

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.3

2024/09/14 10:07:04

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR1954925.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_SRR1954925 /seu_share/home/tujing/220232460/reference/homo_bwa/hsa.fa SRR1954925_1.fastq.gz SRR1954925_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 10:07:04 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR1954925.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,979,714
Mapped reads	14,646,020 / 97.77%
Unmapped reads	333,694 / 2.23%
Mapped paired reads	14,646,020 / 97.77%
Mapped reads, first in pair	7,437,843 / 49.65%
Mapped reads, second in pair	7,208,177 / 48.12%
Mapped reads, both in pair	14,389,510 / 96.06%
Mapped reads, singletons	256,510 / 1.71%
Secondary alignments	0
Supplementary alignments	39,148 / 0.26%
Read min/max/mean length	30 / 100 / 100.1
Duplicated reads (estimated)	834,879 / 5.57%
Duplication rate	4.72%
Clipped reads	5,350,868 / 35.72%

2.2. ACGT Content

Number/percentage of A's	373,004,972 / 28.31%
Number/percentage of C's	253,755,478 / 19.26%
Number/percentage of T's	373,948,627 / 28.38%
Number/percentage of G's	317,032,835 / 24.06%
Number/percentage of N's	61,046 / 0%

GC Percentage	43.31%
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2.3. Coverage

Mean	0.426
Standard Deviation	1.2676

2.4. Mapping Quality

Mean Mapping Quality	54.14
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2.5. Insert size

Mean	42,293.76
Standard Deviation	2,083,577.16
P25/Median/P75	305 / 319 / 333

2.6. Mismatches and indels

General error rate	0.82%
Mismatches	10,486,117
Insertions	205,614
Mapped reads with at least one insertion	1.39%
Deletions	599,889
Mapped reads with at least one deletion	4.01%
Homopolymer indels	53.98%

