

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 21:53:32

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472652.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_SRR3472652 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472652_1.fastq.gz SRR3472652_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 21:53:31 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472652.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	13,377,654
Mapped reads	13,247,668 / 99.03%
Unmapped reads	129,986 / 0.97%
Mapped paired reads	13,247,668 / 99.03%
Mapped reads, first in pair	6,661,075 / 49.79%
Mapped reads, second in pair	6,586,593 / 49.24%
Mapped reads, both in pair	13,167,680 / 98.43%
Mapped reads, singletons	79,988 / 0.6%
Secondary alignments	0
Supplementary alignments	20,218 / 0.15%
Read min/max/mean length	30 / 101 / 99.39
Duplicated reads (estimated)	6,853,470 / 51.23%
Duplication rate	44.72%
Clipped reads	725,577 / 5.42%

2.2. ACGT Content

Number/percentage of A's	357,832,781 / 27.47%
Number/percentage of C's	293,515,629 / 22.54%
Number/percentage of T's	362,794,498 / 27.86%
Number/percentage of G's	287,960,846 / 22.11%
Number/percentage of N's	292,287 / 0.02%

GC Percentage	44.65%
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2.3. Coverage

Mean	0.4208
Standard Deviation	9.0622

2.4. Mapping Quality

Mean Mapping Quality	54.93
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2.5. Insert size

Mean	19,751.57
Standard Deviation	1,424,336.96
P25/Median/P75	154 / 217 / 296

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	5,945,490
Insertions	54,833
Mapped reads with at least one insertion	0.41%
Deletions	67,133
Mapped reads with at least one deletion	0.5%
Homopolymer indels	44.29%

