

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/29 05:26:00

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472677.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_SRR3472677 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472677_1.fastq.gz SRR3472677_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sun Sep 29 05:25:59 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472677.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,546,658
Mapped reads	14,416,401 / 99.1%
Unmapped reads	130,257 / 0.9%
Mapped paired reads	14,416,401 / 99.1%
Mapped reads, first in pair	7,228,199 / 49.69%
Mapped reads, second in pair	7,188,202 / 49.41%
Mapped reads, both in pair	14,326,050 / 98.48%
Mapped reads, singletons	90,351 / 0.62%
Secondary alignments	0
Supplementary alignments	86,811 / 0.6%
Read min/max/mean length	30 / 101 / 99.68
Duplicated reads (estimated)	9,751,704 / 67.04%
Duplication rate	48.18%
Clipped reads	1,135,472 / 7.81%

2.2. ACGT Content

Number/percentage of A's	383,086,689 / 27.07%
Number/percentage of C's	326,787,077 / 23.09%
Number/percentage of T's	382,586,346 / 27.04%
Number/percentage of G's	322,285,762 / 22.78%
Number/percentage of N's	254,721 / 0.02%

GC Percentage	45.87%
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2.3. Coverage

Mean	0.4572
Standard Deviation	21.4359

2.4. Mapping Quality

Mean Mapping Quality	54.78
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2.5. Insert size

Mean	20,273.67
Standard Deviation	1,394,842.15
P25/Median/P75	152 / 208 / 277

2.6. Mismatches and indels

General error rate	0.71%
Mismatches	9,827,272
Insertions	92,736
Mapped reads with at least one insertion	0.64%
Deletions	78,471
Mapped reads with at least one deletion	0.54%
Homopolymer indels	46.92%

