

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/04 12:34:26

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR10173957.sorted.bam -c -nw 400 -hm 3
```

1.2. Alignment

Command line:	/home/luna/Desktop/Software/bwa/bwa mem -t 16 -k 30 -R @RG\tID:Singlecell2022\tLB:Library\tPL:ILLUMINA\tSM:sample_SRR10173957 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR10173957_1.fastq.gz SRR10173957_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Wed Sep 04 12:34:26 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR10173957.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	3,943,464
Mapped reads	3,854,014 / 97.73%
Unmapped reads	89,450 / 2.27%
Mapped paired reads	3,854,014 / 97.73%
Mapped reads, first in pair	1,928,540 / 48.9%
Mapped reads, second in pair	1,925,474 / 48.83%
Mapped reads, both in pair	3,795,900 / 96.26%
Mapped reads, singletons	58,114 / 1.47%
Secondary alignments	0
Supplementary alignments	476,054 / 12.07%
Read min/max/mean length	30 / 133 / 125.55
Duplicated reads (estimated)	3,057,018 / 77.52%
Duplication rate	65.23%
Clipped reads	1,832,668 / 46.47%

2.2. ACGT Content

Number/percentage of A's	130,938,813 / 29.77%
Number/percentage of C's	87,830,062 / 19.97%
Number/percentage of T's	129,774,778 / 29.5%
Number/percentage of G's	91,308,796 / 20.76%
Number/percentage of N's	3,642 / 0%

GC Percentage	40.73%
---------------	--------

2.3. Coverage

Mean	0.1422
Standard Deviation	2.7581

