

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 01:45:21

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354875.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_SRR22354875 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354875_1.fastq.gz SRR22354875_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 01:45:21 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354875.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	23,293,756
Mapped reads	23,059,629 / 98.99%
Unmapped reads	234,127 / 1.01%
Mapped paired reads	23,059,629 / 98.99%
Mapped reads, first in pair	11,540,599 / 49.54%
Mapped reads, second in pair	11,519,030 / 49.45%
Mapped reads, both in pair	23,018,564 / 98.82%
Mapped reads, singletons	41,065 / 0.18%
Secondary alignments	0
Supplementary alignments	1,223,576 / 5.25%
Read min/max/mean length	30 / 150 / 151.91
Duplicated reads (estimated)	14,815,136 / 63.6%
Duplication rate	62.83%
Clipped reads	13,971,280 / 59.98%

2.2. ACGT Content

Number/percentage of A's	745,349,970 / 26.87%
Number/percentage of C's	609,438,539 / 21.97%
Number/percentage of T's	764,989,212 / 27.58%
Number/percentage of G's	653,805,626 / 23.57%
Number/percentage of N's	81,224 / 0%

GC Percentage	45.54%
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2.3. Coverage

Mean	0.8964
Standard Deviation	61.4159

2.4. Mapping Quality

Mean Mapping Quality	53.39
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2.5. Insert size

Mean	522,544.8
Standard Deviation	8,351,465.38
P25/Median/P75	92 / 141 / 212

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	15,900,939
Insertions	449,438
Mapped reads with at least one insertion	1.8%
Deletions	451,497
Mapped reads with at least one deletion	1.85%
Homopolymer indels	41.75%

