

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 16:00:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354856.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_SRR22354856 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354856_1.fastq.gz SRR22354856_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 16:00:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354856.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	22,187,246
Mapped reads	21,245,465 / 95.76%
Unmapped reads	941,781 / 4.24%
Mapped paired reads	21,245,465 / 95.76%
Mapped reads, first in pair	10,643,415 / 47.97%
Mapped reads, second in pair	10,602,050 / 47.78%
Mapped reads, both in pair	21,180,364 / 95.46%
Mapped reads, singletons	65,101 / 0.29%
Secondary alignments	0
Supplementary alignments	329,760 / 1.49%
Read min/max/mean length	30 / 150 / 150.61
Duplicated reads (estimated)	19,403,787 / 87.45%
Duplication rate	84.68%
Clipped reads	5,429,618 / 24.47%

2.2. ACGT Content

Number/percentage of A's	849,686,769 / 28.67%
Number/percentage of C's	623,667,297 / 21.05%
Number/percentage of T's	855,385,087 / 28.86%
Number/percentage of G's	634,646,492 / 21.42%
Number/percentage of N's	14,862 / 0%

GC Percentage	42.46%
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2.3. Coverage

Mean	0.9577
Standard Deviation	23.3228

2.4. Mapping Quality

Mean Mapping Quality	54.19
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2.5. Insert size

Mean	119,718.23
Standard Deviation	3,866,824.25
P25/Median/P75	163 / 249 / 379

2.6. Mismatches and indels

General error rate	0.69%
Mismatches	19,101,300
Insertions	446,344
Mapped reads with at least one insertion	1.95%
Deletions	482,838
Mapped reads with at least one deletion	2.17%
Homopolymer indels	44.2%