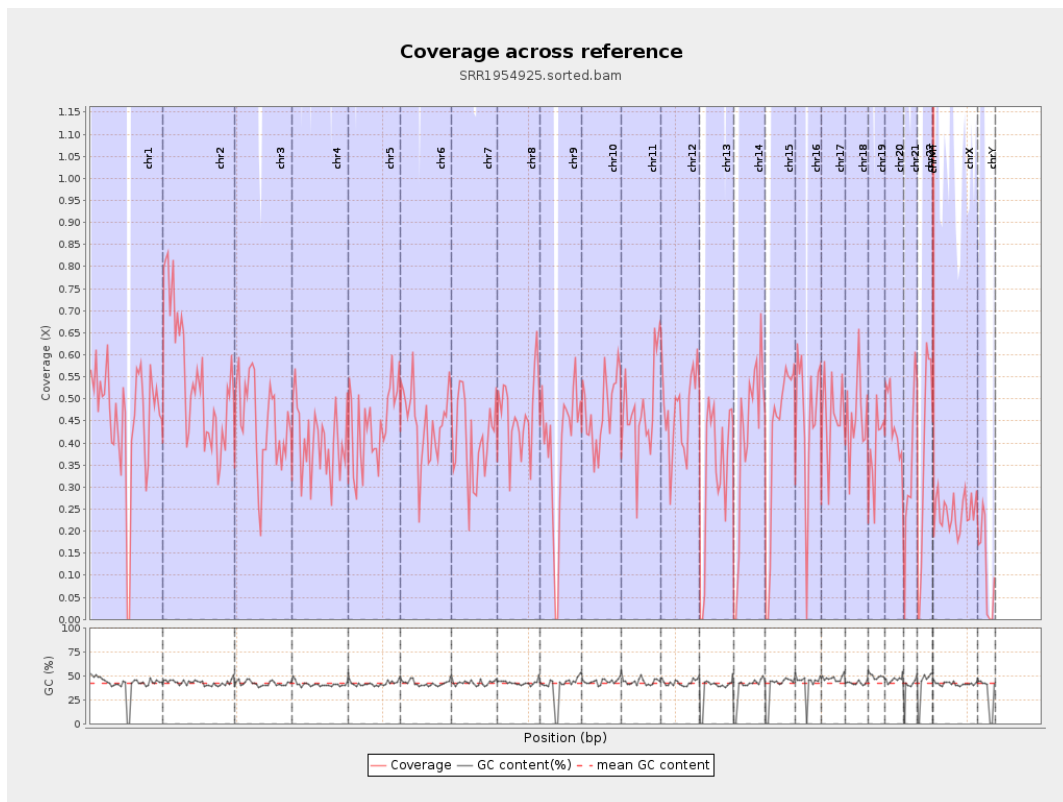
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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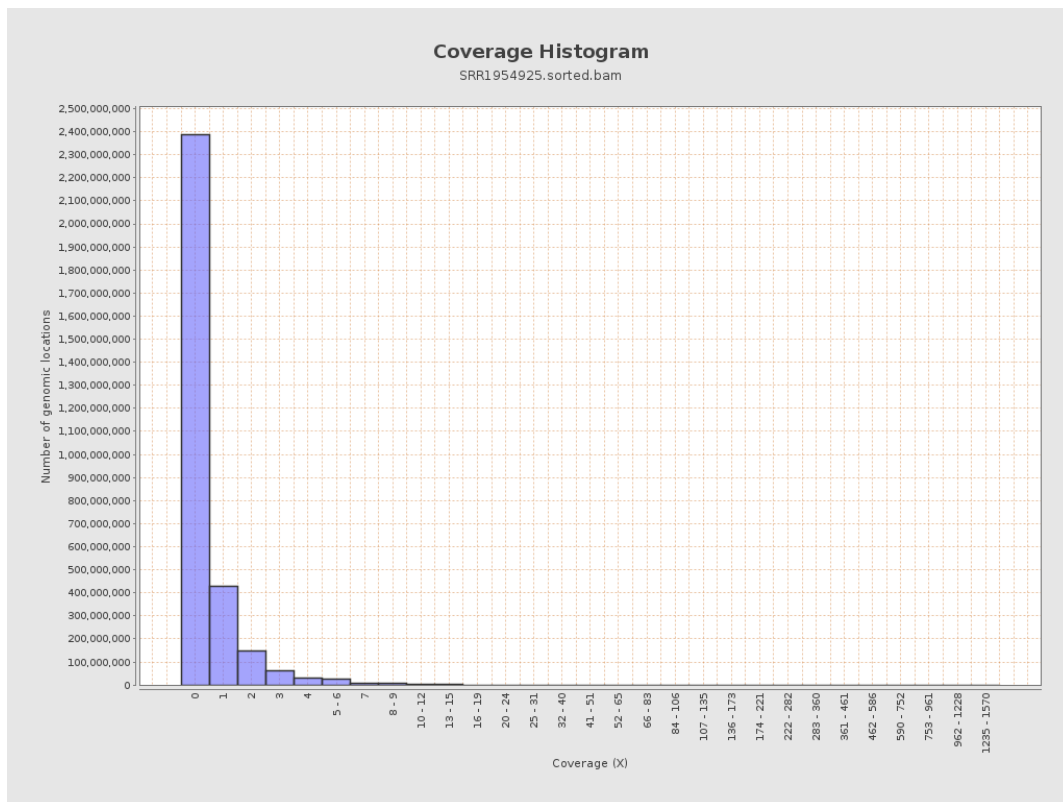
		bases	coverage	deviation
chr1	249250621	113665905	0.456	1.3241
chr2	243199373	132284080	0.5439	2.1112
chr3	198022430	87470119	0.4417	1.0978
chr4	191154276	77307584	0.4044	1.1287
chr5	180915260	80086229	0.4427	1.0942
chr6	171115067	76210800	0.4454	1.1142
chr7	159138663	64796187	0.4072	1.0598
chr8	146364022	68195776	0.4659	1.1941
chr9	141213431	55192817	0.3908	1.3282
chr10	135534747	64279916	0.4743	1.2316
chr11	135006516	64216931	0.4757	1.2933
chr12	133851895	63652165	0.4755	1.1782
chr13	115169878	38441085	0.3338	0.9525
chr14	107349540	44451331	0.4141	1.1294
chr15	102531392	42087947	0.4105	1.106
chr16	90354753	41293923	0.457	1.4593
chr17	81195210	37761110	0.4651	1.2046
chr18	78077248	35577542	0.4557	1.3657
chr19	59128983	22865505	0.3867	1.1417
chr20	63025520	27610642	0.4381	1.1246
chr21	48129895	17061017	0.3545	1.4365
chr22	51304566	19205896	0.3744	1.0925
chrMT	16571	263394	15.8949	12.4438
chrX	155270560	37725813	0.243	0.757

