

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 17:56:54

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525100.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_SRR10525100 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525100.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 17:56:53 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525100.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,467,360
Mapped reads	1,292,672 / 88.1%
Unmapped reads	174,688 / 11.9%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	37,681 / 2.57%
Read min/max/mean length	30 / 101 / 101.95
Duplicated reads (estimated)	38,228 / 2.61%
Duplication rate	1.72%
Clipped reads	1,328,255 / 90.52%

2.2. ACGT Content

Number/percentage of A's	26,102,684 / 26.52%
Number/percentage of C's	19,713,148 / 20.03%
Number/percentage of T's	30,620,687 / 31.12%
Number/percentage of G's	21,969,925 / 22.32%
Number/percentage of N's	3,616 / 0%
GC Percentage	42.36%

2.3. Coverage

Mean	0.0318

Standard Deviation	0.3453
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2.4. Mapping Quality

Mean Mapping Quality	45.98
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2.5. Mismatches and indels

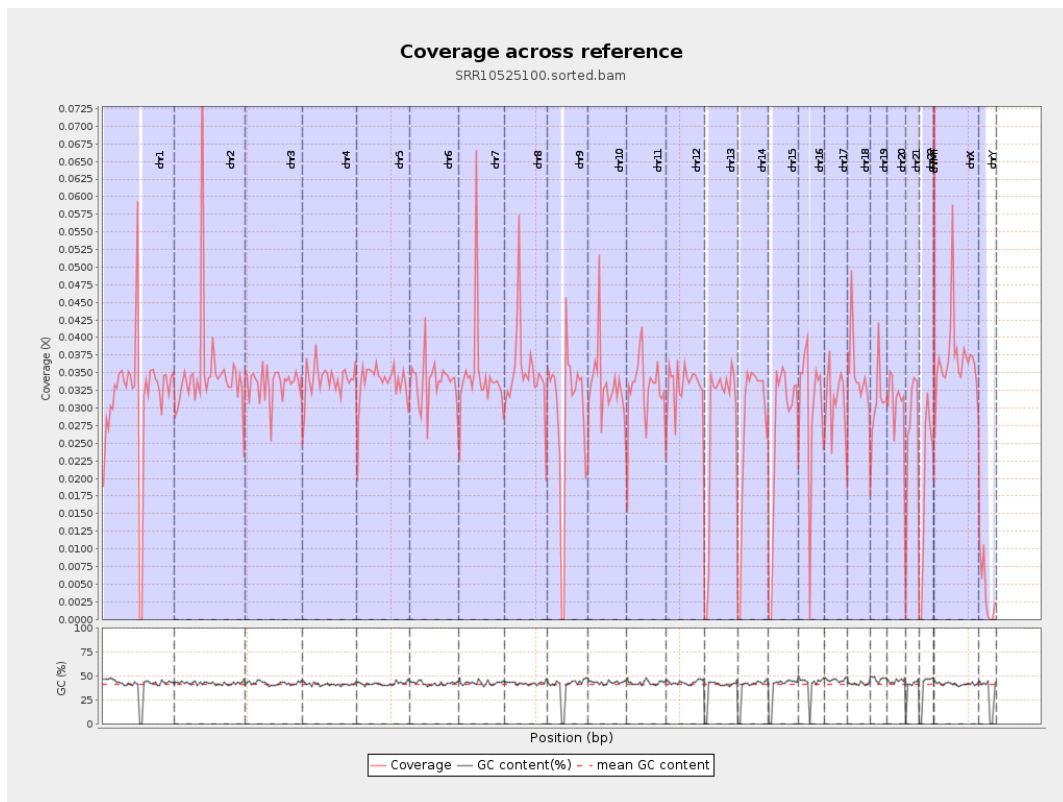
General error rate	0.79%
Mismatches	765,416
Insertions	8,650
Mapped reads with at least one insertion	0.66%
Deletions	23,461
Mapped reads with at least one deletion	1.79%
Homopolymer indels	43.62%

