

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/06/22 19:13:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR504410.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_SRR504410 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR504410_1.fastq.gz SRR504410_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Jun 22 19:13:22 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR504410.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	132,806,906
Mapped reads	131,909,933 / 99.32%
Unmapped reads	896,973 / 0.68%
Mapped paired reads	131,909,933 / 99.32%
Mapped reads, first in pair	66,018,472 / 49.71%
Mapped reads, second in pair	65,891,461 / 49.61%
Mapped reads, both in pair	131,612,634 / 99.1%
Mapped reads, singletons	297,299 / 0.22%
Secondary alignments	0
Supplementary alignments	2,230,315 / 1.68%
Read min/max/mean length	30 / 100 / 99.68
Duplicated reads (estimated)	63,319,451 / 47.68%
Duplication rate	27.81%
Clipped reads	67,883,567 / 51.11%

2.2. ACGT Content

Number/percentage of A's	3,746,484,311 / 29.76%
Number/percentage of C's	2,533,811,332 / 20.13%
Number/percentage of T's	3,765,927,530 / 29.91%
Number/percentage of G's	2,540,868,449 / 20.18%
Number/percentage of N's	1,922,649 / 0.02%

GC Percentage	40.31%
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2.3. Coverage

Mean	4.0679
Standard Deviation	250.7171

2.4. Mapping Quality

Mean Mapping Quality	52.65
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2.5. Insert size

Mean	83,893.34
Standard Deviation	2,773,569.36
P25/Median/P75	127 / 156 / 187

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	63,268,057
Insertions	1,315,256
Mapped reads with at least one insertion	0.99%
Deletions	2,606,182
Mapped reads with at least one deletion	1.95%
Homopolymer indels	49.13%

