Supplemental Material

Table S1. Number of ASVs shared among A) stomach, B) intestine and all environmental sources during visceral regeneration. For each column, the number of total ASVs are listed followed by the percent (%) of total ASVs shared with each sample type. Env. sediment and seawater include samples initially collected at Hamblin and Jehu Ponds, while tank sediment and seawater were collected throughout the experiment from the experimental flow-through tank.

A) Stomach	**All samples (*n* = 67)**	**Initial (*n* = 37)**	**Day 17 (*n* = 6)**	**Day 20 (*n* = 12)**	**Tank Control (*n* = 12)**
Total ASVs	5,810	2,774	1,453	2,486	1,230
Shared with intestine	33.6 %	25.7 %	22.6 %	34.3 %	21.5 %
Shared with tank sediment	17.5 %	23.6 %	30.6 %	29.1 %	42.7 %
Shared with env. sediment	12.9 %	19.8 %	20.4 %	20.9 %	31.2 %
Shared with tank seawater	8.6 %	11.9 %	17.7 %	12.4 %	15.4 %
Shared with env. seawater	3.4 %	5.6 %	7.6 %	5.6 %	9.3 %
Shared with *Gracilaria*	4.2 %	5.4 %	8.3 %	6.1 %	12.4 %
Shared with *Zostera*	2.0 %	2.6 %	3.6 %	2.3 %	4.4 %

B) Intestine	**All samples (*n* = 76)**	**Initial (*n* = 36)**	**Day 13 (*n* = 11)**	**Day 17 (*n* = 6)**	**Day 20 (*n* = 11)**	**Tank Control (*n* = 12)**
Total ASVs	6,689	2,652	1,397	1,089	2,890	937
Shared with stomach	29.2 %	26.9 %	n/a	30.1 %	29.5 %	28.3 %
Shared with tank sediment	13.9 %	18.7 %	27.3 %	34.3 %	22.8 %	31.1 %
Shared with env. sediment	10.7 %	17.8 %	19.3 %	25.7 %	15.8 %	25.5 %
Shared with tank seawater	6.6 %	9.0 %	13.0 %	16.4 %	9.3 %	16.2 %
Shared with env. seawater	3.1 %	6.3 %	6.9 %	8.8 %	4.4 %	11.7 %
Shared with *Gracilaria*	3.6 %	5.0 %	9.7 %	10.3 %	5.0 %	9.5 %
Shared with *Zostera*	1.7 %	2.5 %	3.9 %	3.9 %	1.6 %	3.5 %

Figure S1. Relative abundance barplots of environmental microbial communities from replicate (A) seawater (top row) and (B) sediment (bottom row) samples collected from the field and from the experimental tank on days 13, 17 and 20. Colors represent microbial order-level taxonomy.

