

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/24 00:11:15

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472454.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_SRR3472454 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472454_1.fastq.gz SRR3472454_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Aug 24 00:11:14 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472454.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,173,782
Mapped reads	16,004,664 / 98.95%
Unmapped reads	169,118 / 1.05%
Mapped paired reads	16,004,664 / 98.95%
Mapped reads, first in pair	8,030,351 / 49.65%
Mapped reads, second in pair	7,974,313 / 49.3%
Mapped reads, both in pair	15,925,670 / 98.47%
Mapped reads, singletons	78,994 / 0.49%
Secondary alignments	0
Supplementary alignments	60,146 / 0.37%
Read min/max/mean length	30 / 100 / 99.23
Duplicated reads (estimated)	10,000,196 / 61.83%
Duplication rate	47.1%
Clipped reads	1,158,281 / 7.16%

2.2. ACGT Content

Number/percentage of A's	417,975,016 / 26.68%
Number/percentage of C's	365,712,634 / 23.34%
Number/percentage of T's	420,475,411 / 26.84%
Number/percentage of G's	362,475,500 / 23.13%
Number/percentage of N's	222,860 / 0.01%

GC Percentage	46.47%
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2.3. Coverage

Mean	0.5062
Standard Deviation	16.7666

2.4. Mapping Quality

Mean Mapping Quality	55.14
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2.5. Insert size

Mean	16,142.47
Standard Deviation	1,254,434.39
P25/Median/P75	146 / 201 / 268

2.6. Mismatches and indels

General error rate	0.47%
Mismatches	7,172,114
Insertions	98,861
Mapped reads with at least one insertion	0.61%
Deletions	78,995
Mapped reads with at least one deletion	0.48%
Homopolymer indels	44.19%

