

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/03/30 21:32:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR2046540.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_SRR2046540 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR2046540_1.fastq.gz SRR2046540_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Mar 30 21:32:54 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR2046540.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,251,334
Mapped reads	6,054,407 / 96.85%
Unmapped reads	196,927 / 3.15%
Mapped paired reads	6,054,407 / 96.85%
Mapped reads, first in pair	3,099,235 / 49.58%
Mapped reads, second in pair	2,955,172 / 47.27%
Mapped reads, both in pair	5,885,220 / 94.14%
Mapped reads, singletons	169,187 / 2.71%
Secondary alignments	0
Supplementary alignments	52,313 / 0.84%
Read min/max/mean length	30 / 100 / 100.34
Duplicated reads (estimated)	4,661,794 / 74.57%
Duplication rate	29.32%
Clipped reads	1,727,536 / 27.63%

2.2. ACGT Content

Number/percentage of A's	169,172,526 / 29.52%
Number/percentage of C's	117,761,750 / 20.55%
Number/percentage of T's	168,647,000 / 29.42%
Number/percentage of G's	117,525,119 / 20.5%
Number/percentage of N's	48,711 / 0.01%

GC Percentage	41.05%
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2.3. Coverage

Mean	0.1852
Standard Deviation	40.6261

2.4. Mapping Quality

Mean Mapping Quality	51.05
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2.5. Insert size

Mean	45,576.05
Standard Deviation	2,093,199.45
P25/Median/P75	100 / 127 / 160

2.6. Mismatches and indels

General error rate	0.48%
Mismatches	2,607,713
Insertions	54,184
Mapped reads with at least one insertion	0.88%
Deletions	55,645
Mapped reads with at least one deletion	0.88%
Homopolymer indels	46.26%

