

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/10 15:34:41

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5514746.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_SRR5514746 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5514746.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 10 15:34:40 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5514746.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,300,983
Mapped reads	1,275,326 / 38.63%
Unmapped reads	2,025,657 / 61.37%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	329,658 / 9.99%
Read min/max/mean length	30 / 100 / 102.9
Duplicated reads (estimated)	1,406,976 / 42.62%
Duplication rate	23.77%
Clipped reads	1,394,070 / 42.23%

2.2. ACGT Content

Number/percentage of A's	26,935,838 / 27.99%
Number/percentage of C's	19,604,036 / 20.37%
Number/percentage of T's	27,074,121 / 28.14%
Number/percentage of G's	22,601,539 / 23.49%
Number/percentage of N's	5,290 / 0.01%
GC Percentage	43.86%

2.3. Coverage

Mean	0.0312

Standard Deviation	27.1608
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2.4. Mapping Quality

Mean Mapping Quality	30.95
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2.5. Mismatches and indels

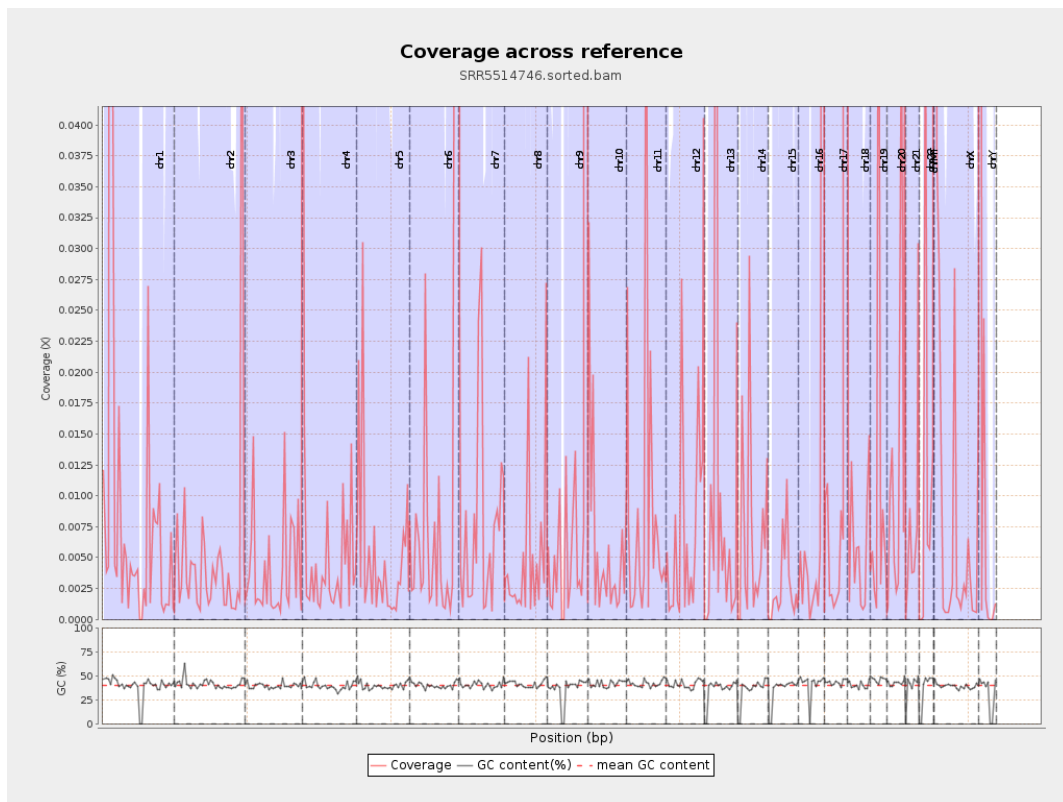
General error rate	1.99%
Mismatches	1,633,335
Insertions	91,703
Mapped reads with at least one insertion	6.6%
Deletions	85,643
Mapped reads with at least one deletion	6.01%
Homopolymer indels	24.43%

