

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/15 01:53:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR5038422.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_SRR5038422 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR5038422_1.fastq.gz SRR5038422_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 15 01:53:31 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR5038422.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	18,986,522
Mapped reads	17,546,904 / 92.42%
Unmapped reads	1,439,618 / 7.58%
Mapped paired reads	17,546,904 / 92.42%
Mapped reads, first in pair	8,900,018 / 46.88%
Mapped reads, second in pair	8,646,886 / 45.54%
Mapped reads, both in pair	17,237,728 / 90.79%
Mapped reads, singletons	309,176 / 1.63%
Secondary alignments	0
Supplementary alignments	244,837 / 1.29%
Read min/max/mean length	30 / 150 / 150.65
Duplicated reads (estimated)	3,474,788 / 18.3%
Duplication rate	14.34%
Clipped reads	8,046,670 / 42.38%

2.2. ACGT Content

Number/percentage of A's	673,443,448 / 28.41%
Number/percentage of C's	476,918,197 / 20.12%
Number/percentage of T's	682,413,318 / 28.79%
Number/percentage of G's	537,487,232 / 22.67%
Number/percentage of N's	192,285 / 0.01%

GC Percentage	42.79%
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2.3. Coverage

Mean	0.7662
Standard Deviation	8.859

2.4. Mapping Quality

Mean Mapping Quality	53.52
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2.5. Insert size

Mean	84,976.17
Standard Deviation	2,875,138.49
P25/Median/P75	197 / 248 / 313

2.6. Mismatches and indels

General error rate	1.28%
Mismatches	29,402,263
Insertions	399,043
Mapped reads with at least one insertion	2.17%
Deletions	831,282
Mapped reads with at least one deletion	4.57%
Homopolymer indels	47.97%

