

Supplementary materials for:

Distinct responses from bacterial, archaeal and fungal streambed communities to severe hydrological disturbances

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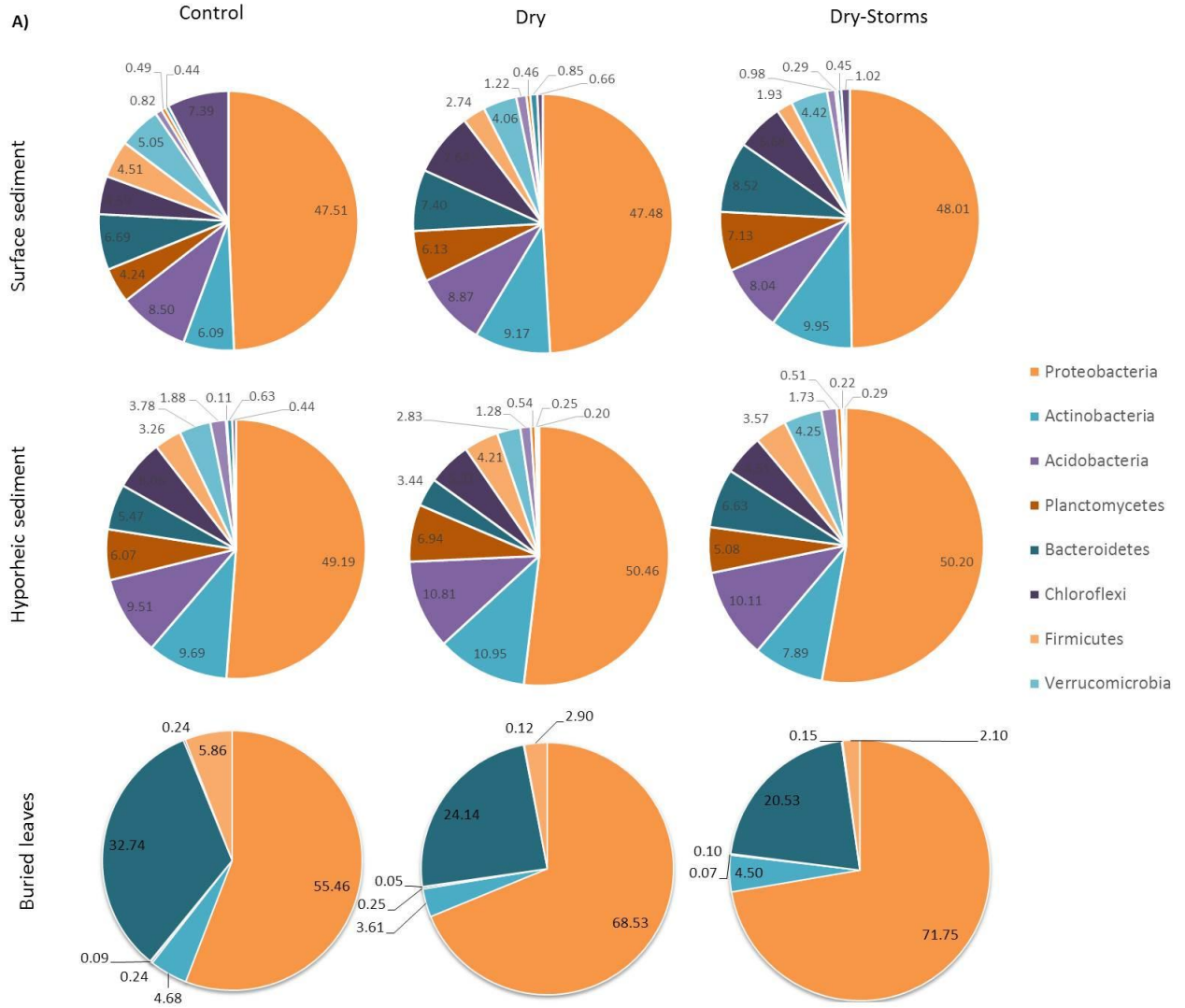
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Bacteria



