

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 05:05:34

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472377.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_SRR3472377 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472377_1.fastq.gz SRR3472377_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 05:05:32 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472377.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	16,135,524
Mapped reads	16,005,609 / 99.19%
Unmapped reads	129,915 / 0.81%
Mapped paired reads	16,005,609 / 99.19%
Mapped reads, first in pair	8,025,758 / 49.74%
Mapped reads, second in pair	7,979,851 / 49.46%
Mapped reads, both in pair	15,934,504 / 98.75%
Mapped reads, singletons	71,105 / 0.44%
Secondary alignments	0
Supplementary alignments	62,004 / 0.38%
Read min/max/mean length	30 / 100 / 99.23
Duplicated reads (estimated)	9,896,579 / 61.33%
Duplication rate	47.44%
Clipped reads	1,178,080 / 7.3%

2.2. ACGT Content

Number/percentage of A's	424,091,990 / 27.09%
Number/percentage of C's	359,781,722 / 22.98%
Number/percentage of T's	425,188,340 / 27.16%
Number/percentage of G's	356,470,258 / 22.77%
Number/percentage of N's	189,173 / 0.01%

GC Percentage	45.75%
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2.3. Coverage

Mean	0.5058
Standard Deviation	16.7735

2.4. Mapping Quality

Mean Mapping Quality	54.97
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2.5. Insert size

Mean	16,474.85
Standard Deviation	1,274,648.46
P25/Median/P75	148 / 206 / 277

2.6. Mismatches and indels

General error rate	0.51%
Mismatches	7,851,943
Insertions	90,717
Mapped reads with at least one insertion	0.56%
Deletions	76,831
Mapped reads with at least one deletion	0.47%
Homopolymer indels	45.35%

