

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 01:15:37

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695929.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/s oftware/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\t PL:ILLUMINA\tSM:sample_SRR1695 929 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695929_1.fastq.gz SRR1695929_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Fri Sep 13 01:15:37 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695929.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	97,216,660
Mapped reads	86,186,774 / 88.65%
Unmapped reads	11,029,886 / 11.35%
Mapped paired reads	86,186,774 / 88.65%
Mapped reads, first in pair	45,333,651 / 46.63%
Mapped reads, second in pair	40,853,123 / 42.02%
Mapped reads, both in pair	78,938,826 / 81.2%
Mapped reads, singletons	7,247,948 / 7.46%
Secondary alignments	0
Supplementary alignments	2,360,173 / 2.43%
Read min/max/mean length	30 / 100 / 100.9
Duplicated reads (estimated)	54,372,223 / 55.93%
Duplication rate	30.11%
Clipped reads	57,697,093 / 59.35%

2.2. ACGT Content

Number/percentage of A's	1,892,874,920 / 26.11%
Number/percentage of C's	1,323,438,397 / 18.25%
Number/percentage of T's	2,331,339,357 / 32.16%
Number/percentage of G's	1,673,430,411 / 23.08%
Number/percentage of N's	29,111,188 / 0.4%

GC Percentage	41.34%
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2.3. Coverage

Mean	2.343
Standard Deviation	21.2865

2.4. Mapping Quality

Mean Mapping Quality	51.8
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2.5. Insert size

Mean	136,178.05
Standard Deviation	3,529,835.84
P25/Median/P75	302 / 321 / 334

2.6. Mismatches and indels

General error rate	1.58%
Mismatches	113,615,511
Insertions	591,895
Mapped reads with at least one insertion	0.68%
Deletions	1,660,006
Mapped reads with at least one deletion	1.9%
Homopolymer indels	46.73%

