## SUPPLEMENTARY MATERIALS

### TABLE S1

The list of all OTUs with significant LEfSe scores is provided in the Supplemental Table (S1) to determine microbial communities that were statistically associated with community compositional differences across stages and across treatments. The LDA scores were normalized by log10. Relative abundance is significant when P < 0.05, logarithmic LDA score ≥ 2.0. Five highlighted OTUs explained the greatest differences across stages, but not across treatments.

| Biomarker | Taxonomy | Abundance | Group | LDA | Pvalue |
|---|---|---|---|---|---|
| Otu00527 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|unclassified\|unclassified\|unclassified\|Otu00527\| | 2.1358 | Two-wk | 3.3874 | 0.0047 |
| Otu00410 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhizobiales\|"Aurantimonadaceae"\|Aurantimonas\|Otu00410\| | 3.4337 | Pre-fed | 3.3205 | 0.0344 |
| Otu00094 | Bacteria\|Firmicutes\|Bacilli\|Lactobacillales\|Carnobacteriaceae\|Carnobacterium\|Otu00094\| | 3.0166 | Two-wk | 2.8297 | 0.0001 |
| Otu00091 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Oceanospirillales\|Halomonadaceae\|Halomonas\|Otu00091\| | 3.4477 | One-wk | 3.1380 | 0.0083 |
| Otu00060 | Bacteria\|"Proteobacteria"\|Betaproteobacteria\|Burkholderiales\|unclassified\|unclassified\|Otu00060\| | 3.3097 | One-wk | 3.0489 | 0.0419 |
| Otu00061 | Bacteria\|"Proteobacteria"\|Betaproteobacteria\|unclassified\|unclassified\|unclassified\|Otu00061\| | 3.5395 | Two-wk | 3.2503 | 0.0045 |
| Otu00117 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Xanthomonadales\|Xanthomonadaceae\|unclassified\|Otu00117\| | 3.0468 | One-wk | 3.1467 | 0.0320 |
| Otu00026 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhizobiales\|Phyllobacteriaceae\|Nitratireductor\|Otu00026\| | 4.0398 | One-wk | 3.7592 | 2.28E-07 |
| Otu00002 | Bacteria\|Firmicutes\|Clostridia\|Clostridiales\|Clostridiaceae_1\|Sarcina\|Otu00002\| | 5.2821 | Two-wk | 4.9588 | 0.0021 |
| Otu00004 | Bacteria\|Firmicutes\|Clostridia\|Clostridiales\|Clostridiaceae_1\|unclassified\|Otu00004\| | 4.7512 | Two-wk | 4.4746 | 0.0005 |
| Otu00042 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhodobacterales\|Rhodobacteraceae\|unclassified\|Otu00042\| | 3.7411 | Two-wk | 3.4403 | 6.30E-09 |
| Otu00048 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhodobacterales\|Rhodobacteraceae\|unclassified\|Otu00048\| | 3.4756 | Two-wk | 3.1857 | 0.0007 |
| Otu00132 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Chromatiales\|Chromatiaceae\|Rheinheimera\|Otu00132\| | 3.0872 | Pre-fed | 3.2073 | 0.0344 |
| Otu00058 | Bacteria\|Firmicutes\|Bacilli\|Lactobacillales\|Streptococcaceae\|Streptococcus\|Otu00058\| | 3.4626 | One-wk | 3.0579 | 0.0356 |
| Otu00052 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhizobiales\|Methylobacteriaceae\|Methylobacterium\|Otu00052\| | 3.7160 | One-wk | 3.4676 | 0.0498 |

