Figure S3 Growth rate distributions in CSM media (n=4) of ten S. cerevisiae strains (white boxes) compared to strains where the mt-n genome combinations were recreated (light gray boxes) or cured of prions (dark gray boxes). Box plots show the 25th percentile (lower edge), median (solid line), 75th percentile (upper edge), and 90th percentile (whisker). Outliers are shown as empty circles.