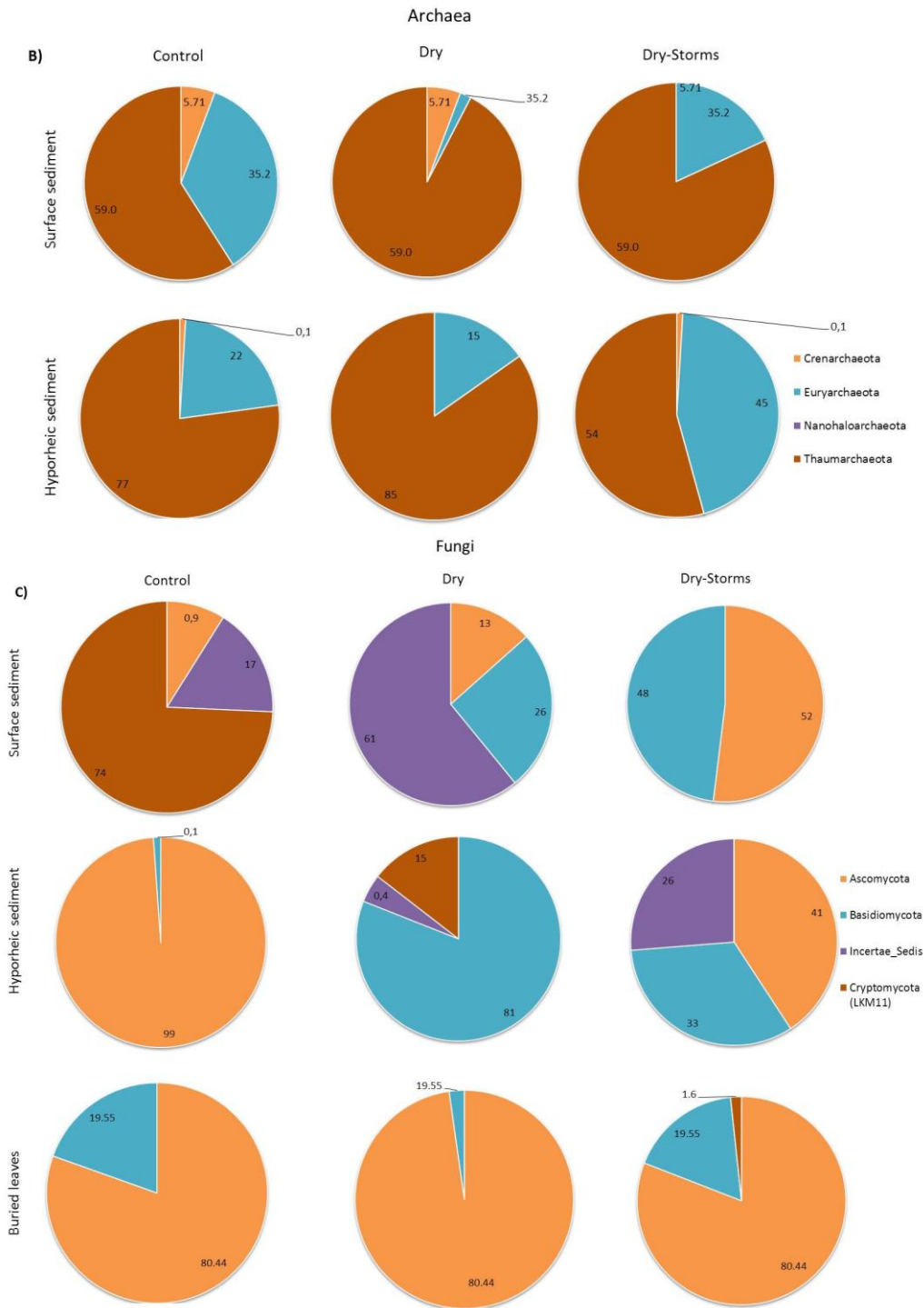


Fig. S1 Cake plots representing initial microbial composition (time 0) for Control, Dry and Dry-Storm treatments in surface and hyporheic sediments and buried leaves for: **A)** bacteria, **B)** archaea, **C)** fungi. These results are associated to those presented in the Table S1.

