

Qualimap Analysis Results

BAM QC analysis

Generated by Qualimap v.2.2.2-dev

2024/09/28 13:34:42

1. Input data & parameters

1.1. QualiMap command line

```
qualimap bamqc -bam SRR3472621.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_SRR3472621 /home/luna/Desktop/database/homo_bwa/hsa.fa SRR3472621_1.fastq.gz SRR3472621_2.fastq.gz
Draw chromosome limits:	yes
Analyze overlapping paired-end reads:	no
Program:	bwa (0.7.17-r1188)
Analysis date:	Sat Sep 28 13:34:41 CST 2024
Size of a homopolymer:	3
Skip duplicate alignments:	no
Number of windows:	400
BAM file:	SRR3472621.sorted.bam

2. Summary

2.1. Globals

Reference size	3,095,693,983
Number of reads	21,710,078
Mapped reads	21,530,162 / 99.17%
Unmapped reads	179,916 / 0.83%
Mapped paired reads	21,530,162 / 99.17%
Mapped reads, first in pair	10,798,334 / 49.74%
Mapped reads, second in pair	10,731,828 / 49.43%
Mapped reads, both in pair	21,401,164 / 98.58%
Mapped reads, singletons	128,998 / 0.59%
Secondary alignments	0
Supplementary alignments	129,998 / 0.6%
