

Supplementary materials

Comparative metagenomic analysis of electrogenic microbial communities in differentially inoculated swine wastewater-fed microbial fuel cells

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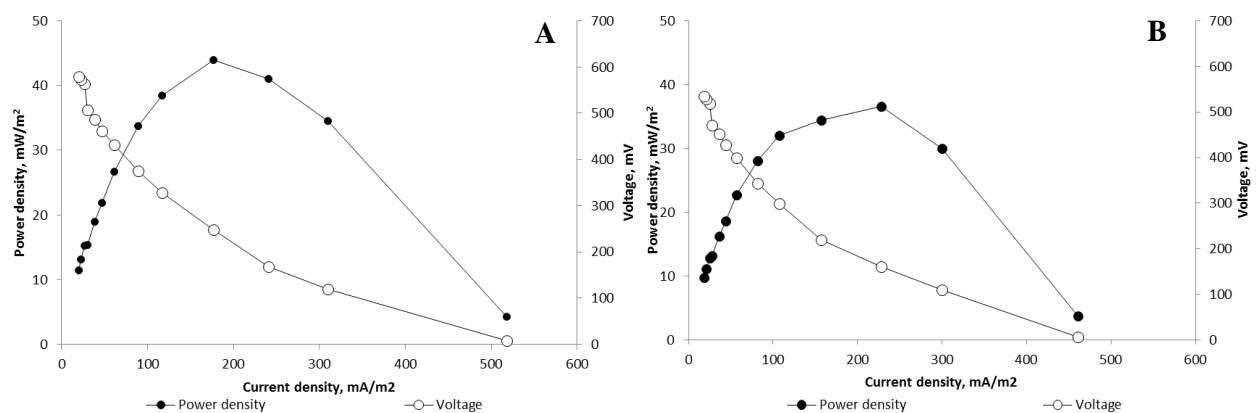


Fig. S1. Cell voltage and power density vs. current density (cell polarization) of MFCs (A) inoculated with swine sludge (SS); (B) inoculated with industrial granular brewery sludge (IGSB). Open circles, voltage; closed circles, power density.

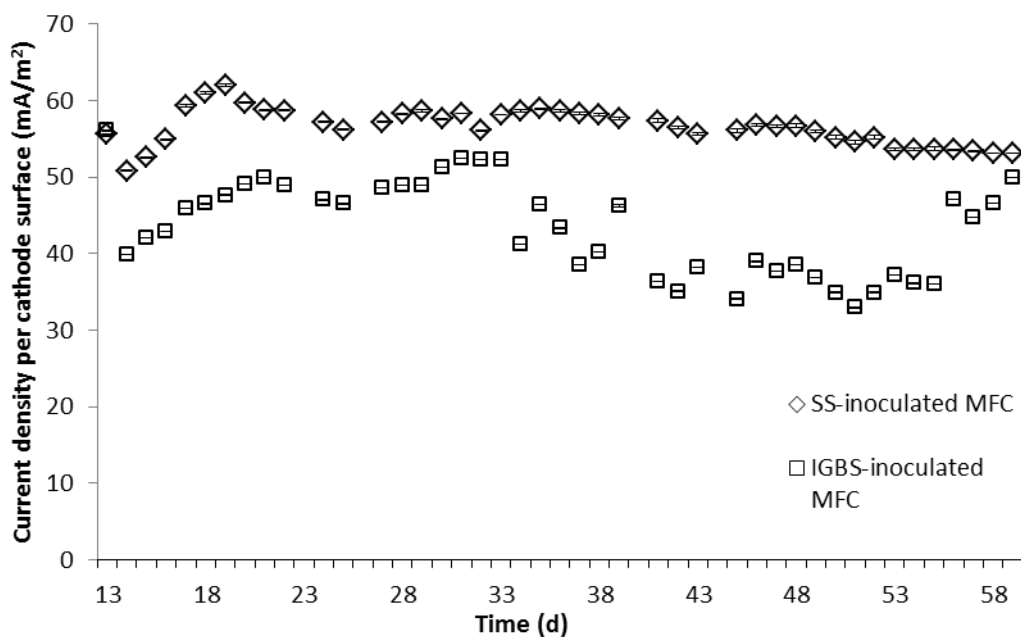


Fig. S2. Current generation during swine wastewater treatment by MFCs inoculated with swine waste sludge and brewery sludge. Mean data from duplicate experiments; error bars indicating \pm SD to not exceed the diameter of the data point symbols. Open boxes, SS-inoculated MFC; open diamonds, IGBS-inoculated MFC.

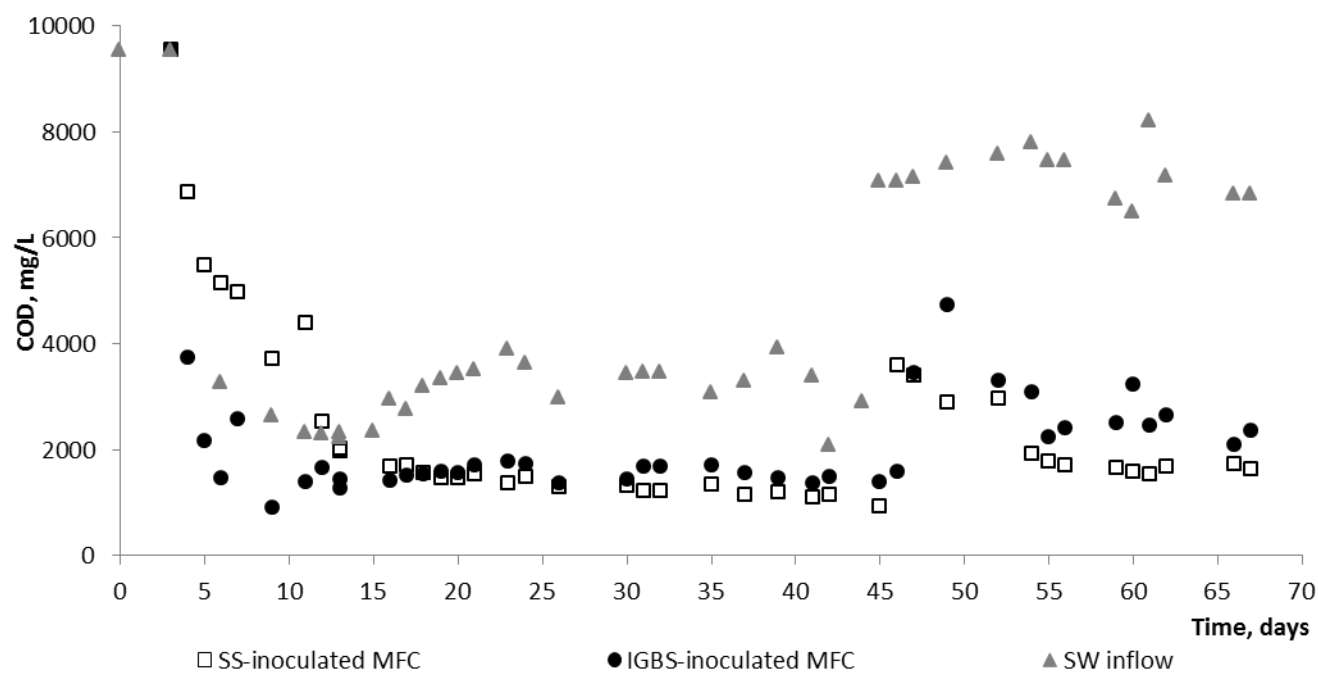


Fig. S3. Total COD concentrations in SW feed and within MFCs inoculated with swine waste sludge and industrial granular brewery sludge. Squares, SS-inoculated MFC; circles, IGBS-inoculated MFC; Mean data from duplicate experiments.

