

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/08 07:57:18

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354879.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_SRR22354879 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354879_1.fastq.gz SRR22354879_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 08 07:57:17 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354879.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,739,416
Mapped reads	19,598,673 / 99.29%
Unmapped reads	140,743 / 0.71%
Mapped paired reads	19,598,673 / 99.29%
Mapped reads, first in pair	9,808,312 / 49.69%
Mapped reads, second in pair	9,790,361 / 49.6%
Mapped reads, both in pair	19,560,192 / 99.09%
Mapped reads, singletons	38,481 / 0.19%
Secondary alignments	0
Supplementary alignments	461,101 / 2.34%
Read min/max/mean length	30 / 150 / 150.91
Duplicated reads (estimated)	7,032,613 / 35.63%
Duplication rate	33.81%
Clipped reads	7,800,055 / 39.52%

2.2. ACGT Content

Number/percentage of A's	744,891,273 / 28.7%
Number/percentage of C's	540,524,431 / 20.83%
Number/percentage of T's	751,537,228 / 28.96%
Number/percentage of G's	558,255,032 / 21.51%
Number/percentage of N's	11,944 / 0%

GC Percentage	42.34%
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2.3. Coverage

Mean	0.8388
Standard Deviation	20.4806

2.4. Mapping Quality

Mean Mapping Quality	54.02
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2.5. Insert size

Mean	212,405.36
Standard Deviation	5,277,993.31
P25/Median/P75	125 / 191 / 276

2.6. Mismatches and indels

General error rate	0.8%
Mismatches	19,165,391
Insertions	491,772
Mapped reads with at least one insertion	2.34%
Deletions	513,577
Mapped reads with at least one deletion	2.49%
Homopolymer indels	44.36%

