

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/14 15:29:29

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6013198.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_SRR6013198 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6013198.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 14 15:29:28 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6013198.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,721,040
Mapped reads	1,385,227 / 80.49%
Unmapped reads	335,813 / 19.51%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	9,770 / 0.57%
Read min/max/mean length	30 / 76 / 76.2
Duplicated reads (estimated)	18,661 / 1.08%
Duplication rate	1.11%
Clipped reads	461,373 / 26.81%

2.2. ACGT Content

Number/percentage of A's	30,348,507 / 31.79%
Number/percentage of C's	16,408,664 / 17.19%
Number/percentage of T's	28,341,782 / 29.69%
Number/percentage of G's	20,334,016 / 21.3%
Number/percentage of N's	39,430 / 0.04%
GC Percentage	38.49%

2.3. Coverage

Mean	0.0309

Standard Deviation	0.2111
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2.4. Mapping Quality

Mean Mapping Quality	49.37
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2.5. Mismatches and indels

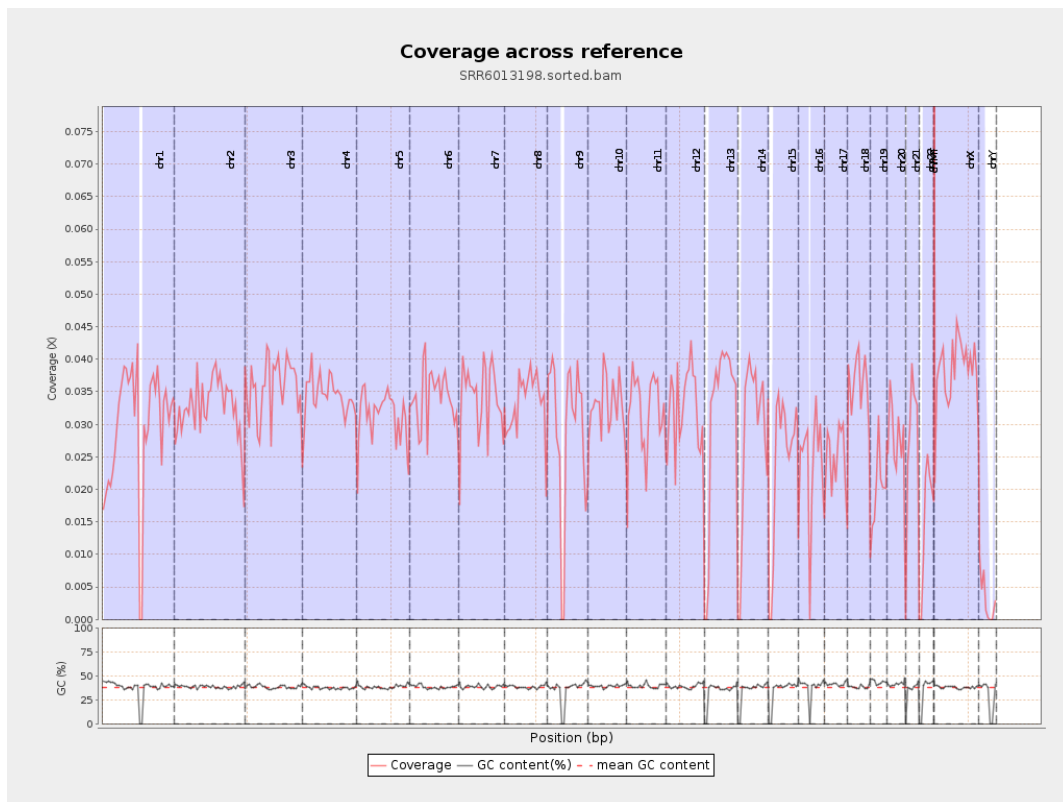
General error rate	1.09%
Mismatches	1,027,929
Insertions	5,777
Mapped reads with at least one insertion	0.41%
Deletions	18,538
Mapped reads with at least one deletion	1.33%
Homopolymer indels	46.53%

