

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 18:25:27

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695918.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 918 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695918_1.fastq.gz SRR1695918_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 18:25:27 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695918.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	431,386,314
Mapped reads	427,950,443 / 99.2%
Unmapped reads	3,435,871 / 0.8%
Mapped paired reads	427,950,443 / 99.2%
Mapped reads, first in pair	214,892,073 / 49.81%
Mapped reads, second in pair	213,058,370 / 49.39%
Mapped reads, both in pair	425,446,176 / 98.62%
Mapped reads, singletons	2,504,267 / 0.58%
Secondary alignments	0
Supplementary alignments	5,035,630 / 1.17%
Read min/max/mean length	30 / 100 / 100.48
Duplicated reads (estimated)	61,032,185 / 14.15%
Duplication rate	13.34%
Clipped reads	31,128,321 / 7.22%

2.2. ACGT Content

Number/percentage of A's	12,557,183,524 / 29.6%
Number/percentage of C's	8,515,415,433 / 20.07%
Number/percentage of T's	12,441,975,761 / 29.32%
Number/percentage of G's	8,800,866,419 / 20.74%
Number/percentage of N's	112,790,417 / 0.27%

GC Percentage	40.81%
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2.3. Coverage

Mean	13.7086
Standard Deviation	16.8592

2.4. Mapping Quality

Mean Mapping Quality	53.88
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2.5. Insert size

Mean	77,964.13
Standard Deviation	2,666,531.49
P25/Median/P75	317 / 325 / 334

2.6. Mismatches and indels

General error rate	0.79%
Mismatches	329,278,019
Insertions	4,287,029
Mapped reads with at least one insertion	0.98%
Deletions	4,135,182
Mapped reads with at least one deletion	0.95%
Homopolymer indels	44.93%

