

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/01 20:49:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432714.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_SRR6432714 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432714_1.fastq.gz SRR6432714_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 01 20:49:41 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432714.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	357,517,404
Mapped reads	357,355,505 / 99.95%
Unmapped reads	161,899 / 0.05%
Mapped paired reads	357,355,505 / 99.95%
Mapped reads, first in pair	178,682,663 / 49.98%
Mapped reads, second in pair	178,672,842 / 49.98%
Mapped reads, both in pair	357,295,574 / 99.94%
Mapped reads, singletons	59,931 / 0.02%
Secondary alignments	0
Supplementary alignments	215,802 / 0.06%
Read min/max/mean length	30 / 150 / 139.9
Duplicated reads (estimated)	163,248,228 / 45.66%
Duplication rate	30.41%
Clipped reads	103,439,455 / 28.93%

2.2. ACGT Content

Number/percentage of A's	13,267,657,082 / 27.11%
Number/percentage of C's	10,716,150,964 / 21.89%
Number/percentage of T's	13,111,084,454 / 26.79%
Number/percentage of G's	11,853,142,965 / 24.22%
Number/percentage of N's	158,640 / 0%

GC Percentage	46.11%
---------------	--------

2.3. Coverage

Mean	15.8269
Standard Deviation	47.1483

2.4. Mapping Quality

Mean Mapping Quality	55.31
----------------------	-------

2.5. Insert size

Mean	97,293.2
Standard Deviation	3,191,988.64
P25/Median/P75	284 / 304 / 321

2.6. Mismatches and indels

General error rate	0.95%
Mismatches	445,810,221
Insertions	10,091,589
Mapped reads with at least one insertion	2.75%
Deletions	31,728,366
Mapped reads with at least one deletion	8.48%
Homopolymer indels	51.08%

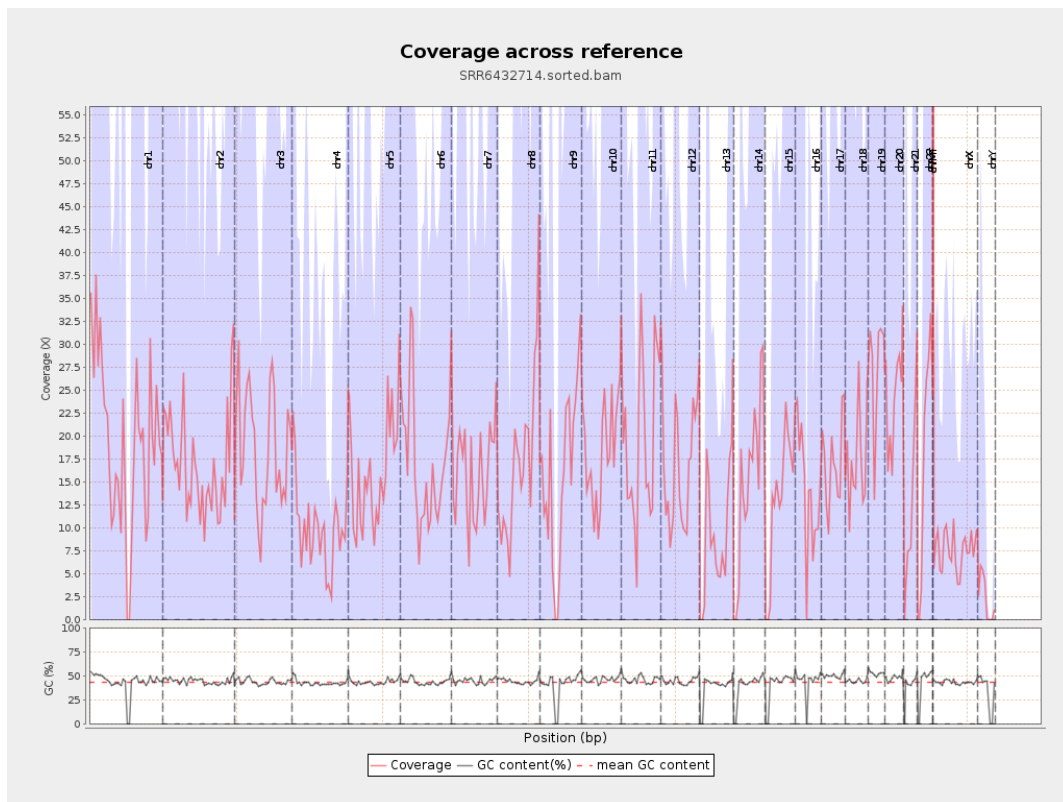
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

