

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/12/10 00:18:49

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3124878.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_SRR3124878 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3124878_1.fastq.gz SRR3124878_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Dec 10 00:18:49 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3124878.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	4,278,302
Mapped reads	4,225,793 / 98.77%
Unmapped reads	52,509 / 1.23%
Mapped paired reads	4,225,793 / 98.77%
Mapped reads, first in pair	2,116,764 / 49.48%
Mapped reads, second in pair	2,109,029 / 49.3%
Mapped reads, both in pair	4,209,942 / 98.4%
Mapped reads, singletons	15,851 / 0.37%
Secondary alignments	0
Supplementary alignments	40,761 / 0.95%
Read min/max/mean length	30 / 151 / 151.47
Duplicated reads (estimated)	613,494 / 14.34%
Duplication rate	14.59%
Clipped reads	3,103,791 / 72.55%

2.2. ACGT Content

Number/percentage of A's	165,137,400 / 29.02%
Number/percentage of C's	117,782,103 / 20.7%
Number/percentage of T's	164,937,002 / 28.98%
Number/percentage of G's	121,203,562 / 21.3%
Number/percentage of N's	25,731 / 0%

GC Percentage	41.99%
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2.3. Coverage

Mean	0.1839
Standard Deviation	1.7817

2.4. Mapping Quality

Mean Mapping Quality	53.84
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2.5. Insert size

Mean	72,736.17
Standard Deviation	2,570,803.33
P25/Median/P75	135 / 166 / 208

2.6. Mismatches and indels

General error rate	1.31%
Mismatches	7,275,480
Insertions	85,995
Mapped reads with at least one insertion	1.97%
Deletions	190,624
Mapped reads with at least one deletion	4.38%
Homopolymer indels	47.21%

