

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 09:49:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524539.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_SRR10524539 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524539.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 09:49:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524539.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	2,546,533
Mapped reads	2,335,634 / 91.72%
Unmapped reads	210,899 / 8.28%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	8,761 / 0.34%
Read min/max/mean length	30 / 76 / 76.12
Duplicated reads (estimated)	145,350 / 5.71%
Duplication rate	4.72%
Clipped reads	2,336,555 / 91.75%

2.2. ACGT Content

Number/percentage of A's	35,765,186 / 26.24%
Number/percentage of C's	27,960,237 / 20.51%
Number/percentage of T's	41,426,490 / 30.39%
Number/percentage of G's	31,162,895 / 22.86%
Number/percentage of N's	2,177 / 0%
GC Percentage	43.37%

2.3. Coverage

Mean	0.044

Standard Deviation	0.3927
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2.4. Mapping Quality

Mean Mapping Quality	45.12
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2.5. Mismatches and indels

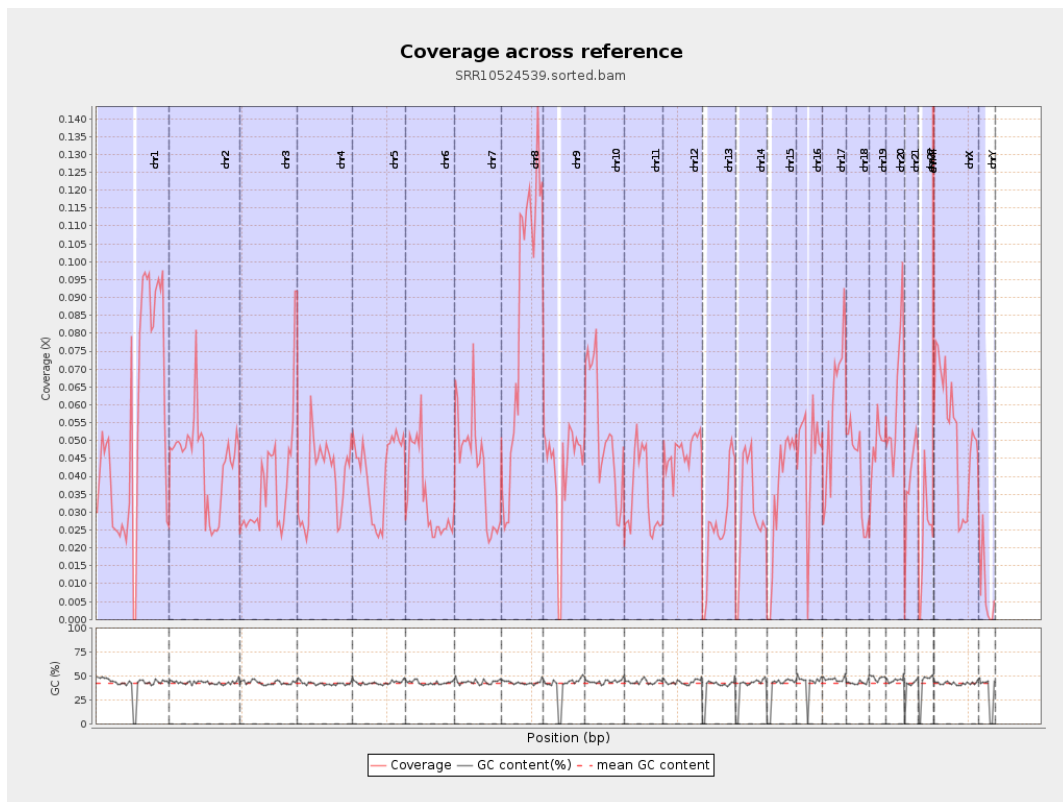
General error rate	0.52%
Mismatches	691,541
Insertions	9,998
Mapped reads with at least one insertion	0.43%
Deletions	25,887
Mapped reads with at least one deletion	1.1%
Homopolymer indels	42.52%