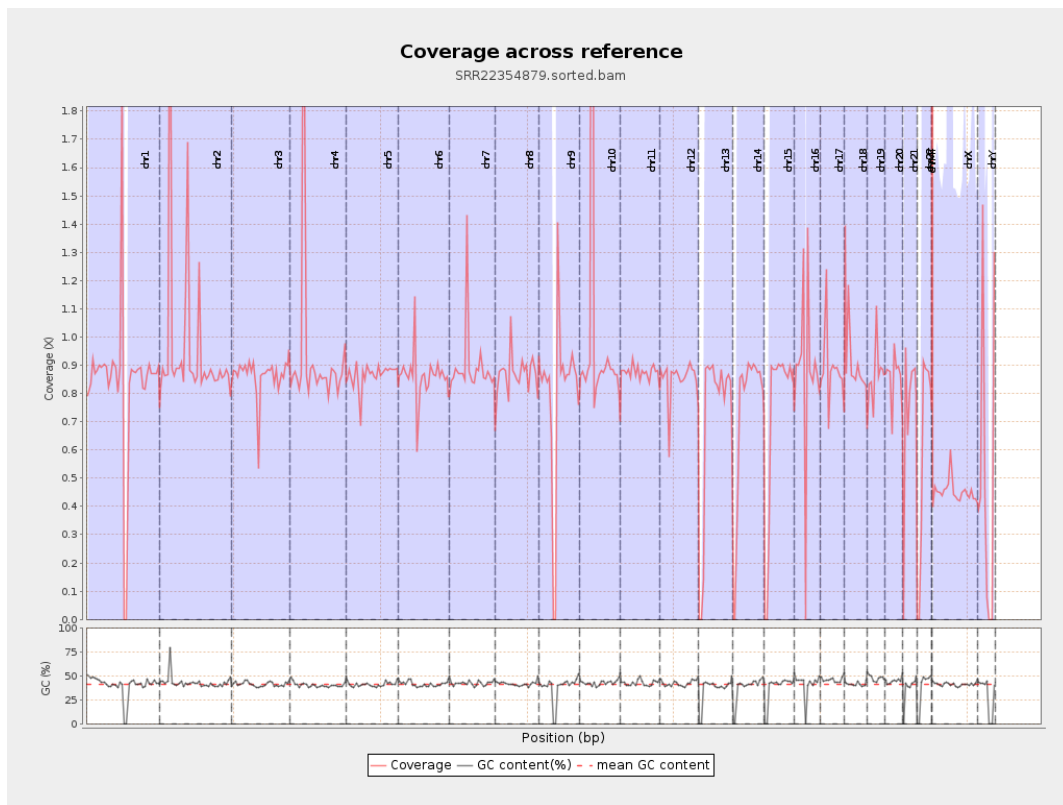
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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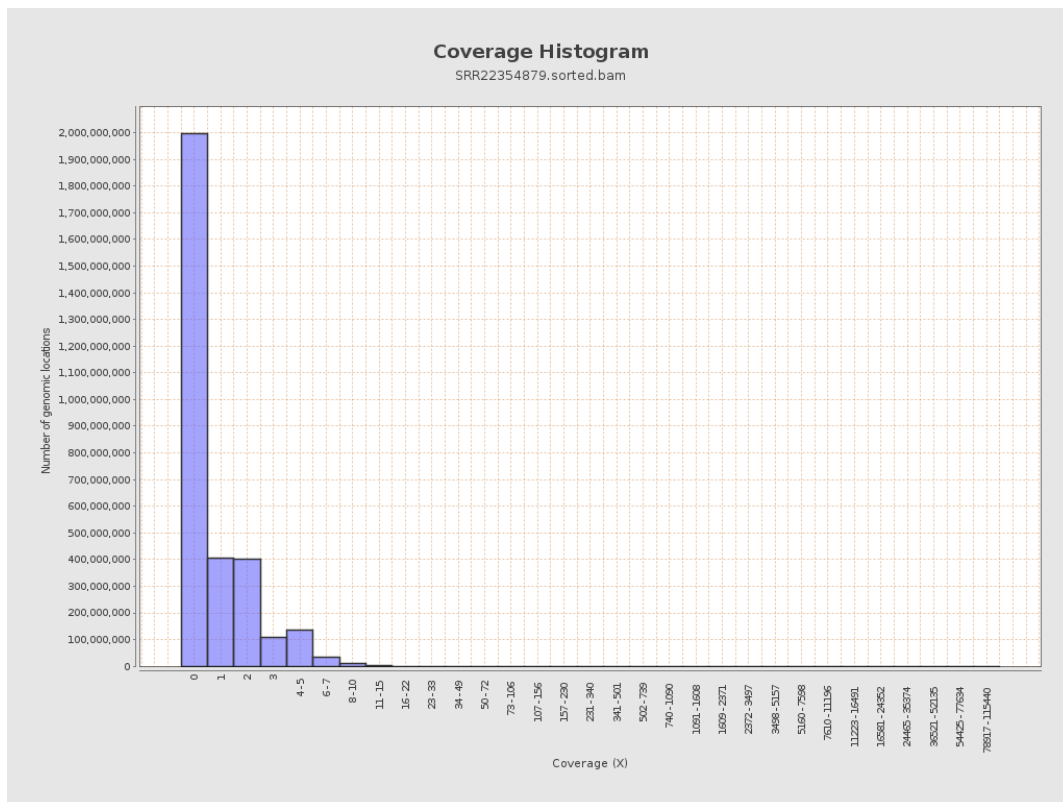
		bases	coverage	deviation
chr1	249250621	211327956	0.8479	23.3789
chr2	243199373	235425471	0.968	61.4069
chr3	198022430	170750286	0.8623	1.8001
chr4	191154276	176747051	0.9246	12.5112
chr5	180915260	156128071	0.863	1.524
chr6	171115067	147804646	0.8638	3.4952
chr7	159138663	141963930	0.8921	12.7694
chr8	146364022	127954164	0.8742	3.5437
chr9	141213431	111304440	0.7882	13.0353
chr10	135534747	143713458	1.0603	28.3172
chr11	135006516	117990265	0.874	4.44
chr12	133851895	114073291	0.8522	1.5285
chr13	115169878	81987315	0.7119	1.3445
chr14	107349540	78088594	0.7274	3.4073
chr15	102531392	73637290	0.7182	1.3485
chr16	90354753	79464411	0.8795	5.5923
chr17	81195210	71691381	0.883	5.1211
chr18	78077248	71508958	0.9159	10.7111
chr19	59128983	51277573	0.8672	11.6045
chr20	63025520	53996996	0.8567	4.1967
chr21	48129895	36368813	0.7556	6.385
chr22	51304566	31044544	0.6051	2.6301
chrMT	16571	11368304	686.0361	127.6333
chrX	155270560	70153832	0.4518	1.8283

