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Correction to: Microbial colonization and persistence in deep fractured shales is guided by metabolic exchanges and viral predation

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Following the publication of the original article [1], the author reported that Figs. 2 and 5 contains extra images at the topmost right that should have not been a part of these figures.

The original article has been updated.

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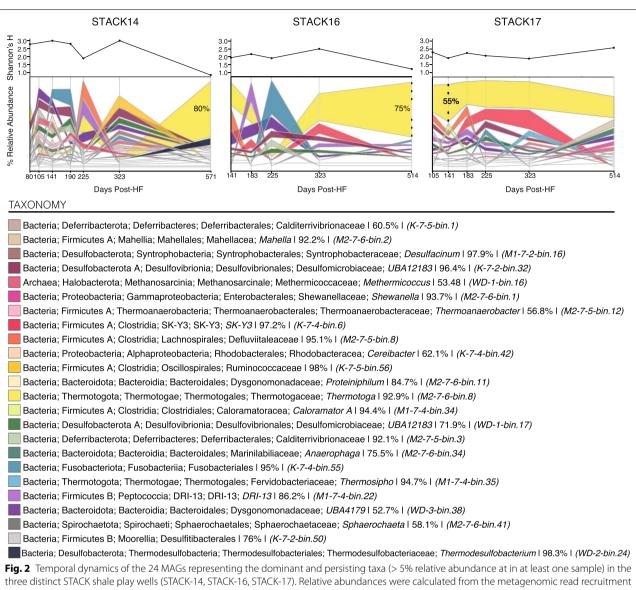
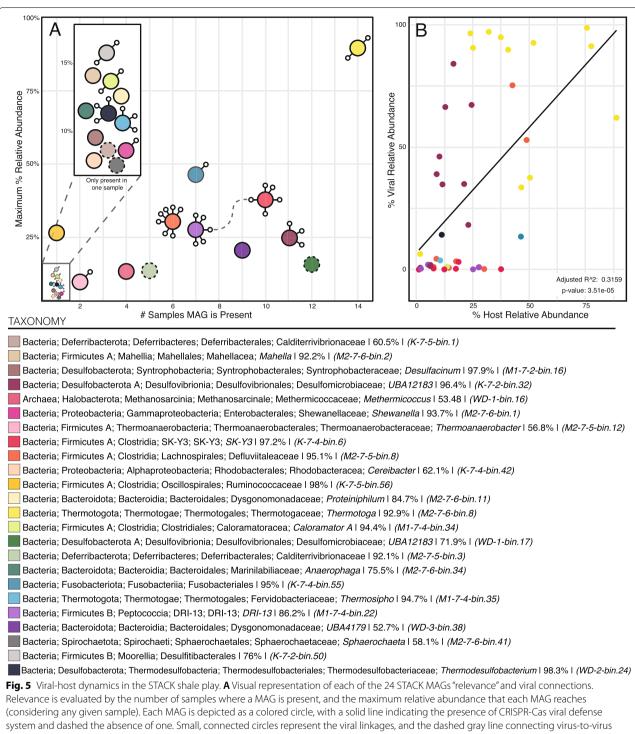


Fig. 2 Temporal dynamics of the 24 MAGs representing the dominant and persisting taxa (> 5% relative abundance at in at least one sample) in the three distinct STACK shale play wells (STACK-14, STACK-16, STACK-17). Relative abundances were calculated from the metagenomic read recruitment to MAGs as described in the methods. The relative abundance of each MAG is indicated by the width of its respective band in the alluvial plot at each timepoint, with the most abundant MAG on top and least abundant on the bottom and colored by respective taxonomy. Completeness estimates for each MAGs are listed following MAG taxonomy, and unique identifiers for each MAG are listed in parentheses. Trends in alpha diversity through time are shown above each plot for each well

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indicates an identical spacer sequence (but likely not an identical virus). B Evaluation of viral and host dynamics where linkages could be made. Relative abundances of hosts and the summed relative abundance of their linked viruses are plotted for each timepoint that the host is present, revealing that the most abundant viruses are associated with the most abundant microbial hosts