

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 01:09:43

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354874.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_SRR22354874 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354874_1.fastq.gz SRR22354874_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 01:09:42 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354874.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,349,652
Mapped reads	23,082,198 / 98.85%
Unmapped reads	267,454 / 1.15%
Mapped paired reads	23,082,198 / 98.85%
Mapped reads, first in pair	11,553,266 / 49.48%
Mapped reads, second in pair	11,528,932 / 49.38%
Mapped reads, both in pair	23,038,358 / 98.67%
Mapped reads, singletons	43,840 / 0.19%
Secondary alignments	0
Supplementary alignments	1,486,936 / 6.37%
Read min/max/mean length	30 / 150 / 152.29
Duplicated reads (estimated)	14,654,005 / 62.76%
Duplication rate	61.57%
Clipped reads	15,566,237 / 66.67%

2.2. ACGT Content

Number/percentage of A's	710,105,435 / 26.64%
Number/percentage of C's	579,996,116 / 21.76%
Number/percentage of T's	722,483,764 / 27.1%
Number/percentage of G's	653,050,761 / 24.5%
Number/percentage of N's	78,426 / 0%

GC Percentage	46.26%
---------------	--------

2.3. Coverage

Mean	0.8616
Standard Deviation	73.2778

2.4. Mapping Quality

Mean Mapping Quality	53.15
----------------------	-------

2.5. Insert size

Mean	662,270.72
Standard Deviation	9,441,948.43
P25/Median/P75	83 / 129 / 198

2.6. Mismatches and indels

General error rate	0.62%
Mismatches	15,030,814
Insertions	446,047
Mapped reads with at least one insertion	1.79%
Deletions	452,477
Mapped reads with at least one deletion	1.86%
Homopolymer indels	41.96%