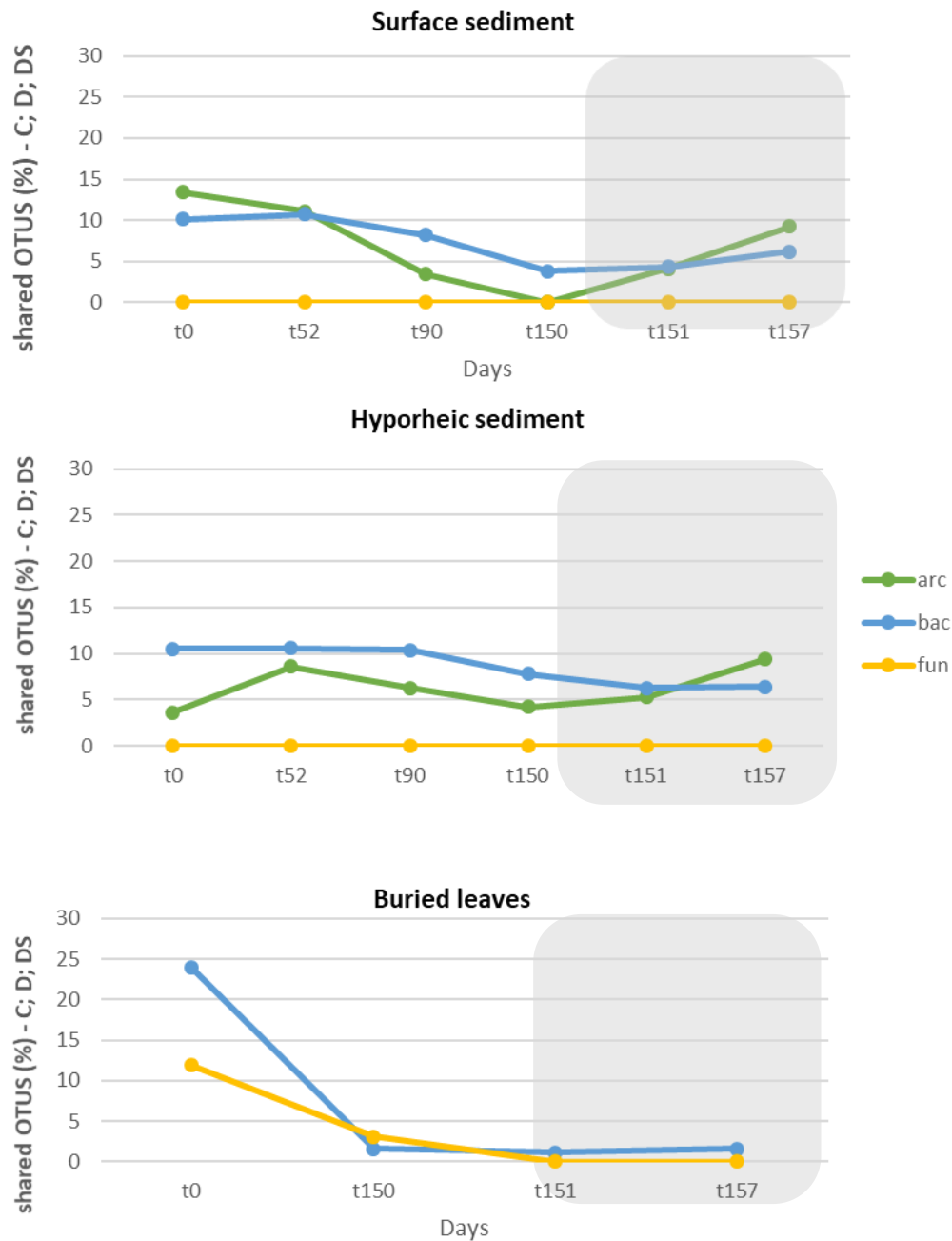


Fig. S2 Percentage of shared OTUs between the three treatments (C, Control; D, Dry; DS, Dry-Storm) reported during the experimental time (0, 52, 90, 150, 157 days), from each community (bac., bacteria; arc., archaea and fun., fungi) inhabiting each habitat (surface and hyporheic sediment and buried leaves). The shaded area indicate rewetting phase.

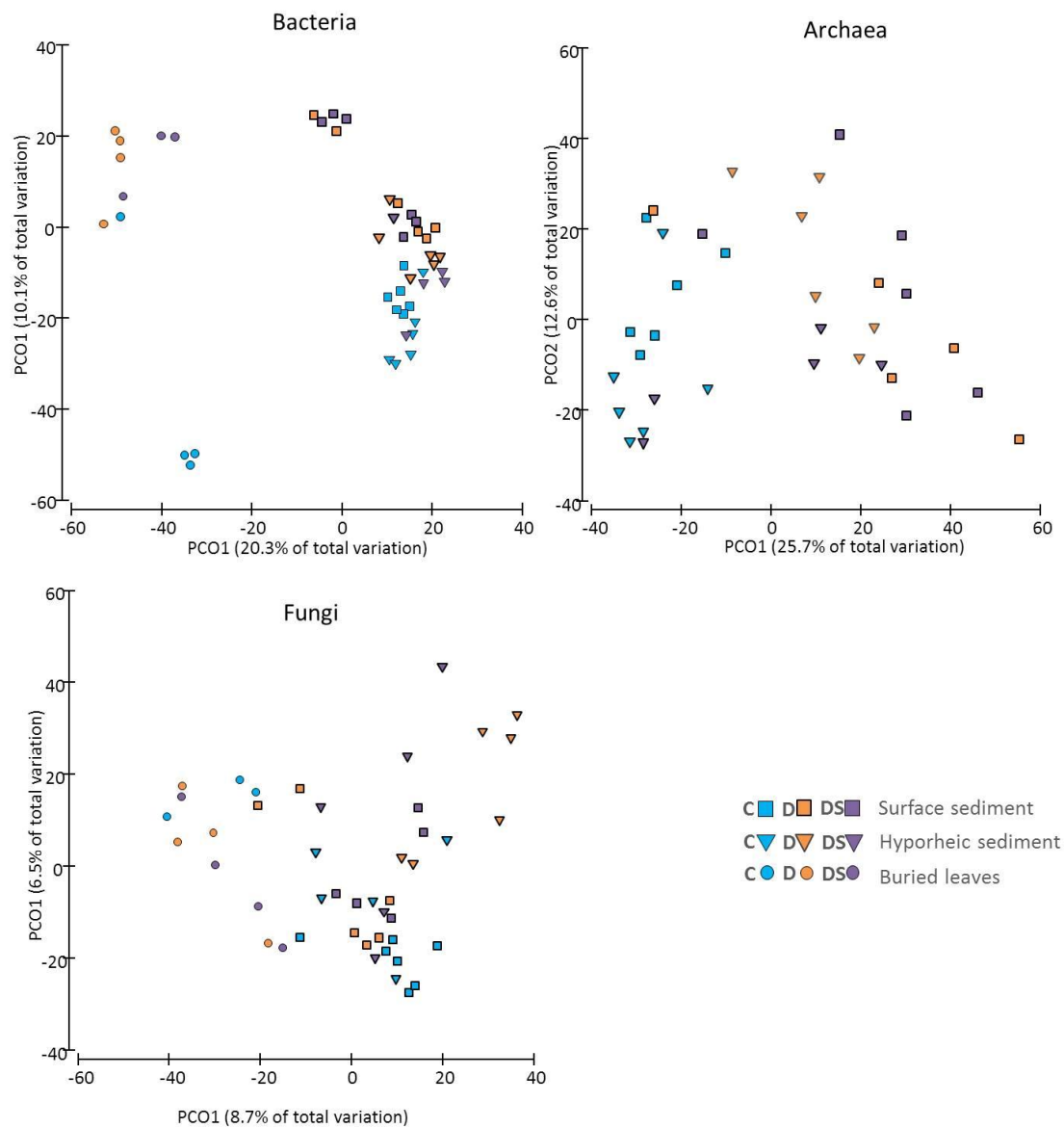


Fig.S3 PCO from bacterial, archaeal and fungal OTUs, inhabiting the three habitats, indicated as: surface sediment; hyporheic sediment; buried leaves. The colour pattern is indicated in the legend for the three treatments: C, Control; D, Dry; DS, Dry-Storm.

