

## Additional file 1

### Tables

**Supplementary Table S1:** Details of seed proteins

| <b>Protein</b>    | <b>Specific location</b>                      | <b>Involvement in root development</b>              | <b>Function</b>                                                                      | <b>Source</b>    |
|-------------------|-----------------------------------------------|-----------------------------------------------------|--------------------------------------------------------------------------------------|------------------|
| <b>ada2</b>       | Primary root (PR), crown root (CR)            | Root elongation of PR and CR, increase number of CR | Auxin or cytokinin signaling                                                         | Literature[1]    |
| <b>aim1</b>       | Root meristem                                 | Root growth                                         | Salicylic acid biosynthesis promotes reactive oxygen species accumulation            | Literature[2]    |
| <b>arf1</b>       | Adventitious root                             | Root formation                                      | Auxin response factor, transcriptional factor                                        | Literature [3]   |
| <b>arf12</b>      | Primary root                                  | Longer primary roots                                | Auxin response factor, transcriptional factor                                        | Literature [3,4] |
| <b>arf25</b>      | Crown root                                    | Root development                                    | Auxin response factor, transcriptional factor                                        | Literature[4]    |
| <b>arl1</b>       | Crown root, lateral root, adventitious root   | Root formation, root development                    | Auxin-mediated cell de-differentiation                                               | Literature [3]   |
| <b>crl4/gnom1</b> | Crown root                                    | Root initiation                                     | Polar auxin transportation                                                           | Literature[5]    |
| <b>ccc1</b>       | Root tip                                      | Root elongation                                     | Osmotic regulation                                                                   | Literature[6]    |
| <b>cinv1</b>      | Primary root, lateral root                    | Root elongation, root formation                     | Cleaves sucrose into glucose and fructose, floral transition, and pollen development | STRING DB        |
| <b>cki1</b>       | Lateral root, adventitious root, primary root | Root elongation, increase the number of roots.      | Involved in ABA and brassinosteroid signaling pathways.                              | STRING DB        |

|                         |                          |                                                                                     |                                                                      |                 |
|-------------------------|--------------------------|-------------------------------------------------------------------------------------|----------------------------------------------------------------------|-----------------|
| <b>ckx4</b>             | Crown root               | Root formation, root emergence, and development increase the number of crown roots. | CK signaling pathway                                                 | Literature[7]   |
| <b>cinv1 (cyt-inv1)</b> | -                        | Root elongation                                                                     | Mutant accumulates sucrose and had reduced levels of hexose          | Literature[8]   |
| <b>d14</b>              | Crown roots              | Root elongation                                                                     | Involved in the strigolactone signaling pathway                      | Literature [9]  |
| <b>DRO1</b>             | Crown roots              | Increases root angle and facilitate root growth more downward                       | enhances nitrogen uptake and cytokinin fluxes                        | Literature [10] |
| <b>el5.1/el5.2</b>      | Root primordia           | Maintains cell viability after the initiation of root primordial formation,         | mediate the degradation of cytotoxic proteins produced in root cells | STRING DB       |
| <b>expa17</b>           | Root hair                | Root elongation                                                                     | Cell wall remodeling                                                 | Literature[11]  |
| <b>expa8</b>            | Root and shoot           | Root elongation, fewer LR, and short root hairs                                     | Encodes for cell wall localized protein                              | Literature[11]  |
| <b>fh1</b>              | Root hair                | Root elongation                                                                     | Actin-binding protein                                                | Literature[12]  |
| <b>gatb</b>             | Primary root, root tip   | Growth, cell division, and elongation                                               | Maintaining mitochondrial structure and function                     | Literature[13]  |
| <b>gcn5</b>             | Primary root, crown root | Root elongation of PR and CR, increase the number of CR                             | Auxin or cytokinin signaling                                         | Literature[1]   |
| <b>glr3.1</b>           | Root meristem (apical)   | Root elongation, maintenance of cell division, survival in                          | Glutamate-gate receptor                                              | Literature[14]  |

|                                      |                          |                                                     |                                                                                                                        |                |
|--------------------------------------|--------------------------|-----------------------------------------------------|------------------------------------------------------------------------------------------------------------------------|----------------|
| the root meristem in early seedlings |                          |                                                     |                                                                                                                        |                |
| <b>glu3</b>                          | -                        | Root elongation                                     | Encodes for putative membrane-bound endo-1,4- $\beta$ -glucans. Mutant lower the cellulose contents in root cell walls | Literature[9]  |
| <b>glu5</b>                          | Lateral root development | Root development                                    | Endohydrolysis of (1->4)-beta-D-glucosidic linkages in cellulose                                                       | STRING DB      |
| <b>gna1</b>                          | Root elongation zone     | Root elongation, maintaining normal root cell shape | Plays an important role in protein and lipid glycosylation                                                             | Literature[15] |
| <b>iaa13</b>                         | Lateral root             | Root formation                                      | Member of IAA gene family, transcriptional factor                                                                      | Literature[16] |
| <b>iaa14</b>                         | Lateral root             | Root initiation                                     | Member of IAA gene family, transcriptional factor                                                                      | Literature[17] |
| <b>mst3</b>                          | Root system              | Root development                                    | Sugar transporter                                                                                                      | STRING DB      |
| <b>mt2c</b>                          | Lateral root             | Root development, root initiation                   | Seed embryo germination by regulating CK level, reactive oxygen species scavenger in the cytosol                       | STRING DB      |
| <b>orc3</b>                          | Lateral root             | Root development                                    | Component of the origin recognition complex that binds origins of replication                                          | Literature[3]  |
| <b>os01t0682001-01</b>               | Seedling roots           | Primary ammonium ions assimilation                  | Reutilization of glutamine in developing organs.                                                                       | STRING DB      |

