

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/10/01 10:15:20

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR6432729.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_SRR6432729 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR6432729_1.fastq.gz SRR6432729_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Oct 01 10:15:20 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR6432729.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	379,687,448
Mapped reads	379,515,021 / 99.95%
Unmapped reads	172,427 / 0.05%
Mapped paired reads	379,515,021 / 99.95%
Mapped reads, first in pair	189,764,891 / 49.98%
Mapped reads, second in pair	189,750,130 / 49.98%
Mapped reads, both in pair	379,449,242 / 99.94%
Mapped reads, singletons	65,779 / 0.02%
Secondary alignments	0
Supplementary alignments	223,752 / 0.06%
Read min/max/mean length	30 / 150 / 140.4
Duplicated reads (estimated)	176,164,448 / 46.4%
Duplication rate	31.19%
Clipped reads	111,555,063 / 29.38%

2.2. ACGT Content

Number/percentage of A's	14,221,941,159 / 27.35%
Number/percentage of C's	11,290,691,129 / 21.71%
Number/percentage of T's	14,028,585,886 / 26.98%
Number/percentage of G's	12,456,995,447 / 23.96%
Number/percentage of N's	1,652,983 / 0%

GC Percentage	45.67%
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2.3. Coverage

Mean	16.8139
Standard Deviation	49.1567

2.4. Mapping Quality

Mean Mapping Quality	55.36
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2.5. Insert size

Mean	86,777.66
Standard Deviation	2,990,056.1
P25/Median/P75	282 / 305 / 324

2.6. Mismatches and indels

General error rate	1.08%
Mismatches	543,425,503
Insertions	10,871,113
Mapped reads with at least one insertion	2.8%
Deletions	34,215,265
Mapped reads with at least one deletion	8.6%
Homopolymer indels	51.28%

