

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/29 18:23:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10525110.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_SRR10525110 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10525110.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 29 18:23:25 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10525110.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	877,227
Mapped reads	805,112 / 91.78%
Unmapped reads	72,115 / 8.22%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	22,116 / 2.52%
Read min/max/mean length	30 / 101 / 101.93
Duplicated reads (estimated)	19,249 / 2.19%
Duplication rate	1.43%
Clipped reads	825,753 / 94.13%

2.2. ACGT Content

Number/percentage of A's	15,876,286 / 25.64%
Number/percentage of C's	11,565,069 / 18.68%
Number/percentage of T's	19,638,129 / 31.72%
Number/percentage of G's	14,831,494 / 23.96%
Number/percentage of N's	2,233 / 0%
GC Percentage	42.63%

2.3. Coverage

Mean	0.02

Standard Deviation	0.2343
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2.4. Mapping Quality

Mean Mapping Quality	46.19
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2.5. Mismatches and indels

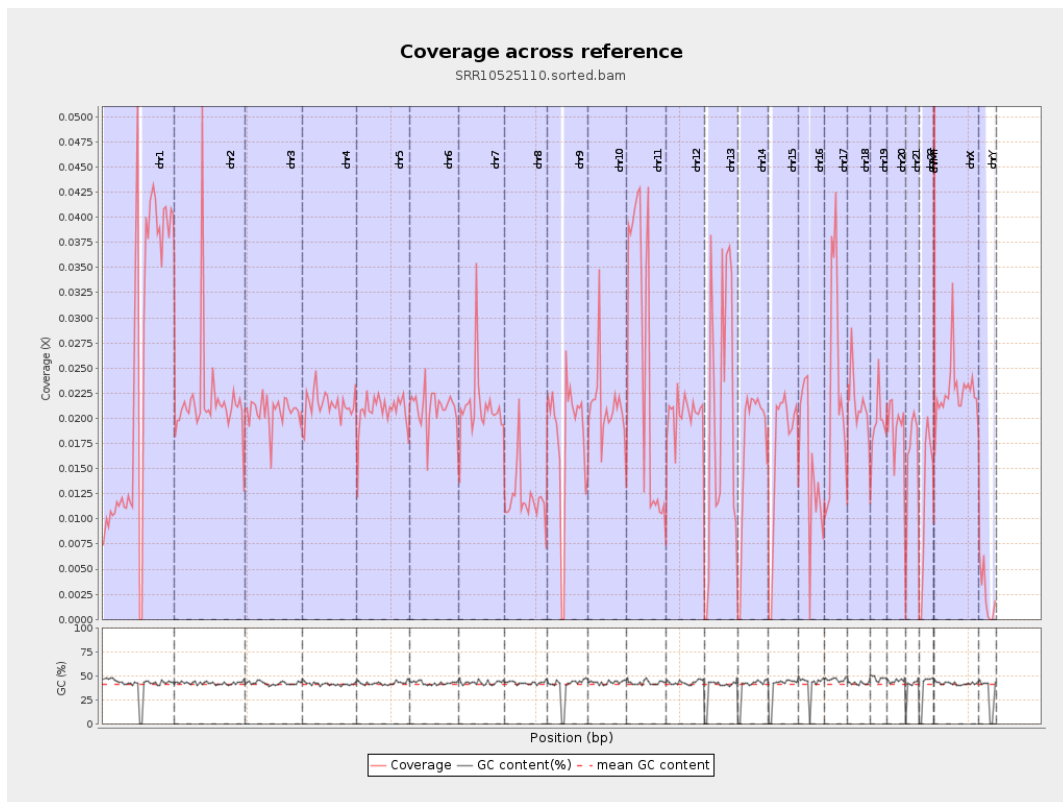
General error rate	0.75%
Mismatches	456,729
Insertions	5,350
Mapped reads with at least one insertion	0.66%
Deletions	13,914
Mapped reads with at least one deletion	1.7%
Homopolymer indels	42.36%

