

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 19:52:24

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354861.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_SRR22354861 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354861_1.fastq.gz SRR22354861_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 19:52:22 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354861.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,083,160
Mapped reads	20,782,259 / 98.57%
Unmapped reads	300,901 / 1.43%
Mapped paired reads	20,782,259 / 98.57%
Mapped reads, first in pair	10,418,619 / 49.42%
Mapped reads, second in pair	10,363,640 / 49.16%
Mapped reads, both in pair	20,700,828 / 98.19%
Mapped reads, singletons	81,431 / 0.39%
Secondary alignments	0
Supplementary alignments	759,057 / 3.6%
Read min/max/mean length	30 / 150 / 151.38
Duplicated reads (estimated)	13,074,118 / 62.01%
Duplication rate	55.47%
Clipped reads	9,589,400 / 45.48%

2.2. ACGT Content

Number/percentage of A's	740,416,733 / 27.76%
Number/percentage of C's	570,909,548 / 21.4%
Number/percentage of T's	750,126,775 / 28.12%
Number/percentage of G's	606,095,037 / 22.72%
Number/percentage of N's	13,180 / 0%

GC Percentage	44.12%
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2.3. Coverage

Mean	0.8621
Standard Deviation	35.6199

2.4. Mapping Quality

Mean Mapping Quality	53.52
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2.5. Insert size

Mean	343,515.44
Standard Deviation	6,736,308.78
P25/Median/P75	112 / 180 / 298

2.6. Mismatches and indels

General error rate	0.78%
Mismatches	19,249,115
Insertions	443,705
Mapped reads with at least one insertion	1.95%
Deletions	437,477
Mapped reads with at least one deletion	1.97%
Homopolymer indels	38.41%

