

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 06:57:25

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695975.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 975 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695975_1.fastq.gz SRR1695975_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Sat Sep 14 06:57:24 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695975.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	399,276,194
Mapped reads	391,265,004 / 97.99%
Unmapped reads	8,011,190 / 2.01%
Mapped paired reads	391,265,004 / 97.99%
Mapped reads, first in pair	197,307,946 / 49.42%
Mapped reads, second in pair	193,957,058 / 48.58%
Mapped reads, both in pair	386,463,750 / 96.79%
Mapped reads, singletons	4,801,254 / 1.2%
Secondary alignments	0
Supplementary alignments	1,265,025 / 0.32%
Read min/max/mean length	30 / 100 / 100.12
Duplicated reads (estimated)	60,331,631 / 15.11%
Duplication rate	10.03%
Clipped reads	23,940,616 / 6%

2.2. ACGT Content

Number/percentage of A's	11,274,744,445 / 29.26%
Number/percentage of C's	7,977,120,487 / 20.7%
Number/percentage of T's	11,263,232,645 / 29.23%
Number/percentage of G's	8,013,514,564 / 20.8%
Number/percentage of N's	7,135,961 / 0.02%

GC Percentage	41.5%
---------------	-------

2.3. Coverage

Mean	12.4518
Standard Deviation	137.0637

2.4. Mapping Quality

Mean Mapping Quality	53.7
----------------------	------

2.5. Insert size

