

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/28 16:42:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10524691.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_SRR10524691 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10524691.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Aug 28 16:42:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10524691.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,698,597
Mapped reads	1,573,557 / 92.64%
Unmapped reads	125,040 / 7.36%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	7,004 / 0.41%
Read min/max/mean length	30 / 76 / 76.14
Duplicated reads (estimated)	65,606 / 3.86%
Duplication rate	3.1%
Clipped reads	1,578,685 / 92.94%

2.2. ACGT Content

Number/percentage of A's	22,584,760 / 24.3%
Number/percentage of C's	16,696,262 / 17.96%
Number/percentage of T's	30,423,041 / 32.73%
Number/percentage of G's	23,229,370 / 24.99%
Number/percentage of N's	12,898 / 0.01%
GC Percentage	42.96%

2.3. Coverage

Mean	0.03

Standard Deviation	0.2824
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2.4. Mapping Quality

Mean Mapping Quality	45.79
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2.5. Mismatches and indels

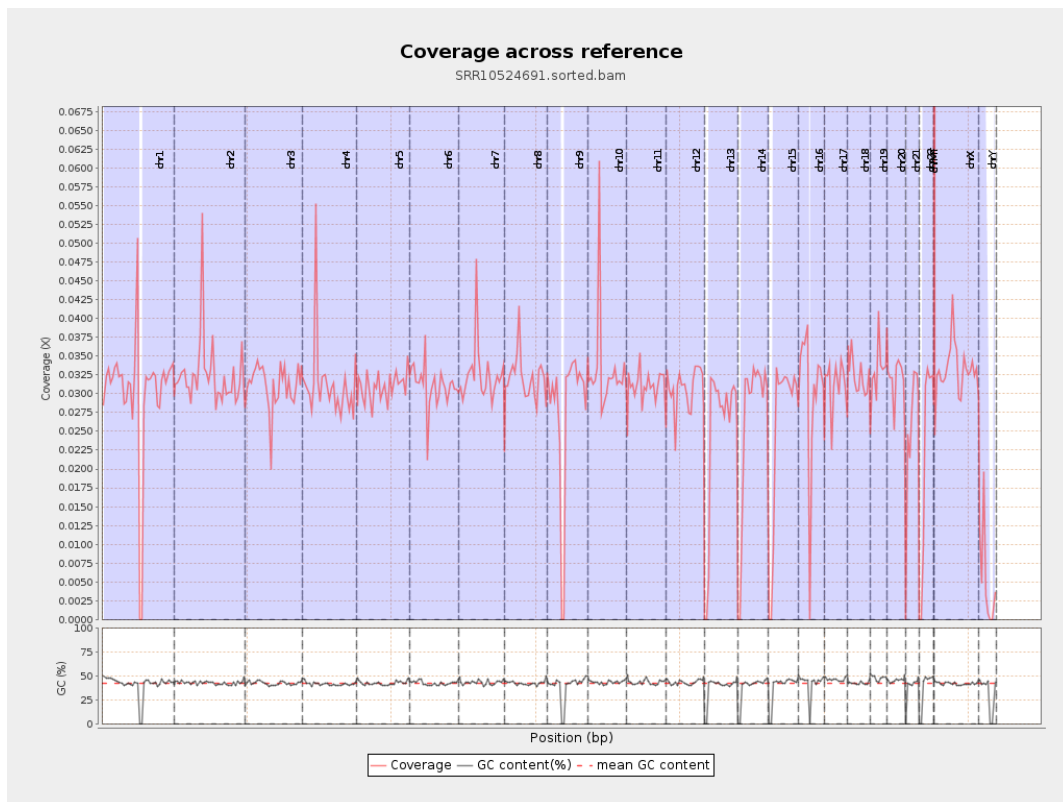
General error rate	0.51%
Mismatches	463,945
Insertions	5,644
Mapped reads with at least one insertion	0.36%
Deletions	17,543
Mapped reads with at least one deletion	1.11%
Homopolymer indels	45.39%