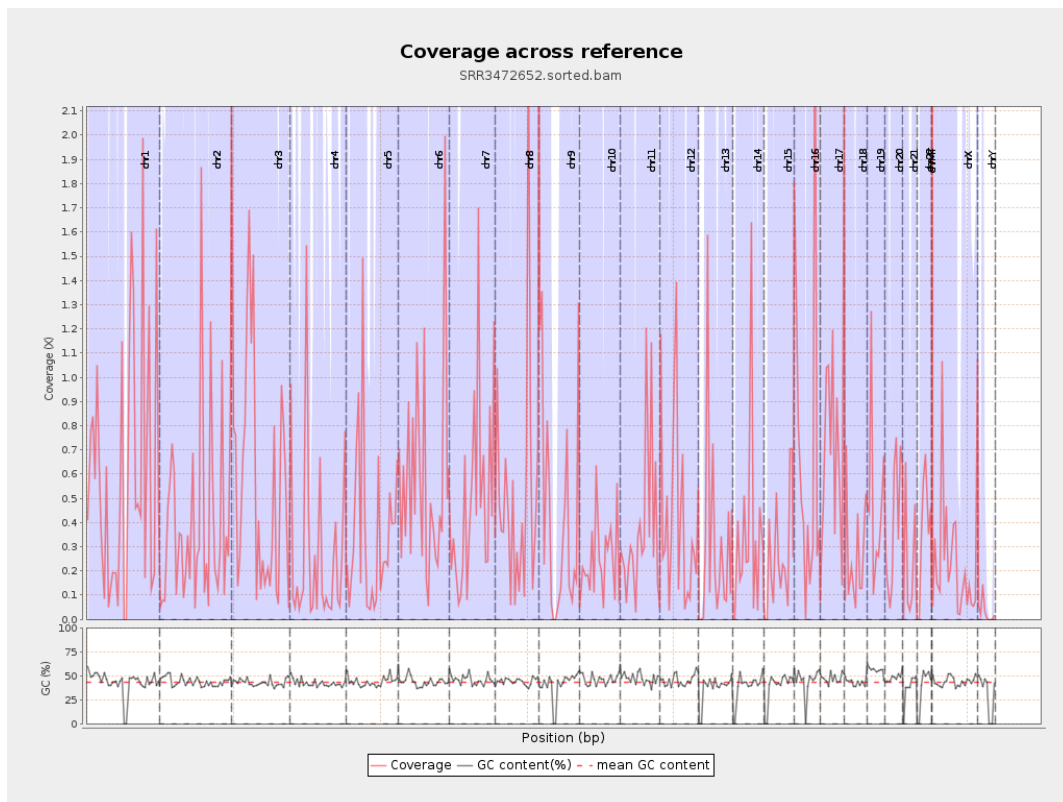
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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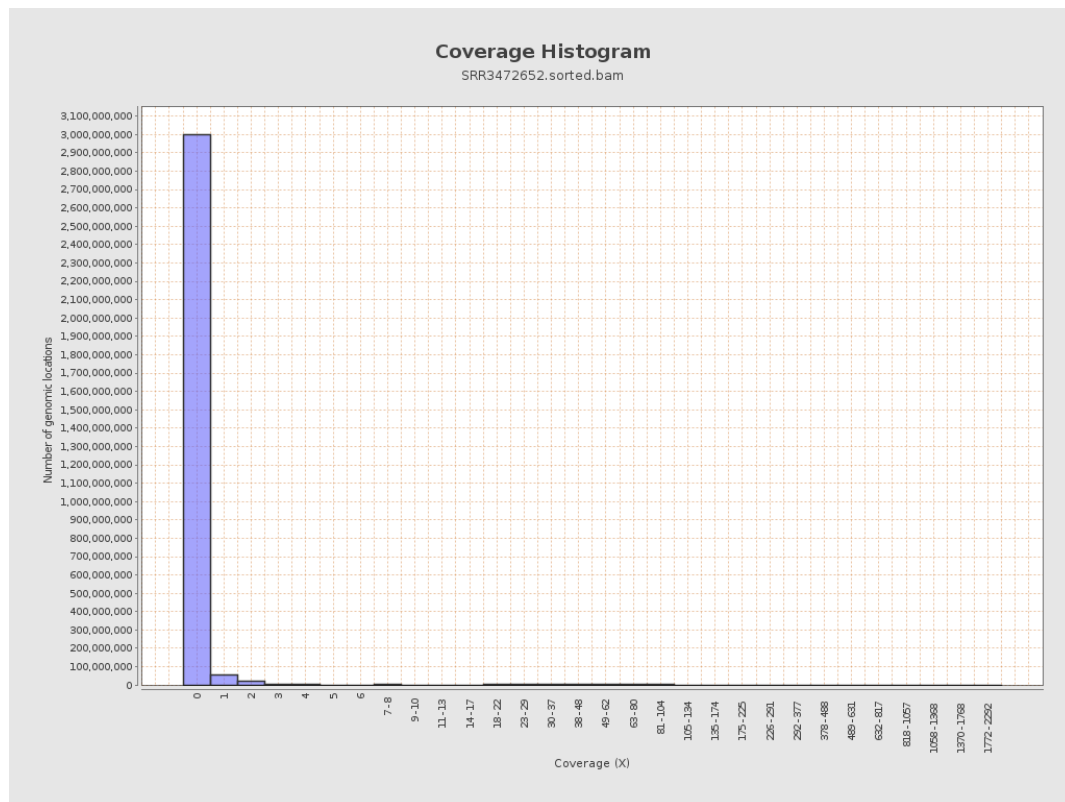
		bases	coverage	deviation
chr1	249250621	152965347	0.6137	11.7775
chr2	243199373	96655974	0.3974	9.3492
chr3	198022430	116734185	0.5895	9.8427
chr4	191154276	49844461	0.2608	7.5826
chr5	180915260	65210221	0.3604	8.2468
chr6	171115067	96069140	0.5614	10.0889
chr7	159138663	79888608	0.502	11.2589
chr8	146364022	76882707	0.5253	10.4785
chr9	141213431	63195610	0.4475	8.2234
chr10	135534747	33536255	0.2474	6.4713
chr11	135006516	50457909	0.3737	8.6901
chr12	133851895	57127523	0.4268	7.6167
chr13	115169878	33325510	0.2894	8.1275
chr14	107349540	35354880	0.3293	7.7015
chr15	102531392	27378933	0.267	6.2508
chr16	90354753	65074696	0.7202	14.4748
chr17	81195210	59886968	0.7376	11.9263
chr18	78077248	21138921	0.2707	6.1585
chr19	59128983	28489994	0.4818	7.0205
chr20	63025520	25269651	0.4009	8.2474
chr21	48129895	10736641	0.2231	9.9664
chr22	51304566	18665200	0.3638	7.728
chrMT	16571	625964	37.7747	11.9979
chrX	155270560	36048251	0.2322	3.9541

