

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 09:45:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1954922.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 922 /seu_share/home/tujing/220232460/r eference/homo_bwa/hsa.fa SRR1954922_1.fastq.gz SRR1954922_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 09:45:00 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1954922.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	15,390,318
Mapped reads	15,041,202 / 97.73%
Unmapped reads	349,116 / 2.27%
Mapped paired reads	15,041,202 / 97.73%
Mapped reads, first in pair	7,633,860 / 49.6%
Mapped reads, second in pair	7,407,342 / 48.13%
Mapped reads, both in pair	14,792,316 / 96.11%
Mapped reads, singletons	248,886 / 1.62%
Secondary alignments	0
Supplementary alignments	28,186 / 0.18%
Read min/max/mean length	30 / 100 / 100.07
Duplicated reads (estimated)	659,699 / 4.29%
Duplication rate	3.69%
Clipped reads	3,551,332 / 23.08%

2.2. ACGT Content

Number/percentage of A's	402,191,153 / 28.61%
Number/percentage of C's	278,892,717 / 19.84%
Number/percentage of T's	401,917,896 / 28.59%
Number/percentage of G's	322,920,917 / 22.97%
Number/percentage of N's	37,654 / 0%

GC Percentage	42.8%
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2.3. Coverage

Mean	0.4545
Standard Deviation	1.3268

2.4. Mapping Quality

Mean Mapping Quality	54.31
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2.5. Insert size

Mean	32,841.88
Standard Deviation	1,833,951.16
P25/Median/P75	343 / 356 / 369

2.6. Mismatches and indels

General error rate	0.86%
Mismatches	11,722,269
Insertions	235,087
Mapped reads with at least one insertion	1.54%
Deletions	671,697
Mapped reads with at least one deletion	4.36%
Homopolymer indels	54.25%