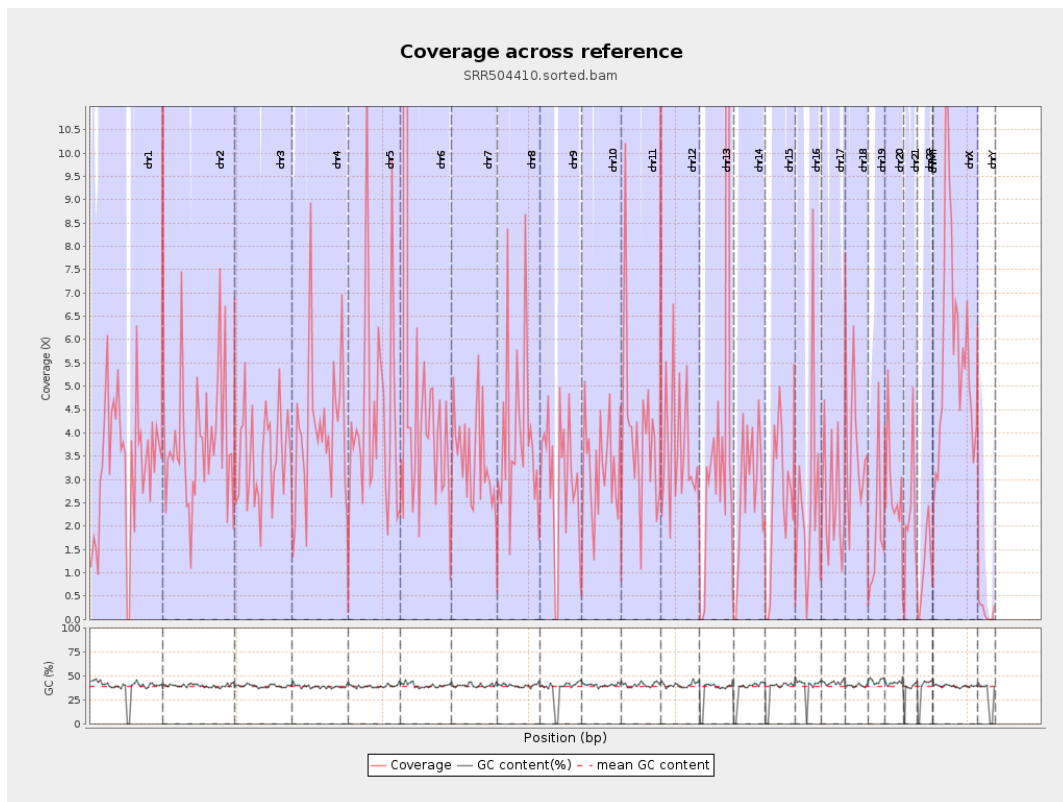
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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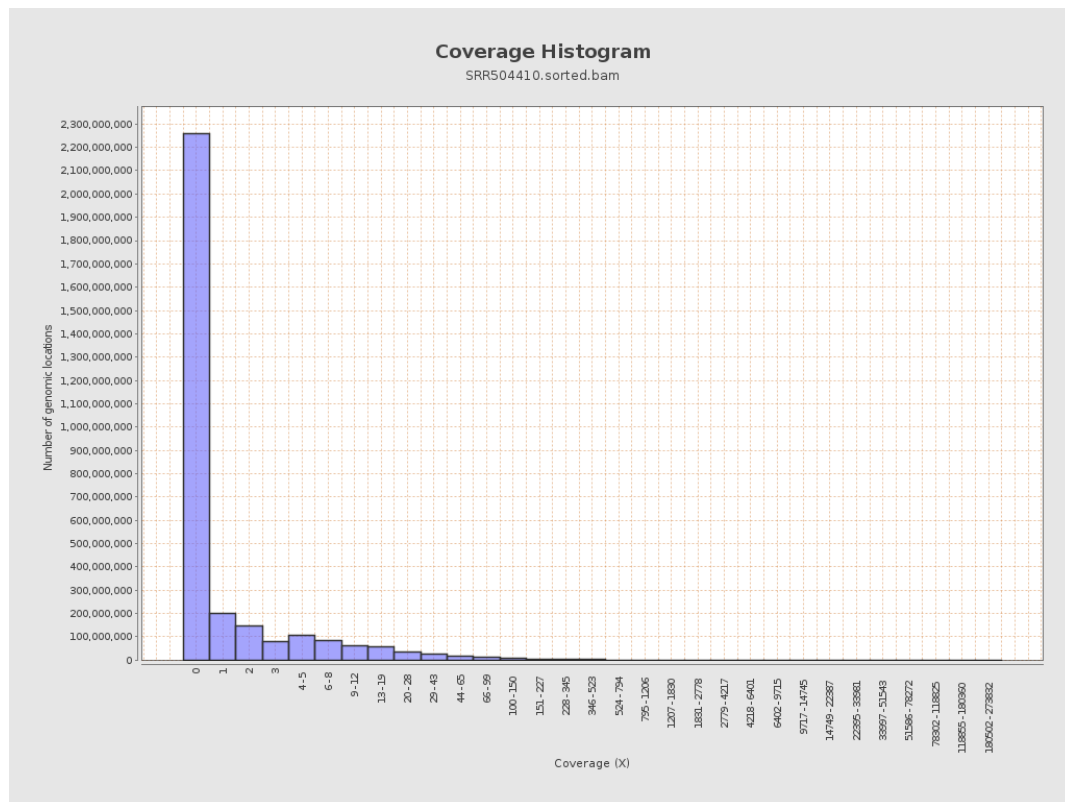
		bases	coverage	deviation
chr1	249250621	845915912	3.3938	27.0445
chr2	243199373	926550845	3.8098	28.8286
chr3	198022430	698309507	3.5264	21.1959
chr4	191154276	783443840	4.0985	29.5536
chr5	180915260	784499743	4.3363	36.6612
chr6	171115067	2348968709	13.7274	1,051.6803
chr7	159138663	546208463	3.4323	25.8496
chr8	146364022	574912984	3.928	26.9352
chr9	141213431	422380611	2.9911	20.3475
chr10	135534747	442913098	3.2679	19.3384
chr11	135006516	549726079	4.0718	45.3834
chr12	133851895	477153206	3.5648	25.2282
chr13	115169878	565541718	4.9105	167.4922
chr14	107349540	297285762	2.7693	16.2035
chr15	102531392	261086978	2.5464	16.4908
chr16	90354753	221121086	2.4473	30.5652
chr17	81195210	203905472	2.5113	18.1293
chr18	78077248	287178788	3.6781	31.0043
chr19	59128983	111905586	1.8926	19.3798
chr20	63025520	176306854	2.7974	17.8098
chr21	48129895	104268737	2.1664	13.3025
chr22	51304566	60046713	1.1704	9.5962
chrMT	16571	13044	0.7872	4.0655
chrX	155270560	893539283	5.7547	37.333