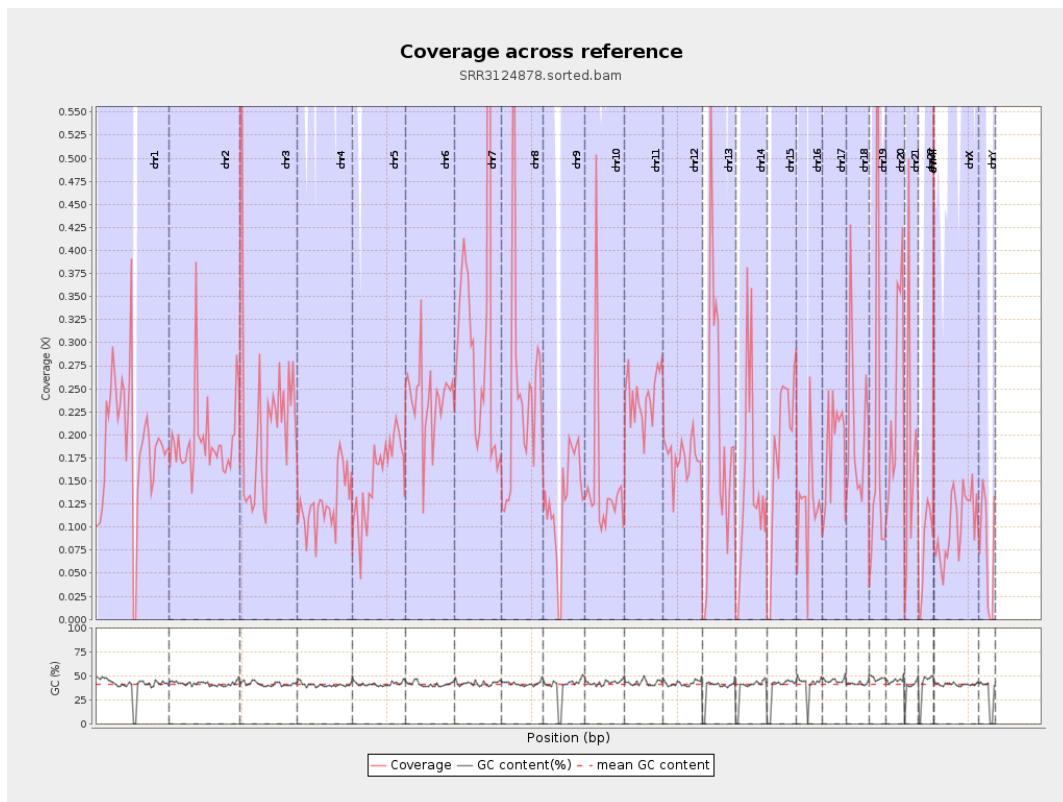
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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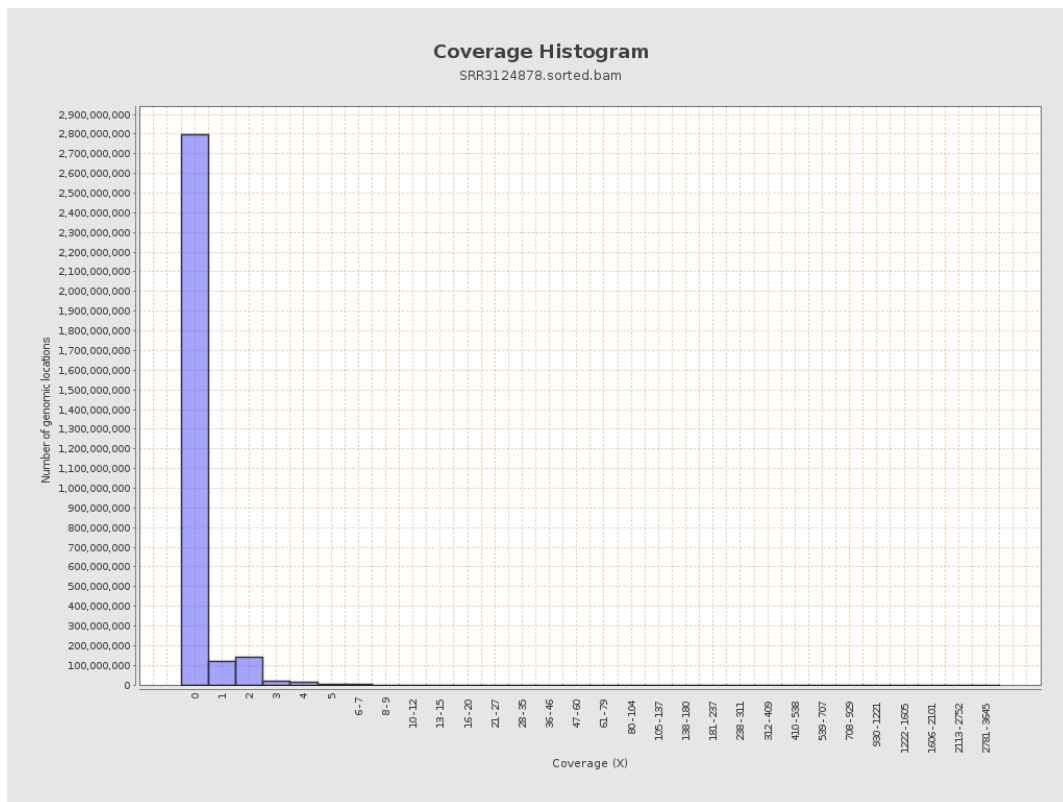
		bases	coverage	deviation
chr1	249250621	47128159	0.1891	3.457
chr2	243199373	47205187	0.1941	1.6144
chr3	198022430	43522343	0.2198	0.7388
chr4	191154276	24041872	0.1258	0.6241
chr5	180915260	27975218	0.1546	0.566
chr6	171115067	40881127	0.2389	1.4728
chr7	159138663	51455842	0.3233	2.7072
chr8	146364022	34669427	0.2369	0.9819
chr9	141213431	18236364	0.1291	1.7692
chr10	135534747	19756620	0.1458	3.8973
chr11	135006516	32194175	0.2385	1.5761
chr12	133851895	23393073	0.1748	0.5949
chr13	115169878	21588505	0.1874	0.6684
chr14	107349540	15661809	0.1459	0.5841
chr15	102531392	18830964	0.1837	0.634
chr16	90354753	11096302	0.1228	1.2467
chr17	81195210	15258609	0.1879	2.1438
chr18	78077248	16376333	0.2097	2.1222
chr19	59128983	11759443	0.1989	1.9255
chr20	63025520	15435125	0.2449	0.7448
chr21	48129895	8600244	0.1787	0.7249
chr22	51304566	3945872	0.0769	0.3947
chrMT	16571	11661	0.7037	1.0664
chrX	155270560	15970355	0.1029	0.6311

