

A transcriptome-wide, organ-specific regulatory map of *Dendrobium officinale*, an important traditional Chinese orchid herb

Yijun Meng^{1, 2, &, *}, Dongliang Yu^{1, &}, Jie Xue^{1, 2}, Jiangjie Lu^{1, 2}, Shangguo Feng^{1, 2}, Chenjia Shen^{1, 2}, Huizhong Wang^{1, 2, *}

1 College of Life and Environmental Sciences, Hangzhou Normal University, Hangzhou 310036, PR China

2 Zhejiang Provincial Key Laboratory for Genetic Improvement and Quality Control of Medicinal Plants, Hangzhou Normal University, Hangzhou 310036, China

&These authors contributed equally to this work.

*Corresponding authors:

Huizhong Wang

Zhejiang Provincial Key Laboratory for Genetic Improvement and Quality Control of Medicinal Plants, College of Life and Environmental Sciences, Hangzhou Normal University. Xuelin Street 16#, Xiasha, Hangzhou 310036, P. R. China

Tel: +86-571-28865330

E-mail: whz62@163.com

Yijun Meng

Zhejiang Provincial Key Laboratory for Genetic Improvement and Quality Control of Medicinal Plants, College of Life and Environmental Sciences, Hangzhou Normal University. Xuelin Street 16#, Xiasha, Hangzhou 310036, P. R. China

Tel: +86-571-28865198

E-mail: mengyijun@zju.edu.cn

Supplementary data introduction

Table S1 Statistical results of the RNA-seq experiment.

Table S2 List of the transcripts highly accumulated in specific organs (root, flower, stem or leaf) of *Dendrobium officinale*. The transcript IDs along with their expression levels (normalized in RPKM and rescaled by log10) in four organs are included in this table. For each organ, there are two biological replicates (“Root1” and “Root2”, for example). ND: not detected.

Table S3 List of organ-specific transcripts potentially involved in specific organ-related biological functions.

Table S4 Organ-specific sRNAs identified in *Dendrobium officinale*. The sRNA sequences along with their accumulation levels (normalized in RPM) in sRNA-seq libraries prepared from specific organs were included in this table. Seven miRNAs were identified to be specifically accumulated in the floral organ.

Table S5 List of 1,047 miRNA candidates identified from *Dendrobium officinale*. The miRNA candidates from *Dendrobium officinale* along with the homologous miRNAs from other species sharing identical sequences according to miRBase (release 21) are provided. The accumulation levels of the miRNA candidates in the sRNA-seq libraries prepared from four organs are also included in this table. For each organ, there are two biological replicates (“Root1” and “Root2”, for example).

Table S6 A partial list of miRNA--target pairs identified from *Dendrobium officinale*. The miRNA IDs, target transcript IDs, target length and target annotations are included in this table. Based on the functional annotations of the target transcripts, the miRNA--target pairs were classified into four functional groups (hormone signaling-, plant development-, secondary metabolism- and Argonaute 1-related groups) for

network construction.

Figure S1 Statistical results of the sRNA-seq experiment.

Figure S2 Certain highly structured transcripts might serve as miRNA precursors. The transcripts were assembled by RNA-seq reads, and the transcript IDs were provided in the figure. The mature miRNA-coding regions on the long stems of the miRNA precursors were marked by red lines, and the mature miRNA IDs were provided. Note, for each mature miRNA, its average accumulation level in either organ (flower, leaf, root or stem; two biological replicates for each organ) of *Dendrobium officinale* should be 5 RPM or higher. The secondary structures of the transcripts were predicted by using RNAfold (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>).

Figure S3 Certain highly structured transcripts might serve as miRNA precursors. The transcripts were assembled by RNA-seq reads, and the transcript IDs were provided in the figure. The mature miRNA- and miRNA*-coding regions on the long stems of the miRNA precursors were marked by red and blue lines respectively, and their IDs were also provided. Note, for each mature miRNA, its average accumulation level in either organ (flower, leaf, root or stem; two biological replicates for each organ; thus, there are a total of eight libraries) of *Dendrobium officinale* should be 5 RPM or higher. Besides, the accumulation level of each miRNA* should be detectable in at least one sRNA-seq library. The secondary structures of the transcripts were predicted by using RNAfold (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>).

Figure S4 Certain highly structured transcripts might serve as miRNA precursors. The transcripts were assembled by RNA-seq reads, and the transcript IDs were provided in the figure. The mature miRNA- and miRNA*-coding regions on the long stems of the miRNA precursors were marked by red and blue lines respectively, and their IDs were also provided. The 5' ends of the degradome signatures supporting the

processing of miRNAs and/or miRNA*s from their precursors are represented by green arrows. Note, for each mature miRNA, its average accumulation level in either organ (flower, leaf, root or stem; two biological replicates for each organ; thus, there are a total of eight libraries) of *Dendrobium officinale* should be 5 RPM or higher. Besides, the accumulation level of each miRNA* should be detectable in at least one sRNA-seq library. The secondary structures of the transcripts were predicted by using RNAfold (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>).

Figure S5 T-plots providing degradome-seq data-based evidences for cleavage actions between specific miRNA--target pairs identified from *Dendrobium officinale*. Four degradome-seq libraries prepared from four organs (root, flower, stem and leaf; represented by four different signs) of *Dendrobium officinale* were included for drawing t-plots. For each miRNA--target pair, two scatter diagrams are provided. The left diagram with target ID provides a global view of degradome signals distributed all along the full-length target transcript. The right diagram with ID(s) of regulatory miRNA(s) provides a detailed view of degradome signals within about 60-nt region surrounding the predicted miRNA binding site (marked by a green horizontal line) on the target transcript. The y axis of each diagram measures the intensity (in RPM) of degradome signals. Please note: only the miRNA--target pairs supported by prominent degradome signatures resided within 10th to 11th nt from the 5' ends of the regulatory miRNAs are included in this figure.

Figure S6 Examples of miRNA--target pairs showing organ-specific regulation.

Data S1 Sequences of the transcripts highly accumulated in specific organs in Table S2.

Data S2 Sequences of the transcripts predicted to be miRNA precursors in Figure S2.

Data S3 Sequences of the transcripts predicted to be miRNA precursors in Figure S3.

Data S4 Sequences of the transcripts predicted to be miRNA precursors in Figure S4.

Data S5 List of miRNA--target pairs identified based on degradome-seq data.

Data S6 Transcript sequences for Data S5 and Table S5.

Data S1 Sequences of the transcripts highly accumulated in specific organs in Table S2.

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Data S2 Sequences of the transcripts predicted to be miRNA precursors in Figure S2.

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Data S3 Sequences of the transcripts predicted to be miRNA precursors in Figure S3.

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Data S4 Sequences of the transcripts predicted to be miRNA precursors in Figure S4.

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Data S5 List of miRNA--target pairs identified based on degradome-seq data.

Target transcript Regulatory miRNA

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comp154657_c0_seq6 dof-miR-606

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comp160962_c0_seq9 dof-miR-839
comp160962_c0_seq10 dof-miR-835

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comp162345_c1_seq3 dof-miR-796
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comp163430_c1_seq2 dof-miR-992
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Data S6 Transcript sequences for Data S5 and Table S5.

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Figure S1 Statistical results of the sRNA-seq experiment.

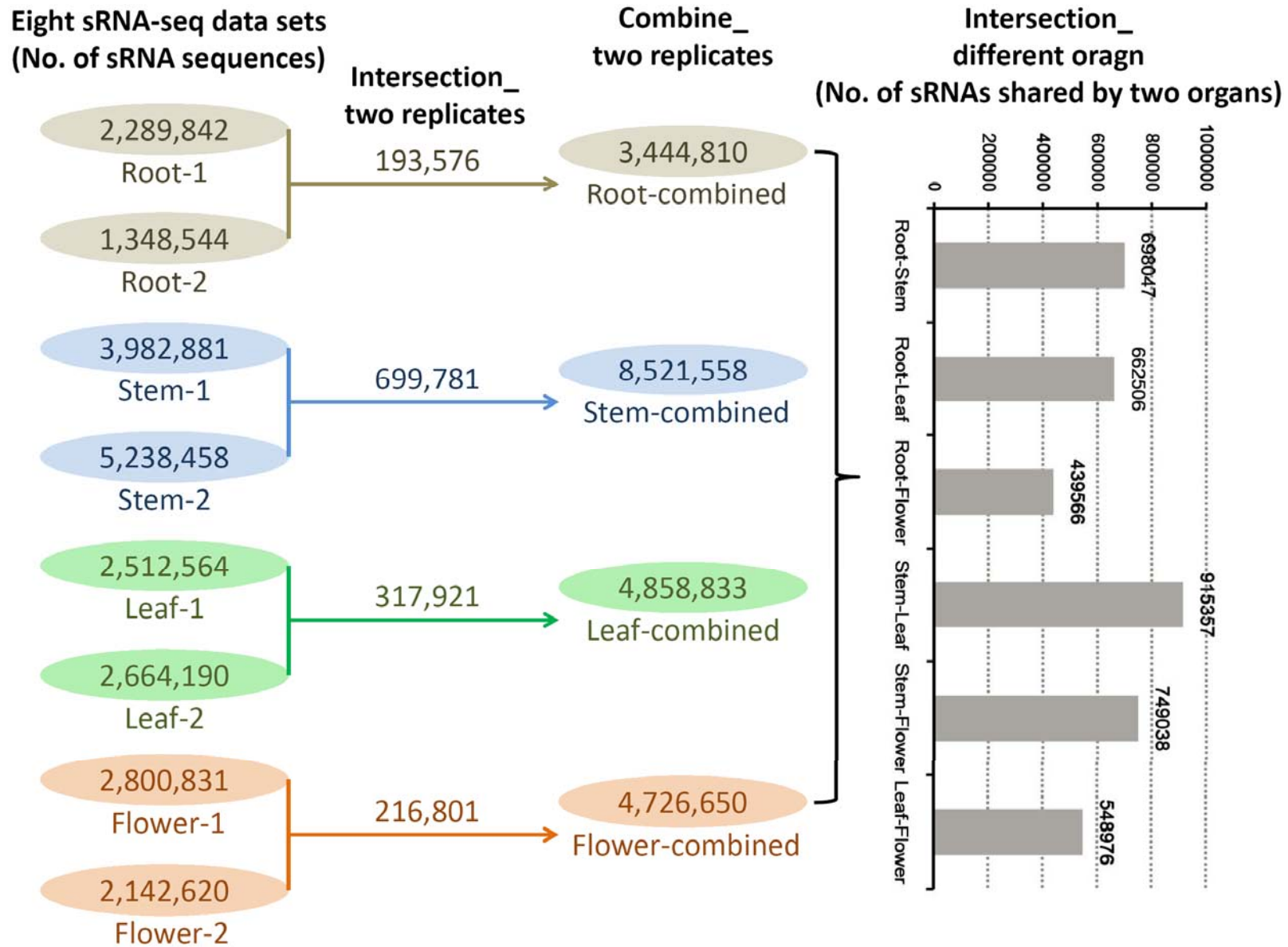
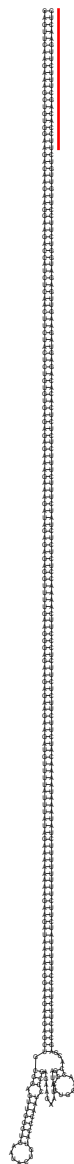


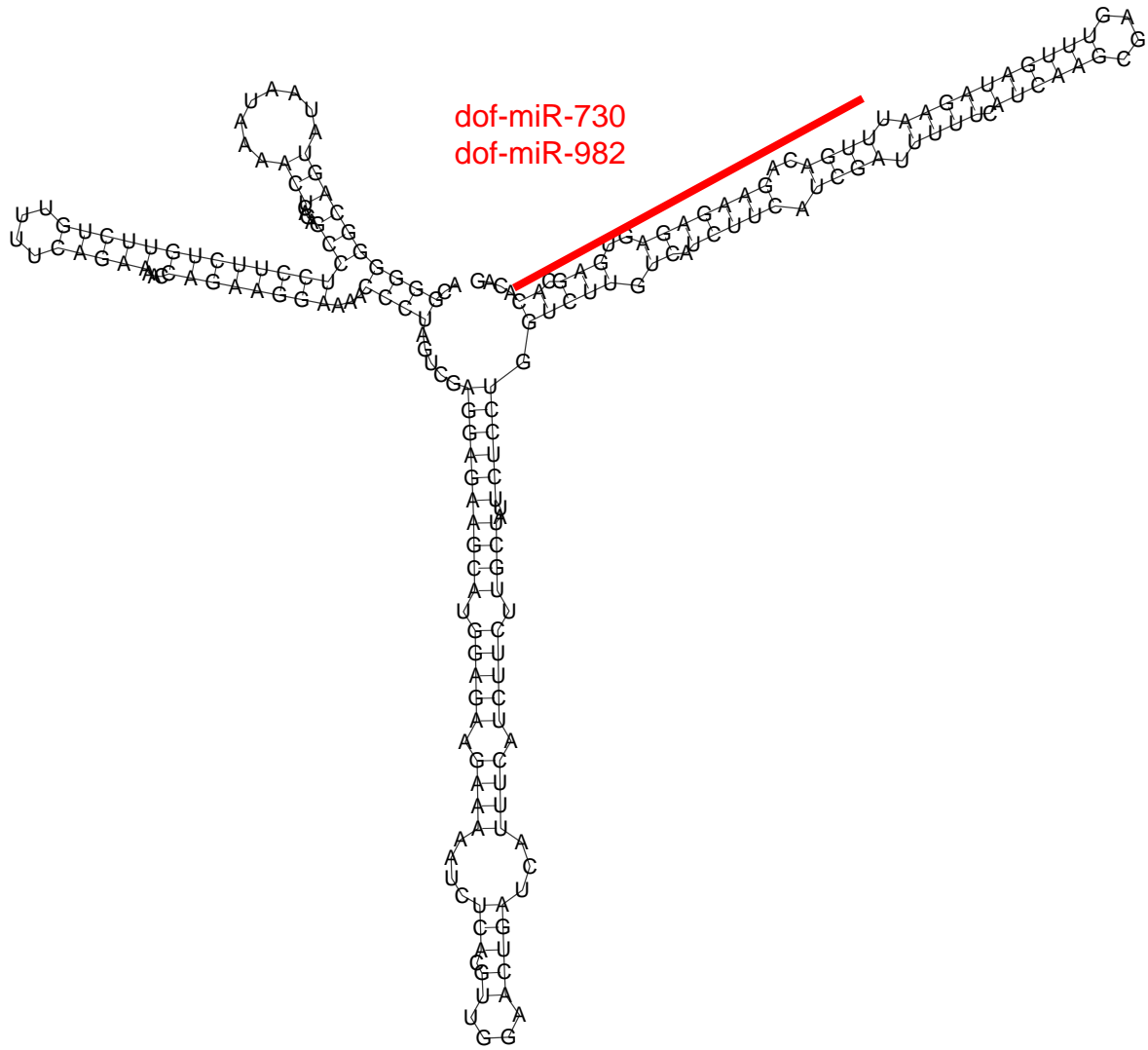
Figure S2 Certain highly structured transcripts might serve as miRNA precursors. The transcripts were assembled by RNA-seq reads, and the transcript IDs were provided in the figure. The mature miRNA-coding regions on the long stems of the miRNA precursors were marked by red lines, and the mature miRNA IDs were provided. Note, for each mature miRNA, its average accumulation level in either organ (flower, leaf, root or stem; two biological replicates for each organ) of *Dendrobium officinale* should be 5 RPM or higher. The secondary structures of the transcripts were predicted by using RNAfold (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>).

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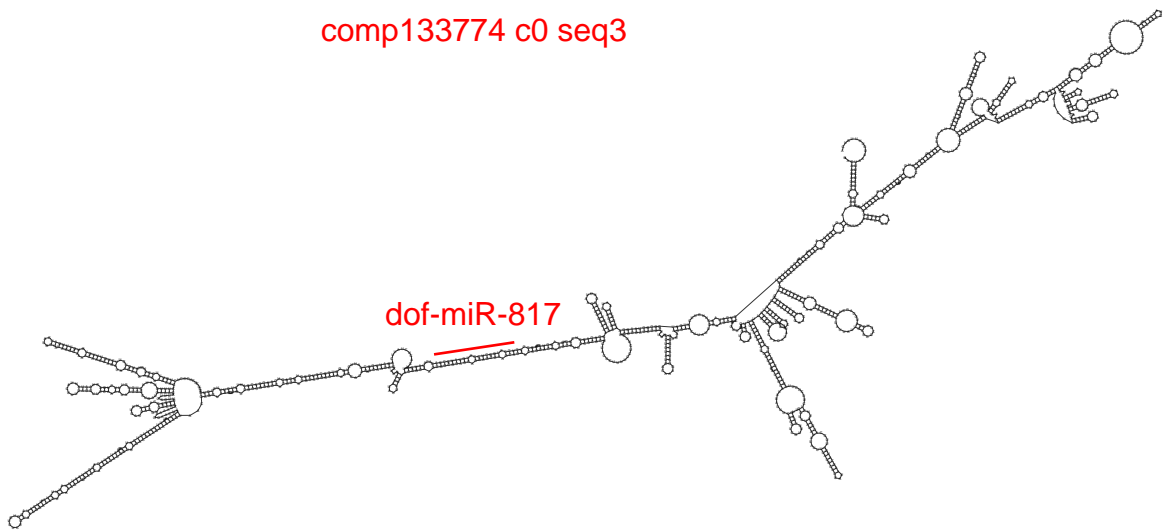


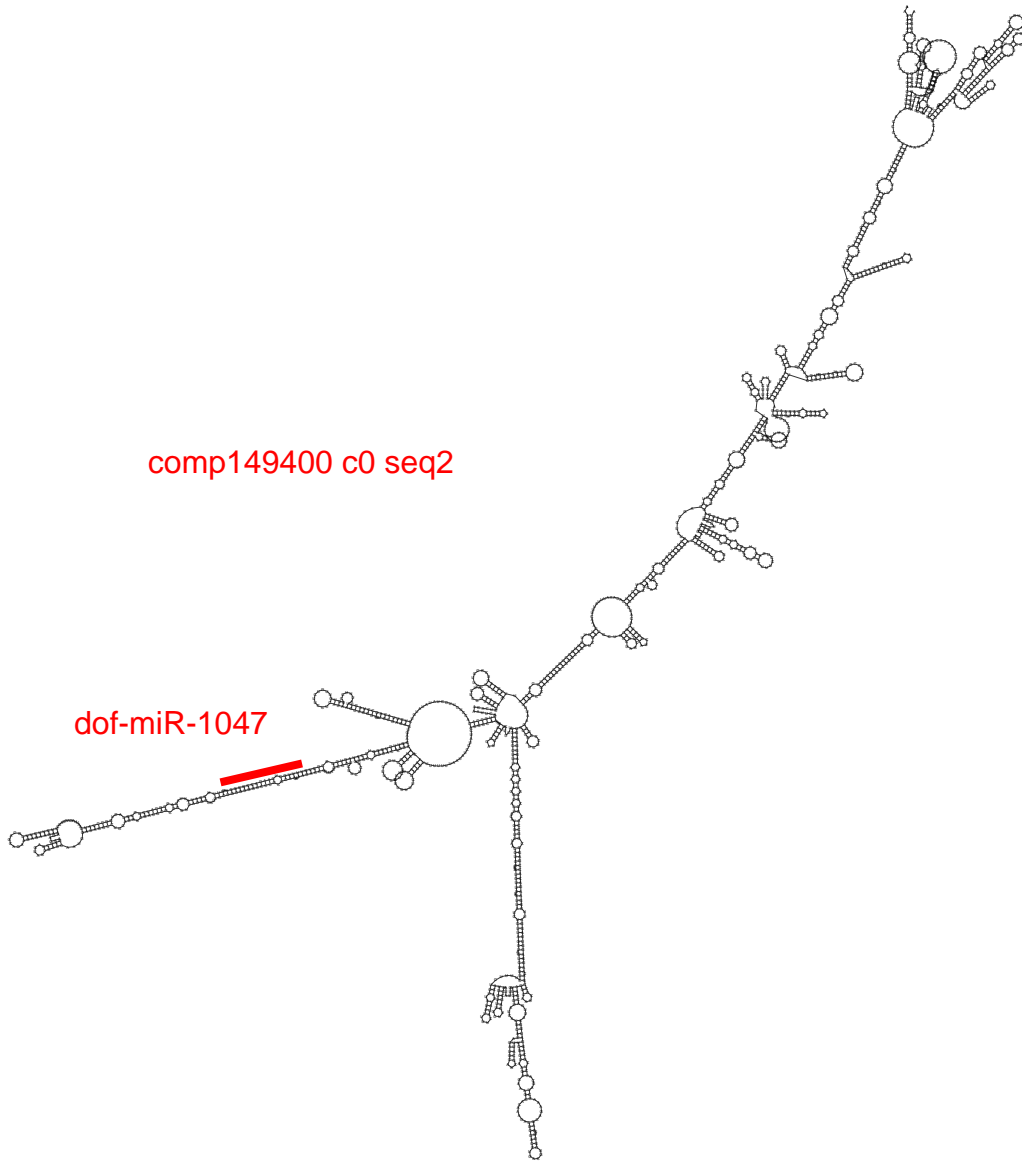
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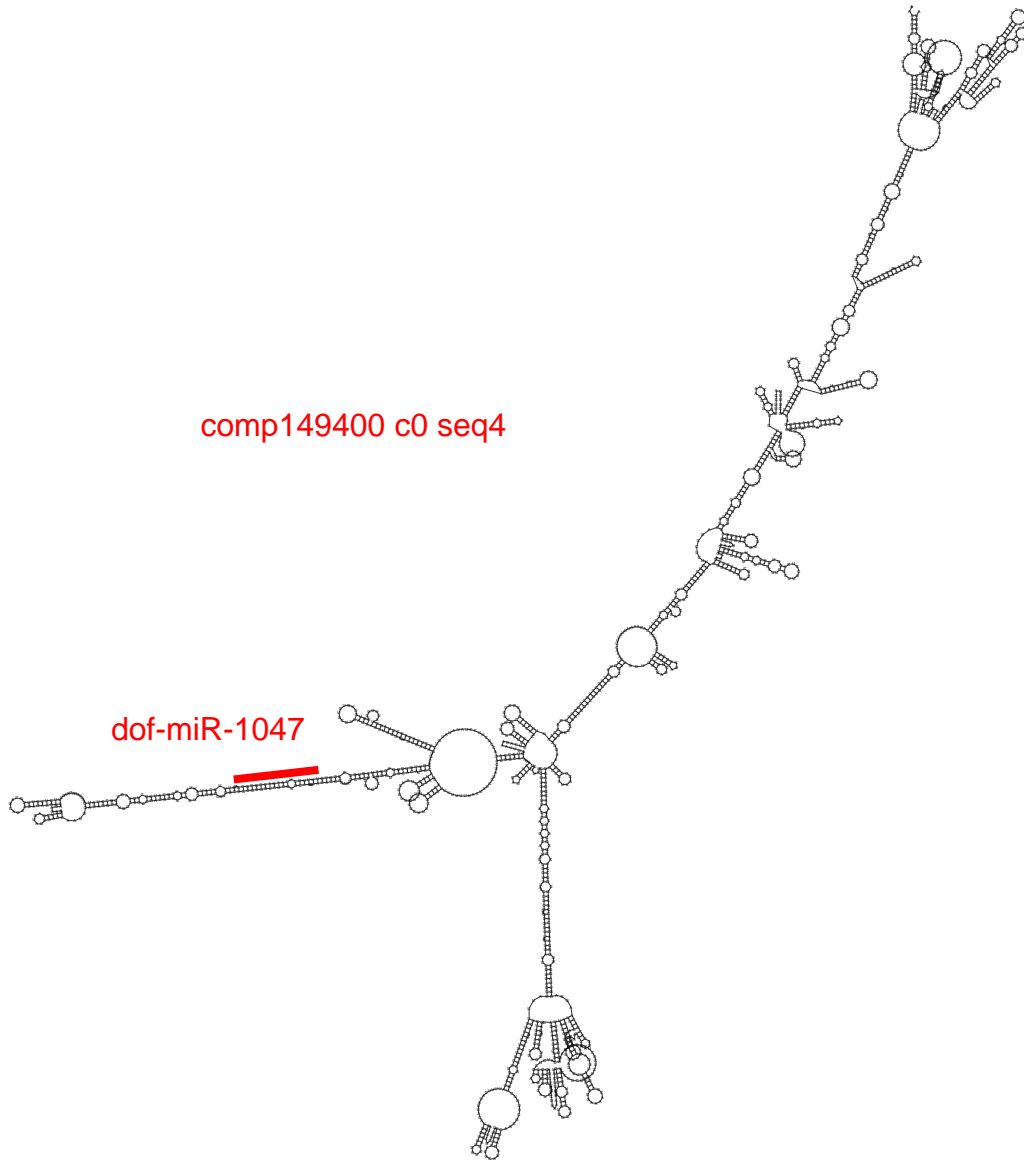
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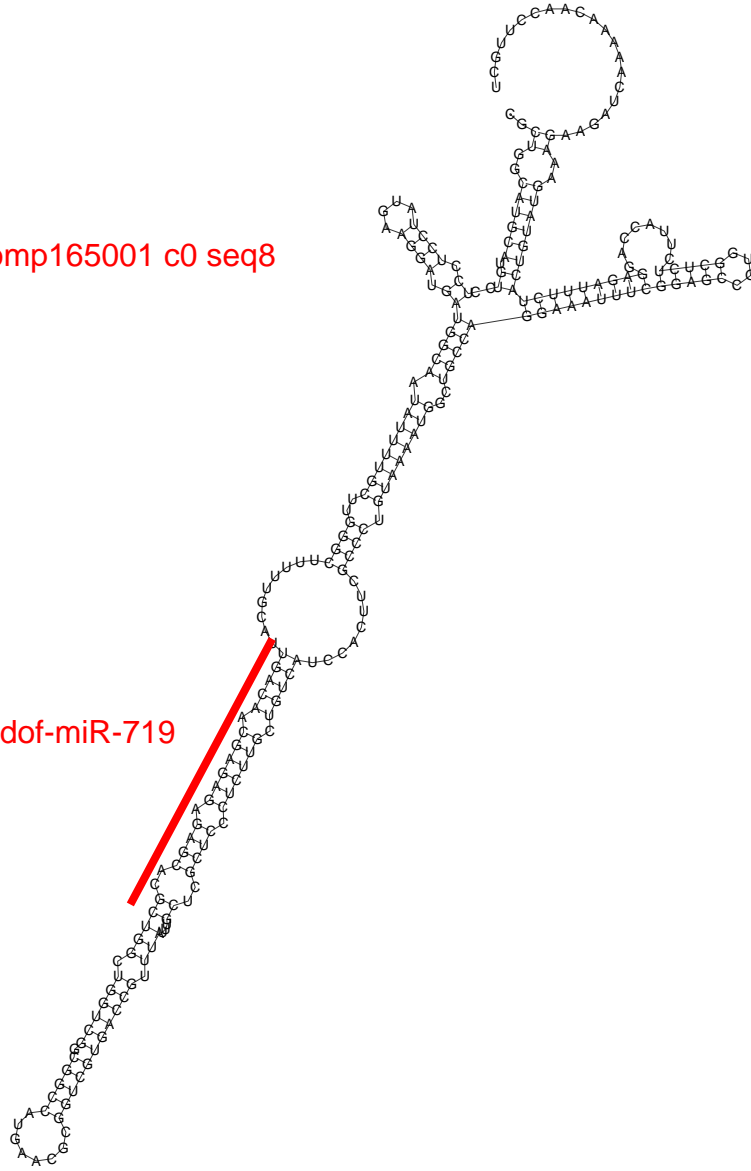


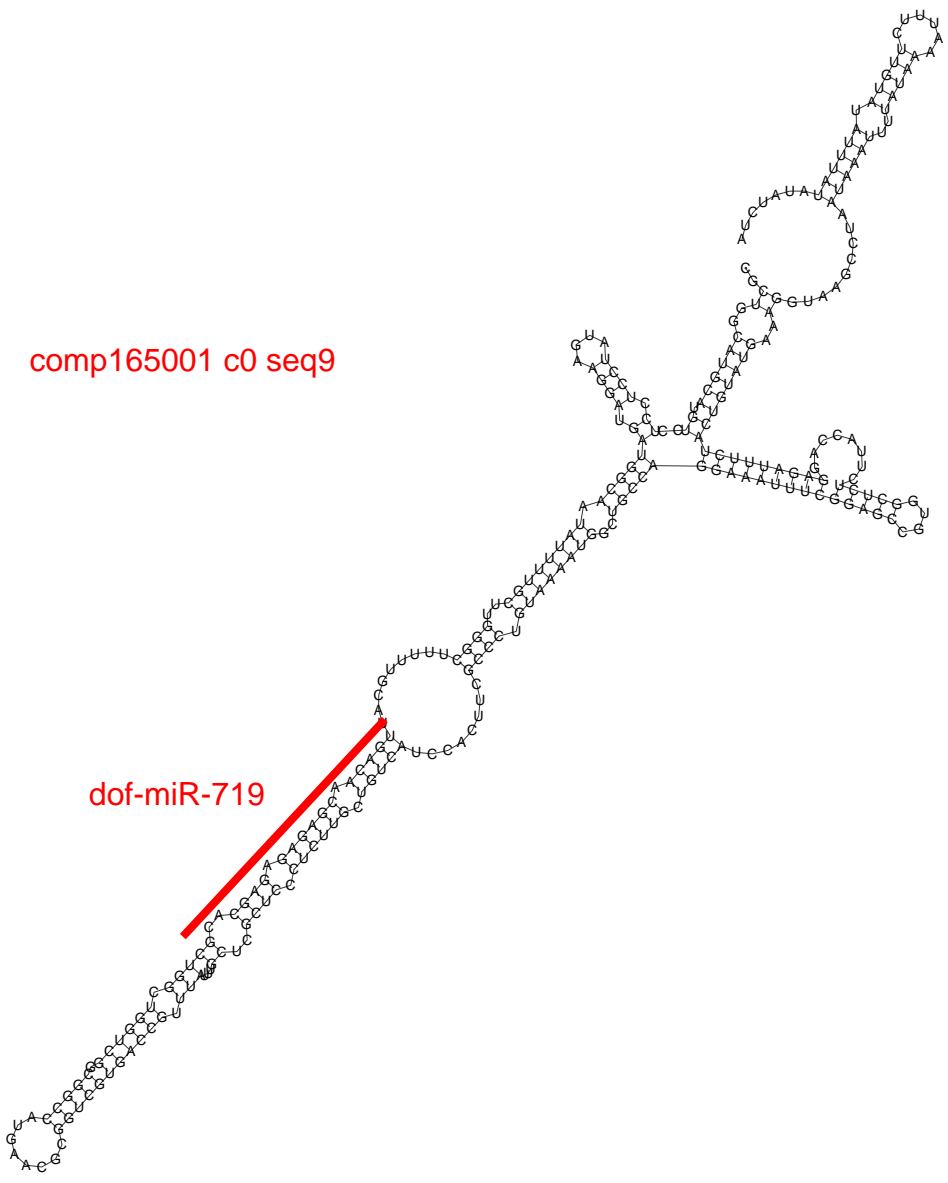




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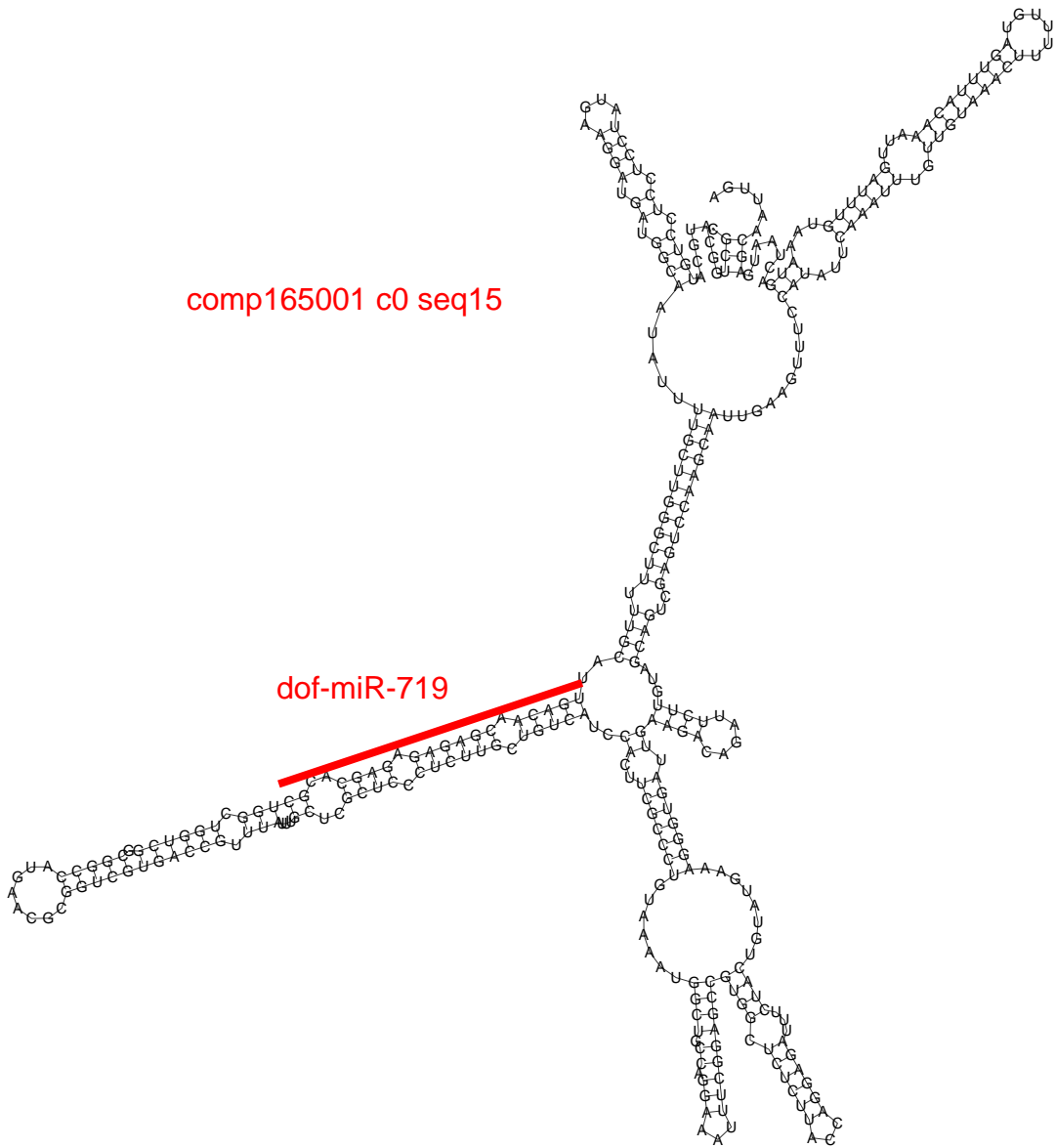


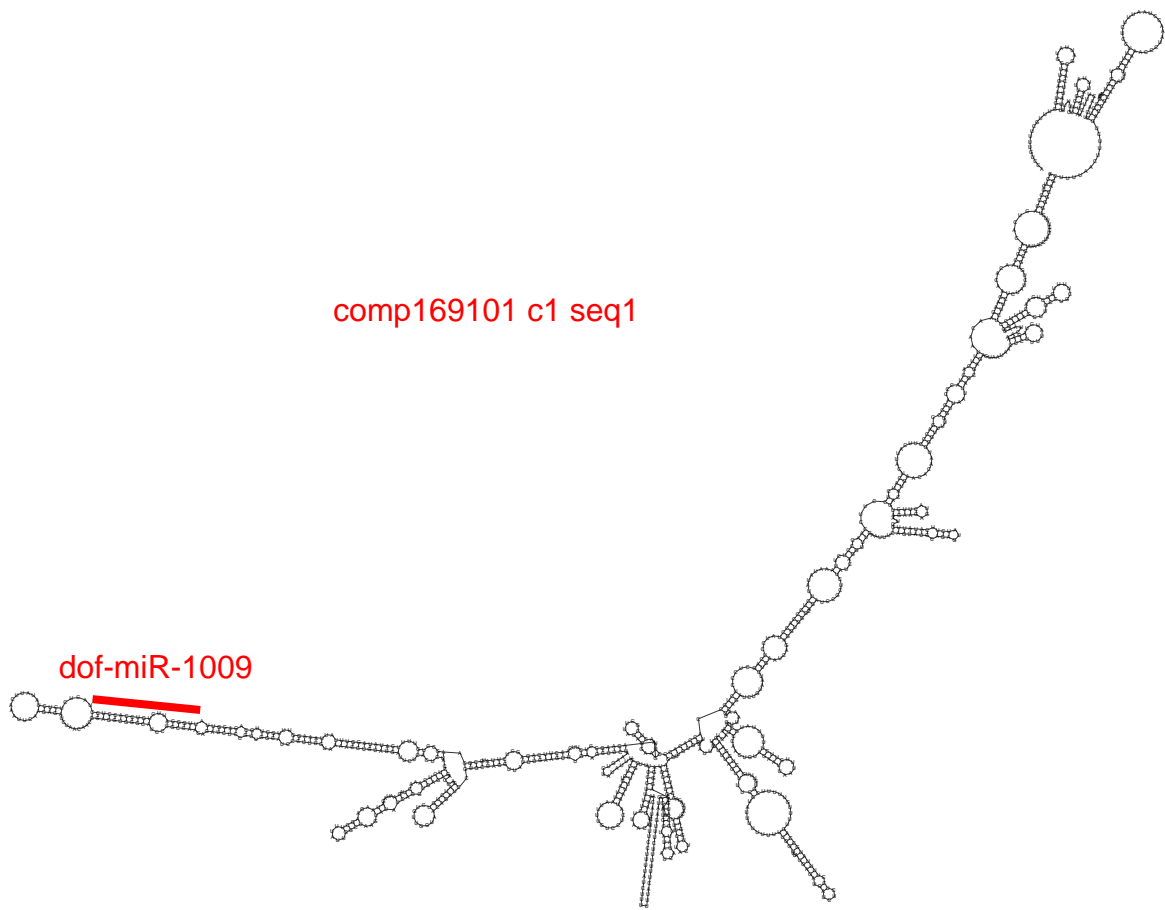
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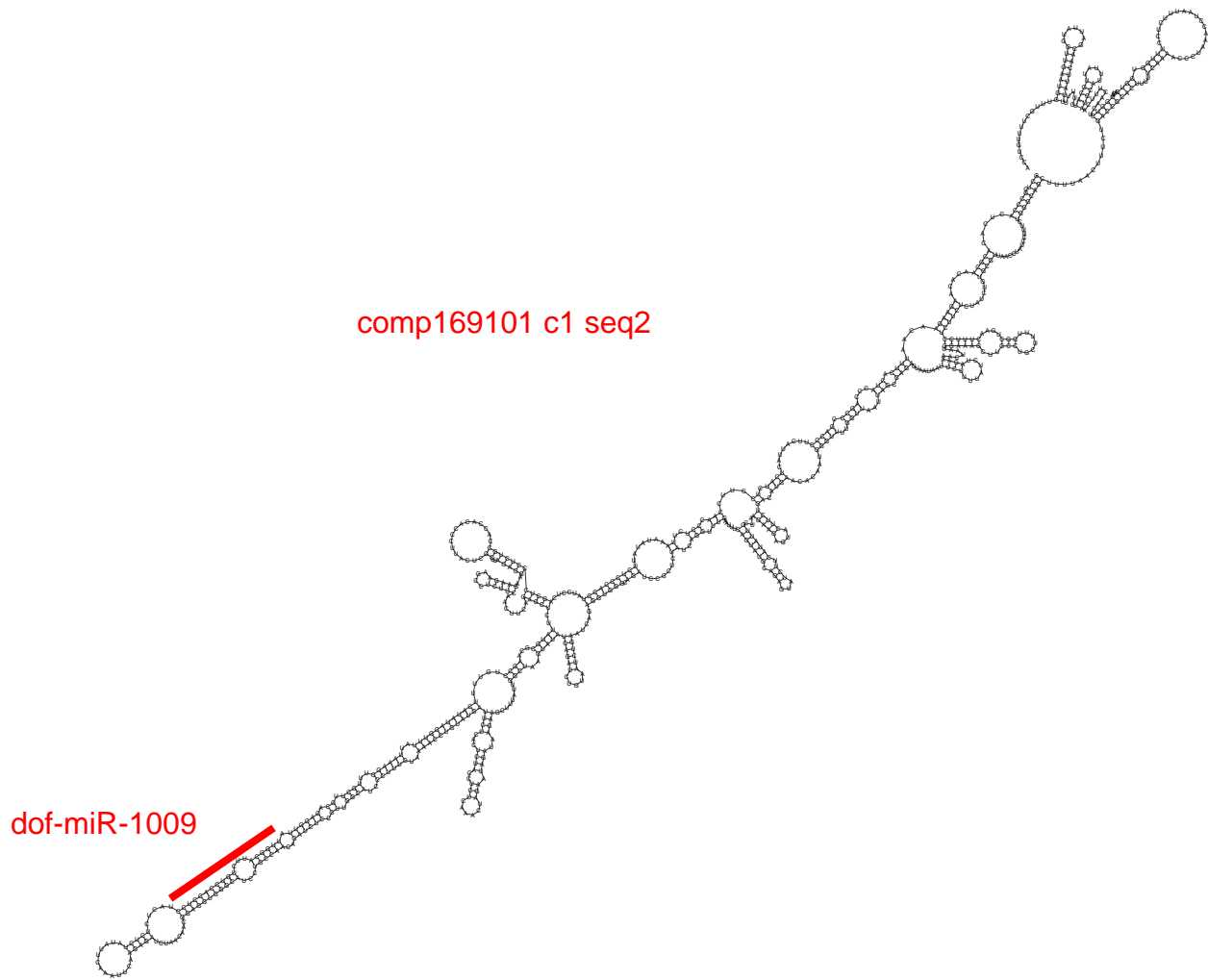
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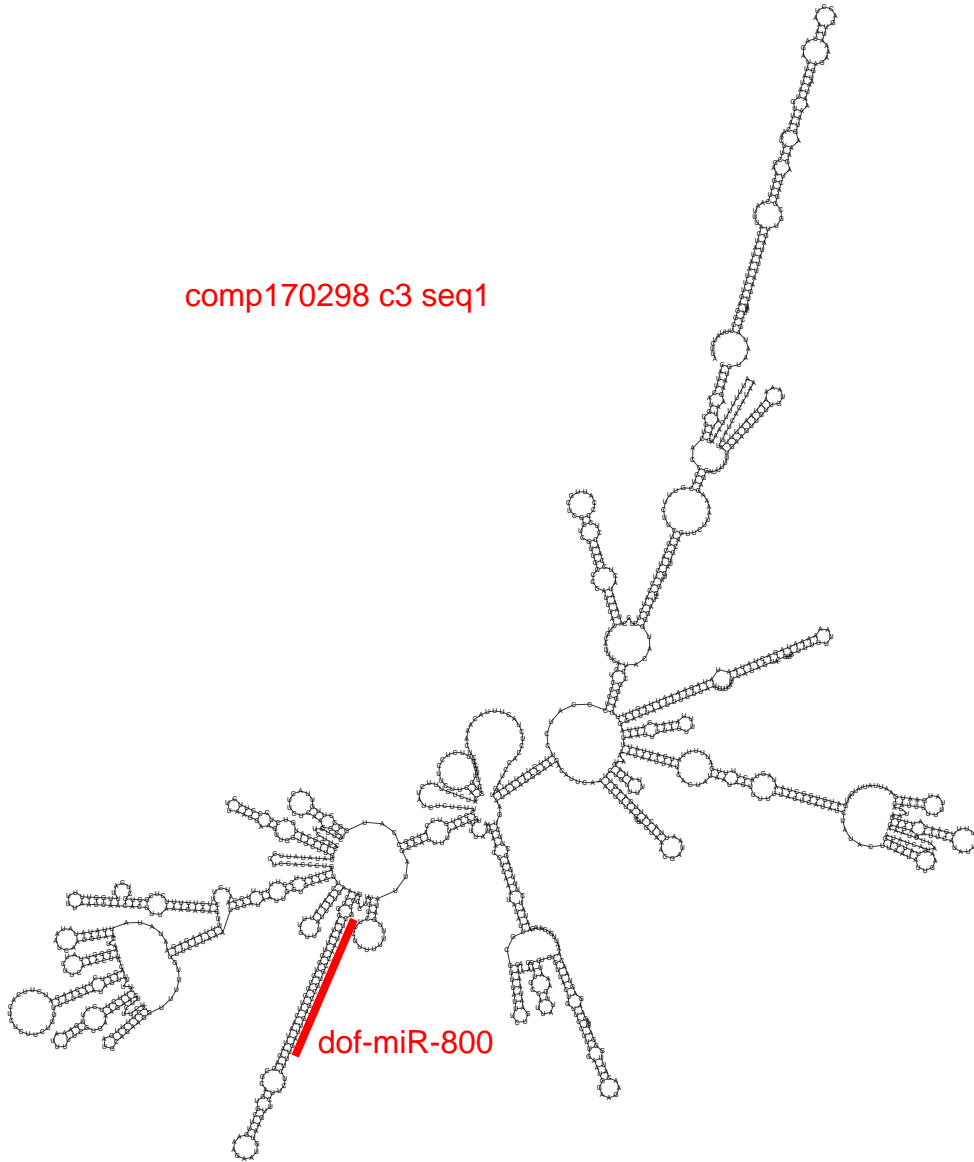
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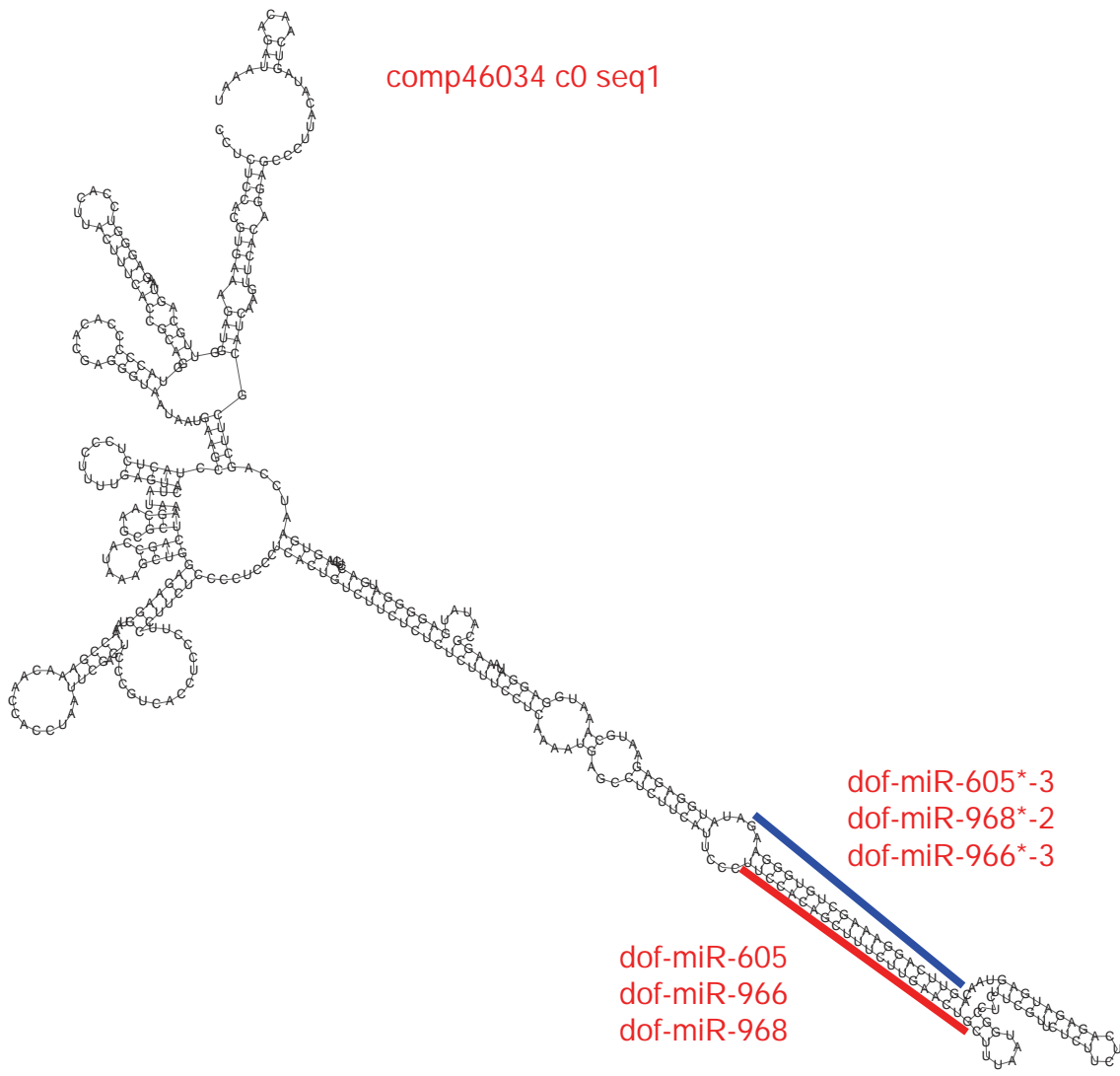


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Figure S3 Certain highly structured transcripts might serve as miRNA precursors. The transcripts were assembled by RNA-seq reads, and the transcript IDs were provided in the figure. The mature miRNA- and miRNA*-coding regions on the long stems of the miRNA precursors were marked by red and blue lines respectively, and their IDs were also provided. Note, for each mature miRNA, its average accumulation level in either organ (flower, leaf, root or stem; two biological replicates for each organ; thus, there are a total of eight libraries) of *Dendrobium officinale* should be 5 RPM or higher. Besides, the accumulation level of each miRNA* should be detectable in at least one sRNA-seq library. The secondary structures of the transcripts were predicted by using RNAfold (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>).



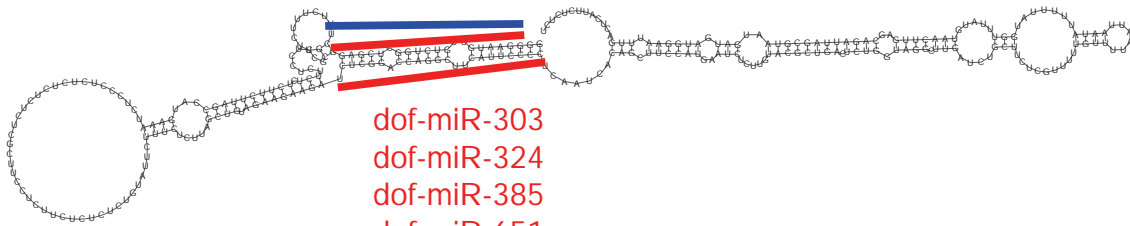
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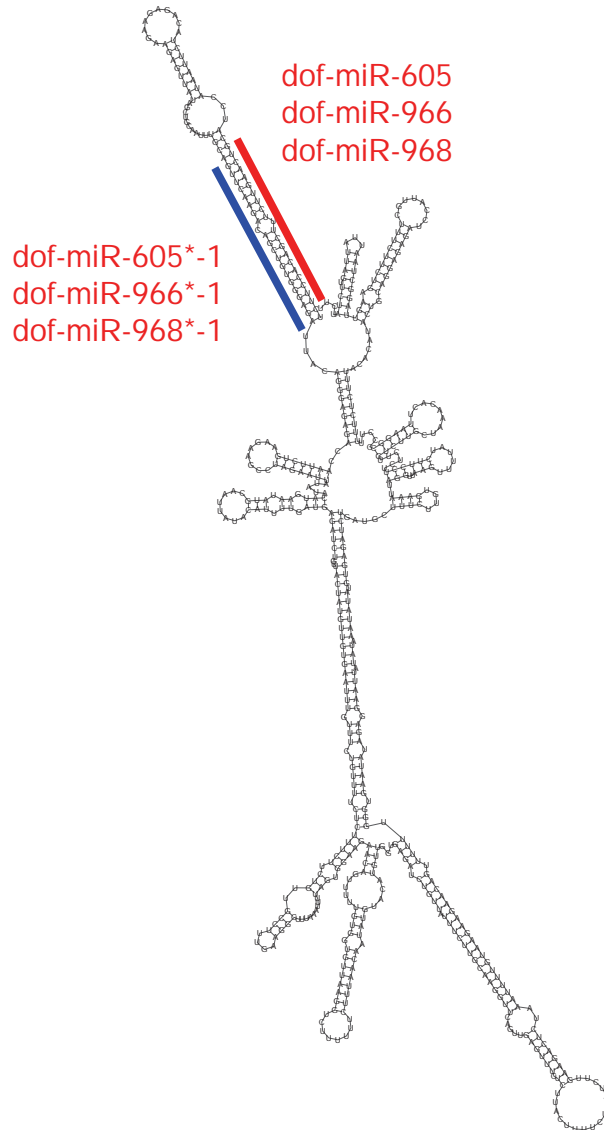
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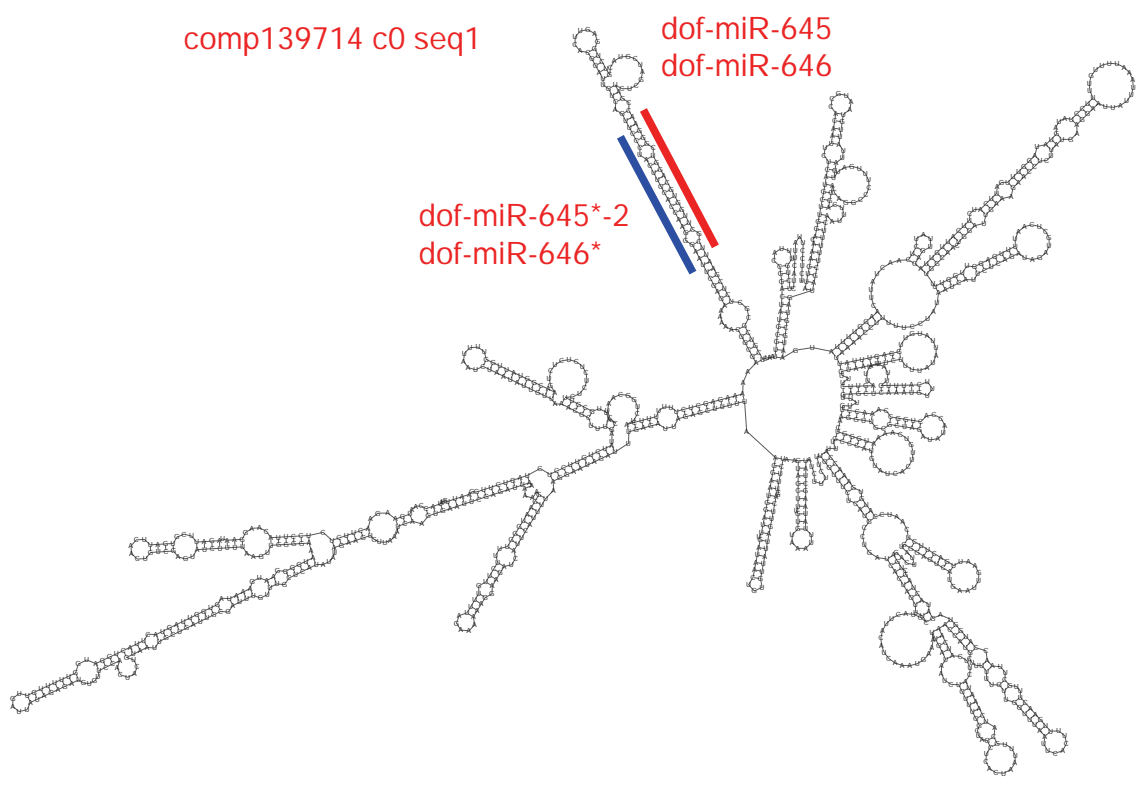
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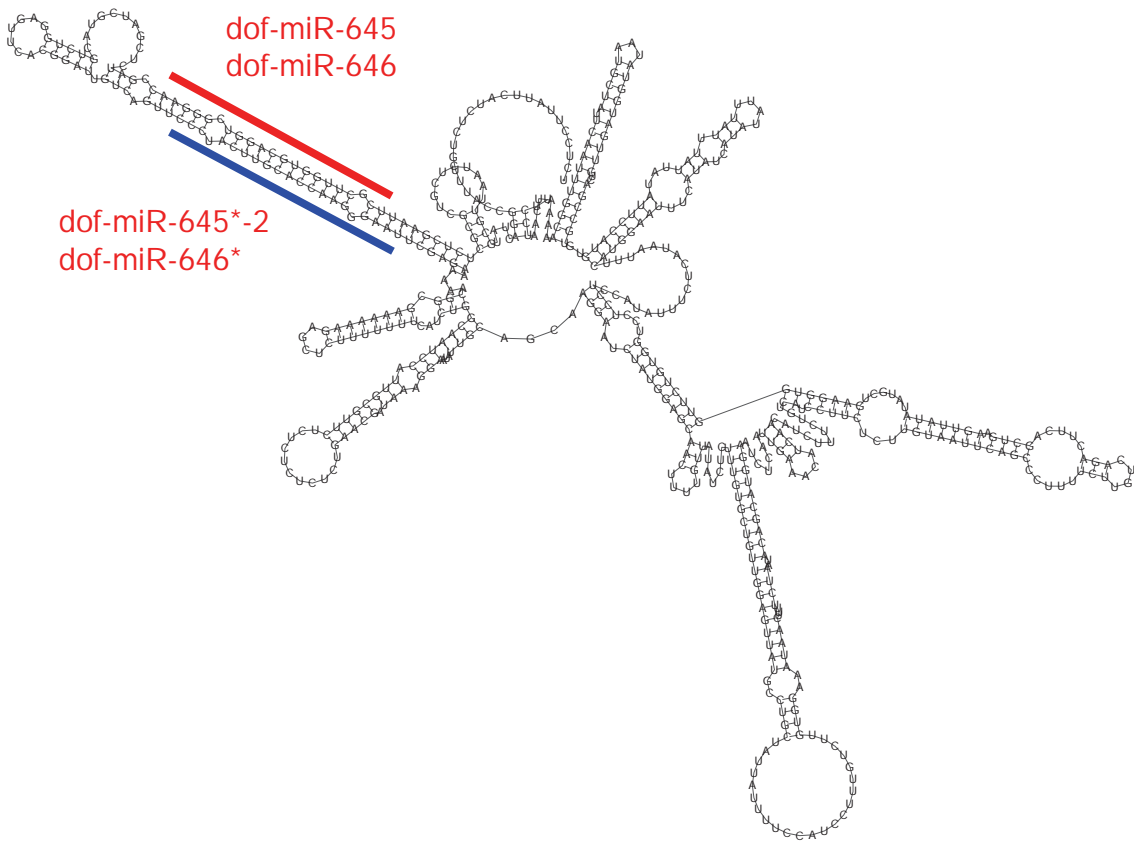
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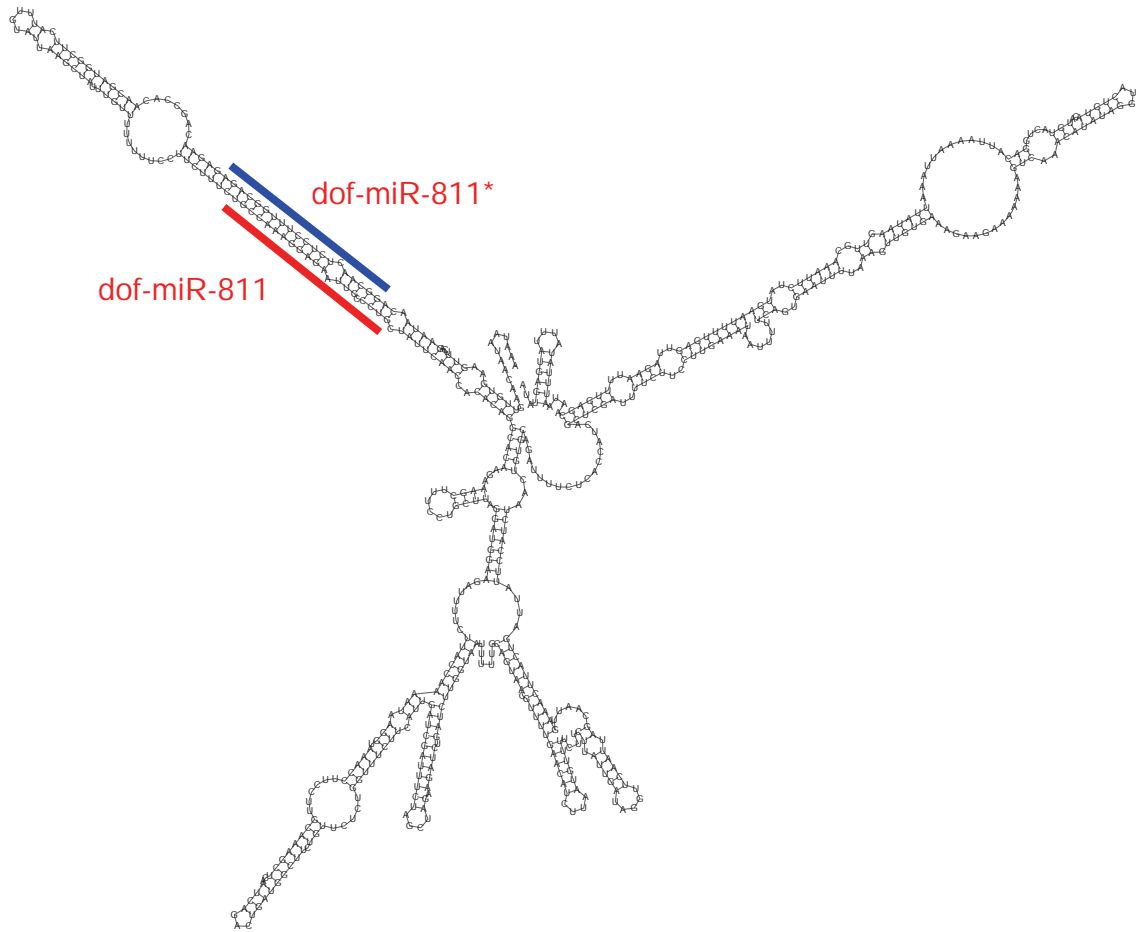




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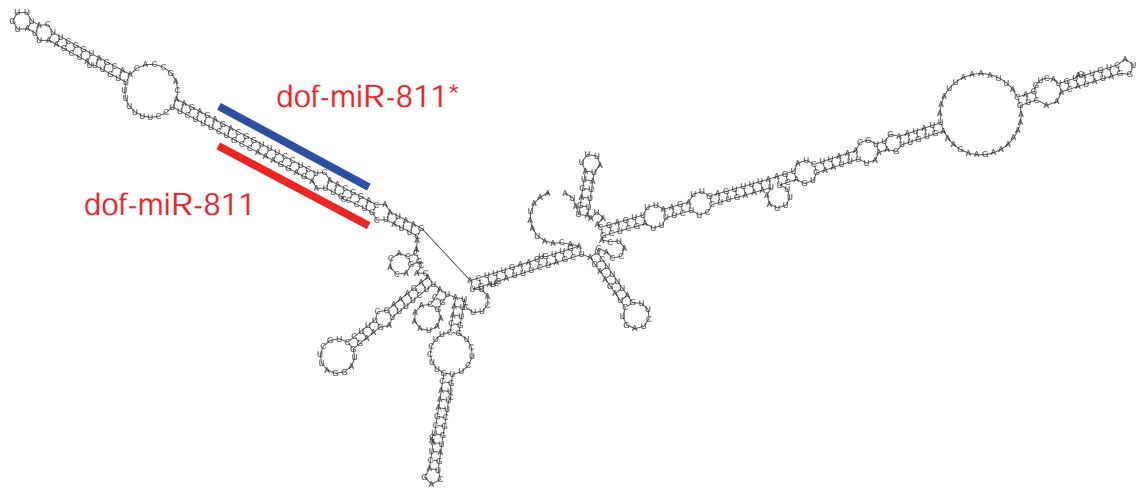
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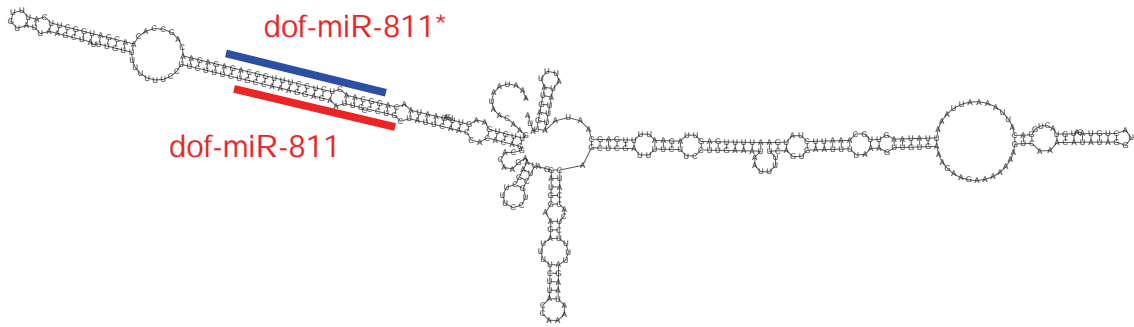
dof-miR-811*

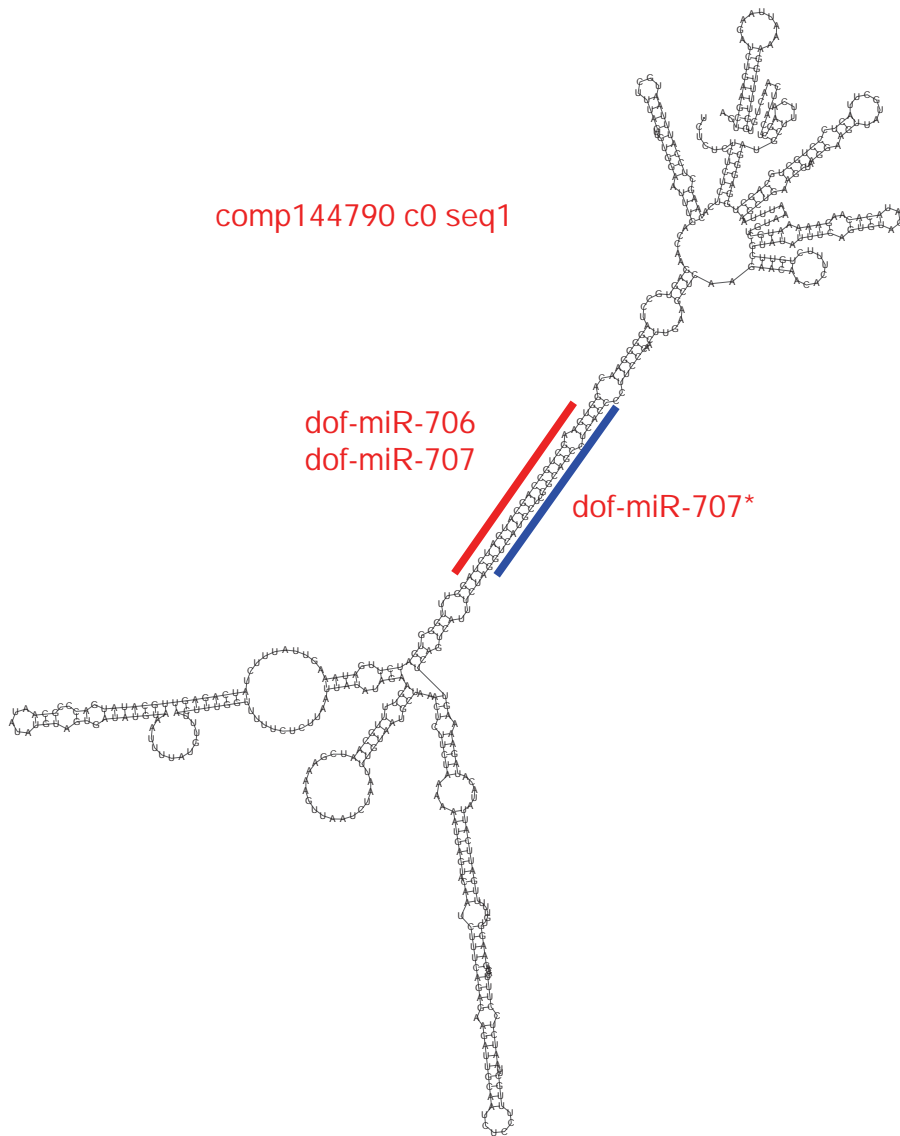
dof-miR-811

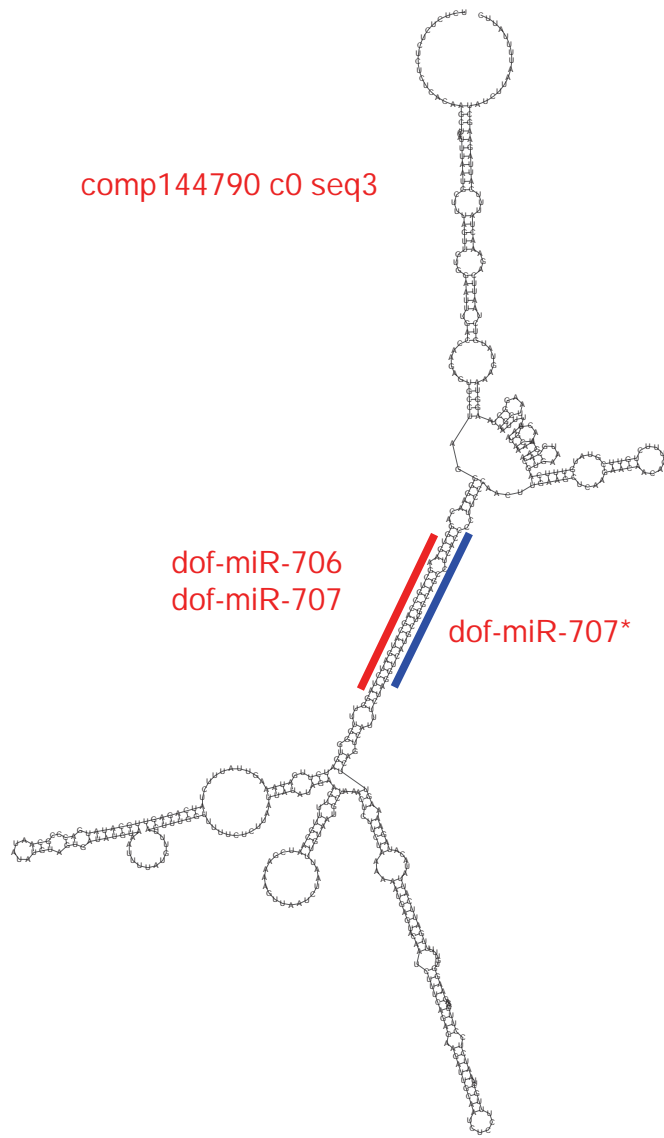
comp140839 c0 seq2



comp140839 c0 seq3



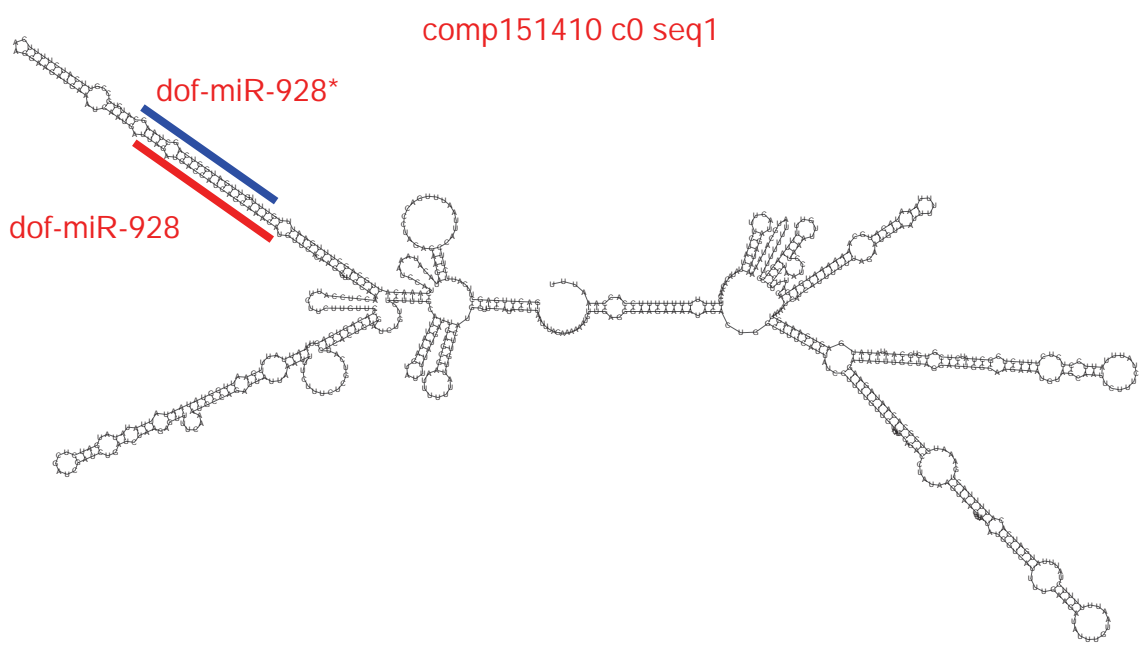




comp144790 c0 seq3

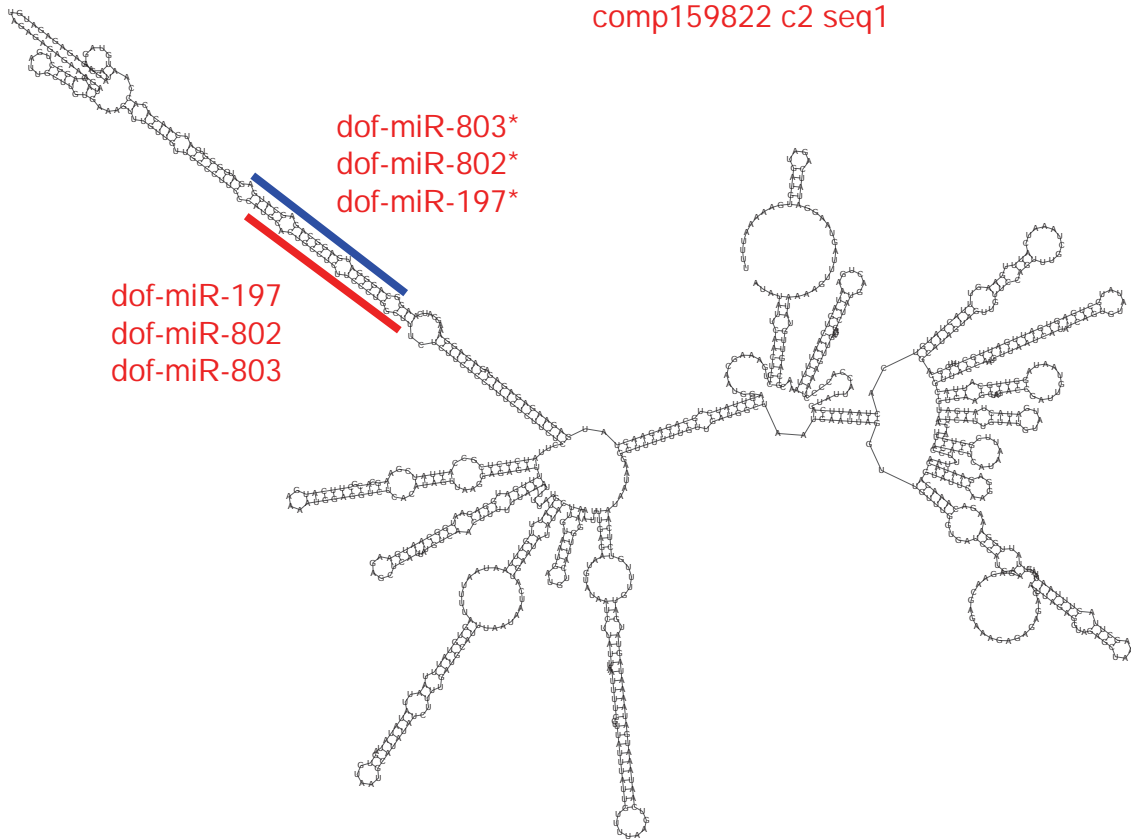
dof-miR-706
dof-miR-707

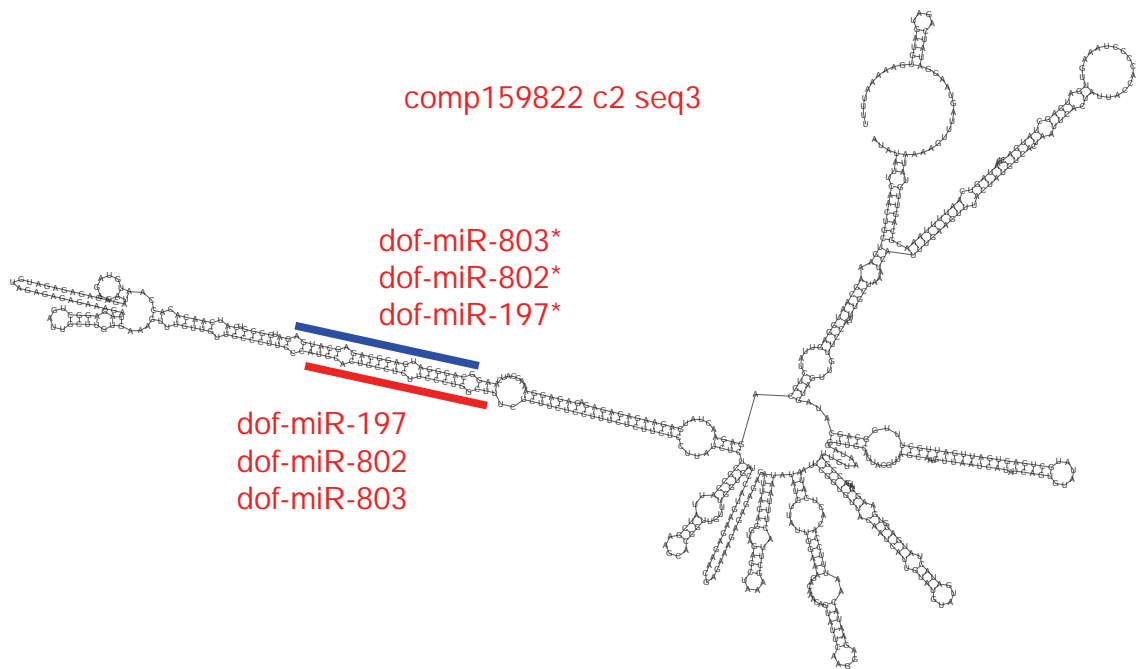
dof-miR-707*

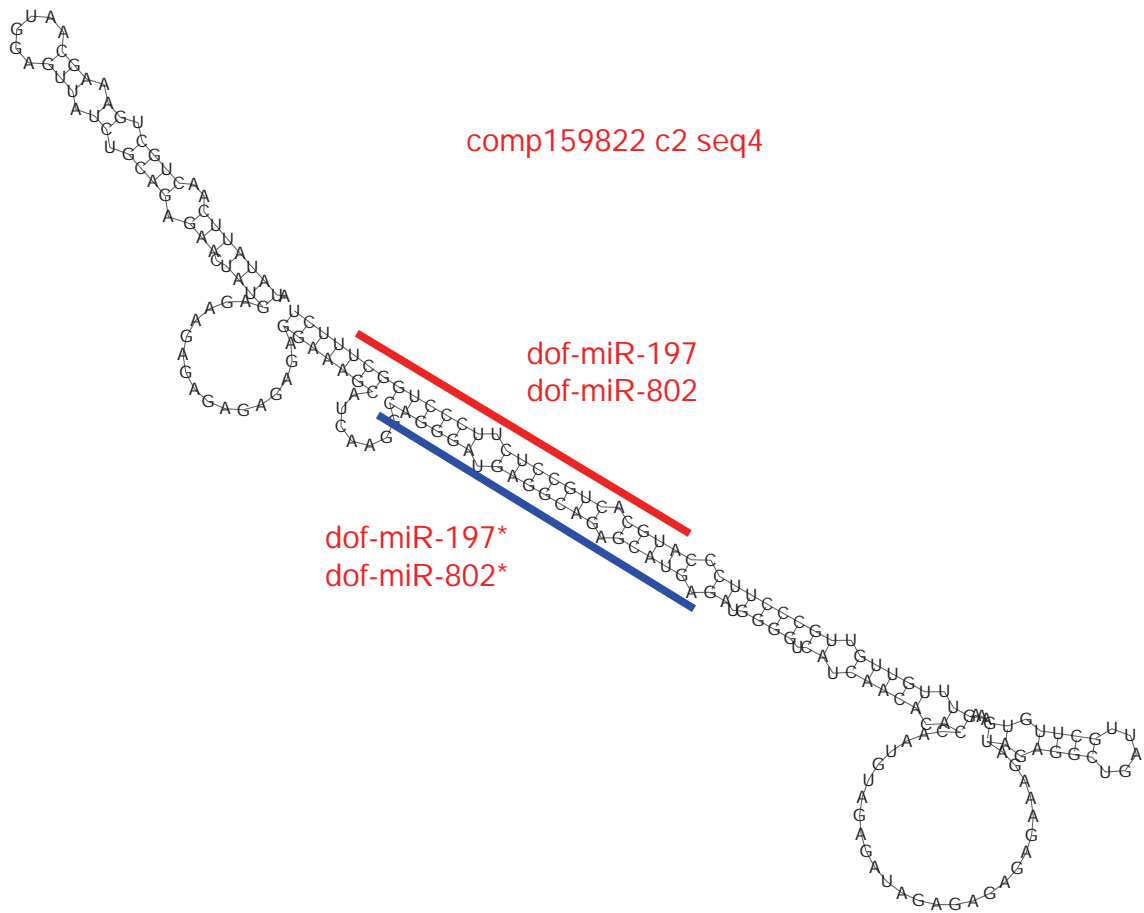




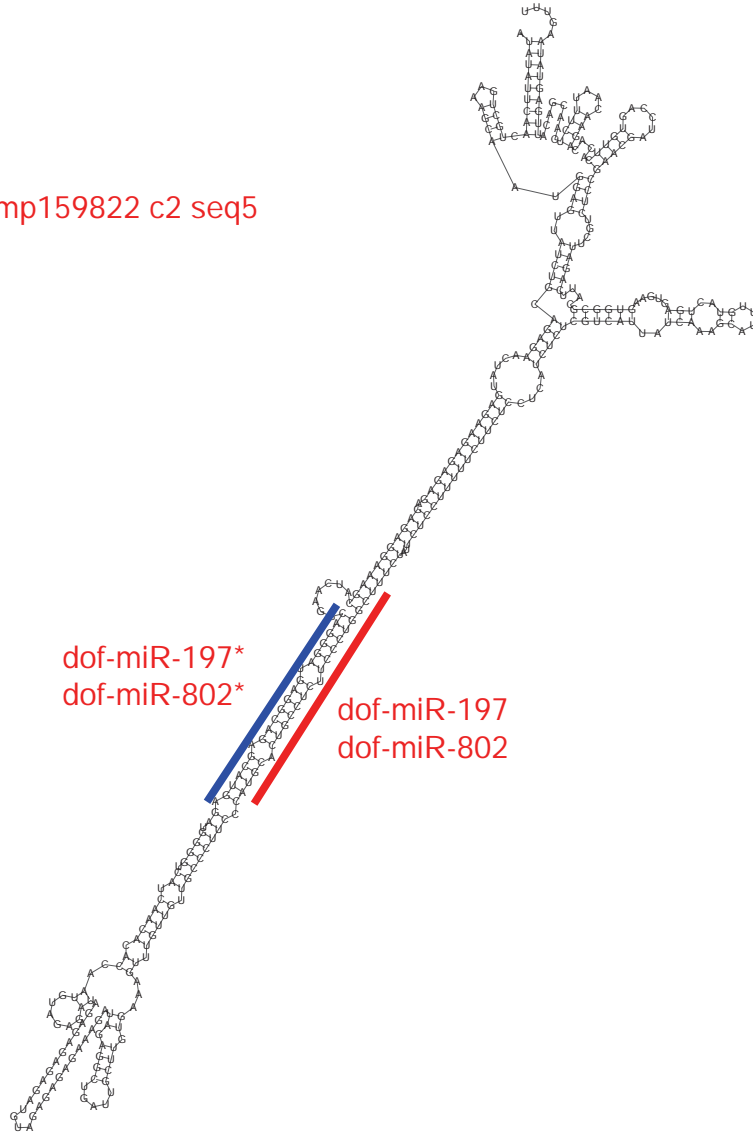
comp159822 c2 seq1







comp159822 c2 seq5



comp160245 c0 seq1



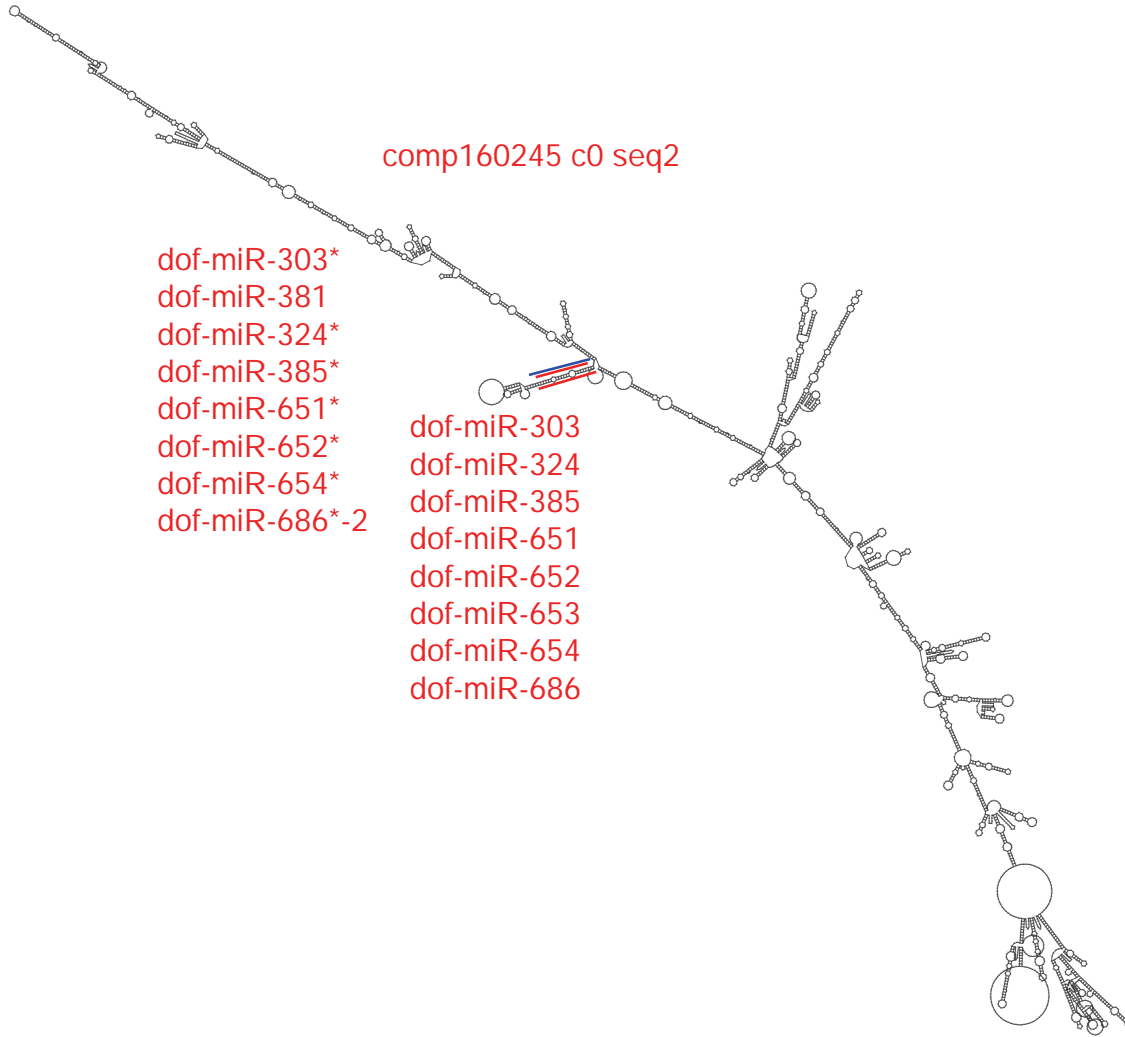
dof-miR-303
dof-miR-324
dof-miR-385
dof-miR-651
dof-miR-652
dof-miR-653
dof-miR-654
dof-miR-686

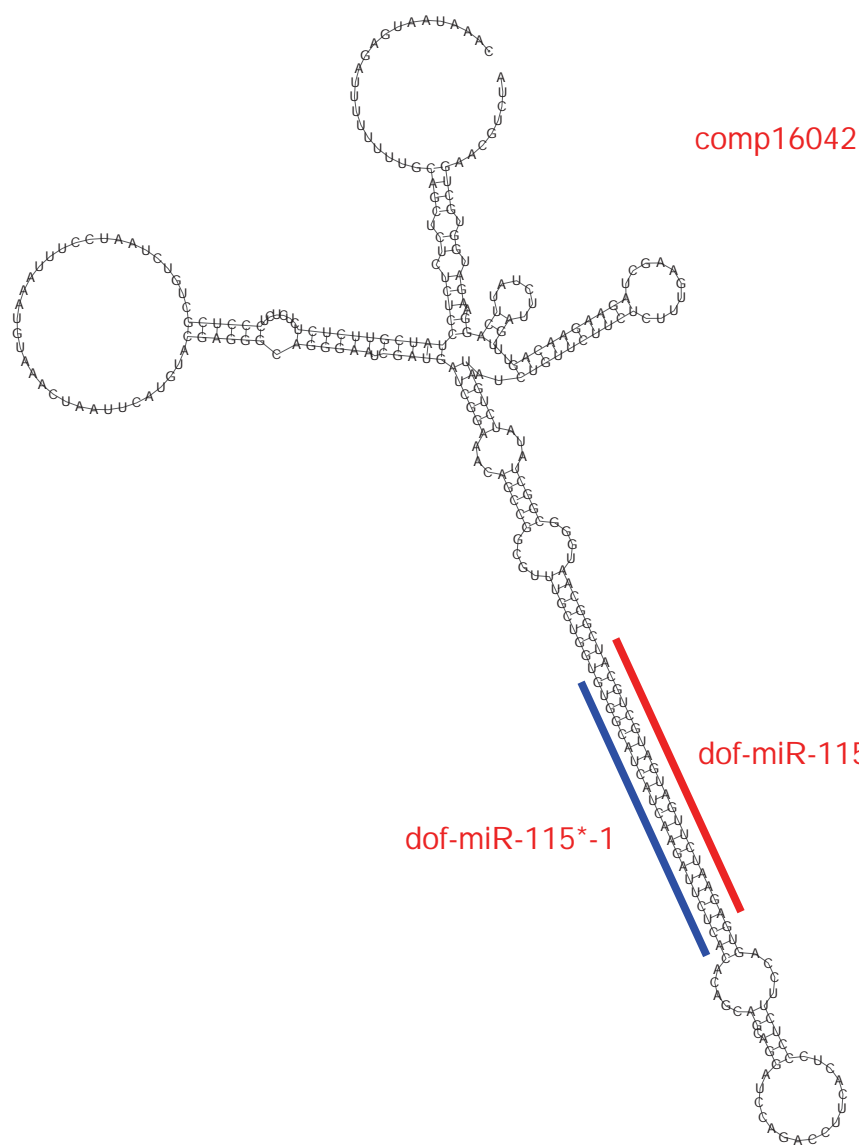
dof-miR-303*
dof-miR-381
dof-miR-324*
dof-miR-385*
dof-miR-651*
dof-miR-652*
dof-miR-654*
dof-miR-686*-2

comp160245 c0 seq2

dof-miR-303*
dof-miR-381
dof-miR-324*
dof-miR-385*
dof-miR-651*
dof-miR-652*
dof-miR-654*
dof-miR-686*-2

dof-miR-303
dof-miR-324
dof-miR-385
dof-miR-651
dof-miR-652
dof-miR-653
dof-miR-654
dof-miR-686