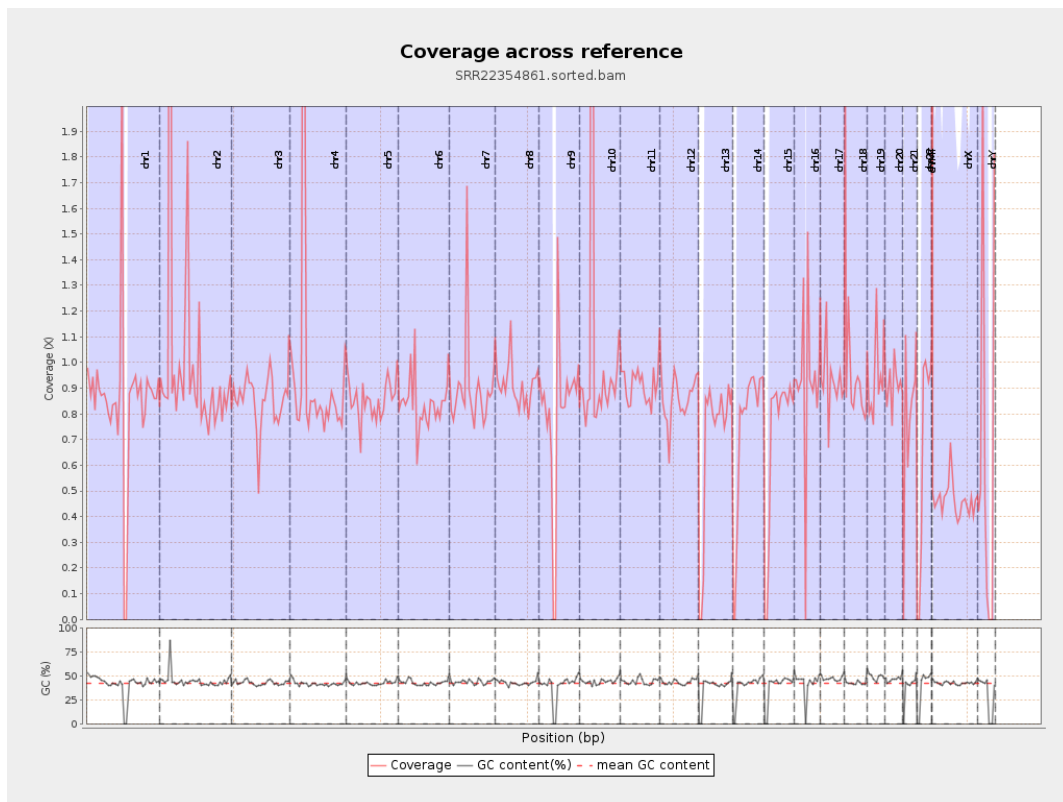
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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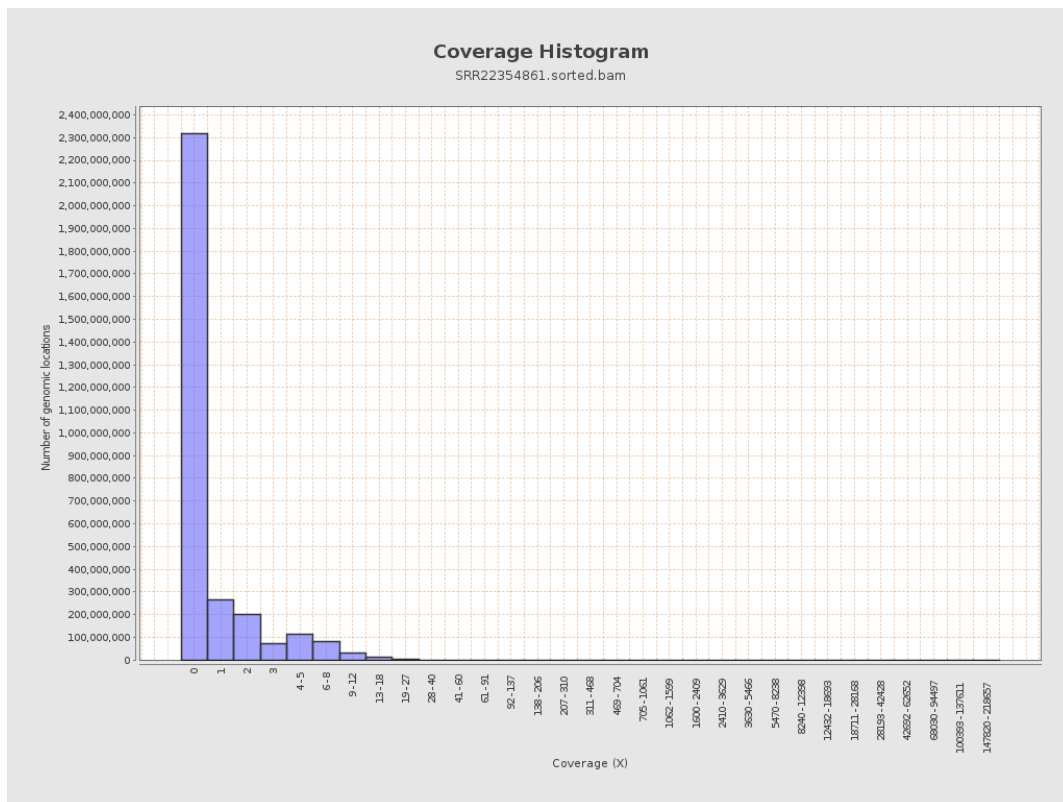
		bases	coverage	deviation
chr1	249250621	215136599	0.8631	30.8098
chr2	243199373	247468727	1.0176	115.4339
chr3	198022430	169127664	0.8541	2.5543
chr4	191154276	179986292	0.9416	18.7085
chr5	180915260	155446626	0.8592	2.2113
chr6	171115067	143968182	0.8414	3.7668
chr7	159138663	142984452	0.8985	17.1618
chr8	146364022	132833592	0.9076	12.0945
chr9	141213431	112797175	0.7988	14.7955
chr10	135534747	154128494	1.1372	34.9575
chr11	135006516	122683950	0.9087	5.8703
chr12	133851895	114696789	0.8569	2.1621
chr13	115169878	79763830	0.6926	1.8984
chr14	107349540	79031830	0.7362	4.8969
chr15	102531392	71848611	0.7007	1.904
chr16	90354753	83828029	0.9278	6.3303
chr17	81195210	74932445	0.9229	5.4011
chr18	78077248	75292887	0.9643	17.2364
chr19	59128983	54938677	0.9291	19.2648
chr20	63025520	57282589	0.9089	6.5135
chr21	48129895	38466108	0.7992	10.5202
chr22	51304566	34471621	0.6719	3.0876
chrMT	16571	14445769	871.75	295.7258
chrX	155270560	71810131	0.4625	2.2968

