Supplementary Fig 1. Sequence analysis of *TNO1*.

A. TNO1 DNA sequence

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TNO1      1  ATGCACGAGAAGGATGATCTTCCGCAGGATTCTATAGCTGATGGAATTGAGAATGATGAC 60
         61  GAGTCTAATGGGCAAGAAGAAGAAGAGCTTGATCCTGACCAGGGAACAGCTTTCGTTGAT 120
        121  AGTAAGGAAGATATGTTTGTTGATGCTCCTGAAGAGTTGAATTTTGATACACCTAGCAAG 180
        181  GAAGCTCTTACCACAGATGACGATGATAATGATGACCTTGGAACTCATTTCAATATTGAG 240
        241  AAGGGGGATTGGGAGAAGGAACTTGCAGGGCTTCAGGAGCAGTTTAAGCTGTTGACTGGT 300
        301  GAGAATGATTTGACAGGTGAAGATGGGAACACTACTGTGGATATTGTCAGTCGCTTCTCG 360
        361  AAGTTCTTAAAAACTGCCAAGGAAGAGCGGATTCAGCATGAGGTTGCACTCAAGGAGCTT 420
        421  CACGGGGTTATTAGTGGGAGGGACGATGAGATTGCTGATCTCACCACAAAAATCTCTGAG 480
        481  CTTTCTTCGTCGCAGCCGGTTTCCGAAATGGGTGATCAGGCACAGAACTTGGAGCACCTT 540
        541  GAGGCTGCAACGGATAGGATTATGGTTTCTCTTAGTAATGTATTTGGGGAAGGGGAGTTG 600
        601  CAGTATGGTTCTTCTATCTCTGAAAAGCTTGCTCATCTGGAGAACCGAGTTTCGTTTTTA 660
        661  GGTGCAAAGTATACTGAGTTTTACTATGGTGCTGATCAGTTAAGGAAGTGTTTGGCTAGT 720
        721  GATGTGTTGGATCTTAGTTTCCAAGAGGATTTTGGTTCAGCTCTTGGTGCTGCTTGTTCT 780
        781  GAGCTATTTGAGCTCAAACAGAAGGAAGCAGCCTTTTTTGAAGGACTTAGTCATCTAGAA 840
        841  GATGAGAATAGGAACTTTGTTGAACAAGTGAACAGAGAGAAAGAAATGTGTGAGTCAATG 900
        901  AGAACAGAATTTGAAAAATTGAAGGCAGAGCTTGAGCTAGAAAAGACTAAGTGTACTAAC 960
        961  ACAAAAGAAAAGCTCAGCATGGCCGTAACAAAGGGGAAGGCGTTAGTTCAGAACCGGGAT 1020
       1021  GCTCTGAAGCATCAATTGTCTGAAAAAACAACAGAGCTTGCGAATAGGTTGACTGAATTA 1080
       1081  CAAGAGAAGGAGATTGCCCTTGAAAGTTCTGAAGTAATGAAGGGGCAGCTGGAACAATCG 1140
       1141  TTAACCGAAAAGACGGATGAACTTGAGAAATGCTATGCTGAATTGAATGATAGGTCCGTA 1200
       1201  TCCCTGGAAGCATATGAGCTAACAAAGAAGGAGTTGGAACAGTCTCTGGCTGAAAAAACA 1260
       1261  AAAGAACTTGAAGAGTGTTTGACGAAACTACAAGAGATGTCAACAGCATTGGATCAATCT 1320
       1321  GAACTCGACAAAGGCGAGTTAGCAAAATCCGATGCTATGGTTGCATCATATCAGGAAATG 1380
       1381  TTATCGGTGAGGAACTCTATCATTGAAAATATTGAAACTATCCTGTCAAACATATATACA 1440
       1441  CCTGAAGAAGGTCACTCTTTTGATATCGTTGAAAAAGTAAGGTCACTTGCAGAAGAGAGG 1500
       1501  AAAGAGCTCACAAATGTTTCCCAGGAATACAACAGACTAAAAGATTTGATCGTTTCCATT 1560
       1561  GACTTACCAGAGGAGATGTCCCAATCCAGCTTAGAAAGTCGCCTAGCTTGGCTTAGAGAA 1620
       1621  TCTTTTCTCCAGGGAAAAGATGAAGTTAATGCCTTGCAAAACCGGATTGAAAGTGTAAGC 1680
       1681  ATGTCTCTTTCAGCAGAAATGGAGGAGAAAAGTAACATTAGAAAGGAACTGGATGATTTA 1740
       1741  AGTTTCAGTTTGAAAAAAATGGAGGAAACTGCAGAGCGAGGTTCGTTGGAGAGGGAGGAA 1800
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1801 ATTGTGAGGAGACTTGTGGAAACCTCTGGCTTGATGACAGAAGGAGTCGAAGATCATACT 1860