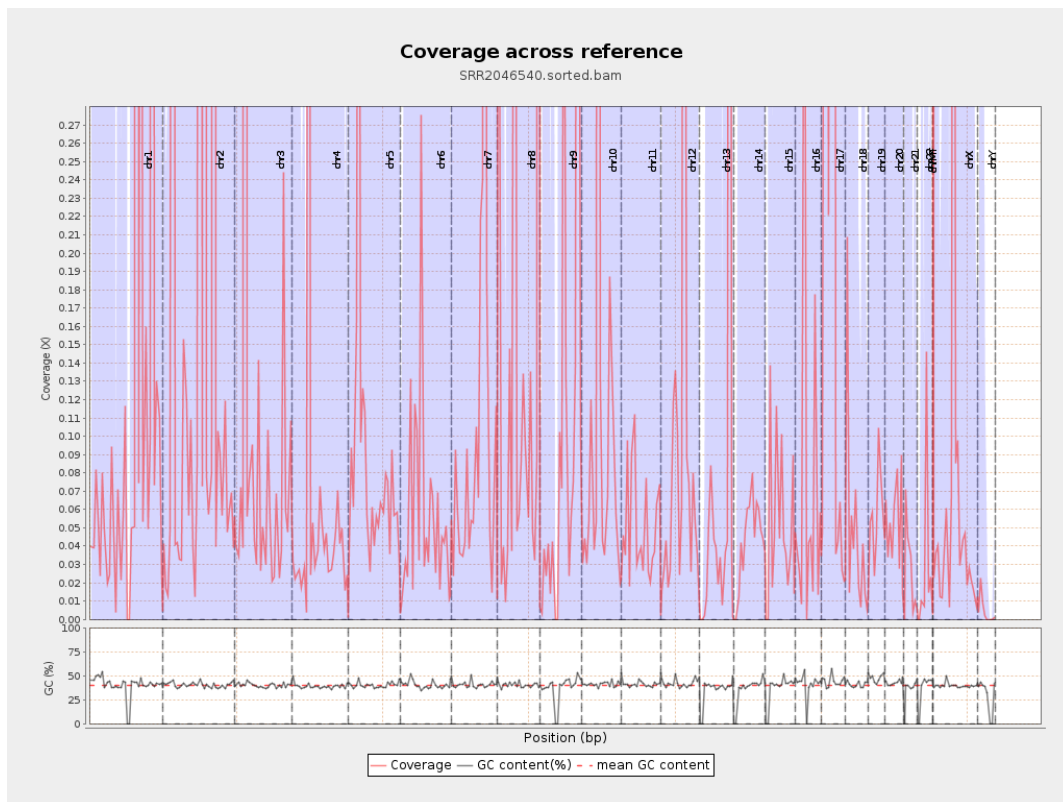
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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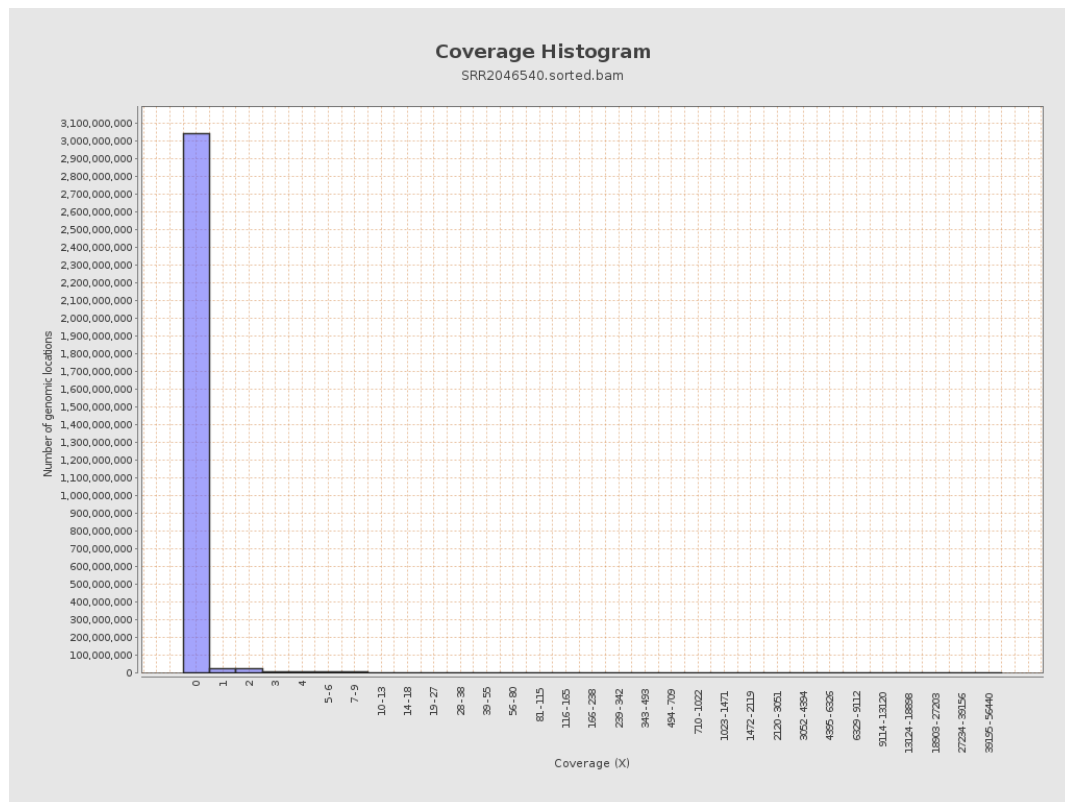
		bases	coverage	deviation
chr1	249250621	76841311	0.3083	40.3987
chr2	243199373	119479271	0.4913	74.3842
chr3	198022430	64555964	0.326	55.3007
chr4	191154276	13619836	0.0713	6.0016
chr5	180915260	16810687	0.0929	9.0491
chr6	171115067	9836506	0.0575	3.2864
chr7	159138663	21166280	0.133	13.1022
chr8	146364022	95807542	0.6546	123.3931
chr9	141213431	16930945	0.1199	18.9966
chr10	135534747	23031040	0.1699	31.3561
chr11	135006516	6735551	0.0499	1.5363
chr12	133851895	13071266	0.0977	10.8562
chr13	115169878	14397358	0.125	18.7544
chr14	107349540	4641942	0.0432	0.9204
chr15	102531392	5380024	0.0525	3.836
chr16	90354753	7195657	0.0796	8.5244
chr17	81195210	37308734	0.4595	46.8094
chr18	78077248	3737287	0.0479	2.7634
chr19	59128983	3359137	0.0568	0.8513
chr20	63025520	3379459	0.0536	1.7349
chr21	48129895	1298008	0.027	0.9086
chr22	51304566	1563991	0.0305	3.2397
chrMT	16571	226194	13.65	6.3703
chrX	155270560	12655071	0.0815	16.7559

