

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 09:38:17

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1954921.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_SRR1954 921 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1954921_1.fastq.gz SRR1954921_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 09:38:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1954921.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,046,350
Mapped reads	14,692,194 / 97.65%
Unmapped reads	354,156 / 2.35%
Mapped paired reads	14,692,194 / 97.65%
Mapped reads, first in pair	7,462,574 / 49.6%
Mapped reads, second in pair	7,229,620 / 48.05%
Mapped reads, both in pair	14,437,440 / 95.95%
Mapped reads, singletons	254,754 / 1.69%
Secondary alignments	0
Supplementary alignments	27,358 / 0.18%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	630,610 / 4.19%
Duplication rate	3.62%
Clipped reads	3,480,461 / 23.13%

2.2. ACGT Content

Number/percentage of A's	392,379,680 / 28.58%
Number/percentage of C's	272,716,957 / 19.86%
Number/percentage of T's	392,087,243 / 28.56%
Number/percentage of G's	315,792,623 / 23%
Number/percentage of N's	71,668 / 0.01%

GC Percentage	42.86%
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2.3. Coverage

Mean	0.4438
Standard Deviation	1.2961

2.4. Mapping Quality

Mean Mapping Quality	54.33
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2.5. Insert size

Mean	31,603.42
Standard Deviation	1,801,115.28
P25/Median/P75	343 / 356 / 369

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	11,796,106
Insertions	229,565
Mapped reads with at least one insertion	1.54%
Deletions	655,121
Mapped reads with at least one deletion	4.36%
Homopolymer indels	54.26%