1861 TCTTCAGATATCAATTTACTTGTTGATAGATCATTCGACAAGATAGAAAAGCAAATCAGG 1920

1921 GATTCTAGTGATAGTTCTTATGGCAACGAAGAAATATTTGAAGCCTTTCAAAGTCTCCTT 1980

1981 TATGTGAGAGATCTGGAGTTTTCACTTTGTAAGGAAATGCTAGGAGAGGGAGAGCTGATT 2040

2041 AGCTTTCAGGTAAGCAATCTCTCAGATGAGCTAAAGATCGCATCTCAAGAACTTGCTTTC 2100

2101 GTGAAAGAAGAAAAAATTGCTTTGGAGAAAGATCTAGAGCGATCAGAGGAGAAATCTGCT 2160

2161 TTGCTCAGAGACAAACTTTCTATGGCTATCAAGAAAGGCAAGGGACTAGTCCAAGATAGG 2220

2221 GAAAAGTTTAAAACTCAGTTGGATGAGAAAAAATCTGAAATCGAAAAGCTGATGCTCGAG 2280

2281 TTGCAGCAGCTAGGTGGTACGGTTGATGGCTACAAGAATCAGATAGATATGTTATCGAGA 2340

2341 GACTTAGAGCGCACGAAAGAGCTAGAGACTGAGCTTGTTGCTACTAAAGAAGAAAGAGAT 2400

2401 CAACTTCAGCAATCCTTATCTCTAATTGACACGTTGTTGCAGAAAGTGATGAAATCAGTT 2460

2461 GAAATTATAGCTCTCCCTGTTGATCTAGCATCTGAAGATCCTTCAGAAAAGATTGACCGA 2520

2521 CTTGCTGGGTACATCCAAGAAGTGCAGCTGGCTAGAGTAGAGGAACAAGAAGAAATAGAA 2580

2581 AAAGTAAAGTCAGAAGTTGATGCGTTAACCAGTAAATTAGCAGAAACCCAAACAGCCCTG 2640

2641 AAGTTGGTTGAGGATGCCTTGTCTACTGCAGAGGATAACATCAGTCGGCTTACTGAGGAG 2700

2701 AATAGAAATGTCCAAGCTGCCAAGGAAAATGCTGAGCTTGAGCTGCAAAAAGCAGTTGCA 2760

2761 GATGCCTCCTCTGTAGCTAGCGAACTGGATGAAGTTCTTGCAACCAAAAGCACACTTGAA 2820

2821 GCTGCACTCATGCAGGCTGAAAGAAATATATCTGATATTATTAGTGAAAAGGAAGAGGCT 2880

2881 CAAGGCAGAACTGCTACTGCAGAGATGGAGCATGAGATGCTGCAAAAAGAAGCTTCAATT 2940

2941 CAGAAGAACAAATTAACAGAAGCACATAGCACCATAAATTCACTTGAAGAAACACTTGCT 3000

3001 CAGACAGAAAGCAACATGGATTCGCTGTCCAAACAAATTGAAGATGACAAAGTTCTTACT 3060

3061 ACAAGTTTAAAGAATGAGTTAGAGAAGCTTAAAATTGAGGCAGAATTTGAGCGTAACAAG 3120

3121 ATGGCCGAAGCTTCCTTGACAATAGTATCCCATGAGGAGGCACTTATGAAKGCAGAGAAT 3180

3181 AGTCTTTCTGCTTTACAAGGAGAAATGGTGAAAGCTGAAGGCGAGATATCAACTCTCAGT 3240

3241 AGTAAACTTAATGTATGCATGGAAGAGTTAGCTGGATCAAGCGGAAACTCACAGAGTAAA 3300

