

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:40:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124790.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_SRR3124790 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124790.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:40:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124790.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	628,702
Mapped reads	627,878 / 99.87%
Unmapped reads	824 / 0.13%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	252,845 / 40.22%
Read min/max/mean length	30 / 151 / 177.32
Duplicated reads (estimated)	877,812 / 139.62%
Duplication rate	17.9%
Clipped reads	558,871 / 88.89%

2.2. ACGT Content

Number/percentage of A's	26,722,253 / 28.63%
Number/percentage of C's	17,642,467 / 18.9%
Number/percentage of T's	29,741,185 / 31.86%
Number/percentage of G's	19,244,813 / 20.62%
Number/percentage of N's	0 / 0%
GC Percentage	39.51%

2.3. Coverage

Mean	0.0302

Standard Deviation	49.1579
--------------------	---------

2.4. Mapping Quality

Mean Mapping Quality	48.32
----------------------	-------

2.5. Mismatches and indels

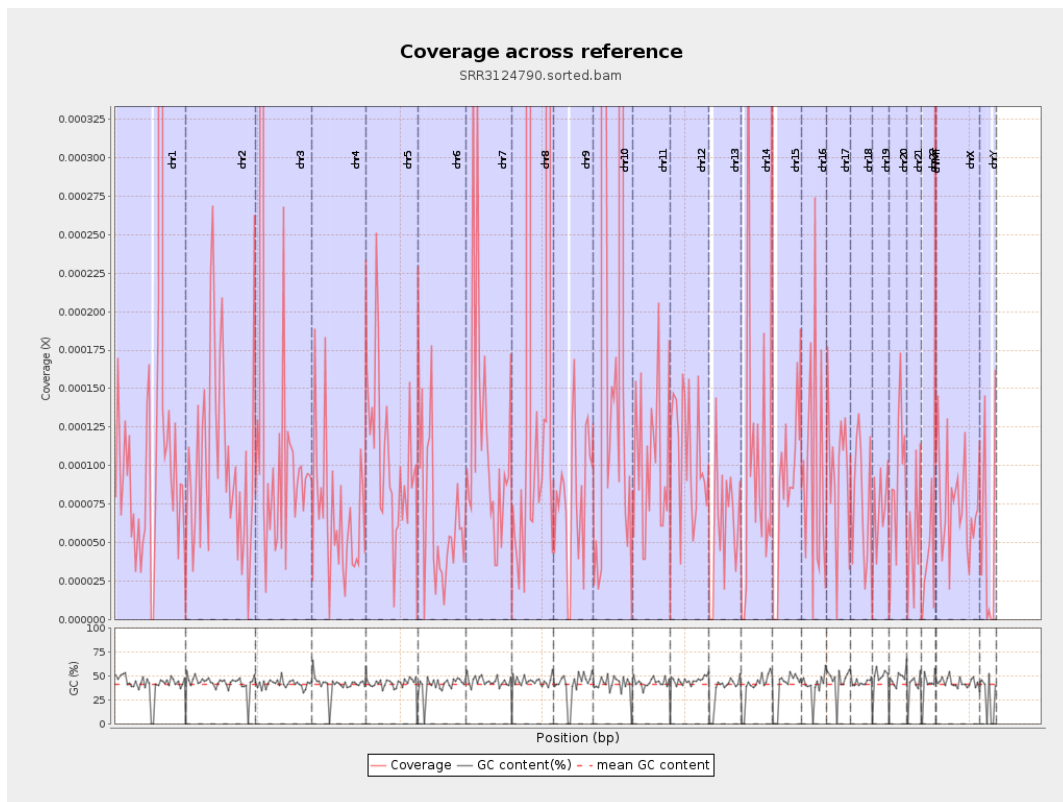
General error rate	0.79%
Mismatches	719,588
Insertions	18,512
Mapped reads with at least one insertion	2.93%
Deletions	47,370
Mapped reads with at least one deletion	7.34%
Homopolymer indels	73.43%