2.4. Mapping Quality

Mean Mapping Quality	52.62
----------------------	-------

2.5. Insert size

Mean	862,934.64
Standard Deviation	8,662,880.88
P25/Median/P75	110 / 162 / 249

2.6. Mismatches and indels

General error rate	0.89%
Mismatches	3,757,405
Insertions	48,761
Mapped reads with at least one insertion	1.22%
Deletions	117,097
Mapped reads with at least one deletion	2.97%
Homopolymer indels	41.26%

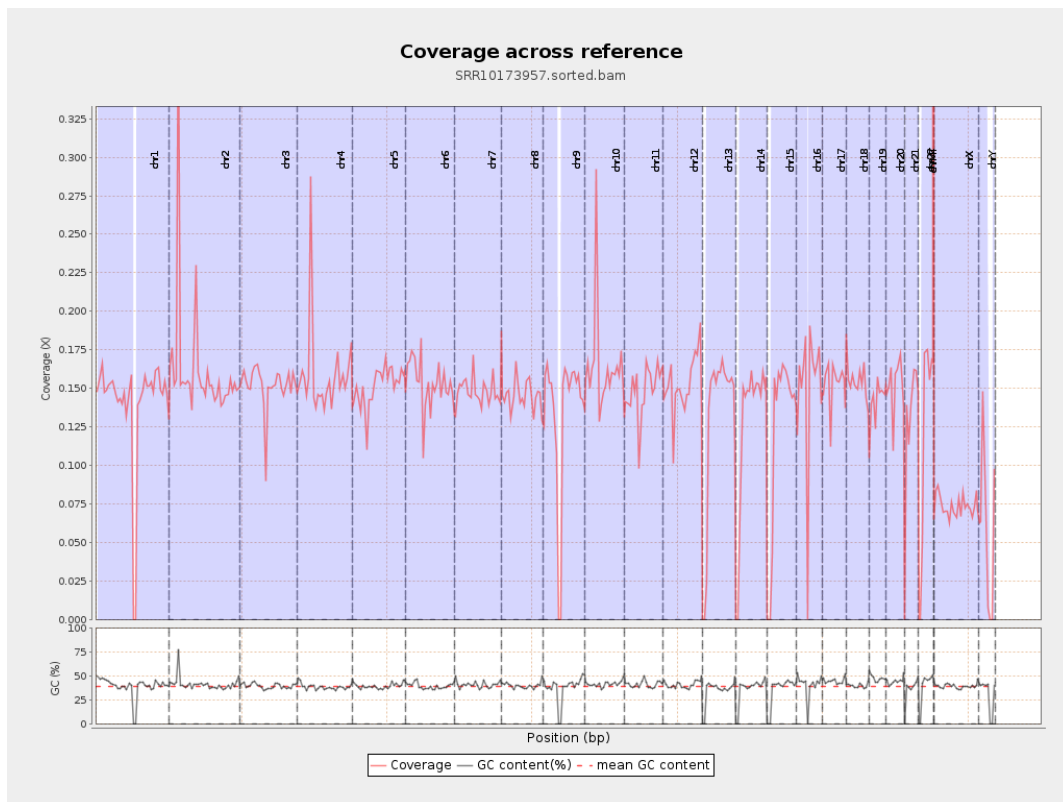
