

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 15:51:39

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046456.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_SRR2046456 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046456_1.fastq.gz SRR2046456_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 15:51:38 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046456.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,006,804
Mapped reads	5,966,799 / 99.33%
Unmapped reads	40,005 / 0.67%
Mapped paired reads	5,966,799 / 99.33%
Mapped reads, first in pair	2,986,187 / 49.71%
Mapped reads, second in pair	2,980,612 / 49.62%
Mapped reads, both in pair	5,939,178 / 98.87%
Mapped reads, singletons	27,621 / 0.46%
Secondary alignments	0
Supplementary alignments	40,504 / 0.67%
Read min/max/mean length	30 / 100 / 100.27
Duplicated reads (estimated)	4,394,700 / 73.16%
Duplication rate	43.61%
Clipped reads	2,106,706 / 35.07%

2.2. ACGT Content

Number/percentage of A's	163,850,443 / 29.51%
Number/percentage of C's	114,380,518 / 20.6%
Number/percentage of T's	161,223,254 / 29.04%
Number/percentage of G's	115,688,985 / 20.84%
Number/percentage of N's	44,479 / 0.01%

GC Percentage	41.44%
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2.3. Coverage

Mean	0.1794
Standard Deviation	16.2907

2.4. Mapping Quality

Mean Mapping Quality	52.32
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2.5. Insert size

Mean	24,964.66
Standard Deviation	1,605,713.15
P25/Median/P75	92 / 119 / 163

2.6. Mismatches and indels

General error rate	0.33%
Mismatches	1,756,539
Insertions	48,297
Mapped reads with at least one insertion	0.8%
Deletions	47,896
Mapped reads with at least one deletion	0.78%
Homopolymer indels	47.16%

