**Supplementary material**

**Table S1.** Rolling leaf (RL) genes of rice and their references

| **SN** | **Gene/QTL** | **Gene name** | **Phenotype of rice leaf** | **Chr** | **MSU Locus ID** | **References** |
| --- | --- | --- | --- | --- | --- | --- |
| 1 | Gene | *NAL4* | Narrow leaf | 4 | Unknown | Yen *et al*. (1968); [http://ejournal.sinica.edu.tw/bbas/content/1968/1/bot091-10.PDF] |
| 2 | Gene | *NAL6* | Narrow leaf | 3 | Unknown | https://shigen.nig.ac.jp/rice/oryzabase/gene/detail/568 |
| 3 | Gene | *RL1* | Inward rolling | 1,12 | Unknown | Yoshimura *et al*. (1997); http://archive.gramene.org/db/genes/search\_gene?acc=GR:0060764 |
| 4 | Gene | *RL2* | Inward rolling | 1 | Unknown | Yoshimura *et al*. (1997); http://archive.gramene.org/db/genes/search\_gene?acc=GR:0060765 |
| 5 | Gene | *RL3* | Inward rolling | 3,12 | Unknown | Yoshimura *et al*. (1997); http://archive.gramene.org/db/genes/search\_gene?acc=GR:0060766 |
| 6 | Gene | *RL4* | Inward rolling | 1 | Unknown | Yoshimura *et al*. (1997); http://archive.gramene.org/db/genes/search\_gene?acc=GR:0060767 |
| 7 | Gene | *RL5* | Inward rolling | 3 | Unknown | Yoshimura *et al*. (1997); http://archive.gramene.org/db/genes/search\_gene?acc=GR:0060768 |
| 8 | Gene | *RFS* | Rolled fine striped leaf | 7 | LOC\_Os07g31450 | Yoshimura *et al*. (1997); Cho *et al*. (2018) |
| 9 | Gene | *OsCHR4* | Narrow albino leaf | 7 | LOC\_Os07g31450 | Zhao *et al*. (2012); Xu *et al*. (2017); Cho *et al*. (2018) |
| 10 | Gene | *CHR729* | Narrow albino leaf | 7 | LOC\_Os07g31450 | Hu *et al*. (2012); Ma *et al*. (2015); Xu *et al*. (2017); Cho *et al*. (2018) |
| 11 | Gene | *NAAL1* | Narrow albino leaf | 7 | LOC\_Os07g31450 | Xu *et al*. (2017) |
| 12 | Gene | *rl6* | Inward rolling | 7 | Unknown | http://archive.gramene.org/db/genes/search\_gene?acc=GR:0060769 |
| 13 | Gene | *rl7* | Inward rolling | 5 | Unknown | Li *et al*. (1998) |
| 14 | Gene | *rl(t)* | Inward rolling | 2 | Unknown | Shao *et al*. (2005a); Pan *et al*. (2011) |
| 15 | Gene | *rl8* | Inward rolling | 5 | Unknown | Shao *et al*., (2005b) |
| 16 | Gene | *DCL1* | Rolling leaf | 3 | LOC\_Os03g02970 | Liu *et al*. (2005) |
| 17 | Gene | *rl9(t)* | Inward rolling | 9 | Unknown | Yan *et al*. (2006) |
| 18 | Gene | *rl10(t)* | Inward rolling | 3 | LOC\_Os03g06654 | Yi *et al*. (2007) |
| 19 | Gene | *RL10* | Inward rolling | 9 | LOC\_Os09g23200 | Luo *et al*. (2007) |
| 20 | Gene | *OsAGO7* | Inward rolling | 3 | LOC\_Os03g33650 | Shi *et al*. (2007) |
| 21 | Gene | ***YABBY1*** | Abaxial rolling | 7 | LOC\_Os07g06620 | Dai *et al*. (2007) |
| 22 | Gene | *NAL1* | Narrow leaf | 4 | LOC\_Os04g52479 | Qi *et al*. (2008) |
| 23 | Gene | *COW1* | Inward rolling | 3 | LOC\_Os03g06654 | Woo *et al*. (2007) |
| 24 | Gene | *NAL7* | Inward rolling | 3 | LOC\_Os03g06654 | Fujino *et al*. (2008) |
| 25 | Gene | *url1(t)* | Inward rolling | 1 | Unknown | Yu *et al*. (2010) |
| 26 | Gene | *RL9* | Inward rolling | 9 | LOC\_Os09g23200 | Yan *et al*. (2008) |
| 27 | Gene | *SLL1* | Inward rolling | 9 | LOC\_Os09g23200 | Zhang *et al*. (2009) |
| 28 | Gene | *ADL1* | Outward rolling | 2 | LOC\_Os02g47970 | Hibara *et al*. (2009) |
| 29 | Gene | *rl11(t)* | Inward rolling | 7, 4 | Unknown | Shi *et al*. (2009); Zhou *et al*. (2010) |
| 30 | Gene | *OsAS2* | Aberrant twisted leaf | 1 | LOC\_Os01g66590 | Ma *et al*. (2009) |
| 31 | Gene | *rl12(t)* | Inward rolling | 10 | Unknown | Luo *et al*. (2009) |
| 32 | Gene | *ND1* | Narrow leaf and dwarf | 12 | LOC\_Os12g36890 | Li *et al*. (2009) |
| 33 | Gene | *DNL3* | Dwarf and narrow leaf  | 12 | LOC\_Os12g36890 | Shi *et al*. (2016) |
| 34 | Gene | *nal3(t)* | Inward rolling | 12 | Unknown | Wang *et al*. (2009); FENG *et al*. (2012) |
