

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 14:29:14

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046434.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_SRR2046434 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046434_1.fastq.gz SRR2046434_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 14:29:13 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046434.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,928,254
Mapped reads	6,897,971 / 99.56%
Unmapped reads	30,283 / 0.44%
Mapped paired reads	6,897,971 / 99.56%
Mapped reads, first in pair	3,453,073 / 49.84%
Mapped reads, second in pair	3,444,898 / 49.72%
Mapped reads, both in pair	6,877,932 / 99.27%
Mapped reads, singletons	20,039 / 0.29%
Secondary alignments	0
Supplementary alignments	26,075 / 0.38%
Read min/max/mean length	30 / 100 / 100.15
Duplicated reads (estimated)	5,022,377 / 72.49%
Duplication rate	41.74%
Clipped reads	2,313,206 / 33.39%

2.2. ACGT Content

Number/percentage of A's	185,604,922 / 28.94%
Number/percentage of C's	135,399,840 / 21.11%
Number/percentage of T's	181,980,232 / 28.37%
Number/percentage of G's	138,309,916 / 21.57%
Number/percentage of N's	50,436 / 0.01%

GC Percentage	42.68%
---------------	--------

2.3. Coverage

Mean	0.2072
Standard Deviation	21.1901

2.4. Mapping Quality

Mean Mapping Quality	52.35
----------------------	-------

2.5. Insert size

Mean	20,508.84
Standard Deviation	1,242,230.16
P25/Median/P75	91 / 117 / 146

2.6. Mismatches and indels

General error rate	0.33%
Mismatches	1,990,630
Insertions	48,555
Mapped reads with at least one insertion	0.69%
Deletions	58,403
Mapped reads with at least one deletion	0.83%
Homopolymer indels	45.93%

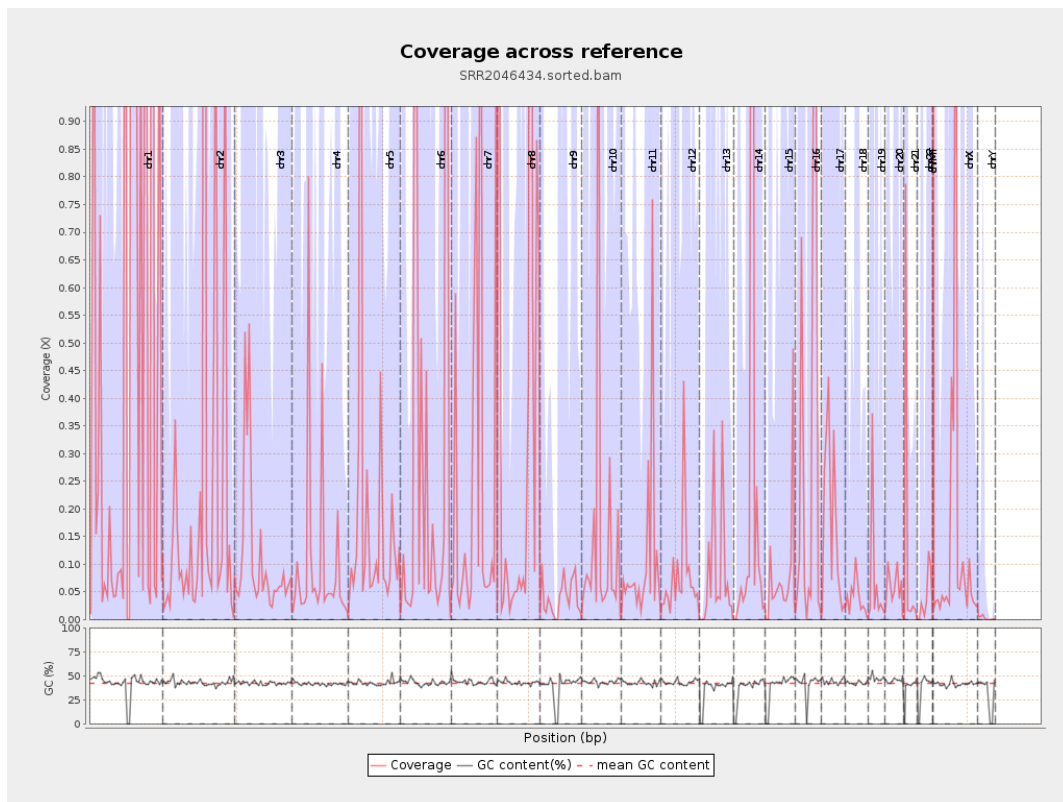
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