Mean	49,763.8
Standard Deviation	2,113,551.49
P25/Median/P75	301 / 308 / 316

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	256,249,043
Insertions	3,900,298
Mapped reads with at least one insertion	0.97%
Deletions	4,617,323
Mapped reads with at least one deletion	1.15%
Homopolymer indels	41.91%

2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

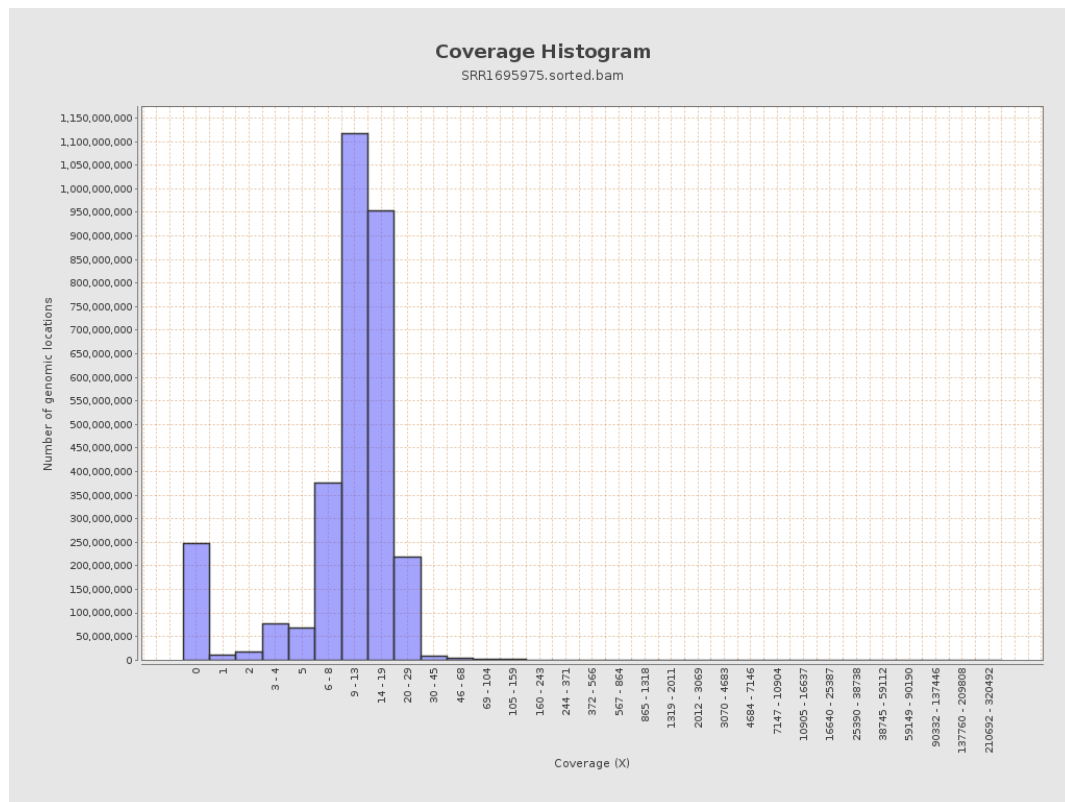
		bases	coverage	deviation
chr1	249250621	3209451126	12.8764	313.1914
chr2	243199373	3359080780	13.812	87.2811
chr3	198022430	2526058306	12.7564	13.8754
chr4	191154276	2503878257	13.0987	93.7817
chr5	180915260	2296584789	12.6943	12.1133
chr6	171115067	2203140547	12.8752	52.4103
chr7	159138663	2083653470	13.0933	114.2115
chr8	146364022	1917366831	13.1	78.162
chr9	141213431	1628055970	11.529	115.9414
chr10	135534747	2132583572	15.7346	357.1337
chr11	135006516	1781515325	13.1958	61.5104
chr12	133851895	1717963908	12.8348	12.3256
chr13	115169878	1187957125	10.3148	9.4298
chr14	107349540	1171777399	10.9155	11.1038
chr15	102531392	1114459942	10.8695	10.6233
chr16	90354753	1255521354	13.8955	98.3471
chr17	81195210	1127946921	13.8918	57.8989
chr18	78077248	1047783714	13.4198	150.0323
chr19	59128983	816247931	13.8045	167.0225
chr20	63025520	833638834	13.227	44.9137
chr21	48129895	533912811	11.0932	55.6588
chr22	51304566	512007247	9.9798	52.3425
chrMT	16571	109818333	6,627.1398	1,033.2307
chrX	155270560	1004279131	6.4679	24.0411

