

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/23 15:15:51

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504421.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_SRR504421 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504421_1.fastq.gz SRR504421_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Jun 23 15:15:50 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504421.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	133,556,838
Mapped reads	132,207,827 / 98.99%
Unmapped reads	1,349,011 / 1.01%
Mapped paired reads	132,207,827 / 98.99%
Mapped reads, first in pair	66,129,993 / 49.51%
Mapped reads, second in pair	66,077,834 / 49.48%
Mapped reads, both in pair	131,784,254 / 98.67%
Mapped reads, singletons	423,573 / 0.32%
Secondary alignments	0
Supplementary alignments	2,189,502 / 1.64%
Read min/max/mean length	30 / 100 / 99.67
Duplicated reads (estimated)	63,047,946 / 47.21%
Duplication rate	33.51%
Clipped reads	67,661,330 / 50.66%

2.2. ACGT Content

Number/percentage of A's	3,749,185,425 / 29.72%
Number/percentage of C's	2,544,239,397 / 20.17%
Number/percentage of T's	3,769,726,975 / 29.88%
Number/percentage of G's	2,550,353,084 / 20.22%
Number/percentage of N's	1,896,472 / 0.02%

GC Percentage	40.38%
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2.3. Coverage

Mean	4.0764
Standard Deviation	153.8157

2.4. Mapping Quality

Mean Mapping Quality	52.73
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2.5. Insert size

Mean	80,894.06
Standard Deviation	2,643,918.94
P25/Median/P75	132 / 163 / 196

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	73,315,677
Insertions	1,252,783
Mapped reads with at least one insertion	0.94%
Deletions	2,421,492
Mapped reads with at least one deletion	1.81%
Homopolymer indels	48.08%

