

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/23 13:17:55

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472429.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_SRR3472429 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472429_1.fastq.gz SRR3472429_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Fri Aug 23 13:17:54 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472429.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	14,522,676
Mapped reads	14,394,720 / 99.12%
Unmapped reads	127,956 / 0.88%
Mapped paired reads	14,394,720 / 99.12%
Mapped reads, first in pair	7,218,683 / 49.71%
Mapped reads, second in pair	7,176,037 / 49.41%
Mapped reads, both in pair	14,325,920 / 98.65%
Mapped reads, singletons	68,800 / 0.47%
Secondary alignments	0
Supplementary alignments	55,722 / 0.38%
Read min/max/mean length	30 / 100 / 99.21
Duplicated reads (estimated)	9,077,391 / 62.5%
Duplication rate	46.83%
Clipped reads	939,288 / 6.47%

2.2. ACGT Content

Number/percentage of A's	384,061,900 / 27.21%
Number/percentage of C's	322,593,545 / 22.86%
Number/percentage of T's	385,683,533 / 27.33%
Number/percentage of G's	318,898,104 / 22.59%
Number/percentage of N's	168,185 / 0.01%

GC Percentage	45.45%
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2.3. Coverage

Mean	0.456
Standard Deviation	16.6615

2.4. Mapping Quality

Mean Mapping Quality	54.6
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2.5. Insert size

Mean	16,323.92
Standard Deviation	1,262,797.54
P25/Median/P75	151 / 208 / 279

2.6. Mismatches and indels

General error rate	0.53%
Mismatches	7,360,753
Insertions	93,475
Mapped reads with at least one insertion	0.64%
Deletions	75,258
Mapped reads with at least one deletion	0.51%
Homopolymer indels	46.43%

