

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/25 07:51:09

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472552.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_SRR3472552 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472552_1.fastq.gz SRR3472552_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Aug 25 07:51:03 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472552.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	20,571,068
Mapped reads	20,324,904 / 98.8%
Unmapped reads	246,164 / 1.2%
Mapped paired reads	20,324,904 / 98.8%
Mapped reads, first in pair	10,188,284 / 49.53%
Mapped reads, second in pair	10,136,620 / 49.28%
Mapped reads, both in pair	20,209,064 / 98.24%
Mapped reads, singletons	115,840 / 0.56%
Secondary alignments	0
Supplementary alignments	105,105 / 0.51%
Read min/max/mean length	30 / 100 / 100.21
Duplicated reads (estimated)	13,173,965 / 64.04%
Duplication rate	46.61%
Clipped reads	1,943,427 / 9.45%

2.2. ACGT Content

Number/percentage of A's	551,916,556 / 27.65%
Number/percentage of C's	448,795,943 / 22.49%
Number/percentage of T's	548,446,079 / 27.48%
Number/percentage of G's	446,262,518 / 22.36%
Number/percentage of N's	309,706 / 0.02%

GC Percentage	44.85%
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2.3. Coverage

Mean	0.6448
Standard Deviation	22.4783

2.4. Mapping Quality

Mean Mapping Quality	55.02
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2.5. Insert size

Mean	39,558.47
Standard Deviation	1,965,611.08
P25/Median/P75	163 / 230 / 313

2.6. Mismatches and indels

General error rate	0.6%
Mismatches	11,687,344
Insertions	105,598
Mapped reads with at least one insertion	0.51%
Deletions	99,006
Mapped reads with at least one deletion	0.48%
Homopolymer indels	45%

