

Table S3. Gene set enrichment analysis of metagenome and metatranscriptome datasets. Pathways with genes differentially present or expressed based on nominal P value (NOM P -val ≤ 0.05) are shown, ranked by normalised enrichment score (NES). Corrected P values for false discovery rate (FDR q-val) and familywise-error rate (FEWER P -val) are shown.

Methane yield group	KEGG Pathway	NES	NOM P -val	FDR val	q-	FEWER P -val
Metagenome						
Low	ko00052-Galactose metabolism	-1.97	0.003	0.017		0.015
Low	ko02060-Phosphotransferase systems (PTS)	-1.82	0.015	0.092		0.120
Low	ko00440-Phosphonate and phosphinate metabolism	-1.62	0.012	0.734		0.602
Low	ko00561- Glycerolipid metabolism	-1.58	0.047	0.544		0.701
Low	ko00290- Valine, leucine, isoleucine biosynthesis	-1.57	0.036	0.496		0.716
Low	ko00791- Atrazine degradation	-1.53	0.040	0.608		0.801
Low	ko01212- Fatty acid metabolism	-1.45	0.043	0.786		0.909
High	ko03070-Bacterial secretion system	1.70	0.019	0.470		0.386
High	ko00983- Drug metabolism and other enzymes	1.55	0.039	0.688		0.773
High	ko00250- Alanine, aspartate and glutamate metabolism	1.55	0.036	0.538		0.782
Metatranscriptome						
Low	ko00052-Galactose metabolism	-1.72	0.010	0.511		0.270
Low	ko00630-Glyoxylate and dicarboxylate metabolism	-1.69	0.005	0.362		0.348
Low	ko00720-Carbon fixation pathways in prokaryotes	-1.64	0.010	0.427		0.507
Low	ko01230-Biosynthesis of amino acids	-1.61	0.035	0.393		0.570
Low	ko00550-Peptidoglycan biosynthesis	-1.60	0.020	0.365		0.612
Low	ko00300-Lysine biosynthesis	-1.58	0.030	0.316		0.669
Low	ko00290-Valine, leucine, isoleucine biosynthesis	-1.55	0.040	0.311		0.736
Low	ko00450-Selenocompound metabolism	-1.52	0.033	0.311		0.792
Low	ko00330-Arginine and proline metabolism	-1.48	0.038	0.373		0.870