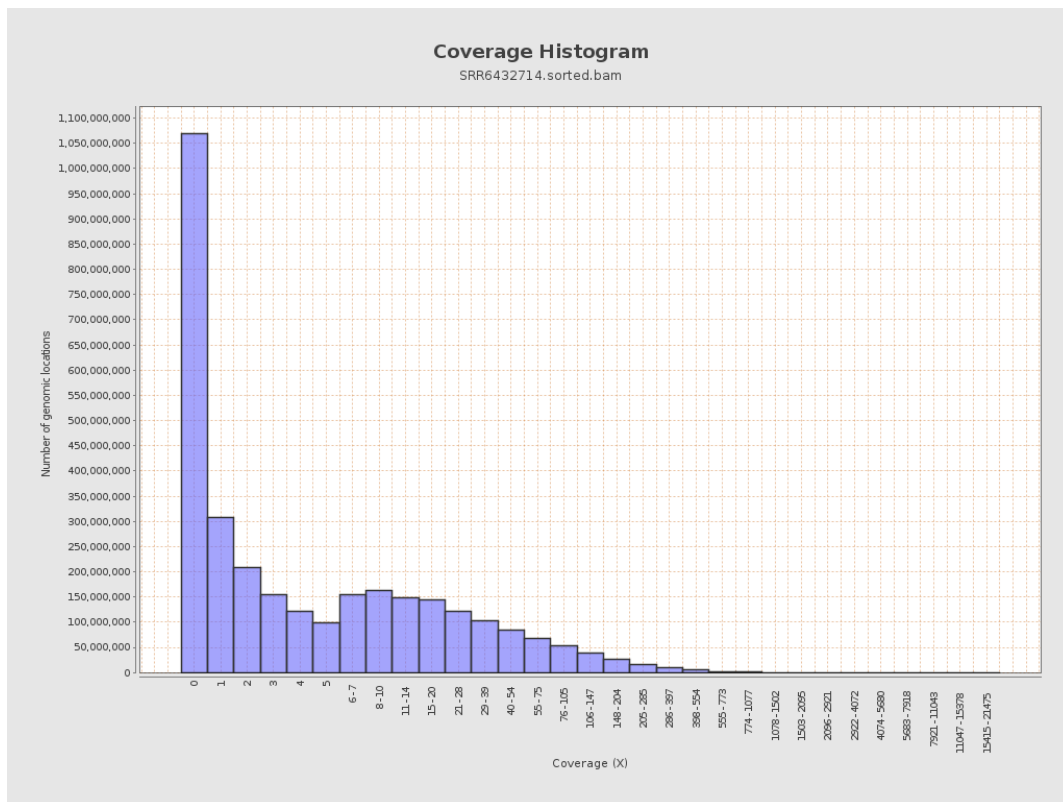
		bases	coverage	deviation
chr1	249250621	4787159461	19.2062	54.3473
chr2	243199373	4112087463	16.9083	53.1941
chr3	198022430	3669063429	18.5285	49.0504
chr4	191154276	1893018021	9.9031	31.5745
chr5	180915260	2952719346	16.321	45.8742
chr6	171115067	2862664367	16.7295	46.5497
chr7	159138663	2593089515	16.2945	44.7638
chr8	146364022	2538017430	17.3404	50.2099
chr9	141213431	2216570623	15.6966	50.4264
chr10	135534747	2459954229	18.15	48.2762
chr11	135006516	2667105322	19.7554	53.2382
chr12	133851895	2268531749	16.9481	46.5968
chr13	115169878	1061740845	9.2189	31.3202
chr14	107349540	1639930362	15.2765	44.6024
chr15	102531392	1330851153	12.9799	38.4011
chr16	90354753	1269769565	14.0532	49.8355
chr17	81195210	1372837841	16.9079	45.0076
chr18	78077248	1328794056	17.019	48.5744
chr19	59128983	1613689470	27.291	72.44
chr20	63025520	1496745771	23.7482	58.4289
chr21	48129895	605778140	12.5863	46.7454
chr22	51304566	927847036	18.0851	53.4013
chrMT	16571	7722369	466.0171	908.3311
chrX	155270560	1177229444	7.5818	22.282

chrY	59373566	142424950	2.3988	20.8989
------	----------	-----------	--------	---------

