

Supplementary dataset S2. Expression data of different NMCPs: *Ppa1*, *Ppa2*, *Osa1*, *Osa2*, *Zma1*, *Zma2*, *Bdi1*, *Bdi2*, *Gma1I*, *Gma1II*, *Gma2II* and *Gma3II* from the eFP browser.

Ppa1

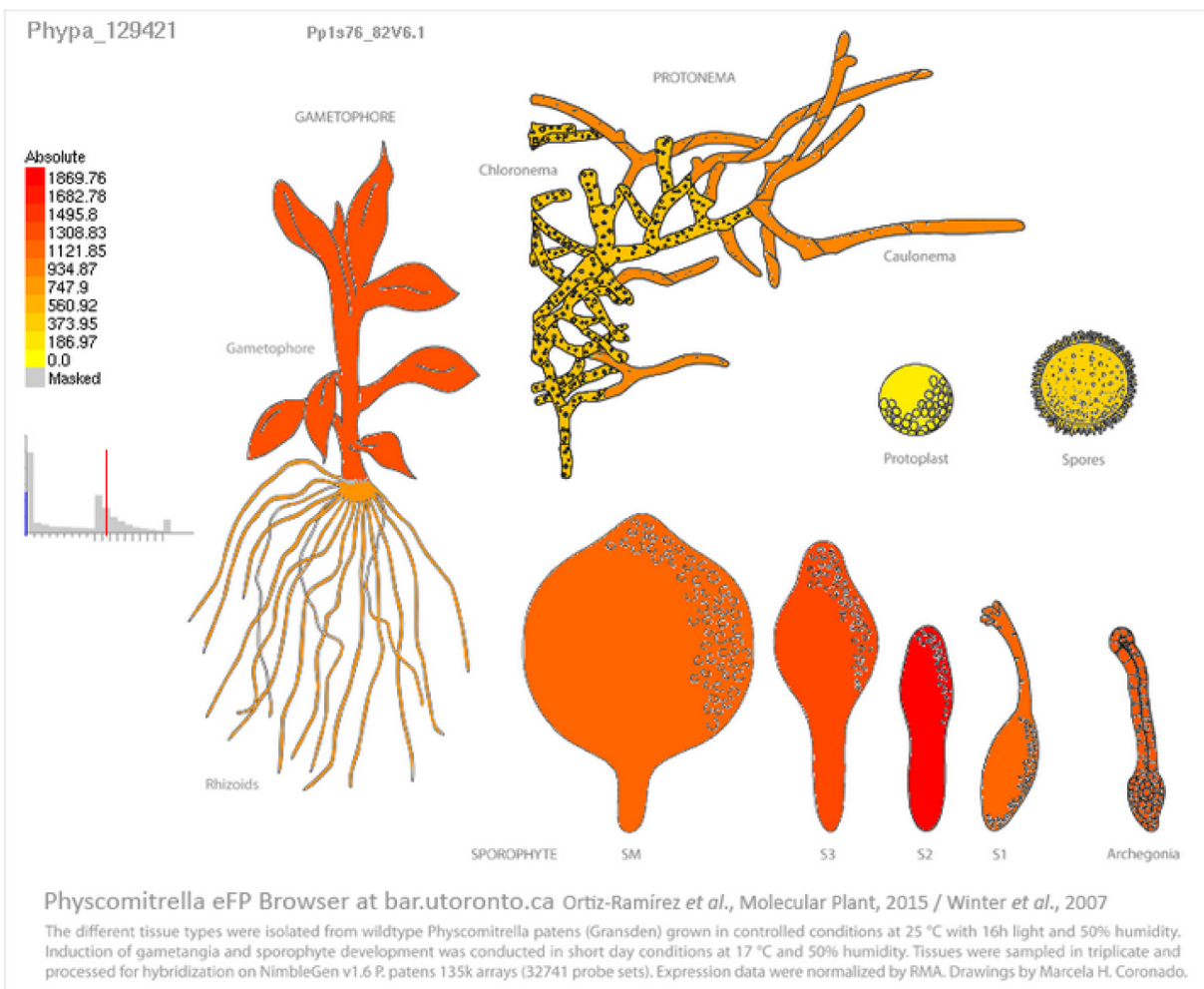
Organism *Physcomitrella patens*
Transcript Name Pp3c2_34830V3.1 (primary)
Alas Pp3c2_34830J5.1 Pp3c2_34830 Phpat.002G143000
Phypa_129421 Pp1s76_81V6 Pp3c2_34830.v3.1



Like 1K

Data Source Mode Primary Gene ID Secondary Gene ID Signal Threshold
Physcomitrella Absolute Pp1s76_82V6.1 Pp1s9_9V6.1 1869.76 Go

• For group1 data, this probe set reaches its maximum expression level (expression potential) of 1869.76 in the Physcomitrella data source.