2.6. Chromosome stats

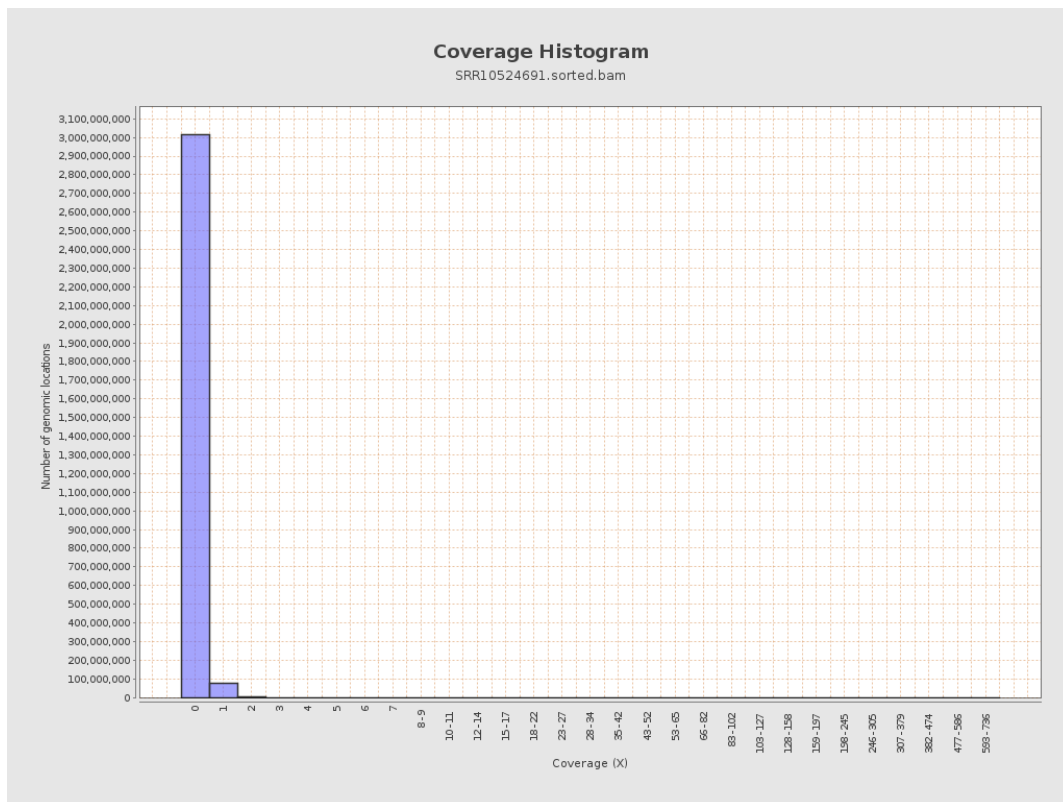
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	7510670	0.0301	0.4841
chr2	243199373	7897407	0.0325	0.3879
chr3	198022430	6161726	0.0311	0.1935
chr4	191154276	5974816	0.0313	0.2241
chr5	180915260	5616582	0.031	0.1932
chr6	171115067	5314980	0.0311	0.2155
chr7	159138663	5182285	0.0326	0.3281

chr8	146364022	4704335	0.0321	0.3011
chr9	141213431	3925932	0.0278	0.2387
chr10	135534747	4493938	0.0332	0.3041
chr11	135006516	4212798	0.0312	0.2505
chr12	133851895	4109616	0.0307	0.193
chr13	115169878	2852437	0.0248	0.1727
chr14	107349540	2812965	0.0262	0.1813
chr15	102531392	2614883	0.0255	0.1758
chr16	90354753	2705136	0.0299	0.2014
chr17	81195210	2537910	0.0313	0.2034
chr18	78077248	2519736	0.0323	0.4355
chr19	59128983	1973595	0.0334	0.376
chr20	63025520	1994302	0.0316	0.1996
chr21	48129895	1229134	0.0255	0.2012
chr22	51304566	1131859	0.0221	0.1624
chrMT	16571	14392	0.8685	1.1751
chrX	155270560	5170749	0.0333	0.2175
chrY	59373566	312146	0.0053	0.1893

