

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:25:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124781.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_SRR3124781 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124781.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:25:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124781.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	479,955
Mapped reads	479,449 / 99.89%
Unmapped reads	506 / 0.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	223,066 / 46.48%
Read min/max/mean length	30 / 151 / 181.45
Duplicated reads (estimated)	701,069 / 146.07%
Duplication rate	40.87%
Clipped reads	461,606 / 96.18%

2.2. ACGT Content

Number/percentage of A's	20,091,821 / 27.89%
Number/percentage of C's	13,847,395 / 19.22%
Number/percentage of T's	23,285,120 / 32.33%
Number/percentage of G's	14,808,176 / 20.56%
Number/percentage of N's	0 / 0%
GC Percentage	39.78%

2.3. Coverage

Mean	0.0233

Standard Deviation	38.1276
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2.4. Mapping Quality

Mean Mapping Quality	27.47
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2.5. Mismatches and indels

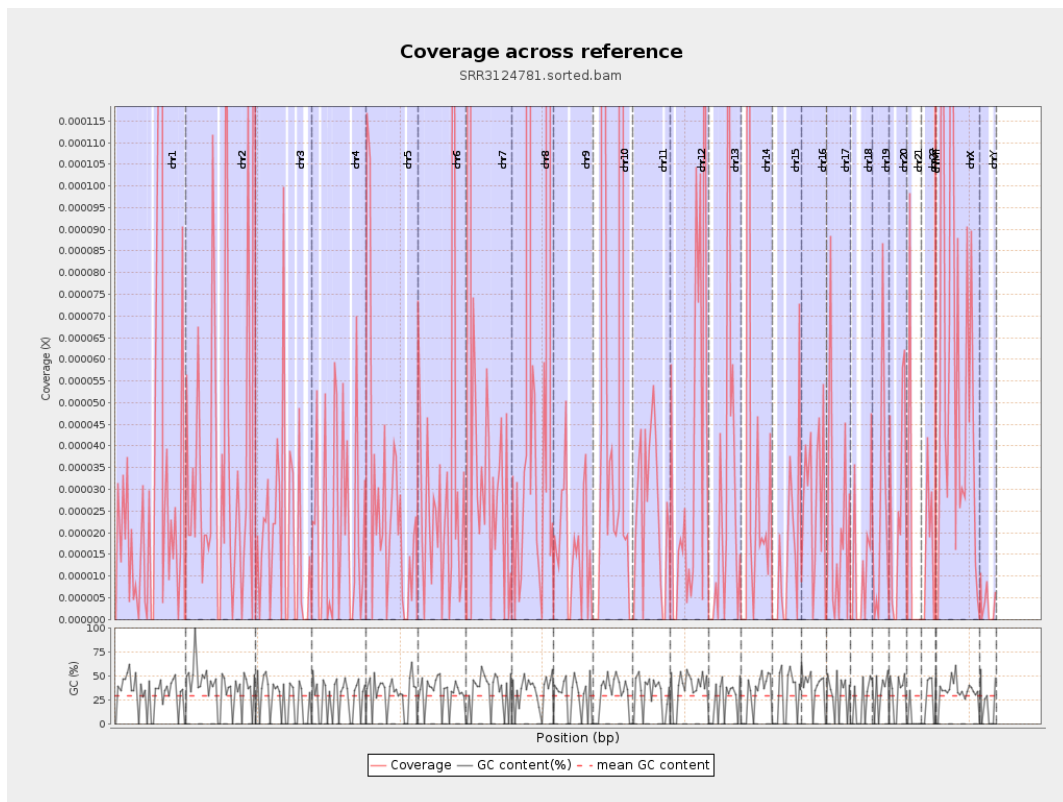
General error rate	0.85%
Mismatches	602,190
Insertions	9,817
Mapped reads with at least one insertion	2.03%
Deletions	43,319
Mapped reads with at least one deletion	8.74%
Homopolymer indels	53.67%