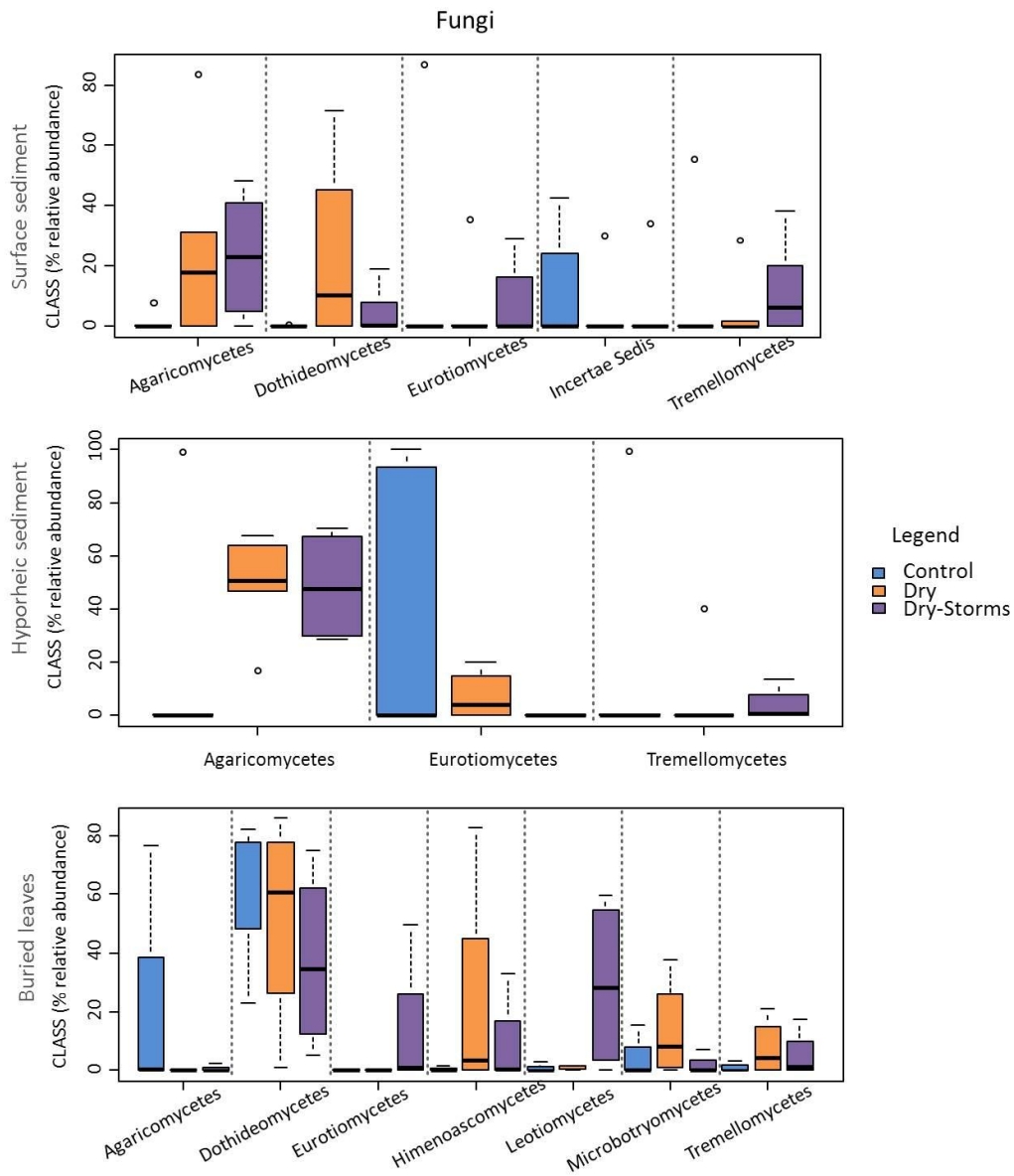


Fig.S4 Boxplots for fungal classes variability (% of relative abundance) considering the whole experimental period. The three habitats are indicated as: surface sediment; hyporheic sediment; buried leaves. The colour pattern is indicated in the legend for the three treatments: C, Control; D, Dry; DS, Dry-Storm. Only the classes presenting relative abundances >5% have been considered.

