

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/09 19:52:52

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR617494.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_SRR617494 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR617494_1.fastq.gz SRR617494_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Oct 09 19:52:51 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR617494.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	6,155,330
Mapped reads	5,753,278 / 93.47%
Unmapped reads	402,052 / 6.53%
Mapped paired reads	5,753,278 / 93.47%
Mapped reads, first in pair	2,907,277 / 47.23%
Mapped reads, second in pair	2,846,001 / 46.24%
Mapped reads, both in pair	5,622,030 / 91.34%
Mapped reads, singletons	131,248 / 2.13%
Secondary alignments	0
Supplementary alignments	30,843 / 0.5%
Read min/max/mean length	30 / 100 / 100.2
Duplicated reads (estimated)	536,399 / 8.71%
Duplication rate	5.6%
Clipped reads	1,275,828 / 20.73%

2.2. ACGT Content

Number/percentage of A's	164,309,787 / 29.59%
Number/percentage of C's	111,948,455 / 20.16%
Number/percentage of T's	163,858,259 / 29.51%
Number/percentage of G's	114,563,823 / 20.63%
Number/percentage of N's	567,065 / 0.1%

GC Percentage	40.79%
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2.3. Coverage

Mean	0.1795
Standard Deviation	1.8542

2.4. Mapping Quality

Mean Mapping Quality	52.61
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2.5. Insert size

Mean	39,650.7
Standard Deviation	1,859,986.96
P25/Median/P75	171 / 214 / 281

2.6. Mismatches and indels

General error rate	1.4%
Mismatches	7,586,802
Insertions	82,833
Mapped reads with at least one insertion	1.41%
Deletions	191,226
Mapped reads with at least one deletion	3.25%
Homopolymer indels	47.54%

