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| --- | --- | --- | --- | --- |
| **Case** | **Lef31** | **Gray Zone** | **Exceeds 99% P.I. *1*** | **Interpretation** |
| 1 | yes | yes or no | yes or no | Evidence of lethal factor gene, could be *B. anthracis* or a *B. cereus* strain carrying the pXO1 plasmid. |
| 2 | no | yes | yes | Possible *B. anthracis* or closely related strain based on high Ba31 counts but genome coverage too low to guarantee seeing the *lef* gene. Requires more sequence coverage and/or validation by PCR or other methods. |
| 3 | no | no | yes | Ba31 matches exceed what is expected by the BCerG error model, but are at a level of genome coverage at which lethal factor should have been detected. Most likely explanation is *B. anthracis* strain cured of pXO1 or unsequenced lineage closely related to *B. anthracis*. |
| 4 | no | yes or no | no | Most likely scenario is that BCerG background produced Ba31 k-mers through random errors but impossible to also rule out presence of low coverage *B. anthracis* |

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***1***Prediction Interval