|                        |                    |                                                                                                                                             |                                                                    |                  |
|------------------------|--------------------|---------------------------------------------------------------------------------------------------------------------------------------------|--------------------------------------------------------------------|------------------|
|                        |                    |                                                                                                                                             | Plays a role in the development of tillers                         |                  |
| <b>os12t0604600-01</b> | Root hair          | Root development                                                                                                                            | Probable GTP-binding protein                                       | STRING DB        |
| <b>osasl1</b>          | Primary root, root | Primary root elongation, normal root growth                                                                                                 | Arginine biosynthesis                                              | Literature[18]   |
| <b>oseil1</b>          | -                  | Root elongation                                                                                                                             | Involved in the ethylene signaling pathway, transcriptional factor | Literature[19]   |
| <b>osj_19760</b>       | Root hair          | Form shorter root hairs                                                                                                                     | Reduced ABA signaling                                              | Literature[20]   |
| <b>osj_28507</b>       | Lateral root       | Influencing auxin-mediated developmental responses root production (ex: cell elongation, apical dominance, general growth, and development) | Auxin efflux and polar auxin transport                             | STRING DB        |
| <b>osj_34384</b>       | Root hair          | Root development                                                                                                                            | Probable GTP-binding protein                                       | STRING DB        |
| <b>pin1</b>            | adventitious root  | Regulation of adventitious root development via auxin pathway                                                                               | Controls the traffic of auxin efflux carrier proteins              | Literature[3,21] |
| <b>pin2</b>            |                    | Root growth angle                                                                                                                           | Component of the auxin efflux carrier                              | Literature[3,21] |
| <b>pin3a</b>           | Crown root         | Root development, response to water stress                                                                                                  | Auxin efflux and polar auxin transport                             | STRING DB        |

|               |              |                                                           |                                                                                                                         |                             |
|---------------|--------------|-----------------------------------------------------------|-------------------------------------------------------------------------------------------------------------------------|-----------------------------|
| <b>raa1</b>   | Root system  | Root development mediate by auxin                         | Cell cycle regulator during root development                                                                            | STRING DB                   |
| <b>rcn1</b>   | Lateral root | Promoting the outgrowth, hypodermal suberization of roots | Essential transporter for growth and development under abiotic stress, required for salt tolerance via Na/K homeostasis | STRING DB                   |
| <b>rhd3</b>   | Root hair    | Root development                                          | Probable GTP-binding protein                                                                                            | Literature[12,22–24]        |
| <b>rr1</b>    | Crown root   | Root development                                          | CK response regulators                                                                                                  | Literature[21,25–30]        |
| <b>rr2</b>    | Crown root   | Root development                                          | CK response regulators                                                                                                  | Literature [21,25,26,28,30] |
| <b>rr3</b>    | Crown root   | Root development                                          | CK response regulators                                                                                                  | Literature[26,30]           |
| <b>rr6</b>    | Crown root   | Suppressed root and vegetative development                | CK response regulators                                                                                                  | Literature[26,30]           |
| <b>sapk10</b> | Root hair    | Produces longer root hairs                                | Aba activated protein kinase 10 production                                                                              | Literature[31]              |
| <b>spl12</b>  | Crown roots  | Root development                                          | Trans-acting factor                                                                                                     | Literature[32]              |
| <b>spl3</b>   | Crown roots  | Increase number of roots                                  | Trans-acting factor                                                                                                     | Literature[32]              |
| <b>vln2</b>   |              | Root gravitropism                                         | Modulation of polar auxin transport                                                                                     | Literature[33]              |
| <b>wox11</b>  | Crown root   | Root elongation, root development                         | CK-regulation                                                                                                           | Literature[1,34]            |