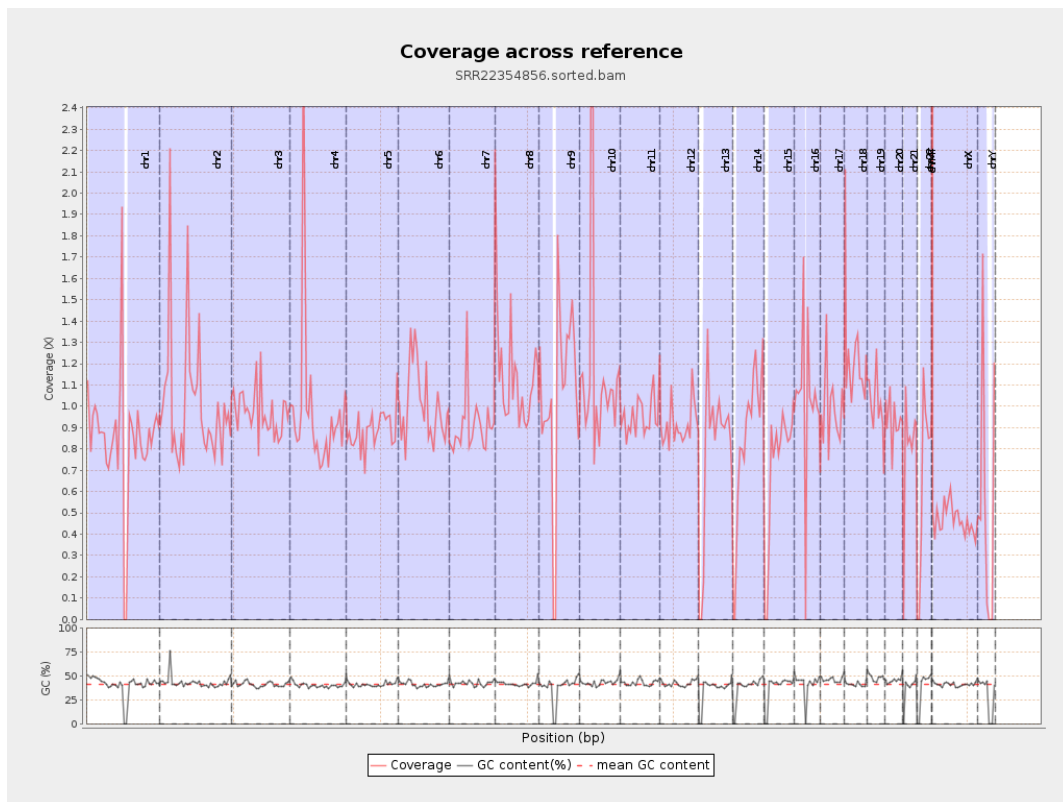
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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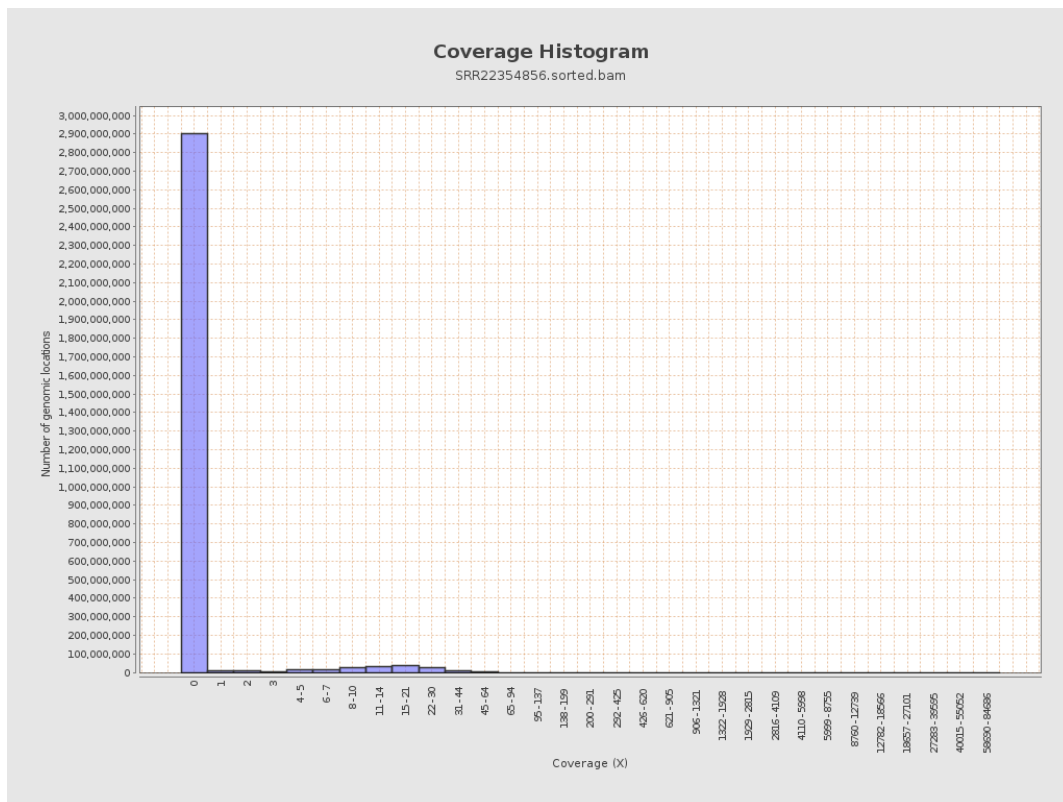
		bases	coverage	deviation
chr1	249250621	212245937	0.8515	25.748
chr2	243199373	246090463	1.0119	47.5446
chr3	198022430	192208004	0.9706	4.6191
chr4	191154276	184357406	0.9644	15.3146
chr5	180915260	161527370	0.8928	4.3824
chr6	171115067	173202658	1.0122	6.0504
chr7	159138663	144979340	0.911	10.9959
chr8	146364022	162536998	1.1105	5.95
chr9	141213431	146407452	1.0368	15.7275
chr10	135534747	161799793	1.1938	24.3343
chr11	135006516	128551145	0.9522	6.0331
chr12	133851895	122052970	0.9119	4.4706
chr13	115169878	91836138	0.7974	4.1538
chr14	107349540	90626331	0.8442	4.6149
chr15	102531392	72724416	0.7093	3.8726
chr16	90354753	93593574	1.0358	6.6997
chr17	81195210	80108664	0.9866	6.8889
chr18	78077248	94597733	1.2116	14.7705
chr19	59128983	59990342	1.0146	13.884
chr20	63025520	58667170	0.9308	6.7751
chr21	48129895	39395900	0.8185	9.0652
chr22	51304566	34892526	0.6801	4.705
chrMT	16571	106228189	6,410.4875	983.9182
chrX	155270560	72475910	0.4668	3.5122