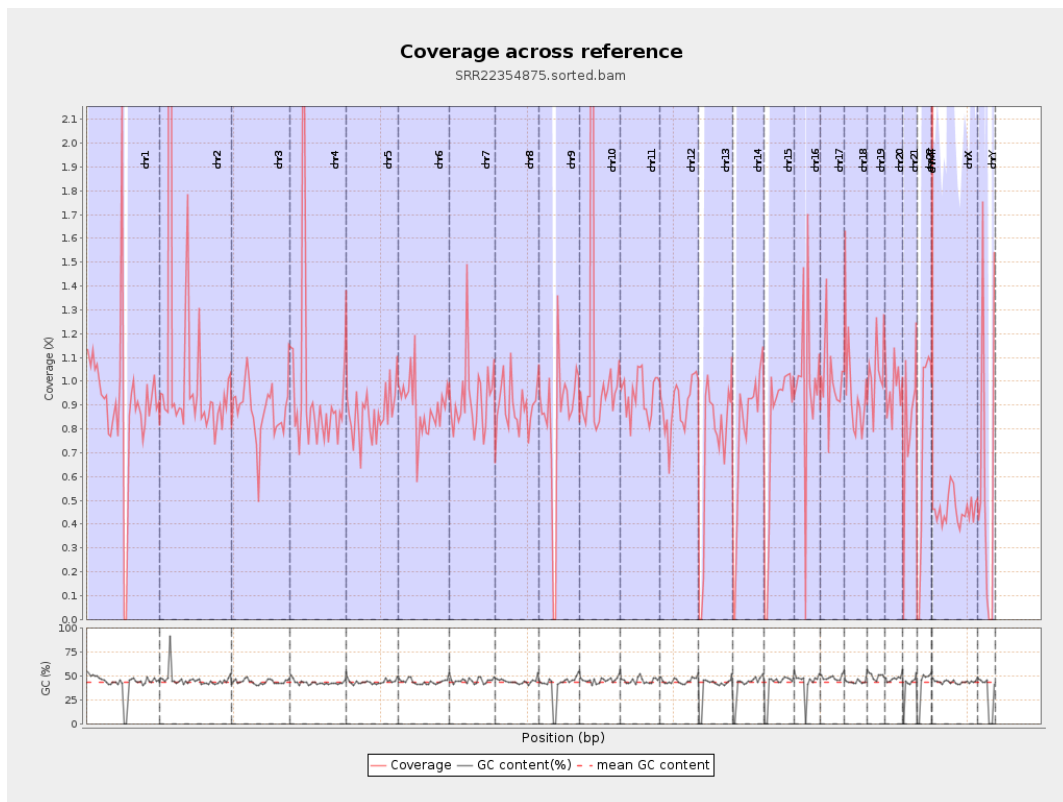
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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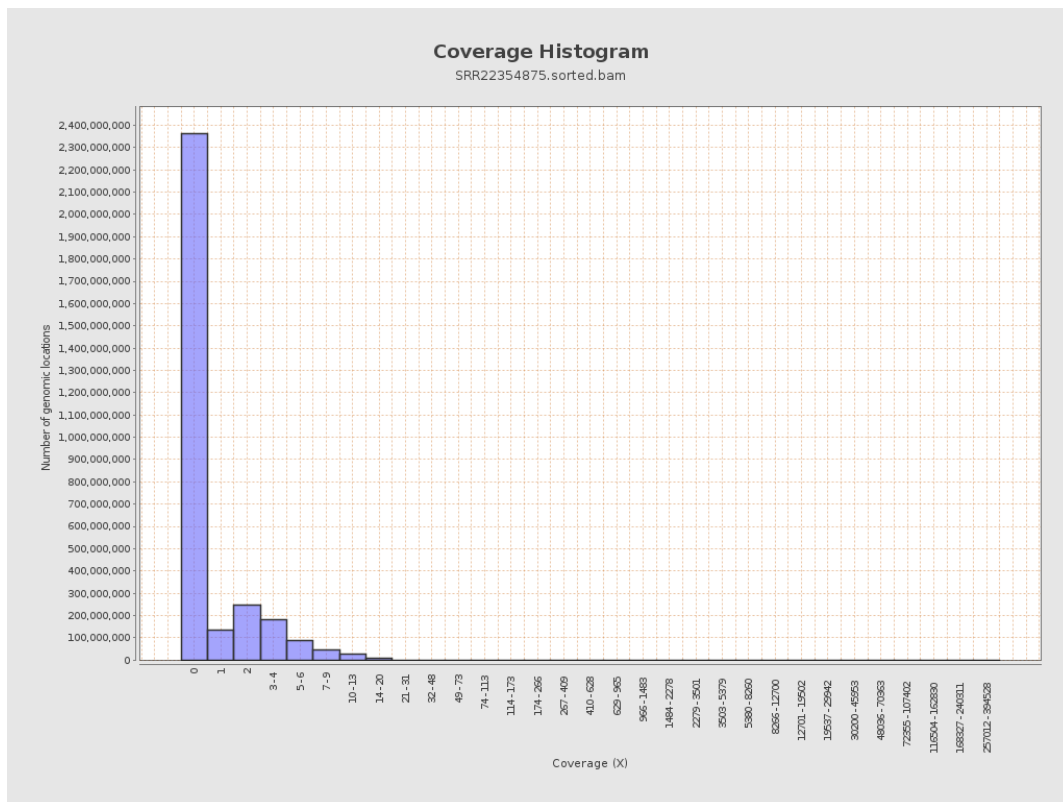
		bases	coverage	deviation
chr1	249250621	226828559	0.91	26.1657
chr2	243199373	272086198	1.1188	213.9008
chr3	198022430	173478504	0.8761	3.035
chr4	191154276	181756940	0.9508	14.3698
chr5	180915260	156944163	0.8675	2.103
chr6	171115067	153157906	0.8951	4.168
chr7	159138663	148251115	0.9316	18.7134
chr8	146364022	131997033	0.9018	3.8247
chr9	141213431	118376887	0.8383	11.0952
chr10	135534747	159413768	1.1762	37.1251
chr11	135006516	127691857	0.9458	5.2833
chr12	133851895	120046188	0.8969	2.1447
chr13	115169878	82908664	0.7199	1.877
chr14	107349540	84316759	0.7854	8.4154
chr15	102531392	81168898	0.7916	1.9765
chr16	90354753	90674050	1.0035	6.6452
chr17	81195210	81573607	1.0047	6.2374
chr18	78077248	73635656	0.9431	11.8215
chr19	59128983	60764972	1.0277	14.4444
chr20	63025520	60937060	0.9669	5.3731
chr21	48129895	40035496	0.8318	8.4437
chr22	51304566	38144656	0.7435	3.1588
chrMT	16571	3377740	203.8344	64.4363
chrX	155270560	71406944	0.4599	2.2373

