Electronic Supplementary Material (ESI) for Environmental Science: Nano.

Supplementary Materials

Toxic effects of carbon quantum dots on the gut–liver axis and gut microbiota in the common carp Cyprinus carpio

Table S1 Primer sequences for qRT-PCR analysis.

Primer	Forward	Reverse	Acc. Num.
40S	CCGTGGGTGACATCGTTACA	TCAGGACATTGAACCTCACTGTCT	XM_019078334
occludin	GACGCCATGGATGAGTACAA	GTGGTTGAGTTTGGCTTTCAG	KF975606.1
claudin-2	CTGGAGTTGATGGGTTTCTTTTG	AGACCTTTCATGCTTTCTACCG	KU200691.1
zonula occludens-1	GATATGTTCGGAGGTGCGCT	ATGTTGCATGGTGCTTGCTG	KY290394.1
nrf-2	GTATGACCCAGAGACAAACC	CCAACCACATACAGACTTCC	XM_019124298.1
ho-1	GCTCATGCATATACGCGCTA	CAGAATTCCCTTGTTGCCACT	XM_019071460.1
tlr4	CGAGTCAGAACCTCAGCC	CCTTGCTCCCCCTCATCC	XM_019090185.1
myd88	CGCCGAAATGATGGACTTCAC	TCTACTGTTGCCTCTGGACG	HQ380208.1
nf-κB/p65	AGAAGAGCAACGACACCACAA	TTGTACGGCTGGTTCTTGGTT	MN167531.1
il-1β	CAAACTGGAGCTGTCTTCGC	CTTCACCAGACGCTCTTCGAT	AB010701.1
tnf-α	AGCCAGGTGTCTTTCCACAT	ATGTAGCCGCCATAGGAATCG	XM_019088899.1
srebp-1c	CACGGCTCTGCTCAACGACAT	TGCGGAGGAGACTGCTGGAA	XM_019073316.1
fas	GAGAAAGTGGTGGTCGCTAAA	CATCACGCACACCCAGAATA	XM_019070657.1
mttp	CGGAGGGTGTTCCTATTC	TATGCGGTTCAGTGTCTT	XM_019122094.1
cpt-1α	CAGATGGAAAGTGTTGCTAATGAC	TGTGTAGAAGTTGCTGTTGACCA	XM_019122018.1
hmgcr	TGGAGCAGGTCATCACGC	GATTGGTCAGGGAGCAGTT	XM_019073034.1
fxr	GGTGCTGAGGAAGGTCTG	GTGGTGGTGGTTGAGGGT	XM_019069273.1
abcg1	AGCAGACGCCGCTGTTAC	TTCTCCACCACGGTCCTTC	XM_019091447.1
abcg8	CAAGCAAACGGTCATAAAG	TCATAGTGCCACCCTCATC	XM_019114412.1
fgf19	TGTGATCCAGAGTCCCAG	GTGTCCCGTGTGCAGTTT	XM_019066901.1
cyp7a1	GTGCTCTTCAGTTTGGGG	GCAGGTTCTCGGTAGTGT	XM_019074263.1
cyp27a1	AGATGTGGTCAATGCGGT	AGCCAATGCGTGTCTCAA	XM_019102935.1

Table S2 Total bases, sequence number, and Good's coverage (i.e., sequencing depth index) from nine samples. CK: control group (CQDs at 0 mg/kg BW); C1: treatment group 1 (CQDs at 2 mg/kg BW); C2: treatment group 2 (CQDs at 20 mg/kg BW).

Samples	**Total bases**	**Sequence number**	**Coverage**
CK_1	23,362,776	47286	0.999247
CK_2	19,584,385	44921	0.99913
CK_3	20,556,309	50768	0.999159
C1_1	24,189,174	69391	0.999184
C1_2	24,954,254	47934	0.998726
C1_3	25,570,431	41146	0.999349
C2_1	22,595,429	45399	0.998902
C2_2	20,120,295	47013	0.999055
C2_3	23,749,973	51377	0.999386

Fig. S1 Mean fluorescence intensity of intestinal tissue in the control and CQD treatment groups. Data are mean ± SEM (n = 10). P values were obtained by two-tailed Student's *t*-test using GraphPad Prism. **$P < 0.01$.