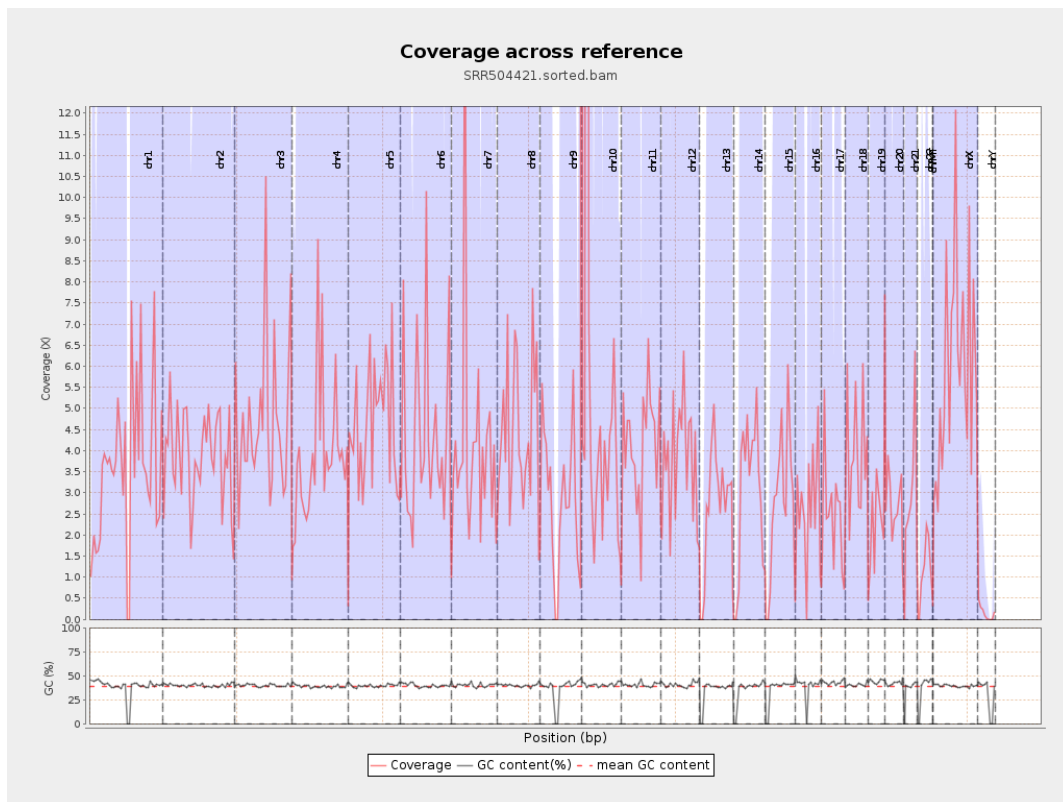
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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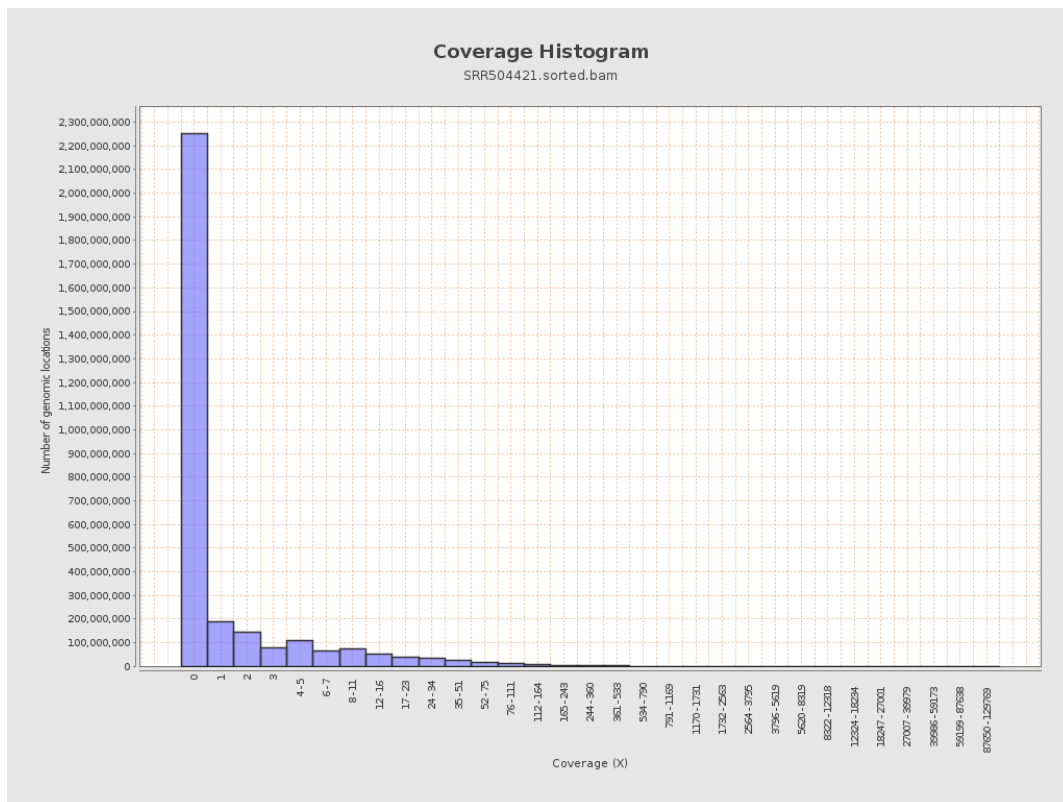
		bases	coverage	deviation
chr1	249250621	896293874	3.596	33.5271
chr2	243199373	944739820	3.8846	22.0825
chr3	198022430	914730524	4.6193	34.6176
chr4	191154276	749905022	3.923	34.1633
chr5	180915260	834850534	4.6146	30.8745
chr6	171115067	750858440	4.388	38.8198
chr7	159138663	648320794	4.0739	152.7459
chr8	146364022	655310295	4.4773	36.4552
chr9	141213431	1197628401	8.481	636.2239
chr10	135534747	859149870	6.339	269.5027
chr11	135006516	563117345	4.171	26.3659
chr12	133851895	504507184	3.7691	19.984
chr13	115169878	310543192	2.6964	17.3211
chr14	107349540	331359738	3.0867	20.5084
chr15	102531392	278829803	2.7195	18.8664
chr16	90354753	228010391	2.5235	14.7456
chr17	81195210	202964282	2.4997	16.1606
chr18	78077248	305917337	3.9181	31.342
chr19	59128983	144320167	2.4408	24.2299
chr20	63025520	175557602	2.7855	17.3214
chr21	48129895	137384974	2.8545	21.0907
chr22	51304566	59976005	1.169	8.3304
chrMT	16571	5077	0.3064	1.3556
chrX	155270560	916113092	5.9001	60.7828