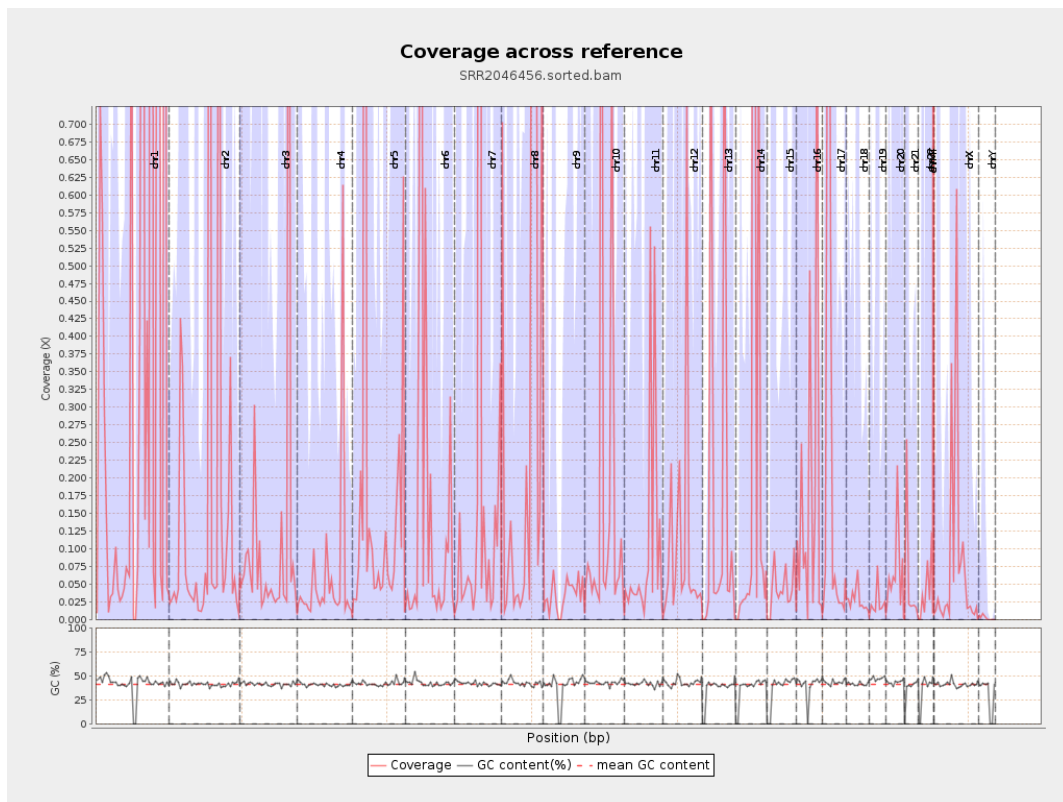
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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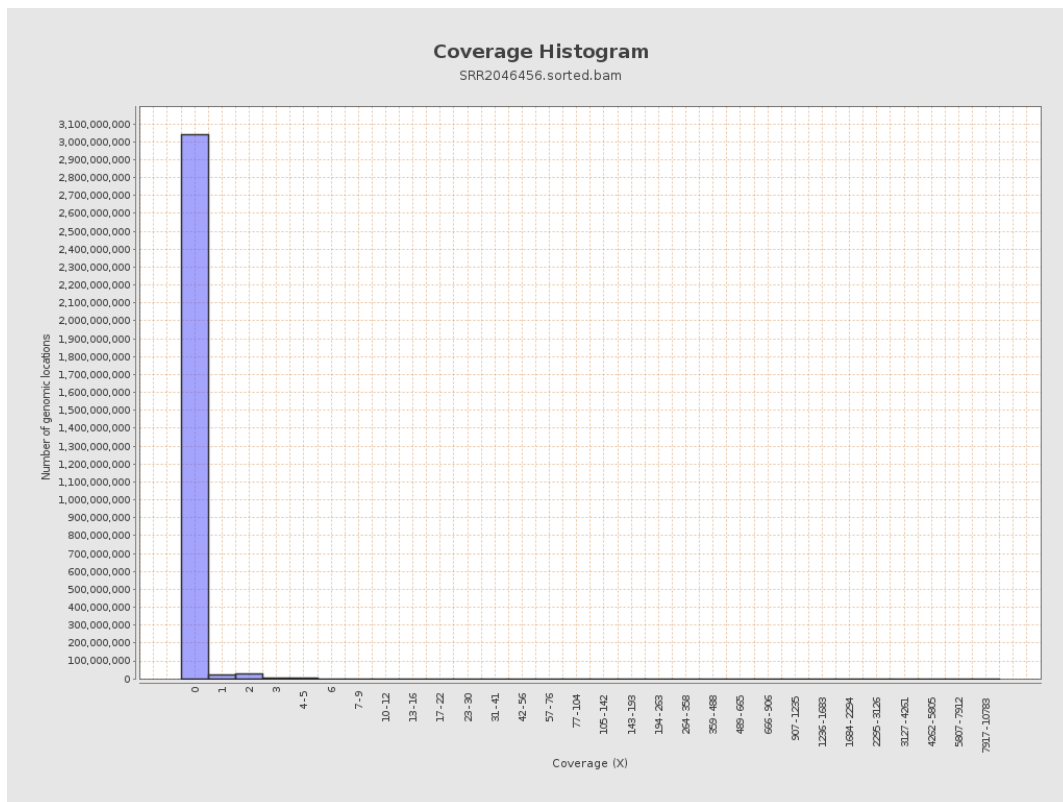
		bases	coverage	deviation
chr1	249250621	129672159	0.5202	32.7108
chr2	243199373	44602292	0.1834	14.4761
chr3	198022430	23374226	0.118	12.1592
chr4	191154276	10743774	0.0562	6.3273
chr5	180915260	38371260	0.2121	15.9673
chr6	171115067	30822223	0.1801	15.6789
chr7	159138663	43413263	0.2728	28.2821
chr8	146364022	68860530	0.4705	25.4798
chr9	141213431	4903041	0.0347	1.1975
chr10	135534747	25724605	0.1898	17.0452
chr11	135006516	13500211	0.1	6.2752
chr12	133851895	14247191	0.1064	9.5576
chr13	115169878	18390430	0.1597	15.6836
chr14	107349540	25114957	0.234	17.6609
chr15	102531392	4419238	0.0431	2.3523
chr16	90354753	17219157	0.1906	11.9915
chr17	81195210	17379715	0.214	13.0279
chr18	78077248	2143664	0.0275	0.7017
chr19	59128983	1397357	0.0236	1.6818
chr20	63025520	4294174	0.0681	3.0175
chr21	48129895	2568541	0.0534	6.1646
chr22	51304566	2171588	0.0423	2.5245
chrMT	16571	83076	5.0133	3.5354
chrX	155270560	11769199	0.0758	6.799