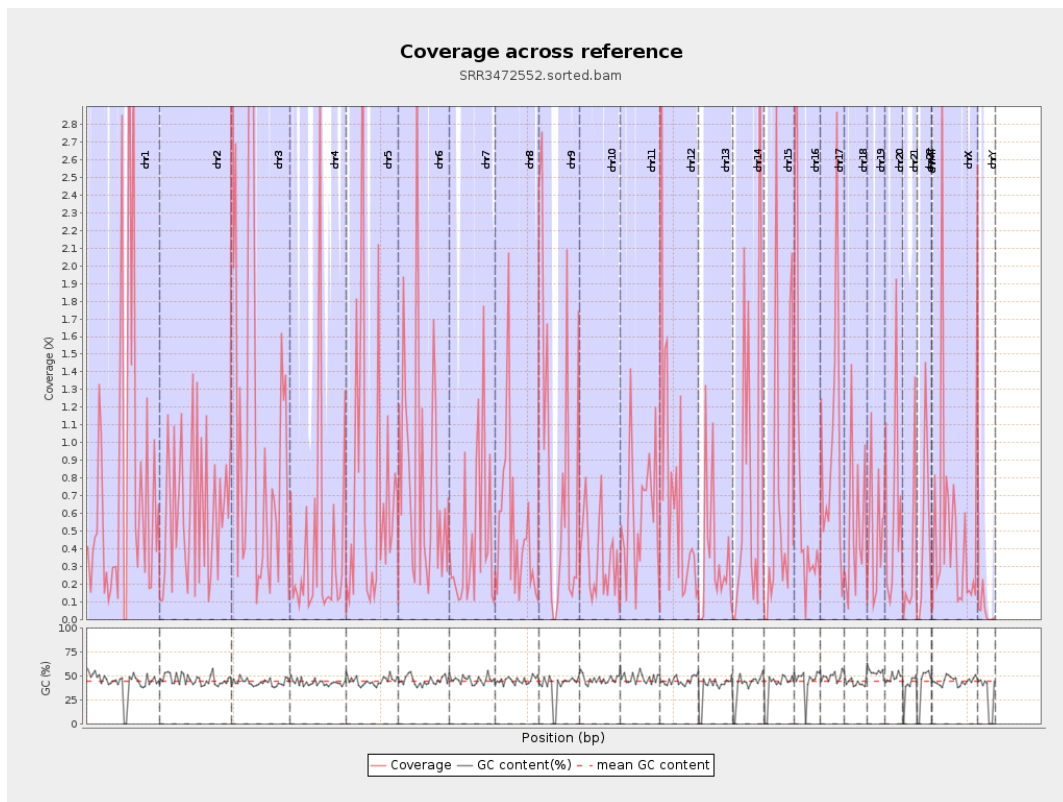
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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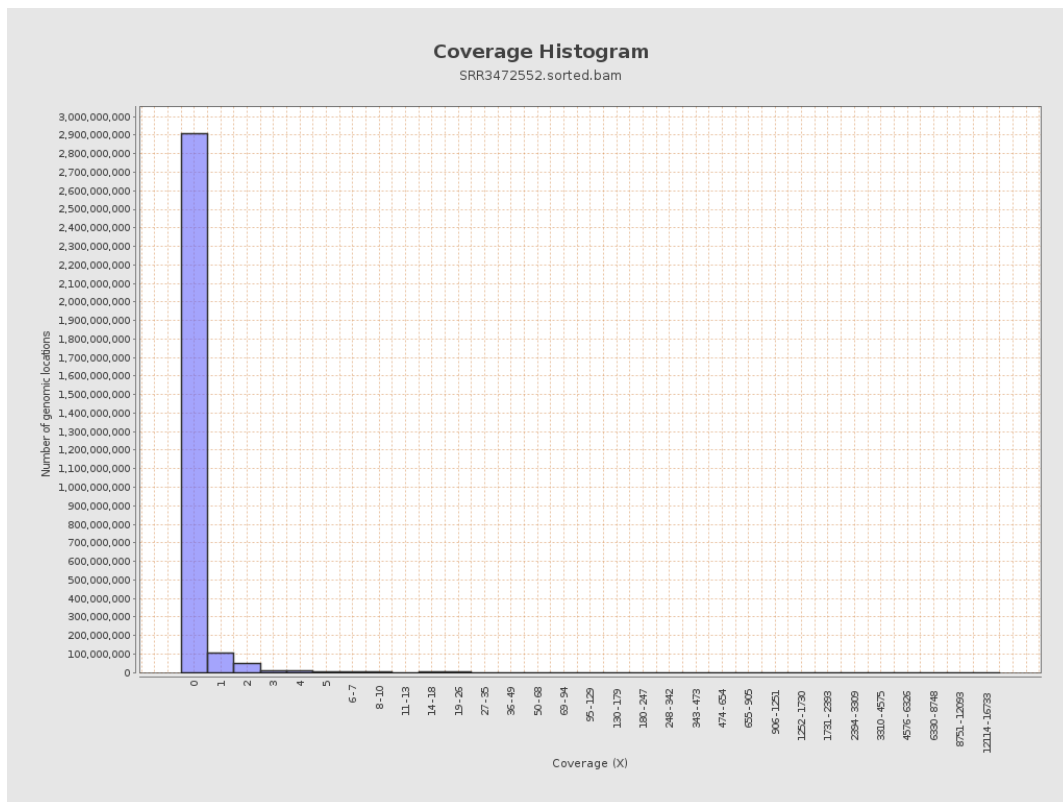
		bases	coverage	deviation
chr1	249250621	190561423	0.7645	30.8246
chr2	243199373	147346824	0.6059	21.434
chr3	198022430	225035938	1.1364	26.8847
chr4	191154276	73402177	0.384	16.4385
chr5	180915260	133674219	0.7389	24.348
chr6	171115067	138783927	0.8111	21.8924
chr7	159138663	71637455	0.4502	16.4255
chr8	146364022	74232388	0.5072	18.1099
chr9	141213431	119844599	0.8487	21.2836
chr10	135534747	47618494	0.3513	13.2345
chr11	135006516	84264511	0.6242	19.2034
chr12	133851895	114156275	0.8529	28.2739
chr13	115169878	40161942	0.3487	11.3011
chr14	107349540	82012687	0.764	43.0486
chr15	102531392	74117890	0.7229	26.1653
chr16	90354753	69645340	0.7708	24.6763
chr17	81195210	76065779	0.9368	21.6722
chr18	78077248	40131254	0.514	20.9602
chr19	59128983	29813308	0.5042	11.5204
chr20	63025520	40005386	0.6347	18.6926
chr21	48129895	15067391	0.3131	14.9822
chr22	51304566	23588522	0.4598	15.0161
chrMT	16571	1920	0.1159	0.4492
chrX	155270560	81726470	0.5263	14.4161

