

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/12 20:56:40

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1695921.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 921 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1695921_1.fastq.gz SRR1695921_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 20:56:40 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1695921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	1,946,536
Mapped reads	1,940,213 / 99.68%
Unmapped reads	6,323 / 0.32%
Mapped paired reads	1,940,213 / 99.68%
Mapped reads, first in pair	971,236 / 49.9%
Mapped reads, second in pair	968,977 / 49.78%
Mapped reads, both in pair	1,936,618 / 99.49%
Mapped reads, singletons	3,595 / 0.18%
Secondary alignments	0
Supplementary alignments	55,992 / 2.88%
Read min/max/mean length	30 / 150 / 151.53
Duplicated reads (estimated)	6,520 / 0.33%
Duplication rate	0.27%
Clipped reads	191,336 / 9.83%

2.2. ACGT Content

Number/percentage of A's	85,257,950 / 29.5%
Number/percentage of C's	59,105,076 / 20.45%
Number/percentage of T's	84,773,185 / 29.33%
Number/percentage of G's	59,845,484 / 20.71%
Number/percentage of N's	35,636 / 0.01%

GC Percentage	41.16%
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2.3. Coverage

Mean	0.0934
Standard Deviation	0.3537

2.4. Mapping Quality

Mean Mapping Quality	54.4
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2.5. Insert size

Mean	64,051.91
Standard Deviation	2,478,298.45
P25/Median/P75	278 / 288 / 296

2.6. Mismatches and indels

General error rate	0.4%
Mismatches	1,080,395
Insertions	34,571
Mapped reads with at least one insertion	1.73%
Deletions	32,519
Mapped reads with at least one deletion	1.62%
Homopolymer indels	47.52%

