

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/04 14:33:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124786.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_SRR3124786 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124786.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Dec 04 14:33:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124786.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	148,011
Mapped reads	138,719 / 93.72%
Unmapped reads	9,292 / 6.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,438 / 5.03%
Read min/max/mean length	30 / 151 / 153.3
Duplicated reads (estimated)	14,447 / 9.76%
Duplication rate	1.39%
Clipped reads	96,047 / 64.89%

2.2. ACGT Content

Number/percentage of A's	5,119,475 / 28.85%
Number/percentage of C's	3,447,307 / 19.42%
Number/percentage of T's	5,198,697 / 29.29%
Number/percentage of G's	3,982,157 / 22.44%
Number/percentage of N's	0 / 0%
GC Percentage	41.86%

2.3. Coverage

Mean	0.0057

Standard Deviation	0.7142
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	50.96
----------------------	-------

2.5. Mismatches and indels

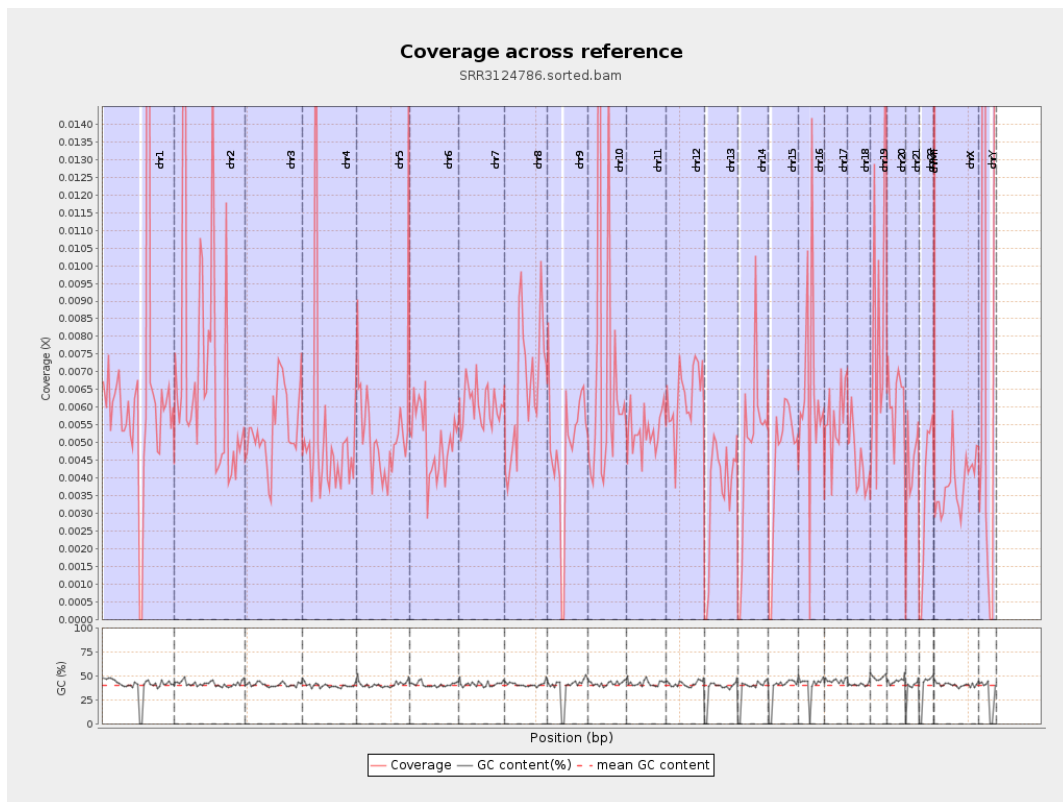
General error rate	1.63%
Mismatches	264,544
Insertions	6,718
Mapped reads with at least one insertion	4.57%
Deletions	9,888
Mapped reads with at least one deletion	6.78%
Homopolymer indels	40.15%

