

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/17 14:55:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6238291.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_SRR6238291 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6238291.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Sep 17 14:55:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6238291.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,250,361
Mapped reads	2,910,701 / 89.55%
Unmapped reads	339,660 / 10.45%
Mapped paired reads	0 / 0%
Secondary alignments	0
Supplementary alignments	26,315 / 0.81%
Read min/max/mean length	30 / 76 / 76.28
Duplicated reads (estimated)	138,532 / 4.26%
Duplication rate	3.52%
Clipped reads	1,468,239 / 45.17%

2.2. ACGT Content

Number/percentage of A's	52,470,019 / 27.51%
Number/percentage of C's	36,847,453 / 19.32%
Number/percentage of T's	58,166,111 / 30.5%
Number/percentage of G's	43,194,378 / 22.65%
Number/percentage of N's	48,500 / 0.03%
GC Percentage	41.97%

2.3. Coverage

Mean	0.0616

Standard Deviation	0.5657
--------------------	--------

2.4. Mapping Quality

Mean Mapping Quality	44.31
----------------------	-------

2.5. Mismatches and indels

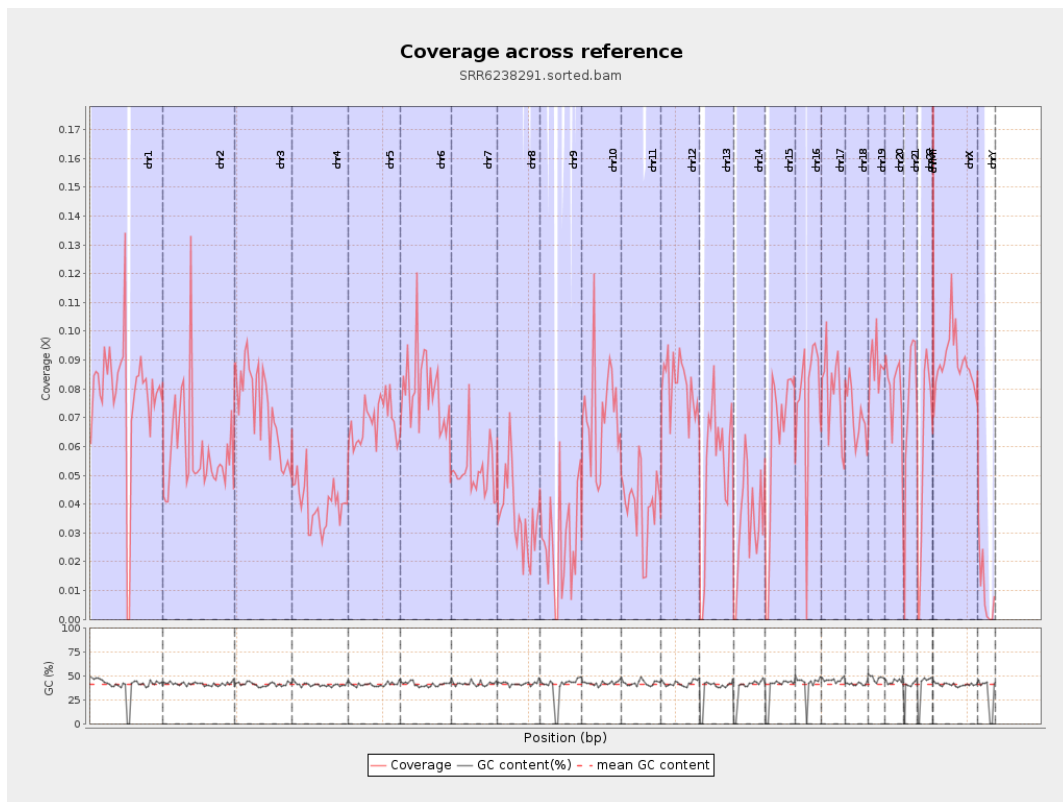
General error rate	0.87%
Mismatches	1,639,748
Insertions	14,617
Mapped reads with at least one insertion	0.5%
Deletions	54,065
Mapped reads with at least one deletion	1.84%
Homopolymer indels	44.94%

