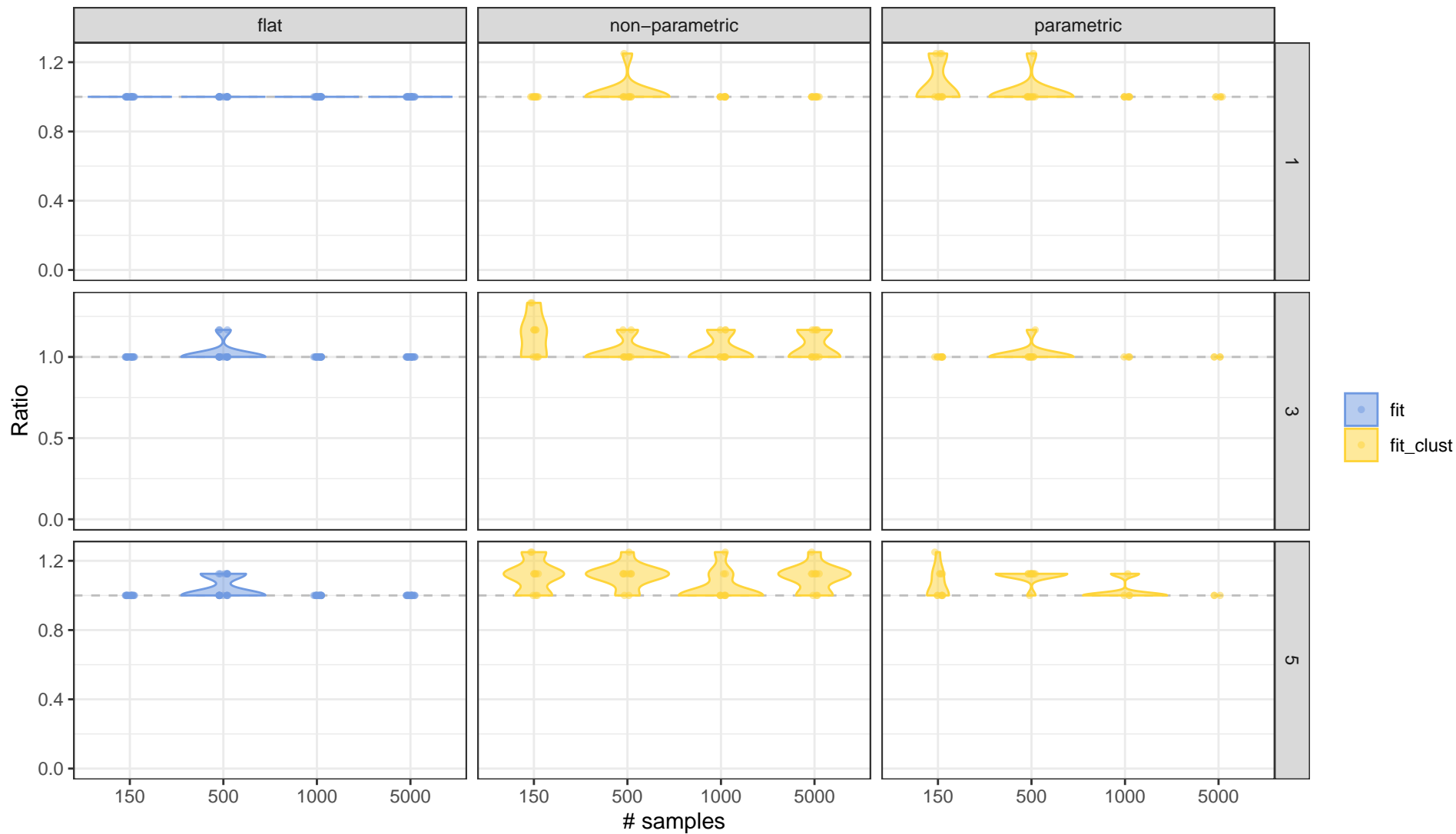
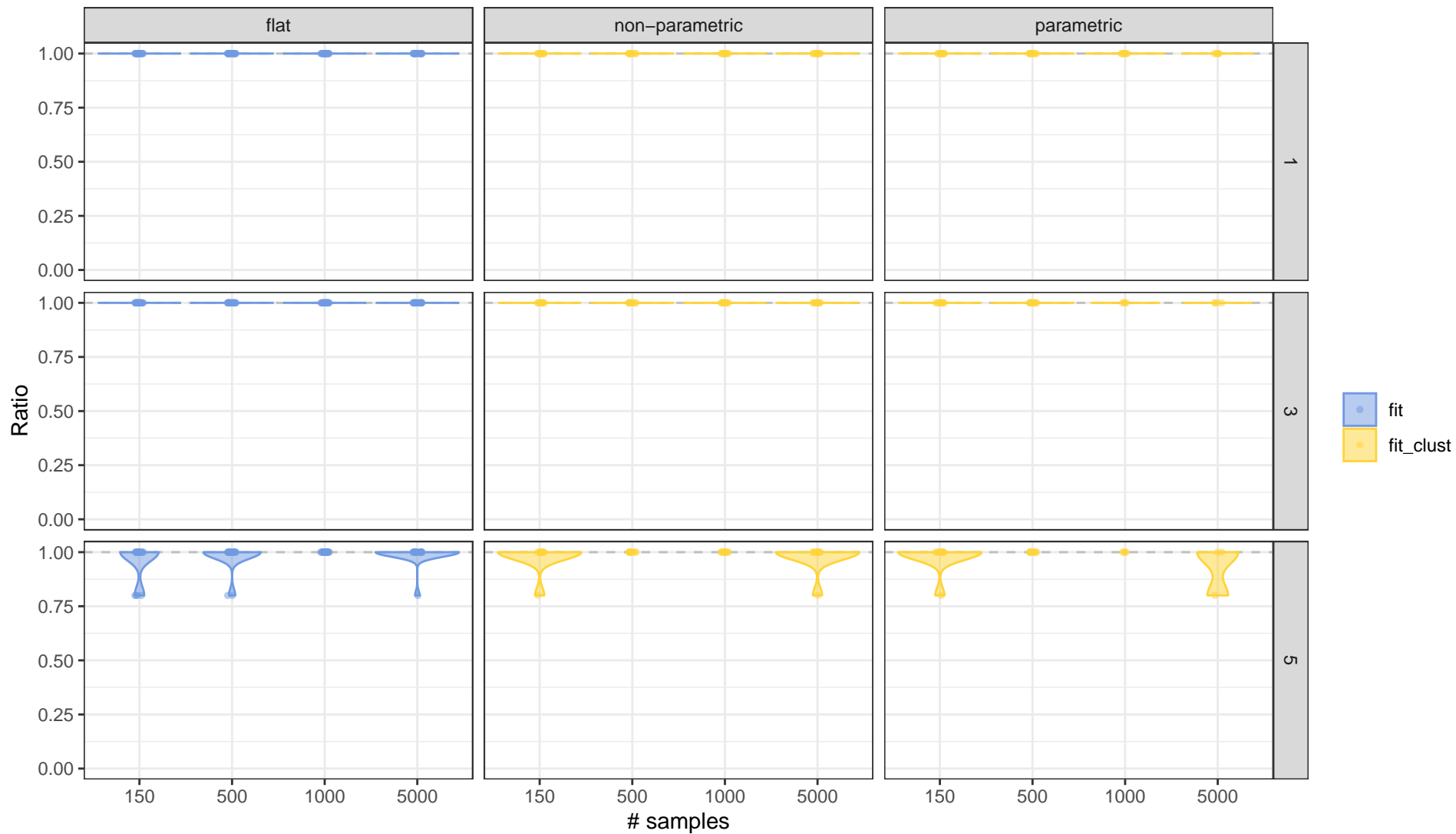