| 35 | Gene | *rl13(t)* | Inward rolling | 9 | Unknown | Chen *et al*. (2010) |
| 36 | Gene | *ACL1* | Outward rolling | 4 | LOC\_Os04g33860 | Li *et al*. (2010) |
| 37 | Gene | *LC2* | Outward rolling | 2 | LOC\_Os02g05840 | Zhao *et al*. (2010) |
| 38 | Gene | *NRL1* | Inward rolling | 12 | LOC\_Os12g36890 | Hu *et al*. (2010); Wu *et al*. (2010) |
| 39 | Gene | *nrl2(t)* | Inward rolling | 3 | Unknown | Wang *et al*. (2011) |
| 40 | Gene | *Roc5* | Outward rolling | 2 | LOC\_Os02g45250 | Zou *et al*. (2011) |
| 41 | Gene | *CFL1* | Inward rolling | 2 | LOC\_Os02g31140 | Wu *et al*. (2011) |
| 42 | Gene | *rl13* | Inward rolling | 6 | Unknown | Tian *et al*. (2012) |
| 43 | Gene | *RL14* | Inward rolling | 10 | LOC\_Os10g40960 | Fang *et al*. (2012) |
| 44 | Gene | *SRL1* | Inward rolling | 7 | LOC-Os07g01240 | Xiang *et al*. (2012) |
| 45 | Gene | *nul1* | narrow & upper-albino leaf | 7 | Unknown | Wang *et al*. (2012a) |
| 46 | Gene | *OsJNBa0003P07* | Rolling leaf | 10 | Unknown | Wang *et al*. (2012b) |
| 47 | Gene | *NAL2* | Narrow leaf | 11 | LOC\_Os11g01130 | Cho *et al*. (2013) |
| 48 | Gene | *NAL3* | Narrow leaf | 12 | LOC\_Os12g01120 | Cho *et al*. (2013) |
| 49 | Gene | *NAL9* | Narrow leaf | 3 | LOC\_Os03g29810 | Li *et al*. (2013b) |
| 50 | Gene | *AGO1a* | Adaxial rolling | 2 | LOC\_Os02g45070 | Li *et al*. (2013a) |
| 51 | Gene | *s1-145* | Adaxial rolling | 2 | Unknown | Xie *et al*., (2013) |
| 52 | Gene | *OsZHD1* | Outward rolling | 9 | LOC\_Os09g29130 | Xu *et al*. (2014) |
| 53 | Gene | *OsMYB103L* | Upward rolling | 8 | LOC\_Os08g05520 | Yang *et al*. (2014) |
| 54 | Gene | *DNAL1* | Narrow leaf | 2 | Unknown | Sang *et al*. (2014) |
| 55 | Gene | *NAL5* | Narrow leaf | 4 | Unknown | Cho *et al*. (2014) |
| 56 | Gene | *rl15(t)* | Inward rolling | 10 | Unknown | Zhang *et al*. (2014) |
| 57 | Gene | *rl28* | Inward rolling | 5 | Unknown | Feng *et al*. (2015) |
| 58 | Gene | *Nrl3(t)* | Adaxial rolling | 2 | Unknown | Zhang *et al*. (2015b) |
| 59 | Gene | *SLL2* | Inward rolling | 7 | LOC\_Os07g38664 | Zhang *et al*. (2015a) |
| 60 | Gene | *REL1* | Inward rolling | 1 | LOC\_Os01g64380 | Chen *et al*. (2015) |
| 61 | Gene | *NAL10* | Narrow leaf | 1 | Unknown | Fang *et al*. (2015) |
| 62 | Gene | *rl16(t)/RL16* | Rolled leaf | 9 | LOC\_Os09g09360 | Liu *et al*. (2015) |
| 63 | Gene | *LRL1* | Late-stage rolled leaf | 9 | Unknown | Zhao *et al*. (2015) |
| 64 | Gene | *NL(t)* | Narrow leaf | 4 | Unknown | Pan *et al*. (2015); Zhang *et al*. (2016) |
| 65 | Gene | *REL2* | Rolling & erect leaf  | 10 | LOC\_Os10g41310 | Yang *et al*. (2016) |
| 66 | Gene | *SRL2* | Inward rolling | 3 | LOC\_Os03g19520 | Liu *et al*. (2016) |
| 67 | Gene | *SCL1* | Semi-curled leaf | 2 | LOC\_Os02g44360 | Zhang *et al*. (2016) |
| 68 | Gene | *SRS5* | Leaf rolling | 11 | LOC\_Os11g14220 | Segami *et al*. (2012) |
| 69 | Gene | *DTL1* | Twisty leaf | 10 | Unknown | Zhang *et al*. (2012) |
| 70 | Gene | *OsLBD3-7* | Narrow and adaxiallyrolled leaf | 3 | LOC\_Os03g57660 | Li *et al*. (2016) |
| 71 | Gene | *NAL11* | Narrow leaf | 7 | LOC\_Os07g09450 | Wu *et al*. (2016); Zhao *et al*. (2017) |
| 72 | Gene | *NRL4* | Narrow and rolling leaf | 3 | LOC\_Os03g19770 | Liang *et al*. (2016) |
| 73 | Gene | *OsARVL4* | Abaxially rolled leaves | 4 | LOC\_Os04g33570 | Wang *et al*. (2016) |
| 74 | Gene | *OsARF18* | Rolled leaves | 6 | LOC\_Os06g47150 | Huang *et al*. (2016) |
| 75 | Gene | *RL15* | Adaxial leaf rolling | 1 | LOC\_Os01g37837 | Lee *et al*. (2016) |
| 76 | Gene | *DNL2* | Dwarf and narrow leaf | 10 | Unknown | Adedze *et al*. (2017) |
| 77 | Gene | *SFL1* | Screw flag leaf | 10 | LOC\_Os10g28060 | Alamin *et al*. (2017) |
