

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/13 09:13:46

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695946.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_SRR1695946 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695946_1.fastq.gz SRR1695946_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 09:13:46 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695946.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	153,320,160
Mapped reads	152,242,275 / 99.3%
Unmapped reads	1,077,885 / 0.7%
Mapped paired reads	152,242,275 / 99.3%
Mapped reads, first in pair	76,310,972 / 49.77%
Mapped reads, second in pair	75,931,303 / 49.52%
Mapped reads, both in pair	151,550,384 / 98.85%
Mapped reads, singletons	691,891 / 0.45%
Secondary alignments	0
Supplementary alignments	2,059,325 / 1.34%
Read min/max/mean length	30 / 100 / 100.55
Duplicated reads (estimated)	16,574,288 / 10.81%
Duplication rate	9.29%
Clipped reads	10,274,064 / 6.7%

2.2. ACGT Content

Number/percentage of A's	4,263,423,336 / 28.24%
Number/percentage of C's	3,247,333,219 / 21.51%
Number/percentage of T's	4,240,460,815 / 28.09%
Number/percentage of G's	3,346,567,091 / 22.17%
Number/percentage of N's	256,380 / 0%

GC Percentage	43.67%
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2.3. Coverage

Mean	4.8785
Standard Deviation	11.701

2.4. Mapping Quality

Mean Mapping Quality	54.06
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2.5. Insert size

Mean	76,402.01
Standard Deviation	2,710,302.4
P25/Median/P75	331 / 338 / 345

2.6. Mismatches and indels

General error rate	0.39%
Mismatches	55,749,022
Insertions	2,005,306
Mapped reads with at least one insertion	1.28%
Deletions	1,742,641
Mapped reads with at least one deletion	1.11%
Homopolymer indels	44.61%