chrY	59373566	128703	0.0022	0.224
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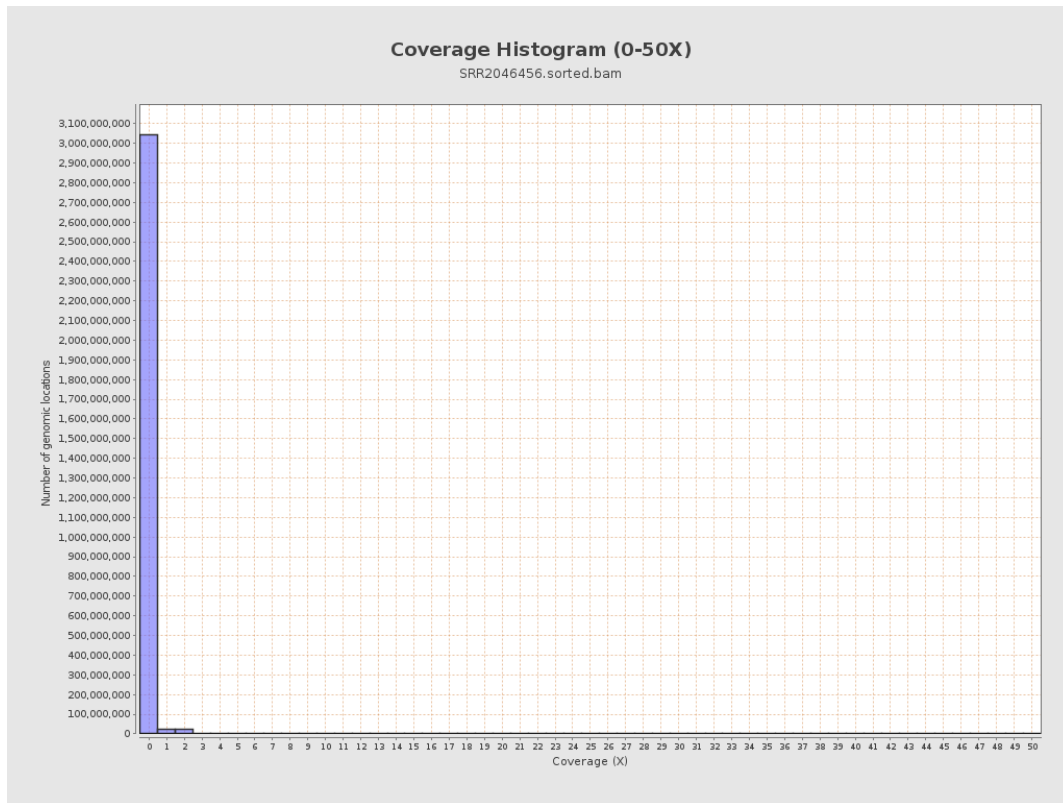
3. Results : Coverage across reference