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
------	--------	--------	------	----------

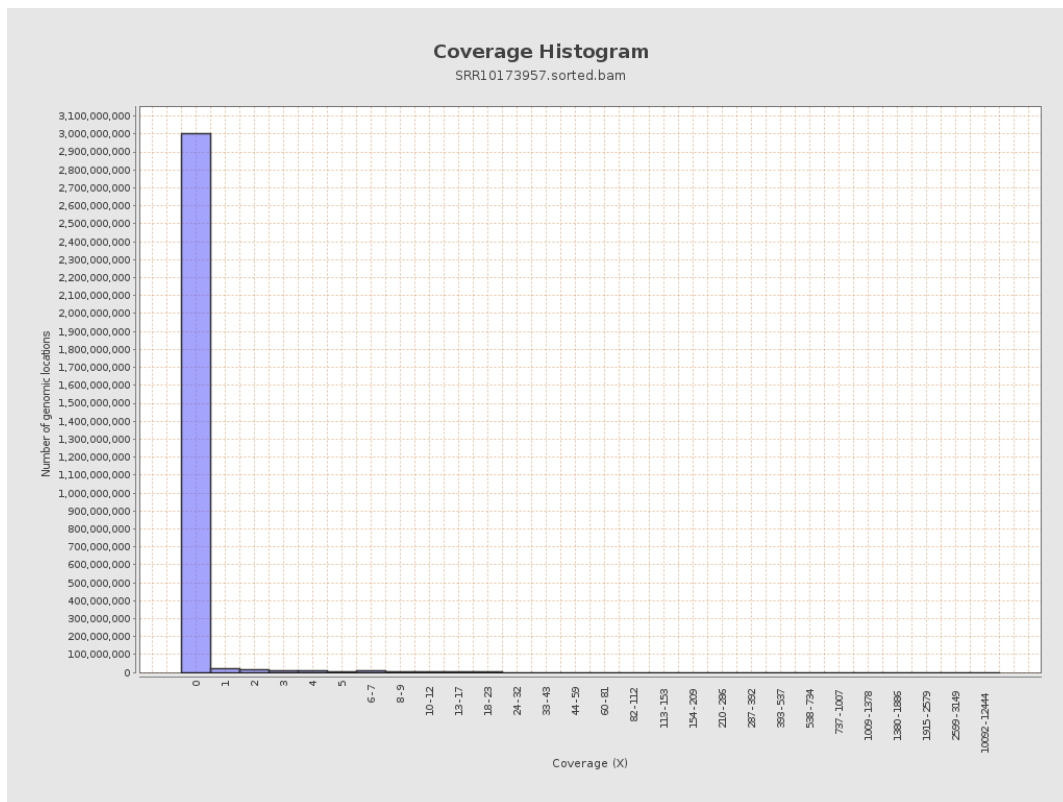
		bases	coverage	deviation
chr1	249250621	35035159	0.1406	1.3912
chr2	243199373	39535738	0.1626	8.7506
chr3	198022430	30053419	0.1518	1.1615
chr4	191154276	30223316	0.1581	1.5845
chr5	180915260	27373251	0.1513	1.1523
chr6	171115067	26148284	0.1528	1.2533
chr7	159138663	23589938	0.1482	1.4142
chr8	146364022	21258985	0.1452	1.5688
chr9	141213431	19013841	0.1346	1.3029