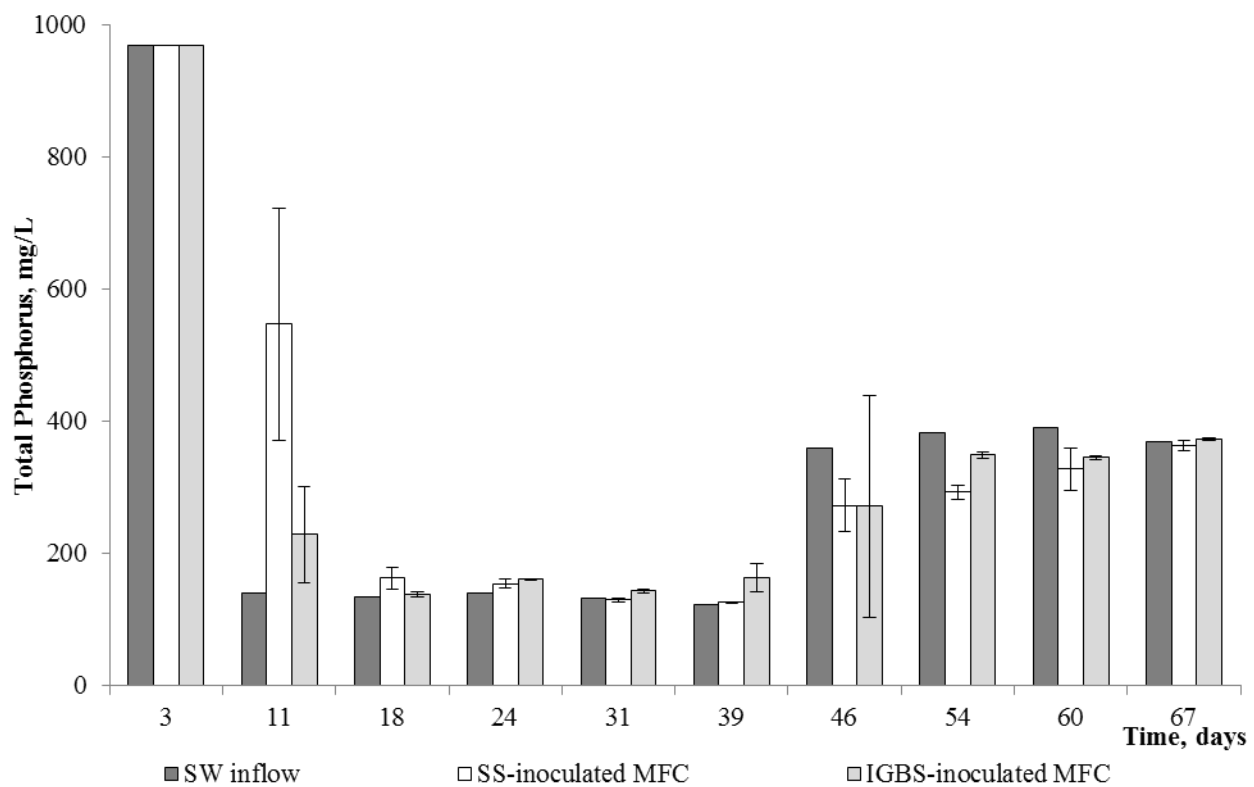


Fig. S4. Change in total phosphorus ($\text{PO}_4^{3-}\text{-P}$) in inflow and outflows of MFCs inoculated with swine wastewater sludge (SS) and industrial granular brewery sludge (IGBS). Mean data from duplicate experiments with error bars ($\pm\text{SD}$).

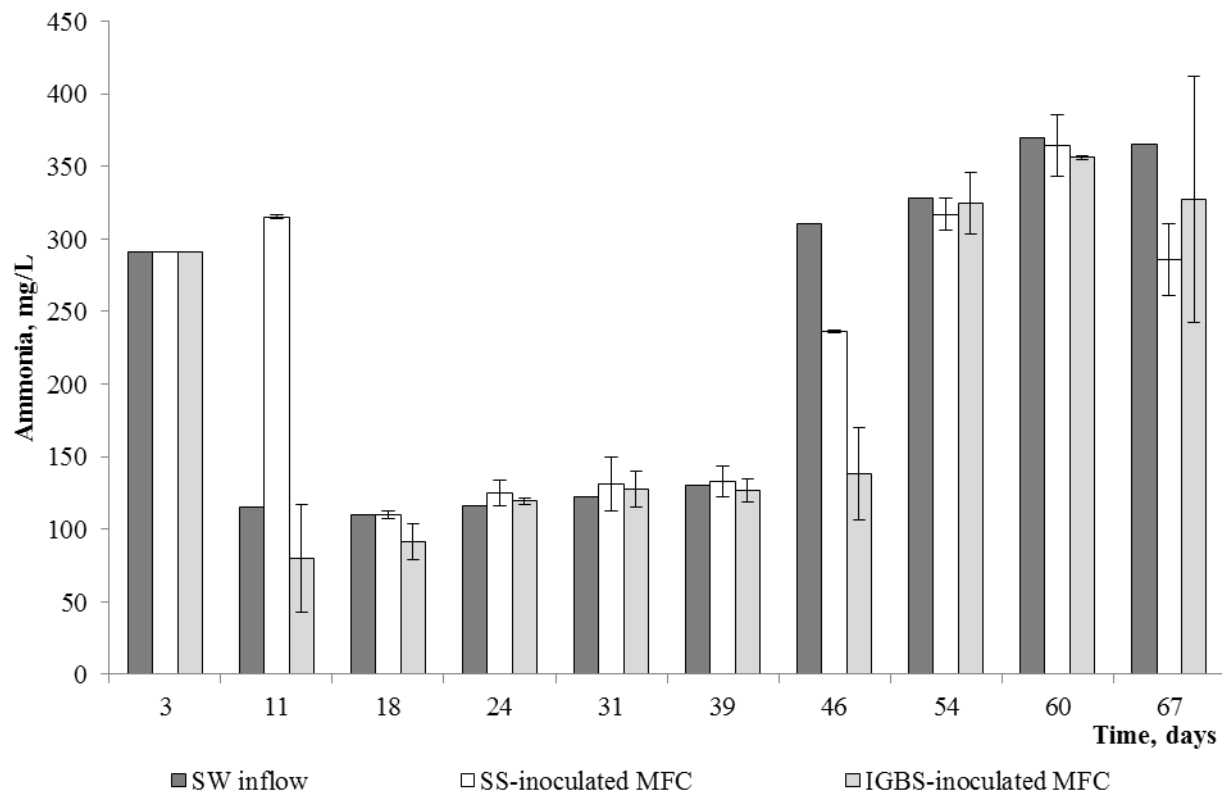


Fig. S5. Changes in ammonia nitrogen ($\text{NH}_4\text{-N}$) in inflow and outflows of MFCs inoculated with swine wastewater sludge (SS) and industrial granular brewery sludge (IGBS). Mean data from duplicate experiments with error bars ($\pm\text{SD}$).

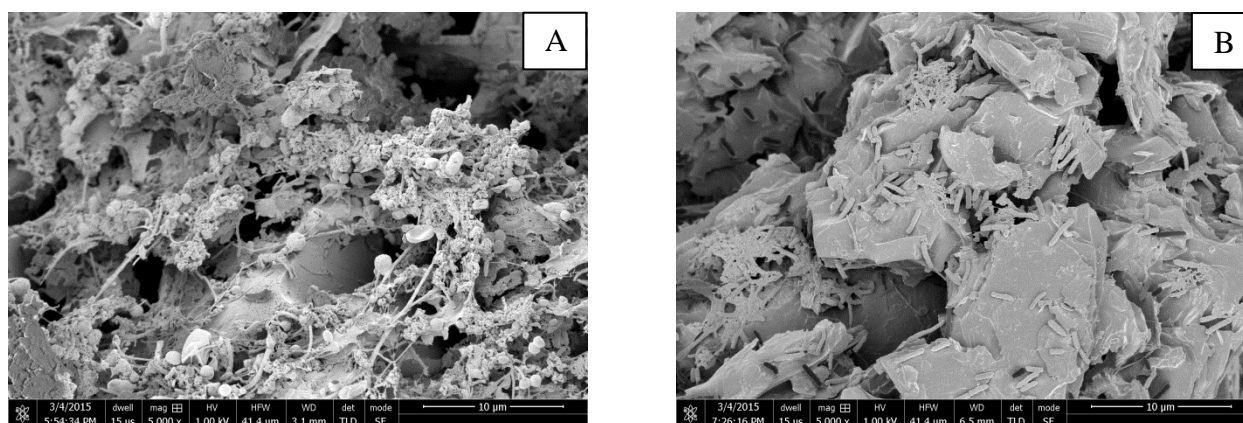


Fig. S6. SEM images of the anodic biofilms the MFCs inoculated with (A) swine waste and (B) brewery sludge. Samples of anode surfaces (activated carbon granules and fiber) the MFCs were taken after 67 days of swine wastewater treatment upon disassembling the MFCs. Slices of anode electrodes (1 cm²) were briefly rinsed with deionized water and fixed in 2.5% glutaraldehyde for 2 h, further in 1% osmium tetroxide. Dehydration of microbial biofilms was carried out using a series of ethanol–water solutions (25, 50, 75, 95, 100%). After gold coating, the obtained specimens were observed using a Focused Ion Beam Scanning electron microscope (Helios NanoLab 650, USA). High resolution images were acquired using an accelerating voltage of 20 kV at a working distance of 3.1–6.5 mm.

