

Supplementary Materials

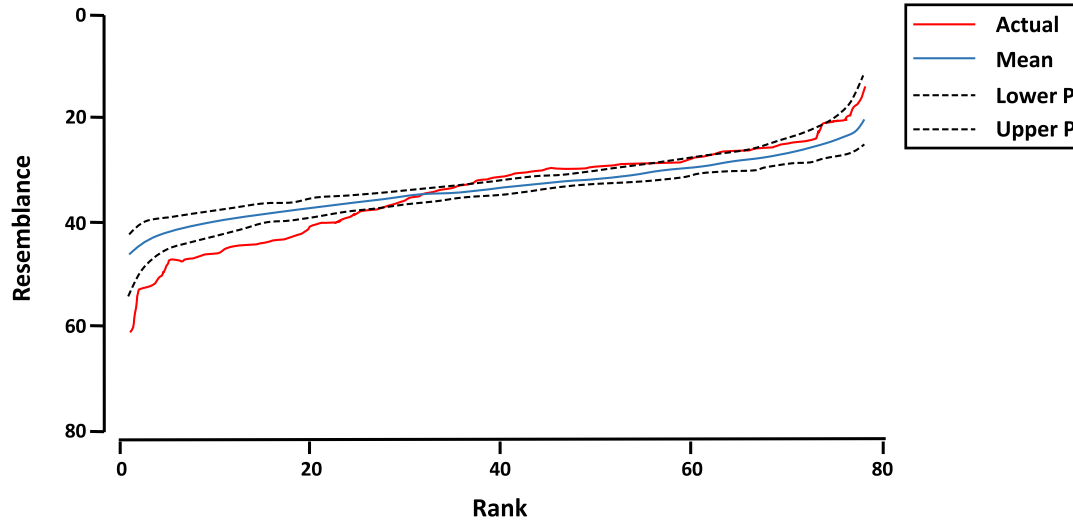


FIGURE S1. SIMPROFs (similarity profiles) based on Bray-Curtis similarity matrix fourth root transformed, showing the departure of the real curve (red line) from its expected shape (blue line) inside an interval of lower and upper probability (dotted lines), under the null hypothesis of no clustering of the samples.

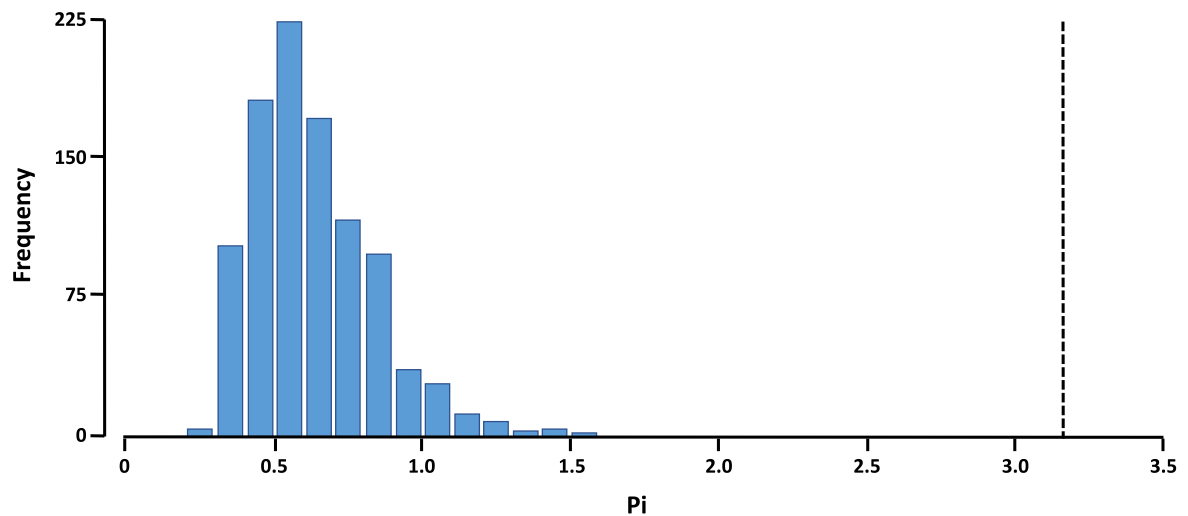


FIGURE S2. SIMPROF. Histogram of null distribution.

