

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/07 19:13:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124844.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_SRR3124844 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124844_1.fastq.gz SRR3124844_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Dec 07 19:13:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124844.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	91,527,834
Mapped reads	86,997,022 / 95.05%
Unmapped reads	4,530,812 / 4.95%
Mapped paired reads	86,997,022 / 95.05%
Mapped reads, first in pair	44,745,367 / 48.89%
Mapped reads, second in pair	42,251,655 / 46.16%
Mapped reads, both in pair	84,117,912 / 91.9%
Mapped reads, singletons	2,879,110 / 3.15%
Secondary alignments	0
Supplementary alignments	2,751,586 / 3.01%
Read min/max/mean length	30 / 150 / 151.41
Duplicated reads (estimated)	37,112,575 / 40.55%
Duplication rate	22.82%
Clipped reads	51,518,094 / 56.29%

2.2. ACGT Content

Number/percentage of A's	3,262,382,396 / 28.83%
Number/percentage of C's	2,173,429,507 / 19.21%
Number/percentage of T's	3,384,750,824 / 29.91%
Number/percentage of G's	2,495,790,082 / 22.05%
Number/percentage of N's	193,138 / 0%

GC Percentage	41.26%
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2.3. Coverage

Mean	3.6598
Standard Deviation	62.617

2.4. Mapping Quality

Mean Mapping Quality	53.19
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2.5. Insert size

Mean	155,548.93
Standard Deviation	3,747,372.62
P25/Median/P75	195 / 251 / 320

2.6. Mismatches and indels

General error rate	1.55%
Mismatches	164,872,041
Insertions	3,001,063
Mapped reads with at least one insertion	3.13%
Deletions	5,599,773
Mapped reads with at least one deletion	6.08%
Homopolymer indels	42.51%