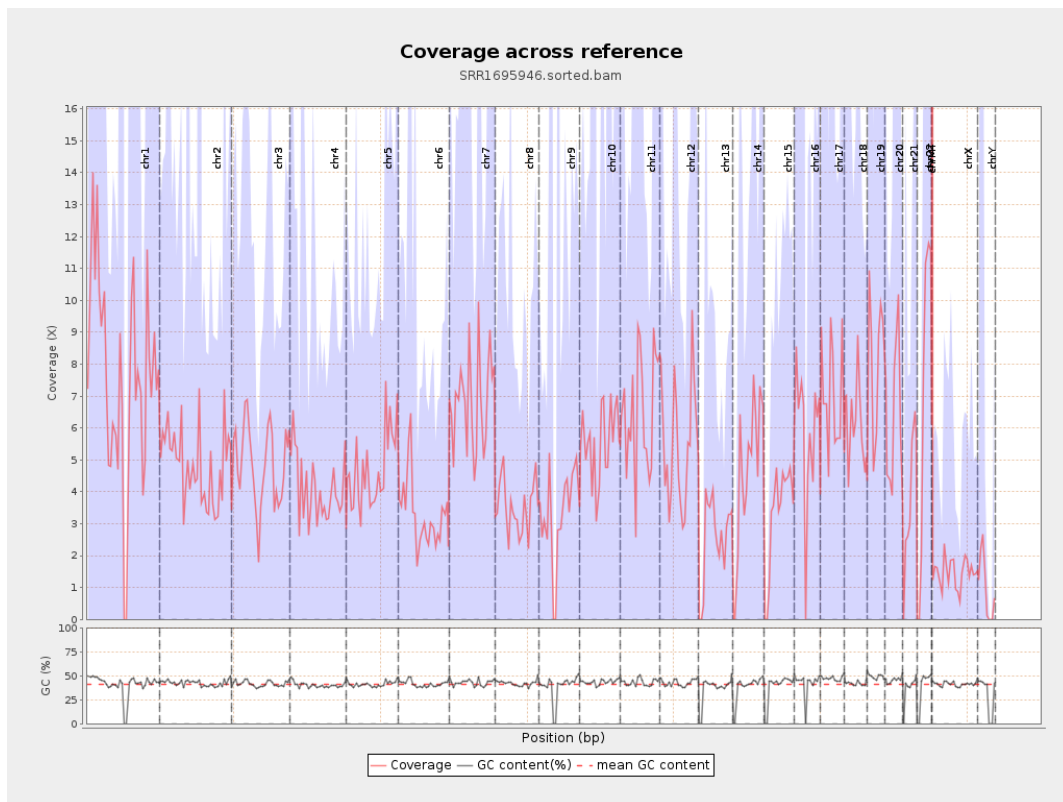
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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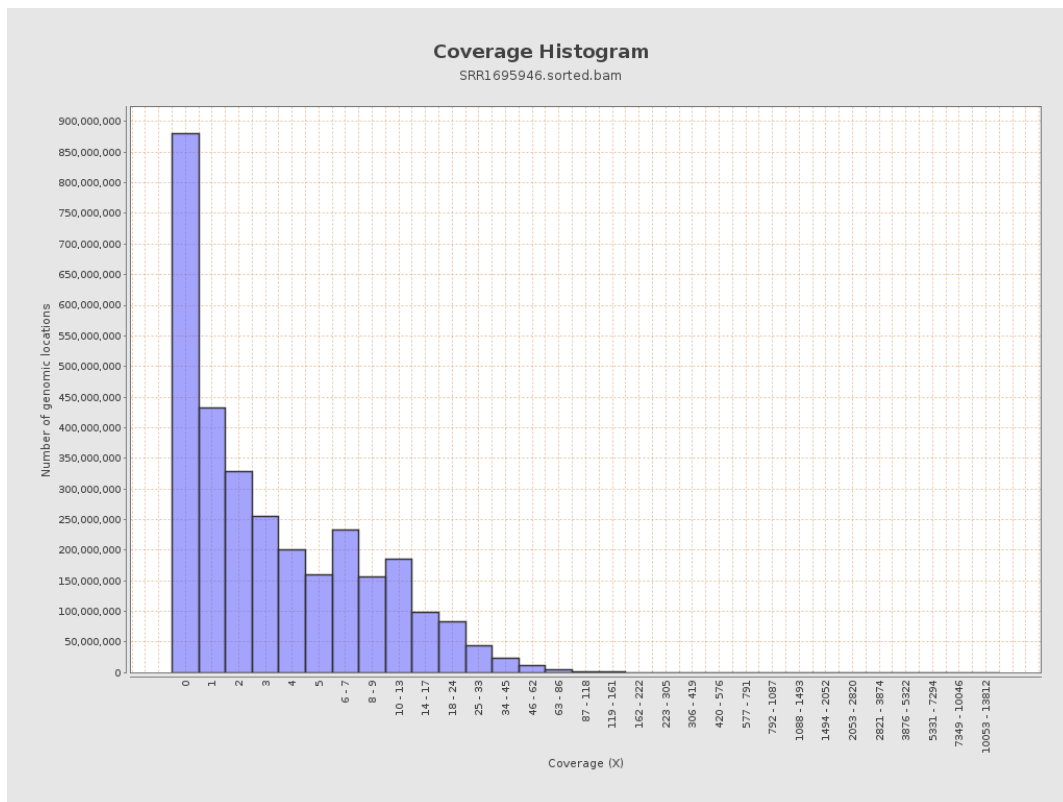
		bases	coverage	deviation
chr1	249250621	1907052451	7.6511	16.7361
chr2	243199373	1172866730	4.8227	16.549
chr3	198022430	959168801	4.8437	7.3467
chr4	191154276	781424517	4.0879	7.4642
chr5	180915260	849814656	4.6973	7.4252
chr6	171115067	559917840	3.2722	7.2448
chr7	159138663	1090884811	6.8549	10.2425
chr8	146364022	519629821	3.5503	6.9799
chr9	141213431	467249286	3.3088	12.7444
chr10	135534747	756040713	5.5782	15.648
chr11	135006516	878750974	6.509	10.7931
chr12	133851895	734814684	5.4898	9.2491
chr13	115169878	291935759	2.5348	6.2008
chr14	107349540	492885788	4.5914	9.6019
chr15	102531392	336374321	3.2807	6.4642
chr16	90354753	528620859	5.8505	15.4013
chr17	81195210	570519234	7.0265	13.6173
chr18	78077248	483526143	6.1929	17.222
chr19	59128983	484630701	8.1962	15.8171
chr20	63025520	407118337	6.4596	10.6003
chr21	48129895	184667023	3.8368	9.0092
chr22	51304566	355267697	6.9247	15.2533
chrMT	16571	2424505	146.3101	49.6922
chrX	155270560	224915827	1.4485	4.6327