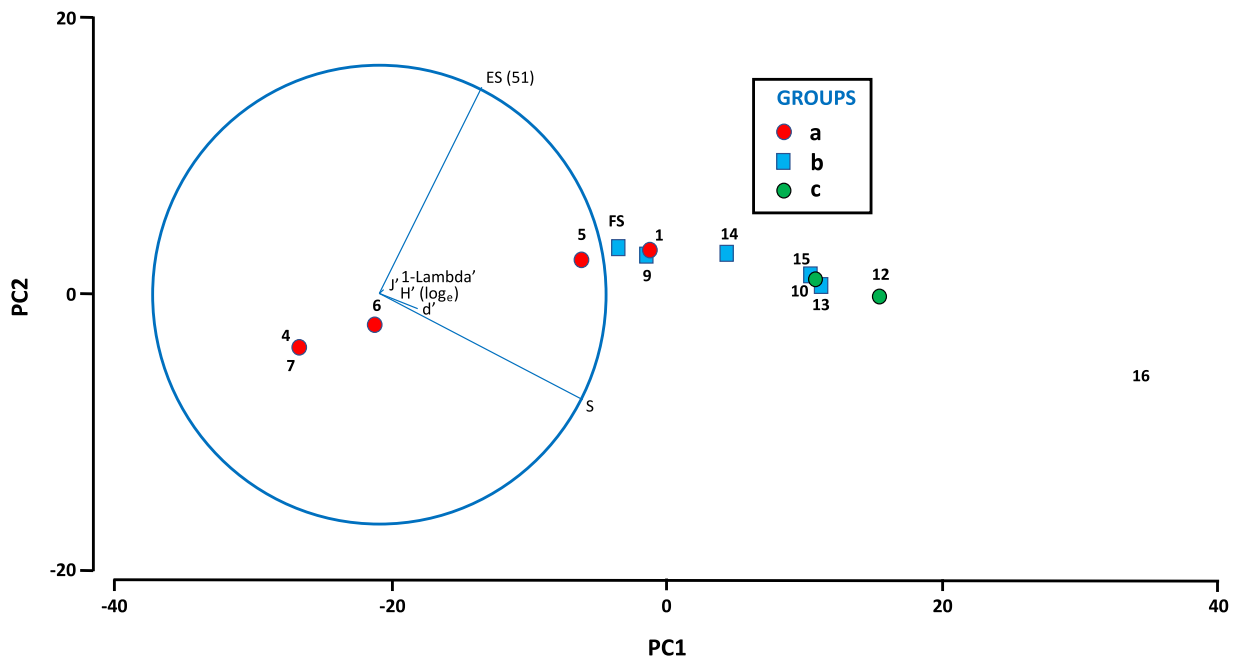


FIGURE S3. Principal component analysis (PCA) ordination of diversity indexes from the sampling sites and CLUSTER groups: species richness (S), Shannon-Wiener diversity index ($H'(\log_e)$), Margalef's diversity index (d'), Pielou's evenness index (J), rarefaction (ES [51]), and 1-Lambda' index.

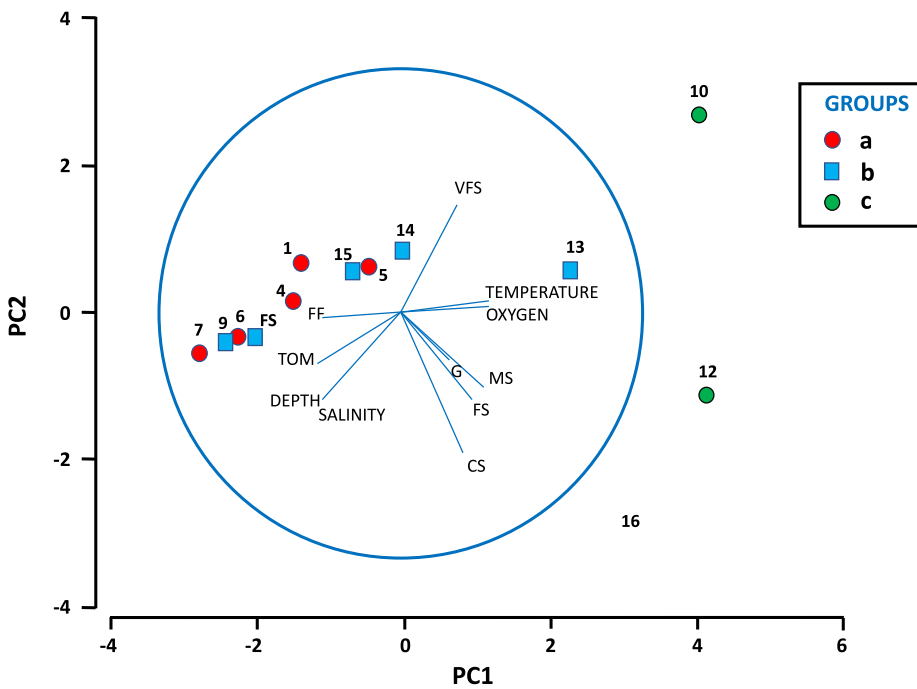


FIGURE S4. Principal component analysis (PCA) ordination of environmental parameters from the sites and CLUSTER groups: mean depth (depth), total organic matter (TOM), fine fraction (FF), very fine sand (VFS), fine sand (FS), medium sand (MS), coarse sand, (CS), gravel (G), temperature, salinity, and oxygen.

Buccal types % by sample

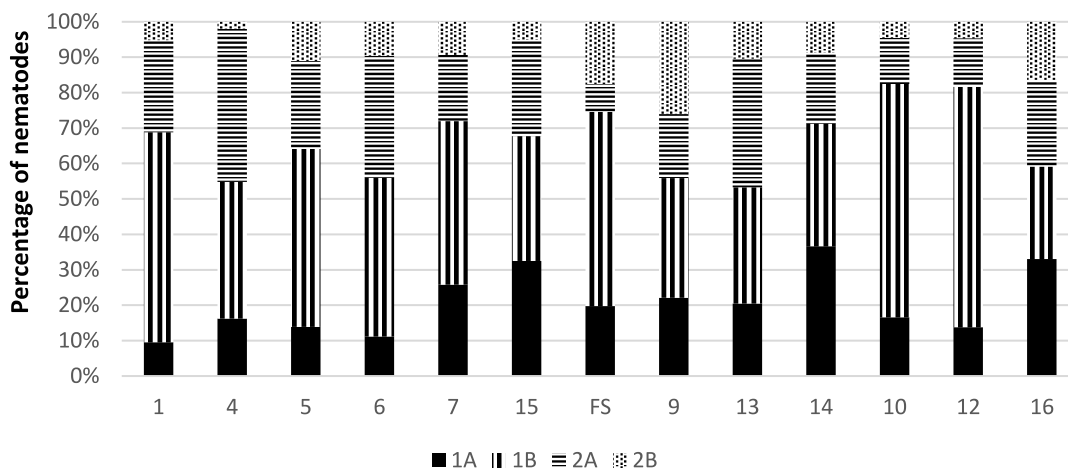


FIGURE S5. Percentage of nematodes from each feeding group, from each site. 1A = selective deposit feeders. 1B = non-selective deposit feeders. 2A = epistrate feeders. 2B = predators/omnivores.