2.6. Chromosome stats

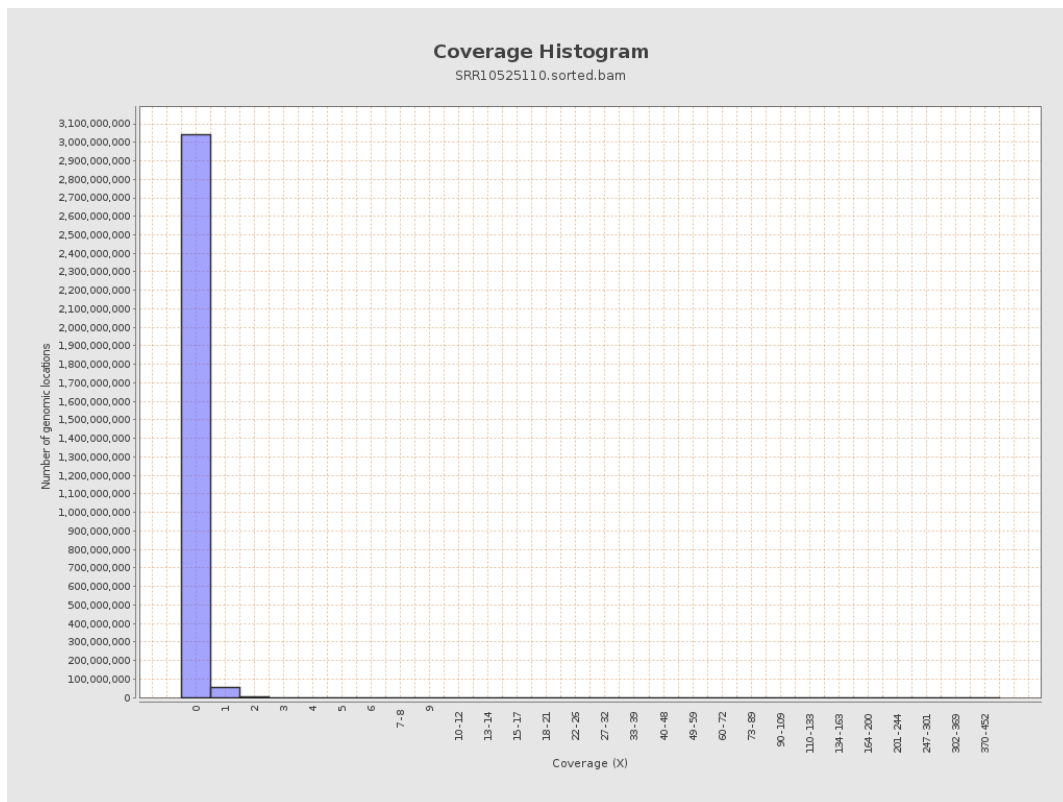
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	6090304	0.0244	0.3996
chr2	243199373	5316402	0.0219	0.3229
chr3	198022430	4096675	0.0207	0.1517
chr4	191154276	4078298	0.0213	0.1578
chr5	180915260	3788013	0.0209	0.1543
chr6	171115067	3594912	0.021	0.1661
chr7	159138663	3371511	0.0212	0.291

chr8	146364022	1768230	0.0121	0.254
chr9	141213431	2573714	0.0182	0.218
chr10	135534747	2862979	0.0211	0.2411
chr11	135006516	3495579	0.0259	0.2874
chr12	133851895	2742693	0.0205	0.1518
chr13	115169878	2260068	0.0196	0.148
chr14	107349540	1863353	0.0174	0.1493
chr15	102531392	1730586	0.0169	0.1368
chr16	90354753	1357550	0.015	0.138
chr17	81195210	1820584	0.0224	0.1813
chr18	78077248	1689596	0.0216	0.3523
chr19	59128983	1165386	0.0197	0.2867
chr20	63025520	1198783	0.019	0.1469
chr21	48129895	781040	0.0162	0.14
chr22	51304566	620314	0.0121	0.1152
chrMT	16571	3667	0.2213	0.5144
chrX	155270560	3527993	0.0227	0.1901
chrY	59373566	138661	0.0023	0.0618

