

Supplement S1. Genes preferentially expressed in wild-type pericycle cells compared to the pericycle of the lateral root initiation mutant *rum1*.

GeneID	p-value ^a	Fold-change ^a	Blastx result ^b [Species] Accession number
Transcription^c			
MEST 24-E09	4.88E-03	7.01	Helix-loop-helix-like protein [<i>O. sativa</i>] AAO72577.1
618015B12.X1	5.56E-03	2.75	Helix-loop-helix protein [<i>A. thaliana</i>] NP_194827.1
MEST 29-G12	1.95E-03	2.75	Pumilio/Mpt5 family RNA-binding protein [<i>O. sativa</i>] BAB89558.1
MEST 27-C10	5.30E-03	2.74	Nucleoid DNA-binding-like protein [<i>O. sativa</i>] BAC15479.1
614089B09.Y1	3.14E-03	2.66	Putative RNA helicase [<i>O. sativa</i>] NP_922213.1
MEST 24-F07	9.34E-03	2.43	U2 Snrnp auxiliary factor [<i>A. thaliana</i>] AAM98156.1
687064E06.Y1	4.67E-04	2.33	DNA methyltransferase ZMET4 [<i>Z. mays</i>] AAK40306.1
707050G12.X1	6.69E-04	2.33	High mobility group protein MNB1b [<i>Z. mays</i>] T03640
MEST 35-G08	5.81E-03	2.28	KH domain protein [<i>A. thaliana</i>] NP_201244.2
614056B02.X1	1.30E-03	2.00	RRNA methylase [<i>A. thaliana</i>] NP_197043.1
Signal transduction mechanism/cellular communication			
486062F10.X1	3.10E-03	2.55	Protein kinase CK2 catalytic subunit CK2 alpha-3 [<i>Z. mays</i>] AAG36872.1
MEST 11-G06	3.12E-03	2.36	Protein kinase [<i>O. sativa</i>] BAA99439.1
687067C03.X1	2.07E-03	2.23	FKBP12 interacting protein (FIP37) [<i>A. thaliana</i>] NP_190985.1
603017B03.X1	6.40E-03	2.19	Receptor-like protein kinase [<i>O. sativa</i>] AAM27467.1
486082B04.X1	6.59E-03	2.02	Protein phosphatase 2A regulatory subunit [<i>O. sativa</i>] AAK13162.1
Cell cycle and DNA processing			
687027G04.X3	1.73E-03	2.57	HD2 type histone deacetylase HDA106 [<i>Z. mays</i>] AF384033_1
606022B03.X1	9.43E-03	2.22	Wee1-like protein [<i>Z. mays</i>] AF123594_1
614051D05.Y1	5.79E-03	2.09	Ran binding protein [<i>O. sativa</i>] NP_910461.1
707090F03.X1	8.74E-03	2.01	Cyclin T2 [<i>O. sativa</i>] BAD17160.1
Metabolism			
707051F04.X1	3.10E-03	5.13	Glyoxalase II [<i>O. sativa</i>] BAB90501.1
486059F07.X3	2.29E-03	3.19	2,3-bisphosphoglycerate-independent phosphoglycerate mutase (BPG-Independent PGAM) [<i>Z. mays</i>] P30792
MEST 166-B10	4.35E-03	3.19	Pyruvate decarboxylase [<i>Z. mays</i>] AAL99744.1
614062G08.Y1	8.13E-03	2.94	Neoxanthin cleavage enzyme [<i>A. thaliana</i>] T51734
687024C07.Y2	9.27E-03	2.82	Aldehyde dehydrogenase [<i>A. thaliana</i>] AAM61211.1
MEST 27-A10	1.05E-03	2.77	Ketol-acid reductoisomerase [<i>O. sativa</i>] BAB86573.1
MEST113-C07	9.19E-03	2.57	Cinnamyl alcohol dehydrogenase [<i>L. perenne</i>] AAL99535.1
MEST 121-G10	2.55E-03	2.56	C2 domain-containing protein [<i>A. thaliana</i>] NP_191525.2
687065B03.X1	5.45E-03	2.40	Nodulin/Glutamate-ammonia ligase [<i>A. thaliana</i>] NP_190886.2
MEST 350-A12	6.15E-03	2.34	Formamidase [<i>O. sativa</i>] BAB63595.1
614031D02.Y1	6.95E-04	2.31	Haloacid dehalogenase-like hydrolase [<i>A. thaliana</i>] NP_974931.1
606034E09.X1	1.67E-03	2.30	S-Adenosylmethionine synthetase 1 [<i>O. sativa</i>] P46611
603014F05.X1	4.20E-04	2.21	Glucose-6-phosphate isomerase [<i>S. oleracea</i>] T09153
707083E03.X1	6.12E-03	2.10	Short-chain dehydrogenase/reductase [<i>A. thaliana</i>] BAB02424.1
MEST 338-H06	9.37E-03	2.09	NADH oxidoreductase [<i>Z. mays</i>] CAB97005.1
Cellular Transport, Transport Facilitation and Transport route			
MEST 197-B05	9.90E-03	257.64	Vesicle soluble NSF attachment protein receptor [<i>O. sativa</i>] BAC16405.1
MEST 233-C02	6.42E-04	3.19	Cation diffusion facilitator 9 [<i>O. sativa</i>] BAD81688.1
603040G10.X1	7.97E-03	3.09	Amino acid transport protein [<i>O. sativa</i>] BAD37472.1
606012C06.X1	3.02E-03	2.50	Membrane protein-1 [<i>M. polymorpha</i>] BAB71817.1
MEST 334-A04	5.67E-04	2.35	Cationic amino acid transporter [<i>O. sativa</i>] AAO73233.1
MEST 31-F02	5.01E-03	2.20	P-Type ATPase [<i>H. vulgare</i>] CAC40031.1
MEST 148-G01	4.50E-03	2.11	Nonclathrin coat protein, gamma [<i>O. sativa</i>] AAN60990.1
MEST 72-G11	1.05E-03	2.09	Allinase [<i>A. thaliana</i>] NP_564436.1
Translation			
614100E06.X1	9.99E-03	2.48	Deoxyhypusine synthase [<i>M. acuminata</i>] AAG53643.1