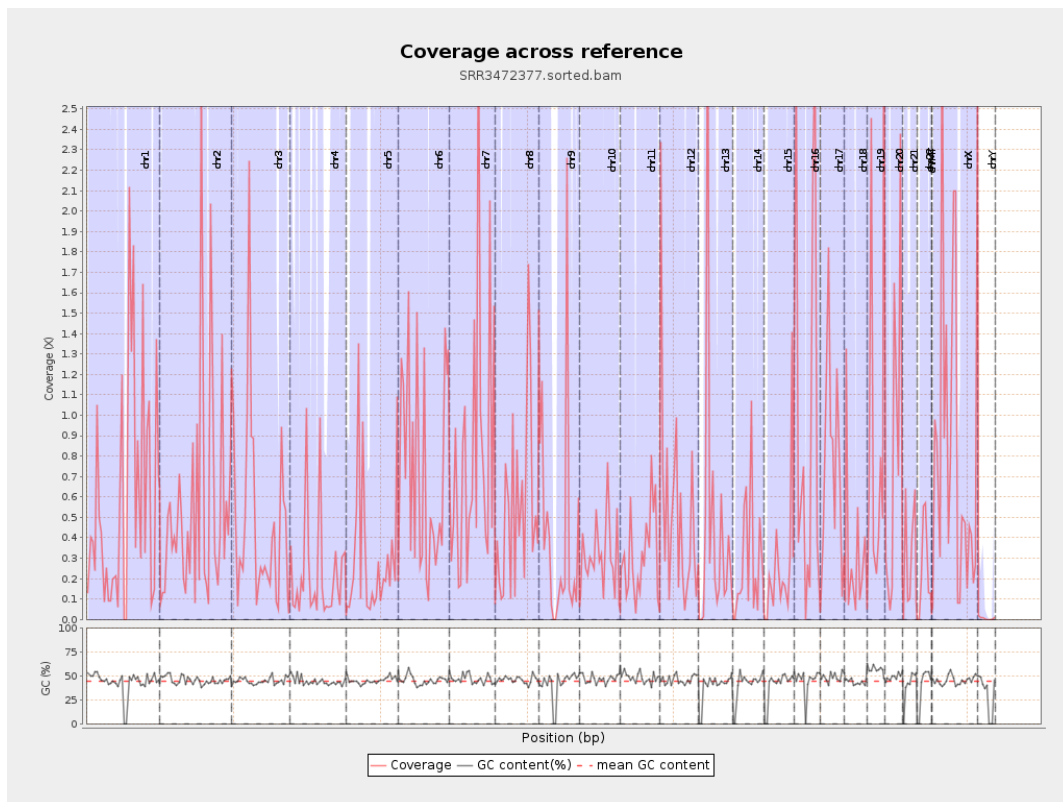
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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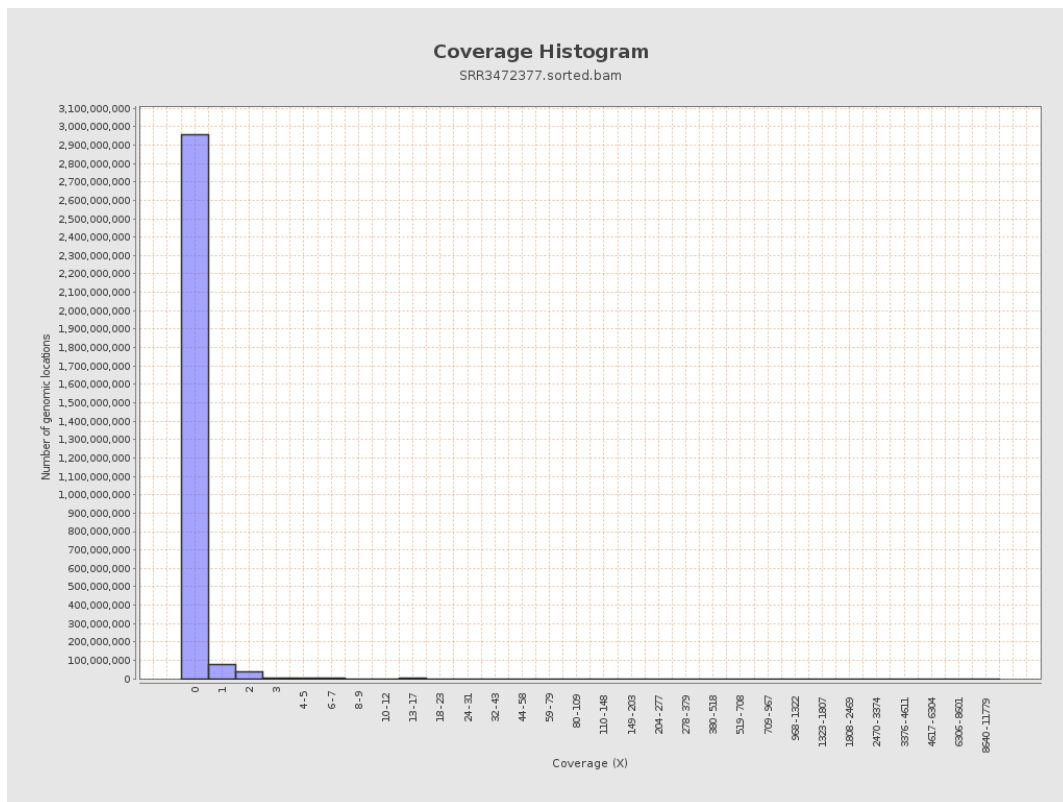
		bases	coverage	deviation
chr1	249250621	148136672	0.5943	17.7727
chr2	243199373	133606850	0.5494	16.3888
chr3	198022430	97598095	0.4929	11.8189
chr4	191154276	41365230	0.2164	8.5455
chr5	180915260	55944345	0.3092	11.2612
chr6	171115067	123235248	0.7202	20.9477
chr7	159138663	131976282	0.8293	23.6588
chr8	146364022	82133957	0.5612	16.1963
chr9	141213431	57699906	0.4086	14.1051
chr10	135534747	42411102	0.3129	9.8283
chr11	135006516	43162984	0.3197	9.8637
chr12	133851895	70780636	0.5288	13.3567
chr13	115169878	52426061	0.4552	21.8531
chr14	107349540	29435983	0.2742	8.9103
chr15	102531392	26838972	0.2618	12.0307
chr16	90354753	87309466	0.9663	35.9495
chr17	81195210	62153281	0.7655	18.7717
chr18	78077248	25396669	0.3253	10.3215
chr19	59128983	48214892	0.8154	21.6548
chr20	63025520	50970256	0.8087	23.2774
chr21	48129895	14949409	0.3106	12.9838
chr22	51304566	12258694	0.2389	6.9878
chrMT	16571	2268	0.1369	0.4833
chrX	155270560	127602431	0.8218	22.2537

