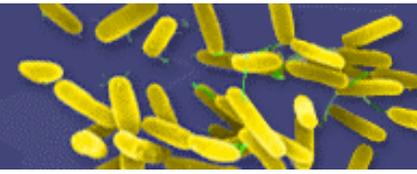


Phylogenetic and functional analysis of microbial communities

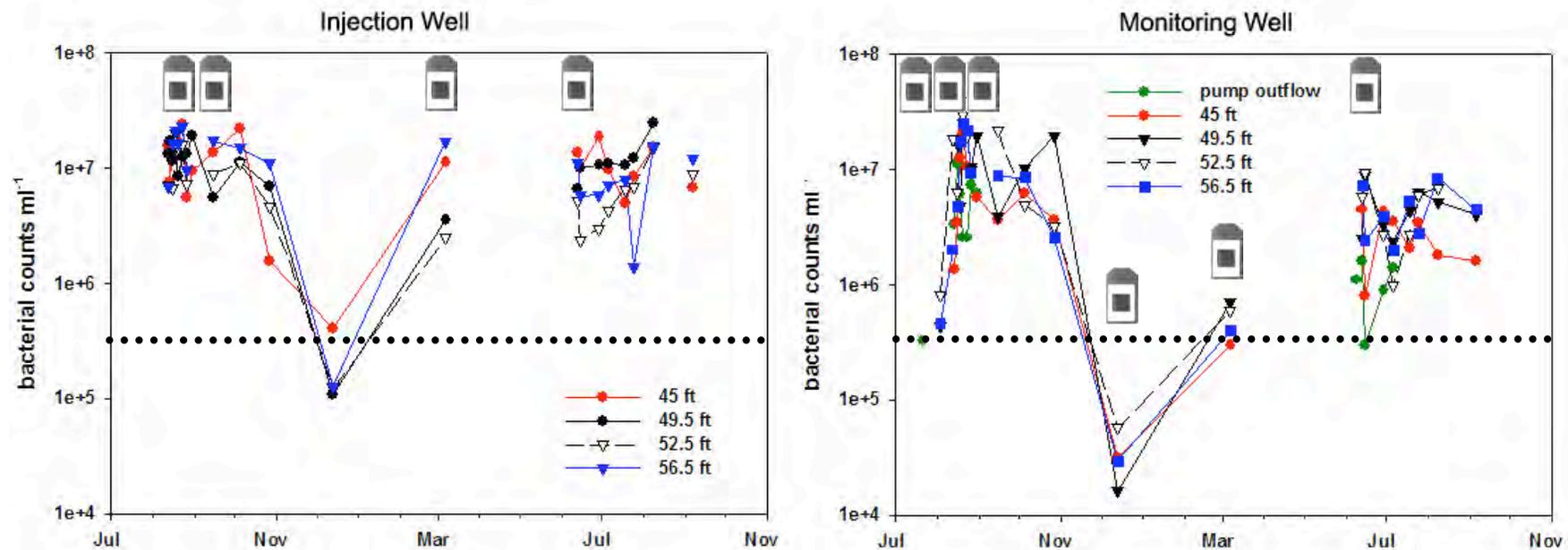
Eoin Brodie
Lawrence Berkeley National Lab
Berkeley, CA, USA
ELBrodie@lbl.gov

vimss.lbl.gov
www-esd.lbl.gov/CEB/index.html

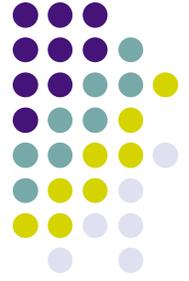
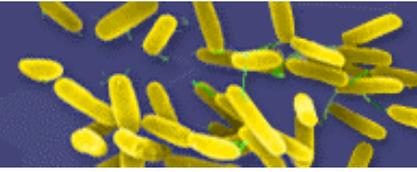
greengenes.lbl.gov
<http://www-esd.lbl.gov/ERT/hanford100h>