2.6. Chromosome stats

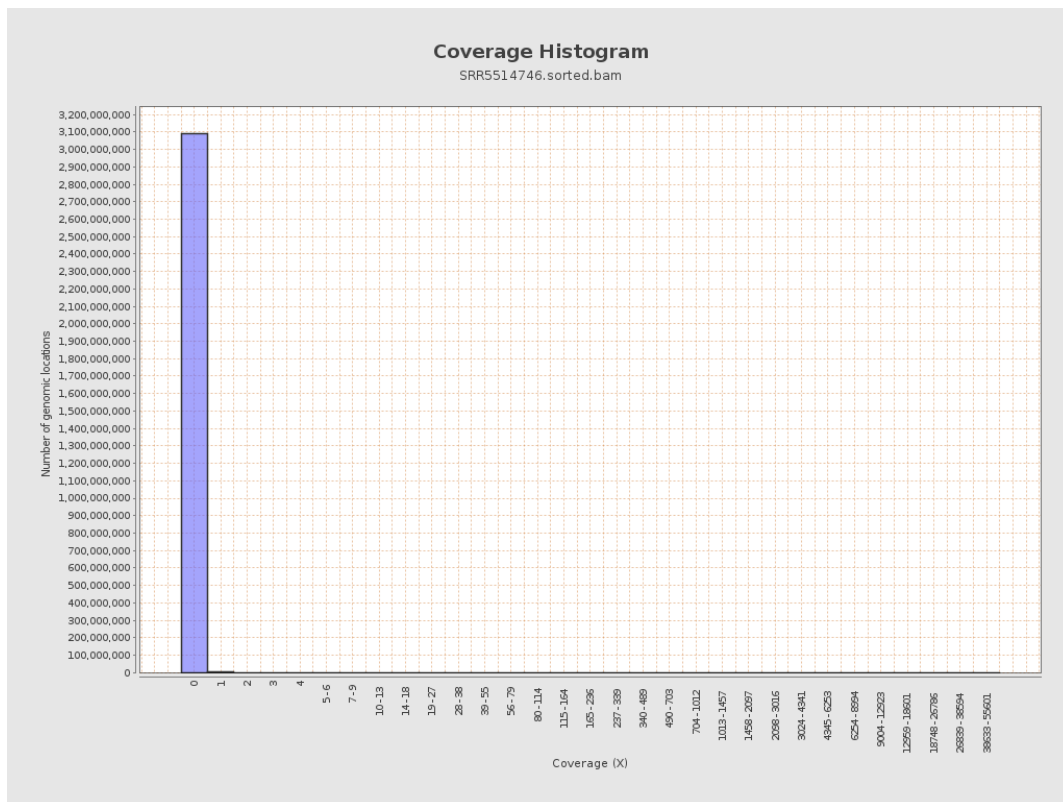
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	3287749	0.0132	4.629
chr2	243199373	1314315	0.0054	3.351
chr3	198022430	795854	0.004	0.3411
chr4	191154276	1347754	0.0071	4.9997
chr5	180915260	946697	0.0052	0.3405
chr6	171115067	18575335	0.1086	60.7886
chr7	159138663	1238623	0.0078	1.4449

chr8	146364022	716677	0.0049	0.5398
chr9	141213431	45003787	0.3187	105.7814
chr10	135534747	805885	0.0059	1.0721
chr11	135006516	1201312	0.0089	4.7199
chr12	133851895	964765	0.0072	1.1832
chr13	115169878	1194678	0.0104	1.9659
chr14	107349540	755362	0.007	0.5374
chr15	102531392	291554	0.0028	0.2788
chr16	90354753	1388381	0.0154	7.2099
chr17	81195210	6857809	0.0845	22.089
chr18	78077248	438313	0.0056	0.5184
chr19	59128983	711198	0.012	1.3899
chr20	63025520	863092	0.0137	1.4186
chr21	48129895	360834	0.0075	0.7248
chr22	51304566	919425	0.0179	8.4919
chrMT	16571	149475	9.0203	12.6288
chrX	155270560	3709408	0.0239	4.3352
chrY	59373566	2753727	0.0464	7.03