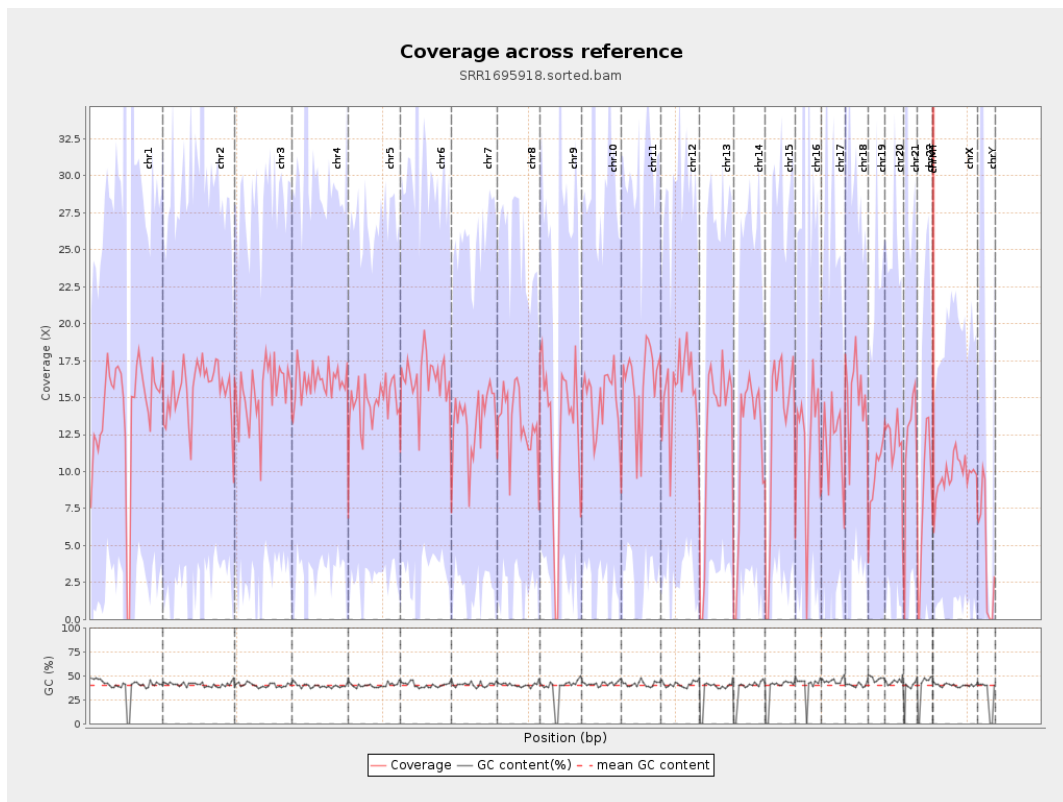
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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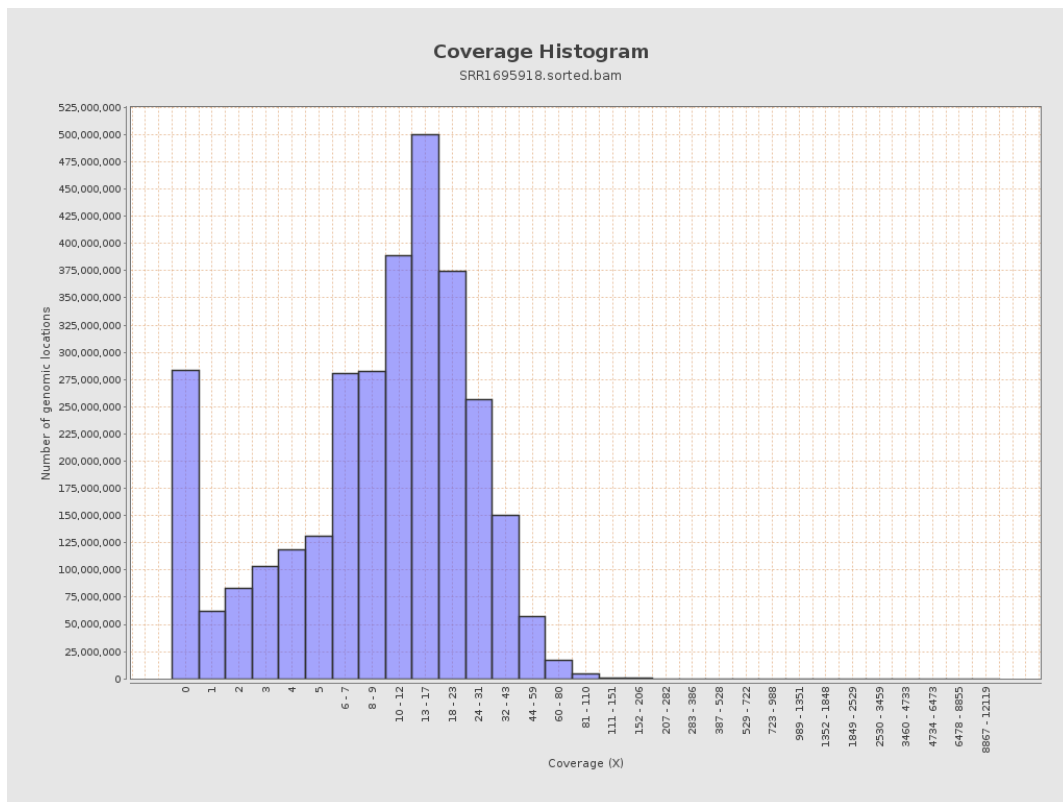
		bases	coverage	deviation
chr1	249250621	3505480658	14.0641	17.5947
chr2	243199373	3766951210	15.4891	19.5193
chr3	198022430	3054358482	15.4243	12.2191
chr4	191154276	3082187885	16.1241	16.6684
chr5	180915260	2652805919	14.6633	11.5405
chr6	171115067	2792189847	16.3176	14.903
chr7	159138663	2132990170	13.4033	11.974
chr8	146364022	1941282664	13.2634	11.3863
chr9	141213431	1794707692	12.7092	15.1219
chr10	135534747	2021738331	14.9168	18.7112
chr11	135006516	2155837147	15.9684	14.2525
chr12	133851895	2075531859	15.5062	12.739
chr13	115169878	1476474678	12.82	12.3215
chr14	107349540	1277870649	11.9038	12.3568
chr15	102531392	1329943766	12.9711	13.2727
chr16	90354753	1053782170	11.6627	19.7644
chr17	81195210	975490989	12.0141	14.9436
chr18	78077248	1180140118	15.115	18.3175
chr19	59128983	587827160	9.9414	12.9324
chr20	63025520	751930843	11.9306	12.9641
chr21	48129895	572955443	11.9044	23.8645
chr22	51304566	426472874	8.3126	11.62
chrMT	16571	49640908	2,995.6495	785.5627
chrX	155270560	1511375497	9.7338	9.0438

