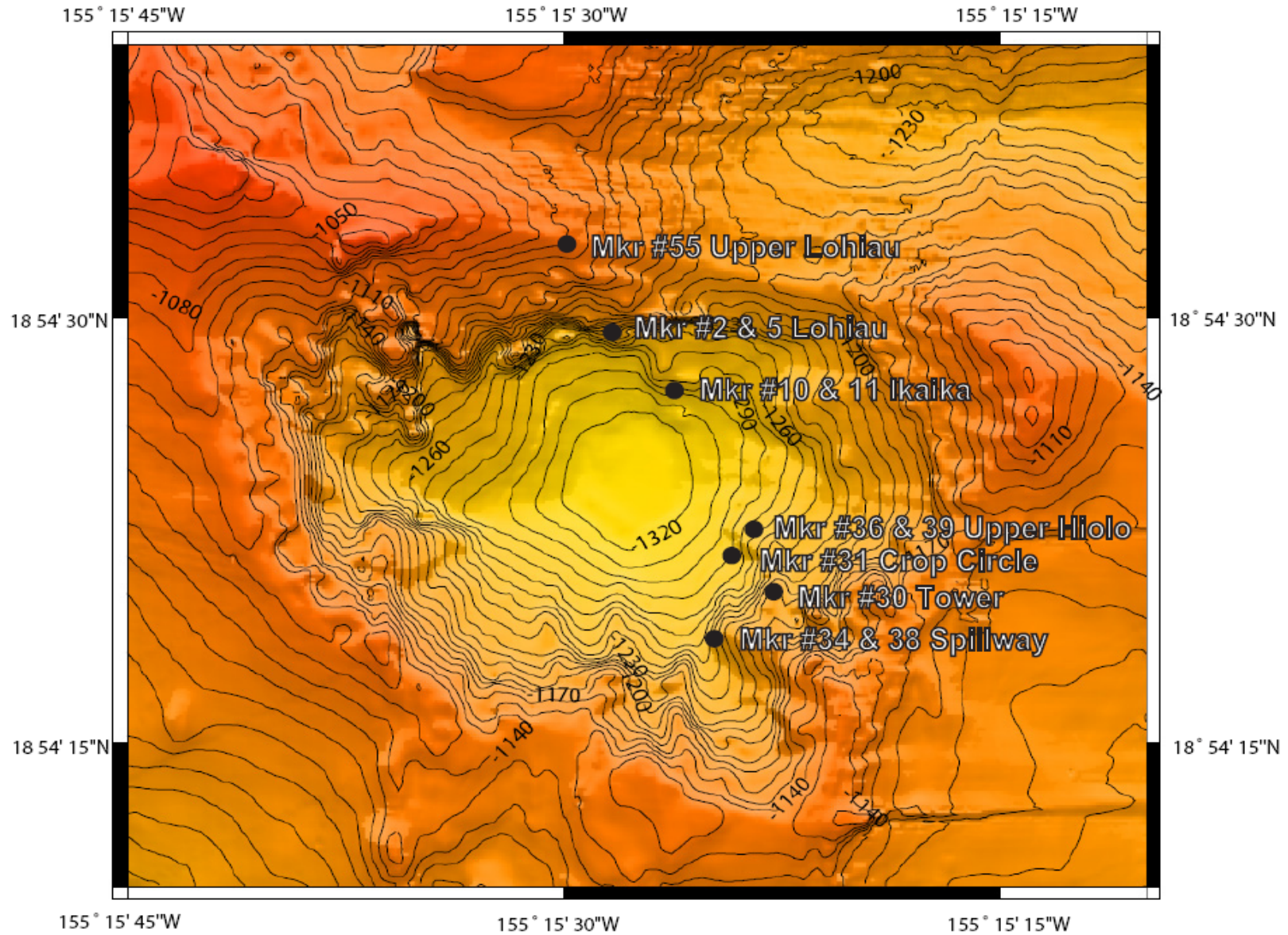


The detection of *Nitratiruptor*  
dominated communities using Bact  
Traps, clone libraries & the FeMO  
T-RFLP database

