

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/01 20:34:22

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524897.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_SRR10524897 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524897.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 01 20:34:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524897.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,832,298
Mapped reads	1,675,139 / 91.42%
Unmapped reads	157,159 / 8.58%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	6,200 / 0.34%
Read min/max/mean length	30 / 76 / 76.11
Duplicated reads (estimated)	71,201 / 3.89%
Duplication rate	3.11%
Clipped reads	1,676,742 / 91.51%

2.2. ACGT Content

Number/percentage of A's	25,117,126 / 25.84%
Number/percentage of C's	17,713,616 / 18.22%
Number/percentage of T's	31,660,220 / 32.57%
Number/percentage of G's	22,704,497 / 23.36%
Number/percentage of N's	12,661 / 0.01%
GC Percentage	41.58%

2.3. Coverage

Mean	0.0314

Standard Deviation	0.314
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2.4. Mapping Quality

Mean Mapping Quality	46.12
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2.5. Mismatches and indels

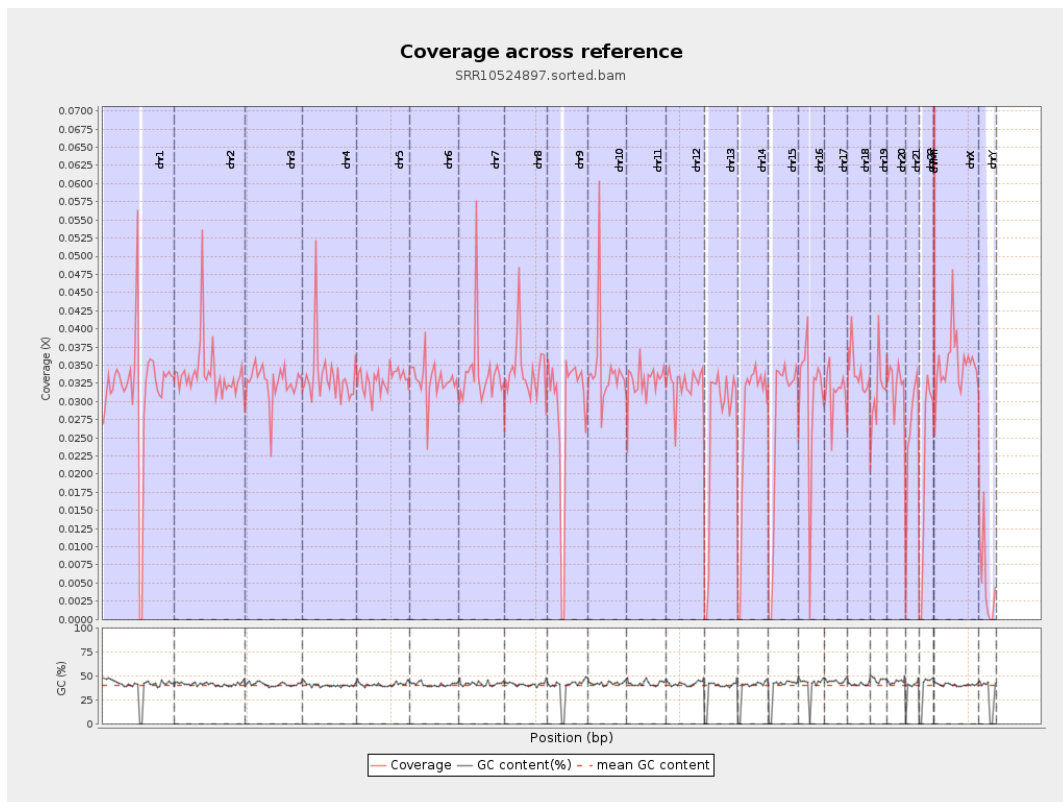
General error rate	0.51%
Mismatches	485,591
Insertions	6,814
Mapped reads with at least one insertion	0.4%
Deletions	18,944
Mapped reads with at least one deletion	1.12%
Homopolymer indels	43.28%