chrY	59373566	305157	0.0051	0.2563
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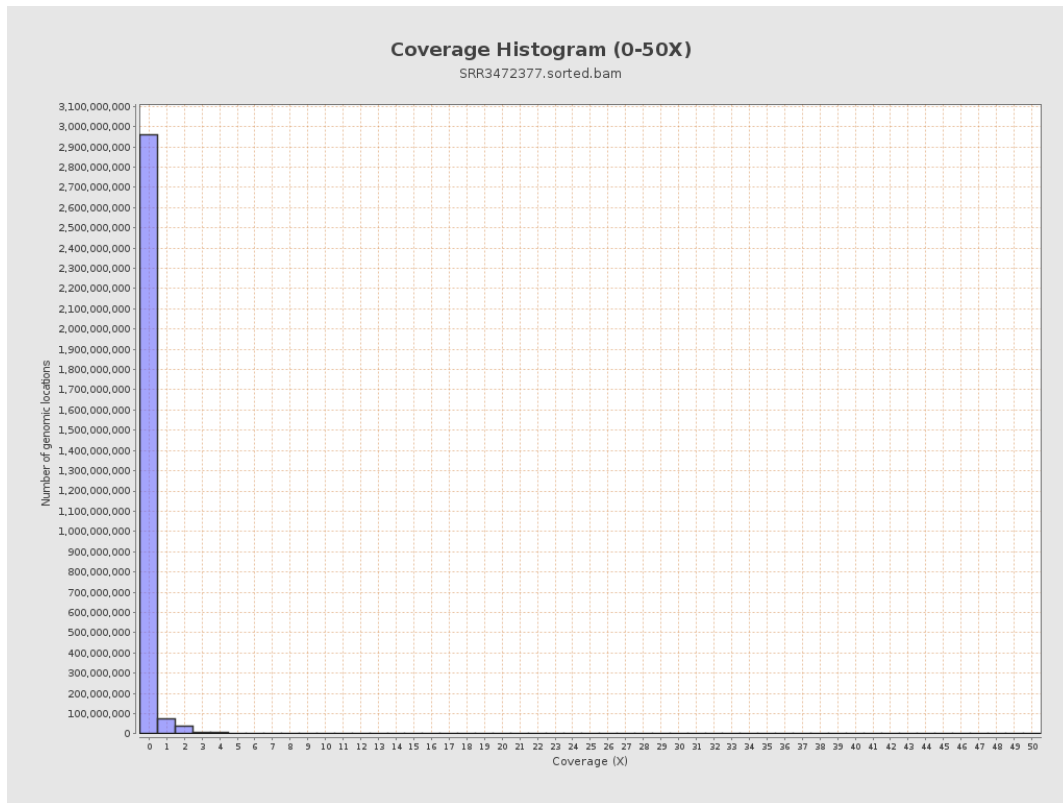
3. Results : Coverage across reference