chrY	59373566	41569558	0.7001	22.8617
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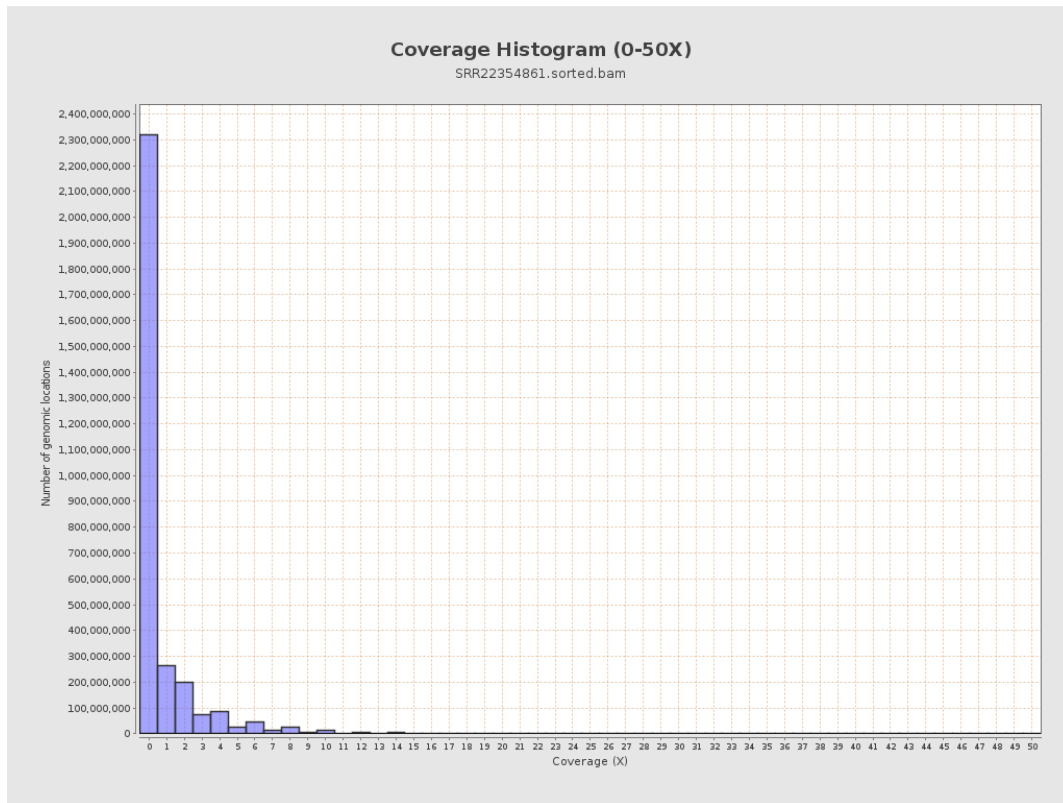
3. Results : Coverage across reference