2.6. Chromosome stats

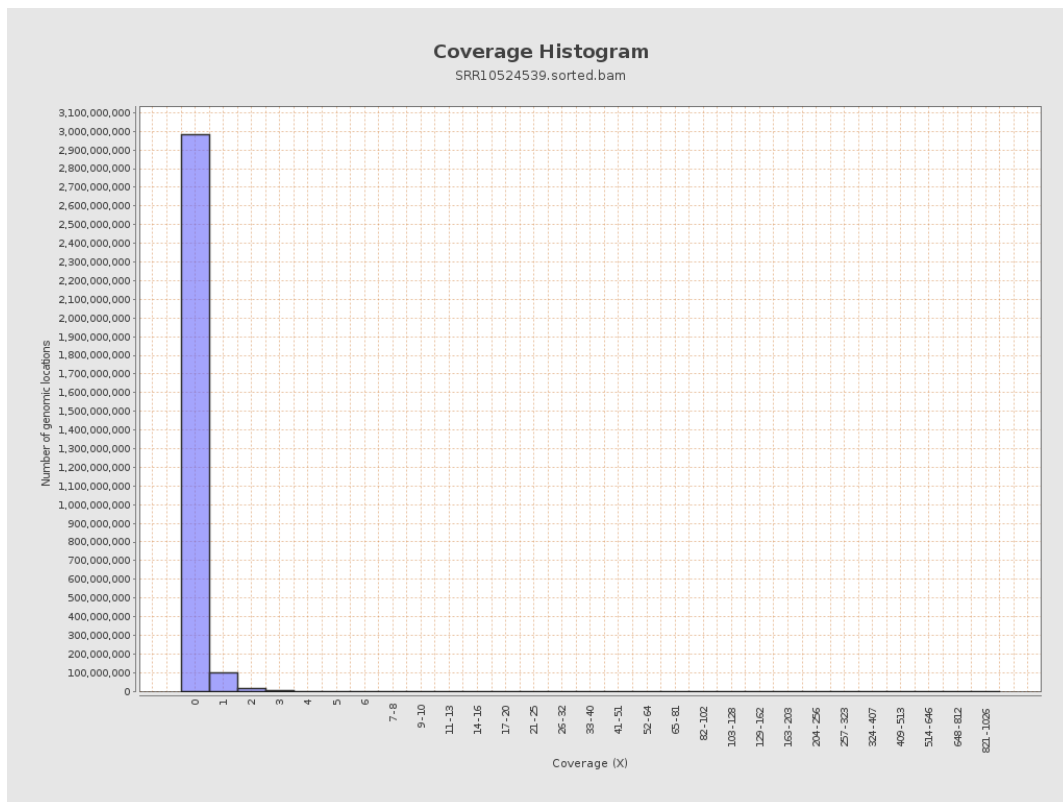
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	13439692	0.0539	0.7556
chr2	243199373	10746504	0.0442	0.4596
chr3	198022430	7388446	0.0373	0.2249
chr4	191154276	7550589	0.0395	0.2791
chr5	180915260	7471389	0.0413	0.2369
chr6	171115067	5837817	0.0341	0.2816
chr7	159138663	6750526	0.0424	0.5021

chr8	146364022	12430492	0.0849	0.4312
chr9	141213431	5844861	0.0414	0.3266
chr10	135534747	7128328	0.0526	0.3848
chr11	135006516	4635758	0.0343	0.3584
chr12	133851895	6295821	0.047	0.2522
chr13	115169878	3024811	0.0263	0.1911
chr14	107349540	3231012	0.0301	0.2052
chr15	102531392	3611694	0.0352	0.2243
chr16	90354753	4216985	0.0467	0.2687
chr17	81195210	4866844	0.0599	0.3079
chr18	78077248	3251933	0.0417	0.612
chr19	59128983	2841747	0.0481	0.4888
chr20	63025520	3944838	0.0626	0.2947
chr21	48129895	1890767	0.0393	0.2633
chr22	51304566	1157137	0.0226	0.173
chrMT	16571	274765	16.5811	10.938
chrX	155270560	8062394	0.0519	0.3046
chrY	59373566	465167	0.0078	0.2419

