

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 12:44:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524611.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_SRR10524611 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524611.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 12:44:39 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524611.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,139,271
Mapped reads	1,048,317 / 92.02%
Unmapped reads	90,954 / 7.98%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	5,185 / 0.46%
Read min/max/mean length	30 / 76 / 76.15
Duplicated reads (estimated)	23,886 / 2.1%
Duplication rate	1.61%
Clipped reads	1,049,591 / 92.13%

2.2. ACGT Content

Number/percentage of A's	16,137,357 / 26.37%
Number/percentage of C's	12,147,463 / 19.85%
Number/percentage of T's	18,879,918 / 30.85%
Number/percentage of G's	14,032,053 / 22.93%
Number/percentage of N's	1,887 / 0%
GC Percentage	42.78%

2.3. Coverage

Mean	0.0198

Standard Deviation	0.1969
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2.4. Mapping Quality

Mean Mapping Quality	45.74
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2.5. Mismatches and indels

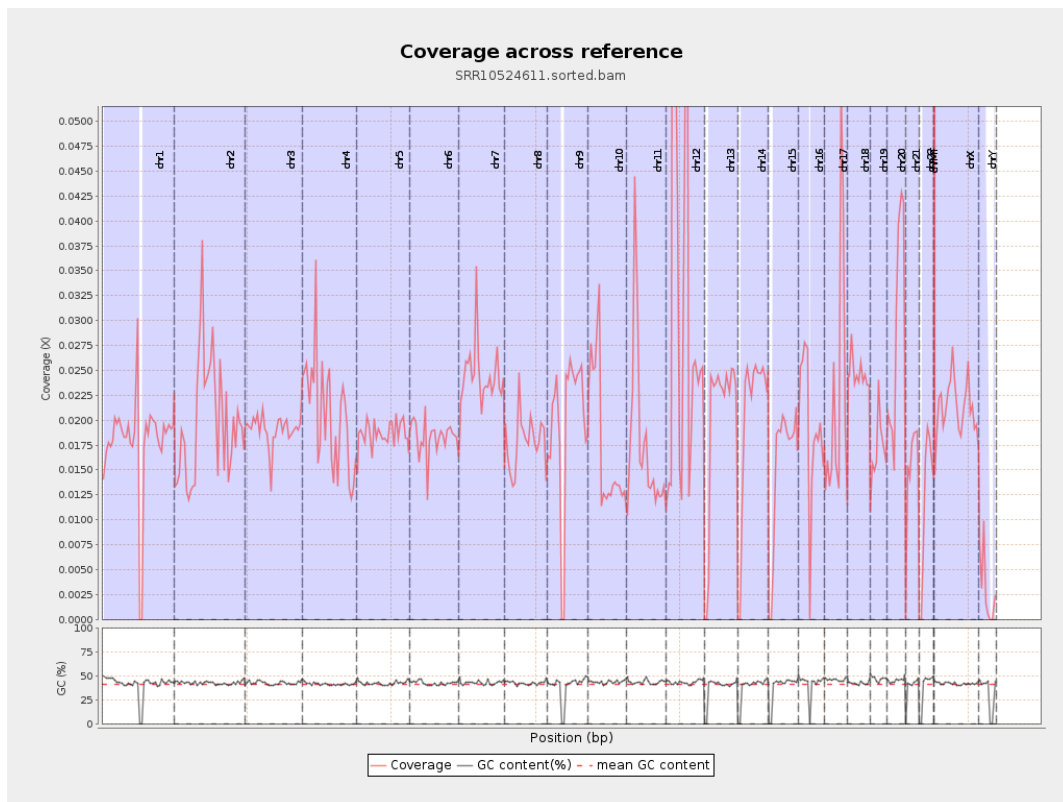
General error rate	0.49%
Mismatches	289,637
Insertions	4,762
Mapped reads with at least one insertion	0.45%
Deletions	10,103
Mapped reads with at least one deletion	0.96%
Homopolymer indels	41.16%

