

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:55:56

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124799.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_SRR3124799 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124799.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:55:55 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124799.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	692,436
Mapped reads	691,702 / 99.89%
Unmapped reads	734 / 0.11%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	298,700 / 43.14%
Read min/max/mean length	30 / 151 / 176.41
Duplicated reads (estimated)	988,359 / 142.74%
Duplication rate	20.36%
Clipped reads	624,020 / 90.12%

2.2. ACGT Content

Number/percentage of A's	32,564,398 / 31.63%
Number/percentage of C's	20,297,796 / 19.72%
Number/percentage of T's	31,330,550 / 30.43%
Number/percentage of G's	18,753,541 / 18.22%
Number/percentage of N's	0 / 0%
GC Percentage	37.93%

2.3. Coverage

Mean	0.0333

Standard Deviation	76.4283
--------------------	---------

2.4. Mapping Quality

Mean Mapping Quality	45.51
----------------------	-------

2.5. Mismatches and indels

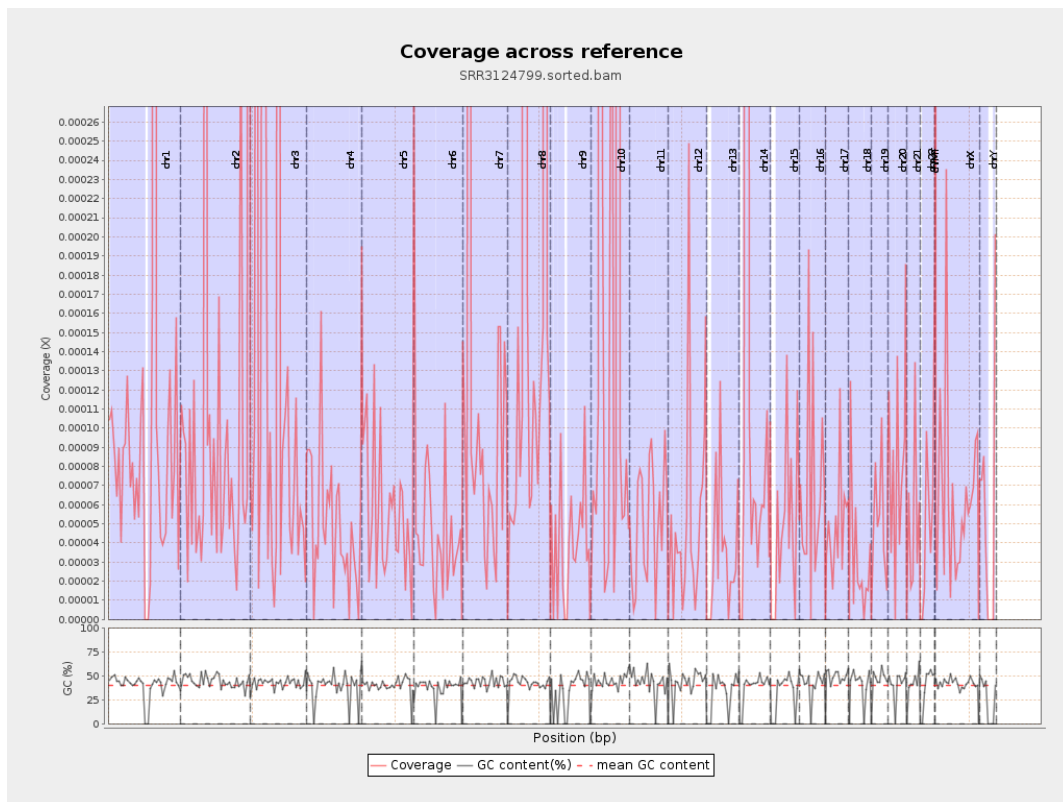
General error rate	0.75%
Mismatches	763,679
Insertions	5,180
Mapped reads with at least one insertion	0.75%
Deletions	44,509
Mapped reads with at least one deletion	6.35%
Homopolymer indels	73.02%