3301 TCTTTGGAGATTATTACTCATCTTGATAATCTCCAGATGCTACTGAAGGATGGAGGKCTA 3360

3361 ATTTCCAAGGTGAATGAATTCCTTCAAAGGAAGTTCAAGAGCCTTAGAGACGTGGATGTC 3420

3421 ATTGCTAGAGATATCACACGAAATATTGGTGAGAATGGATTATTGGCAGGGGAAATGGGC 3480

3481 AACGCTGAGGATGATTCGACTGAGGCAAAATCGTTGTTGAGTGACCTTGATAATTCAGTG 3540

3541 AACACAGAGCCGGAGAATAGTCAAGGGAGTGCAGCTGATGAAGACGAAATTTCTTCATCC 3600

3601 CTTAGGAAGATGGCAGAGGGGGTCAGGCTGAGAAACAAAACCCTCGAGAATAACTTTGAG 3660

3661 GGTTTCTCAACTTCCATTGATACTCTCATAGCGACTTTGATGCAAAACATGACAGCAGCT 3720

3721 AGGGCTGATGTGTTAAATATCGTGGGTCATAATTCATCCTTGGAAGAACAGGTGAGGAGT 3780

3781 GTGGAAAATATTGTTCGTGAACAGGAGAACACTATATCTGCATTACAAAAAGATTTGTCA 3840

3841 TCTTTGATATCTGCATGTGGTGCGGCTGCCAGAGAACTGCAGTTGGAAGTGAAAAATAAC 3900

3901 CTCTTAGAGTTGGTTCAATTCCAAGAAAATGAAAACGGTGGTGAGATGGAATCAACTGAA 3960

3961 GACCCACAGGAGCTTCATGTAAGTGAATGCGCCCAAAGGATAAAAGAATTATCTTCTGCC 4020

4021 GCAGAGAAGGCATGTGCTACTCTTAAACTCTTTGAGACAACAAATAATGCAGCTGCCACT 4080

4081 GTAATCCGAGATATGGAGAACAGGCTAACAGAAGCATCTGTCGCTCTAGAAAAGGCTGTG 4140

4141 TTAGAAAGAGATCTAAACCAAACTAAGGTTTCAAGTTCTGAGGCCAAGGTGGAATCTCTG 4200

4201 GAAGAGCTTCGCCAAGACCTGAAACTTCAGTTGGAAAATCTCAGAGTGAAGGAAGAGAAA 4260

4261 TGGCATGAAAAAAAGGTGGAACTGTCTACGTTATATGATAAACTATTGGTGCAAGAGCAA 4320

4321 GAGGCAAAGGAACATCTAATTCCAGCTTCTGATATGCGAACCCTTTTTGACAAAATAAAT 4380

4381 GGTATTGAAGTGCCATCAGTAGATCTAGTCAACGGATTAGATCCACAGAGTCCATATGAT 4440

4441 GTGAAAAAGCTATTCGCGATTGTTGATAGTGTTACTGAGATGCAGCATCAGATAGACATC 4500

4501 TTATCATATGGACAAAAAGAGCTCAATTCTACTTTGGCAGAAAAGGATCTTGAAATTCAA 4560

4561 GGTCTAAAGAAGGCGACTGAAGCAGAGAGTACGACCGAGCTAGAGTTAGTGAAGGCAAAG 4620

4621 AATGAACTGTCCAAGCTAATATCTGGCTTGGAAAAACTGCTGGGTATATTGGCAAGCAAT 4680

4681 AATCCTGTTGTAGACCCAAACTTCTCCGAGTCATGGACACTCGTACAAGCACTAGAAAAA 4740

4741 AAGATAACTTCCCTTCTCCTAGAATCAGAGAGTTCAAAATCAAGGGCCCAAGAACTTGGT 4800