2.6. Chromosome stats

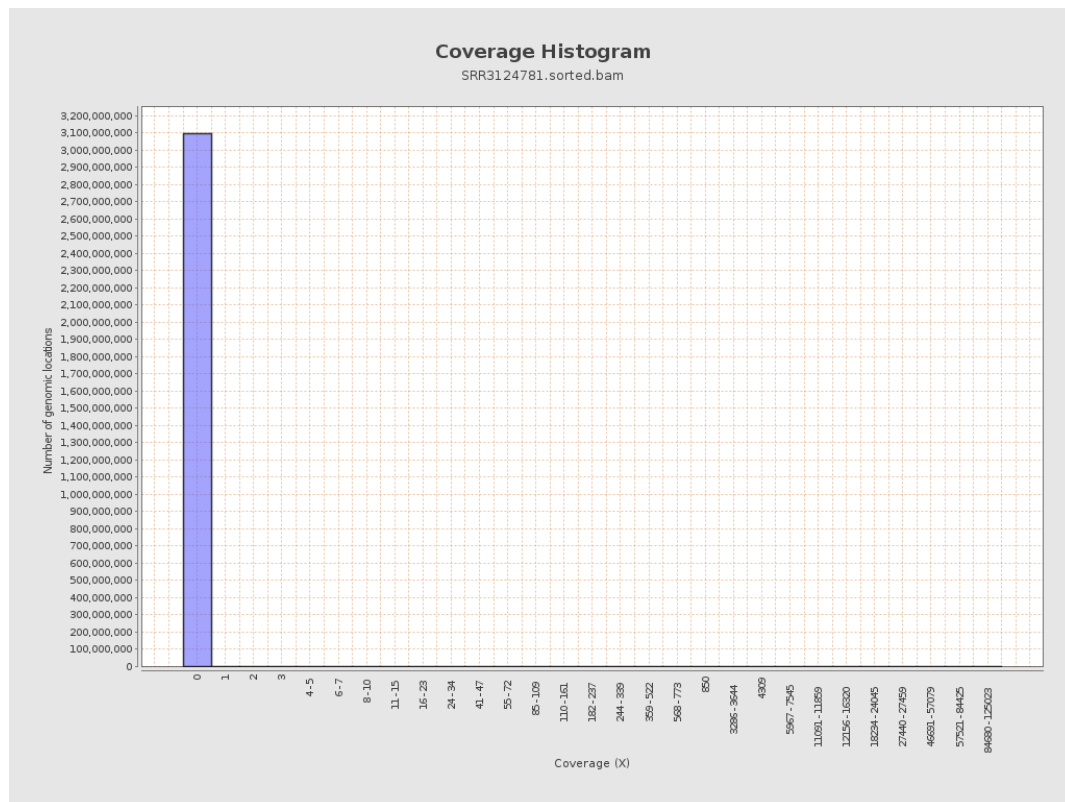
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	16346	0.0001	0.043
chr2	243199373	10116	0	0.0287
chr3	198022430	3637	0	0.0095
chr4	191154276	4248	0	0.0061
chr5	180915260	4897	0	0.0091
chr6	171115067	5749	0	0.0264
chr7	159138663	8658	0.0001	0.0587

chr8	146364022	52167902	0.3564	157.6538
chr9	141213431	2380	0	0.0044
chr10	135534747	19817341	0.1462	79.7683
chr11	135006516	3353	0	0.0081
chr12	133851895	5285	0	0.0151
chr13	115169878	3311	0	0.0139
chr14	107349540	4545	0	0.0396
chr15	102531392	1560	0	0.004
chr16	90354753	2445	0	0.0055
chr17	81195210	1660	0	0.0089
chr18	78077248	893	0	0.0044
chr19	59128983	1377	0	0.0079
chr20	63025520	1572	0	0.006
chr21	48129895	762	0	0.0162
chr22	51304566	702	0	0.0037
chrMT	16571	284	0.0171	0.1293
chrX	155270560	9343	0.0001	0.0193
chrY	59373566	203	0	0.0018