chrY	59373566	36047571	0.6071	18.8711
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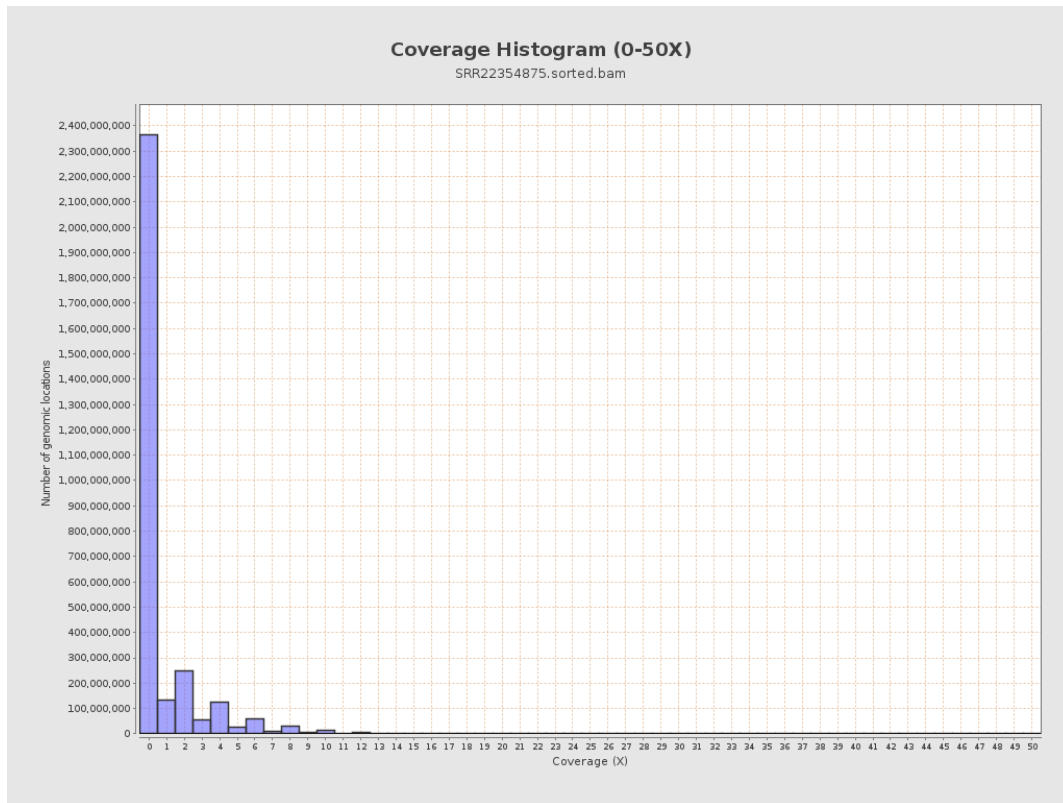
3. Results : Coverage across reference