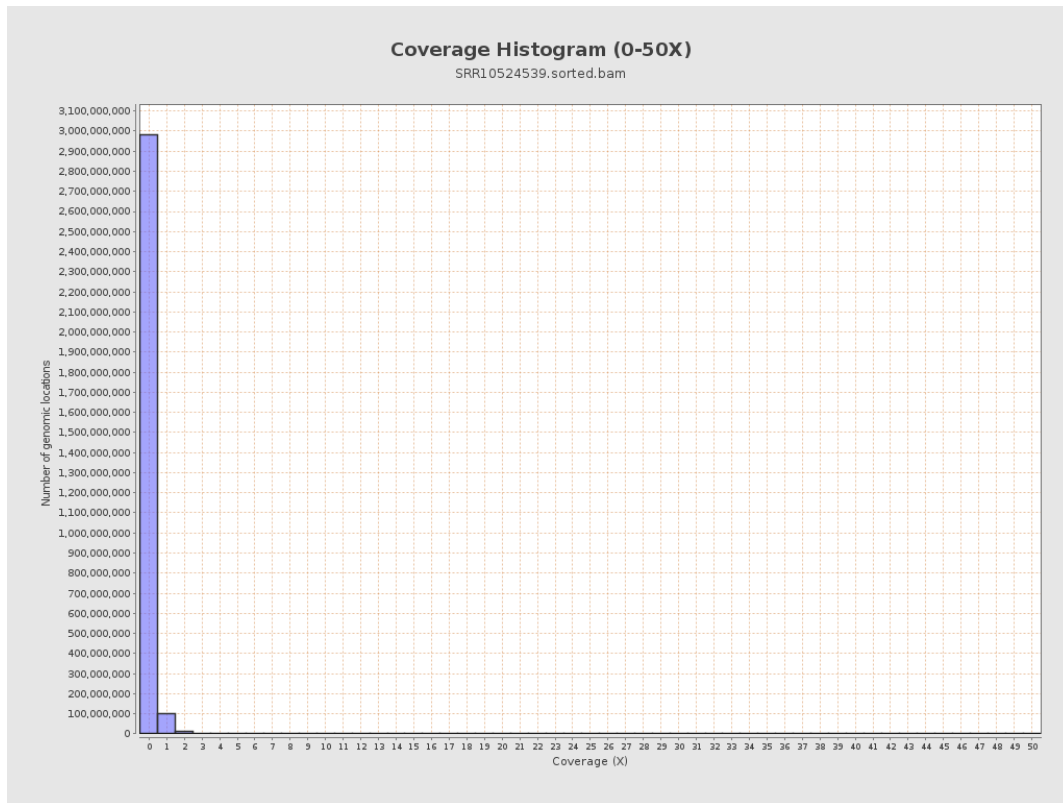
3. Results : Coverage across reference



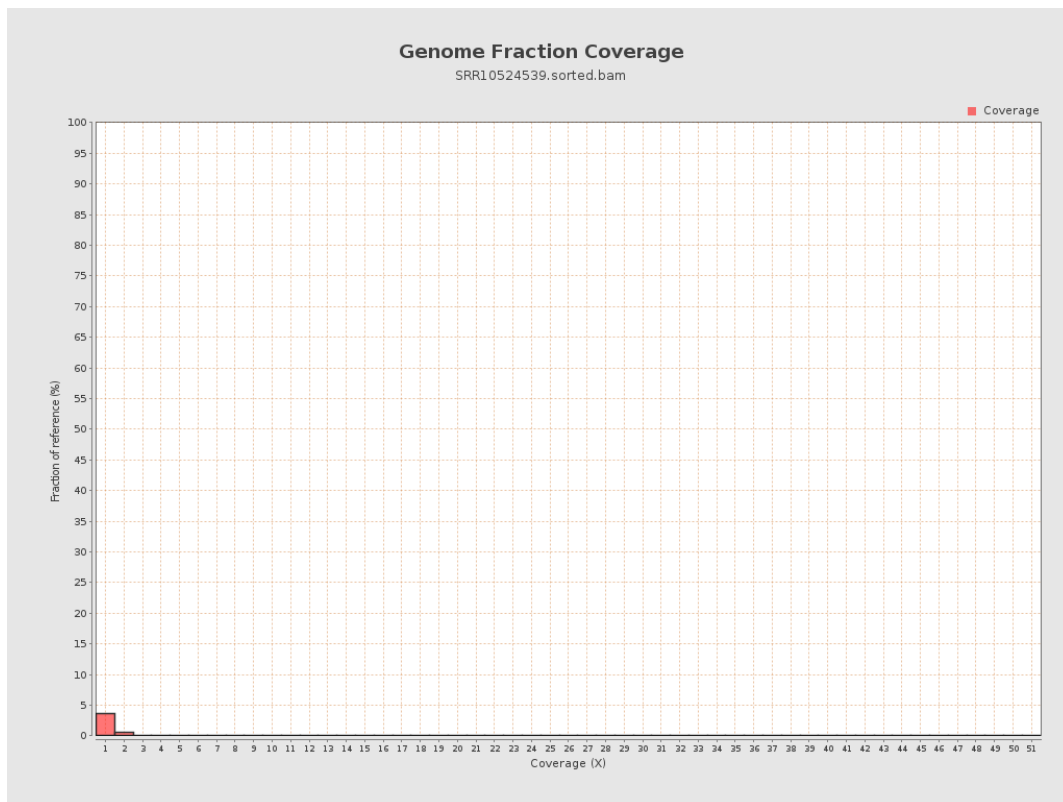
