

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/02 04:45:02

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432715.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_SRR6432715 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432715_1.fastq.gz SRR6432715_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Apr 02 04:45:01 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432715.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	393,256,278
Mapped reads	393,066,363 / 99.95%
Unmapped reads	189,915 / 0.05%
Mapped paired reads	393,066,363 / 99.95%
Mapped reads, first in pair	196,539,420 / 49.98%
Mapped reads, second in pair	196,526,943 / 49.97%
Mapped reads, both in pair	392,997,274 / 99.93%
Mapped reads, singletons	69,089 / 0.02%
Secondary alignments	0
Supplementary alignments	230,363 / 0.06%
Read min/max/mean length	30 / 150 / 140.01
Duplicated reads (estimated)	184,556,028 / 46.93%
Duplication rate	31.28%
Clipped reads	112,955,241 / 28.72%

2.2. ACGT Content

Number/percentage of A's	14,687,234,780 / 27.29%
Number/percentage of C's	11,704,217,024 / 21.74%
Number/percentage of T's	14,520,619,241 / 26.98%
Number/percentage of G's	12,909,811,485 / 23.98%
Number/percentage of N's	3,698,051 / 0.01%

GC Percentage	45.73%
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2.3. Coverage

Mean	17.404
Standard Deviation	50.3999

2.4. Mapping Quality

Mean Mapping Quality	55.41
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2.5. Insert size

Mean	72,916.26
Standard Deviation	2,717,594.97
P25/Median/P75	267 / 286 / 304

2.6. Mismatches and indels

General error rate	1.01%
Mismatches	524,991,478
Insertions	11,204,178
Mapped reads with at least one insertion	2.78%
Deletions	35,142,517
Mapped reads with at least one deletion	8.54%
Homopolymer indels	51.41%