chrY	59373566	8833778	0.1488	1.8168
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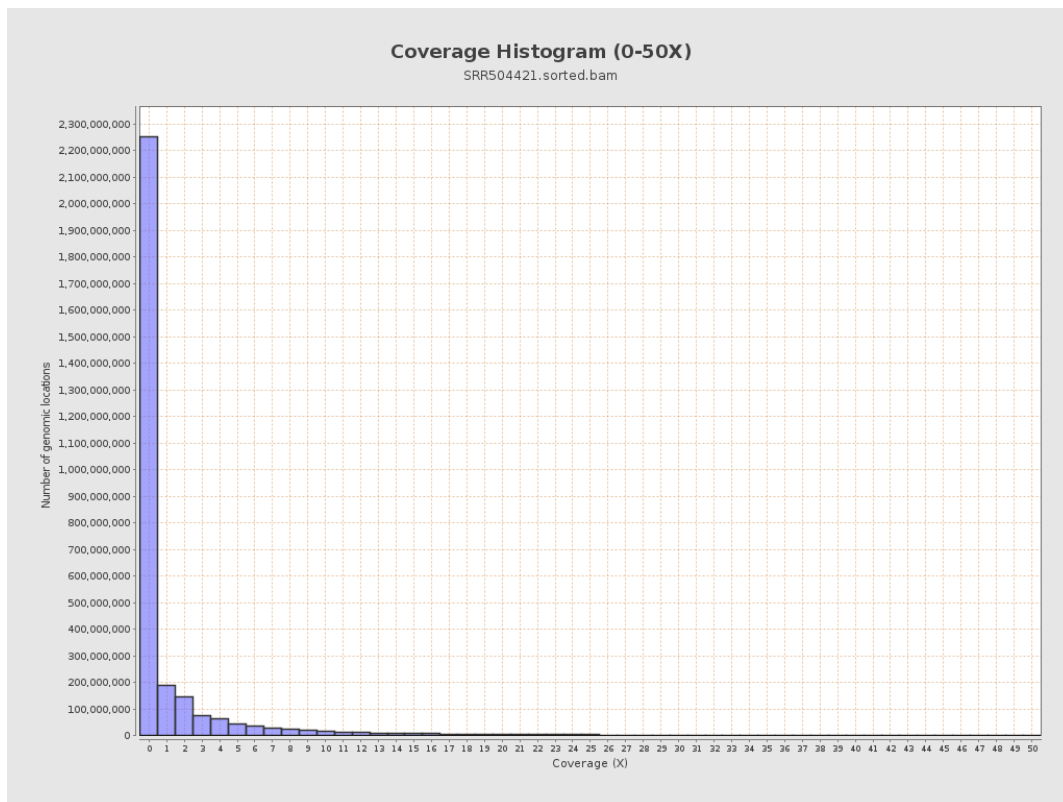
3. Results : Coverage across reference



