

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 05:13:53

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472593.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_SRR3472593 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472593_1.fastq.gz SRR3472593_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 05:13:52 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472593.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	9,569,682
Mapped reads	8,889,621 / 92.89%
Unmapped reads	680,061 / 7.11%
Mapped paired reads	8,889,621 / 92.89%
Mapped reads, first in pair	4,484,879 / 46.87%
Mapped reads, second in pair	4,404,742 / 46.03%
Mapped reads, both in pair	8,692,516 / 90.83%
Mapped reads, singletons	197,105 / 2.06%
Secondary alignments	0
Supplementary alignments	283,800 / 2.97%
Read min/max/mean length	30 / 100 / 101.15
Duplicated reads (estimated)	1,424,525 / 14.89%
Duplication rate	14.01%
Clipped reads	6,845,002 / 71.53%

2.2. ACGT Content

Number/percentage of A's	187,091,017 / 25.93%
Number/percentage of C's	143,205,770 / 19.85%
Number/percentage of T's	216,166,771 / 29.96%
Number/percentage of G's	174,624,851 / 24.2%
Number/percentage of N's	454,623 / 0.06%

GC Percentage	44.05%
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2.3. Coverage

Mean	0.2332
Standard Deviation	2.0593

2.4. Mapping Quality

Mean Mapping Quality	50.61
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2.5. Insert size

Mean	238,372.33
Standard Deviation	4,691,815.31
P25/Median/P75	89 / 126 / 174

2.6. Mismatches and indels

General error rate	1.18%
Mismatches	8,402,801
Insertions	66,143
Mapped reads with at least one insertion	0.73%
Deletions	161,167
Mapped reads with at least one deletion	1.78%
Homopolymer indels	42.69%