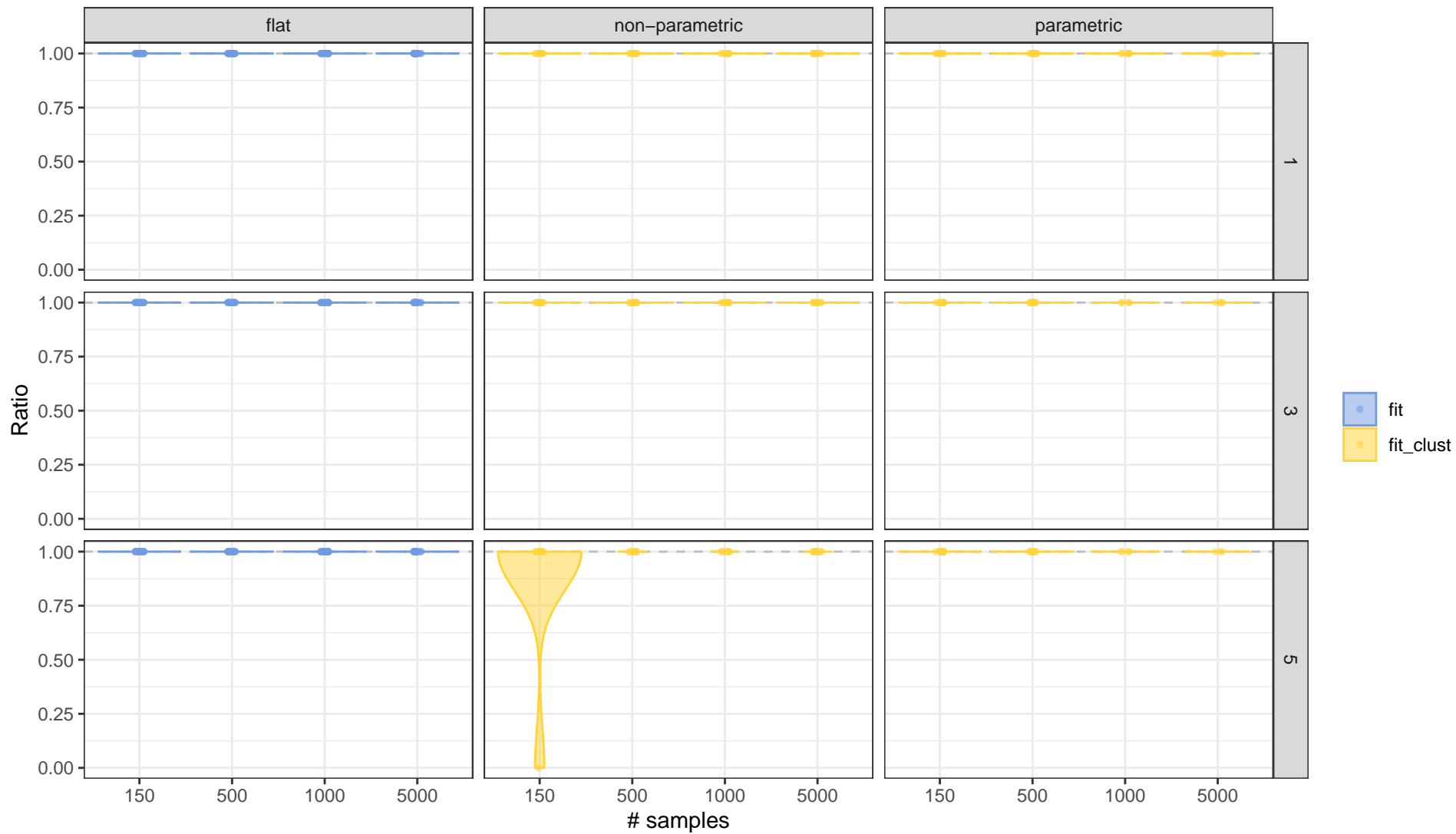
Ratio between number of signatures found and true



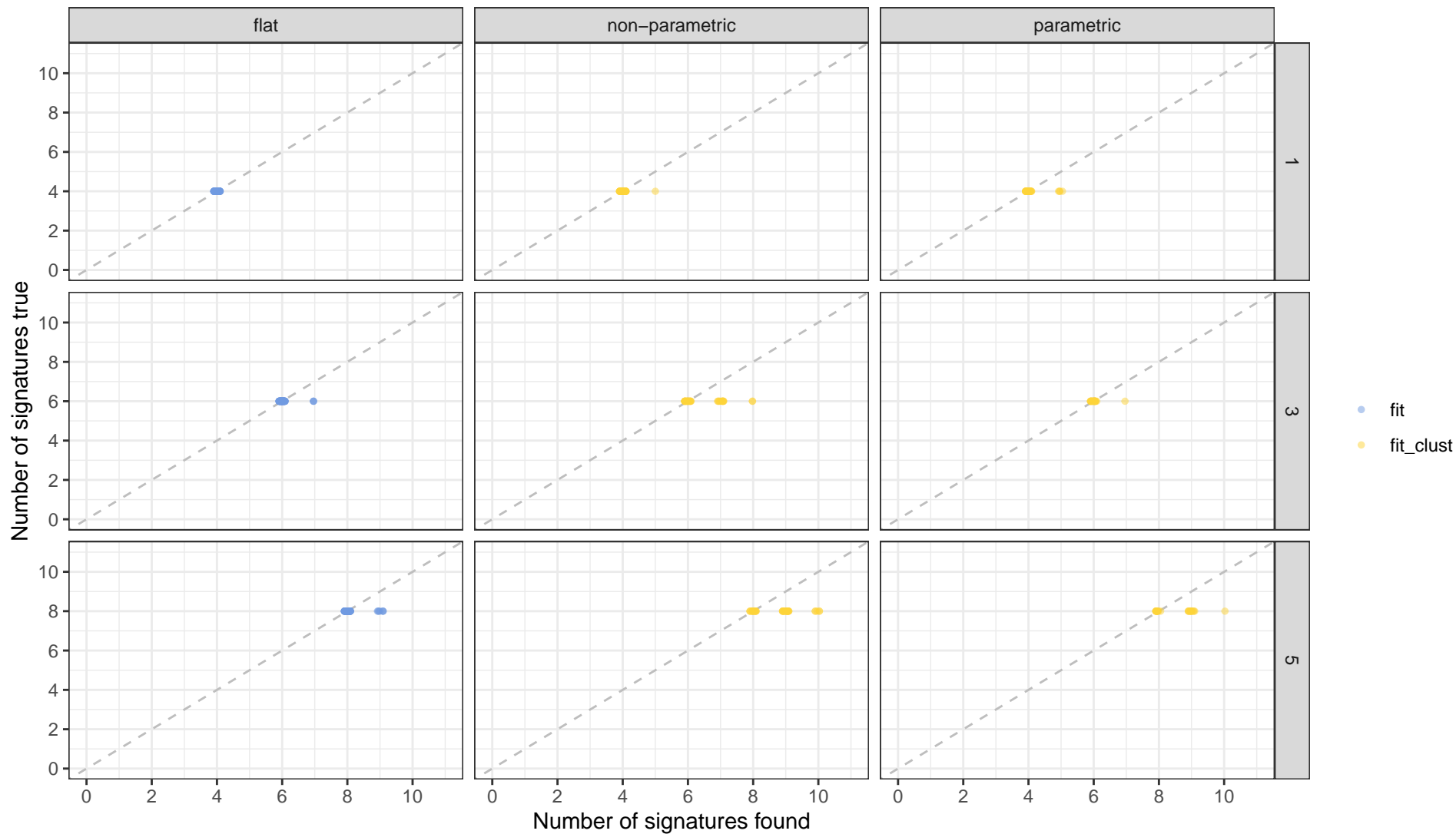
Ratio between number of common signatures found and true



