

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 08:10:28

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3084258.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_SRR3084258 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3084258.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 08:10:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3084258.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,983,629
Mapped reads	2,279,207 / 76.39%
Unmapped reads	704,422 / 23.61%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	15,762 / 0.53%
Read min/max/mean length	30 / 76 / 76.18
Duplicated reads (estimated)	92,171 / 3.09%
Duplication rate	3.37%
Clipped reads	1,219,342 / 40.87%

2.2. ACGT Content

Number/percentage of A's	41,680,043 / 28.5%
Number/percentage of C's	27,872,282 / 19.06%
Number/percentage of T's	44,797,917 / 30.64%
Number/percentage of G's	31,870,325 / 21.8%
Number/percentage of N's	1,666 / 0%
GC Percentage	40.86%

2.3. Coverage

Mean	0.0473

Standard Deviation	0.3286
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2.4. Mapping Quality

Mean Mapping Quality	45.78
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2.5. Mismatches and indels

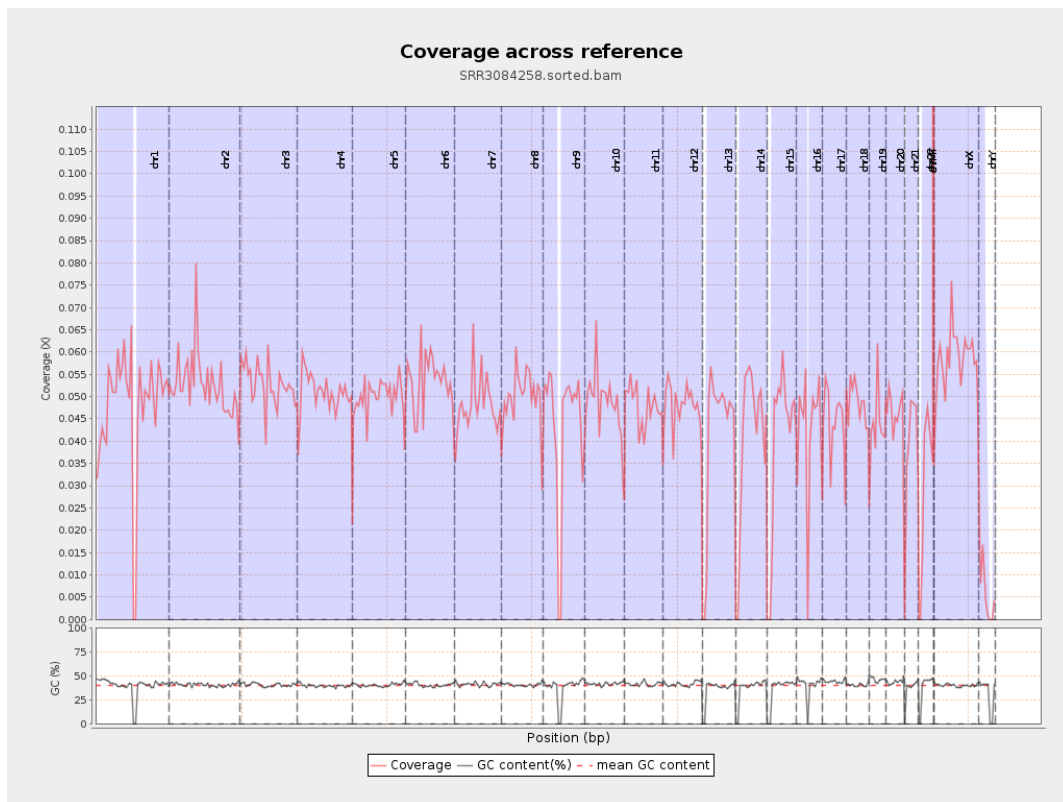
General error rate	0.85%
Mismatches	1,224,040
Insertions	11,044
Mapped reads with at least one insertion	0.48%
Deletions	31,782
Mapped reads with at least one deletion	1.38%
Homopolymer indels	46.49%