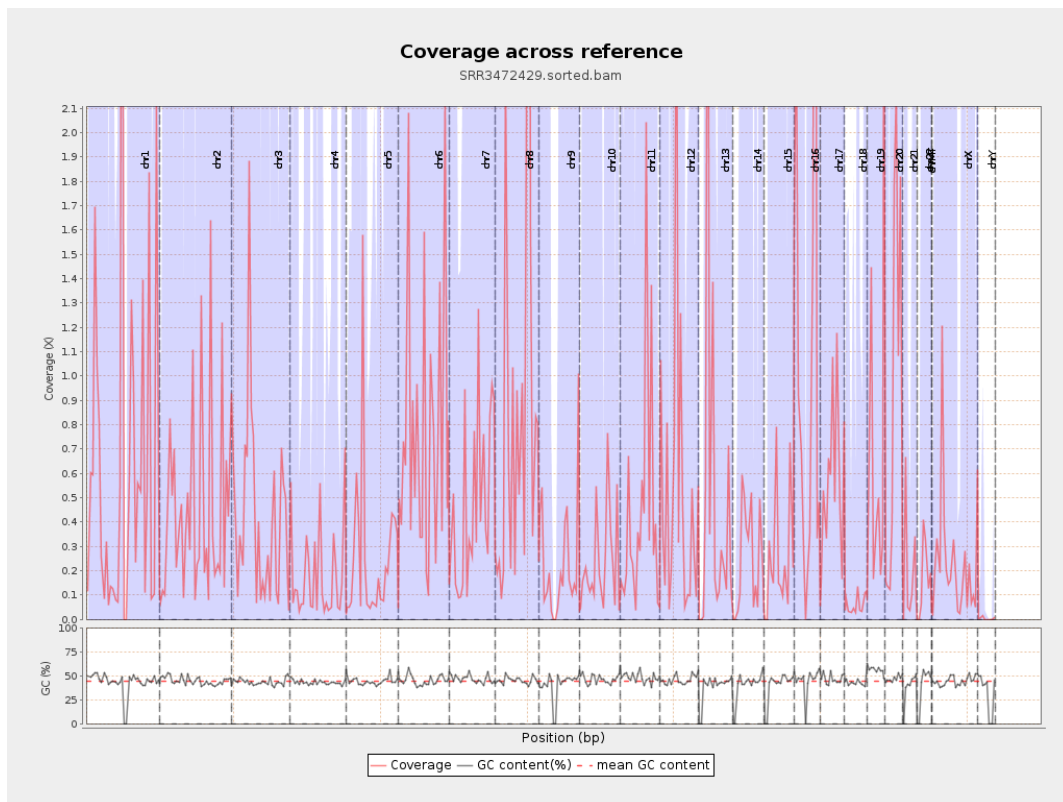
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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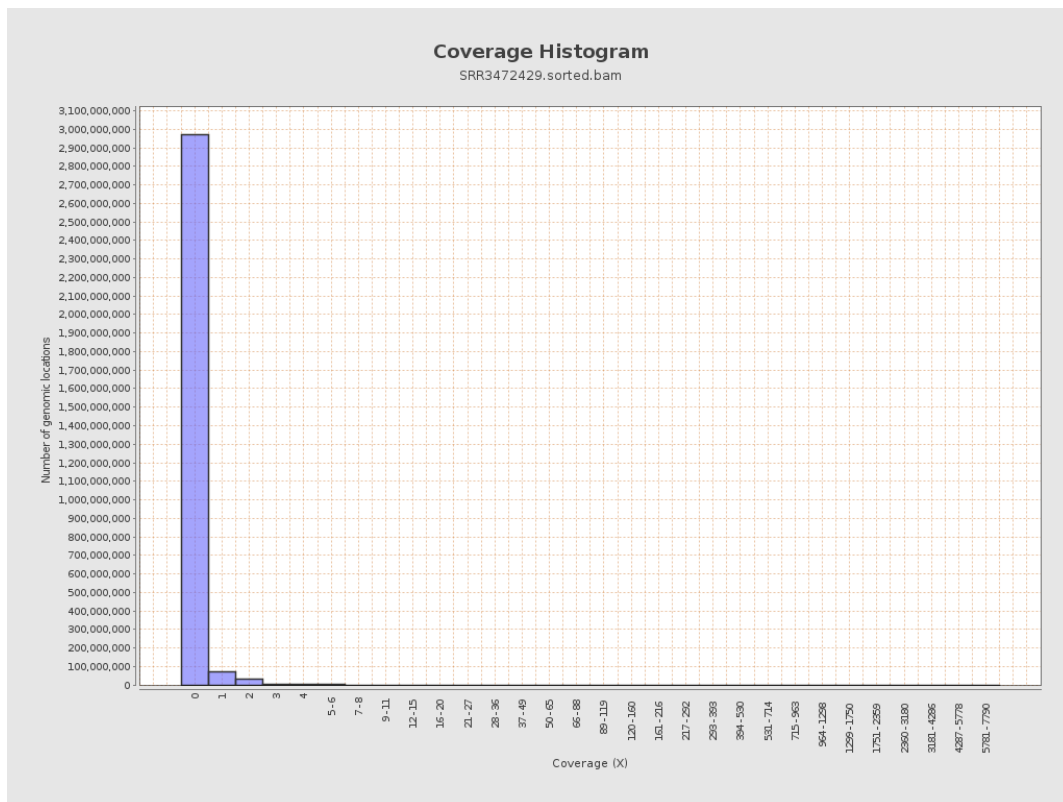
		bases	coverage	deviation
chr1	249250621	167776314	0.6731	22.3563
chr2	243199373	109856550	0.4517	14.5478
chr3	198022430	86381283	0.4362	11.0272
chr4	191154276	33155797	0.1735	5.9649
chr5	180915260	45460782	0.2513	8.0033
chr6	171115067	131151218	0.7665	19.5762
chr7	159138663	76333589	0.4797	15.1856
chr8	146364022	144681062	0.9885	30.5078
chr9	141213431	32526997	0.2303	7.8439
chr10	135534747	31568080	0.2329	9.2276
chr11	135006516	60420386	0.4475	18.6127
chr12	133851895	75033832	0.5606	14.7024
chr13	115169878	59968307	0.5207	24.9582
chr14	107349540	26483154	0.2467	8.239
chr15	102531392	25854482	0.2522	8.3872
chr16	90354753	105590303	1.1686	39.2264
chr17	81195210	46973593	0.5785	12.6407
chr18	78077248	4842685	0.062	2.0189
chr19	59128983	34392151	0.5816	15.7921
chr20	63025520	59828808	0.9493	25.2978
chr21	48129895	9648909	0.2005	9.9351
chr22	51304566	8688902	0.1694	4.8389
chrMT	16571	1634	0.0986	0.3424
chrX	155270560	34697298	0.2235	6.5231