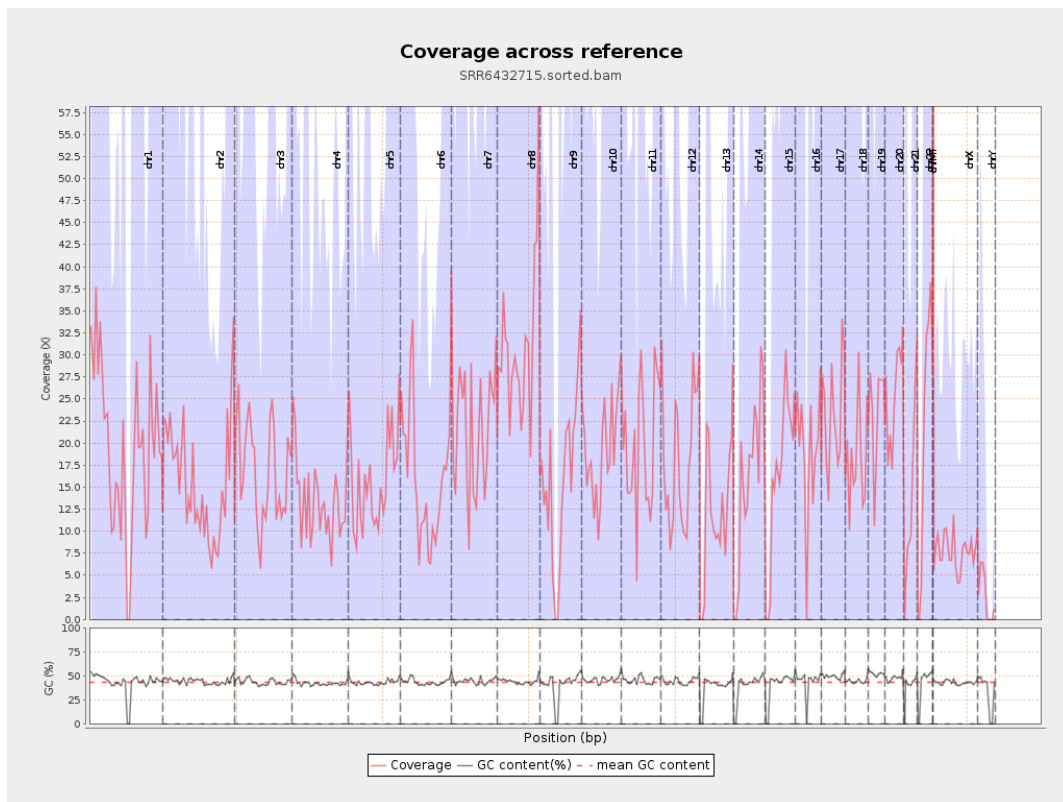
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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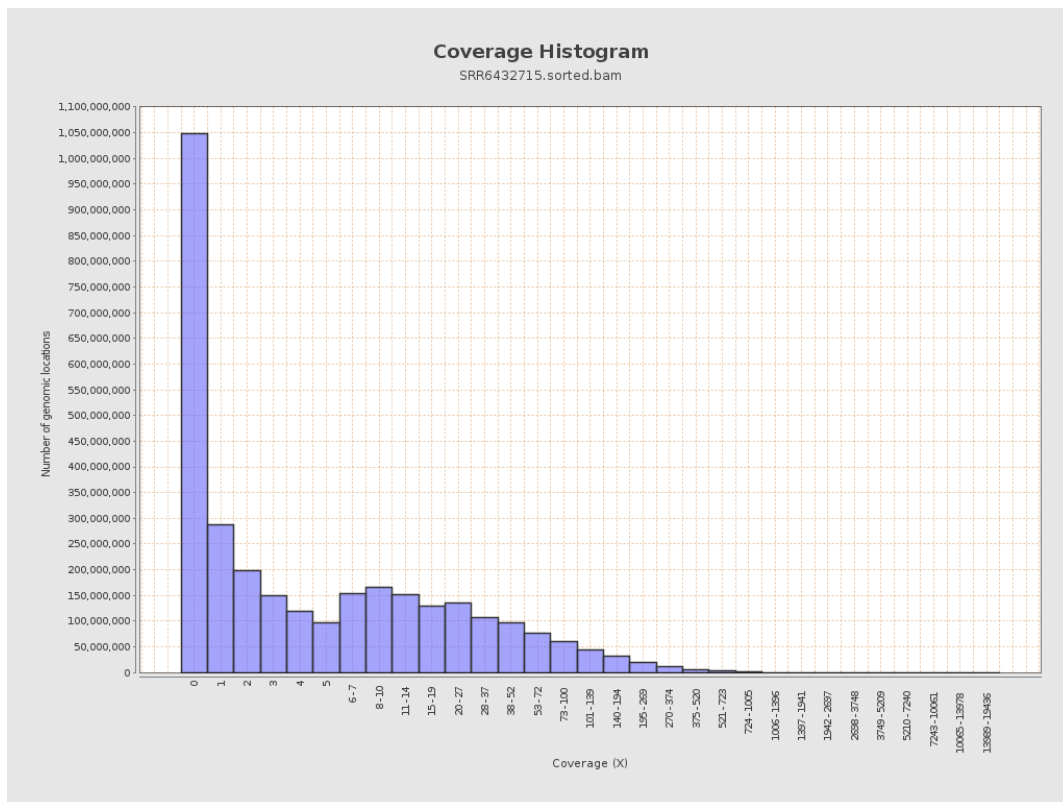
		bases	coverage	deviation
chr1	249250621	4830145544	19.3787	54.408
chr2	243199373	3780433068	15.5446	51.229
chr3	198022430	3303183472	16.6809	43.6619
chr4	191154276	2566466256	13.4262	38.9634
chr5	180915260	2900799221	16.034	43.8953
chr6	171115067	2702179954	15.7916	43.9472
chr7	159138663	3469563236	21.8021	57.0001
chr8	146364022	4547117837	31.0672	77.6332
chr9	141213431	2219329157	15.7161	50.7557
chr10	135534747	2579778467	19.0341	49.6085
chr11	135006516	2671870586	19.7907	50.9701
chr12	133851895	2443606969	18.2561	49.356
chr13	115169878	1370339551	11.8984	36.8567
chr14	107349540	1734585167	16.1583	46.3138
chr15	102531392	1668040856	16.2686	46.4609
chr16	90354753	1722508011	19.0638	59.4154
chr17	81195210	1888145158	23.2544	58.5991
chr18	78077248	1397580754	17.9	50.2413
chr19	59128983	1371230832	23.1905	61.4124
chr20	63025520	1576435659	25.0127	60.1342
chr21	48129895	673473962	13.9928	51.5679
chr22	51304566	1085590609	21.1597	60.4817
chrMT	16571	6366372	384.1876	724.6959
chrX	155270560	1206800199	7.7722	22.4214

