

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:20:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124778.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_SRR3124778 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124778.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:20:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124778.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	612,528
Mapped reads	543,650 / 88.76%
Unmapped reads	68,878 / 11.24%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	227,050 / 37.07%
Read min/max/mean length	30 / 151 / 175.08
Duplicated reads (estimated)	768,477 / 125.46%
Duplication rate	27.85%
Clipped reads	490,711 / 80.11%

2.2. ACGT Content

Number/percentage of A's	23,308,099 / 28.72%
Number/percentage of C's	15,569,932 / 19.18%
Number/percentage of T's	25,876,524 / 31.88%
Number/percentage of G's	16,414,109 / 20.22%
Number/percentage of N's	0 / 0%
GC Percentage	39.4%

2.3. Coverage

Mean	0.0262

Standard Deviation	41.0123
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2.4. Mapping Quality

Mean Mapping Quality	40.61
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2.5. Mismatches and indels

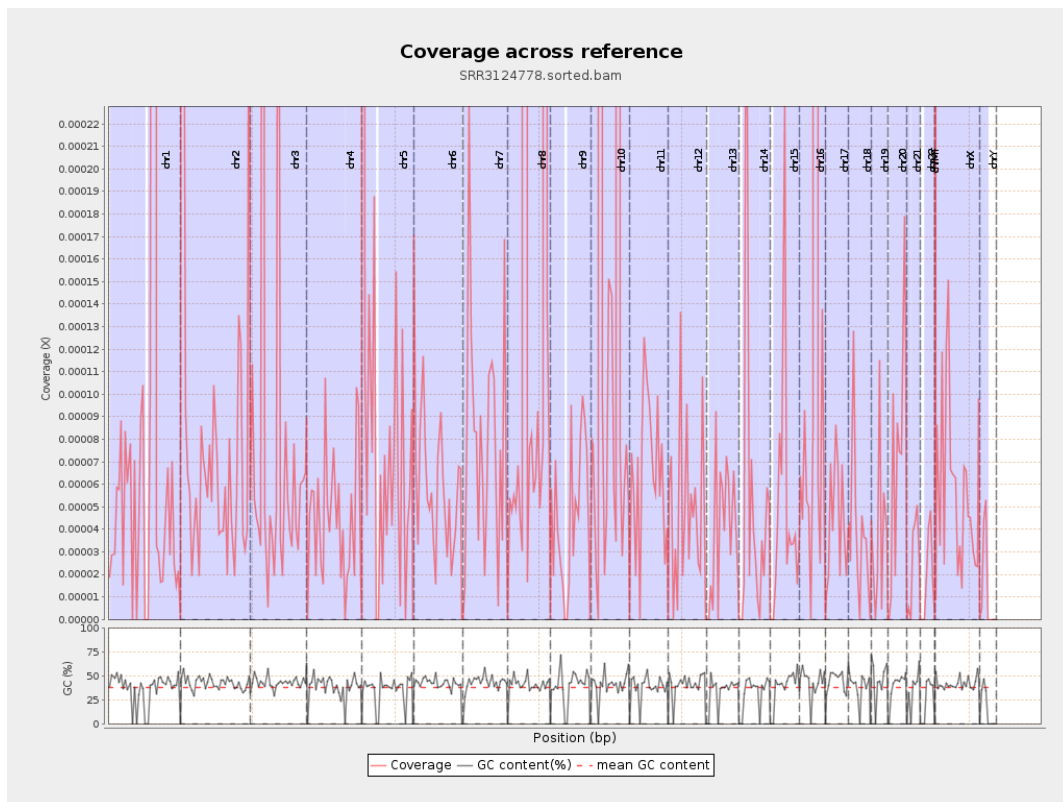
General error rate	0.82%
Mismatches	657,764
Insertions	11,217
Mapped reads with at least one insertion	2.04%
Deletions	33,174
Mapped reads with at least one deletion	5.94%
Homopolymer indels	76.92%