2.6. Chromosome stats

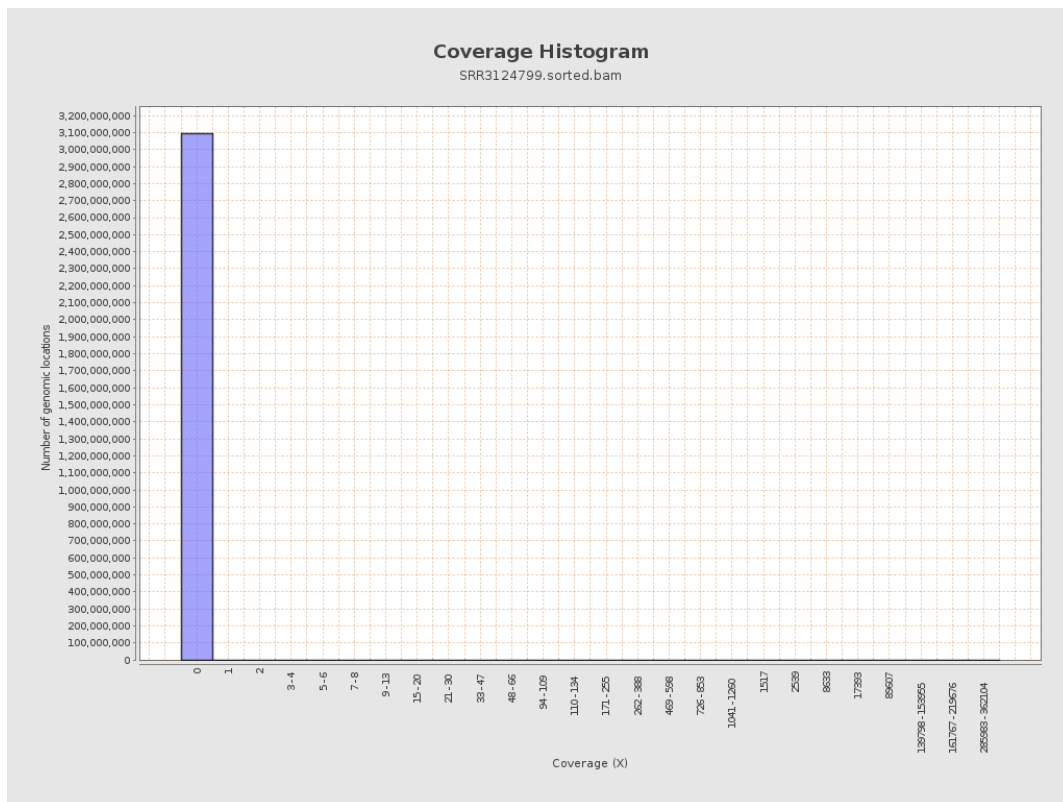
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	160235	0.0006	0.5272
chr2	243199373	33589	0.0001	0.1051
chr3	198022430	36991	0.0002	0.1554
chr4	191154276	9250	0	0.0072
chr5	180915260	10265	0.0001	0.0075
chr6	171115067	8491	0	0.0222
chr7	159138663	22942	0.0001	0.1255

chr8	146364022	185815	0.0013	0.5959
chr9	141213431	5662	0	0.0065
chr10	135534747	102425265	0.7557	365.2629
chr11	135006516	6893	0.0001	0.0126
chr12	133851895	7018	0.0001	0.0261
chr13	115169878	3955	0	0.0059
chr14	107349540	31098	0.0003	0.3692
chr15	102531392	4752	0	0.0072
chr16	90354753	6202	0.0001	0.0084
chr17	81195210	4076	0.0001	0.0072
chr18	78077248	2347	0	0.0055
chr19	59128983	3186	0.0001	0.0073
chr20	63025520	4857	0.0001	0.0091
chr21	48129895	2372	0	0.0095
chr22	51304566	2547	0	0.0074
chrMT	16571	426	0.0257	0.1583
chrX	155270560	9741	0.0001	0.0228
chrY	59373566	3426	0.0001	0.0077