chrY	59373566	260419	0.0044	0.3938
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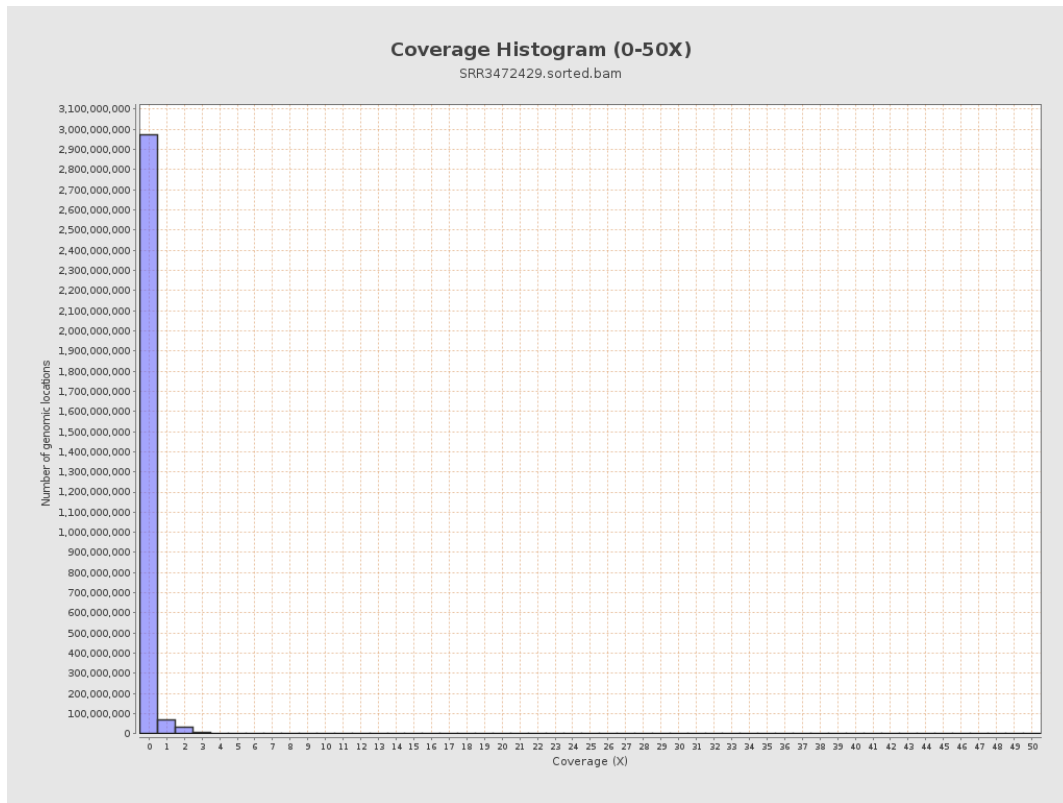
3. Results : Coverage across reference



