

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:28:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124783.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_SRR3124783 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124783.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:28:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124783.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	527,735
Mapped reads	527,253 / 99.91%
Unmapped reads	482 / 0.09%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	244,450 / 46.32%
Read min/max/mean length	30 / 151 / 181.67
Duplicated reads (estimated)	769,318 / 145.78%
Duplication rate	16.94%
Clipped reads	511,794 / 96.98%

2.2. ACGT Content

Number/percentage of A's	21,463,262 / 27.18%
Number/percentage of C's	15,062,725 / 19.07%
Number/percentage of T's	25,581,632 / 32.39%
Number/percentage of G's	16,869,439 / 21.36%
Number/percentage of N's	0 / 0%
GC Percentage	40.43%

2.3. Coverage

Mean	0.0255

Standard Deviation	48.0697
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2.4. Mapping Quality

Mean Mapping Quality	46.95
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2.5. Mismatches and indels

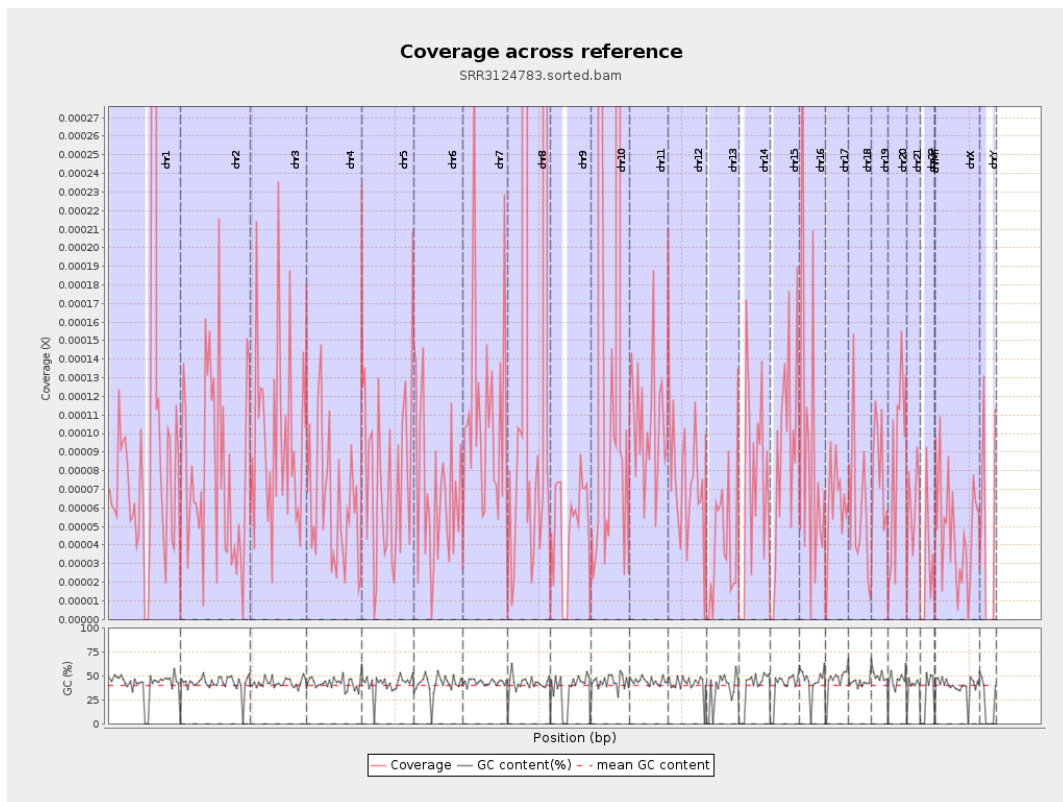
General error rate	0.77%
Mismatches	598,147
Insertions	9,087
Mapped reads with at least one insertion	1.71%
Deletions	35,778
Mapped reads with at least one deletion	6.57%
Homopolymer indels	78.86%