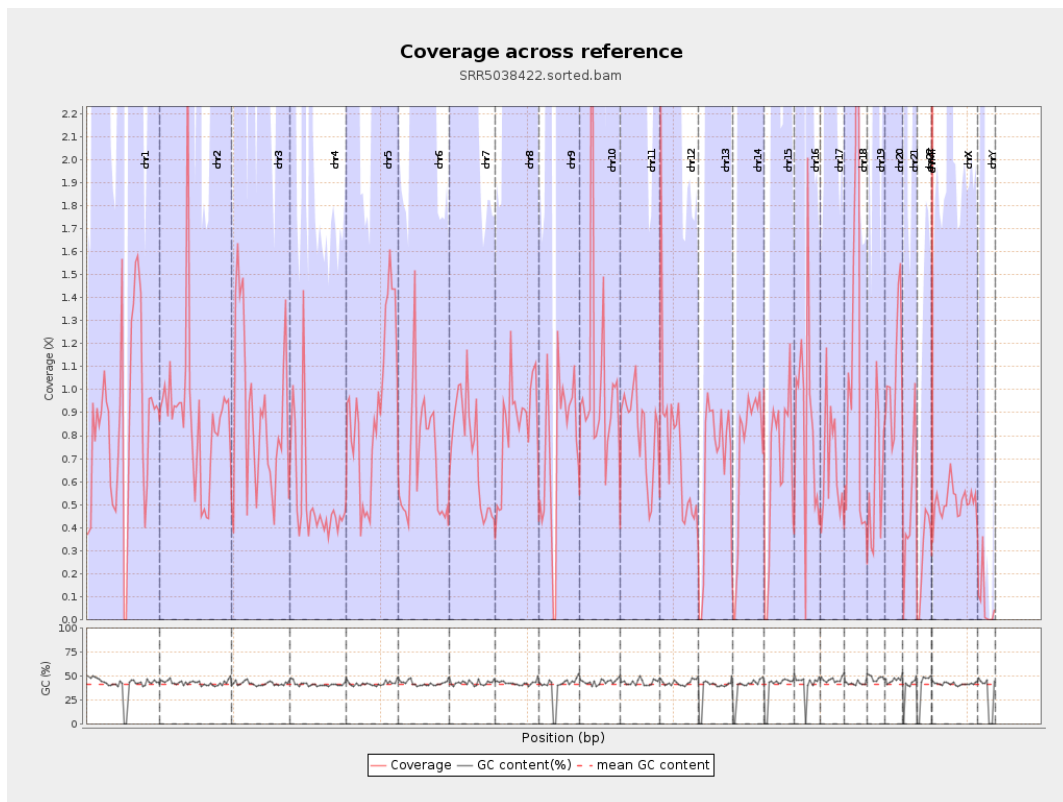
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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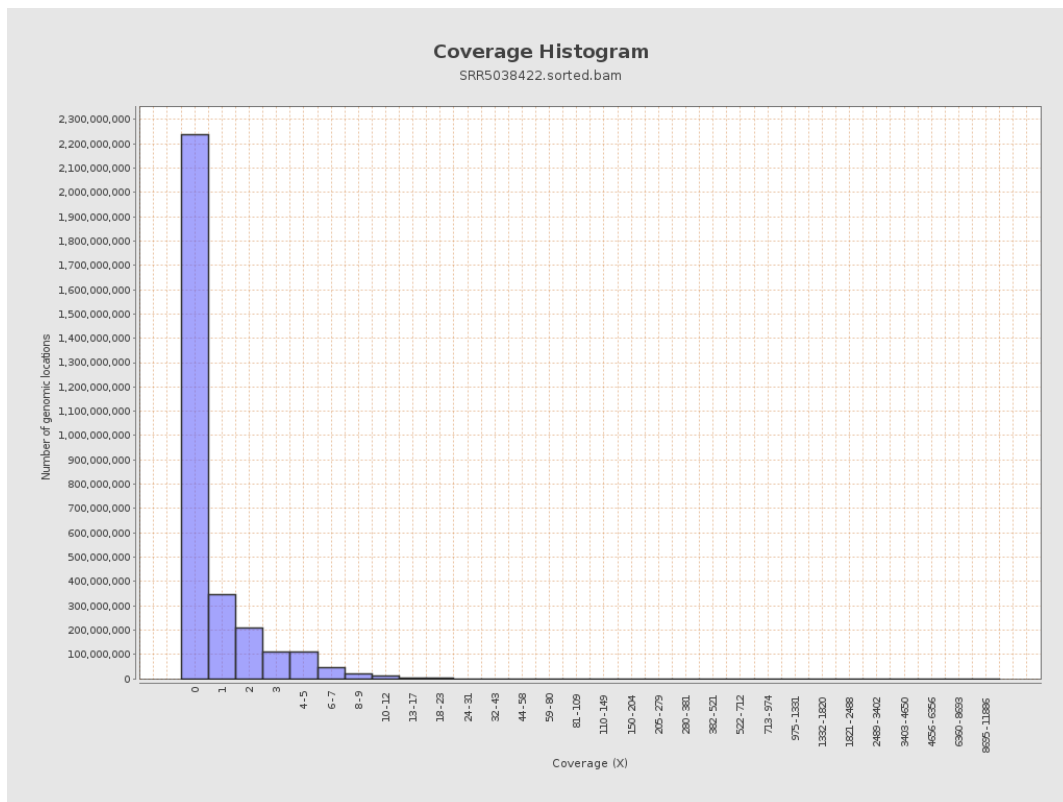
		bases	coverage	deviation
chr1	249250621	212460183	0.8524	12.2943
chr2	243199373	215087374	0.8844	10.3567
chr3	198022430	175957846	0.8886	1.9472
chr4	191154276	100355594	0.525	8.5358
chr5	180915260	165498725	0.9148	1.9077
chr6	171115067	119993555	0.7012	7.0671
chr7	159138663	115801790	0.7277	8.5215
chr8	146364022	126018326	0.861	3.5681
chr9	141213431	103147952	0.7304	14.4013
chr10	135534747	145543388	1.0738	22.3589
chr11	135006516	110335731	0.8173	7.2124
chr12	133851895	101000946	0.7546	1.882
chr13	115169878	78813178	0.6843	1.5992
chr14	107349540	78702392	0.7331	1.7449
chr15	102531392	66998700	0.6534	1.602
chr16	90354753	75810560	0.839	8.7436
chr17	81195210	54181630	0.6673	11.3211
chr18	78077248	95512159	1.2233	10.0276
chr19	59128983	34796835	0.5885	5.6175
chr20	63025520	67452725	1.0702	3.3178
chr21	48129895	24140019	0.5016	4.1303
chr22	51304566	14785715	0.2882	1.0179
chrMT	16571	5928005	357.7337	210.8343
chrX	155270560	79344699	0.511	2.0344

