



Figure 6: PRV by DSI (*left*) and Class (*right*) for predicted interacting pairs of proteins. Left, For each interacting protein pair, the duplication history of the encoding genes was used to calculate DSI, which is equal to WGD retention (1 if both genes have retained their α duplicate, 0.5 if 1 out of 2 has, 0 if neither has) minus small scale duplication (1 if both have been duplicated by small scale events, 0.5 if 1 out of 2 has, 0 if neither has). A DSI of 1 is evidence that the interaction is dosage sensitive, and decreasing values of DSI suggest decreasing levels of dosage sensitivity. Right, Class II is the same as DSI = 1 and Class I is everything else. PRV is calculated as described for GO terms and metabolic networks.