chrY	59373566	1997077	0.0336	1.1689
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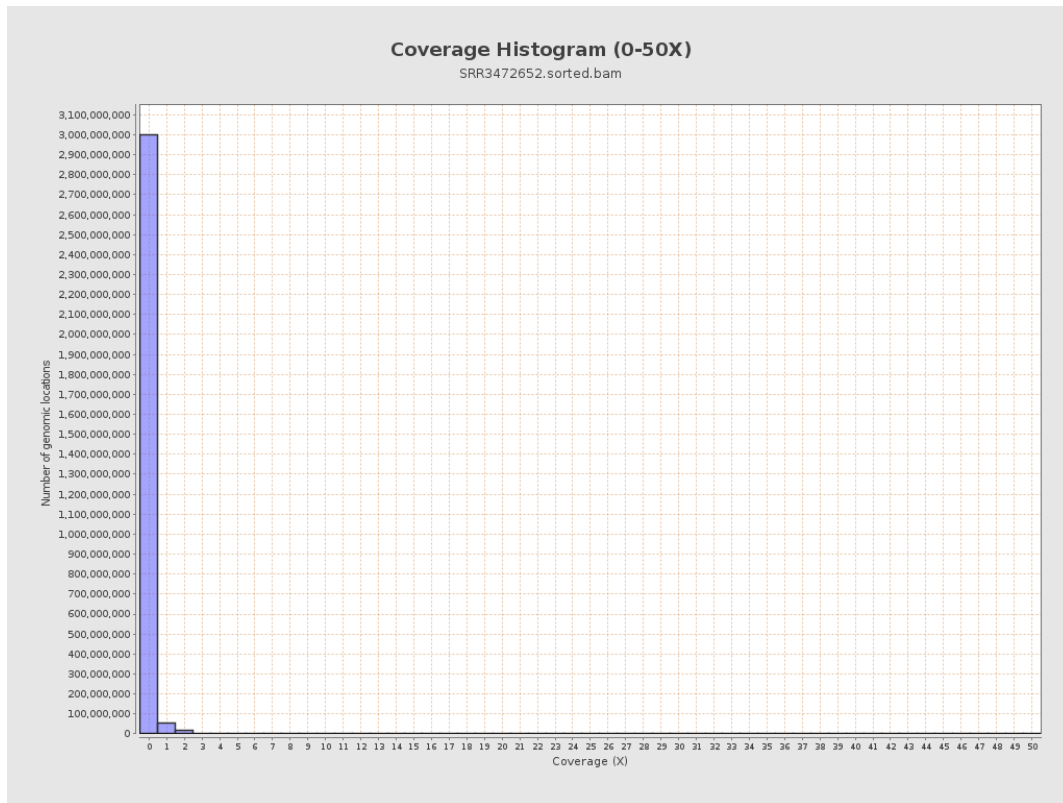
3. Results : Coverage across reference