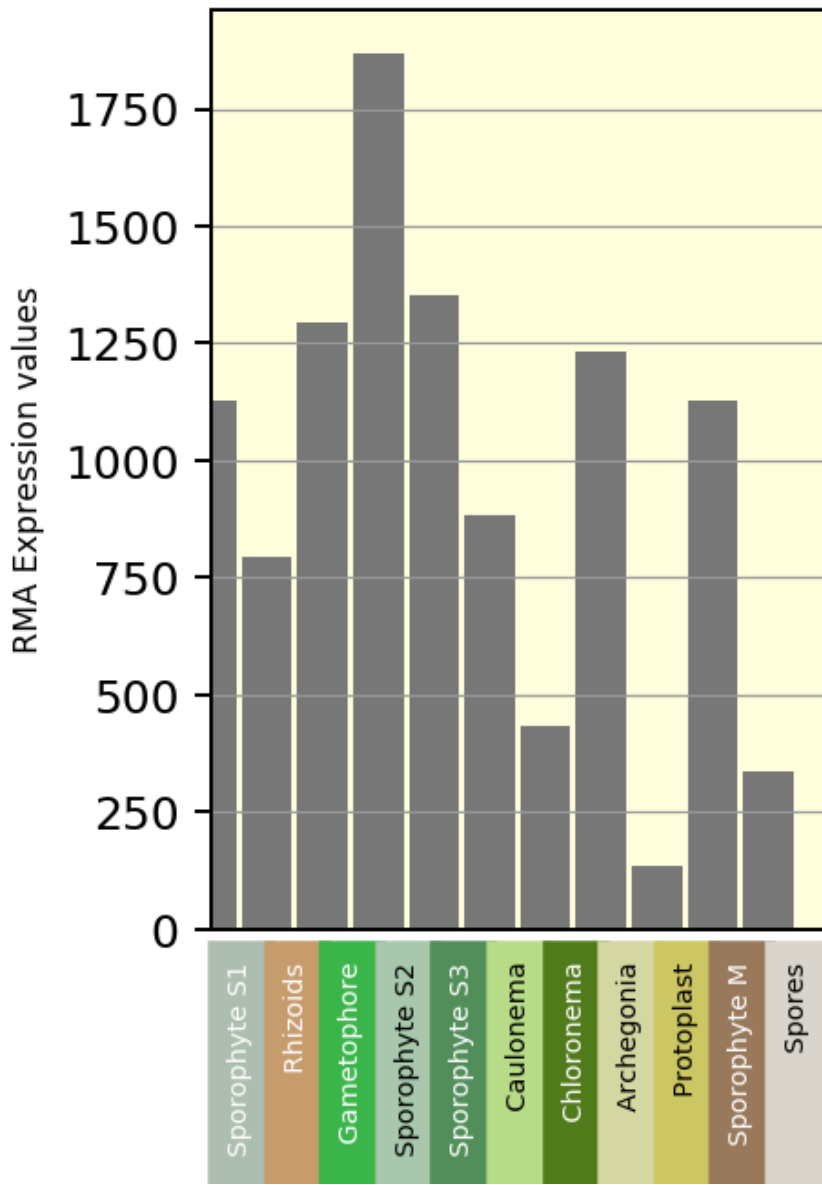


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• Pp1s76_82V6.1 was used as the probe set identifier for your primary query, Phypa_129421 (nuclear matrix constituent protein-related)

Group #	Tissue	Expression Level	Standard Deviation	Samples	Links
1	Sporophyte S1	1128.22	0.0	Sporophyte_S1,	To the Experiment
1	Rhizoids	795.7	0.0	Rhizoids,	To the Experiment
1	Gametophore	1292.66	0.0	Gametophore,	To the Experiment
1	Sporophyte S2	1869.76	0.0	Sporophyte_S2,	To the Experiment
1	Sporophyte S3	1352.67	0.0	Sporophyte_S3,	To the Experiment
1	Caulonema	881.56	0.0	Caulonema,	To the Experiment
1	Chloronema	433.7	0.0	Chloronema,	To the Experiment
1	Archegonia	1233.16	0.0	Archegonia,	To the Experiment
1	Protoplast	133.6	0.0	Protoplast,	To the Experiment
1	Sporophyte M	1129.31	0.0	Sporophyte_M,	To the Experiment
1	Spores	335.2	0.0	Spores,	To the Experiment



Ppa2

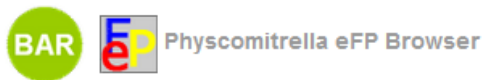
Organism *Physcomitrella patens*

Transcript Name Pp3c1_1360V3.1 (primary)

Alias Pp1s200_64V6.1 Pp3c1_1360E2.1 Pp3c1_1360V1.1

Pp3c1_1360 Pp1s200_64V6 Phpat.001G006400 Pp3c1_1360.v3.1

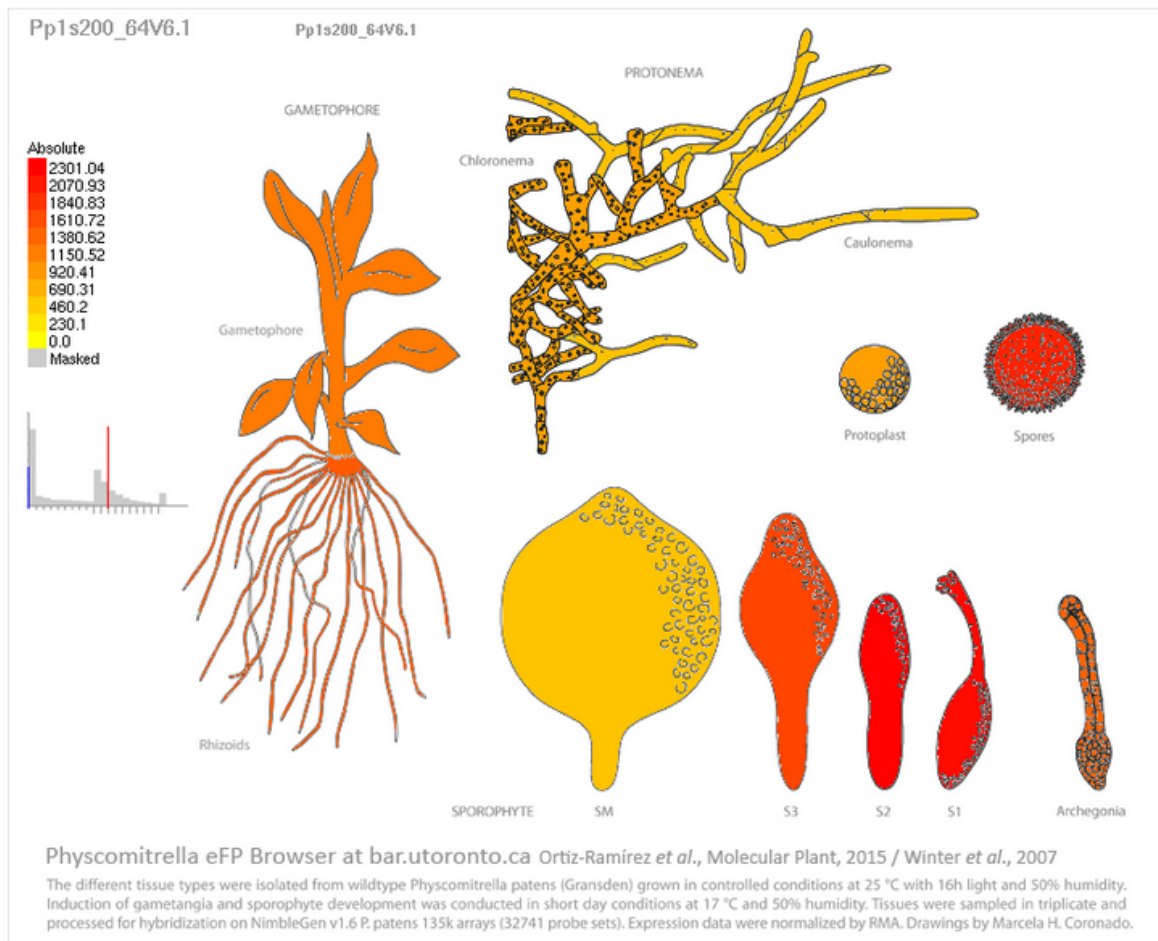
Pp3c1_1360V1.1.v3.1



Like 1K

Data Source: Physcomitrella Mode: Absolute Primary Gene ID: Pp1s200_64V6.1 Secondary Gene ID: Pp1s9_9V6.1 Signal Threshold: 2301.04 Go

- For group1 data, this probe set reaches its maximum expression level (expression potential) of 2301.04 in the Physcomitrella data source.

