

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/27 13:28:59

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR22354865.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_SRR22354865 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR22354865_1.fastq.gz SRR22354865_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Tue Aug 27 13:28:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR22354865.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	163,625,886
Mapped reads	156,904,229 / 95.89%
Unmapped reads	6,721,657 / 4.11%
Mapped paired reads	156,904,229 / 95.89%
Mapped reads, first in pair	78,556,779 / 48.01%
Mapped reads, second in pair	78,347,450 / 47.88%
Mapped reads, both in pair	156,531,170 / 95.66%
Mapped reads, singletons	373,059 / 0.23%
Secondary alignments	0
Supplementary alignments	6,671,641 / 4.08%
Read min/max/mean length	30 / 150 / 151.47
Duplicated reads (estimated)	142,919,902 / 87.35%
Duplication rate	85.75%
Clipped reads	100,192,105 / 61.23%

2.2. ACGT Content

Number/percentage of A's	5,131,776,858 / 27.69%
Number/percentage of C's	3,901,444,085 / 21.05%
Number/percentage of T's	5,169,535,003 / 27.89%
Number/percentage of G's	4,330,692,461 / 23.37%
Number/percentage of N's	399,108 / 0%

GC Percentage	44.42%
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2.3. Coverage

Mean	5.9896
Standard Deviation	360.1994

2.4. Mapping Quality

Mean Mapping Quality	53.55
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2.5. Insert size

Mean	469,510.19
Standard Deviation	7,910,704.8
P25/Median/P75	89 / 133 / 195

2.6. Mismatches and indels

General error rate	0.63%
Mismatches	108,546,256
Insertions	2,963,941
Mapped reads with at least one insertion	1.79%
Deletions	3,205,876
Mapped reads with at least one deletion	1.97%
Homopolymer indels	43.33%