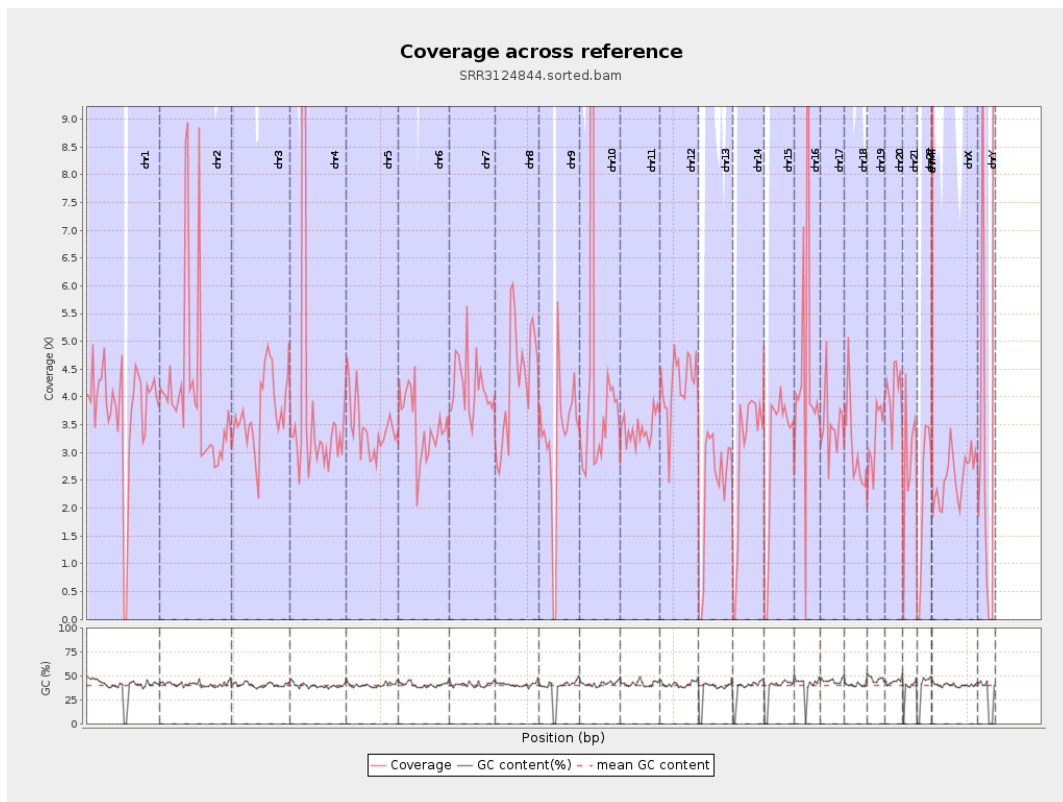
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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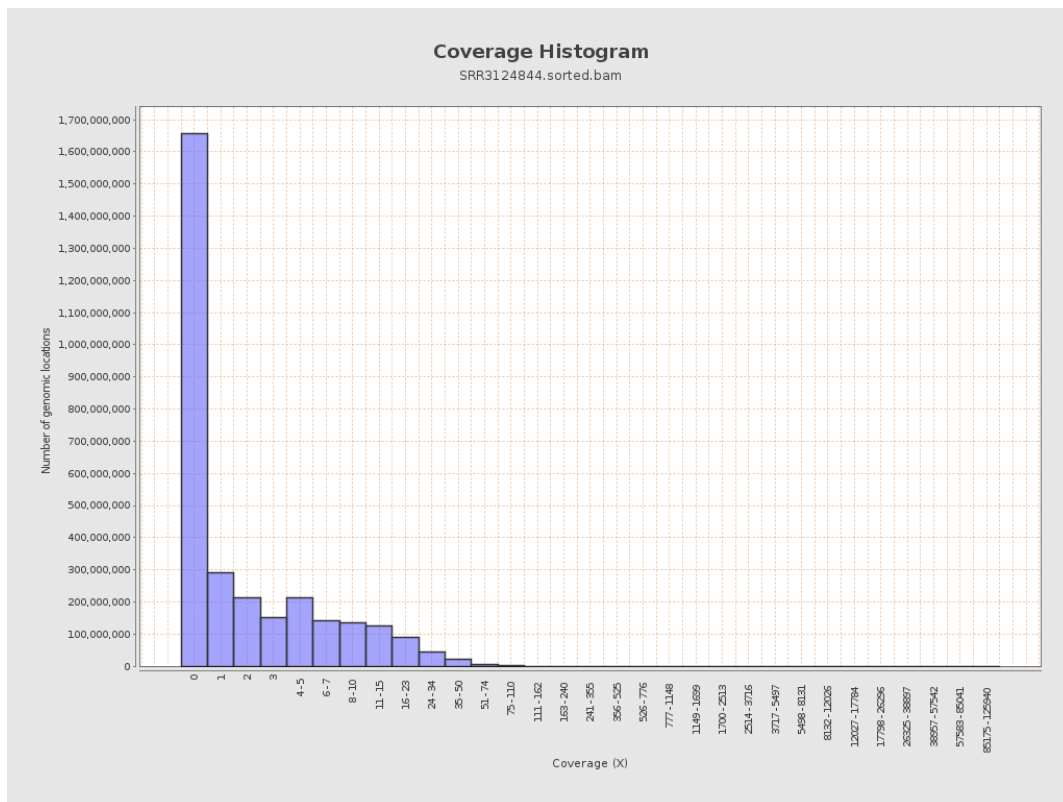
		bases	coverage	deviation
chr1	249250621	940288688	3.7725	24.4768
chr2	243199373	989526718	4.0688	76.2746
chr3	198022430	741271884	3.7434	8.6718
chr4	191154276	753039030	3.9394	116.4762
chr5	180915260	622719996	3.4421	9.7997
chr6	171115067	596175839	3.4841	15.1141
chr7	159138663	664667735	4.1767	32.4436
chr8	146364022	635283272	4.3404	13.0977
chr9	141213431	454966792	3.2218	55.8139
chr10	135534747	661059296	4.8774	184.4714
chr11	135006516	460604449	3.4117	17.1529
chr12	133851895	563187966	4.2075	19.057
chr13	115169878	277861807	2.4126	6.0206
chr14	107349540	325691550	3.0339	9.901
chr15	102531392	310968256	3.0329	10.3892
chr16	90354753	422244209	4.6732	84.2465
chr17	81195210	282086857	3.4742	31.5056
chr18	78077248	239721640	3.0703	48.1612
chr19	59128983	194628203	3.2916	16.4096
chr20	63025520	258858547	4.1072	35.4994
chr21	48129895	140483667	2.9188	50.8493
chr22	51304566	112964875	2.2018	10.0527
chrMT	16571	5919076	357.1949	206.1689
chrX	155270560	396720296	2.555	10.5234