chrY	59373566	472314201	7.955	136.4368
------	----------	-----------	-------	----------

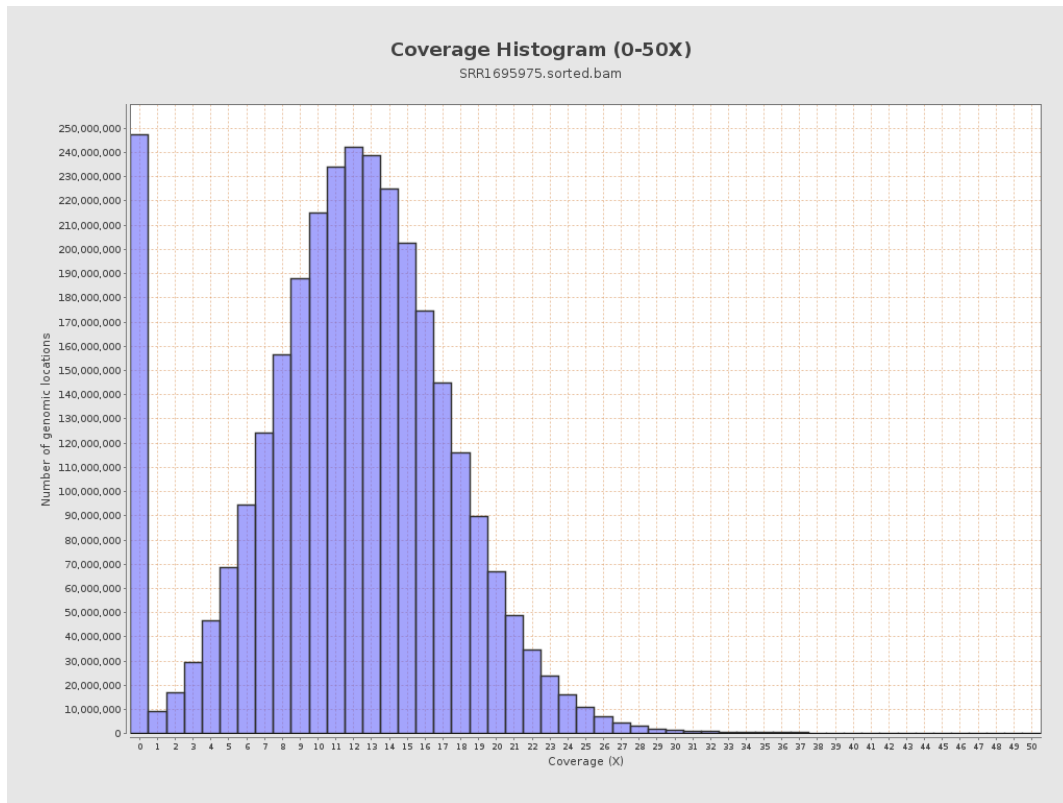
3. Results : Coverage across reference