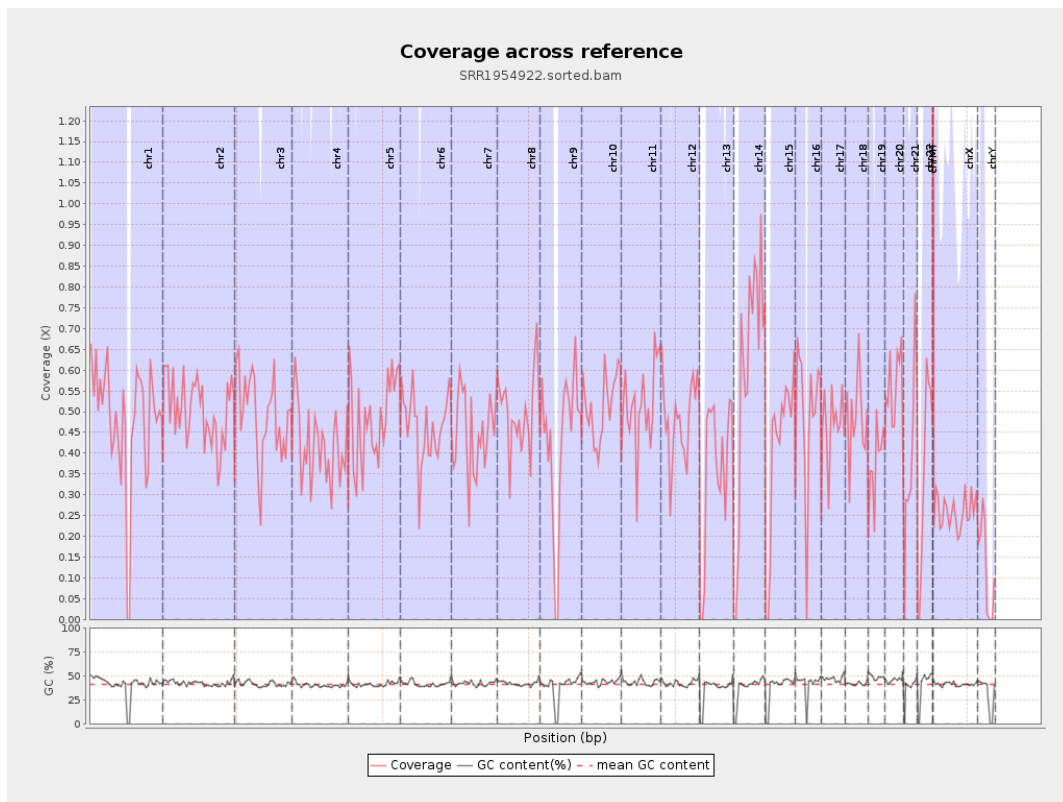
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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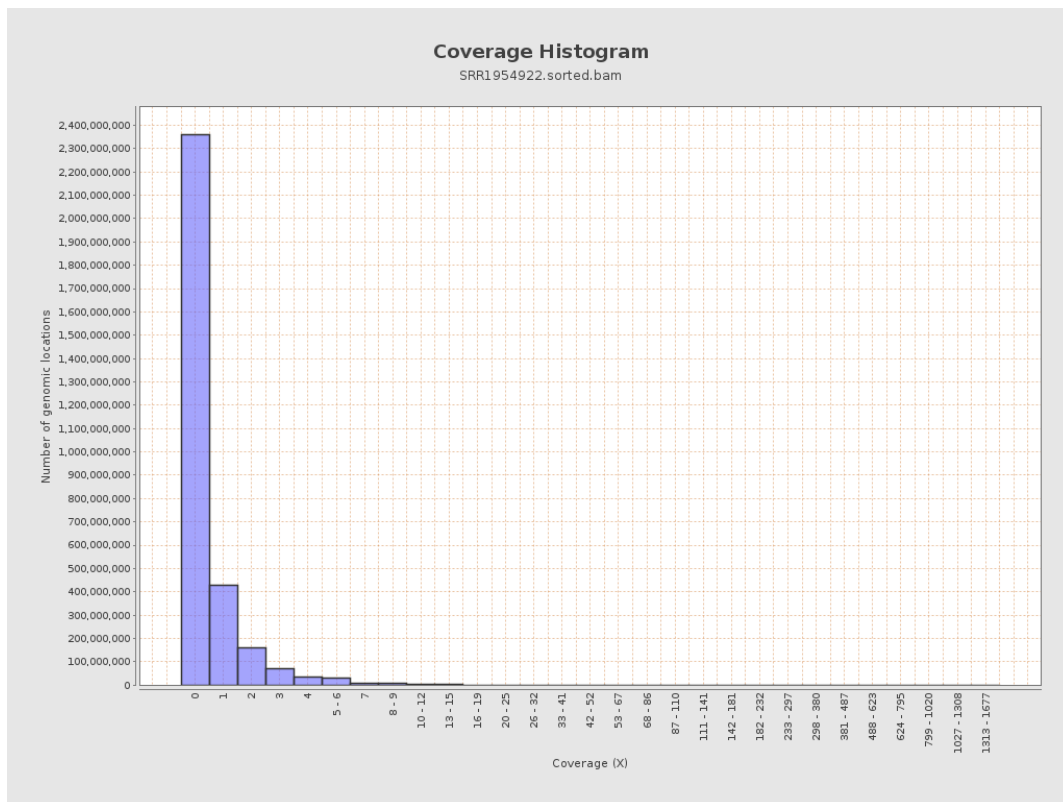
		bases	coverage	deviation
chr1	249250621	119537102	0.4796	1.4179
chr2	243199373	122412517	0.5033	2.1605
chr3	198022430	96124479	0.4854	1.1439
chr4	191154276	80384025	0.4205	1.1369
chr5	180915260	87923857	0.486	1.1444
chr6	171115067	79465224	0.4644	1.1251
chr7	159138663	71211601	0.4475	1.1231
chr8	146364022	72932418	0.4983	1.2187
chr9	141213431	60794327	0.4305	1.4364
chr10	135534747	69628688	0.5137	1.2861
chr11	135006516	69435562	0.5143	1.3324
chr12	133851895	64917932	0.485	1.1673
chr13	115169878	41528715	0.3606	0.9753
chr14	107349540	64484257	0.6007	1.4439
chr15	102531392	41709068	0.4068	1.0882
chr16	90354753	44219044	0.4894	1.5379
chr17	81195210	38379544	0.4727	1.2349
chr18	78077248	37729481	0.4832	1.6149
chr19	59128983	22376505	0.3784	1.1322
chr20	63025520	35695624	0.5664	1.3228
chr21	48129895	19306213	0.4011	1.474
chr22	51304566	18643776	0.3634	1.0712
chrMT	16571	227913	13.7537	10.8902
chrX	155270560	40312438	0.2596	0.7663