2.6. Chromosome stats

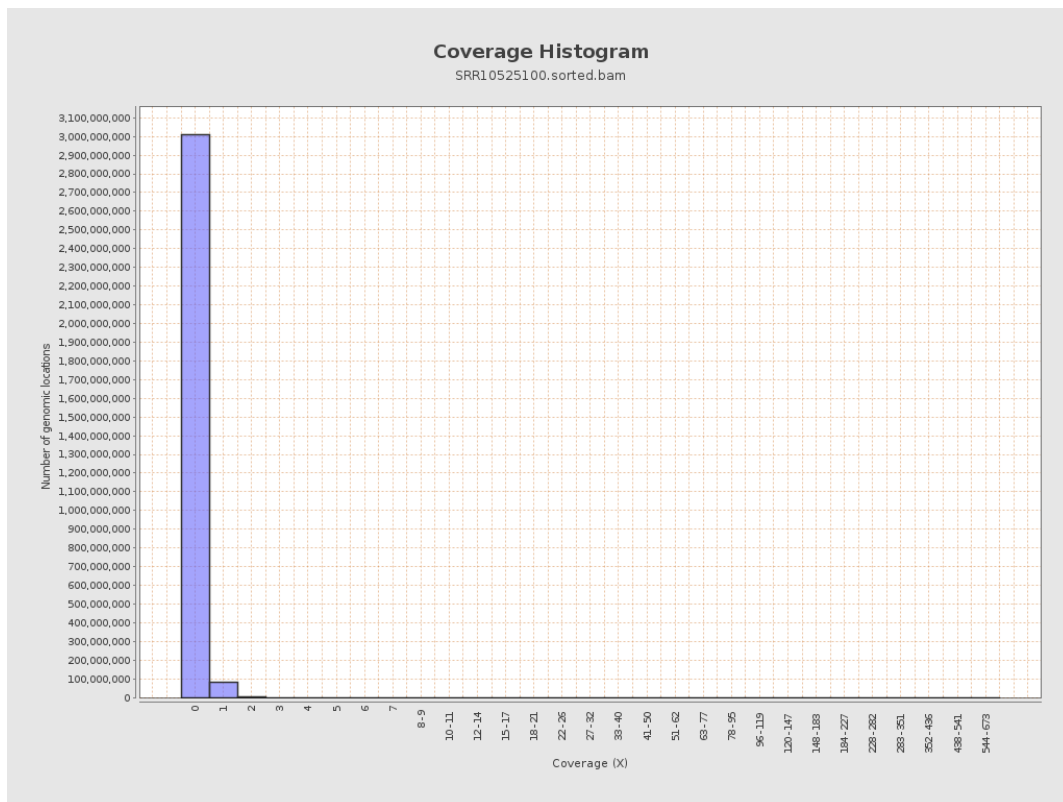
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7799828	0.0313	0.5472
chr2	243199373	8531655	0.0351	0.5156
chr3	198022430	6622437	0.0334	0.1962
chr4	191154276	6485173	0.0339	0.2055
chr5	180915260	6134769	0.0339	0.2034
chr6	171115067	5759094	0.0337	0.2347
chr7	159138663	5513225	0.0346	0.5322

chr8	146364022	5140739	0.0351	0.4592
chr9	141213431	4134680	0.0293	0.3263
chr10	135534747	4495385	0.0332	0.2992
chr11	135006516	4483776	0.0332	0.3334
chr12	133851895	4439505	0.0332	0.1987
chr13	115169878	3195769	0.0277	0.1779
chr14	107349540	2959257	0.0276	0.2136
chr15	102531392	2759874	0.0269	0.176
chr16	90354753	2710836	0.03	0.2061
chr17	81195210	2505134	0.0309	0.2461
chr18	78077248	2735388	0.035	0.5811
chr19	59128983	1835439	0.031	0.392
chr20	63025520	1935396	0.0307	0.1939
chr21	48129895	1297223	0.027	0.1881
chr22	51304566	993068	0.0194	0.1482
chrMT	16571	4843	0.2923	0.6186
chrX	155270560	5755155	0.0371	0.2795
chrY	59373566	222204	0.0037	0.0864