| 78 | Gene | *OsYABBY6* | Adaxial rolling | 12 | LOC\_Os12g42610 | Xia *et al*. (2017) |
| 79 | Gene | *OsI\_14279* | Rolling leaf | 3 | LOC\_Os03g62620 | Wang *et al*. (2017) |
| 80 | Gene | *OsRRK1* | Adaxially rolled leaves | 6 | LOC\_Os06g47820 | Ma *et al*. (2017) |
| 81 | Gene | *OsHB4* | Adaxially rolled leaves | 3 | LOC\_Os03g43930 | Zhang *et al*. (2018) |
| 82 | Gene | *LRRK1* | Adaxially rolled leaves | 6 | LOC\_Os06g07070 | Zhou *et al*. (2018) |
| 83 | Gene | *OsSND2* | Rolled leaf | 5 | LOC\_Os05g48850 | Ye *et al*. (2018) |
| 84 | Gene | *KAN1* | Upward rolling leaf | 9 | Unknown | Adedze *et al*. (2018) |
| 85 | QTL | *QFl4* | Inward rolling | 4 | Unknown | Xu *et al*. (1999) |
| 86 | QTL | *QFl5* | Inward rolling | 5 | Unknown | Xu *et al*. (1999) |
| 87 | QTL | *QFl7* | Inward rolling | 7 | Unknown | Xu *et al*. (1999) |
| 88 | QTL | *QFl9* | Inward rolling | 9 | Unknown | Xu *et al*. (1999) |
| 89 | QTL | *qRL-1* | Outward rolling | 1 | Unknown | Xu *et al*. (1999); Guo *et al*. (2010) |
| 90 | QTL | *qRL3* | Outward rolling | 3 | Unknown | Xu *et al*. (1999) |
| 91 | QTL | *qRL5* | Outward rolling | 5 | Unknown | Xu *et al*. (1999) |
| 92 | QTL | *qRL-7* | Outward rolling | 7 | Unknown | Xu *et al*. (1999); Guo *et al*. (2010) |
| 93 | QTL | *qRL4-2* | Rolled leaf | 4 | Unknown | Gao *et al*. (2007) |
| 94 | QTL | *qRL5-9* | Rolled leaf | 5 | Unknown | Gao *et al*. (2007) |
| 95 | QTL | *qRL5-10* | Rolled leaf | 5 | Unknown | Gao *et al*. (2007) |
| 96 | QTL | *qRL-2-1b* | Rolled leaf | 2 | Unknown | Gao *et al*. (2007) |
| 97 | QTL | *qRL-6* | Rolled leaf | 6 | Unknown | Gao *et al*. (2007); Guo *et al*., (2010) |
| 98 | QTL | *qRL-8-1* | Rolled leaf | 8 | Unknown | Gao *et al*. (2007); Guo *et al*., (2010) |
| 99 | QTL | *qRL-8-2* | Rolled leaf | 8 | Unknown | Gao *et al*. (2007); Guo *et al*. (2010) |
| 100 | QTL | *qRL-9* | Rolled leaf | 9 | Unknown | Gao *et al*. (2007); Guo *et al*. (2010) |
| 101 | QTL | *qRL-10* | Rolled leaf | 10 | Unknown | Gao *et al*. (2007); Guo *et al*., (2010) |
| 102 | QTL | *qRL7b* | Rolled leaf | 7 | Unknown | Zhang *et al*. (2016) |
| 103 | QTL | *qRL9b* | Rolled leaf | 9 | Unknown | Zhang *et al*. (2016) |

**Abbreviation:** Chr, Chromosome

**Table S2.** Conserved domain analysis of the 42 RL proteins identified in this study

| **Protein Name** | **Domain Name** | **Accession** | **Description** | **Interval** | **E-value** |
| --- | --- | --- | --- | --- | --- |
| OsACL1 | No conserved domain found |  | No conserved domain have been identified for this query sequence |  |  |
| OsADL1 | Peptidase\_C2 | pfam00648 | Calpain family cysteine protease | 1707-2006 | 8.65e-120 |
| Calpain\_III super family | cl00165 | Calpain, subdomain III | 2012-2162 | 2.78e-35 |
| LamG super family | cl22861 | Laminin G domain | 1436-1596 | 9.49e-06 |
| OsAGO1a | Piwi-like super family | cl00628 | Piwi-like: PIWI domain | 197-1082 | 0e+00 |
| Gly-rich\_Ago1 | pfam12764 | Glycine-rich region of argonaut | 98-200 | 4.94e-44 |
| OsAGO7 | Piwi\_ago-like | cd04657 | Piwi\_ago-like: PIWI domain, Argonaute-like subfamily. | 575-1016 | 0e+00 |
| ArgoN | pfam16486 | N-terminal domain of argonaute | 197-352 | 1.52e-31 |
| PAZ | pfam02170 | PAZ domain; This domain is named PAZ after the proteins Piwi Argonaut and Zwille. | 438-544 | 2.96e-29 |
| ArgoL1 | pfam08699 | Argonaute linker 1 domain. ArgoL1 is a region found in argonaute proteins. | 363-412 | 1.38e-11 |
| PLN03202 | PLN03202 | protein argonaute; Provisional | 194-1048 | 6.95e-151 |
| OsARF18 | Auxin\_resp | pfam06507 | Auxin response factor. A conserved region of auxin-responsive transcription factors. | 292-375 | 4.85e-45 |