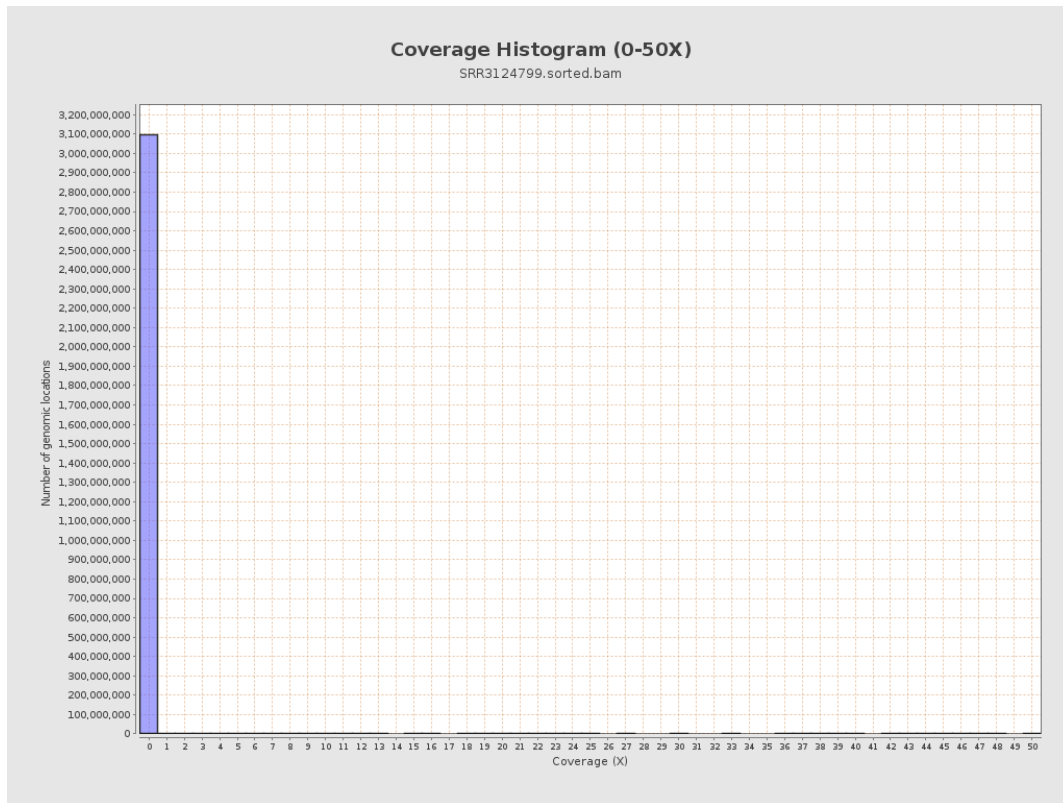
3. Results : Coverage across reference



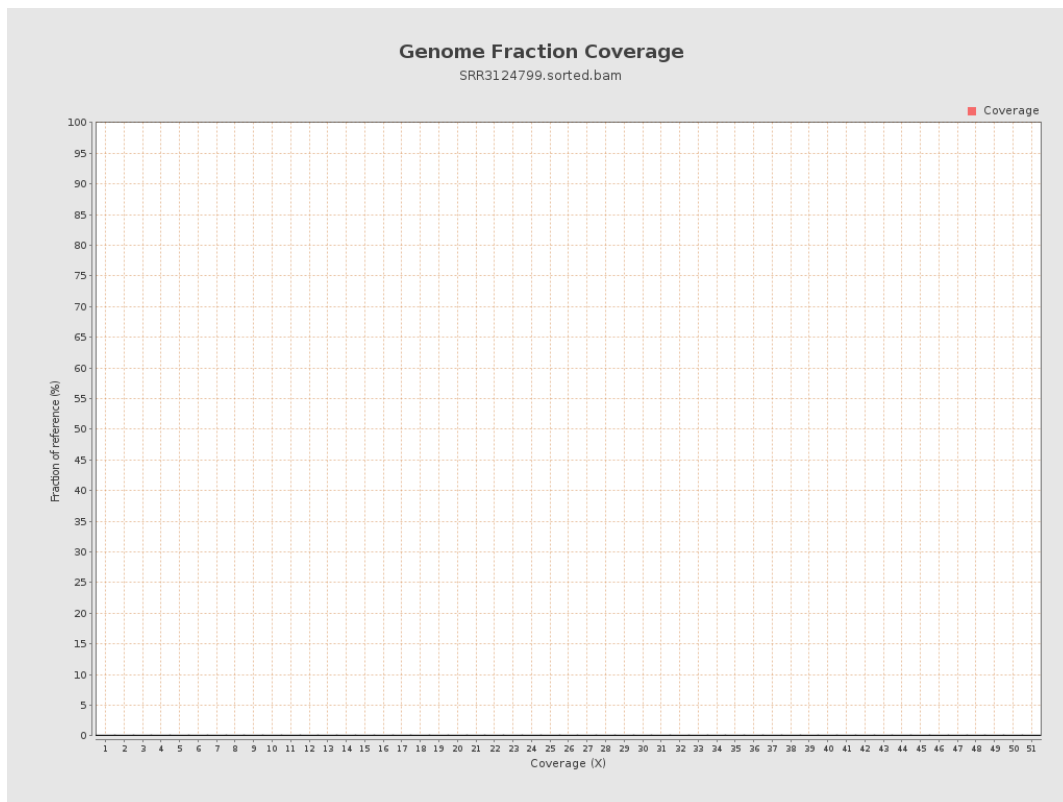