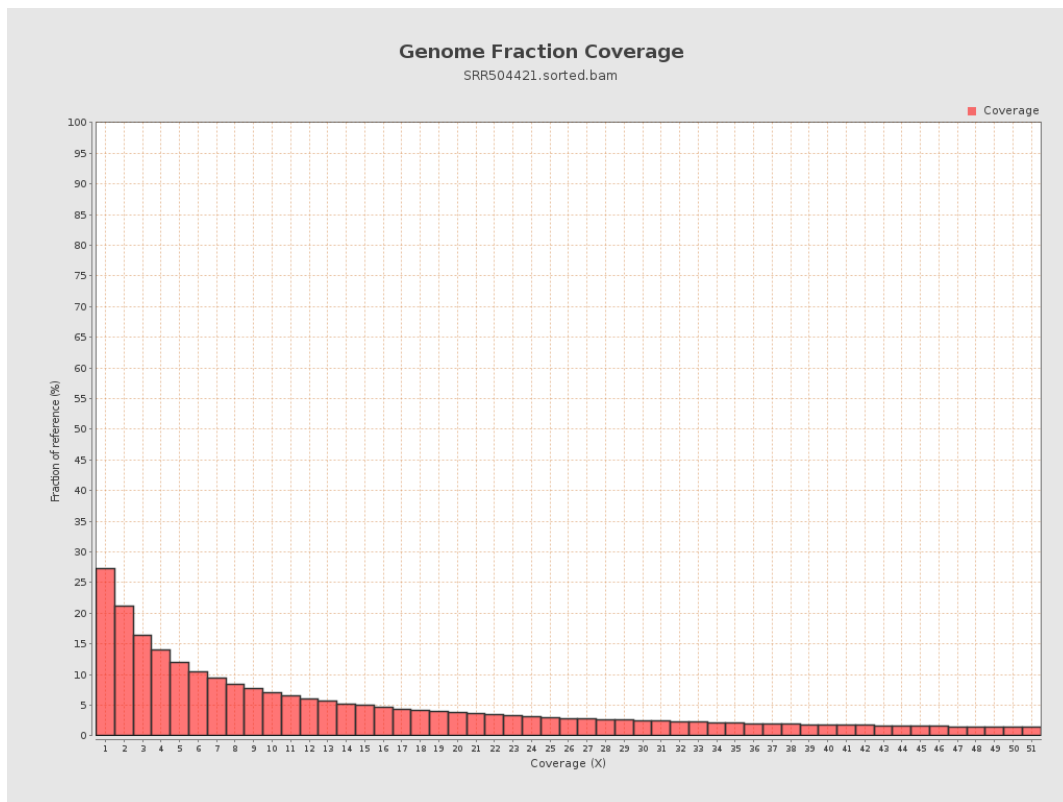
4. Results : Coverage Histogram



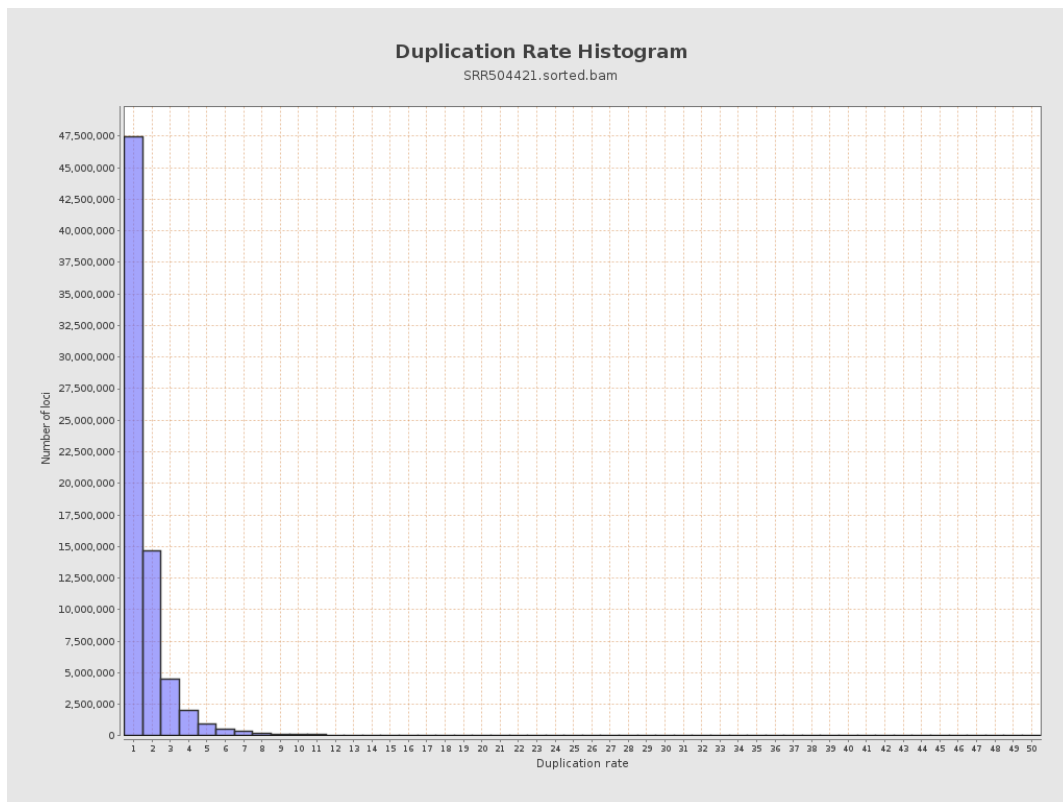
5. Results : Coverage Histogram (0-50X)