chr10	135534747	22220156	0.1639	1.7595
chr11	135006516	20115446	0.149	1.1616
chr12	133851895	20404465	0.1524	1.1729
chr13	115169878	14918392	0.1295	1.0758
chr14	107349540	13560949	0.1263	1.0565
chr15	102531392	12631147	0.1232	1.0523
chr16	90354753	13521731	0.1497	1.2921
chr17	81195210	12404412	0.1528	1.1921
chr18	78077248	12087452	0.1548	1.7129
chr19	59128983	8433743	0.1426	1.2637
chr20	63025520	9556650	0.1516	1.1816
chr21	48129895	6258943	0.13	1.2656
chr22	51304566	5927699	0.1155	1.1387
chrMT	16571	1084802	65.4639	60.2843
chrX	155270560	11447774	0.0737	0.7987

chrY	59373566	3331271	0.0561	1.0496
------	----------	---------	--------	--------

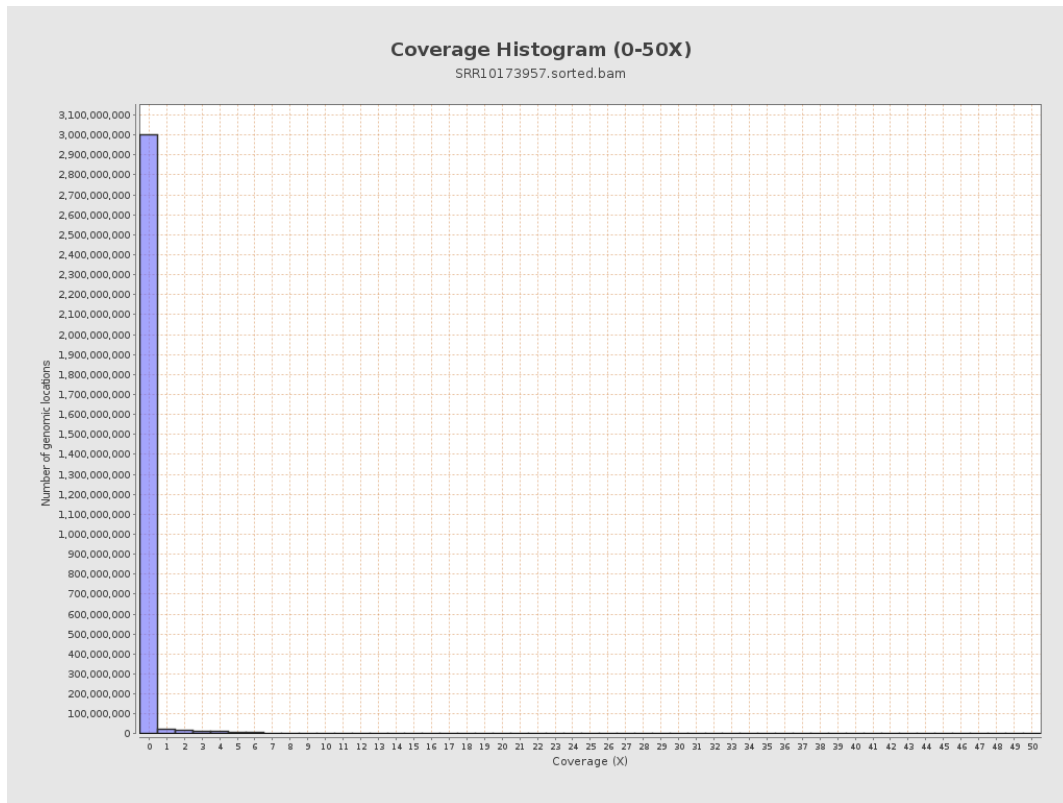
3. Results : Coverage across reference



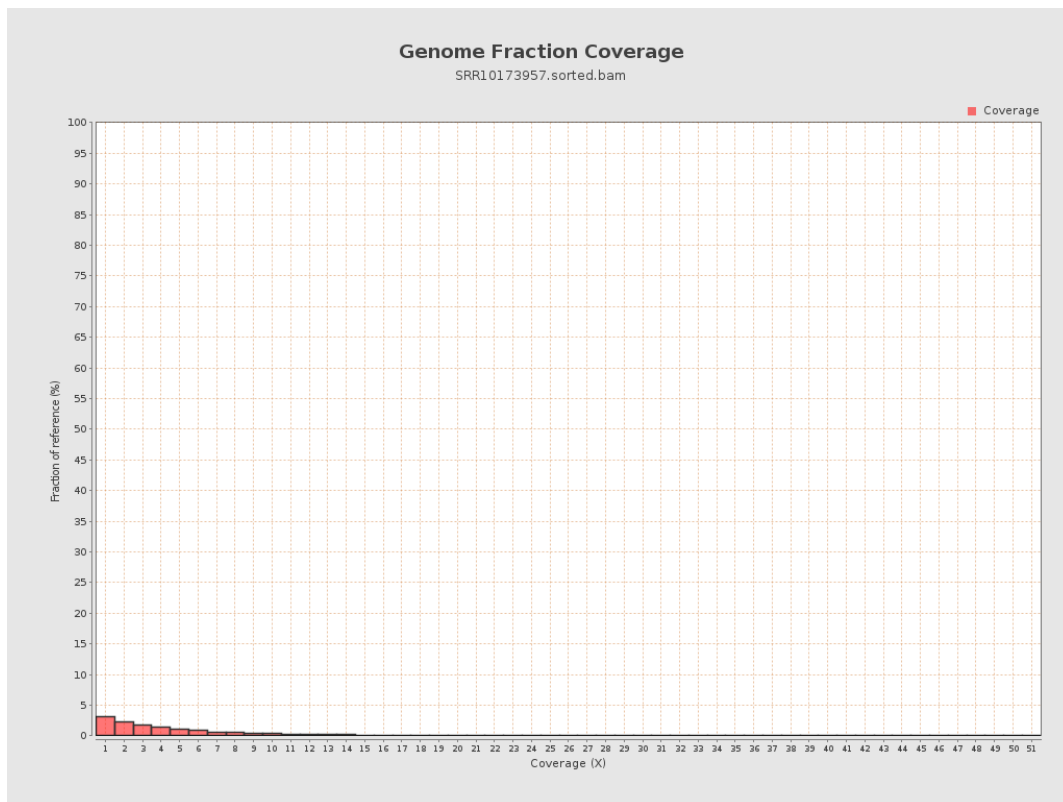
4. Results : Coverage Histogram



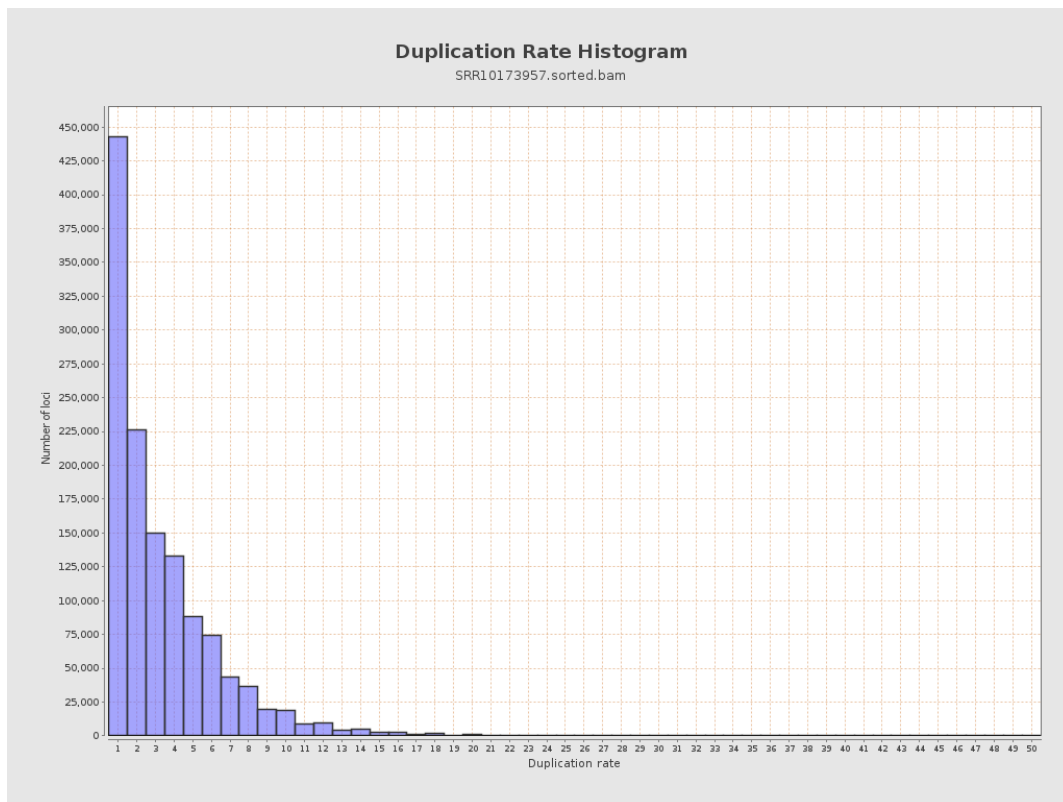
5. Results : Coverage Histogram (0-50X)



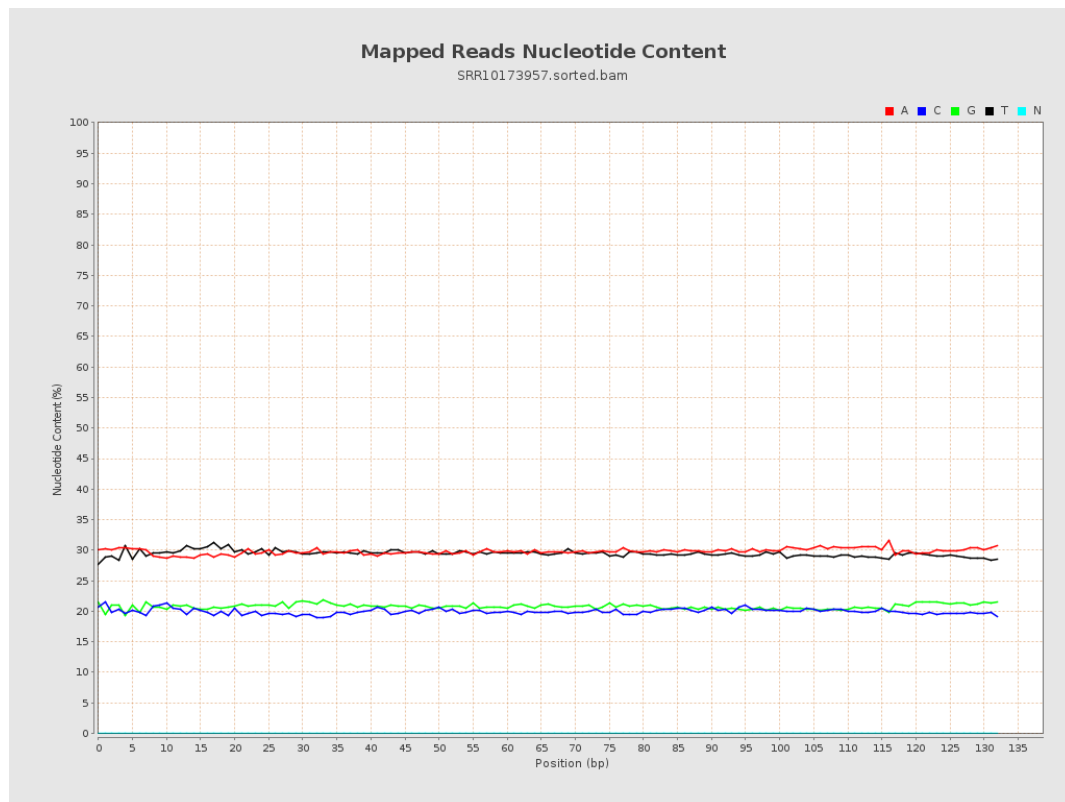