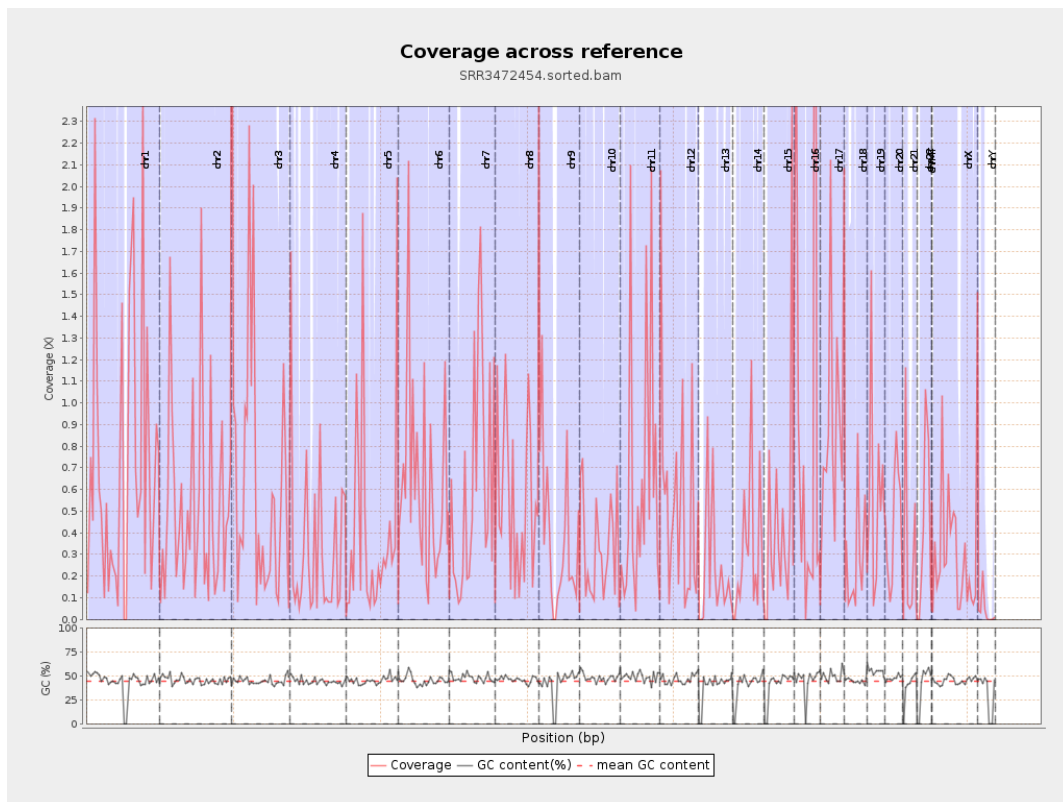
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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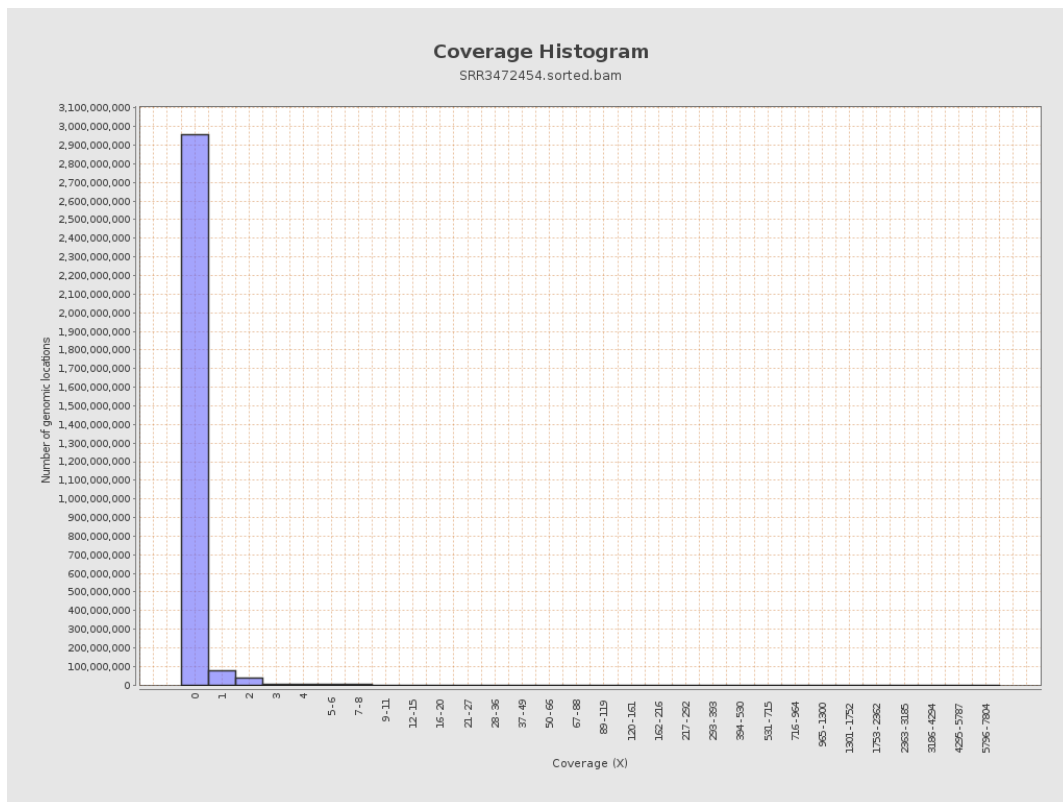
		bases	coverage	deviation
chr1	249250621	184926864	0.7419	22.0987
chr2	243199373	127043114	0.5224	17.7839
chr3	198022430	131066864	0.6619	14.7713
chr4	191154276	59315988	0.3103	13.2807
chr5	180915260	76551890	0.4231	16.7465
chr6	171115067	104936496	0.6133	15.5557
chr7	159138663	97835011	0.6148	22.6469
chr8	146364022	82875147	0.5662	14.7983
chr9	141213431	54088618	0.383	9.4377
chr10	135534747	43534618	0.3212	12.6449
chr11	135006516	86821481	0.6431	23.3232
chr12	133851895	73577121	0.5497	16.9883
chr13	115169878	26545156	0.2305	7.7078
chr14	107349540	32500548	0.3028	8.7111
chr15	102531392	48499346	0.473	20.142
chr16	90354753	90280761	0.9992	28.6064
chr17	81195210	75446423	0.9292	22.7856
chr18	78077248	22424363	0.2872	9.8792
chr19	59128983	35951708	0.608	13.0619
chr20	63025520	28387514	0.4504	13.652
chr21	48129895	15008165	0.3118	21.6595
chr22	51304566	20682217	0.4031	11.5439
chrMT	16571	9072	0.5475	0.9553
chrX	155270560	46118474	0.297	8.1199