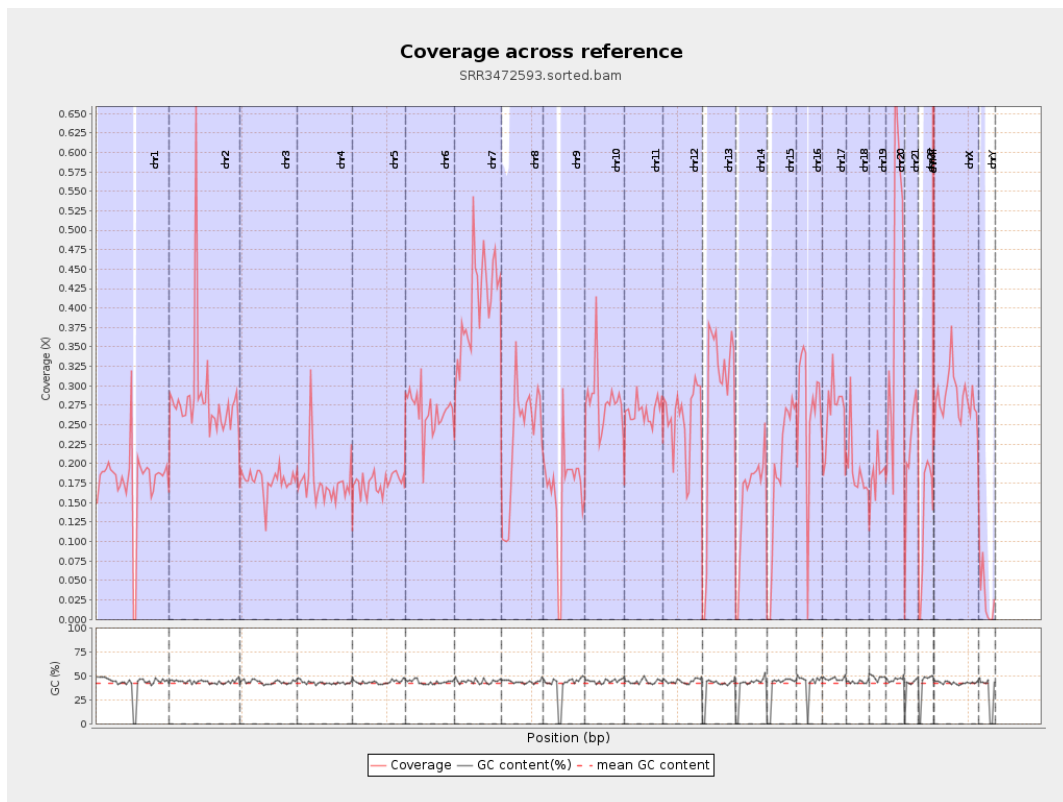
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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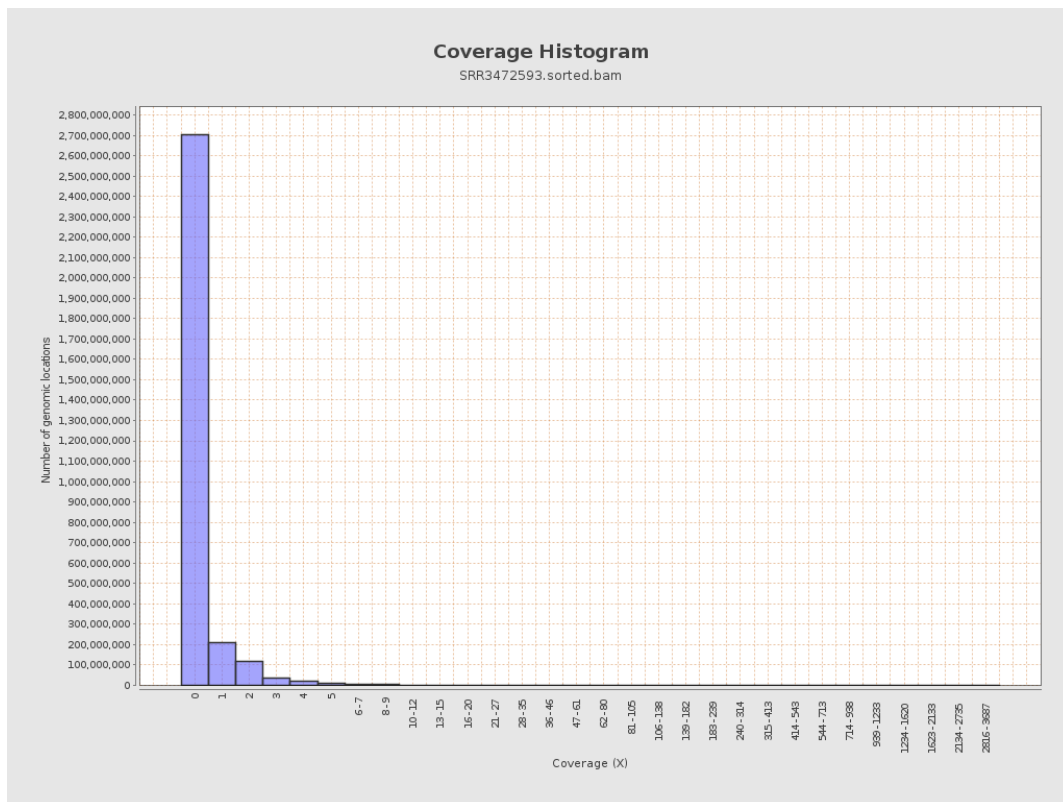
		bases	coverage	deviation
chr1	249250621	44197774	0.1773	2.5819
chr2	243199373	69003591	0.2837	3.1869
chr3	198022430	35214522	0.1778	0.6356
chr4	191154276	33703029	0.1763	1.031
chr5	180915260	31708301	0.1753	0.6642
chr6	171115067	45724307	0.2672	1.2079
chr7	159138663	64990067	0.4084	4.0845
chr8	146364022	33895261	0.2316	1.8503
chr9	141213431	23331637	0.1652	2.1789
chr10	135534747	38077264	0.2809	2.0481
chr11	135006516	35804373	0.2652	2.0408
chr12	133851895	34554886	0.2582	0.8036
chr13	115169878	32551012	0.2826	0.8498
chr14	107349540	16948372	0.1579	3.4447
chr15	102531392	19469174	0.1899	0.6814
chr16	90354753	24409481	0.2702	1.1279
chr17	81195210	21451850	0.2642	1.599
chr18	78077248	15110257	0.1935	3.561
chr19	59128983	11060530	0.1871	1.794
chr20	63025520	27188197	0.4314	1.235
chr21	48129895	10469332	0.2175	0.9344
chr22	51304566	6721035	0.131	0.5603
chrMT	16571	206872	12.484	9.6897
chrX	155270560	44360765	0.2857	1.1913