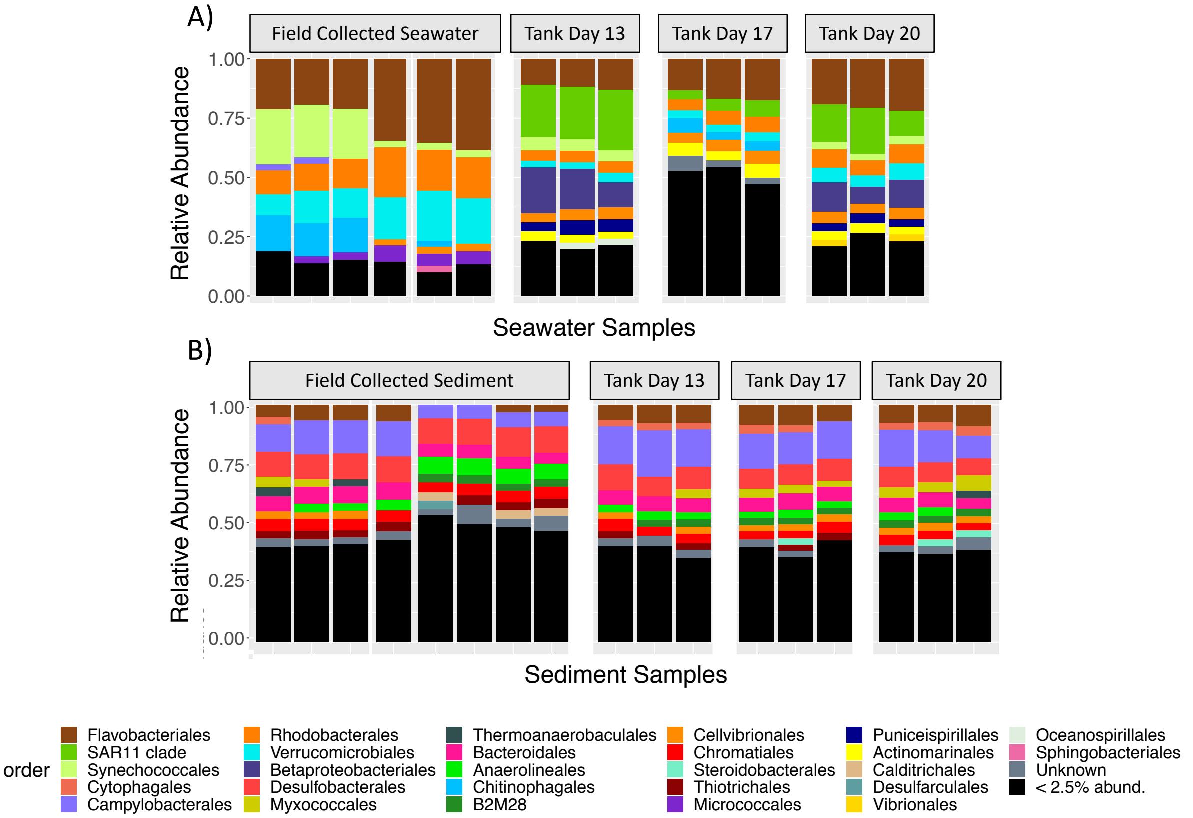

Figure S2. On days 17 and 20, a small ball of sediment was observed within the coelomic cavity of several *S. briareus*. Out of curiosity, this sediment was sampled for microbial communities from *n* = 4 total individual *S. briareus* on days 17 and 20 of regeneration.