chrY	59373566	4372205	0.0736	8.474
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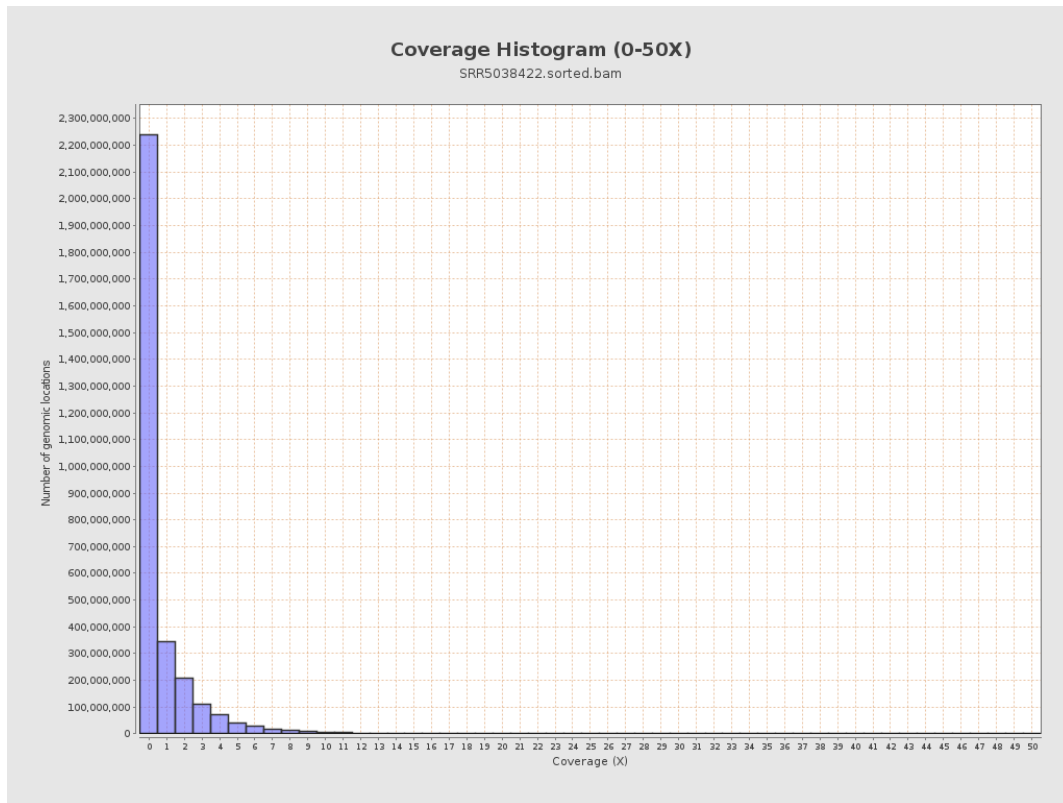
3. Results : Coverage across reference