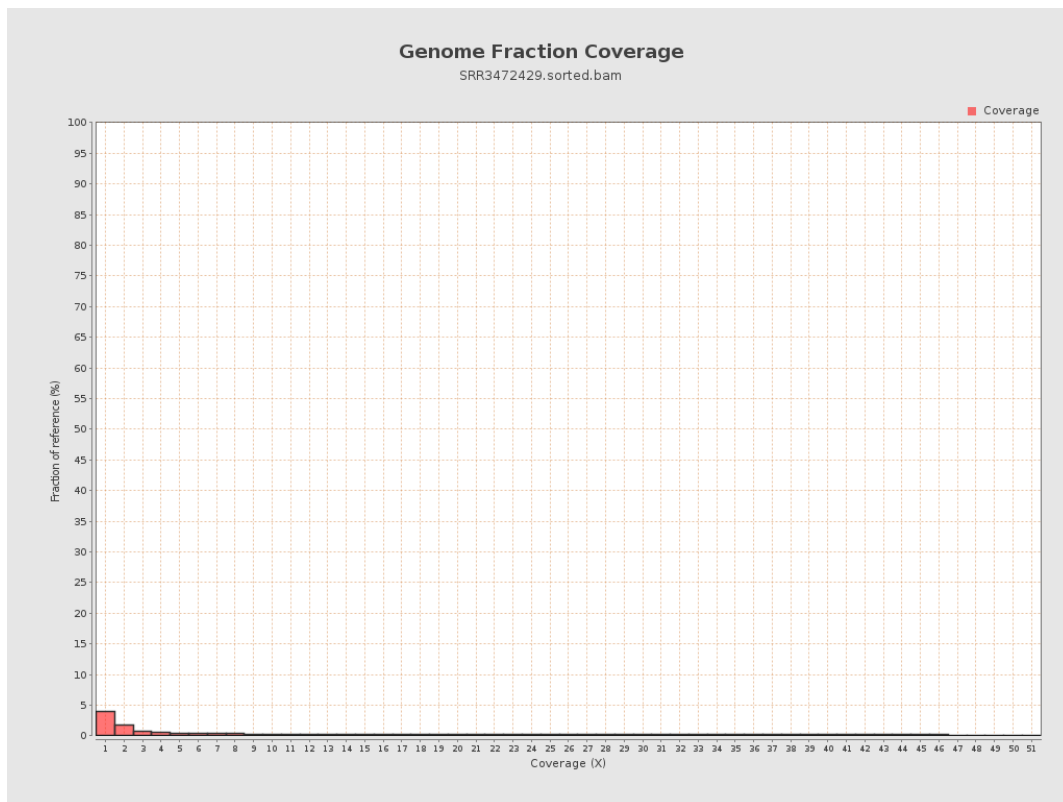
4. Results : Coverage Histogram



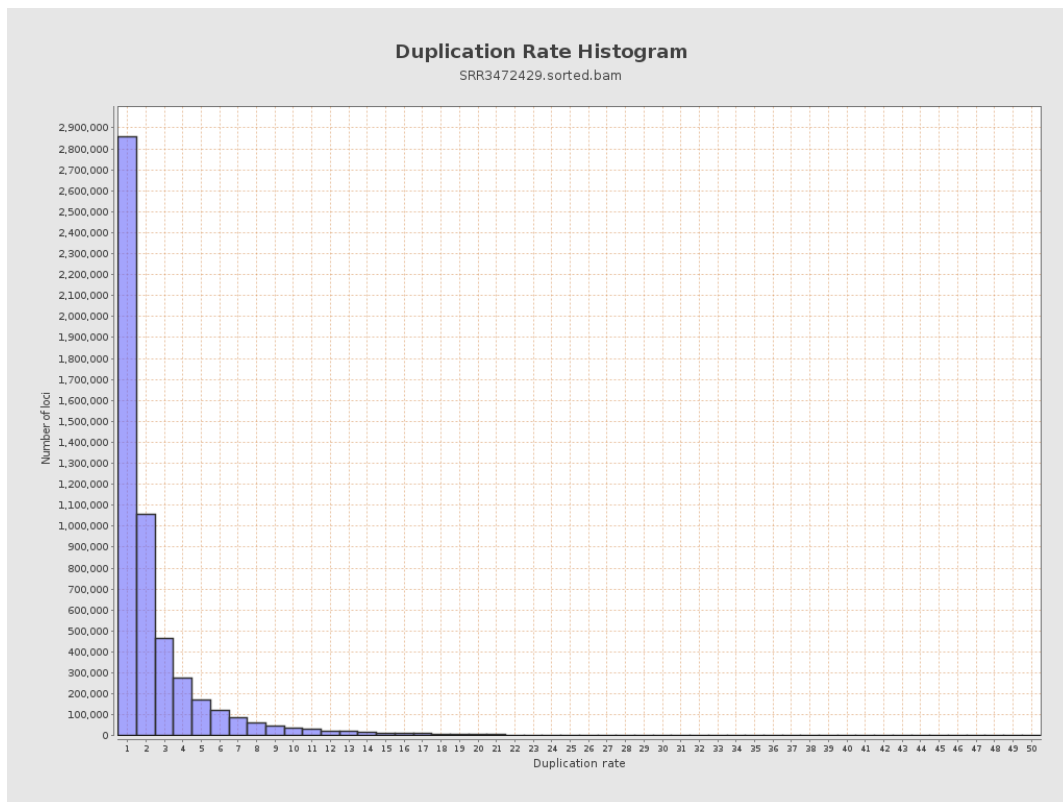
5. Results : Coverage Histogram (0-50X)