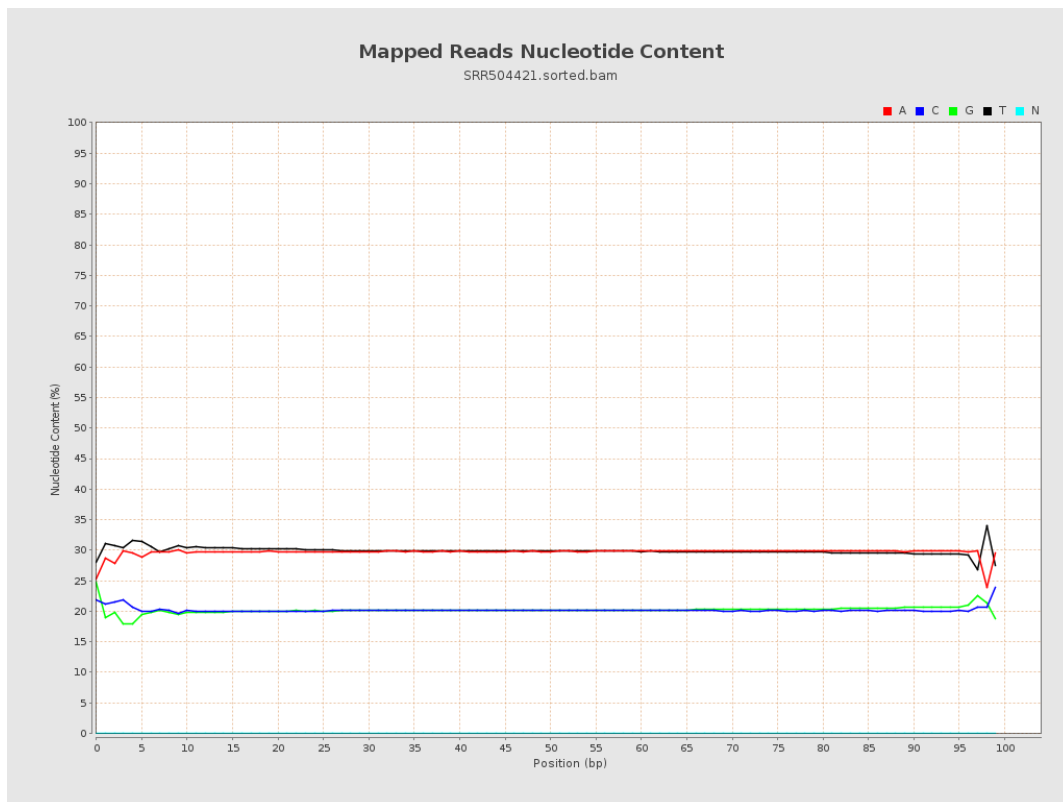
6. Results : Genome Fraction Coverage



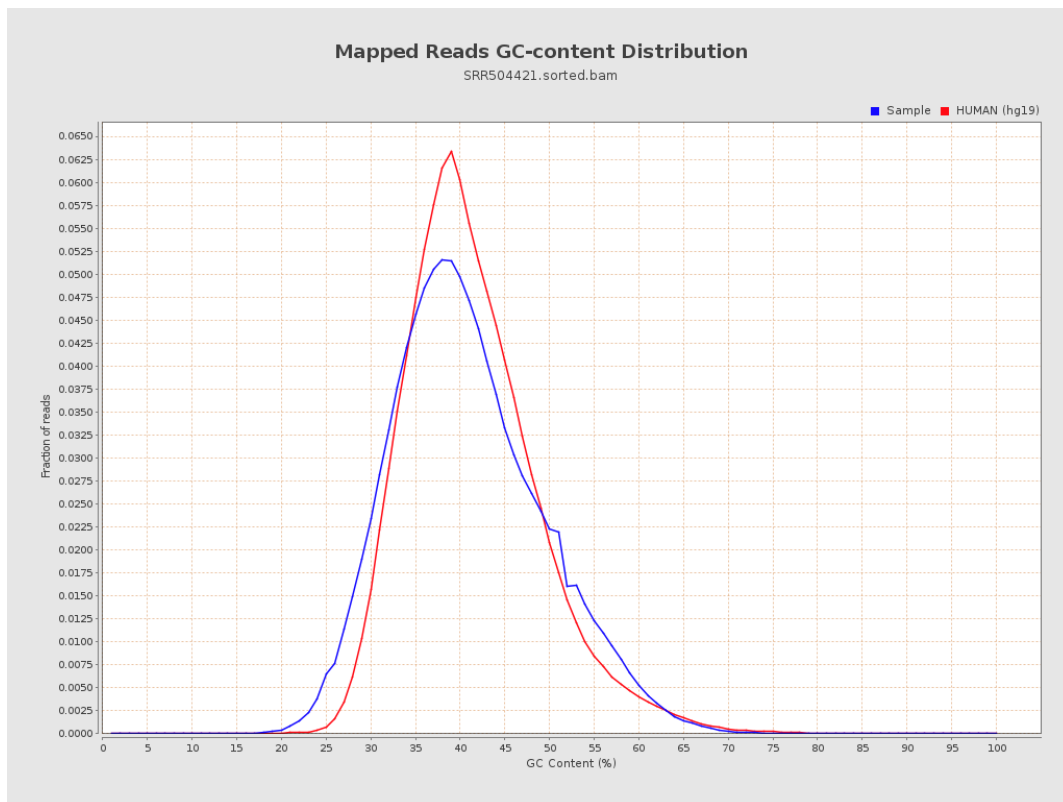