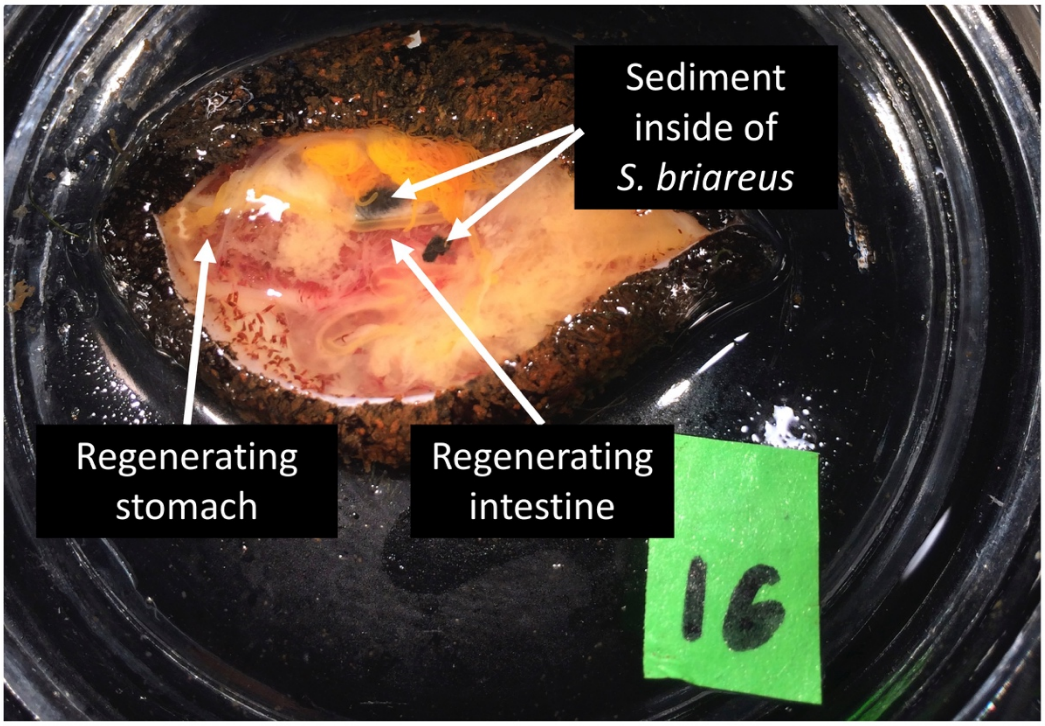

Figure S3. Experimental design. Sea cucumbers (*S. briareus*) were collected in the field from Jehu and Hamblin Ponds, eviscerated to acquire the initial stomach and intestine tissue samples, and randomly placed into cells of a flow-through seawater tank with sediment sourced from Hamblin Pond. Additional sea cucumbers collected at each site were placed directly into the tank without evisceration (Tank Controls). Stomach and intestine tissues were dissected from regenerating sea cucumbers on days 13, 17 and 20 post-evisceration. Stomach and intestine tissues were collected from tank controls using induced evisceration on day 18.

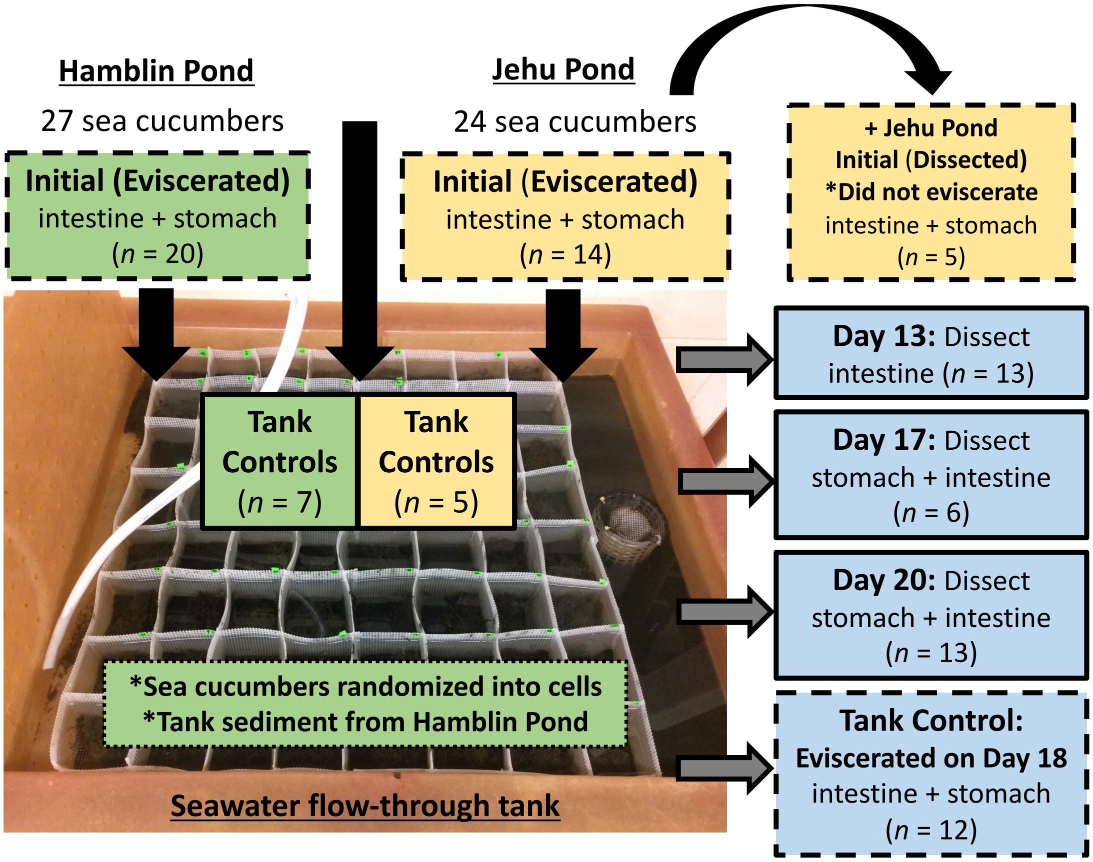

Figure S4. Alpha rarefaction curves, generated in QIIME2, showing the number of observed ASVs vs. sequencing depth for all samples (different colors). Samples were subsequently rarefied to 6,800 sequences per sample (dotted line).