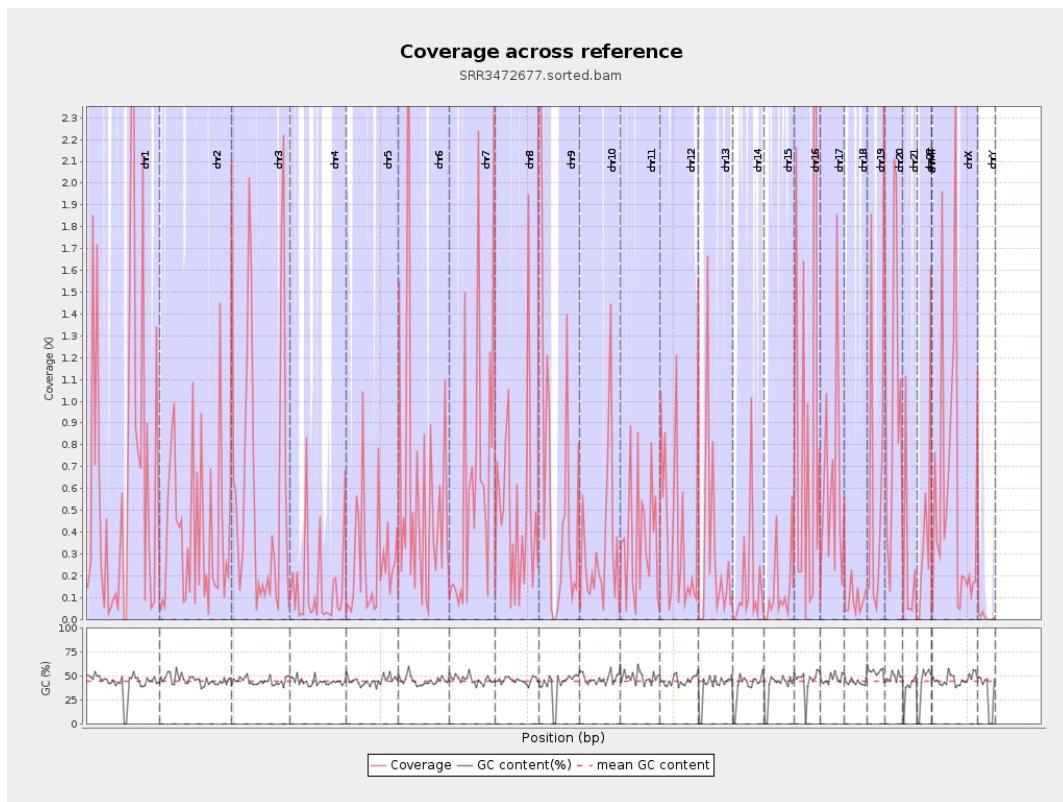
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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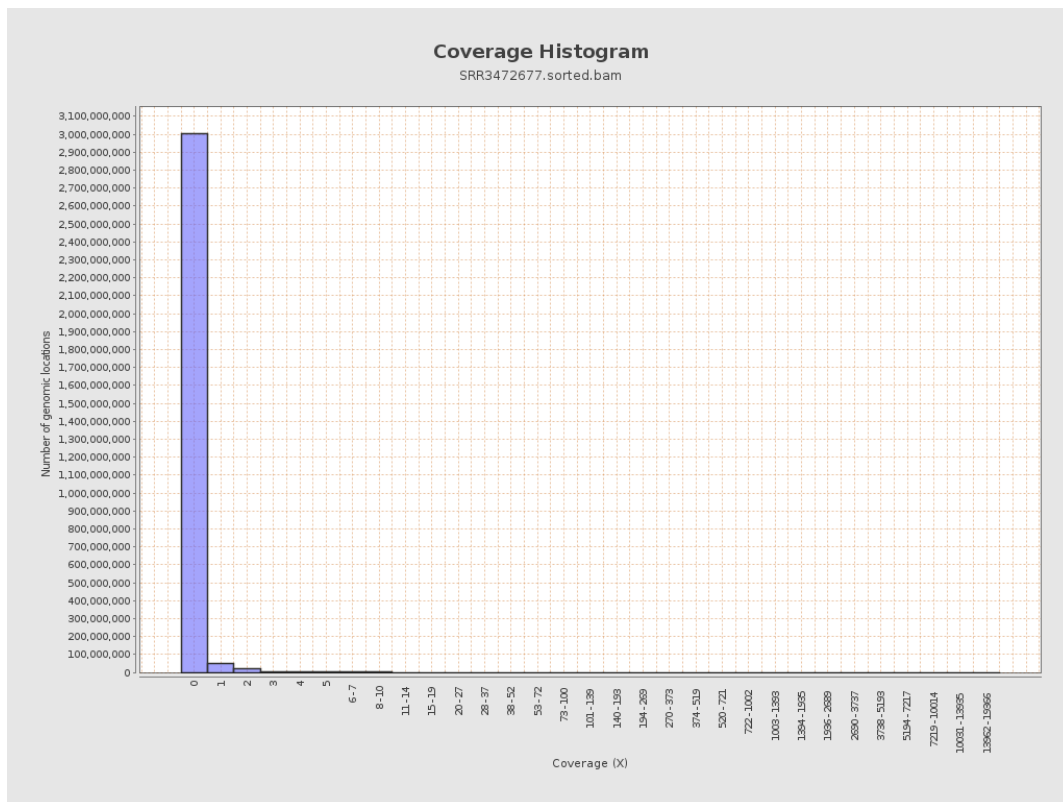
		bases	coverage	deviation
chr1	249250621	166693608	0.6688	26.4065
chr2	243199373	97838250	0.4023	20.512
chr3	198022430	122216422	0.6172	24.0146
chr4	191154276	27148339	0.142	6.9714
chr5	180915260	47349428	0.2617	11.1952
chr6	171115067	96580771	0.5644	24.3996
chr7	159138663	102588453	0.6446	25.6104
chr8	146364022	74376073	0.5082	16.4068
chr9	141213431	96173704	0.6811	23.6742
chr10	135534747	43267090	0.3192	15.8523
chr11	135006516	51909229	0.3845	20.0996
chr12	133851895	54792568	0.4094	14.8579
chr13	115169878	35590977	0.309	12.4993
chr14	107349540	16708999	0.1557	7.159
chr15	102531392	13962168	0.1362	8.0036
chr16	90354753	91924970	1.0174	54.6751
chr17	81195210	49079175	0.6045	20.0661
chr18	78077248	6698333	0.0858	3.5917
chr19	59128983	34718630	0.5872	17.0486
chr20	63025520	63404721	1.006	31.7696
chr21	48129895	11624467	0.2415	21.9888
chr22	51304566	23030744	0.4489	23.6598
chrMT	16571	2182	0.1317	0.4234
chrX	155270560	86841794	0.5593	24.1297