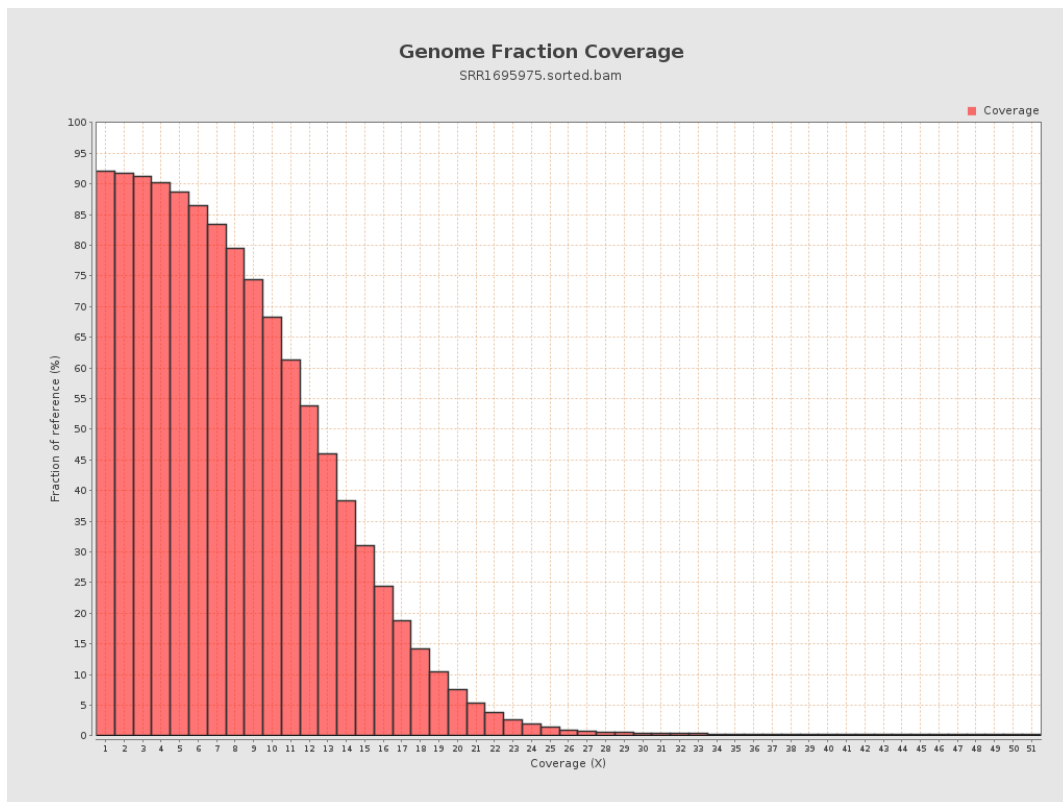
4. Results : Coverage Histogram



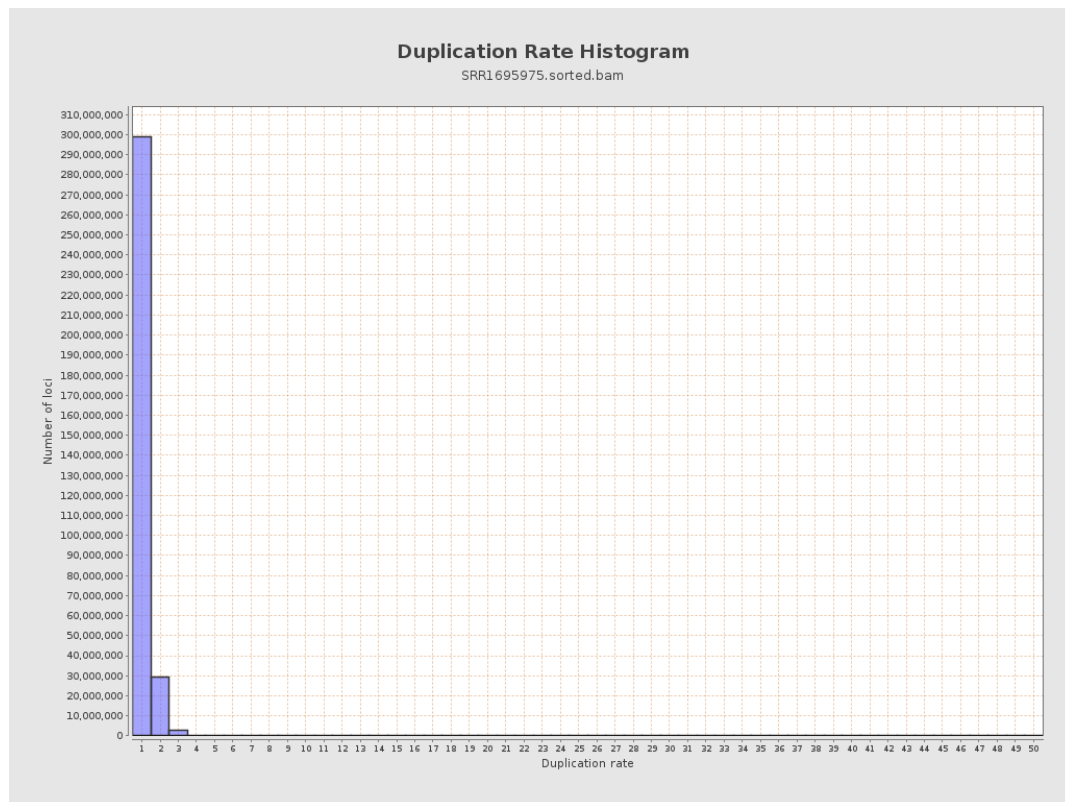
5. Results : Coverage Histogram (0-50X)