Table S1. Summary of MFC operation modes.

| Step | Period, days | Feeding mode | HRT, h | Dilution rate, times | Initial pH | External resistance | Description |
|------|--------------|---|--------|----------------------|------------|---------------------------------|---|
| I | 0-3 | Inoculation of units | - | - | 6.8 | Open circuit | Biofilm formation |
| II | 3-12 | Every 2 days | 48 | - | 6.8 | Open circuit | Biofilm adaptation |
| III | 13-35 | every 2 h, during 2 min 34 sec, V=180mL/day | 24 | 6 | 6.8 | Closed circuit (1000 Ω) | Treatment of wastes |
| IV | 36-41 | every 2 h, during 2 min 34 sec, V=180mL/day | 24 | 6 | 5.5 | Closed circuit (1000 Ω) | Influence of initial pH on treatment processes |
| V | 42-44 | every 2 h, during 2 min 34 sec, V=180mL/day | 24 | 6 | 6.8 | Closed circuit (1000 Ω) | Preparing to mode changing |
| VI | 45-52 | every 2 h, during 2 min 34 sec, V=180mL/day | 24 | 2 | 6.8 | Closed circuit (1000 Ω) | Increasing of initial COD level |
| VII | 53-59 | every 2 h, during 1 min 34 sec, V=90mL/day | 48 | 2 | 6.8 | Closed circuit (1000 Ω) | Optimization of MFC wastes treatment processes |
| VIII | 60-62 | every 2 h, during 1 min 34 sec, V=90mL/day | 48 | 2 | 6.8 | closed circuit (10 Ω) | Influence of low external resistance on MFC wastes treatment |
| IX | 63-64 | every 2 h, during 1 min 34 sec, V=90mL/day | 48 | 2 | 6.8 | From 0 – 2100 Ω | Optimization of external resistance on MFC wastes treatment |
| X | 65-66 | every 2 h, during 1 min 34 sec, V=90mL/day | 48 | 2 | 6.8 | closed circuit (100 Ω) | Influence of middle external resistance on MFC wastes treatment |
| XI | 67 | The End of MFC treatment | | | | | |

Table S2. VFA concentrations in SS-inoculated MFCs.

| | Concentration, mg/L | | | | | | |
|------------|-------------------------|---------------------------|------------------------|--------------------------|--------------------------|-------------------------|-------------------------|
| Time, days | Acetate | Propionate | Isobutyrate | Butyrate | Isovalerate | Valerate | Hexanoate |
| 13 | 33.73 (± 2.08) | 83.44 (± 4.37) | 4.10 (± 0.37) | 30.27 (± 3.83) | 21.16 (± 1.66) | 17.51 (± 2.10) | 11.99 (± 1.88) |
| 18 | 20.04 (± 3.0) | 84.70 (± 8.31) | 6.44 (± 0.53) | 36.34 (± 11.04) | 34.49 (± 0.77) | 38.34 (± 0.79) | 20.43 (± 4.52) |
| 24 | 11.63 (± 2.26) | 55.00 (± 20.76) | 4.11 (± 1.59) | 19.81 (± 14.03) | 22.16 (± 10.57) | 16.39 (± 8.05) | 9.59 (± 5.29) |
| 31 | 6.65 (± 1.01) | 47.95 (± 6.19) | 4.21 (± 0.96) | 9.47 (± 6.62) | 21.46 (± 7.66) | 13.87 (± 6.01) | 7.46 (± 4.57) |
| 39 | 10.61 (± 2.46) | 55.36 (± 15.37) | 3.30 (± 1.36) | 4.27 (± 2.29) | 13.75 (± 8.09) | 8.95 (± 5.61) | 4.30 (± 3.27) |
| 46 | 45.79 (± 3.77) | 202.24 (± 19.87) | 8.26 (± 0.85) | 67.45 (± 14.50) | 49.09 (± 5.37) | 60.49 (± 8.88) | 40.22 (± 9.13) |
| 52 | 9.70 (± 3.09) | 105.76 (± 23.07) | 5.53 (± 1.18) | 3.27 (± 1.85) | 63.22 (± 1.92) | 11.93 (± 6.66) | 7.78 (± 2.37) |
| 60 | 9.43 (± 1.28) | 38.01 (± 13.65) | 0.90 (± 0.49) | 4.91 (± 0.45) | 5.39 (± 2.11) | 3.12 (± 0.14) | 2.64 (± 0.01) |
| 67 | 7.06 (± 3.65) | 59.98 (± 51.37) | 0.90 (± 0.78) | 0.80 (± 0.46) | 5.62 (± 4.79) | 0.98 (± 0.88) | 0.51 (± 0.29) |

* (\pm) Range of variation represent duplicate experiments.

Table S3. VFA concentrations in IGBS-inoculated MFCs.

| | Concentration, mg/L | | | | | | |
|------------|-------------------------|---------------------------|------------------------|--------------------------|--------------------------|-------------------------|-------------------------|
| Time, days | Acetate | Propionate | Isobutyrate | Butyrate | Isovalerate | Valerate | Hexanoate |
| 13 | 18.22 (± 1.54) | 27.44 (± 6.99) | 1.94 (± 0.39) | 12.50 (± 2.03) | 6.65 (± 0.62) | 7.92 (± 0.07) | 6.52 (± 0.06) |
| 18 | 26.14 (± 6.64) | 69.00 (± 31.26) | 4.44 (± 0.37) | 33.95 (± 13.52) | 23.06 (± 0.78) | 25.57 (± 4.79) | 20.80 (± 3.00) |
| 24 | 31.67 (± 3.00) | 68.73 (± 2.64) | 5.15 (± 0.76) | 30.44 (± 1.19) | 27.37 (± 4.89) | 20.64 (± 0.89) | 15.32 (± 0.44) |
| 31 | 16.86 (± 2.72) | 47.74 (± 14.49) | 4.19 (± 0.58) | 17.47 (± 6.65) | 26.34 (± 3.80) | 17.43 (± 5.81) | 13.35 (± 5.01) |
| 39 | 14.04 (± 0.90) | 45.07 (± 3.85) | 3.29 (± 0.03) | 12.09 (± 2.08) | 18.30 (± 0.59) | 11.04 (± 1.10) | 7.03 (± 0.51) |
| 46 | 16.14 (± 3.36) | 48.94 (± 11.57) | 3.09 (± 0.36) | 12.85 (± 3.71) | 20.28 (± 2.44) | 12.50 (± 3.59) | 8.26 (± 2.08) |
| 52 | 15.91 (± 2.02) | 85.48 (± 19.12) | 7.02 (± 1.64) | 17.50 (± 2.56) | 56.10 (± 11.26) | 21.02 (± 3.93) | 14.08 (± 3.56) |
| 60 | 15.05 (± 1.45) | 77.66 (± 6.39) | 5.48 (± 0.24) | 10.10 (± 2.47) | 43.23 (± 0.30) | 12.70 (± 3.29) | 6.76 (± 1.63) |
| 67 | 8.78 (± 3.72) | 108.65 (± 25.54) | 6.24 (± 1.60) | 4.50 (± 1.12) | 40.89 (± 7.41) | 12.26 (± 3.90) | 4.87 (± 0.83) |

* (\pm) Range of variation represent duplicate experiments.

Table S4. Diversity of dominated species in the SW, inocula, anodic and planktonic microbial communities of SS- and IGBS-inoculated MFCs.

Total hit numbers of class *Deltaproteobacteria*

| | Swine wastewater | SS-inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|----------------------------|---------------------|--------------------------------|---|--------------------------------------|---|--------|-----------------|
| <i>Deltaproteobacteria</i> | 28255 | 318508.75 | 70918.25 | 487004.25 | 142937.5 | 149374 | 44033.5 |

Prokaryotes abundance, *Geobacter* species (17 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|----------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Geobacter metallireducens</i> | 824 | 106093 | 2309 | 115774 | 4840 | 5240 | 1152 |
| <i>Geobacter sulfurreducens</i> | 853 | 43073 | 2262 | 80771 | 5860 | 6654 | 1308 |
| <i>Geobacter uraniireducens</i> | 1008 | 14489 | 2571 | 36737 | 6470 | 7026 | 1497 |
| <i>Geobacter lovleyi</i> | 551 | 7149 | 1416 | 31628 | 3062 | 2152 | 680 |
| <i>Geobacter bemidjiensis</i> | 495 | 4420 | 1140 | 12923 | 2543 | 2753 | 662 |
| <i>Geobacter</i> sp. FRC-32 | 267 | 4272 | 895 | 11054 | 2221 | 2458 | 509 |
| <i>Geobacter</i> sp. M18 | 140 | 4092 | 810 | 9996 | 2037 | 2251 | 378 |
| <i>Geobacter</i> sp. M21 | 216 | 2606 | 485 | 6313 | 1082 | 1225 | 292 |
| uncultured <i>Geobacter</i> sp. | 1 | 16 | 8 | 141 | 14 | 13 | 1 |
| <i>Geobacter</i> sp. | 0 | 14 | 11 | 48 | 10 | 10 | 4 |
| <i>Geobacter psychrophilus</i> | 0 | 0 | 0 | 13 | 0 | 0 | 0 |
| <i>Geobacter grbiciae</i> | 0 | 6 | 0 | 6 | 0 | 0 | 0 |
| <i>Geobacter chapelleii</i> | 0 | 0 | 0 | 11 | 0 | 0 | 0 |
| <i>Geobacter thiogenes</i> | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| <i>Geobacter</i> sp. Ply1 | 0 | 0 | 0 | 3 | 0 | 0 | 0 |
| <i>Geobacter pelophilus</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Geobacter</i> sp. Ply4 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Prokaryotes abundance, *Pelobacter* species (5 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|--------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Pelobacter propionicus</i> | 1227 | 12472 | 2919 | 65096 | 6367 | 6325 | 1605 |
| <i>Pelobacter carbinolicus</i> | 987 | 6022 | 1965 | 4919 | 3596 | 4013 | 1186 |
| <i>Pelobacter acidigallici</i> | 1 | 2 | 2 | 4 | 7 | 14 | 2 |
| <i>Pelobacter acetylenicus</i> | 0 | 0 | 0 | 2 | 2 | 3 | 0 |
| <i>Pelobacter massiliensis</i> | 0 | 0 | 0 | 0 | 1 | 1 | 0 |