Read min/max/mean length	30 / 101 / 99.83
Duplicated reads (estimated)	16,127,474 / 74.29%
Duplication rate	50.07%
Clipped reads	1,593,206 / 7.34%

2.2. ACGT Content

Number/percentage of A's	558,358,553 / 26.35%
Number/percentage of C's	504,470,671 / 23.81%
Number/percentage of T's	558,081,514 / 26.34%
Number/percentage of G's	497,352,395 / 23.47%
Number/percentage of N's	396,658 / 0.02%

GC Percentage	47.29%
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2.3. Coverage

Mean	0.6845
Standard Deviation	35.3111

2.4. Mapping Quality

Mean Mapping Quality	54.72
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2.5. Insert size

Mean	25,380.87
Standard Deviation	1,629,712.56
P25/Median/P75	156 / 215 / 290

2.6. Mismatches and indels

General error rate	0.64%
Mismatches	13,308,534
Insertions	121,032
Mapped reads with at least one insertion	0.56%
Deletions	108,785
Mapped reads with at least one deletion	0.5%
Homopolymer indels	47.49%

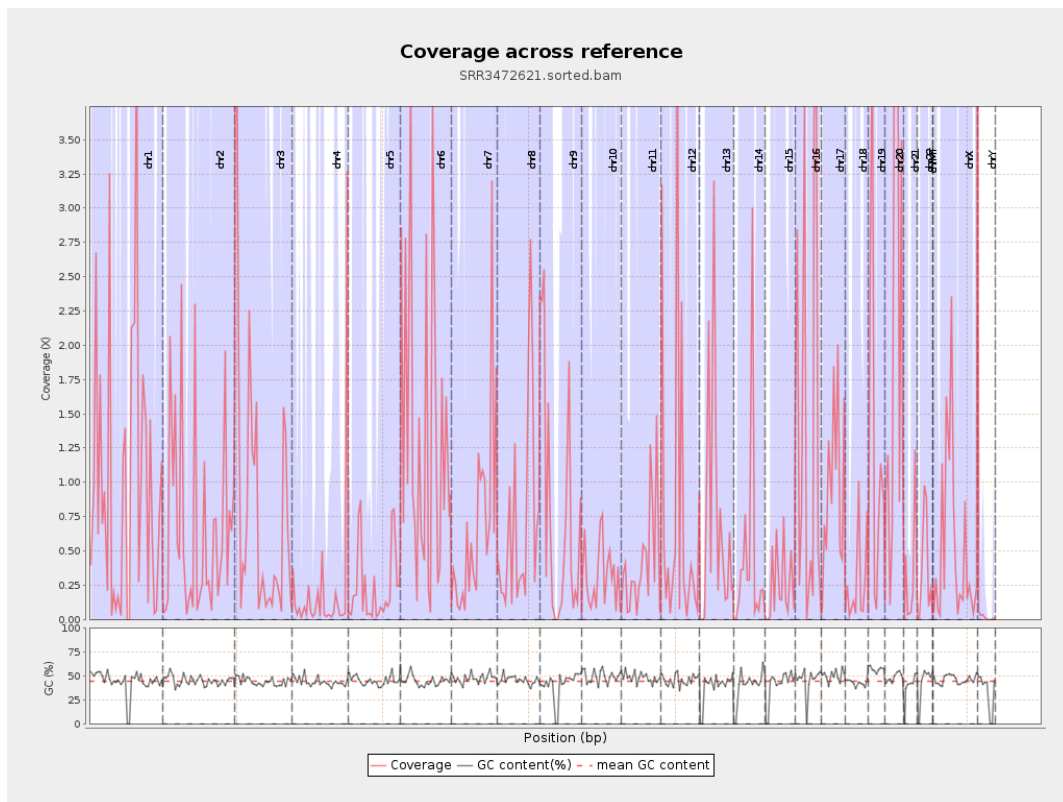
2.7. Chromosome stats

Name	Length	Mapped	Mean	Standard
