

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/08/22 03:12:50

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472375.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_SRR3472375 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472375_1.fastq.gz SRR3472375_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Thu Aug 22 03:12:48 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472375.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	19,418,368
Mapped reads	19,249,122 / 99.13%
Unmapped reads	169,246 / 0.87%
Mapped paired reads	19,249,122 / 99.13%
Mapped reads, first in pair	9,662,418 / 49.76%
Mapped reads, second in pair	9,586,704 / 49.37%
Mapped reads, both in pair	19,139,114 / 98.56%
Mapped reads, singletons	110,008 / 0.57%
Secondary alignments	0
Supplementary alignments	62,703 / 0.32%
Read min/max/mean length	30 / 100 / 99.26
Duplicated reads (estimated)	12,097,583 / 62.3%
Duplication rate	48.75%
Clipped reads	1,447,908 / 7.46%

2.2. ACGT Content

Number/percentage of A's	497,271,337 / 26.41%
Number/percentage of C's	446,030,994 / 23.69%
Number/percentage of T's	497,802,579 / 26.44%
Number/percentage of G's	441,463,429 / 23.45%
Number/percentage of N's	235,756 / 0.01%

GC Percentage	47.14%
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2.3. Coverage

Mean	0.6083
Standard Deviation	16.898

2.4. Mapping Quality

Mean Mapping Quality	54.88
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2.5. Insert size

Mean	17,042.39
Standard Deviation	1,303,846.52
P25/Median/P75	145 / 200 / 270

2.6. Mismatches and indels

General error rate	0.52%
Mismatches	9,675,554
Insertions	104,023
Mapped reads with at least one insertion	0.53%
Deletions	81,389
Mapped reads with at least one deletion	0.42%
Homopolymer indels	45.14%

