Table 1 Suppl. Primers used for qPCR analysis (F - forward, R - reverse).

Gene ID	Gene Name	Function	Primes (5′−3′)
C41346-g1	*E2.4.1.13*	sucrose synthase family protein	F: CACGAGTCAGGTGGCGAAG R: CAATCTGGTGGTGTTGGAG
C70619-g1	*UXS1*	UDP-xylose synthase 4 family protein	F: CATTCGTTACCTGCTTCTC R: CGATCACGTTATCTCCTC
C65600-g1	*glgA*	glycogen synthase family protein	F: CCTGTGAGAGCTACAGCTG R: CTGGTACCTCATCTGCAG
C66251-g1	*GAUT*	glycosyl transferase family 8	F: CAGTTGACTCCATTGATGG R: GTATGCTACTTGACGCAAC
C70726-g1	*XYL4*	beta-glucosidase family protein	F: TCTGTAACACGTCGTTAG R: CTGGGGTCTCGAAATATG
C56919-g1	*UGDH*	UDP-glucose dehydrogenase	F: ACATCTGCGAGTGCAATGG R: TGCCACTCTTCGGCTGGAG
Reference	*UBQ-L*	polyubiquitin 4 like	F:TGAGGCTTAGGGGAGGAACT R:TGTAGTCGCGAGCTGTCTTG

Table 2 Suppl. Correlation of expression of genes involved in saccharide metabolism during embolized xylem vessels refilling and osmotic potential of xylem sap in *Salix. matsudana*. ∗ and ∗∗ - correlation significant at $P < 0.05$ and $P < 0.01$, respectively.

Gene names	Unigene ID	Description	Correlation coefficients
UXS1	*c95333_g1*	UDP-glucuronic acid decarboxylase	-0.783*
UXS1	*c70619_g1*	UDP-xylose synthase 4 family protein	-0.956**
UGDH	*c55418_g1*	UDP-glucose 6-dehydrogenase family protein	-0.966**
BGLU40	*c67131_g1*	hydroxyisourate hydrolase family protein	-0.913**
β-amylase	*c69220_g1*	beta-amylase 1	0.524
E3.1.1.11	*c68272_g1*	pectinesterase family protein	-0.527
UG3	*c62946_g1*	UDP-D-glucuronate 4-epimerase 1 family protein	0.597
PPE8B	*c66969_g1*	pectinesterase inhibitor PPE8B	-0.988**
glgA	*c65600_g1*	glycogen synthase family protein	-0.774*
UG1	*c69293_g2*	UDP-D-glucuronate 4-epimerase 6 family protein	-0.957**
PMEpcrA	*c62377_g1*	pectin methylesterase family protein	-0.876*
XYL4	*c70726_g1*	beta-glucosidase family protein	-0.985**
sacA	*c63969_g1*	beta-fructofuranosidase, insoluble isoenzyme CWINV1	-0.358
HK	*c70420_g1*	hexokinase family protein	-0.873*
E2.4.1.13	*c41346_g1*	sucrose synthase family protein	-0.88*
GAUT	*c66251_g1*	glycosyl transferase family 8	-0.852*
TPS	*c95022_g1*	glycosyl transferase family 20 family protein	0.584
E2.4.1.14	*c70790_g1*	sucrose-phosphate synthase family protein	0.840
GAUT	*c66017_g1*	galacturonosyltransferase 15	-0.840*
UGDH	*c56919_g1*	UDP-glucose dehydrogenase	-0.886**