Bacterial biomass - Direct counts

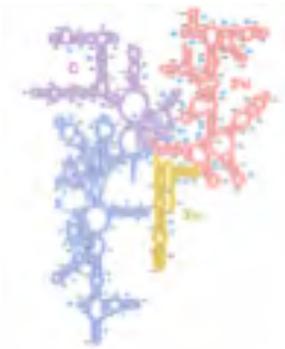


Bacterial biomass enriched rapidly by 2 orders of magnitude – remained elevated over one year later

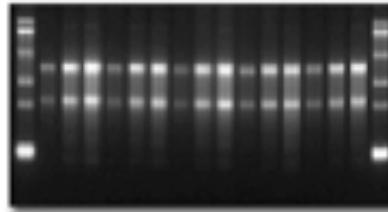


PhyloChip

- PhyloChip – 500,000 probes (300k target 16S)



16S rRNA gene used as biomarker due to large database and availability of “universal” primers.



16S rRNA gene is amplified from genomic extract or 16S rRNA molecules are used directly



Amplicon pool fragmented, biotin labeled



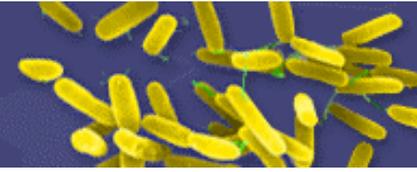
Biotin labeled 16S hybridizes to its complement sequence on the array surface.



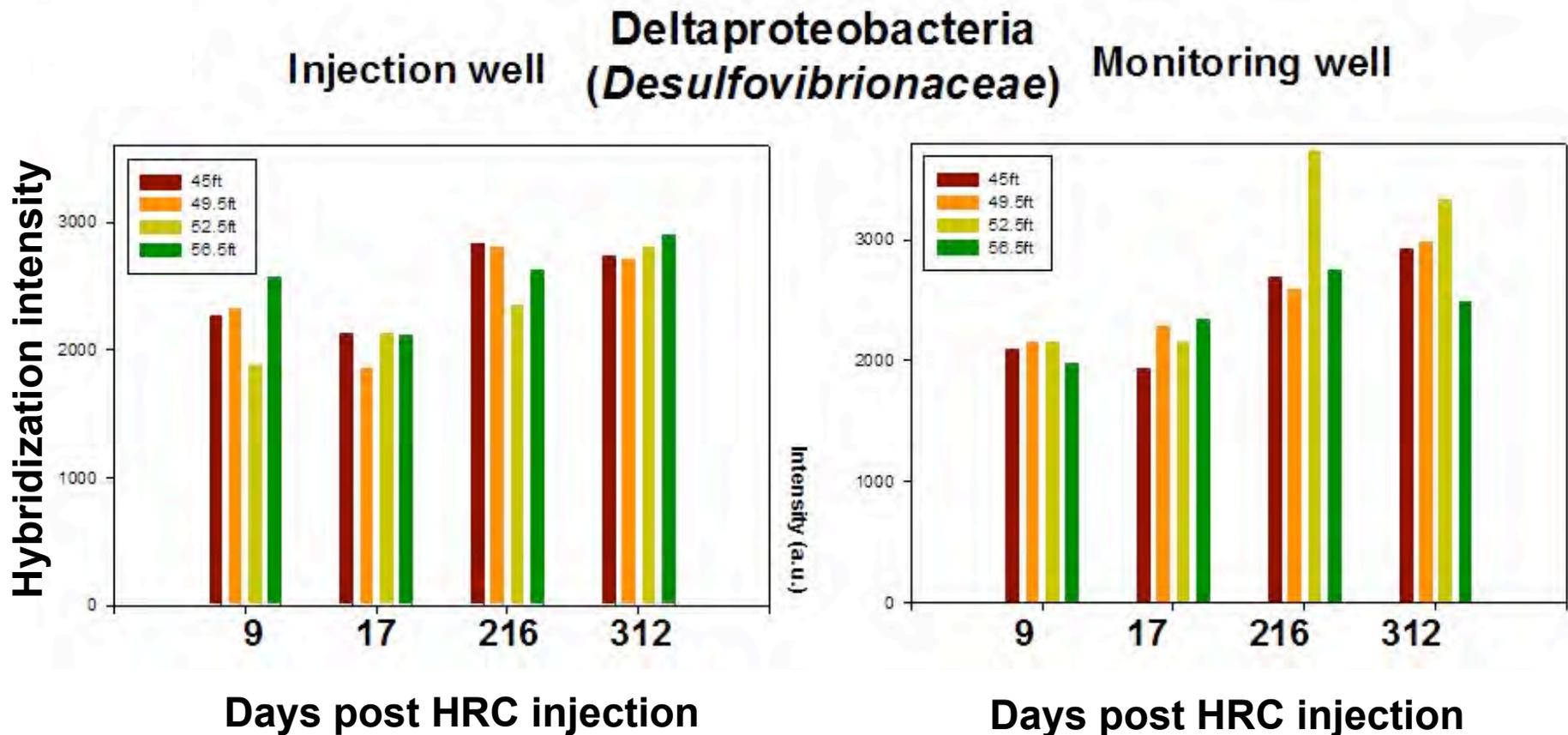
PhyloChip stained and washed using automatic fluidics station