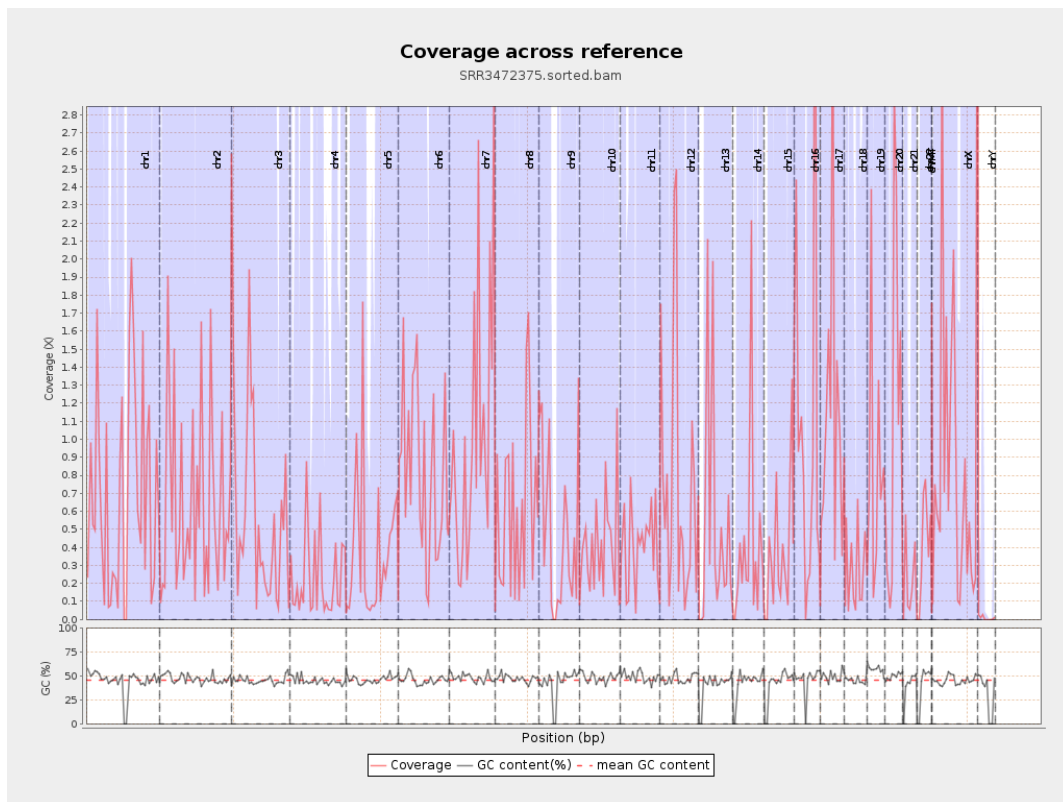
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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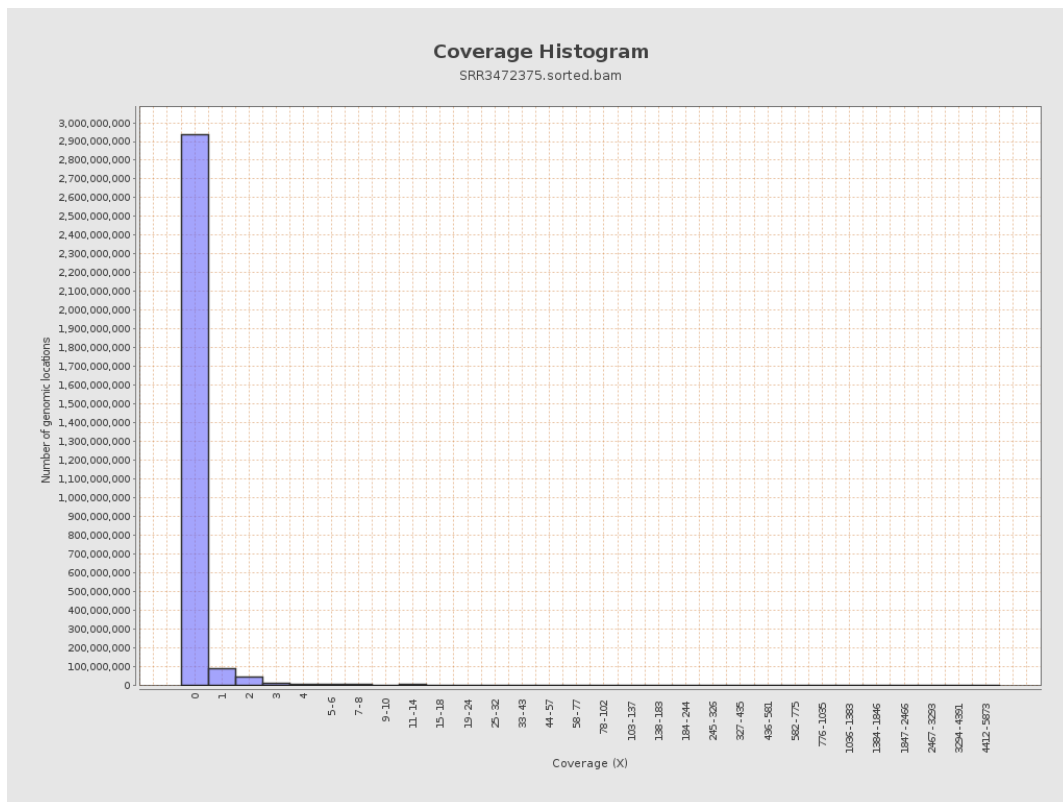
		bases	coverage	deviation
chr1	249250621	177235237	0.7111	19.1055
chr2	243199373	156396357	0.6431	18.6853
chr3	198022430	118527472	0.5986	12.8355
chr4	191154276	43209459	0.226	7.9855
chr5	180915260	68535452	0.3788	11.0397
chr6	171115067	138200118	0.8076	17.6451
chr7	159138663	164006120	1.0306	26.5838
chr8	146364022	92947204	0.635	18.0036
chr9	141213431	69059226	0.489	13.5149
chr10	135534747	55509940	0.4096	14.2472
chr11	135006516	55650966	0.4122	10.4746
chr12	133851895	100875548	0.7536	17.3489
chr13	115169878	59735474	0.5187	16.3163
chr14	107349540	40620101	0.3784	11.5412
chr15	102531392	39405943	0.3843	13.9073
chr16	90354753	99504041	1.1013	27.2532
chr17	81195210	95733371	1.1791	25.9389
chr18	78077248	22186496	0.2842	8.8671
chr19	59128983	51586254	0.8724	18.5408
chr20	63025520	70331088	1.1159	24.5757
chr21	48129895	10687571	0.2221	10.0092
chr22	51304566	20534601	0.4002	12.1074
chrMT	16571	29114	1.7569	2.0234
chrX	155270560	131980183	0.85	18.9842