chrY	59373566	679337	0.0114	0.4581
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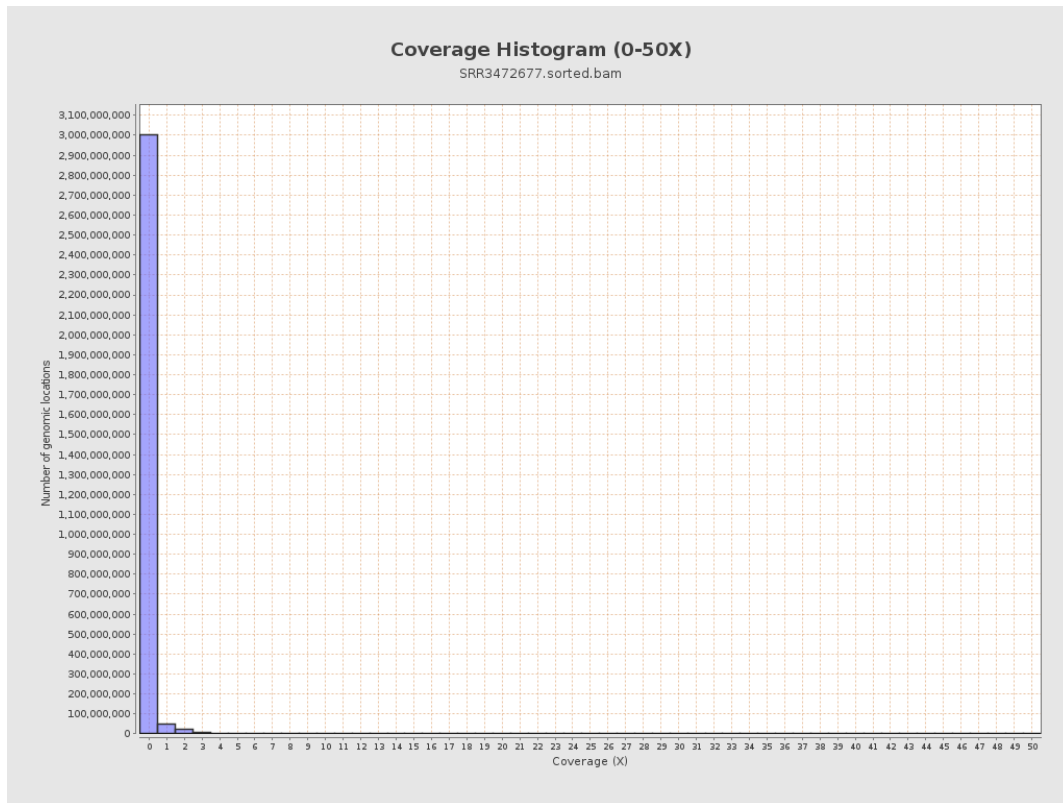
3. Results : Coverage across reference



