

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2022/04/01 08:26:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432713.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_SRR6432713 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432713_1.fastq.gz SRR6432713_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Apr 01 08:26:30 CST 2022
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432713.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	401,666,604
Mapped reads	401,497,524 / 99.96%
Unmapped reads	169,080 / 0.04%
Mapped paired reads	401,497,524 / 99.96%
Mapped reads, first in pair	200,753,190 / 49.98%
Mapped reads, second in pair	200,744,334 / 49.98%
Mapped reads, both in pair	401,439,844 / 99.94%
Mapped reads, singletons	57,680 / 0.01%
Secondary alignments	0
Supplementary alignments	197,061 / 0.05%
Read min/max/mean length	30 / 150 / 140.69
Duplicated reads (estimated)	193,573,363 / 48.19%
Duplication rate	31.68%
Clipped reads	100,357,254 / 24.99%

2.2. ACGT Content

Number/percentage of A's	15,197,037,093 / 27.38%
Number/percentage of C's	12,064,515,227 / 21.74%
Number/percentage of T's	15,052,304,344 / 27.12%
Number/percentage of G's	13,182,981,085 / 23.75%
Number/percentage of N's	284,077 / 0%

GC Percentage	45.49%
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2.3. Coverage

Mean	17.945
Standard Deviation	53.3759

2.4. Mapping Quality

Mean Mapping Quality	55.37
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2.5. Insert size

Mean	53,058.36
Standard Deviation	2,271,622.11
P25/Median/P75	258 / 279 / 299

2.6. Mismatches and indels

General error rate	0.93%
Mismatches	497,325,820
Insertions	11,569,756
Mapped reads with at least one insertion	2.81%
Deletions	38,172,094
Mapped reads with at least one deletion	9.06%
Homopolymer indels	52.22%