chrY	59373566	33652731	0.5668	15.3929
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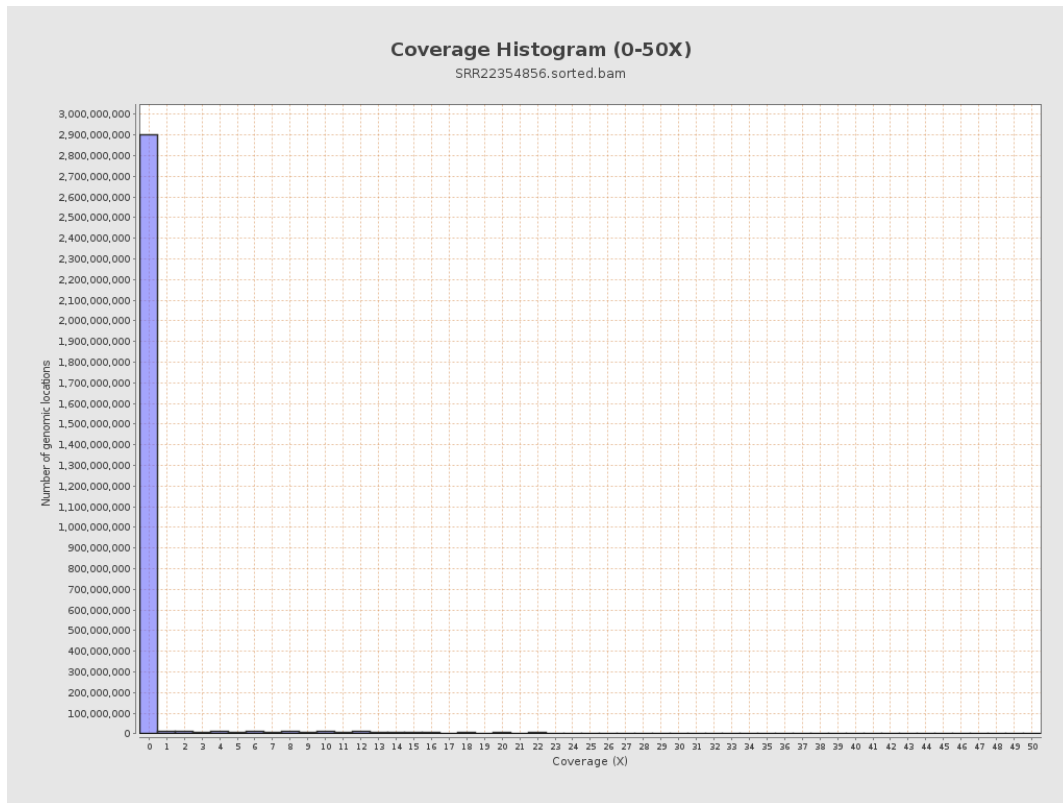
3. Results : Coverage across reference



