

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 13:54:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046422.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_SRR2046422 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046422_1.fastq.gz SRR2046422_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 13:54:02 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046422.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	7,794,098
Mapped reads	7,747,206 / 99.4%
Unmapped reads	46,892 / 0.6%
Mapped paired reads	7,747,206 / 99.4%
Mapped reads, first in pair	3,877,228 / 49.75%
Mapped reads, second in pair	3,869,978 / 49.65%
Mapped reads, both in pair	7,714,162 / 98.97%
Mapped reads, singletons	33,044 / 0.42%
Secondary alignments	0
Supplementary alignments	54,729 / 0.7%
Read min/max/mean length	30 / 100 / 100.29
Duplicated reads (estimated)	5,674,110 / 72.8%
Duplication rate	42.35%
Clipped reads	1,565,991 / 20.09%

2.2. ACGT Content

Number/percentage of A's	218,425,877 / 29.12%
Number/percentage of C's	157,095,249 / 20.94%
Number/percentage of T's	219,754,243 / 29.29%
Number/percentage of G's	154,837,226 / 20.64%
Number/percentage of N's	70,033 / 0.01%

GC Percentage	41.58%
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2.3. Coverage

Mean	0.2424
Standard Deviation	16.6909

2.4. Mapping Quality

Mean Mapping Quality	53.12
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2.5. Insert size

Mean	16,331.45
Standard Deviation	1,206,434.33
P25/Median/P75	110 / 140 / 179

2.6. Mismatches and indels

General error rate	0.43%
Mismatches	3,094,392
Insertions	65,834
Mapped reads with at least one insertion	0.83%
Deletions	78,369
Mapped reads with at least one deletion	0.98%
Homopolymer indels	48.83%