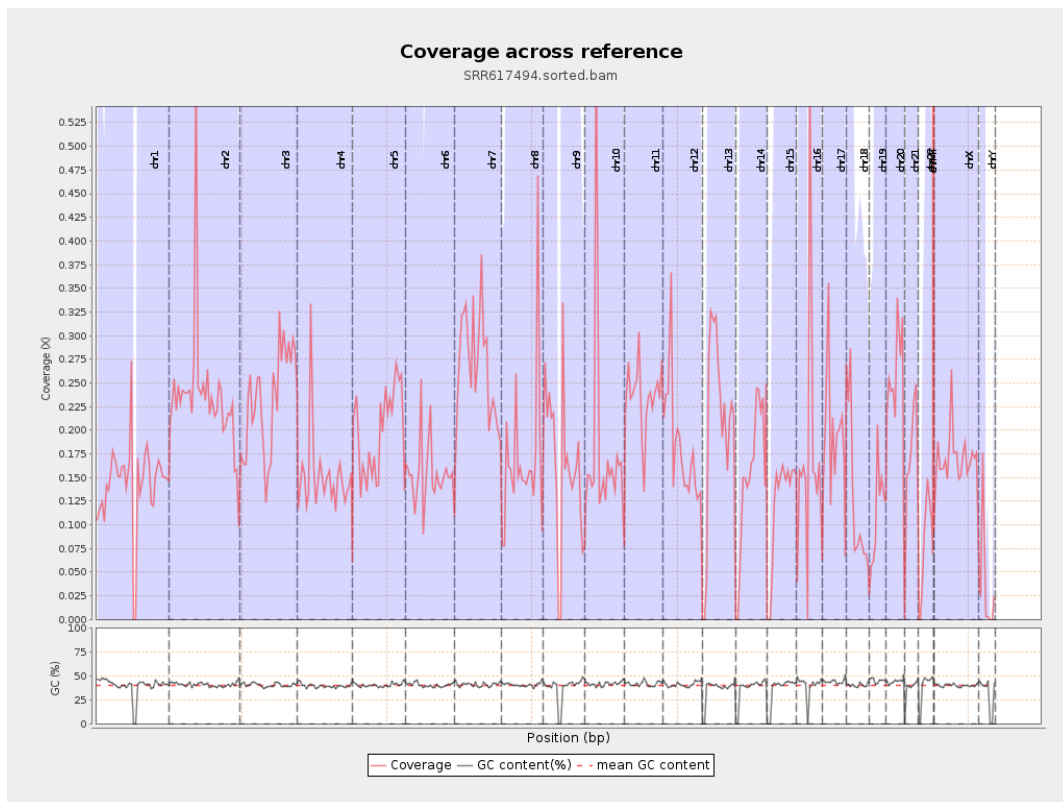
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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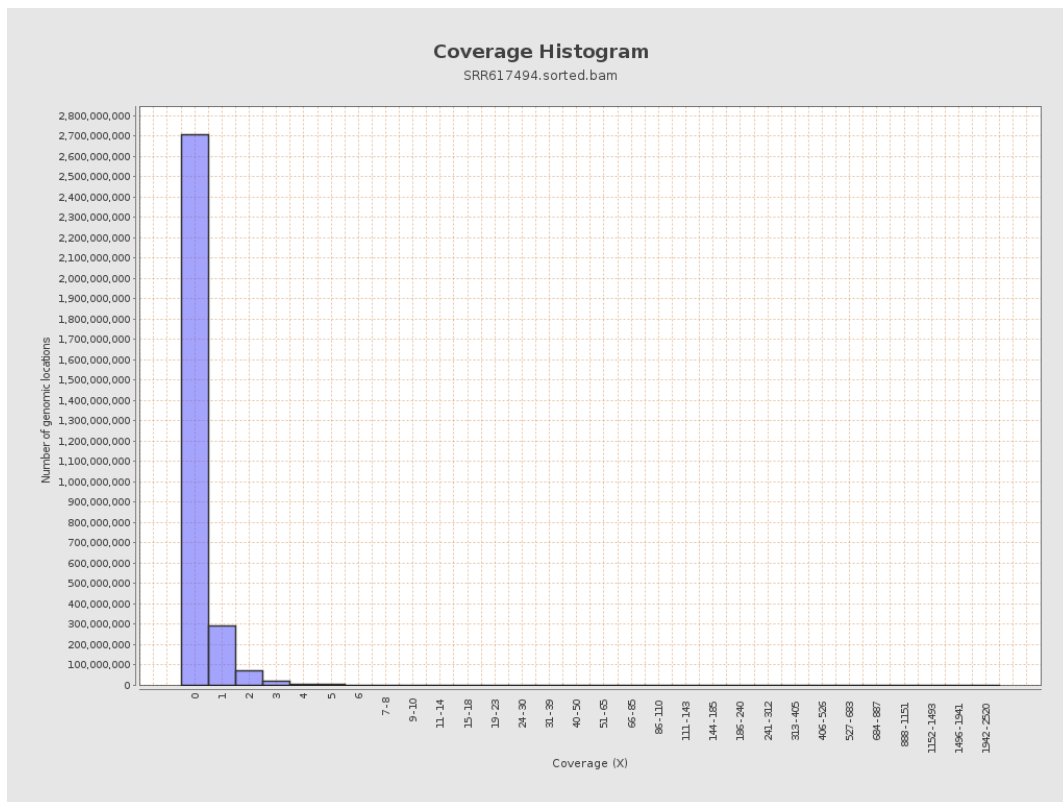
		bases	coverage	deviation
chr1	249250621	35725682	0.1433	1.8
chr2	243199373	57545251	0.2366	2.1642
chr3	198022430	45815067	0.2314	0.6251
chr4	191154276	28682092	0.15	1.1865
chr5	180915260	35716418	0.1974	0.5819
chr6	171115067	26319929	0.1538	1.129
chr7	159138663	42835534	0.2692	2.4831
chr8	146364022	24725847	0.1689	0.833
chr9	141213431	23006980	0.1629	3.4248
chr10	135534747	23507543	0.1734	3.5418
chr11	135006516	31297473	0.2318	2.3786
chr12	133851895	24174560	0.1806	0.554
chr13	115169878	23591555	0.2048	0.5938
chr14	107349540	16172934	0.1507	0.557
chr15	102531392	12438500	0.1213	0.4374
chr16	90354753	15103492	0.1672	2.8793
chr17	81195210	15502170	0.1909	2.5735
chr18	78077248	9898747	0.1268	3.1179
chr19	59128983	6607028	0.1117	1.1361
chr20	63025520	16216441	0.2573	0.714
chr21	48129895	8012634	0.1665	0.8049
chr22	51304566	4091570	0.0798	0.3585
chrMT	16571	395038	23.8391	17.2735
chrX	155270560	26241265	0.169	0.8924

