Figure S8 MIPS functional category enrichment for yeast genome, PIP-Lcut600 and PIC-Lcut600. Each slice reflects either the number of ORFs classified under the respective functional category (in the case of yeast genome), or the number of interactions involving at least one ORF from the respective category (in the case of PIP-Lcut600 and PIC-Lcut600). Both PIP-Lcut600 and PIC-Lcut600 are, compared to yeast genome, enriched by proteins employed for protein synthesis, even though the training set of PIC was deprived from ribosomal proteins. PIC-Lcut600 contains many interactions involving proteins of unclassified function, while PIP-Lcut600 includes few interactions of this kind, mainly because of its dependence on biological function as a predictor.
Figure S8 Continued
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