2.6. Chromosome stats

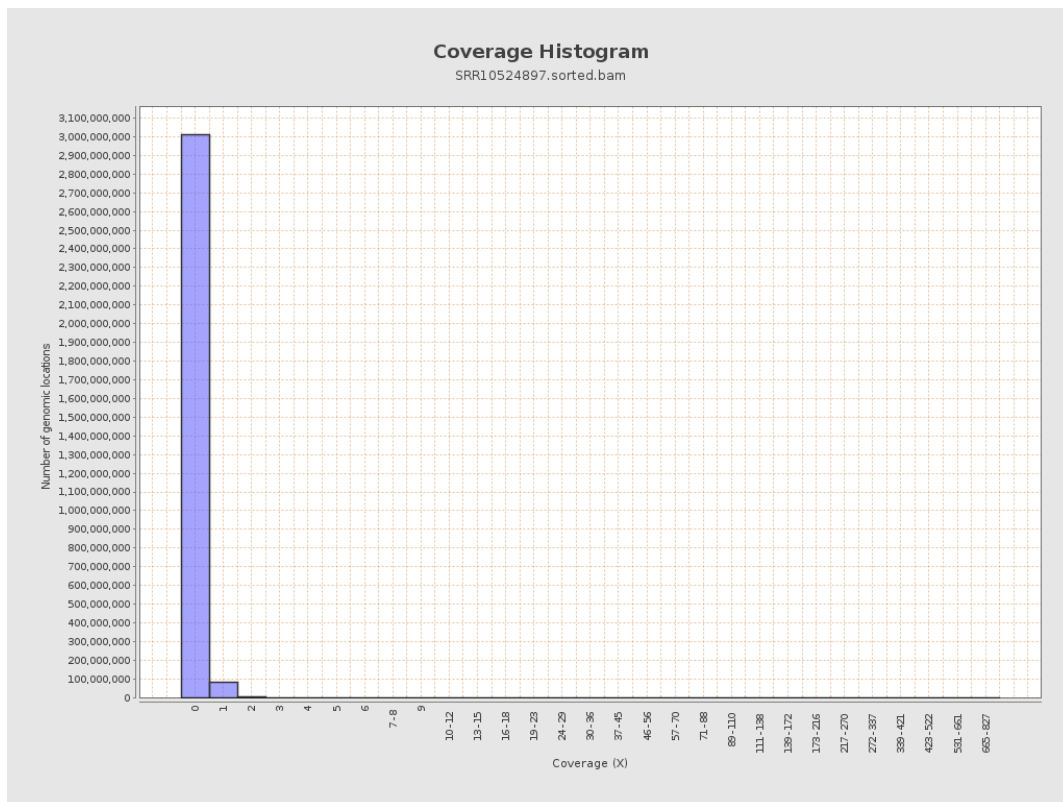
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7802837	0.0313	0.6126
chr2	243199373	8233964	0.0339	0.329
chr3	198022430	6469899	0.0327	0.1965
chr4	191154276	6386661	0.0334	0.2238
chr5	180915260	5977288	0.033	0.1993
chr6	171115067	5631600	0.0329	0.2192
chr7	159138663	5410781	0.034	0.4286

chr8	146364022	5021099	0.0343	0.3272
chr9	141213431	4082774	0.0289	0.2848
chr10	135534747	4669717	0.0345	0.2936
chr11	135006516	4450635	0.033	0.2788
chr12	133851895	4329120	0.0323	0.2019
chr13	115169878	3024413	0.0263	0.1775
chr14	107349540	2962943	0.0276	0.1911
chr15	102531392	2773789	0.0271	0.1805
chr16	90354753	2744178	0.0304	0.208
chr17	81195210	2537820	0.0313	0.2098
chr18	78077248	2654233	0.034	0.5573
chr19	59128983	1866708	0.0316	0.4186
chr20	63025520	2031378	0.0322	0.1976
chr21	48129895	1256360	0.0261	0.1986
chr22	51304566	1107068	0.0216	0.1583
chrMT	16571	29078	1.7548	1.8147
chrX	155270560	5484359	0.0353	0.2393
chrY	59373566	299483	0.005	0.1356