chrY	59373566	9914357	0.167	3.0217
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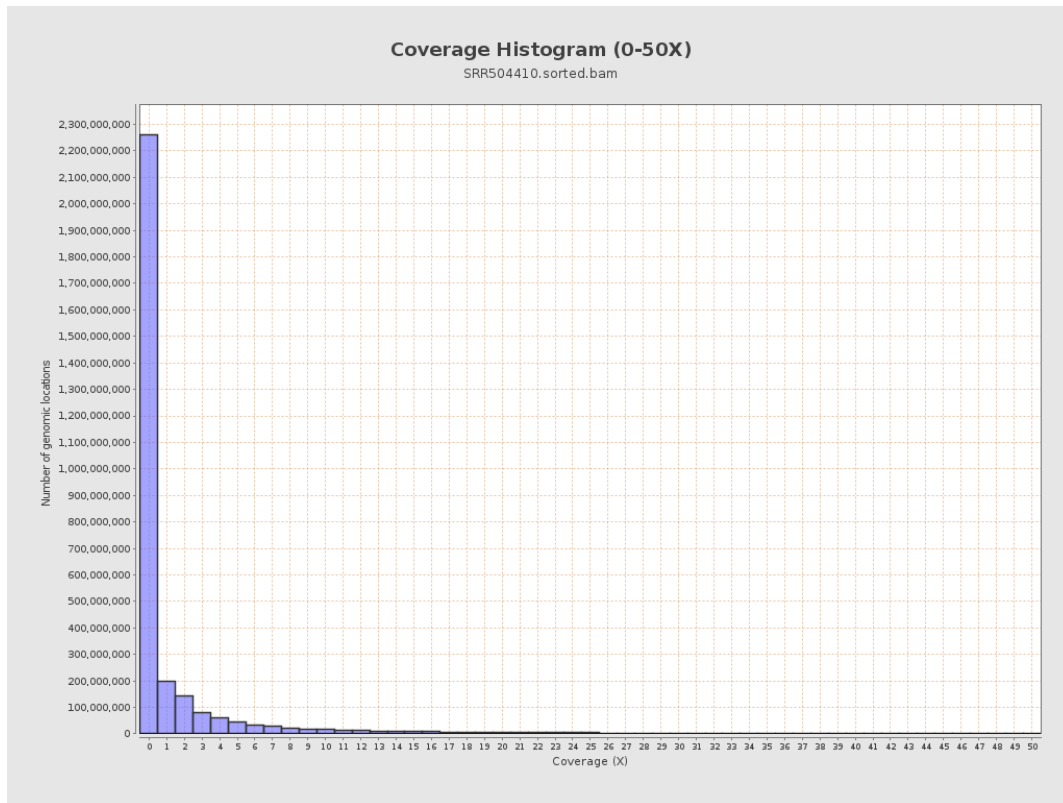
3. Results : Coverage across reference