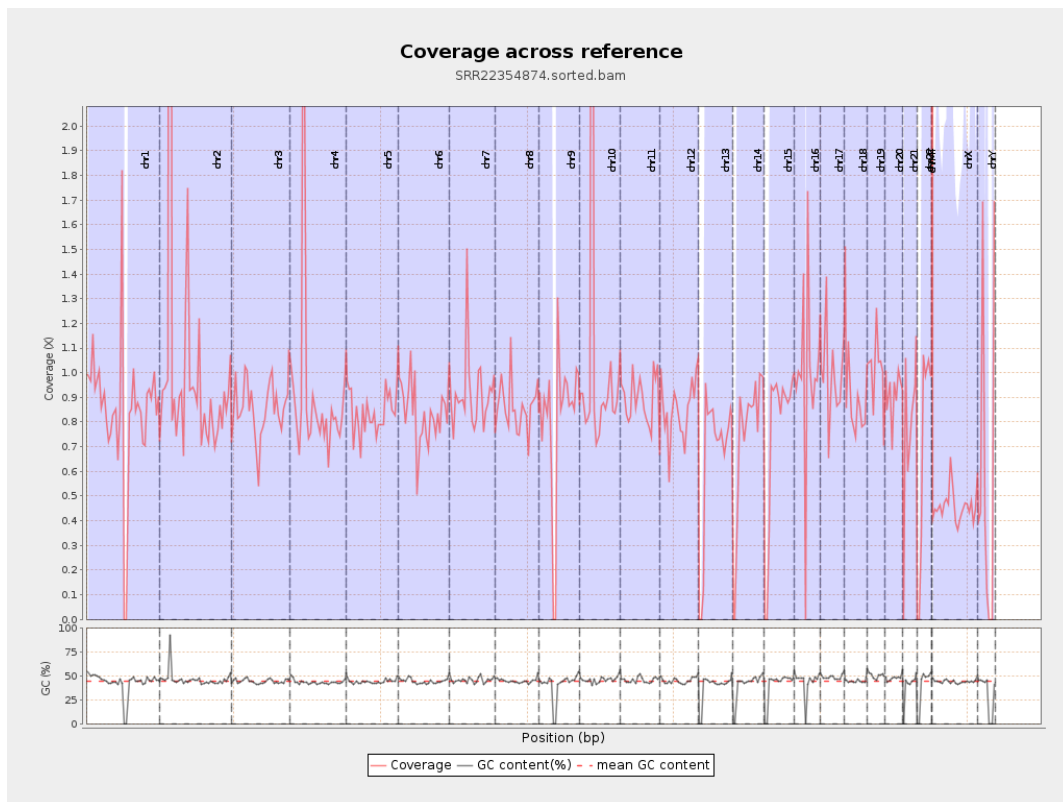
2.7. Chromosome stats

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

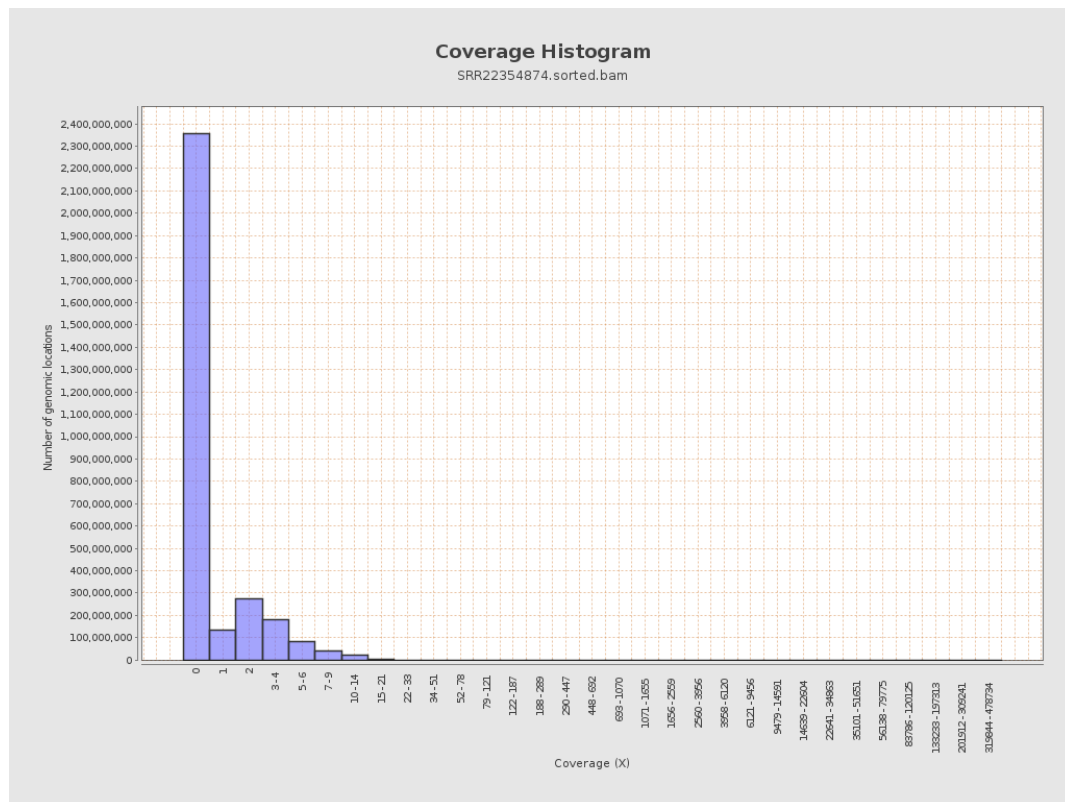
		bases	coverage	deviation
chr1	249250621	211958498	0.8504	22.4464
chr2	243199373	270803428	1.1135	257.3246
chr3	198022430	169623498	0.8566	3.2065
chr4	191154276	172912719	0.9046	14.8501
chr5	180915260	152906173	0.8452	2.1505
chr6	171115067	142500829	0.8328	3.2291
chr7	159138663	145899988	0.9168	22.4785
chr8	146364022	126658472	0.8654	3.6056
chr9	141213431	114186014	0.8086	10.7895
chr10	135534747	151040764	1.1144	36.2329
chr11	135006516	121800724	0.9022	5.199
chr12	133851895	113601860	0.8487	2.0202
chr13	115169878	75959199	0.6595	1.7177
chr14	107349540	78649230	0.7326	10.3242
chr15	102531392	76527628	0.7464	1.8411
chr16	90354753	90258873	0.9989	7.1755
chr17	81195210	79871973	0.9837	5.573
chr18	78077248	69185462	0.8861	11.0054
chr19	59128983	60761795	1.0276	12.4228
chr20	63025520	57662495	0.9149	4.9029
chr21	48129895	37823234	0.7859	7.7267
chr22	51304566	36316987	0.7079	3.0559
chrMT	16571	3751713	226.4023	69.5991
chrX	155270560	70724293	0.4555	2.2174

chrY	59373566	35714420	0.6015	18.9371
------	----------	----------	--------	---------

