

Table S5. Read mapping statistics of metagenome and metatranscriptome data for *lcdA* genes.

	Low methane yield		High methane yield		Fold change	<i>P</i> -value
	Mean read counts (RPM)	Standard deviation	Mean read counts (RPM)	Standard deviation		
Metagenome	6.757	8.176	0.370	0.190	18.26	0.024
Metatranscriptome	0.549	0.369	0.453	0.143	1.21	0.958