Buccal types % by groups

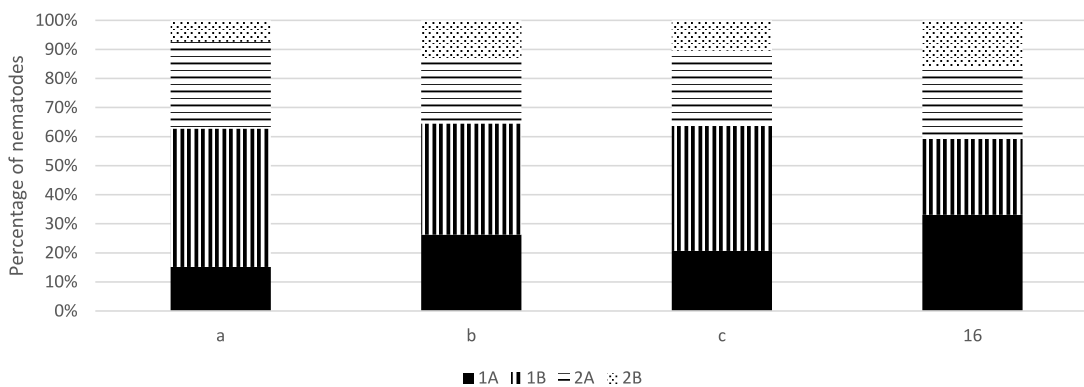


FIGURE S6. Percentage of nematodes from each feeding group, from each ecological group. 1A = selective deposit feeders. 1B = non-selective deposit feeders. 2A = epistrate feeders. 2B = predators/omnivores.

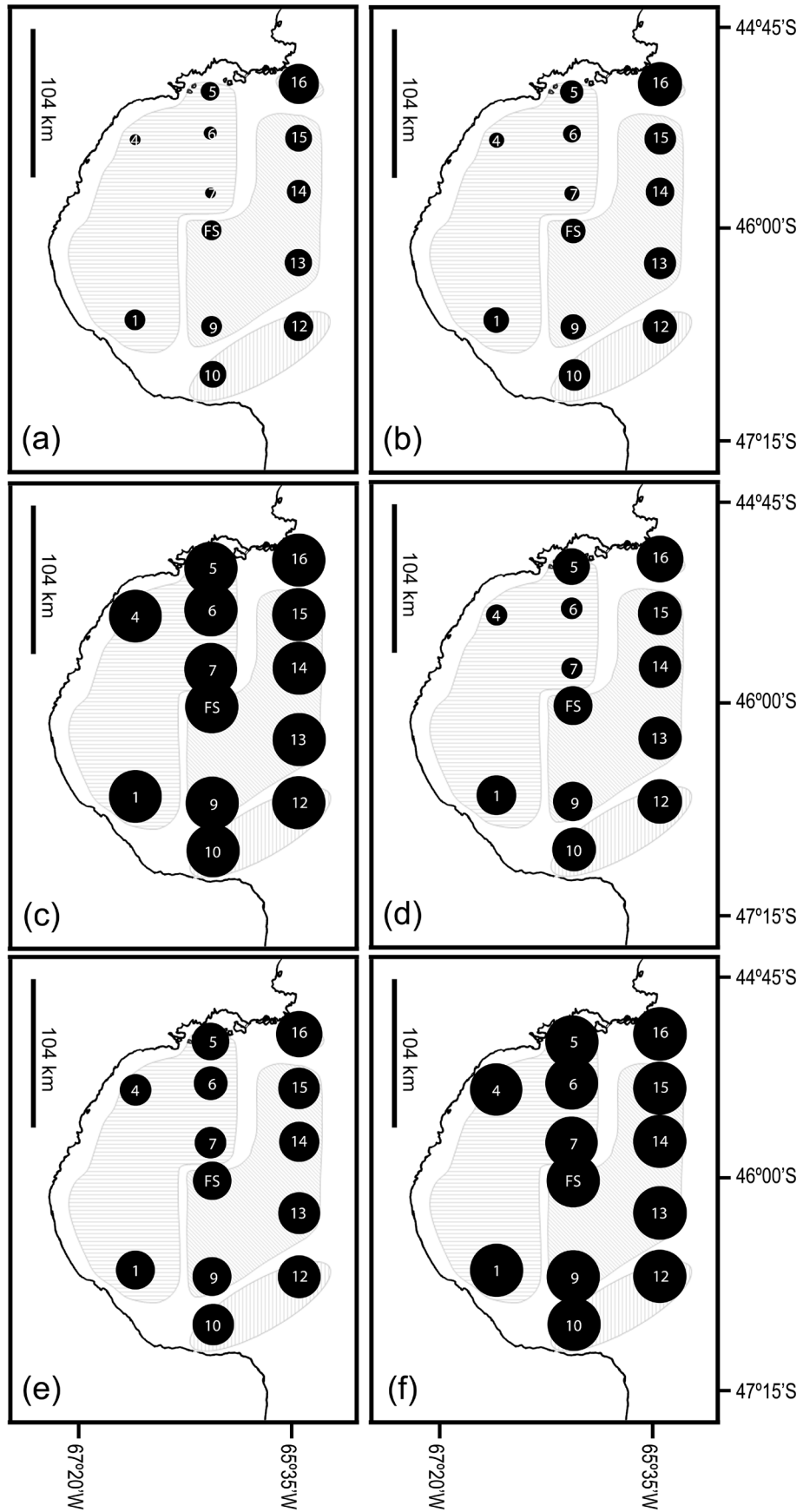


FIGURE S7. Maps of San Jorge Gulf with diversity indexes plotted as different sized circles. (a) Species richness (S). (b) Margalef richness (d'). (c) Pielou's evenness (J'). (d) Rarefaction (ES [51]). (e) Shannon-Wiener diversity index $H'(\log_e)$. (f) $1-\Lambda'$. The sizes of the circles reflect the data displayed in Table 1.

