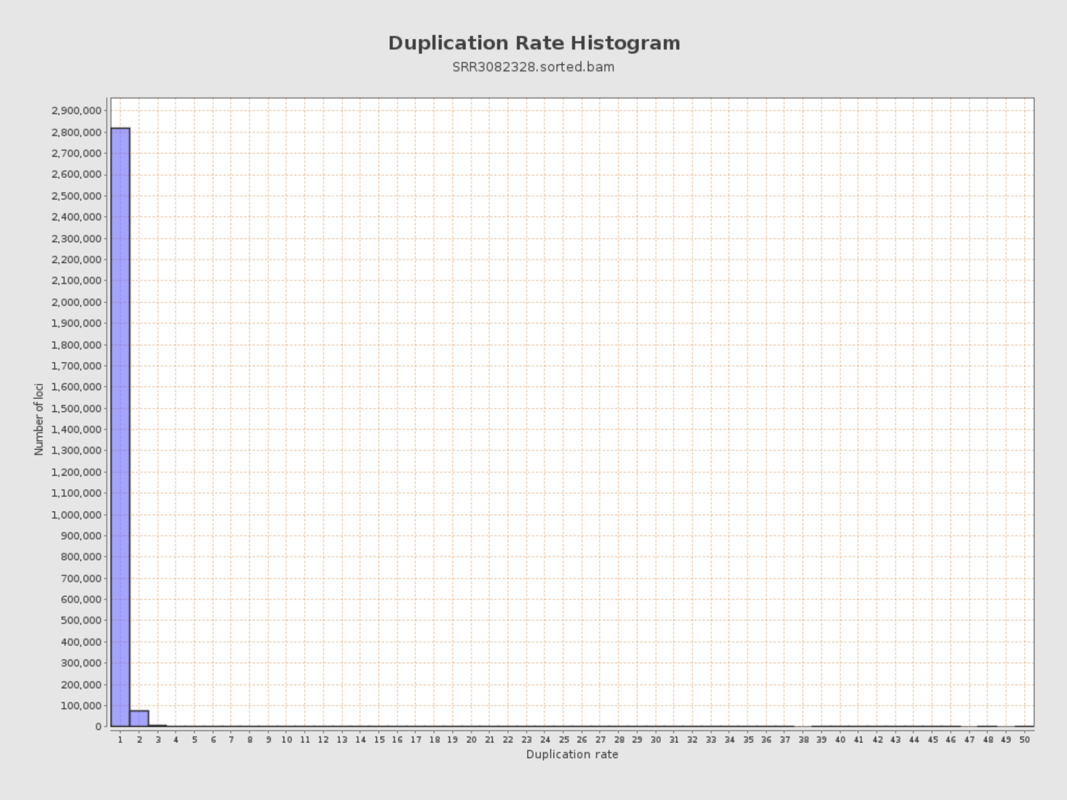
5. Results : Coverage Histogram (0-50X)



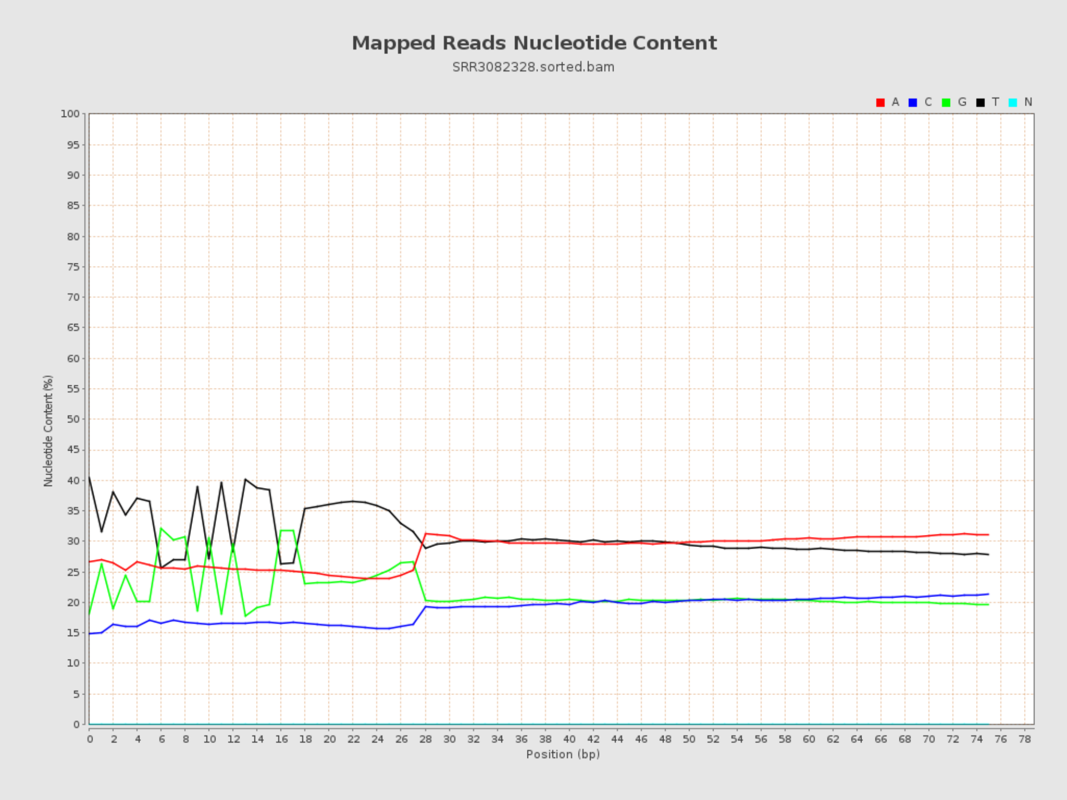
