

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 01:49:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695931.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/seu_share/home/tujing/220232460/software/bwa-0.7.18/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR1695931 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695931_1.fastq.gz SRR1695931_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 01:49:34 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695931.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	29,781,062
Mapped reads	25,536,691 / 85.75%
Unmapped reads	4,244,371 / 14.25%
Mapped paired reads	25,536,691 / 85.75%
Mapped reads, first in pair	13,111,458 / 44.03%
Mapped reads, second in pair	12,425,233 / 41.72%
Mapped reads, both in pair	23,854,620 / 80.1%
Mapped reads, singletons	1,682,071 / 5.65%
Secondary alignments	0
Supplementary alignments	795,153 / 2.67%
Read min/max/mean length	30 / 100 / 100.99
Duplicated reads (estimated)	13,969,639 / 46.91%
Duplication rate	21.84%
Clipped reads	18,744,840 / 62.94%

2.2. ACGT Content

Number/percentage of A's	545,964,651 / 25.85%
Number/percentage of C's	374,116,976 / 17.71%
Number/percentage of T's	693,476,552 / 32.84%
Number/percentage of G's	496,644,858 / 23.52%
Number/percentage of N's	1,732,718 / 0.08%

GC Percentage	41.23%
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2.3. Coverage

Mean	0.6825
Standard Deviation	6.9254

2.4. Mapping Quality

Mean Mapping Quality	51.71
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2.5. Insert size

Mean	140,548.66
Standard Deviation	3,599,191.82
P25/Median/P75	298 / 317 / 332

2.6. Mismatches and indels

General error rate	1.27%
Mismatches	26,565,824
Insertions	168,769
Mapped reads with at least one insertion	0.65%
Deletions	472,932
Mapped reads with at least one deletion	1.83%
Homopolymer indels	46.77%