chrY	59373566	30889632	0.5203	14.8743
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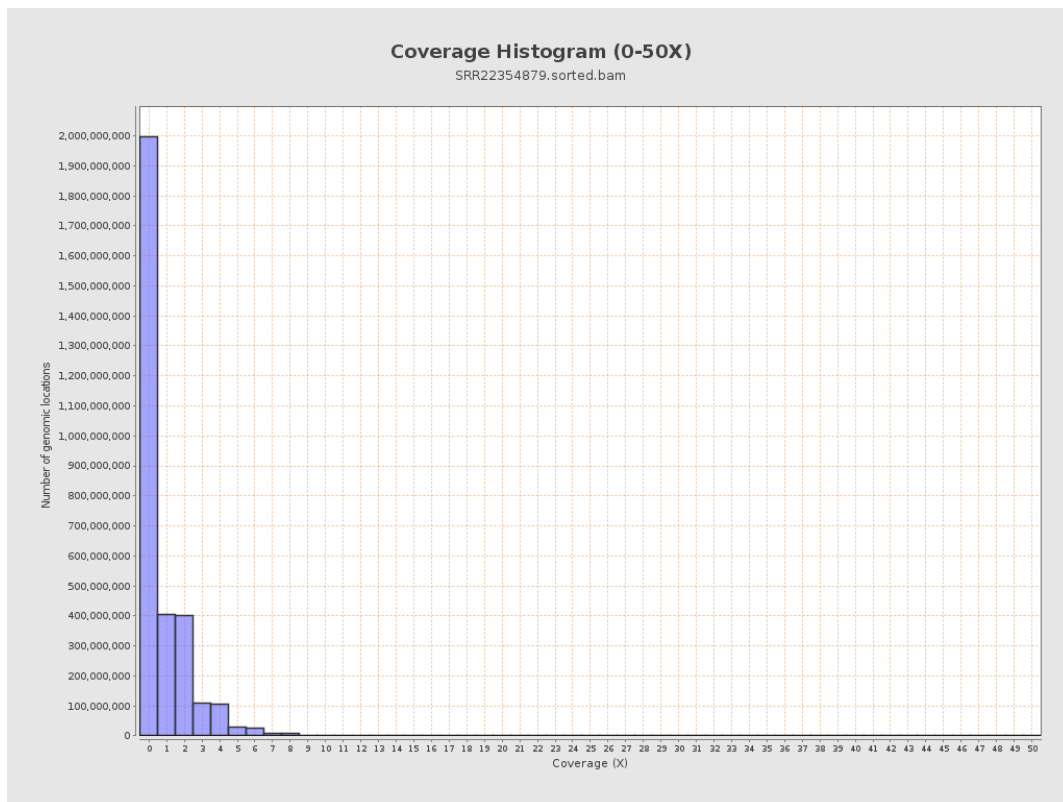
3. Results : Coverage across reference