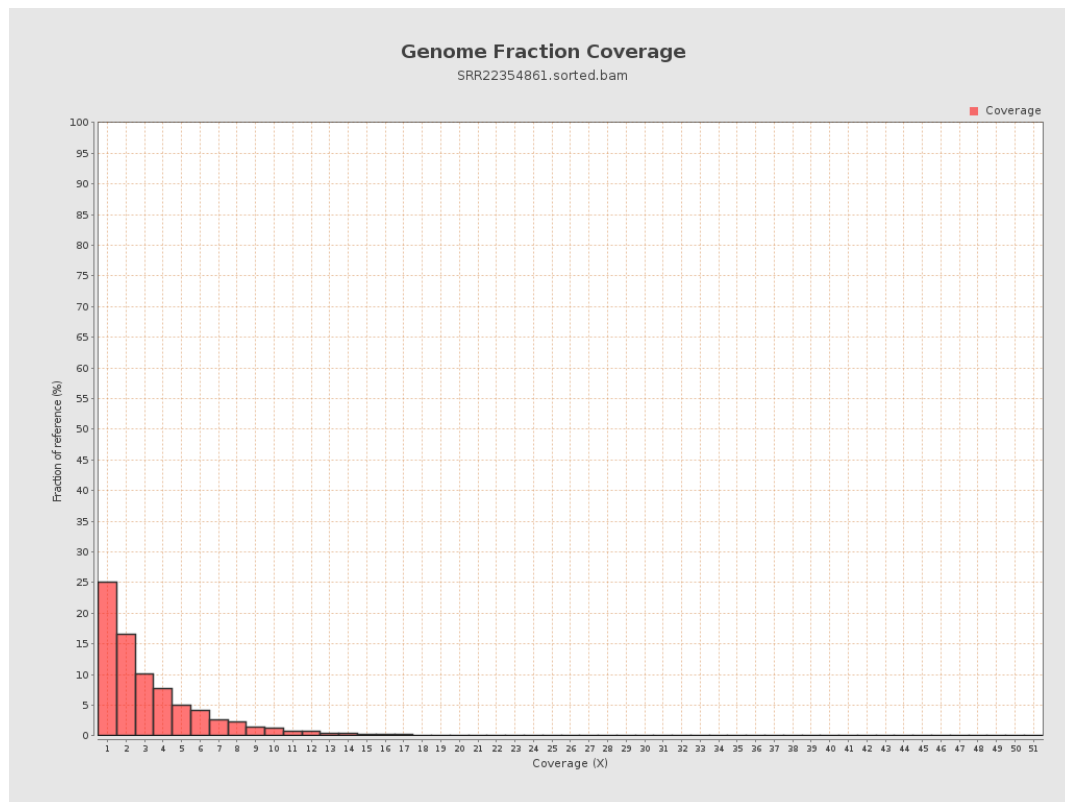
4. Results : Coverage Histogram



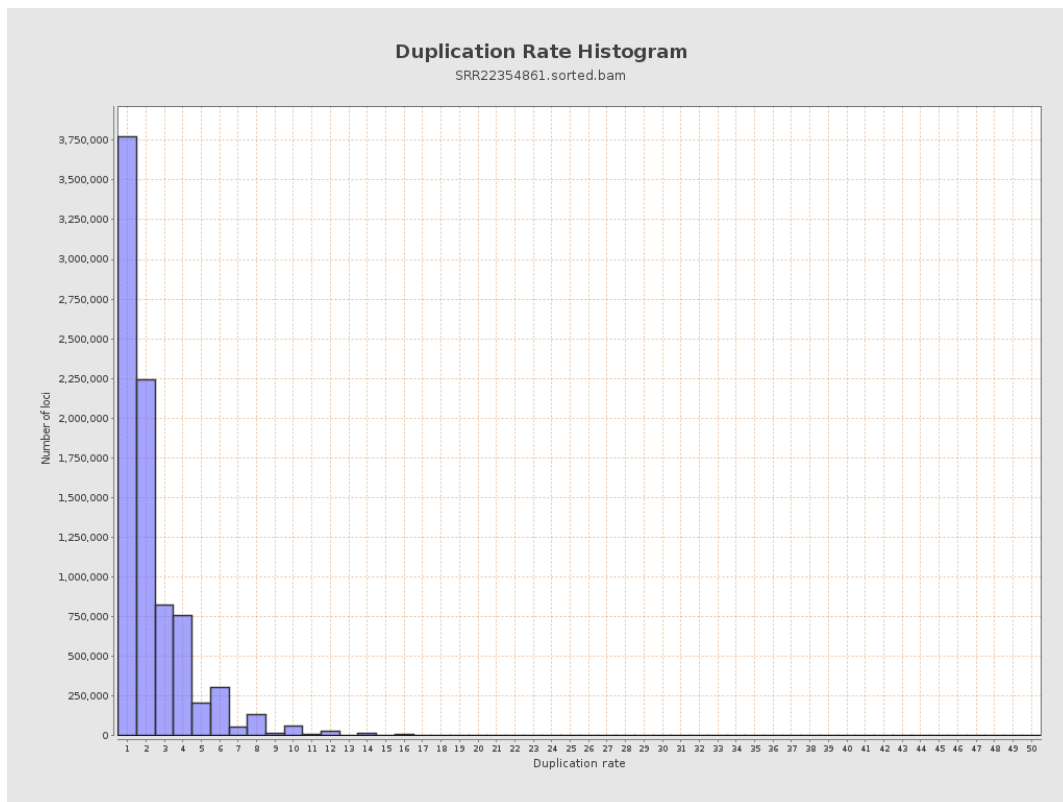
5. Results : Coverage Histogram (0-50X)