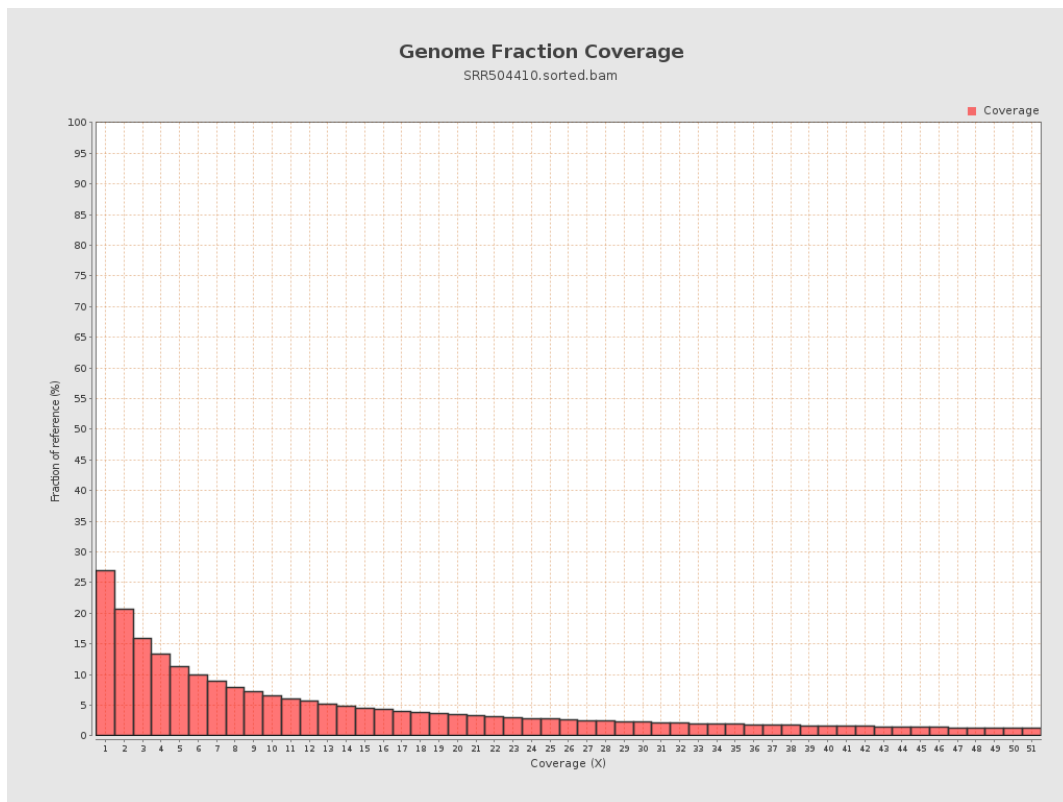
4. Results : Coverage Histogram



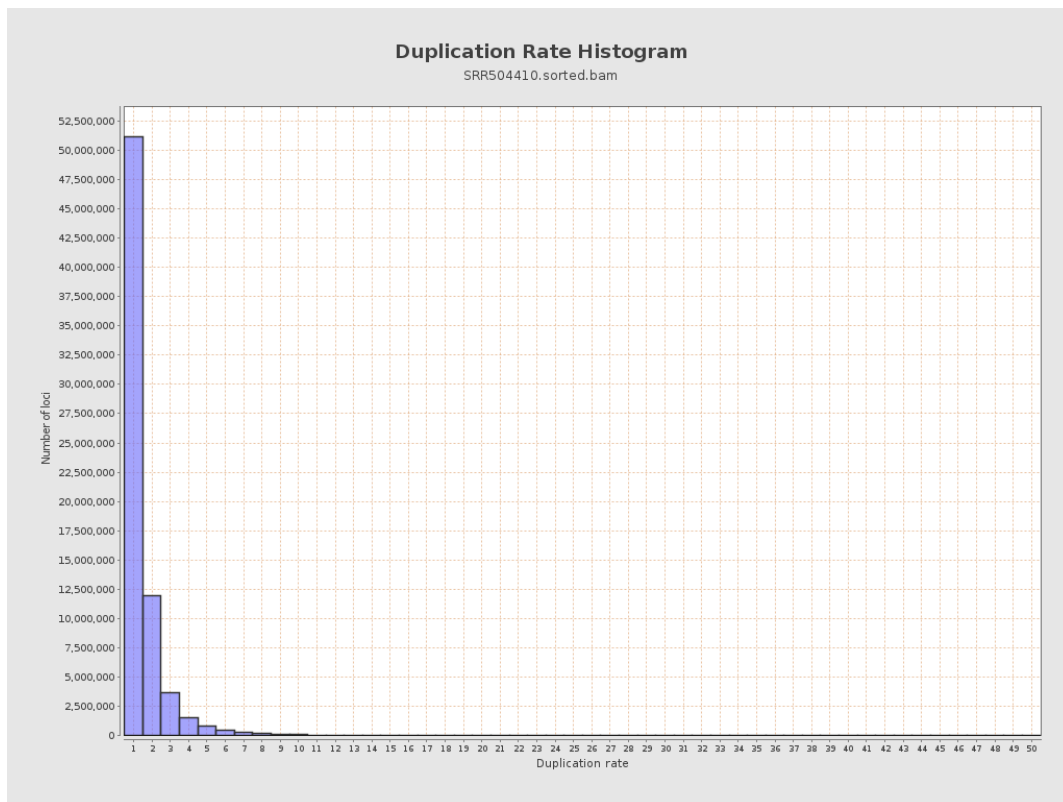
5. Results : Coverage Histogram (0-50X)