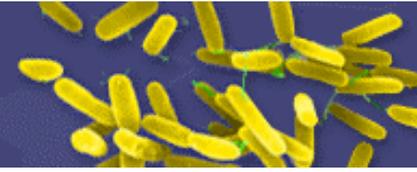
PhyloChip is scanned, fluorescence data analyzed and probe sets with >90% probes positive are considered present



Functional groups – Sulfate reduction



H₂S can abiotically reduce Cr(VI) to Cr(III)

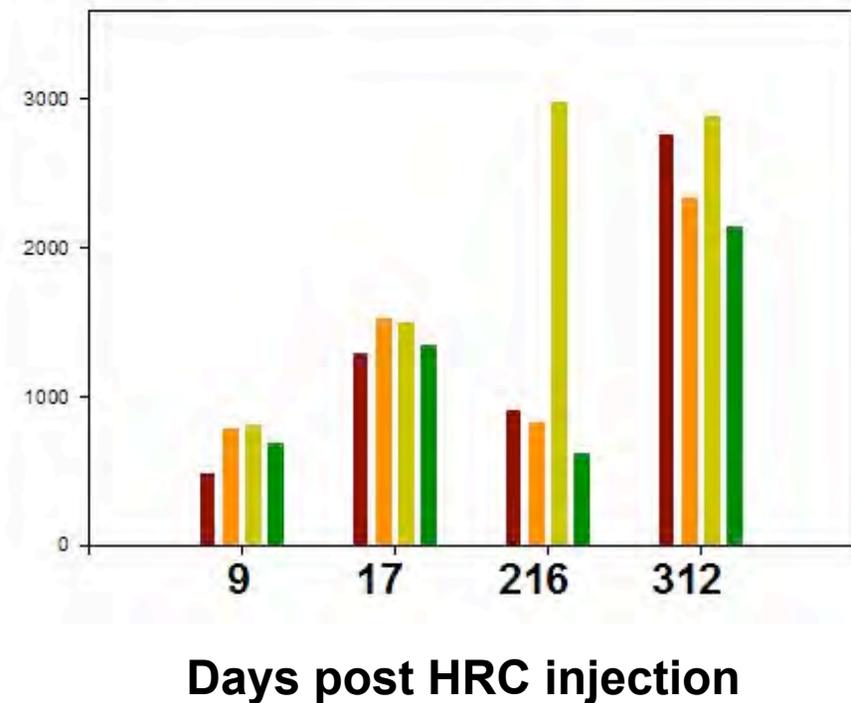
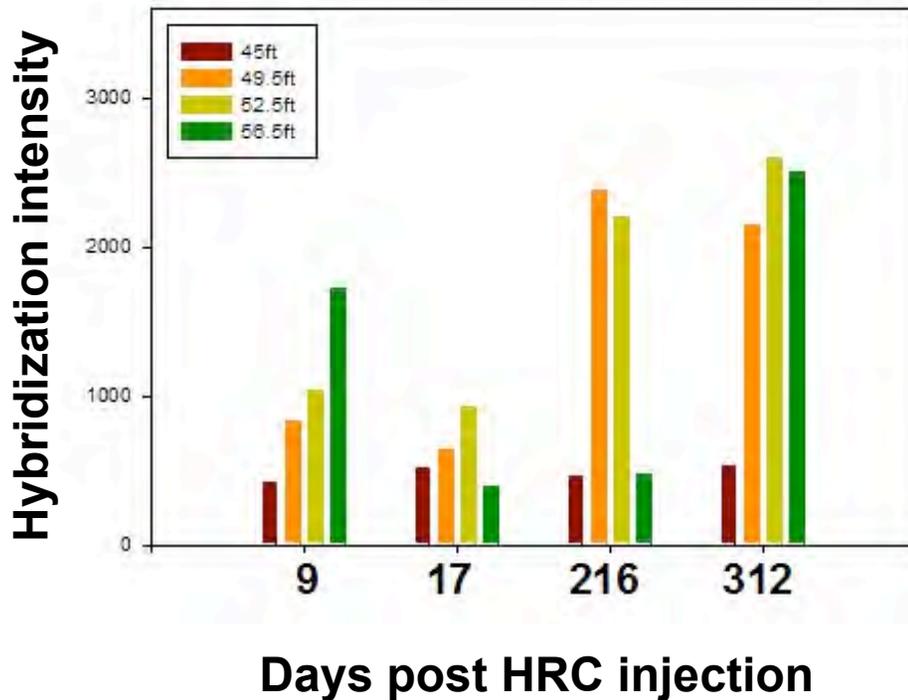


Functional groups – Methanogenesis

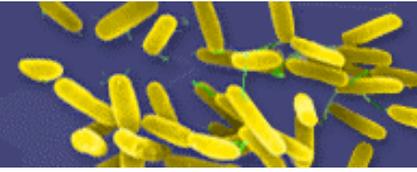
Euryarchaeota (Methanogens)