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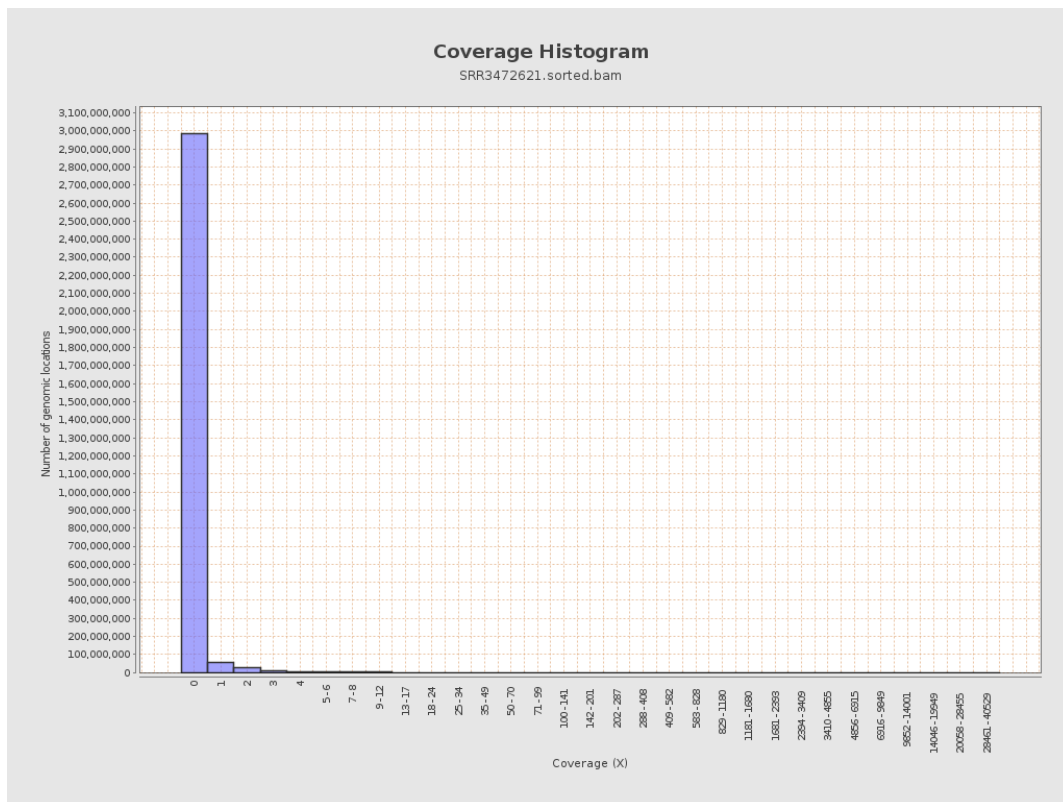
		bases	coverage	deviation
chr1	249250621	247654773	0.9936	39.2246
chr2	243199373	159282978	0.6549	28.9381
chr3	198022430	167518432	0.846	58.6274
chr4	191154276	41044995	0.2147	21.3437
chr5	180915260	43724492	0.2417	12.1335
chr6	171115067	225736509	1.3192	48.3191
chr7	159138663	110645719	0.6953	31.7772
chr8	146364022	103480351	0.707	28.5609
chr9	141213431	98441060	0.6971	25.9495
chr10	135534747	45198706	0.3335	16.5185