2.6. Chromosome stats

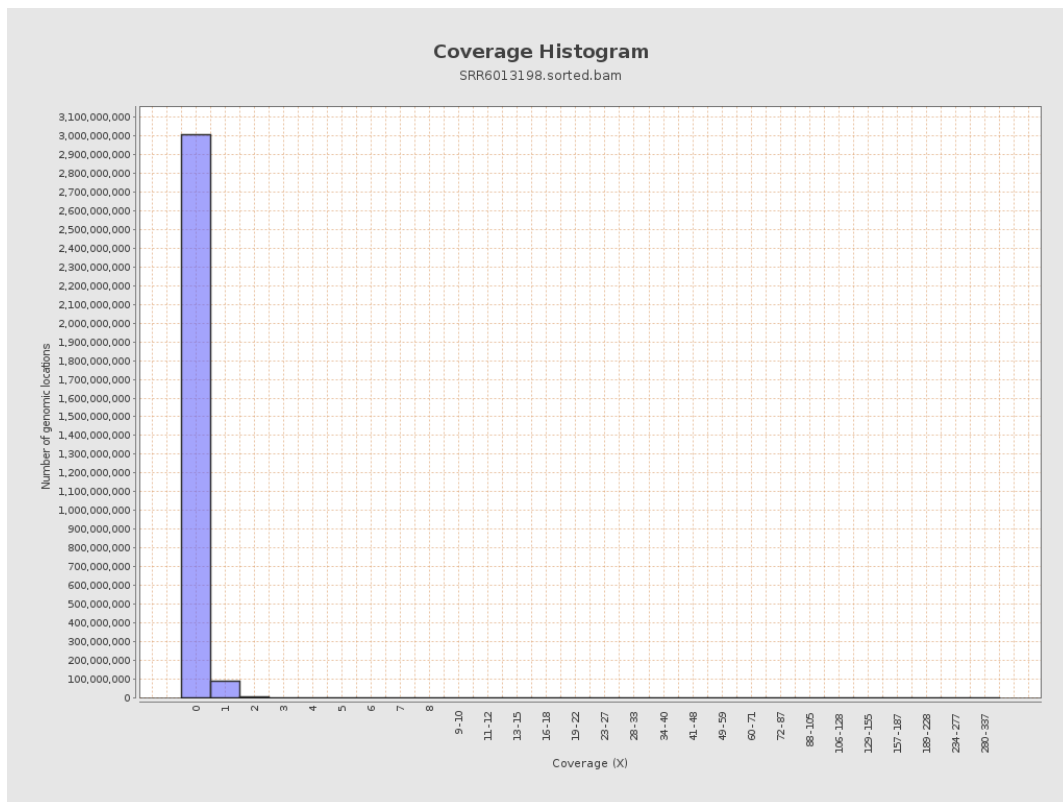
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7391434	0.0297	0.3249
chr2	243199373	7923264	0.0326	0.207
chr3	198022430	7099624	0.0359	0.1944
chr4	191154276	6540987	0.0342	0.1921
chr5	180915260	5709052	0.0316	0.1829
chr6	171115067	5831380	0.0341	0.2042
chr7	159138663	5433113	0.0341	0.2444

chr8	146364022	4890288	0.0334	0.239
chr9	141213431	4131577	0.0293	0.1926
chr10	135534747	4426055	0.0327	0.207
chr11	135006516	4348463	0.0322	0.1991
chr12	133851895	4351167	0.0325	0.1858
chr13	115169878	3612489	0.0314	0.1822
chr14	107349540	3055928	0.0285	0.1759
chr15	102531392	2489137	0.0243	0.1629
chr16	90354753	2112242	0.0234	0.1625
chr17	81195210	2006789	0.0247	0.1681
chr18	78077248	2871487	0.0368	0.2806
chr19	59128983	1202620	0.0203	0.2087
chr20	63025520	1755802	0.0279	0.1739
chr21	48129895	1341739	0.0279	0.1772
chr22	51304566	793839	0.0155	0.1287
chrMT	16571	5091	0.3072	0.6971
chrX	155270560	5997934	0.0386	0.2087
chrY	59373566	181796	0.0031	0.0679