2.6. Chromosome stats

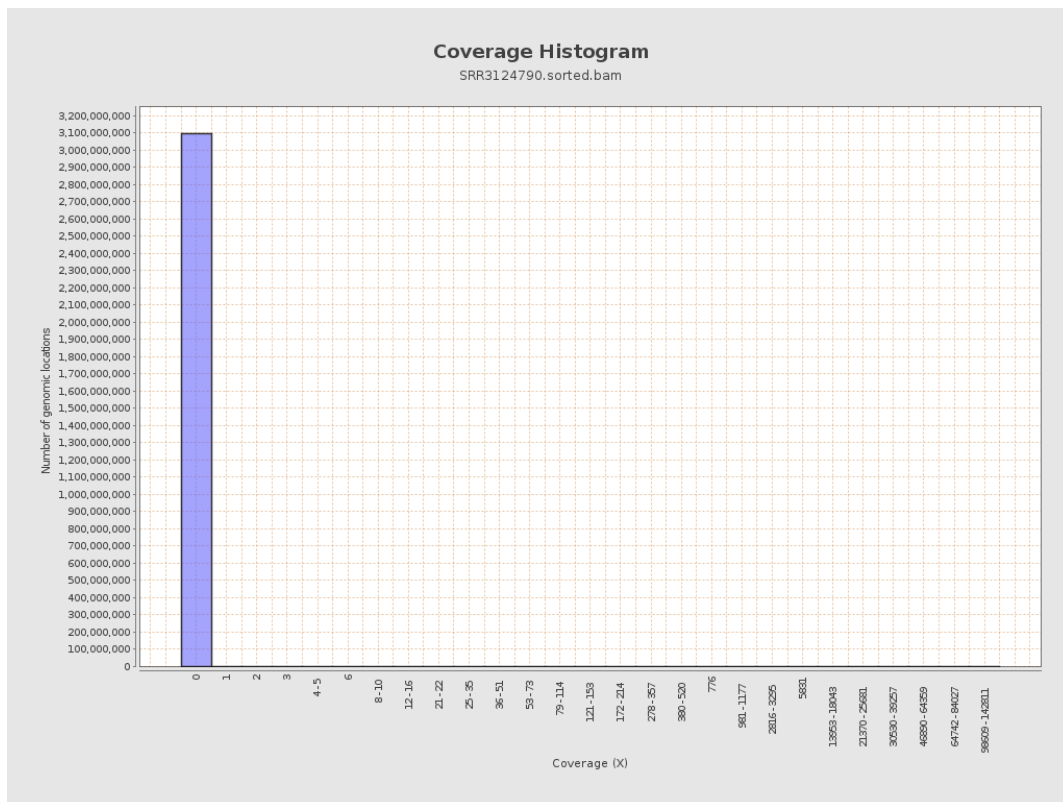
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	61335	0.0002	0.1485
chr2	243199373	24921	0.0001	0.0171
chr3	198022430	29276	0.0001	0.0702
chr4	191154276	12736	0.0001	0.0082
chr5	180915260	18799	0.0001	0.0102
chr6	171115067	11761	0.0001	0.0123
chr7	159138663	19235	0.0001	0.0222

chr8	146364022	67891948	0.4639	208.1052
chr9	141213431	11356	0.0001	0.0091
chr10	135534747	25212486	0.186	91.7923
chr11	135006516	13694	0.0001	0.0107
chr12	133851895	14501	0.0001	0.0104
chr13	115169878	6898	0.0001	0.0077
chr14	107349540	10955	0.0001	0.0326
chr15	102531392	8627	0.0001	0.0092
chr16	90354753	8433	0.0001	0.0097
chr17	81195210	7990	0.0001	0.0099
chr18	78077248	6139	0.0001	0.009
chr19	59128983	4077	0.0001	0.0083
chr20	63025520	5842	0.0001	0.0096
chr21	48129895	2655	0.0001	0.0079
chr22	51304566	2068	0	0.0063
chrMT	16571	303	0.0183	0.1338
chrX	155270560	11687	0.0001	0.009
chrY	59373566	2803	0	0.0069