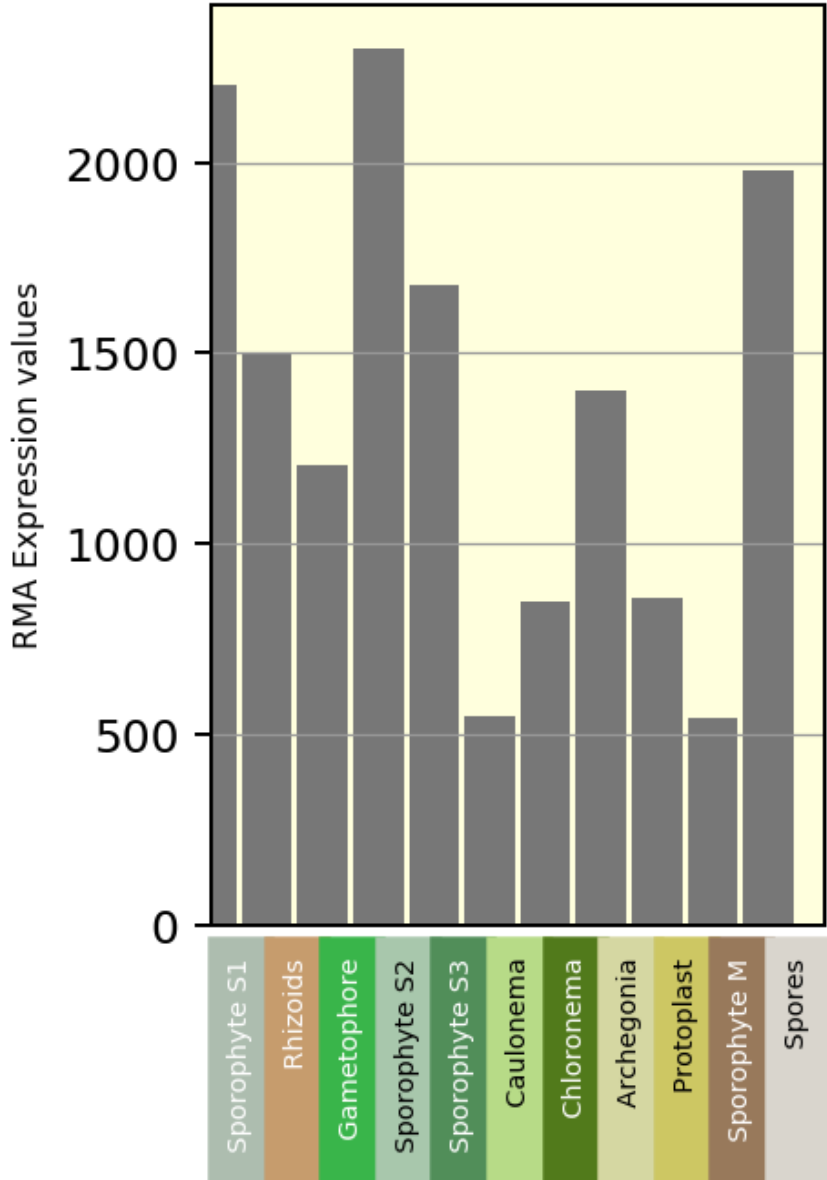


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- Pp1s200_64V6.1 was used as the probe set identifier for your primary query, Pp1s200_64V6.1 (little nuclei1)

Group #	Tissue	Expression Level	Standard Deviation	Samples	Links
1	Sporophyte S1	2204.58	0.0	Sporophyte_S1,	To the Experiment
1	Rhizoids	1495.44	0.0	Rhizoids,	To the Experiment
1	Gametophore	1207.46	0.0	Gametophore,	To the Experiment
1	Sporophyte S2	2301.04	0.0	Sporophyte_S2,	To the Experiment
1	Sporophyte S3	1678.71	0.0	Sporophyte_S3,	To the Experiment
1	Caulonema	546.75	0.0	Caulonema,	To the Experiment
1	Chloronema	849.87	0.0	Chloronema,	To the Experiment
1	Archegonia	1404.33	0.0	Archegonia,	To the Experiment
1	Protoplast	857.88	0.0	Protoplast,	To the Experiment
1	Sporophyte M	540.09	0.0	Sporophyte_M,	To the Experiment
1	Spores	1979.72	0.0	Spores,	To the Experiment



Osa1

Organism *Oryza sariva*
Transcript Name LOC_Os02g48010.1



Data Source: Mode: Primary Gene ID: Secondary Gene ID: Signal Threshold:

- For group1 data, this probe set reaches its maximum expression level (expression potential) of 1386.88 in the rice_mas or ricestigma_mas or ricestress_mas data source.
- For group1 data, note the maximum signal value has increased to 1165.24 from 20.92. Use the [Signal Threshold option to keep it constant at 20.92](#), or enter a value in the Signal Threshold box, such as [1386.88](#). The same colour scheme will then be applied across all views.
- Some samples exhibit high standard deviations for replicates. You can use [standard deviation filtering](#) to mask those with a deviation greater than half their expression value.



Rice eFP Browser at bar.utoronto.ca
LOC_Os02g48010 Os.11658.1.S1_at



eFP by R. Patel. Drawings by R. Patel adapted from images provided by Dr. D. Barar at IRRI as well as images contained within F-Box Proteins in Rice. Genome-wide Analysis, Classification, Temporal, and Spatial Gene Expression during Panicle and Seed Development, and Regulation by Light and Abiotic Stress: Jain M, Nijhawan A, Arora R, Agarwal P et al. Plant Physiol 2007 Apr;143(4):1467-83. Data is derived from the same paper, and normalized by MAS 5.0 and RMA methods. TGT value of 100 was used and all tissues were sampled in triplicate.

[Click Here for Table of Expression Values](#)

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- Os.11658.1.S1_at was used as the probe set identifier for your primary gene, LOC_Os02g48010 (protein nuclear matrix constituent protein 1-like, putative, expressed)

Osa2

Organism *Oryza sariva*
Transcript Name LOC_Os01g56140.1



Data Source: Mode: Primary Gene ID: Secondary Gene ID: Signal Threshold:

- For group1 data, this probe set reaches its maximum expression level (expression potential) of **10446.8** in the **rice_mas** or **ricestigma_mas** or **ricestress_mas** data source.
- For group1 data, note the maximum signal value has increased to 10023.36 from 1165.24. Use the [Signal Threshold option to keep it constant at 1165.24](#), or enter a value in the Signal Threshold box, such as [10446.8](#). The same colour scheme will then be applied across all views.



