Figure S6 Relationship between base substitution mutation rate per effective genome size per generation and effective population size (N_E) in five multicellular eukaryotes (red), seven unicellular eukaryotes (black), and eight prokaryotes (blue; *B. cenocepacia* – green) (Sung *et al.* 2012). The log-linear regression is highly significant (r^2=0.85, p<0.0001, df=19).