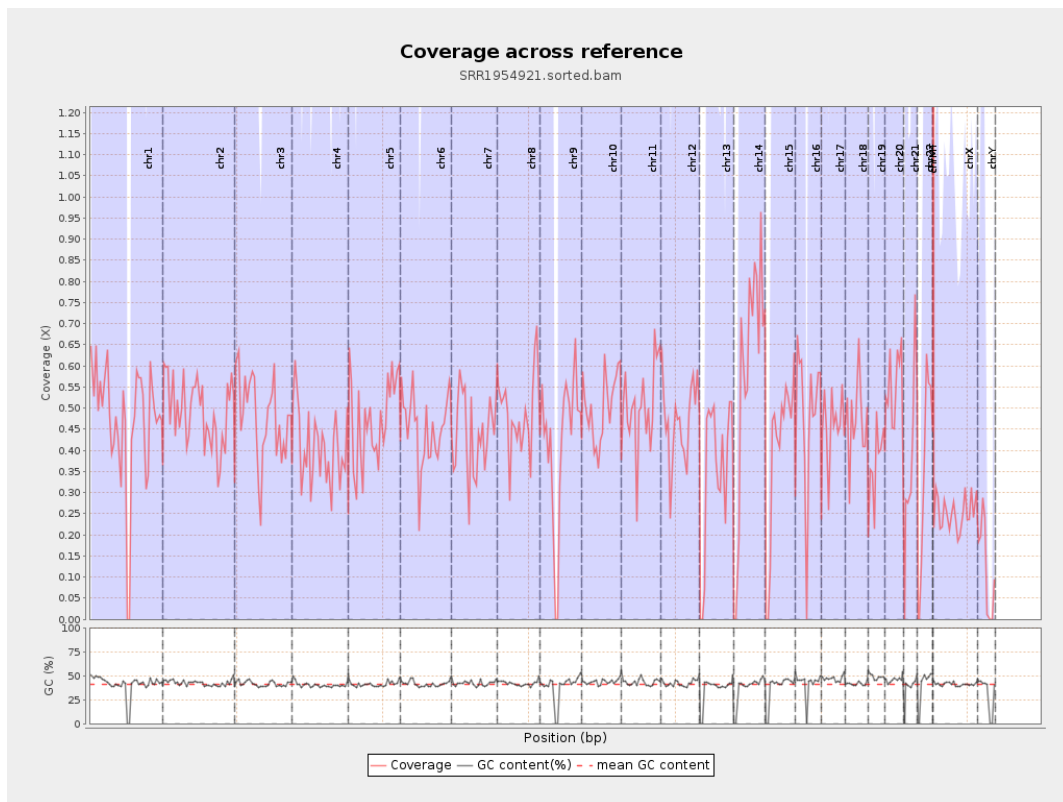
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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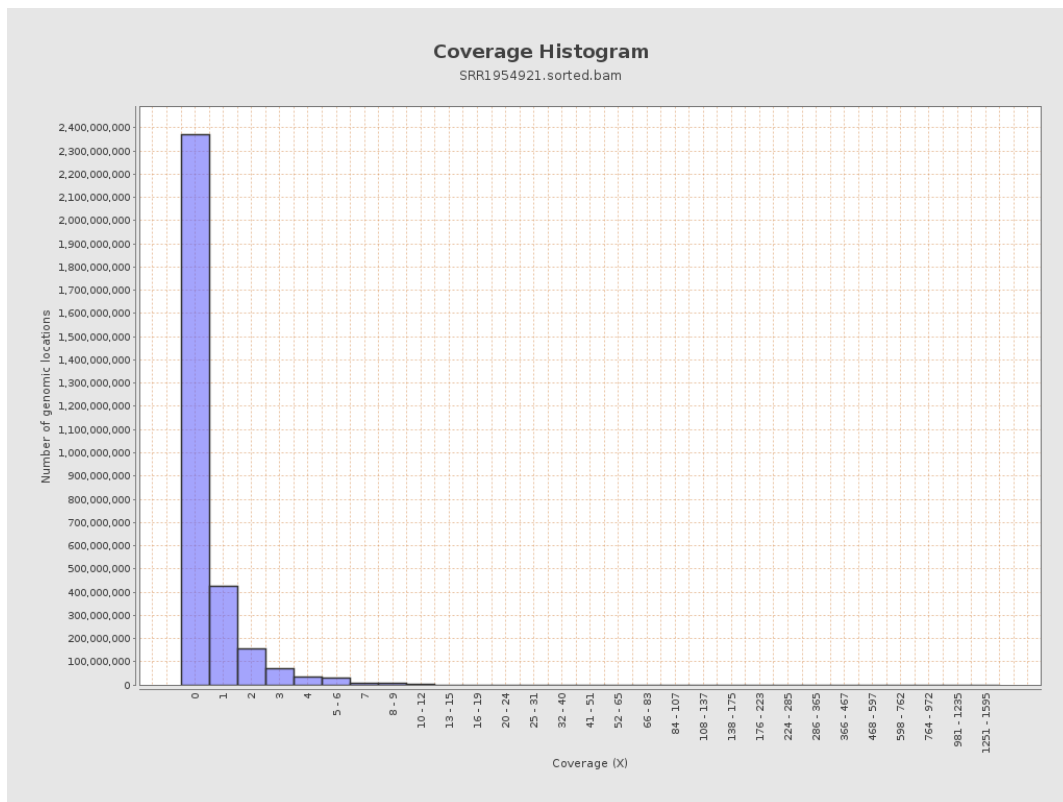
		bases	coverage	deviation
chr1	249250621	116748629	0.4684	1.3793
chr2	243199373	119430296	0.4911	2.0964
chr3	198022430	93876524	0.4741	1.1238
chr4	191154276	78290481	0.4096	1.1163
chr5	180915260	85599849	0.4731	1.1174
chr6	171115067	77329401	0.4519	1.102
chr7	159138663	69620536	0.4375	1.0969
chr8	146364022	71238937	0.4867	1.1967
chr9	141213431	59392942	0.4206	1.385
chr10	135534747	67960288	0.5014	1.2649
chr11	135006516	67957971	0.5034	1.2894
chr12	133851895	63398706	0.4736	1.144
chr13	115169878	40575819	0.3523	0.9578
chr14	107349540	63172433	0.5885	1.4152
chr15	102531392	40678998	0.3967	1.0632
chr16	90354753	43392709	0.4802	1.5283
chr17	81195210	37591604	0.463	1.1966
chr18	78077248	36716539	0.4703	1.5912
chr19	59128983	21956415	0.3713	1.1157
chr20	63025520	35025259	0.5557	1.2974
chr21	48129895	18806776	0.3908	1.4596
chr22	51304566	18408973	0.3588	1.0622
chrMT	16571	206657	12.471	9.1361
chrX	155270560	39204656	0.2525	0.7495