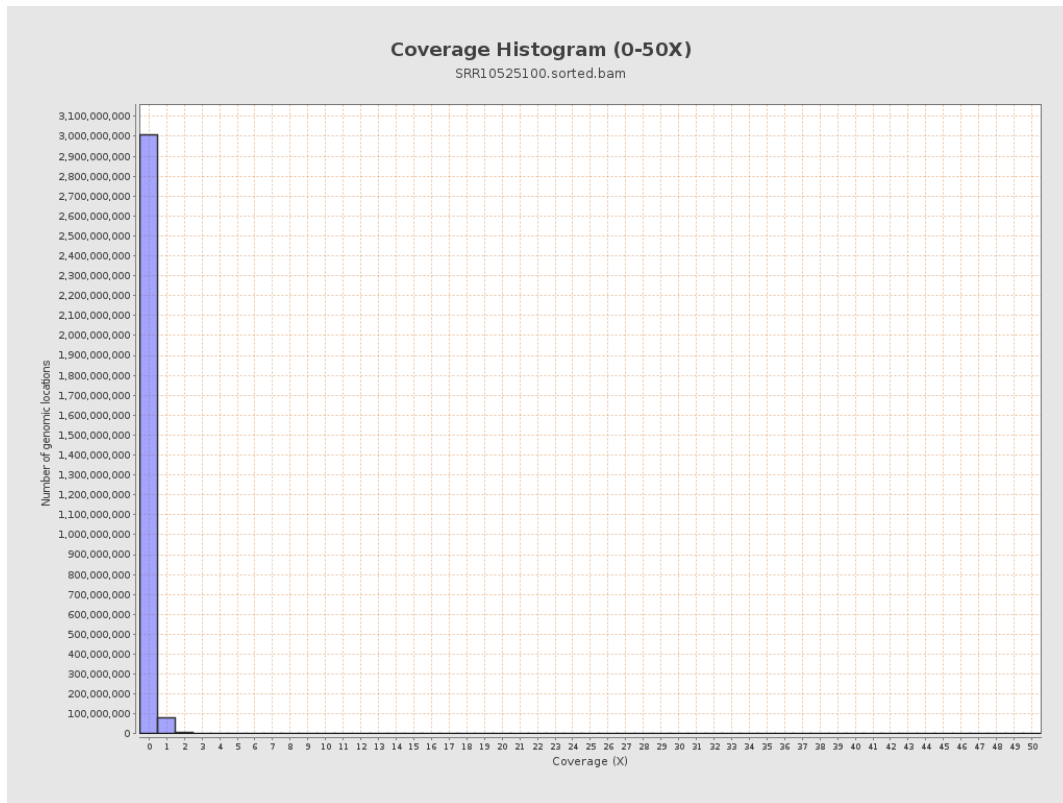
3. Results : Coverage across reference



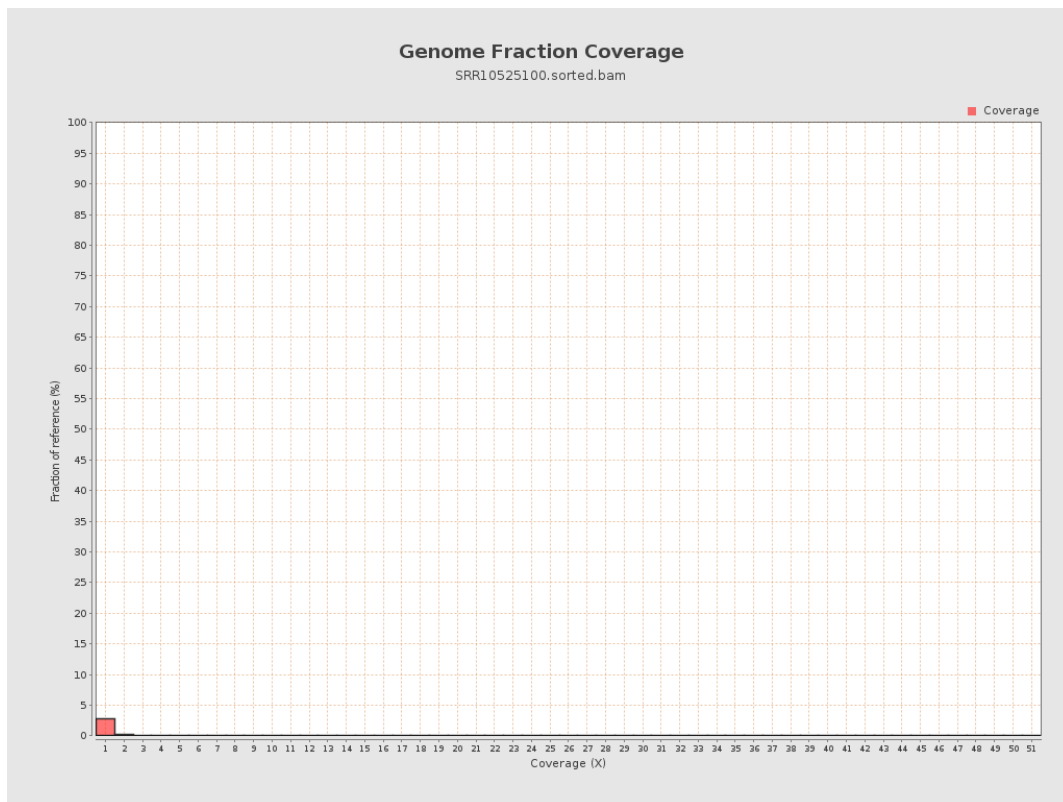