Craig Moyer & Allen Rassa  
Biology Department  
Western Washington University

# Updated Pele's Pit Map with revised "best estimate" sampling locations

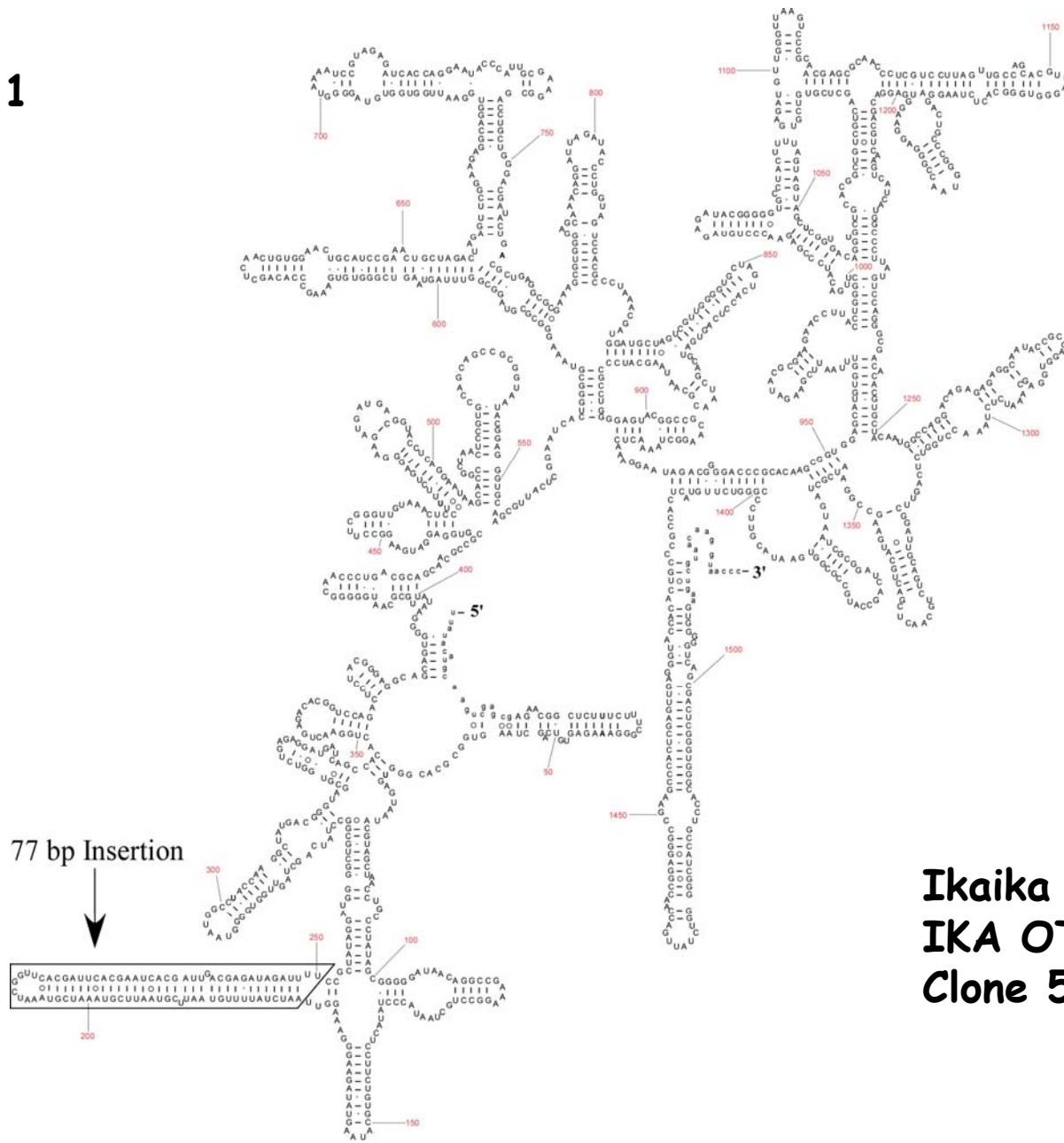


Map courtesy of Brad Bailey