Prokaryotes abundance, *Desulfovibrio* species (18 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|-------------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Desulfovibrio vulgaris</i> | 2352 | 7150 | 2309 | 6780 | 3797 | 3134 | 2945 |
| <i>Desulfovibrio desulfuricans</i> | 2313 | 3910 | 1282 | 5324 | 2042 | 967 | 3825 |
| <i>Desulfovibrio alaskensis</i> | 1094 | 3870 | 1495 | 3510 | 2594 | 2556 | 1359 |
| <i>Desulfovibrio magneticus</i> | 462 | 3831 | 1089 | 4067 | 1803 | 1581 | 619 |
| <i>Desulfovibrio</i> sp. FW1012B | 223 | 2805 | 679 | 2882 | 1137 | 1009 | 371 |
| <i>Desulfovibrio fructosovorans</i> | 203 | 2539 | 707 | 2492 | 1186 | 939 | 326 |
| <i>Desulfovibrio</i> sp. 3_1_syn3 | 983 | 1181 | 465 | 1784 | 748 | 302 | 1566 |
| <i>Desulfovibrio aespoeensis</i> | 215 | 2393 | 625 | 1368 | 943 | 937 | 287 |
| <i>Desulfovibrio salexigens</i> | 397 | 1635 | 695 | 1133 | 957 | 807 | 390 |
| <i>Desulfovibrio piger</i> | 975 | 667 | 335 | 790 | 404 | 285 | 1129 |
| <i>Desulfovibrio gigas</i> | 11 | 67 | 28 | 79 | 64 | 62 | 19 |
| <i>Desulfovibrio</i> sp. | 2 | 10 | 6 | 5 | 3 | 3 | 3 |
| <i>Desulfovibrio africanus</i> | 3 | 4 | 1 | 1 | 0 | 0 | 0 |
| <i>Desulfovibrio butyratiphilus</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Desulfovibrio</i> sp. JD160 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| <i>Desulfovibrio</i> sp. LG-2009 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Desulfovibrio burkinensis</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Desulfovibrio sulfodismutans</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Prokaryotes abundance, *Syntrophus* species (1 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|----------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|-------|-----------------|
| <i>Syntrophus aciditrophicus</i> | 1038 | 11935 | 11550 | 10281 | 19335 | 27383 | 5232 |

Prokaryotes abundance, *Syntrophobacter* species (2 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|-------------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|-------|-----------------|
| <i>Syntrophobacter fumaroxidans</i> | 958 | 8255 | 4860 | 18654 | 20536 | 17987 | 2615 |
| <i>Syntrophobacter pfennigii</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Total hit numbers of class *Gammaproteobacteria*

| | Swine wastewater | SS-inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|----------------------------|---------------------|--------------------------------|---|--------------------------------------|---|--------|-----------------|
| <i>Gammaproteobacteria</i> | 513175.5 | 97953 | 49742 | 131568.75 | 142295.75 | 213992 | 506025.5 |

Prokaryotes abundance, *Acinetobacter* species (56 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGB S | Swine sludge |
|-------------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|----------|-----------------|
| <i>Acinetobacter baumannii</i> | 38509 | 5443 | 3970 | 3326 | 5368 | 309 | 14869 |
| <i>Acinetobacter sp. ADP1</i> | 17655 | 2505 | 1795 | 1698 | 2532 | 167 | 7012 |
| <i>Acinetobacter johnsonii</i> | 16163 | 2146 | 1596 | 1073 | 1831 | 42 | 6034 |
| <i>Acinetobacter lwoffii</i> | 15299 | 1874 | 1364 | 1018 | 1571 | 56 | 5778 |
| <i>Acinetobacter oleivorans</i> | 6340 | 810 | 587 | 447 | 815 | 42 | 2431 |
| <i>Acinetobacter radioresistens</i> | 5024 | 722 | 536 | 477 | 695 | 42 | 1923 |
| <i>Acinetobacter junii</i> | 3322 | 620 | 407 | 333 | 718 | 29 | 1300 |
| <i>Acinetobacter haemolyticus</i> | 2449 | 413 | 261 | 229 | 457 | 26 | 932 |
| <i>Acinetobacter calcoaceticus</i> | 1583 | 223 | 158 | 146 | 246 | 28 | 646 |
| <i>Acinetobacter sp. ATCC 27244</i> | 1556 | 249 | 183 | 143 | 305 | 14 | 568 |
| <i>Acinetobacter pittii</i> | 1509 | 204 | 160 | 148 | 191 | 16 | 589 |
| <i>Acinetobacter nosocomialis</i> | 1174 | 196 | 119 | 144 | 187 | 14 | 469 |
| <i>Acinetobacter venetianus</i> | 165 | 18 | 13 | 8 | 27 | 4 | 75 |
| <i>Acinetobacter sp.</i> | 59 | 11 | 7 | 6 | 10 | 0 | 18 |
| <i>Acinetobacter sp. LUH5605</i> | 42 | 7 | 6 | 2 | 7 | 0 | 16 |
| <i>Acinetobacter sp. P8-3-8</i> | 27 | 4 | 5 | 2 | 5 | 0 | 12 |
| <i>Acinetobacter schindleri</i> | 28 | 1 | 0 | 0 | 3 | 0 | 12 |
| <i>Acinetobacter guillouiae</i> | 26 | 2 | 2 | 2 | 2 | 0 | 7 |
| <i>Acinetobacter sp. SUN</i> | 26 | 1 | 1 | 2 | 2 | 0 | 8 |
| <i>Acinetobacter sp. NFM2</i> | 22 | 2 | 2 | 4 | 3 | 0 | 2 |
| <i>Acinetobacter sp. SE19</i> | 12 | 5 | 1 | 3 | 6 | 0 | 5 |
| <i>Acinetobacter sp. M-1</i> | 15 | 1 | 0 | 0 | 4 | 0 | 3 |
| <i>Acinetobacter sp. XMZ-26</i> | 16 | 0 | 0 | 0 | 0 | 0 | 8 |
| <i>Acinetobacter sp. MO</i> | 9 | 0 | 0 | 0 | 0 | 0 | 6 |
| <i>Acinetobacter baylyi</i> | 6 | 0 | 0 | 0 | 2 | 0 | 4 |
| <i>Acinetobacter sp. BD413</i> | 7 | 1 | 0 | 0 | 1 | 0 | 3 |
| <i>Acinetobacter townneri</i> | 8 | 0 | 0 | 0 | 0 | 0 | 4 |
| <i>Acinetobacter sp. CR1</i> | 9 | 0 | 0 | 0 | 0 | 0 | 3 |
| <i>Acinetobacter bereziniae</i> | 8 | 0 | 0 | 0 | 0 | 0 | 3 |
| <i>Acinetobacter sp. AD513A</i> | 3 | 3 | 1 | 0 | 1 | 0 | 2 |
| <i>Acinetobacter bouvetii</i> | 4 | 1 | 0 | 0 | 1 | 0 | 3 |
| <i>Acinetobacter sp. no. 6</i> | 4 | 1 | 1 | 0 | 0 | 0 | 1 |
| <i>Acinetobacter sp. 1690</i> | 5 | 0 | 0 | 0 | 0 | 0 | 3 |
| <i>Acinetobacter genomosp. 13</i> | 4 | 0 | 0 | 1 | 0 | 0 | 2 |
| <i>Acinetobacter sp. NCIMB9871</i> | 2 | 0 | 0 | 0 | 1 | 0 | 2 |
| <i>Acinetobacter tandooii</i> | 6 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Acinetobacter sp. DM-2005</i> | 4 | 0 | 0 | 0 | 0 | 0 | 2 |
| <i>Acinetobacter sp. G16(2009)</i> | 4 | 0 | 0 | 0 | 0 | 0 | 2 |
| <i>Acinetobacter sp. 511B</i> | 2 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Acinetobacter sp. 20</i> | 1 | 1 | 0 | 0 | 0 | 0 | 1 |
| <i>Acinetobacter sp. 423D</i> | 3 | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | | |
|--|---|---|---|---|---|---|---|
| <i>Acinetobacter</i> sp. HY-7 | 3 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Acinetobacter</i> sp. A3-6 | 2 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Acinetobacter</i> genomosp. 6 | 2 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Acinetobacter</i> ursingii | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Acinetobacter</i> sp. TS25 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| <i>Acinetobacter</i> sp. UA3 | 1 | 0 | 0 | 0 | 0 | 0 | 2 |
| <i>Acinetobacter</i> genomosp. 15TU | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| <i>Acinetobacter</i> glutaminasificans | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Acinetobacter</i> sp. AD321 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Acinetobacter</i> sp. RAG-1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Acinetobacter</i> sp. 48A1 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Acinetobacter</i> sp. 8637 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Acinetobacter</i> sp. PD12 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Acinetobacter</i> sp. isolate 30Bi | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Prokaryotes abundance, *Pseudomonas* species (119 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|--------------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|-------|-----------------|
| <i>Pseudomonas fluorescens</i> | 4055 | 1893 | 1109 | 17643 | 3953 | 13719 | 2337 |
| <i>Pseudomonas aeruginosa</i> | 5319 | 2863 | 868 | 4520 | 5423 | 1488 | 3056 |
| <i>Pseudomonas putida</i> | 3294 | 1430 | 547 | 3179 | 2861 | 1302 | 1882 |
| <i>Pseudomonas mendocina</i> | 4051 | 1203 | 450 | 1774 | 3143 | 513 | 1997 |
| <i>Pseudomonas stutzeri</i> | 3824 | 1482 | 525 | 2001 | 2667 | 497 | 1974 |
| <i>Pseudomonas entomophila</i> | 1005 | 528 | 189 | 1105 | 973 | 416 | 562 |
| <i>Pseudomonas syringae</i> group | 1052 | 440 | 191 | 1063 | 743 | 627 | 656 |
| <i>Pseudomonas</i> genomosp. 3 | | | | | | | |
| <i>Pseudomonas syringae</i> | 769 | 424 | 180 | 1173 | 719 | 470 | 482 |
| <i>Pseudomonas savastanoi</i> | 820 | 434 | 190 | 952 | 789 | 500 | 482 |
| <i>Pseudomonas amygdali</i> | 252 | 99 | 37 | 199 | 168 | 122 | 154 |
| <i>Pseudomonas coronafaciens</i> | 117 | 62 | 18 | 104 | 86 | 62 | 59 |
| <i>Pseudomonas alcaligenes</i> | 21 | 26 | 8 | 27 | 52 | 8 | 9 |
| <i>Pseudomonas resinovorans</i> | 9 | 23 | 7 | 30 | 39 | 7 | 15 |
| <i>Pseudomonas alkylphenolia</i> | 4 | 8 | 2 | 36 | 43 | 6 | 3 |
| <i>Pseudomonas veronii</i> | 0 | 3 | 2 | 28 | 21 | 12 | 0 |
| <i>Pseudomonas chlororaphis</i> | 4 | 6 | 1 | 20 | 8 | 6 | 4 |
| <i>Pseudomonas denitrificans</i> | 4 | 12 | 2 | 26 | 5 | 0 | 1 |
| <i>Pseudomonas nitroreducens</i> | 16 | 4 | 0 | 8 | 10 | 3 | 7 |
| <i>Pseudomonas</i> sp. TJI-51 | 11 | 2 | 1 | 7 | 11 | 2 | 3 |
| <i>Pseudomonas</i> sp. MIS38 | 0 | 0 | 0 | 27 | 2 | 0 | 0 |
| <i>Pseudomonas anguilliseptica</i> | 0 | 7 | 1 | 14 | 2 | 0 | 1 |
| <i>Pseudomonas pseudoalcaligenes</i> | 9 | 2 | 0 | 4 | 6 | 1 | 2 |
| <i>Pseudomonas knackmussii</i> | 1 | 1 | 1 | 5 | 5 | 9 | 1 |
| <i>Pseudomonas brassicacearum</i> | 4 | 1 | 2 | 6 | 0 | 4 | 3 |
| <i>Pseudomonas oleovorans</i> | 9 | 1 | 1 | 3 | 2 | 0 | 1 |
| <i>Pseudomonas</i> sp. CT14 | 1 | 8 | 1 | 4 | 3 | 0 | 0 |
| <i>Pseudomonas</i> sp. Y2 | 3 | 1 | 0 | 4 | 4 | 0 | 4 |
| <i>Pseudomonas</i> sp. MT-1 | 12 | 0 | 0 | 0 | 3 | 0 | 1 |
| <i>Pseudomonas</i> sp. Chol1 | 0 | 5 | 0 | 4 | 5 | 0 | 1 |
| <i>Pseudomonas fragi</i> | 4 | 2 | 0 | 2 | 2 | 1 | 2 |
| <i>Pseudomonas</i> sp. J465 | 3 | 0 | 0 | 0 | 4 | 3 | 2 |
| <i>Pseudomonas</i> sp. S-47 | 2 | 0 | 0 | 6 | 0 | 3 | 1 |
| <i>Pseudomonas</i> sp. JR1 | 1 | 0 | 1 | 3 | 2 | 2 | 1 |
| <i>Pseudomonas tolaasii</i> | 0 | 1 | 1 | 2 | 2 | 3 | 2 |
| <i>Flavobacterium lutescens</i> | 3 | 3 | 0 | 3 | 2 | 0 | 0 |
| <i>Pseudomonas marginalis</i> | 0 | 0 | 0 | 5 | 0 | 6 | 0 |
| <i>Pseudomonas abietaniphila</i> | 0 | 1 | 0 | 5 | 4 | 0 | 0 |