chrY	59373566	61753274	1.0401	13.5271
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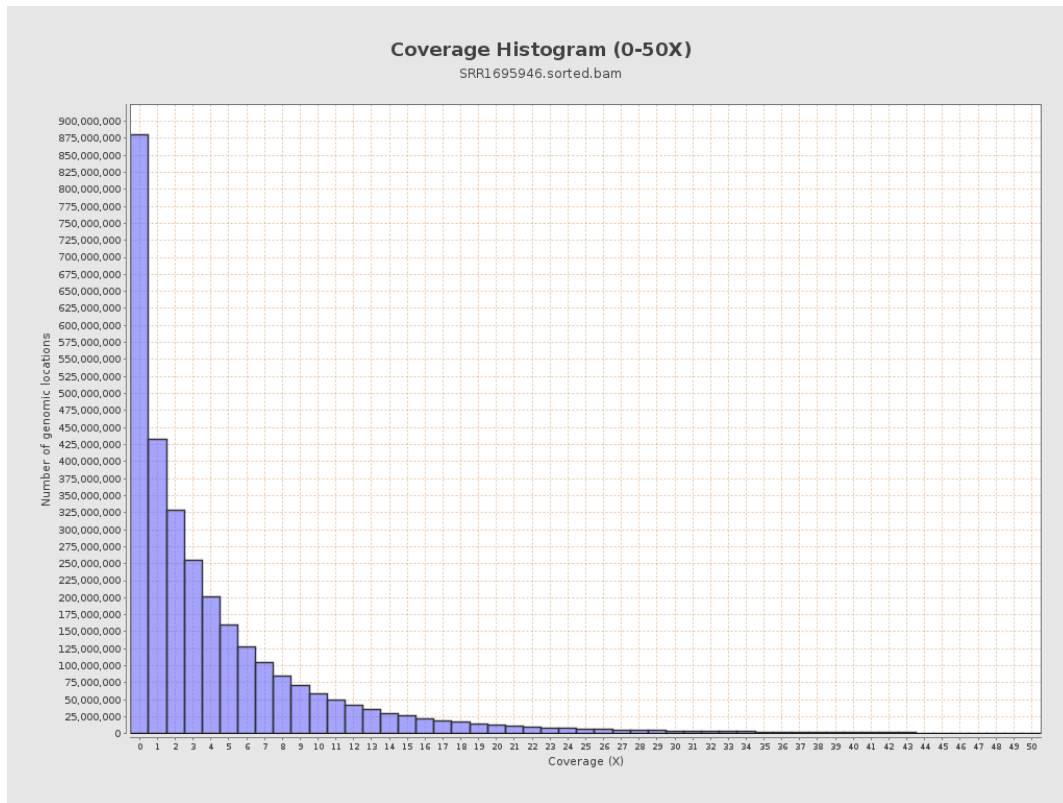
3. Results : Coverage across reference



