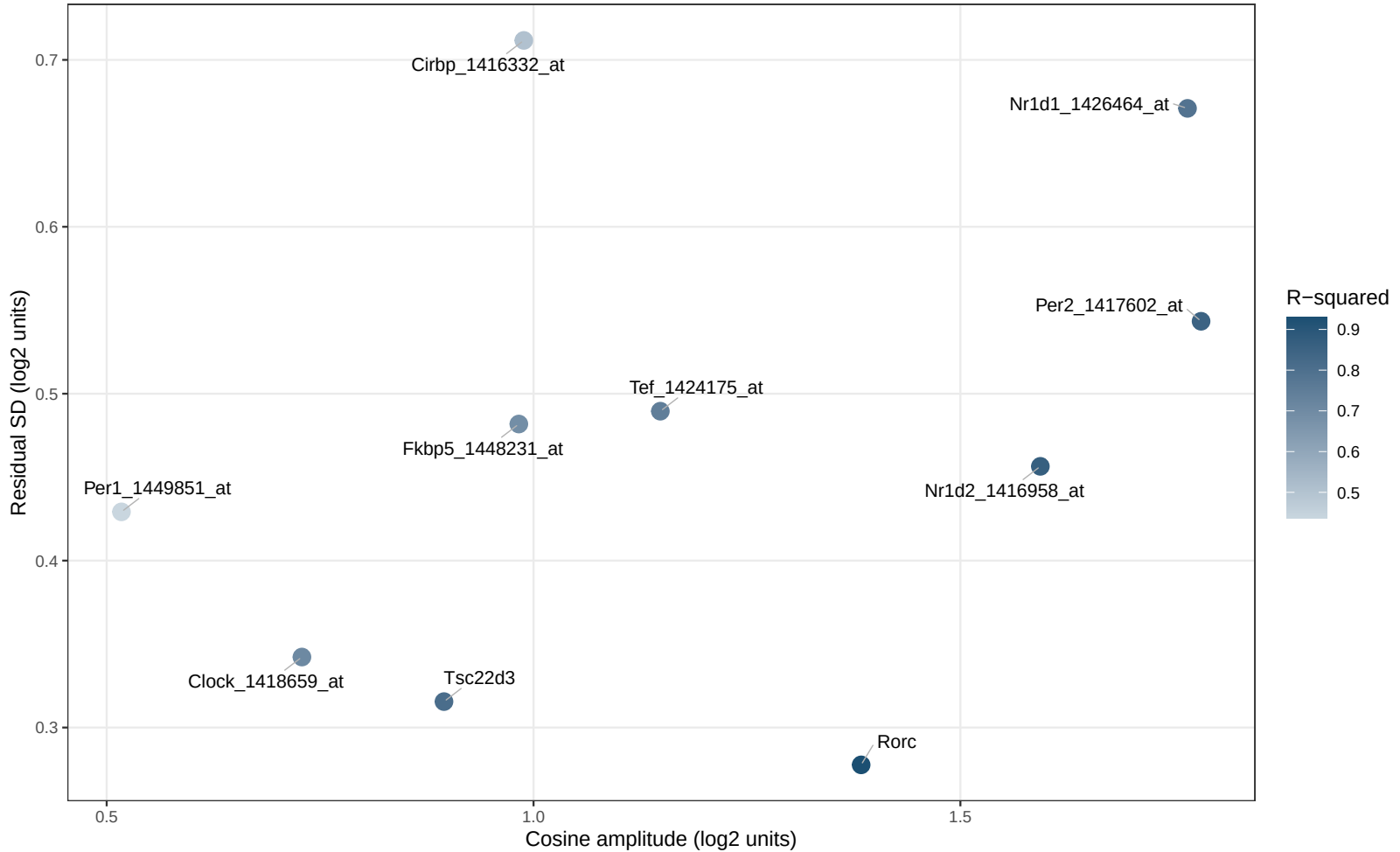
Larger amplitude does not guarantee a better cosine fit

Spearman rho(amplitude, residual SD) = 0.45 across 10 genes



Residual SD: standard deviation of the 24 h cosine residuals over 48 time points (df = 45);
R−squared: fraction of variance explained by the 24 h cosine.