chrY	59373566	4431922	0.0746	0.9917
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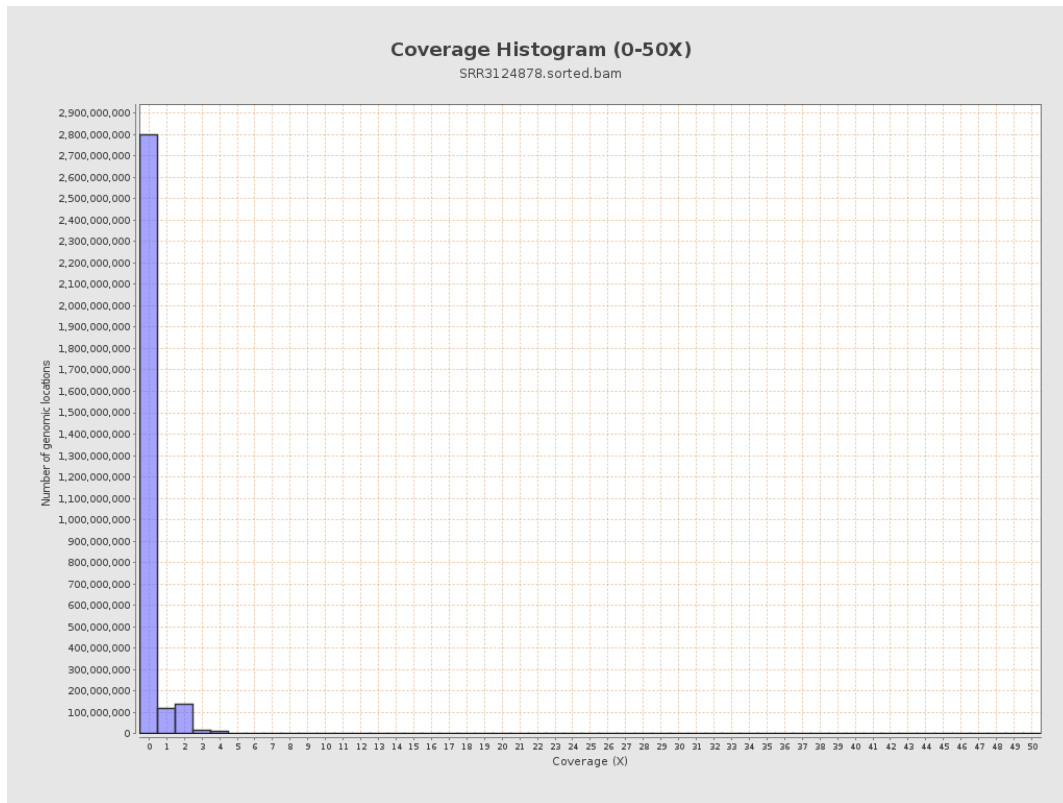
3. Results : Coverage across reference