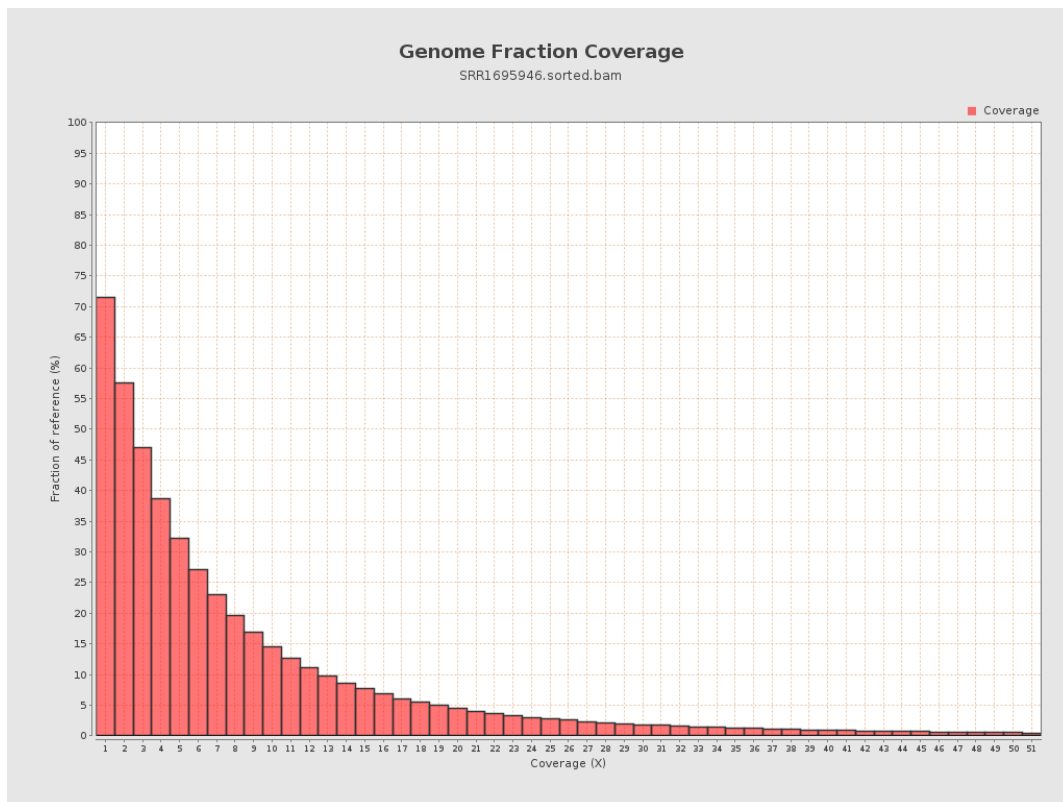
4. Results : Coverage Histogram



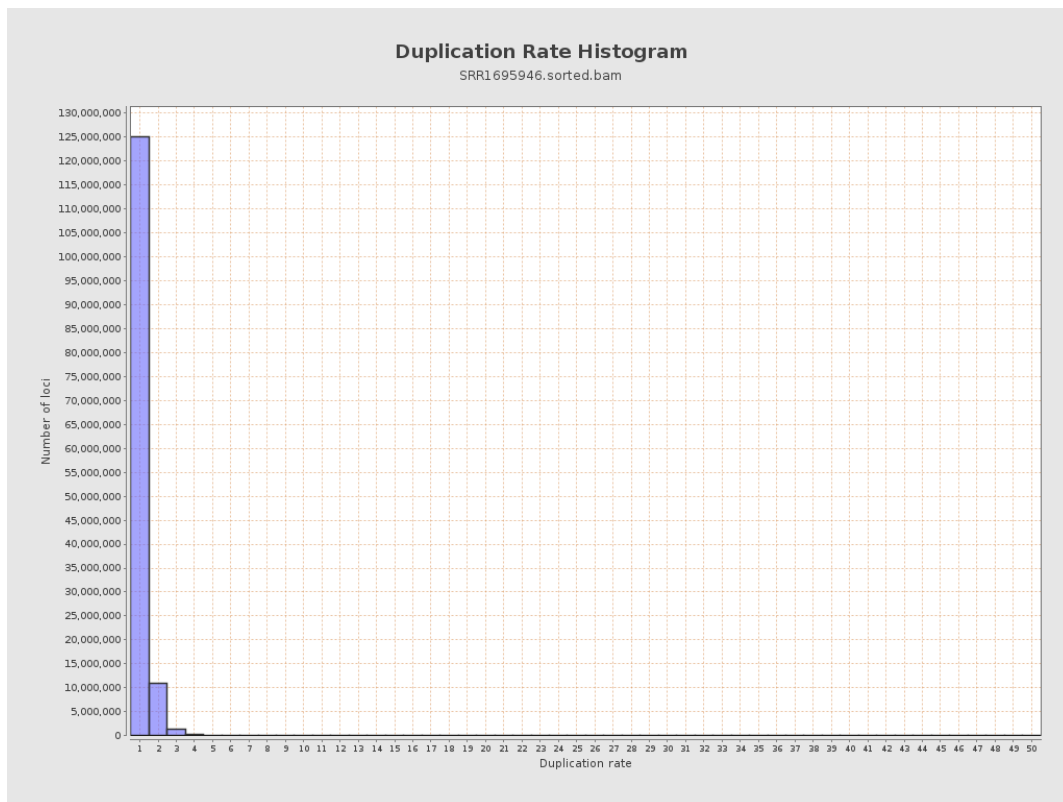
5. Results : Coverage Histogram (0-50X)



