

Next Generation Sequencing (NGS) Report

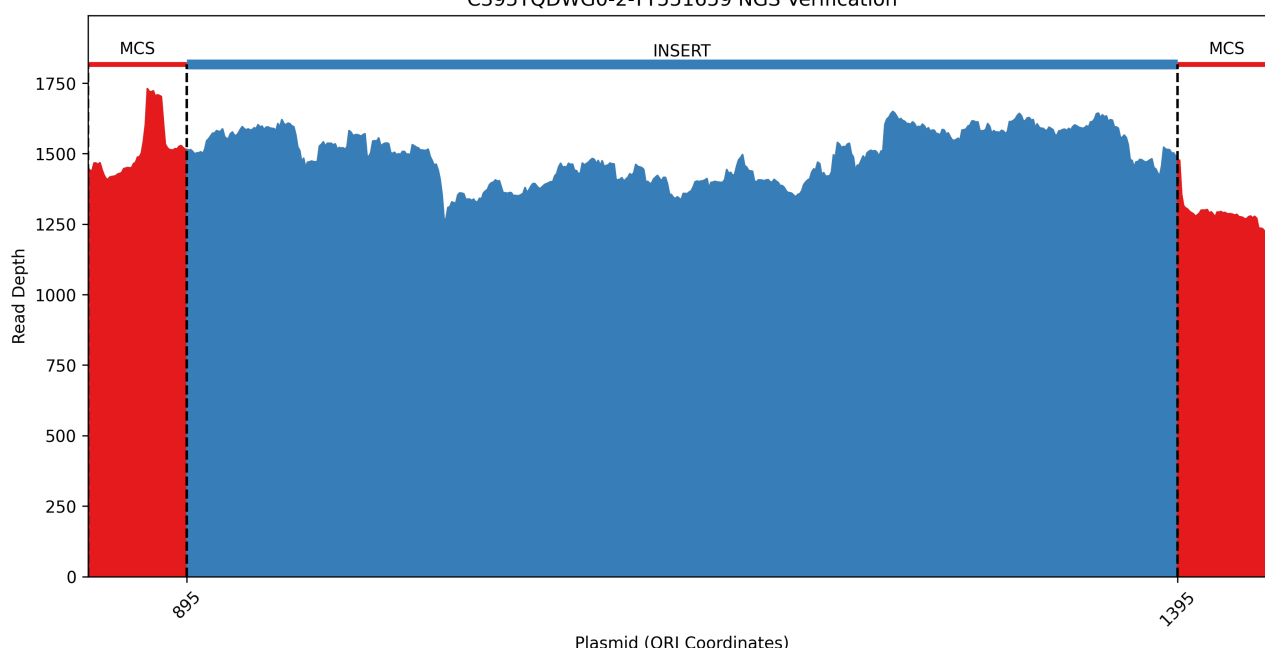
Sample Info

Project ID: C395TQDWG0-2
Clone ID: TY551659

I Insert+f50 Depth

The sequence depth (the frequency of single base (1bp) sequenced in the same site) pattern of **insert and extended 50bp** at both ends. See the single base depth in the region in III. Sequence alignment.

C395TQDWG0-2-TY551659 NGS Verification



II NGS sequencing quality value (Q value)

Quality Scores and BaseCalling Accuracy

Phred Quality Score	Probability of Incorrect Base Call	Base Call Accuracy
10	1 in 10	90%
20	1 in 100	99%
30	1 in 1,000	99.9%
40	1 in 10,000	99.99%
50	1 in 100,000	99.999%

- Total Bases Q30 is 97.23%.
- The Bases Q30 is equal or greater than 75% and meets our analytical requirements.
- Higher Q scores indicate a smaller probability of error.
- Lower Q scores can result in a significant portion of the reads being unusable. They may also lead to increased false-positive variant calls, resulting in inaccurate conclusions.
- A quality score of 30 (Q30) represents an error rate of 1 in 1000 (meaning every 1000 bp sequencing read may contain an error), with a corresponding call accuracy of 99.9%. When sequencing quality reaches Q30, virtually all of the reads will be perfect, with no errors or ambiguities.

III Sequence alignment

X-axis indicates the template sequence, Y-axis indicates the NGS sequence read depth.

[Click to the page of coverage and reads details.](#)