2.6. Chromosome stats

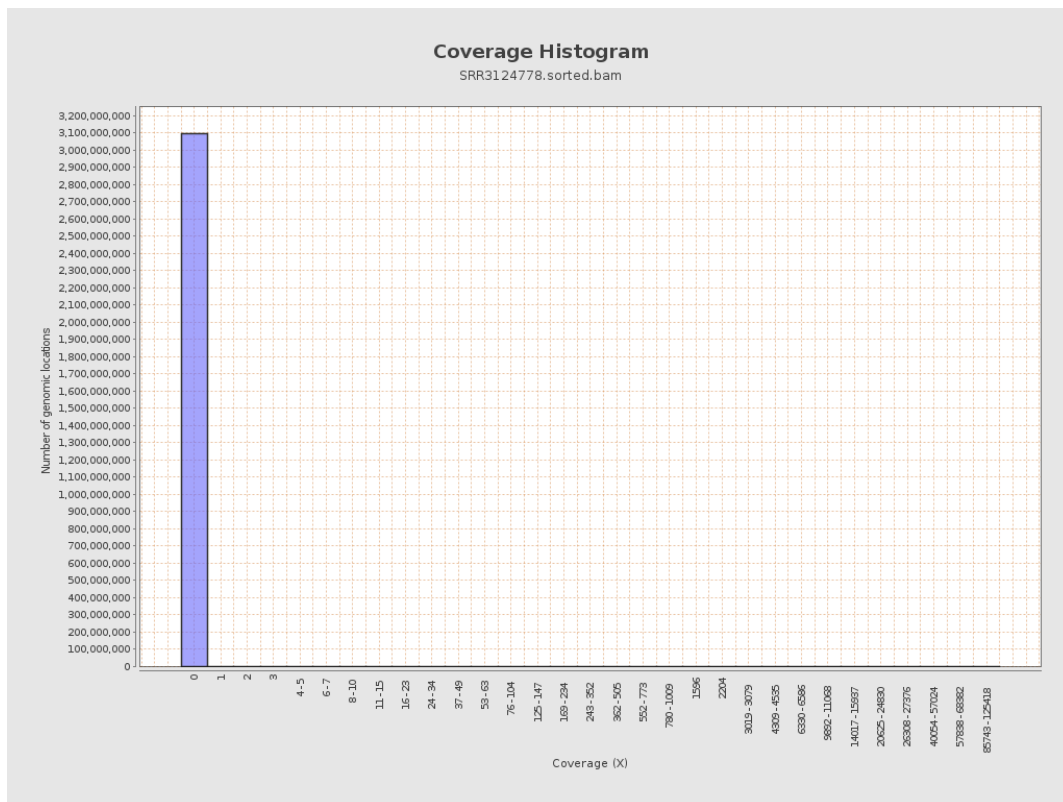
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	46770	0.0002	0.1171
chr2	243199373	21406	0.0001	0.0283
chr3	198022430	17132	0.0001	0.0556
chr4	191154276	8560	0	0.0122
chr5	180915260	58467	0.0003	0.428
chr6	171115067	9946	0.0001	0.0093
chr7	159138663	12341	0.0001	0.0205

chr8	146364022	56712393	0.3875	169.1214
chr9	141213431	6547	0	0.0069
chr10	135534747	24199596	0.1785	86.7757
chr11	135006516	8718	0.0001	0.0117
chr12	133851895	6515	0	0.0071
chr13	115169878	4384	0	0.0062
chr14	107349540	5367	0	0.0361
chr15	102531392	4856	0	0.0215
chr16	90354753	55123	0.0006	0.646
chr17	81195210	3582	0	0.0067
chr18	78077248	2921	0	0.007
chr19	59128983	2109	0	0.006
chr20	63025520	4604	0.0001	0.0089
chr21	48129895	1199	0	0.005
chr22	51304566	974	0	0.0044
chrMT	16571	300	0.0181	0.1333
chrX	155270560	8800	0.0001	0.0148
chrY	59373566	788	0	0.0041