| B3 | pfam02362 | B3 DNA binding domain. This is a family of plant transcription factors with various roles in development. | 128-229 | 5.07e-28 |
| OsARVL4 | PEBP super family | cl00227 | Phosphatidyl Ethanolamine-Binding Protein (PEBP) domain. Phosphatidyl Ethanolamine-Binding Proteins (PEBPs) are represented in all three major phylogenetic divisions (eukaryotes, bacteria, archaea). A number of biological roles for members of the PEBP family include serine protease inhibition, membrane biogenesis, regulation of flowering plant stem architecture, and Raf-1 kinase inhibition. | 1-173 | 9.05e-82 |
| OsAS2 | DUF260 | pfam03195 | Protein of unknown function DUF260. | 38-135 | 4.04e-63 |
| OsCFL1 | WW | pfam00397 | WW domain. The WW domain is a protein module with two highly conserved tryptophans that binds proline-rich peptide motifs in vitro. | 56-86 | 1.37e-03 |
| OsDCL1 | PAZ\_CAF\_like | cd02844 | PAZ domain, CAF\_like subfamily. | 1152-1298 | 1.04e-61 |
| Rnc | COG0571 | dsRNA-specific ribonuclease [Transcription] | 1538-1779 | 6.20e-46 |
| helicase\_insert\_domain super family | cl17041 | helicase\_insert\_domain. This helical domain can be found inserted in a subset of SF2-type DEAD-box related helicases, like archaeal Hef helicase, MDA5-like helicases and FancM-like helicases. | 251-779 | 6.79e-42 |
| Dicer\_dimer | pfam03368 | Dicer dimerisation domain. | 817-906 | 1.45e-30 |
| RIBOc | cd00593 | RIBOc. Ribonuclease III C terminal domain. | 1337-1518 | 1.97e-30 |
| DSRM super family | cl00054 | Double-stranded RNA binding motif. | 1797-1870 | 3.44e-15 |
| OsHB4 | START\_ArGLABRA2\_like | cd08875 | C-terminal lipid-binding START domain of the Arabidopsis homeobox protein GLABRA 2 and related proteins; This subfamily includes the steroidogenic acute regulatory protein (StAR)-related lipid transfer (START) domains of the Arabidopsis homeobox protein GLABRA 2 and related proteins. | 175-391 | 1.47e-69 |
| MEKHLA | pfam08670 | MEKHLA domain; The MEKHLA domain shares similarity with the PAS domain and is found in the 3' end of plant HD-ZIP III homeobox genes, and bacterial proteins. | 715-857 | 2.34e-65 |
| Homeobox | pfam00046 | Homeobox domain | 32-89 | 4.52e-17 |
| bZIP | cd14686 | Basic leucine zipper (bZIP) domain of bZIP transcription factors: a DNA-binding and dimerization domain; Basic leucine zipper (bZIP) factors comprise one of the most important classes of enhancer-type transcription factors. | 84-123 | 2.04e-06 |
| OsI\_14279 | WHy | smart00769 | Water Stress and Hypersensitive response; | 61-155 | 2.23e-23 |
| LEA\_2 | pfam03168 | Late embryogenesis abundant protein; Different types of LEA proteins are expressed at different stages of late embryogenesis in higher plant seed embryos and under conditions of dehydration stress. The function of these proteins is unknown. | 206-301 | 6.86e-18 |
| OsLBD3-7 | M28\_PSMA\_like | cd08022 | M28 Zn-peptidase prostate-specific membrane antigen; Peptidase M28 family; prostate-specific membrane antigen (PSMA, also called glutamate carboxypeptidase II or GCP-II)-like subfamily. | 325-549 | 3.34e-116 |
| PA super family | cl28883 | PA: Protease-associated (PA) domain. | 118-310 | 1.80e-34 |
| TFR\_dimer | pfam04253 | Transferrin receptor-like dimerisation domain; This domain is involved in dimerisation of the transferrin receptor as shown in its crystal structure. | 578-694 | 1.55e-17 |
| OsLC2 | PHD\_Oberon | pfam07227 | PHD - plant homeodomain finger protein; PHD\_oberon is a plant homeodomain finger domain of Oberon proteins from plants. | 143-263 | 1.18e-55 |
| FN3 | cd00063 | Fibronectin type 3 domain; One of three types of internal repeats found in the plasma protein fibronectin. | 343-424 | 2.12e-03 |