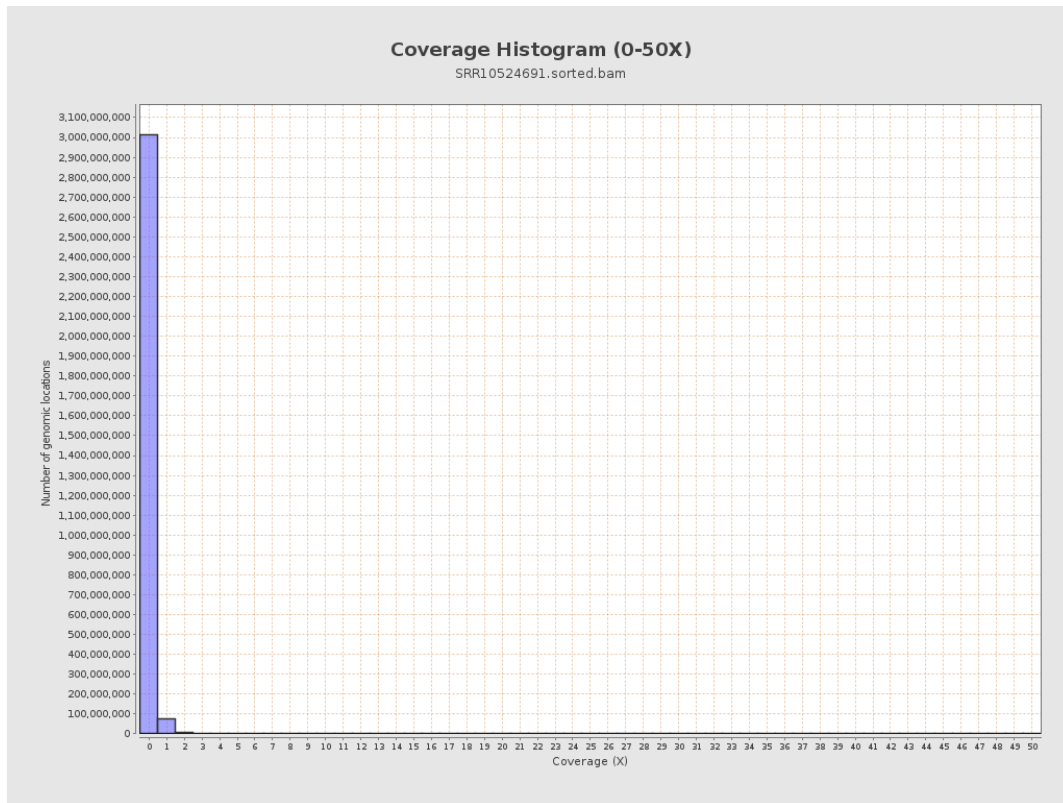
3. Results : Coverage across reference



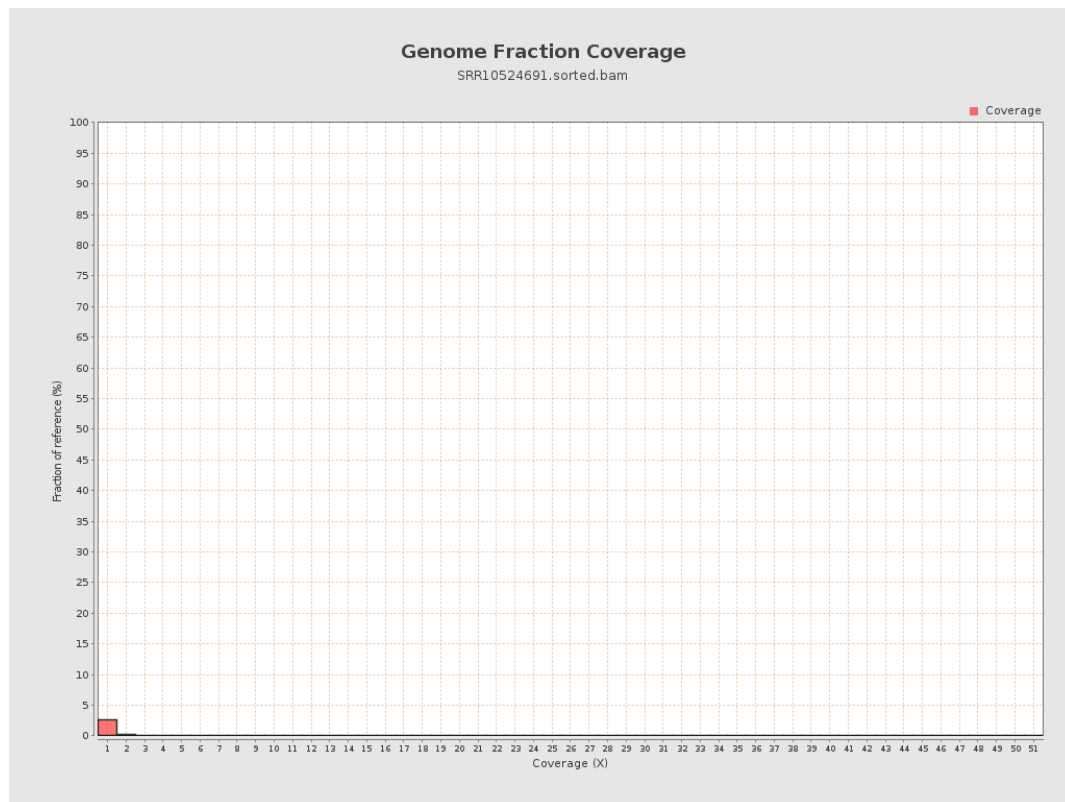