2.6. Chromosome stats

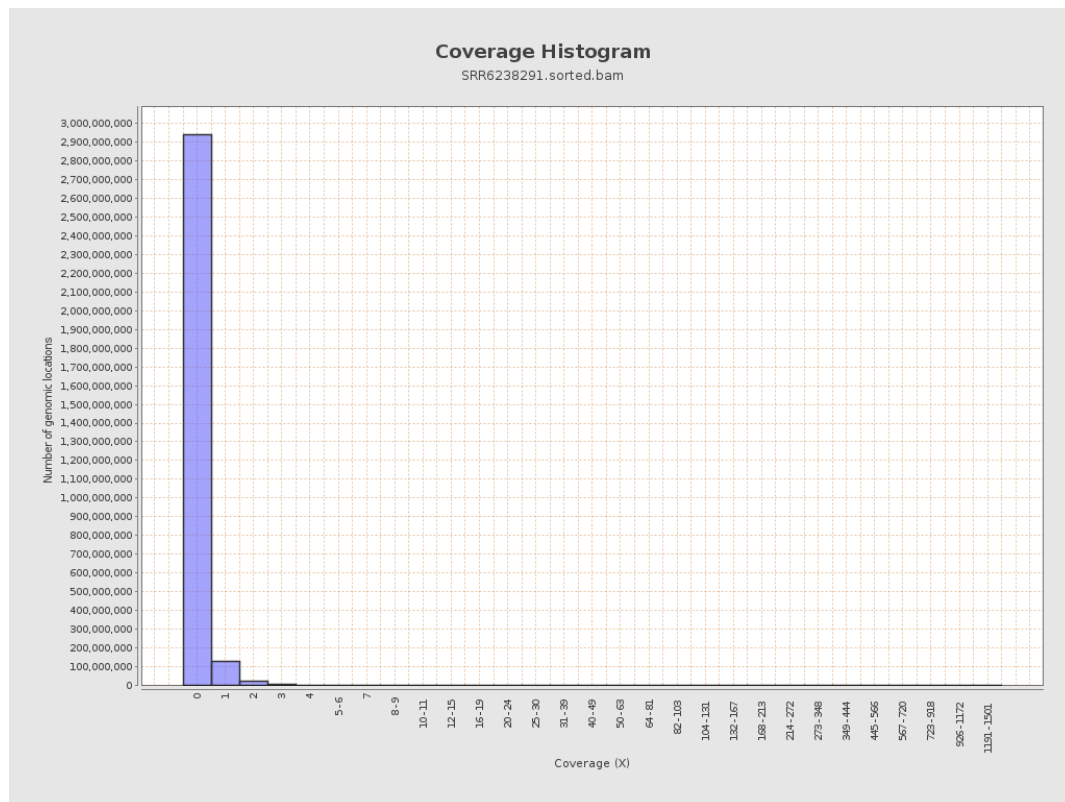
Name	Length	Mapped bases	Mean coverage	Standard deviation
chr1	249250621	19397901	0.0778	1.2246
chr2	243199373	14224586	0.0585	0.676
chr3	198022430	14398191	0.0727	0.324
chr4	191154276	7608440	0.0398	0.2538
chr5	180915260	12391034	0.0685	0.3164
chr6	171115067	13552359	0.0792	0.4754
chr7	159138663	8148440	0.0512	0.4917