chr11	135006516	55758309	0.413	24.3361
chr12	133851895	104285077	0.7791	38.6351
chr13	115169878	83475158	0.7248	37.104
chr14	107349540	45436068	0.4233	23.8762
chr15	102531392	24891860	0.2428	18.6696
chr16	90354753	126858570	1.404	63.5542
chr17	81195210	78974620	0.9727	29.3857
chr18	78077248	19360238	0.248	12.9685
chr19	59128983	76985475	1.302	61.1527
chr20	63025520	131820266	2.0915	67.4491
chr21	48129895	16203466	0.3367	26.1852
chr22	51304566	18897286	0.3683	11.9023
chrMT	16571	4384	0.2646	0.6672
chrX	155270560	92304232	0.5945	29.4518

chrY	59373566	988615	0.0167	0.8936
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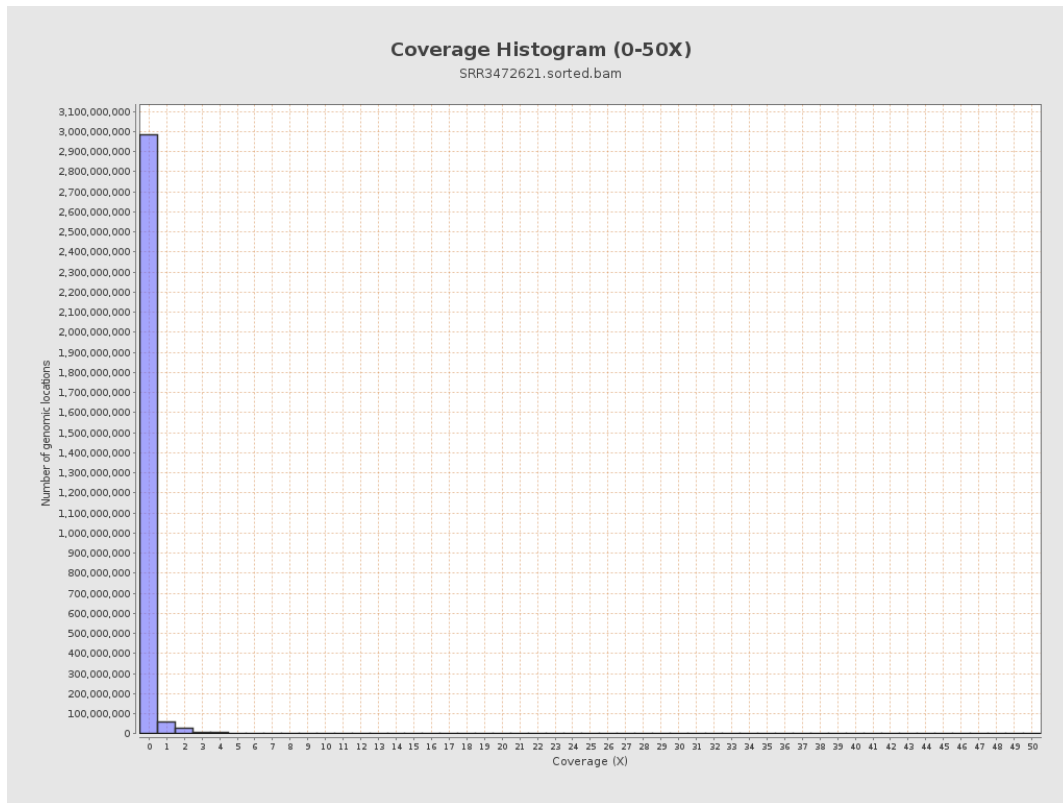
3. Results : Coverage across reference



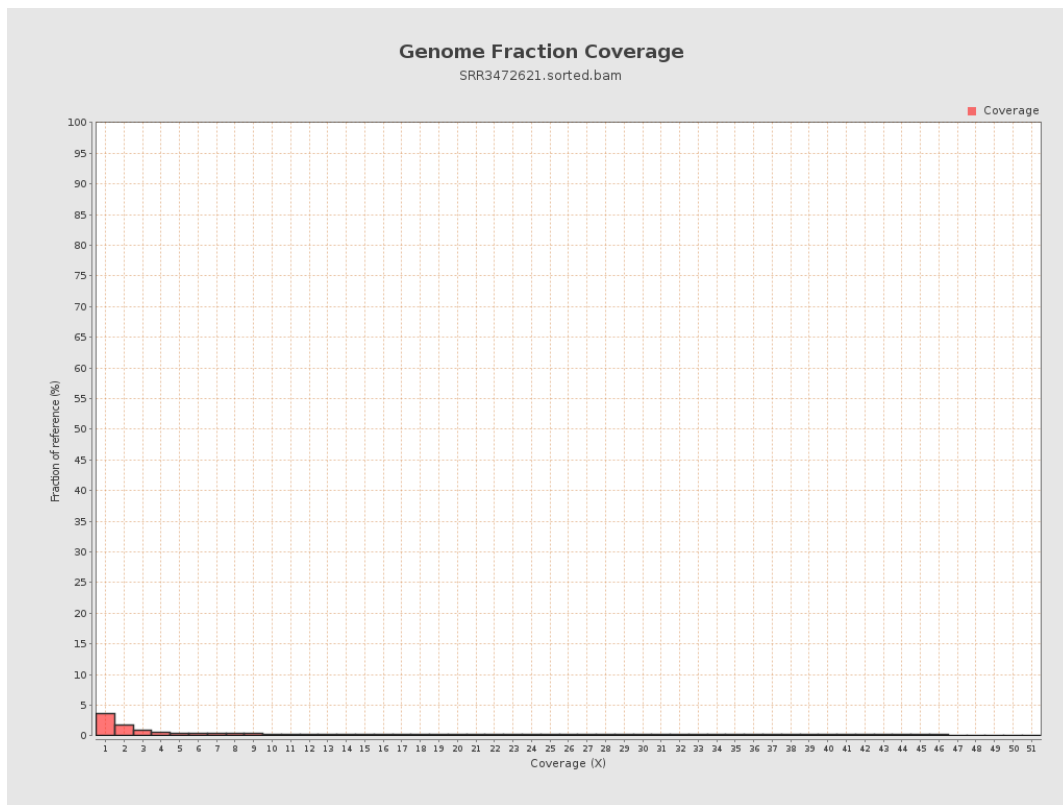
4. Results : Coverage Histogram



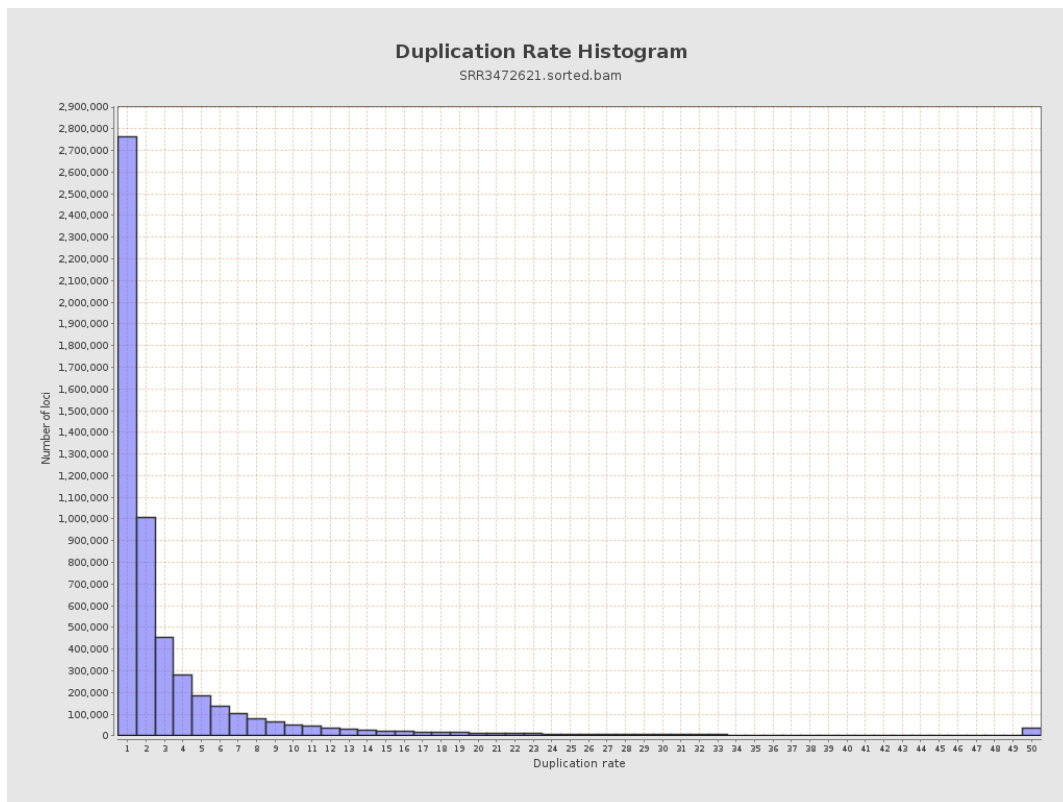
5. Results : Coverage Histogram (0-50X)



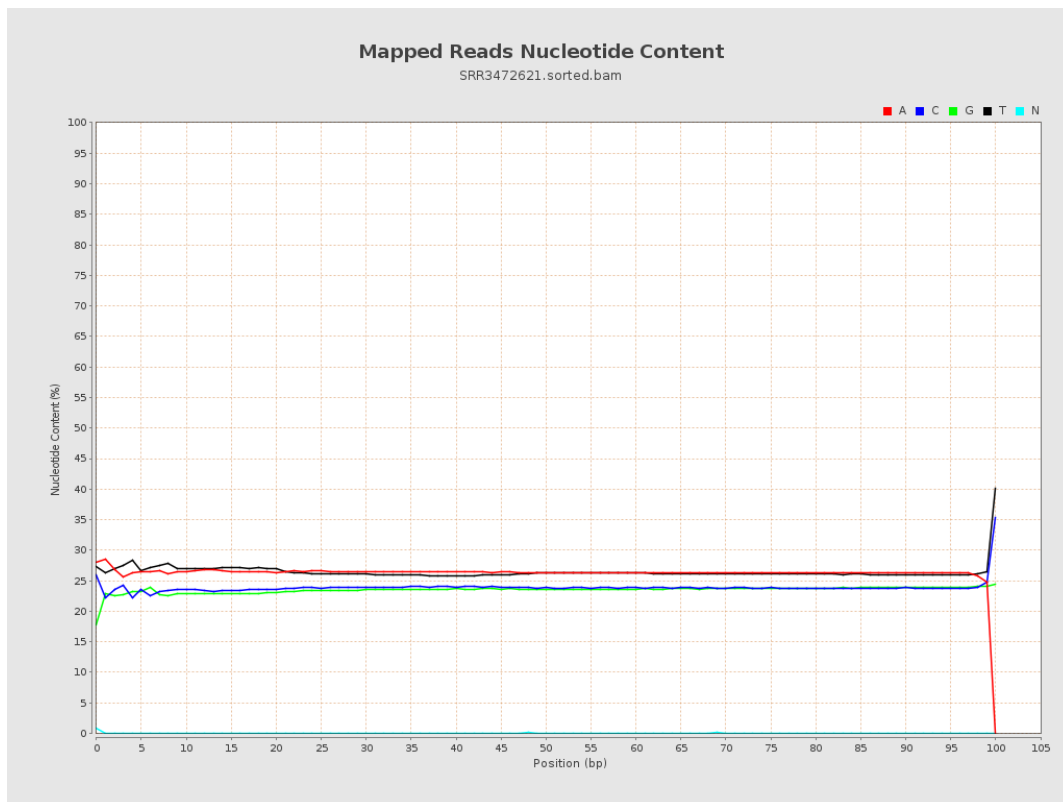
6. Results : Genome Fraction Coverage



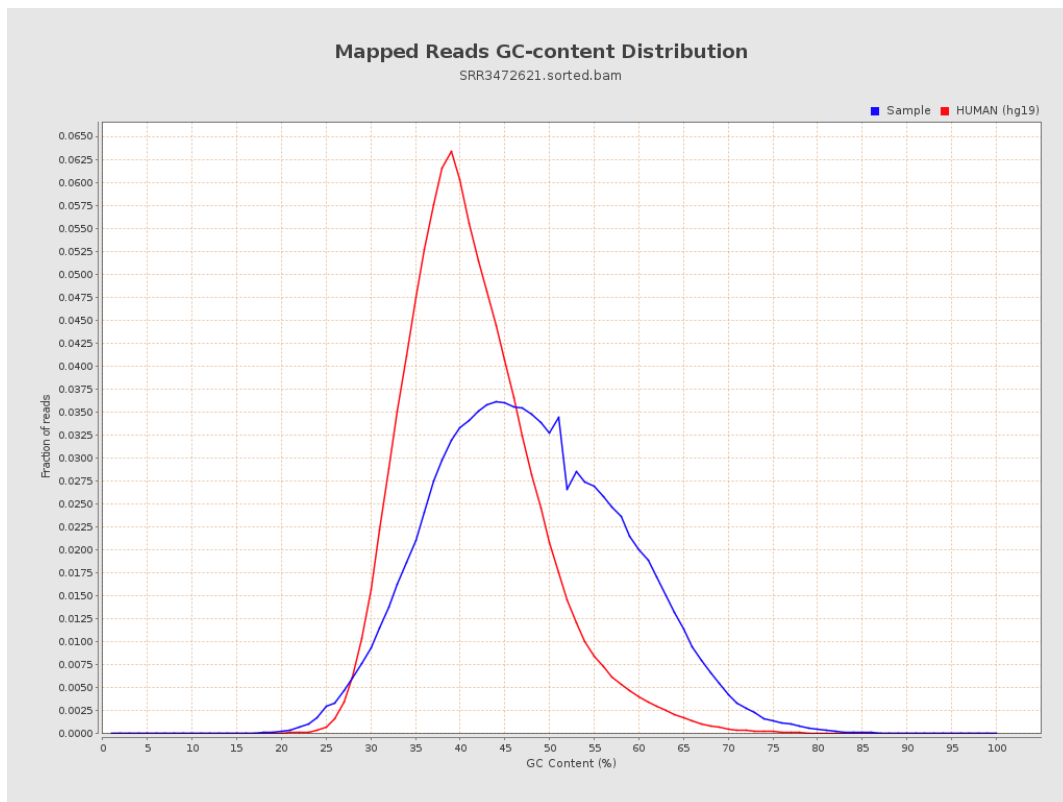
7. Results : Duplication Rate Histogram