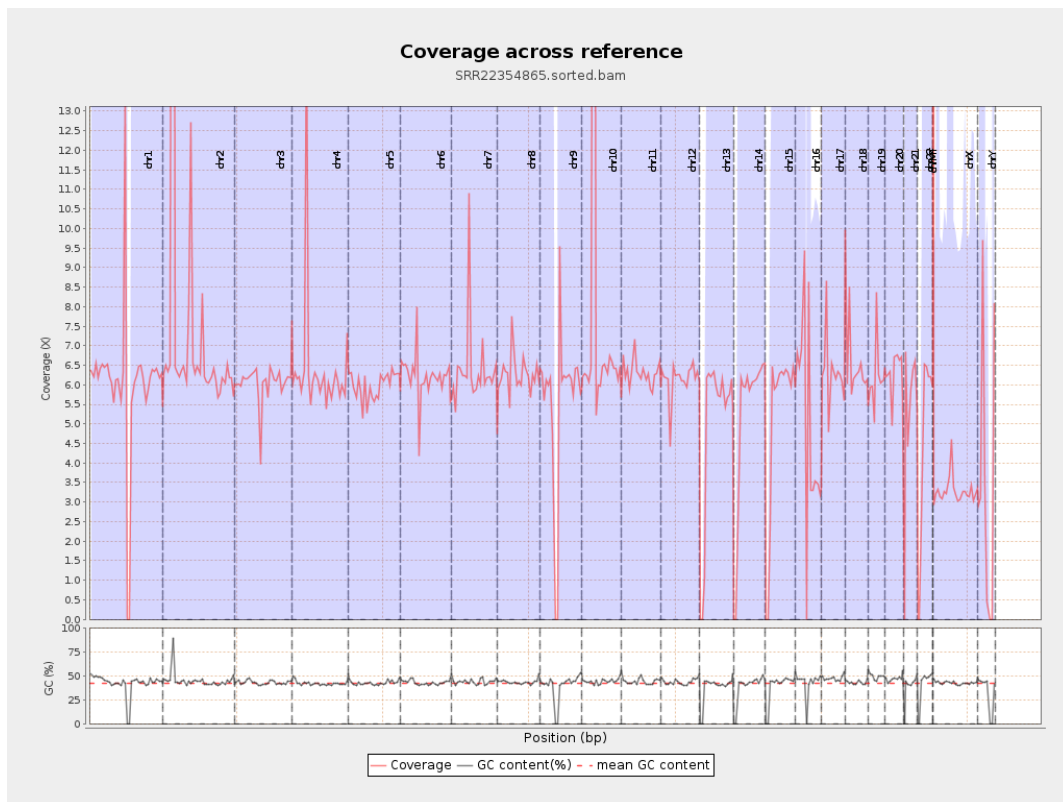
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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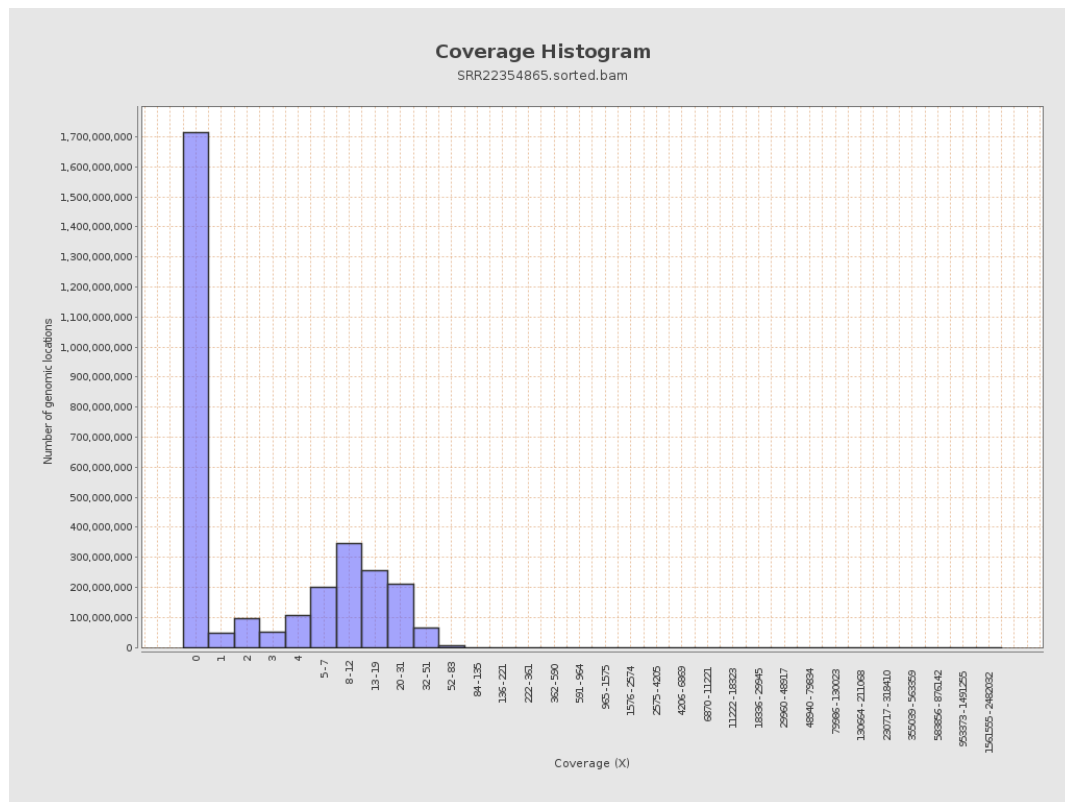
		bases	coverage	deviation
chr1	249250621	1503099862	6.0305	171.7118
chr2	243199373	1852246551	7.6162	1,251.7862
chr3	198022430	1198114205	6.0504	16.2237
chr4	191154276	1229771657	6.4334	63.4118
chr5	180915260	1082439108	5.9831	10.2637
chr6	171115067	1062586777	6.2098	25.3019
chr7	159138663	1016921714	6.3902	141.271
chr8	146364022	916954957	6.2649	21.3761
chr9	141213431	784567958	5.5559	82.3052
chr10	135534747	1032633967	7.619	199.462
chr11	135006516	848653682	6.286	33.4592
chr12	133851895	823491025	6.1523	10.4562
chr13	115169878	572927657	4.9746	8.7837
chr14	107349540	557900614	5.197	46.2672
chr15	102531392	519443128	5.0662	8.7581
chr16	90354753	456066960	5.0475	38.1787
chr17	81195210	515143717	6.3445	37.3118
chr18	78077248	512029149	6.558	81.0874
chr19	59128983	367692394	6.2185	83.699
chr20	63025520	397205843	6.3023	22.8353
chr21	48129895	259526005	5.3922	39.5112
chr22	51304566	227566592	4.4356	19.177
chrMT	16571	87060879	5,253.8096	1,004.8076
chrX	155270560	511174784	3.2922	15.3973