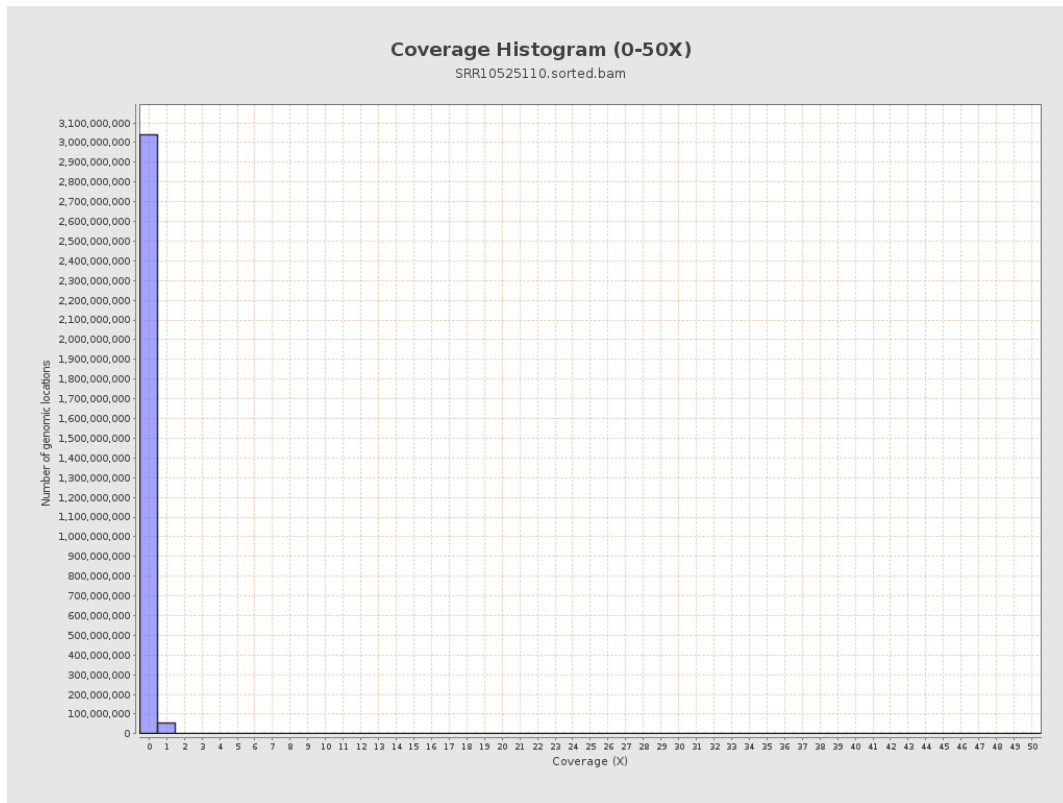
3. Results : Coverage across reference



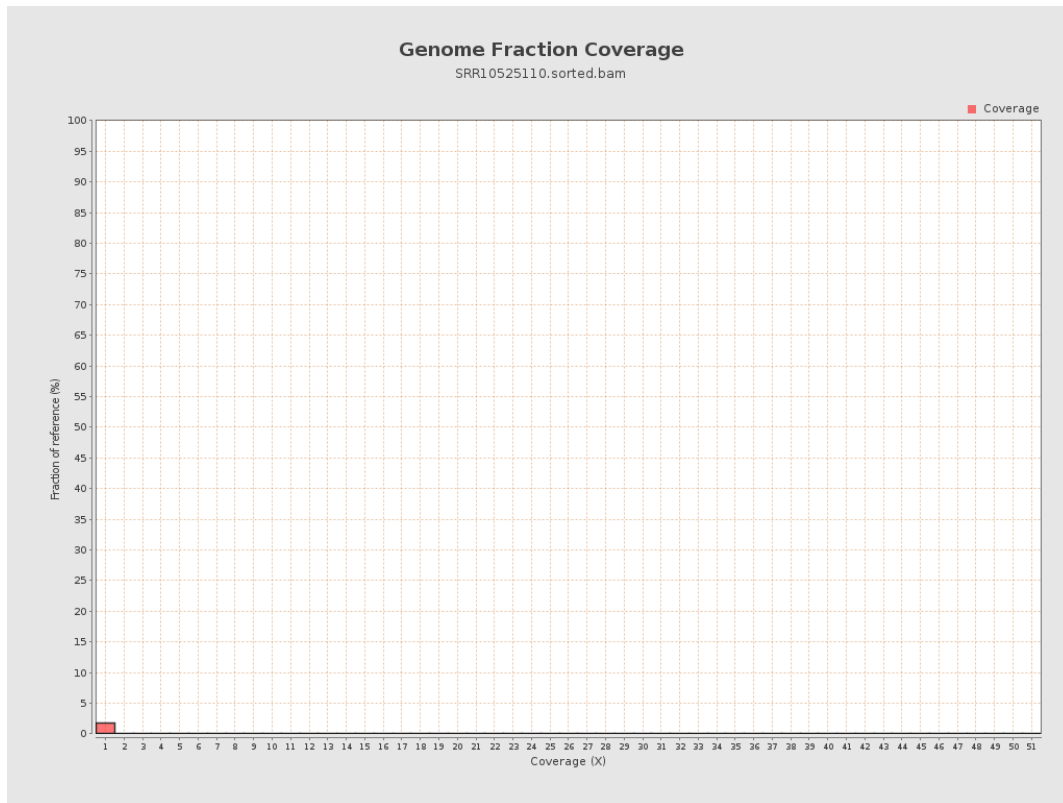
