

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 21:21:35

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10174014.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_SRR10174014 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10174014_1.fastq.gz SRR10174014_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 21:21:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10174014.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,859,012
Mapped reads	6,668,420 / 97.22%
Unmapped reads	190,592 / 2.78%
Mapped paired reads	6,668,420 / 97.22%
Mapped reads, first in pair	3,336,681 / 48.65%
Mapped reads, second in pair	3,331,739 / 48.57%
Mapped reads, both in pair	6,545,680 / 95.43%
Mapped reads, singletons	122,740 / 1.79%
Secondary alignments	0
Supplementary alignments	627,291 / 9.15%
Read min/max/mean length	30 / 133 / 127.88
Duplicated reads (estimated)	5,167,466 / 75.34%
Duplication rate	65.28%
Clipped reads	2,603,212 / 37.95%

2.2. ACGT Content

Number/percentage of A's	238,121,540 / 30.22%
Number/percentage of C's	154,050,317 / 19.55%
Number/percentage of T's	237,132,493 / 30.09%
Number/percentage of G's	158,637,513 / 20.13%
Number/percentage of N's	9,187 / 0%

GC Percentage	39.68%
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2.3. Coverage

Mean	0.2547
Standard Deviation	3.6602

2.4. Mapping Quality

Mean Mapping Quality	52.79
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2.5. Insert size

Mean	667,385.16
Standard Deviation	7,537,993.46
P25/Median/P75	144 / 199 / 281

2.6. Mismatches and indels

General error rate	1.03%
Mismatches	7,940,667
Insertions	79,245
Mapped reads with at least one insertion	1.15%
Deletions	154,203
Mapped reads with at least one deletion	2.25%
Homopolymer indels	43.89%

