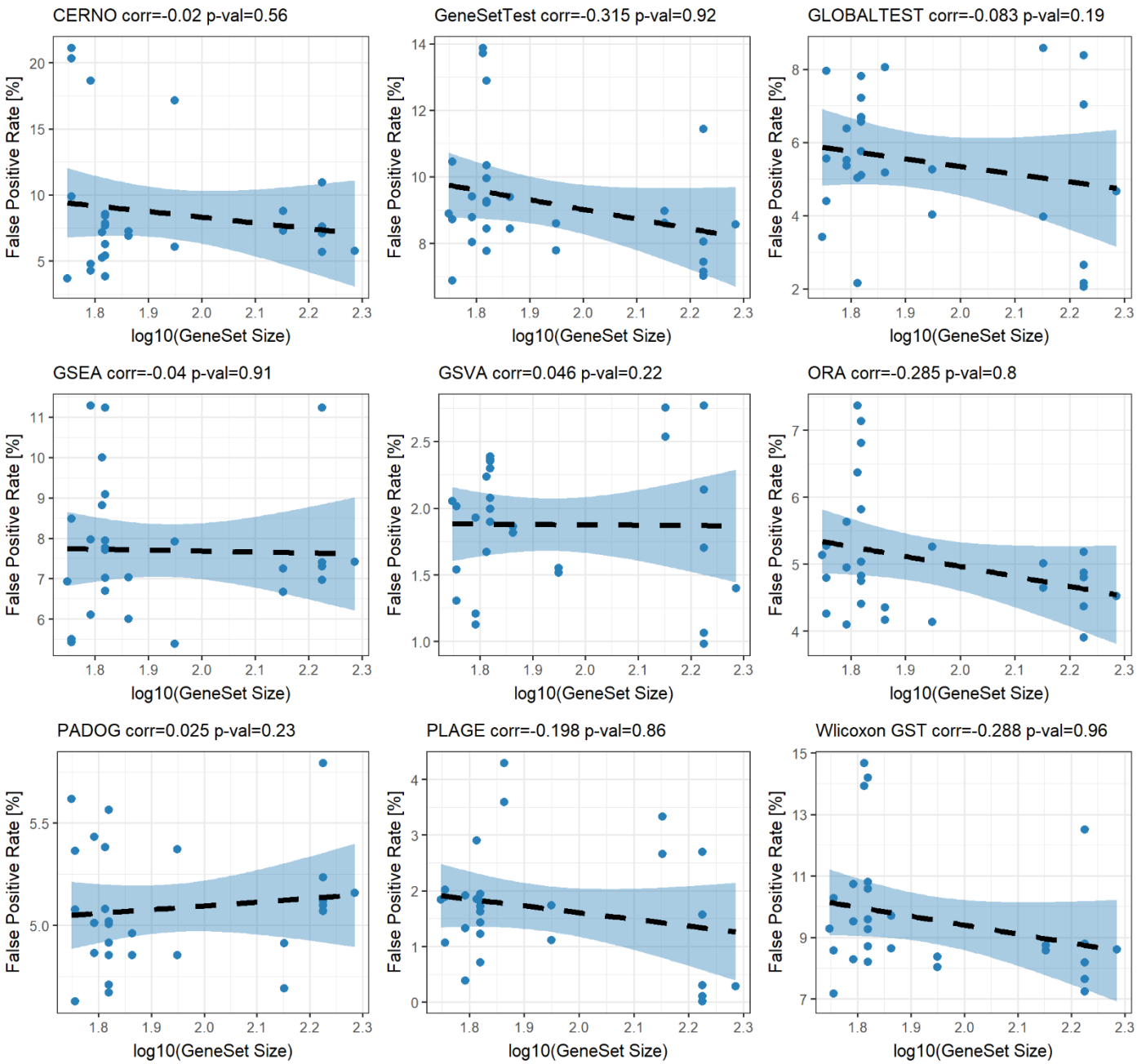Supplement Figure 5. Relation between false positive rate and gene set size in each tested algorithm. Blue dots represents observed outcomes, black dashed line shows linear regression model while blue area represents its 95% confidence interval. To each dependency, Spearman rank correlation coefficient (corr.) with its p-value (p-val) for equality to zero testing is included. X axis scale is presented as log10 of original value.