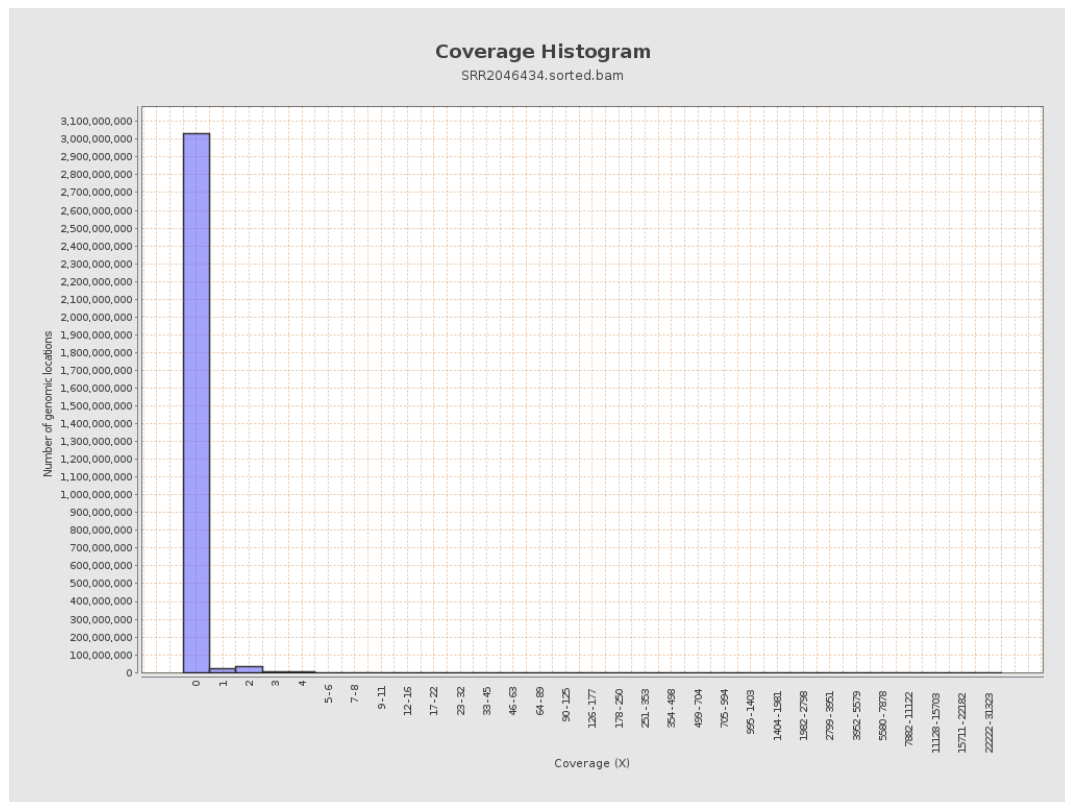
		bases	coverage	deviation
chr1	249250621	141286907	0.5668	48.234
chr2	243199373	70118455	0.2883	24.5916
chr3	198022430	22121170	0.1117	7.3244
chr4	191154276	19207846	0.1005	5.3223
chr5	180915260	37583669	0.2077	15.3339
chr6	171115067	52193616	0.305	22.8402
chr7	159138663	45588828	0.2865	19.2635
chr8	146364022	72200033	0.4933	30.5057
chr9	141213431	5923848	0.0419	2.5981
chr10	135534747	21732322	0.1603	32.1944
chr11	135006516	14583383	0.108	8.1545
chr12	133851895	10266241	0.0767	3.779
chr13	115169878	9098593	0.079	5.7168
chr14	107349540	26468406	0.2466	21.6902
chr15	102531392	8575543	0.0836	4.999
chr16	90354753	26710366	0.2956	19.1066
chr17	81195210	14224305	0.1752	9.3637
chr18	78077248	2995117	0.0384	0.8585
chr19	59128983	4188533	0.0708	8.5645
chr20	63025520	3854535	0.0612	1.1324
chr21	48129895	6648373	0.1381	18.1647
chr22	51304566	2272621	0.0443	3.3337
chrMT	16571	126438	7.6301	4.4256
chrX	155270560	23372919	0.1505	17.8924