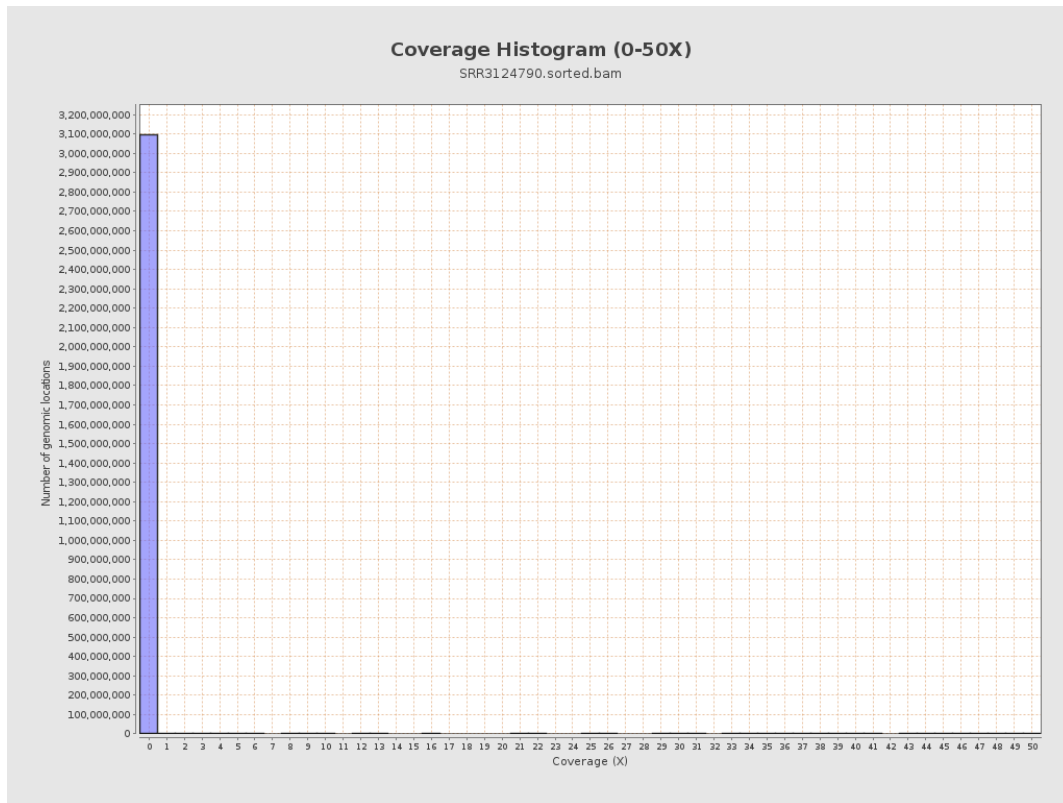
3. Results : Coverage across reference



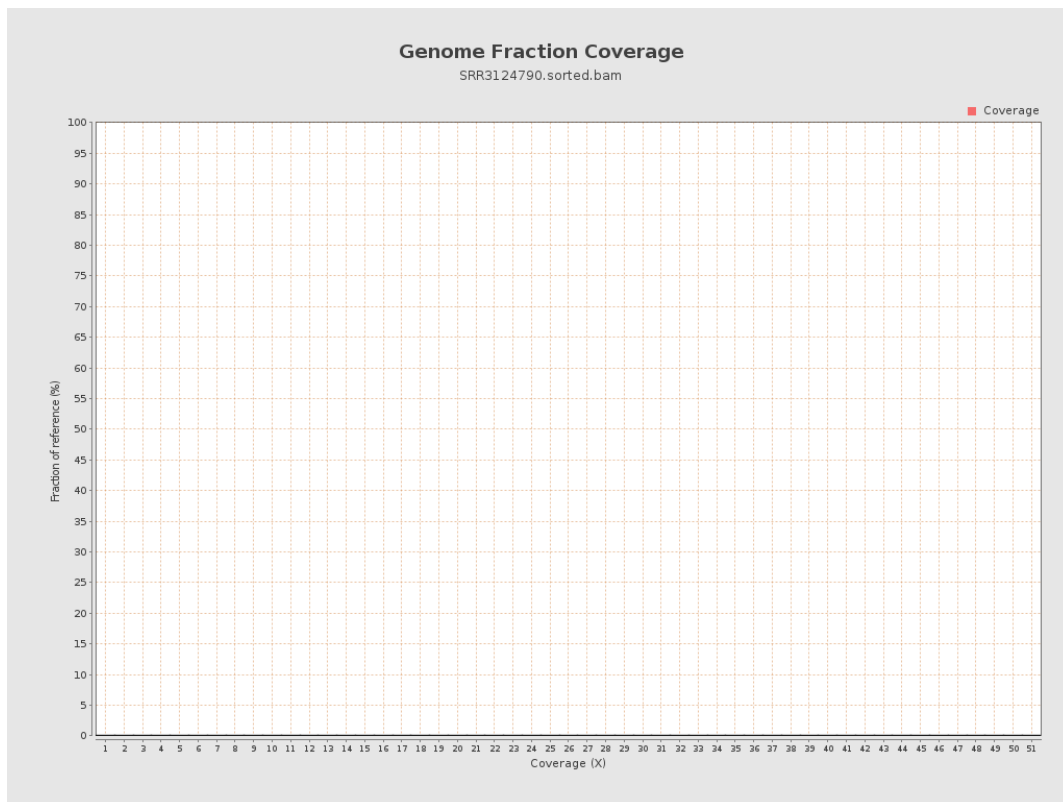