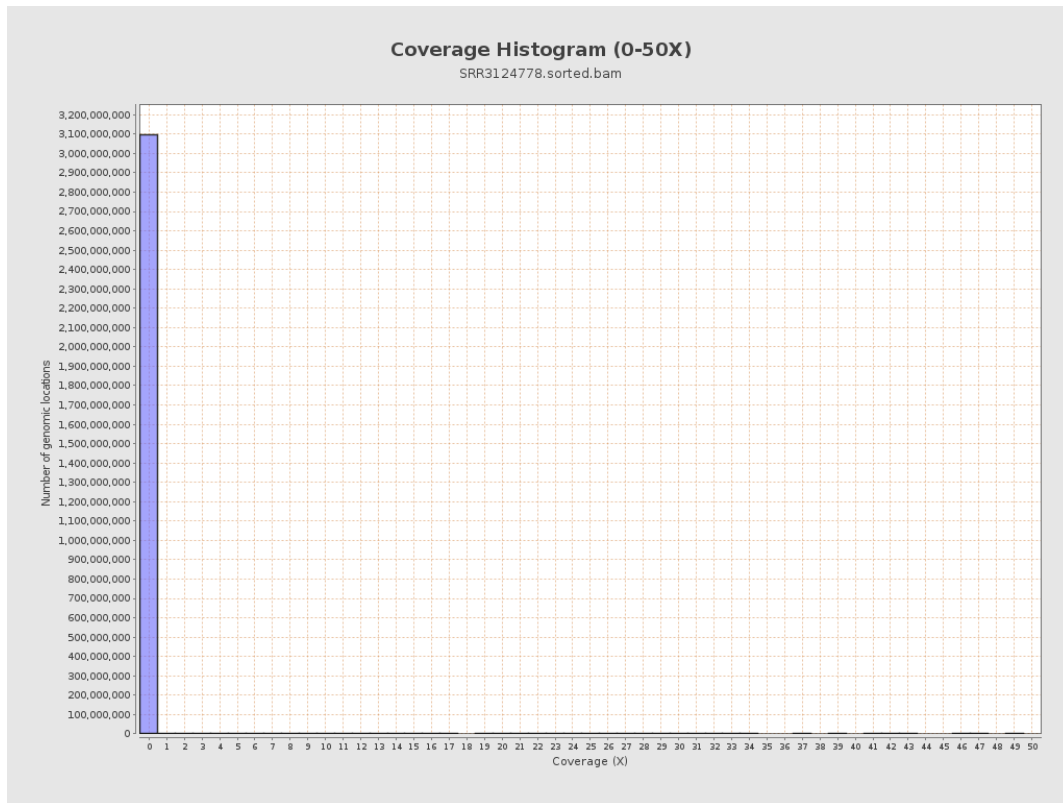
3. Results : Coverage across reference



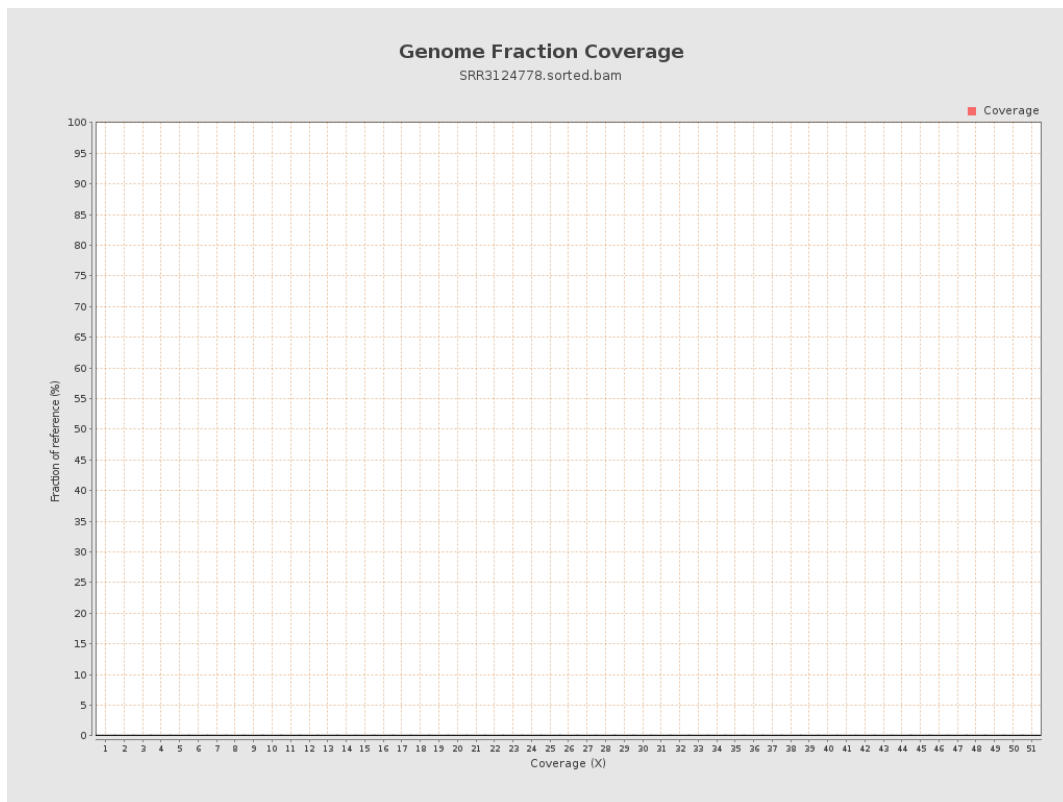