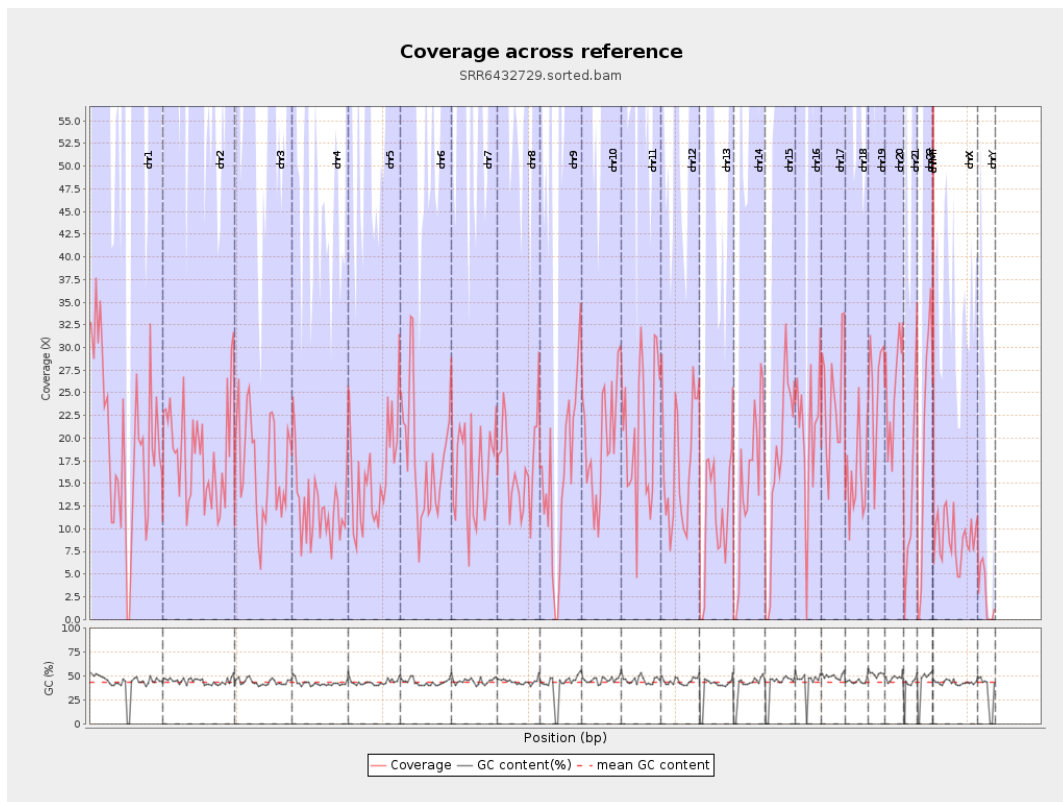
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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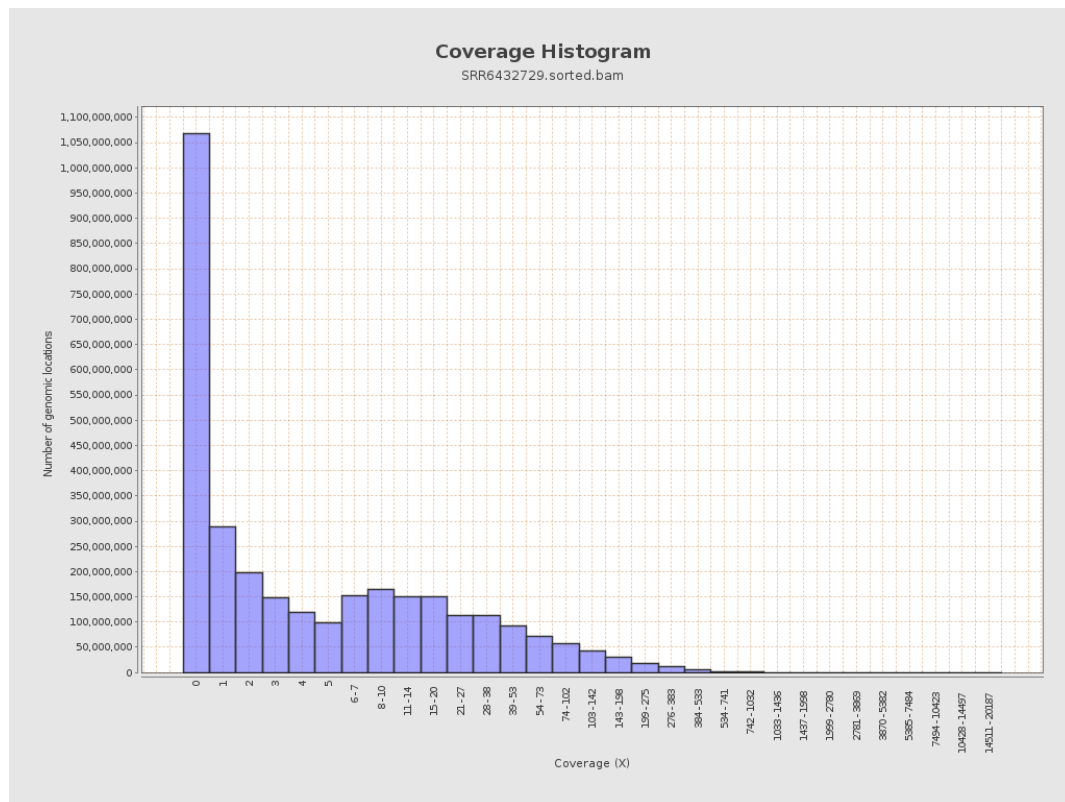
		bases	coverage	deviation
chr1	249250621	4836791724	19.4053	55.2699
chr2	243199373	4440838989	18.2601	55.958
chr3	198022430	3313929548	16.7351	44.5616
chr4	191154276	2371313418	12.4052	36.8103
chr5	180915260	2930627880	16.1989	45.5506
chr6	171115067	3001839250	17.5428	48.315
chr7	159138663	2641947413	16.6015	45.7327
chr8	146364022	2484060266	16.9718	46.248
chr9	141213431	2227808492	15.7762	51.0562
chr10	135534747	2660032595	19.6262	52.1027
chr11	135006516	2778353195	20.5794	53.9027
chr12	133851895	2316606480	17.3072	47.8045
chr13	115169878	1294156652	11.2369	35.1888
chr14	107349540	1617976068	15.072	44.4927
chr15	102531392	1742714899	16.9969	49.3586
chr16	90354753	1876605010	20.7693	63.1723
chr17	81195210	1973445847	24.305	62.4297
chr18	78077248	1200945090	15.3815	44.9876
chr19	59128983	1501148650	25.3877	68.6171
chr20	63025520	1595443664	25.3142	61.8698
chr21	48129895	672051465	13.9633	51.1129
chr22	51304566	1008523323	19.6576	58.2872
chrMT	16571	4978175	300.4149	593.0453
chrX	155270560	1391868970	8.9642	26.0486