chrY	59373566	267798172	4.5104	18.912
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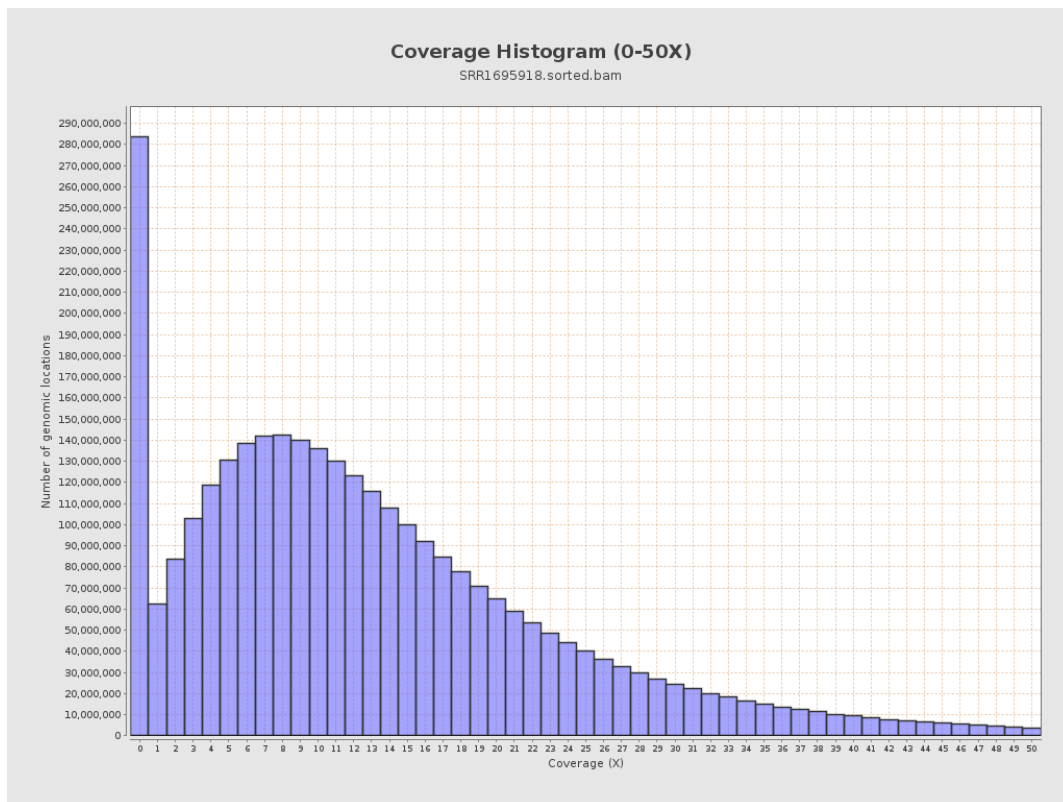
3. Results : Coverage across reference