4. Results : Coverage Histogram



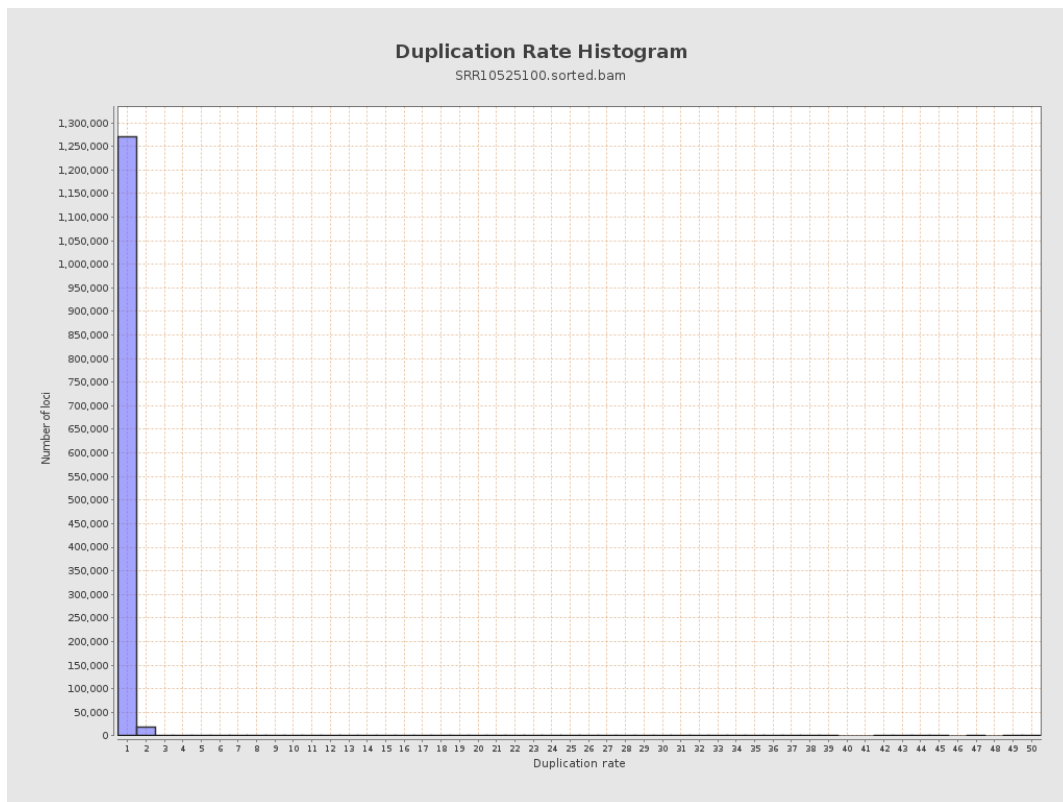
5. Results : Coverage Histogram (0-50X)



