

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 15:22:45

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695917.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_SRR1695917 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1695917_1.fastq.gz SRR1695917_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.18-r1243-dirty)
Analysis date:	Thu Sep 12 15:22:45 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695917.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	435,889,172
Mapped reads	432,435,277 / 99.21%
Unmapped reads	3,453,895 / 0.79%
Mapped paired reads	432,435,277 / 99.21%
Mapped reads, first in pair	217,141,769 / 49.82%
Mapped reads, second in pair	215,293,508 / 49.39%
Mapped reads, both in pair	429,903,508 / 98.63%
Mapped reads, singletons	2,531,769 / 0.58%
Secondary alignments	0
Supplementary alignments	5,502,855 / 1.26%
Read min/max/mean length	30 / 100 / 100.52
Duplicated reads (estimated)	62,318,555 / 14.3%
Duplication rate	13.47%
Clipped reads	32,361,630 / 7.42%

2.2. ACGT Content

Number/percentage of A's	12,734,700,670 / 29.71%
Number/percentage of C's	8,609,659,963 / 20.08%
Number/percentage of T's	12,614,523,494 / 29.43%
Number/percentage of G's	8,900,594,472 / 20.76%
Number/percentage of N's	10,141,678 / 0.02%

GC Percentage	40.85%
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2.3. Coverage

Mean	13.8512
Standard Deviation	17.0476

2.4. Mapping Quality

Mean Mapping Quality	53.85
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2.5. Insert size

Mean	80,971.53
Standard Deviation	2,717,043.02
P25/Median/P75	317 / 325 / 334

2.6. Mismatches and indels

General error rate	0.59%
Mismatches	244,520,594
Insertions	4,273,074
Mapped reads with at least one insertion	0.97%
Deletions	4,165,991
Mapped reads with at least one deletion	0.94%
Homopolymer indels	45.51%

