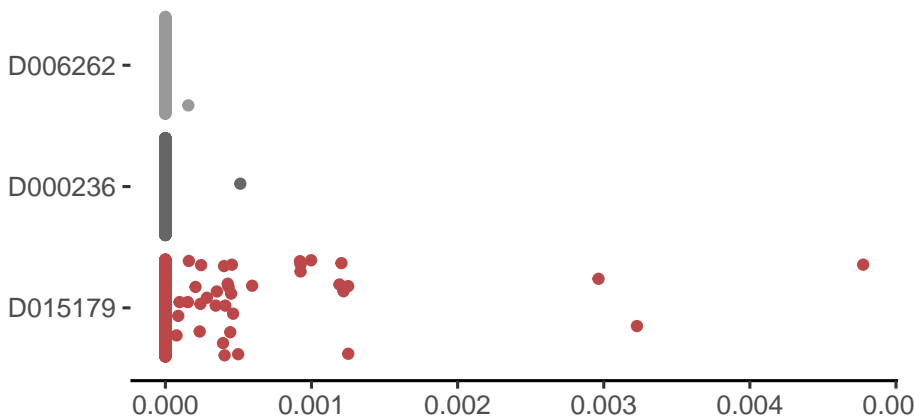
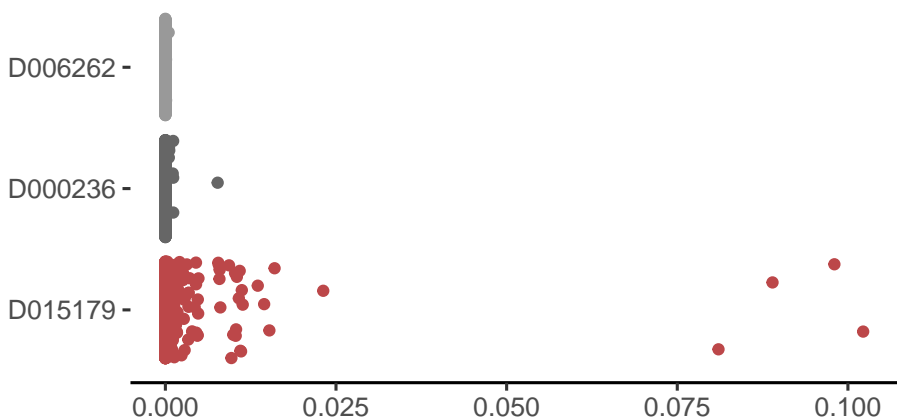


factor(associated.phenotype, level = c("D015179", "D000236", ...

s\_\_Fusobacterium nucleatum



s\_\_Parvimonas micra



s\_\_Peptostreptococcus stomatis