chrY	59373566	2628460	0.0443	3.3303
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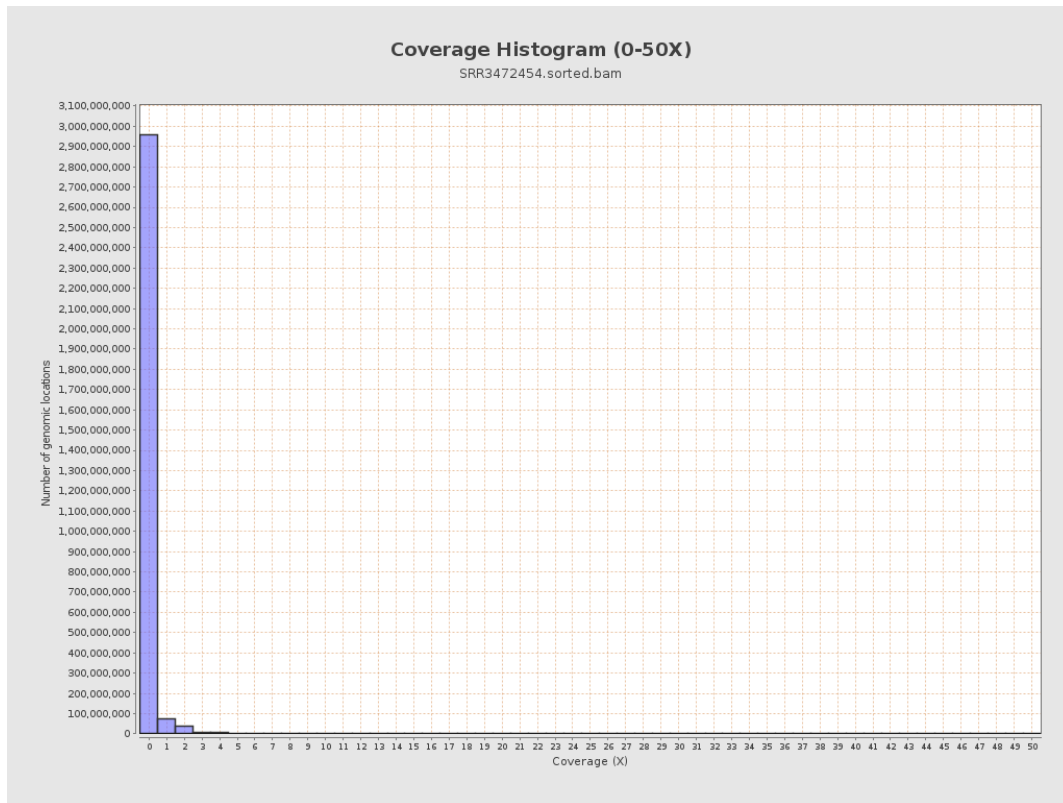
3. Results : Coverage across reference