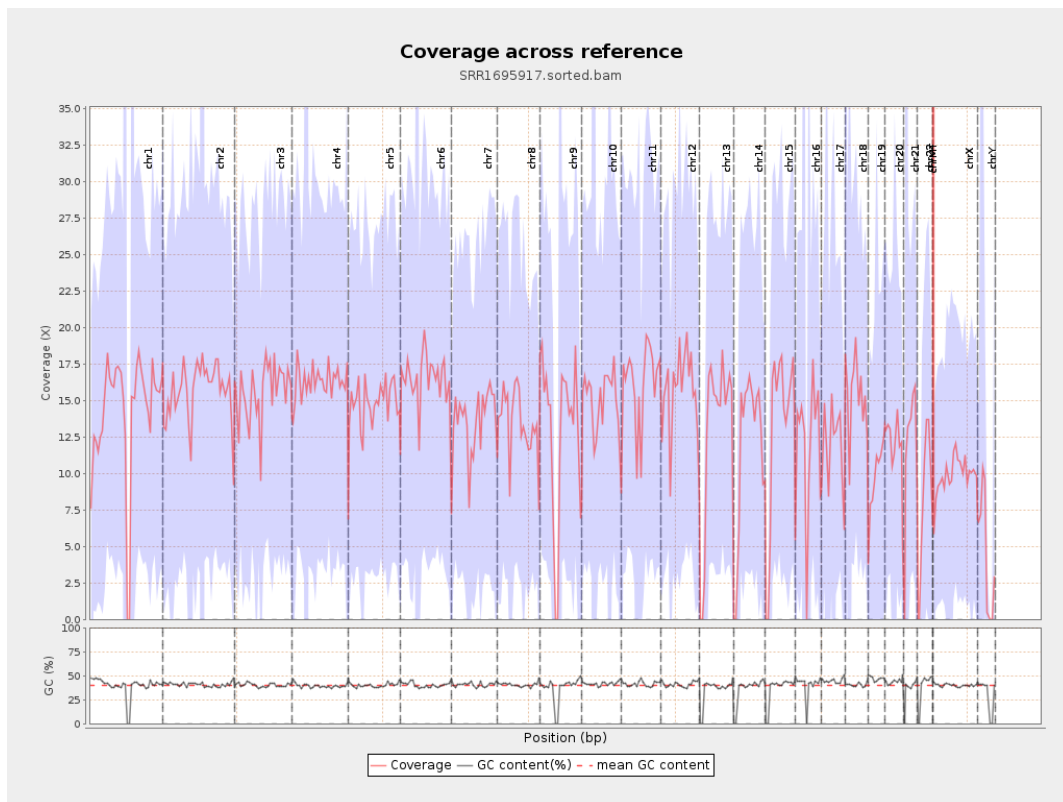
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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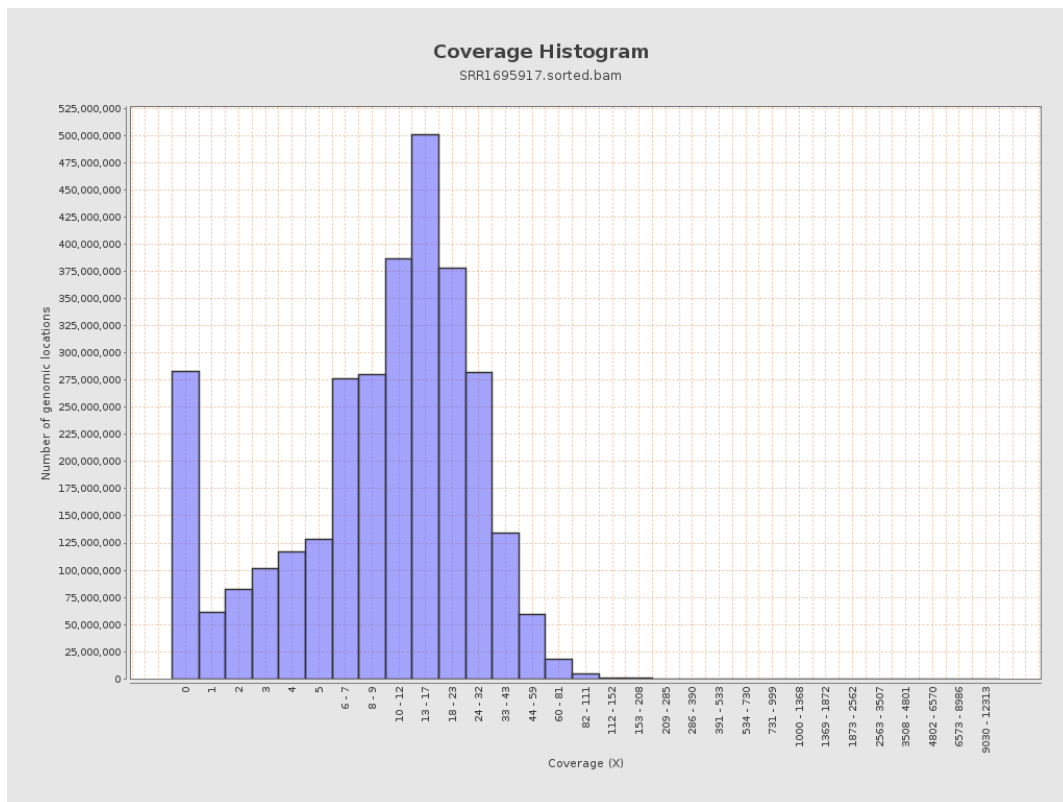
		bases	coverage	deviation
chr1	249250621	3540480174	14.2045	17.8343
chr2	243199373	3805971078	15.6496	19.7921
chr3	198022430	3087380225	15.5911	12.3437
chr4	191154276	3121195574	16.3281	16.8014
chr5	180915260	2680884945	14.8185	11.6681
chr6	171115067	2822722471	16.496	15.0691
chr7	159138663	2156074336	13.5484	12.0807
chr8	146364022	1963328861	13.414	11.5044
chr9	141213431	1812648597	12.8362	15.3544
chr10	135534747	2042815366	15.0723	19.1818
chr11	135006516	2178010101	16.1326	14.4196
chr12	133851895	2098569812	15.6783	12.8435
chr13	115169878	1493048677	12.9639	12.4321
chr14	107349540	1292806661	12.043	12.4708
chr15	102531392	1342587432	13.0944	13.4319
chr16	90354753	1061292303	11.7458	19.9744
chr17	81195210	981658955	12.0901	15.1464
chr18	78077248	1192203974	15.2695	18.6147
chr19	59128983	589006274	9.9614	13.014
chr20	63025520	758379770	12.0329	13.1176
chr21	48129895	579157450	12.0332	24.0767
chr22	51304566	428562917	8.3533	11.7485
chrMT	16571	49883426	3,010.2846	788.0951
chrX	155270560	1529455352	9.8503	9.1685