chrY	59373566	1948195	0.0328	2.5836
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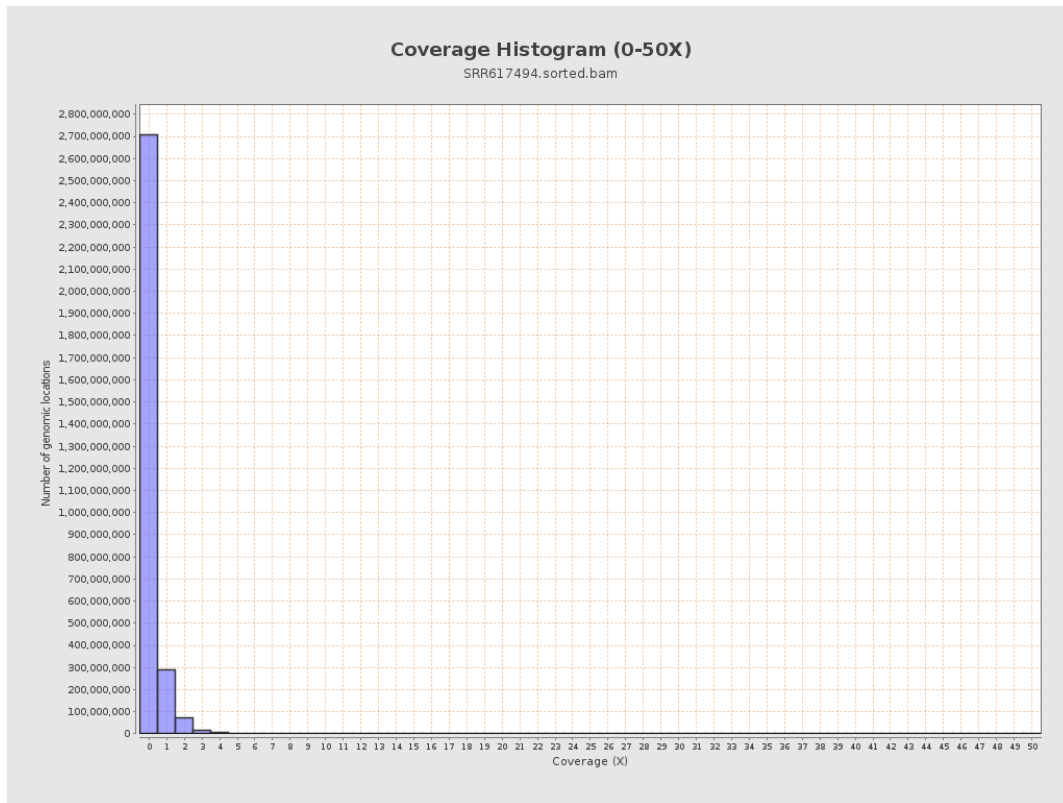
3. Results : Coverage across reference



