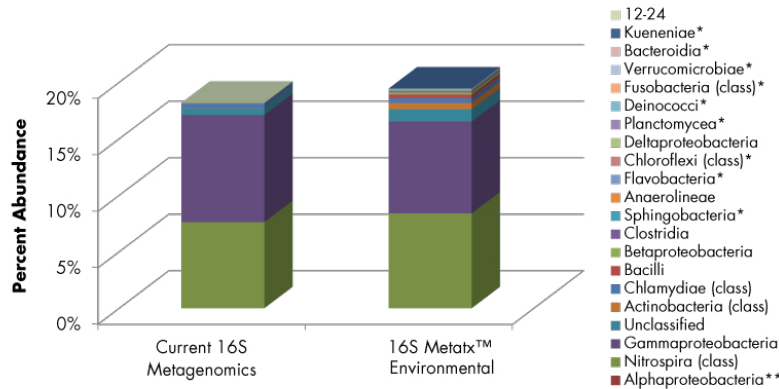


# Case Study: GENEWIZ 16S MetaVx Metagenomics Sequencing vs Traditional 16S V4 Sequencing Approaches

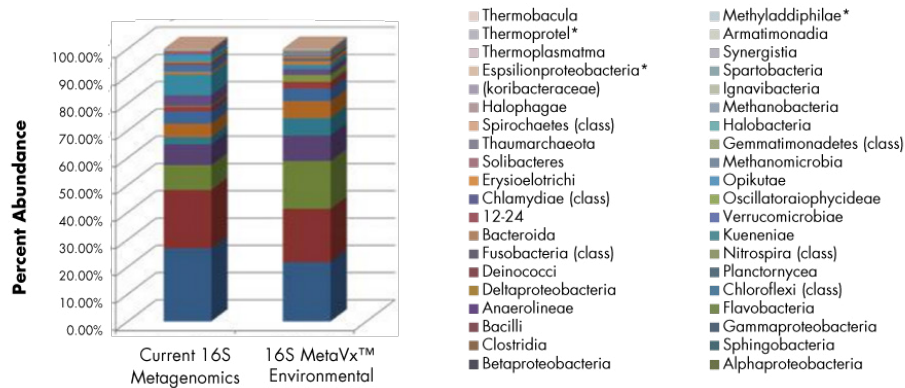
A comparison of 16S MetaVx™ Environmental and a commonly used technique for next generation 16S rRNA amplicon sequencing of the V4 region was performed using the same sample. Both samples were sequenced in the same sequencing run to ensure identical experimental conditions. The data was normalized to an average of 1M reads/sample after sequencing.

## Current 16S Metagenomics vs. 16S MetaVx™ Environmental Experiment #1



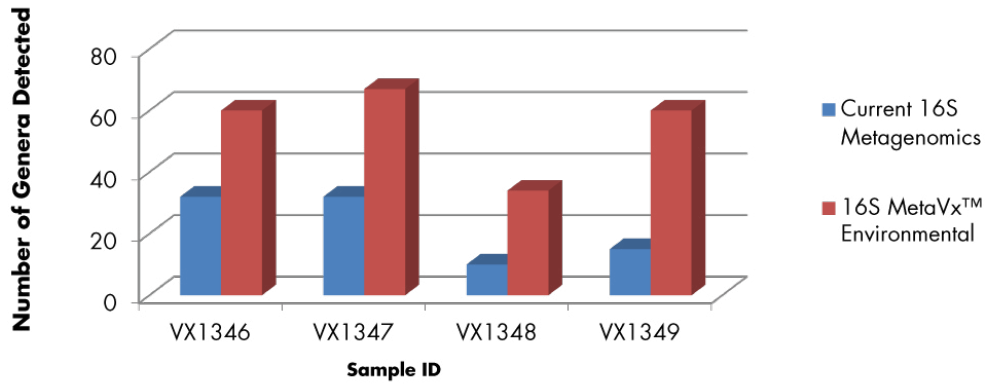
**Figure 6.** One experimental sample was assayed using current 16S metagenomics and 16S MetaVx™. 16S MetaVx™ detected 19 classes of bacteria, while current 16S metagenomics detected 11 classes. \*Detected by 16S MetaVx™ but not by current 16S metagenomics. \*\*The bacterial class with the highest abundance (detected at ~80% of sample with both techniques) was removed for clarity.

## Current 16S Metagenomics vs. 16S MetaVx™ Environmental Experiment #2



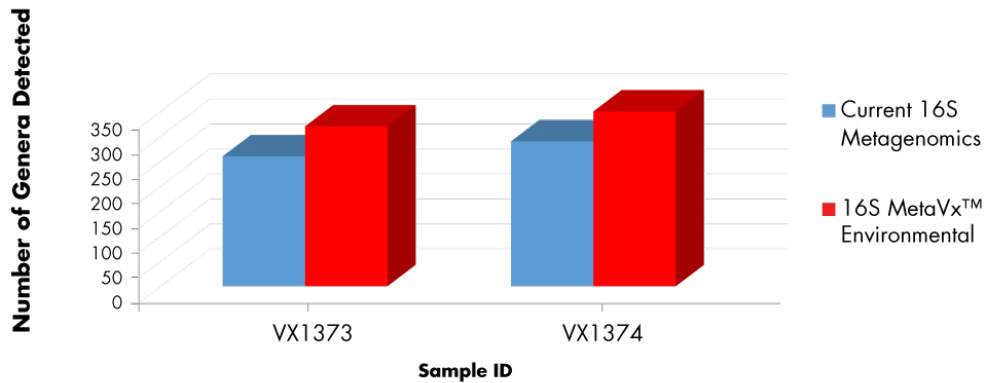
**Figure 7.** One Experimental sample was assayed using current 16S metagenomics and 16S MetaVx™ Environmental. A key element of this comparison was that 16S MetaVx™ Environmental detected 6 archeal classes, while current 16S metagenomics detected 4 classes. \*Detected by 16S MetaVx™ Environmental but not by current 16S metagenomics

### Current 16S Metagenomics vs. 16S MetaVx™ Environmental Comparison #1



**Figure 8.** Across all 4 samples assayed here, 16S MetaVx™ detected up to 4-fold more genera than current 16S metagenomics.

### Current 16S Metagenomics vs. 16S MetaVx™ Environmental Comparison #2



**Figure 9.** Across Both Samples assayed here, 16S MetaVx™ Environmental detected more genera than current 16S metagenomics.