chr8	146364022	5304249	0.0362	0.6849
chr9	141213431	3689695	0.0261	0.4416
chr10	135534747	9604734	0.0709	0.5923
chr11	135006516	5395271	0.04	0.3007
chr12	133851895	10906539	0.0815	0.3503
chr13	115169878	6009328	0.0522	0.2722
chr14	107349540	3634058	0.0339	0.2756
chr15	102531392	6415307	0.0626	0.305
chr16	90354753	6871079	0.076	0.4008
chr17	81195210	6465031	0.0796	0.4279
chr18	78077248	5579365	0.0715	0.8853
chr19	59128983	5217979	0.0882	0.8236
chr20	63025520	4993552	0.0792	0.3536
chr21	48129895	3557099	0.0739	0.3559
chr22	51304566	3015887	0.0588	0.2898
chrMT	16571	5705	0.3443	0.6574
chrX	155270560	13868921	0.0893	0.4162
chrY	59373566	562175	0.0095	0.1777

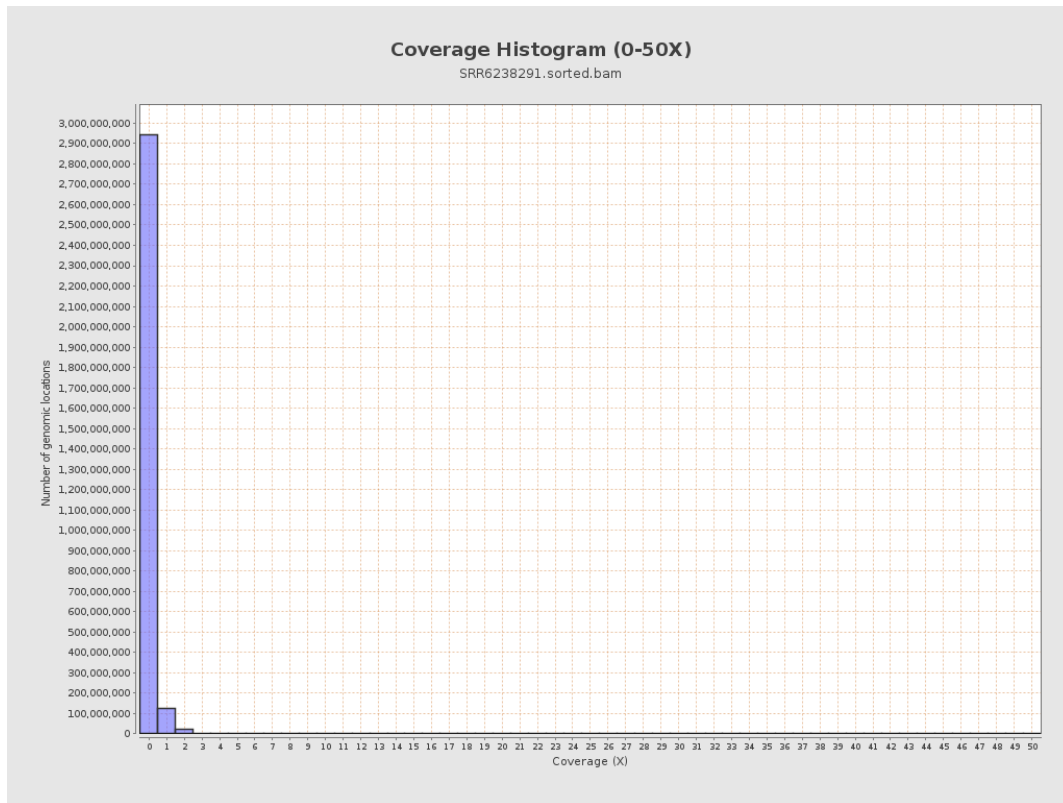
3. Results : Coverage across reference



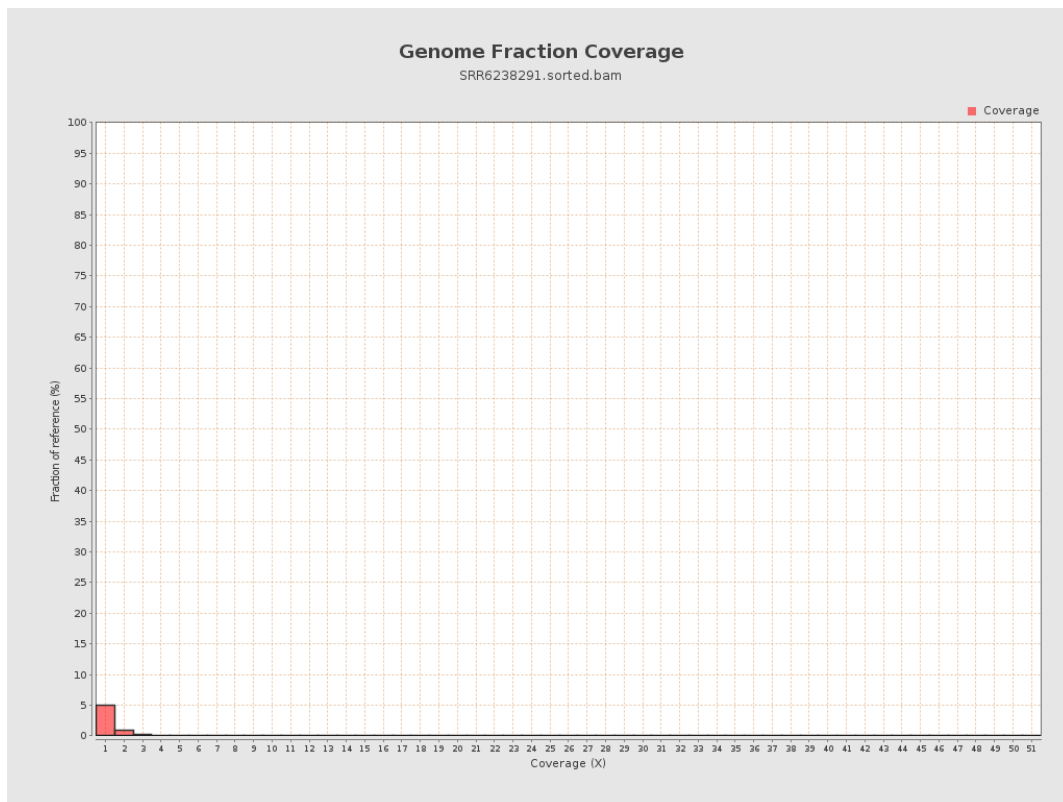
4. Results : Coverage Histogram



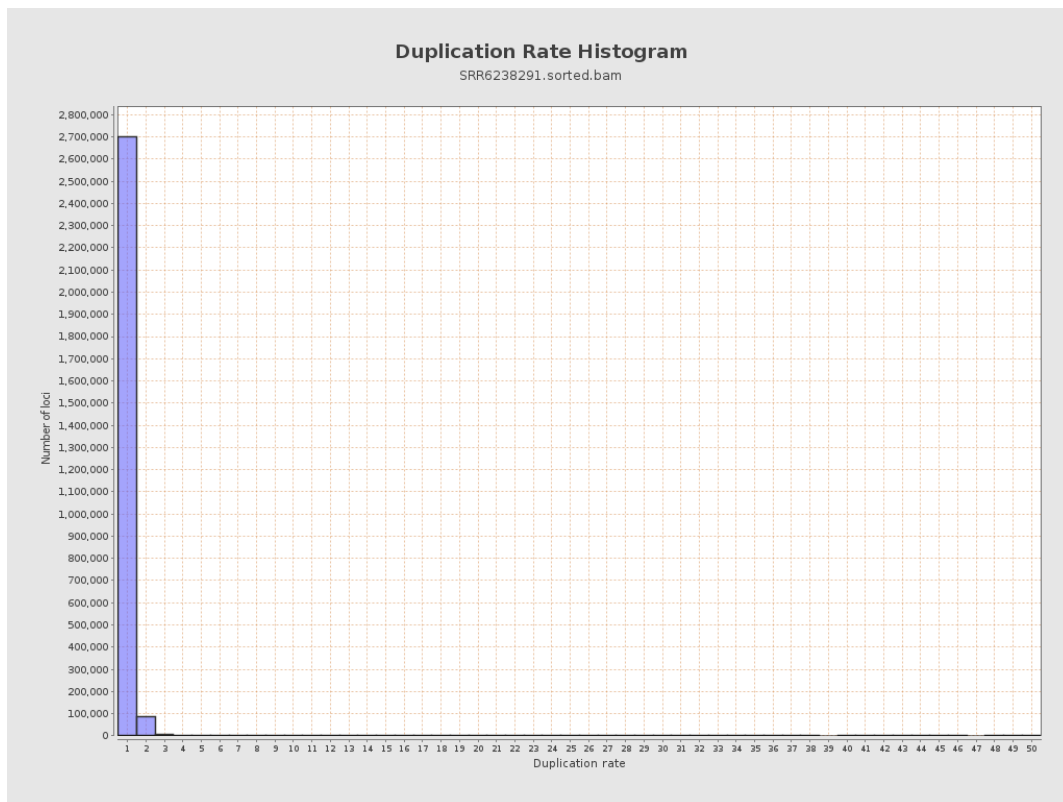
5. Results : Coverage Histogram (0-50X)