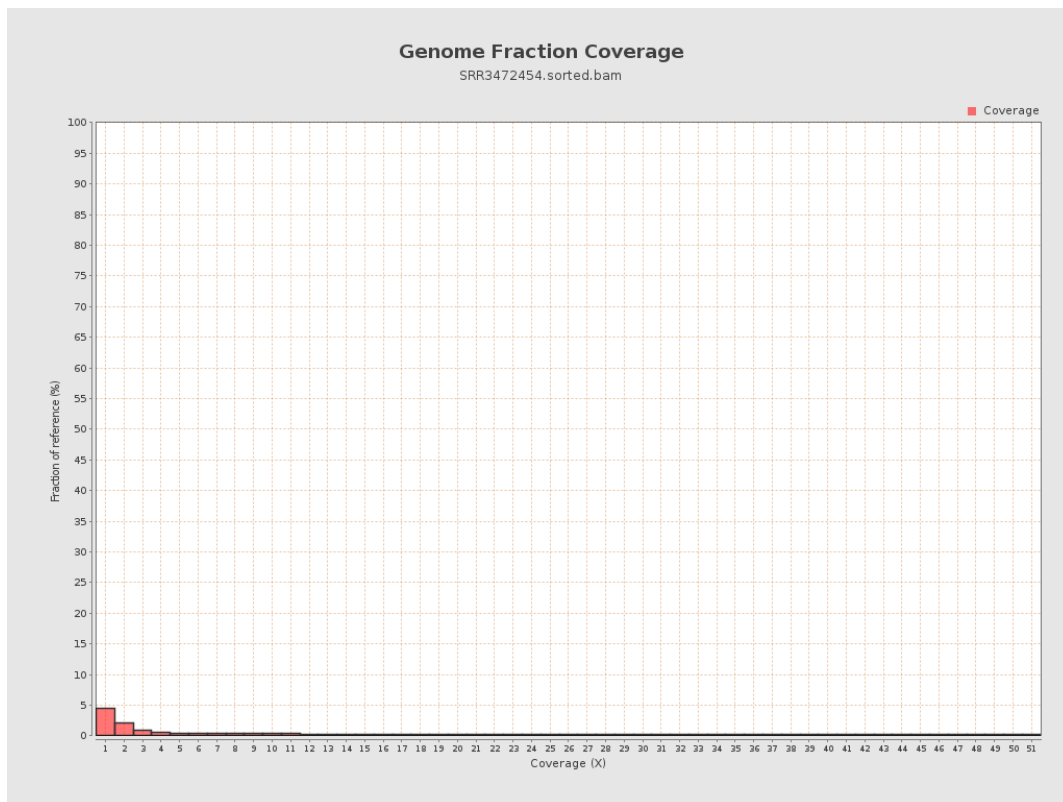
4. Results : Coverage Histogram



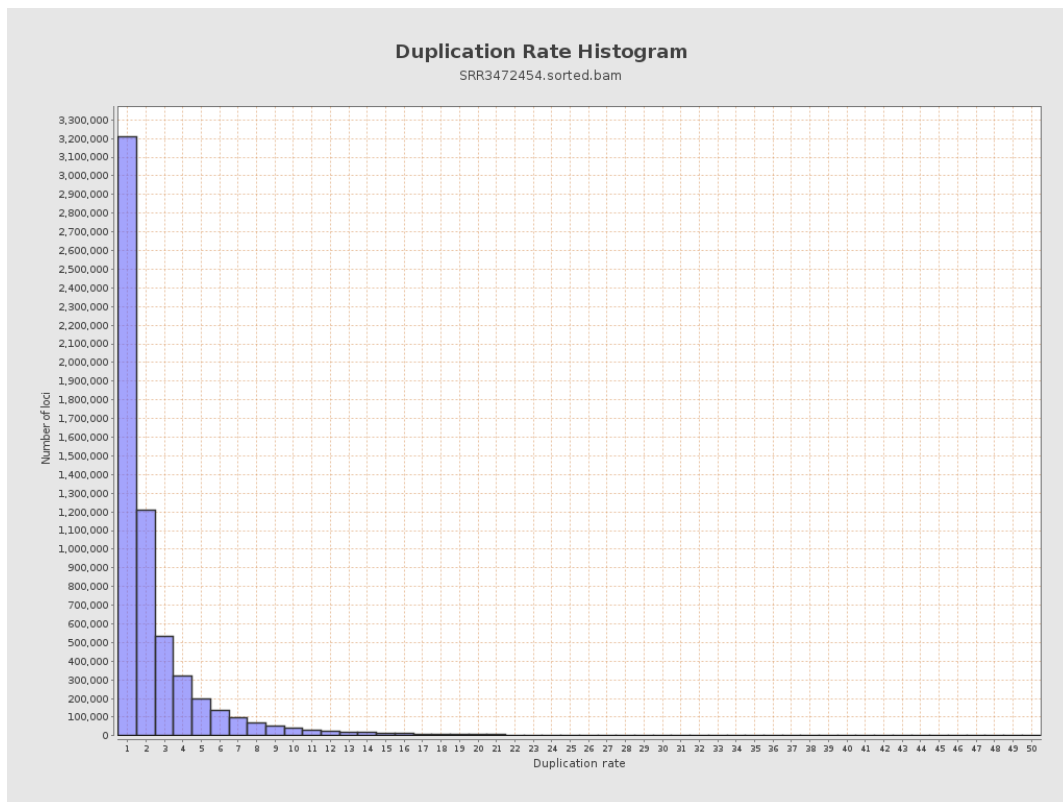
5. Results : Coverage Histogram (0-50X)