chrY	59373566	289979	0.0049	0.2883
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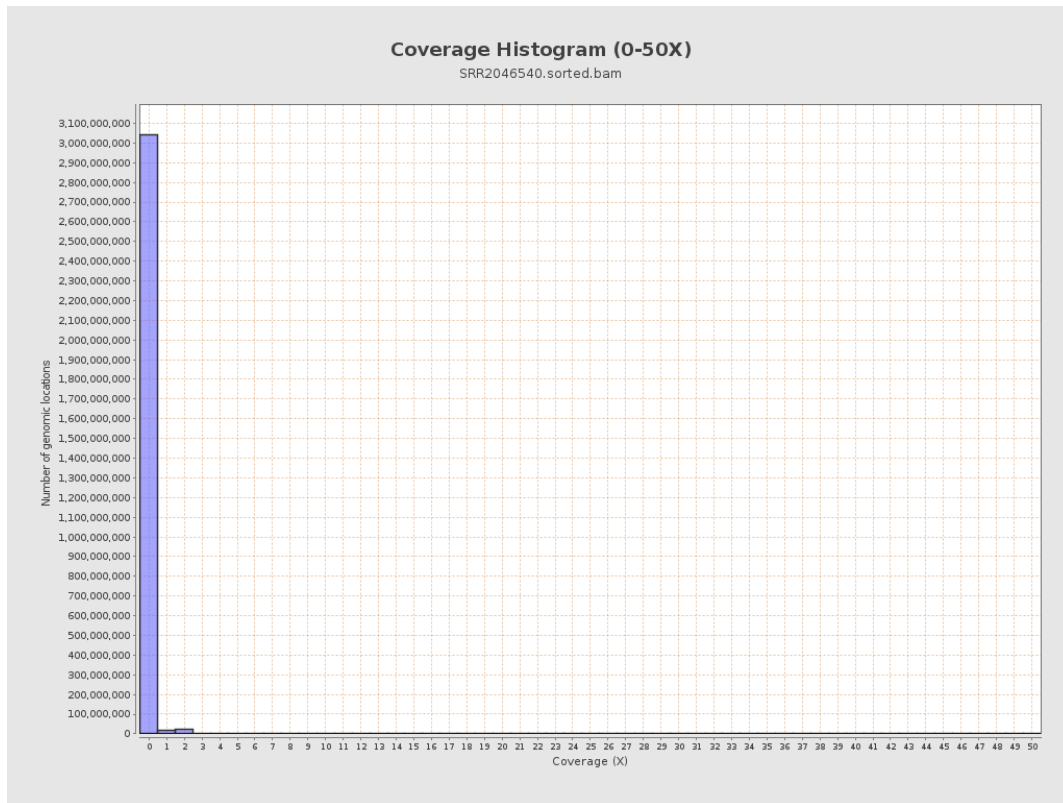
3. Results : Coverage across reference