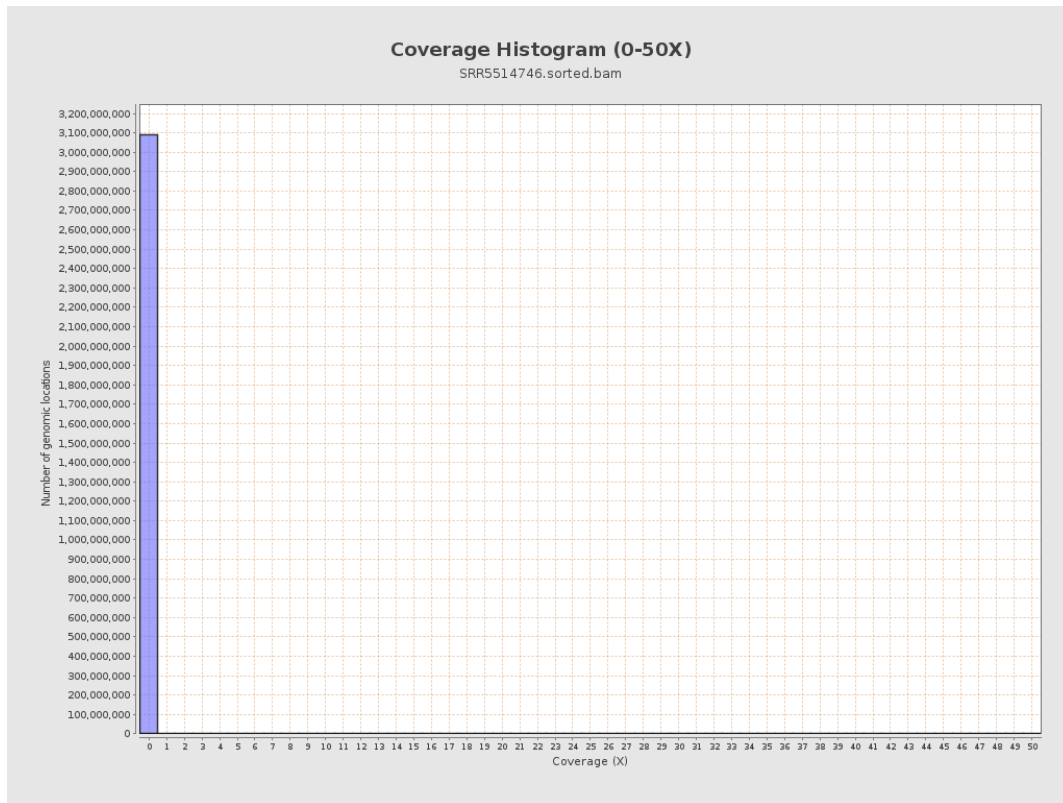
3. Results : Coverage across reference



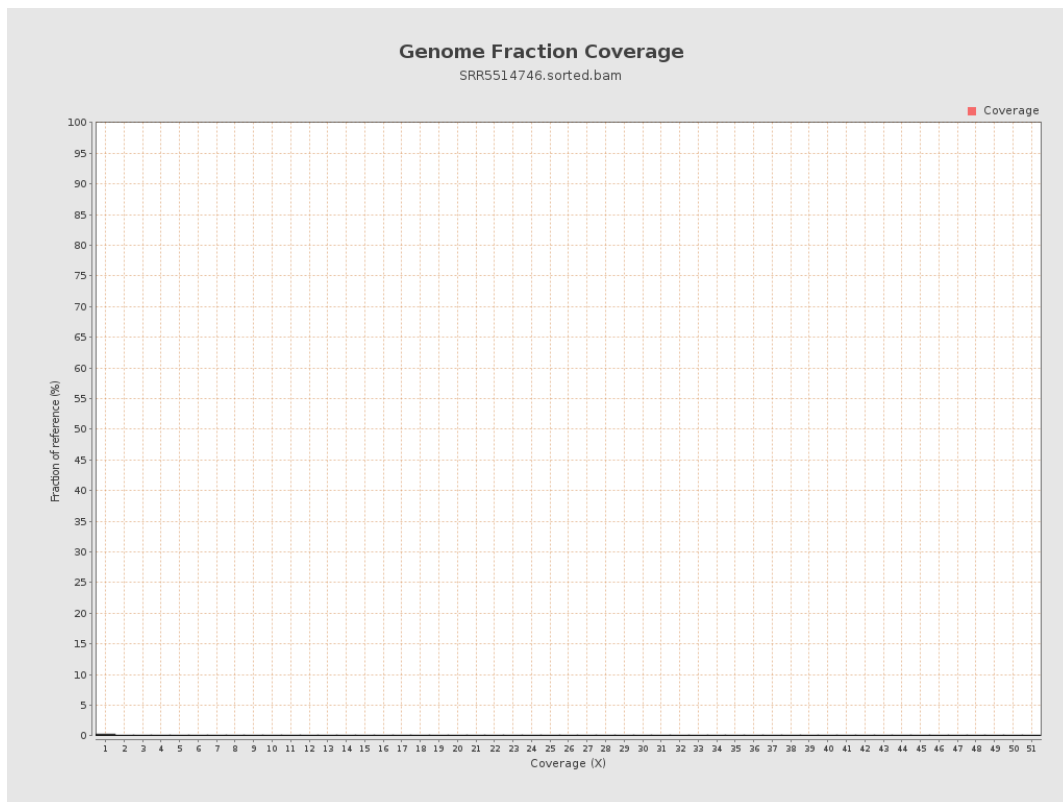