chrY	59373566	166720003	2.808	21.739
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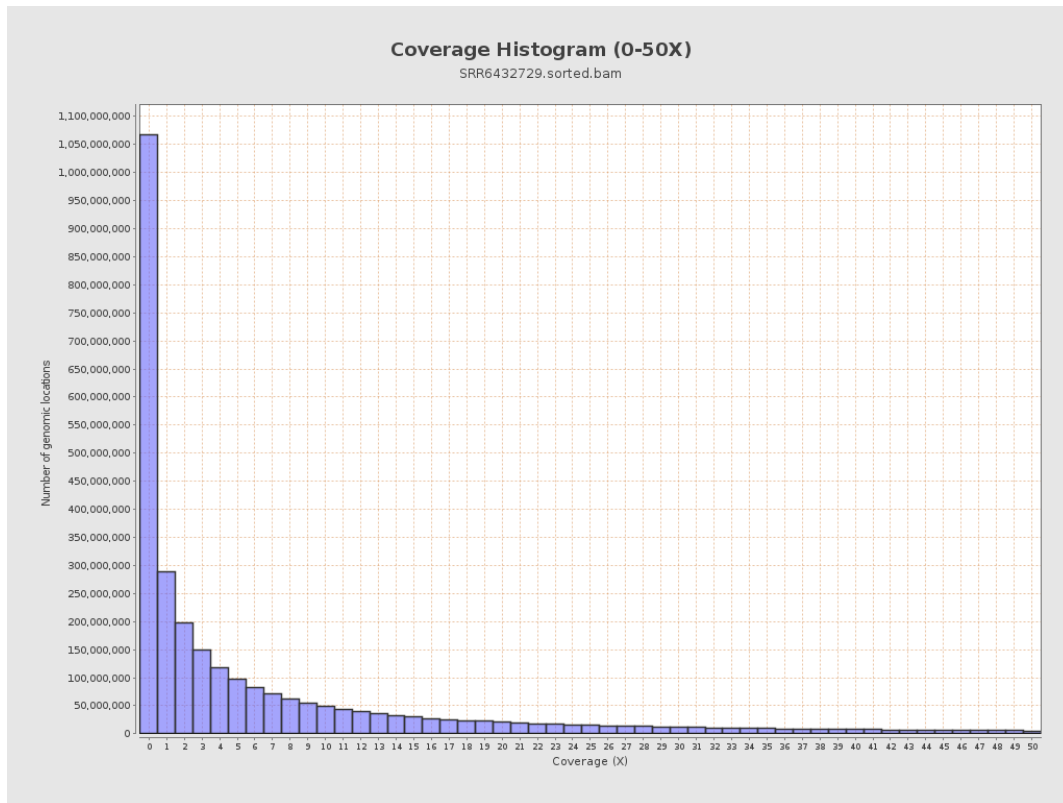
3. Results : Coverage across reference