### Supplementary Table S2:

List of NCBI gene symbols of proteins of extracted network module and the prediction scores for the top 75 candidates

|    | <b>Protein</b>  | <b>Gene symbol</b> | <b>Type of protein<br/>(seed/predicted)</b> | <b>Prediction<br/>score</b> |
|----|-----------------|--------------------|---------------------------------------------|-----------------------------|
| 1  | Os07t0108100-01 | LOC4342208         | Predicted                                   | 398.2289137                 |
| 2  | Osj_06916       | LOC4329481         | Predicted                                   | 398.2289137                 |
| 3  | Os05t0145700-01 | LOC4337795         | Predicted                                   | 394.2489024                 |
| 4  | Os05t0146100-01 | LOC4337797         | Predicted                                   | 394.2489024                 |
| 5  | Os05t0146900-00 | LOC9272414         | Predicted                                   | 394.2489024                 |
| 6  | GNP4            | LOC107277161       | Predicted                                   | 278.8703058                 |
| 7  | PDR16           | LOC4326812         | Predicted                                   | 271.1123074                 |
| 8  | LAX             | LOC4327431         | Predicted                                   | 262.3899959                 |
| 9  | EXPA5           | LOC4330706         | Predicted                                   | 198.1182047                 |
| 10 | P0018C10.5      | LOC4325089         | Predicted                                   | 198.1182047                 |
| 11 | Os11t0540600-01 | LOC4350668         | Predicted                                   | 198.1182047                 |
| 12 | Os06t0610100-00 | Discontinued       | Predicted                                   | 198.1182047                 |
| 13 | Os08t0423600-00 | LOC107276201       | Predicted                                   | 198.1182047                 |
| 14 | Osj_18177       | LOC 4338502        | Predicted                                   | 196.1331962                 |
| 15 | Osj_07614       | LOC4330055         | Predicted                                   | 194.1581821                 |
| 16 | Os11t0143300-02 | LOC4349747         | Predicted                                   | 192.1931623                 |
| 17 | HK6             | LOC107275680       | Predicted                                   | 175.4249306                 |
| 18 | C68             | LOC4328829         | Predicted                                   | 174.1518585                 |
| 19 | Os04t0672900-01 | LOC4337370         | Predicted                                   | 174.1518585                 |
| 20 | Os08t0467500-02 | LOC4345793         | Predicted                                   | 174.1518585                 |
| 21 | Os03t0253200-01 | LOC4332276         | Predicted                                   | 174.1518585                 |
| 22 | Os05t0107300-01 | LOC107275998       | Predicted                                   | 173.900894                  |
| 23 | P0425F05.2      | LOC4340552         | Predicted                                   | 165.5780768                 |
| 24 | Osj_34426       | LOC4350866         | Predicted                                   | 157.7839569                 |
| 25 | Os02t0190300-01 | LOC4328570         | Predicted                                   | 157.7839569                 |
| 26 | Os01t0967100-01 | LOC4324005         | Predicted                                   | 156.1155519                 |
| 27 | Osj_24793       | LOC4343642         | Predicted                                   | 150.6678038                 |
| 28 | HK4             | LOC4333916         | Predicted                                   | 146.4983529                 |
| 29 | Osj_09048       | LOC4331278         | Predicted                                   | 144.1448717                 |
| 30 | HOX9            | LOC4348919         | Predicted                                   | 141.028896                  |
| 31 | Os09t0450600-00 | LOC4347222         | Predicted                                   | 138.1439741                 |
| 32 | Os01t0728200-01 | Discontinued       | Predicted                                   | 138.1439741                 |
| 33 | Os07t0632600-01 | LOC4344004         | Predicted                                   | 132.6048761                 |

|    |                 |              |           |             |
|----|-----------------|--------------|-----------|-------------|
| 34 | Os07t0162600-02 | LOC4342462   | Predicted | 131.4163008 |
| 35 | Os03t0356470-00 | LOC9270588   | Predicted | 131.4163008 |
| 36 | Os03t0377300-01 | LOC9267254   | Predicted | 131.4163008 |
| 37 | Os03t0377500-01 | LOC9271339   | Predicted | 131.4163008 |
| 38 | Osj_34565       | LOC4350998   | Predicted | 131.4163008 |
| 39 | Os10t0485400-01 | Discontinued | Predicted | 131.4163008 |
| 40 | Os08t0547600-00 | LOC9269394   | Predicted | 131.4163008 |
| 41 | Osj_12688       | Discontinued | Predicted | 131.4163008 |
| 42 | Os08t0424100-00 | LOC9267362   | Predicted | 131.4163008 |
| 43 | P0025H07.5      | LOC4347247   | Predicted | 131.4163008 |
| 44 | EXPA31          | LOC4333168   | Predicted | 129.4387881 |
| 45 | Os11t0515500-01 | LOC4350590   | Predicted | 122.7141653 |
| 46 | PT2             | LOC4331637   | Predicted | 122.7141653 |
| 47 | Os01t0728150-00 | LOC107276471 | Predicted | 118.2806568 |
| 48 | PT3             | LOC4348740   | Predicted | 118.2806568 |
| 49 | Osj_32478       | LOC4349400   | Predicted | 115.2765157 |
| 50 | ARF19           | LOC4341978   | Predicted | 103.235112  |
| 51 | ORR5            | LOC4336439   | Predicted | 103.235112  |
| 52 | Os04t0445300-01 | LOC4335958   | Predicted | 102.7645228 |
| 53 | Os06t0697000-02 | LOC4341944   | Predicted | 102.7645228 |
| 54 | Os07t0582850-00 | LOC9266807   | Predicted | 98.06659812 |
| 55 | Os04t0101800-01 | LOC4334888   | Predicted | 98.06659812 |
| 56 | Osj_35591       | Discontinued | Predicted | 98.06659812 |
| 57 | Os09t0467700-01 | LOC4347323   | Predicted | 98.06659812 |
| 58 | CR4             | LOC4333525   | Predicted | 92.21651326 |
| 59 | Osj_22409       | LOC4341879   | Predicted | 90.21339716 |
| 60 | Os08t0564300-04 | LOC4346344   | Predicted | 89.18949213 |
| 61 | Os11t0498600-01 | LOC4350556   | Predicted | 88.88541299 |
| 62 | Os02t0235900-01 | LOC9271032   | Predicted | 86.45738679 |
| 63 | Osj_019622      | LOC9270361   | Predicted | 85.55435509 |
| 64 | Os11t0439600-01 | LOC4350420   | Predicted | 84.9841779  |
| 65 | Os11t0672900-01 | LOC4351100   | Predicted | 84.9841779  |
| 66 | Os03t0303100-01 | LOC4332586   | Predicted | 84.9841779  |
| 67 | Osj_14626       | LOC4335696   | Predicted | 84.15088682 |
| 68 | Os01t0844300-01 | LOC4327507   | Predicted | 81.95702094 |