4. Results : Coverage Histogram



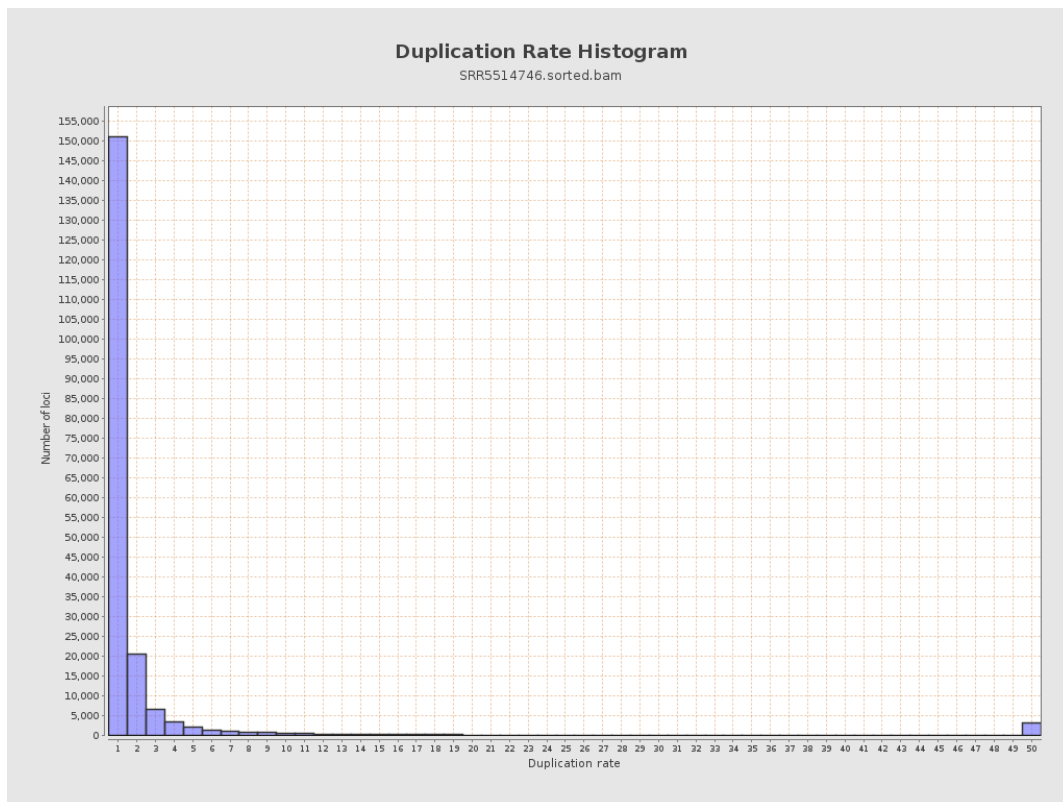
5. Results : Coverage Histogram (0-50X)