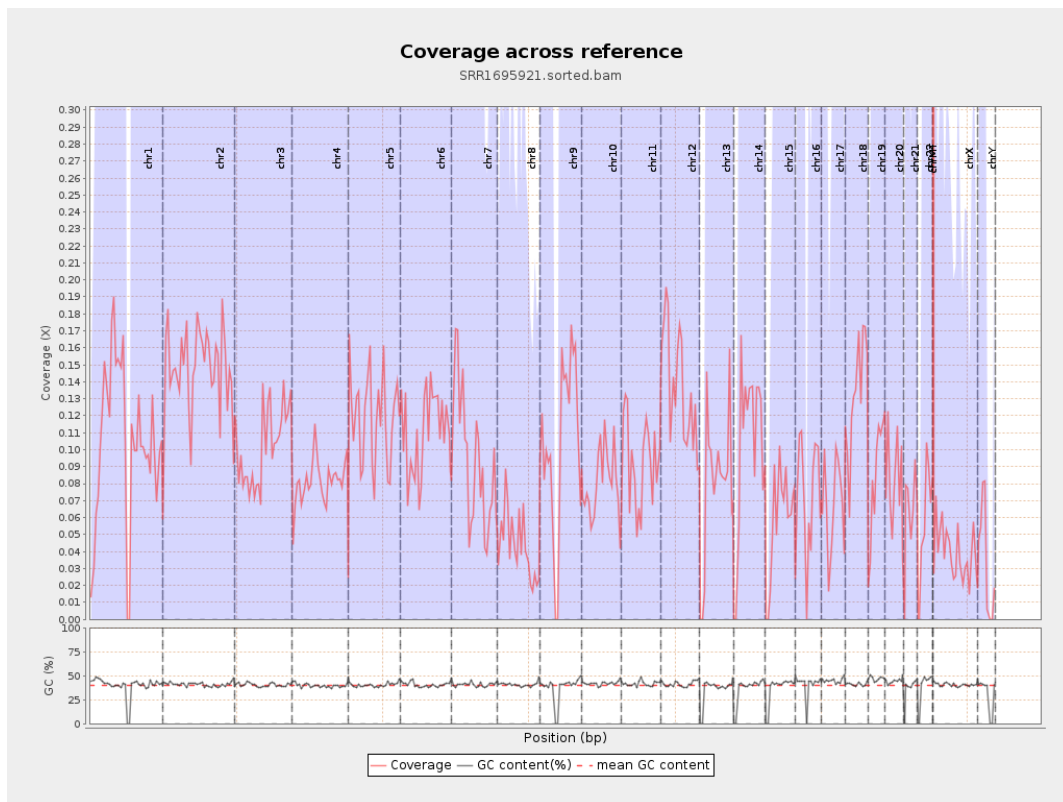
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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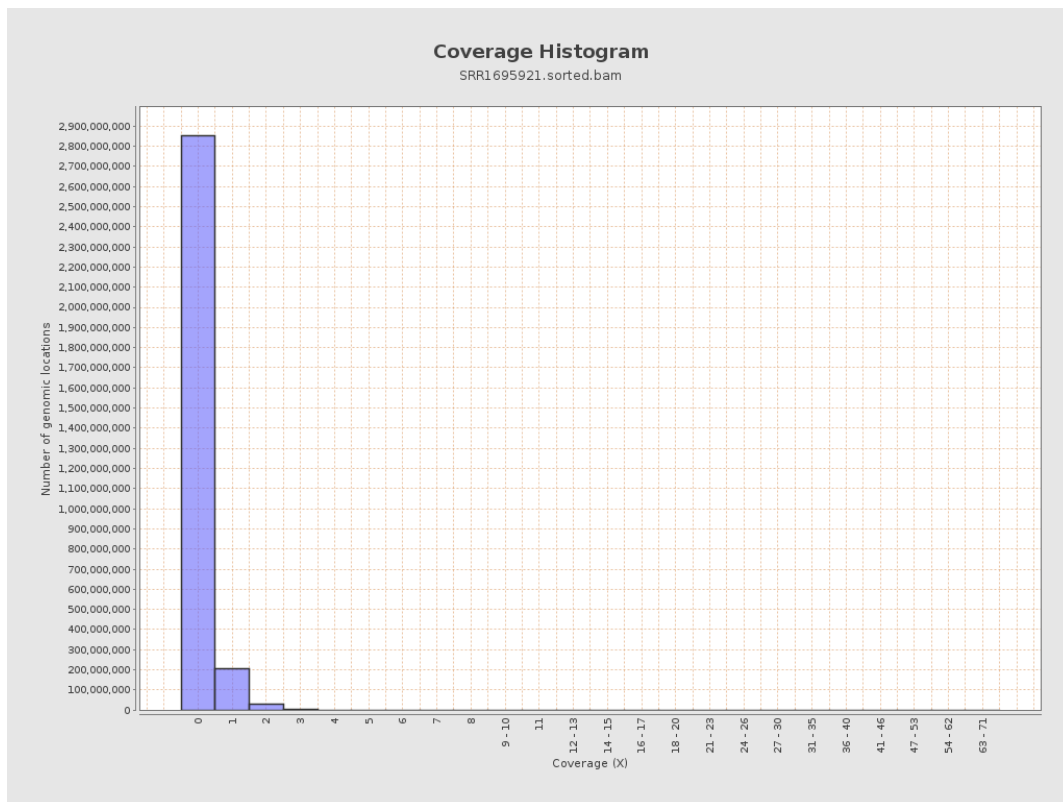
		bases	coverage	deviation
chr1	249250621	25874274	0.1038	0.3763
chr2	243199373	35958390	0.1479	0.4512
chr3	198022430	20156229	0.1018	0.3566
chr4	191154276	15549897	0.0813	0.3368
chr5	180915260	21368215	0.1181	0.3862
chr6	171115067	18894619	0.1104	0.3742
chr7	159138663	14782737	0.0929	0.3443
chr8	146364022	6324600	0.0432	0.2333
chr9	141213431	14727893	0.1043	0.3702
chr10	135534747	10973559	0.081	0.3249
chr11	135006516	12478309	0.0924	0.3434
chr12	133851895	18426782	0.1377	0.4175
chr13	115169878	9320743	0.0809	0.3202
chr14	107349540	11178664	0.1041	0.3655
chr15	102531392	5948789	0.058	0.2715
chr16	90354753	6409370	0.0709	0.3228
chr17	81195210	5632813	0.0694	0.2994
chr18	78077248	10352487	0.1326	0.4154
chr19	59128983	5100669	0.0863	0.3333
chr20	63025520	5171001	0.082	0.3208
chr21	48129895	3139342	0.0652	0.3443
chr22	51304566	2927577	0.0571	0.274
chrMT	16571	256569	15.483	6.5079
chrX	155270560	6038906	0.0389	0.223