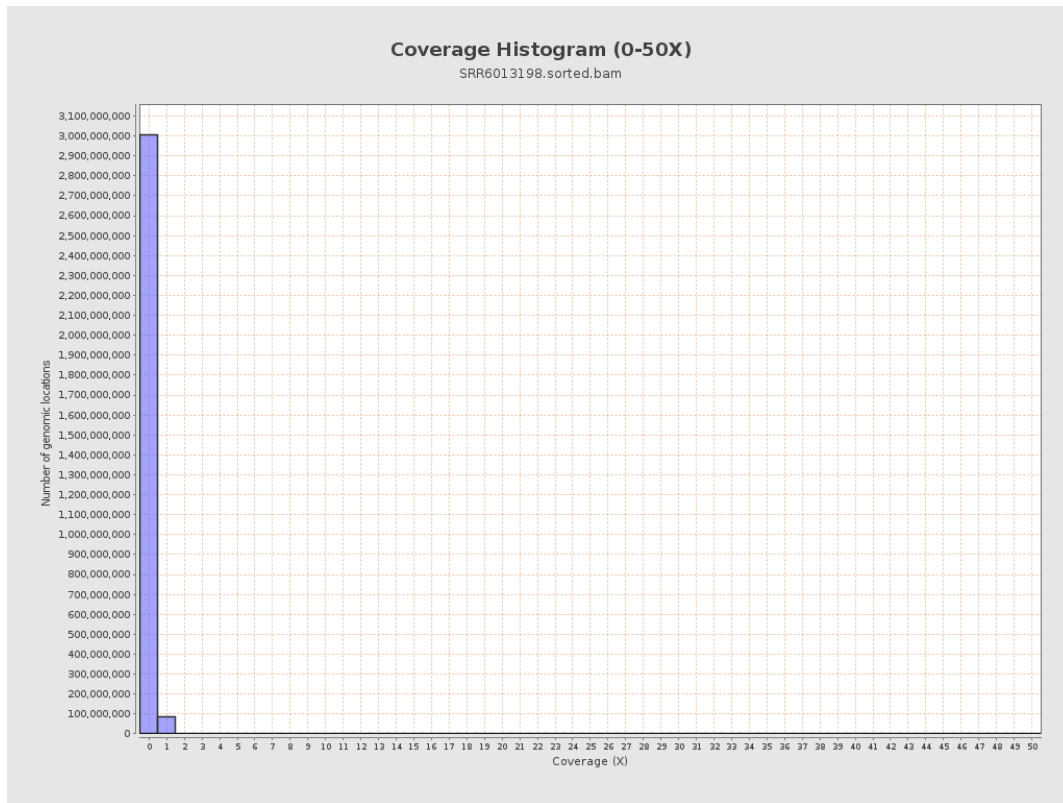
3. Results : Coverage across reference



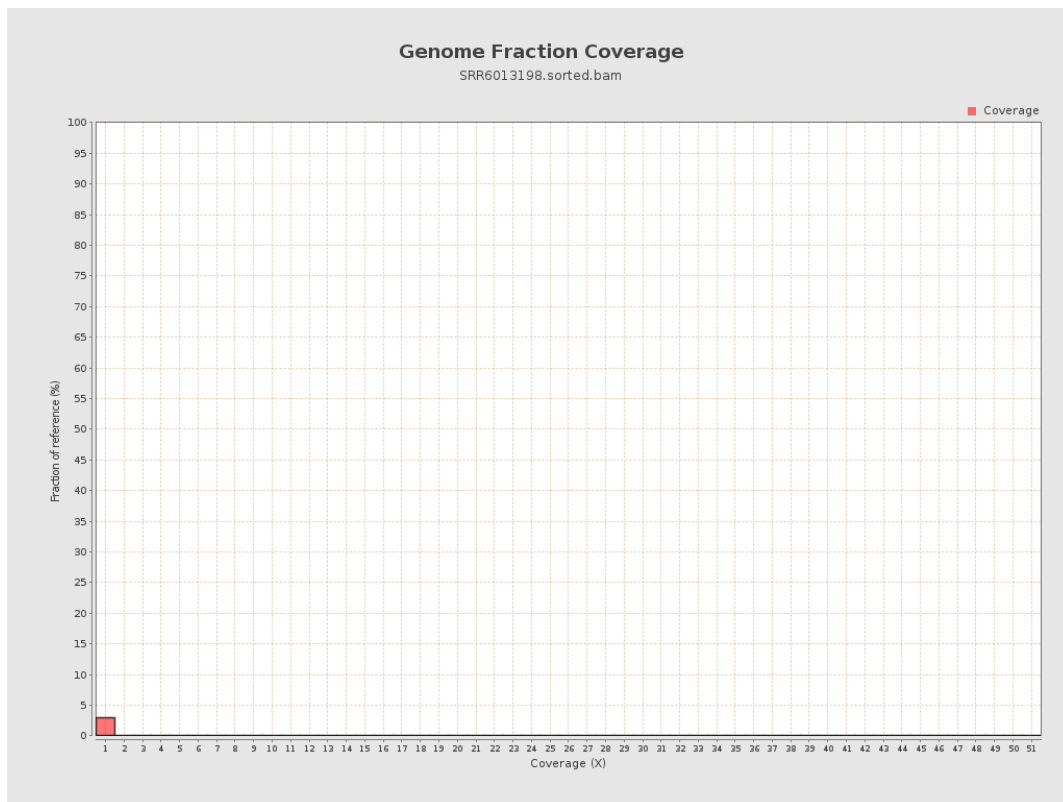
