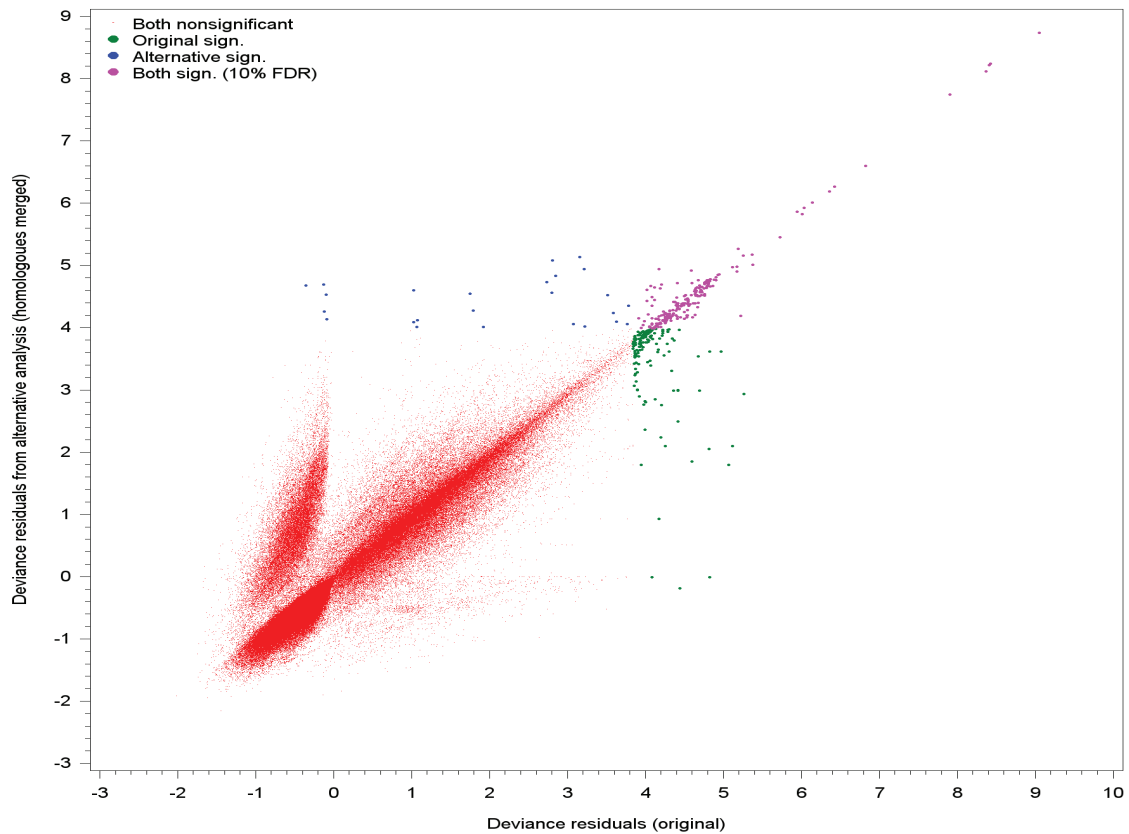
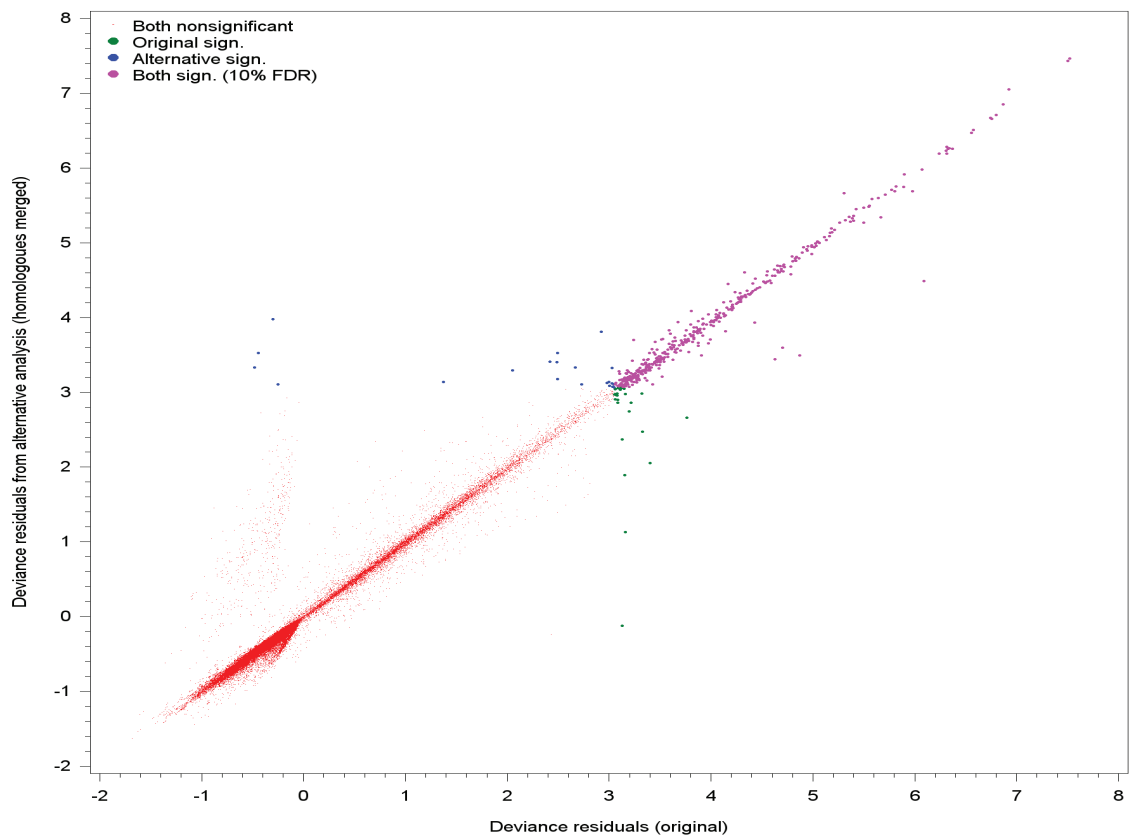


## A Protein complex with merged paralogues Vs original analysis (human)



Exclusion rule: ICE rule (incl. BSO)

## B Protein complex with merged paralogues Vs original analysis (yeast)



Exclusion rule: ICE rule (incl. BSO)

Plot of deviance residuals of the complex-complex interaction predictions where the proteins of high sequence similarity within the same complexes have been merged (Y-axes) against the original calculations (X-axes) for both human (A) and yeast (B). Each data point represents a complex-complex pair. Each datapoint is classified and color-coded according to complex pairs according to their change in significance ( $< 10\%$  FDR) after the merging of the paralogues. It is apparent that the merging of paralogous genes had little impact on the vast majority of both significant and non-significant complex-complex pairs in both organisms. The effect is much greater in human than in yeast possibly due to many more paralogues identified by Ensembl in human. The paralogue information for both human and yeast was sourced from (26).