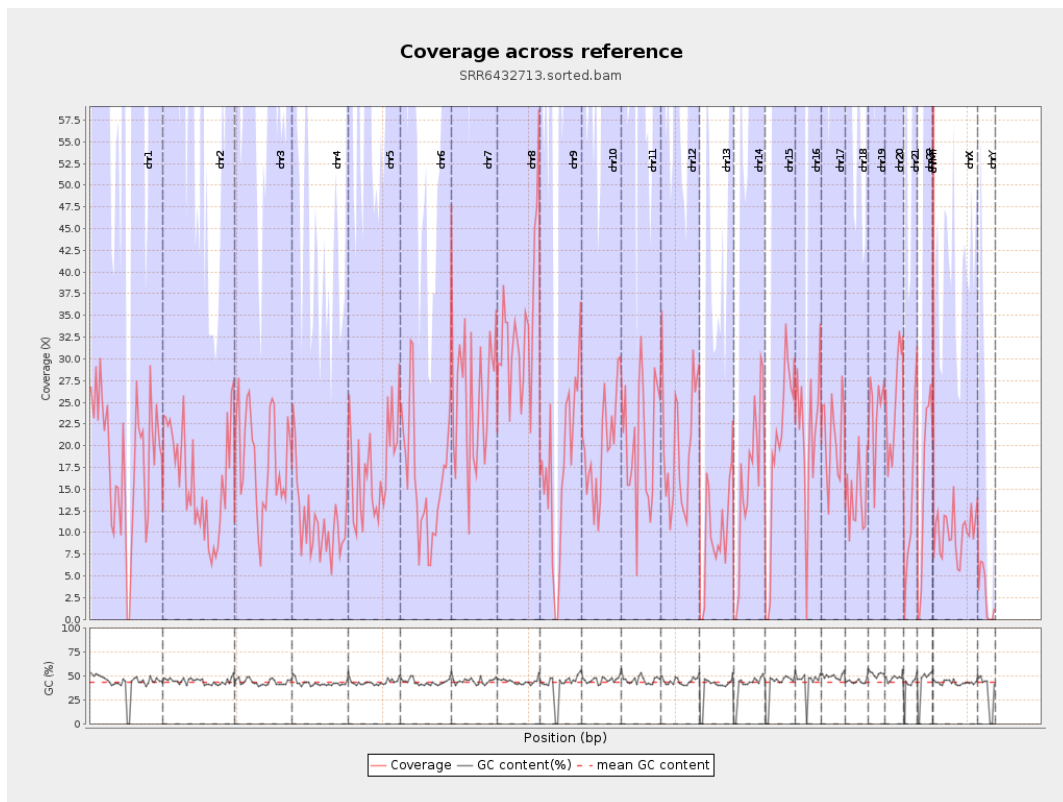
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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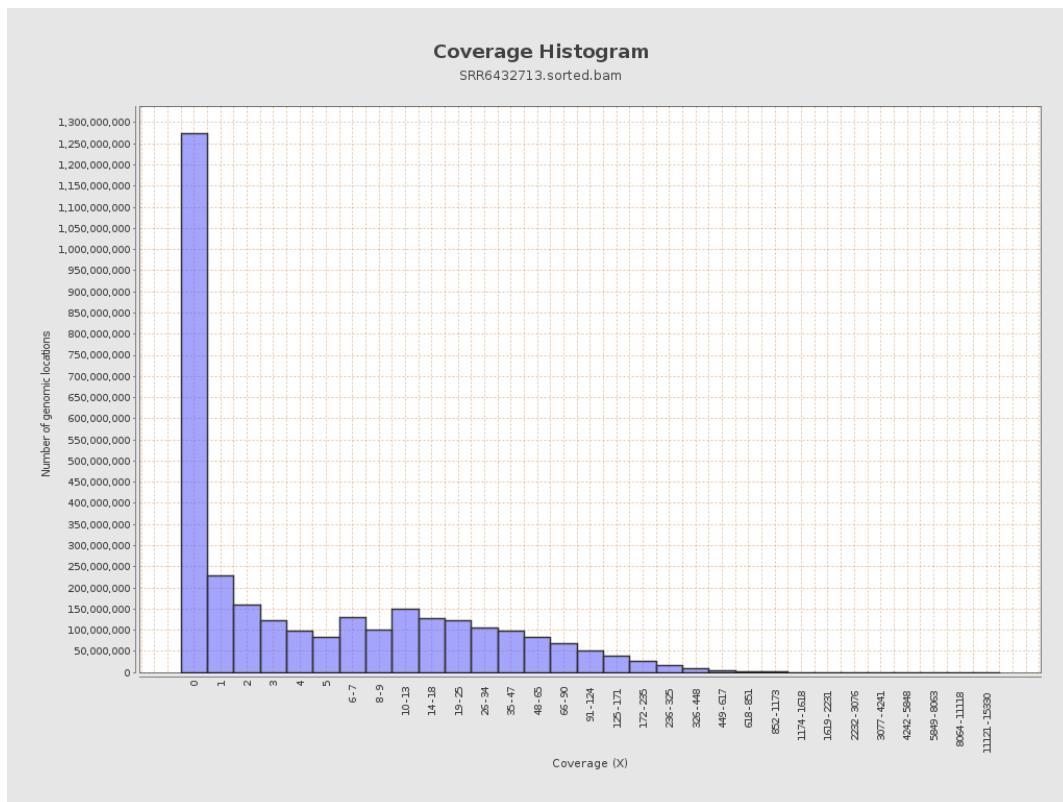
		bases	coverage	deviation
chr1	249250621	4586385056	18.4007	53.5493
chr2	243199373	3892217232	16.0042	51.4855
chr3	198022430	3607652332	18.2184	48.8575
chr4	191154276	2148190269	11.238	35.9693
chr5	180915260	3175223046	17.5509	49.2151
chr6	171115067	2744596686	16.0395	46.5766
chr7	159138663	4101300119	25.7719	68.0662
chr8	146364022	4925833961	33.6547	84.8166
chr9	141213431	2478019751	17.548	56.7779
chr10	135534747	2673328220	19.7243	52.8431
chr11	135006516	2781419204	20.6021	55.2187
chr12	133851895	2692360144	20.1145	54.6741
chr13	115169878	1125323497	9.771	31.8355
chr14	107349540	1710262831	15.9317	47.298
chr15	102531392	1972326768	19.2363	55.8284
chr16	90354753	1958799076	21.679	64.1317
chr17	81195210	1705961491	21.0106	55.7602
chr18	78077248	1079628299	13.8277	42.4561
chr19	59128983	1411234814	23.8671	65.1958
chr20	63025520	1562749767	24.7955	62.3786
chr21	48129895	663130202	13.7779	53.7406
chr22	51304566	811970573	15.8265	49.4306
chrMT	16571	9796889	591.2069	1,019.081
chrX	155270560	1564238093	10.0743	29.9837

