

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/26 14:40:48

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354854.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_SRR22354854 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354854_1.fastq.gz SRR22354854_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Mon Aug 26 14:40:47 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354854.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	37,463,832
Mapped reads	36,839,135 / 98.33%
Unmapped reads	624,697 / 1.67%
Mapped paired reads	36,839,135 / 98.33%
Mapped reads, first in pair	18,493,007 / 49.36%
Mapped reads, second in pair	18,346,128 / 48.97%
Mapped reads, both in pair	36,641,508 / 97.81%
Mapped reads, singletons	197,627 / 0.53%
Secondary alignments	0
Supplementary alignments	699,234 / 1.87%
Read min/max/mean length	30 / 150 / 150.76
Duplicated reads (estimated)	22,322,019 / 59.58%
Duplication rate	59.7%
Clipped reads	9,084,189 / 24.25%

2.2. ACGT Content

Number/percentage of A's	1,479,331,992 / 28.85%
Number/percentage of C's	1,064,795,527 / 20.76%
Number/percentage of T's	1,487,754,620 / 29.01%
Number/percentage of G's	1,096,326,892 / 21.38%
Number/percentage of N's	39,282 / 0%

GC Percentage	42.14%
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2.3. Coverage

Mean	1.6574
Standard Deviation	36.3111

2.4. Mapping Quality

Mean Mapping Quality	54.02
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2.5. Insert size

Mean	162,784.26
Standard Deviation	4,579,579.76
P25/Median/P75	186 / 320 / 489

2.6. Mismatches and indels

General error rate	0.91%
Mismatches	43,761,609
Insertions	859,598
Mapped reads with at least one insertion	2.17%
Deletions	914,193
Mapped reads with at least one deletion	2.36%
Homopolymer indels	43.61%