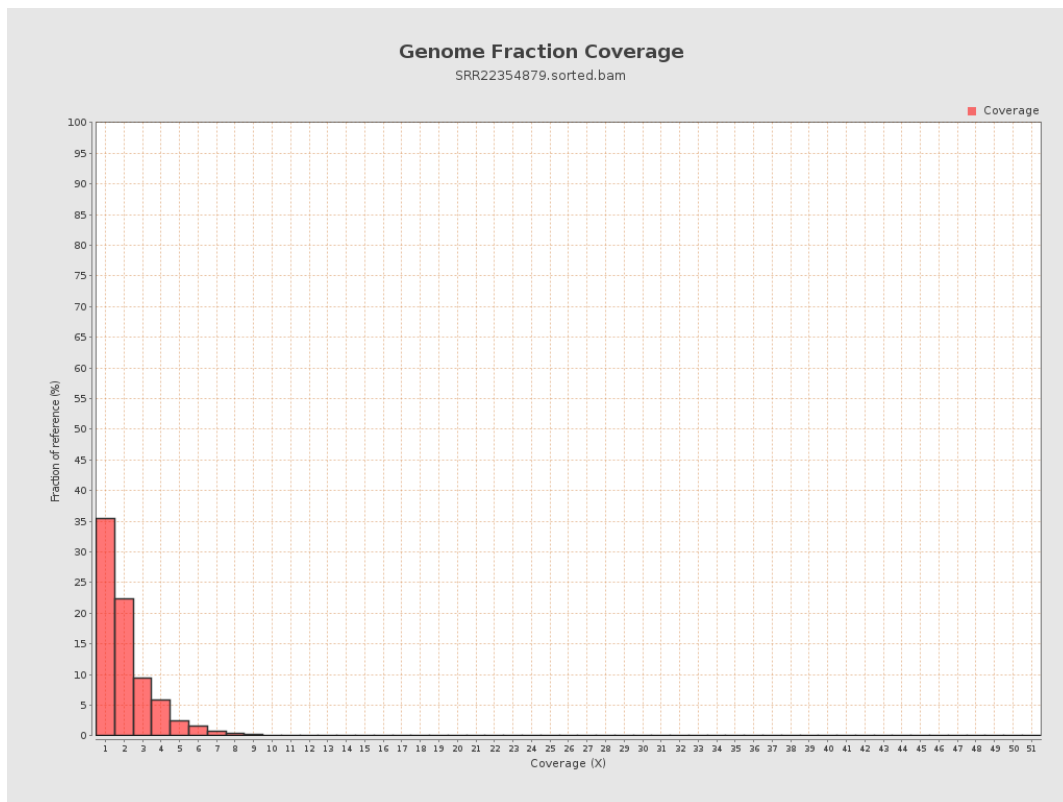
4. Results : Coverage Histogram



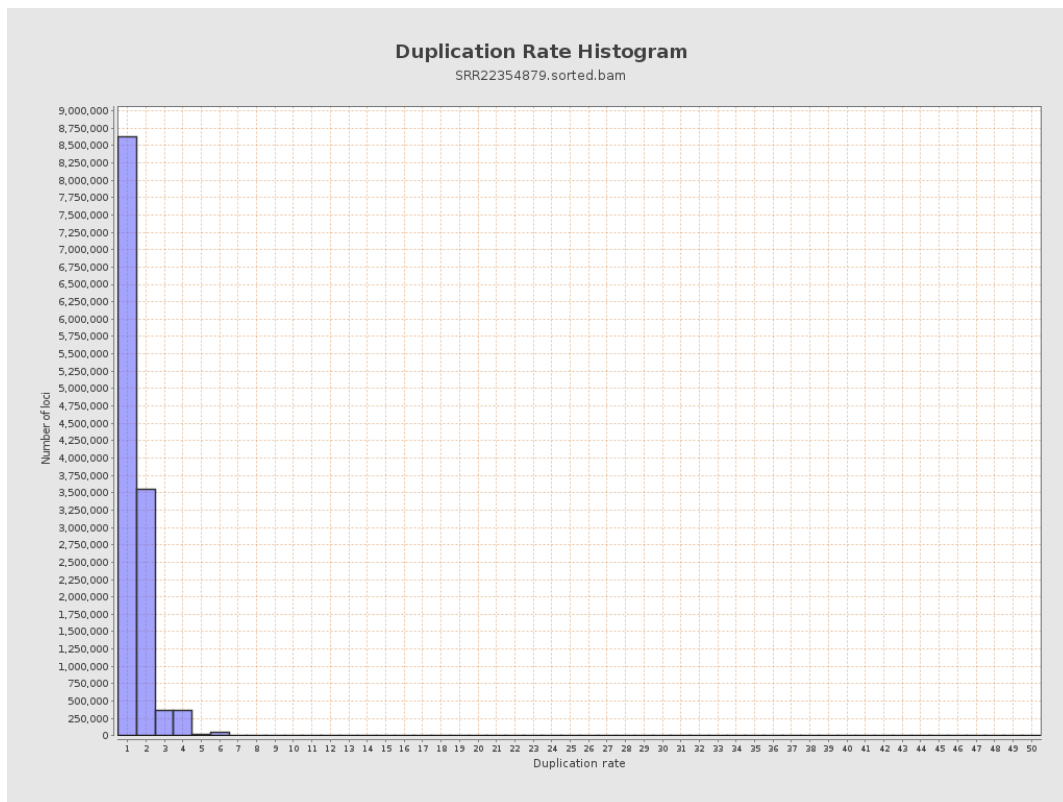
5. Results : Coverage Histogram (0-50X)