4. Results : Coverage Histogram



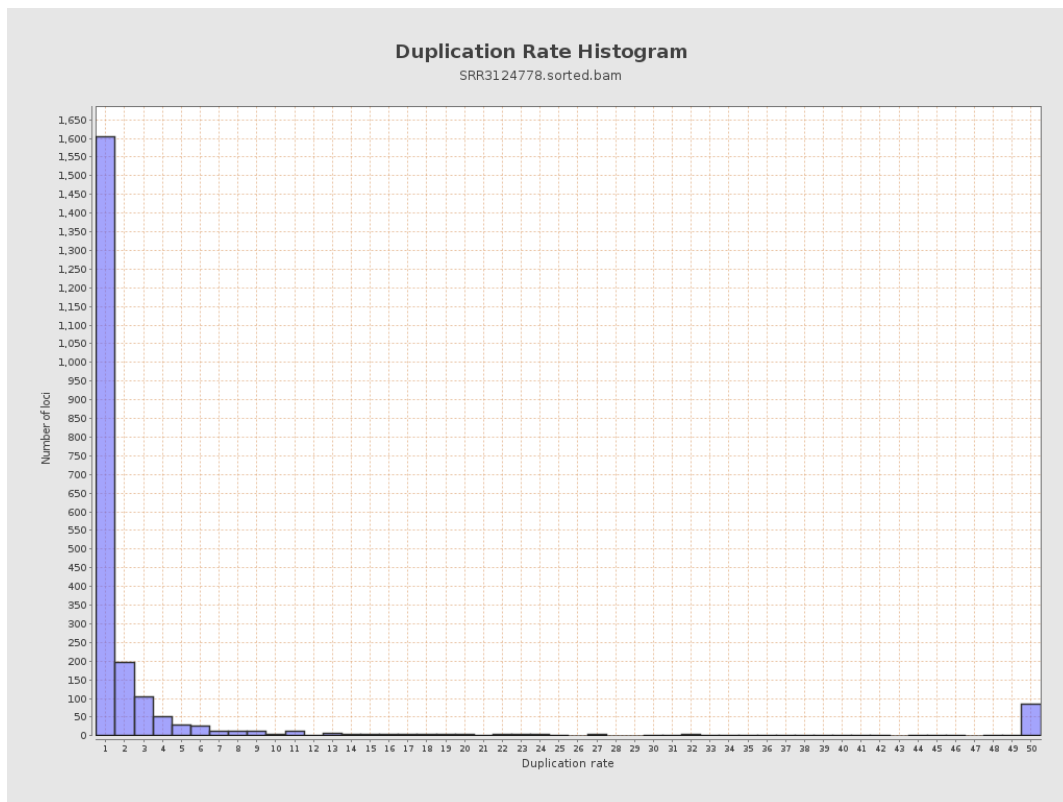
5. Results : Coverage Histogram (0-50X)