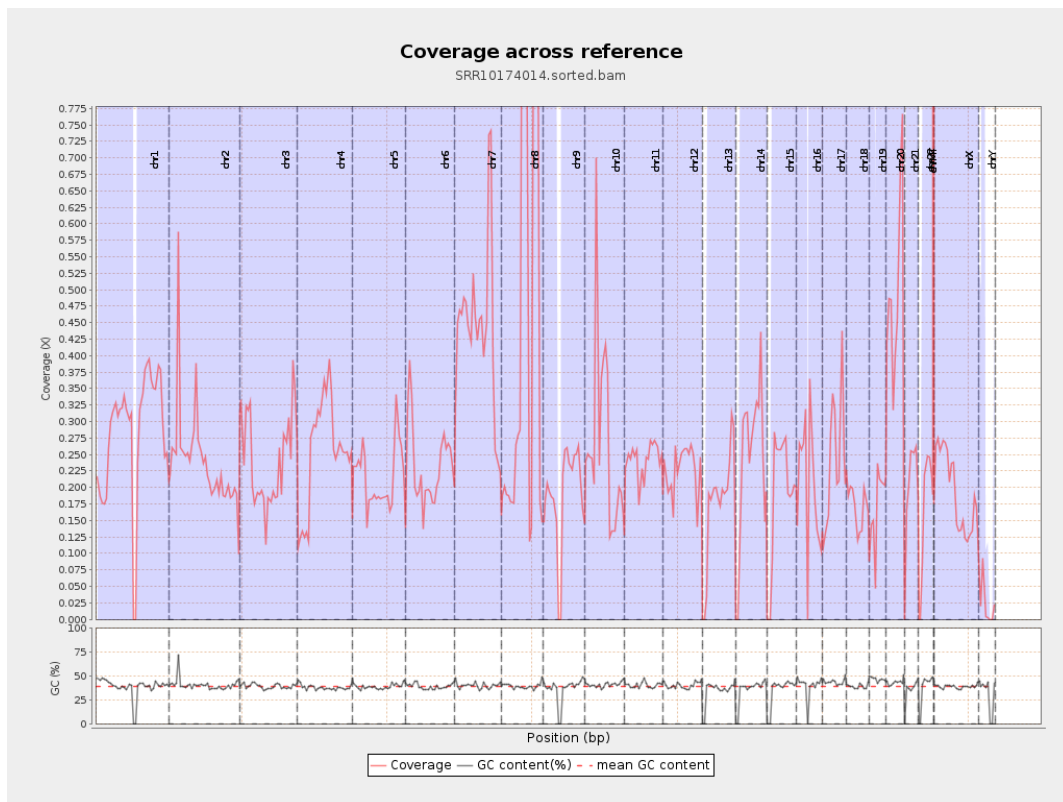
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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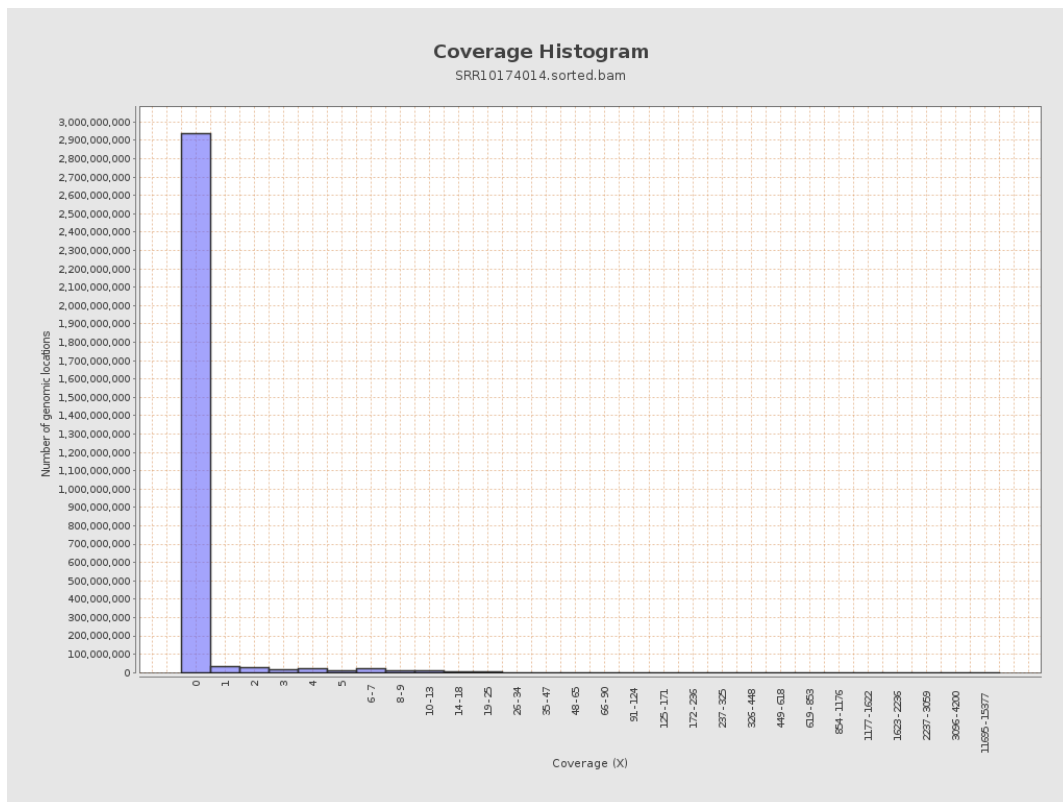
		bases	coverage	deviation
chr1	249250621	70391399	0.2824	1.8654
chr2	243199373	58579242	0.2409	10.7697
chr3	198022430	47846931	0.2416	1.4196
chr4	191154276	48384202	0.2531	1.8249
chr5	180915260	38990075	0.2155	1.3289
chr6	171115067	39357128	0.23	1.4711
chr7	159138663	70895549	0.4455	4.2526
chr8	146364022	77785233	0.5315	2.7534
chr9	141213431	26895229	0.1905	1.6362
chr10	135534747	36389108	0.2685	4.7225
chr11	135006516	32487063	0.2406	1.4591
chr12	133851895	30511961	0.228	1.3851
chr13	115169878	20419573	0.1773	1.2099
chr14	107349540	26069939	0.2429	1.4368
chr15	102531392	19616459	0.1913	1.2532
chr16	90354753	18202635	0.2015	1.8374
chr17	81195210	19707712	0.2427	1.5785
chr18	78077248	13458106	0.1724	2.1707
chr19	59128983	10013250	0.1693	1.5479
chr20	63025520	30953518	0.4911	2.0498
chr21	48129895	9727615	0.2021	1.3972
chr22	51304566	8268475	0.1612	1.1179
chrMT	16571	2060842	124.3644	97.8974
chrX	155270560	29977381	0.1931	1.2663