chrY	59373566	159016	0.0027	0.3216
------	----------	--------	--------	--------

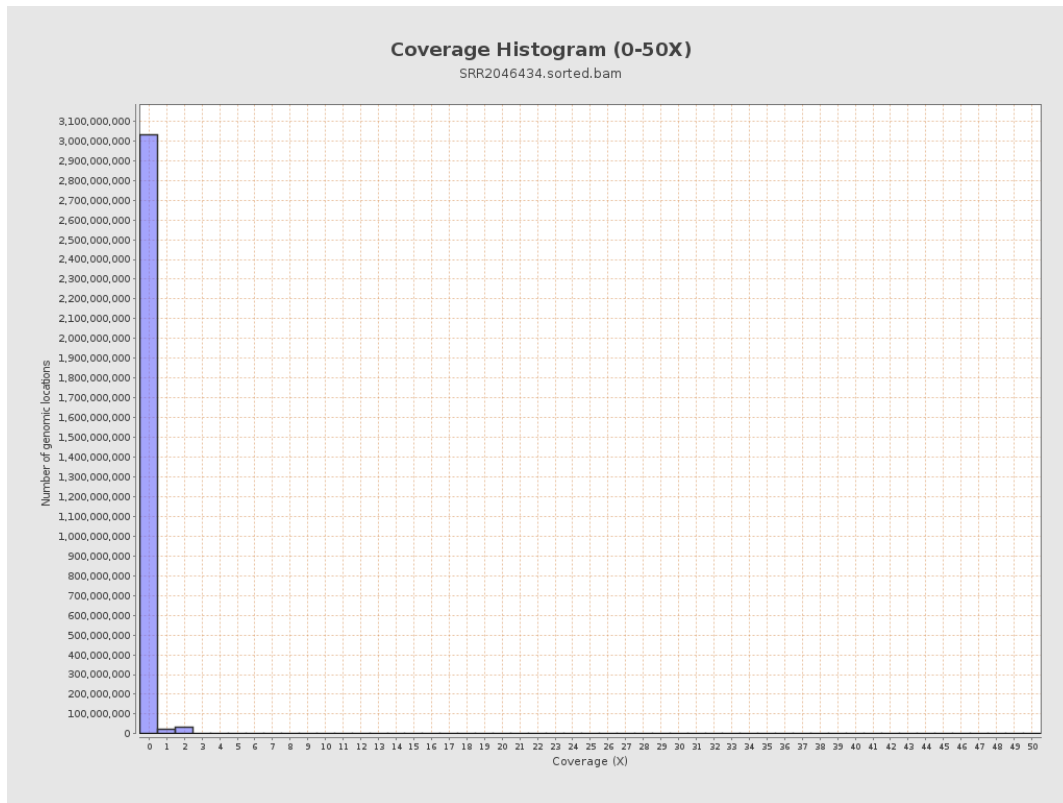
3. Results : Coverage across reference