chrY	59373566	7369279	0.1241	0.768
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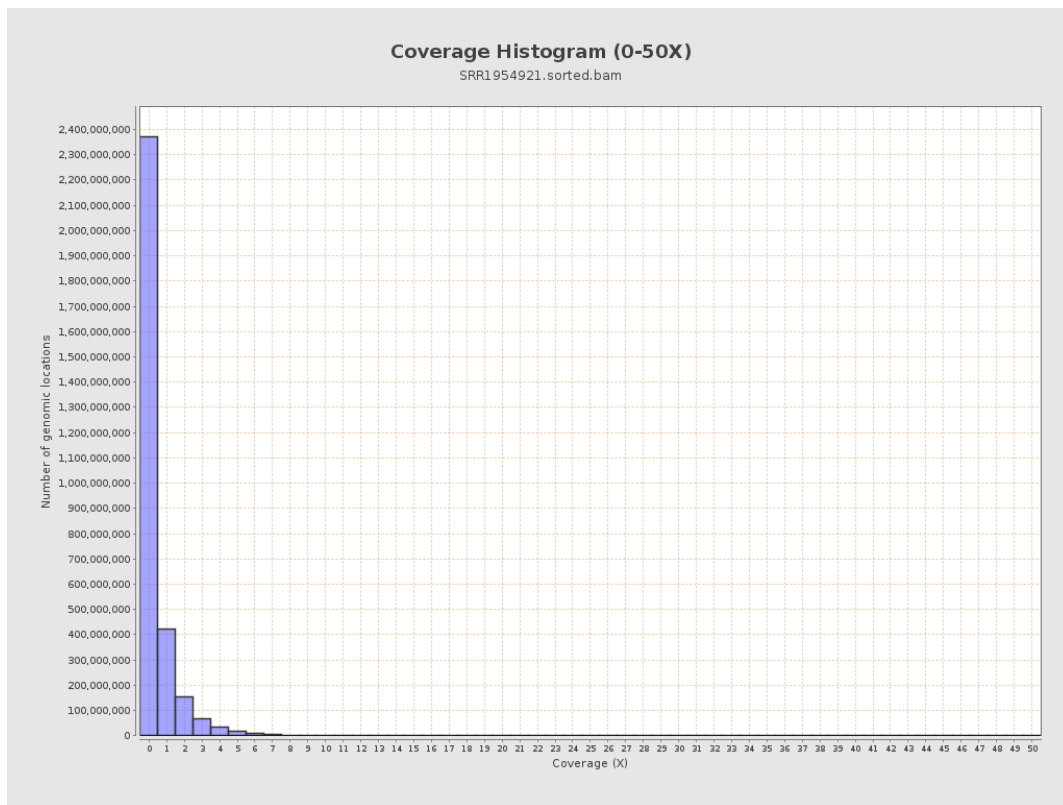
3. Results : Coverage across reference