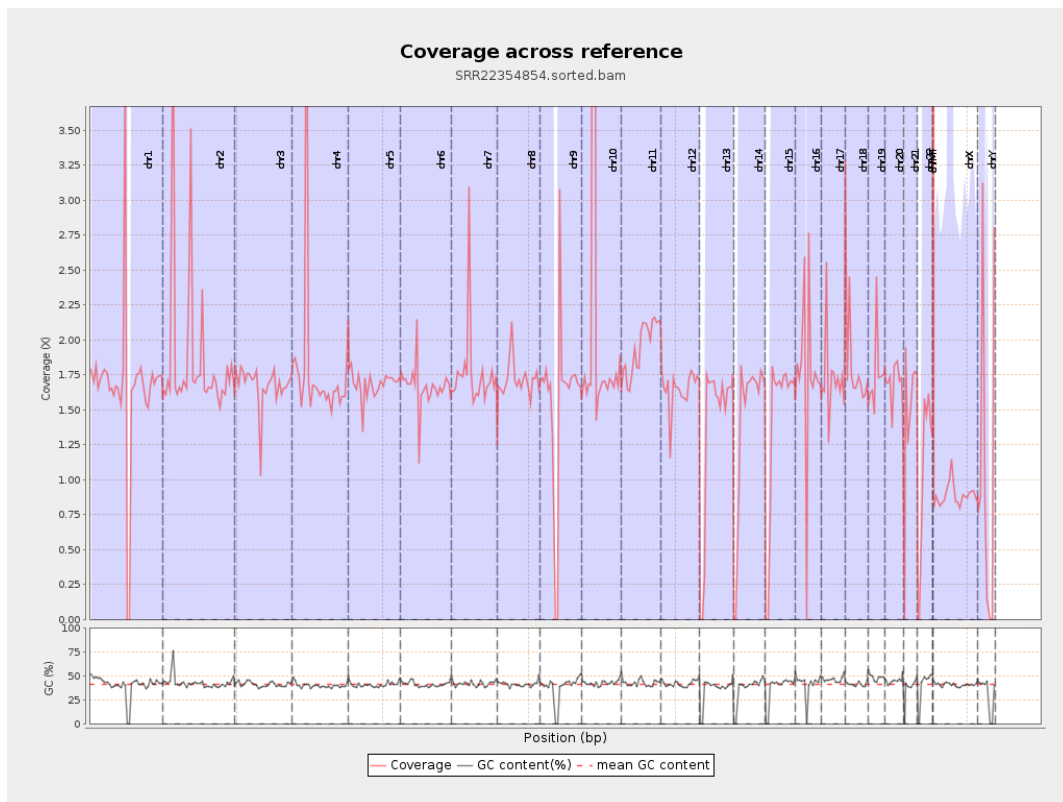
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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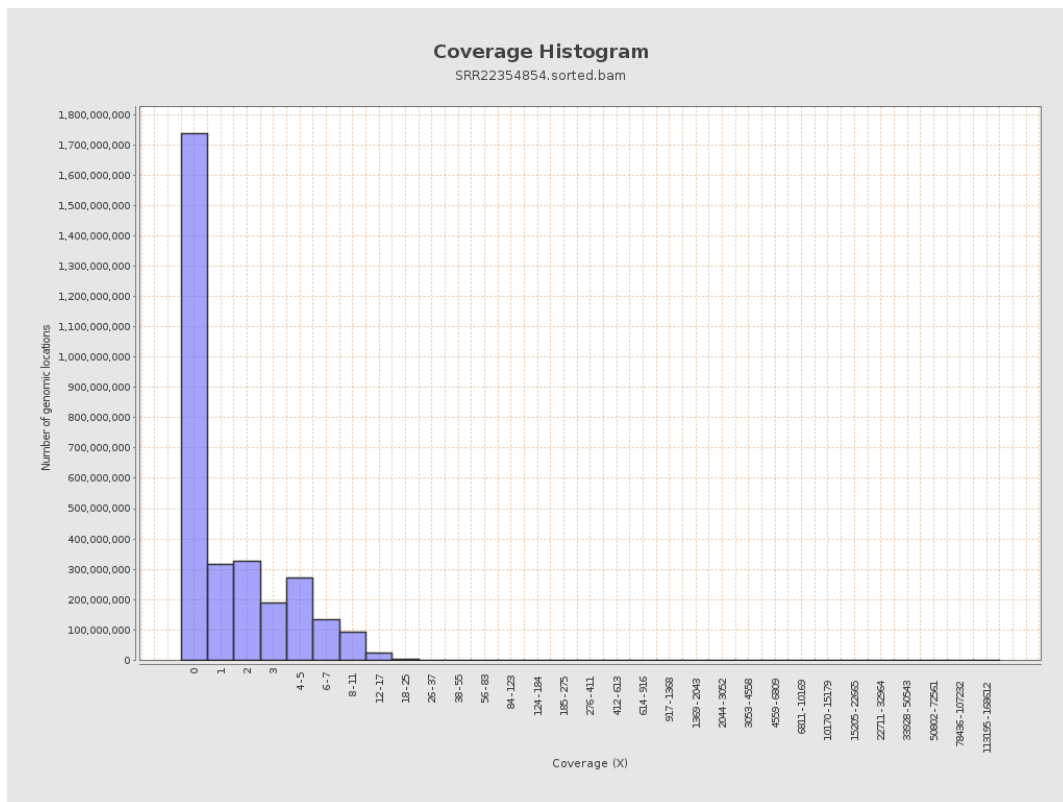
		bases	coverage	deviation
chr1	249250621	414361918	1.6624	51.2153
chr2	243199373	452890545	1.8622	96.4038
chr3	198022430	331524694	1.6742	3.0132
chr4	191154276	343910743	1.7991	27.2792
chr5	180915260	305035774	1.6861	2.8072
chr6	171115067	284931459	1.6651	6.695
chr7	159138663	280884180	1.765	28.8031
chr8	146364022	251537964	1.7186	18.5962
chr9	141213431	221944871	1.5717	31.0943
chr10	135534747	280354874	2.0685	52.2706
chr11	135006516	262209659	1.9422	8.9284
chr12	133851895	221108055	1.6519	2.7153
chr13	115169878	158487141	1.3761	2.4411
chr14	107349540	153405351	1.429	4.3751
chr15	102531392	143245895	1.3971	2.47
chr16	90354753	157512803	1.7433	10.4047
chr17	81195210	140603892	1.7317	10.4959
chr18	78077248	142286894	1.8224	24.6771
chr19	59128983	104118898	1.7609	28.7584
chr20	63025520	106646168	1.6921	9.1721
chr21	48129895	72557137	1.5075	14.151
chr22	51304566	53933322	1.0512	4.831
chrMT	16571	44397376	2,679.2213	426.0638
chrX	155270560	138199450	0.8901	3.2579