chrY	59373566	161883947	2.7265	22.6087
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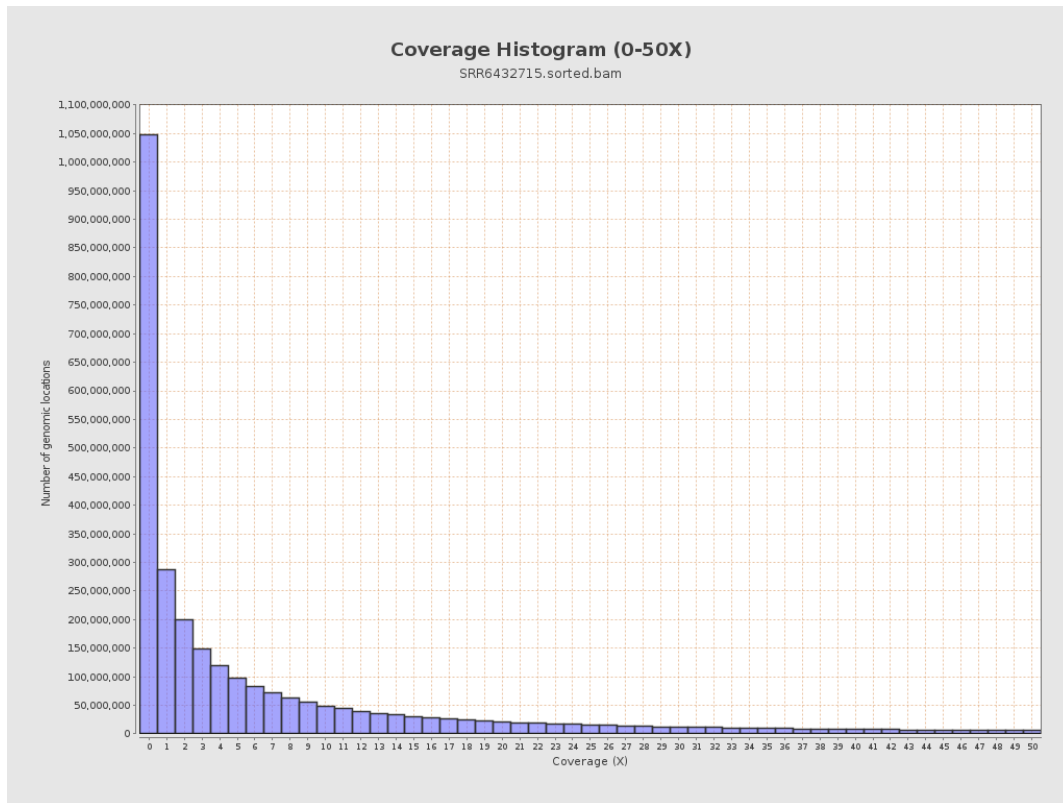
3. Results : Coverage across reference