| OsLRRK1 | STKc\_IRAK | cd14066 | Catalytic domain of the Serine/Threonine kinases, Interleukin-1 Receptor Associated Kinases and related STKs; STKs catalyze the transfer of the gamma-phosphoryl group from ATP to serine/threonine residues on protein substrates. | 54-321 | 1.87e-92 |
| OsMYB103L | Myb\_DNA-binding | pfam00249 | Myb-like DNA-binding domain. This family contains the DNA binding domains from Myb proteins, as well as the SANT domain family. | 67-112 | 6.27e-16 |
| Myb\_DNA-binding | pfam00249 | Myb-like DNA-binding domain. This family contains the DNA binding domains from Myb proteins, as well as the SANT domain family. | 14-61 | 1.29e-15 |
| SANT | smart00717 | SANT SWI3, ADA2, N-CoR and TFIIIB'' DNA-binding domains | 67-114 | 5.92e-15 |
| SANT | smart00717 | SANT SWI3, ADA2, N-CoR and TFIIIB'' DNA-binding domains | 14-63 | 1.69e-12 |
| OsNAL1 | No conserved domain found |  | No conserved domain have been identified for this query sequence |  |  |
| OsNAL11 | DnaJ super family | cl02542 | DnaJ domain or J-domain. DnaJ/Hsp40 (heat shock protein 40) proteins are highly conserved and play crucial roles in protein translation, folding, unfolding, translocation, and degradation. | 1-103 | 1.19e-22 |
| OsNAL2 | Homeobox | pfam00046 | Homeobox domain | 7-61 | 7.68e-13 |
| OsNAL3/OsWOX3 | Homeobox | pfam00046 | Homeobox domain | 7-61 | 1.39e-12 |
| OsNAL7/OsCOW1 | Pyr\_redox\_3 | pfam13738 | Pyridine nucleotide-disulphide oxidoreductase | 27-220 | 6.31e-17 |
| NADB\_Rossmann super family | cl21454 | Rossmann-fold NAD(P)(+)-binding proteins; A large family of proteins that share a Rossmann-fold NAD(P)H/NAD(P)(+) binding (NADB) domain. | 334-386 | 1.86e-04 |
| CzcO | COG2072 | Predicted flavoprotein CzcO associated with the cation diffusion facilitator CzcD [Inorganic ion transport and metabolism] | 27-351 | 2.86e-50 |
| OsNAL9 | S14\_ClpP\_2 | cd07017 | Caseinolytic protease (ClpP) is an ATP-dependent, highly conserved serine protease. | 84-252 | 4.11e-78 |
| OsNRL1 | Glyco\_tranf\_GTA\_type super family | cl11394 | Glycosyltransferase family A (GT-A) includes diverse families of glycosyl transferases with a common GT-A type structural fold. | 643-956 | 7.14e-19 |
| RING super family | cl17238 | RING-finger (Really Interesting New Gene) domain. | 175-202 | 1.72e-06 |
| PLN02248 | PLN02248 | Cellulose synthase-like protein D4 (CLSD4) | 22-1215 | 0e+00 |
| OsNRL4 | No conserved domain found |  | No conserved domain have been identified for this query sequence |  |  |
| OsREL1 | No conserved domain found |  | No conserved domain have been identified for this query sequence |  |  |
| OsREL2 | DUF632 | pfam04782 | Protein of unknown function (DUF632). | 325-631 | 2.07e-113 |
| DUF630 | pfam04783 | Protein of unknown function (DUF630). | 1-59 | 2.74e-27 |
| OsRFS | SNF2\_N super family | cl26465 | SNF2 family N-terminal domain. | 595-1123 | 1.33e-136 |
| PHD2\_CHD\_II | cd15532 | PHD finger 2 found in class II Chromo domain-Helicase-DNA binding (CHD) proteins. | 35-76 | 3.70e-22 |
| SANT\_TRF | cd11660 | Telomere repeat binding factor-like DNA-binding domains of the SANT/myb-like family. | 1645-1689 | 2.10e-08 |
| DUF1087 super family | cl05792 | Domain of Unknown Function (DUF1087). | 1206-1255 | 5.49e-08 |
| CHROMO | cd00024 | Chromatin organization modifier (chromo) domain. | 476-526 | 8.88e-08 |
| Atrophin-1 super family | cl26464 | Atrophin-1 family. | 1907-2192 | 7.00e-06 |
| Chromo | pfam00385 | Chromo (CHRromatin Organisation MOdifier) domain | 533-554 | 7.16e-04 |
| OsRL14 | 2OG-FeII\_Oxy | pfam03171 | 2OG-Fe(II) oxygenase superfamily | 1-93 | 3.84e-32 |
| OsRL15 | PLN02678 | PLN02678 | seryl-tRNA synthetase | 1-445 | 0e+00 |