chrY	59373566	278624383	4.6927	153.6098
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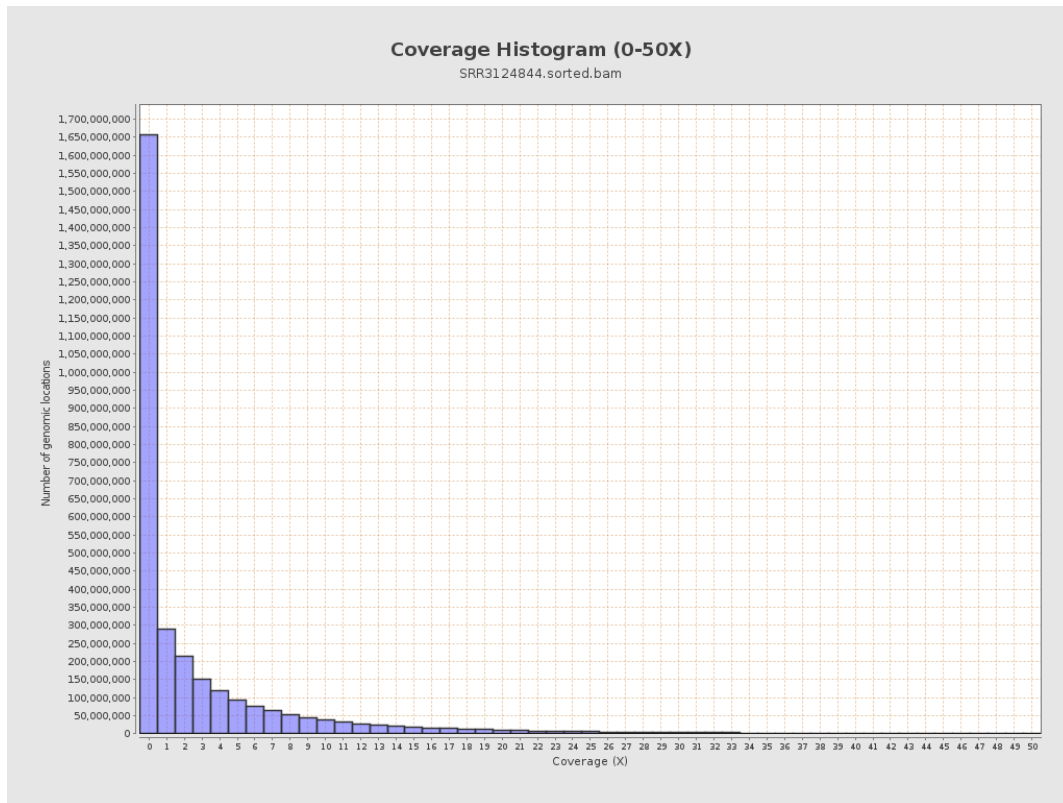
3. Results : Coverage across reference



