

Seasonal dynamics of the microbiome-host response to pharmaceuticals and pesticides in *Mytilus galloprovincialis* farmed in the Northwestern Adriatic Sea

Supplementary material

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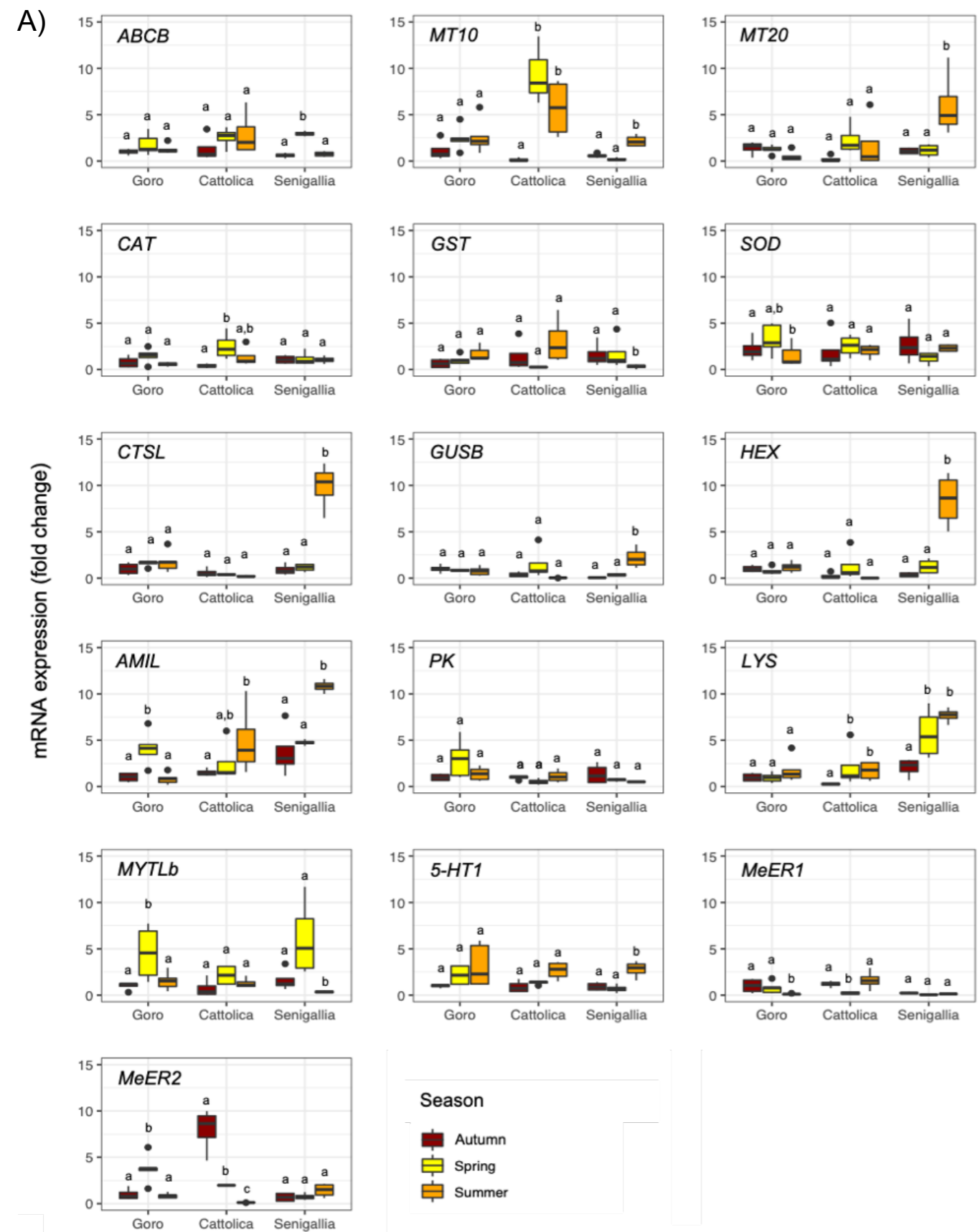
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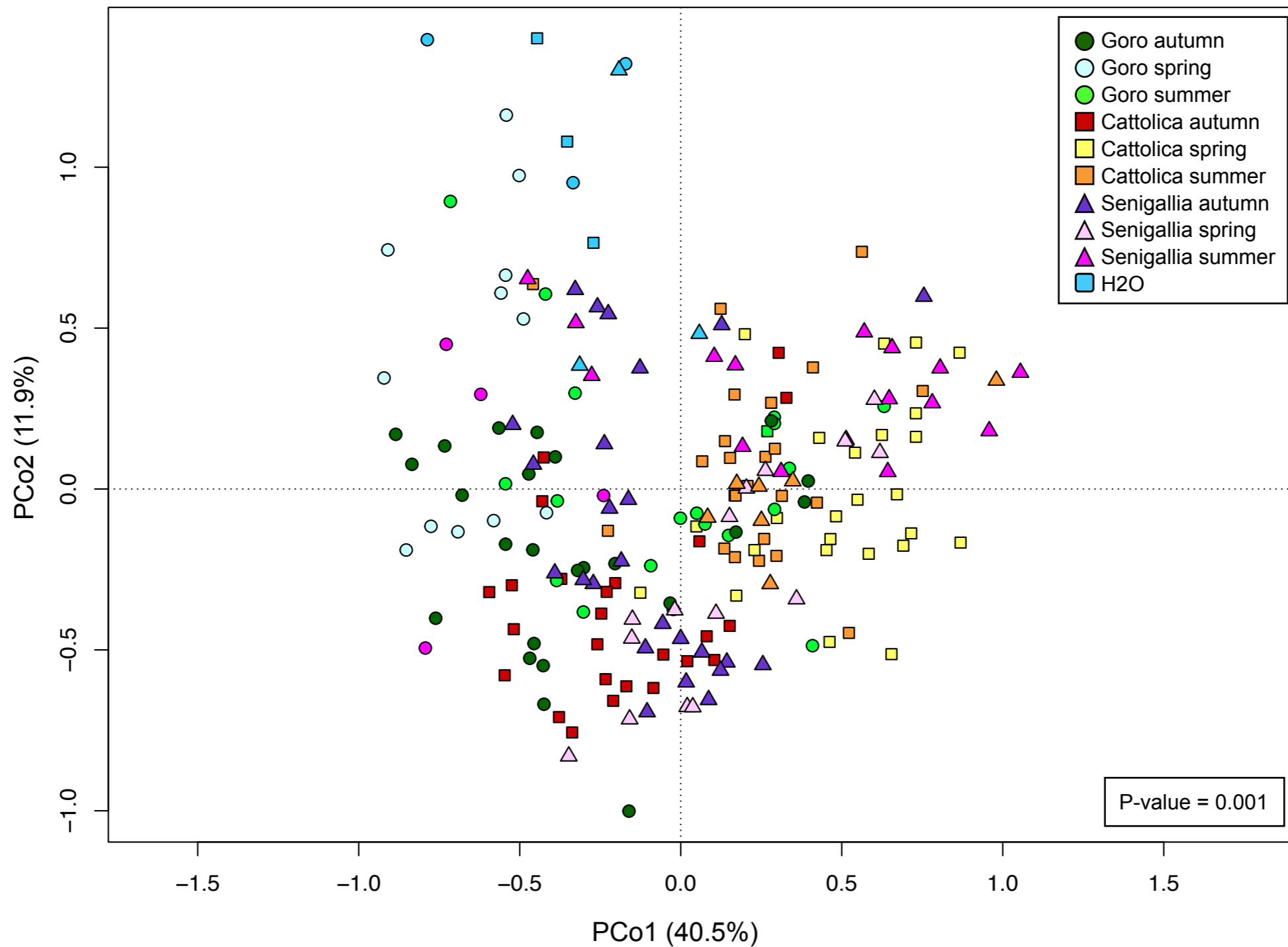


