

S4 Table. Metabolic gene identification.

Metabolism	Gene	KEGG id	<i>Marinosulfonomonas</i> ^a		<i>Rhodobac- teraceae</i>	<i>Thiotrich- aceae</i>	<i>Flavobac- teriaceae</i>
			MAG 1	MAG 2			
Cytochrome Oxidases	UQCRFS1	K00411	X	X	X	X	
	coxA	K02274			X	X	
	ccoN	K00404	X	X	X		
	cydA	K00425		X			
	cyoB	K02298			X		
Aerobic CODH	coxS ^b	K03518					
	coxM ^b	K03519					
	coxL ^b	K03520					
Methanogenesis	mcrA ^b	K00399					
	mcrB ^b	K00401					
	mcrG ^b	K00402					
Methane Oxidation or Nitrification	pmoA ^b	K10944					
	pmoB ^b	K10945					
	pmoC ^b	K10946					
Sulfur Oxidation	soxA	K17222	X	X	X		
	soxX	K17223	X	X	X		
	soxB	K17224	X	X	X		
	soxC	K17225	X	X	X		
	soxY	K17226	X		X		
	soxZ	K17227	X		X		
General Nitrogen Metabolism	narG	K00370	X	X	X		
	narH	K00371	X	X	X		
Dissimilatory Nitrate Reduction	nirB	K00362		X	X	X	
	nirD	K00363		X		X	
	nrfA ^b	K03385					
Denitrification	nirK	K00368			X		
	norB	K04561			X		
	norC	K02305			X		
	nosZ	K00376			X		
MAG Completeness (%) ^c			88.4	88.2	93.7	66.1	44.3
MAG Contamination (%) ^c			16.4	0.6	1.4	11.8	1.6

^a *Marinosulfonomonas* MutY contig belongs to two separate MAGs and each are reported separately as MAG 1 and MAG 2, respectively.

^b KEGG ID gene not identified in any MAG and not reported in Table 2.

^c Completeness and contamination scores generated by CheckM v1.0.5 as described in Brazelton et al 2022 [35].

A KEGG ID analysis was used to identify the potential metabolic strategies of the MutY encoding organisms at the LCHF. The full metabolic KEGG ID search is shown above.