Weston Solutions qPCR Report - Sample Results

**Client:** County of San Diego  
**Project:** Rainbow Creek  
**Date Received:** 08/19 and 08/20/19  
**n Samples:** 14  
**Survey:** Event 3  
**No Template Controls:** passed  
**Positive Extraction Controls:** passed  
**Inhibition Control:** HF183 (B.dorei)  
**File name(s):** Plate S46 HF183TMaMan dd ka  
**Date ddPCR:** 09/04/19 Plate 547

<table>
<thead>
<tr>
<th>Sample ID</th>
<th>Site ID</th>
<th>Weston DNA ID</th>
<th>Date Sampled</th>
<th>Matrix</th>
<th>Sample Result</th>
<th>Qualifier</th>
<th>Sample Concentration</th>
<th>Sample Stdev</th>
<th>Units</th>
<th>SLDO*</th>
<th>SLQQ*</th>
<th>cpr</th>
<th>Inhibition Result 1</th>
</tr>
</thead>
<tbody>
<tr>
<td>MS4-SMG-095</td>
<td>MS4-SMG-095</td>
<td>6842MS4-SMG-095</td>
<td>08/19/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>MS4-SMG-057</td>
<td>MS4-SMG-057</td>
<td>6844MS4-SMG-057</td>
<td>08/19/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>MS4-SMG-057-DUP</td>
<td>MS4-SMG-057-DUP</td>
<td>6846MS4-SMG-057-DUP</td>
<td>08/19/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>FB-081919</td>
<td>FB-081919</td>
<td>6848FB-081919</td>
<td>08/19/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>HST01</td>
<td>HST01</td>
<td>6850HST01</td>
<td>08/19/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>RVT02</td>
<td>RVT02</td>
<td>6854RVT02</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>RBC02</td>
<td>RBC02</td>
<td>6856RBC02</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>RBC04</td>
<td>RBC04</td>
<td>6858RBC04</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>RGT01</td>
<td>RGT01</td>
<td>6860RGT01</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>SMG05</td>
<td>SMG05</td>
<td>6862SMG05</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>WGT01</td>
<td>WGT01</td>
<td>6864WGT01</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>SMG06</td>
<td>SMG06</td>
<td>6866SMG06</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>SMG06-DUP</td>
<td>SMG06</td>
<td>6868SMG06-DUP</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
<tr>
<td>FB-082019</td>
<td>FB-082019</td>
<td>6870FB-082019</td>
<td>08/20/19</td>
<td>FW</td>
<td>ND</td>
<td>§&lt;</td>
<td>14</td>
<td>0</td>
<td>copies/100mL</td>
<td>43</td>
<td>43</td>
<td>1</td>
<td>0</td>
</tr>
</tbody>
</table>

**Abbreviations:**  
Avg = Average; BDL = Below Detection Limit; cpr = copies per reaction; Cq = quantification (threshold) cycle; DNQ = Detectable But Not Quantifiable; FB = Field Blank; FW = Fresh Water; GW = Ground Water; L = Salt Water; SW = Storm Water; LOD = Limit of Quantification; LOQ = Lower Limit of Quantification; LOD = Limit of Detection; n=number; N/A = Not Applicable; ND = Not Detected; NDsub = substitution value for nondetects; PCR = Polymerase chain reaction; rsx = reactions; StdDev = Standard Deviation; sub = substitution; TSC = Target Sequence Copies; ROQ = Range of Quantification; SLLOQ = Sample Specific Lower Limit of Quantification; SLOD = Sample Specific Limit of Detection.

**Footnotes:**  
1Sample Process Control (SPC), Sketa assay for salmon sperm.  
2Inhibition Control = assay used for 2 well spike with DNA dilution method.  
3Suggestion for conversion of sample result into categorical results: ROQ and DNQ = positive; ND = negative; BDL = equivocal (see explanation on Part B).  
4If shown: Average computed for ND result by a) qPCR: substituting Cq with maximum number of cycles (Boehm et al., 2013) or b) ddPCR: substituting with 1 cpr.  
5Concentration = mean of at least 3 technical replicates.  
6Standard Deviation of at least 3 technical replicates.  
7For enterococci, results are given in Target Sequence Copies (TSC), as per EPA Method 1611 (standard concs in TSC/ul = copies/ul x 4).  
8SLLOQ and SLOD: sample specific detection and quantification limits calculated based on sample specific processing volumes see more information on Part B.  
9Inhibition: 0 = no inhibition observed, 1 = inhibition observed, but overcome in diluted sample; 2 = inhibition not overcome in diluted sample: The given concentration may be underestimated for positive samples, 3 = Dilution needed to overcome inhibition did not yield amplification. Given concentration may be underestimated. NT = not tested. See Part B for additional comments.
Weston Solutions qPCR Report - Standard Curve Metrics

**Client:** County of San Diego  
**Project:** Rainbow Creek  
**Survey:** Event 3  
**Date Received:** 08/19 and 08/20/19

### QA/QC Information

**Assay** Human Bacteroidales - HF183TMCaMan

<table>
<thead>
<tr>
<th>Method Detection Limits</th>
<th>ND sub</th>
<th>LOD</th>
<th>LLOQ</th>
</tr>
</thead>
<tbody>
<tr>
<td>cpr (copies per reaction)</td>
<td>1.0</td>
<td>3</td>
<td>3</td>
</tr>
</tbody>
</table>

**standard source:** genomic DNA

**Samples:**

- **copies per genome:** 7
- **AVG Filtration Volume:** 100 mL  
  (eluted 1/2 volume to keep SLODs analog to evts 1 and 2)

Sample result calculations use cpr values based on the following definitions:

- **ND:** Cq=maximum cycle number, negative result.
- **BDL:** 0<Cq≤LOD, Equivocal result.
- **DNQ:** LOD<Cq≤LLOQ, positive binary result.
- **ROQ:** Cq>LLOQ, positive result.
- **LLOQ:** lowest concentration with amplification rate of 100% (>20 reps).

In addition, SLOD and SLLOQ values are provided. These are sample specific detection limits which take into account sample processing, for example volumes or mass.

**Categorical Results:**

- **ROQ and DNQ = positive; ND = negative**
- **BDL results are categorized as "equivocal" because a signal was observed below the limit of detection. The result can therefore not be classified as either a negative or positive with great confidence. Weston uses BDL concentration values to compute averages unless directed otherwise by Client. Sites with chronic BDL results may warrant additional monitoring.**

**Abbreviations:**

- **Avg** = Average; **BDL** = Below Detection Limit; **cpr** = copies per reaction; **Cq** = quantification (threshold) cycle; **DNQ** = Detectable But Not Quantifiable; **FB** = Field Blank; **LLOQ** = Lower Limit of Quantification; **LOD** = Limit of Detection; **n** = number; **N/A** = Not Applicable; **ND** = Not Detected; **NDsub** = substitution value for nondetects; **PCR** = Polymerase chain reaction; **rxs** = reactions; **StdDev** = Standard Deviation; **sub** = substitution; **TSC** = Target Sequence Copies; **ROQ** = Range of Quantification; **SLLOQ** = Sample Specific Lower Limit of Quantification; **SLOD** = Sample Specific Limit of Detection.

---

**Satomi Yonemasu**  
QC Officer (Satomi Yonemasu)  
9/5/2019  
Date

Report template version 7.04