chrY	59373566	3073045	0.0518	1.7382
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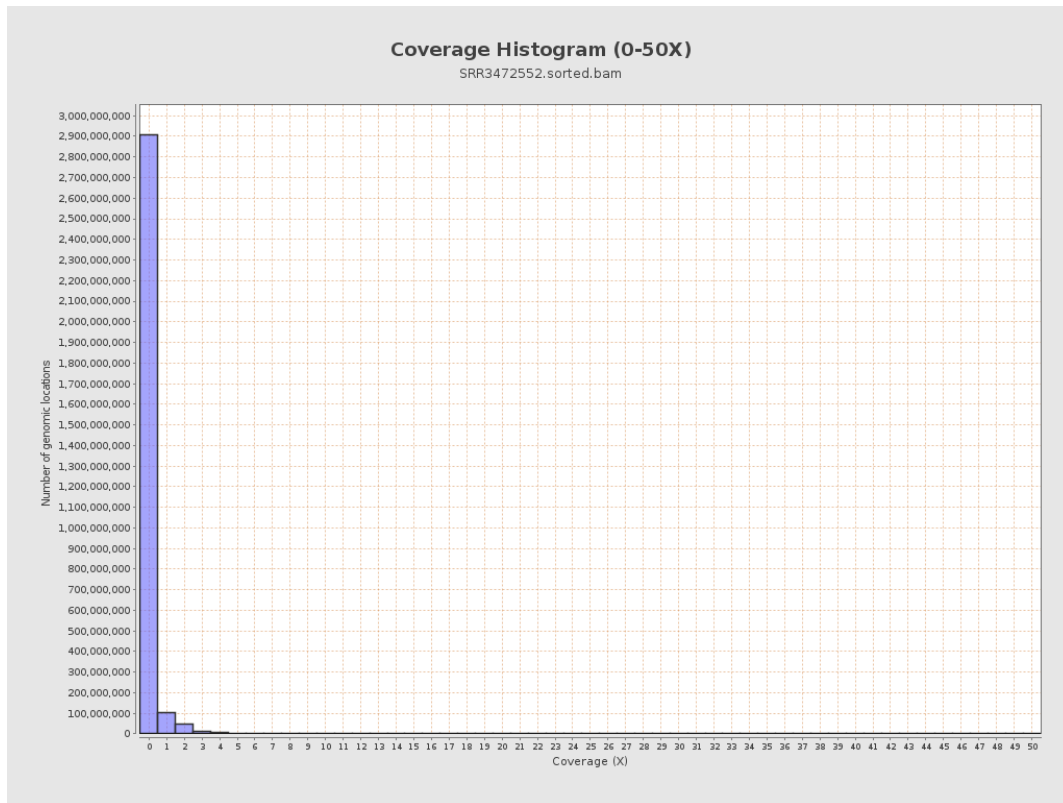
3. Results : Coverage across reference