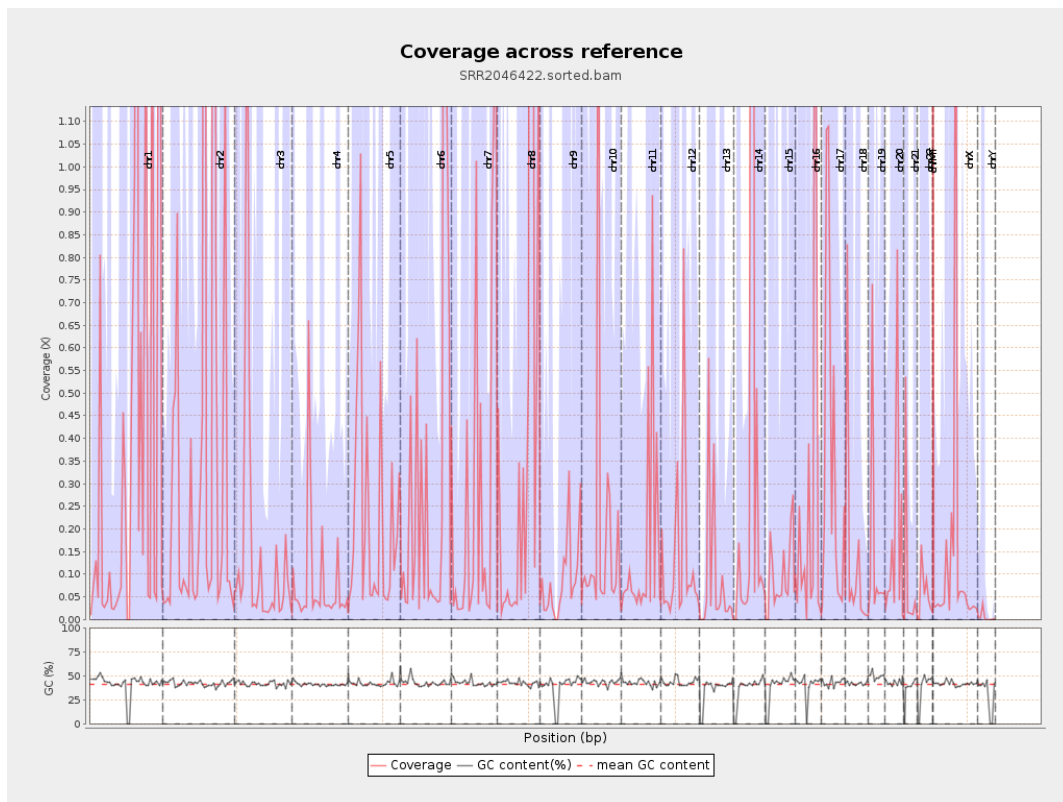
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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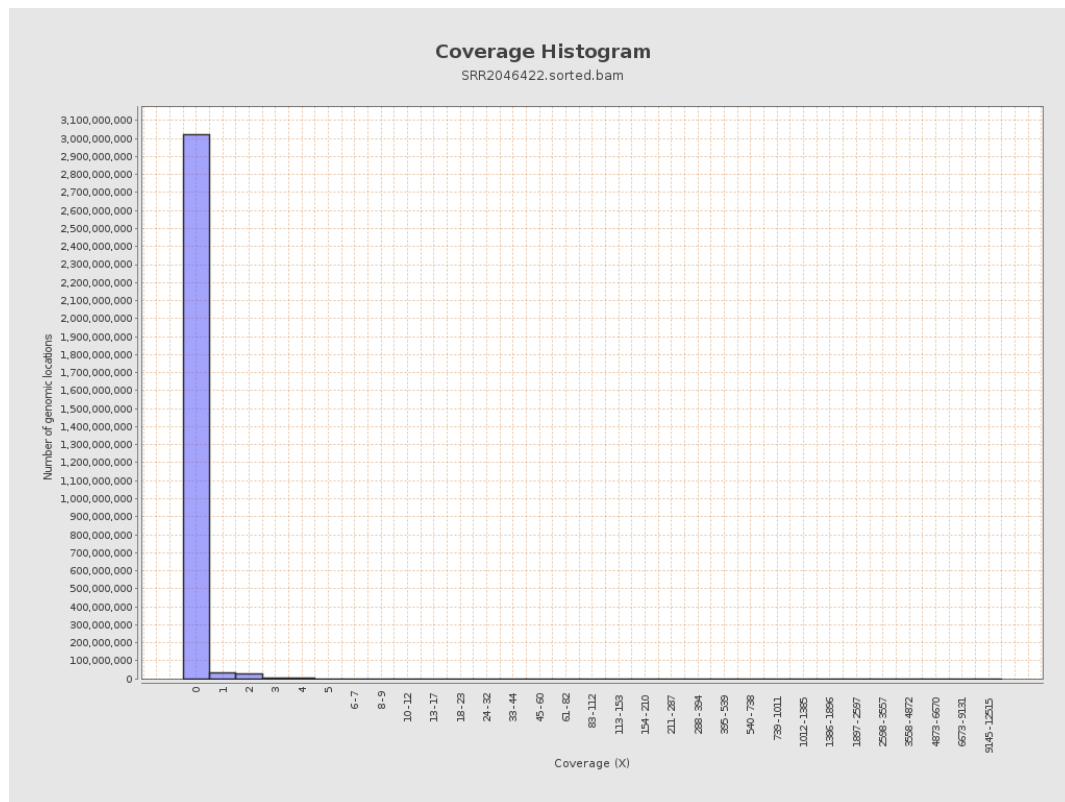
		bases	coverage	deviation
chr1	249250621	103284722	0.4144	21.9949
chr2	243199373	116242970	0.478	28.6836
chr3	198022430	31372246	0.1584	12.0939
chr4	191154276	16252351	0.085	4.5142
chr5	180915260	40541204	0.2241	11.4479
chr6	171115067	54044568	0.3158	19.9085
chr7	159138663	46761649	0.2938	18.0262
chr8	146364022	81120150	0.5542	28.268
chr9	141213431	12264444	0.0869	4.6848
chr10	135534747	27755646	0.2048	14.1022
chr11	135006516	20911099	0.1549	9.9808
chr12	133851895	17547461	0.1311	6.4131
chr13	115169878	10085531	0.0876	6.0163
chr14	107349540	51609123	0.4808	24.6511
chr15	102531392	10222214	0.0997	5.2085
chr16	90354753	22942860	0.2539	15.3136
chr17	81195210	27838008	0.3429	15.472
chr18	78077248	9933672	0.1272	7.2662
chr19	59128983	8545241	0.1445	5.9144
chr20	63025520	11611659	0.1842	13.5287
chr21	48129895	4793989	0.0996	12.2606
chr22	51304566	2945169	0.0574	4.4787
chrMT	16571	40601	2.4501	2.3025
chrX	155270560	21378213	0.1377	19.7708