# Fortuitous Phylotype Detection

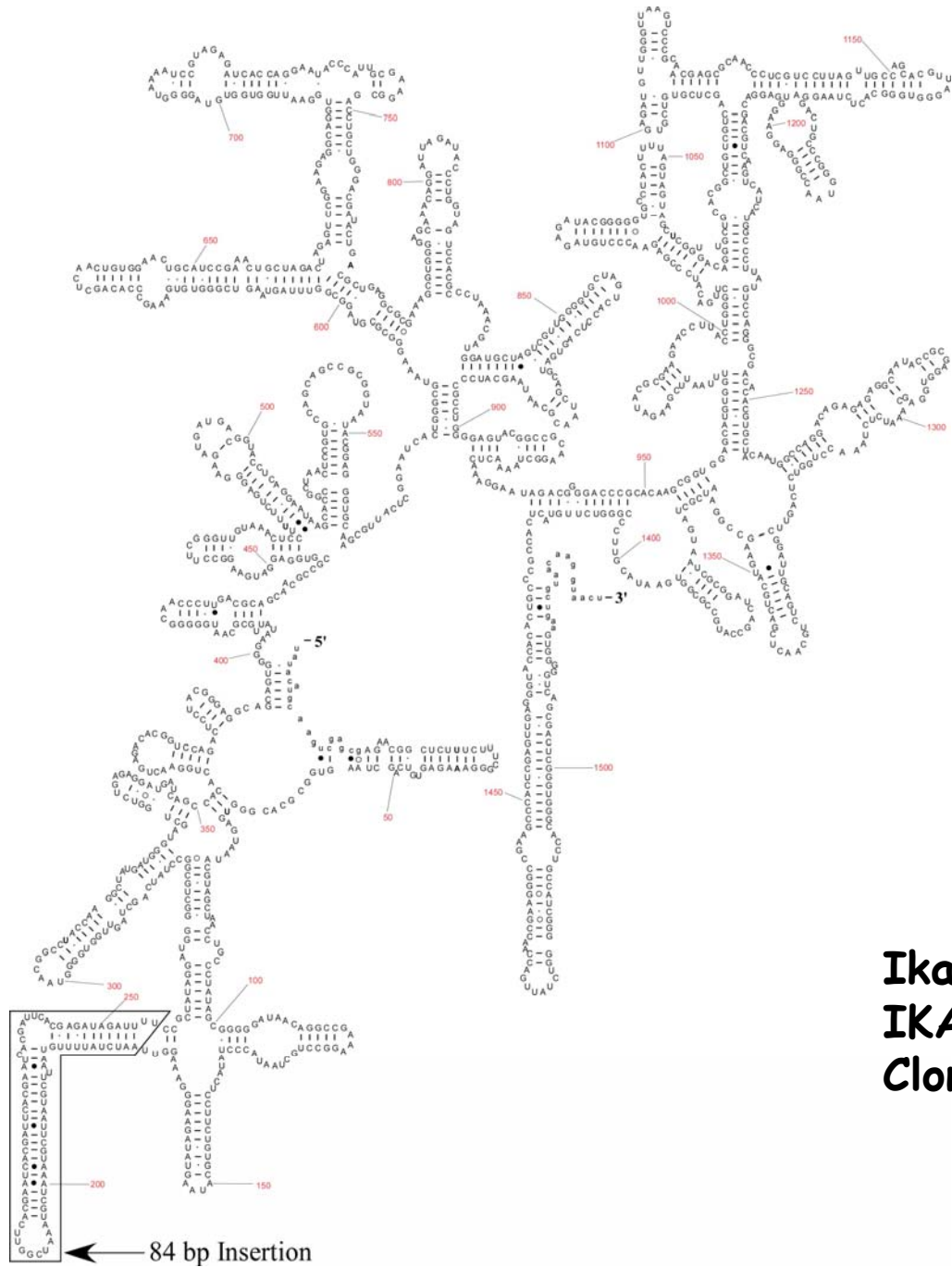
- Clone library from Ikaika (aka Jet) vents yielded a pair of unusual clones with strange inserts in the cruciform region (see 2<sup>o</sup> structure maps; Figs 1 & 2).