2.6. Chromosome stats

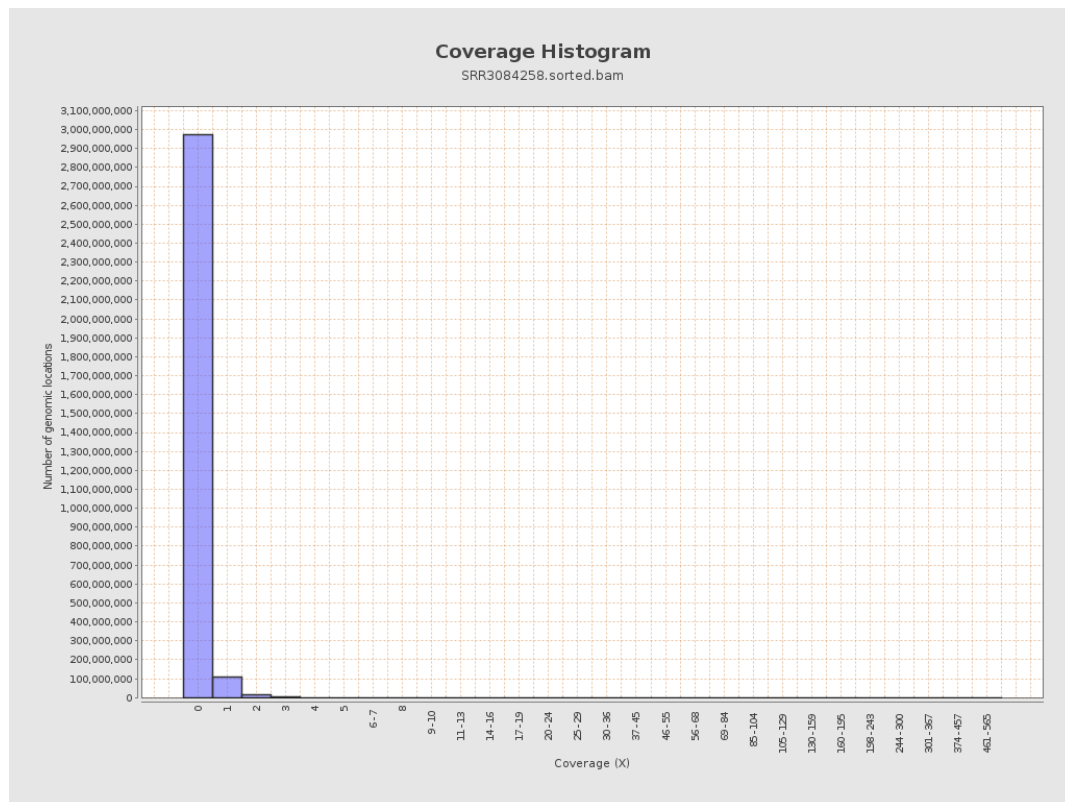
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	11925872	0.0478	0.5062
chr2	243199373	12822825	0.0527	0.4212
chr3	198022430	10444604	0.0527	0.2611
chr4	191154276	9738479	0.0509	0.266
chr5	180915260	9037893	0.05	0.2533
chr6	171115067	9119689	0.0533	0.3012
chr7	159138663	7719149	0.0485	0.382

chr8	146364022	7307558	0.0499	0.3381
chr9	141213431	6107119	0.0432	0.307
chr10	135534747	6634368	0.0489	0.3454
chr11	135006516	6404879	0.0474	0.2855
chr12	133851895	6425668	0.048	0.2522
chr13	115169878	4720661	0.041	0.2304
chr14	107349540	4351052	0.0405	0.2379
chr15	102531392	4064157	0.0396	0.232
chr16	90354753	3831441	0.0424	0.2549
chr17	81195210	3555046	0.0438	0.2596
chr18	78077248	3805262	0.0487	0.5403
chr19	59128983	2605459	0.0441	0.394
chr20	63025520	2905727	0.0461	0.2492
chr21	48129895	1855269	0.0385	0.2343
chr22	51304566	1491448	0.0291	0.1932
chrMT	16571	29547	1.7831	1.9198
chrX	155270560	9016031	0.0581	0.294
chrY	59373566	353256	0.0059	0.1208