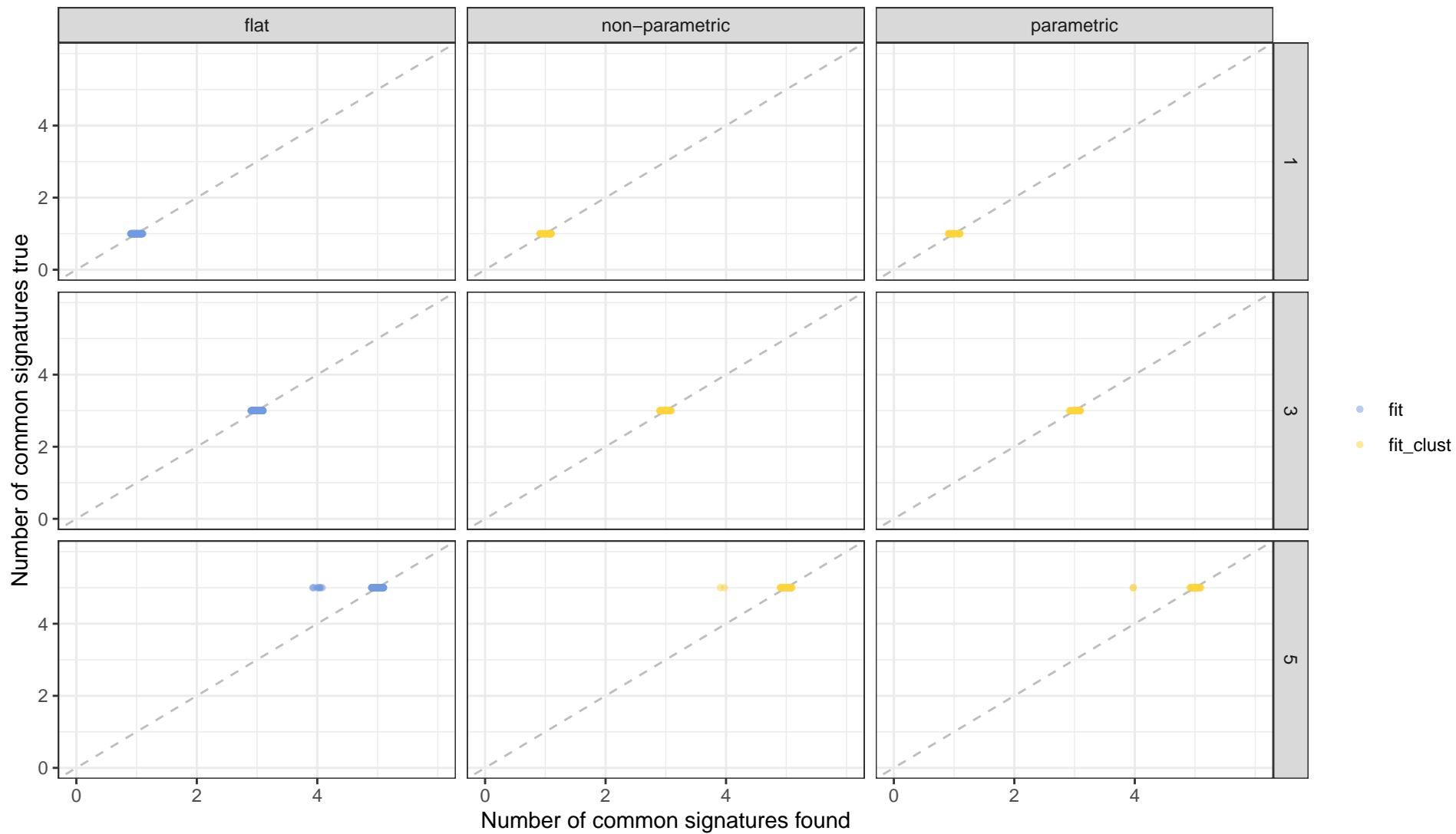
Ratio between number of rare signatures found and true



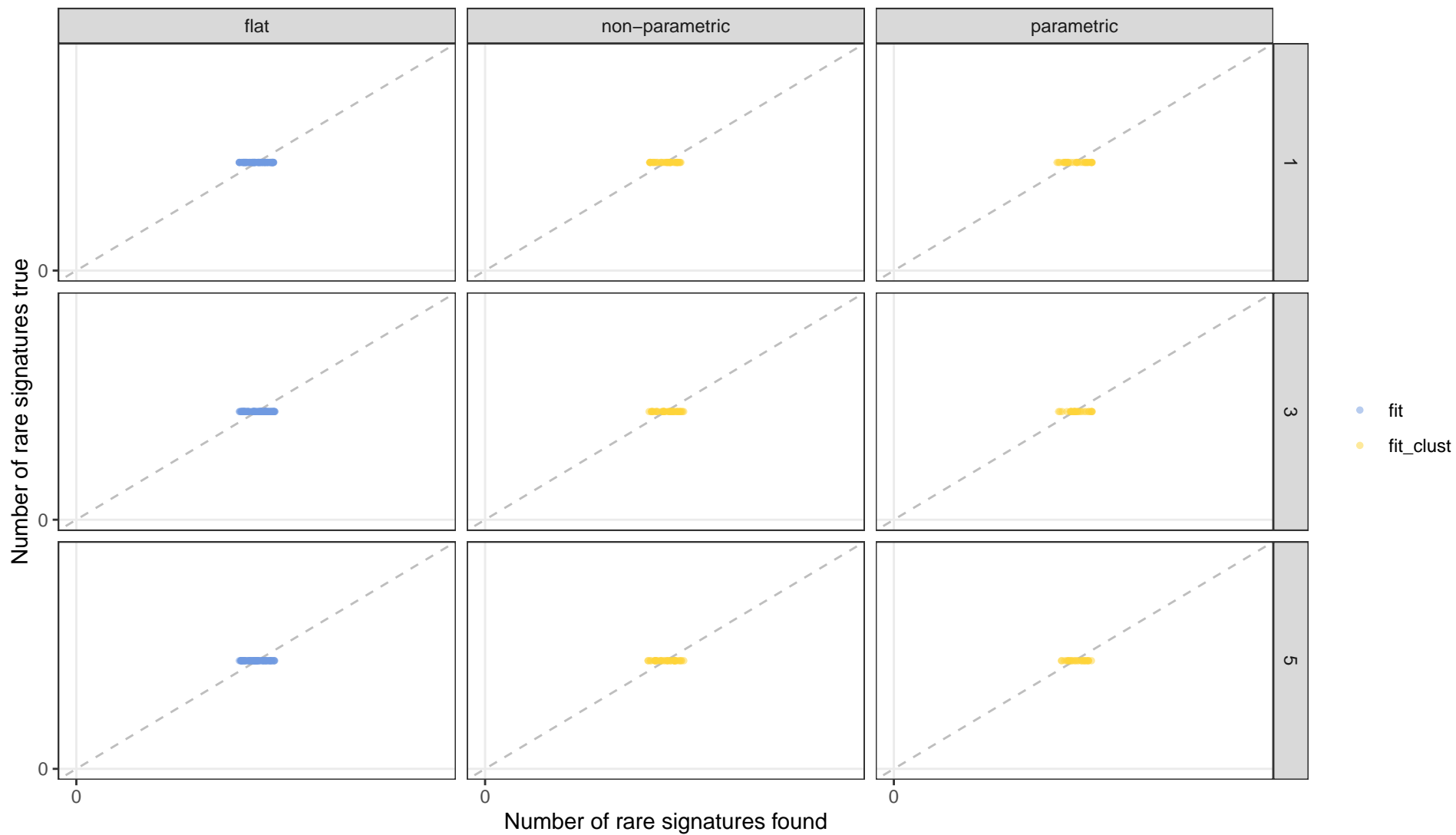
Number of signatures found (x) and true (y)



