



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) |

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|-----------------------------|----------------|---------|----------------------------------|-----|-----------------------------------|
| <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'CTCATTAAGAAC 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 |