chrY	59373566	2109440	0.0355	0.2341
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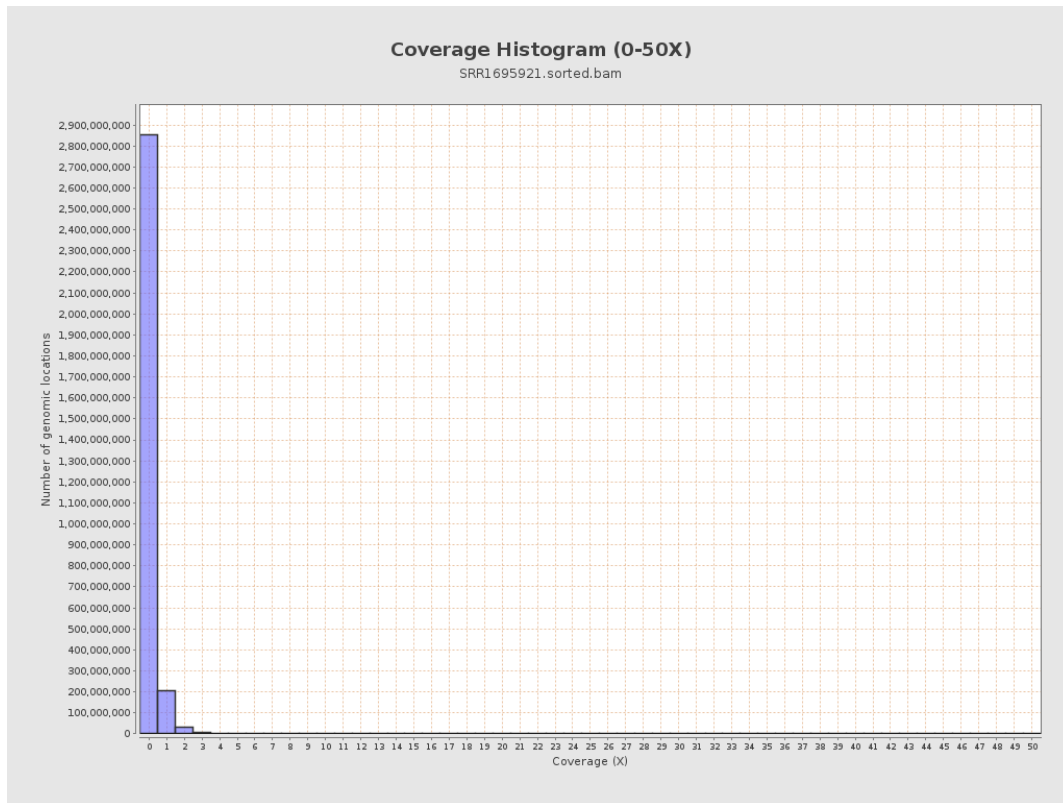
3. Results : Coverage across reference