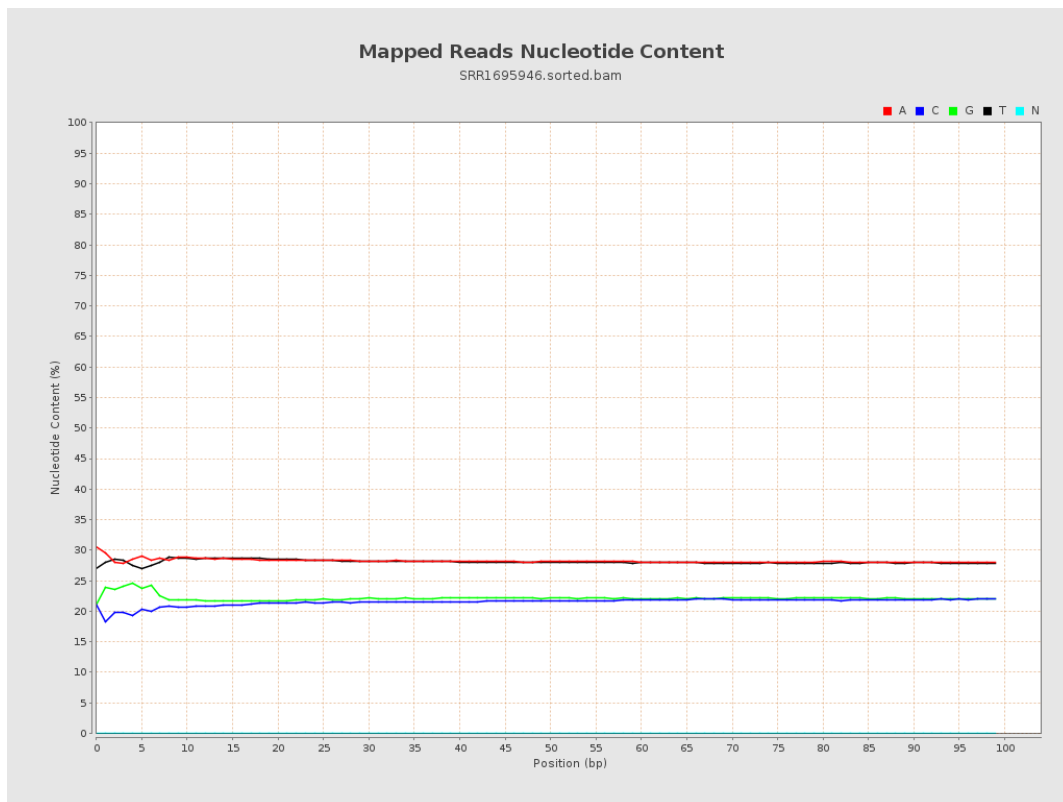
6. Results : Genome Fraction Coverage



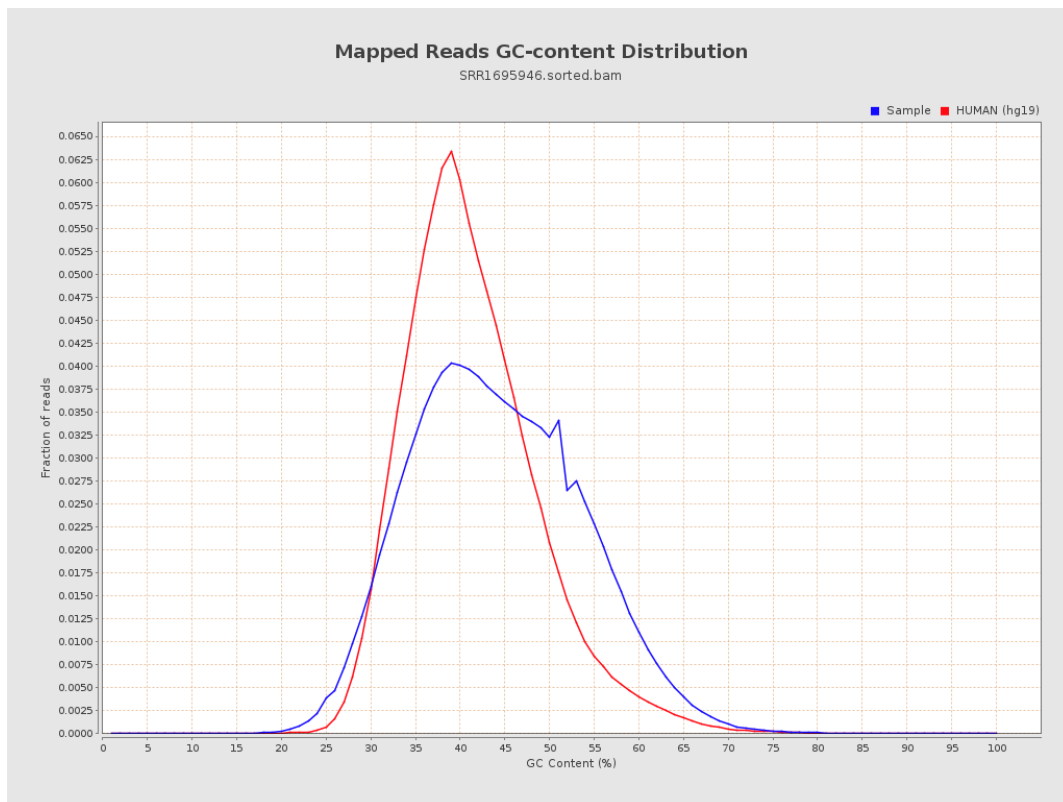