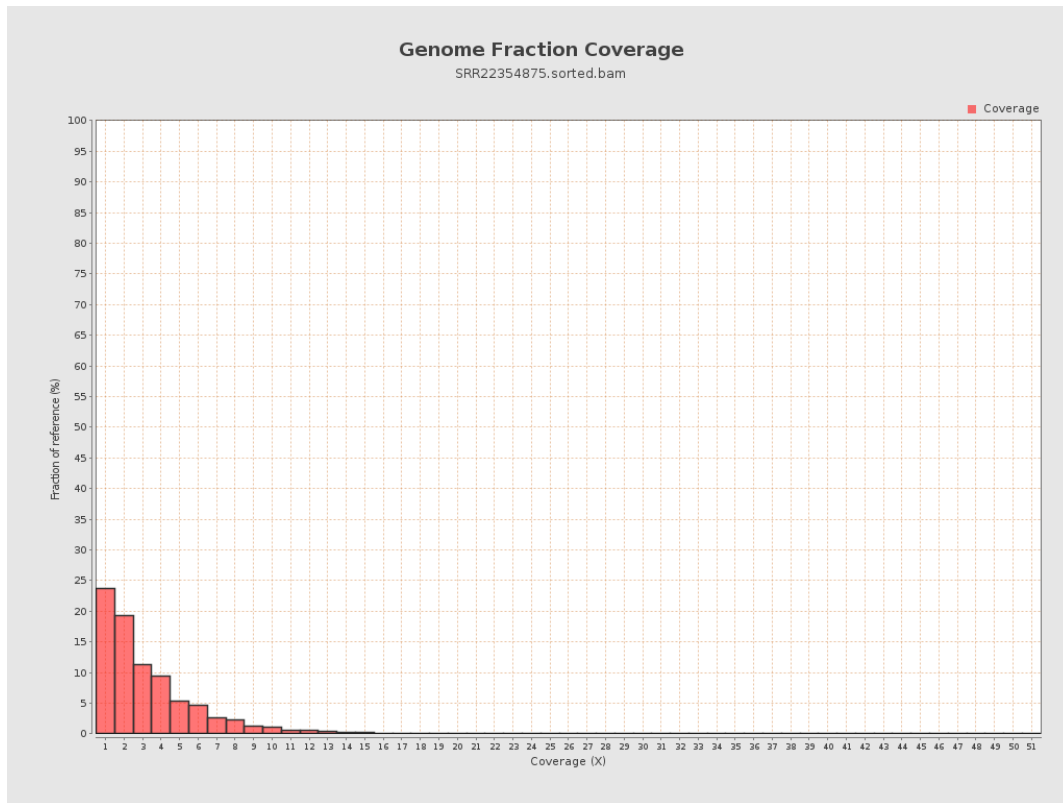
4. Results : Coverage Histogram



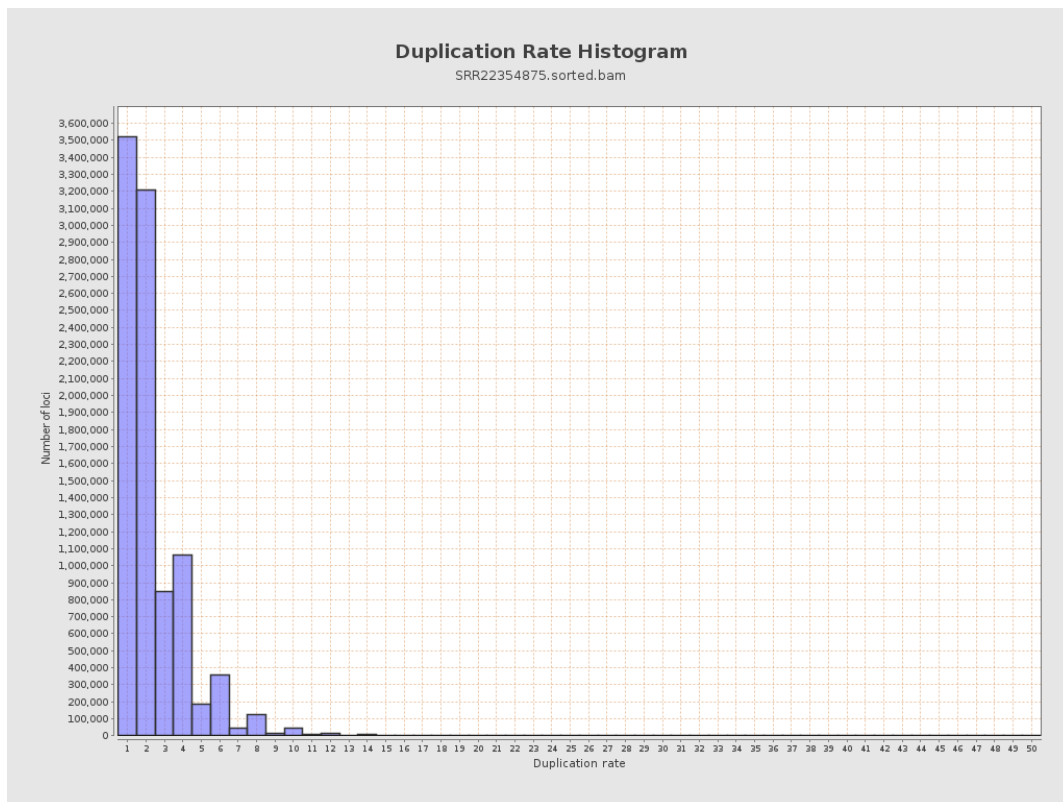
5. Results : Coverage Histogram (0-50X)