7. Results : Duplication Rate Histogram



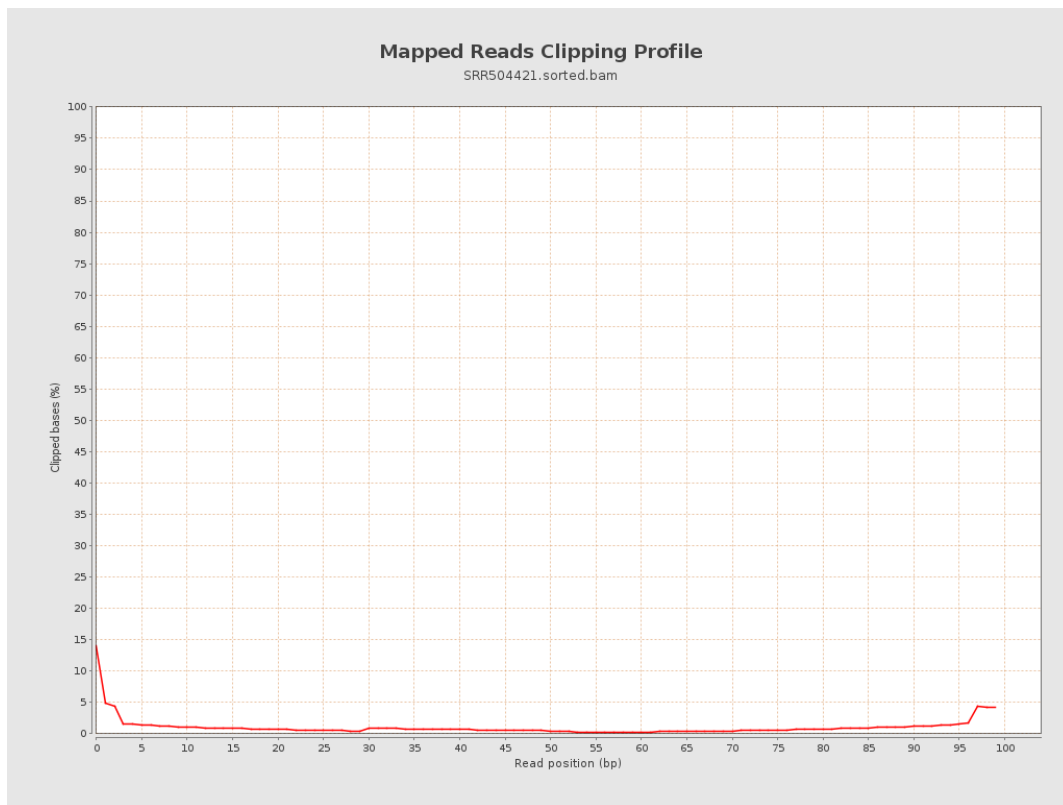
8. Results : Mapped Reads Nucleotide Content



