

## Additional file 1. – Model validation

Correlation plot of the connectivity from  $P_{G_{KroganHigh}}$  and normalized peptide counts from Krogan *et al.* Each data point corresponds to an interaction in  $G_{KroganFull} - G_{KroganHigh}$ , many of which are expected to be indirect. x-axis: connectivity entry in  $P_{G_{KroganHigh}}$ , using  $\hat{p} = 0.5$ . y-axis: peptide count, normalized by protein lengths. The resulting linear regression showed a strong correlation (regression p-value  $8.17 \times 10^{-11}$ , Student *t*-test), suggesting that many interactions in  $G_{KroganFull} - G_{KroganHigh}$  are indirect and are the result of direct interactions in  $G_{KroganHigh}$ .