2.6. Chromosome stats

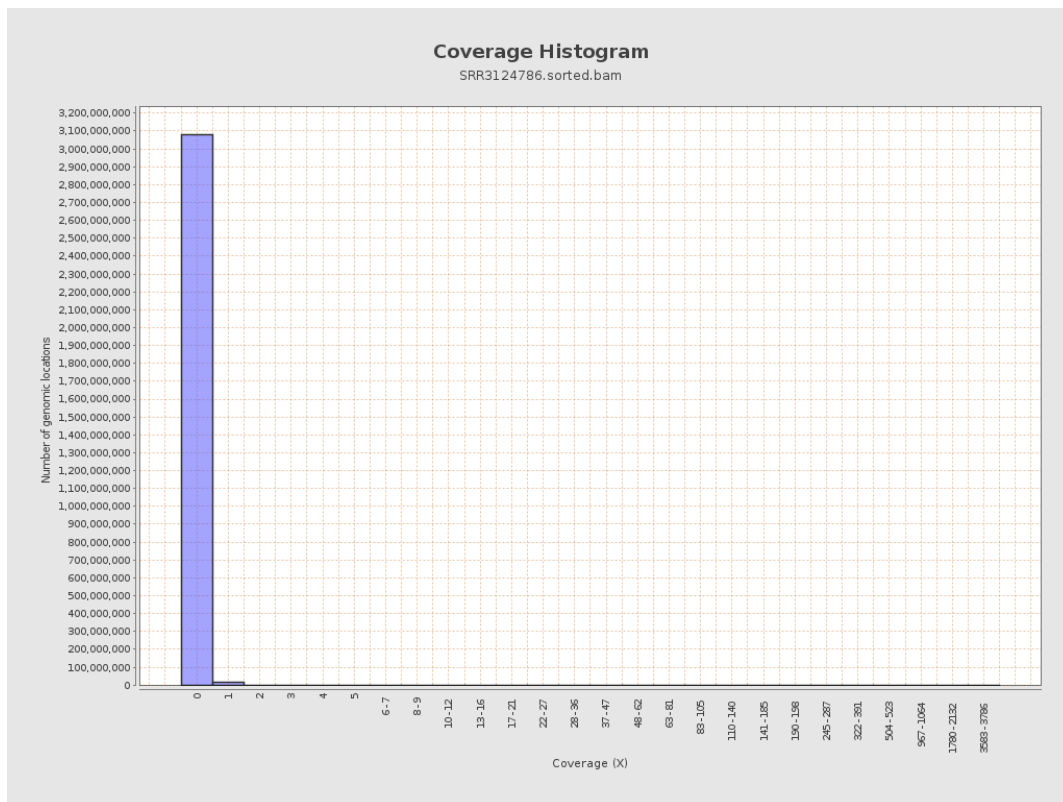
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	1682372	0.0067	1.0931
chr2	243199373	1696794	0.007	0.6489
chr3	198022430	1080320	0.0055	0.076
chr4	191154276	994138	0.0052	0.1071
chr5	180915260	934744	0.0052	0.1431
chr6	171115067	860624	0.005	0.075
chr7	159138663	964072	0.0061	0.0889

chr8	146364022	960359	0.0066	0.1164
chr9	141213431	690346	0.0049	0.1386
chr10	135534747	994081	0.0073	0.5167
chr11	135006516	720681	0.0053	0.0778
chr12	133851895	841515	0.0063	0.0813
chr13	115169878	412963	0.0036	0.0606
chr14	107349540	524178	0.0049	0.2862
chr15	102531392	461046	0.0045	0.0698
chr16	90354753	573852	0.0064	0.1464
chr17	81195210	465117	0.0057	0.1808
chr18	78077248	346801	0.0044	0.09
chr19	59128983	515125	0.0087	0.9088
chr20	63025520	392123	0.0062	0.0838
chr21	48129895	205623	0.0043	0.0853
chr22	51304566	181126	0.0035	0.1029
chrMT	16571	10830	0.6536	0.8755
chrX	155270560	598524	0.0039	0.0657
chrY	59373566	661351	0.0111	4.2276