chrY	59373566	64763129	1.0908	30.4212
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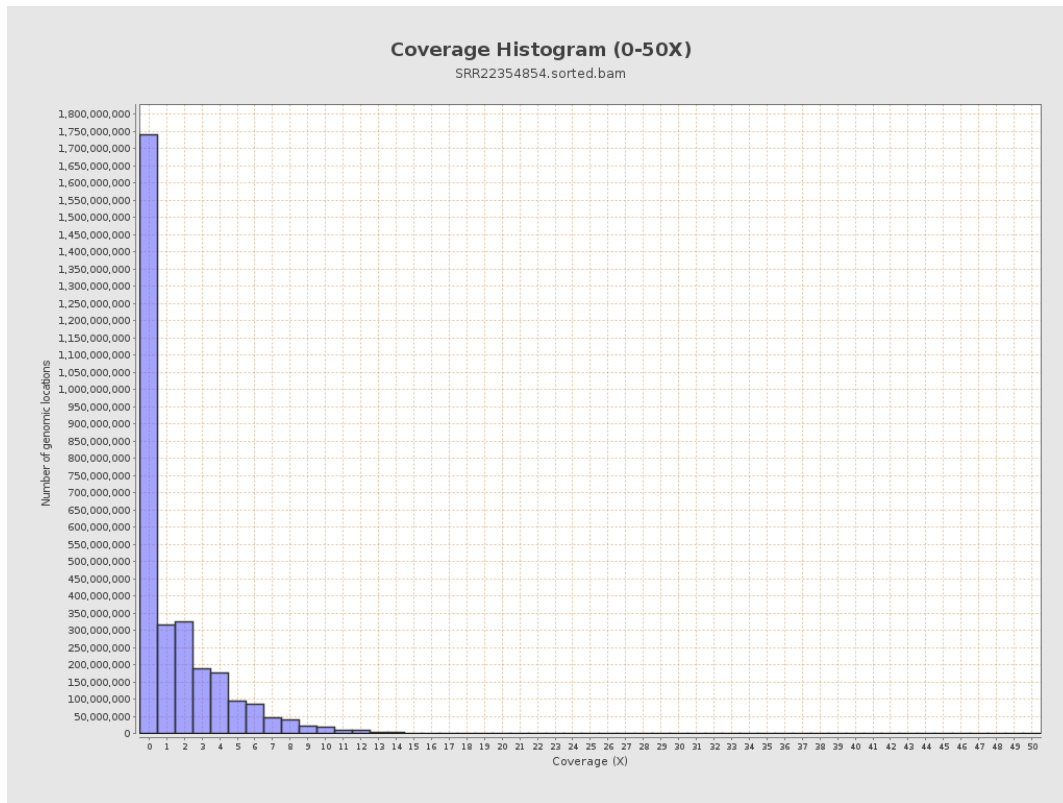
3. Results : Coverage across reference



