

SUPPLEMENTARY TABLE

Table S1. Sequence similarities of bacterial bands excised from DGGE.

| Band (Accession N°) | Most closely related organisms (Accession N°) | % Sequence similarity (N° of bases) ^a | Taxonomic group ^b |
|------------------------|--|--|------------------------------|
| CFS | | | |
| 1 (MG736956) | <i>Roseobacter</i> sp. (KT461667) | 99% (516) | Alphaproteobacteria |
| 2 (MG736955) | Uncultured <i>Flavobacterium</i> sp. (KM580154) | 98% (527) | Bacteroidetes |
| 3 (MG736954) | Uncultured Alphaproteobacterium clone (KF177382) | 99% (534) | Alphaproteobacteria |
| 4 (MG736953) | <i>Marinoscillum luteum</i> (NR108992) | 99% (531) | Bacteroidetes |
| 5 (MG736952) | <i>Marinobacter</i> sp. (KC295406) | 99% (541) | Gammaproteobacteria |
| 6 (MG736951) | <i>Saccharospirillum</i> sp. (KM033262) | 99% (430) | Gammaproteobacteria |
| 7 (MG736950) | Uncultured bacterium clone (KM042643) | 94% (478) | Zetaproteobacteria |
| 8 (MG736949) | <i>Polaribacter</i> sp. (AB557510) | 99% (552) | Flavobacteria |
| 9 (MG736948) | Uncultured bacterium clone (JF514279) | 94% (503) | Alphaproteobacteria |
| 10 (MG736947) | Gammaproteobacteria bacterium (CP013099) | 93% (434) | Gammaproteobacteria |
| 11 (MG736946) | Kordiimonadales bacterium (KC295399) | 98% (513) | Alphaproteobacteria |
| 12 (MG736945) | Kordiimonadales bacterium (KC295399) | 99% (514) | Alphaproteobacteria |
| 13 (MG736944) | Kordiimonadales bacterium (KC295367) | 97% (451) | Alphaproteobacteria |
| STS | | | |
| 14 (MG736943) | <i>Sagittula</i> sp. (KP297965) | 96% (505) | Alphaproteobacteria |
| 15 (MG736942) | <i>Paracoccus</i> sp. (KJ786454) | 99% (542) | Alphaproteobacteria |
| 16 (MG736941) | <i>Loktanella salsilacus</i> (KP860543) | 99% (545) | Alphaproteobacteria |
| 17 (MG736940) | <i>Marinobacter</i> sp. (KC295406) | 99% (542) | Gammaproteobacteria |
| 18 (MG736939) | <i>Reichenbachiella agariperforans</i> (NR113854) | 97% (381) | Bacteroidetes |
| 19 (MG736938) | Flammeovirgaceae bacterium (KM279027) | 99% (533) | Bacteroidetes |
| 20 (MG736937) | Flammeovirgaceae bacterium (KM279027) | 99% (538) | Bacteroidetes |
| 21 (MG736936) | Flammeovirgaceae bacterium (KM279027) | 99% (538) | Bacteroidetes |
| 22 (MG736935) | <i>Marinoscillum luteum</i> (NR108992) | 99% (539) | Bacteroidetes |
| Seawater Bulk | | | |
| 23 (MG736934) | Uncultured bacterium clone (JQ199247) | 99% (497) | Bacteroidetes/Flavobacteria |
| 24 (MG736933) | Uncultured bacterium clone (KM520728) | 97% (532) | Cyanobacteria |
| 25 (MG736932) | Uncultured Rhodobacteraceae bacterium clone (HQ242021) | 96% (500) | Alphaproteobacteria |
| 26 (MG736931) | Uncultured <i>Synechococcus</i> sp. (AY033297) | 99% (526) | Cyanobacteria |
| 27 (MG736930) | Uncultured marine bacterium clone (KM223850) | 99% (528) | Bacteroidetes/Flavobacteria |
| 28 (MG736929) | Uncultured Alphaproteobacterium clone (DQ436582) | 97% (443) | Alphaproteobacteria |

^a Number of bases used to calculate percentage of similarity with reference sequence.

^b Uncultured clone taxonomic groups were inferred through the phylogenetic analysis of the partial sequences.

SUPPLEMENTARY FIGURE

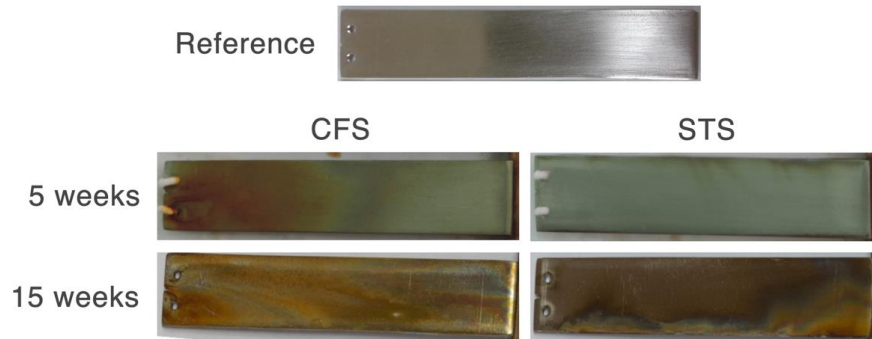


Figure S1. Visual analysis of the coupons after exposure to natural seawater. Representative images of visual inspection of the 316L stainless steel coupons that were under different conditions: i) Reference, coupons not exposed to natural seawater. ii) CFS, coupons continuously exposed to natural seawater for 5 and 15 weeks. iii) STS, coupons exposed to simulated tidal conditions for 5 and 15 weeks.