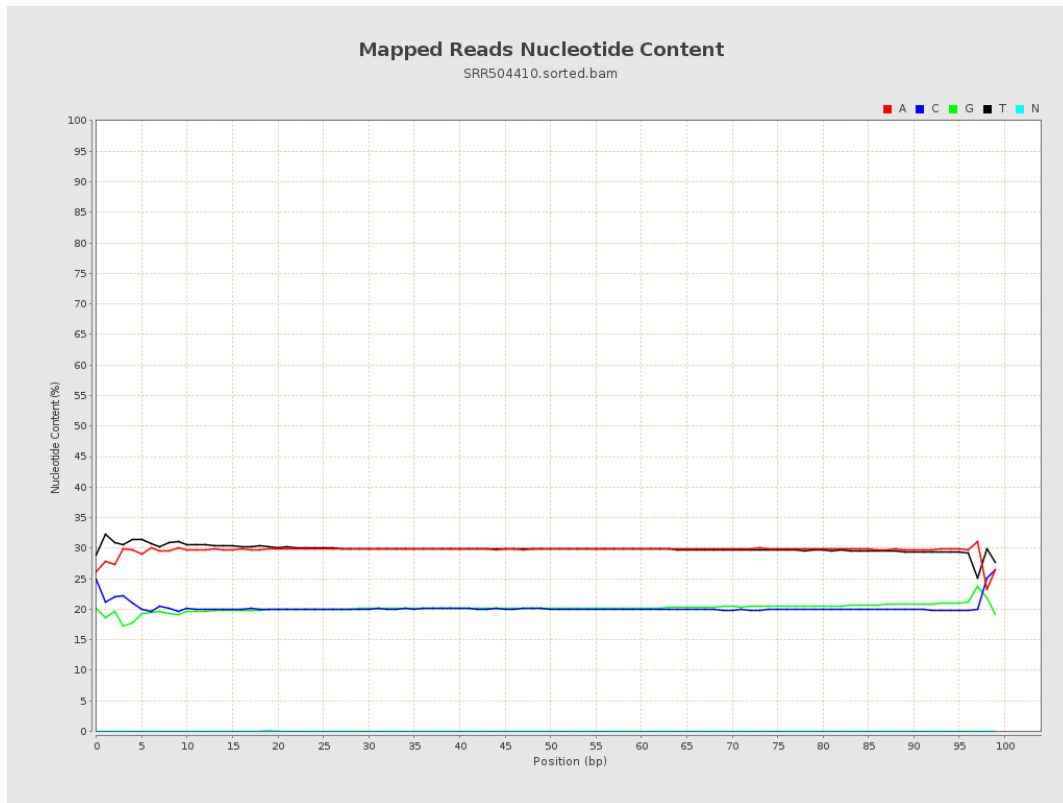
6. Results : Genome Fraction Coverage



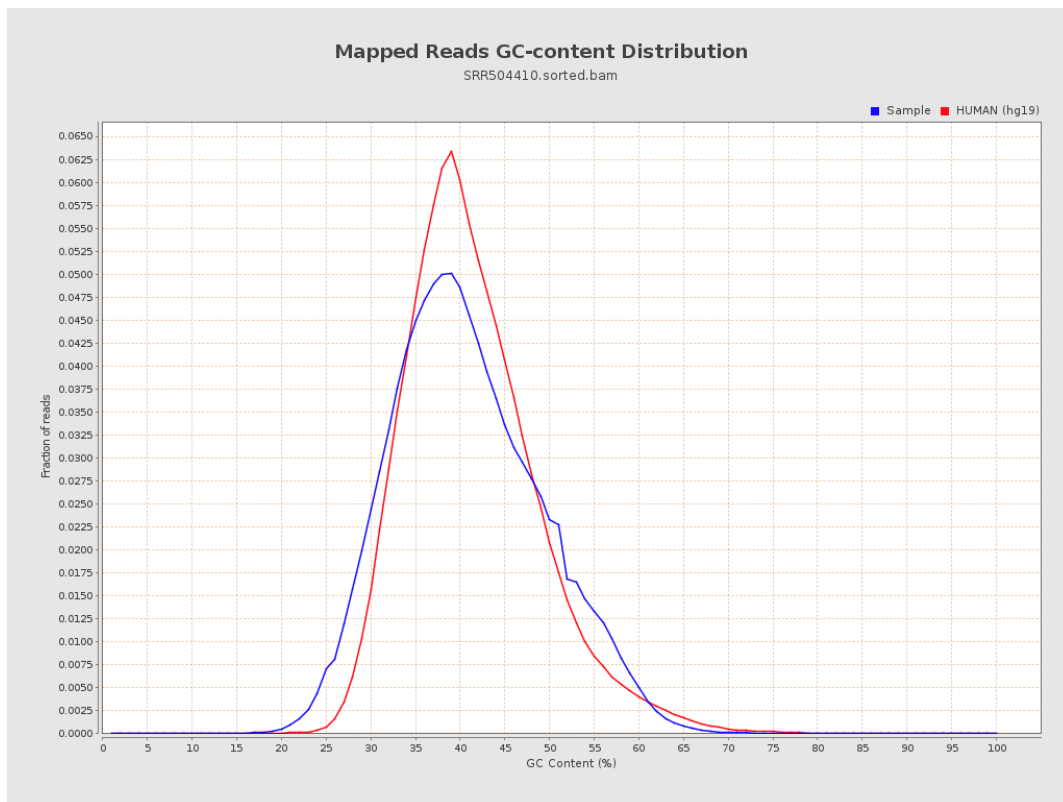