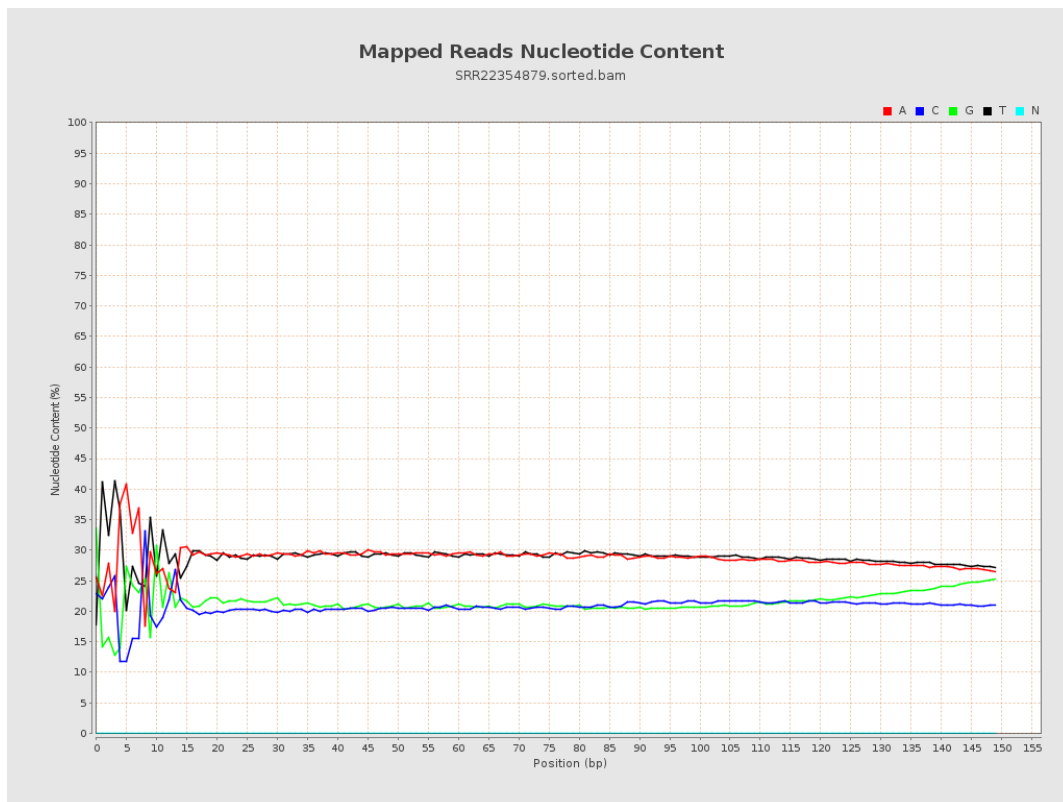
6. Results : Genome Fraction Coverage



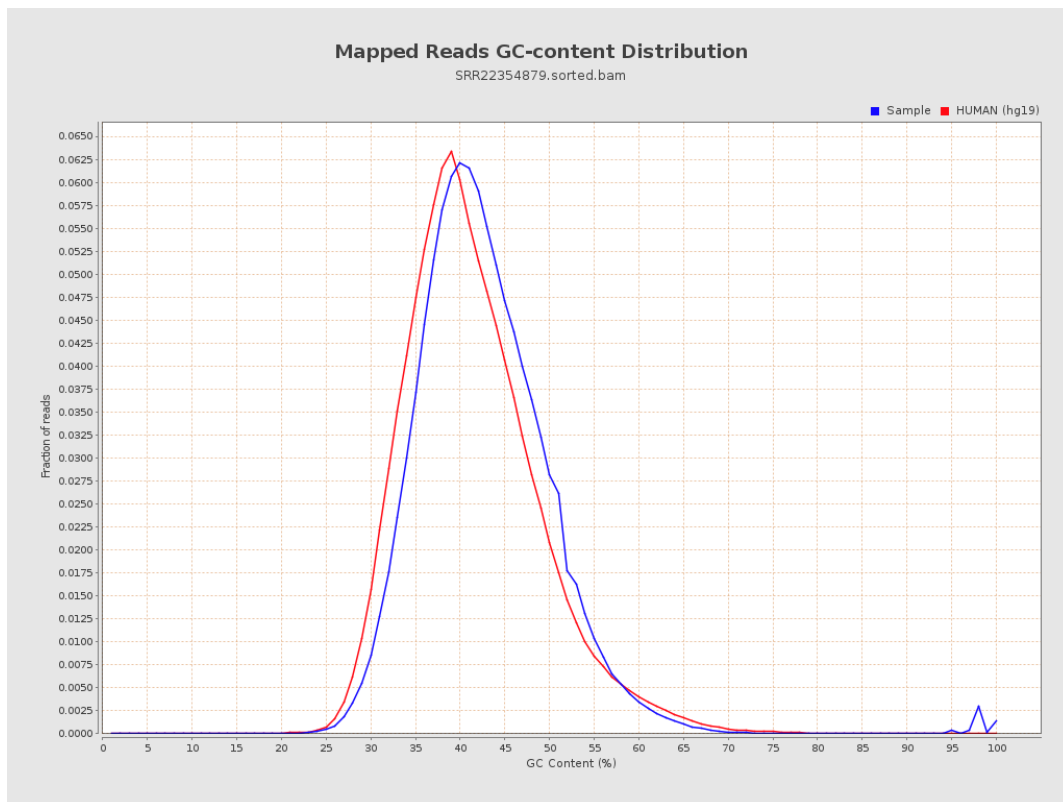