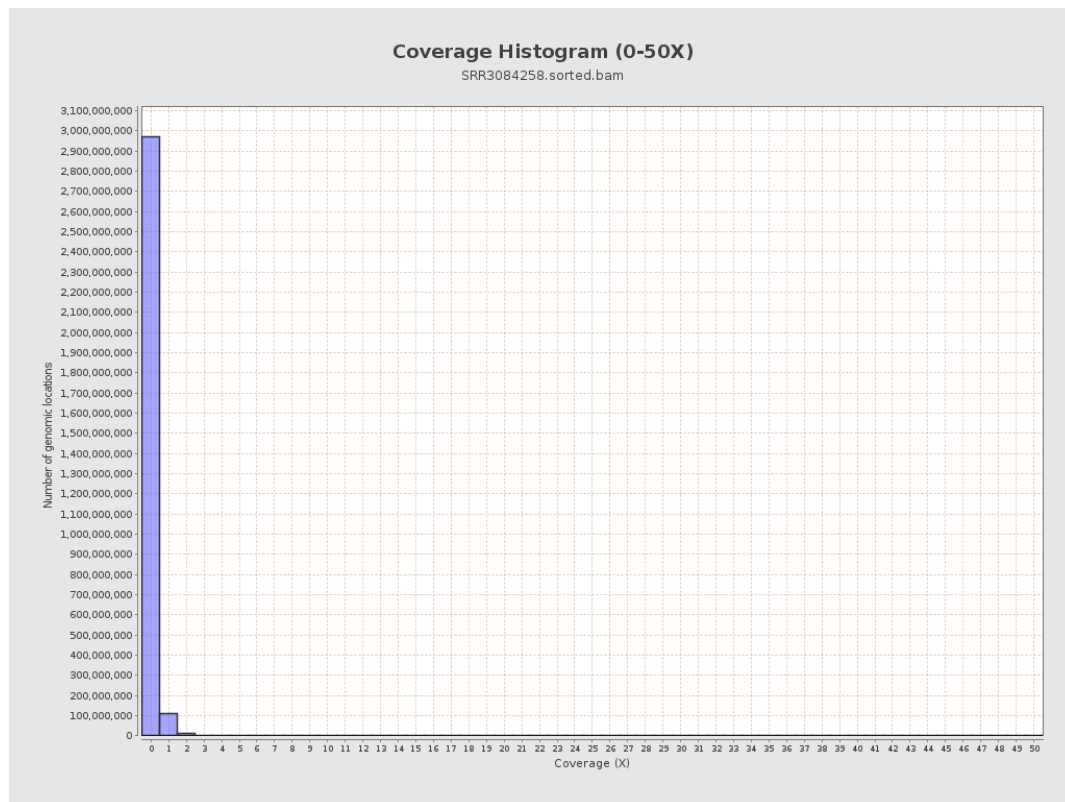
3. Results : Coverage across reference



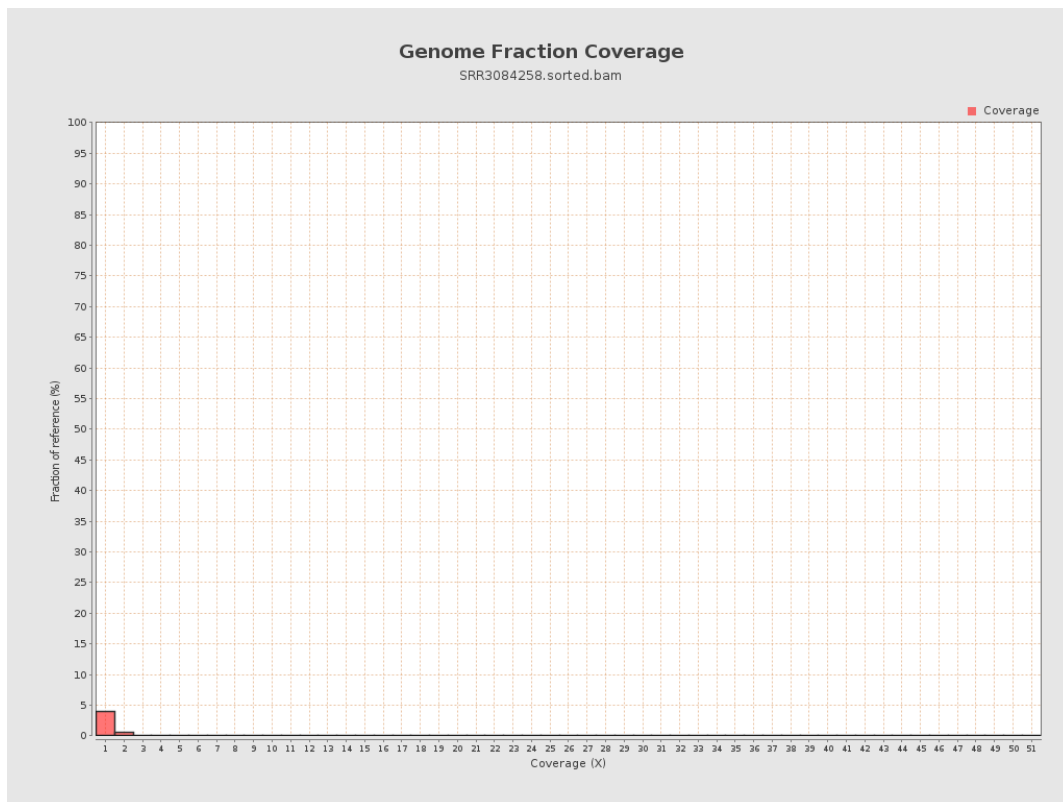