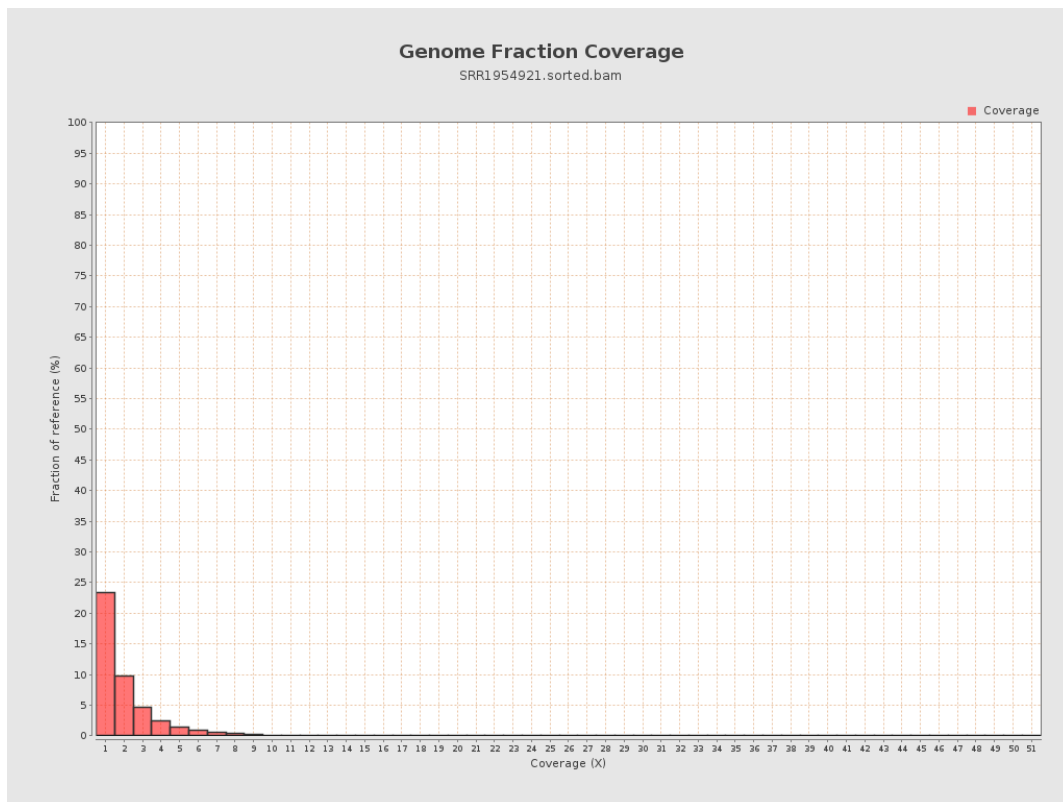
4. Results : Coverage Histogram



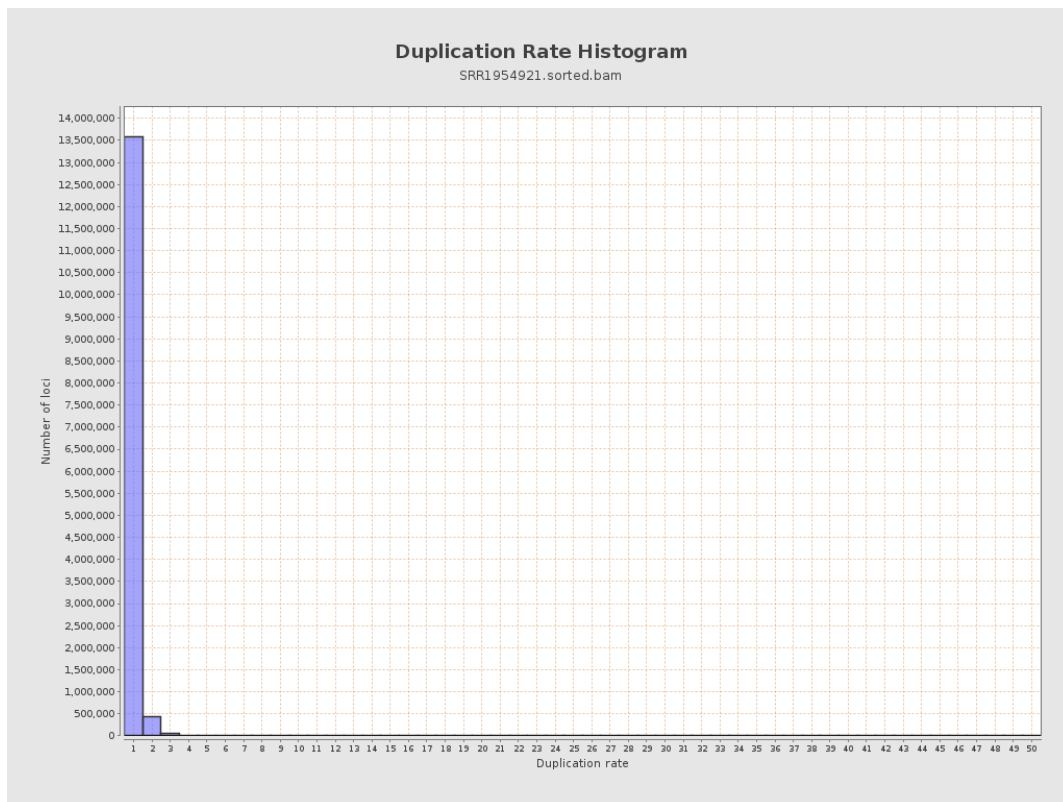
5. Results : Coverage Histogram (0-50X)