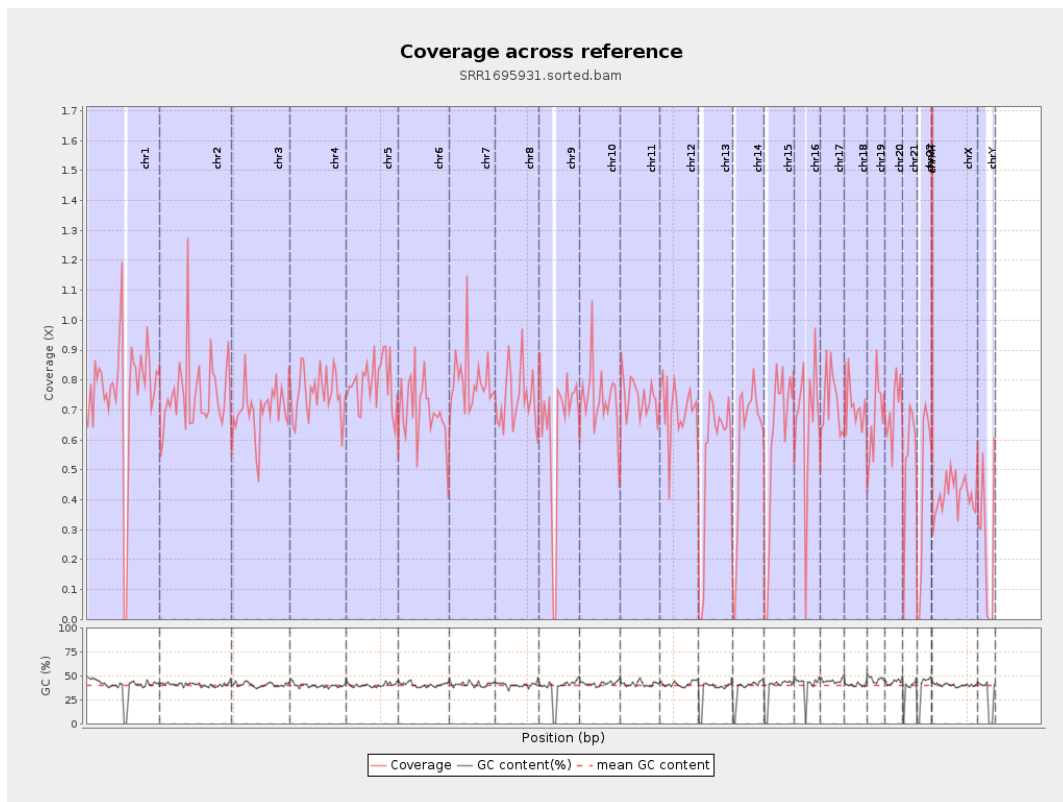
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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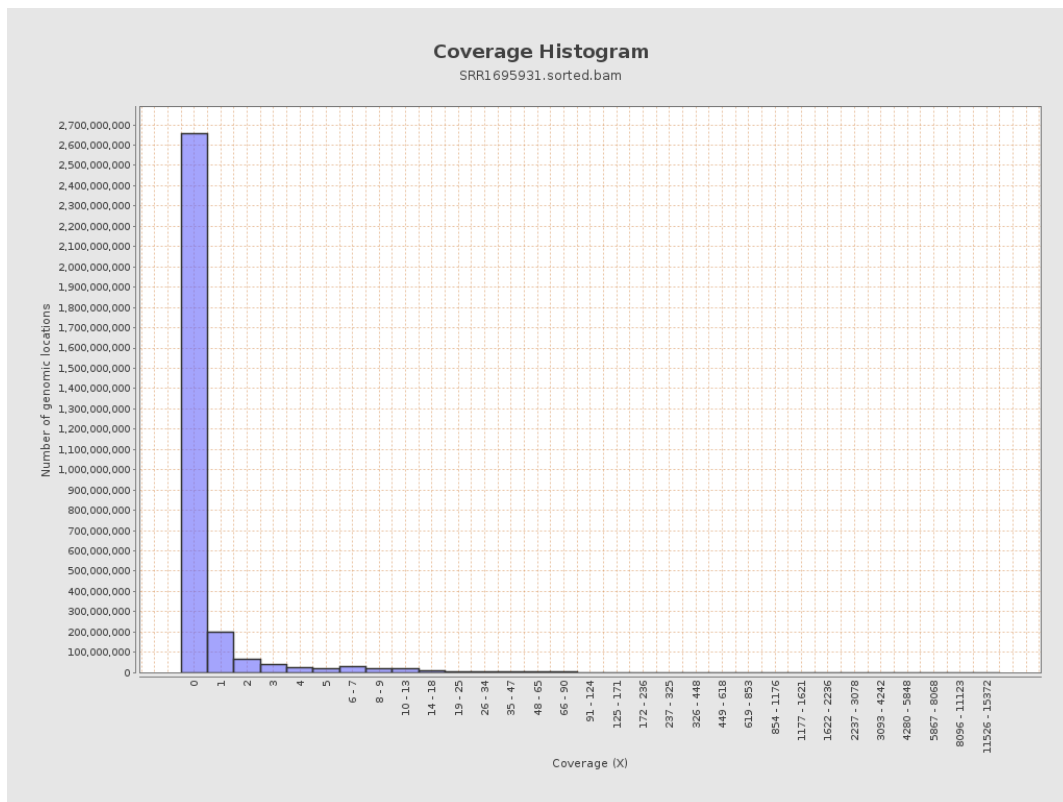
		bases	coverage	deviation
chr1	249250621	190825118	0.7656	10.0944
chr2	243199373	183304347	0.7537	7.8127
chr3	198022430	138298937	0.6984	4.2847
chr4	191154276	144386211	0.7553	4.6429
chr5	180915260	142339532	0.7868	4.6747
chr6	171115067	119519019	0.6985	5.2271
chr7	159138663	126375076	0.7941	9.8841
chr8	146364022	106758223	0.7294	11.6937
chr9	141213431	89665230	0.635	5.7284
chr10	135534747	100320968	0.7402	6.3732
chr11	135006516	99569570	0.7375	5.9151
chr12	133851895	93663850	0.6998	4.3681
chr13	115169878	62284234	0.5408	3.7402
chr14	107349540	64133110	0.5974	4.1501
chr15	102531392	60812138	0.5931	3.9514
chr16	90354753	59494809	0.6585	4.1205
chr17	81195210	59043353	0.7272	4.6355
chr18	78077248	55400153	0.7096	16.1742
chr19	59128983	39689356	0.6712	7.4367
chr20	63025520	43952995	0.6974	4.4776
chr21	48129895	26525949	0.5511	4.1692
chr22	51304566	22758904	0.4436	3.8611
chrMT	16571	3394462	204.8435	164.5131
chrX	155270560	64634010	0.4163	3.6812