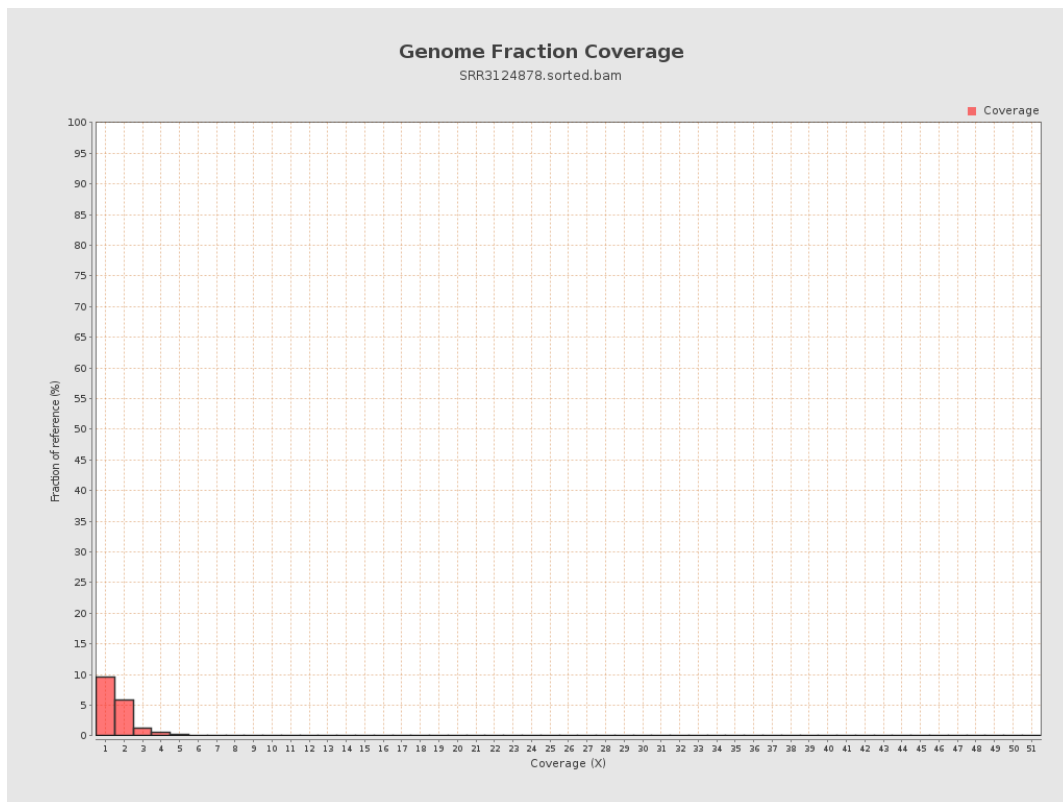
4. Results : Coverage Histogram



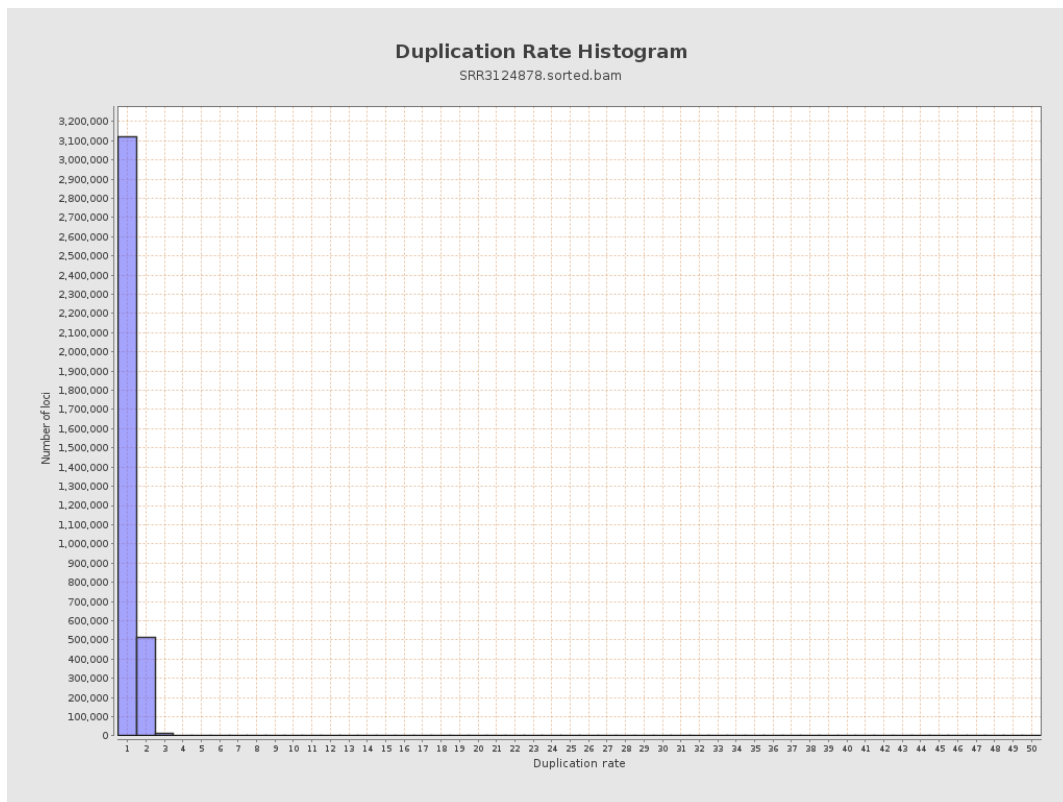
5. Results : Coverage Histogram (0-50X)