chrY	59373566	271091377	4.5659	19.127
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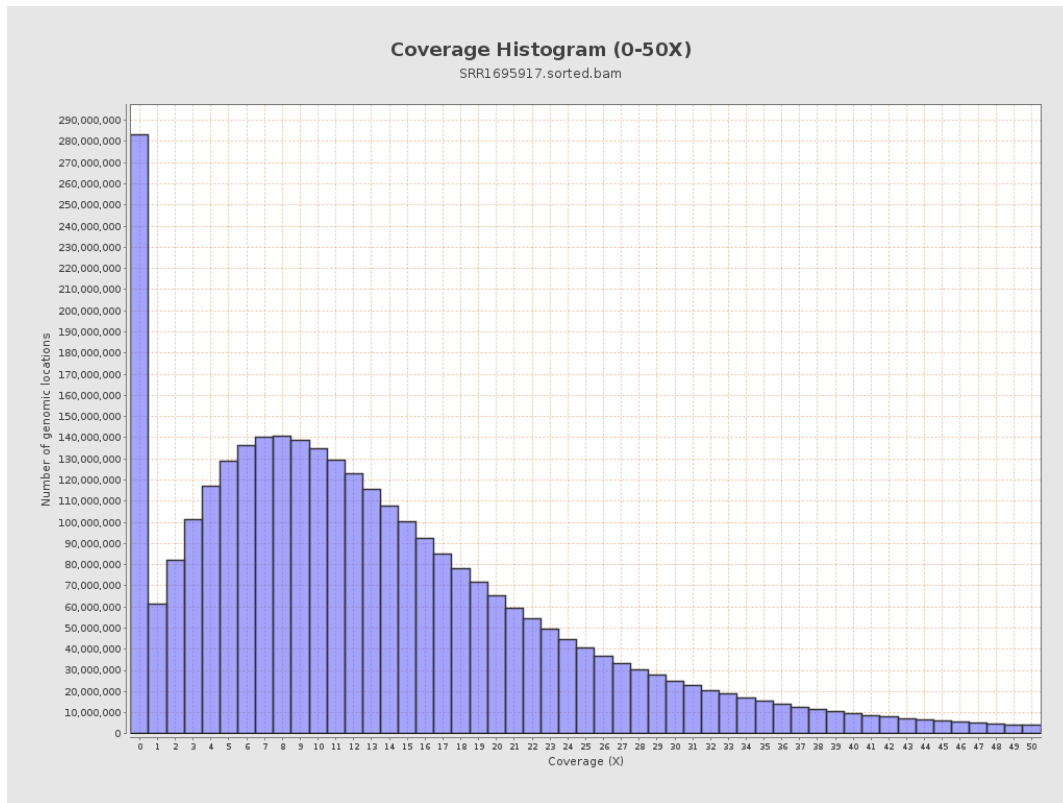
3. Results : Coverage across reference