chrY	59373566	1688630	0.0284	0.7941
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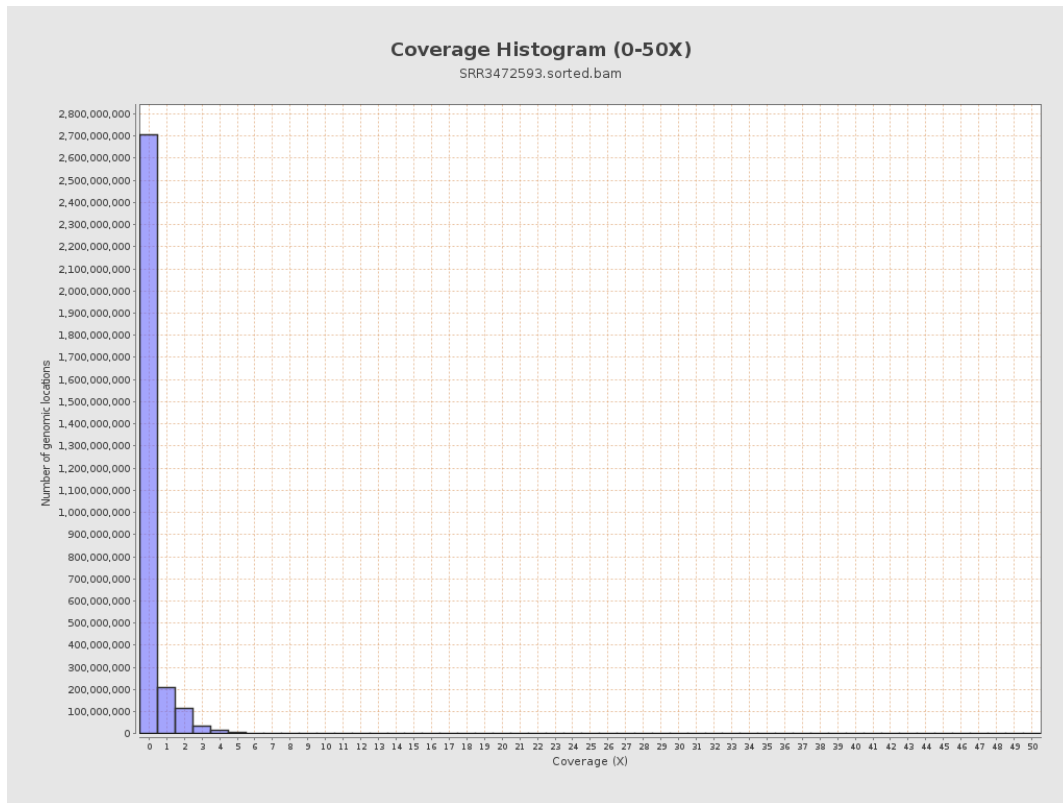
3. Results : Coverage across reference