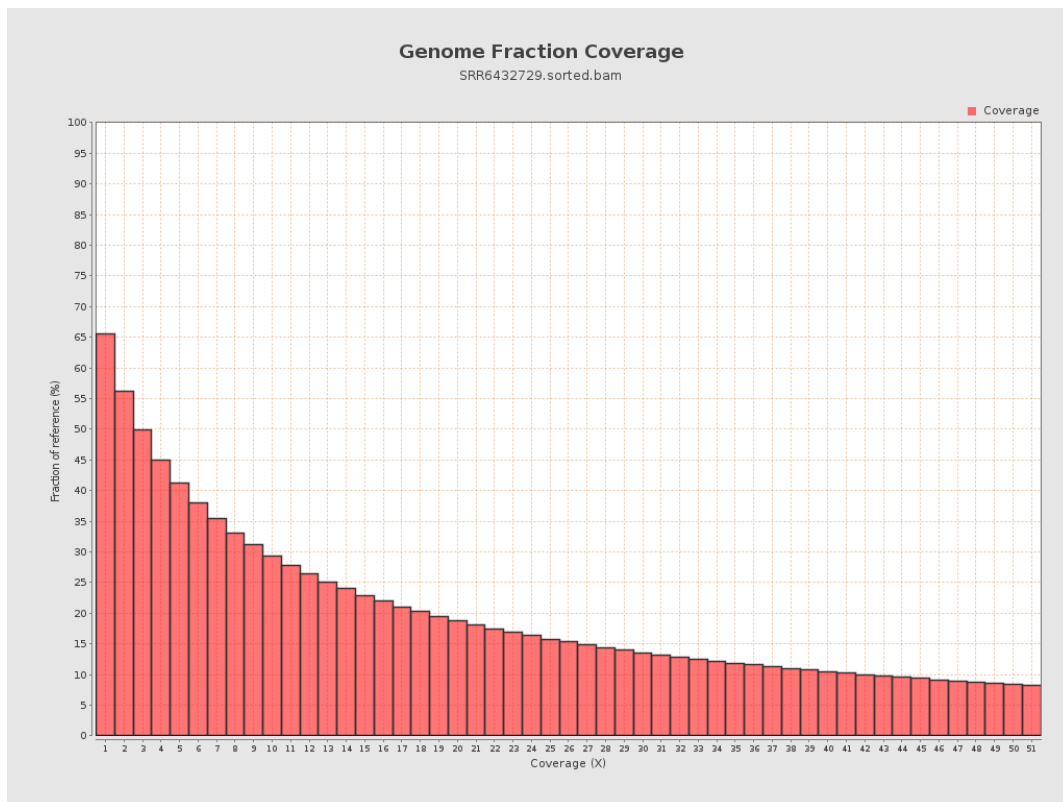
4. Results : Coverage Histogram



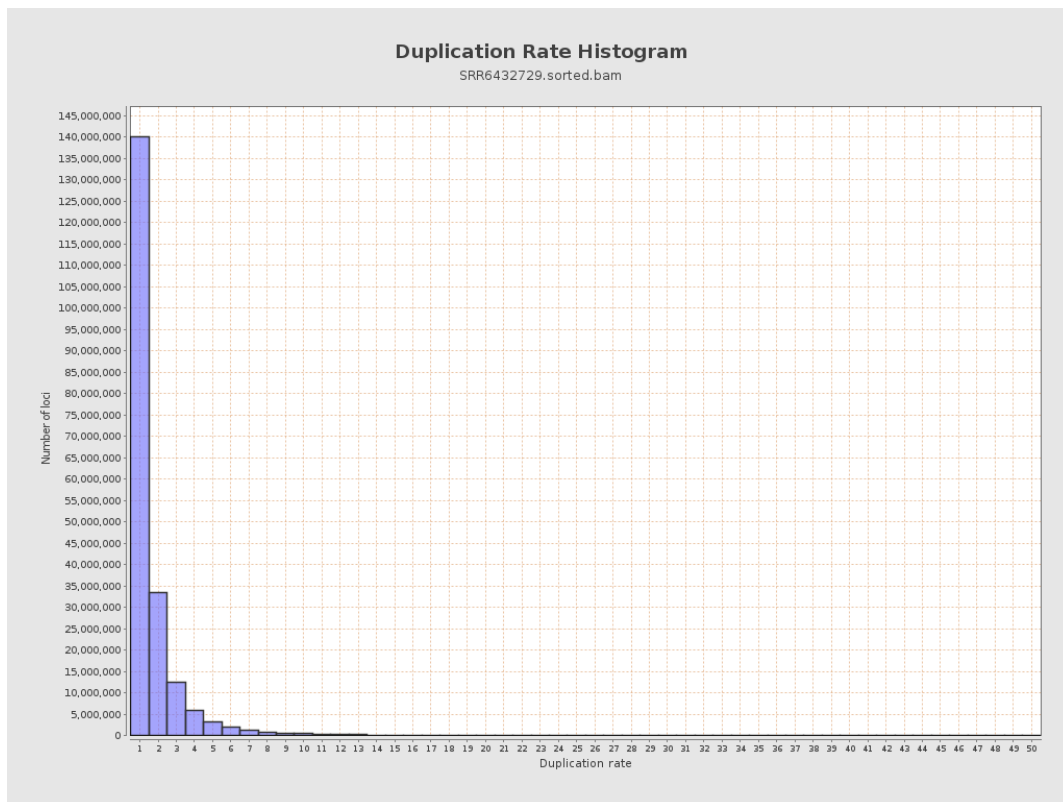
5. Results : Coverage Histogram (0-50X)