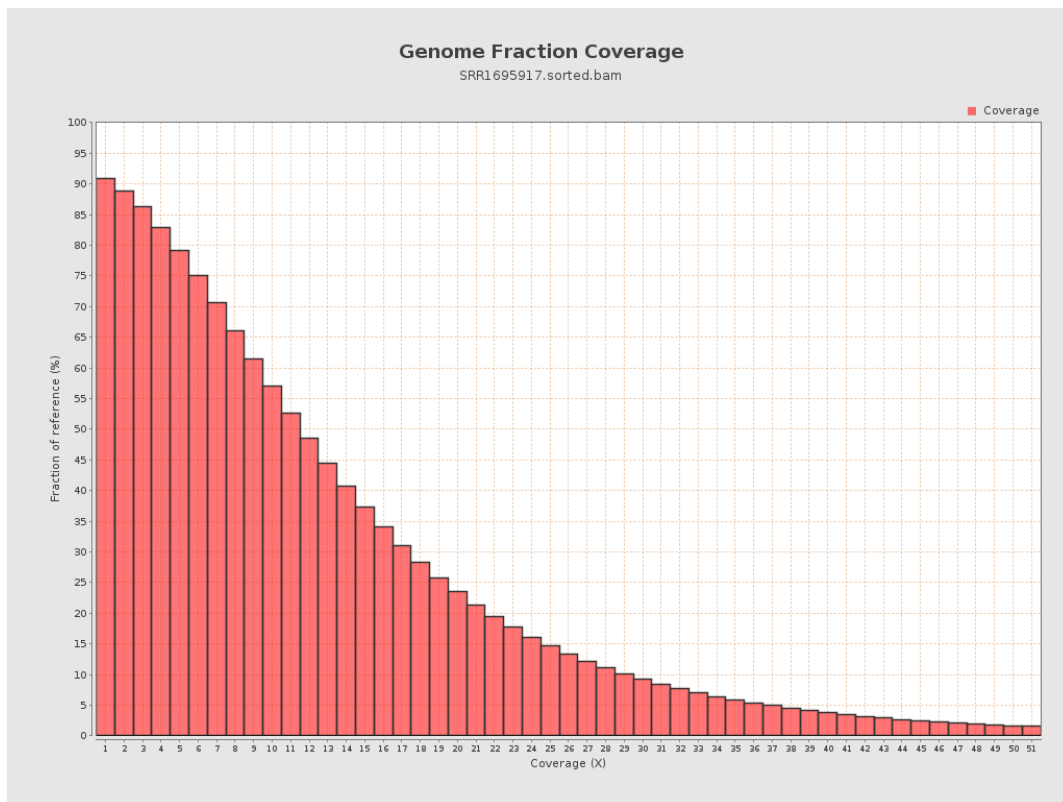
4. Results : Coverage Histogram



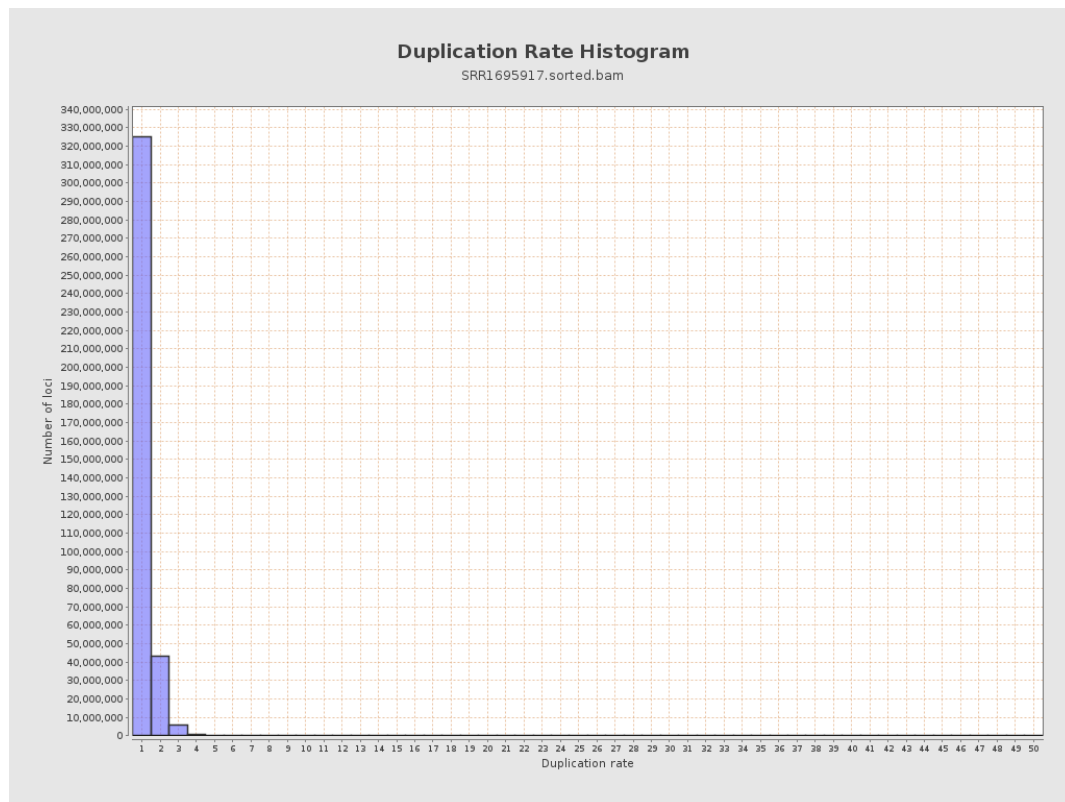
5. Results : Coverage Histogram (0-50X)