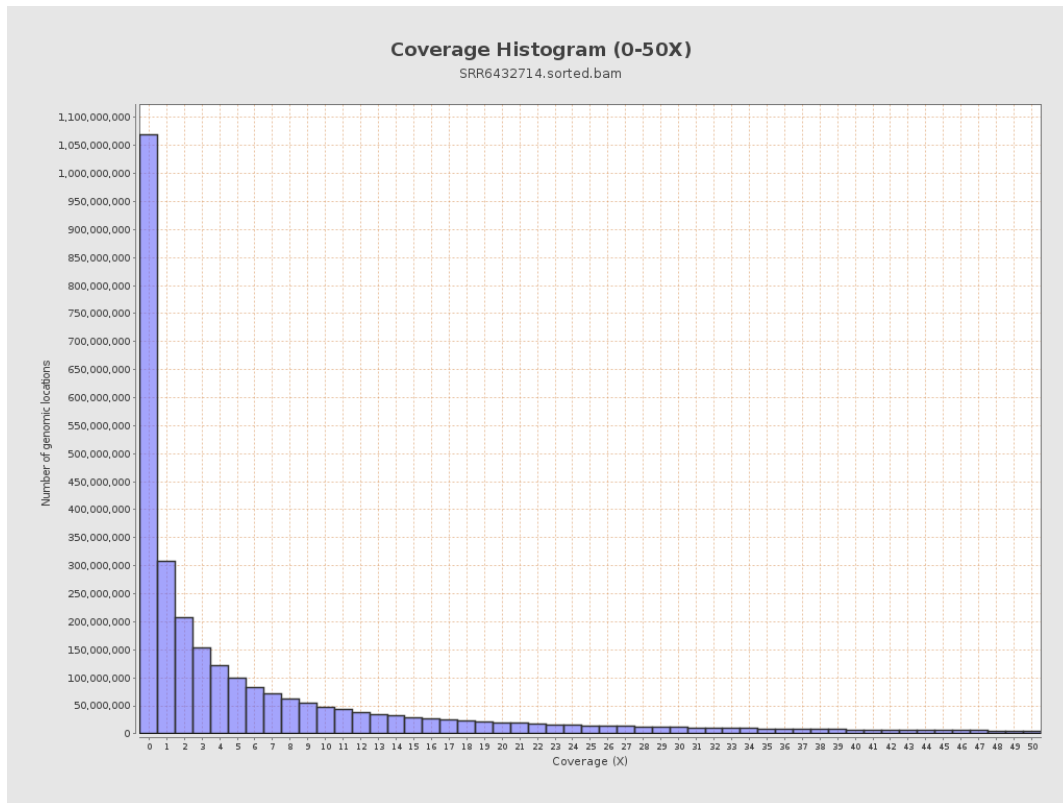
3. Results : Coverage across reference



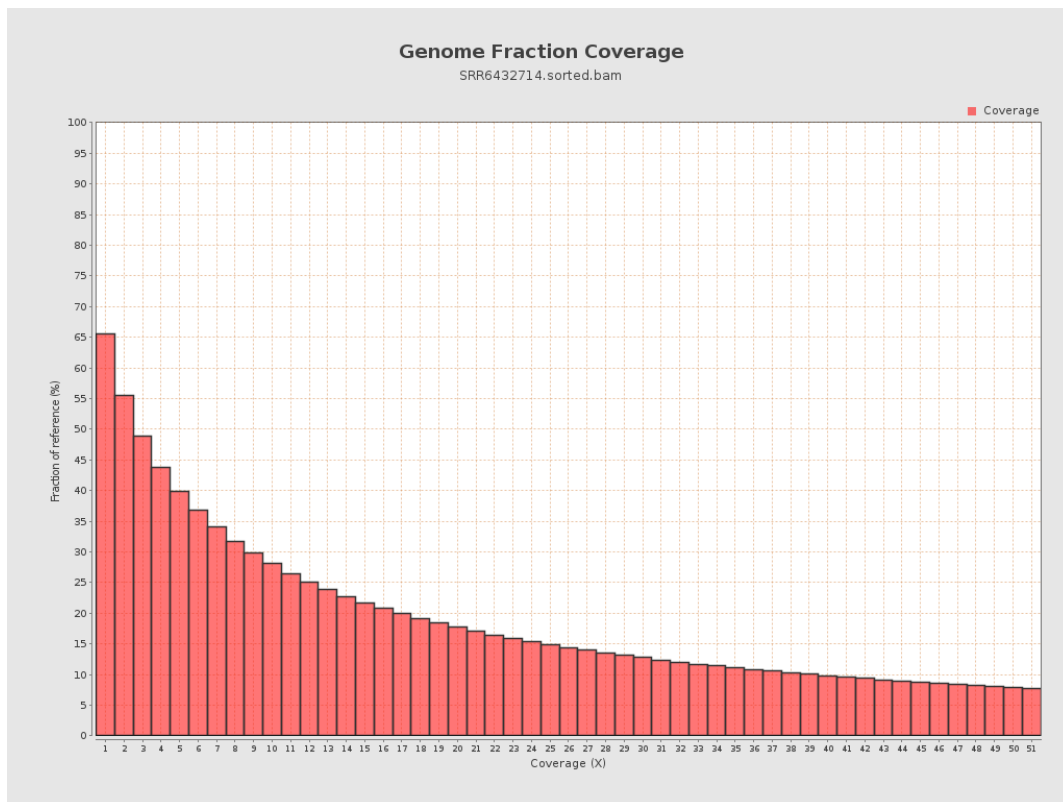