Rice eFP Browser at bar.utoronto.ca
LOC_Os01g56140 Os.26362.1.S1_at



eFP by R. Patel. Drawings by R. Patel adapted from images provided by Dr. D. Brar at IRRRI as well as images contained within F-Box Proteins in Rice. Genome-wide Analysis, Classification, Temporal, and Spatial Gene Expression during Panicle and Seed Development, and Regulation by Light and Abiotic Stress: Jain M, Nijhawan A, Arora R, Agarwal P et al. Plant Physiol 2007 Apr;143(4):1467-83. Data is derived from the same paper, and normalized by MAS 5.0 and RMA methods. TGT value of 100 was used and all tissues were sampled in triplicate.

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- Os.26362.1.S1_at was used as the probe set identifier for your primary gene, LOC_Os01g56140 (protein expressed protein)

Zma1

Organism

Zea mays

Transcript Name

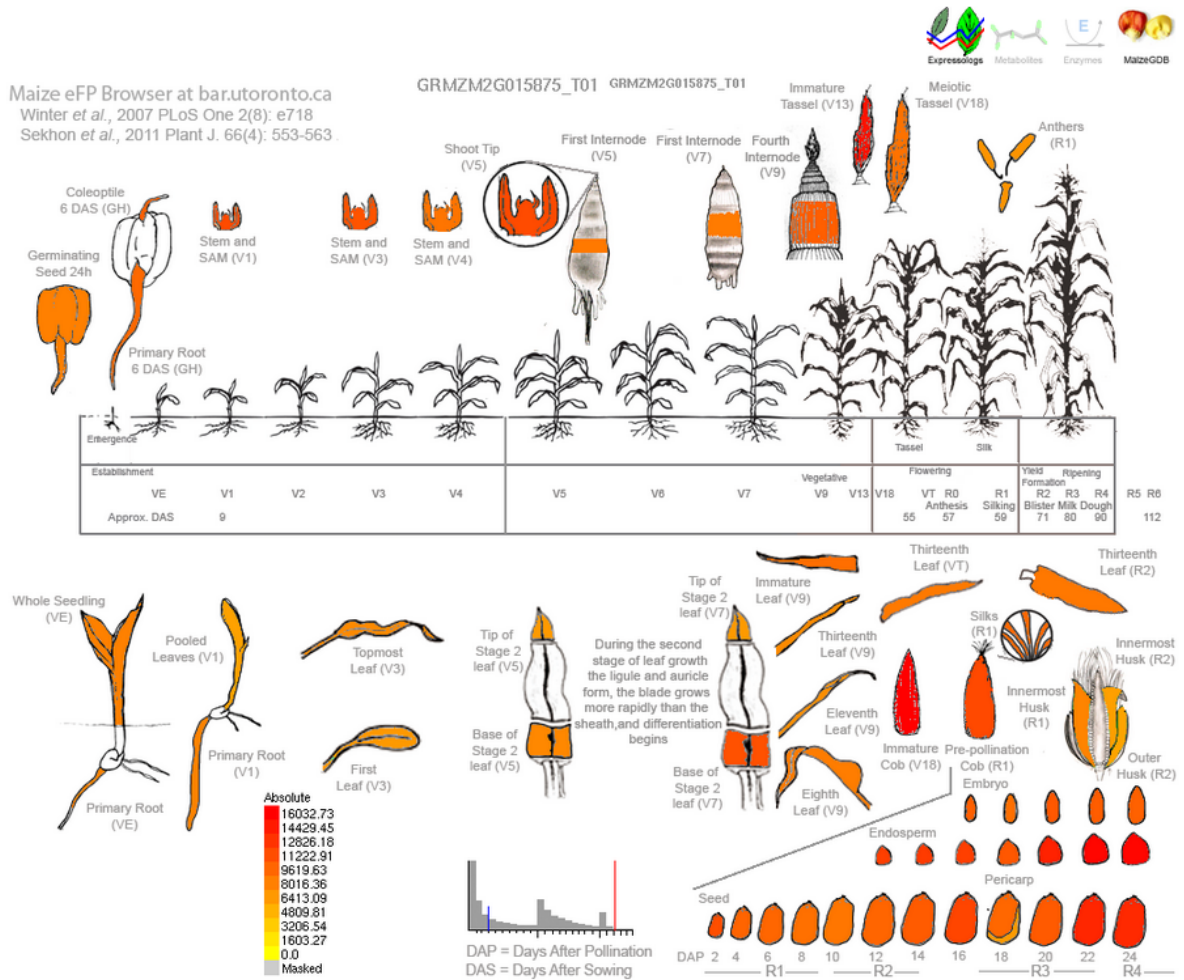
GRMZM2G015875_T01



Like 1K

Data Source: Sekhon et al Atlas | Mode: Absolute | Primary Gene ID: GRMZM2G015875 | Secondary Gene ID: GRMZM2G011169 | Signal Threshold: 16032.73 | Go

- For group1 data, this probe set reaches its maximum expression level (expression potential) of 17821.3 in the maize_RMA_linear data source.
- For group1 data, note the maximum signal value has increased to 16032.73 from 20.92. Use the [Signal Threshold option to keep it constant at 20.92](#), or enter a value in the Signal Threshold box, such as [17821.3](#). The same colour scheme will then be applied across all views.



eFP by R. Patel. Images provided by Shawn Kaeppeler's group at University of Wisconsin - Madison. Data were derived from Genome-wide atlas of transcription during maize development: R. Sekhon et al., (2011) The Plant Journal 66(4): 553-563. Data were Nimblegen derived and were normalized using RMA and are provided as linearized data. All tissues were sampled in triplicate.