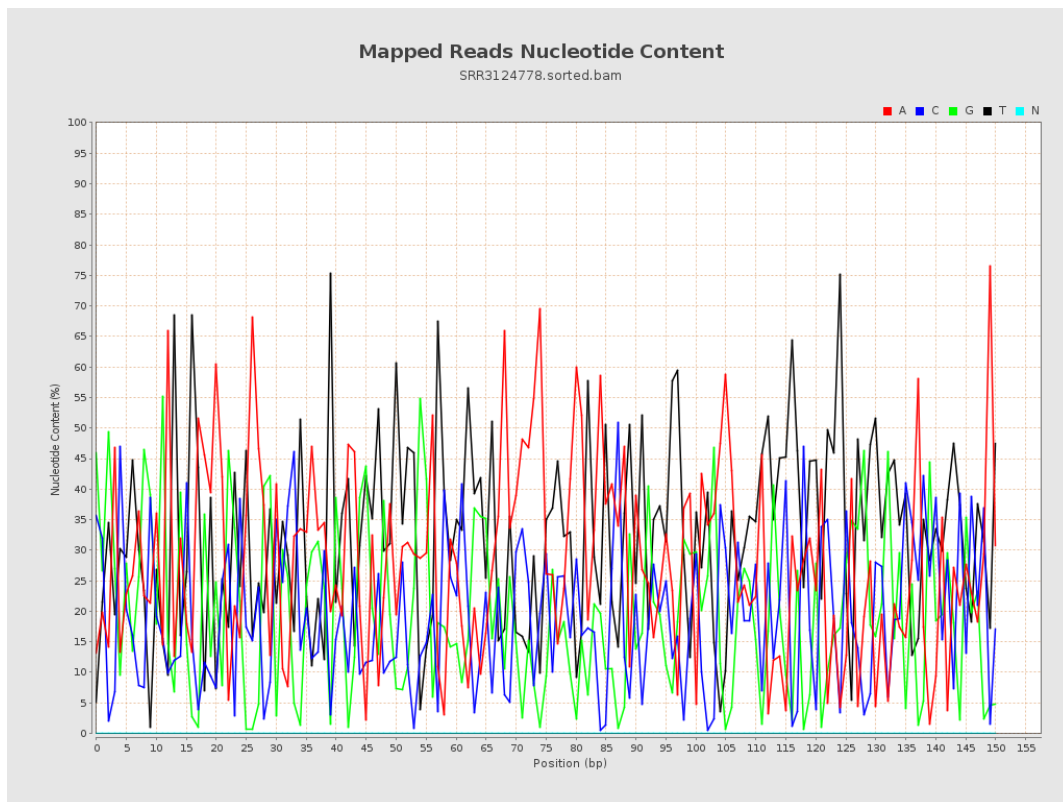
6. Results : Genome Fraction Coverage



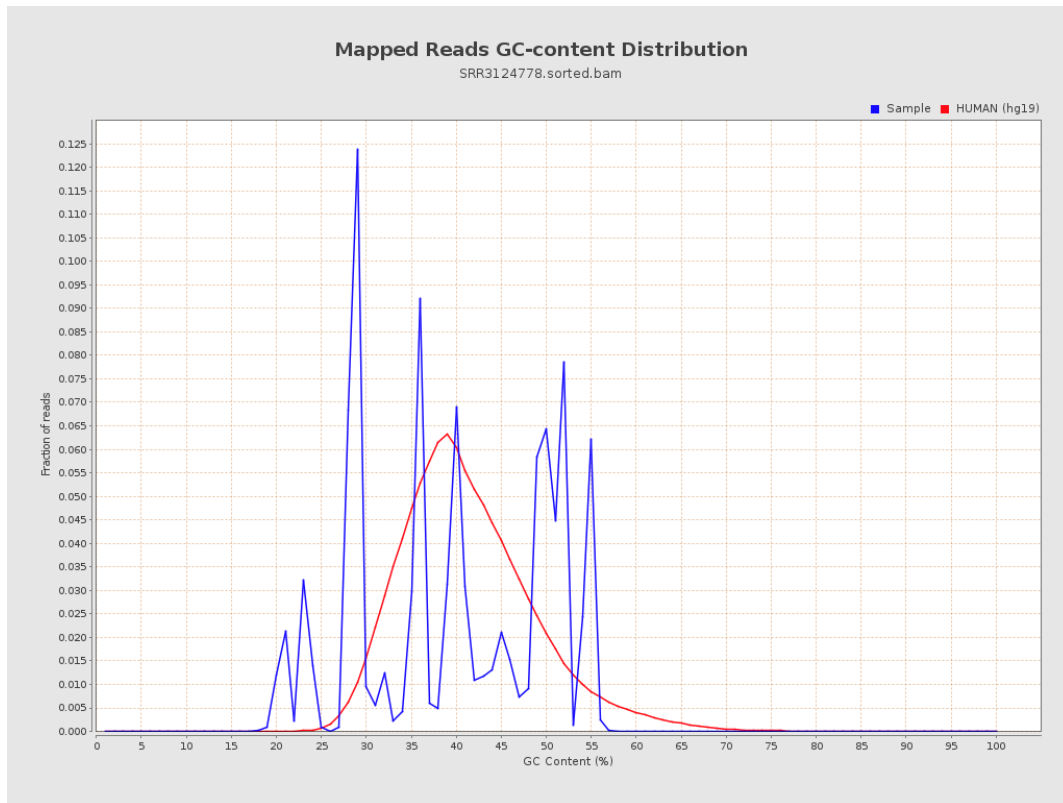