| | | | | | | | |
|---------------------------------------|---|---|---|---|---|---|---|
| <i>Pseudomonas extremaustralis</i> | 1 | 1 | 0 | 3 | 1 | 2 | 0 |
| <i>Pseudomonas</i> sp. HR199 | 2 | 1 | 0 | 1 | 3 | 1 | 1 |
| <i>Pseudomonas viridiflava</i> | 2 | 0 | 0 | 1 | 1 | 1 | 3 |
| <i>Pseudomonas citronellolis</i> | 2 | 1 | 1 | 1 | 2 | 2 | 1 |
| <i>Pseudomonas</i> sp. ND6 | 1 | 0 | 0 | 4 | 2 | 1 | 0 |
| <i>Pseudomonas</i> sp. WBC-3 | 0 | 2 | 4 | 1 | 1 | 0 | 0 |
| <i>Pseudomonas</i> sp. 2663 | 0 | 2 | 0 | 3 | 2 | 0 | 0 |
| <i>Pseudomonas chloritidis</i> mutans | 5 | 0 | 0 | 0 | 0 | 0 | 3 |
| <i>Pseudomonas cichorii</i> | 0 | 1 | 0 | 0 | 0 | 3 | 1 |
| <i>Pseudomonas</i> sp. NCIMB 10558 | 0 | 1 | 0 | 4 | 0 | 1 | 0 |
| <i>Pseudomonas</i> sp. M1 | 0 | 0 | 0 | 2 | 1 | 1 | 1 |
| <i>Pseudomonas</i> sp. 1-7 | 0 | 1 | 0 | 1 | 2 | 1 | 0 |
| <i>Pseudomonas</i> sp. OM2164 | 0 | 1 | 0 | 1 | 1 | 0 | 1 |
| <i>Pseudomonas corrugata</i> | 3 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. WO24 | 0 | 2 | 0 | 1 | 2 | 0 | 0 |
| <i>Pseudomonas</i> sp. CG21 | 0 | 0 | 0 | 0 | 1 | 1 | 1 |
| <i>Pseudomonas mediterranea</i> | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Pseudomonas</i> sp. PCL1171 | 0 | 0 | 0 | 2 | 0 | 0 | 0 |
| <i>Pseudomonas otitidis</i> | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Pseudomonas fulva</i> | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. OPS1 | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| <i>Pseudomonas</i> sp. UK4 | 0 | 0 | 0 | 2 | 0 | 1 | 0 |
| <i>Pseudomonas</i> sp. 7197 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. JS189 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. NyZ402 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. PC17 | 1 | 0 | 0 | 0 | 0 | 0 | 2 |
| <i>Pseudomonas</i> sp. SLT2001 | 1 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. TW3 | 0 | 1 | 1 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas synxantha</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas alcaliphila</i> | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Pseudomonas</i> sp. 61-3 | 0 | 0 | 0 | 0 | 1 | 1 | 0 |
| <i>Pseudomonas</i> sp. TS44 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| <i>Pseudomonas fuscovaginae</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas psychrophila</i> | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Pseudomonas</i> sp. B-0831 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. In5 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Pseudomonas tuomuerensis</i> | 2 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas frederiksbergensis</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. CT07 | 0 | 0 | 0 | 1 | 0 | 1 | 0 |
| <i>Pseudomonas</i> sp. S11 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. XJUH-X-1 | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas diterpeniphila</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas reinekei</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. 122 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| <i>Pseudomonas</i> sp. Tik3 | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas azotoformans</i> | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| <i>Pseudomonas grimonii</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas hydrogenovora</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas qianpuensis</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. LQ26 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| <i>Pseudomonas</i> sp. ST41 | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| <i>Pseudomonas</i> sp. SY4 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas mosselii</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas reactans</i> | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| <i>Pseudomonas</i> sp. AC2 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. AR(2010) | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. C6-9 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. CMR5c | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas</i> sp. S9 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |

| | | | | | | | |
|-----------------------------------|---|---|---|---|---|---|---|
| <i>Pseudomonas thermotolerans</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas oryzihabitans</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas pertucinogena</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas sp. PT03</i> | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| <i>Pseudomonas sp. R125</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas sp. SK38</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas sp. TAC II 18</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas wisconsinensis</i> | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Pseudomonas azotifigens</i> | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| <i>Pseudomonas mucidolens</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Pseudomonas sp. ED3</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |

Prokaryotes abundance, *Azotobacter* species (4 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGB S | Swine sludge |
|--------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|----------|-----------------|
| <i>Azotobacter vinelandii</i> | 2448 | 1567 | 450 | 3387 | 3517 | 641 | 1638 |
| <i>Azotobacter chroococcum</i> | 20 | 32 | 10 | 99 | 52 | 6 | 24 |
| <i>Azotobacter sp. FA8</i> | 0 | 3 | 0 | 3 | 11 | 0 | 5 |
| <i>Azotobacter salinestris</i> | 0 | 1 | 0 | 4 | 4 | 0 | 3 |

Prokaryotes abundance, *Xanthomonas* species (20 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGB S | Swine sludge |
|-----------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|----------|-----------------|
| <i>Xanthomonas campestris</i> | 1248 | 2204 | 527 | 2849 | 2243 | 379 | 642 |
| <i>Xanthomonas oryzae</i> | 671 | 1303 | 338 | 1693 | 1406 | 276 | 357 |
| <i>Xanthomonas citri</i> | 667 | 1161 | 267 | 1542 | 1293 | 195 | 341 |
| <i>Xanthomonas albilineans</i> | 427 | 875 | 194 | 1355 | 1041 | 128 | 227 |
| <i>Xanthomonas euvesicatoria</i> | 548 | 806 | 209 | 1109 | 950 | 147 | 258 |
| <i>Xanthomonas fuscans</i> | 221 | 473 | 93 | 622 | 505 | 70 | 134 |
| <i>Xanthomonas axonopodis</i> | 9 | 35 | 3 | 21 | 21 | 1 | 4 |
| <i>Xanthomonas vesicatoria</i> | 6 | 8 | 0 | 8 | 7 | 0 | 3 |
| <i>Xanthomonas sp. T22</i> | 0 | 1 | 0 | 1 | 2 | 3 | 1 |
| <i>Xanthomonas perforans</i> | 2 | 3 | 0 | 1 | 1 | 0 | 1 |
| <i>Xanthomonas vasicola</i> | 1 | 1 | 0 | 0 | 2 | 0 | 0 |
| <i>Xanthomonas translucens</i> | 0 | 0 | 0 | 0 | 1 | 0 | 0 |
| <i>Xanthomonas sp. CIP 102397</i> | 0 | 0 | 0 | 1 | 0 | 0 | 0 |
| <i>Xanthomonas gardneri</i> | 0 | 1 | 0 | 0 | 0 | 0 | 0 |

Prokaryotes abundance, *Shewanella* species (25 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|-----------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Shewanella baltica</i> | 1770 | 585 | 331 | 747 | 588 | 1676 | 632 |
| <i>Shewanella sp. W3-18-1</i> | 1688 | 182 | 97 | 374 | 317 | 2337 | 583 |
| <i>Shewanella oneidensis</i> | 676 | 234 | 164 | 324 | 332 | 1133 | 304 |
| <i>Shewanella putrefaciens</i> | 556 | 225 | 100 | 357 | 208 | 1429 | 210 |
| <i>Shewanella sediminis</i> | 616 | 425 | 296 | 425 | 532 | 416 | 312 |
| <i>Shewanella amazonensis</i> | 727 | 333 | 248 | 390 | 479 | 366 | 299 |
| <i>Shewanella pealeana</i> | 520 | 326 | 181 | 338 | 448 | 325 | 279 |
| <i>Shewanella frigidimarina</i> | 634 | 298 | 171 | 351 | 346 | 275 | 258 |
| <i>Shewanella sp. ANA-3</i> | 619 | 260 | 119 | 287 | 237 | 478 | 232 |
| <i>Shewanella loihica</i> | 506 | 279 | 191 | 321 | 357 | 265 | 255 |
| <i>Shewanella denitrificans</i> | 596 | 228 | 144 | 310 | 324 | 193 | 238 |
| <i>Shewanella woodyi</i> | 333 | 172 | 150 | 196 | 265 | 199 | 152 |
| <i>Shewanella sp. MR-7</i> | 315 | 118 | 85 | 160 | 162 | 361 | 140 |
| <i>Shewanella halifaxensis</i> | 244 | 179 | 96 | 172 | 199 | 171 | 133 |
| <i>Shewanella piezotolerans</i> | 261 | 126 | 94 | 139 | 198 | 175 | 110 |
| <i>Shewanella sp. MR-4</i> | 200 | 125 | 83 | 129 | 125 | 270 | 108 |
| <i>Shewanella violacea</i> | 272 | 84 | 64 | 88 | 106 | 190 | 135 |
| <i>Shewanella benthica</i> | 218 | 91 | 49 | 91 | 116 | 120 | 97 |
| <i>Shewanella sp. 33B</i> | 0 | 4 | 0 | 9 | 35 | 1 | 0 |
| <i>Shewanella livingstonensis</i> | 7 | 0 | 0 | 0 | 0 | 0 | 2 |
| <i>Shewanella hanedai</i> | 0 | 3 | 2 | 0 | 1 | 1 | 1 |
| <i>Shewanella algae</i> | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Shewanella sp.</i> | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| <i>Shewanella colwelliana</i> | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| <i>Shewanella sp. DB6705</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Prokaryotes abundance, *Methylobacter* species (3 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|------------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Methylobacter tundripaludum</i> | 180 | 4363 | 511 | 5889 | 8092 | 495 | 184 |
| <i>Methylobacter marinus</i> | 0 | 0 | 0 | 2 | 3 | 1 | 0 |
| <i>Methylobacter bovis</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Total hit numbers of class *Epsilonproteobacteria*

| | Swine wastewater | SS-inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|------------------------------|---------------------|--------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Epsilonproteobacteria</i> | 45137 | 24913.25 | 15848 | 26223 | 61311.25 | 4260 | 20853 |

Prokaryotes abundance, *Arcobacter* species (11 OTUs)

| | inflow SW | MFC1_a | MFC1_p | MFC3_a | MFC3_p | rIS | rSW |
|---|-----------|--------|--------|--------|--------|-----|-------|
| <i>Arcobacter butzleri</i> | 27488 | 4304 | 3454 | 5211 | 25344 | 185 | 12601 |
| <i>Arcobacter nitrofigilis</i> | 4289 | 887 | 737 | 1026 | 3301 | 107 | 1861 |
| <i>Arcobacter cryaerophilus</i> | 30 | 4 | 9 | 0 | 13 | 0 | 12 |
| <i>Arcobacter sp. L</i> | 13 | 2 | 2 | 2 | 11 | 0 | 8 |
| <i>Arcobacter skirrowii</i> | 20 | 1 | 1 | 1 | 1 | 0 | 7 |
| <i>Arcobacter cibarius</i> | 9 | 0 | 2 | 0 | 1 | 0 | 2 |
| <i>Arcobacter cf. butzleri</i> LCDC134322 | | 0 | 0 | 0 | 1 | 0 | 0 |
| <i>Arcobacter trophiarum</i> | 3 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Arcobacter defluvii</i> | 0 | 0 | 0 | 0 | 2 | 0 | 0 |
| <i>Arcobacter cf. butzleri</i> LCDC132072 | | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Arcobacter mytili</i> | 0 | 0 | 0 | 0 | 1 | 0 | 0 |

Total hit numbers of phylum *Firmicutes*

| | Swine wastewater | SS-inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|-------------------|---------------------|--------------------------------|---|--------------------------------------|---|----------|-----------------|
| <i>Firmicutes</i> | 841540.5 | 229422.25 | 219750.5 | 143203.5 | 151085.25 | 119895.5 | 574808 |

Prokaryotes abundance, *Clostridium* species (77 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|------------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Clostridium botulinum</i> | 15215 | 5154 | 5083 | 3010 | 4017 | 2094 | 10268 |
| <i>Clostridium thermocellum</i> | 9754 | 6740 | 5567 | 3559 | 3574 | 2253 | 7088 |
| <i>Clostridium phytofermentans</i> | 14049 | 3200 | 2844 | 1691 | 1491 | 621 | 7910 |
| <i>Clostridium beijerinckii</i> | 11976 | 2782 | 3020 | 1529 | 2429 | 895 | 7981 |
| <i>Clostridium saccharolyticum</i> | 12916 | 2889 | 2459 | 1477 | 1203 | 386 | 8155 |
| <i>Clostridium perfringens</i> | 7065 | 2282 | 2271 | 1275 | 1924 | 916 | 4647 |
| <i>Clostridium kluyveri</i> | 6266 | 2782 | 2389 | 1563 | 1575 | 910 | 4642 |
| <i>Clostridium leptum</i> | 6471 | 1840 | 3113 | 946 | 1032 | 328 | 5926 |
| <i>Clostridium cellulolyticum</i> | 4923 | 3003 | 2456 | 1568 | 1588 | 771 | 3435 |
| <i>Clostridium acetobutylicum</i> | 5098 | 1665 | 1629 | 1088 | 1179 | 670 | 3406 |
| <i>Clostridium boltea</i> | 4902 | 1131 | 983 | 693 | 615 | 297 | 4179 |
| <i>Clostridium cellulovorans</i> | 4309 | 1552 | 1480 | 833 | 928 | 446 | 2932 |
| <i>Clostridium asparagiforme</i> | 4047 | 1369 | 1074 | 794 | 673 | 434 | 2571 |
| <i>Clostridium tetani</i> | 3180 | 1488 | 1361 | 885 | 955 | 704 | 2192 |