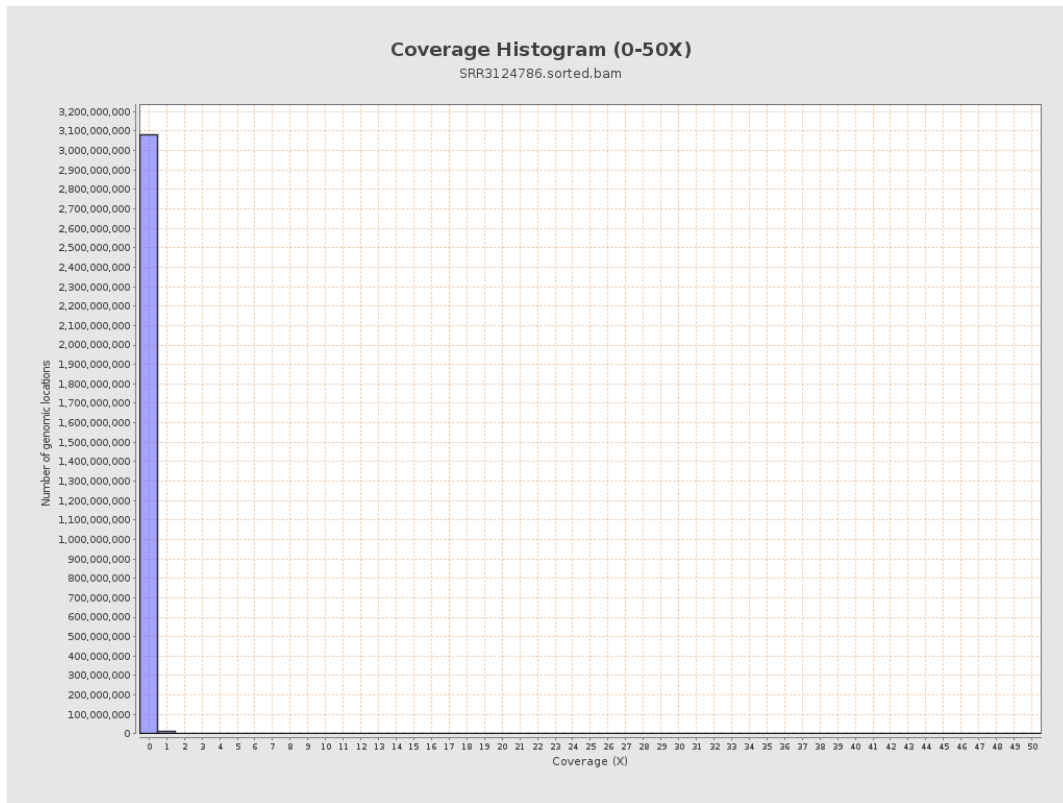
3. Results : Coverage across reference



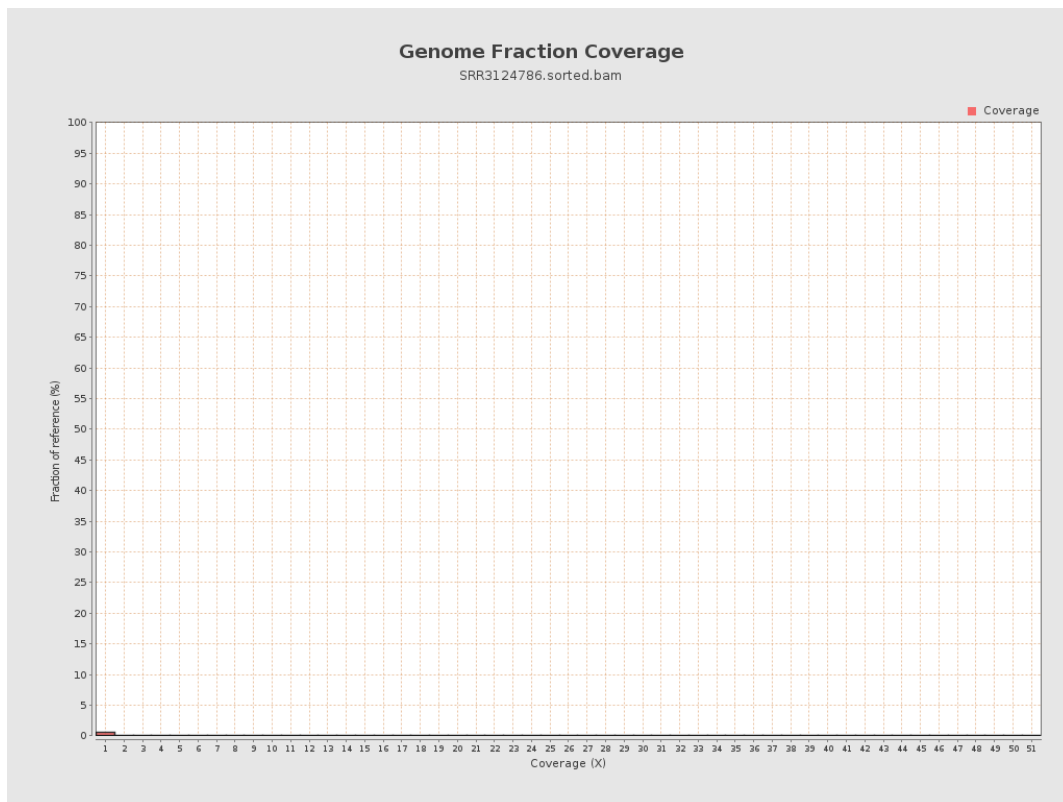