4. Results : Coverage Histogram



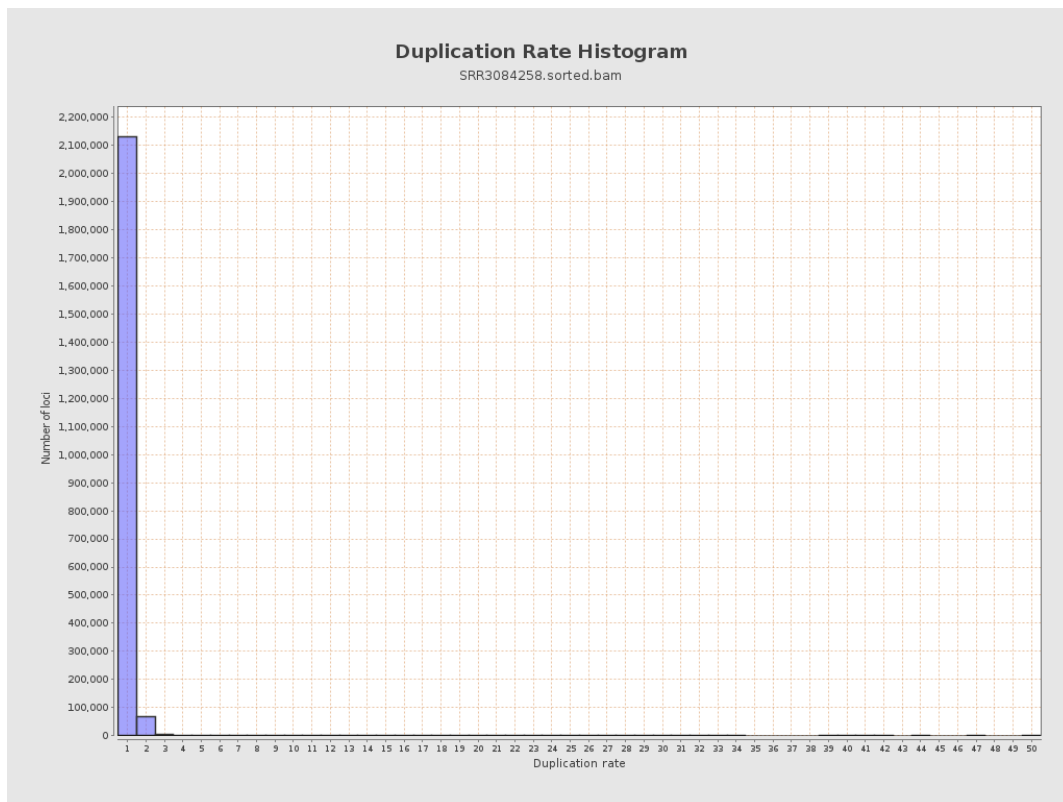
5. Results : Coverage Histogram (0-50X)



