

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 18:15:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354872.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_SRR22354872 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354872_1.fastq.gz SRR22354872_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 18:15:58 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354872.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	25,710,216
Mapped reads	25,472,926 / 99.08%
Unmapped reads	237,290 / 0.92%
Mapped paired reads	25,472,926 / 99.08%
Mapped reads, first in pair	12,746,788 / 49.58%
Mapped reads, second in pair	12,726,138 / 49.5%
Mapped reads, both in pair	25,430,592 / 98.91%
Mapped reads, singletons	42,334 / 0.16%
Secondary alignments	0
Supplementary alignments	1,151,565 / 4.48%
Read min/max/mean length	30 / 150 / 151.64
Duplicated reads (estimated)	16,293,231 / 63.37%
Duplication rate	63.49%
Clipped reads	14,511,903 / 56.44%

2.2. ACGT Content

Number/percentage of A's	854,324,379 / 27.27%
Number/percentage of C's	681,439,391 / 21.75%
Number/percentage of T's	872,940,071 / 27.87%
Number/percentage of G's	723,738,140 / 23.1%
Number/percentage of N's	91,902 / 0%

GC Percentage	44.86%
---------------	--------

2.3. Coverage

Mean	1.0124
Standard Deviation	56.9371

2.4. Mapping Quality

Mean Mapping Quality	53.55
----------------------	-------

2.5. Insert size

Mean	435,734.31
Standard Deviation	7,602,506.97
P25/Median/P75	98 / 148 / 216

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	18,258,642
Insertions	529,975
Mapped reads with at least one insertion	1.93%
Deletions	532,060
Mapped reads with at least one deletion	1.98%
Homopolymer indels	42.4%