4. Results : Coverage Histogram



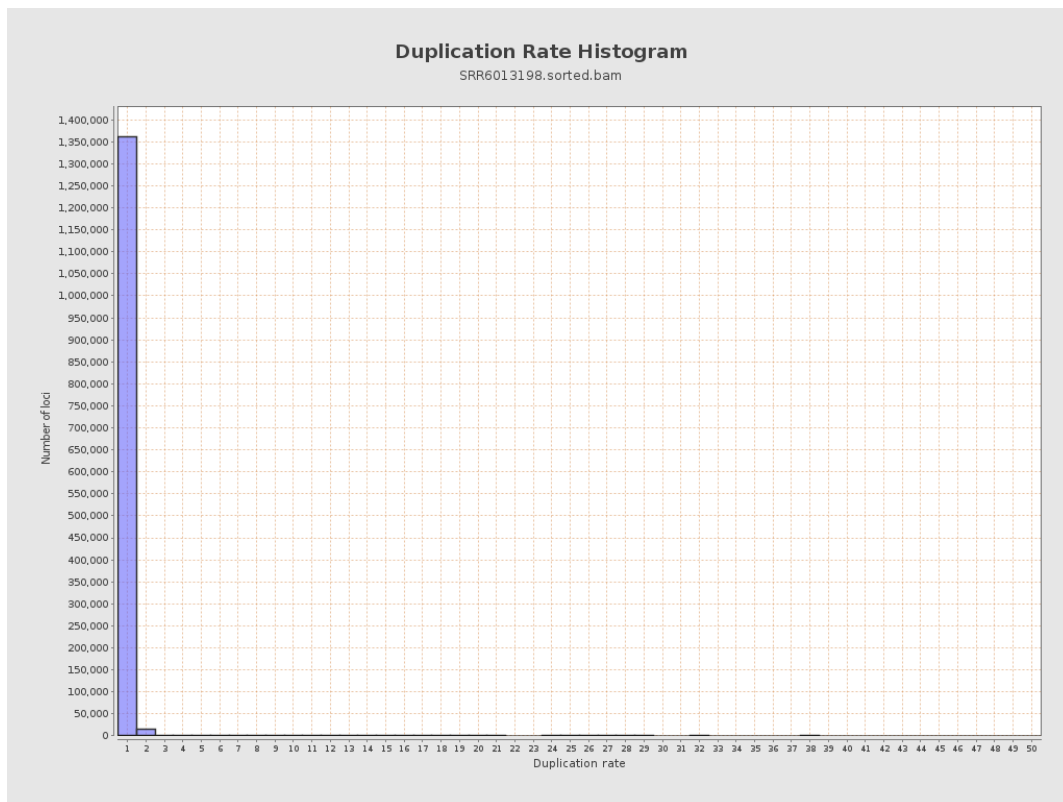
5. Results : Coverage Histogram (0-50X)