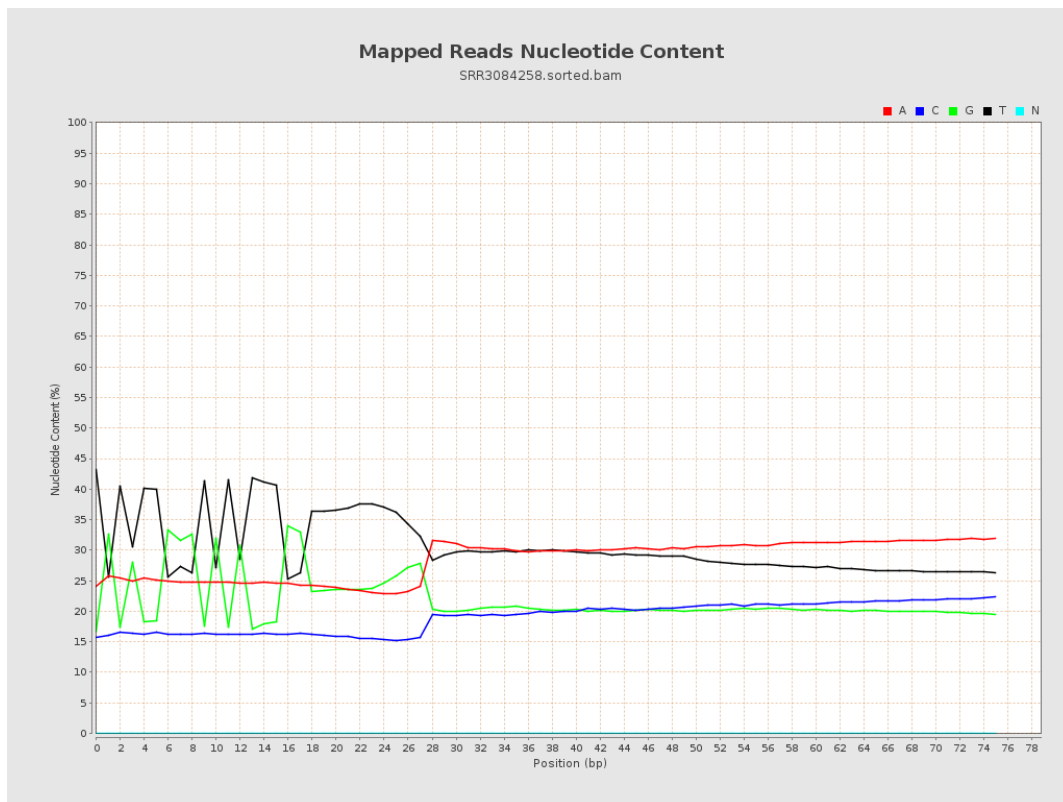
6. Results : Genome Fraction Coverage



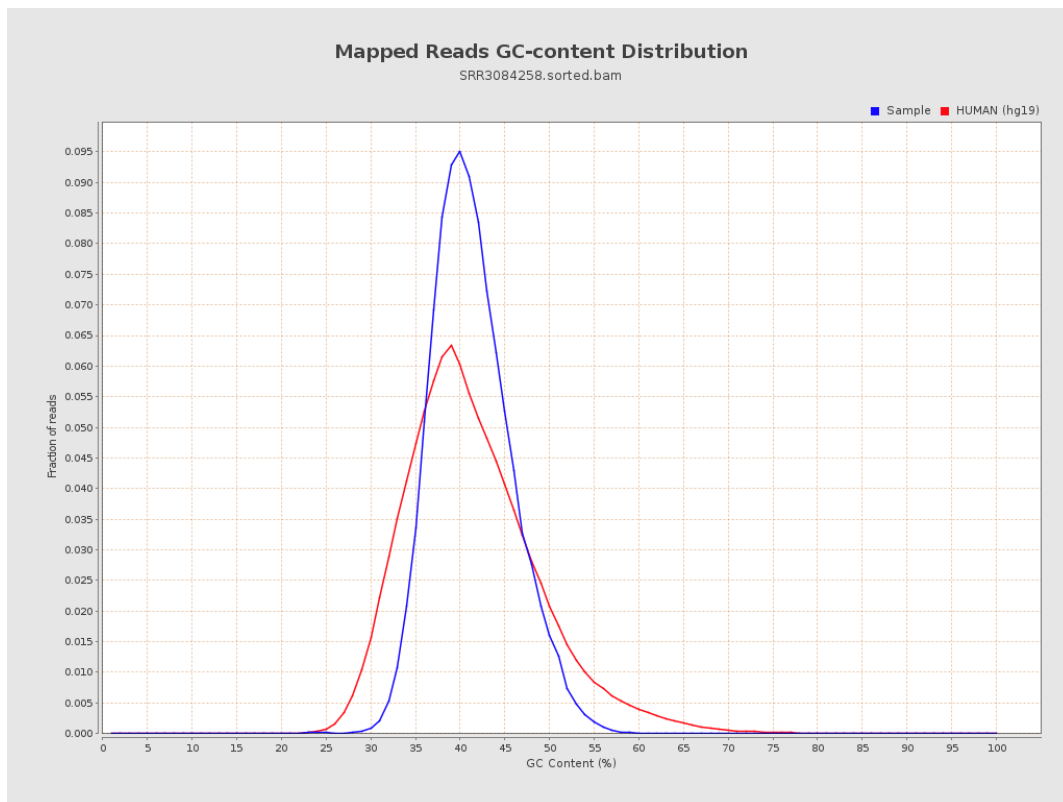