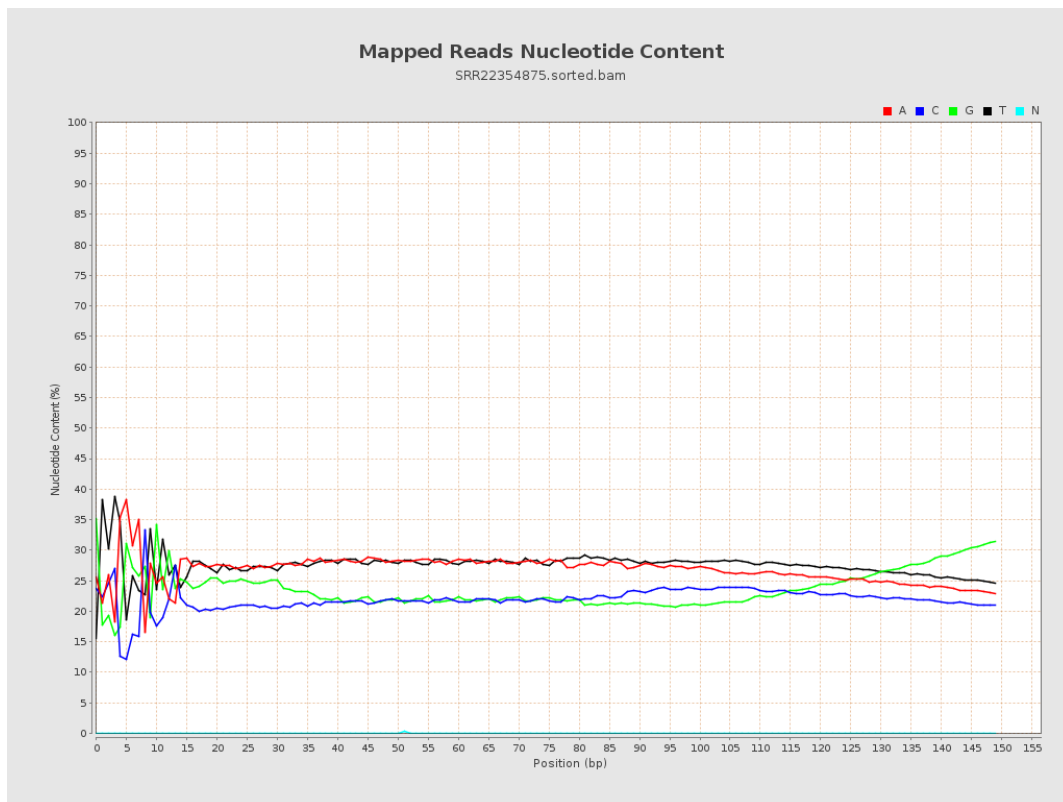
6. Results : Genome Fraction Coverage



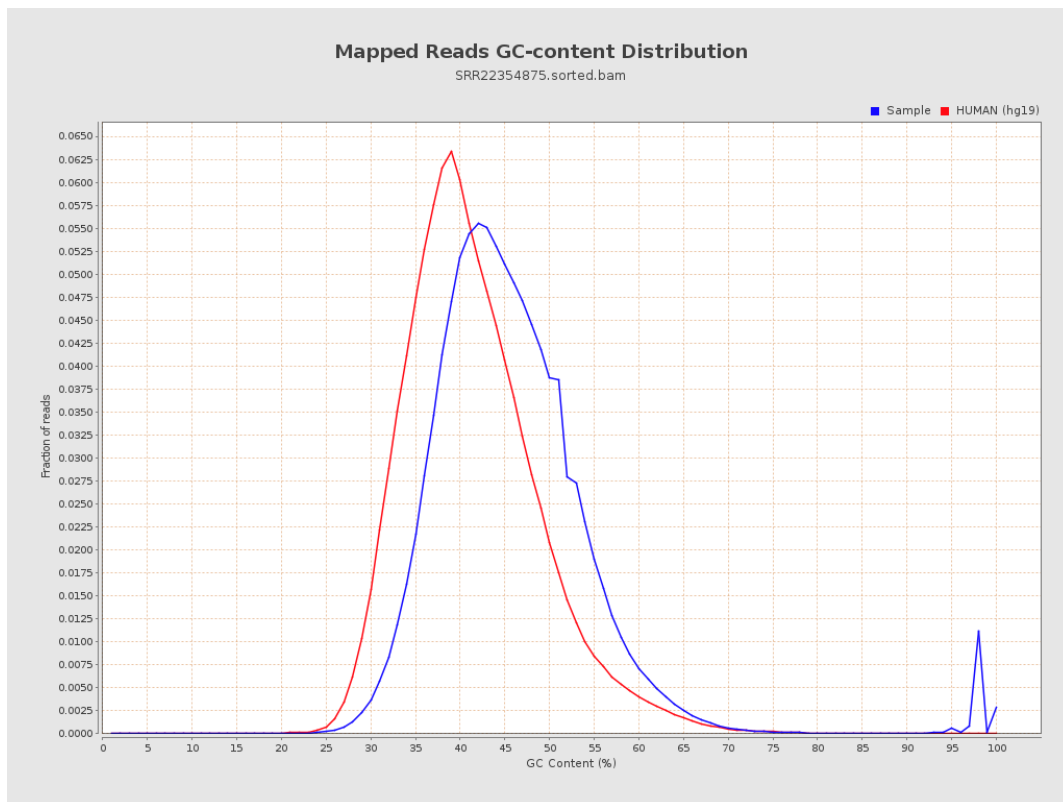