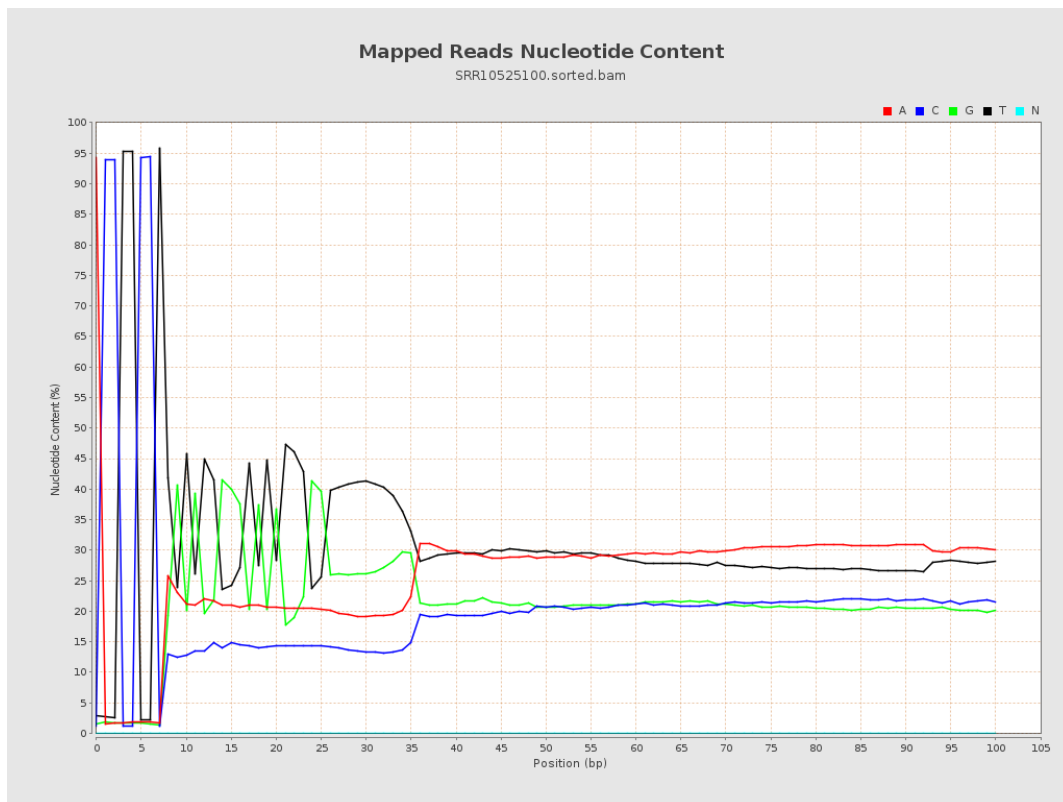
6. Results : Genome Fraction Coverage



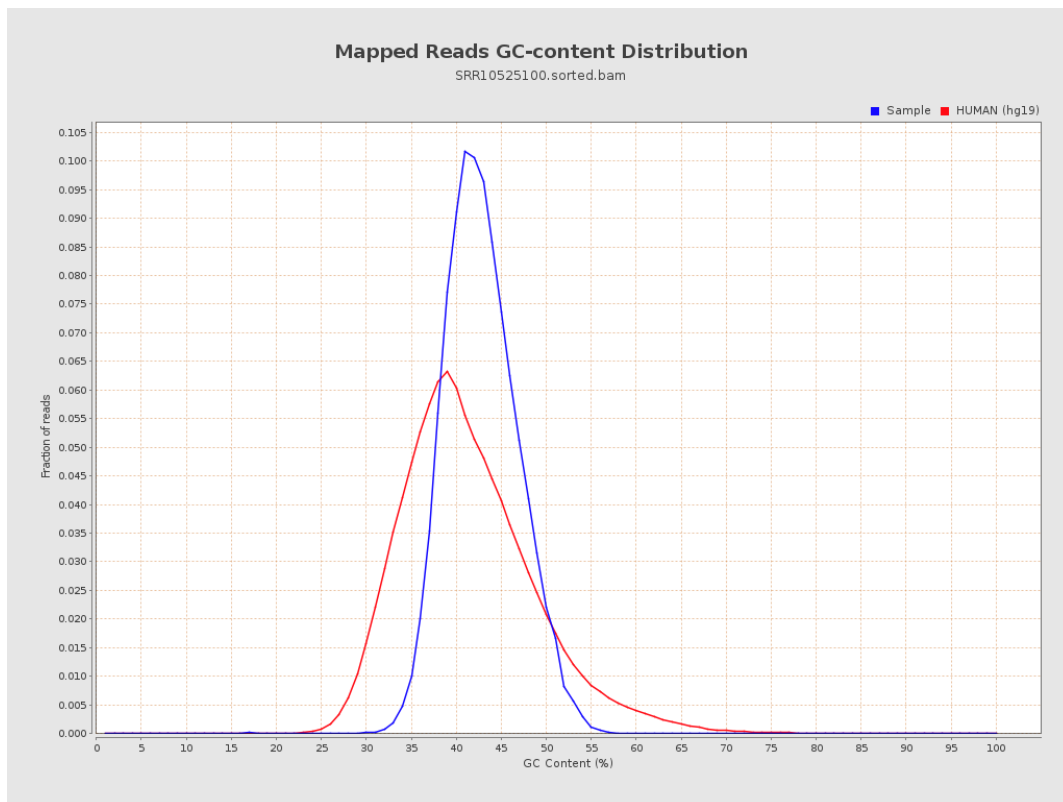