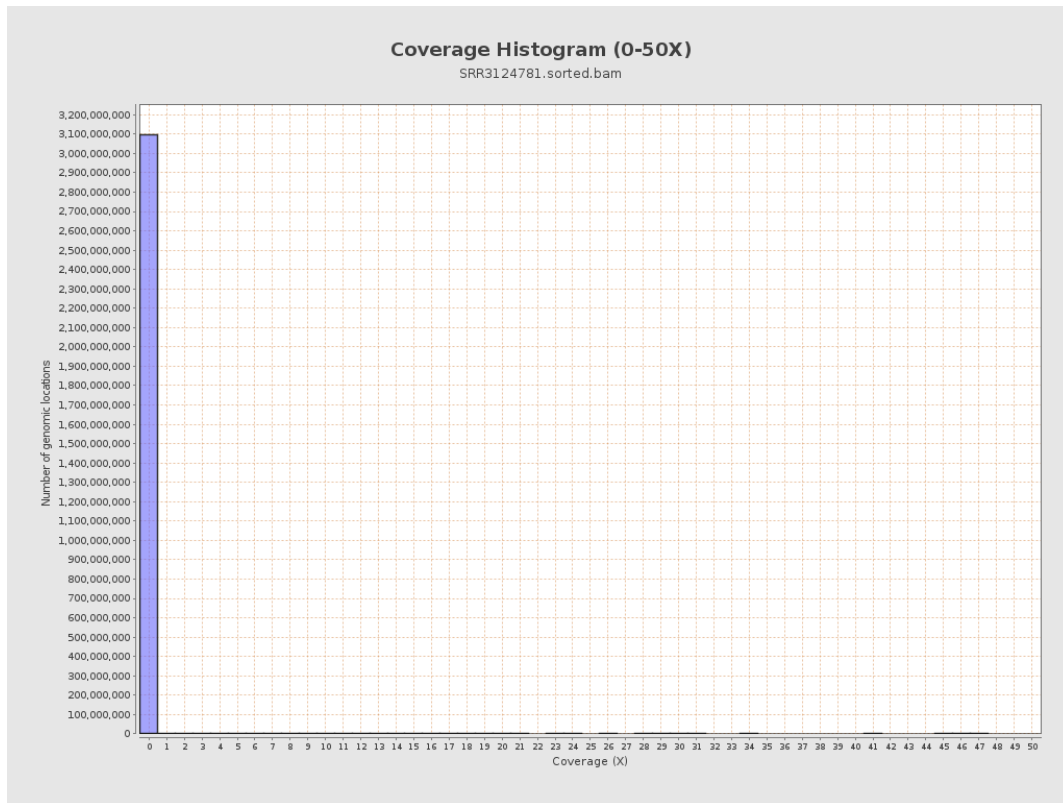
3. Results : Coverage across reference



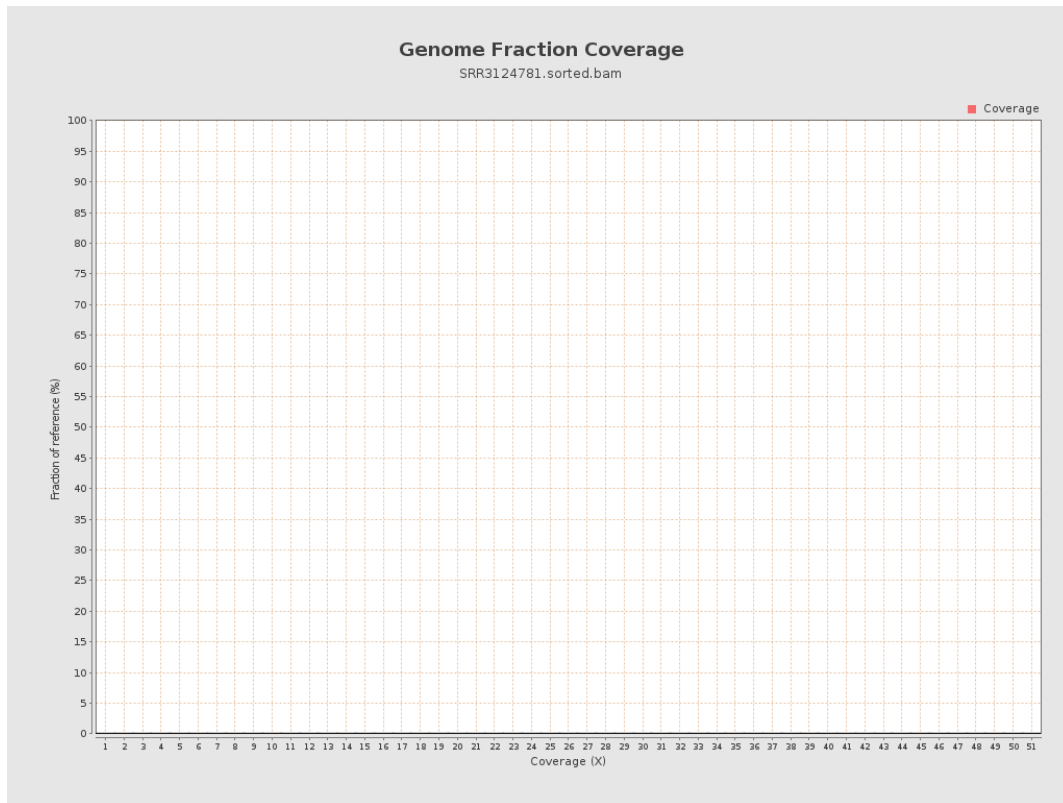