4. Results : Coverage Histogram



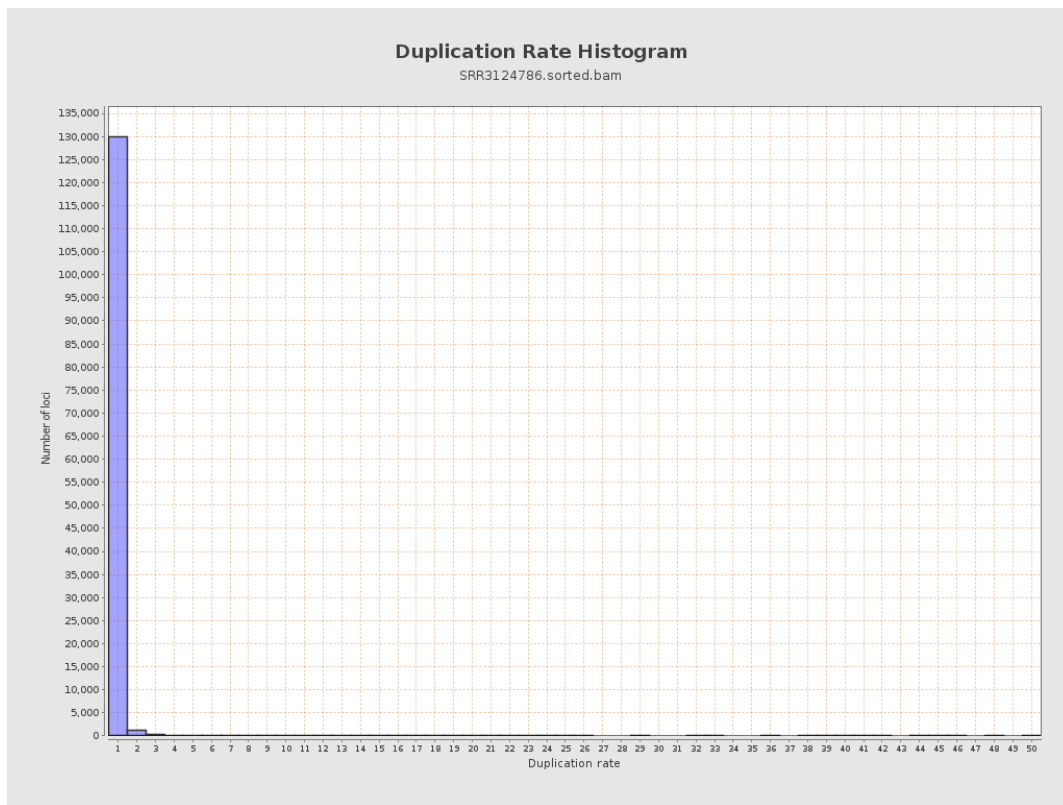
5. Results : Coverage Histogram (0-50X)