2.6. Chromosome stats

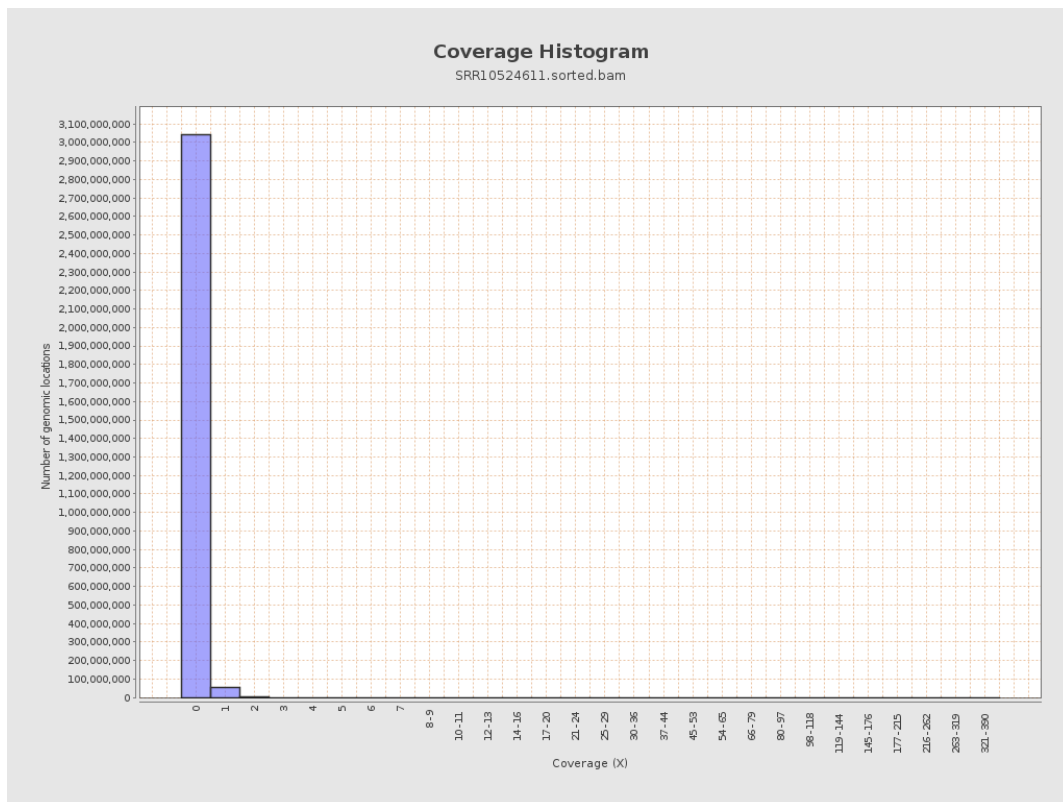
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	4432271	0.0178	0.3181
chr2	243199373	4798796	0.0197	0.2038
chr3	198022430	3772881	0.0191	0.1451
chr4	191154276	3897921	0.0204	0.1633
chr5	180915260	3398195	0.0188	0.1452
chr6	171115067	3126675	0.0183	0.1494
chr7	159138663	3887378	0.0244	0.2494

chr8	146364022	2618168	0.0179	0.1857
chr9	141213431	2787047	0.0197	0.1924
chr10	135534747	2400425	0.0177	0.2001
chr11	135006516	2360571	0.0175	0.1697
chr12	133851895	4535774	0.0339	0.2091
chr13	115169878	2281542	0.0198	0.1482
chr14	107349540	2178255	0.0203	0.1606
chr15	102531392	1580607	0.0154	0.1304
chr16	90354753	1721969	0.0191	0.1529
chr17	81195210	1807210	0.0223	0.1619
chr18	78077248	1928509	0.0247	0.3419
chr19	59128983	1024742	0.0173	0.2427
chr20	63025520	1822848	0.0289	0.1828
chr21	48129895	732713	0.0152	0.1397
chr22	51304566	616799	0.012	0.1154
chrMT	16571	7432	0.4485	0.7254
chrX	155270560	3320247	0.0214	0.1677
chrY	59373566	176588	0.003	0.0847