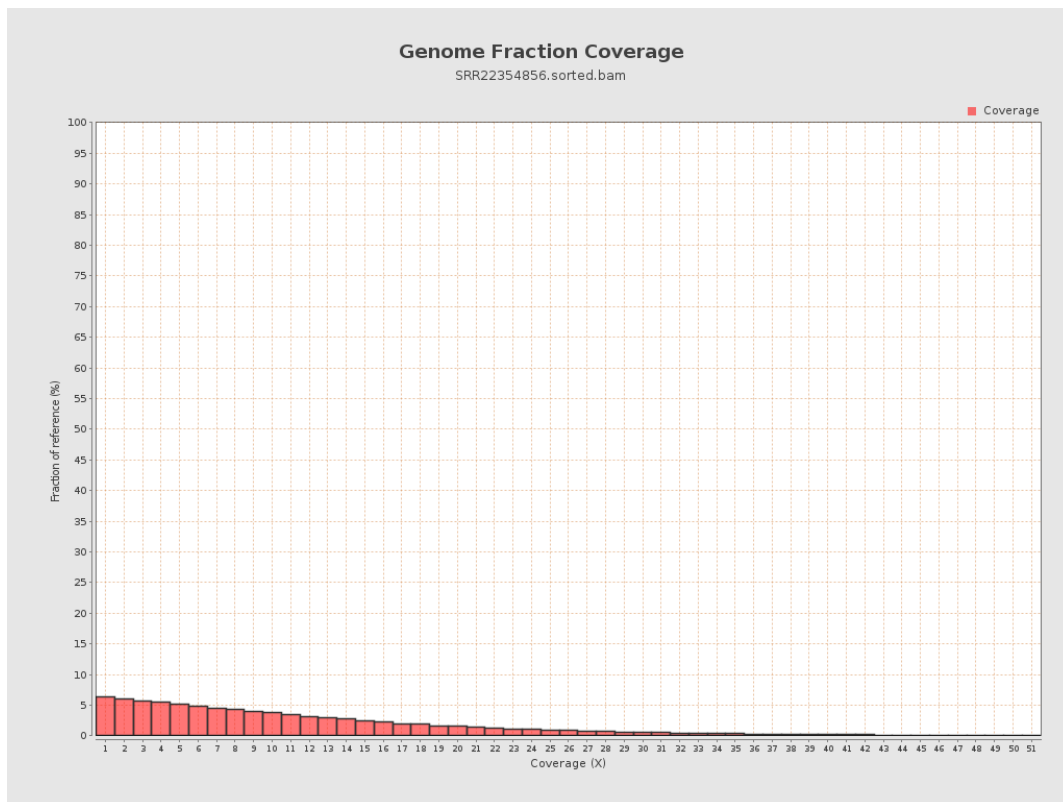
4. Results : Coverage Histogram



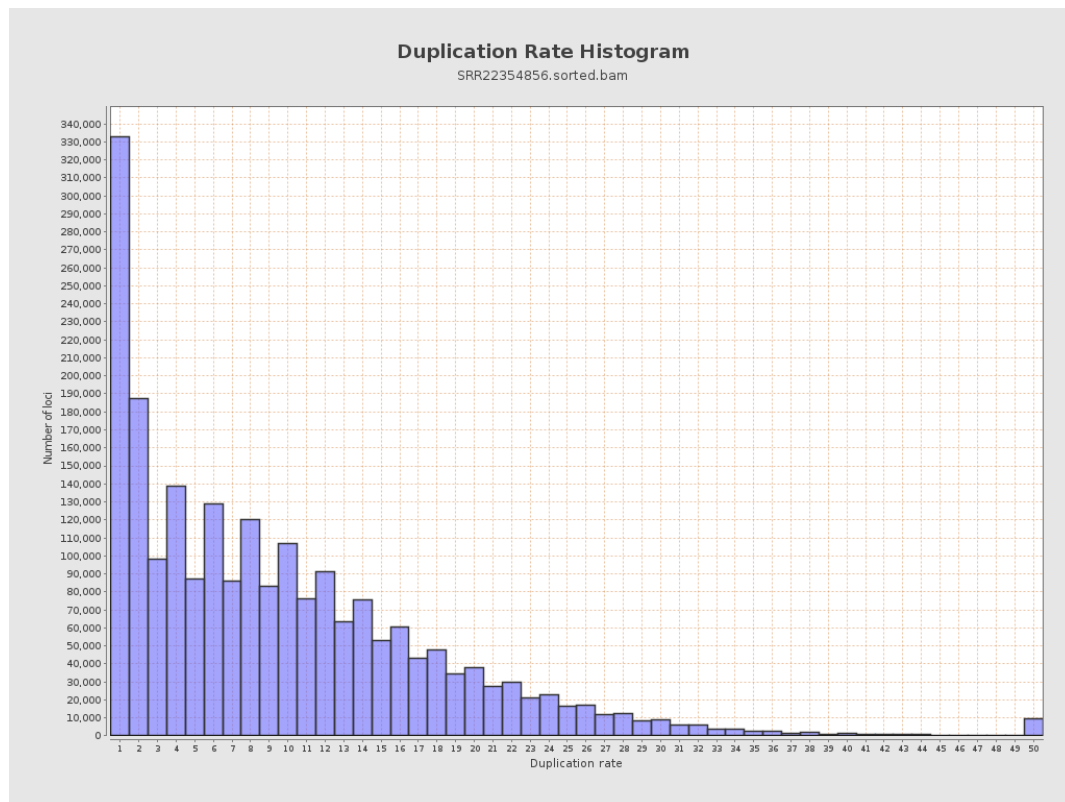
5. Results : Coverage Histogram (0-50X)



