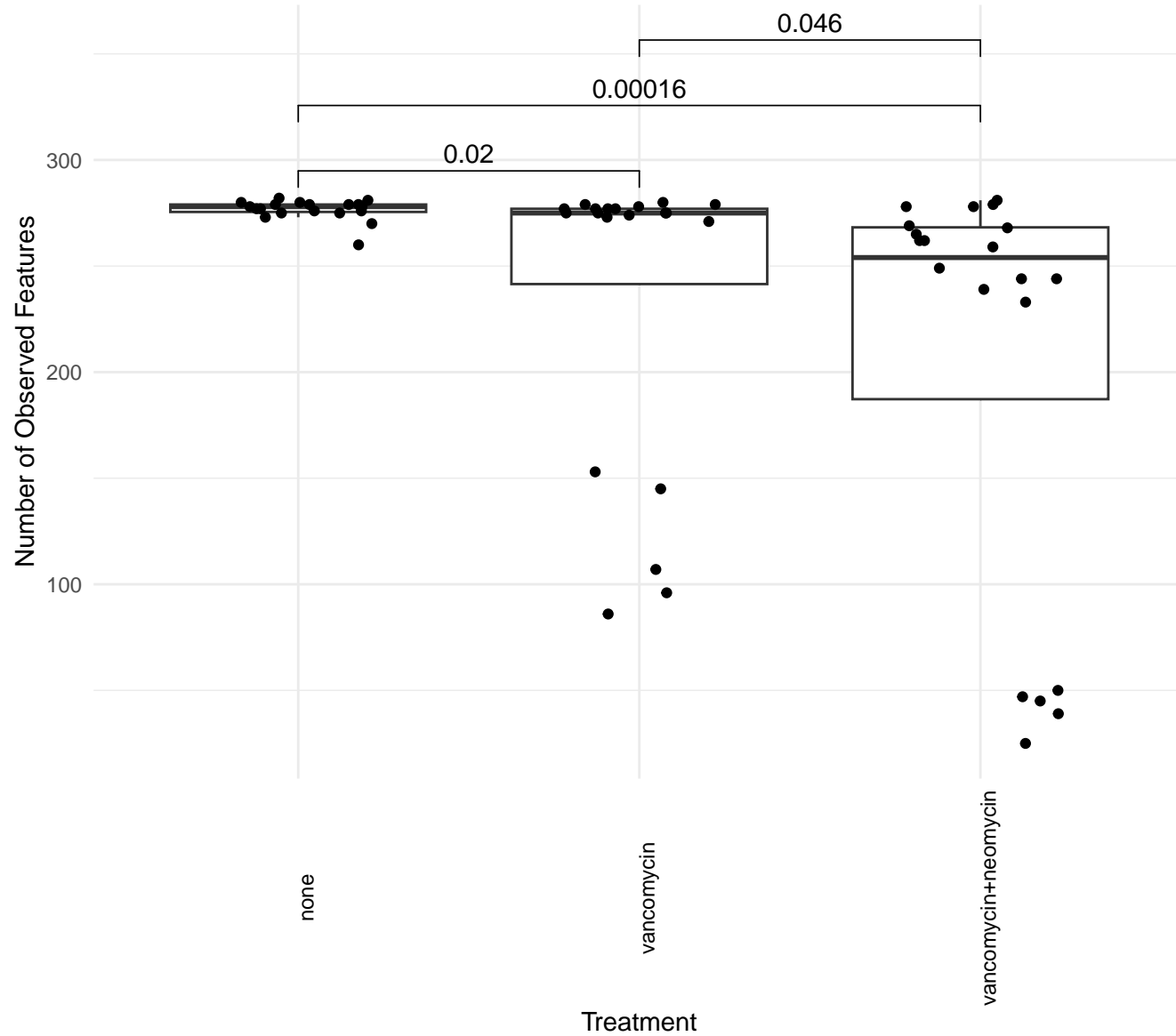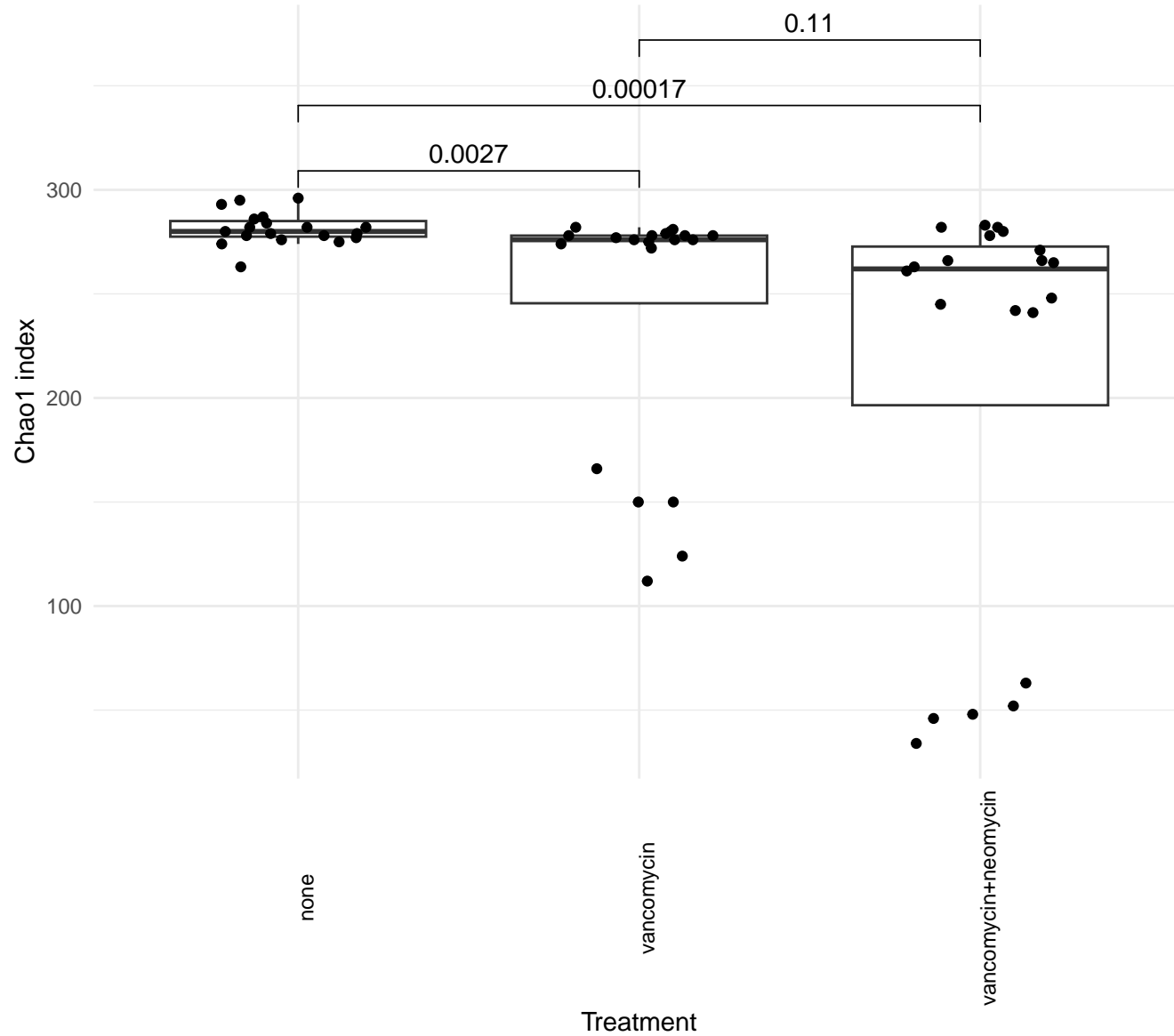Alpha Diversity Plot | k__Bacteria
Feature must be >50PPM in at least 5% of samples
Taxonomy information must come from >70% contigs in at least 50% of samples
Taxon genome completeness must be >5% in at least 5% of samples
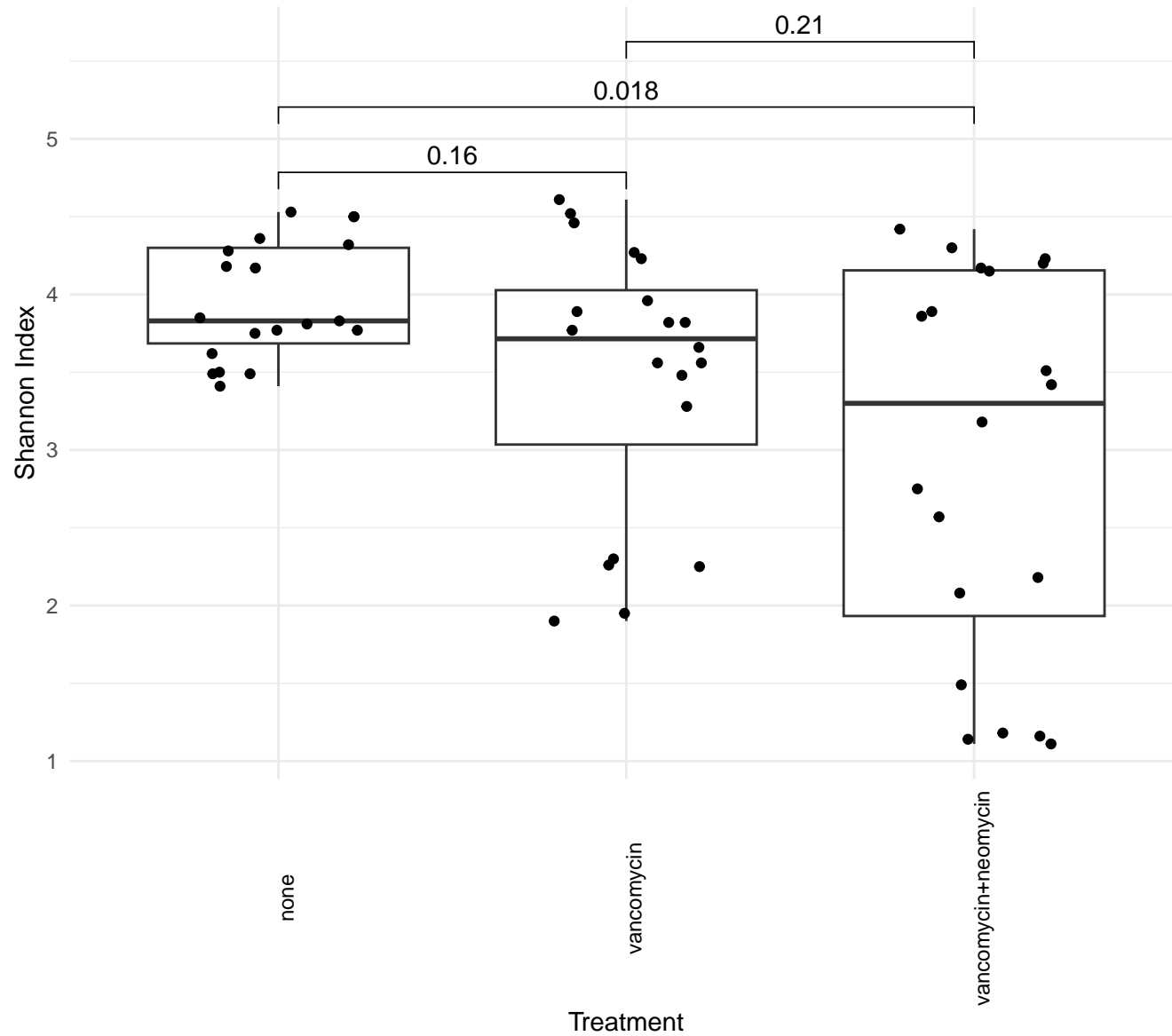Number of Observed Features