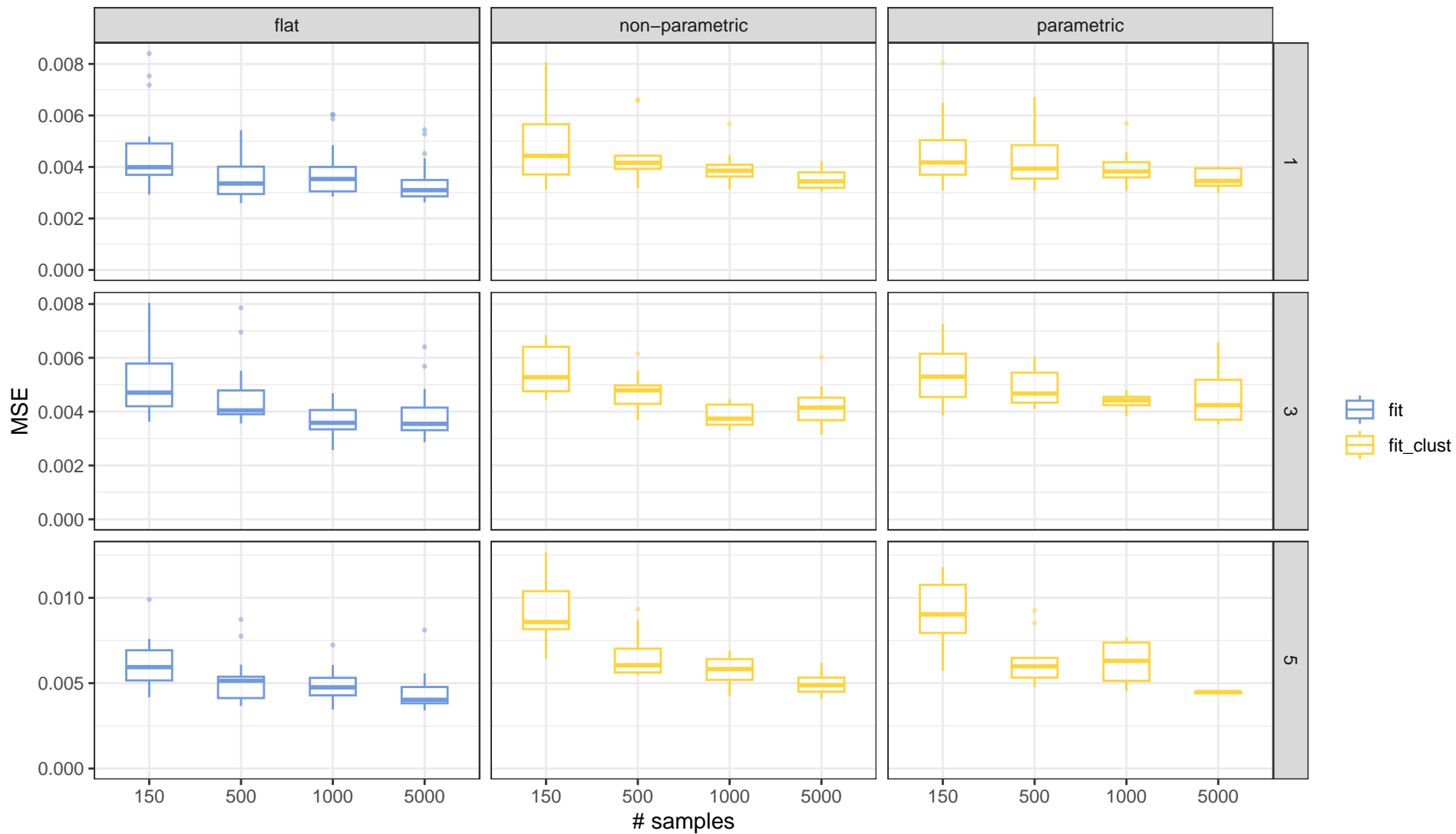
Number of common signatures found (x) and true (y)



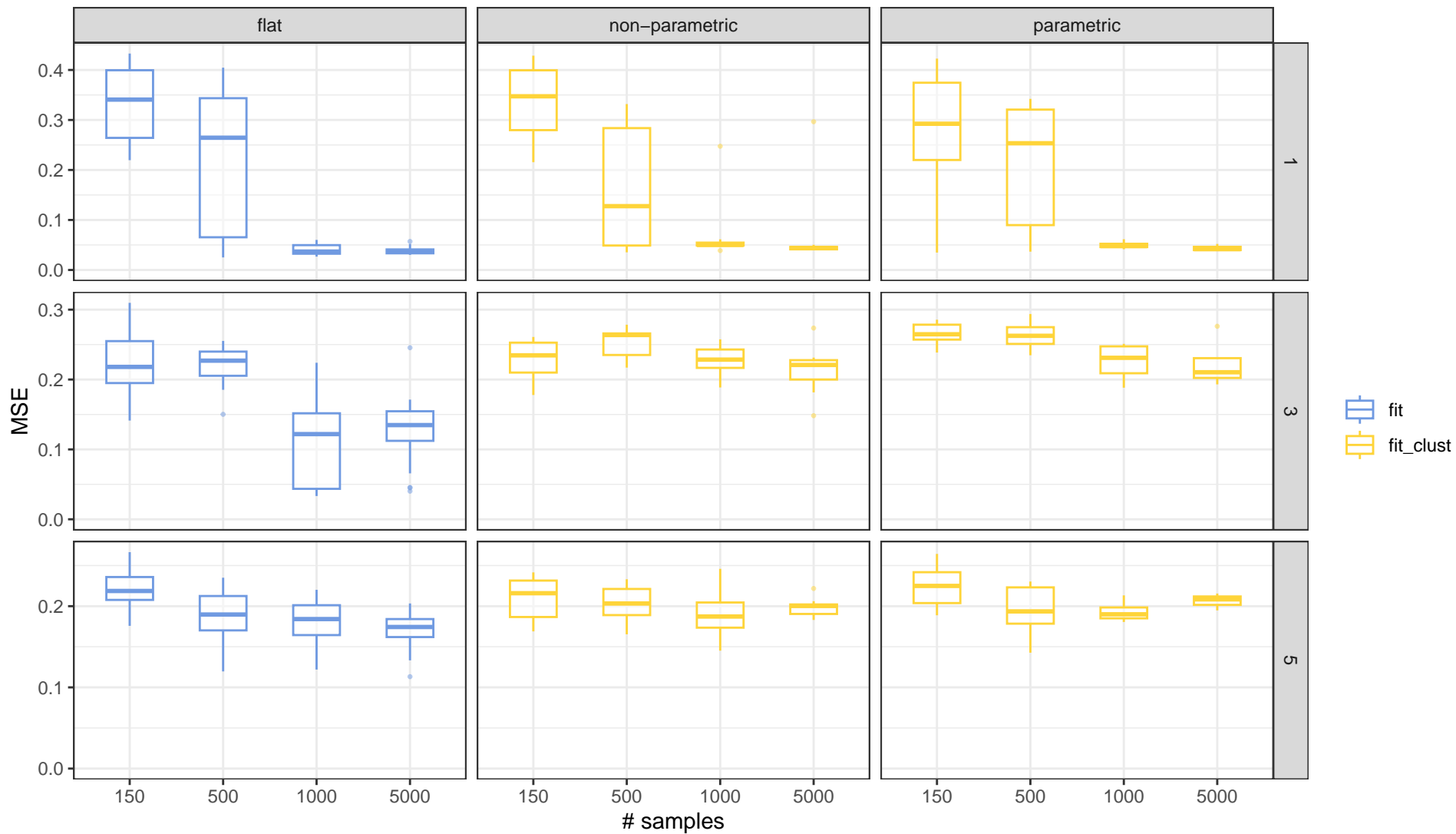
Number of rare signatures found (x) and true (y)