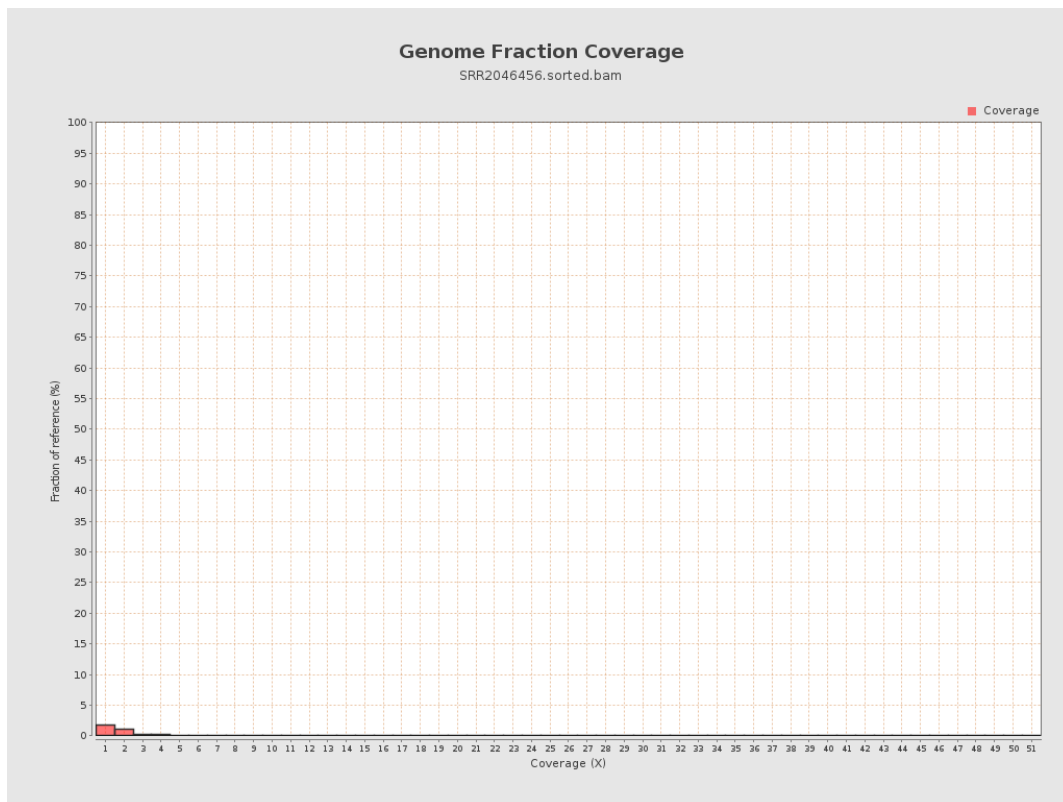
4. Results : Coverage Histogram



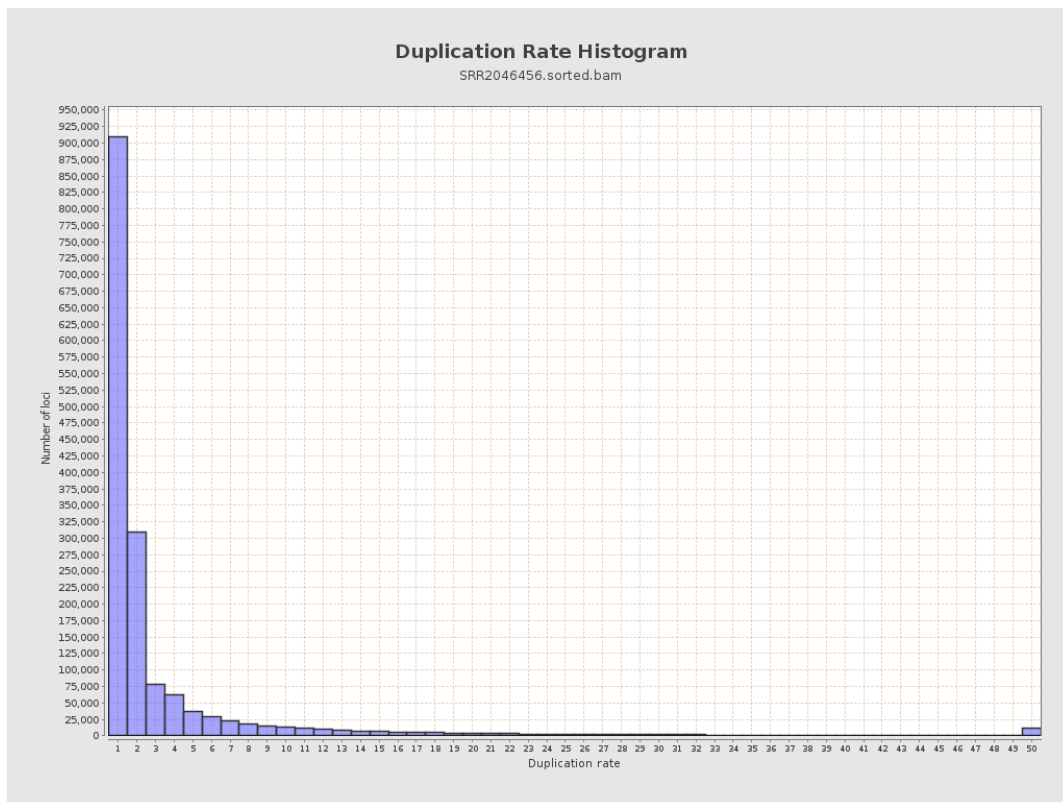
5. Results : Coverage Histogram (0-50X)