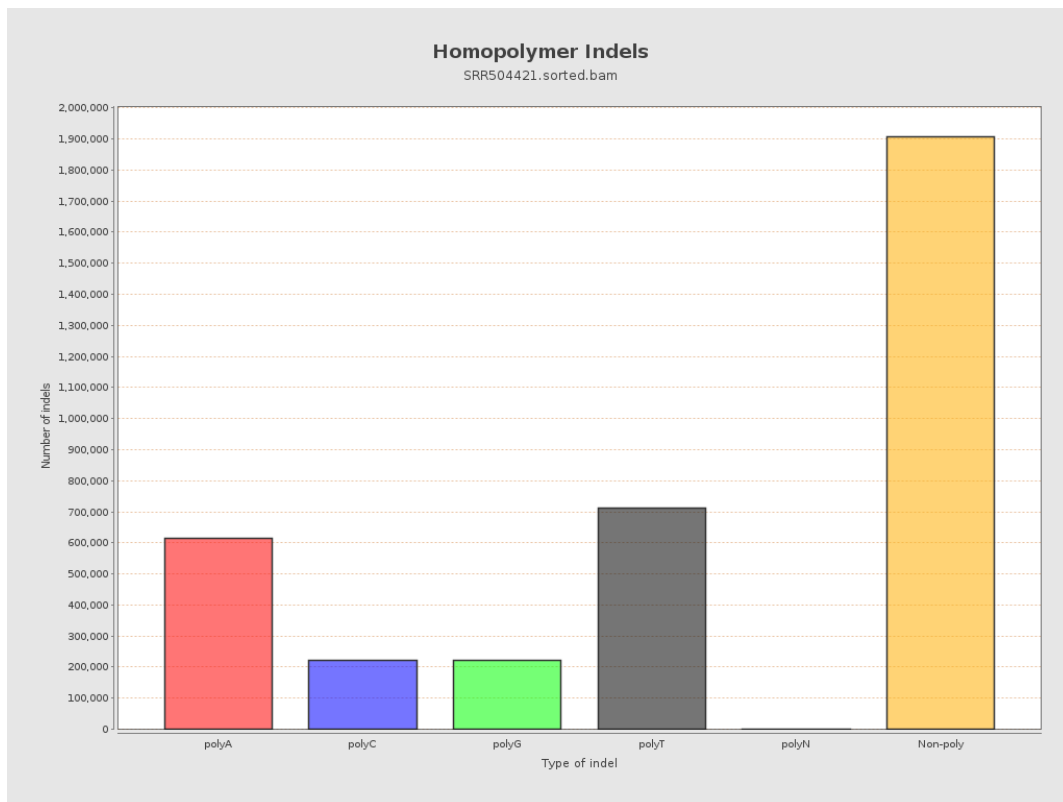
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