MSE computed between true and inferred counts

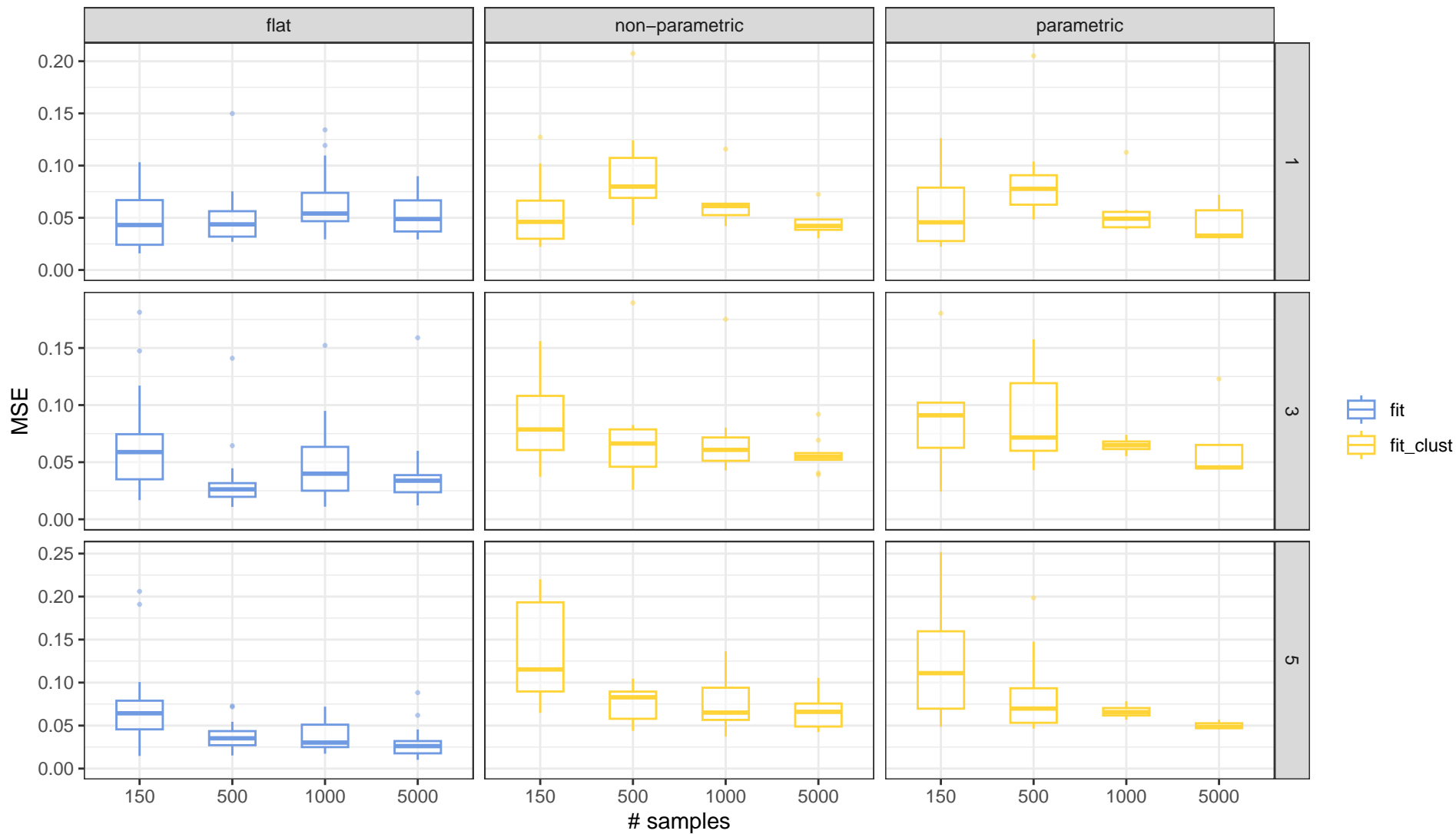


MSE computed between true and inferred exposures

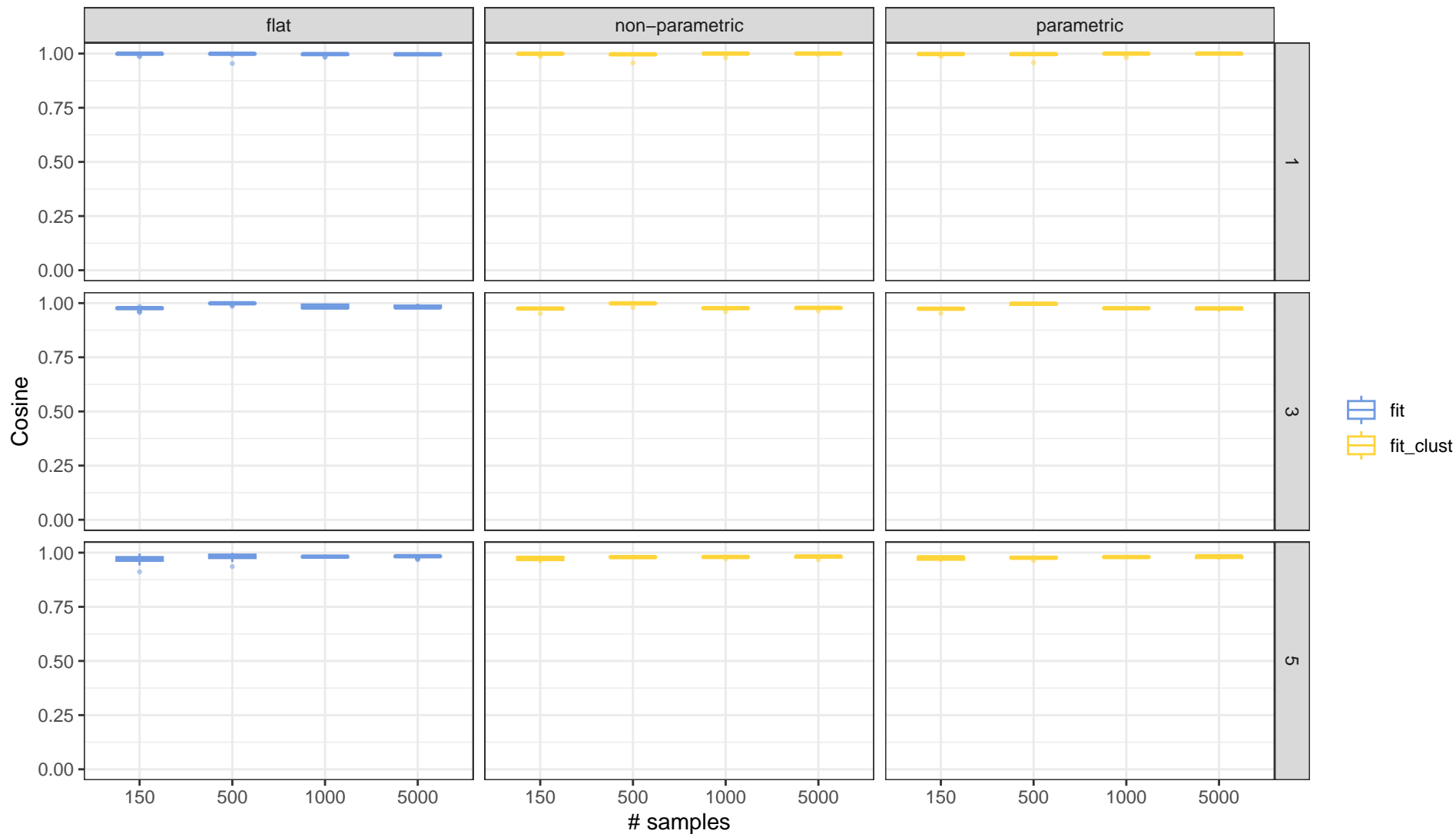




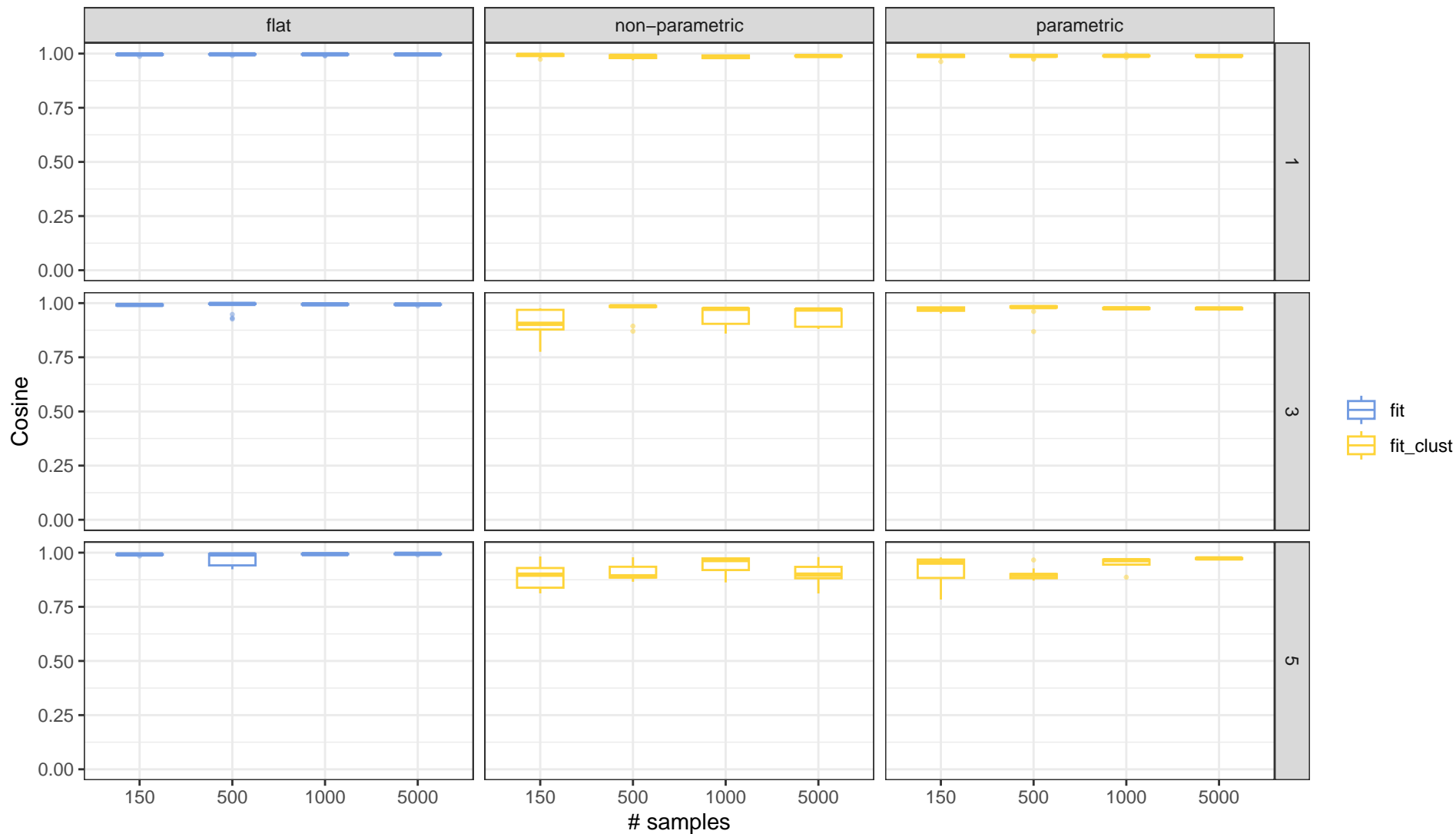
MSE computed between true and inferred rare exposures