7. Results : Duplication Rate Histogram



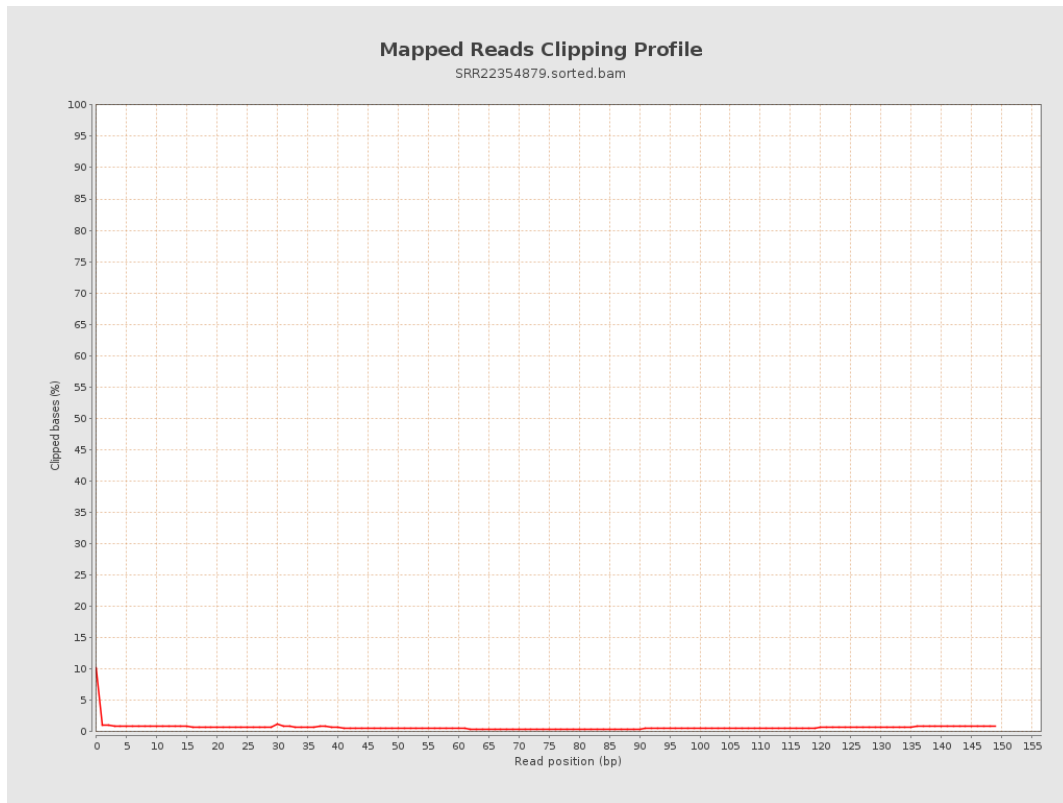
8. Results : Mapped Reads Nucleotide Content