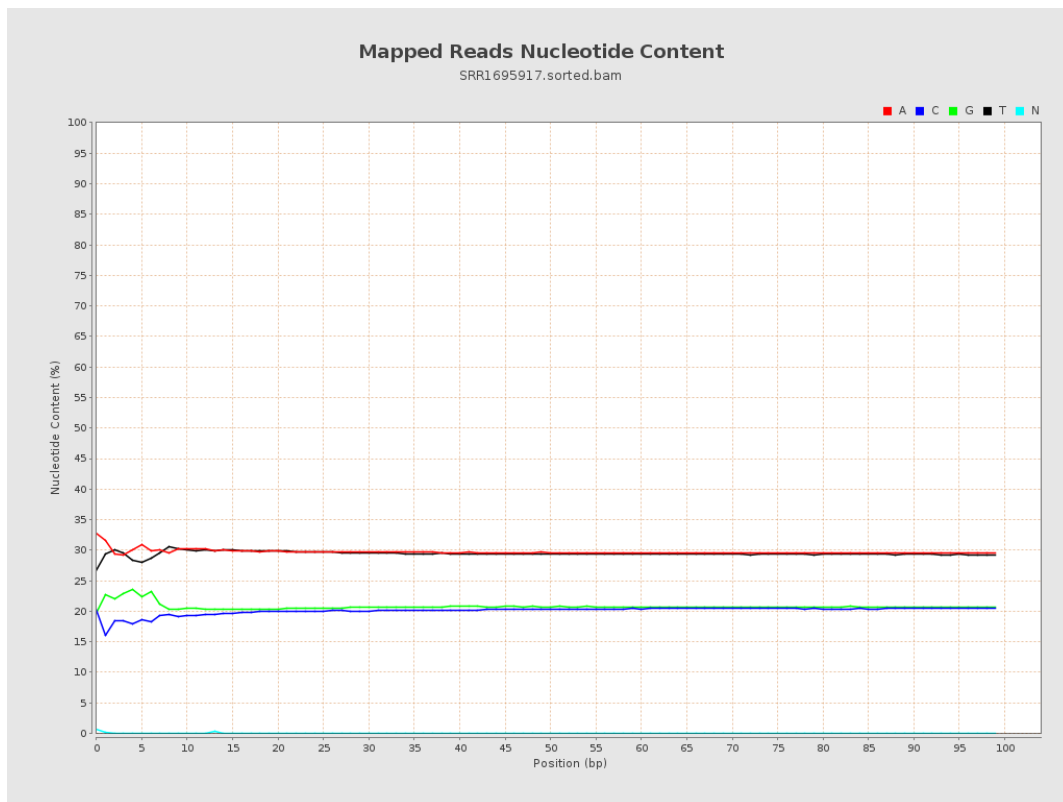
6. Results : Genome Fraction Coverage



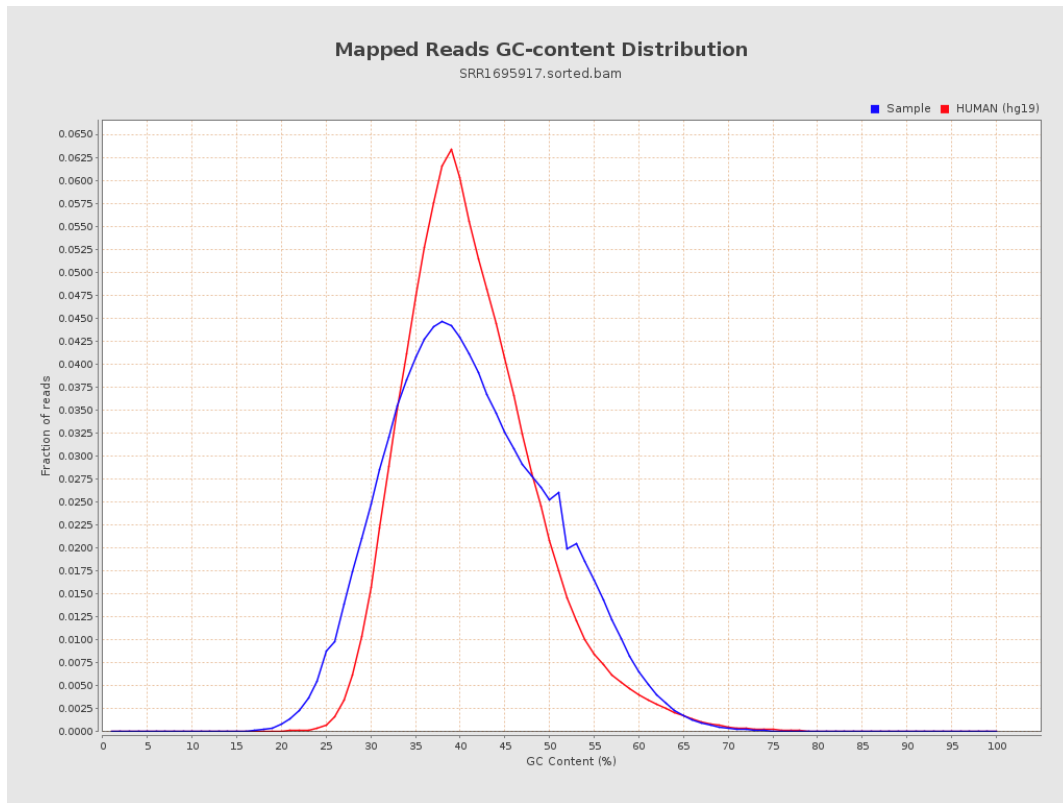
