

## ***Interactive comment on “Reviews and synthesis: Carbon capture and storage monitoring – an integrated biological, biophysical and chemical approach” by N. Hicks et al.***

**Anonymous Referee #2**

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This is an interesting and important subject. However, I find it a bit vague on specifics. For one things, how about we see some diagrams from actual published studies that show the shift in composition of a) functional gene relative abundances b) relative abundances of different phyla? Surely the authors could ask permission from publishers of other papers to add these in. Also they should discuss some of the actual results found in more detail: which gene categories became more abundant, which less, and what are the real implications for ecosystem shifts? How do the patterns for sediment bacteria compare to those seen for larger organisms under increased CO<sub>2</sub>.

In monitoring CO<sub>2</sub> leakage effects: What other environmental factors might give 'false positives'? What might give 'false negatives'? (e.g. if CaCO<sub>3</sub> in sediment is buffering  
C4918

changes).

Can results from microcosm systems really scale up to natural systems? what are the limitations of such simplifications?

What sequencing platforms are best used? Can TRFLP still be useful?

I think the authors need to give more specifics and add in some nice colored diagrams to help make the point of what next gen sequencing can offer, and what the results look like.

I suggest these are made as revisions before the paper can be accepted.

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Interactive comment on Biogeosciences Discuss., 12, 8909, 2015.