2.6. Chromosome stats

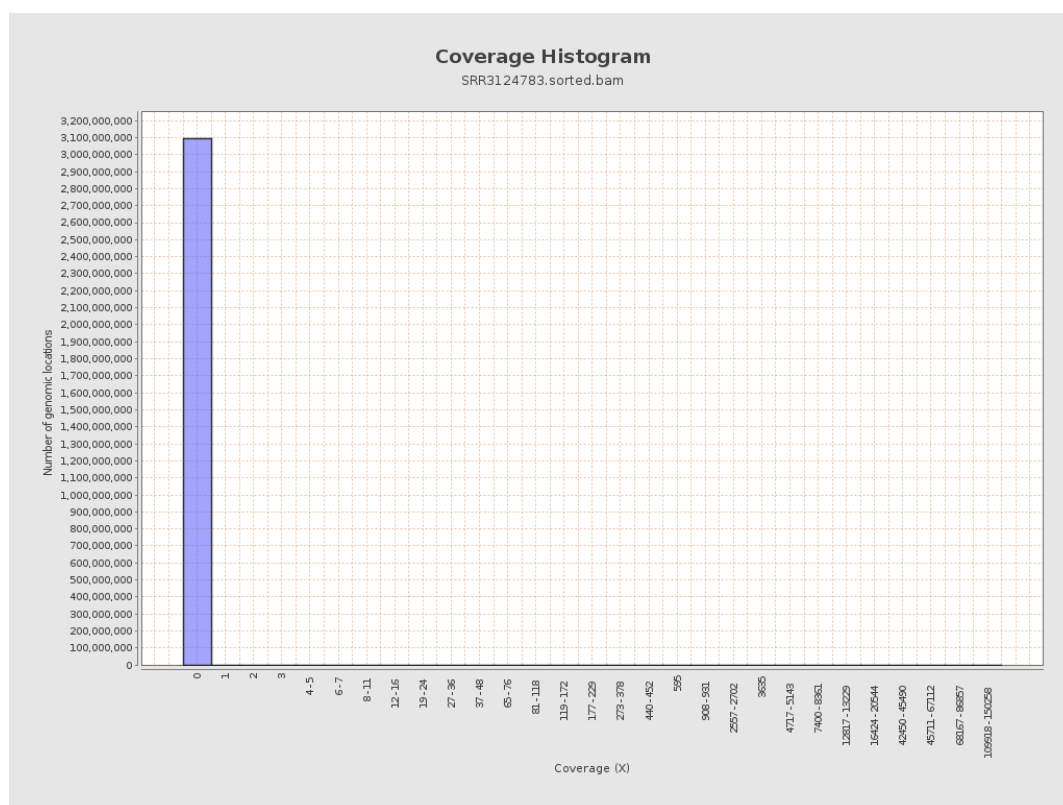
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	89986	0.0004	0.2659
chr2	243199373	19344	0.0001	0.0098
chr3	198022430	19677	0.0001	0.0147
chr4	191154276	11610	0.0001	0.008
chr5	180915260	13519	0.0001	0.0086
chr6	171115067	11857	0.0001	0.0099
chr7	159138663	17231	0.0001	0.0108

chr8	146364022	61814816	0.4223	210.6255
chr9	141213431	6995	0	0.007
chr10	135534747	16924630	0.1249	69.7826
chr11	135006516	14317	0.0001	0.0113
chr12	133851895	9832	0.0001	0.0086
chr13	115169878	4791	0	0.0064
chr14	107349540	7420	0.0001	0.0158
chr15	102531392	8930	0.0001	0.0102
chr16	90354753	8608	0.0001	0.0233
chr17	81195210	5051	0.0001	0.0079
chr18	78077248	4551	0.0001	0.0077
chr19	59128983	4706	0.0001	0.0089
chr20	63025520	5445	0.0001	0.0093
chr21	48129895	2877	0.0001	0.0077
chr22	51304566	1411	0	0.0053
chrMT	16571	0	0	0
chrX	155270560	7328	0	0.007
chrY	59373566	2495	0	0.0067