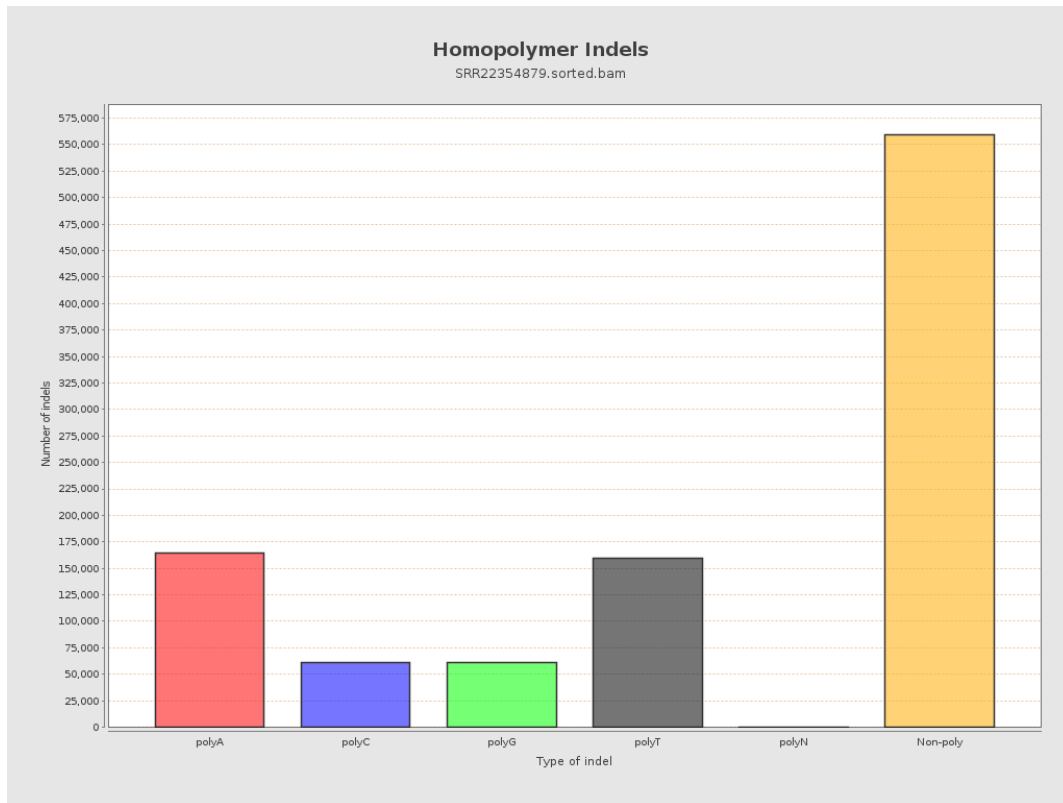
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