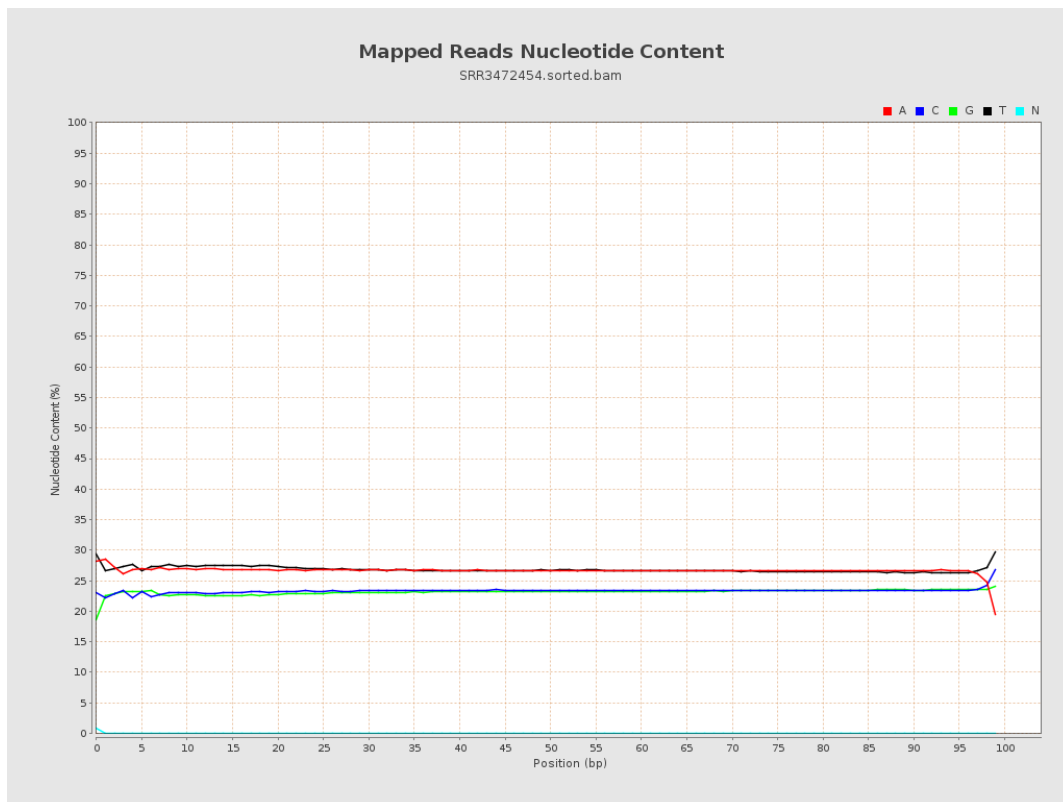
6. Results : Genome Fraction Coverage



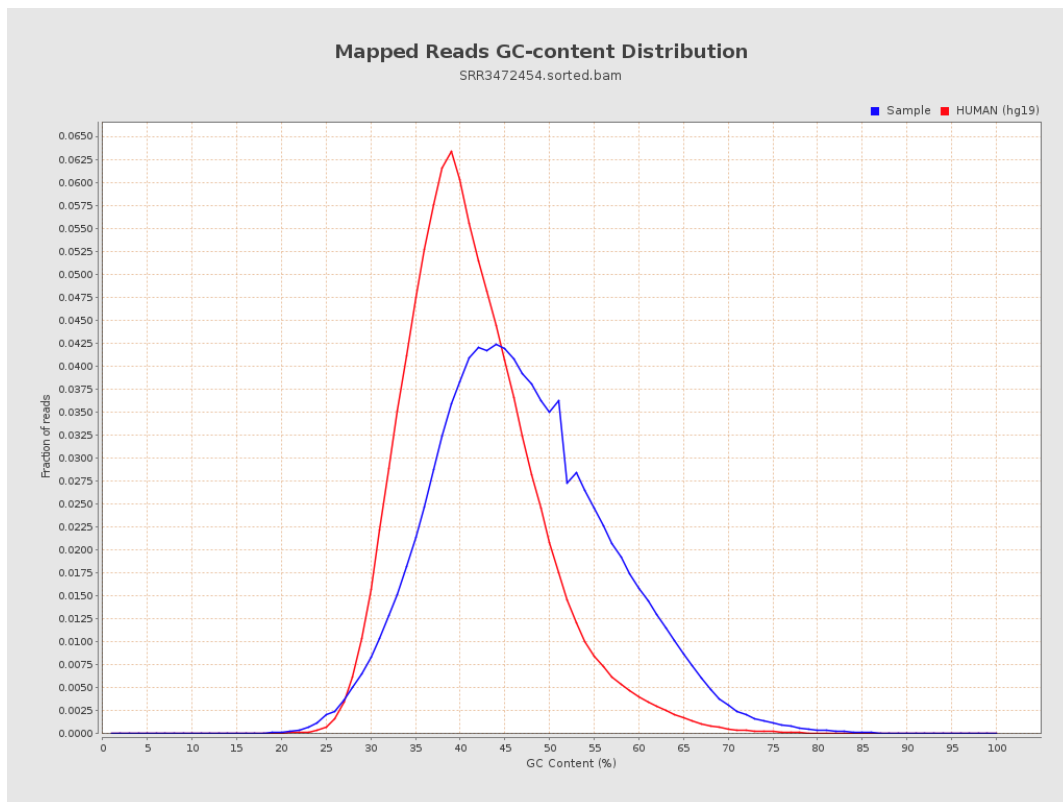