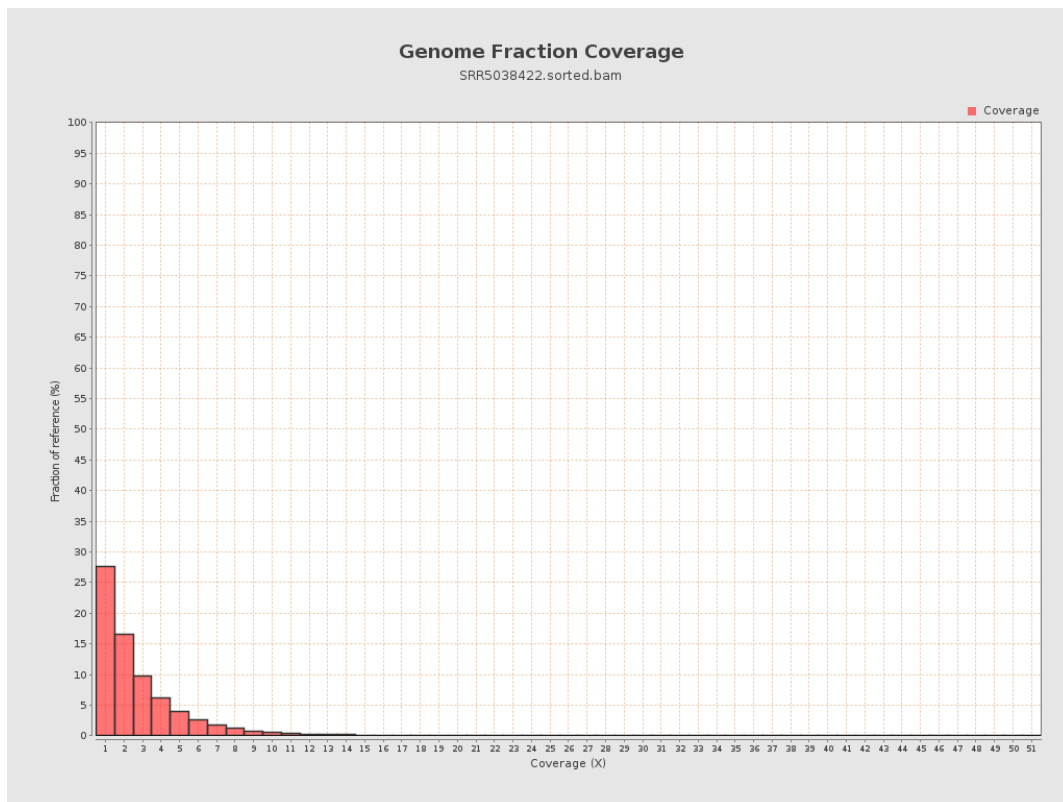
4. Results : Coverage Histogram



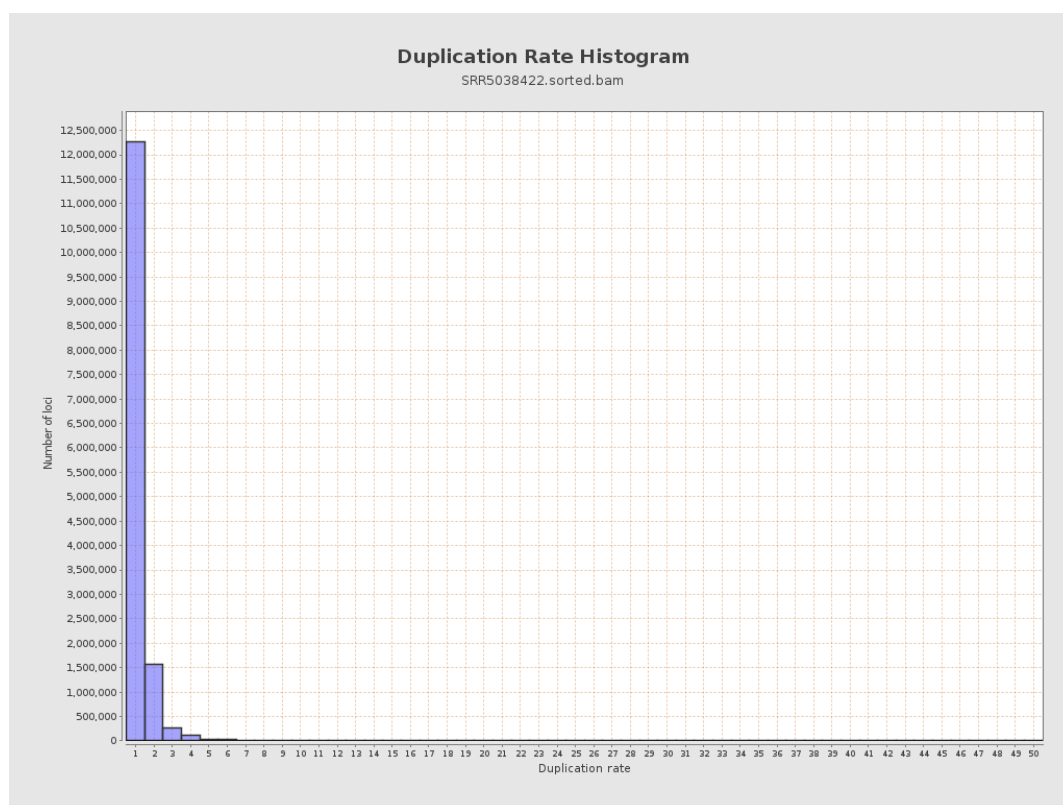
5. Results : Coverage Histogram (0-50X)