4. Results : Coverage Histogram



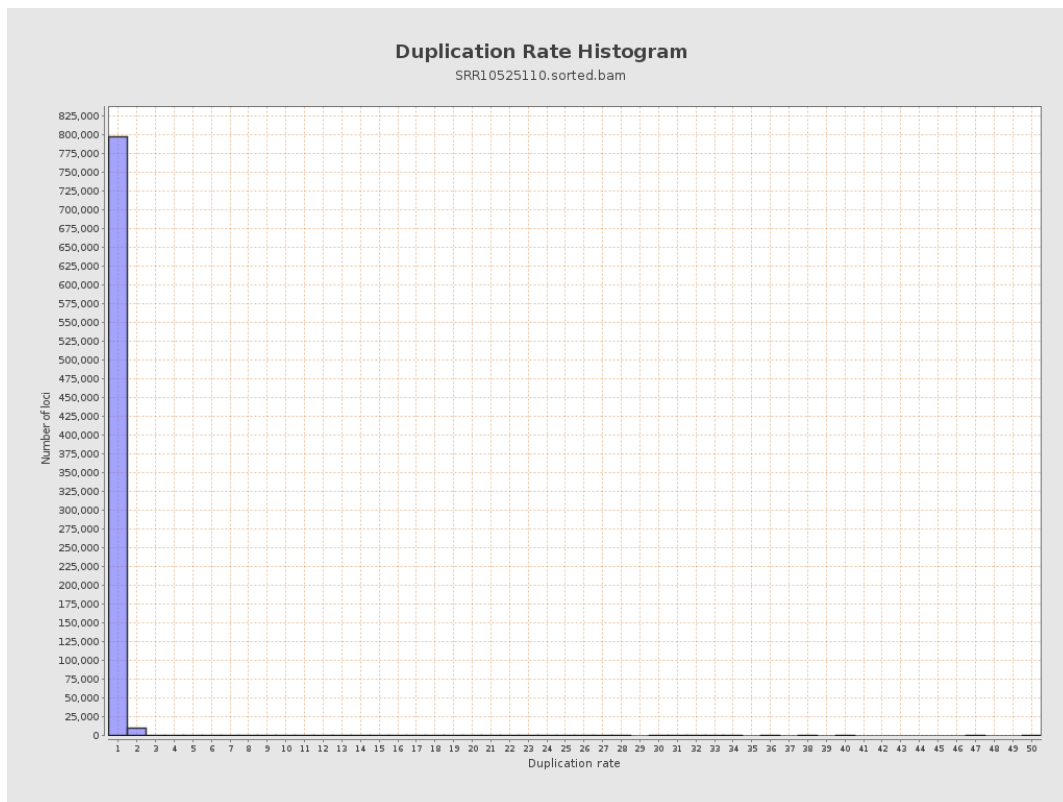
5. Results : Coverage Histogram (0-50X)