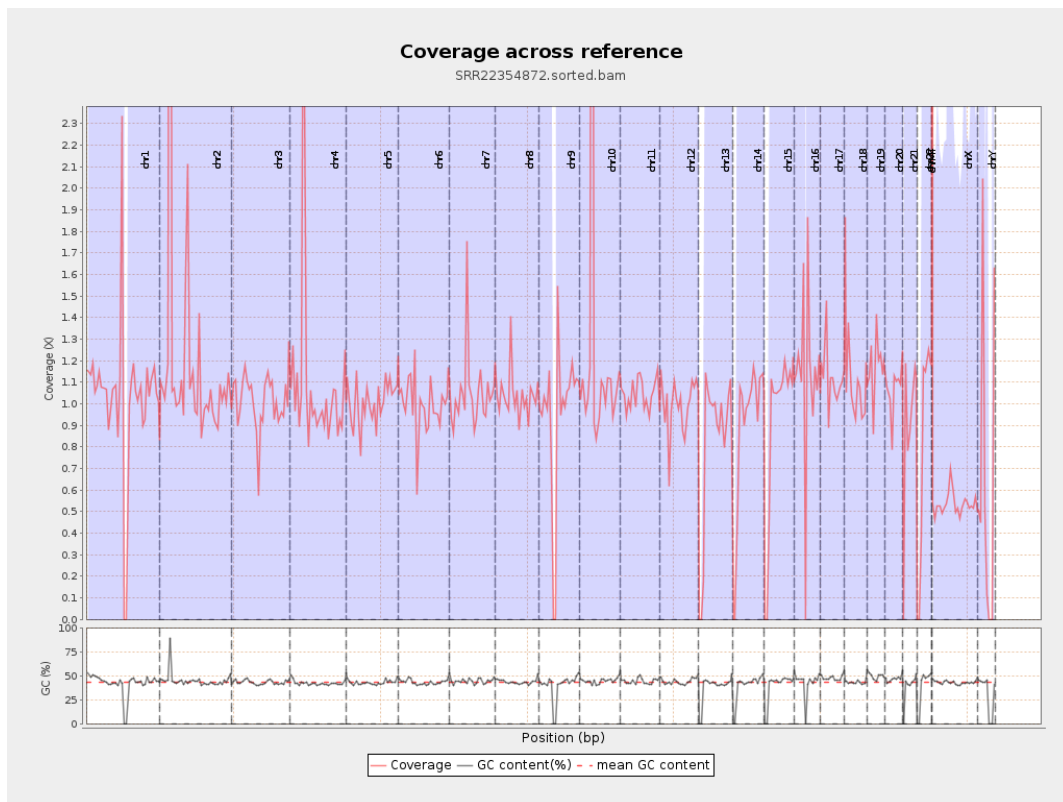
2.7. Chromosome stats

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

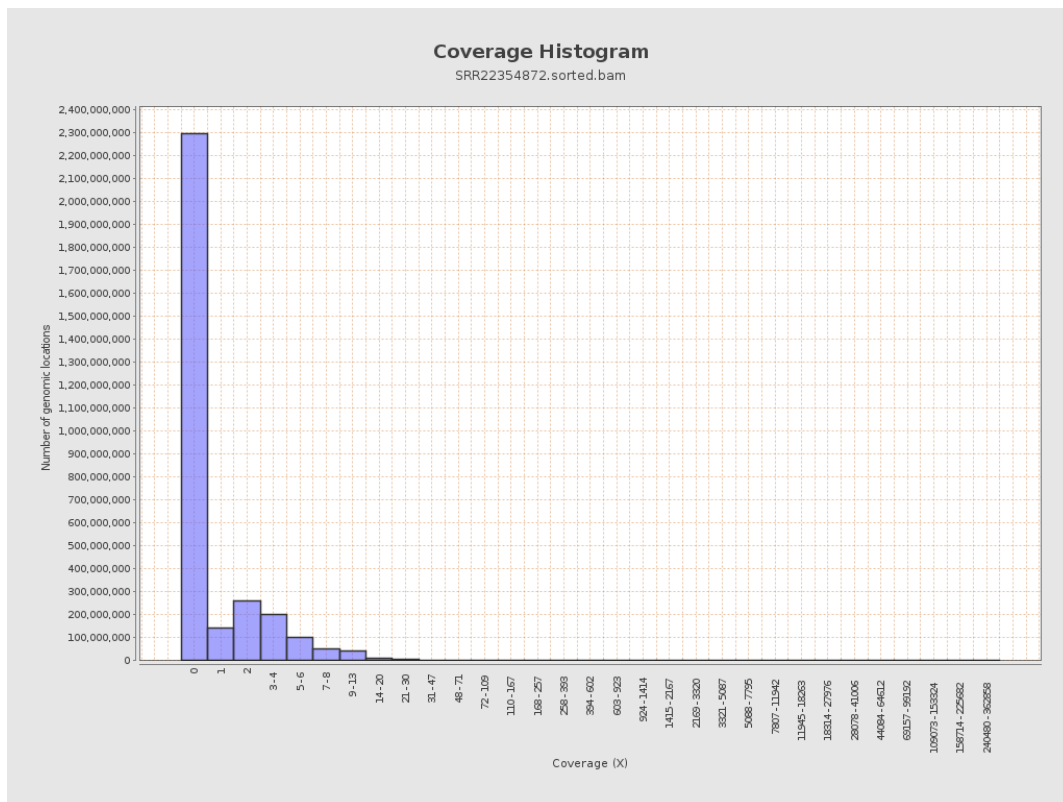
		bases	coverage	deviation
chr1	249250621	257677306	1.0338	29.7592
chr2	243199373	303878217	1.2495	196.2466
chr3	198022430	199781542	1.0089	3.1062
chr4	191154276	206641310	1.081	16.4329
chr5	180915260	182634177	1.0095	2.3425
chr6	171115067	170275426	0.9951	4.2784
chr7	159138663	166581501	1.0468	18.9404
chr8	146364022	151833769	1.0374	4.5328
chr9	141213431	133050623	0.9422	13.9211
chr10	135534747	175957314	1.2982	40.1445
chr11	135006516	141932219	1.0513	5.6054
chr12	133851895	133195110	0.9951	2.3225
chr13	115169878	94827802	0.8234	2.0375
chr14	107349540	94556020	0.8808	7.486
chr15	102531392	92178162	0.899	2.1559
chr16	90354753	103350301	1.1438	7.6867
chr17	81195210	90848357	1.1189	6.9525
chr18	78077248	85603011	1.0964	13.3266
chr19	59128983	69369711	1.1732	16.1417
chr20	63025520	67064941	1.0641	5.9455
chr21	48129895	44347462	0.9214	8.8976
chr22	51304566	42233274	0.8232	3.1655
chrMT	16571	3942563	237.9194	64.098
chrX	155270560	82906284	0.5339	2.6407

chrY	59373566	39437883	0.6642	20.9171
------	----------	----------	--------	---------