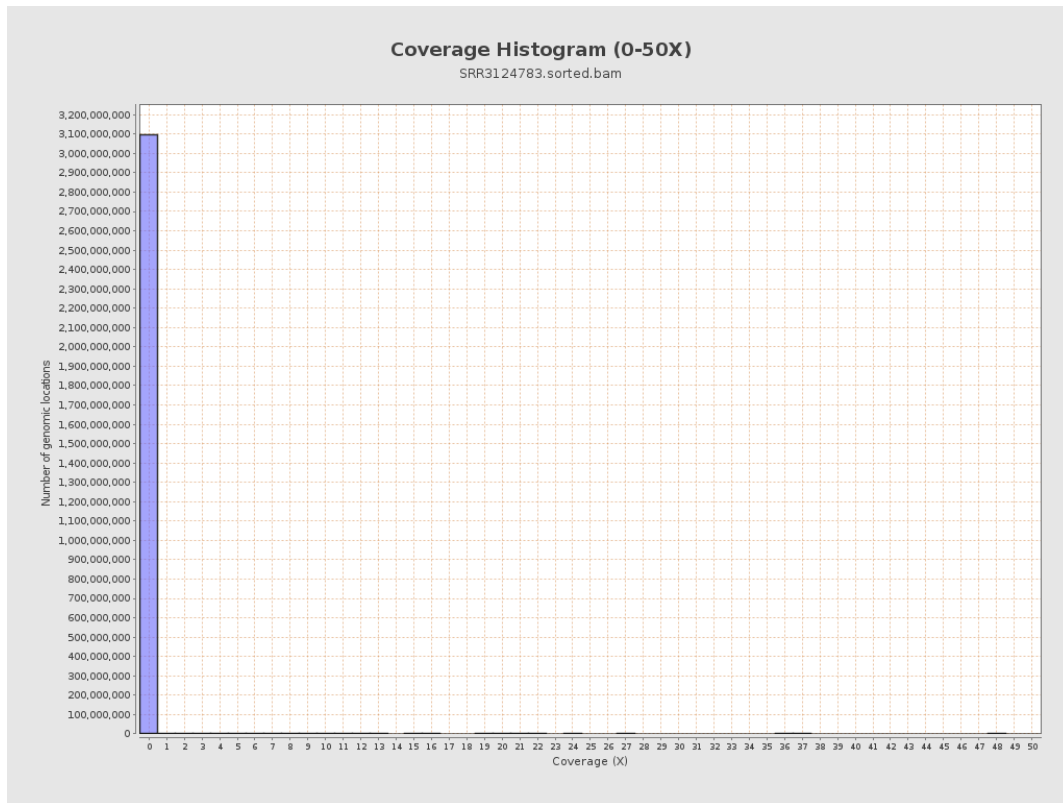
3. Results : Coverage across reference



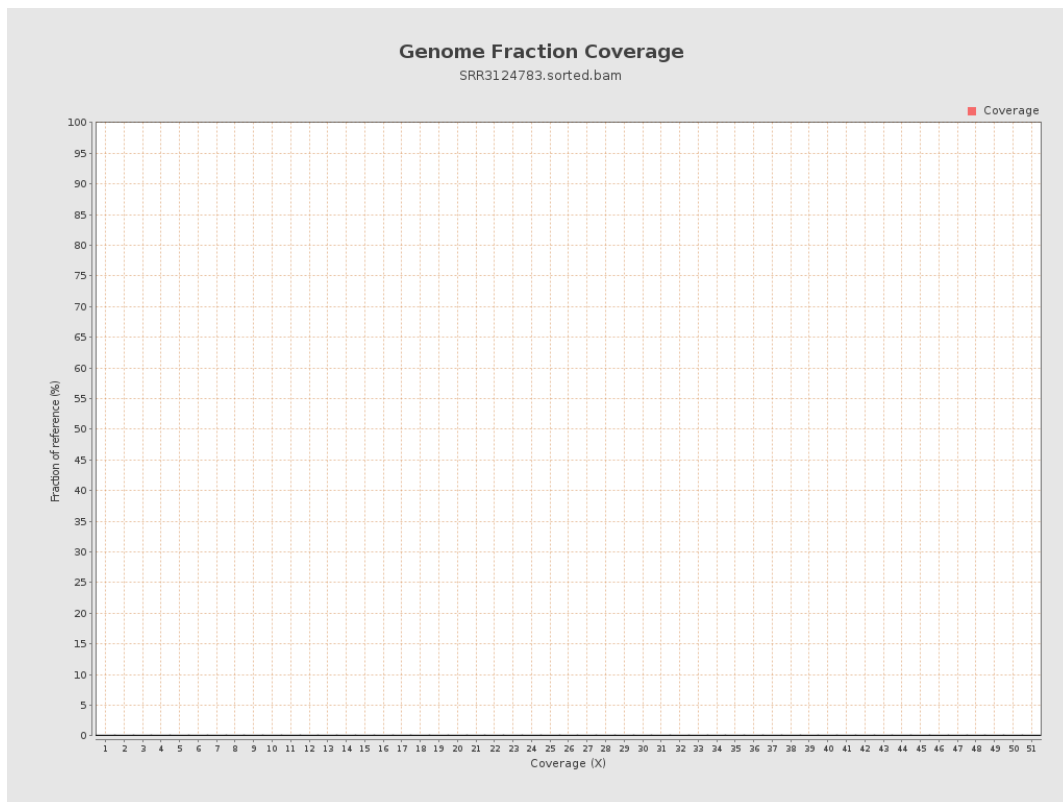