GenelD	p-value ^a	Fold-change ^a	Blastx result ^b [Species] Accession number
683007G04.X1	2.12E-03	2.02	Argonaute [<i>A. thaliana</i>] NP_175274.1
Cell fate			
707077G05.X1	9.86E-03	28.40	Growth-regulating factor 1 [<i>O. sativa</i>] BAC22210.1
Protein fate (folding, modification, destination)			
MEST 39-D10	3.90E-03	3.01	Serine carboxypeptidase [<i>O. sativa</i>] AAL73563.1
MEST 20-A09	8.72E-03	2.02	Translocation protein-related [<i>A. thaliana</i>] NP_566671.1
Subcellular localization			
614006A06.X2	6.44E-03	2.26	Arginine N-methyltransferase [<i>A. thaliana</i>] BAB01859.1
486019C01.X5	4.51E-03	2.02	Myosin-like protein My5 [<i>O. sativa</i>] BAC01233.1
Defence, cell rescue and virulence			
MEST 42-C07	7.83E-03	2.43	Herbicide safener binding protein 1 [<i>Z. mays</i>] T01354
Transposable elements, viral and plasmid protein			
MEST 35-A04	3.13E-03	3.26	Gag-pol polyprotein [<i>Z. mays</i>] AAL76001.1
Unknown function			
486043B11.X3	1.38E-03	10.85	No database hit
606018A05.X1	7.92E-03	5.77	Unknown protein [<i>A. thaliana</i>] NP_177175.2
486073E10.X2	9.92E-03	4.68	Unknown protein [<i>A. thaliana</i>] NP_177698.1
707087E08.X1	1.44E-03	4.45	Unknown protein [<i>O. sativa</i>] BAB92207.1
Mest12-A10	1.00E-03	3.89	Unknown Protein [<i>O. Sativa</i>] BAA96580.1
MEST 9-E07	5.94E-03	3.88	No database hit
945030c08.Y1	4.28E-03	3.44	Unknown Protein [<i>O. Sativa</i>] BAB91997.1
486051G05.X2	1.89E-03	3.39	No database hit
605004D07.X1	7.77E-03	3.38	No database hit
614028G09.Y1	6.38E-03	3.37	Unknown protein [<i>A. thaliana</i>] NP_200633.1
MEST 19-A08	4.73E-03	2.99	Unknown protein [<i>O. sativa</i>] BAB86427.1
496014F12.X1	4.19E-03	2.96	No database hit
486039H05.X3	7.67E-03	2.92	No database hit
486068D05.X1	9.69E-04	2.78	Unknown protein [<i>A. thaliana</i>] NP_195064.2
MEST 15-G04	5.31E-03	2.78	No database hit
614067C02.X1	2.58E-03	2.72	No database hit
Mest233-G08	3.95E-04	2.60	Unknown Protein [<i>A. Thaliana</i>] NP_565993.1
MEST 356-F08	7.73E-03	2.51	No database hit
MEST 73-E06	9.47E-03	2.45	Unknown protein [<i>A. thaliana</i>] NP_173410.1
486052C05.X2	9.61E-03	2.41	No database hit
614051D08.X2	3.18E-03	2.31	No database hit
603043E01.X1	8.71E-03	2.24	No database hit
614006G05.X2	6.72E-03	2.23	Unknown protein [<i>O. sativa</i>] AAO37540.1
614091F06.X1	9.12E-03	2.22	No database hit
618038C04.X1	3.45E-03	2.21	No database hit
486092F07.Y1	1.91E-03	2.20	Unknown protein [<i>O. sativa</i>] AAN59771.1
606054G11.X2	9.61E-03	2.12	No database hit
687027A12.X3	4.13E-03	2.12	No database hit
603014E11.X1	2.63E-03	2.10	No database hit
MEST 250-F04	5.47E-03	2.10	No database hit
606063G10.X1	7.44E-04	2.08	No database hit
486058E11.X2	2.38E-03	2.06	Unknown protein [<i>A. thaliana</i>] BAB02568.1
687066H09.Y1	4.92E-03	2.05	No database hit
687028D11.X4	4.60E-03	2.02	Unknown protein [<i>O. sativa</i>] BAB16337.1
707087A08.X1	7.87E-03	2.02	Unknown protein [<i>A. thaliana</i>] NP_182078.1
683007C10.X1	7.79E-03	2.02	No database hit
605033E06.X1	7.00E-03	2.01	No database hit
614092H09.X1	5.50E-03	2.01	No database hit
MEST 113-B05	6.91E-03	2.00	No database hit