4. Results : Coverage Histogram



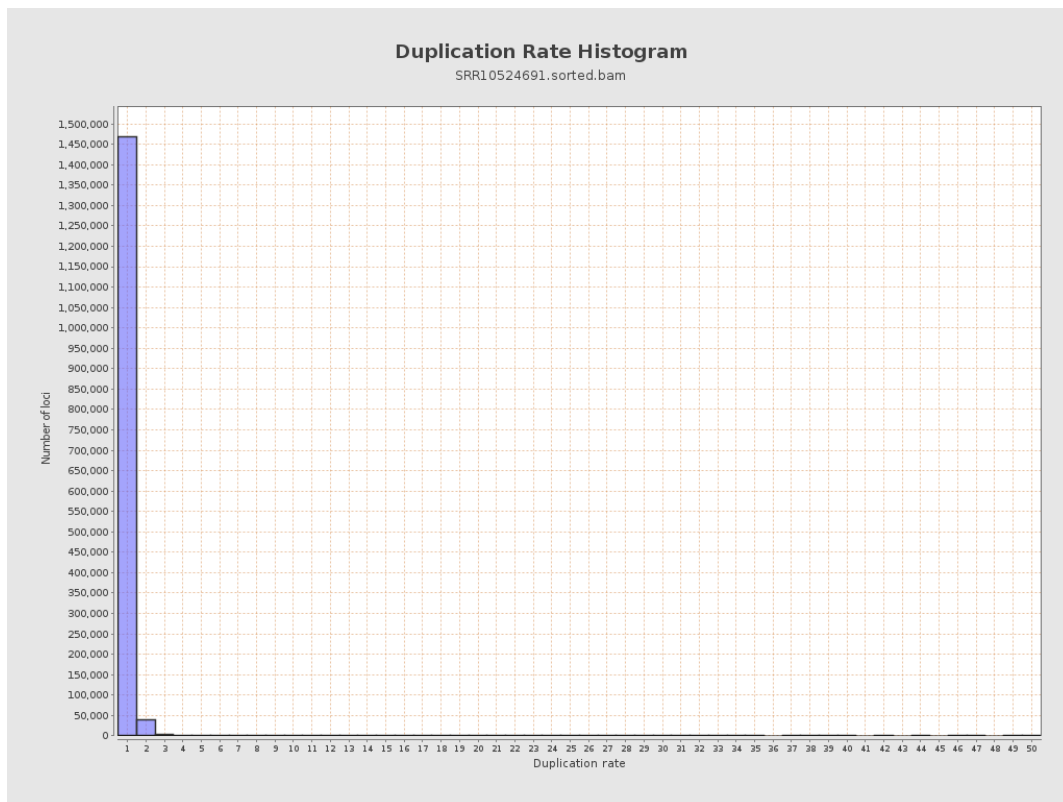
5. Results : Coverage Histogram (0-50X)