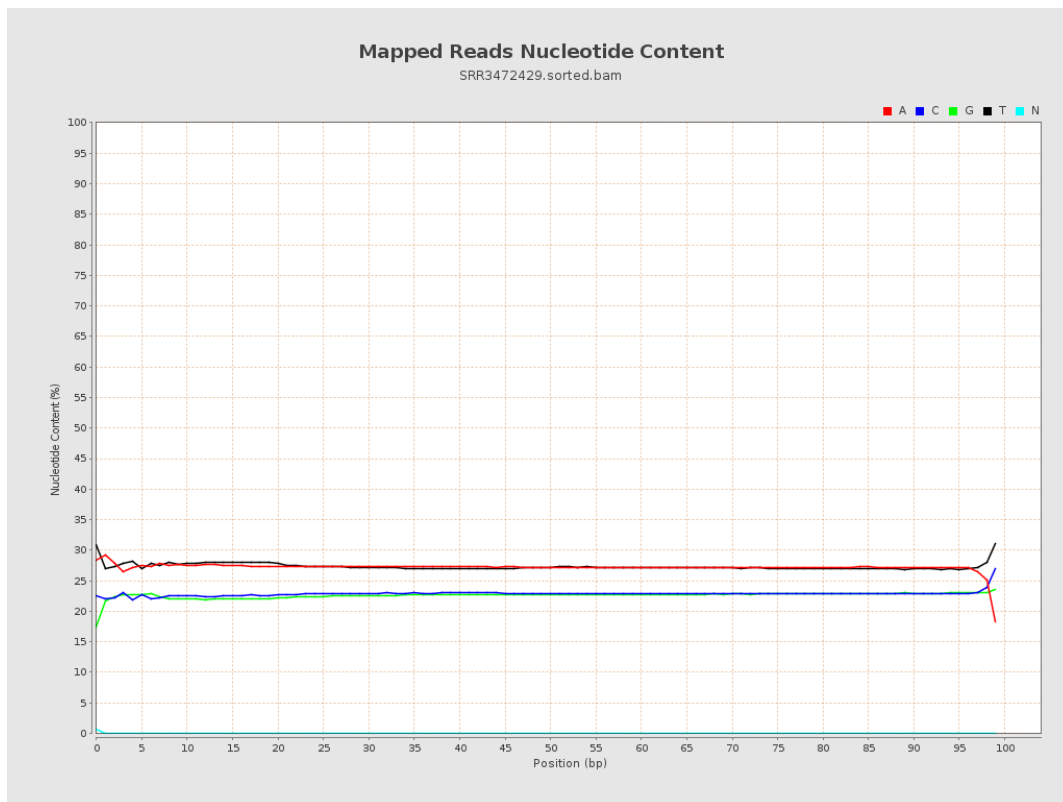
6. Results : Genome Fraction Coverage



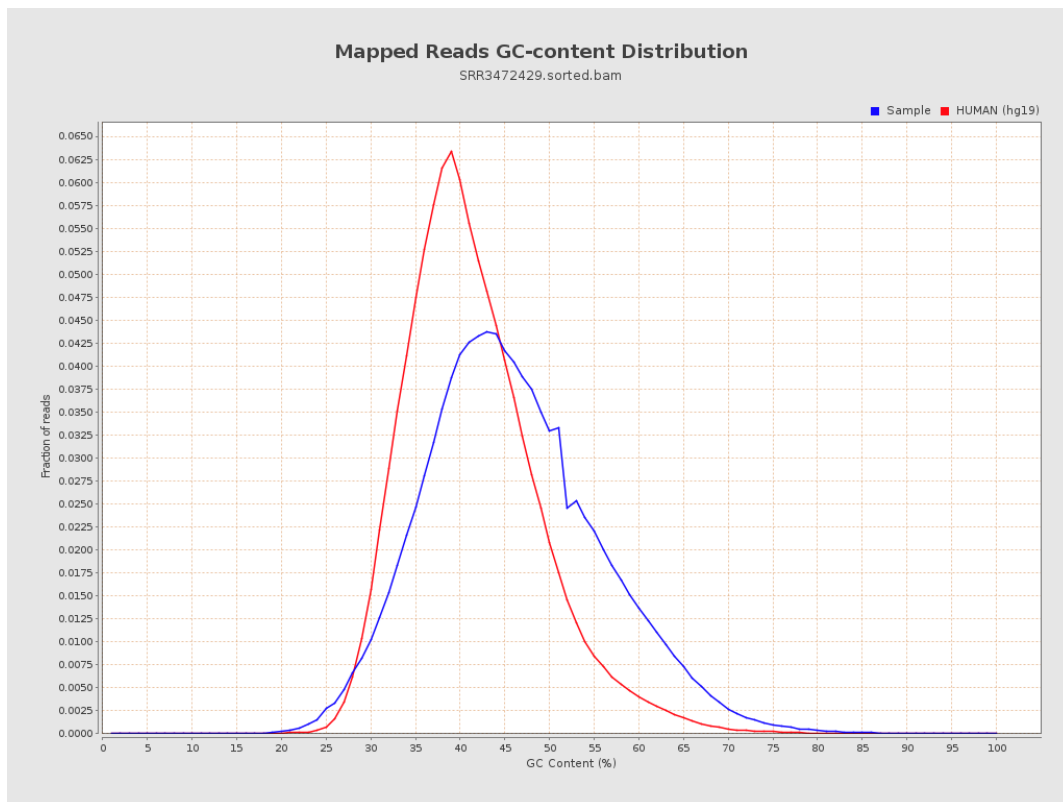