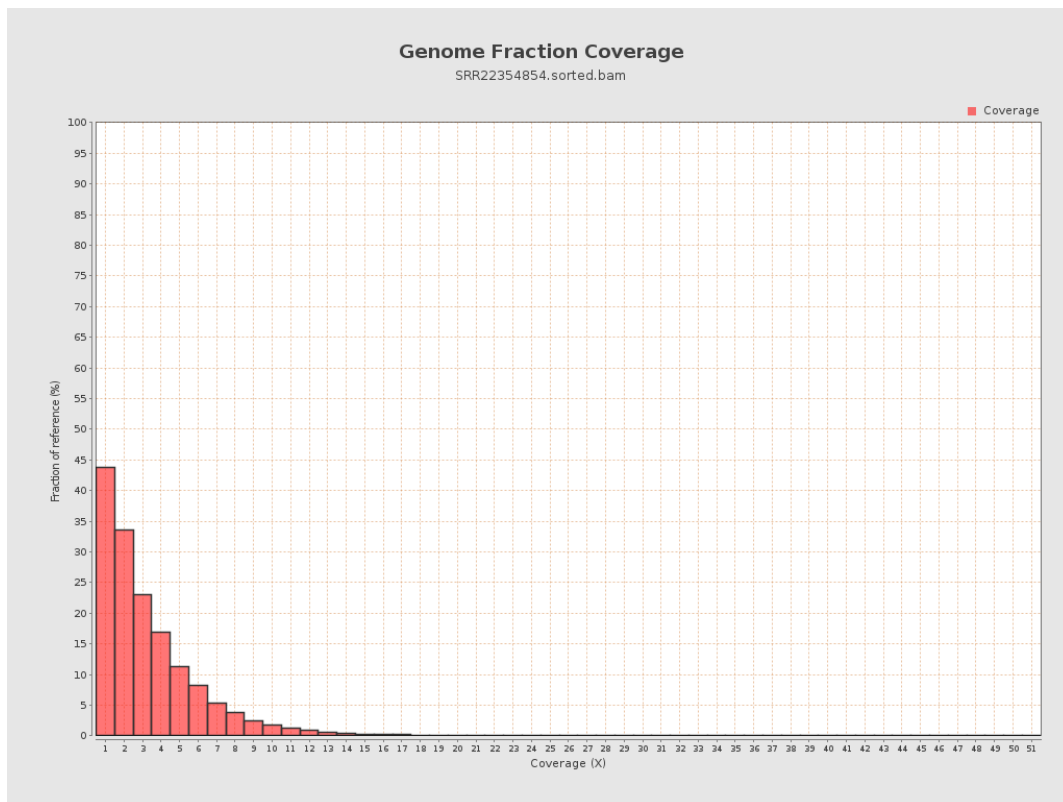
4. Results : Coverage Histogram



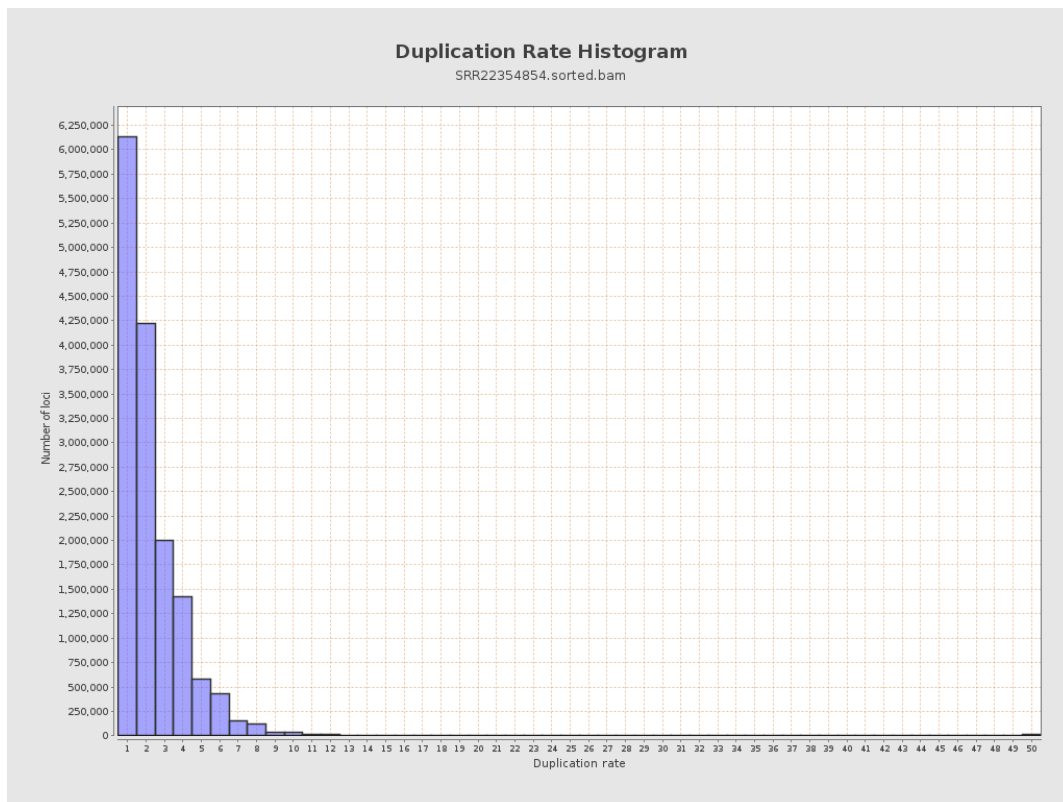
5. Results : Coverage Histogram (0-50X)