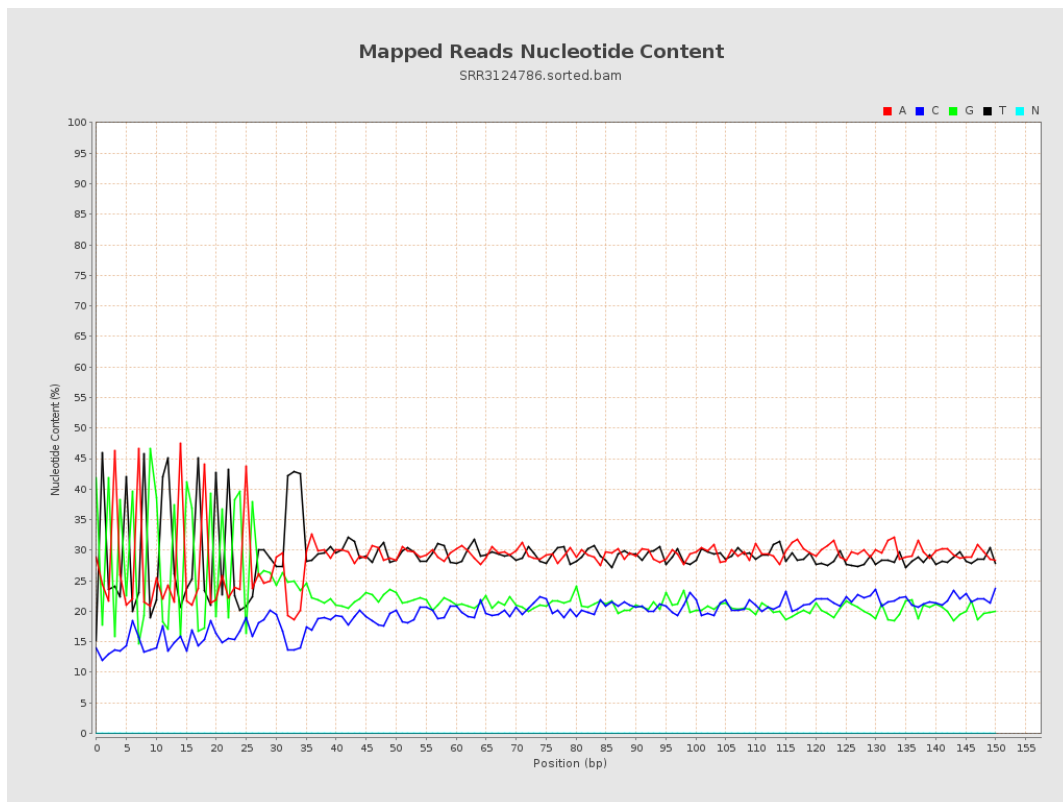
6. Results : Genome Fraction Coverage



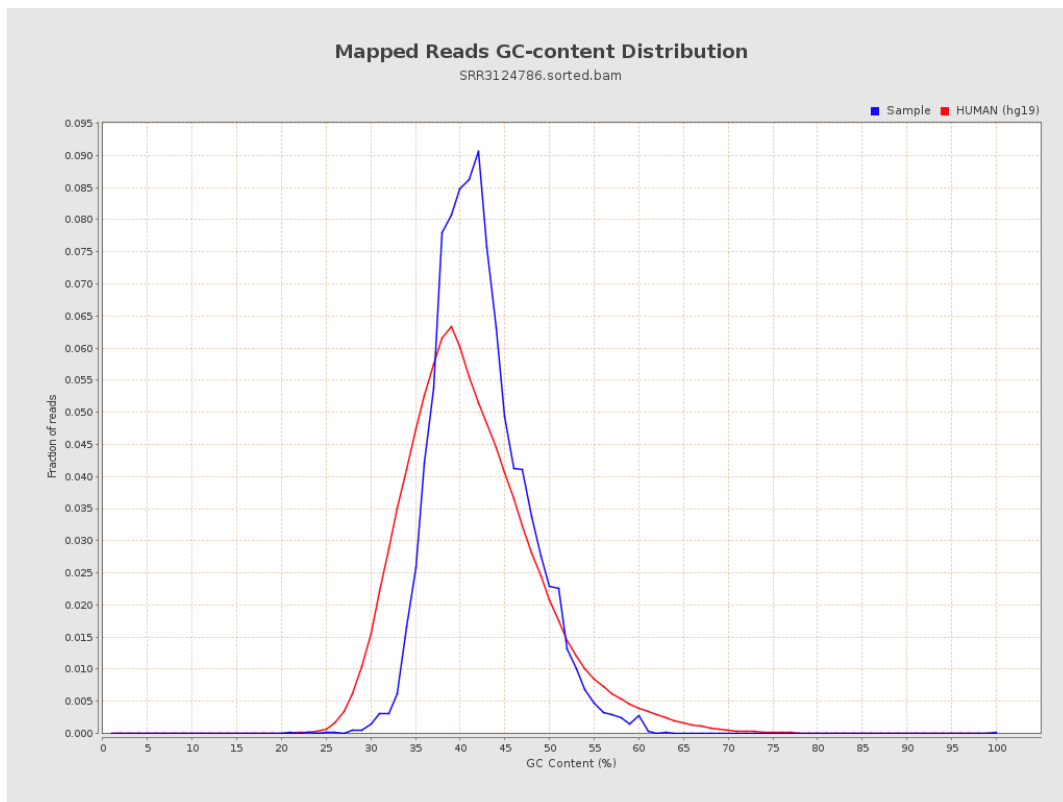