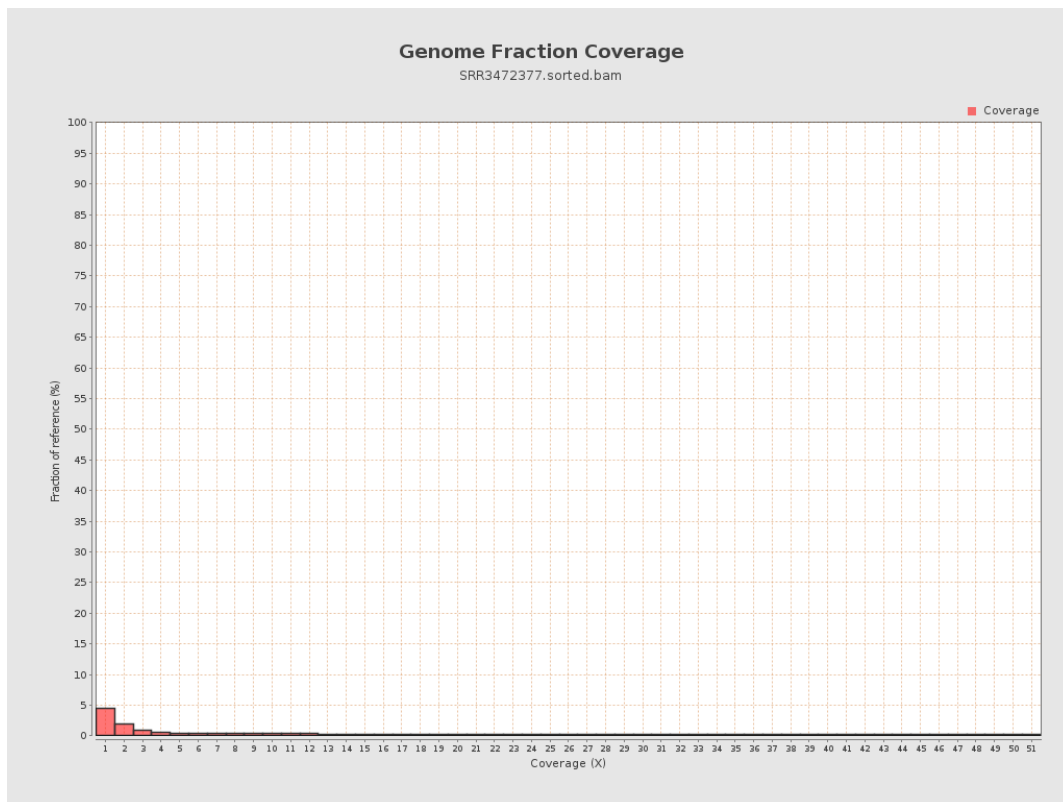
4. Results : Coverage Histogram



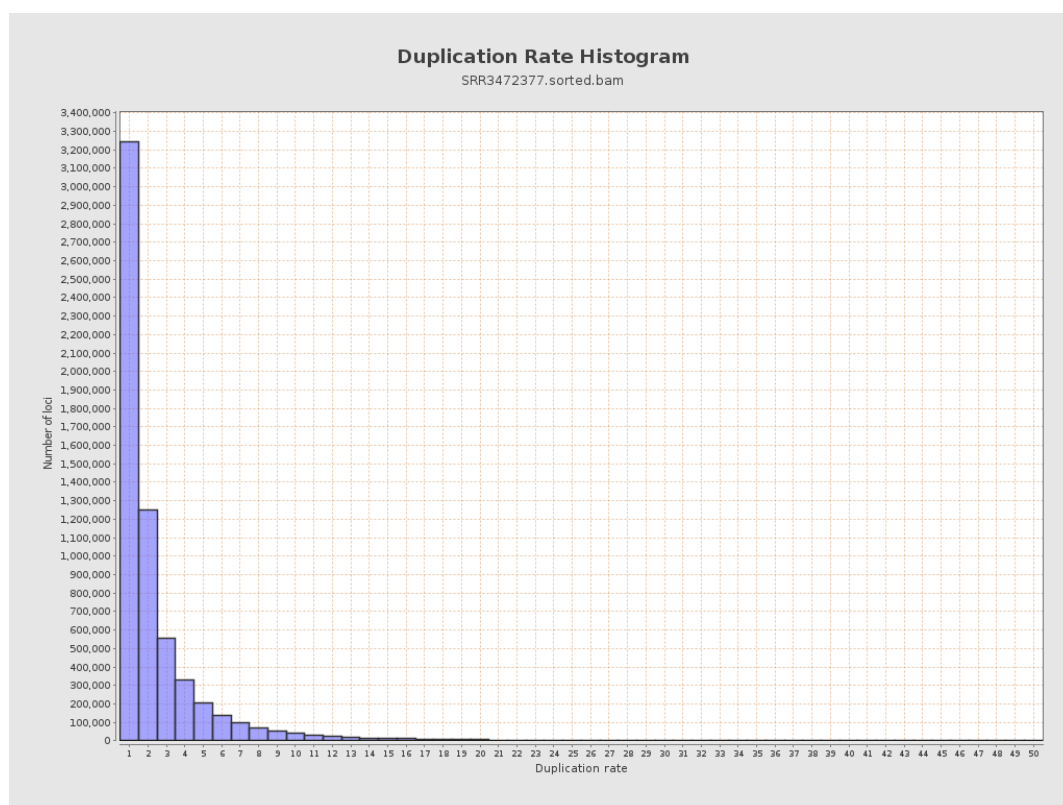
5. Results : Coverage Histogram (0-50X)