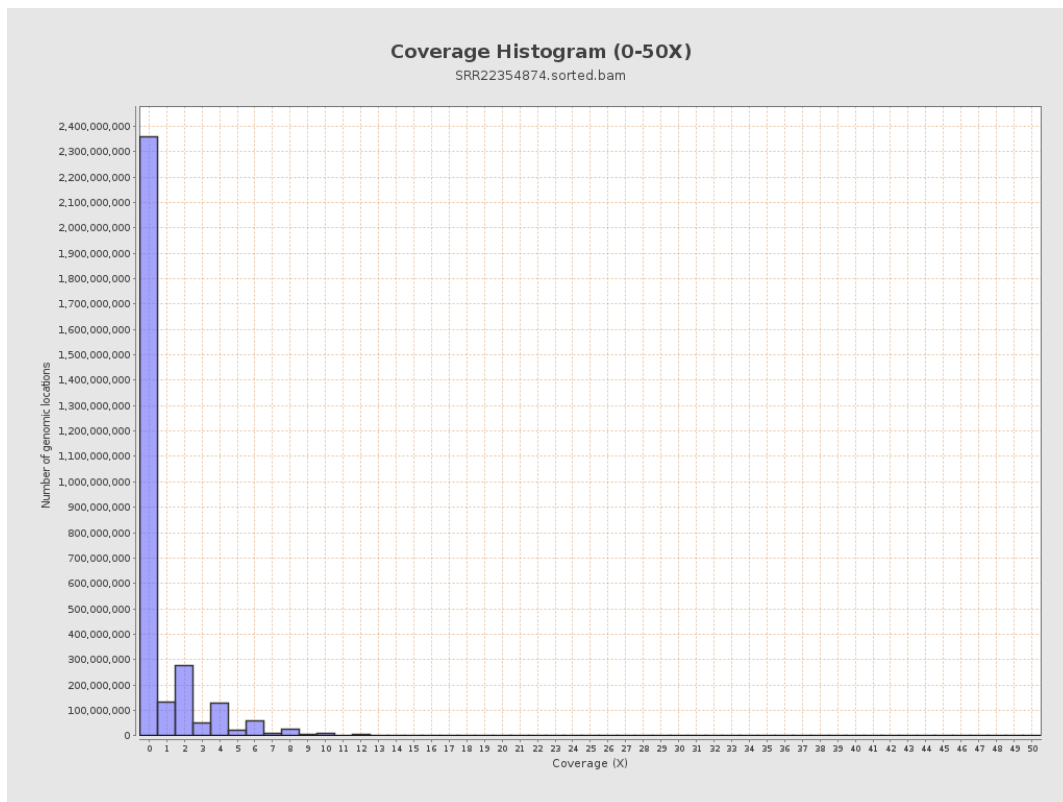
3. Results : Coverage across reference



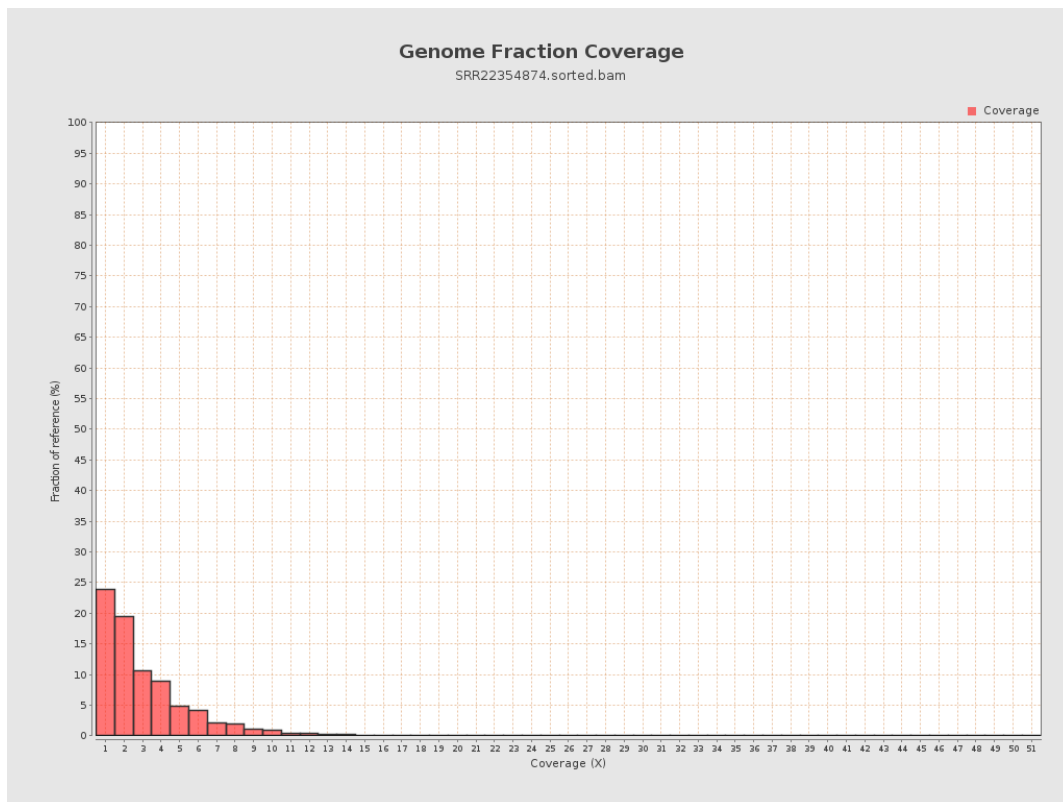
