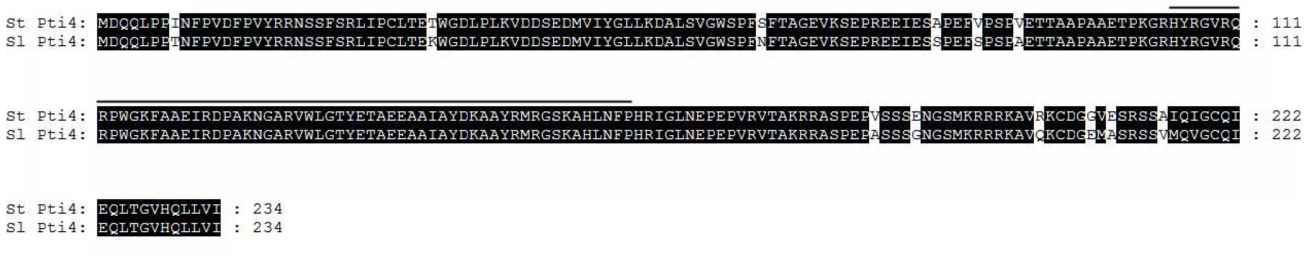
Supplemental Data González-Lamothe et al. (2008) The Transcriptional Activator Pti4 Is Required for the Recruitment of a Repressosome Nucleated by Repressor SEBF at the Potato *PR-10a* Gene



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St Pti4: MDQQLPPINFPVDFPVYRRNSSFSRLIPCLTETWGDLPLKVDDSEDMVIYGLLKDALSVGWSPFSFTAGEVKSEPREEIESAPEFVPSPVETTAAPAAETPKGRHYRGVRQ : 111
Sl Pti4: MDQQLPPTNFPVDFPVYRRNSSFSRLIPCLTEKWGDLPLKVDDSEDMVIYGLLKDALSVGWSPFNFTAGEVKSEPREEIESSPEFSPSPAETTAAPAAETPKGRHYRGVRQ : 111

St Pti4: RPWGKFAAEIRDPAKNGARVWLGTYETAEEAAIAYDKAAYRMRGSKAHLNFPHRIGLNEPEPVRVTAKRRASPEPVSSSENGSMKRRRKAVRKCDGGVESRSSAIQIGCQI : 222
Sl Pti4: RPWGKFAAEIRDPAKNGARVWLGTYETAEEAAIAYDKAAYRMRGSKAHLNFPHRIGLNEPEPVRVTAKRRASPEPASSSGNGSMKRRRKAVQKCDGEMASRSSVMQVGCQI : 222

St Pti4: EQLTGVHQLLVI : 234
Sl Pti4: EQLTGVHQLLVI : 234
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Supplemental Figure 1. Protein Sequence Alignment between Tomato and Potato Pti4.

Protein sequence comparison between potato St Pti4 and tomato Sl Pti4 was performed using CLUSTALW software (Thompson et al., 1994) and edited using the GeneDoc program. Black shading indicates that a residue is conserved in both sequences. The bar above the sequences indicates the position of the ERF motif.

Nicolas, K.B., and Nicolas, H.B. GeneDoc: a tool for editing and annotating multiple sequence alignment; http://www.psc.edu/biomed/genedoc.

Thompson, J.D., Higgins, D.G., and Gibson, T.J. (1994). CLUSTAL W: Improving the sensitivity of progressive multiple sequence alignment through sequence weighting, position-specific gap penalties and weight matrix choice. Nucleic Acids Res. **22,** 4673-4680.