| OsRL16 | PGAP1 | pfam07819 | PGAP1-like protein; The sequences found in this family are similar to PGAP1. | 79-347 | 2.23e-101 |
| OsRL9/OsSLL1 | myb\_SHAQKYF | TIGR01557 | myb-like DNA-binding domain, SHAQKYF class. | 325-378 | 1.58e-21 |
| OsRoc5 | START\_ArGLABRA2\_like | cd08875 | C-terminal lipid-binding START domain | 309-545 | 8.42e-115 |
| Homeobox | pfam00046 | Homeobox domain | 101-154 | 2.19e-22 |
| bZIP super family | cl21462 | Basic leucine zipper (bZIP) domain of bZIP transcription factors: a DNA-binding and dimerization domain | 136-181 | 4.90e-04 |
| OsRRK1 | PKc\_like super family | cl21453 | Protein Kinases, catalytic domain; The protein kinase superfamily is mainly composed of the catalytic domains of serine/threonine-specific and tyrosine-specific protein kinases. It also includes RIO kinases, which are atypical serine protein kinases, aminoglycoside phosphotransferases, and choline kinases. | 75-339 | 9.36e-87 |
| OsSCL1 | GRAS super family | cl15987 | GRAS domain family | 363-708 | 6.47e-92 |
| OsSFL1 | PLN03169 super family | cl28398 | Chalcone synthase family protein; Provisional | 96-514 | 0e+00 |
| OsSLL2 | No conserved domain found |  | No conserved domain have been identified for this query sequence |  |  |
| OsSND2 | NAM | pfam02365 | No apical meristem (NAM) protein. This is a family of no apical meristem (NAM) proteins these are plant development proteins. | 179-206 | 3.09e-03 |
| OsSRL1 | No conserved domain found |  | No conserved domain have been identified for this query sequence |  |  |
| OsSRL2 | No conserved domain found |  | No conserved domain have been identified for this query sequence |  |  |
| OsSRS5 | PLN00221 | PLN00221 | Tubulin alpha chain; Provisional | 1-438 | 0e+00 |
| OsYABBY1 | YABBY | pfam04690 | YABBY protein; YABBY proteins are a group of plant-specific transcription involved in the specification of abaxial polarity in lateral organs. | 5-146 | 3.37e-76 |
| OsYABBY6 | YABBY | pfam04690 | YABBY protein; YABBY proteins are a group of plant-specific transcription involved in the specification of abaxial polarity in lateral organs. | 6-176 | 1.39e-95 |
| OsZHD1 | ZF-HD\_dimer | pfam04770 | ZF-HD protein dimerization region. | 56-108 | 3.03e-35 |
| homeo\_ZF\_HD | TIGR01565 | homeobox domain, ZF-HD class. | 215-271 | 1.97e-26 |

**Table S3.** The enriched GO terms for all rolling leaf genes identified in this study

| **GO term** | **Ontology** | **Description** | **Genes** | **Number in****input list** | **P-value** |
| --- | --- | --- | --- | --- | --- |
| GO:0007275 | BP | multicellular organismal development | *OsAS2, OsSCL1, OsAGO1a, OsRoc5, OsADL1, OsHB4, OsLBD3-7, OsSND2, OsARF18, OsYABBY1, OsRL9, OsNAL2, OsNAL3, OsNRL1, OsYABBY6* | 15 | 4.92E-10 |
| GO:0009908 | BP | flower development | *OsAS2, OsHB4, OsLBD3-7, OsARF18, OsYABBY1, OsRL9, OsNAL2, OsNAL3, OsYABBY6* | 9 | 5.4E-08 |
| GO:0045449 | BP | regulation of transcription | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 6.5E-06 |
| GO:0019219 | BP | regulation of nucleobase, nucleoside, nucleotide and nucleic acid metabolic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 6.8E-06 |
| GO:0051171 | BP | regulation of nitrogen compound metabolic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 6.8E-06 |
| GO:0031326 | BP | regulation of cellular biosynthetic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 8.7E-06 |
| GO:0009889 | BP | regulation of biosynthetic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 8.7E-06 |
| GO:0010556 | BP | regulation of macromolecule biosynthetic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 8.7E-06 |
| GO:0010468 | BP | regulation of gene expression | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 9.4E-06 |