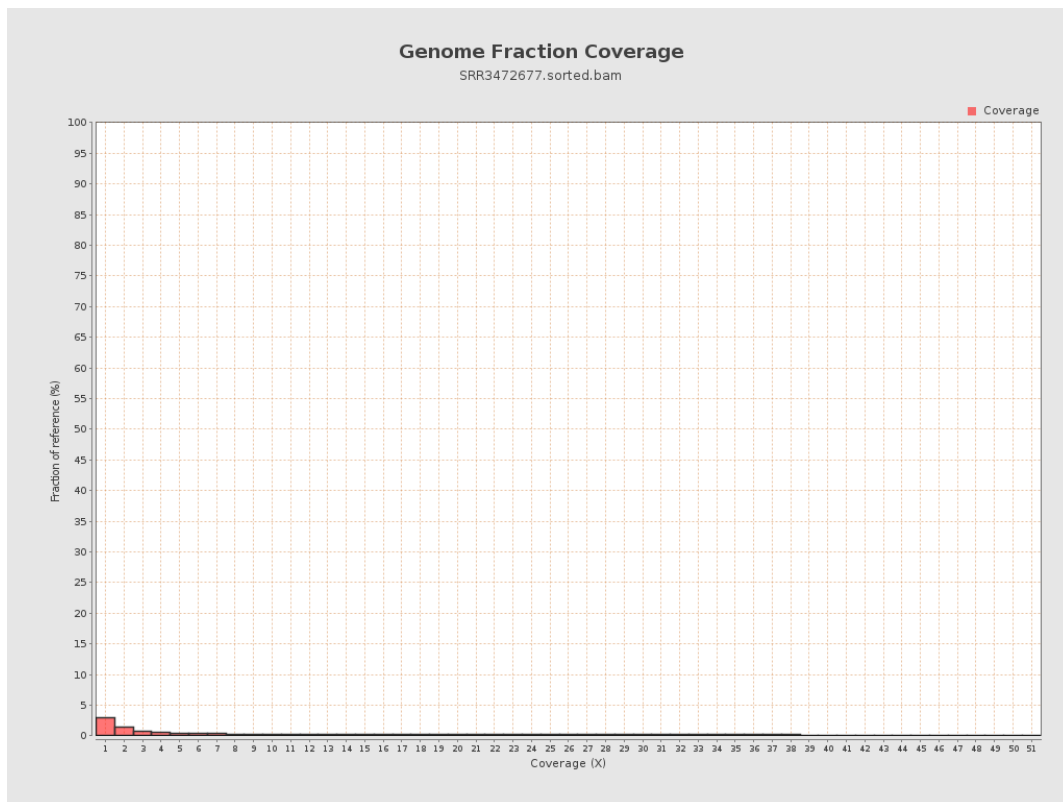
4. Results : Coverage Histogram



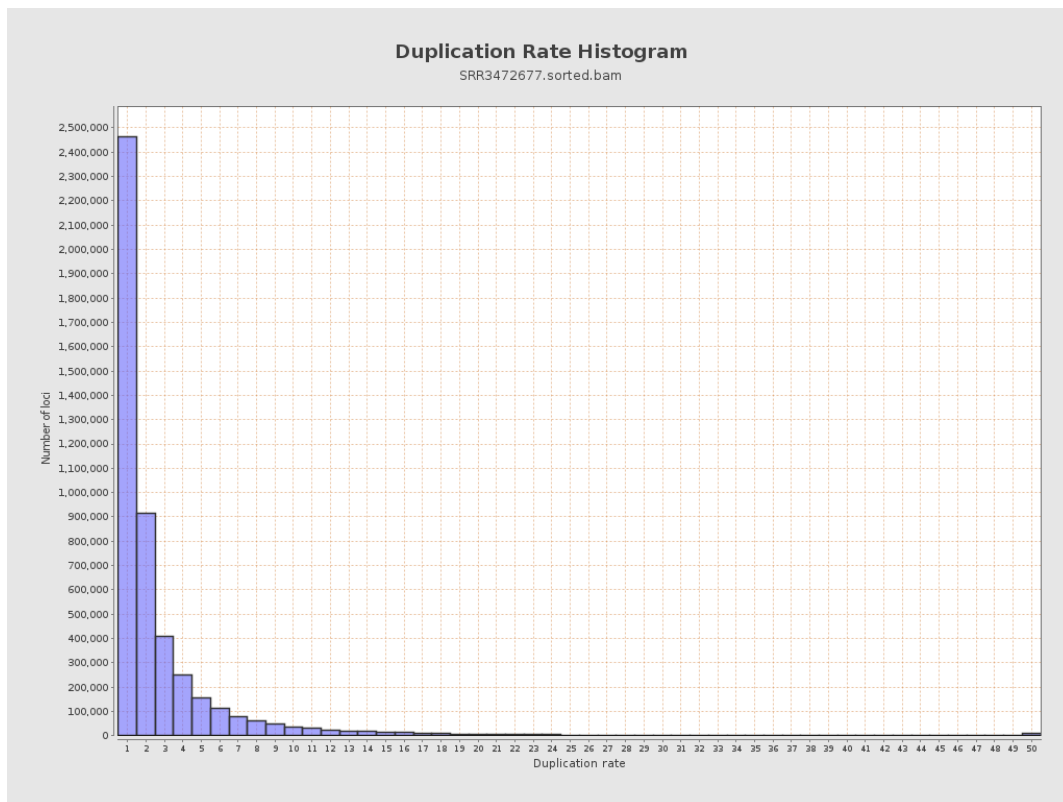
5. Results : Coverage Histogram (0-50X)