7. Results : Duplication Rate Histogram



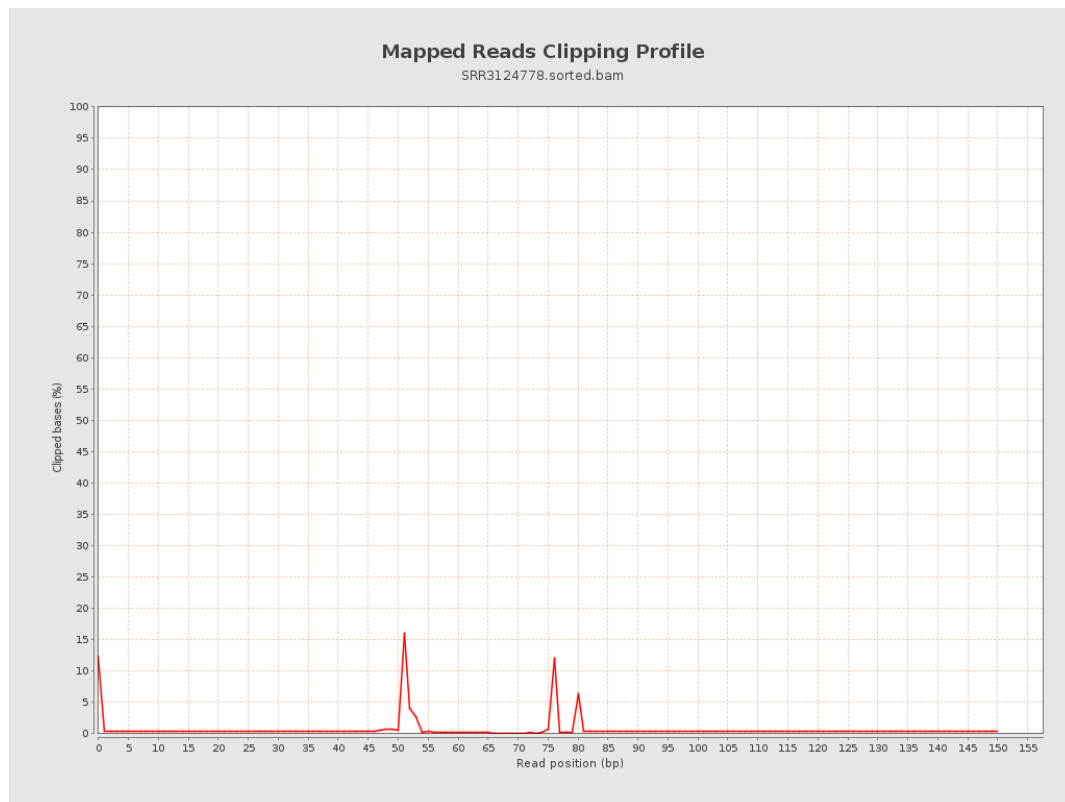
8. Results : Mapped Reads Nucleotide Content