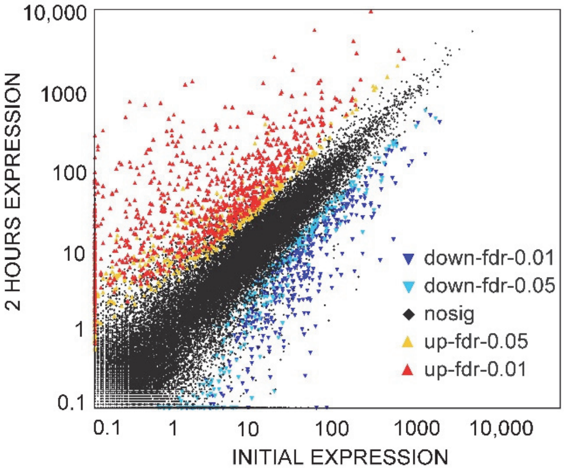

Fig. 1 Suppl. The differential expressions of genes at the beginning and after 2-h soaking. The horizontal and vertical coordinates represent the expression of the genes in the two samples (FPKM value), each point represents a specific gene. The horizontal coordinate value was the expression of the gene in the initial sample, and the vertical coordinate value was the expression of the gene in the treated sample. The red dot indicates the significantly up-regulated gene which the screening thresholds of FDR(false discovery rate) $\leqslant 0.01$, the yellow dot indicates the significantly up-regulated gene which the screening thresholds of FDR ≤ 0.05, the dark blue dot indicates the significantly down-regulated gene which the screening thresholds of FDR ≤ 0.01, the light blue dot indicates the significantly down-regulated gene which the screening thresholds of FDR ≤ 0.05 and the black point indicates the non-significant difference genes. The closer the gene was to zero, the lower the expression was, and the greater the degree of deviation from diagonal, the greater the difference in expression between the two samples.