Alpha Diversity Plot | k__Bacteria
Feature must be >50PPM in at least 5% of samples
Taxonomy information must come from >70% contigs in at least 50% of samples
Taxon genome completeness must be >5% in at least 5% of samples
Chao1 index

Alpha Diversity Plot | k__Bacteria
Feature must be >50PPM in at least 5% of samples
Taxonomy information must come from >70% contigs in at least 50% of samples
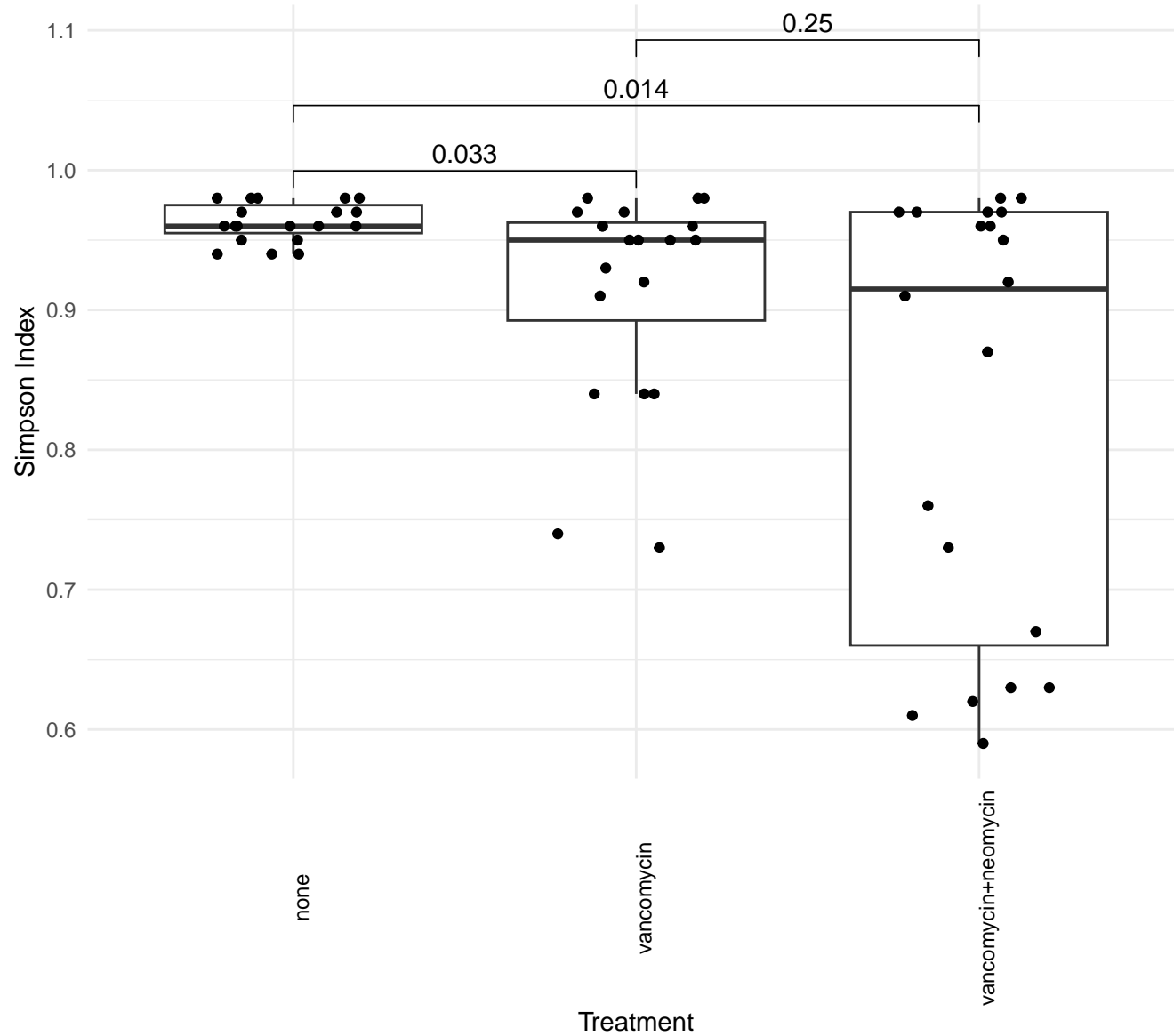Taxon genome completeness must be >5% in at least 5% of samples
Shannon Index

Alpha Diversity Plot | k__Bacteria
Feature must be >50PPM in at least 5% of samples
Taxonomy information must come from >70% contigs in at least 50% of samples
Taxon genome completeness must be >5% in at least 5% of samples
Simpson Index

Alpha Diversity Plot | k__Bacteria
Feature must be >50PPM in at least 5% of samples
Taxonomy information must come from >70% contigs in at least 50% of samples
Taxon genome completeness must be >5% in at least 5% of samples
Inverse Simpson Index