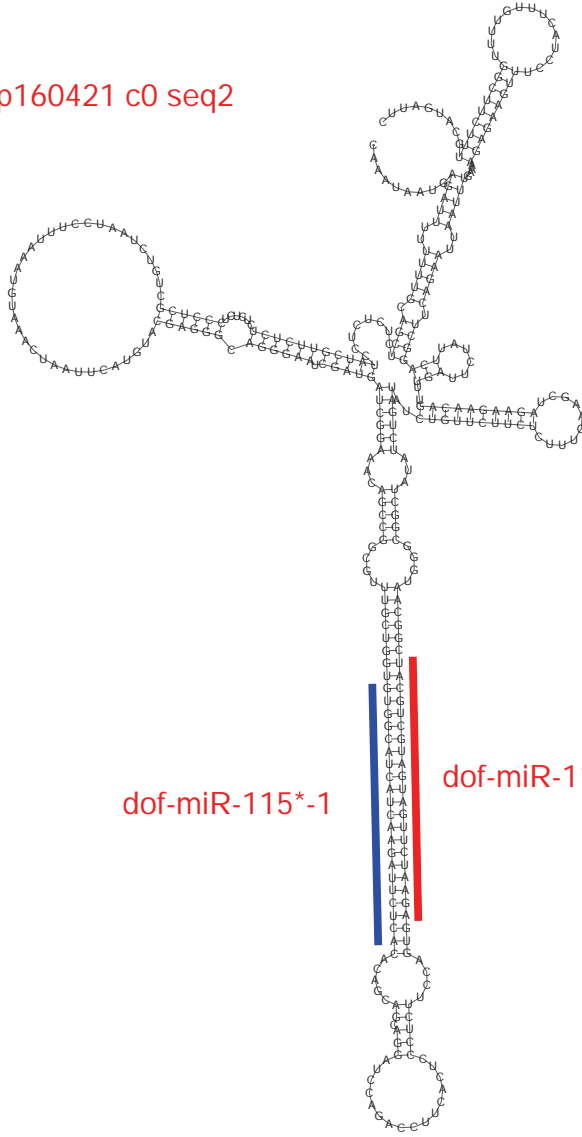


comp160421 c0 seq1

dof-miR-115

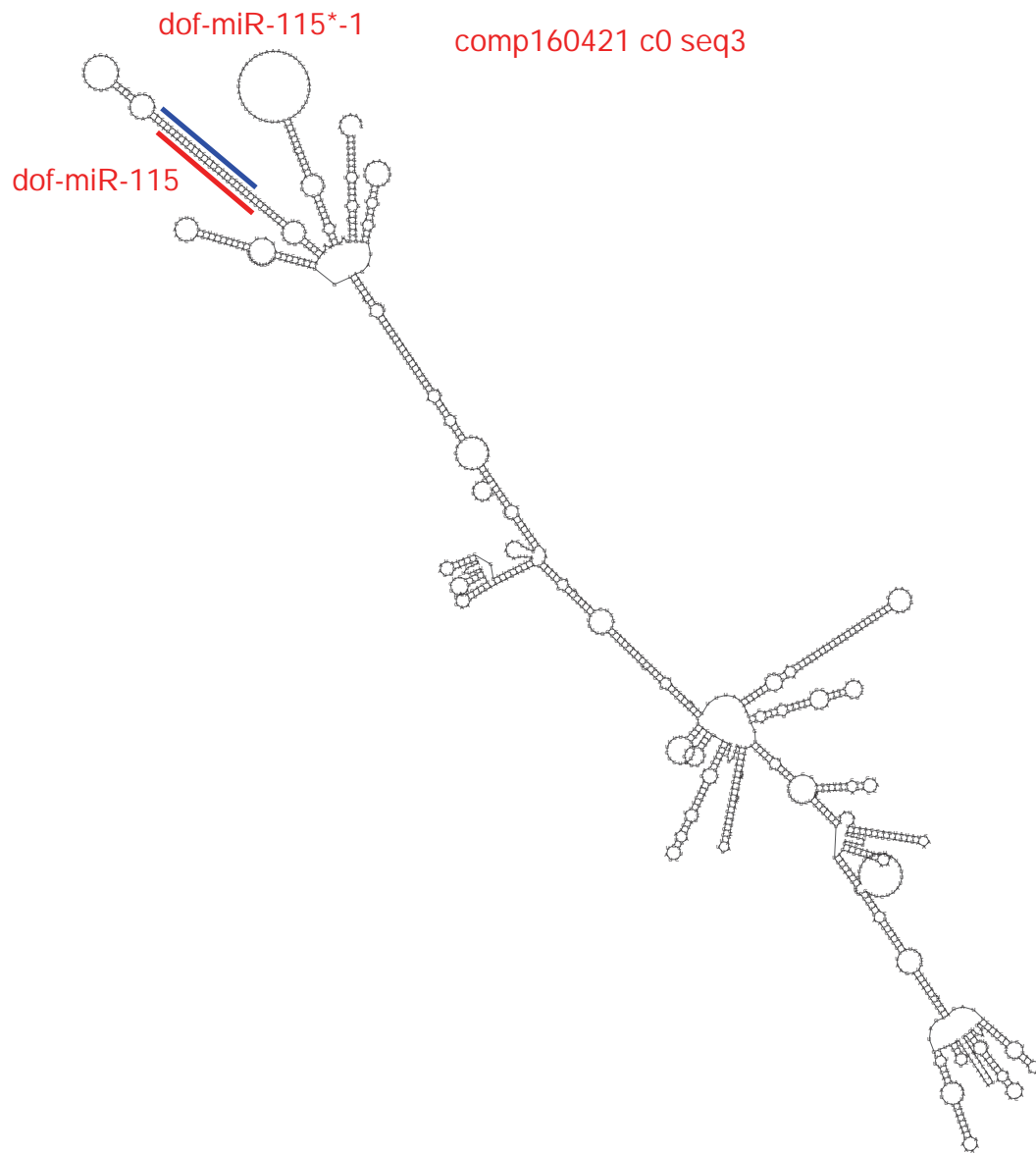
dof-miR-115*-1

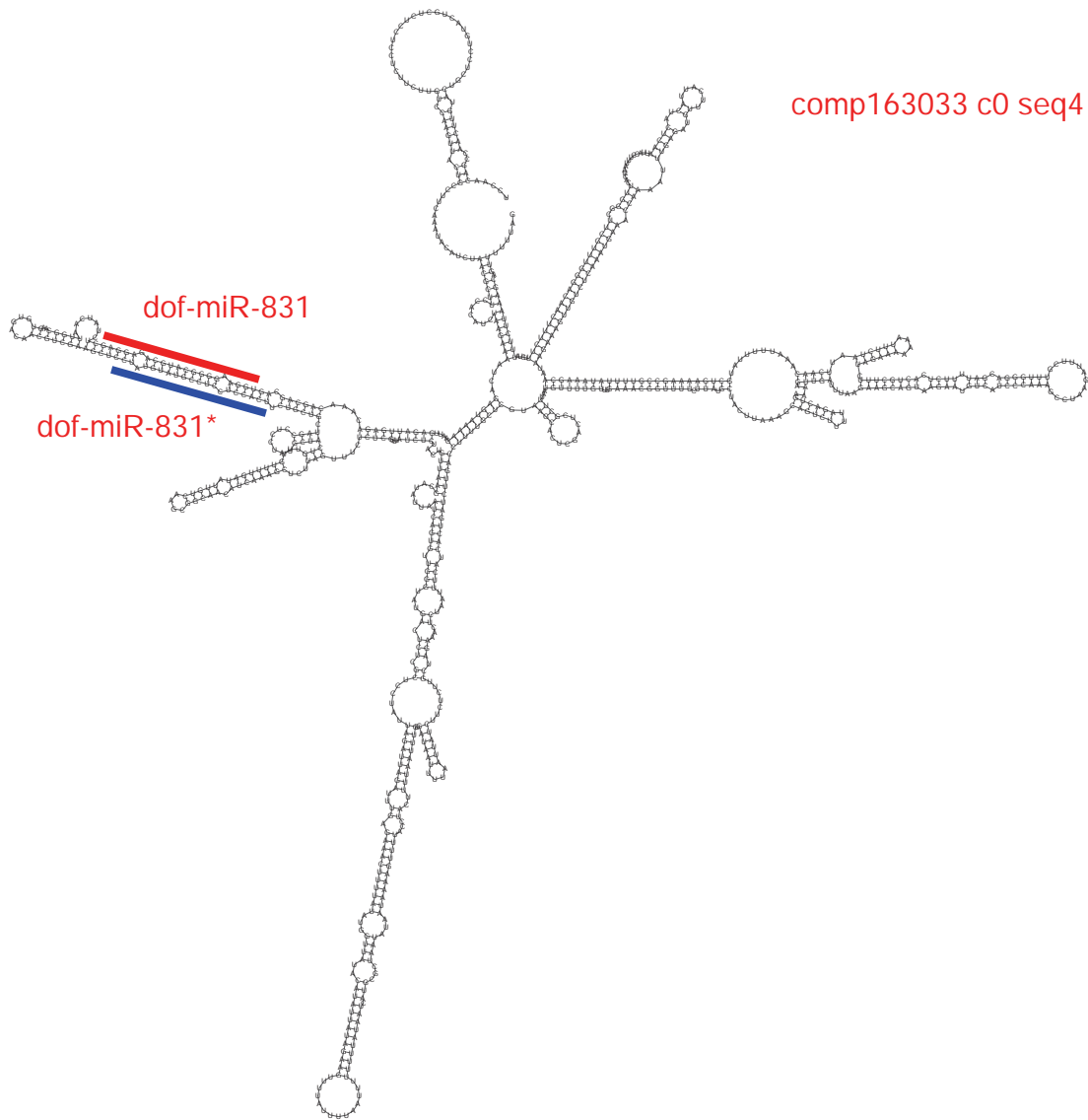
comp160421 c0 seq2



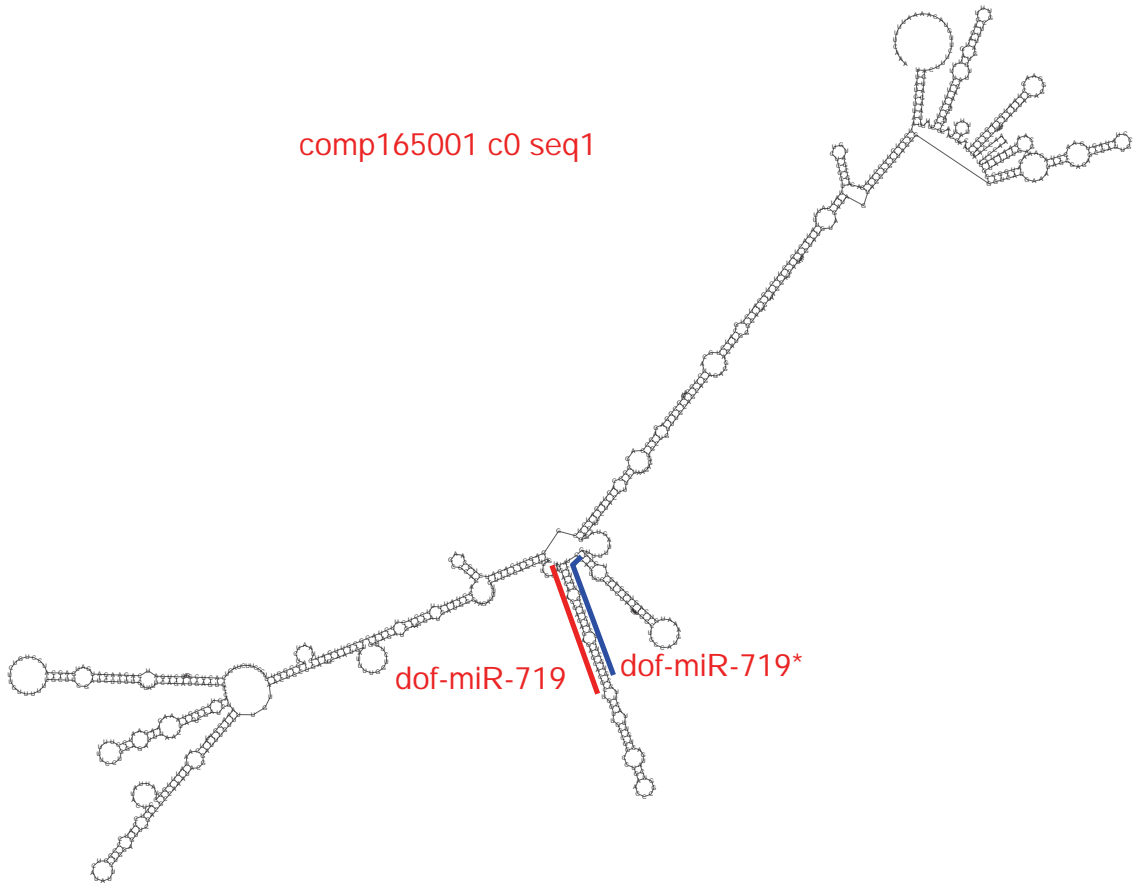
dof-miR-115*-1

dof-miR-115

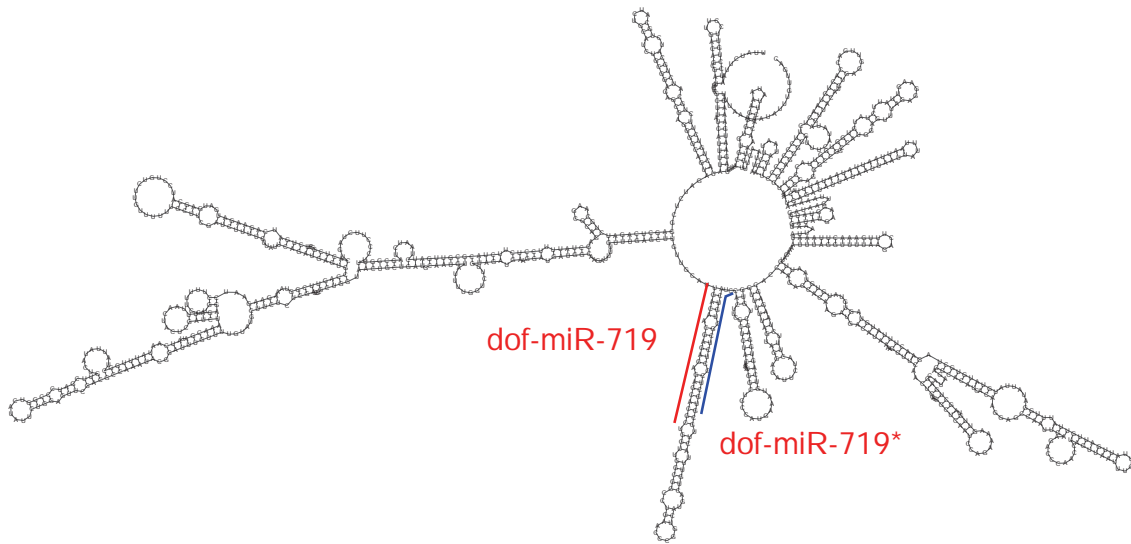




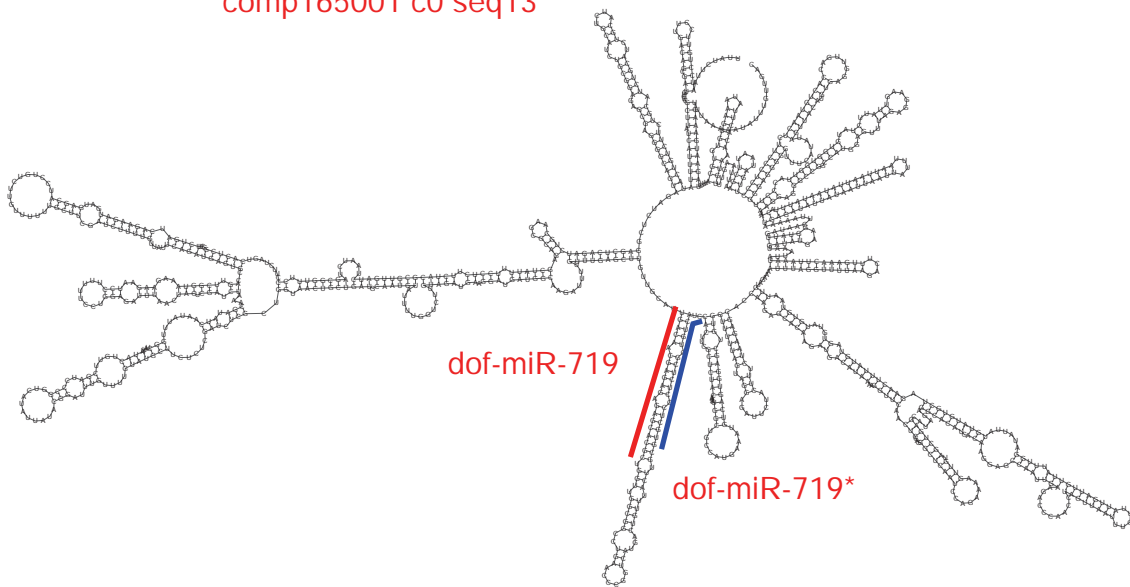
comp165001 c0 seq1



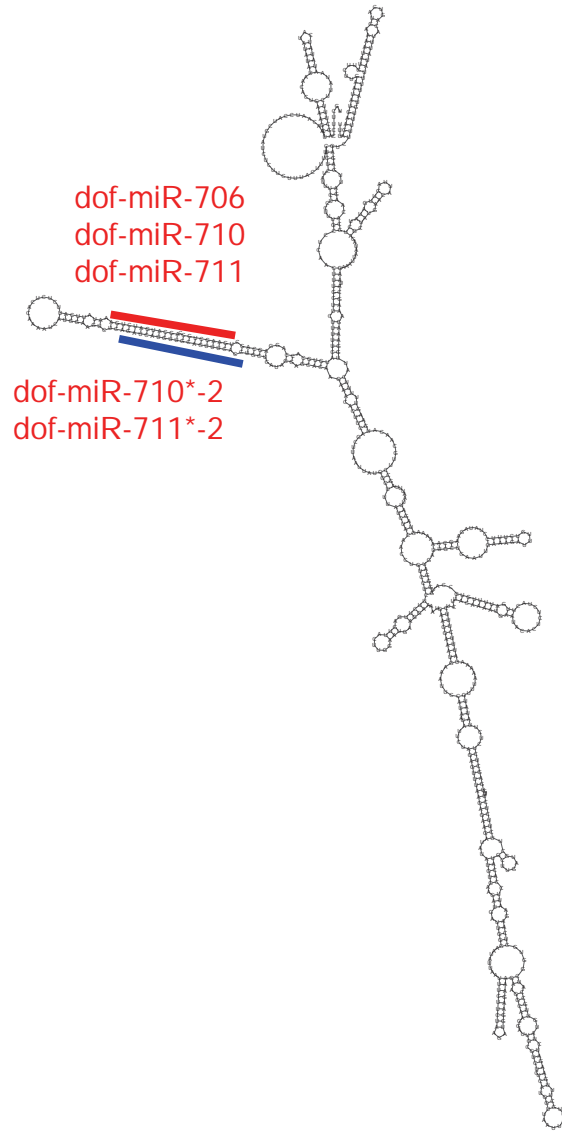
comp165001 c0 seq4



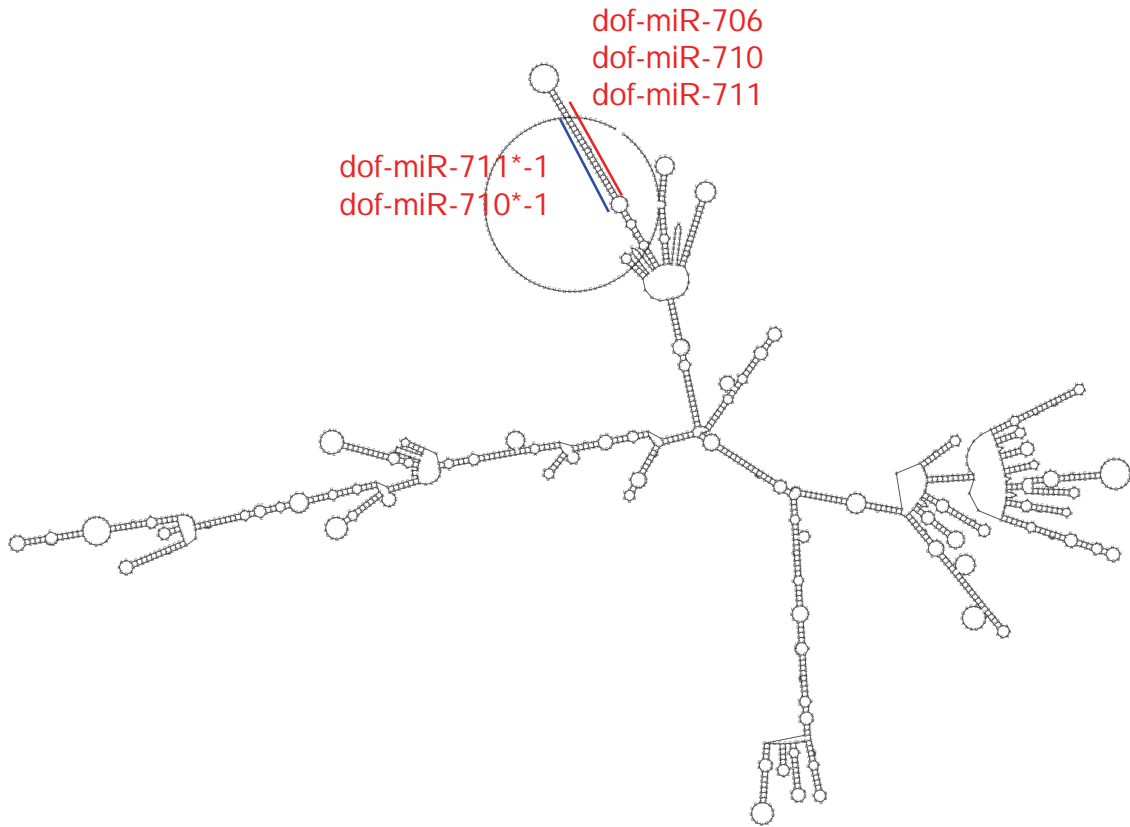
comp165001 c0 seq13



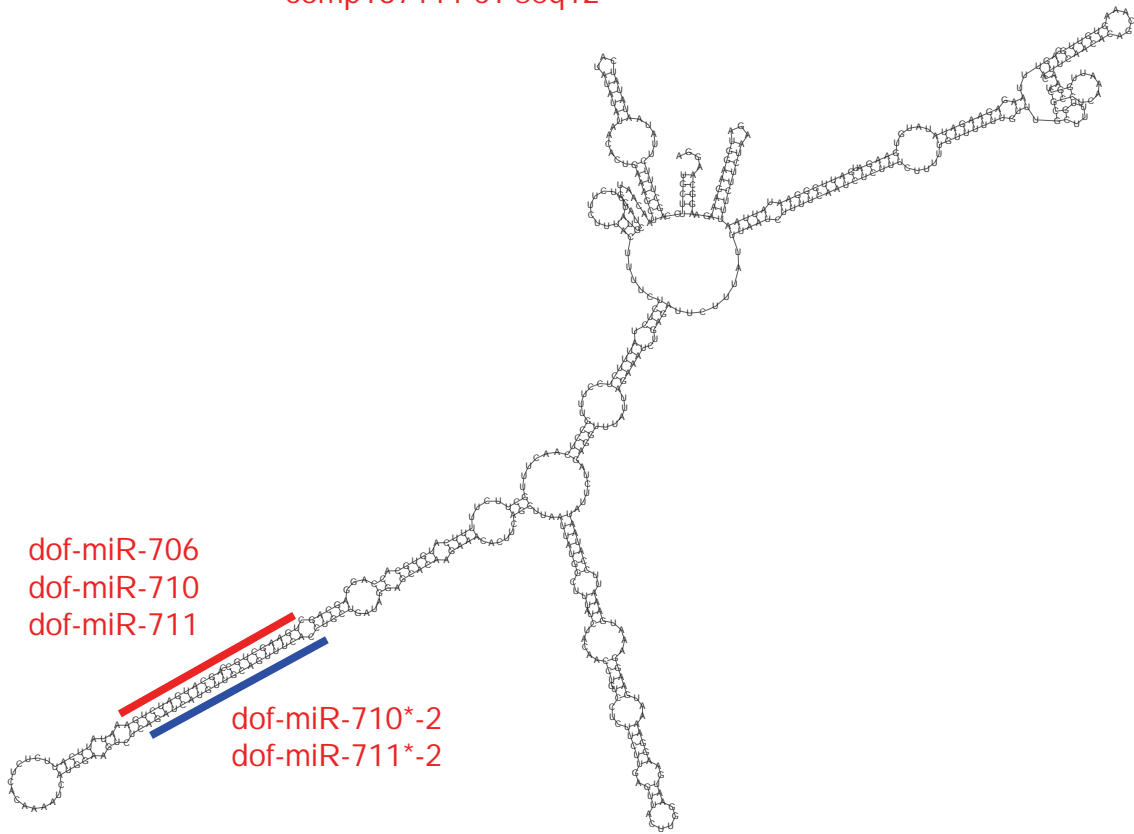
comp167111 c1 seq1



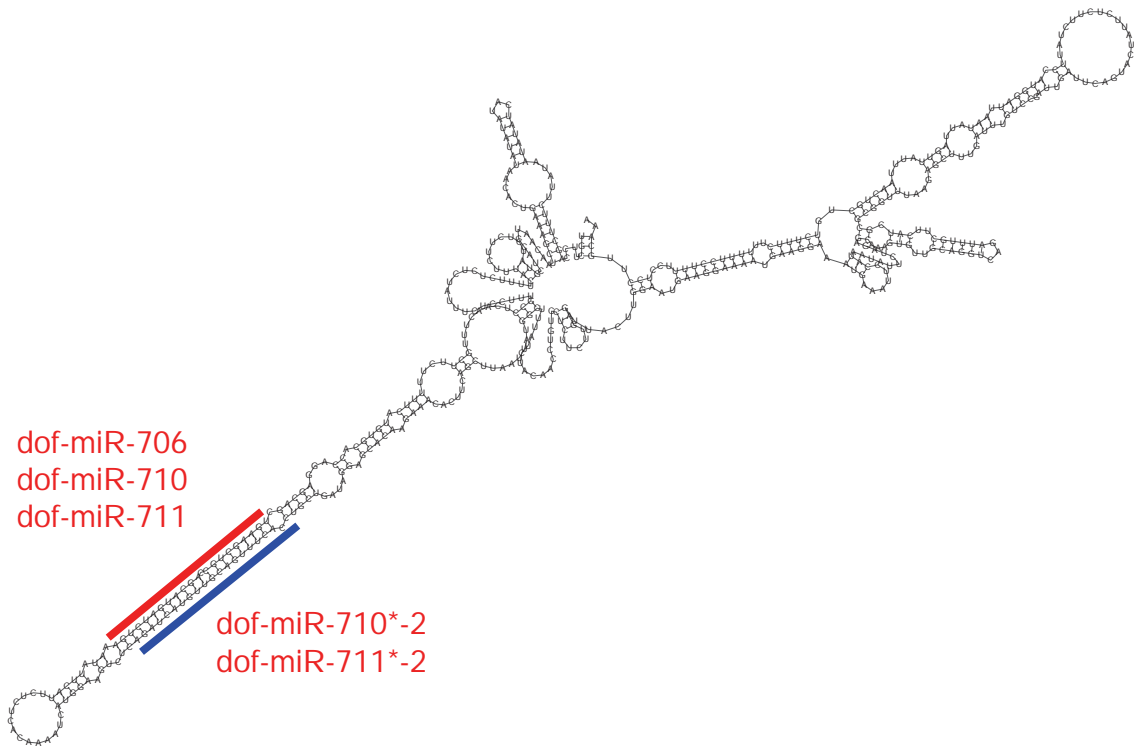
comp167111 c1 seq7



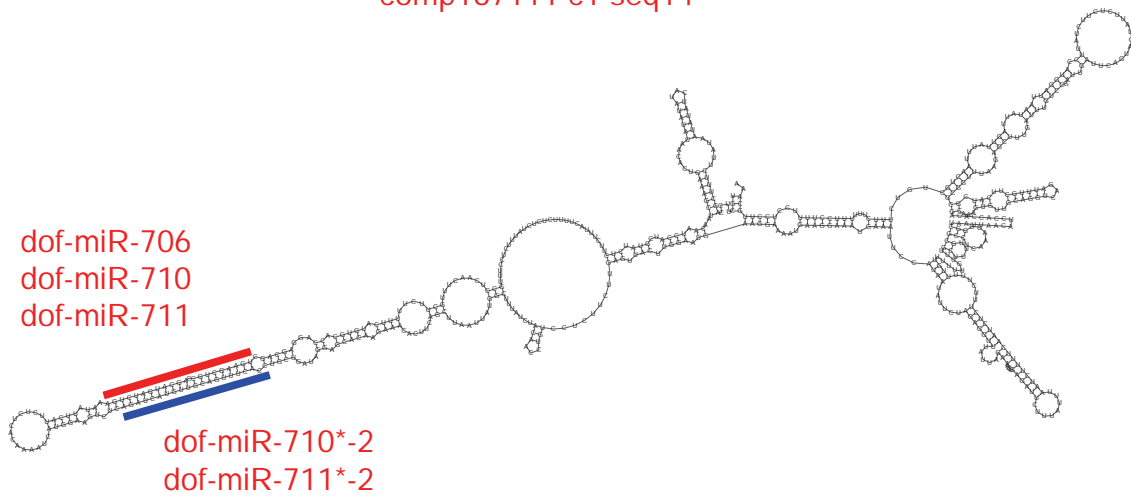
comp167111 c1 seq12



comp167111 c1 seq13



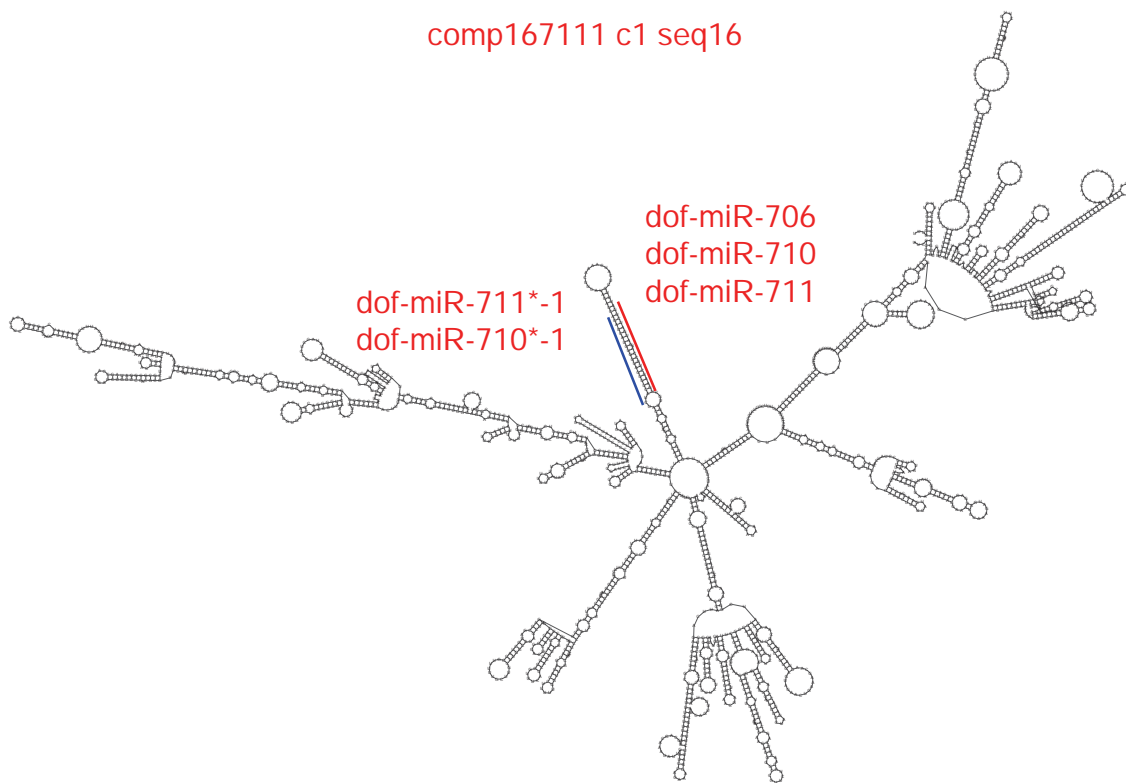
comp167111 c1 seq14

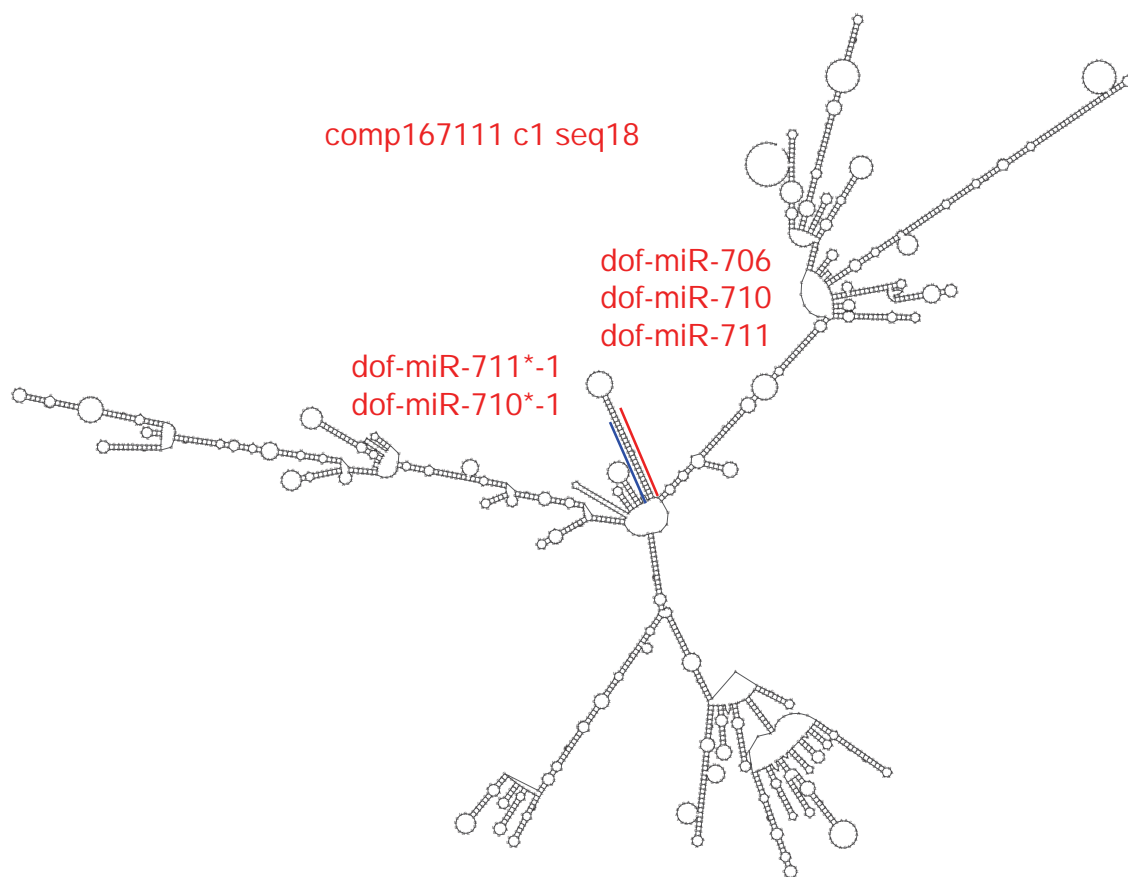


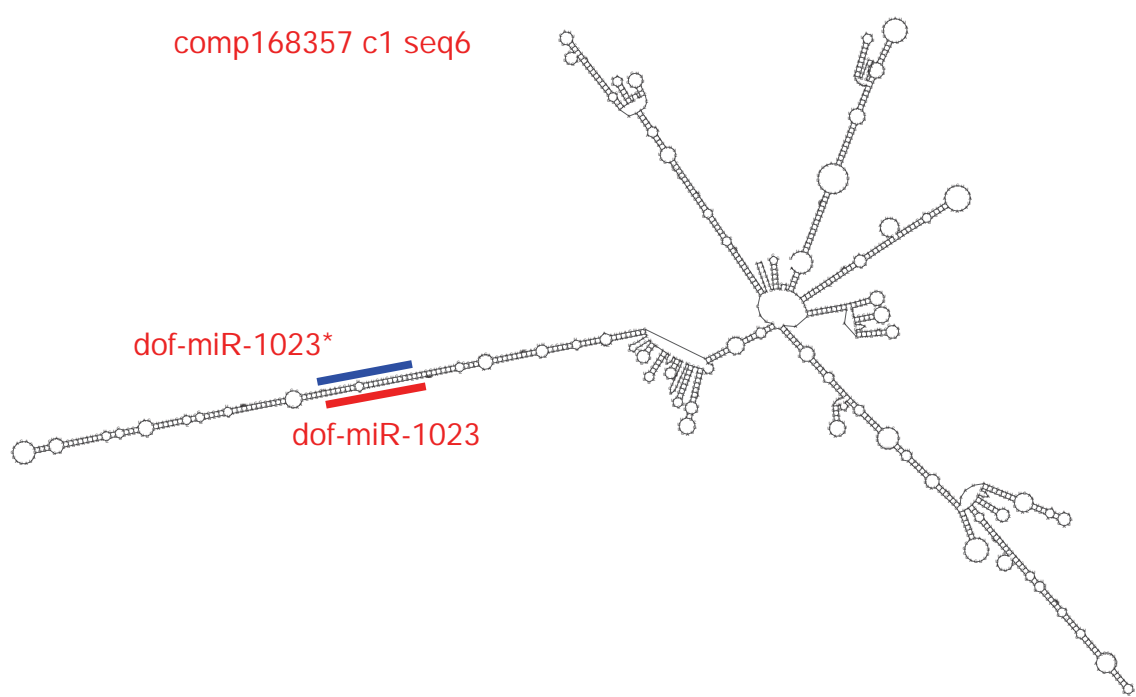
dof-miR-706
dof-miR-710
dof-miR-711

dof-miR-710*-2
dof-miR-711*-2

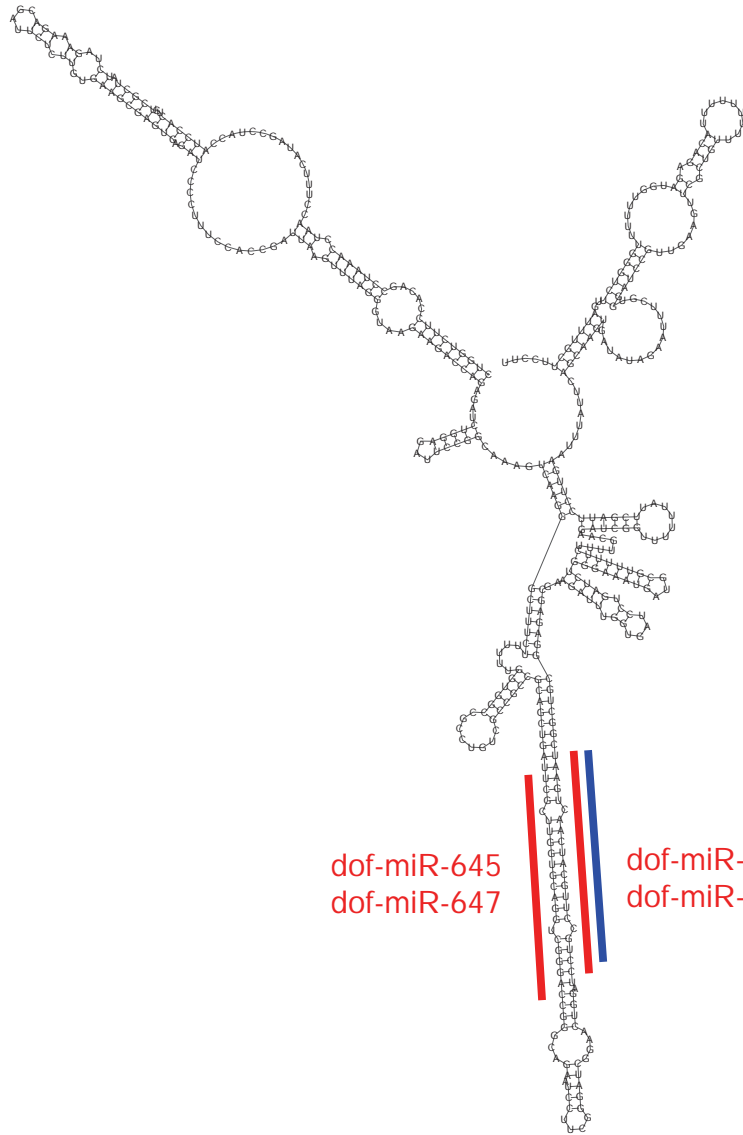
comp167111 c1 seq16







comp168949 c1 seq1



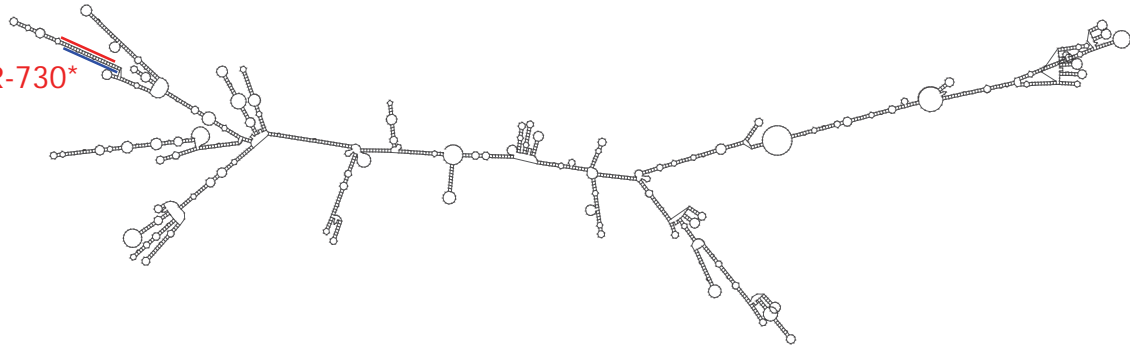
dof-miR-645
dof-miR-647

dof-miR-296
dof-miR-645*-1

comp170626 c2 seq1

dof-miR-730

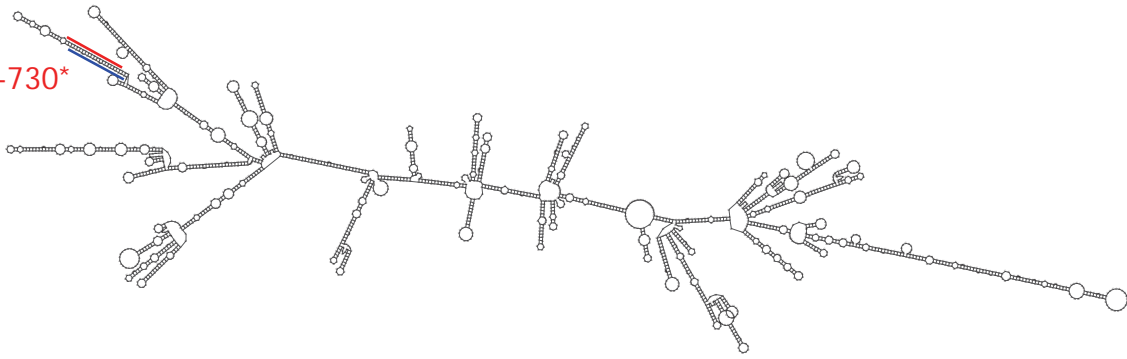
dof-miR-730*



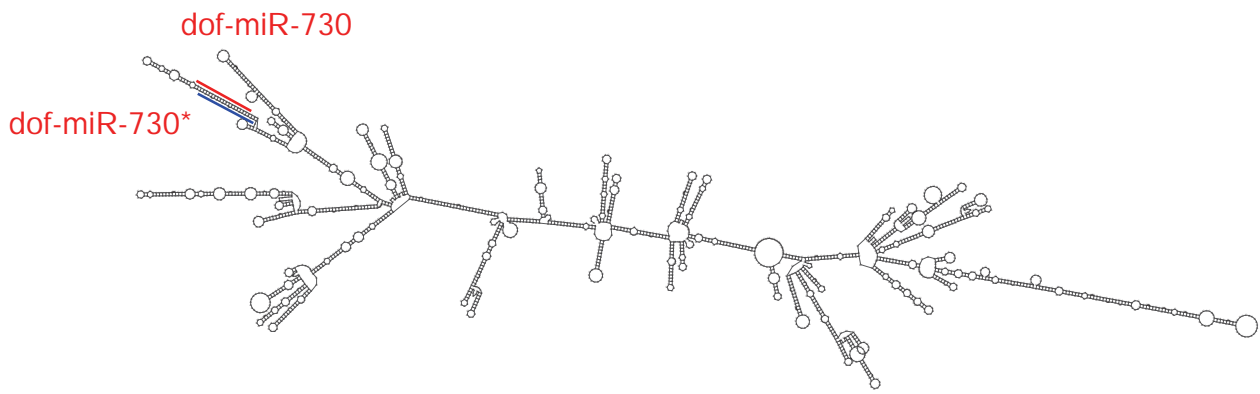
comp170626 c2 seq3

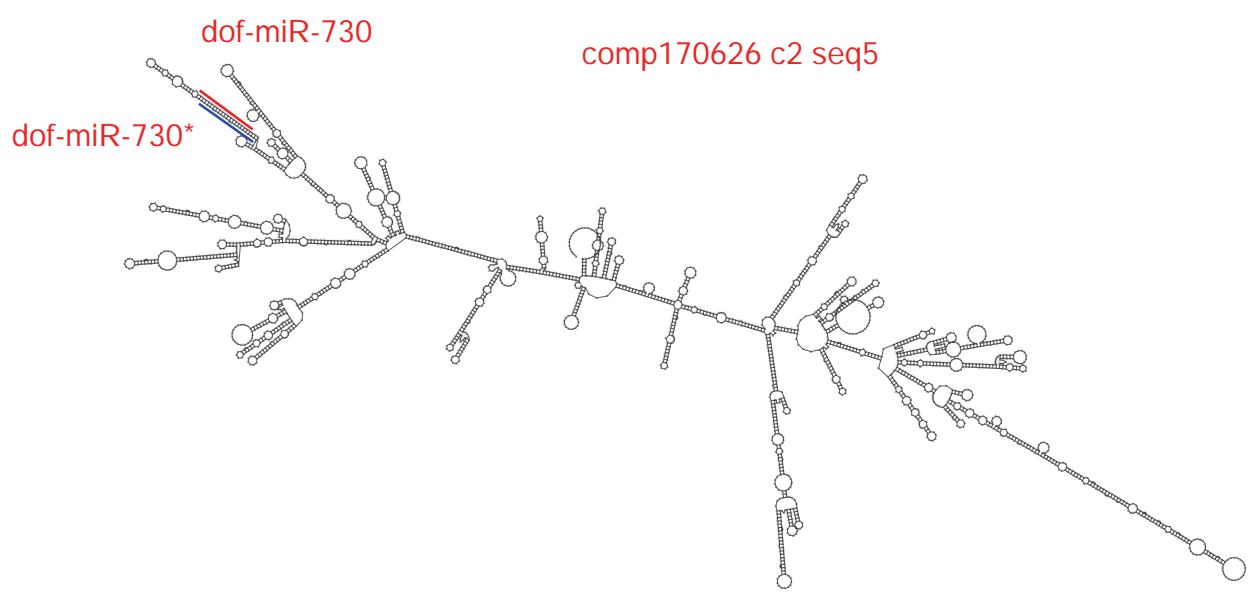
dof-miR-730

dof-miR-730*



comp170626 c2 seq4

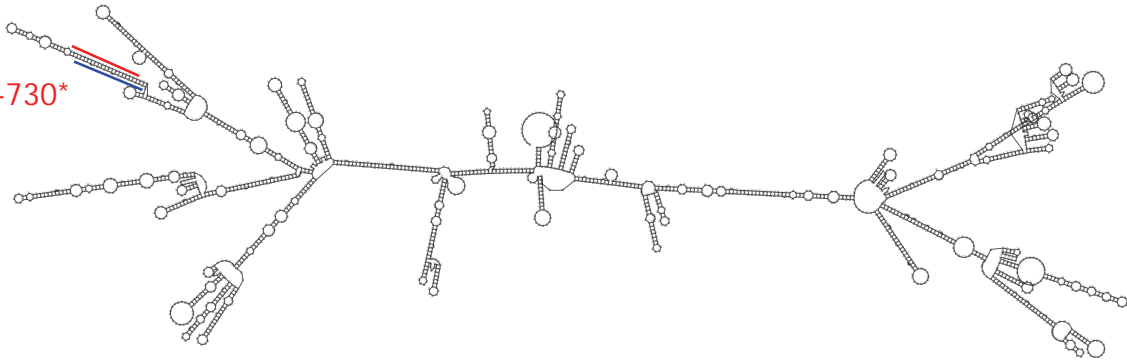


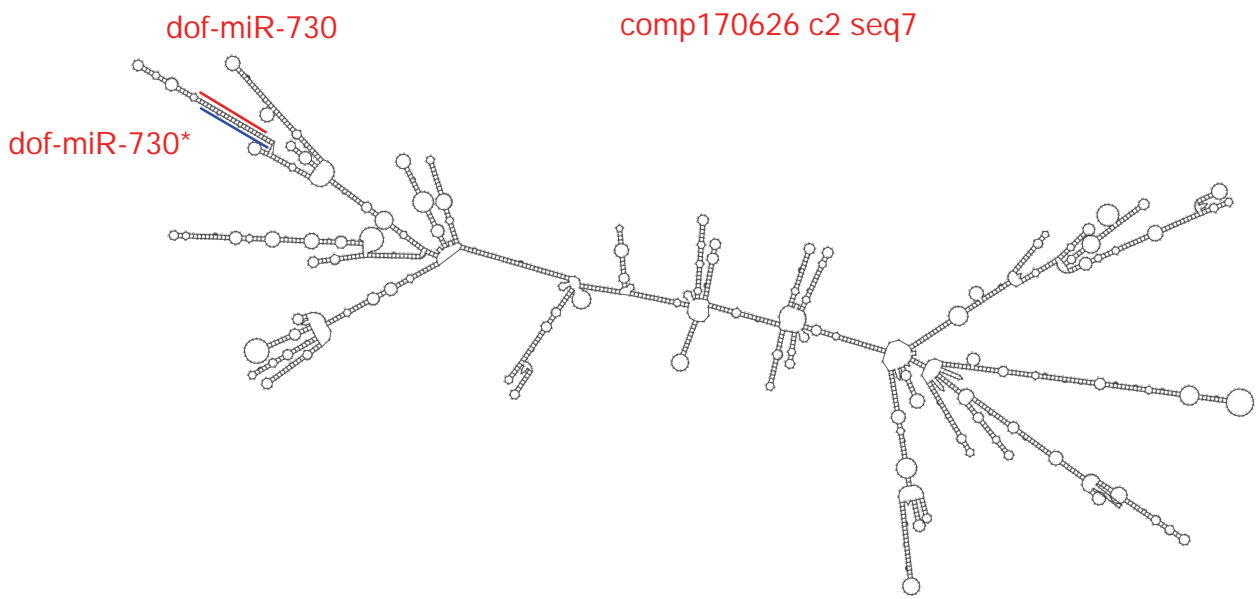


comp170626 c2 seq6

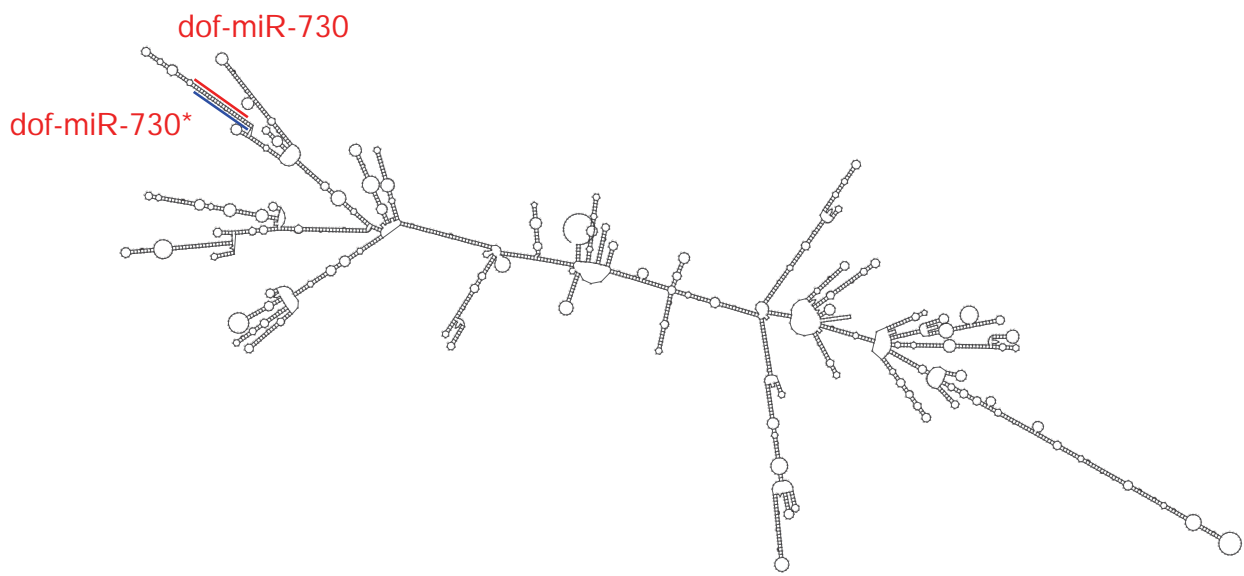
dof-miR-730

dof-miR-730*





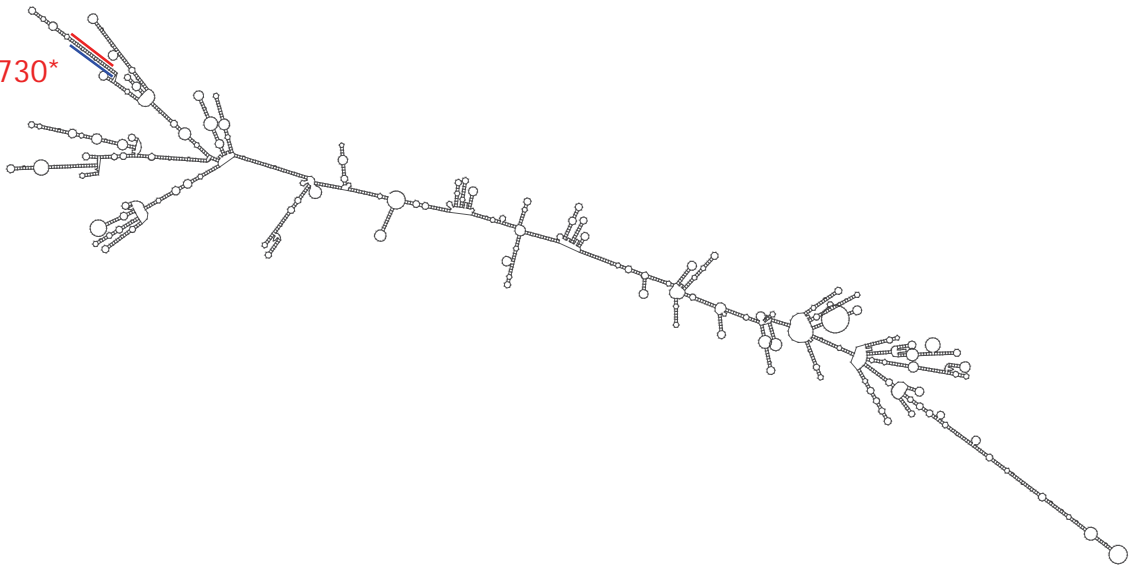
comp170626 c2 seq8



comp170626 c2 seq9

dof-miR-730

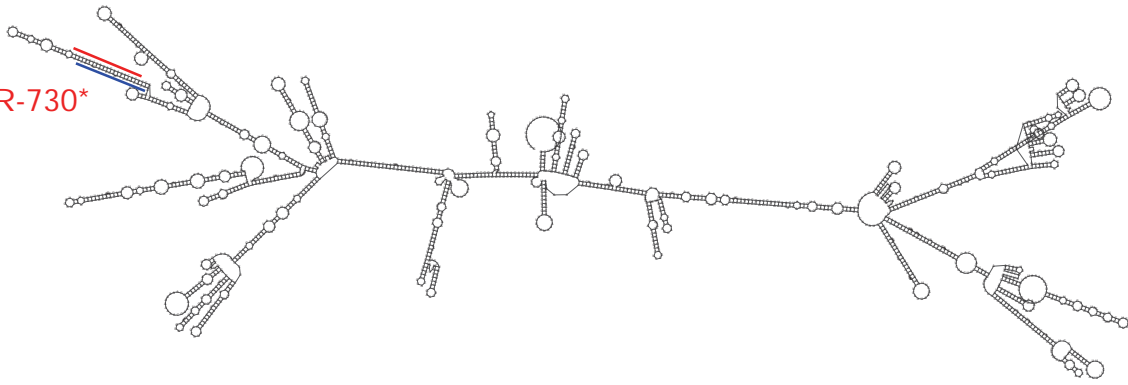
dof-miR-730*

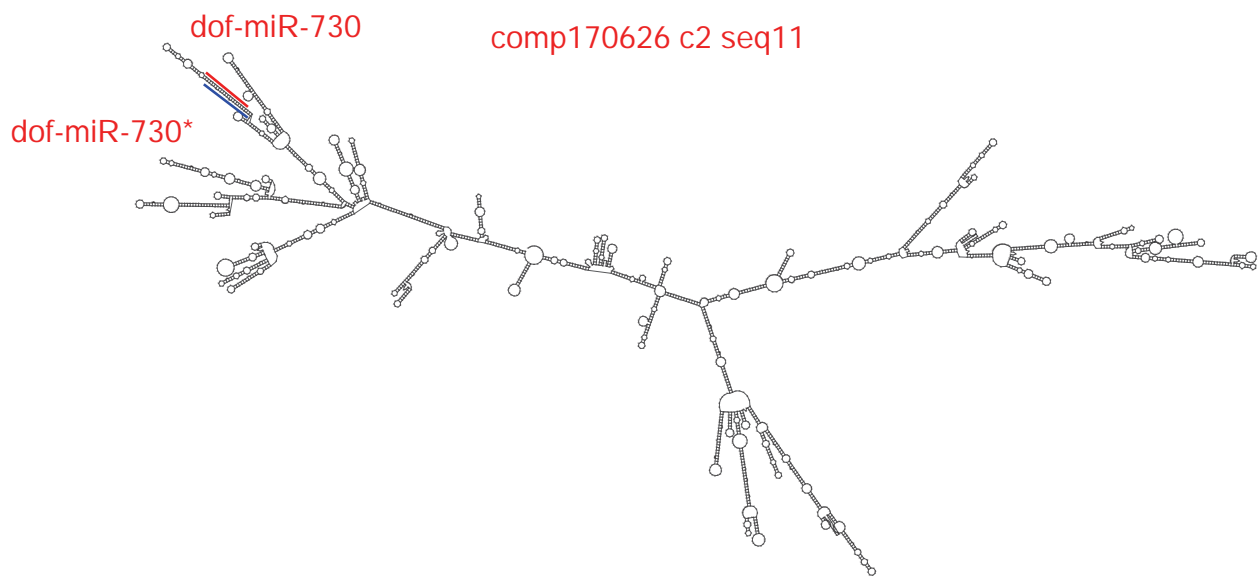


comp170626 c2 seq10

dof-miR-730

dof-miR-730*

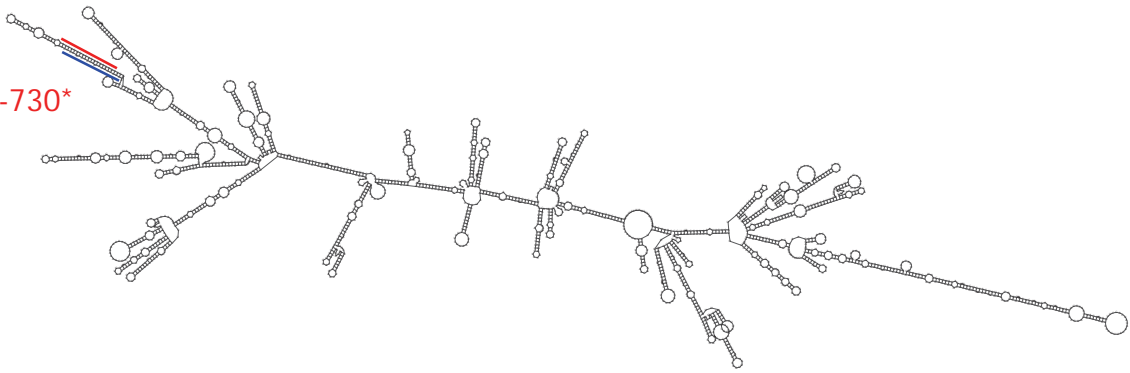




comp170626 c2 seq13

dof-miR-730

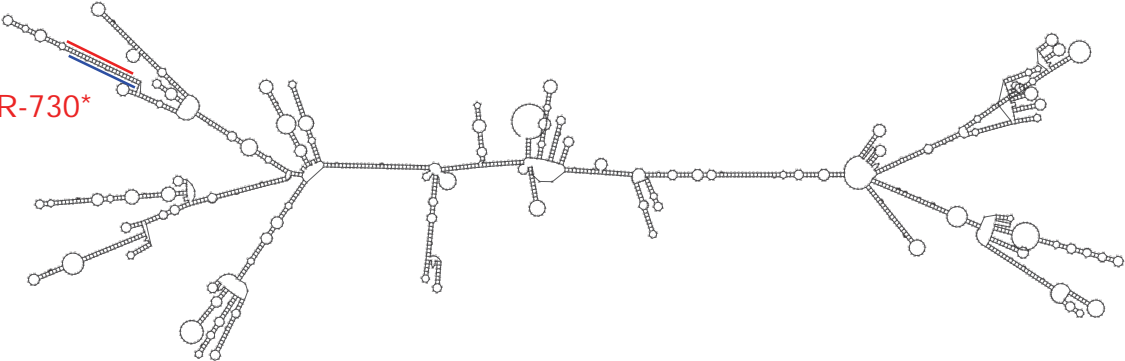
dof-miR-730*



comp170626 c2 seq15

dof-miR-730

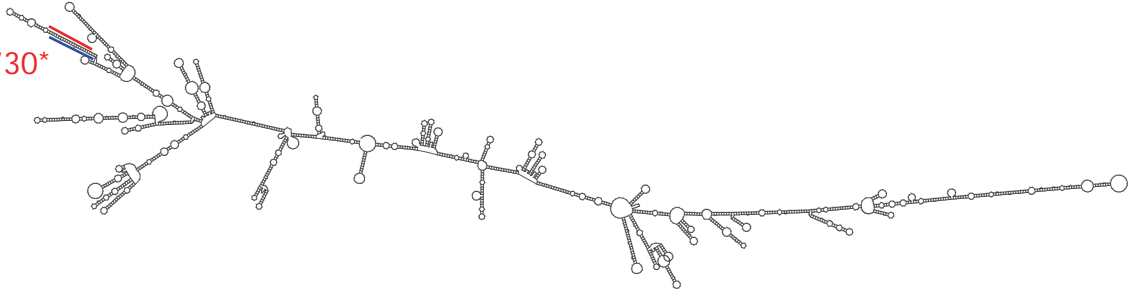
dof-miR-730*



comp170626 c2 seq16

dof-miR-730

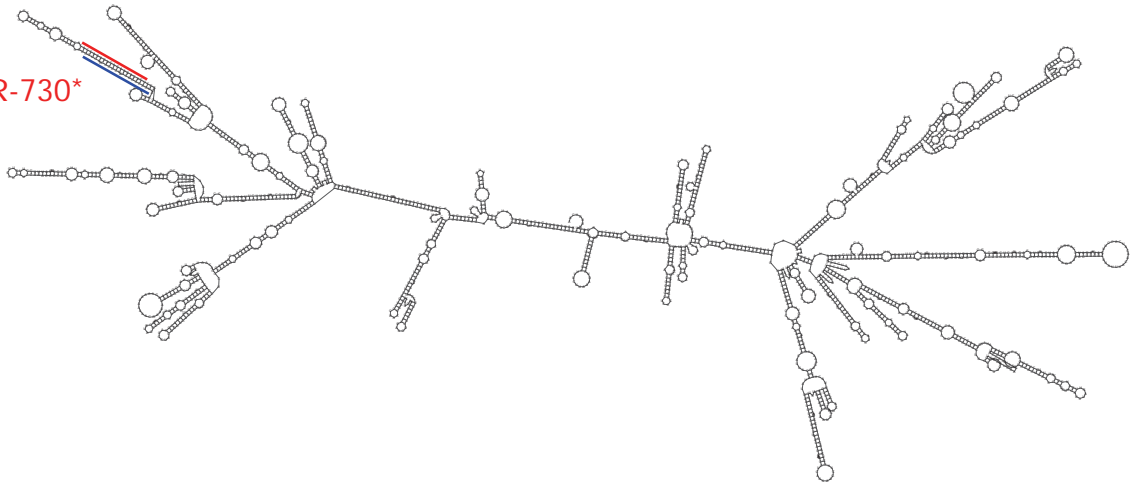
dof-miR-730*



comp170626 c2 seq18

dof-miR-730

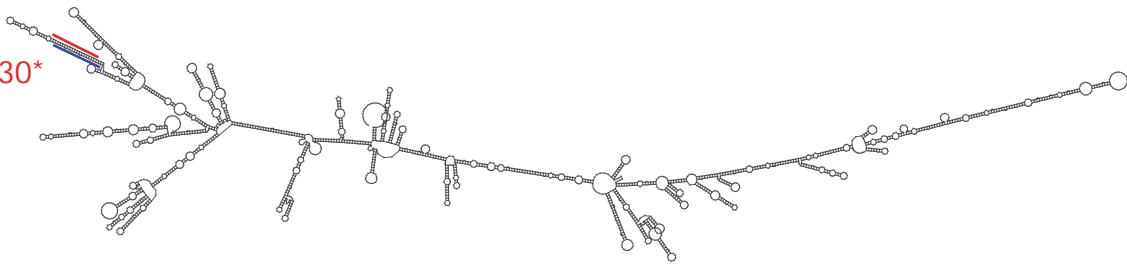
dof-miR-730*



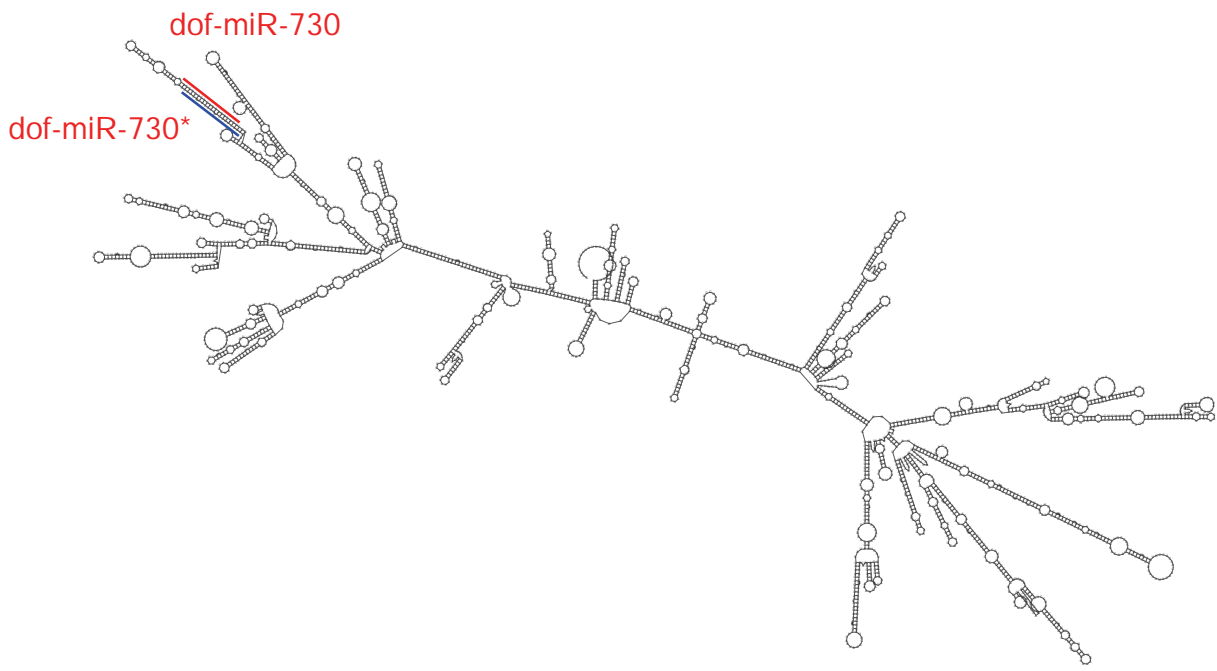
comp170626 c2 seq19

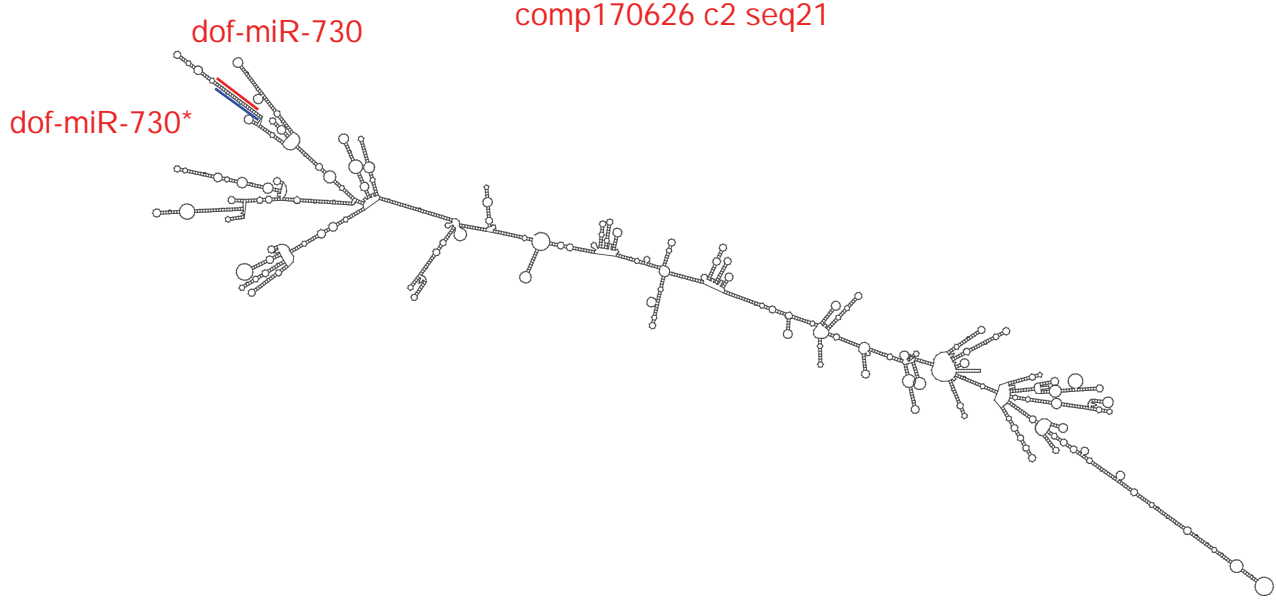
dof-miR-730

dof-miR-730*



comp170626 c2 seq20

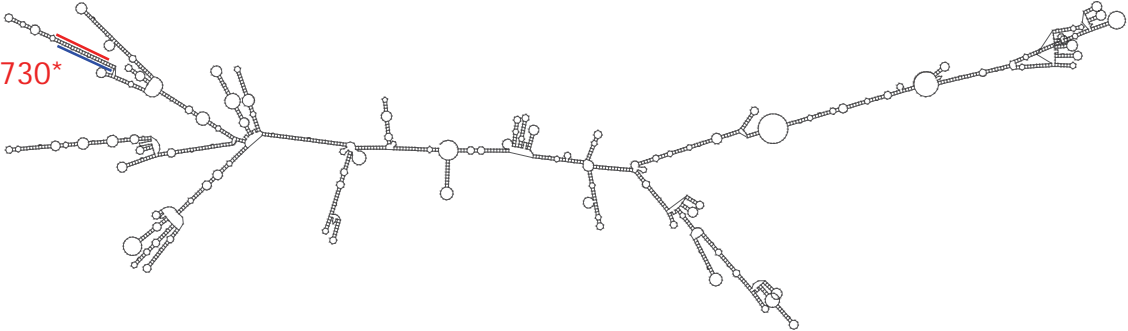




comp170626 c2 seq22

dof-miR-730

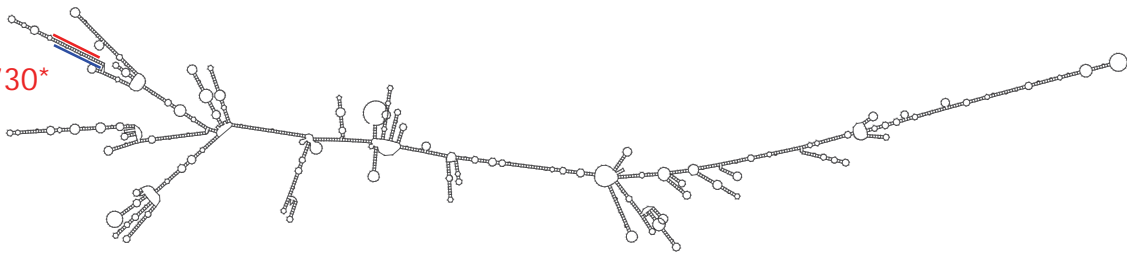
dof-miR-730*



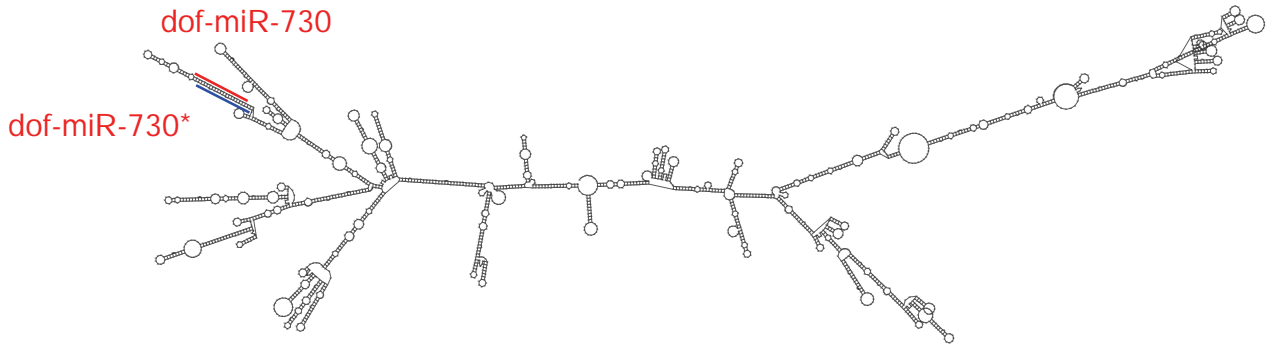
comp170626 c2 seq23

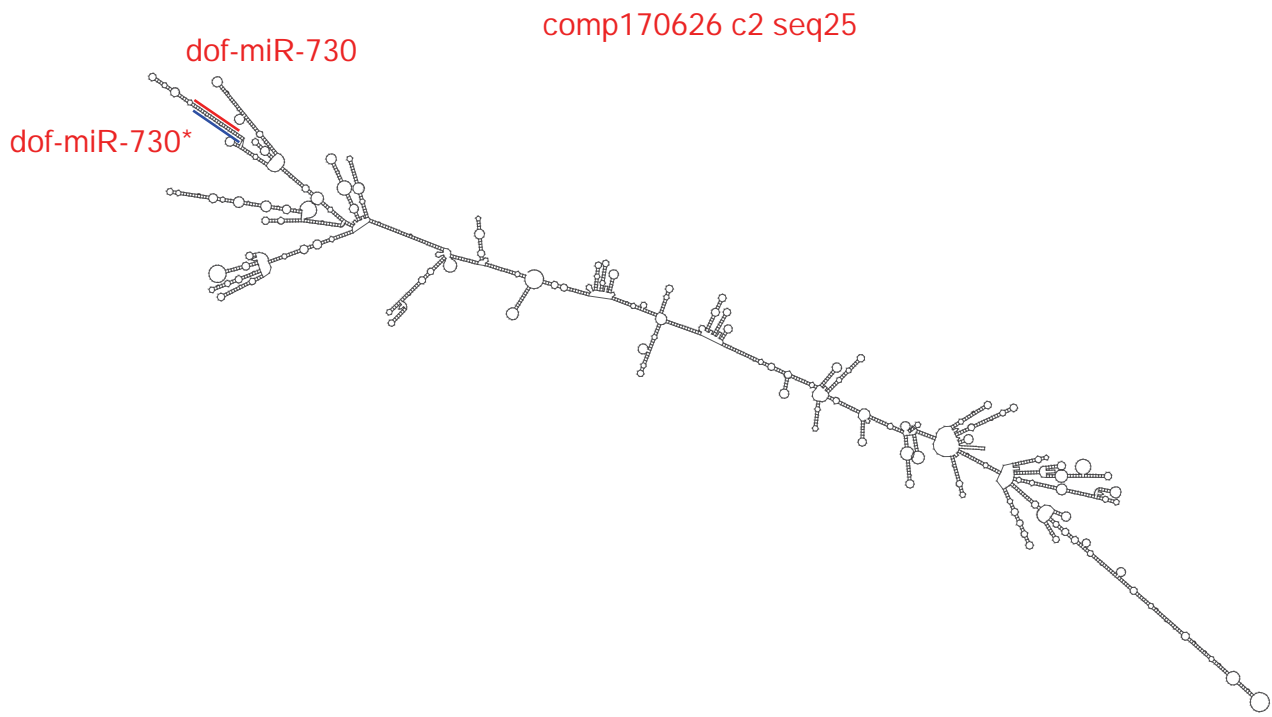
dof-miR-730

dof-miR-730*



comp170626 c2 seq24

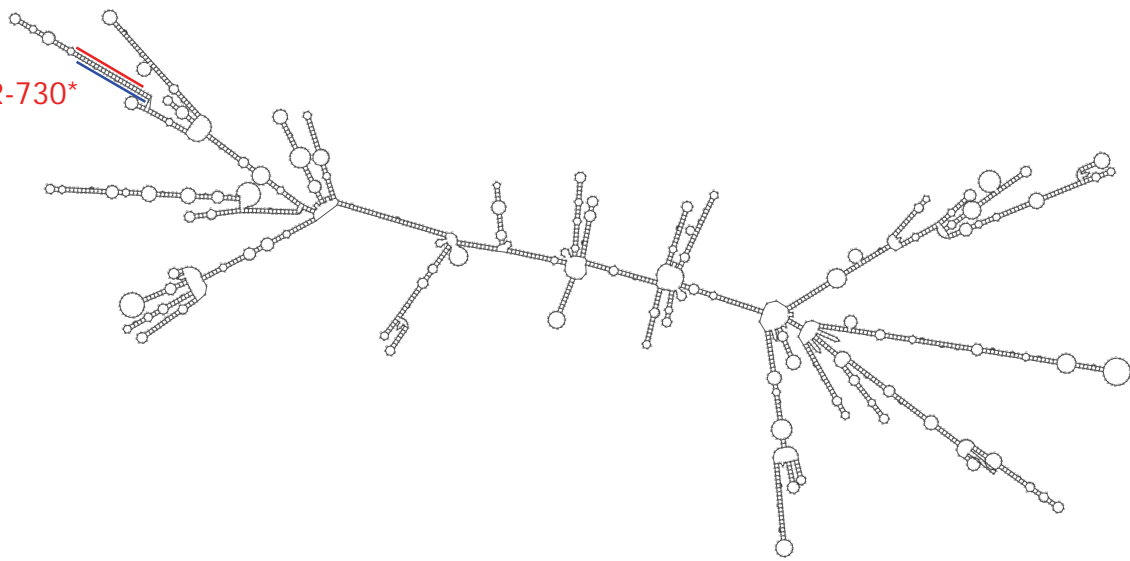




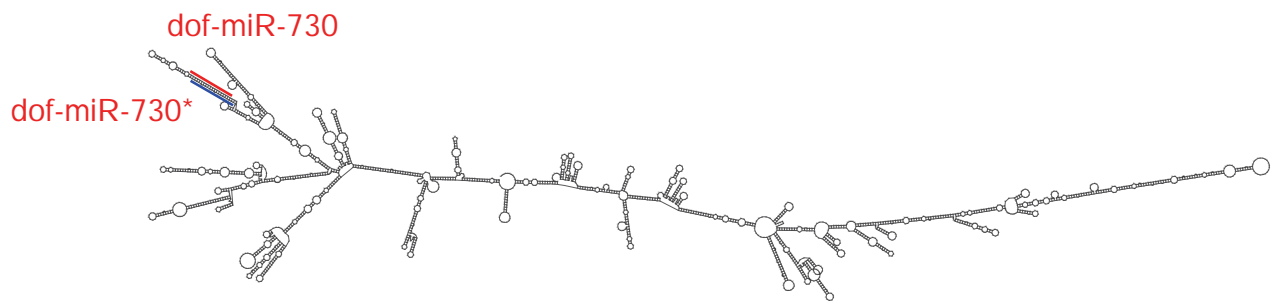
comp170626 c2 seq26

dof-miR-730

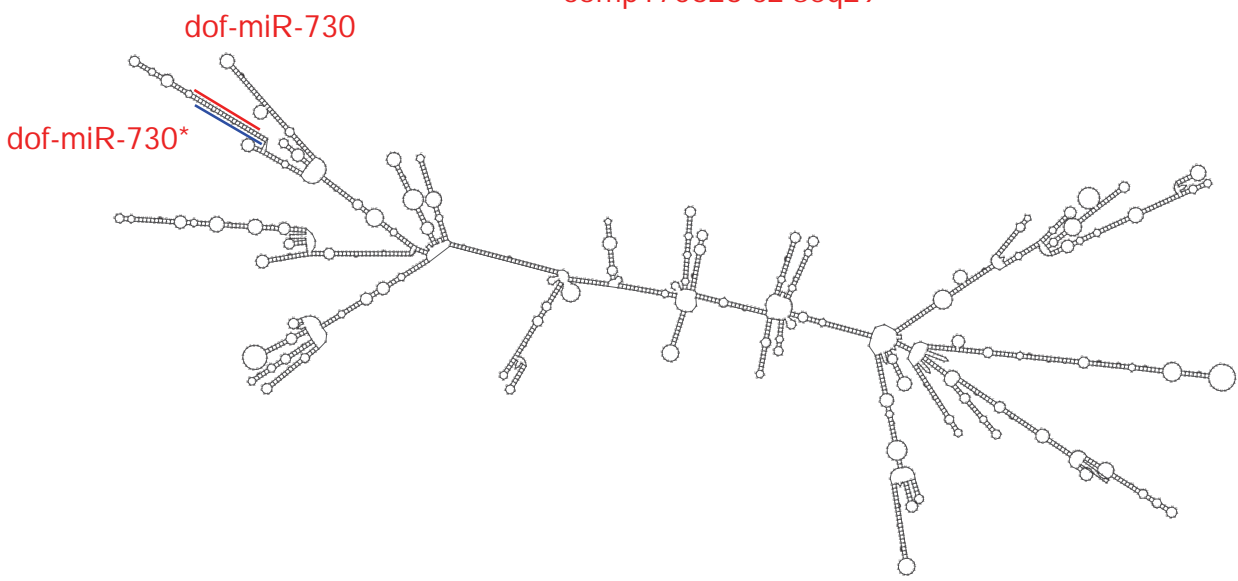
dof-miR-730*



comp170626 c2 seq28



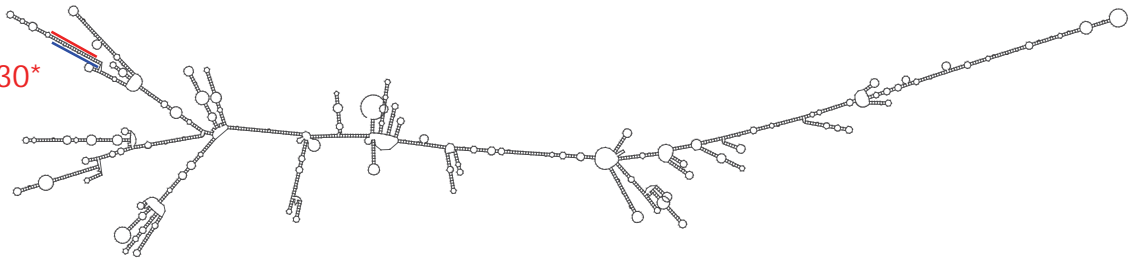
comp170626 c2 seq29



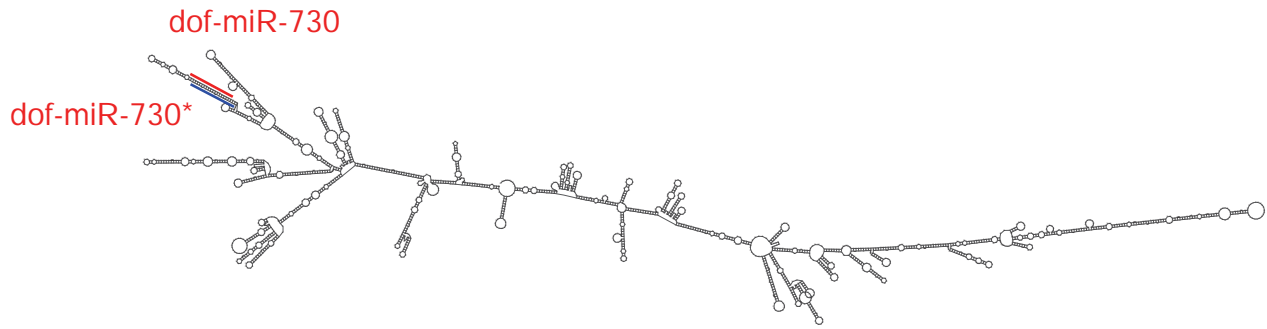
comp170626 c2 seq30

dof-miR-730

dof-miR-730*



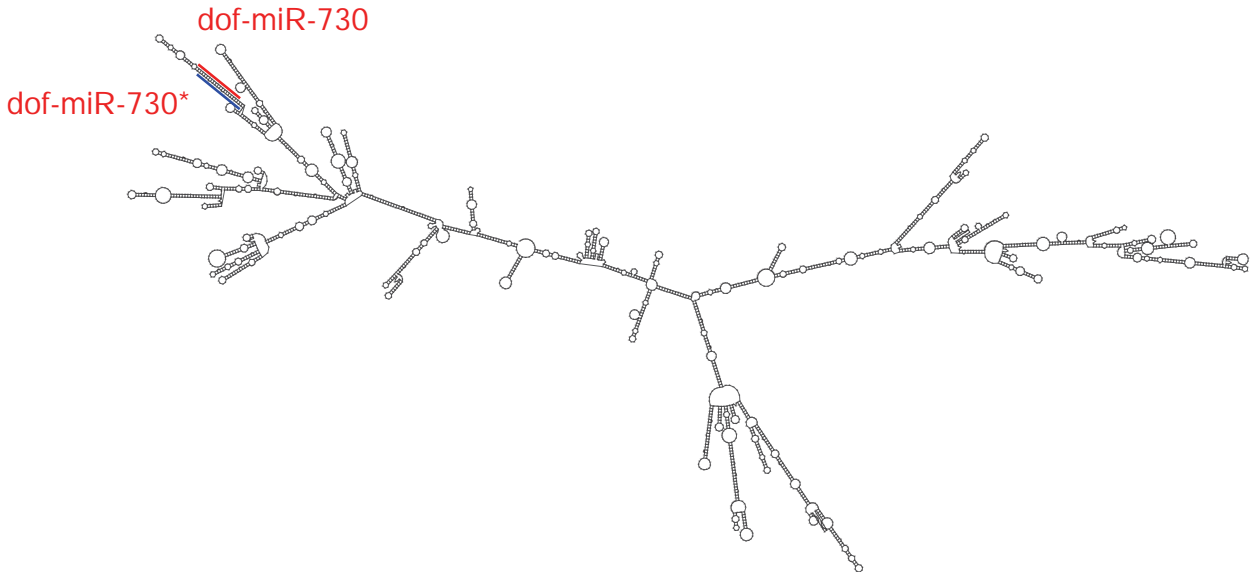
comp170626 c2 seq31



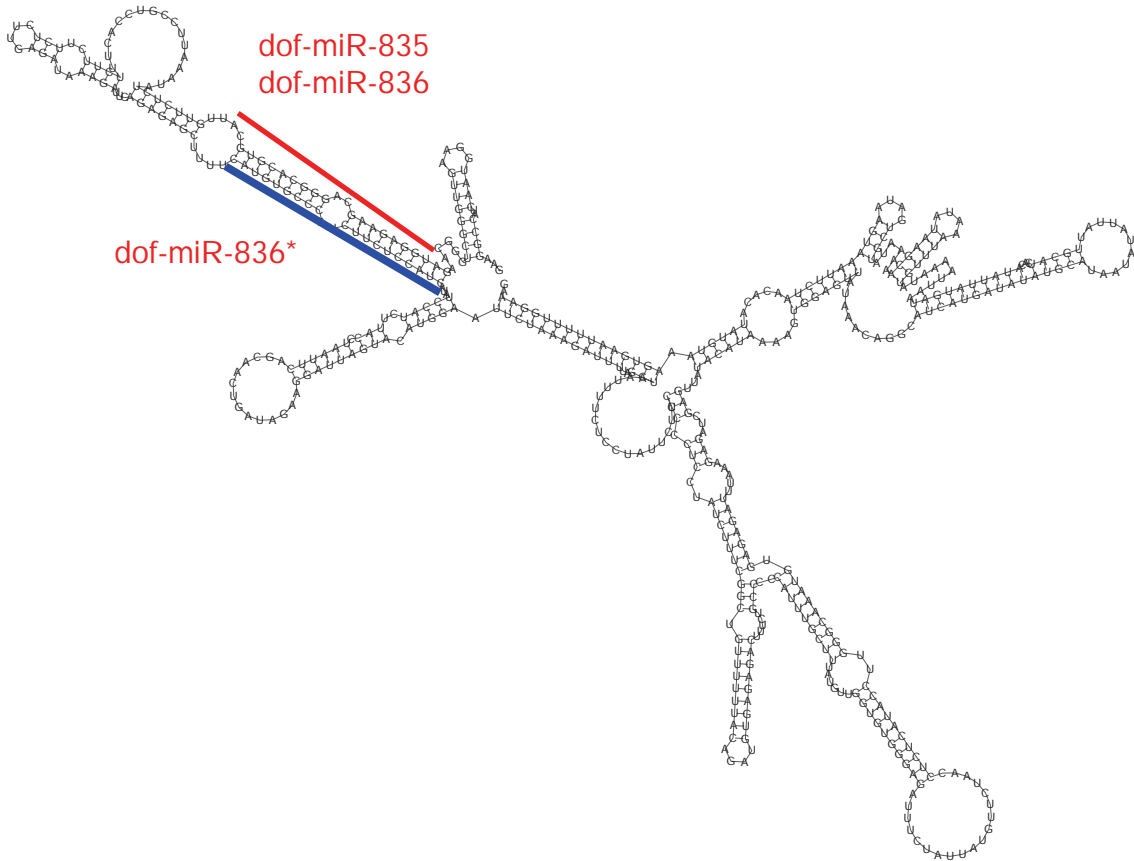
comp170626 c2 seq33



comp170626 c2 seq34



comp177735 c0 seq1



comp218447 c0 seq1

dof-miR-522

dof-miR-522*

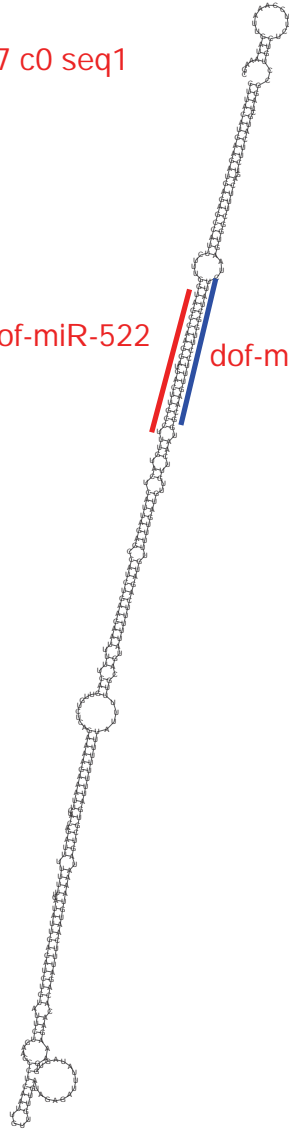
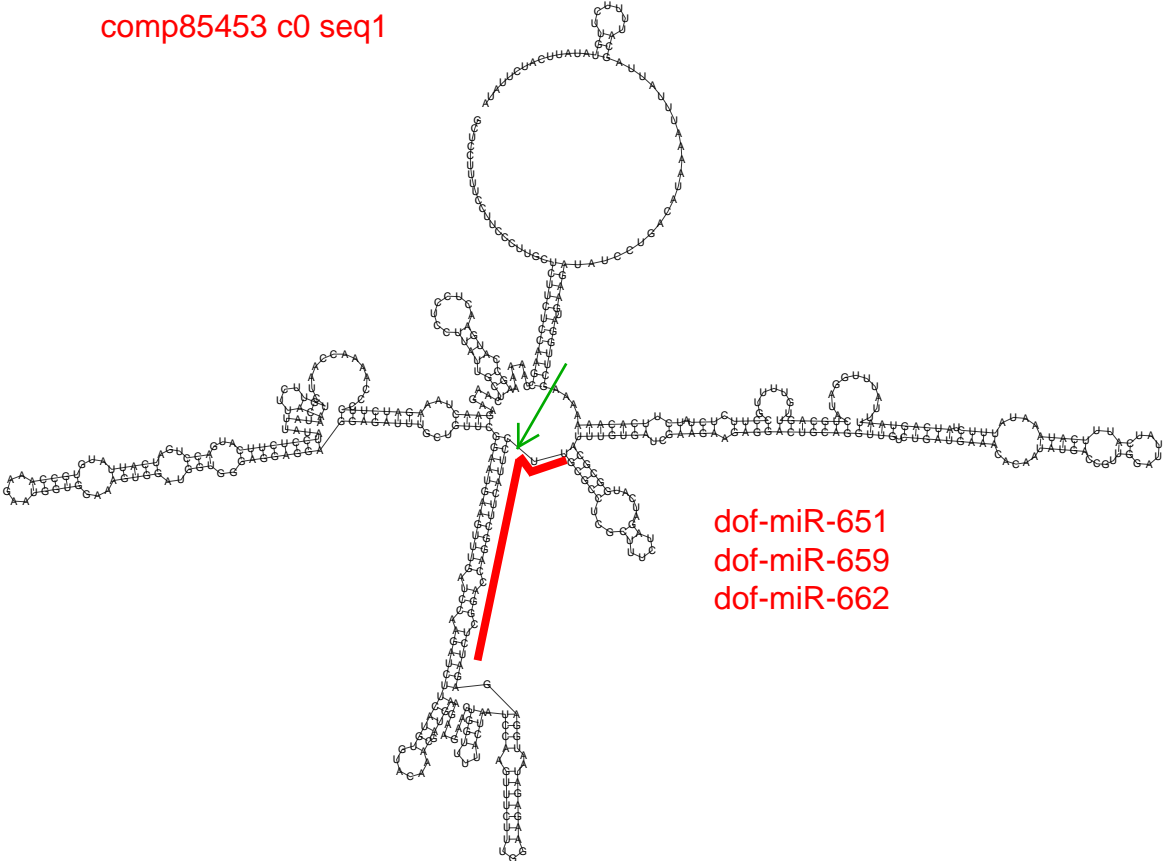


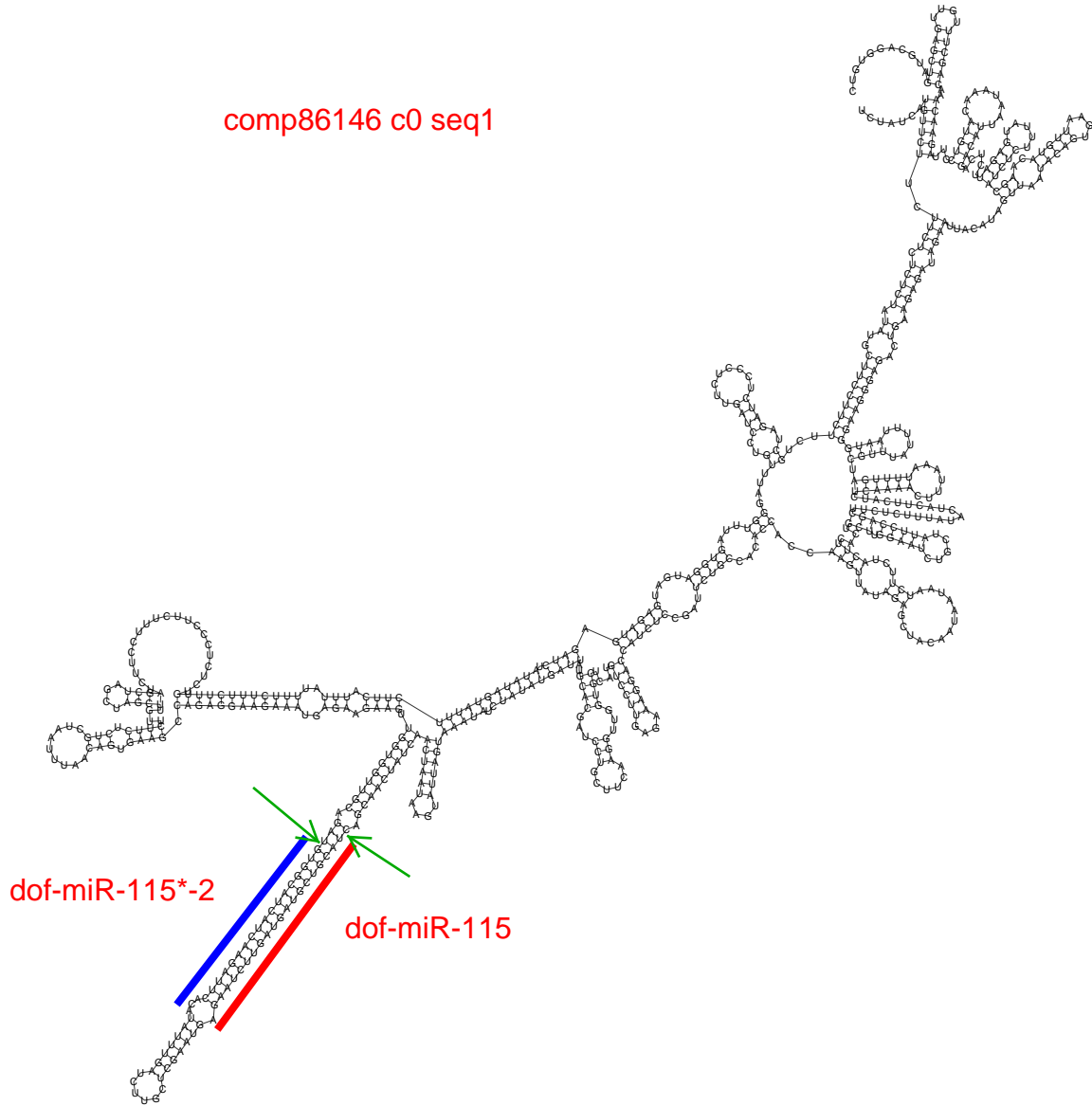
Figure S4 Certain highly structured transcripts might serve as miRNA precursors. The transcripts were assembled by RNA-seq reads, and the transcript IDs were provided in the figure. The mature miRNA- and miRNA*-coding regions on the long stems of the miRNA precursors were marked by red and blue lines respectively, and their IDs were also provided. The 5' ends of the degradome signatures supporting the processing of miRNAs and/or miRNA*s from their precursors are represented by green arrows. Note, for each mature miRNA, its average accumulation level in either organ (flower, leaf, root or stem; two biological replicates for each organ; thus, there are a total of eight libraries) of *Dendrobium officinale* should be 5 RPM or higher. Besides, the accumulation level of each miRNA* should be detectable in at least one sRNA-seq library. The secondary structures of the transcripts were predicted by using RNAfold (<http://rna.tbi.univie.ac.at/cgi-bin/RNAfold.cgi>).