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|---|---|---|---|---|---|
| Otu00054 | Bacteria\|"Proteobacteria"\|Betaproteobacteria\|Burkholderiales\|Comamonadaceae\|Hydrogenophaga\|Otu00054\| | 3.8101 | Pre-fed | 3.4362 | 0.0182 |
| Otu00024 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Xanthomonadales\|Xanthomonadaceae\|Stenotrophomonas\|Otu00024\| | 4.3703 | Pre-fed | 3.9573 | 7.85E-05 |
| Otu00027 | Bacteria\|Firmicutes\|Bacilli\|Bacillales\|Planococcaceae\|Jeotgalibacillus\|Otu00027\| | 3.8985 | Two-wk | 3.5961 | 1.90E-07 |
| Otu00023 | Bacteria\|"Proteobacteria"\|Betaproteobacteria\|Burkholderiales\|Comamonadaceae\|unclassified\|Otu00023\| | 4.3195 | Pre-fed | 4.0130 | 0.0003 |
| Otu00029 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|"Vibrionales"\|Vibrionaceae\|Vibrio\|Otu00029\| | 4.1601 | One-wk | 3.8736 | 3.59E-11 |
| Otu00020 | Bacteria\|"Actinobacteria"\|Actinobacteria\|Actinomycetales\|Micrococcaceae\|unclassified\|Otu00020\| | 4.4156 | Pre-fed | 3.9467 | 0.0021 |
| Otu00038 | Bacteria\|"Proteobacteria"\|Betaproteobacteria\|Burkholderiales\|Burkholderiaceae\|Ralstonia\|Otu00038\| | 4.1446 | Pre-fed | 3.6999 | 0.0100 |
| Otu00034 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Xanthomonadales\|Xanthomonadaceae\|Stenotrophomonas\|Otu00034\| | 4.0837 | Pre-fed | 3.7844 | 0.0261 |
| Otu00030 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhodobacterales\|Rhodobacteraceae\|Loktanella\|Otu00030\| | 4.0715 | One-wk | 3.7751 | 8.19E-05 |
| Otu02230 | Bacteria\|"Bacteroidetes"\|"Bacteroidia"\|"Bacteroidales"\|"Porphyromonadaceae"\|unclassified\|Otu02230\| | 1.6612 | Pre-fed | 3.9043 | 0.0344 |
| Otu00795 | Bacteria\|Firmicutes\|Bacilli\|Lactobacillales\|Streptococcaceae\|Lactococcus\|Otu00795\| | 2.0566 | Two-wk | 3.1392 | 0.0010 |
| Otu00005 | Bacteria\|Firmicutes\|Bacilli\|Bacillales\|Bacillales_Incertae_Sedis_XII\|Exiguobacterium\|Otu00005\| | 4.7475 | One-wk | 4.4294 | 4.57E-05 |
| Otu00009 | Bacteria\|Firmicutes\|Clostridia\|Clostridiales\|Clostridiaceae_1\|unclassified\|Otu00009\| | 4.4099 | Two-wk | 4.0842 | 2.50E-05 |
| Otu00011 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Pseudomonadales\|Pseudomonadaceae\|Pseudomonas\|Otu00011\| | 4.5397 | Pre-fed | 4.2259 | 0.0122 |
| Otu00680 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Sphingomonadales\|Sphingomonadaceae\|Sphingomonas\|Otu00680\| | 2.4556 | One-wk | 3.5219 | 0.0183 |
| Otu00377 | Bacteria\|Firmicutes\|Bacilli\|Bacillales\|Staphylococcaceae\|Jeotgalicoccus\|Otu00377\| | 2.5935 | Pre-fed | 3.2566 | 0.0344 |
| Otu00015 | Bacteria\|"Actinobacteria"\|Actinobacteria\|Actinomycetales\|Corynebacteriaceae\|Turicella\|Otu00015\| | 4.5914 | Pre-fed | 4.1666 | 0.0085 |
| Otu00551 | Bacteria\|"Actinobacteria"\|Actinobacteria\|Actinomycetales\|unclassified\|unclassified\|Otu00551\| | 2.5276 | One-wk | 3.1669 | 0.0183 |
| Otu00017 | Bacteria\|"Actinobacteria"\|Actinobacteria\|Actinomycetales\|Corynebacteriaceae\|Corynebacterium\|Otu00017\| | 4.2374 | One-wk | 3.9257 | 0.0026 |
| Otu00016 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Pseudomonadales\|Pseudomonadaceae\|Pseudomonas\|Otu00016\| | 4.1440 | Two-wk | 3.8142 | 0.0002 |
| Otu00012 | Bacteria\|"Actinobacteria"\|Actinobacteria\|Actinomycetales\|Corynebacteriaceae\|Corynebacterium\|Otu00012\| | 4.5504 | Pre-fed | 4.0733 | 0.0004 |
| Otu00353 | Bacteria\|"Bacteroidetes"\|Flavobacteria\|"Flavobacteriales"\|Flavobacteriaceae\|Chryseobacterium\|Otu00353\| | 2.7309 | One-wk | 3.0988 | 0.0064 |
| Otu00014 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Pseudomonadales\|Moraxellaceae\|Acinetobacter\|Otu00014\| | 4.2644 | Pre-fed | 3.9722 | 0.0082 |
| Otu00010 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhodobacterales\|Rhodobacteraceae\|Paracoccus\|Otu00010\| | 4.4173 | Pre-fed | 4.1726 | 0.0048 |
| Otu00013 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhodobacterales\|Rhodobacteraceae\|Paracoccus\|Otu00013\| | 4.1647 | One-wk | 3.5870 | 0.0191 |

