Erratum to: Eukaryotic diversity in premise drinking water using 18S rDNA sequencing: implications for health risks

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Because some of the eukaryotic species listed in Table 1 under “Algae” and “Dinoflagellates” were incorrectly grouped into those categories, we have listed them below under the correct grouping.

Erratum (I): Table 1 Sequence homologies and number of clones obtained for each major representative eukaryotic group

Erratum (II): Fig 2. Relative abundance of 18S rDNA clone in various eukaryotic groups.

The above listed species were of low abundance in our clone libraries therefore discussion of our results was not affected by these changes as well as the major findings of our study.

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Table 1 Sequence homologies and number of clones obtained for each major representative eukaryotic group

Group	Sequence length (bp)	Accession no. ^a	Closest Relative	no. clones	% Similarity ^b
Algae	613	HQ912625	<i>Cyclotella</i> sp. L04-2	16	99 %
Dinoflagellates	629	JN615412	<i>Amphidoma languida</i> strain SMI	1	91 %
	615	HQ324899	<i>Azadinium poporum</i> isolate UTHD4	2	91 %
	677	EF492492	<i>Gymnodinium</i> sp. CCMP425	92	98 %
	614	AJ415515	<i>Scrippsiella trochoidea</i>	1	93 %
	614	AY443025	<i>Woloszynskia leopoliensis</i>	3	98 %
	701	EF058253	<i>Woloszynskia pascheri</i> strain CCAC0075	37	99 %
Misc	617	EF455761	<i>Malawimonas jakobiformis</i>	9	99 %
	601	FJ424512	<i>Parvilucifera prorocentri</i>	1	78 %

a, Accession no. for closest relative

b, For each clone sequence, query coverage range, 74 - 100 %, and e value range, 0.0-1e⁻¹⁷

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Fig. 2