comp85453 c0 seq1

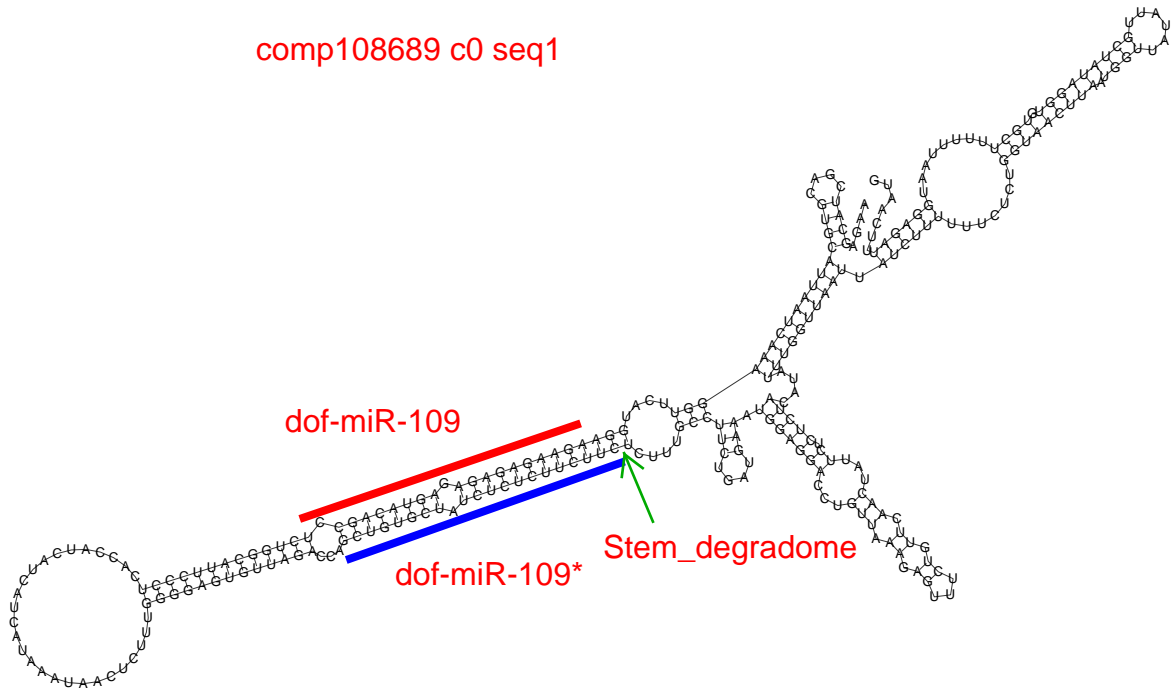


dof-miR-651
dof-miR-659
dof-miR-662

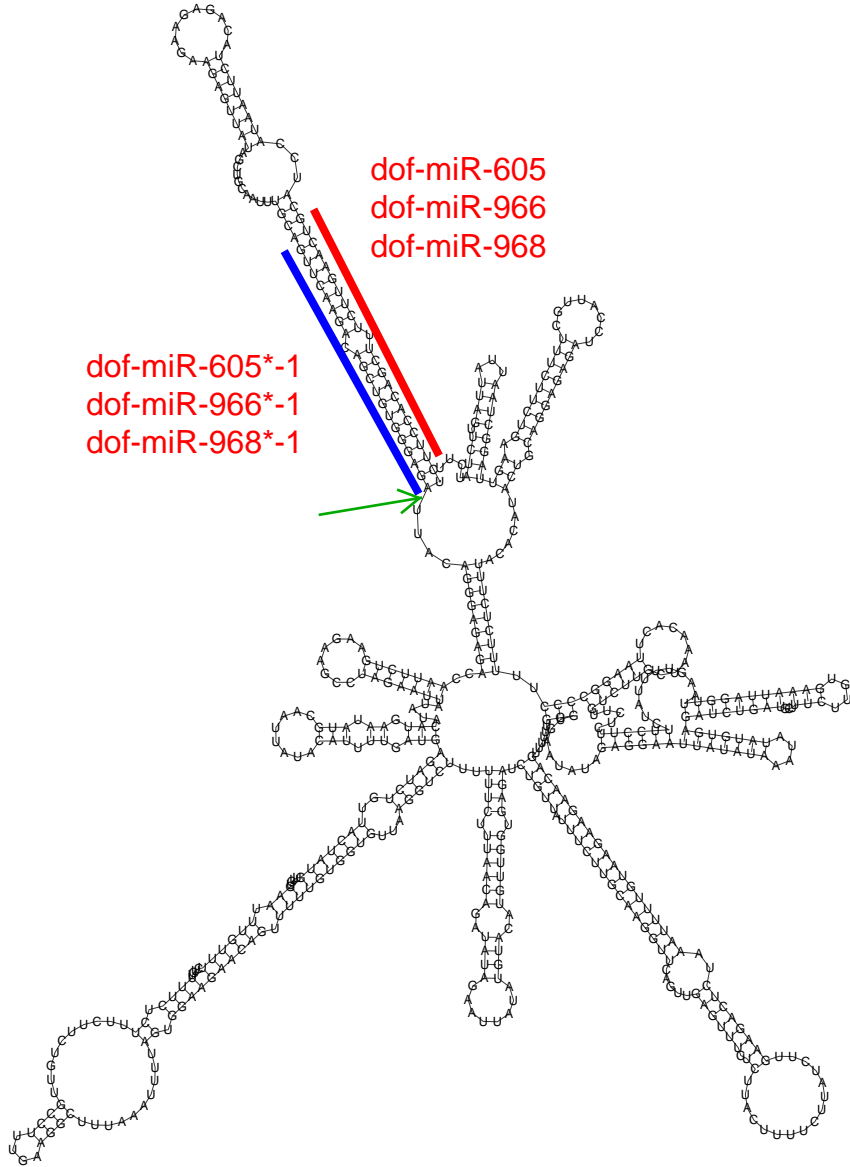
comp86146 c0 seq1



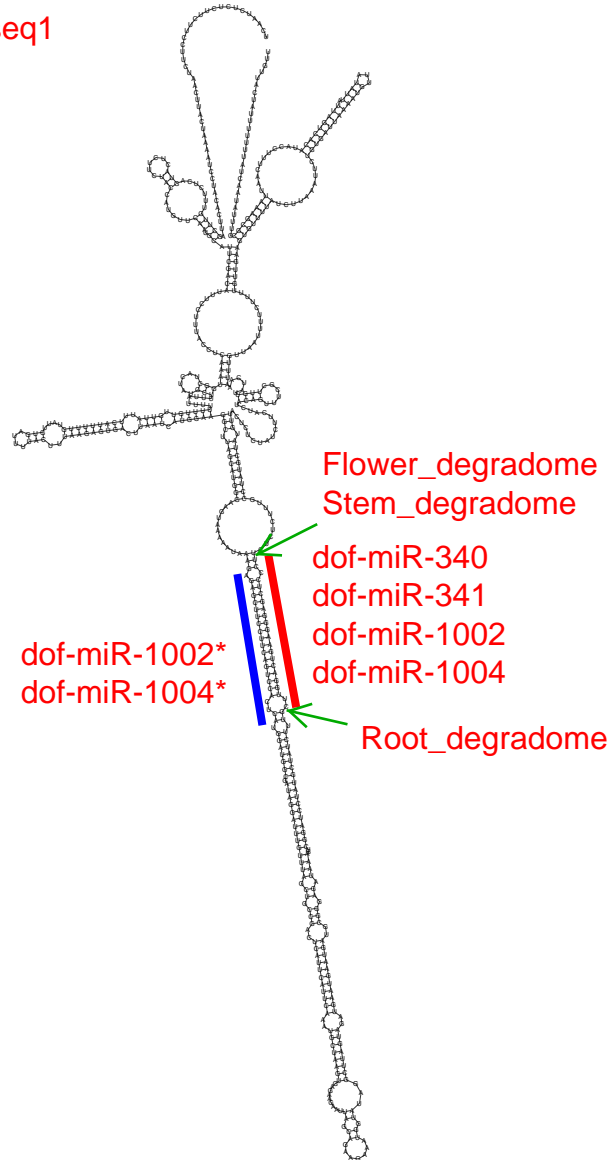
comp108689 c0 seq1

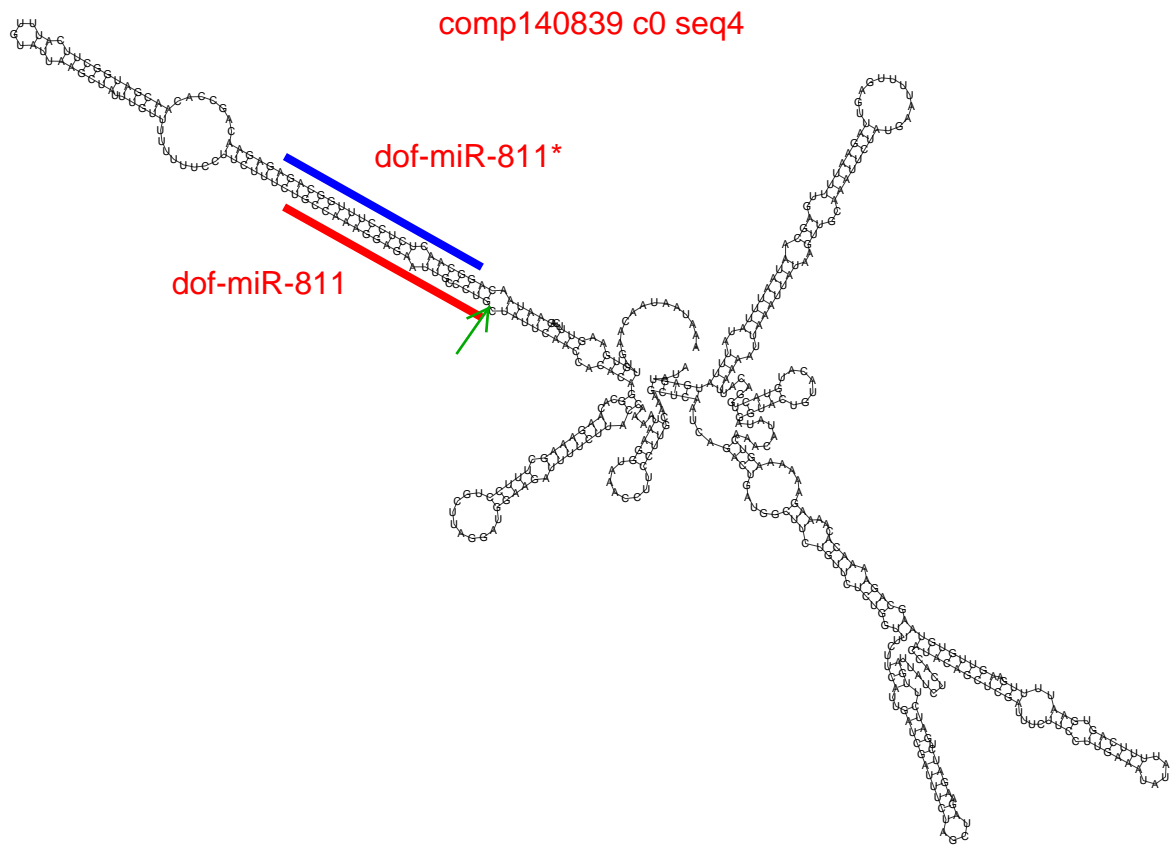


comp112901 c0 seq2

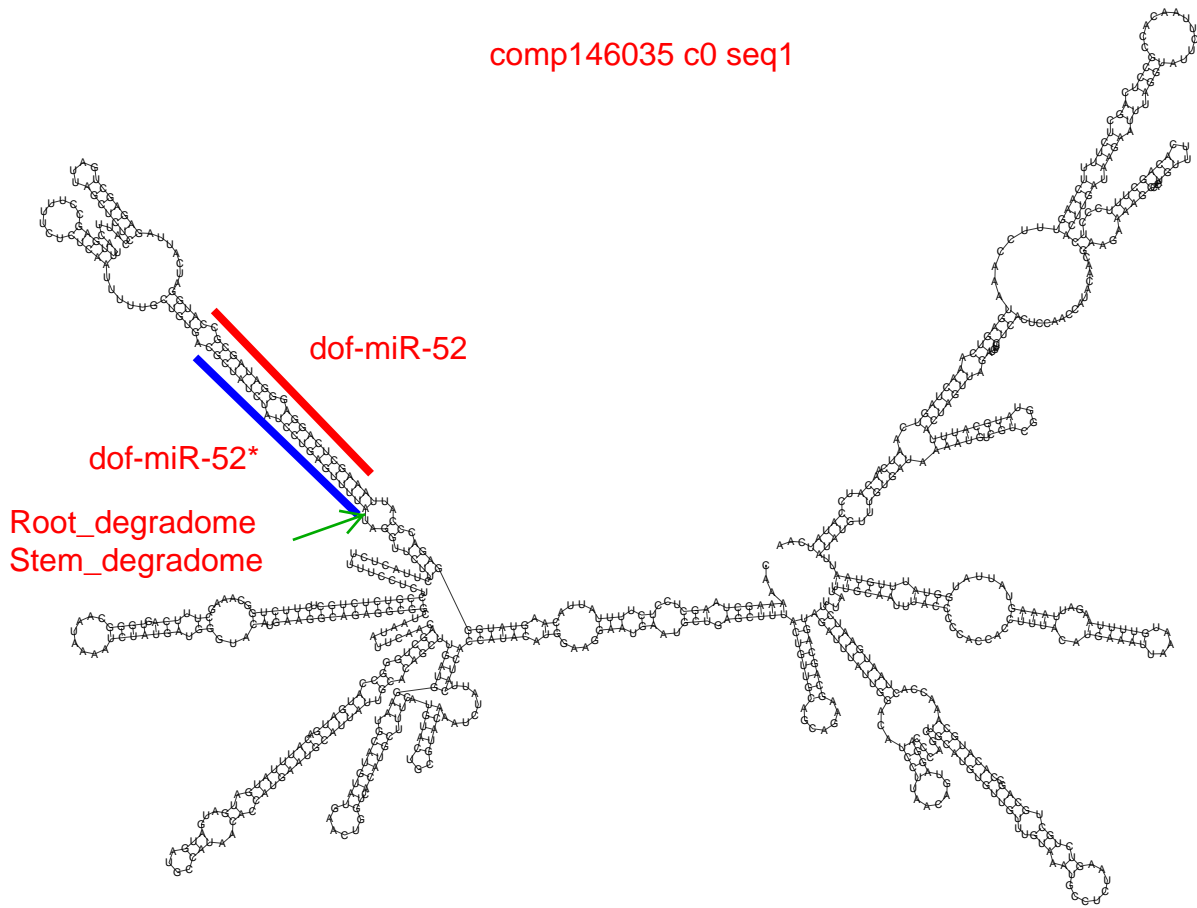


comp124801 c0 seq1

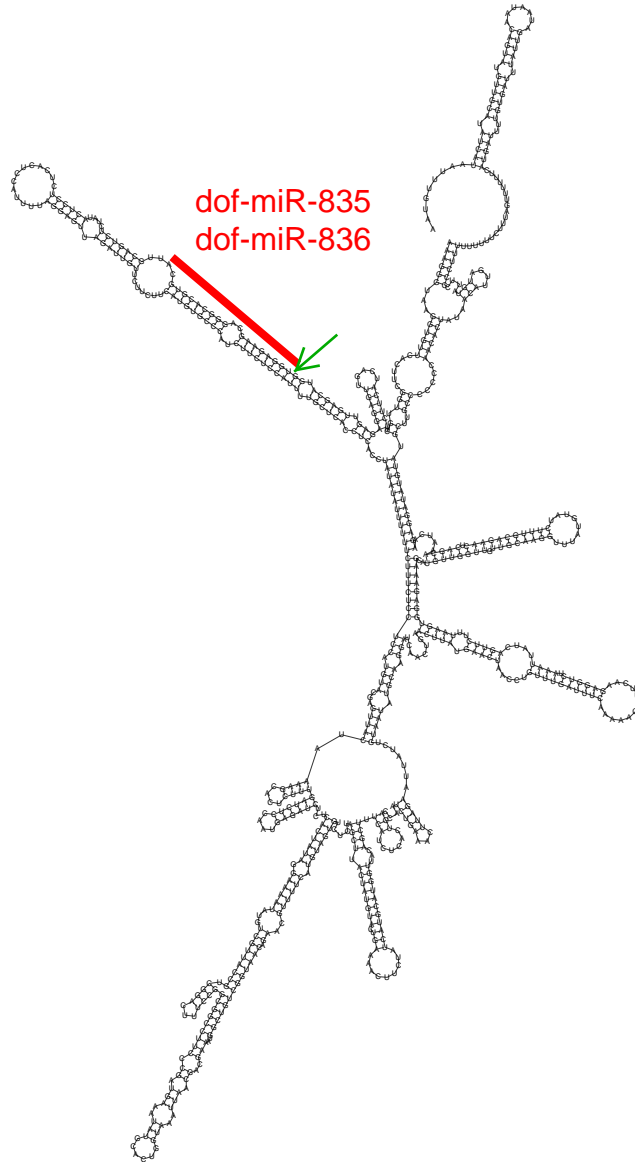




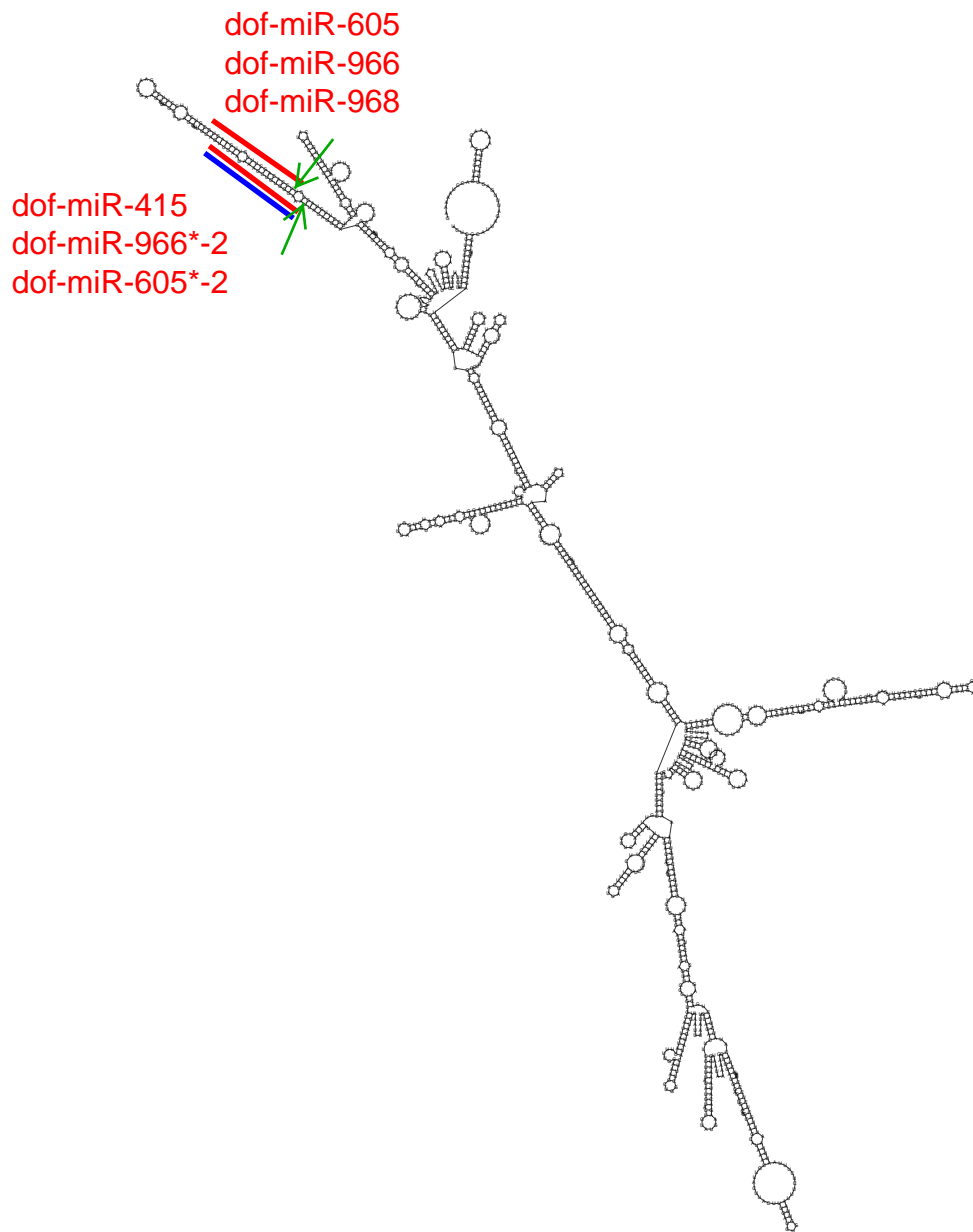
comp146035 c0 seq1



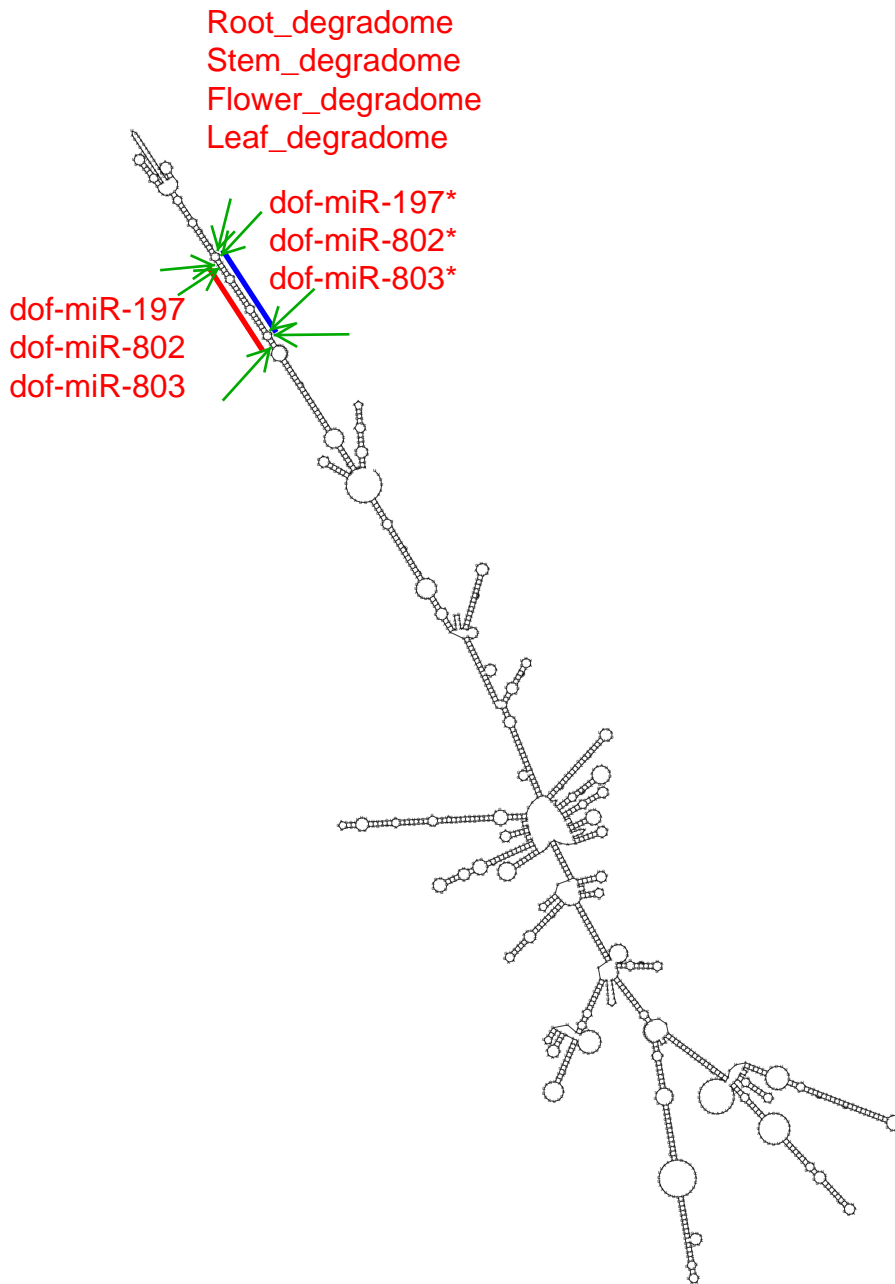
comp146186 c2 seq1



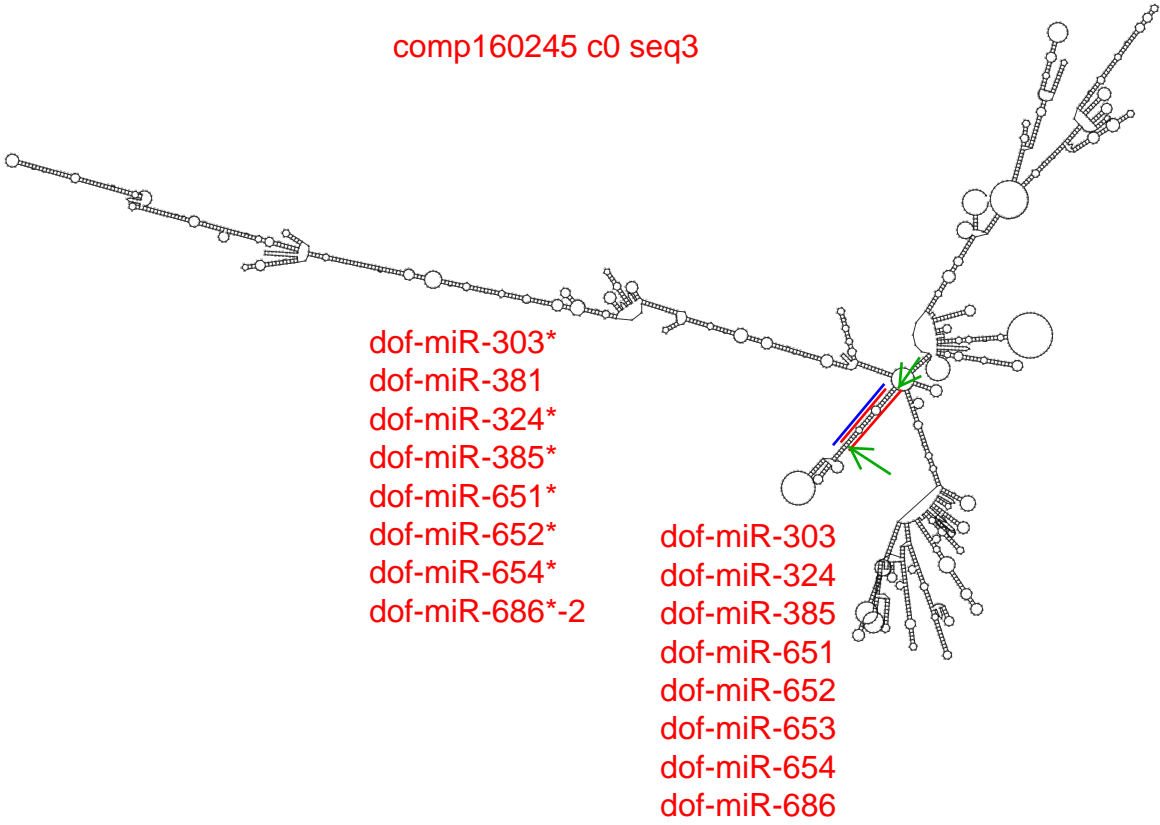
comp153713 c0 seq2



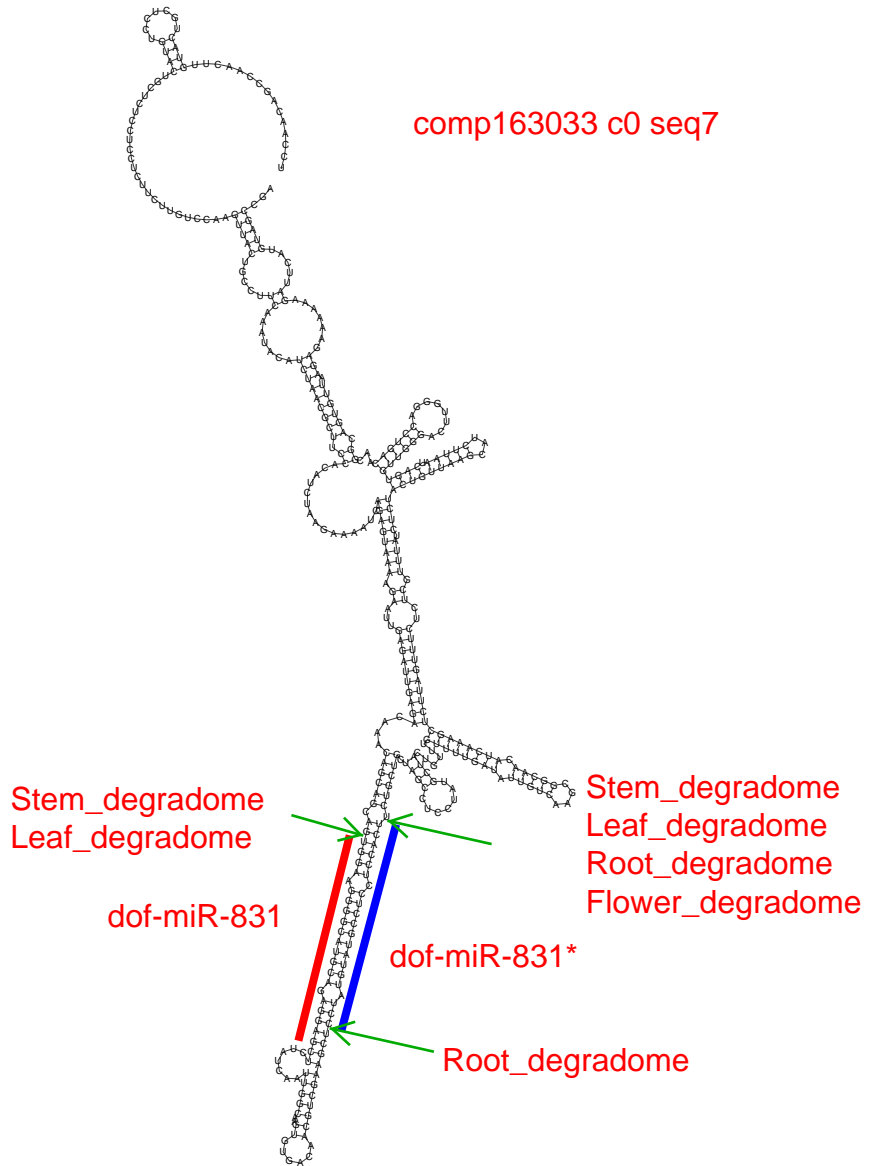
comp159822 c2 seq6



comp160245 c0 seq3



comp163033 c0 seq7



Stem_degradome
Leaf_degradome

dof-miR-831

Stem_degradome
Leaf_degradome
Root_degradome
Flower_degradome

dof-miR-831*

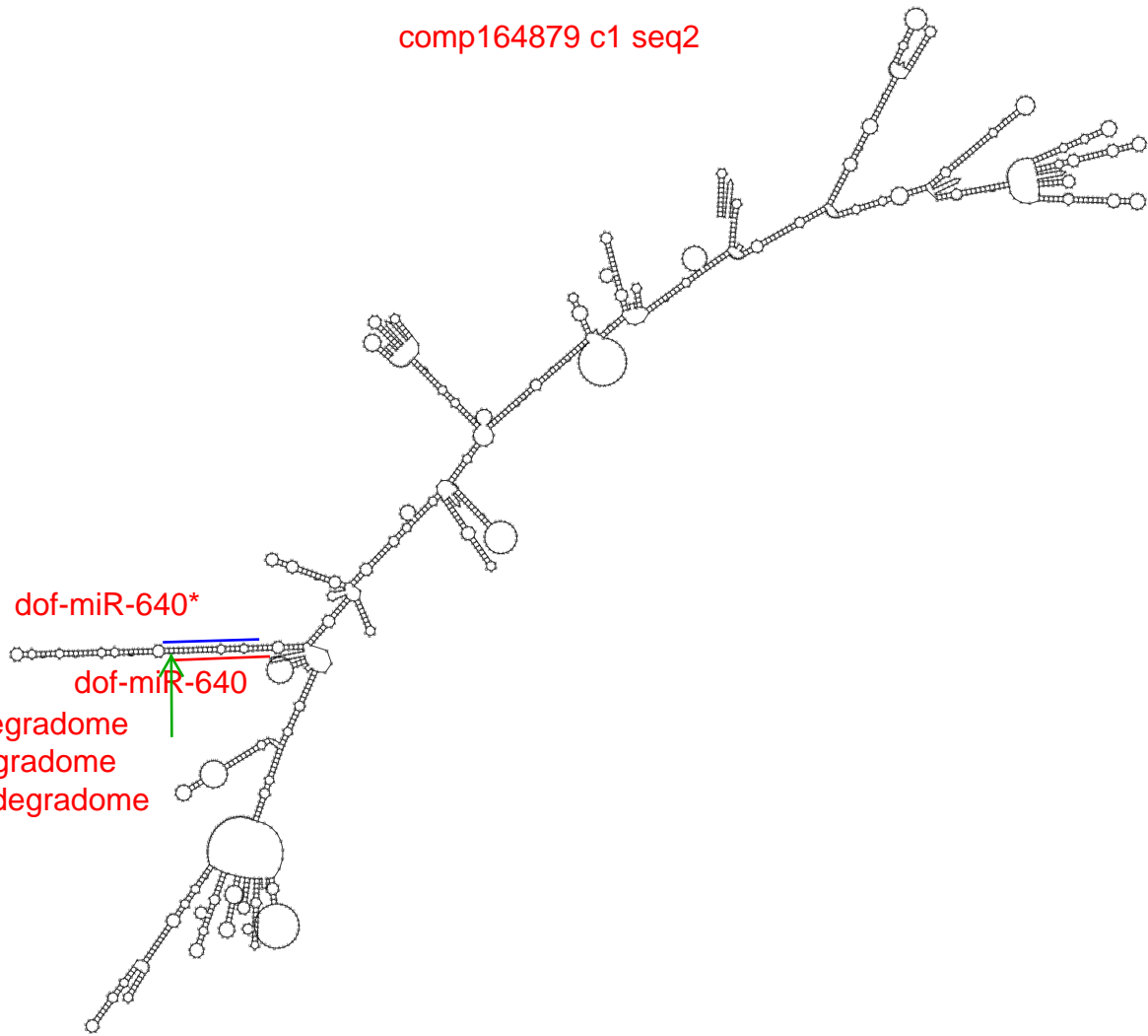
Root_degradome

comp164879 c1 seq2

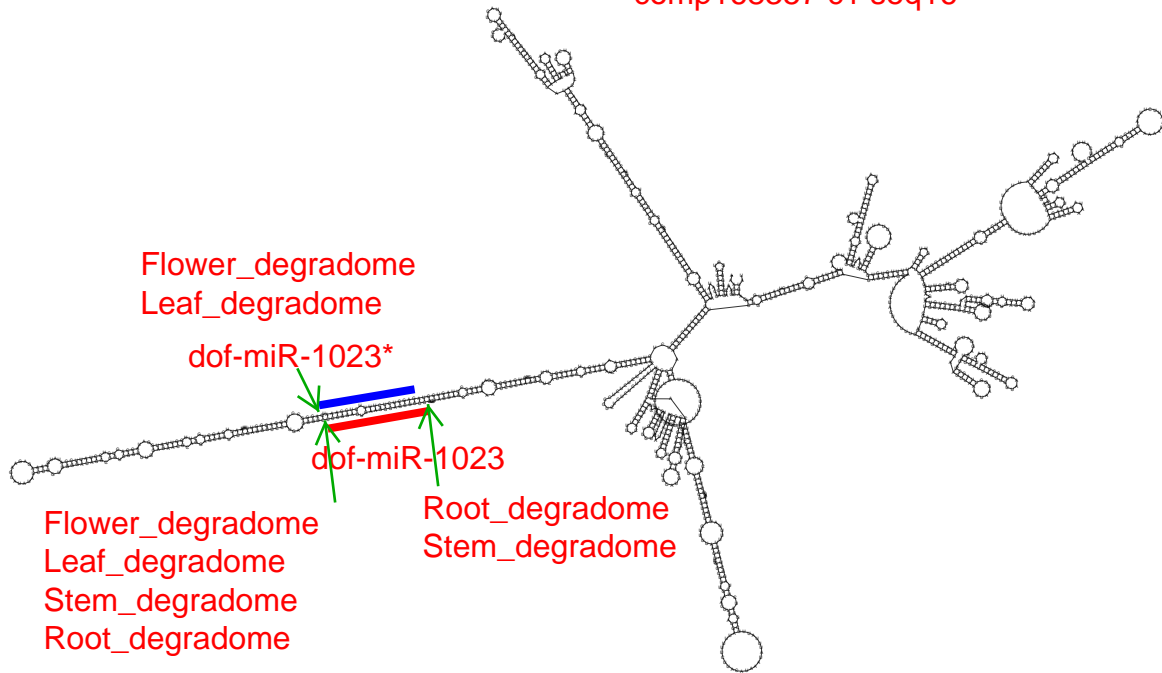
dof-miR-640*

dof-miR-640

Stem_degradome
Leaf_degradome
Flower_degradome



comp168357 c1 seq16



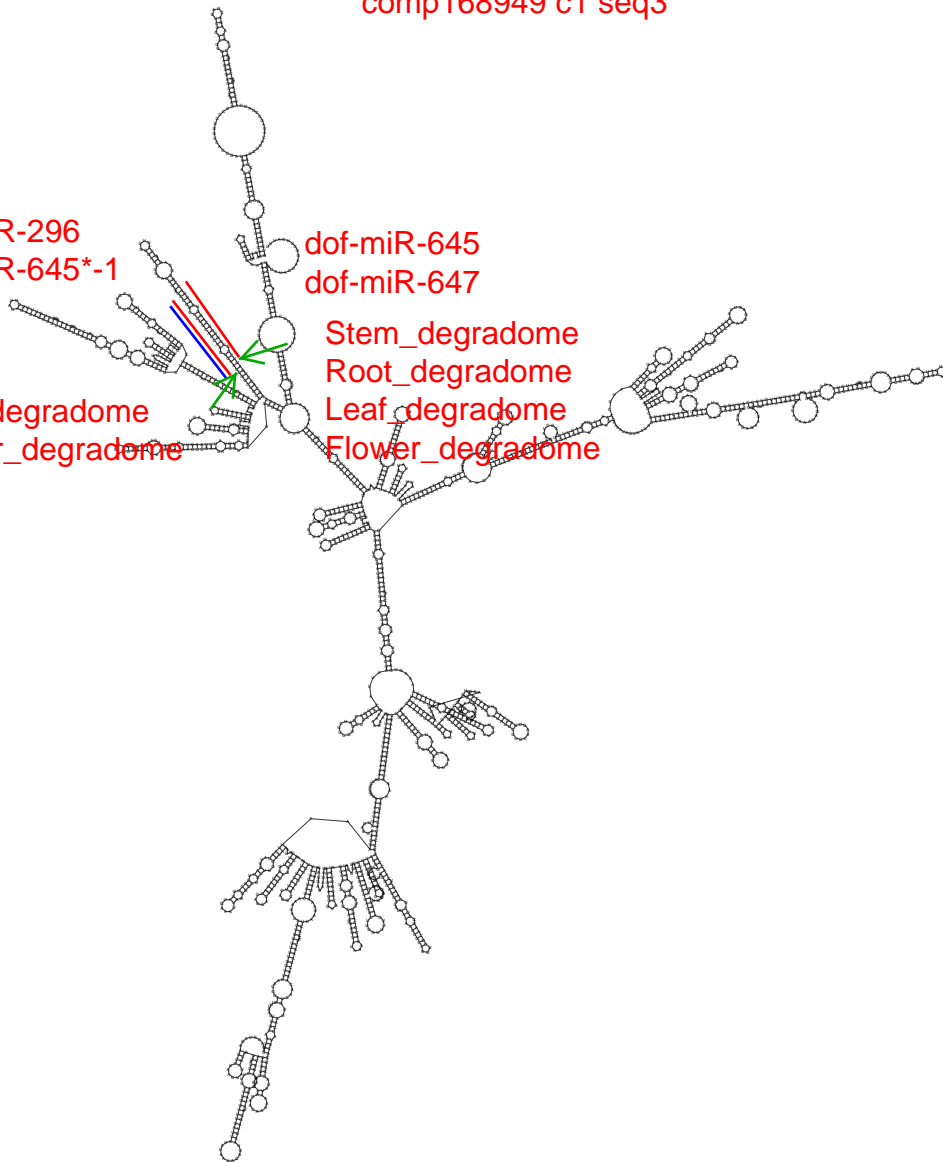
comp168949 c1 seq3

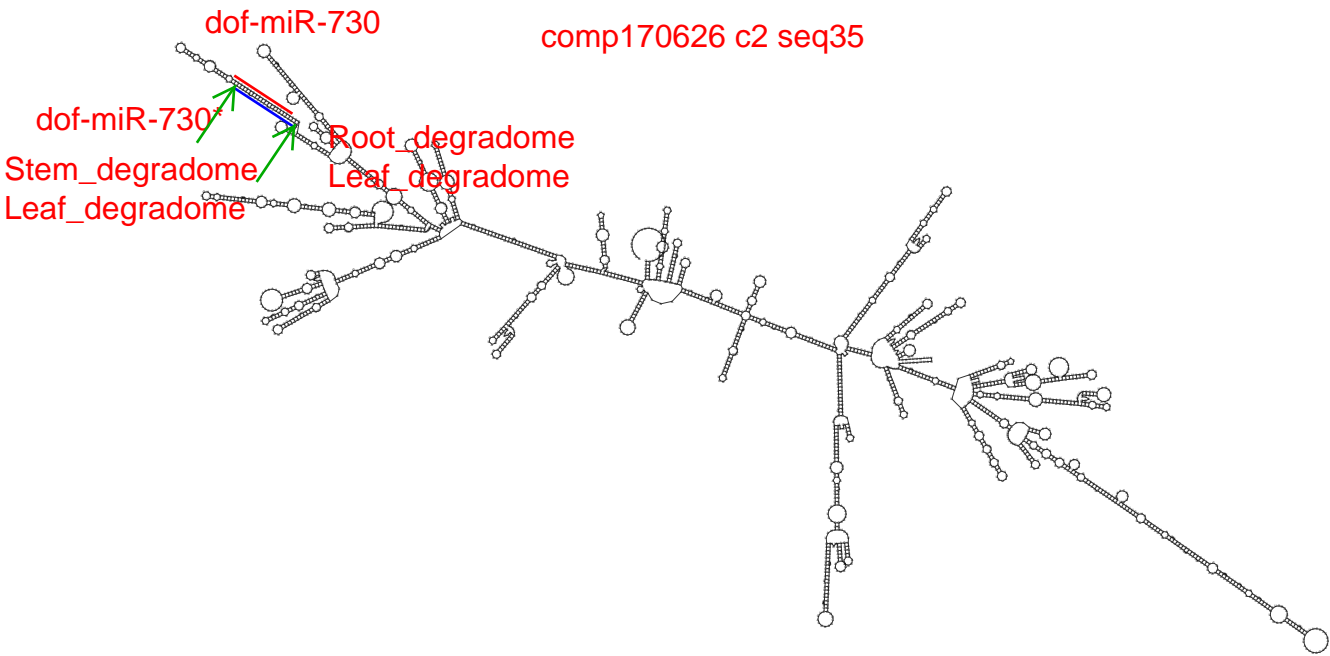
dof-miR-296
dof-miR-645*-1

dof-miR-645
dof-miR-647

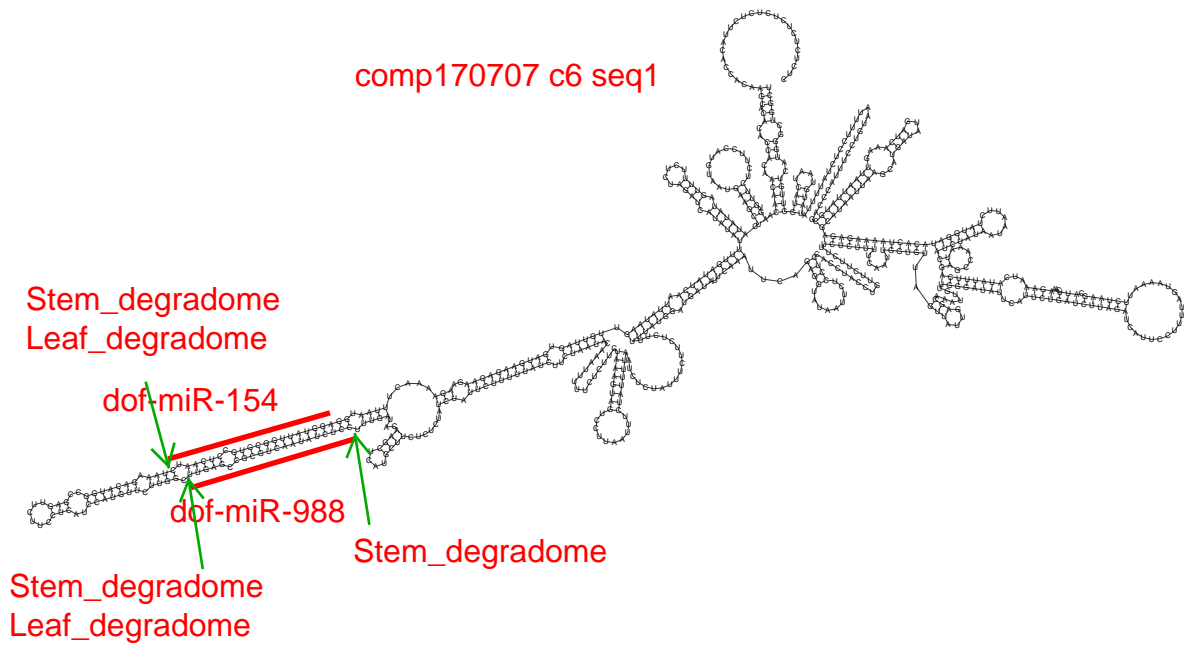
Leaf_degradome
Flower_degradome

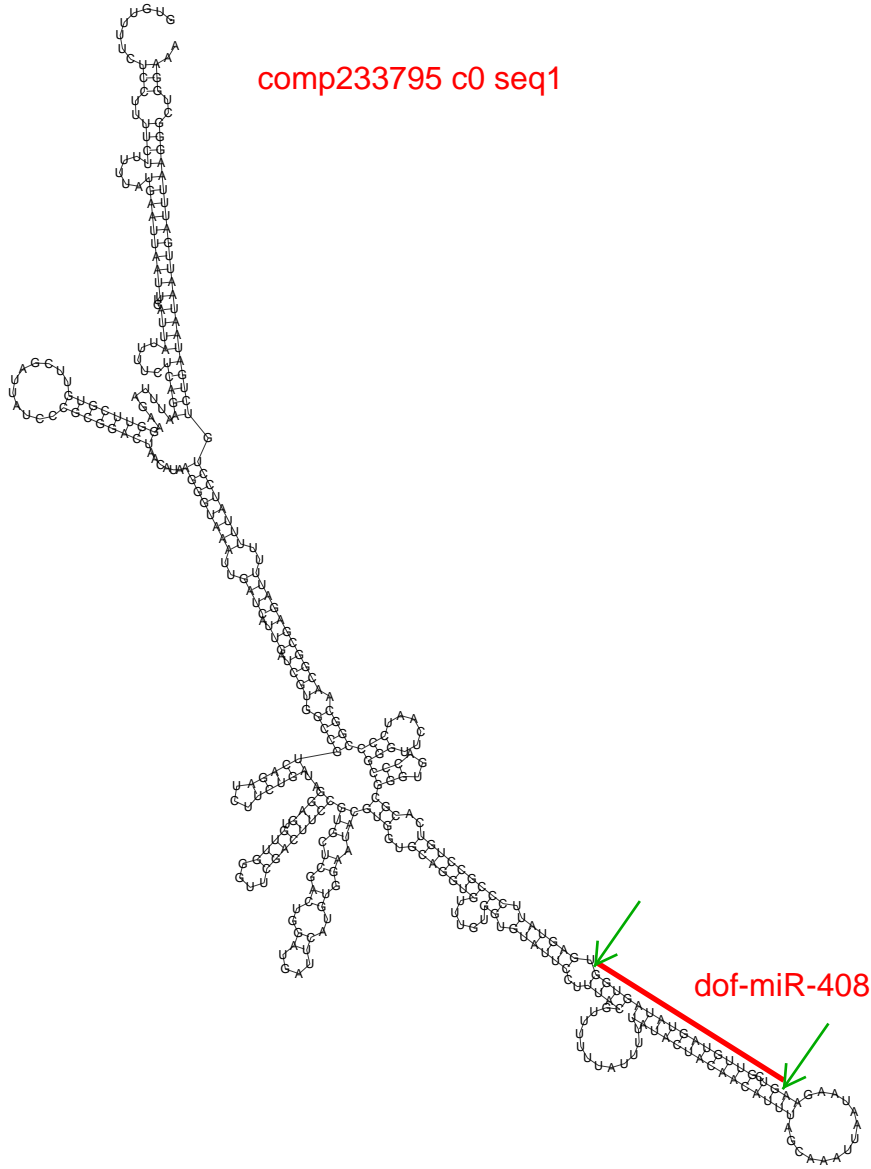
Stem_degradome
Root_degradome
Leaf_degradome
Flower_degradome





comp170707 c6 seq1

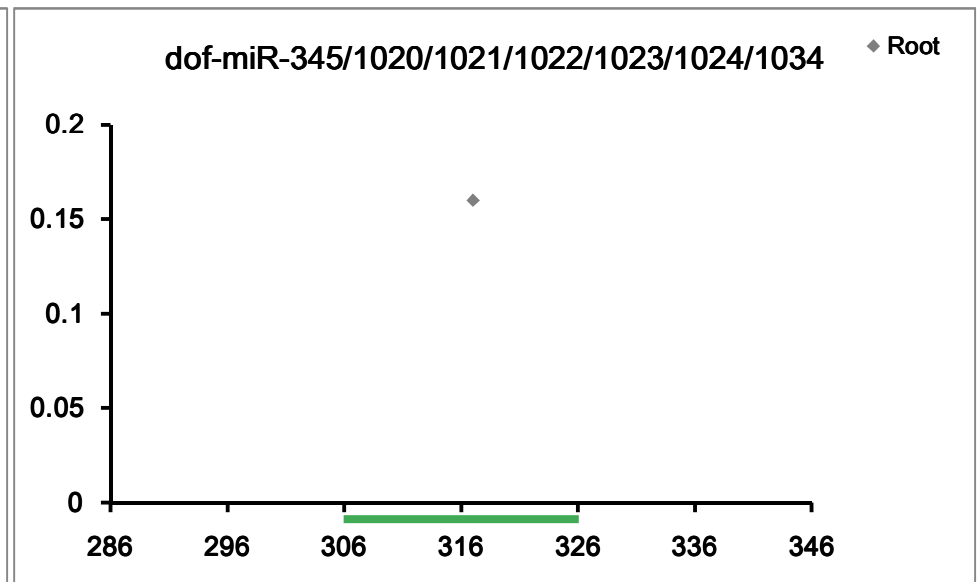
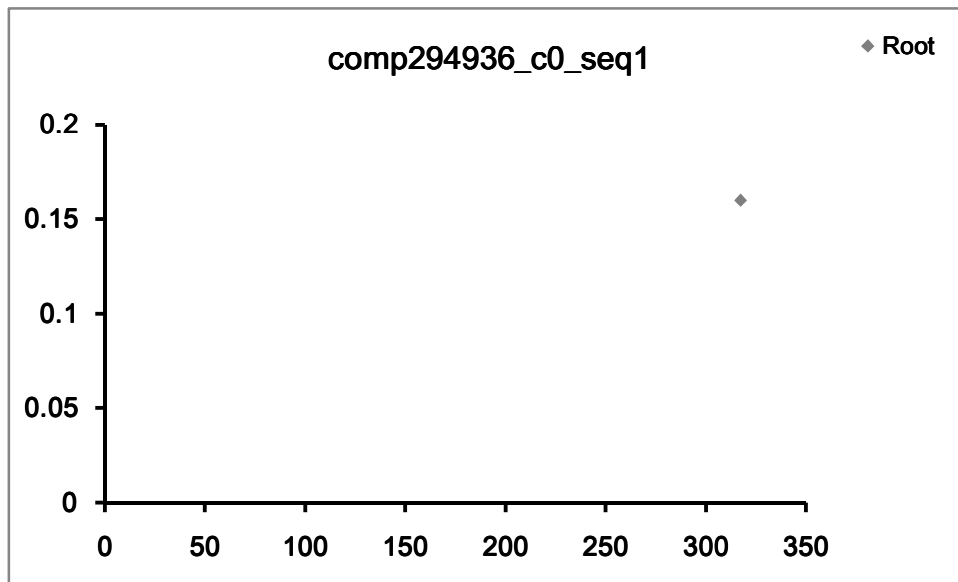
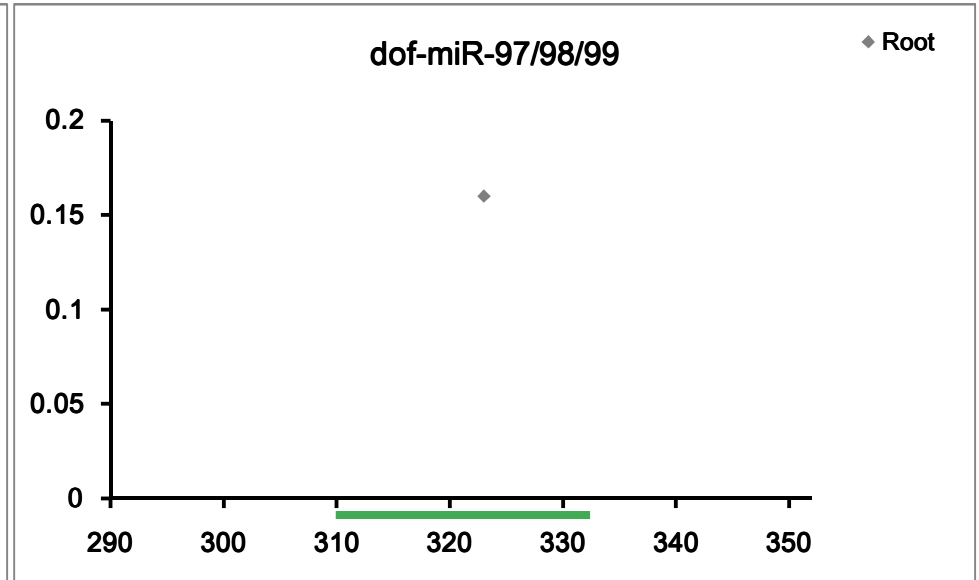
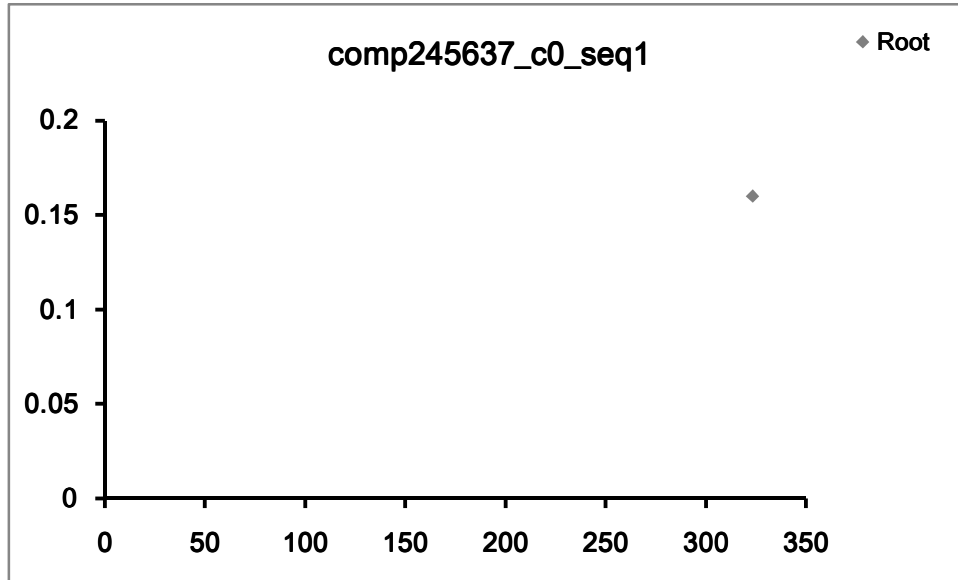


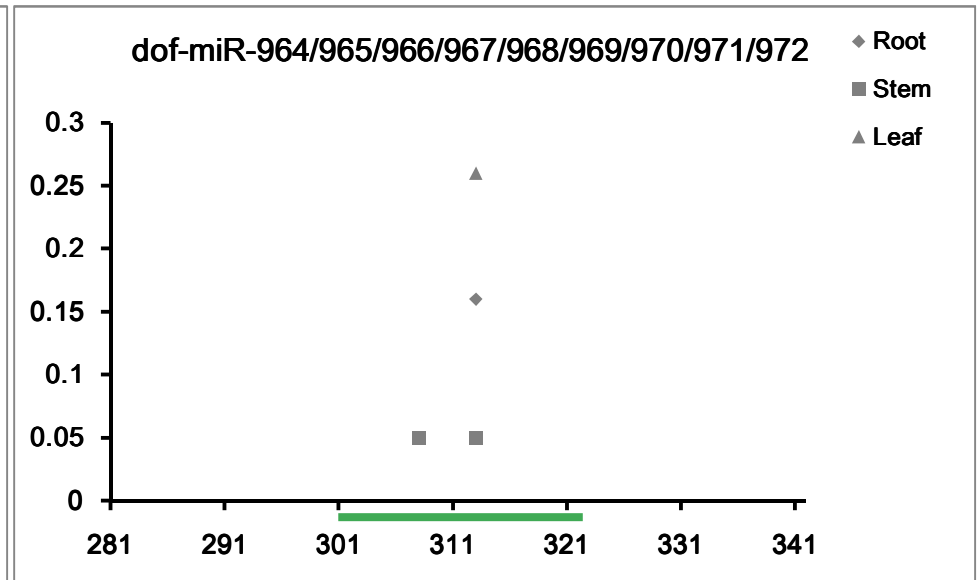
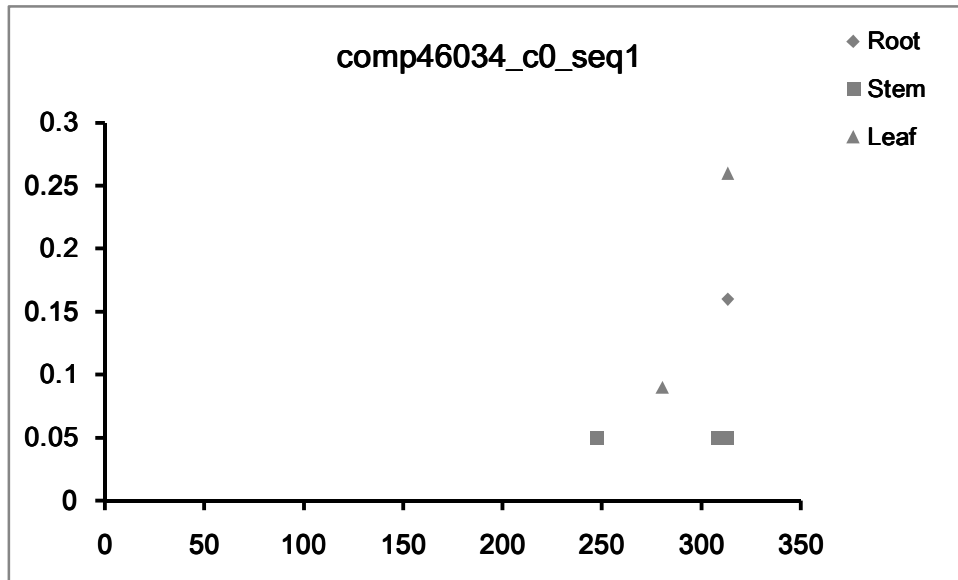
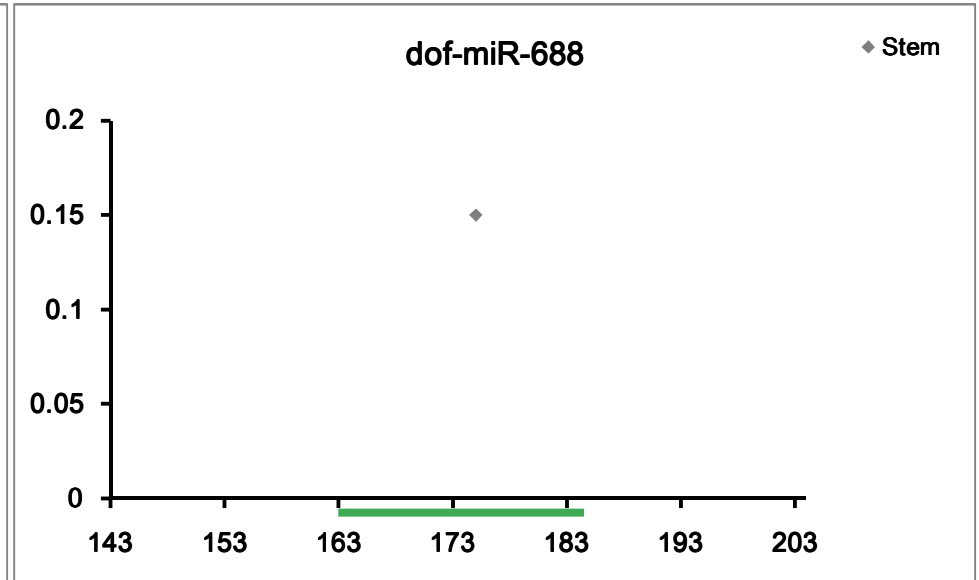
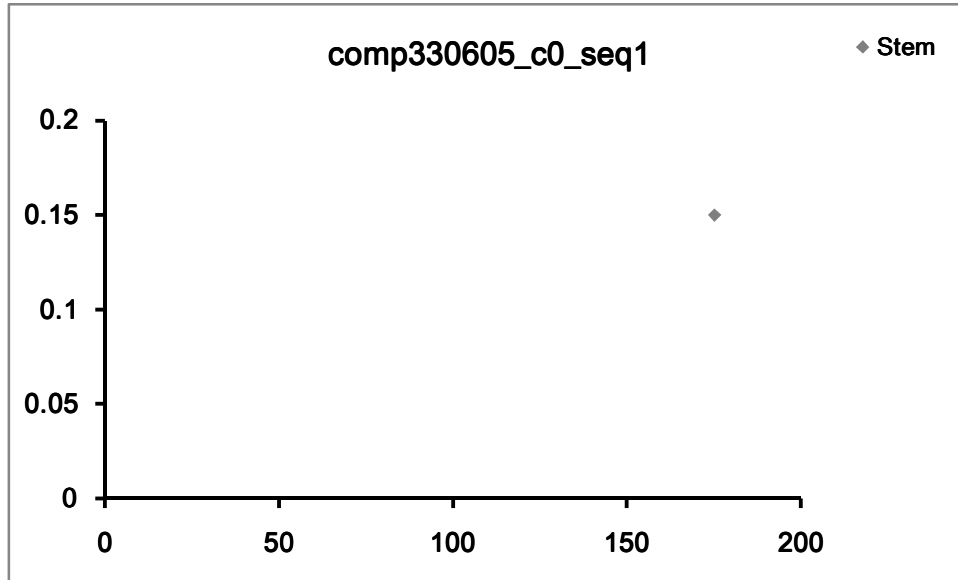


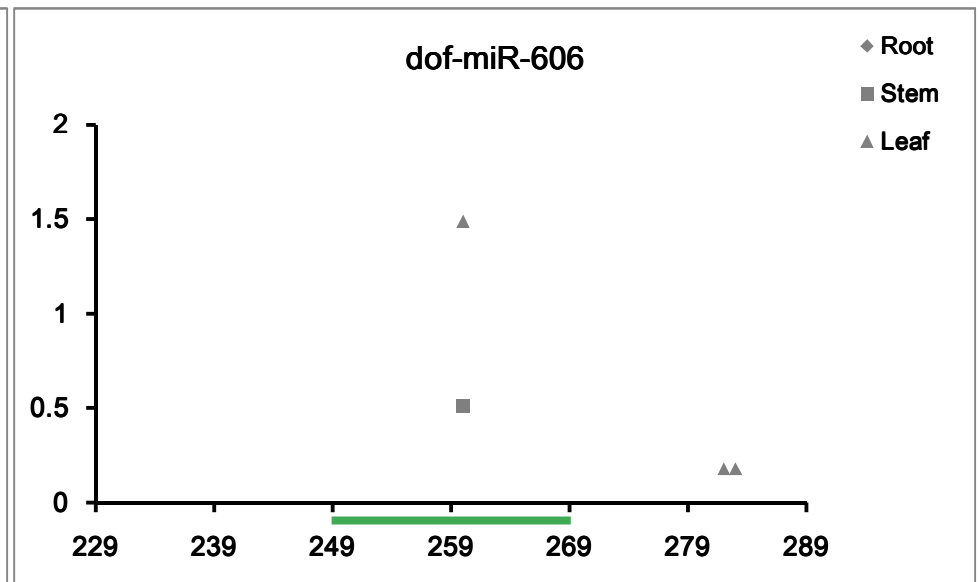
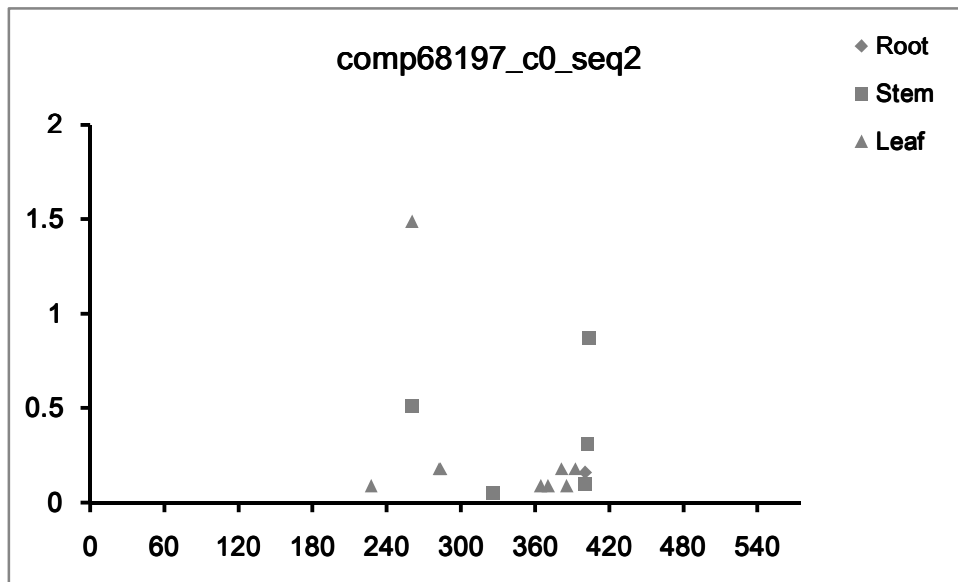
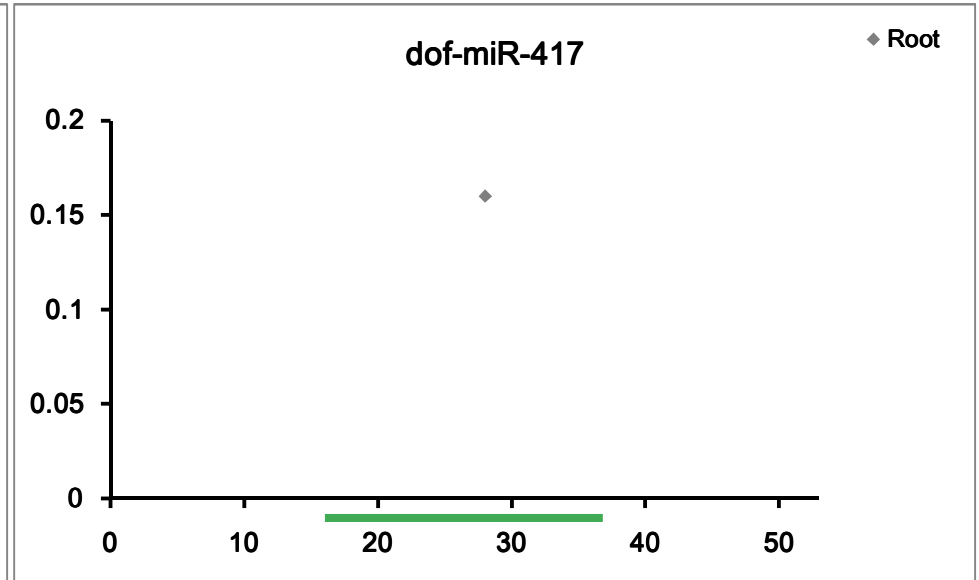
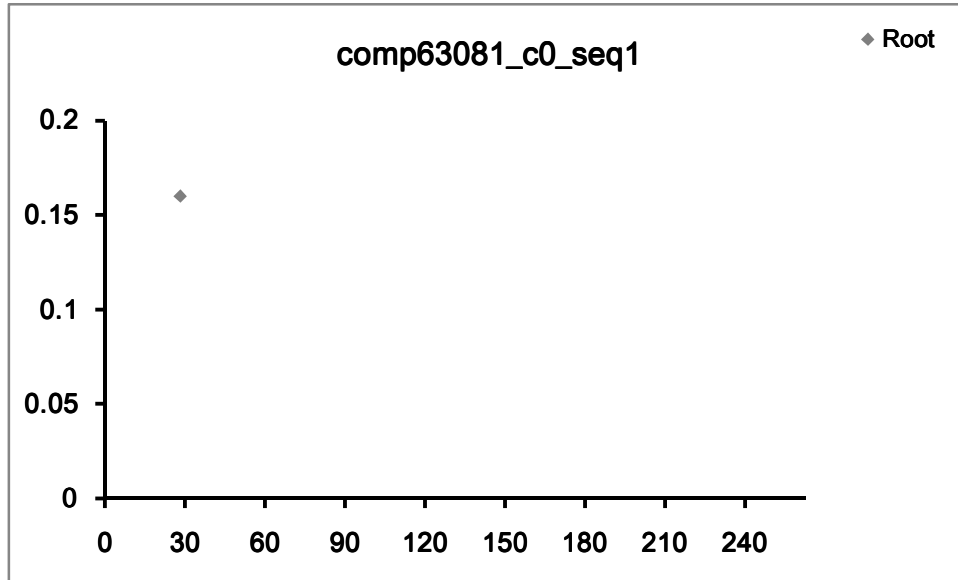
comp233795 c0 seq1

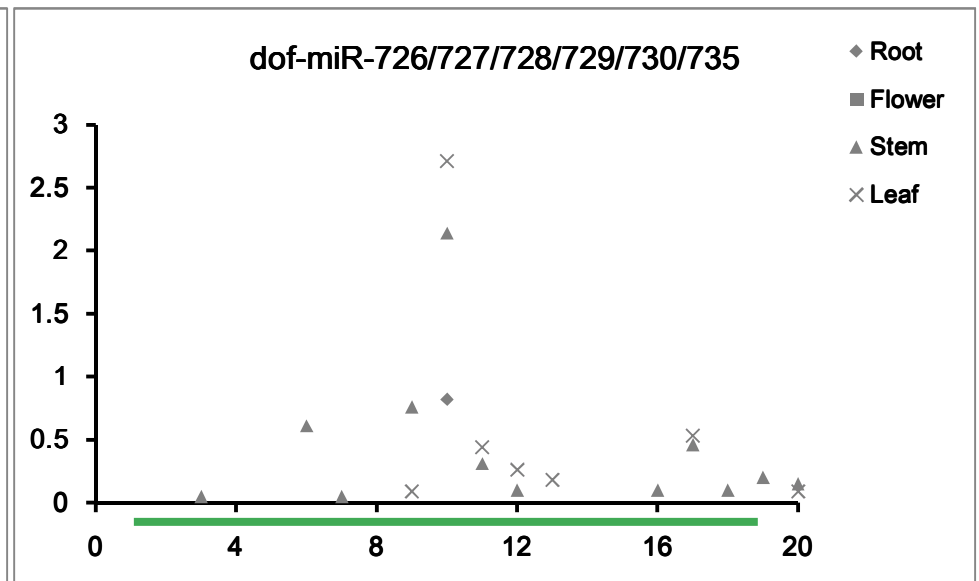
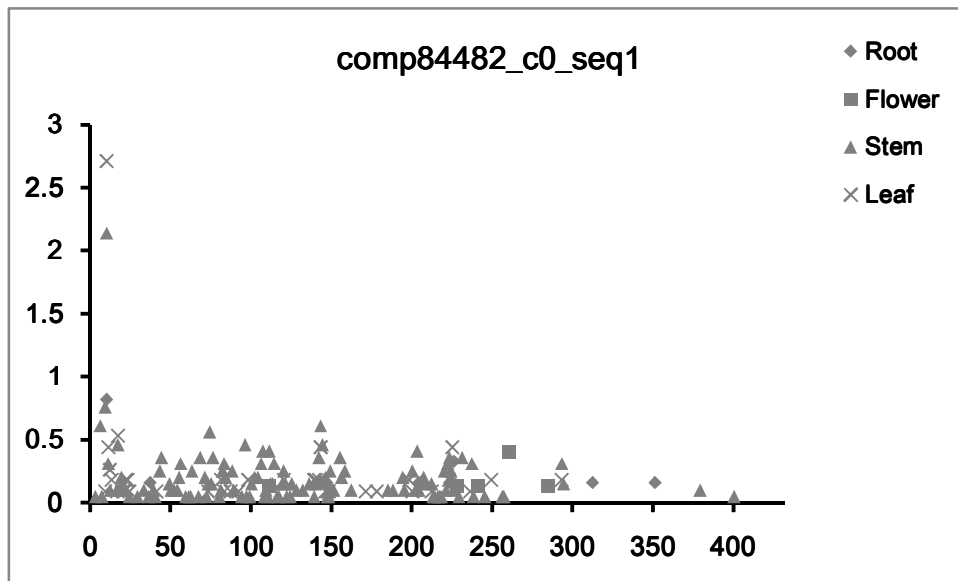
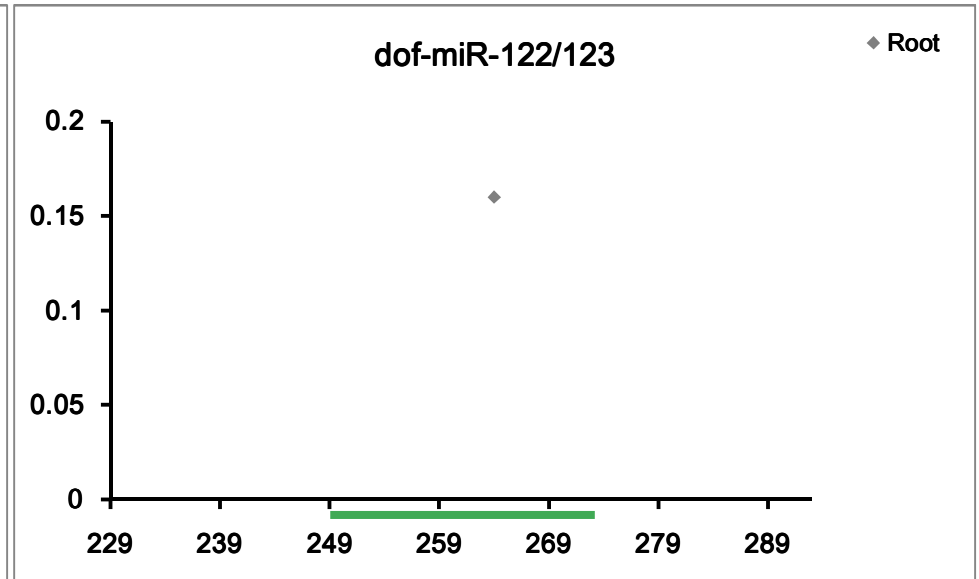
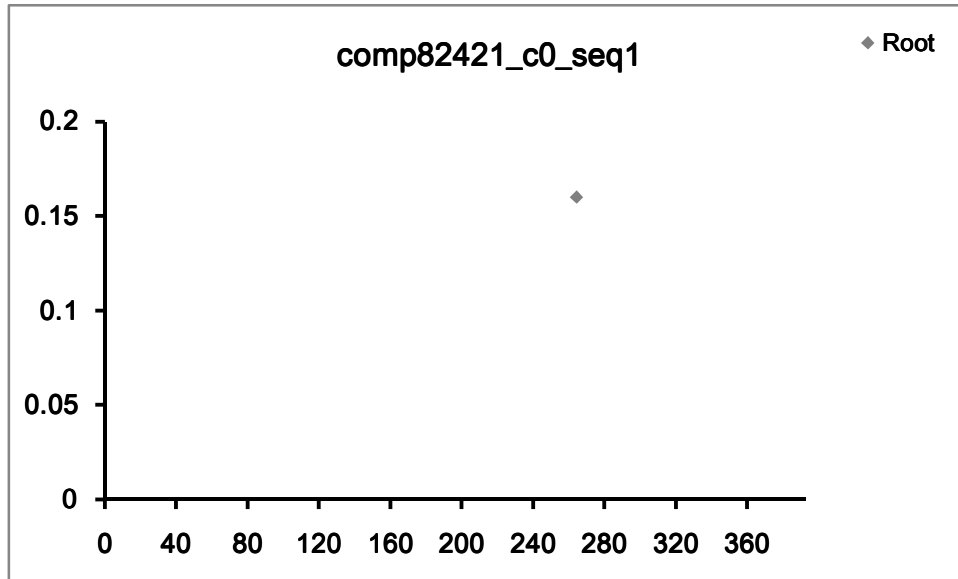
dof-miR-408

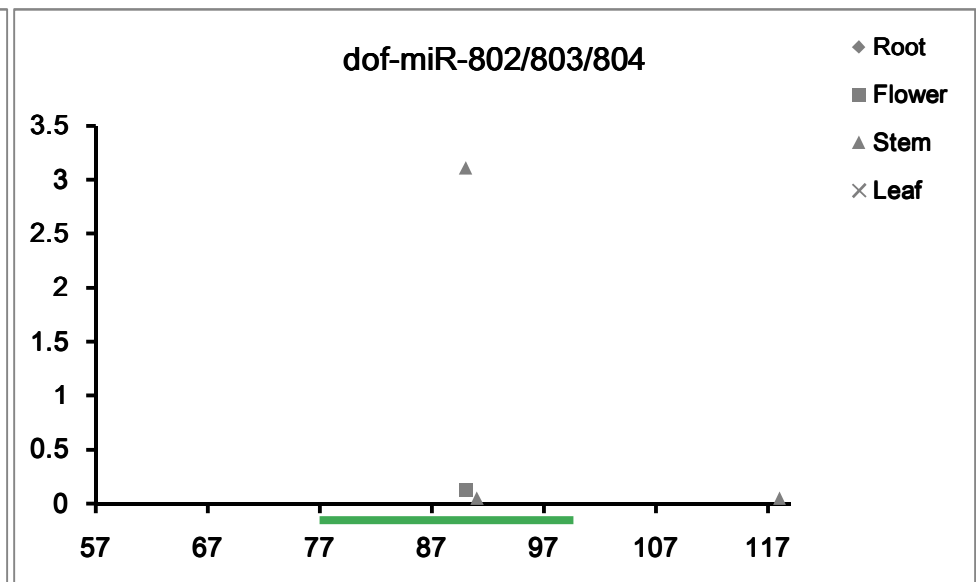
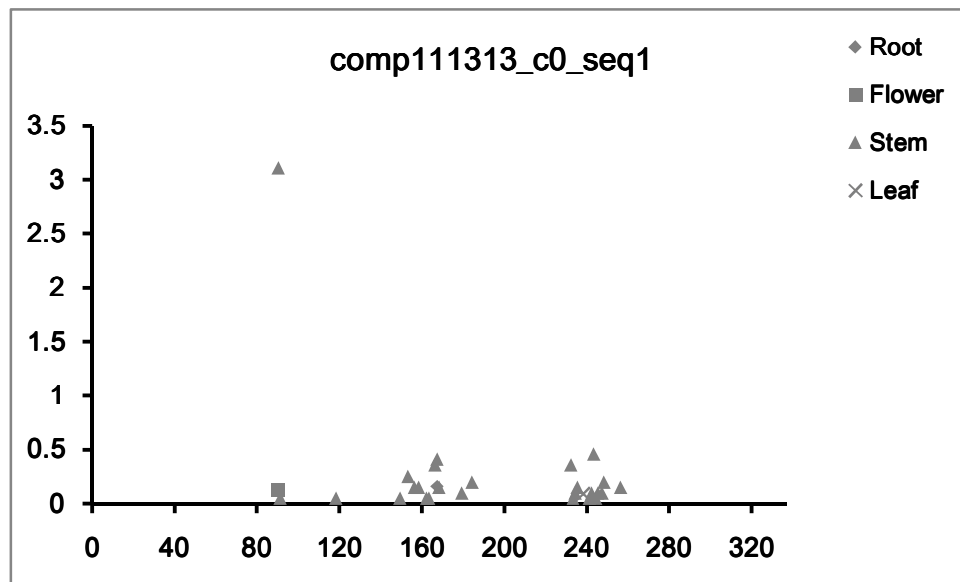
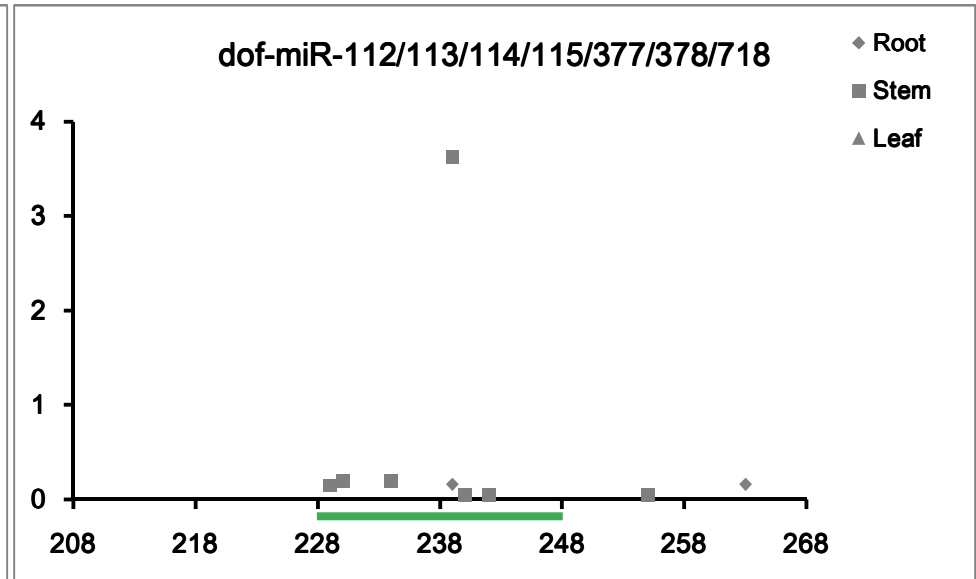
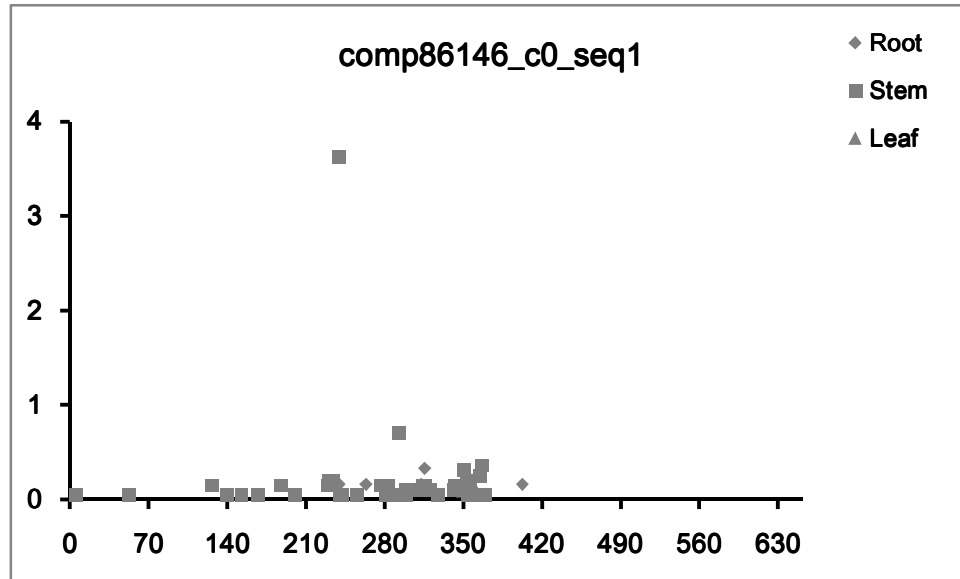
Figure S5 T-plots providing degradome-seq data-based evidences for cleavage actions between specific miRNA--target pairs identified from *Dendrobium officinale*. Four degradome-seq libraries prepared from four organs (root, flower, stem and leaf; represented by four different signs) of *Dendrobium officinale* were included for drawing t-plots. For each miRNA--target pair, two scatter diagrams are provided. The left diagram with target ID provides a global view of degradome signals distributed all along the full-length target transcript. The right diagram with ID(s) of regulatory miRNA(s) provides a detailed view of degradome signals within about 60-nt region surrounding the predicted miRNA binding site (marked by a green horizontal line) on the target transcript. The y axis of each diagram measures the intensity (in RPM) of degradome signals. Please note: only the miRNA--target pairs supported by prominent degradome signatures resided within 10th to 11th nt from the 5' ends of the regulatory miRNAs are included in this figure.

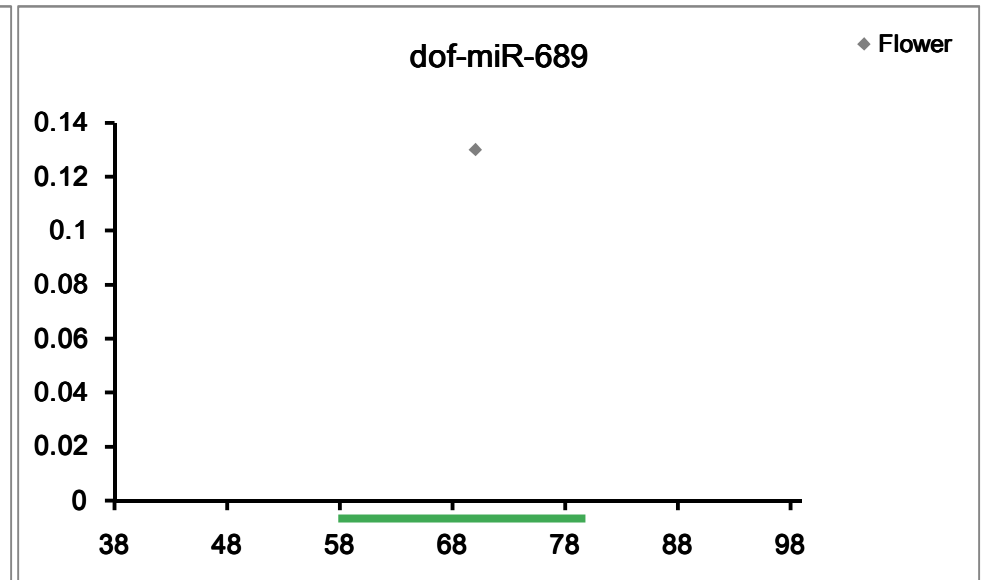
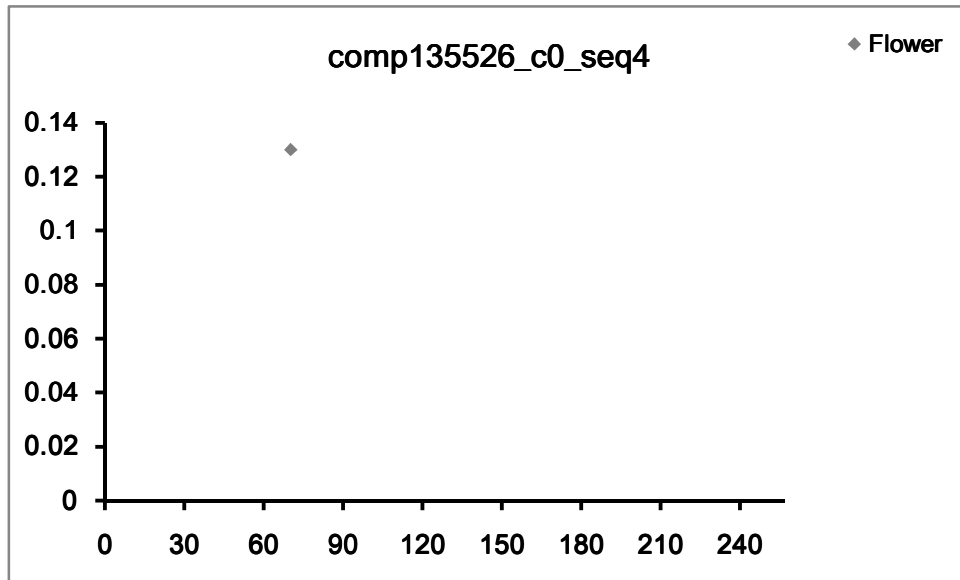
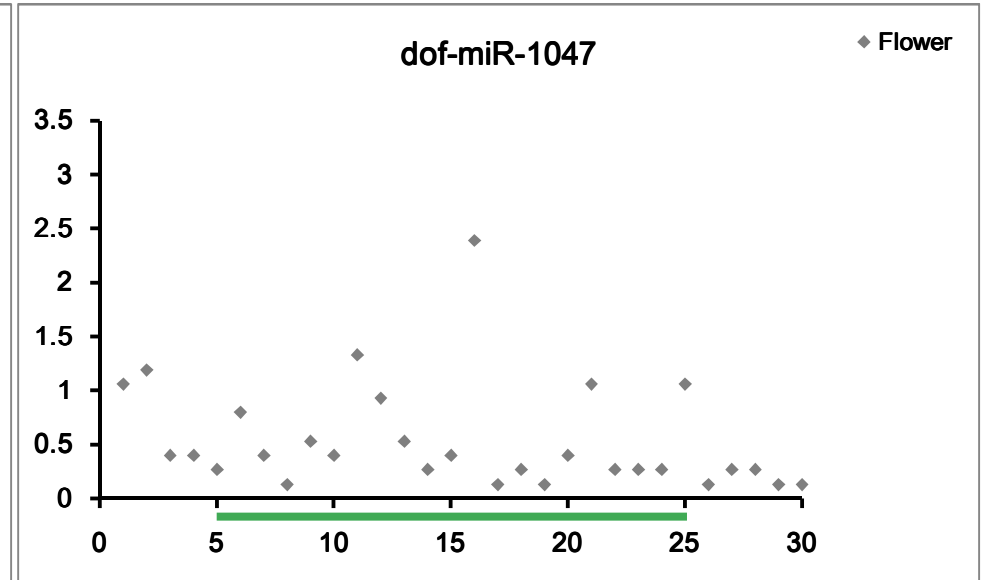
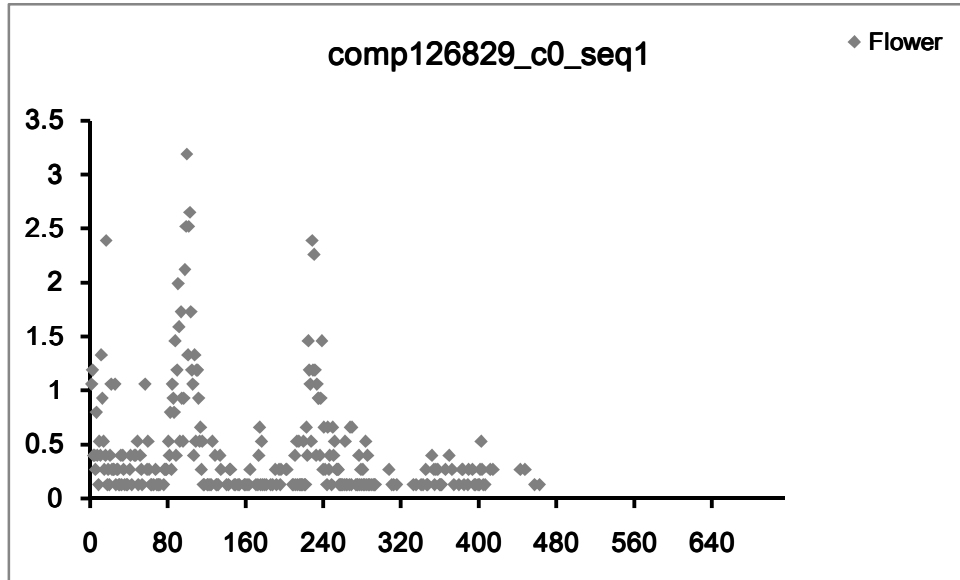


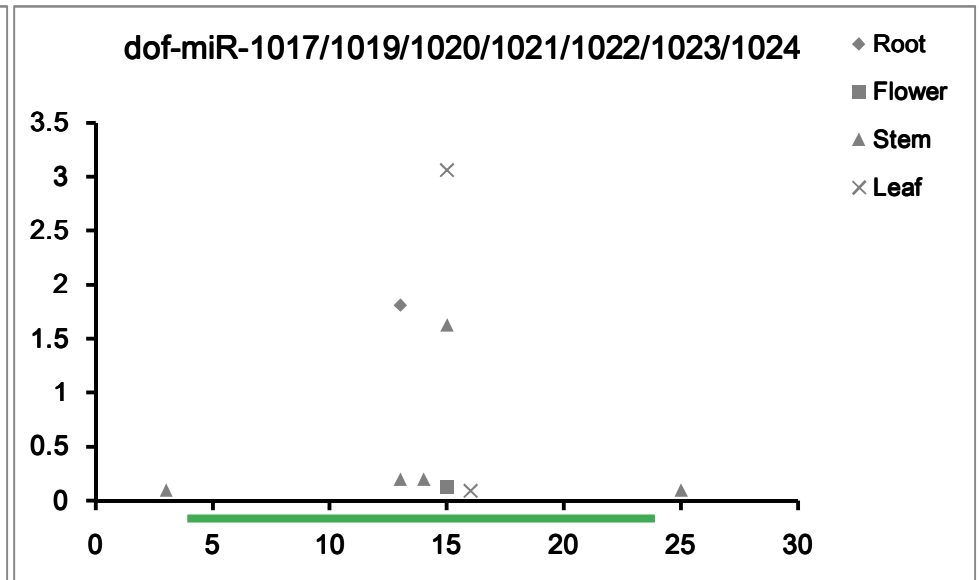
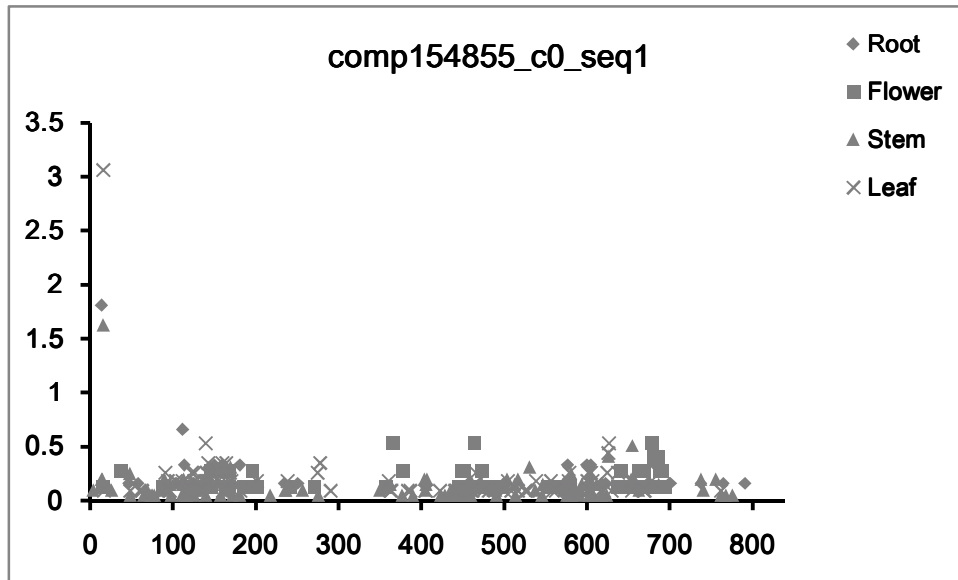
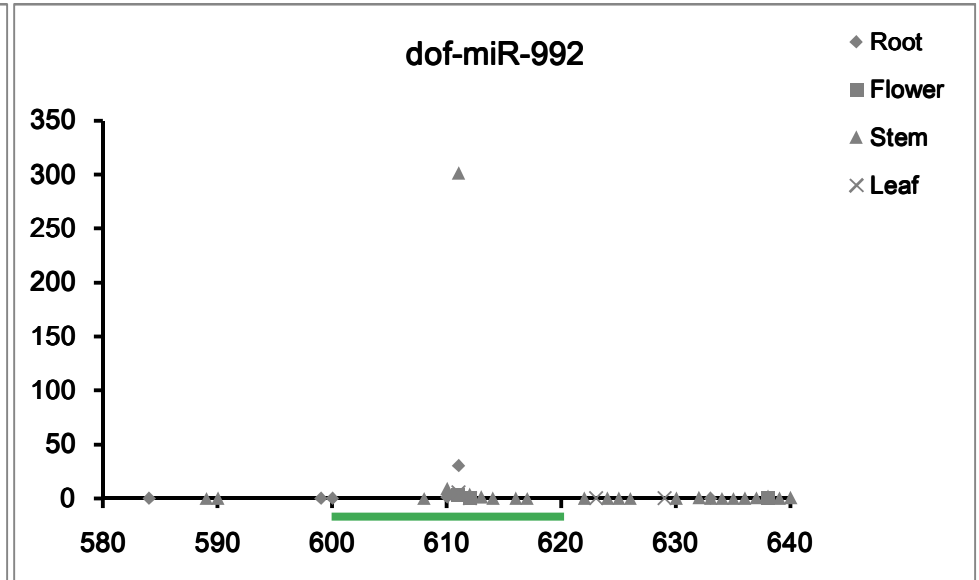
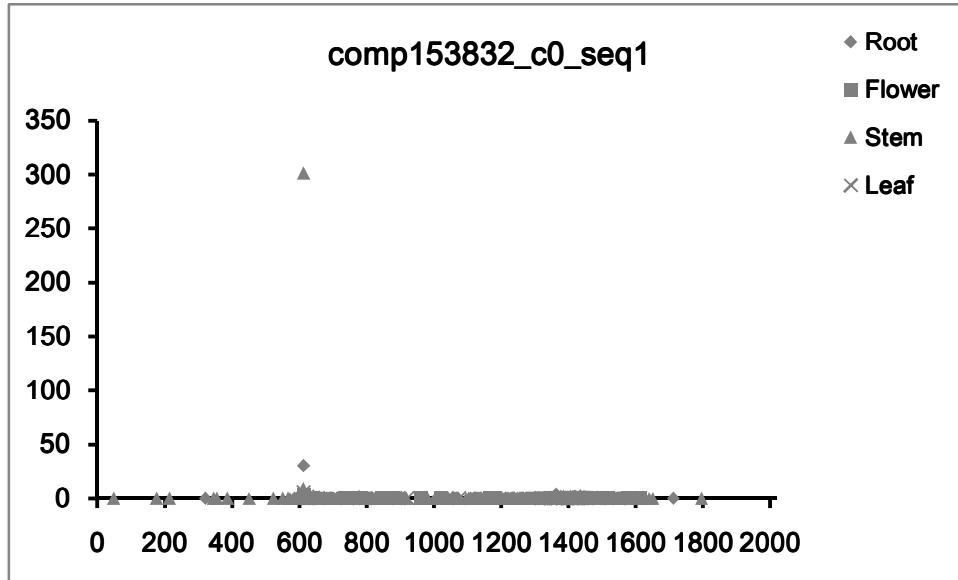


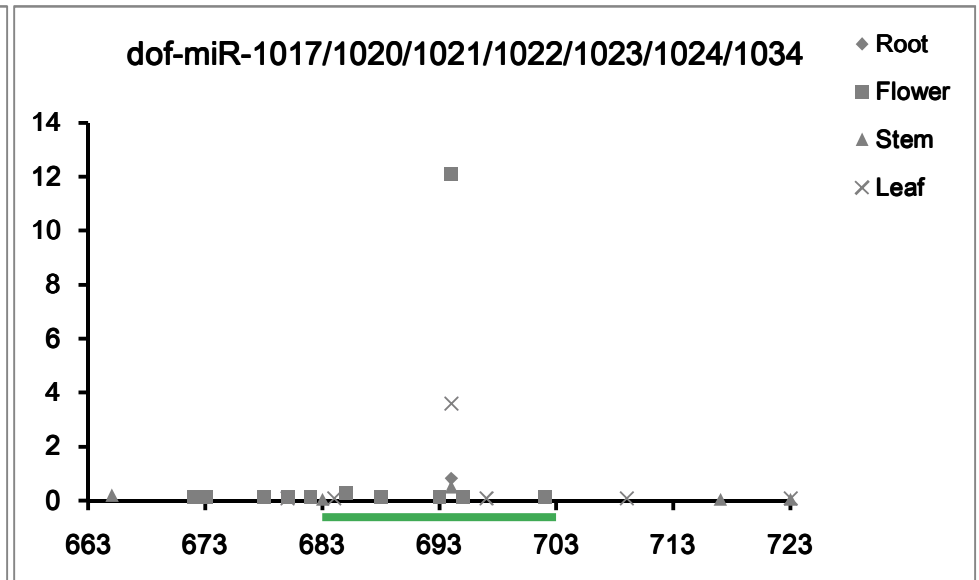
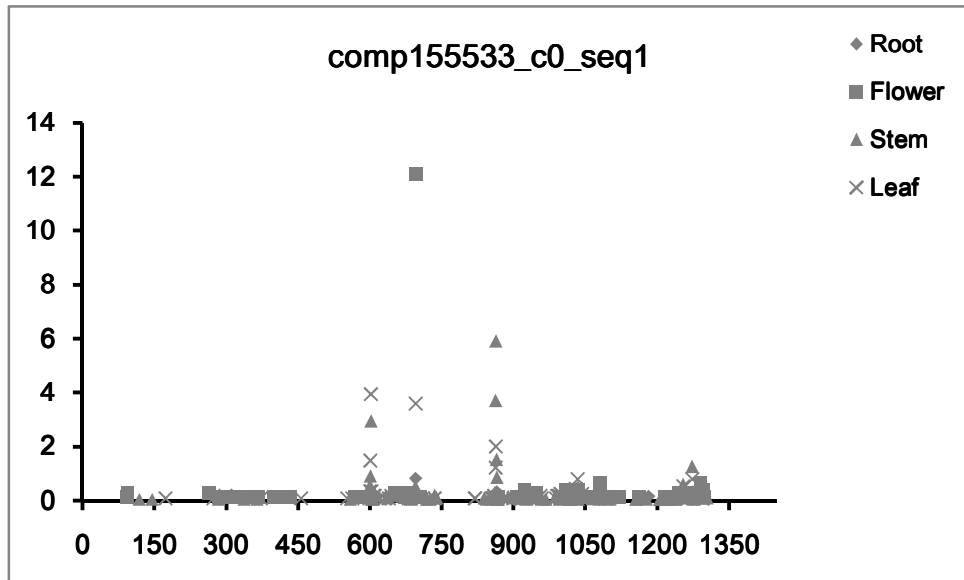
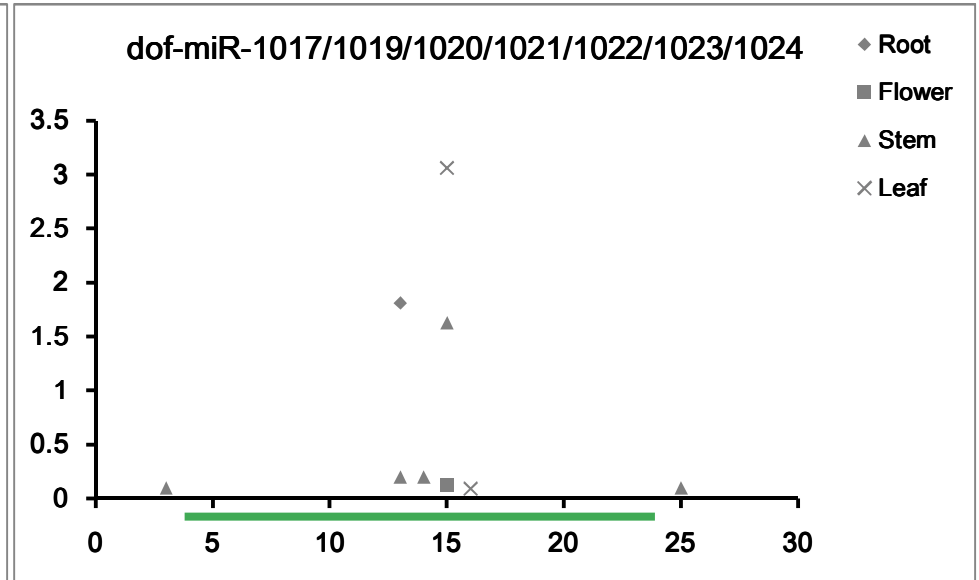
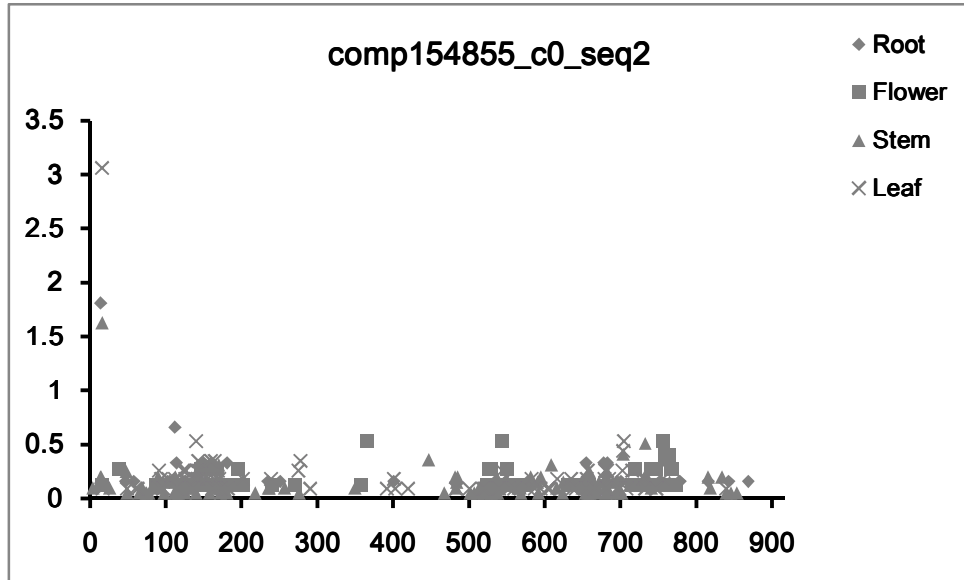


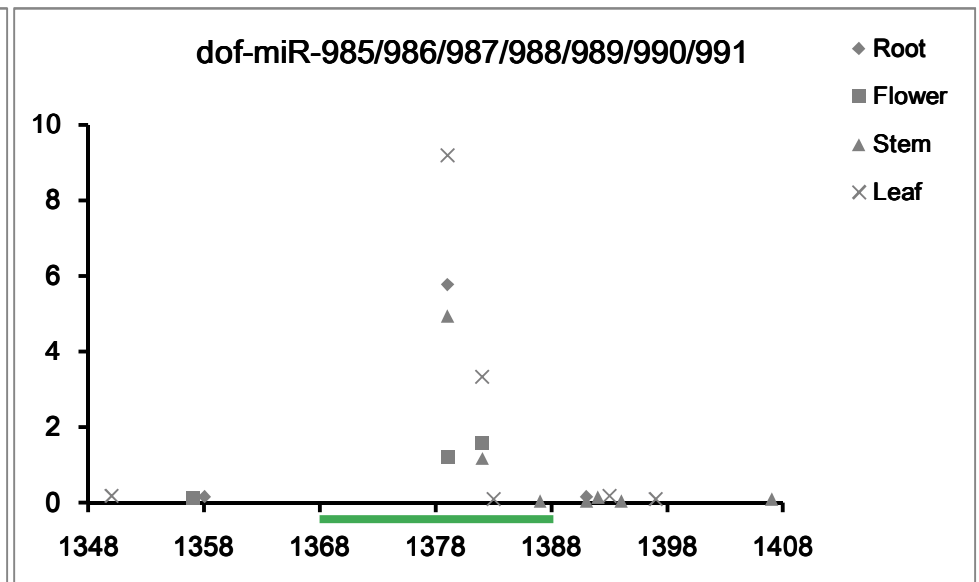
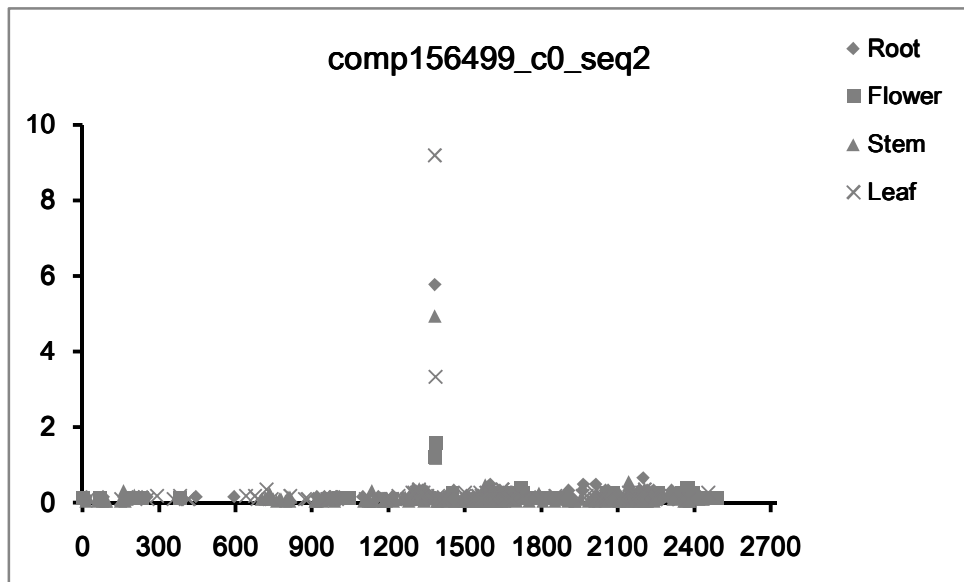
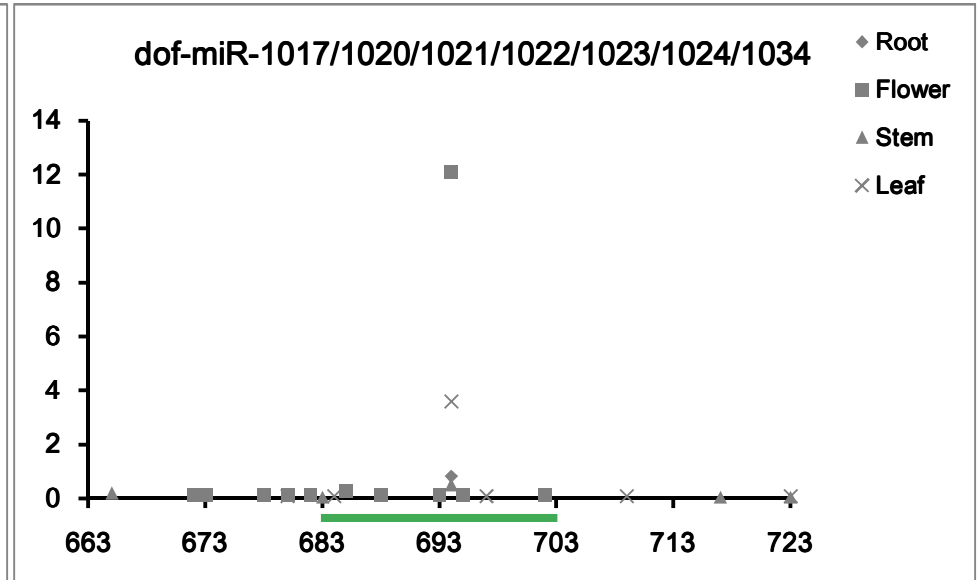
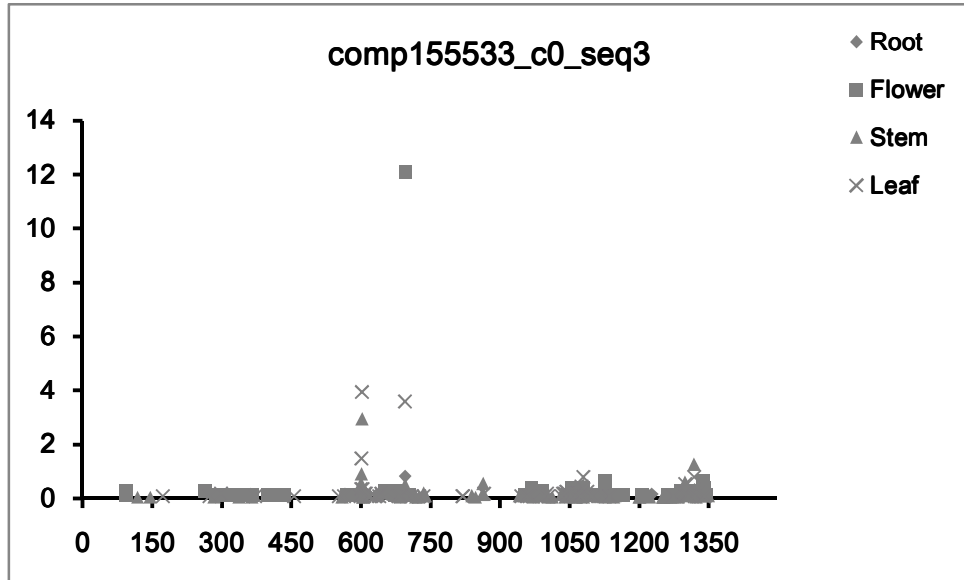


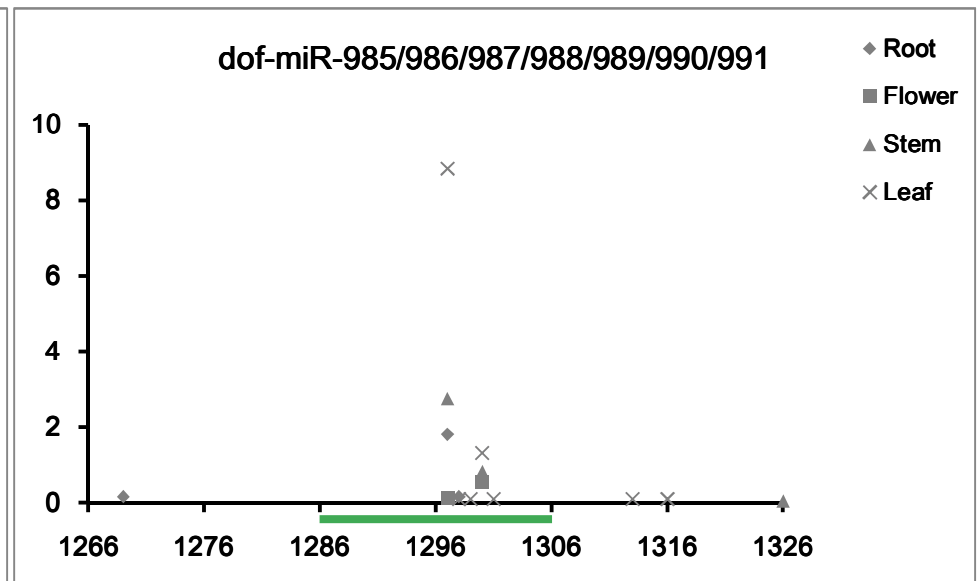
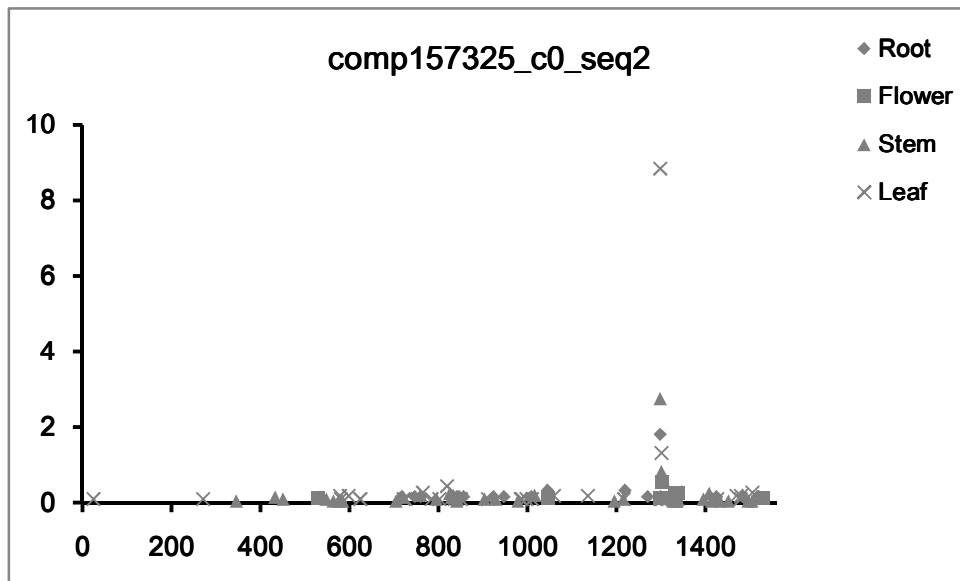
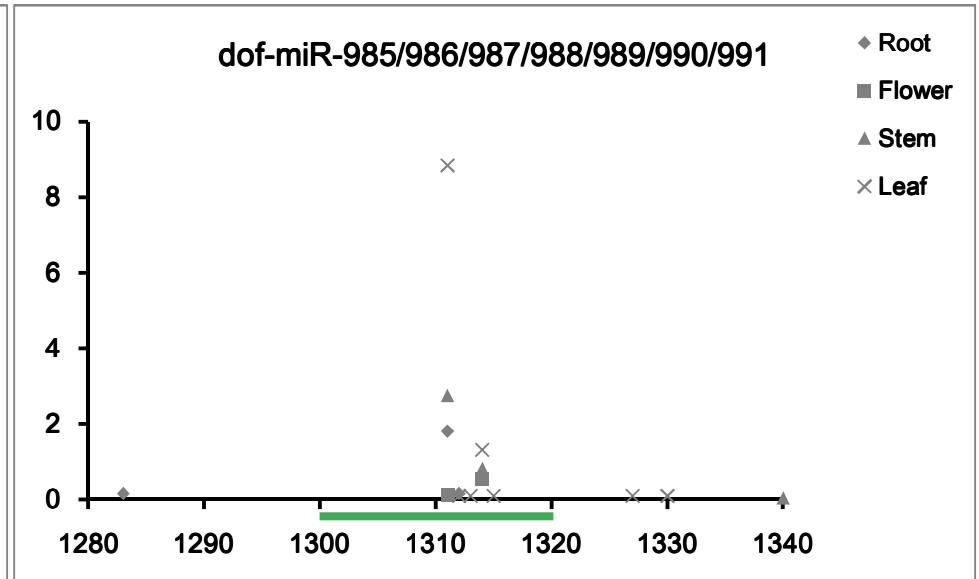
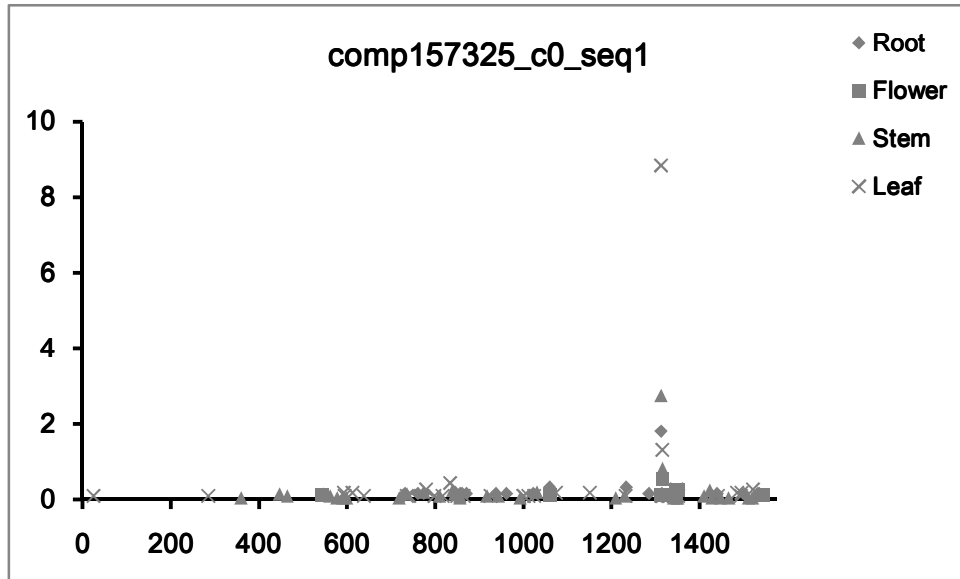


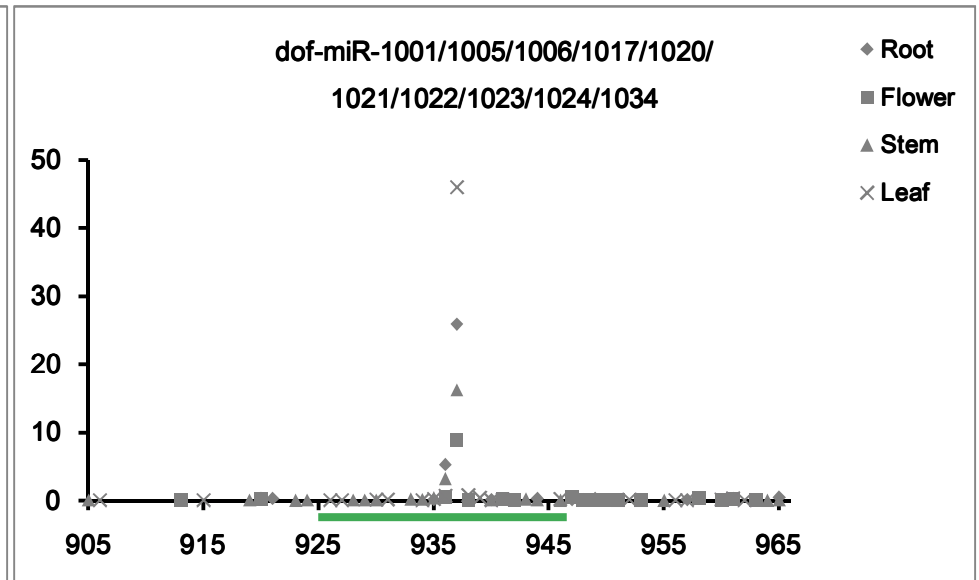
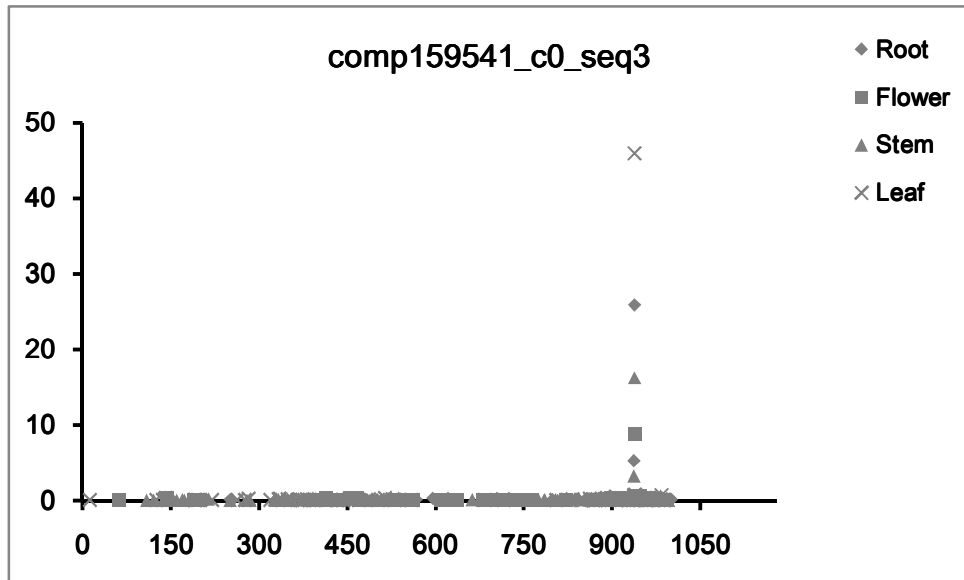
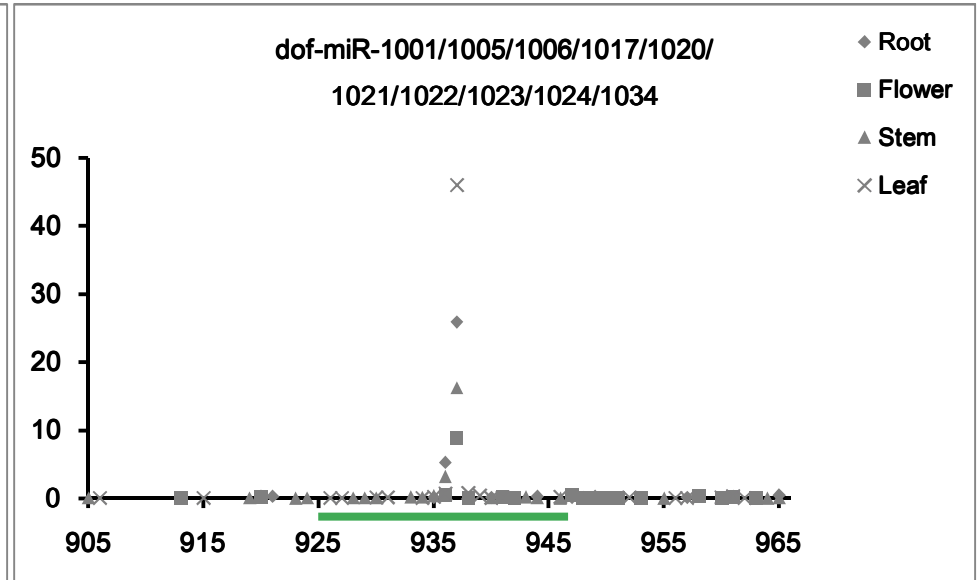
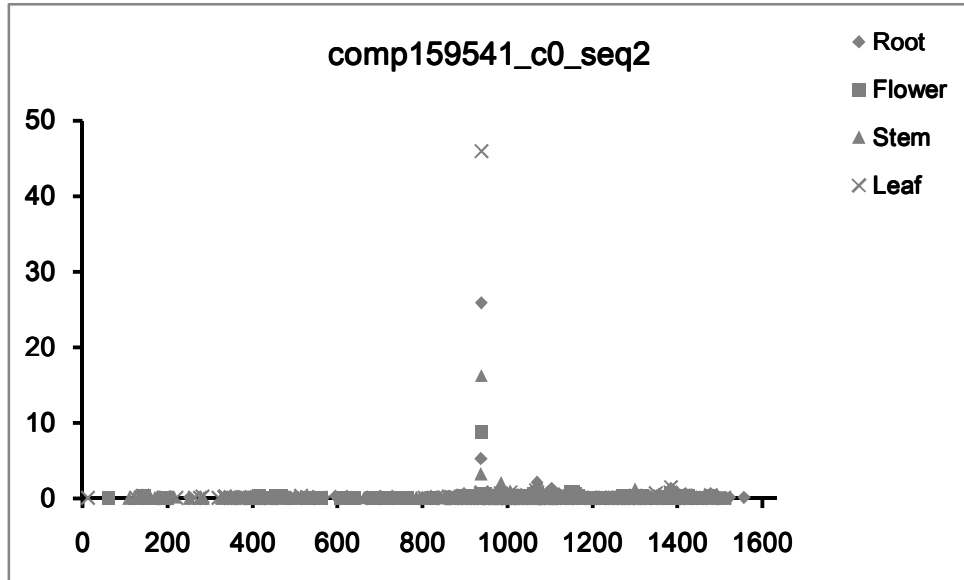


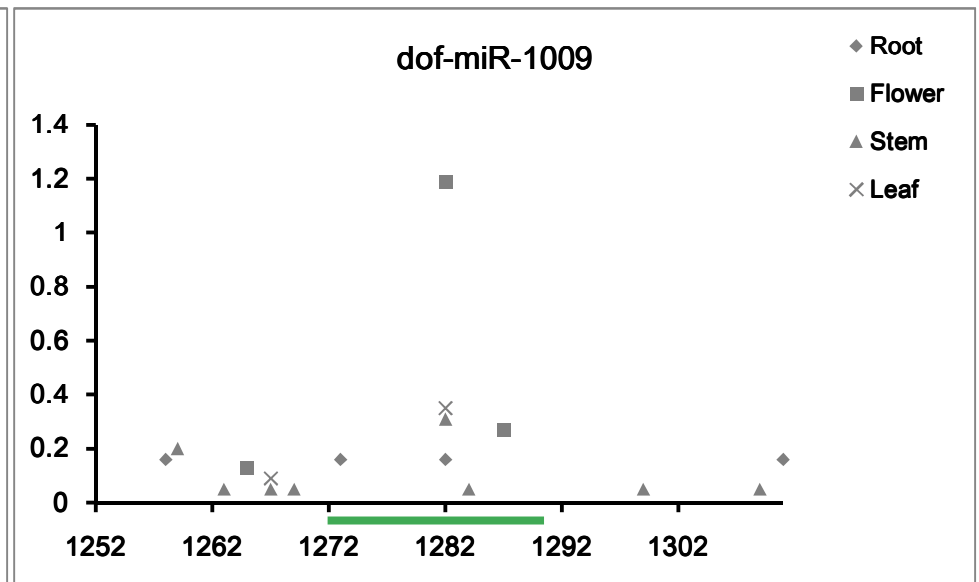
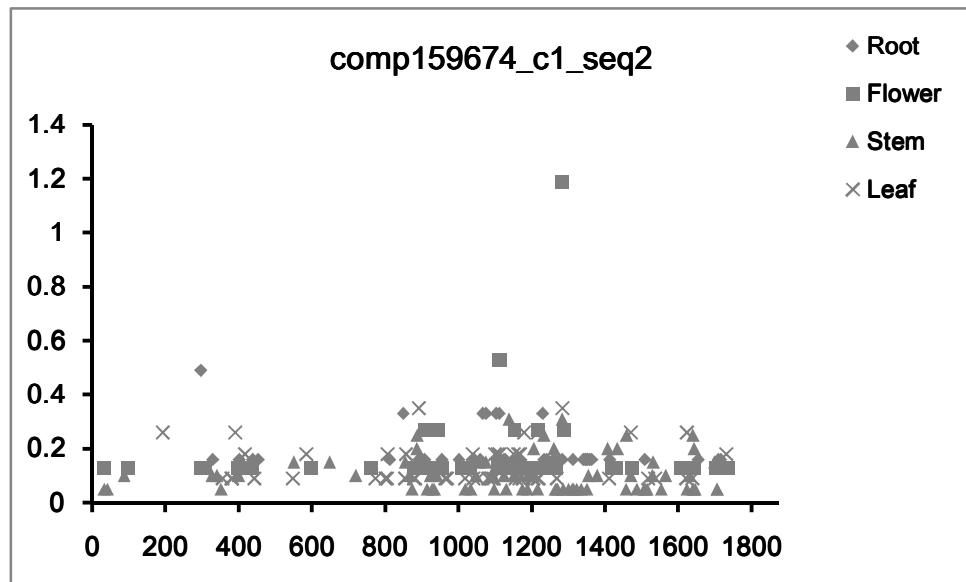
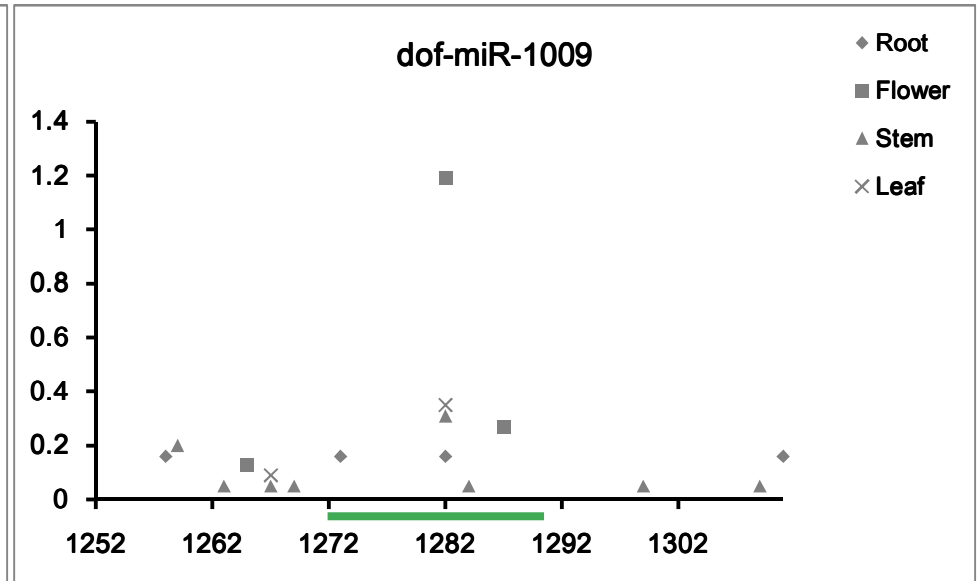
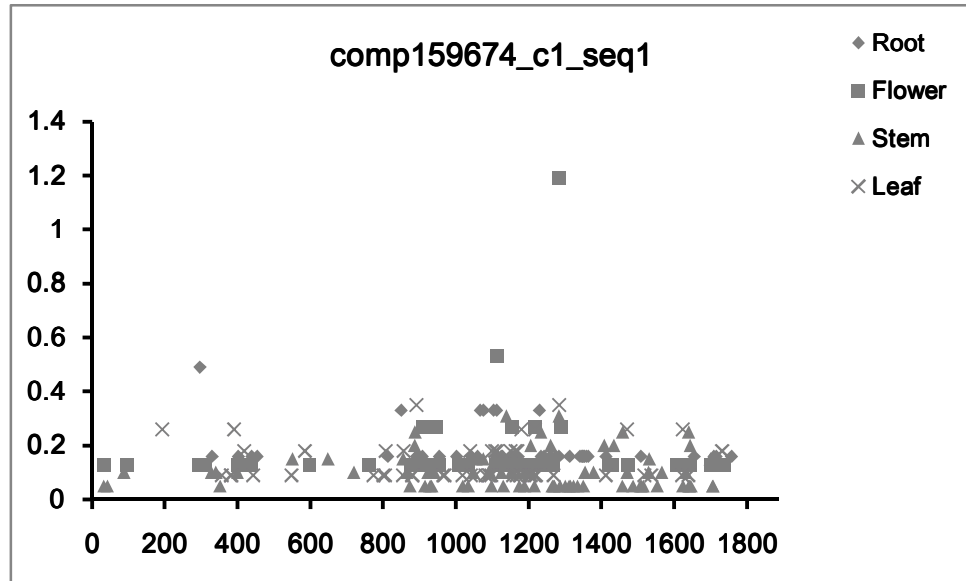