B)

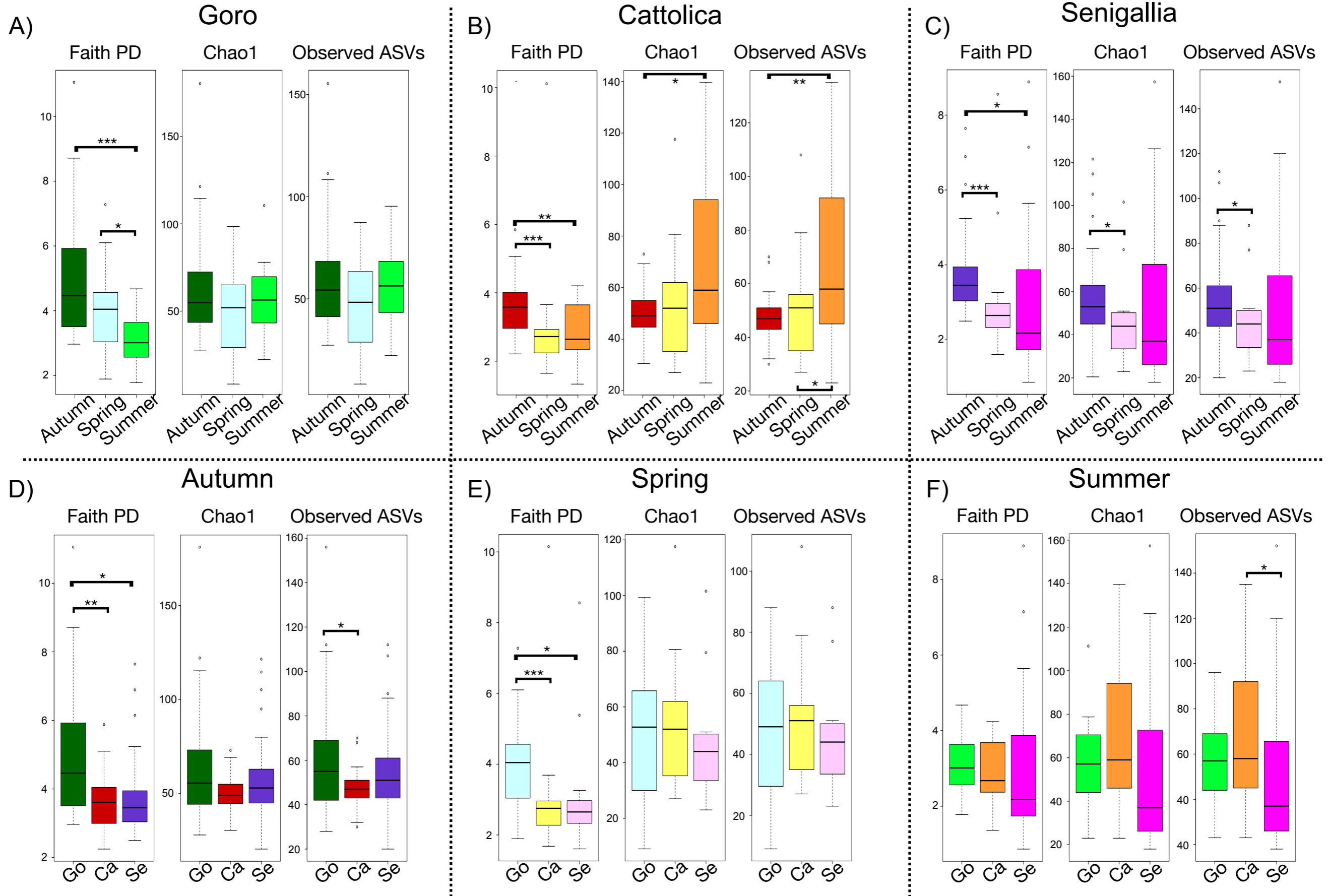
Target transcripts	Autumn			Spring			Summer			
	Go-Ca	Go-Se	Ca-Se	Go-Ca	Go-Se	Ca-Se	Go-Ca	Go-Se	Ca-Se	
ABCB	t	0.17	1.97	0.99	0.99	2.01	0.83	1.55	2.08	2.31
	P(perm)	0.971	0.127	0.410	0.353	0.121	0.614	0.172	0.082	0.030
MT10	t	2.25	0.91	3.21	4.89	5.06	11.51	1.85	0.26	2.46
	P(perm)	0.059	0.526	0.038	0.007	0.025	0.026	0.122	0.829	0.056
MT20	t	3.01	0.53	3.61	1.49	0.38	1.45	0.69	5.72	2.36
	P(perm)	0.059	0.742	0.032	0.199	0.74	0.23	0.648	0.012	0.117
CAT	t	1.12	0.85	2.88	1.27	0.55	1.79	0.64	0.34	0.40
	P(perm)	0.298	0.436	0.053	0.261	0.573	0.114	0.537	0.734	0.801
GST	t	0.77	1.41	0.35	4.16	0.61	2.29	0.50	4.32	3.18
	P(perm)	0.471	0.192	0.651	0.013	0.67	0.03	0.626	0.01	0.033
SOD	t	0.55	0.27	0.69	0.61	2.40	1.90	0.79	1.47	0.80
	P(perm)	0.61	0.77	0.49	0.57	0.06	0.11	0.44	0.15	0.41
CTSL	t	1.06	0.19	0.95	8.84	1.71	3.94	3.90	6.25	16.73
	P(perm)	0.27	0.91	0.327	0.01	0.149	0.037	0.017	0.006	0.03
GUSB	t	2.52	5.53	2.63	0.63	5.17	1.54	3.87	2.88	6.29