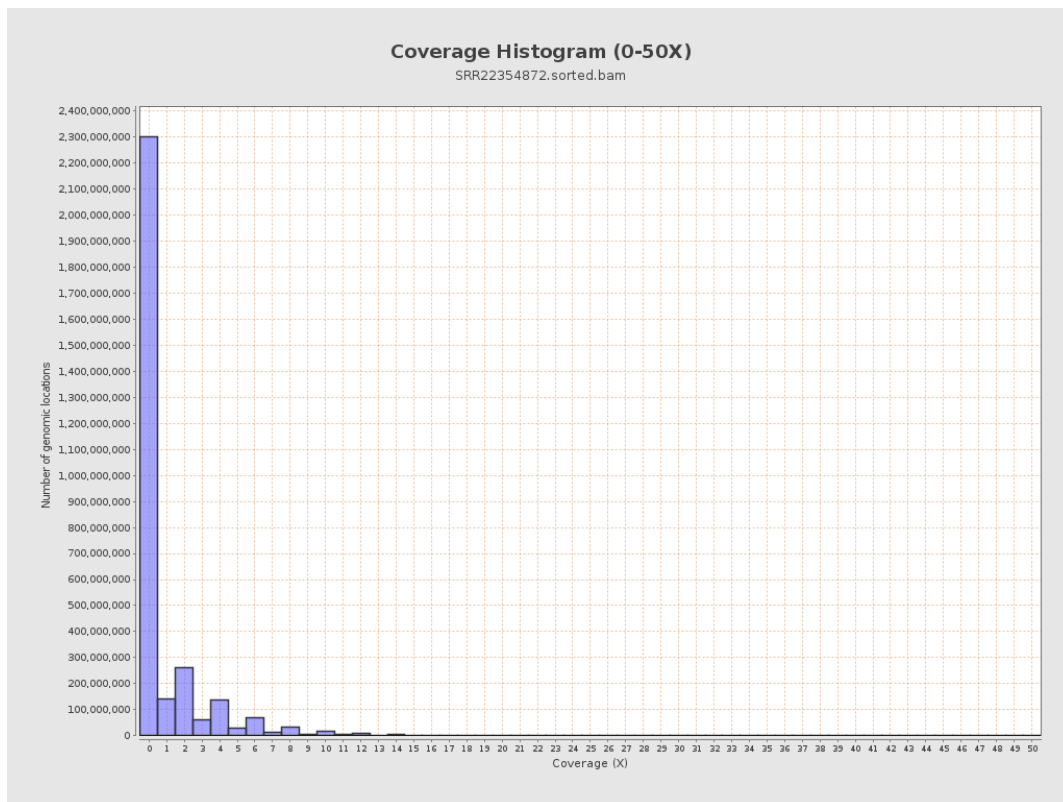
3. Results : Coverage across reference



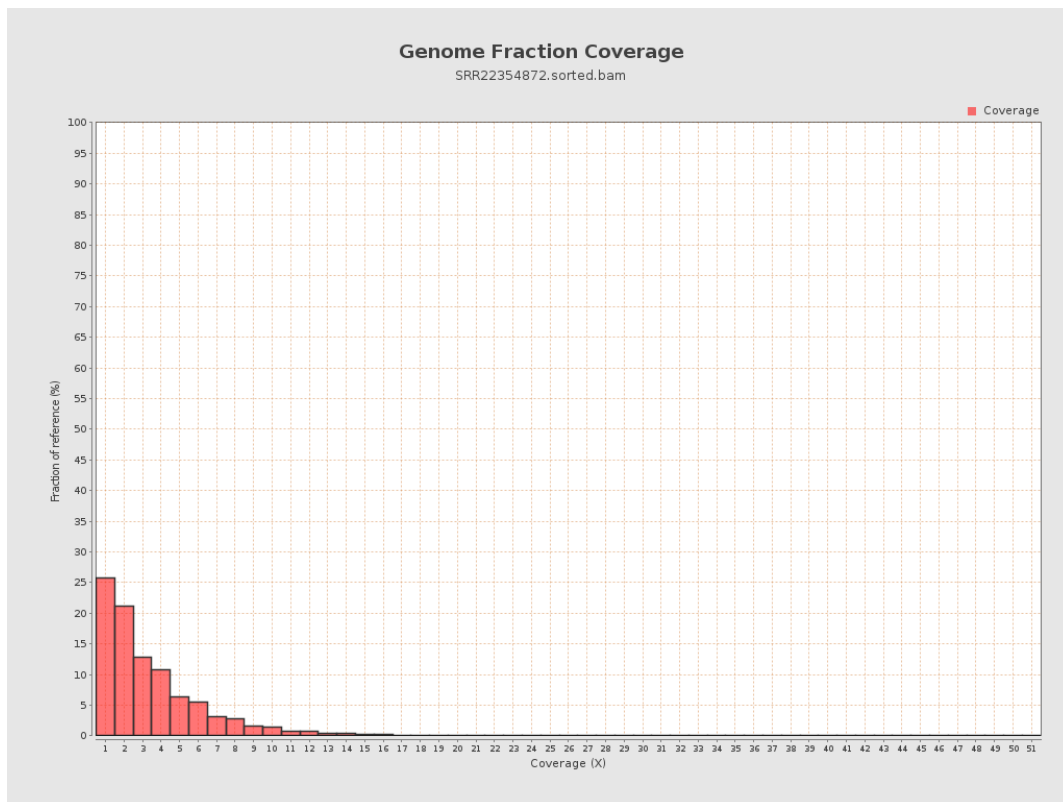
