Supporting Information

S2 Table. The matrix of stimulus coordinates for the MDS model of independent associations among common parasites.[1]

	Balintidium	Blastocystis	Entamoeba coli	Entamoeba sp.	Hookworm	Oesophagostomum	Probstmayria	Strongyloides	Troglocorys	Troglodytella
Balintidium coli	0									
Blastocystis sp.	2.616	0								
Entamoeba coli	2.486	2.252	0							
Entamoeba sp.	2.554	3.345	2.751	0						
Hookworm	2.165	2.23	1.444	2.042	0					
Oesophagostomum sp.	1.401	2.693	2.186	1.822	1.333	0				
Probstmayria gombensis	3.034	2.028	2.498	2.158	1.982	2.563	0			
Strongyloides sp.	2.111	2.539	1.994	1.59	0.989	1.366	1.713	0		
Troglocorys cava	2.969	3.24	3.023	0.992	2.309	2.287	1.744	1.667	0	
Troglodytella abrassarti	2.403	2.997	1.947	1.123	1.165	1.489	2.049	0.905	1.565	0

[1] The table shows the optimally scaled data (disparities) for the MDS analysis of independent associations among biweekly parasite prevalence (frequency of positive samples). Disparities represent the strength of association among the variables included in the model. Larger disparities are equivalent of a weak association. Only parasites detected in >5% of faecal samples were included in the model.