chrY	59373566	206794892	3.4829	86.6619
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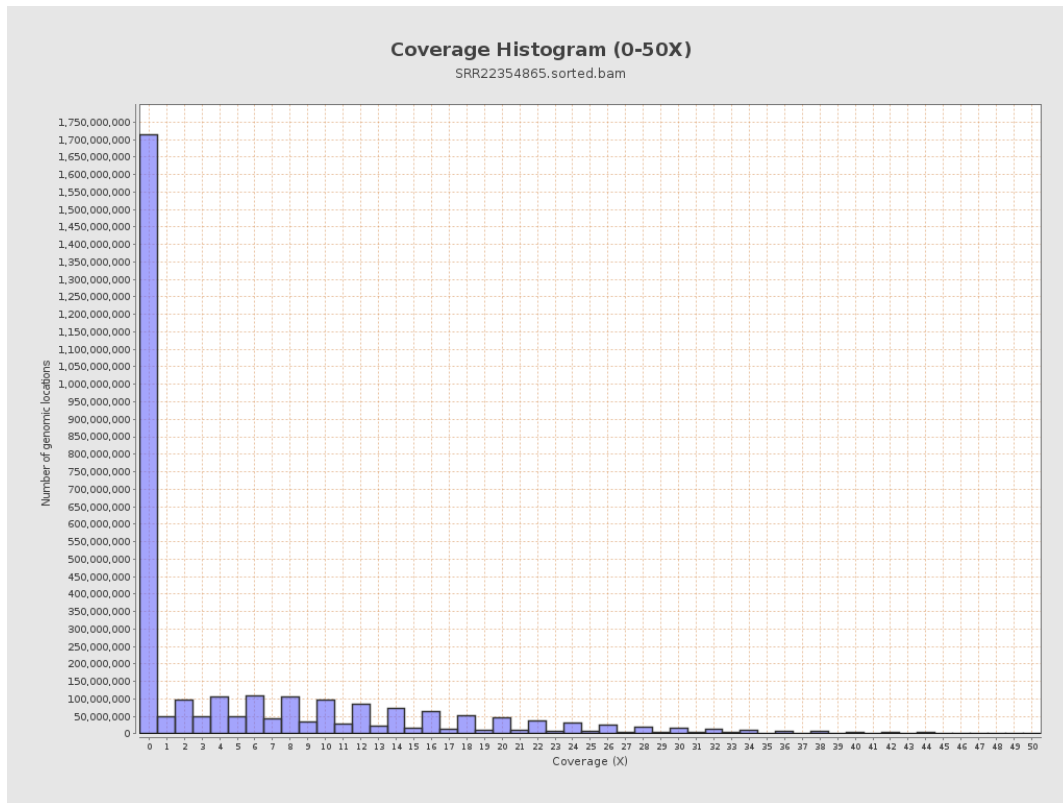
3. Results : Coverage across reference