7. Results : Duplication Rate Histogram



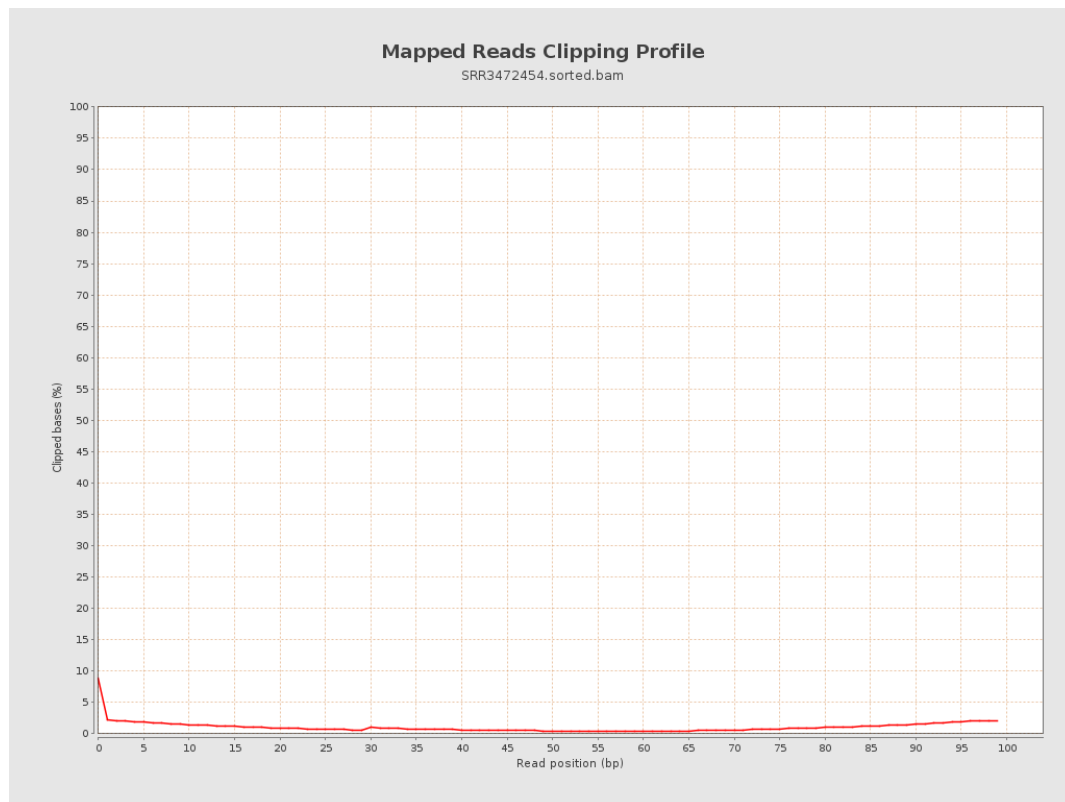
8. Results : Mapped Reads Nucleotide Content