7. Results : Duplication Rate Histogram



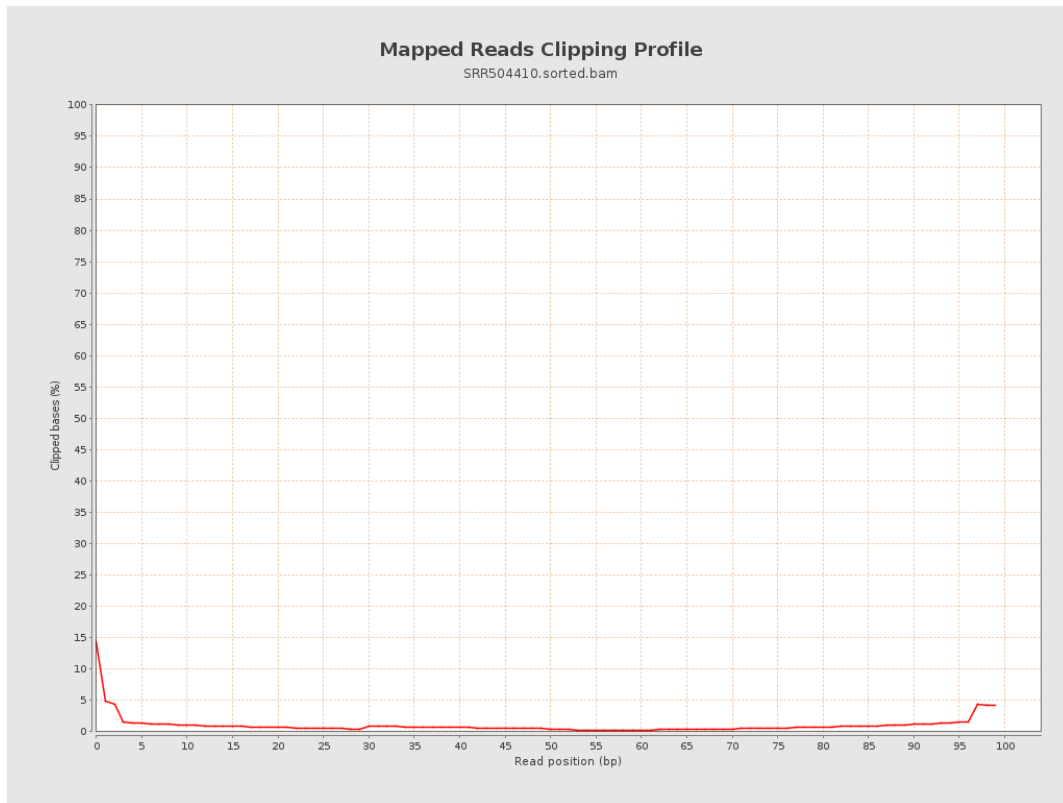
8. Results : Mapped Reads Nucleotide Content



