Figure S6  Growth rate distributions of strains containing native or non-native mt-n genome pairs, separated by isolation habitat. Each box indicates the 25th percentile (lower edge), median (solid line), 75th percentile (upper edge) and 90th percentile (whisker). Note the that fitness scale on the y axis is not the same for each plot. Significant differences between native and non-native mt-n genome combinations, as determined by ANOVAs are indicated. ***<0.001, **<0.01  (A) CSM  (B) EG (C) 37°C