| | | | | | | | |
|--|------|------|------|-----|------|-----|------|
| <i>Clostridium novyi</i> | 2979 | 1392 | 1281 | 775 | 935 | 618 | 2043 |
| <i>Clostridium hathewayi</i> | 3665 | 880 | 729 | 492 | 420 | 213 | 2466 |
| <i>Clostridium ljungdahlii</i> | 2821 | 1121 | 955 | 683 | 762 | 506 | 2001 |
| <i>Clostridium butyricum</i> | 3138 | 802 | 958 | 388 | 880 | 144 | 2455 |
| <i>Clostridium nexile</i> | 4169 | 572 | 595 | 278 | 289 | 112 | 2389 |
| <i>Clostridium methylpentosum</i> | 2690 | 1206 | 1151 | 635 | 564 | 215 | 1867 |
| <i>Clostridium scindens</i> | 3484 | 707 | 637 | 388 | 346 | 177 | 2423 |
| <i>Clostridium sp. M62/1</i> | 3513 | 714 | 667 | 405 | 337 | 127 | 2058 |
| <i>Clostridium sp. 7_2_43FAA</i> | 2441 | 834 | 947 | 363 | 1003 | 195 | 1752 |
| <i>Clostridium carboxidivorans</i> | 1892 | 1117 | 930 | 699 | 773 | 579 | 1466 |
| <i>Clostridium papyrosolvens</i> | 1602 | 1275 | 944 | 685 | 686 | 347 | 1056 |
| <i>Clostridium symbiosum</i> | 2662 | 757 | 624 | 364 | 354 | 142 | 1690 |
| <i>Clostridium hylemonae</i> | 2390 | 700 | 547 | 392 | 329 | 199 | 1628 |
| <i>Clostridium sp. L2-50</i> | 2347 | 428 | 418 | 243 | 212 | 78 | 1230 |
| <i>Clostridium sp. SS2/1</i> | 2146 | 367 | 394 | 199 | 213 | 90 | 1191 |
| <i>Clostridium sporogenes</i> | 366 | 217 | 216 | 129 | 181 | 123 | 284 |
| <i>Clostridium sp. HGF2</i> | 556 | 135 | 141 | 86 | 67 | 29 | 375 |
| <i>Clostridium citroniae</i> | 141 | 35 | 47 | 19 | 13 | 0 | 80 |
| <i>Clostridium pasteurianum</i> | 84 | 29 | 23 | 20 | 21 | 17 | 64 |
| <i>Clostridium sp. enrichment culture clone 7-14</i> | 116 | 37 | 19 | 18 | 17 | 2 | 47 |
| <i>Clostridium saccharobutylicum</i> | 49 | 18 | 15 | 13 | 18 | 13 | 27 |
| <i>Clostridium subterminale</i> | 18 | 32 | 22 | 24 | 32 | 15 | 9 |
| <i>Clostridium sp. D5</i> | 65 | 6 | 11 | 3 | 5 | 0 | 36 |
| <i>Clostridium stercorarium</i> | 41 | 11 | 10 | 11 | 7 | 10 | 15 |
| <i>Clostridium tetanomorphum</i> | 19 | 16 | 15 | 7 | 6 | 4 | 12 |
| <i>Clostridium aminobutyricum</i> | 4 | 13 | 10 | 10 | 10 | 14 | 11 |
| <i>Clostridium sp. 7_3_54FAA</i> | 30 | 3 | 4 | 2 | 5 | 0 | 11 |
| <i>Clostridium clariflavum</i> | 6 | 13 | 9 | 3 | 4 | 2 | 9 |
| <i>Clostridium clostridioforme</i> | 23 | 1 | 4 | 1 | 1 | 0 | 15 |
| <i>Clostridium longisporum</i> | 18 | 1 | 2 | 0 | 3 | 0 | 15 |
| <i>Clostridium sp. enrichment culture clone 7-25</i> | 16 | 2 | 2 | 2 | 2 | 0 | 11 |
| <i>Clostridium sartagoforme</i> | 17 | 0 | 1 | 1 | 0 | 5 | 5 |
| <i>Clostridium scatologenes</i> | 3 | 6 | 5 | 3 | 1 | 4 | 3 |
| <i>Clostridium saccharoperbutylacetonicum</i> | 8 | 3 | 2 | 4 | 3 | 0 | 2 |
| <i>Clostridium tyrobutyricum</i> | 4 | 3 | 2 | 8 | 2 | 1 | 3 |
| <i>Clostridium septicum</i> | 7 | 1 | 2 | 0 | 1 | 0 | 6 |
| <i>Clostridium cochlearium</i> | 5 | 3 | 4 | 0 | 0 | 1 | 1 |
| <i>Clostridium histolyticum</i> | 3 | 1 | 1 | 0 | 3 | 3 | 1 |
| <i>Clostridium magnum</i> | 1 | 2 | 1 | 1 | 2 | 0 | 5 |
| <i>Clostridium cylindrosporum</i> | 4 | 0 | 2 | 0 | 1 | 0 | 5 |
| <i>Clostridium sp. M-E</i> | 1 | 3 | 1 | 2 | 1 | 1 | 1 |
| <i>Clostridium propionicum</i> | 2 | 1 | 1 | 0 | 1 | 1 | 3 |
| <i>Clostridium hungatei</i> | 0 | 3 | 0 | 4 | 1 | 0 | 0 |
| <i>Clostridium sp.</i> | 3 | 0 | 1 | 0 | 0 | 1 | 1 |
| <i>Clostridium josui</i> | 1 | 0 | 0 | 1 | 1 | 1 | 3 |
| <i>Clostridium cellobioparum</i> | 2 | 2 | 0 | 1 | 0 | 0 | 1 |
| <i>Clostridium argentinense</i> | 0 | 0 | 0 | 0 | 1 | 2 | 0 |
| <i>Clostridium aminovaleERICUM</i> | 2 | 0 | 1 | 0 | 0 | 0 | 1 |
| <i>Clostridium acidurici</i> | 0 | 0 | 0 | 0 | 0 | 1 | 1 |
| <i>Clostridium limosum</i> | 0 | 1 | 0 | 0 | 1 | 0 | 0 |
| <i>Clostridium sp. MCF-1</i> | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Clostridium paraputrificum</i> | 0 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Clostridium sp. Kas107-2</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Clostridium cadaveris</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Clostridium diolis</i> | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| <i>Clostridium chauvoei</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 |

| | | | | | | |
|--------------------------------|---|---|---|---|---|-----|
| <i>Clostridium multunense</i> | 0 | 0 | 0 | 0 | 0 | 0 0 |
| <i>Clostridium aceticum</i> | 0 | 0 | 0 | 0 | 0 | 0 0 |
| <i>Clostridium</i> sp. CA6 | 0 | 0 | 0 | 0 | 0 | 0 0 |
| <i>Clostridium</i> sp. DL-VIII | 1 | 0 | 0 | 0 | 0 | 0 0 |

Total hit numbers of phylum *Bacteroidetes*

| | Swine wastewater | SS-inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|----------------------|---------------------|--------------------------------|---|--------------------------------------|---|---------|-----------------|
| <i>Bacteroidetes</i> | 953059 | 177280.25 | 259630.25 | 125597.5 | 148800.25 | 44250.5 | 300106 |

Prokaryotes abundance, *Flavobacterium* species (15 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|-------------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Flavobacterium johnsoniae</i> | 7892 | 4405 | 5334 | 3969 | 4264 | 971 | 2843 |
| <i>Flavobacterium psychrophilum</i> | 3370 | 2710 | 3497 | 2333 | 2537 | 489 | 1412 |
| <i>Flavobacterium columnare</i> | 11 | 9 | 16 | 7 | 9 | 1 | 9 |
| <i>Flavobacterium</i> sp. | 9 | 8 | 5 | 5 | 5 | 2 | 6 |
| <i>Flavobacterium</i> sp. 4214 | 4 | 1 | 5 | 0 | 2 | 1 | 3 |
| <i>Flavobacterium</i> sp. 4H | 3 | 1 | 5 | 1 | 5 | 0 | 0 |
| <i>Flavobacterium hibernum</i> | 1 | 2 | 1 | 0 | 2 | 0 | 2 |
| <i>Flavobacterium frigidimaris</i> | 3 | 0 | 0 | 1 | 1 | 0 | 0 |
| <i>Flavobacterium</i> sp. KP1 | 4 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Flavobacterium aquatile</i> | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Flavobacterium</i> sp. TN17 | 1 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Flavobacterium frigidis</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Flavobacterium</i> sp. 4221 | 0 | 0 | 0 | 0 | 0 | 1 | 0 |
| <i>Flavobacterium</i> sp. 92 | 0 | 1 | 0 | 0 | 0 | 0 | 0 |
| <i>Flavobacterium</i> sp. LW53 | 0 | 0 | 0 | 0 | 0 | 0 | 1 |

