



Figure S1. Visualization of the synteny relationship between *P. vulgaris* and *G. max*. The synteny relationship between *P. vulgaris* and *G. max* is shown for four chromosomes of *P. vulgaris* (Chr1, Chr4, Chr7 and Chr9). Each chromosomal fragment of *G. max*, linked to the *P. vulgaris* chromosome, is situated next to the *P. vulgaris* chromosome and the start and end of each fragment is shown in megabase pairs. The chromosomal location of the galactinol- and RFO synthase genes of *P. vulgaris* and *G. max* is shown underneath the genetic linkage map. The figure is adapted from McClean *et al.* (2010) [61].

Table S1. Overview of the enzymes used for the identification of the galactinol- and RFO synthase genes in *P. vulgaris* and *G. max*. The amino acid sequences of these enzymes have also been used to build the phylogenetic trees shown in Figures 1 and 2.

Species	Accession number	Name	Function	Protein length (AA)	Reference
<i>Arabidopsis thaliana</i>	AT2G47180.1	AtGolS1	Galactinol synthase	344	Taji <i>et al.</i> (2002)
	AT1G56600.1	AtGolS2		335	Taji <i>et al.</i> (2002)
	AT1G09350.1	AtGolS3		334	Taji <i>et al.</i> (2002)
	AT1G60470.1	AtGolS4		334	Taji <i>et al.</i> (2002)
	AT5G23790.1	AtGolS5		333	Taji <i>et al.</i> (2002)
	AT4G26250.1	AtGolS6		336	Taji <i>et al.</i> (2002)
	AT1G60450.1	AtGolS7		332	Taji <i>et al.</i> (2002)
	AT5G30500.1	AtGolS10		328	Sun <i>et al.</i> (2013)
	AMP59727.1	CaGolS1		339	Salvi <i>et al.</i> (2018)
	AMP59729.1	CaGolS2		325	Salvi <i>et al.</i> (2018)
<i>Arabidopsis thaliana</i>	NP_198855.1	AtRS	Raffinose synthase	783	Egert <i>et al.</i> (2013)
<i>Pisum sativum</i>	CAD20127.2	PsRS		798	Peterbauer <i>et al.</i> (2002)
<i>Oryza sativa</i>	XP_015621501.1	OsRS		840	Li <i>et al.</i> (2007)
<i>Zea mays</i>	NP_001354805.1	ZmRS		790	Li <i>et al.</i> (2017)
<i>Arabidopsis thaliana</i>	NP_192106.3	AtSS		857	Gangl <i>et al.</i> (2015)
<i>Vigna angularis</i>	CAB64363.1	VaSS	Stachyose synthase	857	Peterbauer <i>et al.</i> (1999)

<i>Arabidopsis thaliana</i>	OAP05273.1	AtSIP2		773	Shaun Peters <i>et al.</i> (2010)
	AAQ07251.2	ZmAGA1		756	Zhao <i>et al.</i> (2006)
<i>Zea mays</i>	NP_001105794.2	ZmAGA2	Alkaline α -galactosidase	843	Zhao <i>et al.</i> (2006)
	NP_001105775.2	ZmAGA3		747	Zhao <i>et al.</i> (2006)
<i>Cucumis melo</i>	AAM75139.1	CmAGA1		754	Carmi <i>et al.</i> (2003)
	AAM75140.1	CmAGA2		772	Carmi <i>et al.</i> (2003)
<i>Arabidopsis thaliana</i>	NP_191190.2	AtAGAL3		437	Imaizumi <i>et al.</i> (2017)
<i>Solanum lycopersicum</i>	AAF04591.1	SLAGAL	α -galactosidase	409	Tsaniklidis <i>et al.</i> (2016)
<i>Arabidopsis thaliana</i>	NP_001031855.1	AtAGAL2		370	Imaizumi <i>et al.</i> (2017)

Table S2. Primers used for qRT-PCR.

Accession number	Function	Forward Primer	Tm (°C)	Reverse Primer	Tm (°C)	Amplicon length (nt)
Phvul.001G215300	Galactinol synthase	5'CGCGTAGGAG ATGACTTTG ^{3'}	60.5	5'GCACATGGG TGAGTAGATTG ^{3'}	60.4	103
Phvul.001G223700	Galactinol synthase	5'ACAGTGCCCTA ATAAAGTCAG ^{3'}	60.4	5'GTCAGAAA GTCCTGCTCAG ^{3'}	60.2	168
Phvul.007G203400	Galactinol synthase	5'GAATTGGGA GTTGTGGAG ^{3'}	58.9	5'AGAACAGTTAT CAGGCAAGTC ^{3'}	59.6	161
Phvul.004G007100	Raffinose synthase	5'GACAATATT CGGTGTGCGT ^{3'}	61	5'TAGAACGGTTGA AGCTTCCC ^{3'}	60.9	155
Phvul.009G175400	Raffinose synthase	5'GACCCATTAC GTTAGTGATTGTG ^{3'}	61.8	5'CACCTGTATGTT TGTTGAGATTCC ^{3'}	61.8	131
Phvul.001G214300	Stachyose synthase	5'CTCATTAAGAAG CTTGTCTTCCC ^{3'}	61.1	5'CTCCTCCATACT TATTGAAGTTCC ^{3'}	60.5	144
CV530631 (Pereira <i>et al.</i> , 2017)	β -Tubulin	5'CCGTTGTGGA GCCTTACAAT ^{3'}	62.4	5'GCTGGGGTC CTGAAACAA ^{3'}	62.4	117