7. Results : Duplication Rate Histogram



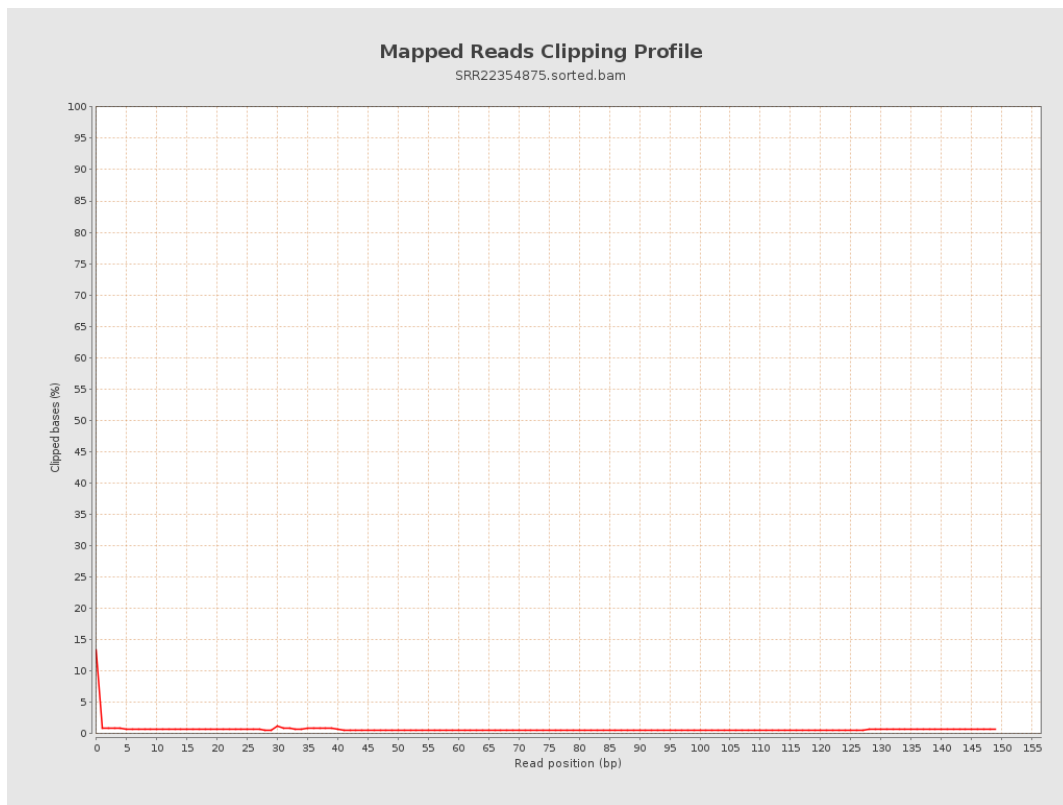
8. Results : Mapped Reads Nucleotide Content