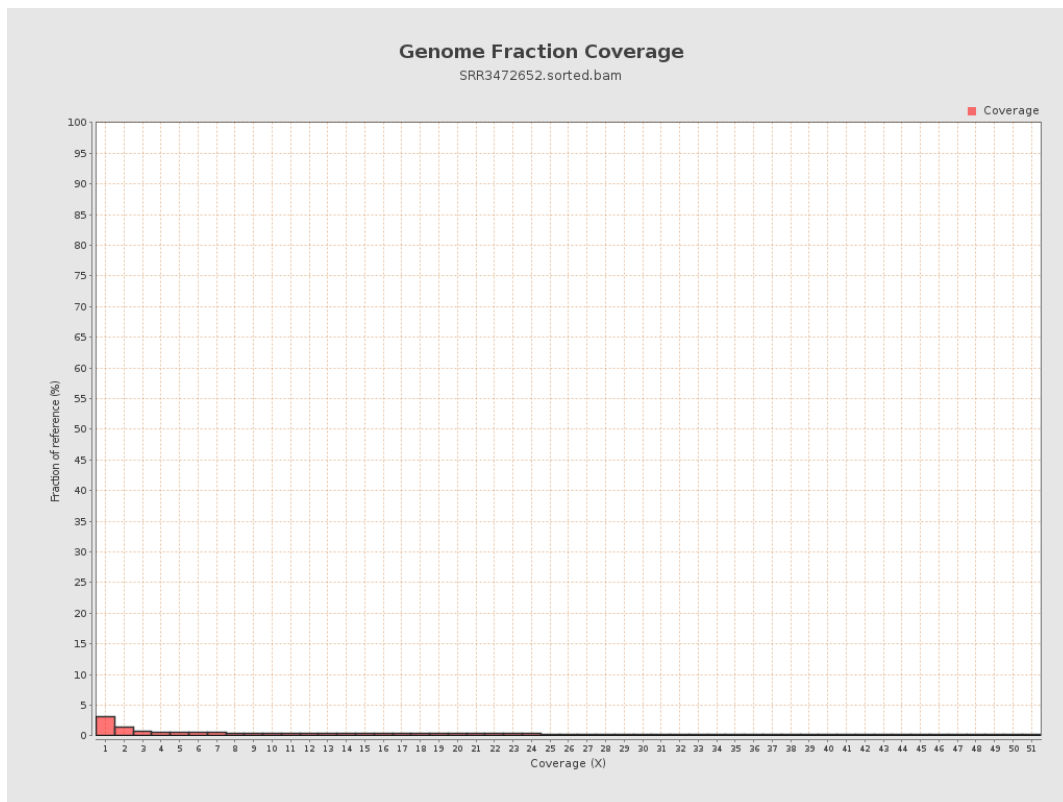
4. Results : Coverage Histogram



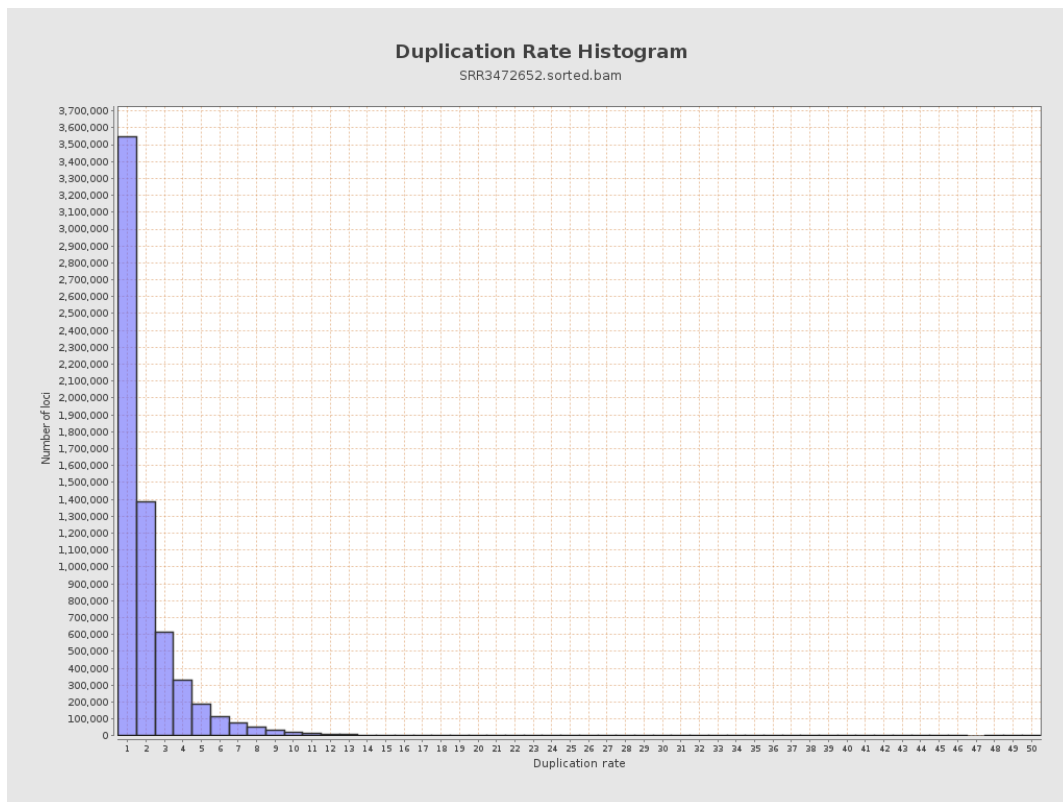
5. Results : Coverage Histogram (0-50X)