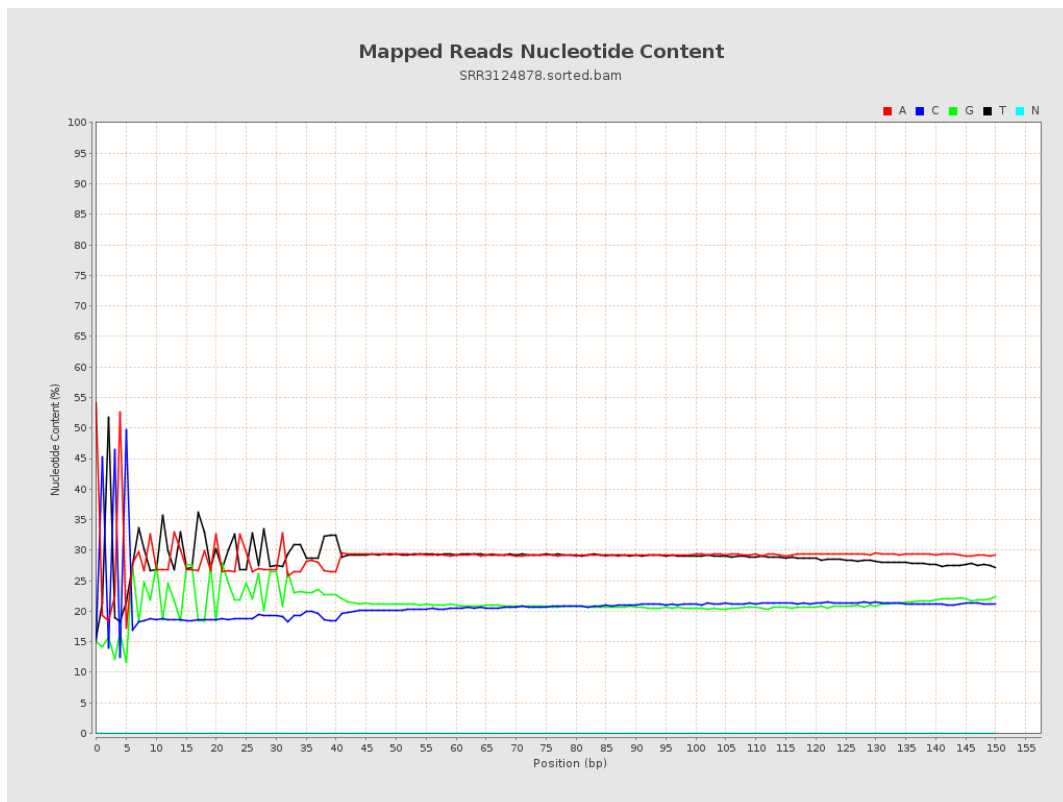
6. Results : Genome Fraction Coverage



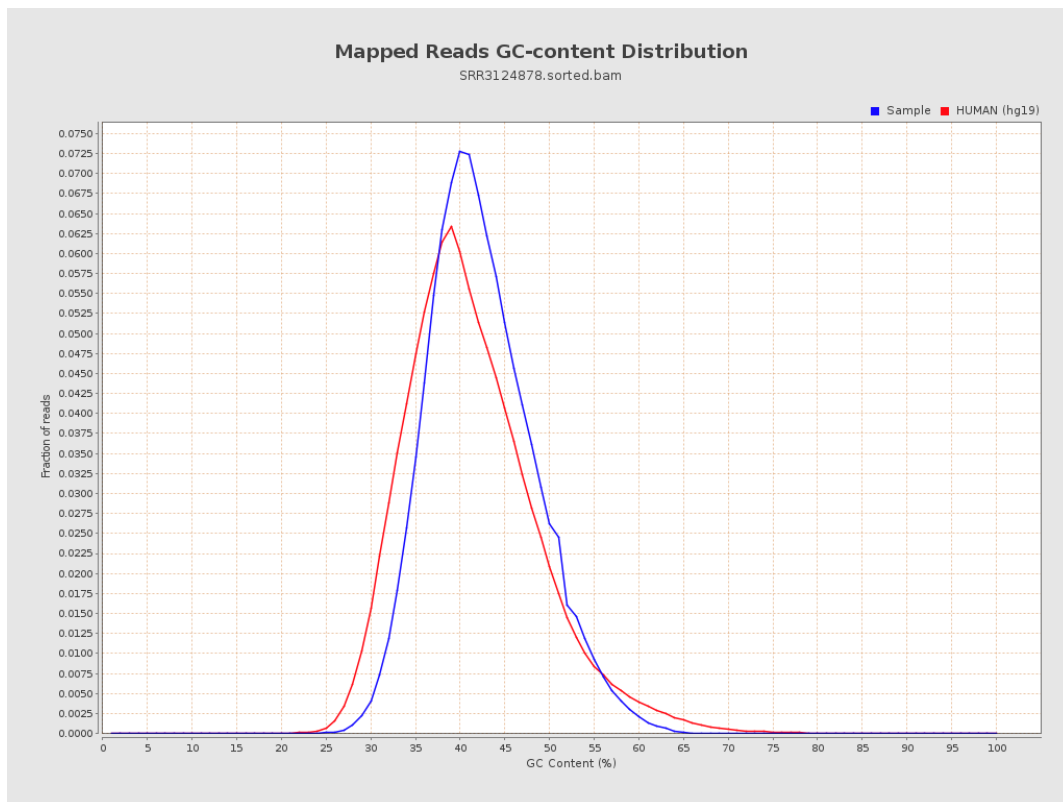