TABLE S1. Summary of environmental data, variables selected using the BEST biota-environment routine (% fine fraction, % medium sand, % coarse sand, and salinity), and hierarchical cluster analysis (CLUSTER).

Samples	Date	Latitude	Longitude	% Fine Fraction	%Medium Sand	%Coarse Sand	Salinity (PSU)	CLUSTER Groups
1	11/2/2014	-46.59	-66.91	4.59	0.00	0.00	33.40	a
4	11/2/2014	-45.50	-66.87	3.82	0.00	0.00	33.40	a
5	12/2/2014	-45.20	-66.18	4.54	0.00	0.00	33.40	a
6	12/2/2014	-45.46	-66.19	5.16	0.00	0.00	33.40	a
7	12/2/2014	-45.83	-66.19	6.70	0.00	0.00	33.40	a
9	12/2/2014	-46.65	-66.21	7.62	0.00	0.00	33.30	b
10	13/2/2014	-46.94	-66.21	0.65	0.52	0.00	33.10	c
12	13/2/2014	-46.63	-65.43	0.52	0.47	0.60	33.10	c
13	13/2/2014	-46.27	-65.42	1.22	0.25	0.00	33.20	b
14	13/2/2014	-45.82	-65.42	0.87	0.00	0.00	33.20	b
15	13/2/2014	-45.50	-65.42	0.78	0.00	0.00	33.30	b
16	14/2/2014	-45.16	-65.42	0.17	0.90	0.76	33.40	
FS	14/2/2014	-45.94	-65.55	3.81	0.00	0.00	33.30	b

TABLE S2. Nematode species identified at 13 sites in San Jorge Gulf, including 79 new records of known species and 101 new species (*), with four identified up to genus (**), two identified up to family (***), and two unidentified species. Total counts at the end of the table. Feeding types (FT): 1A = selective deposit feeders. 1B = non-selective deposit feeders. 2A = epistrate feeders. 2B = predators/omnivores.

Species	FT	Samples													FS
		1	4	5	6	7	9	10	12	13	14	15	16		
<i>Actinonema</i> sp. 1*	2A	0	0	0	0	0	5	0	0	4	12	0	4	0	
<i>Aegialoalaimus</i> sp. 1*	1A	0	0	0	0	0	0	0	0	0	0	1	0	0	
<i>Alaimella</i> sp. 1*	1A	0	0	0	0	0	2	0	0	0	0	0	2	0	
<i>Ammotheristus</i> sp. 1*	1B	0	0	0	0	0	0	0	3	0	0	0	1	0	
<i>Amphimnystera</i> sp. 1*	1B	2	0	1	0	9	1	2	1	1	5	1	1	0	
<i>Amphimnystera</i> sp. 2*	1B	0	0	0	0	0	0	0	2	2	0	1	0	0	
<i>Aponema papillatum</i>	1A	0	0	6	3	0	0	7	0	0	0	1	0	0	
<i>Anticoma campbelli</i>	1A	0	0	0	0	0	1	0	2	0	0	0	0	0	
<i>Axonolaimus</i> sp. 1*	1B	5	6	0	0	0	8	0	1	15	28	4	0	27	
<i>Biarmifer madrynsis</i>	2A	0	0	0	0	0	0	0	2	0	0	0	0	0	
<i>Biarmifer</i> sp. 2*	2A	0	0	0	0	0	4	0	0	0	0	0	0	0	
<i>Ironidae</i> ***	2B	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Microalaimus papillatus</i>	2A	0	0	0	0	0	0	0	0	0	0	0	2	0	
<i>Calyptronema retrocellatum</i>	2B	0	0	0	0	0	0	0	0	1	0	0	0	0	
<i>Campylaimus gerlachi</i>	1A	0	0	0	0	0	0	0	0	0	3	0	0	0	
<i>Campylaimus patagonicus</i>	1A	0	0	0	0	0	0	0	0	0	6	5	0	0	
<i>Campylaimus arcuatus</i>	1A	8	0	2	0	16	8	0	1	5	7	7	0	6	
<i>Campylaimus</i> sp. 1*	1A	2	0	0	0	0	4	1	0	0	0	0	1	11	
<i>Cervonema proberti</i>	1A	0	0	0	0	0	0	0	0	0	0	0	2	0	
<i>Cervonema multispira</i>	1A	0	0	0	0	0	0	0	0	0	10	5	1	0	
<i>Cervonema chilensis</i>	1A	0	0	8	0	0	0	0	0	1	0	0	0	0	
<i>Cervonema hermani</i>	1A	0	0	0	0	0	0	0	3	0	0	0	0	0	
<i>Cervonema tenuicaudata</i>	1A	0	0	0	0	0	0	0	3	5	0	0	0	0	
<i>Cervonema</i> sp. 1*	1A	0	0	0	2	0	1	0	0	0	0	0	0	1	
<i>Cervonema</i> sp. 2*	1A	0	0	0	0	0	0	0	0	0	0	0	0	4	
<i>Cheironchus</i> sp. 1*	2B	0	0	0	0	0	0	0	0	0	0	1	1	0	
<i>Comesa</i> sp. 1*	2B	4	1	21	3	16	3	1	4	2	0	0	8	1	
<i>Comesoma</i> **	1B	0	0	0	0	0	0	0	0	2	0	0	0	0	
<i>Comesoma</i> sp. 1*	1B	0	0	8	1	0	0	0	0	0	0	1	0	1	
<i>Comesoma</i> sp. 2*	1B	0	0	0	0	0	0	0	0	0	0	0	1	0	
<i>Craspodema</i> sp. 1*	2A	4	1	2	8	0	7	0	0	27	7	6	0	0	
<i>Craspodema</i> sp. 2*	2A	0	0	0	0	0	0	0	0	5	0	0	0	0	
<i>Crestanema patagonicum</i>	2A	2	0	0	0	0	4	3	0	0	0	1	2	1	
<i>Croconema otti</i>	2A	0	0	0	0	0	6	0	0	1	2	0	2	3	