chrY	59373566	170263345	2.8677	23.1726
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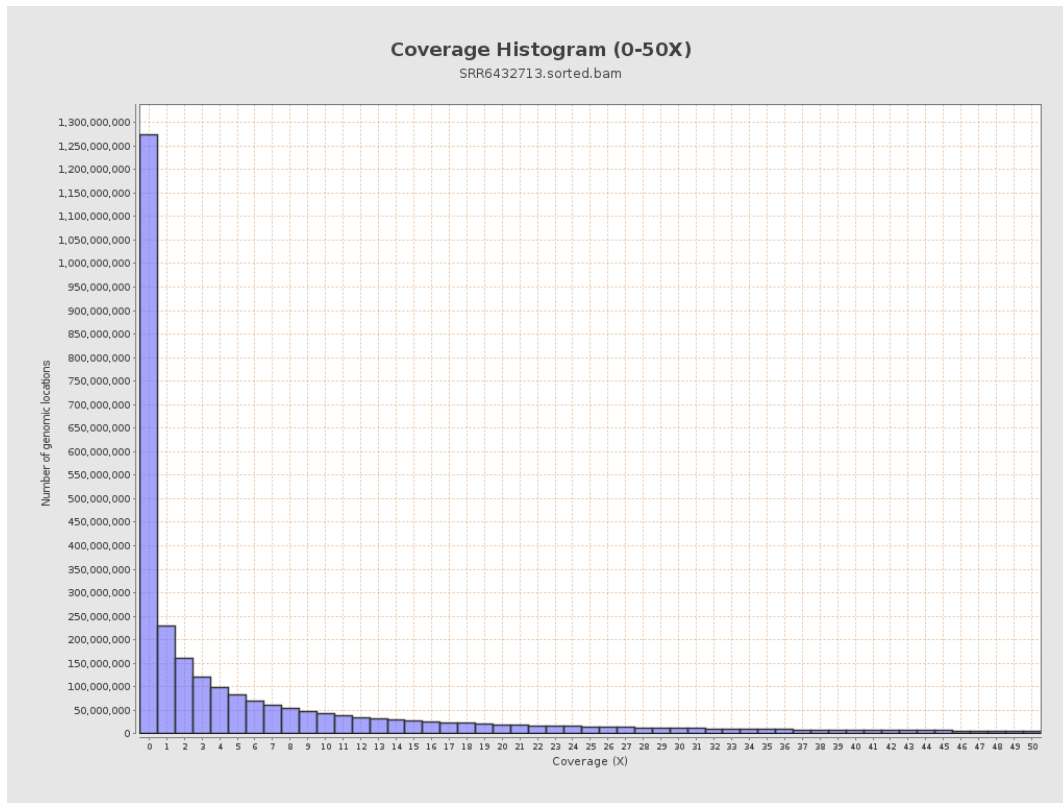
3. Results : Coverage across reference