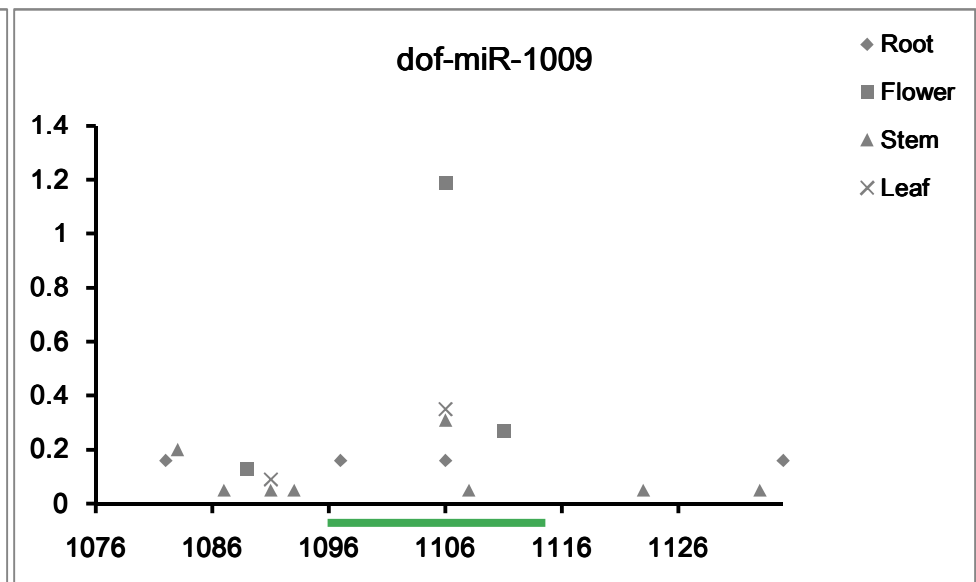
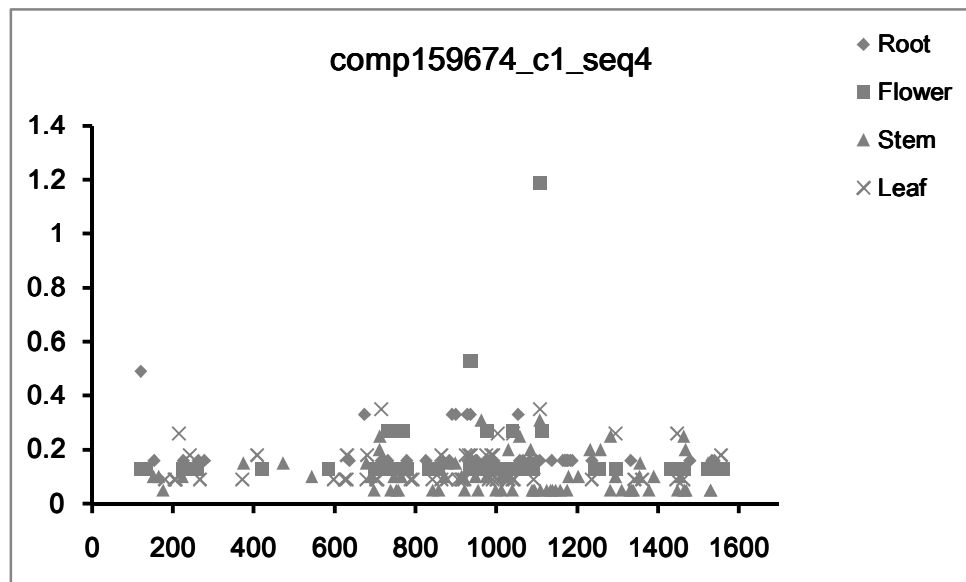
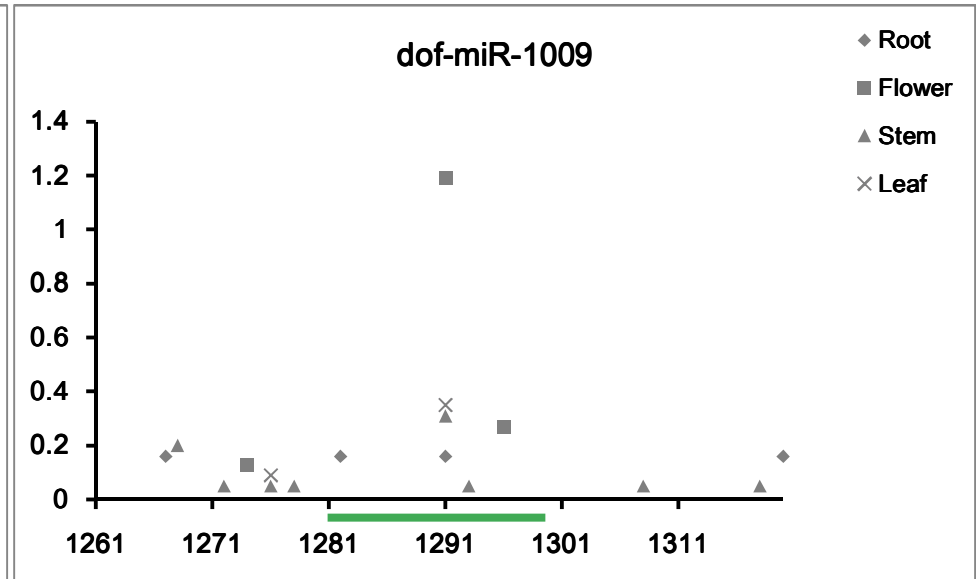
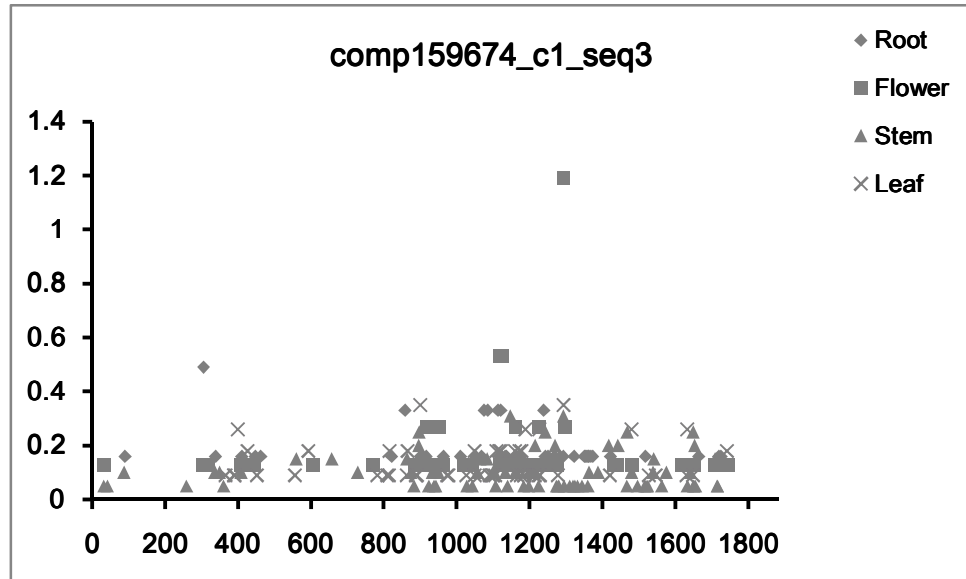


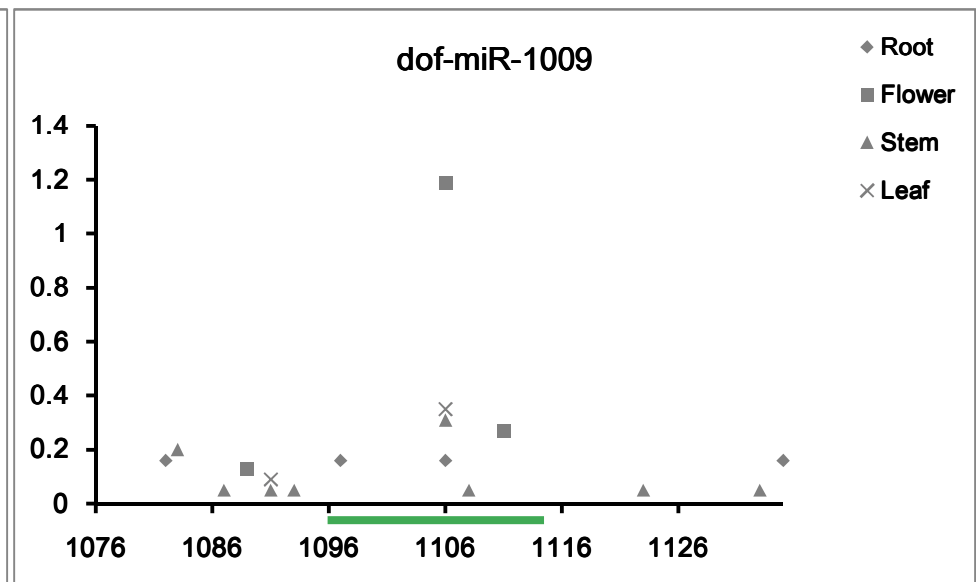
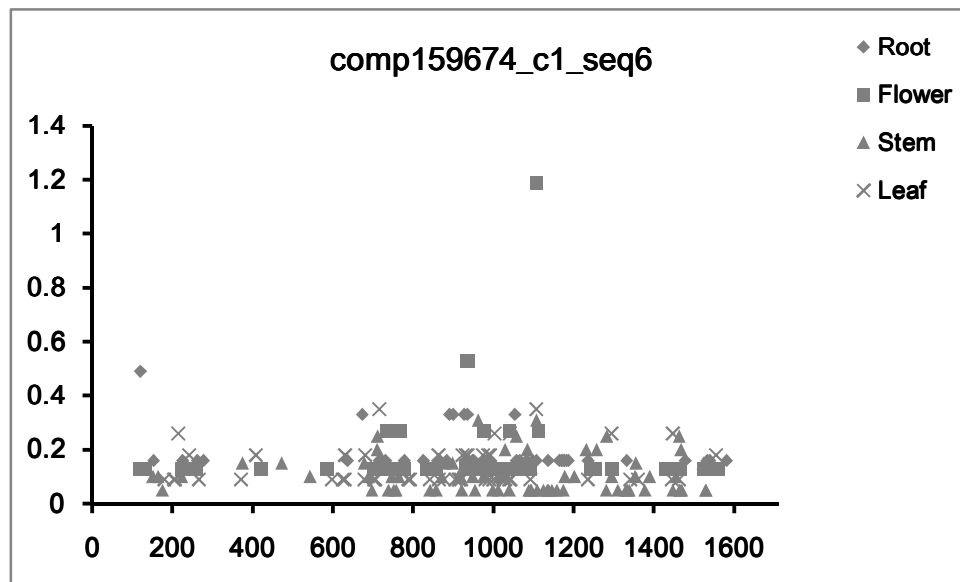
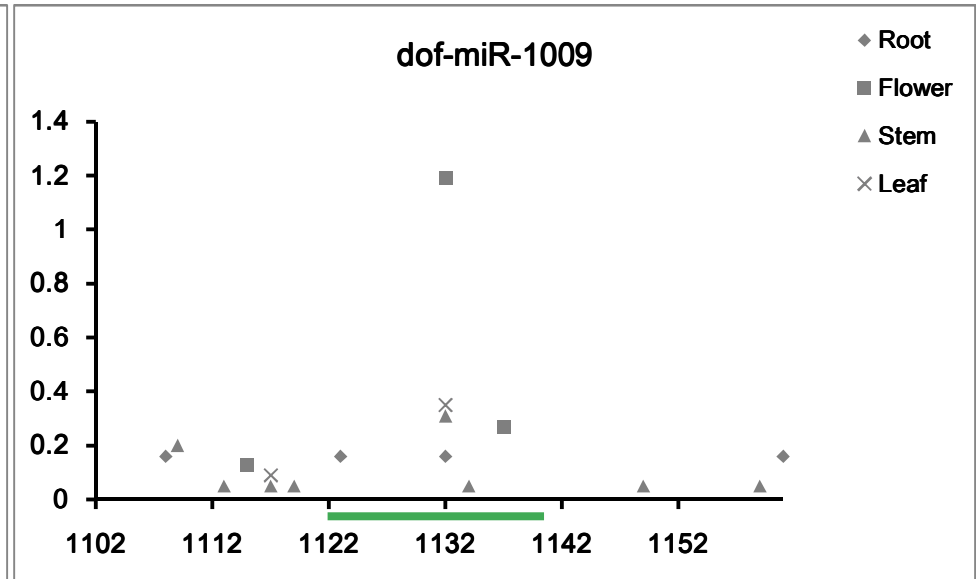
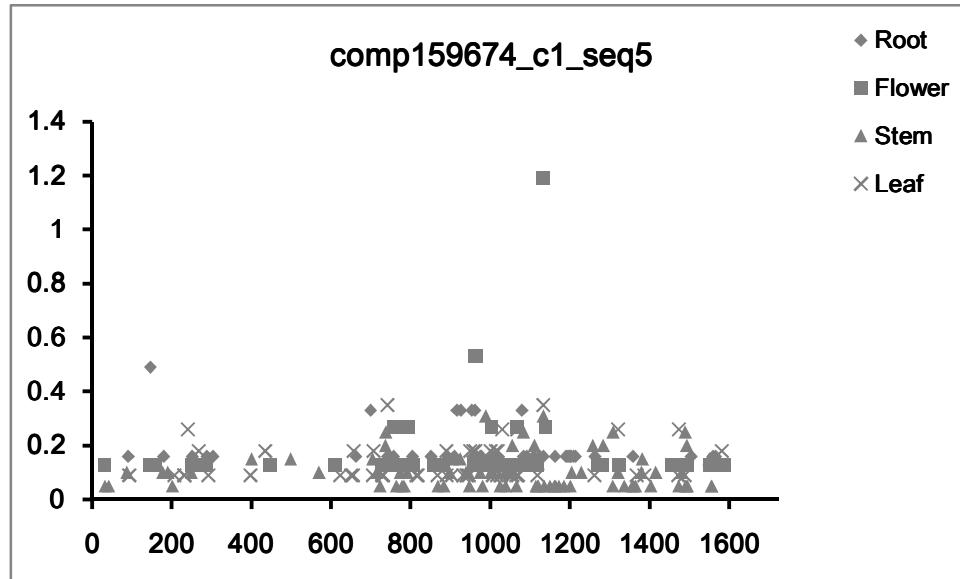


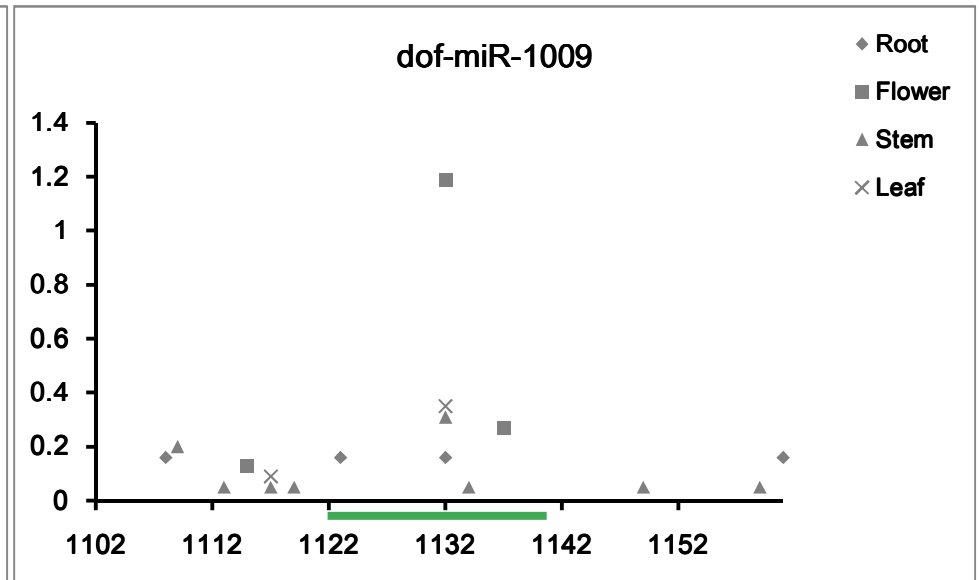
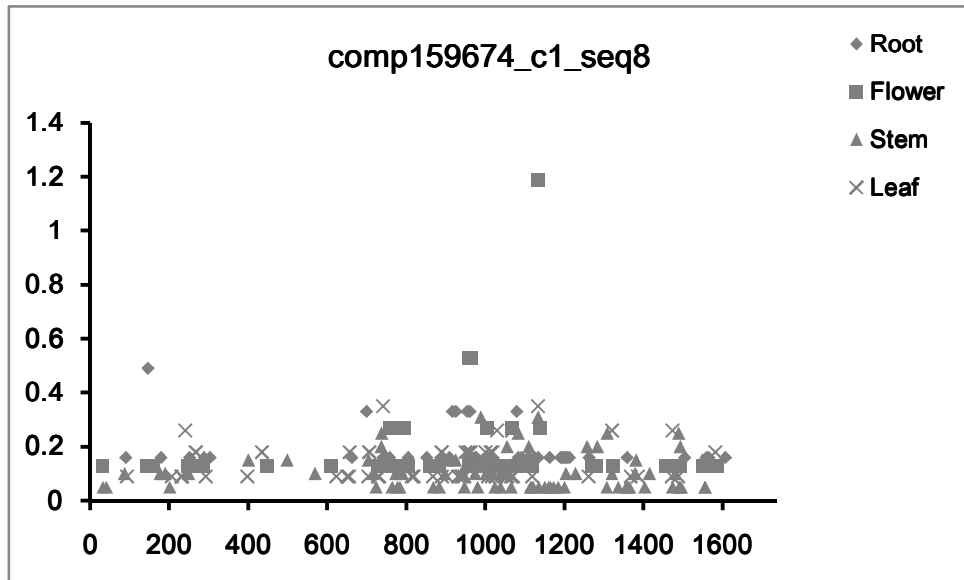
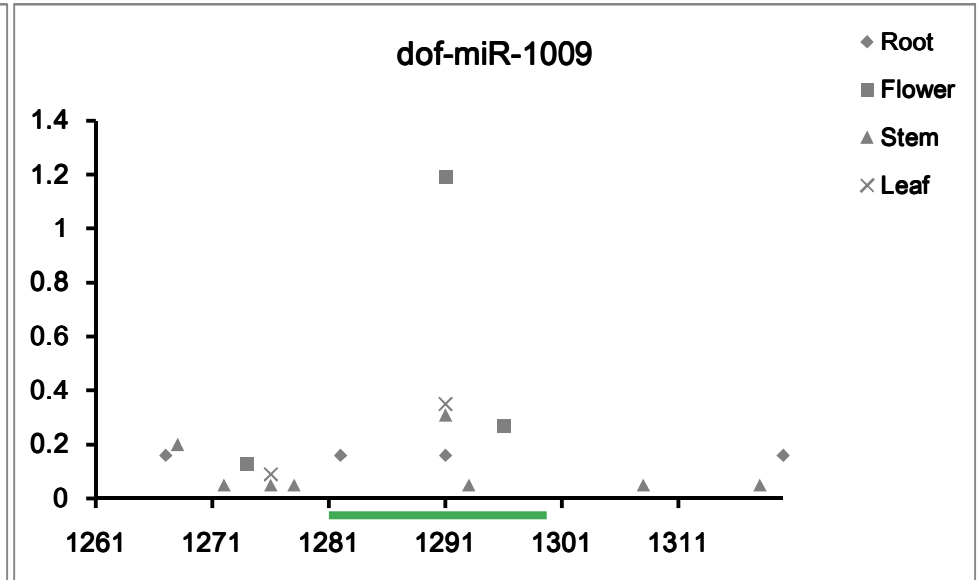
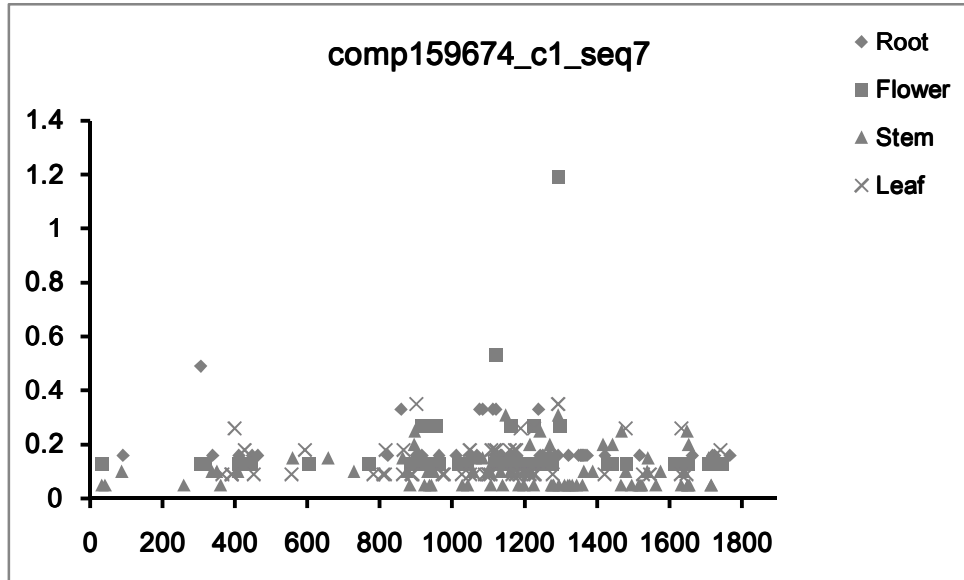


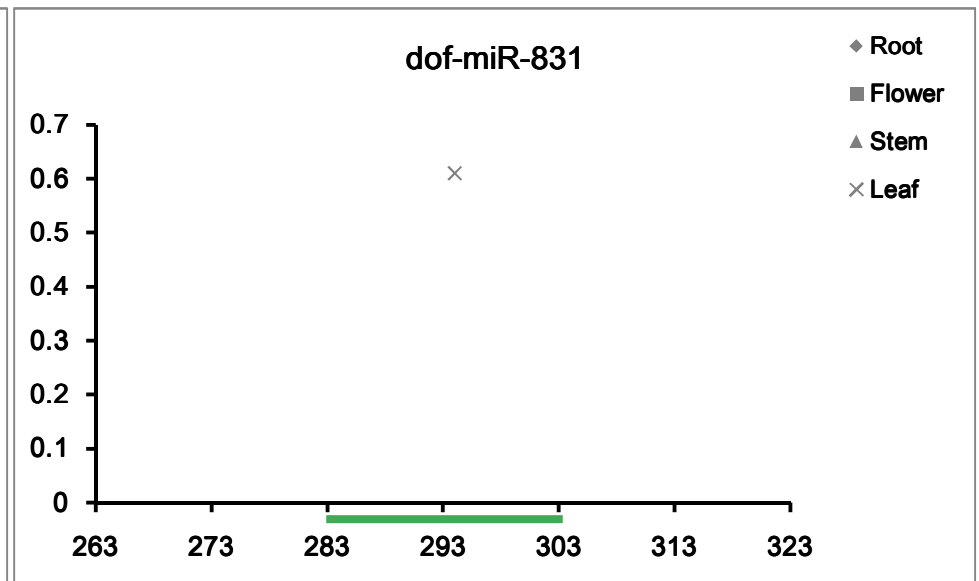
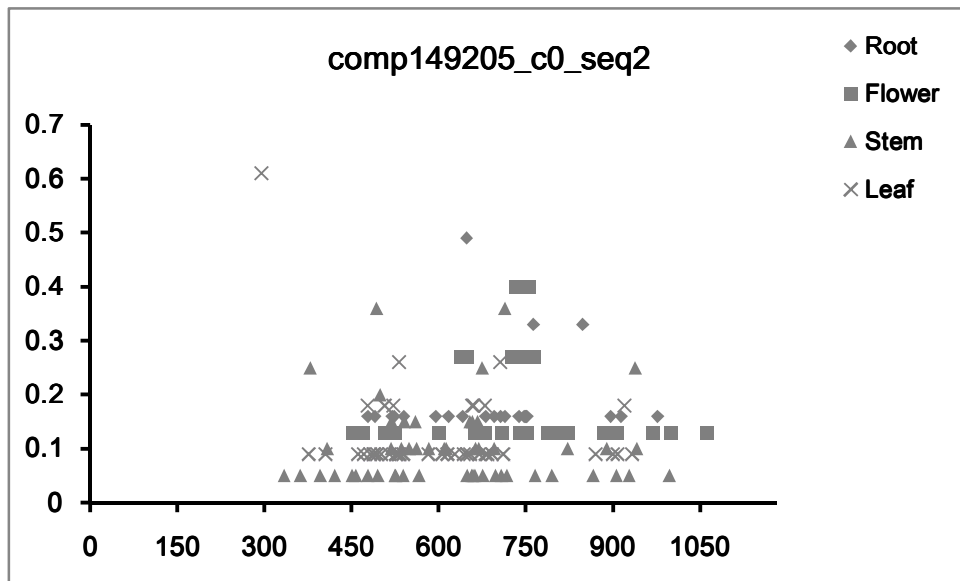
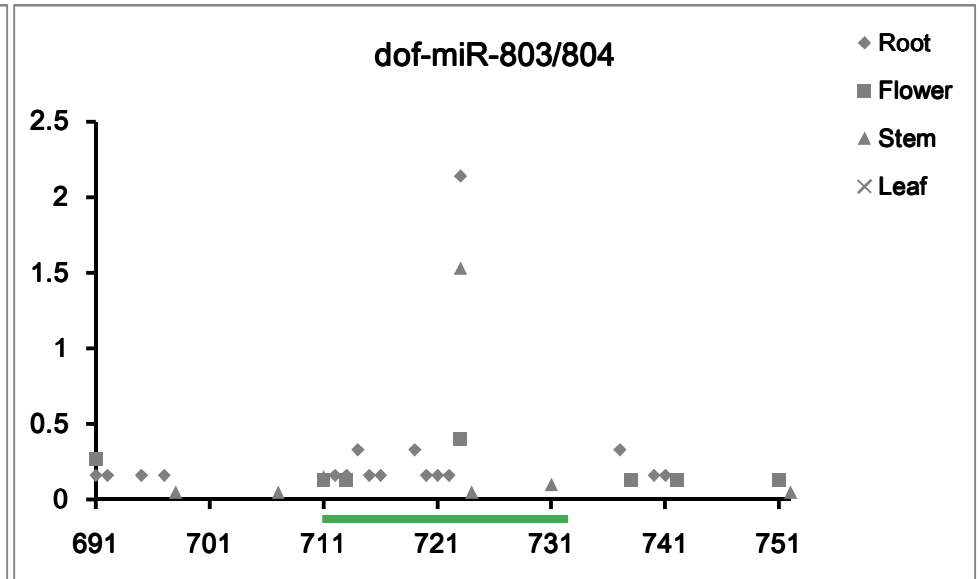
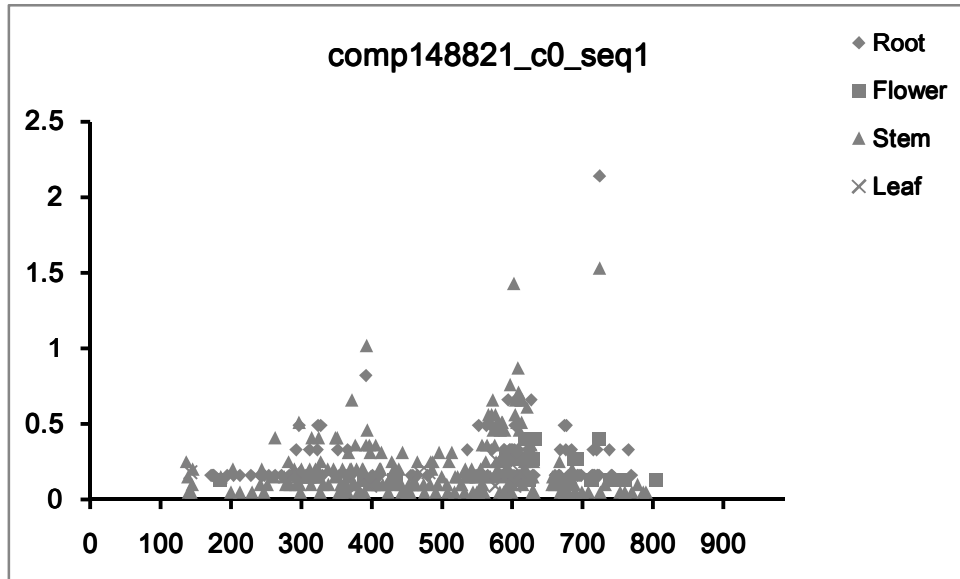


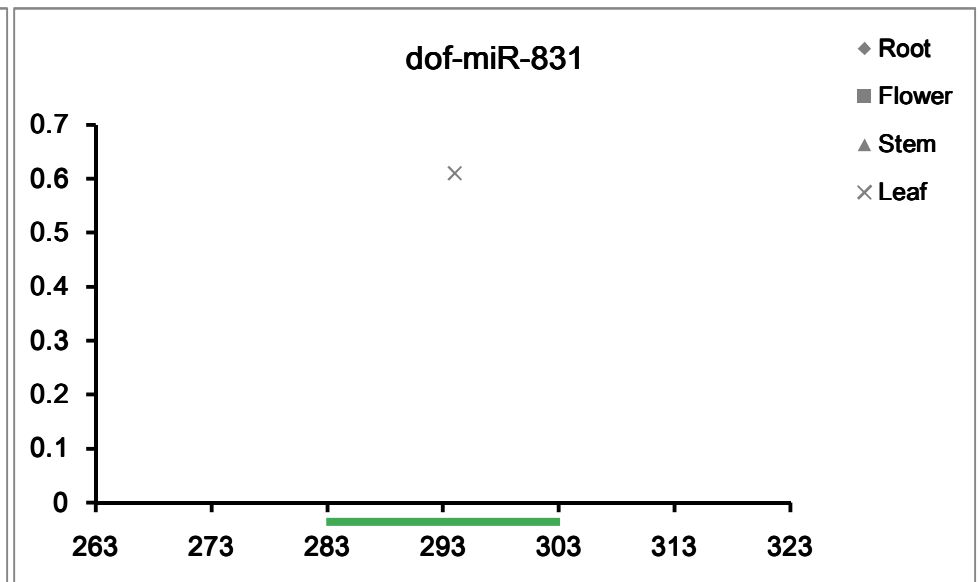
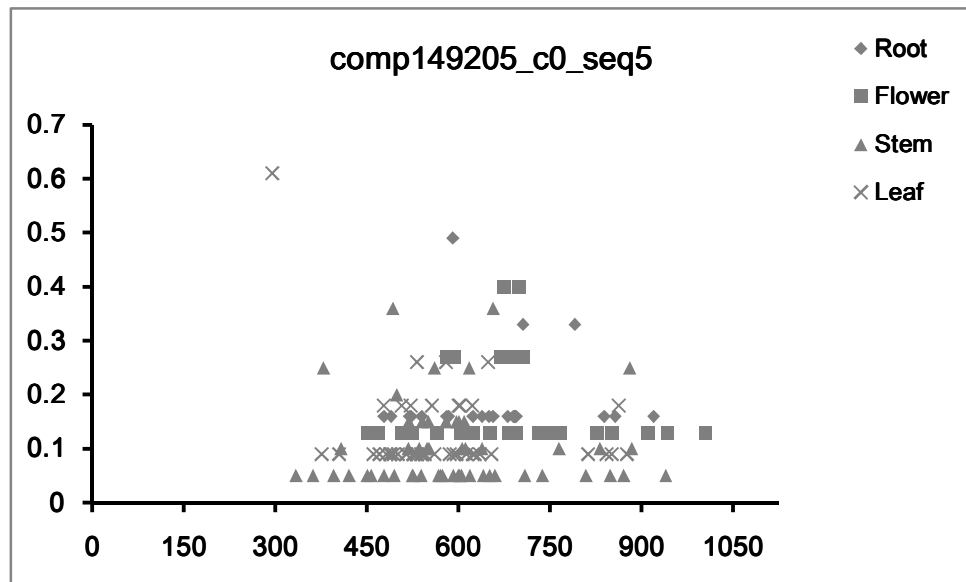
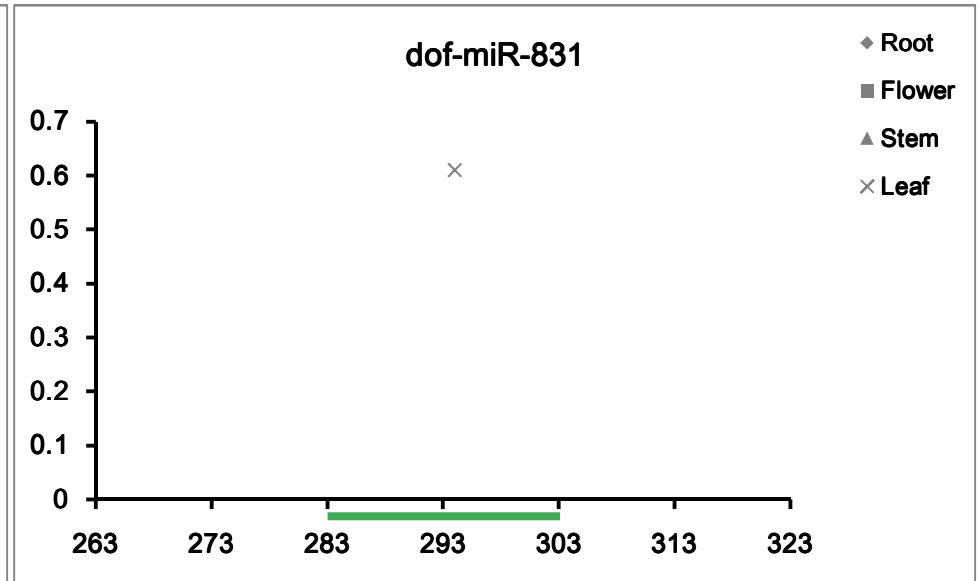
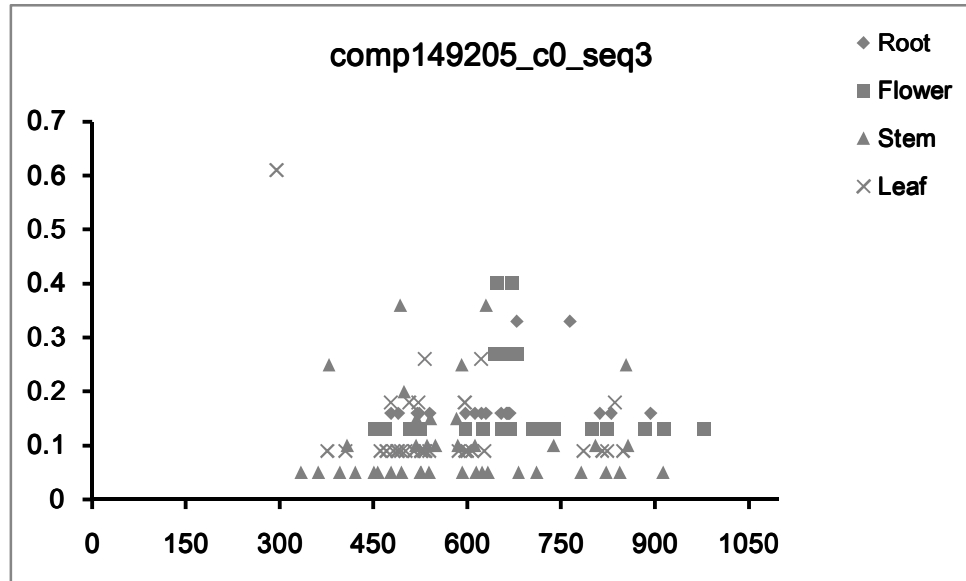


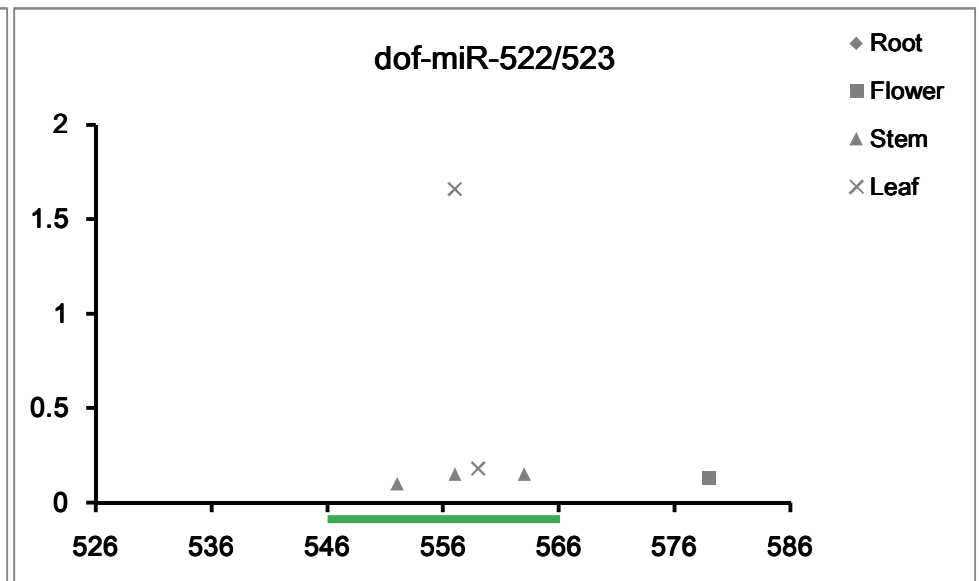
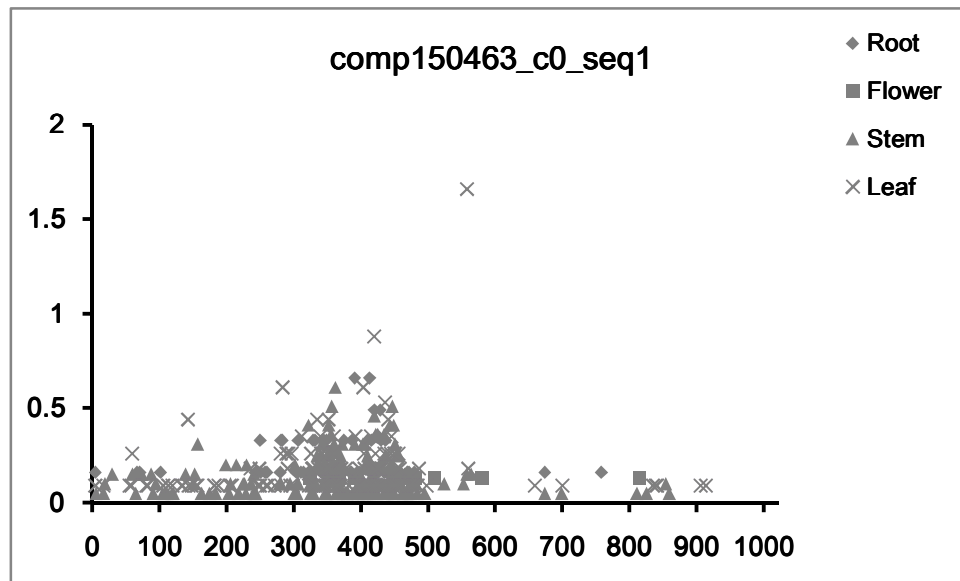
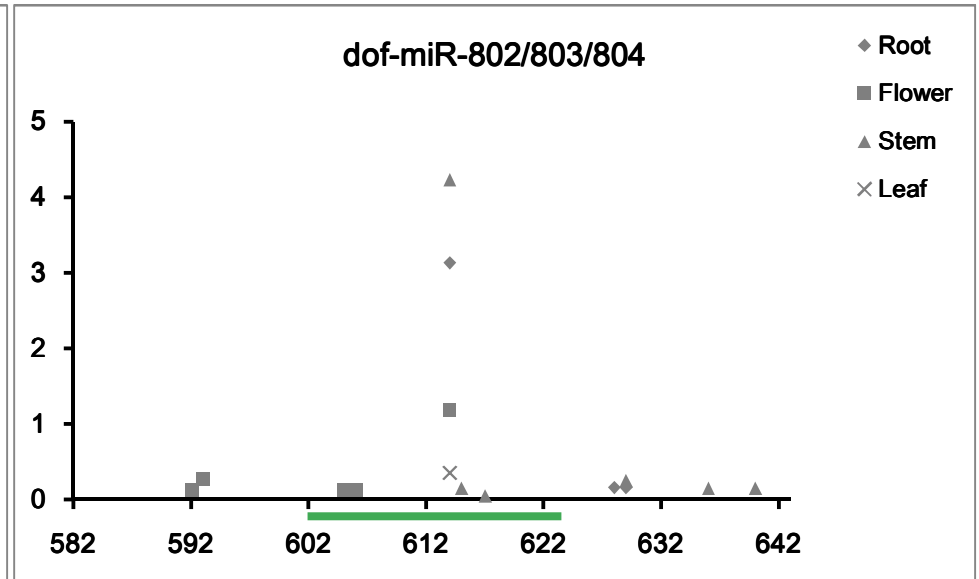
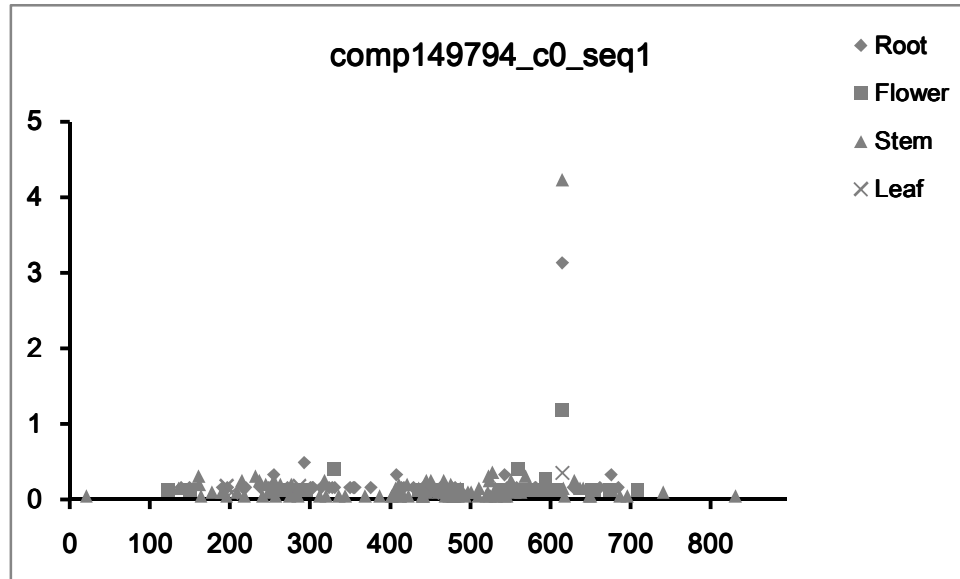


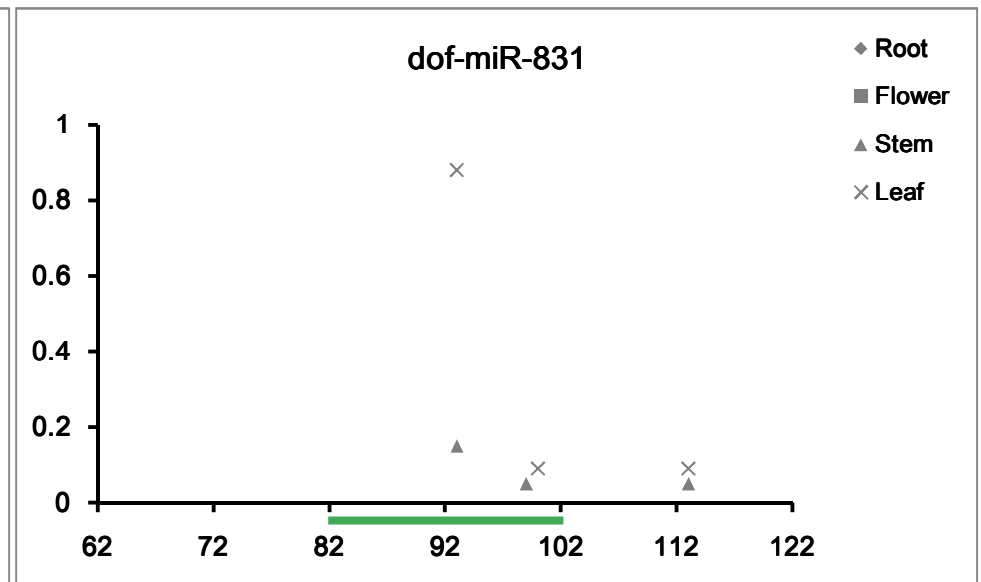
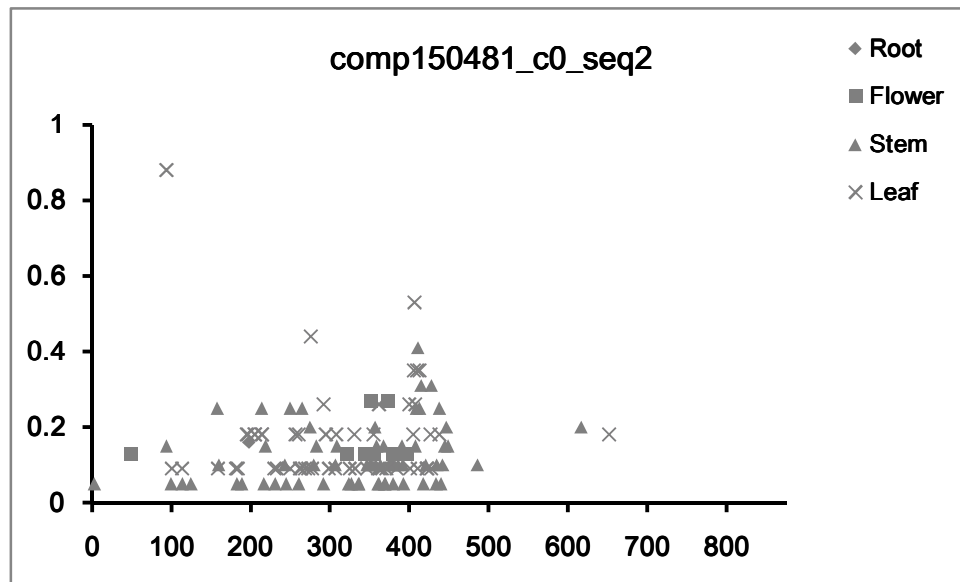
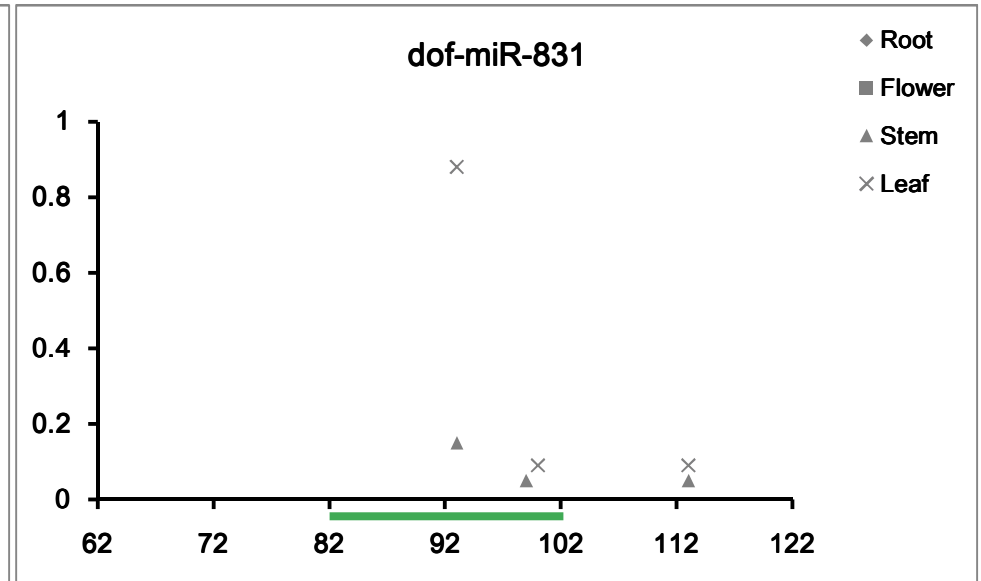
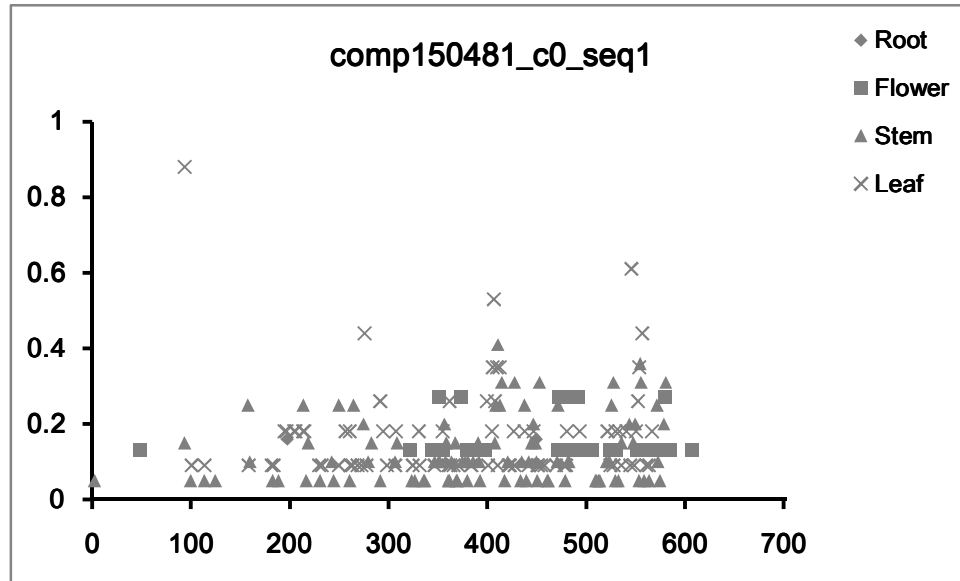


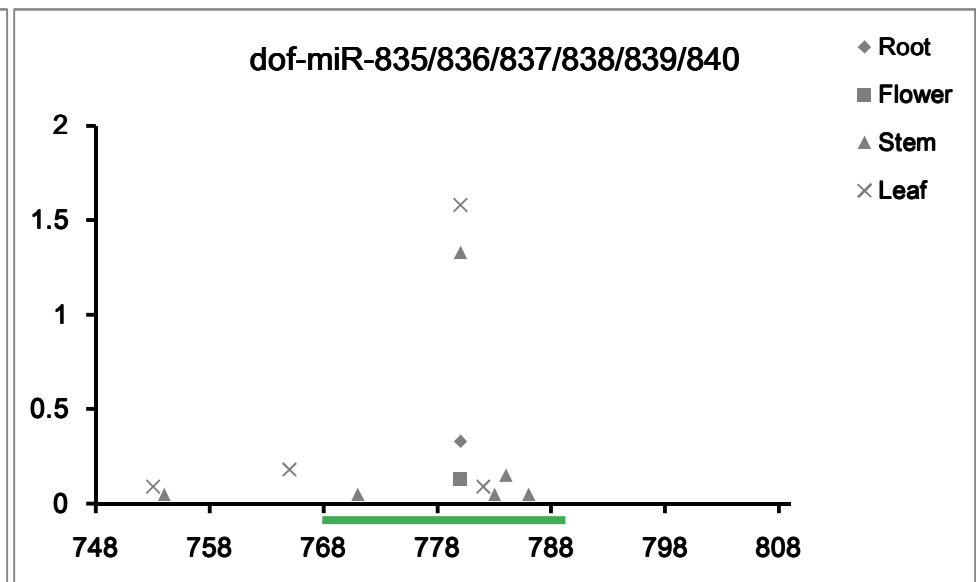
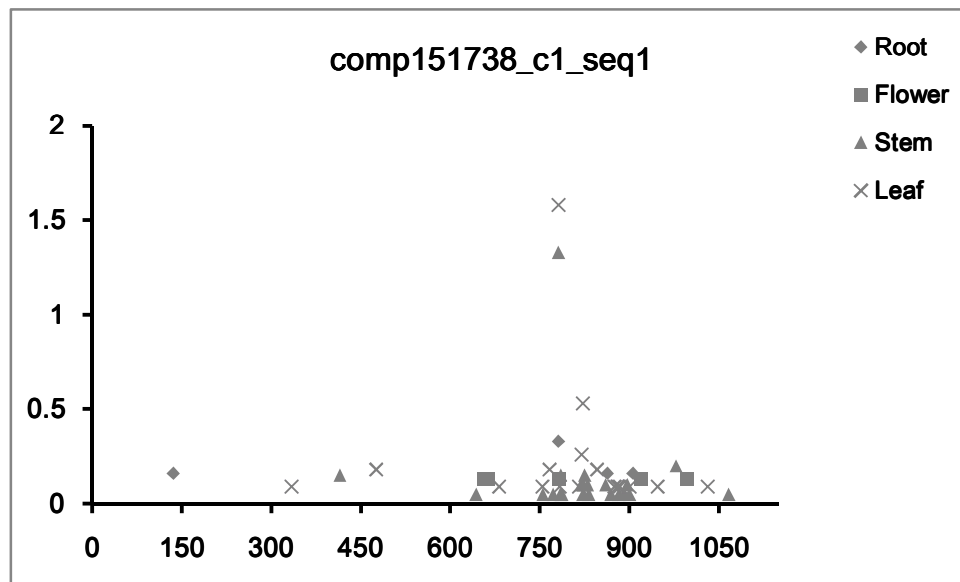
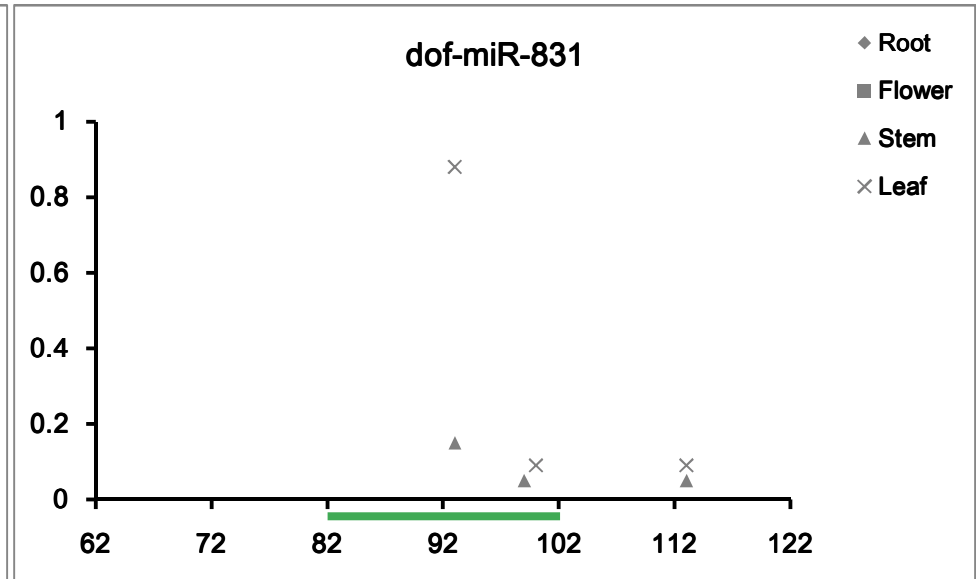
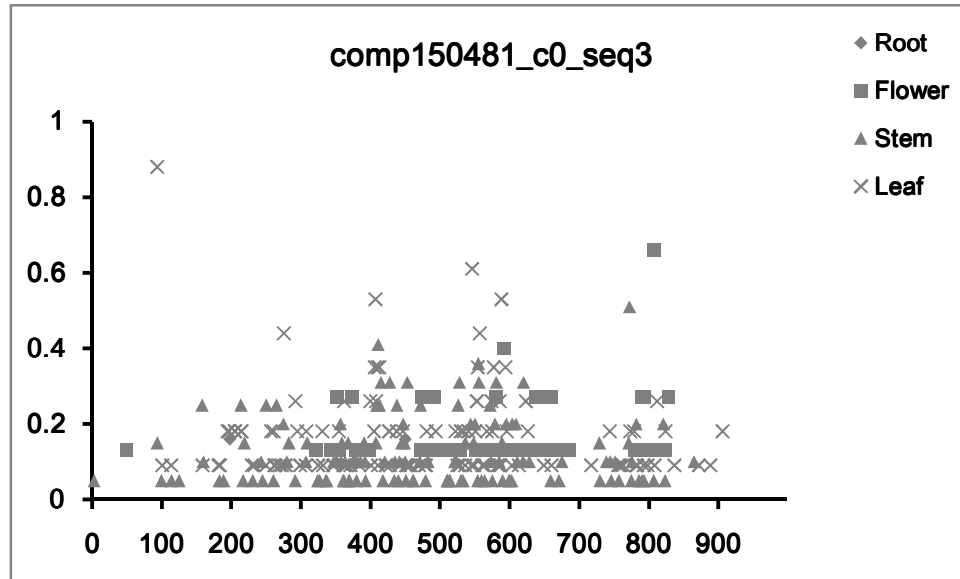


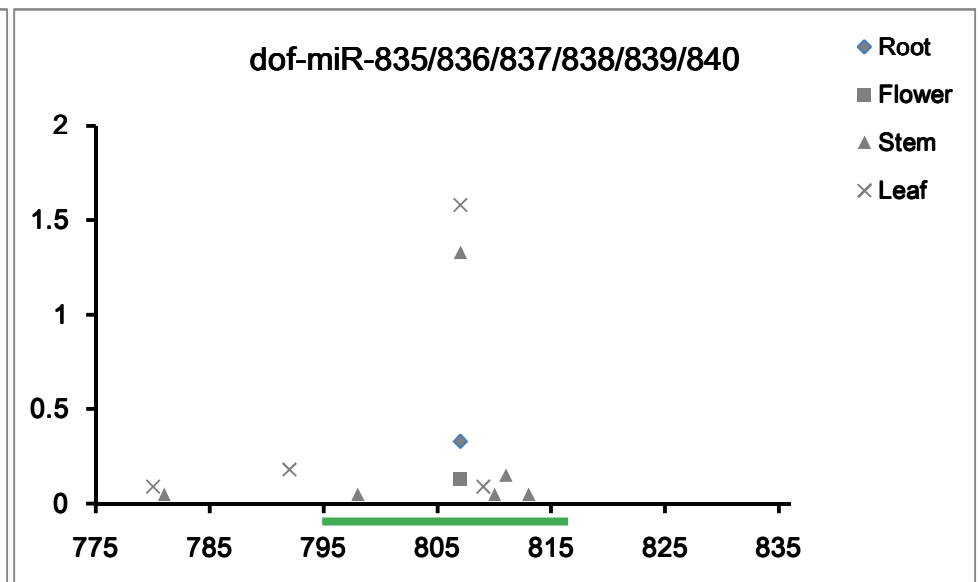
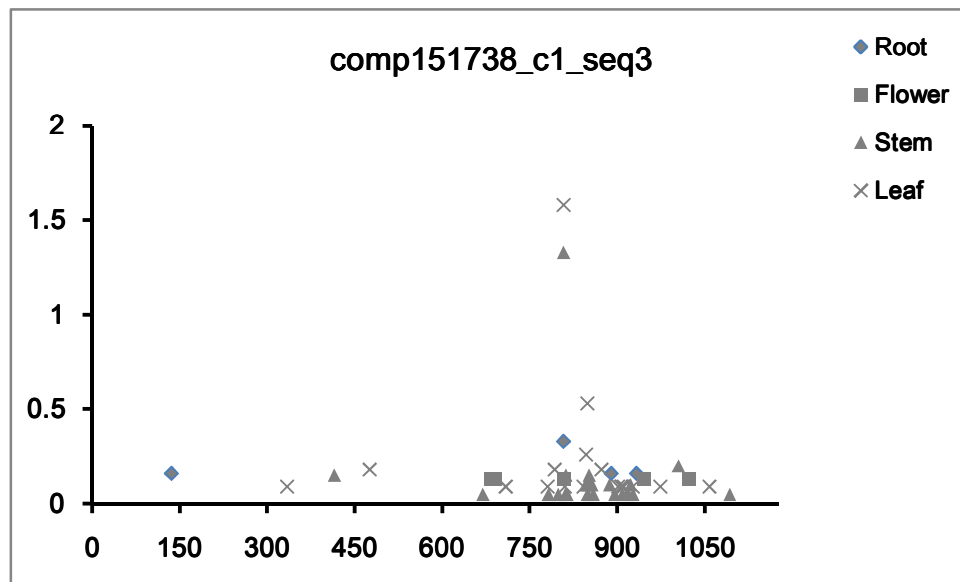
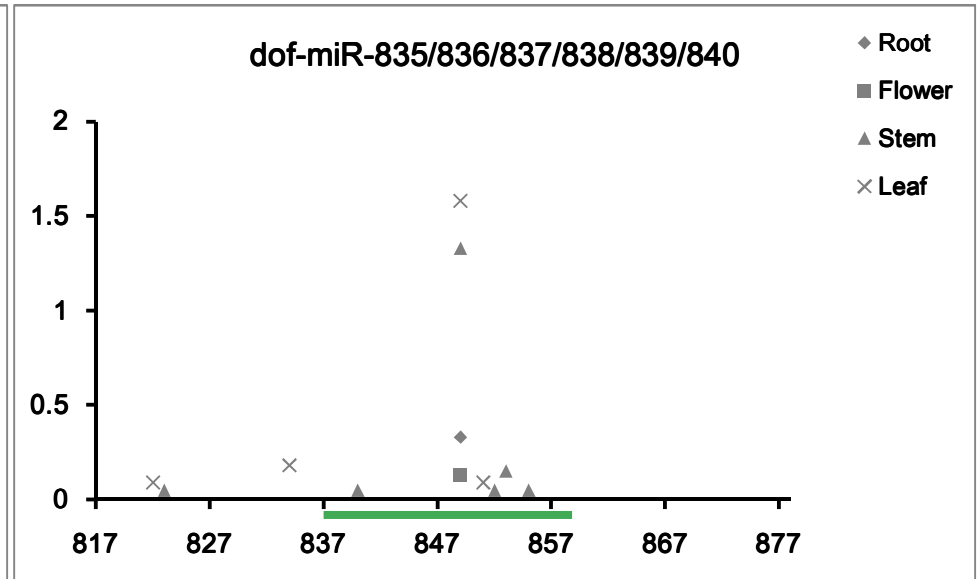
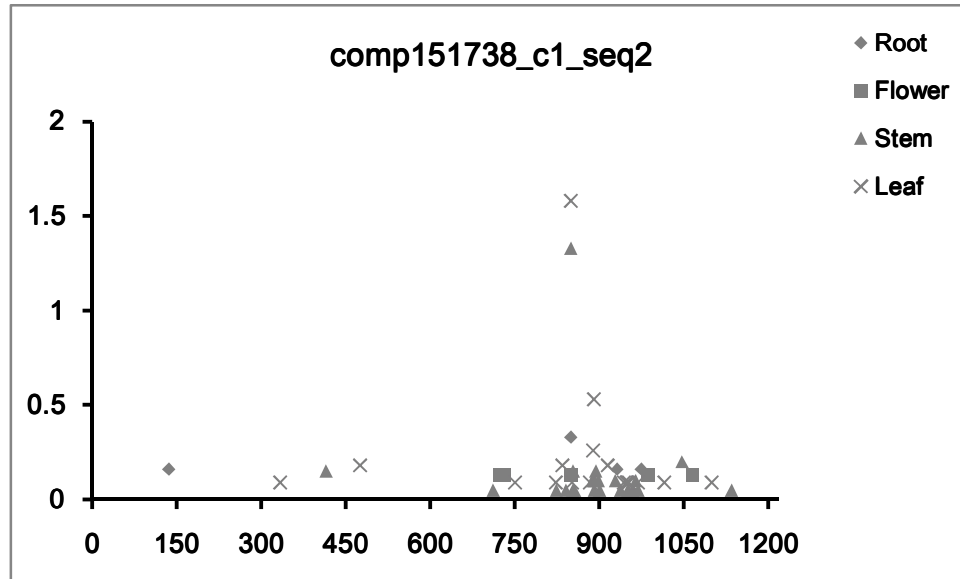


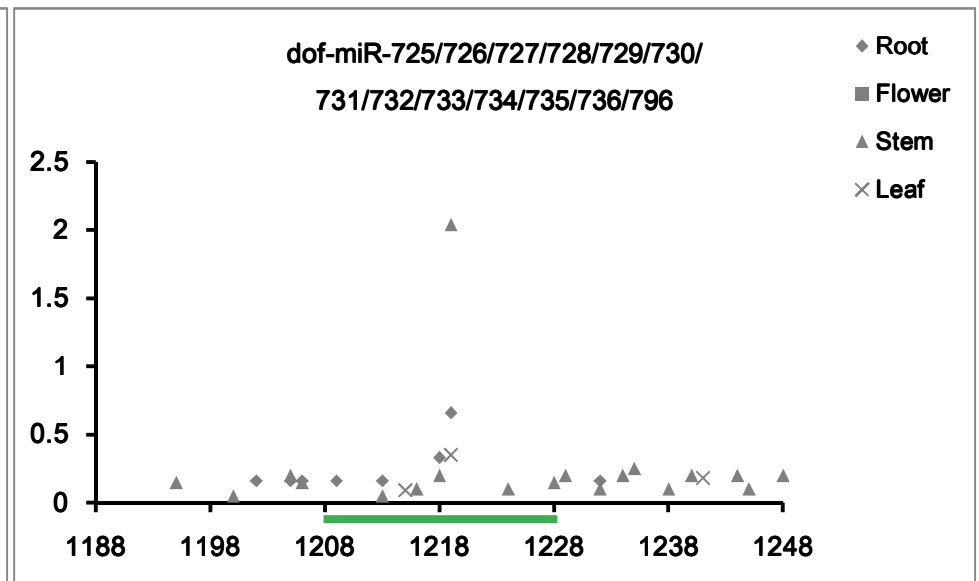
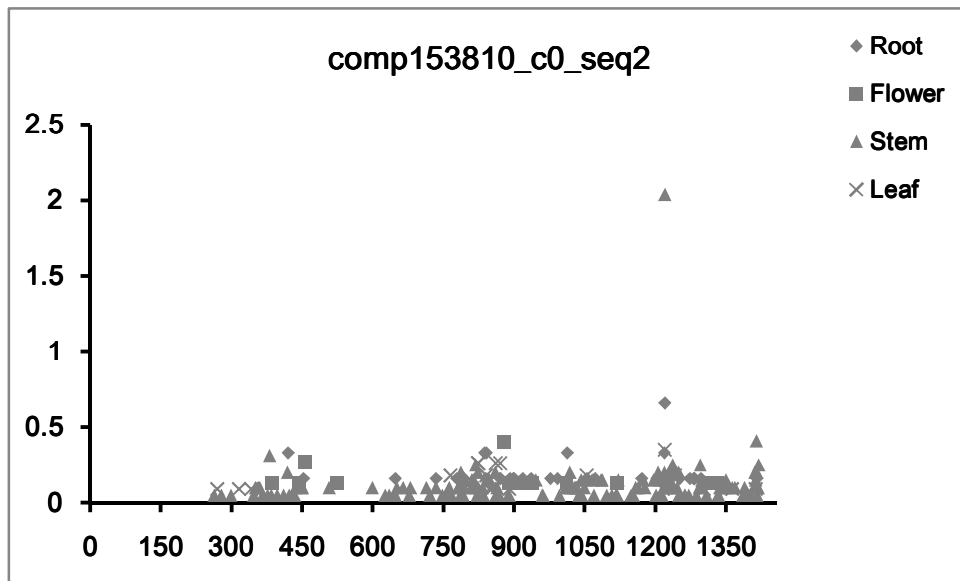
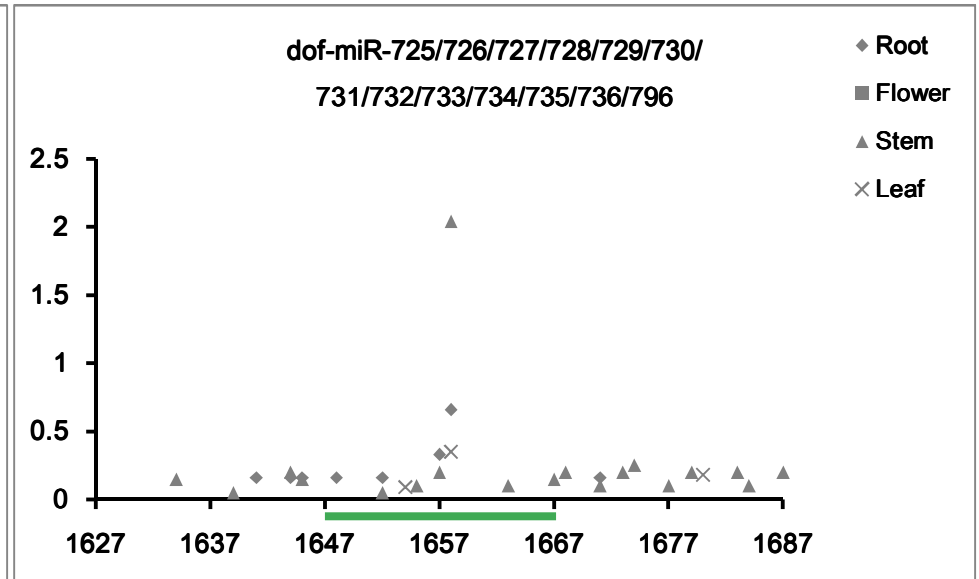
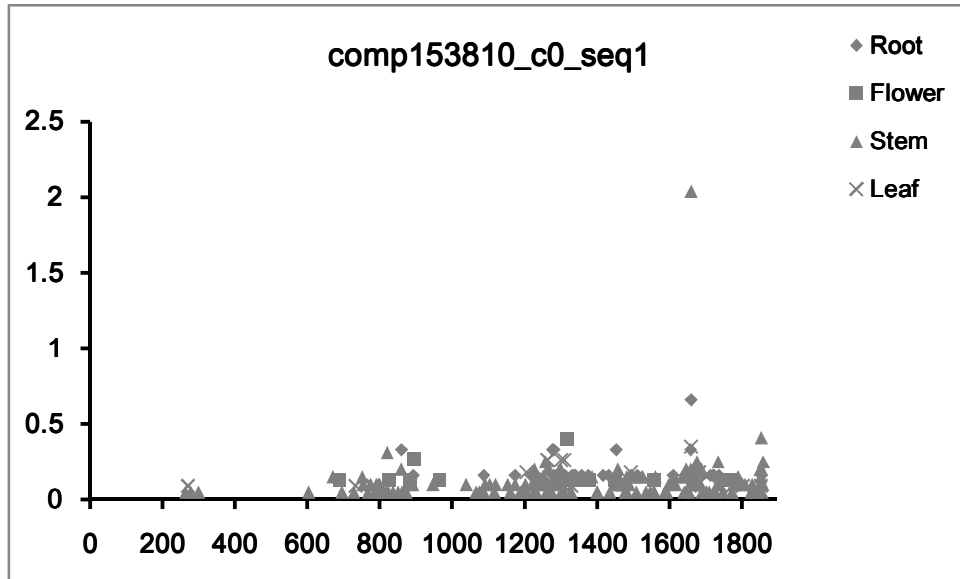


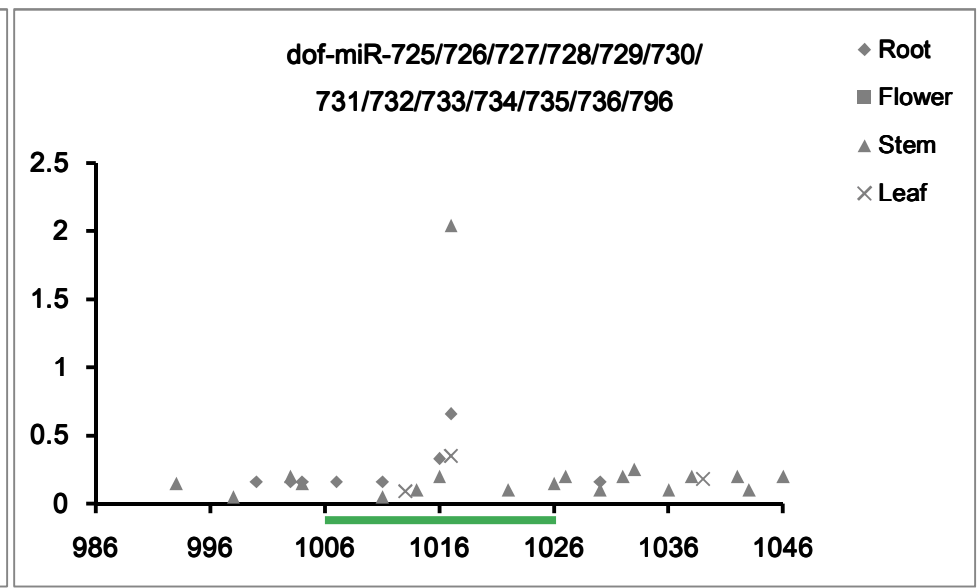
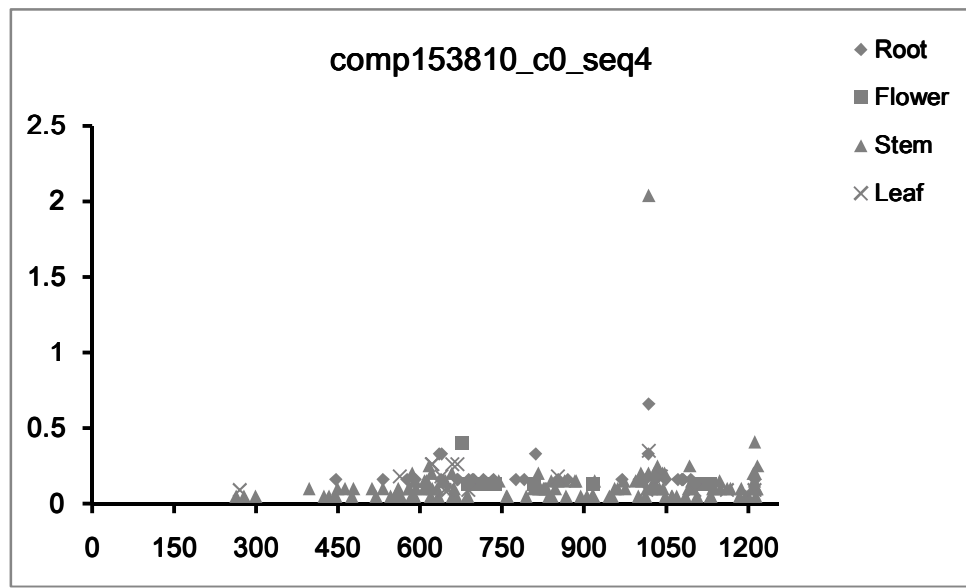
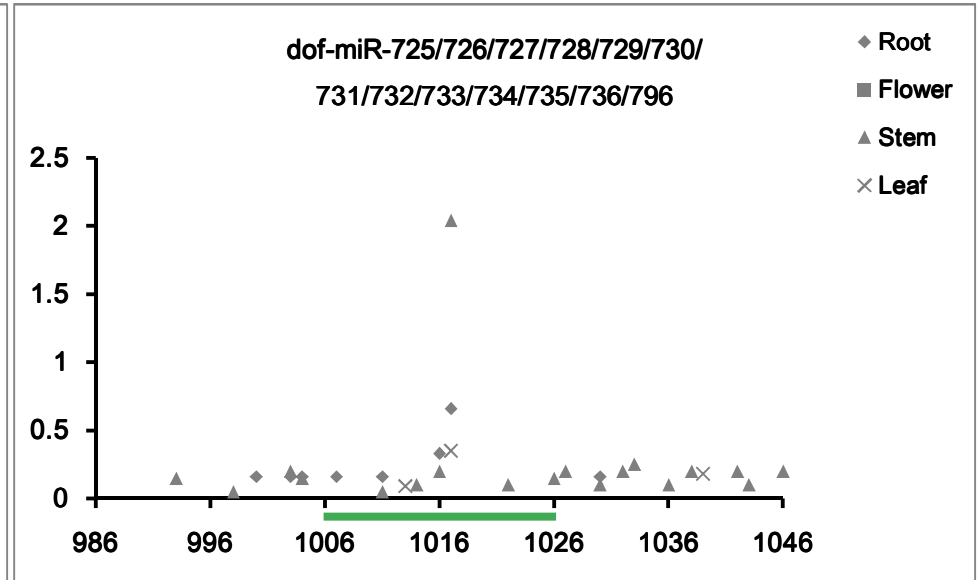
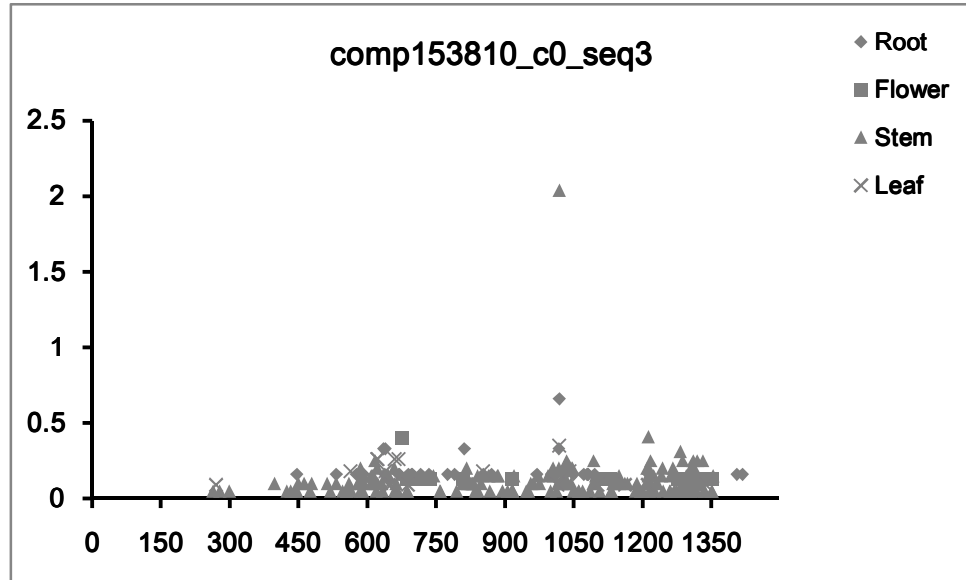


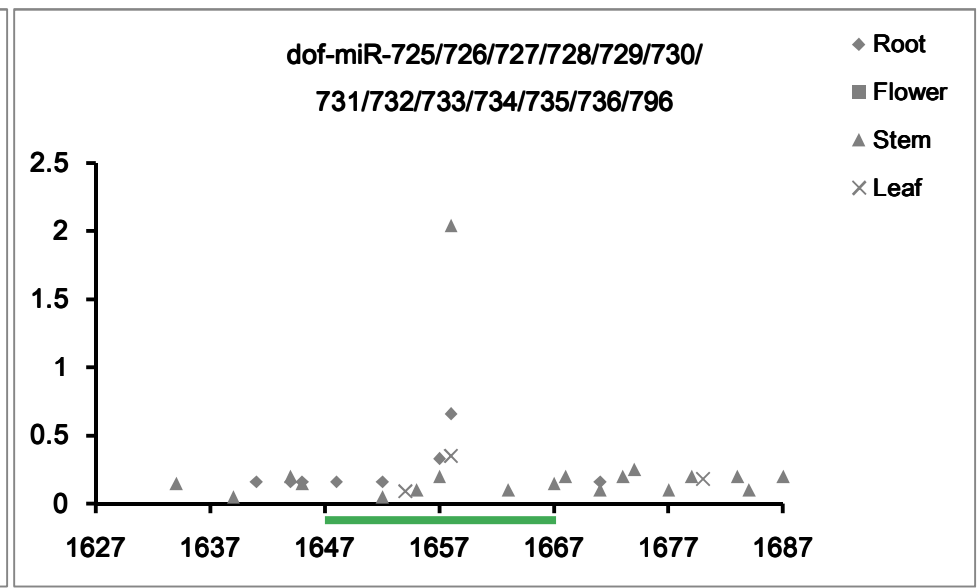
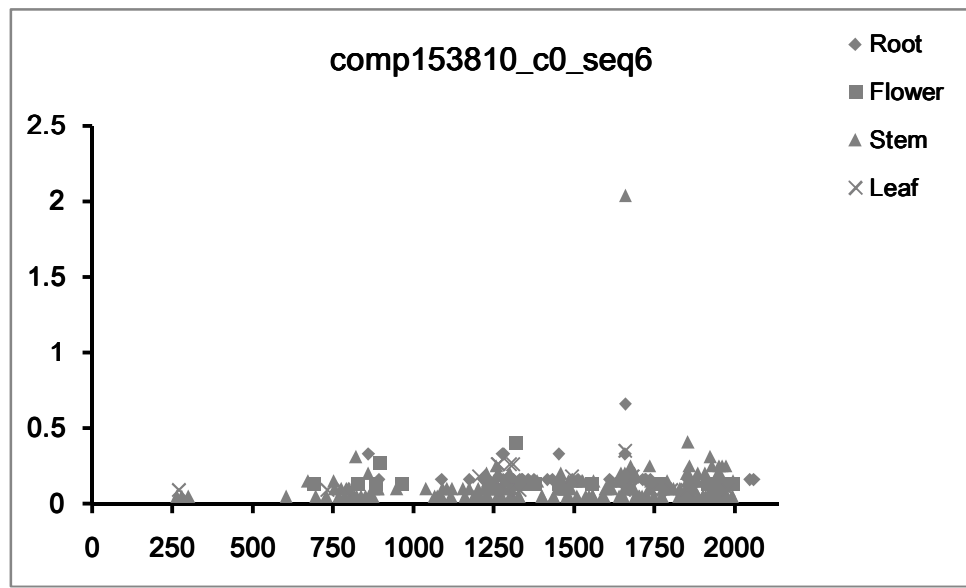
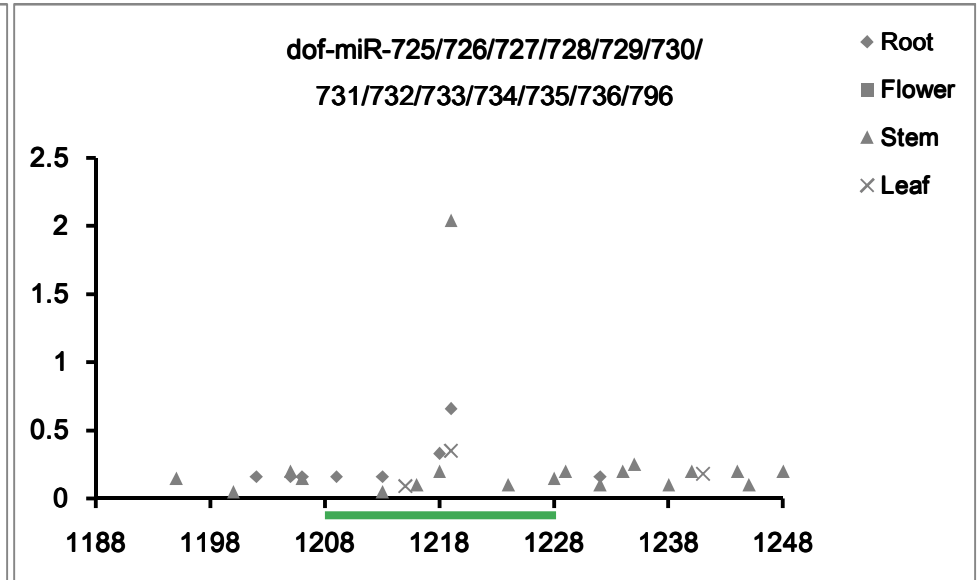
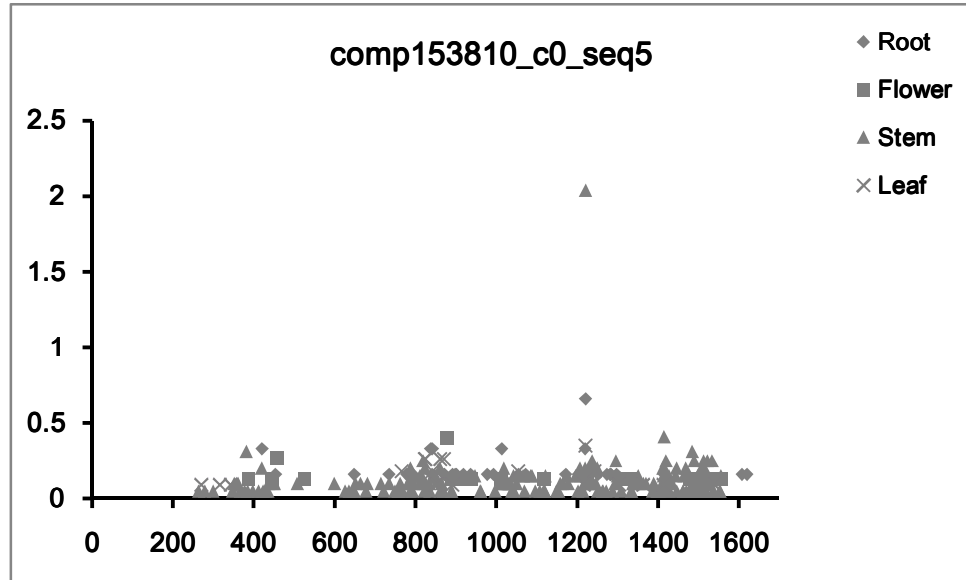


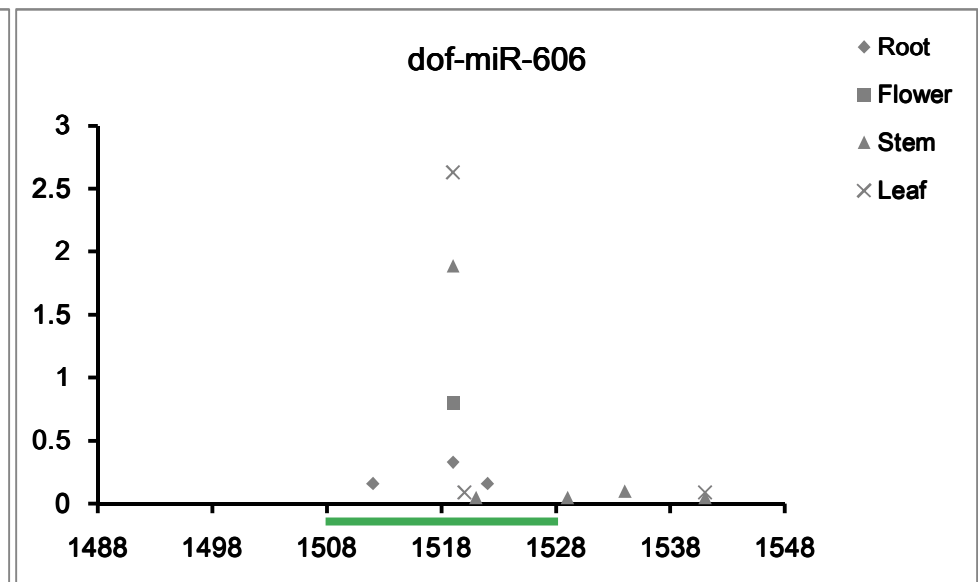
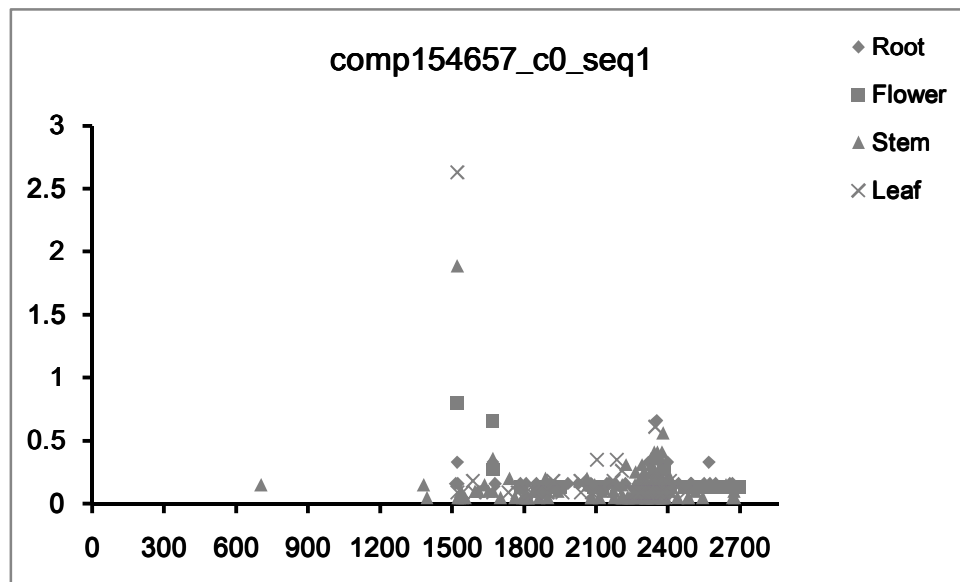
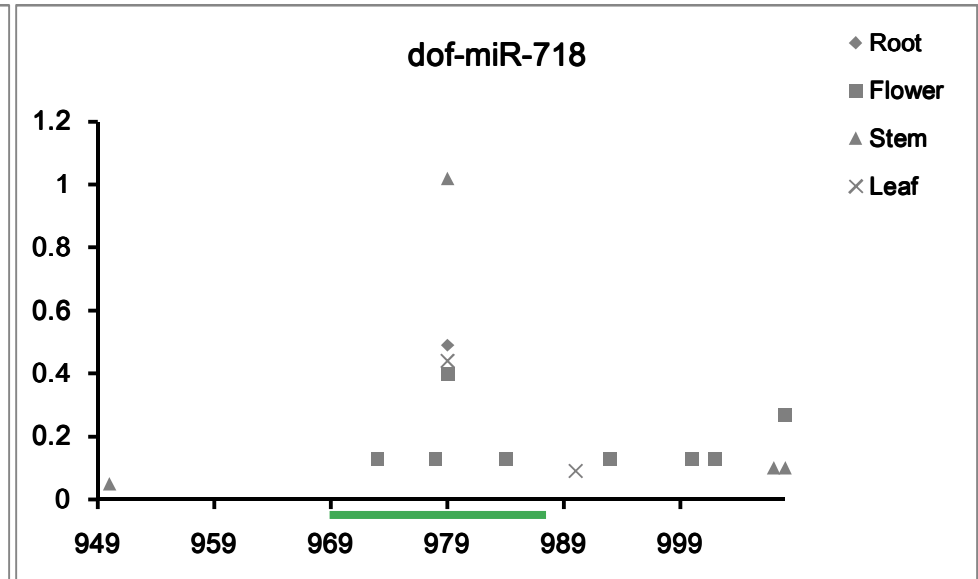
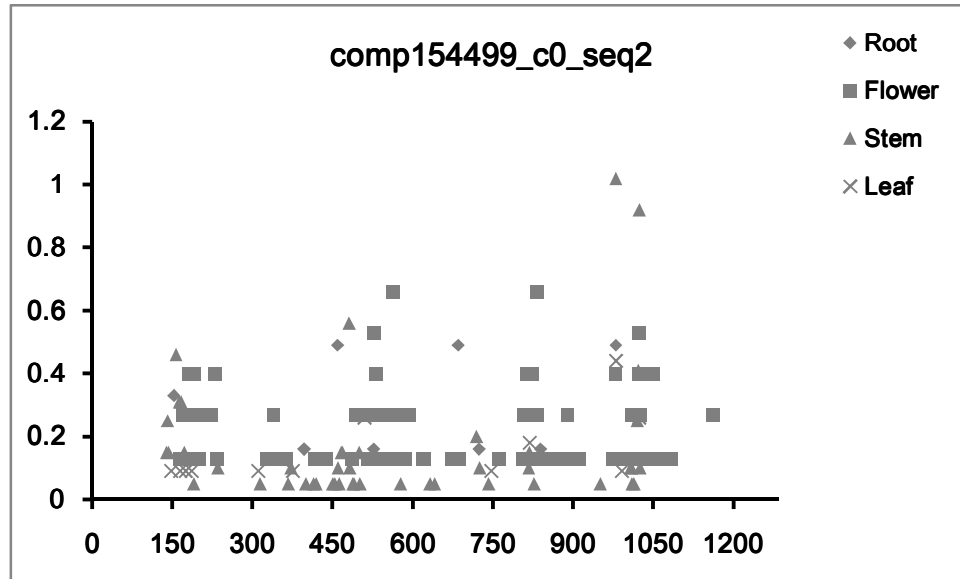


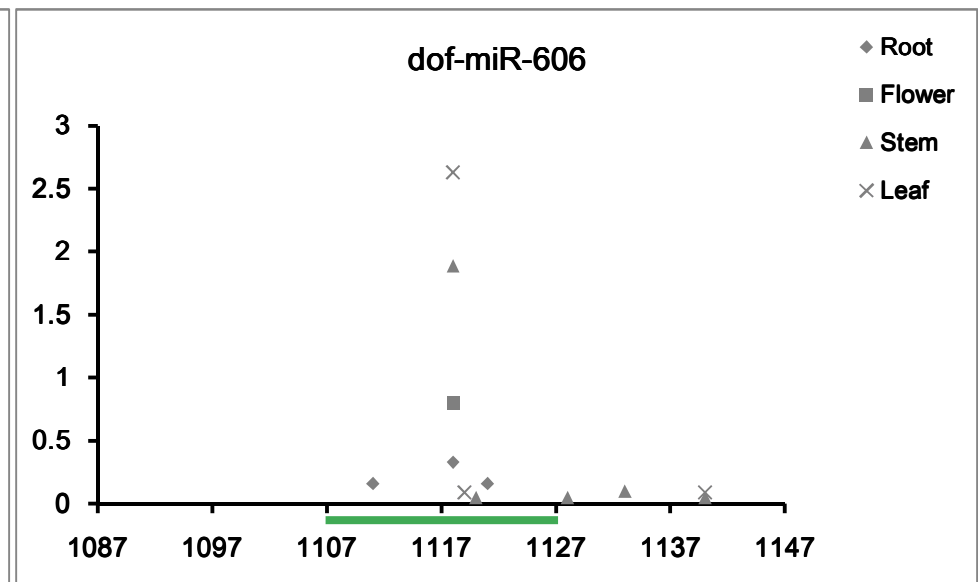
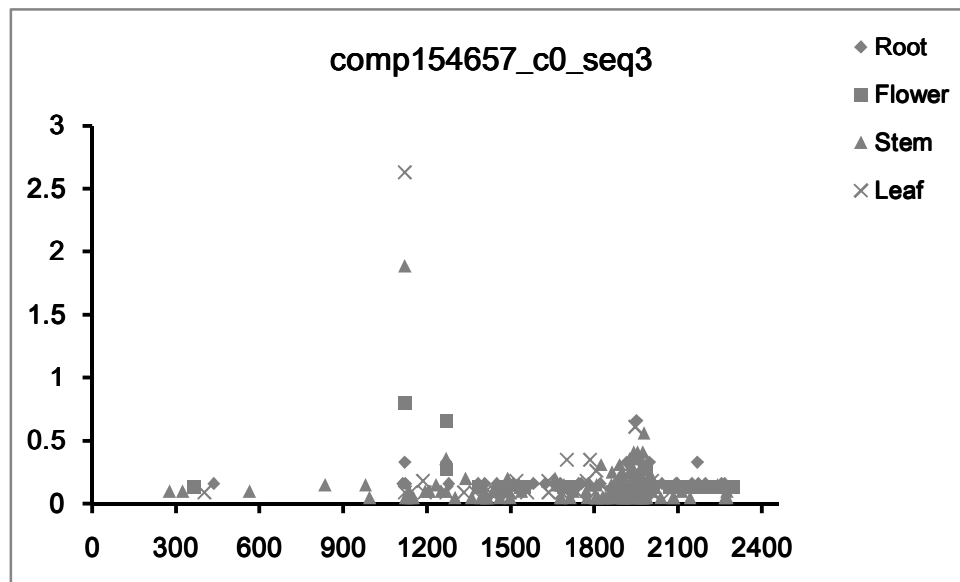
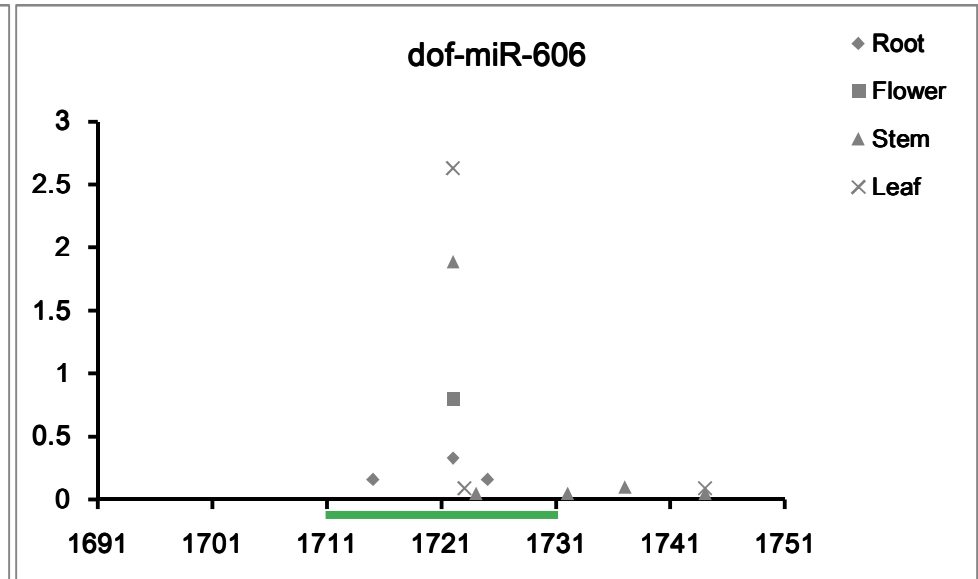
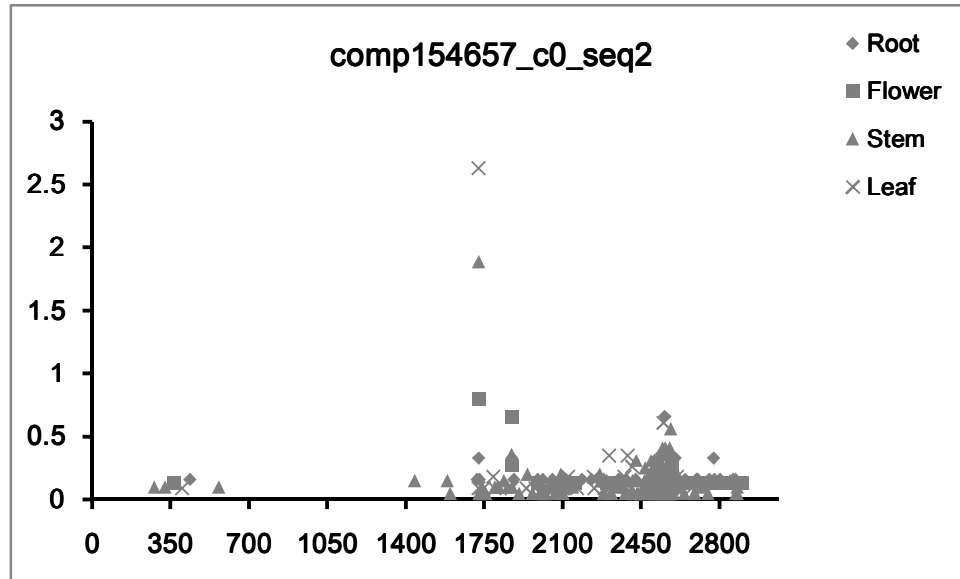


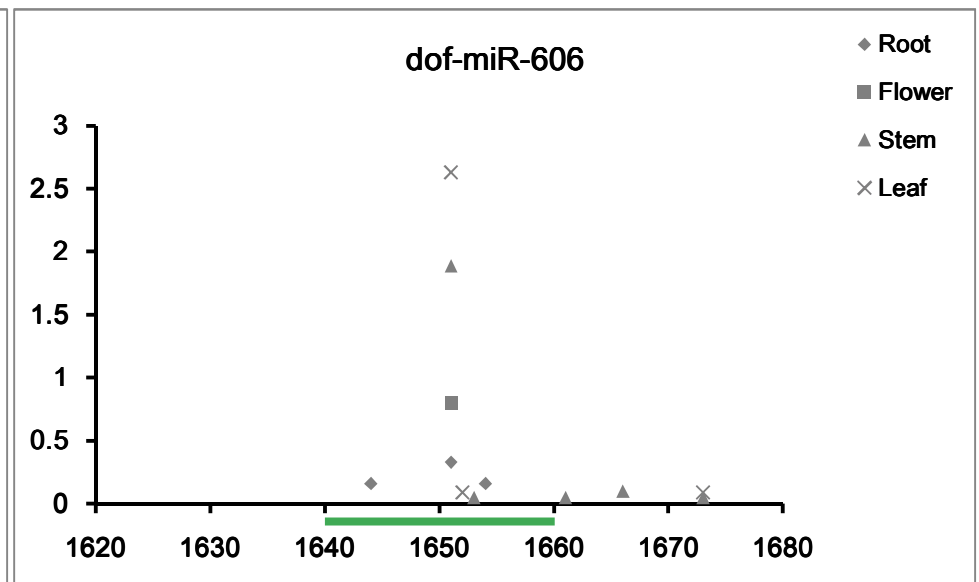
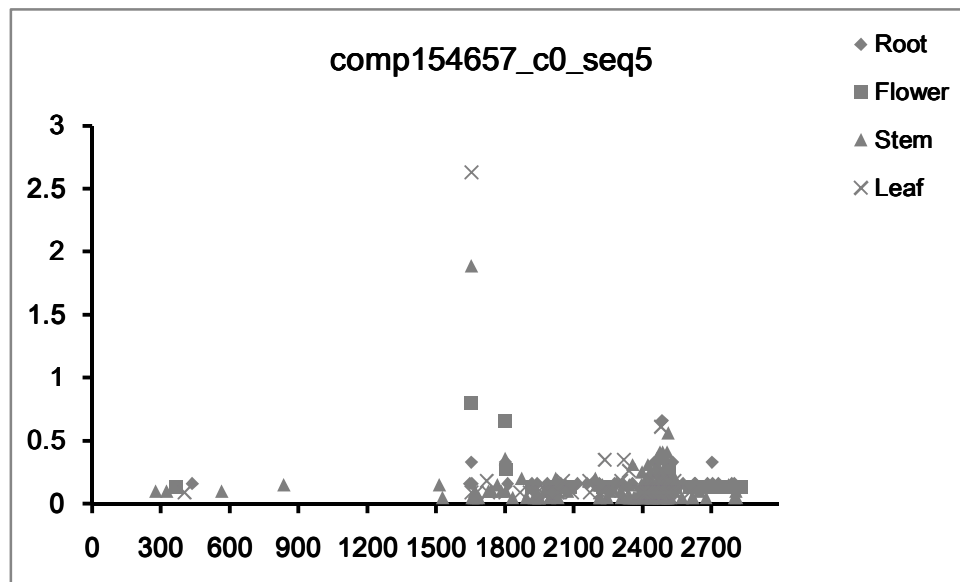
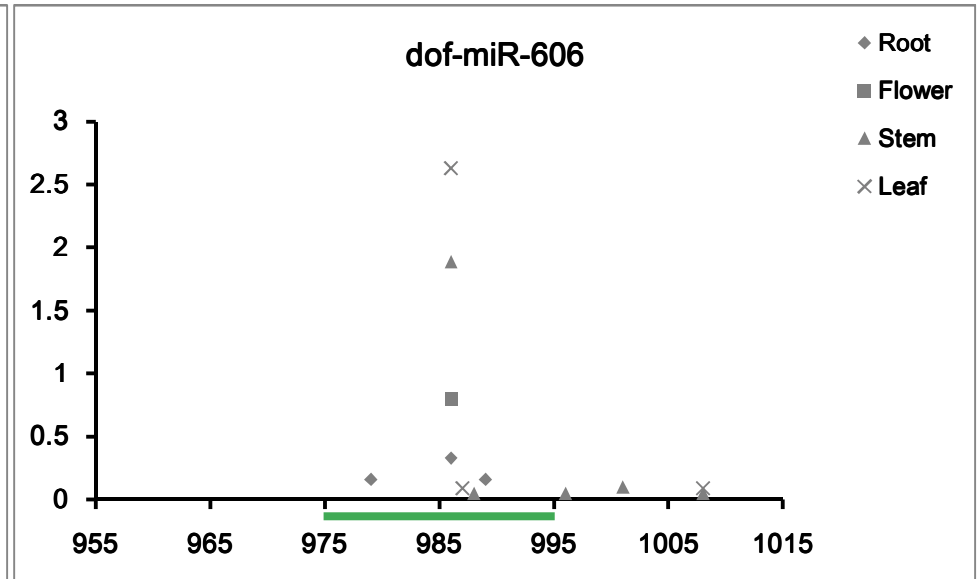
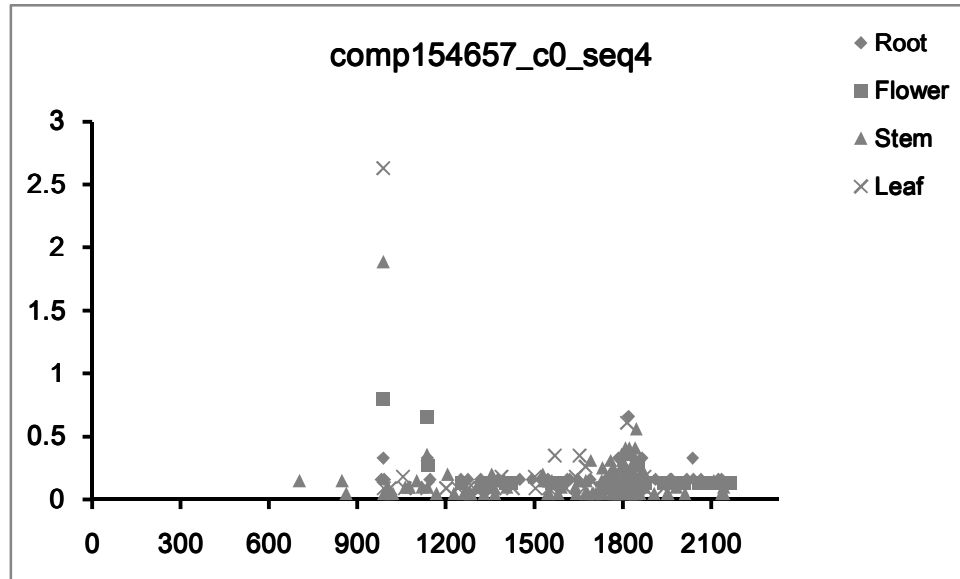


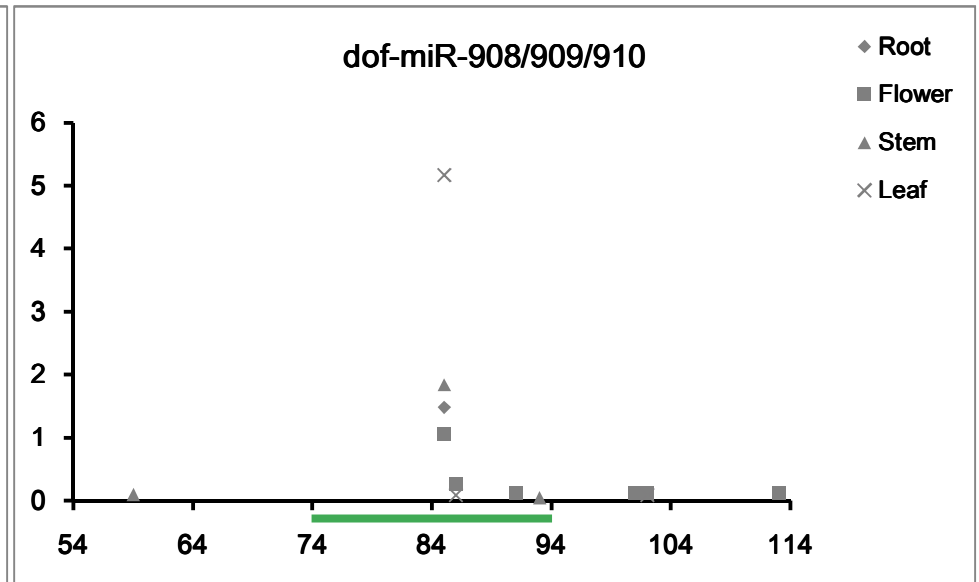
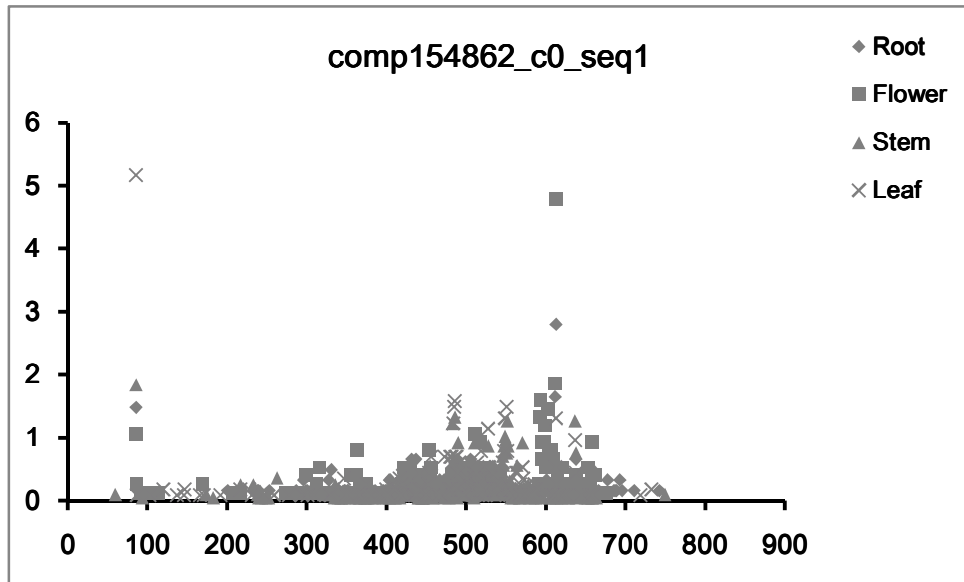
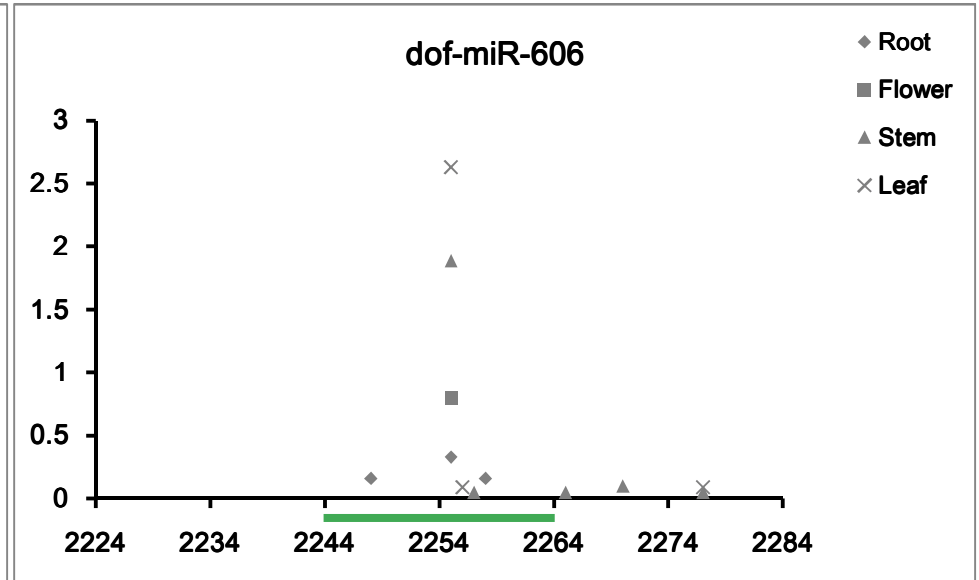
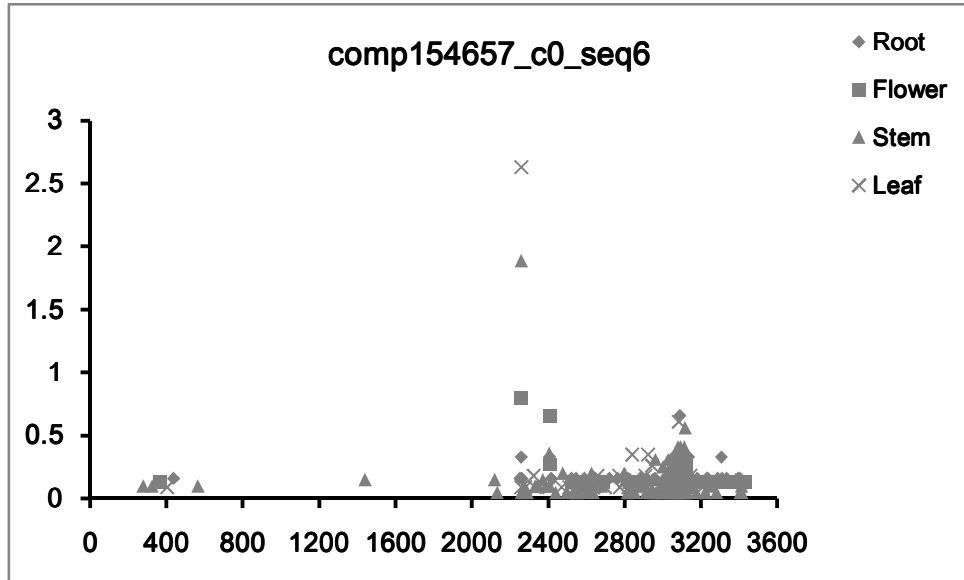


