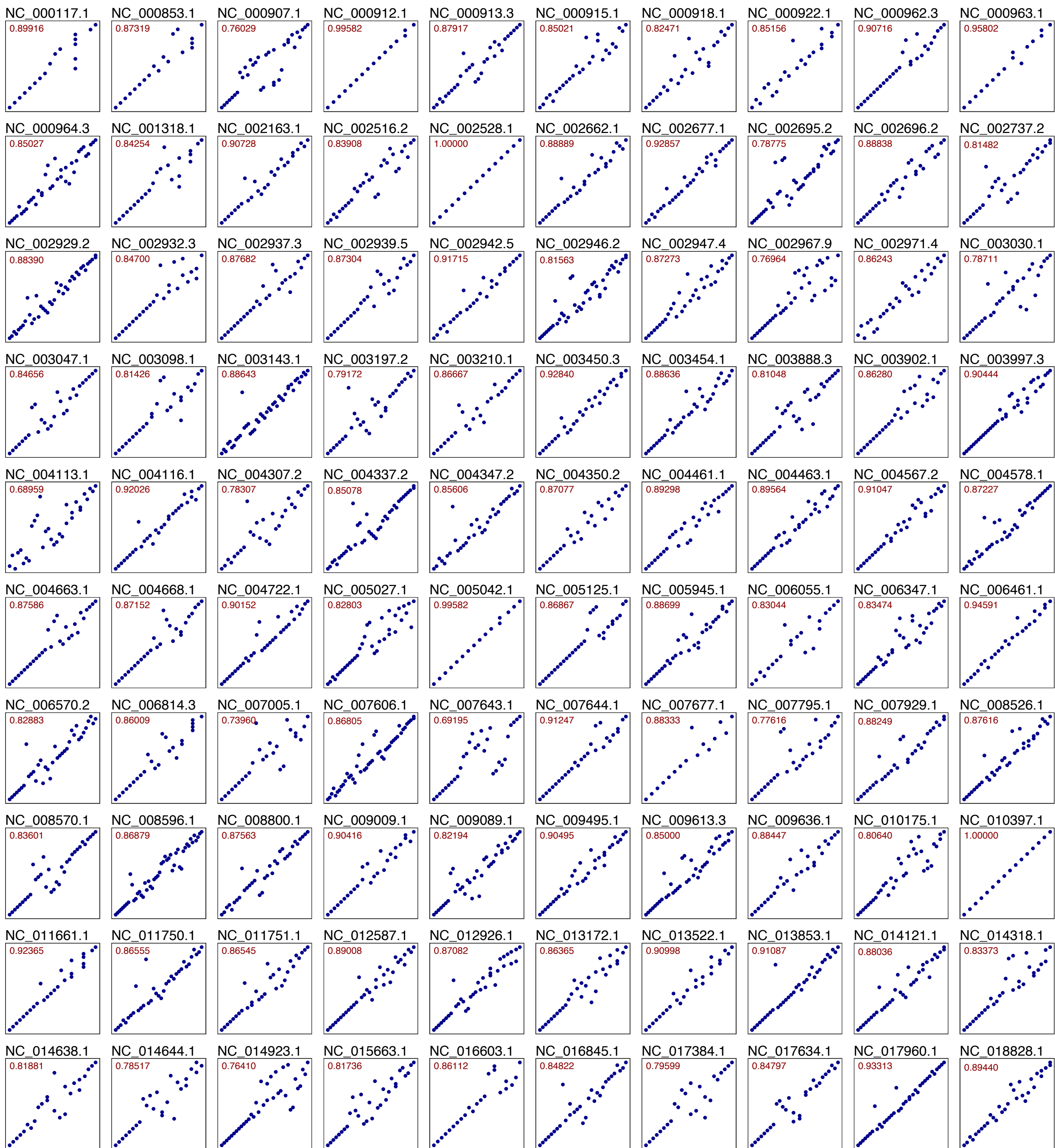


# Per-genome ALE score rank vs identity rank

ALE score rank



identity rank

**Figure S8:** ALE score vs identity rank correlations for each of the 100 simulated-read genomes. Each plot contains all unique assembly sequences available for that genome. ALE scores were produced by ALE using short-read alignments to the assembly. Identity was determined using global alignment of the assembly to the original reference sequence. The number in each plot is the Kendall rank correlation coefficient (tau). Of all predictors of assembly quality tested, ALE score had the highest mean tau value (Table S3).