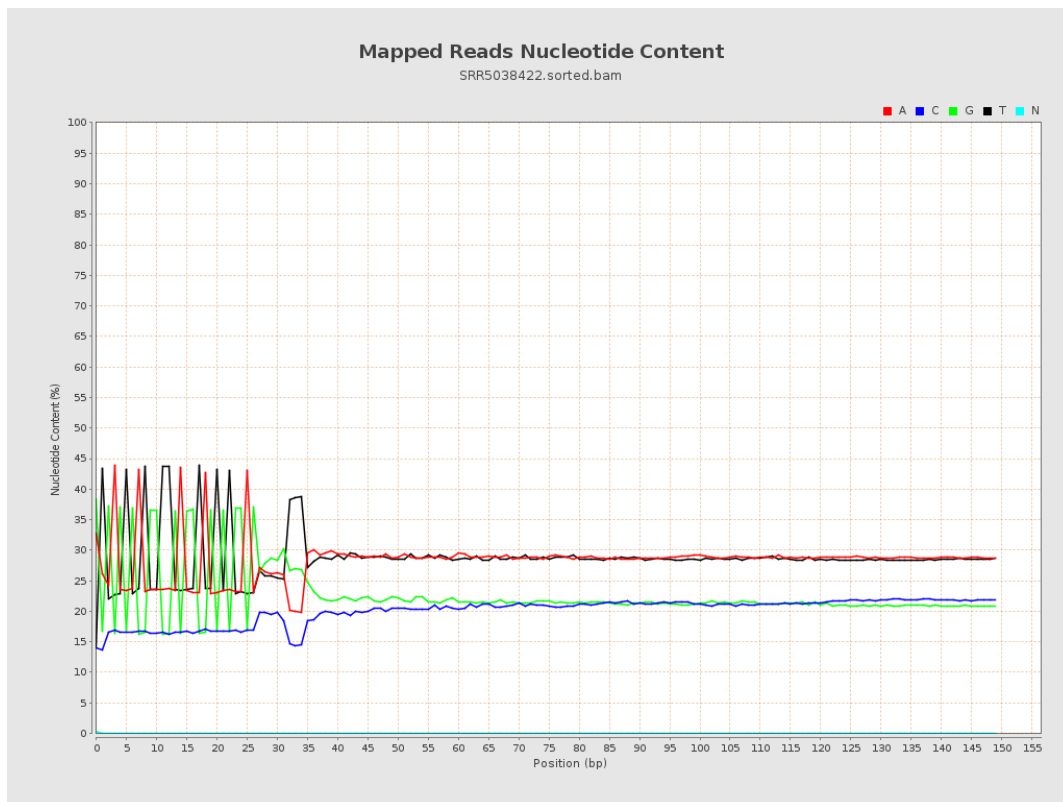
6. Results : Genome Fraction Coverage



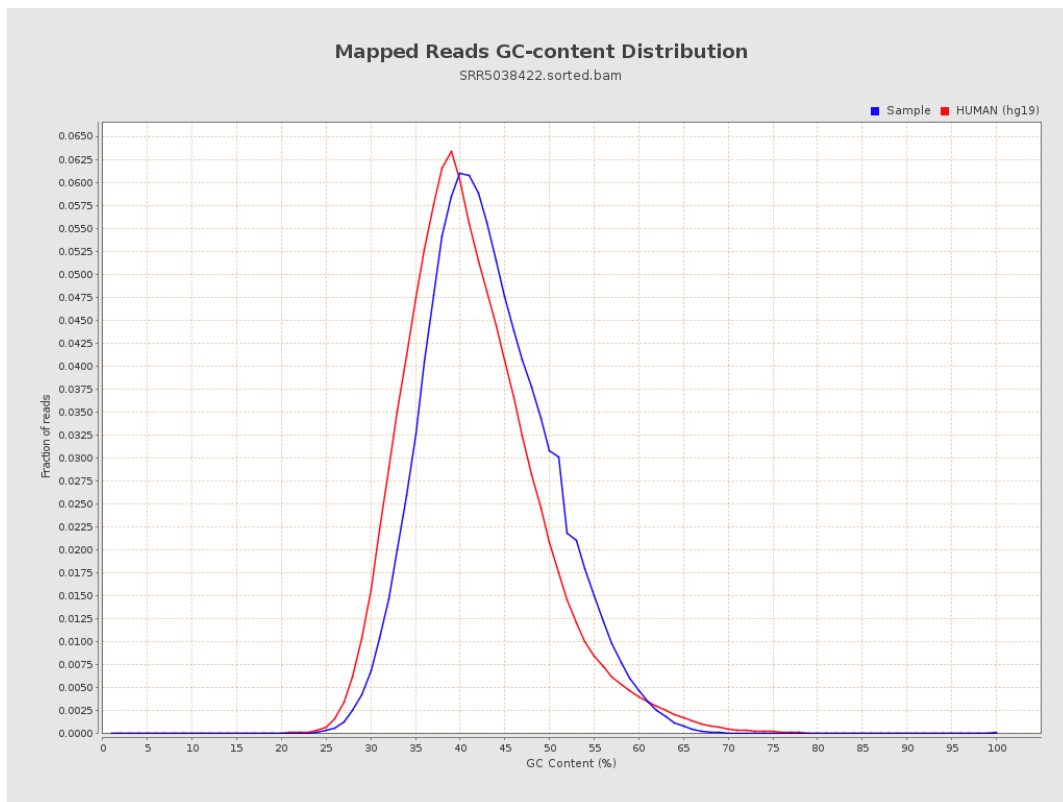