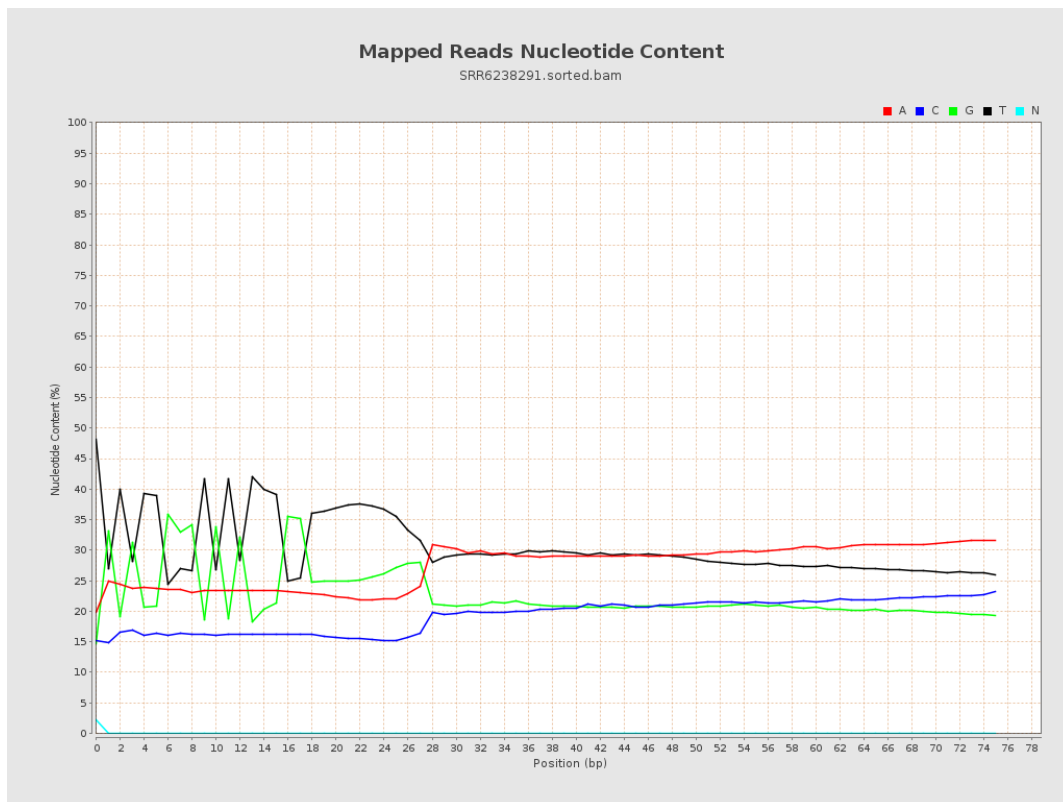
6. Results : Genome Fraction Coverage



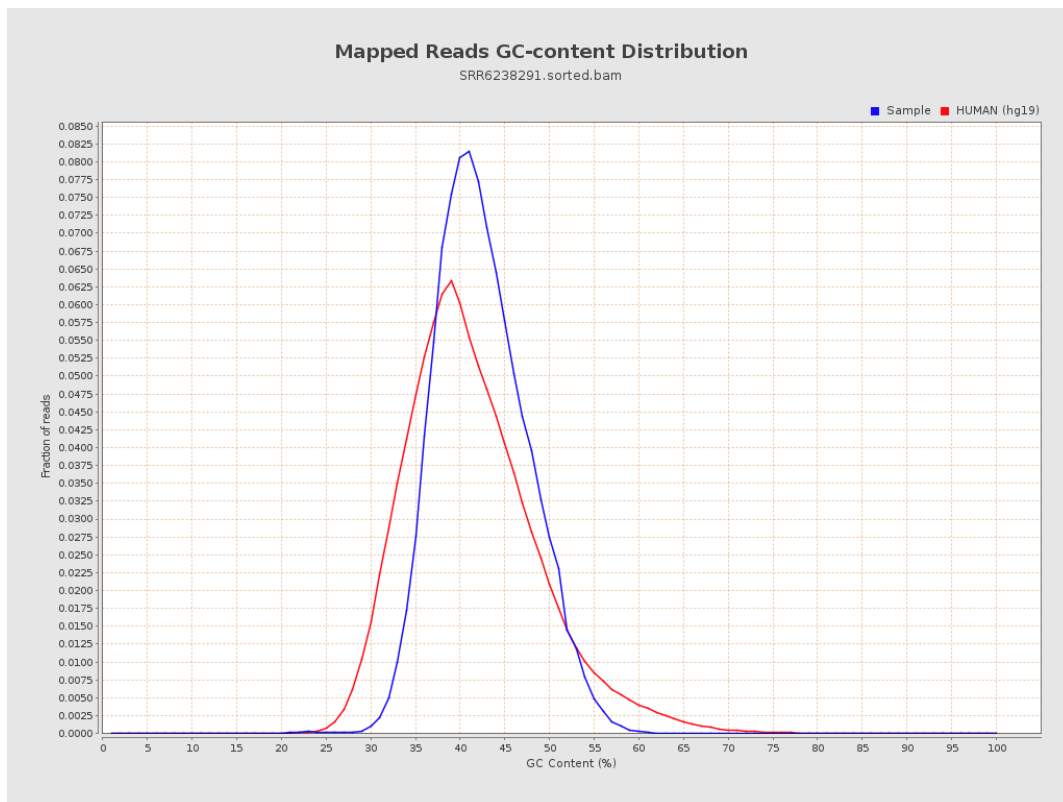