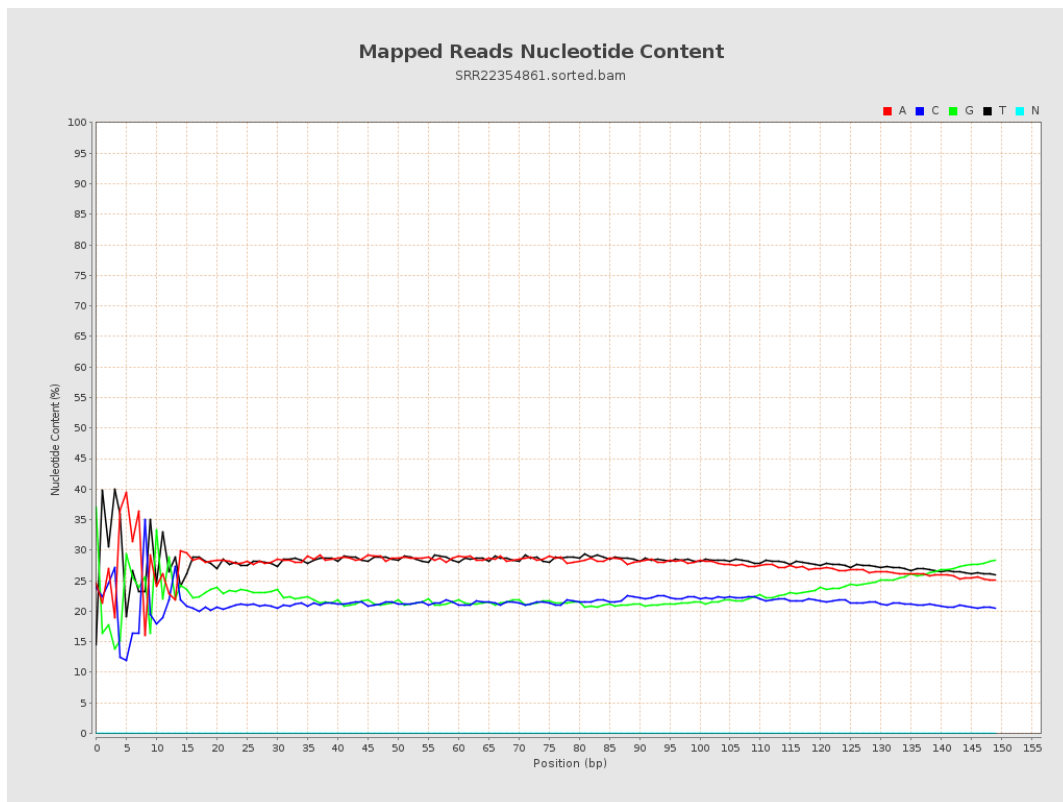
6. Results : Genome Fraction Coverage



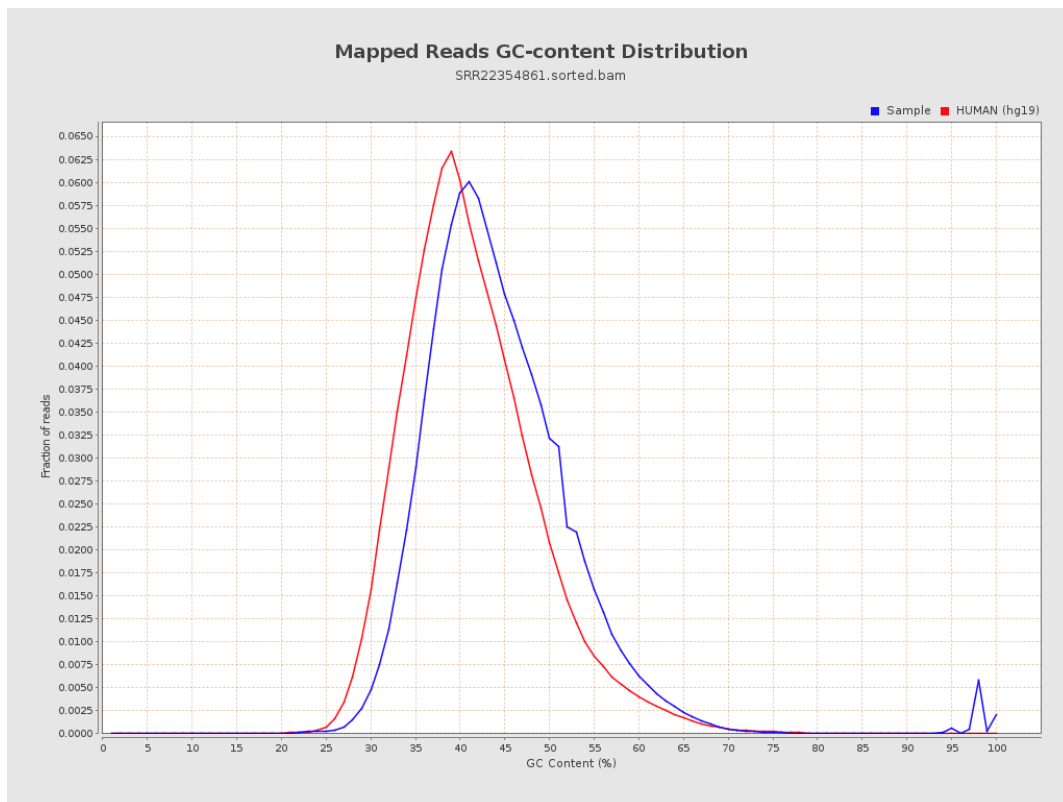