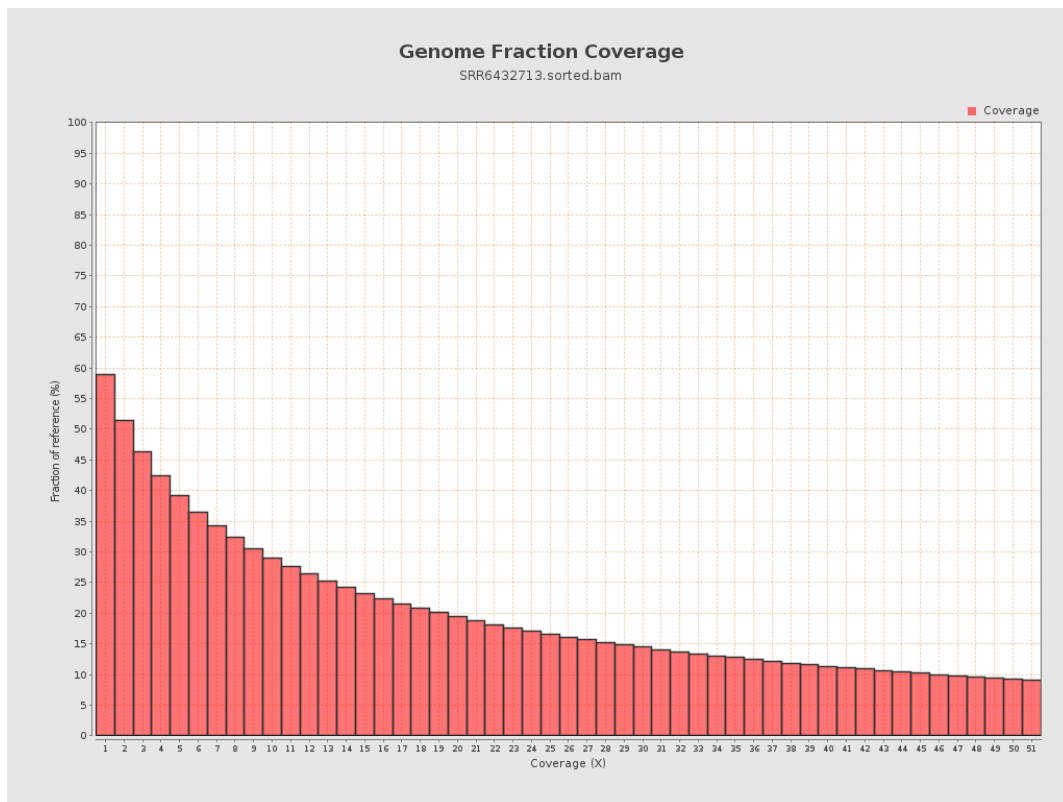
4. Results : Coverage Histogram



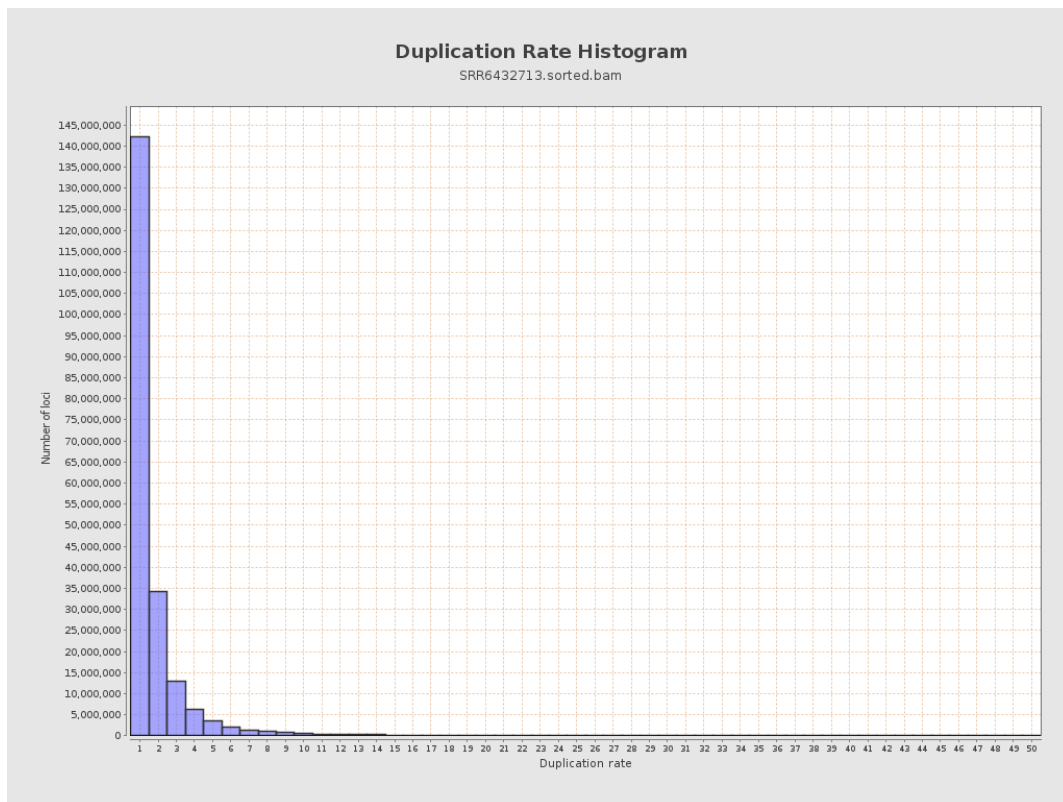
5. Results : Coverage Histogram (0-50X)