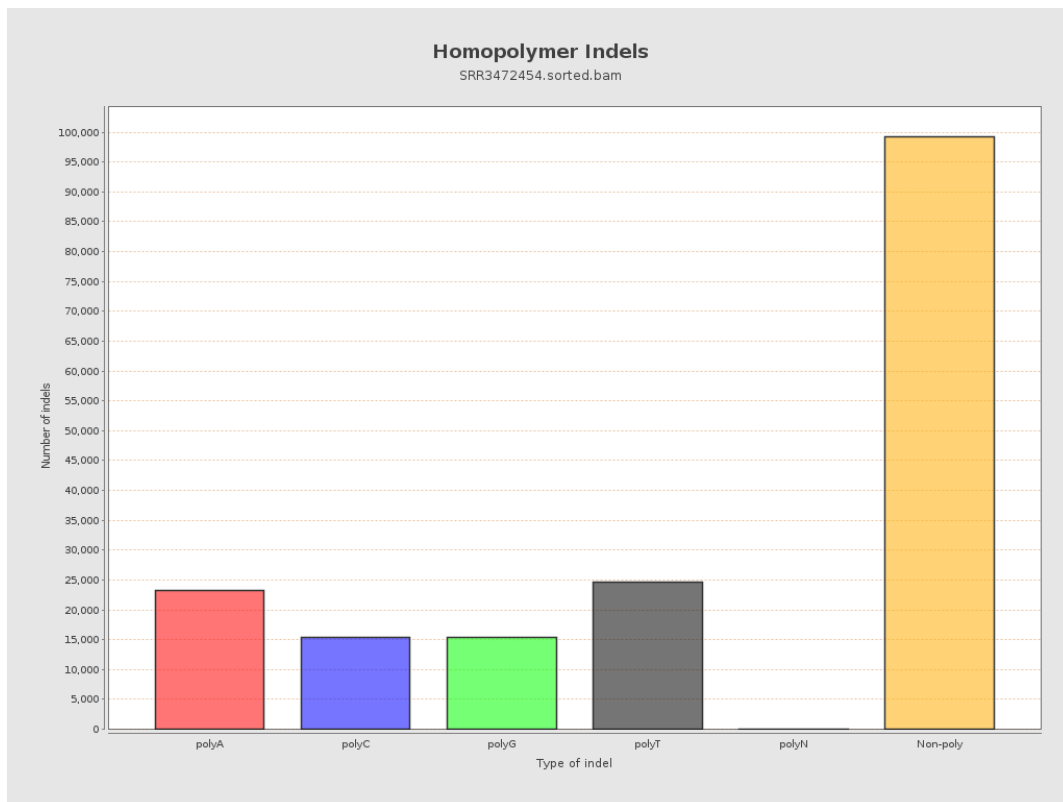
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



