

Table S3. Top genes enriched in “In Gfp^{basal}” population.

Genes in orange are expected to be enriched in this population; YJR087W* partially overlaps with *STE18*; shaded *kch1* and *whi3* mutants are a source of false positives and are described further in the text.

Systematic Name	Common Name	Log2 Fold Change	padj	Individually Tested Phenotype	Newly Made Mutant Phenotype
YFL026W	STE2	3.70176	1.06E-71		No induction
YCL032W	STE50	3.52653	1.61E-90		Lower basal; lower induced (See Figure 3)
YJR087W*	YJR087W*	3.38461	2.78E-35		Lower basal; lower induced
YNL197C	WHI3	2.82035	6.48E-52	Very low basal; modest induction	Lower basal; lower induced
YJL157C	FAR1	2.72306	5.50E-40	Wild-type	
YOR246C	ENV9	2.28854	2.38E-31	Lower basal	Lower basal
YHL007C	STE20	2.22878	5.57E-21		Lower basal; lower induced (See Figure 3)
YIL043C	CBR1	2.05992	1.50E-34	Lower basal	Lower basal
YIL116W	HIS5	1.97992	3.66E-31	Wild-type	
YJR054W	KCH1	1.97460	1.15E-27	Lower basal; lower induced	Wild-type
YDR410C	STE14	1.95821	1.04E-58		Lower basal
YOR144C	ELG1	1.90017	6.74E-18		
YIL055C	YIL055C	1.89938	5.08E-50	Wild-type	
YIL101C	XBP1	1.84533	2.22E-33	Wild-type	
YIL123W	SIM1	1.83481	2.55E-10	Wild-type	
YCL060C	YCL060C	1.82481	2.66E-06		
YDR181C	SAS4	1.69610	1.83E-06		
YMR052W	FAR3	1.67344	3.96E-12	Wild-type	
YIL160C	POT1	1.64078	4.15E-15	Wild-type	
YJL142C	IRC9	1.63983	5.73E-07		
YBL039C	URA7	1.63740	7.54E-11		
YDL021W	GPM2	1.61446	1.54E-07	No induction	Wild-type
YNL127W	FAR11	1.60648	9.23E-07		
YDR102C	YDR102C	1.57243	2.46E-25		
YIL111W	COX5B	1.56441	1.51E-17	Wild-type	
YHR108W	GGA2	1.55728	2.92E-13		
YMR029C	FAR8	1.55177	1.21E-05	Wild-type	
YOR083W	WHI5	1.54981	3.60E-15	Wild-type	
YGL032C	AGA2	1.54217	1.21E-08	Wild-type	