7. Results : Duplication Rate Histogram



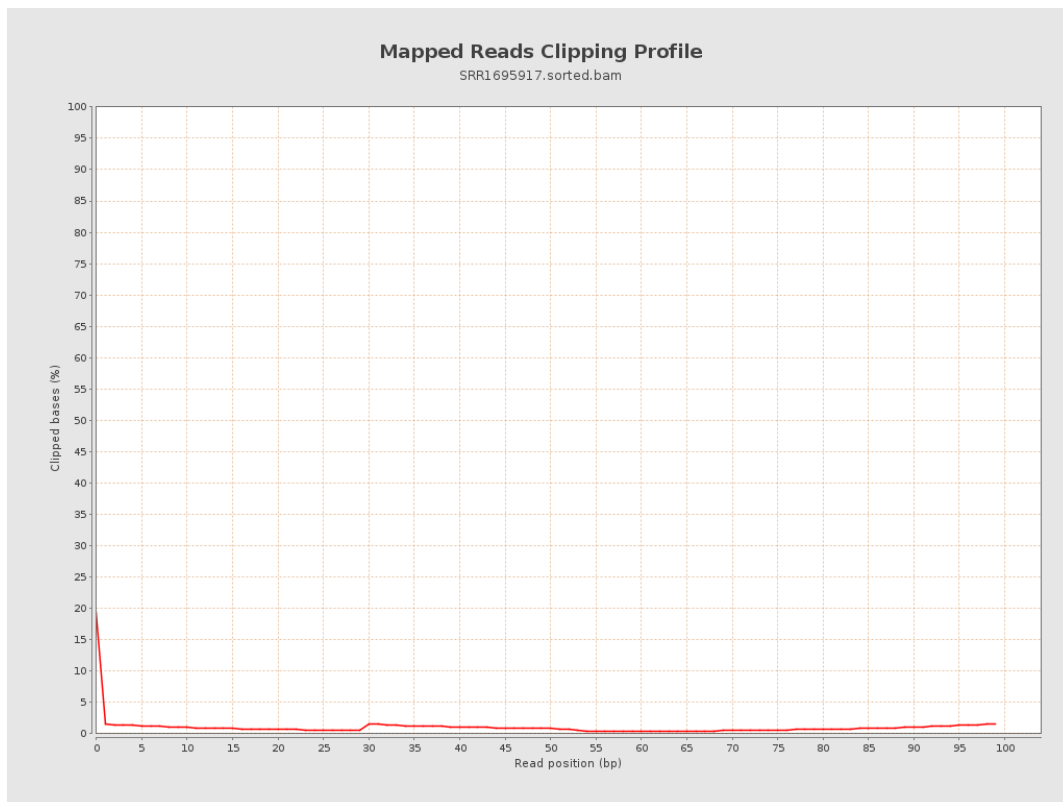
8. Results : Mapped Reads Nucleotide Content