7. Results : Duplication Rate Histogram



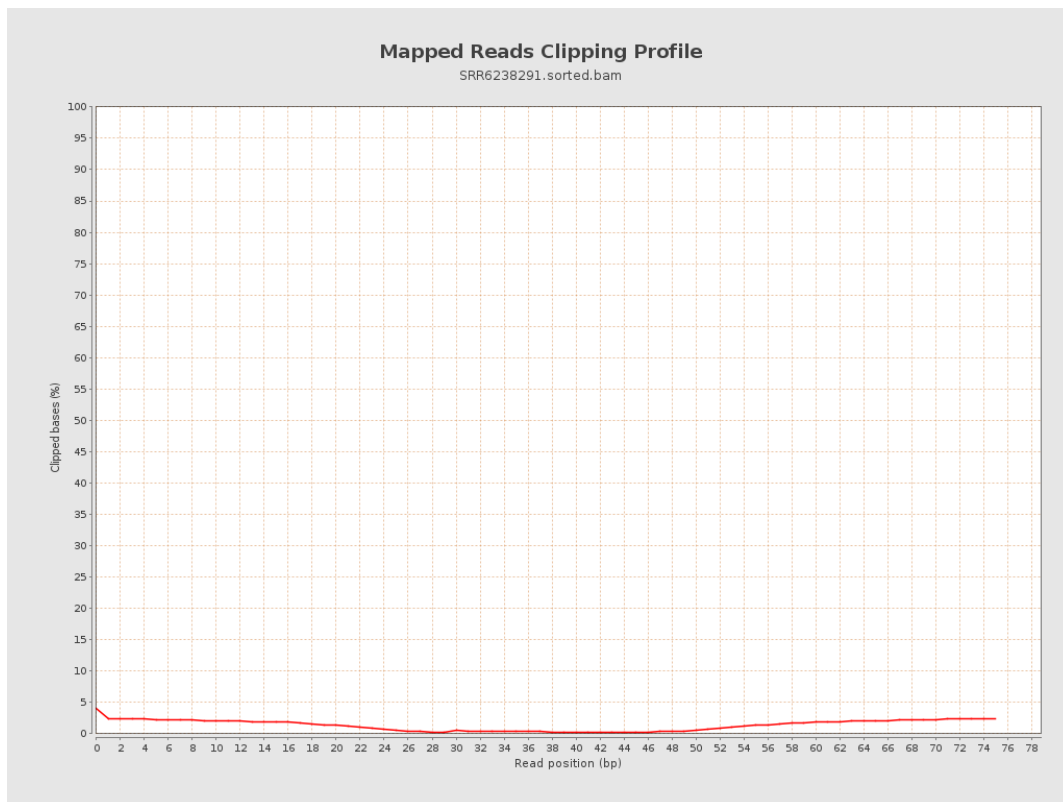
8. Results : Mapped Reads