

Table S4. NanoCLUST average percent identity of Clusters at the species level. Species with percentage of identity ≥ 98.7 based on the full sequence of 16S rRNA gene and relative abundance $\geq 0.2\%$.

Species identifies by NanoCLUST	FW	Average identity (%) \pm SD				
		10PSU- GSC	20PSU- GSC	32PSU- GSC	32PSU- SS	32PSU- FD
<i>Acidovorax radialis</i>			99.2 \pm 0.00			
<i>Acinetobacter johnsonii</i> *	95.2 \pm 3.67	95.3 \pm 3.85	91.5 \pm 0.00	93.4 \pm 2.29	99.3 \pm 0.00	99.2 \pm 0.00
<i>Akkermansia muciniphila</i>		99.2 \pm 0.00				
<i>Aliivibrio wodanis</i> *				99.0 \pm 0.00		
<i>Alistipes onderdonkii</i>		91.6 \pm 3.15	99.0 \pm 0.00			
<i>Alistipes putredinis</i>		94.1 \pm 7.42	99.8 \pm 0.00			
<i>Anaerostipes glycerini</i>			99.4 \pm 0.00			
<i>Arcobacter venerupis</i>		99.6 \pm 0.00				
<i>Bacillus cereus</i>	99.1 \pm 0.00					99.8 \pm 0.00
<i>Bacteroides caccae</i>		99.4 \pm 0.00				
<i>Bradyrhizobium mercantei</i>	99.0 \pm 0.00					
<i>Bradyrhizobium rifense</i>		99.4 \pm 0.00				
<i>Cloacibacterium caeni</i>		99.5 \pm 0.00				
<i>Cloacibacterium normanense</i>			99.4 \pm 0.00			
<i>Cutibacterium acnes</i>		99.7 \pm 0.00	99.9 \pm 0.00			
<i>Elizabethkingia anophelis</i>						99.0 \pm 0.00
<i>Eubacterium rectale</i>		99.5 \pm 0.00				
<i>Flavobacterium cheniae</i>		99.3 \pm 0.00				
<i>Flavobacterium succinicans</i> *		98.1 \pm 7.25	98.8 \pm 4.22			
<i>Heliomonas saccharivorans</i>						98.9 \pm 0.00
<i>Herbaspirillum huttiense</i>						99.0 \pm 0.00
<i>Lactococcus raffinolactis</i>		93.0 \pm 0.49	99.5 \pm 0.00			
<i>Megasphaera massiliensis</i>		99.1 \pm 0.00				
<i>Methylobacterium brachiatum</i>				99.1 \pm 0.00		
<i>Methylobacterium radiotolerans</i>	97.5 \pm 0.00					
<i>Microbacterium ginsengisoli</i>	99.6 \pm 0.00	99.8 \pm 0.00				

<i>Microbacterium mangrovi</i>				94.6±0.00	
<i>Micrococcus luteus</i>				99.7±0.00	
<i>Moraxella osloensis</i>	98.6±0.00	98.6±0.00		99.3±0.00	99.0±0.00
<i>Morganella morganii</i>		97.6±1.60	98.7±0.00		
<i>Paraburkholderia fungorum</i>				98.5±0.00	99.2±0.00
<i>Pelomonas saccharophila</i>					99.1±0.00
<i>Phascolarctobacterium succinatutens</i>		99.0±0.00			
<i>Phocaeicola coprocola</i>		99.2±0.00			
<i>Providencia rettgeri</i> *		98.9±0.00			
<i>Pseudomonas brenneri</i>		99.4±0.00			
<i>Pseudomonas cedrina</i>					99.4±0.00
<i>Pseudomonas migulae</i>	98.5±0.00	99.1±0.00	95.5±0.00	99.3±0.00	
<i>Rahnella aquatilis</i>		99.2±0.00			
<i>Ralstonia insidiosa</i>					99.4±0.00
<i>Rhizobium zoeae</i>	99.6±0.00	99.4±0.00			
<i>Shigella flexneri</i>	97.3±2.47	99.5±0.00	97.0±3.38	95.9±0.34	
<i>Shigella sonnei</i>			93.5±0.00	98.9±0.00	
<i>Sphingobium yanoikuyae</i>				99.5±0.00	
<i>Staphylococcus aureus</i>			99.6±0.00	96.9±0.00	
<i>Streptococcus thermophilus</i>	99.8±0.00		99.5±0.00	98.9±0.00	
<i>Thermosiphon melanesiensis</i>					100.0±0.00
<i>Uruburuella suis</i>		99.6±0.00			

SD: Standard deviation; *indicate fish-pathogenic bacteria. FW: Freshwater previous treatment group, GSC: gradual salinity change at 10 PSU, 20 PSU and 32 PSU groups; 32PSU-SS Salinity shock at 32-PSU group; 32PSU-FD: Salinity shock at 32 PSU group previously feeding with a functional diet.