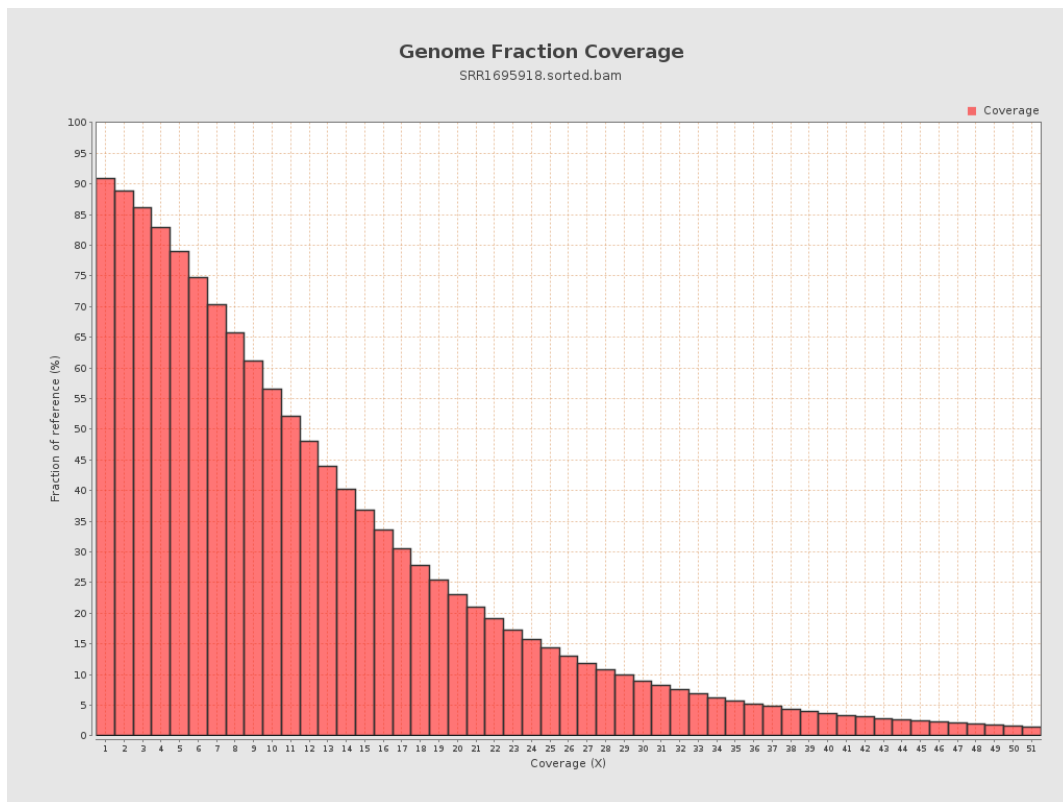
4. Results : Coverage Histogram



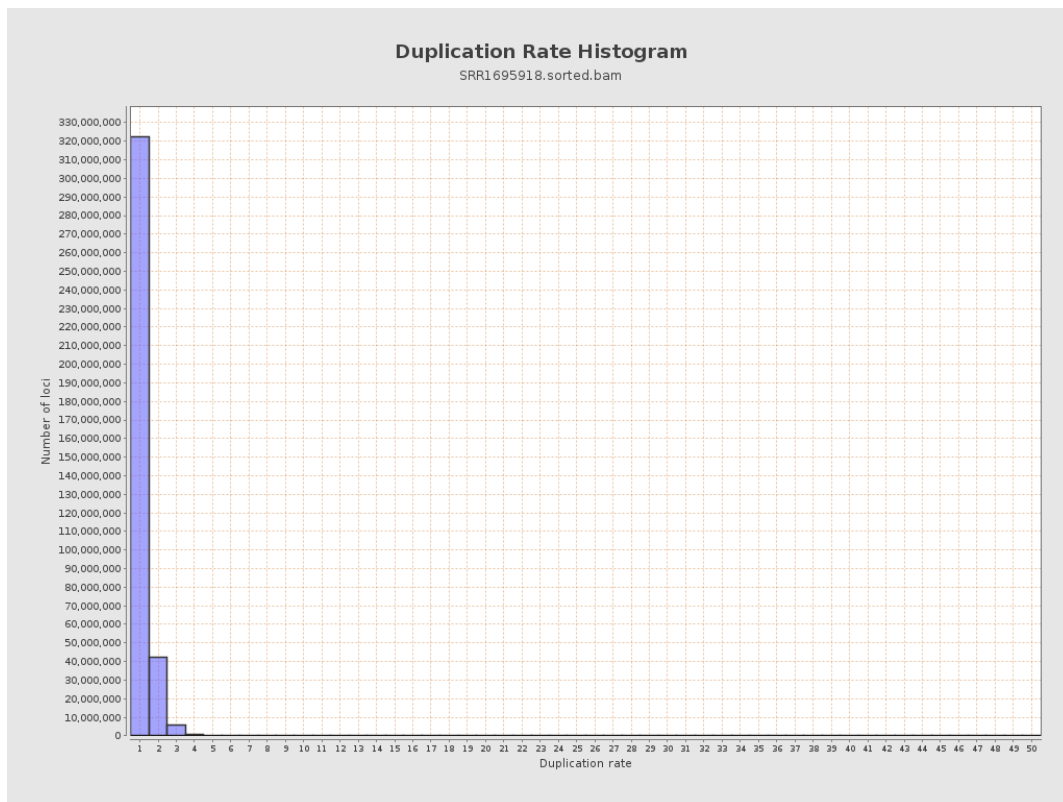
5. Results : Coverage Histogram (0-50X)