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TABLE S2. Continued...

<i>Chromadorella filiformis</i>	2A	0	0	0	0	0	0	0	0	0	1	0	1	0
<i>Chromadorella</i> sp. 1*	2A	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>Chromaspirina</i> sp. 1*	2A	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Cyartonema</i> sp. 2*	1A	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Daptonema concordense</i>	1B	23	28	0	3	1	11	1	0	3	0	4	2	5
<i>Daptonema lopezi</i>	1B	9	0	0	0	0	6	5	2	17	1	6	1	2
<i>Daptonema rectangulatum</i>	1B	0	0	0	0	0	0	2	1	2	0	2	0	0
<i>Daptonema setosum</i>	1B	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Daptonema romanelloi</i>	1B	0	1	0	0	0	0	0	0	0	0	0	1	3
<i>Daptonema</i> sp. 1*	1B	4	0	0	0	0	4	2	3	2	0	0	0	0
<i>Daptonema</i> sp. 2*	1B	1	0	0	0	0	0	0	1	0	0	16	4	3
<i>Daptonema</i> sp. 3*	1B	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Daptonema</i> sp. 4*	1B	1	0	0	0	0	0	6	0	0	0	0	0	1
<i>Daptonema</i> sp. 5*	1B	0	0	0	0	0	0	8	0	0	0	0	1	0
<i>Daptonema</i> **	1B	0	0	5	2	0	0	0	2	0	0	2	0	0
<i>Dasynemoides</i> sp. 1*	1A	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Desmoscolescidae</i> ***	1A	0	0	0	0	0	1	0	0	0	1	0	0	0
<i>Desmolaimus</i> sp. 1*	1B	0	0	0	0	0	0	0	0	0	0	1	0	1
<i>Didelta scutatatum</i>	1B	0	0	0	0	0	0	0	2	1	0	0	0	0
<i>Diplopetloides</i> sp. 1*	1A	0	0	0	0	0	0	2	0	0	0	0	0	0
<i>Disconema</i> sp. 1*	1A	0	0	0	0	0	0	1	0	0	0	2	0	0
<i>Eleutherolaimus</i> sp. 1*	1B	1	0	0	0	0	0	0	0	0	0	0	2	0
<i>Deontolaimus tardus</i>	2A	0	0	0	0	0	0	0	2	0	0	1	2	0
<i>Endeolophos</i> sp. 1*	2A	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Gammanema</i> sp. 1*	2B	1	0	0	0	0	0	0	0	0	0	0	4	0
<i>Gomphionema</i> sp. 1*	2A	1	0	0	0	0	0	1	0	0	0	1	0	0
<i>Gomphionchus</i> sp. 1*	2A	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>Gomphionchus</i> sp. 2*	2A	0	0	0	2	1	0	0	0	0	0	0	0	0
<i>Gomphionchus</i> sp. 3*	2A	0	0	0	0	0	0	2	0	0	0	0	0	0
<i>Halalaimus deseadensis</i>	1A	2	1	0	0	1	3	2	0	4	9	3	7	4
<i>Halalaimus setosus</i>	1A	0	0	0	0	0	0	2	0	5	8	0	2	0
<i>Halalaimus diacros</i>	1A	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Halalaimus</i> sp. 1*	1A	0	0	2	0	3	6	0	0	1	0	1	0	0
<i>Halalaimus</i> sp. 2*	1A	0	0	0	0	0	4	0	0	0	0	0	0	0
<i>Halichoanolaimus minutissimus</i>	2B	0	0	0	0	0	0	0	0	0	0	0	2	0
<i>Halichoanolaimus</i> sp. 1*	2B	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Halichoanolaimus</i> sp. 2*	2B	0	0	0	0	0	0	0	0	0	0	0	1	0

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TABLE S2. Continued...