4801 TTAAAGTTGGCCGGTAGCGAGAAACTTGTCGATAAACTATCATTAAGAGTCAAAGAGTTT 4860

4861 GAAGAGAAACTTCAAACCAAAGCAATTCAGCCTGATATTGTTCAAGAAAGAAGCATCTTC 4920

4921 GAAACACCGAGAGCACCTTCTACCTCAGAGATATCCGAGATTGAGGACAAGGGAGCCTTG 4980

4981 GGAATAAAATCAATATCACCGGTGCCTACAGCAGCACAAGTGAGAACAGTGAGGAAGGGA 5040

5041 TCGACGGATCATCTTTCAATCAACATAGATTCAGAGTCCGAGCATCTGATGAACAACAAC 5100

5101 GAAACAGATGAAGATAAAGGACATGTTTTCAAGTCTCTCAACATGTCTGGTCTGATTCCA 5160

5161 ACGCAAGGAAAGATAATAGCAGATCGGGTTGATGGAATATGGGTCTCAGGTGGAAGAGTA 5220

5221 TTGATGAGCCGTCCTCAAGCAAGGCTTGGCGTTATGGTATACAGTCTCTTATTGCATCTG 5280

5281 TGGCTCCTAGCCTCCATCTTGTAA 5304

B. TNO1 amino acid sequence

TNO1 1 MHEKDDLPQDSIADGIENDDESNGQEEEELDPDQGTAFVDSKEDMFVDAPEELNFDTPSK 60

61 EALTTDDDDNDDLGTHFNIEKGDWEKELAGLQEQFKLLTGENDLTGEDGNTTVDIVSRFS 120

121 KFLKTAKEERIQHEVALKELHGVISGRDDEIADLTTKISELSSSQPVSEMGDQAQNLEHL 180

181 EAATDRIMVSLSNVFGEGELQYGSSISEKLAHLENRVSFLGAKYTEFYYGADQLRKCLAS 240

241 DVLDLSFQEDFGSALGAACSELFELKQKEAAFFEGLSHLEDENRNFVEQVNREKEMCESM 300

301 RTEFEKLKAELELEKTKCTNTKEKLSMAVTKGKALVQNRDALKHQLSEKTTELANRLTEL 360

361 QEKEIALESSEVMKGQLEQSLTEKTDELEKCYAELNDRSVSLEAYELTKKELEQSLAEKT 420

421 KELEECLTKLQEMSTALDQSELDKGELAKSDAMVASYQEMLSVRNSIIENIETILSNIYT 480

481 PEEGHSFDIVEKVRSLAEERKELTNVSQEYNRLKDLIVSIDLPEEMSQSSLESRLAWLRE 540

541 SFLQGKDEVNALQNRIESVSMSLSAEMEEKSNIRKELDDLSFSLKKMEETAERGSLEREE 600

601 IVRRLVETSGLMTEGVEDHTSSDINLLVDRSFDKIEKQIRDSSDSSYGNEEIFEAFQSLL 660

661 YVRDLEFSLCKEMLGEGELISFQVSNLSDELKIASQELAFVKEEKIALEKDLERSEEKSA 720

721 LLRDKLSMAIKKGKGLVQDREKFKTQLDEKKSEIEKLMLELQQLGGTVDGYKNQIDMLSR 780

781 DLERTKELETELVATKEERDQLQQSLSLIDTLLQKVMKSVEIIALPVDLASEDPSEKIDR 840

841 LAGYIQEVQLAR VEEQEEIEKVKSEVDALTSKLAETQTALKLVEDALSTAEDNISRLTEE 900