4. Results : Coverage Histogram



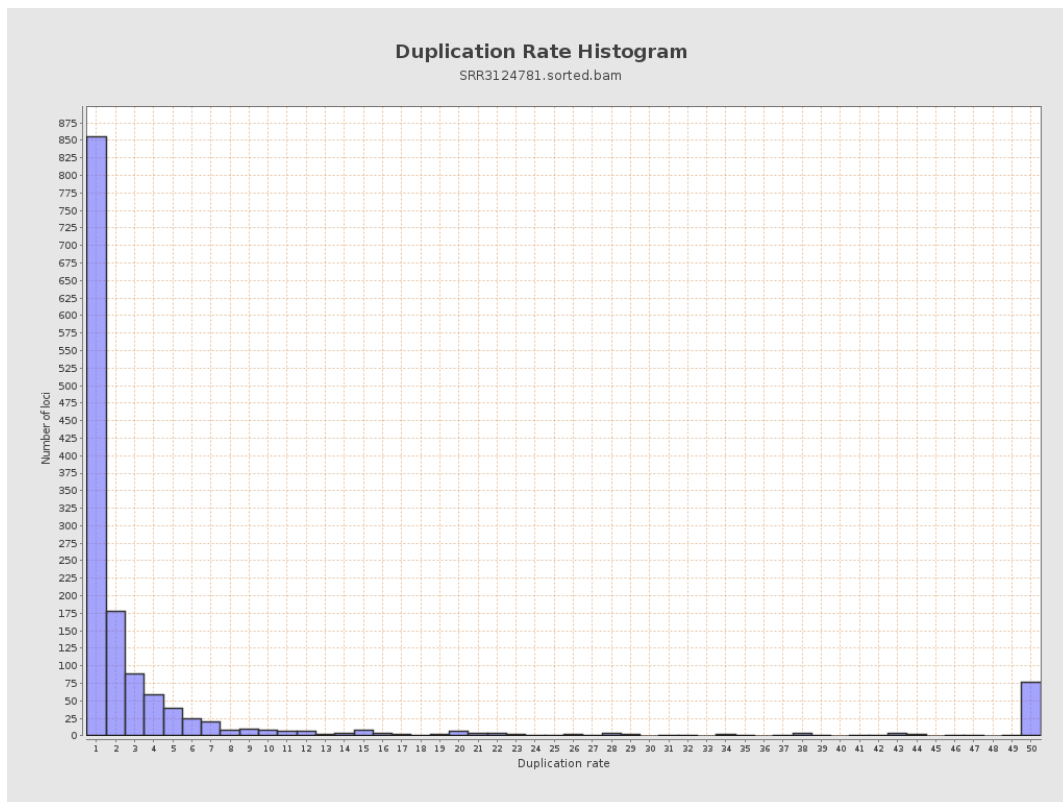
5. Results : Coverage Histogram (0-50X)



