

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 20:04:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013293.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_SRR6013293 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013293.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 20:04:23 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013293.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,337,151
Mapped reads	1,205,647 / 90.17%
Unmapped reads	131,504 / 9.83%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,709 / 0.5%
Read min/max/mean length	30 / 76 / 76.17
Duplicated reads (estimated)	45,075 / 3.37%
Duplication rate	2.57%
Clipped reads	501,673 / 37.52%

2.2. ACGT Content

Number/percentage of A's	23,112,743 / 28.46%
Number/percentage of C's	14,800,961 / 18.22%
Number/percentage of T's	25,780,275 / 31.74%
Number/percentage of G's	17,505,461 / 21.55%
Number/percentage of N's	17,366 / 0.02%
GC Percentage	39.78%

2.3. Coverage

Mean	0.0262

Standard Deviation	0.3341
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2.4. Mapping Quality

Mean Mapping Quality	45.13
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2.5. Mismatches and indels

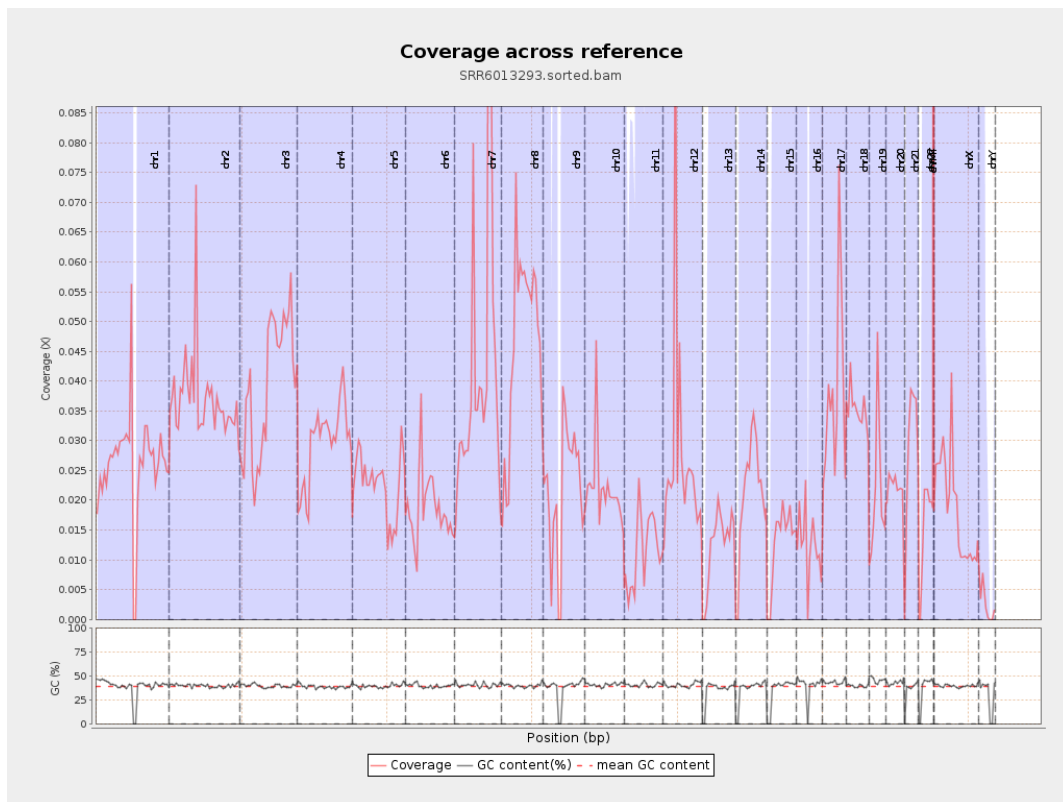
General error rate	0.84%
Mismatches	674,584
Insertions	6,321
Mapped reads with at least one insertion	0.52%
Deletions	19,846
Mapped reads with at least one deletion	1.63%
Homopolymer indels	46.89%