<i>Hopperia americana</i>	2A	17	58	16	15	9	1	14	5	0	0	0	1	0
<i>Hopperia arntzi</i>	2A	1	1	3	12	0	0	0	2	4	0	0	1	0
<i>Hopperia patagonica</i>	2A	0	1	0	0	0	2	0	5	5	1	5	2	3
<i>Hopperia beaglense</i>	2A	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Laimella longicauda</i>	2A	0	0	9	0	0	0	1	4	0	0	0	0	0
<i>Laimella filipjevi</i>	2A	0	0	0	0	0	0	4	0	0	0	0	0	0
<i>Laimella sandrae</i>	2A	1	0	5	0	0	0	1	3	1	1	1	0	0
<i>Laimella subterminata</i>	2A	0	20	0	0	0	0	0	0	0	0	0	0	1
<i>Laimella annae</i>	2A	4	0	4	3	5	0	0	0	0	0	0	0	0
<i>Laimella</i> sp. 1*	2A	0	0	0	0	2	0	0	0	0	0	0	1	0
<i>Laimella</i> sp. 2*	2A	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Ledovitia fallae</i>	2B	0	0	0	0	0	0	0	1	1	0	0	0	5
<i>Leptolaimus vinnulus</i>	1A	1	0	1	2	8	9	2	2	1	1	0	0	0
<i>Leptolaimus</i> sp. 1*	1A	1	0	0	0	0	2	0	0	0	0	0	0	0
<i>Leptolaimus</i> sp. 2*	1A	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Leptolaimus</i> sp. 3*	1A	0	0	0	0	0	0	0	0	0	0	0	4	0
<i>Leptolaimoides</i> sp. 1*	1A	1	0	2	2	1	0	0	0	0	1	5	0	0
<i>Linhomoeus</i> sp. 1*	2A	0	0	0	0	0	0	0	0	1	0	0	1	0
<i>Linhomoeus</i> sp. 2*	2A	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Linhomoeus</i> sp. 3*	2A	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Marylynnia quadriseta</i>	2B	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Marylynnia</i> sp. 1*	2B	0	0	0	8	0	0	1	2	0	0	0	1	0
<i>Mesacanthoides</i> sp. 1*	2B	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Metachromadora zaixsi</i>	2B	0	0	0	0	0	54	2	0	3	6	4	2	5
<i>Metadesmolaimus</i> sp. 1*	1B	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Metalinhomoeus gloriae</i>	1B	33	0	0	0	0	0	10	11	0	0	0	0	0
<i>Metalinhomoeus parafilliformis</i>	1B	0	0	0	0	20	0	1	0	0	0	5	0	0
<i>Metalinhomoeus retrosetosus</i>	1B	0	2	12	6	0	0	0	1	3	4	0	0	0
<i>Metalinhomoeus typicus</i>	1B	0	0	0	0	0	0	0	2	0	0	0	0	0
<i>Metalinhomoeus</i> sp. 1*	1B	2	3	15	6	0	0	0	0	0	0	0	3	5
<i>Meyersia</i> sp. 1*	2B	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Microlaimus cyatholaimoides</i>	2A	0	0	0	0	16	2	0	0	0	0	3	0	0
<i>Microlaimus decoratus</i>	2A	1	0	2	3	0	0	0	0	5	7	6	0	1
<i>Microlaimus gerlachi</i>	2A	0	0	4	0	0	0	0	0	0	0	0	0	0
<i>Microlaimus</i> sp. 1*	2A	0	0	0	0	0	0	0	0	0	0	0	3	0
<i>Microlaimus</i> sp. 2*	2A	0	0	0	0	0	0	0	0	0	0	1	1	0
<i>Molgolaimus</i> sp. 1*	1A	4	21	1	1	0	0	0	0	0	0	0	36	0
<i>Molgolaimus</i> sp. 2*	1A	0	0	0	0	0	0	0	0	0	0	0	1	0

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TABLE S2. Continued...

<i>Mudwigglus</i> sp. 1*	1A	1	4	3	2	0	0	4	0	19	19	15	0	5
<i>Mudwigglus</i> sp. 2*	1A	0	0	0	0	0	0	0	2	0	1	12	1	0
<i>Mudwigglus nellyae</i>	1A	0	0	0	0	0	0	0	0	0	3	0	1	0
<i>Mudwigglus plebeius</i>	1A	0	0	2	0	2	1	0	1	0	0	0	0	3
<i>Neochromadora papillosa</i>	2A	3	0	2	0	0	6	0	0	19	5	1	2	5
<i>Neochromadora</i> sp. 1*	2A	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Neochromadora</i> sp. 2*	2A	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Oxystomina elongata</i>	1A	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Oxystomina</i> sp. 1*	1A	0	0	0	0	4	0	0	0	0	0	0	0	0
<i>Oxystomina</i> sp. 2*	1A	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Oncholaimellus paracarlbergi</i>	2B	0	0	0	0	0	0	1	0	2	0	0	0	0
<i>Onyx</i> sp. 1*	2A	0	0	0	0	0	0	0	4	1	0	0	0	0
<i>Paranticoma</i> sp. 1*	1A	0	0	0	0	0	0	0	0	0	1	0	0	0
<i>Paracanthonchus longicaudatus</i>	2A	0	0	0	0	0	0	0	0	0	0	0	9	0
<i>Paracanthonchus</i> sp. 1*	2A	0	0	0	0	0	0	3	0	0	0	0	0	0
<i>Paracanthonchus</i> sp. 2*	2A	0	0	0	0	0	0	0	0	0	0	0	5	0
<i>Paracyatholaimus</i> sp. 1*	2A	0	0	2	0	0	0	0	0	0	0	0	0	0
<i>Paralinhomoeus</i> sp. 1*	1B	0	0	10	0	0	0	1	9	1	1	0	13	0
<i>Paralinhomoeus</i> sp. 2*	1B	0	0	0	0	0	0	0	3	0	0	0	0	0
<i>Paralinhomoeus</i> sp. 3*	1B	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Paralongicyatholaimus</i> **	2A	27	20	2	0	2	0	1	0	1	0	17	0	1
<i>Paralinhomoeus visitus</i>	1B	0	0	0	0	0	0	0	12	0	0	0	0	0
<i>Paramesacanthion inaequale</i>	2B	0	0	0	0	0	1	0	1	3	7	5	0	3
<i>Paramonohystera zizichi</i>	1B	6	0	0	0	0	6	0	0	0	12	0	1	0
<i>Paramonohystera megacephala</i>	1B	13	25	1	2	1	0	19	0	0	4	4	0	1
<i>Paramonohystera parabutschlii</i>	1B	0	0	0	0	0	0	1	0	0	0	0	0	0
<i>Paramonohystera proteus</i>	1B	0	0	1	0	0	0	3	0	0	0	0	3	5
<i>Pomponema tautraense</i>	2B	0	0	0	0	0	1	5	0	0	0	0	0	0
<i>Pomponema</i> sp. 1*	2B	1	0	0	1	0	0	0	0	0	1	1	0	0
<i>Pomponema</i> sp. 2*	2B	0	0	0	0	0	0	0	0	0	0	0	3	0
<i>Pomponema</i> sp. 3*	2B	0	0	0	0	0	0	0	0	1	0	0	0	0
<i>Pomponema</i> sp. 4*	2B	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Pseudochromadora</i> sp. 1*	2A	0	0	0	0	0	1	0	0	0	2	0	1	0
<i>Pseudopelagonema</i> sp. 1*	2A	0	0	0	0	0	3	0	0	0	1	0	0	3
<i>Pseudosteineria scopae</i>	1B	0	0	0	0	0	0	4	0	0	0	0	0	0
<i>Pselionema</i> sp. 1*	1A	0	0	0	0	0	0	0	0	1	2	0	0	0
<i>Pseudolella</i> sp. 1*	2B	0	0	0	0	0	0	0	0	0	0	6	0	0
<i>Pterygonema</i> sp. 1*	1A	0	0	0	0	0	0	0	0	0	0	0	1	0
Unidentified 1	1A	0	0	0	0	0	0	0	0	0	1	0	0	0
Unidentified 2	1A	0	0	0	0	0	0	0	0	0	0	0	0	1