4. Results : Coverage Histogram



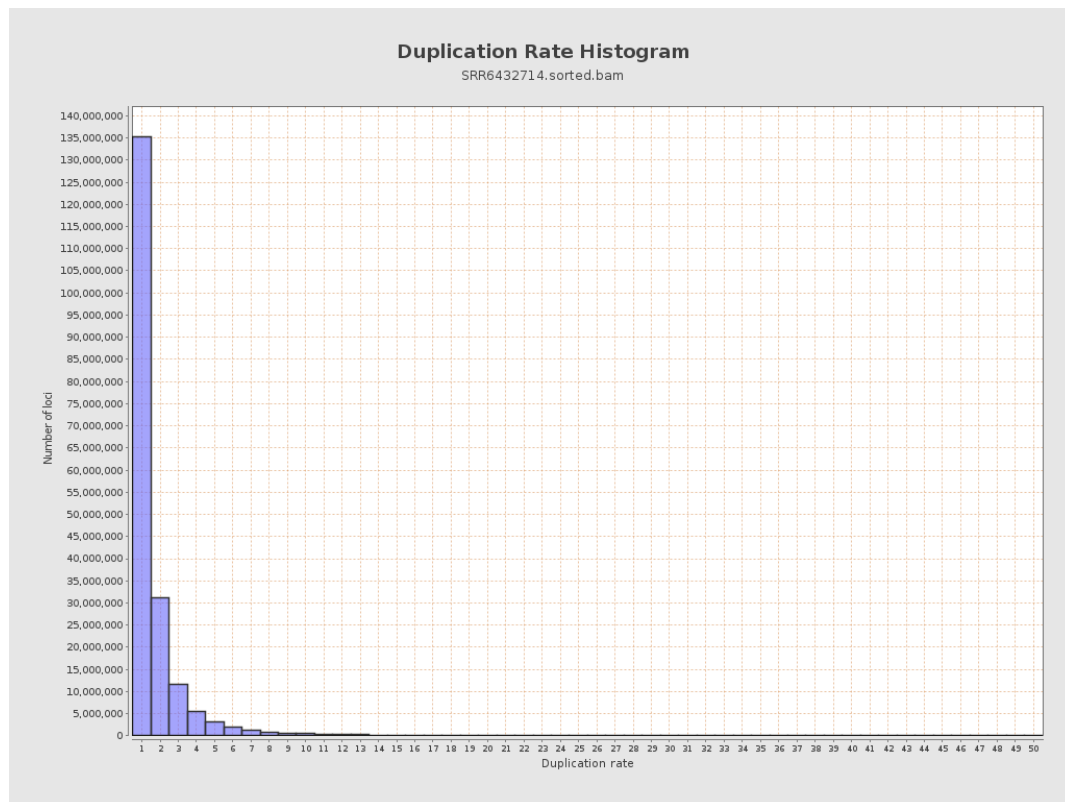
5. Results : Coverage Histogram (0-50X)