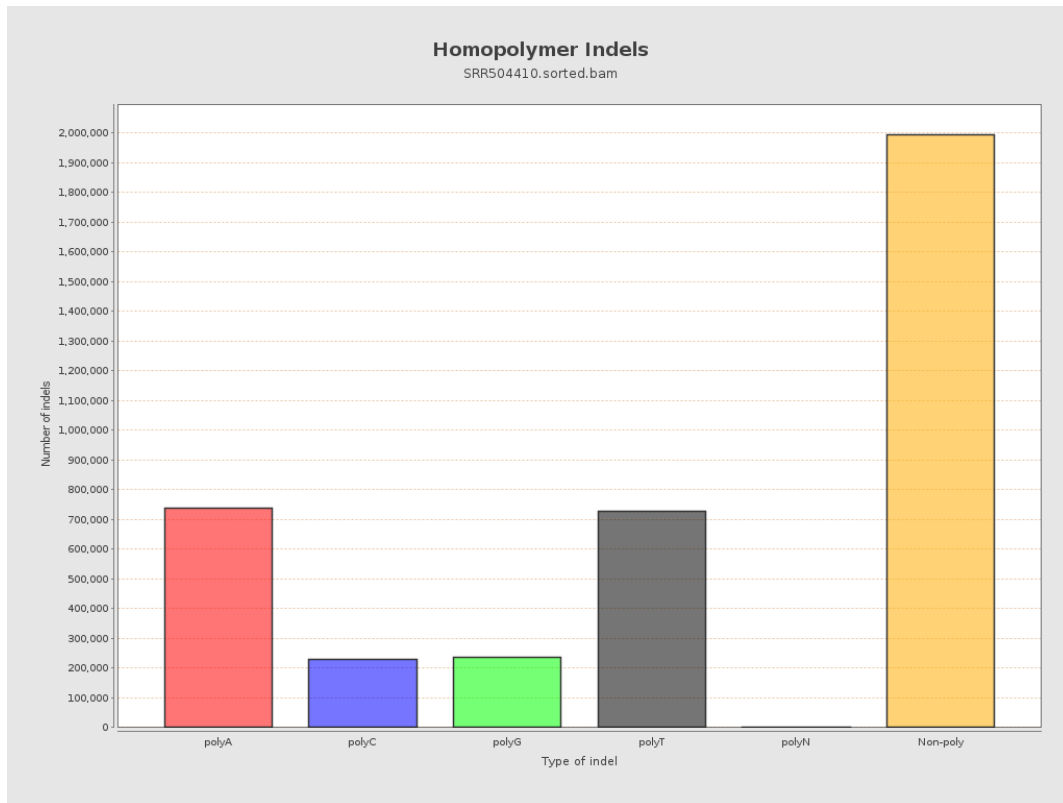
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



