

Supplementary Table 1

Position of putative transcription factor binding sequences present in the PHO89 promoter
Higher probability sequences are denoted in bold.

factor	start	end	sequence	weight	Pvalue	ln(Pval)
Crz1	-620	-612	CGAAGCCAG	6.1	4.8e-04	-7.642
Mig1/2	-584	-578	CACCCGC	4.5	8.3e-04	-7.094
Crz1	-555	-547	TCGCGCCAC	6.8	2.8e-04	-8.181
Crz1	-513	-505	CACAGCCAC	8.6	2.0e-05	-10.820
Mig1/2	-466	-460	CCCCACG	8.4	7.5e-05	-9.498
Pho4	-464	-457	CAACGTGG	7.3	1.6e-04	-8.740
Nrg1/2	-440	-429	TTAAGGGCCCAC	8.8	1.3e-05	-11.251
Pho4	-324	-317	CCACGTGC	10.3	1.3e-05	-11.251
Crz1	-275	-267	CACAGCCAC	8.6	2.0e-05	-10.820
Nrg1/2	-265	-254	AGAAGGATCCAA	0.4	9.4e-04	-6.970
Crz1	-166	-158	CTAAGCCCG	6.4	3.8e-04	-7.875