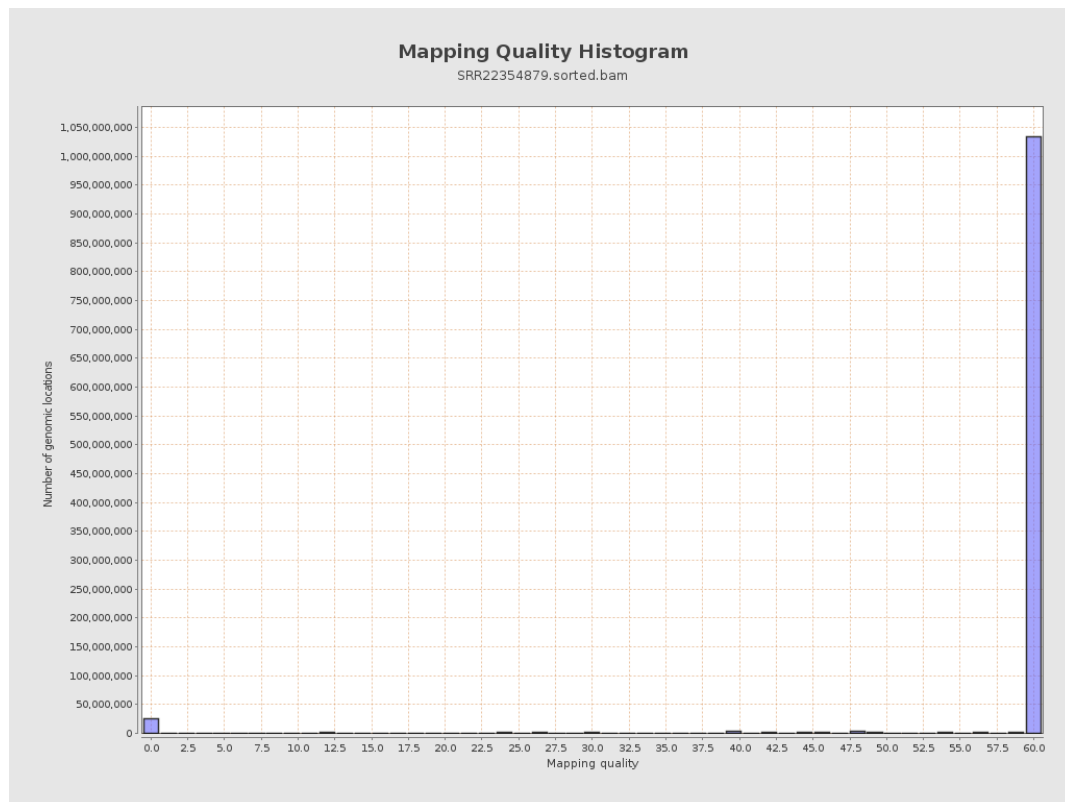
11. Results : Homopolymer Indels



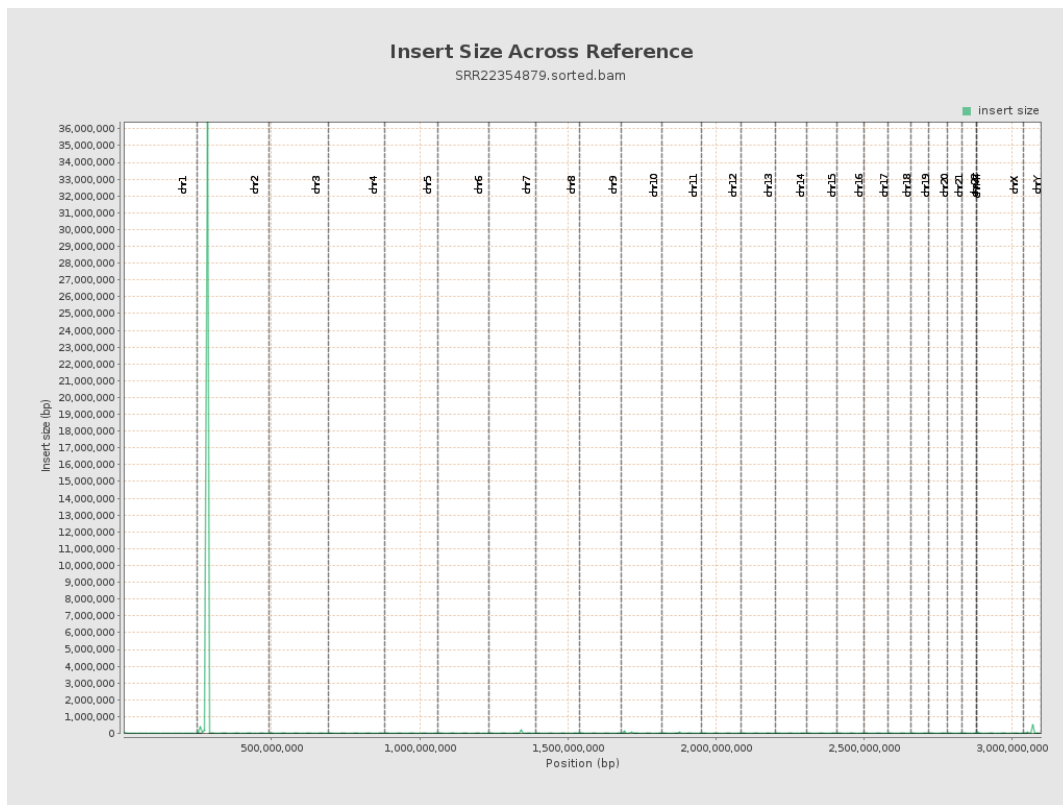
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

