

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 02:17:31

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695934.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_SRR1695934 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695934_1.fastq.gz SRR1695934_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 02:17:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695934.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,433,486
Mapped reads	14,228,370 / 92.19%
Unmapped reads	1,205,116 / 7.81%
Mapped paired reads	14,228,370 / 92.19%
Mapped reads, first in pair	7,163,775 / 46.42%
Mapped reads, second in pair	7,064,595 / 45.77%
Mapped reads, both in pair	13,910,252 / 90.13%
Mapped reads, singletons	318,118 / 2.06%
Secondary alignments	0
Supplementary alignments	241,290 / 1.56%
Read min/max/mean length	30 / 100 / 100.63
Duplicated reads (estimated)	4,813,118 / 31.19%
Duplication rate	16.26%
Clipped reads	7,916,774 / 51.3%

2.2. ACGT Content

Number/percentage of A's	341,535,688 / 27.11%
Number/percentage of C's	280,001,920 / 22.22%
Number/percentage of T's	347,188,867 / 27.55%
Number/percentage of G's	290,806,577 / 23.08%
Number/percentage of N's	454,039 / 0.04%

GC Percentage	45.3%
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2.3. Coverage

Mean	0.4072
Standard Deviation	7.5719

2.4. Mapping Quality

Mean Mapping Quality	50.55
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2.5. Insert size

Mean	498,980.4
Standard Deviation	6,888,621.52
P25/Median/P75	285 / 296 / 305

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	14,417,062
Insertions	149,317
Mapped reads with at least one insertion	1.02%
Deletions	192,837
Mapped reads with at least one deletion	1.32%
Homopolymer indels	40.26%