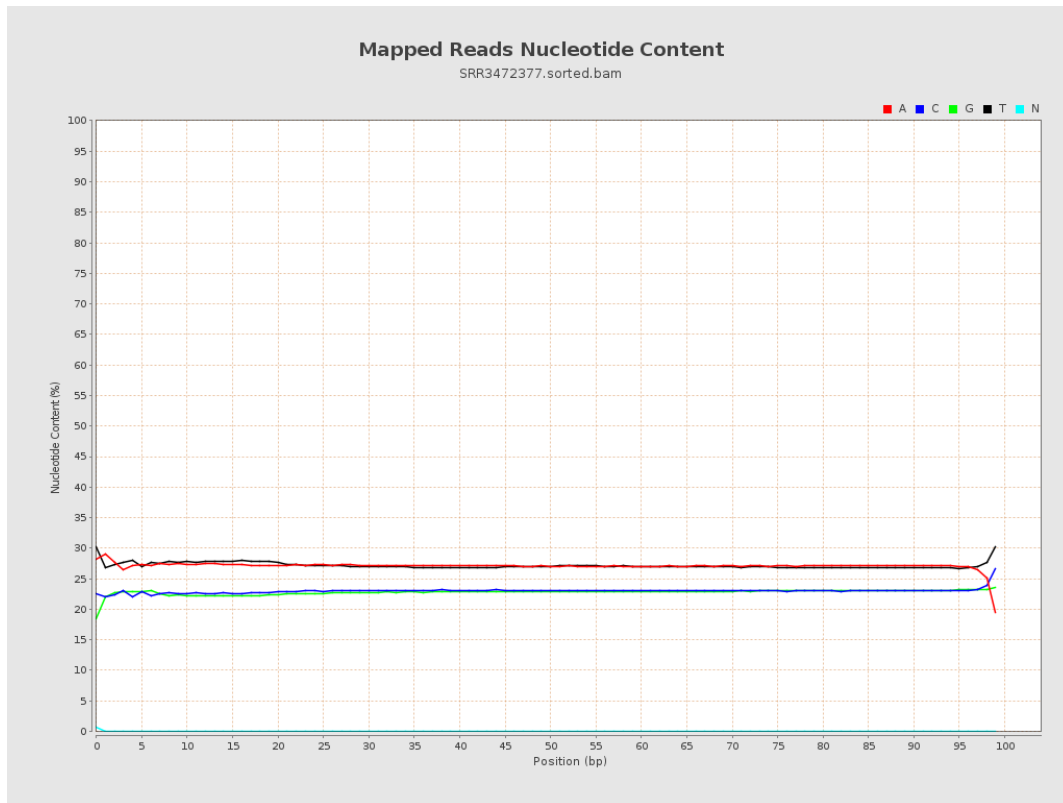
6. Results : Genome Fraction Coverage



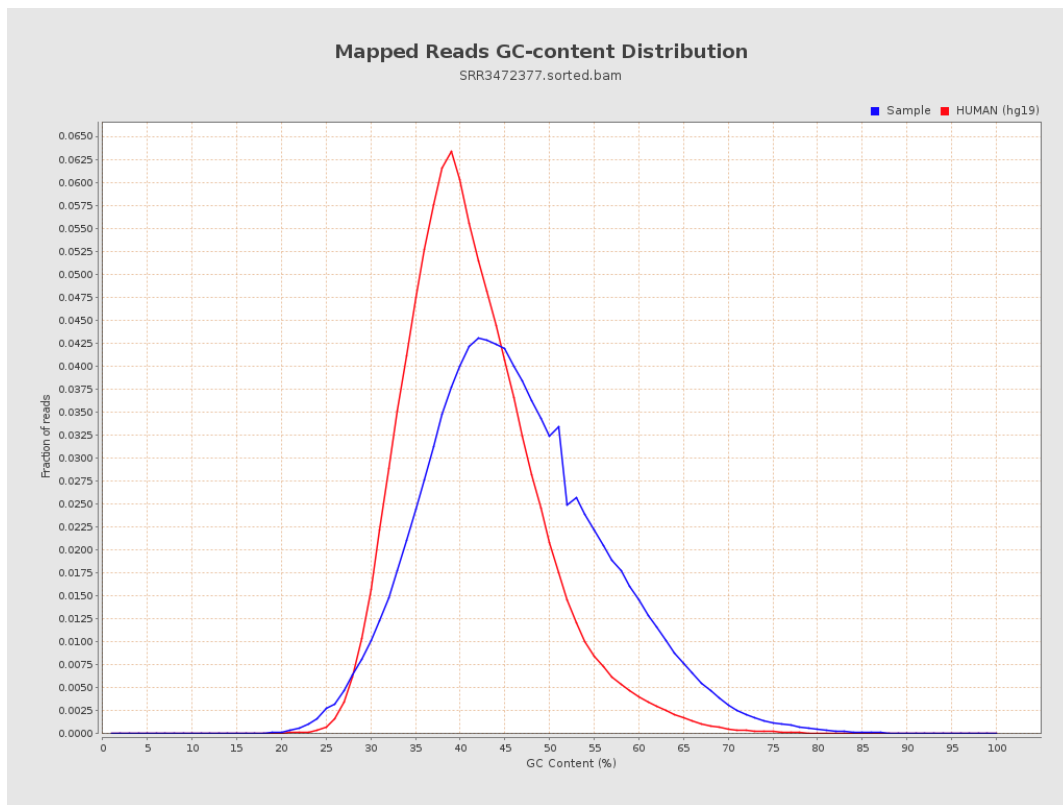