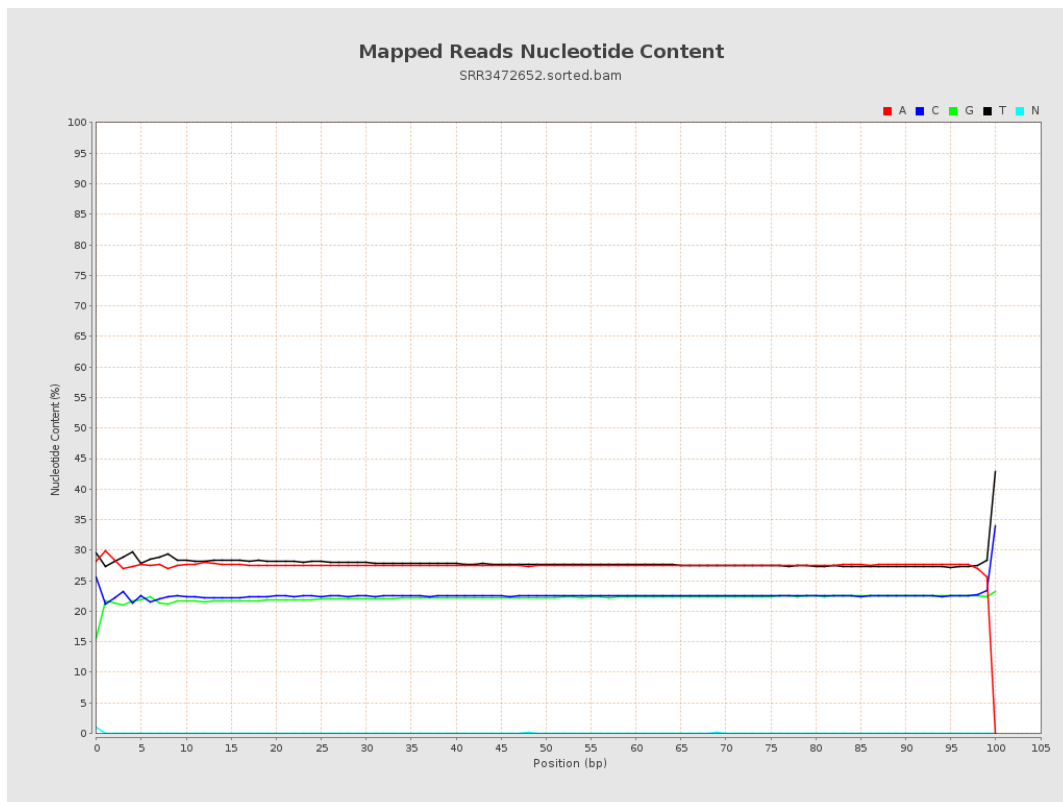
6. Results : Genome Fraction Coverage



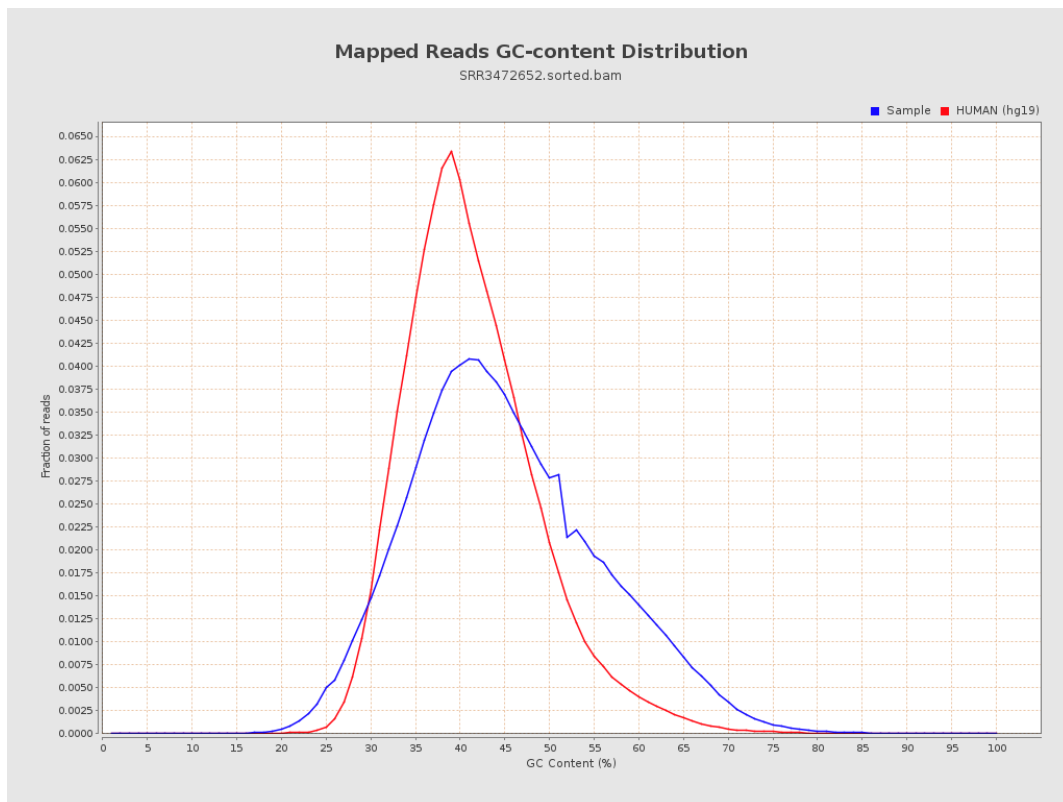