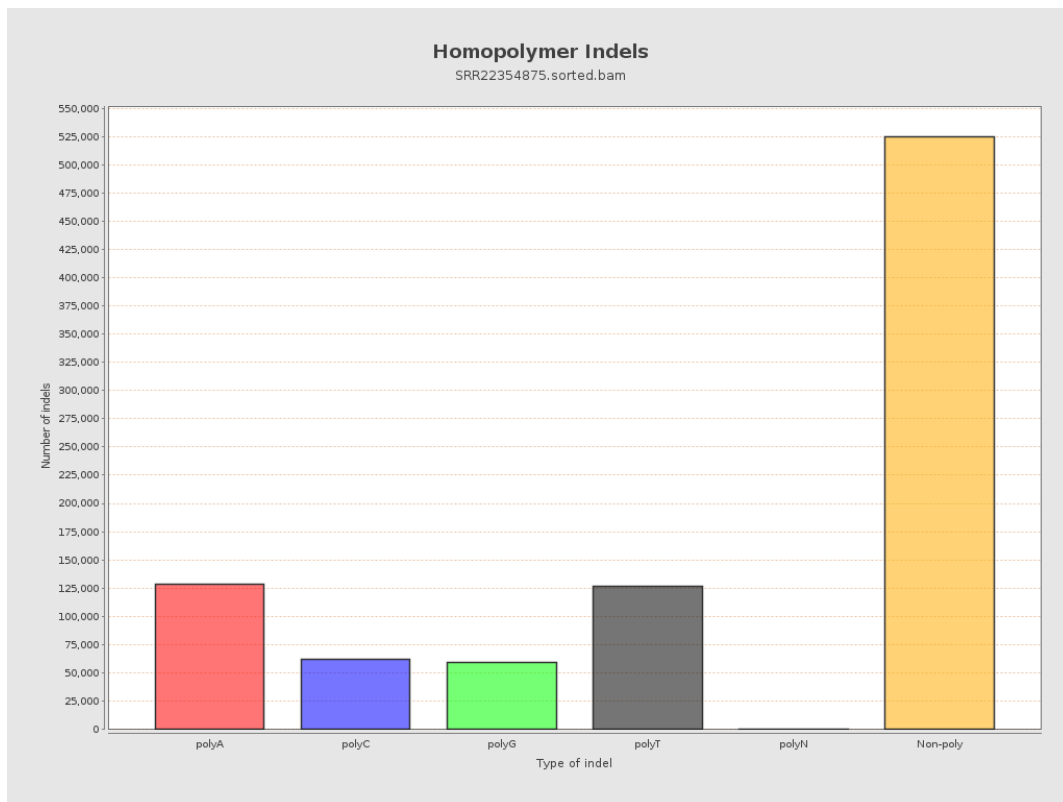
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