7. Results : Duplication Rate Histogram



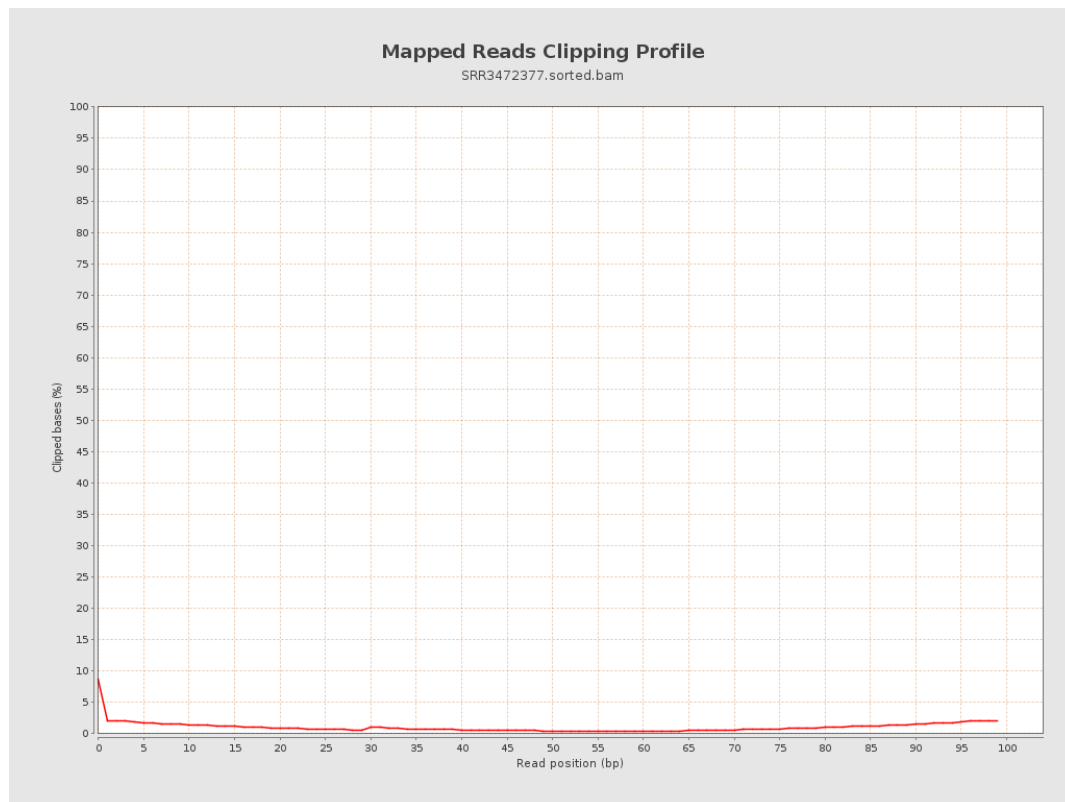
8. Results : Mapped Reads Nucleotide Content