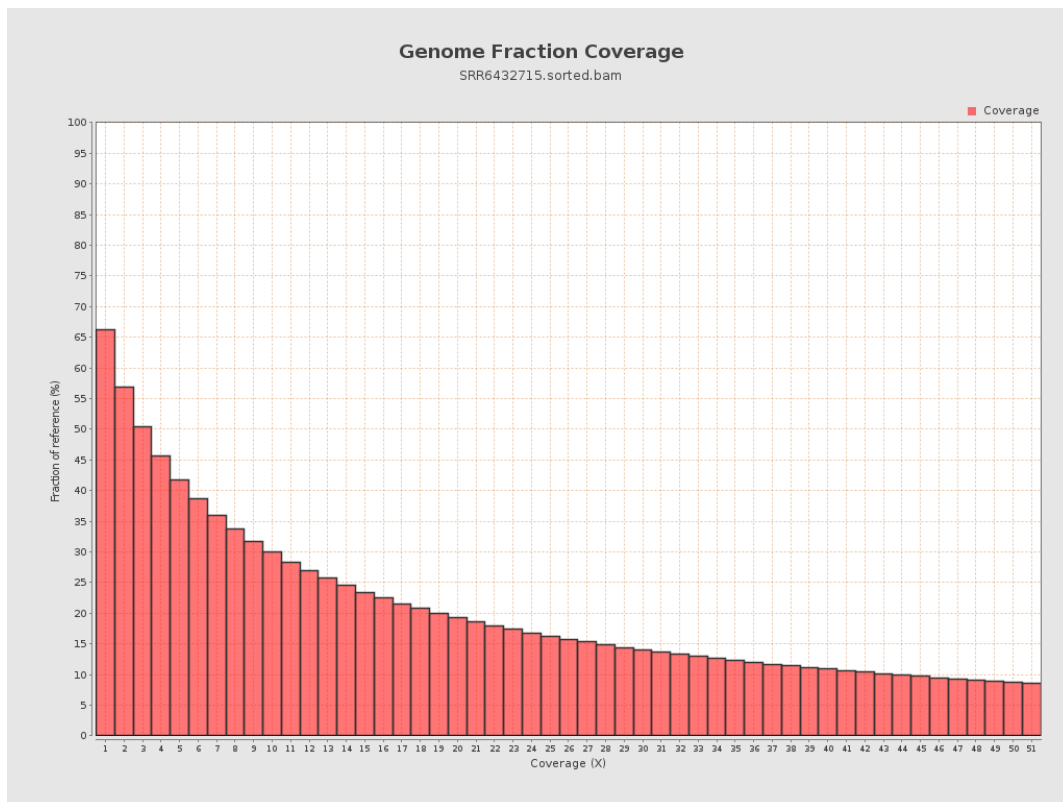
4. Results : Coverage Histogram



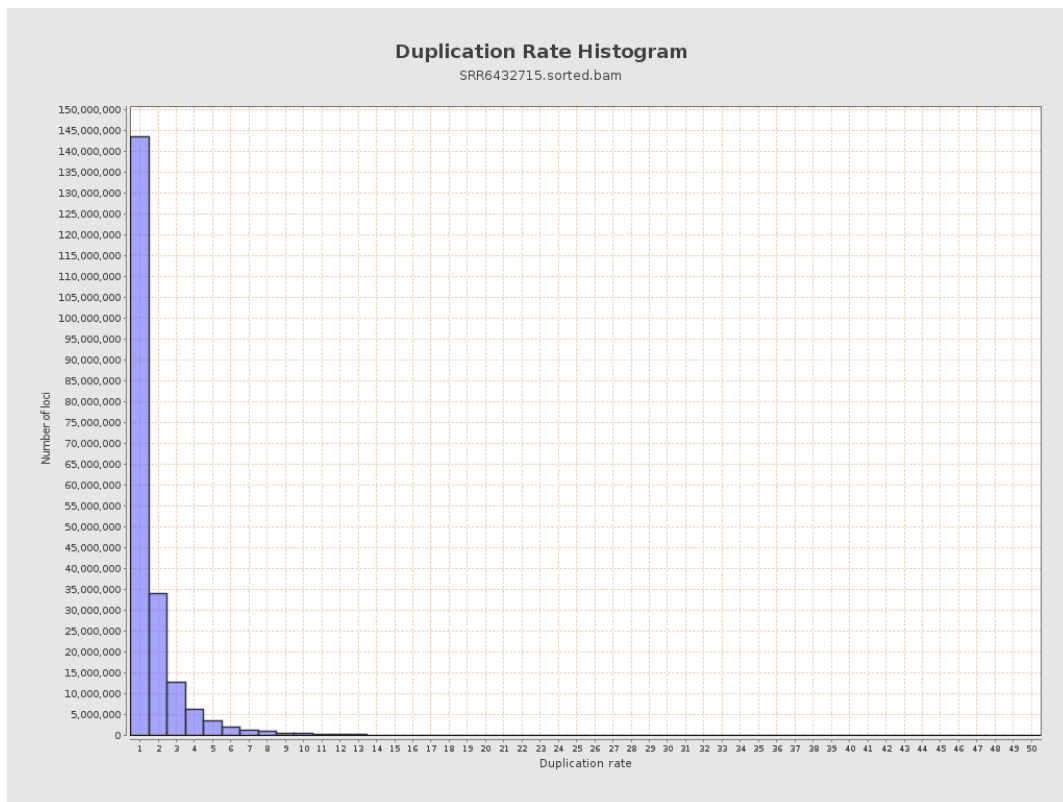
5. Results : Coverage Histogram (0-50X)