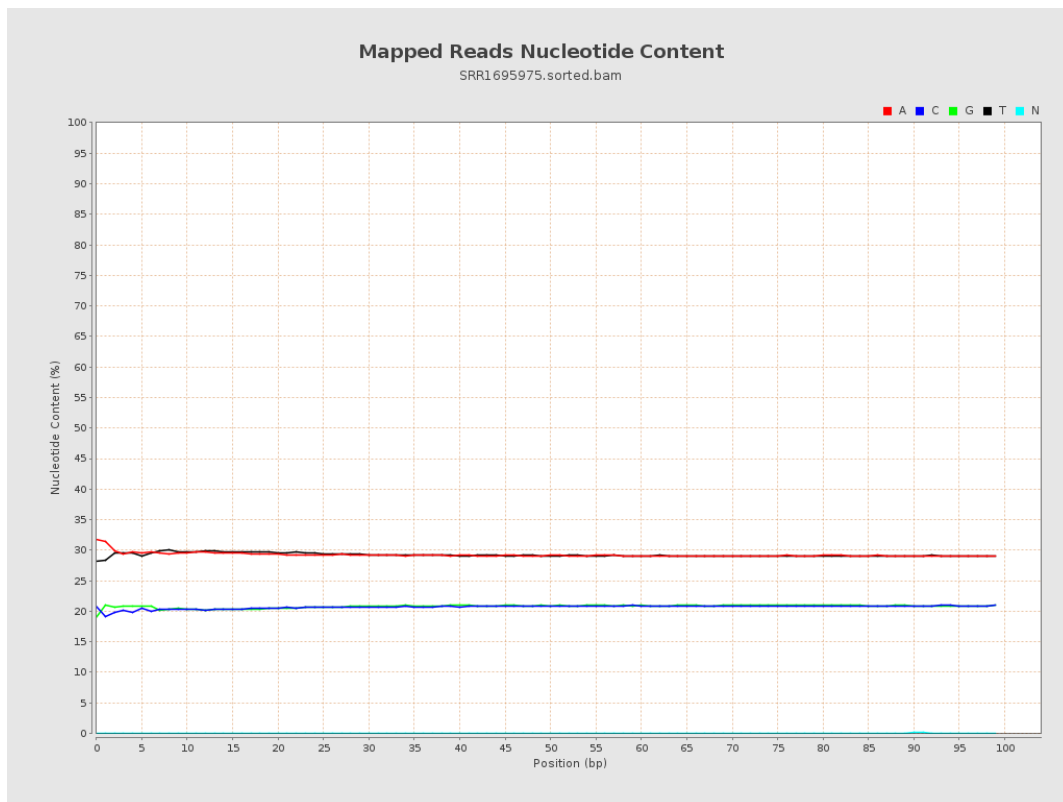
6. Results : Genome Fraction Coverage



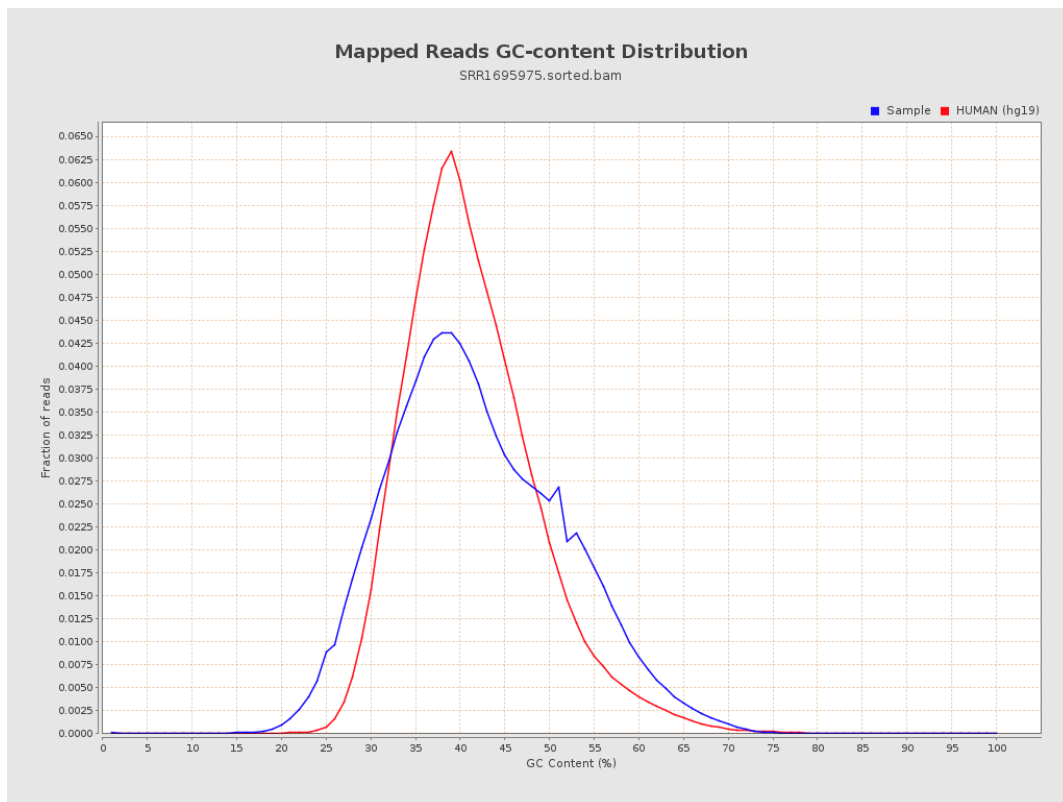