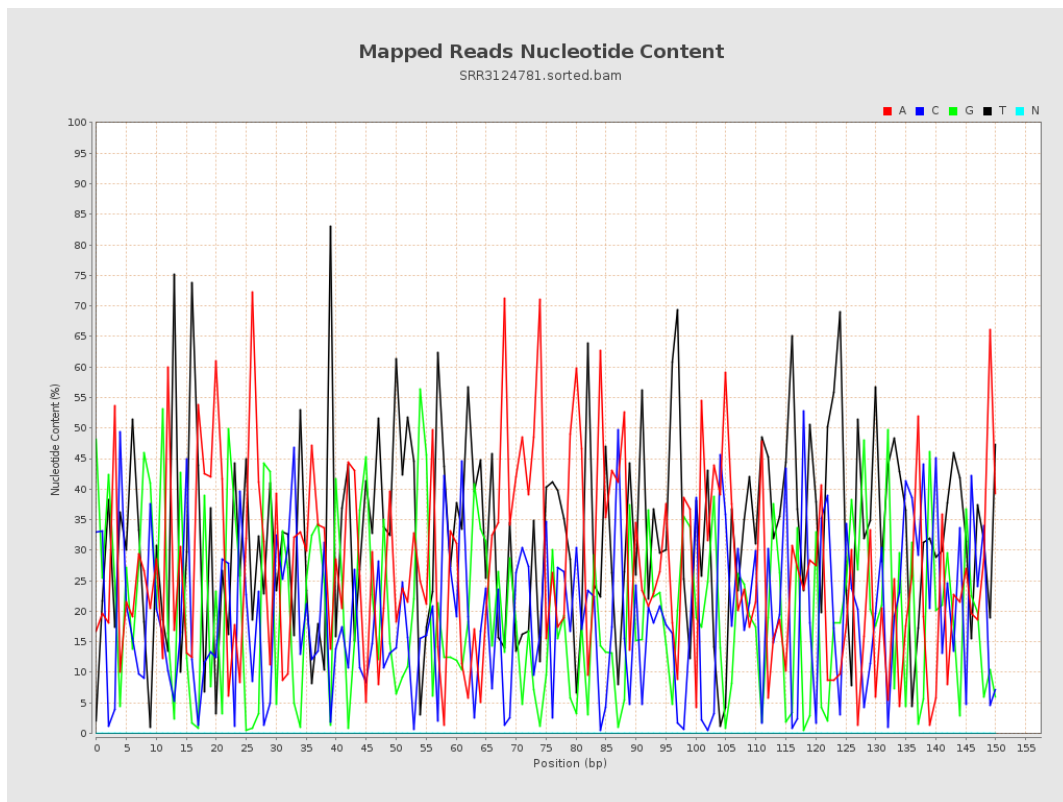
6. Results : Genome Fraction Coverage



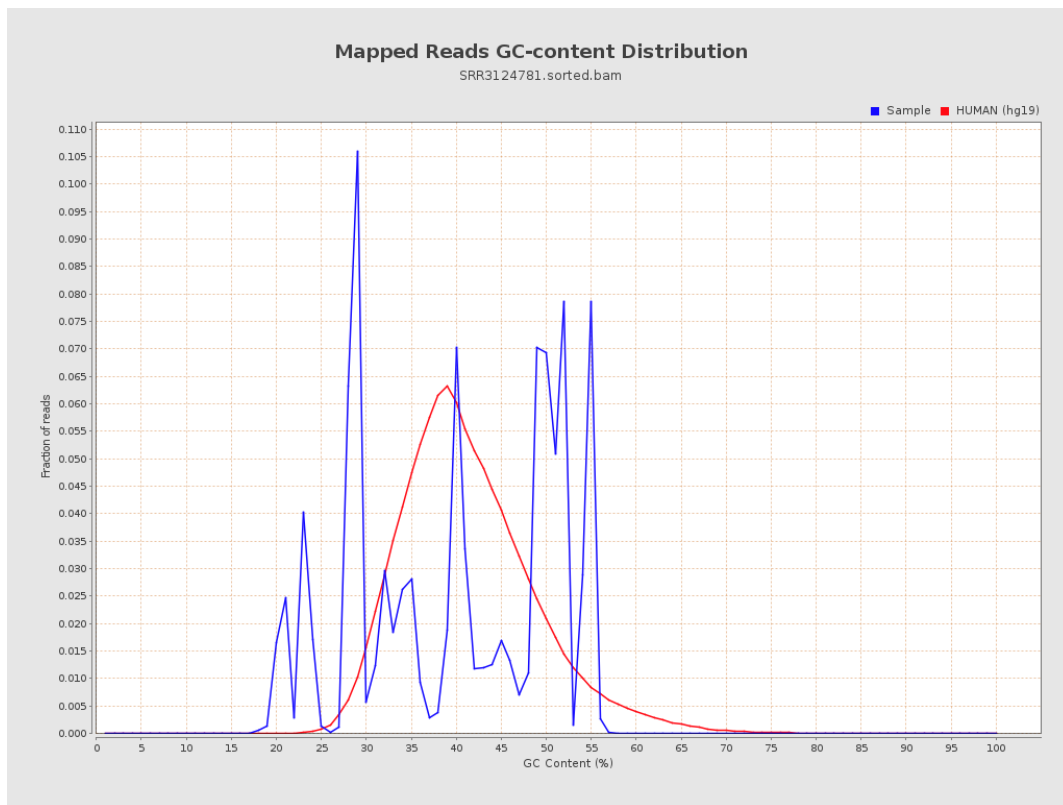
