



Figure S2. Diagnostic plots of simple linear regression models for T_d and T_{G1} values of yeast (A-D), and human (E-H) cells. The log-transformed T_d and T_{G1} values shown in Tables S1 and S2 were used to build simple linear regression models. **A, E.** Plot of residuals (y-axis) against fitted values (x-axis). Numbered data points indicate problematic outliers. **B, F.** Normal Q-Q plot of the ordered standardized residuals (y-axis), against the expected order statistics from a standard normal distribution (x-axis). Points away from the straight dashed line indicate departures from normality. **C, G.** Scale-Location plot of the square root of the absolute residuals (y-axis) against fitted values (x-axis), in order to diminish skewness. **D, H.** Plot of residuals (y-axis) against leverages (x-axis). The residual-leverage plot shows contours (shown with dashed red lines) of equal Cook's distance (by default 0.5 and 1). Plots in **B, C, D, F, G, H** use standardized residuals which have identical variance (under the hypothesis of normality). The solid red lines in **A, C, D, E, G, H** indicate the locally weighted scatterplot smoothing.