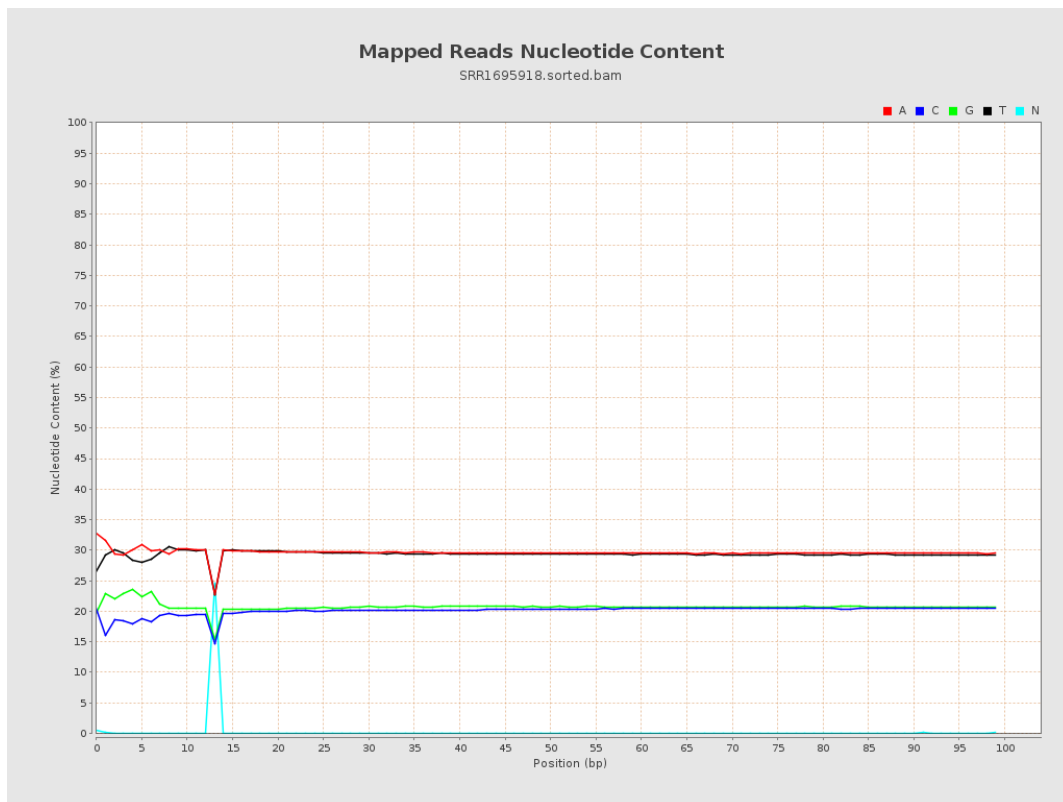
6. Results : Genome Fraction Coverage



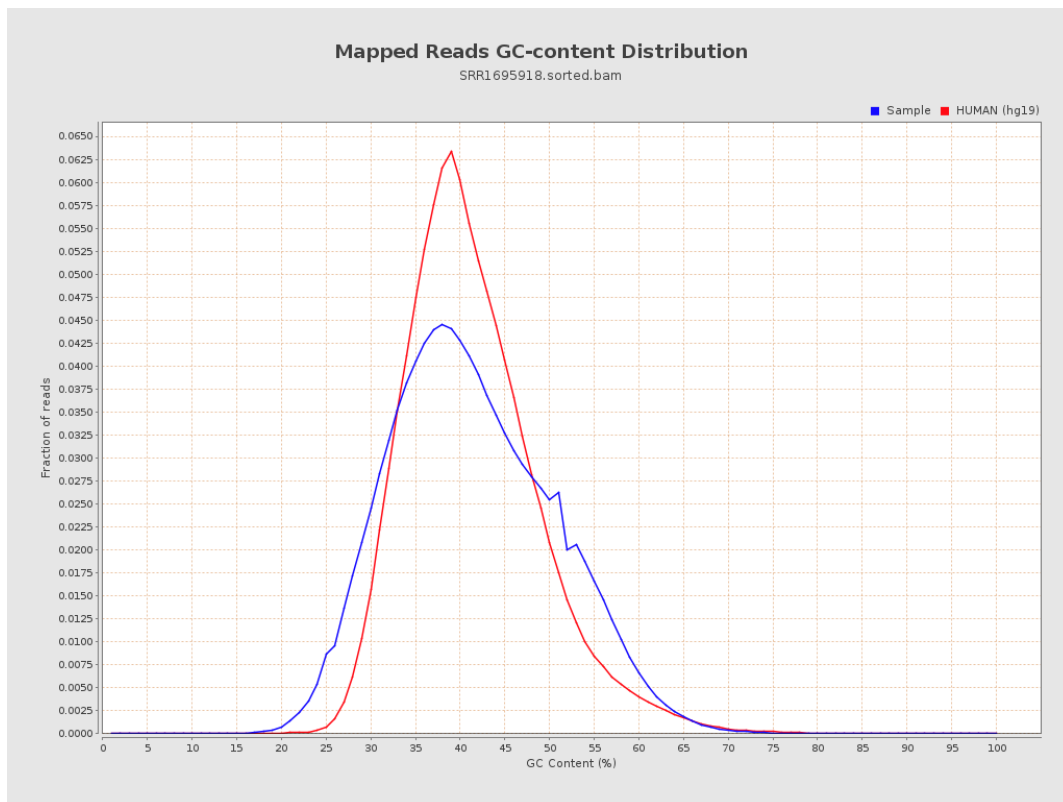