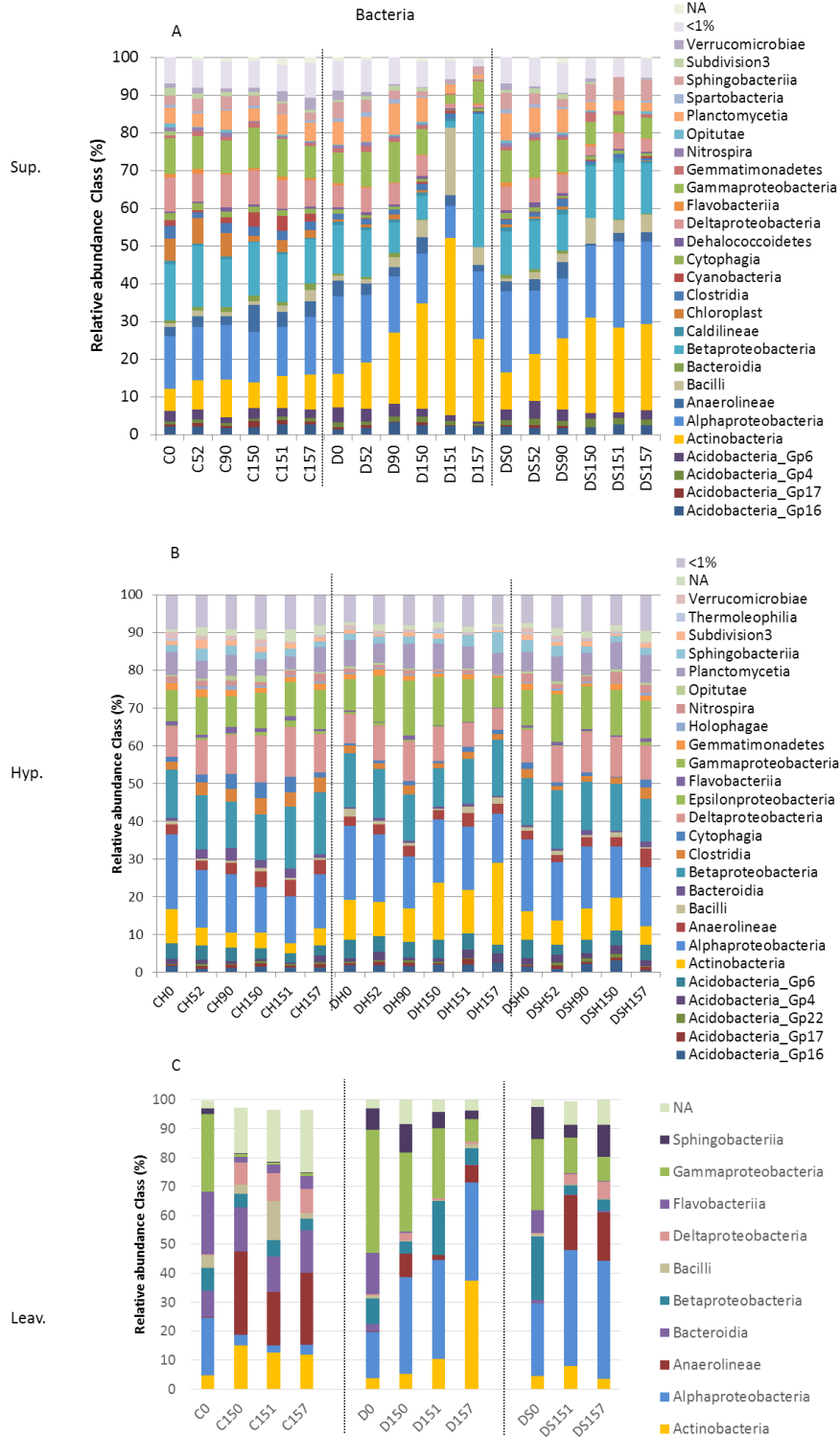


Fig.S5A-B-C Histogram of bacterial class composition (% of relative abundance) inhabiting surface (A) and hyporheic (B) sediment and buried leaves (C). In the *x-axis* the three treatments are indicated (C, D, DS) for each sampling time (day 0, 52, 90, 150, 151, 157).