6. Results : Genome Fraction Coverage



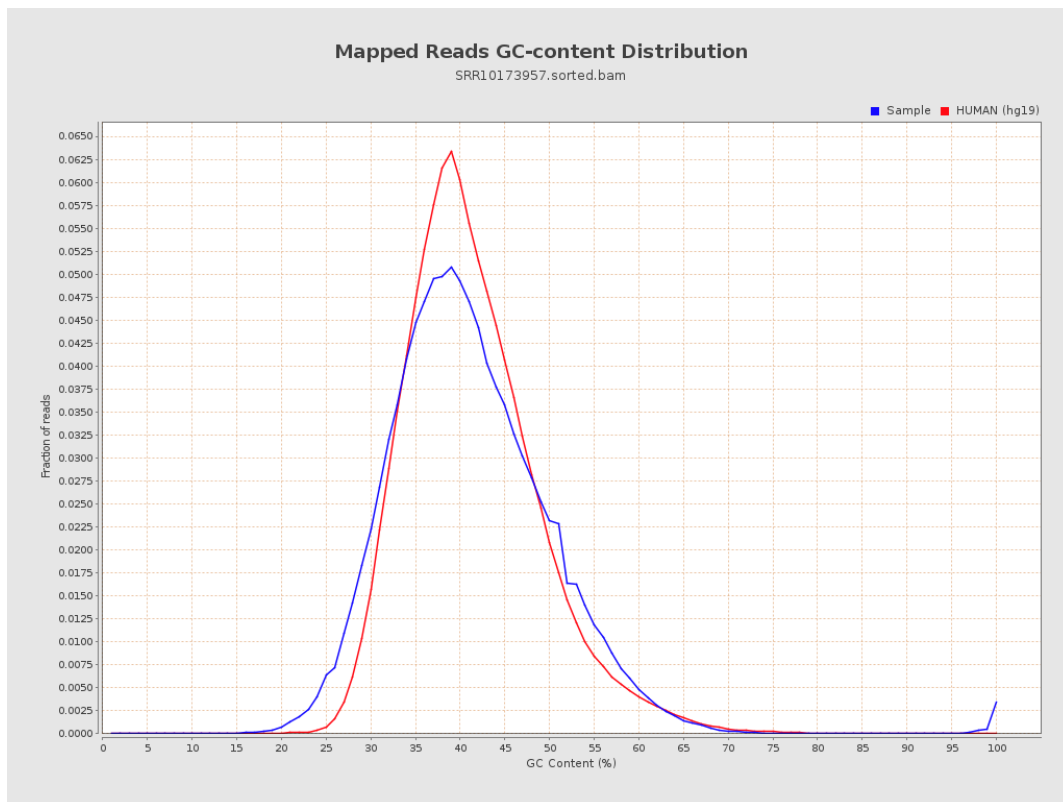
7. Results : Duplication Rate Histogram



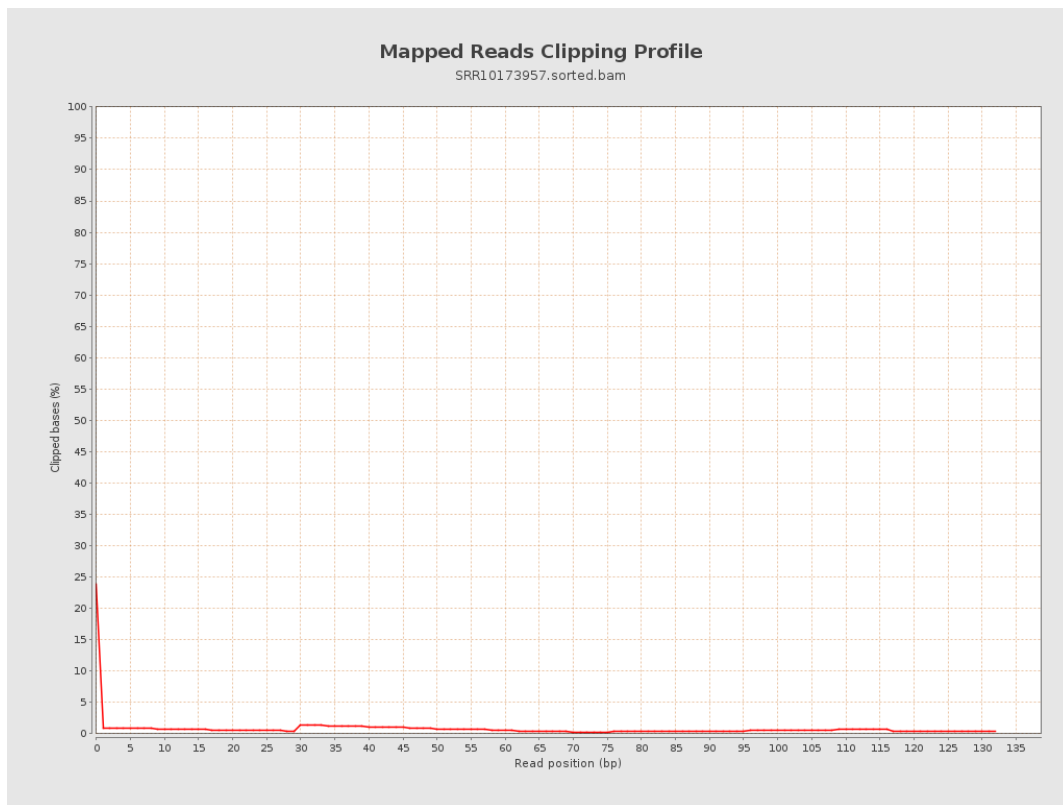
8. Results : Mapped Reads Nucleotide Content



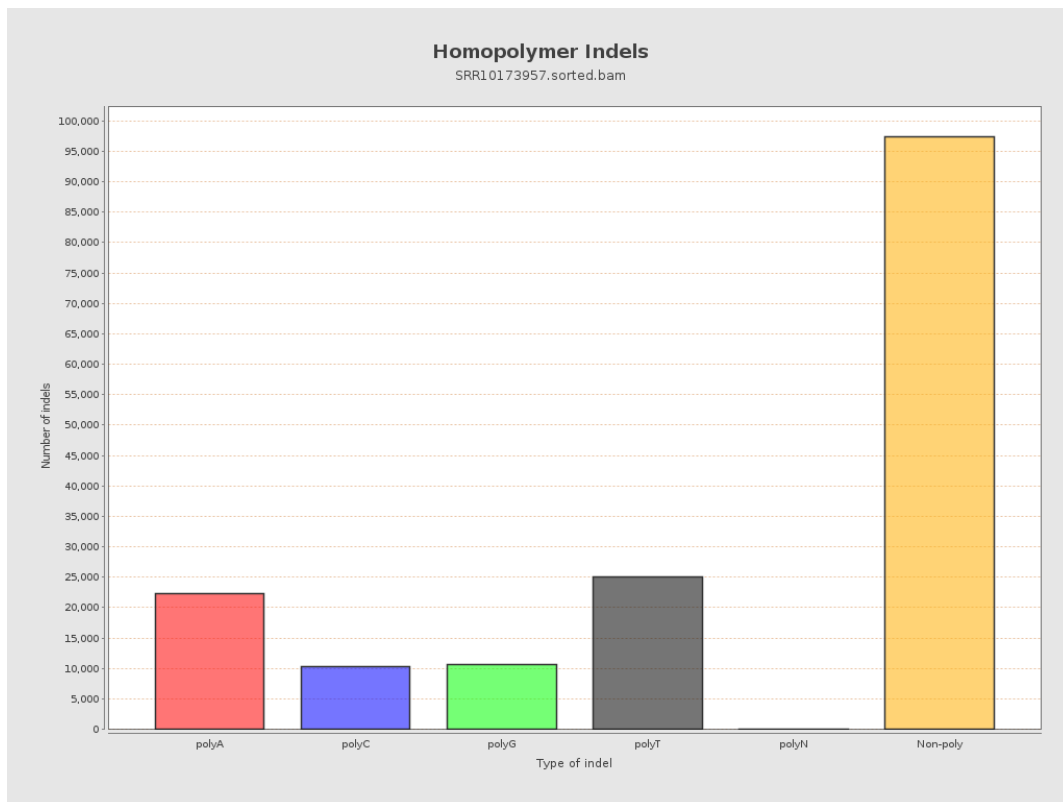
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



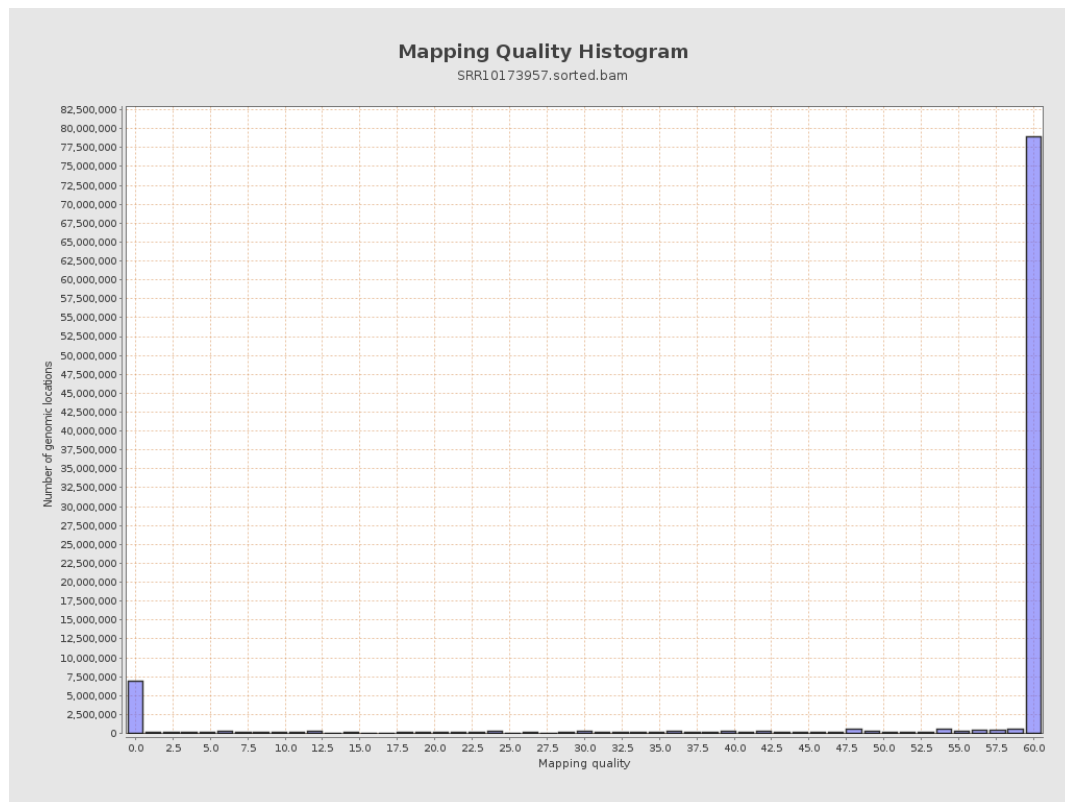
11. Results : Homopolymer Indels



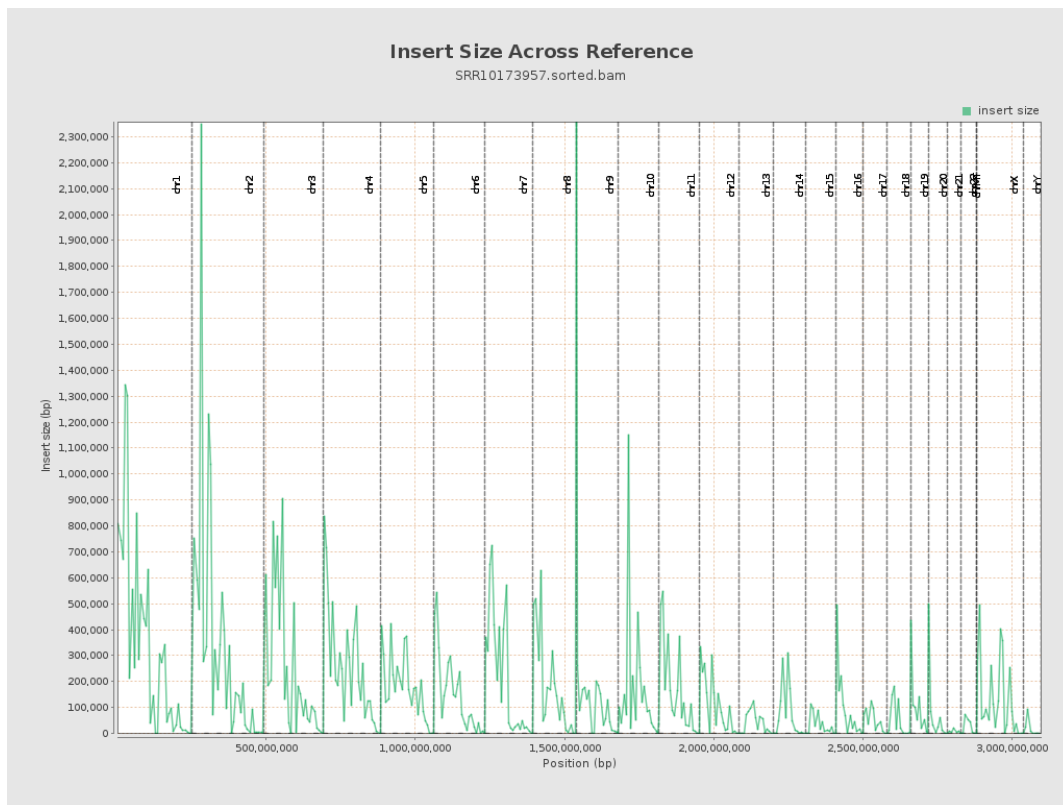
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