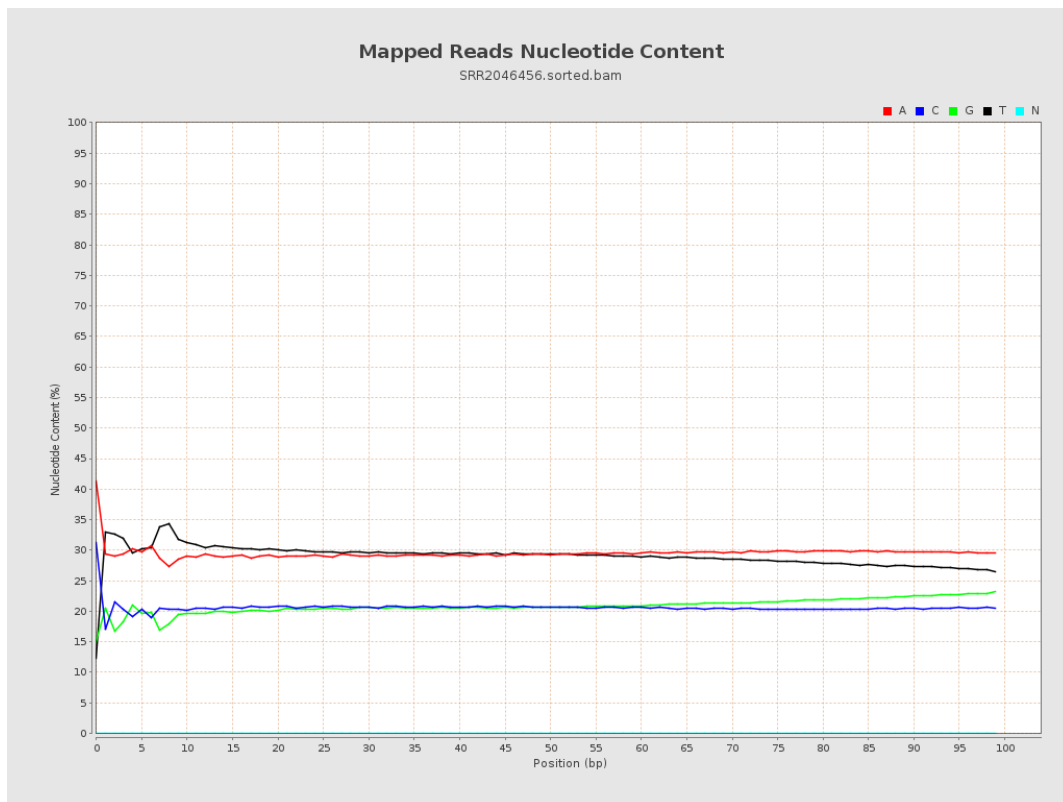
6. Results : Genome Fraction Coverage



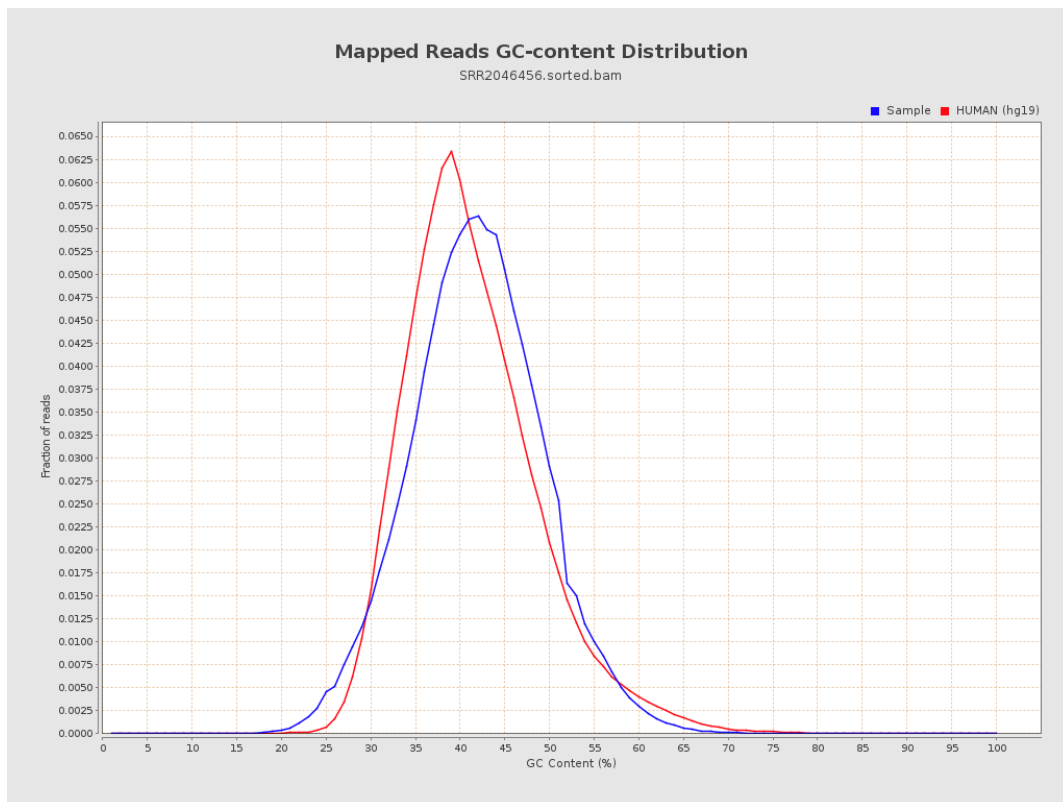
7. Results : Duplication Rate Histogram