7. Results : Duplication Rate Histogram



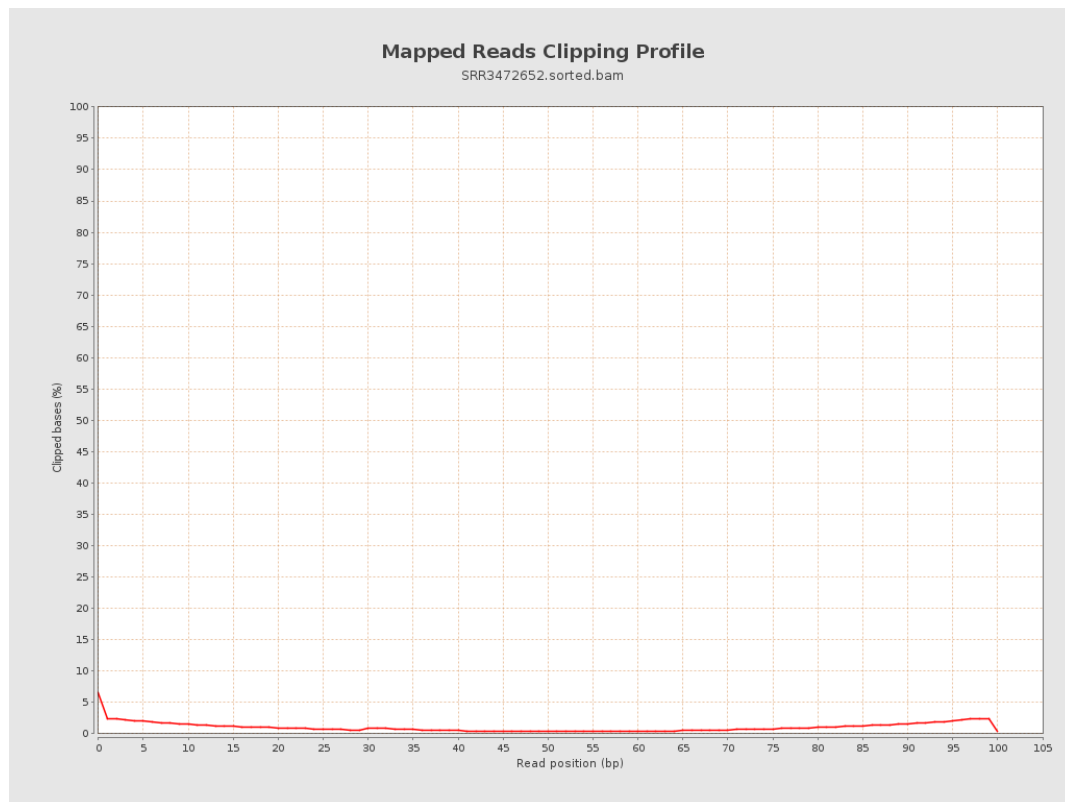
8. Results : Mapped Reads Nucleotide Content