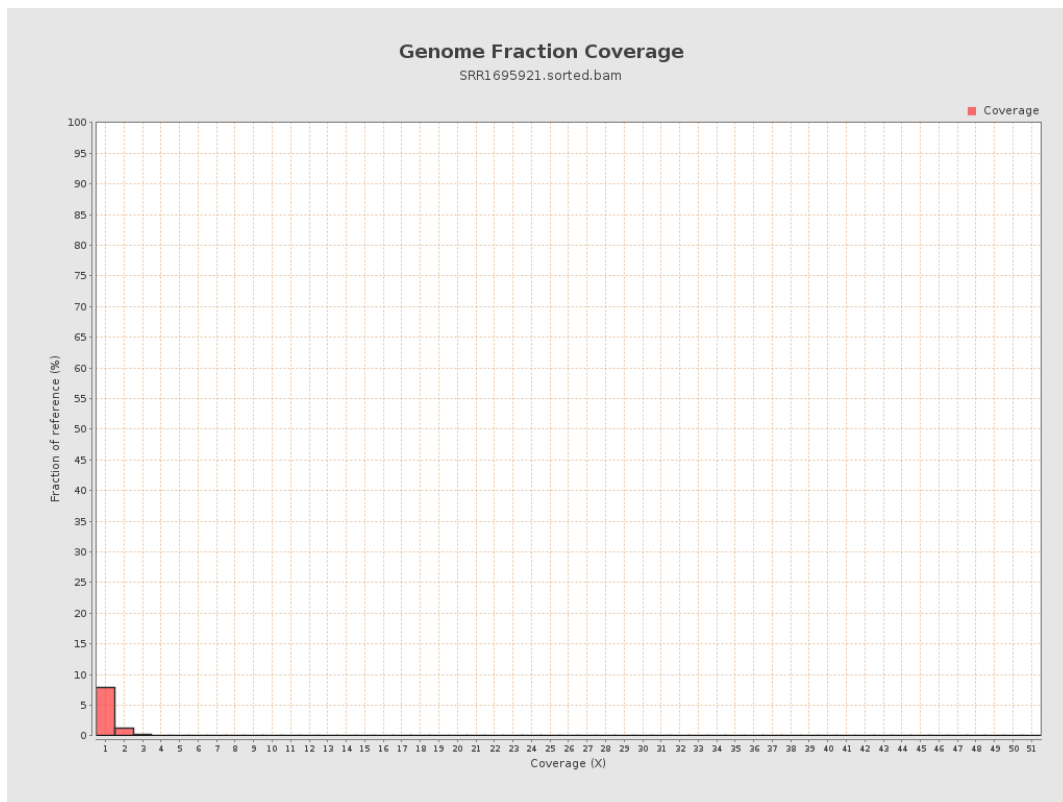
4. Results : Coverage Histogram



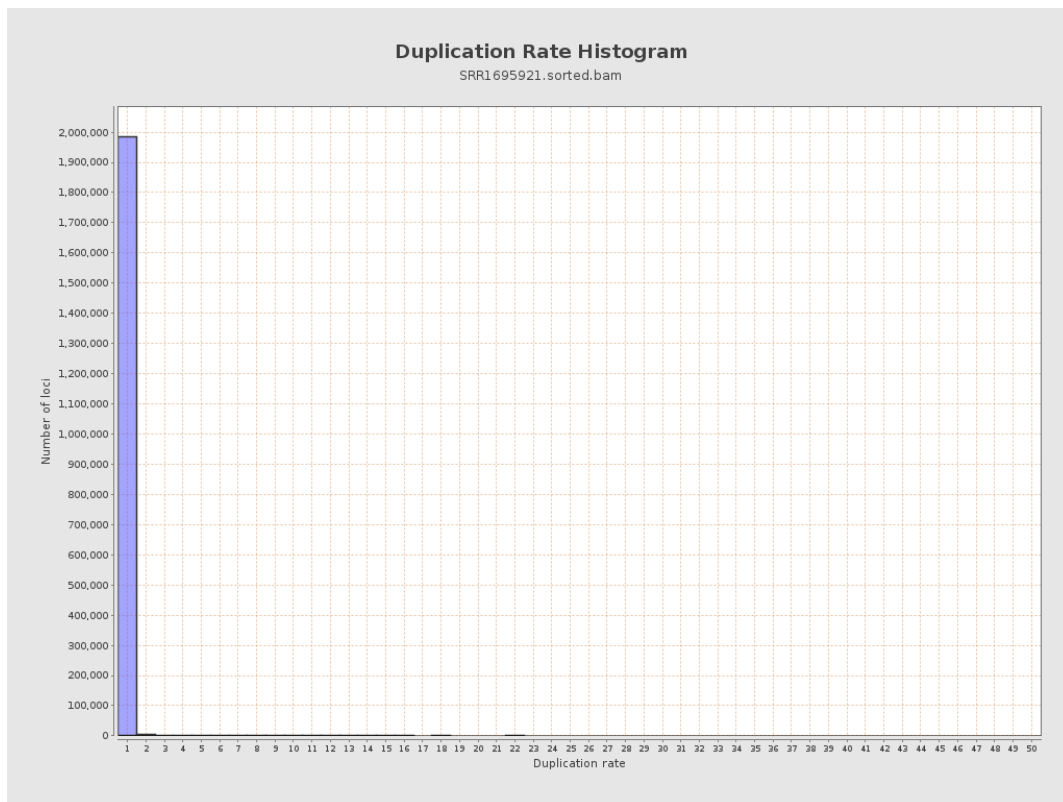
5. Results : Coverage Histogram (0-50X)