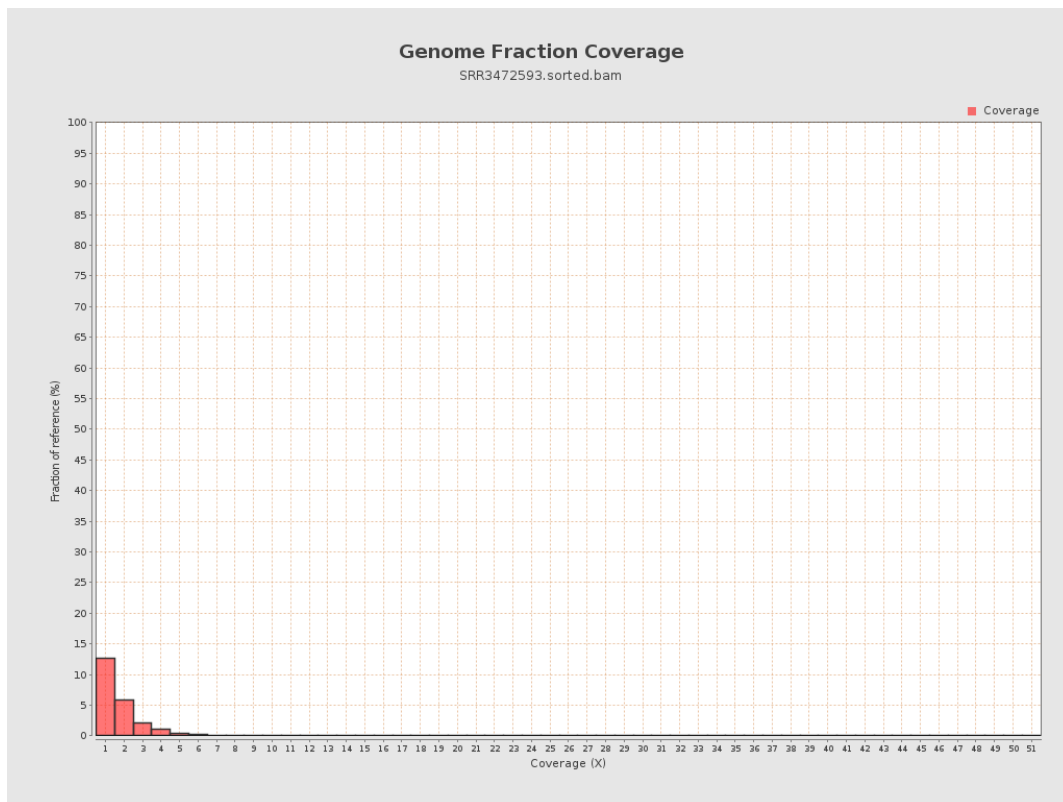
4. Results : Coverage Histogram



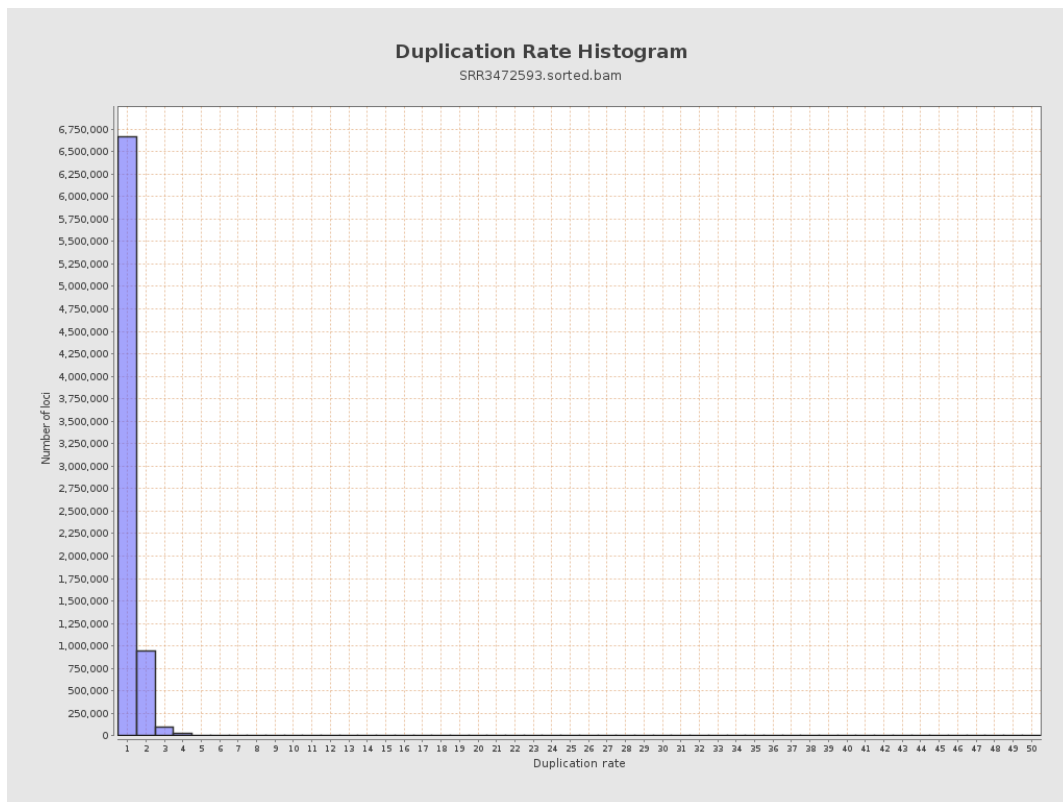
5. Results : Coverage Histogram (0-50X)