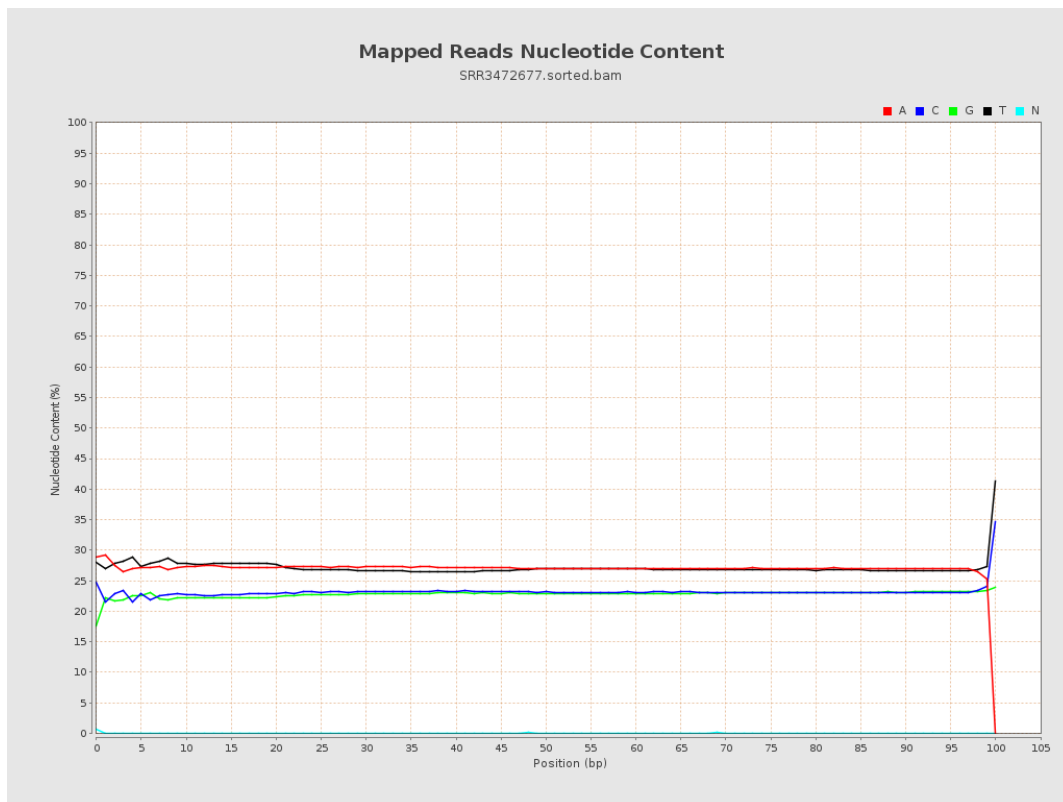
6. Results : Genome Fraction Coverage



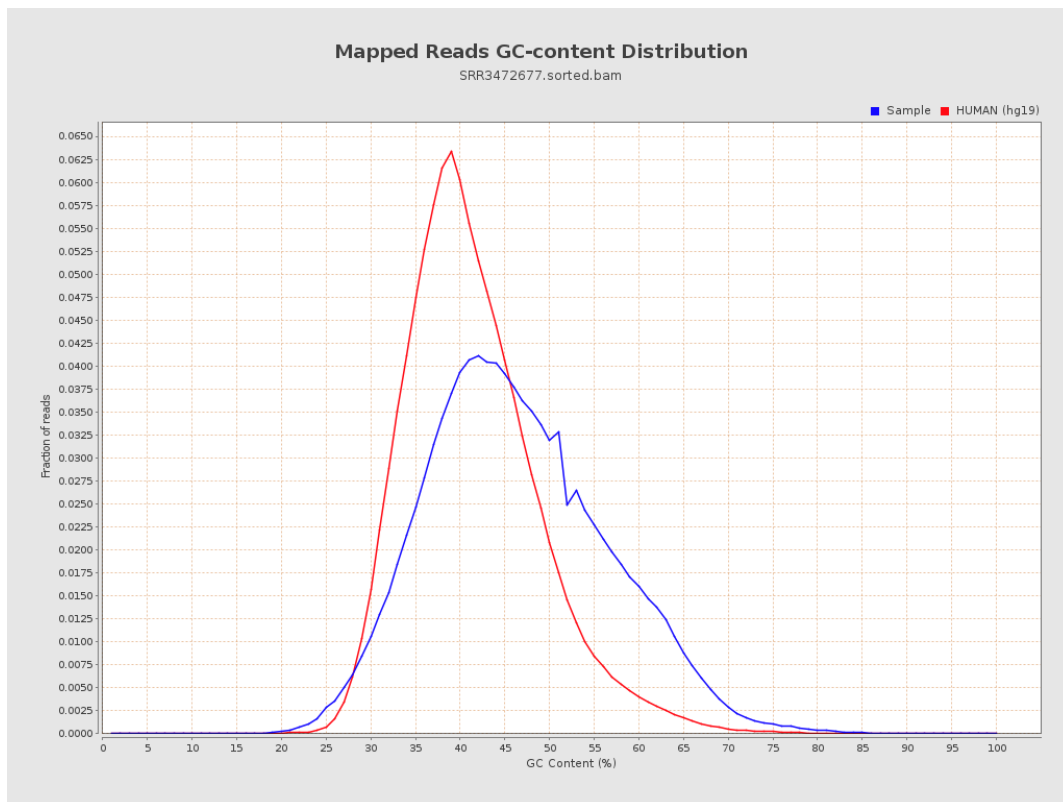