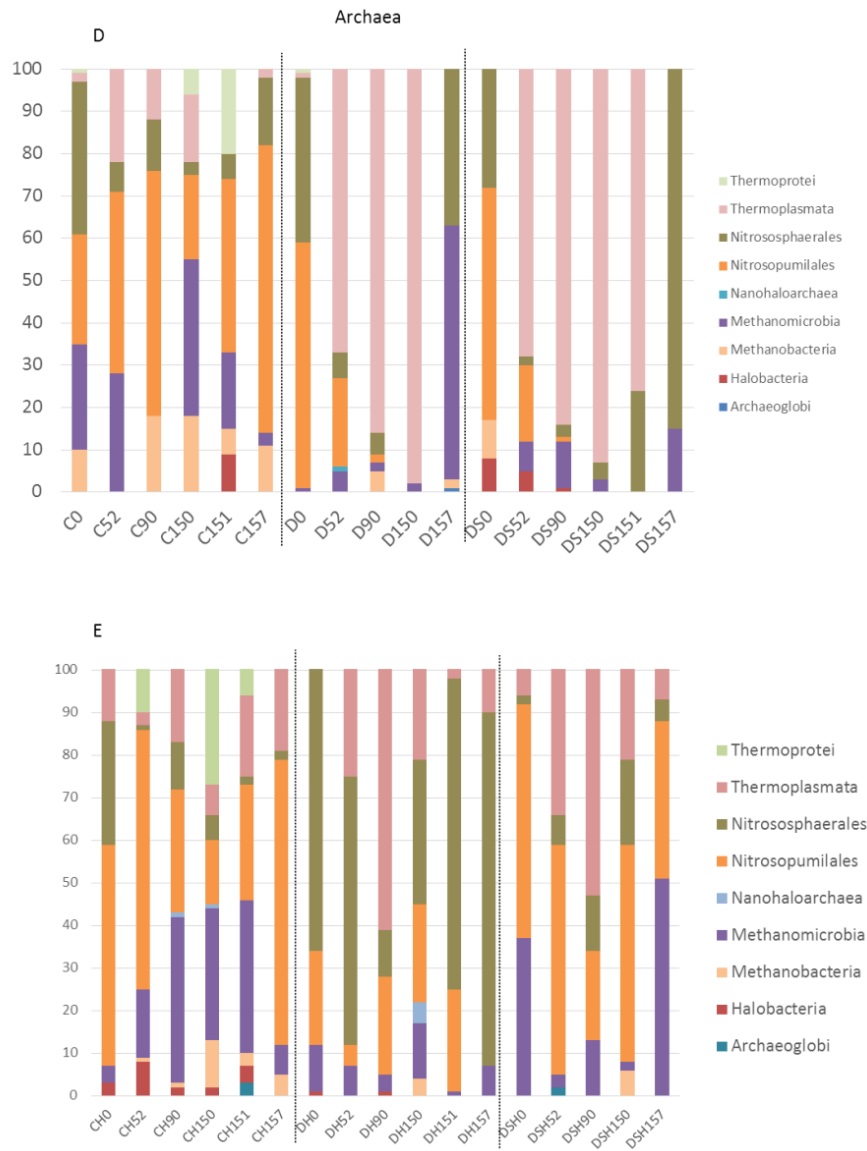


Fig.S5D-E Histogram of archaeal class composition (% of relative abundance) inhabiting surface (D) and hyporheic (E) sediment. In the *x*-axis the three treatments are indicated (C, D, DS) for each sampling time (day 0, 52, 90, 150, 151, 157).

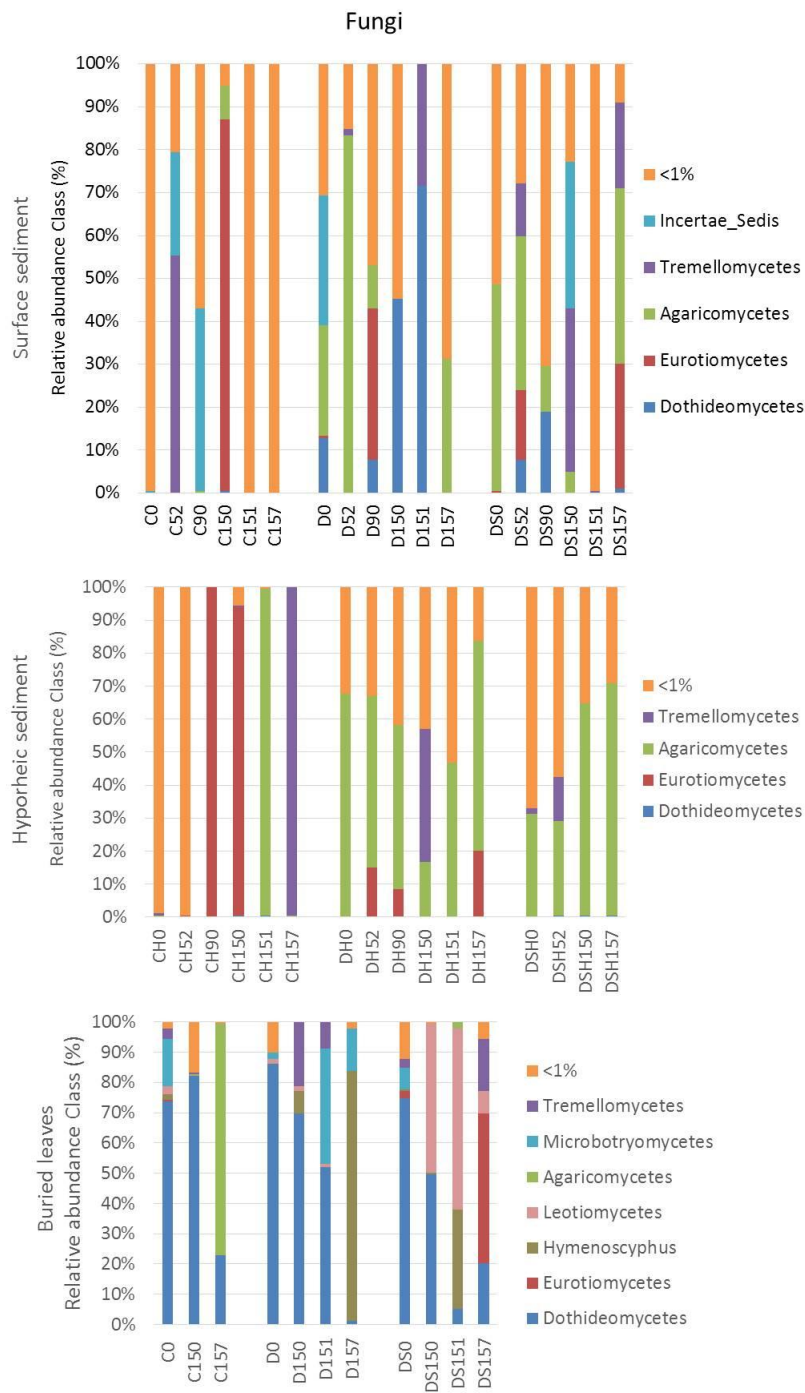


Fig.S6 Histograms of fungal class composition (% of relative abundance) for the three habitats studied, indicated as: surface sediment; hyporheic sediment; buried leaves. In the x-axis the three treatments are indicated (C, D, DS) for each sampling time (day 0, 52, 90, 150, 151, 157).

Table S1. Results (p-values) from the PERMANOVA analyses applied over the initial communities (referred to Figure S1). The acronyms SUR and HYP state for Surface and Hyporheic sediment, respectively. The letters C, D and DS state for the three treatments Control, Dry and Dry-Storms respectively.