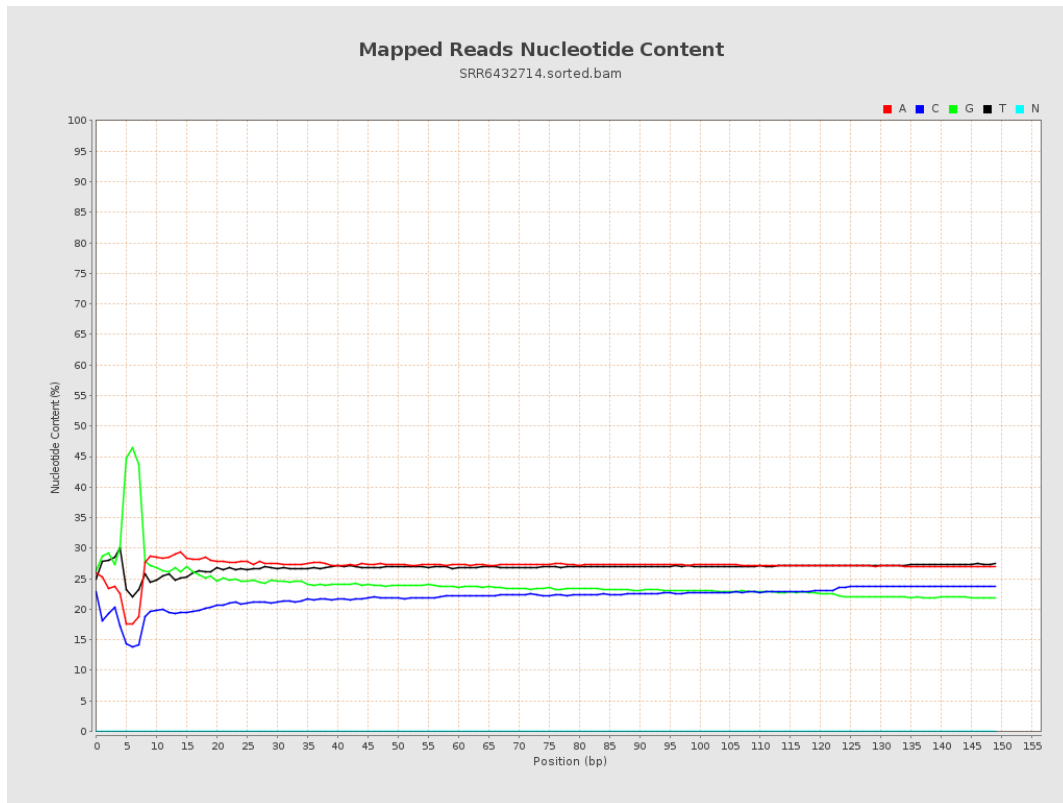
6. Results : Genome Fraction Coverage



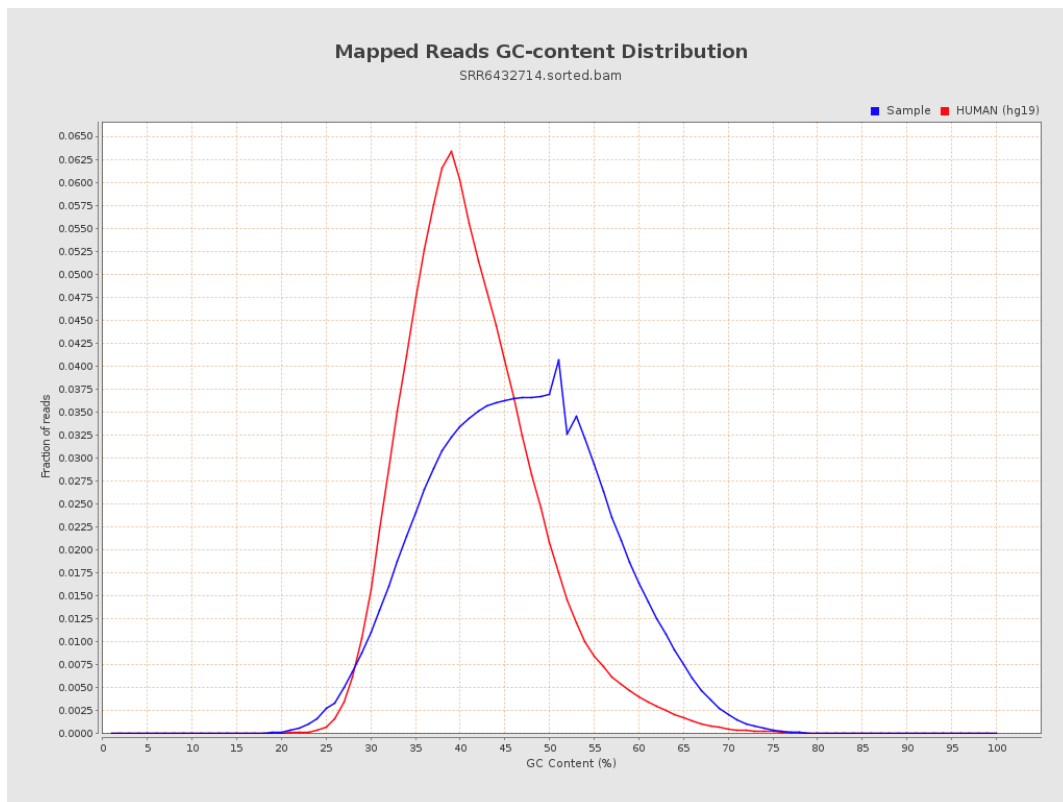