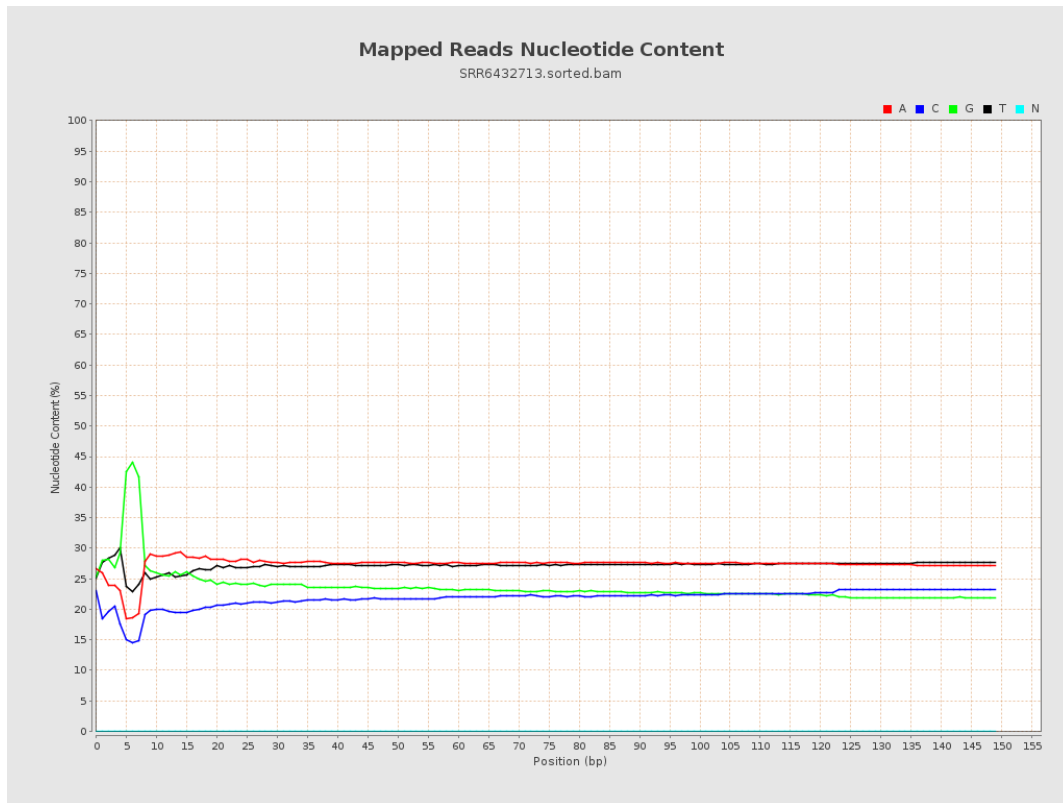
6. Results : Genome Fraction Coverage



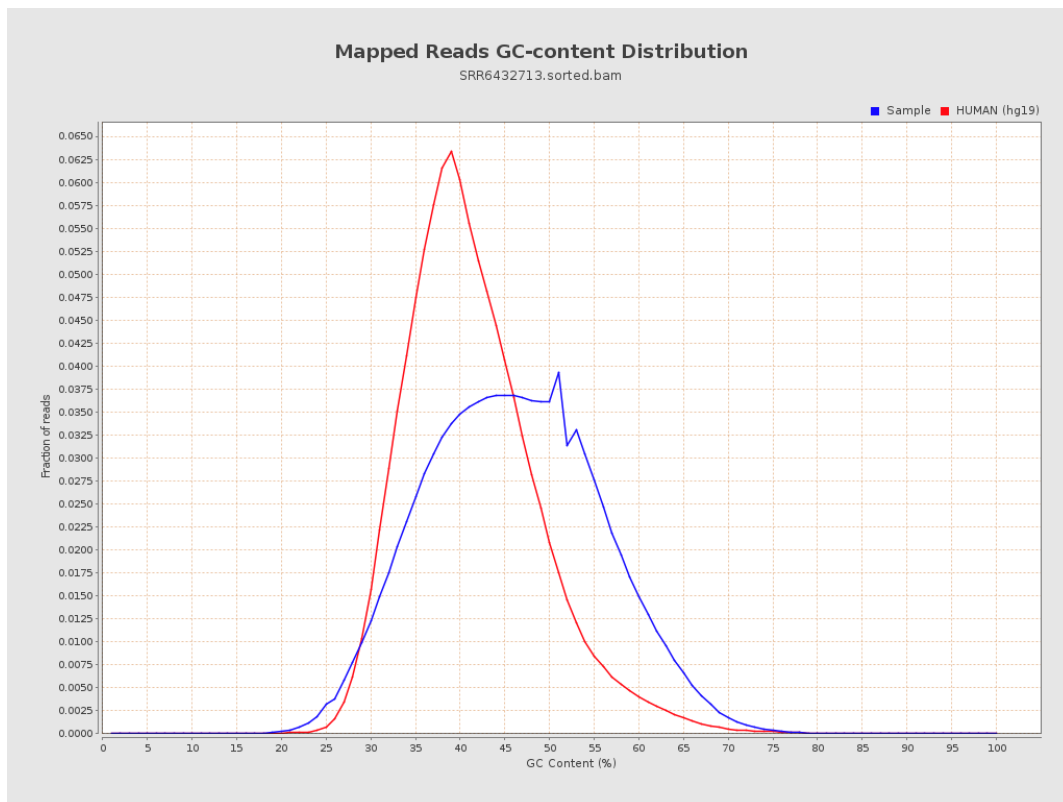