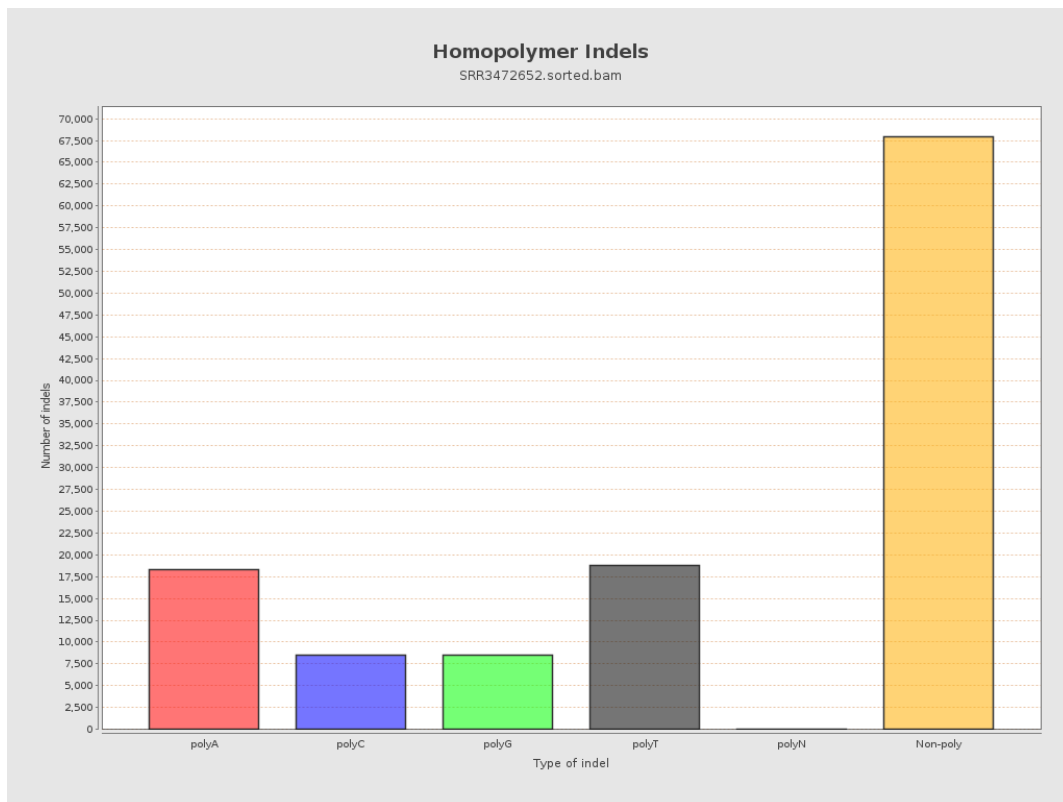
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