|     |                 |              |           |             |
|-----|-----------------|--------------|-----------|-------------|
| 69  | Os05t0490600-00 | LOC4339167   | Predicted | 80.30566578 |
| 70  | OsGLHAT1        | LOC107275998 | Predicted | 80.30566578 |
| 71  | HOX10           | LOC4331345   | Predicted | 79.86774383 |
| 72  | IAA30           | LOC4352721   | Predicted | 79.86774383 |
| 73  | ASMT            | LOC4346795   | Predicted | 78.05777595 |
| 74  | Osj_20964       | LOC4340753   | Predicted | 78.05777595 |
| 75  | Osj_30022       | LOC4347587   | Predicted | 78.05777595 |
| 76  | ADA2            | LOC4334126   | Seed      | -           |
| 77  | ARF12           | LOC4337363   | Seed      | -           |
| 78  | ARF25           | LOC4352783   | Seed      | -           |
| 79  | ARL1            | LOC9271993   | Seed      | -           |
| 80  | CCC1            | LOC4345272   | Seed      | -           |
| 81  | CINV1           | LOC4329626   | Seed      | -           |
| 82  | CKI1            | LOC4330018   | Seed      | -           |
| 83  | CKX4            | LOC4326515   | Seed      | -           |
| 84  | D14             | LOC4331983   | Seed      | -           |
| 85  | DRO1            | LOC4347169   | Seed      | -           |
| 86  | EL5.1           | LOC107276751 | Seed      | -           |
| 87  | EL5.2           | LOC4329685   | Seed      | -           |
| 88  | EXPA17          | LOC107276467 | Seed      | -           |
| 89  | EXPA8           | LOC4327217   | Seed      | -           |
| 90  | FH1             | LOC4325107   | Seed      | -           |
| 91  | GATB            | LOC4350686   | Seed      | -           |
| 92  | GCN5            | LOC4348629   | Seed      | -           |
| 93  | GLR3.1          | LOC4336790   | Seed      | -           |
| 94  | GLU3            | LOC4336284   | Seed      | -           |
| 95  | GLU5            | LOC4324643   | Seed      | -           |
| 96  | GNA1            | LOC4347432   | Seed      | -           |
| 97  | IAA13           | LOC4334069   | Seed      | -           |
| 98  | IAA14           | LOC4334431   | Seed      | -           |
| 99  | MST3            | LOC4342198   | Seed      | -           |
| 100 | MT2C            | LOC4337596   | Seed      | -           |
| 101 | ORC3            | LOC4324643   | Seed      | -           |
| 102 | Os01t0682001-01 | LOC4324398   | Seed      | -           |
| 103 | Os12t0604600-01 | LOC4352733   | Seed      | -           |