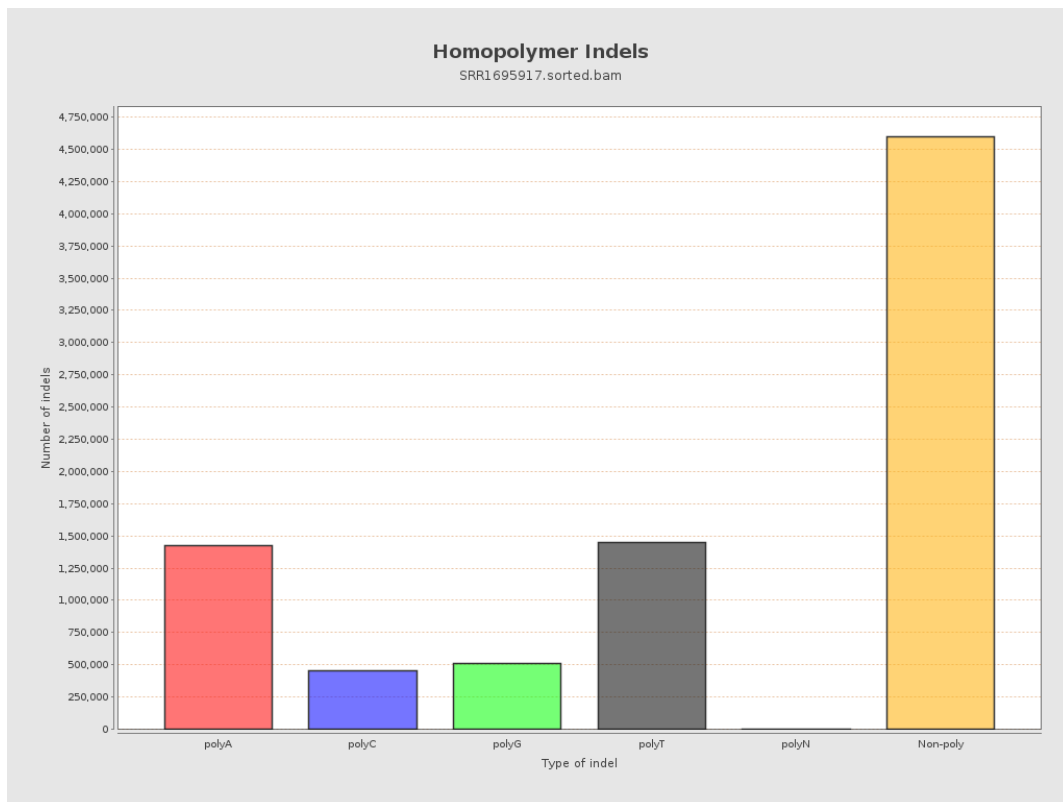
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



