Table S1: Confirmation of ActR protein expression in *R. lacicola* by MS. The band marked ActR in panel 3B, lane 1, was subjected to tryptic digestion. The fragments produced were analyzed by mass spectrometry, and the protein identification was made based on a database match of 95% confidence or greater, including four MSMS matches with >99% confidence to *R. lacicola* actinorhodopsin protein.

Table S2: Predicted carotenoid biosynthetic genes and gene products from the sequence genome of *R. lacicola*. Two separate pathways are predicted, both of which are hypothesized to produce C50 carotenoids.

Figure S1: Full sized agarose and polyacrylamide gels. (**A**) Expression of *actR* was analyzed by RT-PCR. Lane marked L is the 100 bp DNA ladder, lanes with numbers and letters are the day cells were harvested (day 3, 5, 7, or 10), and whether they were grown in the light (L) or dark (D). The partial *actR* transcript was present in both the light and dark cultures at all time points (top set of wells, RT+). No genomic DNA contamination was detected in any sample (bottom set of wells, RT-). (**B**) Expression of *rpoB* was monitored by RT-PCR as a loading control. Lanes are labeled in the same way as panel A. The partial *rpoB* transcript was present in both the light and dark cultures at all time points (top set of wells, RT+). No genomic DNA contamination was detected in any sample (bottom set of wells, RT-). (**C**) ActR protein expression. Second lane - protein present in *R. lacicola* membrane fractions. Fourth lane - positive control of protein from *E. coli*/pRET04/pTAR membrane preparations. Seventh lane – Perfect Protein molecular weight marker.

Calc. Mass	Obs. Mass	± da	± ppm	Start Seq.	End Seq.	Sequence
959.5269	959.5251	-0.0018	-2	113	121	AAQSSILNR
1278.694	1278.6653	-0.0287	-22	223	234	EVGYSIADILAK
1425.7922	1425.77	-0.0222	-16	235	246	CLFGLIIYSIAR
1425.7922	1425.7722	-0.02	-14	235	246	CLFGLIIYSIAR
1772.9615	1772.92	-0.0415	-23	122	139	LVPAAAAMIVLGYPGDAK
1772.9615	1772.9221	-0.0394	-22	122	139	LVPAAAAMIVLGYPGDAK
2100.0947	2100.0696	-0.0251	-12	47	65	IAVMVSATVTAIAAYHYFR
2100.0947	2100.0701	-0.0246	-12	47	65	IAVMVSATVTAIAAYHYFR
2723.158	2723.1399	-0.0181	-7	66	89	MFDNFSHAFAGAENNPDAYNVGYR
2723.158	2723.1438	-0.0142	-5	66	89	MFDNFSHAFAGAENNPDAYNVGYR

Locus	Hypothesized gene product and function
Rhol_00010860	CrtB - phytoene synthase
Rhol_00010870	CrtI - phytoene desaturase (lycopene-forming)
Rhol_00010880 Rhol_00010890	C50 carotenoid cyclase
Rhol_00010900	Lycopene elongase
Rhol_00000870	CrtD - 1-hydroxycarotenoid 3,4-dehydrogenase
Rhol_00000880	Lycopene elongase

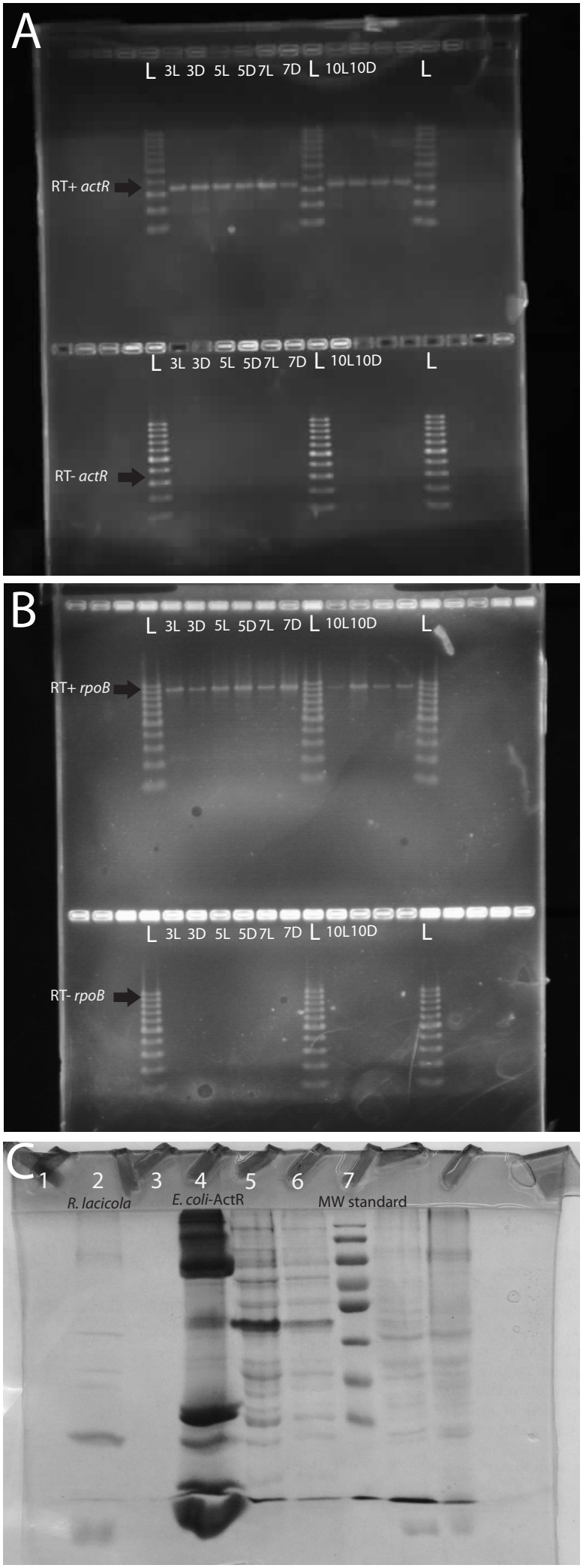

Figure S1. (A) full gel of actR RT-PCR. RT(+) in top set of wells, RT(-) in bottom set of wells. (B) full gel of rpoB RT-PCR. RT(+) in top set of wells, RT(-) in bottom set of wells. (C) full gel of ActR SDS-PAGE.