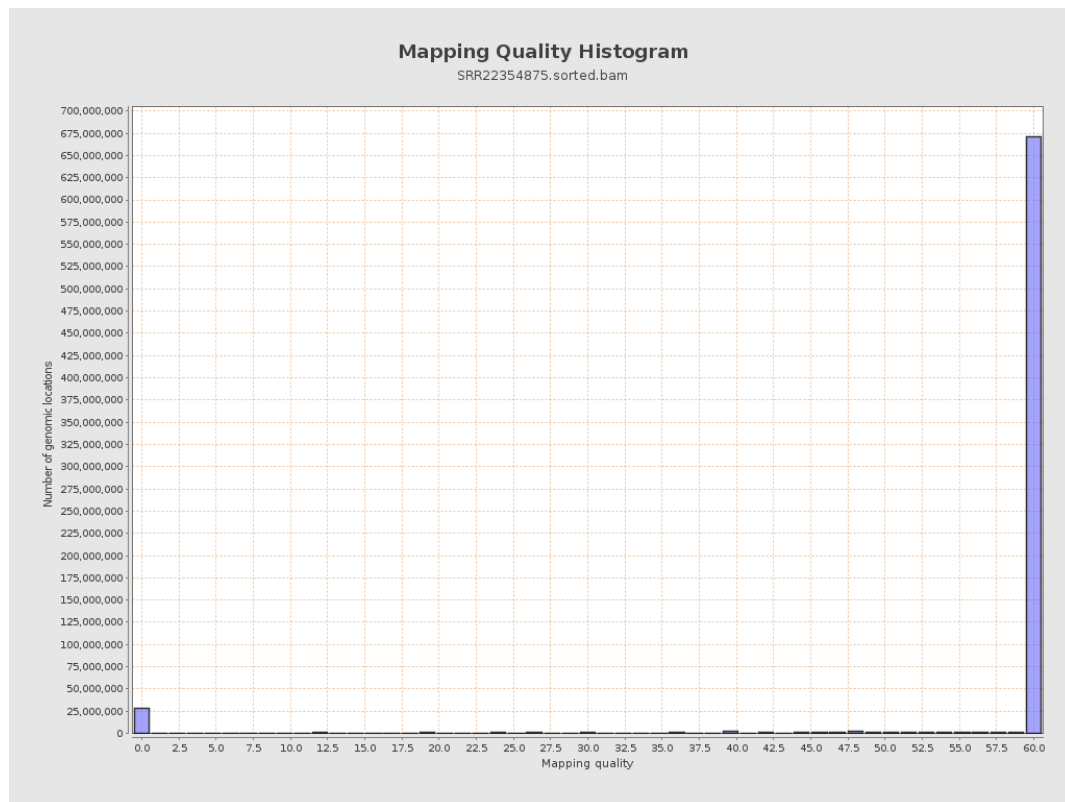
11. Results : Homopolymer Indels



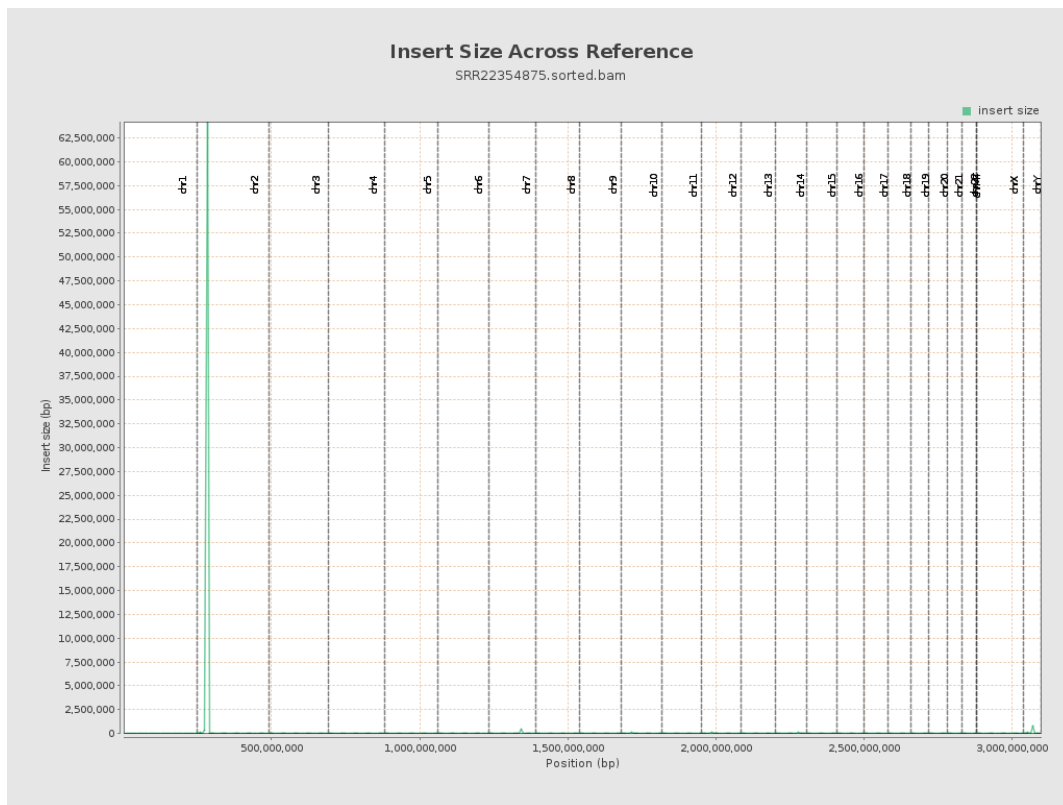
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