chrY	59373566	1363663	0.023	0.9844
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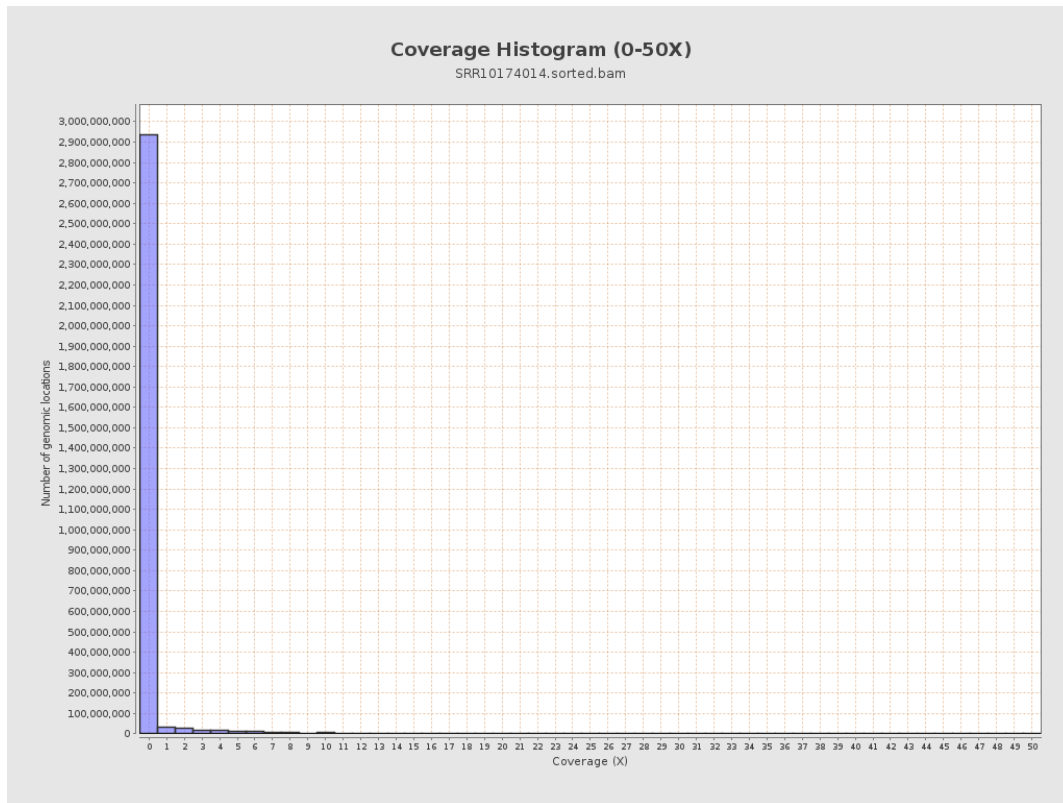
3. Results : Coverage across reference