Continues next page...

TABLE S2. Continued...

<i>Rhabdocoma</i> sp. 1*	1A	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Richtersia argentiniae</i>	2A	0	0	0	0	0	0	2	2	0	0	0	7	0
<i>Sabatieria arcuata</i>	1B	0	0	0	0	0	0	38	1	0	0	6	0	0
<i>Sabatieria flecha</i>	1B	0	0	0	0	0	0	0	36	5	0	0	15	0
<i>Sabatieria sanjosensis</i>	1B	0	0	0	0	0	0	0	2	0	0	0	0	0
<i>Sabatieria mortenseni</i>	1B	0	0	0	0	0	1	6	0	1	0	0	0	0
<i>Sabatieria wieseri</i>	1B	35	12	40	33	65	30	6	40	2	13	7	3	58
<i>Sphaerolaimus gracilis</i>	2B	0	0	2	0	2	0	0	0	6	0	1	0	10
<i>Sphaerolaimus pacificus</i>	2B	5	3	0	0	0	0	0	0	2	2	2	2	10
<i>Sphaerolaimus</i> sp. 1*	2B	0	0	0	0	0	0	0	0	0	0	0	0	3
<i>Setosabatieria conicaudata</i>	1B	0	1	12	3	0	9	0	3	12	3	3	1	4
<i>Setosabatieria</i> sp. 1*	1B	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Siphonolaimus</i> sp. 1*	2B	0	0	0	0	0	0	1	0	0	1	0	0	0
<i>Symplocostoma tenuicolle</i>	2B	0	0	0	0	0	0	0	0	1	1	0	0	0
<i>Synonchiella</i> sp. 1*	2B	0	0	0	0	0	0	0	0	0	0	0	2	0
<i>Southerniella</i> sp. 1*	1A	0	0	0	0	0	2	2	0	0	0	0	0	0
<i>Spirinia</i> sp. 1*	2A	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Spiliphera</i> sp. 1*	2A	0	0	0	0	0	0	0	0	0	0	8	0	0
<i>Spilophorella</i> sp. 1*	2A	0	0	0	0	0	0	2	0	0	1	0	0	0
<i>Steineria pilosa</i>	1B	0	0	0	0	0	0	12	0	0	0	0	1	0
<i>Tarvaia</i> sp. 1*	1A	0	0	0	0	0	0	2	0	0	0	0	0	0
<i>Thalassoalaimus nestori</i>	1A	0	0	0	0	0	0	0	0	0	0	0	3	0
<i>Thalassoalaimus macrosmaticus</i>	1A	0	0	0	0	0	1	0	0	0	0	0	0	0
<i>Thalassomonhystera</i> sp. 1*	1B	1	0	0	0	0	0	0	0	0	0	0	0	0
<i>Theristus rectangulatum</i>	1B	0	0	0	0	0	0	0	1	0	0	0	0	0
<i>Theristus</i> sp. 1*	1B	0	0	0	0	0	0	0	1	1	0	0	3	0
<i>Terschellingia longicaudata</i>	1A	1	4	1	2	0	0	7	6	0	0	1	4	2
<i>Terschellingia sulfidrica</i>	1a	0	0	1	0	0	0	0	0	0	0	0	0	0
<i>Terschellingia</i> sp. 1*	1A	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Terschellingia</i> sp. 2*	1A	0	0	0	0	0	0	0	2	0	1	0	3	1
<i>Terschellingia</i> **	1A	0	0	0	0	0	0	0	0	0	0	0	1	0
<i>Trefusia</i> sp. 1*	1A	0	0	0	0	0	0	0	2	0	0	0	1	0
<i>Trochamus</i> sp. 1*	2A	0	0	0	0	0	0	0	0	0	0	1	0	0
<i>Valvaelaimus</i> sp. 1*	2A	0	0	0	0	0	0	0	0	0	0	0	2	0
<i>Vasostoma</i> sp. 1*	1B	0	0	0	0	0	0	0	2	0	0	0	0	0
<i>Viscosia</i> sp. 2*	2B	0	0	0	0	0	0	0	0	0	0	0	3	0
<i>Viscosia separabilis</i>	2B	0	1	0	0	0	0	1	1	1	0	0	0	0
<i>Viscosia macramphida</i>	2B	0	0	0	0	0	0	0	0	0	0	0	4	0
Total		231	215	209	125	185	226	208	210	212	205	204	218	213