7. Results : Duplication Rate Histogram



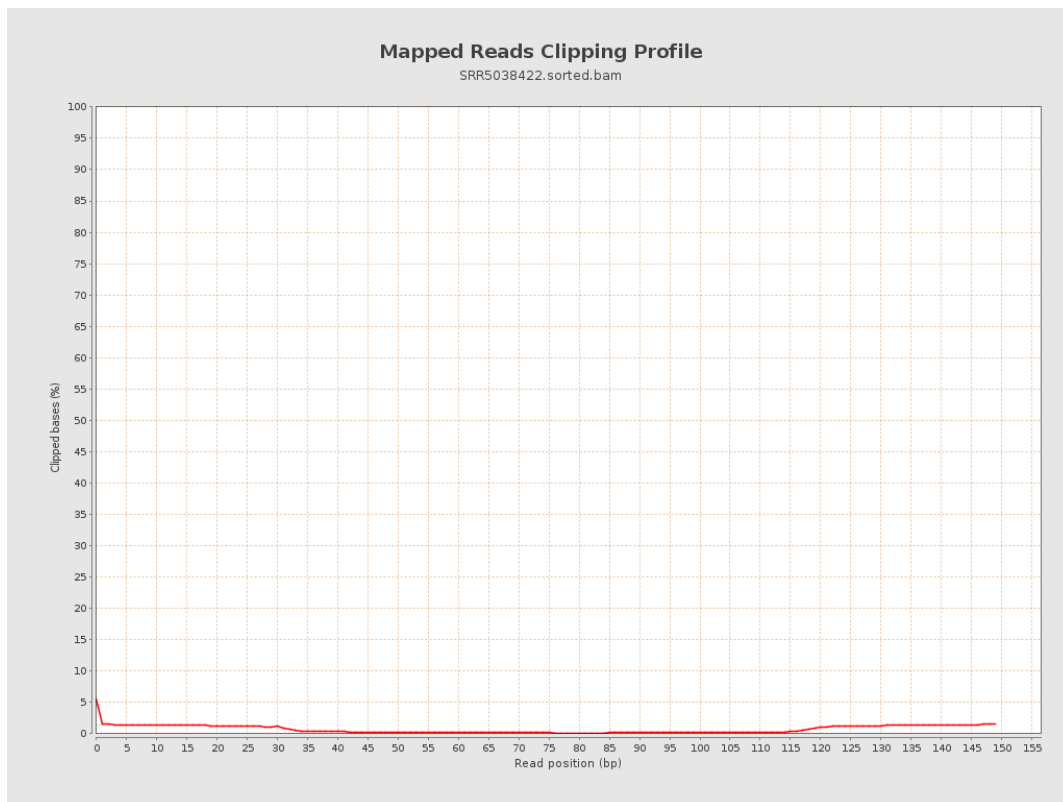
8. Results : Mapped Reads Nucleotide Content