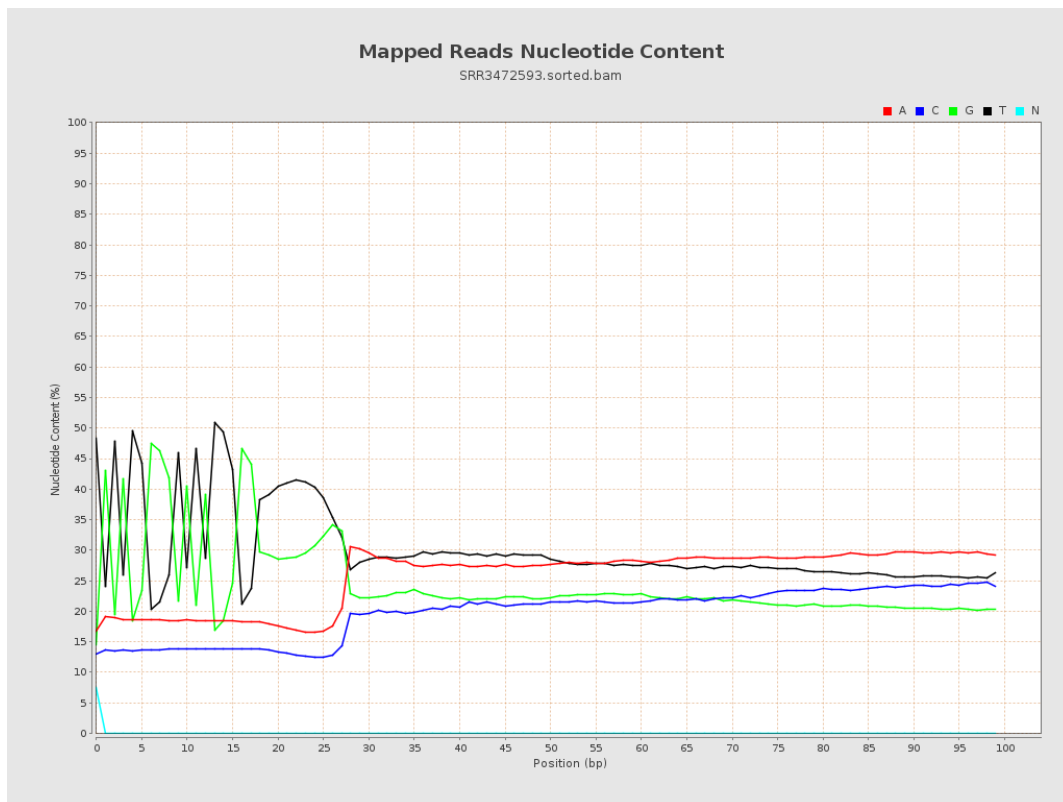
6. Results : Genome Fraction Coverage



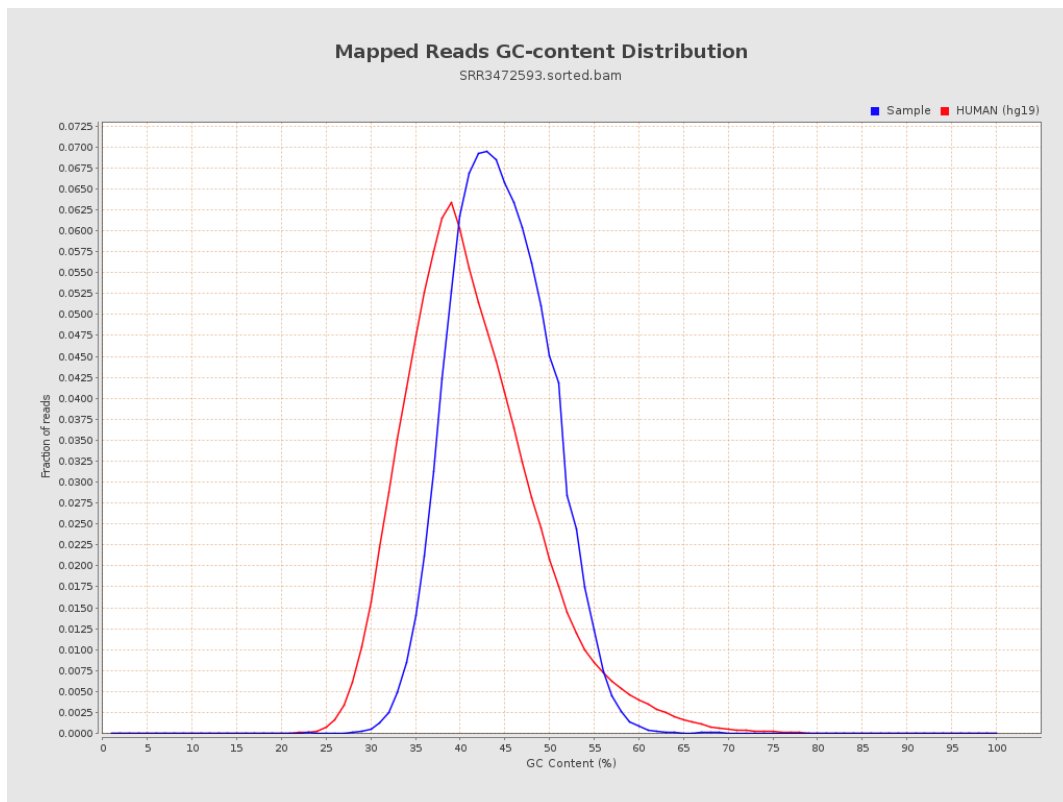