4. Results : Coverage Histogram



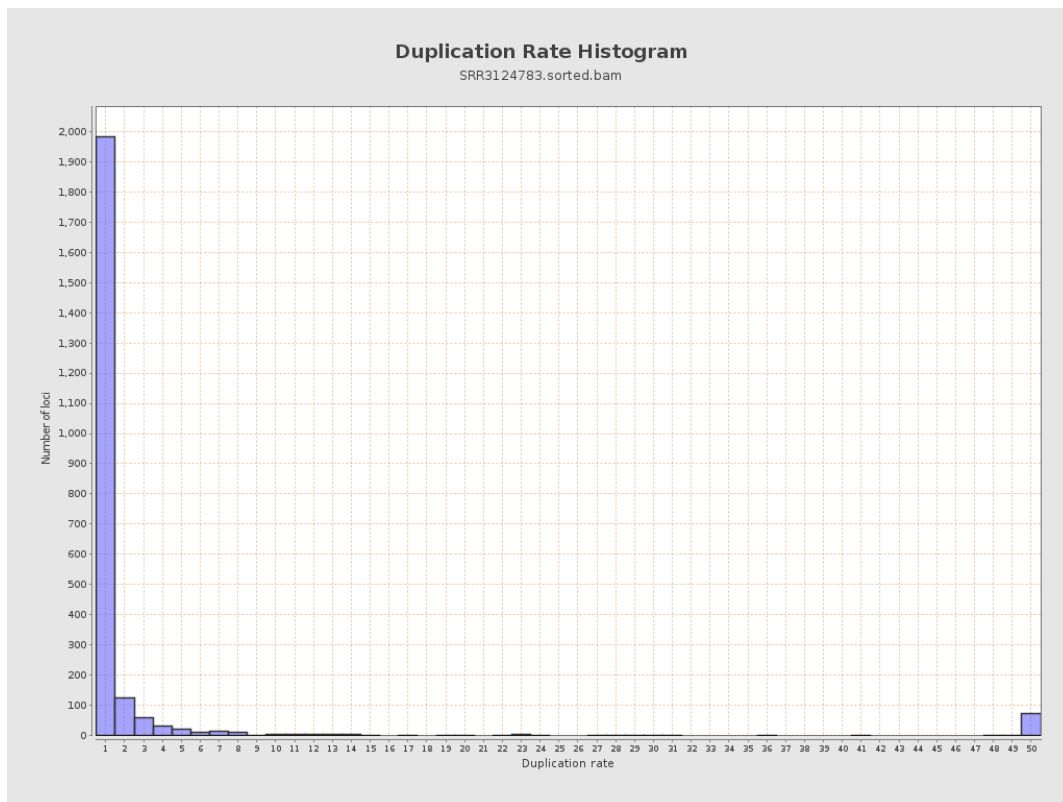
5. Results : Coverage Histogram (0-50X)