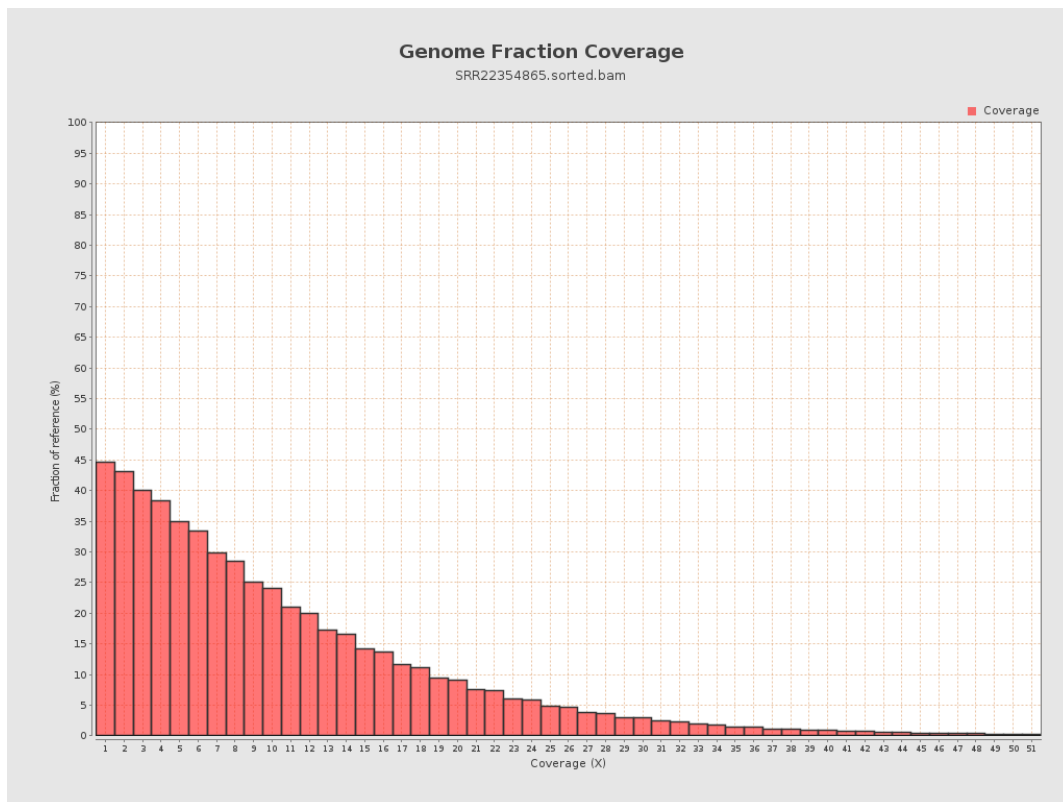
4. Results : Coverage Histogram



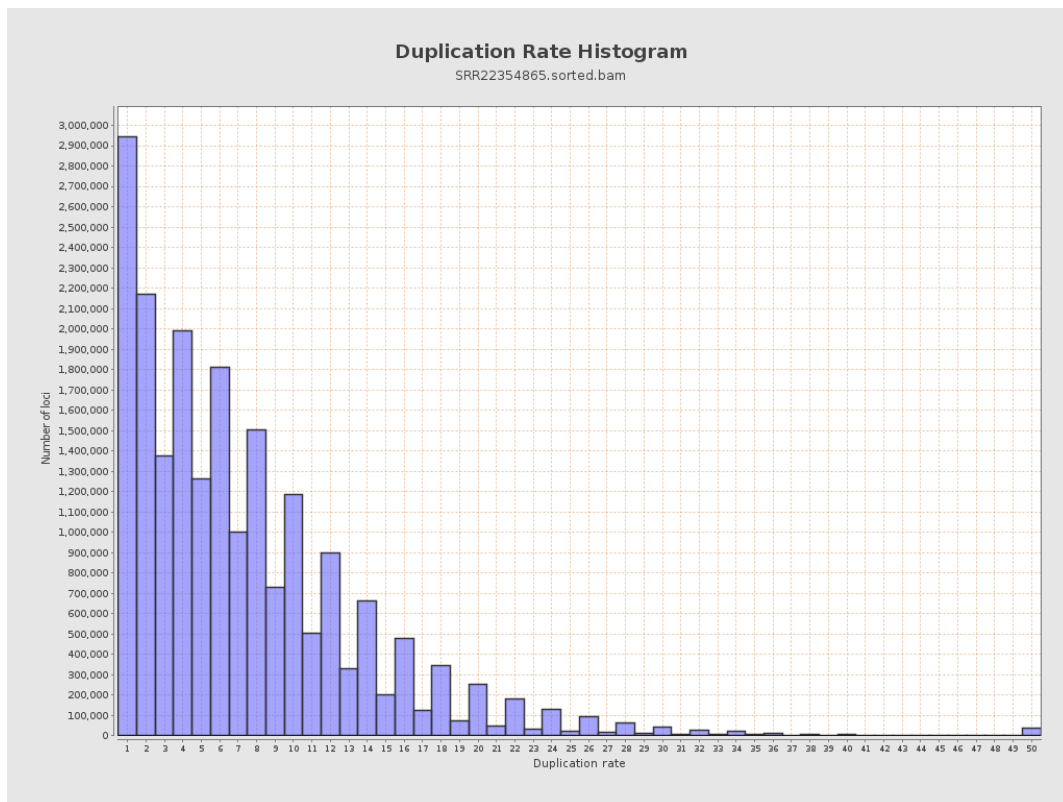
5. Results : Coverage Histogram (0-50X)