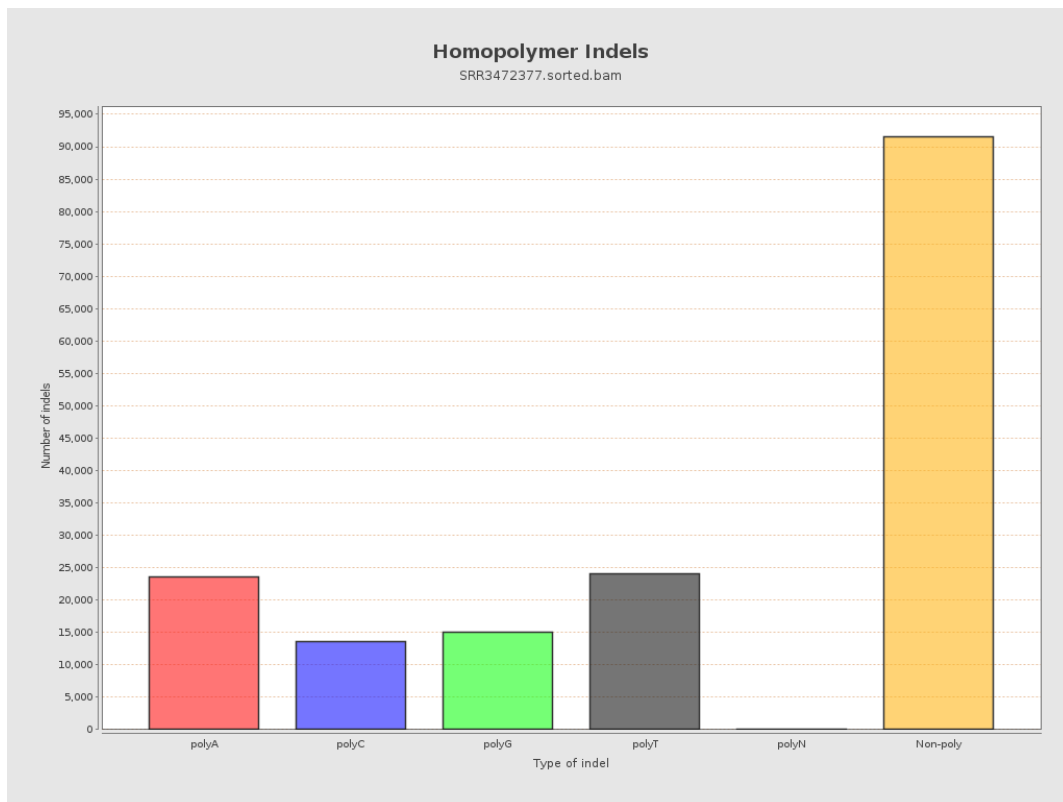
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