chrY	59373566	352731	0.0059	1.4092
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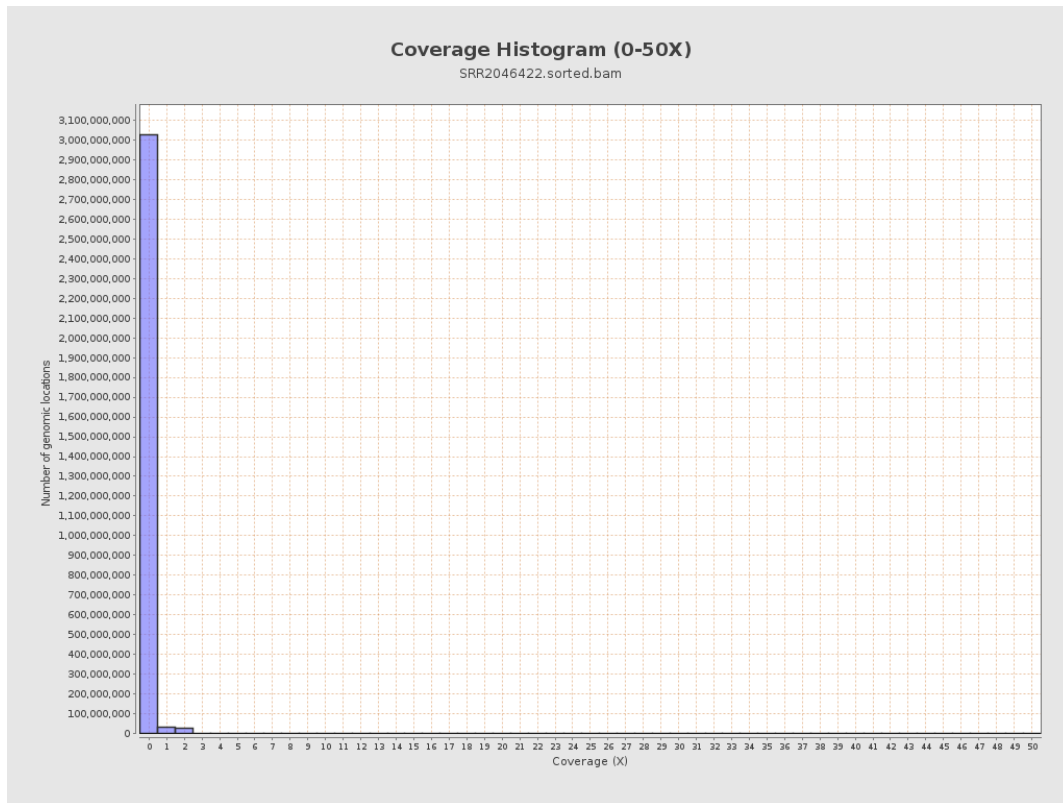
3. Results : Coverage across reference