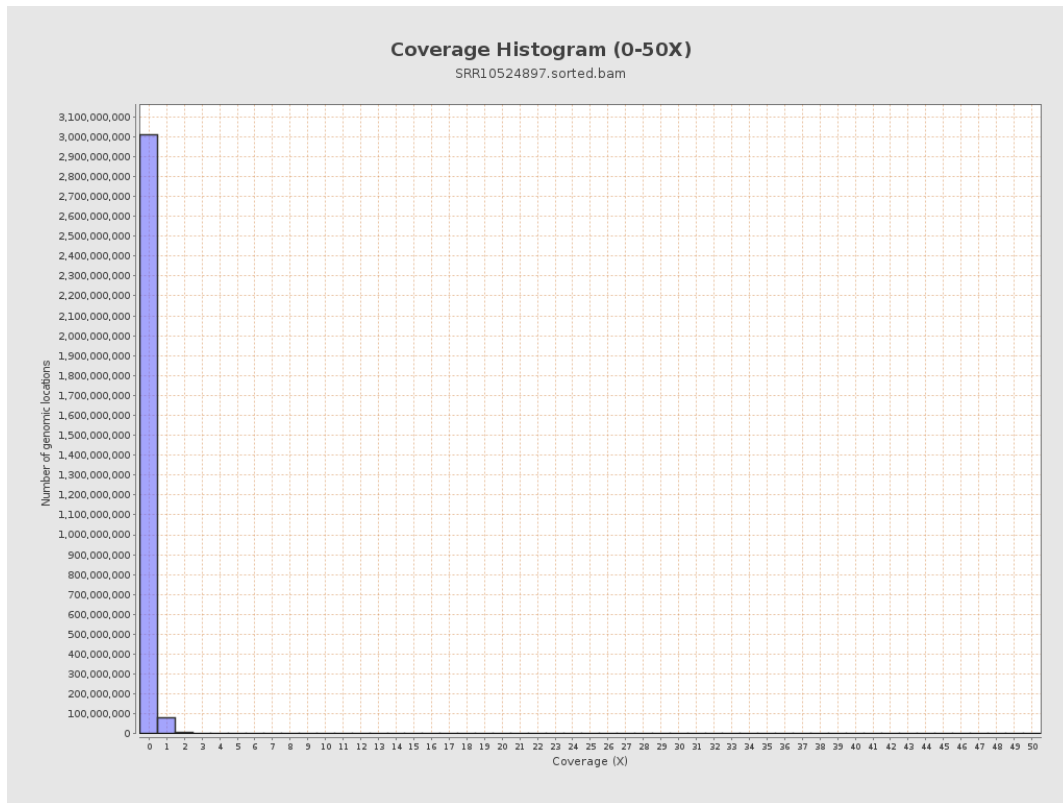
3. Results : Coverage across reference



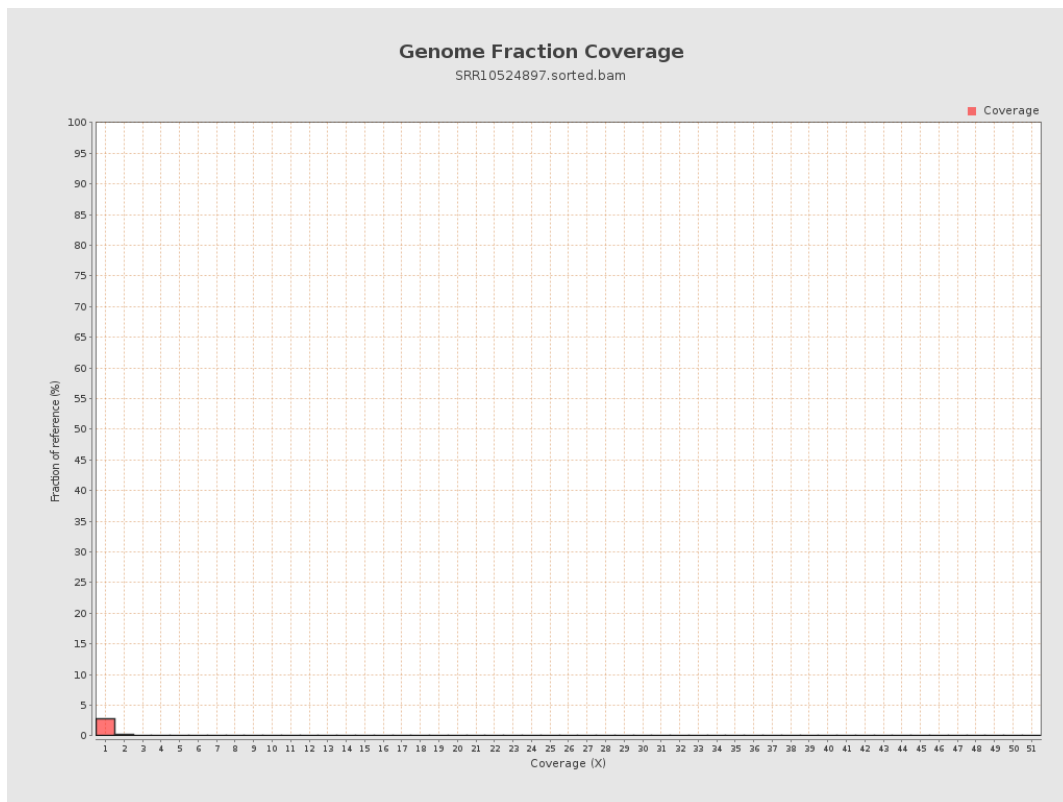