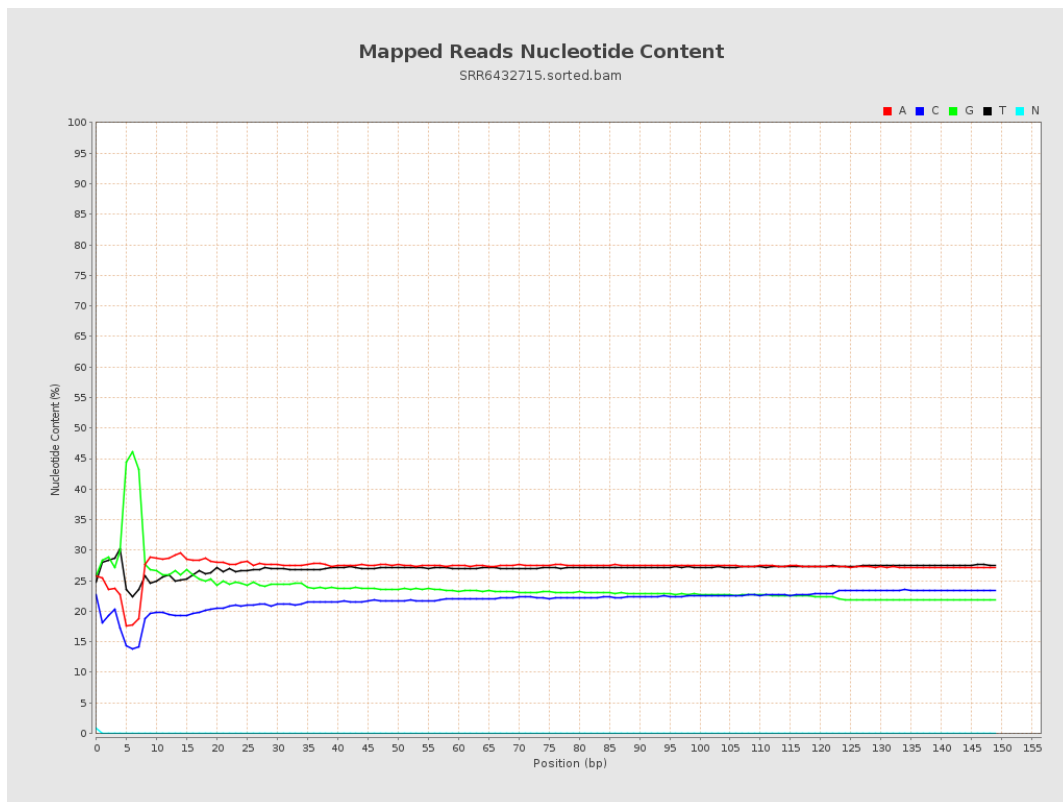
6. Results : Genome Fraction Coverage



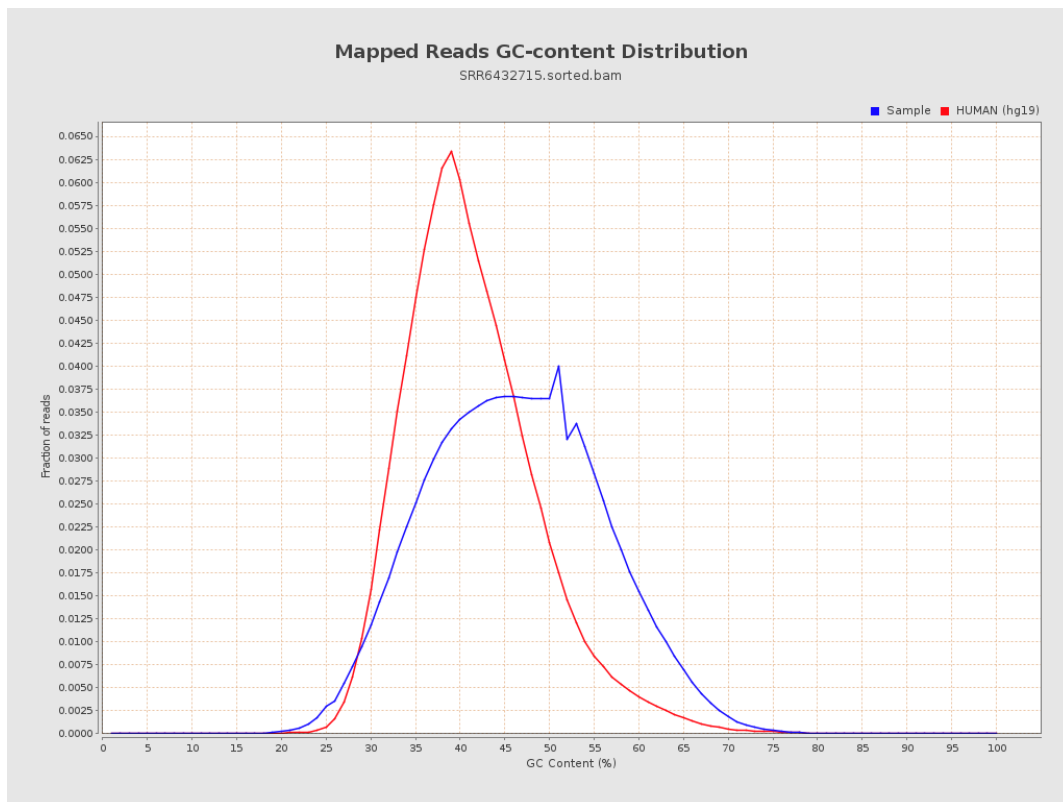