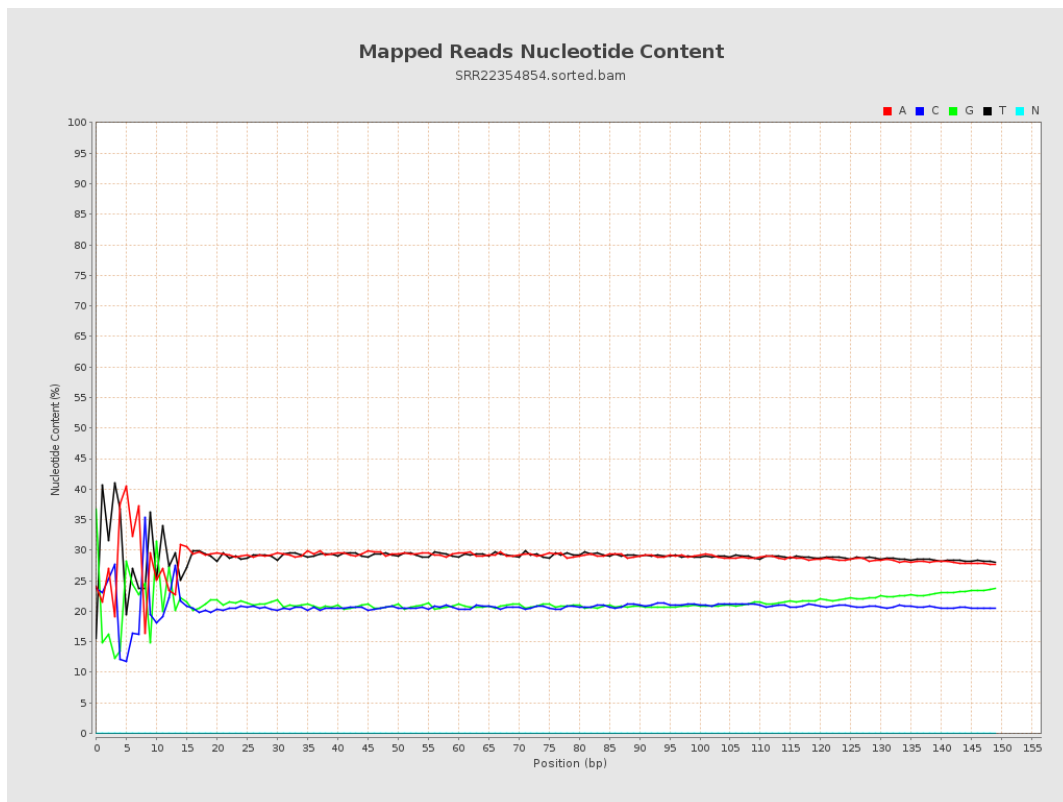
6. Results : Genome Fraction Coverage



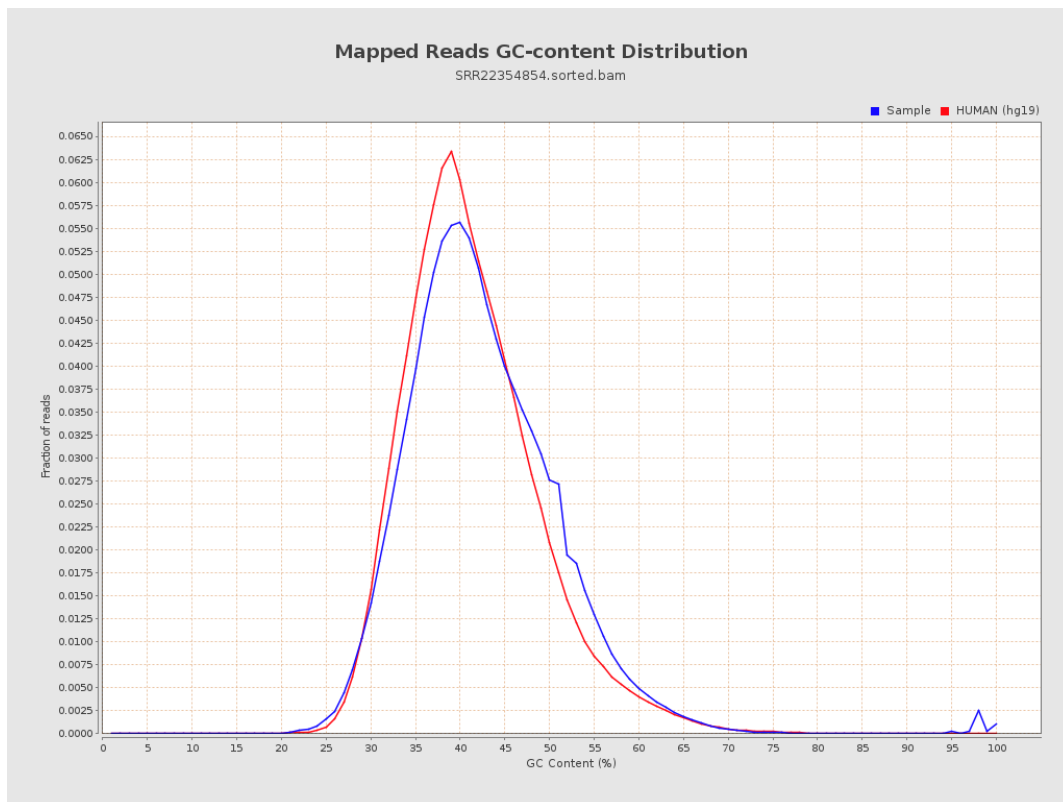