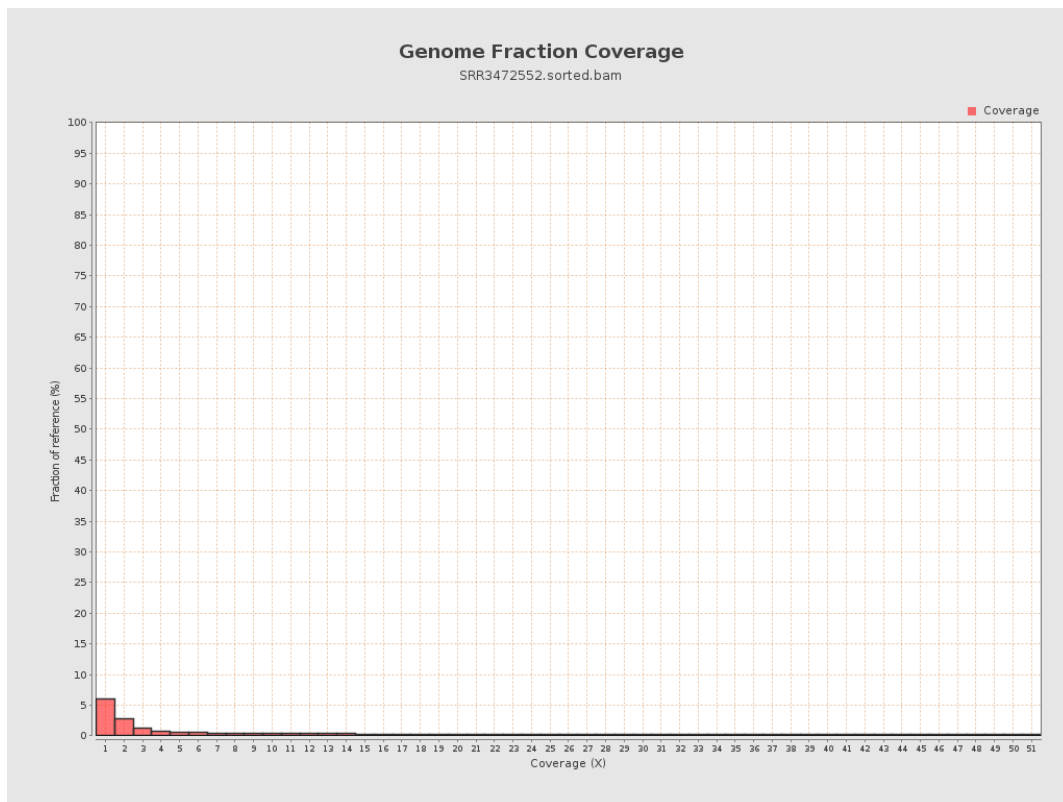
4. Results : Coverage Histogram



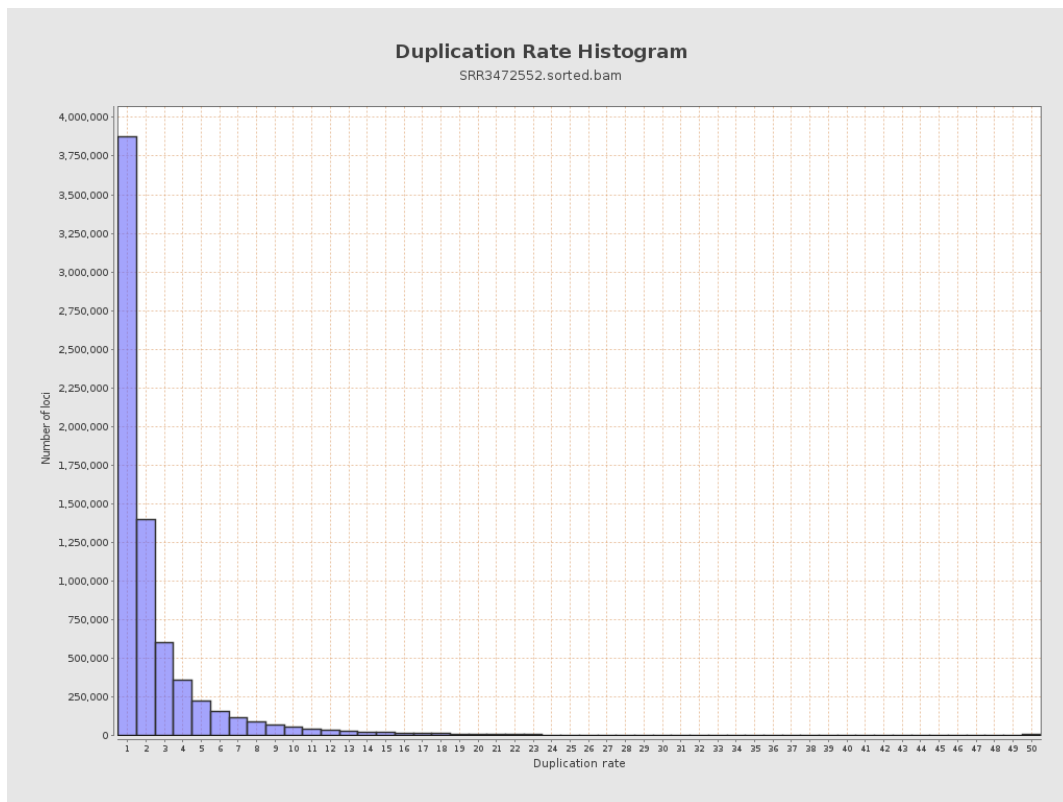
5. Results : Coverage Histogram (0-50X)