6. Results : Genome Fraction Coverage



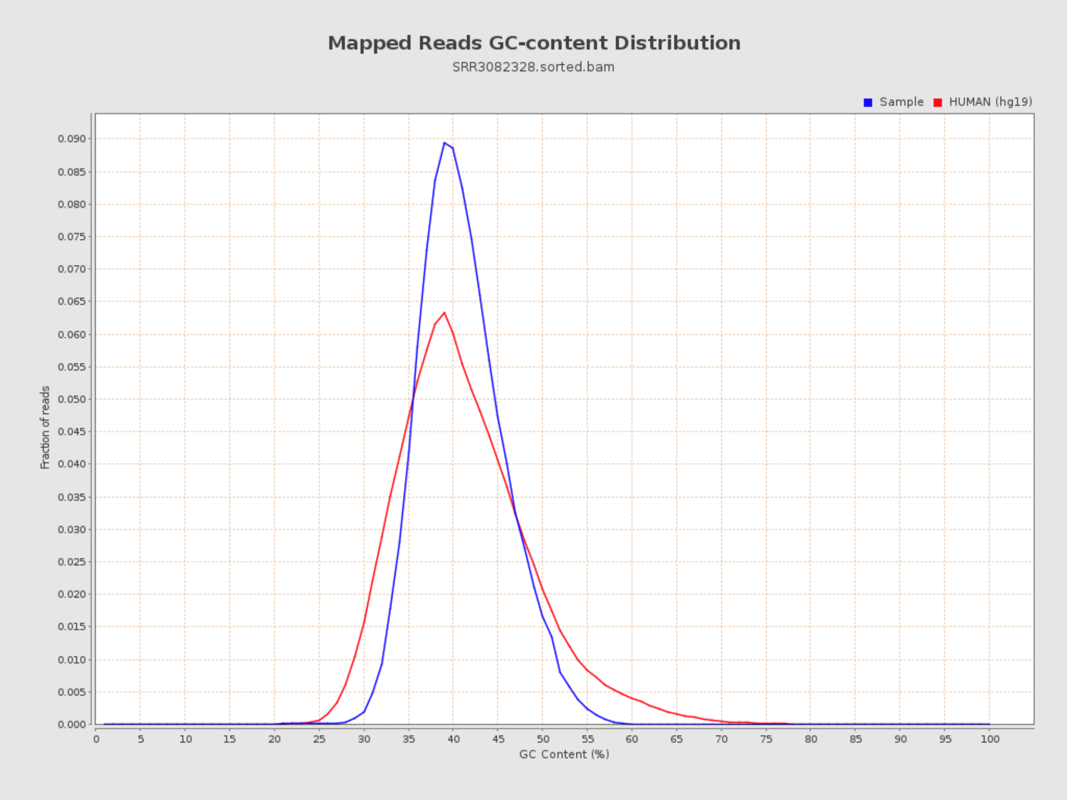
7. Results : Duplication Rate Histogram