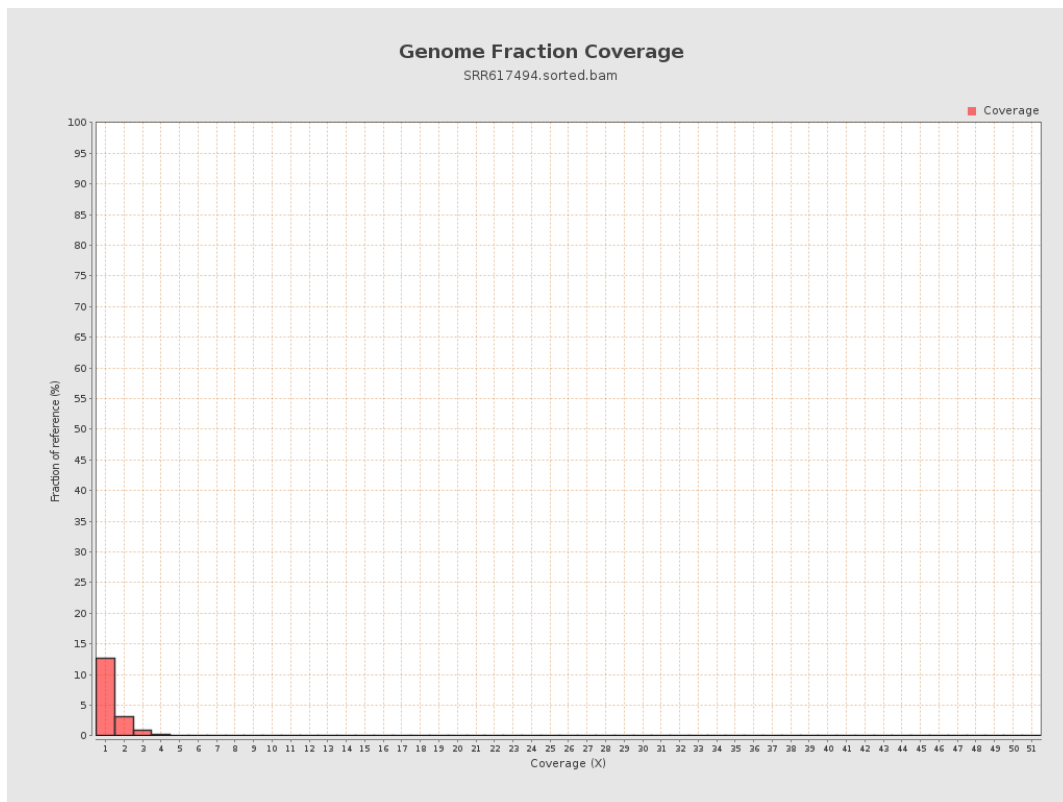
4. Results : Coverage Histogram



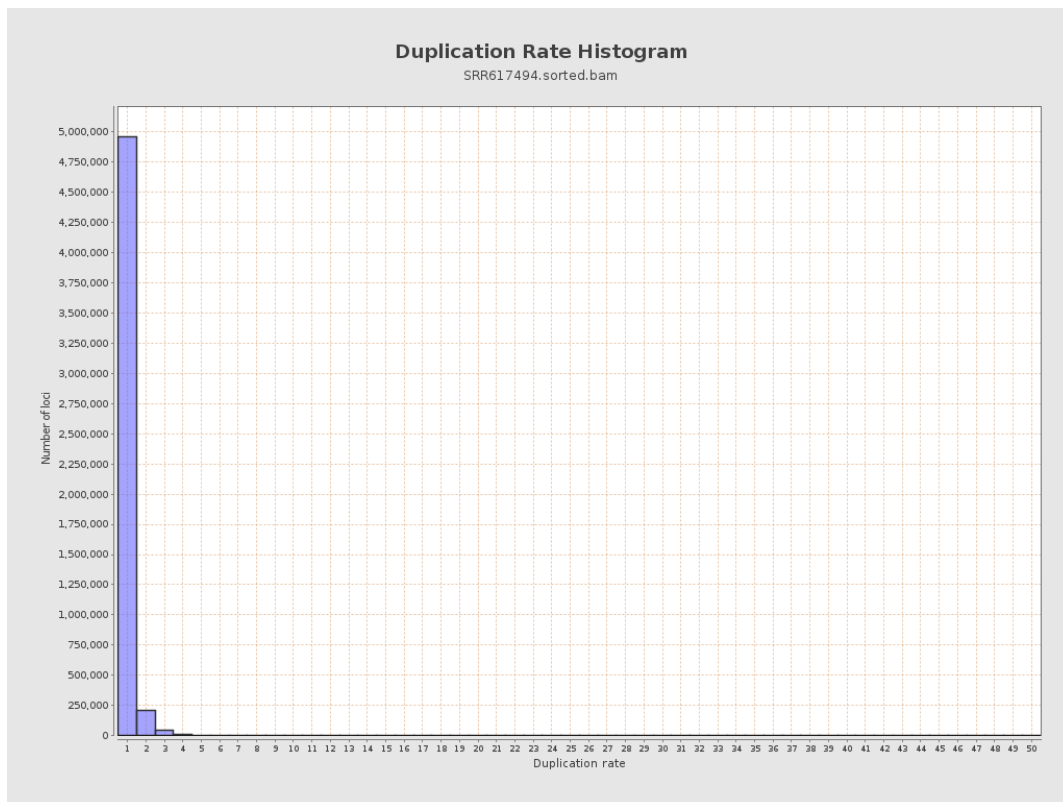
5. Results : Coverage Histogram (0-50X)