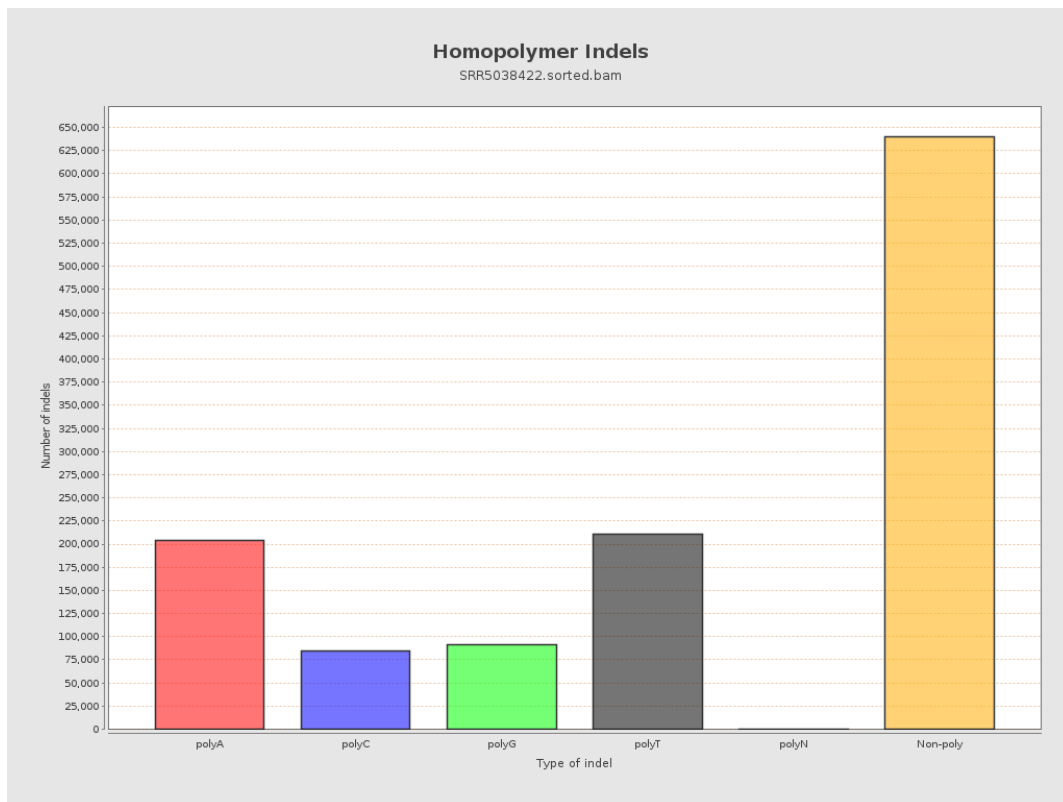
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