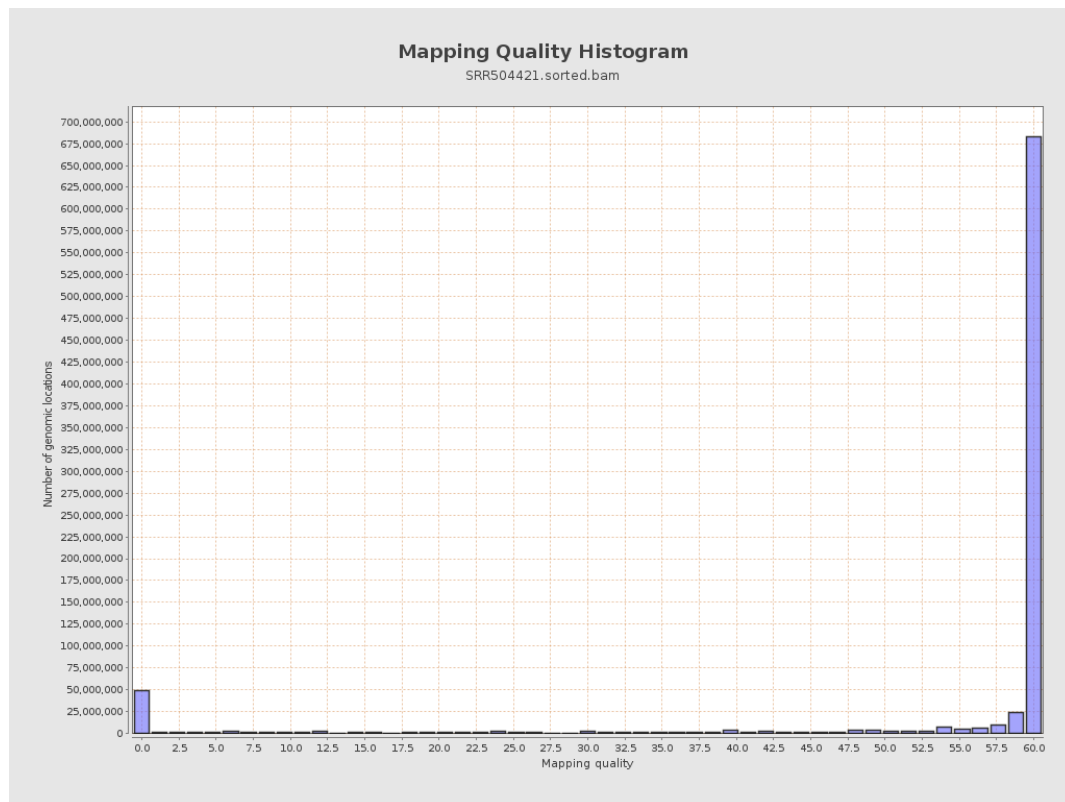
11. Results : Homopolymer Indels



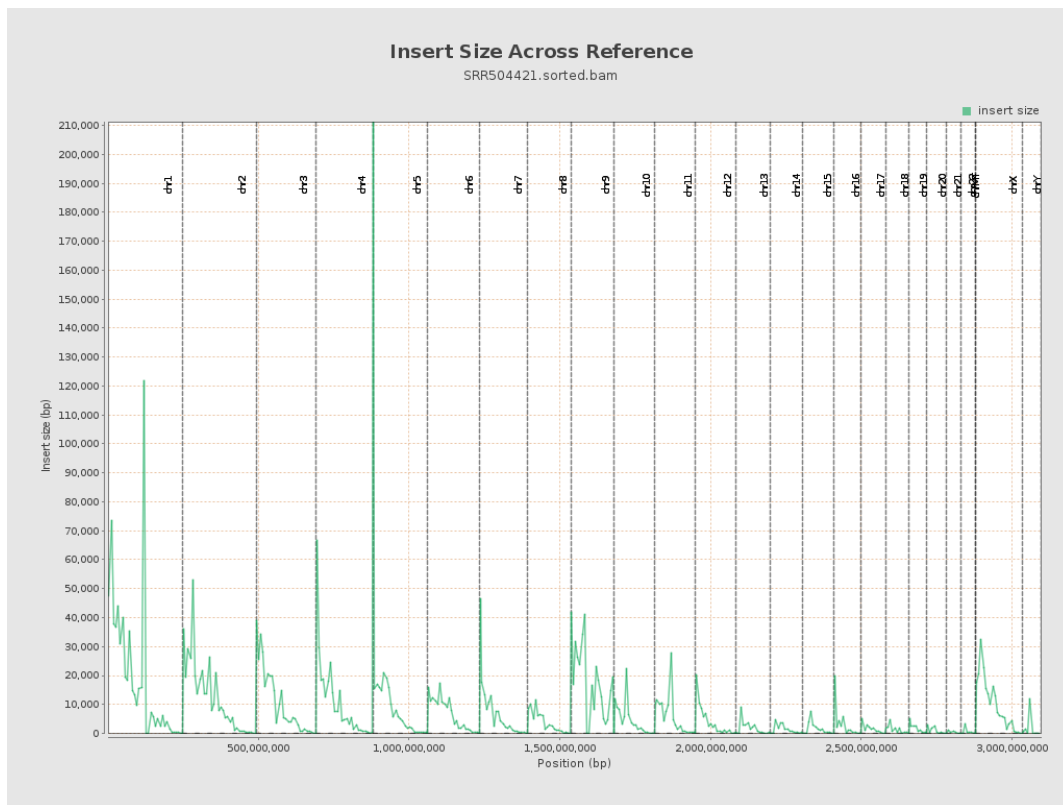
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