Injection well

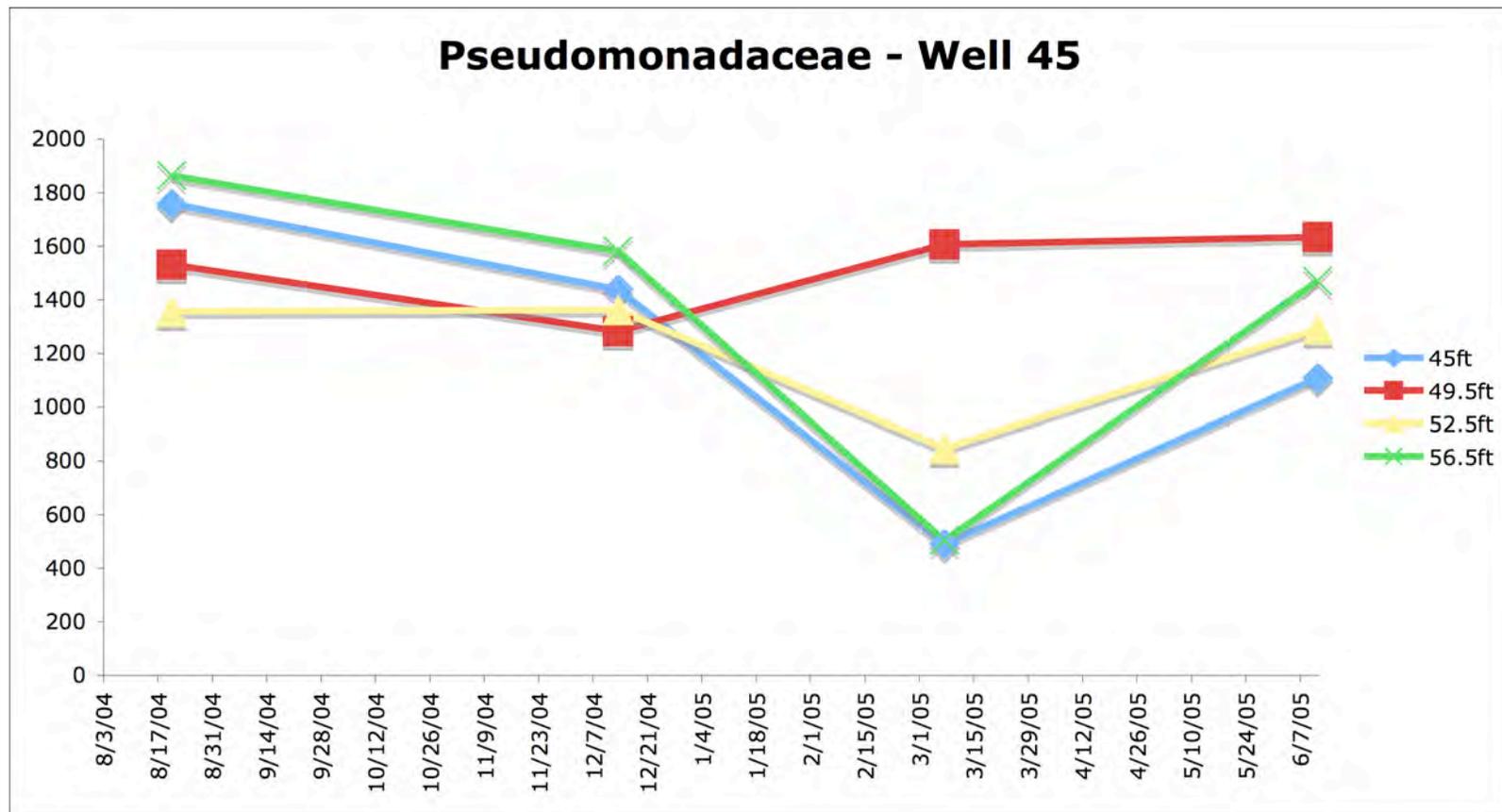
Monitoring well



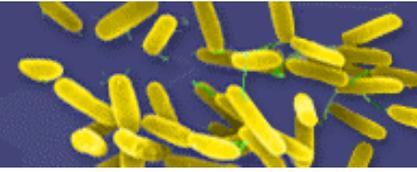
Presence of methanogens indicates strongly reducing conditions