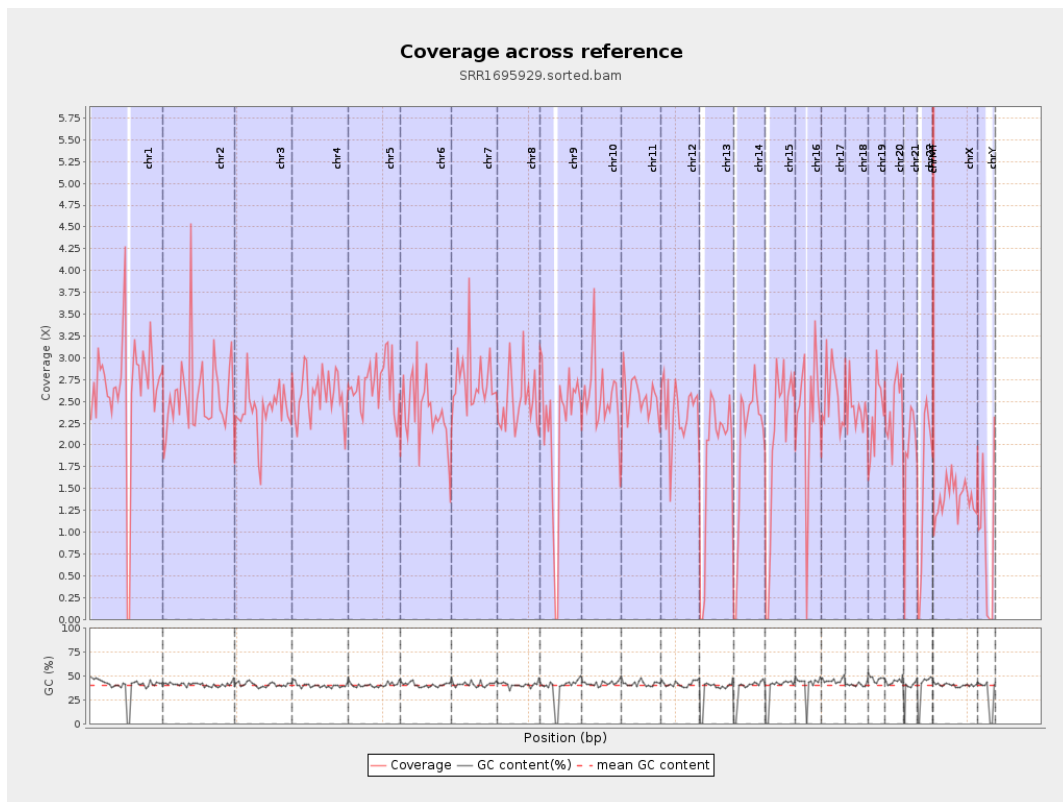
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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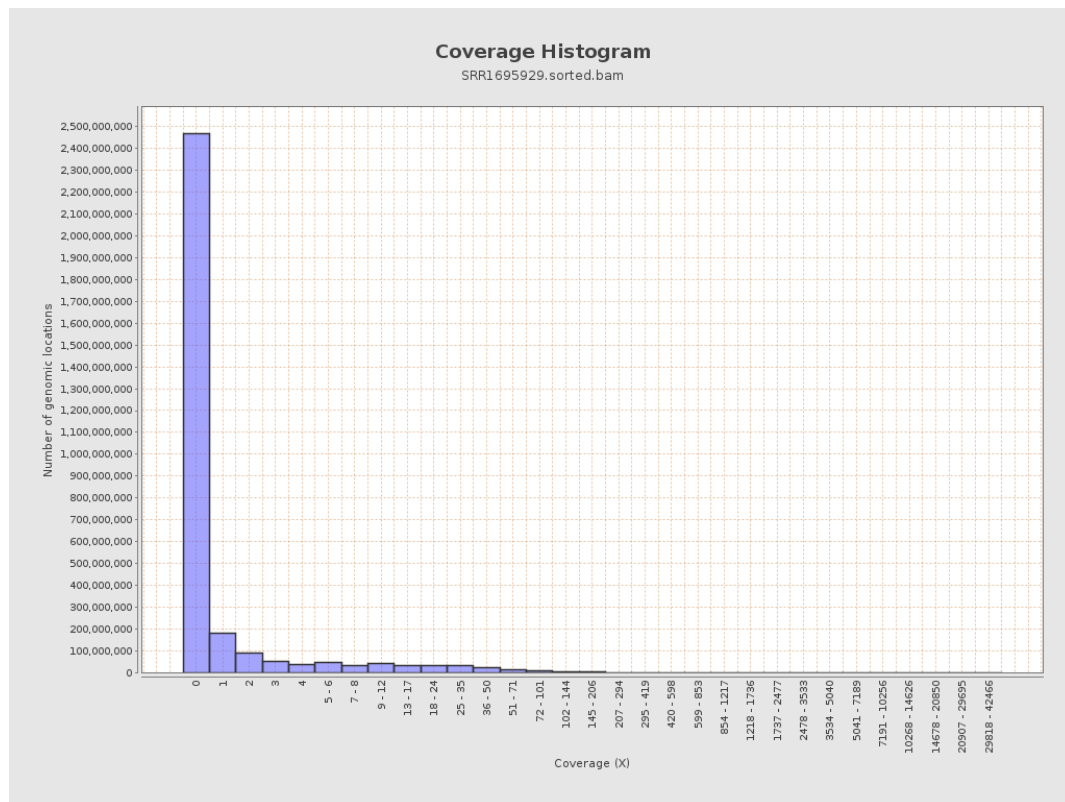
		bases	coverage	deviation
chr1	249250621	659624350	2.6464	35.8581
chr2	243199373	626528657	2.5762	24.3837
chr3	198022430	472150970	2.3843	11.2906
chr4	191154276	492354782	2.5757	12.4754
chr5	180915260	485114565	2.6814	12.1321
chr6	171115067	407484823	2.3813	15.3656
chr7	159138663	434085455	2.7277	27.7211
chr8	146364022	365246572	2.4955	37.6845
chr9	141213431	307860967	2.1801	18.1669
chr10	135534747	345883262	2.552	19.7104
chr11	135006516	342046327	2.5336	18.2246
chr12	133851895	320451589	2.3941	11.7098
chr13	115169878	212391577	1.8442	9.949
chr14	107349540	219327251	2.0431	11.1817
chr15	102531392	209095120	2.0393	10.512
chr16	90354753	208457884	2.3071	11.6283
chr17	81195210	207953488	2.5612	13.5805
chr18	78077248	189140234	2.4225	46.4072
chr19	59128983	140057710	2.3687	23.4699
chr20	63025520	152720599	2.4232	12.4006
chr21	48129895	91951882	1.9105	11.9735
chr22	51304566	79623725	1.552	11.1022
chrMT	16571	11200106	675.8859	475.6499
chrX	155270560	217156018	1.3986	10.2164

