FIG. 6.—Model predictions and observed codon usage frequencies as a function of estimated protein synthesis rate $\Phi$ for the S. cerevisiae S288c genome. The units for $\Phi$ are proteins/t and time $t$ is scaled such that the prior for $\Phi$ satisfies $E(\Phi) = 1$. Each amino acid is represented by a separate subplot. Solid, dashed, and dotted lines represent the without $\Phi$, with $\Phi$ ROC SEMPPR model fits, and a simple logistic regression approach where the estimation.