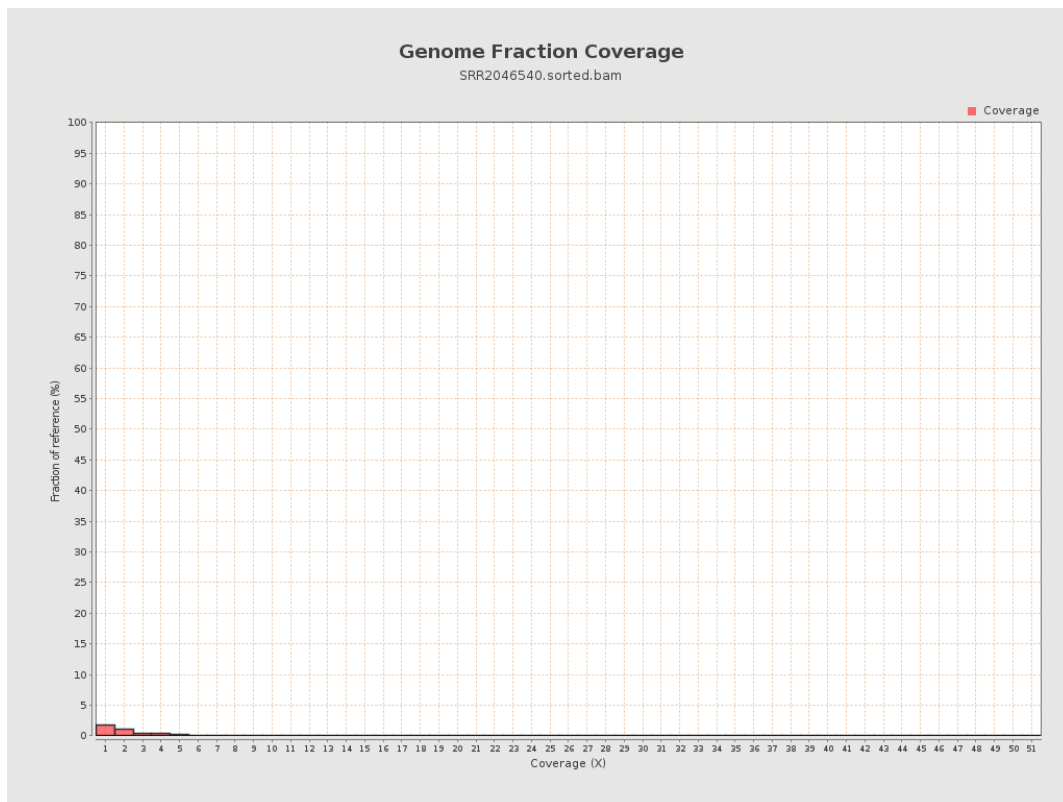
4. Results : Coverage Histogram



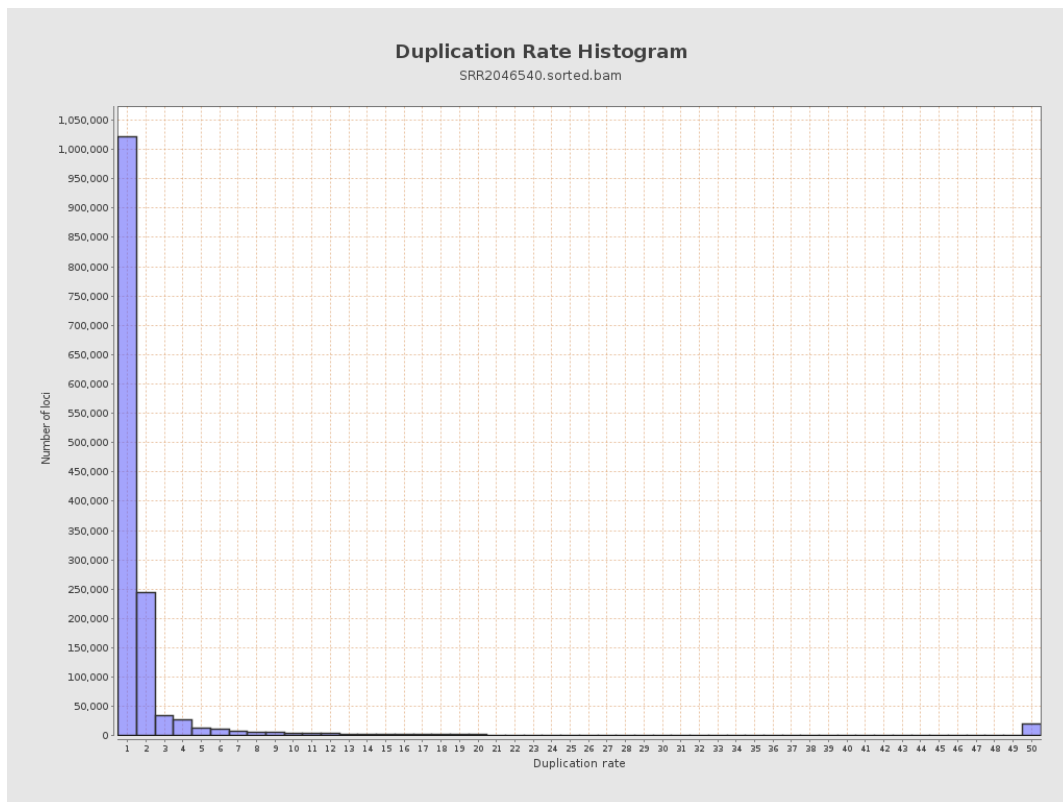
5. Results : Coverage Histogram (0-50X)



