**Additional file**

to

**In-situ pilot application of nZVI embedded in activated carbon** **for remediation of chlorinated ethene contaminated groundwater: effect on microbial communities**

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**Table S1**. Specific primer pairs used for qPCR method

|  |  |  |  |  |  |
| --- | --- | --- | --- | --- | --- |
| **Name** | **Sequence (5′→3′)** | **Product size (bp)** | **Tm(°C)** | **Target organism(s); gene(s)** | **Reference** |
| U16SRT-F | ACTCCTACGGGAGGCAGCAGT | 180 | 60 | *Bacteria*; 16S rRNA genes | [1] |
| U16SRT-R | TATTACCGCGGCTGCTGGC |
| vcrA880F | CCCTCCAGATGCTCCCTTTA | 139 | 60 | *Dehalococcoides* sp.strain VS; *vcrA* | [2] |
| vcrA1018R | ATCCCCTCTCCCGTGTAACC |
| bvcA277F | TGGGGACCTGTACCTGAAAA | 247 | 60 | *Dehalococcoides* sp. strain BAV-1; *bvcA* | [2] |
| bvcA523R | CAAGACGCATTGTGGACATC |
| Dsb406F | GTACGACGAAGGCCTTCGGGT | 213 | 60 | *Desulfitobacterium* sp.;16S rRNA genes | [3] |
| Dsb619R | CCCAGGGTTGAGCCCTAGGT |
| DHC793f | GGGAGTATCGACCCTCTCTG | 191 | 60 | *Dehalococcoides* sp.;16S rRNA genes | [4] |
| DHC946r | CGTTYCCCTTTCRGTTCACT |
| RTC-f | ACCCTGGTCGGTGTKSTYTC | 106 | 60 | ethenotrophs; α subunit of AkMO, *EtnC* | [5] |
| RTC-r | TCATGTAMGAGCCGACGAAGTC |
| RTE-f | CAGAAYGGCTGYGACATYATCCA | 151 | 60 | ethenotrophs; α subunit of EaCoMT, *EtnE* | [5] |
| RTE-r | CSGGYGTRCCCGAGTAGTTWCC |
| Dre441F | GTTAGGGAAGAACGGCATCTGT | 205 | 55 | *Dehalobacter* sp.; 16S rRNA genes | [3] |
| Dre645R | CCTCTCCTGTCCTCAAGCCATA |
| Dhg1243f | GGYACAATGGGTTGCCACCGG | 127 | 68 | *Dehalogenimonas* sp.; 16S rRNA genes | [6] |
| Dhg1351r | AACGCGCTATGCTGACACGCGT |
| Gall-122F-H | ATATCGGAACATATCCGGAAGT | 262 | 60 | *Gallionella ferruginea*; 16S r RNA gene | [7] |
| Gall-384R-H | GGTATGGCTGGATCAGGC |
| Geo564f | AAGCGTTGTTCGGAWTTAT | 276 | 55 | Geobacteraceae; 16S r RNA genes | [8] |
| Geo840r | GGCACTGCAGGGGTCAATA |

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**Figure S1.** Alpha-diversity measures: comparison of wells based on Chao 1 and Inv. Simpson alpha-diversity indexes.

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