7. Results : Duplication Rate Histogram



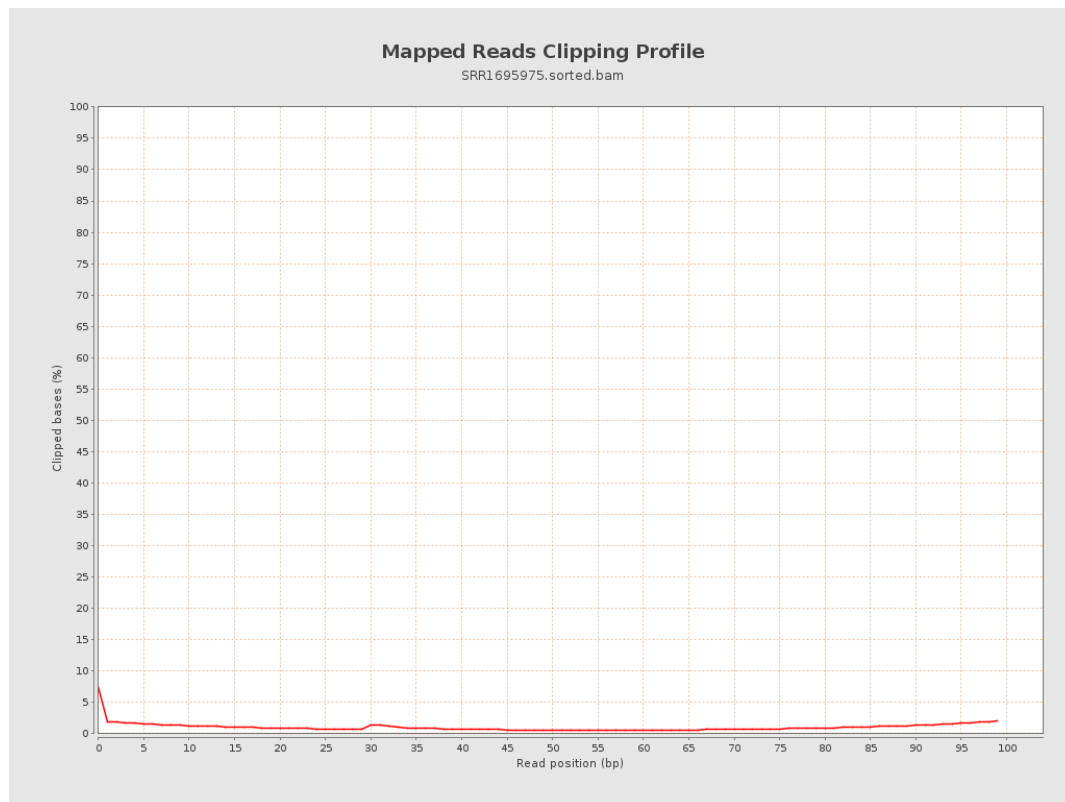
8. Results : Mapped Reads Nucleotide Content