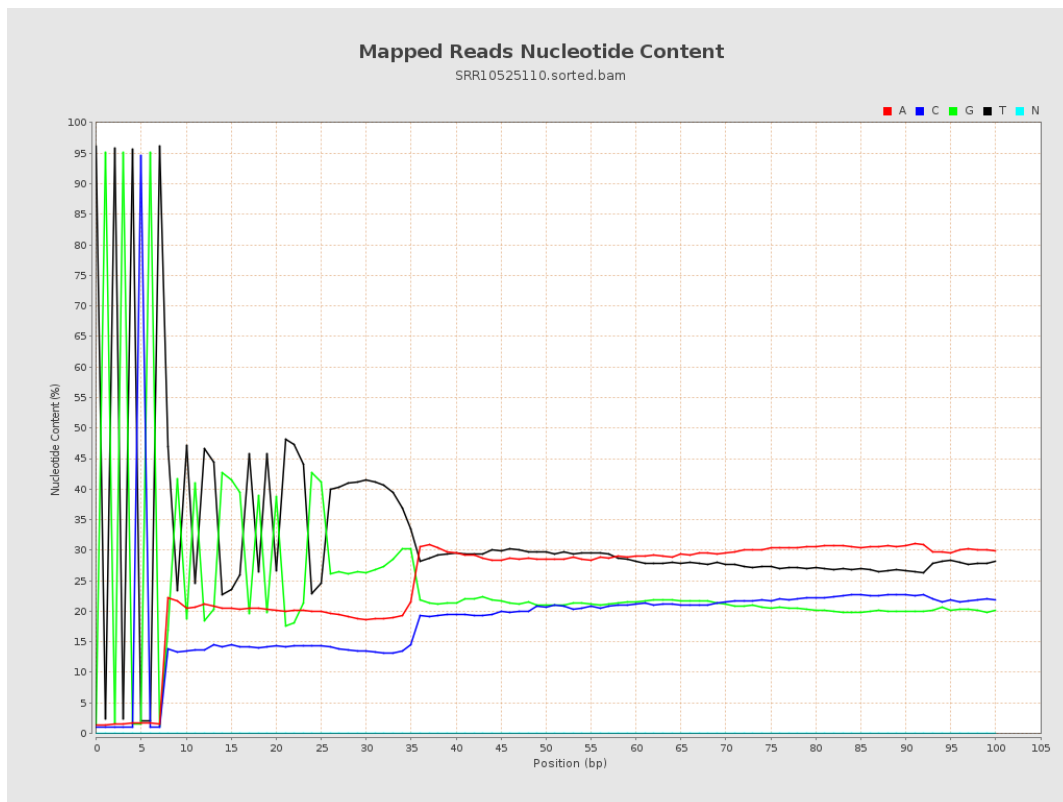
6. Results : Genome Fraction Coverage



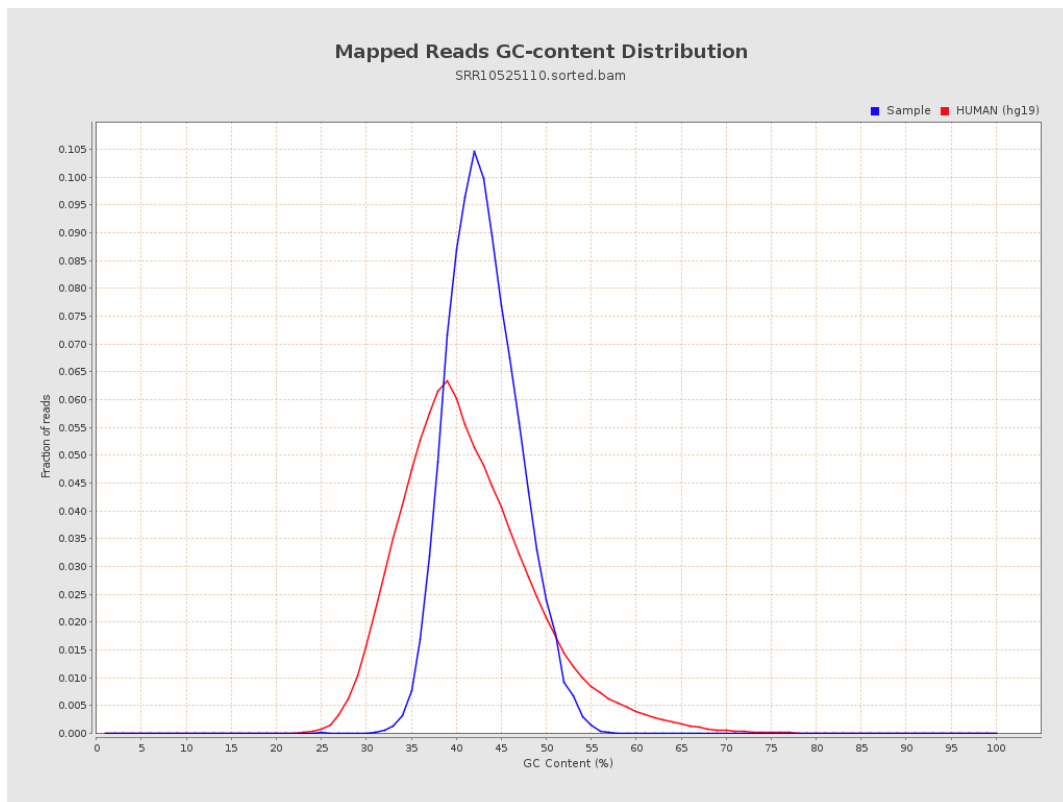
