

Supplemental Table S1: Matrix showing the percent identity between the three protein alignments in Figure S1.

	<i>C. reinhardtii</i> AAB97101	<i>P. tricornutum</i> Phatr3_EG00333	<i>P. multistriata</i> VEU40048.1
<i>C. reinhardtii</i> AAB97101.1	100.0		
<i>P. tricornutum</i> Phatr3_EG00333	31.84	100	
<i>P. multistriata</i> VEU40048.1	34.63	49.88	100

Alignments were made with the MUSCLE algorithm. Numbers represent the percent identical residues between the alignments.