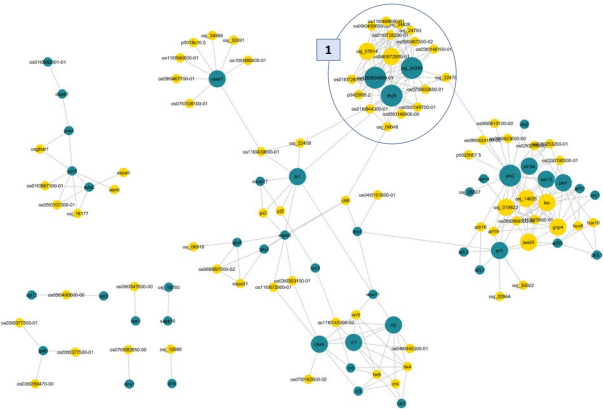
|            |           |                |      |   |
|------------|-----------|----------------|------|---|
| <b>104</b> | OsASL1    | LOC4332596     | Seed | - |
| <b>105</b> | OsEIL1    | LOC4332697     | Seed | - |
| <b>106</b> | Ost_28507 | LOC4346497     | Seed | - |
| <b>107</b> | Osj_34384 | LOC4350788     | Seed | - |
| <b>108</b> | PIN1      | LOC4330700     | Seed | - |
| <b>109</b> | PIN2      | LOC4341736     | Seed | - |
| <b>110</b> | PIN3A     | LOC4326565     | Seed | - |
| <b>111</b> | RAA1      | LOC4326229     | Seed | - |
| <b>112</b> | RCN1      | LOC4332449     | Seed | - |
| <b>113</b> | RHD3      | LOC4326314     | Seed | - |
| <b>114</b> | RR1       | LOC4335937     | Seed | - |
| <b>115</b> | RR2       | LOC4329677     | Seed | - |
| <b>116</b> | RR3       | LOC4331245     | Seed | - |
| <b>117</b> | RR6       | LOC4337372     | Seed | - |
| <b>118</b> | SAPK10    | LOC4333435     | Seed | - |
| <b>119</b> | VLN2      | New submission | Seed | - |
| <b>120</b> | WOX11     | LOC4344325     | Seed | - |

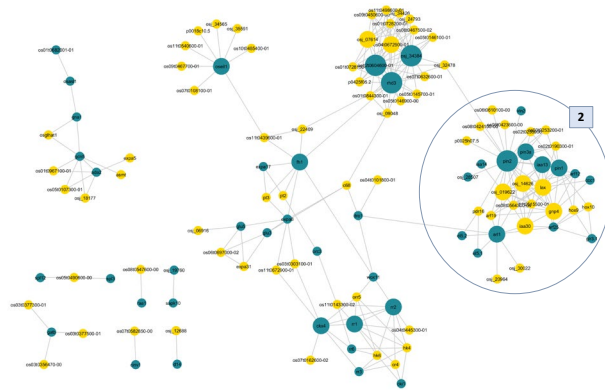
**Supplementary Table S3:** Details of missing seed proteins

| <b>Absent in raw dataset</b> | <b>Removed by filtering</b> |
|------------------------------|-----------------------------|
| AIM1                         | Osj_19760                   |
| CARK                         | HO1                         |
| SPL12                        | SPL3                        |

Supplementary Table S4: Details of sub-modules

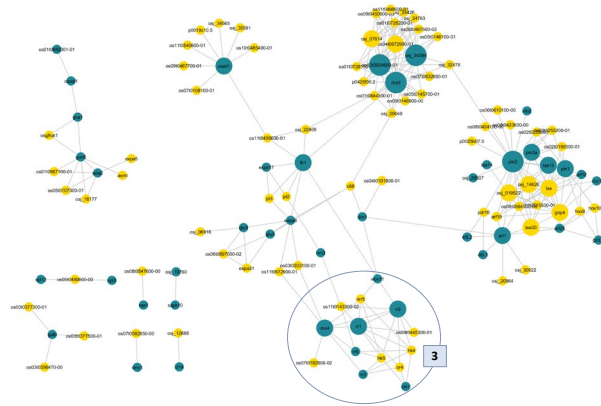
| SUB-MODULE | SEEDS                                | Functions of seeds    | PREDICTED CANDIDATES                                                                                                                                                                                                                                                                         |
|------------|--------------------------------------|-----------------------|----------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------------|
| 1          | RHD3<br>Osj_34384<br>Os12t0604600-01 | Root hair development | Osj_32478<br>Osj_07614<br>Osj_24793<br>P0425F05.2<br>Os01t0728200-01<br>Os07t0632600-01<br>Os05t0146900-00<br>Osj_09048<br>Os09t0450600-00<br>Os01t0728150-00<br>Os05t0145700-01<br>Os04t0672900-01<br>Os05t0146100-01<br>Os08t0467500-02<br>Osj_34384<br>Os01t0844300-01<br>Os11t0498600-01 |