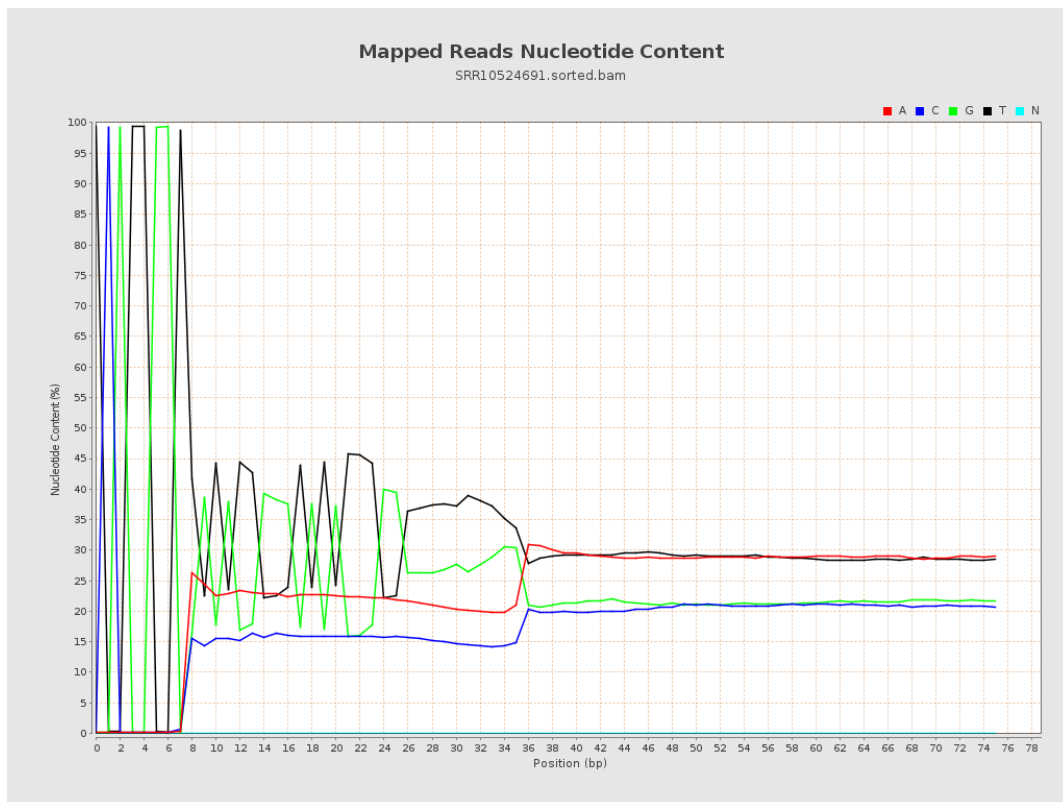
6. Results : Genome Fraction Coverage



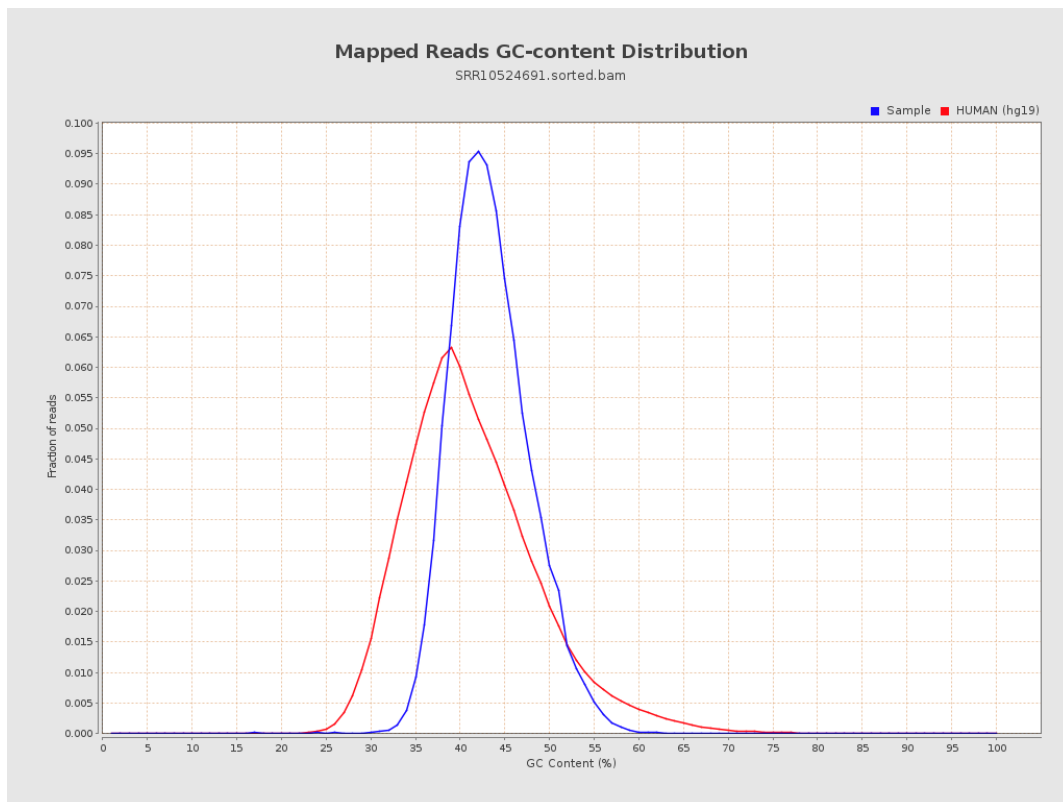