7. Results : Duplication Rate Histogram



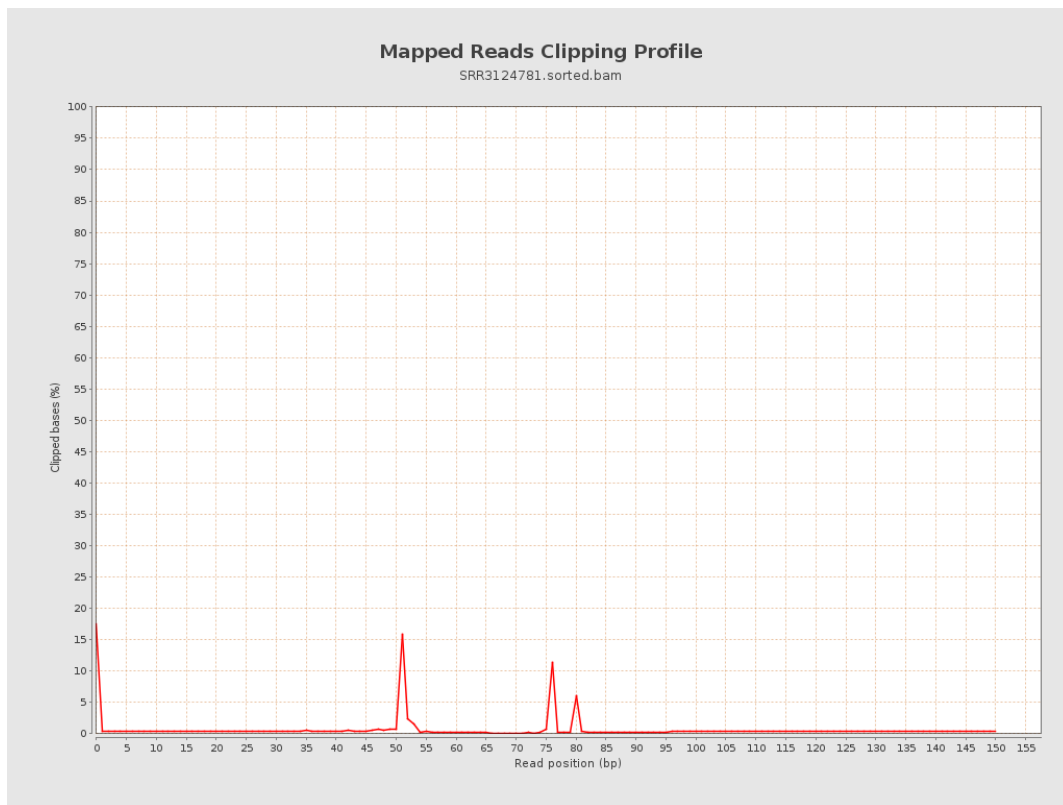
8. Results : Mapped Reads Nucleotide Content