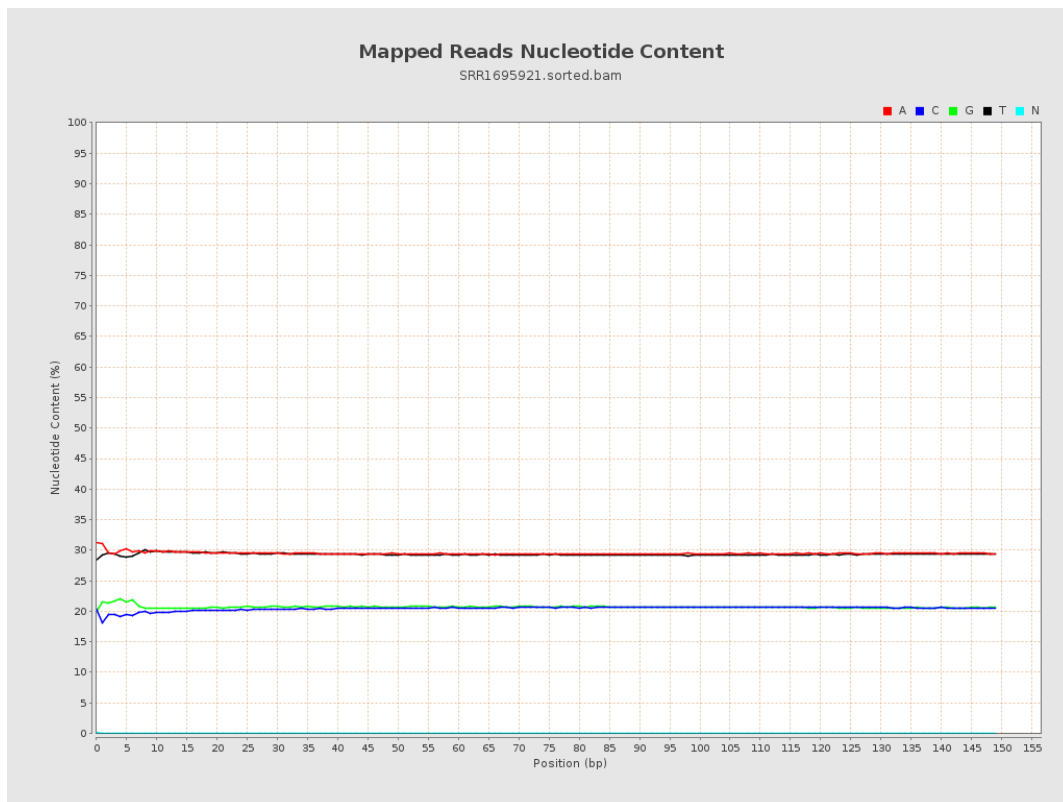
6. Results : Genome Fraction Coverage



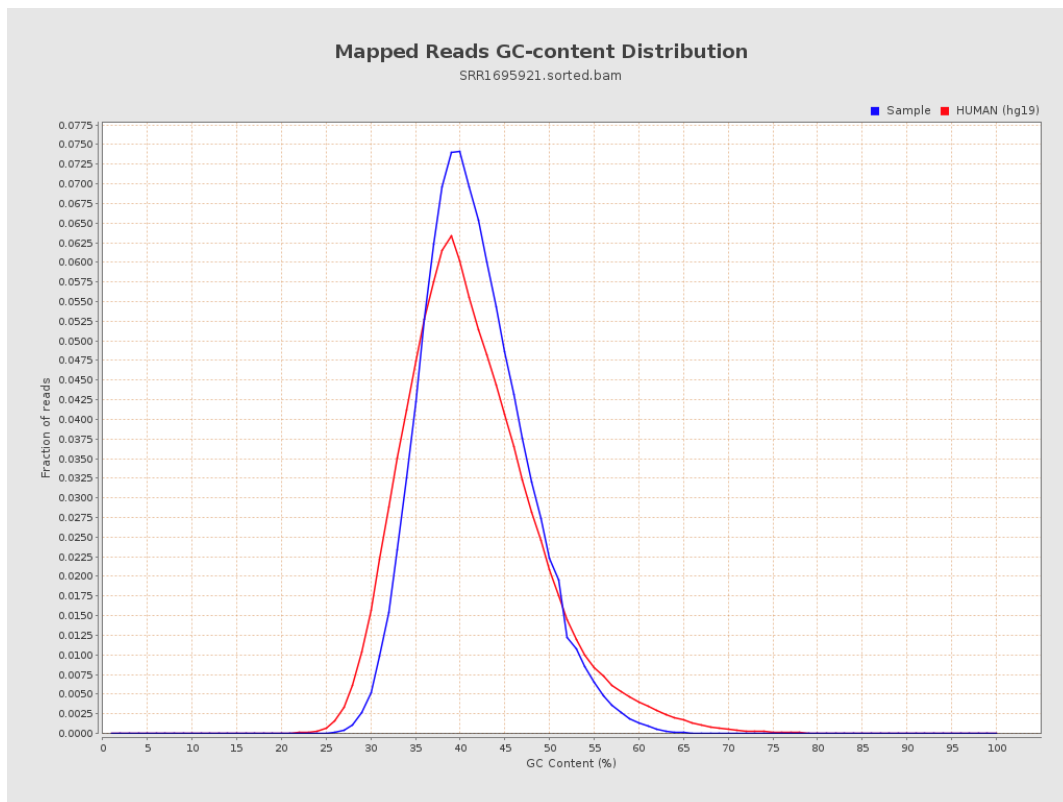