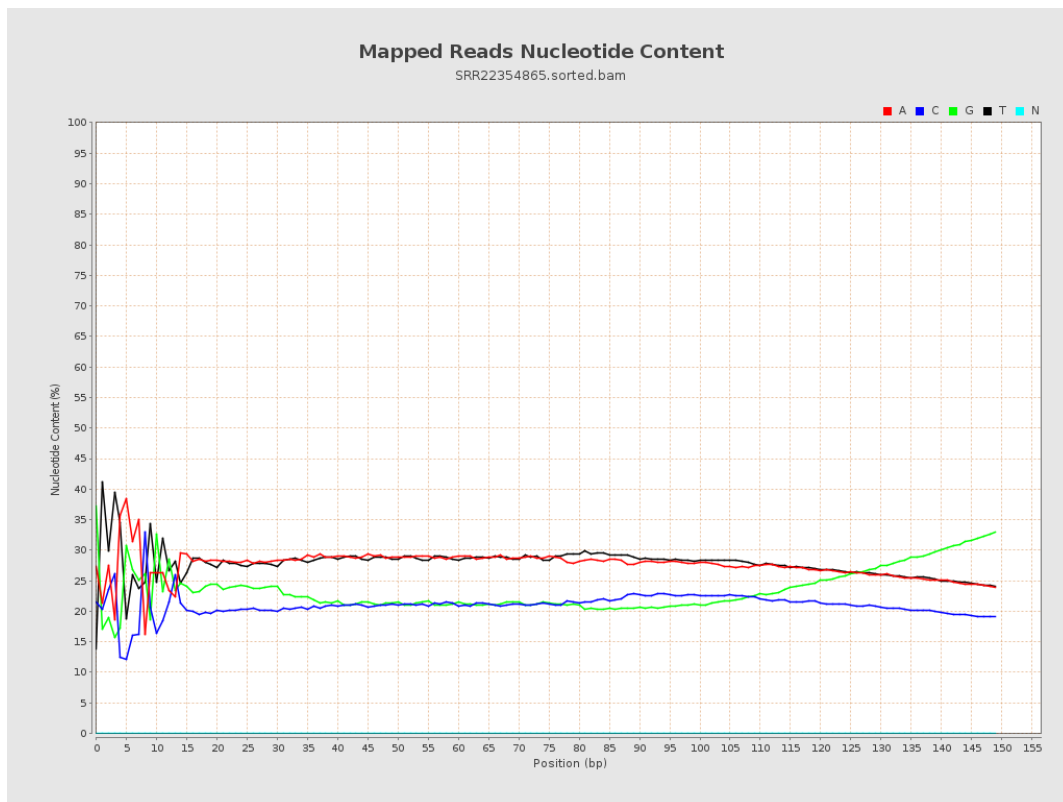
6. Results : Genome Fraction Coverage



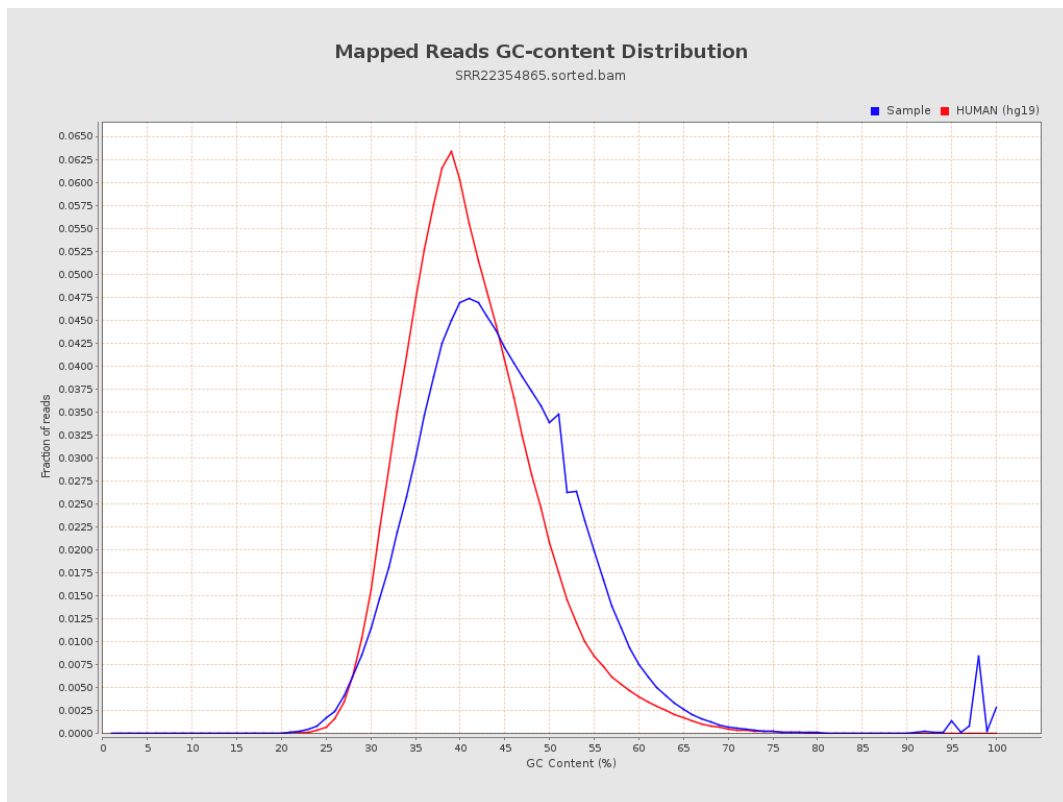