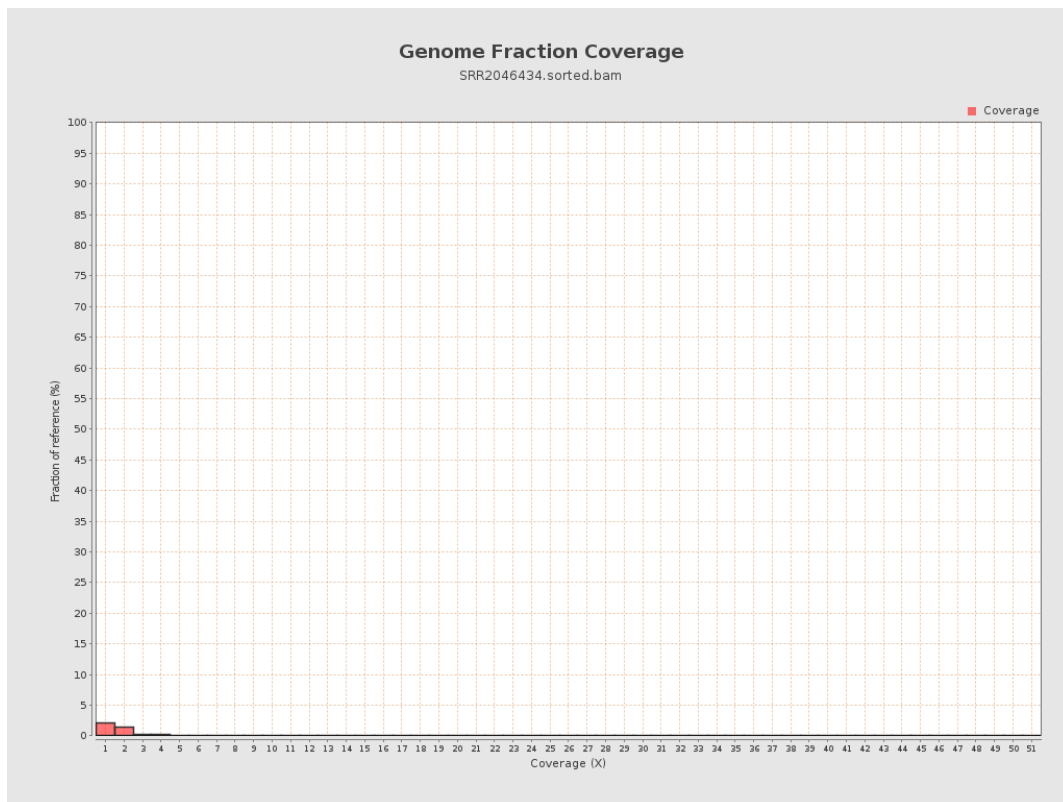
4. Results : Coverage Histogram



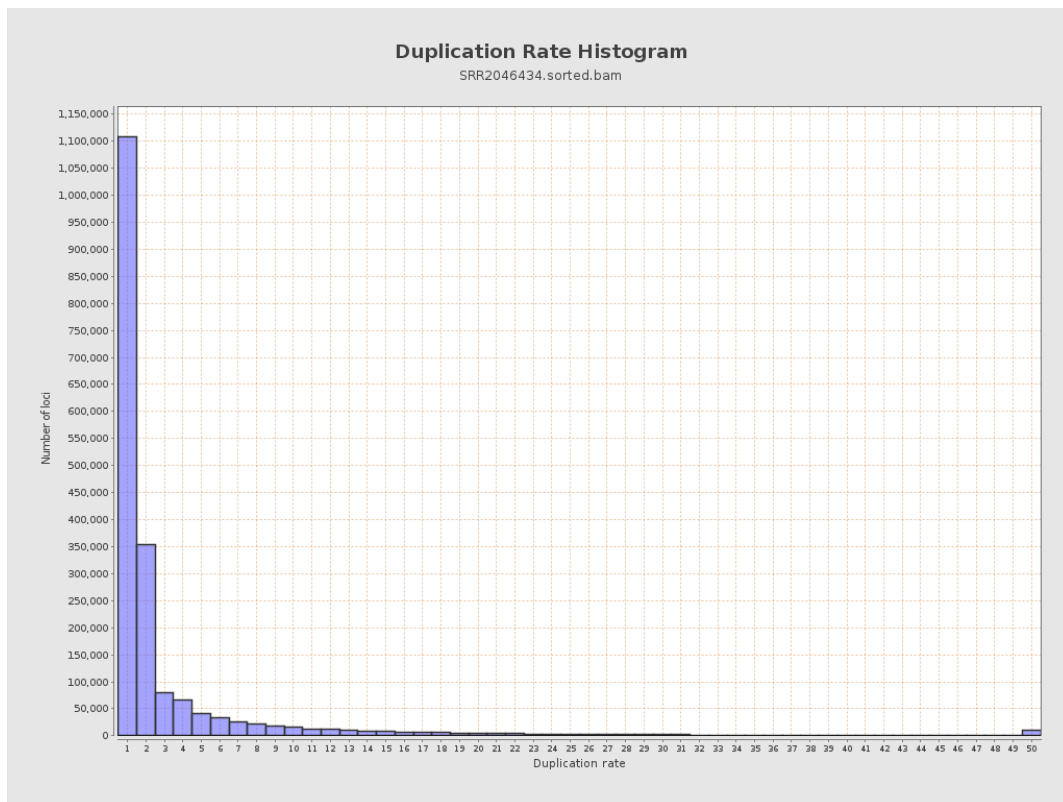
5. Results : Coverage Histogram (0-50X)