7. Results : Duplication Rate Histogram



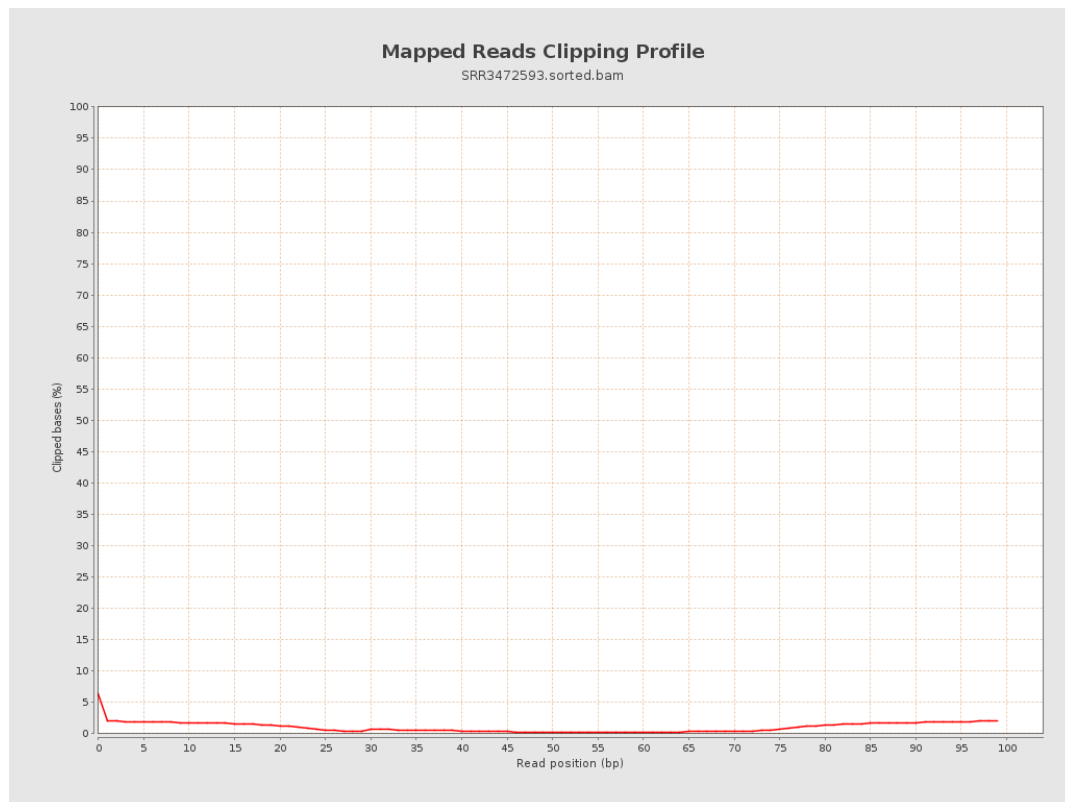
8. Results : Mapped Reads Nucleotide Content