chrY	59373566	6932539	0.1168	0.7676
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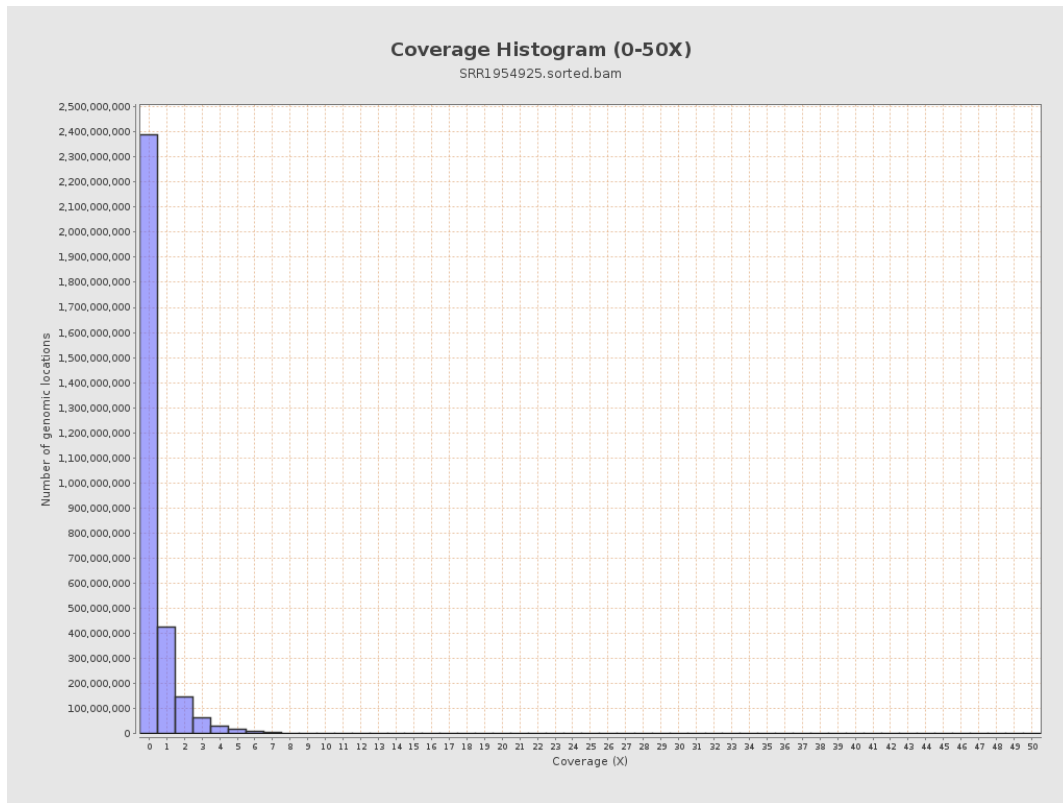
3. Results : Coverage across reference