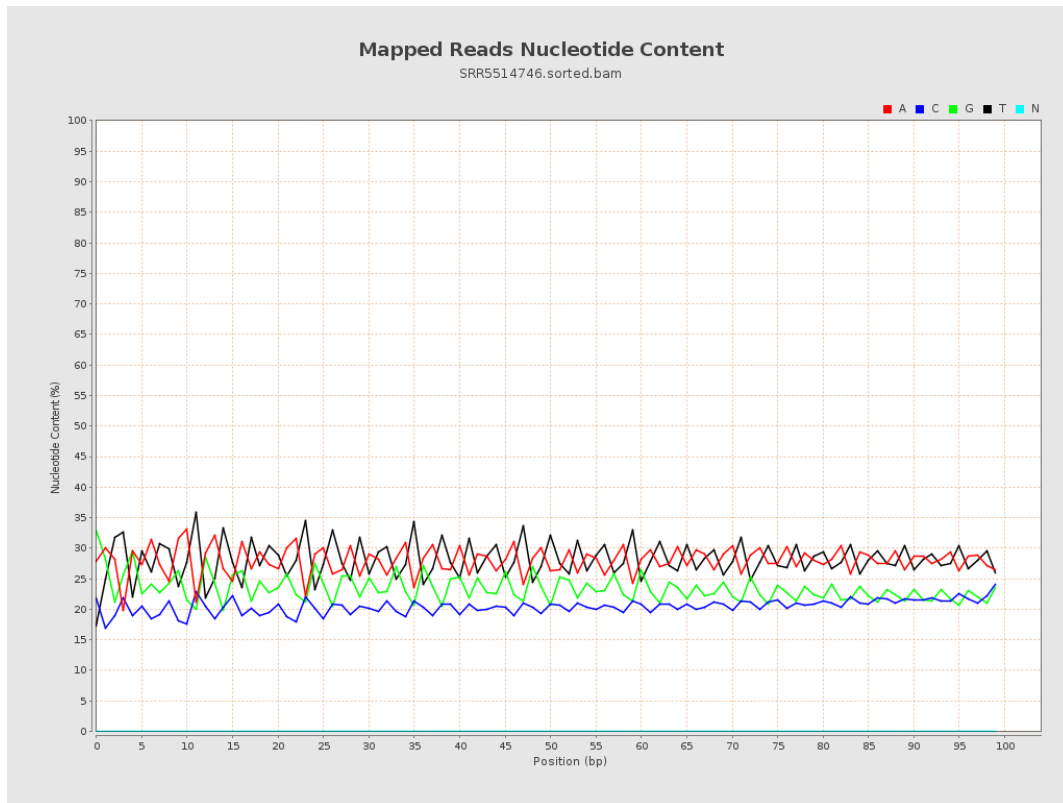
6. Results : Genome Fraction Coverage



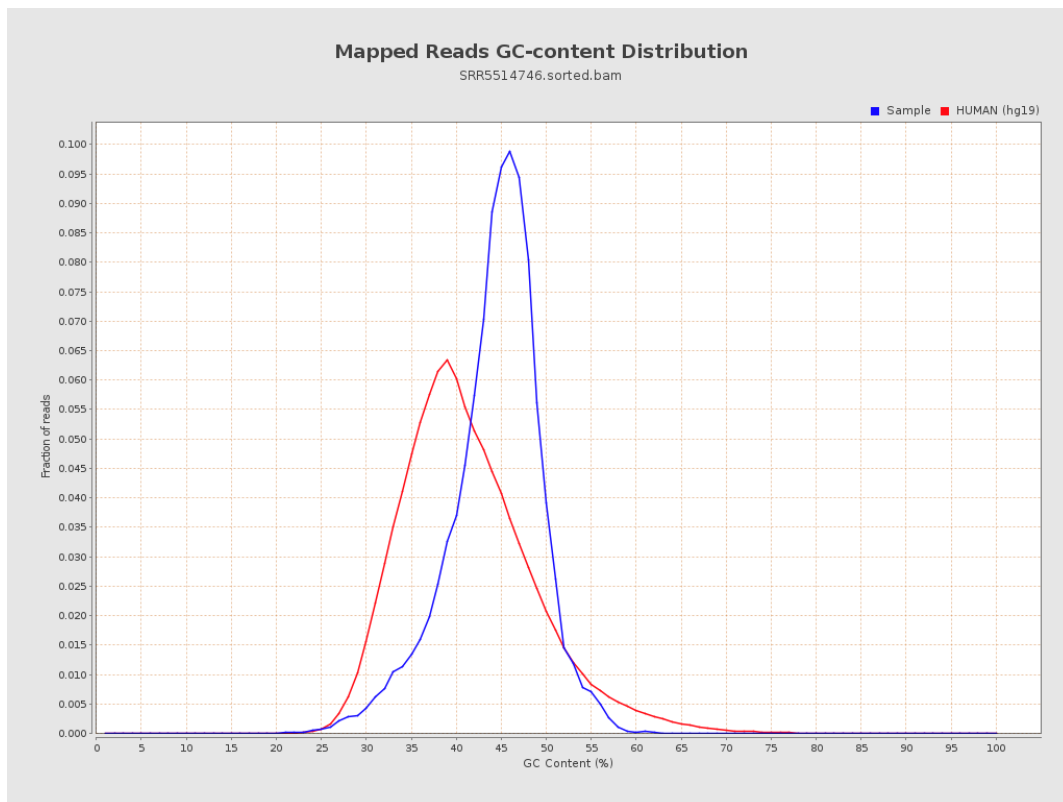