7. Results : Duplication Rate Histogram



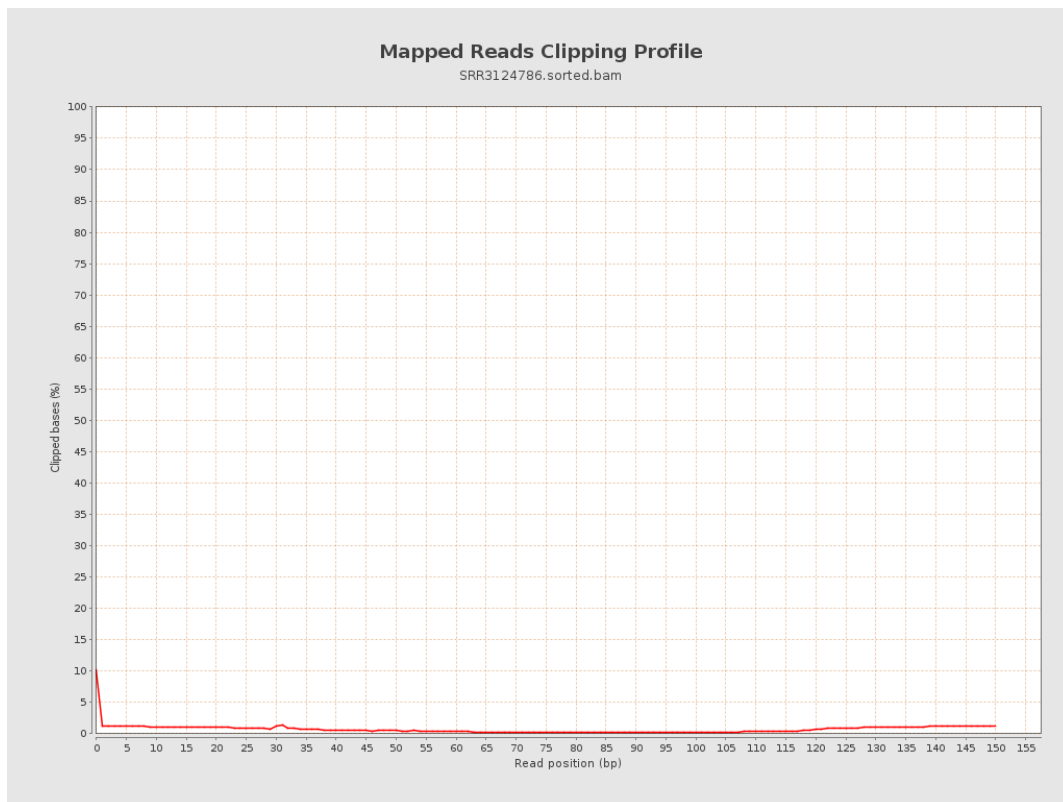
8. Results : Mapped Reads Nucleotide Content