chrY	59373566	516496	0.0087	0.7309
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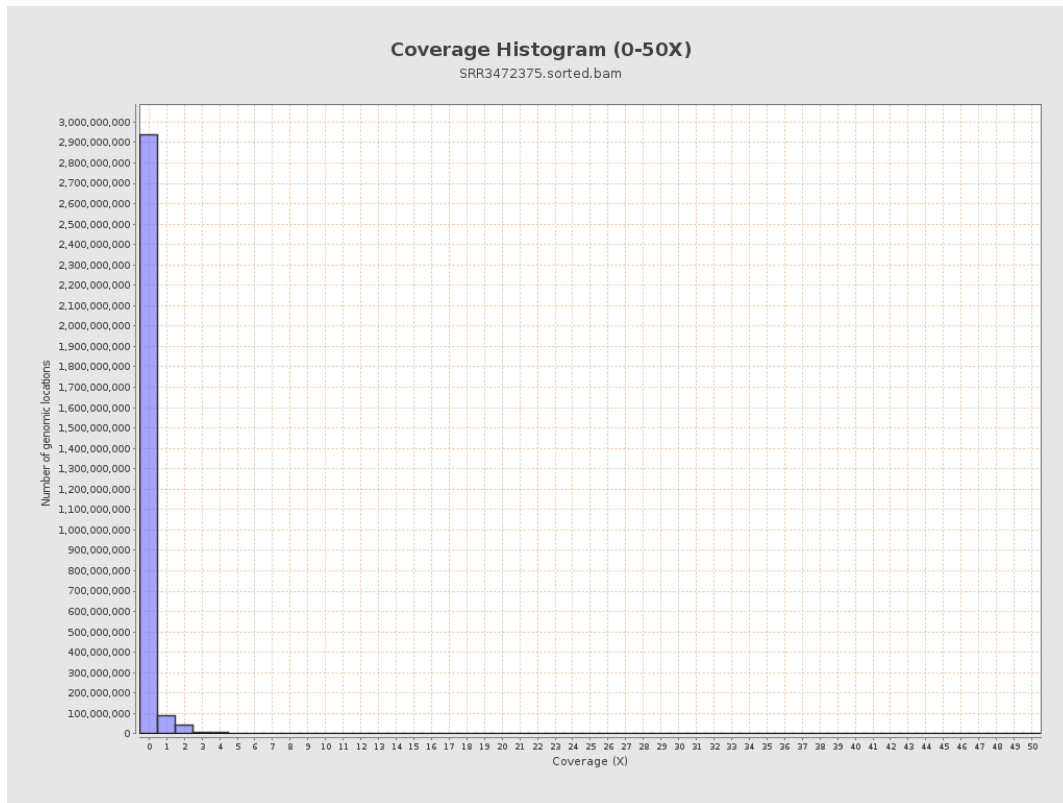
3. Results : Coverage across reference