4. Results : Coverage Histogram



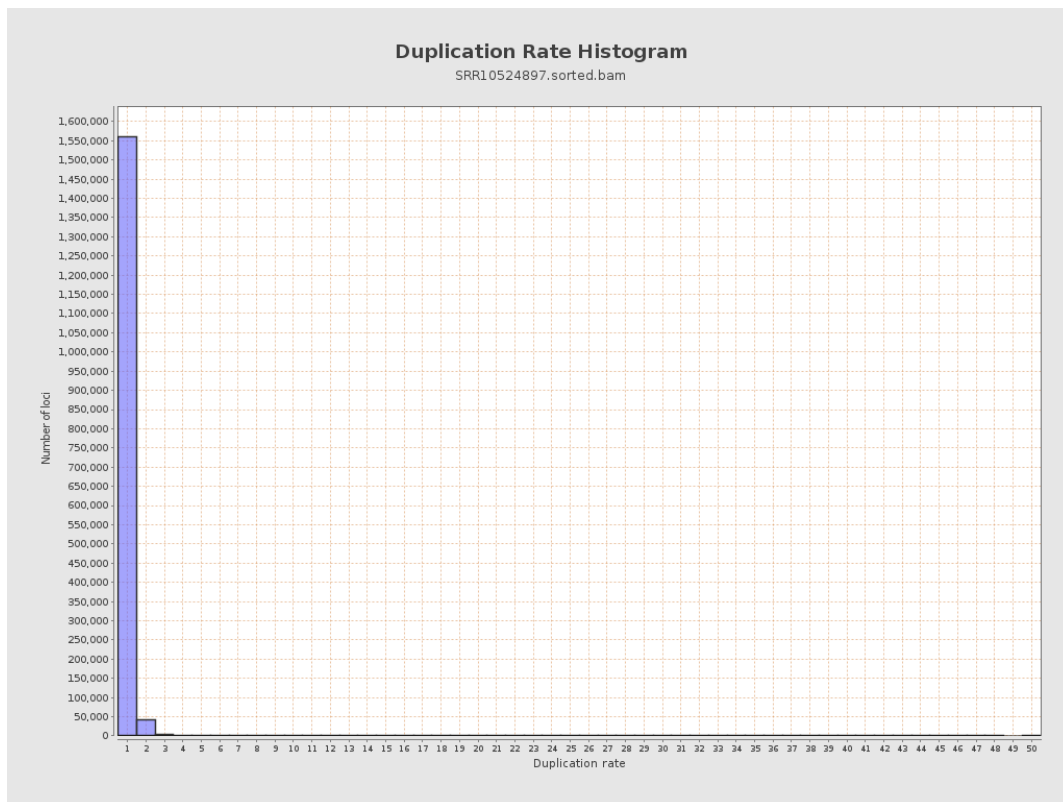
5. Results : Coverage Histogram (0-50X)