7. Results : Duplication Rate Histogram



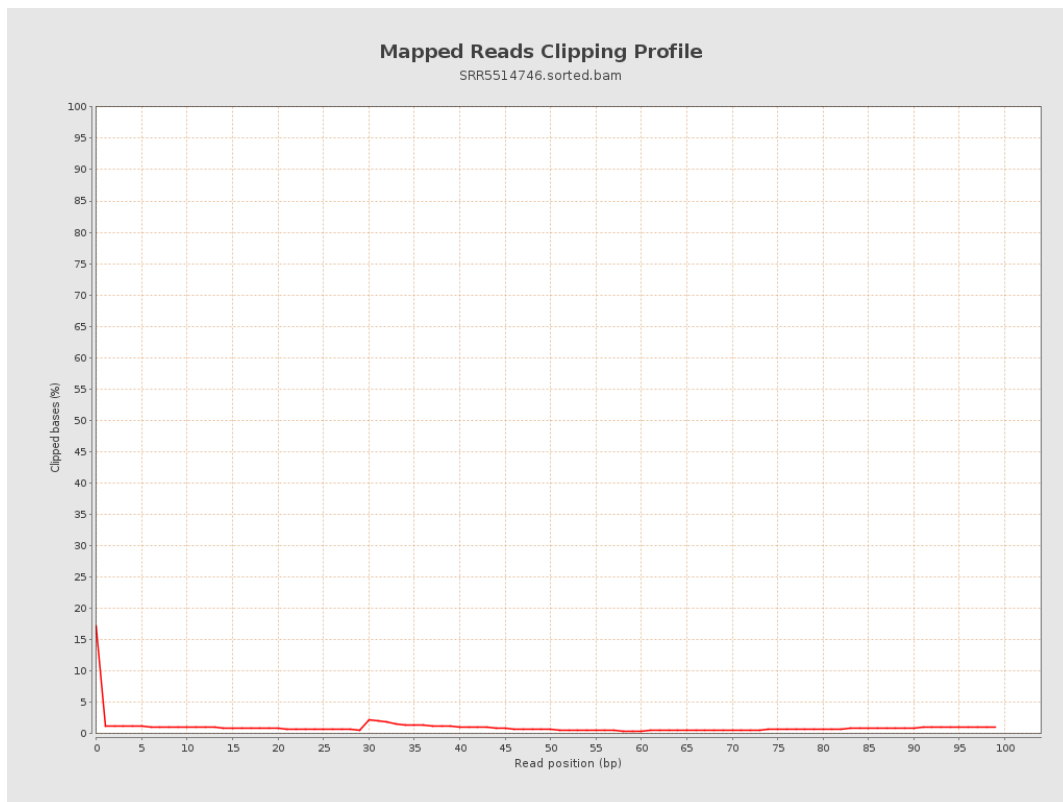
8. Results : Mapped Reads Nucleotide Content