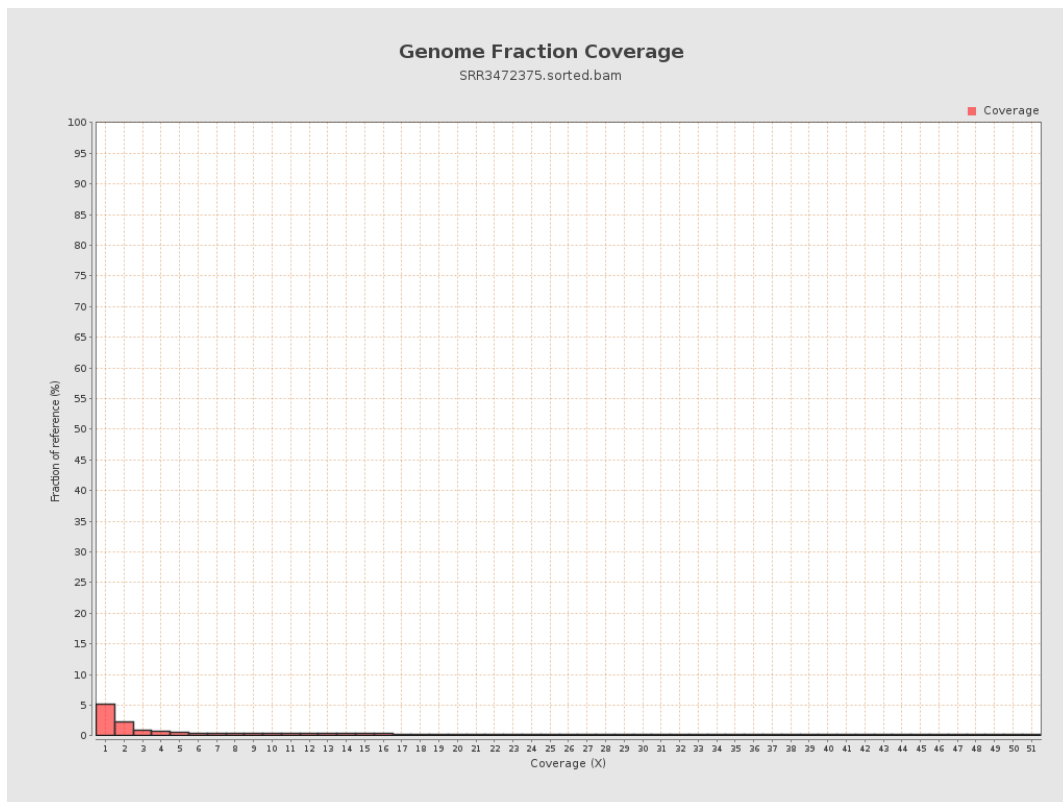
4. Results : Coverage Histogram



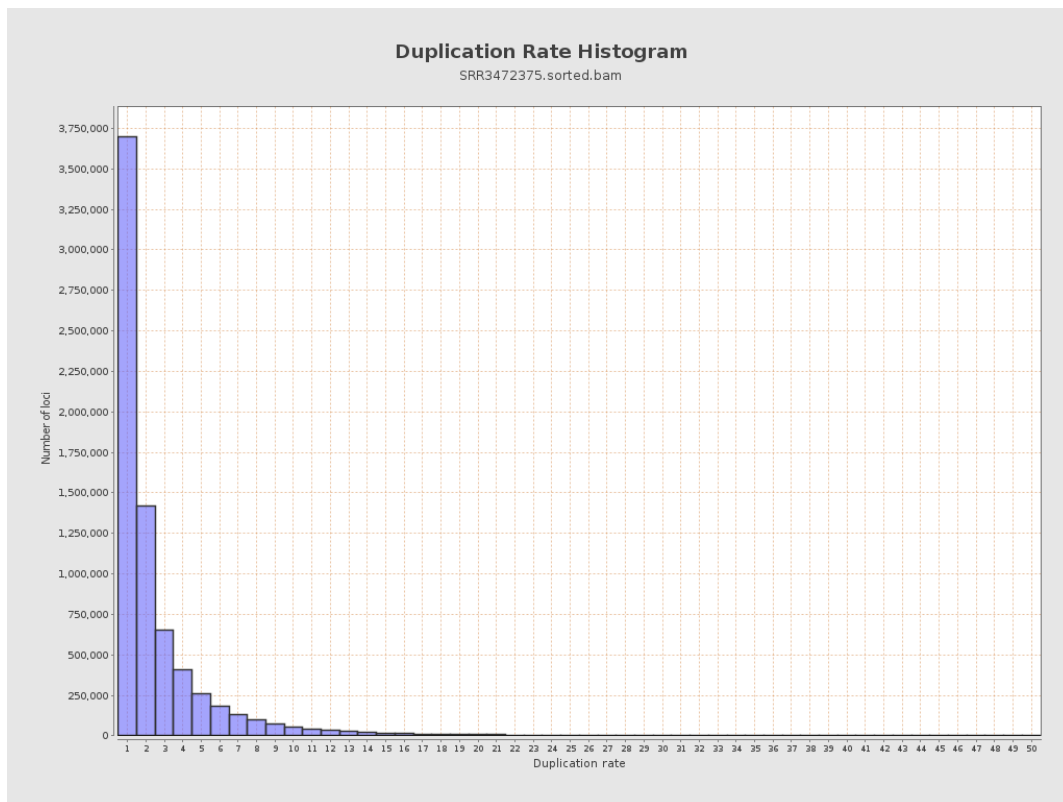
5. Results : Coverage Histogram (0-50X)