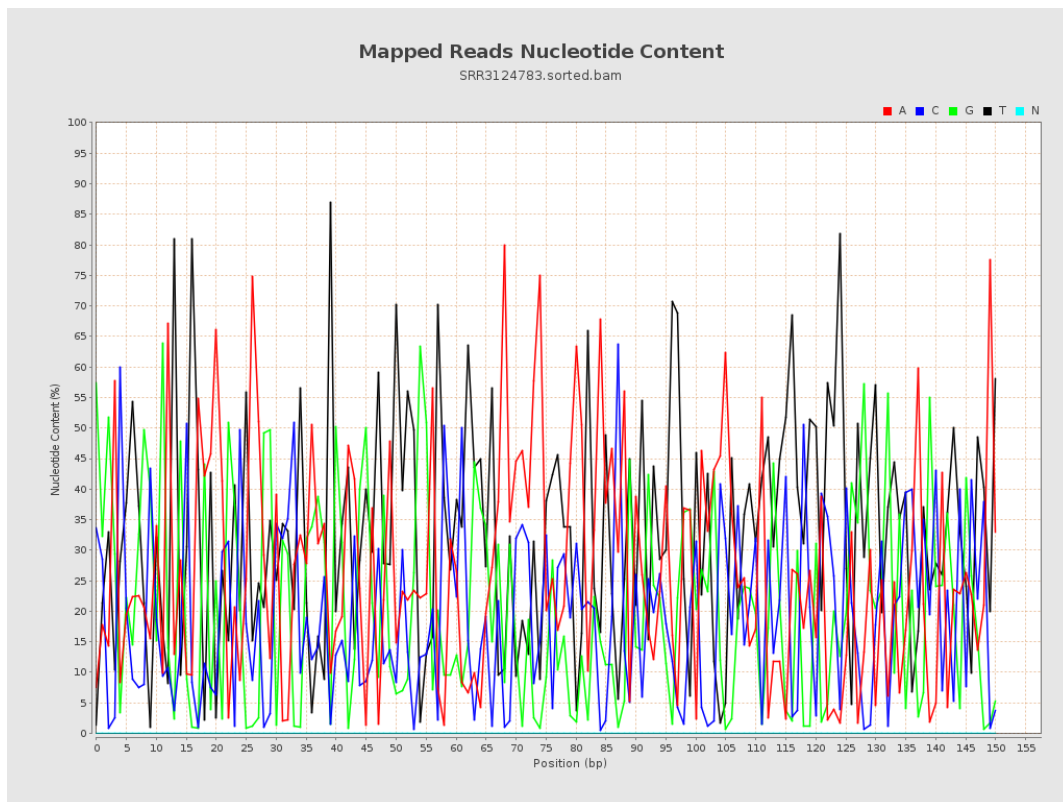
6. Results : Genome Fraction Coverage



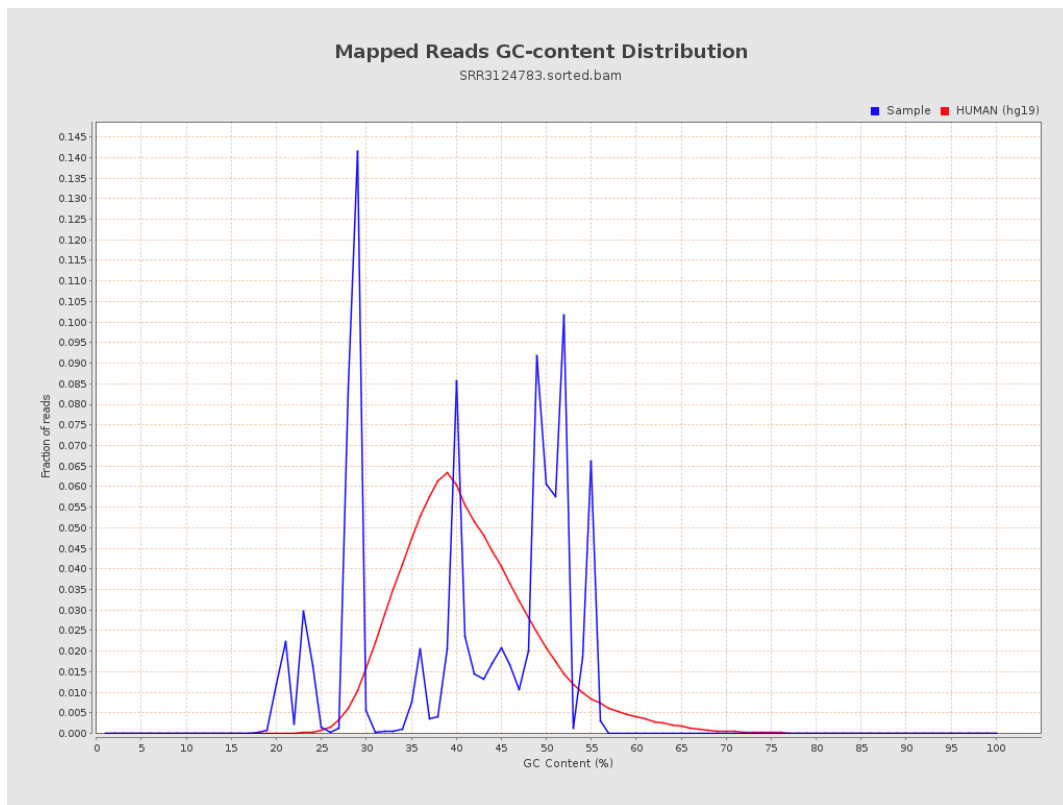