	BACTERIA			ARCHAEA		FUNGI		
	SUR	HYP	LEAVES	SUR	HYP	SUR	HYP	LEAVES
C, D	0.329	0.662	0.671	0.670	0.332	0.670	0.664	0.663
C, DS	0.335	1.000	0.672	0.669	0.336	0.333	1.000	0.669
D, DS	1.000	0.343	1.000	0.671	0.327	0.666	1.000	0.672

Table S2. Richness (S) and Shannon diversity (H), based on number of OTUs of bacterial, archaeal and fungal assemblages at four dry-phase times (t0, t52, t90, t150) and at two rewetting-phase times (t151, t157), for three different habitats (SUR, surface sediment; HYP, hyporheic sediment; LEAVES, buried leaves) and three treatments (C, Control; D, Dry; DS, Dry-Storms).

		t0		t52		t90		t150		t151		t157		
Habitat	Treat.	S	H	S	H	S	H	S	H	S	H	S	H	
Bacteria	C	3107.1	6.98	3055.2	7.02	2094.1	6.64	2391.5	6.72	2282.4	6.73	2127.1	6.63	
	SUR	D	2880.8	7.03	3388.2	7.22	2897.5	7.03	2335.3	6.63	1140.7	4.58	1585.7	5.18
		DS	3317.1	7.15	3886.3	7.35	2931.6	7.00	1807.8	6.08	1962.6	6.18	2348.6	6.46
		C	3092.7	7.09	3218.8	7.18	3271.0	7.18	2697.5	7.00	2738.1	6.96	2801.2	7.06
	HYP	D	2711.5	6.90	3538.4	7.26	3577.8	7.27	3204.7	7.17	1938.1	6.53	2150.8	6.40
		DS	2751.6	6.91	2912.5	7.09	3272.8	7.20	2071.0	6.65	2201.1	6.75	2201.1	6.75
		C	925.1	4.55	na	na	na	na	1041.2	4.50	1125.5	4.80	998.7	4.81
	LEAVES	D	766.0	4.40	na	na	na	na	672.1	4.42	856.0	4.45	489.2	4.35
		DS	964.6	4.67	na	na	na	na	1064.4	4.77	1164.3	4.87	910.4	4.96
C		33.0	2.54	17.0	1.89	11.0	1.92	12.0	2.14	23.5	2.27	21.0	1.40	
Archaea	SUR	D	16.0	1.77	16.5	2.42	19.0	1.99	9.0	1.71	na	na	5.0	0.91
		DS	20.5	1.83	20.0	2.50	16.0	1.84	6.0	0.59	6.0	1.08	12.0	2.01
		C	18.5	2.10	25.5	2.28	47.5	2.89	29.5	2.94	33.0	2.72	39.0	2.35
	HYP	D	14.7	2.09	20.5	1.55	22.0	2.39	16.5	2.55	12.0	1.90	10.0	1.82
		DS	11.0	1.49	17.5	2.31	22.0	2.68	22.2	2.10	na	na	17.0	2.16
		C	4.0	0.76	6.0	1.55	8.5	1.55	8.5	0.60	6.0	1.22	3.0	0.58
Fungi	SUR	D	7.0	1.57	5.0	0.96	14.0	2.30	6.0	1.12	3.0	0.63	3.0	0.74
		DS	7.0	1.39	16.2	2.45	9.0	1.63	5.0	1.30	5.0	1.35	11.0	1.76
		C	8.0	0.76	4.0	1.55	1.0	1.55	9.0	0.60	4.5	1.22	2.0	0.58
	HYP	D	5.0	1.57	18.5	0.96	7.0	2.30	5.0	1.12	6.0	0.63	7.0	0.74
		DS	6.0	1.39	12.5	2.45	na	1.63	3.0	1.30	na	1.35	3.0	1.76
		C	31.5	1.76	na	na	na	na	25.0	1.02	na	na	6.0	0.68
LEAVES	D	21.7	1.53	na	na	na	na	46.0	2.14	7.0	1.45	5.0	0.58	
	DS	19.3	1.68	na	na	na	na	22.0	1.84	6.0	1.06	17.0	1.75	

Table S3. *p*-values from PERMANOVA analyses from complete PCO (Fig. S3). Differences between *Treatments* (C, D, and DS), type of *Habitats* (surface and hyporheic sediment, buried leaves) and the interaction *Treatment x Habitats* were assessed for each microbial community (bacteria, archaea, fungi). *p*-values indicating significant difference ($p < 0.05$) are indicated in boldface while *p*-values at the limit of significance ($p < 0.1$) are indicated in italic.

	Bacteria	Archaea	Fungi
<i>Treatment</i>	<0.001	<0.001	0.516
<i>Habitats</i>	<0.001	0.025	<0.001
<i>Treatment x Habitats</i>	0.003	<i>0.080</i>	0.047

Table S4. A) Dissolved oxygen (DO) in the sediment monitored during the experimental period and the average (\pm SD) for each treatment and habitat; **B)** Water sediment content (\pm SD) assessed at each sampling time. The habitats are indicated with the abbreviations as SUP: surface sediment and HYP: hyporheic sediment whereas the three treatments are stated as C: Control, D: Dry, DS: Dry-Storms.