chrY	59373566	7503130	0.1264	0.776
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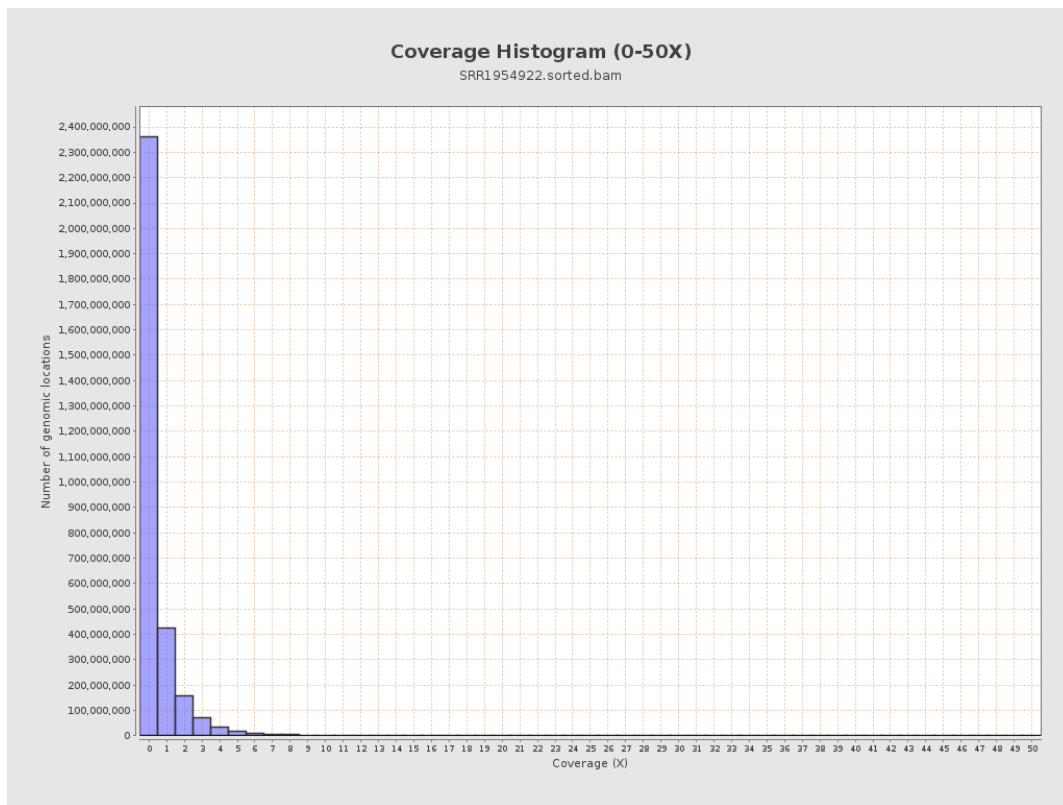
3. Results : Coverage across reference