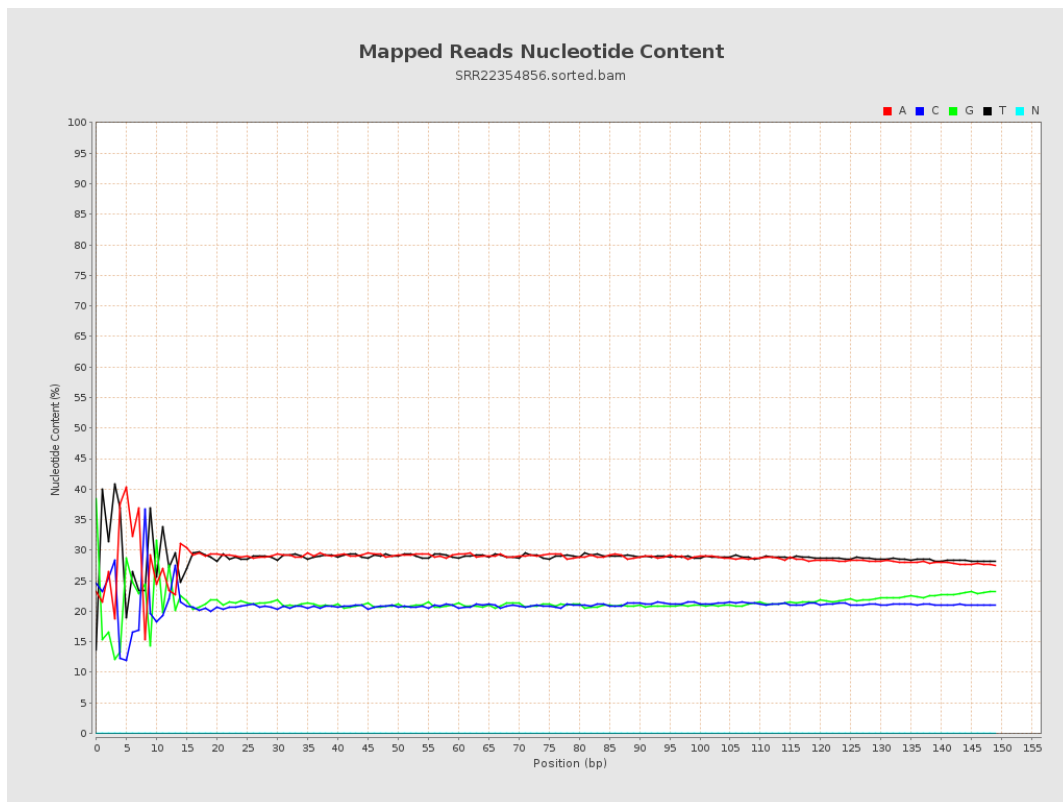
6. Results : Genome Fraction Coverage



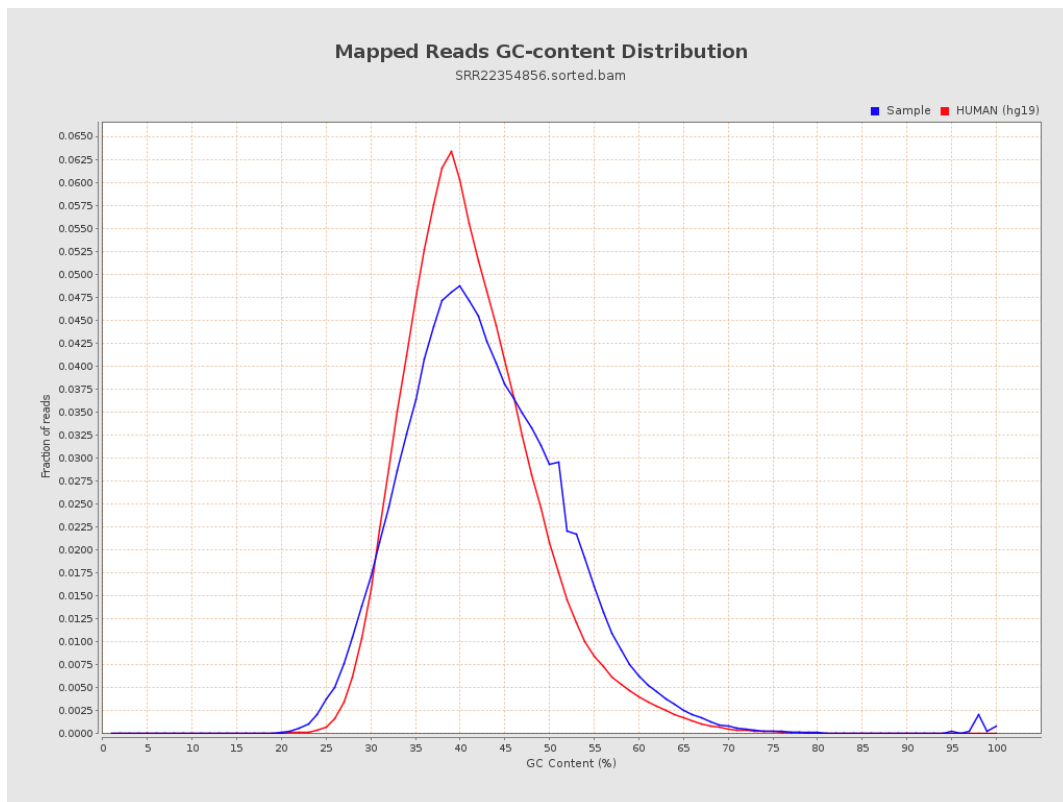