4. Results : Coverage Histogram



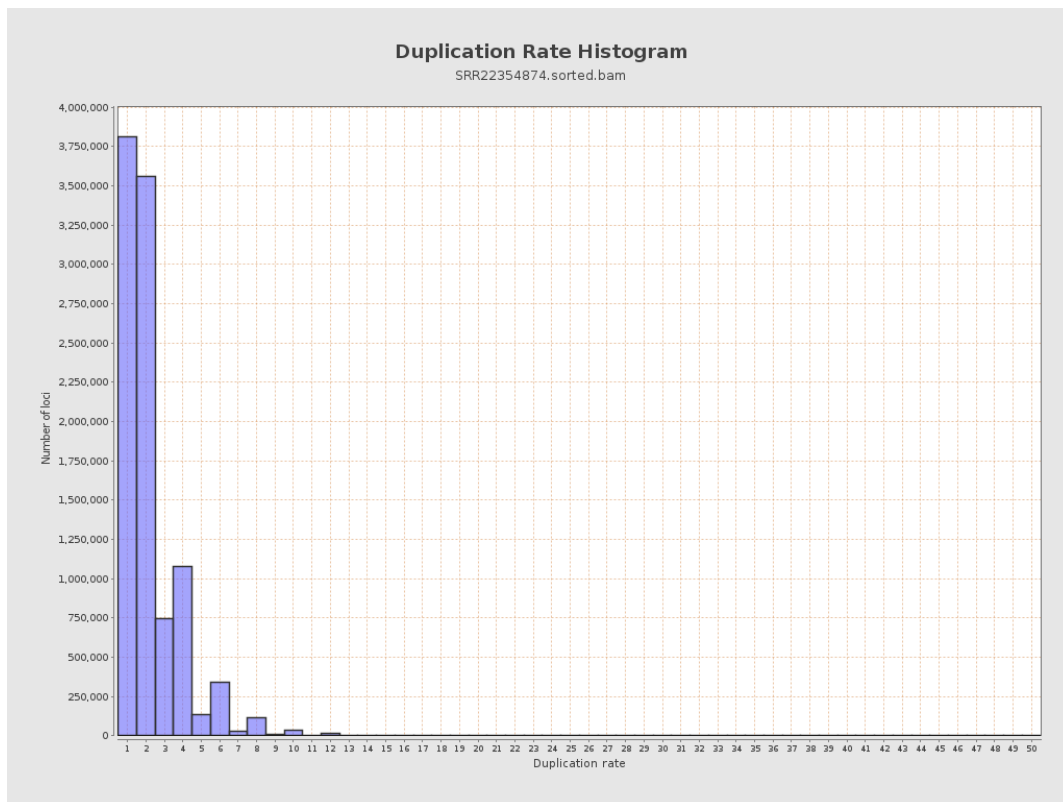
5. Results : Coverage Histogram (0-50X)