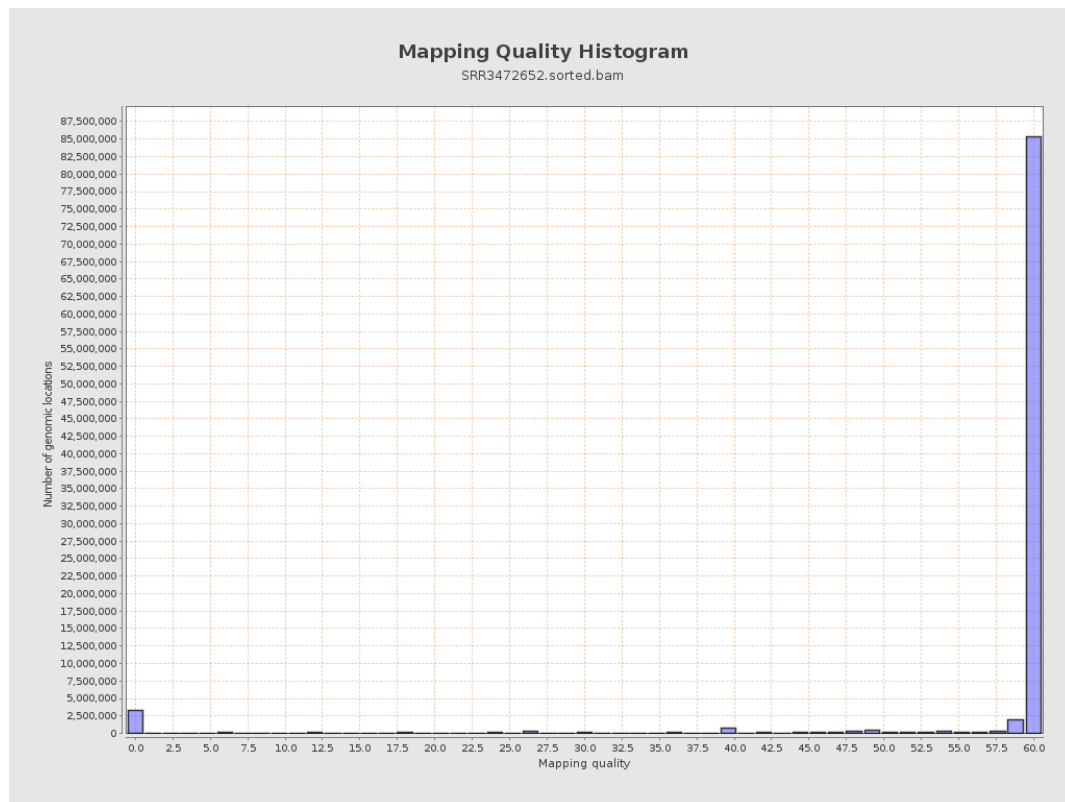
11. Results : Homopolymer Indels



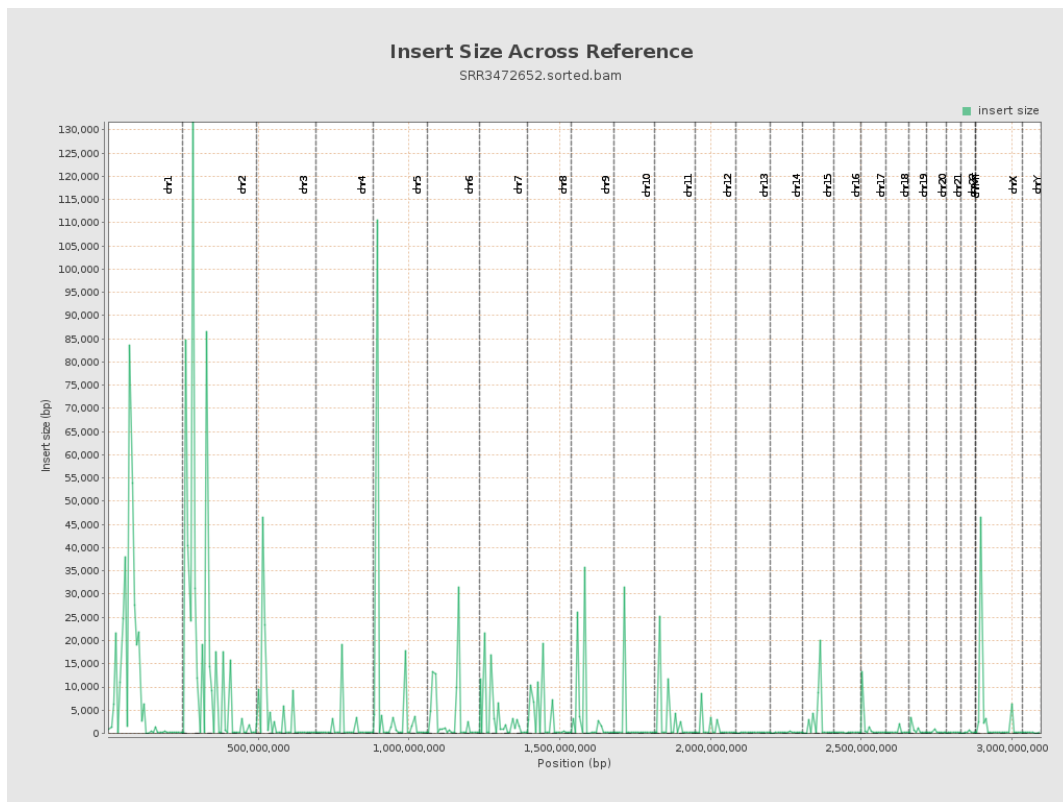
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