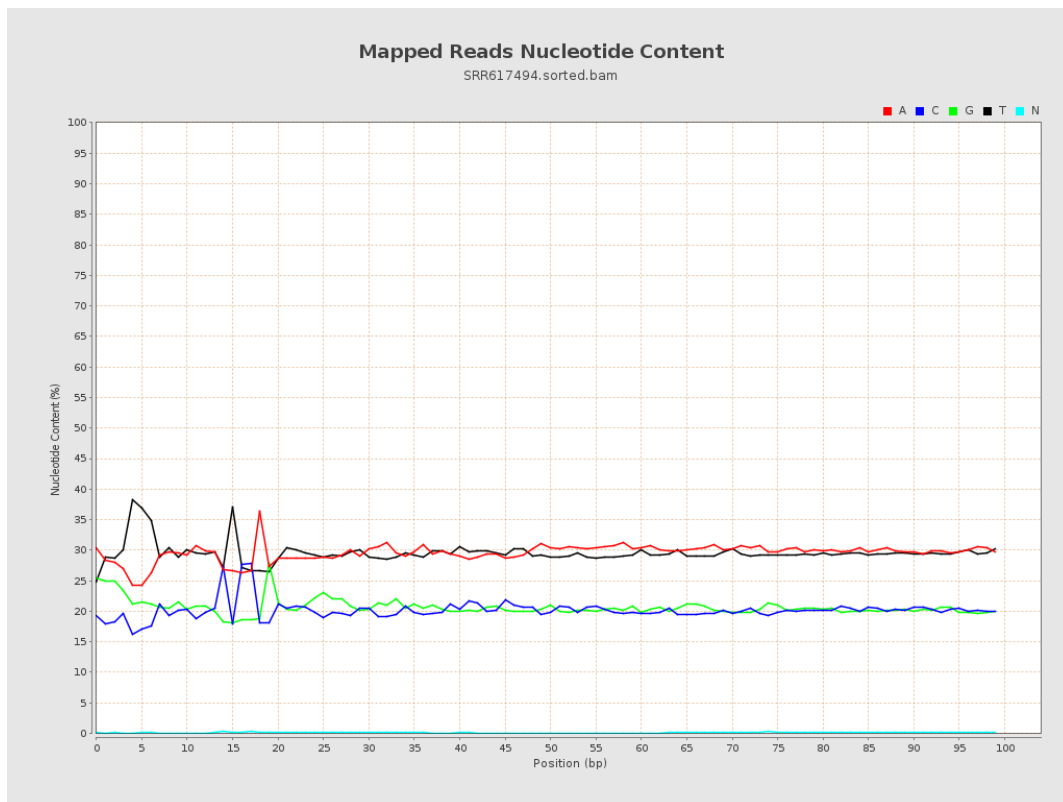
6. Results : Genome Fraction Coverage



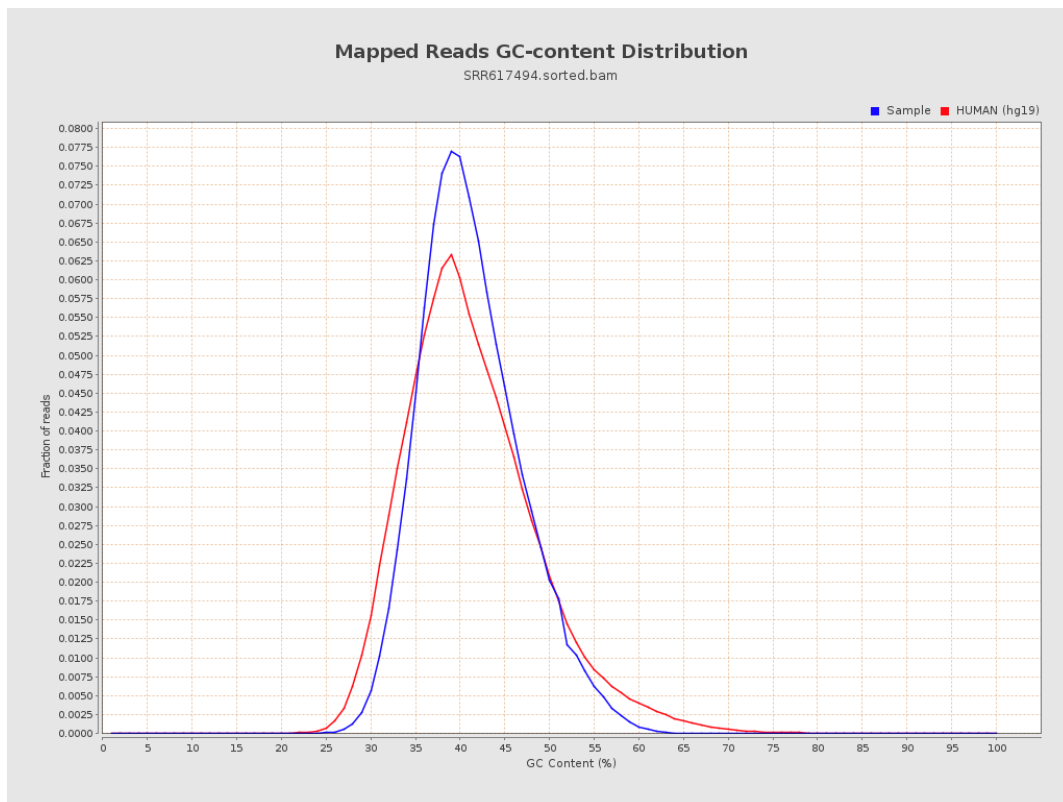
7. Results : Duplication Rate Histogram