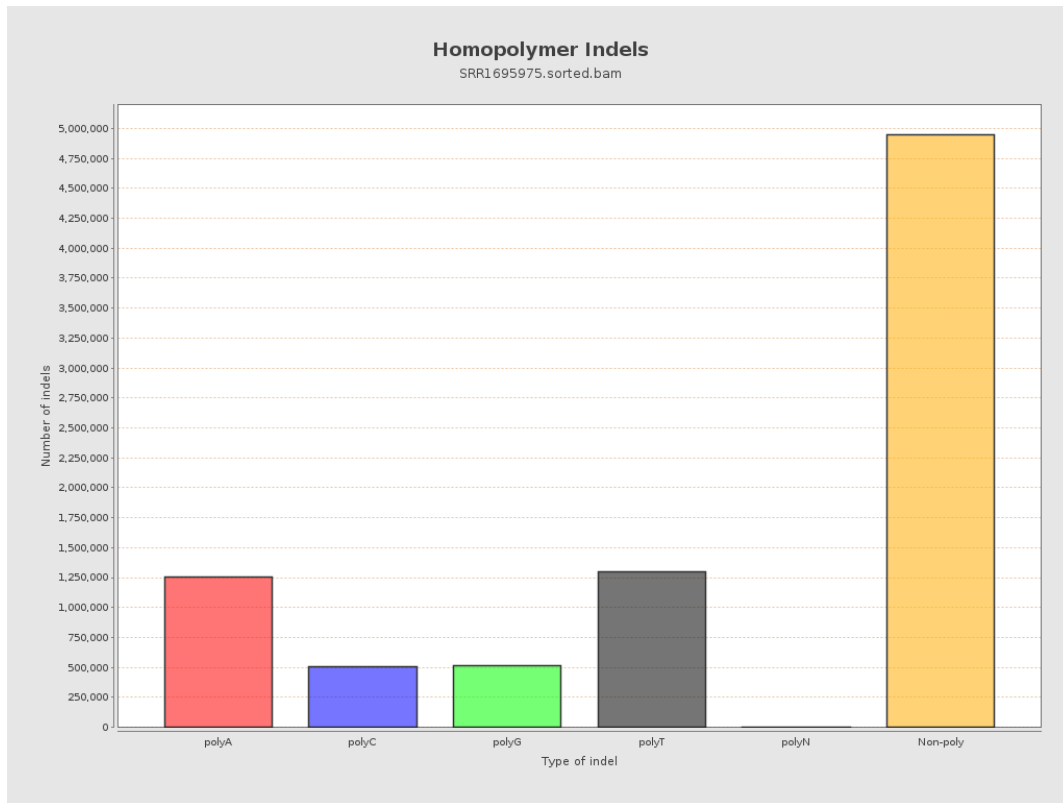
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