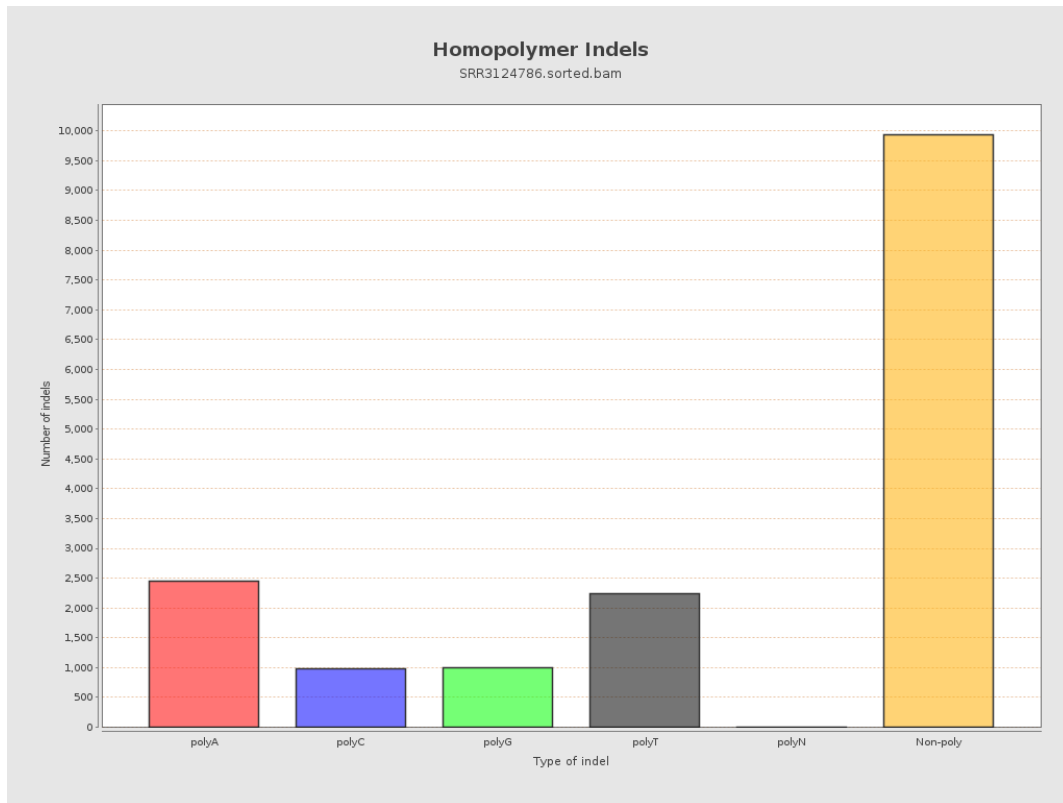
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