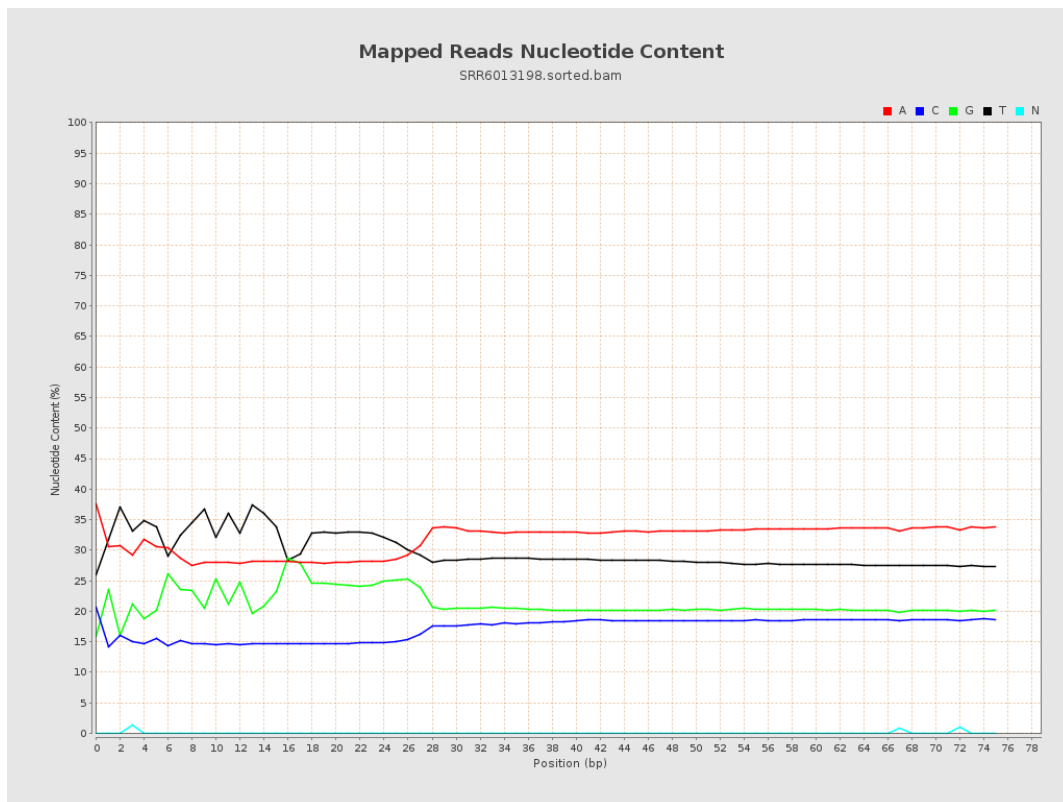
6. Results : Genome Fraction Coverage



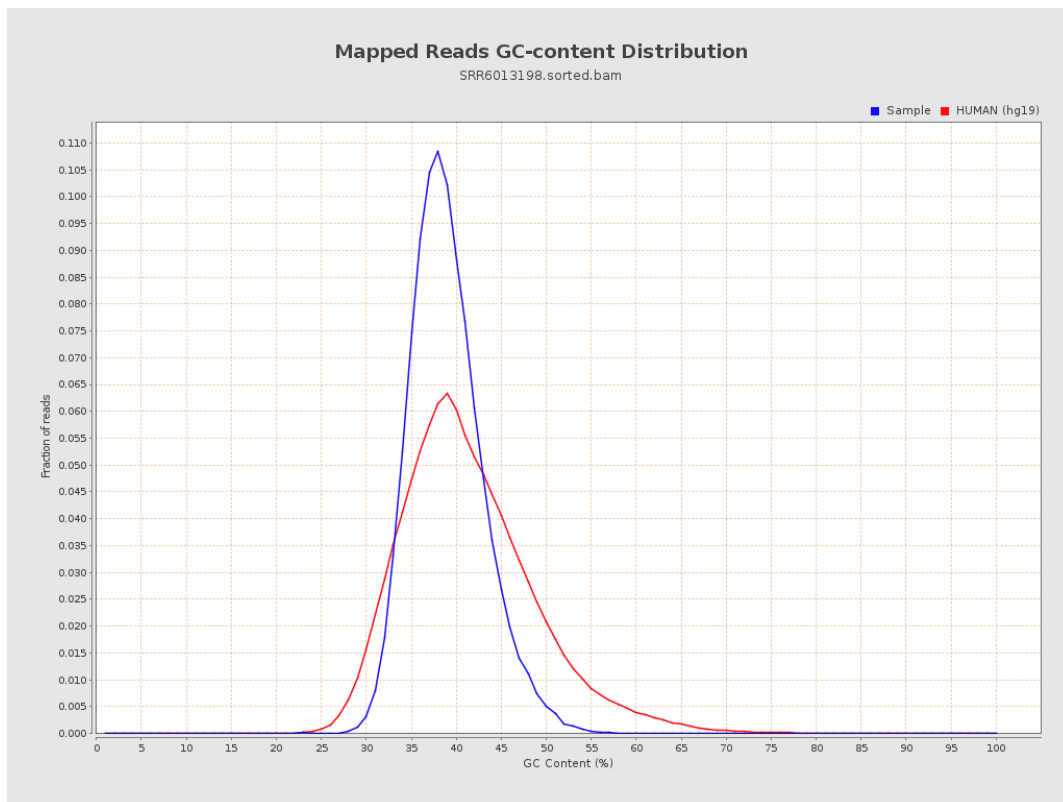