4. Results : Coverage Histogram



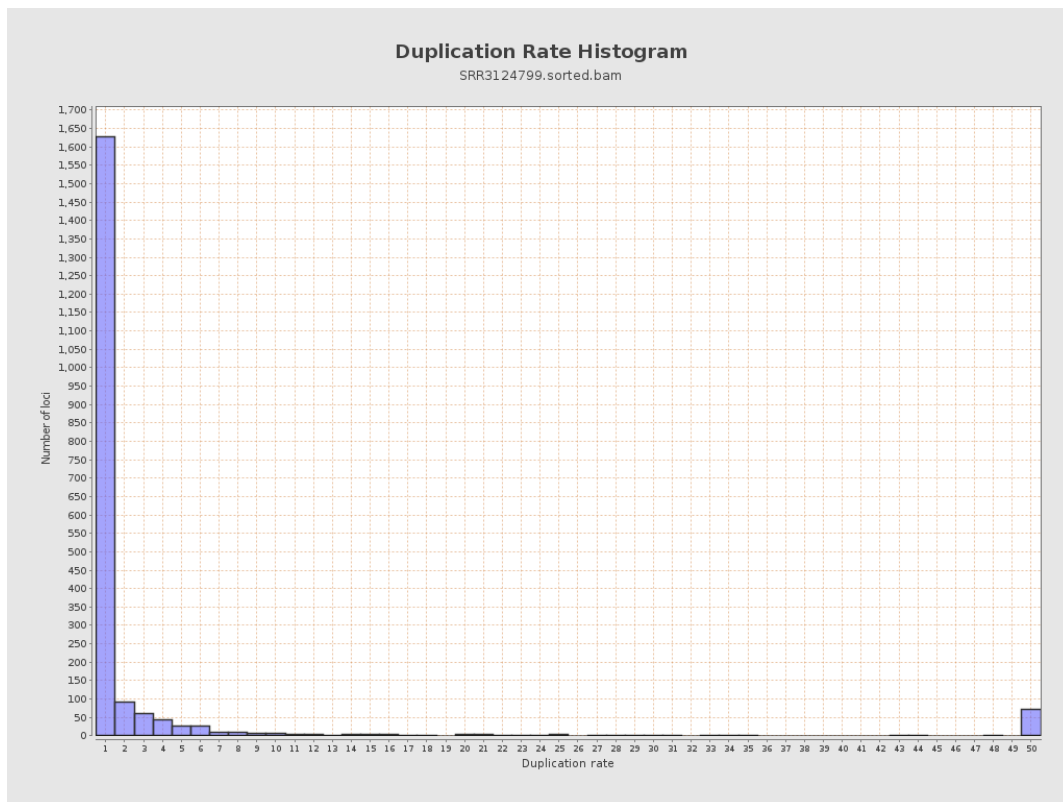
5. Results : Coverage Histogram (0-50X)