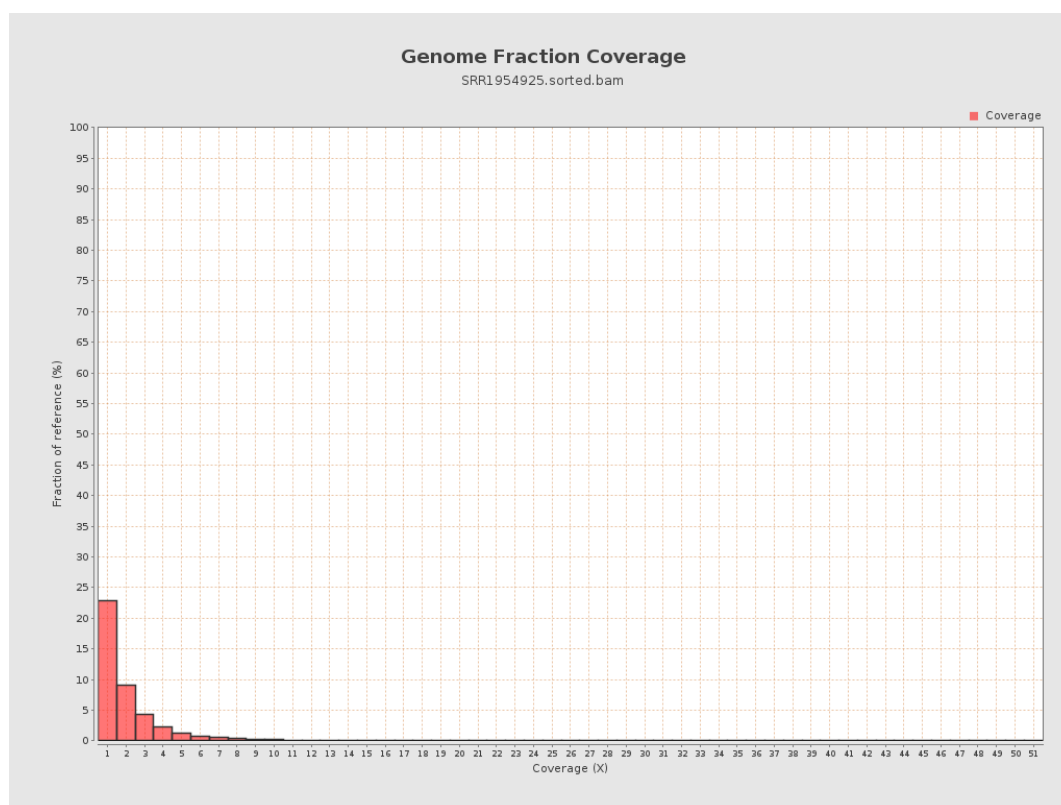
4. Results : Coverage Histogram



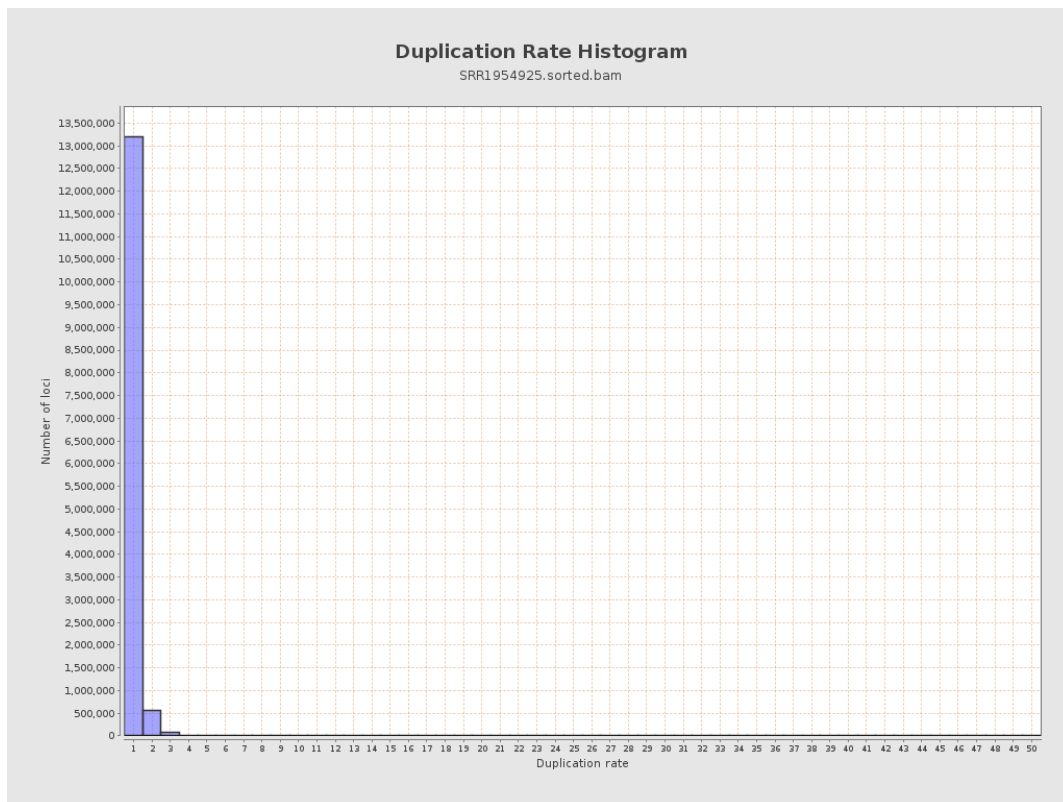
5. Results : Coverage Histogram (0-50X)