4. Results : Coverage Histogram



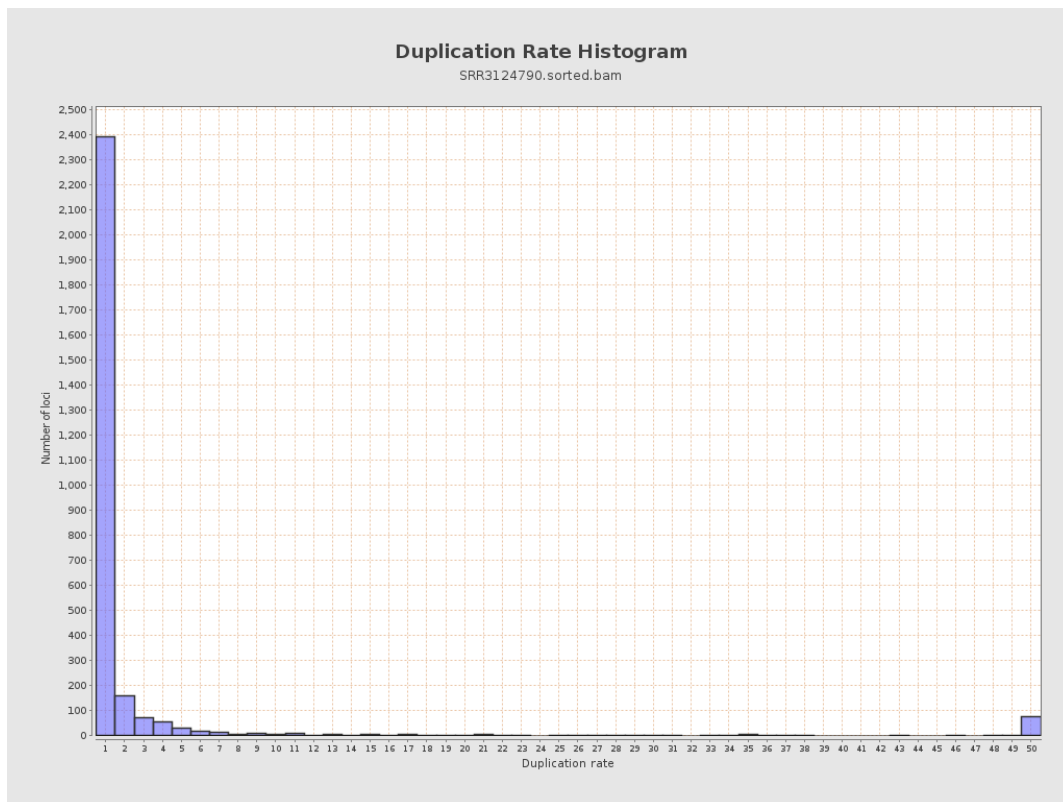
5. Results : Coverage Histogram (0-50X)