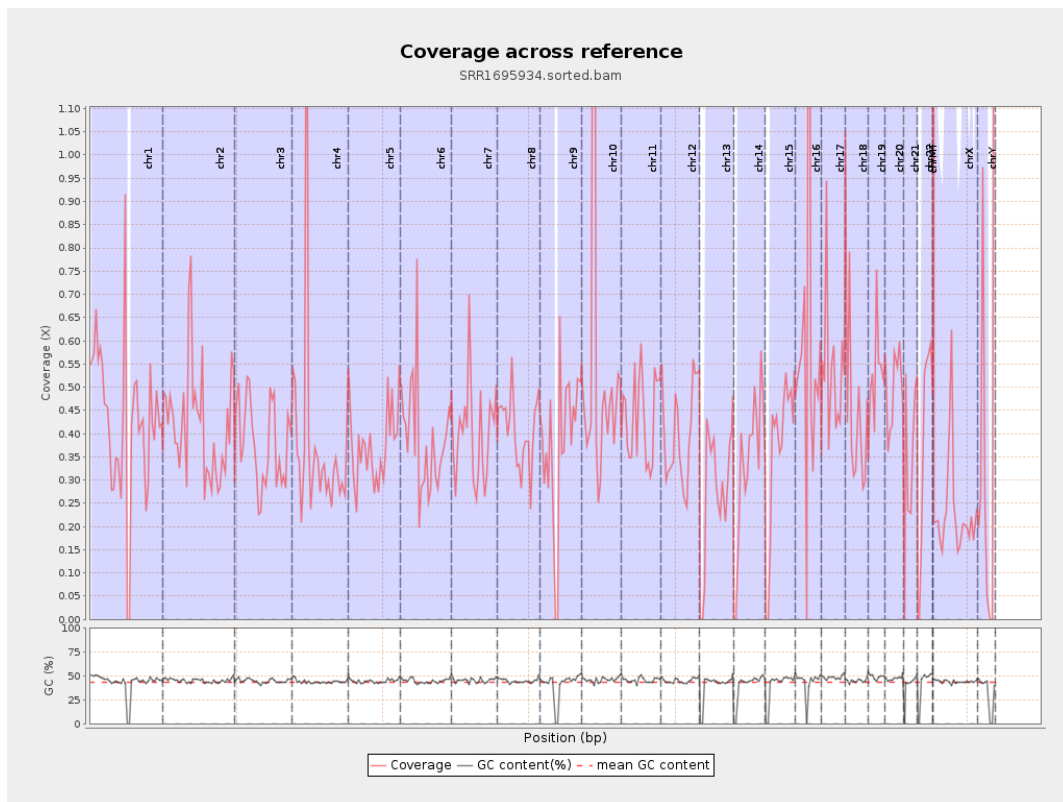
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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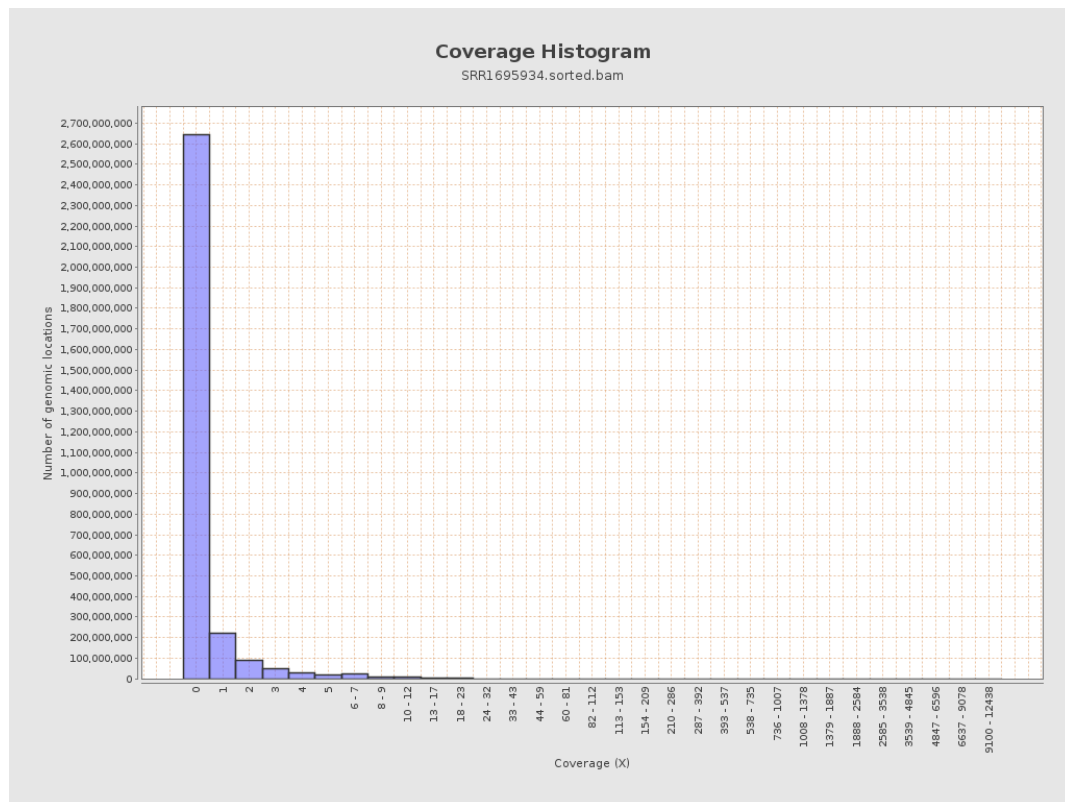
		bases	coverage	deviation
chr1	249250621	105605813	0.4237	10.0093
chr2	243199373	102275498	0.4205	4.2357
chr3	198022430	74887683	0.3782	1.4461
chr4	191154276	73249953	0.3832	7.9922
chr5	180915260	68228007	0.3771	1.7188
chr6	171115067	65987603	0.3856	7.4812
chr7	159138663	64177215	0.4033	4.3784
chr8	146364022	59225718	0.4046	2.6895
chr9	141213431	53317278	0.3776	5.3851
chr10	135534747	71466386	0.5273	16.2168
chr11	135006516	58619463	0.4342	1.8485
chr12	133851895	53582606	0.4003	1.9006
chr13	115169878	31878230	0.2768	1.1629
chr14	107349540	36295841	0.3381	1.406
chr15	102531392	37011539	0.361	1.3347
chr16	90354753	56084761	0.6207	14.911
chr17	81195210	43762002	0.539	5.9207
chr18	78077248	34547307	0.4425	11.4973
chr19	59128983	31566951	0.5339	12.9314
chr20	63025520	31027102	0.4923	3.458
chr21	48129895	17147848	0.3563	3.6212
chr22	51304566	19674471	0.3835	1.4609
chrMT	16571	8098473	488.7136	1,131.2645
chrX	155270560	35826420	0.2307	3.4521