7. Results : Duplication Rate Histogram



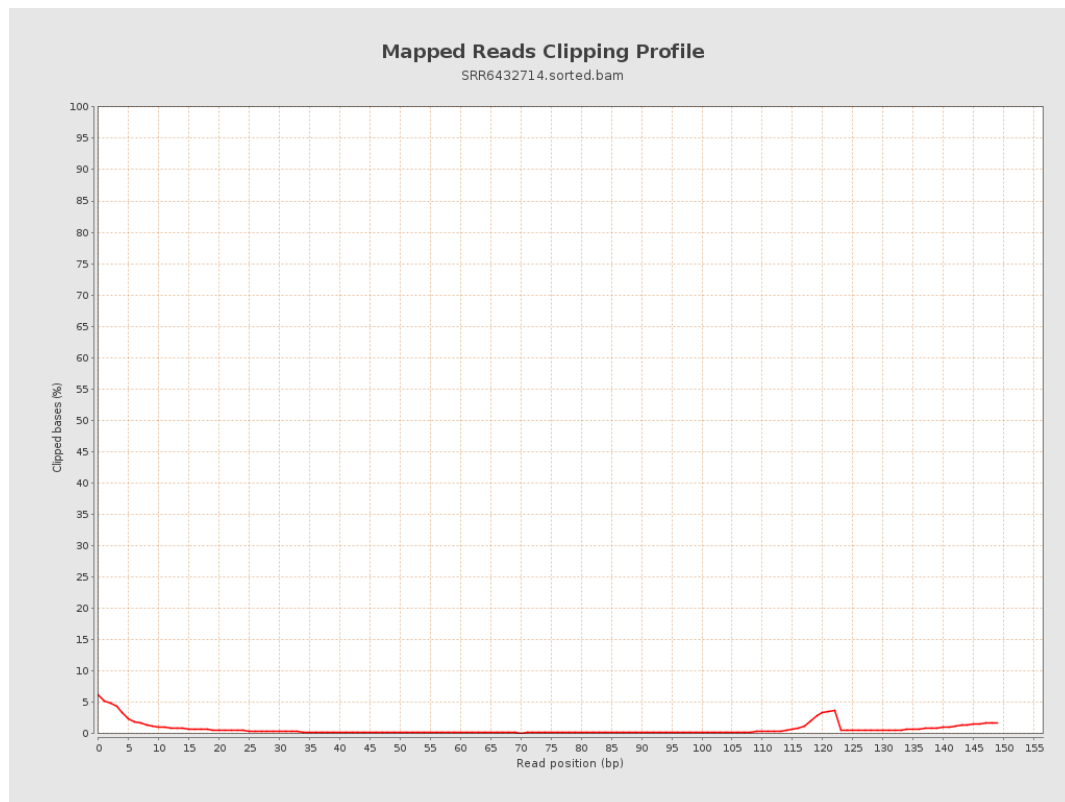
8. Results : Mapped Reads Nucleotide Content