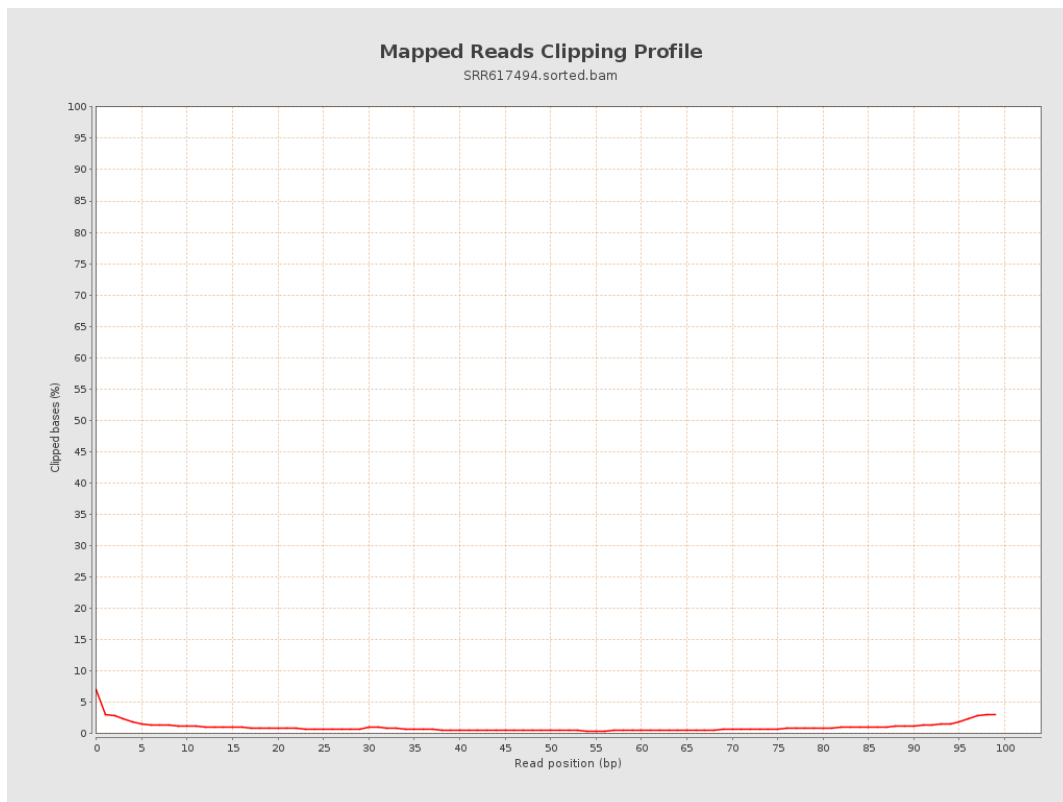
8. Results : Mapped Reads Nucleotide Content



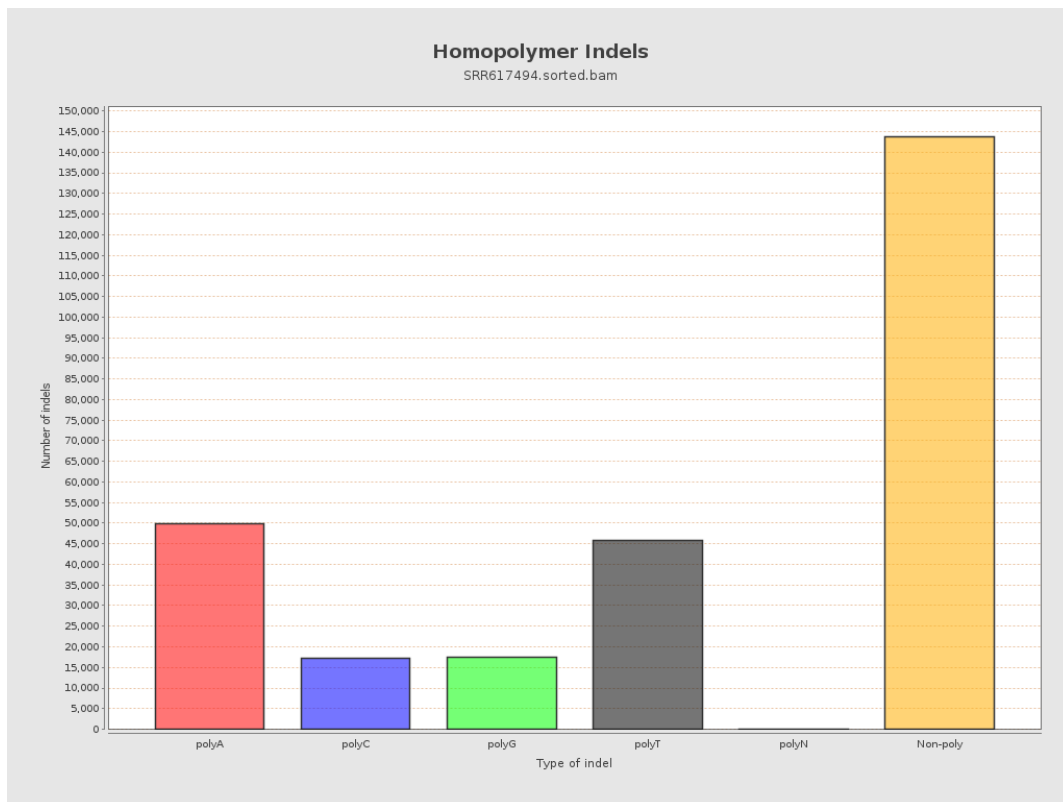
9. Results : Mapped Reads GC-content Distribution