4. Results : Coverage Histogram



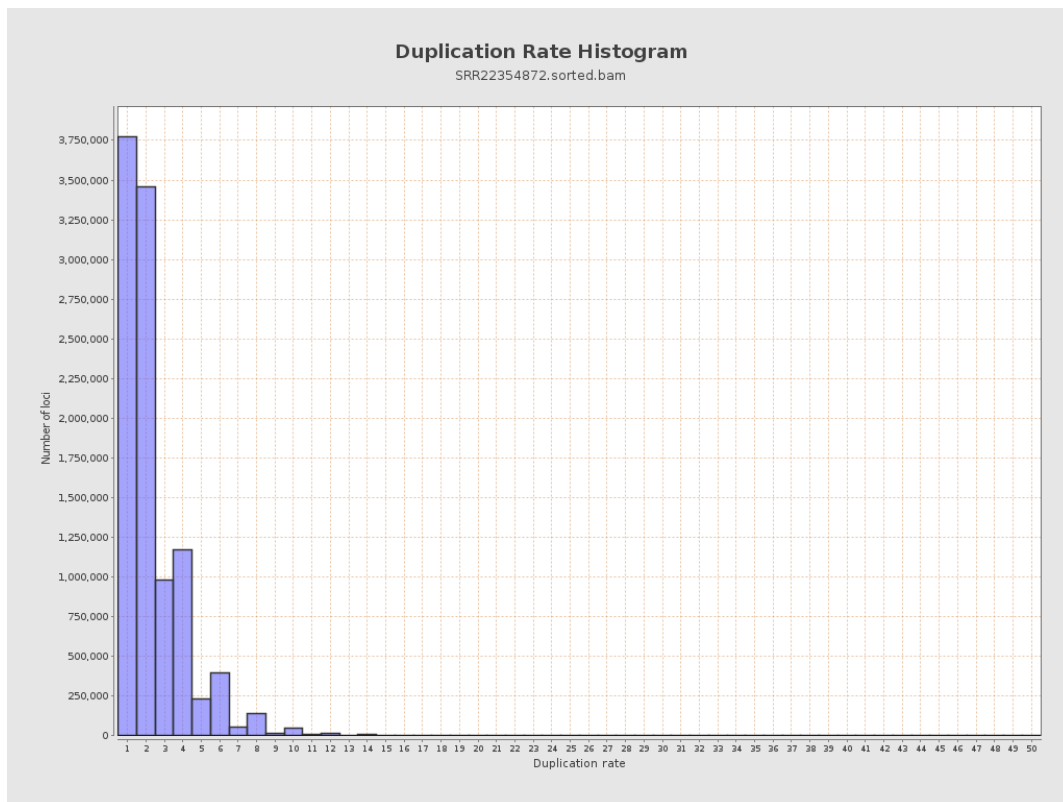
5. Results : Coverage Histogram (0-50X)