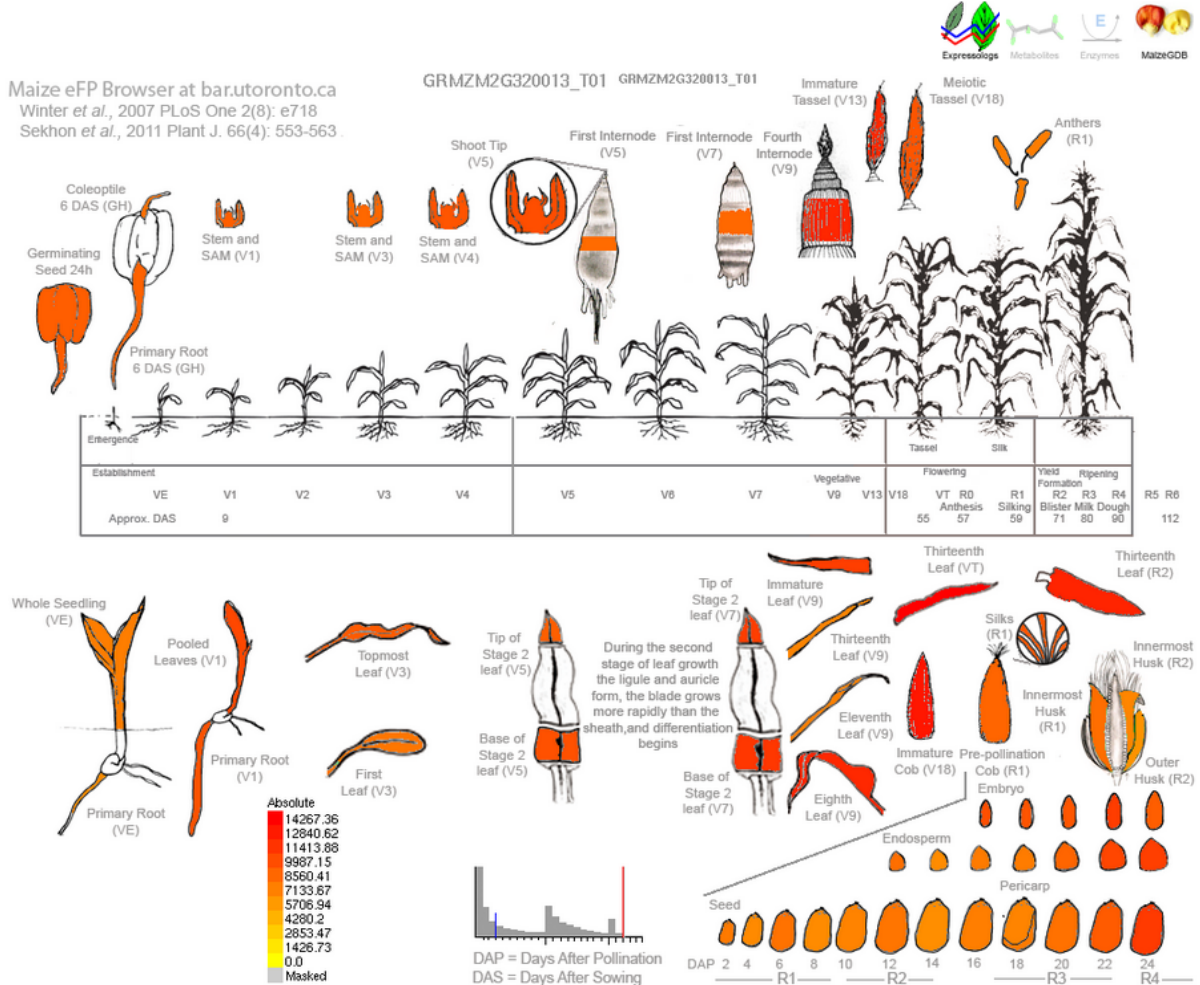
Zma2

Organism *Zea mays*
 Transcript Name GRMZM2G320013_T01



Data Source: Sekhon et al Atlas | Mode: Absolute | Primary Gene ID: GRMZM2G320013 | Secondary Gene ID: GRMZM2G011169 | Signal Threshold: 14267.36 | Go

- For group1 data, this probe set reaches its maximum expression level (expression potential) of 16128.5 in the maize_RMA_linear data source.
- For group1 data, note the maximum signal value has increased to 14267.36 from 35.01. Use the [Signal Threshold option to keep it constant at 35.01](#), or enter a value in the Signal Threshold box, such as [16128.5](#). The same colour scheme will then be applied across all views.



eFP by R. Patel. Images provided by Shawn Kaeppeler's group at University of Wisconsin - Madison. Data were derived from Genome-wide atlas of transcription during maize development: R. Sekhon et al., (2011) The Plant Journal 66(4): 553-563. Data were Nimblegen derived and were normalized using RMA and are provided as linearized data. All tissues were sampled in triplicate.

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- GRMZM2G320013_T01 was used as the probe set identifier for your primary gene, GRMZM2G320013_T01 (expressed protein)