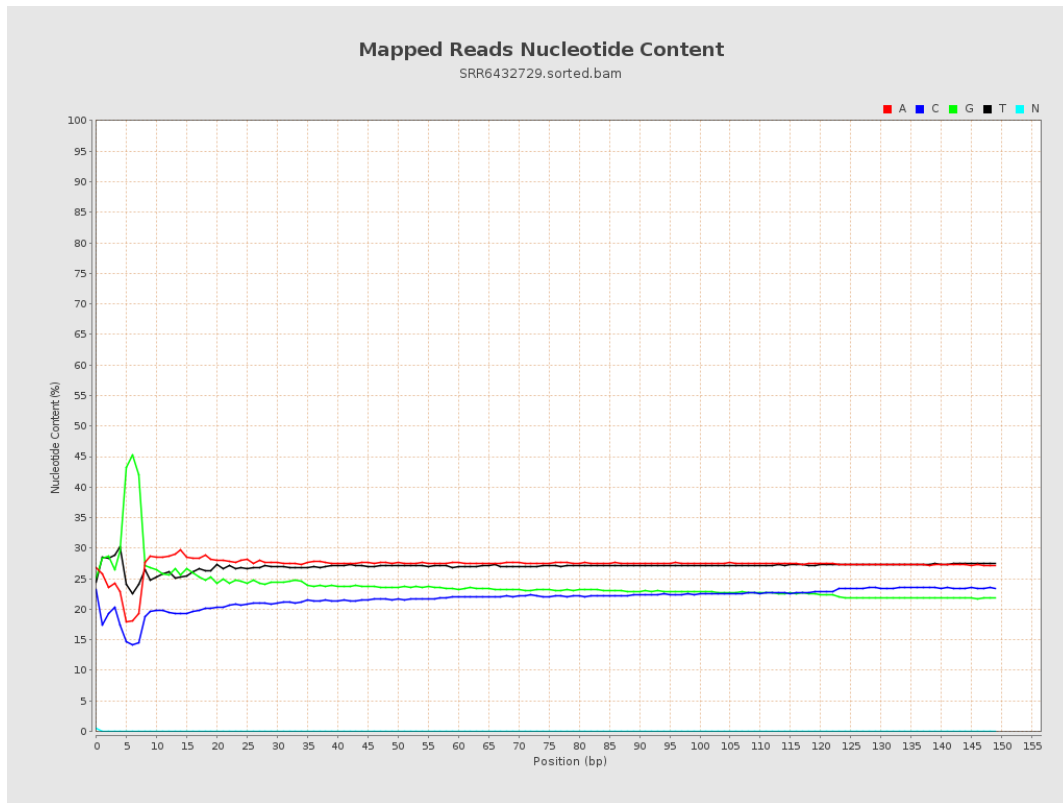
6. Results : Genome Fraction Coverage



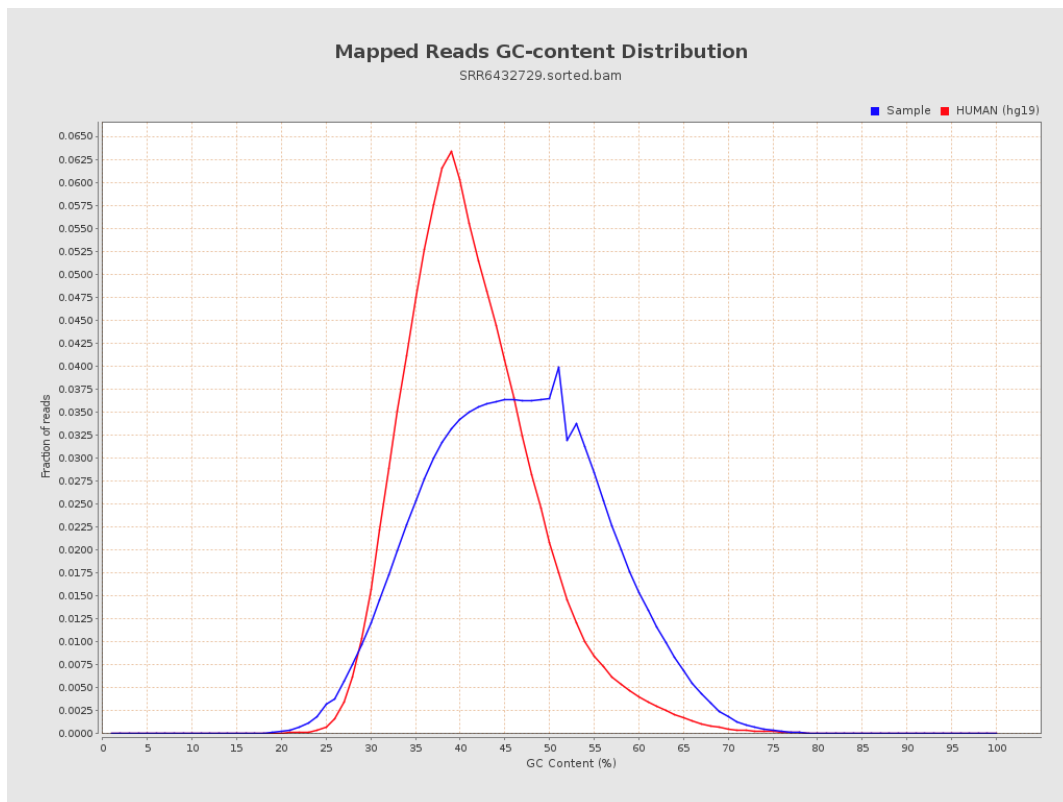