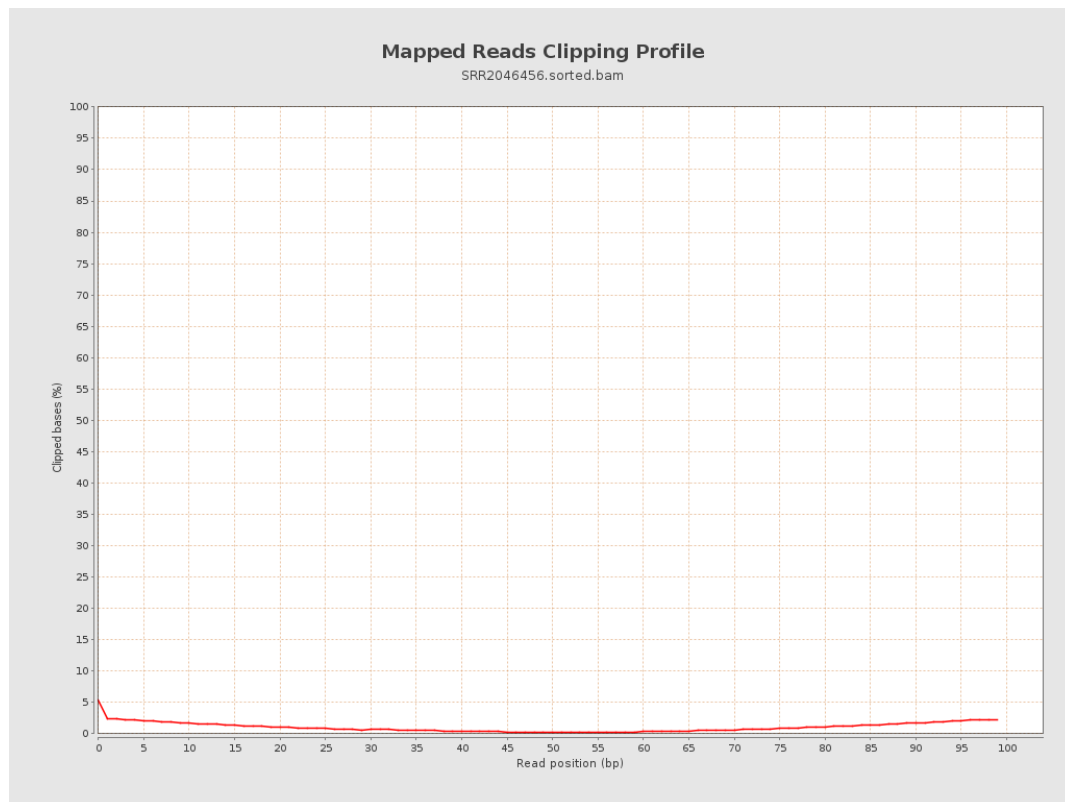
8. Results : Mapped Reads Nucleotide Content



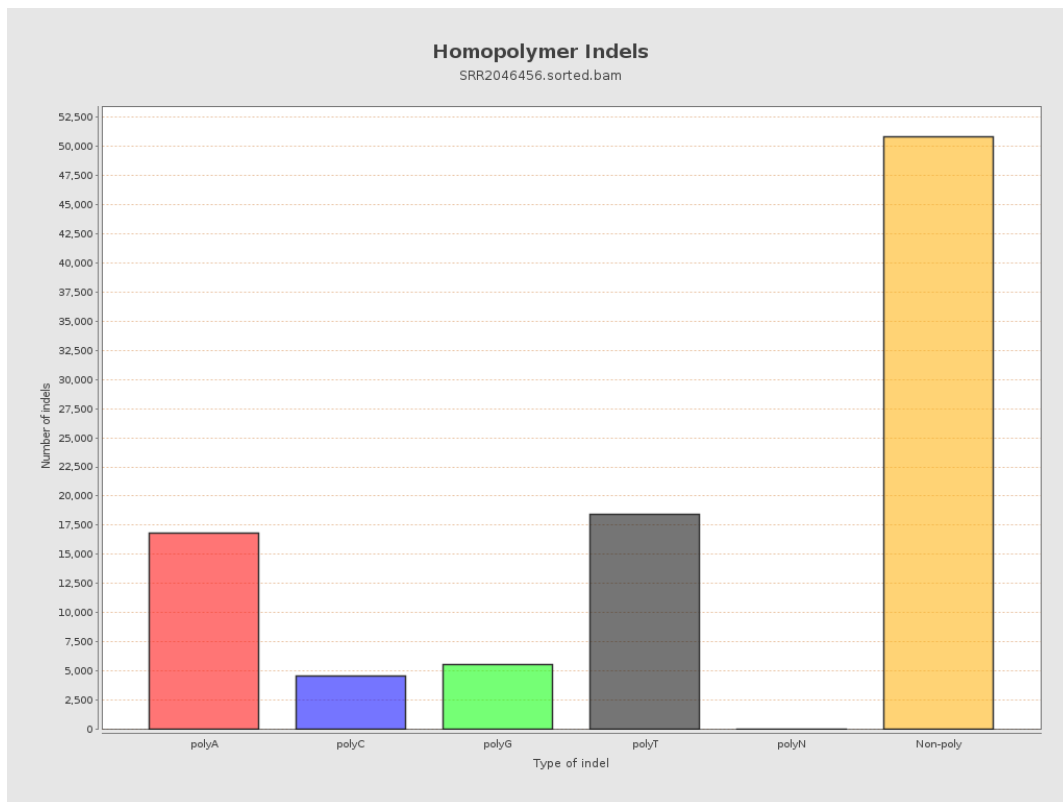
9. Results : Mapped Reads GC-content Distribution



