Correction: Taxonomic and functional heterogeneity of the gill microbiome in a symbiotic coastal mangrove lucinid species

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Since publication of the original paper, the authors noticed that a typesetting error meant Table 2 was typeset incorrectly. The correctly laid out table is displayed below. The HTML and PDF versions of this paper have also been updated. The publisher wish to apologise for any inconvenience caused.

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Table 2 Comparison of genomic features among *Ca.* Sedimenticola endophacoides, free-living *Sedimenticola* spp. (Flood et al. 2015; Louie et al. 2016), and bacterial symbionts, including the lucinid thioautotrophic symbiont clade A (Petersen et al. 2016; König et al. 2016), a vesicomyid clam gill symbiont (*Ca. Ruthia Magnifica*; Roeselers et al. 2010), a solemyid clam gill symbiont (Dnytrenko et al. 2014), bathymodiolin mussel gill symbionts (*Bathymodiolus septemdiem* and *Bathymodiolus thermophilus*; Ikuta et al. 2016; Ponudurai et al. 2017), deep-sea tubeworm trophosomal symbionts (*Ridgeia piscesae*, *Riftia pachyptila* and *Tevnia jerichonana*; Gardebrecht et al. 2012; Perez and Juniper 2016), a marine nematode ectosymbiont (*Ca. Thiosymbion oneisti*; Petersen et al. 2016), and a deep-sea scaly-foot snail esophageal gland symbiont (Nakagawa et al. 2014).

Function	<i>Ca.</i> Sedimenticola endophacoides	<i>S. thio-</i> <i>taurini</i>	<i>S. selenati-</i> <i>reducens</i>	<i>Ca. Thio-</i> diazotropha endoloripes	<i>Ca. Thio-</i> diazotropha endolucinida	<i>Ca. Ruthia</i> magnifica	<i>Solemya velum</i> symbiont	<i>Bathymodiolus</i> spp. symbionts	Deep-sea tubeworm symbionts	<i>Ca.</i> Thiosymbion oneisti	<i>Cryomallon</i> <i>squamiferum</i> symbiont
Sulfur oxidation	Sqr type VI	Sqr types I and VI			Sqr types I, III and VI	Sqr type I	Sqr type I	Sqr types I and VI			Sqr type I
Hydrogen oxidation	Groups 1 and 2b (NAD-dependent) Ni-Fe hydrogenase			Groups 1 and 2a Ni-Fe hydrogenase		–	Groups 1 and 2b (NAD-dependent) Ni-Fe hydrogenase	Groups 1 and 2a Ni-Fe hydrogenase	–		Groups 1 and 2a Ni-Fe hydrogenase
Carbon fixation	RuBisCo II	RuBisCO Ia and II	RuBisCO Ia and II	RuBisCo Ia and II	RuBisCo Ia and II	RuBisCO II	RuBisCO Ia and II	RuBisCO Ia and II	RuBisCO II	RuBisCO Ia and II	RuBisCO Ia and II
Nitrogen fixation	–	+	–	+	+	–	–	–	–	+	–
Assimilatory nitrate and nitrite reduction	–	–	–	+	–	–	–	+	+	+	+
Urea hydrolysis	+	+	–	+	–	–	+	–	–	+	–
Oxygen respiration	cbb3 type terminal oxidase	cbb3, aa3 and cytochrome d ubiquinol oxidases		cbb3 and aa3 type terminal oxidases							cbb3, aa3 and cytochrome d ubiquinol oxidases

‘+’ denotes a feature annotated in a genome while ‘–’ denotes a feature not yet sequenced in a genome

Sqr sulfide:quinone oxidoreductase, *RuBisCO* ribulose-1,5-bisphosphate carboxylase/oxygenase