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|---|---|---|---|---|---|
| Otu01775 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhodobacterales\|Rhodobacteraceae\|unclassified\|Otu01775\| | 1.3576 | Two-wk | 3.8146 | 0.0078 |
| Otu00398 | Bacteria\|"Proteobacteria"\|Gammaproteobacteria\|Alteromonadales\|Alteromonadaceae\|Alteromonas\|Otu00398\| | 2.5945 | One-wk | 3.1229 | 0.0183 |
| Otu00082 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Rhizobiales\|Hyphomicrobiaceae\|Devosia\|Otu00082\| | 3.2004 | One-wk | 3.0175 | 4.53E-05 |
| Otu00084 | Bacteria\|"Actinobacteria"\|Actinobacteria\|Actinomycetales\|Mycobacteriaceae\|Mycobacterium\|Otu00084\| | 3.2788 | One-wk | 3.0152 | 0.0352 |
| Otu00008 | Bacteria\|"Proteobacteria"\|Alphaproteobacteria\|Caulobacterales\|Caulobacteraceae\|Brevundimonas\|Otu00080\| | 4.8780 | Pre-fed | 4.5864 | 0.0041 |

TABLE S2

Relative abundance of predominant taxa defined at threshold > 0.01, for all fish gut microbiomes samples across four treatment groups, denoted as **S** (fish raised in natal stream, fed live Artemia); **Sp** (fish raised in natal stream, fed live Artemia fish mixed with retentate); **GW** (fish raised in groundwater, fed live Artemia); **GWp** (fish raised in groundwater, fed live Artemia mixed with retentate). These are the most abundant 30 taxa that were selected based on the predefined threshold of 0.01

| | | **Pre-feeding** | | | | **One-week active feeding** | | | | **Two-week active feeding** | | | |
|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| **Phylum** | **Genus** | **GW** | **GWp** | **S** | **Sp** | **GW** | **GWp** | **S** | **Sp** | **GW** | **GWp** | **S** | **Sp** |
| Actinobacteria | Turicella | 0.026 | 0.111 | rare | rare | rare | rare | rare | rare | rare | rare | rare | rare |
| Actinobacteria | Corynebacteria | 0.060 | 0.042 | 0.059 | 0.037 | 0.034 | rare | 0.011 | 0.032 | rare | rare | rare | rare |
| Actinobacteria | Janibacter | rare | 0.012 | rare | rare | rare | rare | rare | rare | rare | rare | rare | rare |
| Actinobacteria | Micrococcus | 0.015 | rare | rare | 0.010 | rare | rare | rare | rare | rare | rare | rare | rare |
| Actinobacteria | unclassified | 0.023 | 0.027 | 0.045 | 0.024 | 0.014 | rare | 0.015 | 0.026 | rare | rare | rare | rare |
| Bacteroidetes | Bacteroides | rare | rare | rare | 0.011 | rare | rare | rare | rare | rare | rare | rare | rare |
| Bacteroidetes | Parabacteroides | rare | rare | 0.011 | rare | rare | rare | rare | rare | rare | rare | rare | rare |
| Bacteroidetes | unclassified | rare | 0.047 | 0.016 | 0.061 | 0.010 | rare | rare | 0.023 | rare | rare | rare | rare |
| Bacteroidetes | Wautersiella | rare | rare | 0.011 | rare | rare | rare | rare | rare | rare | rare | rare | rare |
| Firmicutes | Clostridium sensu_stricto | rare | rare | 0.115 | 0.011 | rare | 0.650 | 0.231 | 0.162 | 0.180 | 0.148 | 0.439 | 0.369 |
| Firmicutes | Exiguobacterium | rare | rare | 0.011 | rare | 0.164 | 0.023 | 0.167 | 0.038 | 0.056 | 0.037 | 0.098 | 0.110 |
| Firmicutes | Jeotgalibacillus | rare | rare | rare | rare | 0.023 | rare | rare | rare | 0.015 | 0.014 | 0.010 | 0.011 |
| Firmicutes | Sarcina | rare | rare | 0.020 | rare | 0.227 | 0.049 | 0.206 | 0.123 | 0.212 | 0.348 | 0.272 | 0.377 |