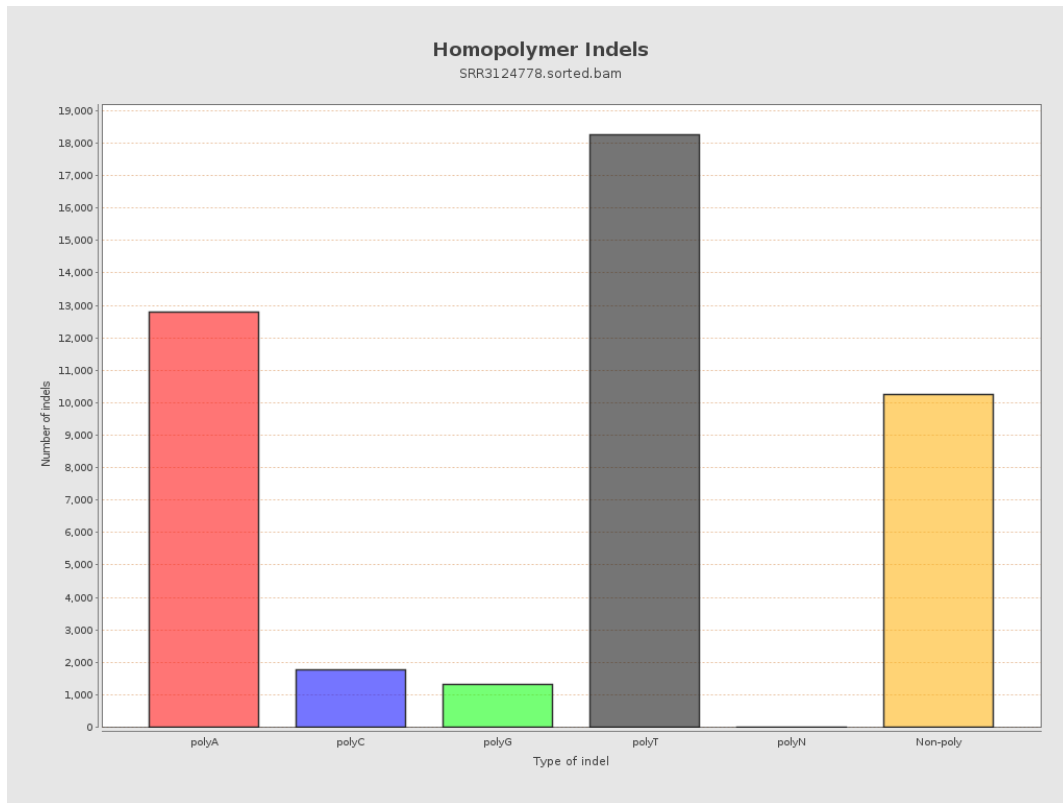
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