7. Results : Duplication Rate Histogram



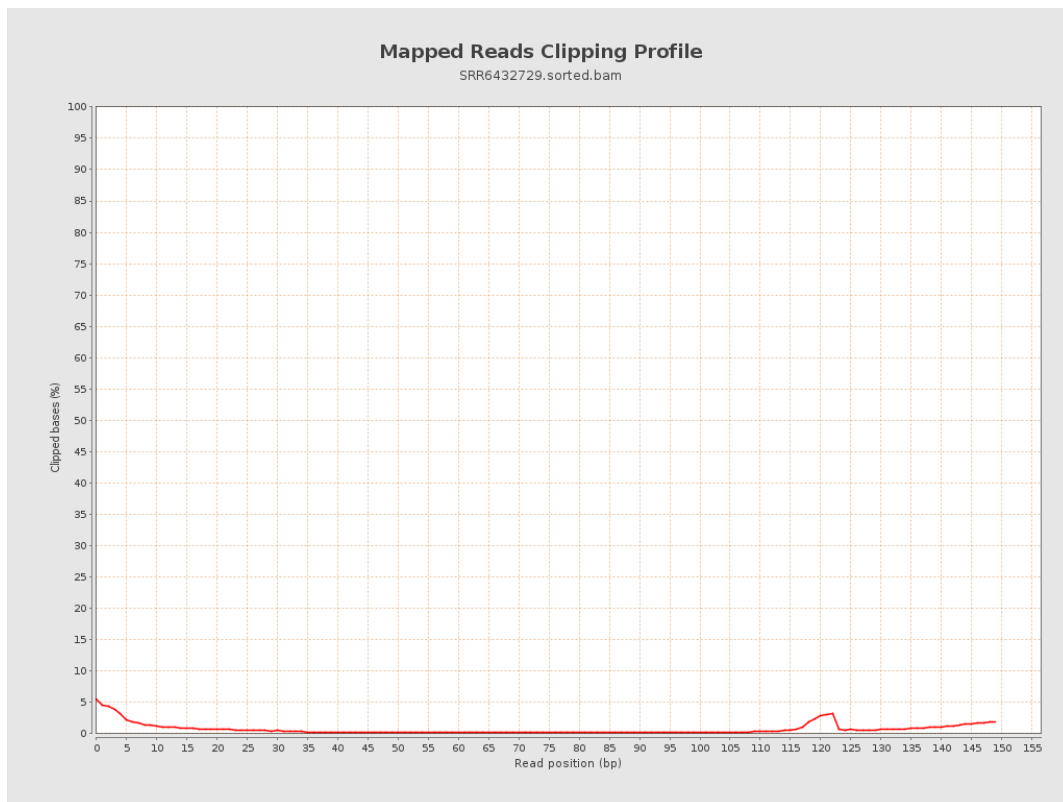
8. Results : Mapped Reads Nucleotide Content