7. Results : Duplication Rate Histogram



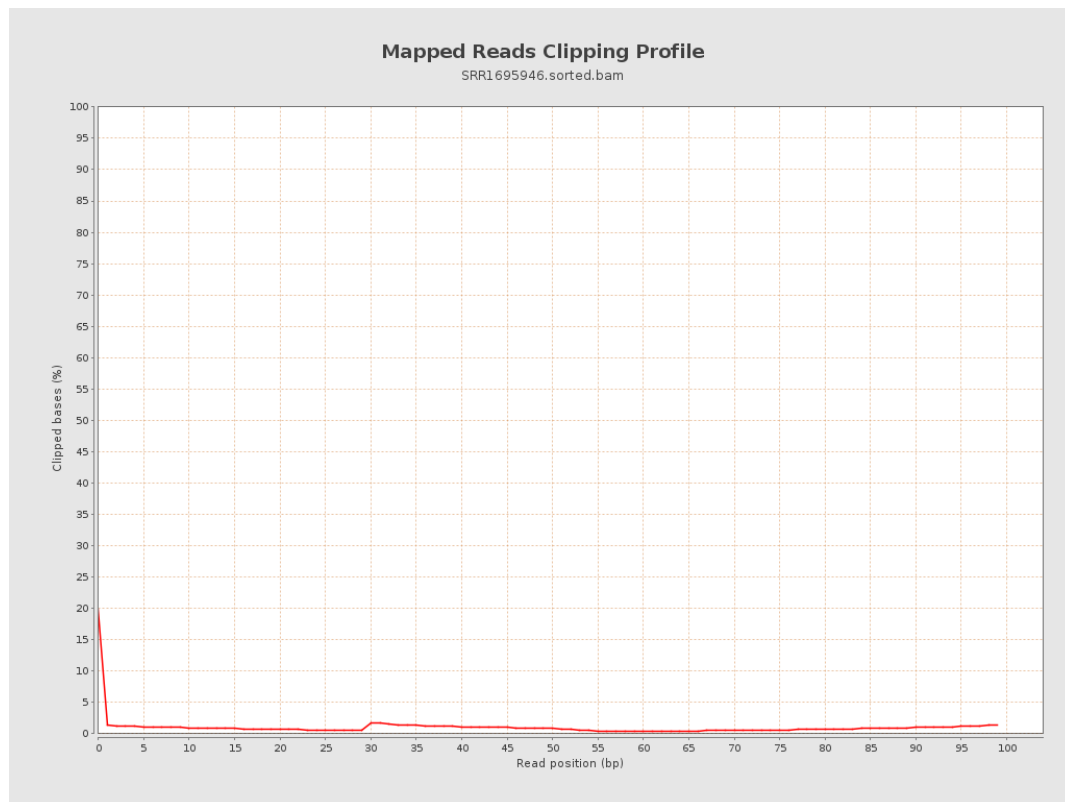
8. Results : Mapped Reads Nucleotide Content