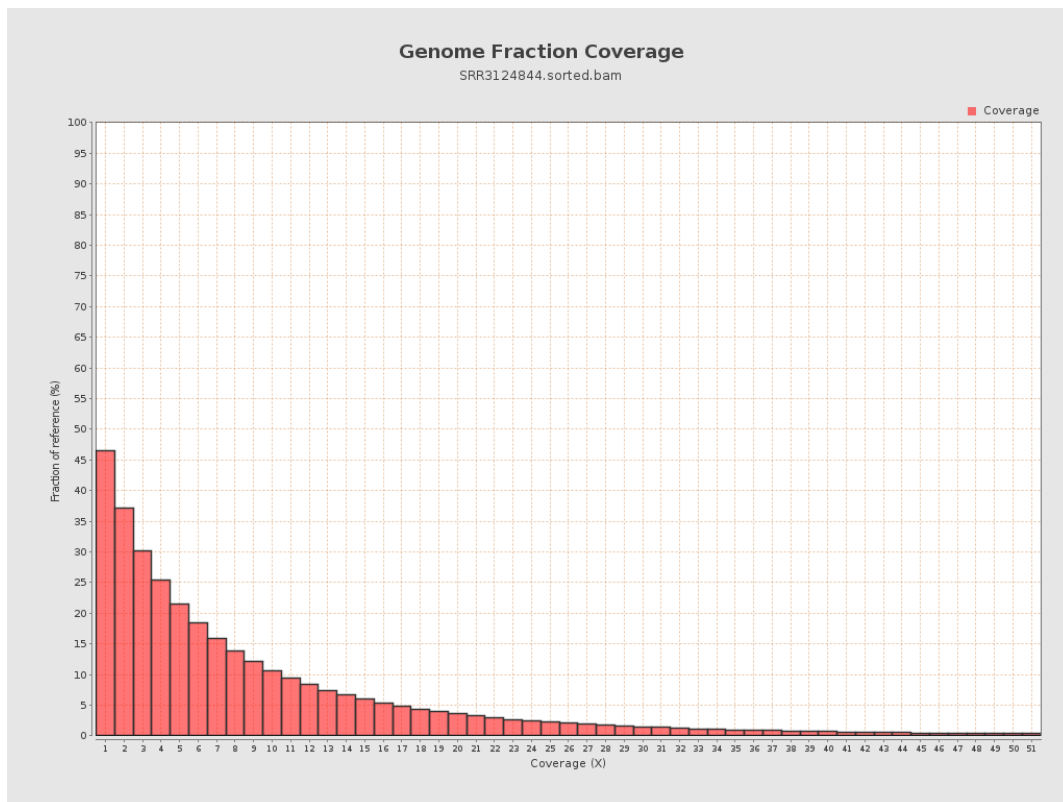
4. Results : Coverage Histogram



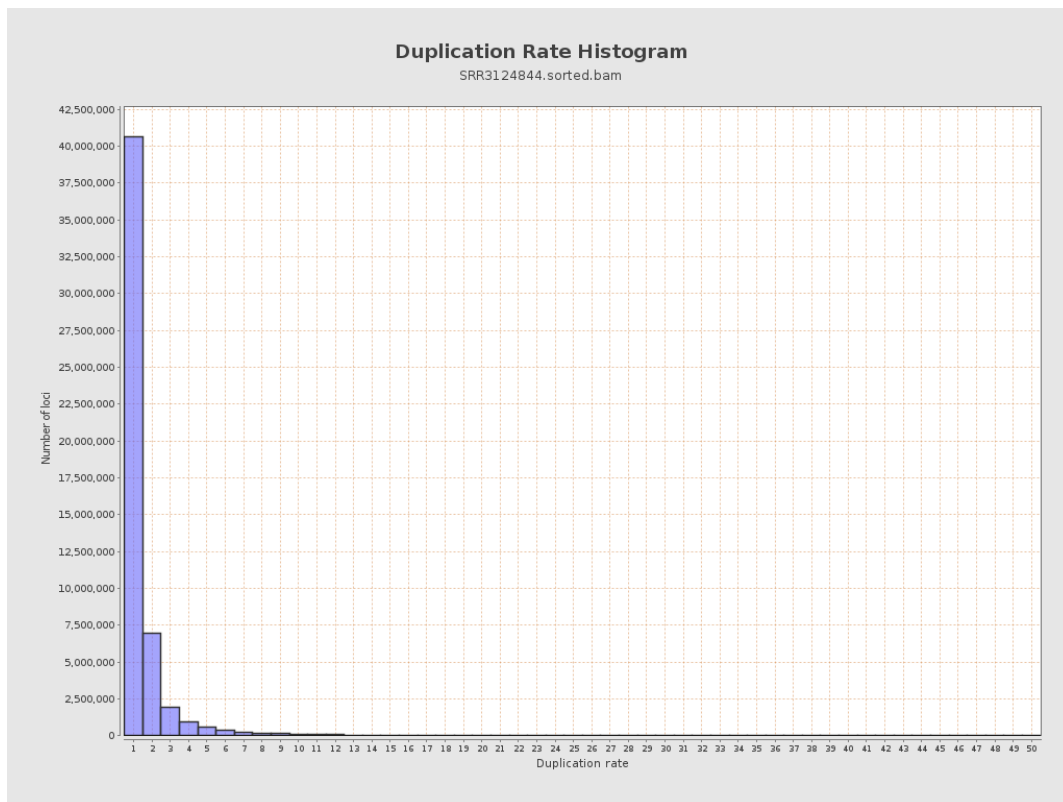
5. Results : Coverage Histogram (0-50X)