7. Results : Duplication Rate Histogram



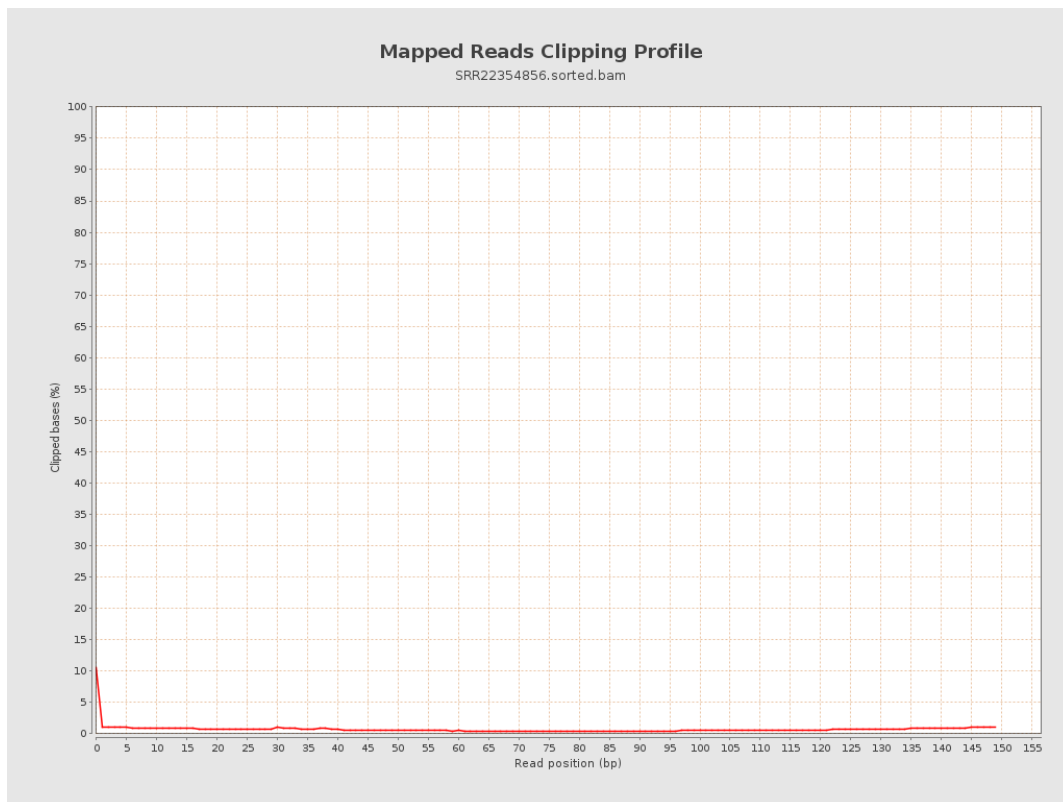
8. Results : Mapped Reads Nucleotide Content