7. Results : Duplication Rate Histogram



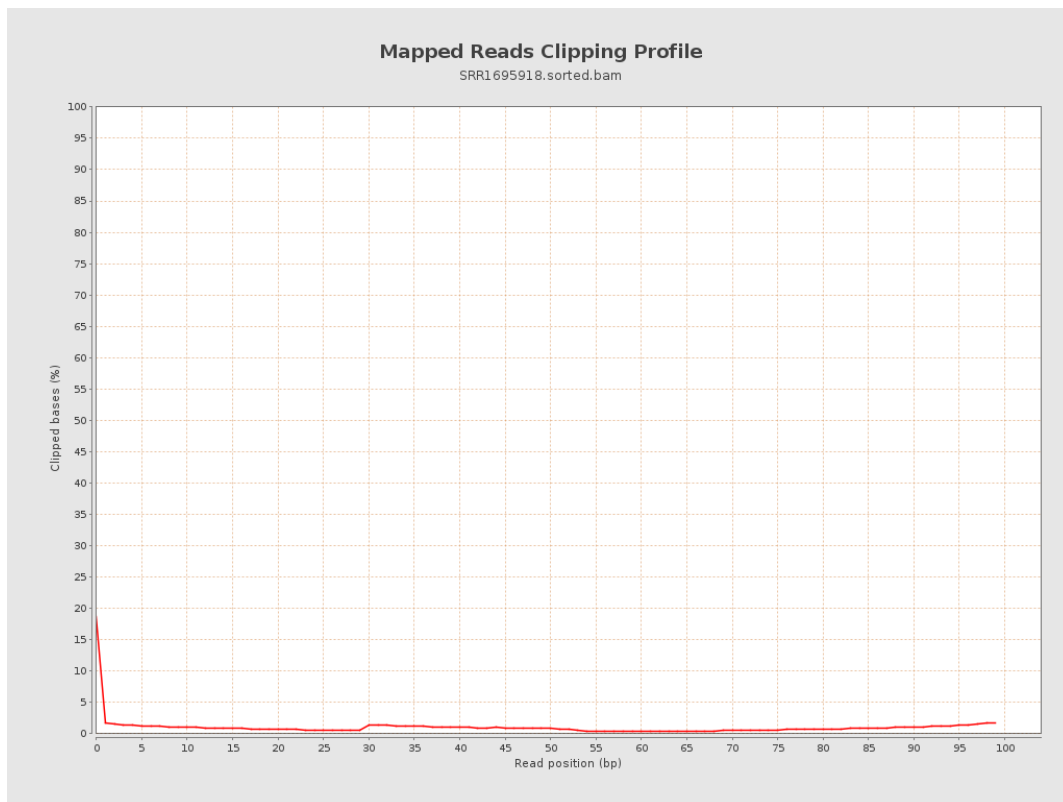
8. Results : Mapped Reads Nucleotide Content