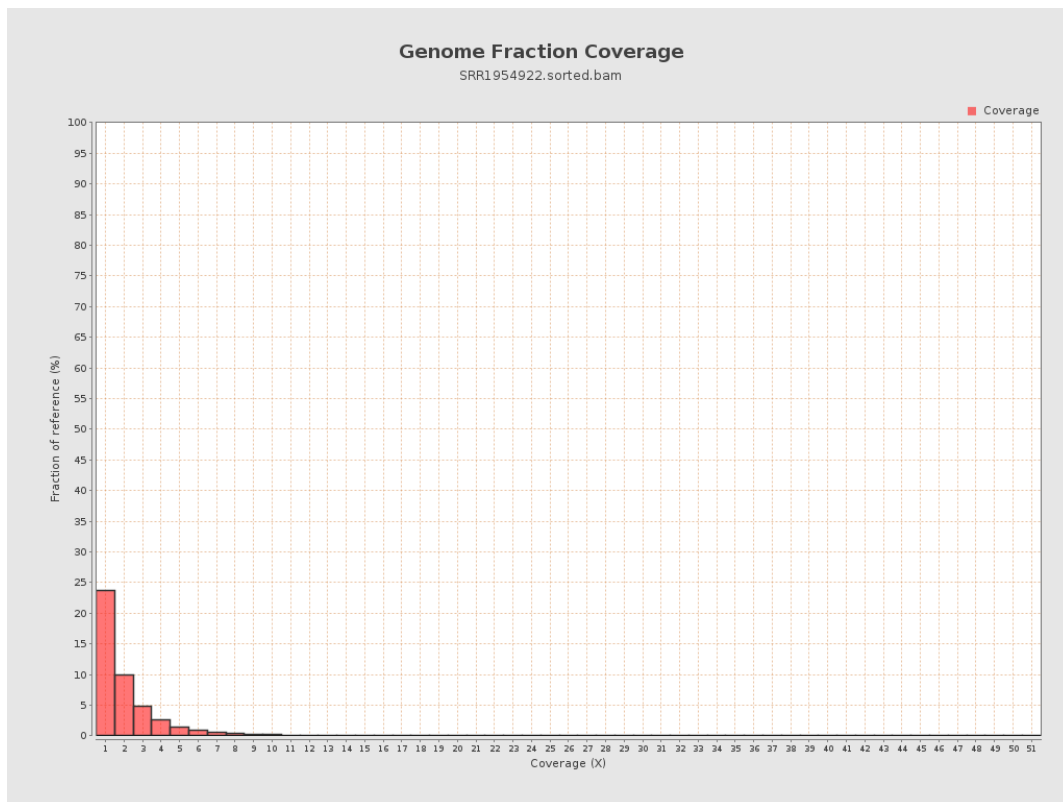
4. Results : Coverage Histogram



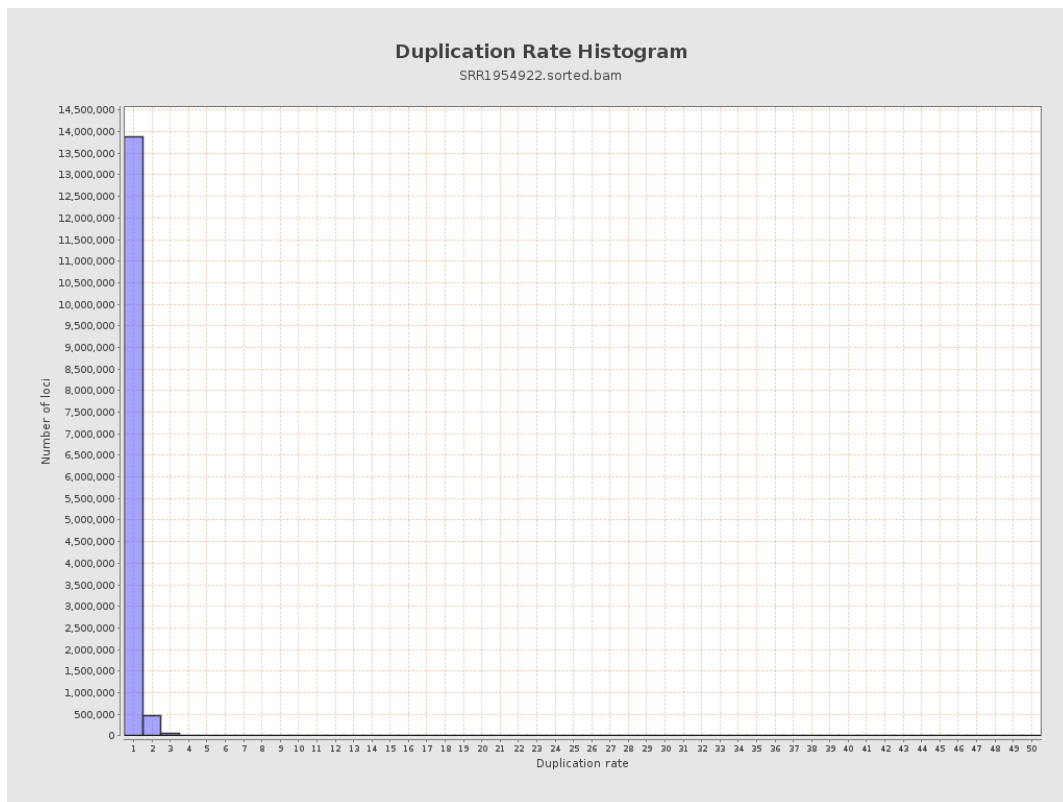
5. Results : Coverage Histogram (0-50X)