7. Results : Duplication Rate Histogram



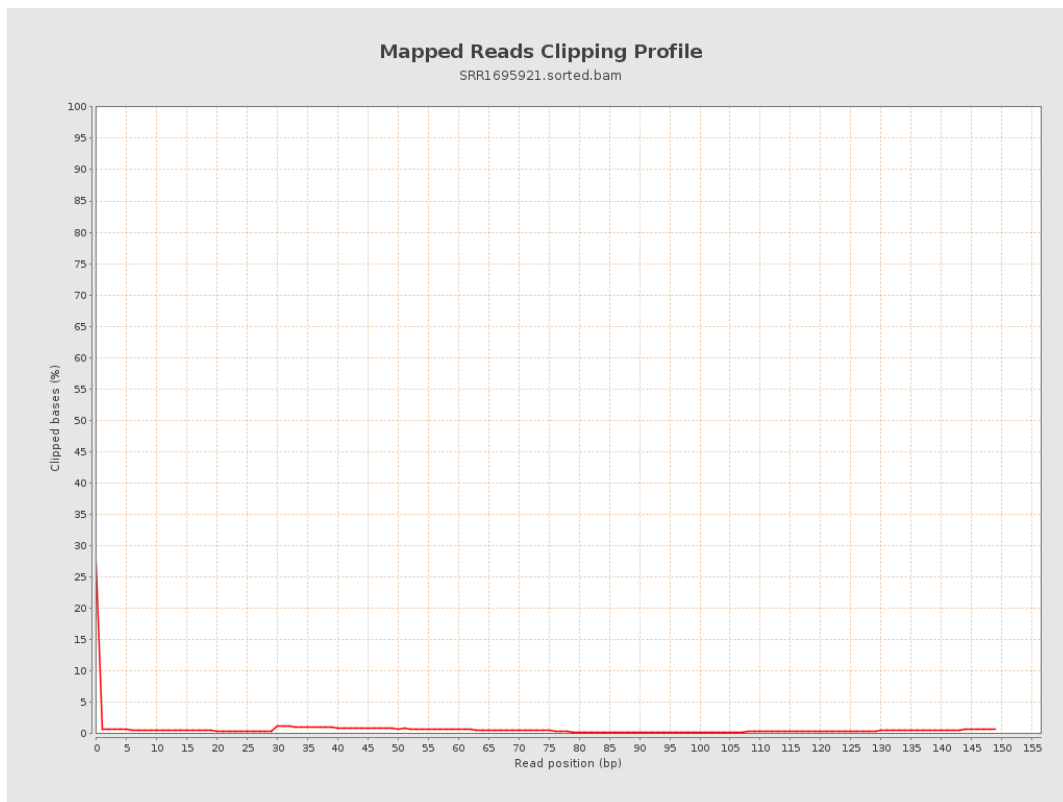
8. Results : Mapped Reads Nucleotide Content