chrY	59373566	15618032	0.263	3.4036
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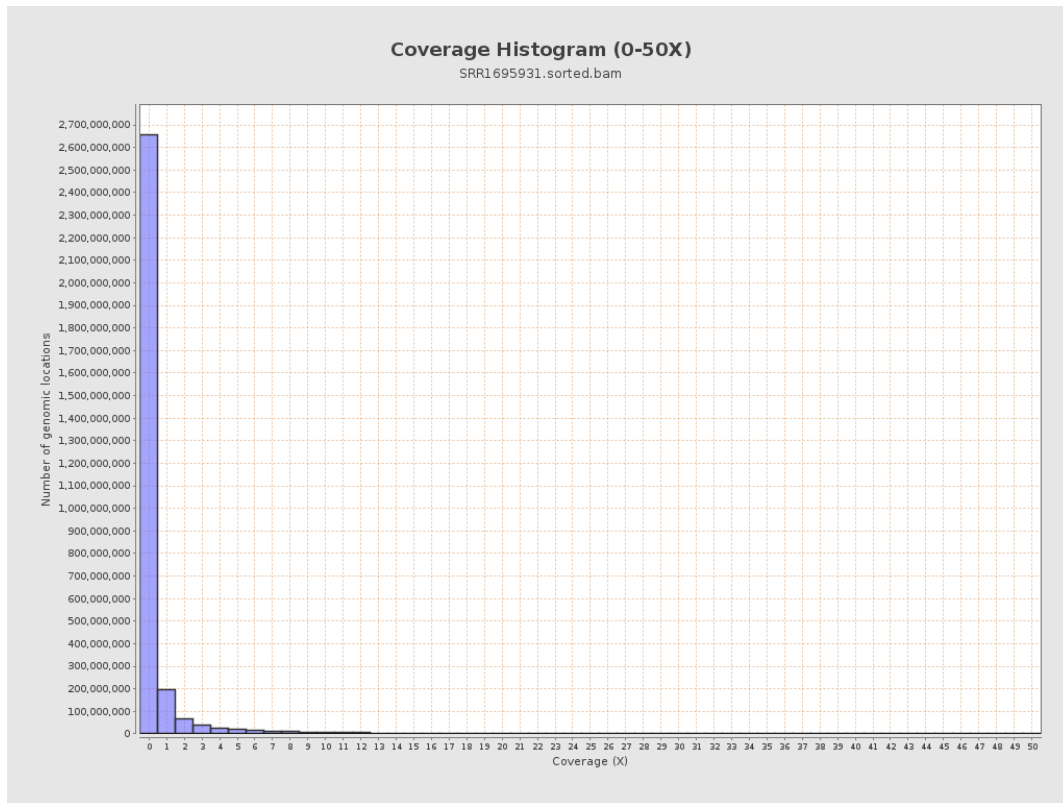
3. Results : Coverage across reference