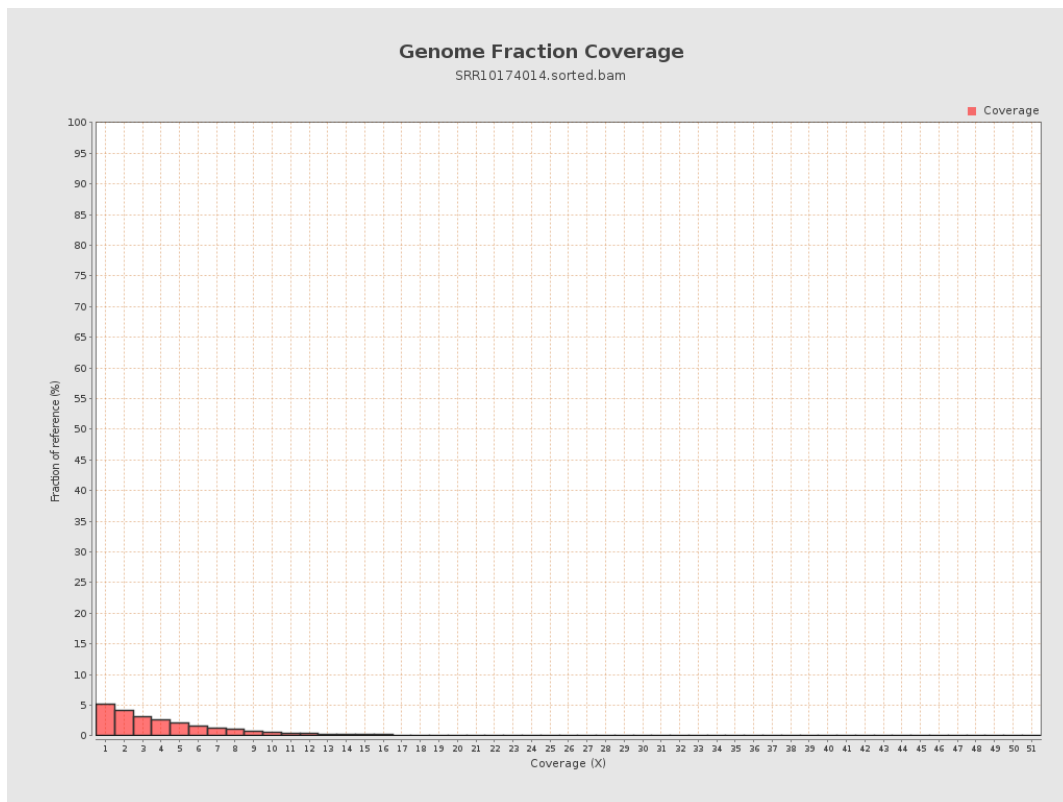
4. Results : Coverage Histogram



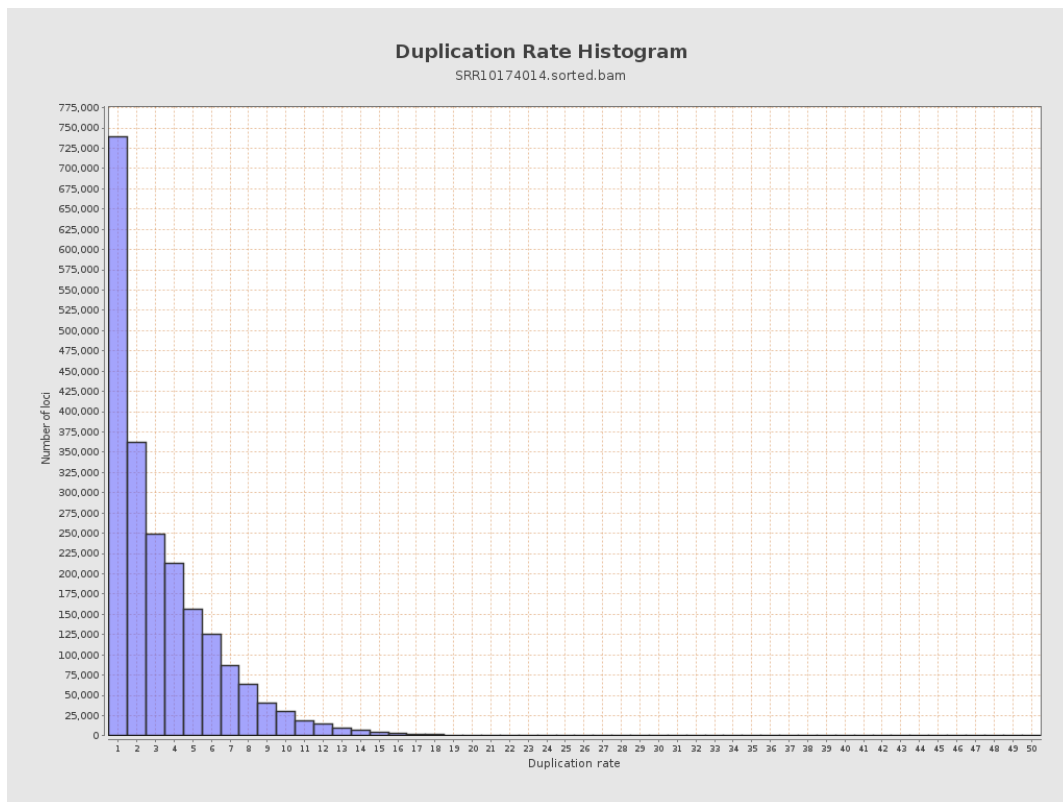
5. Results : Coverage Histogram (0-50X)