chrY	59373566	55216496	0.93	11.6697
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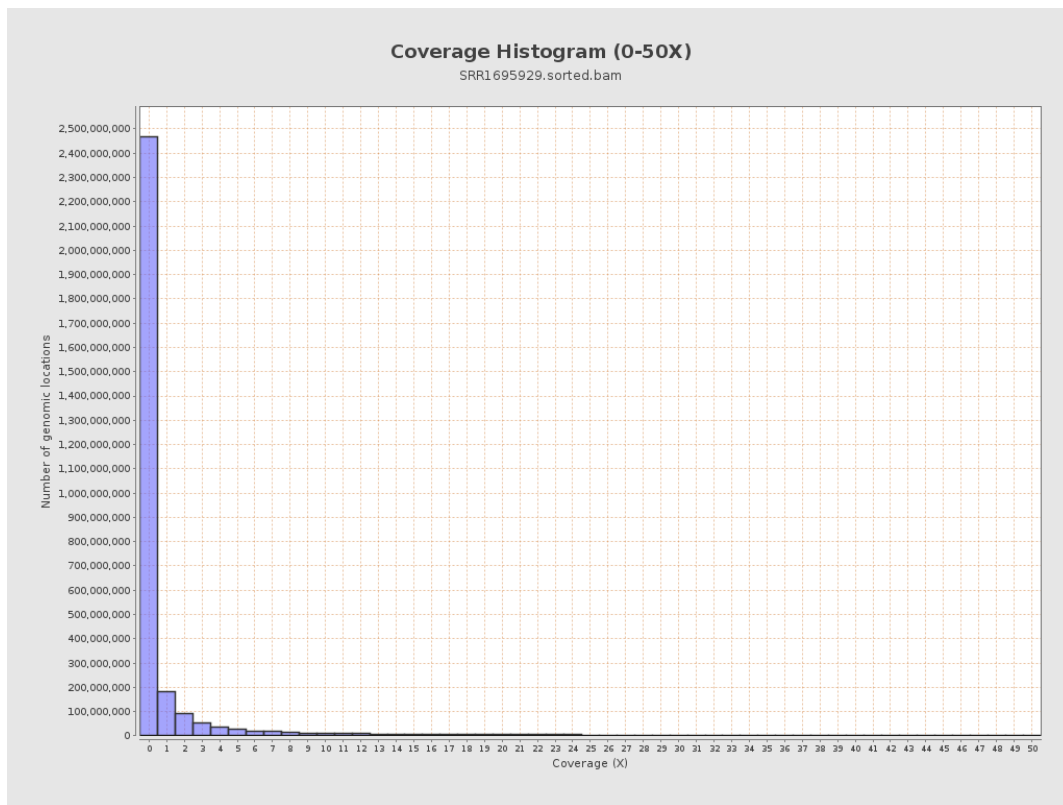
3. Results : Coverage across reference