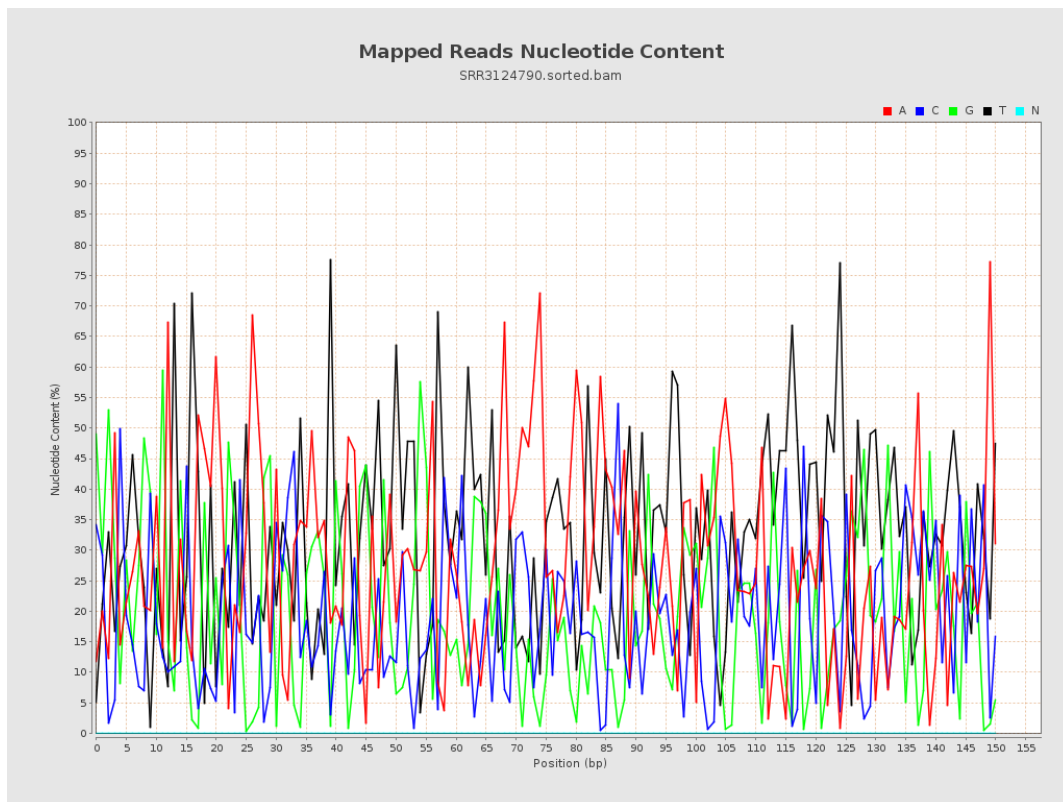
6. Results : Genome Fraction Coverage



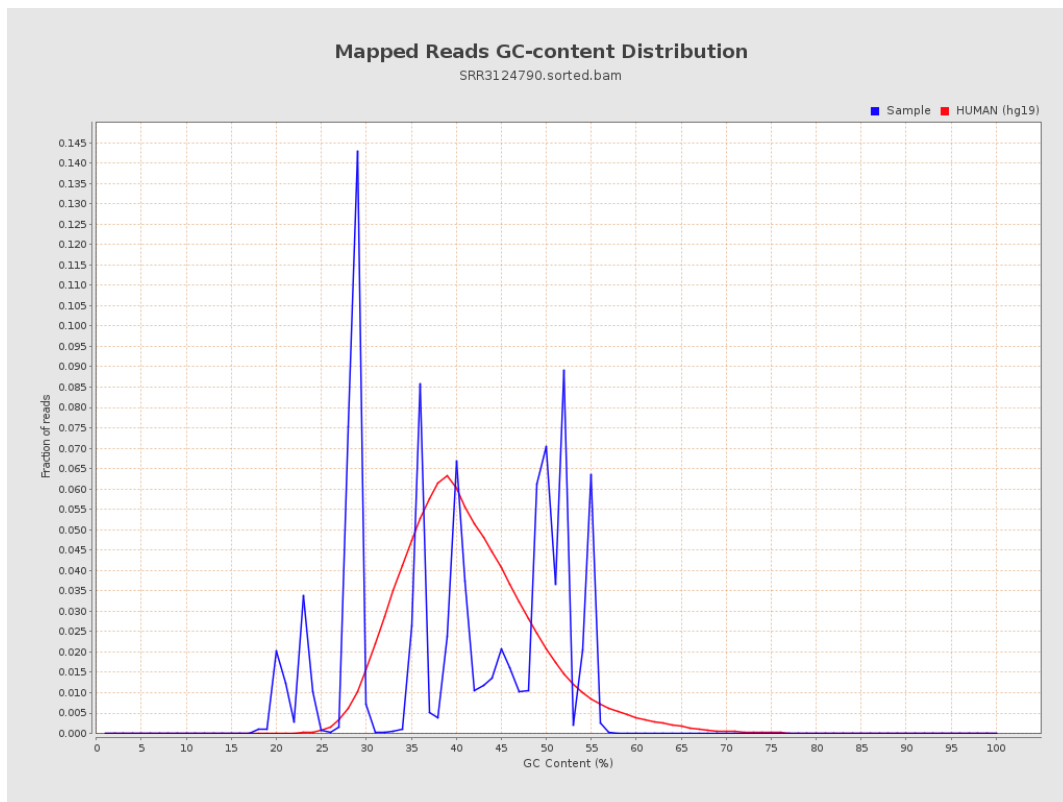