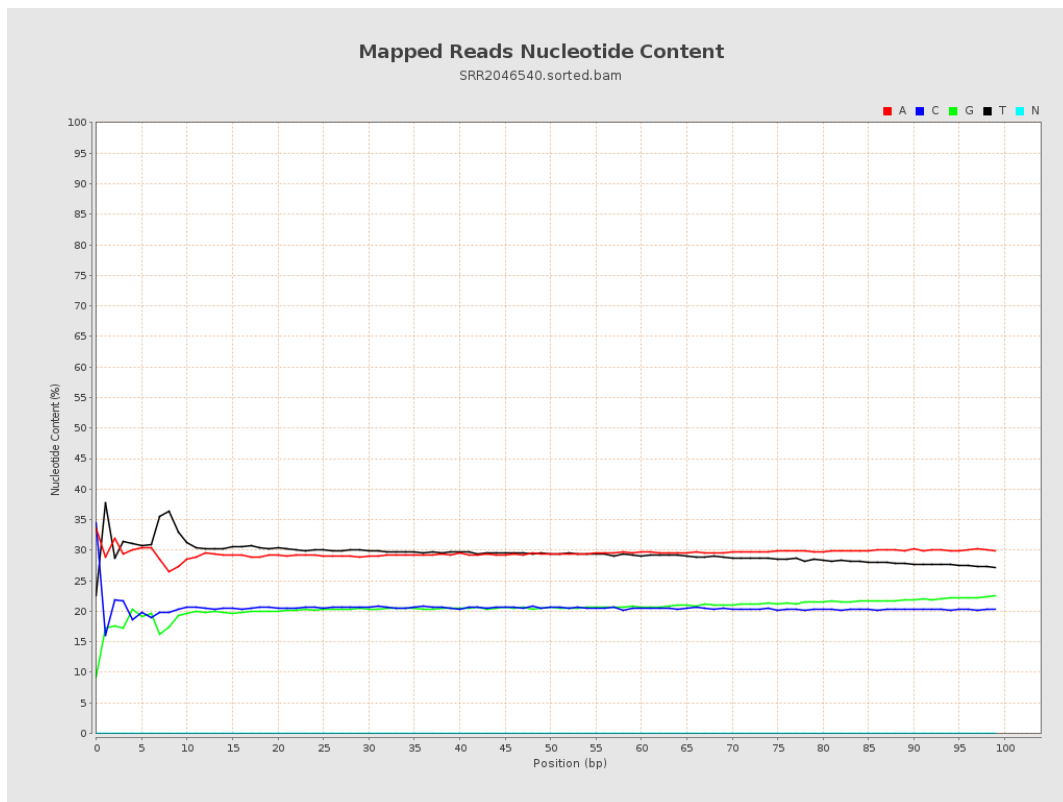
6. Results : Genome Fraction Coverage



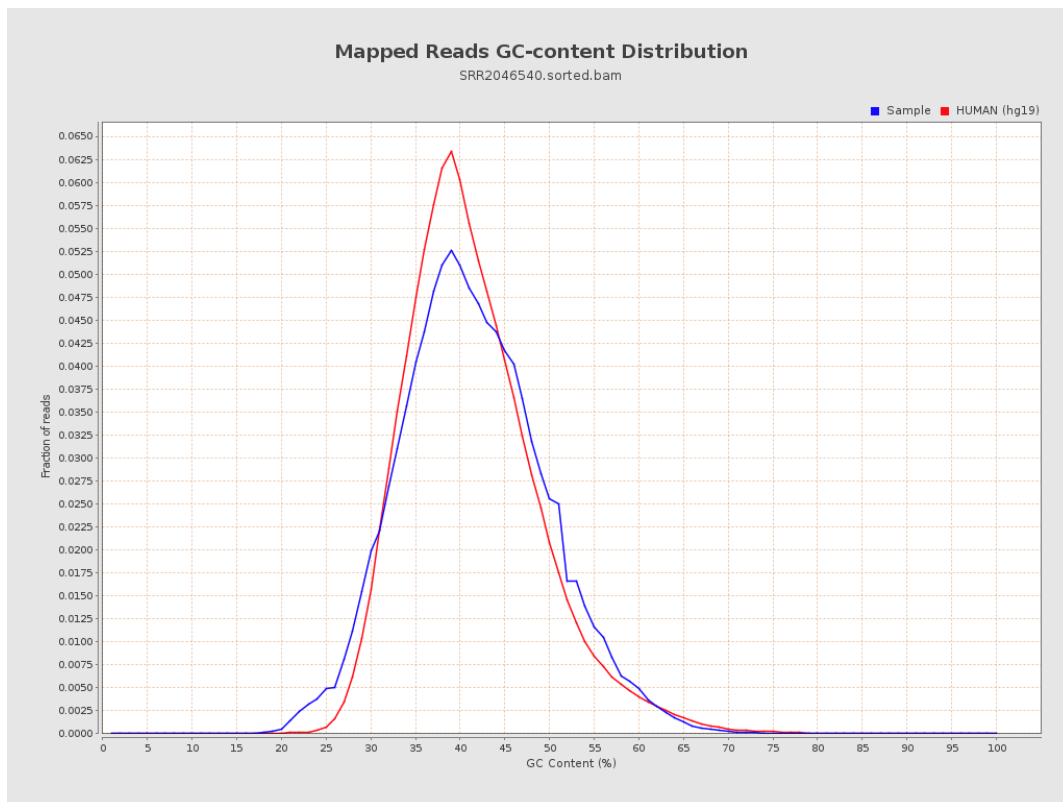