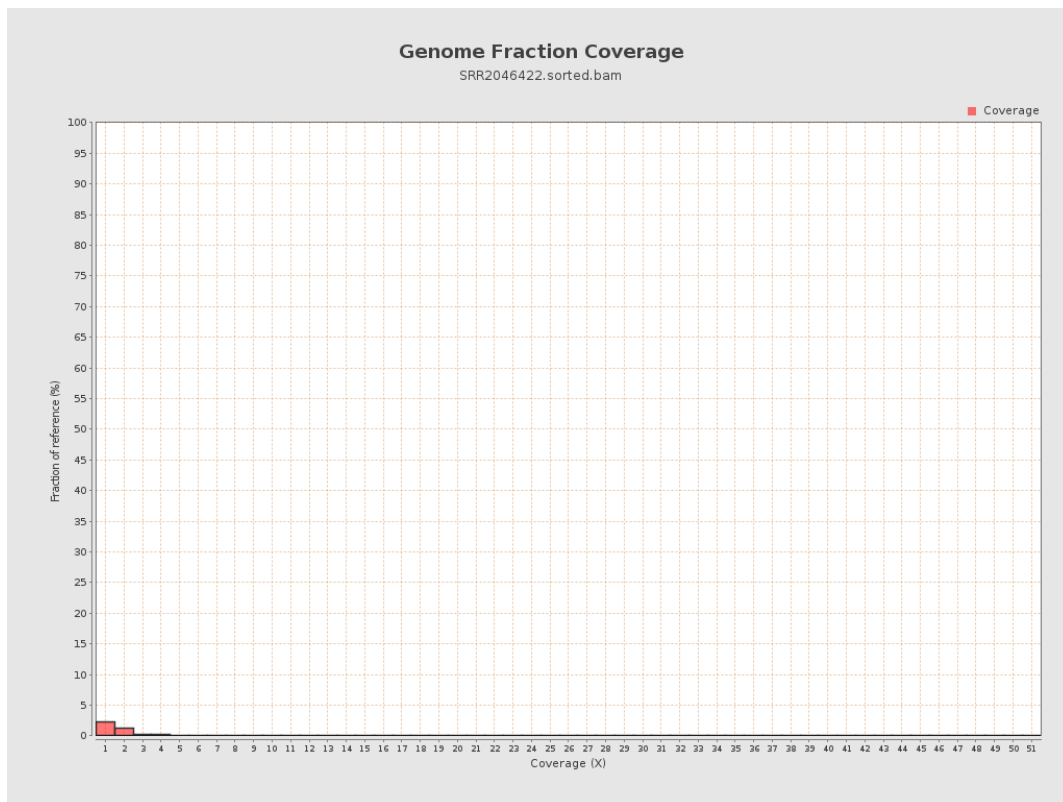
4. Results : Coverage Histogram



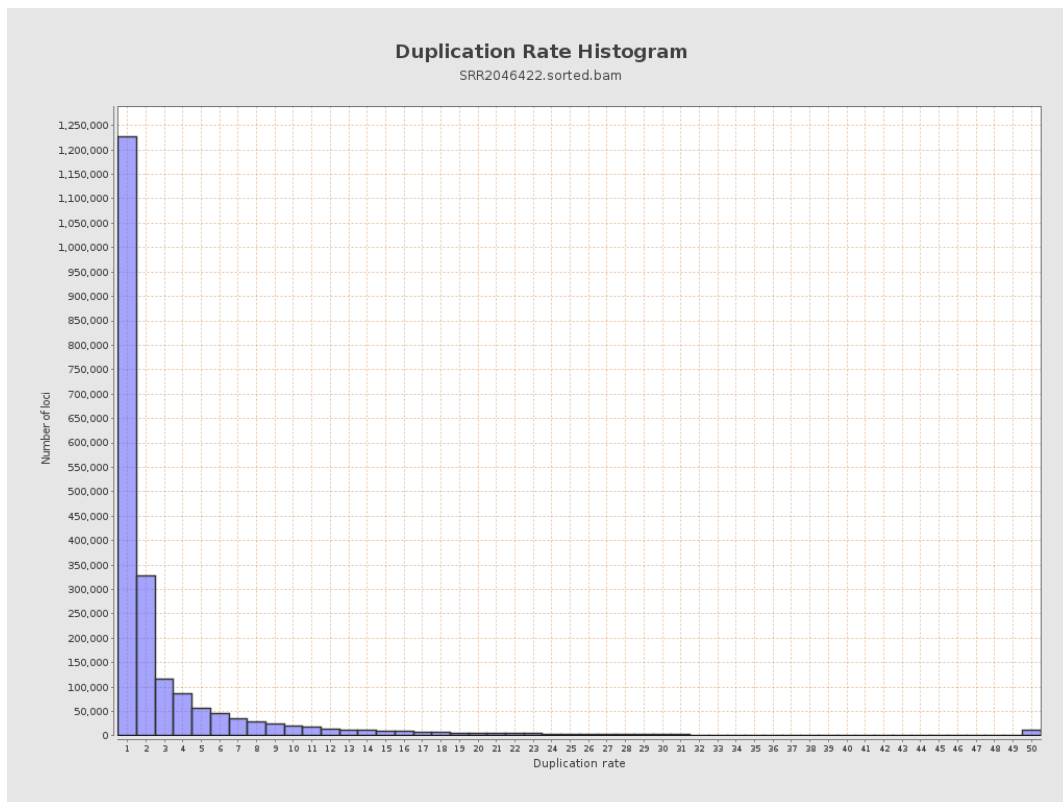
5. Results : Coverage Histogram (0-50X)