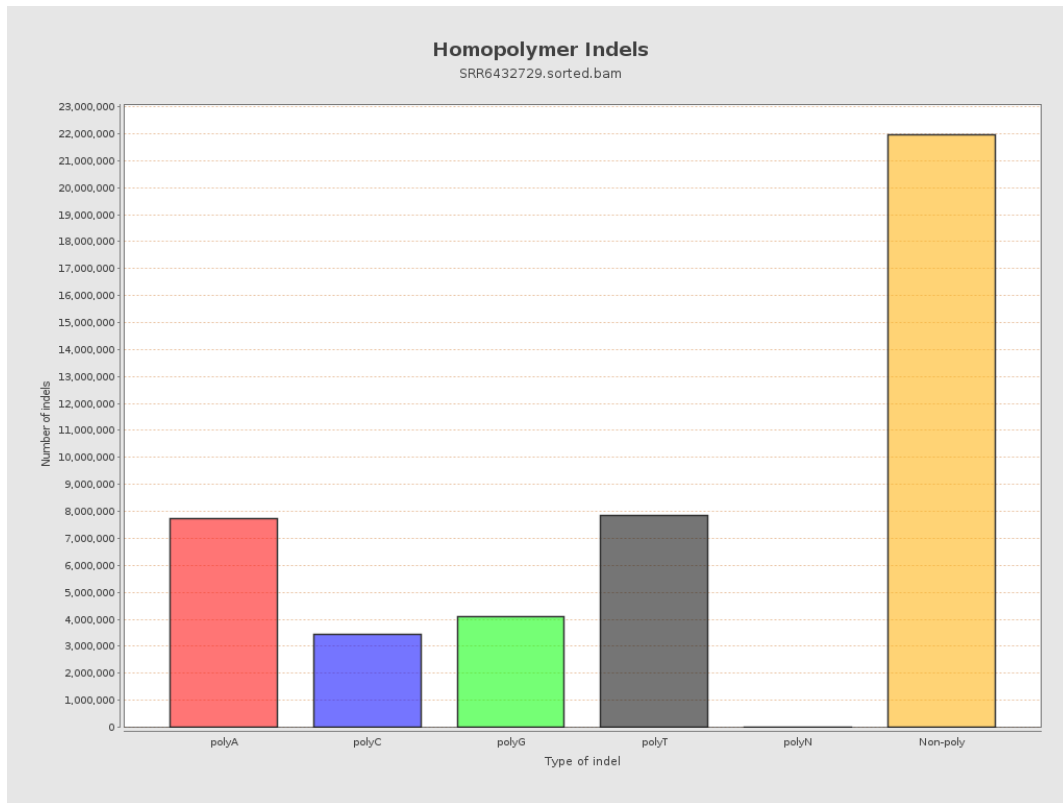
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