7. Results : Duplication Rate Histogram



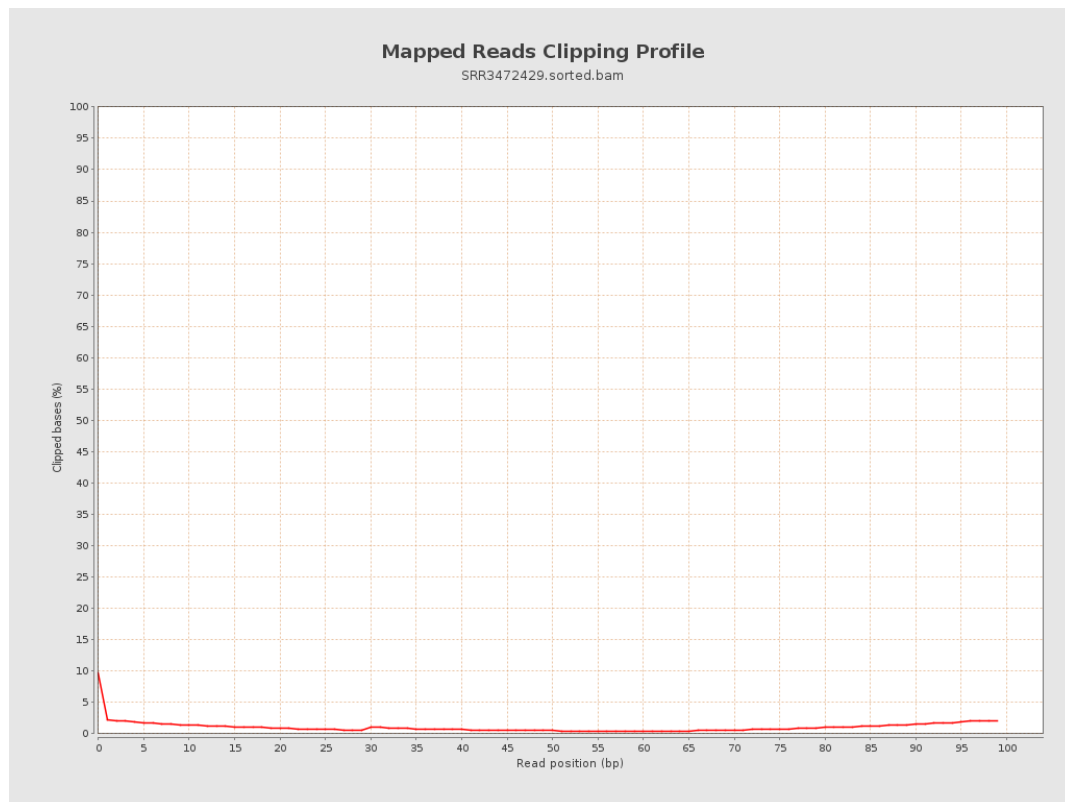
8. Results : Mapped Reads Nucleotide Content