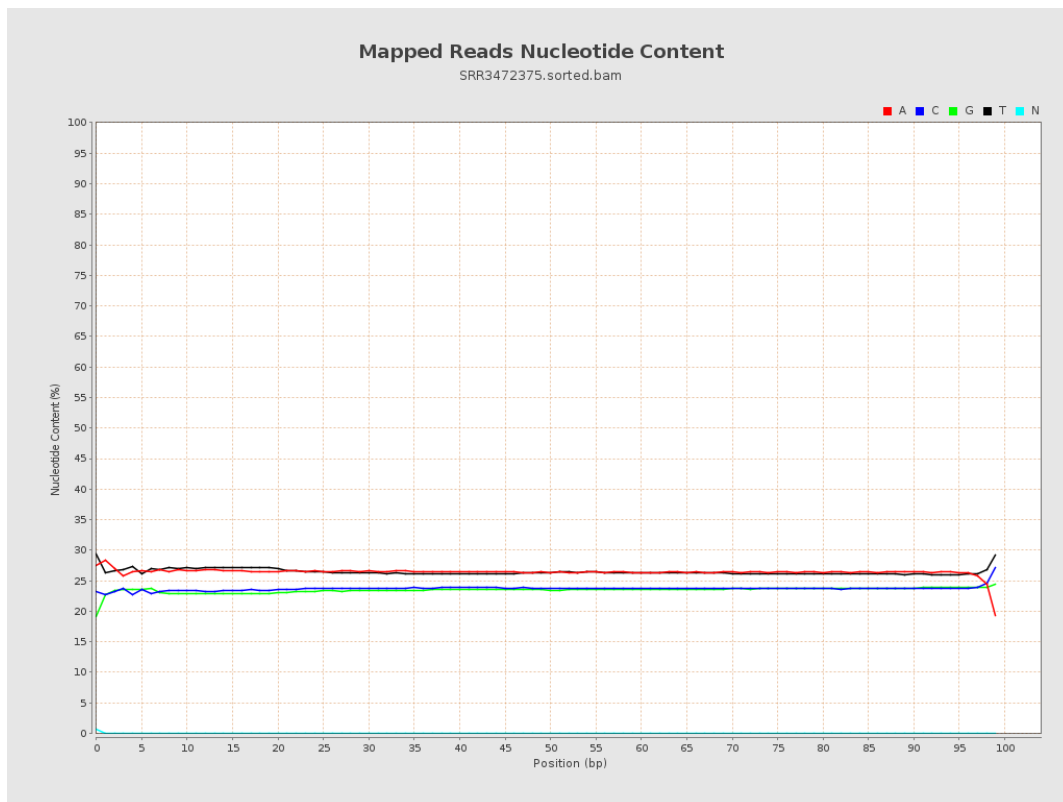
6. Results : Genome Fraction Coverage



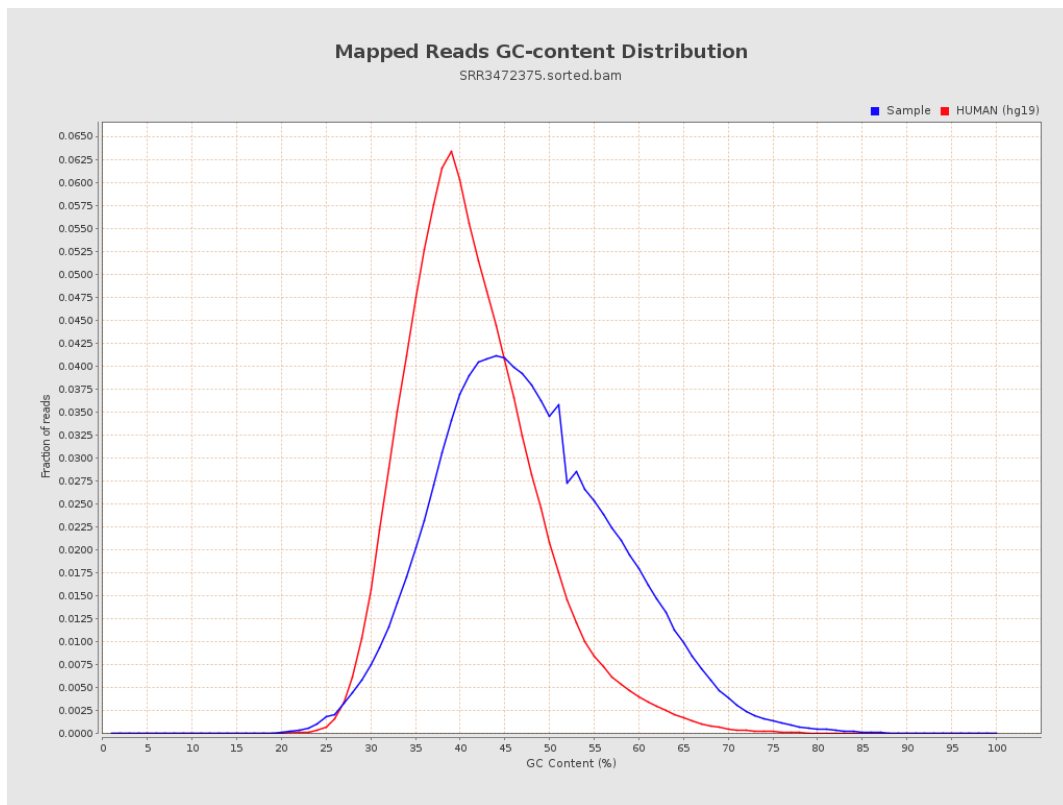