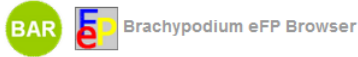
Bdi1

Organism

Brachypodium distachyon

Transcript Name

Bradi3g53047.1



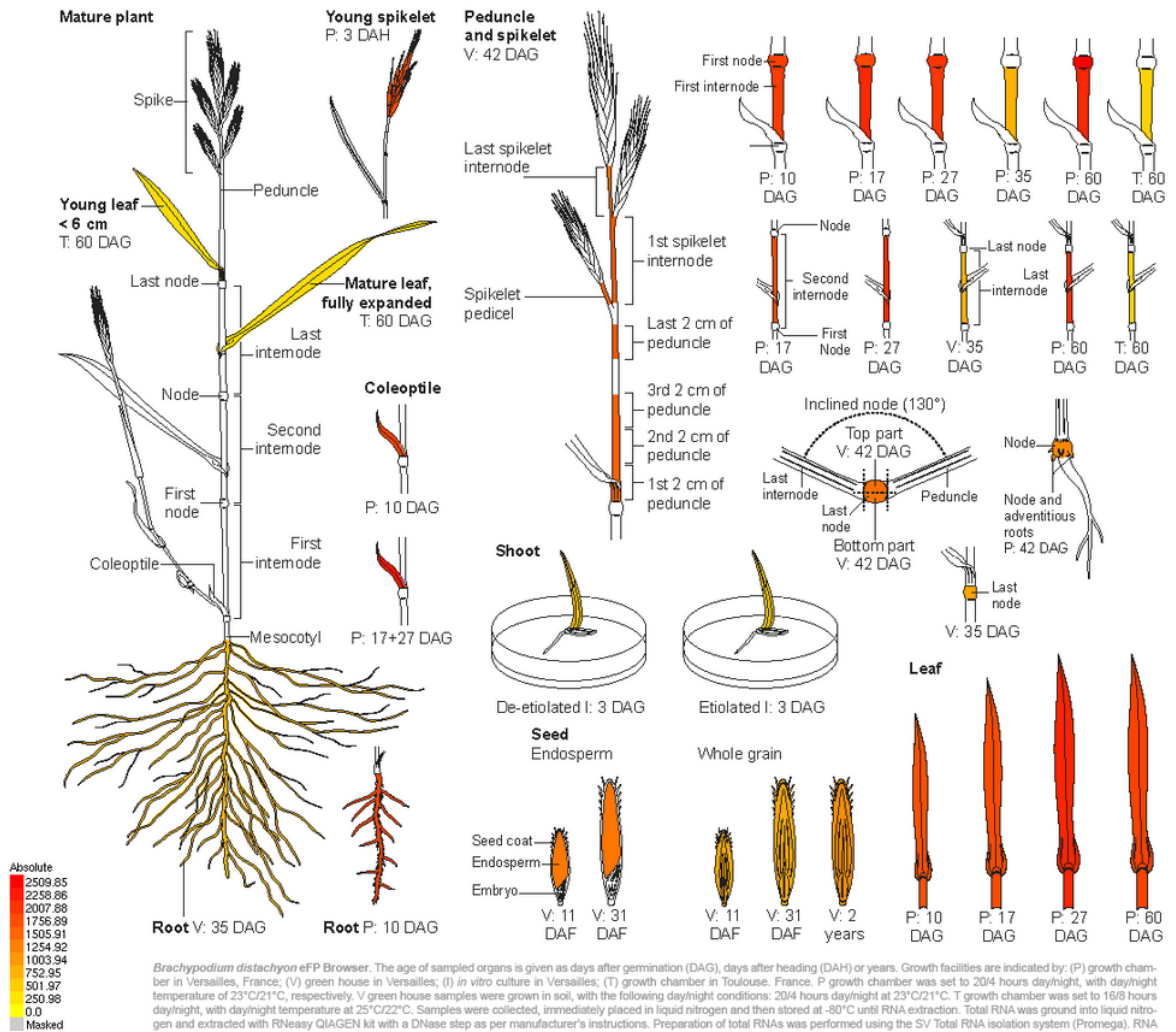
Like 1K

Data Source: Brachypodium Atlas | Mode: Absolute | Primary Gene ID: Bradi3g53047.1 | Secondary Gene ID: Bradi4g08230.1 | Signal Threshold: 2509.85 | Go

For group1 data, this probe set reaches its maximum expression level (expression potential) of 2533.3 in the Brachypodium Atlas data source.

Bradi3g53047.1 Bradi3g53047.1

Brachypodium distachyon eFP Browser at <http://bar.utoronto.ca>
Sibout et al., 2017; Winter et al., 2007. PLoS One 2: e718



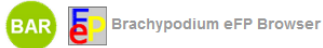
Bdi2

Organism

Brachypodium distachyon

Transcript Name

Bradi2g50990.1



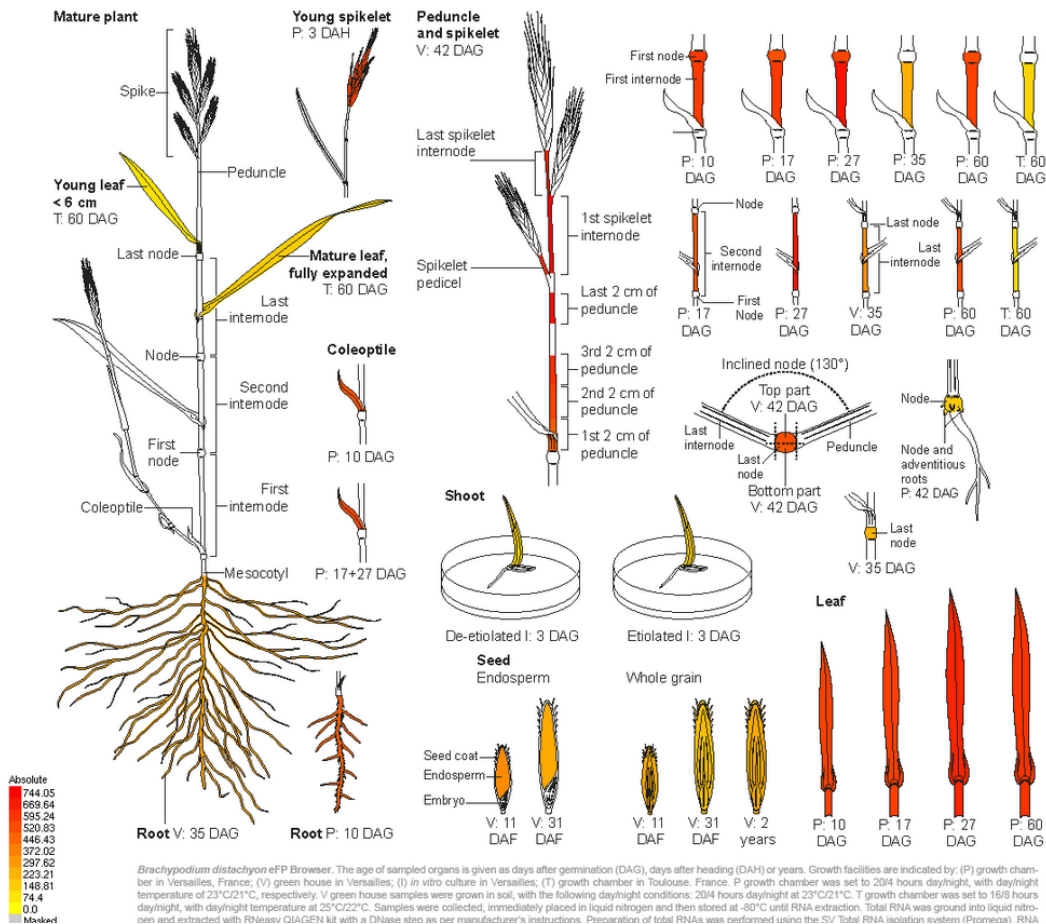
Like 1K

Data Source: Brachypodium Atlas | Mode: Absolute | Primary Gene ID: Bradi2g50990.1 | Secondary Gene ID: Bradi4g08230.1 | Signal Threshold: 744.05 | Go

For group1 data, this probe set reaches its maximum expression level (expression potential) of 802.8 in the Brachypodium Atlas data source.

Bradi2g50990.1 Bradi2g50990.1

Brachypodium distachyon eFP Browser at <http://bar.utoronto.ca>
Sibout et al., 2017; Winter et al., 2007. PLoS One 2: e718



Gma11

Organism

Glycine max

Transcript Name

Glyma.18G280500.1 (Glyma18g51560)