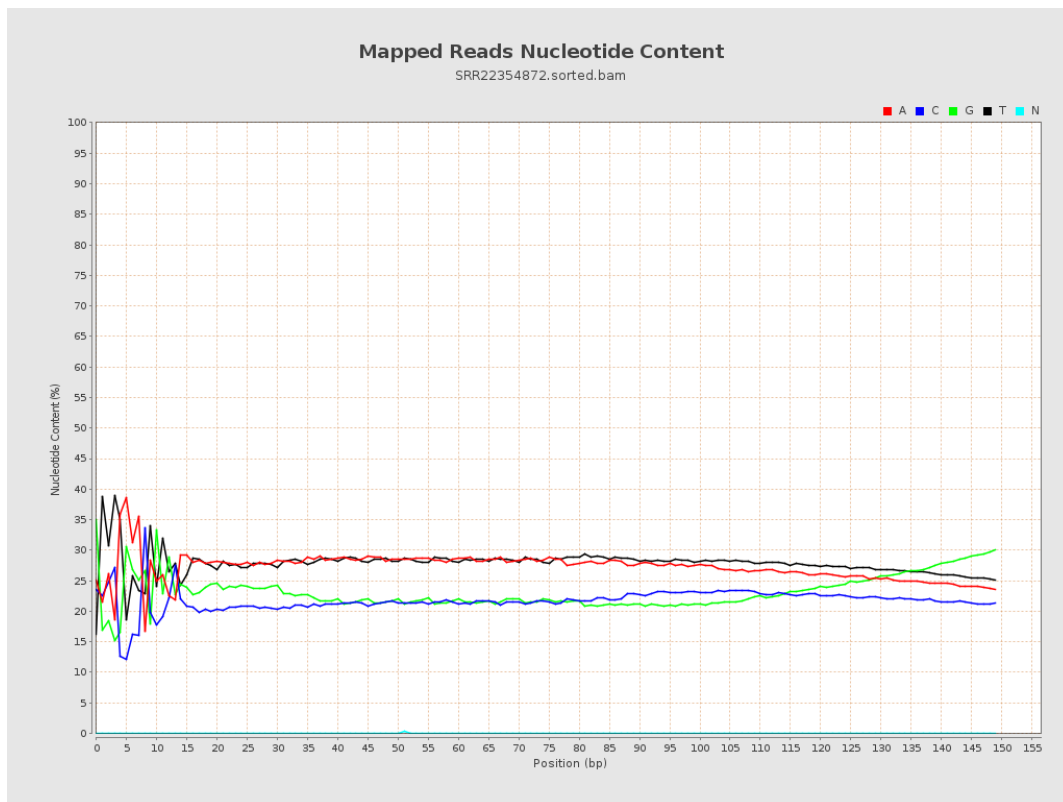
6. Results : Genome Fraction Coverage



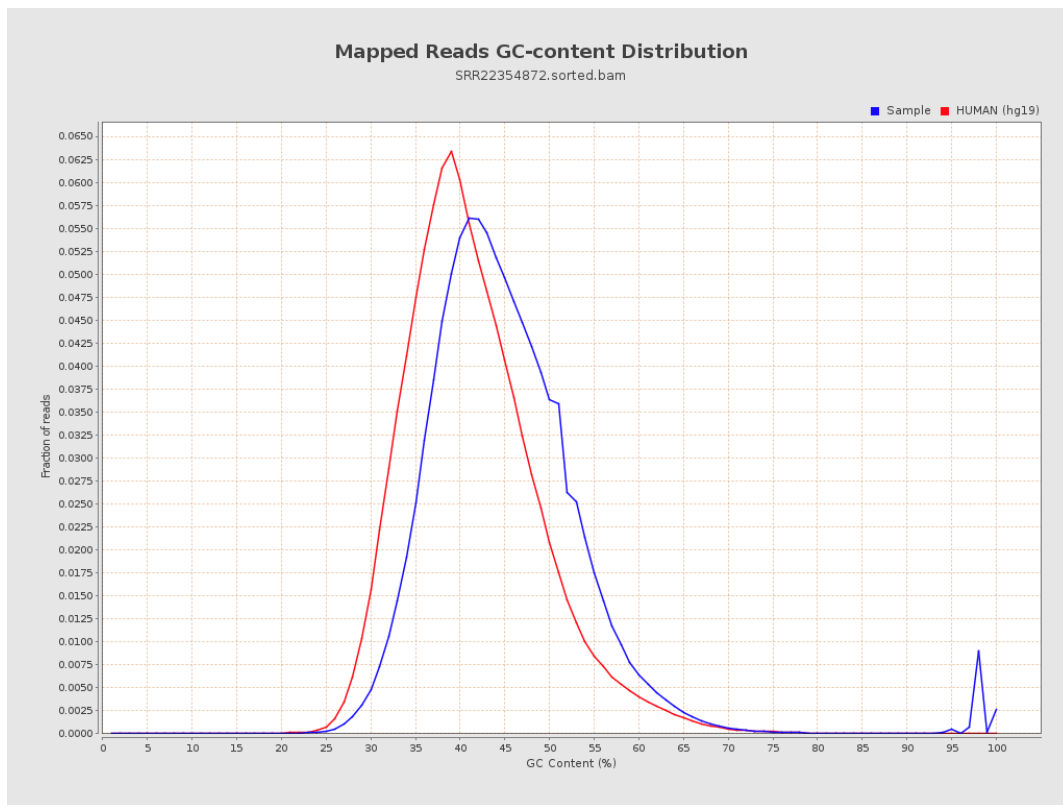