2.6. Chromosome stats

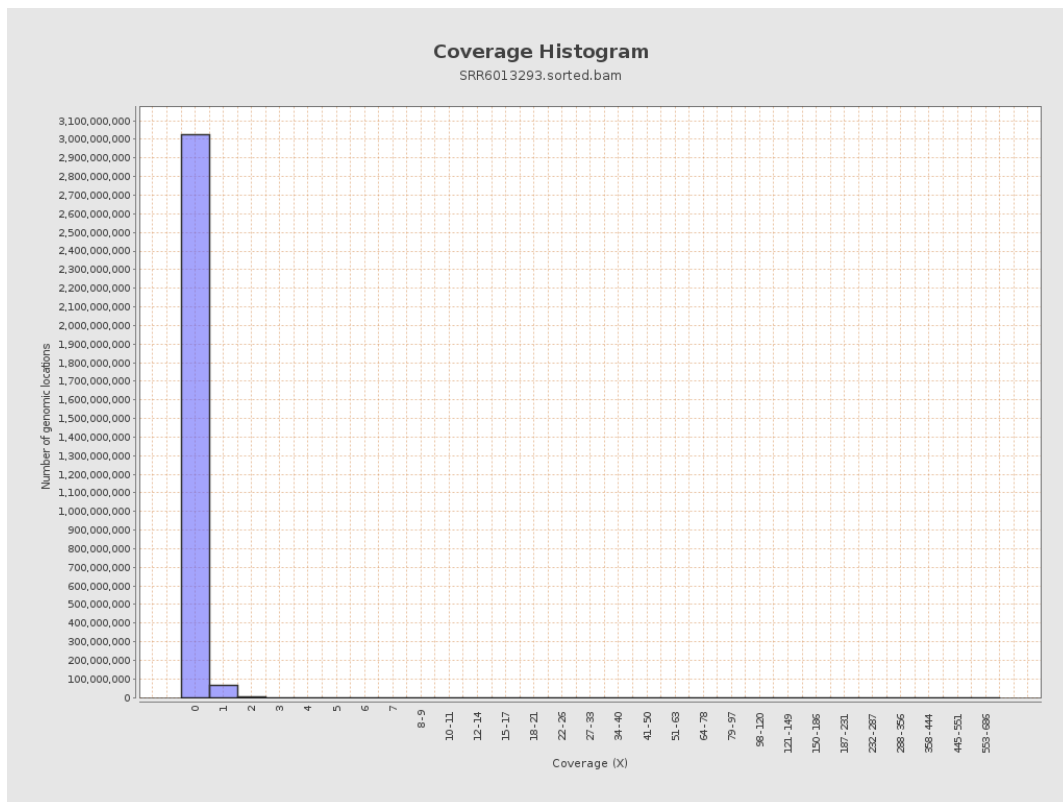
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6522529	0.0262	0.5897
chr2	243199373	9036762	0.0372	0.3805
chr3	198022430	7777989	0.0393	0.2135
chr4	191154276	5671812	0.0297	0.1927
chr5	180915260	4104091	0.0227	0.1638
chr6	171115067	3209807	0.0188	0.1957
chr7	159138663	7004950	0.044	0.6863

chr8	146364022	6785149	0.0464	0.4421
chr9	141213431	3062075	0.0217	0.2997
chr10	135534747	2966695	0.0219	0.3172
chr11	135006516	1538945	0.0114	0.1988
chr12	133851895	3738161	0.0279	0.1894
chr13	115169878	1432370	0.0124	0.1189
chr14	107349540	2276839	0.0212	0.1741
chr15	102531392	1338904	0.0131	0.1243
chr16	90354753	1123434	0.0124	0.1552
chr17	81195210	3024338	0.0372	0.2394
chr18	78077248	2760502	0.0354	0.5537
chr19	59128983	1305185	0.0221	0.3999
chr20	63025520	1386817	0.022	0.1626
chr21	48129895	1391048	0.0289	0.1938
chr22	51304566	758294	0.0148	0.1287
chrMT	16571	7415	0.4475	0.7772
chrX	155270560	2874884	0.0185	0.1694
chrY	59373566	151633	0.0026	0.0804