	P(perm)	0.058	0.029	0.032	0.783	0.005	0.09	0.019	0.03	0.024
HEX	t	3.28	2.95	0.72	0.37	1.07	0.26	6.08	7.52	13.34
	P(perm)	0.058	0.036	0.491	0.832	0.278	0.827	0.013	0.012	0.026
AMIL	t	1.67	2.45	1.76	1.41	0.86	2.23	3.33	11.55	2.67
	P(perm)	0.200	0.080	0.148	0.227	0.496	0.147	0.02	0.007	0.06
PK	t	0.02	0.34	0.35	3.11	2.75	1.23	0.59	2.74	1.86
	P(perm)	0.948	0.698	0.776	0.034	0.052	0.305	0.534	0.035	0.151
LYS	t	3.63	1.75	4.20	1.04	5.27	2.30	0.06	5.46	5.83
	P(perm)	0.025	0.09	0.031	0.4	0.011	0.09	0.98	0.016	0.029
MYTLb	t	0.79	0.91	1.38	1.53	0.59	2.07	0.28	2.88	4.43
	P(perm)	0.444	0.463	0.195	0.158	0.524	0.173	0.753	0.026	0.029
5-HT1	t	0.55	0.45	0.19	1.45	3.01	2.64	0.13	0.01	0.21
	P(perm)	0.67	0.731	0.823	0.18	0.047	0.064	0.933	1	0.795
MeER1	t	0.65	2.04	6.69	1.93	2.83	2.83	4.32	0.55	3.69
	P(perm)	0.608	0.124	0.033	0.094	0.019	0.026	0.008	0.589	0.026
MeER2	t	7.10	0.79	7.95	7.10	0.79	7.95	2.36	4.87	5.61
	P(perm)	0.025	0.486	0.027	0.025	0.486	0.027	0.049	0.03	0.028