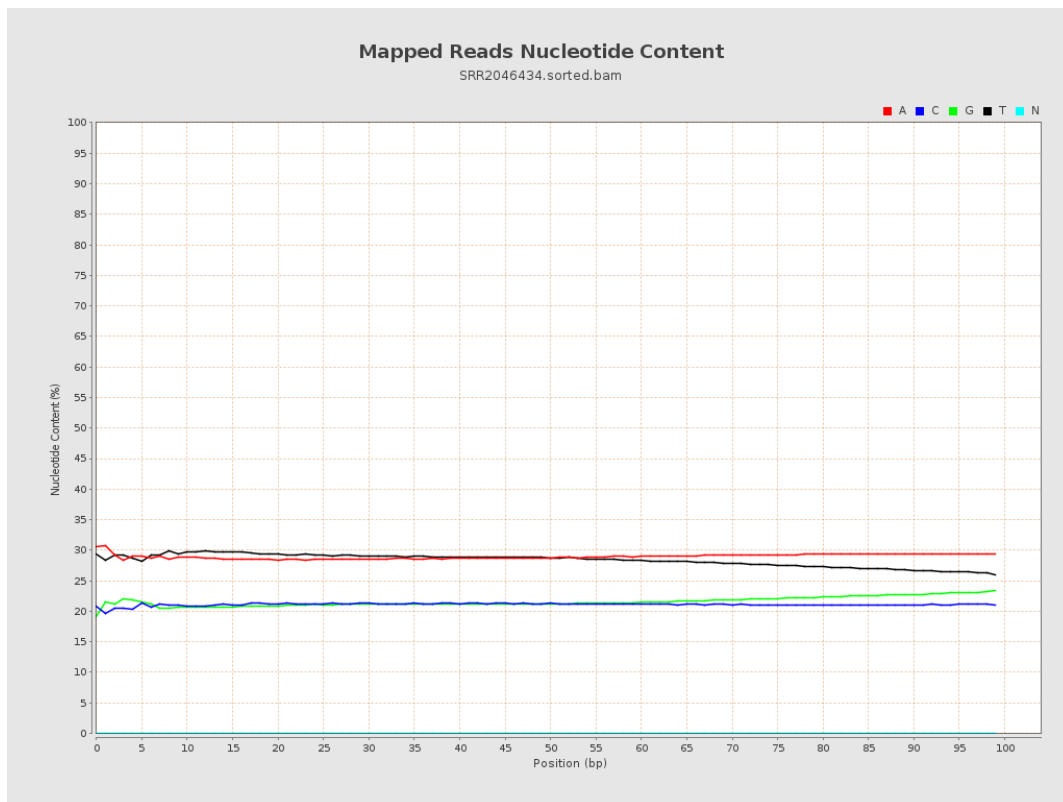
6. Results : Genome Fraction Coverage



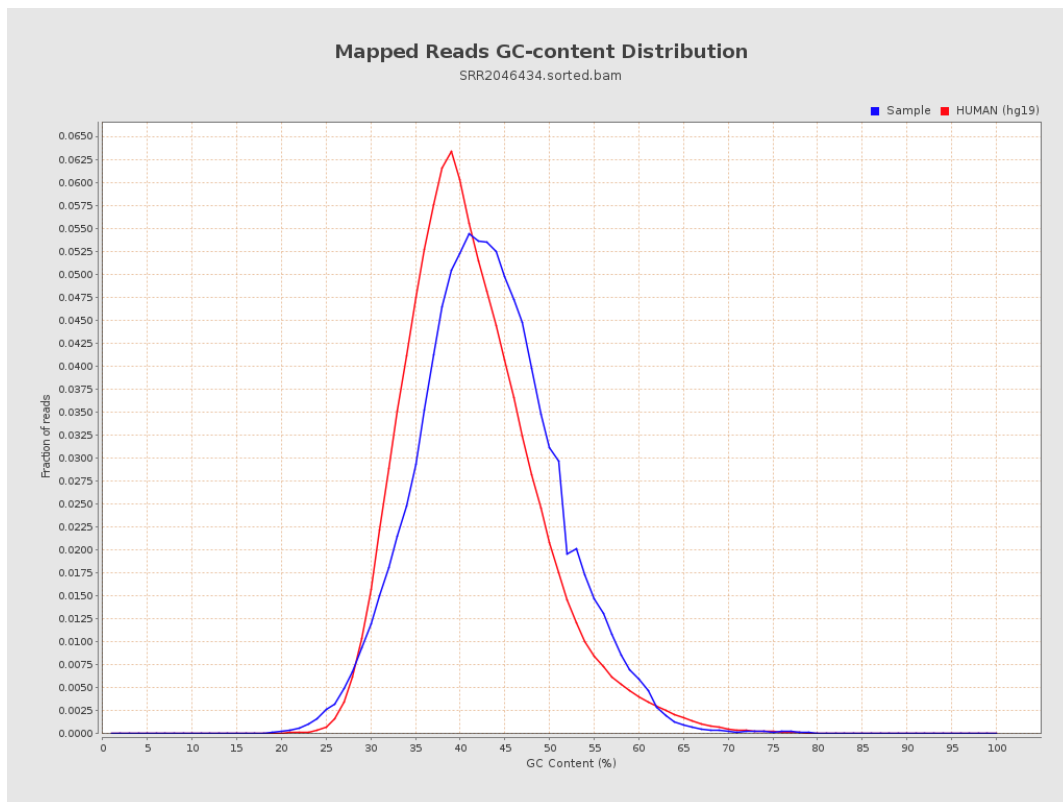
7. Results : Duplication Rate Histogram