chrY	59373566	26885808	0.4528	11.8992
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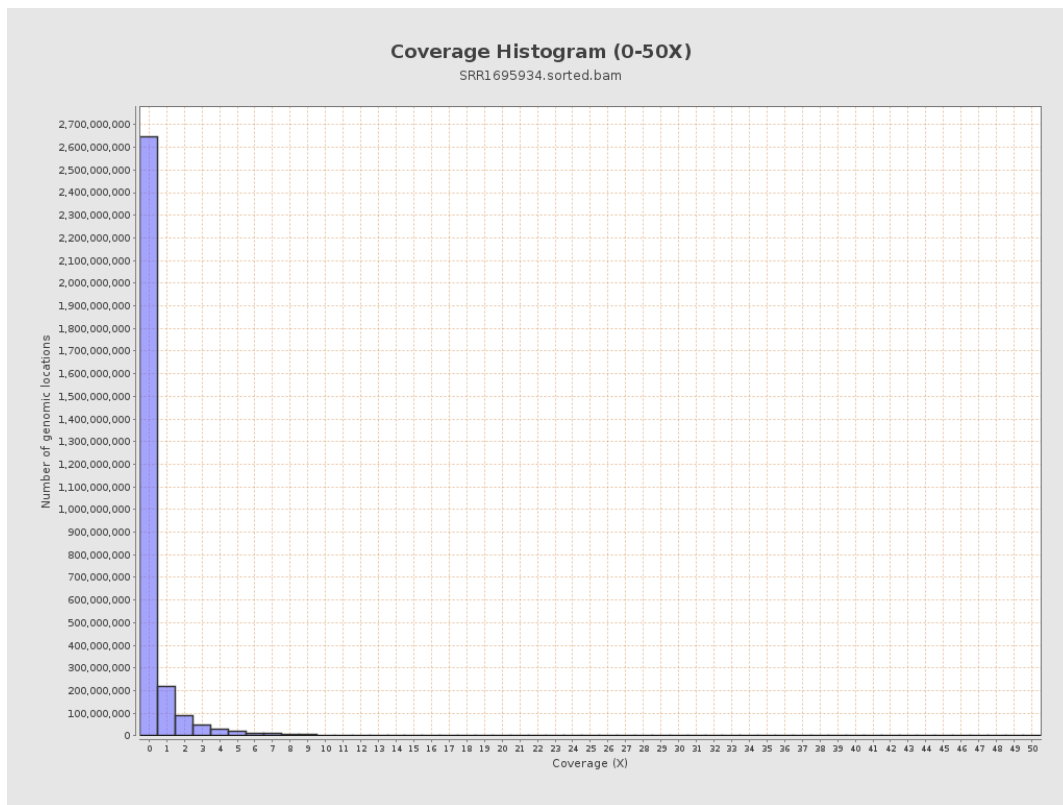
3. Results : Coverage across reference