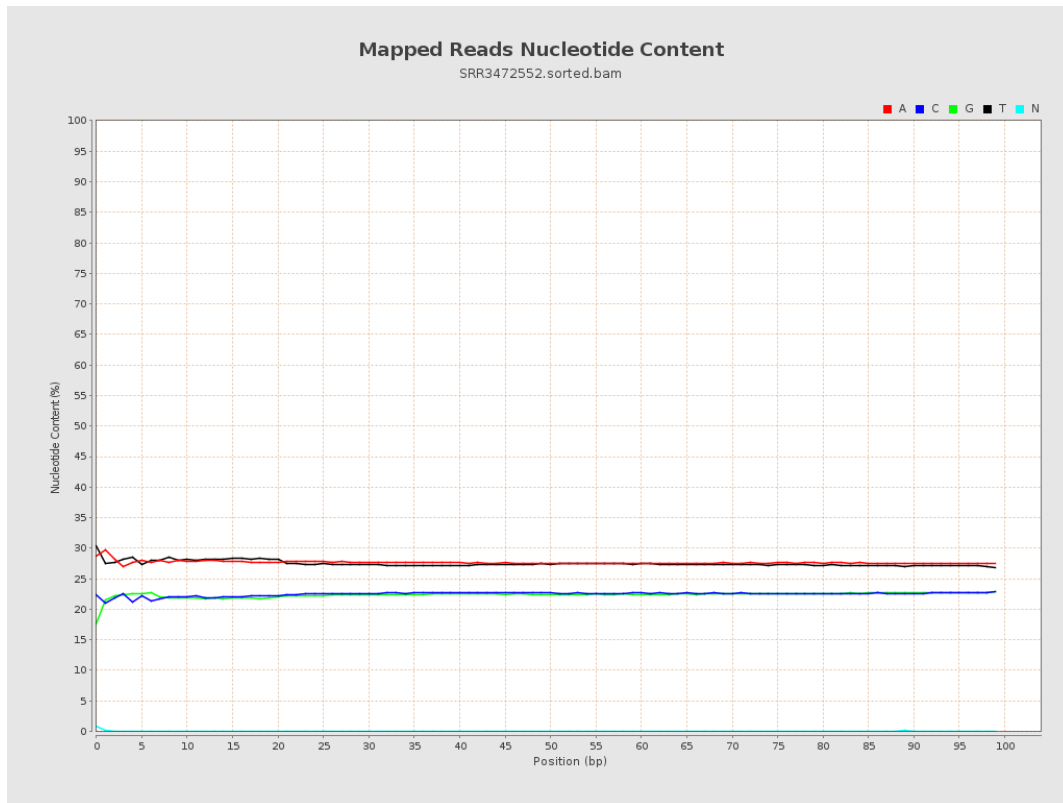
6. Results : Genome Fraction Coverage



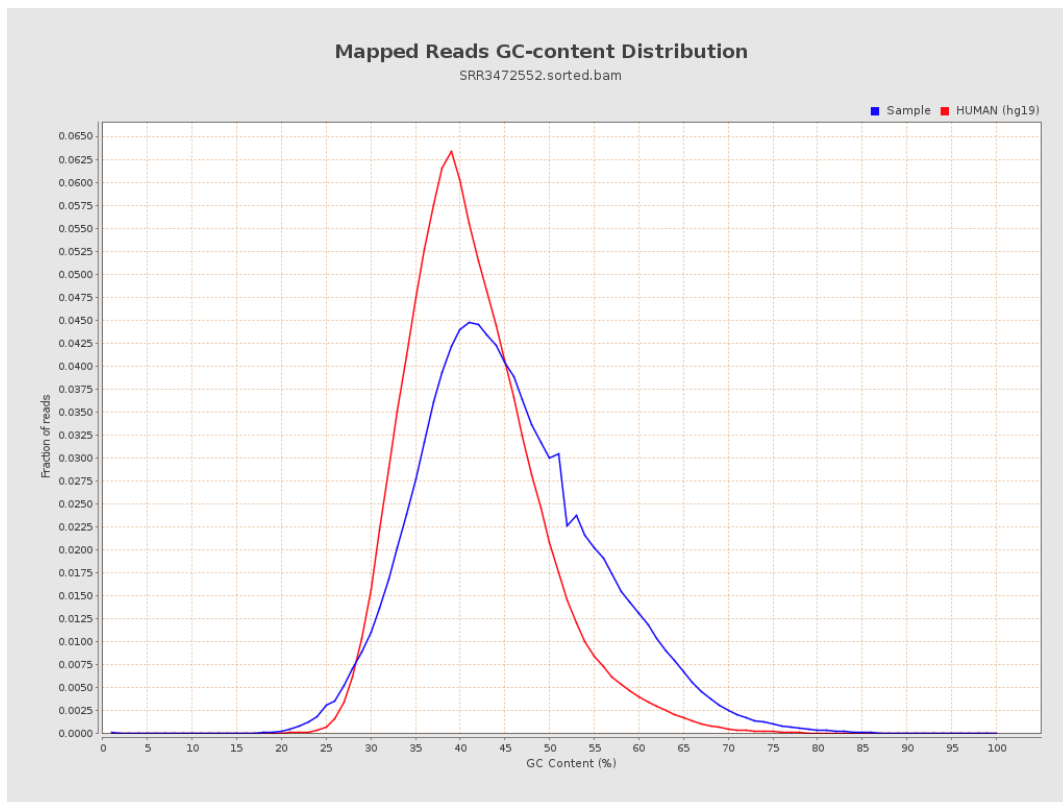