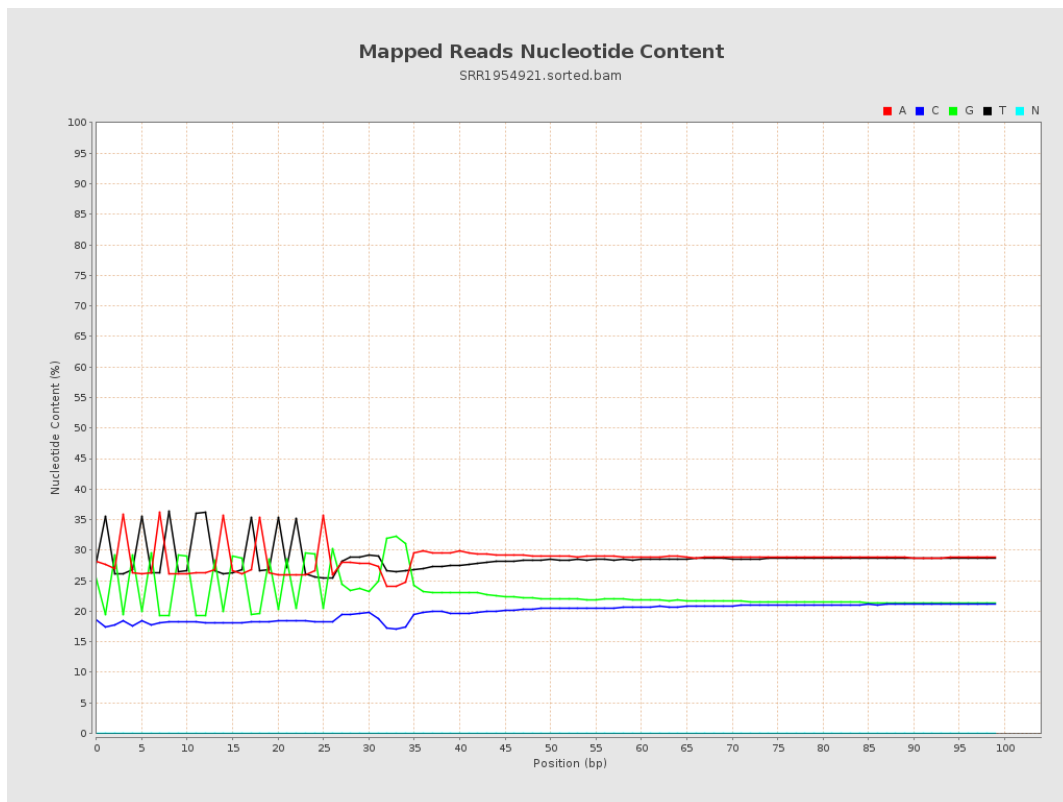
6. Results : Genome Fraction Coverage



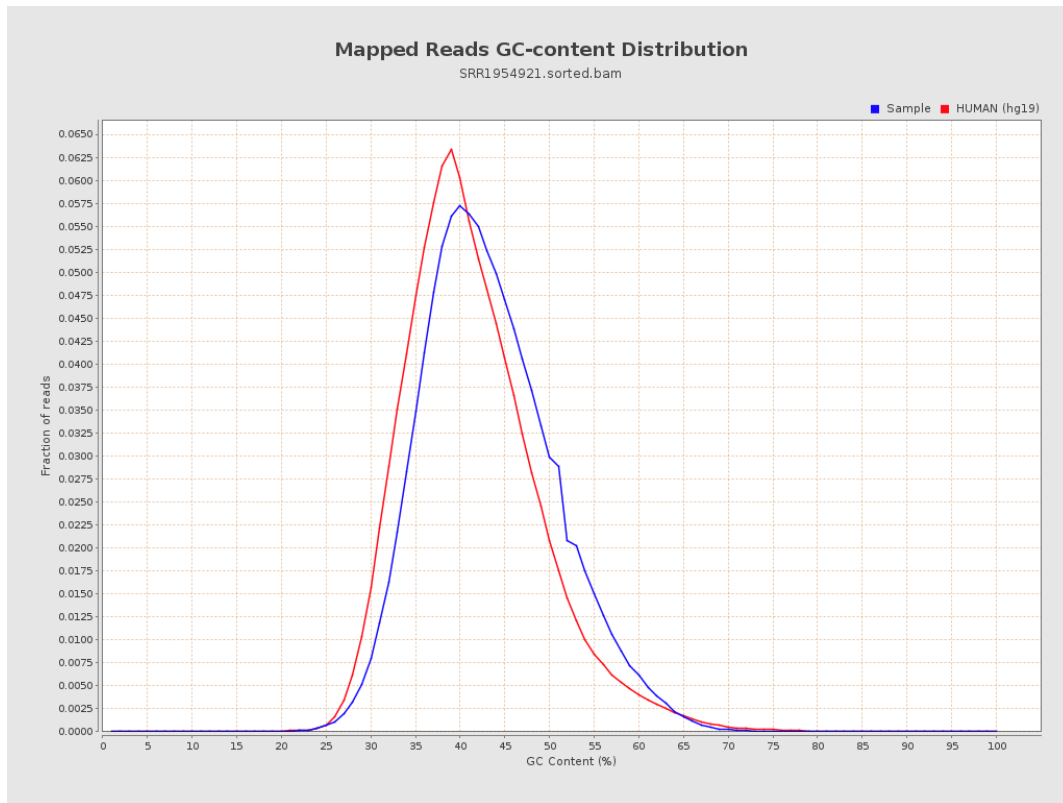