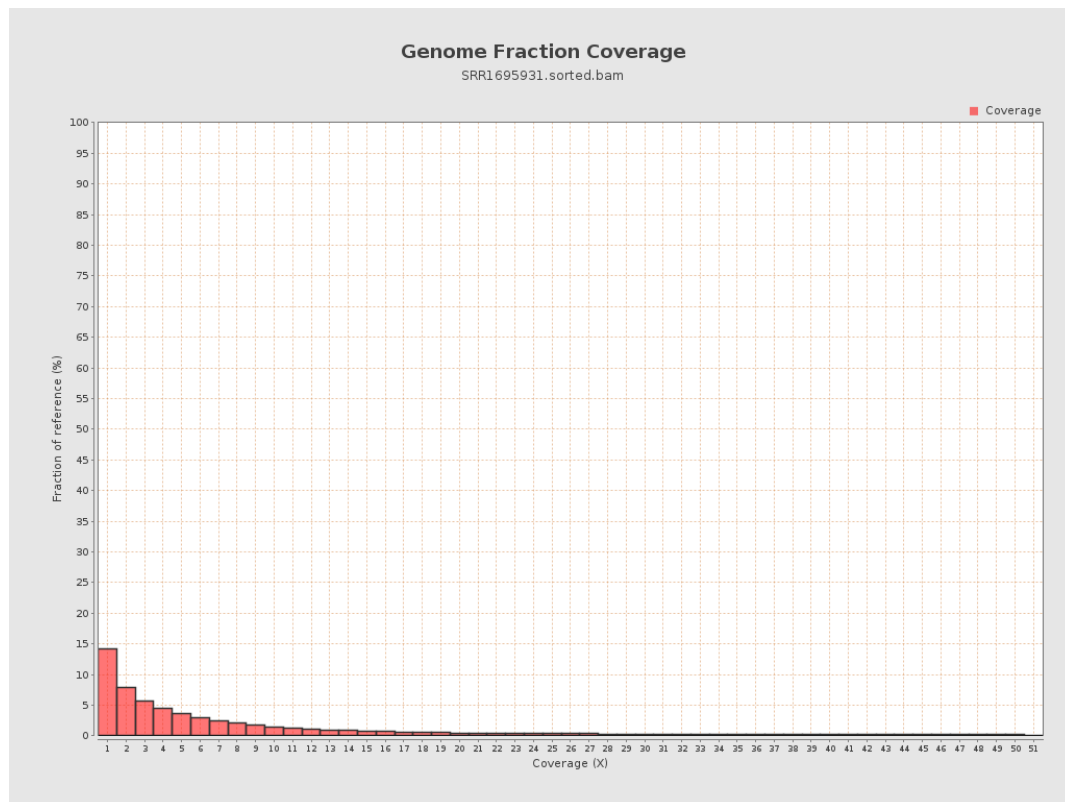
4. Results : Coverage Histogram



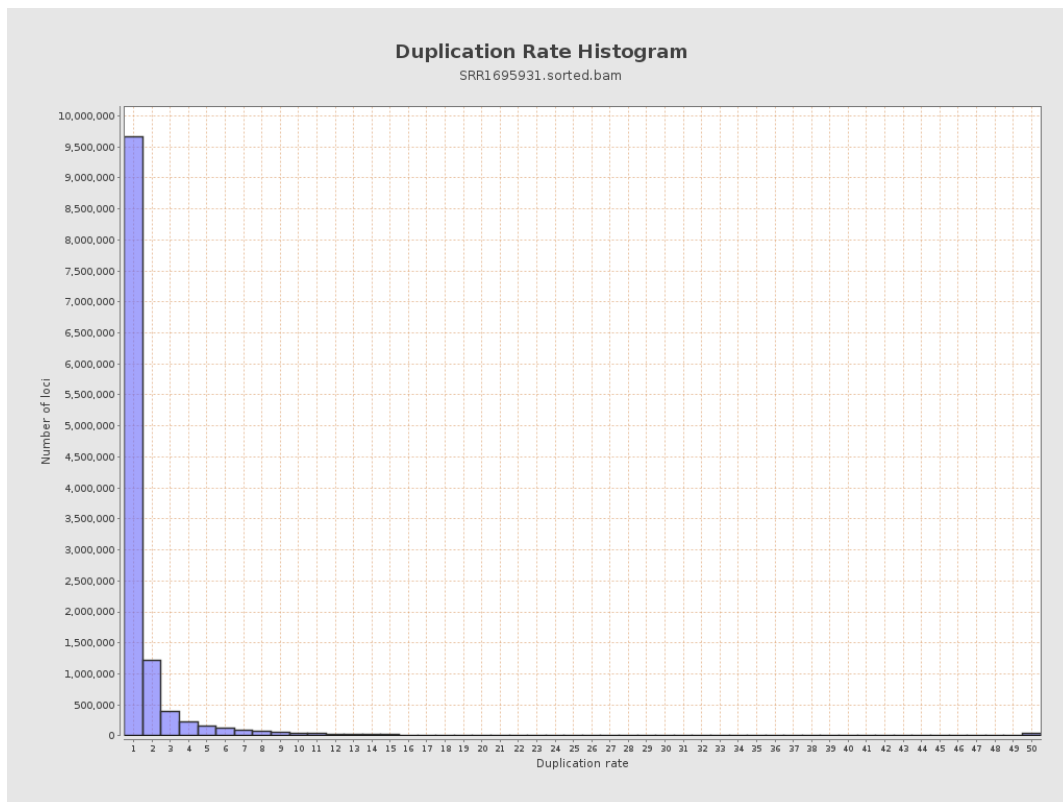
5. Results : Coverage Histogram (0-50X)