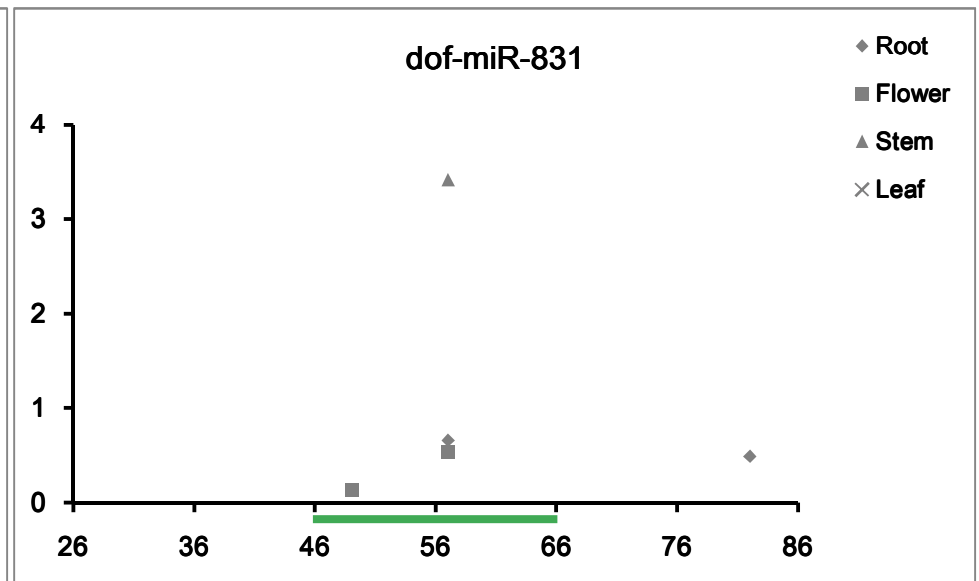
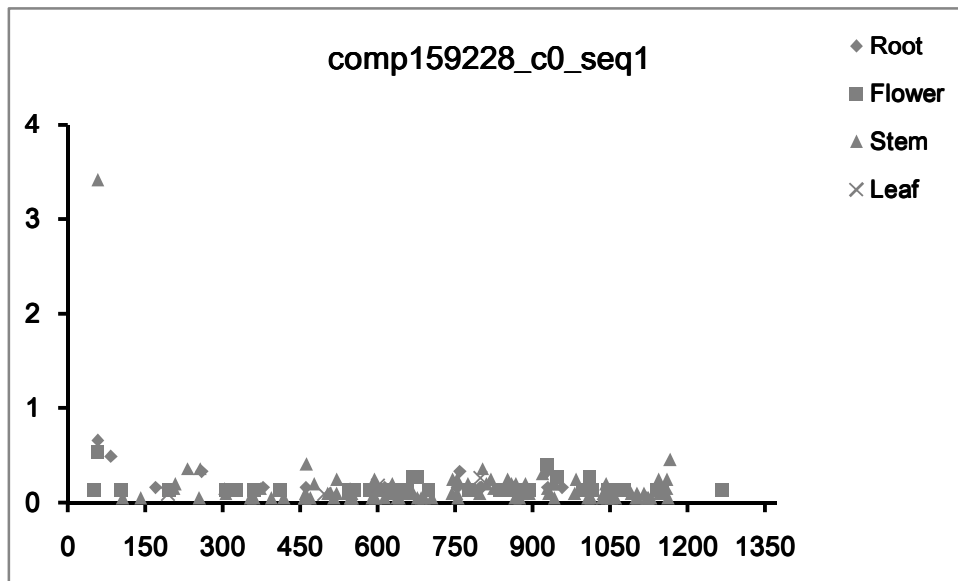
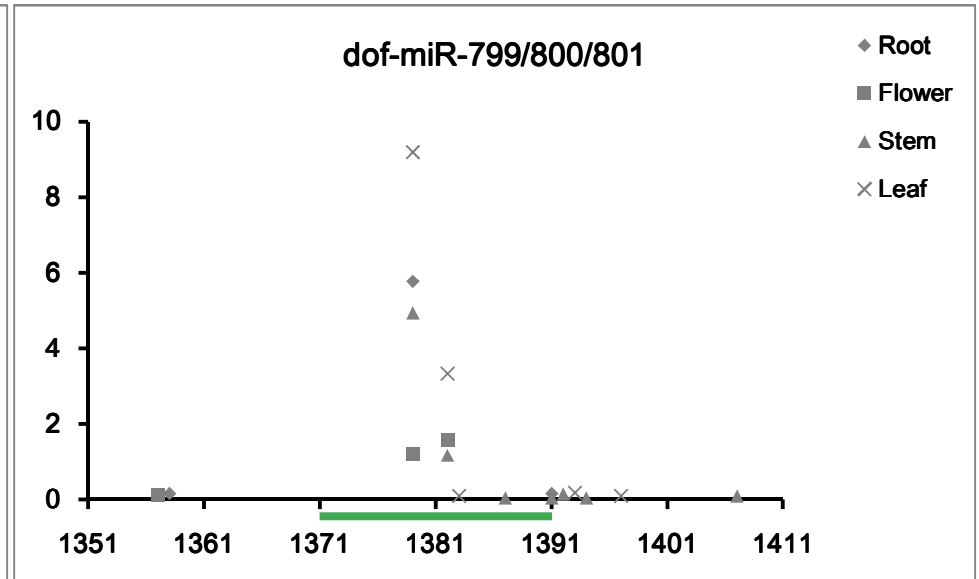
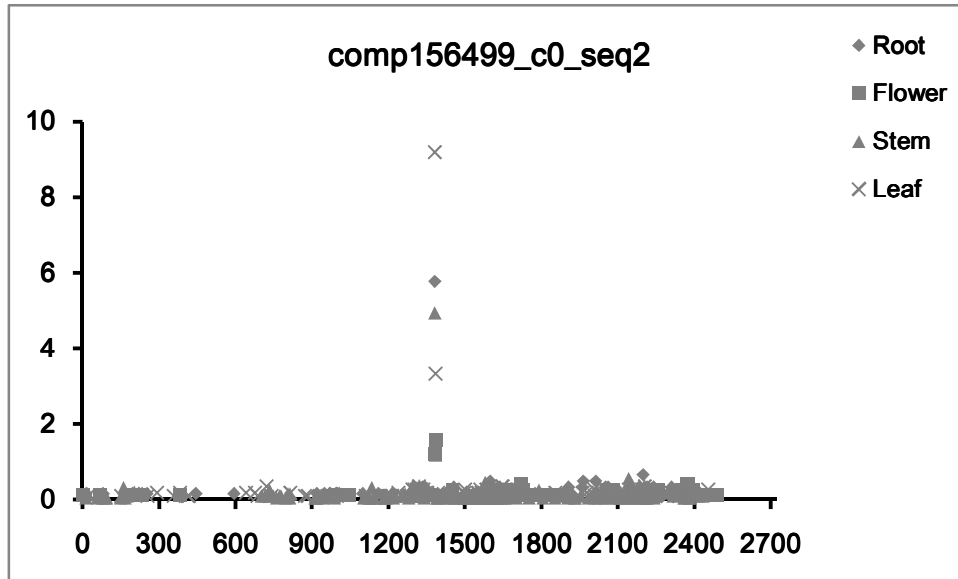


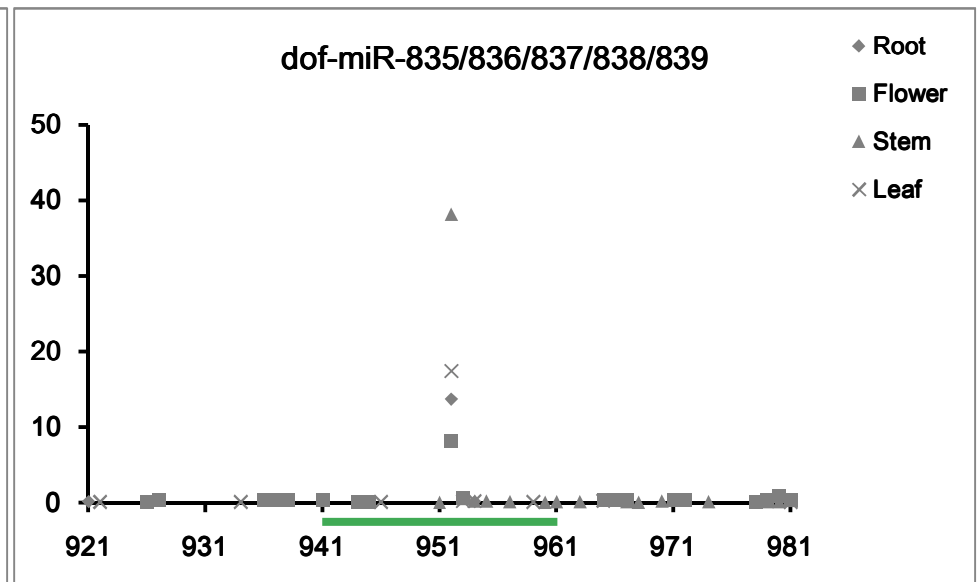
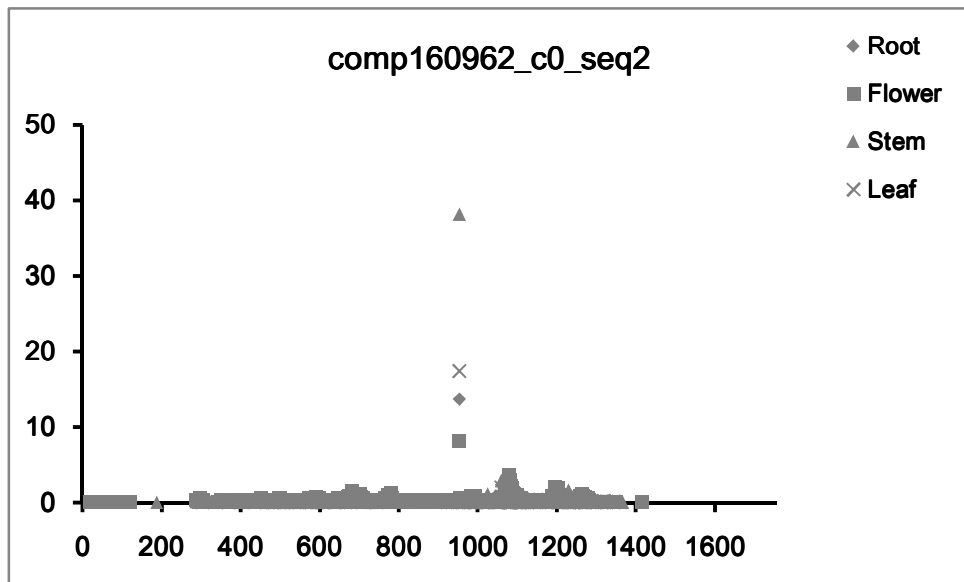
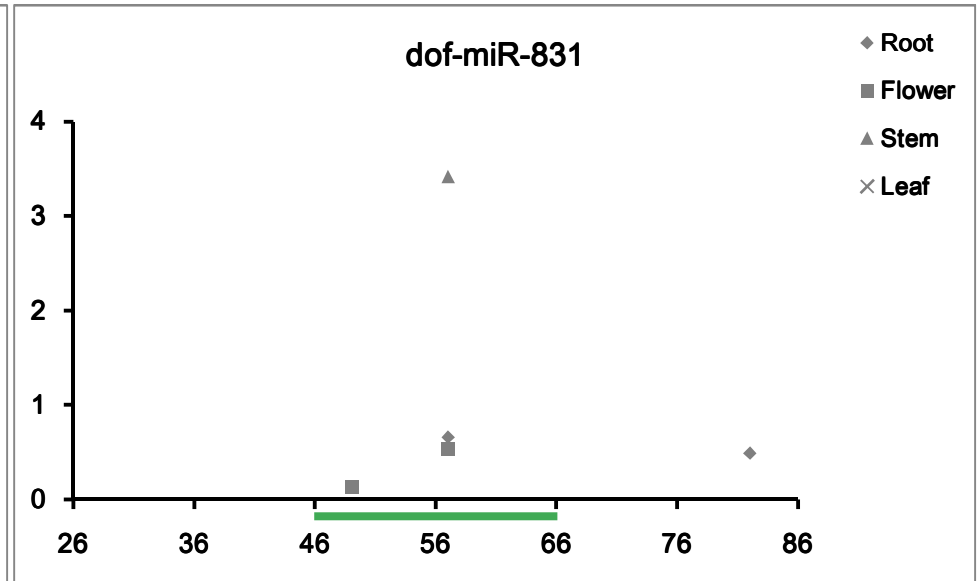
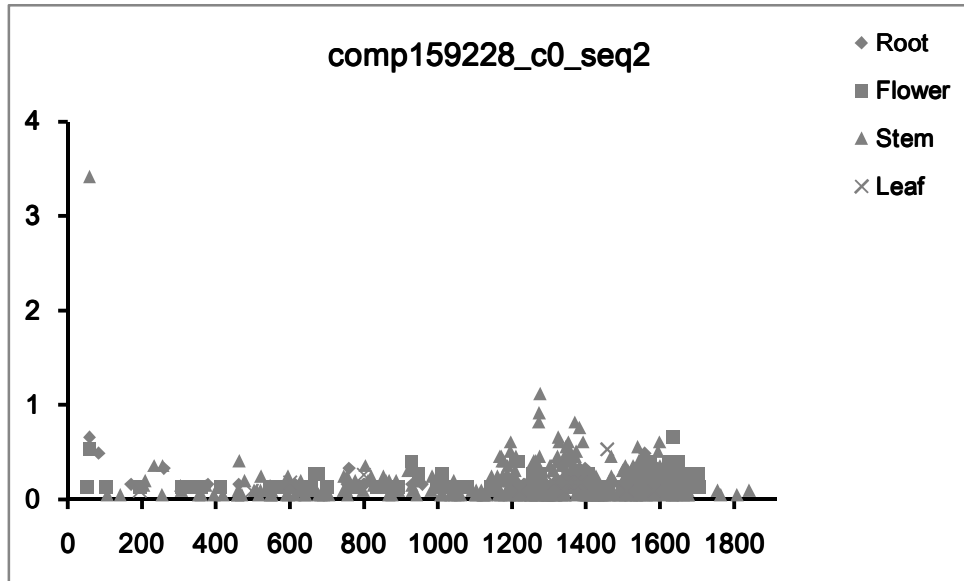


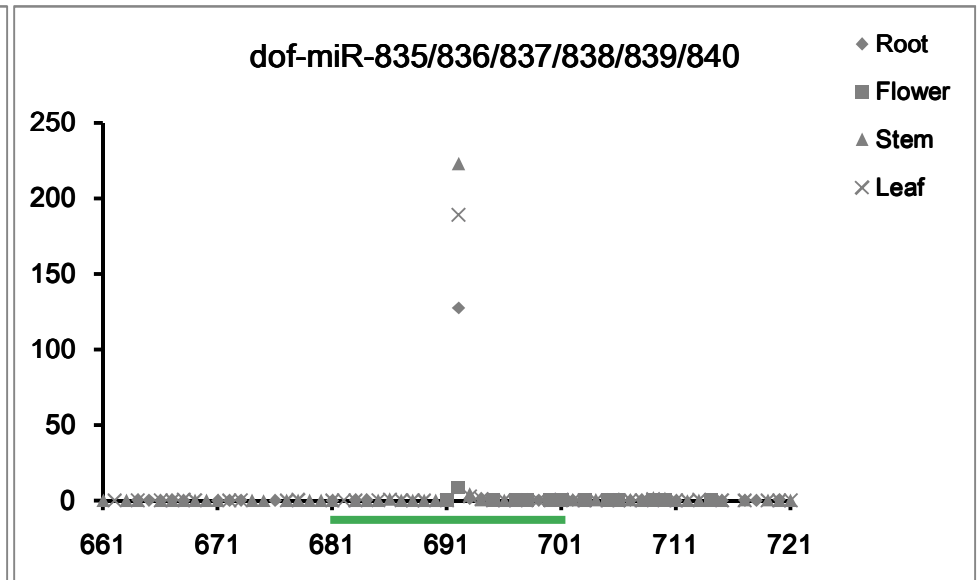
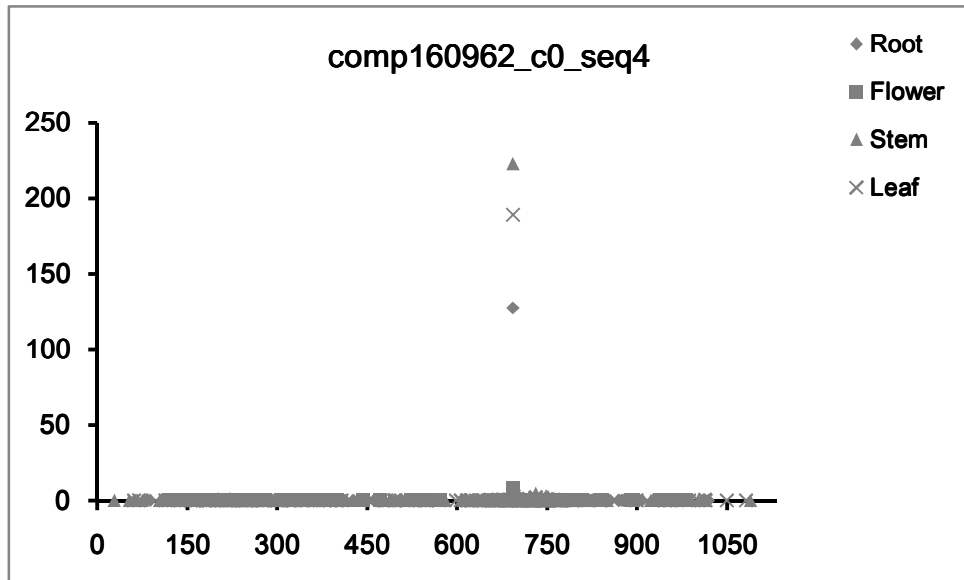
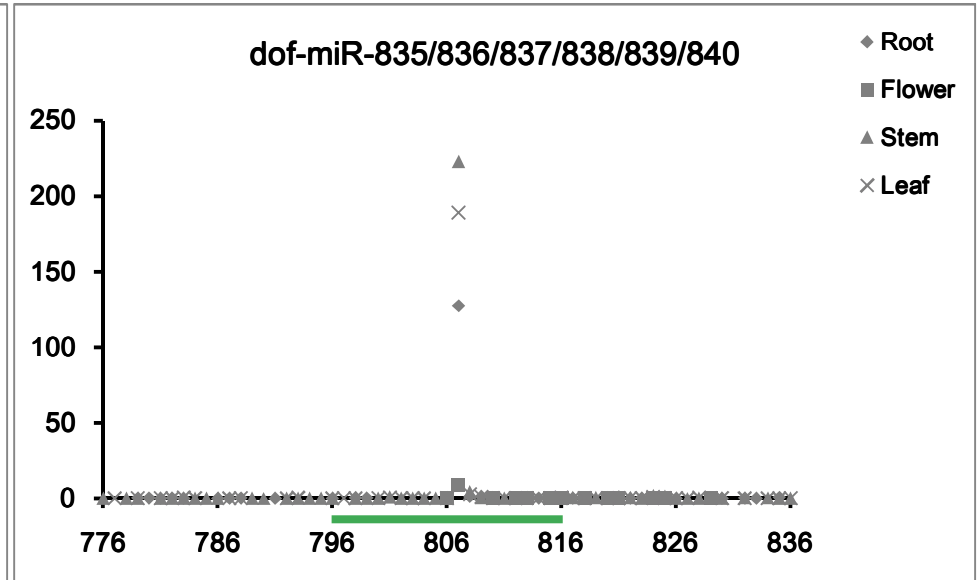
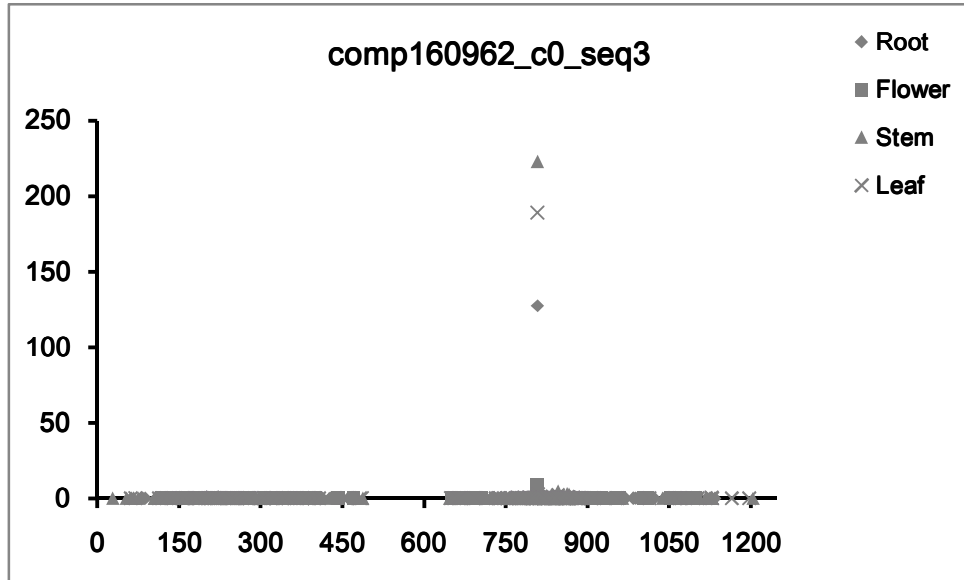


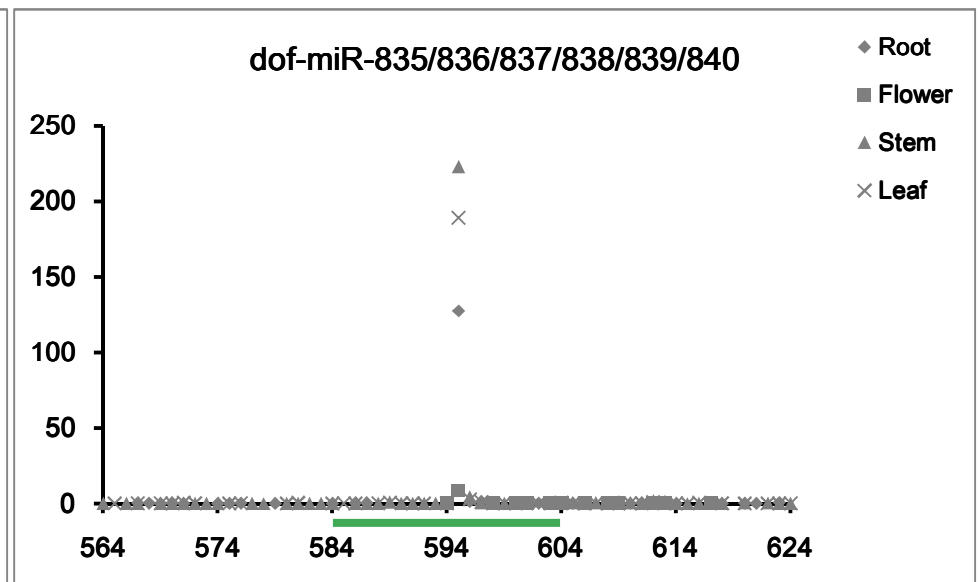
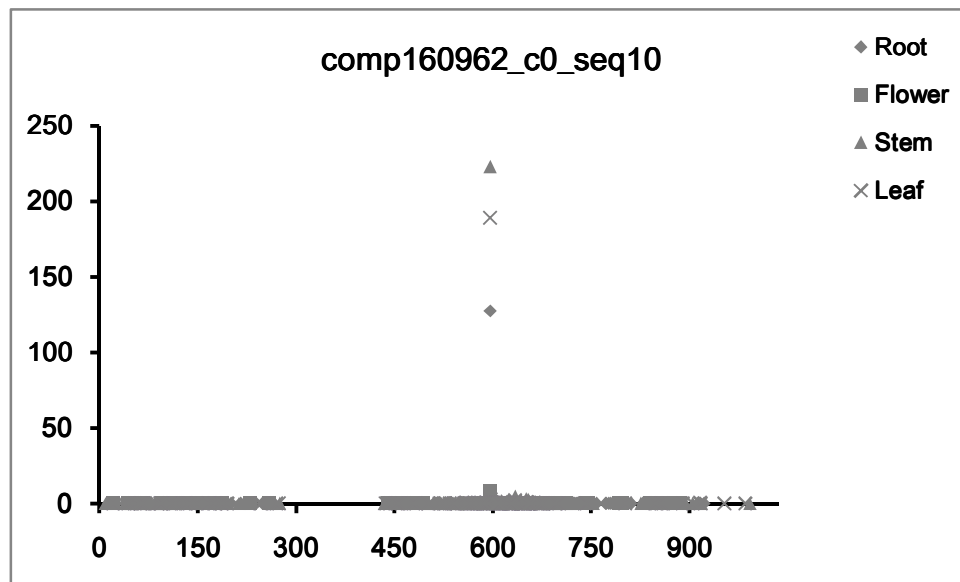
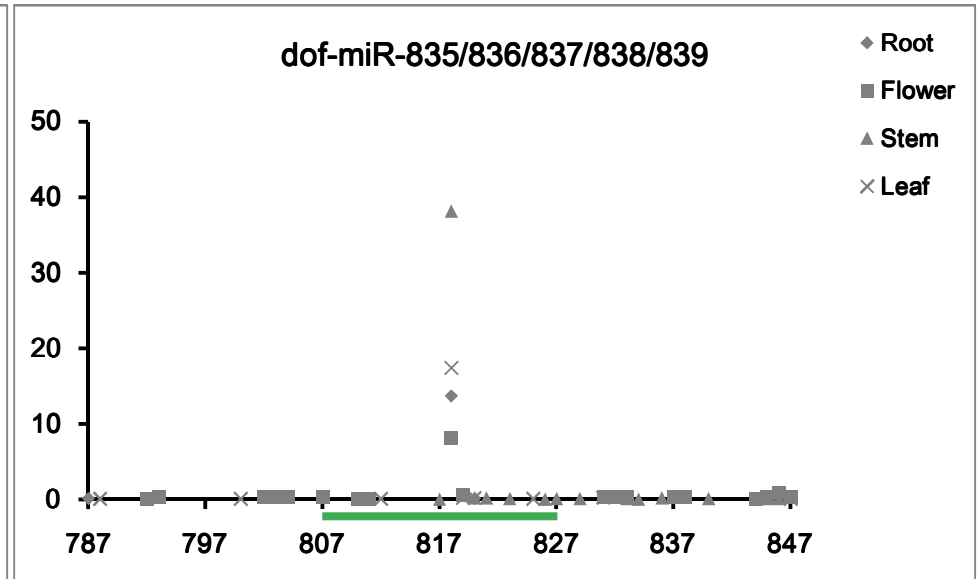
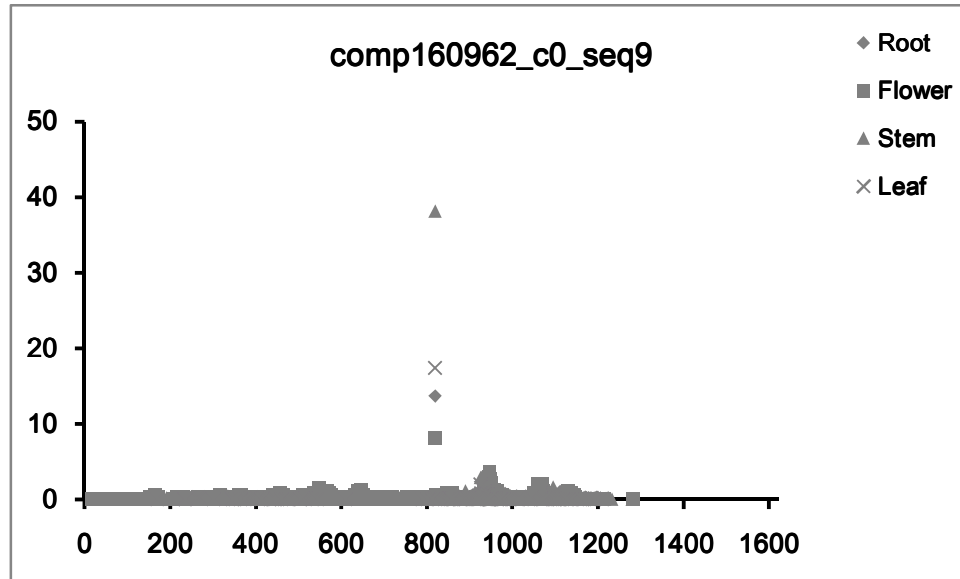


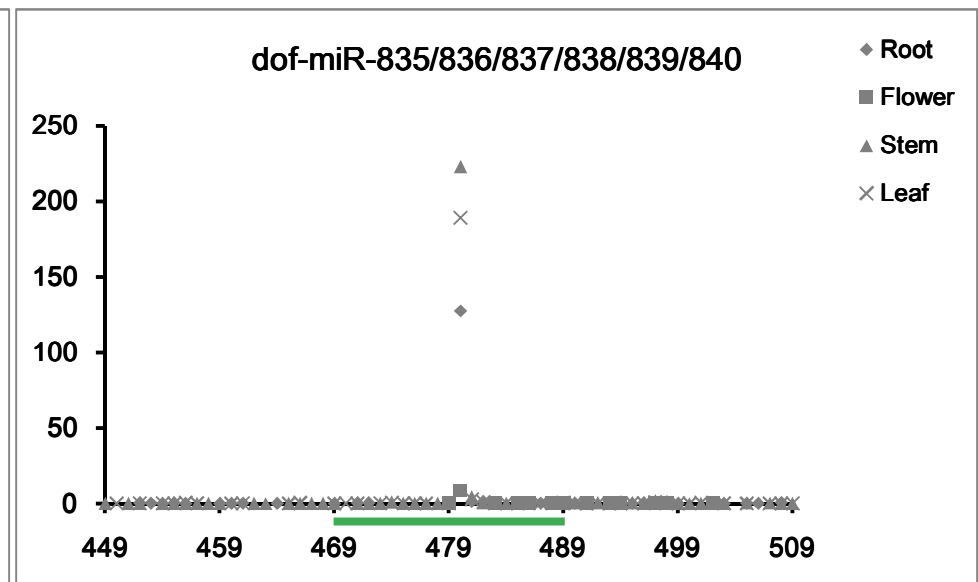
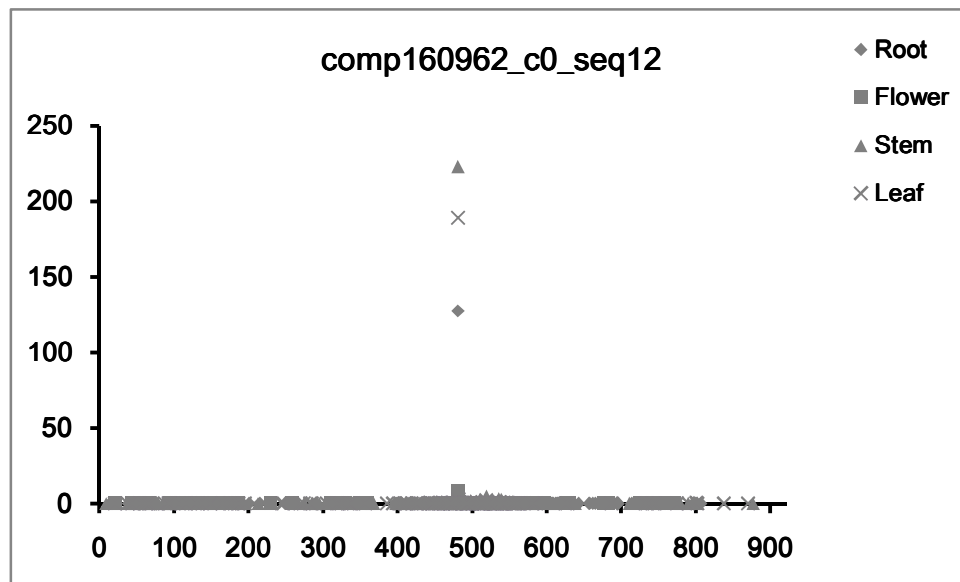
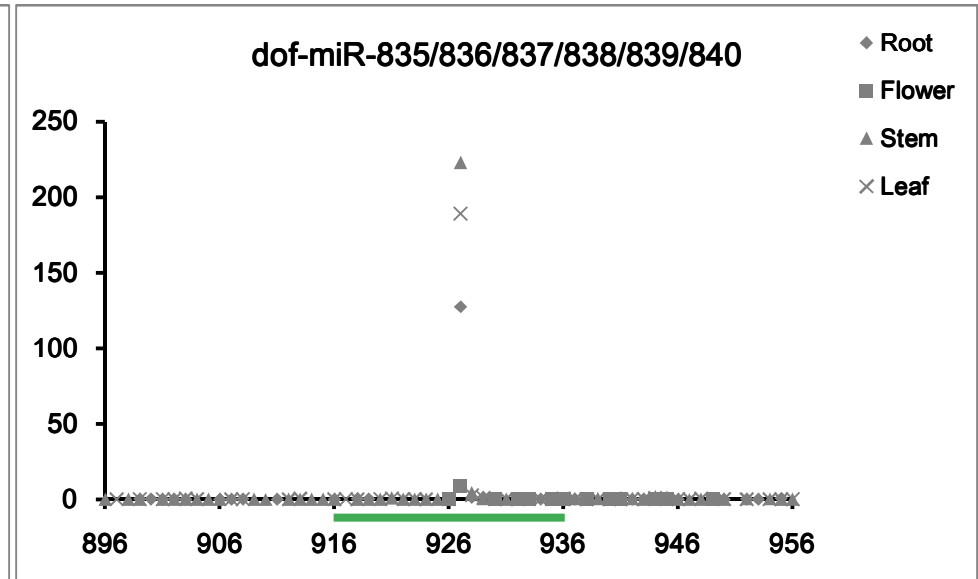
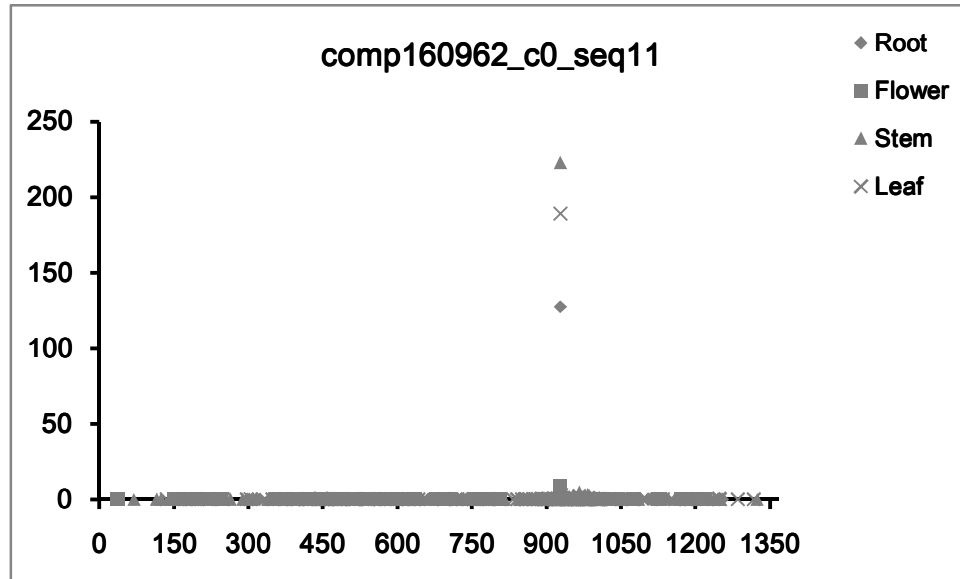


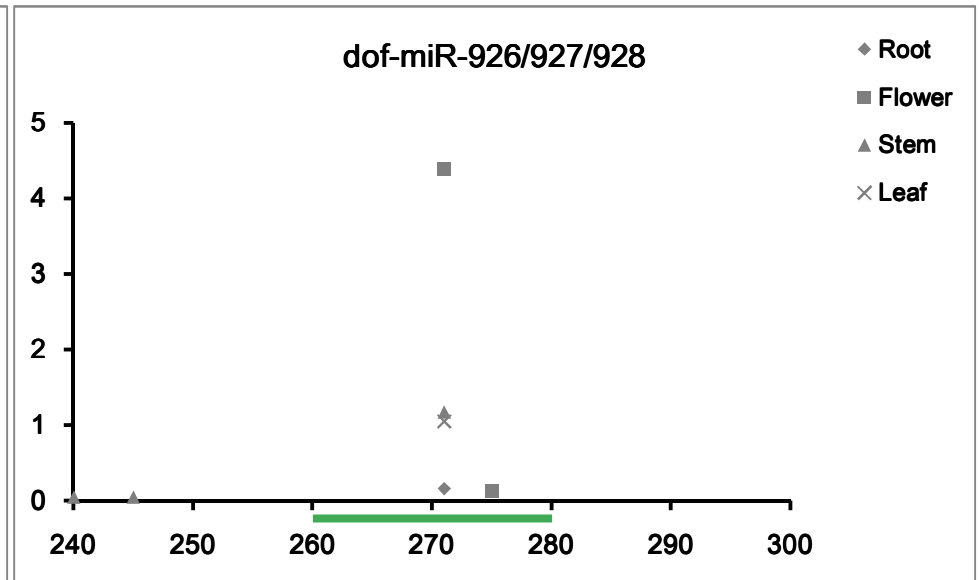
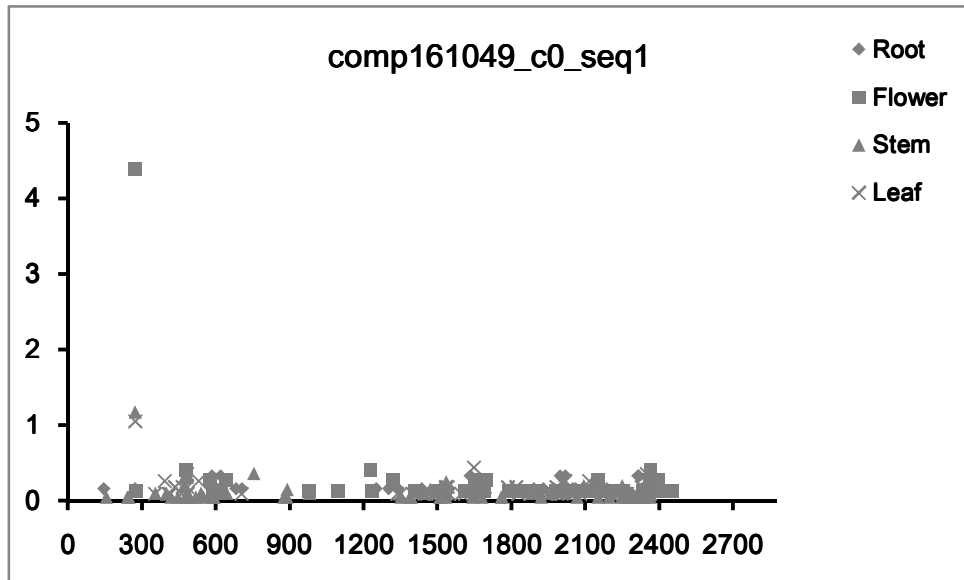
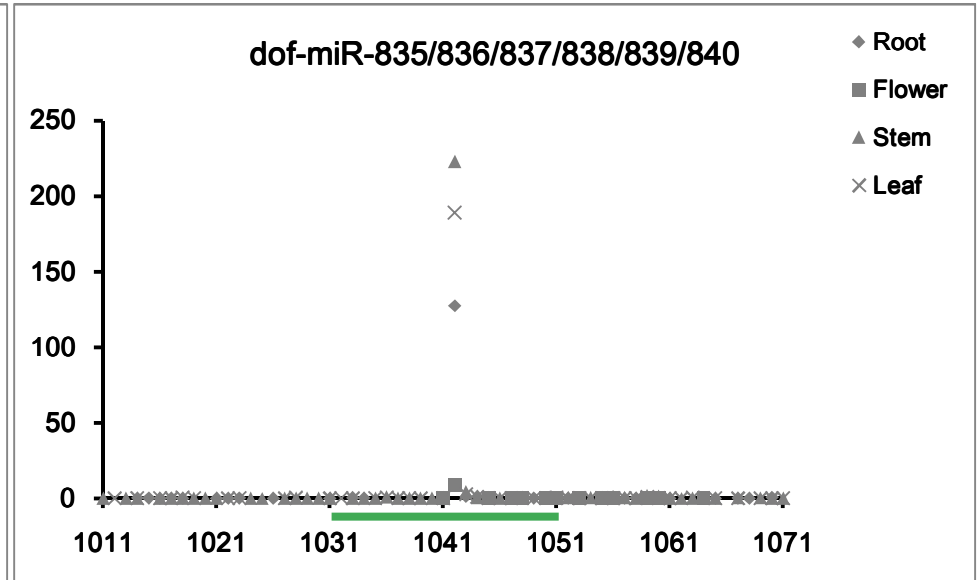
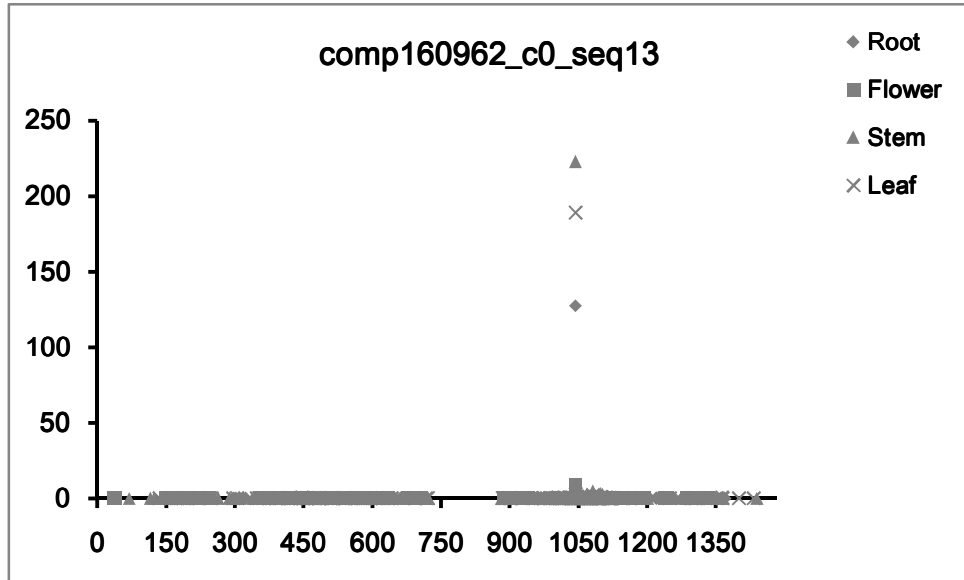


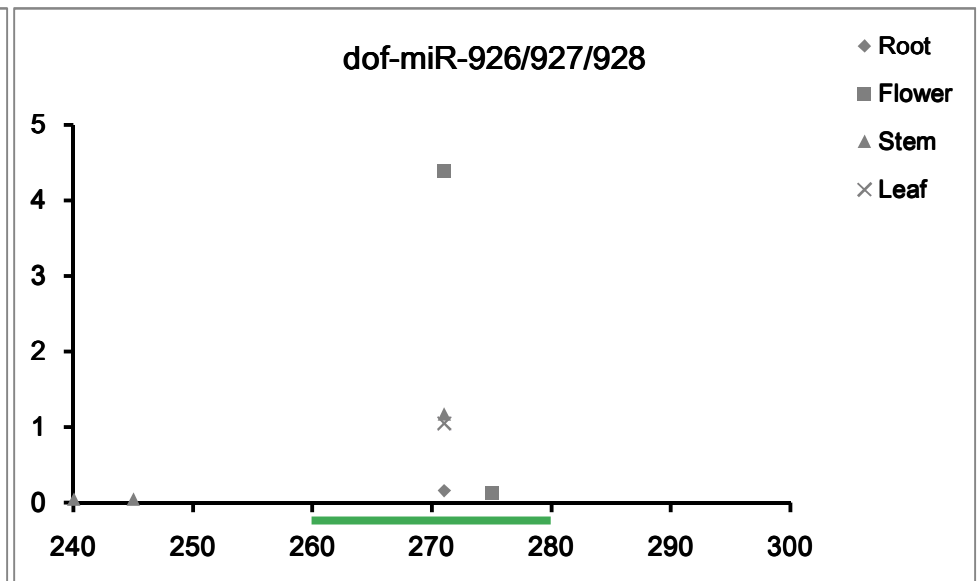
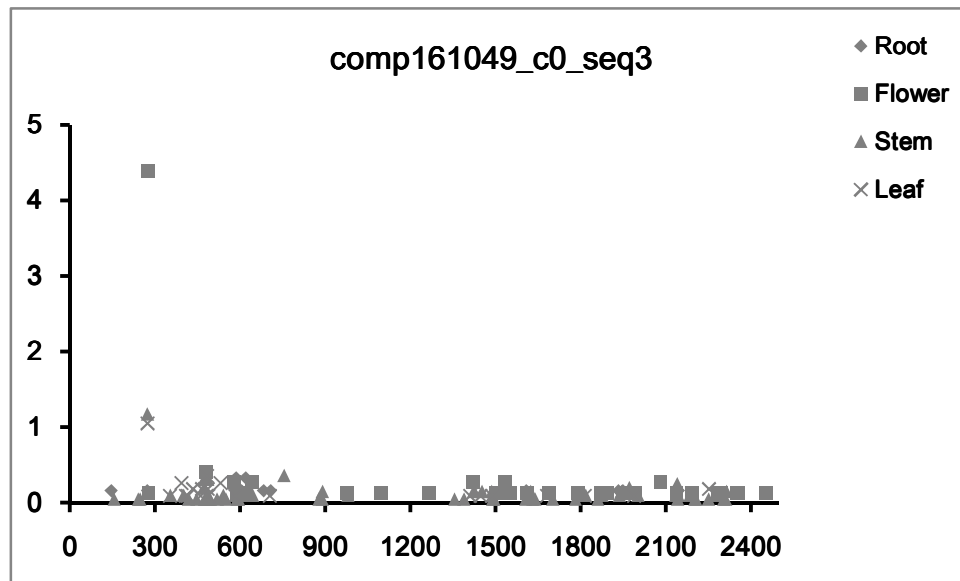
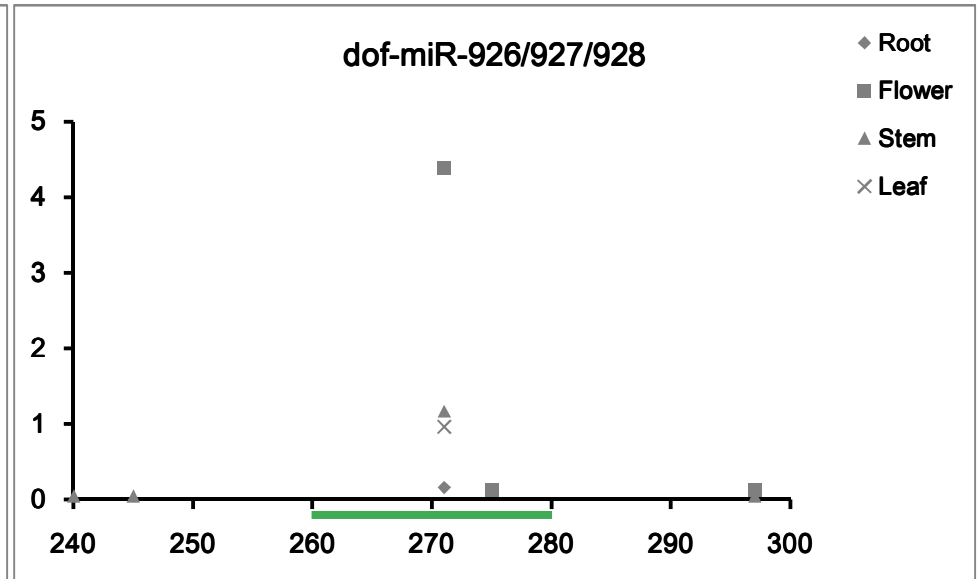
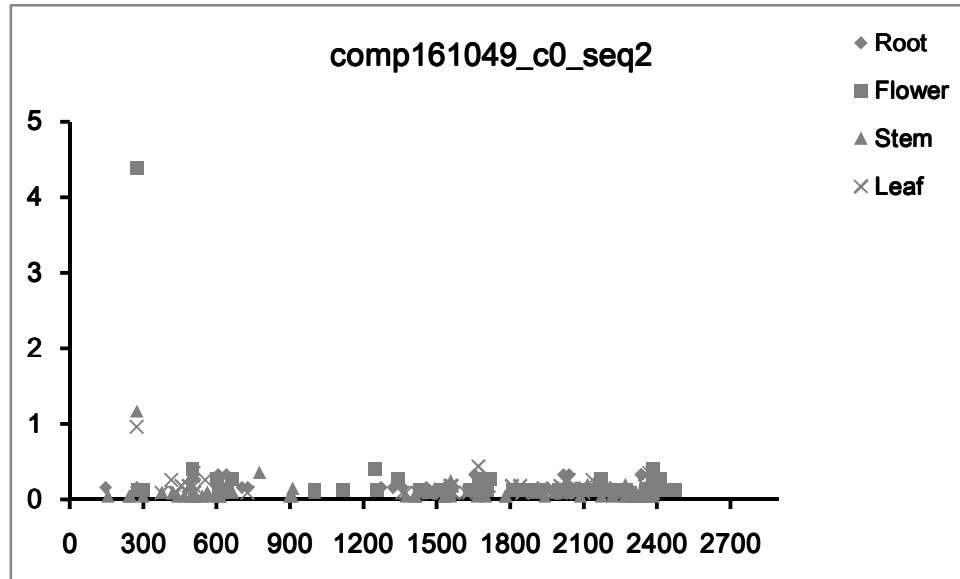


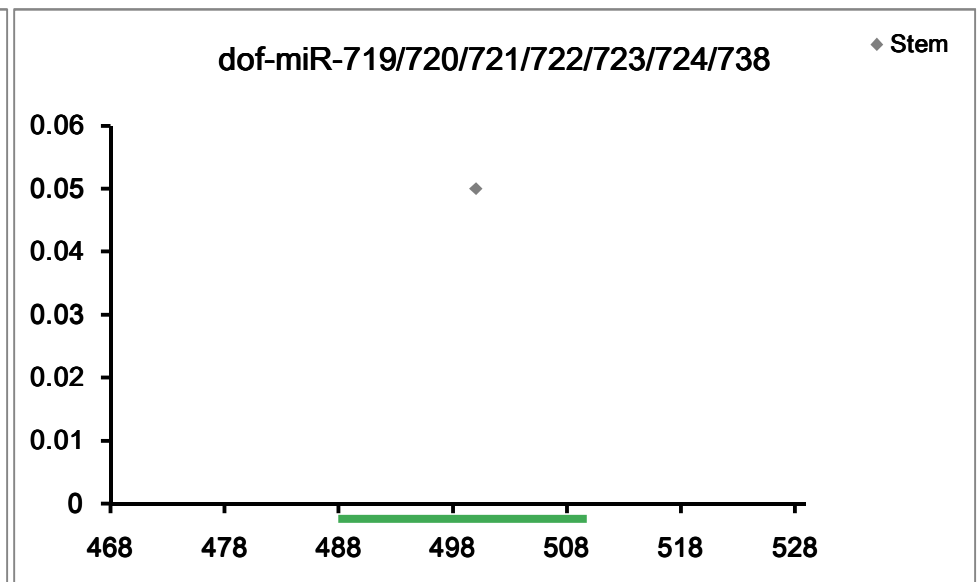
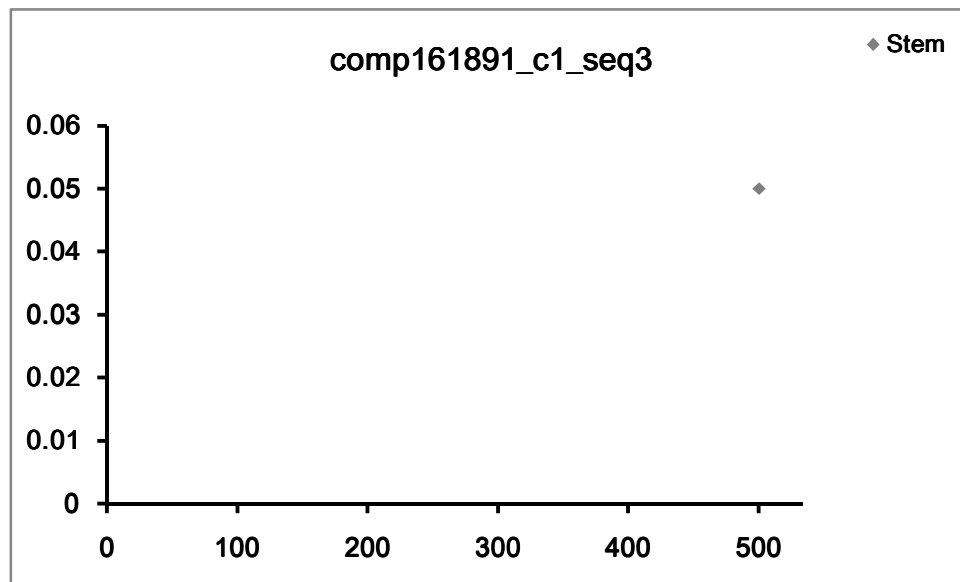
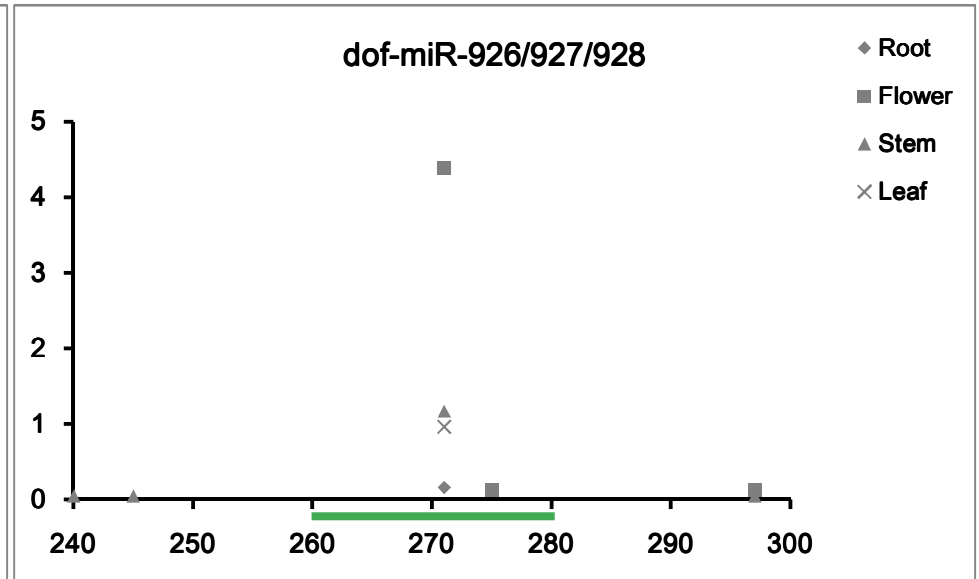
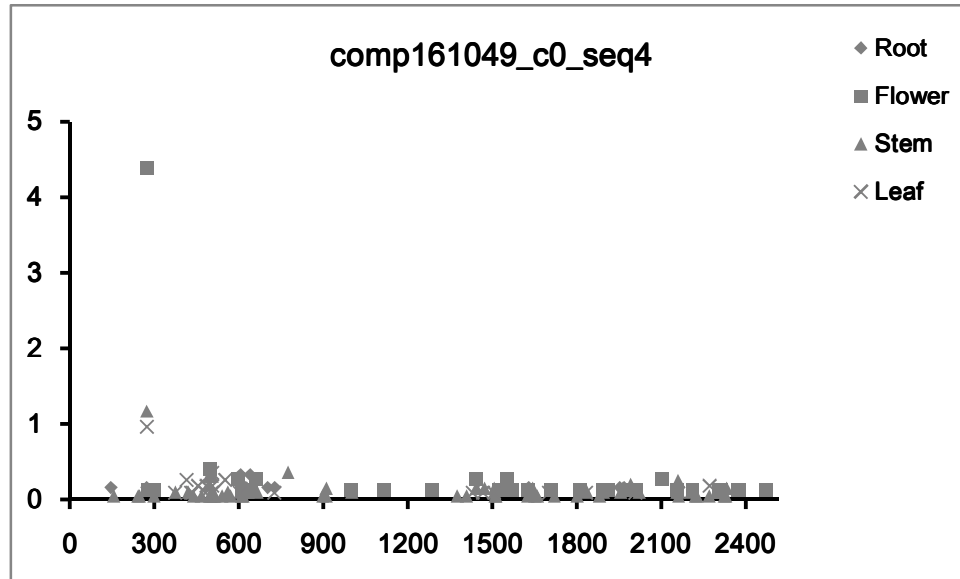


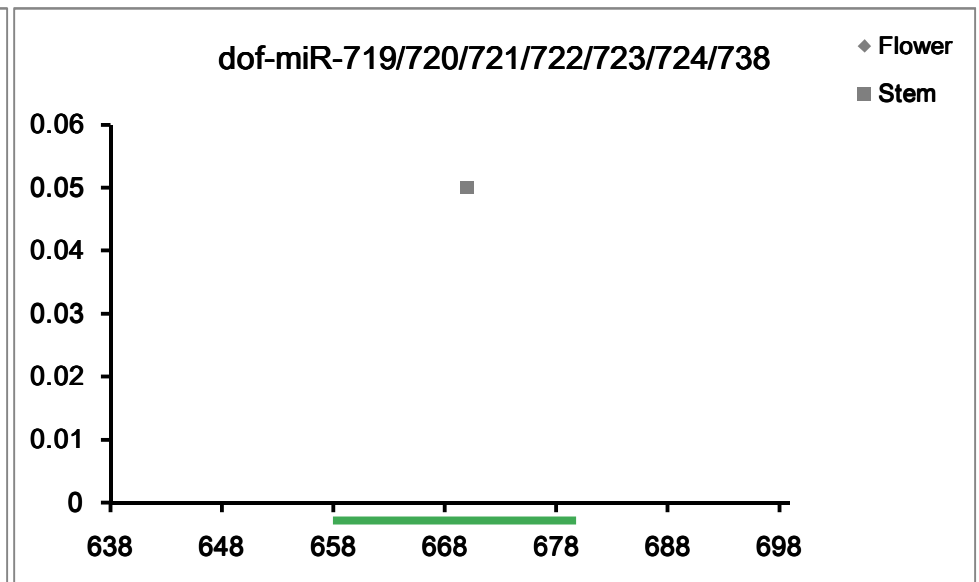
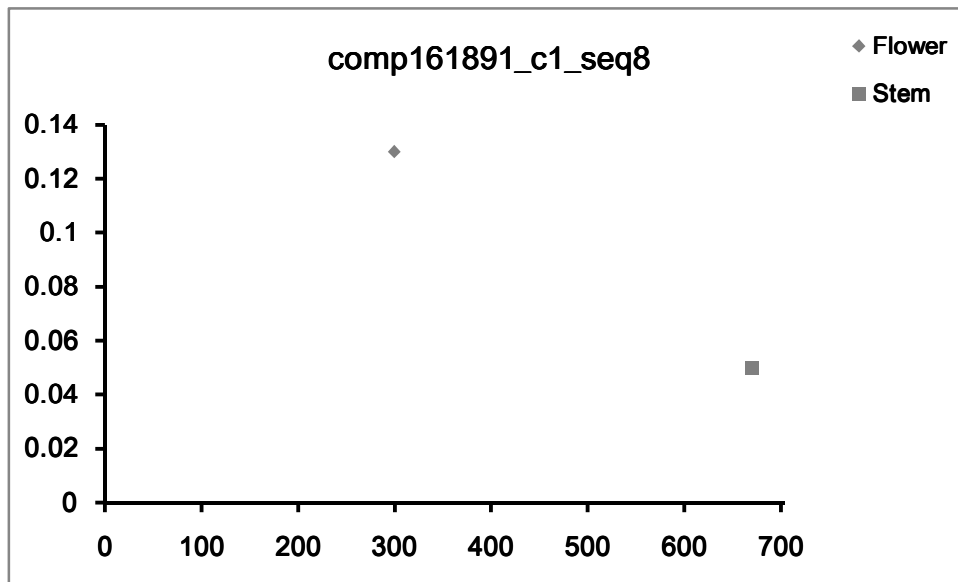
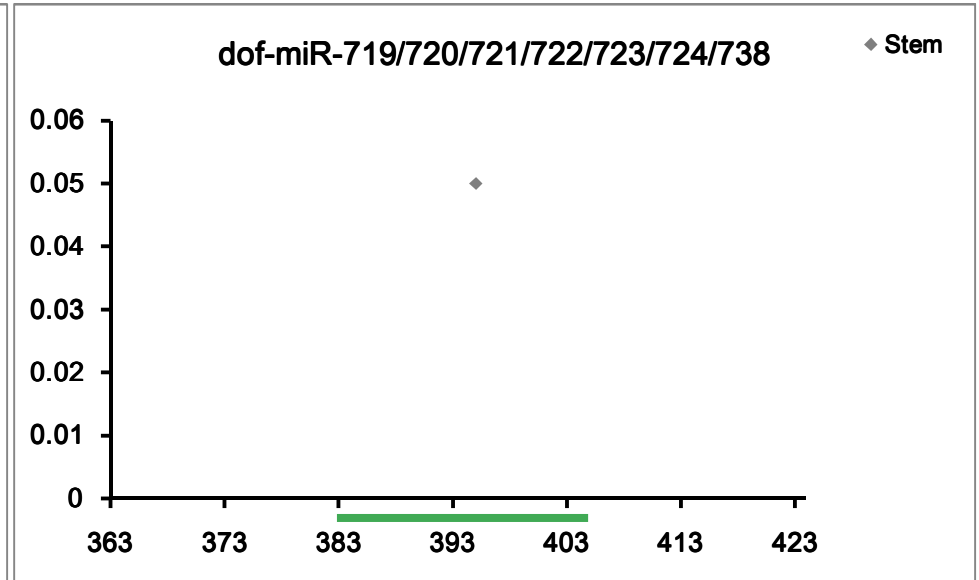
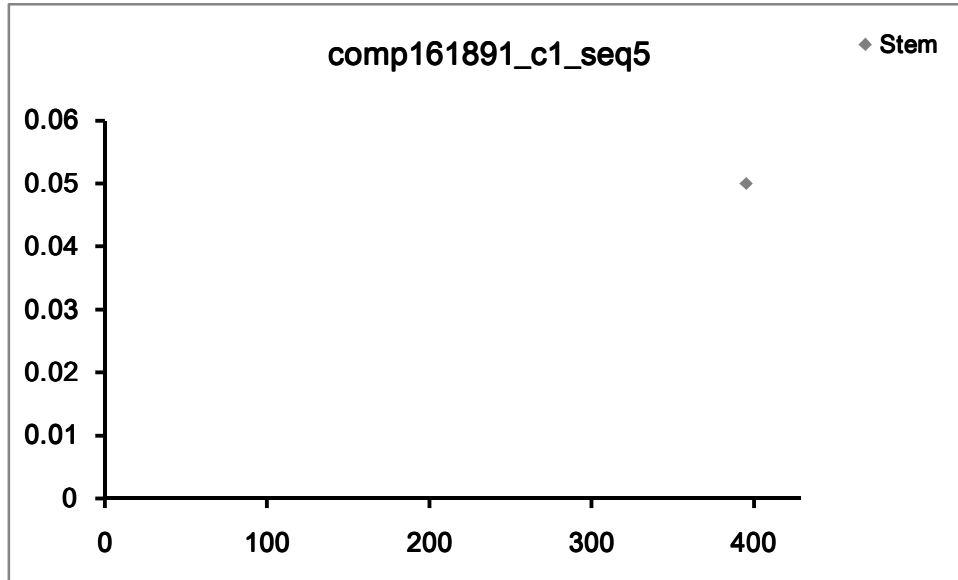


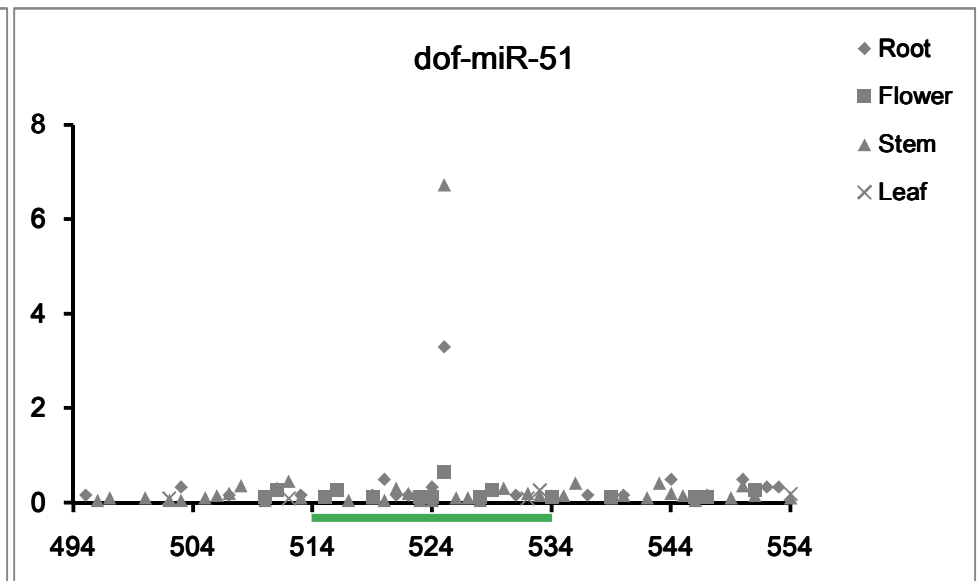
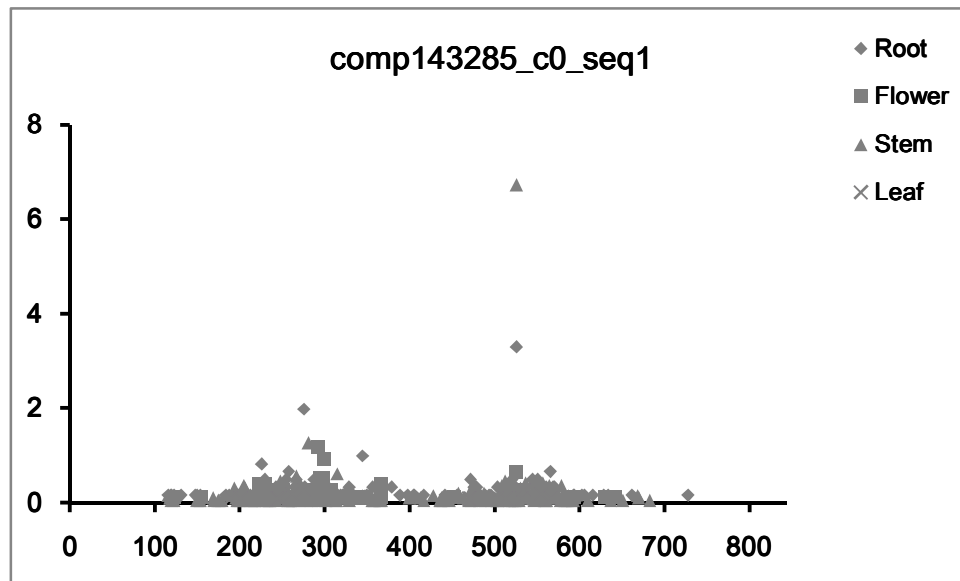
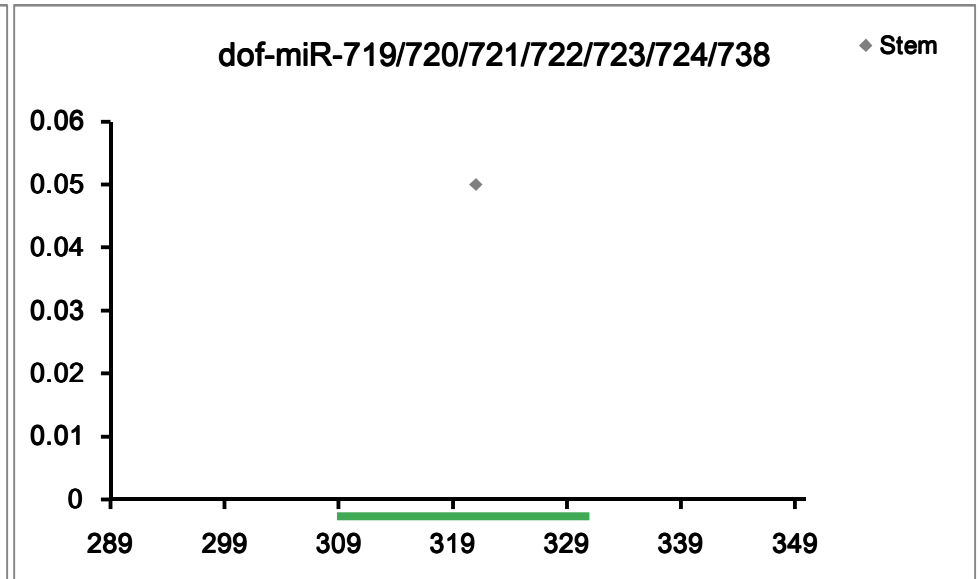
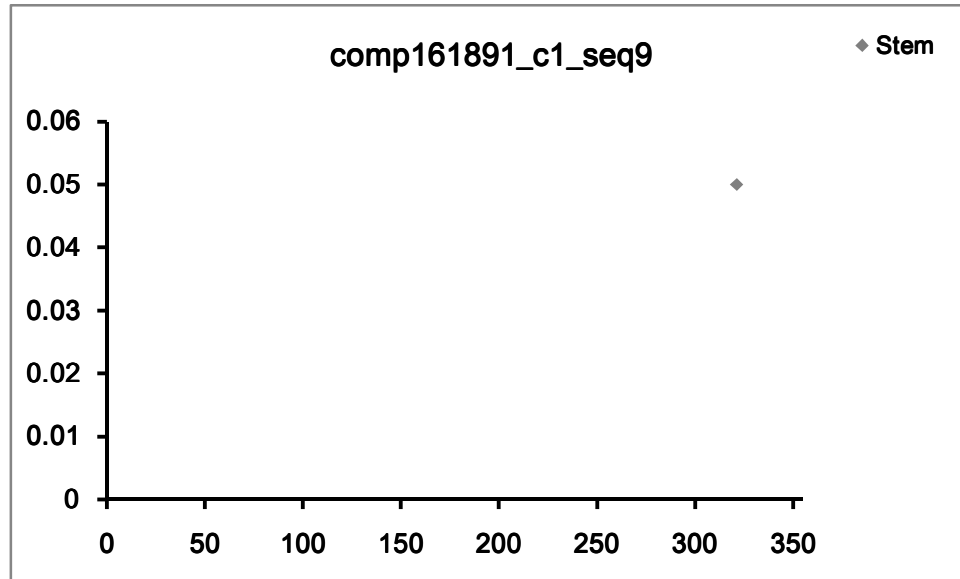


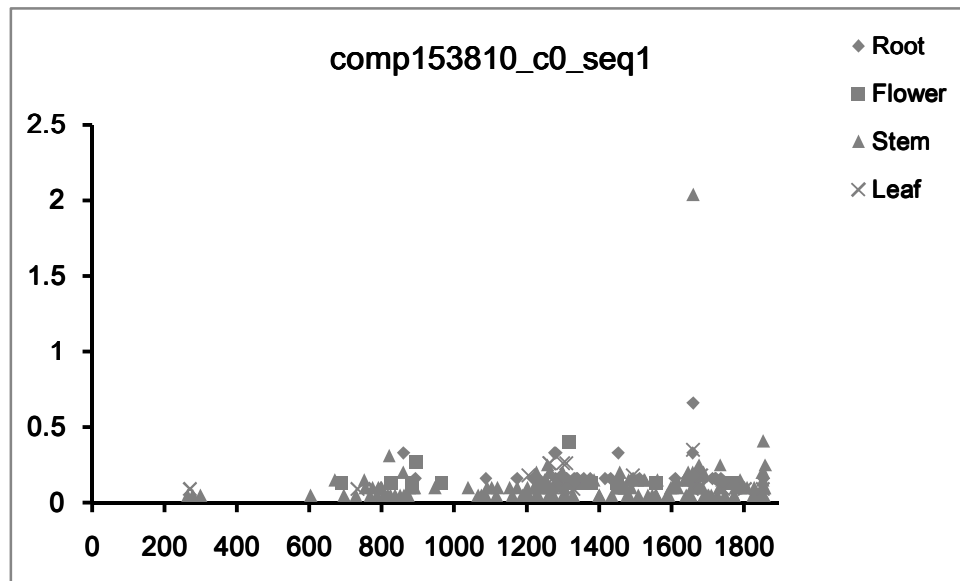
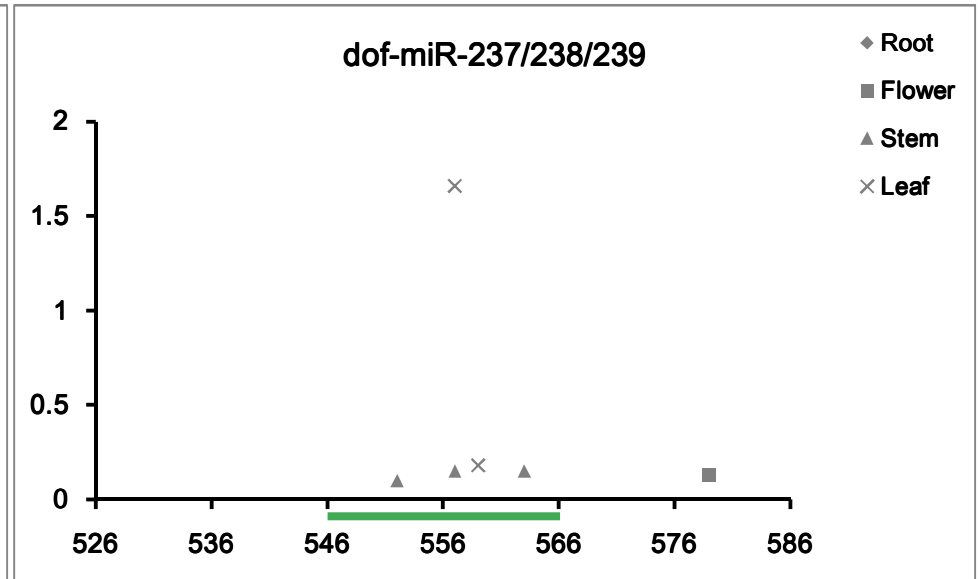
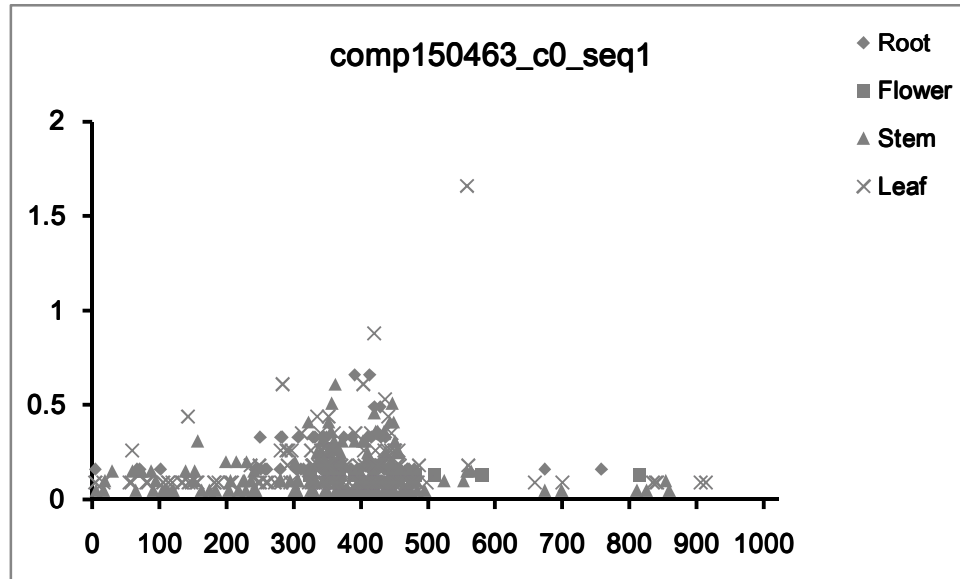


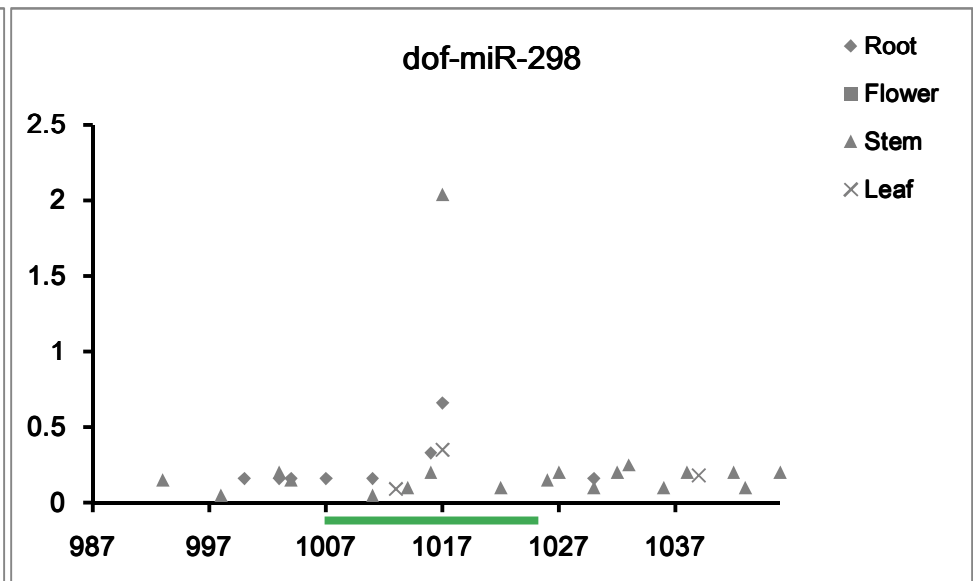
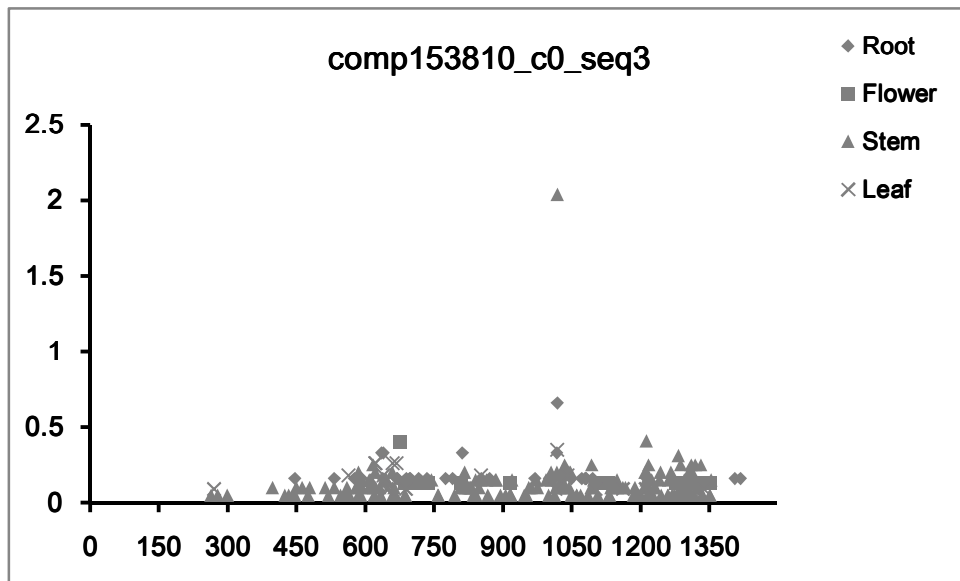
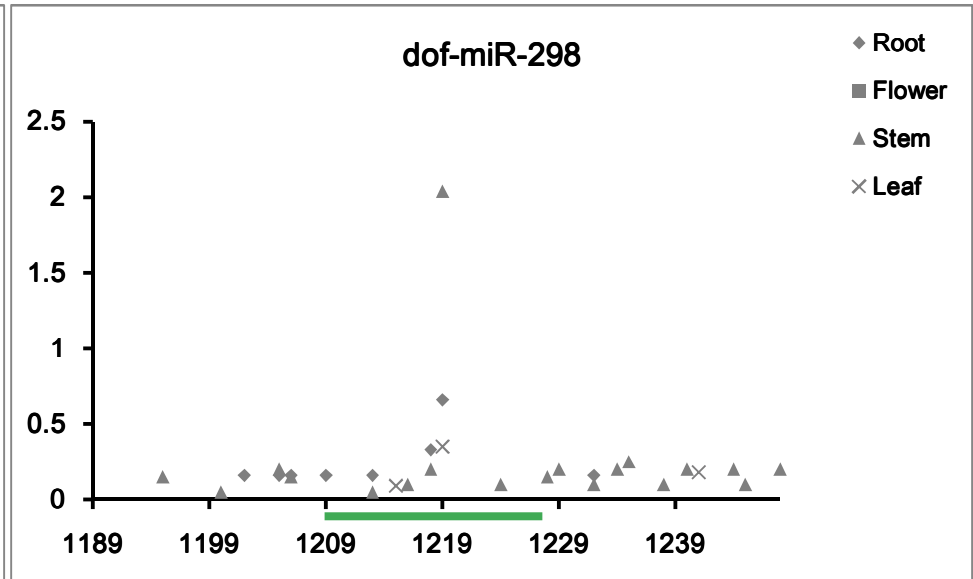
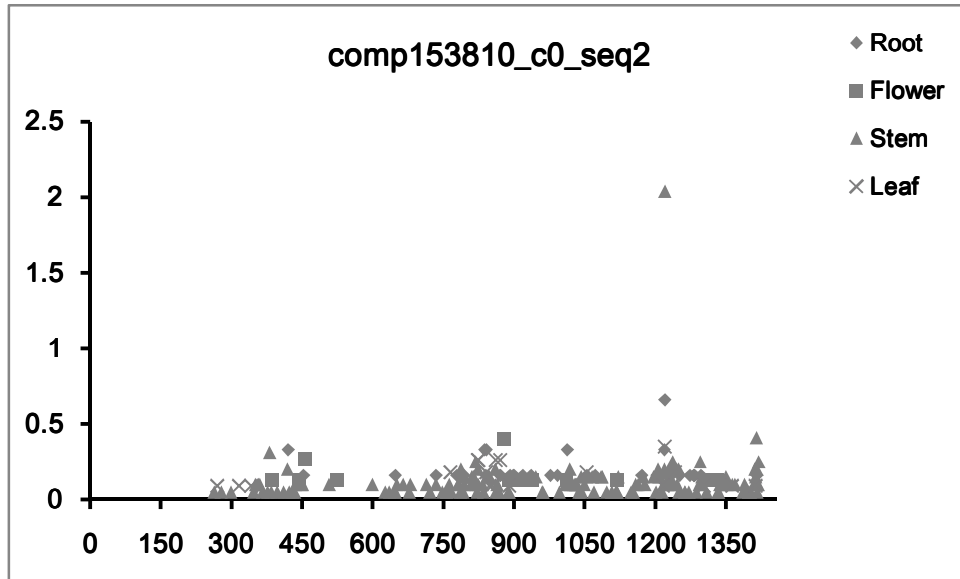


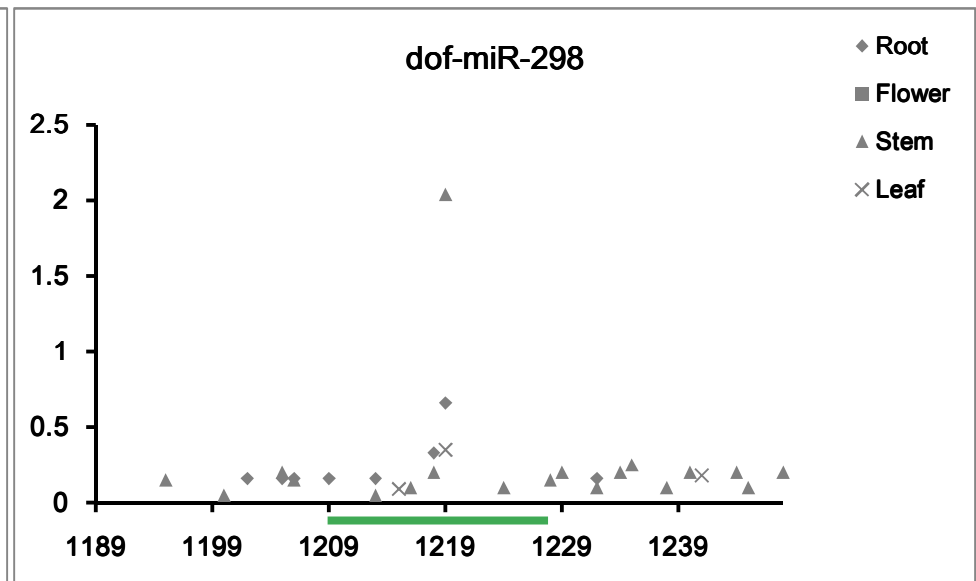
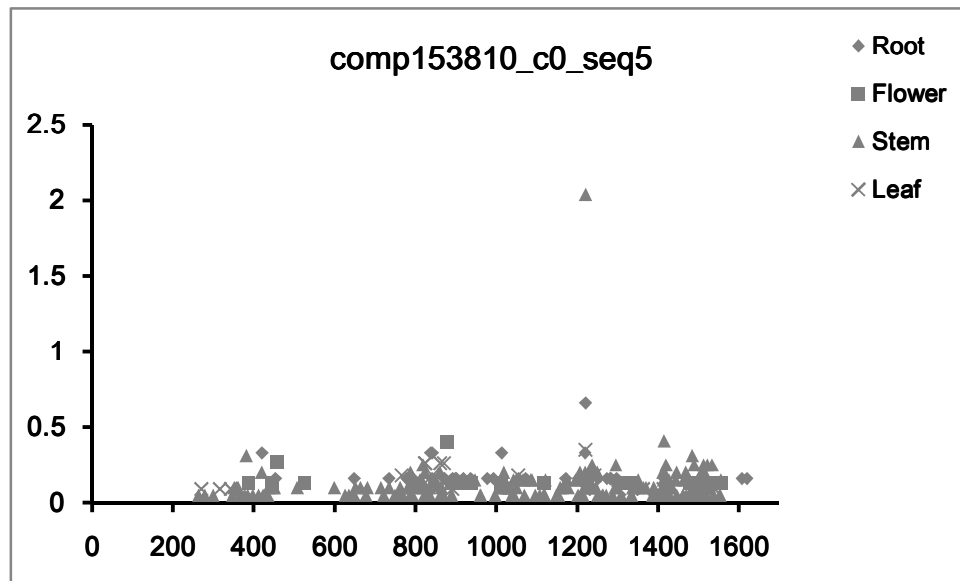
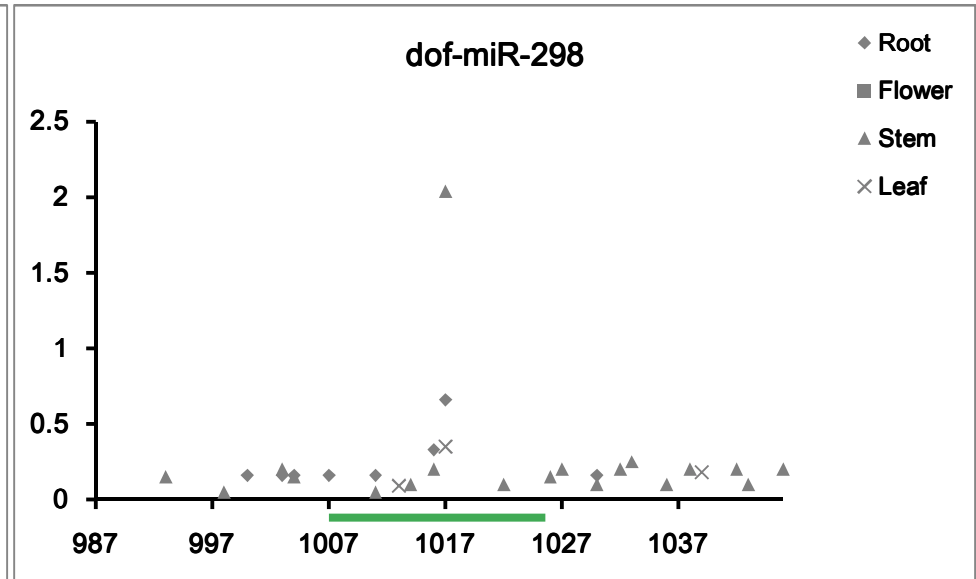
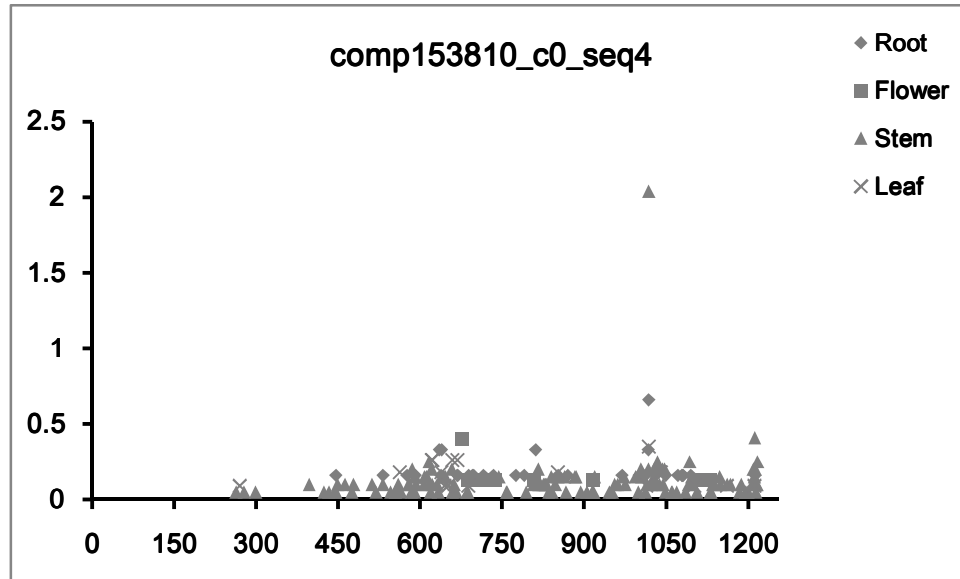


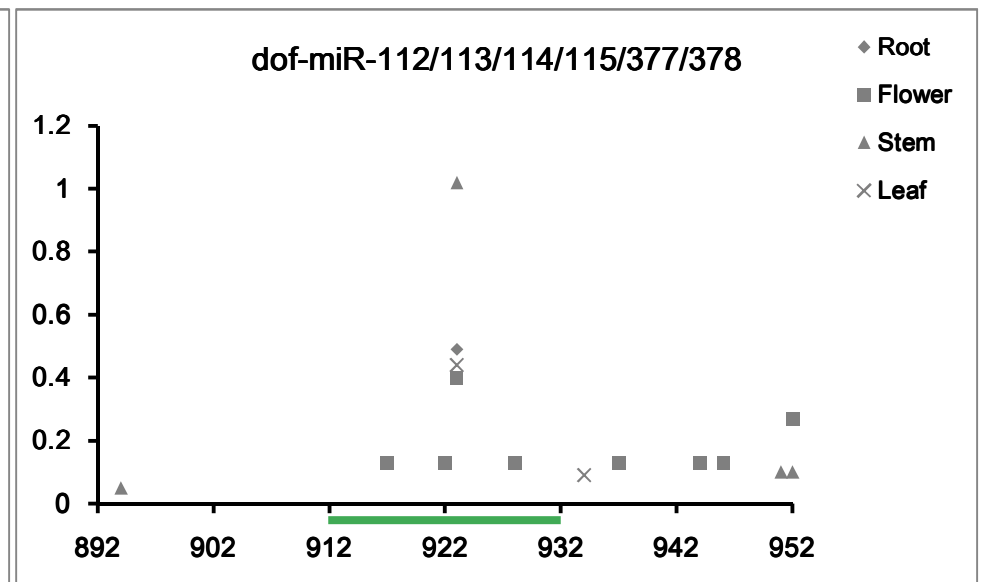
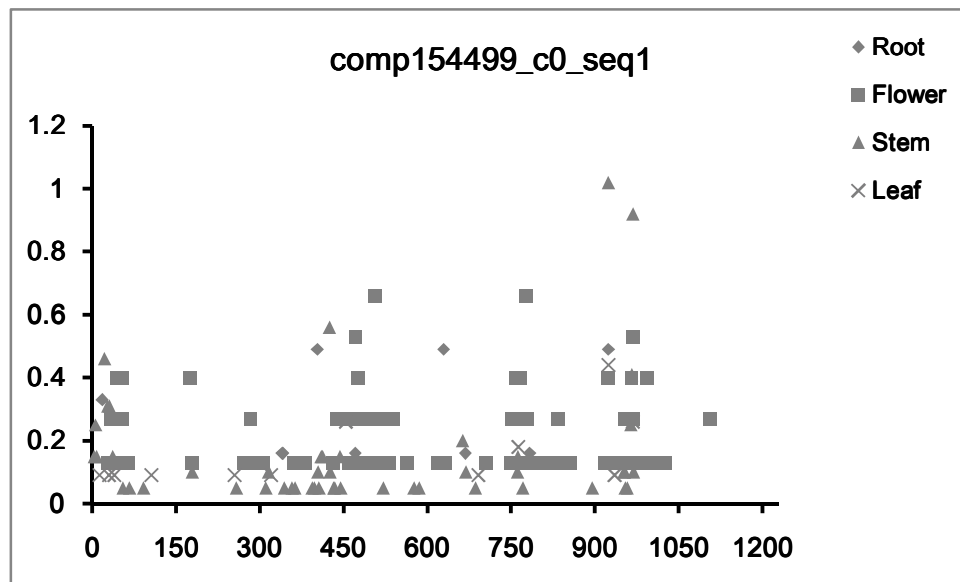
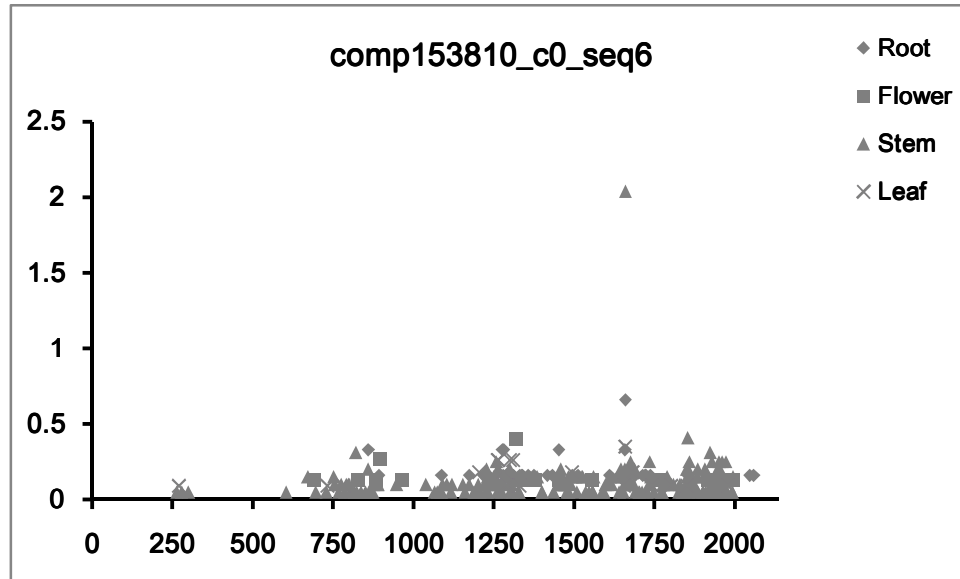


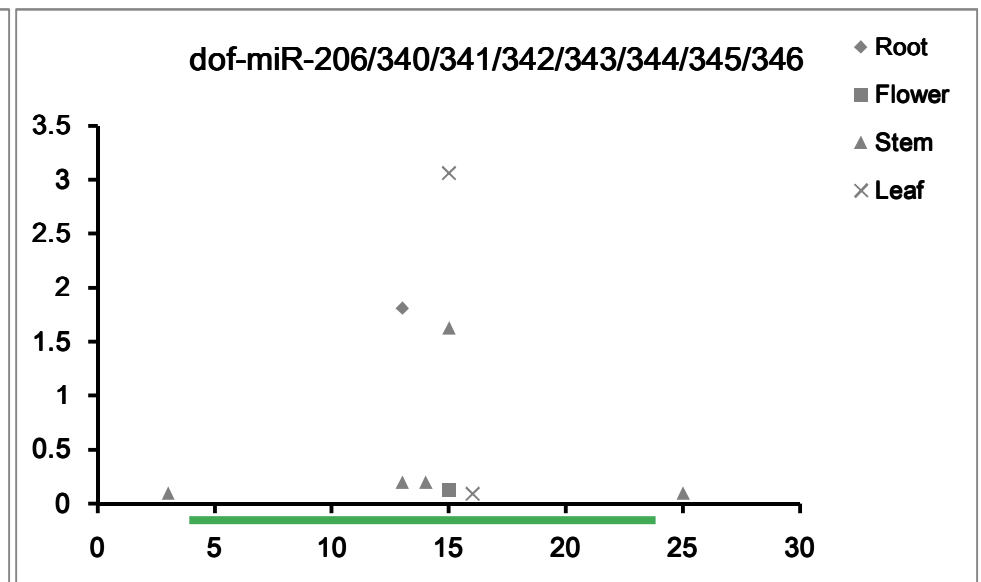
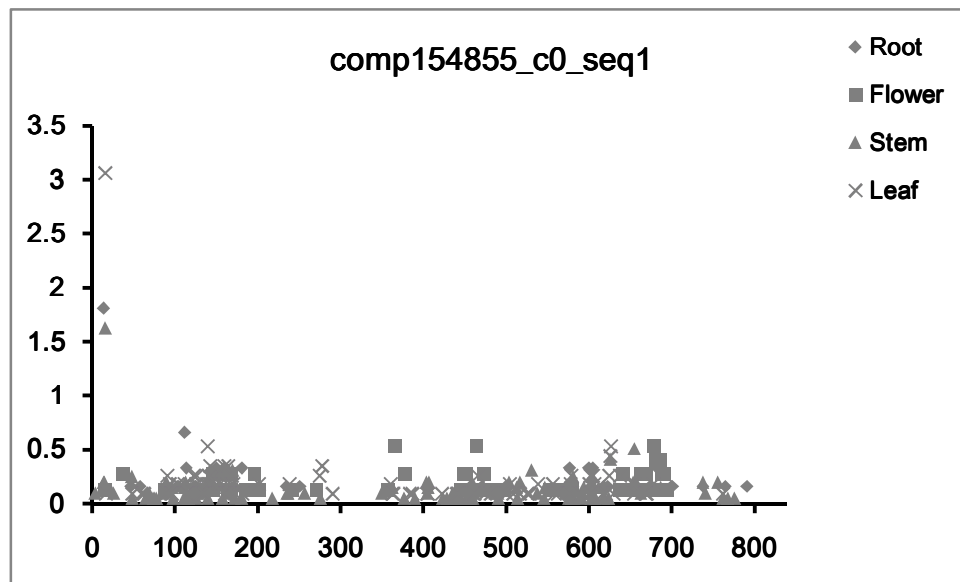
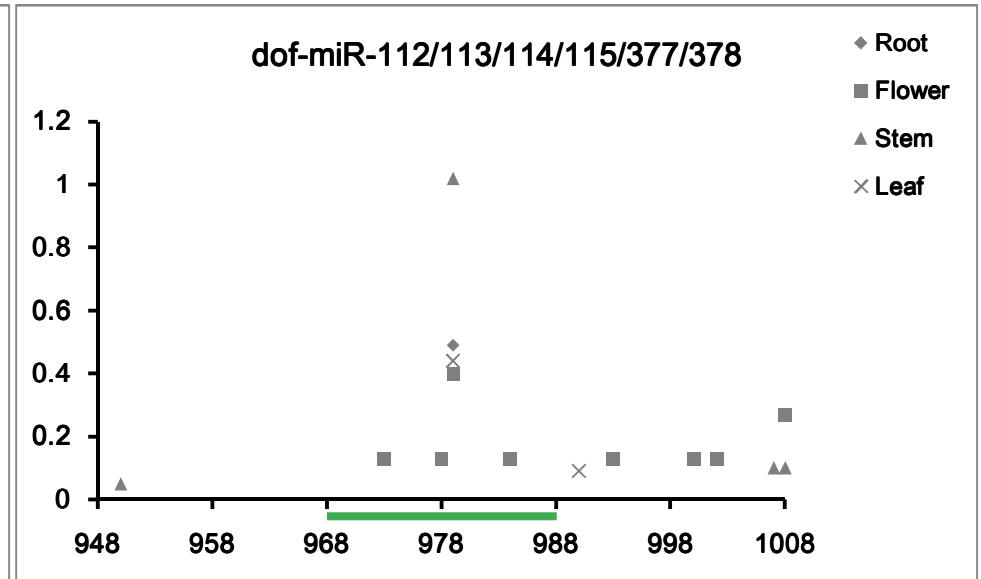
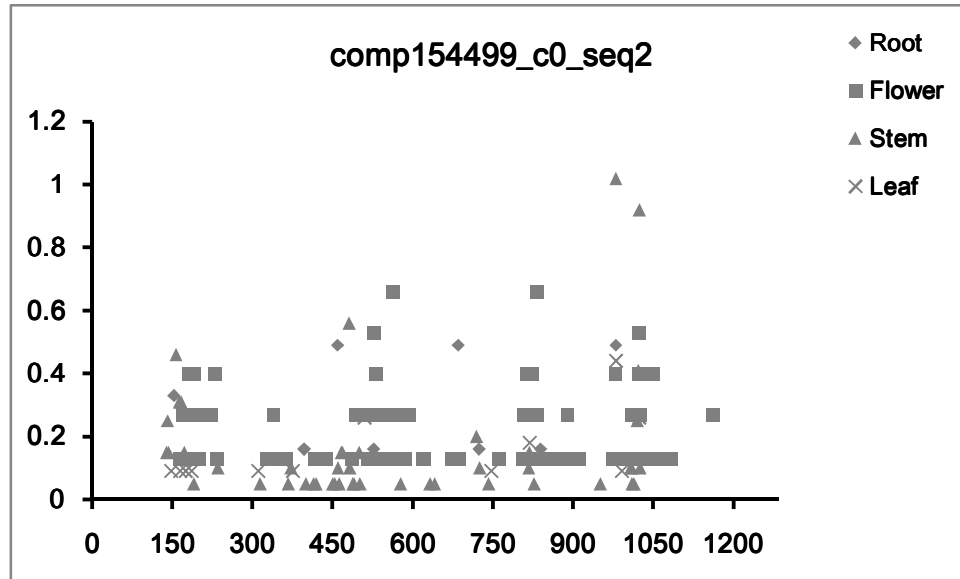