7. Results : Duplication Rate Histogram



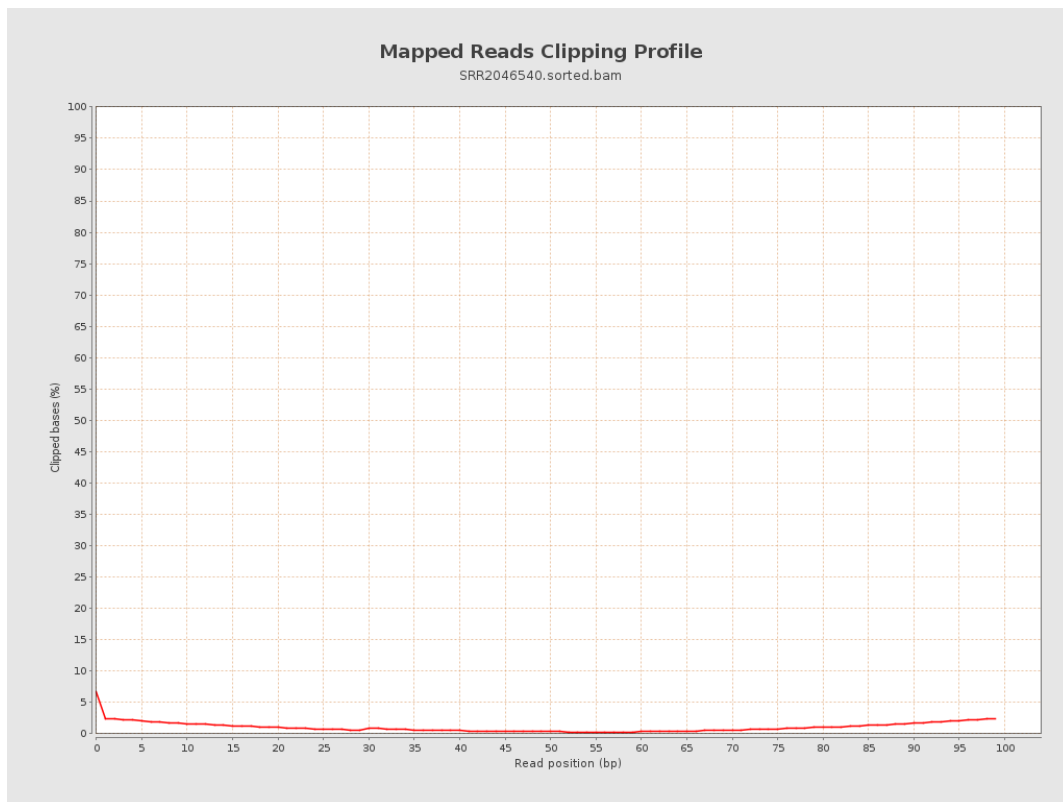
8. Results : Mapped Reads Nucleotide Content