7. Results : Duplication Rate Histogram



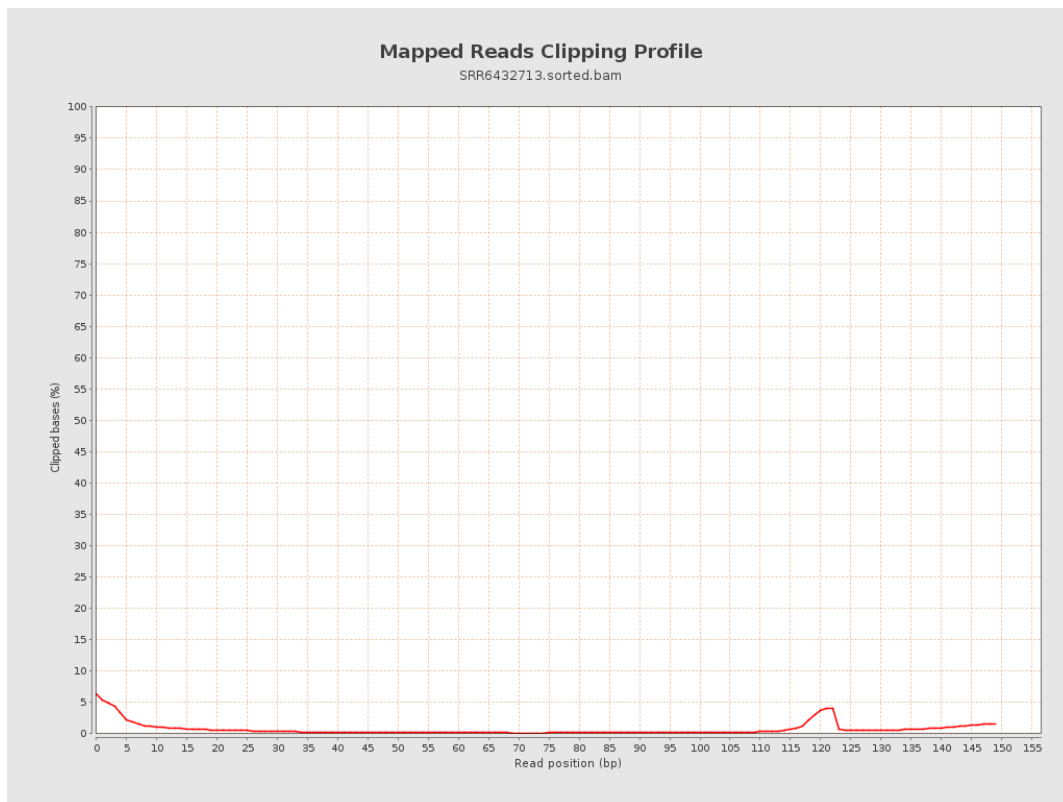
8. Results : Mapped Reads Nucleotide Content