7. Results : Duplication Rate Histogram



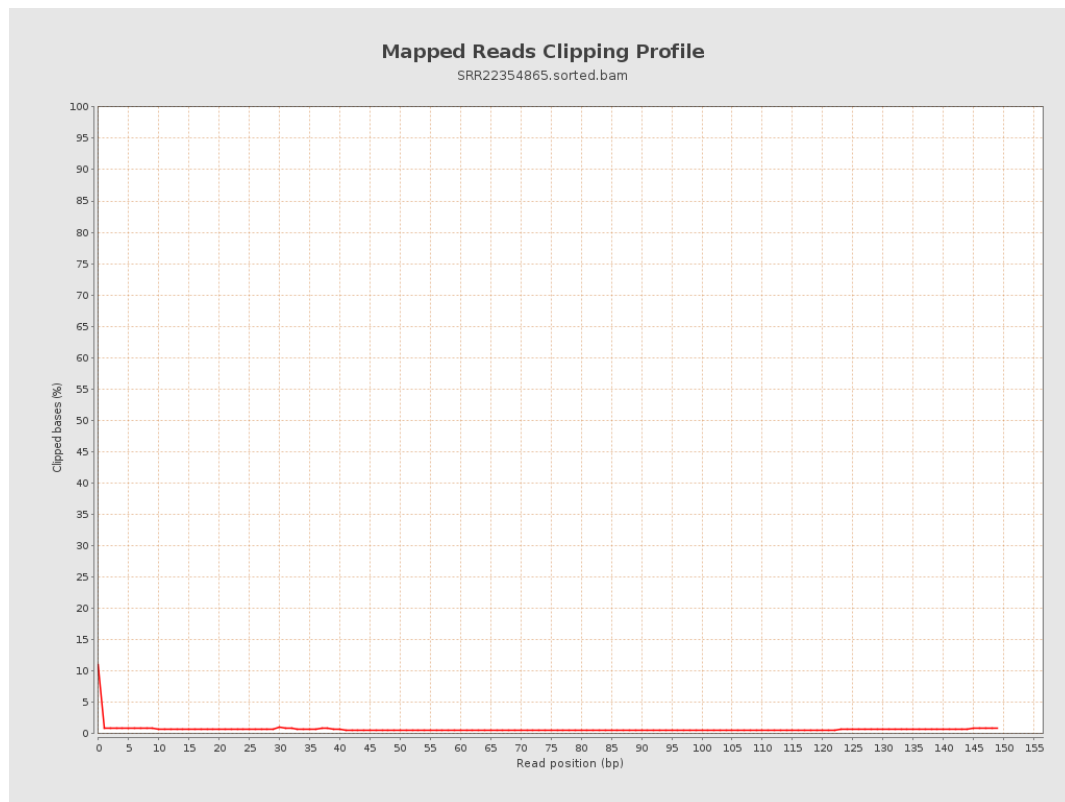
8. Results : Mapped Reads Nucleotide Content