7. Results : Duplication Rate Histogram



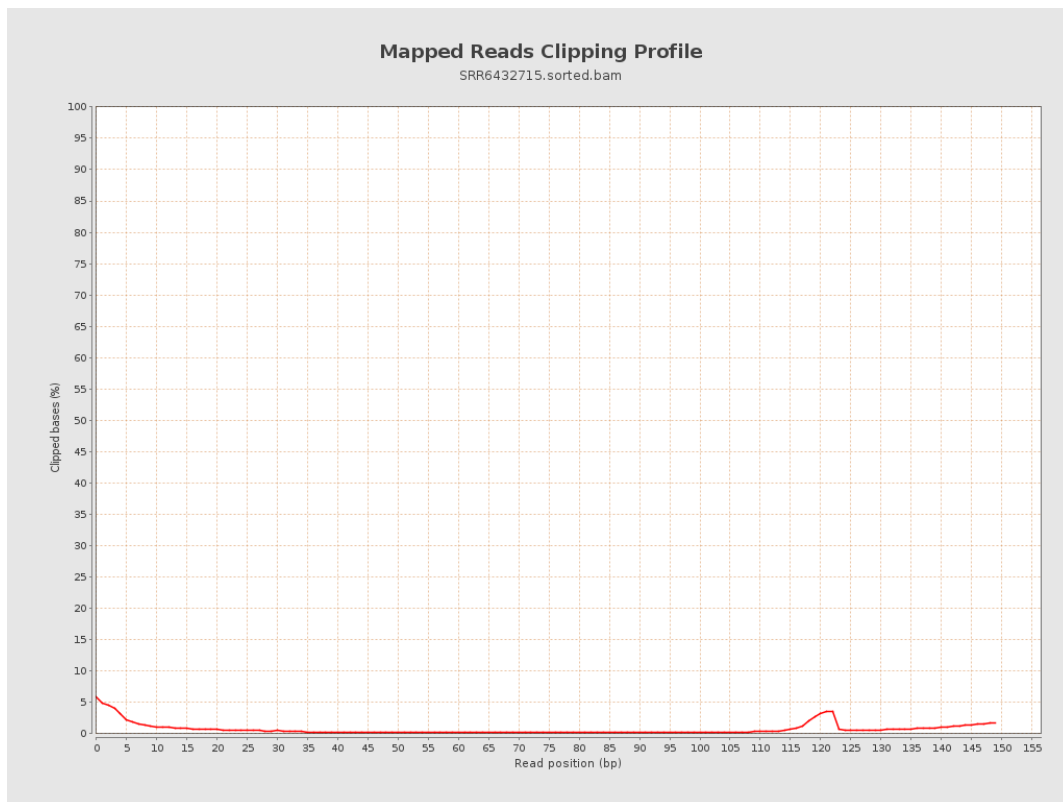
8. Results : Mapped Reads Nucleotide Content