7. Results : Duplication Rate Histogram



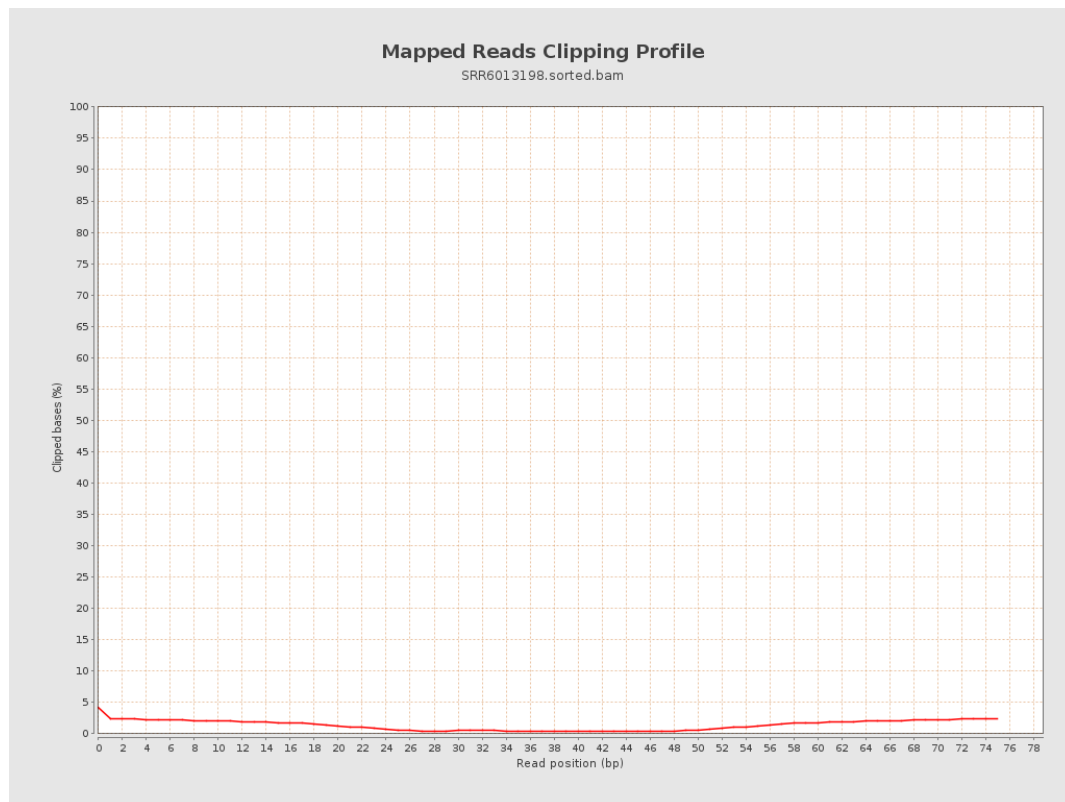
8. Results : Mapped Reads Nucleotide Content