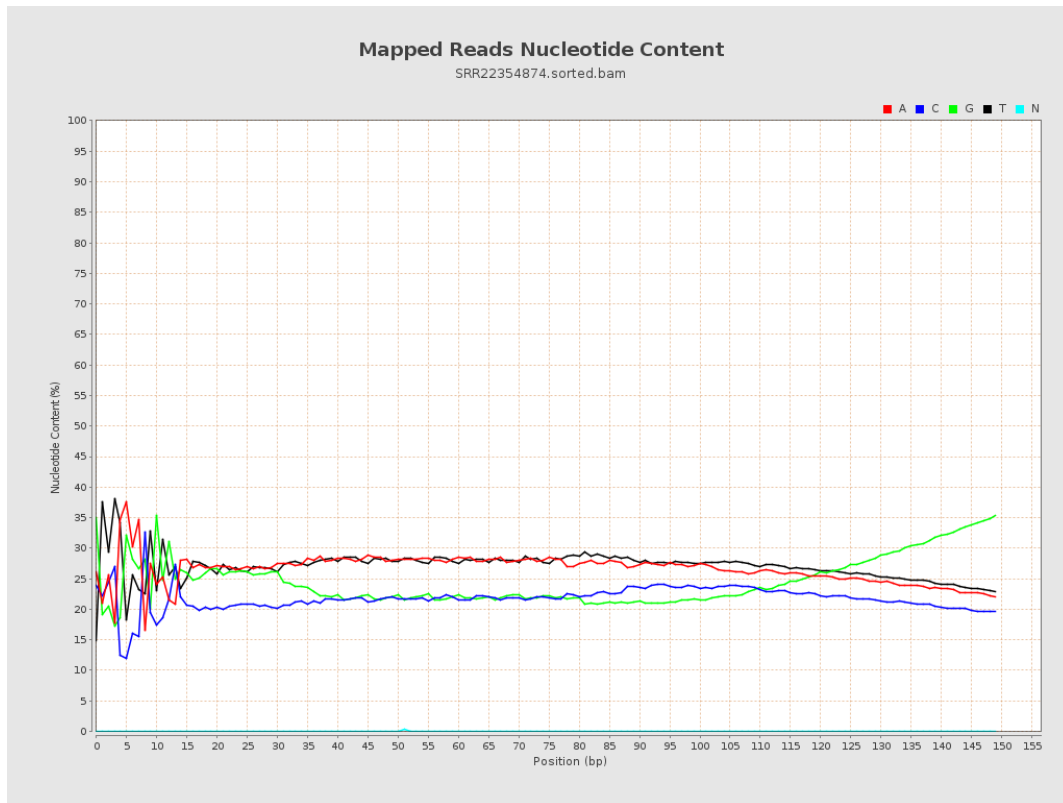
6. Results : Genome Fraction Coverage



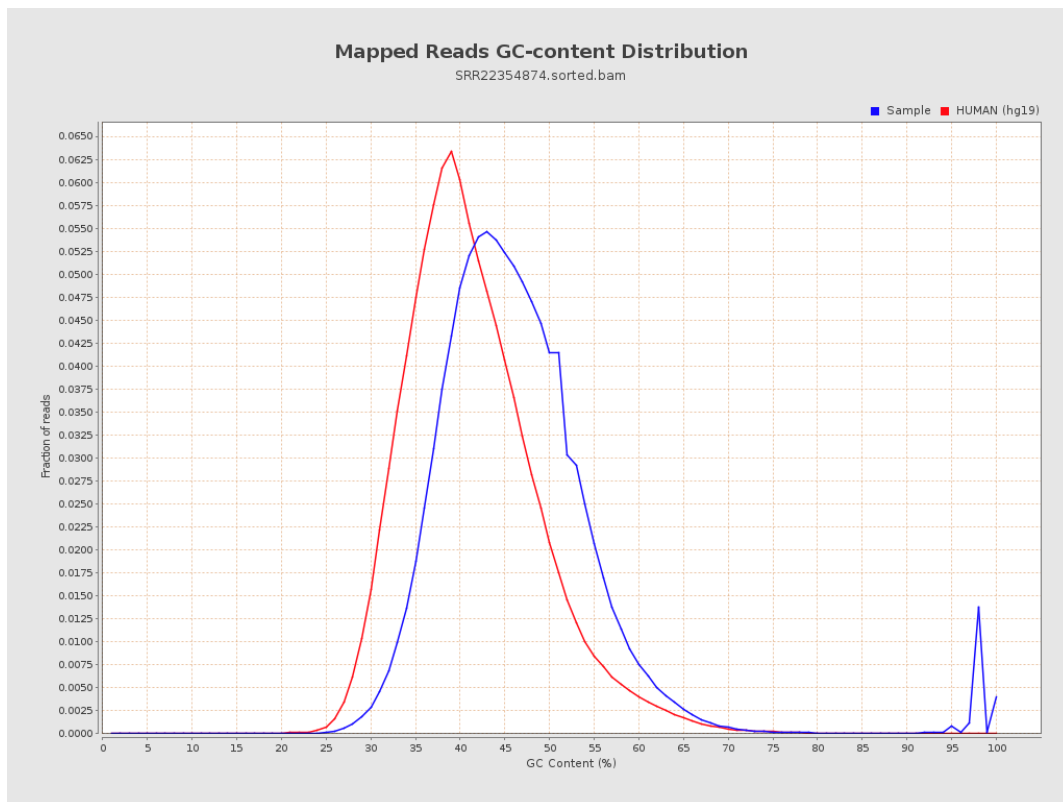