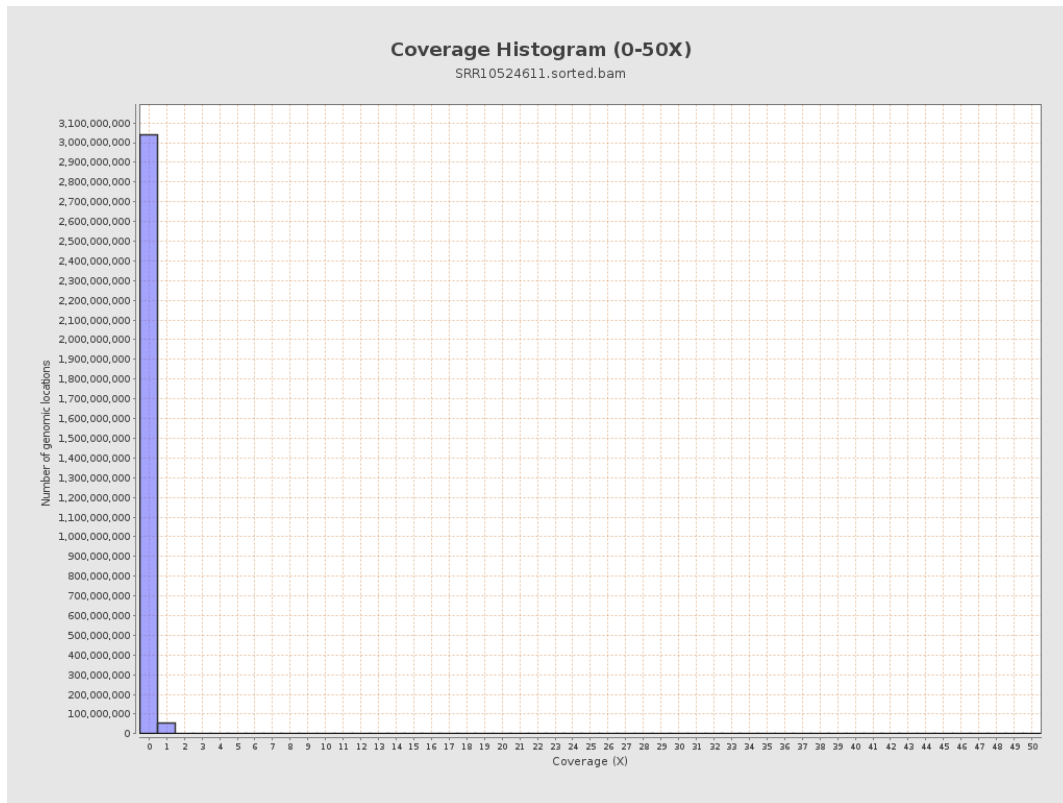
3. Results : Coverage across reference



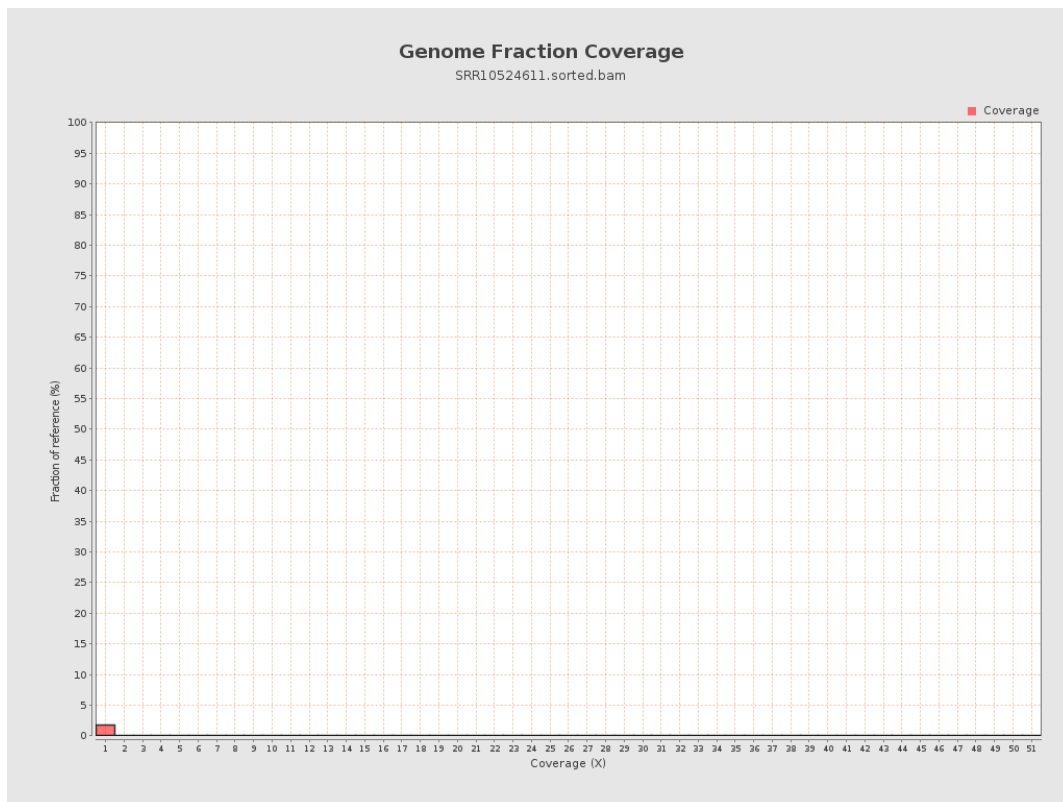