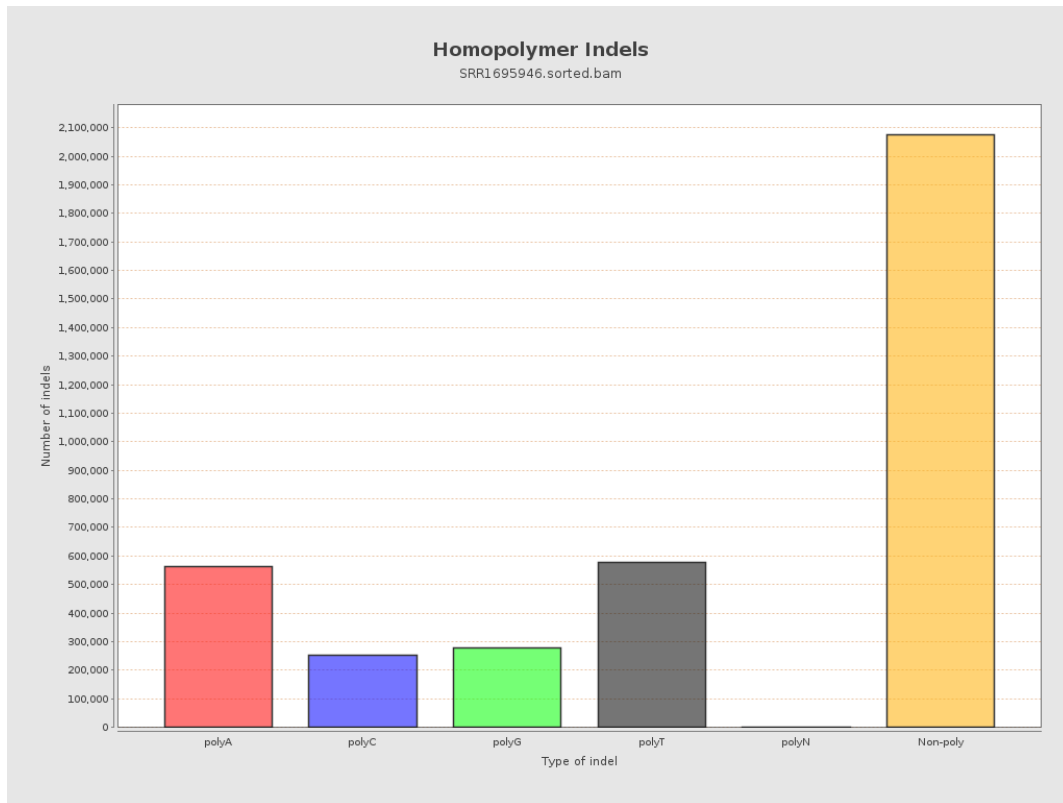
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