7. Results : Duplication Rate Histogram



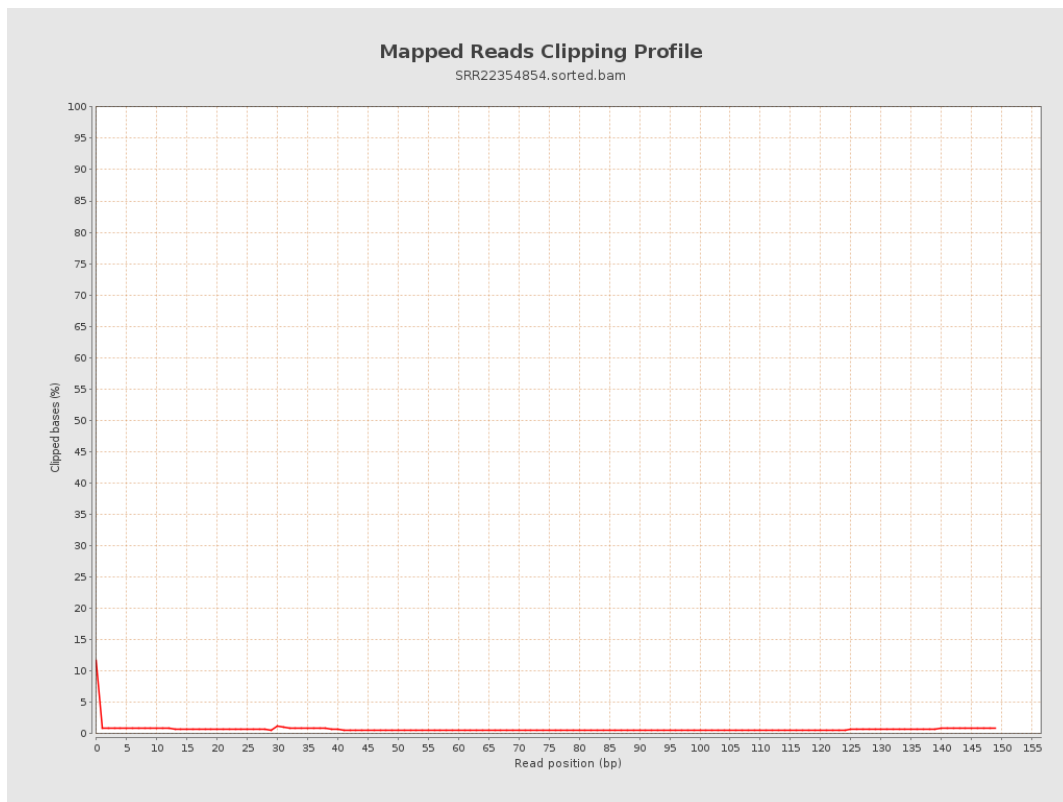
8. Results : Mapped Reads Nucleotide Content