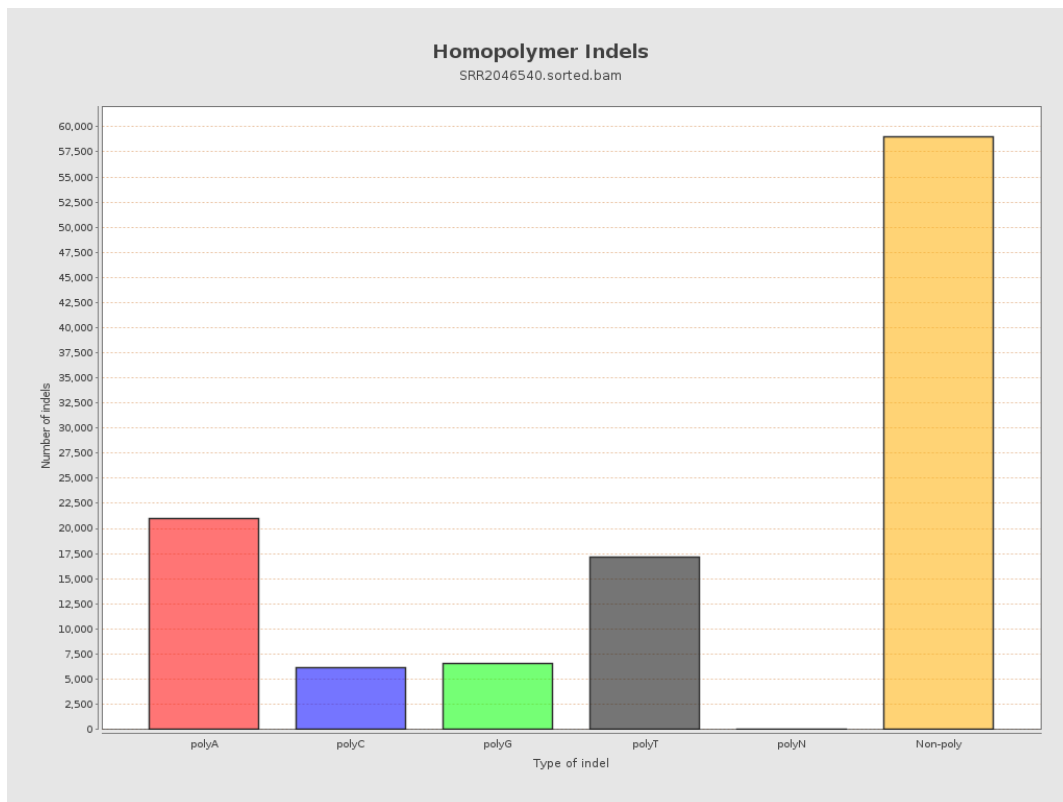
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