7. Results : Duplication Rate Histogram



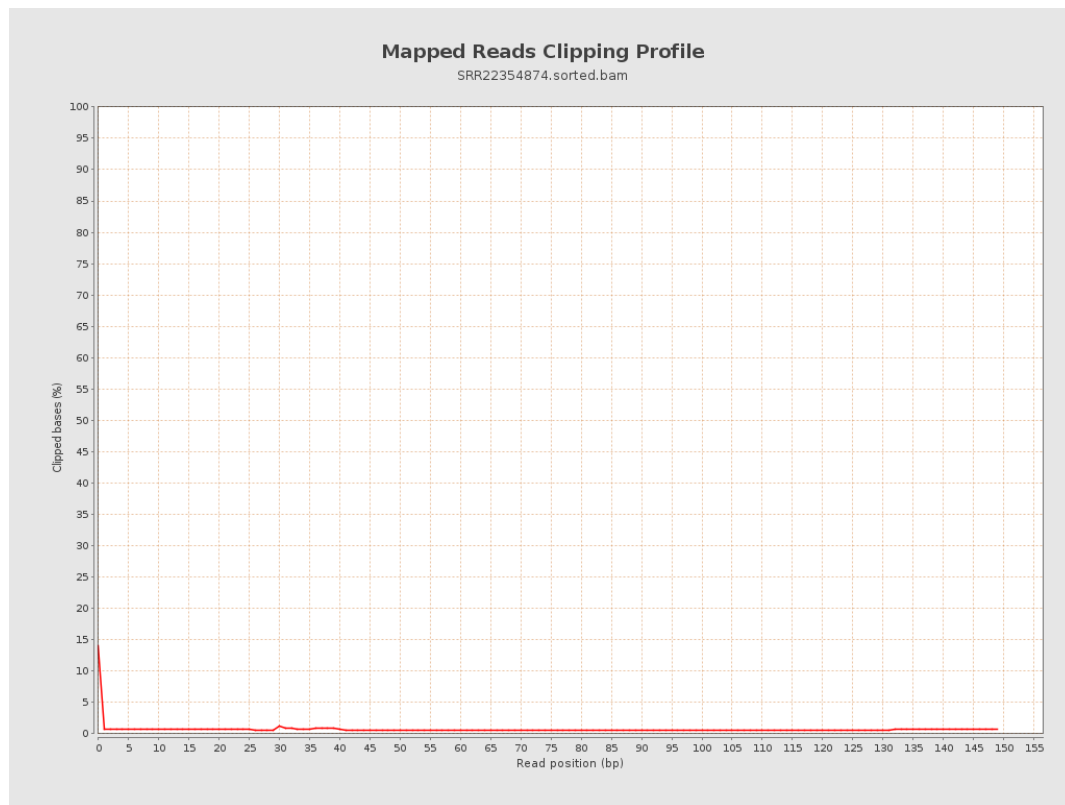
8. Results : Mapped Reads Nucleotide Content