7. Results : Duplication Rate Histogram



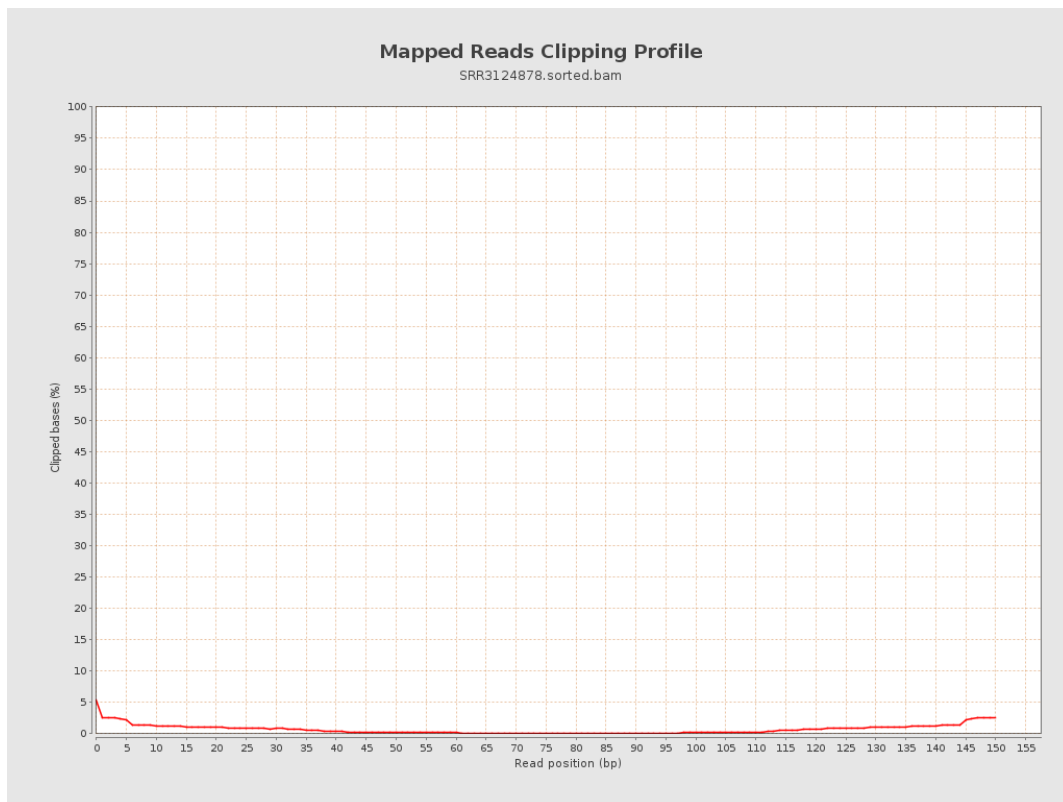
8. Results : Mapped Reads Nucleotide Content