7. Results : Duplication Rate Histogram



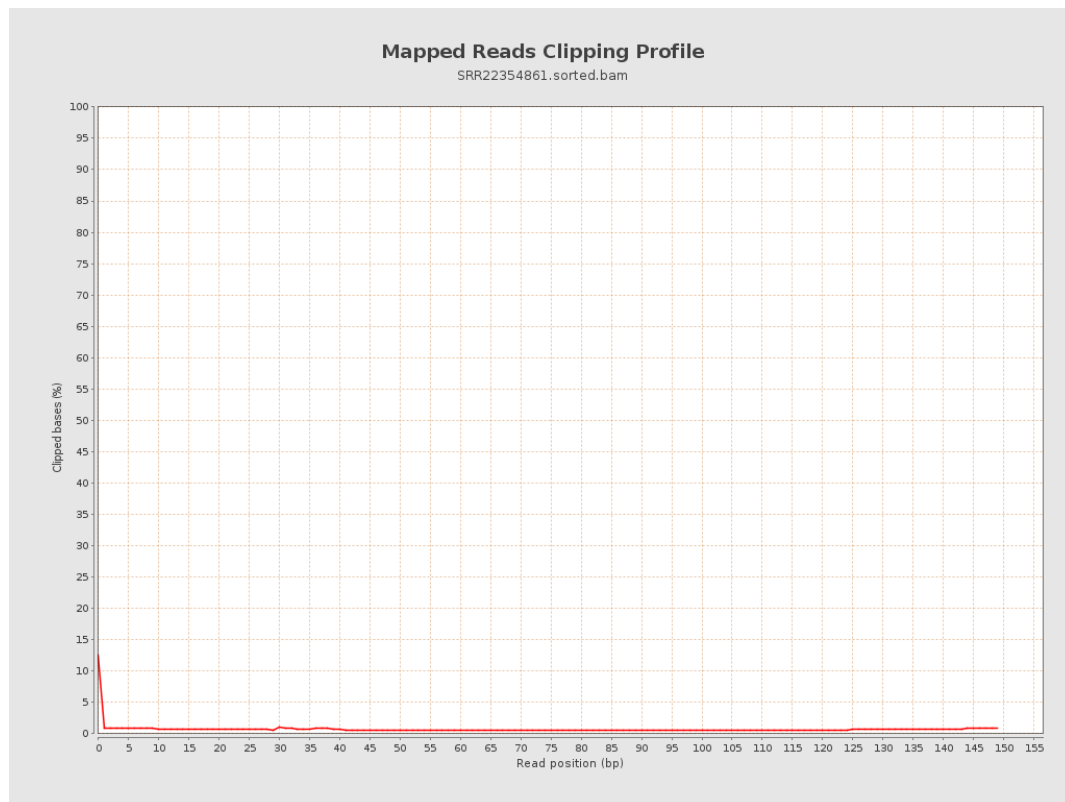
8. Results : Mapped Reads Nucleotide Content