901 NRNVQAAKENAELELQKAVADASSVASELDEVLATKSTLEAALMQAERNISDIISEKEEA 960

961 QGRTATAEMEHEMLQKEASIQKNKLTEAHSTINSLEETLAQTESNMDSLSKQIEDDKVLT 1020

1021 TSLKNELEKLKIEAEFERNKMAEASLTIVSHEEALMKAENSLSALQGEMVKAEGEISTLS 1080

1081 SKLNVCMEELAGSSGNSQSKSLEIITHLDNLQMLLKDGGLISKVNEFLQRKFKSLRDVDV 1140

1141 IARDITRNIGENGLLAGEMGNAEDDSTEAKSLLSDLDNSVNTEPENSQGSAADEDEISSS 1200

1201 LRKMAEGVRLRNKTLENNFEGFSTSIDTLIATLMQNMTAARADVLNIVGHNSSLEEQVR S 1260

1261 VENIVREQENTISALQKDLSSLISACGAAARELQLEVKNNLLELVQFQENENGGEMESTE 1320

1321 DPQELHVSECAQRIKELSSAAEKACATLKLFETTNNAAATVIRDMENRLTEASVALEKAV 1380

1381 LERDLNQTKVSSSEA**KVESLEELRQDLKLQLENLRV**KEEKWHEKKVELSTLYDKLLVQEQ 1440

1441 EAKEHLIPASDMRTLFDKINGIEVPSVDLVNGLDPQSPYDVKKLFAIVDSVTEMQHQIDI 1500

1501 LSYGQKELNSTLAEKDLEIQGLKKATEAESTTELELVKAKNELSKLISGLEKLLGILASN 1560

1561 NPVVDPNFSESWTLVQALEKKITSLLLESESSKSRAQELGLKLAGSEKLVDKLSLRVKEF 1620

1621 EEKLQTKAIQPDIVQERSIFETPRAPSTSEISEIEDKGALGIKSISPVPTAAQVRTVRKG 1680

1681 STDHLSINIDSESEHLMNNNETDEDKGHVFKSLNMSGLIPTQGKIIADRVDGIWVSGGRV 1740

1741 LMSRPQARLGVMVYSLLLHLWLLASIL 1767

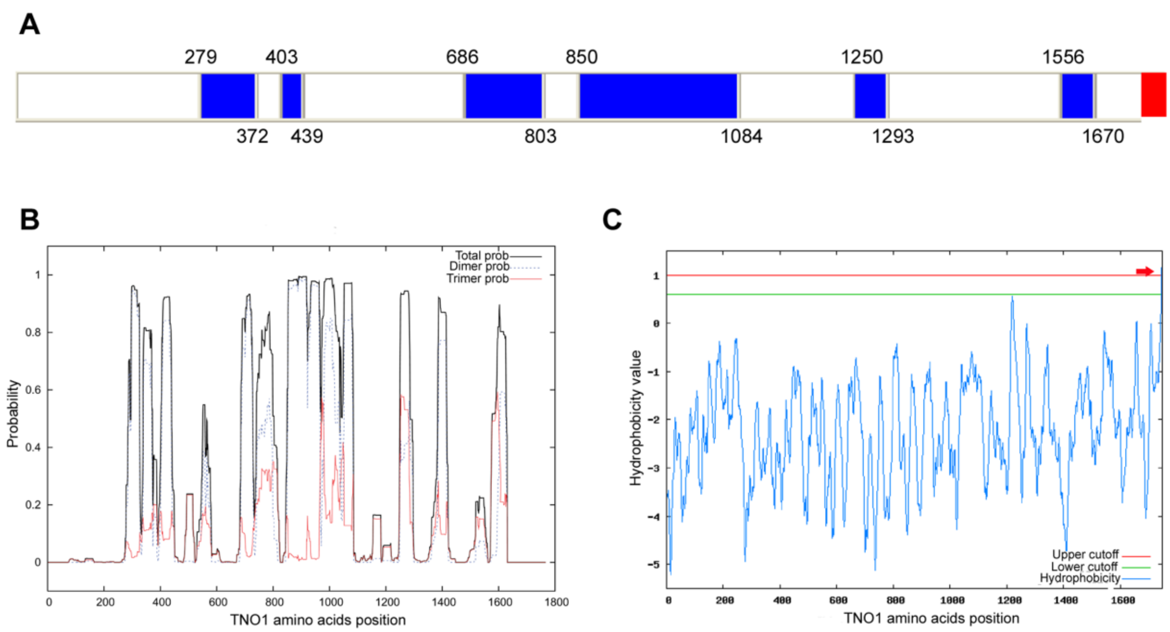
A. *TNO1* cDNA sequence.

Sequence of the open reading frame of *TNO1*. The extra exon encoded by the *TNO1* sequence compared with that in the TAIR database is marked in red.

B. *TNO1* amino acid sequence.

The extra amino acids predicted by our sequence are marked in red, and the predicted transmembrane domain is marked in green. Nine peptides identified by tandem mass spectrometry are marked in blue.

Supplementary Fig 2. TNO1 domain prediction.



A. Position of predicted coiled-coil domains and *trans*-membrane domain.

Positions are relative to the initiation amino acid. Blue boxes represent coiled-coil domains, and the red box represents a transmembrane domain.

