Supplementary Table 1. Robustness of drug-induced modules to redundancy removal parameters. Redundancies among modules were eliminated within each cell line using the recommended standard procedure ISAUnique (R 'eisa' package). We used a correlation (cor.) threshold of 0.3. Subsequently, modules were subjected to a second round of redundancy removal based on gene overlap between modules (Fisher test, p-value $<10^{-5}$, using the same priority as pre-defined by ISA). Additionally, we explored a wide range of parameters here (cor. threshold: from 1 to 0.1 in decrements of 0.1 and overlap p-value cutoffs 10^{-2}, 10^{-5}, and 10^{-10}) and assessed the effect on the resulting non-redundant set of modules (percentages in parentheses indicate the coverage of the non-redundant set of modules described in the main text). In conclusion, the combination of these redundancy removal routines yields similar results across a broad range of parameter settings and is thus quite robust to the actual parameters used (shaded in gray).

ISAUnique (cor.) threshold	# of modules after ISAUnique	# of non-redundant modules after removal of (gene) overlapping modules [% overlap with final set] Threshold for Fisher test P value (FDR corr.)		
MCF7		10^{-2}	10^{-5}	10^{-10}
1.0	1909	28 [84%]	31 [96%]	35 [92%]
0.9	740	28 [84%]	31 [96%]	35 [92%]
0.8	246	26 [84%]	31 [96%]	35 [92%]
0.7	119	25 [84%]	31 [96%]	34 [92%]
0.6	96	25 [84%]	31 [96%]	33 [92%]
0.5	69	25 [84%]	31 [96%]	33 [92%]
0.4	47	24 [84%]	28 [96%]	31 [96%]
0.3	35	23 [88%]	25 [100%]	29 [96%]
0.2	29	21 [80%]	23 [92%]	27 [92%]
0.1	22	17 [68%]	20 [80%]	22 [80%]
PC3		10^{-2}	10^{-5}	10^{-10}
1.0	1405	24 [68%]	30 [100%]	34 [100%]
0.9	447	25 [71%]	30 [100%]	34 [100%]
0.8	157	24 [71%]	30 [100%]	33 [100%]
0.7	86	24 [71%]	30 [100%]	33 [100%]
0.6	67	23 [71%]	30 [100%]	33 [100%]
0.5	60	23 [71%]	30 [100%]	33 [100%]
0.4	50	22 [75%]	28 [100%]	31 [100%]
0.3	38	22 [75%]	28 [100%]	30 [100%]
0.2	32	21 [71%]	27 [96%]	29 [96%]
0.1	25	19 [68%]	24 [86%]	25 [86%]
HL60		10^{-2}	10^{-5}	10^{-10}
1.0	1472	28 [76%]	33 [97%]	39 [100%]
0.9	492	28 [76%]	33 [97%]	39 [100%]
0.8	193	28 [76%]	33 [97%]	39 [100%]
0.7	106	28 [79%]	33 [97%]	39 [100%]
0.6	94	27 [79%]	32 [97%]	37 [100%]
0.5	78	26 [86%]	31 [100%]	36 [100%]
0.4	62	26 [86%]	30 [100%]	36 [100%]
0.3	42	25 [86%]	29 [100%]	35 [100%]
0.2	34	25 [86%]	29 [100%]	33 [100%]
0.1	24	22 [76%]	23 [79%]	24 [79%]