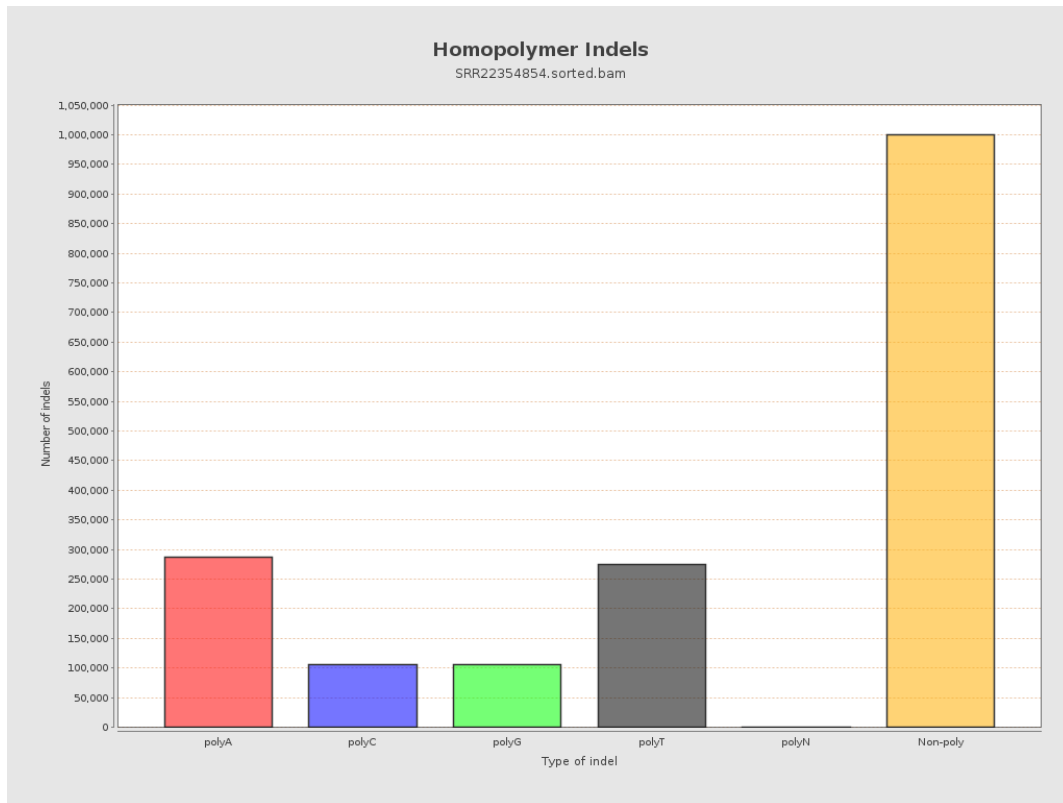
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