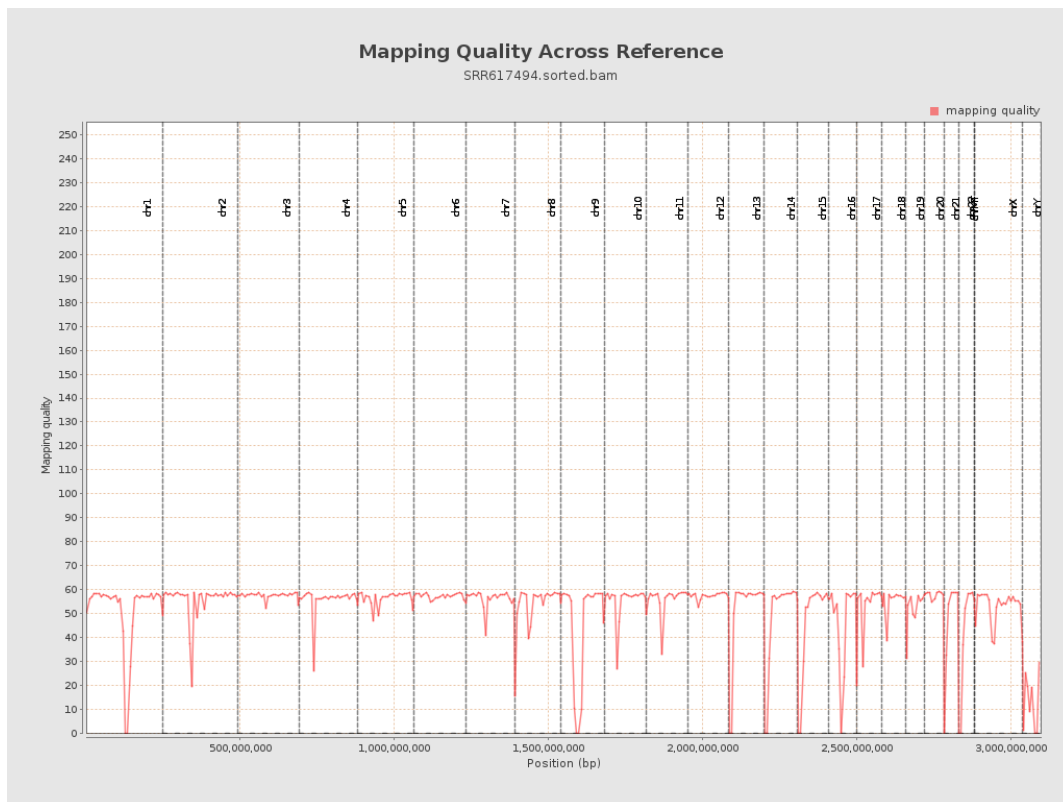
10. Results : Mapped Reads Clipping Profile