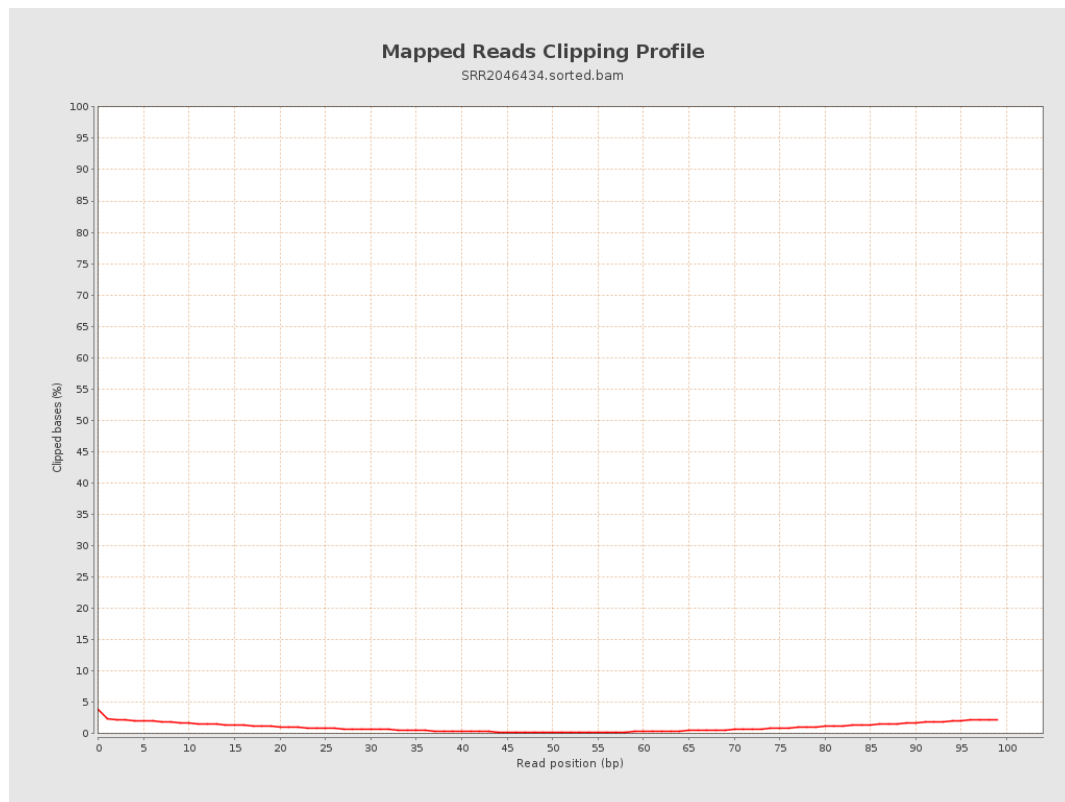
8. Results : Mapped Reads Nucleotide Content



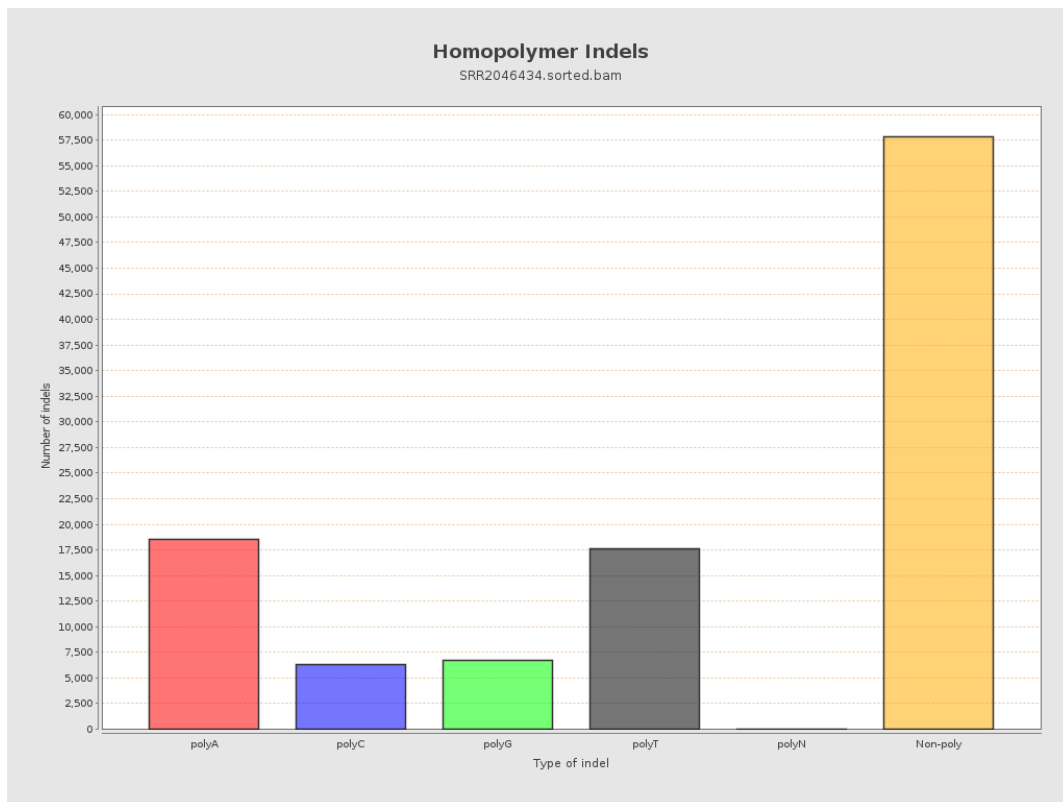
9. Results : Mapped Reads GC-content Distribution