7. Results : Duplication Rate Histogram



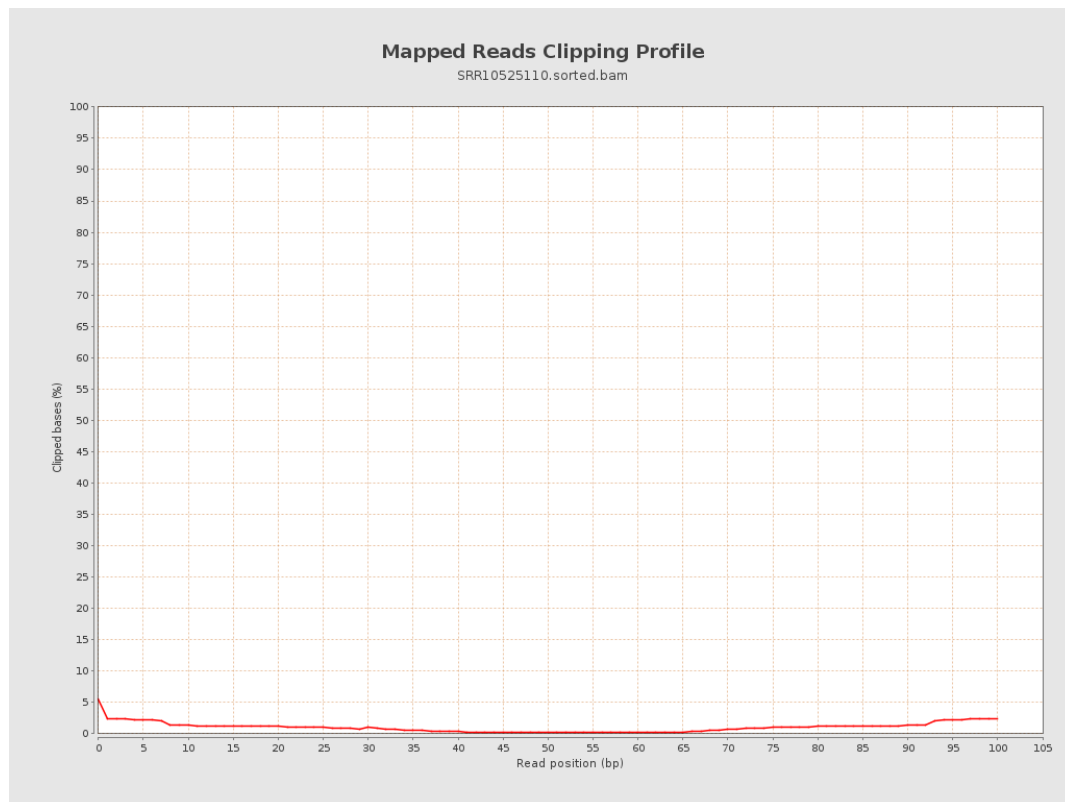
8. Results : Mapped Reads Nucleotide Content