TABLE S3. Similarity percentage (SIMPER) matrix. Species determined by SIMPER analysis for nematode associations in different groups, with their contributions (percent) to the similarity (within each group) and dissimilarities (between groups). * indicates newly identified species.

	Group a		
Group a	Sabatieria wieseri		
	<i>Hopperia americana</i>		
	<i>Comesa sp1*</i>		
	<i>Paramonohystera megacephala</i>		
	<i>Daptonema concordiense</i>		
	<i>Laimella annae</i>		
	<i>Paracyatholaimus sp1*</i>	44.8%	
	<i>Metalinhomoeus sp1*</i>		
	<i>Mudwigglus sp1*</i>		
	<i>Craspodema sp1*</i>		
		Group b	
Group b	<i>Hopperia americana</i>	<i>Axonolaimus sp1*</i>	
	<i>Metachromadora zaixsi</i>	Sabatieria wieseri	
	<i>Paramesacanthion inaequale</i>	<i>Campylaimus arcuatus</i>	
	<i>Axonolaimus sp1*</i>	<i>Metachromadora zaixsi</i>	
	<i>Daptonema lopezi</i>	<i>Setosabatieria conicaudata</i>	
	<i>Neochromadora papillosa</i>	<i>Halalaimus deseadensis</i>	
	<i>Laimella annae</i>	<i>Neochromadora papillosa</i>	
	<i>Molgolaimus sp1*</i>	<i>Paramesacanthion inaequale</i>	
	<i>Hopperia patagonica</i>	<i>Daptonema lopezi</i>	43.9%
	<i>Croconema otti</i>	<i>Hopperia patagonica</i>	66.9%
	<i>Metalinhomoeus sp1*</i>	<i>Mudwigglus sp1*</i>	
	<i>Paralongicyatholaimus sp1*</i>	<i>Craspodema sp1*</i>	
			Group c
Group c	<i>Sabatieria arcuata</i>	<i>Metalinhomoeus gloriae</i>	<i>Metalinhomoeus gloriae</i>
	<i>Metalinhomoeus gloriae</i>	<i>Sabatieria arcuata</i>	Sabatieria wieseri
	<i>Sabatieria flecha</i>	<i>Neochromadora papillosa</i>	<i>Terschellingia longicaudata</i>
	<i>Richtersia argentinae</i>	<i>Hopperia americana</i>	<i>Hopperia americana</i>
	<i>Paralinhomoeus sp1*</i>	<i>Axonolaimus sp1*</i>	<i>Daptonema lopezi</i>
	<i>Daptonema lopezi</i>	<i>Craspodema sp1*</i>	<i>Daptonema sp1*</i>
	<i>Metalinhomoeus sp1</i>	<i>Laimella longicauda</i>	<i>Leptolaimus vinnulus</i>
	<i>Laimella annae</i>	<i>Richtersia argentinae</i>	<i>Richtersia argentinae</i>
	<i>Daptonema rectangulatum</i>	<i>Maryllynnia sp1*</i>	<i>Amphimonhystera sp1*</i>
	<i>Daptonema sp1*</i>	<i>Campylaimus arcuatus</i>	<i>Comesa sp1*</i>

TABLE S4. Results from PCA diversity index, showing the eigenvalues and eigenvectors or group of indexes constituting each PC that explain the highest percentage of total variation in the data. Species richness (S), Shannon-Wiener diversity index ($H'[\log_e]$), Margalef's diversity index (d), Pielou's evenness index (J'), rarefaction (ES [51]), and 1-Lambda' index.

Eigenvalues			
PC	Eigenvalues	%Var.	Cum.% Var.
1	308.00	96.20	96.20
2	12.10	3.80	100.00

Eigenvectors		
Variable	PC1	PC2
S	0.87	-0.45
d	0.17	-0.66
J'	0.00	0.00
ES (51)	0.45	0.89
$H'(\log_e)$	0.02	0.01
1-Lambda'	0,00	0.00

TABLE S5. Results from PCA of environmental variables, showing eigenvalues and eigenvectors or groups of variables constituting each PC that explain the highest percentage of the total variation in data. TOM = total organic matter. FF = fine fraction.

Eigenvalues			
PC	Eigenvalues	%Var.	Cum.%Var.
1	6.33	57.5	57.5
2	1.75	15.9	73.5

Eigenvectors		
Variable	PC1	PC2
Mean depth	-0.29	-0.32
TOM	-0.34	-0.21
FF	-0.33	-0.03
Very fine sand	0.23	0.44
Fine sand	0.29	-0.35
Medium sand	0.34	-0.30
Coarse sand	0.25	-0.57
Gravel	0.20	-0.19
Temperature	0.36	0.05
Salinity	-0.28	-0.30
Oxygen	0.37	0.03