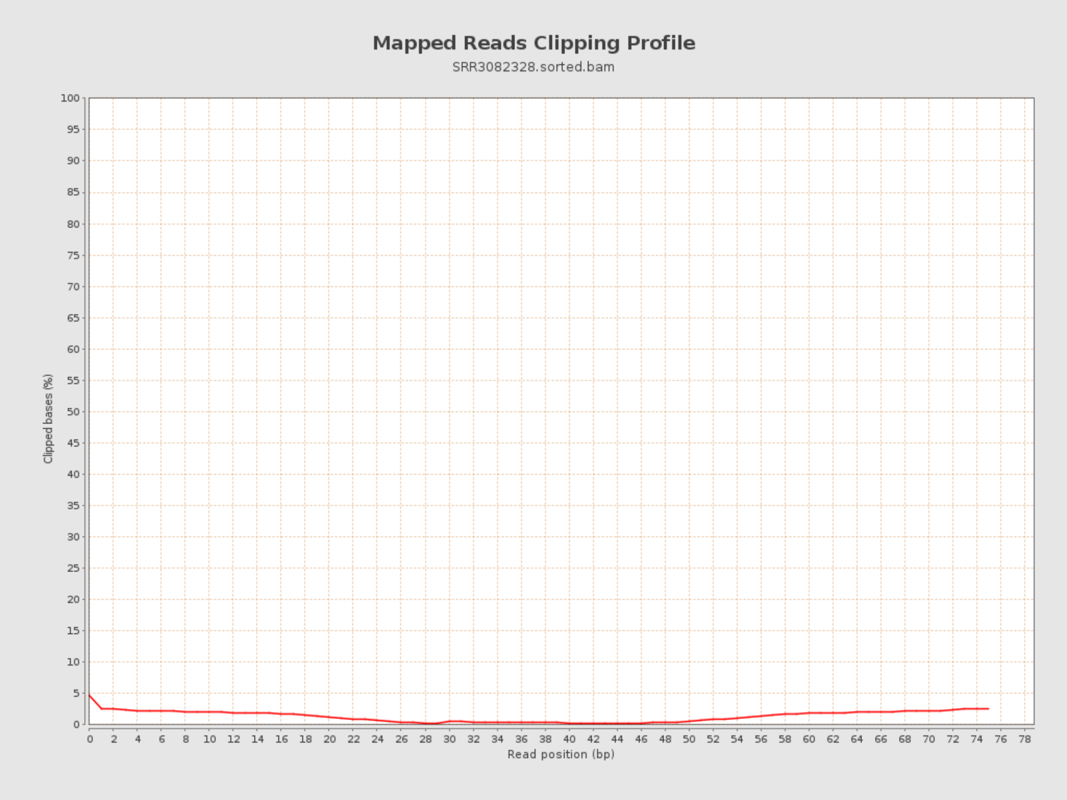
8. Results : Mapped Reads Nucleotide Content



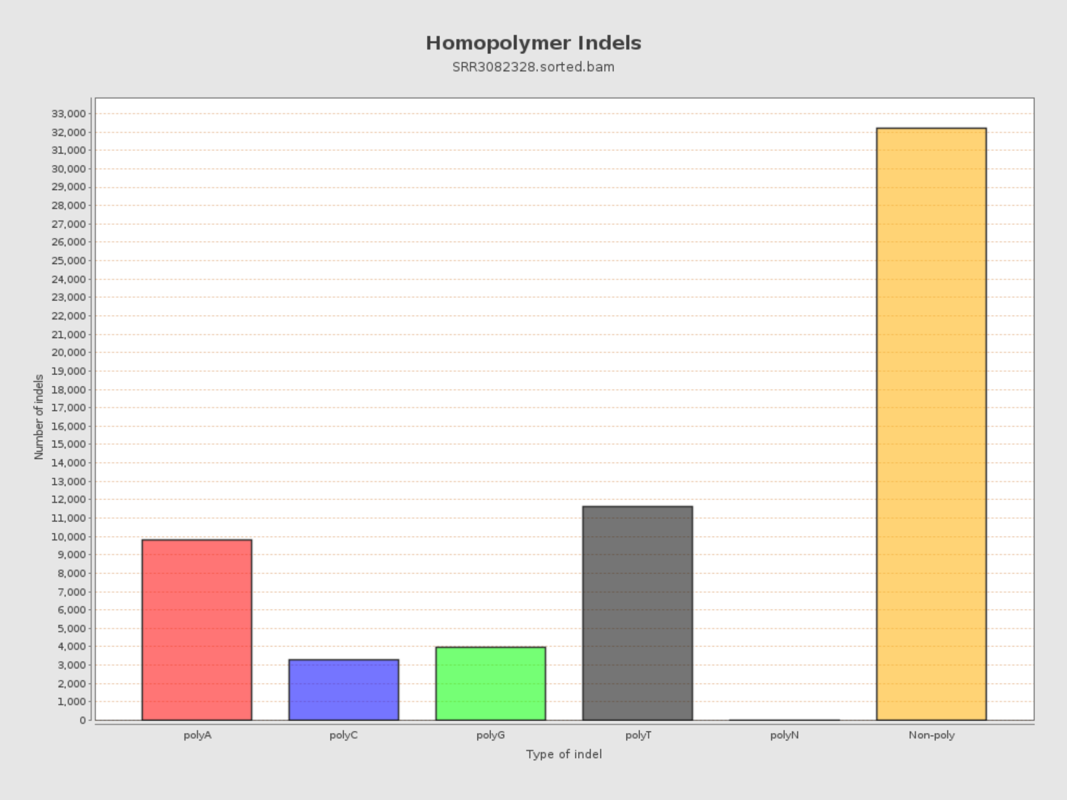