| GO:0031323 | BP | regulation of cellular metabolic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 0.00001 |
| GO:0010467 | BP | gene expression | *OsZHD1, OsHB4, OsDCL1, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL15, OsRL9, OsNAL3, OsARF18* | 12 | 1.1E-05 |
| GO:0080090 | BP | regulation of primary metabolic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 1.2E-05 |
| GO:0006350 | BP | transcription | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 1.2E-05 |
| GO:0060255 | BP | regulation of macromolecule metabolic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 1.3E-05 |
| GO:0019222 | BP | regulation of metabolic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 1.5E-05 |
| GO:0009791 | BP | post-embryonic development | *OsLC2, OsAGO1a, OsADL1, OsAGO7, OsHB4, OsLBD3-7, OsI\_14279, OsZHD1, OsYABBY6* | 9 | 2.29E-05 |
| GO:0000003 | BP | reproduction | *OsLC2, OsAGO1a, OsADL1, OsHB4, OsI\_14279, OsARF18, OsZHD1, OsYABBY6* | 8 | 4.05E-05 |
| GO:0030154 | BP | cell differentiation | *OsSCL1, OsAGO1a, OsRoc5, OsADL1, OsYABBY1, OsRL9, OsYABBY6* | 7 | 4.37E-05 |
| GO:0050794 | BP | regulation of cellular process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 6E-05 |
| GO:0006139 | BP | nucleobase-containing compound (nucleobase, nucleoside, nucleotide and nucleic acid) metabolic process | *OsRL15, OsSCL1, OsRoc5, OsAGO7, OsHB4, OsSND2, OsARF18, OsYABBY1, OsMYB103L, OsRL9, OsZHD1, OsNAL2, OsNAL3, OsYABBY6* | 14 | 6.33E-05 |
| GO:0050789 | BP | regulation of biological process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 8.1E-05 |
| GO:0065007 | BP | biological regulation | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsRL9, OsNAL3, OsARF18* | 10 | 0.00012 |
| GO:0016070 | BP | RNA metabolic process | *OsHB4, OsDCL1, OsNAL2, OsRoc5, OsRL15, OsNAL3, OsARF18* | 7 | 0.00025 |
| GO:0009790 | BP | embryo development | *OsAGO1a, OsADL1, OsHB4, OsLBD3-7, OsI\_14279, OsZHD1* | 6 | 0.00041 |
| GO:0006351 | BP | transcription, DNA-templated | *OsSCL1, OsRoc5, OsHB4, OsARF18, OsRL9, OsNAL2* | 6 | 0.00076 |
| GO:0006355 | BP | regulation of transcription, DNA-templated | *OsSCL1, OsRoc5, OsHB4, OsSND2, OsARF18, OsMYB103L, OsRL9, OsNAL2* | 8 | 0.00172 |
| GO:0051252 | BP | regulation of RNA metabolic process | *OsNAL3, OsHB4, OsRoc5, OsARF18, OsNAL2* | 5 | 0.0018 |
| GO:0032774 | BP | RNA biosynthetic process | *OsNAL3, OsHB4, OsRoc5, OsARF18, OsNAL2* | 5 | 0.0023 |
| GO:0009653 | BP | anatomical structure morphogenesis | *OsSCL1, OsAGO1a, OsRoc5, OsHB4, OsRL9, OsYABBY6* | 6 | 0.00265 |
| GO:0009058 | BP | biosynthetic process | *OsSCL1, OsRoc5, OsHB4, OsSND2, OsARF18, OsYABBY1, OsMYB103L, OsRL9, OsZHD1, OsNAL2, OsNAL3, OsNRL1, OsYABBY6* | 13 | 0.00309 |
| GO:0009628 | BP | response to abiotic stimulus | *OsLC2, OsAGO1a, OsRoc5, OsLBD3-7, OsI\_14279, OsSFL1, OsSRS5, OsNRL1* | 8 | 0.00866 |
| GO:0044249 | BP | cellular biosynthetic process | *OsZHD1, OsHB4, OsSFL1, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsNRL1, OsRL9, OsNAL3, OsARF18, OsRL15* | 13 | 0.013 |
| GO:0034645 | BP | cellular macromolecule biosynthetic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsNRL1, OsRL9, OsNAL3, OsARF18, OsRL15* | 12 | 0.014 |
| GO:0009059 | BP | macromolecule biosynthetic process | *OsZHD1, OsHB4, OsSND2, OsRFS, OsNAL2, OsRoc5, OsMYB103L, OsNRL1, OsRL9, OsNAL3, OsARF18, OsRL15* | 12 | 0.014 |
| GO:0044238 | BP | primary metabolic process | *OsZHD1, OsMYB103L, OsHB4, OsSFL1, OsNAL9, OsSND2, OsRL16, OsRFS, OsNAL2, OsLBD3-7, OsRoc5, OsADL1, OsNAL3, OsNRL1, OsRL9, OsRRK1, OsLRRK1, OsARF18, OsRL15, OsDCL1* | 20 | 0.029 |