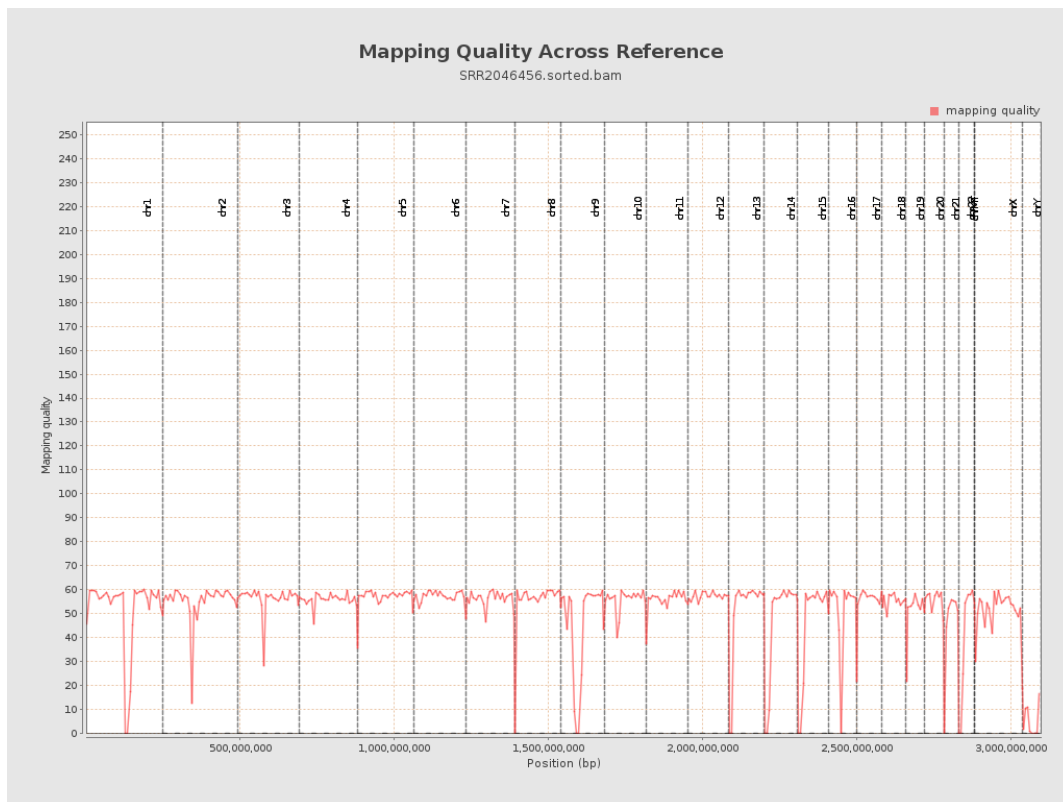
10. Results : Mapped Reads Clipping Profile



