Supplementary Table 2. Tests for extreme branch lengths inferred from promoters of the membrane protein group.

species	branch length, membrane group[a]	branch length, genome[b]	p^c
S. paradoxus	0.077	0.082 (.0026)	0.020
S. cerevisiae	0.129	0.131 (.0034)	0.236
S. mikatae	0.194	0.192 (.0038)	0.753
S. kudriavzevii	0.176	0.180 (.0038)	0.196
S. bayanus	0.276	0.257 (.0054)	0.999

[a] Evolutionary rate, in substitutions per site, for the terminal branch in the *Saccharomyces* phylogeny leading to the indicated species, inferred from the concatenated promoters of the membrane protein regulon and normalized with respect to total tree length.

[b] Evolutionary rate, in substitutions per site, for the terminal branch in the *Saccharomyces* phylogeny leading to the indicated species normalized with respect to total tree length, as an average of inferences from the concatenated promoters of each of 10,000 randomly chosen gene groups. The standard deviation is given in parentheses.

[c] Significance of a one-sided resampling test relative to the genomic null for short length of the terminal branch to the indicated species.