APPENDIX A: LIFECHECK RESOURCES GLOSSARY OF TERMS

Term	Description
Quality Controls	Internal DNA controls are used to ensure accurate and precise qPCR quantification.
Sulfate Reducing Bacteria	Sulfate reducing bacteria (SRB) gain energy for growth by reducing sulfate (SO_4^{2-}) to sulfide (H_2S). Sulfide production can cause souring of a system. SRB can also cause MIC by directly removing electrons from steel surfaces, and indirectly by producing corrosive by-products such as sulfide which react with iron to produce iron sulfide (FeS) deposits.
Methanogens	These anaerobic Archaea produce methane during their metabolism. Can lead to MIC by removing electrons directly from steel surfaces or indirectly through syntrophic interactions with other microbes.
***micH* Methanogens**	Biomarker found in some methanogens that is associated with severe cases of MIC. The *micH* gene encodes a nickel-iron hydrogenase that accelerates MIC attack on iron. Found primarily in biofilms (sessile deposits), but more recently in planktonic environments also.
Iron Reducing Bacteria	Iron reducing bacteria (IRB) gain energy for growth by reducing ferric iron (Fe^{3+}) to ferrous iron (Fe^{2+}). Fe^{3+} reduction can remove protective oxide coatings, exposing the surface beneath to further corrosion.
Halanaerobium	A sulfide producing microbe, increasingly common to oil and gas reservoirs stimulated by hydraulic fracturing methods. Sulfide production occurs via the use of thiosulfate and not sulfate, making this microbe a non-traditional SRB, undetectable by culture media bottle methods. Sulfide production poses both a souring and corrosion-based risk.
Acid Producing Bacteria	Many bacteria form different organic acids during their metabolism, these acids can lead to corrosion of metal surfaces.
Sulfur Cycling	A broad-spectrum qPCR target evaluating the genetic capacity for microbial conversion of sulfur related compounds. Supplementary to the total SRB qPCR primer set, the presence of "sulfur cycling" genes indicates a potential for microbial souring and/or MIC.
Sulfate Reducing Archaea	Sulfate reducing archaea (SRA) gain energy for growth by reducing sulfate (SO_4^{2-}) to sulfide (H_2S). Sulfide production can cause souring of a system, and/or MIC.
Microbe	A unifying term used to describe bacteria and archaea (microscopic, unicellular organisms).
Sulfur Oxidizing Bacteria	A qPCR primer targeting the oxidation of sulfur-related compounds (sulfide, sulfur, thiosulfate) to sulfate. Often considered a beneficial group of microbes as they function to remove sulfide (H_2S) from a system and are stimulated (used) in nitrate injection strategies for souring control. Recent research has indicated select SOB species can cause MIC by oxidizing sulfide to sulfuric acid (H_2SO_4).

Nitrate Reducing Bacteria	Nitrate reducing bacteria (NRB) gain energy for growth by reducing nitrate to nitrite. Nitrate reduction is energetically favorable – NRB can outcompete SRB for growth on the same organics. Nitrite is itself corrosive but is also a potent inhibitor of SRB.
16S	16S is an rRNA gene found universally in all microbes (it encodes for highly important protein building machinery) that is analogous to a fingerprint – it can be used to identify the microbe(s) down to the species level. The 16S gene can be used in several molecular MIC tests.
Archaea	A domain of microorganisms (microbes) very similar, yet distinct from bacteria.
ATP	Adenosine Triphosphate or ATP is the energy currency of cells. All cells (microbe or even human) use energy in the form of ATP to do work.
Bacteria	Single cell, microscopic organisms. Bacteria are found everywhere (capable of living under a very wide range of habitats including extreme environments).
Gene	A functional region/unit of DNA within an organism (microbe). Genes have codes to make proteins that provide a specific function to the microbe. Example, the *dsrAB* gene(s) codes for proteins that are used in sulfate reduction by SRB.
Metagenomics	Sequencing all of the 16S genes (reading all of the fingerprints) in a sample gives a list of all the microbes present, along with relative abundance percentages (semi-quantitative assay).
MIC	Microbiologically Influenced Corrosion (MIC) describes the corrosive damage to surfaces caused by microbes, including bacteria and archaea.
MMM	Molecular Microbiological Methods (MMM) are culture-independent, genetic-based assays for MIC diagnostics.
qPCR	Quantitative Polymerase Chain Reaction (qPCR) is a molecular microbiological method (MMM) that functions by counting/enumerating instances of a gene of interest in a given sample. For example, by counting the number of 16S genes in a sample, one can quantify the total number of microbes.