		Exp 1	Exp 2	Exp 3	Average 2EΔCt	SD 2EΔCt
WT-U Why1	PR10 Ct	31.37804	29.33421	30.24562		
	Actin Ct	35.25327	33.77821	34.89632		
	ΔCt	3.87523	4.444	4.6507		
	2EΔCt	14.67	21.77	25.11	**20.51666667**	**5.331653902**
WT-U SEBF	PR10 Ct	21.64085	22.55351	22.40737		
	Actin Ct	32.89126	33.98562	35.01739		
	ΔCt	11.25041	11.43211	12.21002		
	2EΔCt	2436.19	2763.17	4737.86	**3312.406667**	**1245.257758**
WT-U Pti4	PR10 Ct	20.93902	19.62159	23.42584		
	Actin Ct	32.87523	31.71806	34.82645		
	ΔCt	11.93621	12.09647	11.40061		
	2EΔCt	3918.84	4379.26	2703.5	**3667.2**	**865.7568432**
WT-W Why1	PR10 Ct	24.85135	23.68054	23.94752		
	Actin Ct	35.37766	35.00201	34.88123		
	ΔCt	10.52631	11.32147	10.93371		
	2EΔCt	1474.81	2559.12	1956.03	**1996.653333**	**543.2952562**
WT-W SEBF	PR10 Ct	24.11711	29.48868	27.96593		
	Actin Ct	30.89002	35.99157	34.6655		
	ΔCt	6.77291	6.50289	6.69957		
	2EΔCt	109.36	90.69	103.94	**101.33**	**9.604754031**
WT-W Pti4	PR10 Ct	26.55533	22.76632	28.28434		
	Actin Ct	33.4583	29.76921	34.98715		
	ΔCt	6.90297	7.00289	6.70281		
	2EΔCt	119.67	128.26	104.17	**117.3666667**	**12.20905538**
WT-E Why1	PR10 Ct	17.16795	24.05903	22.54951		
	Actin Ct	28.96348	35.85911	35.00561		
	ΔCt	11.79653	11.80008	12.4561		
	2EΔCt	3557.21	3565.97	5619.01	**4247.396667**	**1187.860066**
WT-E SEBF	PR10 Ct	23.66904	20.61982	27.91585		
	Actin Ct	30.15827	27.02021	34.6248		
	ΔCt	6.48923	6.40039	6.70895		
	2EΔCt	89.84	84.47	104.62	**92.97666667**	**10.43477998**
WT-E Pti4	PR10 Ct	28.50038	28.10748	27.93515		
	Actin Ct	34.48261	34.00731	33.95047		
	ΔCt	5.98223	5.89983	6.01532		
	2EΔCt	63.22	59.71	64.68	**62.53666667**	**2.554492774**
#5-U SEBF	PR10 Ct	24.18392	23.44011	24.22214		
	Actin Ct	28.45063	28.178	29.11998		
	ΔCt	4.26671	4.73789	4.89784		
	2EΔCt	19.25	26.68	29.81	**25.24666667**	**5.423949975**
#5-U Pti4	PR10 Ct	23.88816	29.83268	29.31684		
	Actin Ct	28.9902	35.23365	35.02943		
	ΔCt	5.10204	5.40097	5.71259		
	2EΔCt	34.35	42.25	52.44	**43.01333333**	**9.069125279**
#14-U SEBF	PR10 Ct	25.14659	28.36627	23.59425		
	Actin Ct	31.67782	35.05601	29.90337		
	ΔCt	6.53123	6.68974	6.30912		
	2EΔCt	92.49	103.23	79.29	**91.67**	**11.99104666**
#14-U Pti4	PR10 Ct	27.06047	27.3171	22.66439		
	Actin Ct	32.55657	33.38233	29.00446		
	ΔCt	5.4961	6.06523	6.34007		
	2EΔCt	45.13	66.96	81.01	**64.36666667**	**18.08003411**

Supplemental Figure 2. Data from the ChIP Experiments of Figure 4B.