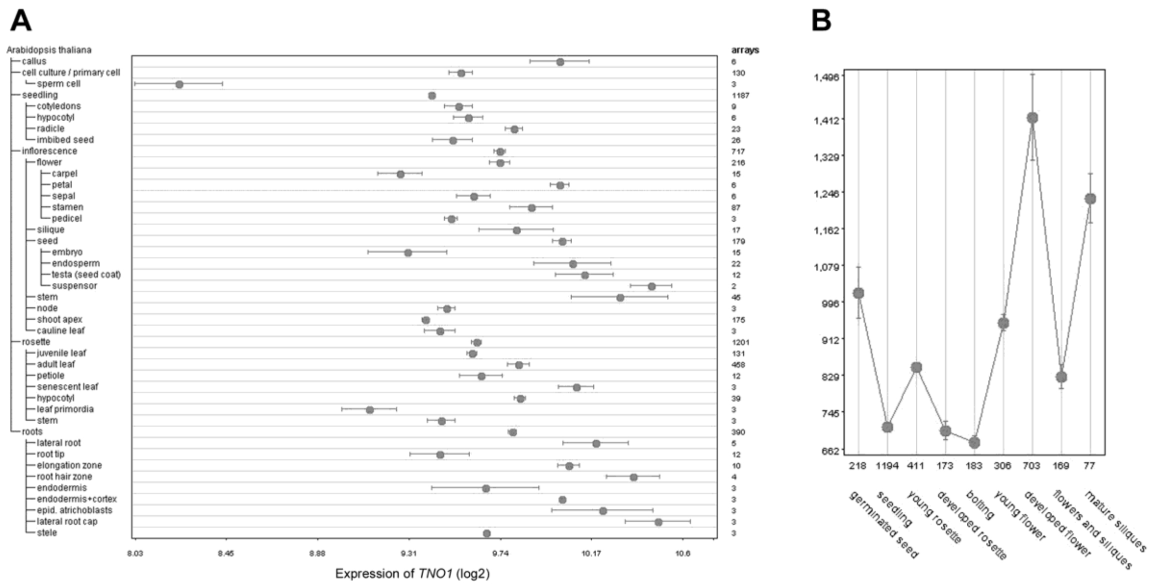
B. Probability of coiled-coil domain.

Probability of coiled-coil domains as determined by Multicoil, a coiled-coil domain prediction algorithm. Total probability, black solid line; dimer probability, black dotted line; trimer probability, red solid line.

C. Hydrophobicity value of TNO1.

Hydrophobicity value of TNO1 is determined by TopPred, a transmembrane topology prediction algorithm; amino acids 1749-1767 are predicted to form a transmembrane domain.

Supplementary Fig 3. Expression pattern of *TNO1* by microarray analysis.



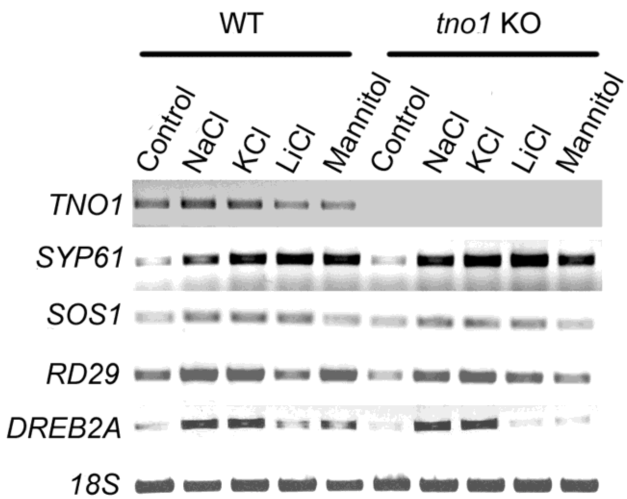
A. Expression of *TNO1* in diverse tissues in Arabidopsis.

Expression of *TNO1* in diverse tissues in Arabidopsis was determined using GENEVESTIGATOR. The number of arrays used to determine the transcript level of *TNO1* is shown at right. The scale is logarithmic. Error bars indicate standard error.

B. Expression of *TNO1* during development

Expression of *TNO1* during development was determined using GENEVESTIGATOR. X-axis represents developmental stage and the number of arrays used to calculate the mean intensities are indicated. Y-axis represents the intensity of *TNO1* transcript. Error bars indicate standard error.

Supplementary Fig 4. Salt/ osmotic stress responsive gene expression in wild-type and *tno1* mutant.



RT-PCR was performed with *TNO1*, *SYP61*, *SOS1*, *DREB2A* and *RD29*-specific primers using RNA extracted from wild-type and *tno1* mutant seedlings after the indicated treatments. Treatments were as follows: control (no treatment), NaCl (300 mM NaCl), KCl (300 mM), LiCl (40 mM LiCl), Mannitol (600 mM).