7. Results : Duplication Rate Histogram



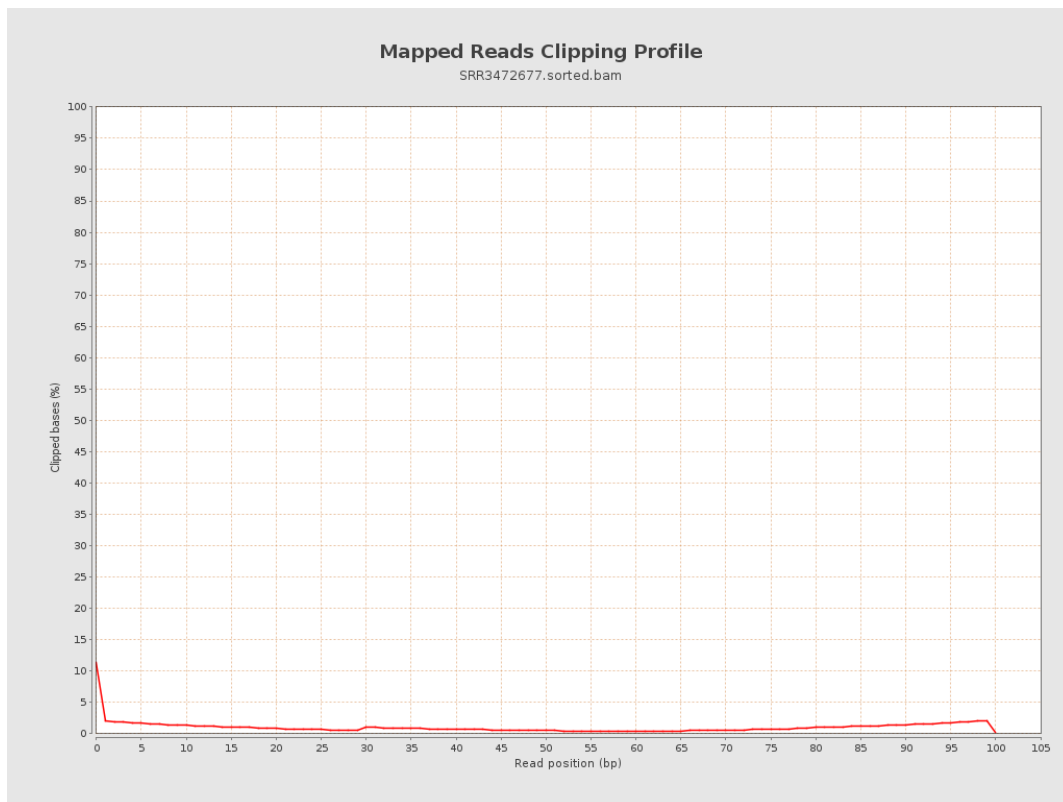
8. Results : Mapped Reads Nucleotide Content