Abbreviations: Go = Goro; Ca = Cattolica; Se = Senigallia.

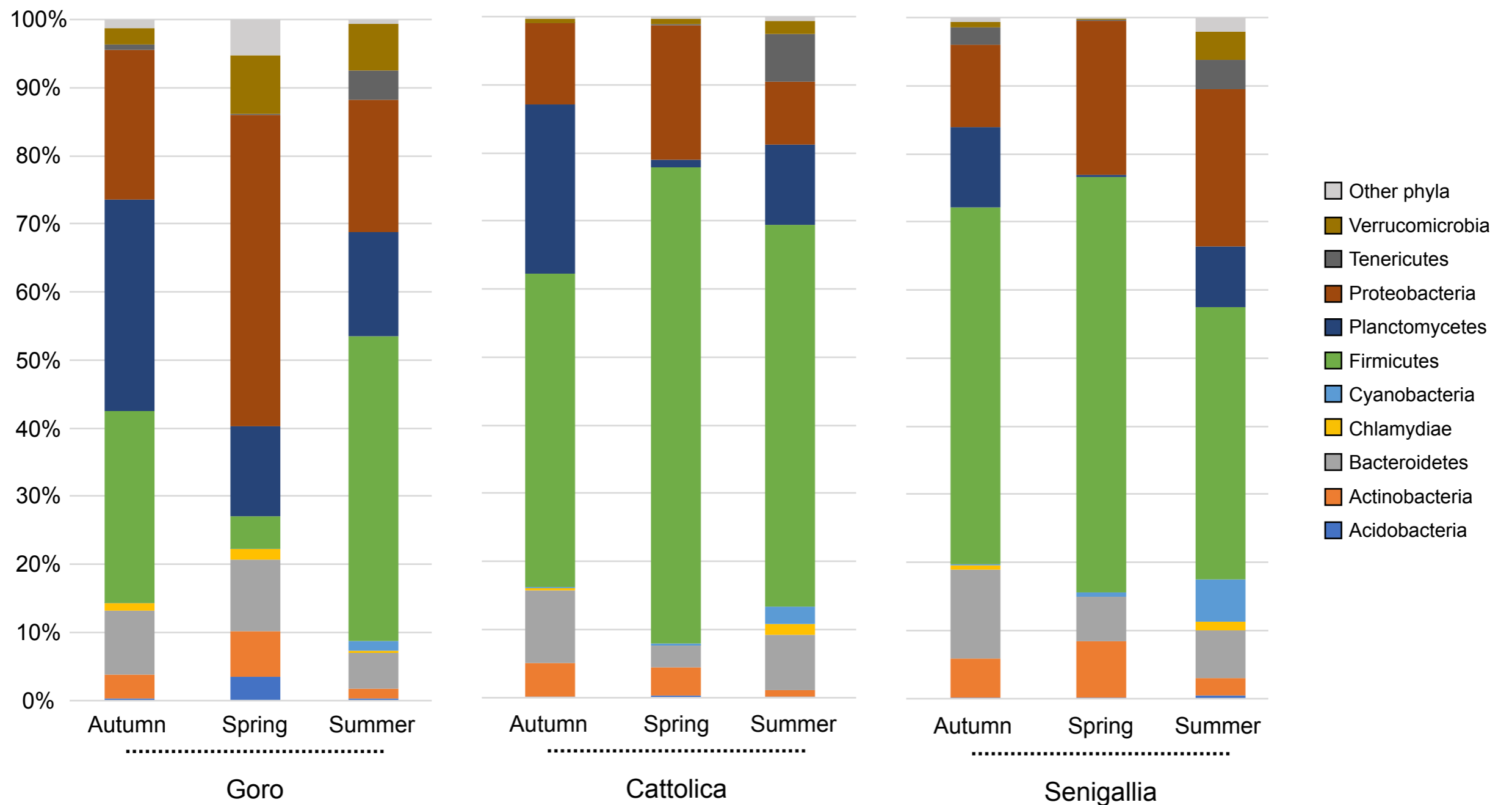
Supplementary Figure S1 - Transcriptional profiles assessed in mussels sampled at the different farm sites and seasons in the Adriatic Sea. A) Transcriptional profiles of cytoprotective/detoxification (ABCB, MT10, MT20), antioxidant (CAT, GST, SOD), lysosomal (*HEX*, *CTSL*, *GUSB*), metabolic (*AMIL*, *PK*, *LYS*, *MYTLb*), and neuroendocrine-relates (*5-HT1*, *MeER1*, *MeER2*) mRNAs. For each target transcript box plots (median, upper and lower quartiles; N = 21) show transcriptional profiles across the sampling sites and seasons. Different letters indicate statistical differences between sampling seasons within each site (P < 0.05, pairwise PERMANOVA comparisons). B) Season-based comparisons (PERMANOVA) among sites. Abbreviations: ABCB, P-glycoprotein; MT10, 10kDa metallothionein; MT20, 20kDa metallothionein; CAT, catalase; GST, glutathione s-transferase; SOD, superoxide dismutase; CTSL, cathepsin L; GUSB, β -glucuronidase; HEX, hexosaminidase; AMIL, amilase; PK, pyruvate kinase; LYS, lysozyme; MYTLb, mytilin b; 5-HT1, type 1 serotonin receptor; MeER1, type 1 estrogen receptor; MeER2, type 2 estrogen receptor.