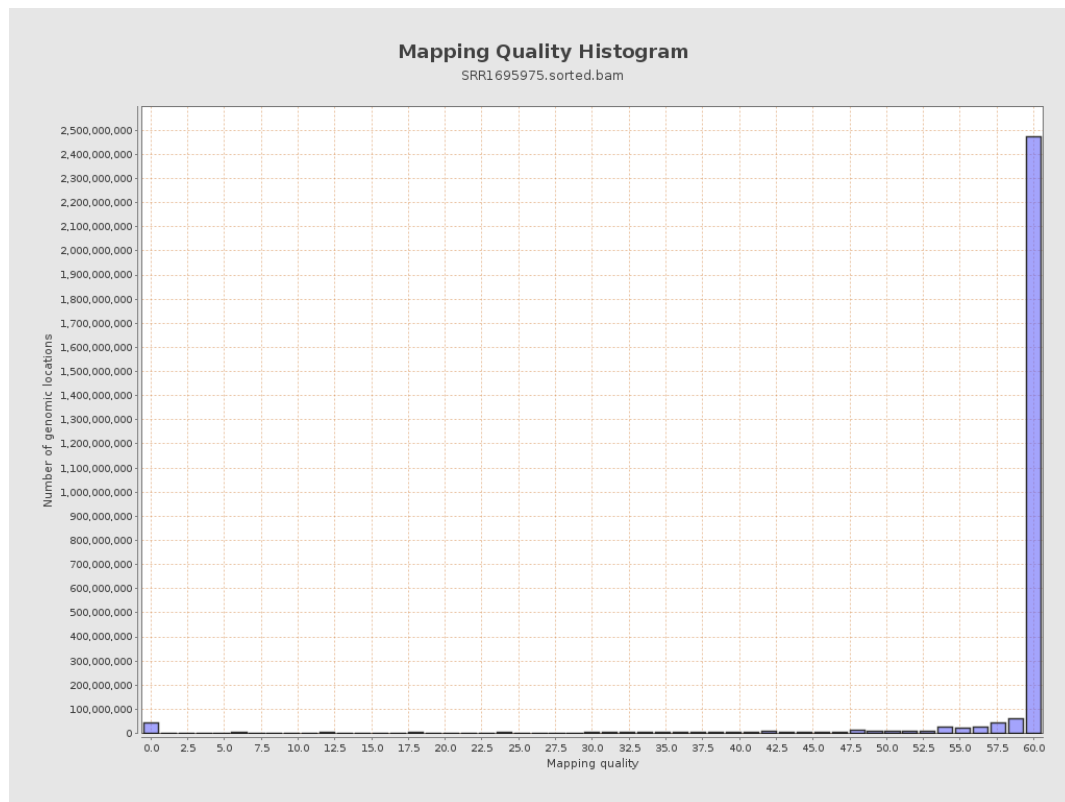
11. Results : Homopolymer Indels



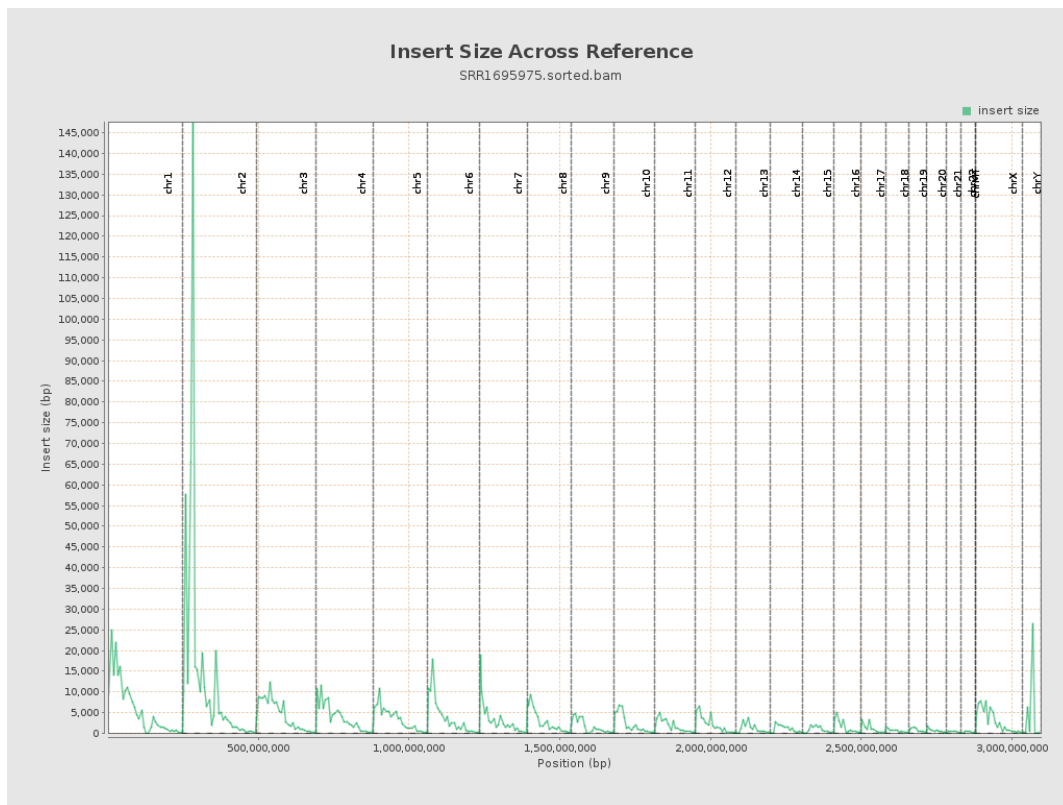
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