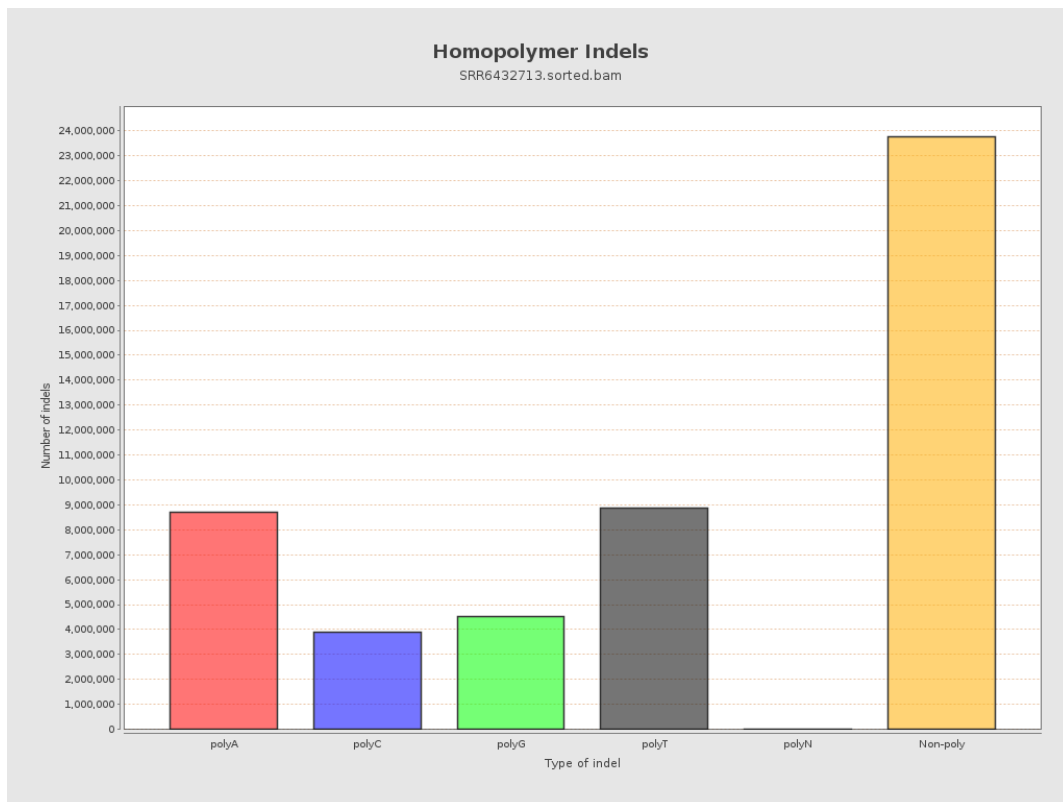
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