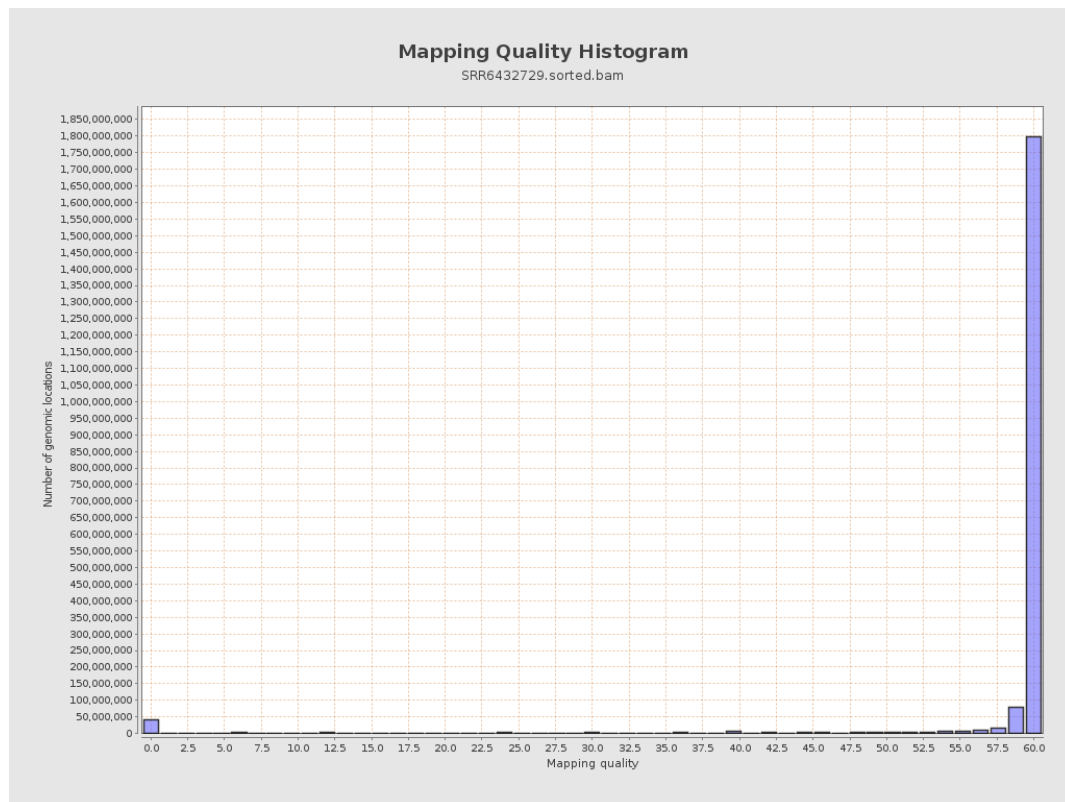
11. Results : Homopolymer Indels



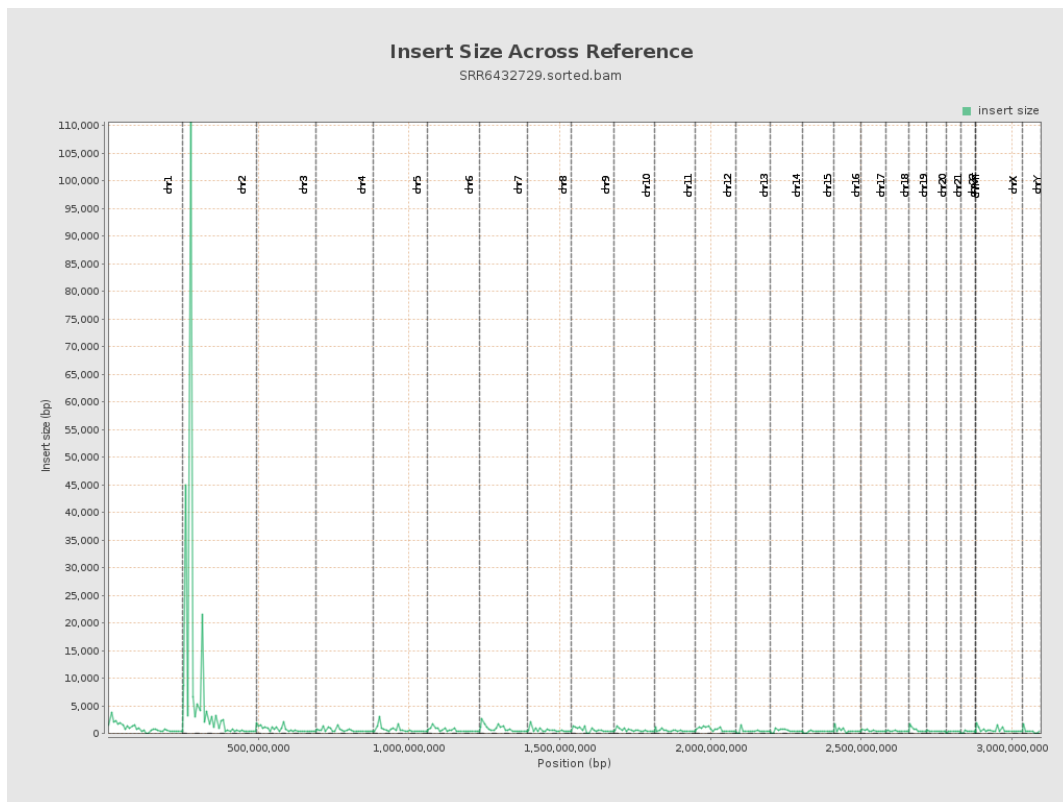
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