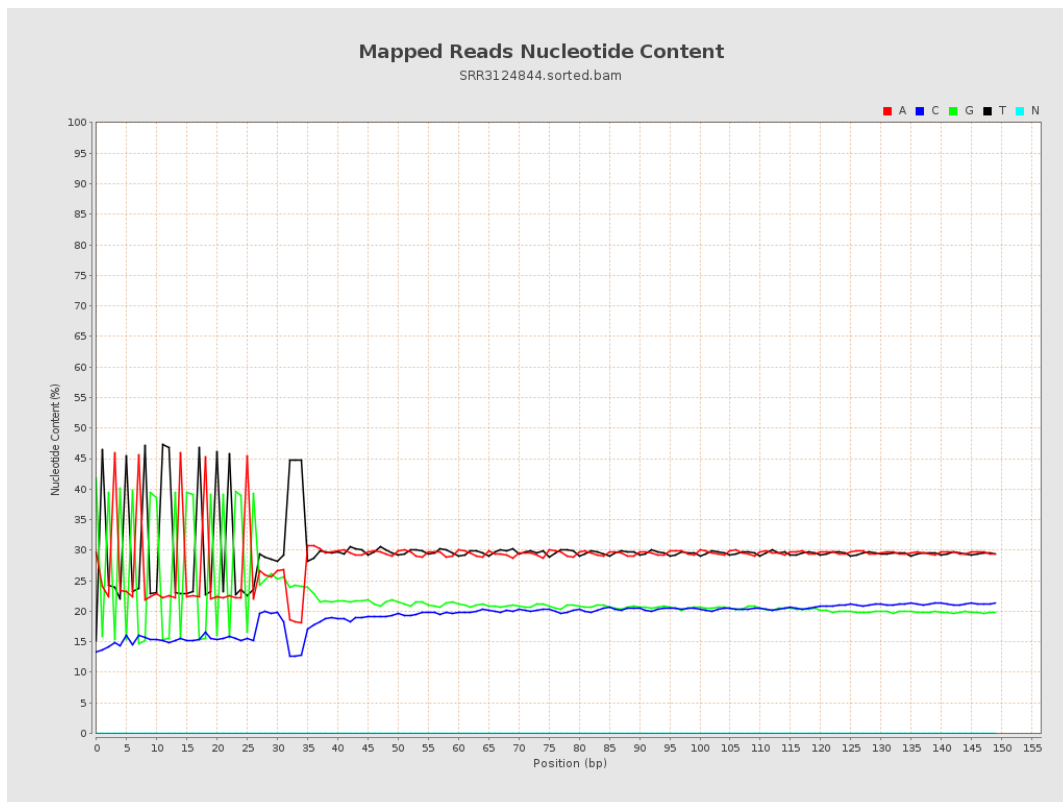
6. Results : Genome Fraction Coverage



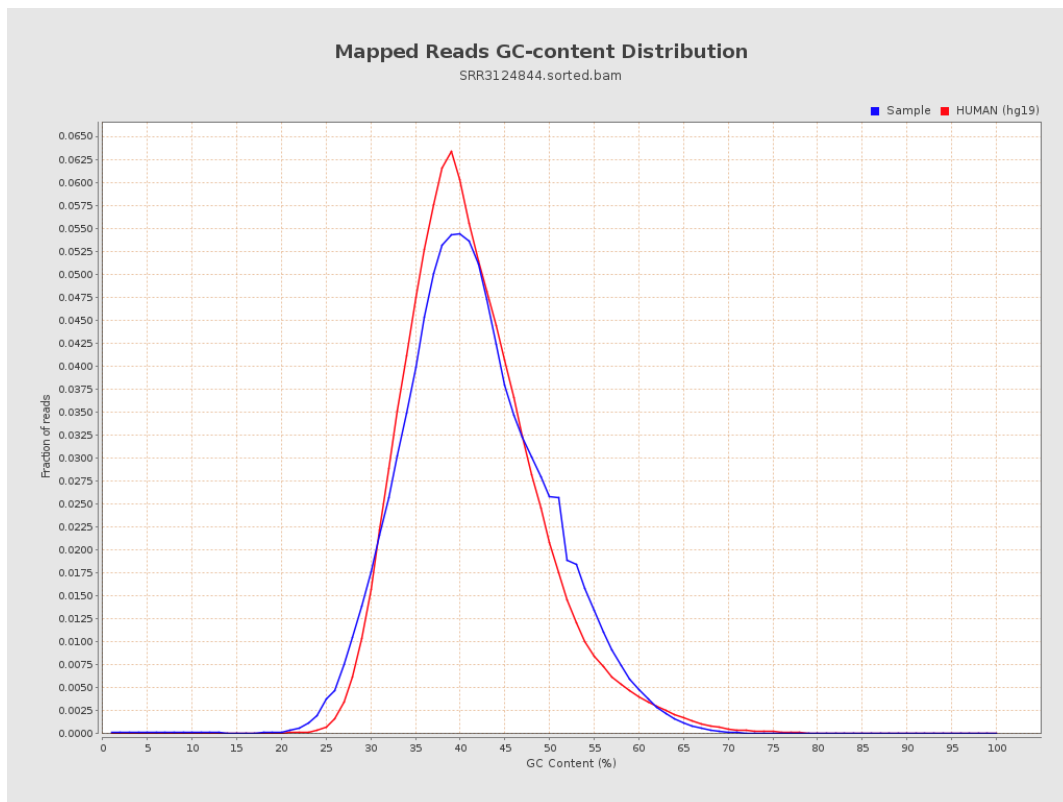