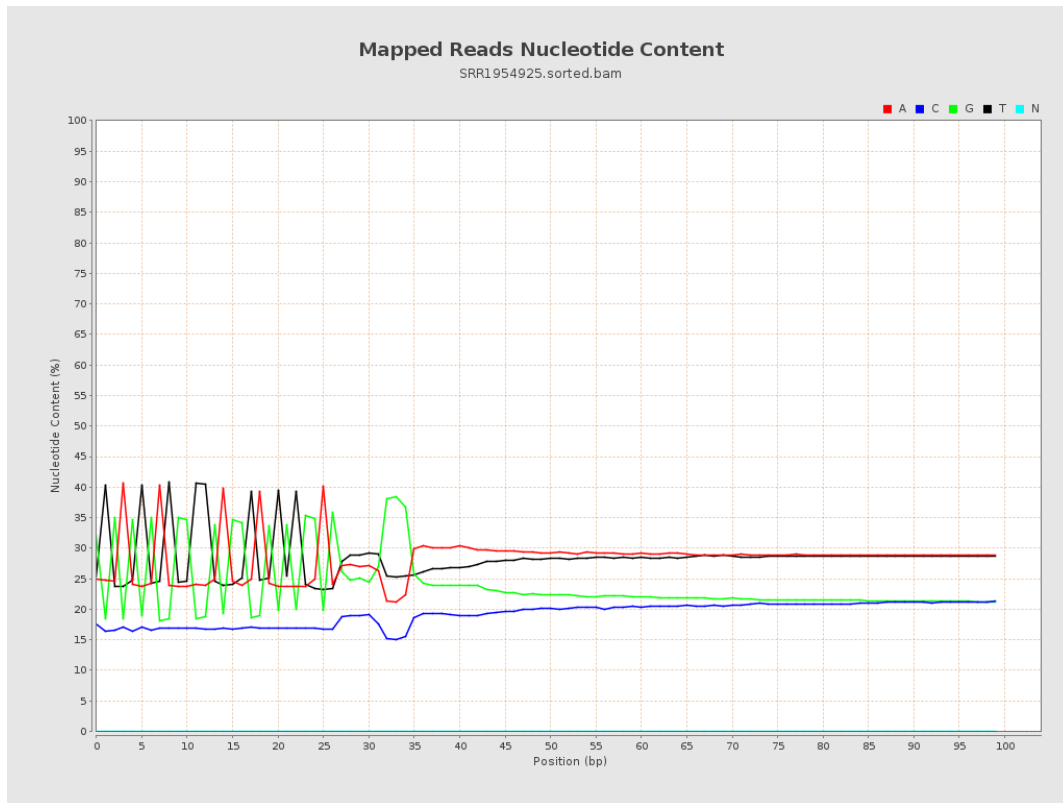
6. Results : Genome Fraction Coverage



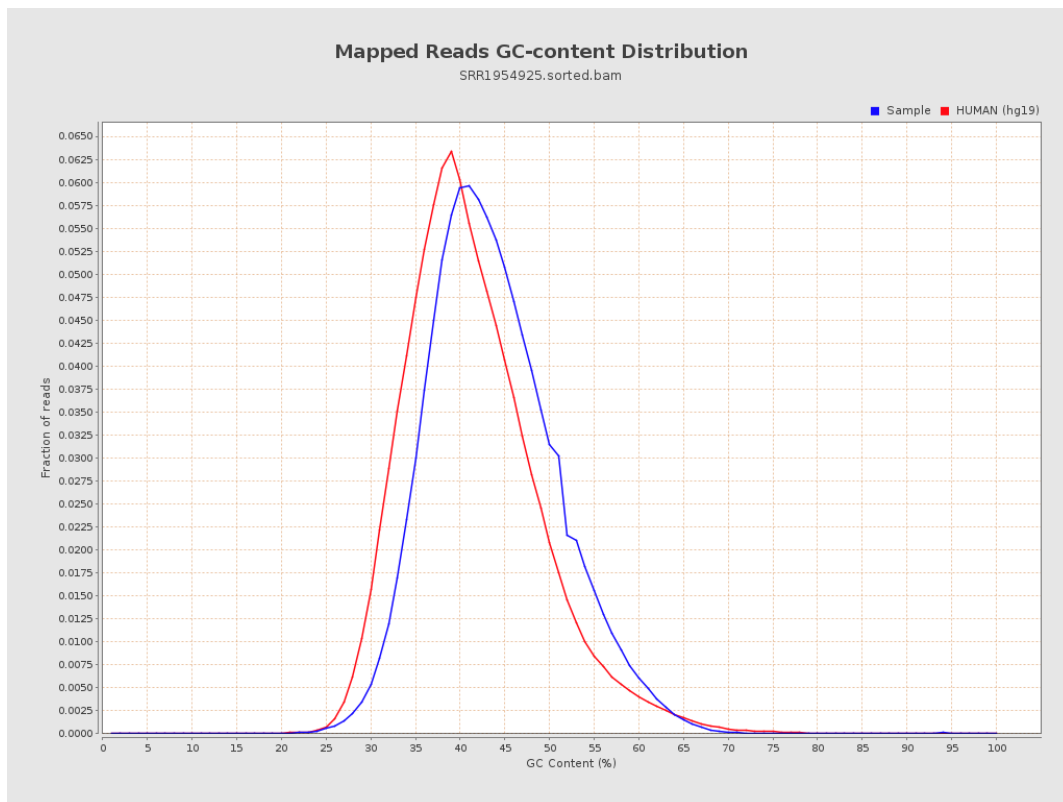
