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**Fig. S1** Transmission electron micrographs (TEM) of typical normal cell and plasmolyzed cell of the *Brassica napus* genotype ‘W10’ suspension cells. (A) Growth performance of normal cells. Scale bar, 1 μm. (B) Representative cell presented plasma membrane retracting from cell wall (indicated by the arrow) with abnormal organelles. Scale bar, 2 μm.

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**Fig. S2** Atomic force microscopy (AFM) deflection and height images of the cell and cell wall (CW) of the *Brassica napus* cultivar ‘W10’ under suspension cell system. CWs were extracted from suspension cells of rapeseed cultivated in the medium containing 50 μM B for 12 d. Images, 5×5 μm.

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**Fig. S3** Root system architecture variation of the *Brassica napus* genotypes ‘QY10’ and ‘W10’ seedlings after a long-term (12 d) hydroponic culture in 0.2 and 25 μM B. (A) Root growth performance taken by a scanner. (B) Root tips number. (C) Total root length. (D) Root average diameter. (E) Total surface area and (F) Total root volume of two genotypes. Bars denote the means (n = 6), and error bars denote the standard error (SE). Different letters show significant difference at *P* < 0.05 (Duncan's test).

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**Fig. S4** Fourier-transform infrared spectra (FT-IR) of the cell wall (CW) and cell wall without pectin (CW-P) of the *Brassica napus* genotypes ‘QY10’ and ‘W10’ suspension cells cultured in 0.1, 0.25, 50 μM B, respectively. (A) FT-IR of the CW. CWs mainly contain pectin in 1740: C=O stretching vibration of alkyl ester, 1630: COO- symmetric bending, 1400: COO- symmetric bending, 1320: Ring vibration, 1243: C-O stretching and 1046: O-C-O asymmetric stretching, hemicelluloses (895, 944, 1042, 1075, 1130, 1370 cm-1), cellulose (895, 1030, 1160, 1370, 1426 cm-1), and a small amount of protein (1550, 1650 cm-1)(He *et al*. 2015). (B) FT-IR of the CW-P. Compared with the result of CW, the characteristic peak of pectin in CW-P was significantly weakened or vanished. Lines denote the means (n = 3).

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**Fig. S5** Plant growth performance and pectin concentrations in the leaves of the *Brassica napus* genotypes ‘QY10’ and ‘W10’. The plants were treated with 25 and 0.2 μM B under hydroponic culture system for 12 d, respectively. (A) Growth performance of ‘QY10’ and ‘W10’. A typical B-deficient symptom of curved leaves was indicated in the red box. Scale bar: 5 cm. (B) Pectin concentrations in the leaves of ‘QY10’ and ‘W10’. Values denote the mean (n=4), and error bars denote the standard error (SE). Different letters show significant difference at *P* < 0.05 (Duncan'stest).

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**Fig. S6** Quantitative real-time PCR results of the genes related to pectin biosynthesis in the leaves of the *Brassica napus* genotypes ‘QY10’ and ‘W10’. The plants were treated with 25 and 0.2 μM B under hydroponic culture systems for 12 d, respectively. The expression level of the indicated gene of ‘QY10’ in 25 μM B is set to 1. Bars denote the means (n = 3), and error bars denote the standard error (SE). Different letters show significant difference for the same gene among the treatments at *P* < 0.05 (Duncan's test).

**Table S1** Solution compositions of different culture medium

**B5 medium**

|  |  |
| --- | --- |
| Component | Concentration（mg L-1） |
| (NH4)2SO4 | 134 |
| KNO3 | 2500 |
| CaCl2·2H2O | 150 |
| MgSO4 | 122 |
| NaH2PO4 | 130.4 |
| ZnSO4·7H2O | 2 |
| H3BO3 | 3 |
| KI | 0.75 |
| Na2MoO4·2H2O | 0.25 |
| CuSO4·5H2O | 0.025 |
| CoCl2·6H2O | 0.025 |
| MnSO4·H2O | 10 |
| Thiamine Hydrochloride | 10 |
| Pyridoxine hydrochloride  Nicotinic acid  Myo-inositol | 1  1  100 |
| Na2EDTA | 37.25 |
| FeSO4·7H2O | 27.85 |
| Sucrose | 30,000 |
| Agar | 8,000 |