7. Results : Duplication Rate Histogram



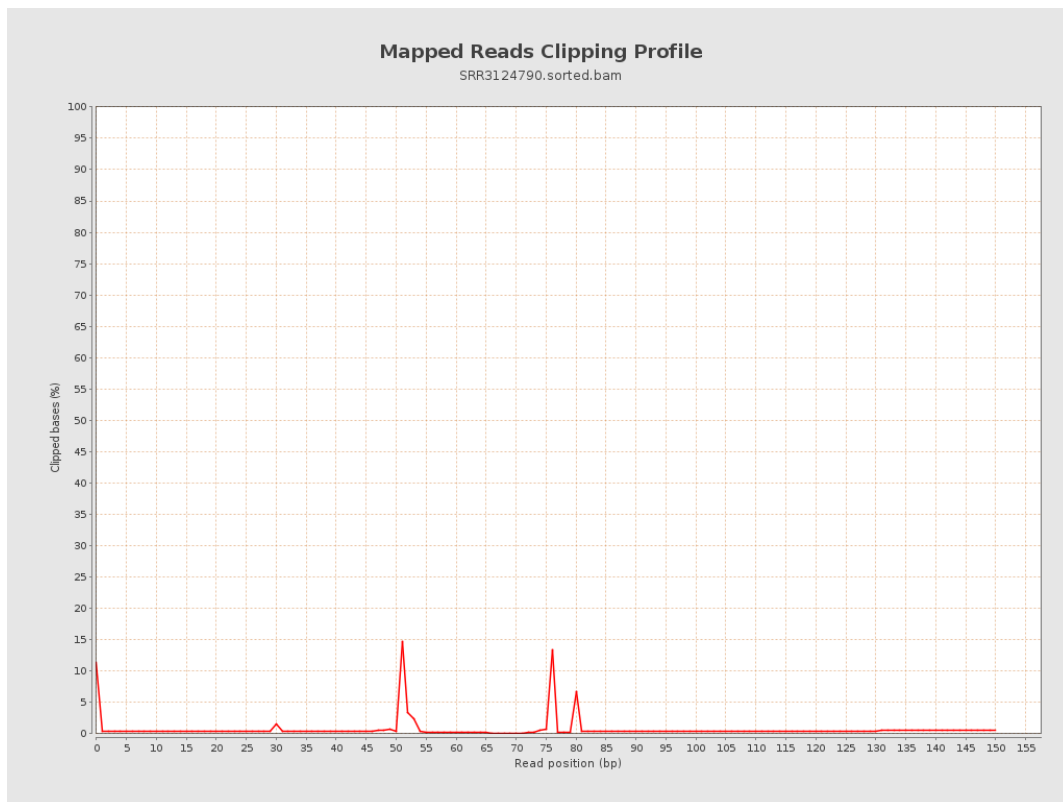
8. Results : Mapped Reads Nucleotide Content