7. Results : Duplication Rate Histogram



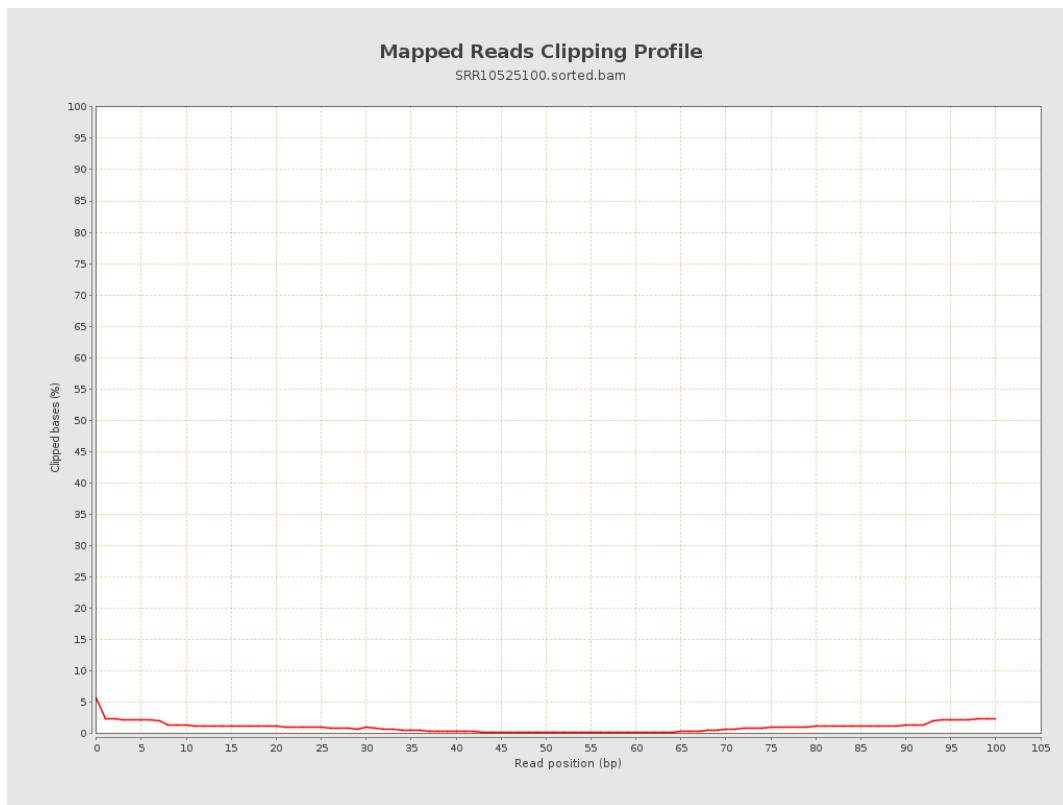
8. Results : Mapped Reads Nucleotide Content