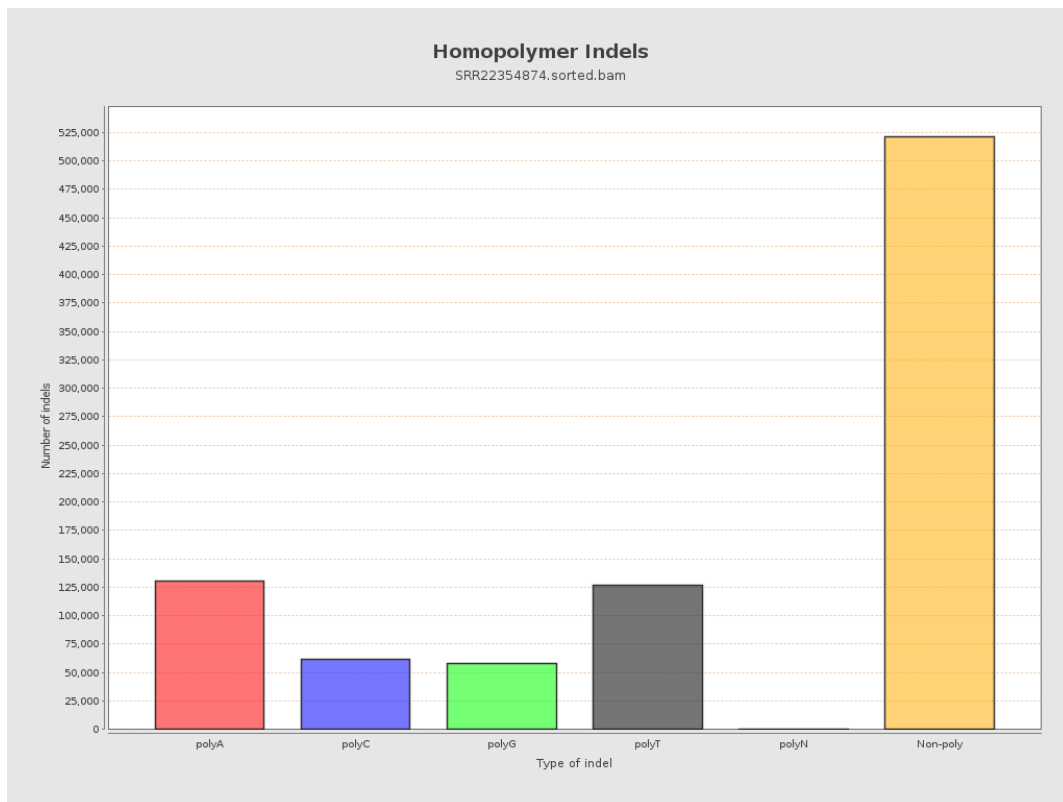
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