7. Results : Duplication Rate Histogram



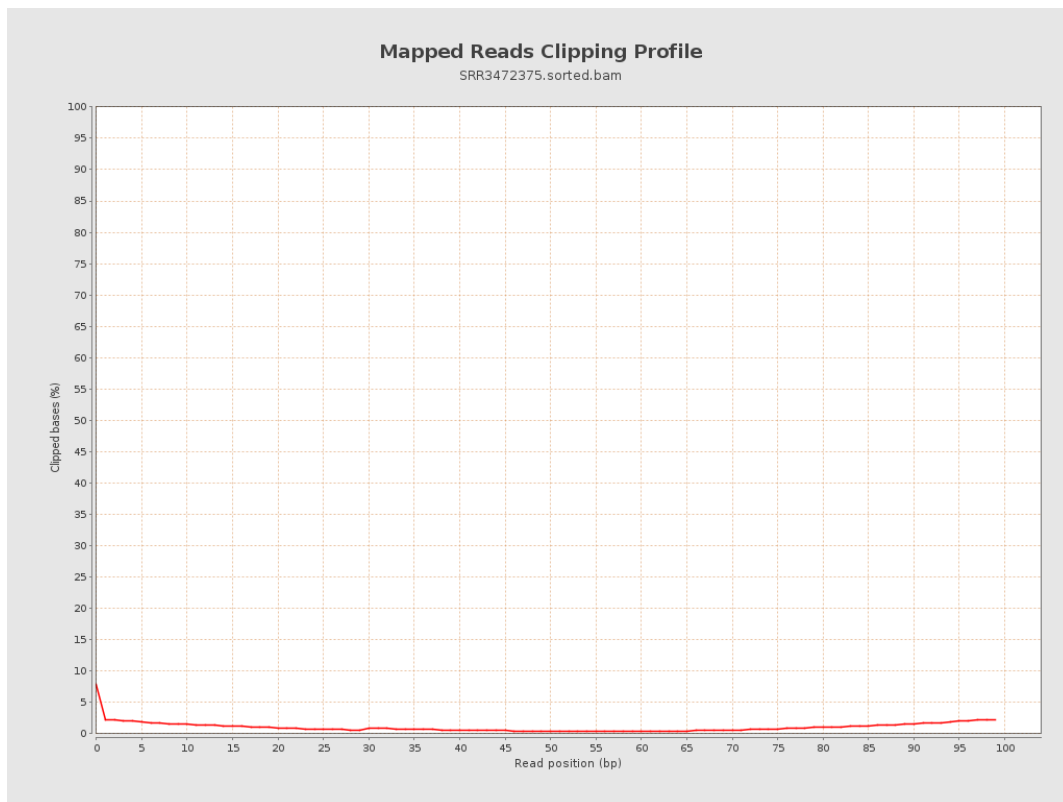
8. Results : Mapped Reads Nucleotide Content