|           |                                                                                             |                 |
|-----------|---------------------------------------------------------------------------------------------|-----------------|
| EL5.2     | Degradation of cytotoxic proteins                                                           | ARF19           |
| EL5.1     | produced in root cells                                                                      | GNP4            |
|           |                                                                                             | HOX10           |
| ARF25     | Auxin response factors                                                                      | HOX9            |
| ARF12     |                                                                                             | IAA30           |
| Osj_28507 | Influence in auxin-mediated developmental responses                                         | LAX             |
| CCC1      | Osmotic regulation                                                                          | Os02t0190300-01 |
| ARL1      | Auxin-mediated cell dedifferentiation                                                       | Os02t0235900-01 |
| PIN3A     | Auxin efflux and polar auxin transport                                                      | Os03t0253200-01 |
| PIN2      |                                                                                             | Os06t0610100-00 |
| PIN1      |                                                                                             | Os08t0423600-00 |
| IAA13     | Members of the IAA family                                                                   | Os08t0424100-00 |
| IAA14     |                                                                                             | Os08t0564300-04 |
| VLN2      | Modulation of polar auxin transport                                                         | Os11t0515500-01 |
| GLR3.1    | The glutamate-gate receptor may regulate cell proliferation and cell death in the root apex | Osj_019622      |
|           |                                                                                             | Osj_14626       |
|           |                                                                                             | Osj_20964       |
|           |                                                                                             | Osj_30022       |
|           |                                                                                             | P0025H07.5      |
|           |                                                                                             | PDR16           |

3



CKI1

Involved in ABA and  
brassinosteroid signaling pathways.

CR4

HK4

HK6

RR6

CK response regulators

ORR5

RR1

Os04t0445300-01

RR2

Os07t0162600-02

RR3

Os11t0143300-02

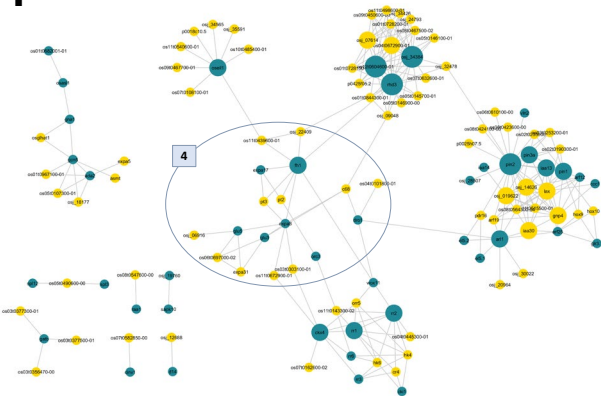
CKX4

CK signaling pathway

WOX11

CK-regulation

4



FH1

Root hair development

C68

GLU3

Encoded for putative membrane-  
bound

EXPA31

Endo-1,4- $\beta$ -glucanase, mutant lower  
the cellulose contents in its root cell  
walls

Os03t0303100-01

Os04t0101800-01

Os06t0697000-02

Os11t0439600-01

Os11t0672900-01

GLU5

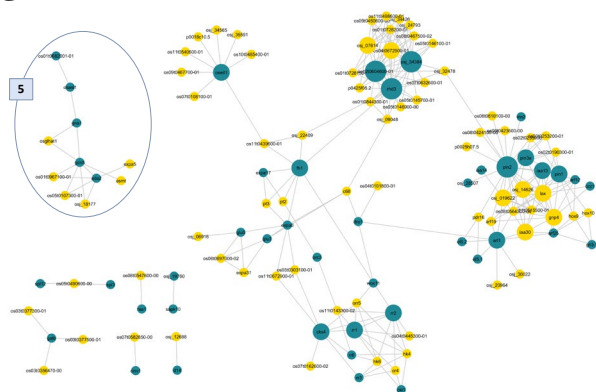
Endohydrolysis of (1->4)-beta-D-  
glucosidic linkages in cellulose

Osj\_06916

Osj\_22409

|  |        |                                                                               |            |
|--|--------|-------------------------------------------------------------------------------|------------|
|  | ORC3   | Component of the origin recognition complex that binds origins of replication | PT2<br>PT3 |
|  | EXPA8  | Cell wall localized protein                                                   |            |
|  | EXPA17 | Cell wall remodeling                                                          |            |
|  | DRO1   | Enhances nitrogen uptake and cytokinin fluxes, regulating root growth angle   |            |

5



|                 |                                                                                             |                                          |
|-----------------|---------------------------------------------------------------------------------------------|------------------------------------------|
| GNA1            | Plays an important role in protein and lipid glycosylation                                  | ASMT<br>EXPA5                            |
| ADA2            | Auxin or cytokinin signaling                                                                | Os01t0967100-01                          |
| Os01t0682001-01 | Reutilization of glutamine in developing organs. Plays a role in the development of tillers | Os05t0107300-01<br>OsGLHAT1<br>Osj_18177 |
| gcn5            | Auxin and cytokinin signaling                                                               |                                          |
| osasl1          | Arginine biosynthesis                                                                       |                                          |