4. Results : Coverage Histogram



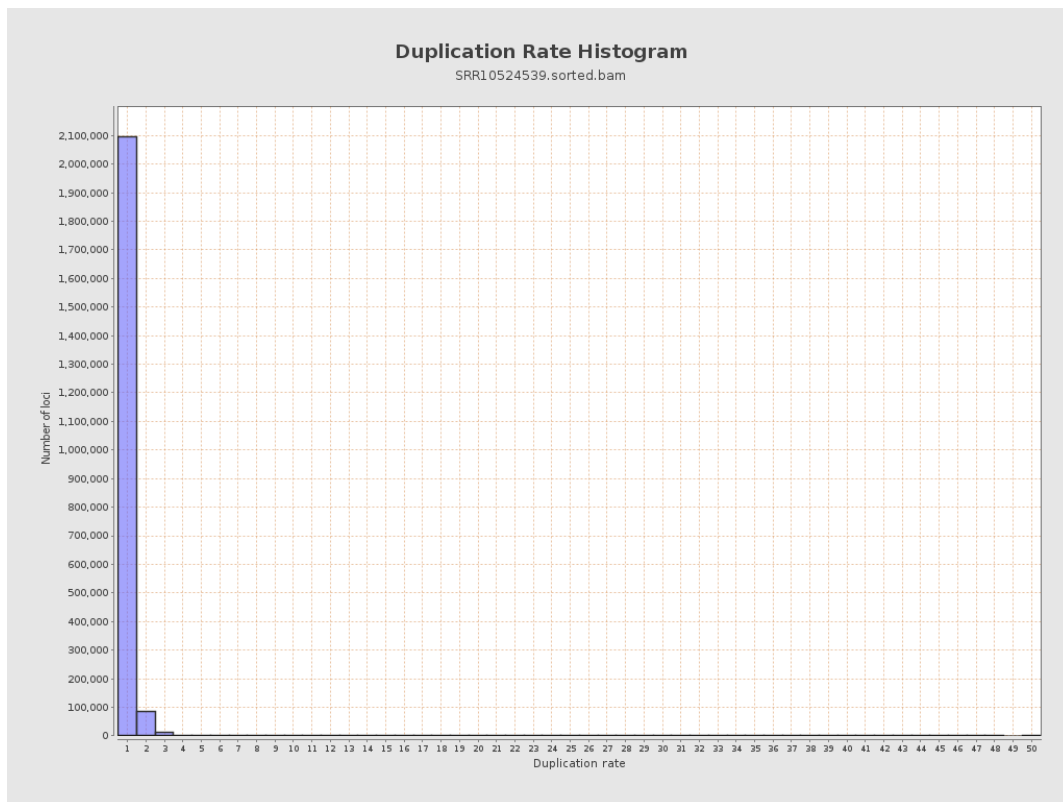
5. Results : Coverage Histogram (0-50X)