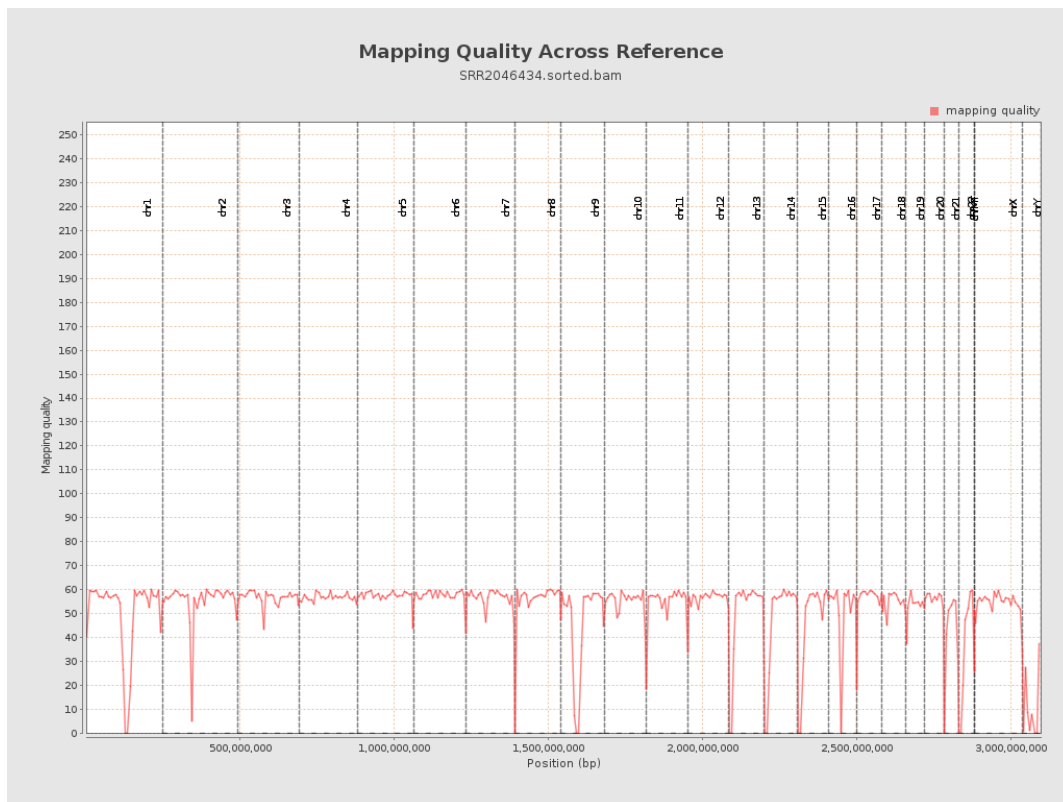
10. Results : Mapped Reads Clipping Profile



