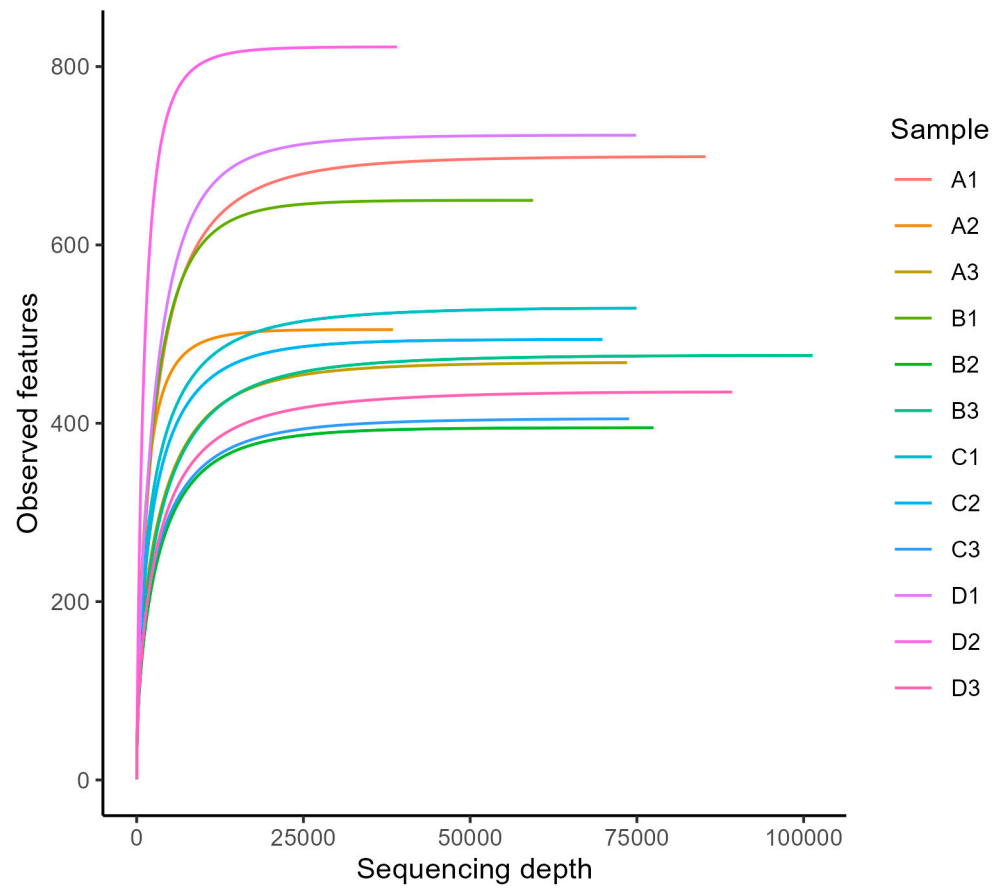


Supplementary materials

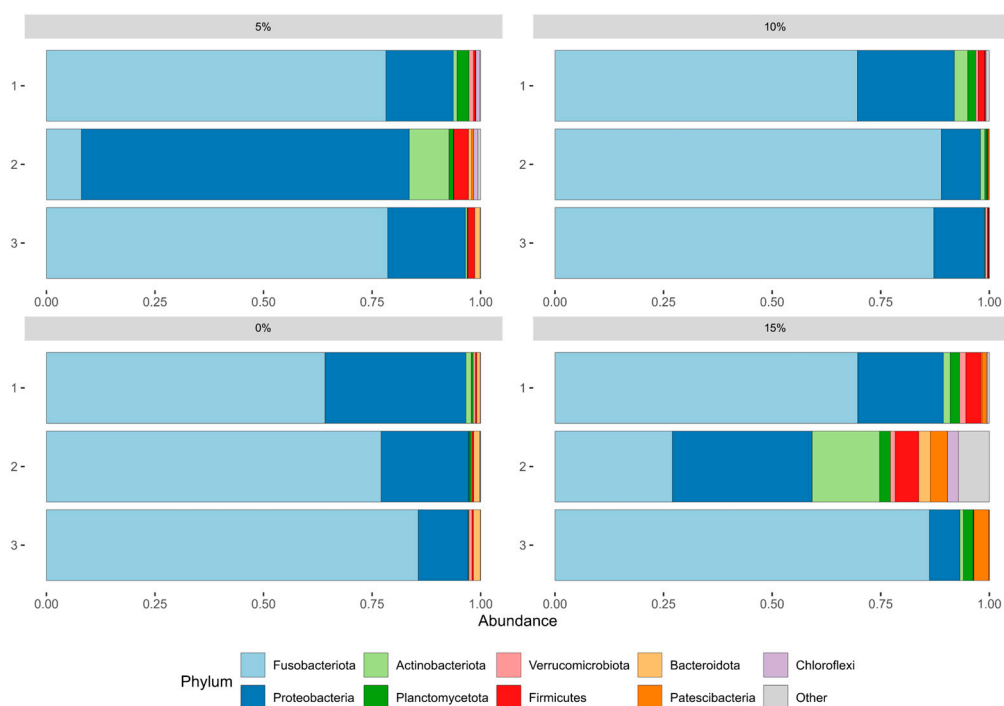
Supplementary Table S1. Summary of the number of sequences during each step of the preprocessing pipeline.