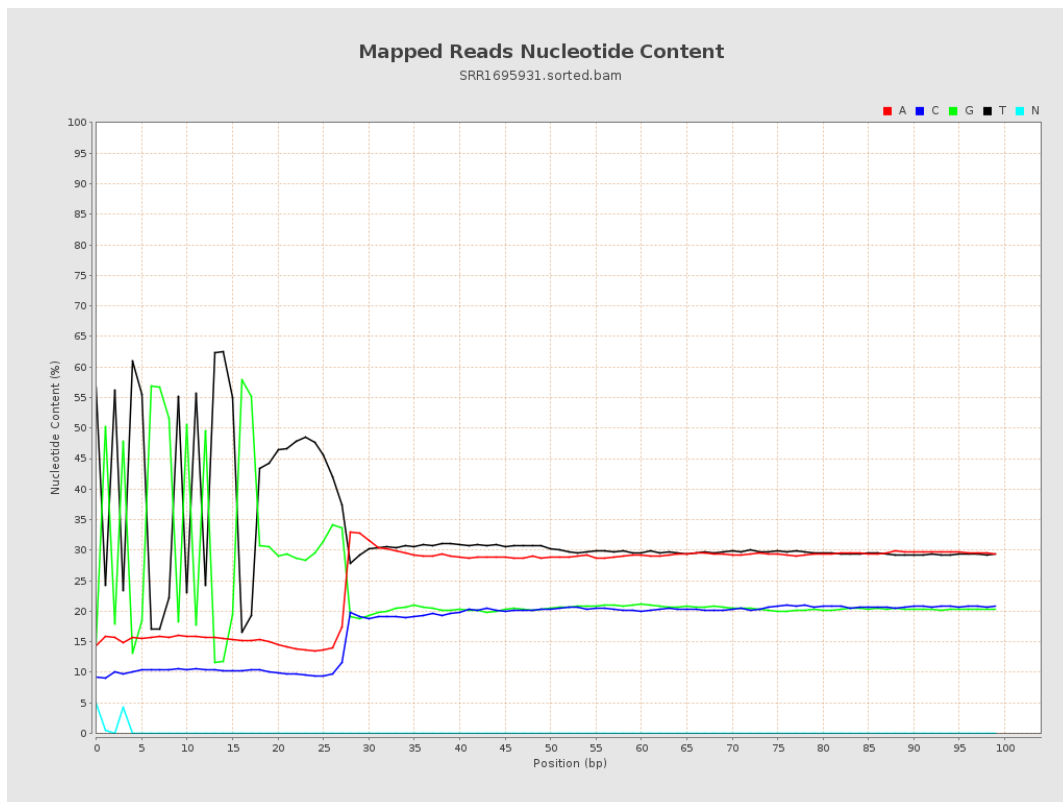
6. Results : Genome Fraction Coverage



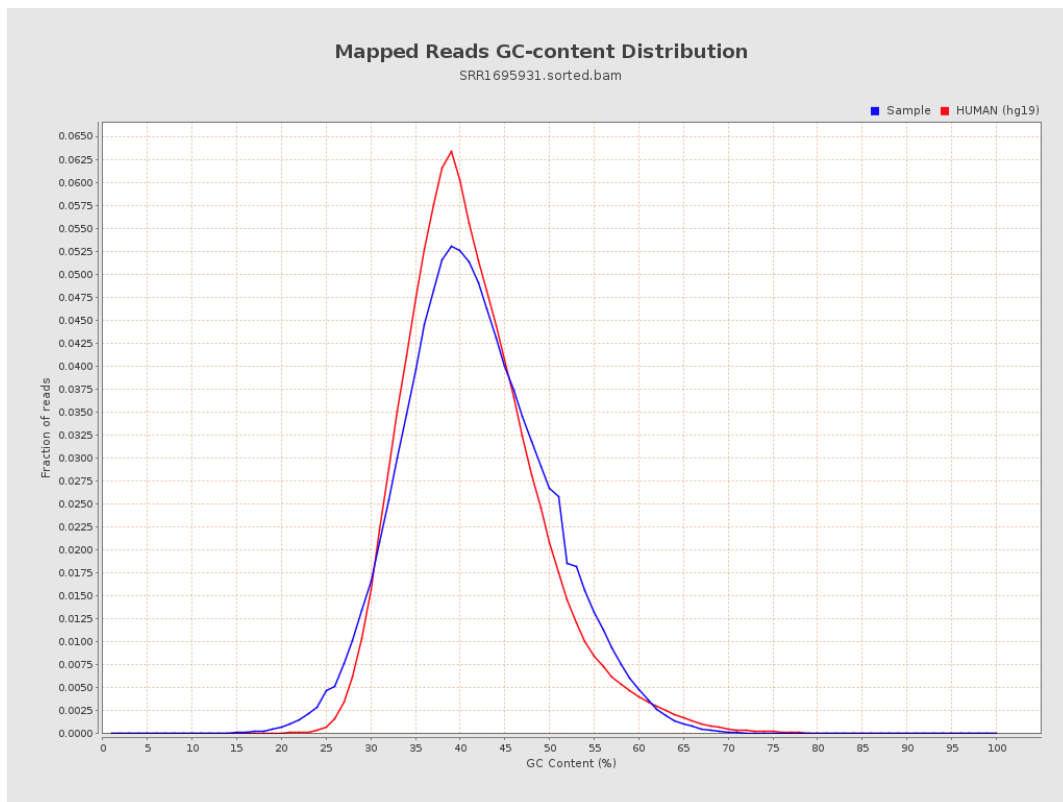