7. Results : Duplication Rate Histogram



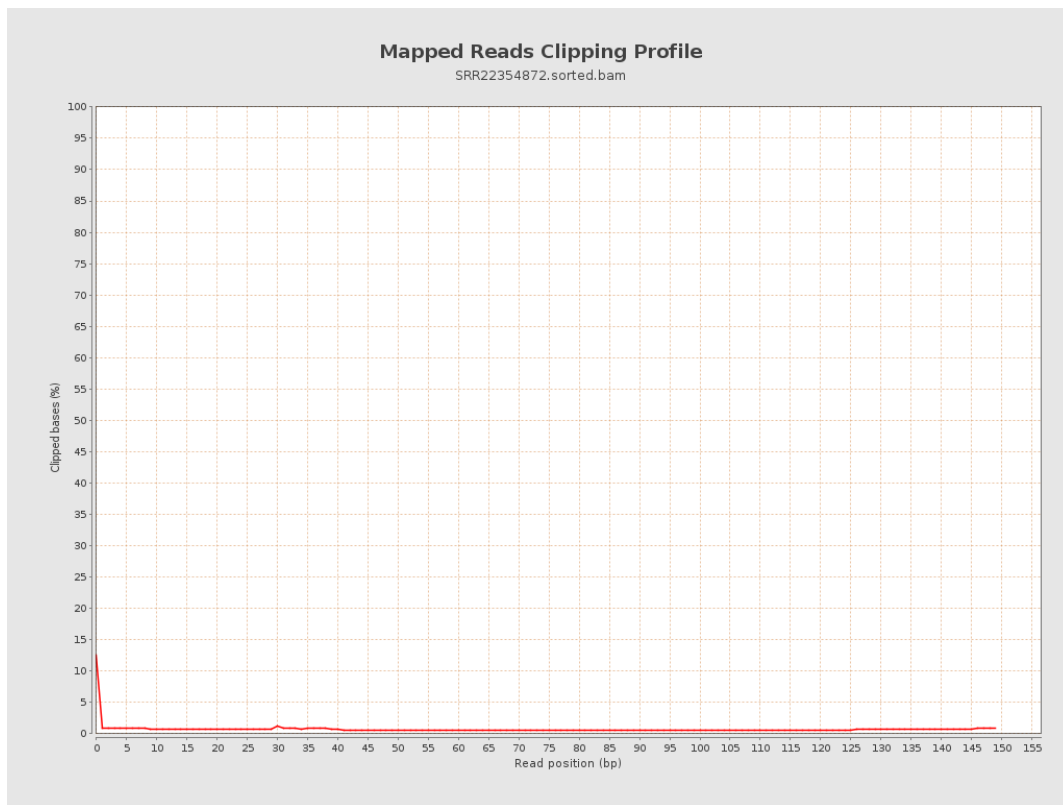
8. Results : Mapped Reads Nucleotide Content