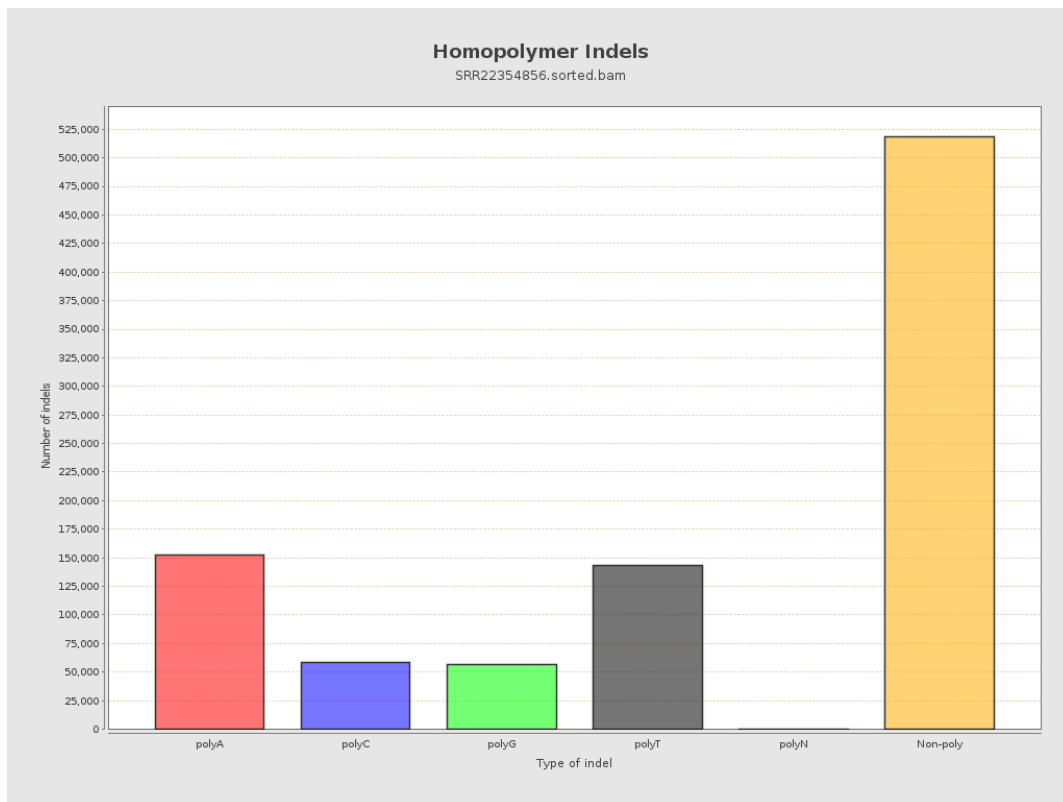
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



