

Supplemental Figure S1. Predicted protein product of *orf641*

(A) Amino acid sequence of Orf641

MDKDKKS PDKDKKSPFSKKVWKK APKQPNI GKKEPNI GPKEPYI GPKEPYA
GQKQLNV GQKQLNV GQKQPNI GQKQPNI GPKEPYV GQKQLNV GQKQPNI
GQKQPNI GPKEPYV GQKQLNV GQKQANI GKKEPNI GPKEPYA GQKQLNV
GQKQLNV GQKQPNI GQKQPNI GPKEPYV GQKQLNV GQKQPNI GQKQPNI
GPKEPYV GQKQLNV GQKQPNI GKKEPYV GPKEPYV GQKQLNV GQKQPNI
GKKEPYV GPKEPYV GQKQLNV GQKQANI GQKQPNI GQKQPNI GPKEPNI
GKKPPNL GQKQANI GQKQPNI GQKQPNI GQKQPYI GKKEPYV GPKEPYV
GQKQLNI GKKQANI SPKQANI GPKQPNI GKKPPNI SPKQPNL GKKPPNL
GPKQPYV GKKQANI GKMKPYI GKMEPYV GKKQPNV GQKQPYI GQKPPYI
GKMESNV GQKQPNV GQKQPNV GQKQPYI GQKQPNV GQKQPNV GQKQPYI
GQKQPNV GQKQPYI GQKSPYI SKKSPYI SKKSPYI SKKSPYI VKKRK
KGKRPFRI RCPQIKSGDQISYRNVRLINKFLSRKTAEIFPRRITKLTFKQQRLLS
SAIKQARILSLLPFFKYPEKRFTKDQKRFFKDKTRFKKYKKRRIQKT

N-terminal region containing 73 copies of repeat with GQKQPNI consensus sequence is shown in yellow. Rps18-like region is shown in grey.

(B) Consensus sequence of the repeat

Position	1	2	3	4	5	6	7
Number of occurrences	G-67; S-5; A-1	Q-40; K-17; P-16	K-70; M-3	Q-46; E-18; S-4; P-4; K-1	P-52; L-11; A-6; S-4	N-47; Y-26	I-39; V-29; L-3; A-2



(C) Alignment of amino acid sequences of Rps18-like region of Orf641 of *Drosera rotundifolia* and 86 a.a. long consensus sequence of chloroplast Rps18 domain (CHL00077)

Orf641 1 MDKDKKS--KGKRPFRI RCPQIKSGDQISYRNVRLINKFLSRKTAEIFPRRITKLTFKQQR 59
MDK K+ K KR FR R P I+SGD+I Y+N+ L+++F+S + +I RR+T+LT KQQR
1 MDKSKRPFRKSKRSFRRRLPPIQSGDRIDYKNMSLLSRFIS-EQGKILSRRVTRLTLKQQR 60
Orf641 60 LLSSAIKQARILSLLPFFKYPEKRFTKDQKRFFKDKTRFKKYKKRRIQKT
L++ AIKQARILSLLPF EK+F +
61 LITKAIKQARILSLLPFLNN-EKQFER 86

Rps18-like region in Orf641 is shown in grey.