---

6

oseil1

Involved in the ethylene signaling  
pathway

Os07t0108100-01

Os09t0467700-01

Os10t0485400-01

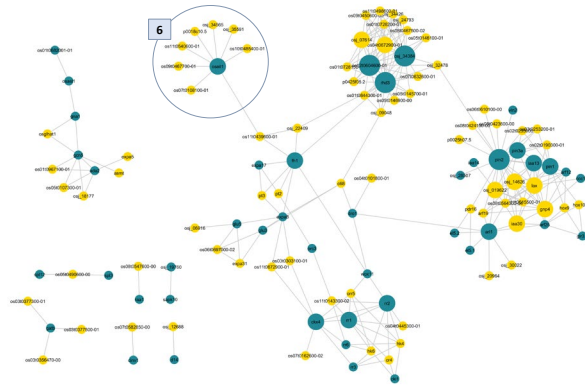
Os11t0540600-01

OSj\_34565

Osj\_35591

P0018C10.5

---



## References

- [1] Zhou S, Jiang W, Long F, Cheng S, Yang W, Zhao Y, et al. Rice Homeodomain Protein WOX11 Recruits a Histone Acetyltransferase Complex to Establish Programs of Cell Proliferation of Crown Root Meristem. *The Plant Cell* 2017;29:1088–104. <https://doi.org/10.1105/tpc.16.00908>.
- [2] Xu L, Zhao H, Ruan W, Deng M, Wang F, Peng J, et al. ABNORMAL INFLORESCENCE MERISTEM1 Functions in Salicylic Acid Biosynthesis to Maintain Proper Reactive Oxygen Species Levels for Root Meristem Activity in Rice. *The Plant Cell* 2017;29:560–74. <https://doi.org/10.1105/tpc.16.00665>.
- [3] Wang L, Guo M, Li Y, Ruan W, Mo X, Wu Z, et al. LARGE ROOT ANGLE1, encoding OsPIN2, is involved in root system architecture in rice. *Journal of Experimental Botany* 2018;69:385–97.
- [4] Liu H, Jia S, Shen D, Liu J, Li J, Zhao H, et al. Four AUXIN RESPONSE FACTOR genes downregulated by microRNA167 are associated with growth and development in *Oryza sativa*. *Functional Plant Biol* 2012;39:736–44. <https://doi.org/10.1071/FP12106>.
- [5] Kitomi Y, Ogawa A, Kitano H, Inukai Y. *CRL4* regulates crown root formation through auxin transport in rice. *Plant Root* 2008;2:19–28. <https://doi.org/10.3117/plantroot.2.19>.
- [6] Henderson SW, Wege S, Gilliam M. Plant Cation-Chloride Cotransporters (CCC): Evolutionary Origins and Functional Insights. *International Journal of Molecular Sciences* 2018;19:492. <https://doi.org/10.3390/ijms19020492>.
- [7] Gao S, Fang J, Xu F, Wang W, Sun X, Chu J, et al. CYTOKININ OXIDASE/DEHYDROGENASE4 Integrates Cytokinin and Auxin Signaling to Control Rice Crown Root Formation. *Plant Physiology* 2014;165:1035–46. <https://doi.org/10.1104/pp.114.238584>.
- [8] Gao J, van Kleeff PJM, Oecking C, Li KW, Erban A, Kopka J, et al. Light modulated activity of root alkaline/neutral invertase involves the interaction with 14-3-3 proteins. *The Plant Journal* 2014;80:785–96. <https://doi.org/10.1111/tpj.12677>.
- [9] Zhou H-L, He S-J, Cao Y-R, Chen T, Du B-X, Chu C-C, et al. OsGLU1, a putative membrane-bound endo-1, 4-β-d-glucanase from rice, affects plant internode elongation. *Plant Molecular Biology* 2006;60:137–51.
- [10] Arai-Sanoh Y, Takai T, Yoshinaga S, Nakano H, Kojima M, Sakakibara H, et al. Deep rooting conferred by DEEPER ROOTING 1 enhances rice yield in paddy fields. *Scientific Reports* 2014;4:1–6.
- [11] Ma N, Wang Y, Qiu S, Kang Z, Che S, Wang G, et al. Overexpression of OsEXPA8, a root-specific gene, improves rice growth and root system architecture by facilitating cell extension. *PLoS One* 2013;8.
- [12] Huang J, Kim CM, Xuan Y, Liu J, Kim TH, Kim B-K, et al. Formin homology 1 (OsFH1) regulates root-hair elongation in rice (*Oryza sativa*). *Planta* 2013;237:1227–39.

