

Case	Lef31	Gray Zone	Exceeds 99% P.I	Interpretation
1	yes	yes or no	yes or no	Evidence of lethal factor gene, could be <i>B. anthracis</i> or a <i>B. cereus</i> strain carrying the pXO1 plasmid.
2	no	yes	yes	Possible <i>B. anthracis</i> or closely related strain based on high Ba31 counts but genome coverage too low to guarantee seeing the <i>lef</i> 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 <i>B. anthracis</i> strain cured of pXO1 or unsequenced lineage closely related to <i>B. anthracis</i> .
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 <i>B. anthracis</i>