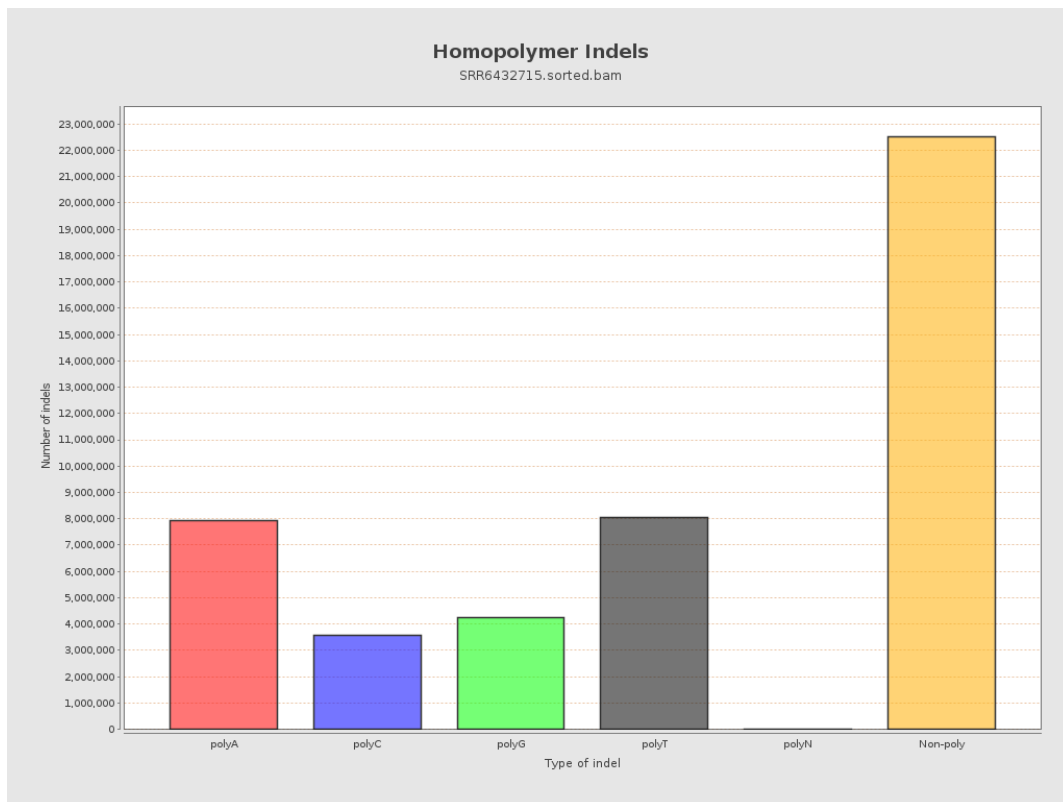
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



