

# Light rare earth element depletion during *Deepwater Horizon* blowout methanotrophy

**Authors:** A.M. Shiller<sup>1\*</sup>, E.W. Chan<sup>2</sup>, DJ. Joung<sup>1</sup>, M.C. Redmond<sup>3</sup>, J.D. Kessler<sup>2</sup>

<sup>1</sup>Center for Trace Analysis, University of Southern Mississippi, Stennis Space Center, MS 39529, USA.

<sup>2</sup>Earth and Environmental Sciences, University of Rochester, Rochester, NY 14627, USA.

<sup>3</sup>Dept. of Biological Sciences, University of North Carolina at Charlotte, Charlotte, NC 28223, USA.

\*Correspondence to: alan.shiller@usm.edu; 228-688-1178

**Supplementary Information:** Table S1 and Figure S1.

Table S1. Summary of metagenome sequences

Sample Name	<b>GOM15B</b>	<b>GOM15C</b>
IMG ID	3300008252	3300008227
Genome Size	802,871,420	845,437,039
Gene Count	1,680,640	1,822,033
Scaffold Count	1,244,072	1,379,518
%GC	42.5	41.8
16S rRNA Gene Count	1252	1304
16S rRNA Reads	268,350	290,117
soxB Gene Count	125	184
soxB Reads	10,307	11,247
soxA Gene Count	46	46
soxA Reads	12,225	11,130
soxA Gene Count	220	206
soxA Reads	13,396	15,615

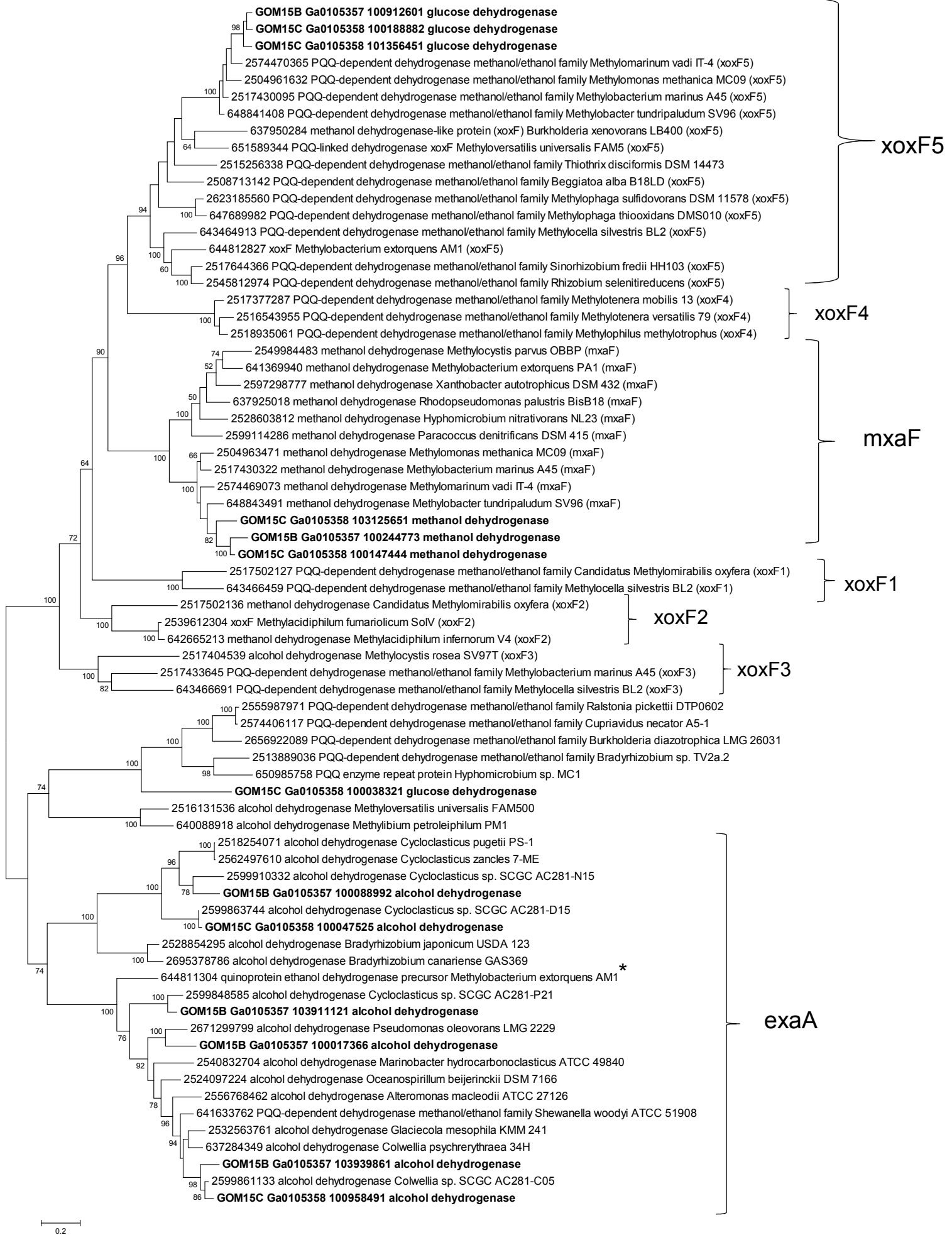


Figure S1: Maximum likelihood tree of *mxαF* and *xoxF* methanol dehydrogenase and *exaA* alcohol dehydrogenase sequences. Selected sequences from incubation metagenomes are indicated in bold and identified by IMG locus tags. La-requiring *exaA* from *Methylobacterium extorquens* AM1 is shown with \*. Reference sequences are shown with IMG gene IDs and annotations. *xoxF* sequences are also classified according to the five clade system used by Keltjens et al. (2014), shown in parentheses. Bootstrap values below 50% are not shown.