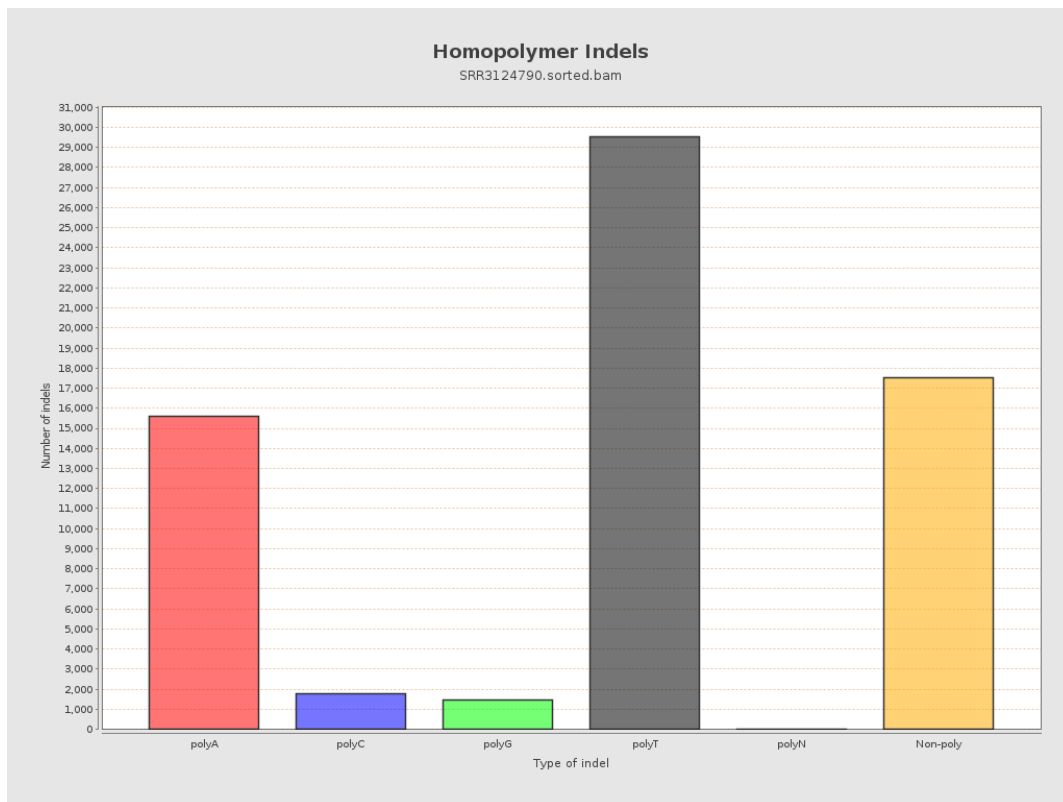
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