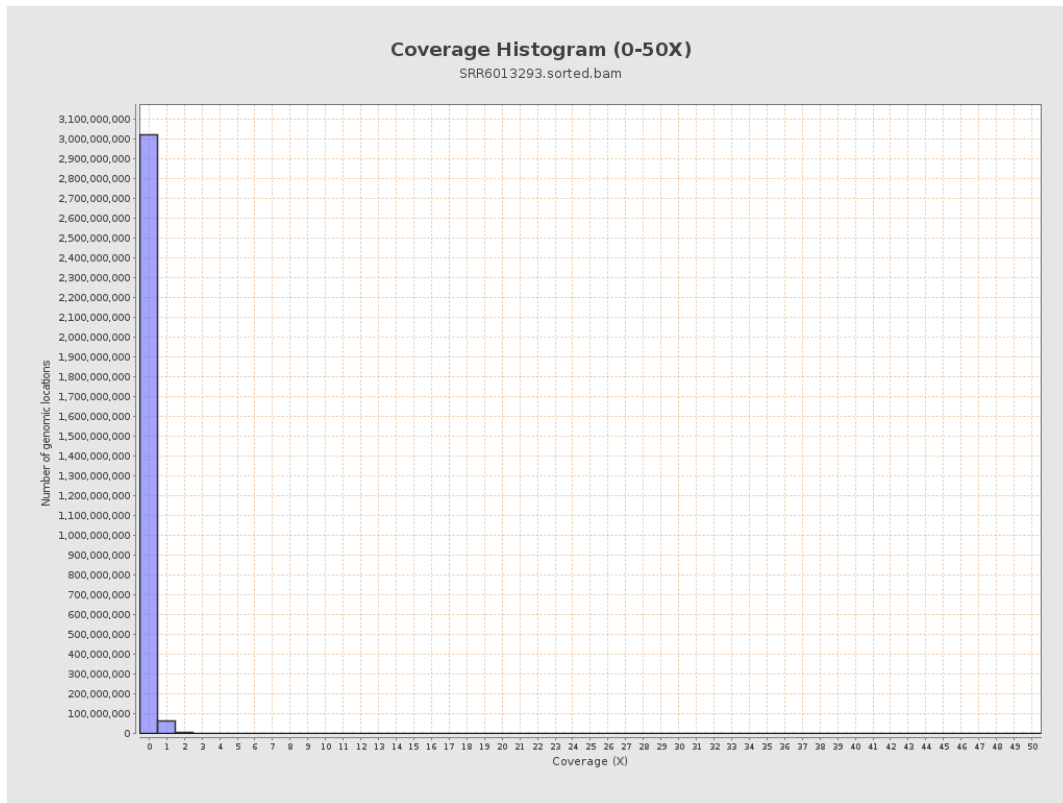
3. Results : Coverage across reference



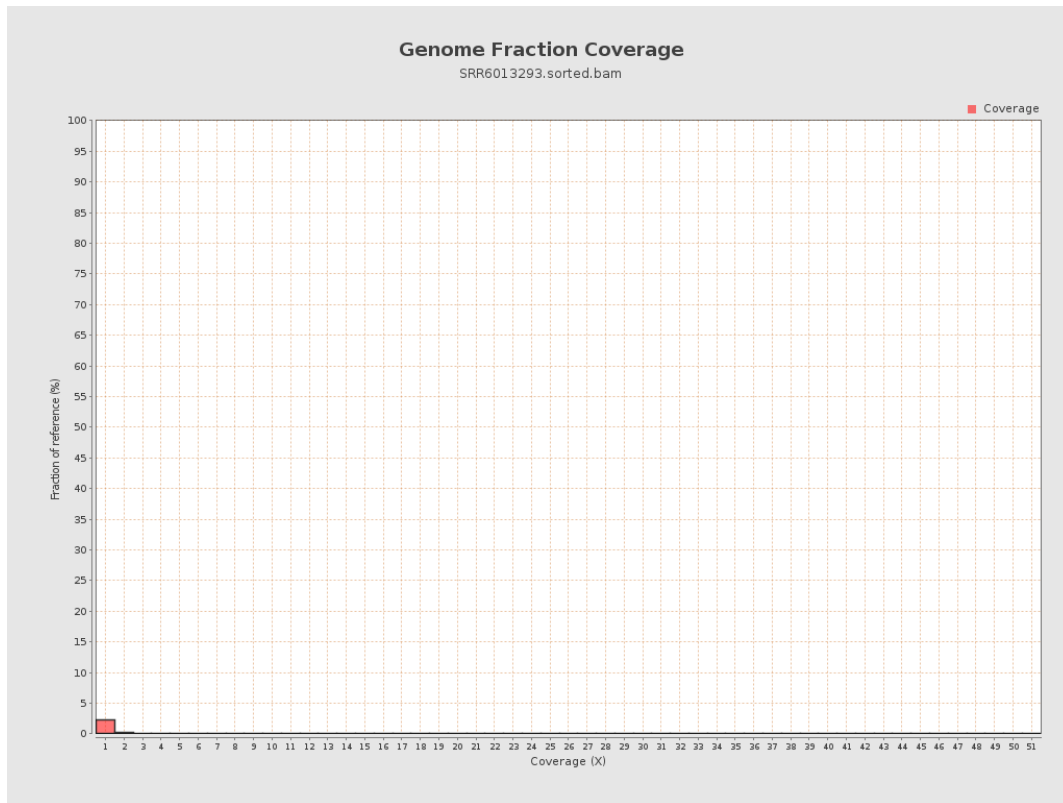