Like 1K

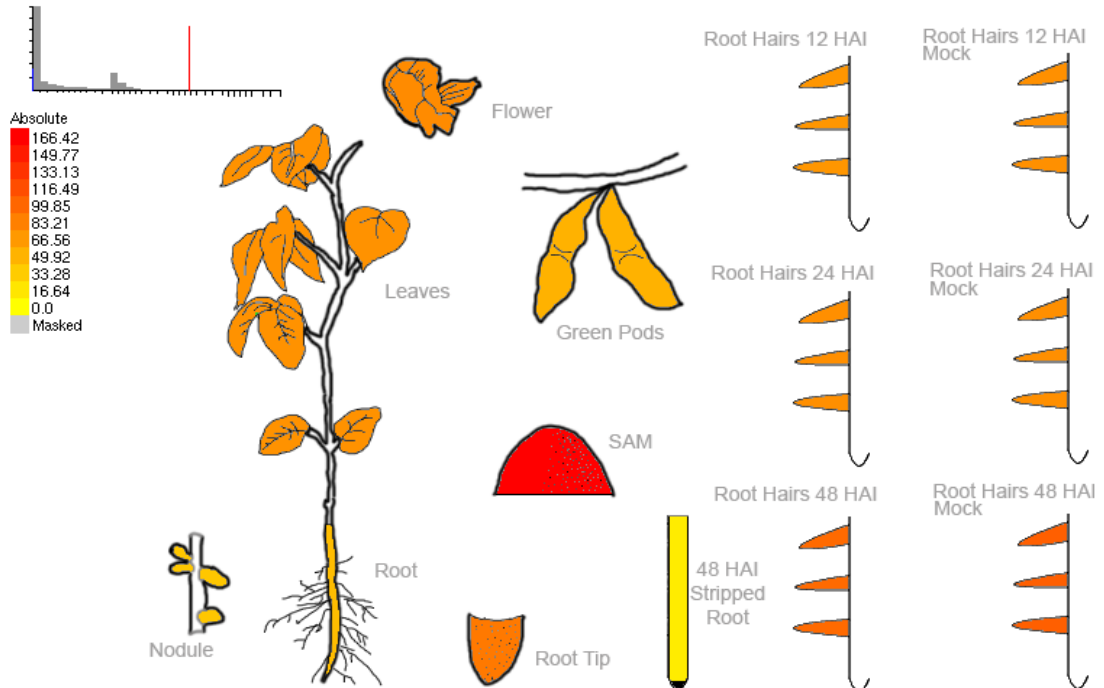
Data Source: soybean Mode: Absolute Primary Gene ID: Glyma.18G280500 Secondary Gene ID: Glyma06g47390 Signal Threshold: 166.42 Go

- For group1 data, this probe set reaches its maximum expression level (expression potential) of 166.42 in the Soybean data source.



Soybean eFP Browser at bar.utoronto.ca
Glyma.18g280500 Glyma18g51560

HAI = Hours after Inoculation



eFP by R. Patel. Drawings by R. Patel. Data for Root Hair series from Complete Transcriptome of Soybean Root Hair Cell, a Single Cell Model, and its alteration in response to *Bradyrhizobium japonicum* infection: Libault, M., Farmer, A., Brechnmacher, L et al. (2010). Plant Physiol. 152, 541-552. All other data from An Integrated Transcriptome Atlas of the Crop Model *Glycine max*, and its use in Comparative Analyses in Plants: Libault, M., et al. (2010) The Plant Journal 63, 86-99. Data is mRNA-Seq derived data and all samples were sampled in triplicate.

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- Glyma18g51560 was used as the probe set identifier for your primary gene, Glyma.18g280500 (LINC1 little nuclei1)

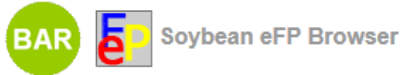
Gma1H

Organism

Glycine max

Transcript Name

Glyma.08G256300.1 (Glyma08g28630)



Like 1K

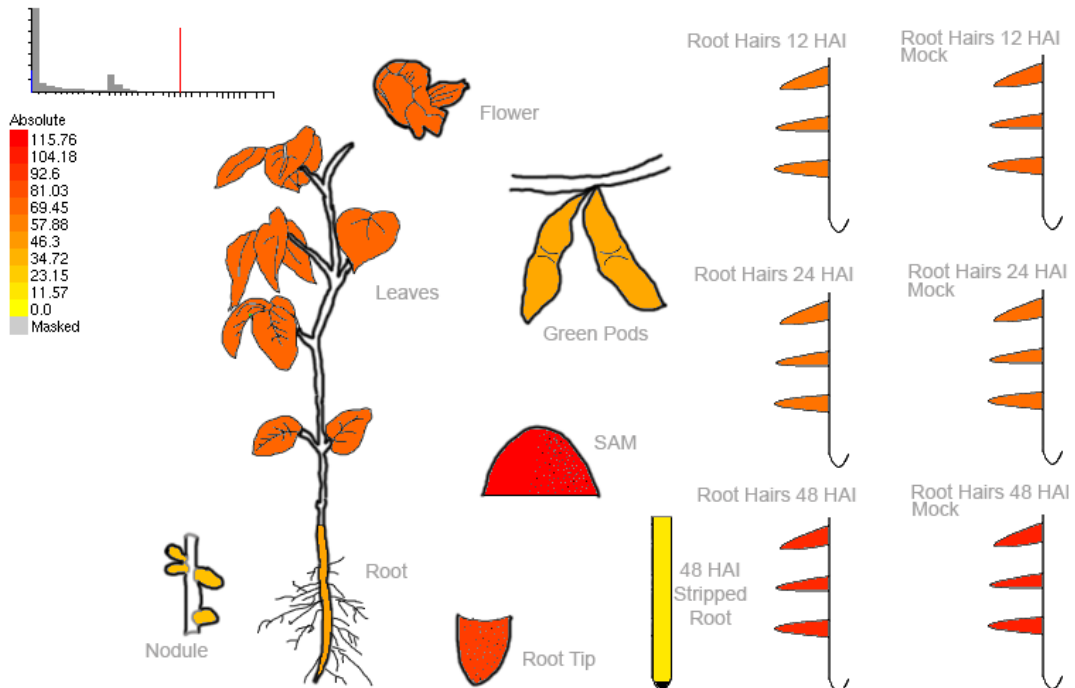
Data Source: soybean Mode: Primary Gene ID: Glyma.08G256300 Secondary Gene ID: Glyma06g47390 Signal Threshold: 115.76 Go

For group1 data, this probe set reaches its maximum expression level (expression potential) of 115.76 in the Soybean data source.



Soybean eFP Browser at bar.utoronto.ca
Glyma.08g256300 Glyma08g28630

HAI = Hours after Inoculation



eFP by R. Patel. Drawings by R. Patel. Data for Root Hair series from Complete Transcriptome of Soybean Root Hair Cell, a Single Cell Model, and its alteration in response to *Bradyrhizobium japonicum* infection: Libault, M., Farmer, A., Brechnmacher, L et al. (2010). Plant Physiol. 152, 541-552. All other data from An Integrated Transcriptome Atlas of the Crop Model *Glycine max*, and its use in Comparative Analyses in Plants: Libault, M., et al. (2010) The Plant Journal 63, 86-99. Data is mRNA-Seq derived data and all samples were sampled in triplicate.

