

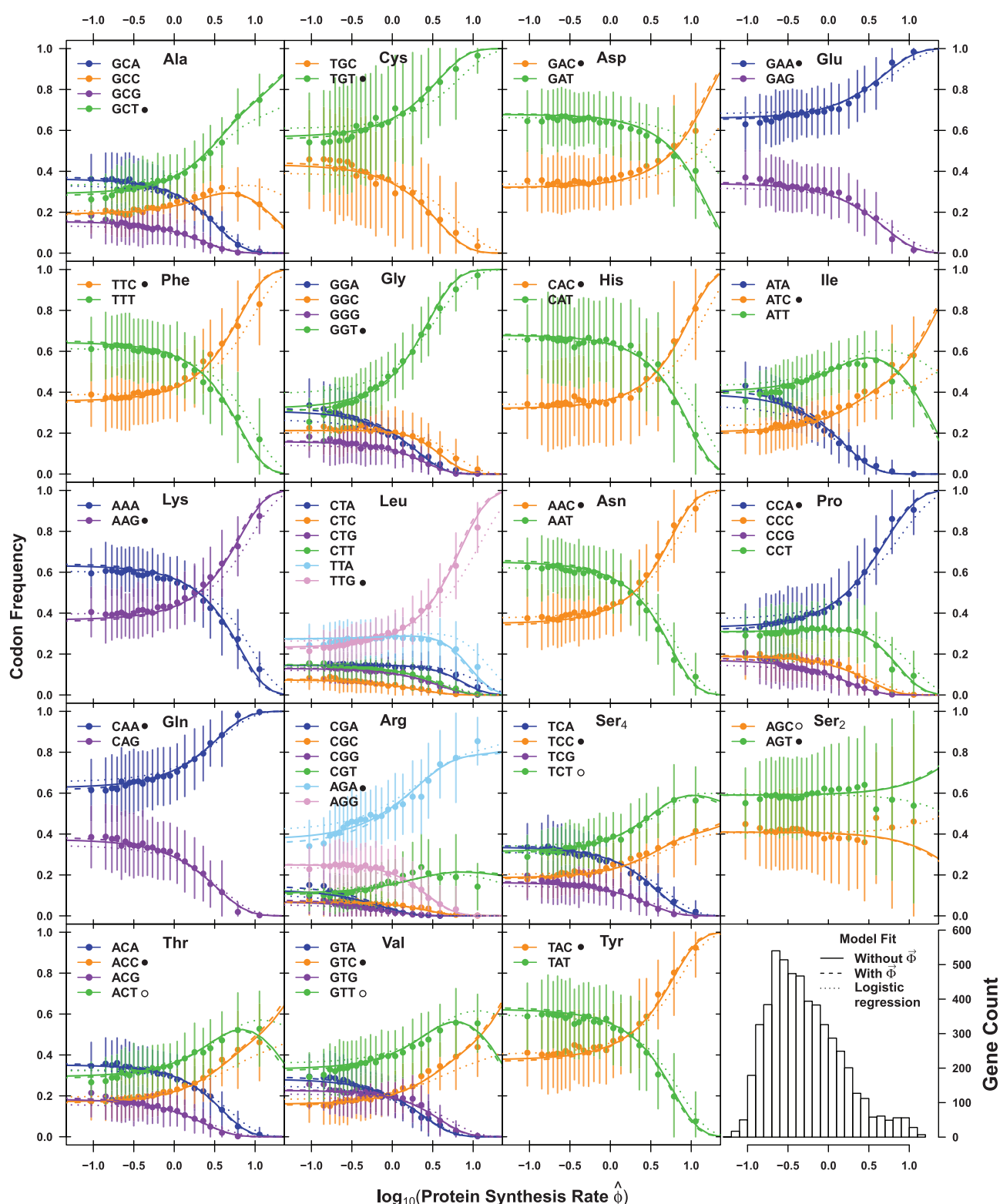


Fig. 6.—Model predictions and observed codon usage frequencies as a function of estimated protein synthesis rate Φ for the *S. cerevisiae* S288c genome. The units for Φ are proteins/ t and time t is scaled such that the prior for Φ satisfies $E(\Phi) = 1$. Each amino acid is represented by a separate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

(continued)