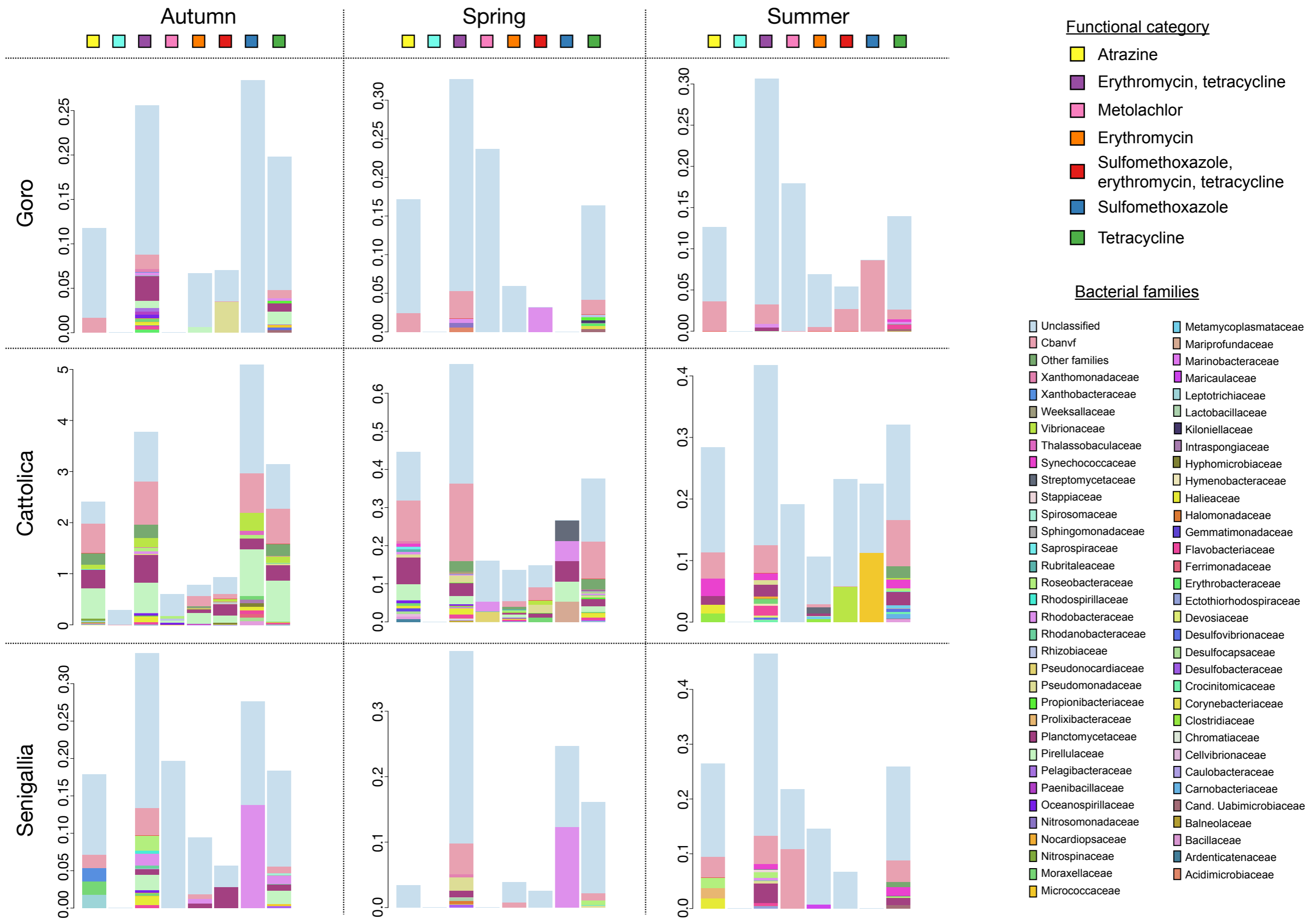
Supplementary Figure S2 - Overall microbiome compositional structure of *M. galloprovincialis* digestive gland and the surrounding seawater. Principal Coordinates Analysis (PCoA) based on weighted UniFrac distances between microbial profiles of mussel digestive gland and seawater samples in all sampling sites (Goro, Cattolica, Senigallia) and seasons (autumn, spring, summer) shows a significant separation between the groups (permutation test with pseudo-F ratio, p-value = 0.001).