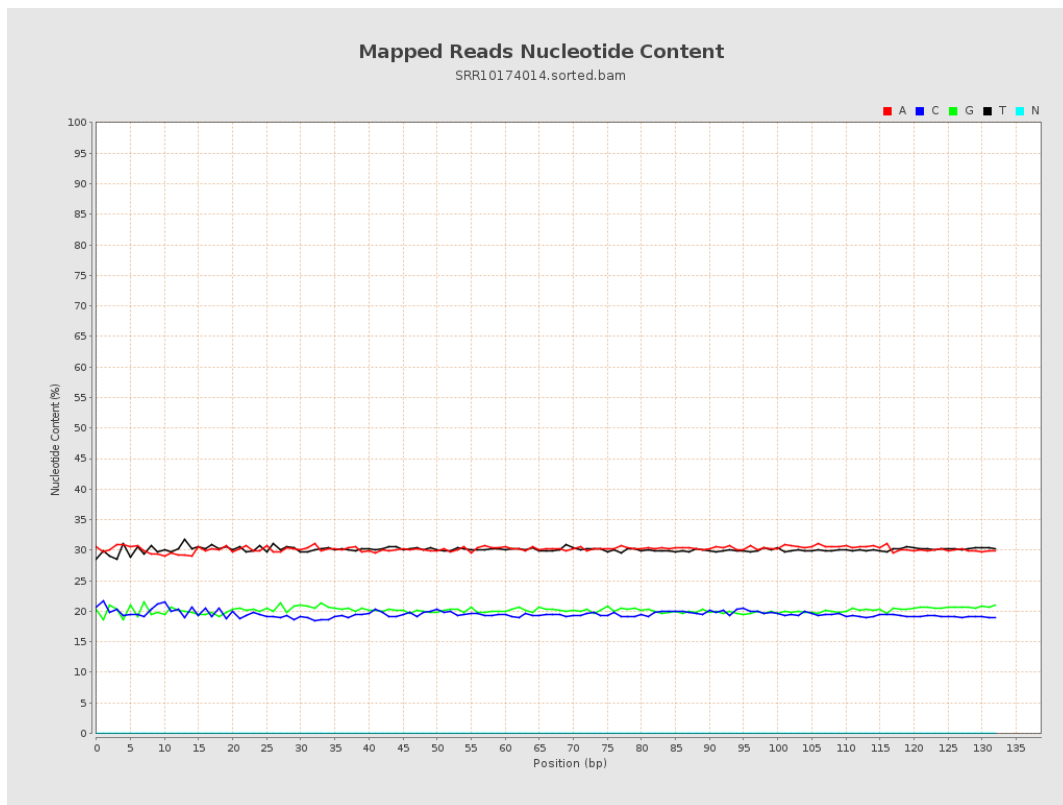
6. Results : Genome Fraction Coverage



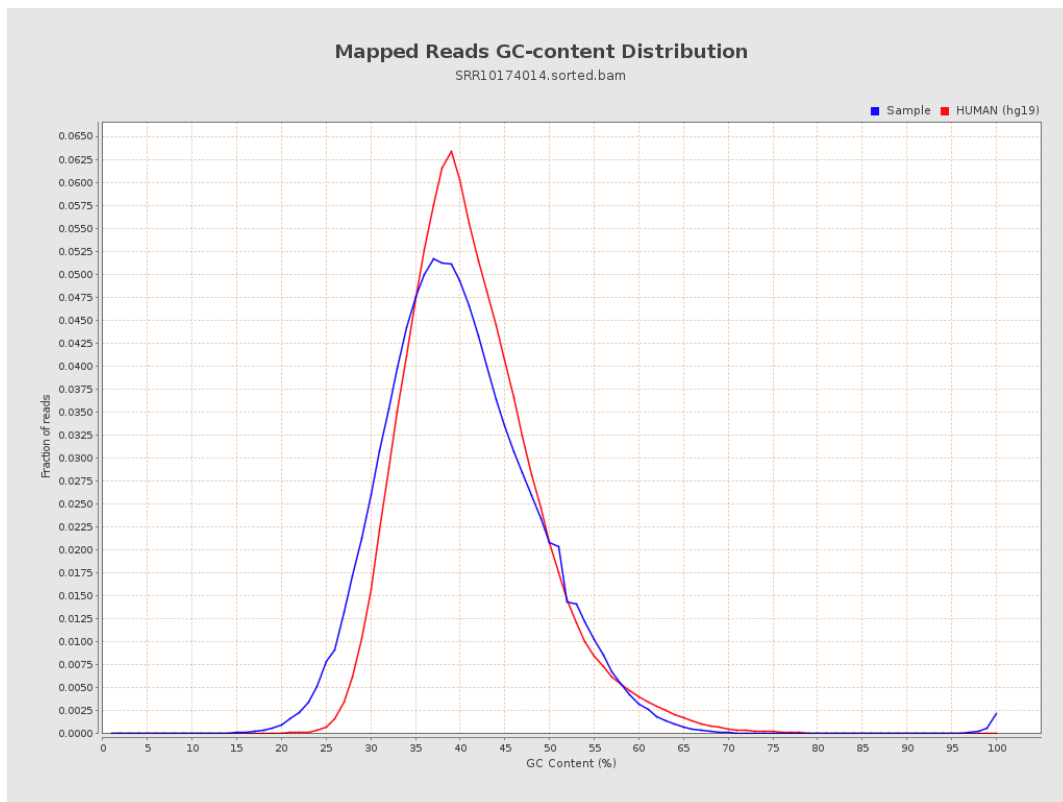