7. Results : Duplication Rate Histogram



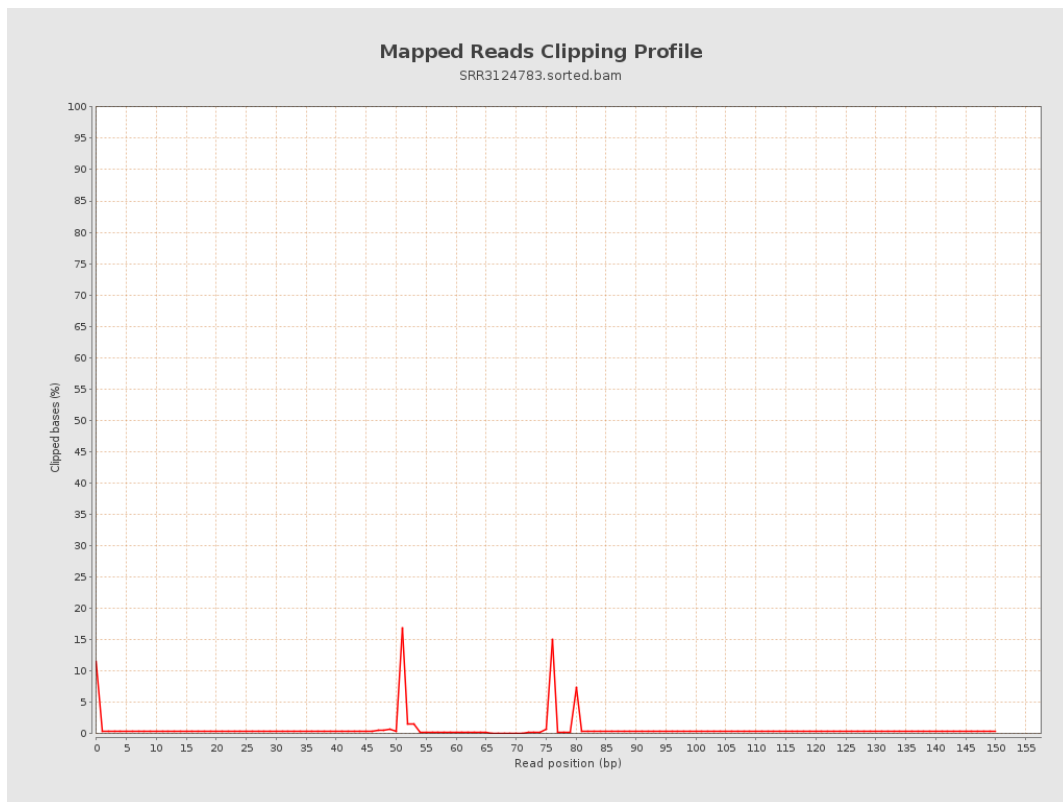
8. Results : Mapped Reads Nucleotide Content