7. Results : Duplication Rate Histogram



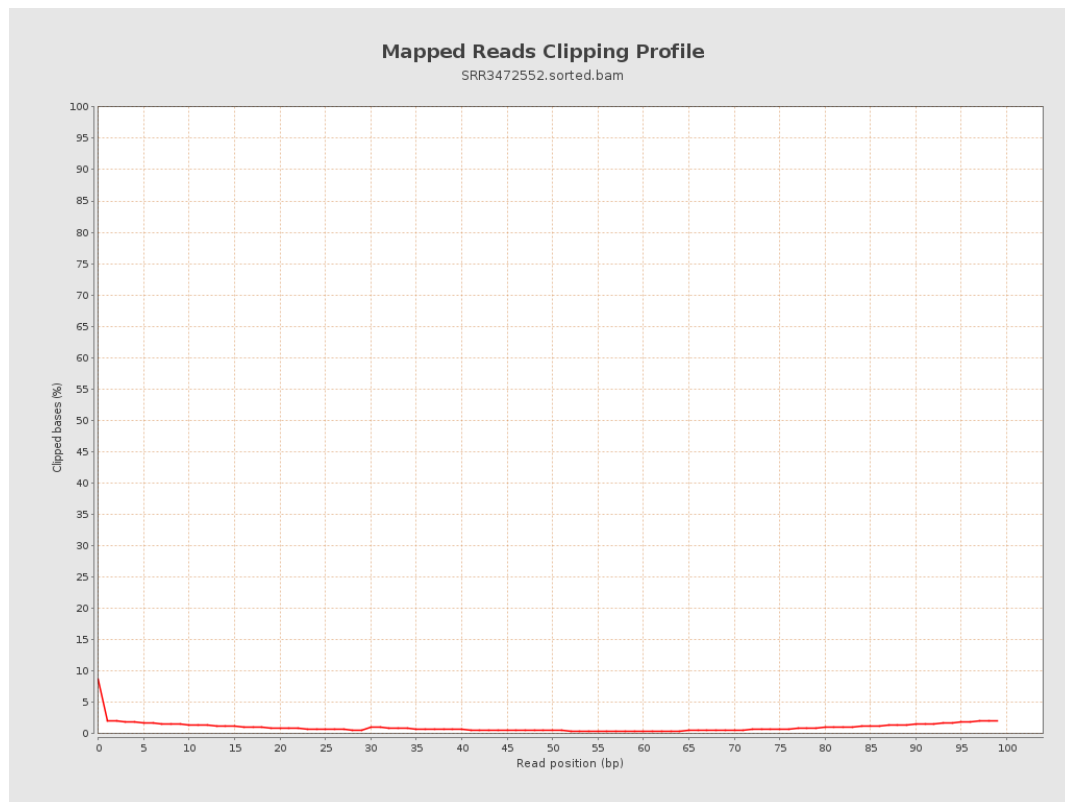
8. Results : Mapped Reads Nucleotide Content