4. Results : Coverage Histogram



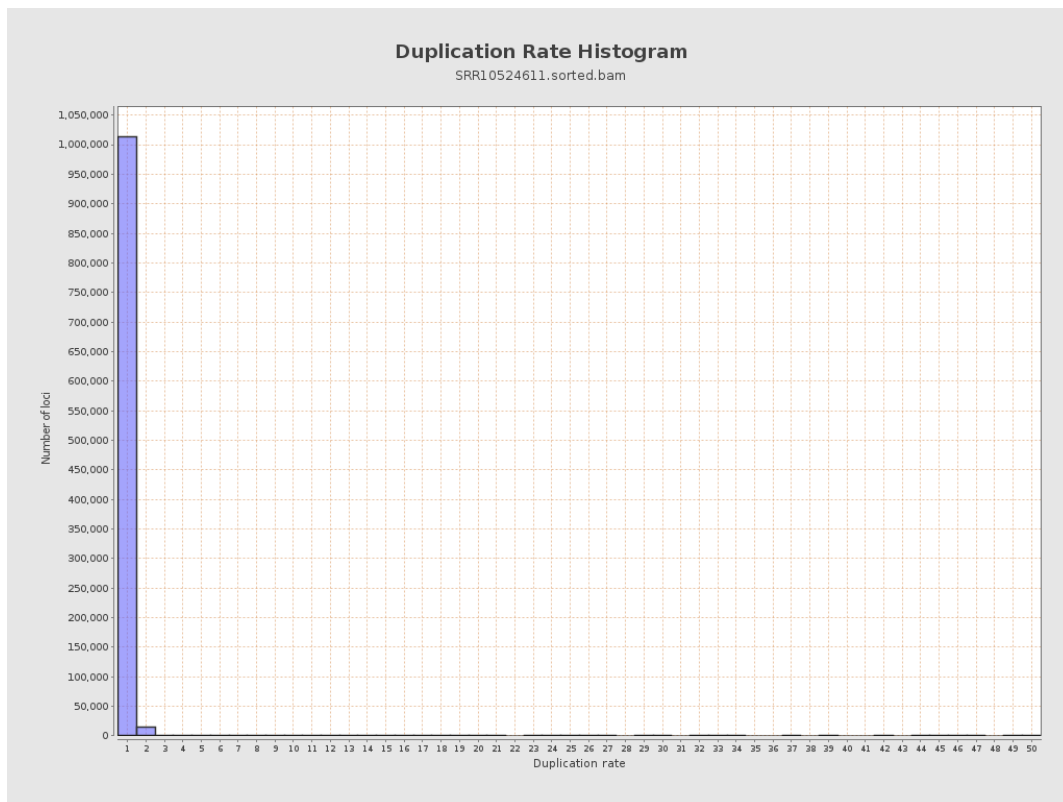
5. Results : Coverage Histogram (0-50X)