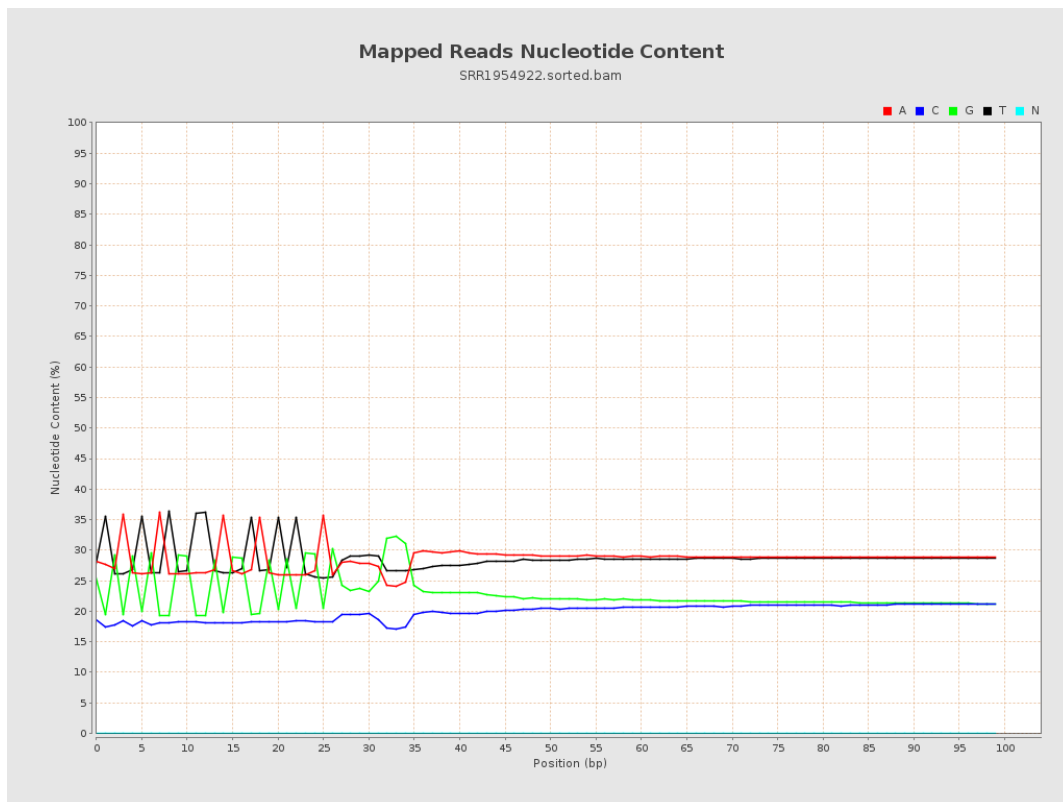
6. Results : Genome Fraction Coverage



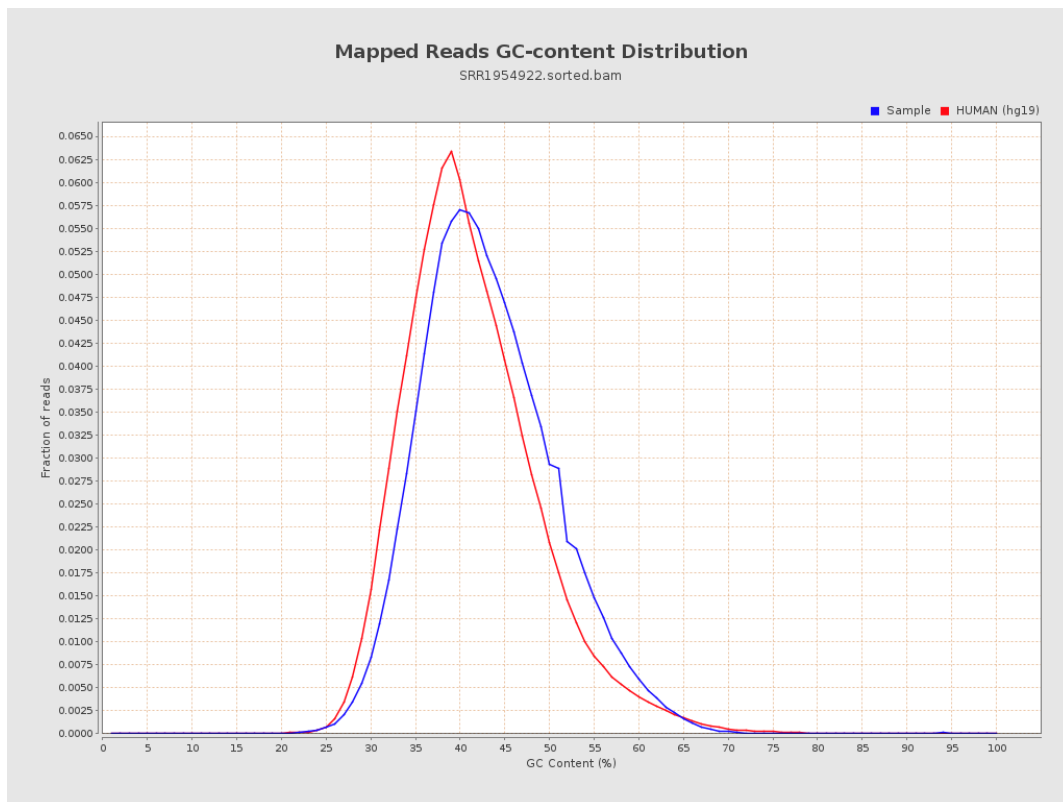