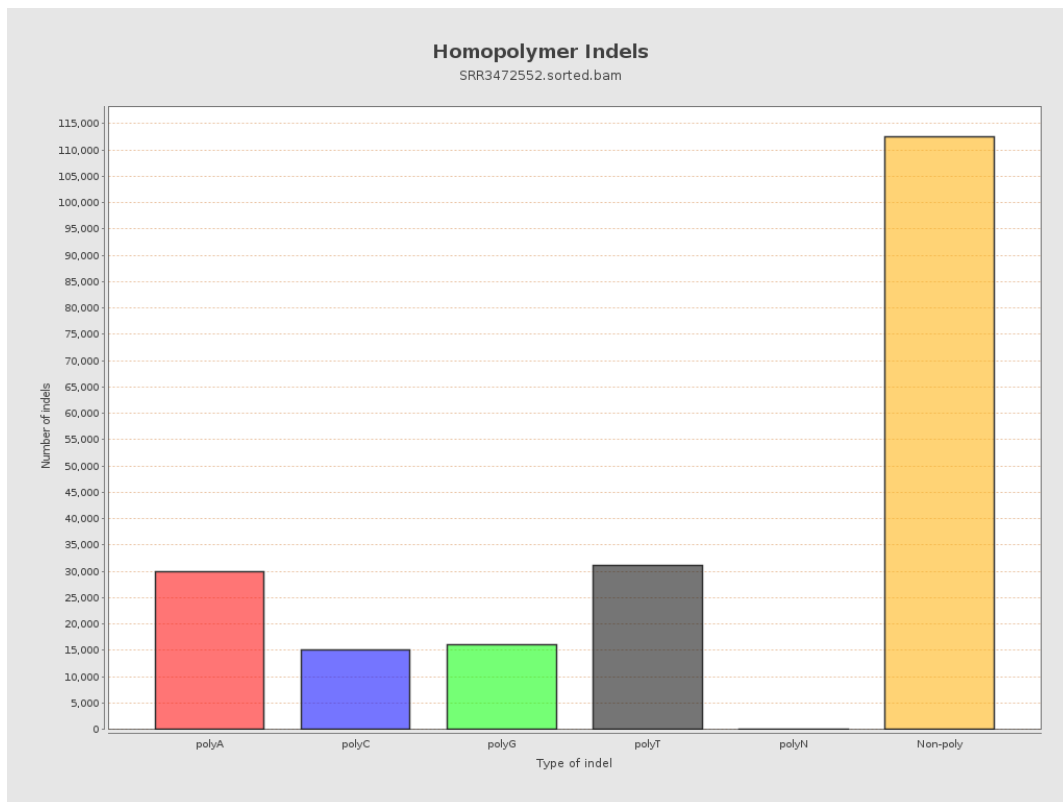
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