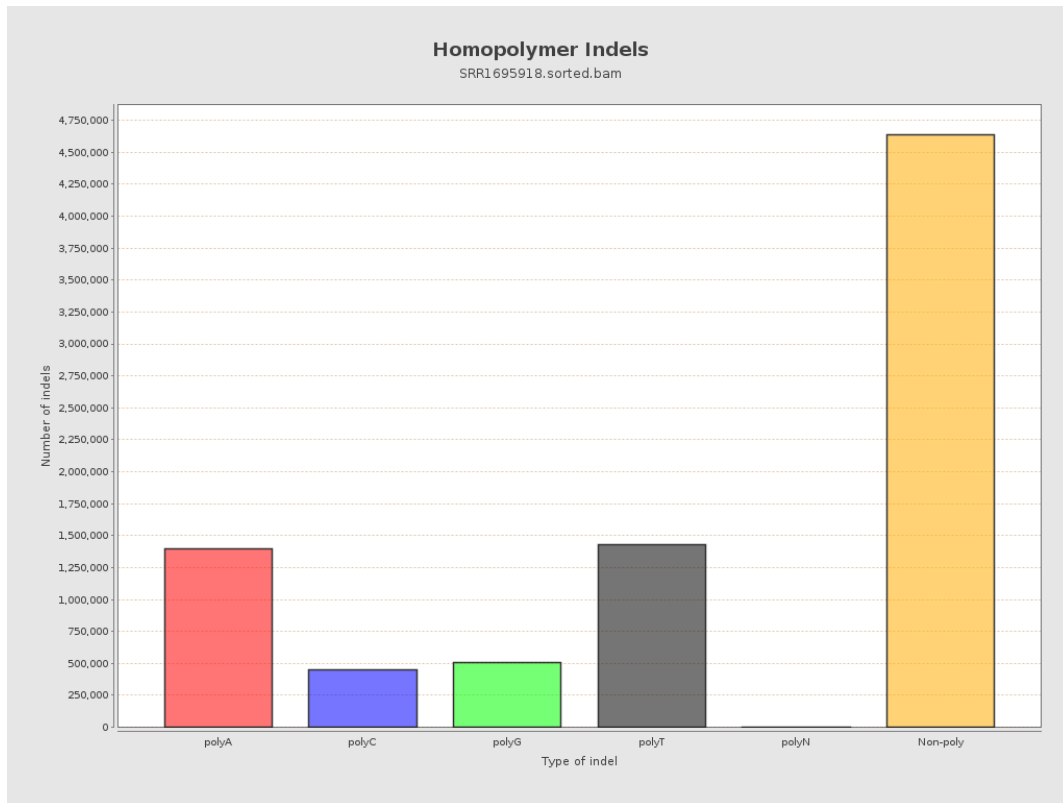
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