7. Results : Duplication Rate Histogram



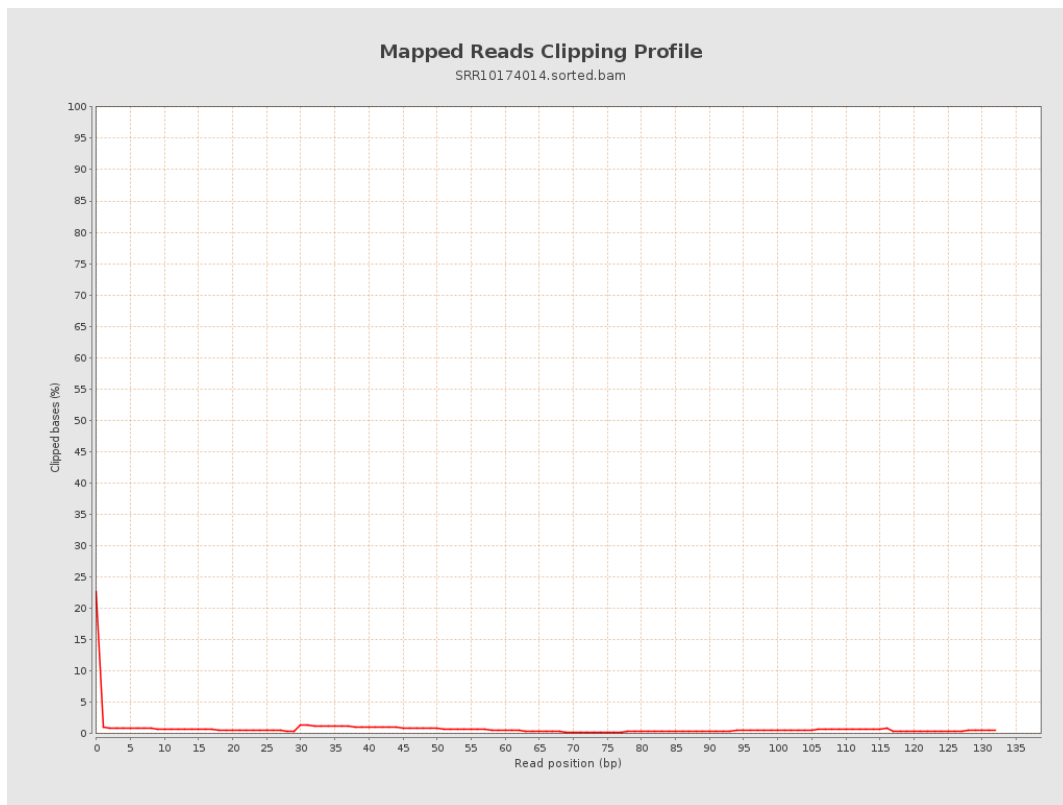
8. Results : Mapped Reads Nucleotide Content