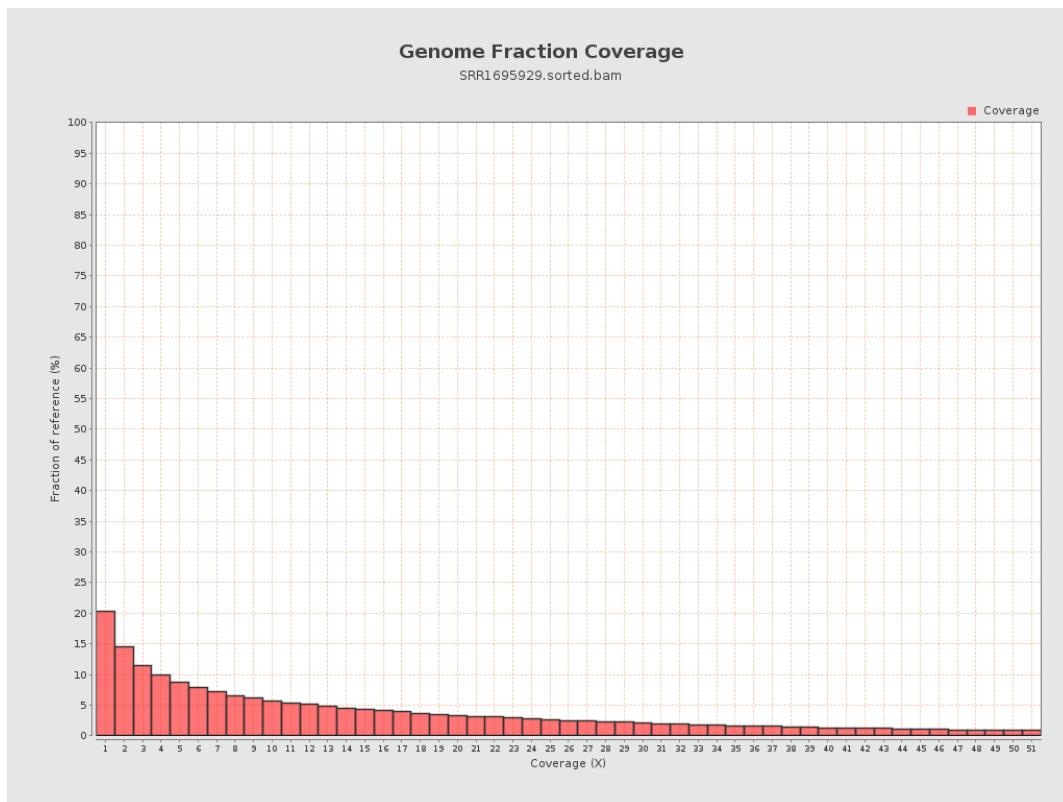
4. Results : Coverage Histogram



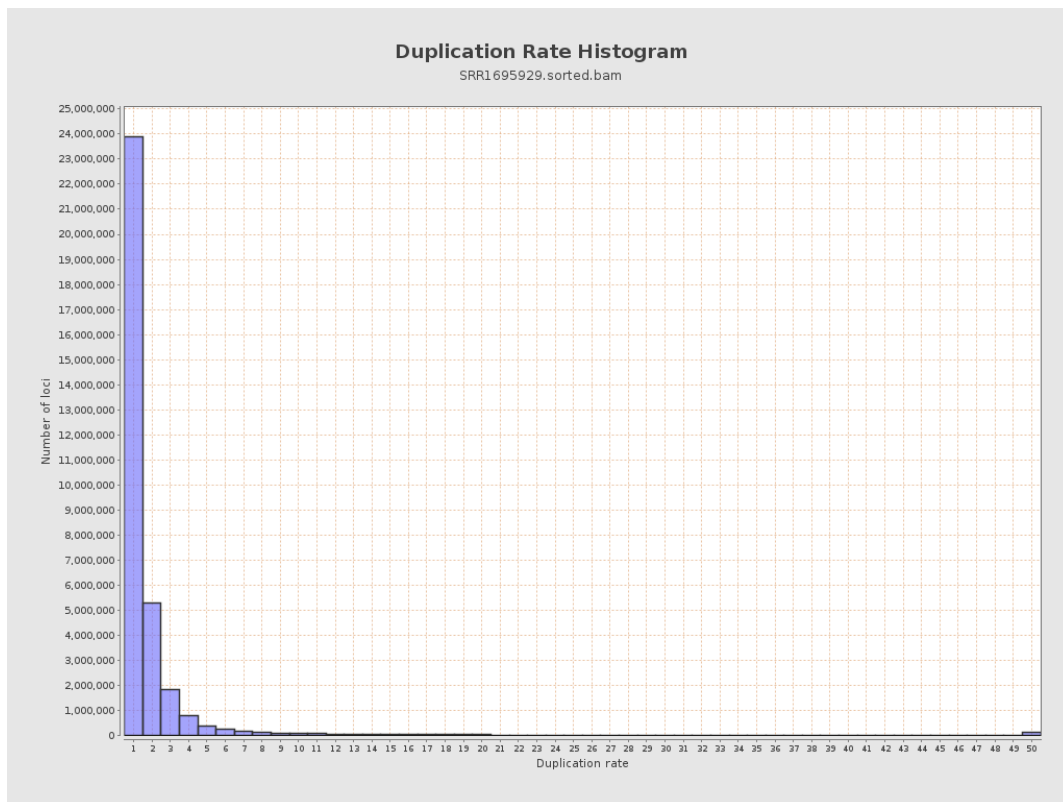
5. Results : Coverage Histogram (0-50X)