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|---|---|---|---|---|---|---|---|---|---|---|---|---|---|
| Firmicutes | Staphyloccoccus | 0.011 | 0.029 | 0.017 | rare | rare | rare | rare | rare | rare | rare | rare | rare |
| Firmicutes | Streptococcus | 0.023 | 0.023 | 0.010 | 0.050 | rare | rare | rare | 0.015 | rare | rare | rare | rare |
| Firmicutes | unclassified | 0.023 | 0.031 | 0.023 | 0.042 | rare | 0.108 | 0.073 | 0.091 | 0.210 | 0.130 | 0.122 | 0.064 |
| Proteobacteria | Acinetobacter | 0.027 | 0.015 | 0.070 | 0.022 | 0.030 | 0.010 | rare | 0.057 | rare | rare | rare | rare |
| Proteobacteria | Brevundimonas | 0.010 | 0.019 | rare | rare | rare | rare | rare | rare | rare | rare | rare | rare |
| Proteobacteria | Deefgea | rare | rare | rare | rare | rare | 0.018 | rare | rare | 0.205 | 0.216 | 0.013 | rare |
| Proteobacteria | Loktanella | rare | rare | rare | rare | 0.098 | rare | rare | rare | rare | rare | rare | rare |
| Proteobacteria | Nitratireductor | rare | rare | rare | rare | rare | rare | 0.039 | 0.023 | 0.011 | rare | rare | rare |
| Proteobacteria | Pseudomonas | 0.239 | 0.163 | 0.165 | 0.138 | 0.037 | rare | 0.050 | 0.043 | rare | rare | rare | 0.003 |
| Proteobacteria | Paracoccus | 0.053 | 0.072 | 0.015 | 0.035 | 0.067 | 0.024 | rare | 0.066 | 0.032 | 0.019 | rare | rare |
| Proteobacteria | Rheinheimera | rare | rare | 0.083 | rare | rare | rare | rare | rare | rare | rare | rare | rare |
| Proteobacteria | Stenotrophomonas | 0.045 | 0.049 | 0.044 | 0.029 | rare | rare | 0.028 | 0.022 | rare | rare | rare | rare |
| Proteobacteria | Vibrio | rare | rare | rare | rare | 0.048 | rare | 0.020 | 0.010 | rare | rare | rare | rare |
| Proteobacteria | unclassified | 0.138 | 0.056 | 0.082 | 0.202 | 0.067 | 0.020 | 0.028 | 0.084 | 0.034 | 0.049 | rare | 0.010 |
| Unclassified | unclassified | 0.022 | 0.026 | 0.026 | 0.060 | 0.017 | rare | 0.012 | 0.014 | rare | rare | rare | rare |
| Others | | 0.285 | 0.279 | 0.177 | 0.272 | 0.163 | 0.097 | 0.121 | 0.170 | 0.045 | 0.039 | 0.045 | 0.055 |

At the genus level pre-feeding gut communities across all treatment groups were dominated by *Proteobacteria* from the genus *Pseudomonas,* comprising between 13 to 23% of total community composition. This genus was also present in food and water, although at considerably lower levels (~1%). Upon initiation of feeding, several *Firmicutes* genera including *Sarcina, Exiguobacterium*, and *Clostridium* emerged as the predominant taxa in the lake sturgeon larval gut microbiota sampled after one week of active feeding. As fish aged, *Sarcina* persisted among predominate taxa comprising ~20-30% of the gut community in all **GW, GWp, S**, and **Sp** groups. However, fish raised in stream water (**S, Sp**) had

*Clostridium* as the most predominant taxa after two weeks of active feeding, whereas *Deefgea* in the phylum *Proteobacteria* was as prevalent as *Sarcina* in fish raised in the ground water treatment.