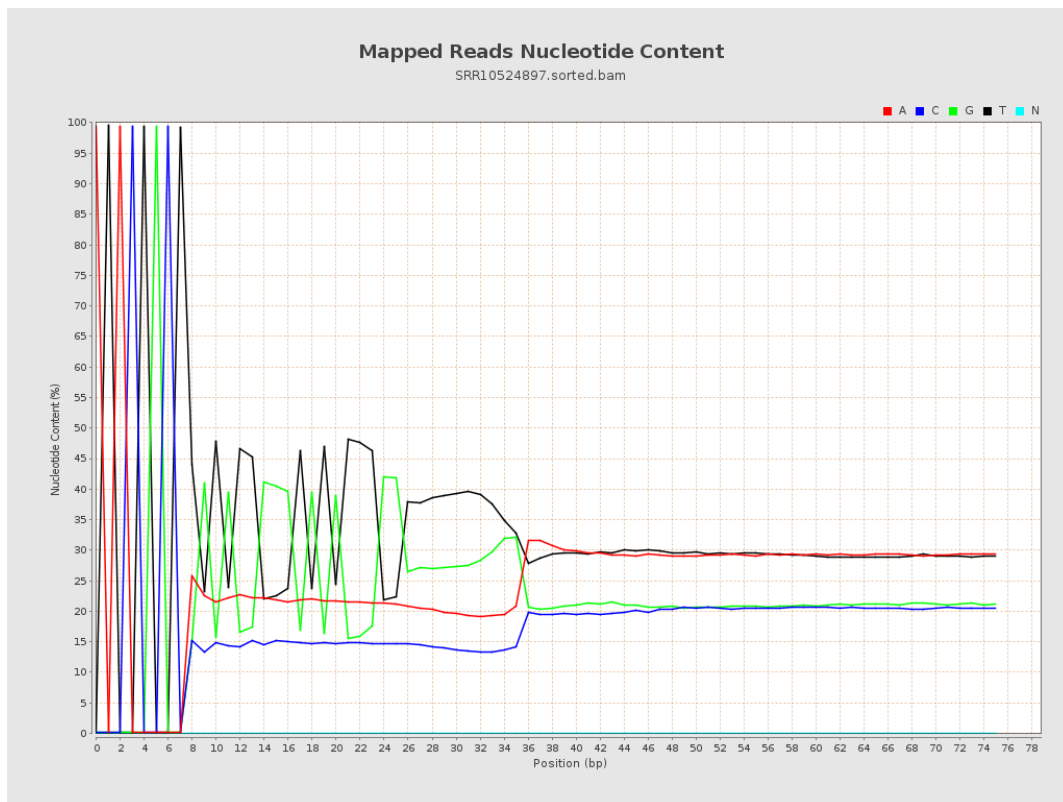
6. Results : Genome Fraction Coverage



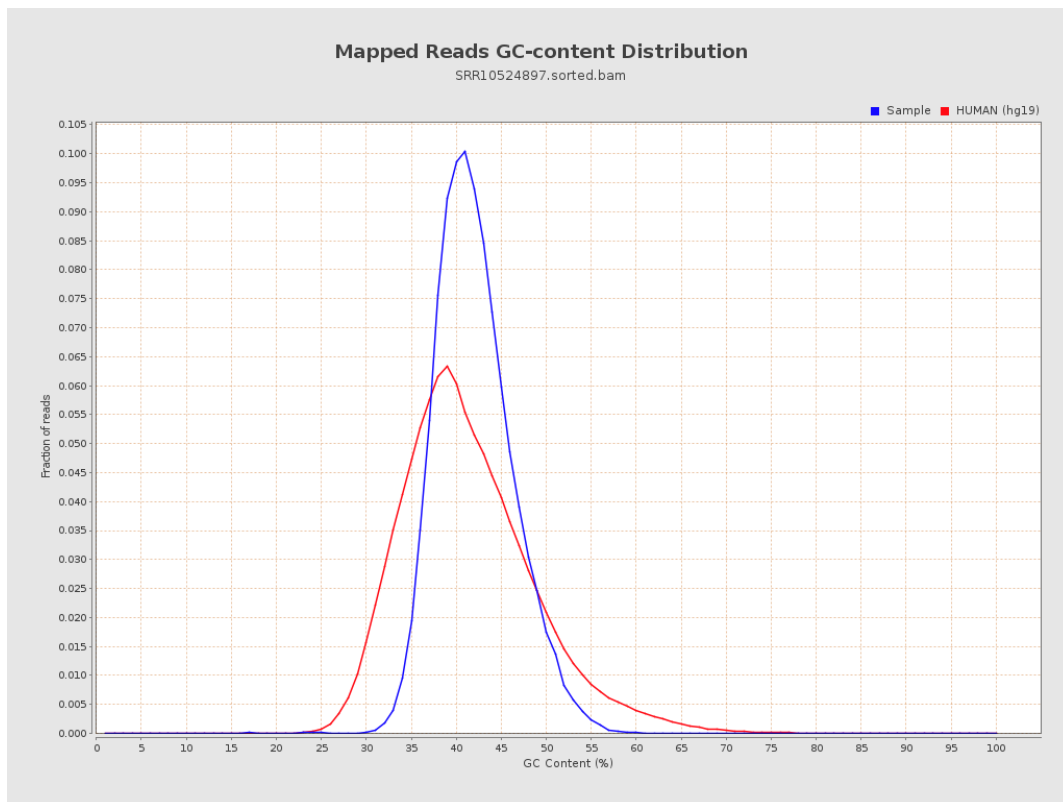