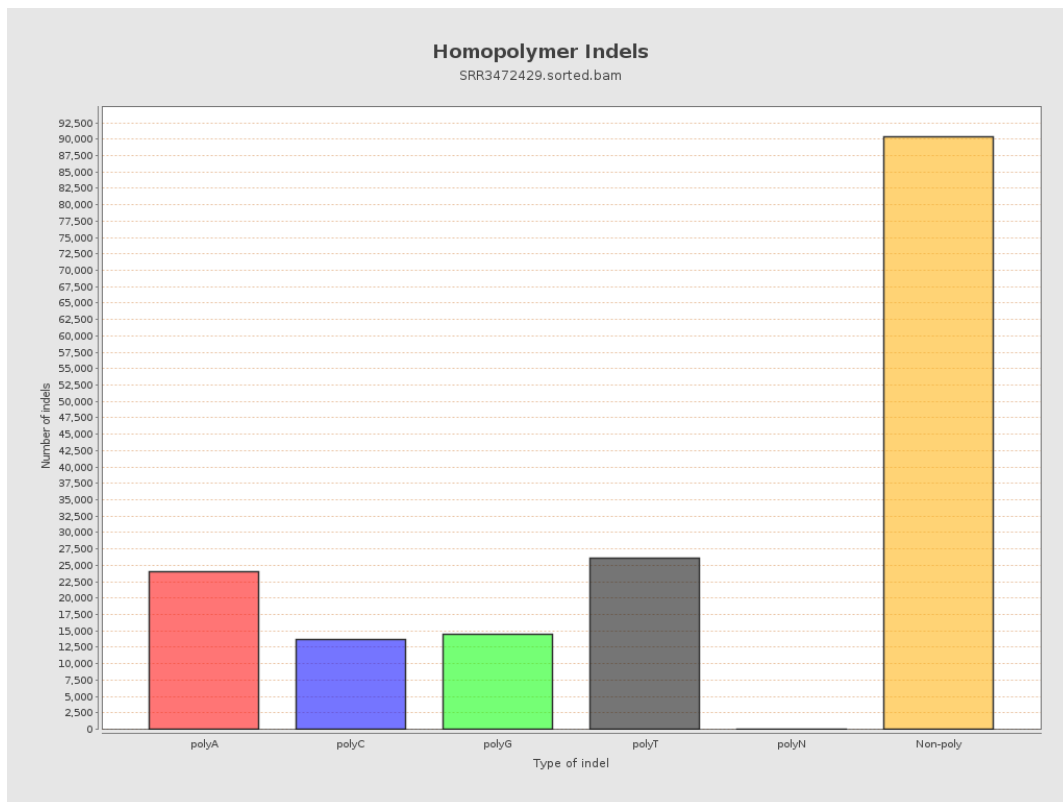
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