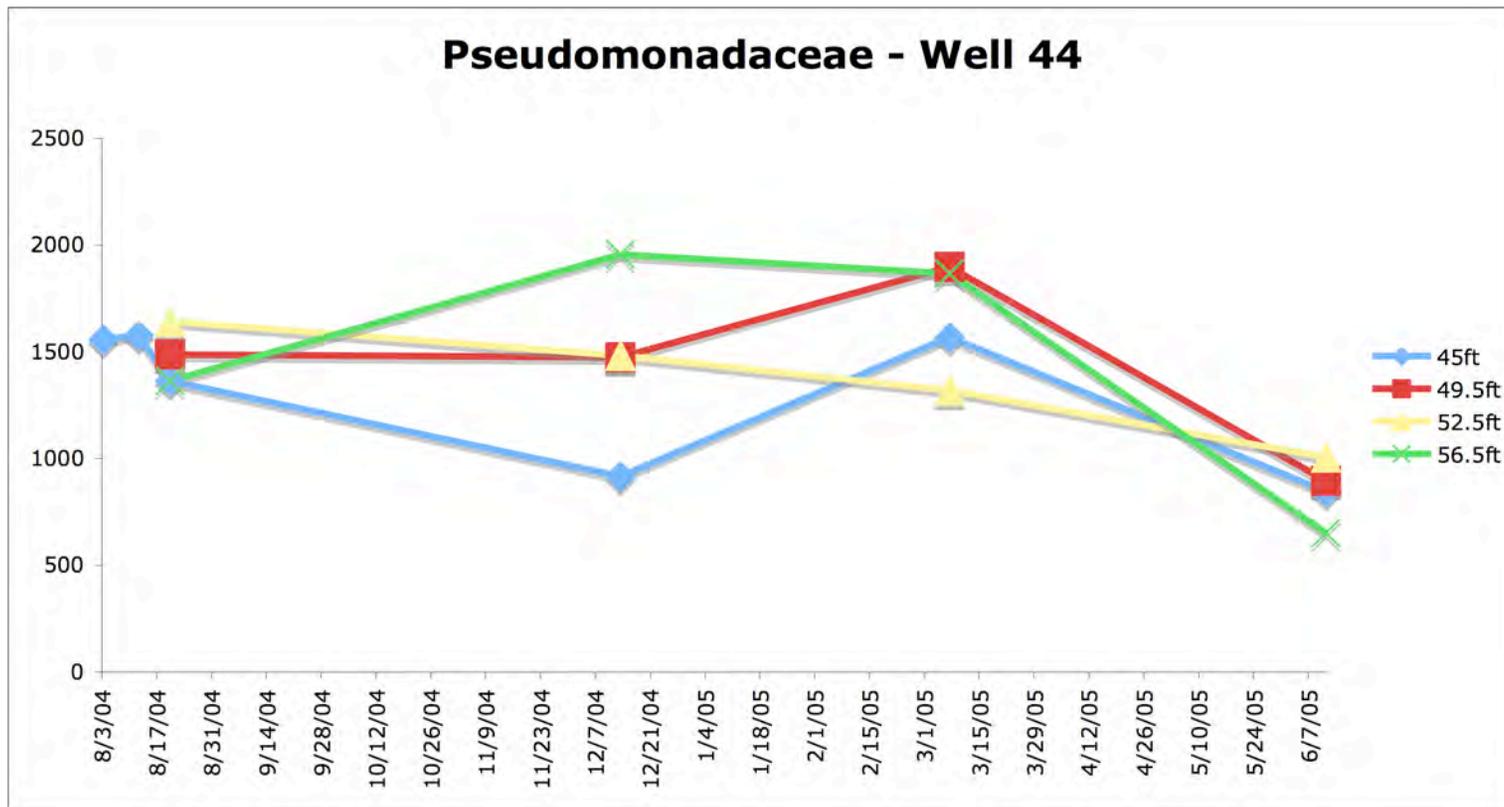
Functional groups – Nitrate & Cr(VI)



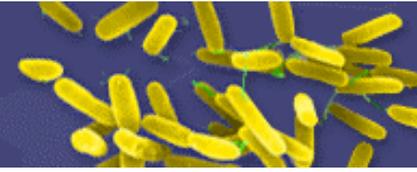
Enrichment of *Pseudomonas* species capable of nitrate and Cr(VI) reduction