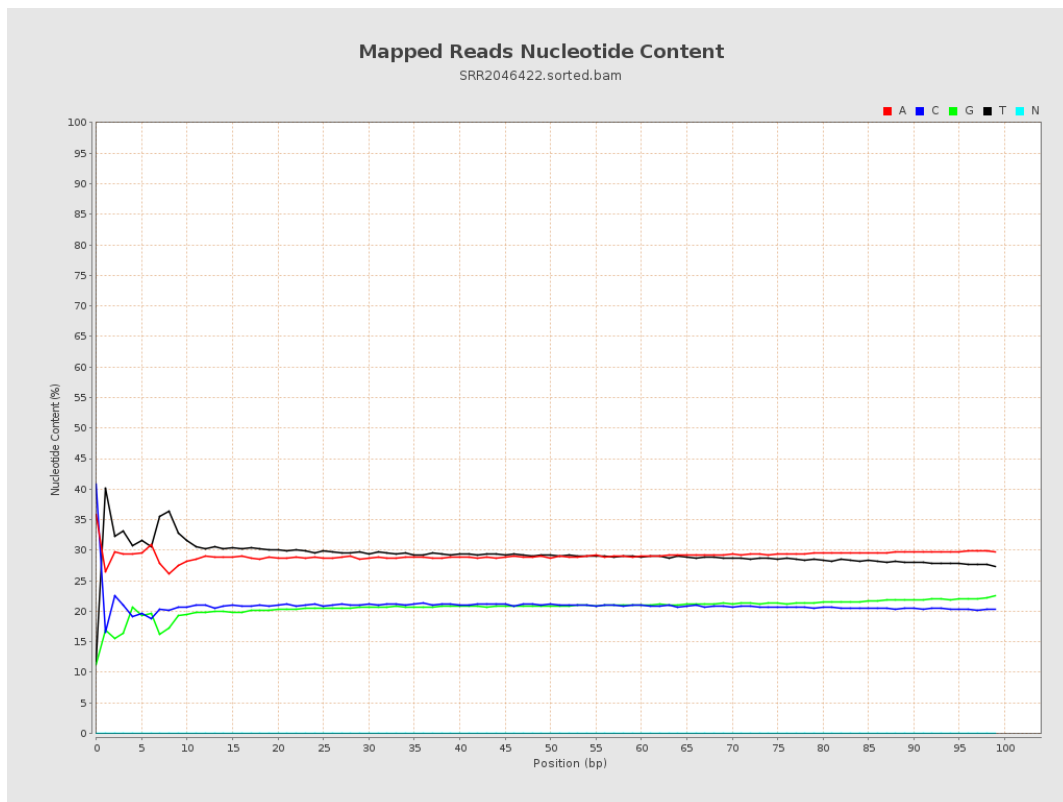
6. Results : Genome Fraction Coverage



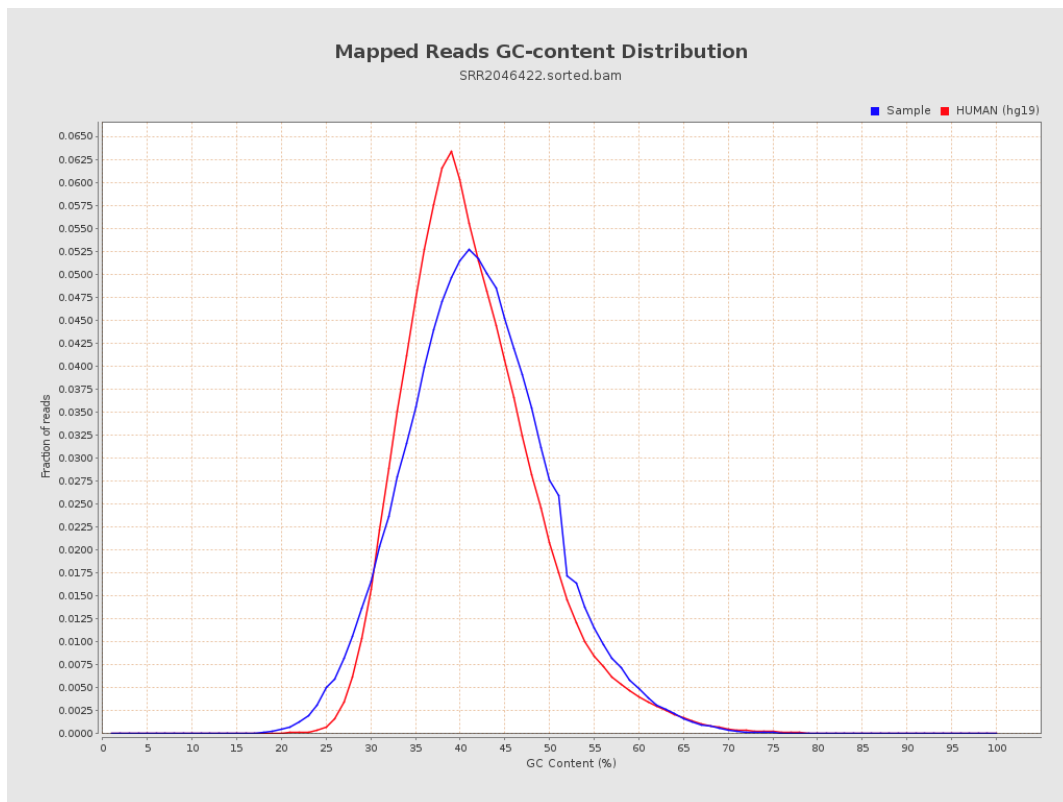
7. Results : Duplication Rate Histogram