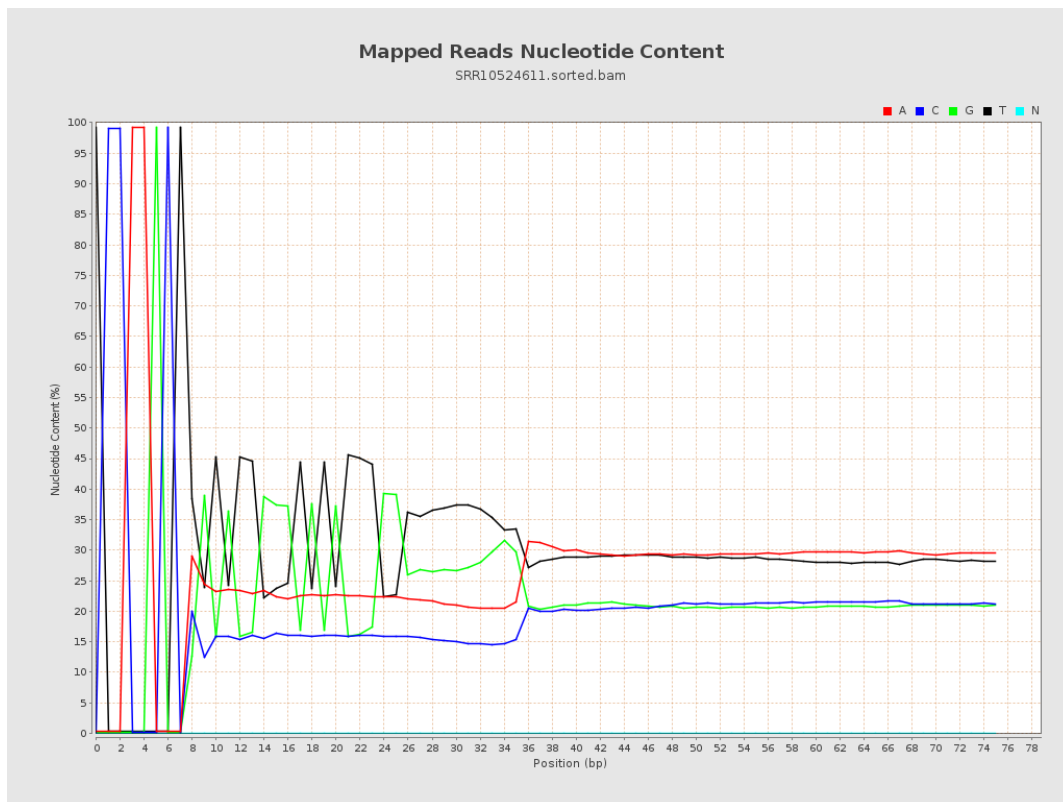
6. Results : Genome Fraction Coverage



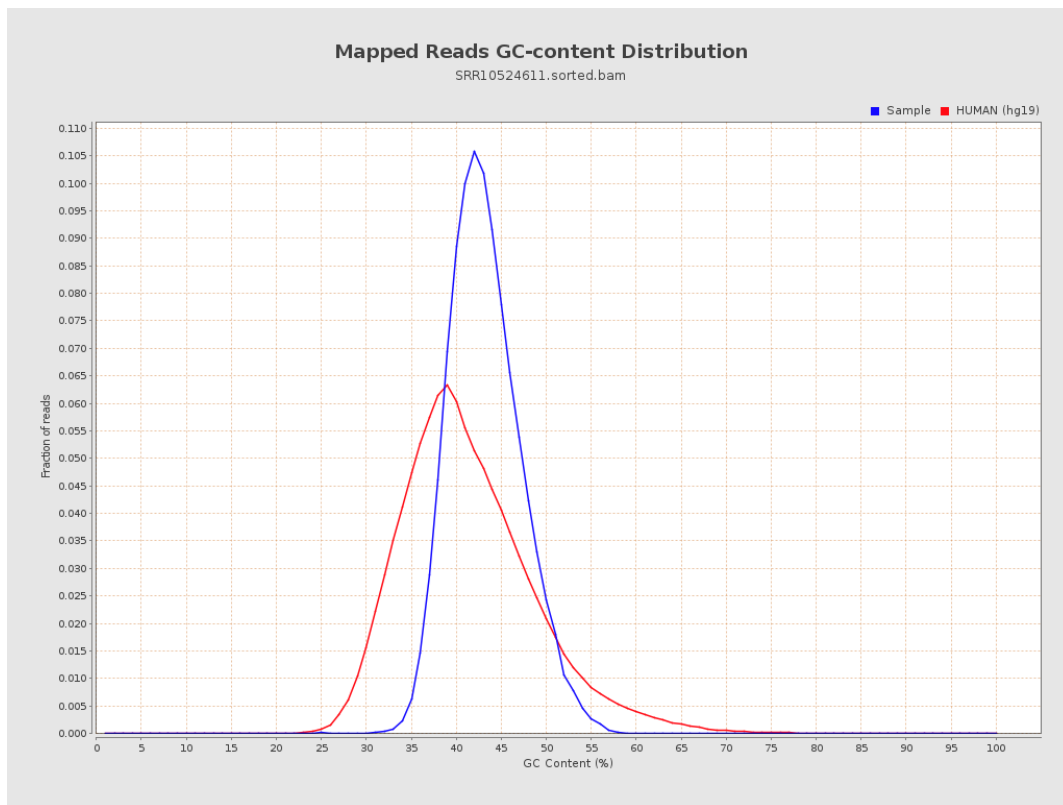