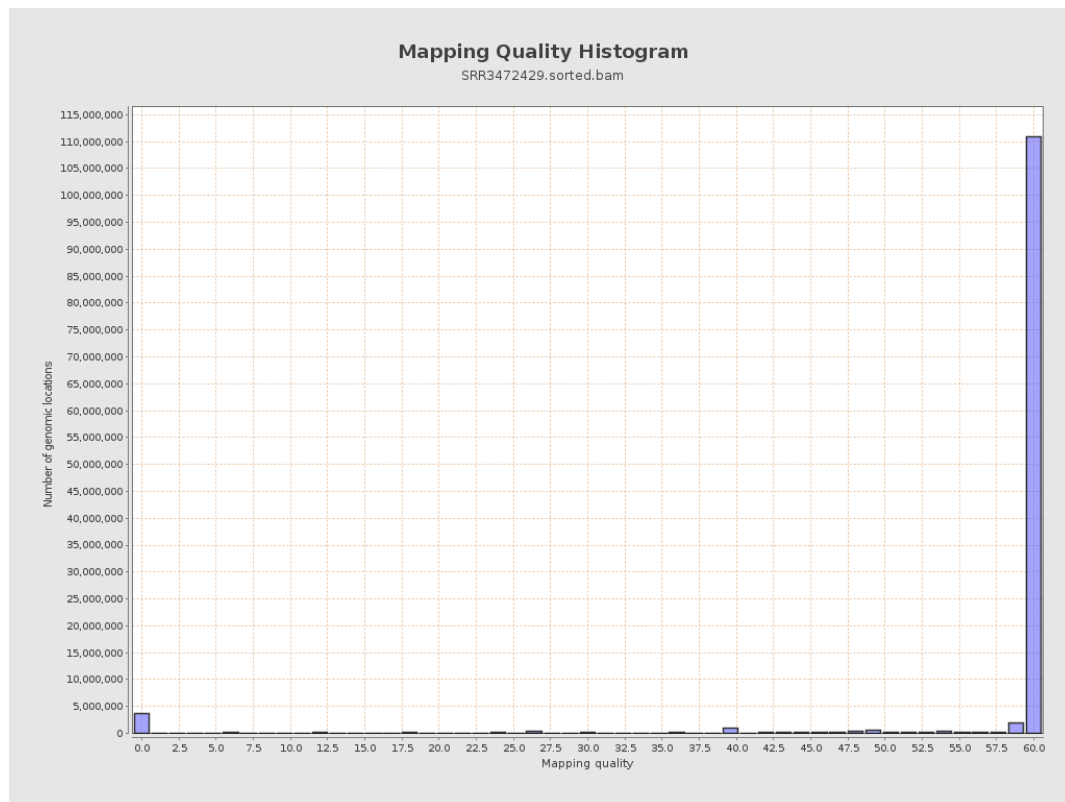
11. Results : Homopolymer Indels



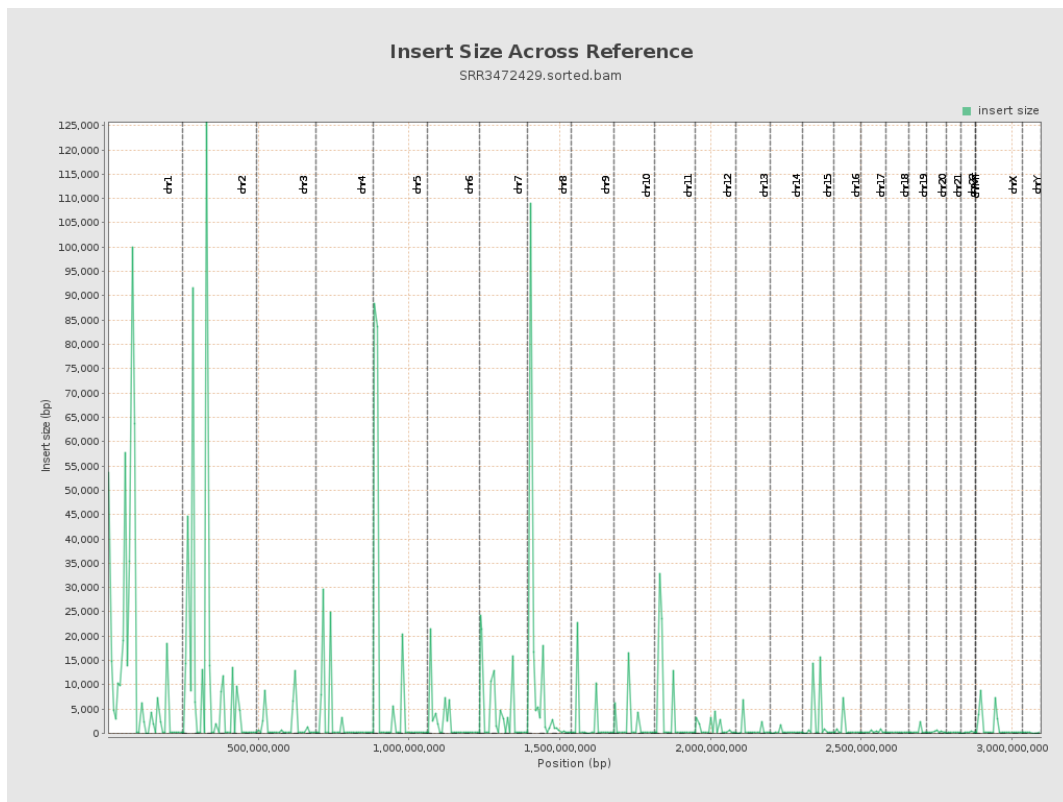
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