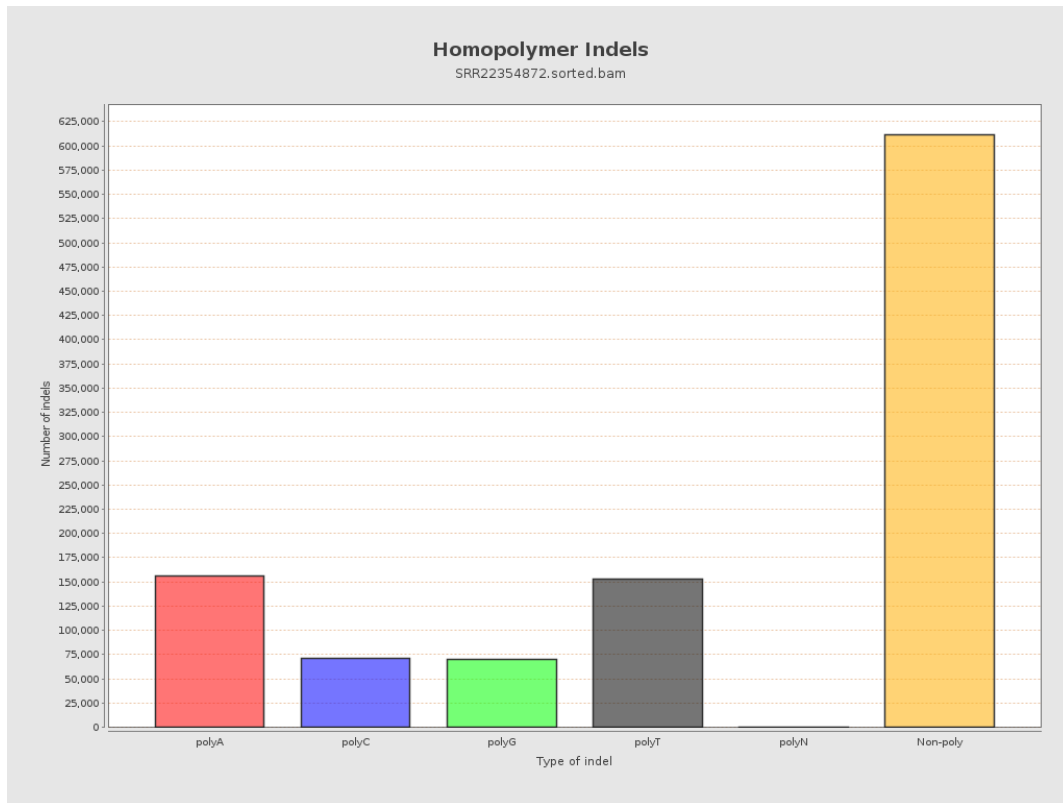
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