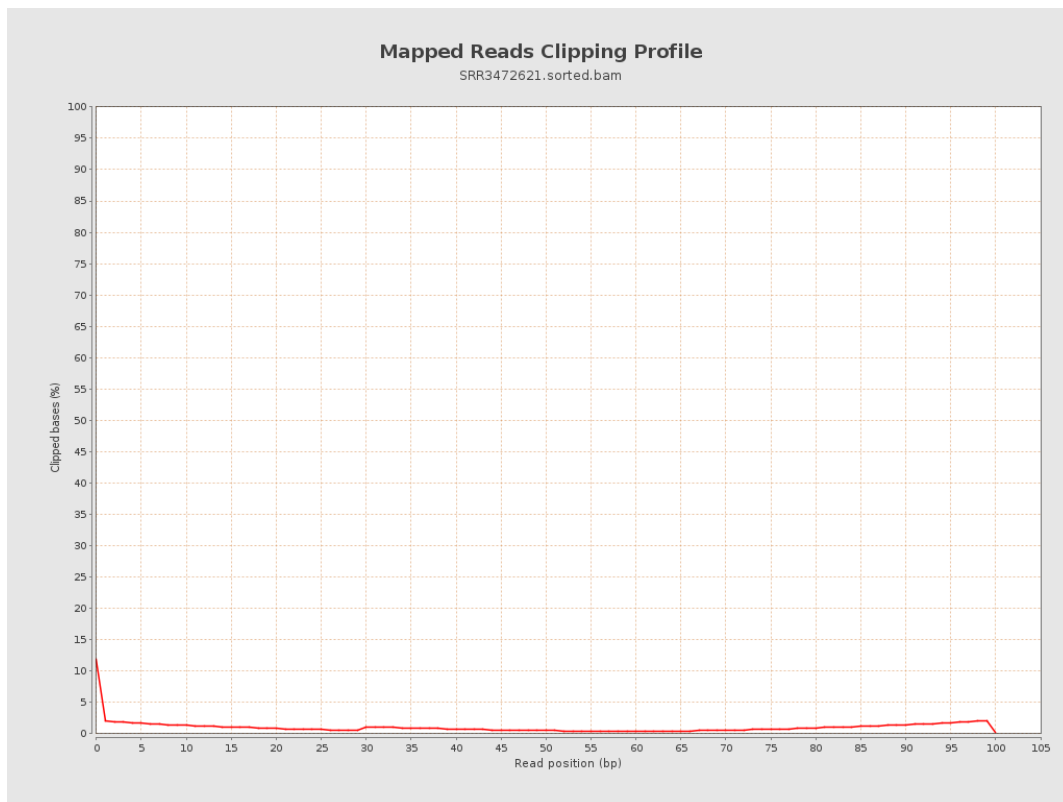
8. Results : Mapped Reads Nucleotide Content



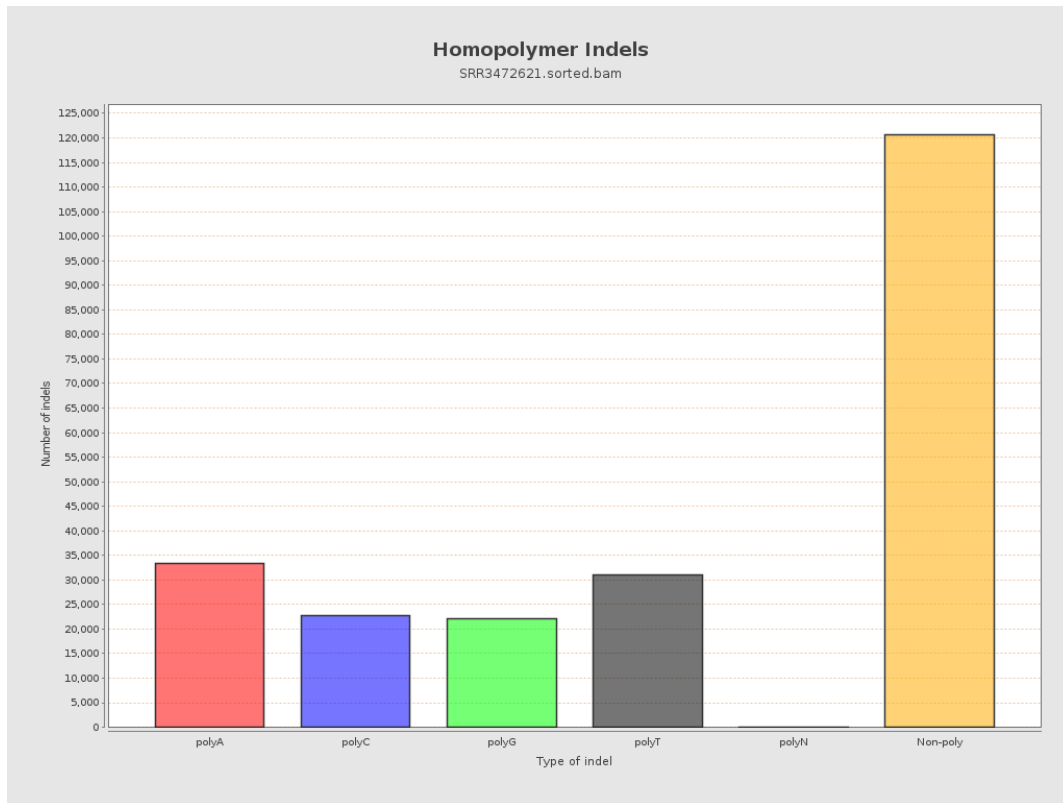
9. Results : Mapped Reads GC-content Distribution



10. Results : Mapped Reads Clipping Profile



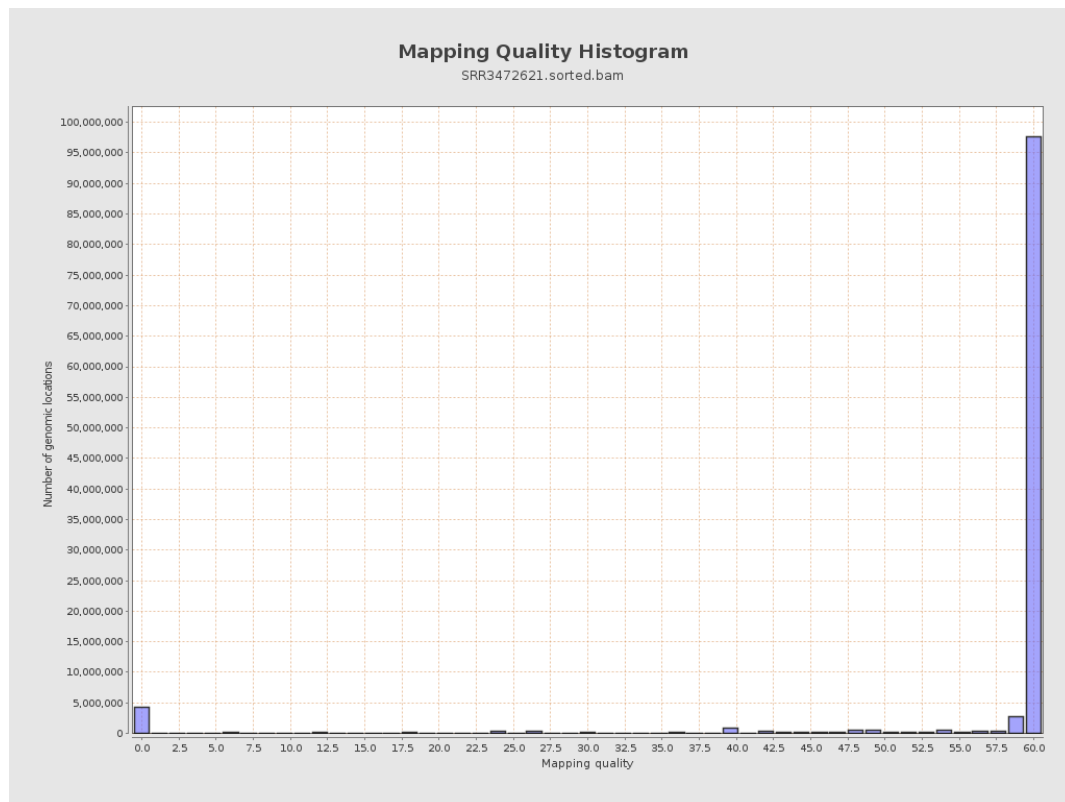
11. Results : Homopolymer Indels



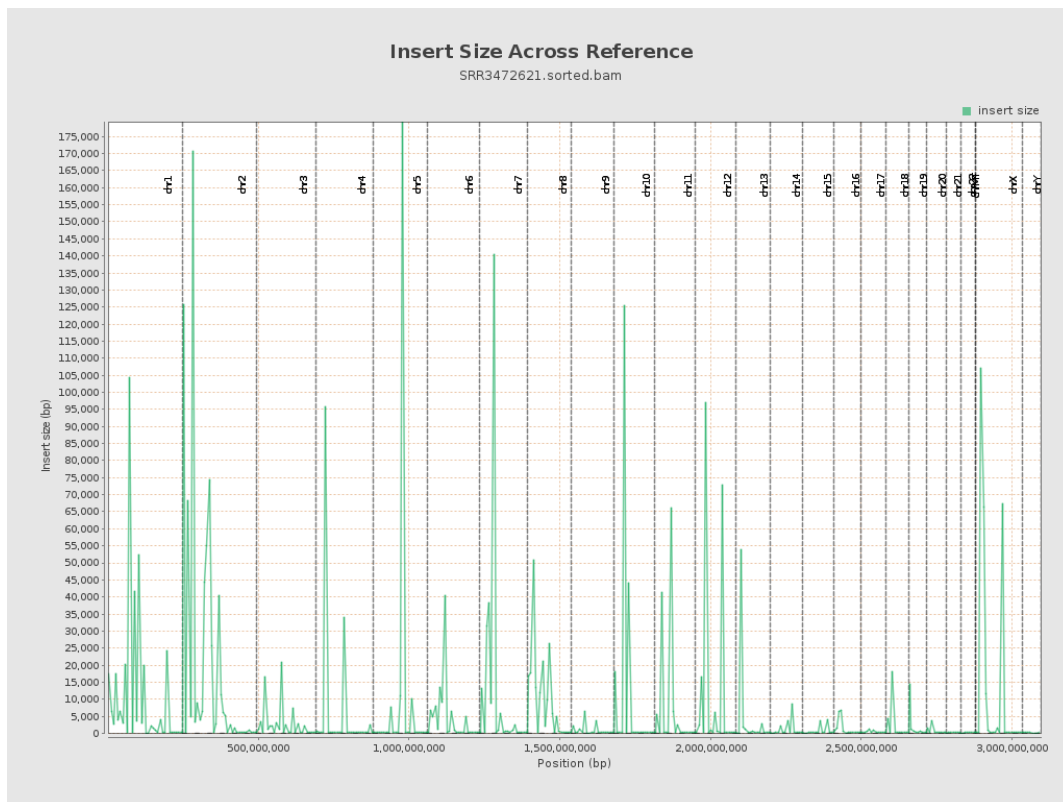
12. Results : Mapping Quality Across Reference



13. Results : Mapping Quality Histogram



14. Results : Insert Size Across Reference



15. Results : Insert Size Histogram