Sample	Input	Filtered	Denoised F	Denoised R	Merged	Non-chimeric
A1	137964	118906	117923	118081	116302	85291
A2	86292	71602	71111	71079	70076	38436
A3	120168	104691	103963	104117	103137	73540
B1	104321	89729	89197	89197	88141	59431
B2	117215	101657	101289	101435	100931	77484
B3	154965	136912	136406	136531	135721	101327
C1	133851	117199	116392	116552	114801	74941
C2	111448	97342	96927	96919	96192	69817
C3	117915	101657	101323	101355	100870	73838
D1	125507	109026	108518	108418	107322	74878
D2	78796	67646	66824	66603	64286	39045
D3	156258	137479	136385	136602	134975	89299

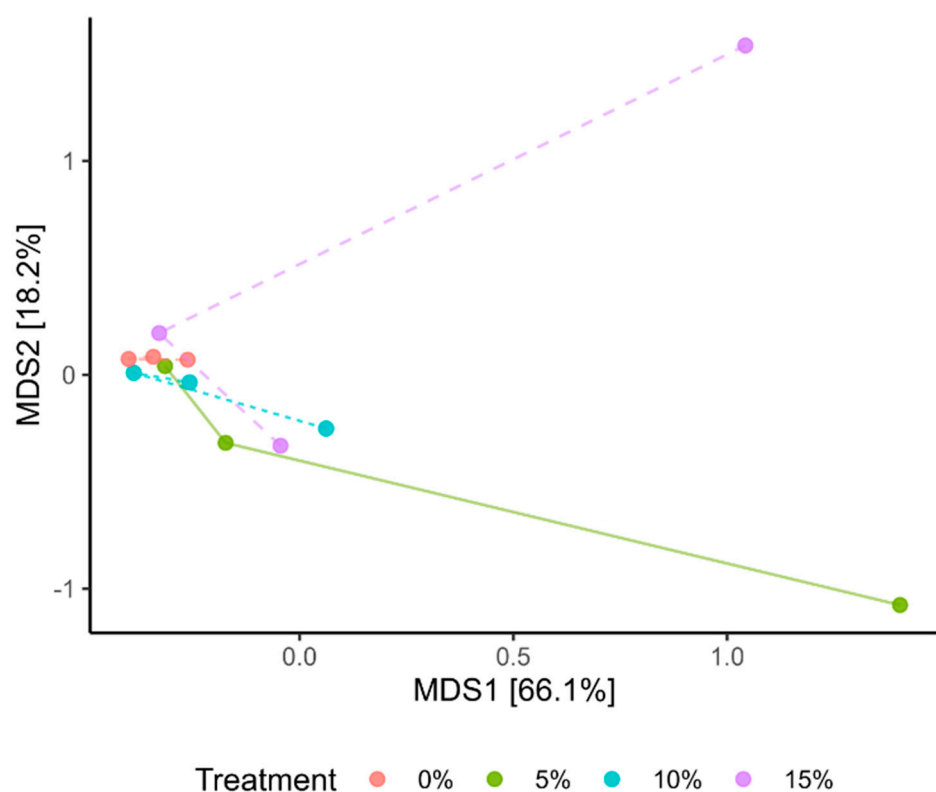
Denoised F = denoised forward sequences. Denoised R = denoised reverse sequences. The number non-chimeric sequences represent the final amount of reads after preprocessing. The 5% supplementation is represented with letter "A", 10% with "B", 15% with "D" and the control group with "C". Associated number to the sample refers to each of the triplicates.



Supplementary Figure S1. Rarefaction curves of observed features (amplicon sequence variants, ASVs) per sample. All the analyzed samples converged before reaching the 25000 reads, indicating that ASV richness was obtained. The 5% supplementation is represented with letter "A", 10% with "B", 15% with "D" and the control group with "C". Associated number to the sample refers to each of the triplicates.



Supplementary Figure S2. Relative abundance of top 10 most abundant phyla in the gut microbiota of tilapia fry fed with *A. maxima* supplemented feed. Associated number refers to the replica.



Supplementary Figure S3. Principal Coordinate Analysis of gut microbiota of tilapia fry. None of the values presented a significant difference per treatment ($p > 0.05$)

Supplementary Table S2. Top 50 predicted metabolic pathways annotated with PICRUST.

Abbreviation	Pathway
PWY-3781	Aerobic respiration I (cytochrome C)
NONOXIPENT-PWY	Pentose phosphate (non-oxidative branch)
PWY-7111	Pyruvate fermentation to isobutanol
PWY-6588	Pyruvate fermentation to acetone
PWY-5676	Acetyl-CoA fermentation to butanoate
PWY-5101	L-isoleucine biosynthesis II
CALVIN-PWY	Calvin-Benson-Bassham cycle
DTDPRHAMSYN-PWY	dTDP-beta-L-rhamnose biosynthesis
PWY-5104	L-isoleucine biosynthesis IV
PWY-5103	L-isoleucine biosynthesis III
PWY-7663	Gondoate biosynthesis (anaerobic)
PWY-5973	Cis-vaccenate biosynthesis
PWY-5667	CDP-diacylglycerol biosynthesis I
PWY0-1319	CDP-diacylglycerol biosynthesis II
PWY-6609	Adenine and adenosine salvage III
ILEUSYN-PWY	L-isoleucine biosynthesis I (from threonine)
VALSYN-PWY	L-valine biosynthesis
PWY0-1296	Purine ribonucleosides degradation
P161-PWY	Acetylene degradation (anaerobic)
PWY-7229	Adenosine nucleotides <i>de novo</i> biosynthesis I
PWY-5686	UMP biosynthesis I
PWY0-162	Pyrimidine ribonucleotides <i>de novo</i> biosynthesis
PWY-2942	L-lysine biosynthesis III
PWY-7208	Pyrimidine nucleobases salvage
PWY-7220	Adenosine deoxyribonucleotides <i>de novo</i> biosynthesis II
PWY-7222	Guanosine deoxyribonucleotides <i>de novo</i> biosynthesis I
PWY-5695	Inosine 5'-phosphate degradation
PWY-6126	Adenosine nucleotides <i>de novo</i> biosynthesis II
BRANCHED-CHAIN-AA-SYN-PWY	Branched chain amino acid biosynthesis
PHOSLIPSYN-PWY	Phospholipid biosynthesis III
PWY-7219	Adenosine ribonucleotides <i>de novo</i> biosynthesis
PPGPPMET-PWY	ppGpp metabolism
PWY-5097	L-lysine biosynthesis VI
PWY-6386	UDP-N-acetylmuramoyl-pentapeptide biosynthesis II
PWY-3001	L-isoleucine biosynthesis I
PWY4FS-7	Phosphatidylglycerol biosynthesis I
PWY4FS-8	Phosphatidylglycerol biosynthesis I
ANAGLYCOLYSIS-PWY	Glycolysis III (from glucose)
PWY-7184	Pyrimidine deoxyribonucleotides <i>de novo</i> biosynthesis I
PWY-6387	UDP-N-acetylmuramoyl-pentapeptide biosynthesis III
PWY-7228	Guanosine nucleotides <i>de novo</i> biosynthesis I
GLYCOGENSYNTH-PWY	Glycogen biosynthesis I (from ADP-D-Glucose)
THRESYN-PWY	L-threonine biosynthesis
PWY-841	Purine nucleotides <i>de novo</i> biosynthesis I
OANTINGEN-PWY	O-antigen building blocks biosynthesis (E. coli)
PEPTIDOLYCANSYN-PWY	Peptidoglycan biosynthesis I
PWY-6385	Peptidoglycan biosynthesis III (mycobacteria)
PWY-6125	Guanosine nucleotides <i>de novo</i> biosynthesis II
PWY-6892	Thiazole component of thiamine diphosphate biosynthesis I
PWY0-1297	Purine deoxyribonucleosides degradation

Supplementary Table S3. Unique genera in the gut microbiota of tilapia fry fed with *A. maxima* supplemented feed.

Treatment	Unique genera				
Control	<i>Candidatus</i> Megaira	<i>Candidatus</i> Metachlamydia	<i>Clostridium</i> sensu stricto 13	<i>Fastidiosipila</i>	Flammeovirgaceae Family
	Flavobacteriales Order	<i>Fonticella</i>	Obscuribacteraceae Family	<i>Oceanivirga</i>	<i>Rothia</i>
	<i>Rubellimicrobium</i>				
5% supplementation	<i>Ammonii bacillus</i>	<i>Anaerobacterium</i>	<i>Anaeromyxobacter</i>	<i>Arcticibacter</i>	<i>Aridibacter</i>
	<i>Blastopirellula</i>	<i>Candidatus</i> Ovatusbacter	<i>Candidatus</i> Woesebacteria Order	<i>Candidatus</i> Woykebacteria Order	<i>Candidimonas</i>
	Corynebacteriaceae Family	<i>Deinococcus</i>	<i>Delftia</i>	<i>Glycocalis</i>	Gracilibacteria Class
	<i>Kocuria</i>	<i>Kouleothrix</i>	Ktedonobacteraceae Family	<i>Lunatimonas</i>	Micrococcaceae Family
	Micromonosporaceae Family	<i>Mycoplasma</i>	<i>Oscillochloris</i>	<i>Parviterribacter</i>	Phycisphaeraceae Family
	<i>Pseudorhodoplanes</i>	<i>Roseiflexus</i>	<i>Salinarimonas</i>	Saprospiraceae Family	<i>Sediminibacterium</i>
	<i>Synechococcus</i> PCC-7942	<i>Tsakumurella</i>	Vampirovibrionales Order	Weeksellaceae Family	ASV2509
10% supplementation	Acidobacteriae Class	<i>Aquicola</i>	<i>Aurantimicrobium</i>	<i>Chitinivorax</i>	<i>Defluviimonas</i>
	Gammaproteobacteria Incertae Sedis Order	<i>Haemophilus</i>	<i>Hydrogenophilus</i>	Hyphomicrobiaceae Family	Legionellaceae Family
	<i>Paraclostridium</i>	Parcubacteria Class	Planococcaceae Family	<i>Propioniceella</i>	<i>Prosthemicrobium</i>
	Proteobacteria Phylum	<i>Rickettsiella</i>	Simkaniaceae Family	<i>Streptococcus</i>	<i>Terrimicrobium</i>
15% supplementation	<i>Abditibacterium</i>	Acetobacteraceae Family	<i>Acidibacter</i>	Acidimicrobiaceae Family	<i>Acidisphaera</i>
	<i>Actinobacillus</i>	Actinobacteriota Phylum	<i>Actinomyces</i>	<i>Actinomycetospira</i>	<i>Actinotignum</i>
	<i>Adhaeribacter</i>	<i>Aeromicrobium</i>	<i>Aetherobacter</i>	<i>Agromyces</i>	<i>Akkermansia</i>
	<i>Alishewanella</i>	Alphaproteobacteria Class	<i>Alsobacter</i>	<i>Amaricoccus</i>	Anaerolineaceae Family
	<i>Anaerosinus</i>	<i>Anaerosphaera</i>	<i>Ancalomicrobium</i>	<i>Archangium</i>	<i>Arenimonas</i>
	Armatimonadales Order	Bacteriodales Order	Bdellovibrionaceae Family	<i>Belnapia</i>	<i>Bifidobacterium</i>
	Blastocatellaceae Family	Blastocatellia Class	<i>Blastococcus</i>	<i>Brevibacillus</i>	<i>Bryobacter</i>
	<i>Butyrivibrio</i>	<i>Caenimonas</i>	<i>Candidatus</i> Entotheonella	<i>Candidatus</i> Pacebacteria Order	<i>Candidatus</i> Peribacteria Order
	<i>Candidatus</i> Solibacter	<i>Candidatus</i> Udaeobacter	Caulobacteraceae Family	<i>Cellulomonas</i>	<i>Cellvibrio</i>
	Cellvibrionaceae Family	Christensenellaceae Family	<i>Chromohalobacter</i>	Clostridia Class	Clostridioides
	<i>Clostridium</i> sensu stricto 12	<i>Couchioplanes</i>	<i>Craurococcus</i> - <i>Caldovatus</i>	<i>Crossiella</i>	<i>Dactylosporangium</i>
	<i>Desulfatiglans</i>	<i>Desulfovibrio</i>	<i>Devosia</i>	Dojkabacteria Class	<i>Duganella</i>
	<i>Elstera</i>	Elsterales Order	<i>Enhydrobacter</i>	Entomoplasmatales Order	Entotheonellaceae Family
	Euzebyaceae Family	<i>Falsarthrobacter</i>	<i>Finegoldia</i>	<i>Flavisolibacter</i>	<i>Fusibacter</i>
	<i>Fusicatenibacter</i>	<i>Fusobacterium</i>	<i>Gallibacterium</i>	<i>Gemella</i>	Gemmatimonadaceae Family
	Gemmatimonadota Phylum	<i>Geodermatophilus</i>	<i>Haliangium</i>	<i>Hassallia</i>	<i>Holdemanella</i>
	Holophagae Class	Hungateiclostridiaceae Family	Hydrogenispora Order	<i>Hydrogenophaga</i>	<i>Hymenobacter</i>
	<i>Illumatobacter</i>	<i>Insolitipirillum</i>	<i>Jatrophihabitans</i>	<i>Jeotgalicoccus</i>	Kallotenuales Order
	<i>Klenkia</i>	<i>Krasilnikovia</i>	<i>Kribbella</i>	<i>Kroppenstedtia</i>	<i>Kutzneria</i>
	<i>Lechevalieria</i>	<i>Leuconostoc</i>	<i>Limosilactobacillus</i>	<i>Loigolactobacillus</i>	Longimicrobiaceae Family
	<i>Luedemannella</i>	<i>Luteitalea</i>	<i>Marinobacter</i>	<i>Marmoricola</i>	<i>Methanosaeta</i>
	<i>Methyloversatilis</i>	<i>Micromonospora</i>	Microscillaceae Family	<i>Modestobacter</i>	Muribaculaceae Family
	Myxococcaceae Family	<i>Nannocystis</i>	<i>Nevskia</i>	<i>Nissabacter</i>	Nitrosococcaceae Family
	Nitrosomonadaceae Family	<i>Nitrospira</i>	<i>Novosphingobium</i>	<i>Olivibacter</i>	<i>Ornithinibacter</i>
	Oscillospirales Order	Oxalobacteraceae Family	<i>Oxalophagus</i>	<i>Pajaroellobacter</i>	<i>Paludibacter</i>
	<i>Pasteuria</i>	<i>Pedobacter</i>	Pedosphaeraceae Family	<i>Pelosinus</i>	<i>Phenylobacterium</i>