7. Results : Duplication Rate Histogram



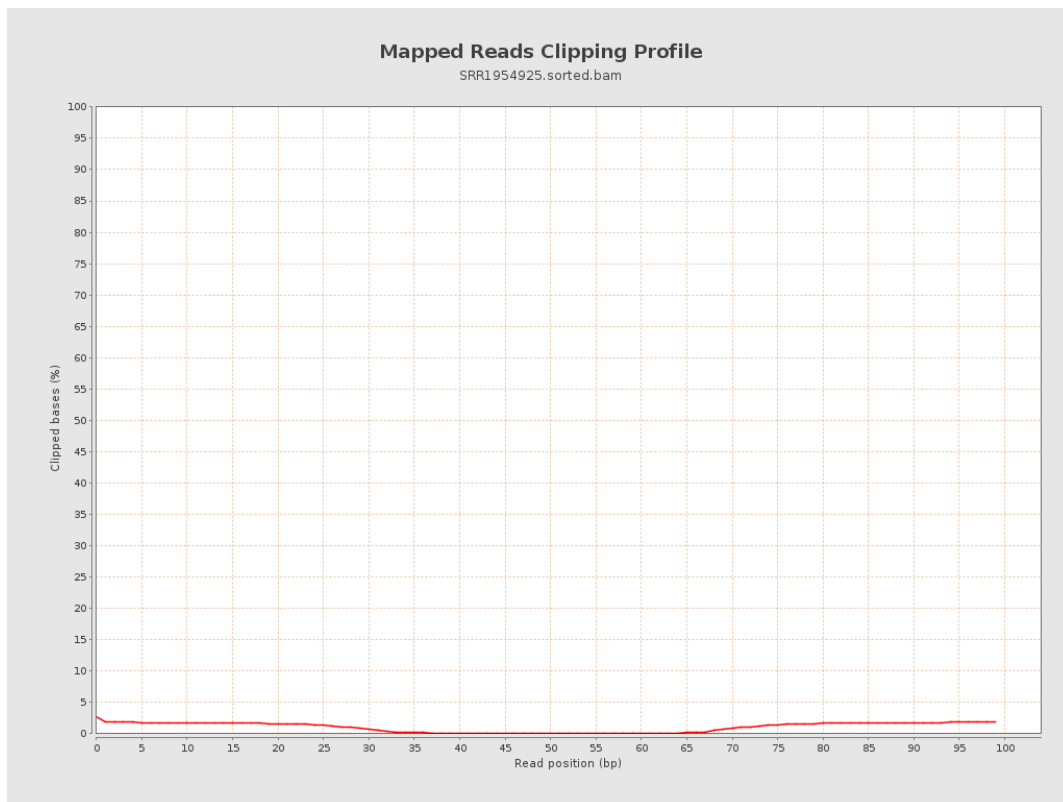
8. Results : Mapped Reads Nucleotide Content