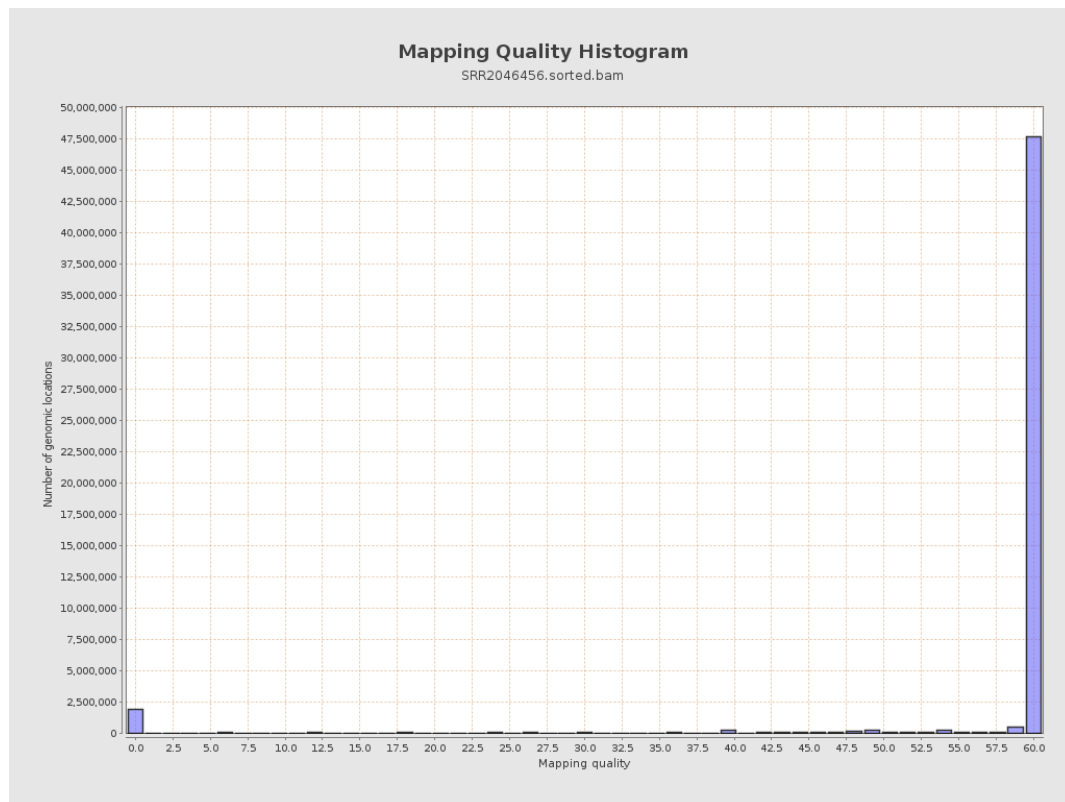
11. Results : Homopolymer Indels



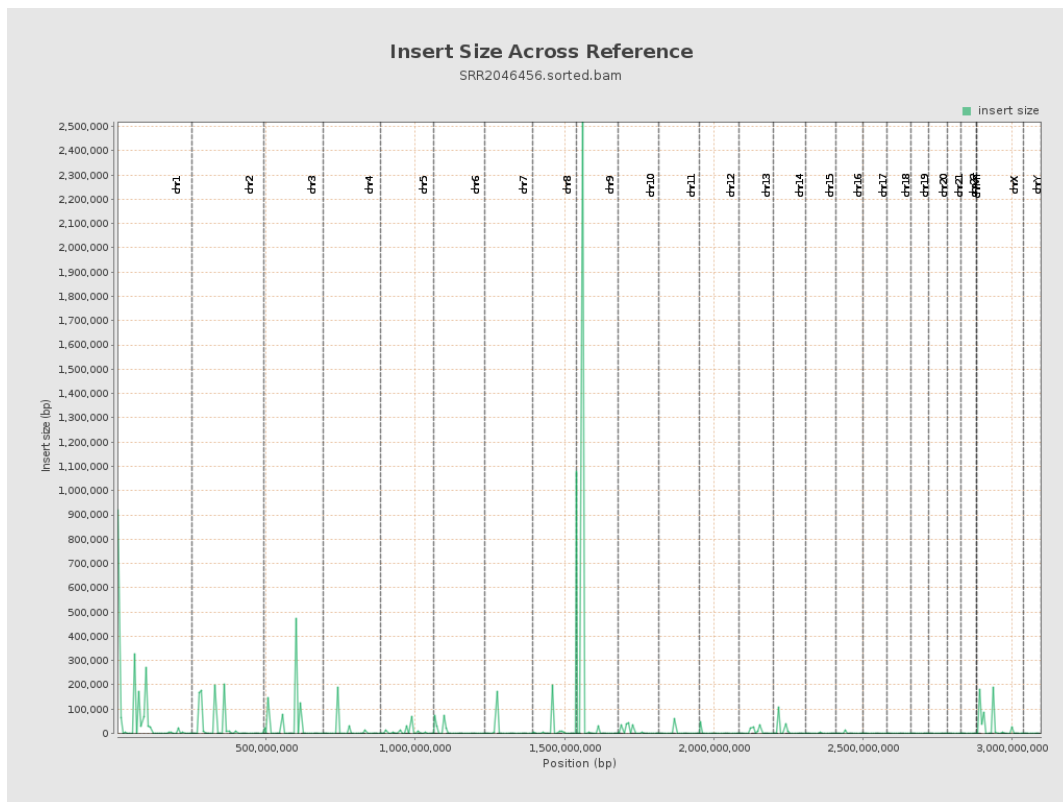
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