7. Results : Duplication Rate Histogram



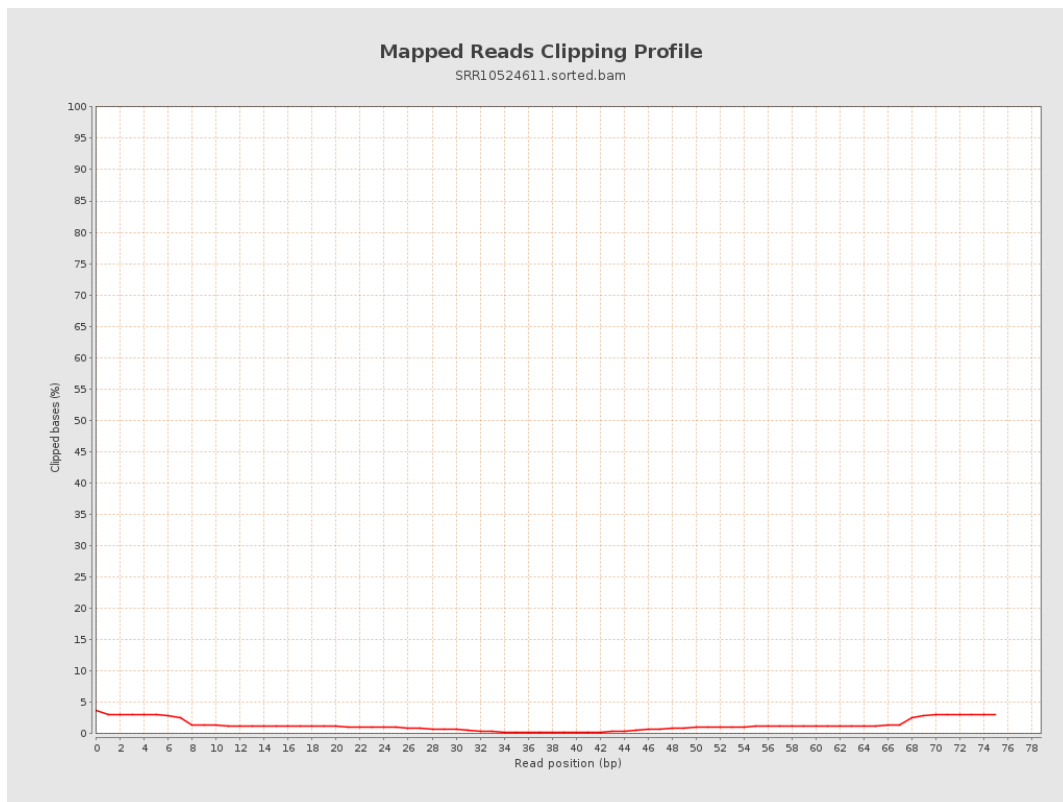
8. Results : Mapped Reads Nucleotide Content