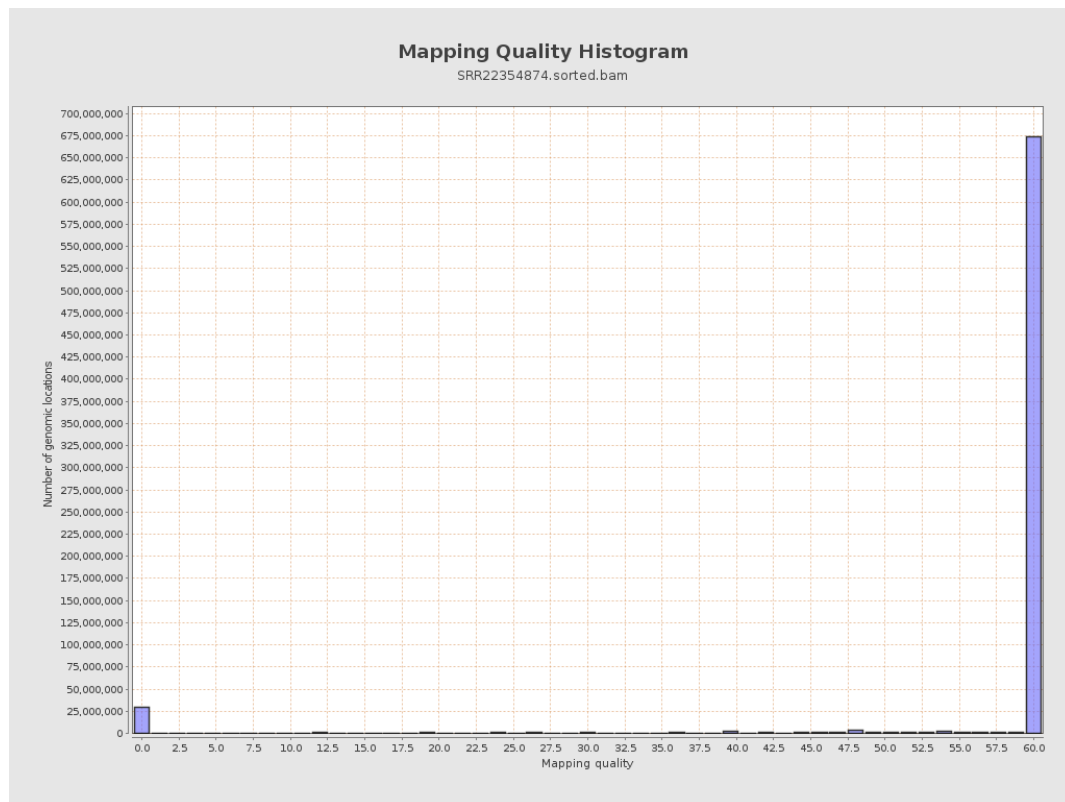
11. Results : Homopolymer Indels



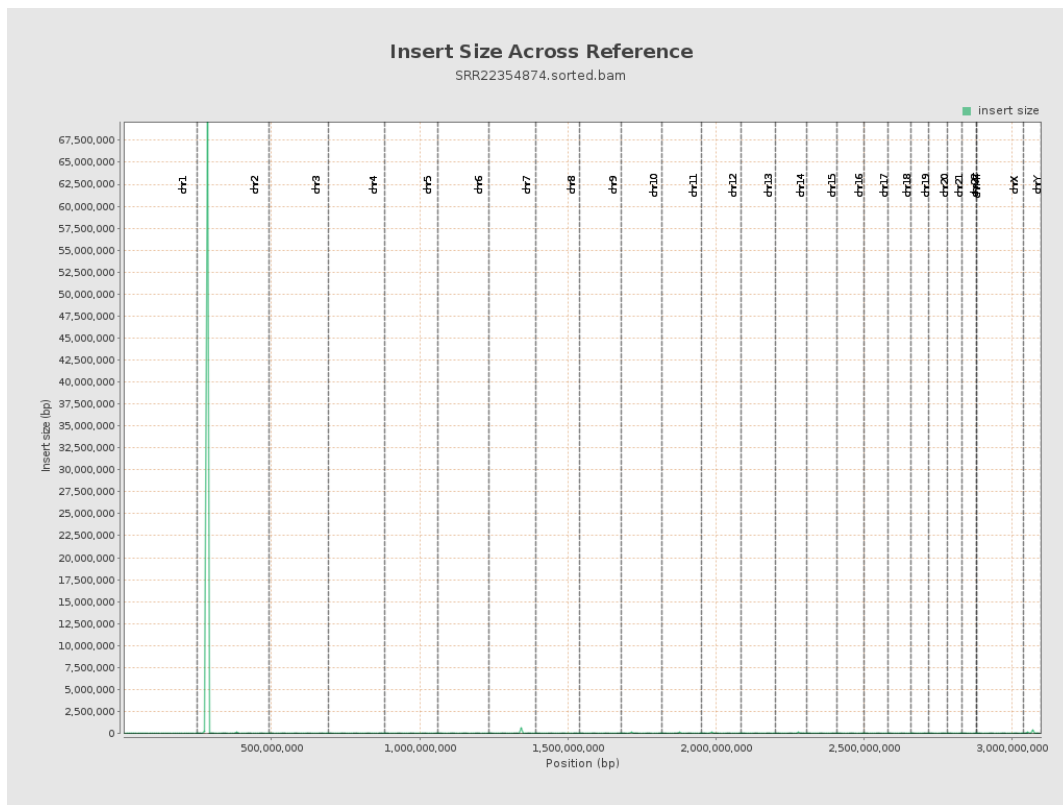
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