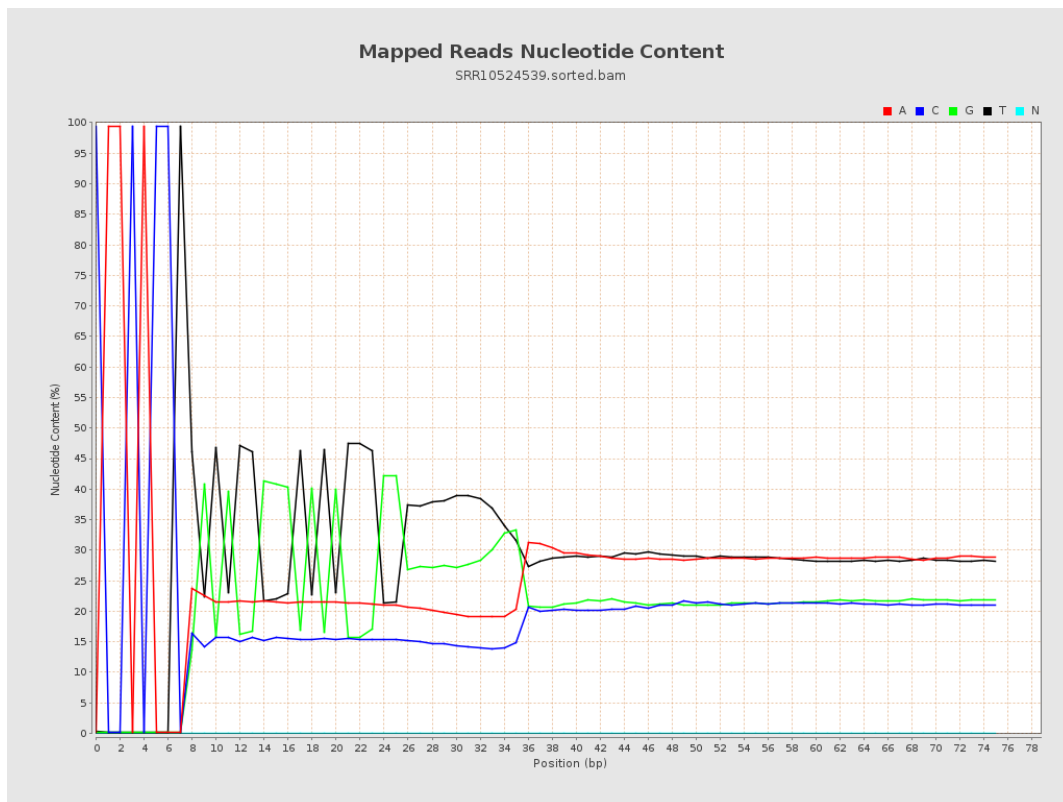
6. Results : Genome Fraction Coverage



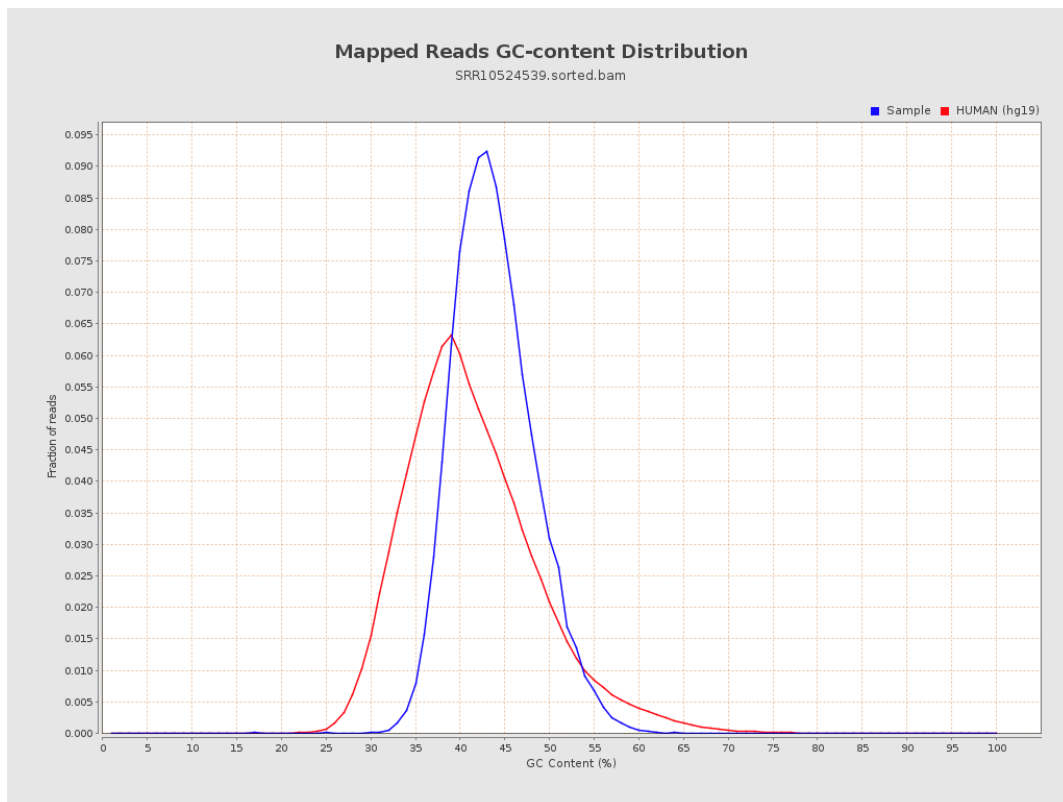