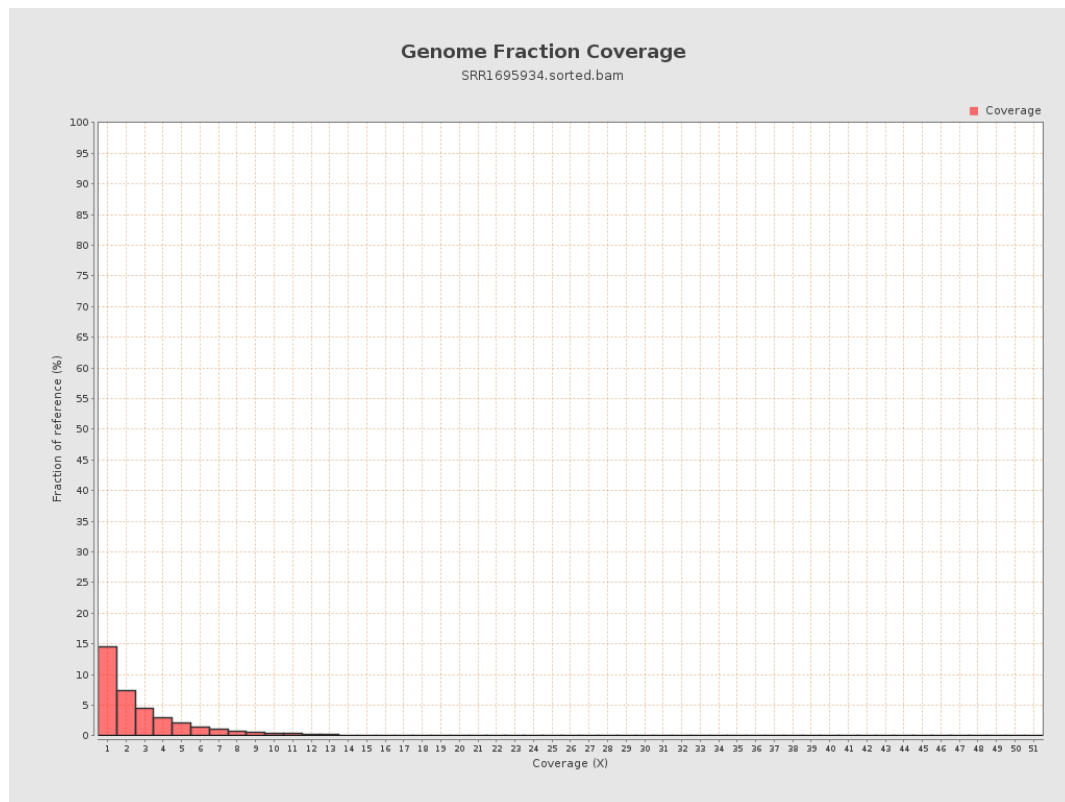
4. Results : Coverage Histogram



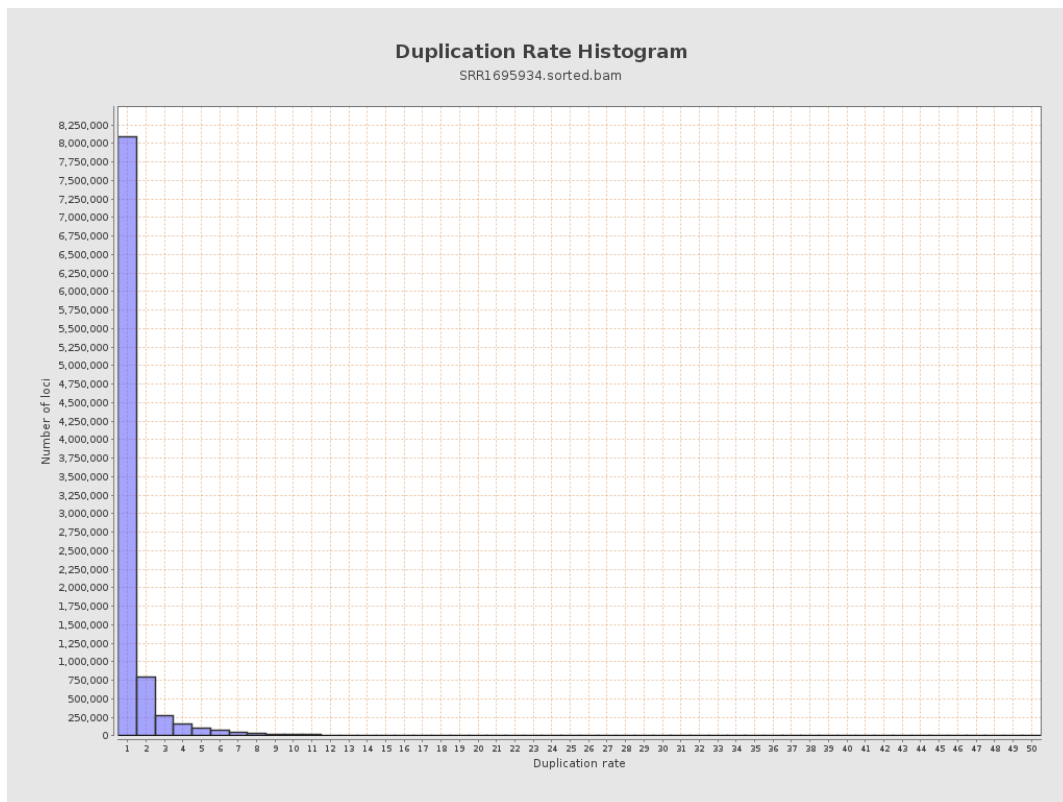
5. Results : Coverage Histogram (0-50X)