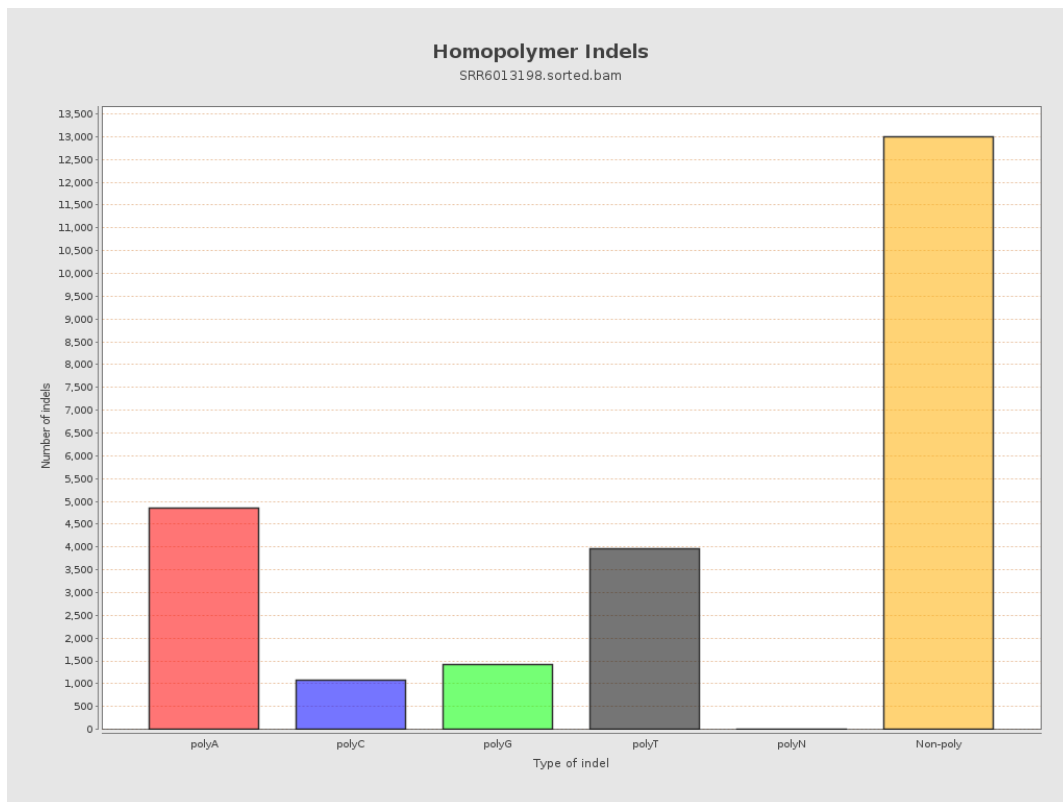
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