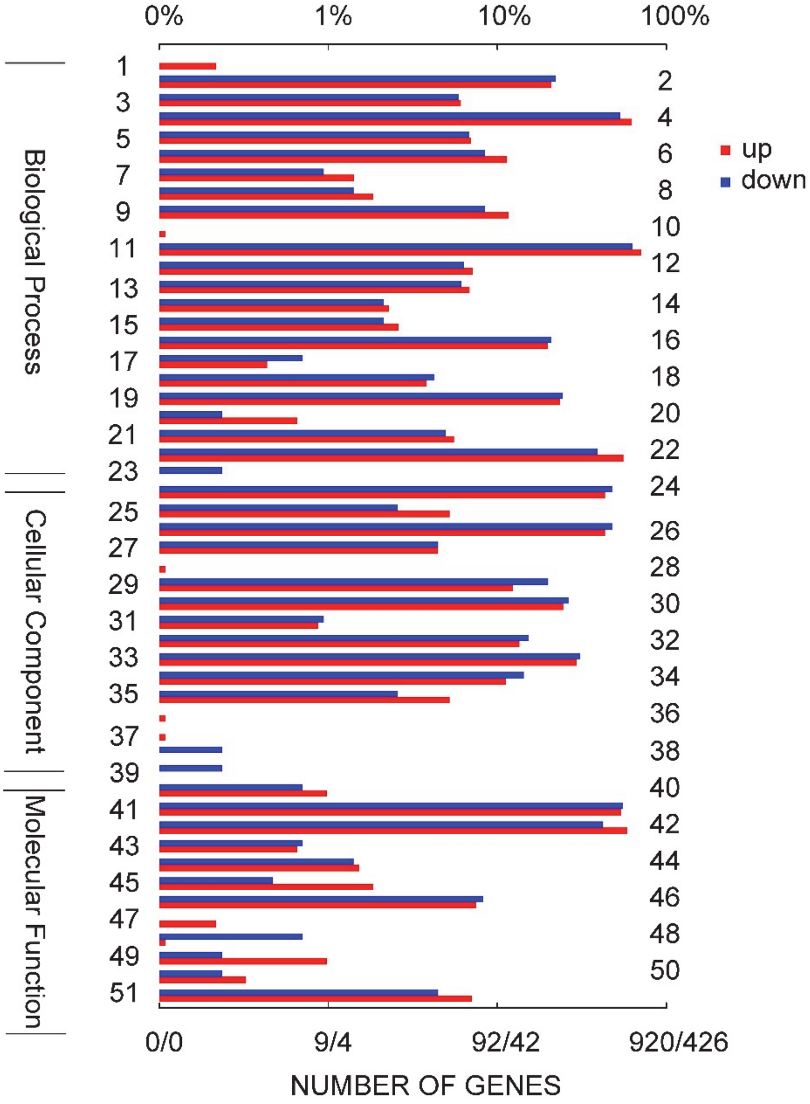

Fig. 2 Suppl. Gene ontology (GO) classification of unigenes: 1 - biological adhesion; 2 - biological regulation; 3 - cellular component organization or biogenesis; 4 - cellular process; 5 - developmental process; 6 - establishment of localization; 7 - growth; 8 - immune system process; 9 - localization;10 - locomotion; 11 - metabolic process; 12 - multicellular organismal process; 13 - multi-organism process; 14 - negative regulation of biological process; 15 - positive regulation of biological process; 16 - regulation of biological process; 17 - reproduction; 18 - reproductive process; 19 - response to stimulus; 20 - rhythmic process; 21 - signaling; 22 - single-organism process; 23 - cell killing; 24 - cell; 25 - cell junction; 26 - cell part; 27 - extracellular region; 28 - extracellular region part; 29 - macromolecular complex; 30 - membrane; 31 - membrane-enclosed lumen; 32 - membrane part; 33 - organelle; 34 - organelle part; 35 - symplast; 36 - virion; 37 - virion part; 38 - extracellular matrix; 39 - nucleoid; 40 - antioxidant activity; 41 - binding; 42 - catalytic activity; 43 - electron carrier activity; 44 - enzyme regulator activity; 45 - molecular transcription factor activity; 46 - nucleic acid binding transcription factor activity; 47 - nutrient reservoir activity; 48 - protein binding transcription factor activity; 49 - receptor activity; 50 - structural molecule activity; 51 - transporter activity.

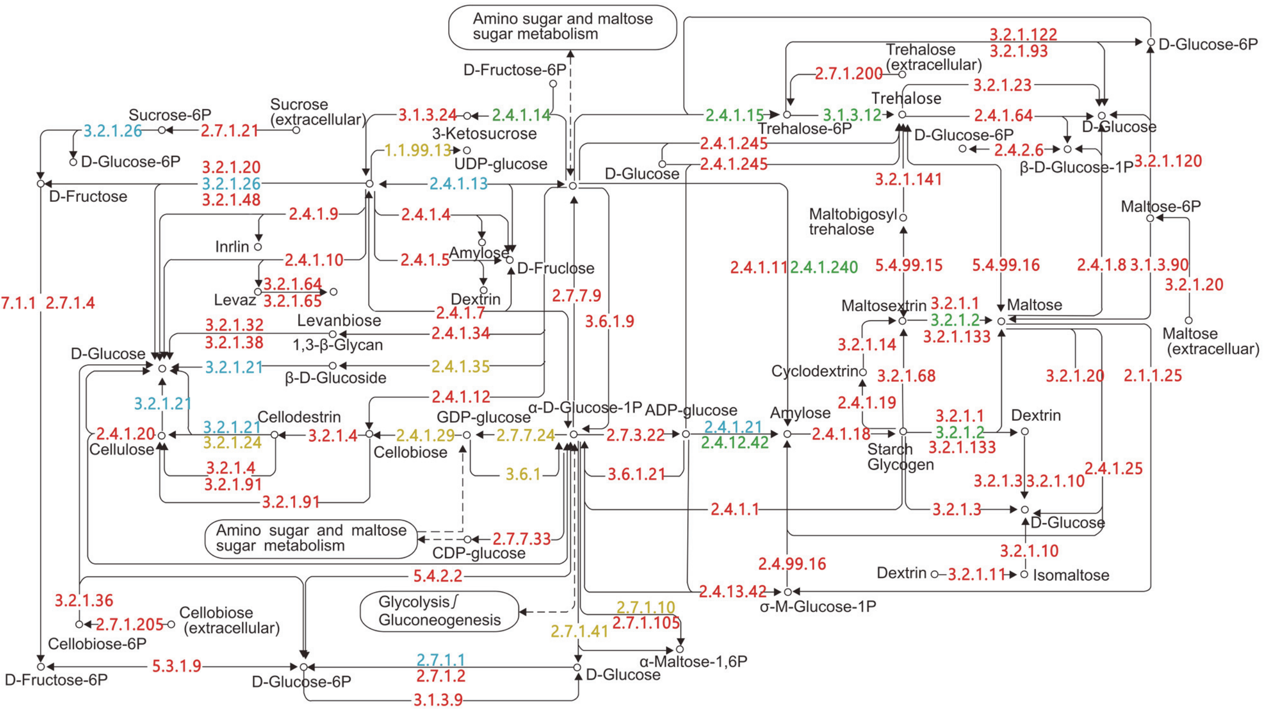

Fig. 3 Suppl. Saccharide metabolism pathways in *Salix matsudana.* The general starch and sucrose metabolism pathways were generated from the *KEGG* pathway, which outlines the steps involved in starch and sucrose metabolism. The numbers represent the standardized international numbers of enzymes in the pathways. The *red font* denotes enzyme genes belonging to the *KEGG ORTHOLOGY* (*KO*) classification system, while the *yellow font* denotes those which are not including in *KO*. The differently expressed genes which were sequenced were marked with *blue* and *green font*. *Blue* means up-regulation genes and *green* represents down-regulation genes.