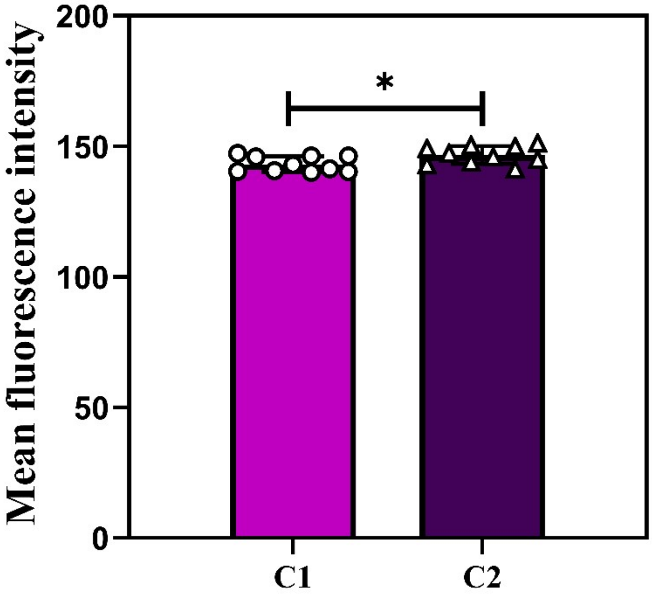

Fig. S2 Mean fluorescence intensity of liver tissue in the control and CQD treatment groups. Data are mean ± SEM (n = 10). P values were obtained by two-tailed Student's *t*-test using GraphPad Prism. $^{**}P < 0.01$.

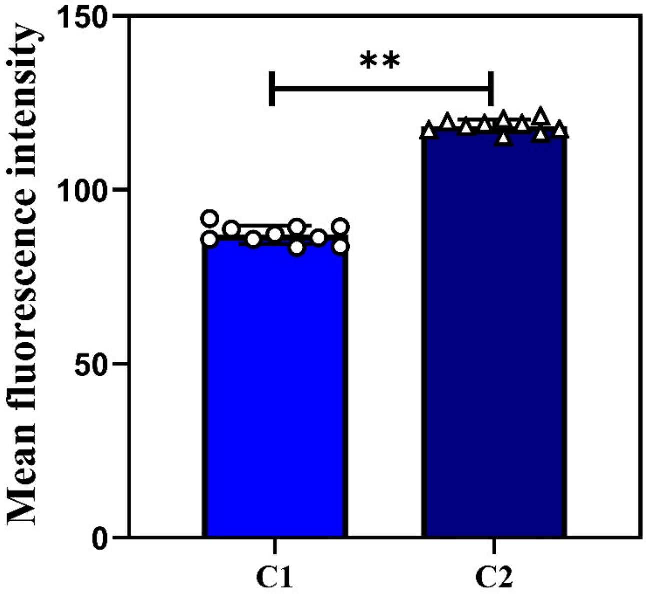

Fig. S3 Rank–abundance curves of bacterial OTUs in the control and CQD treatment groups.

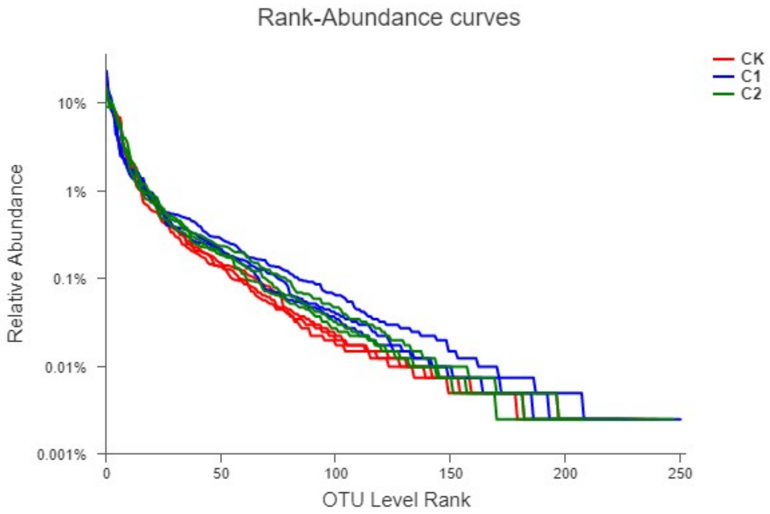

Fig. S4 PICRUSt analysis based on clusters of orthologous groups (COGs). The functional composition of the gut microbiota metagenome was predicted by COGs for the treatment groups.