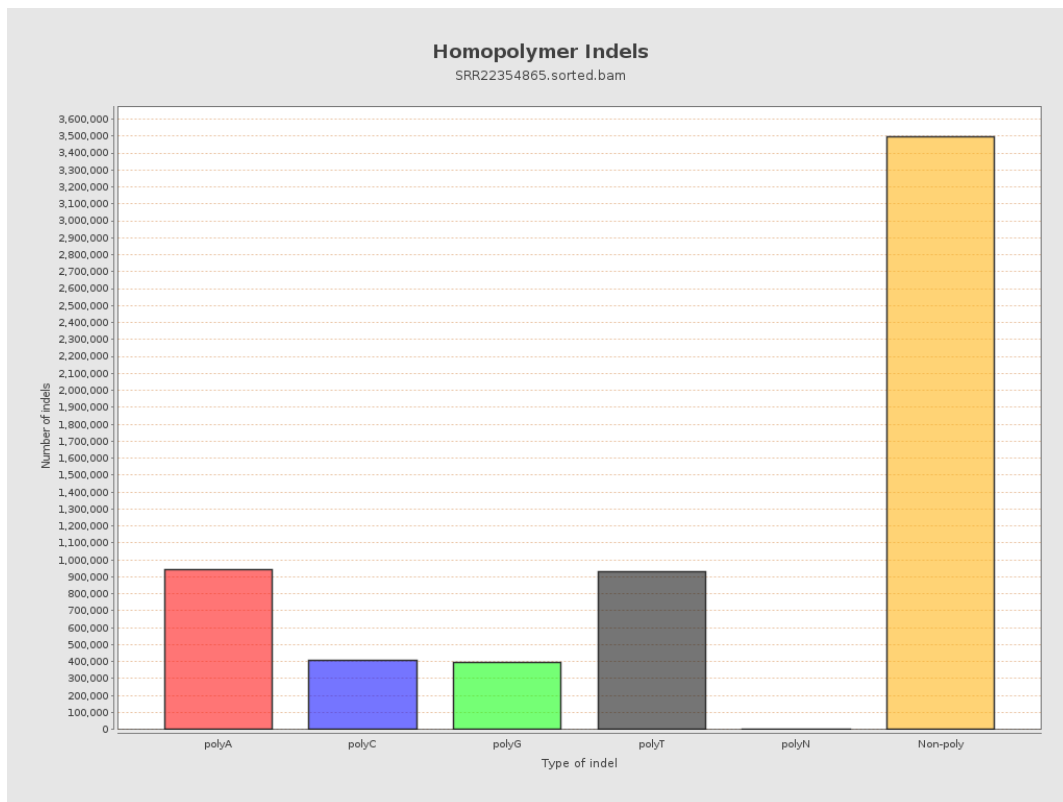
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