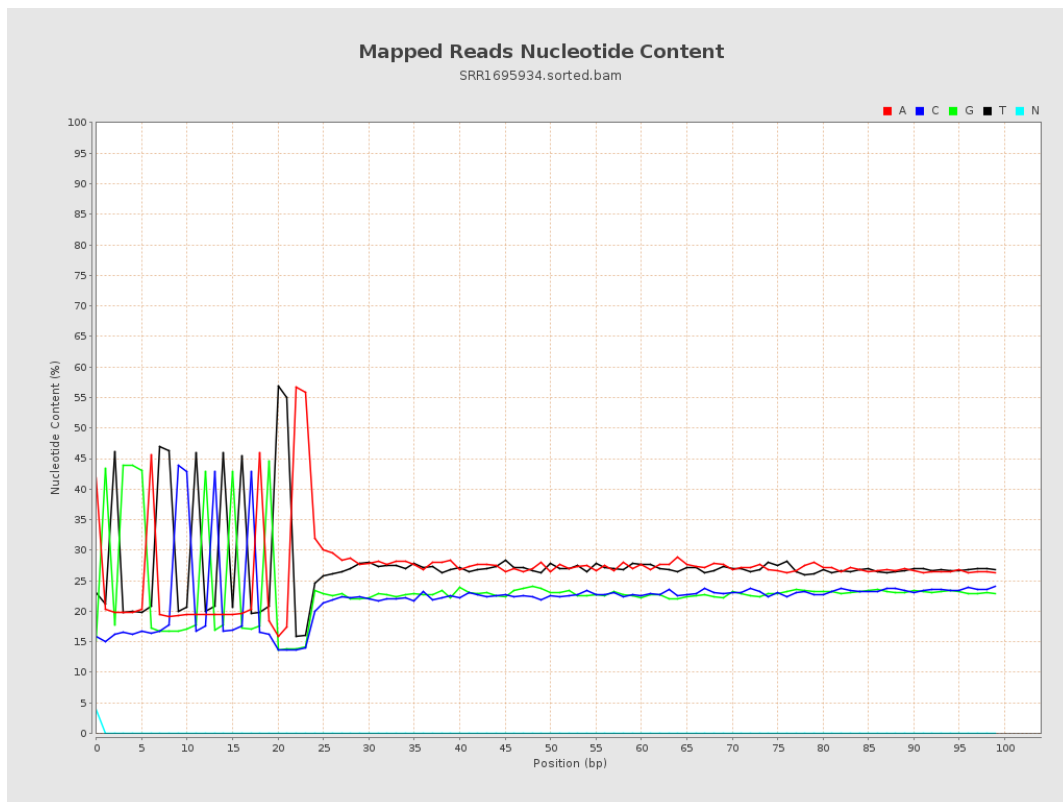
6. Results : Genome Fraction Coverage



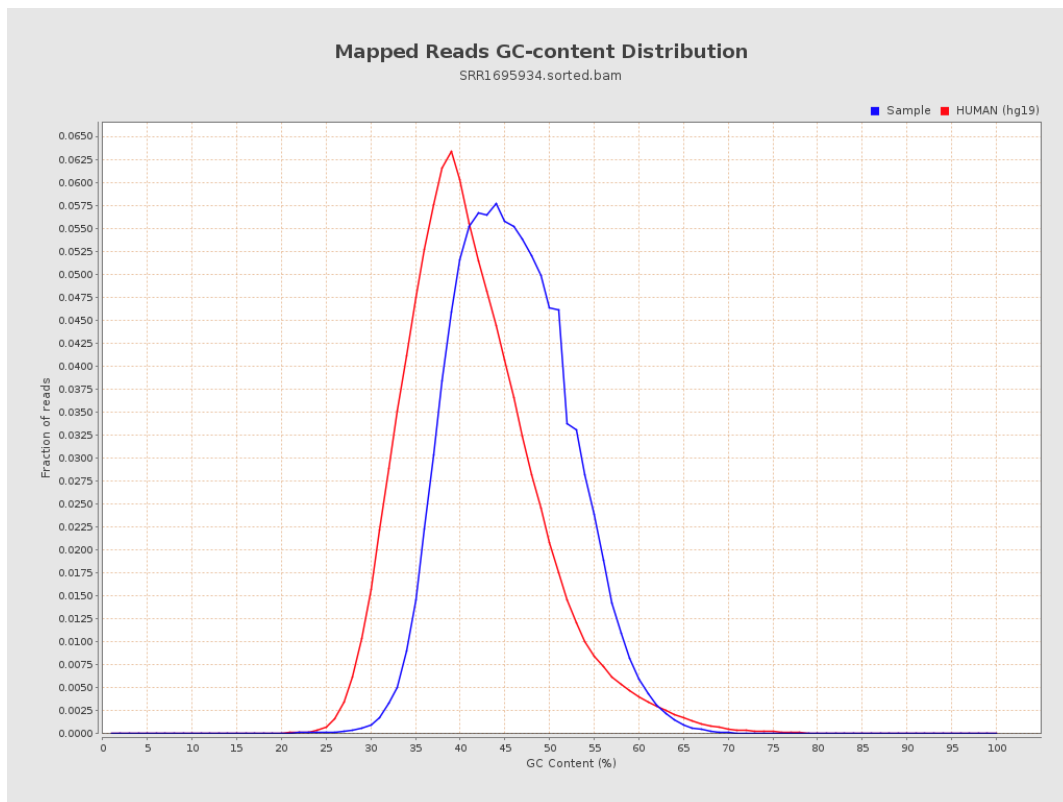