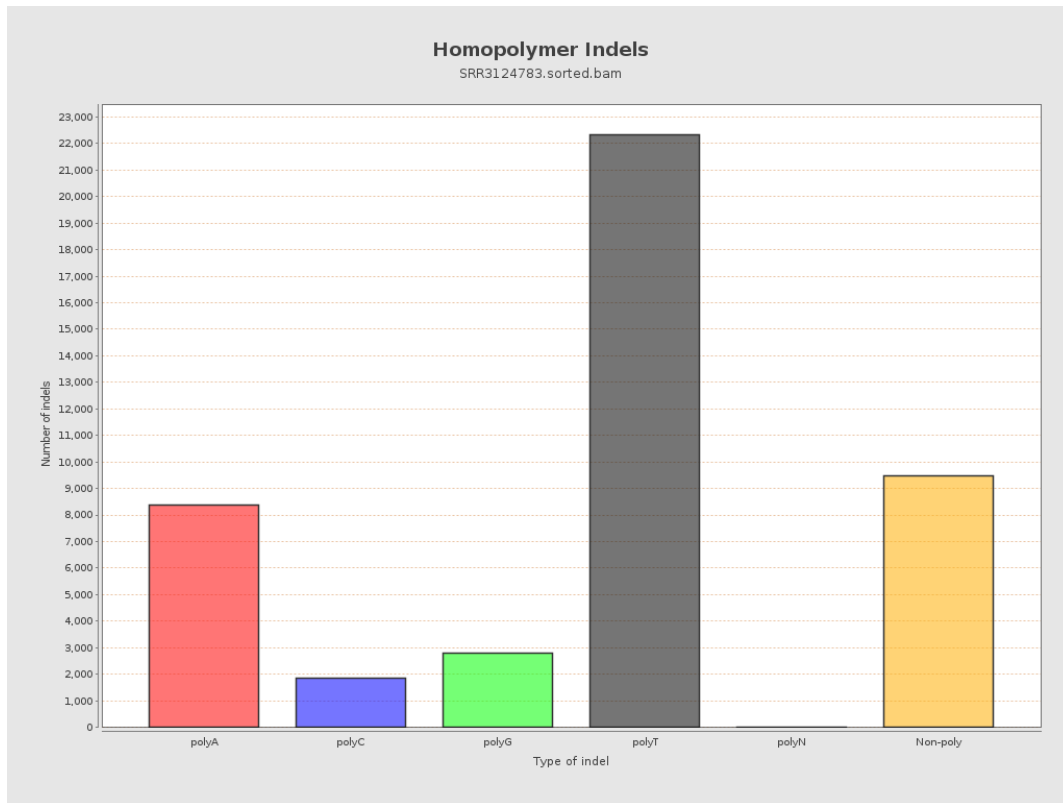
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