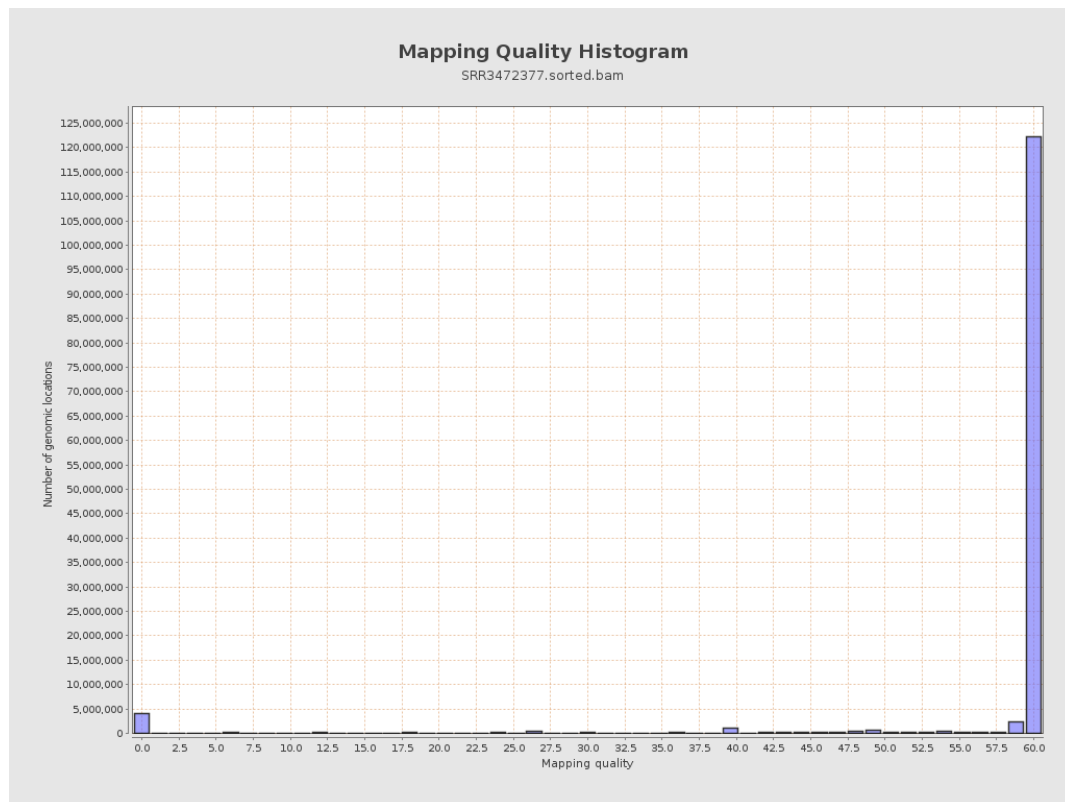
11. Results : Homopolymer Indels



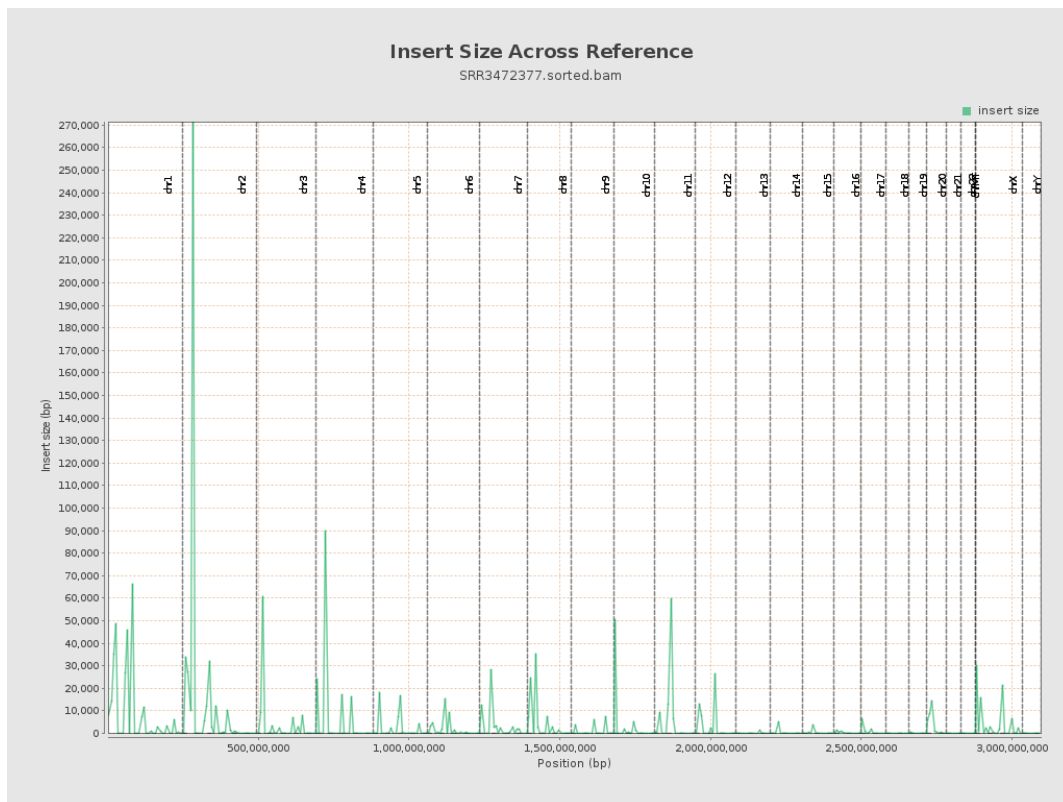
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