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Gma2II

Organism

Glycine max

Transcript Name

Glyma.17G157900.1



Like 1K

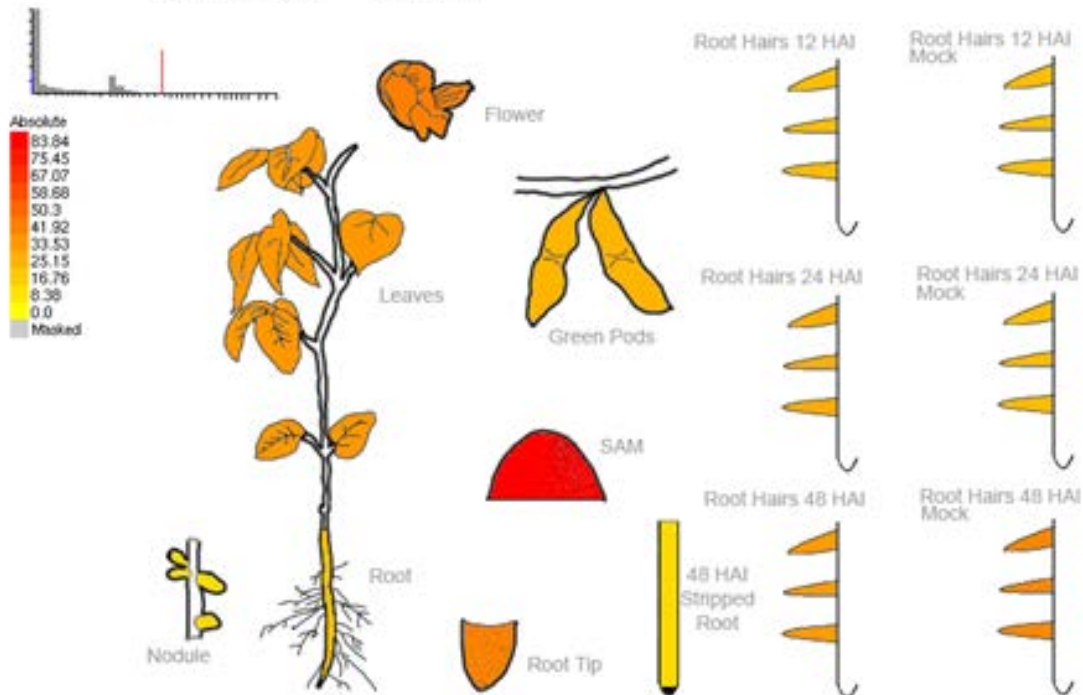
Data Source: soybean Mode: Absolute Primary Gene ID: Glyma.17G157900 Secondary Gene ID: Glyma06g17390 Signal Threshold: 83.84 Go

For group1 data, this probe set reaches its maximum expression level (expression potential) of 83.84 in the Soybean data source.



Soybean eFP Browser at bar.utoronto.ca
Glyma.17g157900 Glyma17g16970

HAI = Hours after Inoculation



eFP by R. Patel. Drawings by R. Patel. Data for Root Hair series from Complete Transcriptome of Soybean Root Hair Cell, a Single Cell Model, and its alteration in response to *Bradyrhizobium japonicum* infection: Libault, M., Farmer, A., Brechtmacher, L et al. (2010) Plant Physiol. 152, 541-552. All other data from An Integrated Transcriptome Atlas of the Crop Model *Glycine max*, and its use in Comparative Analyses in Plants: Libault, M., et al. (2010) The Plant Journal 63, 86-99. Data is mRNA-Seq derived data and all samples were sampled in triplicate.

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Glyma17g16970 was used as the probe set identifier for your primary gene, Glyma.17g157900 (LINC4 little nucleid)

Gma3II

Organism

Glycine max

Transcript Name

Glyma.01G090100.1



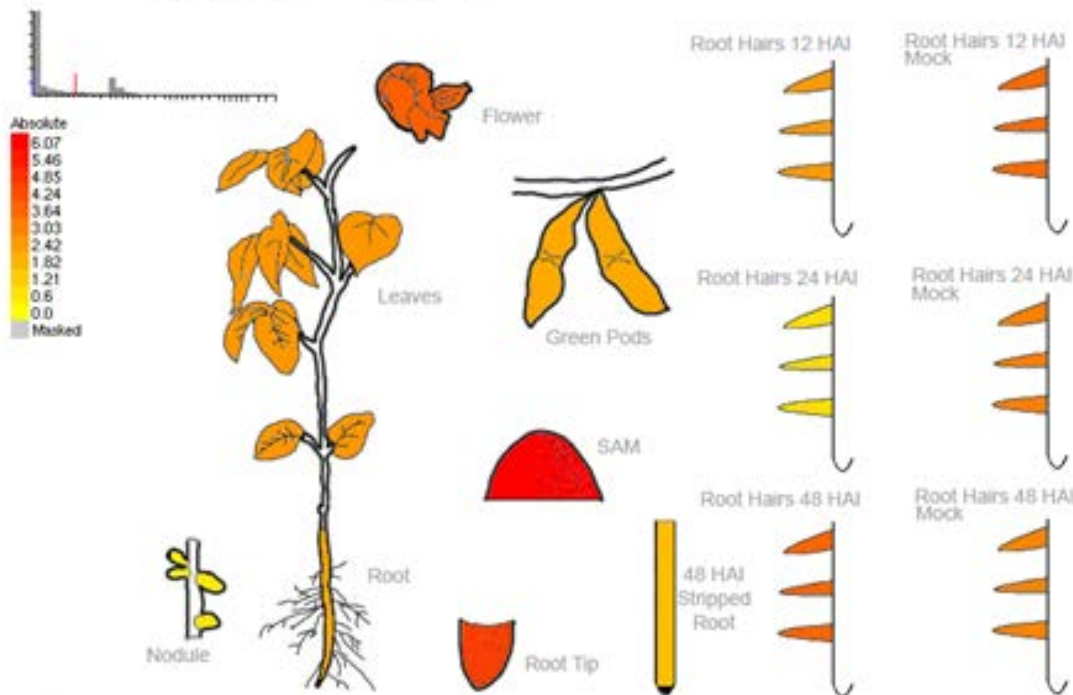
Data Source: soybean Mode: Absolute Primary Gene ID: Glyma.01G090100 Secondary Gene ID: Glyma06g47390 Signal Threshold: 6.07 Go

For group1 data, this probe set reaches its maximum expression level (expression potential) of 6.08 in the Soybean data source.



Soybean eFP Browser at bar.utoronto.ca
Glyma.01g090100 Glyma01g22710

HAI = Hours after Inoculation



eFP by R. Patel. Drawings by R. Patel. Data for Root Hair series from Complete Transcriptome of Soybean Root Hair Cell, a Single Cell Model, and its alteration in response to *Bradyrhizobium japonicum* infection; Libault, M., Farmer, A., Brechtmacher, L et al. (2010) Plant Physiol. 152, 541-552. All other data from An Integrated Transcriptome Atlas of the Crop Model *Glycine max*, and its use in Comparative Analyses in Plants; Libault, M., et al. (2010) The Plant Journal 63, 86-99. Data is mRNA-Seq derived data and all samples were sampled in triplicate.

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Glyma01g22710 was used as the probe set identifier for your primary gene, Glyma.01g090100 (LINC1 little nucleol1)