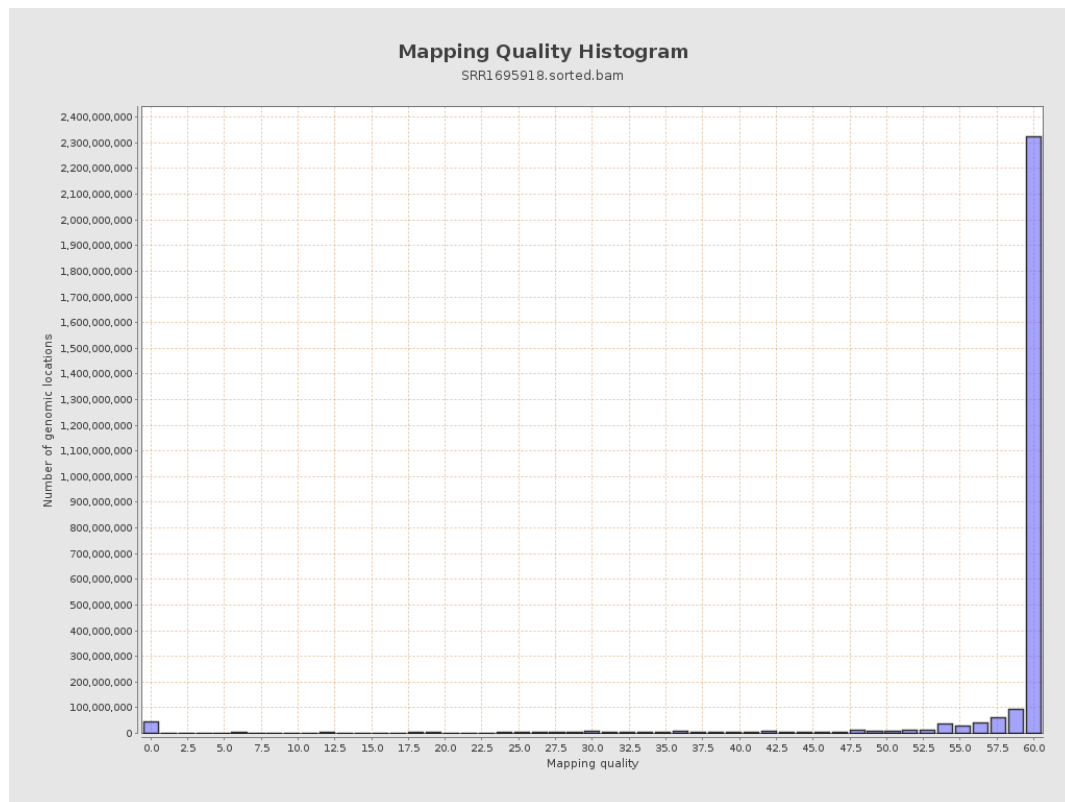
11. Results : Homopolymer Indels



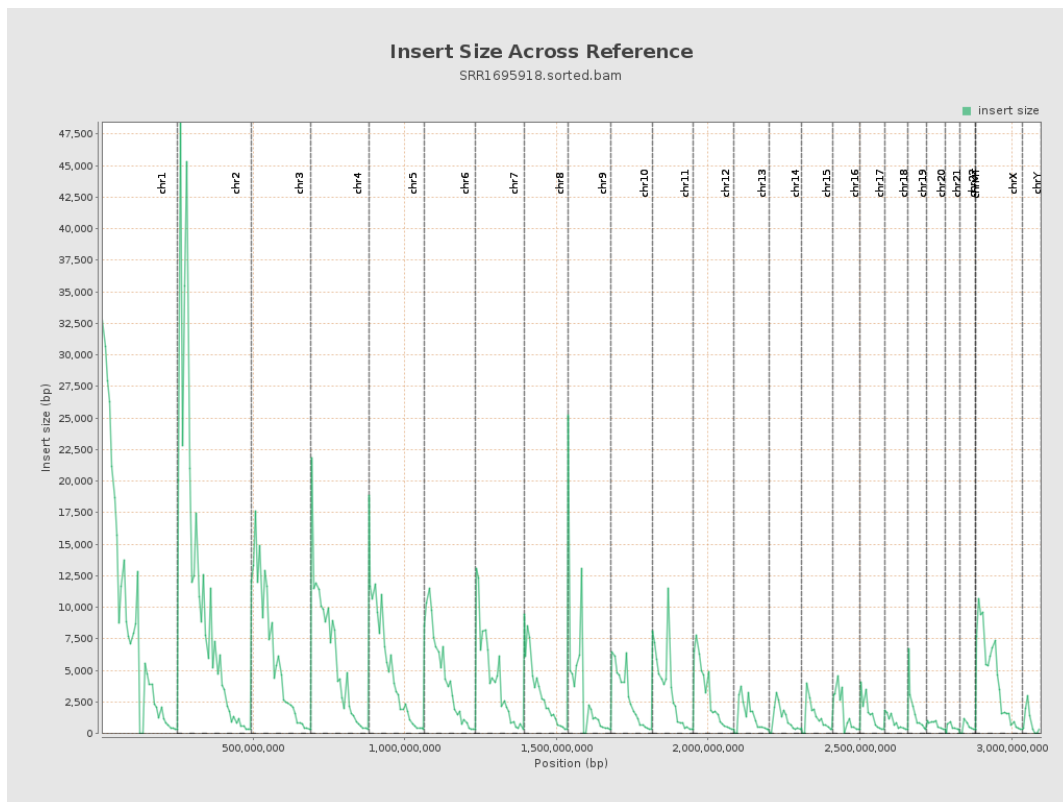
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