7. Results : Duplication Rate Histogram



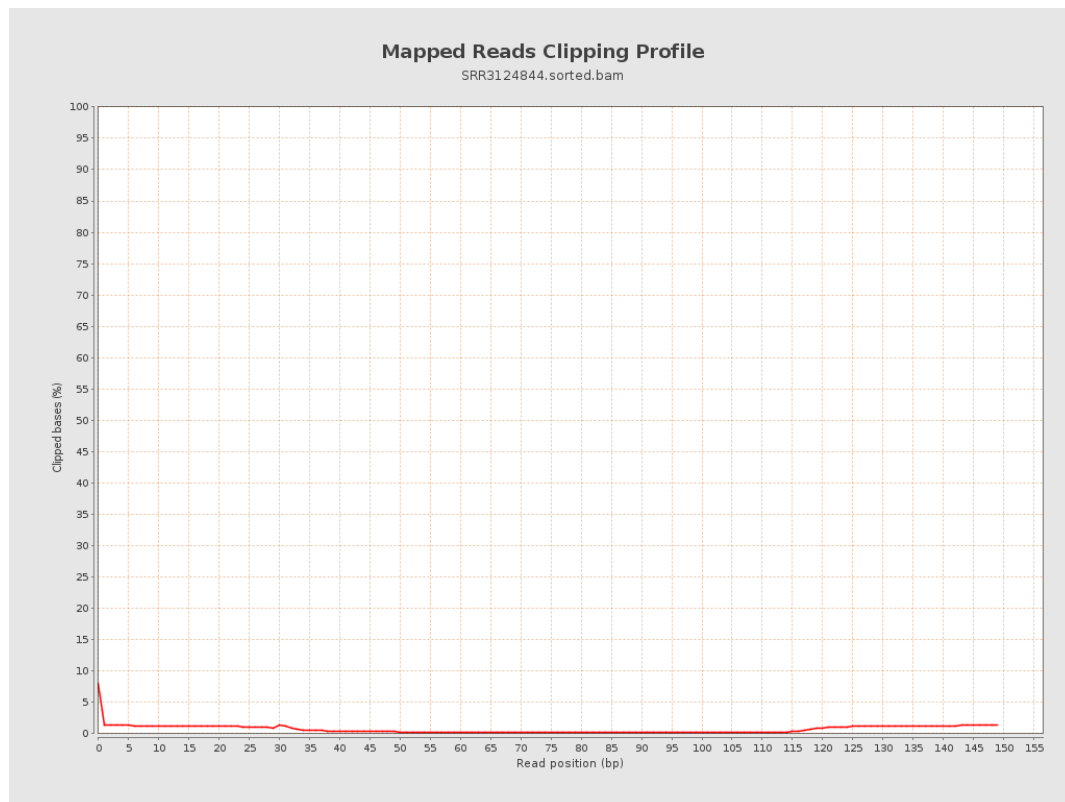
8. Results : Mapped Reads Nucleotide Content