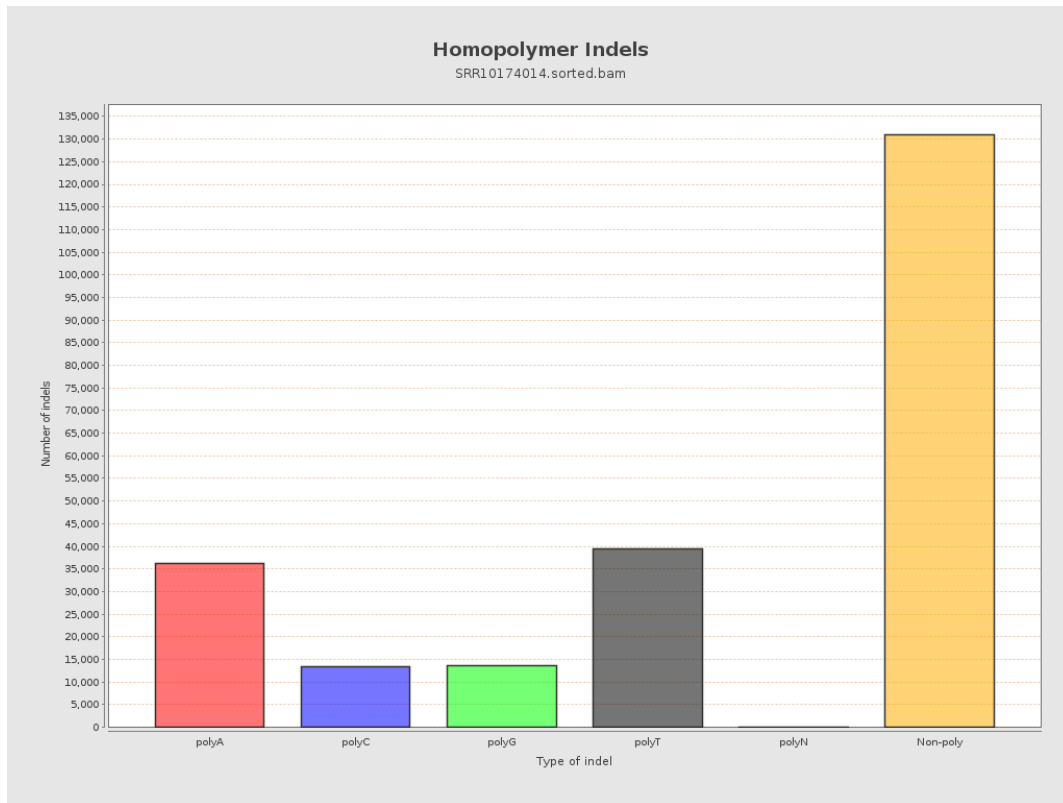
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