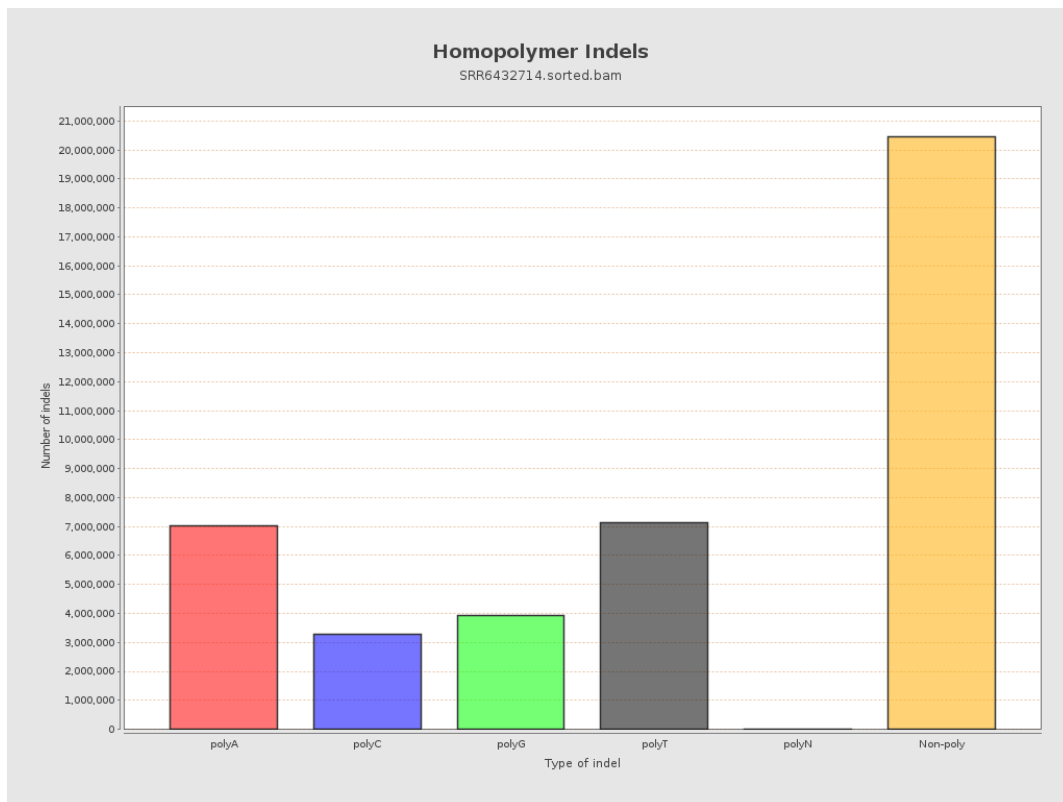
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