7. Results : Duplication Rate Histogram



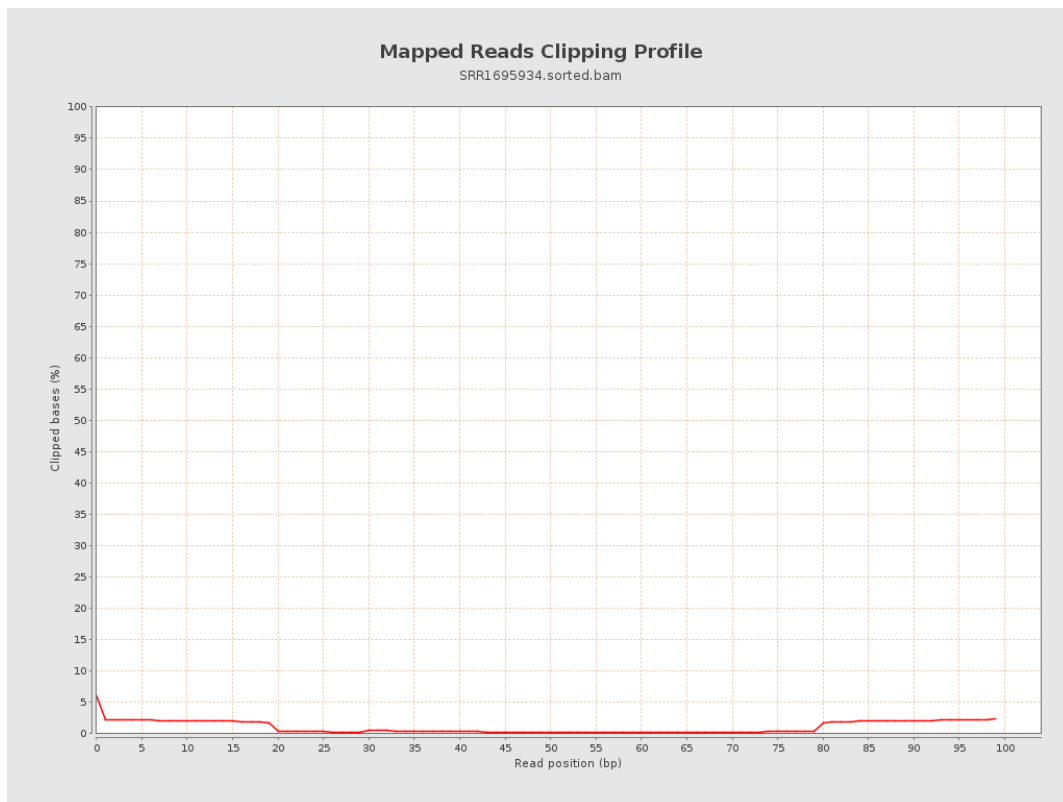
8. Results : Mapped Reads Nucleotide Content



