

gene of unknown function	genes with similar target sets	n	cellular process (SGD)	goTermMapper result
IES6	RTG1 AEP2 CKA2 MED2 MRT4 RSM18 RTS1 SHE4 TUP1	2 1 1 1 1 1 1 1 1	protein localization protein biosynthesis G1/S transition of mitotic cell cycle transcription from Pol II promoter ribosomal large subunit biogenesis protein biosynthesis protein biosynthesis mRNA localization, intracellular negative regulation of transcription	metabolism 9(9)
KIN3	STE12 SWI4 SWI5 DIG1 SWI6 ANP1 BUD14 ERG2 FKS1 GAS1 QCR2 RMD7 SHE4 SPF1 STE18 STE7 TEC1	3 3 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1 1	invasive growth cell cycle G1-specific transcription in mitotic cell cycle invasive growth G1/S-specific transcription in mitotic cell cycle cell cycle N-linked glycosylation bud site selection ergosterol biosynthesis beta-1,3 glucan biosynthesis cell wall organization and biogenesis aerobic respiration cell wall organization and biogenesis mRNA localization, intracellular calcium ion homeostasis signal transduction of mating signal protein amino acid phosphorylation pseudohyphal growth	cell growth and/or maintenance 13(17)
YEL008W	GCN4 SWI4 GLN3 RTG1 ANP1 CKB2 CLB2 ERG2 ERG28 ERG3 NPR2 RAD57 RMD7 RRP6 SGS1 UBR1	3 3 2 2 1 1 1 1 1 1 1 1 1 1 1 1	amino acid biosynthesis cell cycle nitrogen metabolism protein localization N-linked glycosylation G1/S transition of mitotic cell cycle G2/M transition of mitotic cell cycle ergosterol biosynthesis ergosterol biosynthesis ergosterol biosynthesis proline transport DNA recombinase assembly cell wall organization and biogenesis 35S primary transcript processing DNA unwinding monoubiquitination	metabolism 13(16)
YEL033W	RTG1 ANP1 BUD21 BUD22 MRT4 RPL12A TUP1	2 1 1 1 1 1 1	protein localization N-linked glycosylation processing of 20S pre-rRNA bud site selection ribosomal large subunit biogenesis protein biosynthesis negative regulation of transcription	metabolism 6(7)

YHL029C	GCN4	3 amino acid biosynthesis	metabolism 19/24
	SWI4	3 cell cycle G1-specific transcription in mitotic cell	
	SWI5	3 cycle	
	GLN3	2 nitrogen metabolism regulation of transcription from Pol II	
	HIR2	2 promoter	
	RTG1	2 protein localization	
	ANP1	1 N-linked glycosylation	
	CKB2	1 G1/S transition of mitotic cell cycle	
	CLB2	1 G2/M transition of mitotic cell cycle	
	CUP5	1 copper homeostasis	
	ERG2	1 ergosterol biosynthesis	
	ERG28	1 ergosterol biosynthesis	
	ERG3	1 ergosterol biosynthesis	
	NPR2	1 proline transport	
	RAD57	1 DNA recombinase assembly	
	RMD7	1 cell wall organization and biogenesis	
	RRP6	1 35S primary transcript processing	
	RTS1	1 protein biosynthesis	
	SGS1	1 DNA unwinding	
	SPF1	1 calcium ion homeostasis	
	STE24	1 a-factor processing (proteolytic)	
	UBR1	1 monoubiquitination	
	YEL008W	1 biological_process unknown	
	YMR010W	1 biological_process unknown	
YJL206C		regulation of transcription from Pol II	
	MCM1	2 promoter	
YMR010W	CLB2	1 G2/M transition of mitotic cell cycle	metabolism 2(3)
	ERG2	1 ergosterol biosynthesis	
	ERG28	1 ergosterol biosynthesis	
YMR031W-A	GCN4	3 amino acid biosynthesis	metabolism 18(23)
	SWI4	3 cell cycle	
	GLN3	2 nitrogen metabolism regulation of transcription from Pol II	
	HIR2	2 promoter	
	MAC1	2 cadmium homeostasis	
	RTG1	2 protein localization	
	AFG3	1 protein complex assembly	
	ANP1	1 N-linked glycosylation	
	CEM1	1 hexadecanal biosynthesis	
	CKB2	1 G1/S transition of mitotic cell cycle	
	CLB2	1 G2/M transition of mitotic cell cycle	
	ERG2	1 ergosterol biosynthesis	
	ERG28	1 ergosterol biosynthesis	
	ERG3	1 ergosterol biosynthesis	
	RAD57	1 DNA recombinase assembly	
	RMD7	1 cell wall organization and biogenesis	
	SGS1	1 DNA unwinding	
	STE24	1 a-factor processing (proteolytic)	
	UBR1	1 monoubiquitination	
	YEL008W	1 biological_process unknown	
	YHL029C	1 biological_process unknown	
	YMR010W	1 biological_process unknown	
	YMR293C	1 aerobic respiration	

YMR269W	BUD22	1 bud site selection	cell growth and/or maintenance 3(6)
	IES6	1 biological_process unknown	
	MRT4	1 ribosomal large subunit biogenesis	
	RPL12A	1 protein biosynthesis	
	RPL8A	1 protein biosynthesis	
	RPS24A	1 protein biosynthesis	

Predictions made for genes with "biological process unknown" annotation in SGD using target set similarities $p \leq 0.01$; we compared target sets from the mutant network, the *in-silico* network and the combined chip networks (see netCombination.pdf); we list all genes with similar target sets as the query gene; n is number of similar target sets for each gene pair; the last column contains the GO term which describes the set genes best (using goTermMapper from SGD);