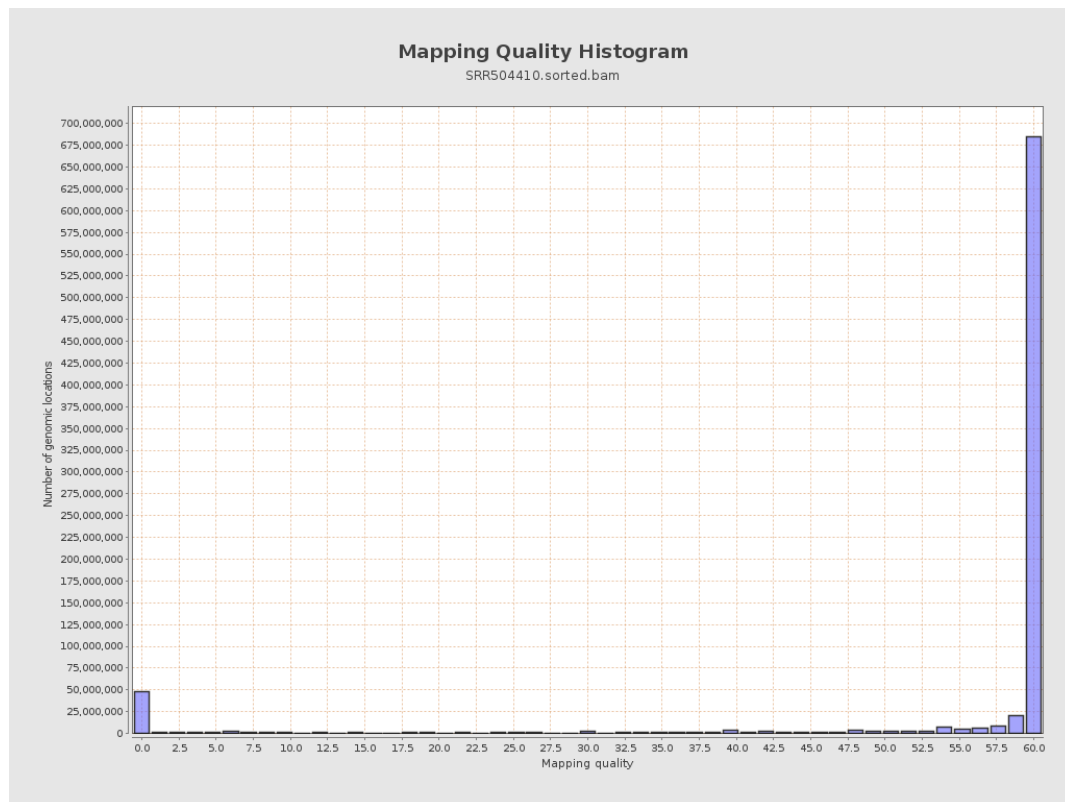
11. Results : Homopolymer Indels



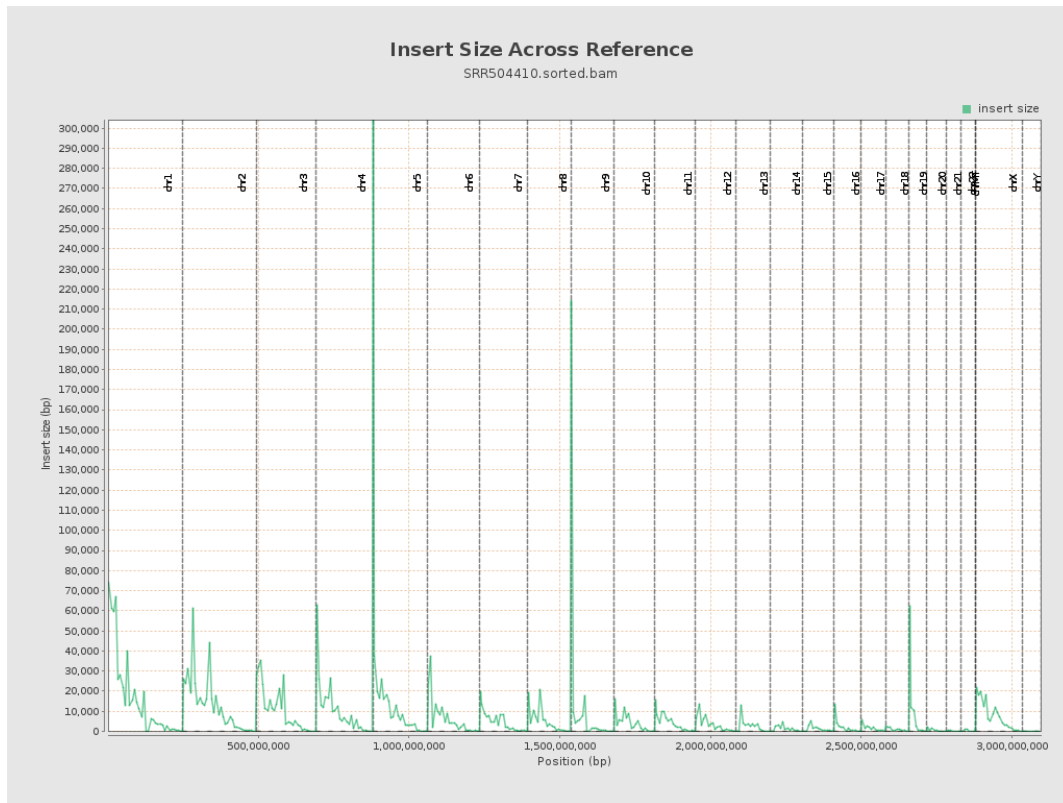
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