^a p-value and fold changes of the highest available scan setting for each gene are given

^b In cases where no blast hit for the EST was found the blast hit for the EST contig (ZmTUC) that includes the EST are given

⁹Functional classification according to the MIPS database (Munich Information Center for Protein sequences; version 2.0;
<http://mips.gsf.de/proj/thal/db>)

Supplement S2. Genes upregulated in the pericycle of the lateral root initiation mutant *rum1* compared to wild-type pericycle cells.

GeneID	p-value ^a	Fold-change ^a	Blastx result ^b [Species] Accession number
Transcription^c			
707020F12.y1	4.11E-03	2.90	Transcription factor HBP-1a (c14) [<i>T. aestivum</i>] A54415
707074G06.x1	4.51E-04	2.61	Drought responsive element-binding factor 1 [<i>Z. mays</i>] AAM80486.1
707061E09.x1	5.47E-03	2.20	Susceptibility homeodomain transcription factor [<i>O. sativa</i>] BAD54334.1
486068H10.y1	3.03E-03	2.12	Zinc finger protein [<i>O. sativa</i>] BAB07996.1
Signal transduction mechanism/cellular communication			
486068C07.x1	8.16E-03	2.53	Serine/ threonine kinase [<i>S. bicolor</i>] AM47579.1
707049E12.x1	8.33E-03	2.29	Receptor-like kinase [<i>A. thaliana</i>] NP_172608.1
614098A03.y1	8.42E-03	2.12	Coatomer complex subunit [<i>A. thaliana</i>] NP_175645.1
Metabolism			
MEST62-E09	3.23E-03	2.46	O-Methyltransferase ZRP4 (OMT) [<i>Z. mays</i>] P47917
MEST93-A01	2.46E-03	2.22	Indole-3-glycerol phosphate synthase [<i>O. sativa</i>] BAC22396.1
603009B04.x1	6.42E-04	2.12	Thiazole biosynthetic enzyme 1-1. chloroplast precursor [<i>Z. mays</i>] Q41738
MEST310-E10	2.87E-04	2.09	(1-4)-beta-mannan endohydrolase [<i>O. sativa</i>] BAB56016.1
606066D09.x1	7.58E-03	2.08	Thiolase [<i>O. sativa</i>] AAK54299.1
707016C11.y1	6.38E-03	2.05	Ribulose-5-phosphate kinase [<i>T. aestivum</i>] CAA41020.1
MEST81-H01	7.42E-03	2.04	Caffeoyl-CoA 3-O-methyltransferase [<i>O. sativa</i>] BAA81774.1
Energy			
945002F02.X3	4.49E-03	5.18	NADH-ubiquinone oxidoreductase B8 subunit [<i>A. thaliana</i>] NP_199600.1
606014D04.x1	4.83E-03	2.39	NADPH-quinone oxidoreductase [<i>O. sativa</i>] BAB64708.1
MEST12-B06	2.29E-03	2.37	Ubiquinol-cytochrome c reductase complex protein [<i>S. tuberosum</i>] P48502
MEST41-D06	3.66E-03	2.17	ATP synthase epsilon chain [<i>Z. mays</i>] Q41898