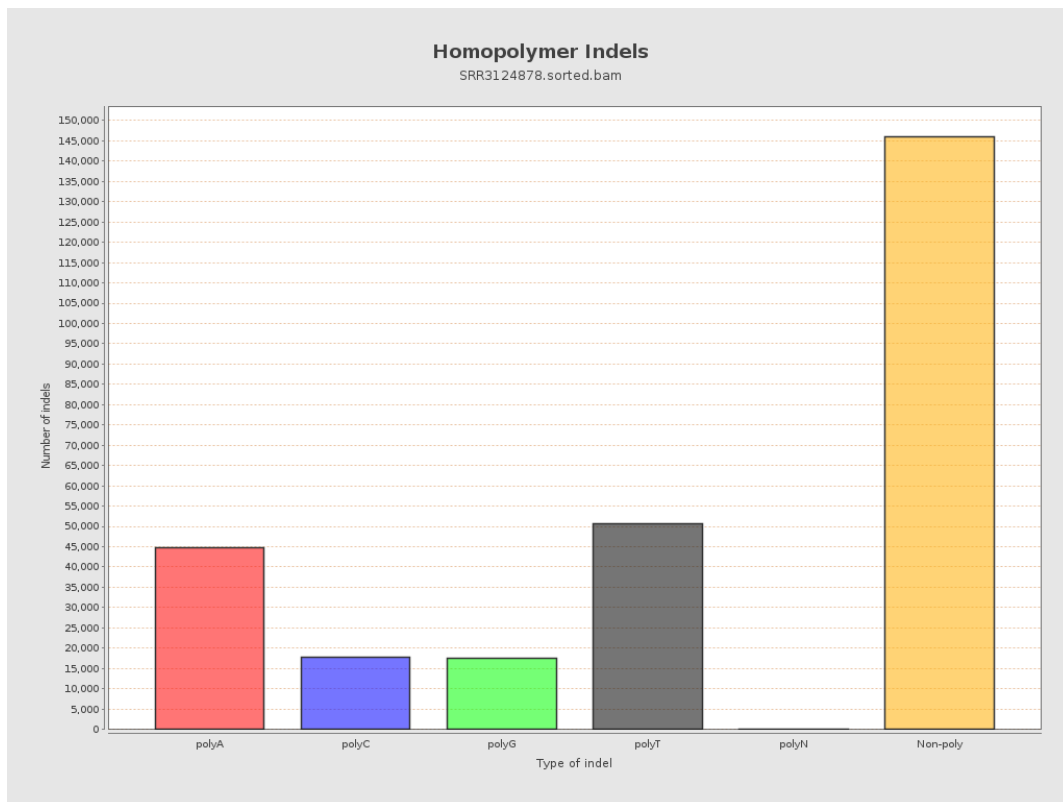
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