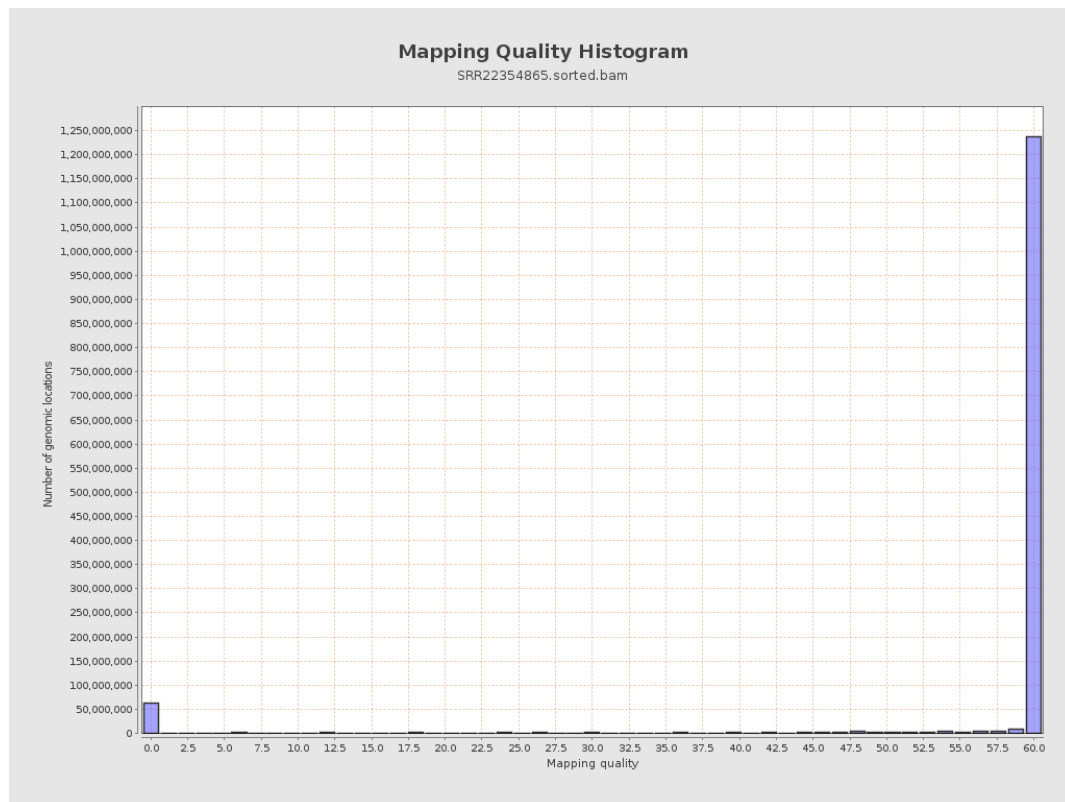
11. Results : Homopolymer Indels



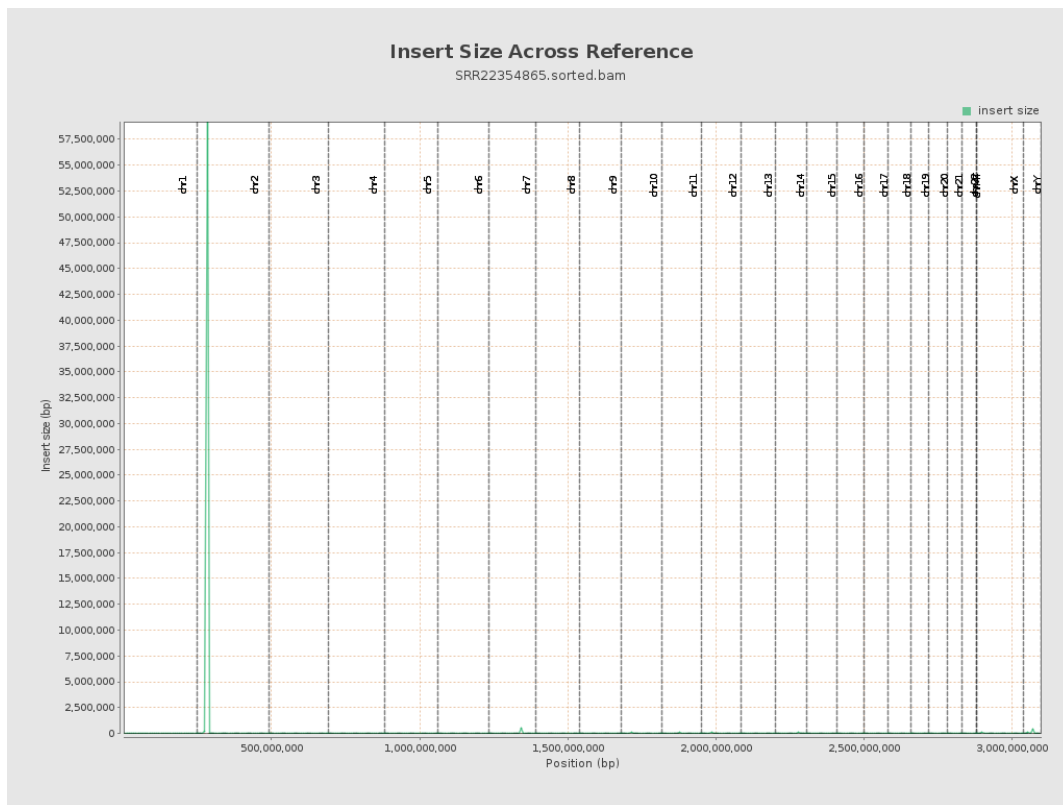
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