Figure 1



Ikaika Clone Library  
IKA OTU 5  
Clone 59

Figure 2

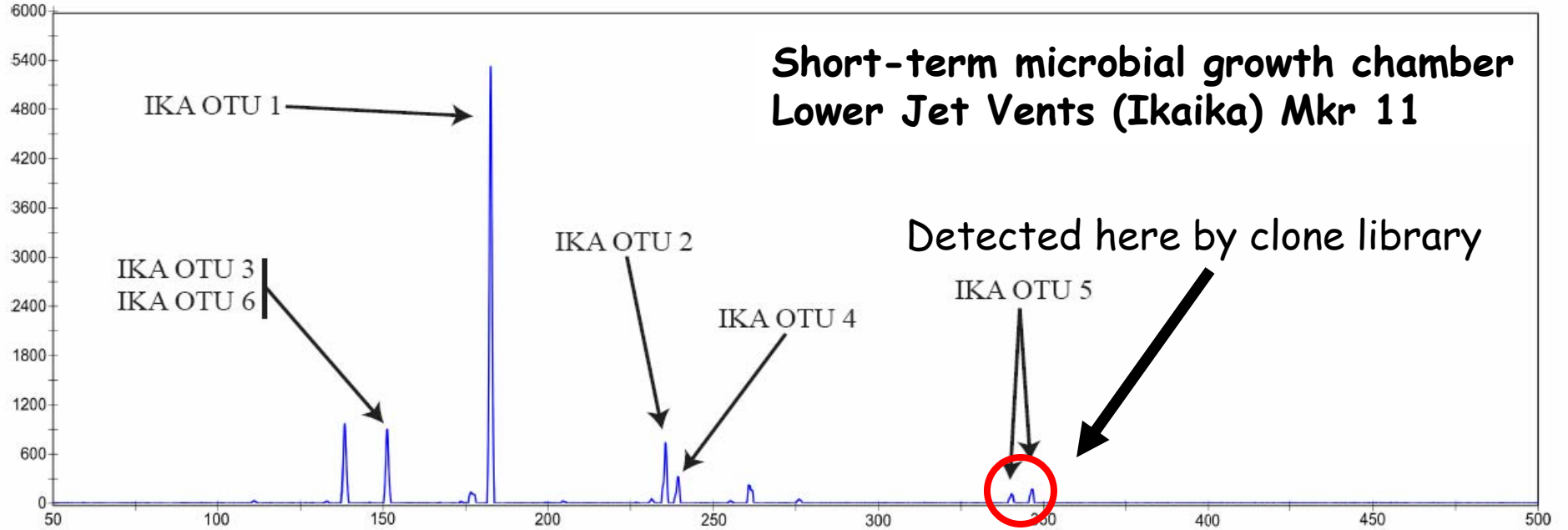


Ikaika Clone Library  
IKA OTU 5  
Clone 37

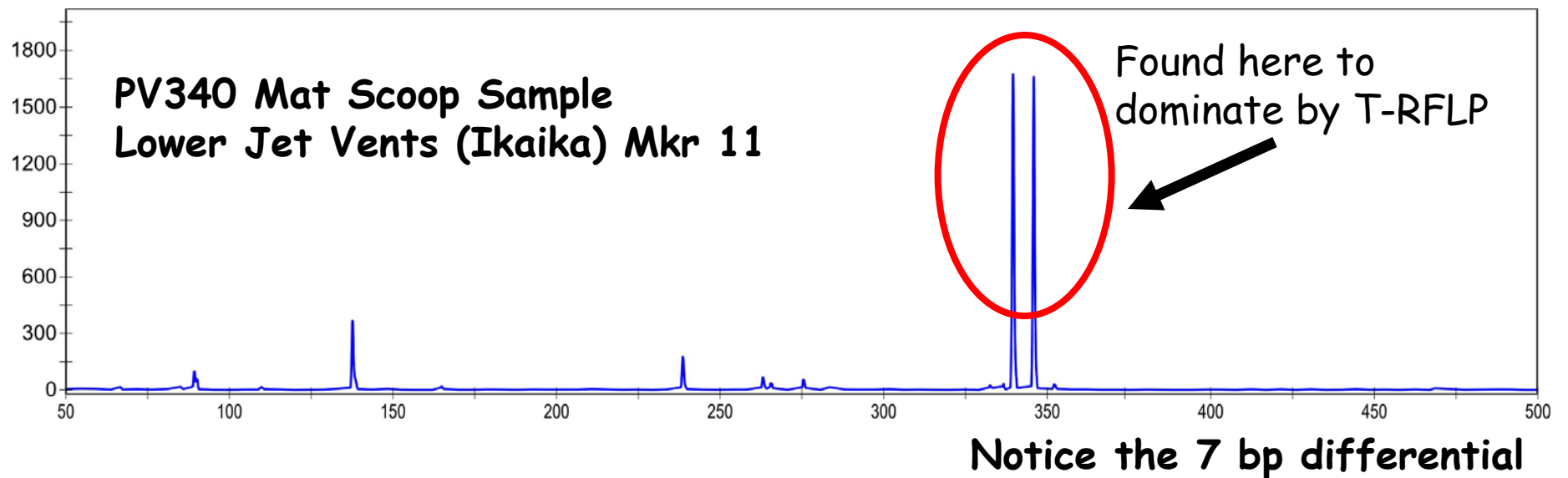
# Fortuitous Phylotype Detection

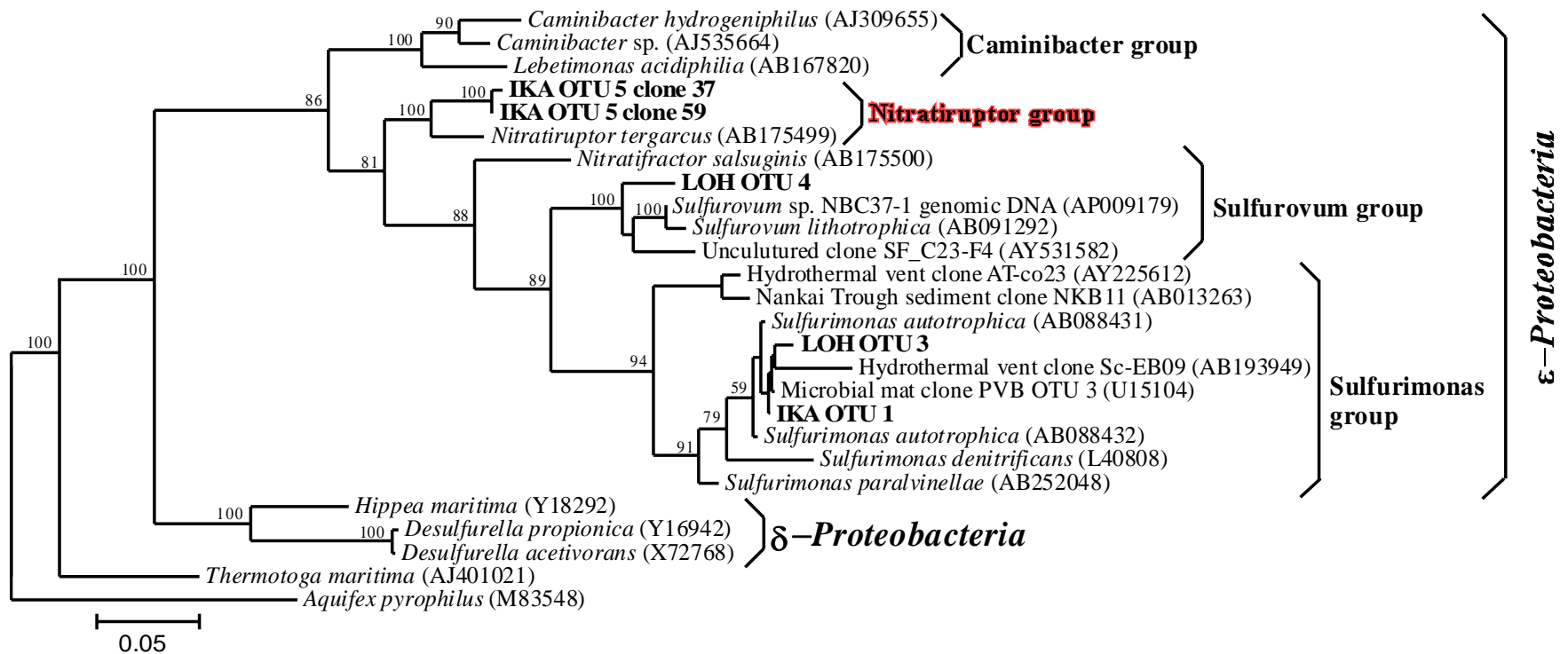
- T-RFLP analysis showed only minor peaks from the clone library source community (Fig 3A), but after further interrogation of the T-RFLP database we uncovered evidence for a community dominated by *Nitratiruptor* populations (Fig 3B) at the same location.
- Currently looking for other sites as well, e.g., Marker #39 @ Upper Hiolo Ridge.