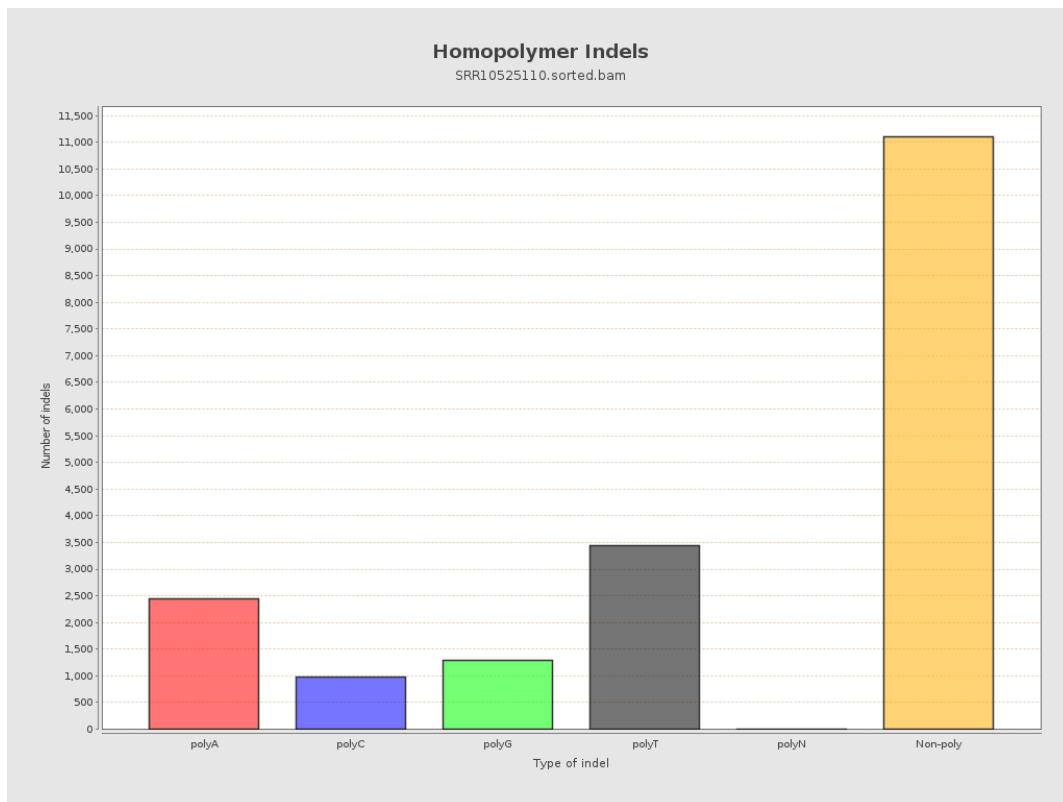
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