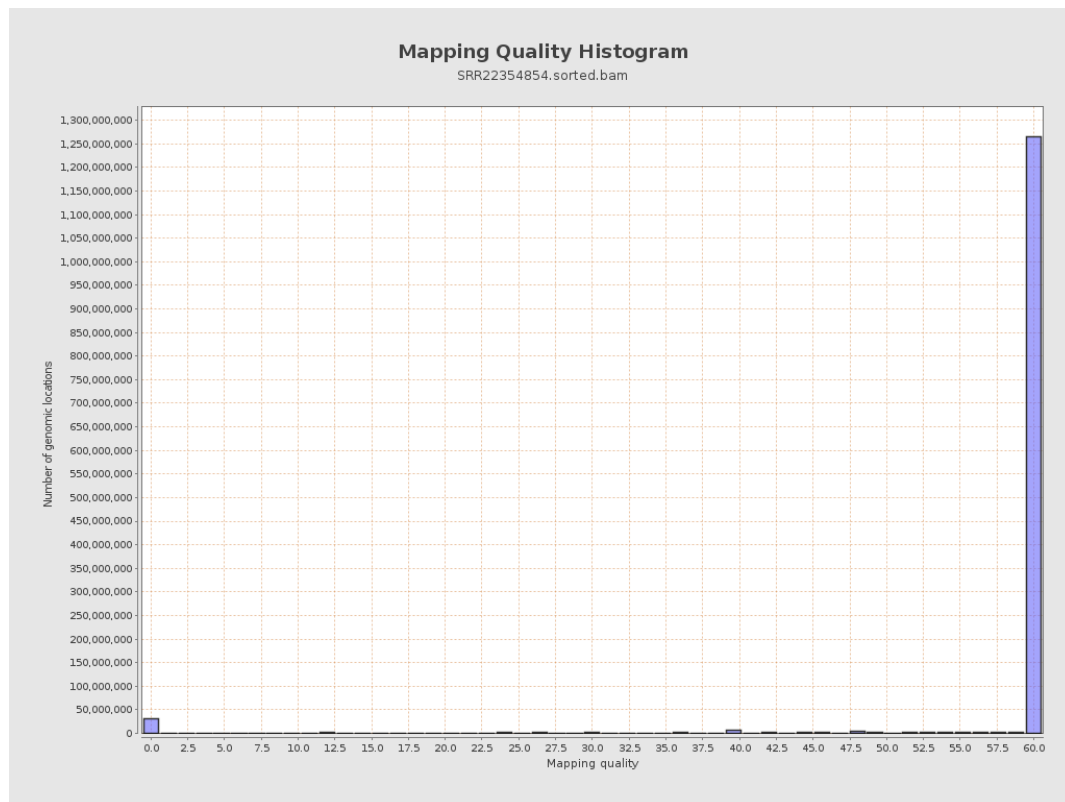
11. Results : Homopolymer Indels



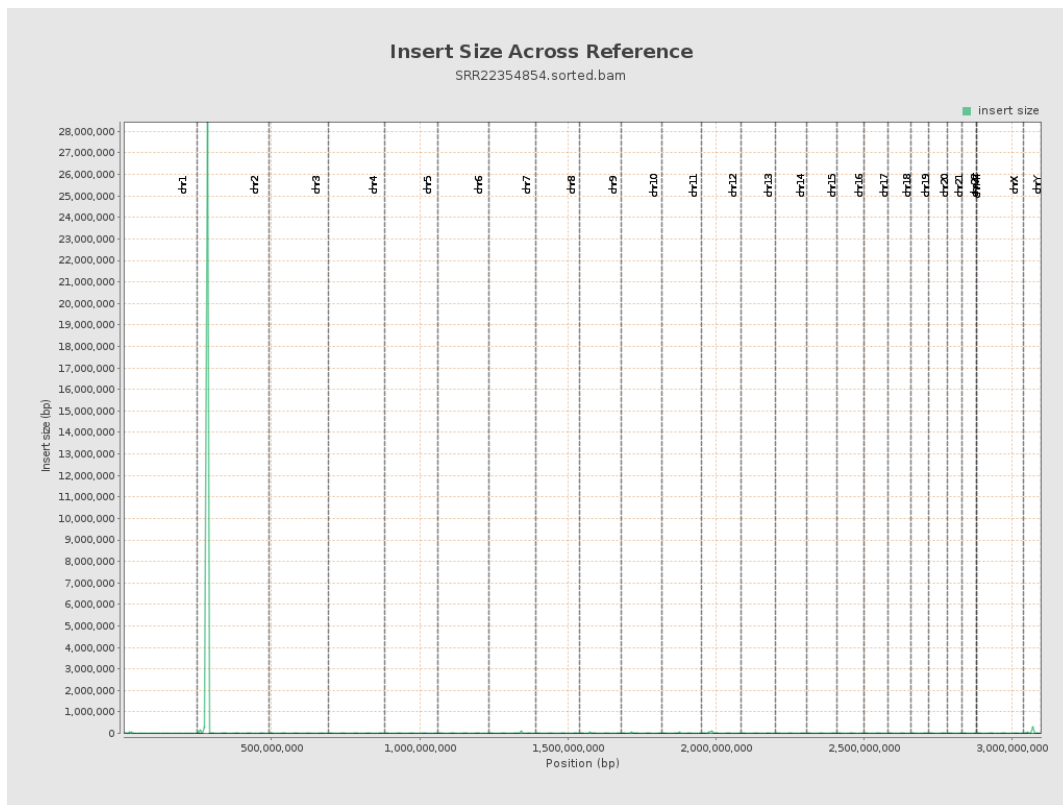
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