7. Results : Duplication Rate Histogram



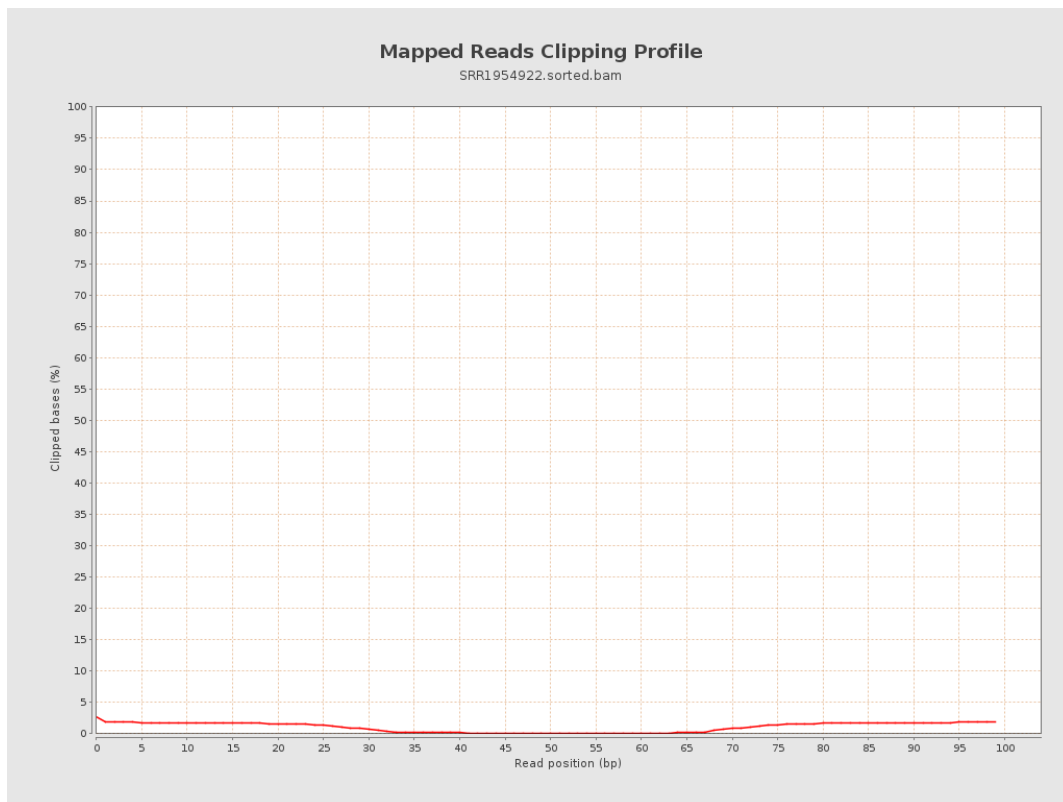
8. Results : Mapped Reads Nucleotide Content