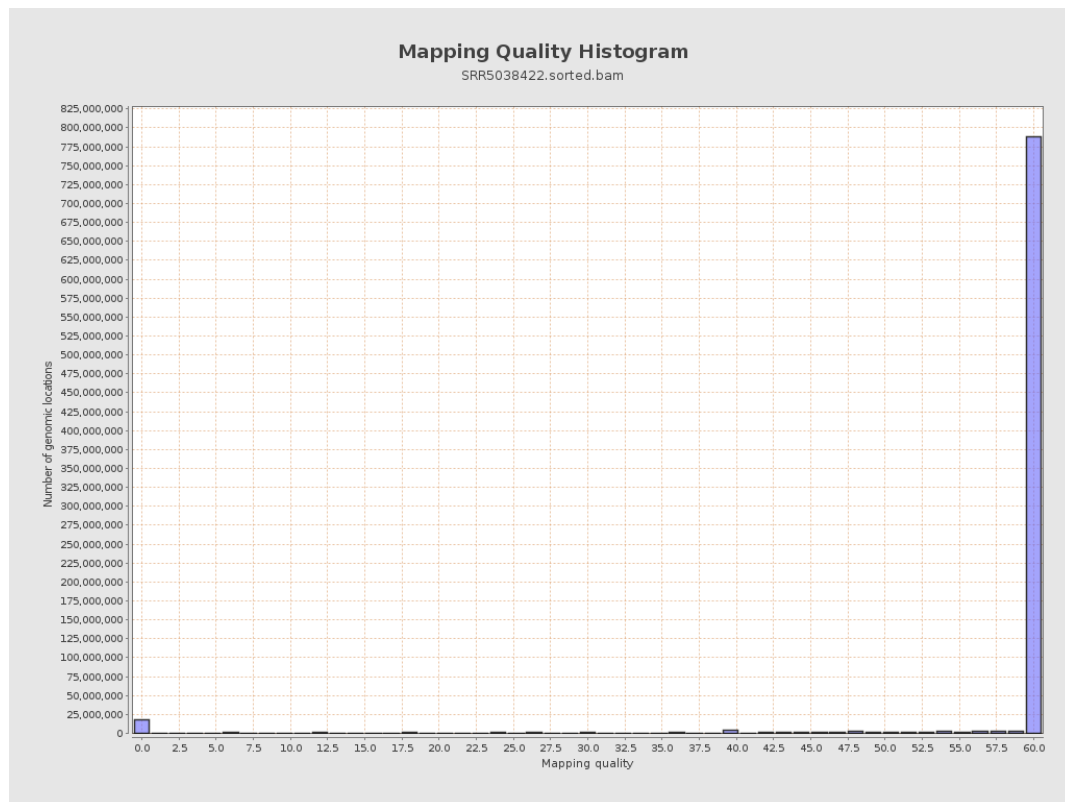
11. Results : Homopolymer Indels



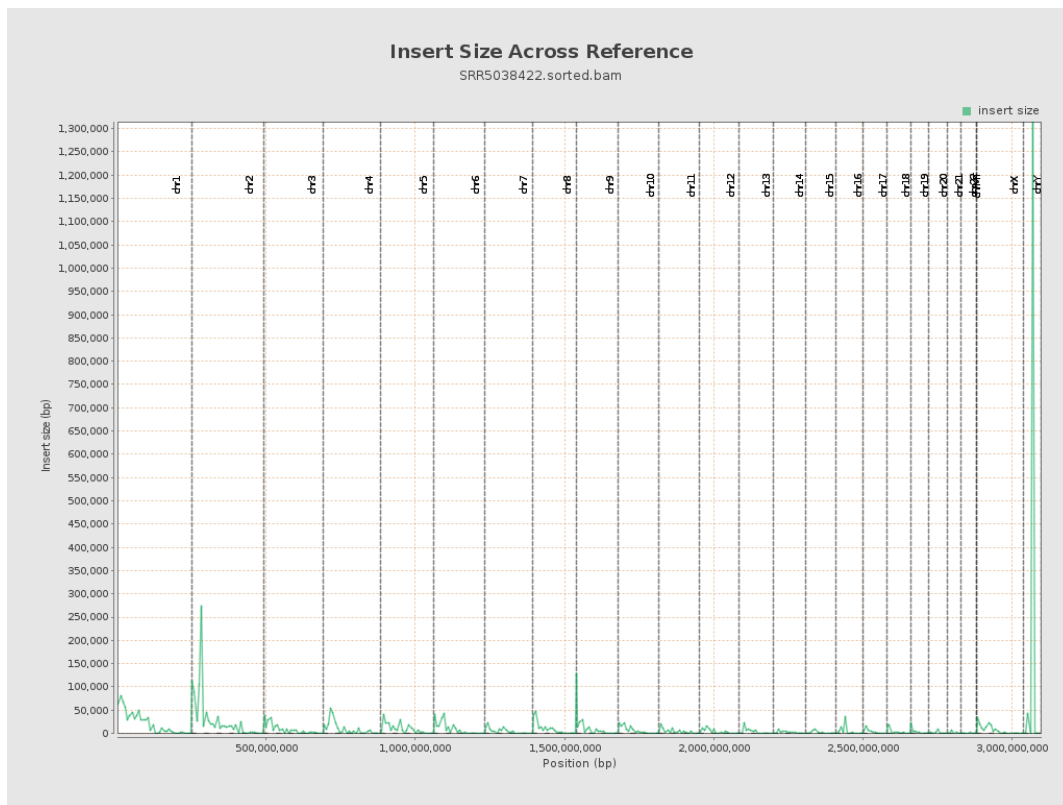
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