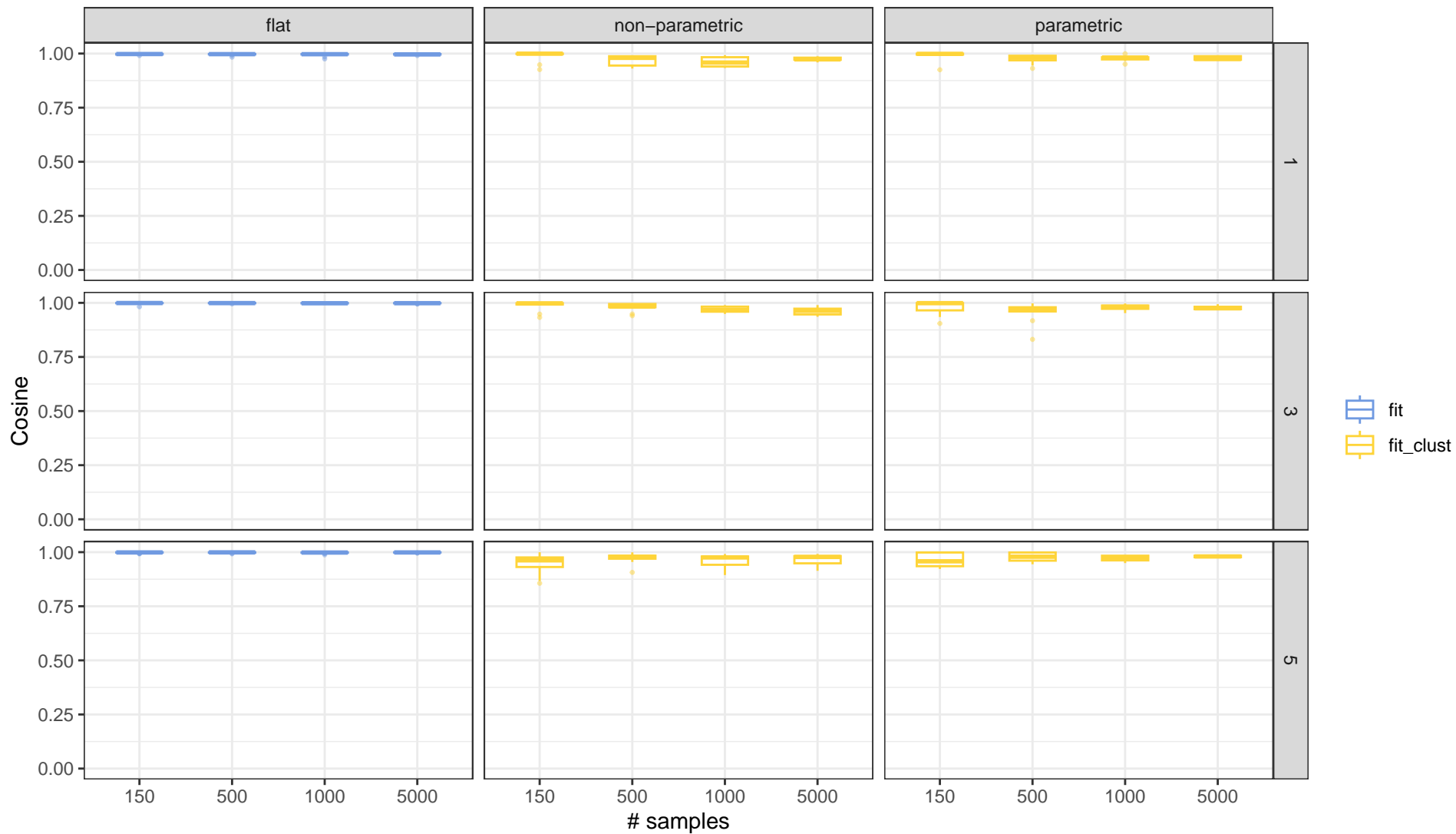
Cosine computed between true and inferred signatures



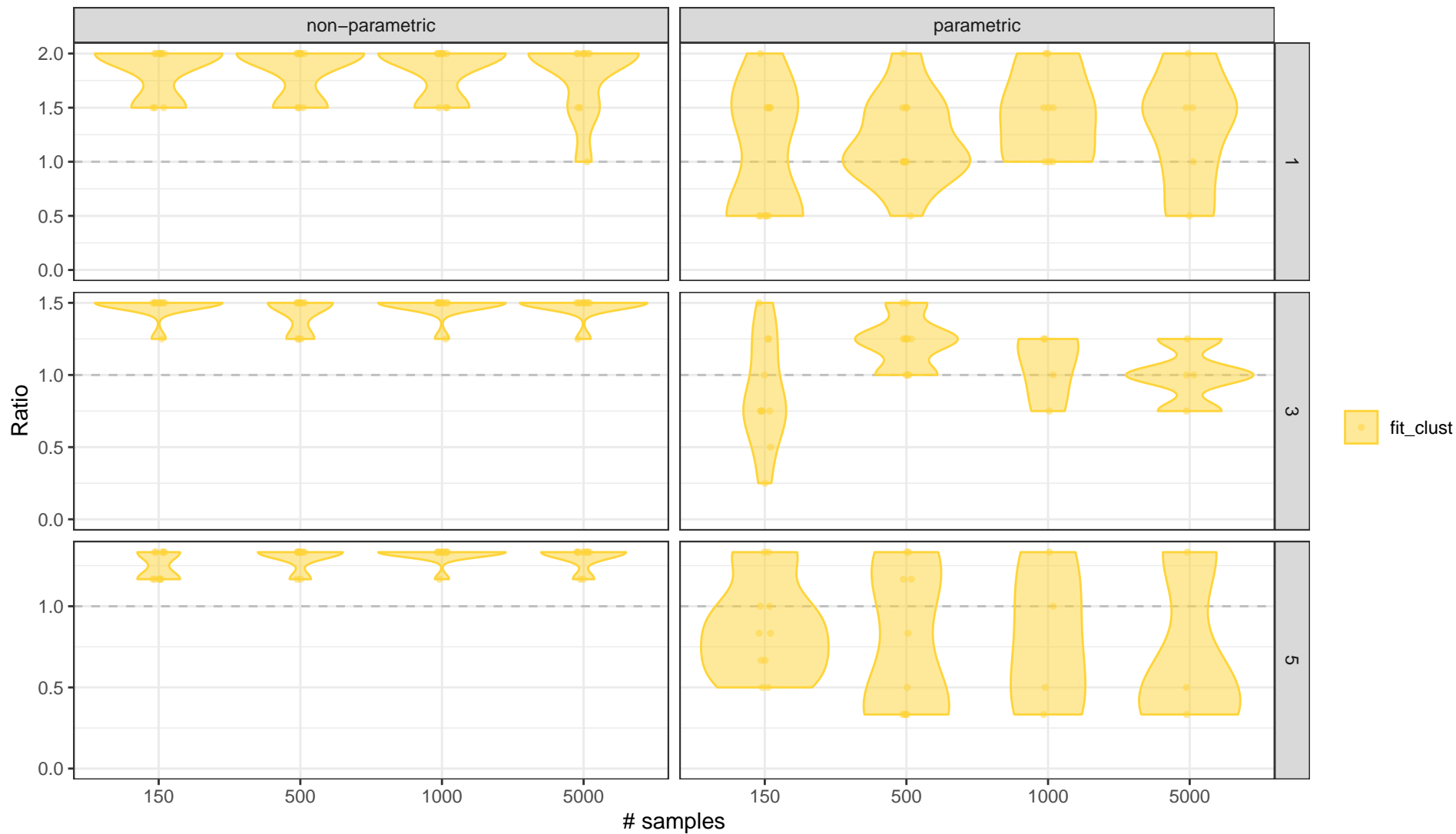
Cosine computed between true and inferred exposures