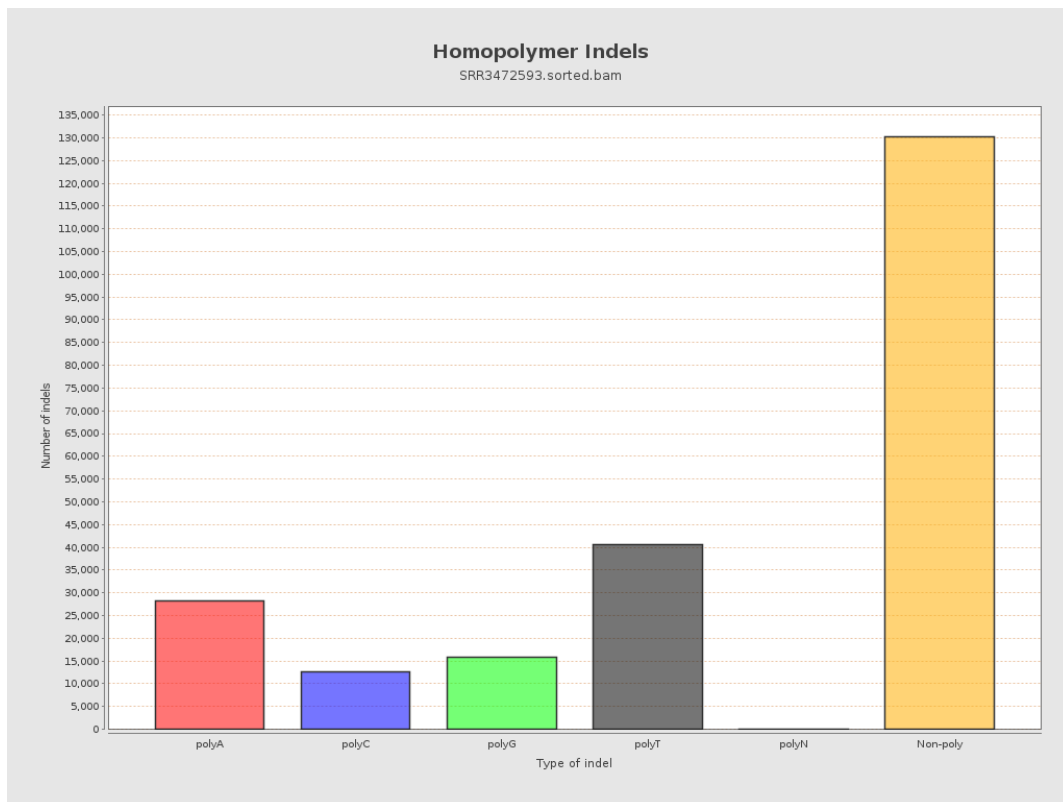
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