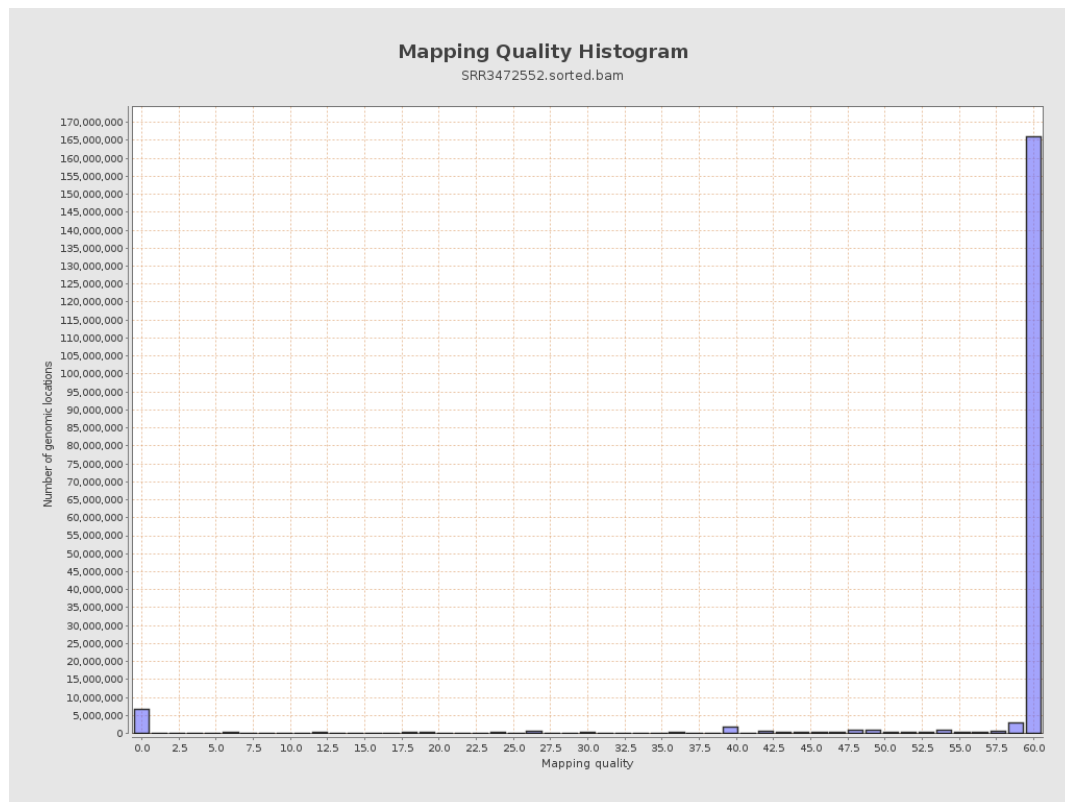
11. Results : Homopolymer Indels



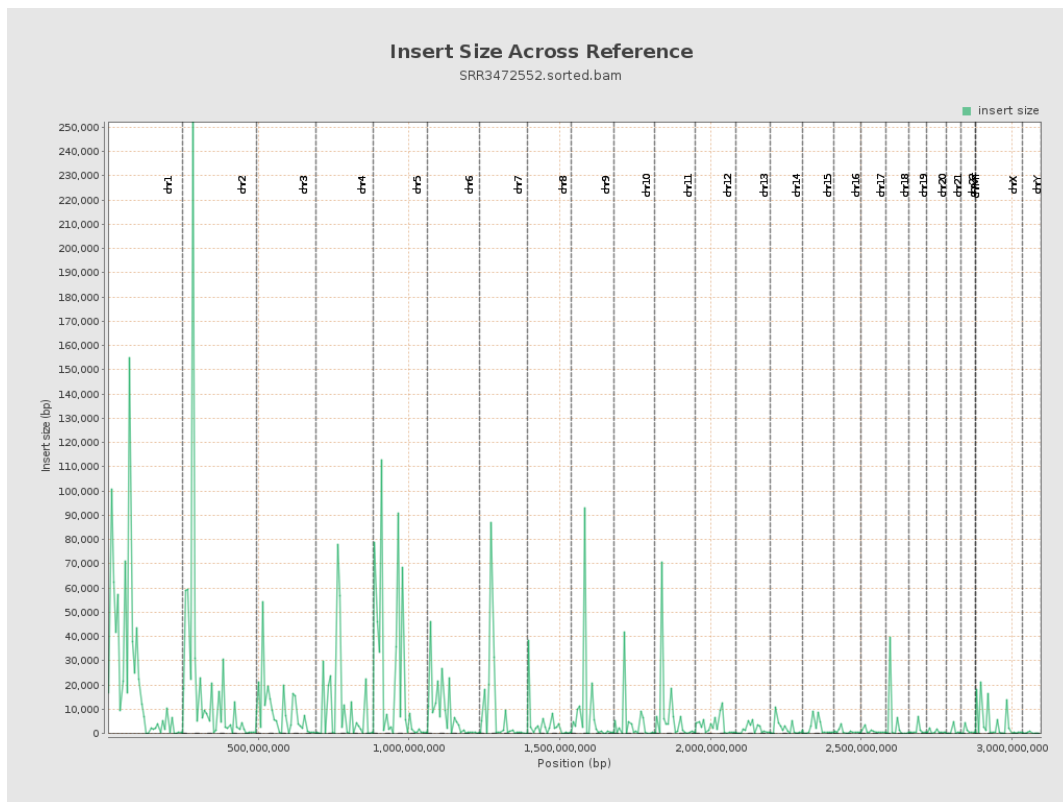
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