Nucleotide Content



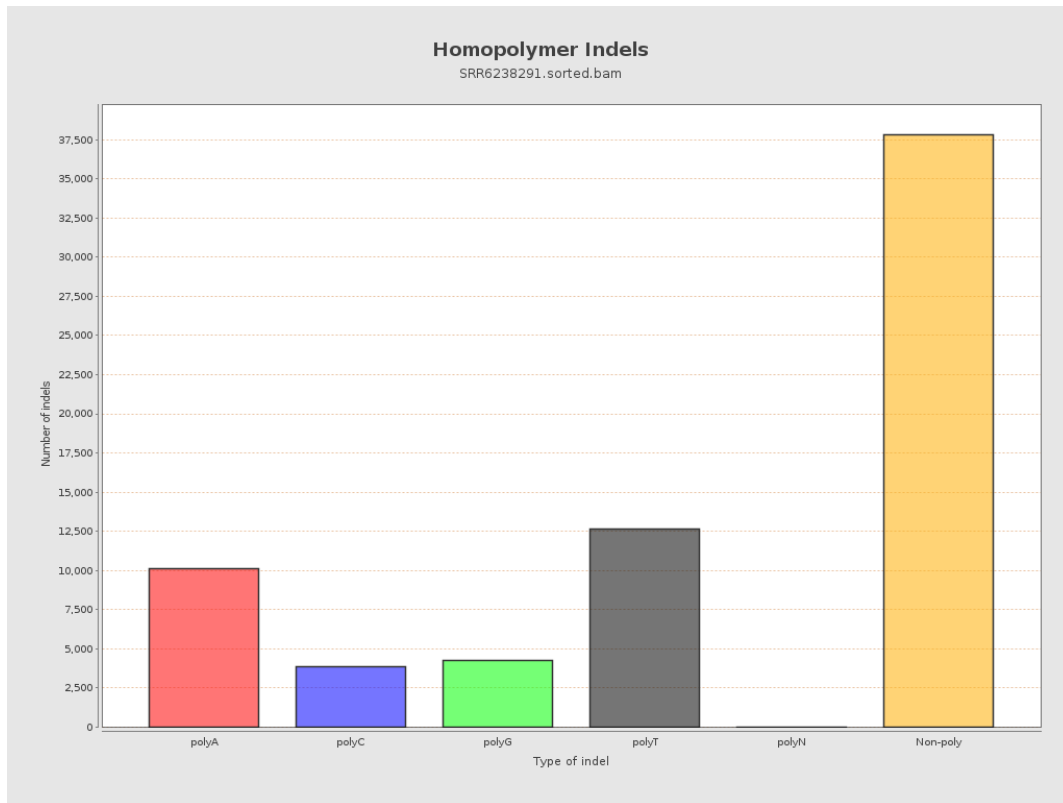
9. Results : Mapped Reads GC-content Distribution