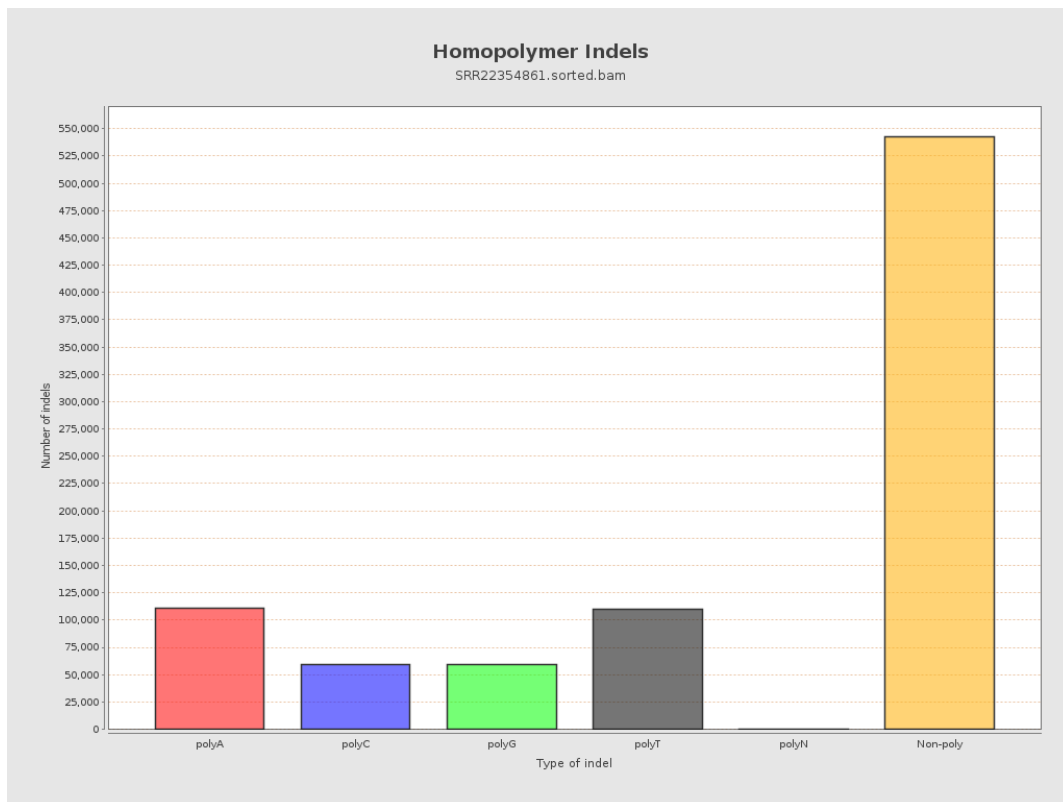
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