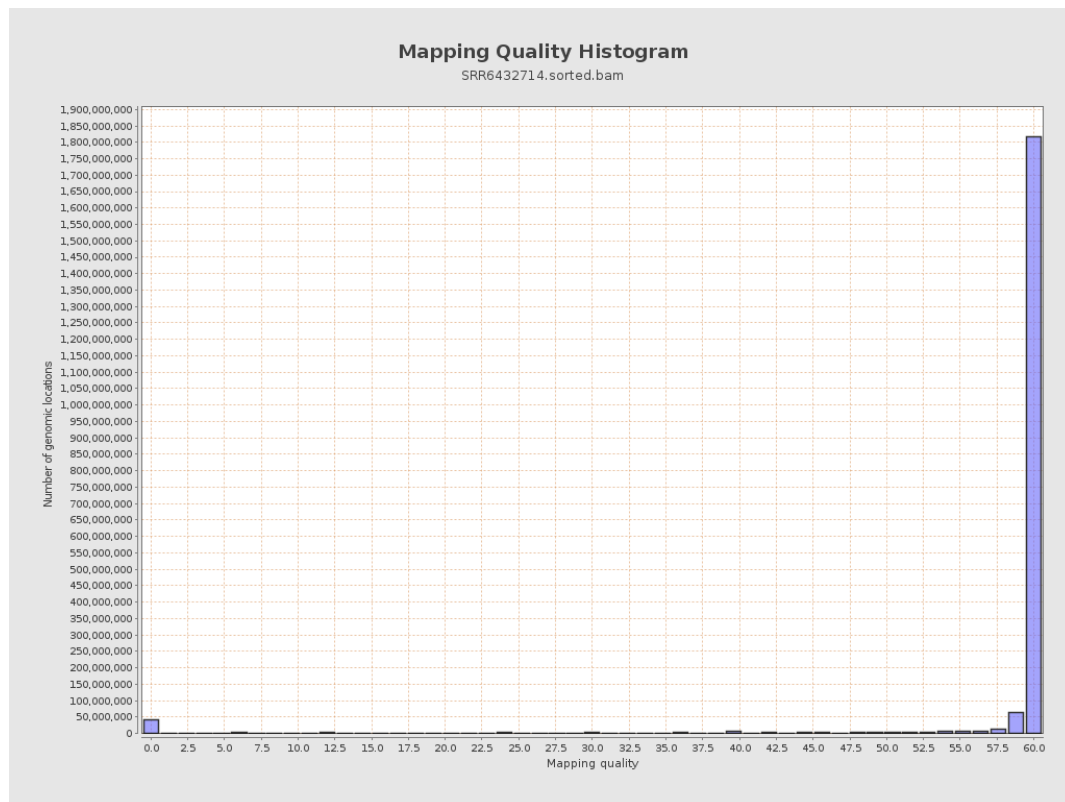
11. Results : Homopolymer Indels



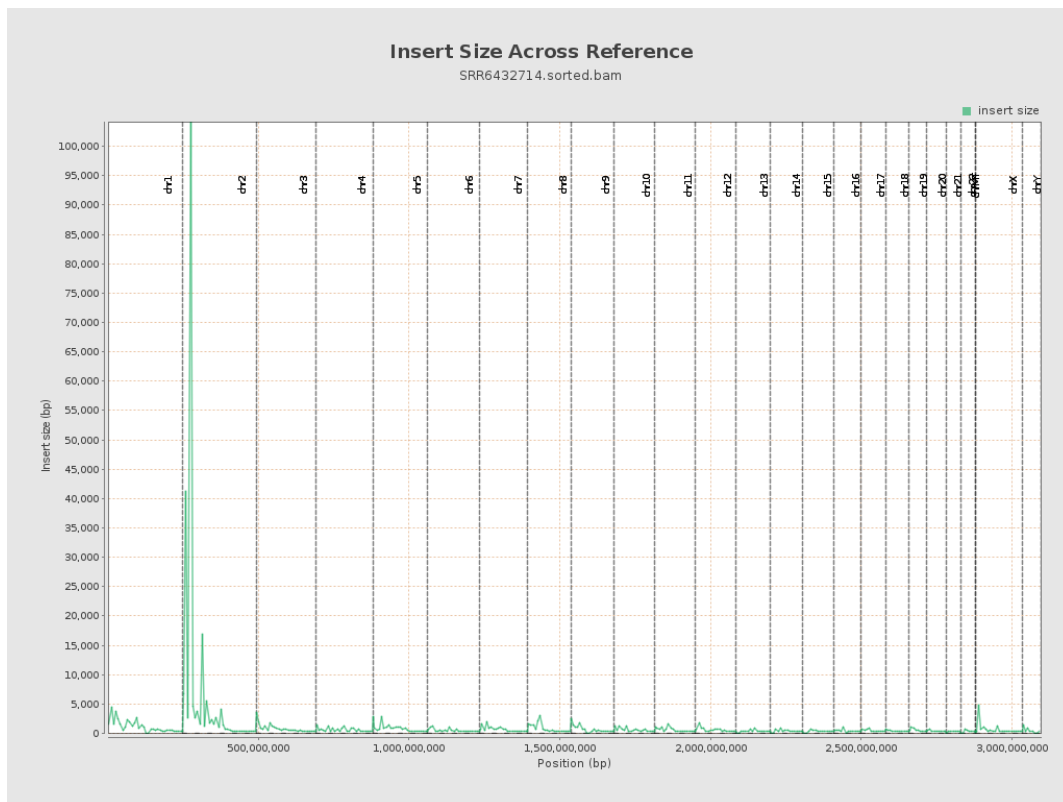
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