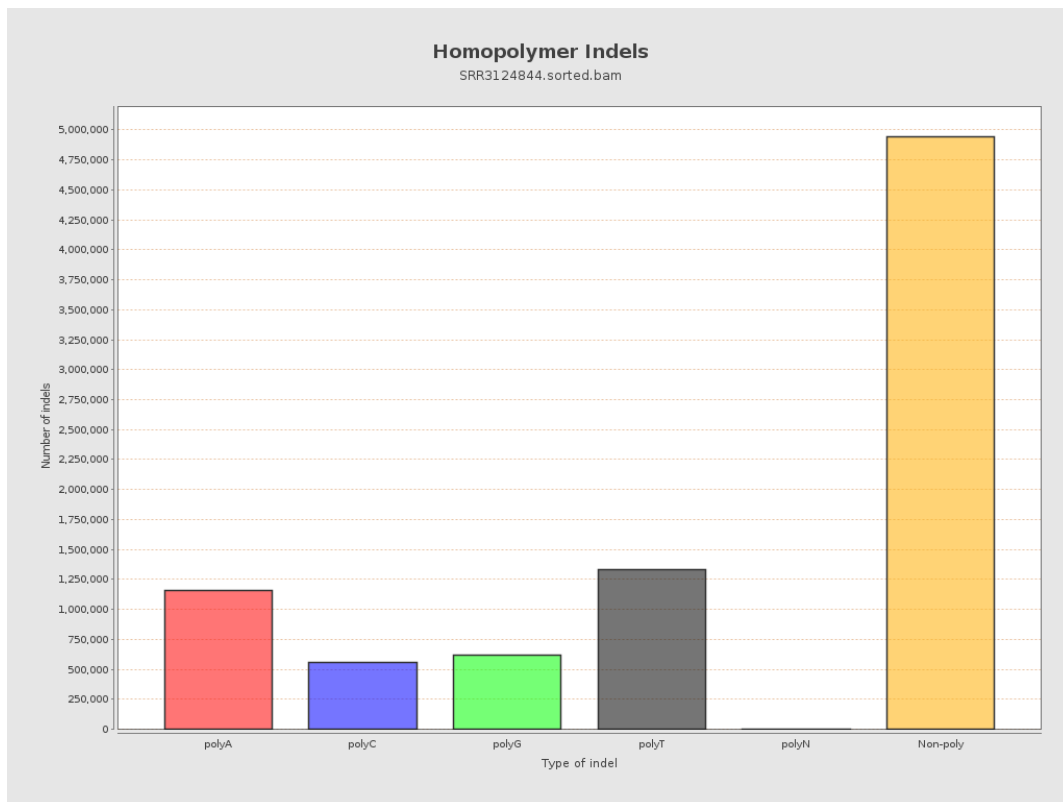
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