7. Results : Duplication Rate Histogram



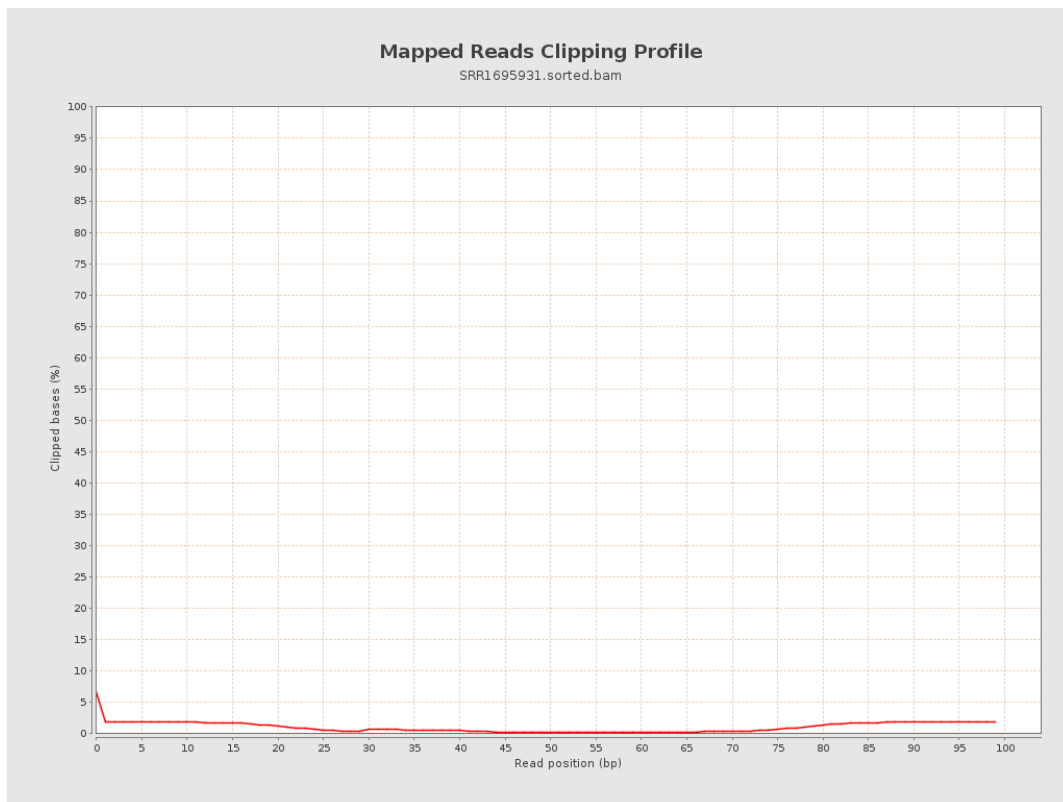
8. Results : Mapped Reads Nucleotide Content