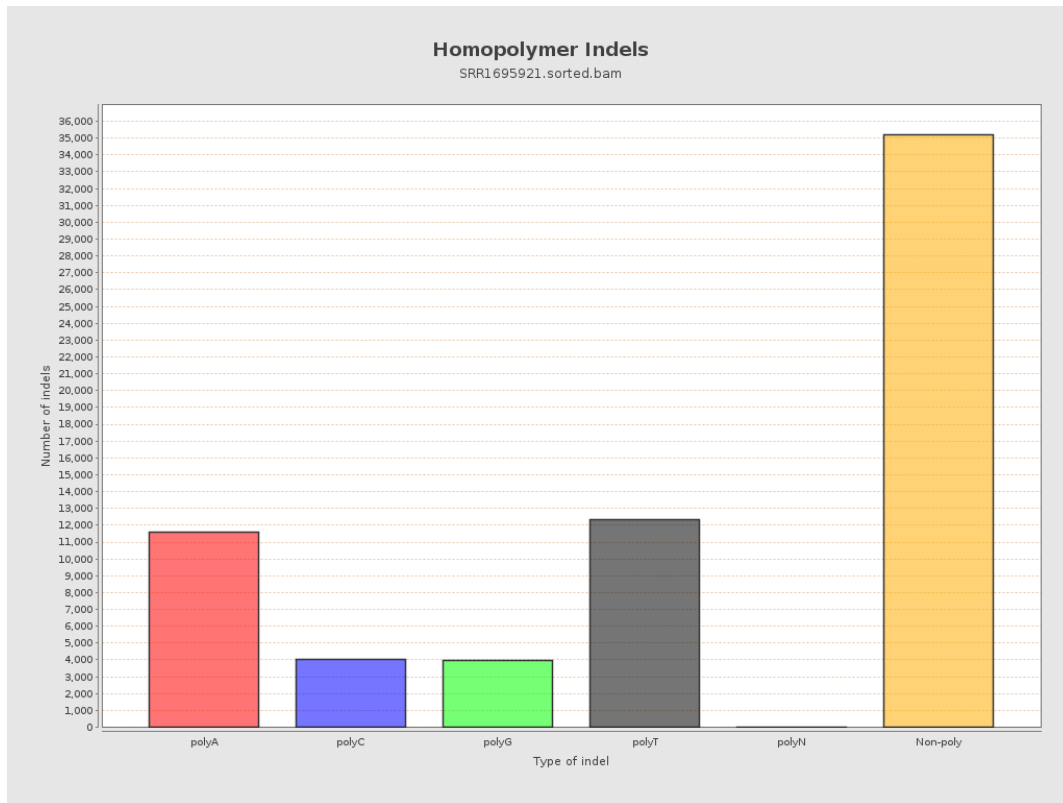
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