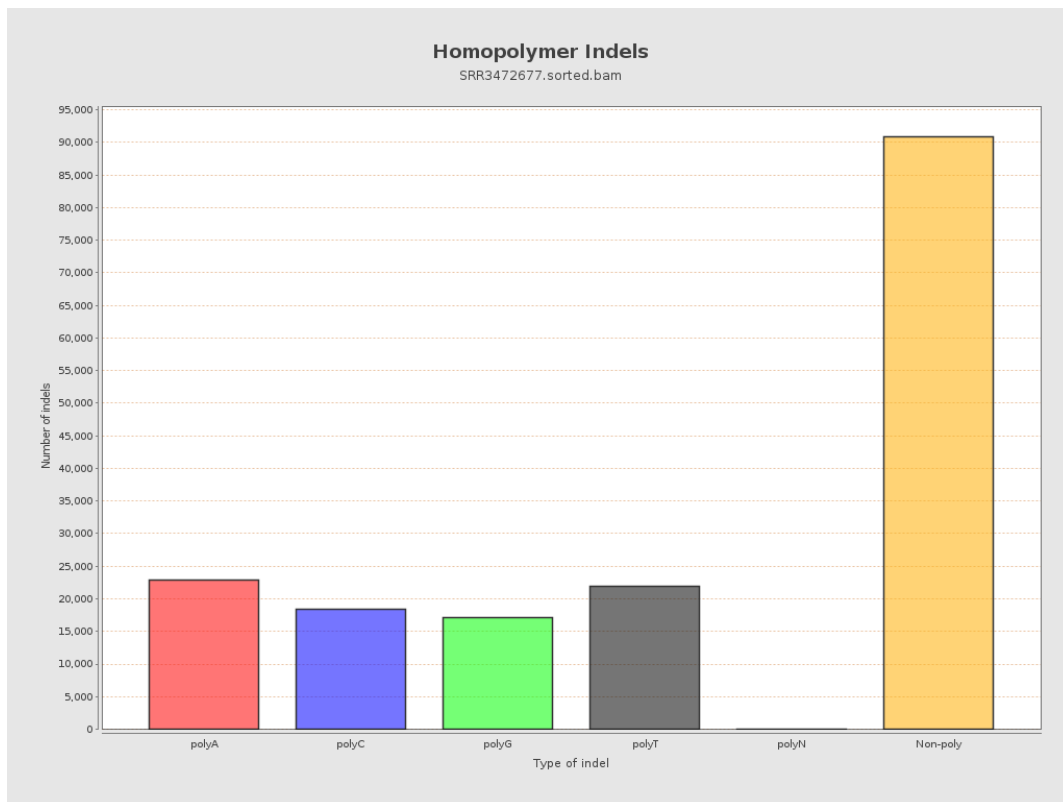
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