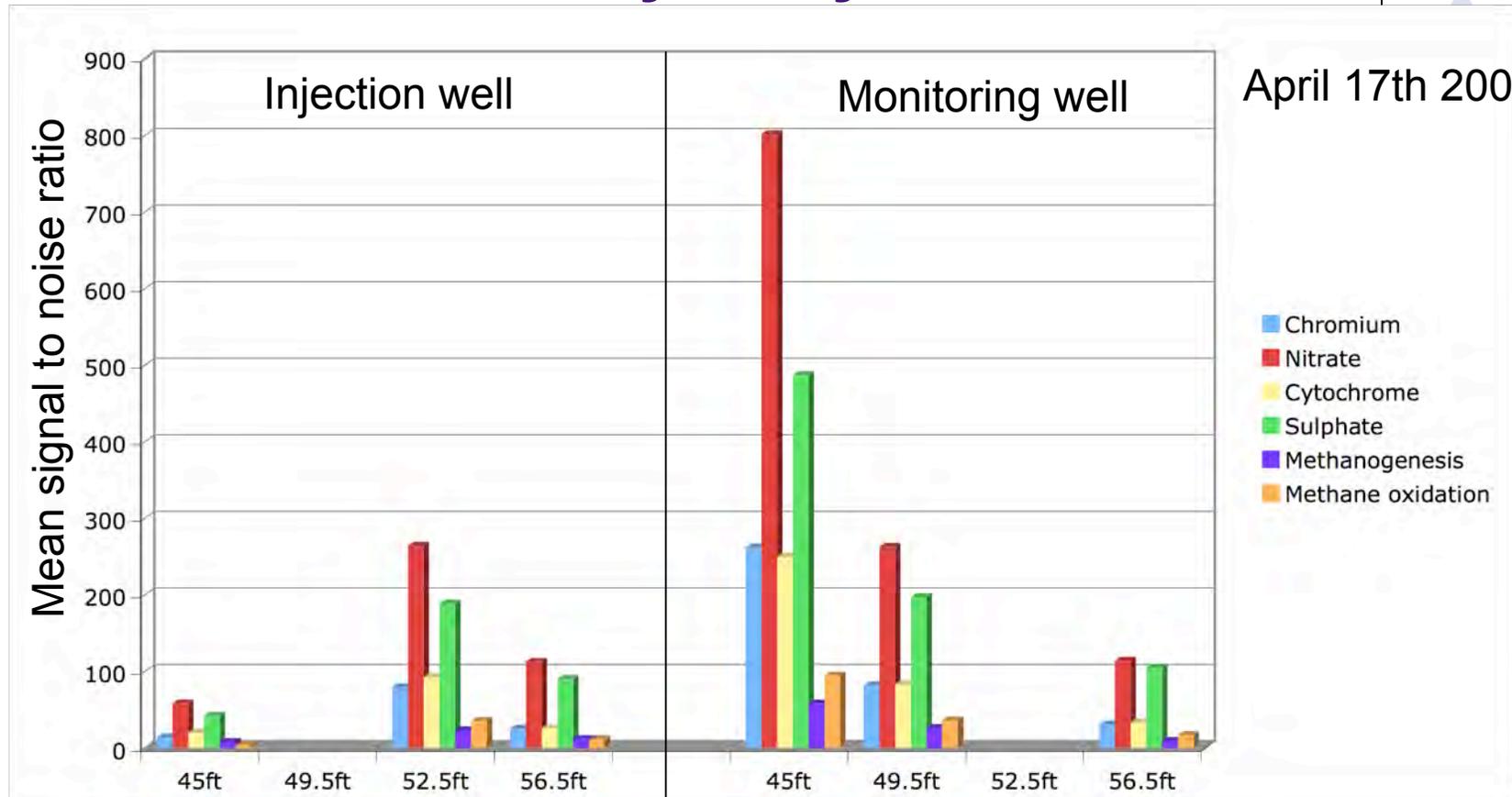
Functional groups – Nitrate & Cr(VI)



Enrichment of *Pseudomonas* species capable of nitrate and Cr(VI) reduction



Functional microarray analysis



Nitrate, Sulfate, Iron reduction. Methanogenesis, Methane oxidation, Sulfur oxidation.
Many chromium tolerance/reduction genes, including a *Pseudomonas* chromate reductase.