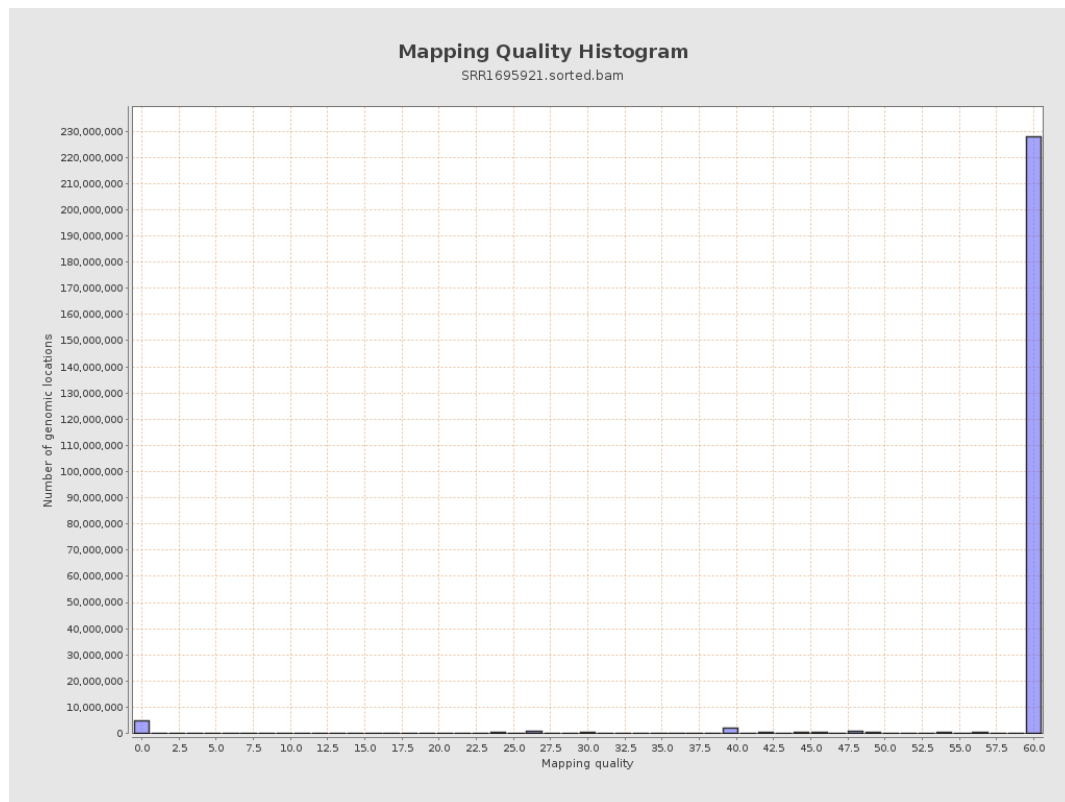
11. Results : Homopolymer Indels



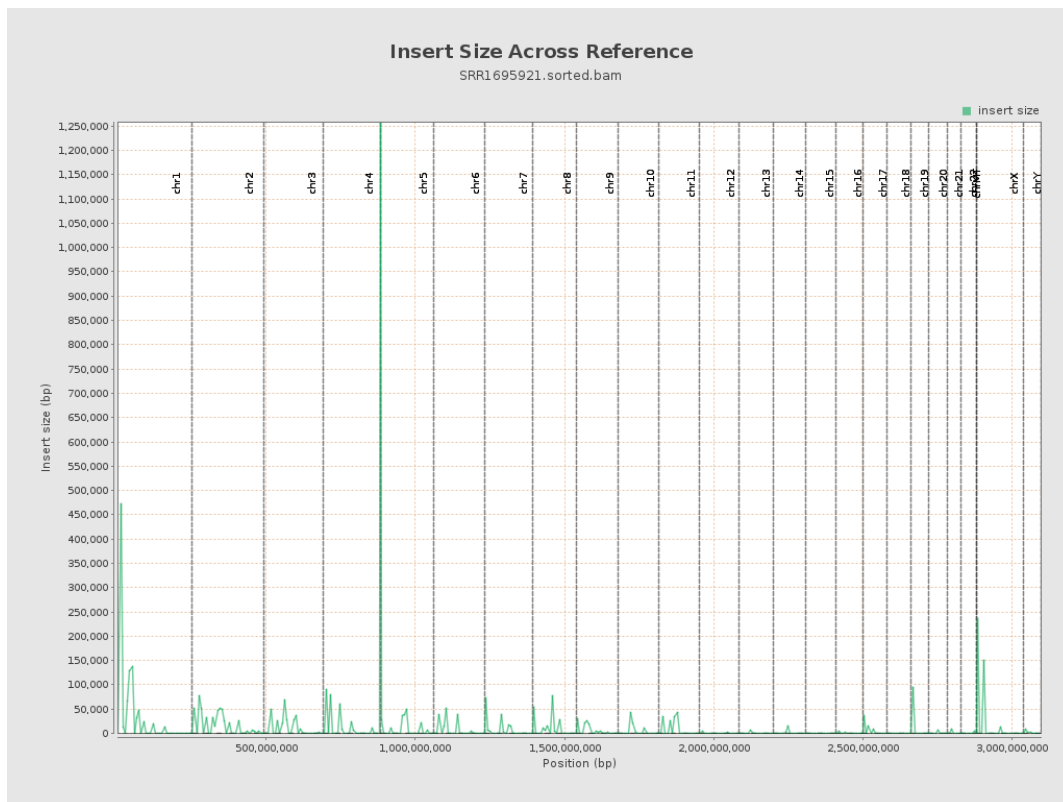
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