4. Results : Coverage Histogram



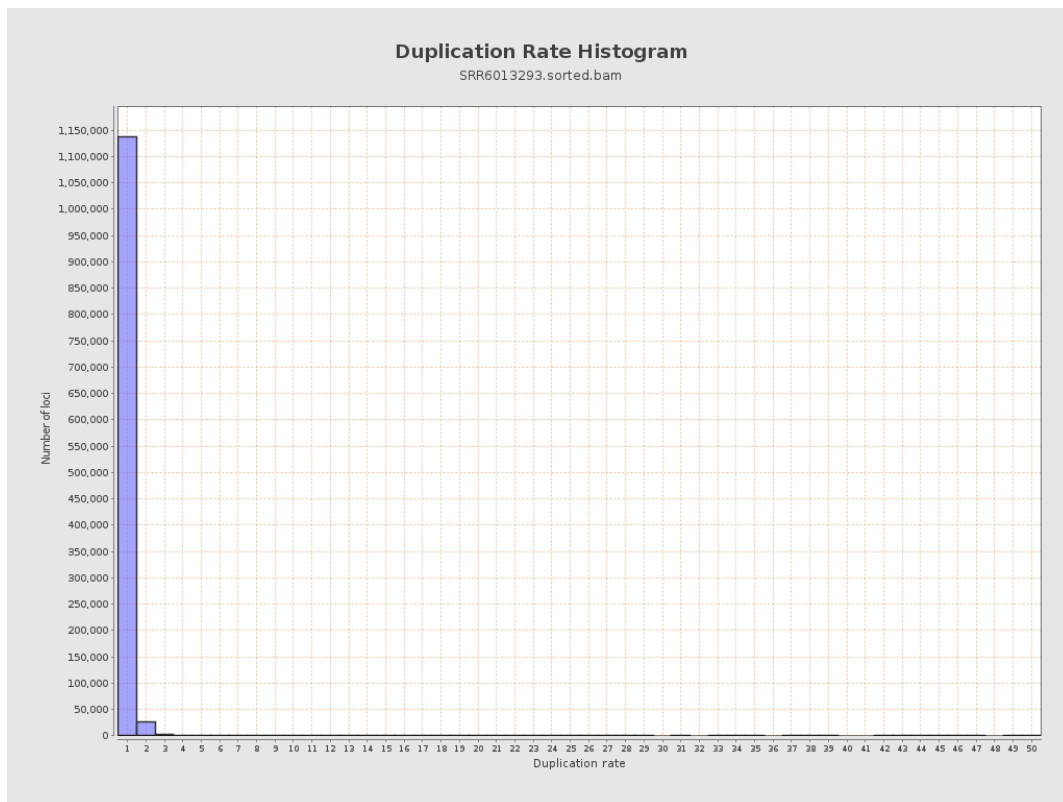
5. Results : Coverage Histogram (0-50X)