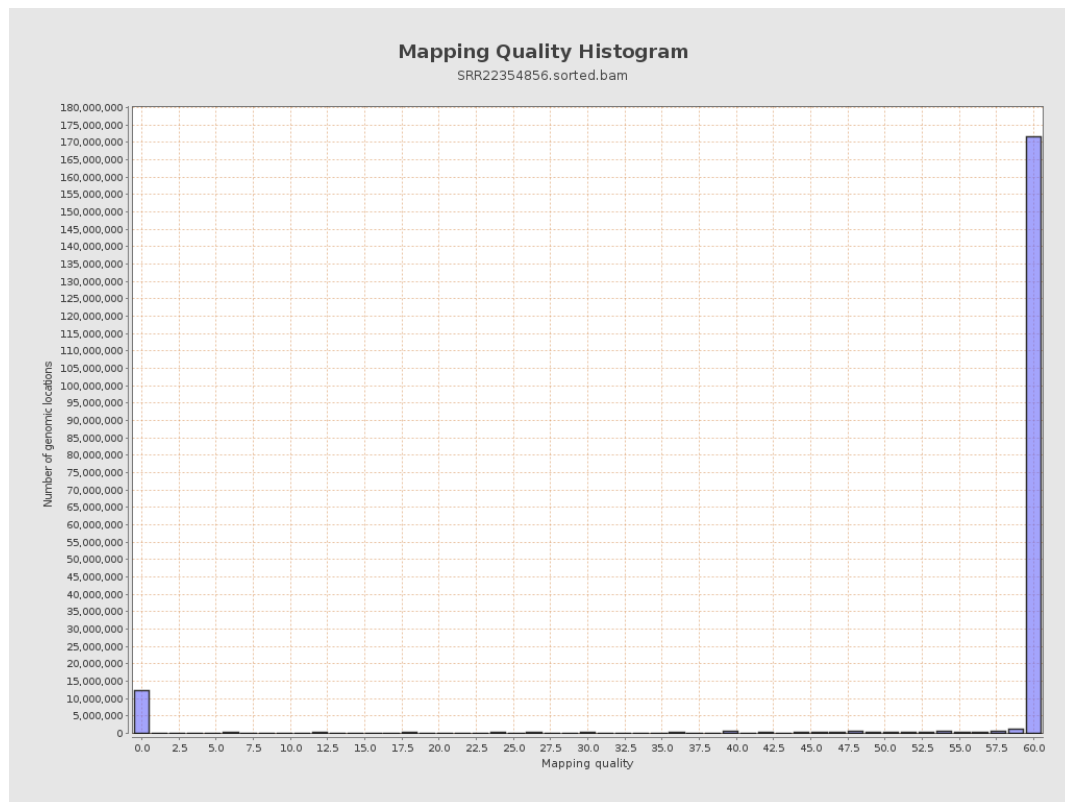
11. Results : Homopolymer Indels



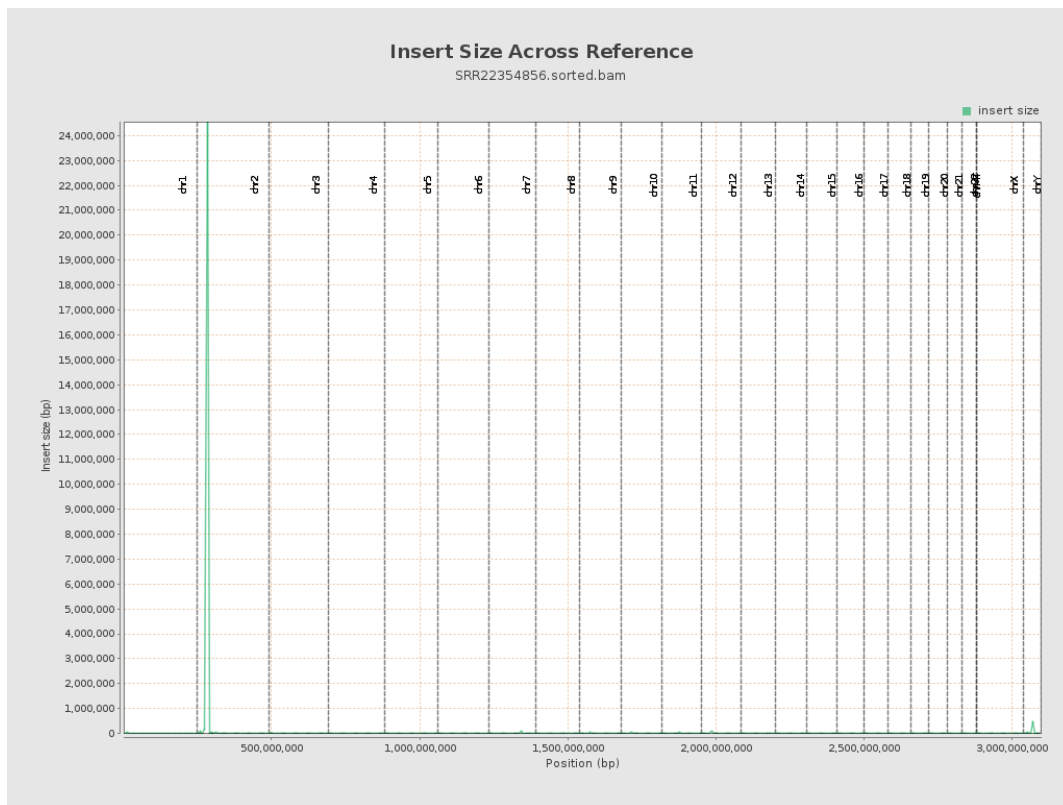
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