707018A04.y1	6.28E-03	2.11	Ubiquinol-cytochrome c reductase [<i>O. sativa</i>] BAA95821.1
486058C09.x2	5.51E-03	2.06	Ubiquinol-cytochrome c reductase [<i>A. thaliana</i>] NP_190841.1
614042E11.x2	8.99E-03	2.02	Cytochrome c oxidase polypeptide VC [<i>H. vulgare</i>] Q42841
Cellular transport, transport facilitation and transport routes			
486093D03.y1	7.57E-03	2.18	Mitochondrial carrier protein family [<i>A. thaliana</i>] NP_201302.1
Translation			
614008G05.x2	7.19E-03	2.20	60S ribosomal protein L38 [<i>O. sativa</i>] BAC45072.1
Protein fate			
MEST18-C05	8.48E-03	4.53	Serine carboxypeptidase II-1 precursor [<i>H. vulgare</i>] P55747
614041D02.x2	7.09E-03	3.48	IAA2.3 deduced protein [<i>N. tabacum</i>] AAD32142.1
618002E08.x2	3.02E-03	2.51	Copper chaperone homolog CCH [<i>O. sativa</i>] T50779
707030G07.x2	6.98E-03	2.50	Cystatin II [<i>Z. mays</i>] BAB32902.1
MEST18-C06	3.11E-03	2.11	Clathrin assembly protein [<i>O. sativa</i>] AAN08659.1
Subcellular localization			
MEST14-B04	1.84E-03	12.07	Beta-expansin 5 [<i>Z. mays</i>] AAK56128.1
683003D07.x1	1.01E-03	2.07	Beta-expansin [<i>O. sativa</i>] AAL04421.1
614041F07.y1	4.84E-03	2.02	CTD-like phosphatase domain-containing protein [<i>O. sativa</i>] BAB92447.1
Cell rescue, defense and virulence			
707020E03.x1	8.55E-03	3.13	Heat-shock protein [<i>O. sativa</i>] BAB32902.1
MEST11-C11	6.87E-03	2.74	Disease resistance response protein [<i>A. thaliana</i>] NP_176762.1
605001F08.x1	8.73E-03	2.39	Tetratricopeptide repeat (TPR)-containing protein [<i>O. sativa</i>] BAD17488.1
486026D12.x1	8.14E-03	2.10	Defensin [<i>T. aestivum</i>] BAC10287.1
MEST15-C12	4.84E-03	2.04	Heat shock protein 82 [<i>O. sativa</i>] P33126
Transposable elements, viral and plasmid proteins			
603009C09.x1	6.83E-03	2.00	Rice retroelement 2 [<i>Z. mays</i>] AAL75972.1
Unclassified proteins			
MEST340-E12	7.45E-03	2.19	Striated muscle activator-like protein [<i>O. sativa</i>] AAT81723.1
MEST39-B6	7.10E-03	2.17	Pollen specific protein C13 precursor [<i>O. sativa</i>] AAM08621.1
707074D06.x1	1.48E-04	2.07	Pollen specific protein C13 precursor [<i>Z. mays</i>] P33050
Unknown function			
945001C11.Y1	9.92E-03	17.72	No database hit
945001E08.X3	2.39E-03	7.95	Unknown protein [<i>O. sativa</i>] AAO38494.1
614059G05.y1	9.41E-04	4.93	No database hit
614028F01.y1	1.54E-03	2.81	Unknown protein [<i>A. thaliana</i>] C86271