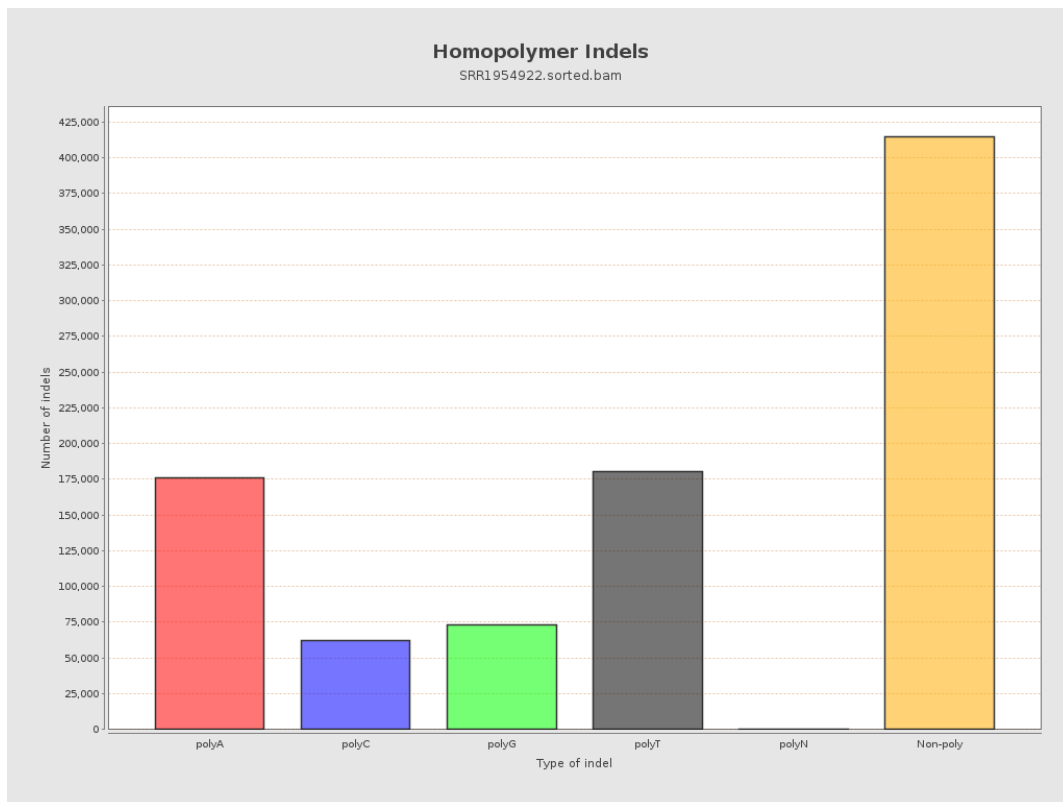
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