| GO:0043170 | BP | macromolecule metabolic process | *OsZHD1, OsHB4, OsADL1, OsNAL9, OsSND2, OsRFS, OsNAL2, OsLBD3-7, OsRoc5, OsMYB103L, OsNAL3, OsNRL1, OsRL9, OsRRK1, OsLRRK1, OsARF18, OsRL15, OsDCL1* | 18 | 0.033 |
| GO:0009793 | BP | embryo development ending in seed dormancy | *OsAGO1a, OsADL1, OsI\_14279* | 3 | 0.034 |
| GO:0008150 | BP | biological\_process | *OsRL15, OsCFL1, OsSCL1, OsSRL2, OsAGO7, OsI\_14279, OsARVL4, OsACL1, OsNAL1, OsARF18, OsSRL1, OsREL2, OsNAL2, OsNAL3, OsNRL1* | 15 | 0.04107 |
| GO:0005634 | CC | nucleus | *OsAS2, OsLC2, OsAGO1a, OsRoc5, OsHB4, OsSND2, OsARF18, OsYABBY1, OsMYB103L, OsRL9, OsNAL2, OsNAL3, OsYABBY6* | 13 | 0.0008 |
| GO:0005575 | CC | cellular\_component | *OsLC2, OsCFL1, OsAGO7, OsLBD3-7, OsI\_14279, OsARVL4, OsNAL1, OsSRL1, OsYABBY1, OsNAL11, OsREL2, OsSRS5* | 12 | 0.0225 |
| GO:0003700 | MF | sequence-specific DNA binding transcription factor activity | *OsSCL1, OsRoc5, OsHB4, OsSND2, OsARF18, OsYABBY1, OsMYB103L, OsRL9, OsZHD1, OsNAL2, OsNAL3, OsYABBY6* | 12 | 3.16E-06 |
| GO:0003677 | MF | DNA binding | *OsRoc5, OsHB4, OsSND2, OsARF18, OsYABBY1, OsMYB103L, OsRL9, OsZHD1, OsREL2, OsNAL2* | 10 | 0.00424 |

**Abbreviation:** BP, Biological process; CC, Cellular component; MF, Molecular function.

**Table S4.** Identified rolling leaf genes KEGG orthologous (KO) and their description

|  |  |  |
| --- | --- | --- |
| **Gene** | **KO** | **Definition** |
| *OsAGO1a* | K11593 | ELF2C; eukaryotic translation initiation factor 2C |
| *OsNAL7* | K11816 | YUCCA; indole-3-pyruvate monooxygenase [EC:1.14.13.168] |
| *OsNAL9* | K01358 | clpP; ATP-dependent Clp protease, protease subunit [EC:3.4.21.92] |
| *OsNAL11* | K09539 | DNAJC19; DnaJ homolog subfamily C member 19 |
| *OsNRL1* | K00770 | E2.4.2.24; 1,4-beta-D-xylan synthase [EC:2.4.2.24] |
| *OsAGO7* | K11593 | ELF2C; eukaryotic translation initiation factor 2C |
| *OsLBD3-7* | K01301 | NAALAD; N-acetylated-alpha-linked acidic dipeptidase [EC:3.4.17.21] |
| *OsMYB103L* | K09422 | MYBP; transcription factor MYB, plant |
| *OsRoc5* | K09338 | HD-ZIP; homeobox-leucine zipper protein |
| *OsSFL1* | K15397 | KCS; 3-ketoacyl-CoA synthase [EC:2.3.1.199] |
| *OsSRL2* | K21842 | EFR3; protein EFR3 |
| *OsSRS5* | K07374 | TUBA; tubulin alpha |
| *OsHB4* | K09338 | HD-ZIP; homeobox-leucine zipper protein |
| *OsRL15* | K01875 | SARS; seryl-tRNA synthetase [EC:6.1.1.11] |



**Fig. S1.**  Gene structure of 42 rolling leaf genes. The blue color area at the start is representing the upstream, the blue color area at the end is representing the downstream, the yellow color area is representing the exon (CDS) and the black color line is representing the intron of each gene. The intron phase is indicated by the numbers 0, 1 and 2. The exon/intron structure was constructed using the Gene Structure Display Server 2.0 (GSDS2.0: http://gsds.cbi.pku.edu.cn).



**Fig. S2.**  Phylogenetic tree and conserved domain organization of 42 rolling leaf proteins of interest identified in this study. (a) Phylogenetic tree: The tree was constructed based on multiple aligned sequences by maximum likelihood method with bootstrap of 1000 in MEGA6. Multiple sequence alignment was performed using ClustalW program in MEGA6. The colored shapes indicate different clusters of RL proteins. The roman numerals I-Vd indicates groups and subgroups of RL genes. (b) Domain organization: Domains are indicated with different colors except for black along with domain names (for more details about domains see Table S2). Domain organization was done using online Conserved Domain Database (CDD) tool “Batch CD-Search” of NCBI (https://www.ncbi.nlm.nih.gov/Structure/bwrpsb/bwrpsb.cgi).

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