

Enrichment of extended up-regulated genes

	Maps		Process networks	
	Average # of significant maps (FDR of 0.05)	# of new and original significant maps recovered*	Average # of significant processes (FDR of 0.2)	# of new and original significant processes recovered*
Original set (no random added)	12	0 and 12	6	0 and 6
50 random	9.58	1 and 11	3.2	4 and 6
100 random	9.7	0 and 11	3.1	4 and 6
200 random	8.8	1 and 11	2.1	0 and 4
300 random	8.8	0 and 8	1.4	0 and 3
400 random	3.7	0 and 9	0.9	0 and 2
500 random	2.3	0 and 7	0.9	0 and 1
1,000 random	0.3	0 and 0	0.5	0 and 0

100 randomizations were performed for each size of random gene set

*Only maps significant in at least 10% of randomizations were counted

Enrichment of extended up-regulated proteins

	Maps		Process networks	
	Average # of significant maps (FDR of 0.05)	# of new and original significant maps recovered*	Average # of significant processes (FDR of 0.2)	# of new and original significant processes recovered*
Original set (no random added)	14	1 and 14	6	0 and 6
50 random	7.28	0 and 8	4.9	1 and 6
100 random	3.55	0 and 2	5.1	4 and 6
200 random	3.2	0 and 2	3.4	0 and 6
300 random	2.7	0 and 2	3.9	0 and 4
400 random	2.7	0 and 2	3.5	0 and 3
500 random	1.42	0 and 2	2.8	0 and 2
1,000 random	0.26	0 and 0	2.3	0 and 2

100 randomizations were performed for each size of random gene set

*Only maps significant in at least 10% of randomizations were counted