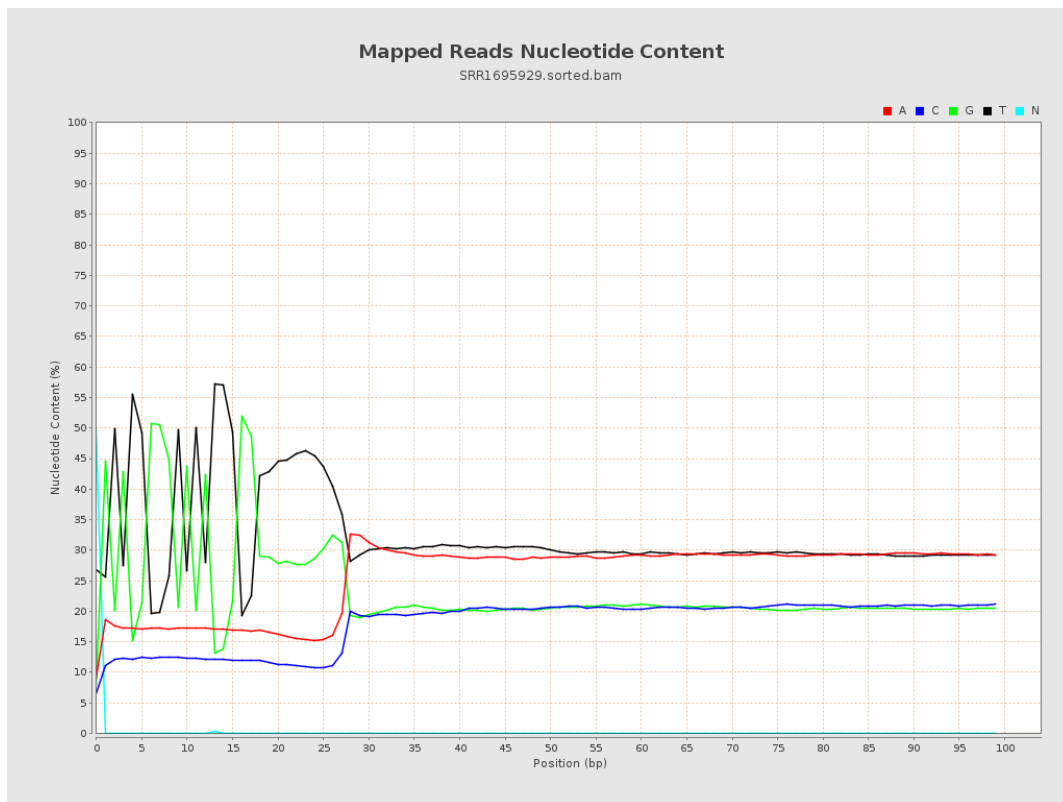
6. Results : Genome Fraction Coverage



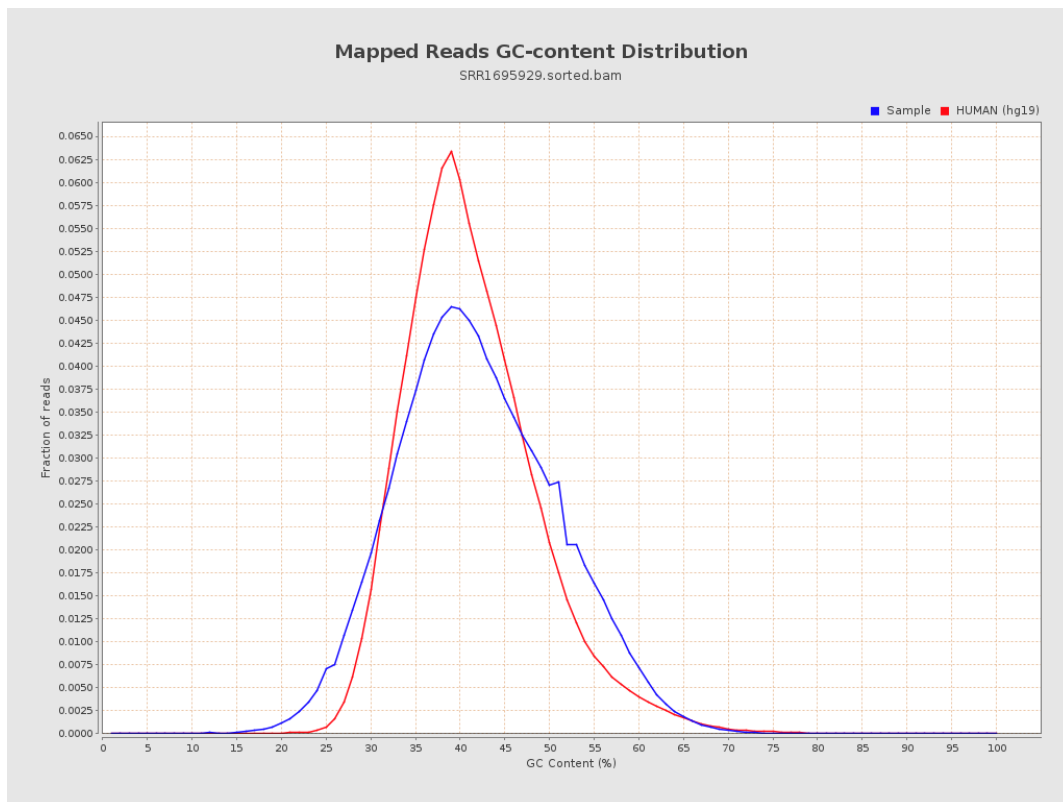