A

Sampling date (day)		DO (mg/l)									DO average	SD
		19-feb	03-mar	17-mar	05-apr	19-apr	04-may	24-may	25-jun	15-jul		
SUP	C	3.90	5.75	6.08	5.42	5.51	1.15	1.94	4.03	2.87	4.07	1.68
	D	7.42	8.09	8.87	8.70	8.90	8.74	8.92	8.52	8.68	8.54	0.46
	DS	7.50	8.29	8.81	8.76	8.81	9.67	8.97	8.69	8.86	8.71	0.55
HYP	C	0.08	0.08	0.03	0.06	0.03	0.17	0.04	0.07	0.07	0.07	0.04
	D	7.08	7.78	9.06	8.80	8.86	8.96	8.80	8.48	8.68	8.50	0.61
	DS	4.32	8.32	8.73	8.65	9.02	9.46	9.20	8.24	8.80	8.31	1.46

B

Sampling time (day)		Water content average (%) \pm SD					
		0	52	90	150	151	157
SUP	C	17.27 \pm 2.19	29.5 \pm 0.54	28.48 \pm 0.43	29.25 \pm 1.29	21.96 \pm 1.33	23.86 \pm 4.43
	D	15.58 \pm 1.55	0.83 \pm 0.54	0.34 \pm 0.37	0.44 \pm 0.91	13.68 \pm 1.33	22.71 \pm 4.43
	DS	16.57 \pm 1.26	1.14 \pm 0.54	0.36 \pm 0.37	2.73 \pm 0.91	12.63 \pm 1.33	21.58 \pm 4.43
HYP	C	43.29 \pm 1.30	27.74 \pm 1.51	26.61 \pm 0.90	27.45 \pm 1.21	20.57 \pm 2.11	23.73 \pm 2.68
	D	44.71 \pm 1.06	4.04 \pm 1.06	2.82 \pm 0.64	0.65 \pm 1.05	18.46 \pm 2.11	22.06 \pm 2.68
	DS	43.43 \pm 1.3	4.55 \pm 1.06	2.86 \pm 0.64	5.48 \pm 1.05	20.01 \pm 2.11	20.31 \pm 2.68

Table S5. Physicochemical parameters in stream water monitored during the experimental period and further checked with the ACA dataset (“Agència Catalana de l’Aigua” dataset January 2016 - August 2016). During the study period the stream was in base flow conditions and no storms occurred.

	Mean value	Unit
N-NO₂	0.05 \pm 0.12	mg/L
N-NO₃	0.14 \pm 0.12	mg/L
P-PO₄	0.83 \pm 0.12	mg/L
DOC	10.43 \pm 1.38	mg/L
Water T^o (range)	7 - 15.6	°C
Dissolved Oxygen	10.18 \pm 3.58	mg/L
Conductivity	488 \pm 41.39	μ S/cm
pH	8.54 \pm 0.06	

Suppl. Info. S2. Results from the repeated measures for Shannon-Wiener diversity (H) and Richness (S) indices and for the Unifrac distance (proxy of phylogenetic distance). The acronyms TR, TI and HAB indicate Treatments, Time and Habitats (surface and hyporheic zone), respectively.

BACTERIA - H index			ARCHAEA - H index			FUNGI - H index		
Origin	F	Sign.	Origin	F	Sign.	Origin	F	Sign.
Intercept	18,598,808	,000	Intercept	1,074,519	,000	Intercept	158,212	,000
TR	3,732	,062	TR	5,710	,029	TR	4,758	,044
TI	9,101	,002	TI	1,735	,233	TI	2,949	,084
HAB	14,188	,004	HAB	8,695	,018	HAB	5,242	,051
TR * TI	3,105	,044	TR * TI	2,117	,150	TR * TI	,623	,763
TR * HAB	1,971	,190	TR * HAB	,250	,785	TR * HAB	3,699	,073
TI * HAB	2,507	,101	TI * HAB	3,288	,066	TI * HAB	1,633	,256

BACTERIA – S index			ARCHAEA – S index			FUNGI – S index		
Origin	F	Sign.	Origin	F	Sign.	Origin	F	Sign.
Intercept	7,810,217	,000	Intercept	248,703	,000	Intercept	103,463	,000
TR	1,657	,239	TR	11,250	,005	TR	,933	,432
TI	48,502	,000	TI	,968	,490	TI	2,400	,130
HAB	19,662	,001	DE	5,431	,048	HAB	1,796	,217
TR * TI	7,657	,002	TR * TI	,754	,669	TR * TI	1,518	,283
TR * HAB	11,459	,003	TR * DE	1,892	,212	TR * HAB	2,607	,134
TI * HAB	7,602	,003	TI * DE	2,604	,110	TI * HAB	1,548	,277

BACTERIA Unifrac			ARCHAEA Unifrac			FUNGI Unifrac		
Origin	F	Sign.	Origin	F	Sign.	Origin	F	Sign.
Intercept	2,523,566	,000	Intercept	775,760	,000	Intercept	520,677	,000
TR	14,794	,001	TR	,894	,446	TR	1,578	,264
TI	1,553	,259	TI	1,722	,235	TI	,285	,908
HAB	21,557	,001	HAB	11,416	,010	HAB	1,223	,301
TR * TI	,935	,541	TR * TI	1,127	,441	TR * TI	,600	,779
TR * HAB	14,658	,001	TR * HAB	3,875	,067	TR * HAB	5,205	,036
TI * HAB	,220	,946	TI * HAB	2,000	,183	TI * HAB	,492	,774

BACTERIA - H index			LEAVES	FUNGI - H index			LEAVES
Origin	F	Sign.		Origin	F	Sign.	
Intercept	26,234,067	,000		Intercept	80,404	,000	
TR	17,734	,003		TR	,891	,467	
TI	2,529	,154		TI	1,452	,333	

BACTERIA – S index			LEAVES	FUNGI – S index			LEAVES
Origin	F	Sign.		Origin	F	Sign.	
Intercept	1,675,366	,000		Intercept	33,297	,002	
TR	23,995	,001		TR	,165	,853	
TI	5,374	,039		TI	3,766	,094	