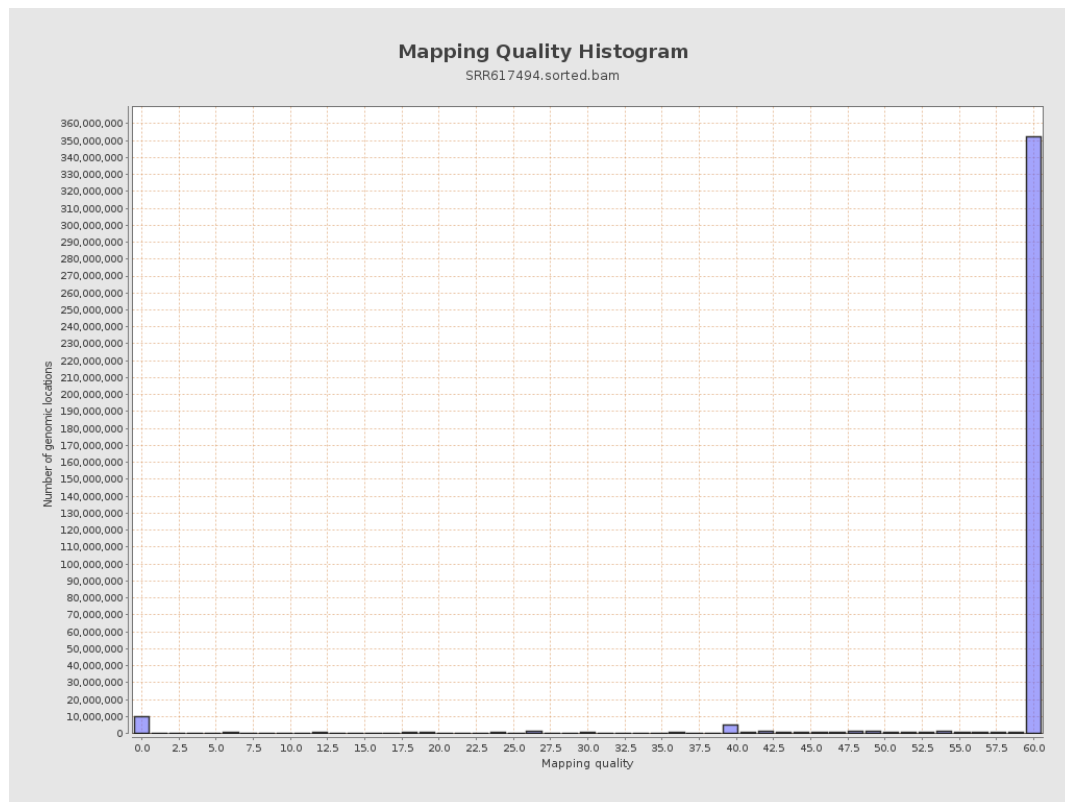
11. Results : Homopolymer Indels



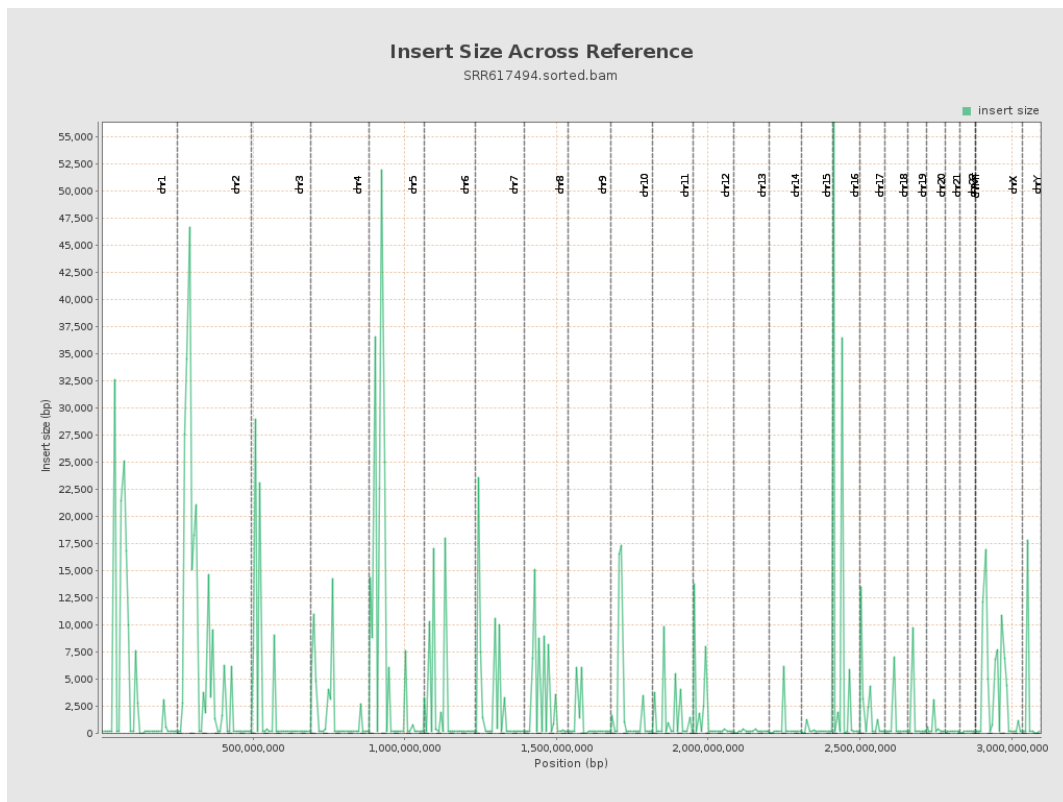
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