7. Results : Duplication Rate Histogram



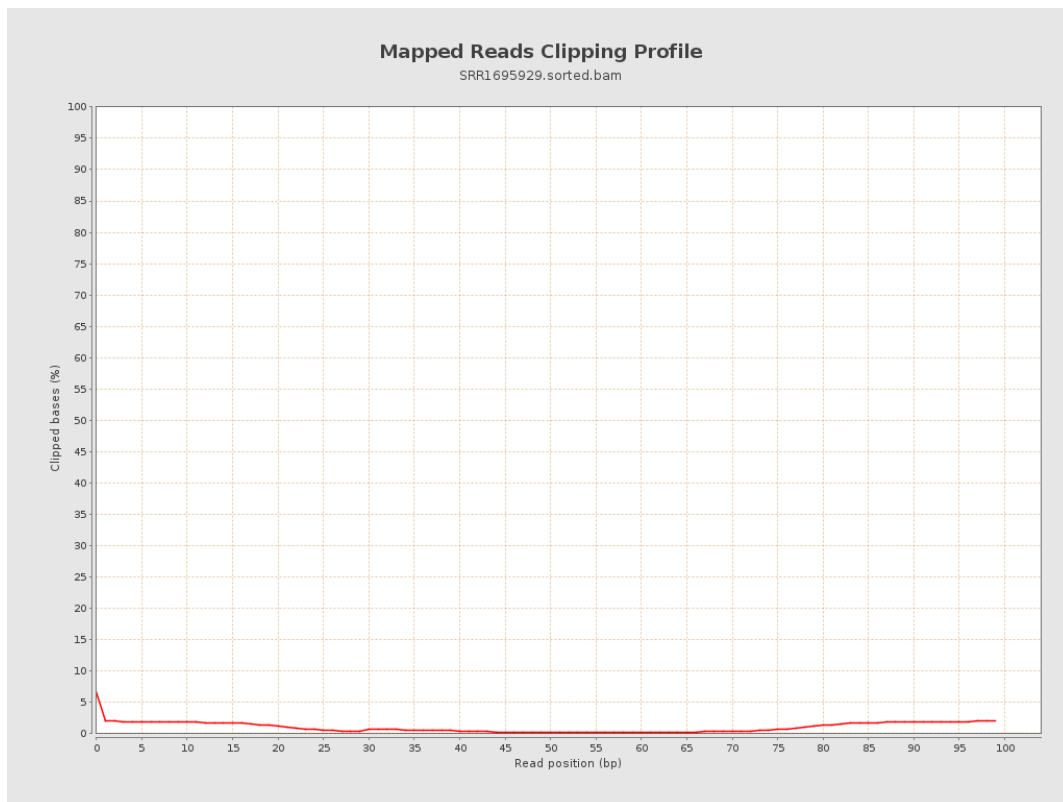
8. Results : Mapped Reads Nucleotide Content