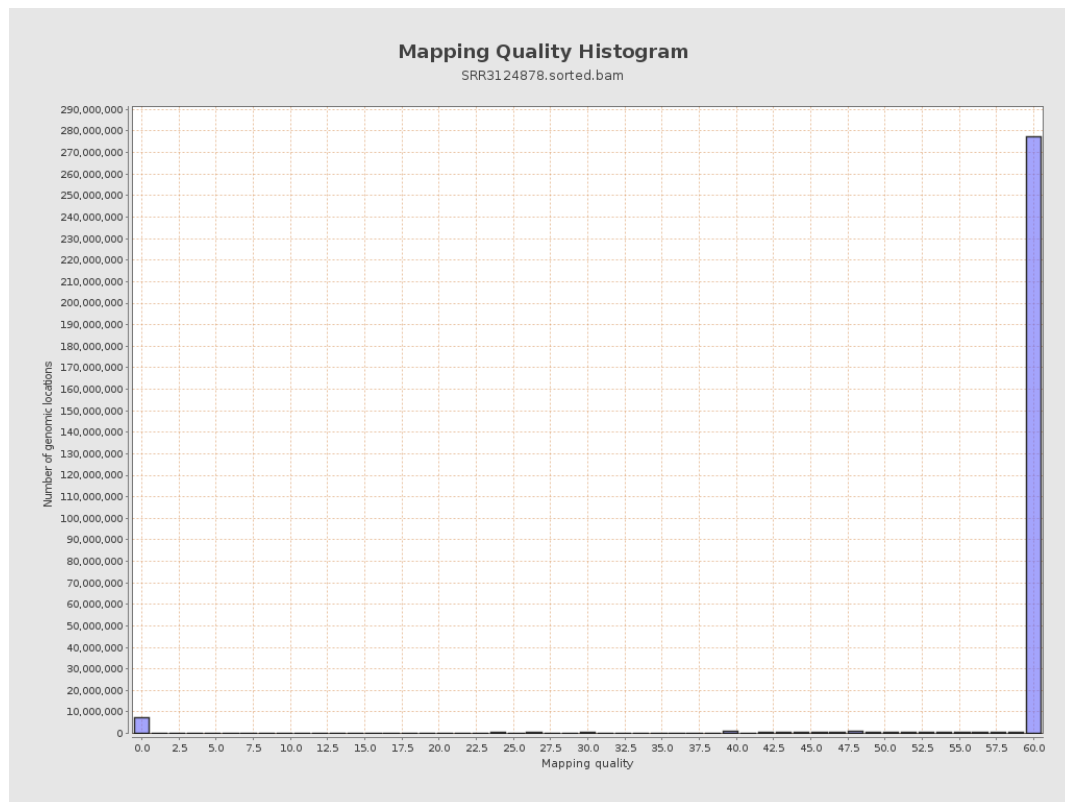
11. Results : Homopolymer Indels



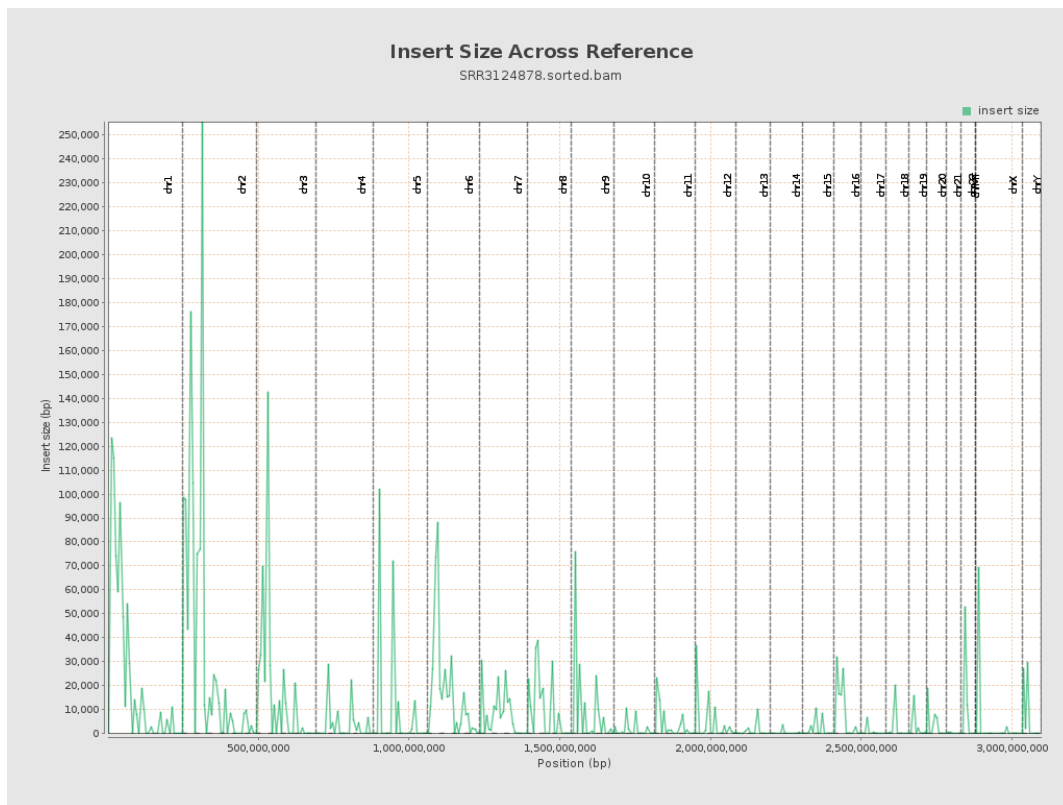
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