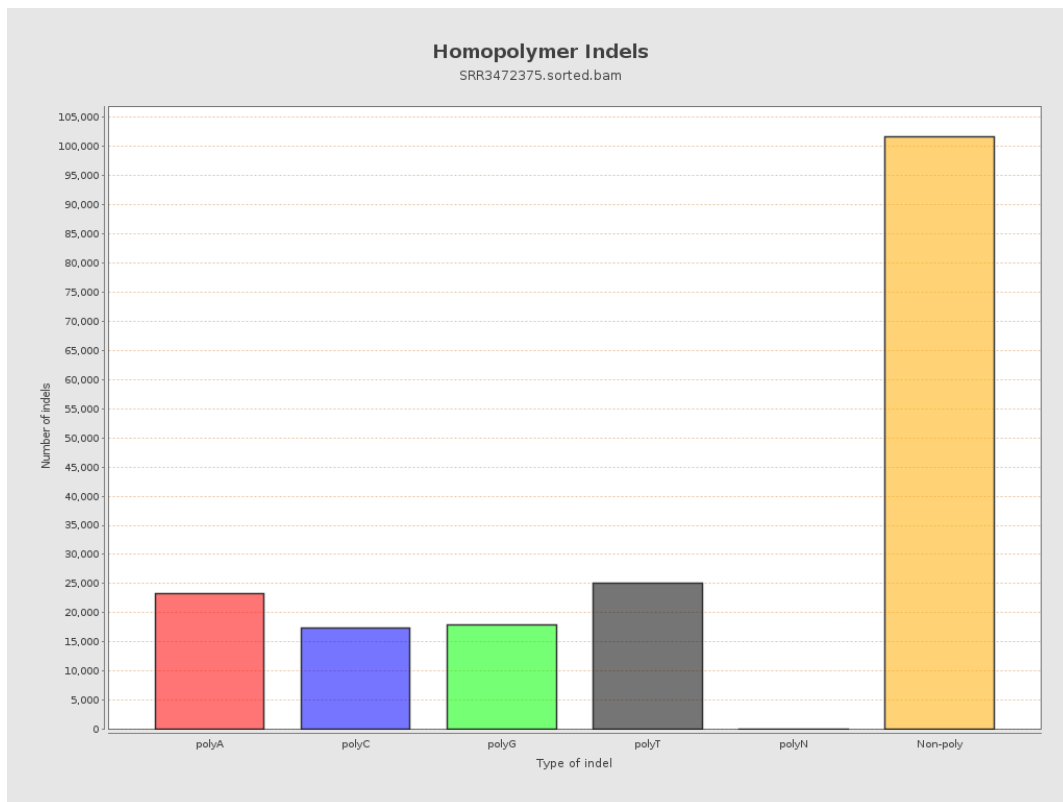
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