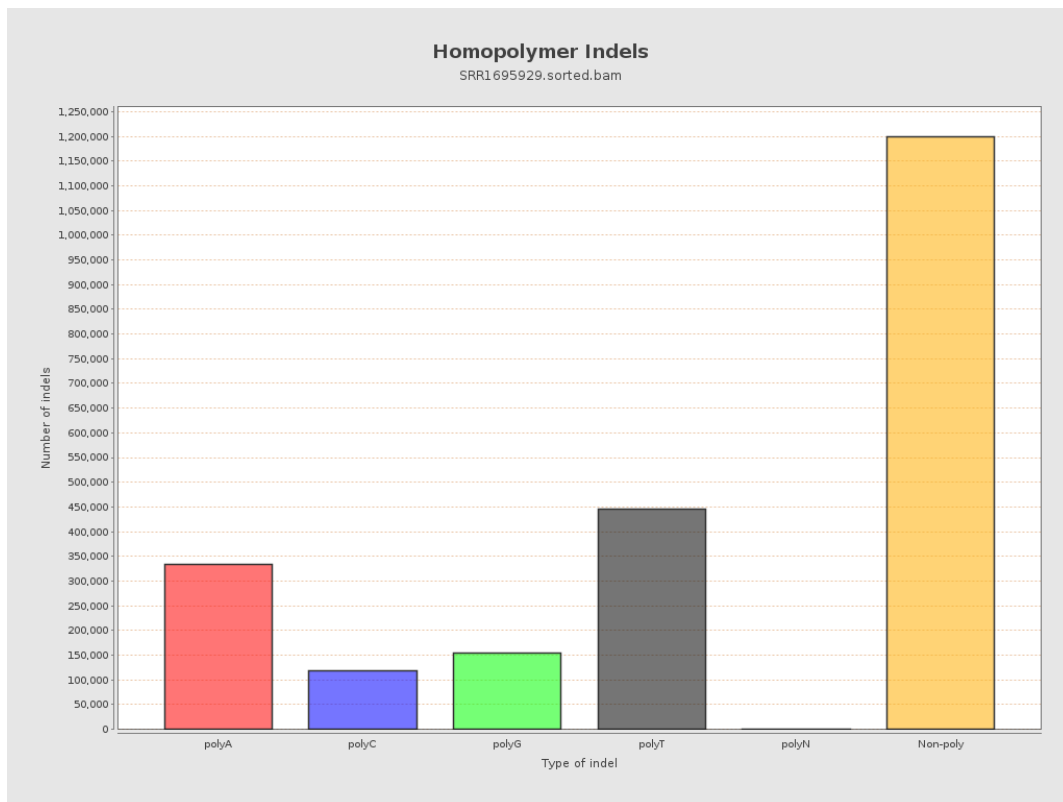
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