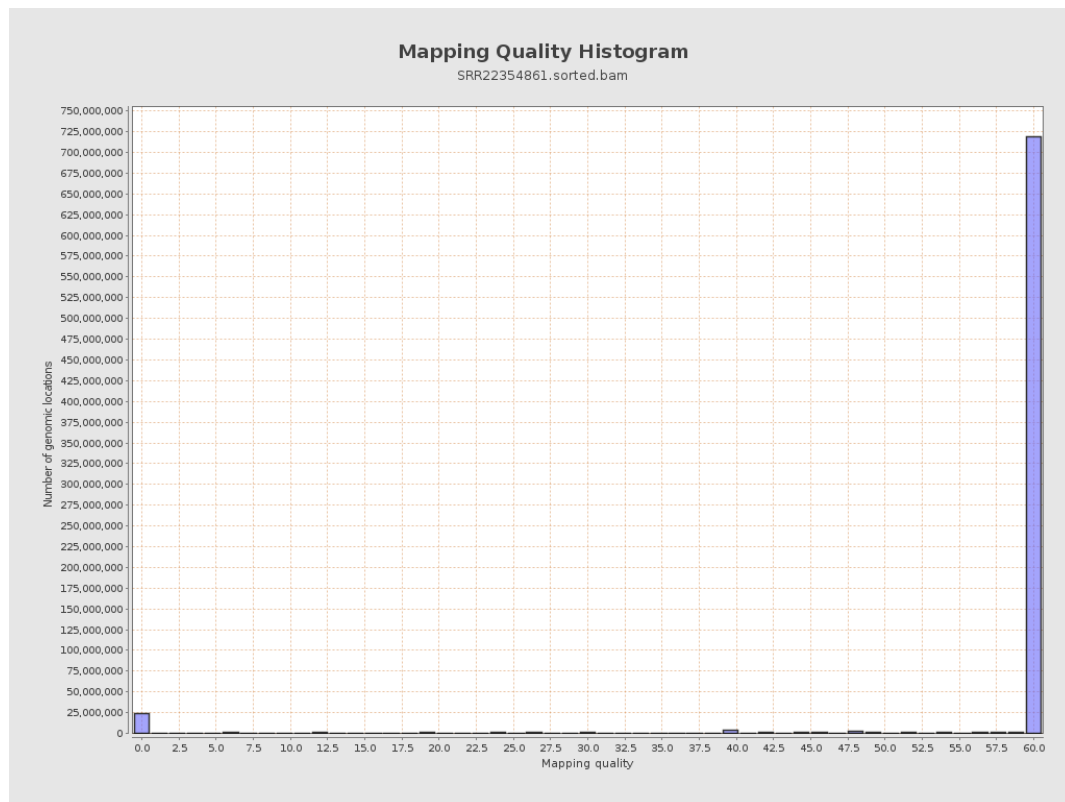
11. Results : Homopolymer Indels



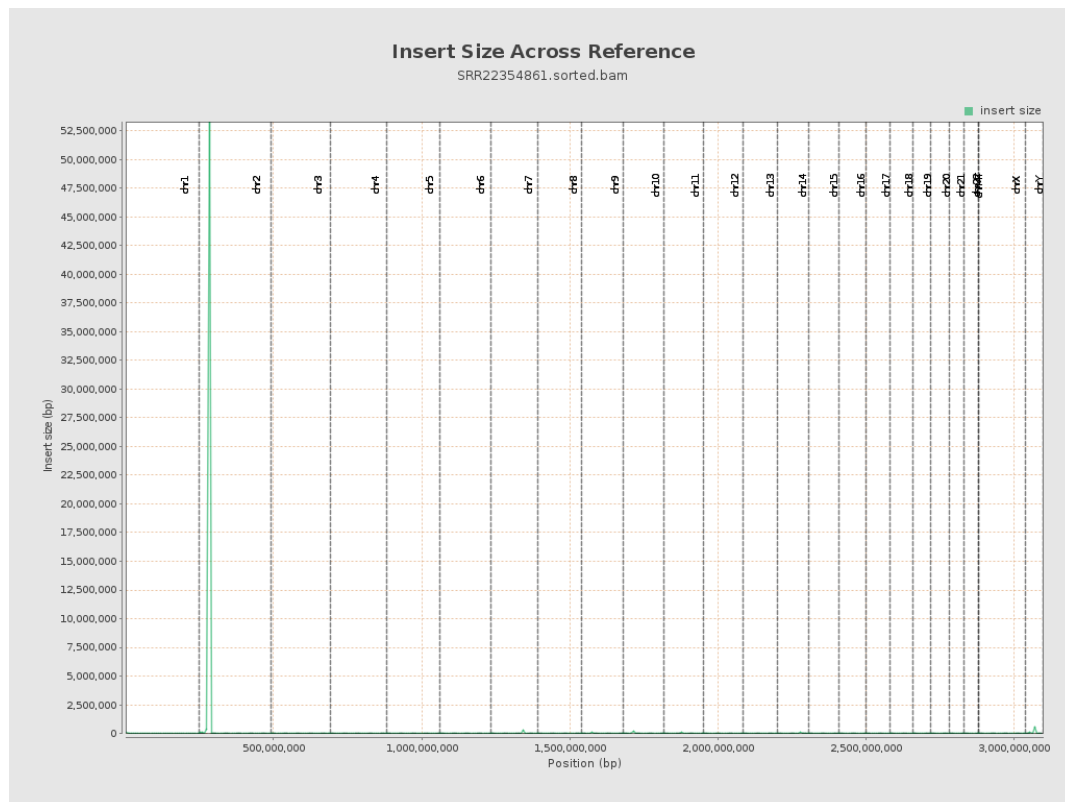
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