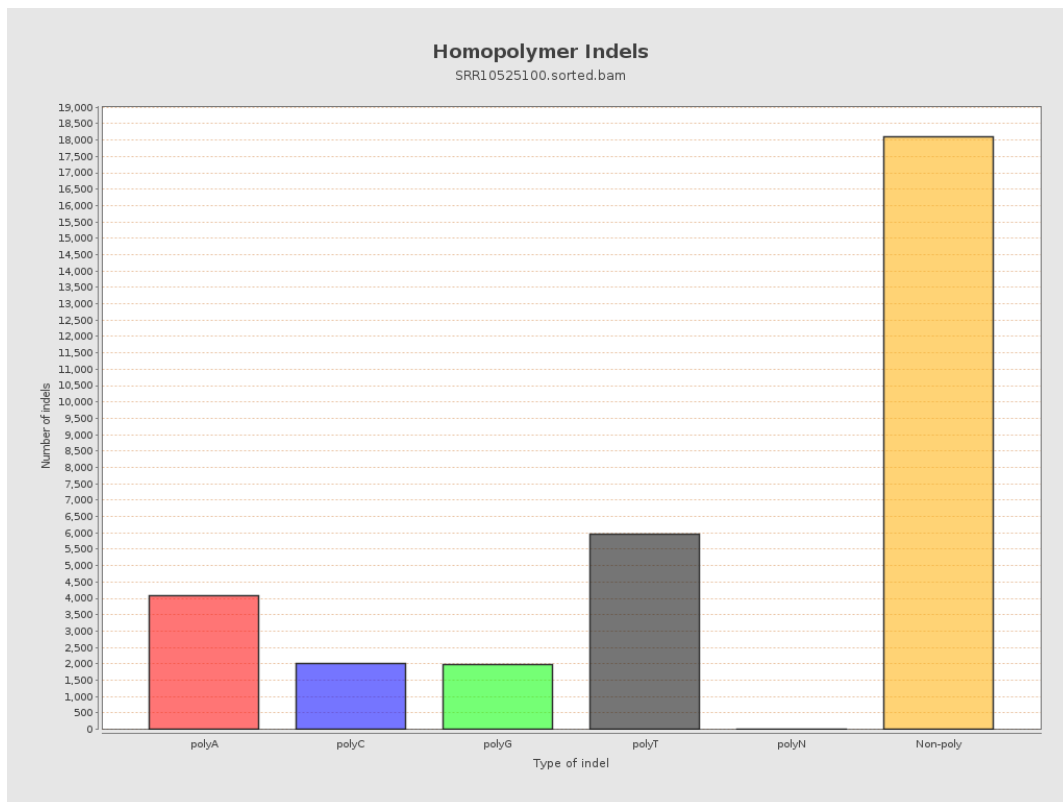
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