		Exp 1	Exp 2	Average 2EΔCt	SD 2EΔCt
PVX-00#1	PR10 Ct	16.55307	20.24065		
SEBF	Actin Ct	27.38911	31.56322		
	ΔCt	10.83604	11.32257		
	2EΔCt	1827.99	2561.14	**2194.565**	**518.4153366**
PVX-00#1	PR10 Ct	17.468	19.81824		
Pti4	Actin Ct	28.37006	31.44671		
	ΔCt	10.90206	11.62847		
	2EΔCt	1913.58	3166.05	**2539.815**	**885.6300302**
VIGS#1	PR10 Ct	28.6722	25.85549		
SEBF	Actin Ct	33.99715	30.68479		
	ΔCt	5.32495	4.82934		
	2EΔCt	40.08	28.43	**28.43**	**8.237794001**
VIGS#1	PR10 Ct	24.64282	22.32973		
Pti4	Actin Ct	29.11485	27.03207		
	ΔCt	4.47203	4.70234		
	2EΔCt	22.19	26.03	**24.11**	**2.71529004**
VIGS#2	PR10 Ct	28.14033	29.17724		
SEBF	Actin Ct	32.44661	32.97134		
	ΔCt	4.30628	3.7941		
	2EΔCt	19.78	13.87	**16.825**	**4.179001077**
VIGS#2	PR10 Ct	27.30008	25.2324		
Pti4	Actin Ct	30.99789	28.15387		
	ΔCt	3.69781	2.92147		
	2EΔCt	12.98	7.58	**10.28**	**3.818376618**

Supplemental Figure 3. Data from the ChIP Experiments of Figure 6B.

Supplemental Table 1. Sequence of the Primers Used for Constructing the Protein Fusions Analyzed in Yeast Two-Hybrid Assays.

Oligonucleotide name	**Sequence (5’-3’)**
Oligo 1 (SEBF fragments 1 to 4) sense	TTTTGTTCGGATCCTAACCCTTTC
Oligo 2 (SEBF fragments 5 to 7) antisense	CTCCTGGACCCTCGAGCCTTTTCTC
Oligo 3 (SEBF fragments 1 and 10) antisense	GACGAGCTCGAGCTCAATTACACGGATG
Oligo 4 (SEBF fragments 2 and 9) antisense	ACGTAGACTCGAGTGGATCAGTCCATACTC
Oligo 5 (SEBF fragments 3 and 8) antisense	GGCTCGAGCTGGCCCTCAATTCACCCTCAG
Oligo 6 (SEBF fragment 4) antisense	CAAAGACTCGAGGGTCTCAATTGGCATTAC
Oligo 7 (SEBF fragments 5, 8, 9 and 10) sense	ATGGGATCCTGACCTTAAAATCTTTGTTG
Oligo 8 (SEBF fragment 6) sense	GGGATCCCTGGGCCAGCACCACCCAAAAG
Oligo 9 (SEBF fragment 7) sense	GGGAGGATCCACAGTTCCAACAGAGTCTAC
Oligo 14 (Pti4 fragments 1 to 3) sense	GATATACTCGAGGATCAACAGTTACCAC
Oligo 15 (Pti4 fragments 4 to 7) antisense	GTGCTCGAGTCAGACCAATAGTTGATG
Oligo 16 (Pti4 fragments 1, 8 to 10) antisense	CATTCAACTCGAGCCGTCACGGGAAATTC
Oligo 17 (Pti4 fragment 2) antisense	GTCTAACTCGAGTTCAATGTCTTCCCTTC
Oligo 18 (Pti4 fragment 3) antisense	CACCGGCTCGAGTACTCATTCAGGCGCTG
Oligo 19 (Pti4 fragments 4 and 8) sense	ATCCCCTGTGAATTCGAAACATGGGGAG
Oligo 20 (Pti4 5 fragments and 9) sense	GCGCCTGAATTCGTACCTTCTCCGGTG
Oligo 21 (Pti4 fragments 6, 10 and 11) sense	GAAGGGAGAATTCTATAGAGGCGTTAGAC
Oligo 22 (Pti4 fragment 7) sense	CACATTTGGAATTCCCGCACCGGATC
Oligo 23 (Pti4 fragment 11) antisense	GTTTCCTCGAGCCGTTTCACGACGAGCTTAC