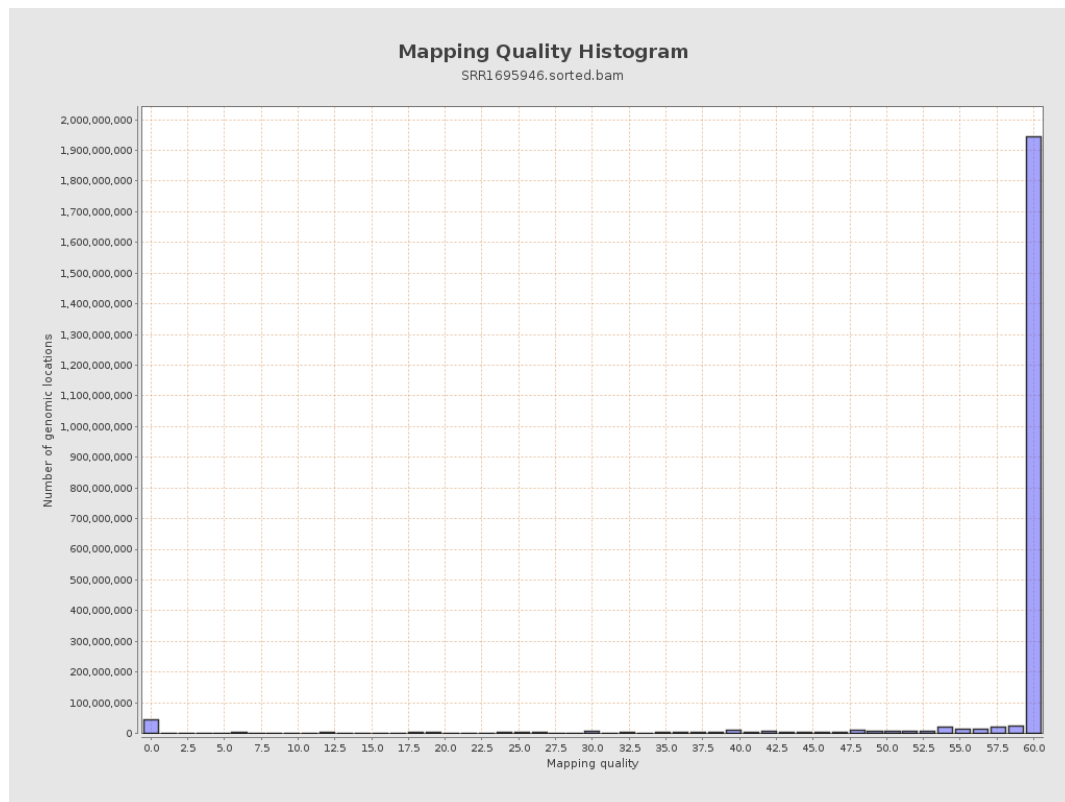
11. Results : Homopolymer Indels



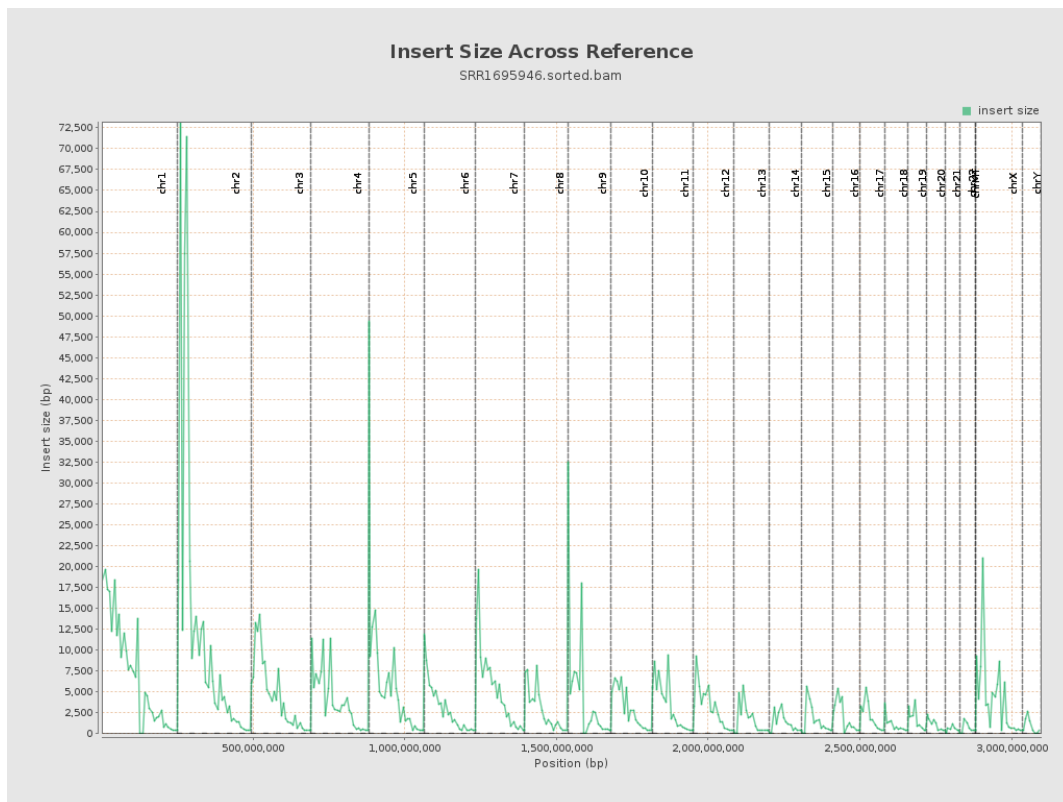
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