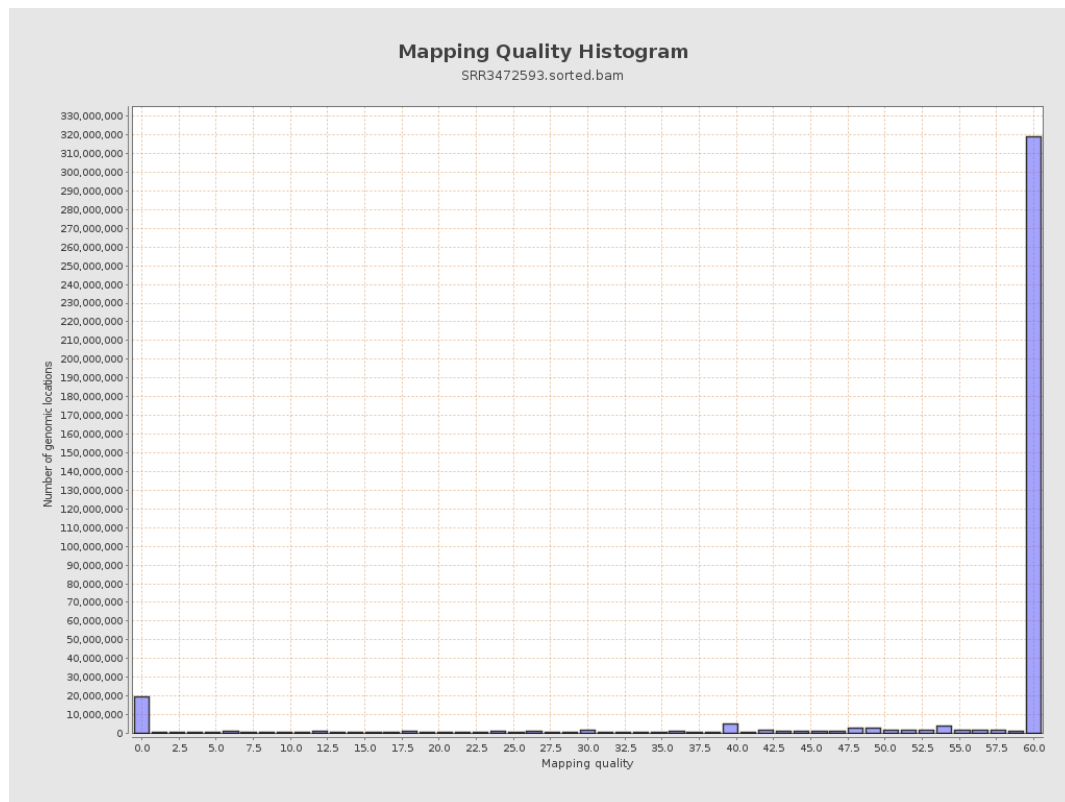
11. Results : Homopolymer Indels



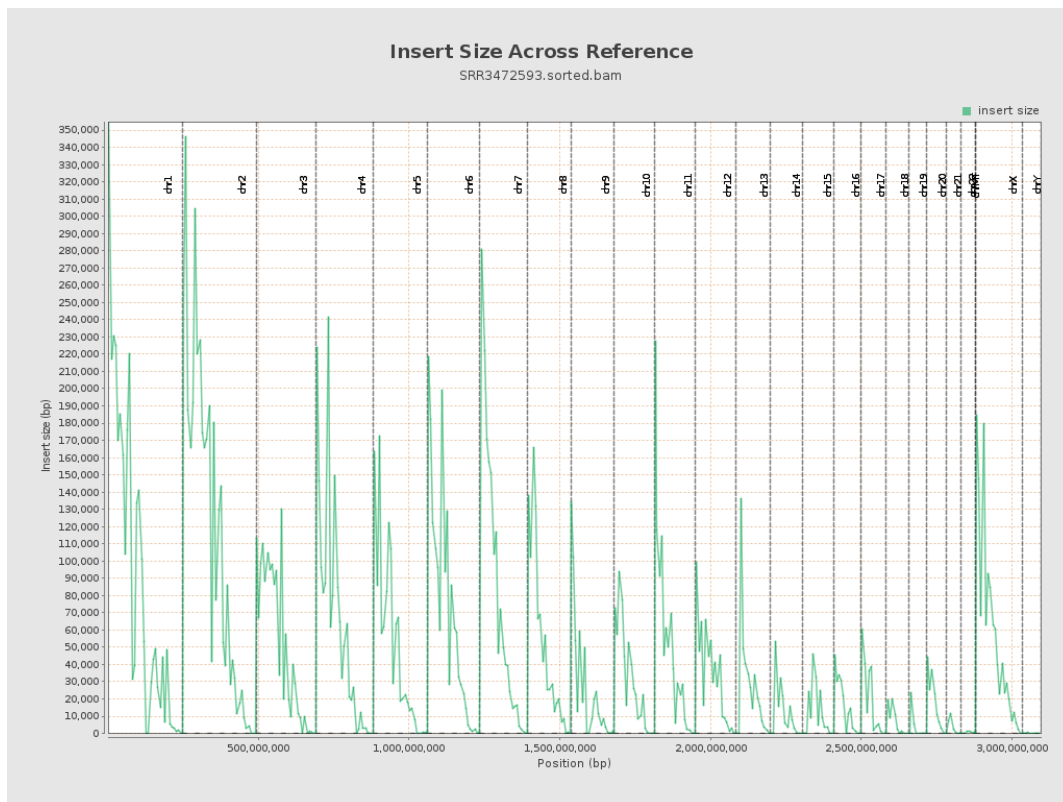
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