**Figure 3A**



**Figure 3B**

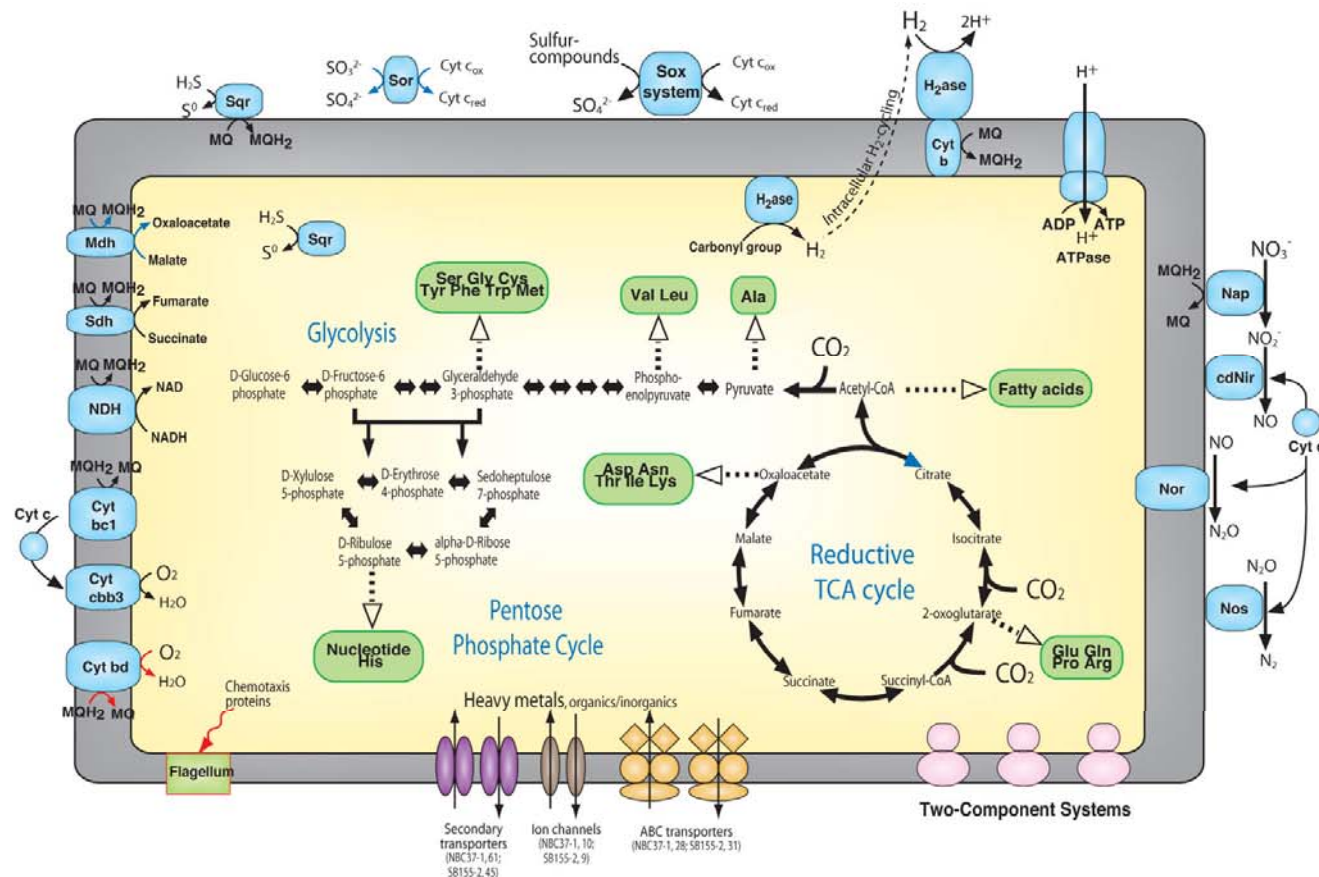




*Nitratiruptor* sp. are obligate chemoautolithotrophs denitrifying via nitrate reduction coupled to H<sub>2</sub>-oxidation forming N<sub>2</sub> under microaerophilic conditions (Nakagawa *etal.*, IJSEM, 2005).

They are also capable of rTCA for carbon-fixing and sulfur-oxidation with thiosulphate, in some cases (Nakagawa *etal.*, PNAS, 2007).





**Fig. 2.** Central metabolism and solute transport in the deep-sea vent  $\epsilon$ -Proteobacteria. Pathways for which no predictable enzymes were found in strains SB155-2 and NBC37-1 genomes are shown in blue and red arrows, respectively. Numbers of transport machineries are shown for both strains. The KEGG database was used for the reconstruction of metabolic pathways. Cyt, cytochrome; H<sub>2</sub>ase, hydrogenase; Sqr, sulfide-quinone oxidoreductases; Nap, periplasmic nitrate reductase; cdNir, cytochrome *cd*, nitrite reductase; Nor, nitric oxide reductase; Nos, nitrous oxide reductase; Mdh, malate dehydrogenase; Sdh, succinate dehydrogenase.

(Nakagawa *et al.*, PNAS, 2007).

# Summary

- This new discovery was essentially made possible by having the FeMO T-RFLP database available to look for characteristic peaks along with using tools from RDP, Greengenes & Arb.
- We will now also try to track down the corresponding geochemical parameters to help us define the "multidimensional-hyperspace" these populations inhabit.