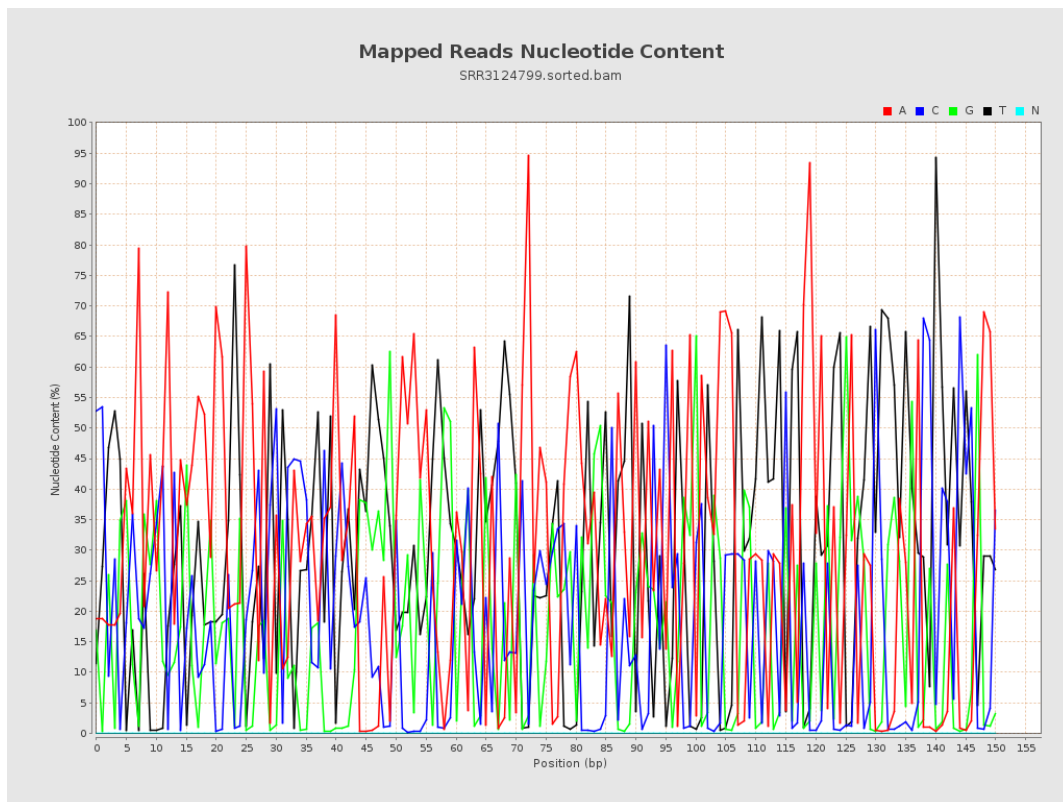
6. Results : Genome Fraction Coverage



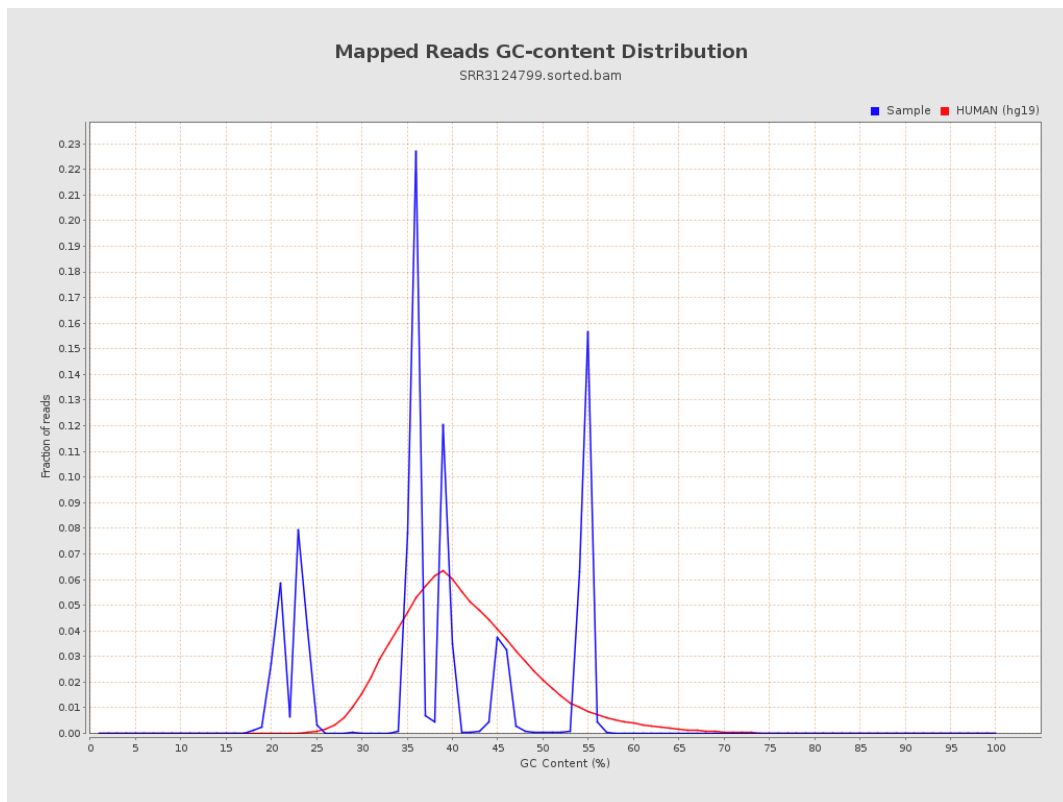