<i>Phytomonospora</i>	Planctomycetota Phylum	Polyangiales Order	<i>Prevotella</i>	<i>Prevotella_9</i>
<i>Propionicimonas</i>	<i>Pseudoxanthomonas</i>	<i>Psychroglaciecola</i>	Pyrinomonadaceae Family	<i>Rhizobacter</i>
Rhodanobacteraceae Family	<i>Rhodopirellula</i>	<i>Rhodoplanes</i>	Rikenellaceae Family	Rokubacteriales Order
<i>Rubrobacter</i>	<i>Ruminiclostridium</i>	<i>Saccharothrix</i>	<i>Sandaracinaceae</i>	<i>Sandaracinus</i>
<i>Schlesneria</i>	<i>Segetibacter</i>	Sericytochromatia Class	<i>Shinella</i>	<i>Skermanella</i>
<i>Solirubrobacter</i>	Solirubrobacteraceae Family	<i>Sphaerisporangium</i>	Sporichthyaceae Family	<i>Stenotrophobacter</i>
<i>Steroidobacter</i>	Streptomycetaceae Family	Streptosporangiaceae Family	Succinivibrionaceae Family	<i>Symbiobacterium</i>
Synthrophales Order	<i>Tepidimonas</i>	Tepidisphaerales Order	<i>Terrimonas</i>	<i>Tetragenococcus</i>
Thermoanaerobaculaceae Family	Thermoplasmata Class	<i>Variovorax</i>	Vibrionaceae Family	Vicinamibacteraceae Family
Vicinamibacterales Order	<i>Virgisporangium</i>			

Genera represented as other taxonomic ranks or the ASV number must be interpreted as an unidentified genus from specified rank or ASVs number, respectively.