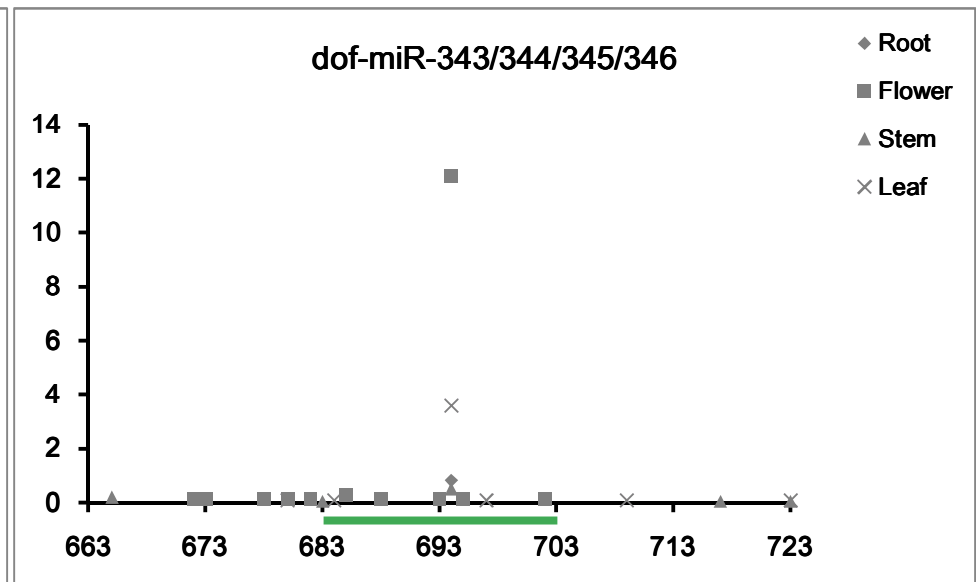
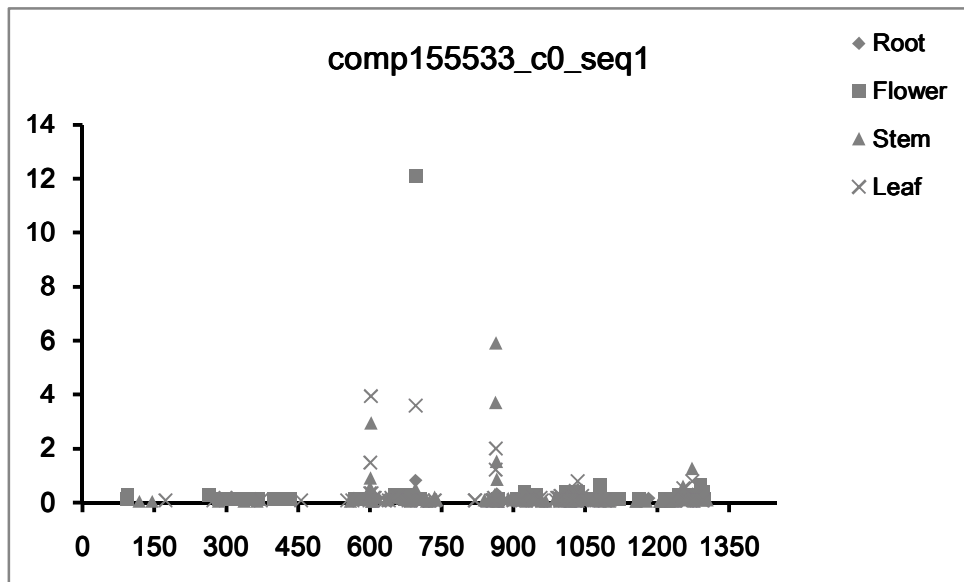
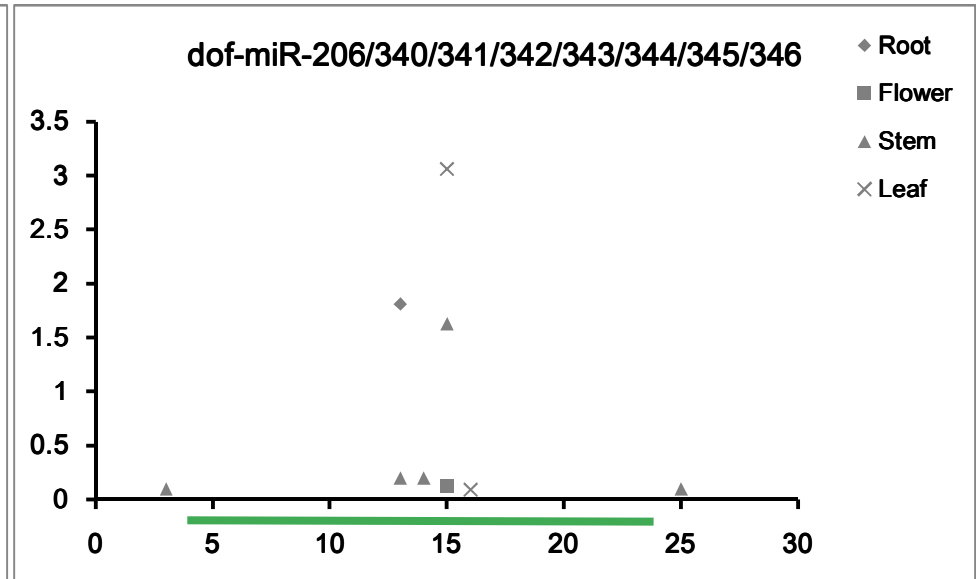
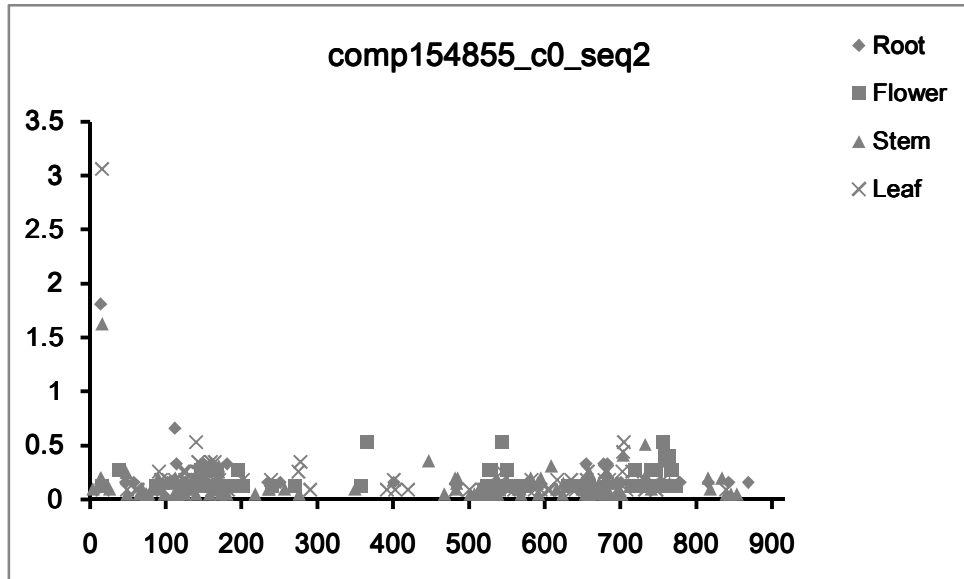


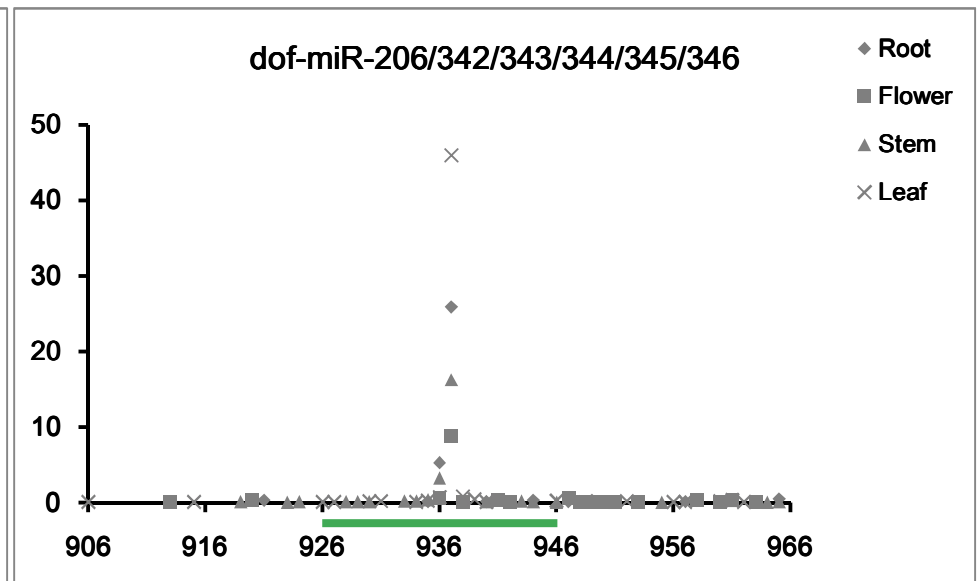
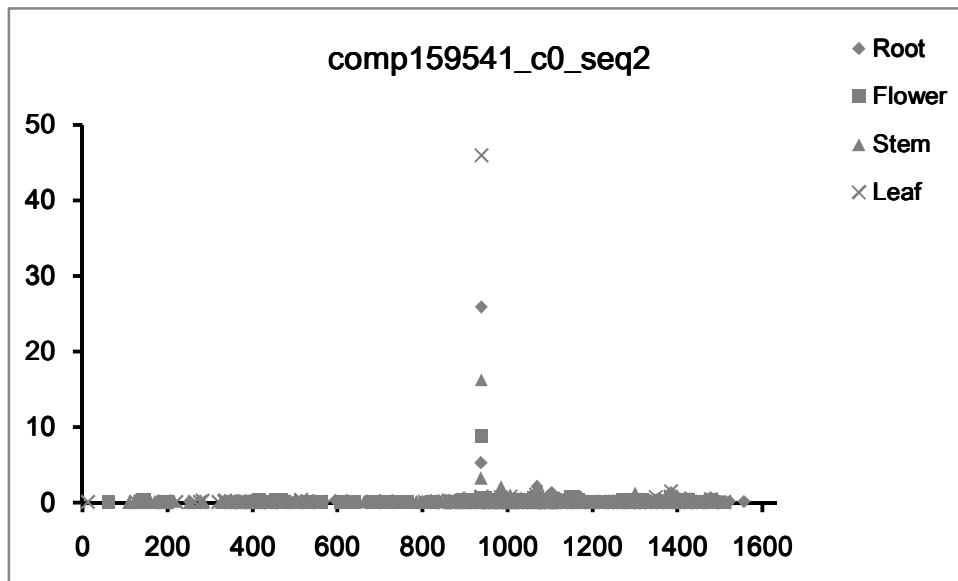
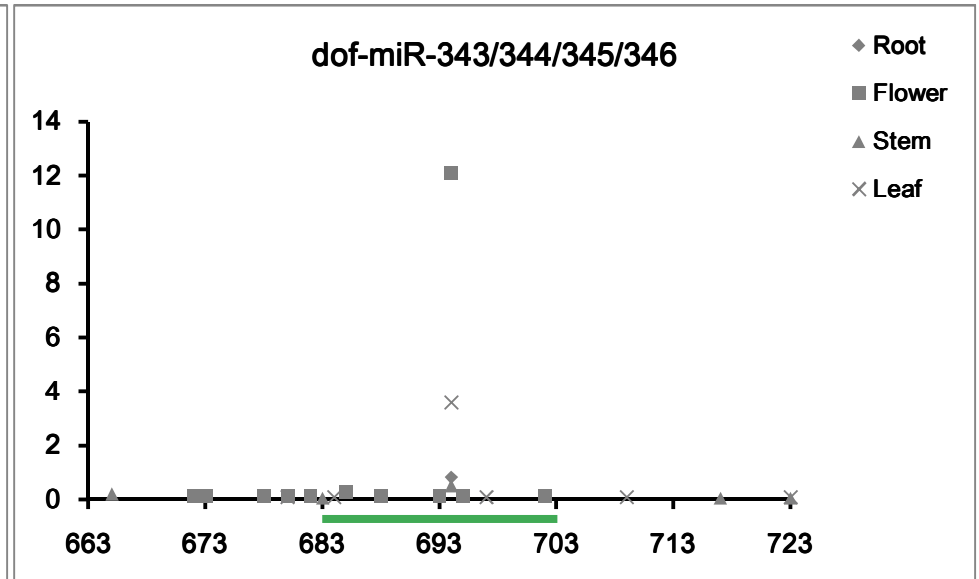
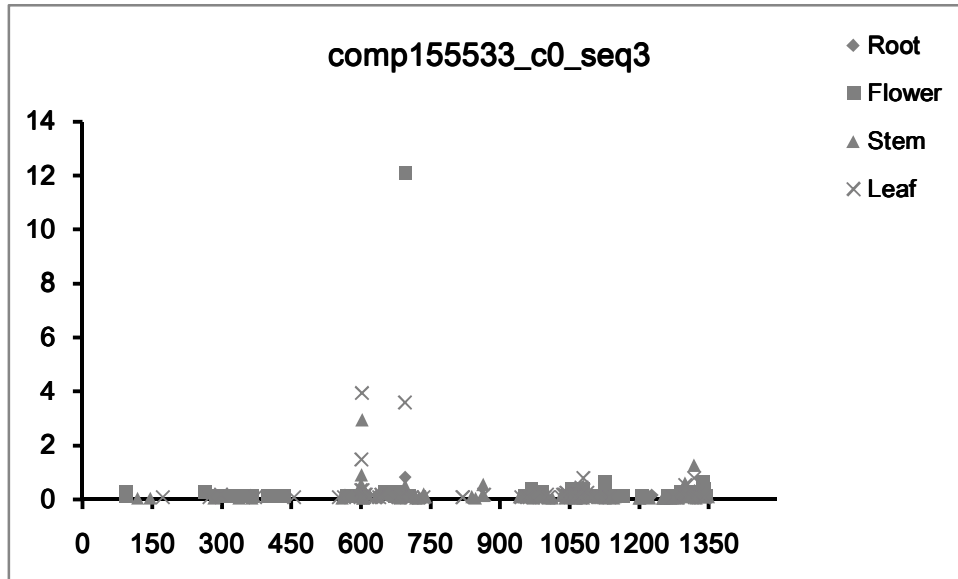


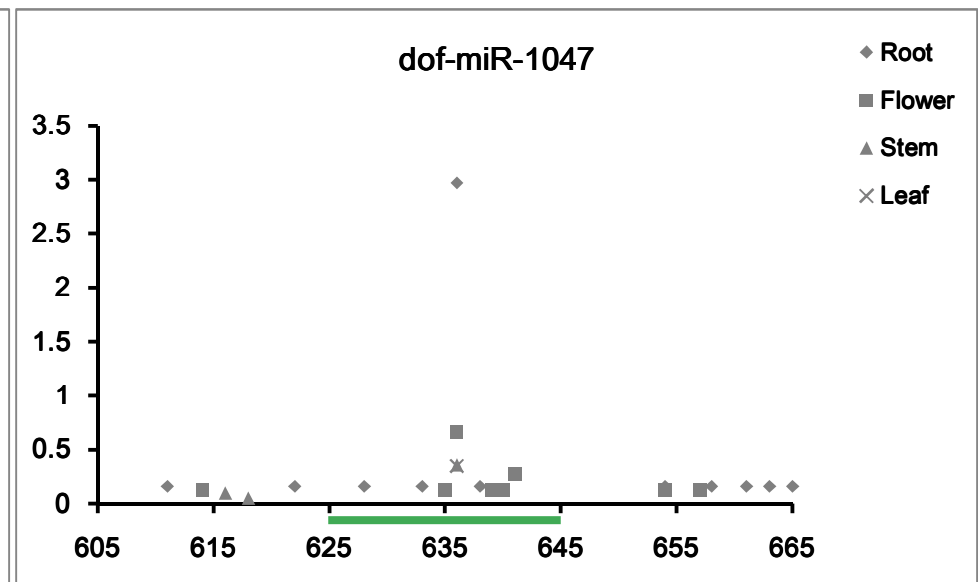
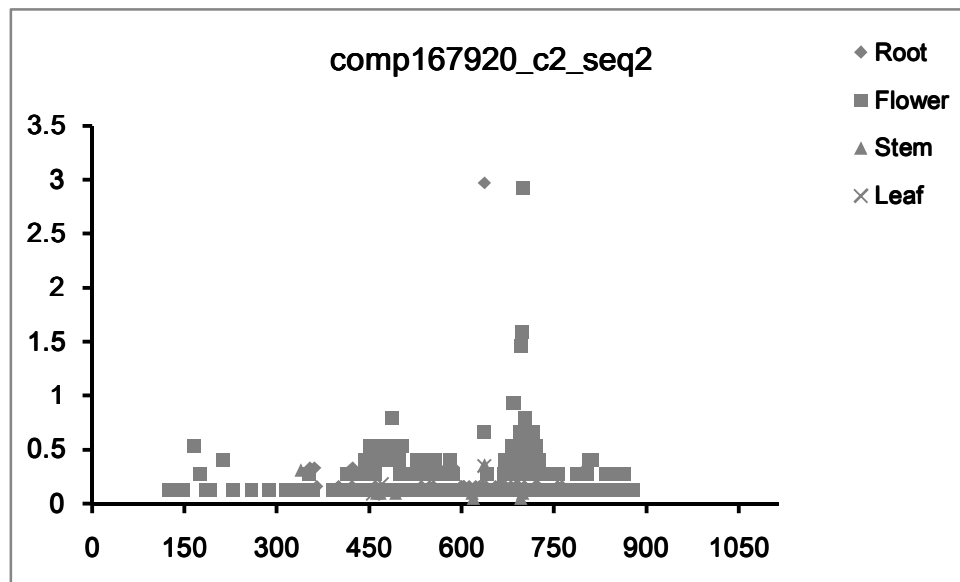
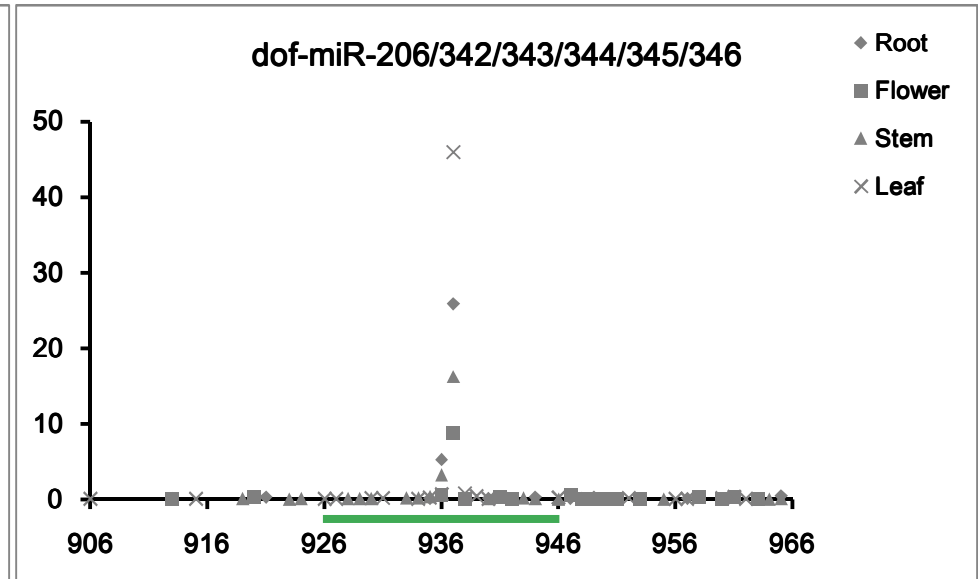
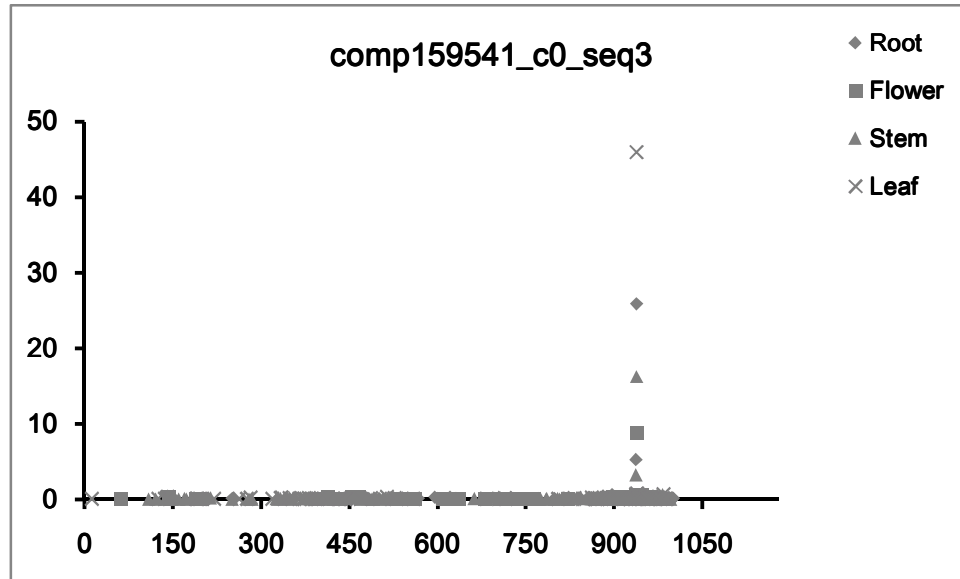


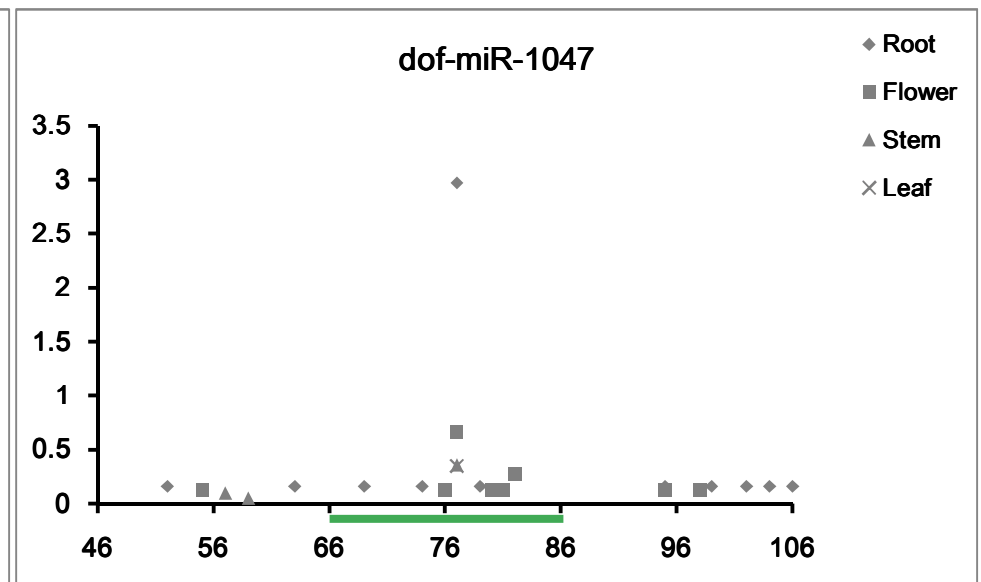
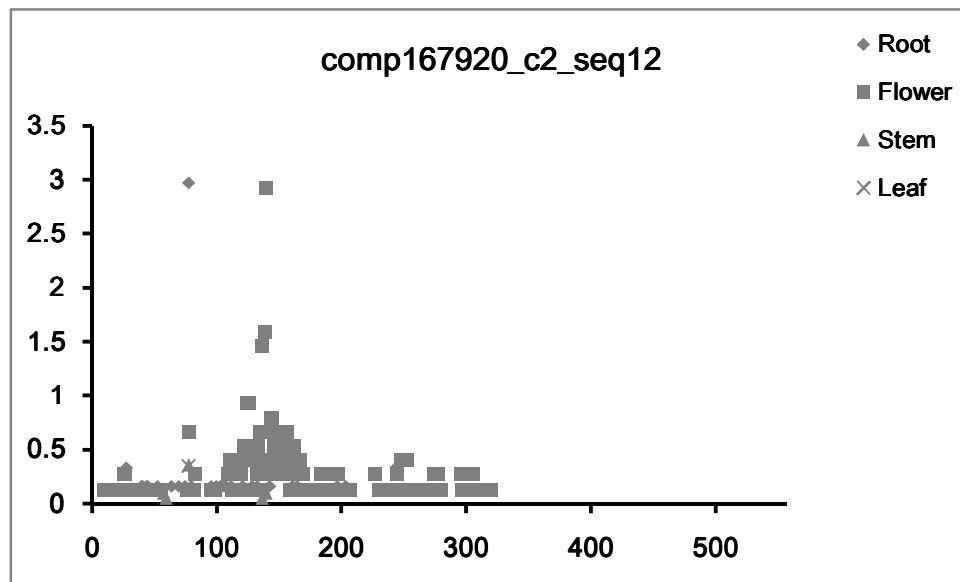
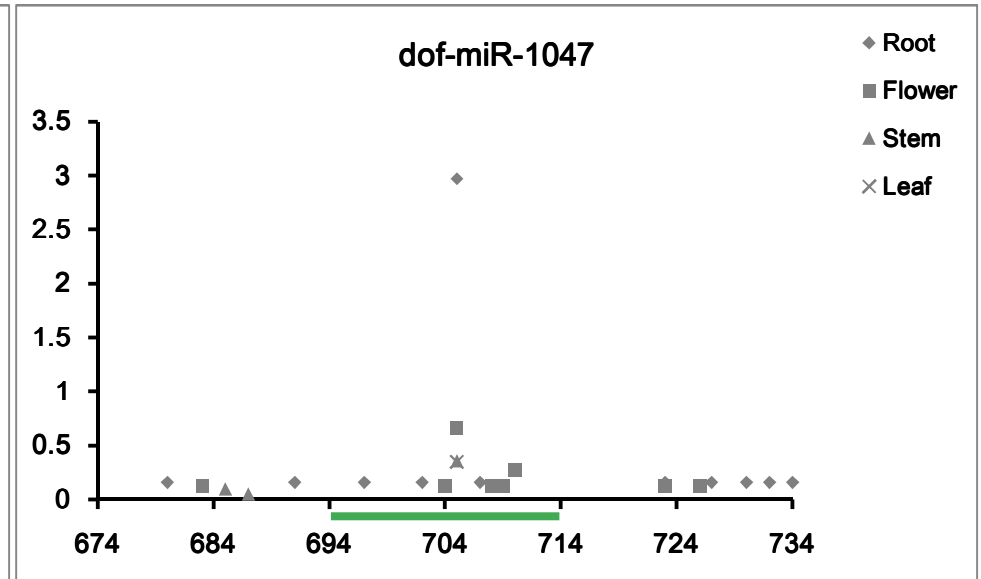
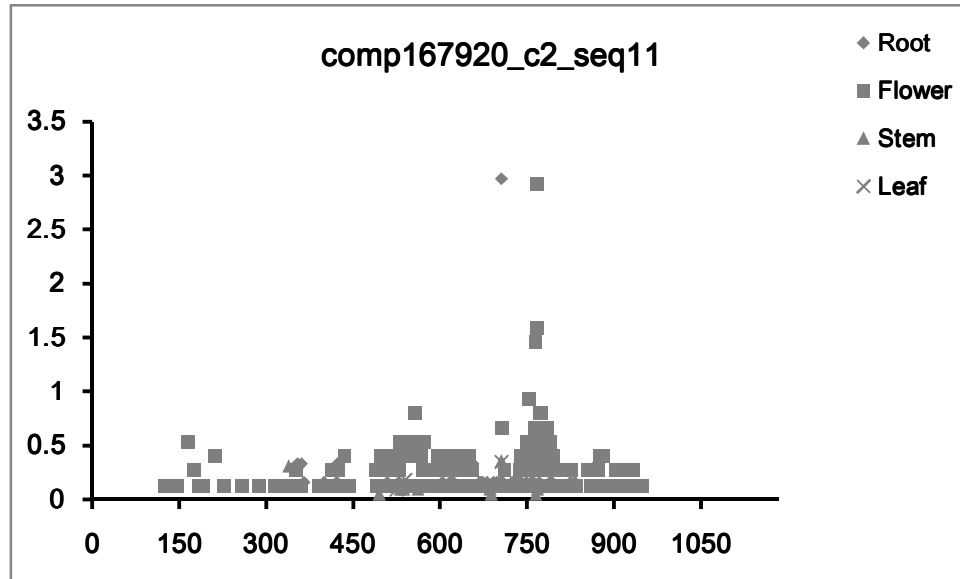


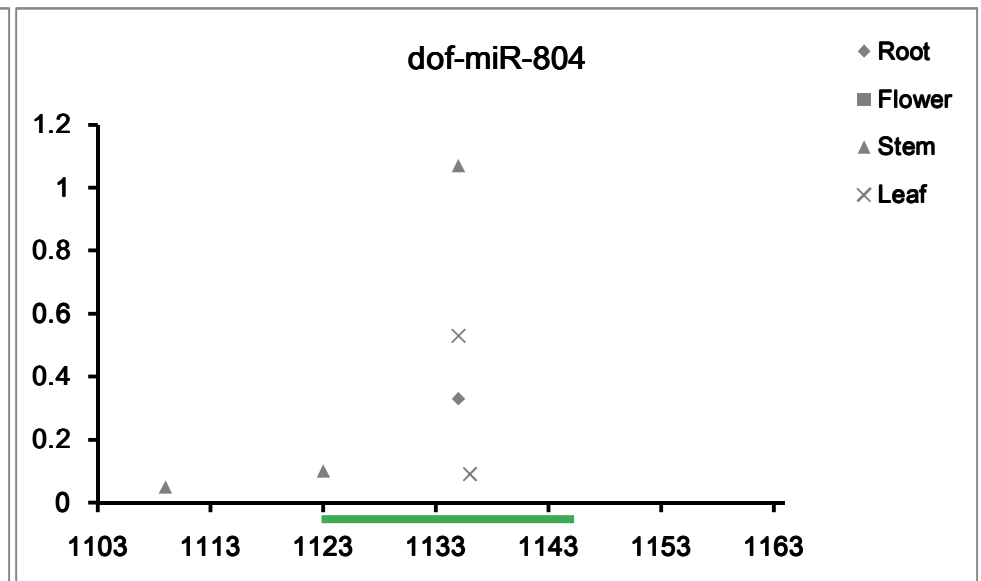
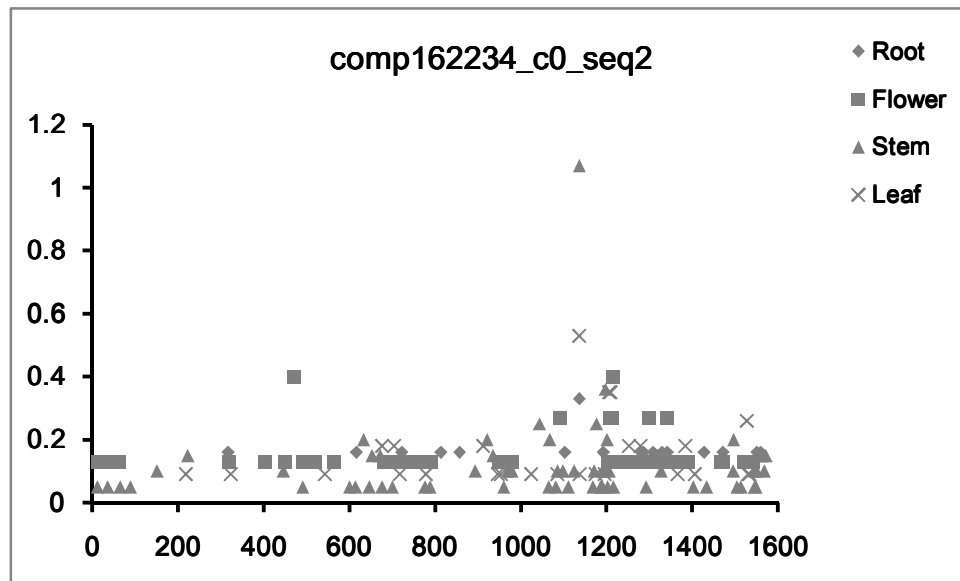
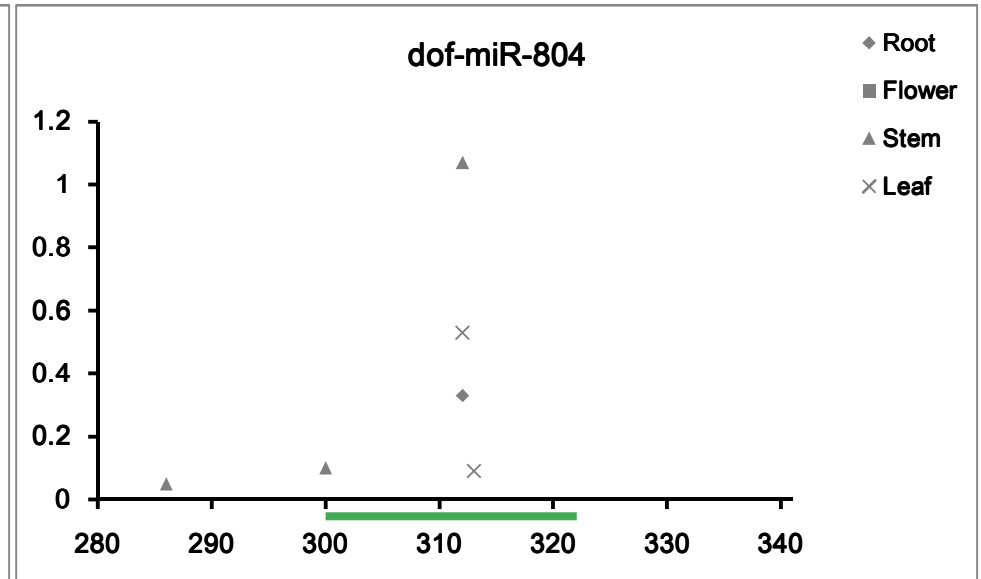
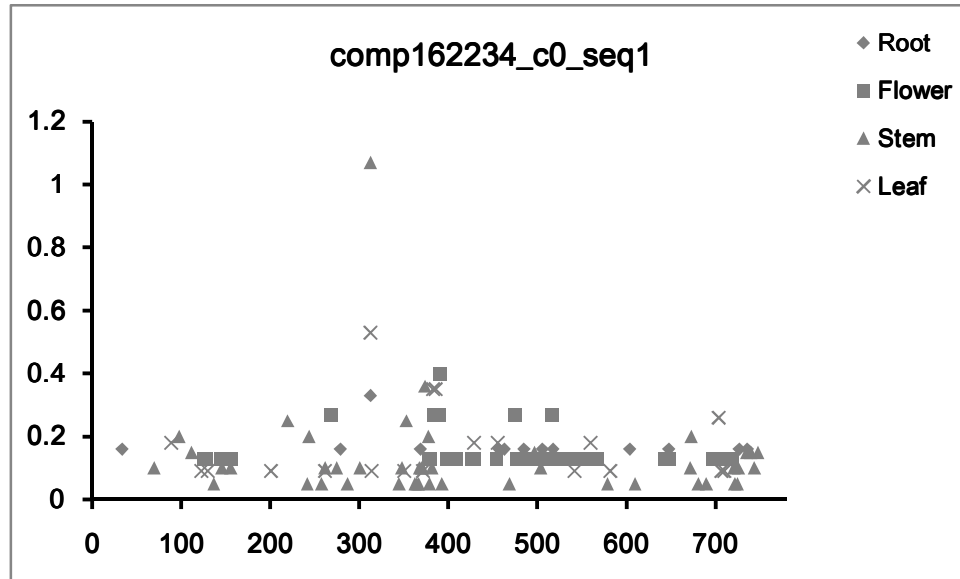


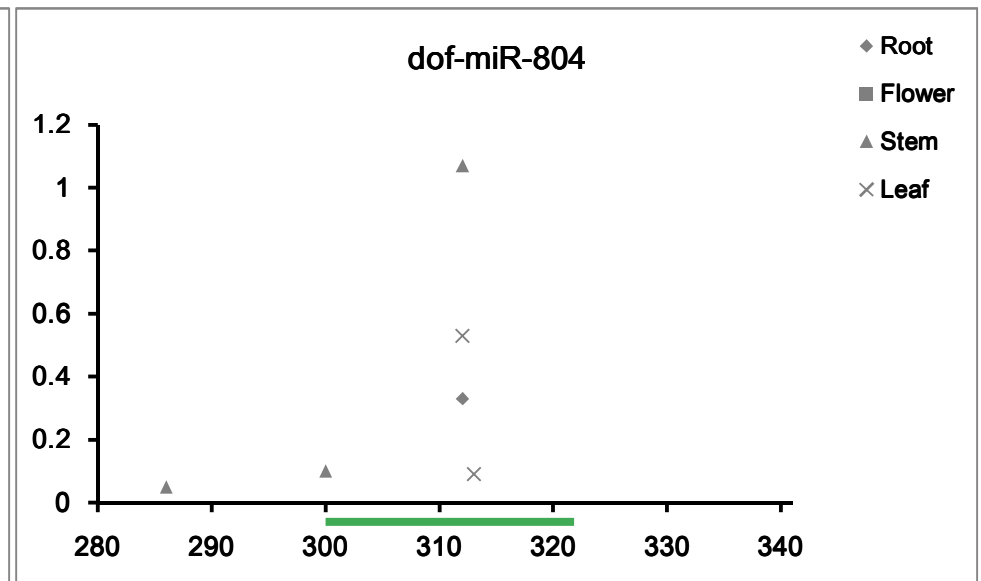
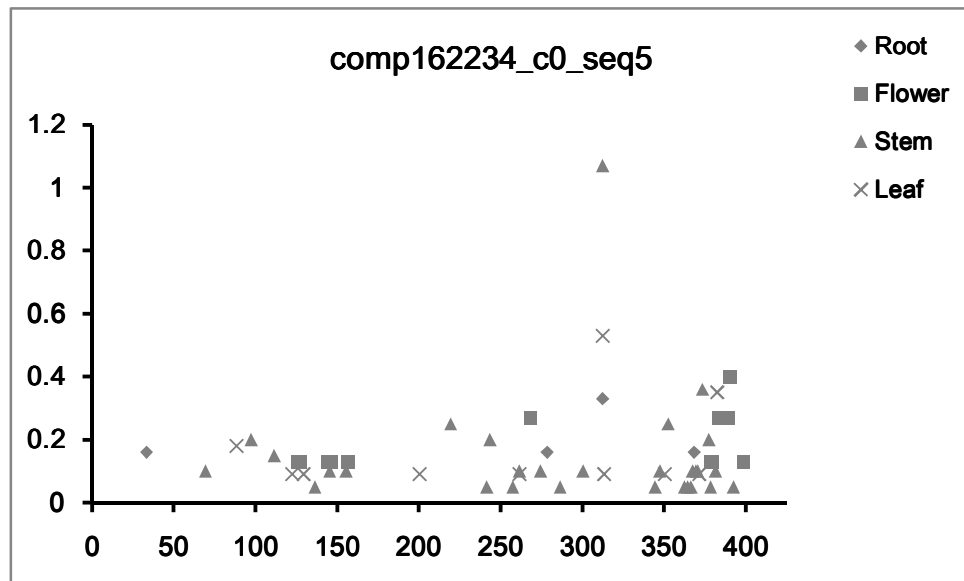
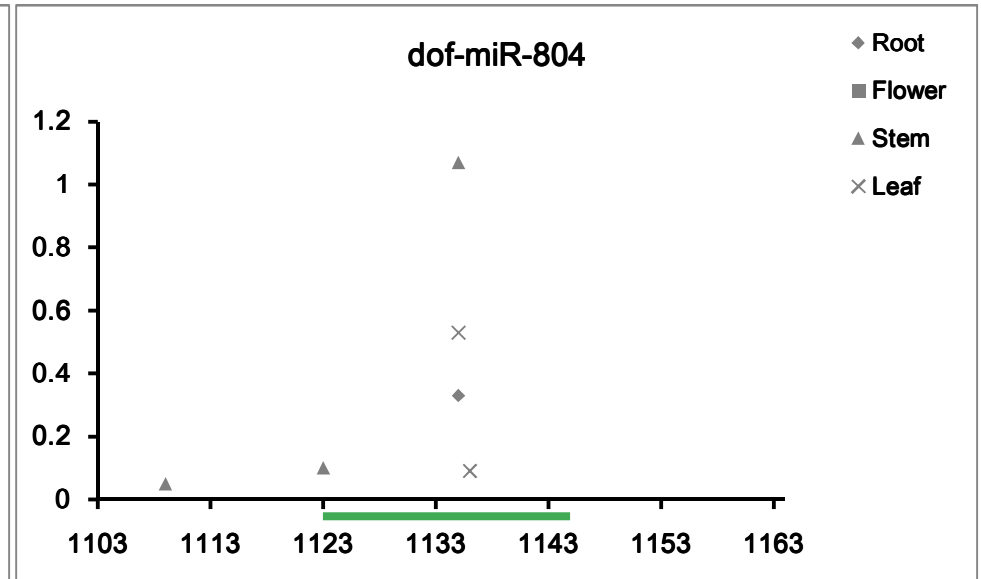
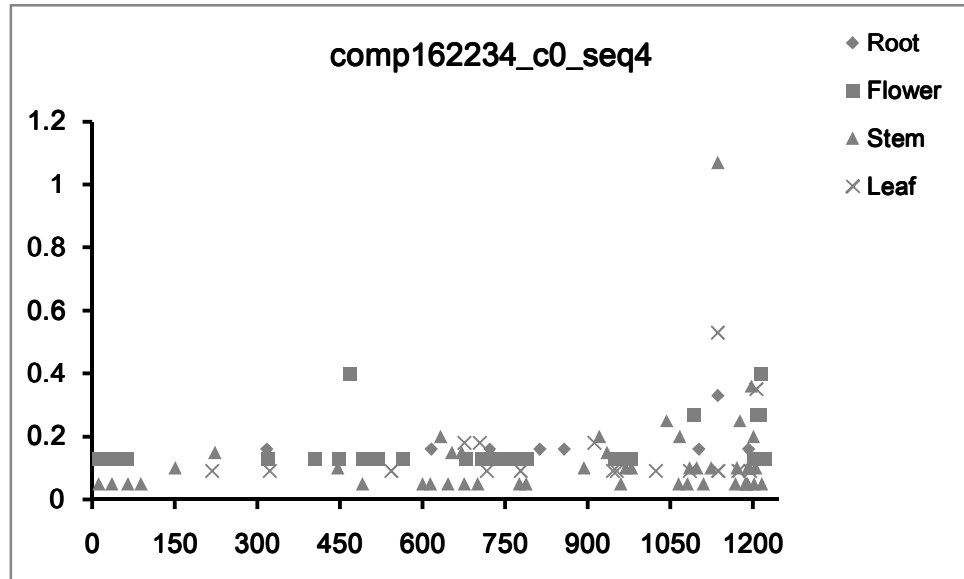


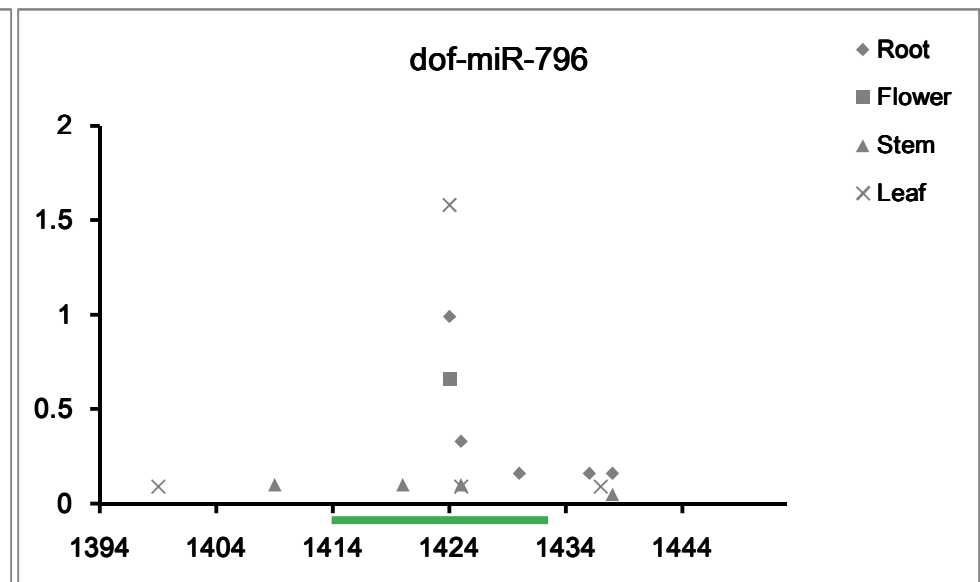
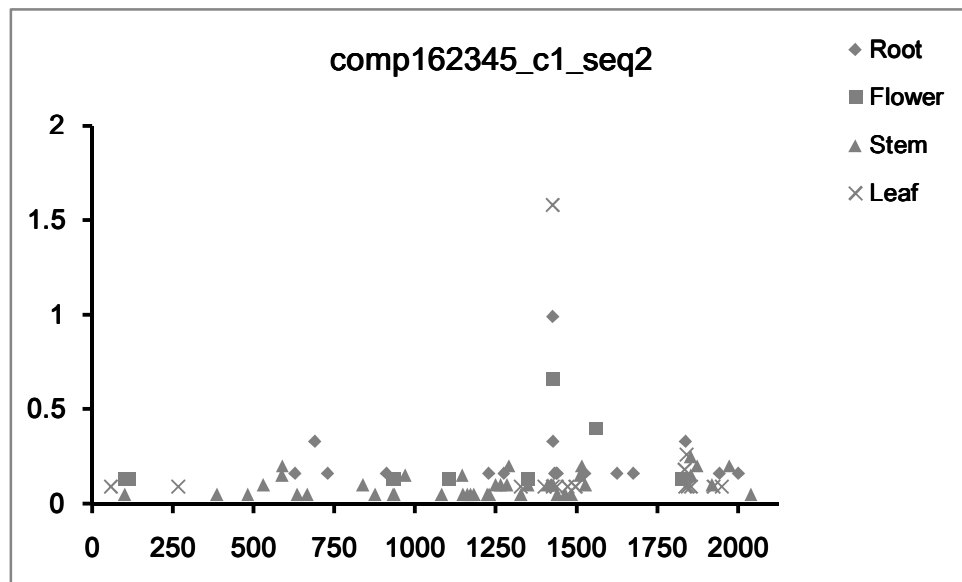
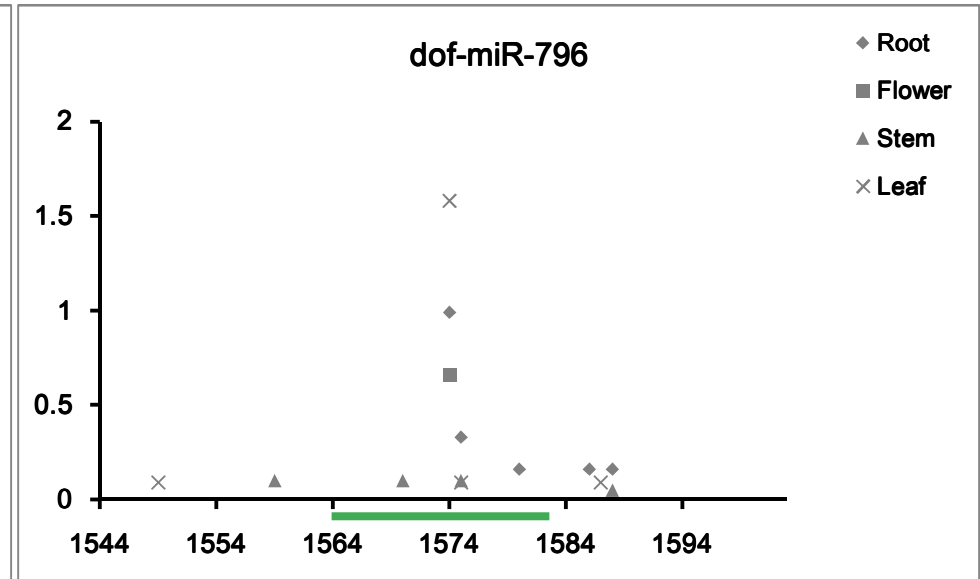
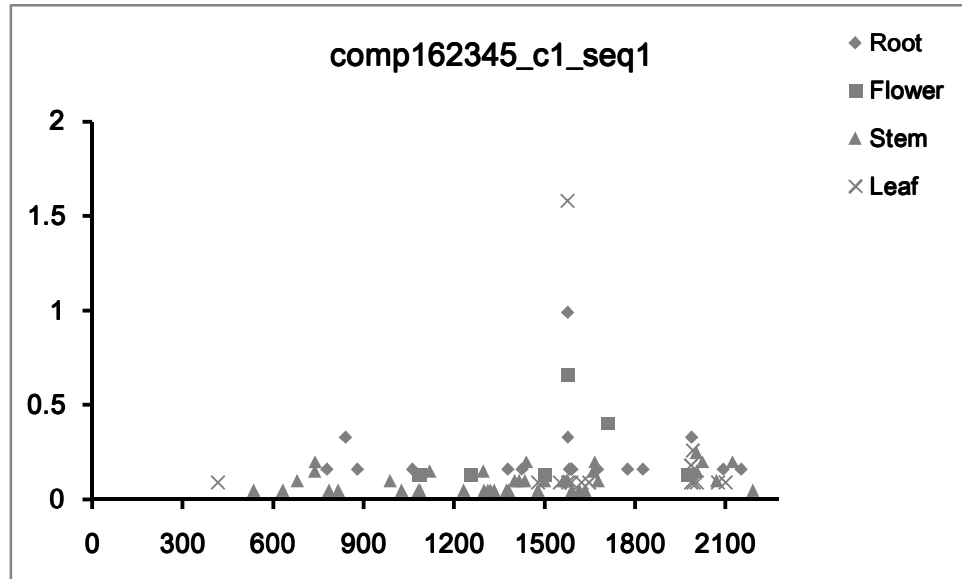


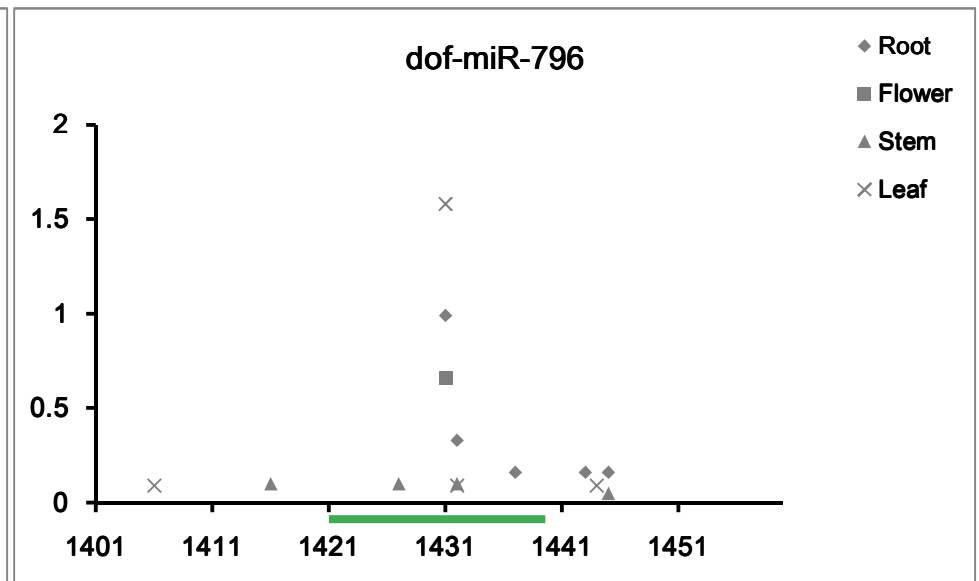
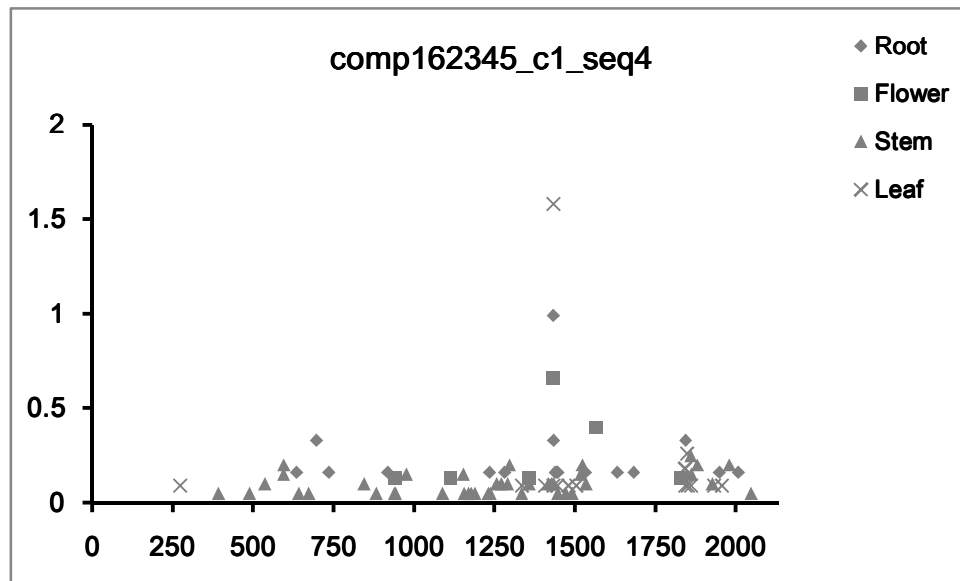
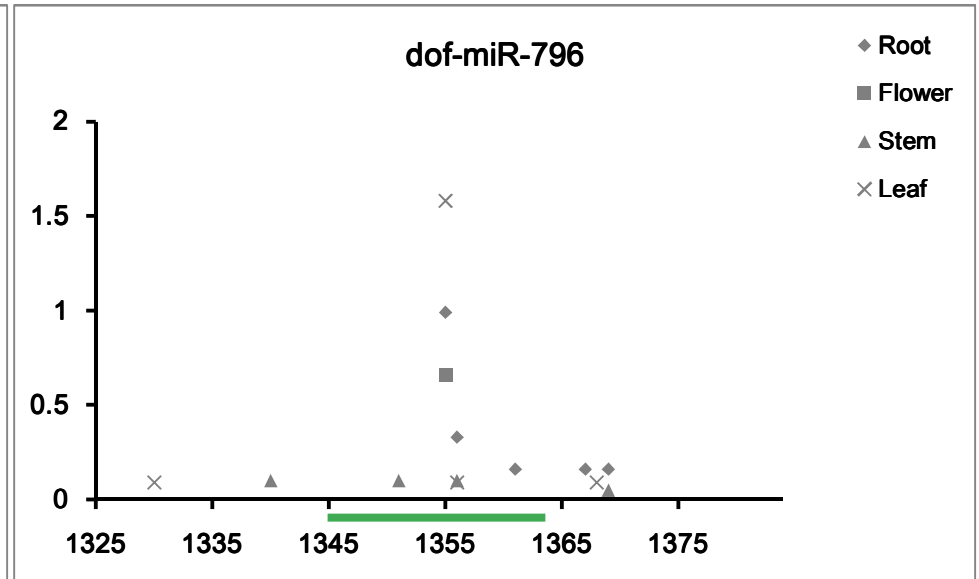
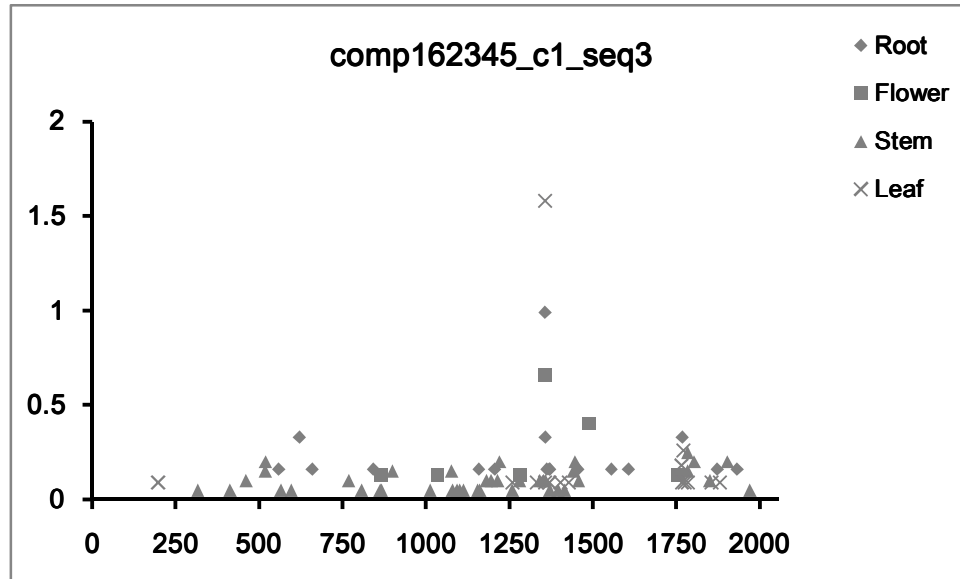


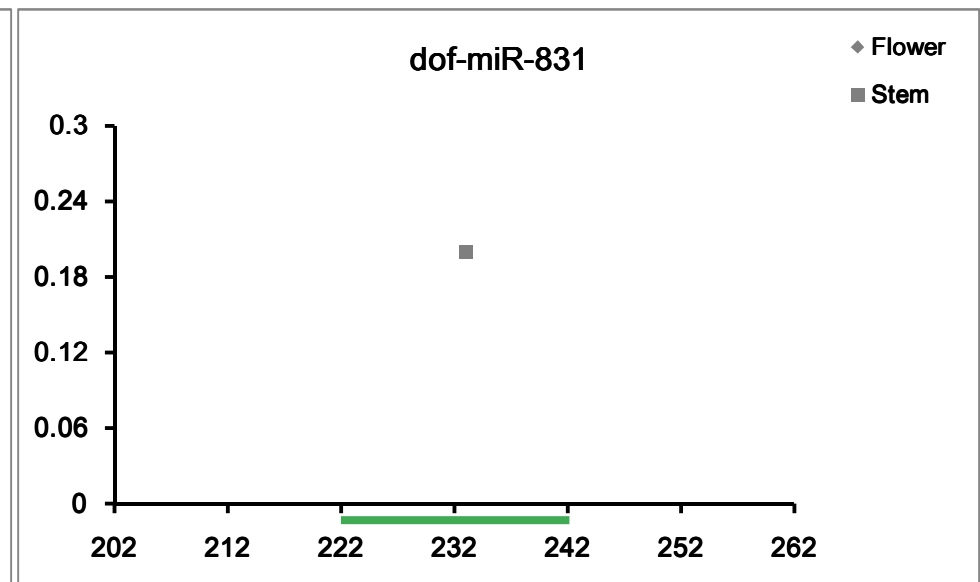
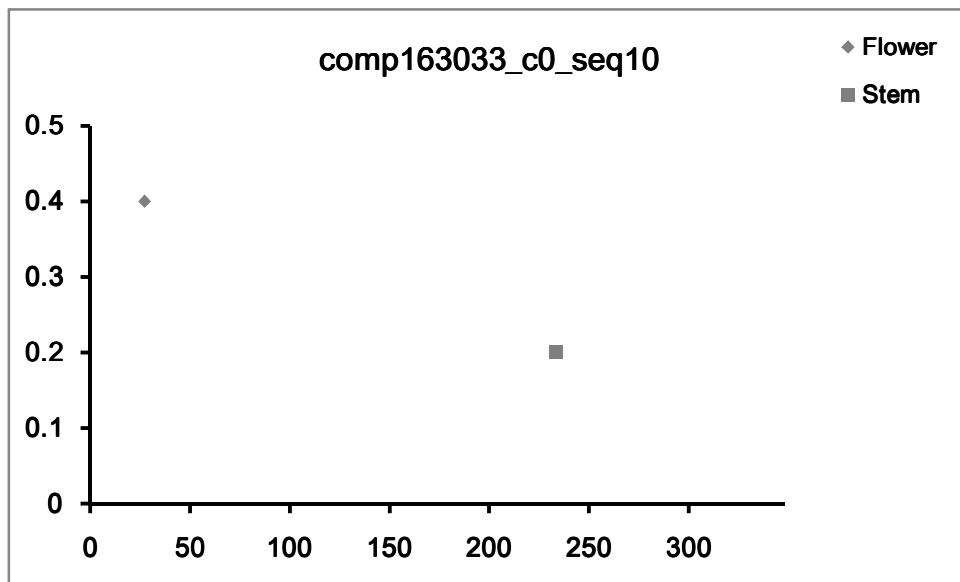
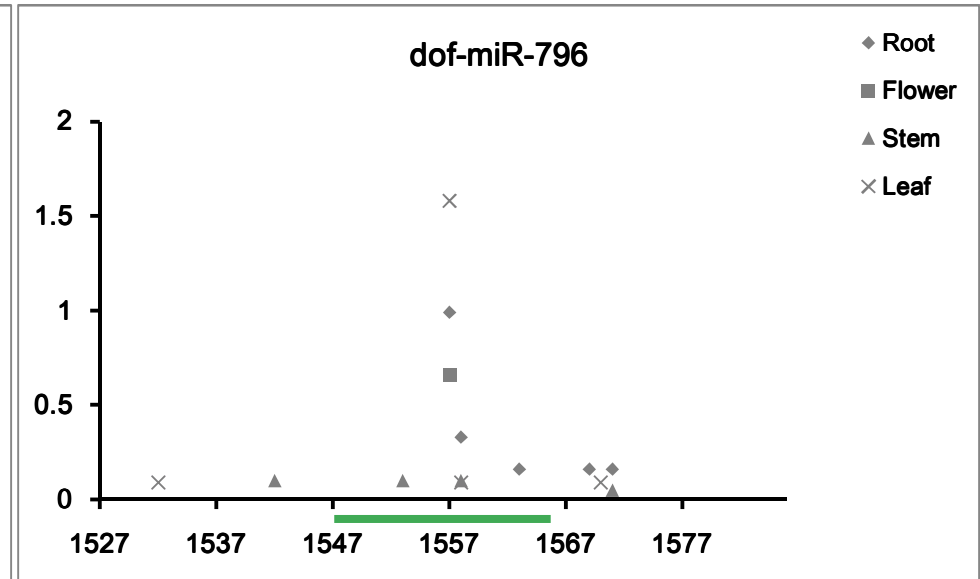
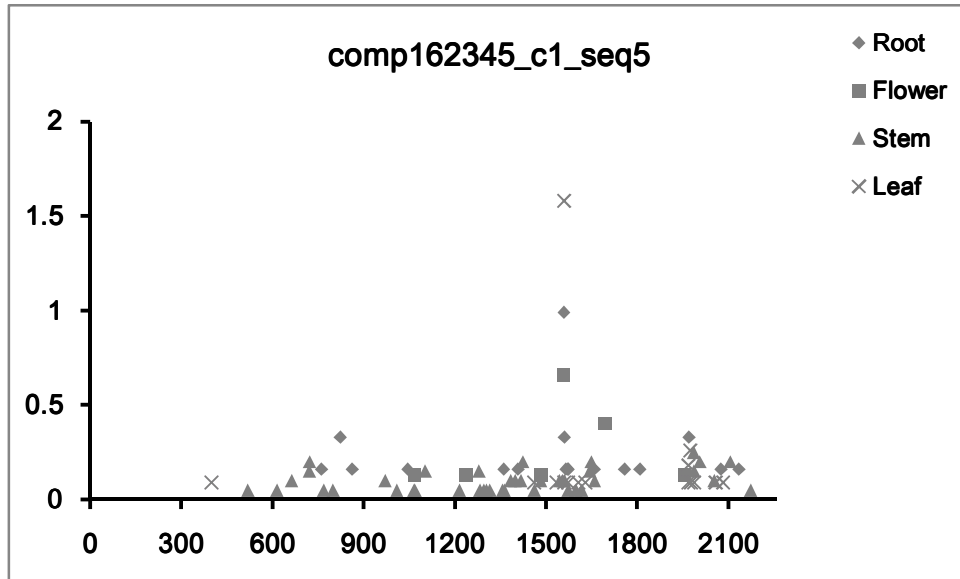


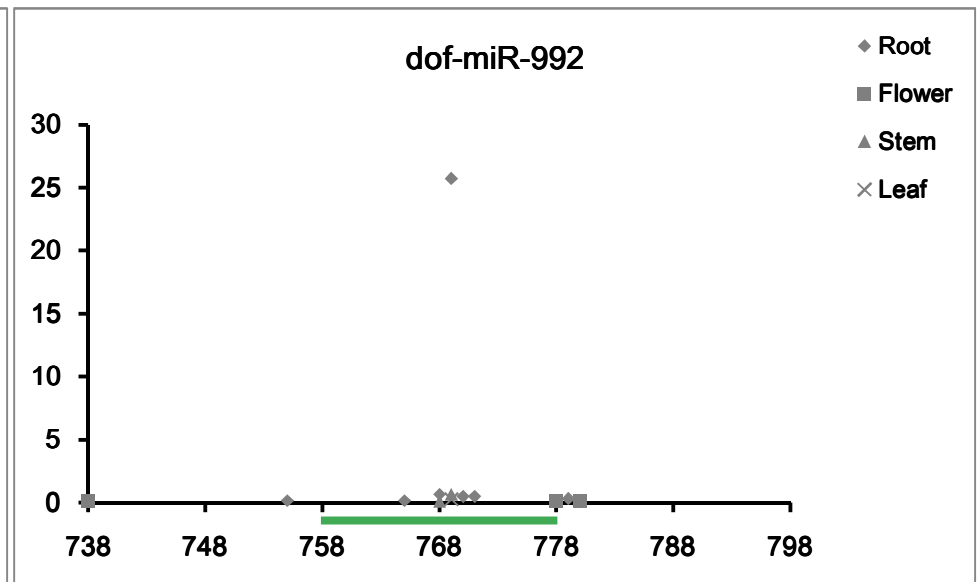
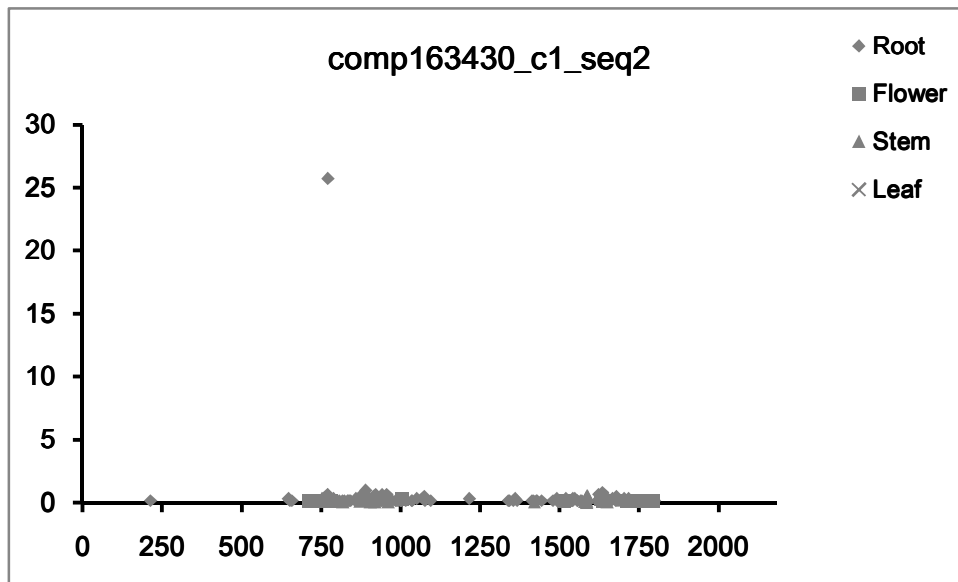
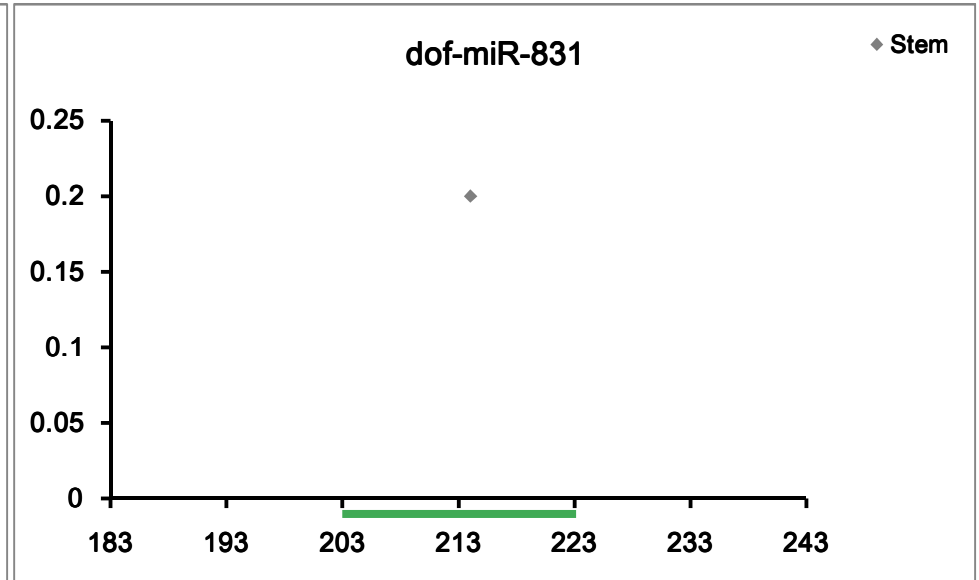
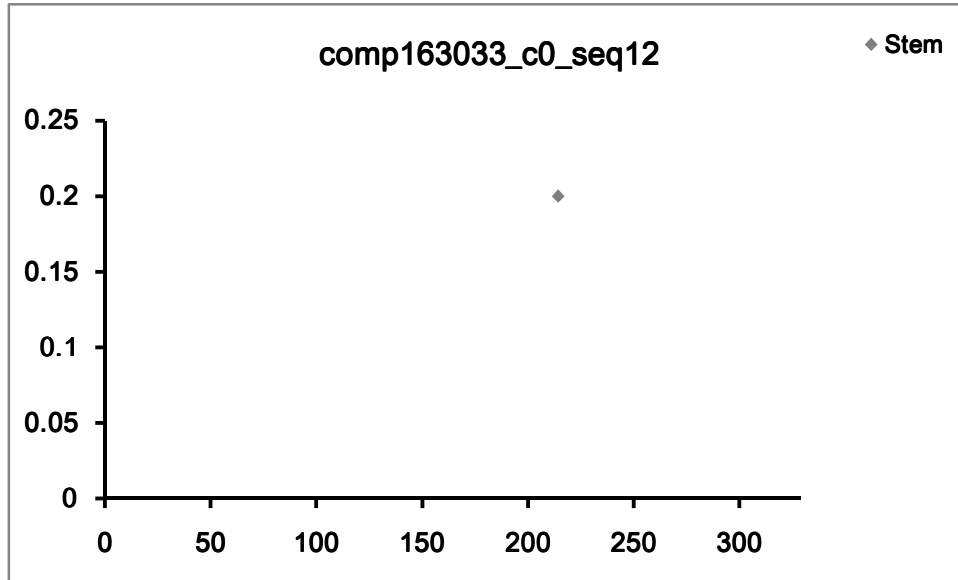


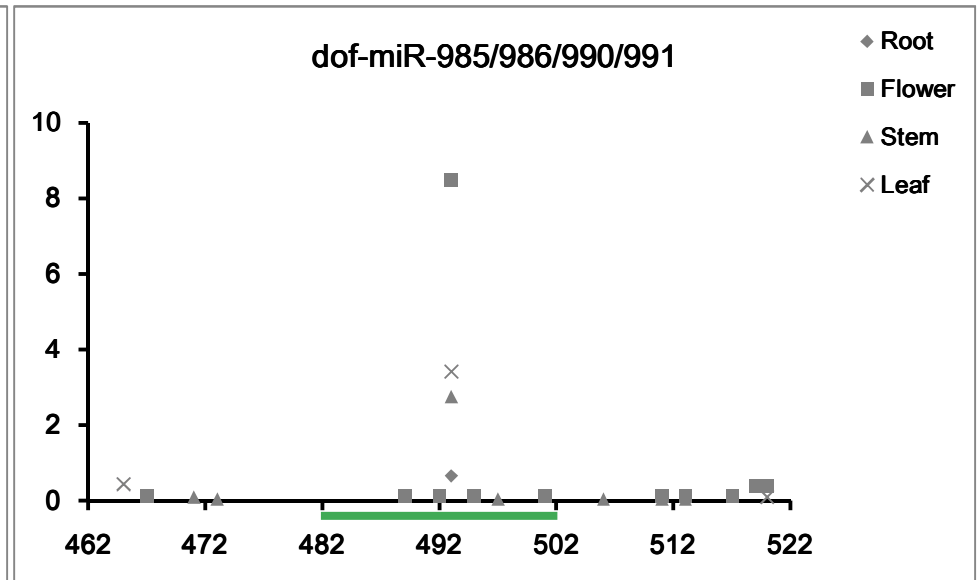
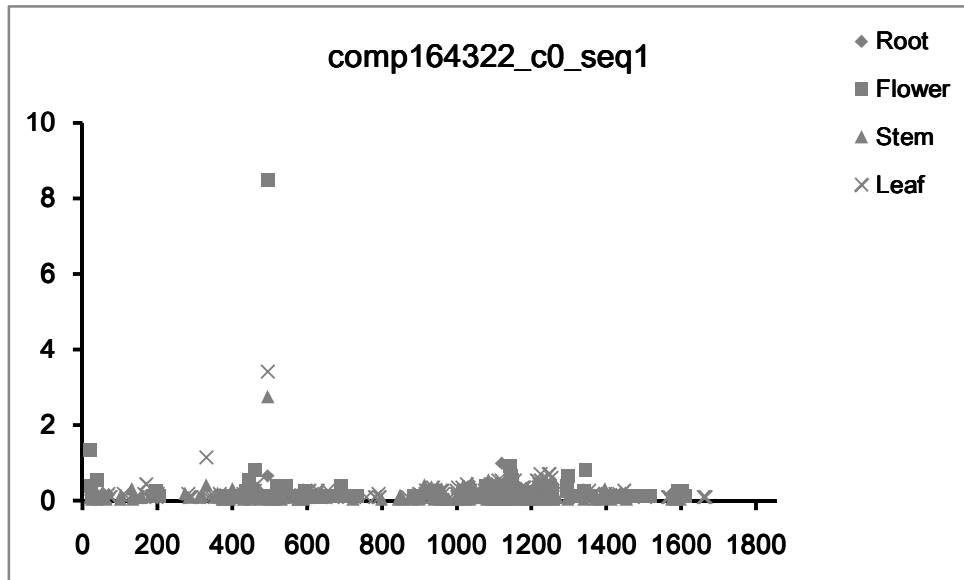
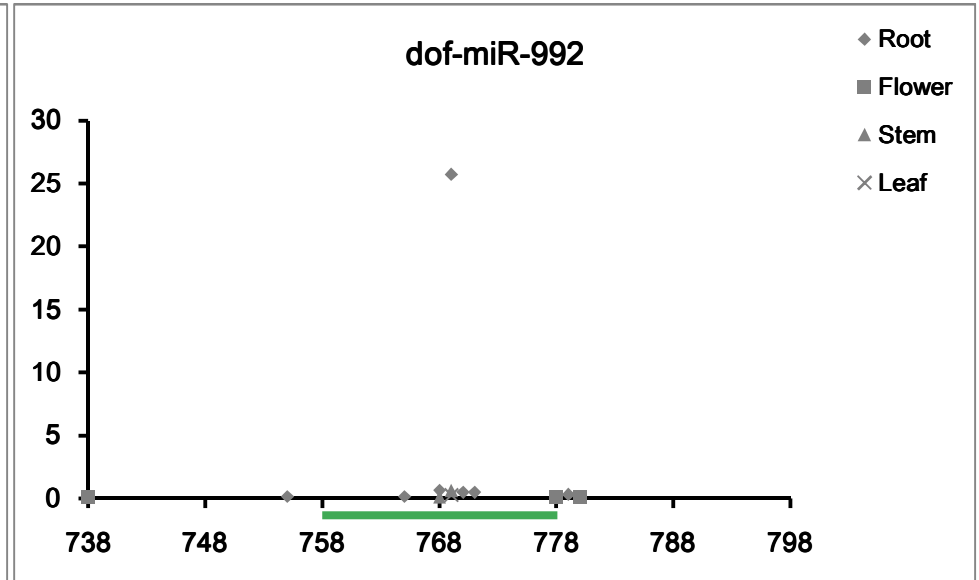
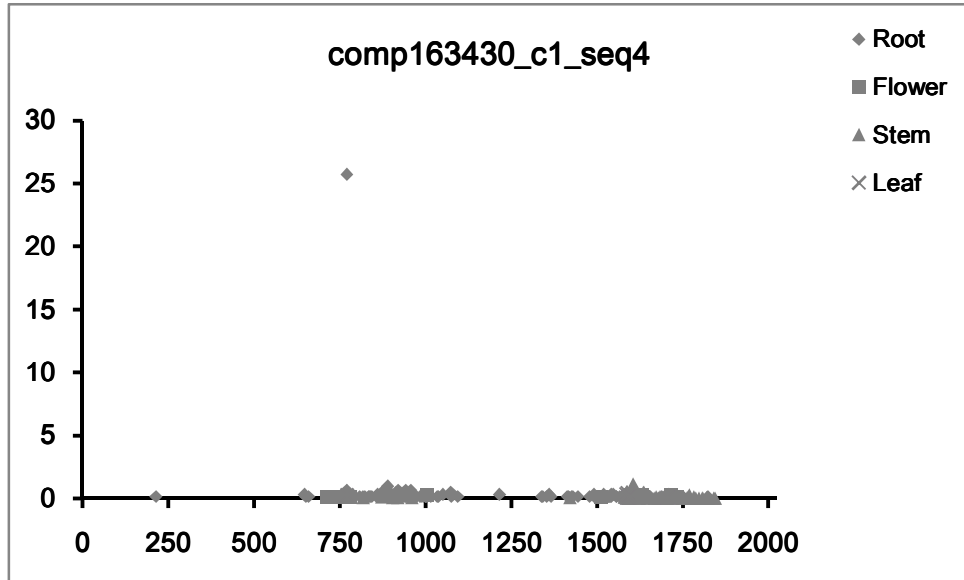


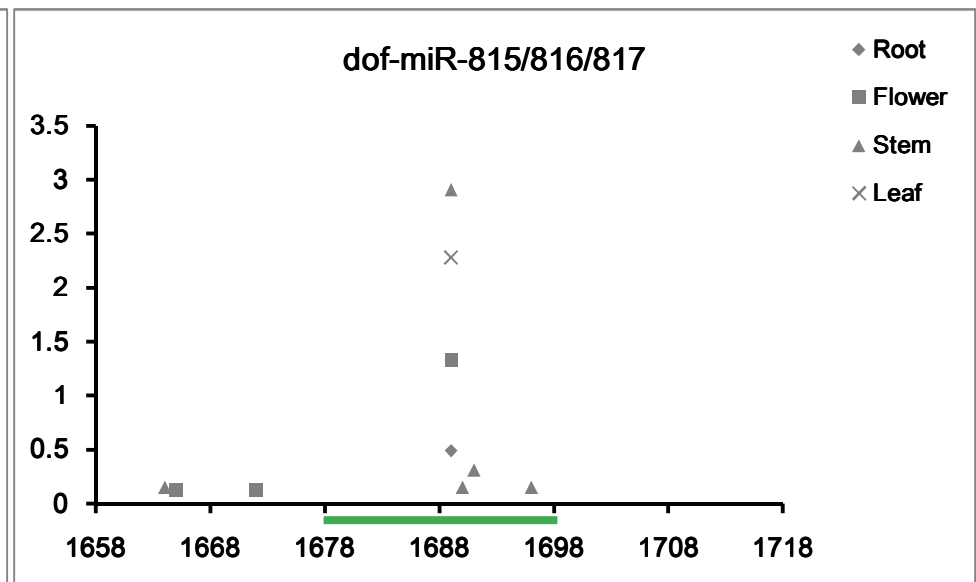
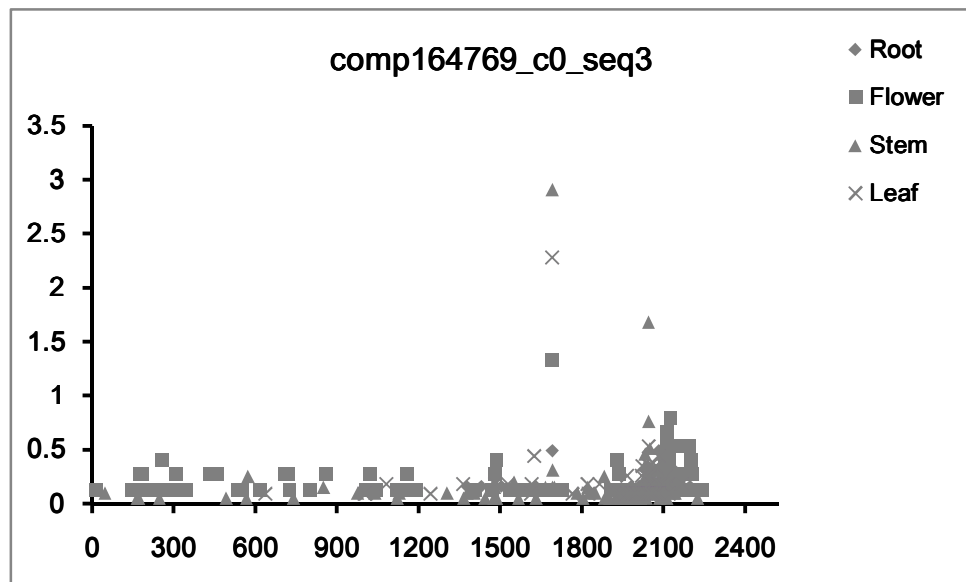
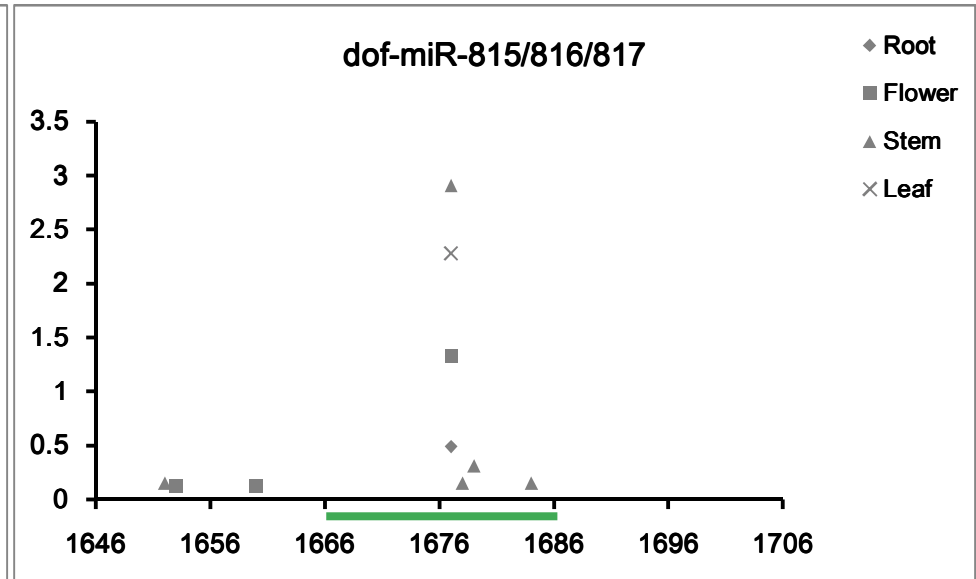
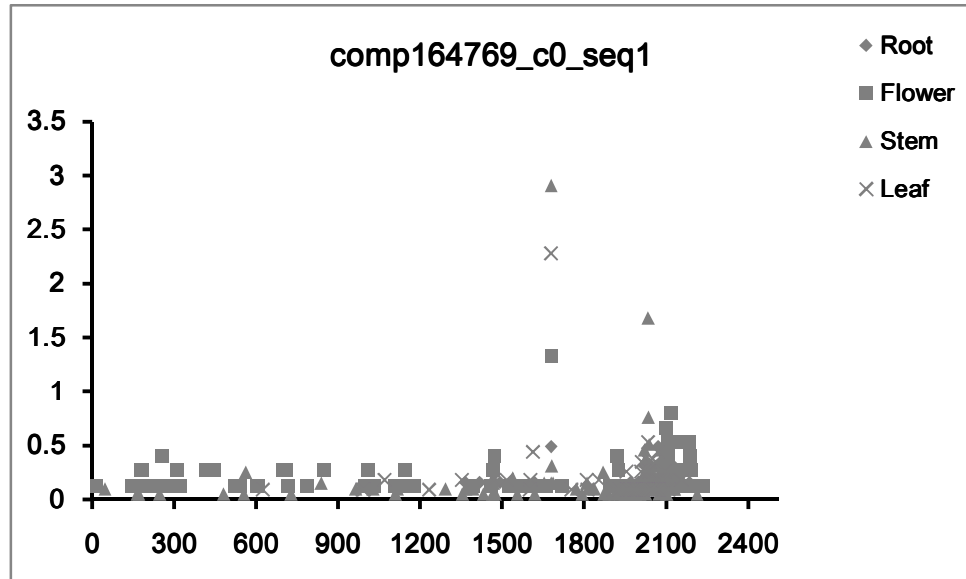


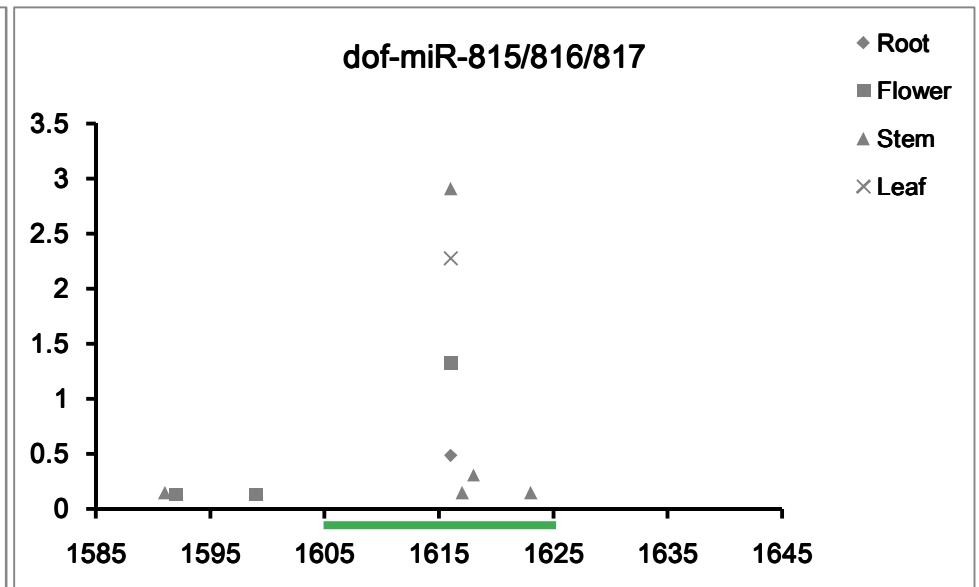
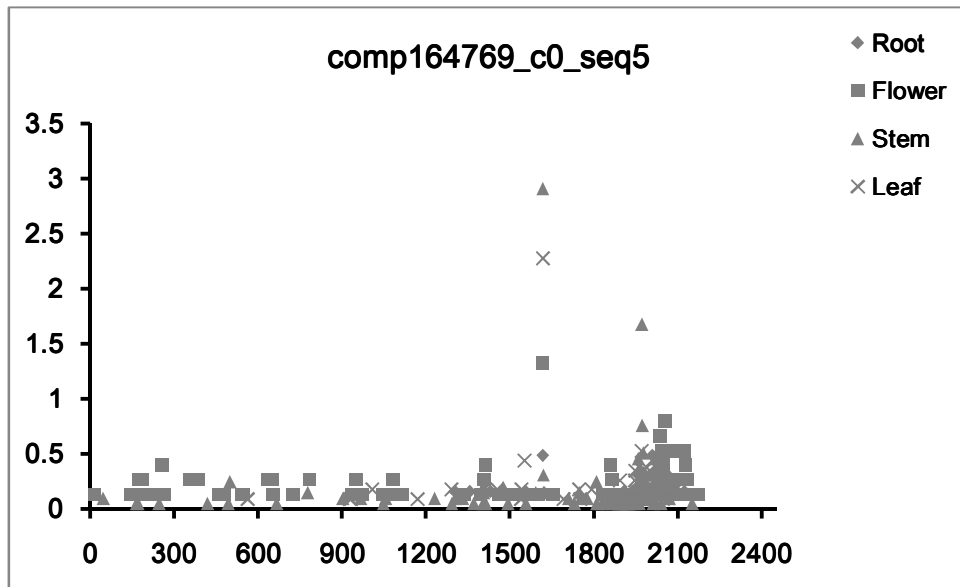
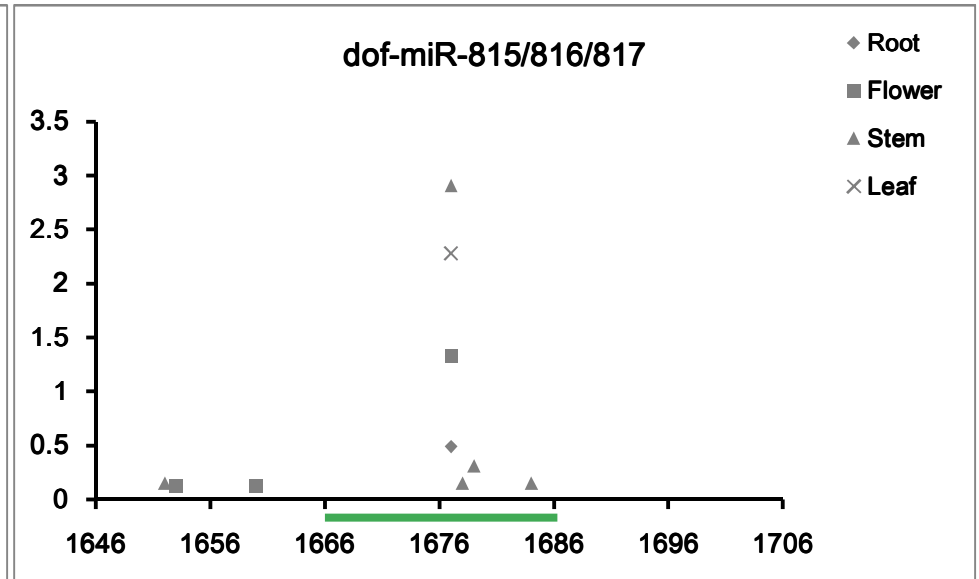
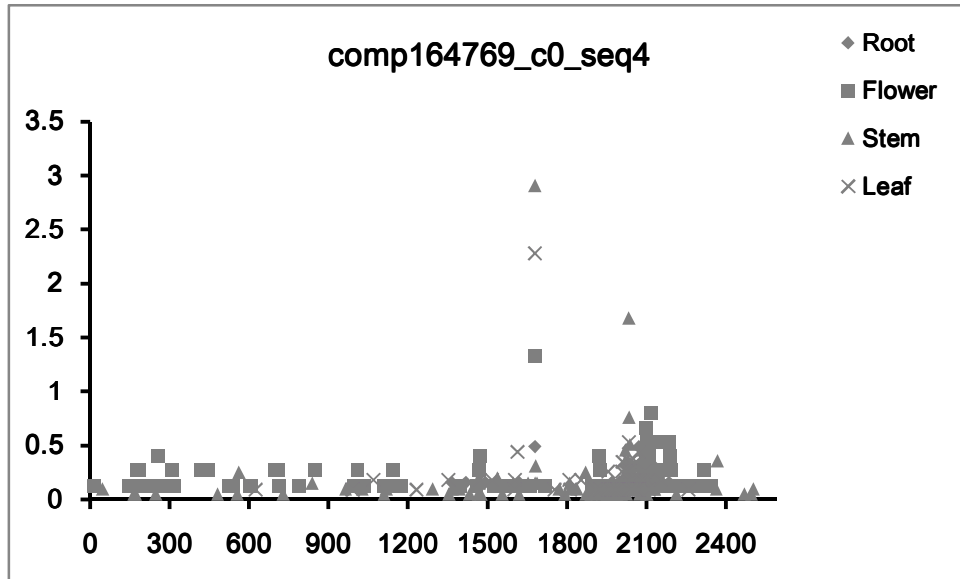


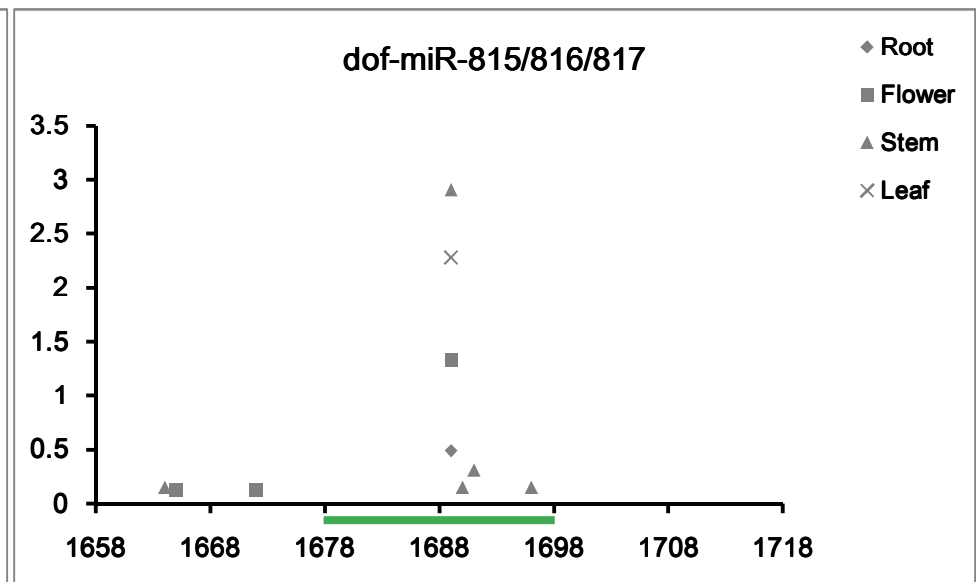
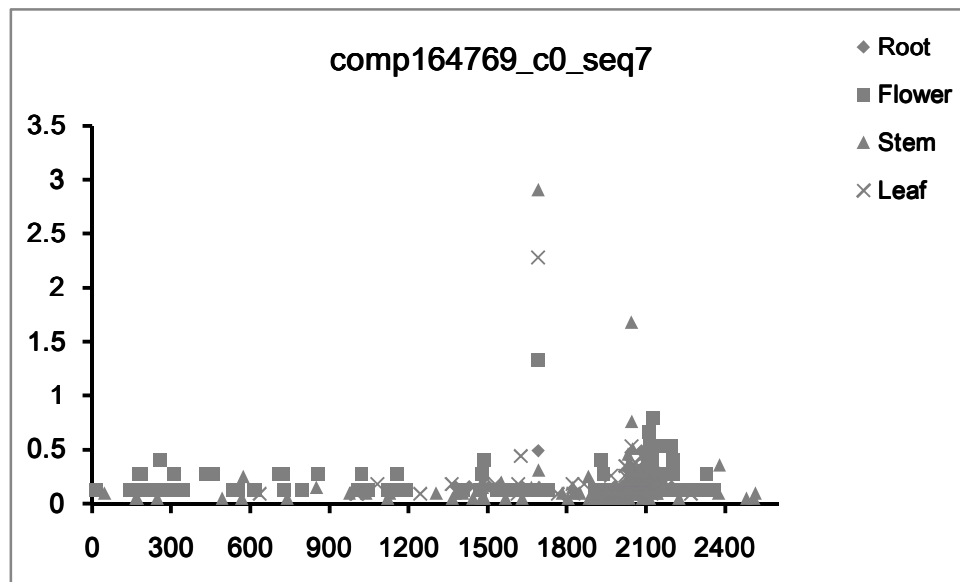
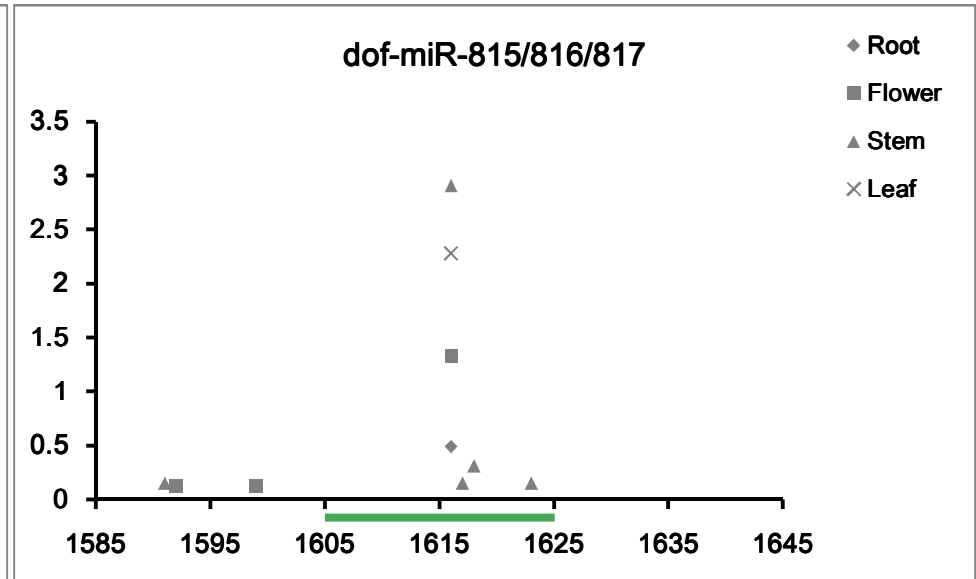
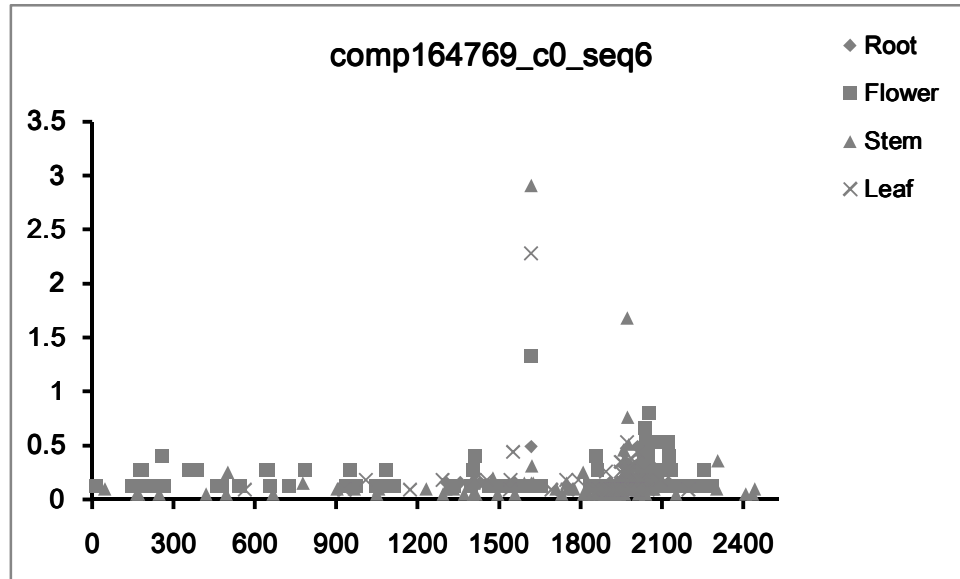


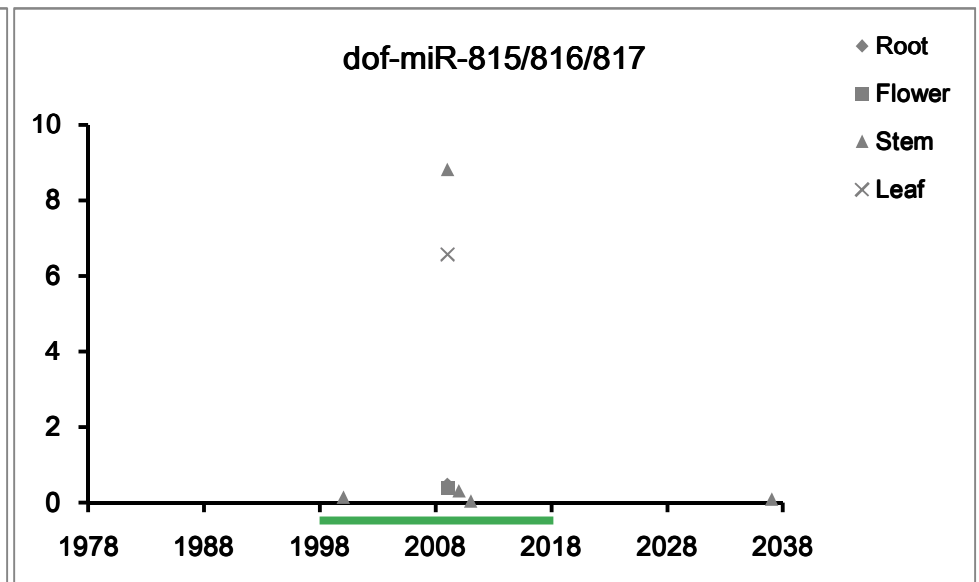
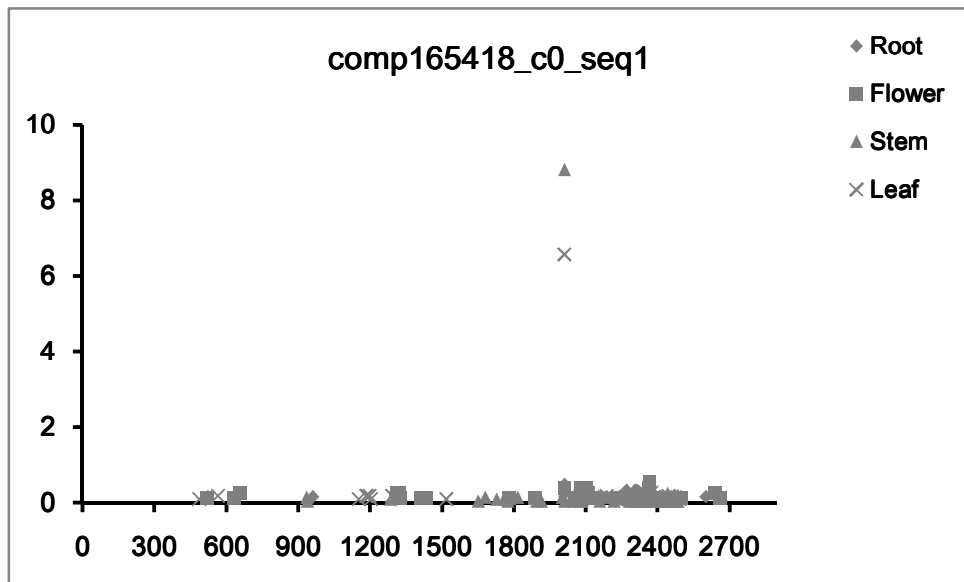
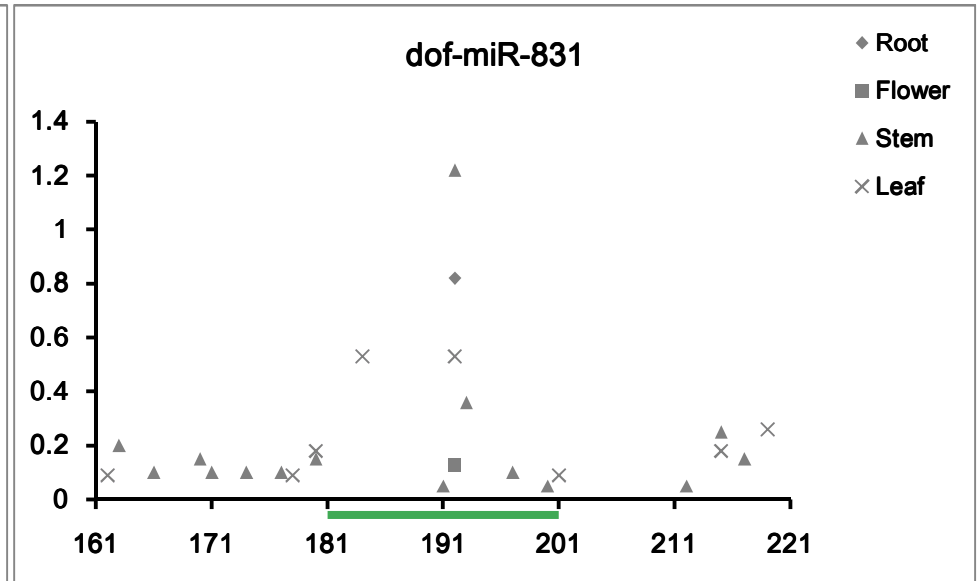
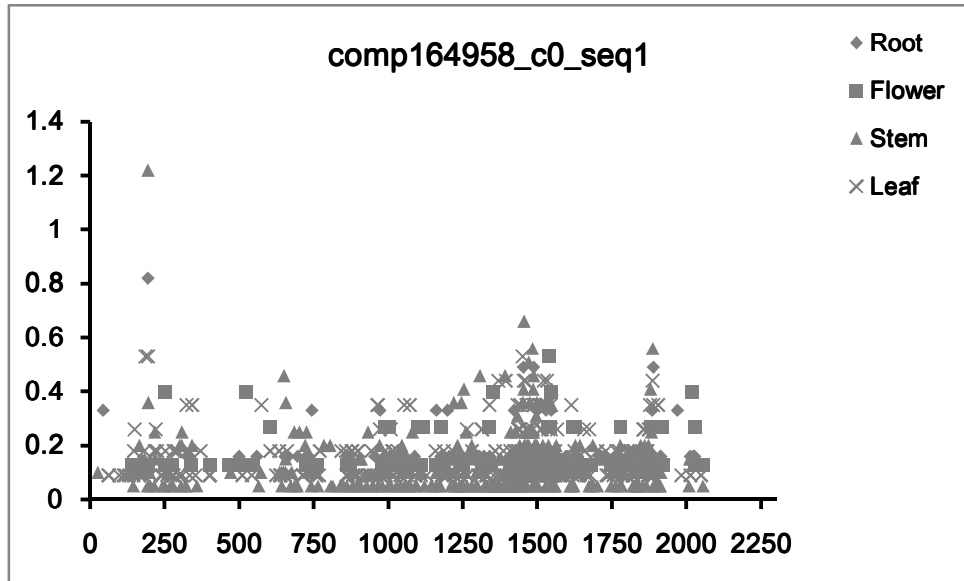


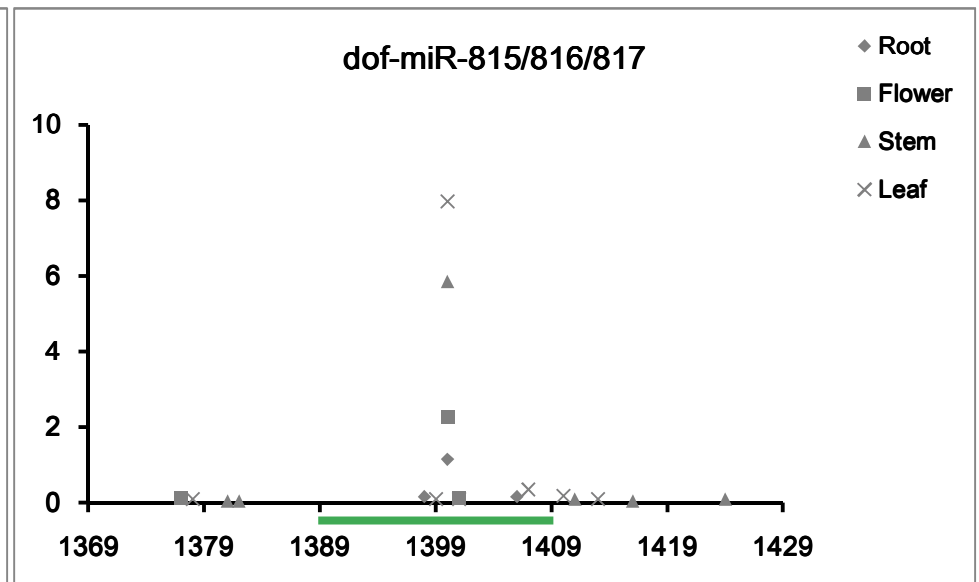
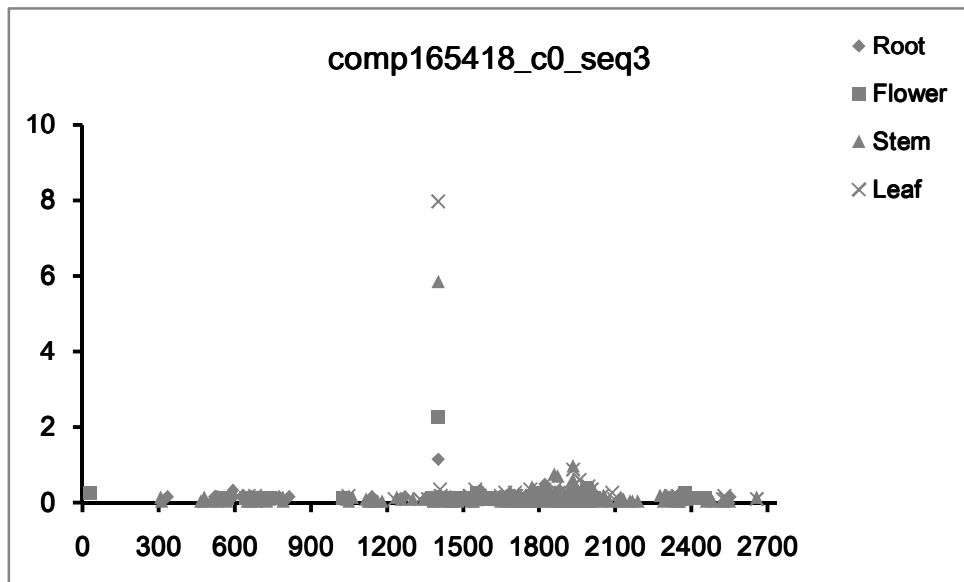
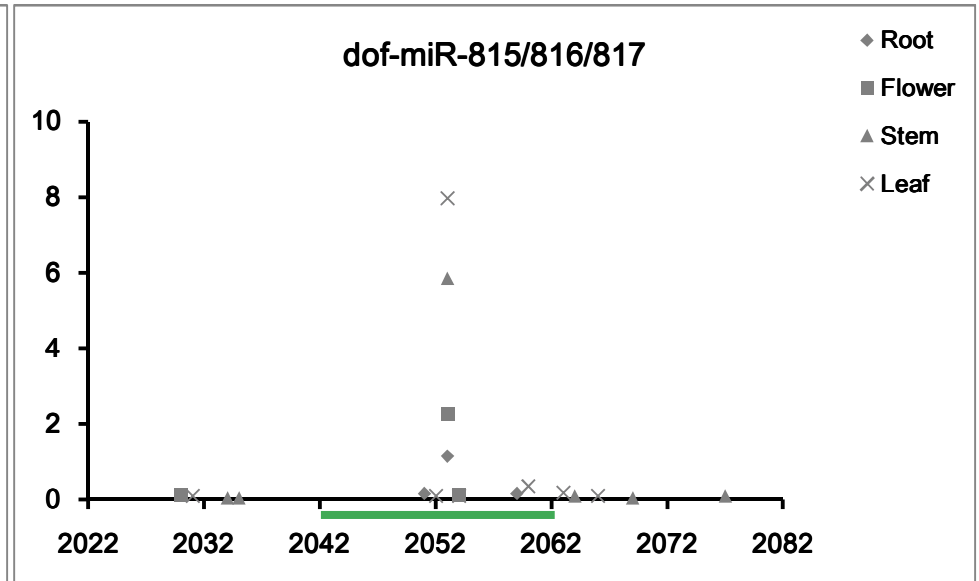
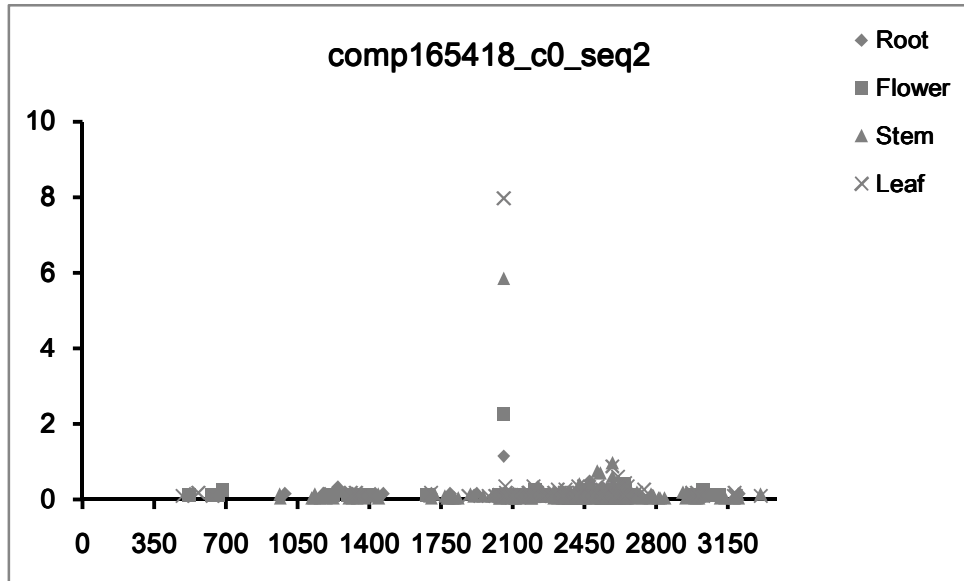