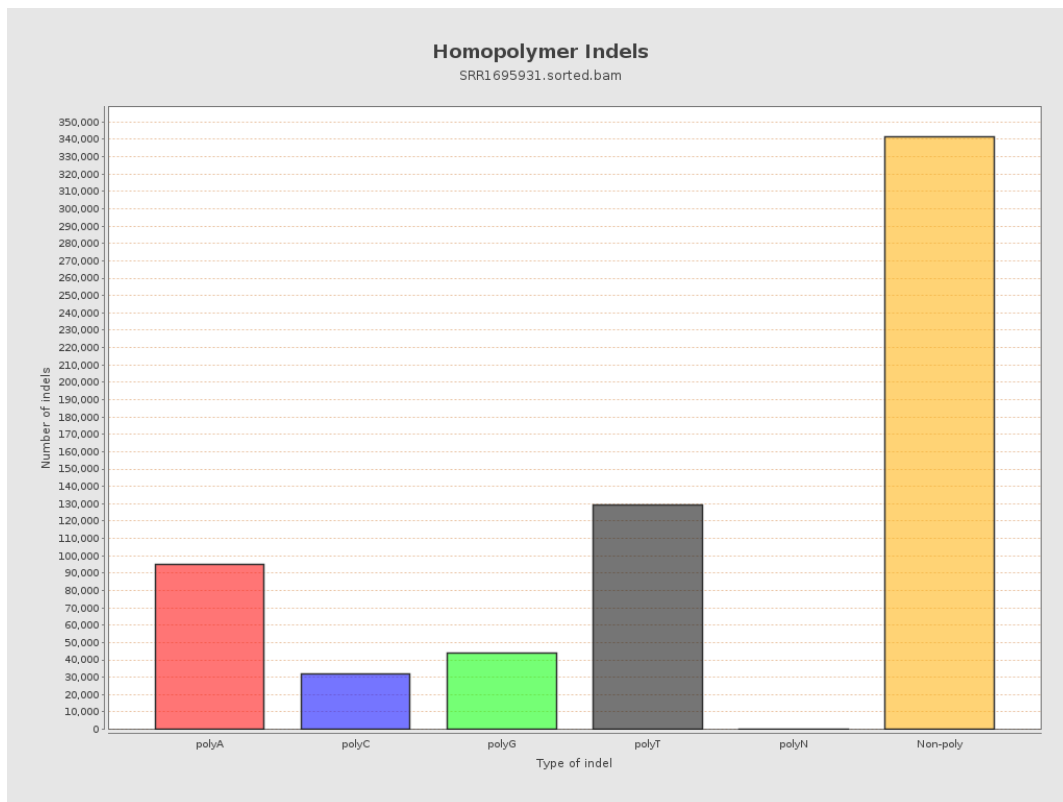
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