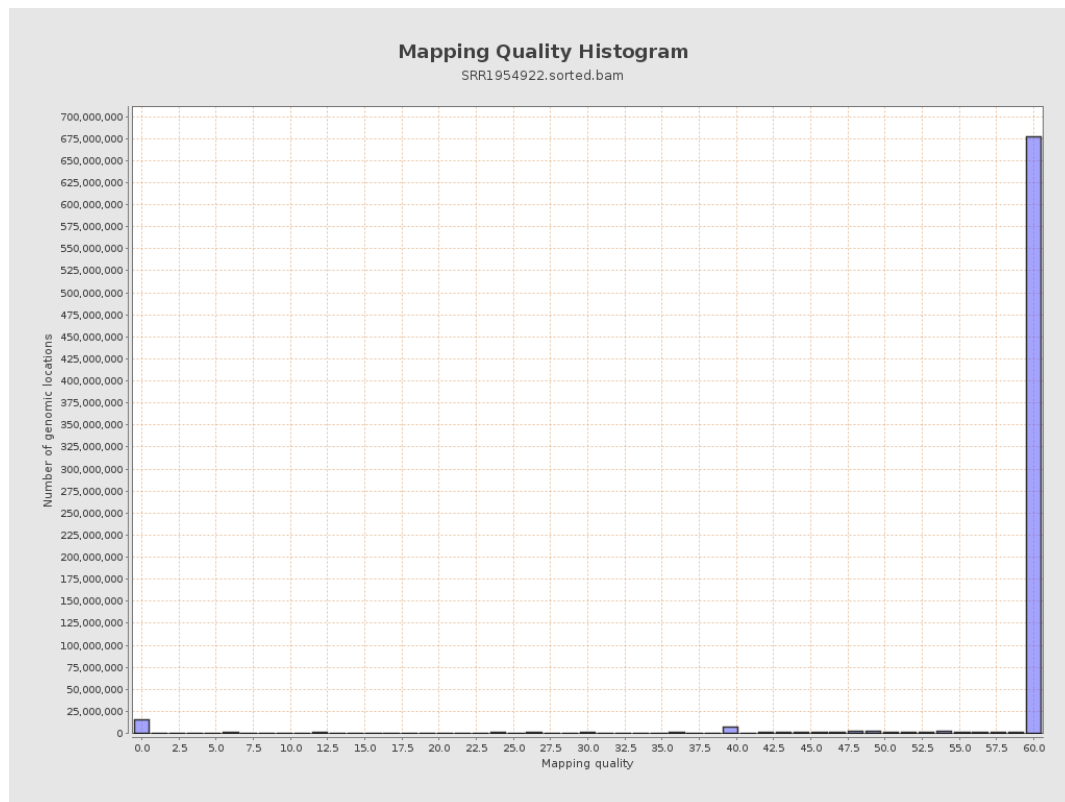
11. Results : Homopolymer Indels



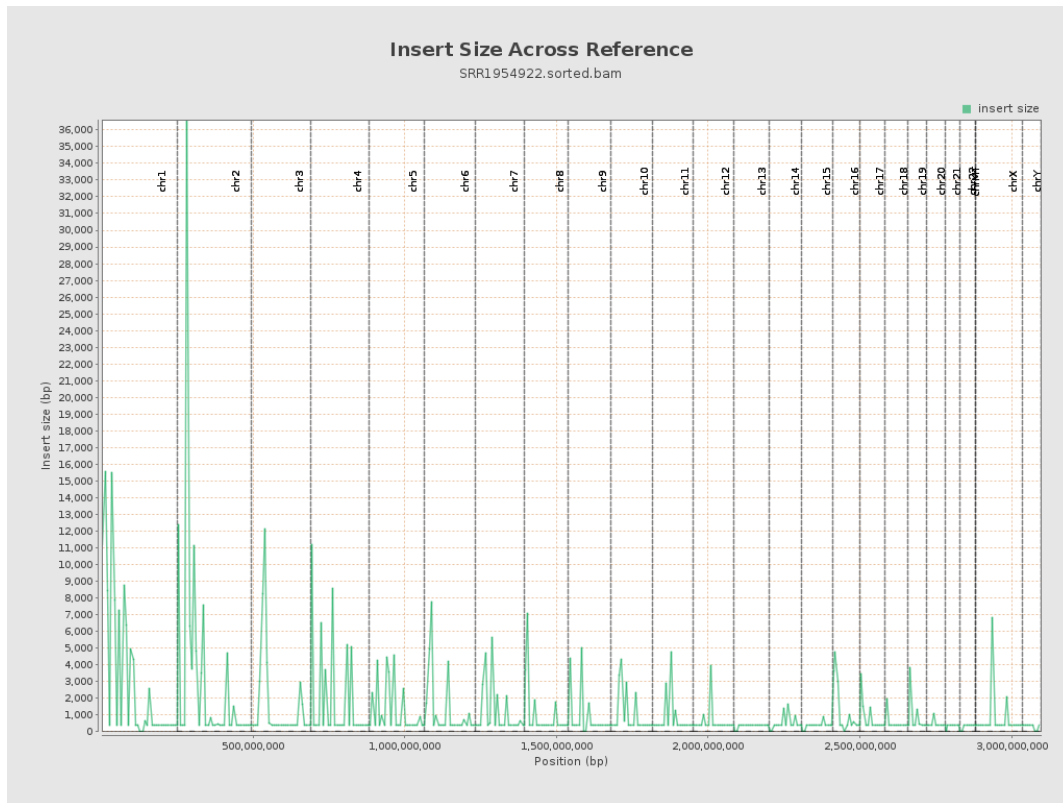
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