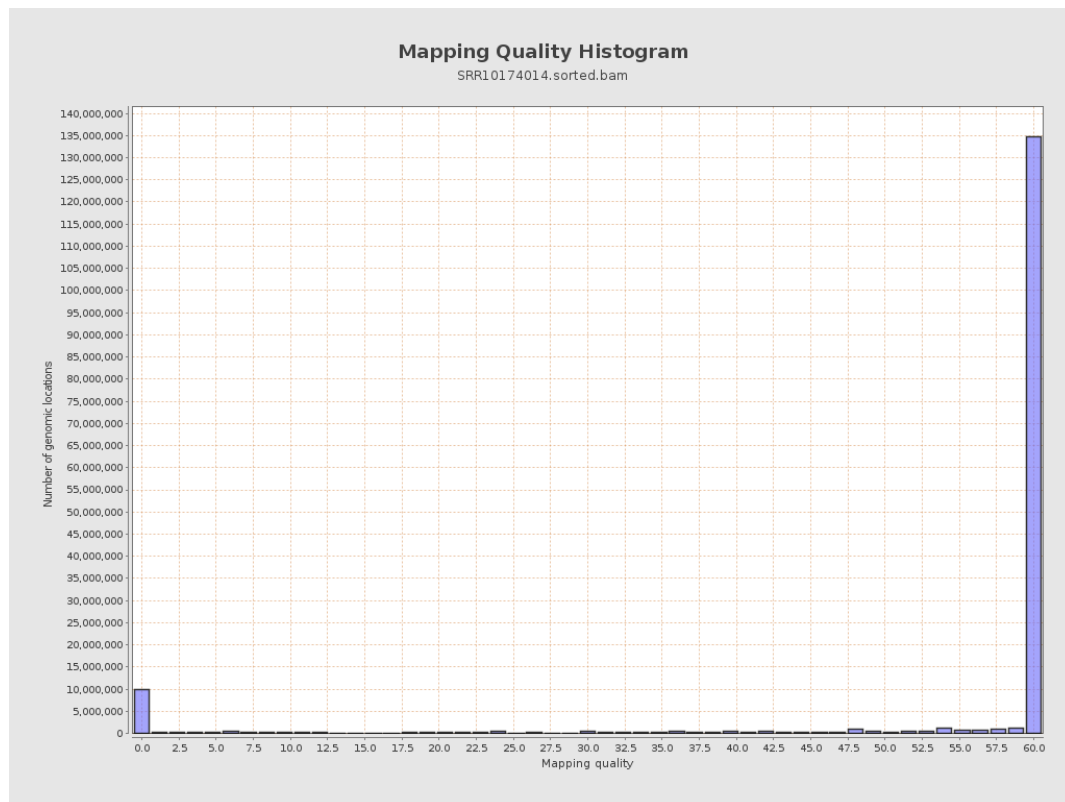
11. Results : Homopolymer Indels



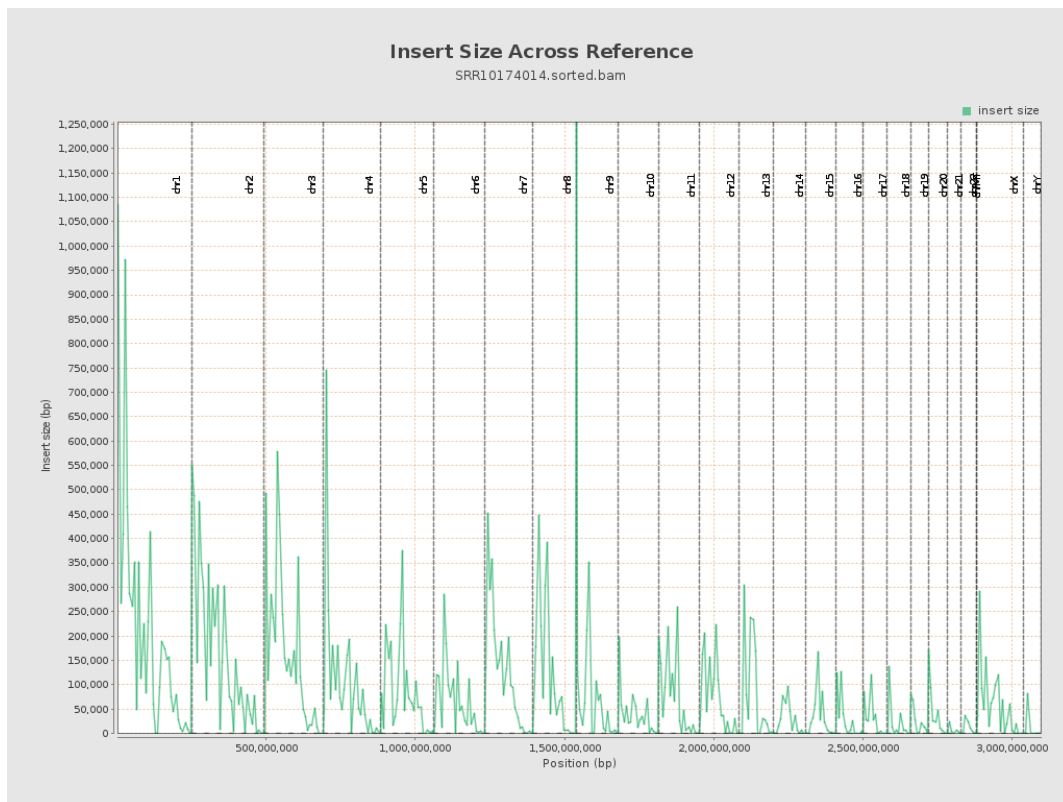
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