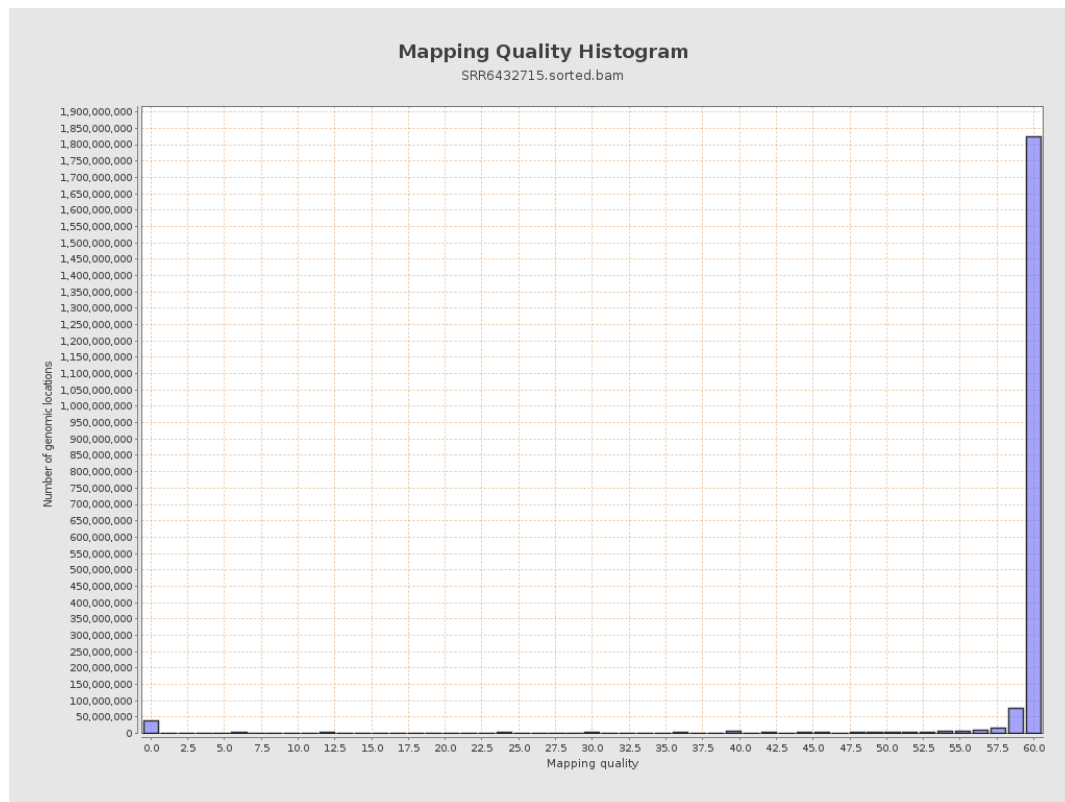
11. Results : Homopolymer Indels



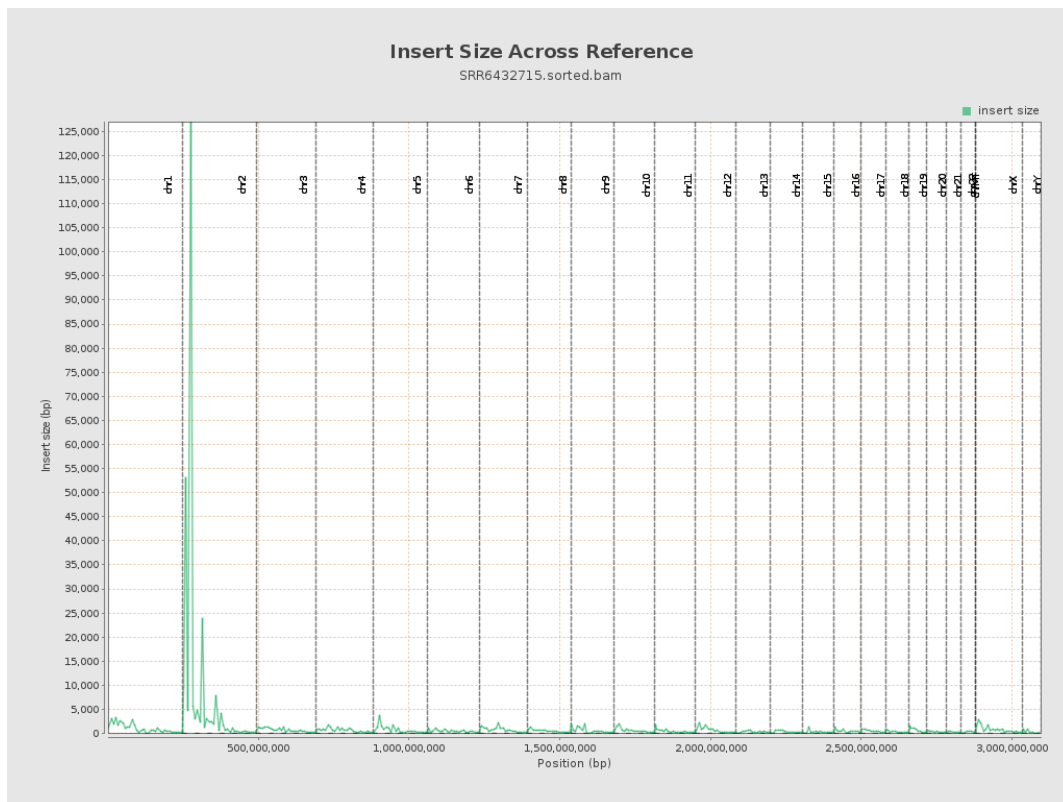
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