7. Results : Duplication Rate Histogram



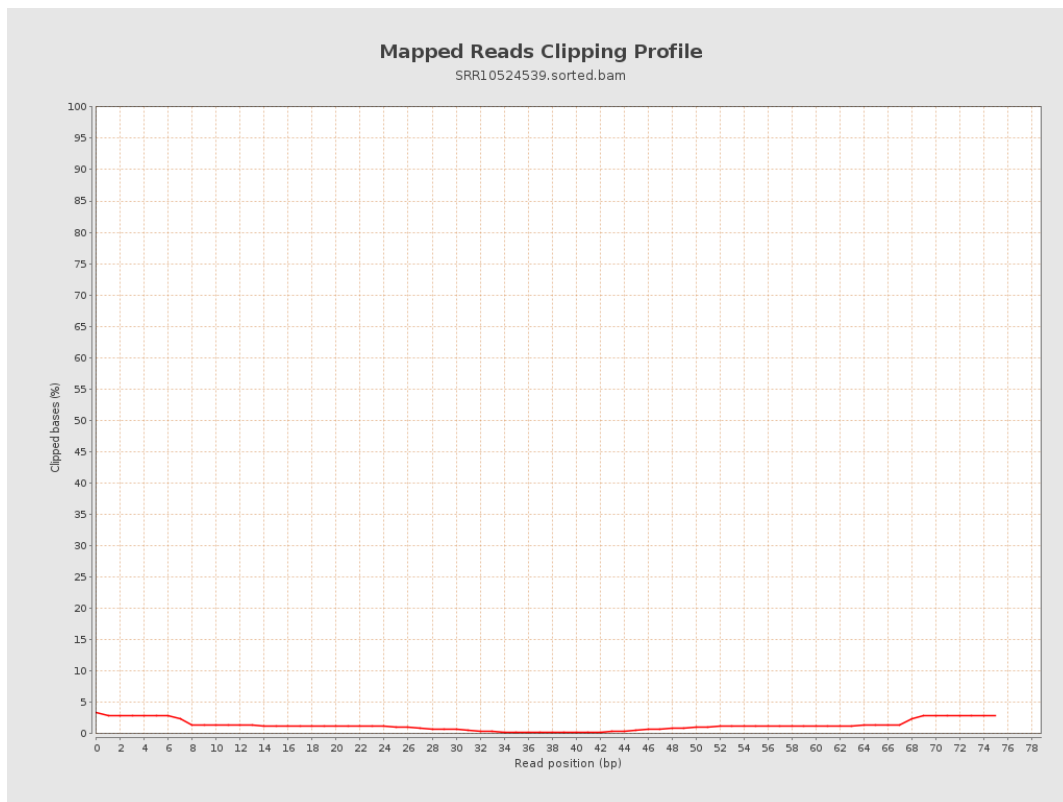
8. Results : Mapped Reads Nucleotide Content