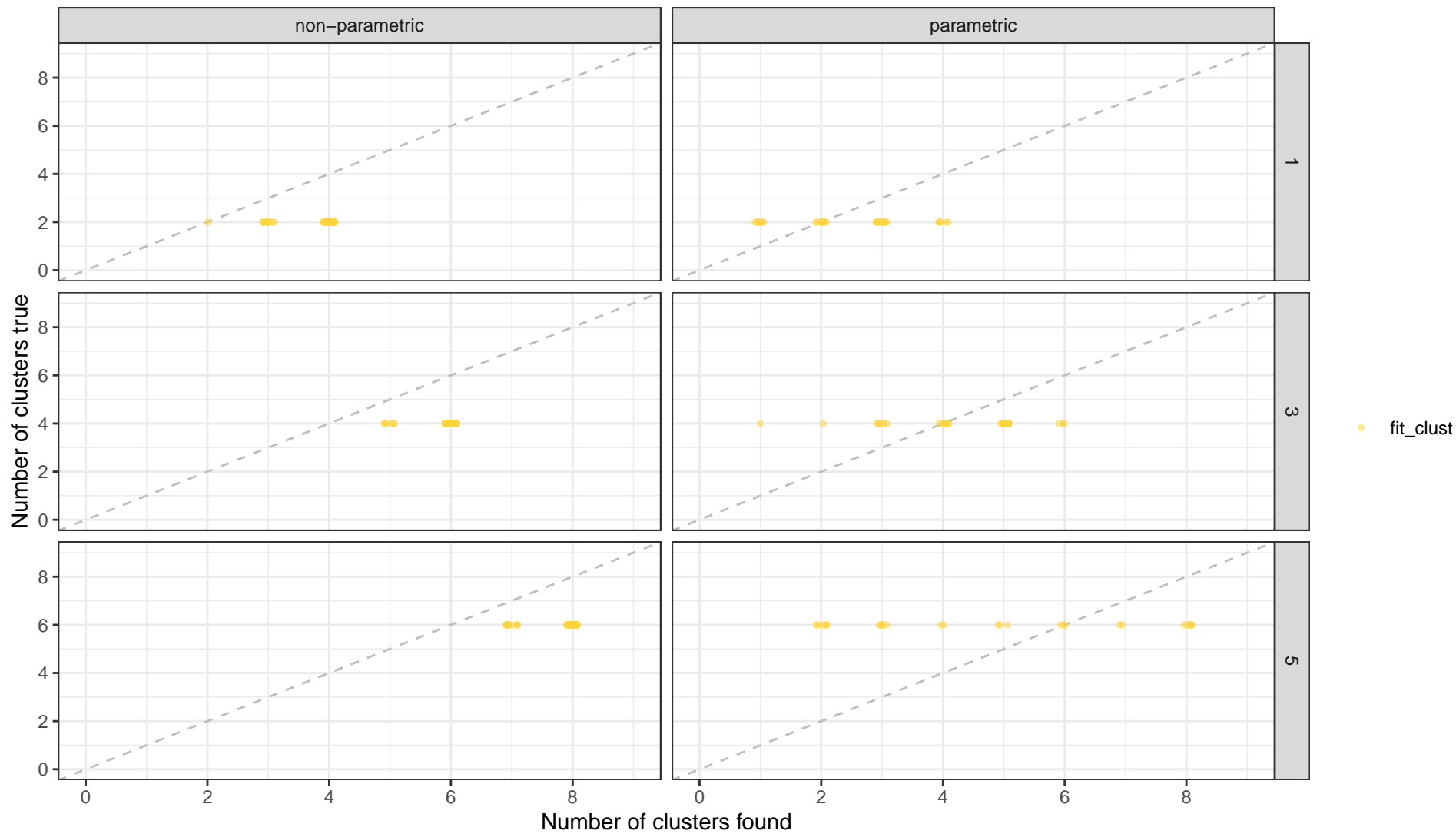
Cosine computed between true and inferred rare exposures



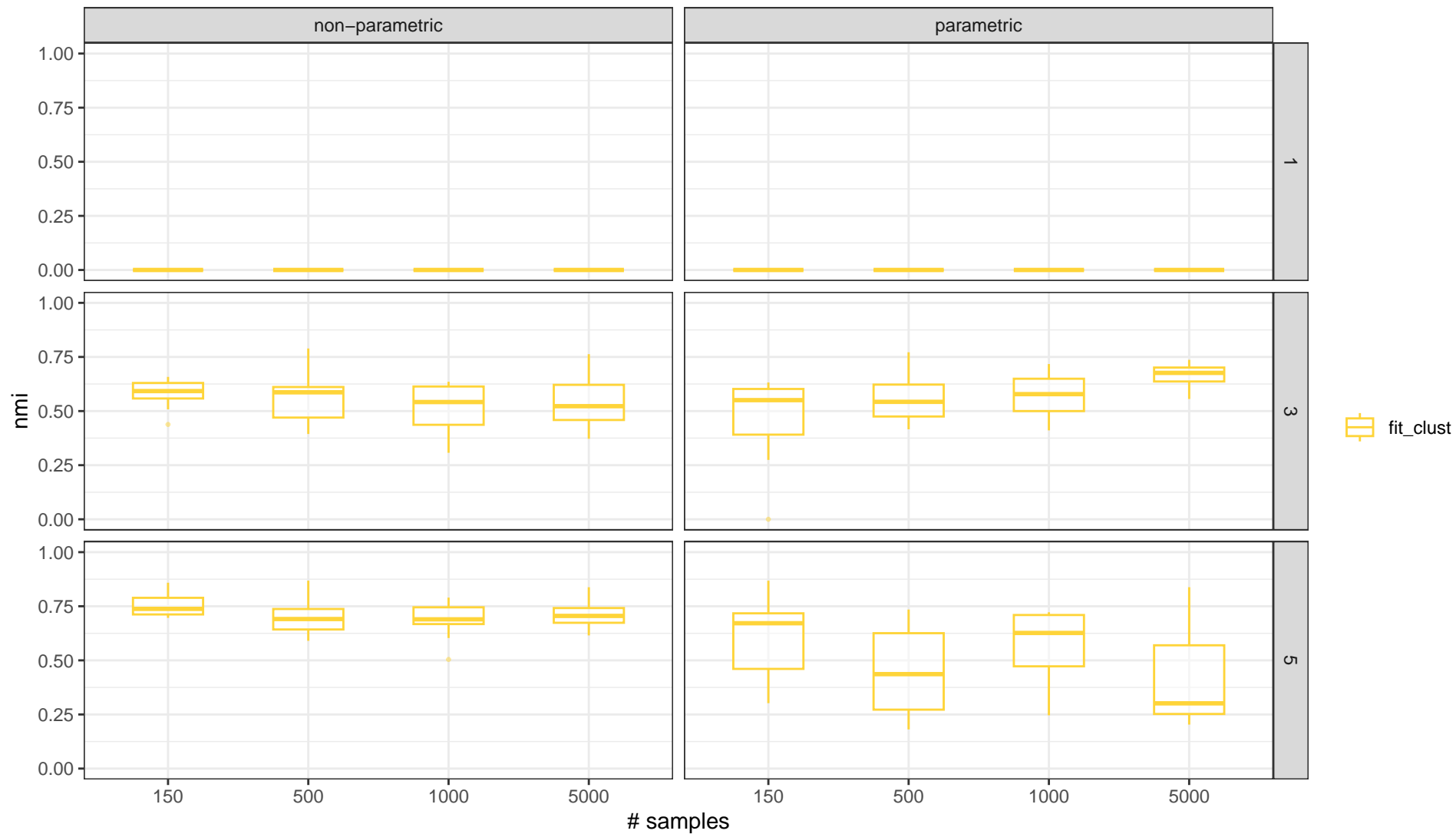
Ratio between number of clusters found and true