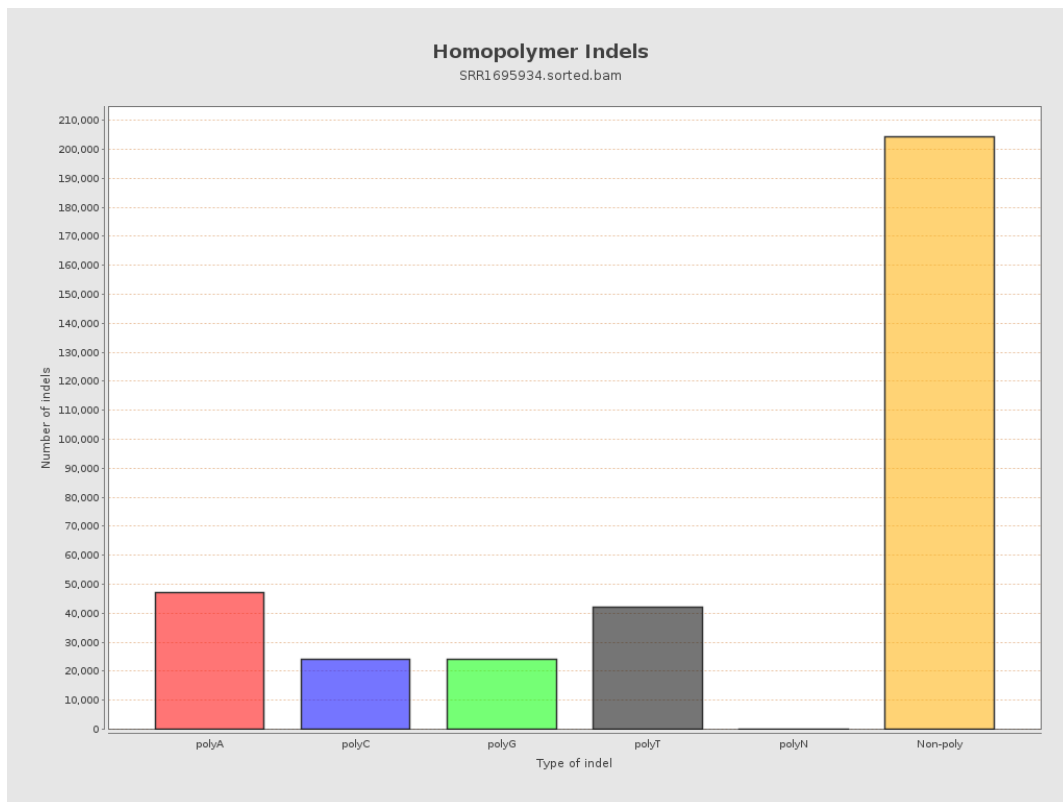
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