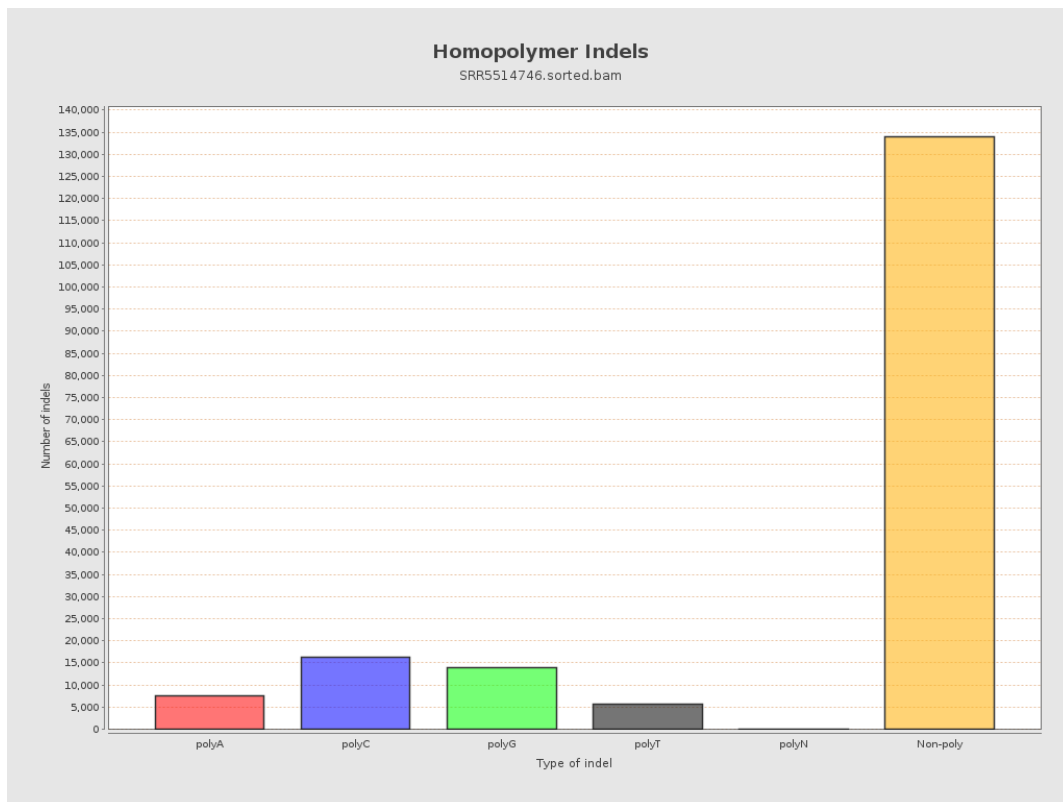
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