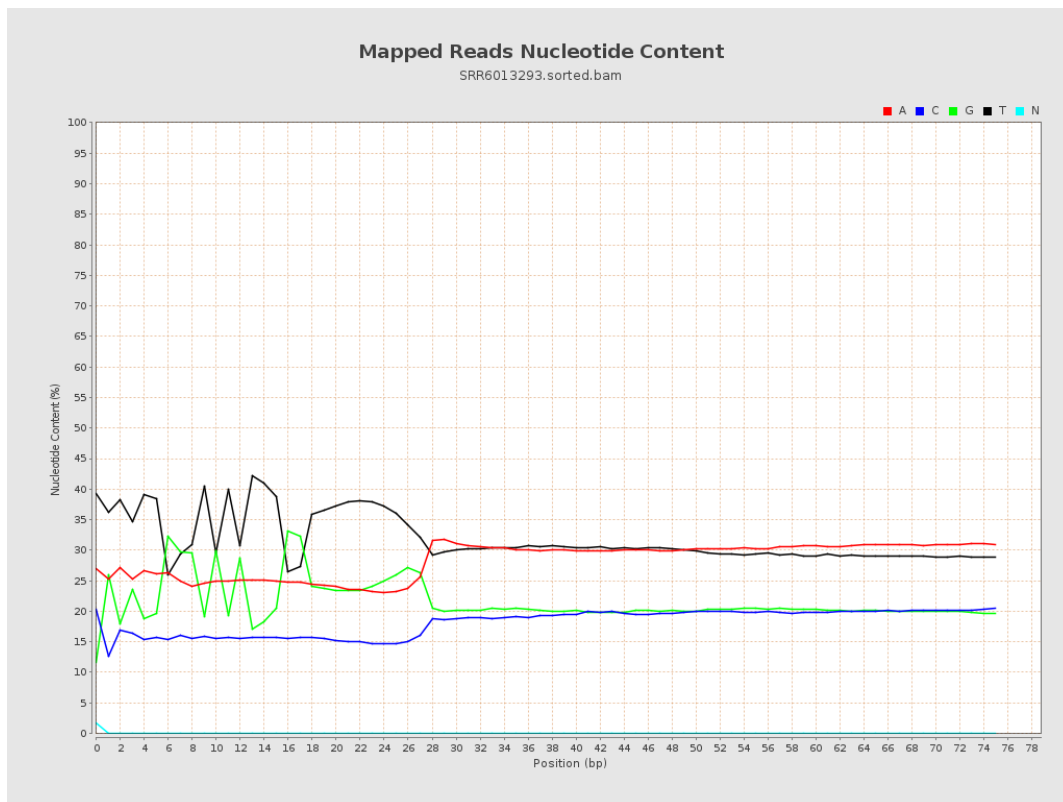
6. Results : Genome Fraction Coverage



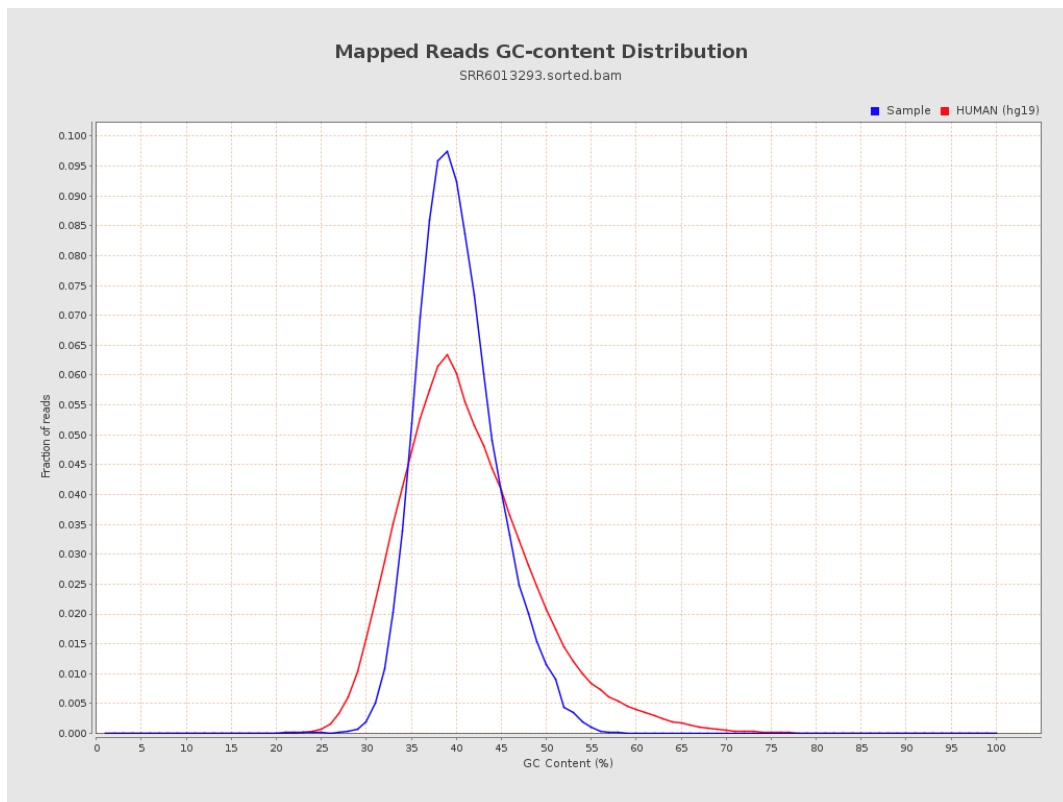