7. Results : Duplication Rate Histogram



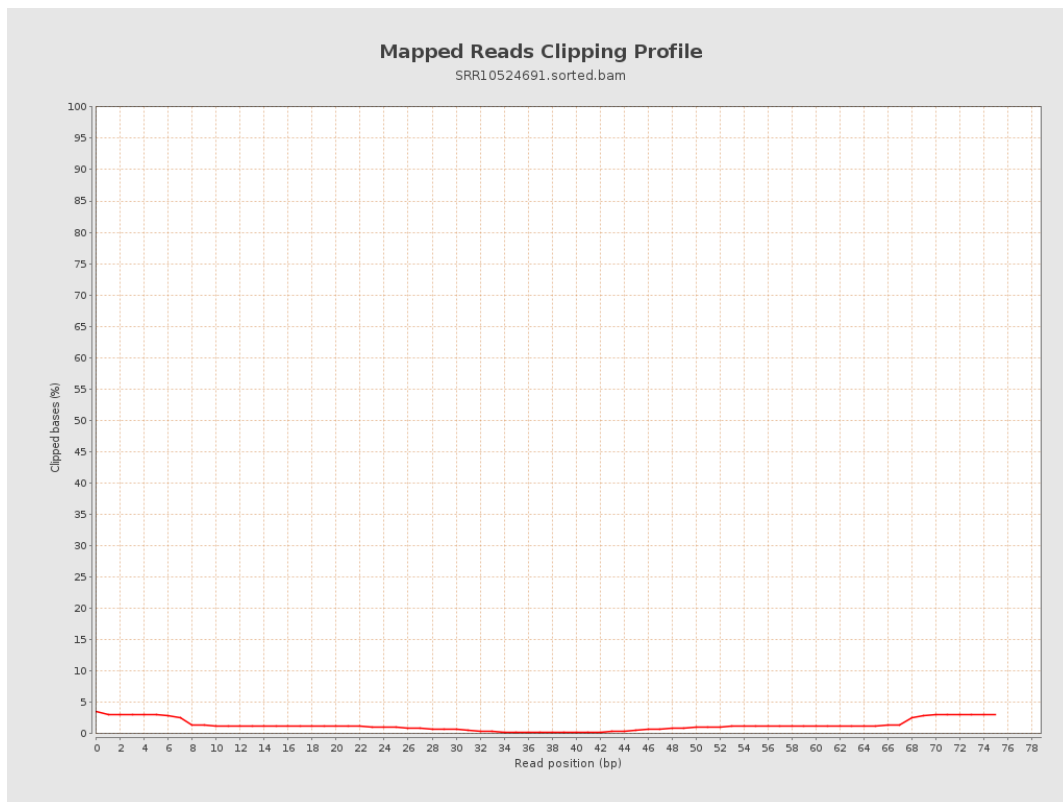
8. Results : Mapped Reads Nucleotide Content