**Induction and subculture medium**

|  |  |
| --- | --- |
| Component | Concentration（mg L-1） |
| (NH4)2SO4 | 134 |
| KNO3 | 2500 |
| CaCl2·2H2O | 150 |
| MgSO4 | 122 |
| NaH2PO4 | 130.4 |
| ZnSO4·7H2O | 2 |
| H3BO3 | 3 |
| KI | 0.75 |
| Na2MoO4·2H2O | 0.25 |
| CuSO4·5H2O | 0.025 |
| CoCl2·6H2O | 0.025 |
| MnSO4·H2O | 10 |
| Thiamine Hydrochloride | 10 |
| Pyridoxine hydrochloride  Nicotinic acid  Myo-inositol | 1  1  100 |
| Na2EDTA | 37.25 |
| FeSO4·7H2O | 27.85 |
| Casein hydrolysate | 300 |
| L-Proline | 500 |
| Sucrose | 30,000 |
| 2,4-dichlorophenoxyacetic acid | 2.5 |
| 6-Benzyl aminopurine | 0.5 |
| Citric acid | 0.1 |
| Agar | 8,000 |

**BA medium**

|  |  |
| --- | --- |
| Component | Concentration（mg L-1） |
| CaCl2·2H2O | 440 |
| KH2PO4 | 170 |
| MgSO4 | 180.5 |
| KCl | 2940 |
| KI | 0.83 |
| CoCl2·6H2O | 0.025 |
| H3BO3 | \* |
| Na2MoO4·2H2O | 0.25 |
| MnSO4·H2O | 16.9 |
| CuSO4·5H2O | 0.025 |
| ZnSO4·7H2O | 8.6 |
| myo-inositol | 100 |
| Thiamine Hydrochloride | 0.5 |
| Na2EDTA | 37.25 |
| FeSO4·7H2O | 27.85 |
| Glycine | 75 |
| L-Glutamine | 877 |
| L-Aspartic acid | 266 |
| L-Arginine | 228 |
| Sucrose | 25,000 |
| 2,4-dichlorophenoxyacetic acid | 3 |
| Citric acid | 0.1 |

\*Boron was added according to the experimental design.

**Table S2** Primer sequences used for quantitative real-time PCR

|  |  |
| --- | --- |
| Gene | Primer sequences |
| *BnaNIP5;1s*  *BnaA3.GAE1*  *BnaC7.GAE6* | F-5′-CACTCAAAGCAGTTTTCCATCCTTTC-3′  R-5′-AACTCAAGAGCAAAGGCTTGTCC-3′  F-5′-CTCAACGACGGTAAGCTCATGTCA-3′  R-5′-GCAAGTCTCGAGGAGGTTGACTAGG-3′  F-5′-TCTTCTCTTCCTCCTCCGCCTC-3′ |
|  | R-5′-TTGCTGTTGAGGATTGTCTCACG-3′ |
| *BnaCnn.GUT1*  *BnaKDSA1s*  *BnaAnn.BOR2* | F-5′-CTCAACCAGGGGATGCGTTTCAC-3′  R-5′-AGTCCAGTTCAACAGCTTCTCACCTGC-3′  F-5′-GATAAGGCTAACCGAACTTCT-3′  R-5′-TTCACACTGATACGCCTCA-3′  F-5′-CGACGACATTCACAGGGAATCTA-3′ |
| *BnaC4.BOR2* | R-5′-GCAACACATCCTCCAACCATTAA-3′  F-5′-CGAGACATTCACGGGAAATCTT-3′  F-5′-CAACACATCCTCCAACCATCAC-3′ |
| *Actin* | F-5′- ACAGTGTCTGGATCGGTGGTTC -3′  R-5′- TGCCTCATCATACTCAGCCTTG -3′ |