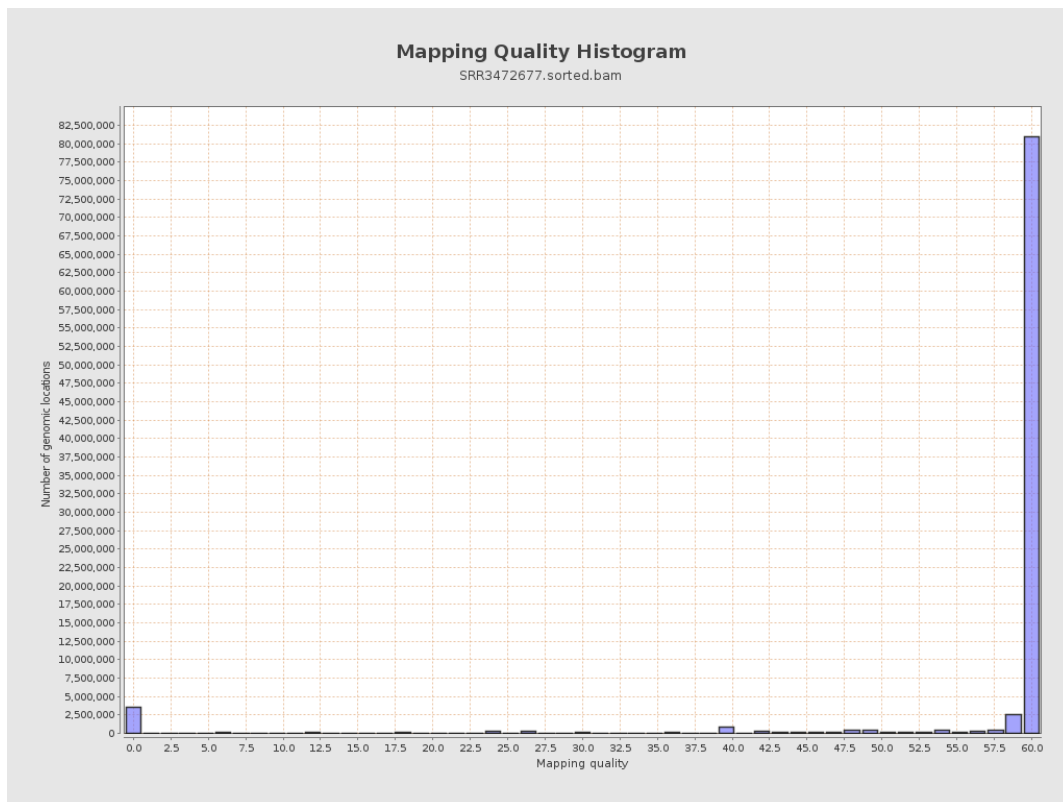
11. Results : Homopolymer Indels



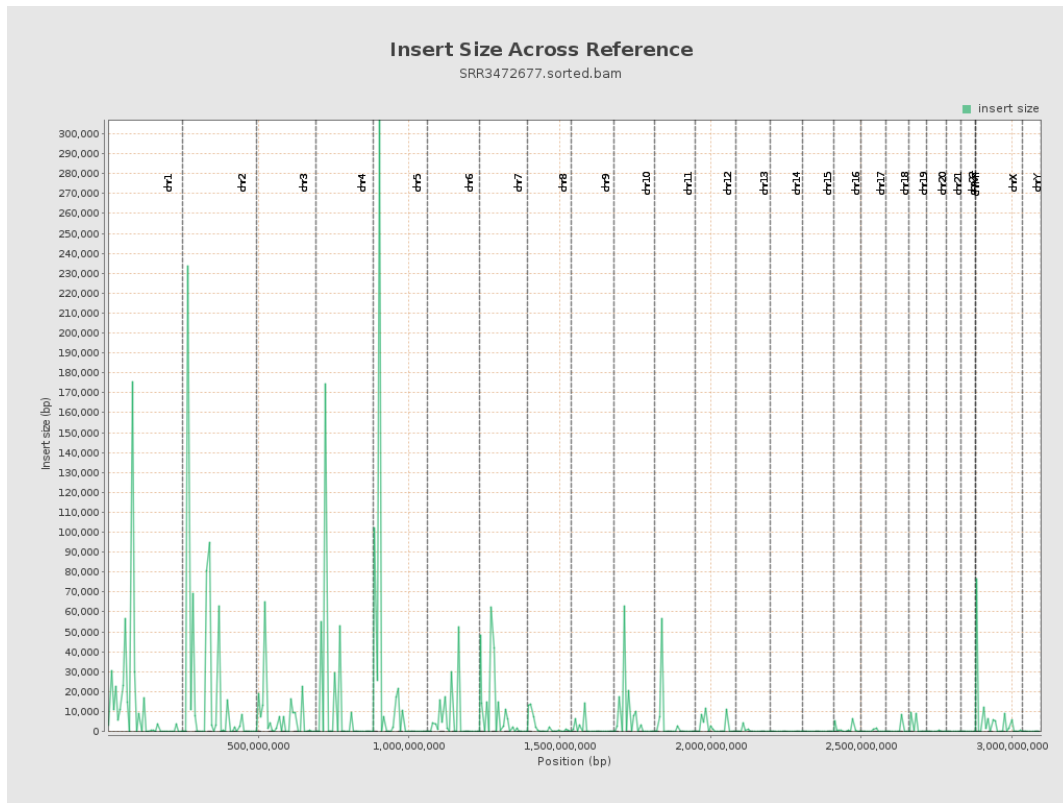
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