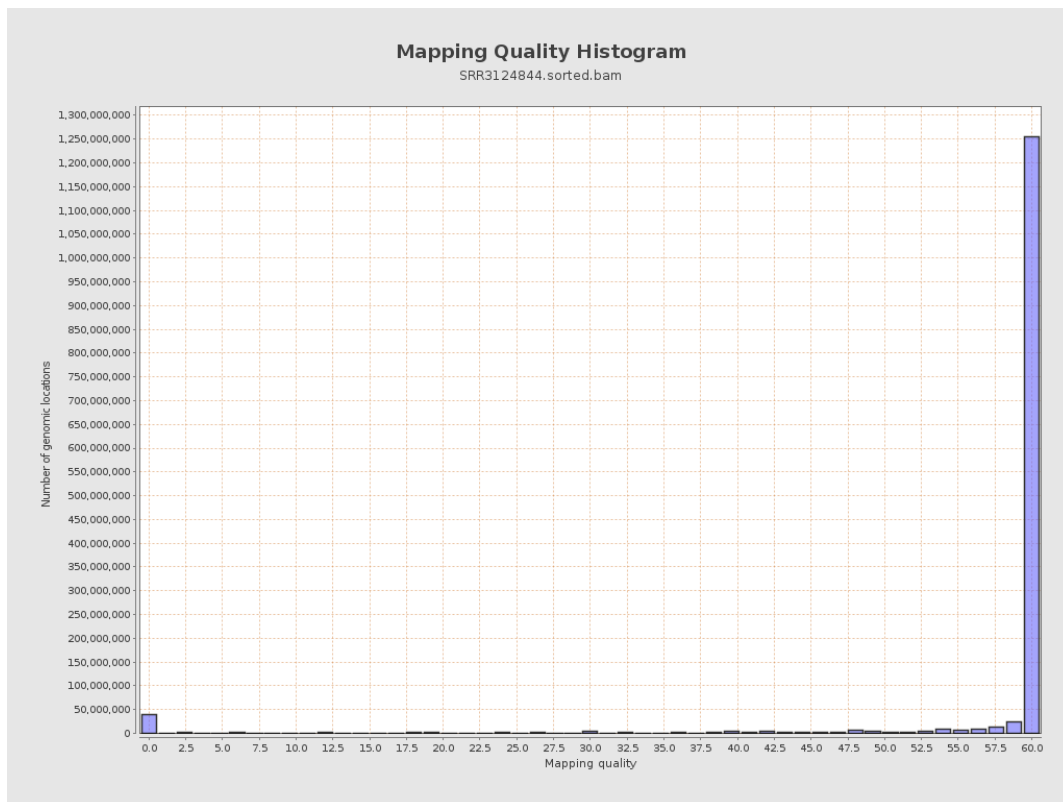
11. Results : Homopolymer Indels



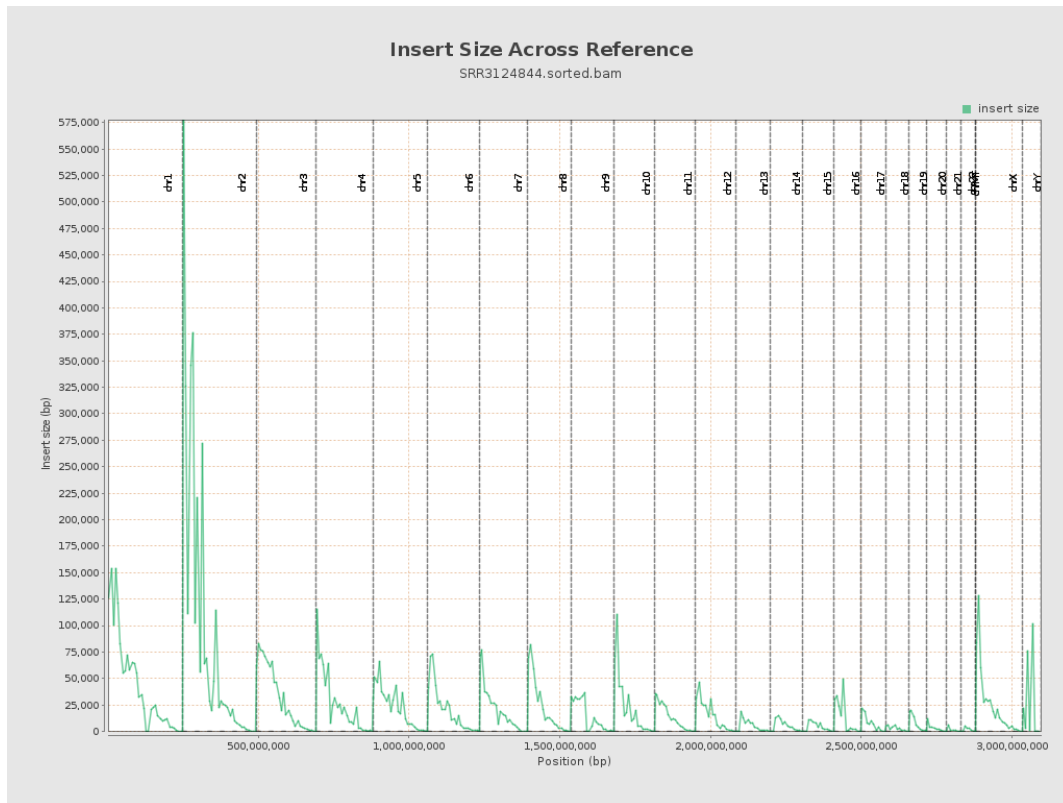
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