7. Results : Duplication Rate Histogram



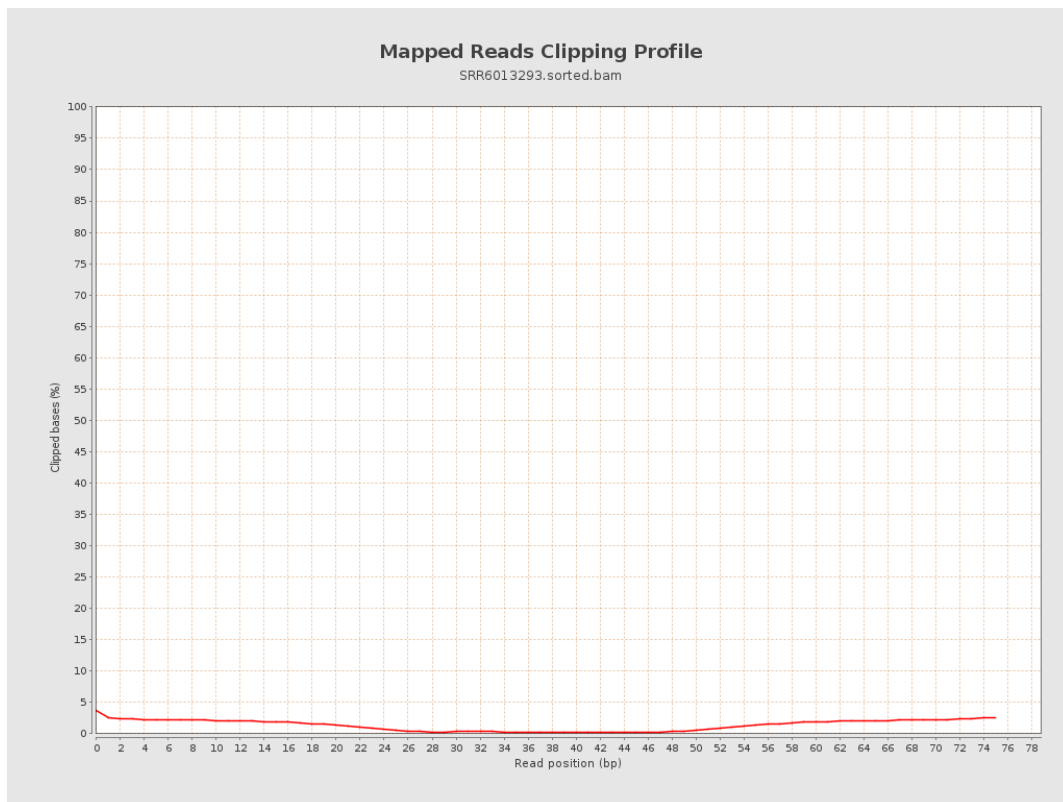
8. Results : Mapped Reads Nucleotide Content