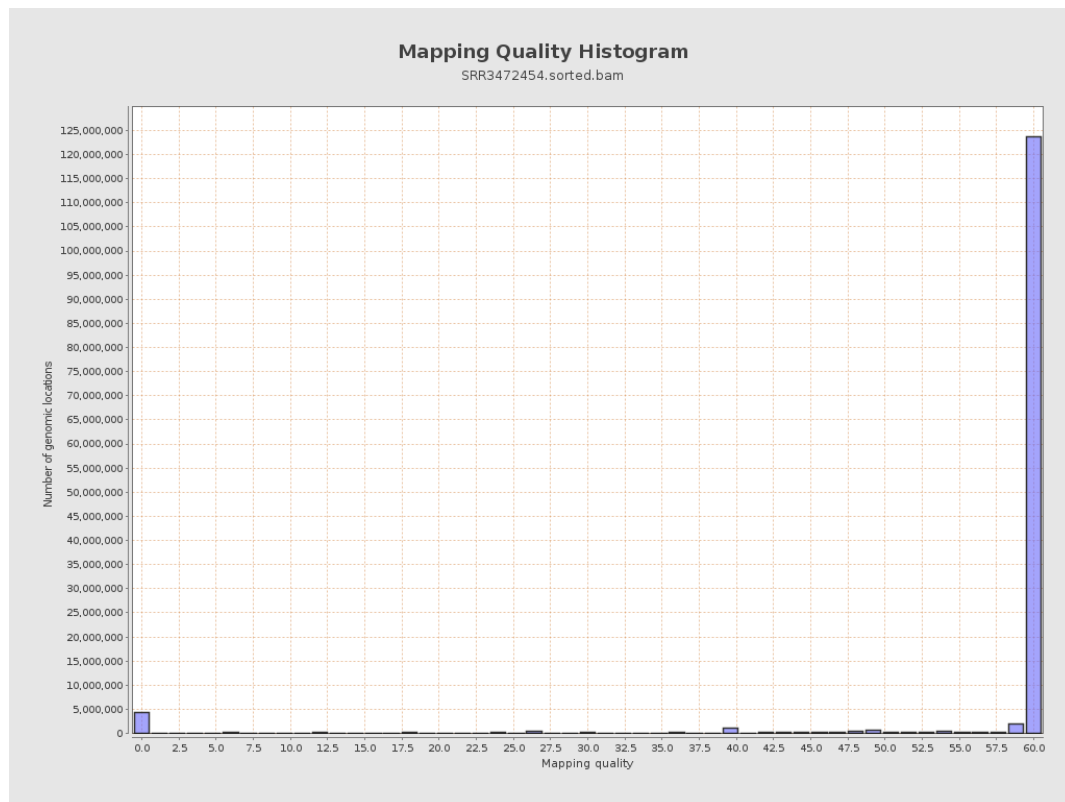
11. Results : Homopolymer Indels



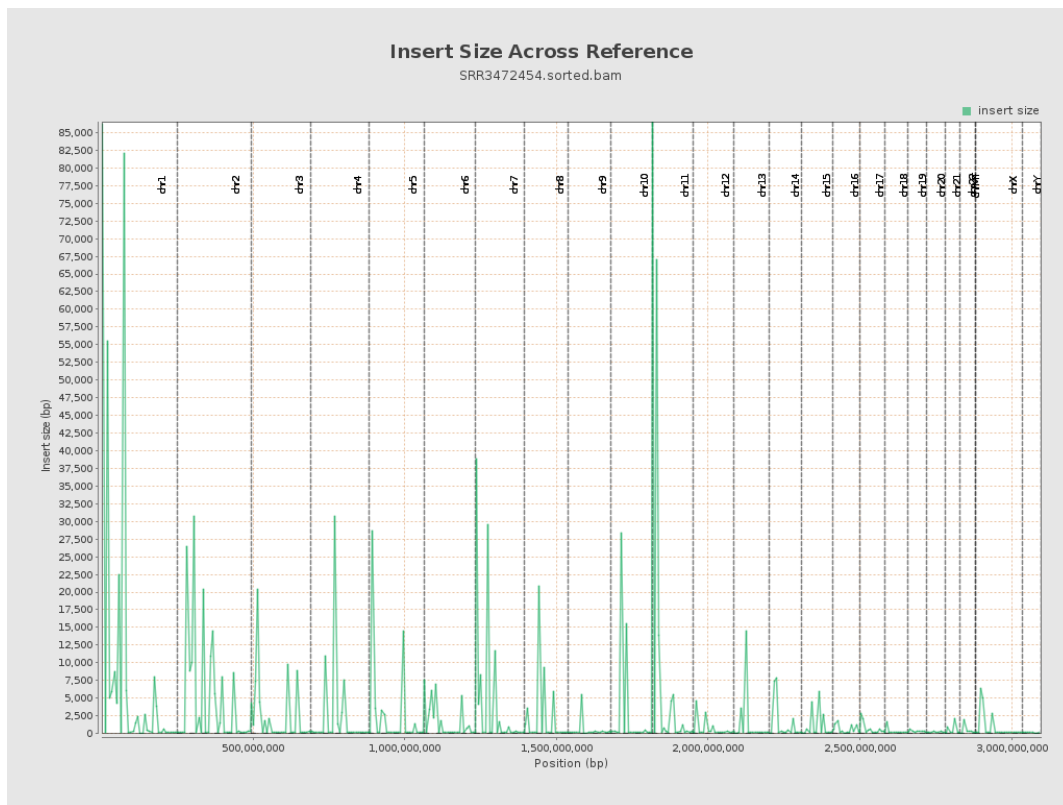
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