- [13] Qin C, Cheng L, Zhang H, He M, Shen J, Zhang Y, et al. OsGatB, the Subunit of tRNA-Dependent Amidotransferase, Is Required for Primary Root Development in Rice. *Frontiers in Plant Science* 2016;7.
- [14] Li J, Zhu S, Song X, Shen Y, Chen H, Yu J, et al. A Rice Glutamate Receptor–Like Gene Is Critical for the Division and Survival of Individual Cells in the Root Apical Meristem. *The Plant Cell* 2006;18:340–9. <https://doi.org/10.1105/tpc.105.037713>.
- [15] Jiang H, Wang S, Dang L, Wang S, Chen H, Wu Y, et al. A Novel Short-Root Gene Encodes a Glucosamine-6-Phosphate Acetyltransferase Required for Maintaining Normal Root Cell Shape in Rice. *Plant Physiology* 2005;138:232–42. <https://doi.org/10.1104/pp.104.058248>.
- [16] Inahashi H, Shelley IJ, Yamauchi T, Nishiuchi S, Takahashi-Nosaka M, Matsunami M, et al. OsPIN2, which encodes a member of the auxin efflux carrier proteins, is involved in root elongation growth and lateral root formation patterns via the regulation of auxin distribution in rice. *Physiologia Plantarum* 2018;164:216–25. <https://doi.org/10.1111/ppl.12707>.
- [17] Leyser O. Auxin signaling. *Plant Physiology* 2018;176:465–79.
- [18] Xia J, Yamaji N, Ma JF. An appropriate concentration of arginine is required for normal root growth in rice. *Plant Signaling & Behavior* 2014;9:e28717. <https://doi.org/10.4161/psb.28717>.
- [19] Mao C, Wang S, Jia Q, Wu P. OsEIL1, a rice homolog of the Arabidopsis EIN3 regulates the ethylene response as a positive component. *Plant Molecular Biology* 2006;61:141.
- [20] Munir MZ, Ud Din S, Imran M, Zhang Z, Pervaiz T, Han C, et al. Transcriptomic and Anatomic Profiling Reveal Etiolation Promotes Adventitious Rooting by Exogenous Application of 1-Naphthalene Acetic Acid in Robinia pseudoacacia L. *Forests* 2021;12:789. <https://doi.org/10.3390/f12060789>.
- [21] Takatsuka H, Umeda M. Hormonal control of cell division and elongation along differentiation trajectories in roots. *Journal of Experimental Botany* 2014;65:2633–43.
- [22] Wang H, Lockwood SK, Hoeltzel MF, Schiefelbein JW. The ROOT HAIR DEFECTIVE3 gene encodes an evolutionarily conserved protein with GTP-binding motifs and is required for regulated cell enlargement in Arabidopsis. *Genes & Development* 1997;11:799–811.
- [23] Chen J, Stefano G, Brandizzi F, Zheng H. Arabidopsis RHD3 mediates the generation of the tubular ER network and is required for Golgi distribution and motility in plant cells. *Journal of Cell Science* 2011;124:2241–52.
- [24] Zheng H, Chen J. Emerging aspects of ER organization in root hair tip growth: lessons from RHD3 and Atlastin. *Plant Signaling & Behavior* 2011;6:1710–3.
- [25] Kieber JJ, Schaller GE. Cytokinin signaling in plant development. *Development* 2018;145:149344.
- [26] Du L, Jiao F, Chu J, Jin G, Chen M, Wu P. The two-component signal system in rice (*Oryza sativa* L.): a genome-wide study of cytokinin signal perception and transduction. *Genomics* 2007;89:697–707.



- [27] Uga Y, Sugimoto K, Ogawa S, Rane J, Ishitani M, Hara N, et al. Control of root system architecture by DEEPER ROOTING 1 increases rice yield under drought conditions. *Nature Genetics* 2013;45:1097.
- [28] Paszkowski U, Kroken S, Roux C, Briggs SP. Rice phosphate transporters include an evolutionarily divergent gene specifically activated in arbuscular mycorrhizal symbiosis. *Proceedings of the National Academy of Sciences* 2002;99:13324–9.
- [29] Spirin V, Mirny LA. Protein complexes and functional modules in molecular networks. *Proceedings of the National Academy of Sciences*, vol. 100, 2003, p. 12123–8.
- [30] Heyl A, Schmülling T. Cytokinin signal perception and transduction. *Current Opinion in Plant Biology* 2003;6:480–8.
- [31] Wang T, Li C, Wu Z, Jia Y, Wang H, Sun S, et al. Absciscic Acid Regulates Auxin Homeostasis in Rice Root Tips to Promote Root Hair Elongation. *Frontiers in Plant Science* 2017;8.
- [32] Shao Y, Zhou H-Z, Wu Y, Zhang H, Lin J, Jiang X, et al. OsSPL3, an SBP-Domain Protein, Regulates Crown Root Development in Rice. *Plant Cell* 2019;31:1257–75. <https://doi.org/10.1105/tpc.19.00038>.
- [33] Wu S, Xie Y, Zhang J, Ren Y, Zhang X, Wang J, et al. VLN2 Regulates Plant Architecture by Affecting Microfilament Dynamics and Polar Auxin Transport in Rice. *The Plant Cell* 2015;27:2829–45. <https://doi.org/10.1105/tpc.15.00581>.
- [34] Zhao Y, Cheng S, Song Y, Huang Y, Zhou S, Liu X, et al. The Interaction between Rice ERF3 and WOX11 Promotes Crown Root Development by Regulating Gene Expression Involved in Cytokinin Signaling. *The Plant Cell* 2015;27:2469–83. <https://doi.org/10.1105/tpc.15.00227>.