7. Results : Duplication Rate Histogram



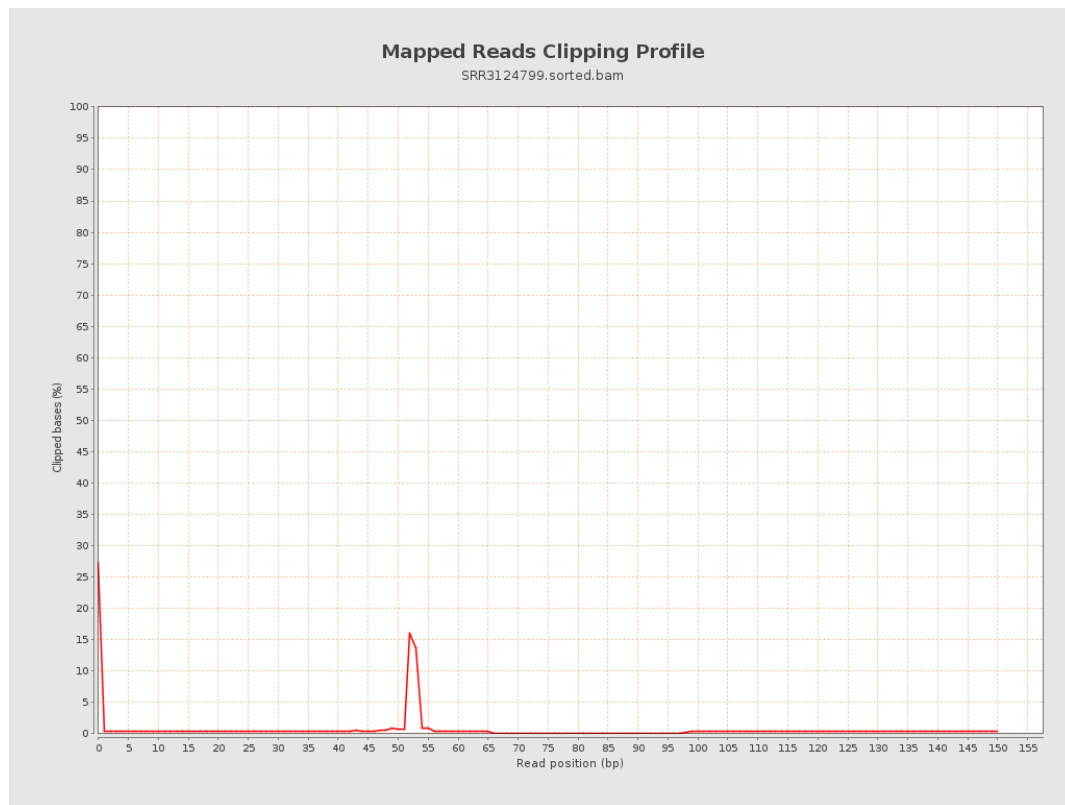
8. Results : Mapped Reads Nucleotide Content