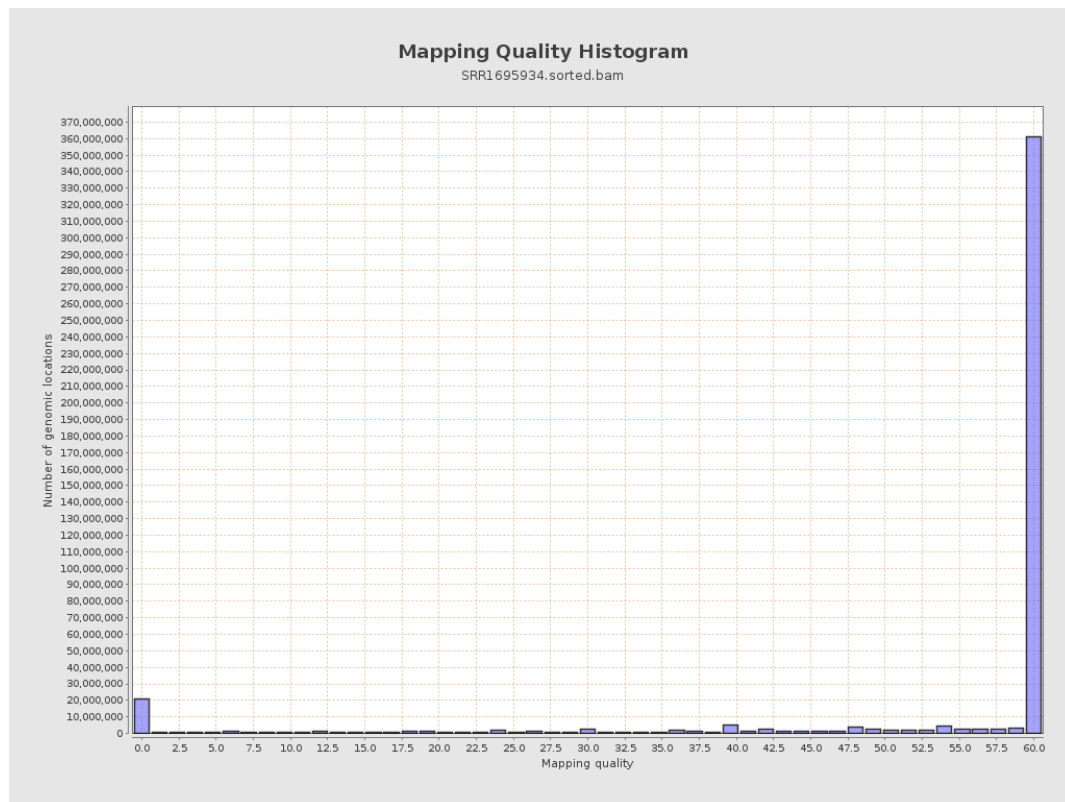
11. Results : Homopolymer Indels



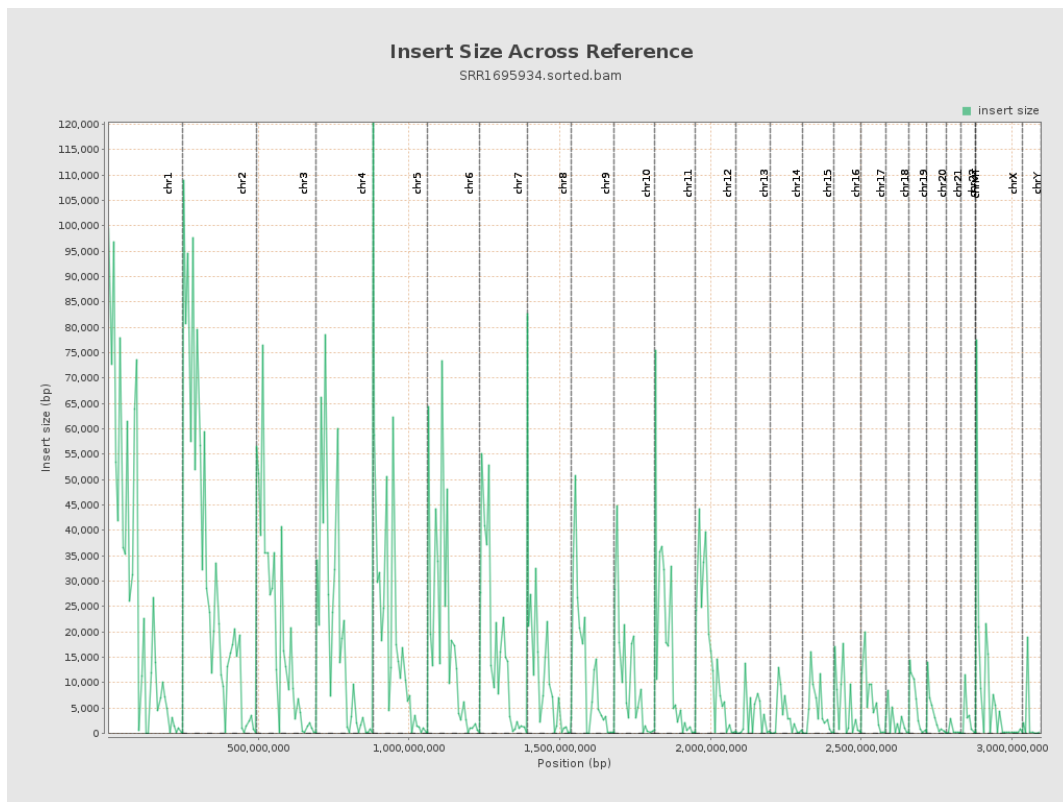
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