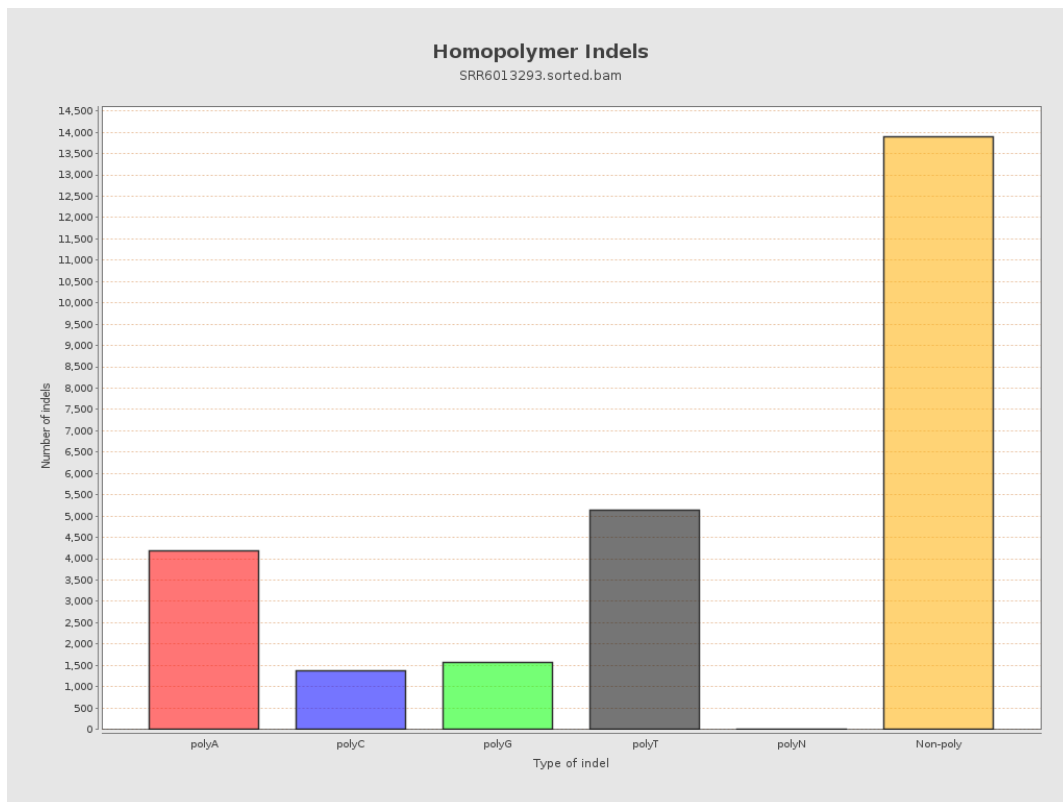
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