7. Results : Duplication Rate Histogram



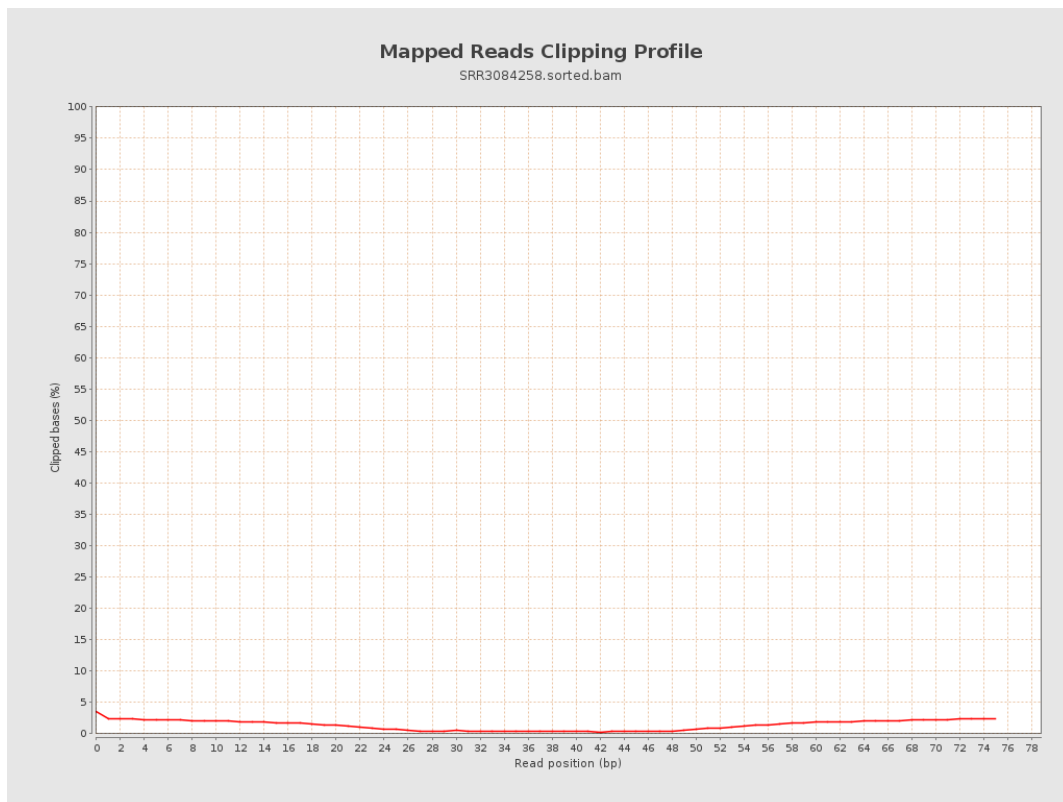
8. Results : Mapped Reads Nucleotide Content