7. Results : Duplication Rate Histogram



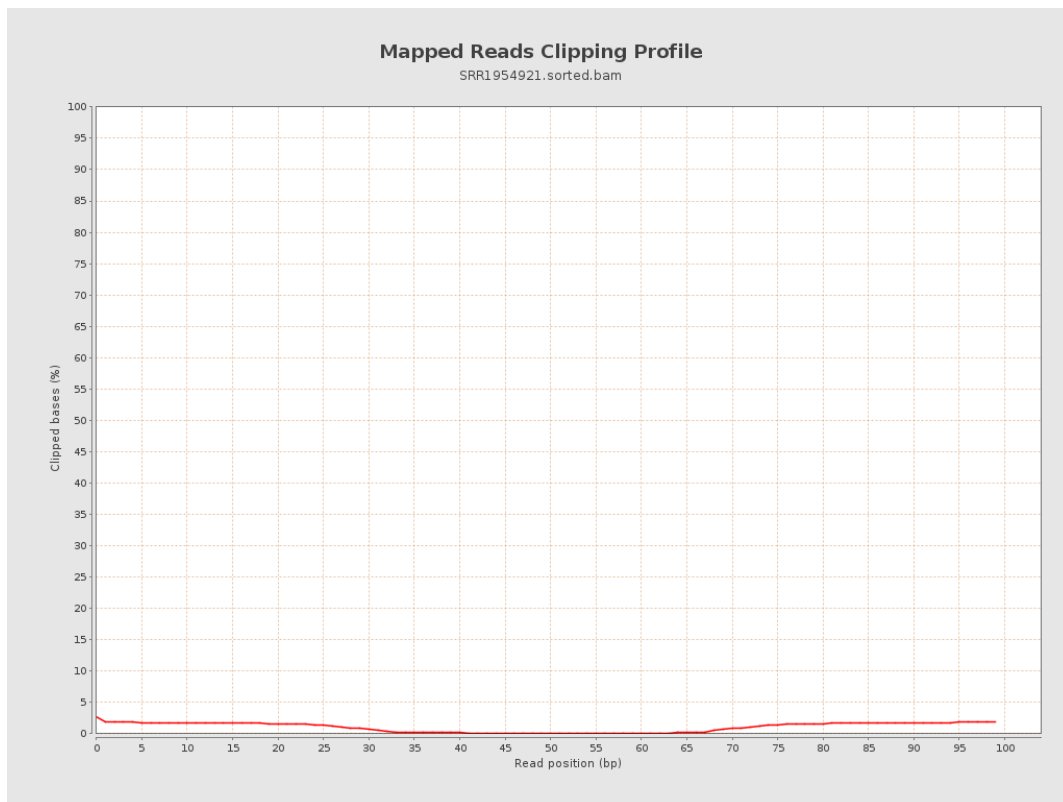
8. Results : Mapped Reads Nucleotide Content