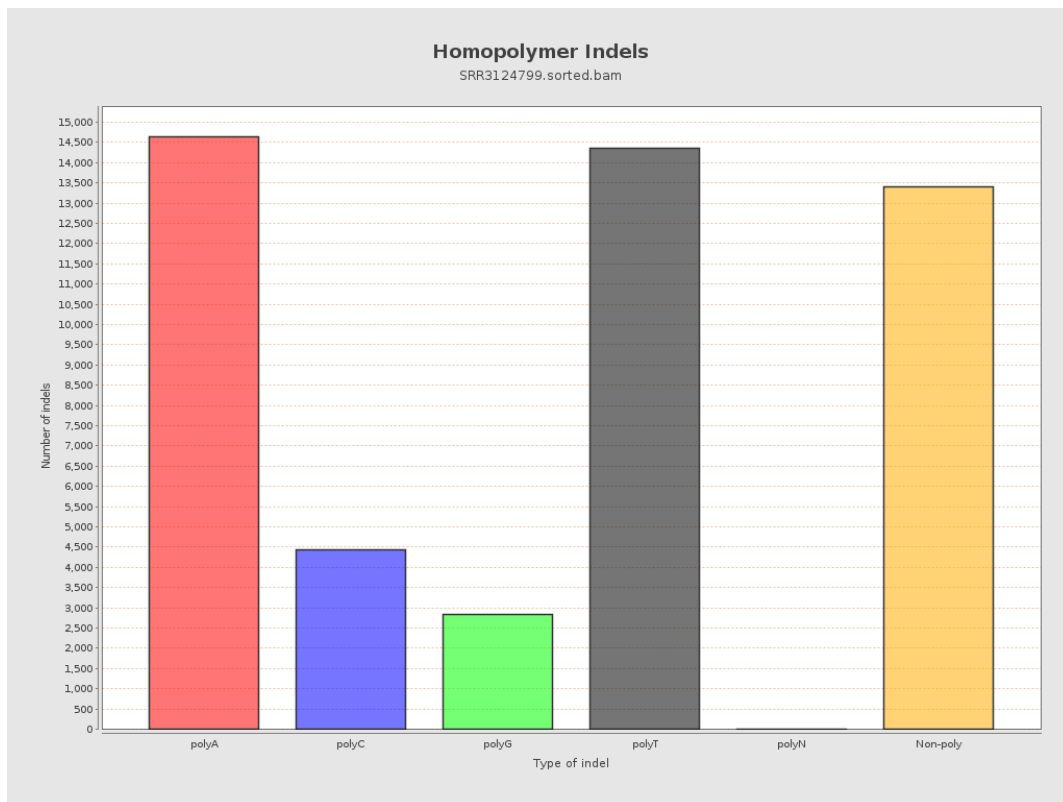
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