9. Results : Mapped Reads GC-content Distribution



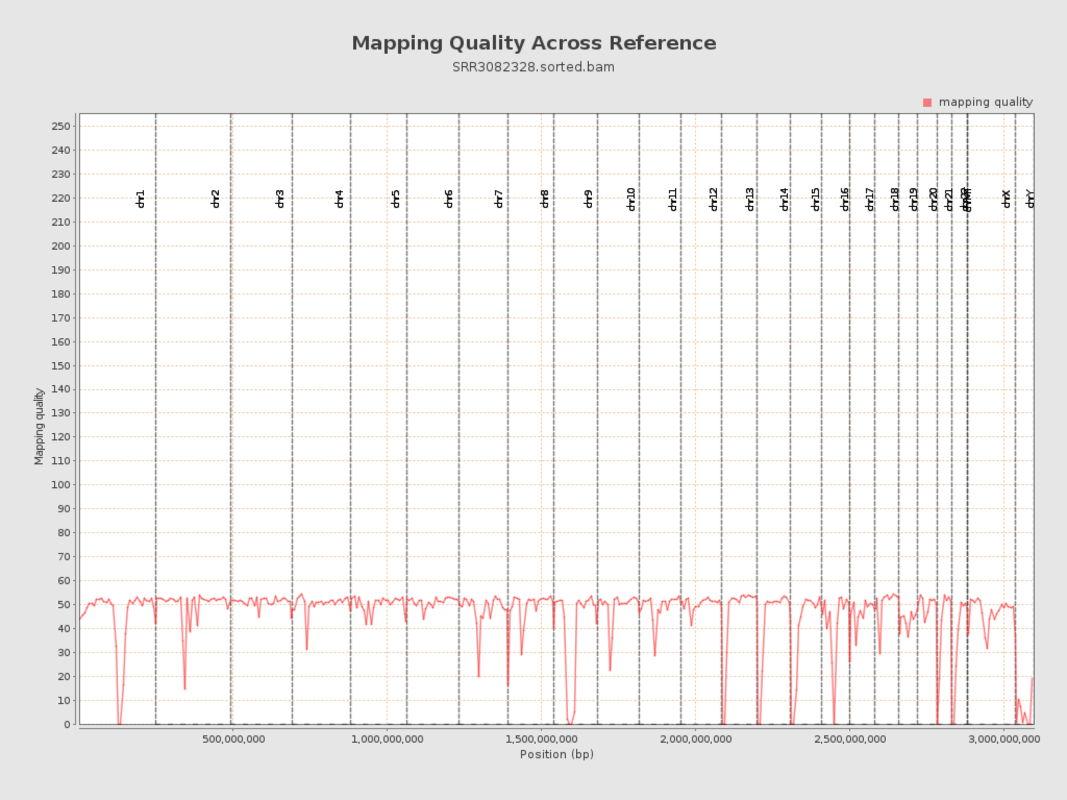
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram