

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/17 23:18:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1006191.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_SRR1006191 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR1006191_1.fastq.gz SRR1006191_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Apr 17 23:18:52 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1006191.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	8,991,720
Mapped reads	7,776,043 / 86.48%
Unmapped reads	1,215,677 / 13.52%
Mapped paired reads	7,776,043 / 86.48%
Mapped reads, first in pair	3,917,317 / 43.57%
Mapped reads, second in pair	3,858,726 / 42.91%
Mapped reads, both in pair	7,185,636 / 79.91%
Mapped reads, singletons	590,407 / 6.57%
Secondary alignments	0
Read min/max/mean length	39 / 39 / 39
Duplicated reads (estimated)	318,074 / 3.54%
Duplication rate	3.45%
Clipped reads	487,090 / 5.42%

2.2. ACGT Content

Number/percentage of A's	82,038,219 / 27.28%
Number/percentage of C's	66,431,447 / 22.09%
Number/percentage of T's	83,673,347 / 27.82%
Number/percentage of G's	68,584,230 / 22.8%
Number/percentage of N's	35,578 / 0.01%
GC Percentage	44.89%

2.3. Coverage

Mean	0.0972
Standard Deviation	0.5723

2.4. Mapping Quality

Mean Mapping Quality	47.55
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2.5. Insert size

Mean	54,995.76
Standard Deviation	2,263,420.67
P25/Median/P75	69 / 101 / 136

2.6. Mismatches and indels

General error rate	0.32%
Mismatches	963,775
Insertions	8,979
Mapped reads with at least one insertion	0.12%
Deletions	31,208
Mapped reads with at least one deletion	0.4%
Homopolymer indels	42.09%

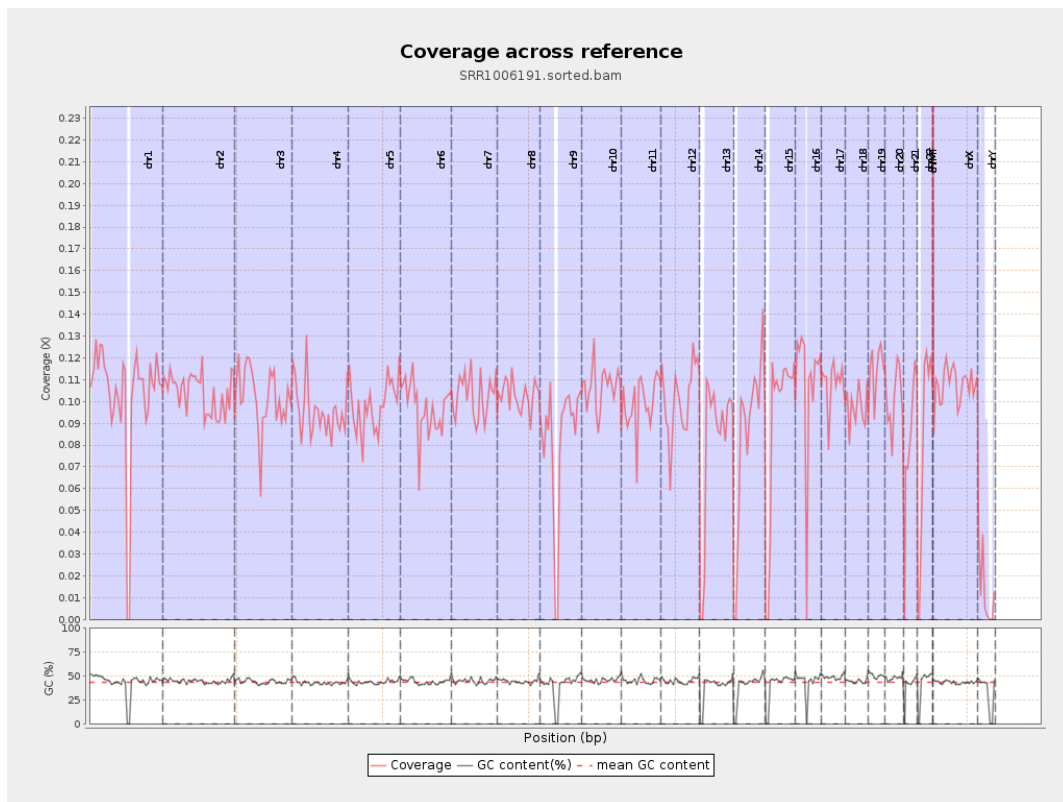
2.7. Chromosome stats

Name	Length	Mapped bases	Mean coverage	Standard deviation

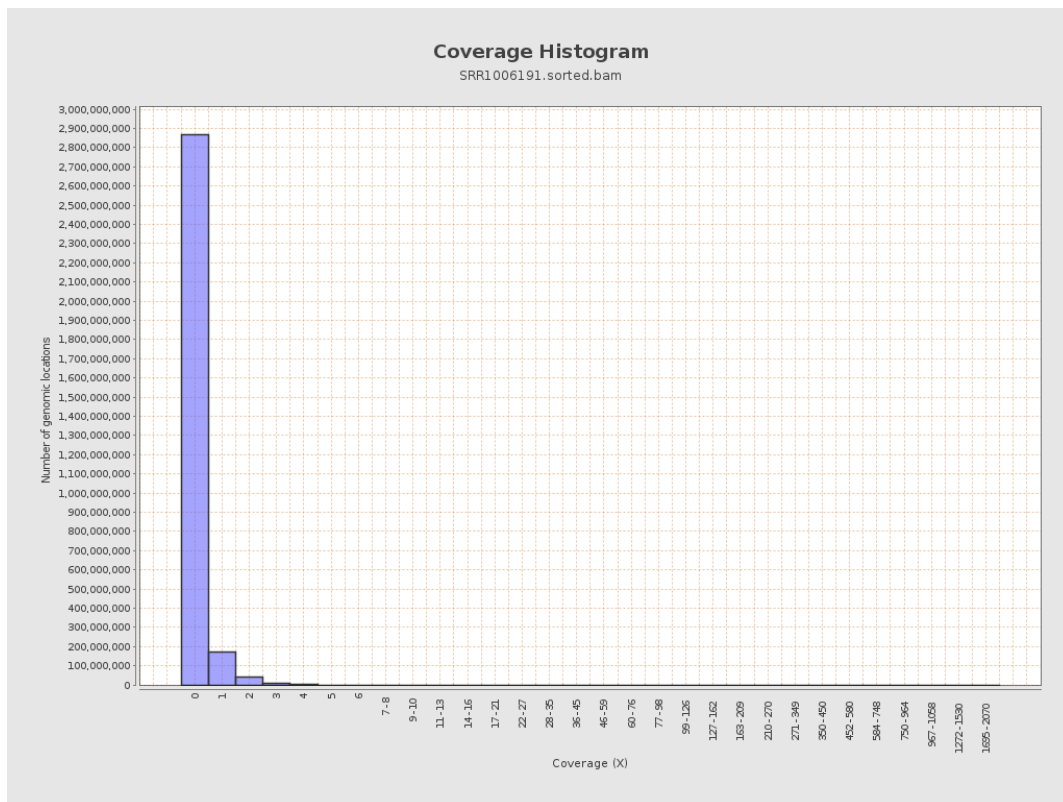
chr1	249250621	25632633	0.1028	0.6788
chr2	243199373	25277570	0.1039	0.4886
chr3	198022430	20130718	0.1017	0.3983
chr4	191154276	18325532	0.0959	0.4285
chr5	180915260	17847100	0.0986	0.3943
chr6	171115067	16563118	0.0968	0.4279
chr7	159138663	16380182	0.1029	0.5795
chr8	146364022	15044367	0.1028	1.0865
chr9	141213431	11569905	0.0819	0.4161
chr10	135534747	14428125	0.1065	0.5399
chr11	135006516	13349102	0.0989	0.4752
chr12	133851895	13582694	0.1015	0.4038
chr13	115169878	9302328	0.0808	0.3608
chr14	107349540	9320991	0.0868	1.329
chr15	102531392	9179189	0.0895	0.3772
chr16	90354753	9699928	0.1074	0.4725
chr17	81195210	8836865	0.1088	0.4403
chr18	78077248	7574139	0.097	0.6513
chr19	59128983	6764112	0.1144	0.5803
chr20	63025520	6340378	0.1006	0.4278
chr21	48129895	4010424	0.0833	0.4296
chr22	51304566	4184417	0.0816	0.4155
chrMT	16571	6257	0.3776	0.7788
chrX	155270560	16706904	0.1076	0.439

chrY	59373566	748432	0.0126	0.2756
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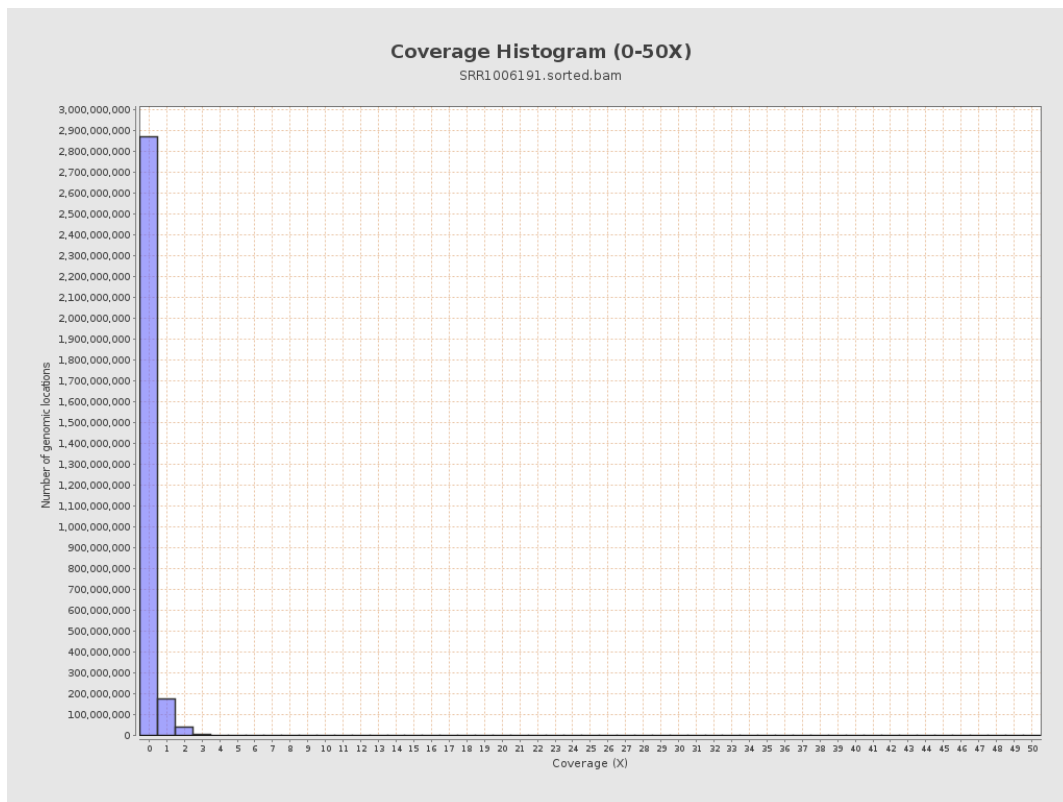
3. Results : Coverage across reference



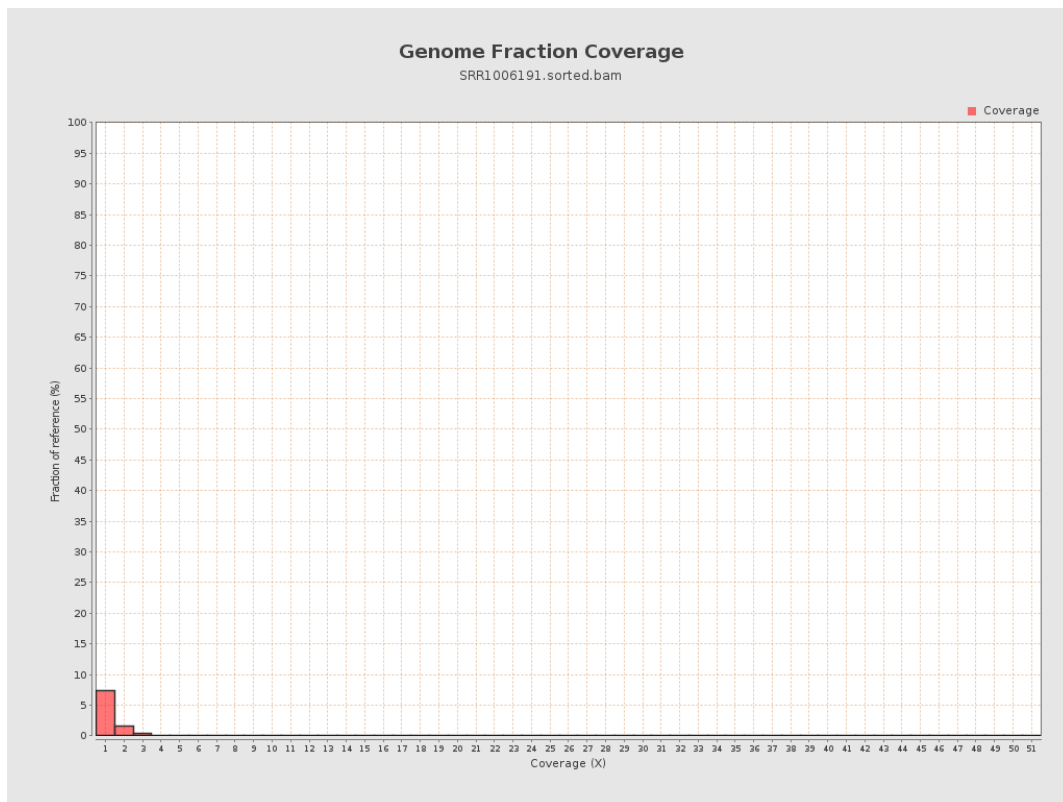
4. Results : Coverage Histogram



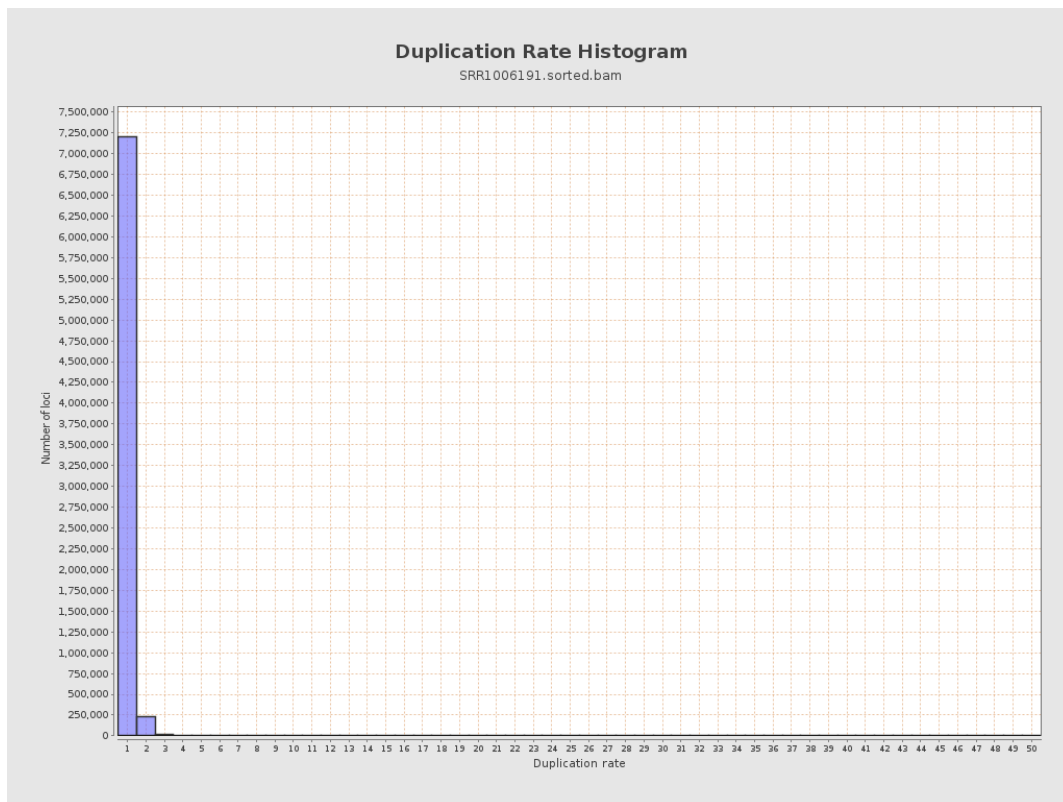
5. Results : Coverage Histogram (0-50X)



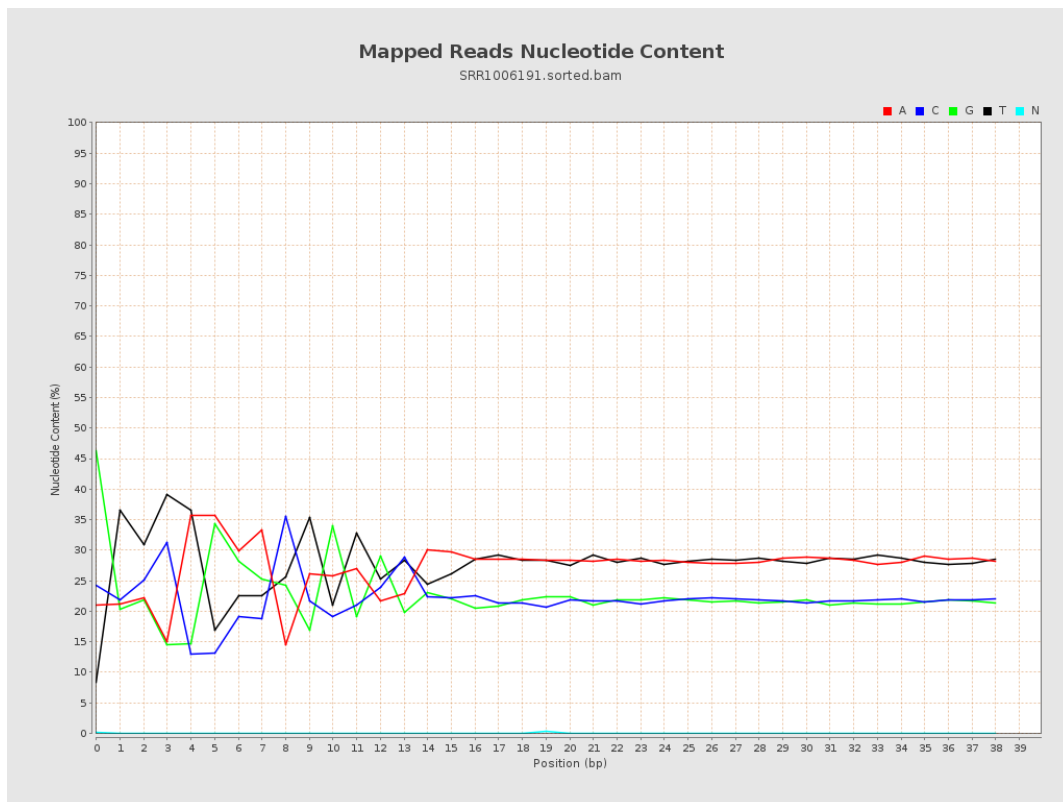
6. Results : Genome Fraction Coverage



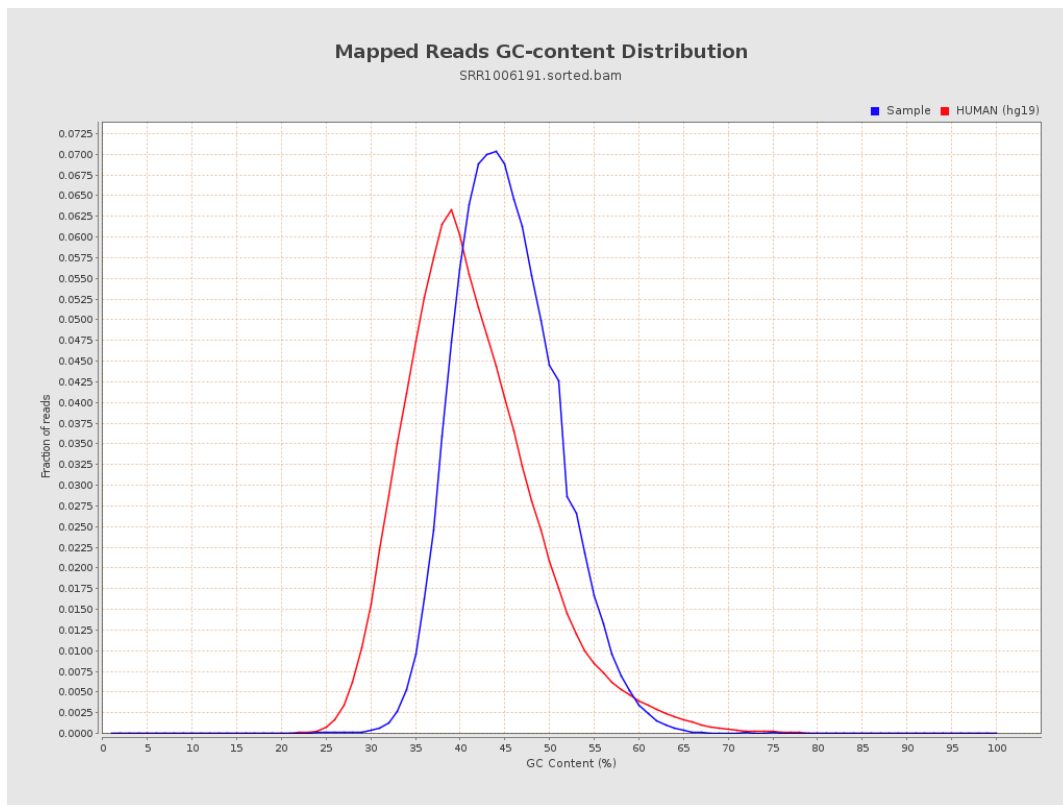
7. Results : Duplication Rate Histogram



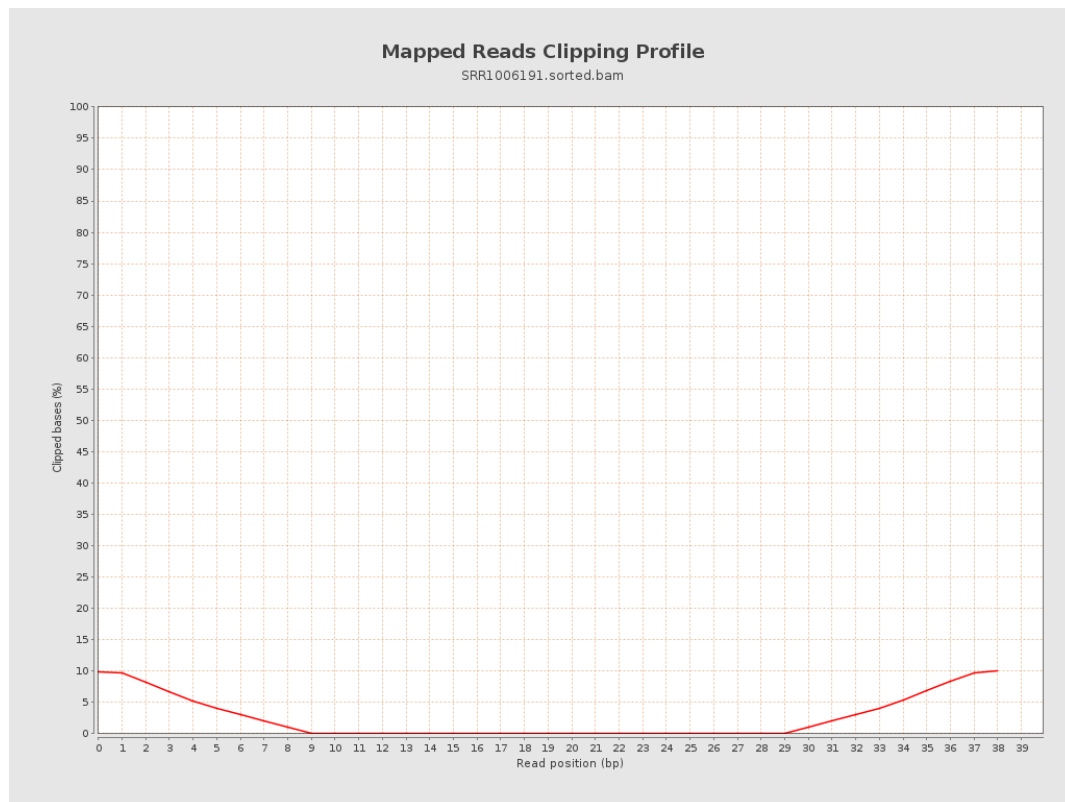
8. Results : Mapped Reads Nucleotide Content



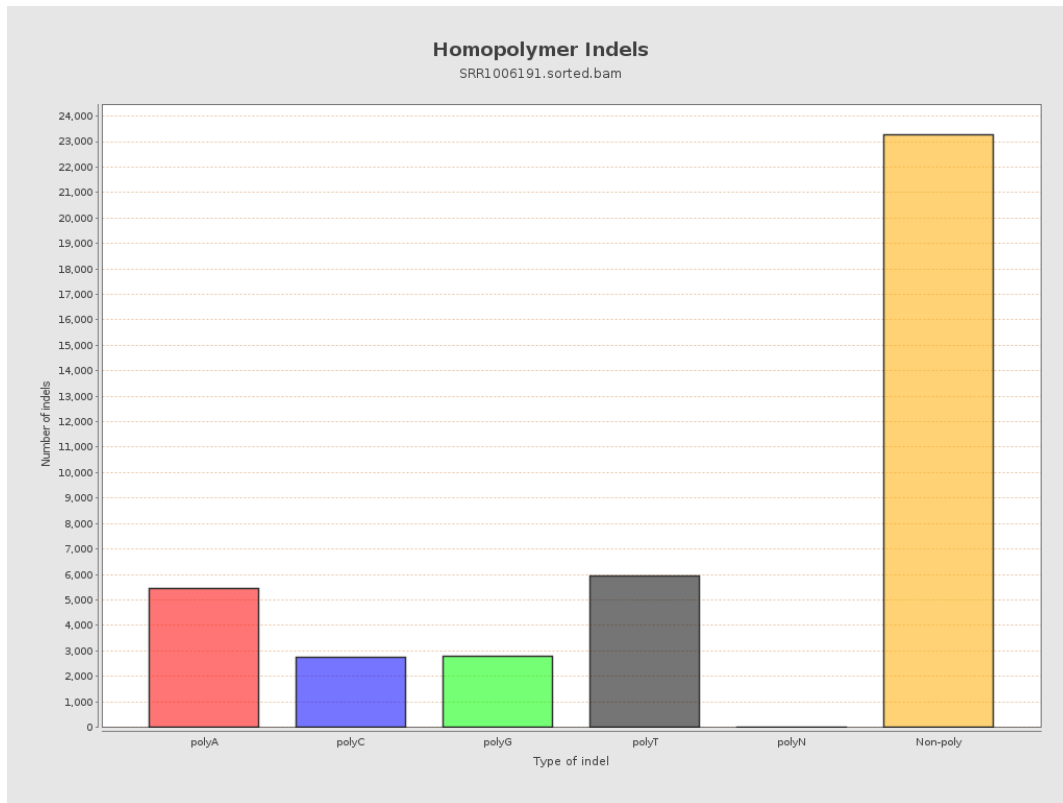
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



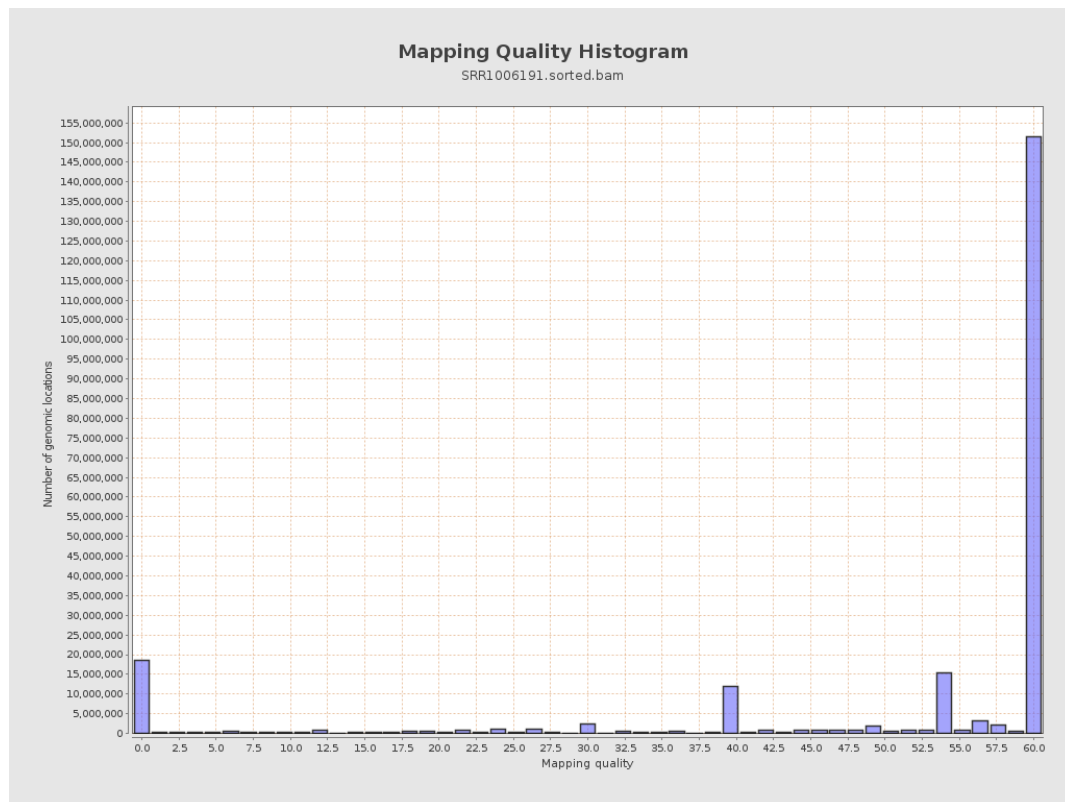
11. Results : Homopolymer Indels



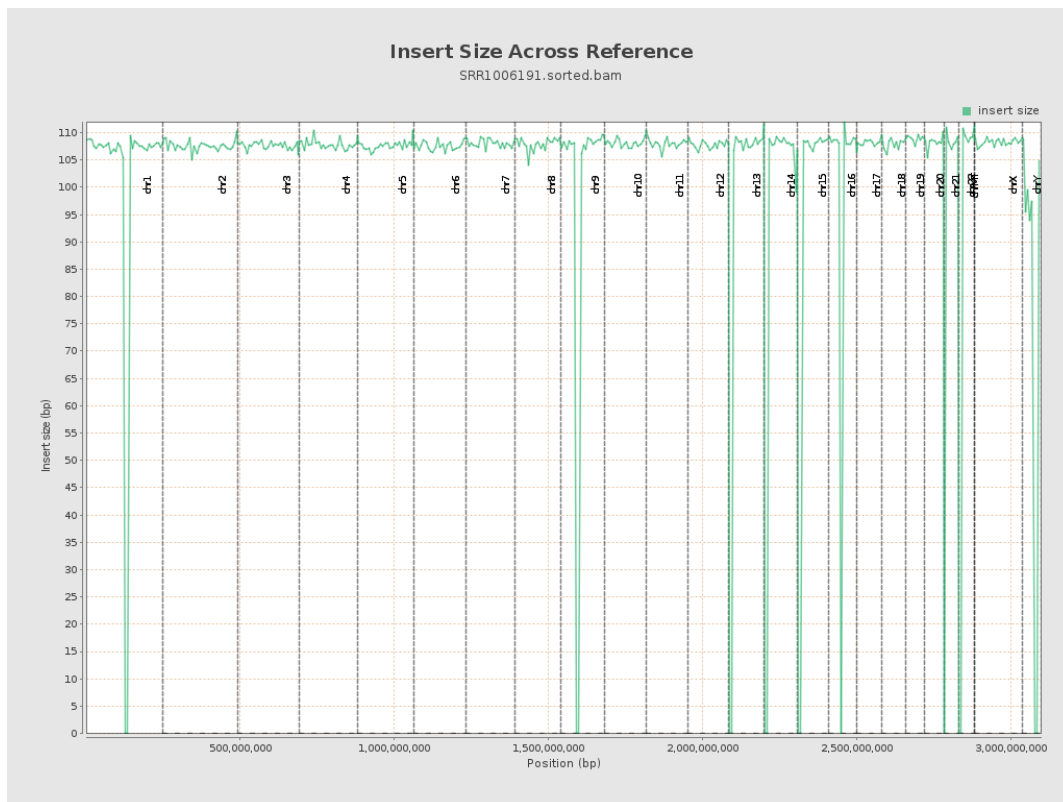
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