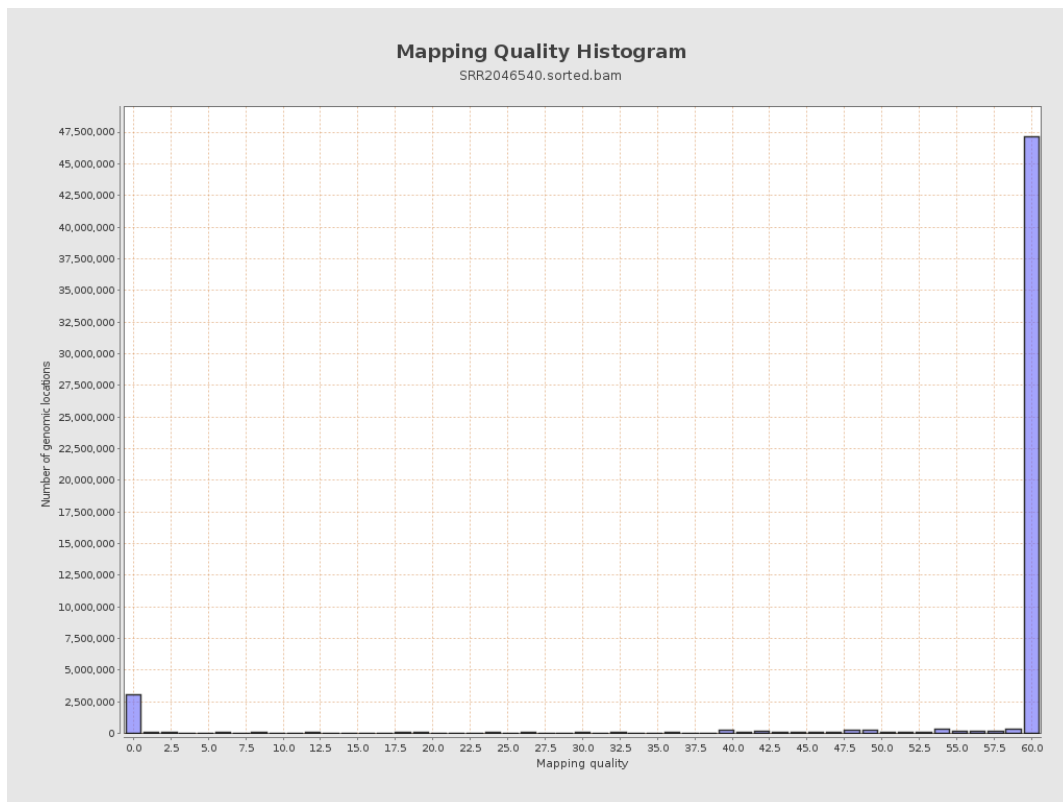
11. Results : Homopolymer Indels



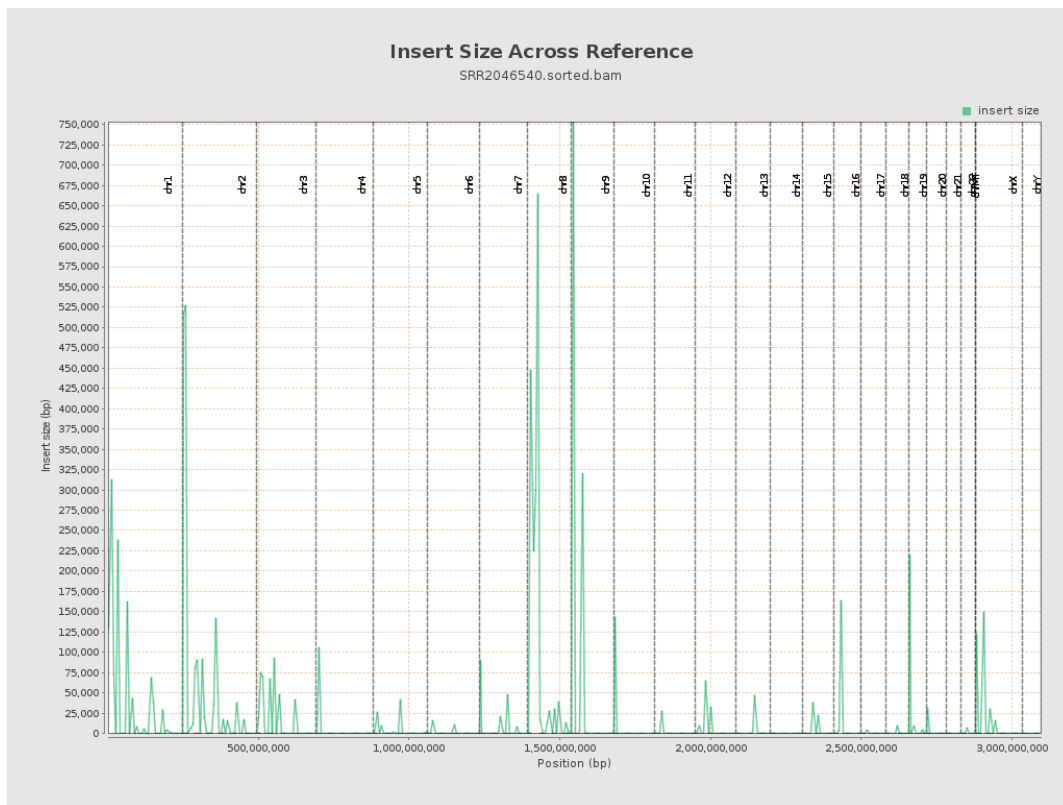
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