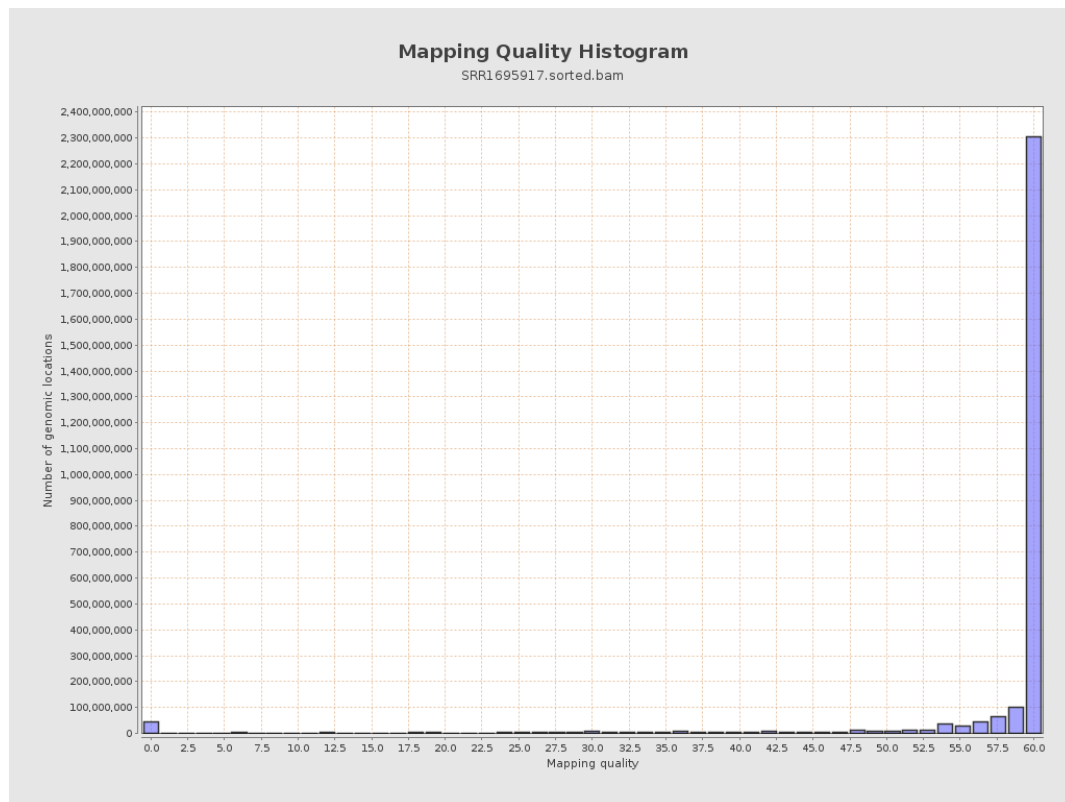
11. Results : Homopolymer Indels



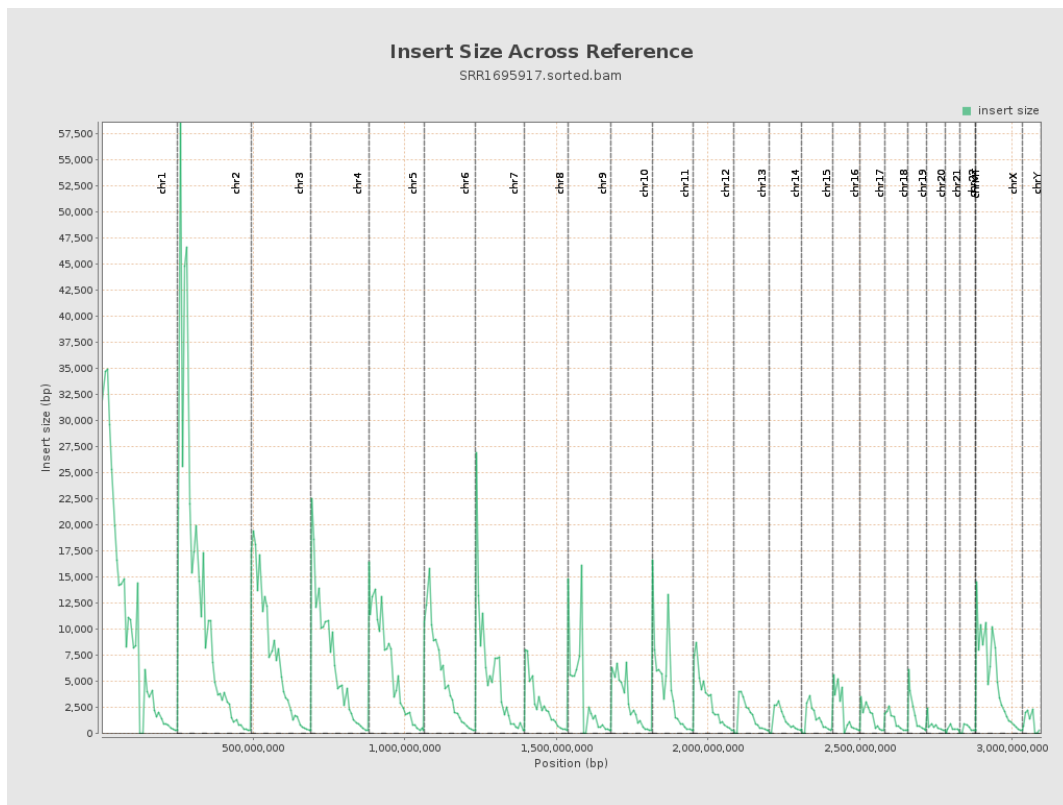
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