**Table S3** Genes involved in pectin biosynthesis and dRG-II-B crosslinking in *Brassica napus*

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| Gene name | | Gene ID | Physical locus | Description |
| *GAE* | *BnaCnn.GAE1* | BnaCnng70410D | chrCnn\_random:70436164-70437454 | GAE1, UDP-glucuronate 4-epimerase |
| *BnaA1.GAE1* | BnaA01g06610D | chrA01:3072465-3073755 | GAE1, UDP-glucuronate 4-epimerase |
| *BnaC4.GAE1* | BnaC04g08650D | chrC04:6487050-6487347 | GAE1, UDP-glucuronate 4-epimerase |
| *BnaA3.GAE1* | BnaA03g50170D | chrA03:26032819-26034296 | GAE1, UDP-glucuronate 4-epimerase |
| *BnaC7.GAE1* | BnaC07g42640D | chrC07:42041241-42042716 | GAE1, UDP-glucuronate 4-epimerase |
| *BnaAnn.GAE3* | BnaAnng18570D | chrAnn\_random:19851668-19853300 | GAE3, UDP-glucuronate 4-epimerase |
| *BnaA3.GAE4* | BnaA03g56770D | chrA03\_random:864404-865712 | GAE4, UDP-glucuronate 4-epimerase |
| *BnaC3.GAE4* | BnaC03g25270D | chrC03:14200552-14201860 | GAE4, UDP-glucuronate 4-epimerase |
| *BnaA2.GAE5* | BnaA02g21470D | chrA02:13831904-13833517 | GAE5, UDP-glucuronate 4-epimerase |
| *BnaC2.GAE5* | BnaC02g28500D | chrC02:27065179-27066777 | GAE5, UDP-glucuronate 4-epimerase |
| *BnaA9.GAE5* | BnaA09g21060D | chrA09:13803448-13805048 | GAE5, UDP-glucuronate 4-epimerase |
| *BnaC9.GAE5* | BnaC09g23320D | chrC09:20883995-20885613 | GAE5, UDP-glucuronate 4-epimerase |
| *BnaA1.GAE6* | BnaA01g23480D | chrA01:15848337-15850113 | GAE6, UDP-glucuronate 4-epimerase |
| *BnaC3.GAE6* | BnaC03g74010D | chrC03\_random:1980893-1982997 | GAE6, UDP-glucuronate 4-epimerase |
| *BnaCnn.GAE6* | BnaCnng44170D | chrCnn\_random:43279631-43281526 | GAE6, UDP-glucuronate 4-epimerase |
| *BnaA7.GAE6* | BnaA07g06190D | chrA07:6485582-6487302 | GAE6, UDP-glucuronate 4-epimerase |
| *BnaC7.GAE6* | BnaC07g07730D | chrC07:12297301-12298874 | GAE6, UDP-glucuronate 4-epimerase |
| *BnaA3.GAE6* | BnaA03g37120D | chrA03:18348695-18350683 | GAE6, UDP-glucuronate 4-epimerase |
| *GUT* | *BnaCnn.GUT1* | BnaCnng24560D | chrCnn\_random:22998310-23000506 | GUT1, glucuronyltransferase |
| *BnaA6.GUT1* | BnaA06g21350D | chrA06:14795886-14797694 | GUT1, glucuronyltransferase |
| *BnaA7.GUT2* | BnaA07g36650D | chrA07\_random:593088-594713 | GUT2, glucuronyltransferase |
| *BnaC3.GUT2* | BnaC03g57690D | chrC03:46909855-46912172 | GUT2, glucuronyltransferase |
| *BnaC7.GUT2* | BnaC07g11500D | chrC07:17070176-17072022 | GUT2, glucuronyltransferase |
| *BnaA8.GUT2* | BnaA08g18970D | chrA08:14699956-14702076 | GUT2, glucuronyltransferase |
| *KDSA1* | *BnaC2.KDSA1*  *BnaCnn.KDSA1*  *BnaA7.KDSA1*  *BnaC6.KDSA1* | BnaC02g25840D  BnaCnng62300D  BnaA07g20320D  BnaC06g19810D | chrC02:23113206-23116078  chrCnn\_random:62108676-62110984  chrA07:15959383-15962465  chrC06:21946765-21949920 | KDOP,3-deoxy-8-phosphooctulonate synthase  KDOP,3-deoxy-8-phosphooctulonate synthase  KDOP,3-deoxy-8-phosphooctulonate synthase  KDOP,3-deoxy-8-phosphooctulonate synthase |
| *BOR2* | *BnaAnn.BOR2* | BnaAnng31830D | chrAnn:36401392-36403419 | borate transmembrane transporter activity |
|  | *BnaC4.BOR2* | BnaC04g21390D | ChrC04:22286377-22289443 | borate transmembrane transporter activity |