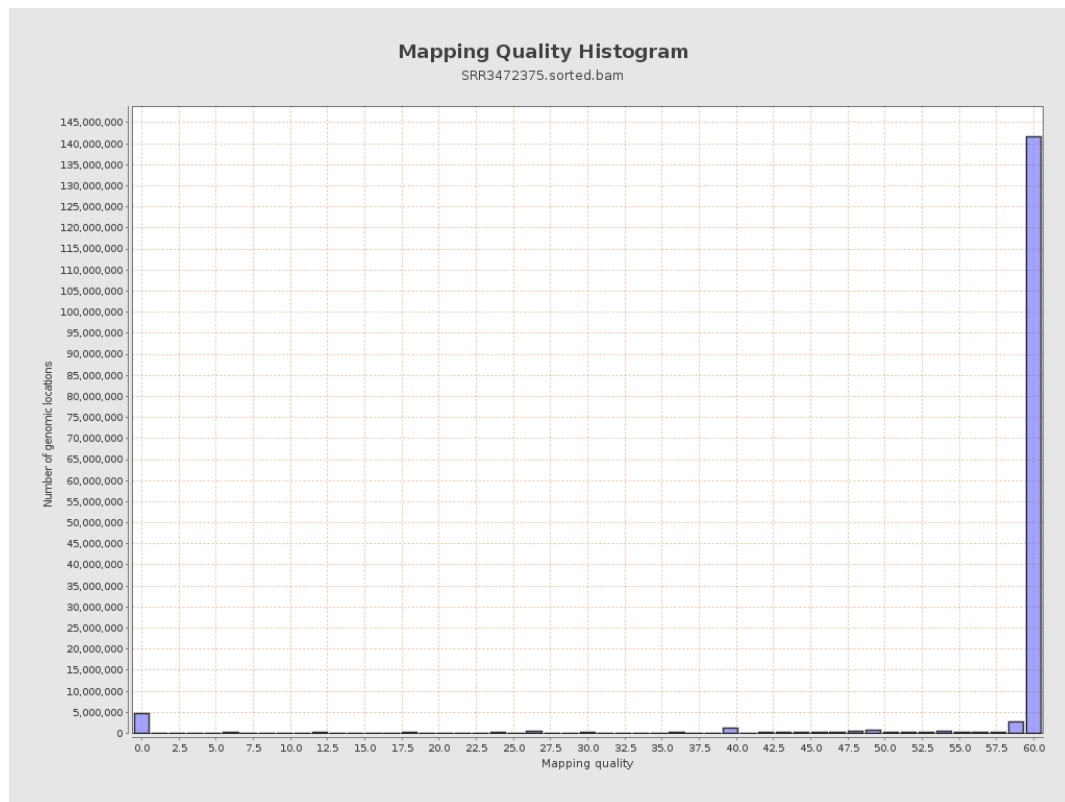
11. Results : Homopolymer Indels



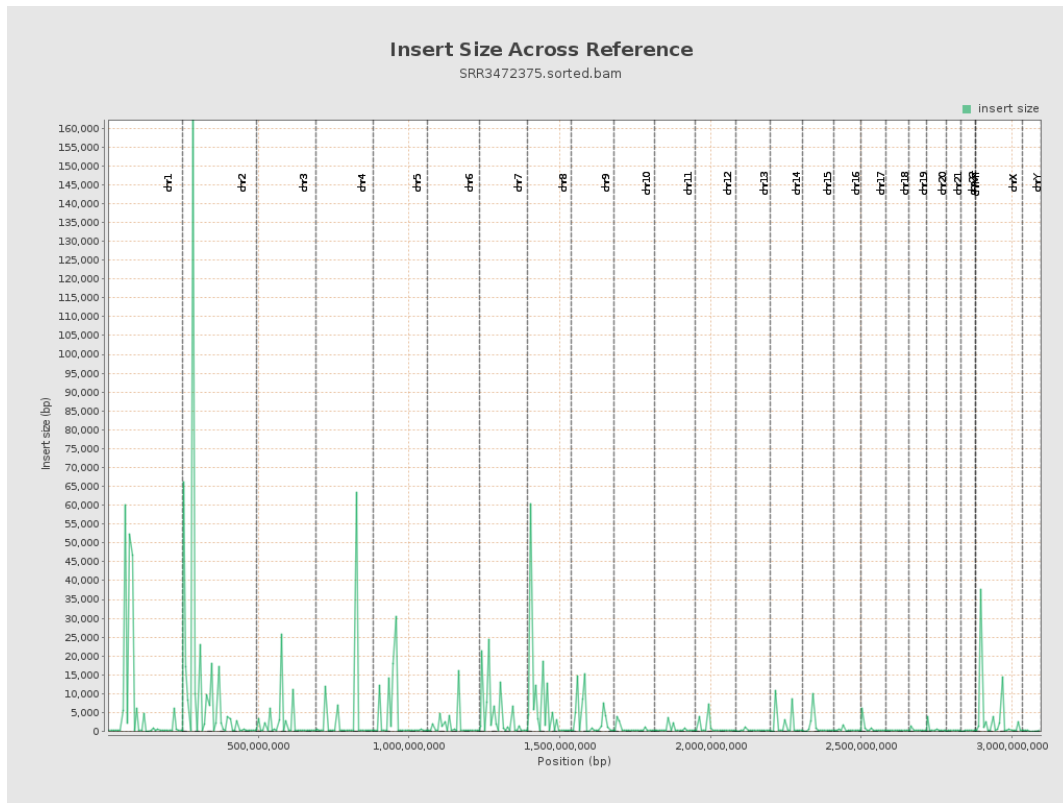
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