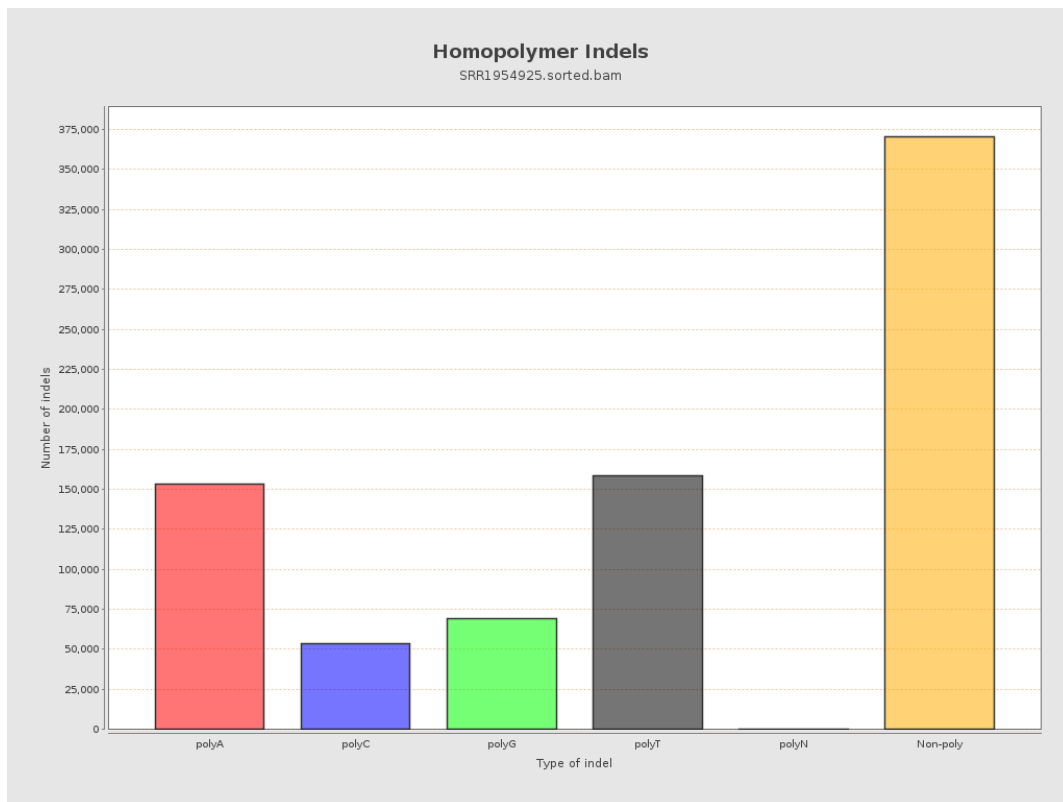
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