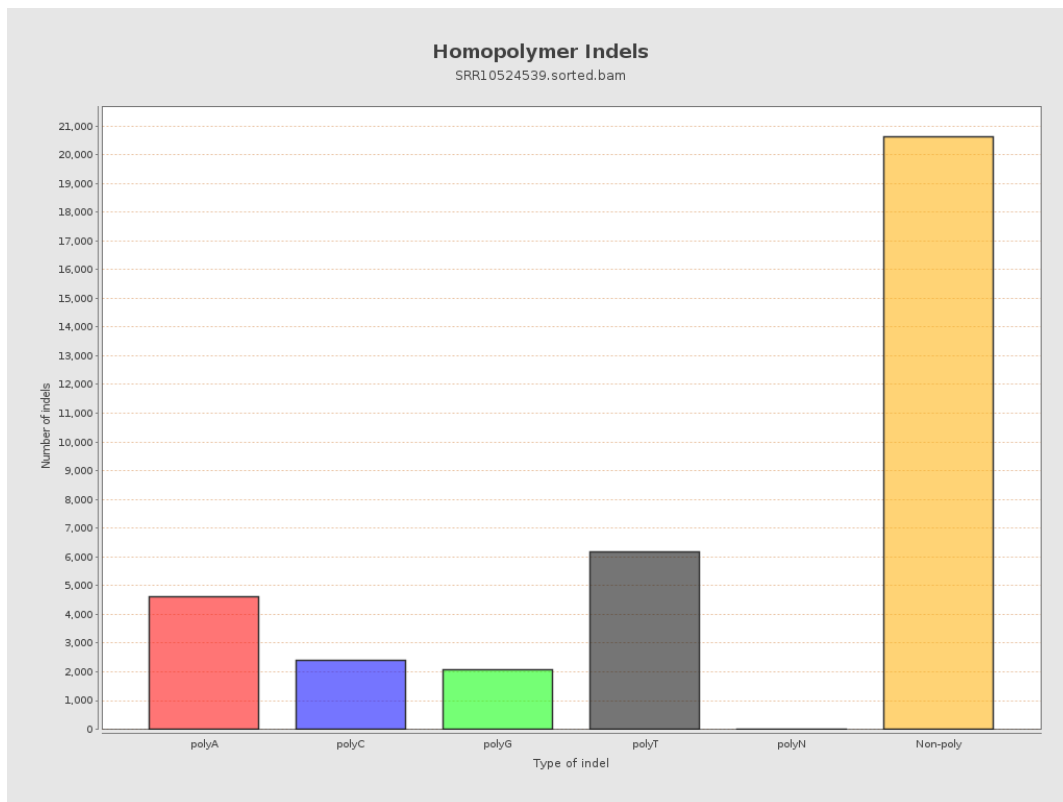
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