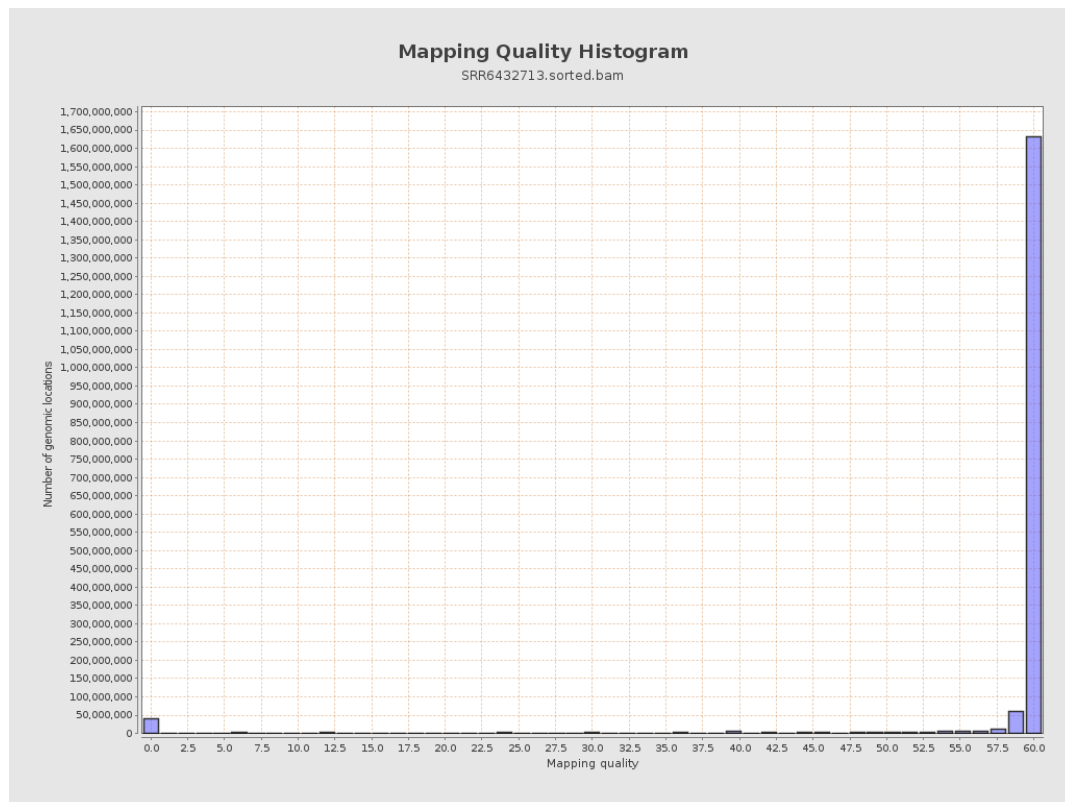
11. Results : Homopolymer Indels



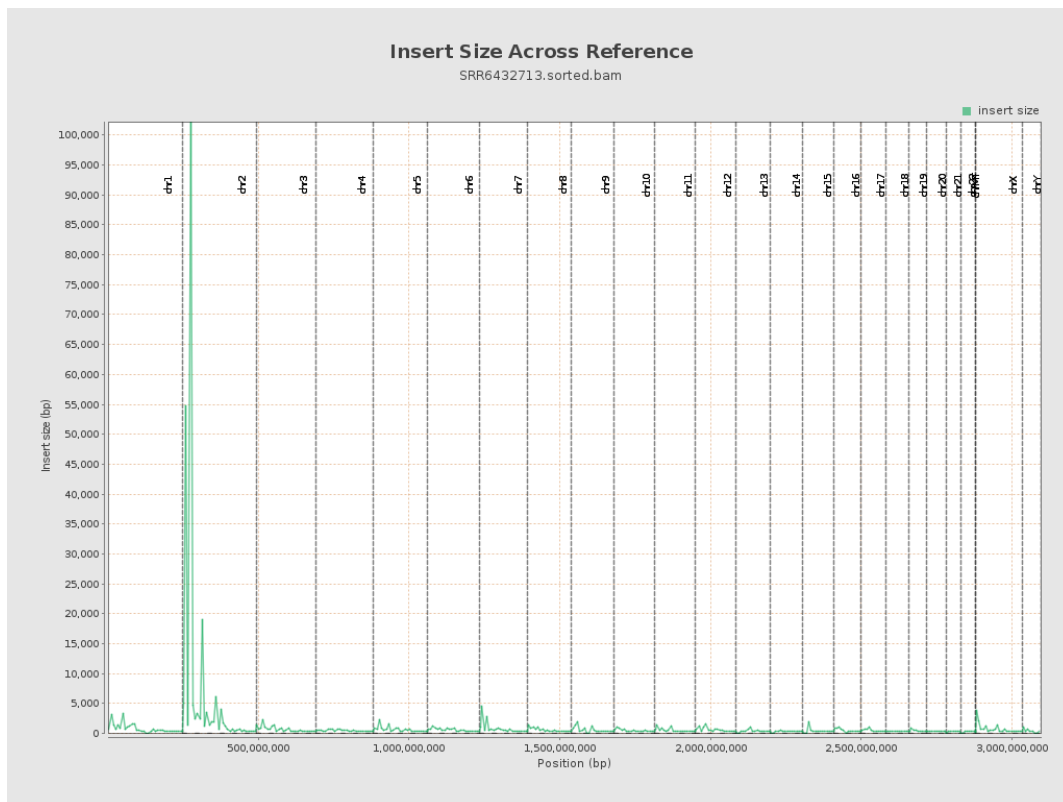
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