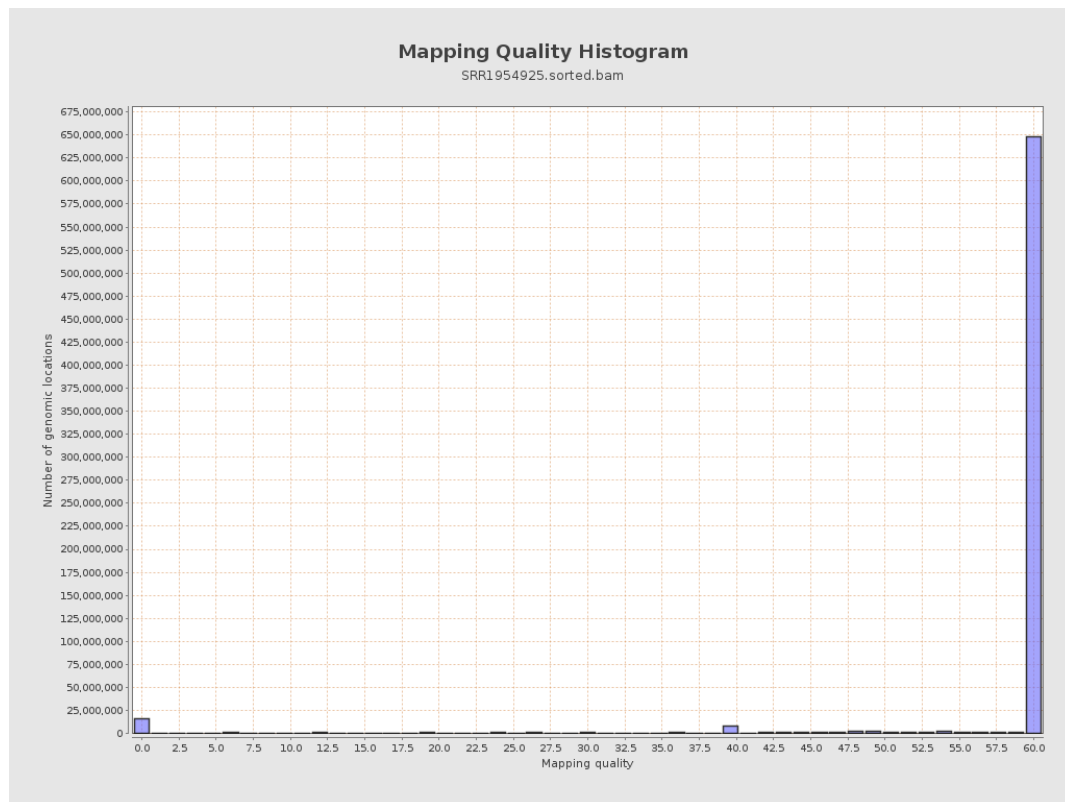
11. Results : Homopolymer Indels



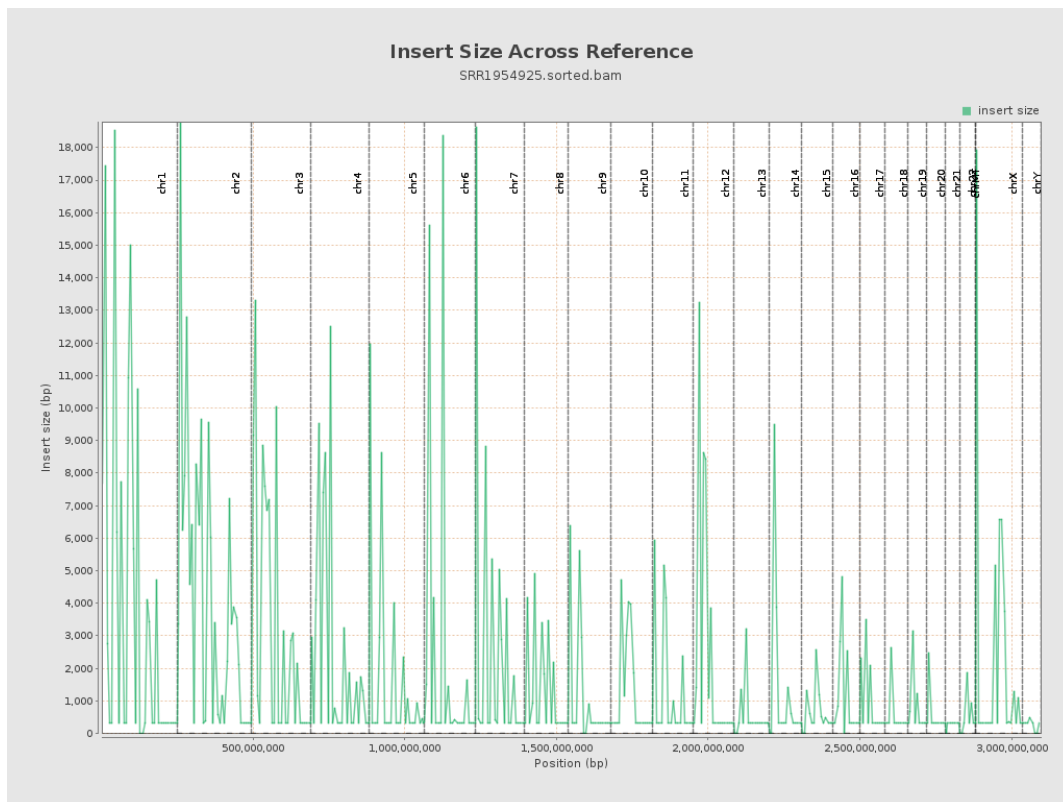
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

