

Supplementary Table 5. P values for overlap among datasets

	Interactions	Overlap with LexA map (N=1,814)	Overlap with Gal4 map (N=20,439)
Yeast interlogs (hub/spoke)	67,238	24 (1.32%; P<0.0001)	251 (1.23%; P<0.0001)
Yeast interlogs (matrix)*	244,202	25 (1.46%; P<0.0001)	294 (1.44%; P<0.0001)
Worm interlogs	37,863	3 (0.17%; P<0.1436)	61 (0.30%; P<0.0001)
Drosophila genetic	2,751	4 (0.22%; P<0.0024)	22 (0.11%; P<0.0001)
Reference set	47	8 (0.44%; P<0.0001)	6 (.03%; P<0.0001)
Ref set (common BD)	20	3 (0.17%; P<0.0001)	2 (.01%; P<0.0001)

Data from Table 3. P values indicate the chances of finding the number of overlapping interactions with a random set of interactions. The random sets were generated by replacing the AD proteins in each of the maps with a random set of proteins, keeping the BD proteins, the number of interactions per BD protein and AD protein, and the topologies of the maps the same (see Methods).

Supplementary Table 6. Interactions from the LexA and Gal4 screens that successfully used the same BD bait proteins.

	Interactions	Overlap with LexA map (N=859)	Overlap with Gal4 map (N=243)	Overlap in common
Yeast interlogs (hub/spoke)	67,238	19 (2.21%)	6 (2.47%)	4
Worm interlogs	37,863	3 (0.35%)	1 (0.41%)	0
Drosophila genetic	2,751	1 (0.12%)	4 (1.65%)	0
Ref set (common BD)	20	3 (0.35%)	2 (.82%)	0

Of the 154 BDs used in both screens (Supplementary Table 1), 14 had interactions only in the Gal4 screens, 60 had interactions only in the LexA screens, and 46 were used successfully to detect interactions in both the LexA and Gal4 screens. With these 46 BDs, the LexA screens detected 859 interactions and the Gal4 screens detected 243. The table shows the overlap among these interactions and the 3 datasets as described in Table 2 and Methods.