TABLE S3

Relative abundance of predominant taxa defined at threshold > 0.01 for all microbial communities from water samples denoted as **WaterS** (stream); **WaterGW** (groundwater that was UV-treated). These are the most abundant 40 taxa that were selected based on the predefined threshold of 0.01

| | | **Pre-feeding** | | **One-week active feeding** | | **Two-week active feeding** | |
|---|---|---|---|---|---|---|---|
| **Phylum** | **Genus** | **WaterGW** | **WaterS** | **WaterGW** | **WaterS** | **WaterGW** | **WaterS** |
| Acidobacteria | Gp1 | 0.022 | 0.027 | 0.032 | rare | rare | rare |
| Acidobacteria | Gp2 | rare | rare | rare | 0.022 | rare | rare |
| Acidobacteria | Gp3 | rare | rare | rare | 0.024 | rare | rare |
| Acidobacteria | Gp4 | rare | 0.010 | rare | 0.028 | rare | rare |
| Acidobacteria | Gp5 | 0.013 | 0.013 | rare | rare | rare | rare |
| Acidobacteria | Gp6 | rare | rare | 0.041 | rare | rare | 0.024 |
| Acidobacteria | Gp10 | rare | rare | rare | rare | rare | 0.025 |
| Acidobacteria | Gp21 | rare | rare | rare | rare | 0.044 | rare |
| Actinobacteria | Turicella | rare | 0.079 | 0.185 | rare | rare | 0.097 |
| Actinobacteria | Corynebacteria | 0.039 | 0.094 | 0.117 | rare | 0.033 | 0.094 |
| Actinobacteria | Janibacter | rare | rare | rare | rare | rare | 0.014 |
| Actinobacteria | Micrococcus | rare | 0.024 | 0.040 | rare | 0.108 | 0.047 |
| Actinobacteria | unclassified | 0.024 | 0.062 | 0.020 | 0.052 | 0.048 | 0.058 |
| Bacteroidetes | Porphyromonas | rare | rare | 0.017 | rare | rare | rare |
| Bacteroidetes | Prevotella | 0.025 | rare | rare | rare | rare | rare |
| Bacteroidetes | unclassified | 0.111 | 0.017 | rare | 0.091 | 0.066 | 0.019 |

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|---|---|---|---|---|---|---|---|
| Firmicutes | Clostridium sensu_stricto | 0.014 | rare | rare | rare | rare | rare |
| Firmicutes | Clostridium XVIII | 0.016 | rare | rare | rare | rare | rare |
| Firmicutes | Erysipelothrix | 0.013 | rare | rare | rare | rare | rare |
| Firmicutes | Paenibacillus | 0.013 | rare | rare | rare | rare | rare |
| Firmicutes | Staphyloccoccus | | rare | rare | rare | 0.033 | 0.015 |
| Firmicutes | Streptococcus | 0.040 | 0.029 | rare | rare | 0.058 | rare |
| Firmicutes | unclassified | 0.060 | 0.045 | 0.034 | rare | rare | 0.038 |
| Planctomycetes | unclassified | rare | rare | 0.057 | 0.017 | rare | rare |
| Proteobacteria | Acinetobacter | 0.216 | 0.159 | rare | rare | rare | rare |
| Proteobacteria | Aeromonas | rare | 0.022 | rare | rare | rare | rare |
| Proteobacteria | Desulfonatronum | rare | rare | 0.062 | rare | rare | rare |
| Proteobacteria | Hydrogenophaga | rare | rare | rare | rare | rare | 0.036 |
| Proteobacteria | Massilia | 0.019 | rare | 0.073 | rare | rare | rare |
| Proteobacteria | Pseudomonas | 0.022 | 0.018 | rare | rare | rare | rare |
| Proteobacteria | Paracoccus | 0.017 | 0.012 | rare | rare | rare | rare |
| Proteobacteria | Ralstonia | 0.011 | 0.025 | rare | rare | rare | 0.022 |
| Proteobacteria | Sphingomonas | rare | 0.020 | rare | rare | rare | rare |
| Proteobacteria | Stenotrophomonas | 0.014 | 0.028 | rare | rare | 0.044 | rare |
| Proteobacteria | unclassified | 0.108 | 0.075 | 0.173 | 0.271 | 0.143 | 0.172 |
| Verrucomicrobia | 3genus incertae_sedis | rare | rare | rare | 0.042 | rare | rare |
| Verrucomicrobia | Spartobacteria genera_incertae sedis | rare | 0.013 | rare | 0.085 | rare | rare |
| Verrucomicrobia | unclassified | rare | rare | rare | rare | rare | 0.046 |
| Unclassified | unclassified | rare | 0.071 | 0.054 | 0.176 | 0.211 | 0.184 |
| Other | | 0.202 | 0.157 | 0.094 | 0.191 | 0.212 | 0.111 |