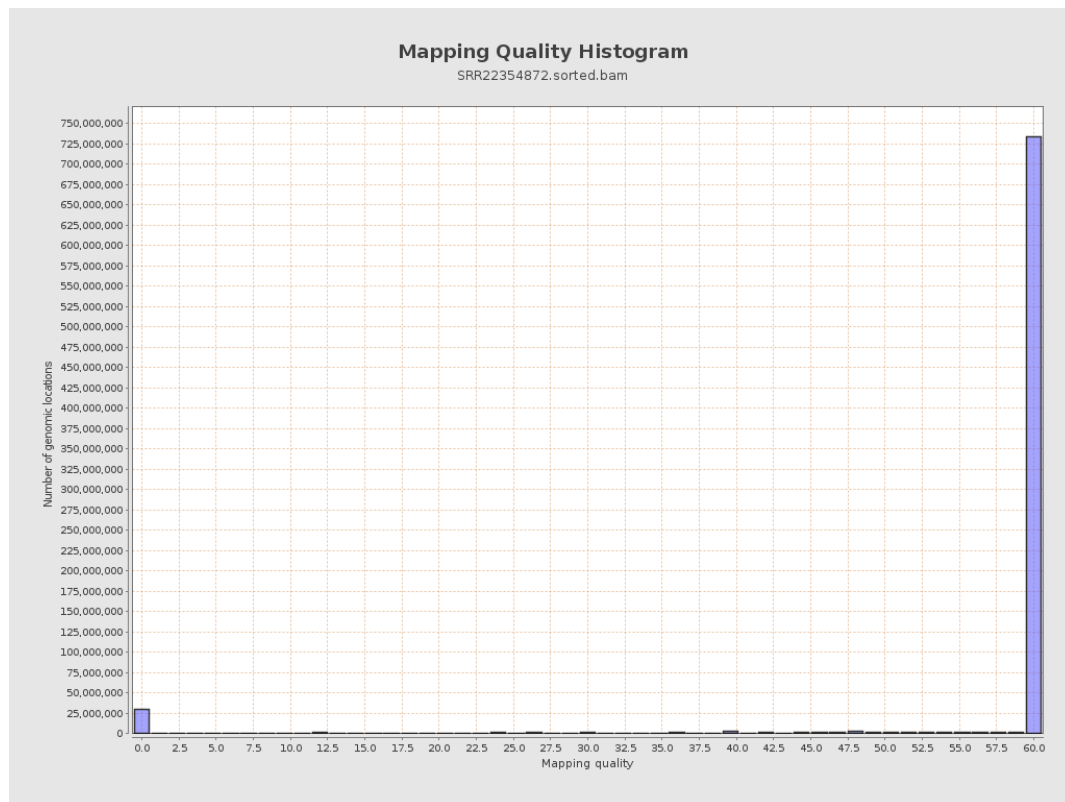
11. Results : Homopolymer Indels



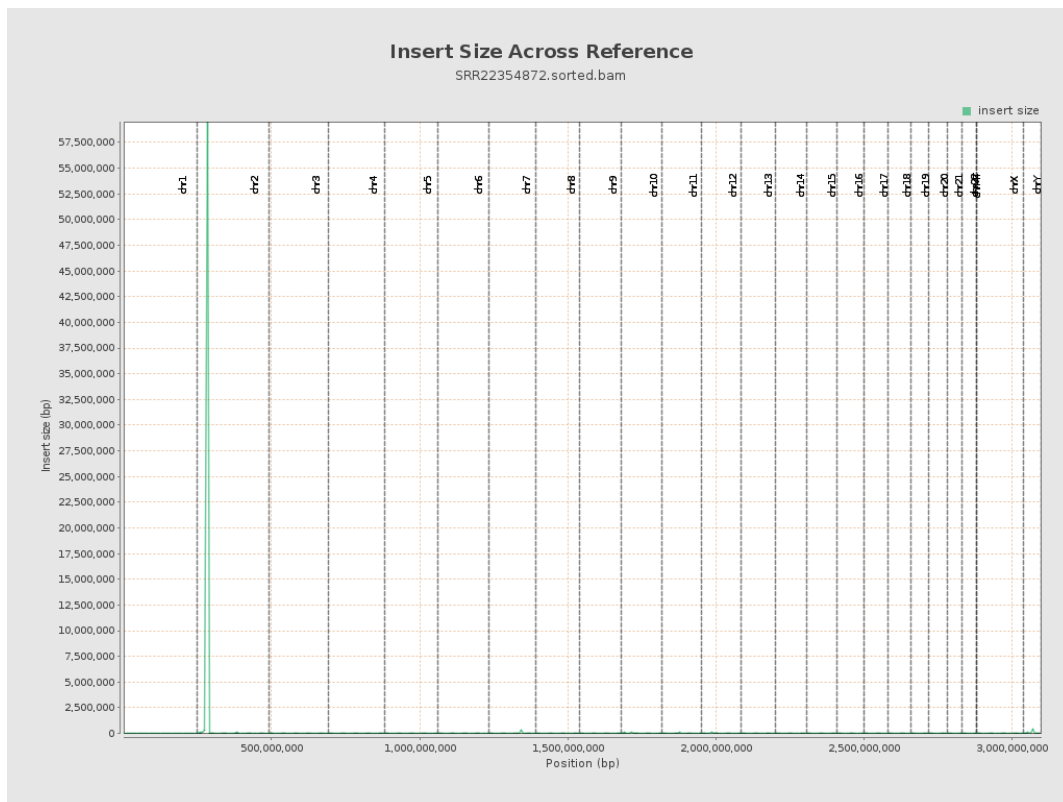
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