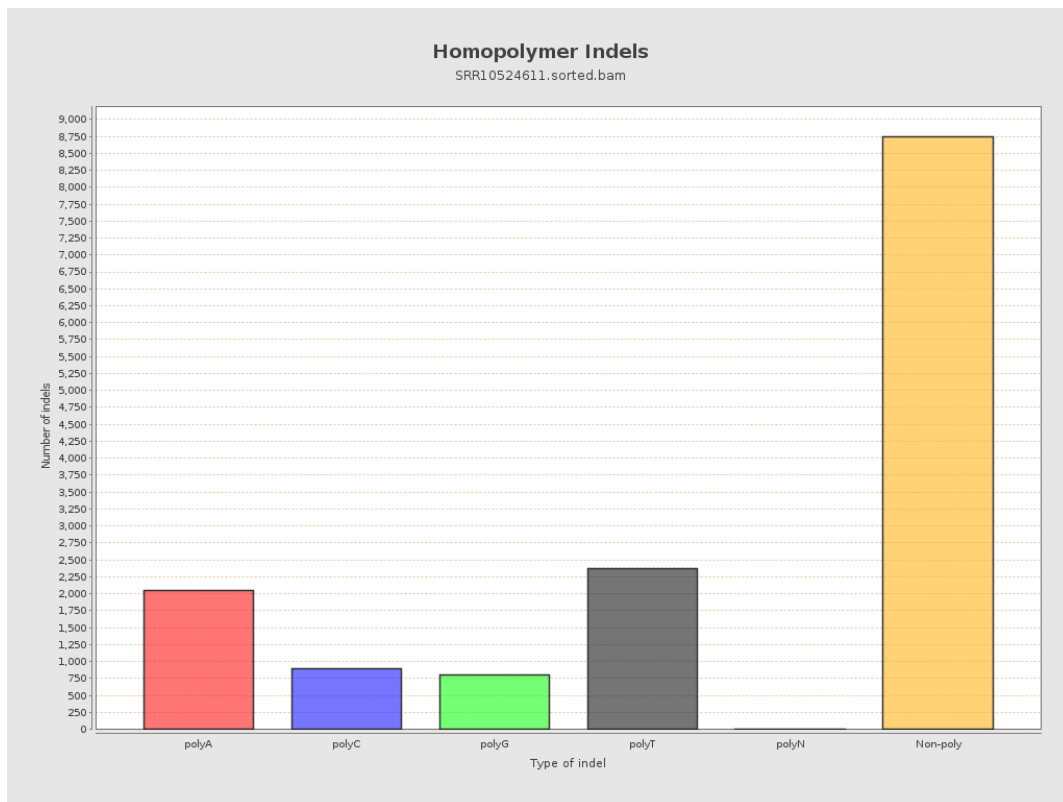
9. Results : Mapped Reads GC-content Distribution



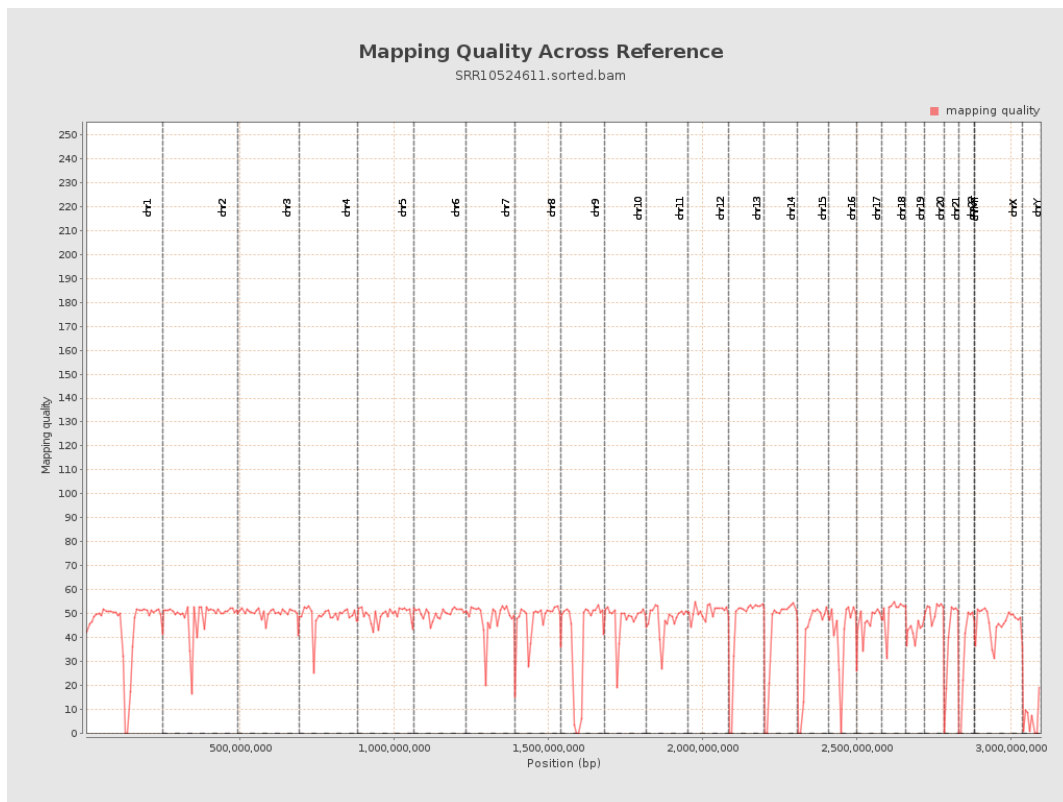
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

