

Bacterial phylum/class	Clone	% of clones	Highest BLAST search (% Similarity)
<i>α-proteobacteria</i>	MRT19-10 (JX014547)	34	<i>Acidiphilium</i> sp. JL2 (EU711079) (98%)
	MW07E (JX014614)	2.5	<i>Acidiphilium</i> sp. JL2 (97.6%)
<i>γ-proteobacteria</i>	MW 11C (JX014624)	5	<i>Thiobacillus prosperus</i> strain V6 (97.0%)
	MW 04E (JX035877)	2.5	<i>Klebsiella</i> sp. Q11 (95.3%)
<i>Acidobacteria</i>	MW 01C (JX014595)	2.5	<i>Acidobacterium capsulatum</i> ATCC 51196 (97.0%)
<i>Bacteroidetes</i>	MW 12D (JX014629)	55	<i>Meniscus glaucopsis</i> strain ATCC 29398 (95.6%)
	MW 10A (JX014620)	2.5	<i>Meniscus glaucopsis</i> strain ATCC 29398 (93.5%)
	MW 02C (JX014600)	2.5	<i>Sphingobacteria</i> bacterium JAM-BA0302 (95.6%)
	MW 10D (JX014622)	2.5	Cytophaga Bacteria strain XB45 (95.4%)
	MW 02E (JX014602)	7.5	<i>Prolixibacter bellariivorans</i> JCM 13498 (97.1%)
	MW 01A (JX014593)	2.5	<i>Prolixibacter bellariivorans</i> JCM 13498 (97.9%)
<i>Firmicutes</i>	MRT18-01 (JX014555)	56	<i>Alicyclobacillus aeris</i> strain. ZJ-6 (98.7%)
	MRT18-06 (JX014560)	10	<i>Alicyclobacillus aeris</i> strain. ZJ-6 (96.7%)
	MW 04C (JX014606)	2.5	<i>Dehalobacterium formicoaceticum</i> (89.8%)
<i>Clostridia</i>	MW 03C (JX014604)	2.5	<i>Dehalobacter</i> sp. MS (97.3%)
	MW 09A (JX014618)	2.5	<i>Anaerotruncus colihominis</i> strain HKU19 (94.1%)
	MW 08D (JX014616)	2.5	<i>Christensenella minuta</i> (93.0%)
	MW 01E (JX014597)	2.5	<i>Clostridium</i> sp. TG60-1 (93.8%)
	MW 11D (JX01462)	2.5	<i>Alkalibaculum bacchi</i> strain CP11 (95.4%)

Table S1: Clone library 16S rRNA gene sequences from *Mary Rose* stem post wood and iron and sulfur enrichment culture SM18. Clones from co-culture SM18 shaded in dark grey. GenBank numbers in parenthesis.