7. Results : Duplication Rate Histogram



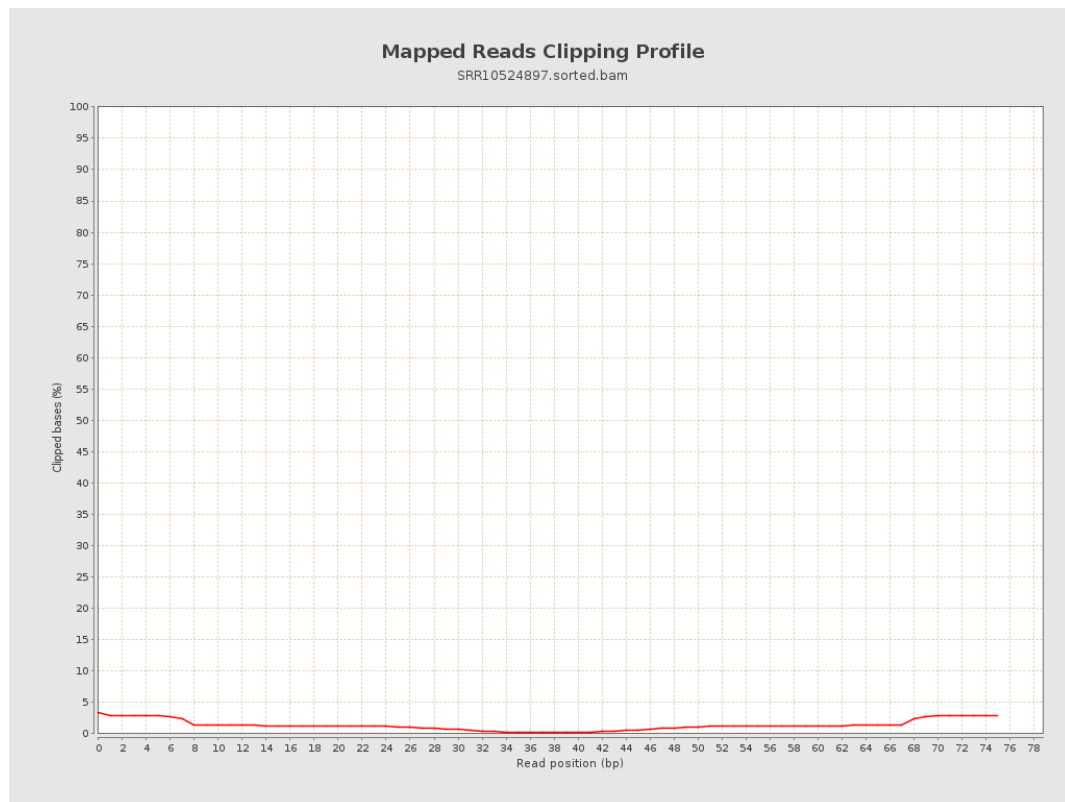
8. Results : Mapped Reads Nucleotide Content