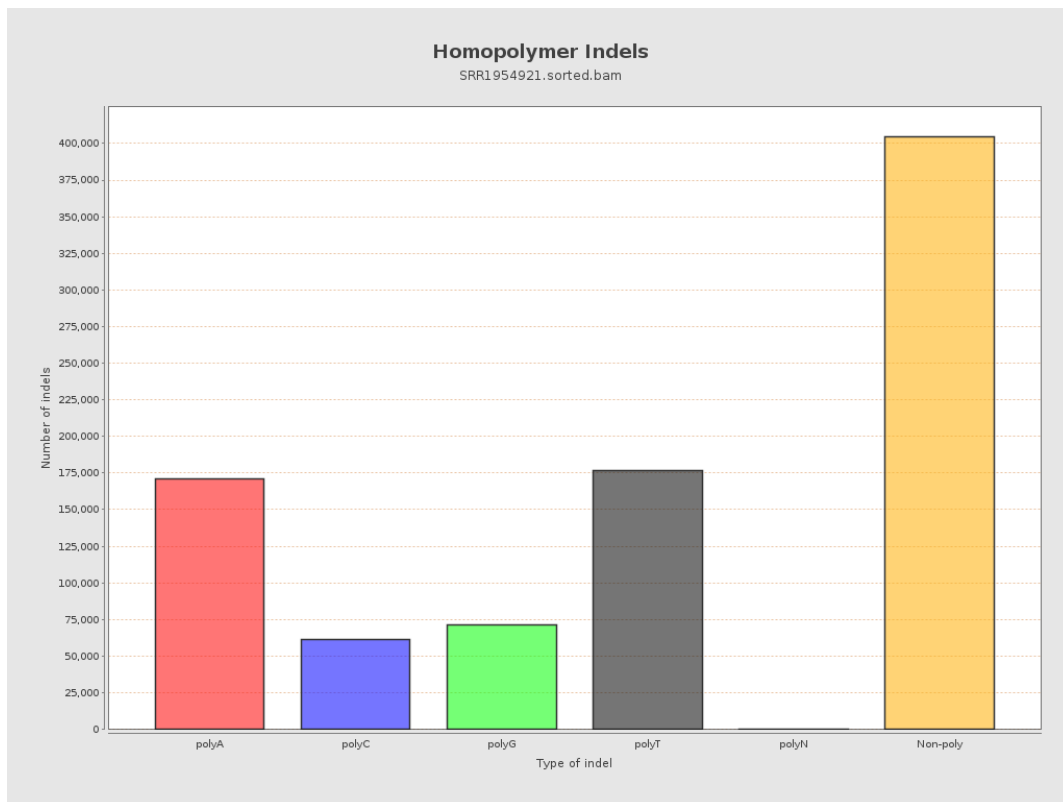
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