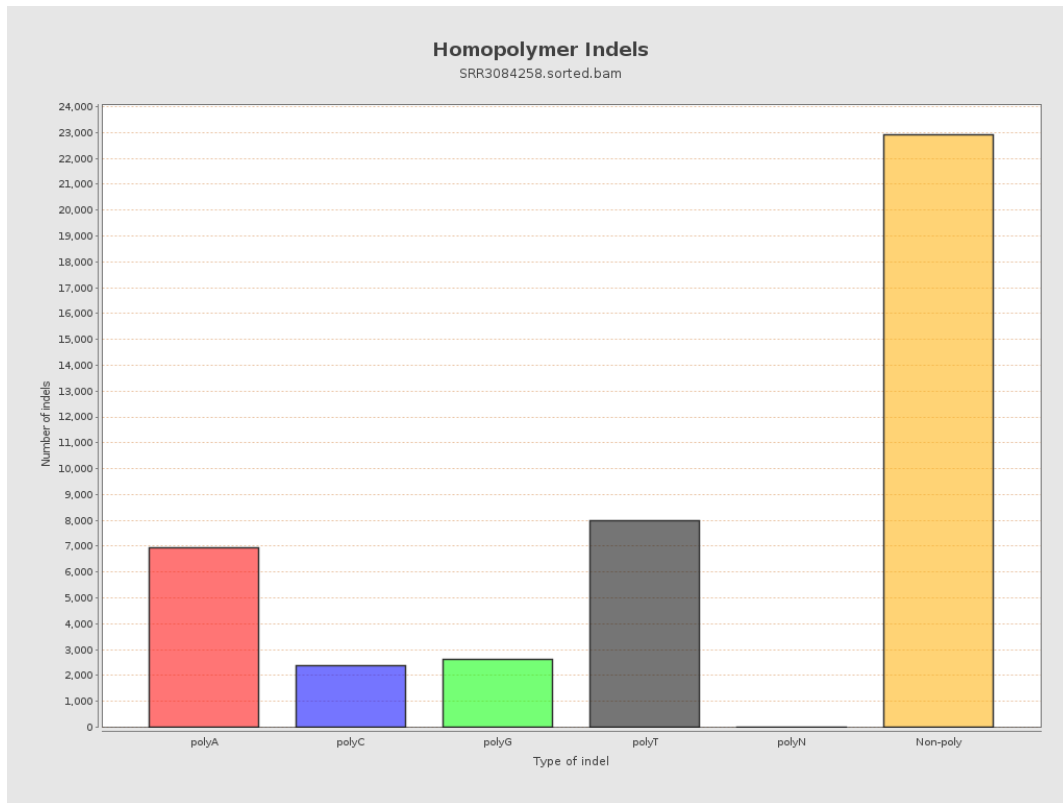
9. Results : Mapped Reads GC-content Distribution



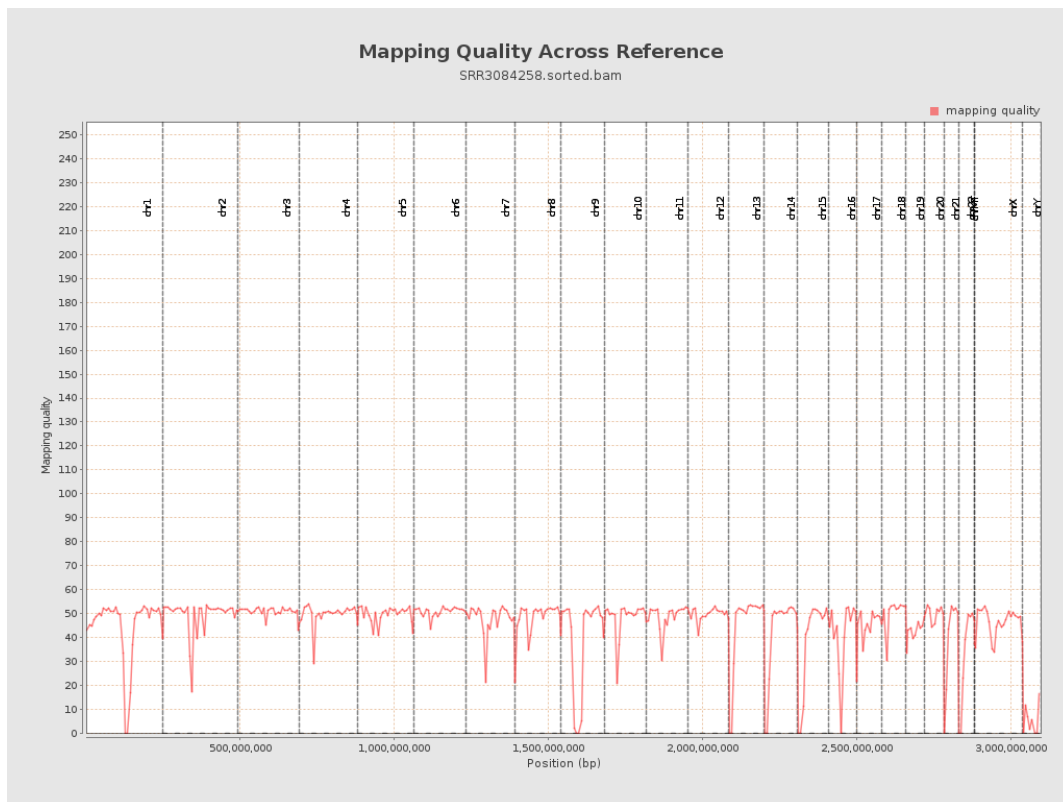
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