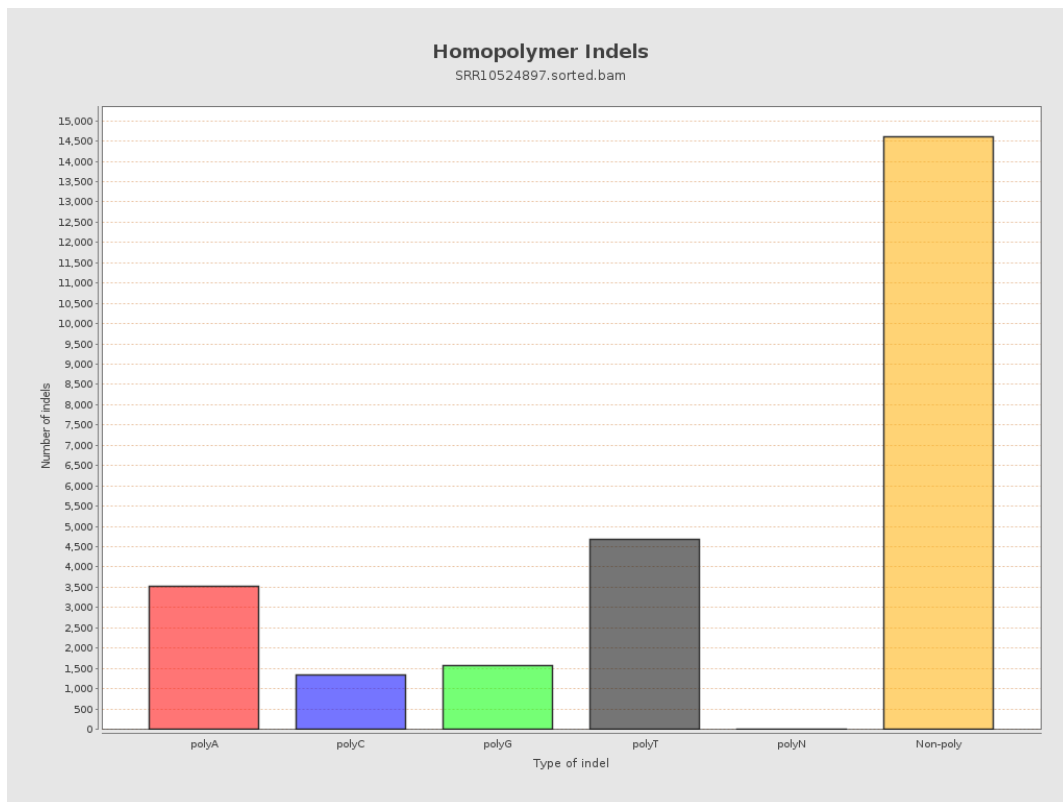
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