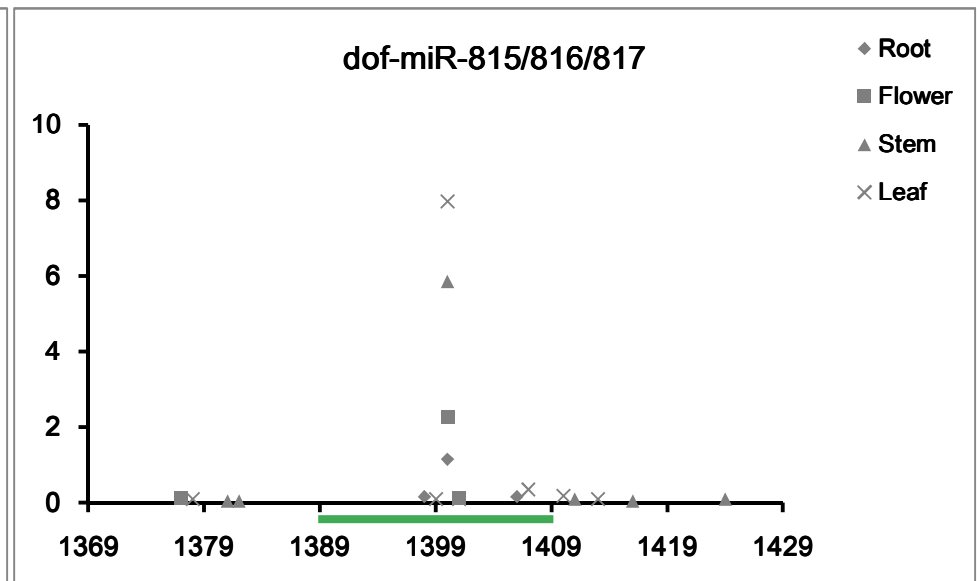
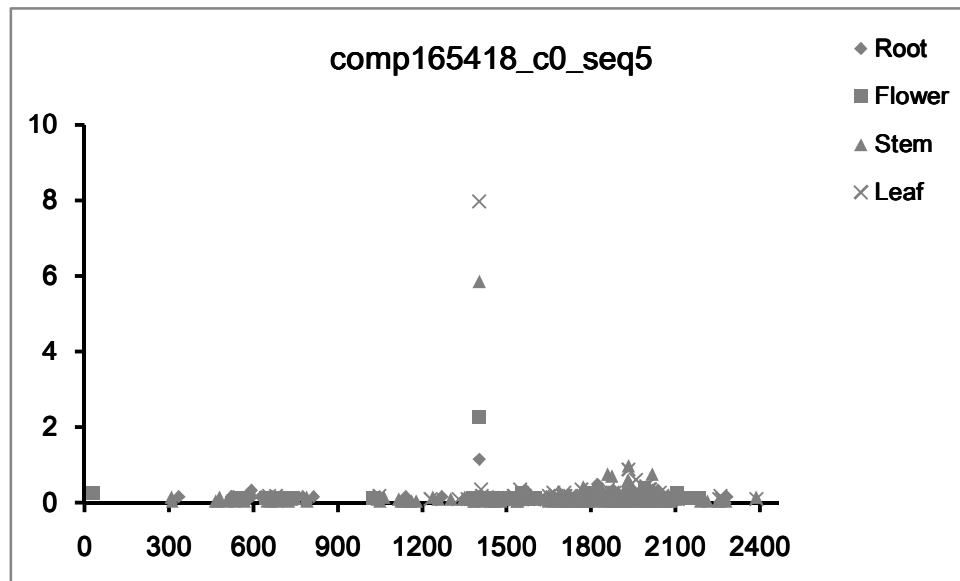
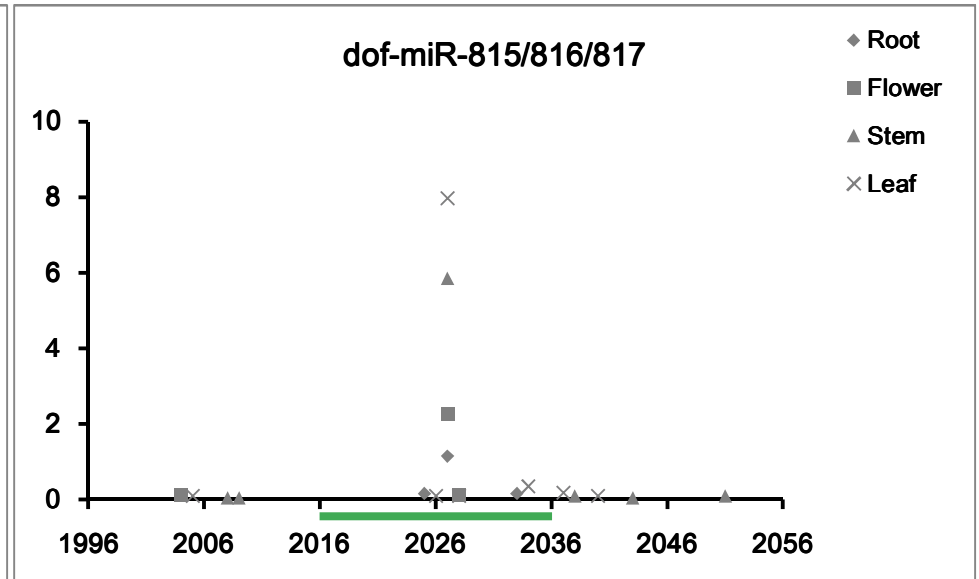
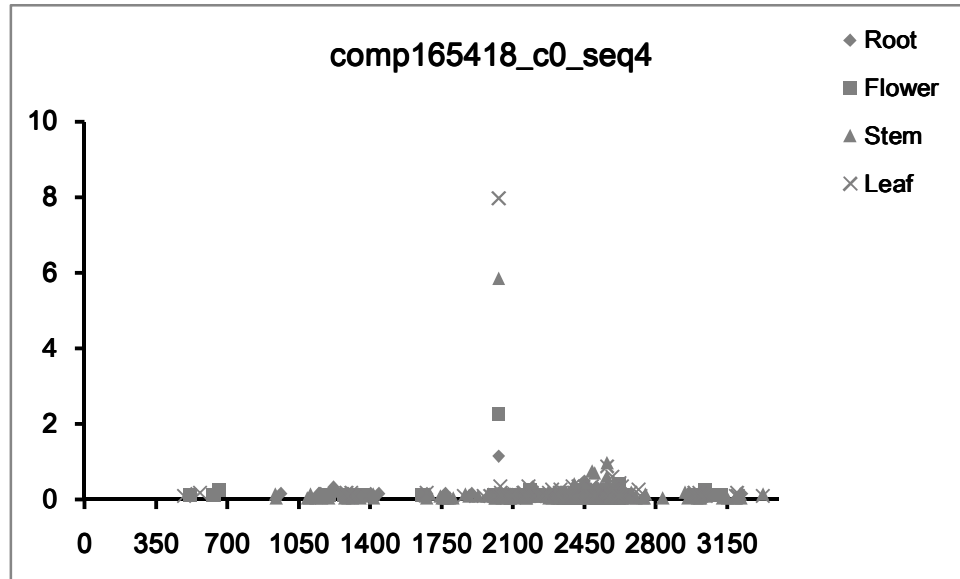


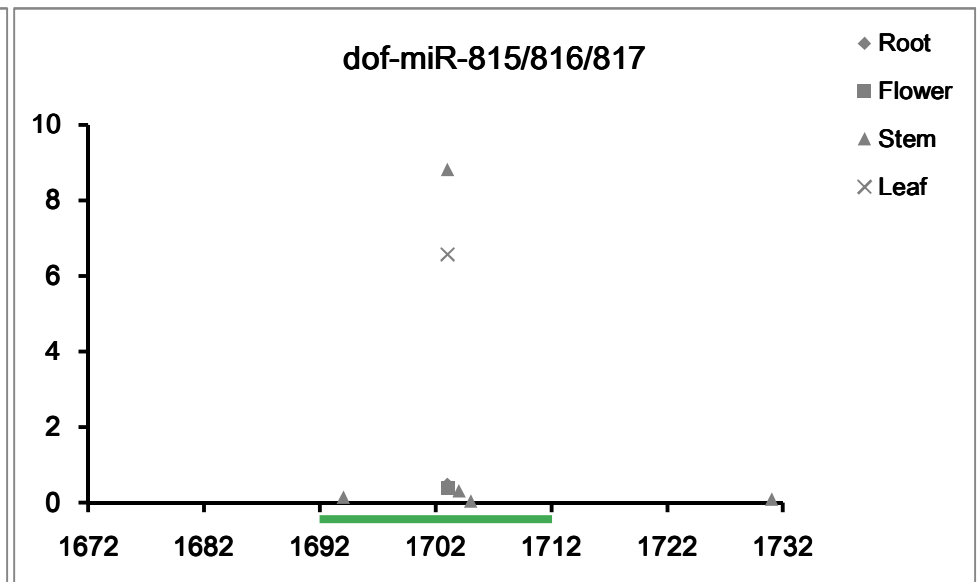
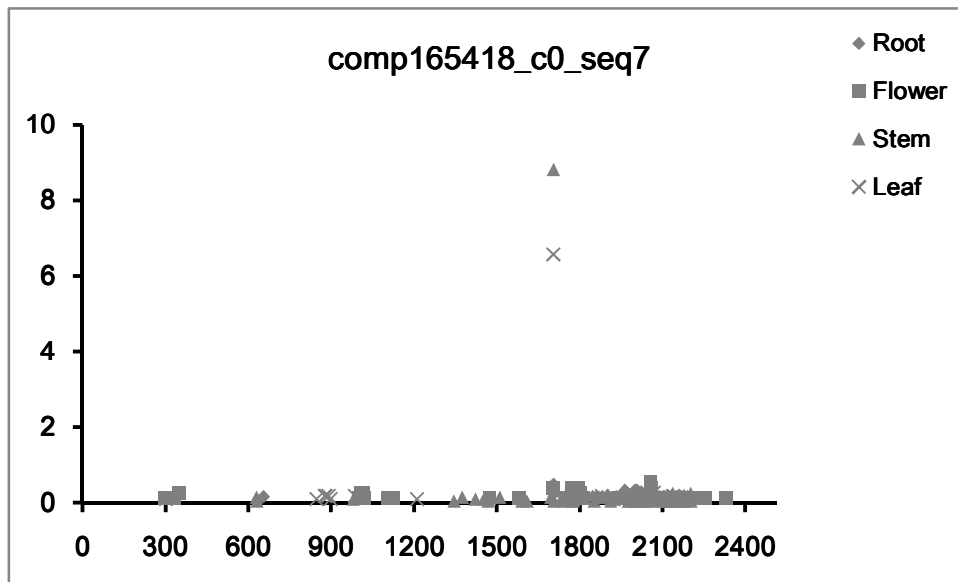
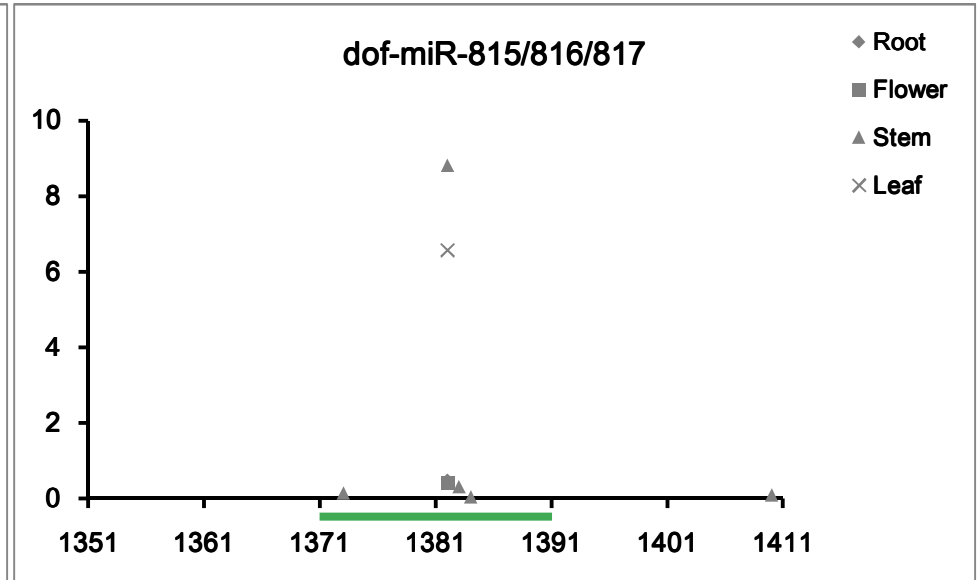
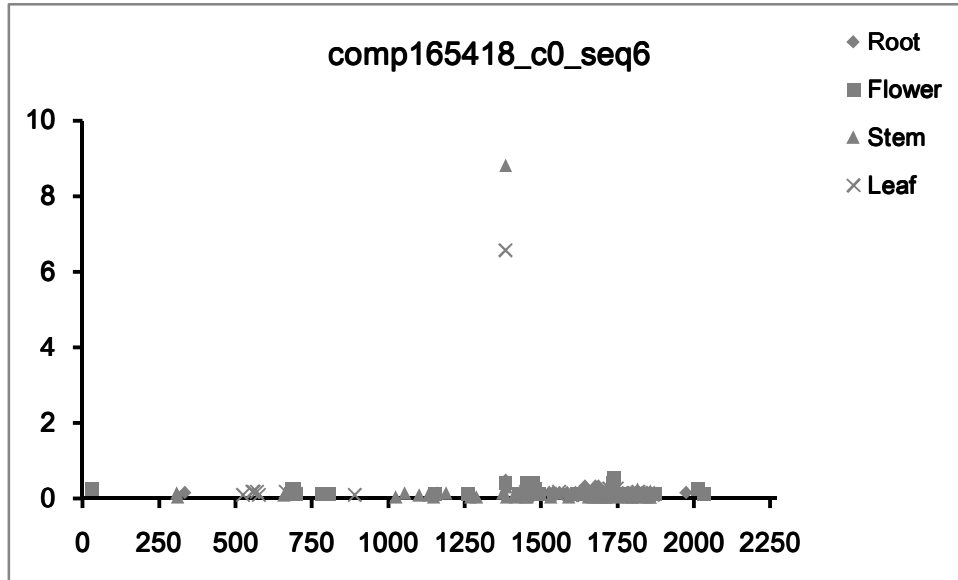


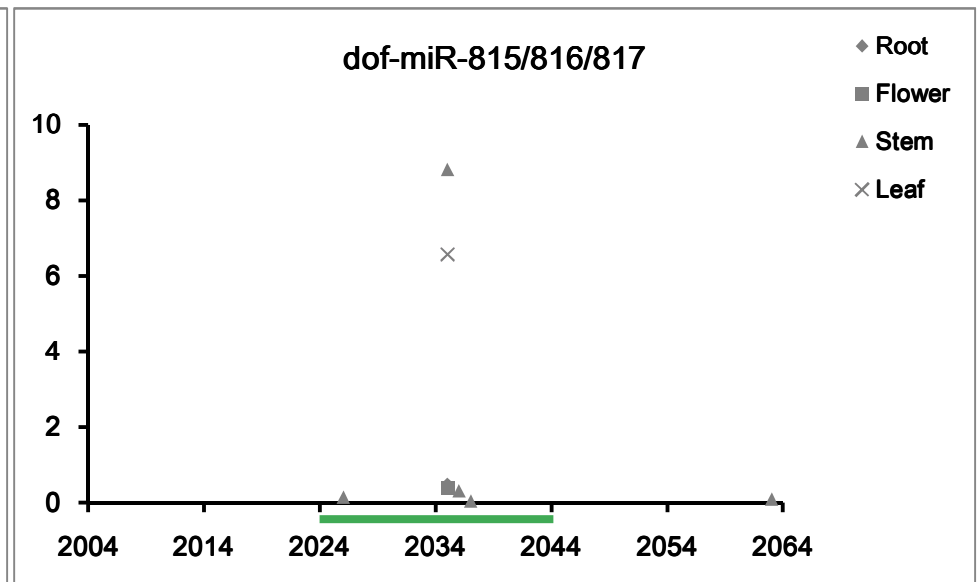
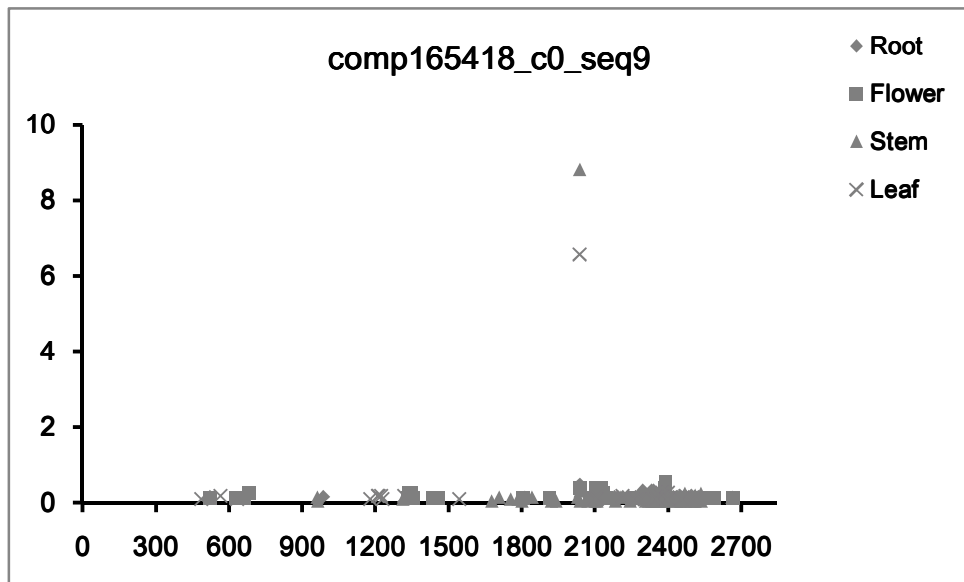
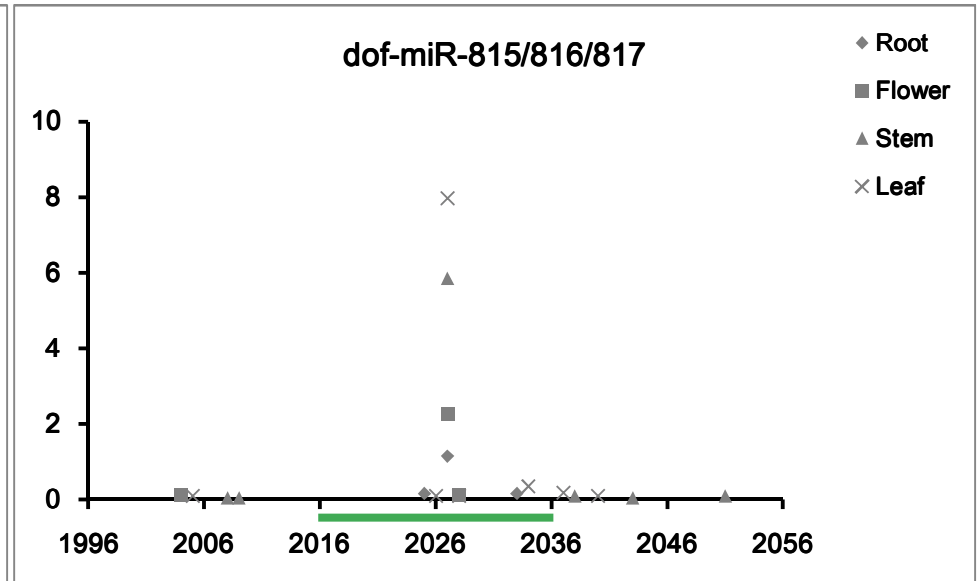
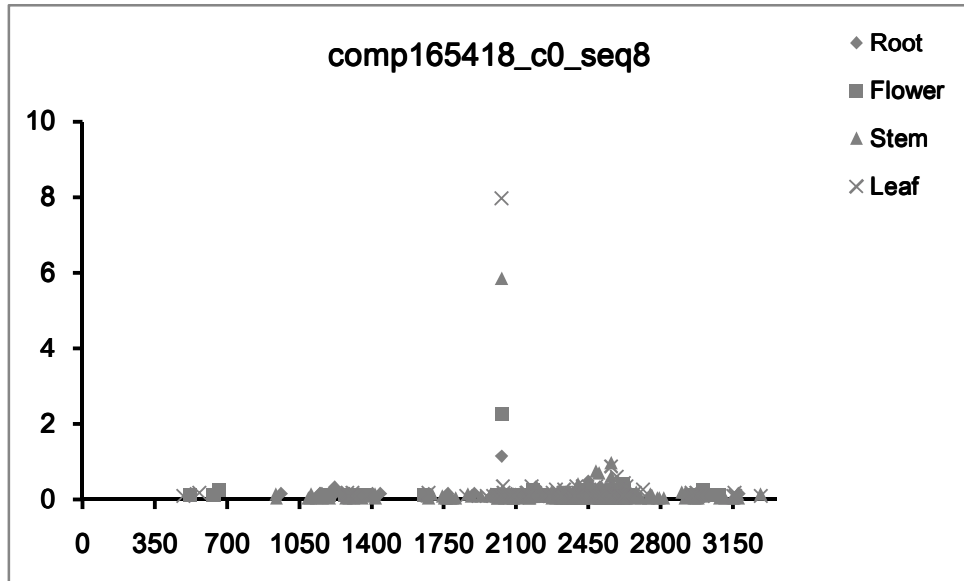


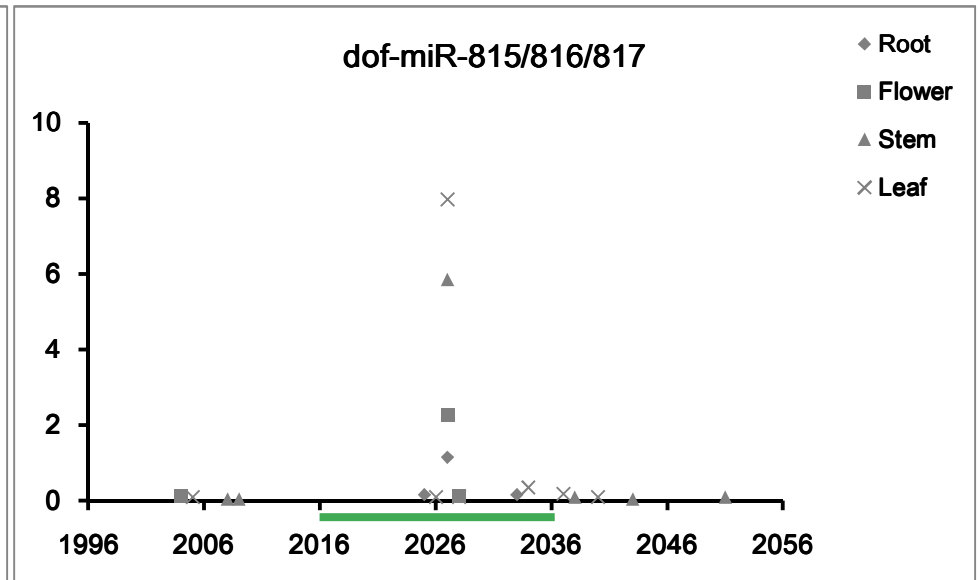
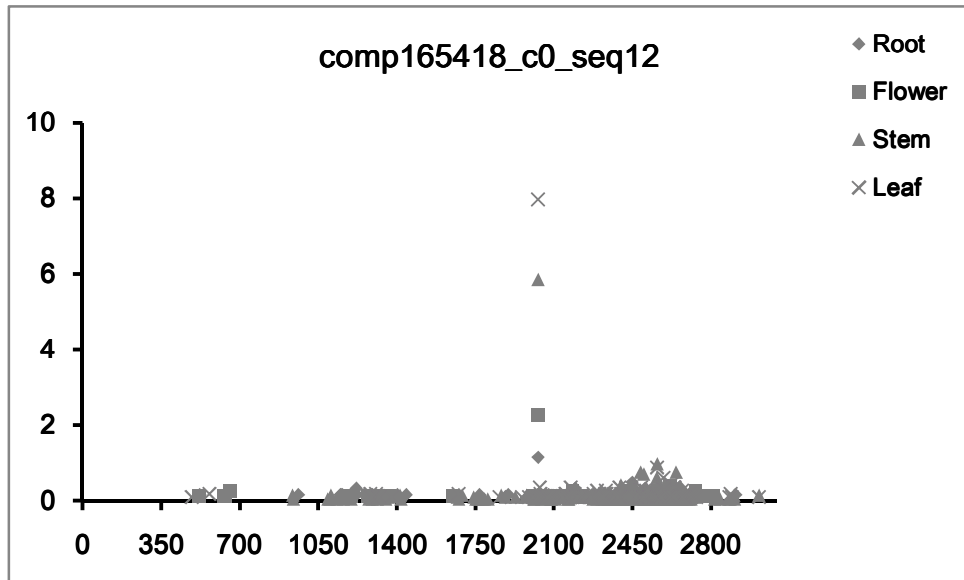
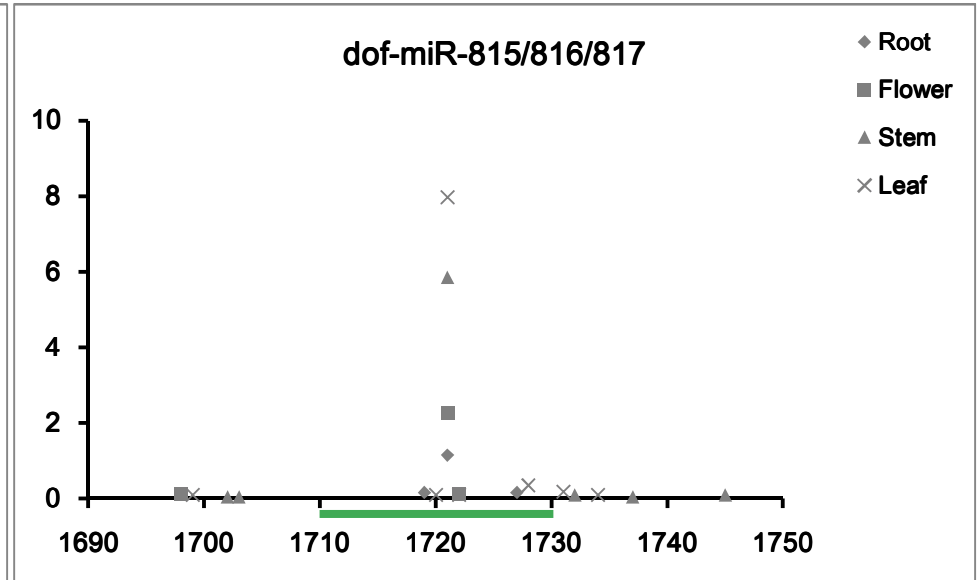
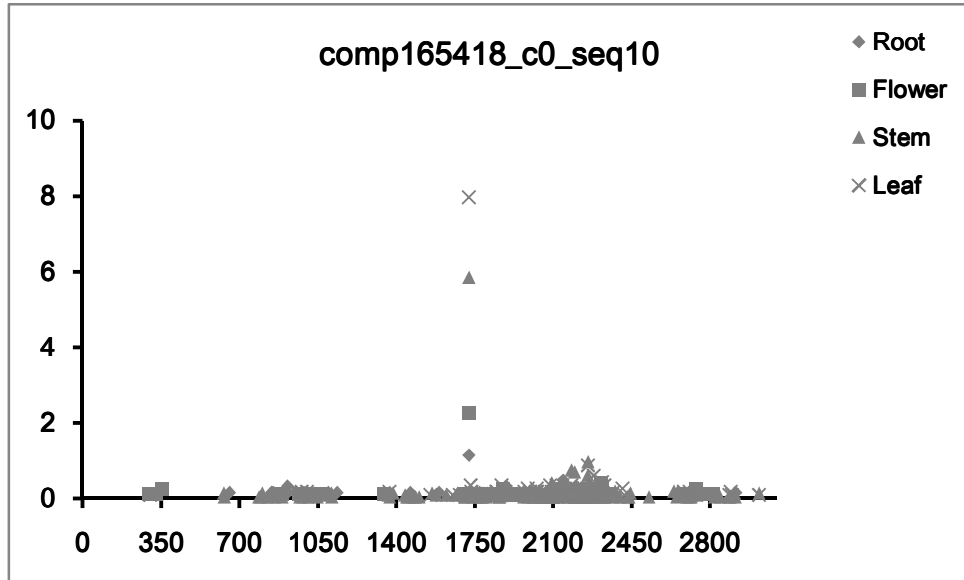


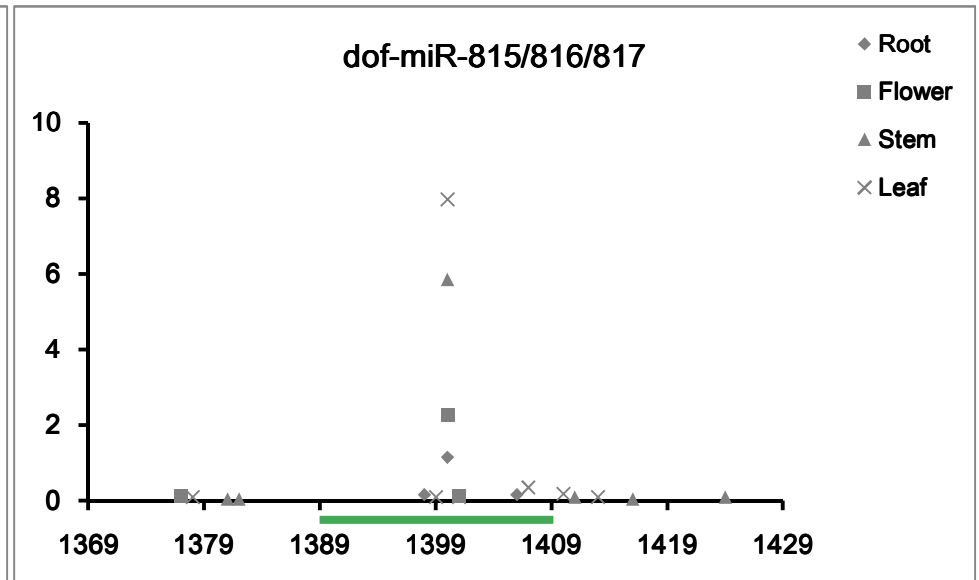
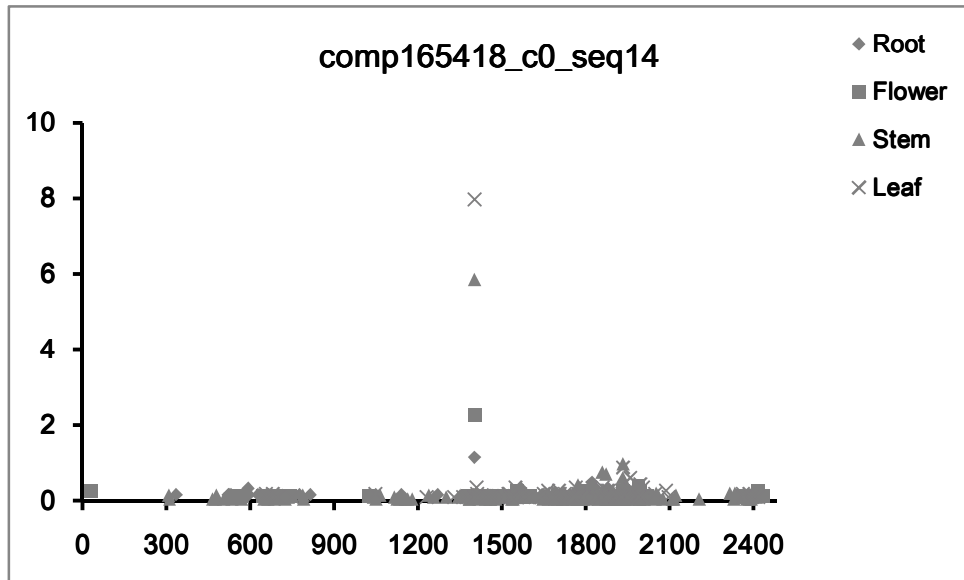
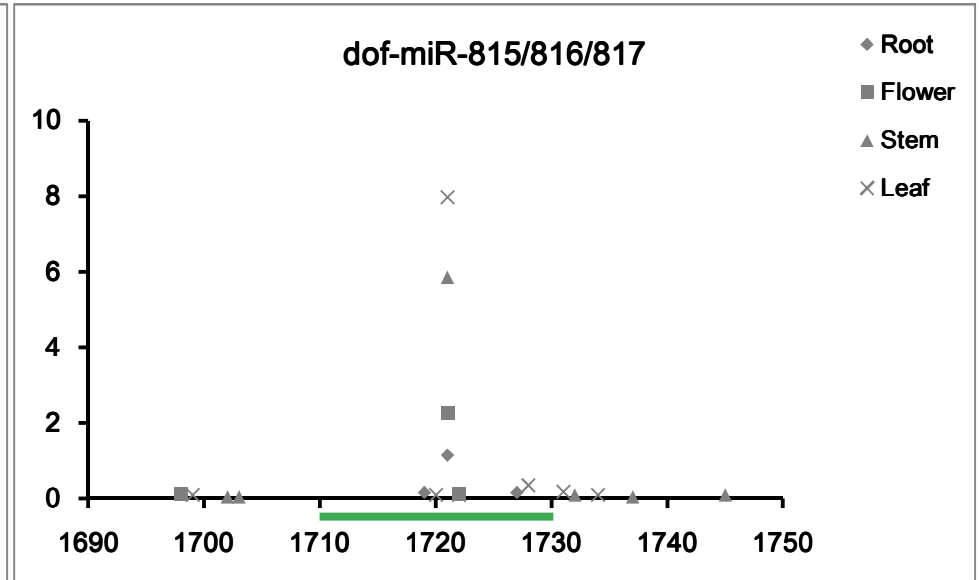
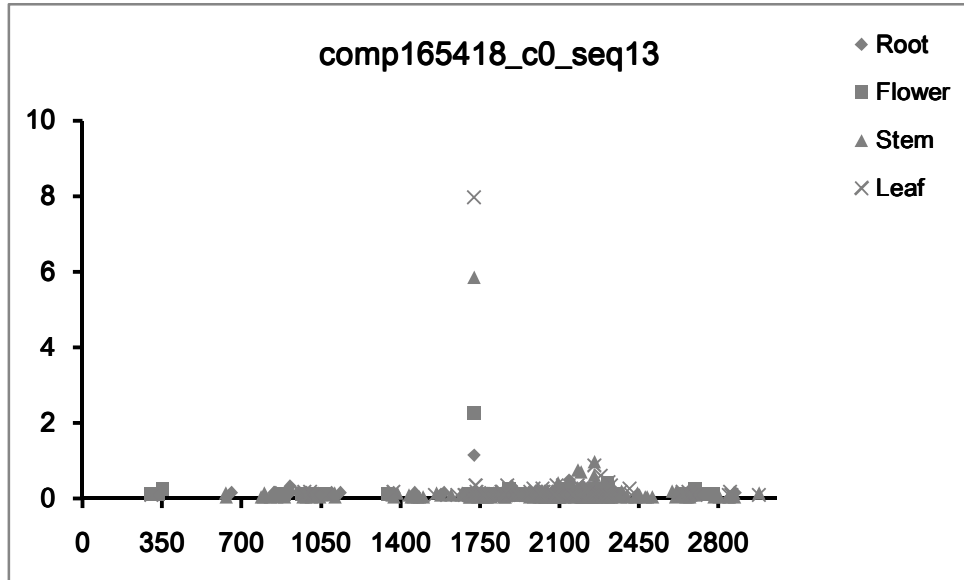


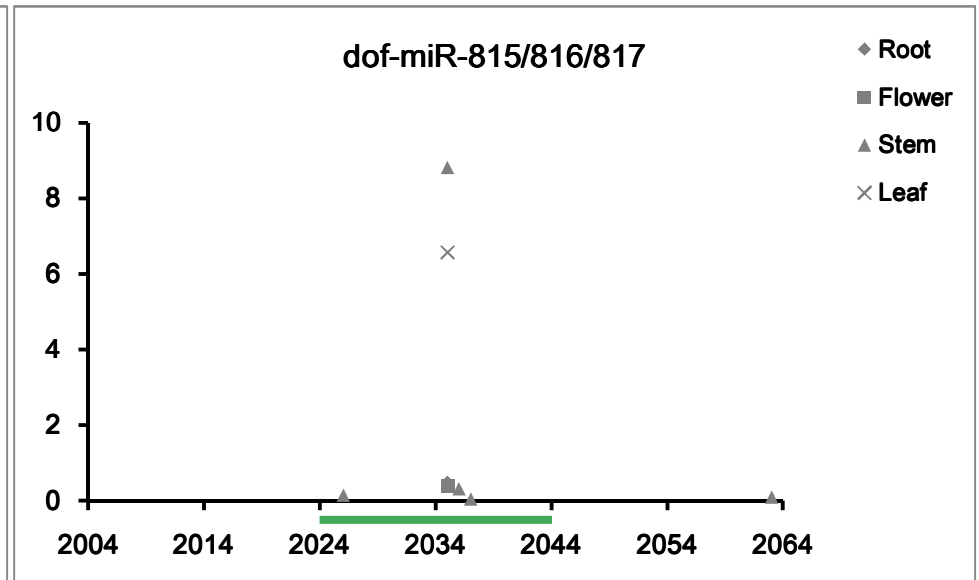
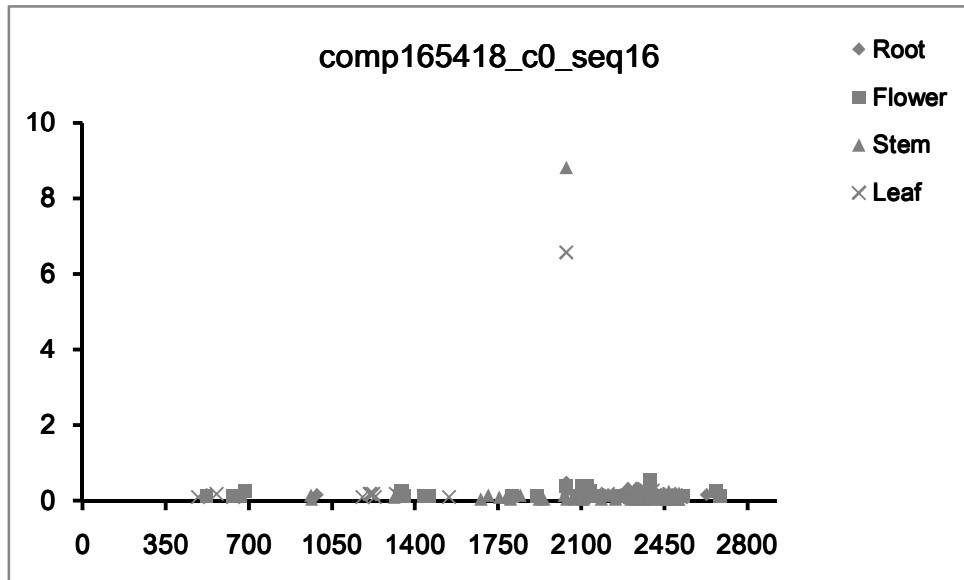
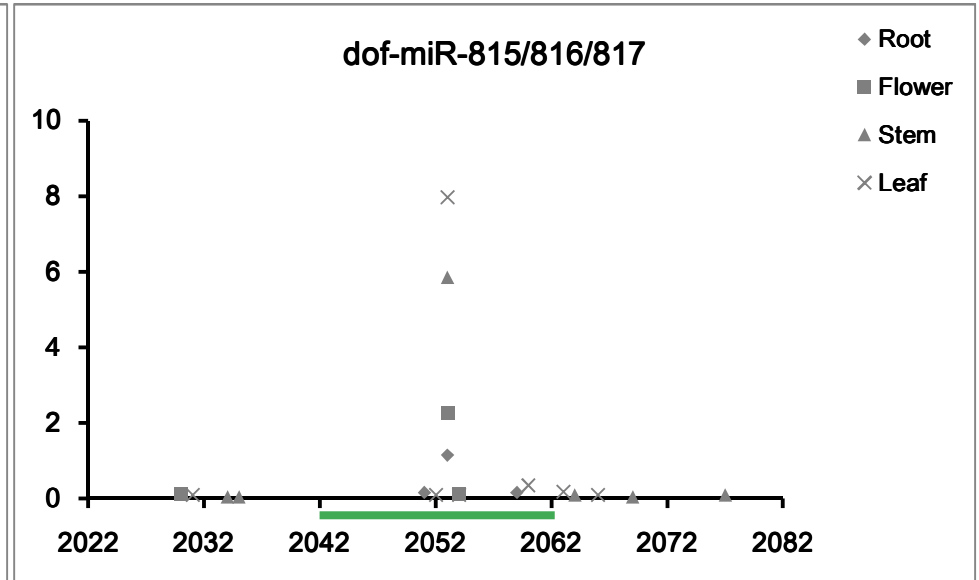
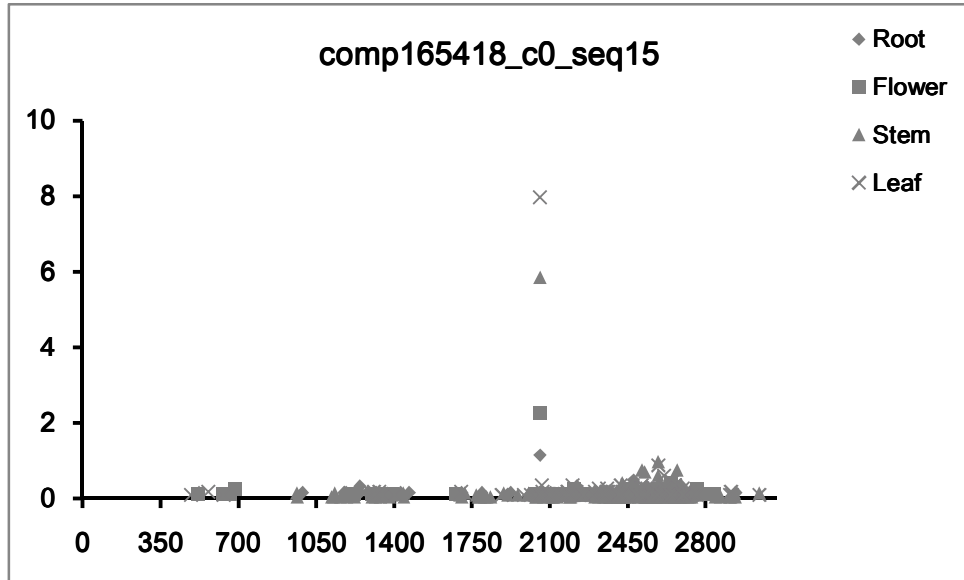


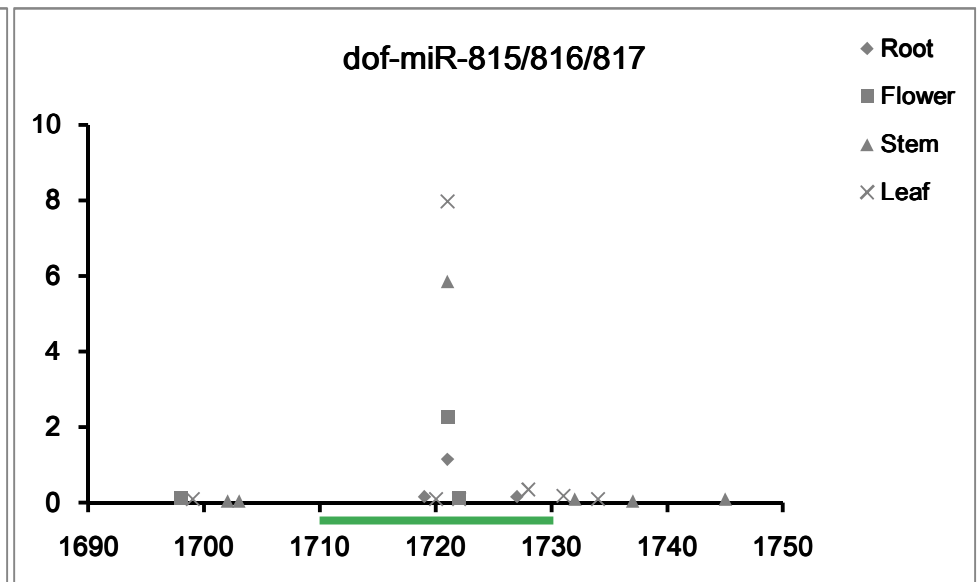
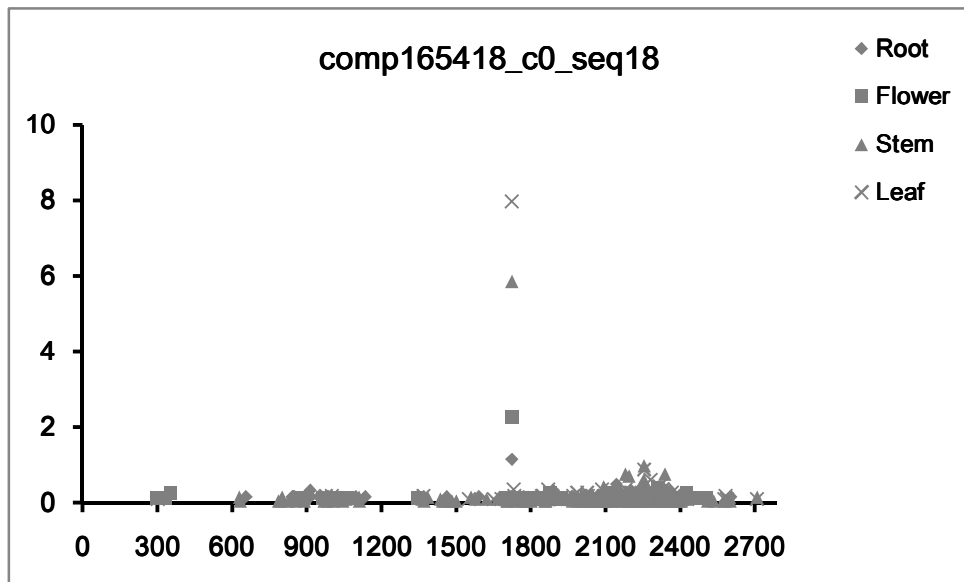
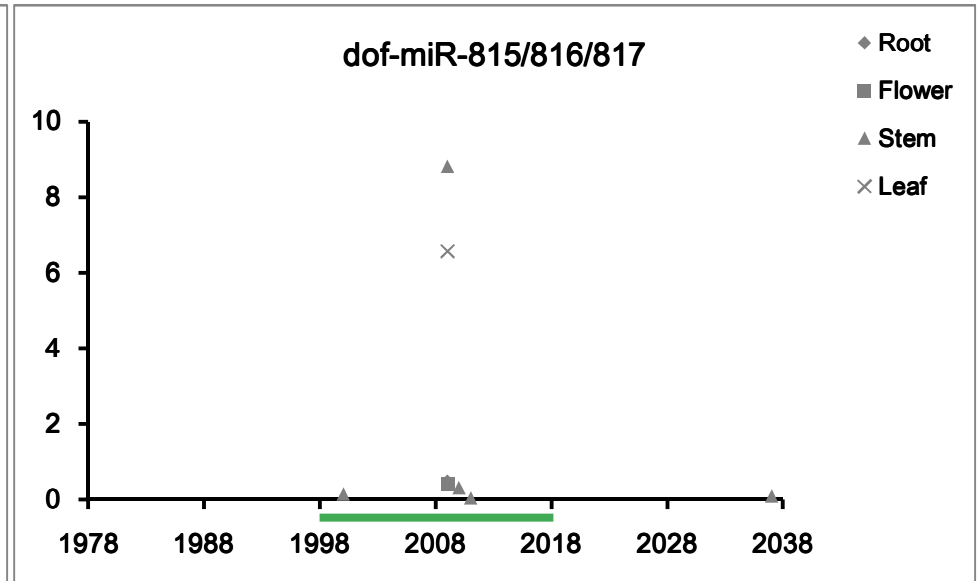
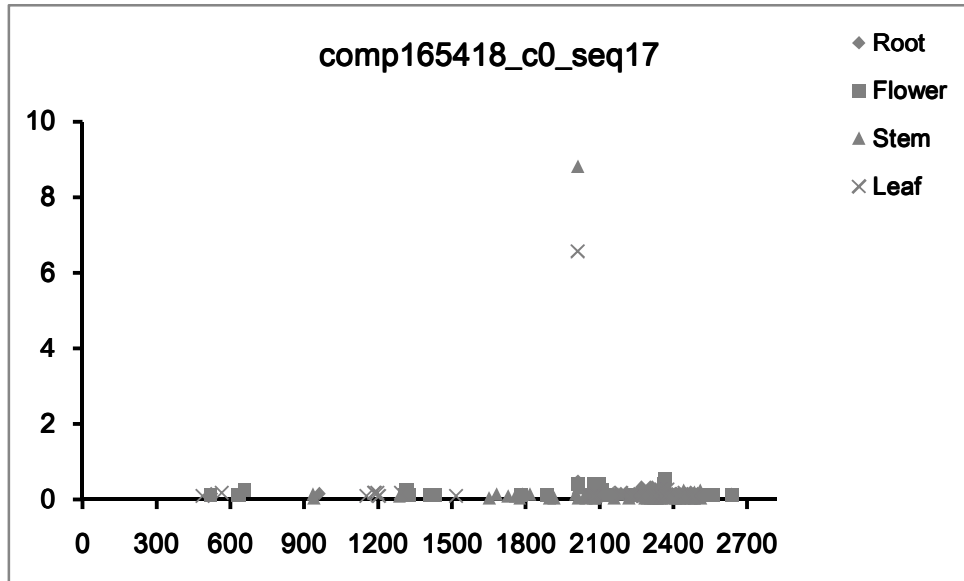


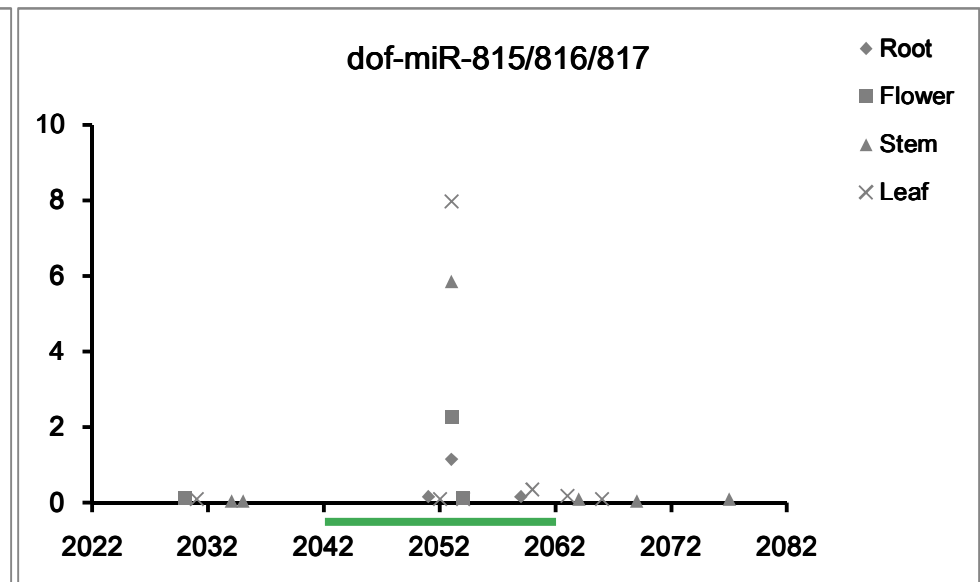
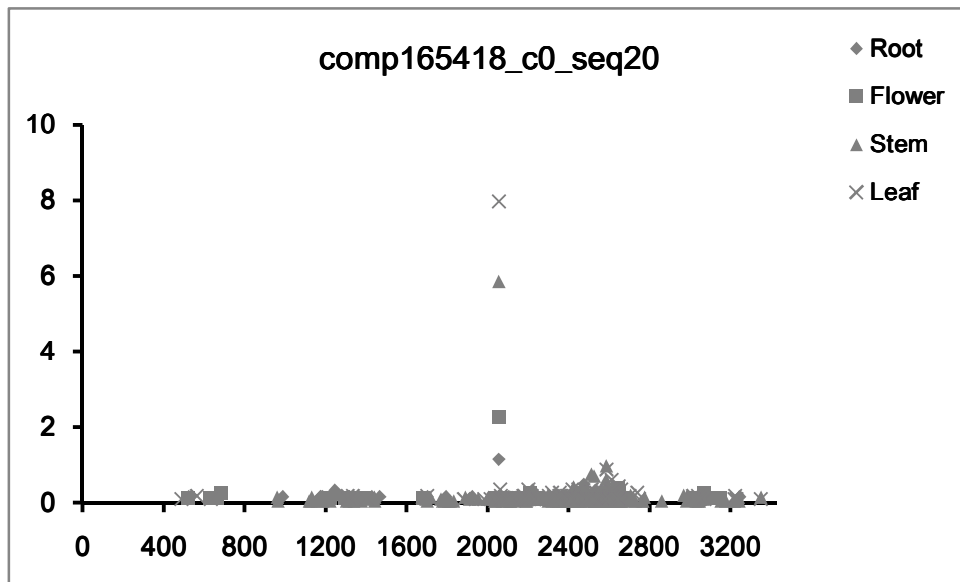
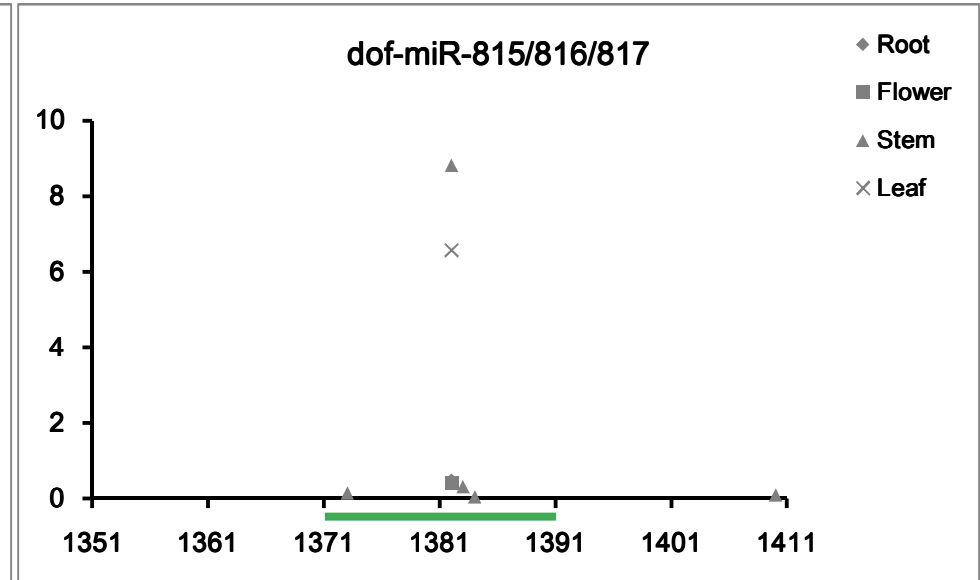
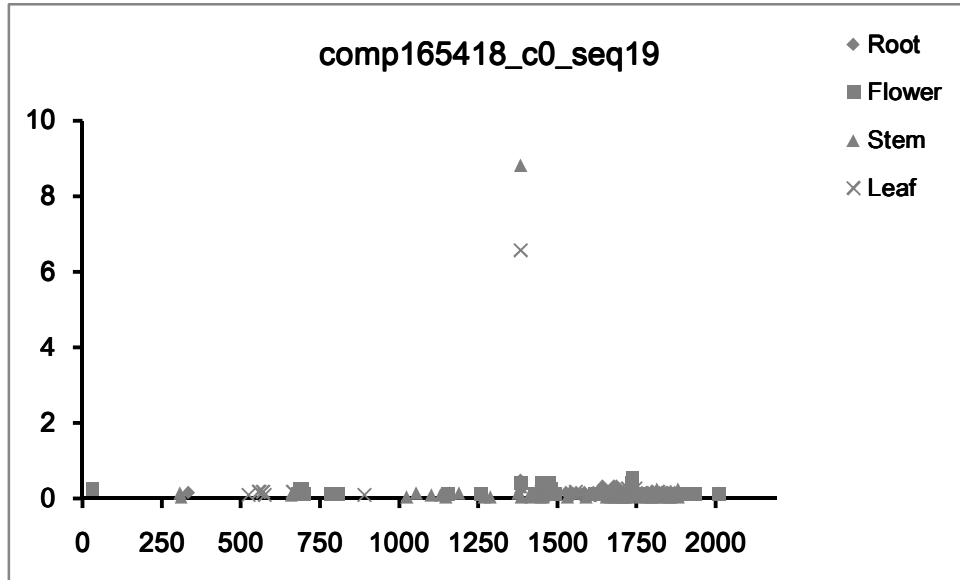


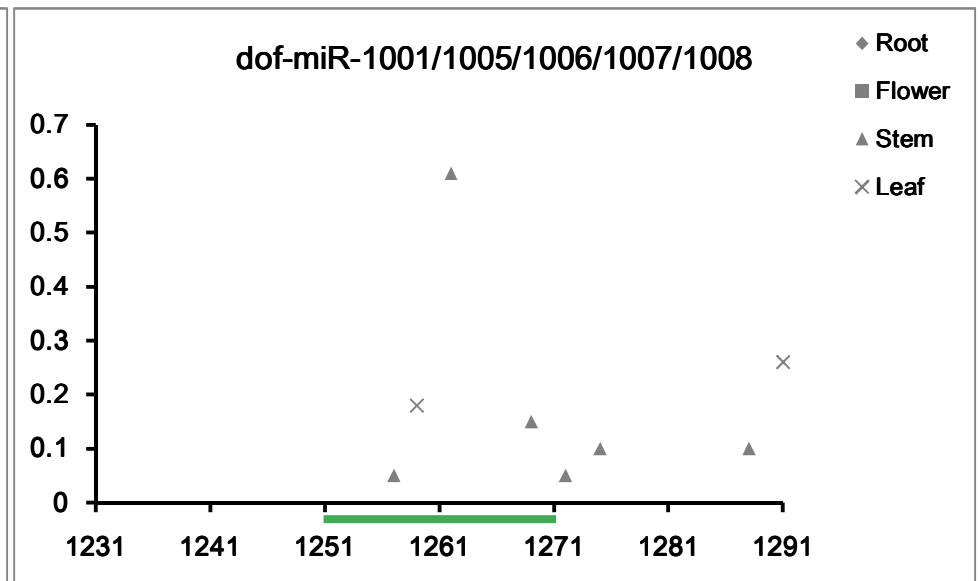
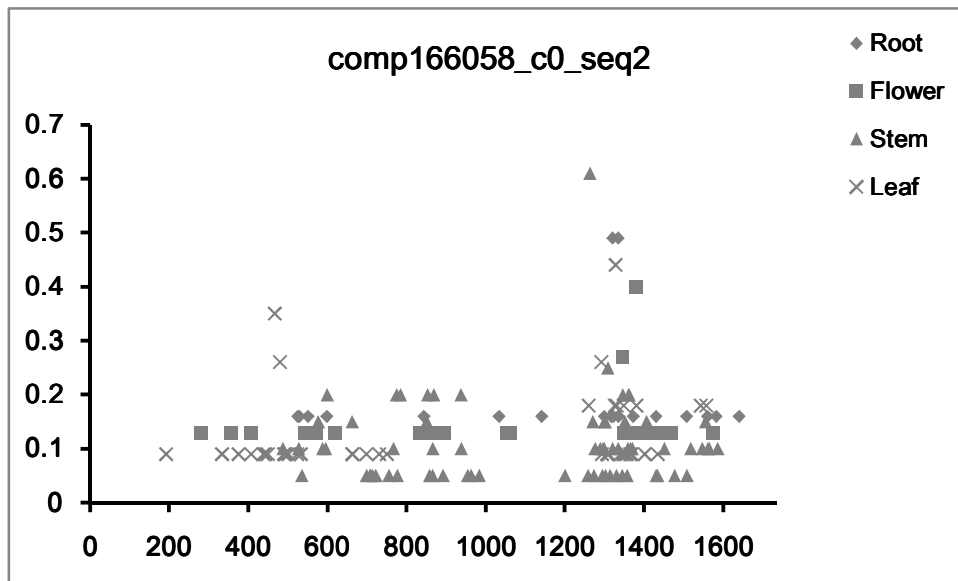
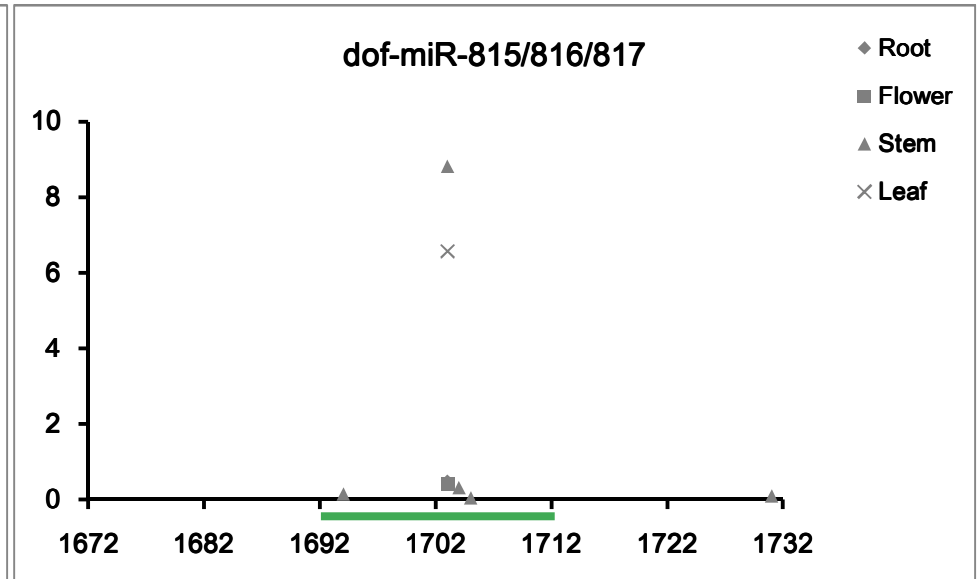
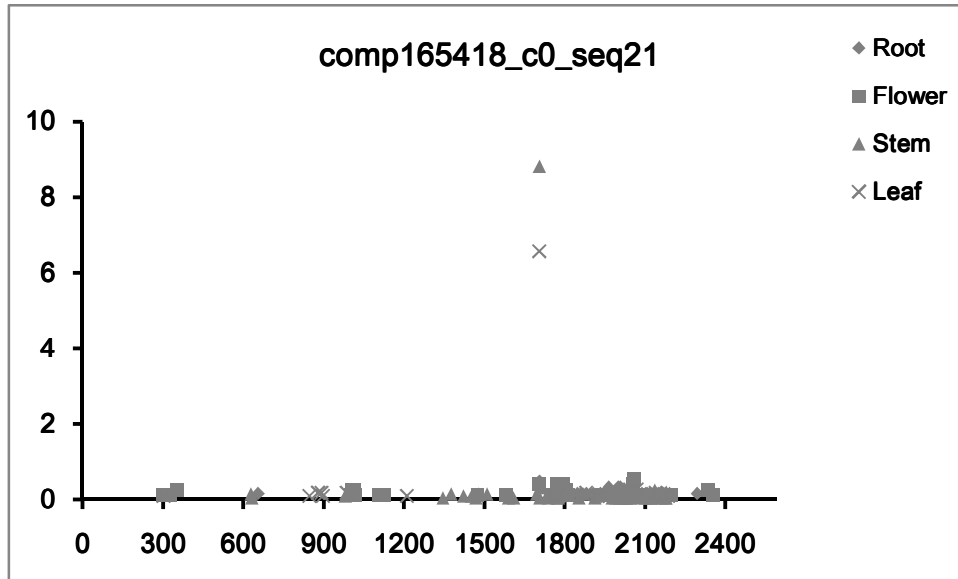


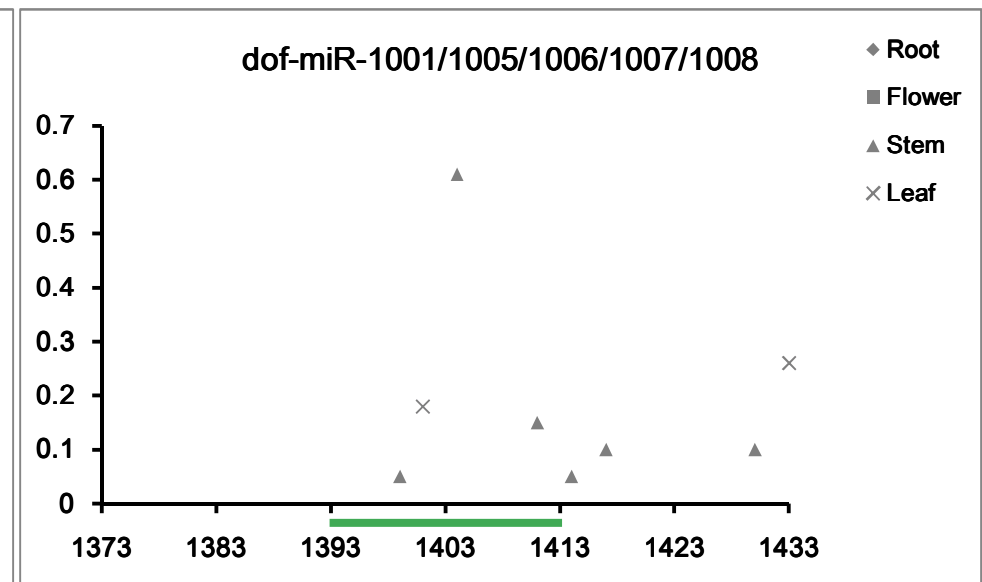
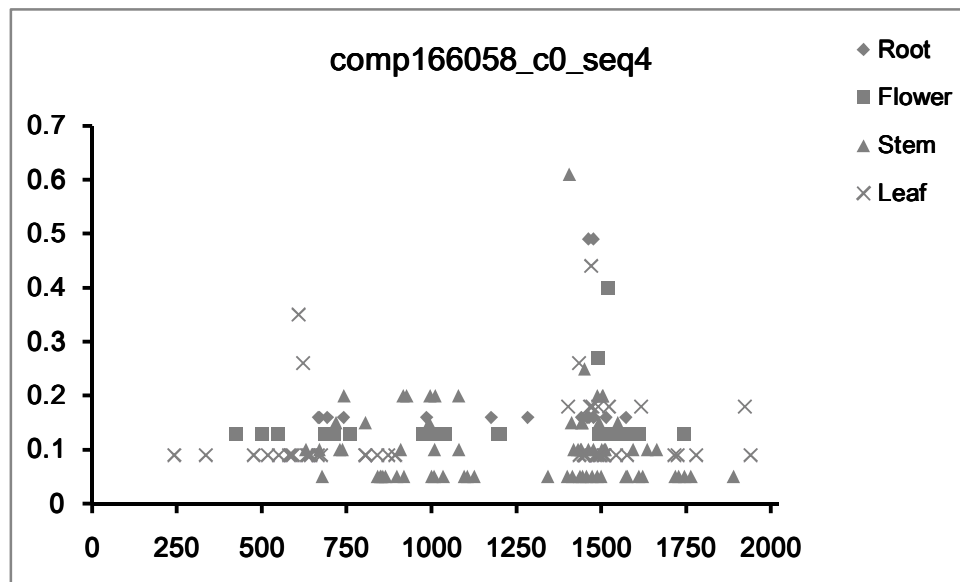
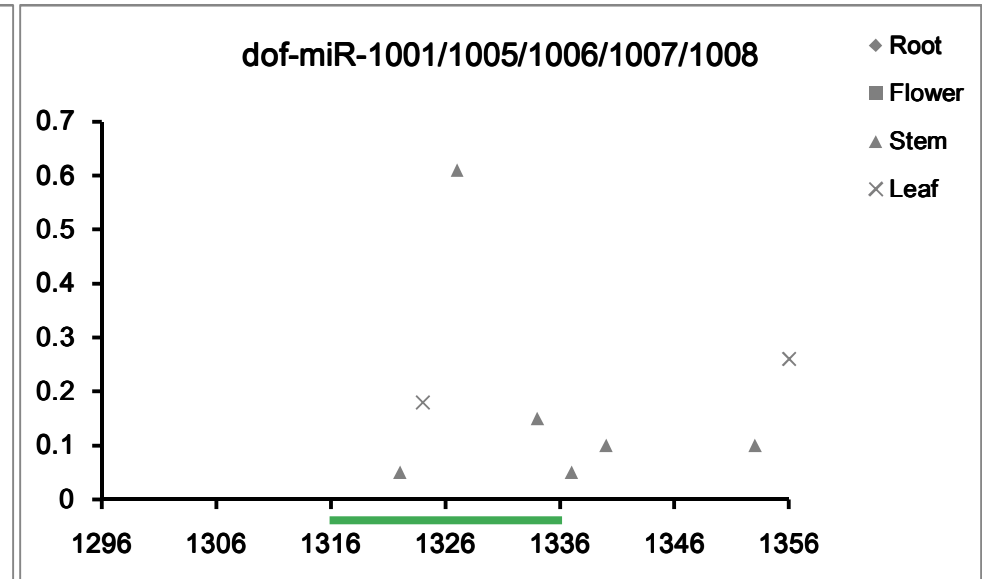
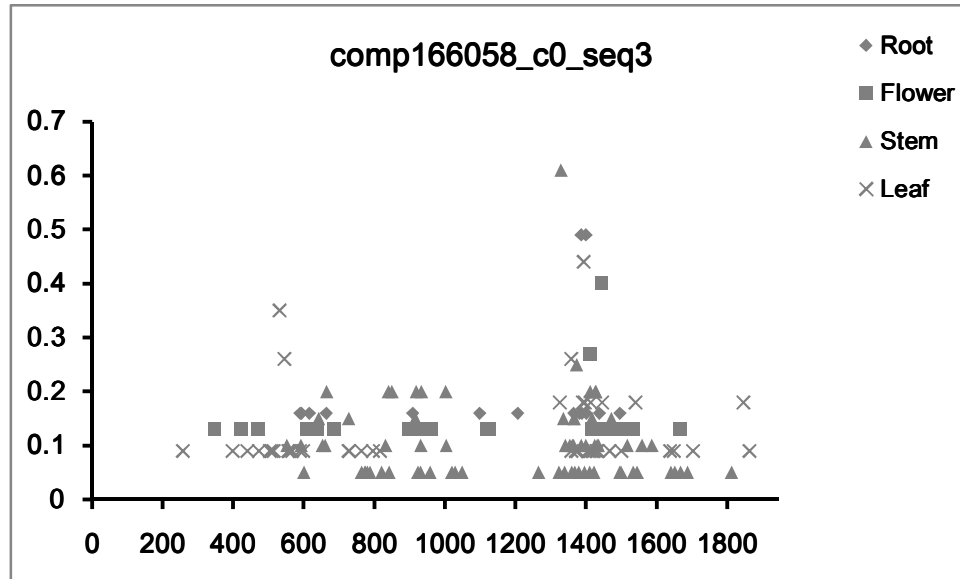


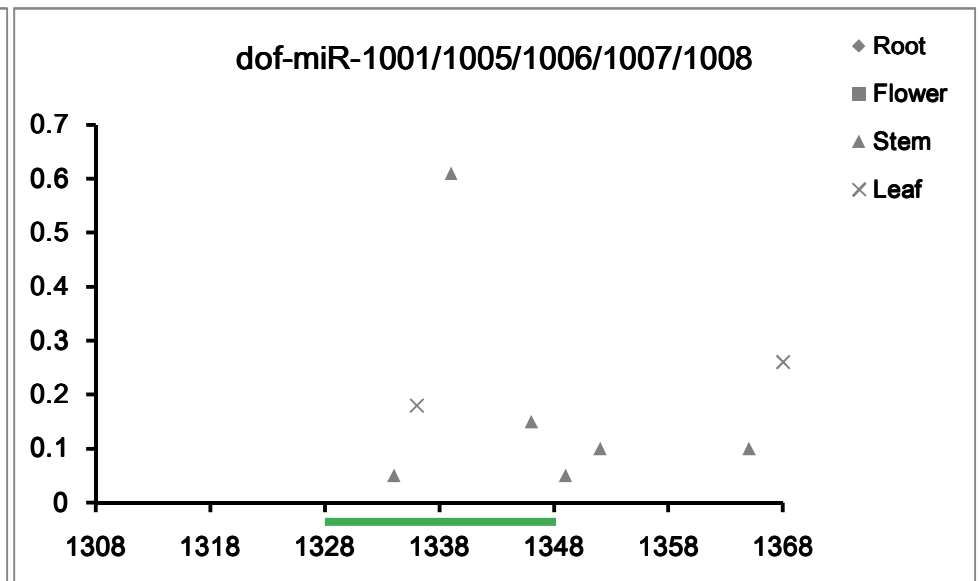
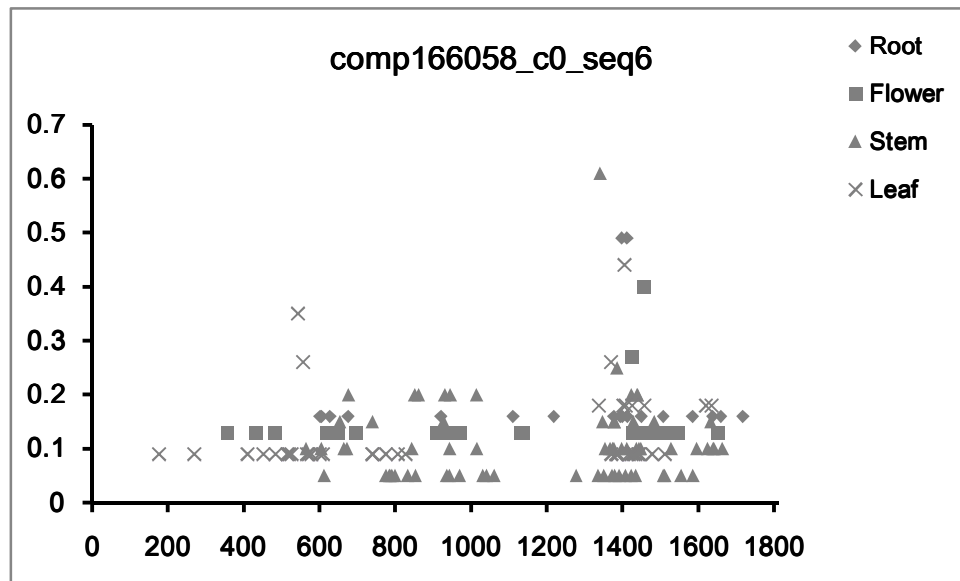
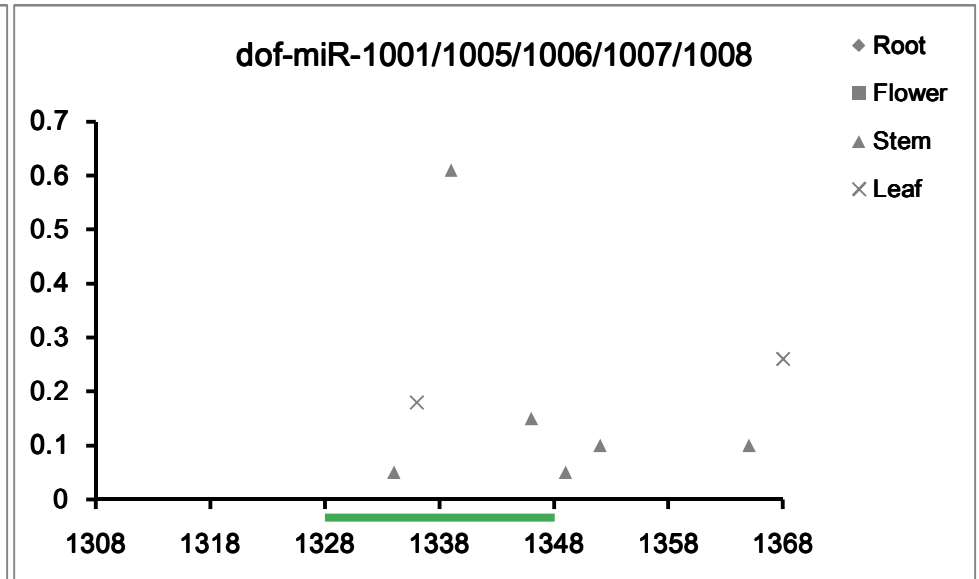
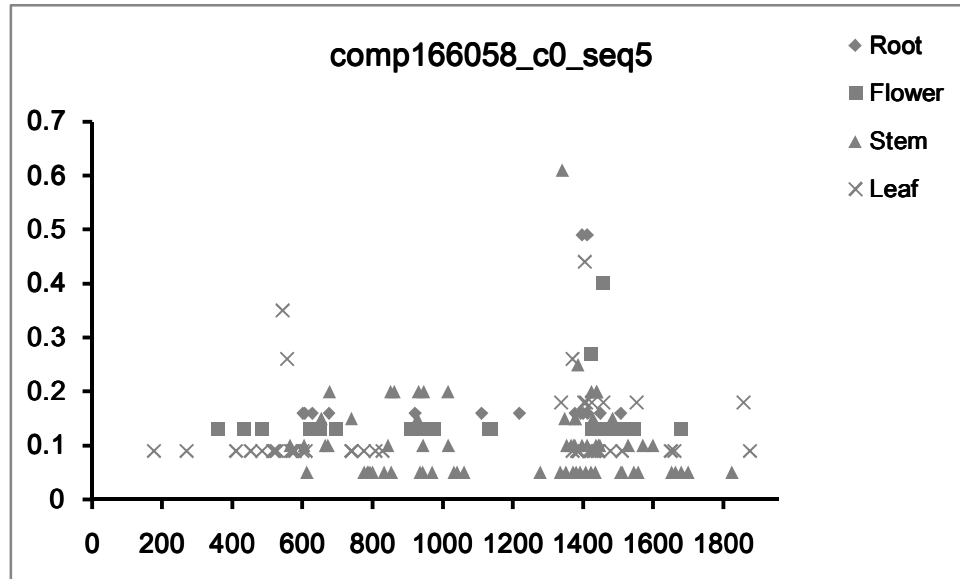


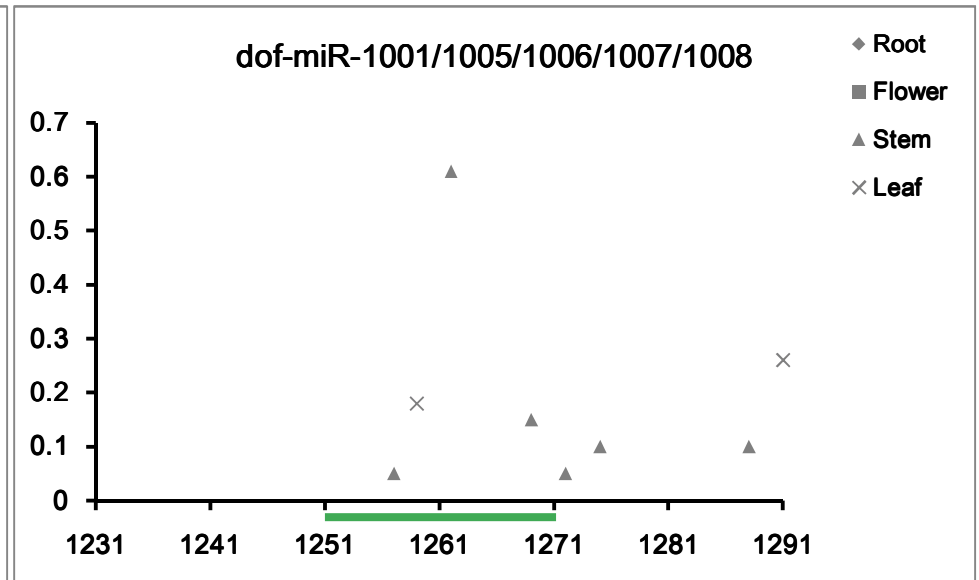
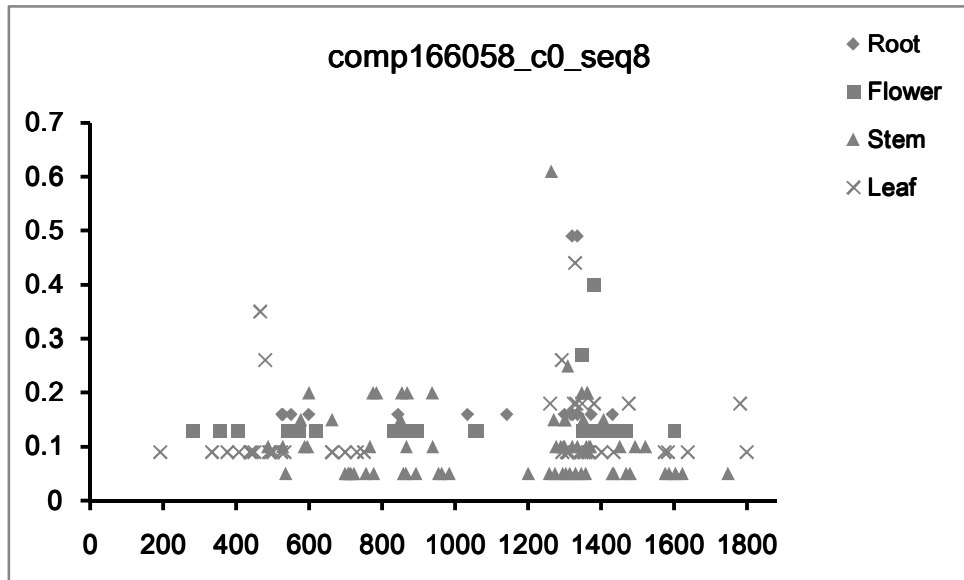
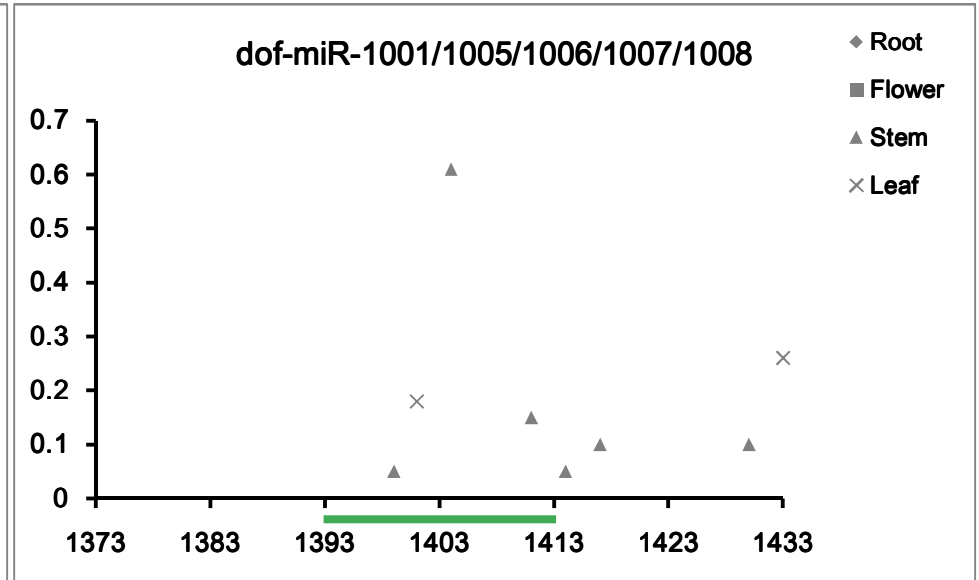
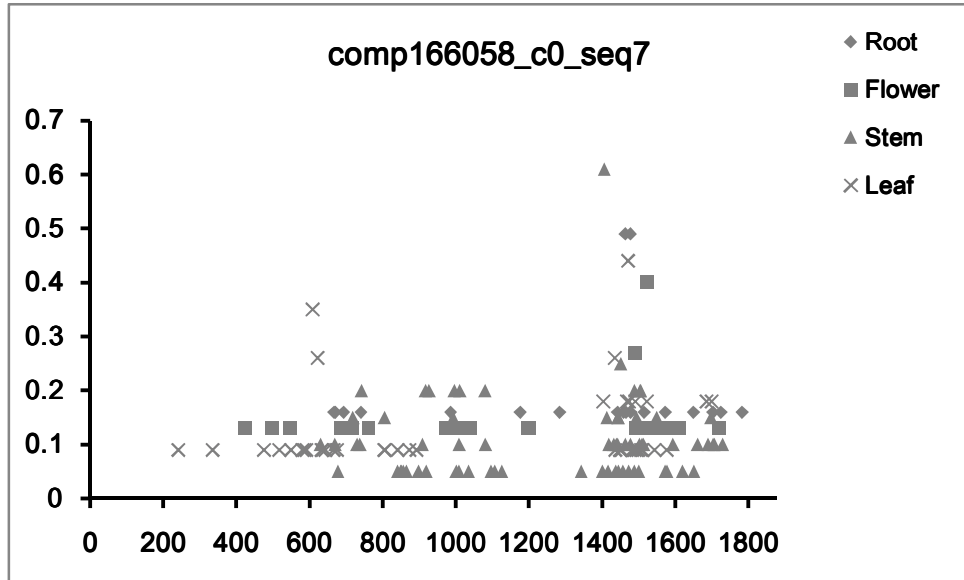


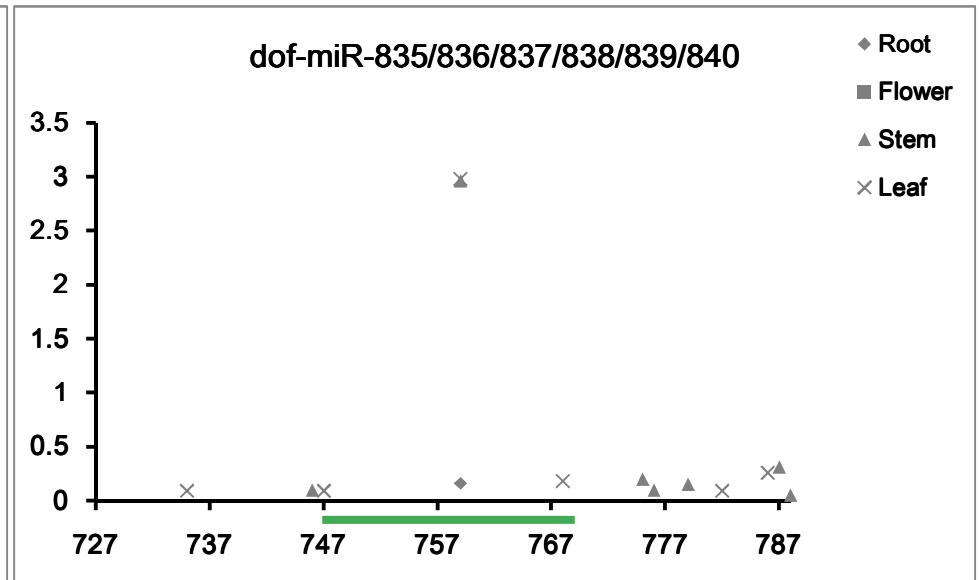
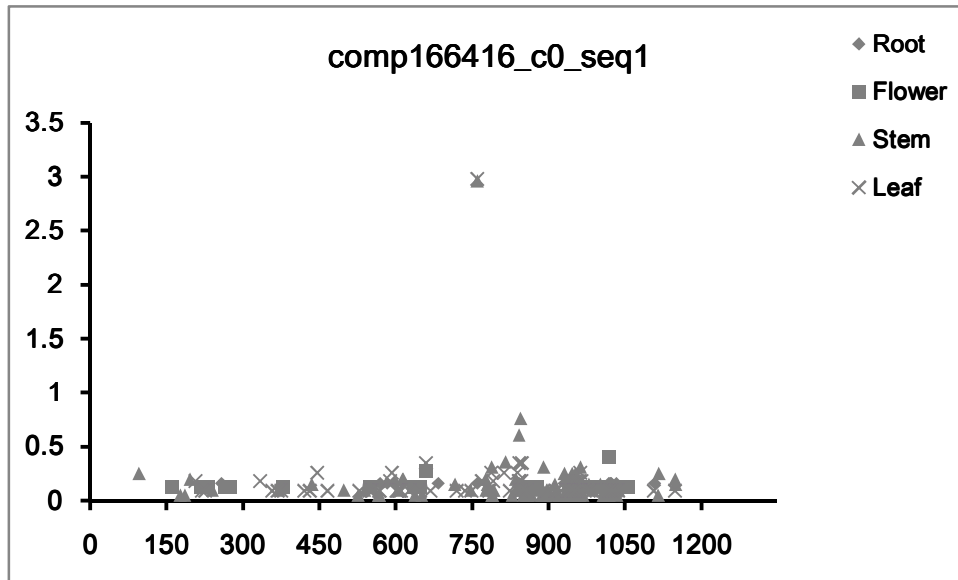
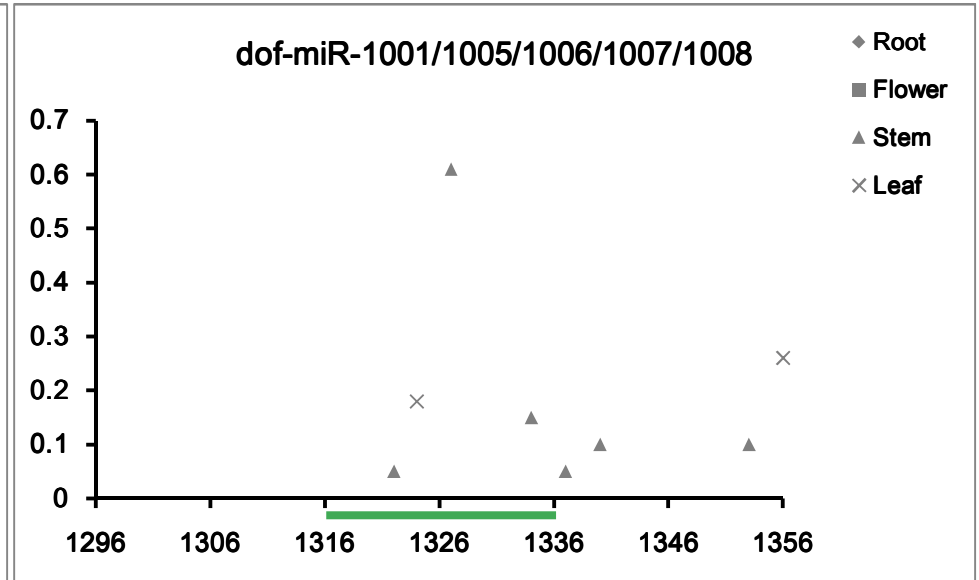
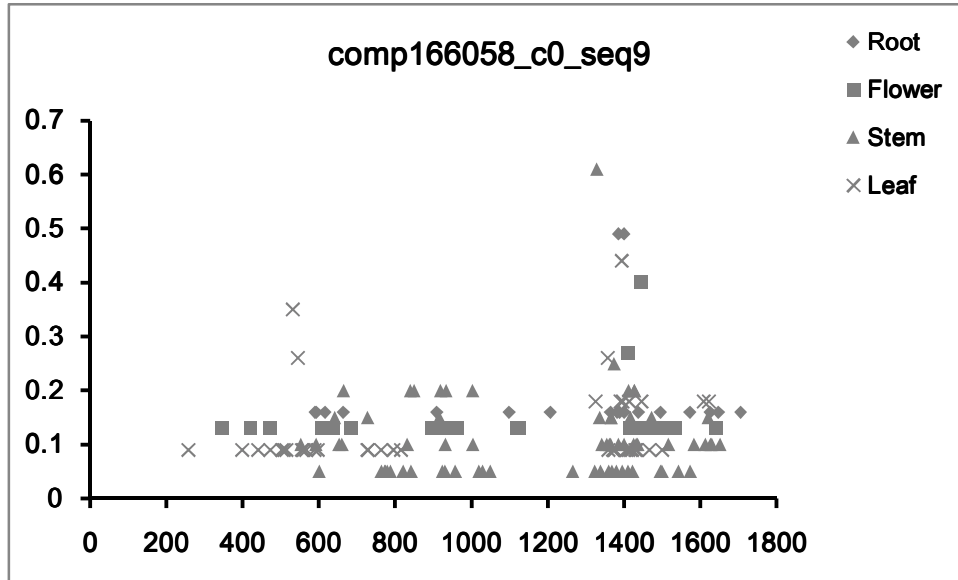


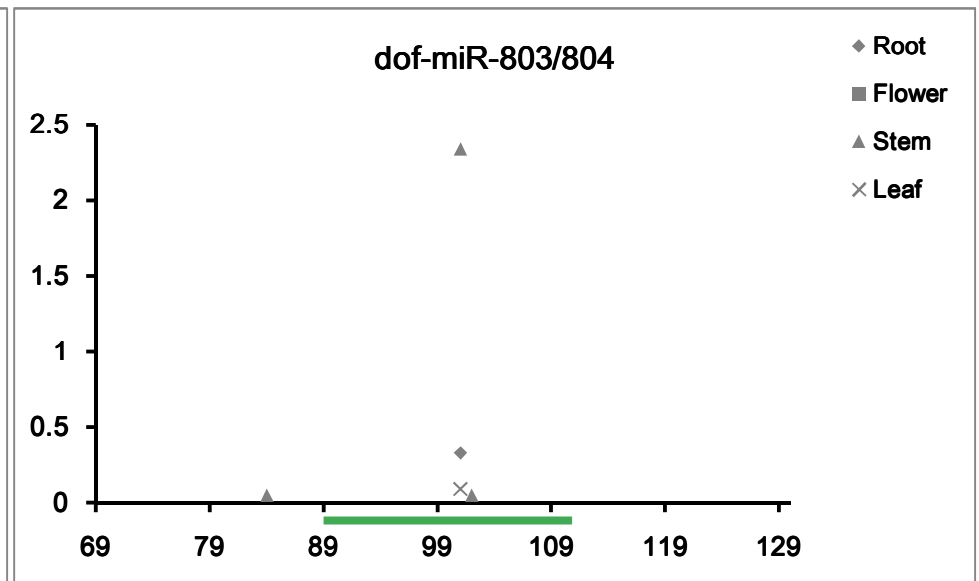
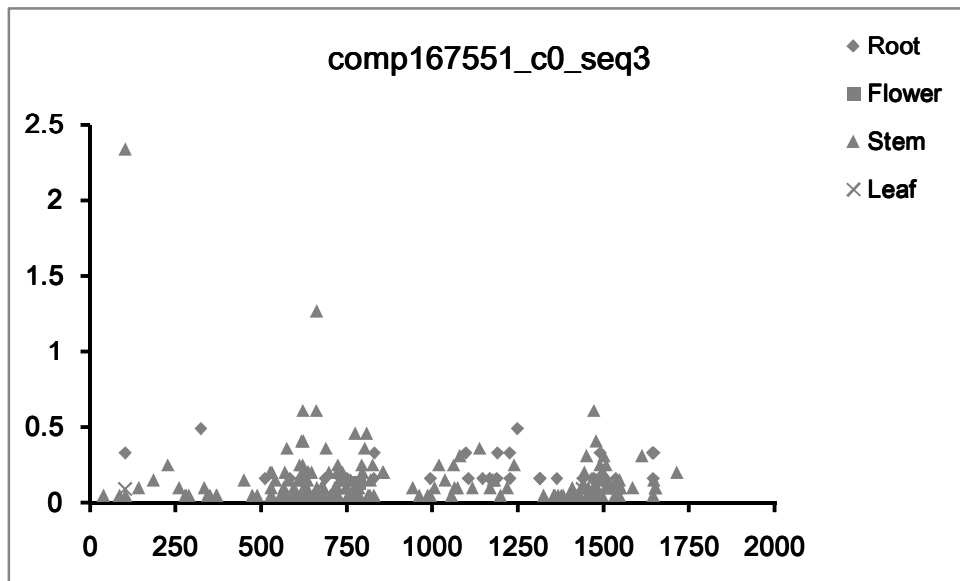
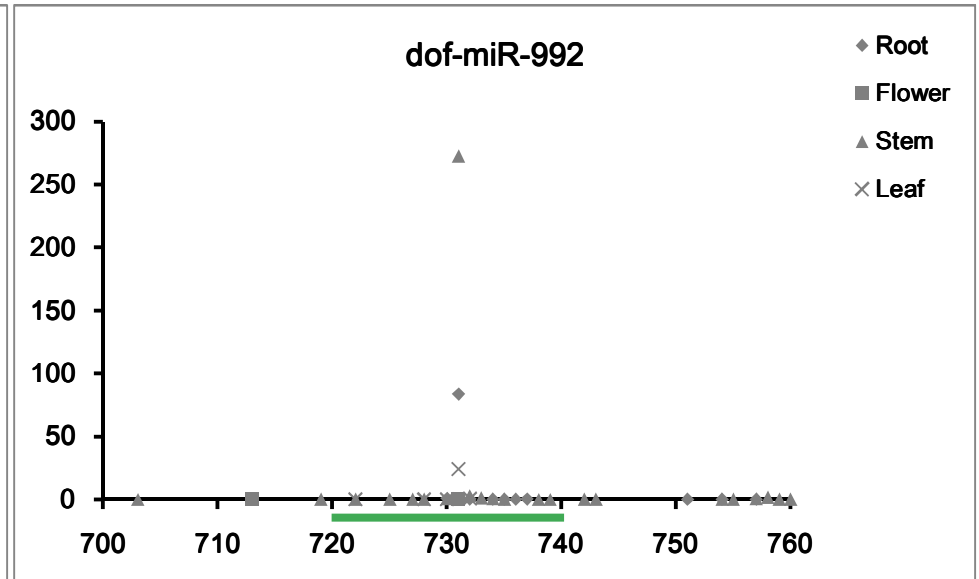
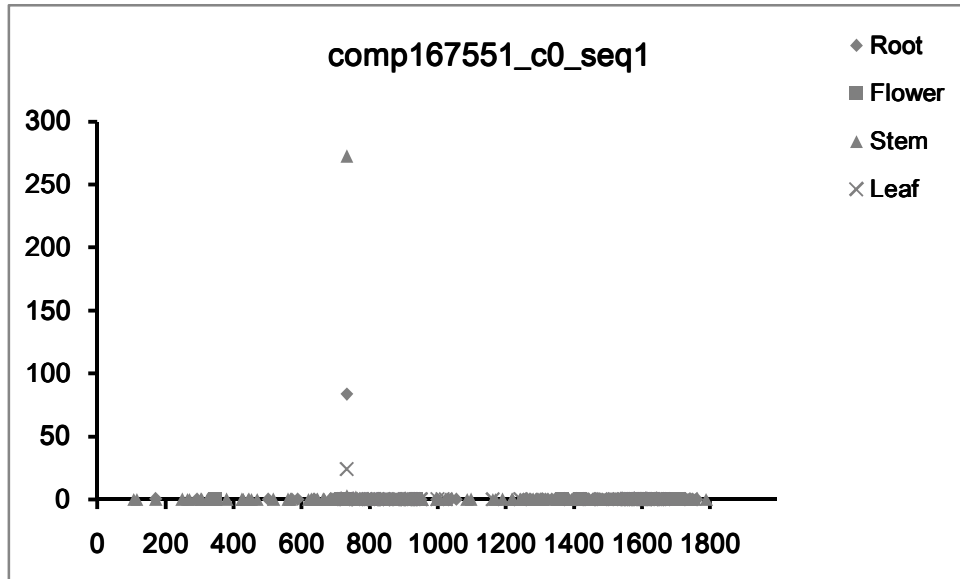


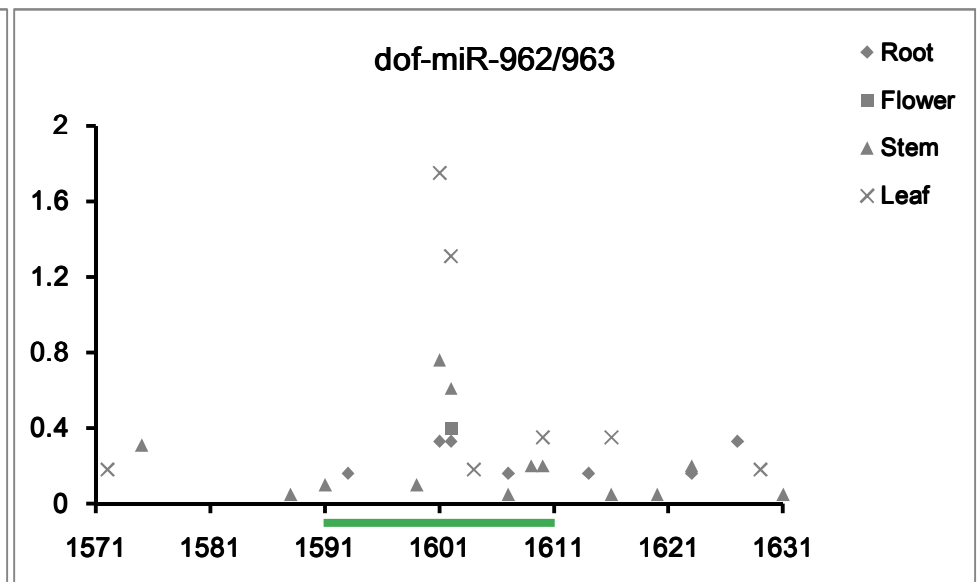
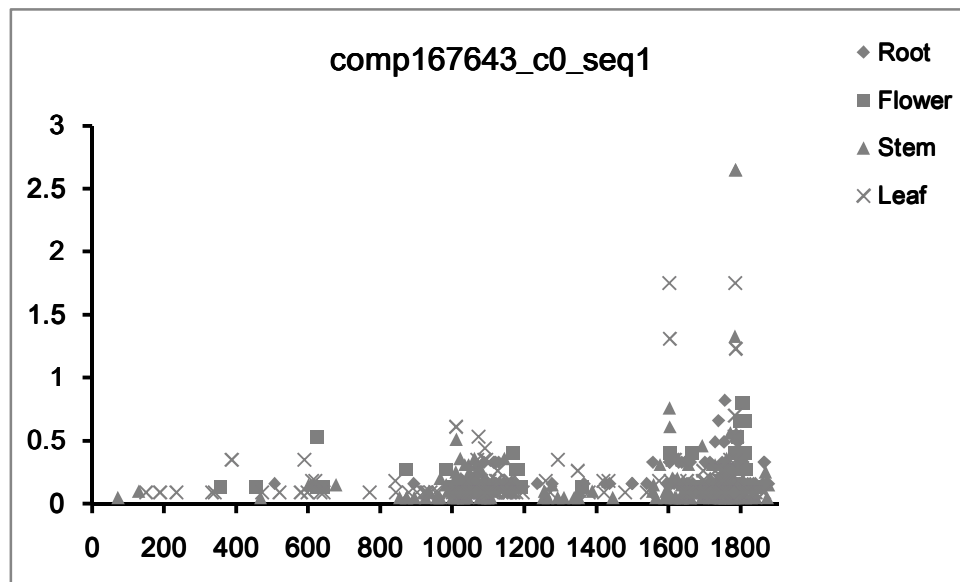
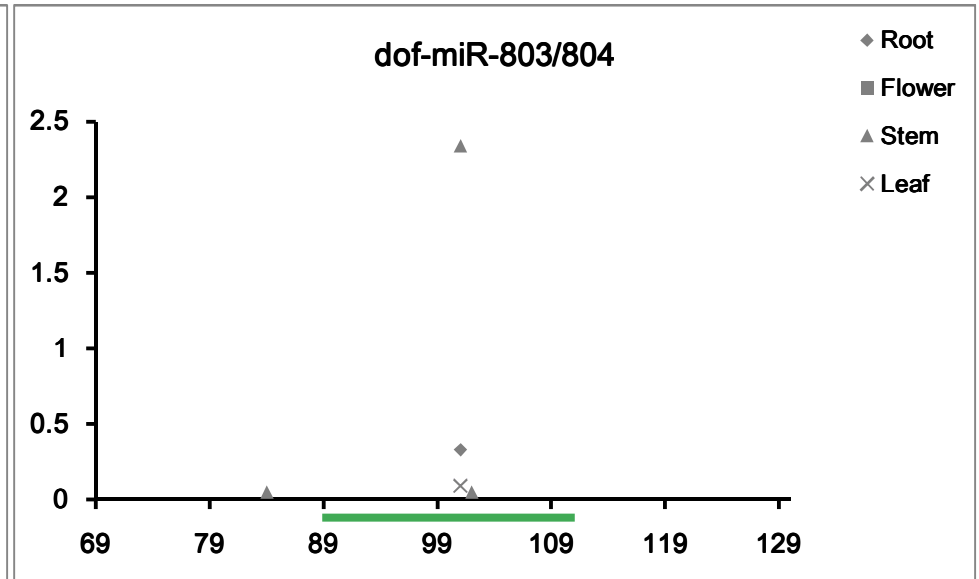
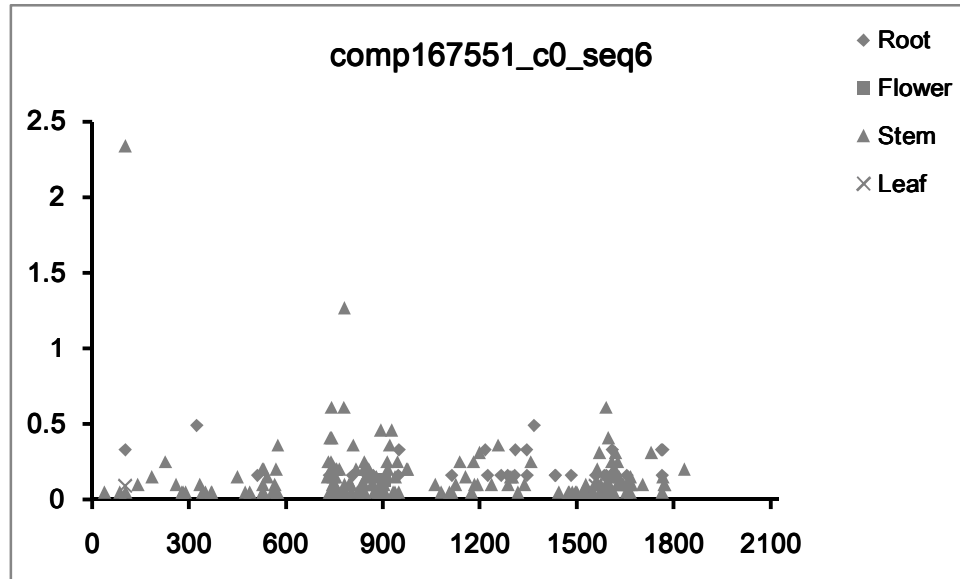