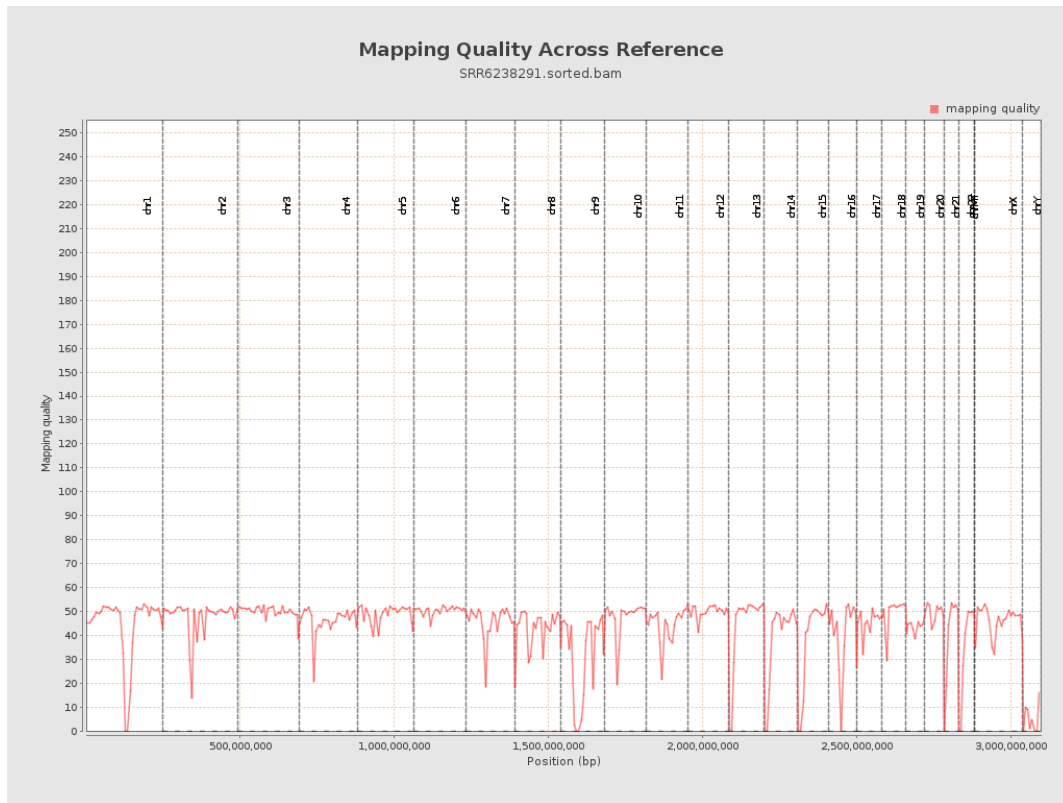
10. Results : Mapped Reads Clipping Profile



11. Results : Homopolymer Indels



12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram

