## Supplementary Materials

# 1 Materials and methods

## 1.1 Chemicals

The detailed information of all chemicals, standards, materials and plants is shown in Table S1.

## 1.2 Treatment of wastewater PFOS by the VFCW

Figure S1 shows the layout and structure of the experimental VFCW. The characteristics of the wastewater are shown in Table S2.

## 1.3 Determination of PFOS

The PFOS was analyzed using HPLC (Dionex Ultimate 3000, USA) with API 3200 triple quadrupole tandem mass spectrometry (AB Company, Canada). The MS/MS was operated in electrospray negative ionization and multiple reactions monitoring mode. Under optimum conditions, 10 μL of sample volume was injected, and an HPLC BEH C18 column (3.0 mm × 150 mm, 3.5 μm, Waters, USA) for separation of the target analytes at a flow rate of 0.3 mL/min. Methanol (A) and 10 mM ammonium acetate aqueous solution (B) were used as mobile phases at a flow rate of 0.3 mL/min. The HPLC gradient elution started at 40% A and 60% B, continued with a linear change to 90% A up to 8 min (held for 4 min), and then immediately restored to 40% A (held for 3 min). Information on other MS parameters is shown in Table S3. The method detect limit (MDL) and (method quantification limit (MQL) data of the extraction method are shown in Table S4.

## 1.4 Analysis of the soil microbial community in the VFCW

An agarose gel image of the extracted genomic DNA is shown in Fig. S2.

## 2 Results and discussion

The mass of root and aerial parts of *E. crassipes and C. alternifolius* was shown in Table S5. The analysis of significance of difference on pH, COD, TN, TP and ammonia nitrogen removal of different PFOS concentrations was shown in Table S6. Figure S3 shows the Change of pH of wetland effluent under different PFOS concentration stress. Figure S4 shows the Shannon index curve for each sample. Figure S5 shows the analysis of bacterial COG gene prediction and clustering information of all samples.

## 3 Tables and figures

Table S1 Detailed information of chemicals and materials

| Chemicals and materials | Grade | Manufacturer |
|---|---|---|
| PFOS | 95% | Silworld Chemical Co. Ltd (Wuhan, China) |
| $^{13}C_8$-PFOS(Na) | 98% | Wellington Laboratories Inc. (Ontario, Canada) |
| $^{13}C_2$-PFOA | 98% | Wellington Laboratories Inc. (Ontario, Canada) |
| Ammonium acetate | HPLC | Merck (Darmstadt, Germany) |
| Methanol | HPLC | Merck (Darmstadt, Germany) |
| Quartz sand | 2–8 mm | Huilong Environmental Protection Technology Co., Ltd (Yixing, China) |
| Cobble stone | 8–32 mm | Huilong Environmental Protection Technology Co., Ltd (Yixing, China) |
| *E. crassipes* | Seedlings | Hangzhou Jacob Agricultural Technology Co., Ltd (Hangzhou, China) |
| *C. alternifolius* | Seedlings | Hangzhou Jacob Agricultural Technology Co., Ltd (Hangzhou, China) |

Table S2 The original properties of the wastewater

| Index | Value |
|---|---|
| pH | 6.69 ± 0.25 |
| COD (mg/L) | 180.55 ± 2.98 |
| TN (mg/L) | 34.62 ± 1.96 |
| TP (mg/L) | 9.13 ± 1.38 |
| $NH_3$-N (mg/L) | 20.04 ± 1.76 |

Table S3 Parameters of mass spectrometer when PFOS was determined

| Chemicals | Q1 (m/z) | Q3 (m/z) | DP (V) | EP (V) | CEP (V) | CE | CXP |
|---|---|---|---|---|---|---|---|
| Object (PFOS) | 498.8 | 98.9 | –85 | –10 | –24 | –66 | 0 |
| Purification internal standards (13C8-PFOS) | 506.9 | 80.0 | –70 | –4 | –34 | –86 | 0 |
| Sampling internal standards (13C2-PFOA) | 414.9 | 370 | –15 | –4 | –16 | –10 | –4 |

Table S4 The MDL and MQL data of the extraction methods

| Samples | Chemicals | Sample amount | MDL (ng/g) | MQL (ng/g) | Standard recovery rate (%) |
|---|---|---|---|---|---|
| Plant, soil | PFOS | 0.5 g | 0.50 | 2.00 | 109 |
| Plant, soil | F53B | 0.5 g | 0.17 | 0.71 | 79.5–129 |
| Water | PFOS | 500 mL | 0.48 | 1.94 | 107 |

Table S5 The mass of root and aerial parts of *E. crassipes and C. alternifolius*

| Plant species | PFOS concentration (mg/L) | Roots (mg) | Aerial parts (mg) | Total mass (mg) |
|---|---|---|---|---|
| *E. crassipes* | 0 | 248.70 ± 8.99 | 1663.68 ± 11.87 | 1912.38 ± 13.45 |
| | $10^{-3}$ | 412.43 ± 39.07 | 1585.06 ± 61.05 | 1997.49 ± 92.11 |
| | 0.1 | 507.37 ± 44.87 | 1656.25 ± 56.19 | 2163.62 ± 64.80 |
| | 10 | 514.77 ± 49.77 | 1673.62 ± 46.22 | 2188.38 ± 168.15 |
| *C. alternifolius* | 0 | 125.43 ± 9.15 | 632.4 ± 15.34 | 757.83 ± 14.67 |
| | $10^{-3}$ | 261.72 ± 23.48 | 777.45 ± 96.06 | 1039.18 ± 91.54 |
| | 0.1 | 156.14 ± 5.50 | 496.69 ± 52.86 | 652.83 ± 5.43 |
| | 10 | 129.09 ± 3.80 | 470.25 ± 16.55 | 599.35 ± 16.59 |

Table S6 The analysis of significance of difference on pH, COD, TN, TP and ammonia nitrogen removal of different PFOS concentrations

| Index | Concentration of PFOS (mg/L) | | | |
|---|---|---|---|---|
| | 0 | $10^{-3}$ | 0.1 | 10 |
| pH | 7.41 ± 0.05 | 7.29 ± 0.04[b)] | 7.16 ± 0.04[a)] | 7.23 ± 0.05[a)] |
| COD (%) | 60.57 ± 2.31 | 53.14 ± 1.93[a)] | 58.07 ± 2.91[c)] | 47.36 ± 2.76[a)] |
| TN (%) | 67.36 ± 2.89 | 62.07 ± 2.81[c)] | 61.43 ± 1.66[c)] | 53.36 ± 2.33[a)] |
| TP (%) | 61.64 ± 3.75 | 61.14 ± 2.22 | 63.64 ± 2.83[c)] | 53.50 ± 3.04[a)] |
| $NH_3$-N (%) | 62.43 ± 2.08 | 65.07 ± 1.27[b,c)] | 58.43 ± 1.31[c)] | 52.57 ± 0.942[a)] |

Notes: Compared with the PFOS concentration of 0 mg/L group, the difference was statistically significant, a) $P < 0.05$;

Compared with the PFOS concentration of 0.1 mg/L group, the difference was statistically significant, b) $P < 0.05$;

Compared with the PFOS concentration of 10 mg/L group, the difference was statistically significant, c) $P < 0.05$

