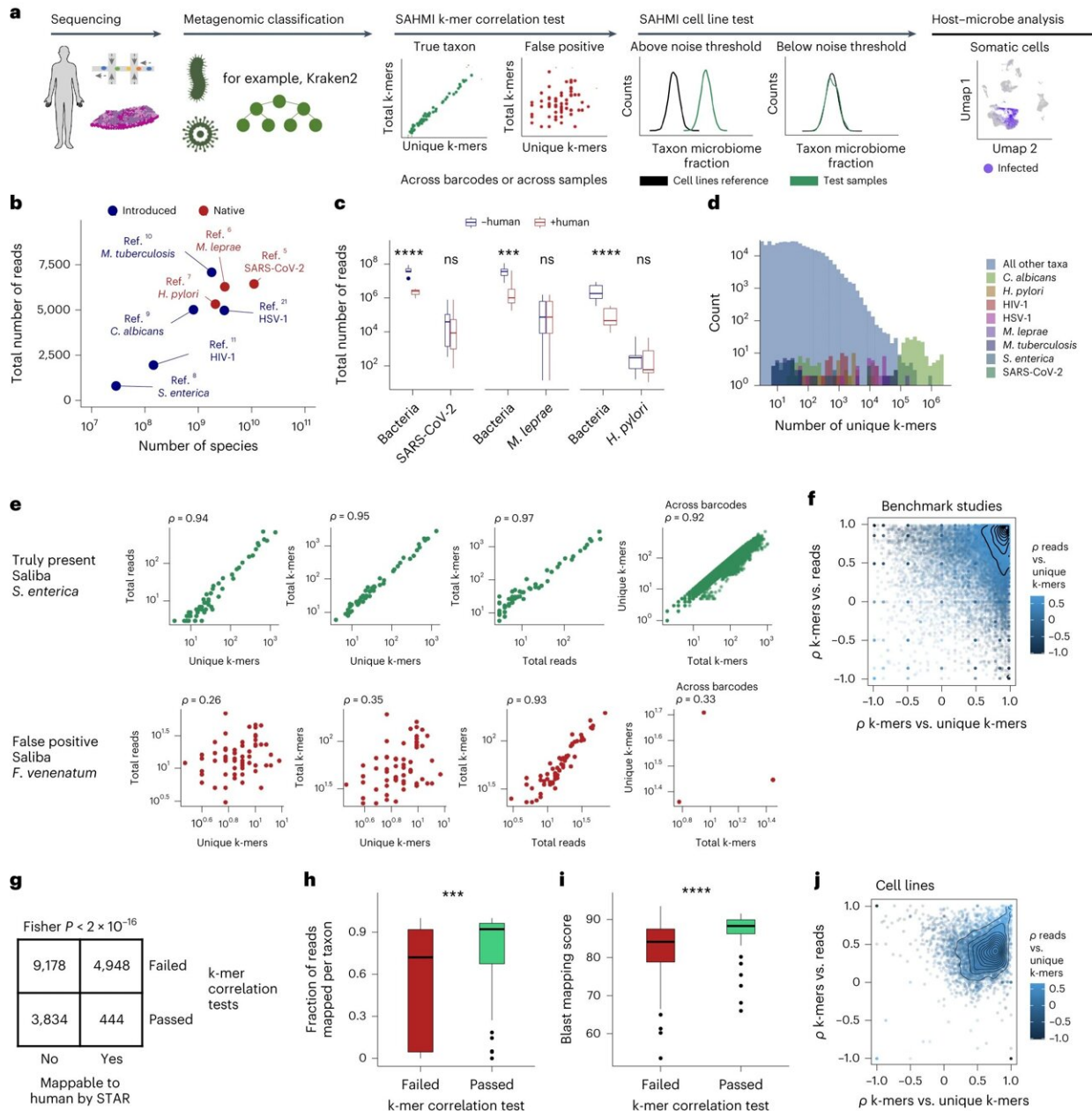


New analytical tool improves genetic analysis and research accuracy

October 9 2023, by Andrew Smith



a, Schematic of the SAHMI pipeline. SAHMI identifies taxa that are truly present in tissues using a k-mer correlation test and identifies false positives and contaminants by comparing taxa distributions to an extensive negative control reference. **b**, Scatter plot showing the total number of sequencing reads and species detected in each study. Blue, experimentally introduced pathogen; red, natural infection involving a human tissue. See Methods for definitions of the microorganisms/viruses. **c**, Box plots showing significantly increased reads assigned to bacteria when the human genome is not included as a reference during taxonomic classification. Box plots show the median (line), 25th and 75th percentiles (box) and 1.5× interquartile range (whiskers); the black dot is an outlier. Two-sided t-tests; *****P*

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