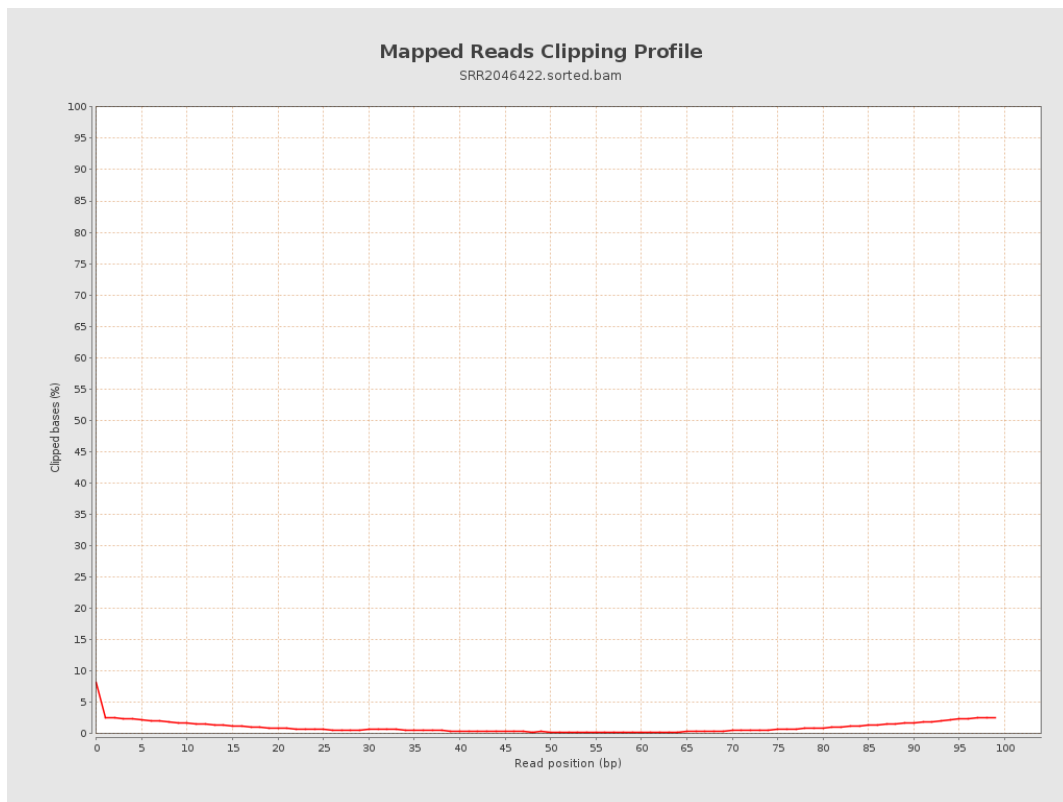
8. Results : Mapped Reads Nucleotide Content



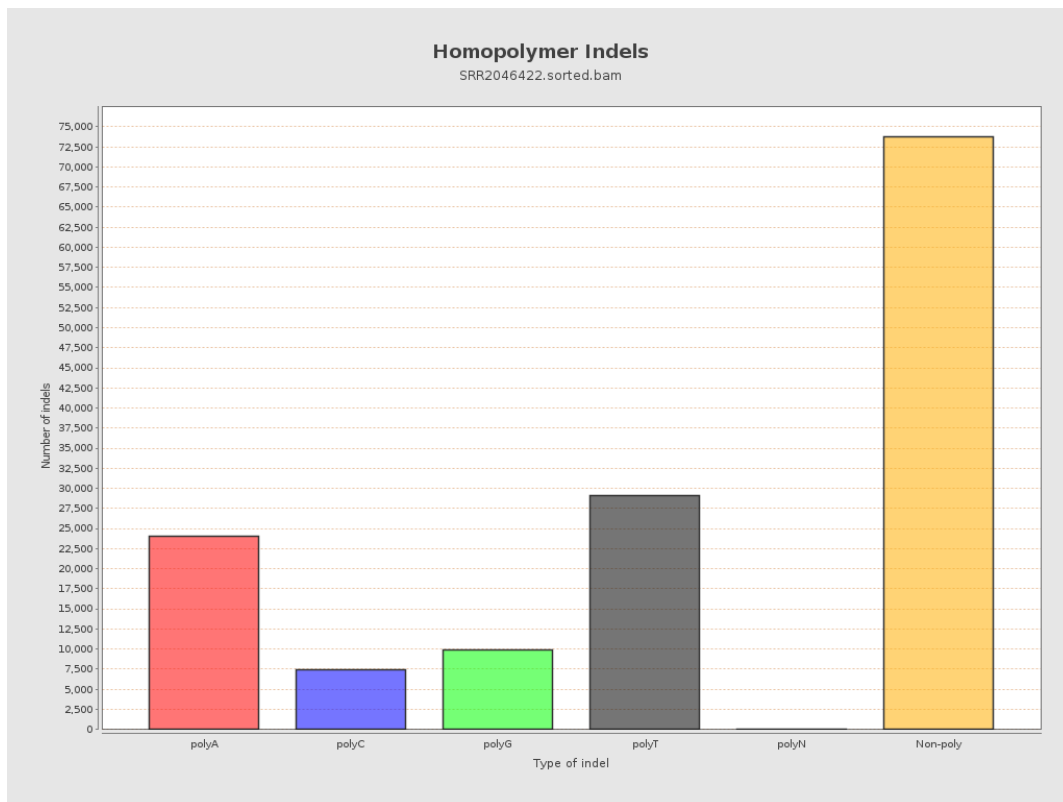
9. Results : Mapped Reads GC-content Distribution