Supplementary Figure S3 - Microbiome alpha diversity of *M. galloprovincialis* digestive gland. Box-and-whiskers distribution of alpha diversity metrics, estimated by Faith's Phylogenetic Diversity (Faith PD), Chao1 and number of observed ASVs, of the mussel digestive gland-associated microbiome from different sites (Goro, Cattolica, and Senigallia) and seasons (autumn, spring, and summer). Significant p-values (Wilcoxon rank-sum test controlled for multiple testing using FDR) are reported with the following symbols: p-value ≤ 0.05 *; p-value ≤ 0.01 **, p-value ≤ 0.001 ***. Go = Goro, Ca = Cattolica, Se = Senigallia.



Supplementary Figure S4 - *M. galloprovincialis* digestive gland microbiome composition at phylum level. Bar plots of the average microbiome composition at the phylum level, associated with mussel digestive gland by sampling site (Goro, Cattolica, and Senigallia) and season (autumn, spring, and summer). Phyla with relative abundance >0.5% in at least 10% of samples are shown.



Supplementary Figure S5 - Taxonomic classification of metagenomics reads assigned to xenobiotic degradation genes. Reads assigned to xenobiotic degradation genes were taxonomically characterized using Kaiju “marDB” database, in order to retrieve the mussels digestive gland associated microbiome components involved in xenobiotic degradation. For each of the 8 different functional categories of xenobiotic degradation genes, bar plots representing the associated microbiome families are shown. On the x-axis the functional categories of xenobiotic degradation are represented. On the y-axis, the CPM assigned to xenobiotic degradation genes are represented as the sum of the gene belonging to each category on the total functional genes CPM assigned to the respective family. Abbreviations: Cbanvf = cannot be assigned to a non-viral family; Cand = Candidatus.

Supplementary Table S1 - Seawater parameters at the selected sampling sites as monitored by the Regional Agency for Prevention, Environment and Energy of Emilia-Romagna and Marche regions.

Site	Season	SST (°C)	Chl-a (µg/L)	Turbidity (m)	Salinity (psu)
Goro	Autumn	12.9	6.6	0.435	27.5
	Spring	19.0	5.9	0.559	26.2
	Summer	27.0	6.0	0.691	28.1
Cattolica	Autumn	13.8	4.2	0.435	29.4
	Spring	17.5	3.6	0.559	35.0
	Summer	25.7	2.1	0.552	33.7
Senigallia	Autumn	14.1	5.2	0.285	29.7
	Spring	17.3	5.1	0.184	35.2
	Summer	25.6	1.9	0.139	35.9

Supplementary Table S2 - Biometric parameters of mussels sampled at different sites and seasons. SD = standard deviation.

Site	Season		Shell weight (g)	Soft tissue weight (g)	Shell length (cm)
Goro	Autumn	Mean	2.99	5.81	4.96
		SD	0.34	1.17	0.21
	Spring	Mean	6.66	5.87	6.21
		SD	1.69	2.06	0.49
	Summer	Mean	4.07	4.99	5.15
		SD	0.64	0.87	0.32
Cattolica	Autumn	Mean	2.66	5.82	5.50
		SD	2.93	4.17	5.42
	Spring	Mean	8.10	11.89	7.35
		SD	1.53	3.41	0.48
	Summer	Mean	8.02	7.70	6.91
		SD	1.83	2.83	0.58
Senigallia	Autumn	Mean	5.77	3.58	5.50
		SD	5.04	3.75	5.41
	Spring	Mean	7.24	7.51	6.88
		SD	1.03	2.25	0.38
	Summer	Mean	7.33	6.76	6.26
		SD	1.60	1.96	0.46

Supplementary Table S3 - LC-MS experimental conditions.