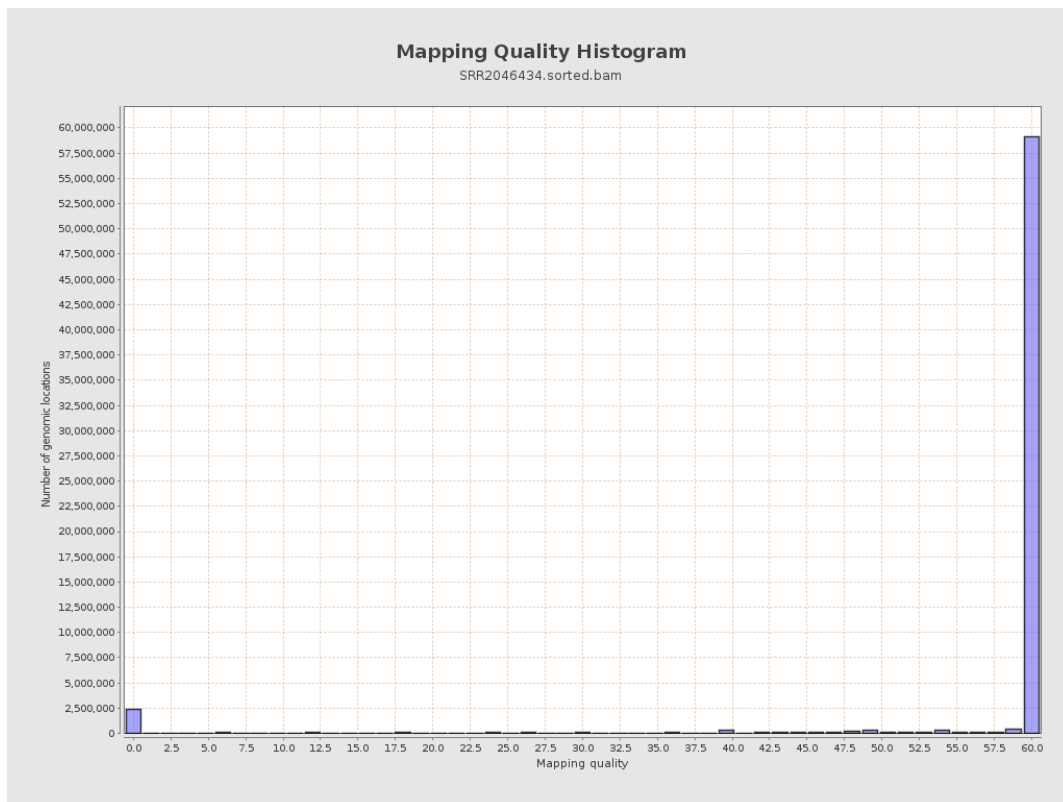
11. Results : Homopolymer Indels



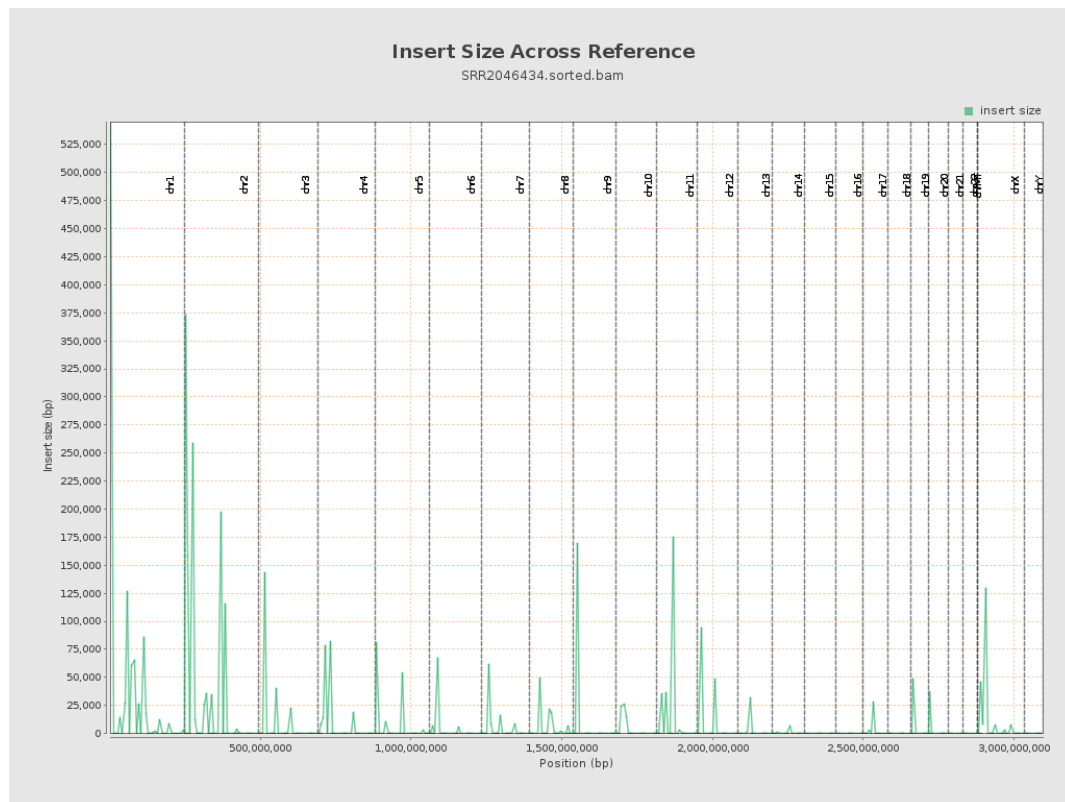
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