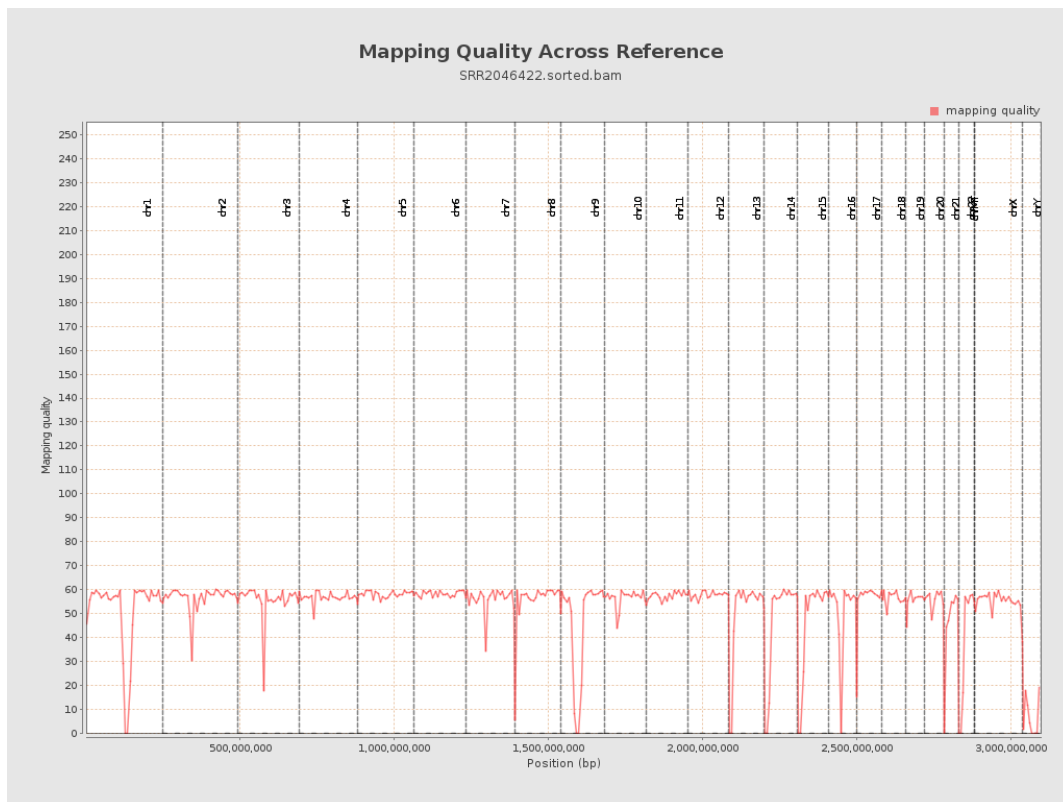
10. Results : Mapped Reads Clipping Profile