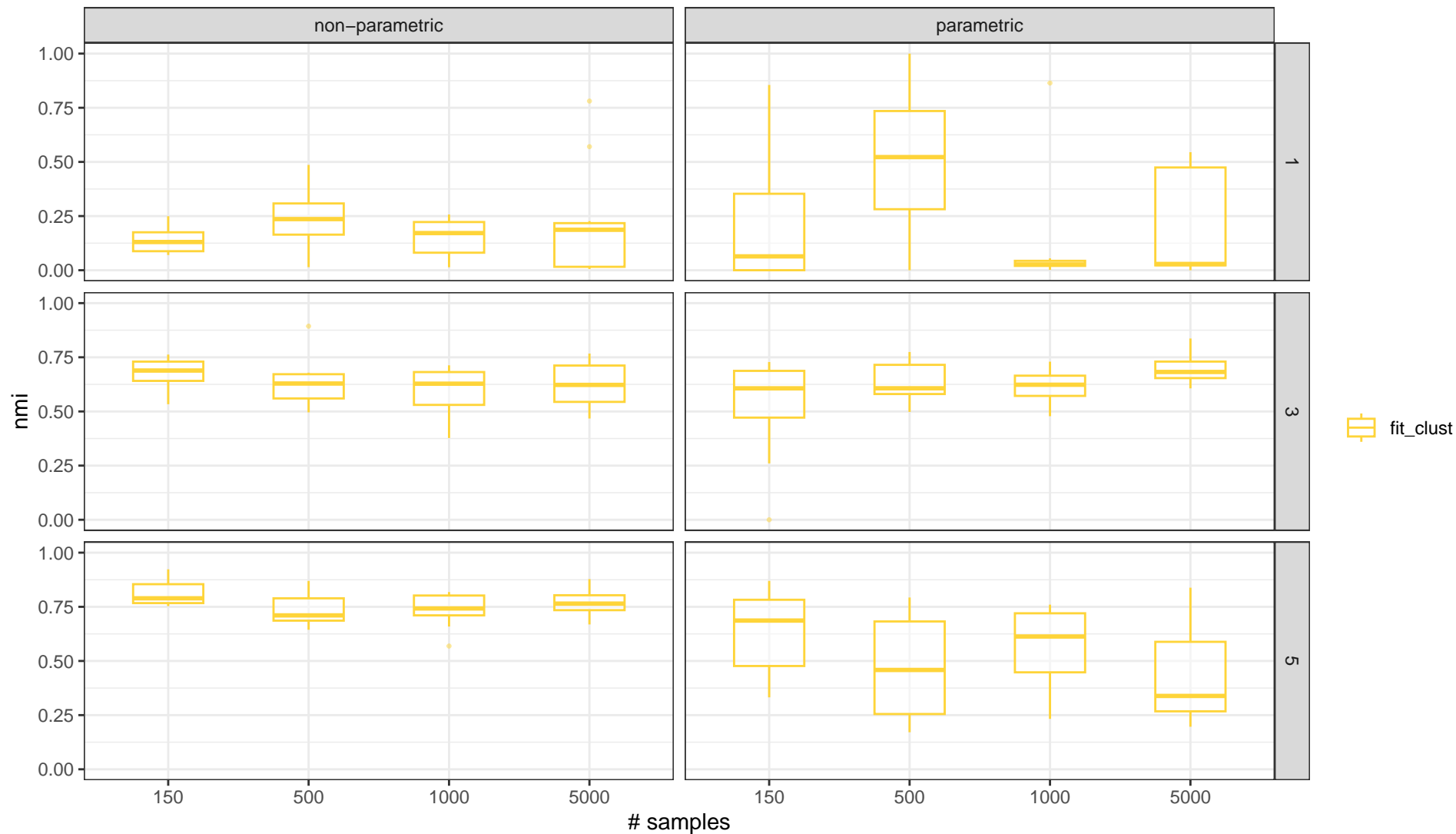
Number of clusters found (x) and true (y)



nmi computed between true and inferred NA

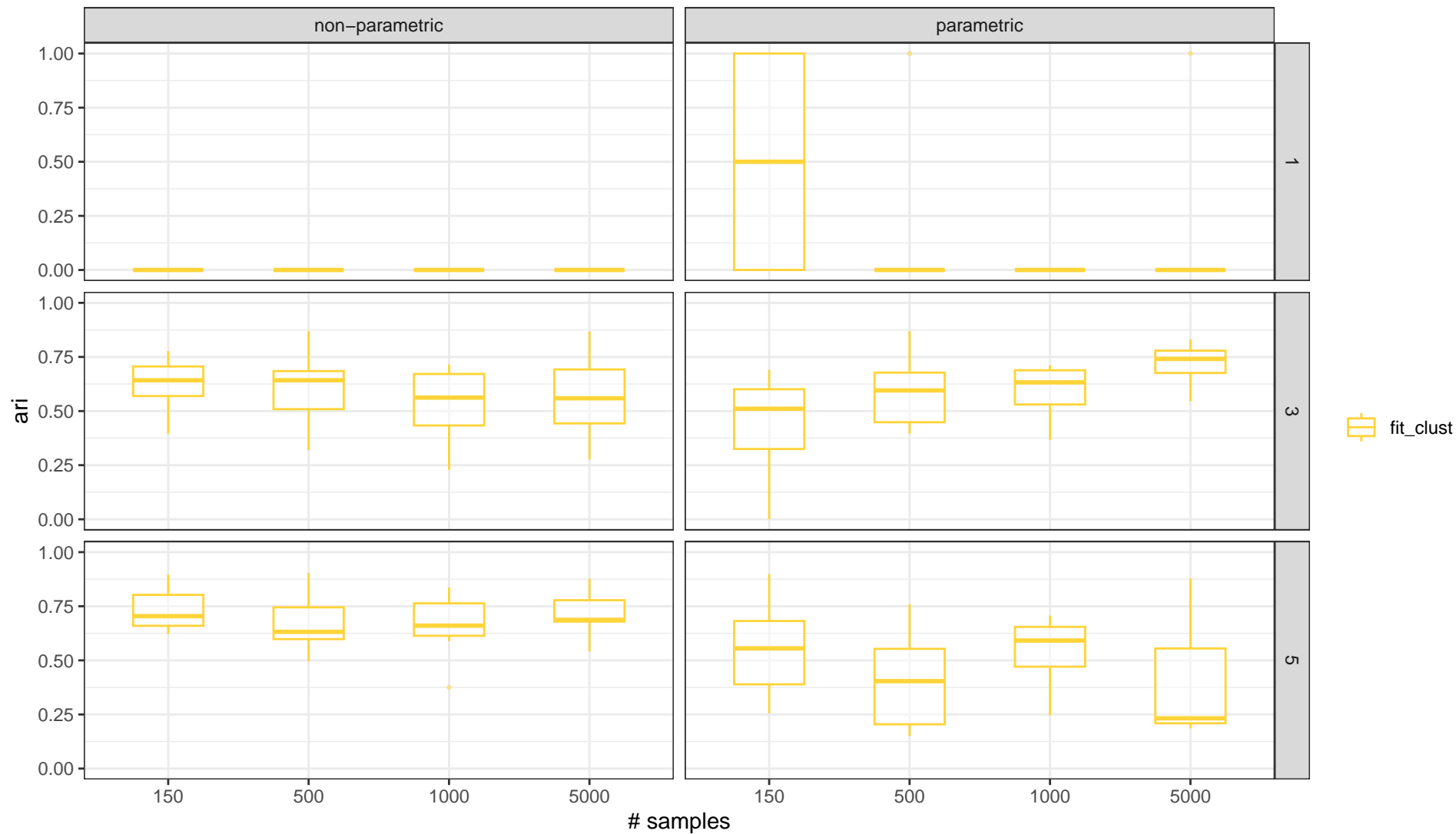


nmi computed between true and inferred rare





ari computed between true and inferred NA



ari computed between true and inferred rare