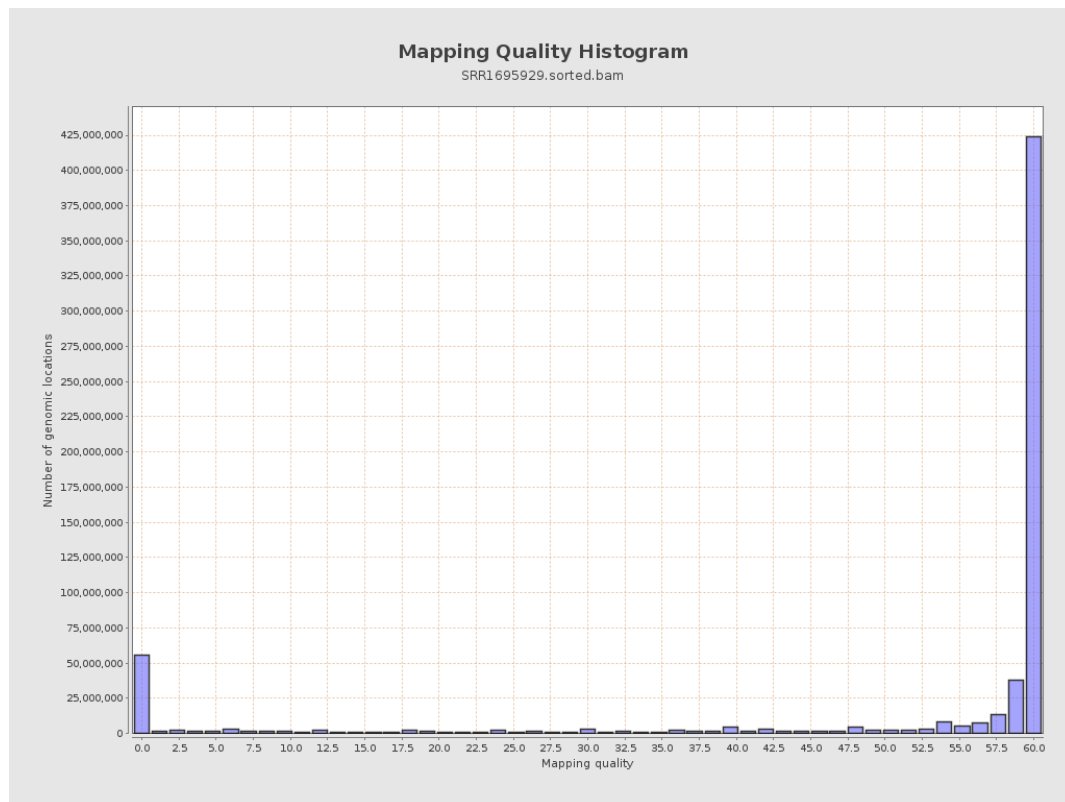
11. Results : Homopolymer Indels



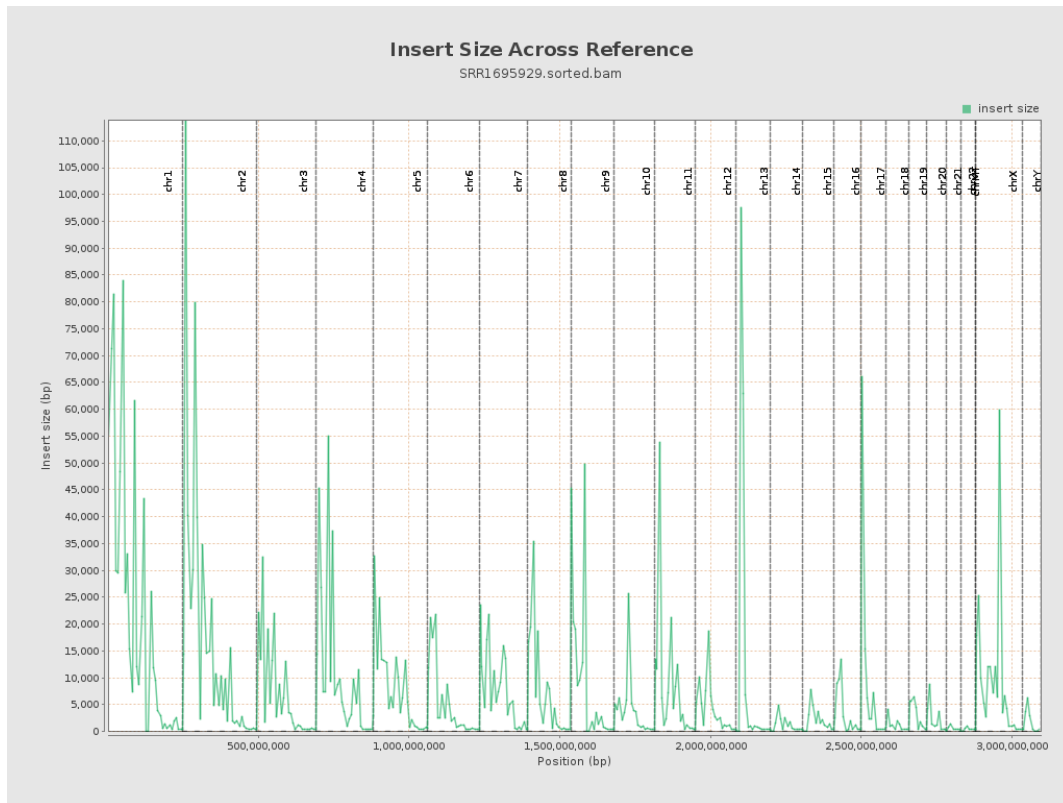
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