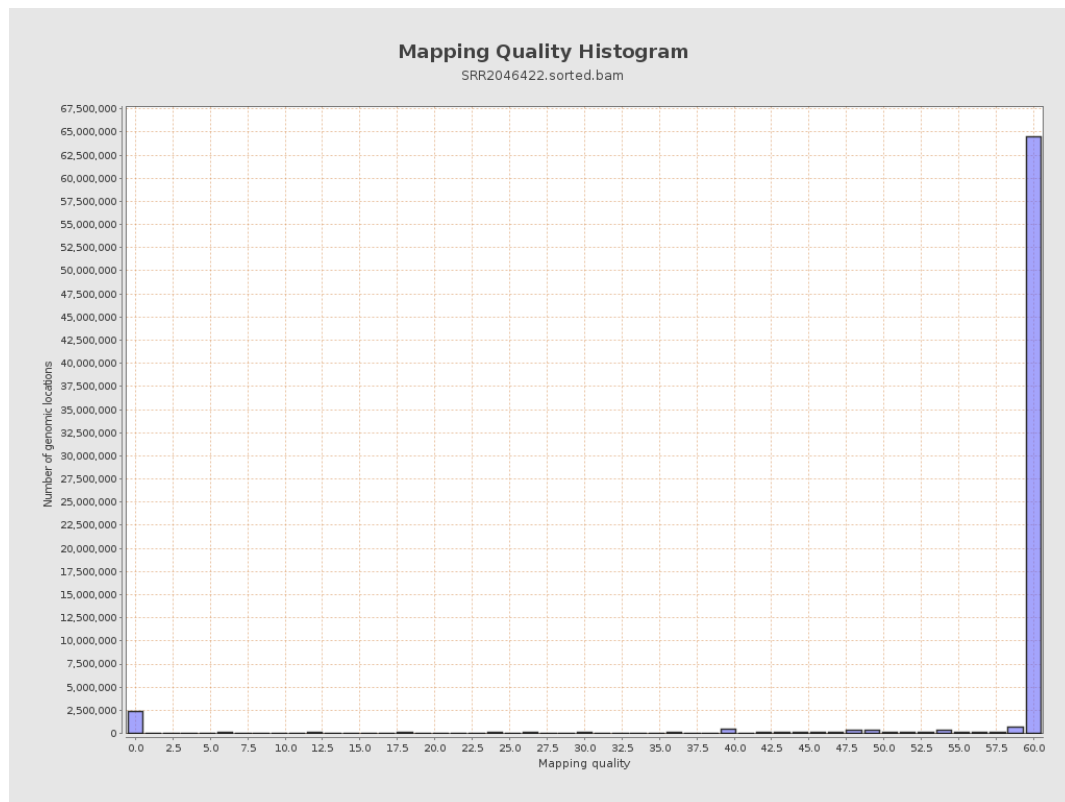
11. Results : Homopolymer Indels



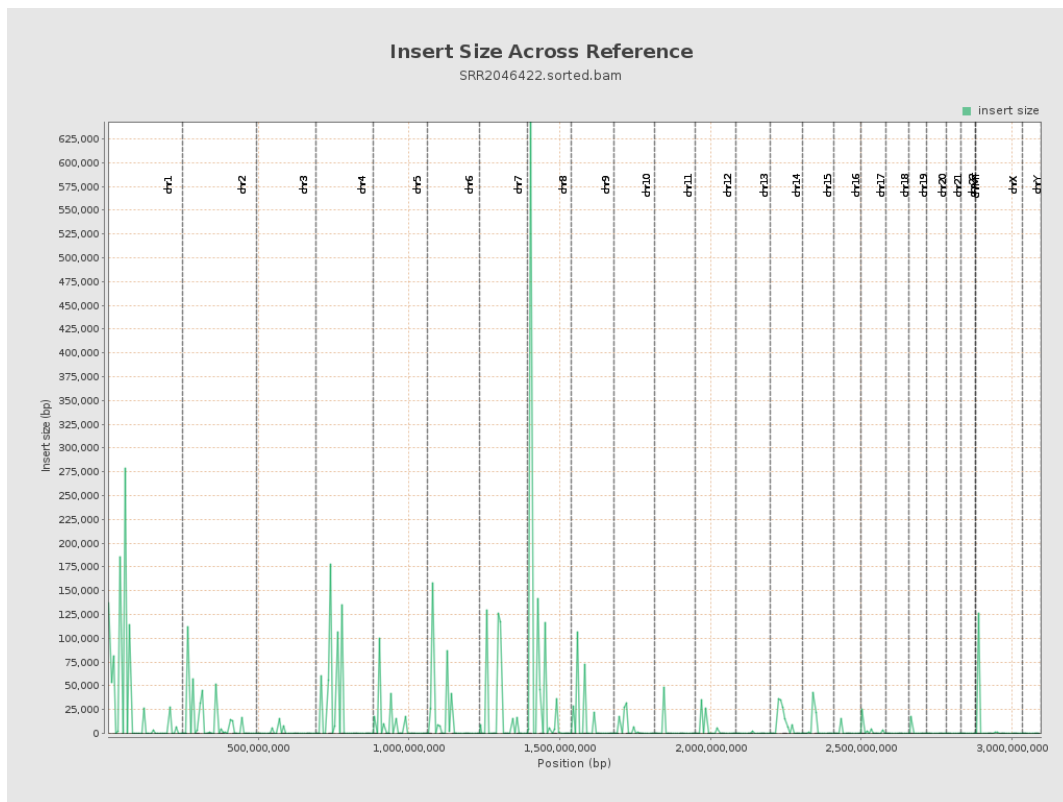
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