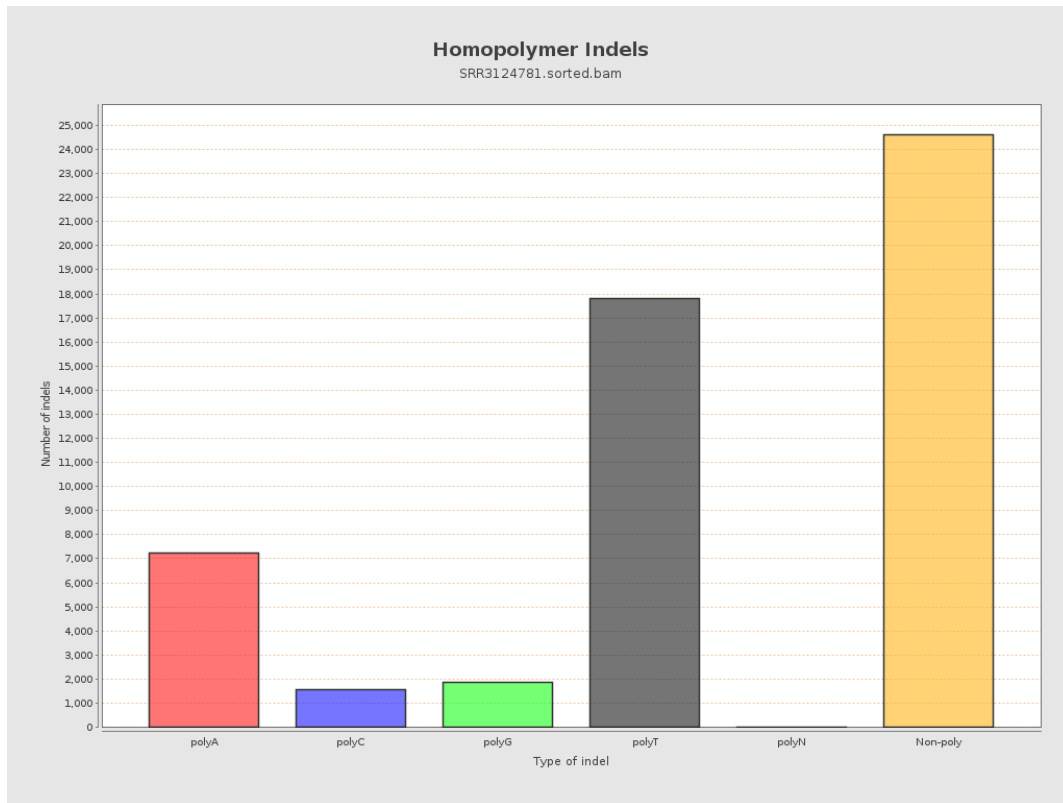
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