COMPOUND	RETENTION TIME (min)	TRANSITIONS	COLLISION ENERGY (eV)	CONE (Volts)
Amoxicillin trihydrate	4.28	[365.69] > [349.03]; [365.69] > [208.14]	12	15
Carbamazepine	19.10	[237.12] > [194.05]; [237.12] > [237.12]	20	30
Carbamazepine- ¹³ C ₆	19.06	[243.02] > [200.13]; [243.02] > [243.02]	20	30
Sulfamethoxazole	17.60	[253.63] > [155.99]; [253.63] > [108.46]	12	30
Sulfamethoxazole- (phenyl- ¹³ C ₆)	17.60	[260.05] > [162.06]; [260.05] > [260.05]	12	30
Erythromycin A dehydrate	16.54	[733.84] > [576.35]; [733.84] > [158.20]	15	35
Tetracycline	16.42	[444.59] > [427.38]; [444.59] > [409.99]	17	20
Doxycycline hyclate	17.40	[444.62] > [428.20]; [444.62] > [282.85]	14	20
N,N-Diethyl-meta-toluamide (DEET)	20.13	[192.13] > [119.10]; [192.13] > [91.07]	15	25
Metolachlor	22.48	[284.04] > [252.03]; [253.63] > [155.89]	12	25
Metolachlor-(2-ethyl-6-methylphenyl-d ₁₁)	22.37	[295.1] > [263.13]; [295.1] > [295.1]	15	25
Alachlor	22.41	[238.32] > [162.13]; [270.12] > [161.35]	15	30
Alachlor-d ₁₃	22.48	[251.13] > [175.23]; [251.13] > [251.13]	15	30
Atrazine	20.02	[216.34] > [174.02]; [216.34] > [104.13]	12	30
Atrazine-d ₅	19.98	[221.09] > [179.11]; [221.09] > [221.09]	15	30
Atrazine-desethyl-desisopropyl	5.77	[146.03] > [104.13]; [146.03] > [110.08]	18	30

Supplementary Methods

Standard and sample solutions

The extraction procedure was as follow: 250 mg dry weight (dw) of whole mussel powder were transferred into a centrifuge tube 10 µL of IS mixture and extracted twice with 1 mL of cold ACN:MeOH (50:50 v/v) mixture (10 µL of EDTA 25 mM and 0,25 g of MgSO₄ were added). The sample was vortexed for 2 min, cooled for 10 min at -20°C, centrifuged and the supernatant collected. The sample powder pellet underwent a second double extraction with 1 mL of a refrigerated Hexane:Acetone (50:50 v/v) solution, and the addition of 10 µL of EDTA 25 mM. The sample was vortexed for 2 min, cooled for 10 min at -20°C and centrifuged. The supernatants were collected and mixed with the ones obtained with ACN:MeOH (50:50 v/v) mixture. The extracted solution was vacuum dried, the oily residue was re-dissolved in 200 µL of CHAPS 0,6% (m/v) aqueous solution. The sample was vortexed for 1 min and centrifuged, the supernatant was collected. 100 µL of MeOH were added to the remaining residues, the sample was vortexed and centrifuged, the supernatant was collected and joined with the previously collected supernatant. This solution was centrifuged and 100 µL of the filtered (0.45 µm syringe filter) supernatant were injected in the LC-MS system.

LC-MS analysis

Liquid chromatography-mass spectrometry (LC-MS) was performed using a 2690 Alliance system (Waters, Milford, MA, USA) coupled to an ESI source and a triple quadruple mass spectrometer (Quattro-LC, Micromass) in the multiple reaction monitoring (MRM) acquisition mode. The analytical column was an Atlantis T3 (5 µm, 2.1 mm X 150 mm, Waters), the gradient elution was obtained with a mobile phase composed of 0.01% acetic acid in water (A) and 0,01% acetic acid in a solution of methanol and acetonitrile 65:35 (v/v) (B). Gradient elution was as follow: 10% of solvent B were held for 5 min, solvent B to 60% over 7 min, to 80% over 3 min and to 90% over 2 min, these conditions were held for 25 min. Finally mobile phase B was returned to its initial conditions over 10 min. The flow rate was 0.14 mL/min, the column temperature was 20°C and injection volume was of 5 µL.

The MS/MS detection was performed in positive mode (2500 V) and the spectra were acquired in multiple reaction monitoring (MRM) mode. Argon was the collision gas and nitrogen the nebulizer and heater gas. Nitrogen was used as nebulizer gas at 117 L/h flow rate and as desolvation gas at 622 L/h. Ion source block and desolvation temperatures were 120 °C and 180 °C, respectively. Capillary and cone voltages were 2,90 kV and 60 V, respectively.