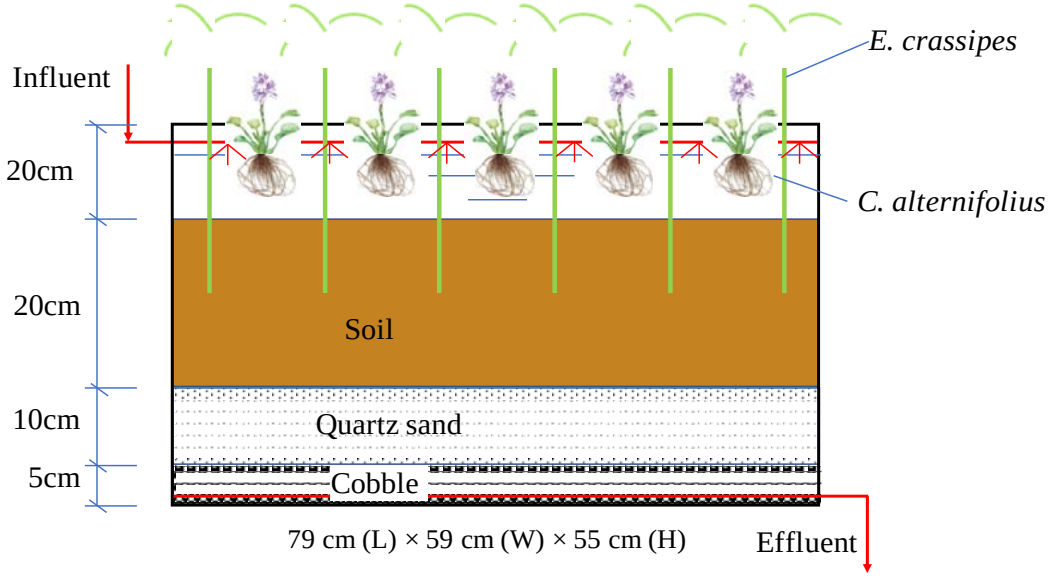


Fig. S1 Schematic diagram of artificial wetland equipment

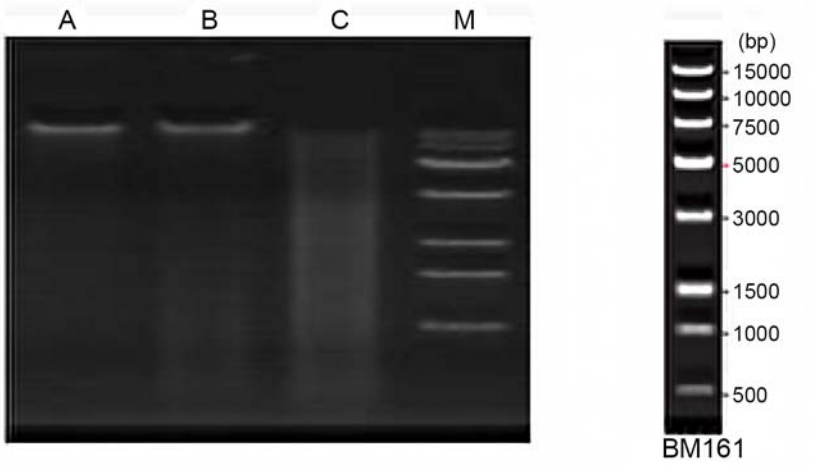


Fig. S2 The agarose electrophoresis of the extracted genomic DNA in soil. Marker is a DNA Marker, which only detects genomic contamination and does not represent RNA strip size. Dot sequence: A, B, C, M, M: DNA Marker, A: initial soil, B: 42 d control group, C: 42 d add 10 mg/L PFOS group

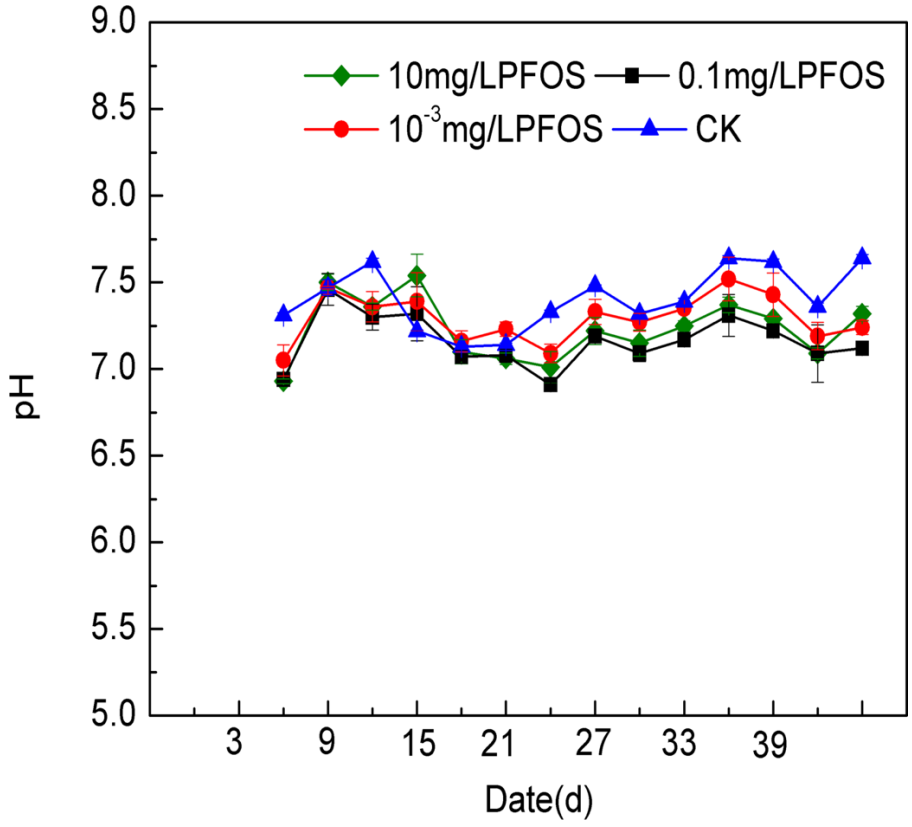


Fig. S3 Change of pH of wetland effluent under different PFOS concentration stress