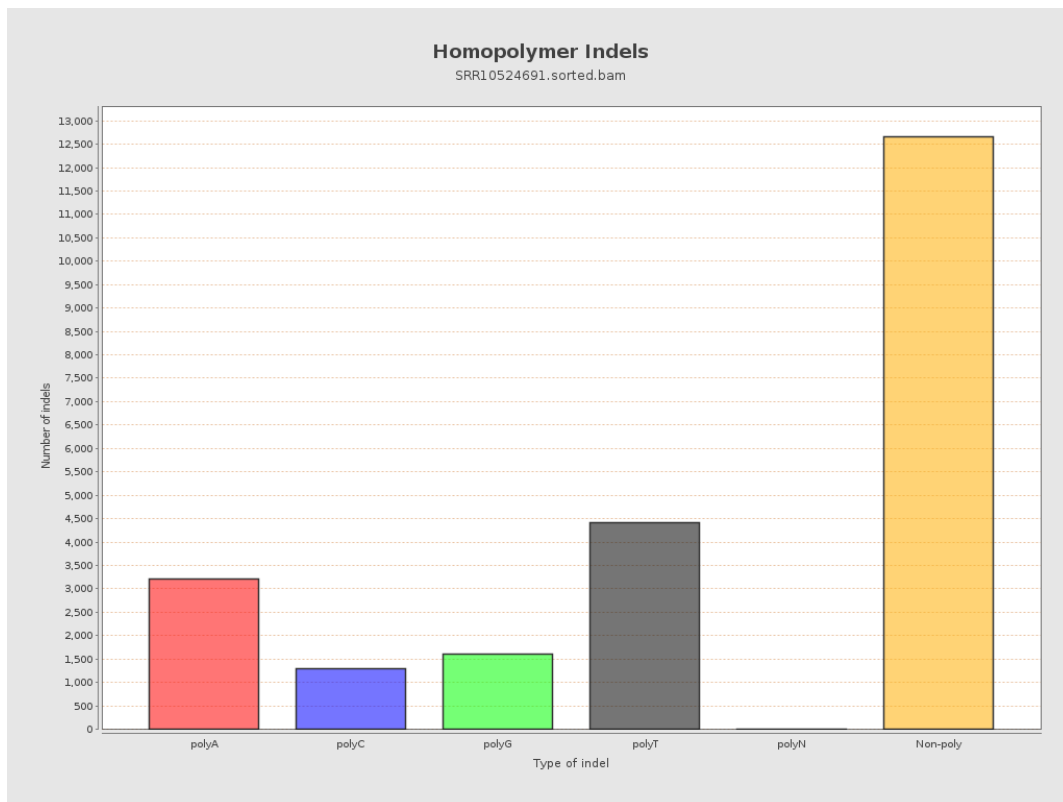
9. Results : Mapped Reads GC-content Distribution



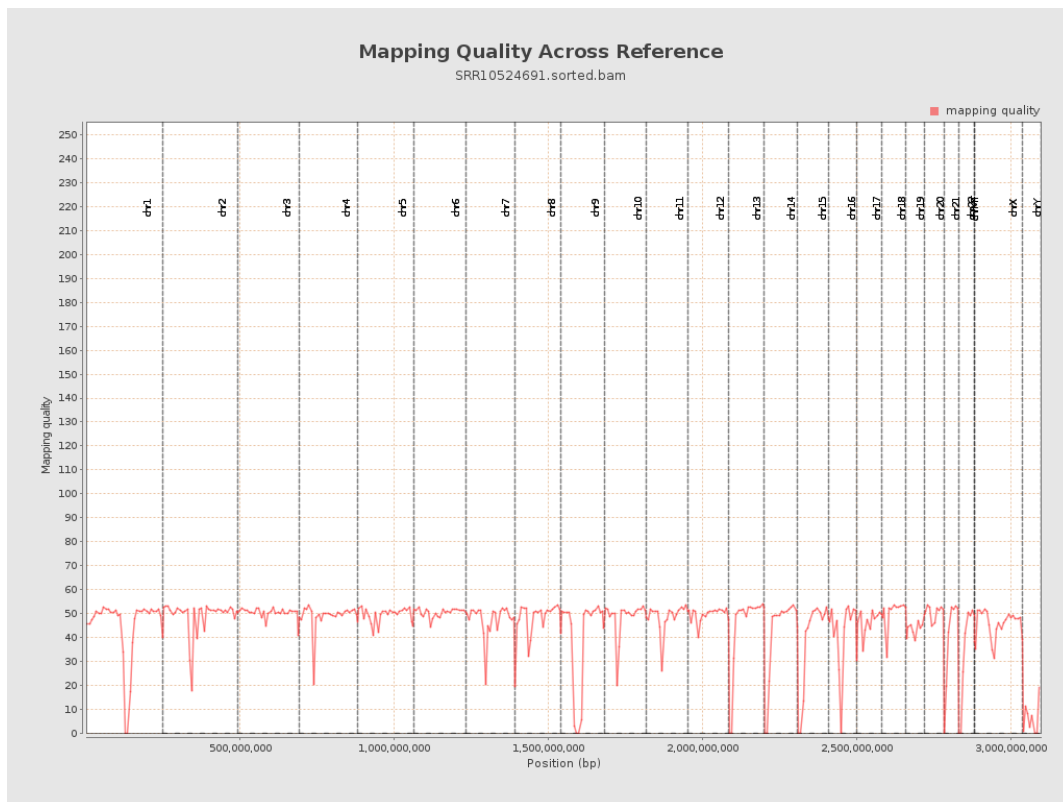
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