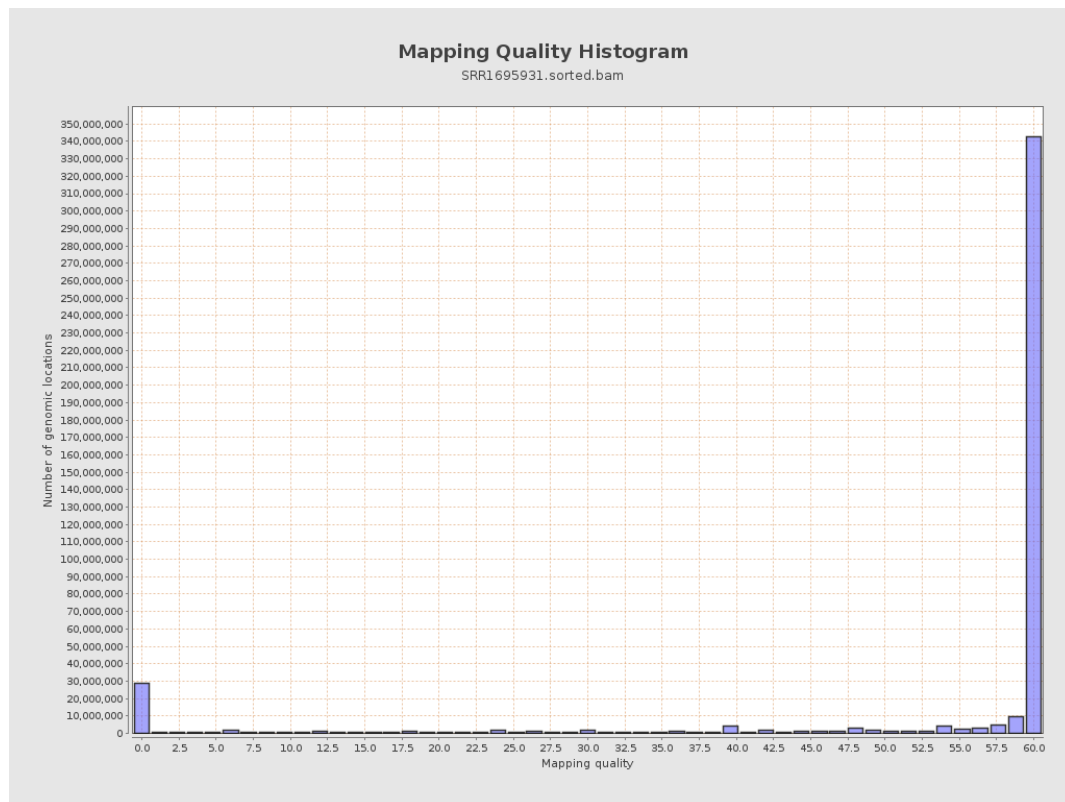
11. Results : Homopolymer Indels



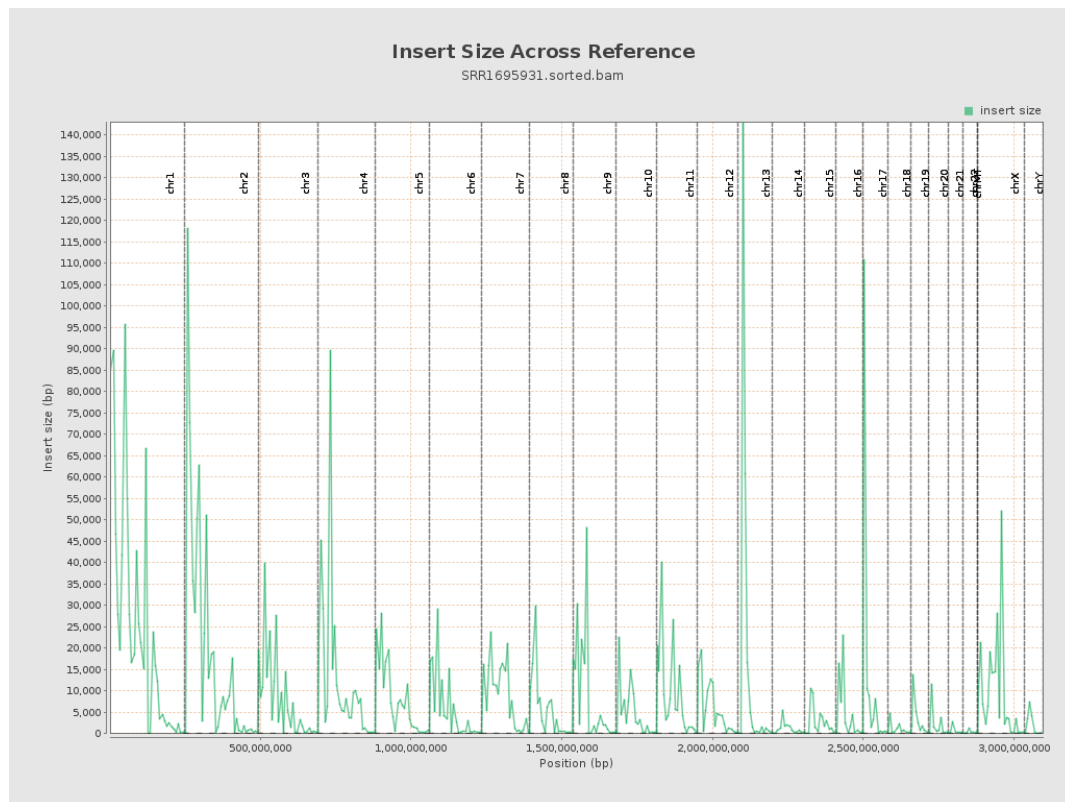
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