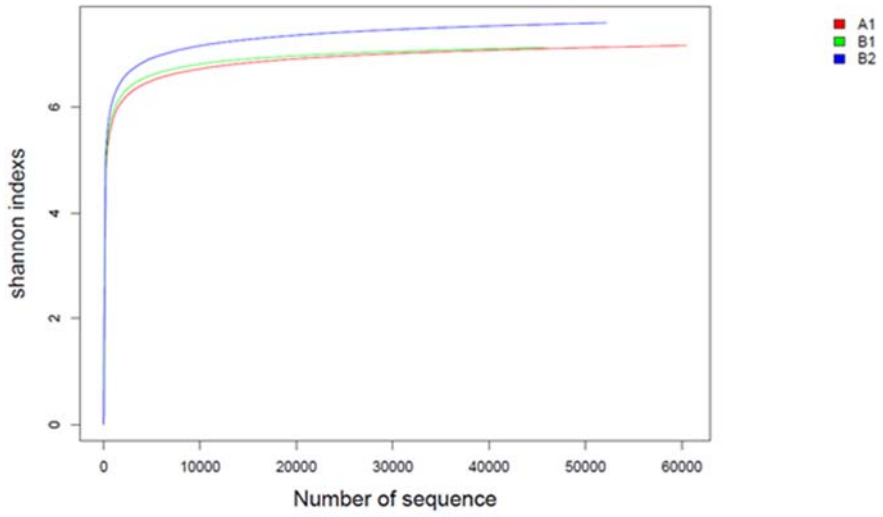


Fig. S4 Shannon index curve for each sample. A1: original soil sample; B1: Soil samples of control group after 42 d; B2: Soil samples after adding 10mg/L PFOS group for 42 d

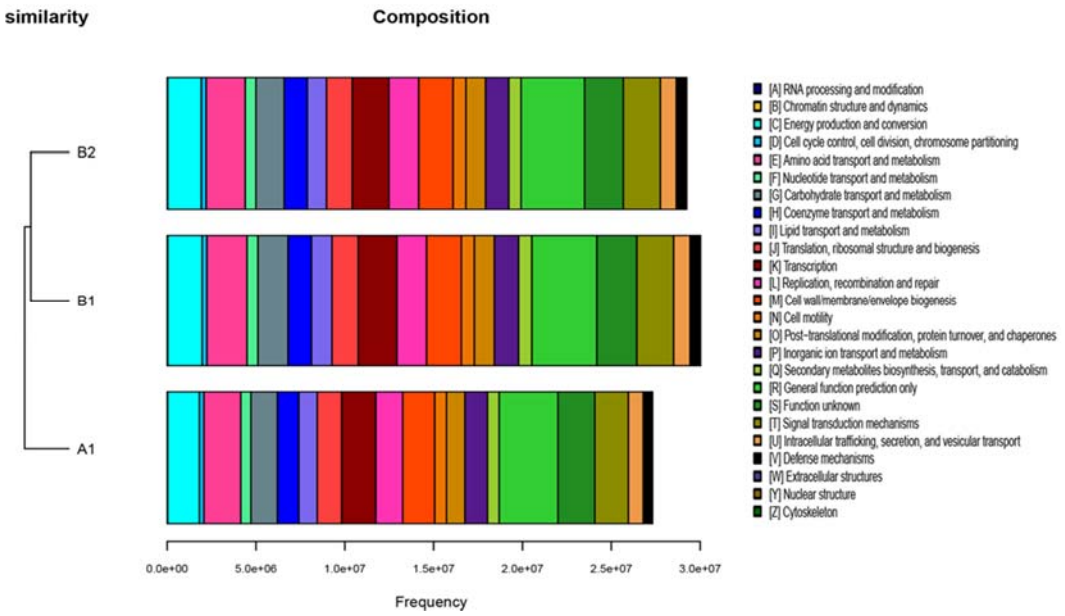


Fig. S5 Analysis of bacterial COG gene prediction and clustering information of all samples. Left: sample clustering tree diagram based on Bray-Curtis; Middle: species bacterial COG gene prediction; Right: pictorial representation of species. A1: original soil sample; B1: Soil samples of control group after 42 d; B2: Soil samples after adding 10mg/L PFOS group for 42 d