GeneID	p-value ^a	Fold-change ^a	Blastx result ^b [Species] Accession number
707058F12.x2	7.26E-05	2.80	No database hit
605005G03.x1	2.08E-03	2.74	Unknown protein [<i>O. sativa</i>] BAB20639.1
MEST137-F12	6.61E-03	2.66	No database hit
707030B03.x2	7.59E-03	3.55	Unknown protein [<i>A. thaliana</i>] AAM10390.1
603010F04.x1	7.24E-03	2.41	Unknown protein [<i>O. sativa</i>] BAB92454.1
Unknown function (continued)			
496036D12.x1	8.53E-03	2.35	No database hit
707041B02.x1	4.01E-03	2.33	No database hit
614078E02.x1	4.57E-03	2.31	No database hit
618043E10.x1	8.48E-03	2.29	No database hit
614001E05.x1	2.85E-03	2.25	No database hit
603013D04.x1	8.94E-03	2.23	No database hit
603034F04.x1	4.98E-03	2.23	No database hit
707078G10.x1	5.22E-03	2.22	Unknown protein [<i>O. sativa</i>] BAA94780.1
606011B08.x1	5.53E-04	2.20	Unknown protein [<i>A. thaliana</i>] NP_175397.1
486068D12.x1	5.39E-03	2.20	No database hit
618044G06.x1	1.08E-03	2.19	No database hit
MEST66-G04	7.42E-04	2.17	Unknown protein [<i>O. sativa</i>] AAO65857.1
614067G07.y1	7.93E-03	2.14	No database hit
707050E12.x1	2.92E-03	2.14	No database hit
614048E03.y1	4.88E-03	2.12	No database hit
486085B08.x2	1.04E-03	2.11	No database hit
496008A03.x1	7.86E-03	2.10	No database hit
614040C04.y1	3.31E-03	2.08	Unknown protein [<i>O. sativa</i>] BAB92380.1
606007A04.x1	5.66E-03	2.08	No database hit
618037B11.x1	8.68E-03	2.08	No database hit
606021A06.x2	6.84E-03	2.07	No database hit
606026C01.x2	3.18E-03	2.01	Unknown protein [<i>O. sativa</i>] AAD27681.1
MEST106-A02	9.89E-03	2.01	Unknown protein [<i>O. sativa</i>] AAN87739.1
614028B01.y1	5.54E-03	2.01	Unknown protein [<i>A. thaliana</i>] T48183

^a p-value and fold changes of the highest available scan setting for each gene are given

^b In cases where no blast hit for the EST was found the blast hit for the EST contig (ZmTUC) that includes the EST are given

^c Functional classification according to the MIPS database (Munich Information Center for Protein sequences; version 2.0; <http://mips.gsf.de/proj/thal/db>)