Prokaryotes abundance, *Bacteroides* species (45 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|--------------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Bacteroides fragilis</i> | 40447 | 7677 | 10712 | 5096 | 5533 | 1517 | 13746 |
| <i>Bacteroides vulgatus</i> | 33183 | 3715 | 6287 | 2466 | 2832 | 760 | 9948 |
| <i>Bacteroides</i> sp. 1_1_6 | 19812 | 3147 | 4713 | 2134 | 2398 | 607 | 6318 |
| <i>Bacteroides</i> sp. 4_3_47FAA | 19687 | 2910 | 4782 | 1927 | 2194 | 446 | 5938 |
| <i>Bacteroides thetaiotaomicron</i> | 17194 | 2848 | 4051 | 1906 | 2032 | 567 | 5585 |
| <i>Bacteroides helcogenes</i> | 16184 | 2227 | 3480 | 1542 | 1613 | 361 | 5264 |
| <i>Bacteroides</i> sp. 20_3 | 9379 | 3310 | 4348 | 2131 | 2384 | 694 | 3827 |
| <i>Bacteroides cellulosilyticus</i> | 9959 | 1583 | 2241 | 1085 | 1170 | 412 | 3178 |
| <i>Bacteroides intestinalis</i> | 8839 | 1462 | 2082 | 985 | 1064 | 295 | 2764 |
| <i>Bacteroides coprocola</i> | 8966 | 1397 | 2239 | 888 | 1010 | 228 | 2750 |
| <i>Bacteroides plebeius</i> | 8516 | 1420 | 2327 | 912 | 1029 | 266 | 2827 |
| <i>Bacteroides eggerthii</i> | 6611 | 1148 | 1639 | 750 | 825 | 246 | 2224 |
| <i>Bacteroides ovatus</i> | 7418 | 819 | 1268 | 651 | 612 | 152 | 2289 |
| <i>Bacteroides uniformis</i> | 6176 | 1104 | 1539 | 761 | 824 | 224 | 1992 |
| <i>Bacteroides</i> sp. D2 | 6673 | 771 | 1111 | 622 | 623 | 152 | 1978 |
| <i>Bacteroides coprophilus</i> | 5515 | 1066 | 1542 | 702 | 782 | 219 | 1883 |
| <i>Bacteroides</i> sp. 2_2_4 | 6293 | 817 | 1191 | 594 | 567 | 128 | 1984 |
| <i>Bacteroides stercoris</i> | 4777 | 942 | 1337 | 627 | 664 | 139 | 1661 |
| <i>Bacteroides finegoldii</i> | 5075 | 666 | 974 | 500 | 516 | 112 | 1670 |
| <i>Bacteroides</i> sp. D20 | 4213 | 773 | 1034 | 546 | 556 | 172 | 1391 |
| <i>Bacteroides caccae</i> | 4289 | 727 | 959 | 519 | 531 | 165 | 1408 |
| <i>Bacteroides</i> sp. D1 | 4395 | 576 | 860 | 399 | 437 | 75 | 1346 |
| <i>Bacteroides</i> sp. 2_1_56FAA | 3658 | 717 | 984 | 450 | 558 | 164 | 1335 |
| <i>Bacteroides dorei</i> | 4364 | 526 | 838 | 349 | 348 | 89 | 1281 |
| <i>Bacteroides</i> sp. 9_1_42FAA | 3907 | 515 | 899 | 406 | 416 | 97 | 1285 |
| <i>Bacteroides</i> sp. 1_1_14 | 3248 | 523 | 796 | 363 | 430 | 128 | 1063 |
| <i>Bacteroides</i> sp. 2_1_16 | 2728 | 586 | 819 | 373 | 415 | 105 | 935 |
| <i>Bacteroides</i> sp. 2_1_33B | 2181 | 652 | 833 | 413 | 484 | 130 | 893 |
| <i>Bacteroides</i> sp. 3_1_33FAA | 1961 | 179 | 345 | 131 | 141 | 49 | 576 |
| <i>Bacteroides</i> sp. 2_1_7 | 1460 | 281 | 414 | 189 | 208 | 75 | 499 |
| <i>Bacteroides</i> sp. D22 | 1700 | 162 | 251 | 120 | 113 | 30 | 533 |
| <i>Bacteroides</i> sp. 3_1_23 | 1544 | 165 | 212 | 129 | 116 | 37 | 484 |
| <i>Bacteroides</i> sp. 3_1_19 | 1098 | 279 | 341 | 158 | 195 | 75 | 444 |
| <i>Bacteroides</i> sp. 3_2_5 | 1076 | 272 | 362 | 157 | 164 | 53 | 353 |
| <i>Bacteroides xylanisolvens</i> | 950 | 143 | 205 | 113 | 100 | 30 | 302 |
| <i>Bacteroides</i> sp. 4_1_36 | 859 | 105 | 138 | 66 | 71 | 17 | 291 |
| <i>Bacteroides</i> sp. 3_1_40A | 786 | 50 | 88 | 33 | 37 | 8 | 216 |
| <i>Bacteroides</i> sp. 1_1_30 | 443 | 66 | 113 | 45 | 46 | 2 | 144 |
| <i>Bacteroides coprosuis</i> | 263 | 46 | 55 | 14 | 20 | 0 | 74 |
| <i>Bacteroides</i> sp. 2_1_22 | 216 | 18 | 36 | 18 | 14 | 5 | 60 |
| <i>Bacteroides fluxus</i> | 34 | 5 | 4 | 2 | 3 | 0 | 4 |
| <i>Bacteroides</i> sp. | 1 | 0 | 1 | 0 | 1 | 2 | 0 |
| <i>Bacteroides</i> sp. WA1 | 1 | 0 | 0 | 0 | 0 | 0 | 1 |
| <i>Bacteroides graminisolvens</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |
| <i>Bacteroides propionicifaciens</i> | 0 | 0 | 0 | 0 | 0 | 0 | 0 |

Prokaryotes abundance, *Parabacteroides* species (4 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|-----------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Parabacteroides distasonis</i> | 23579 | 7320 | 9467 | 4863 | 5299 | 1546 | 9982 |
| <i>Parabacteroides johnsonii</i> | 8714 | 2707 | 3383 | 1827 | 1975 | 552 | 4139 |
| <i>Parabacteroides merdae</i> | 7966 | 2523 | 3117 | 1764 | 1860 | 537 | 3876 |
| <i>Parabacteroides sp. D13</i> | 8131 | 2594 | 3269 | 1798 | 1873 | 552 | 3300 |

Total hit numbers of domain *Archaea*

| | Swine wastewater | SS-inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|----------------|---------------------|--------------------------------|---|--------------------------------------|---|---------|-----------------|
| <i>Archaea</i> | 14263 | 84409.25 | 61551.75 | 85687.5 | 125856 | 85814.5 | 42164.5 |

Prokaryotes abundance, *Methanosarcina* species (4 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|-----------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Methanosarcina barkeri</i> | 876 | 20354 | 10729 | 2693 | 6296 | 2378 | 11534 |
| <i>Methanosarcina acetivorans</i> | 673 | 4801 | 2980 | 2533 | 4230 | 2897 | 2755 |
| <i>Methanosarcina mazei</i> | 541 | 4683 | 2765 | 1720 | 3176 | 2302 | 3133 |
| <i>Methanosarcina thermophila</i> | 7 | 117 | 70 | 45 | 92 | 62 | 76 |

Prokaryotes abundance, *Methanothermobacter* species (3 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|---|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Methanothermobacter thermautrophicus</i> | 385 | 1878 | 1494 | 14287 | 19238 | 7214 | 1010 |
| <i>Methanothermobacter marburgensis</i> | 114 | 876 | 689 | 8024 | 10747 | 3944 | 390 |
| <i>Methanothermobacter wolfeii</i> | 0 | 4 | 2 | 17 | 23 | 6 | 1 |

Prokaryotes abundance, *Methanosaeta* species (3 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|----------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Methanosaeta thermophila</i> | 246 | 3646 | 2346 | 5375 | 12650 | 8927 | 2688 |
| <i>Methanosaeta harundinacea</i> | 7 | 115 | 87 | 244 | 522 | 456 | 90 |
| <i>Methanosaeta concilii</i> | 4 | 42 | 25 | 62 | 131 | 95 | 33 |

Prokaryotes abundance, *Methanospirillum* species (2 OTUs)

| | Swine wastewater | SS- inoculated MFC, Anode | SS- inoculated MFC, Planktonic | IGBS- inoculated MFC, Anode | IGBS- inoculated MFC, Planktonic | IGBS | Swine sludge |
|----------------------------------|---------------------|------------------------------------|---|--------------------------------------|---|------|-----------------|
| <i>Methanospirillum hungatei</i> | 591 | 10919 | 7019 | 3368 | 3598 | 4102 | 2415 |
| <i>Methanospirillum lacunae</i> | 0 | 1 | 0 | 0 | 0 | 0 | 0 |