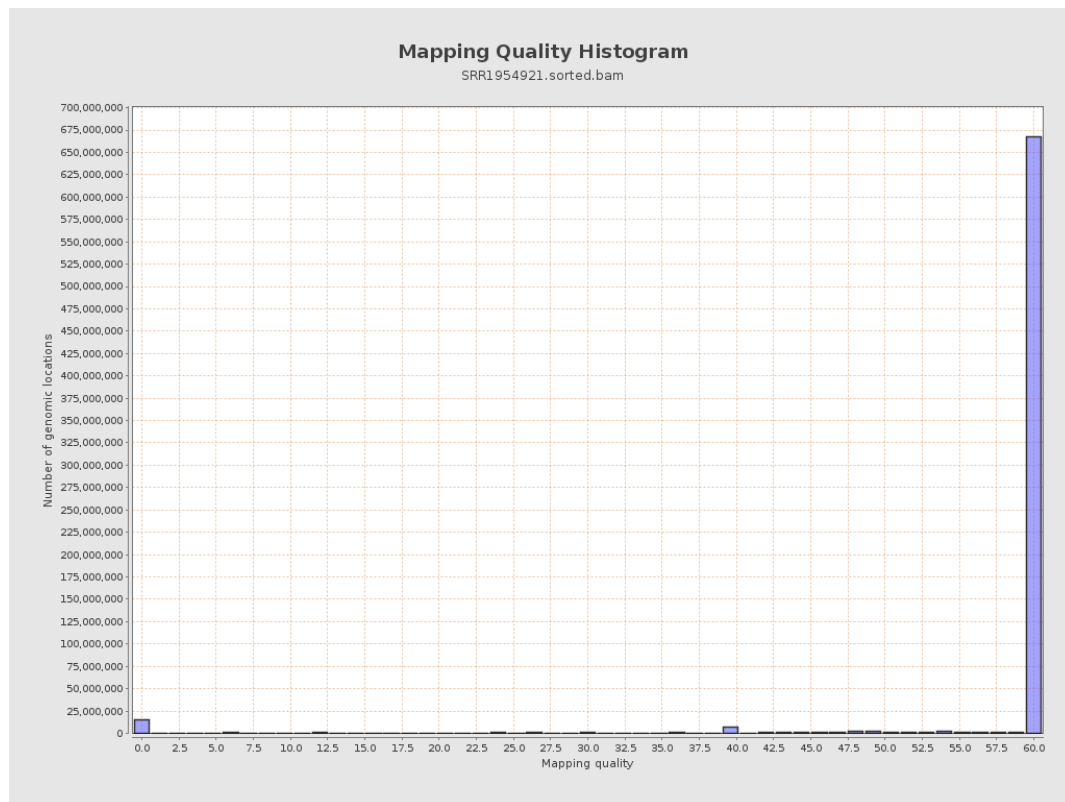
11. Results : Homopolymer Indels



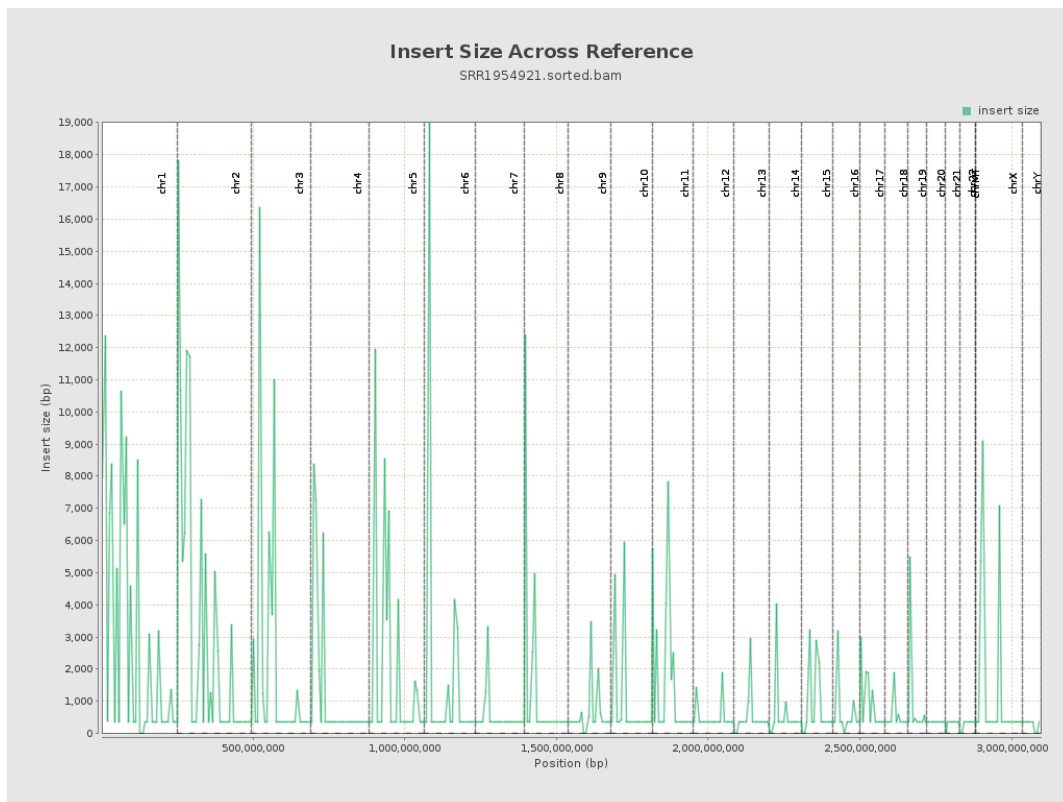
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