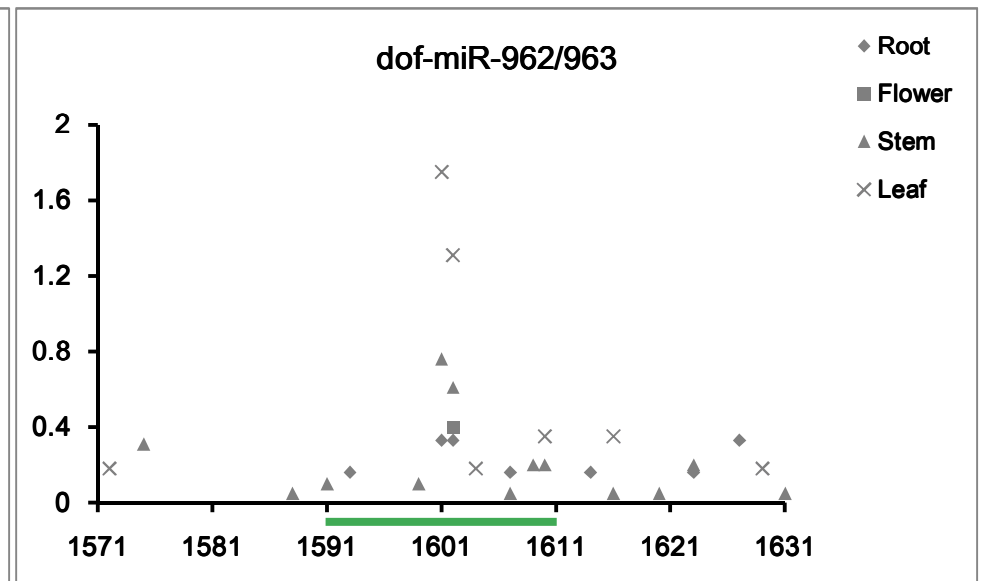
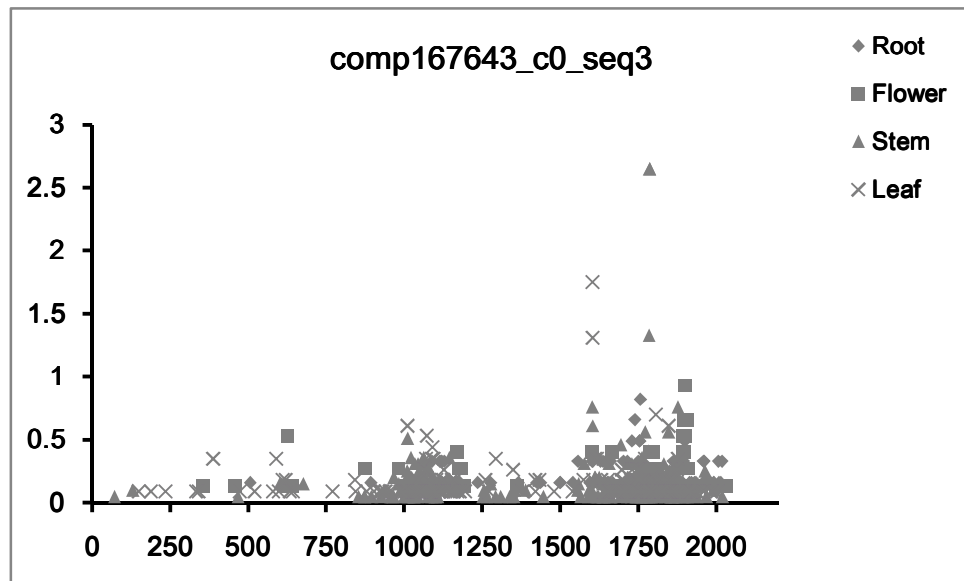
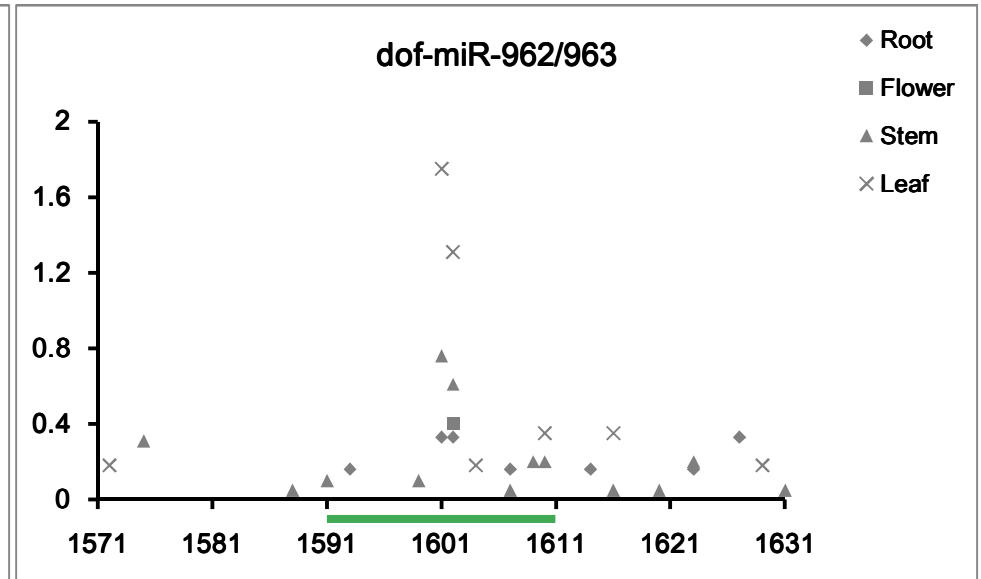
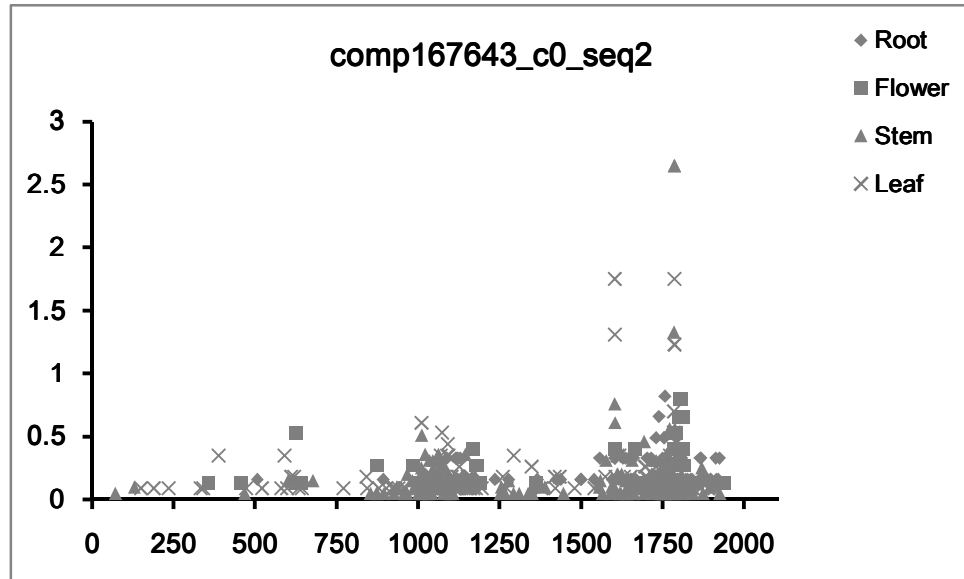


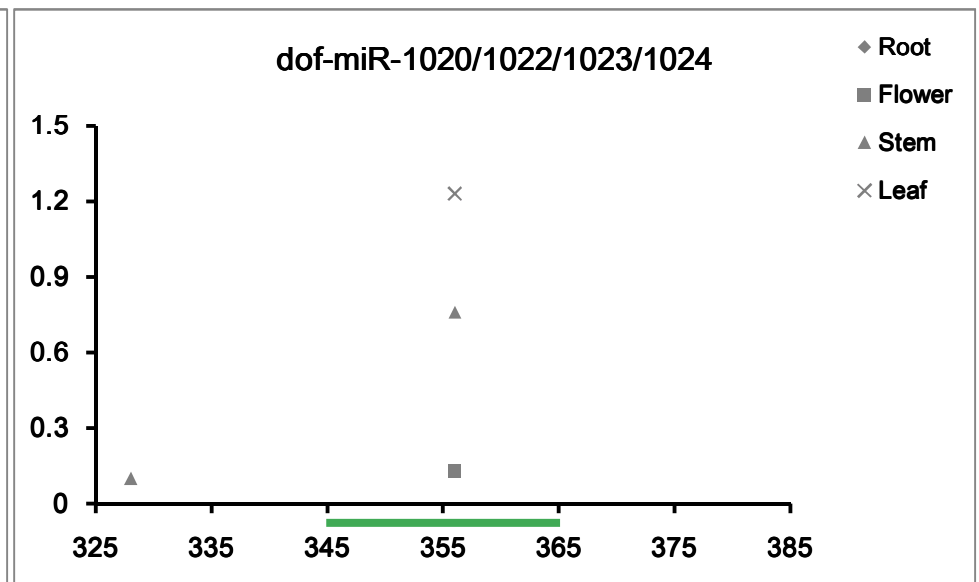
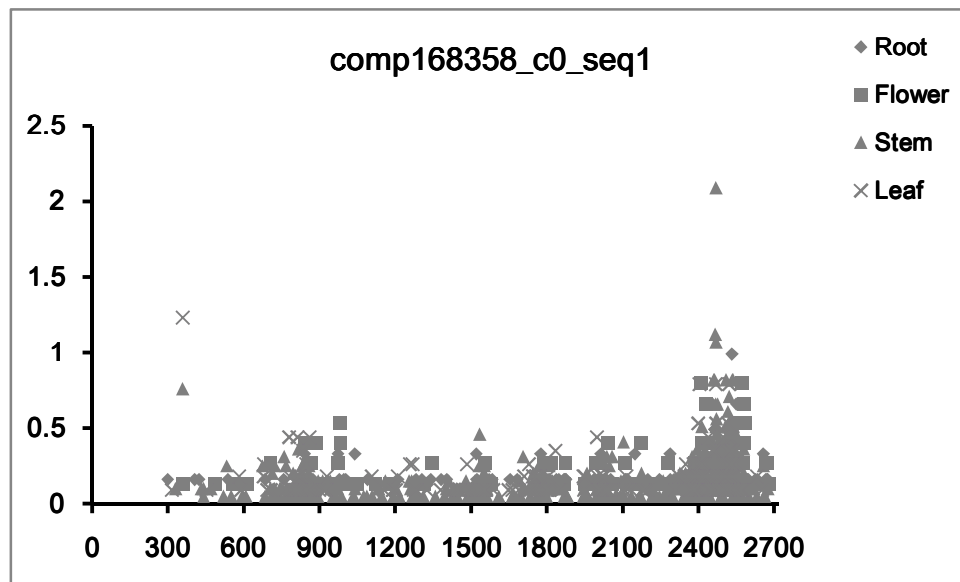
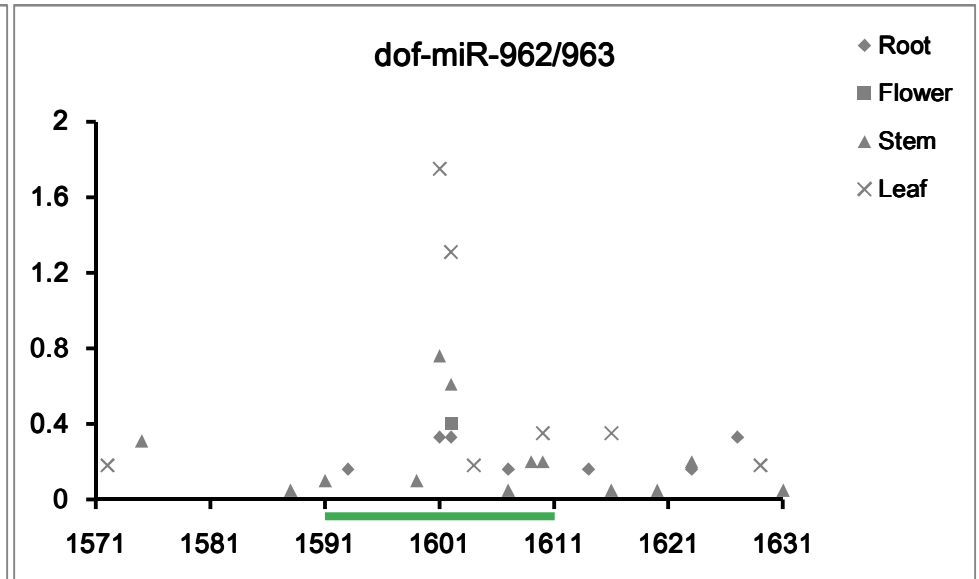
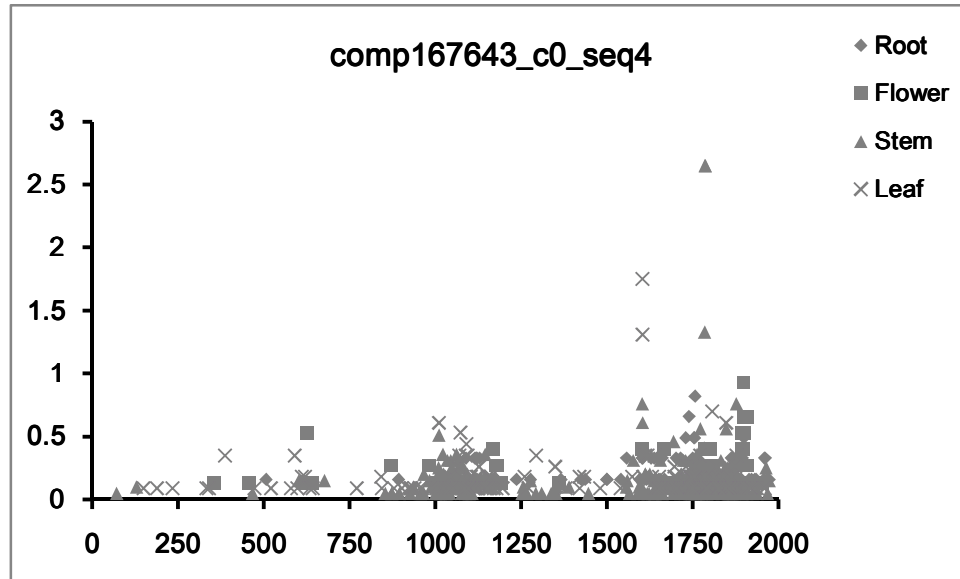


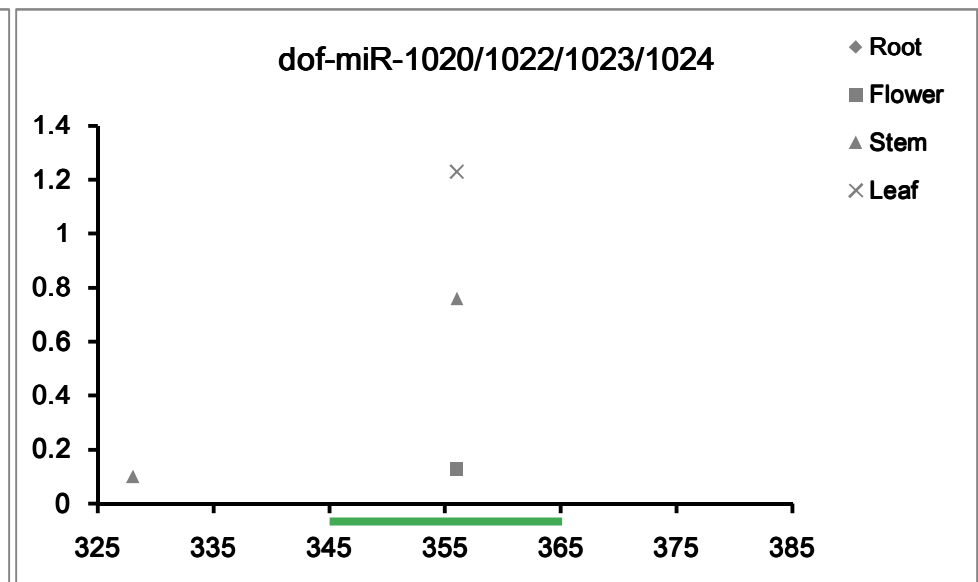
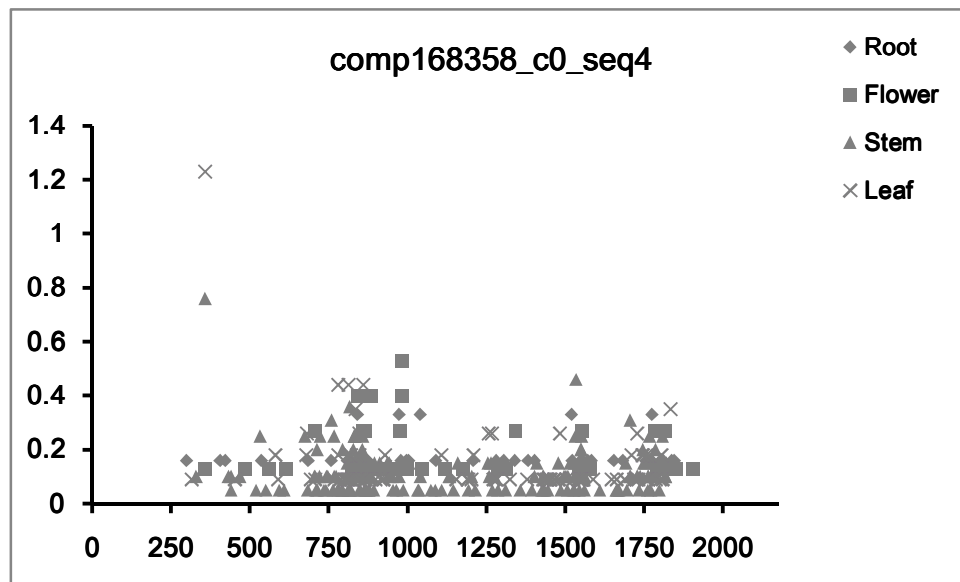
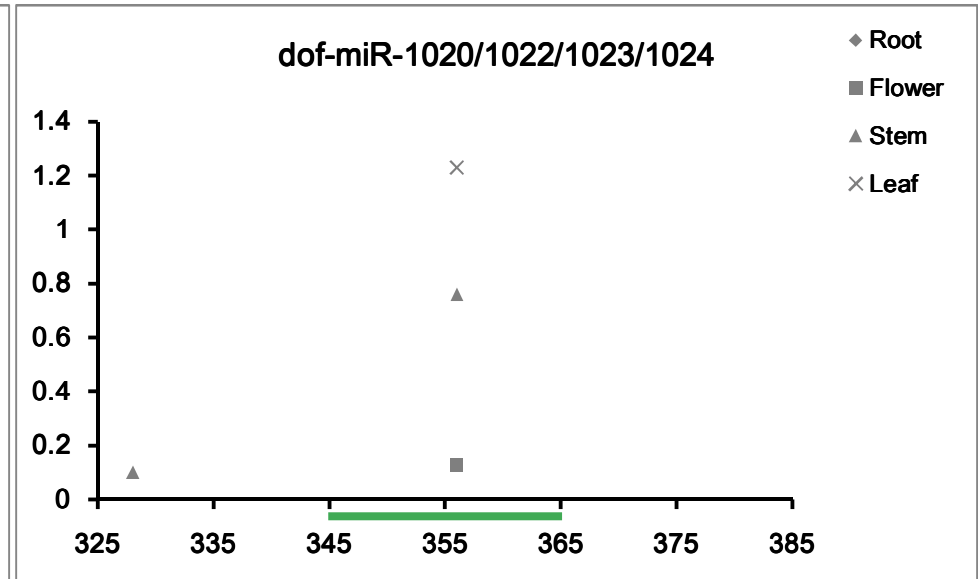
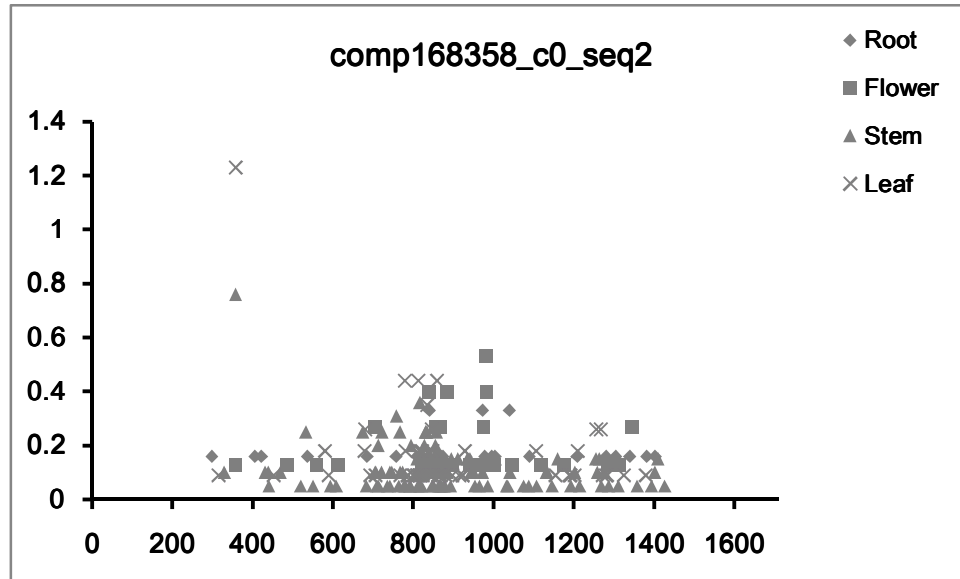


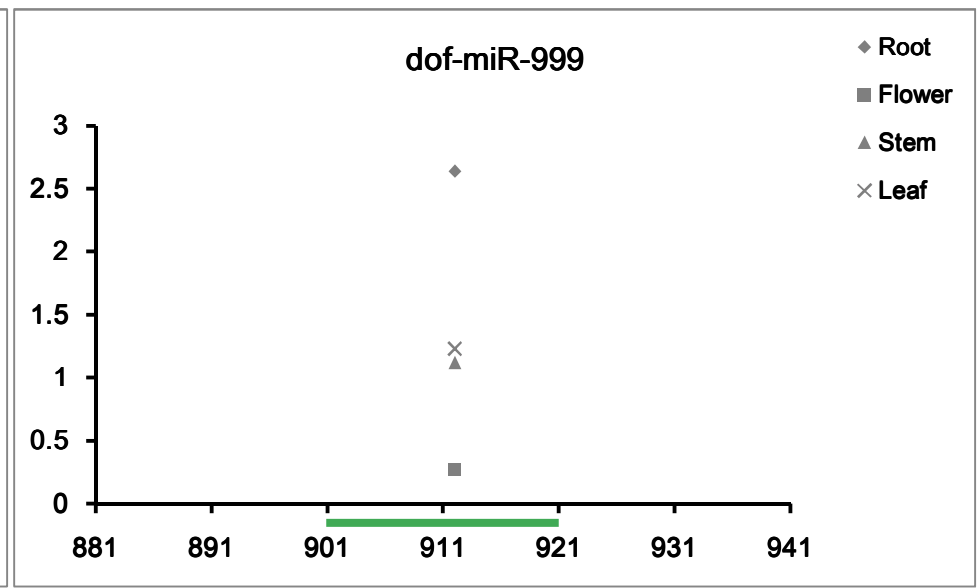
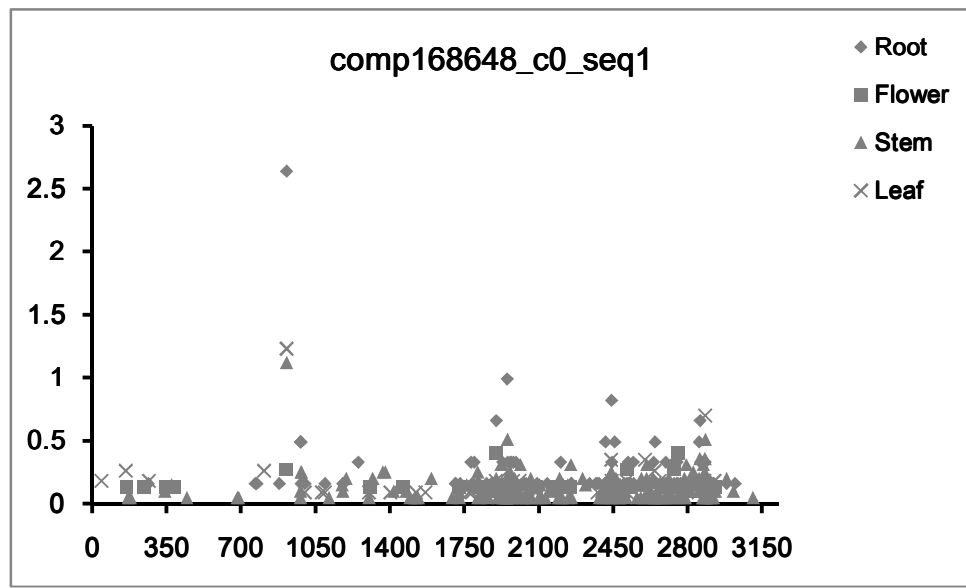
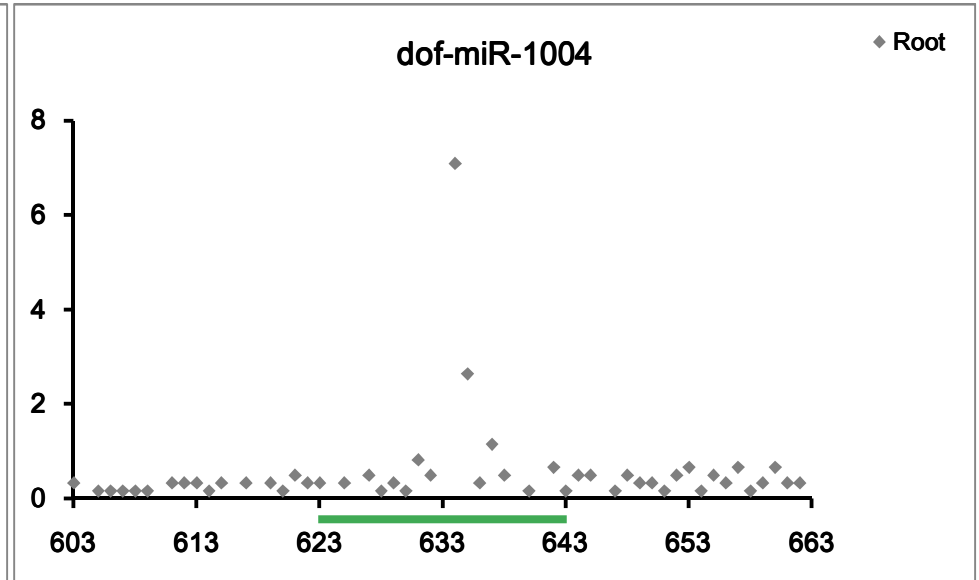
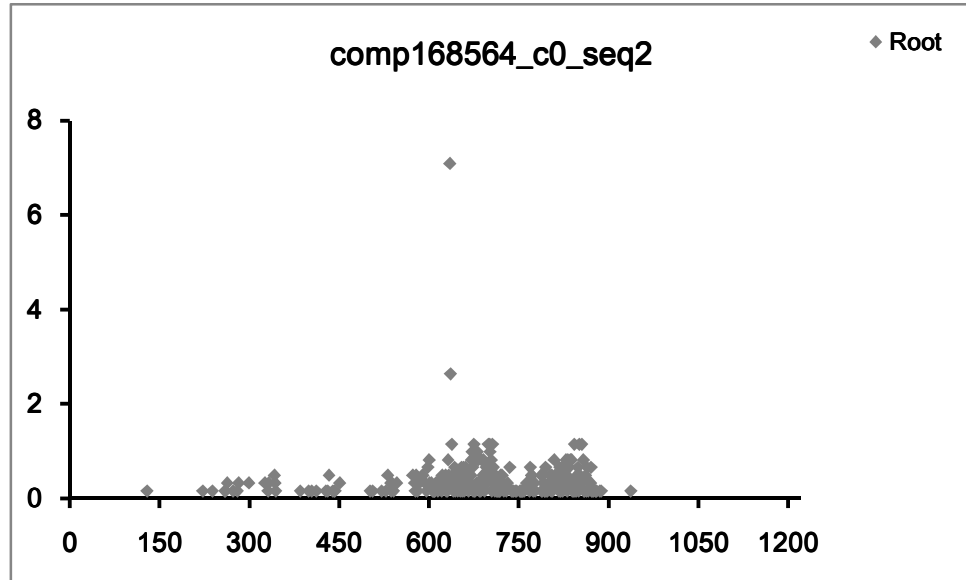


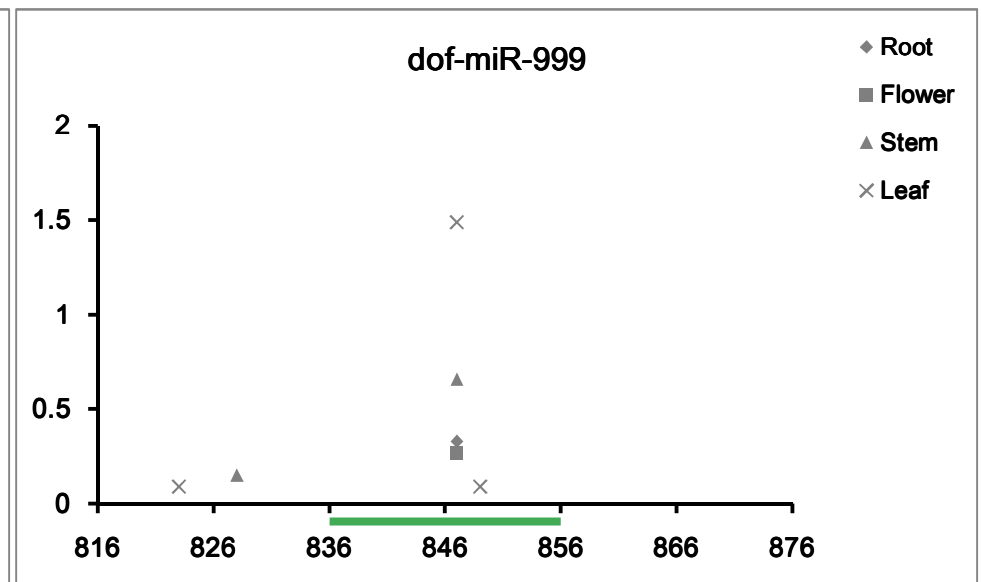
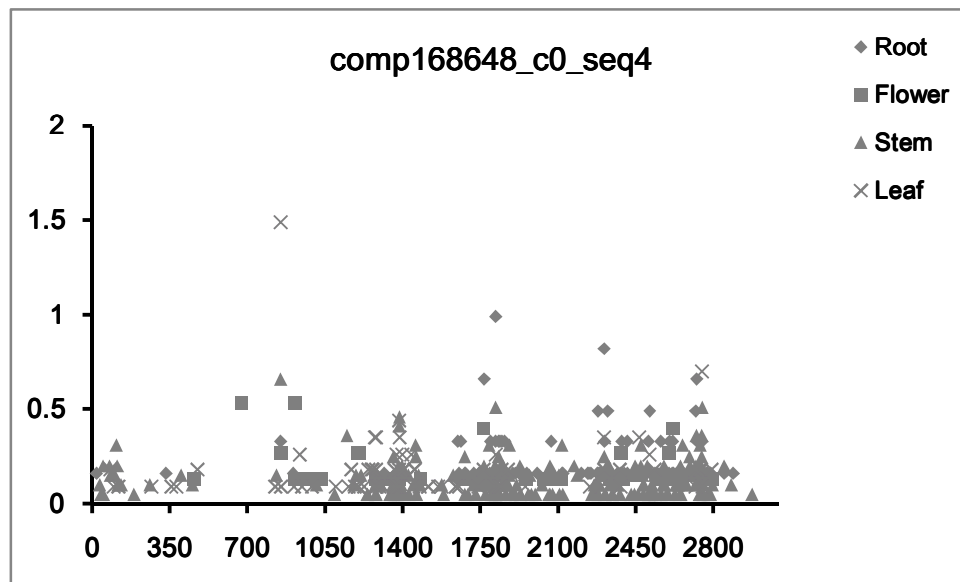
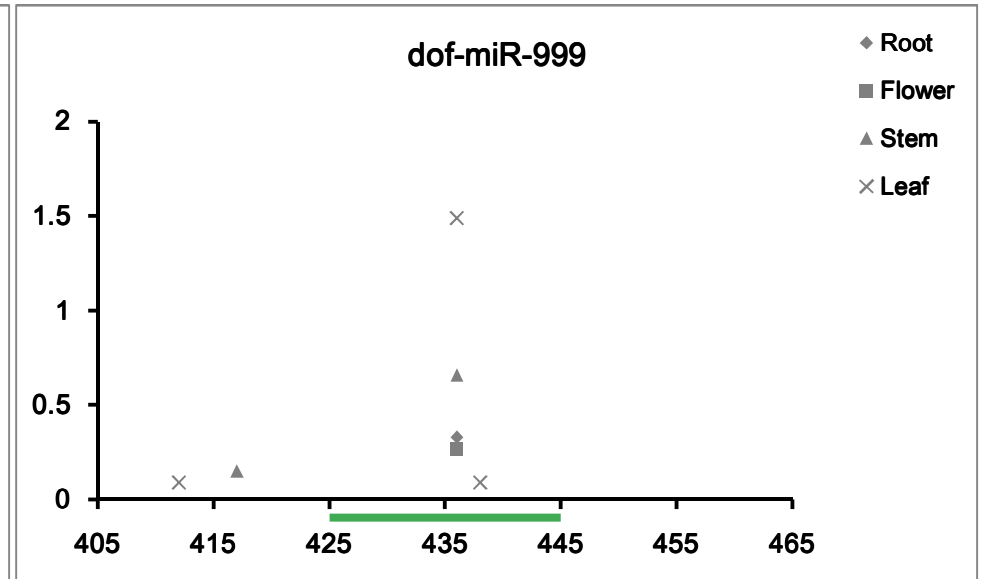
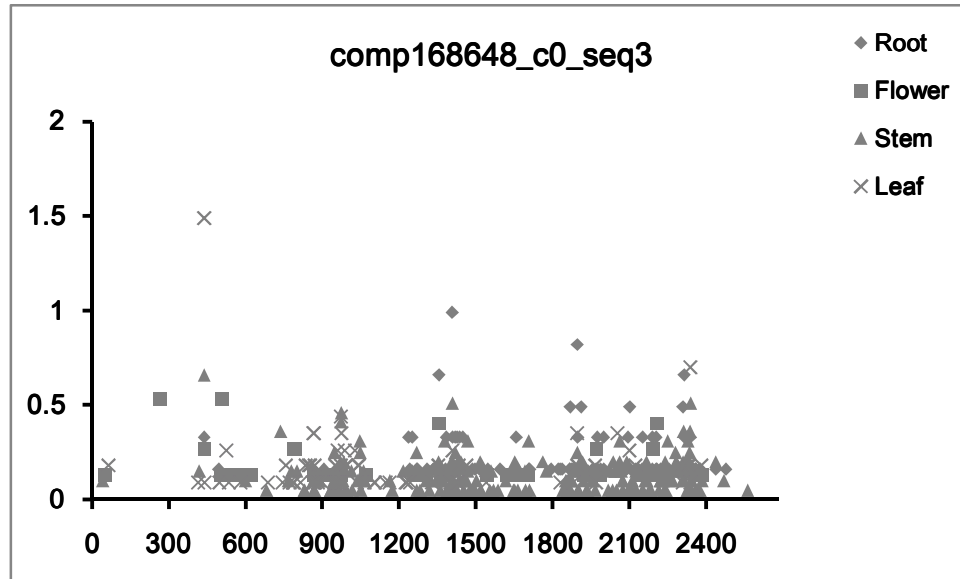


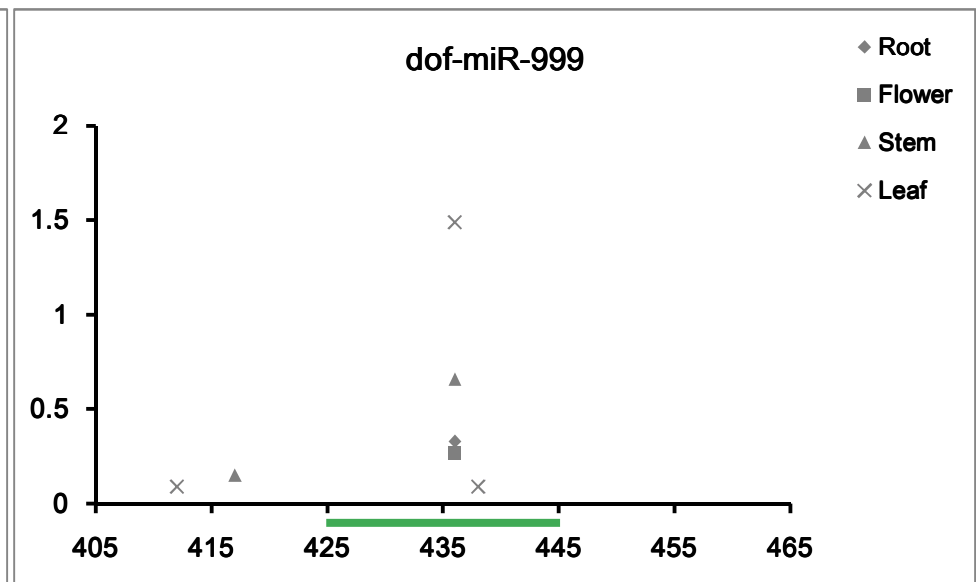
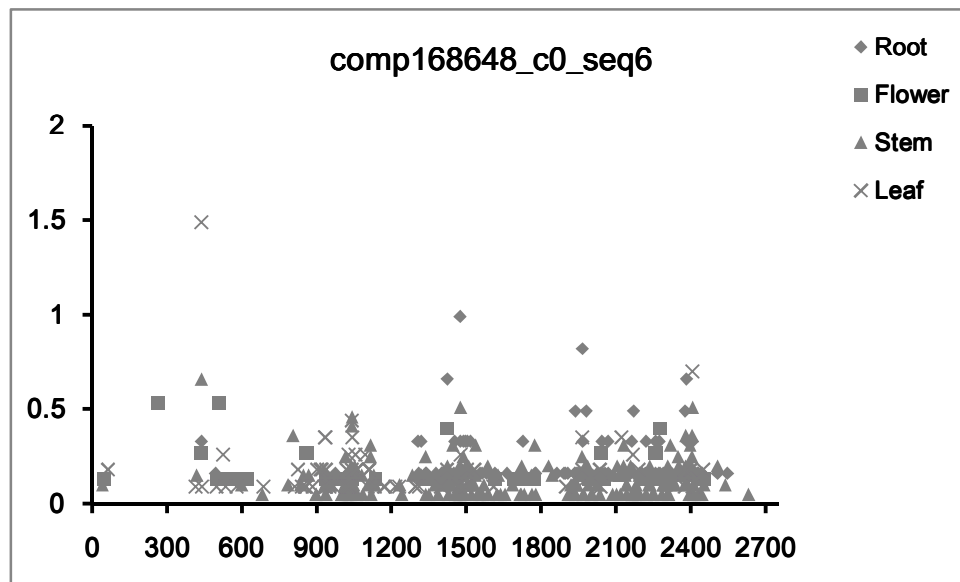
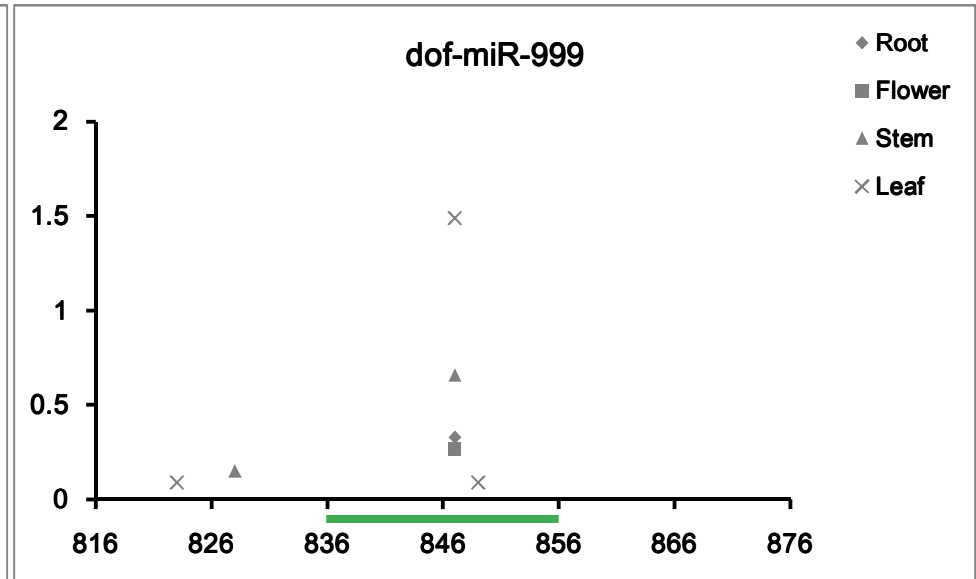
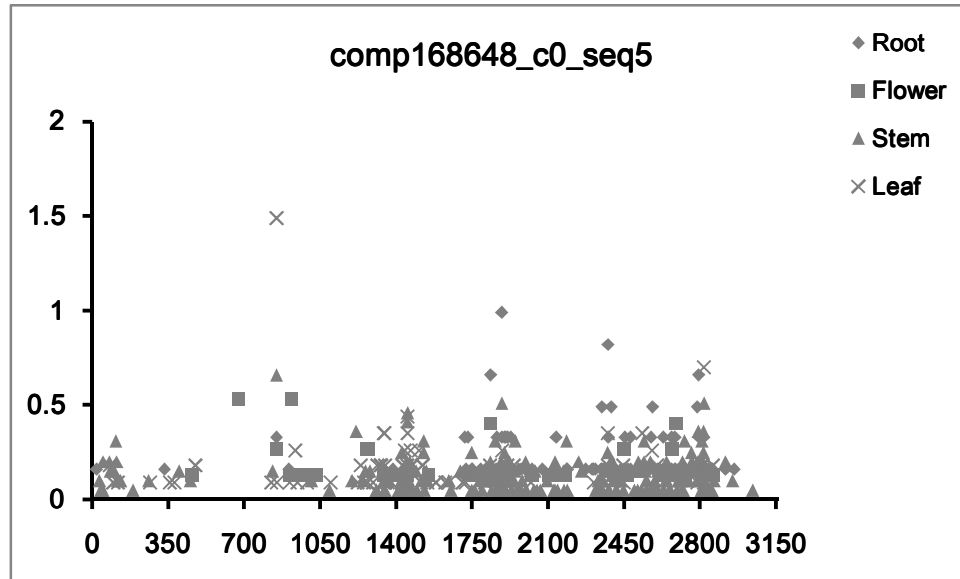


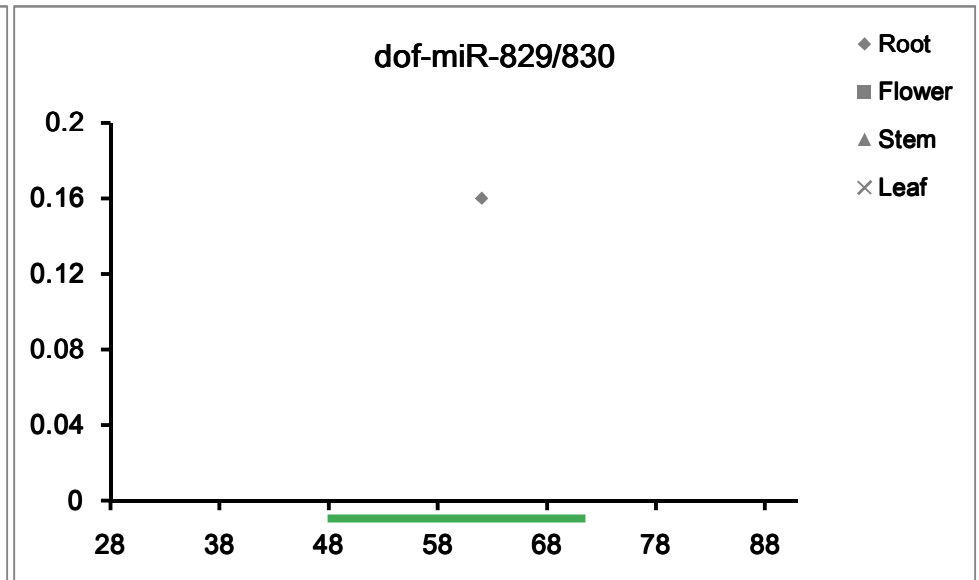
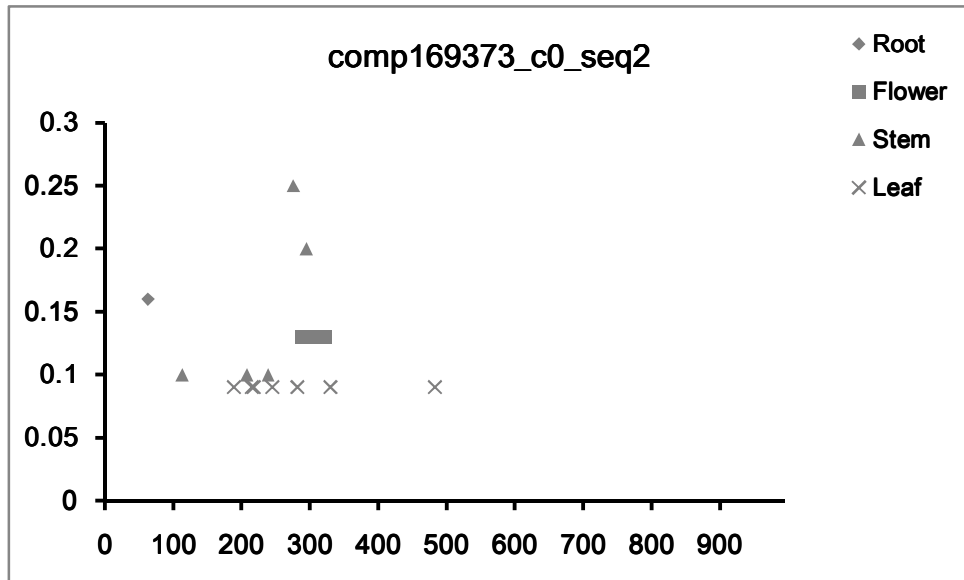
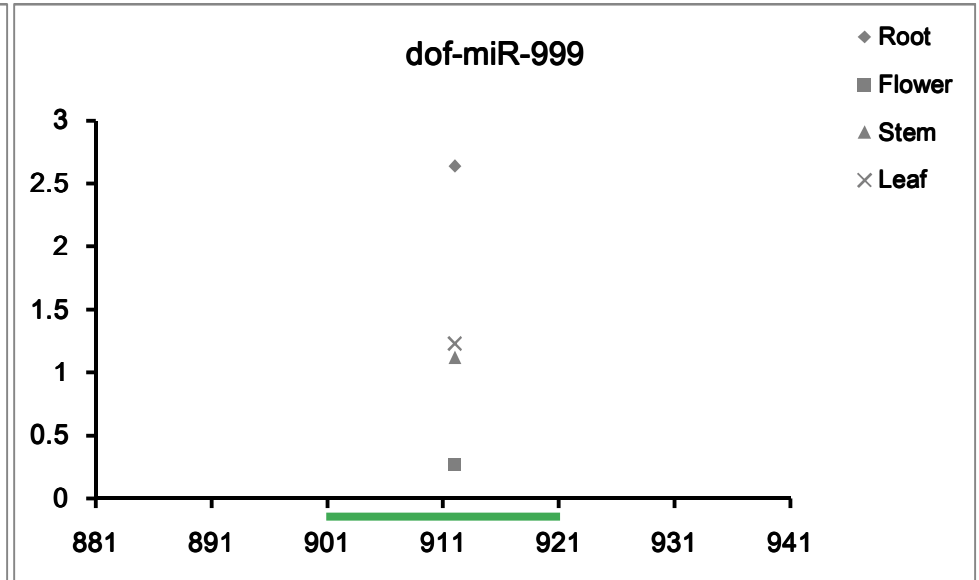
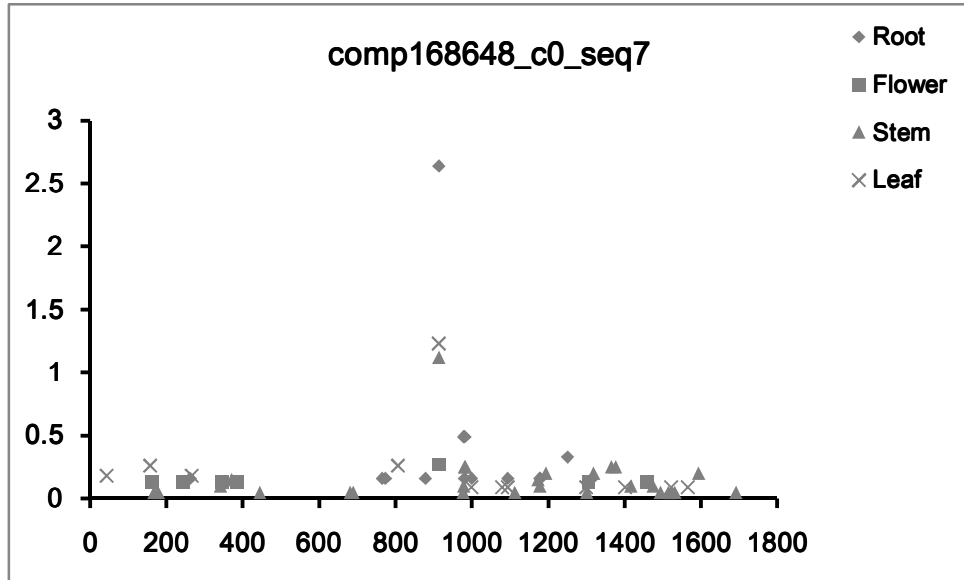


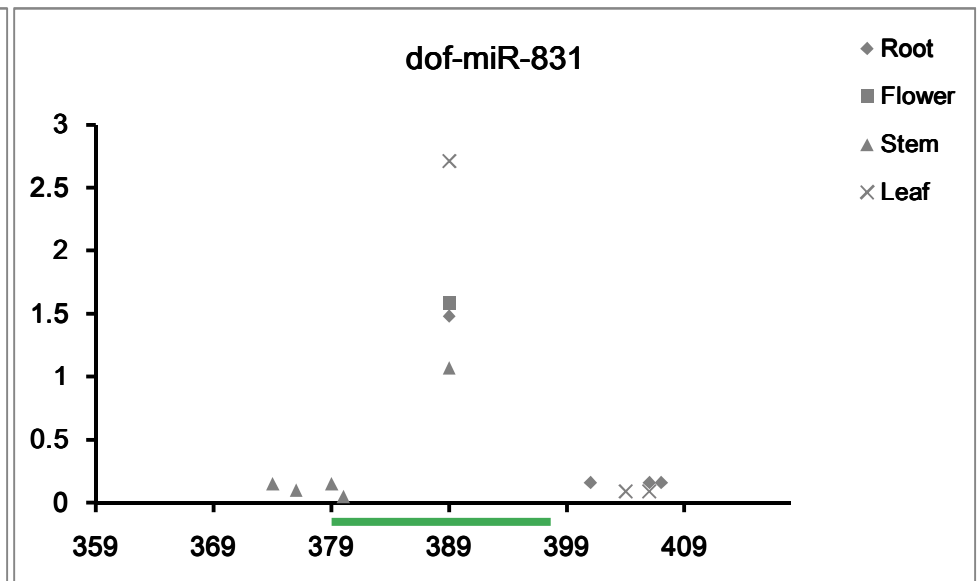
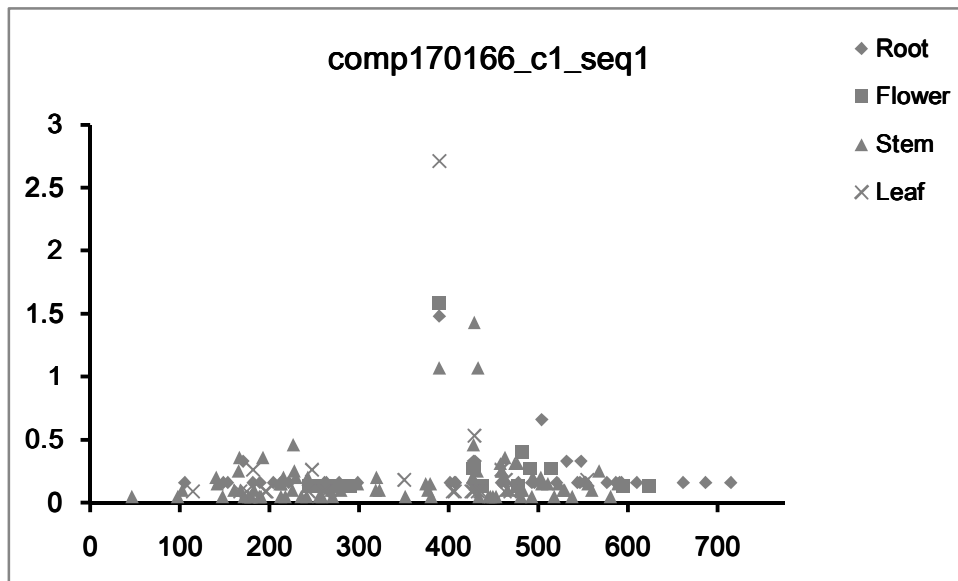
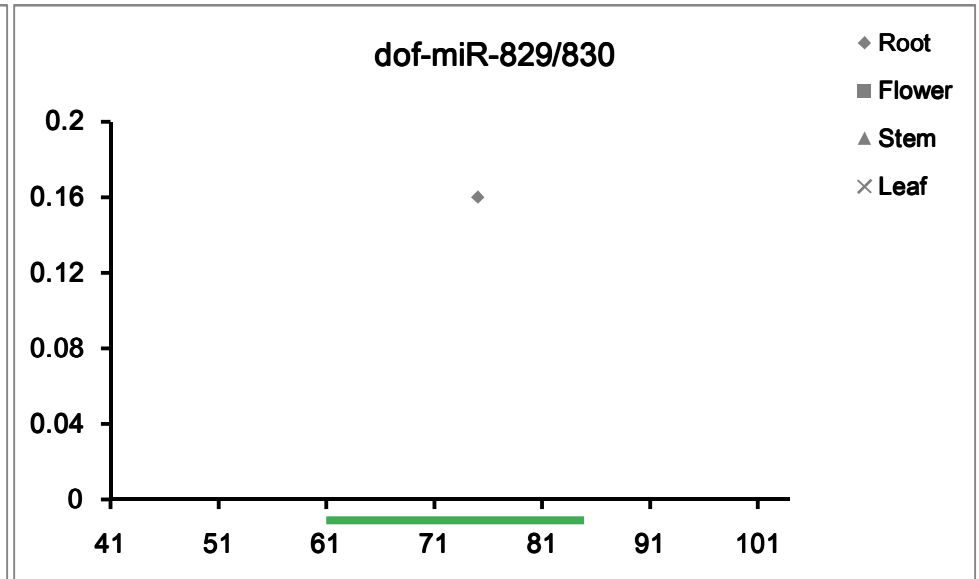
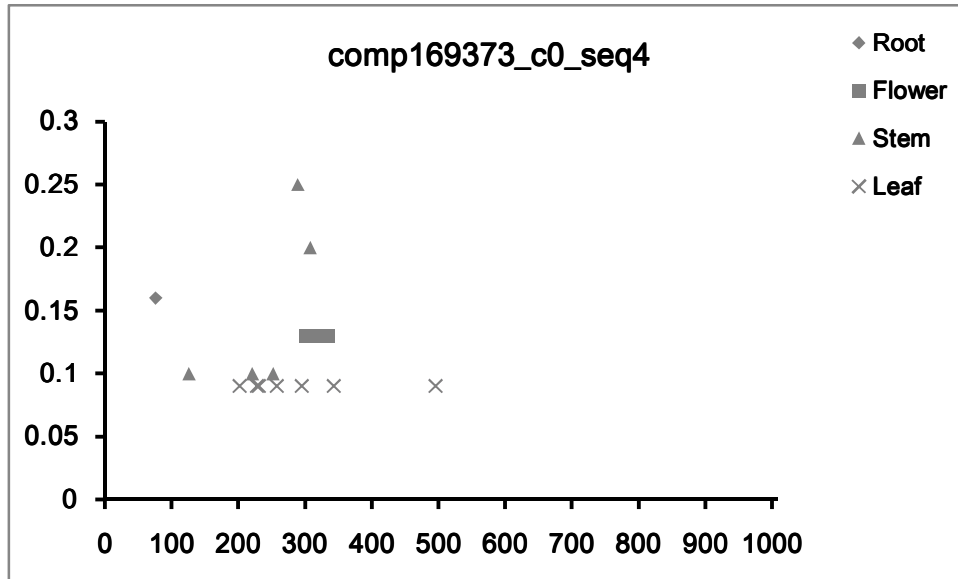


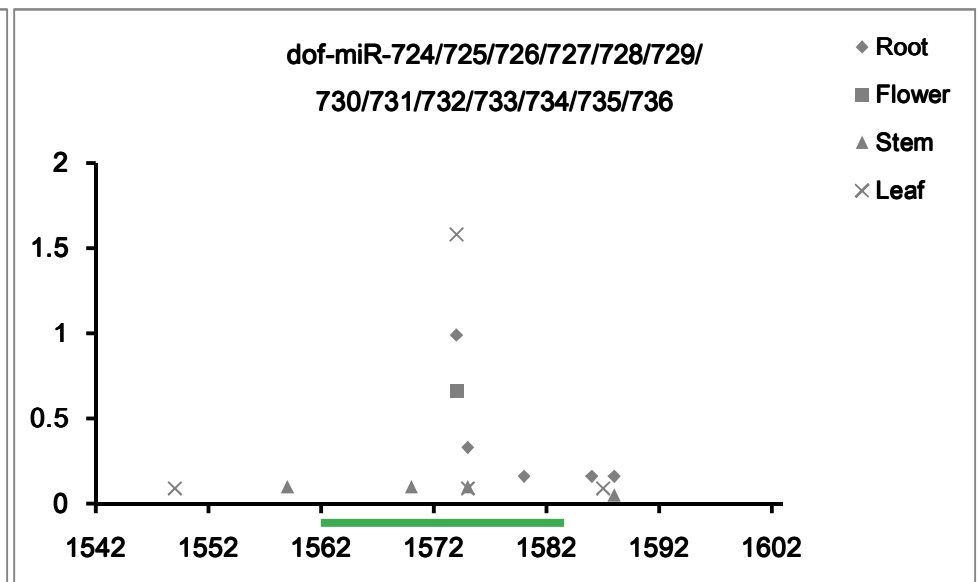
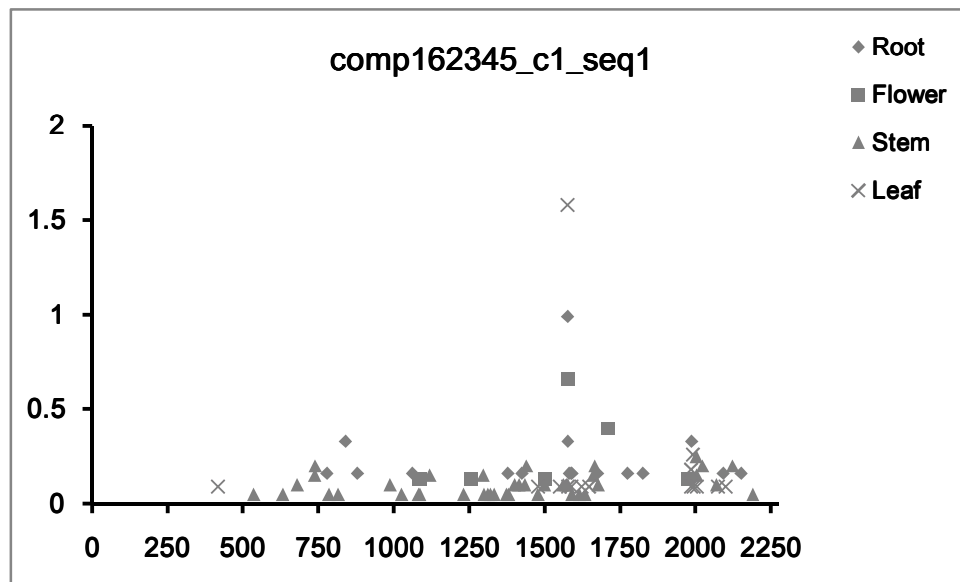
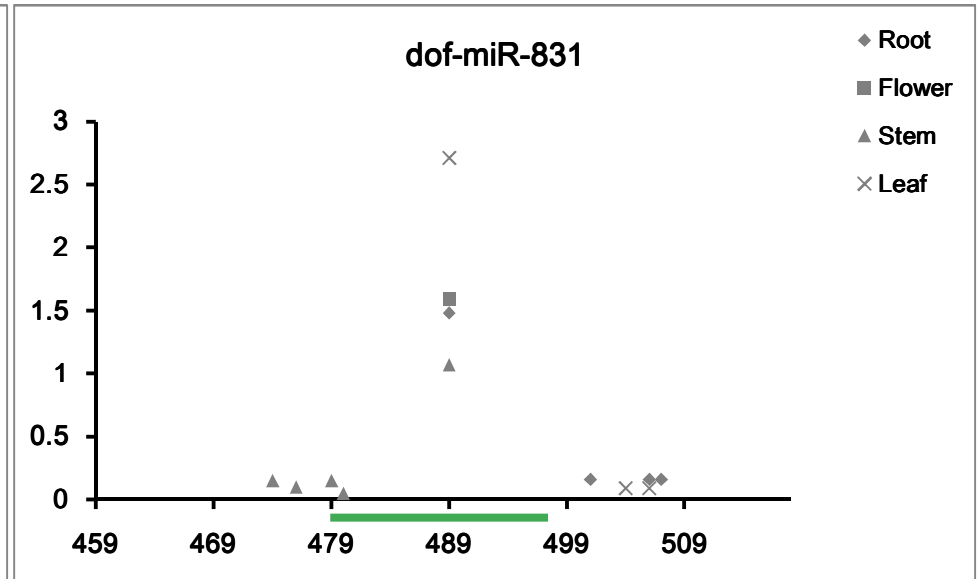
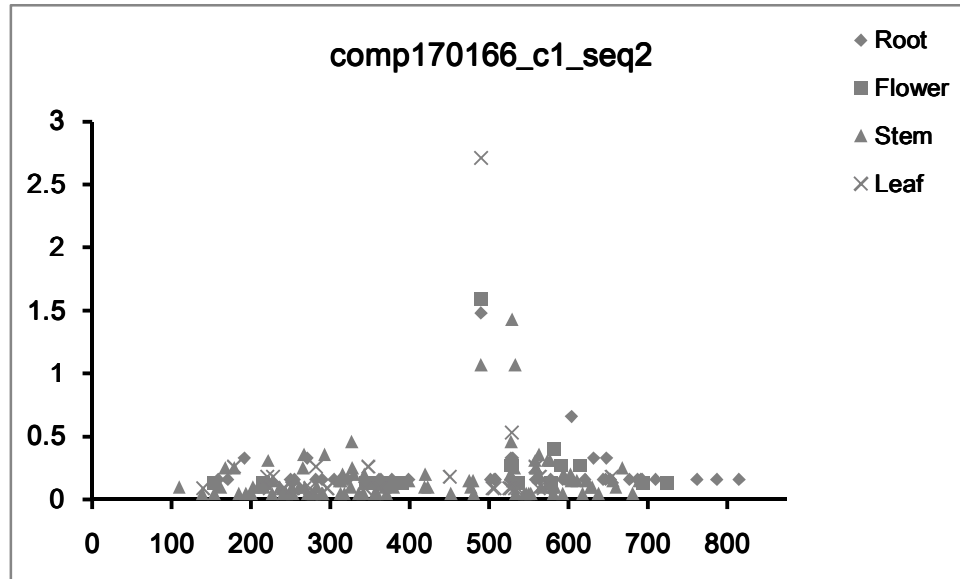


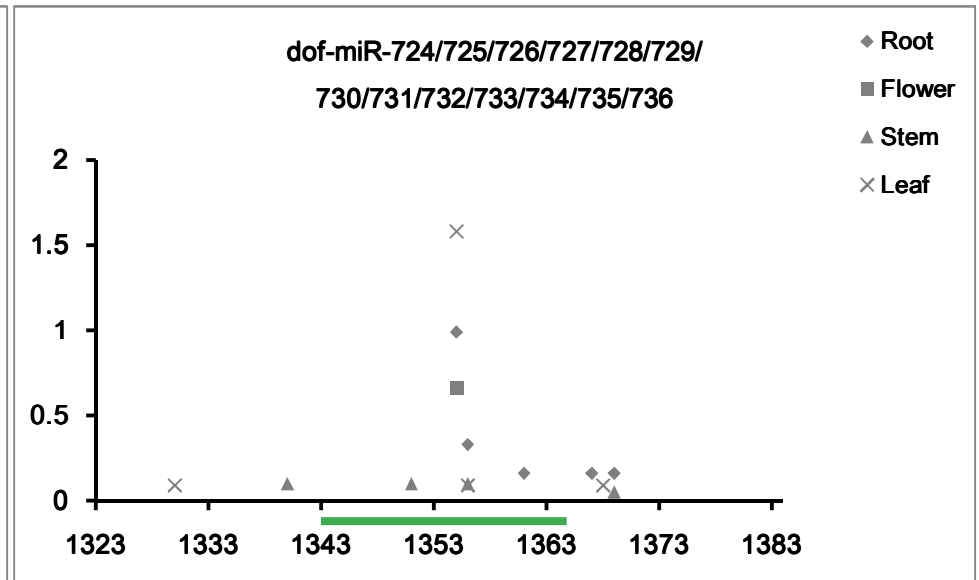
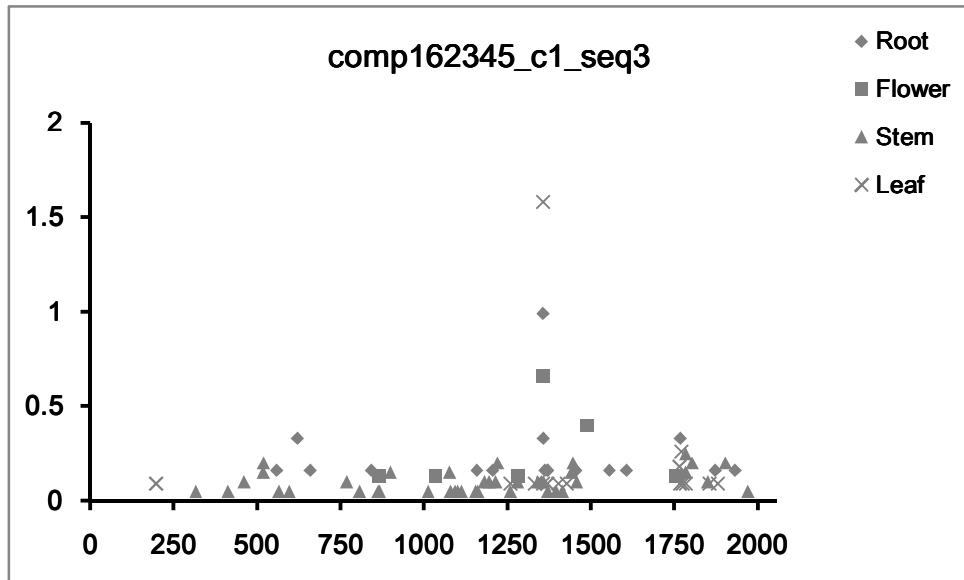
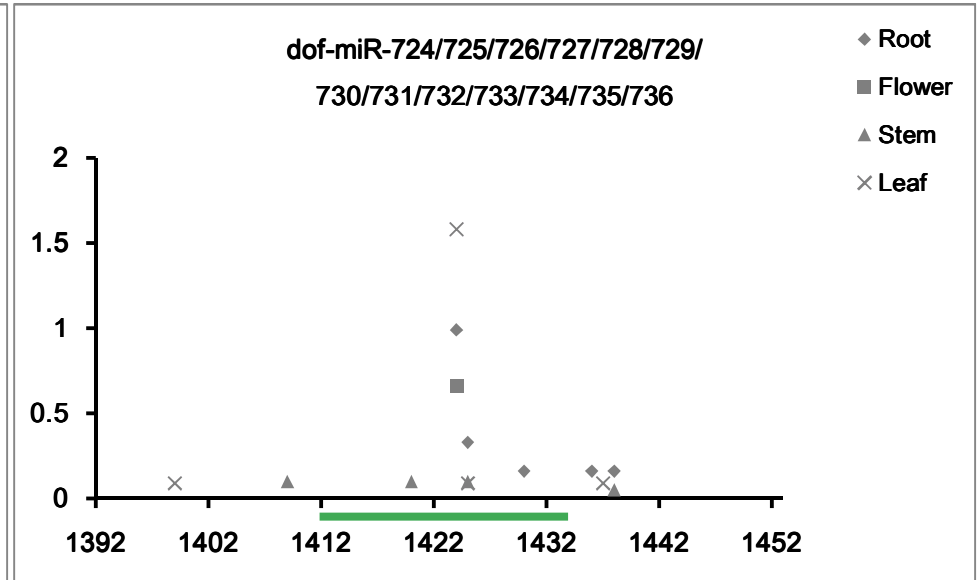
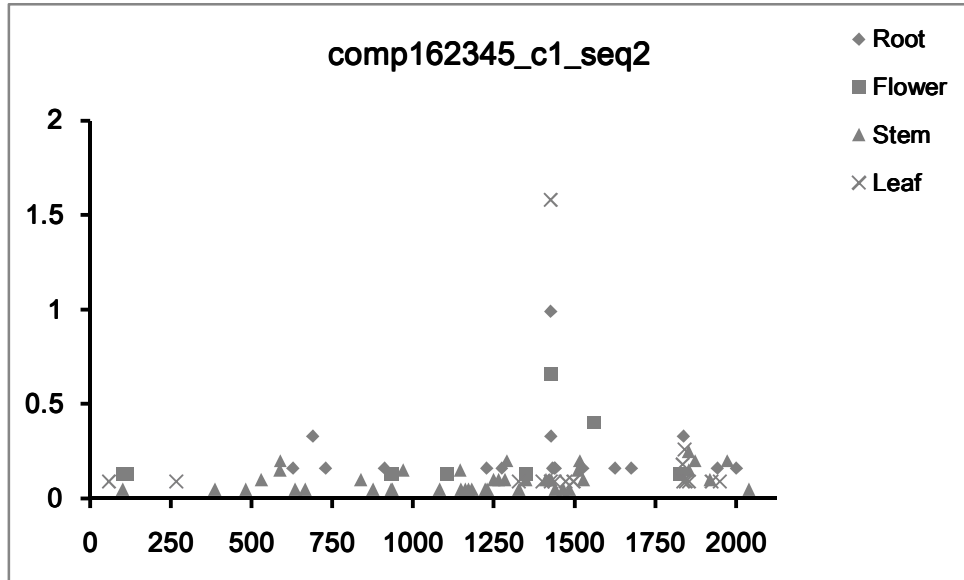


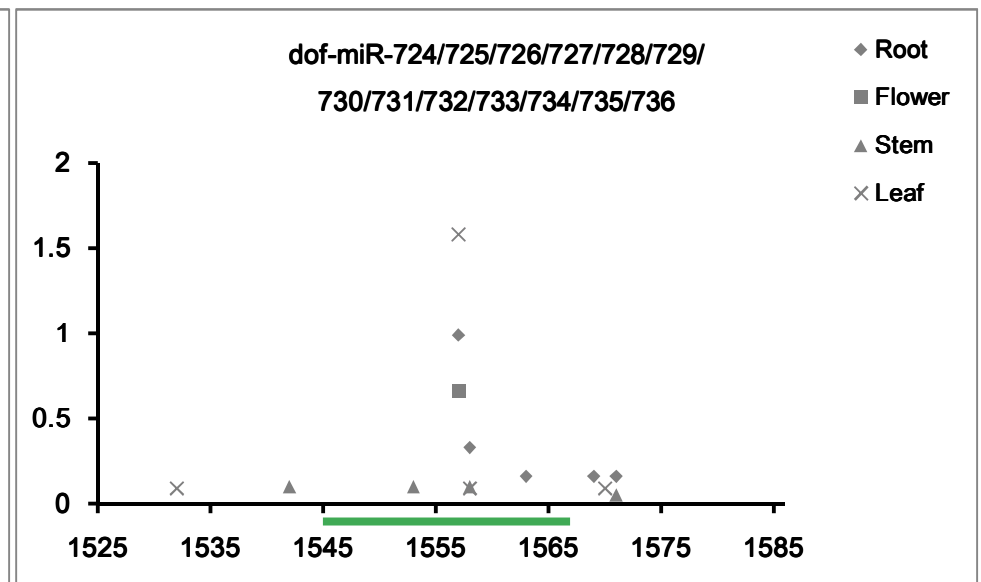
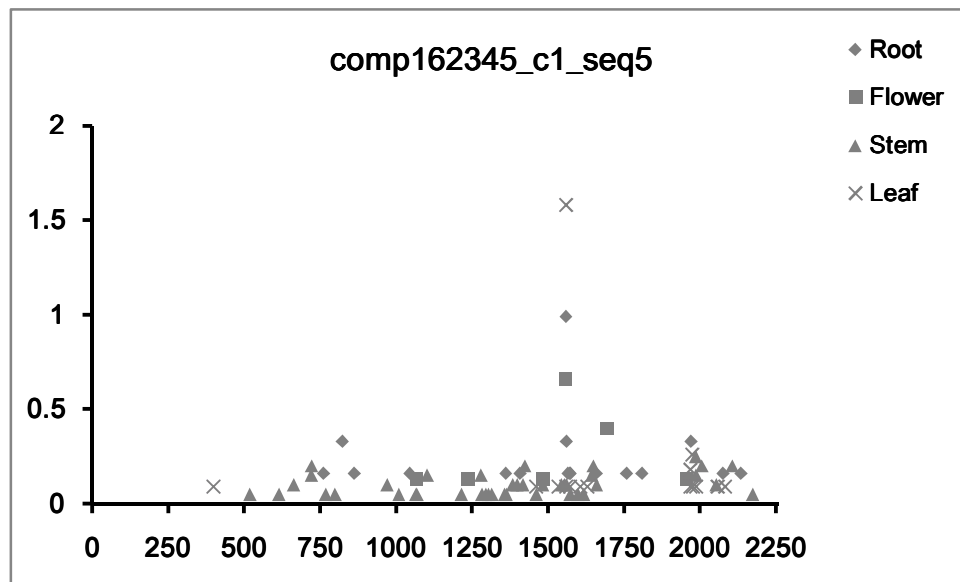
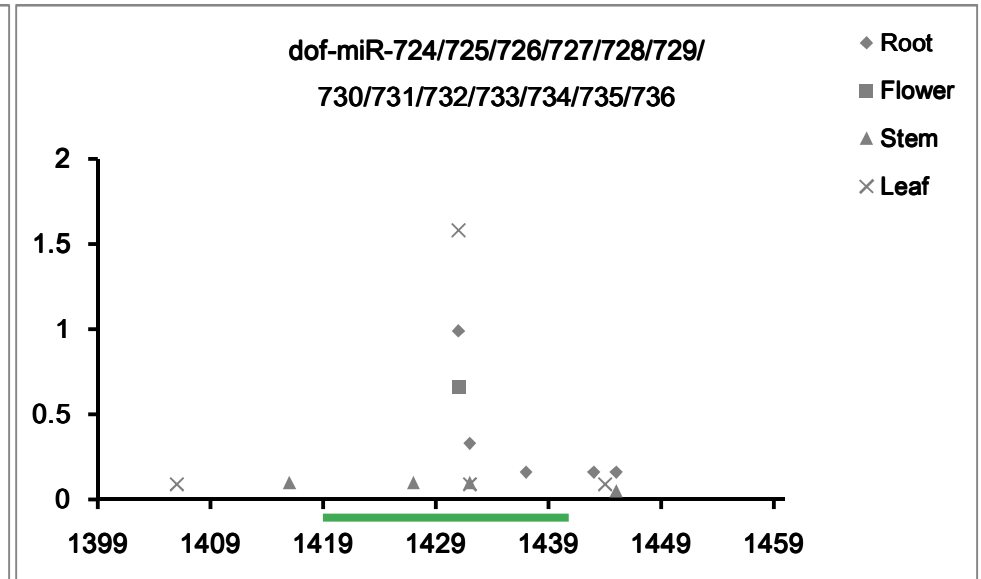
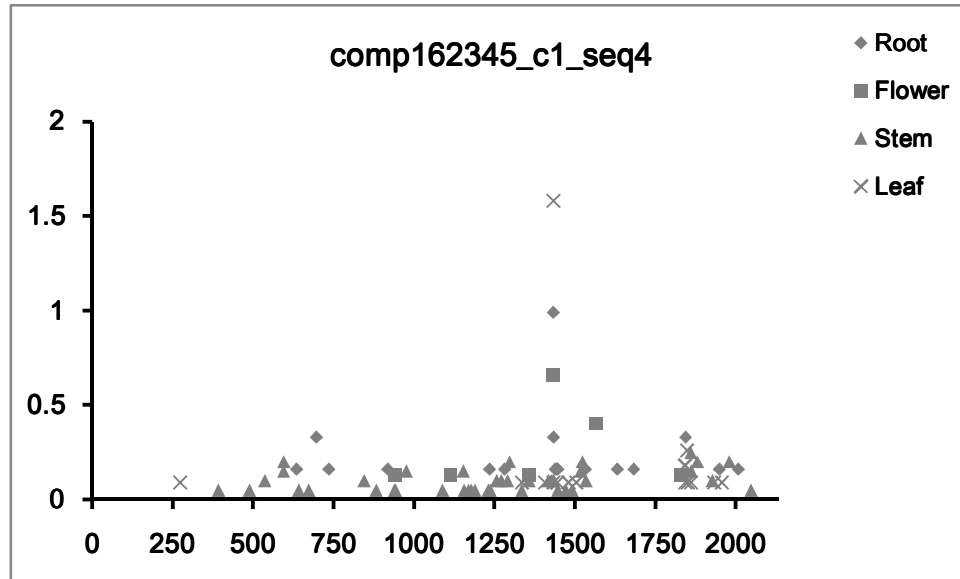


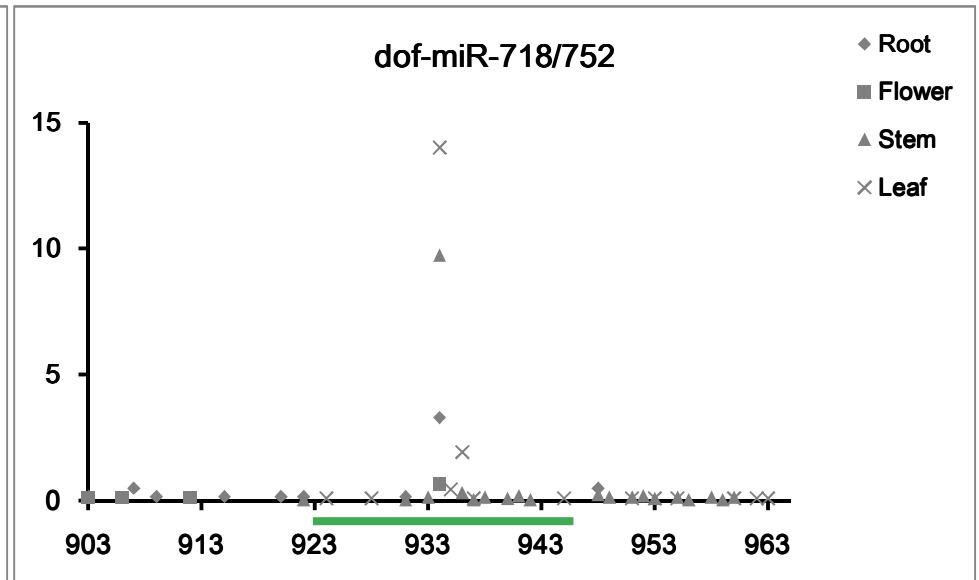
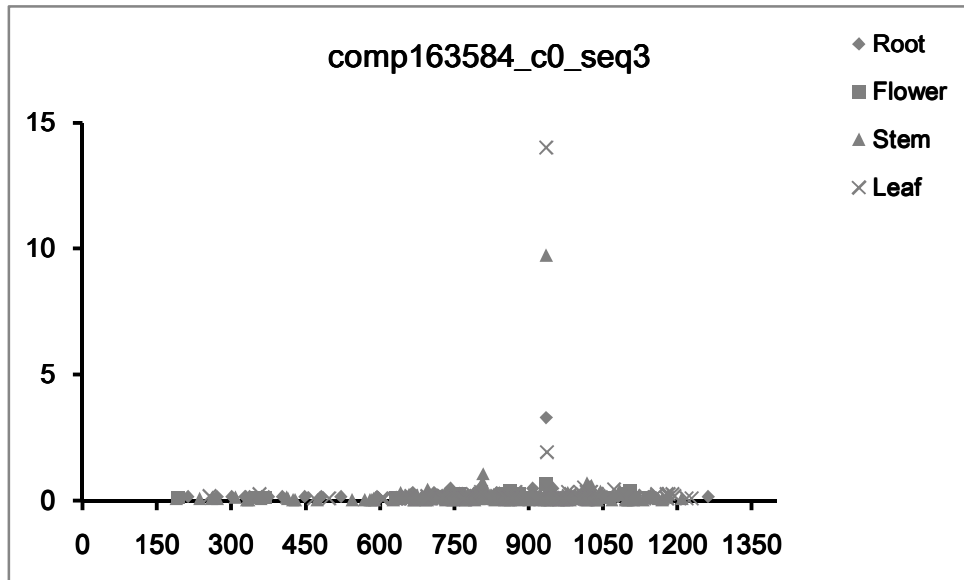
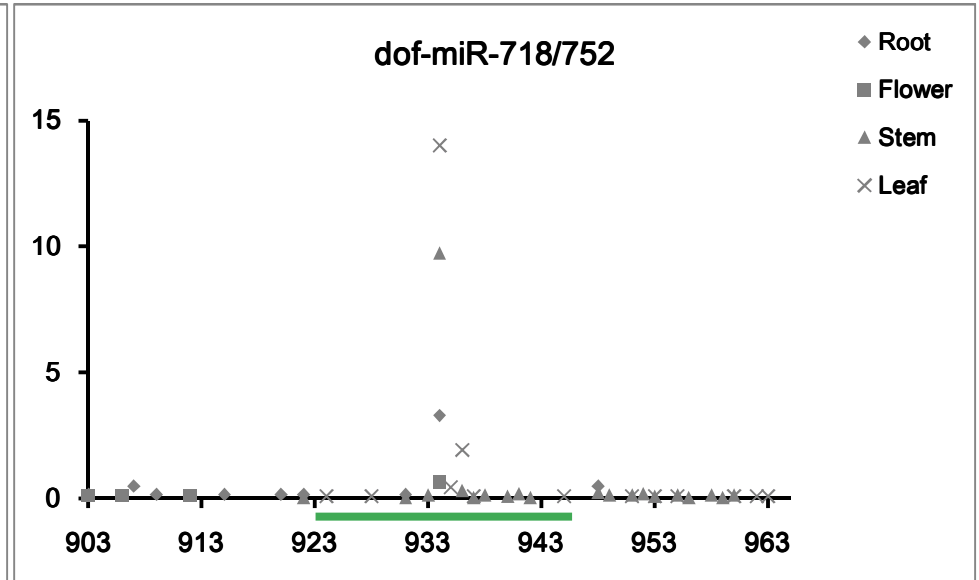
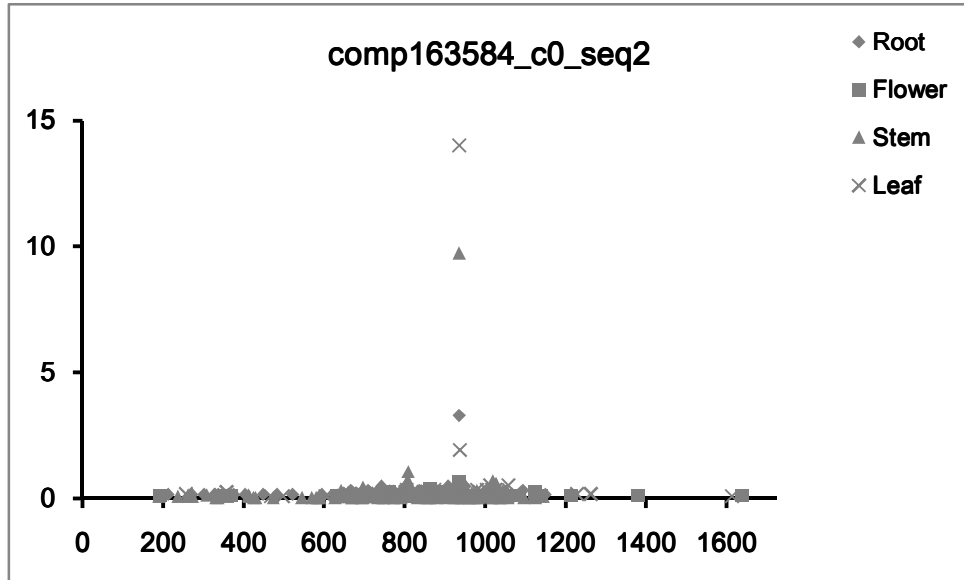


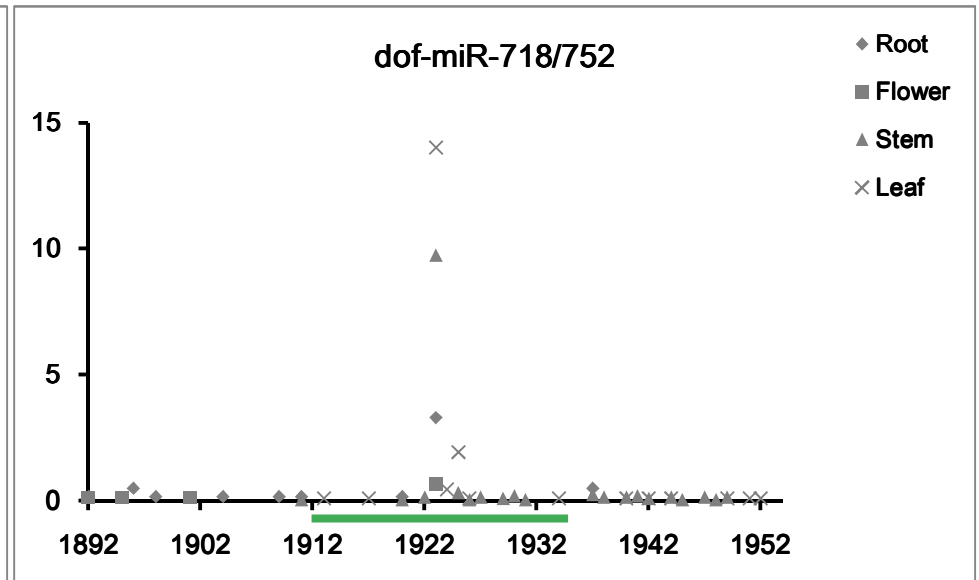
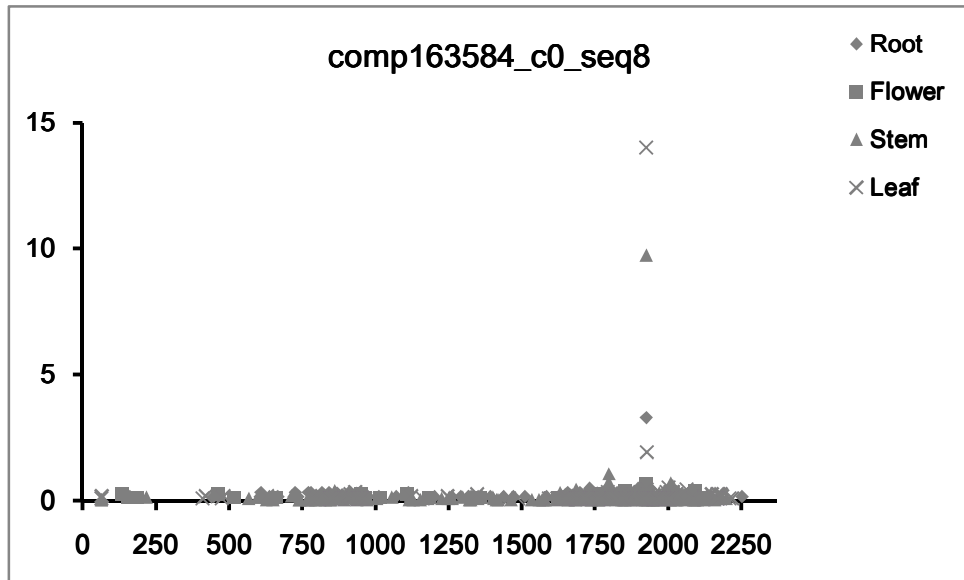
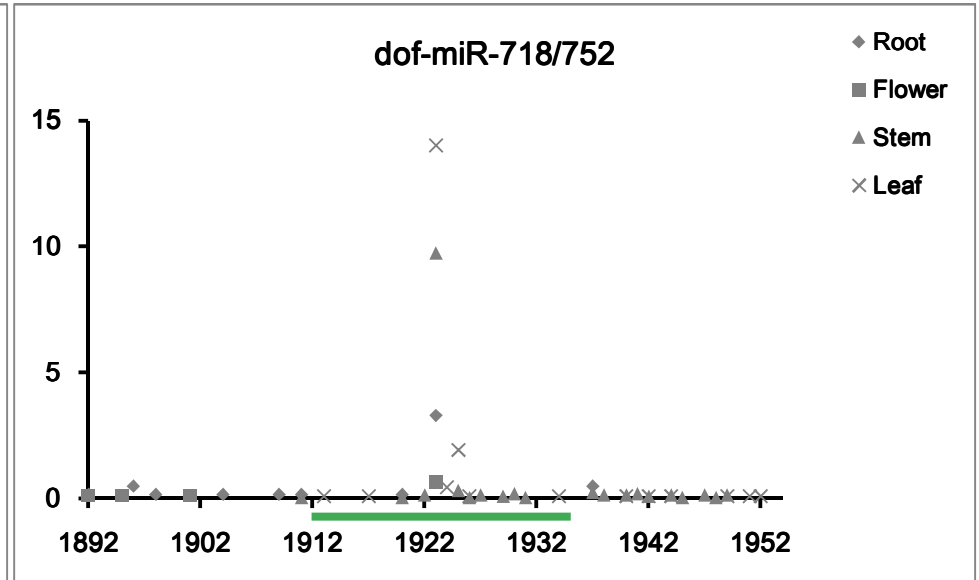
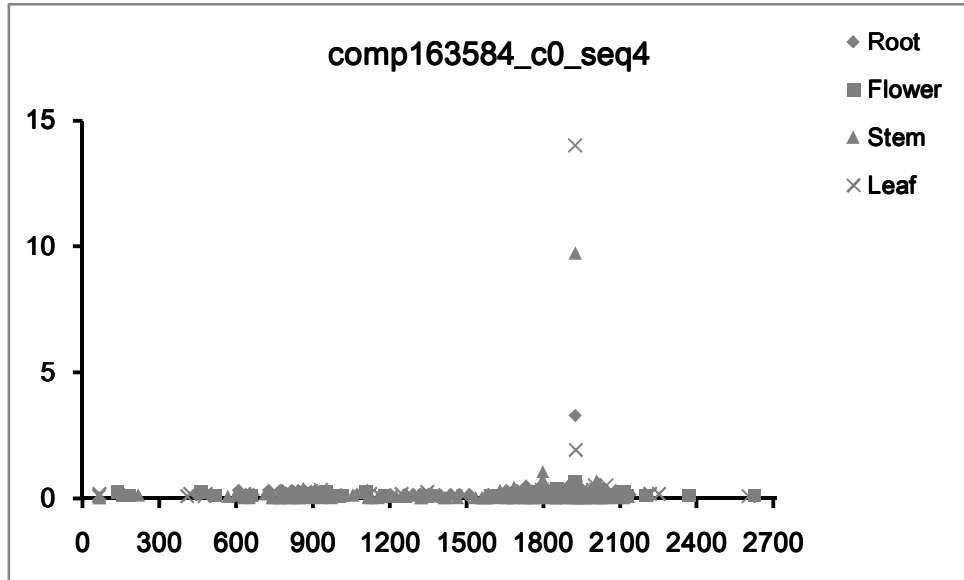


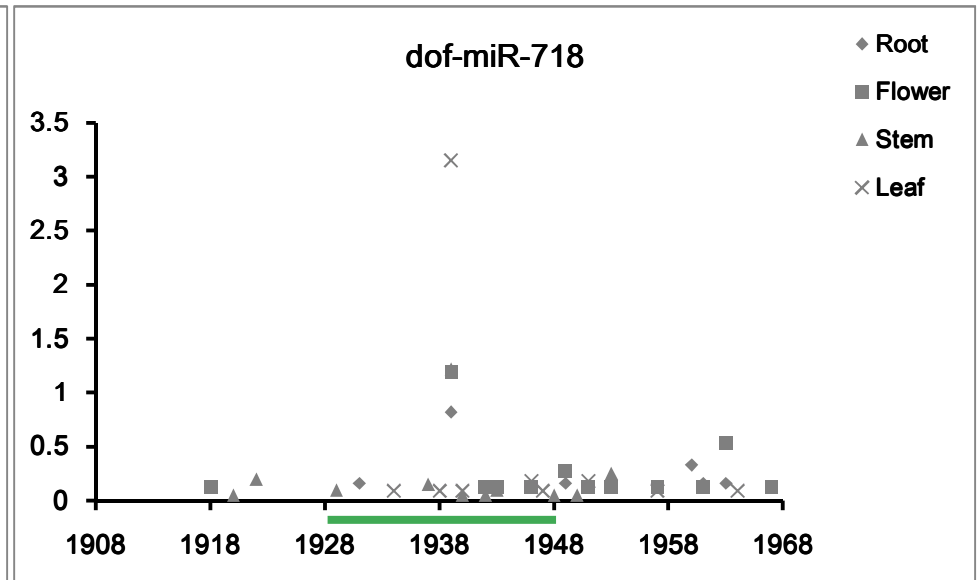
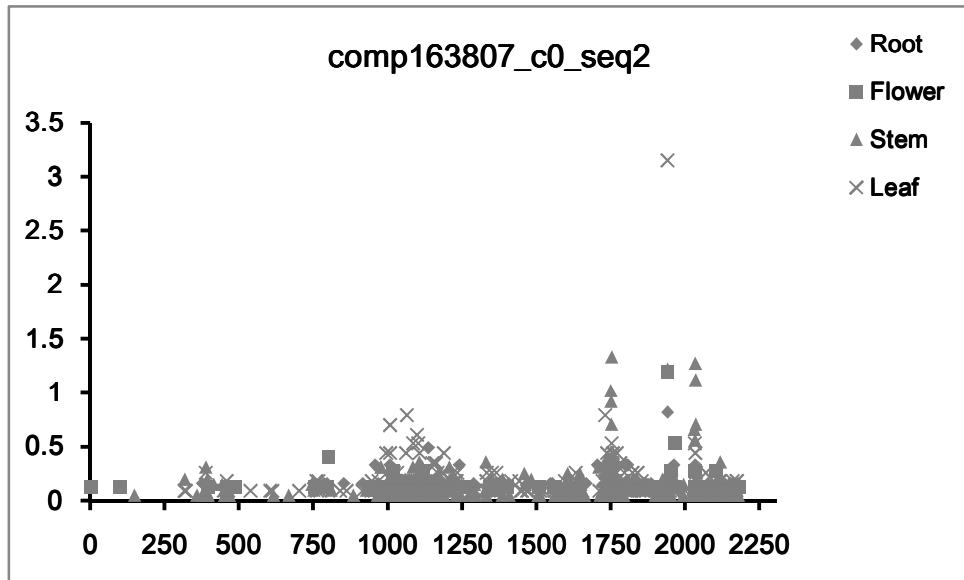
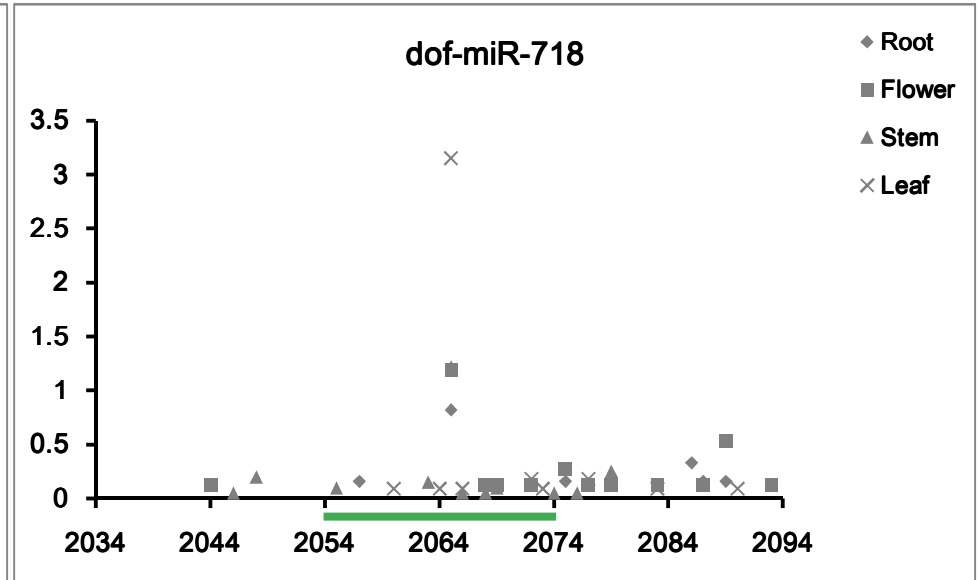
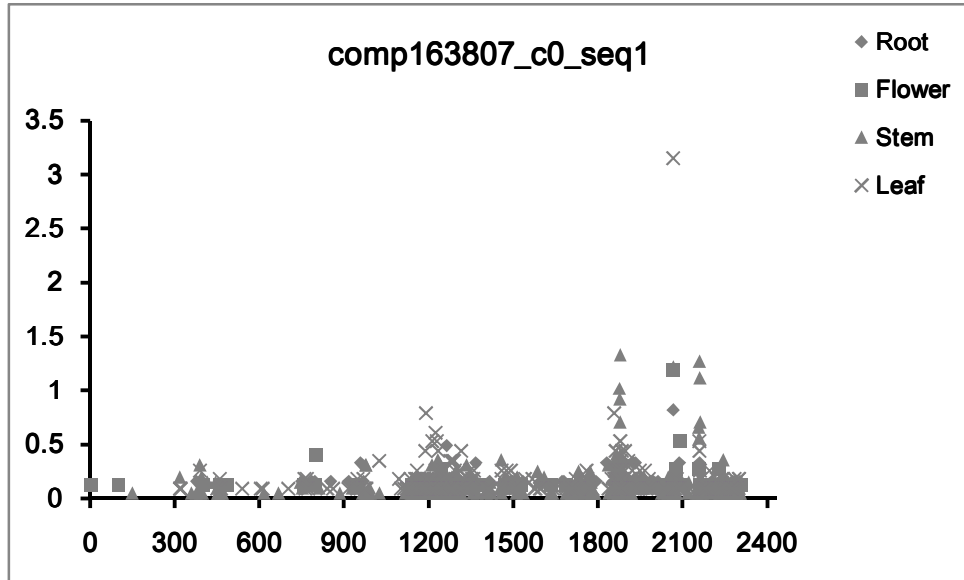


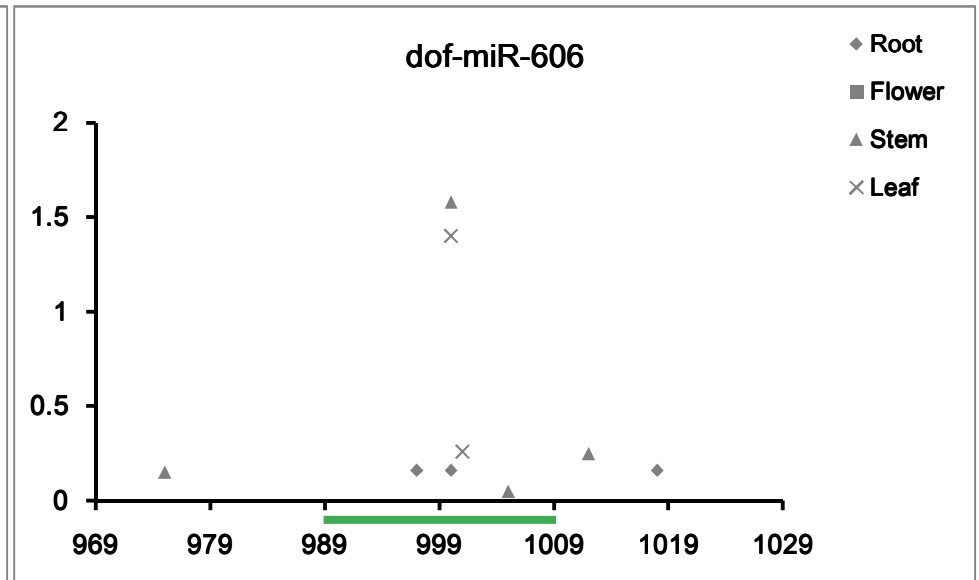
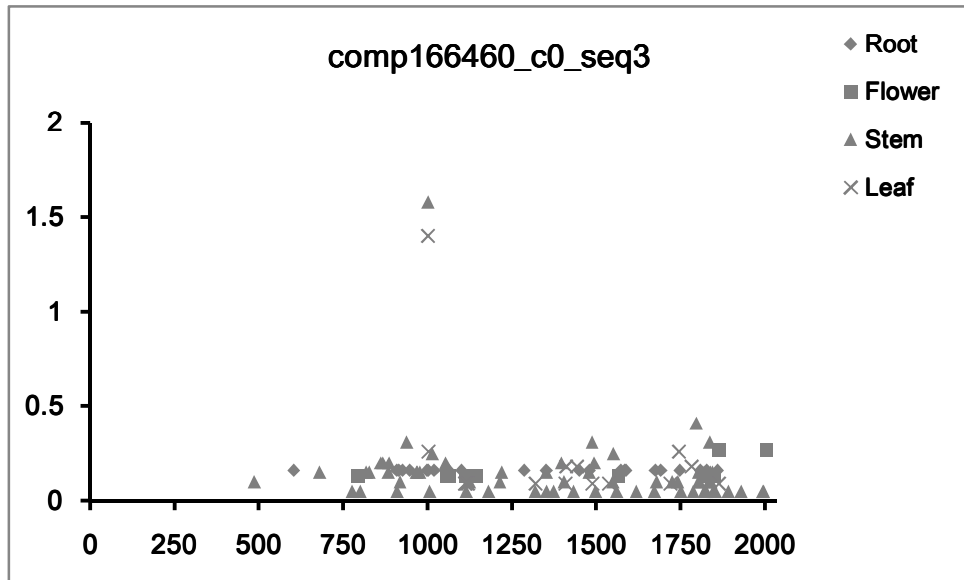
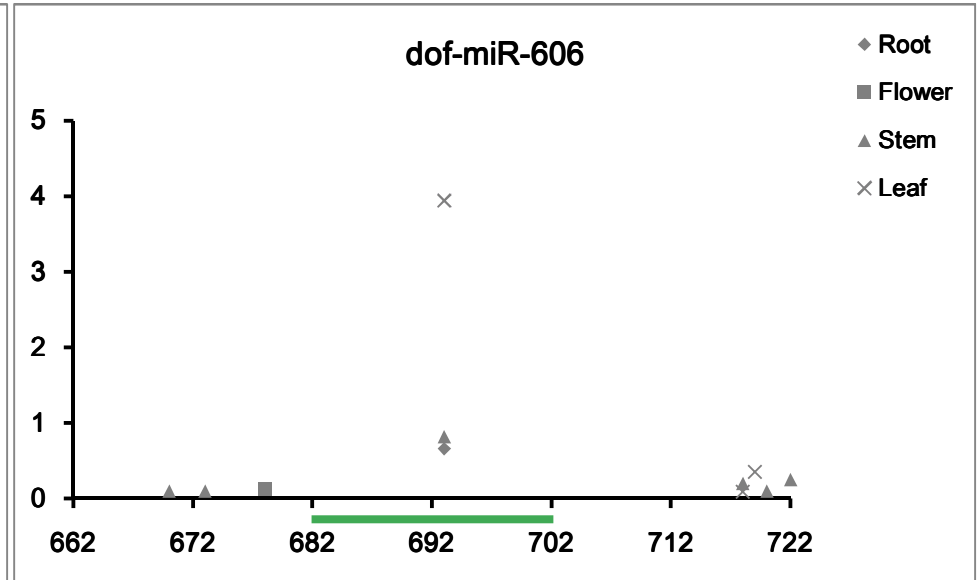
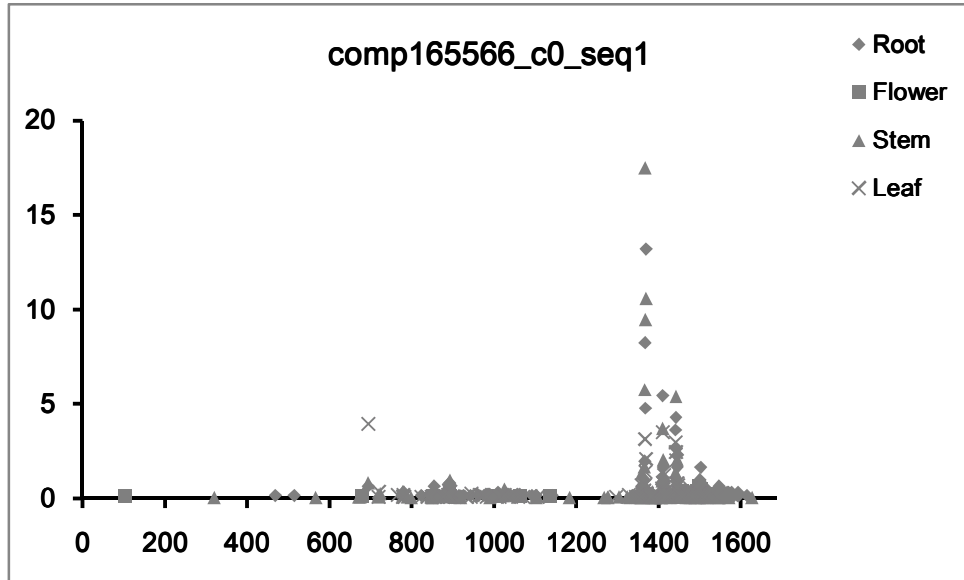


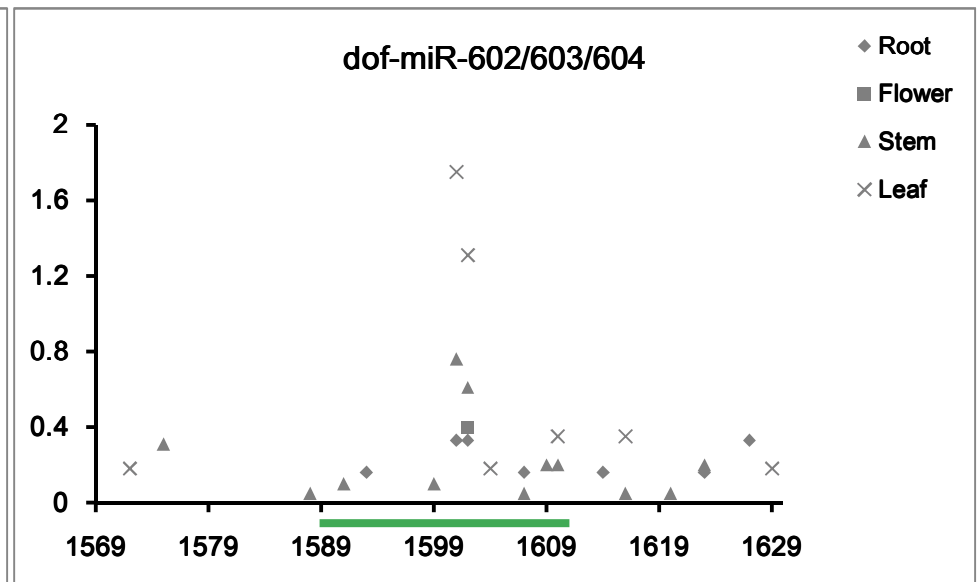
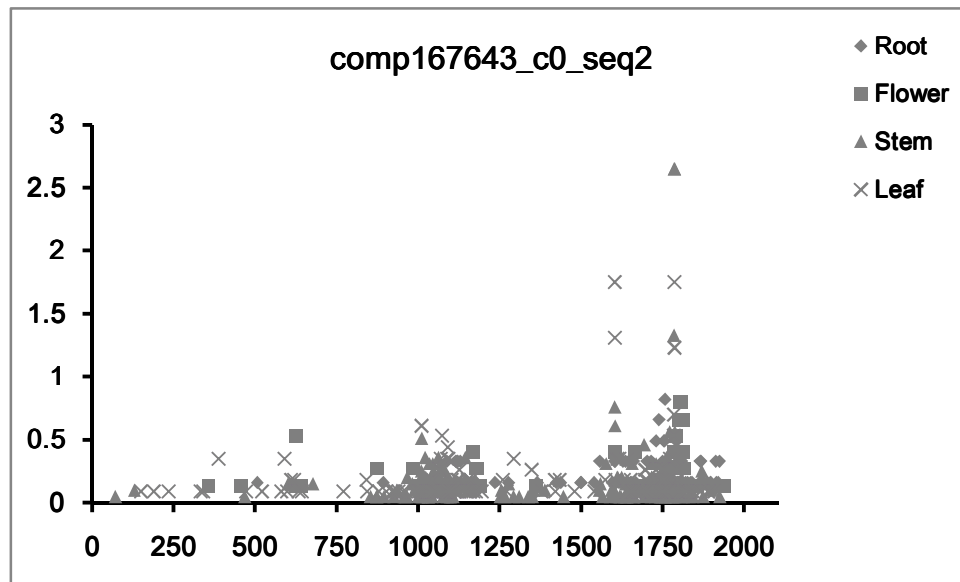
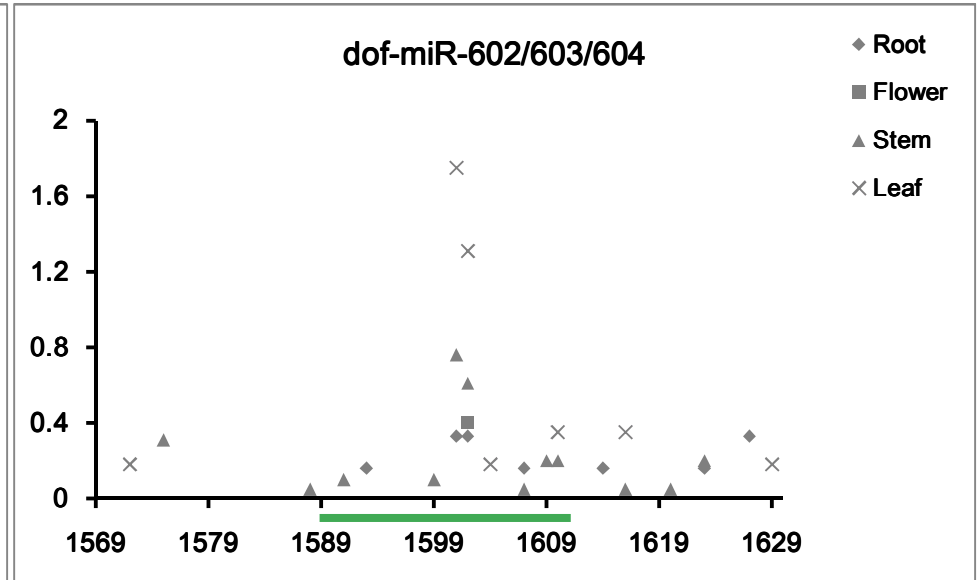
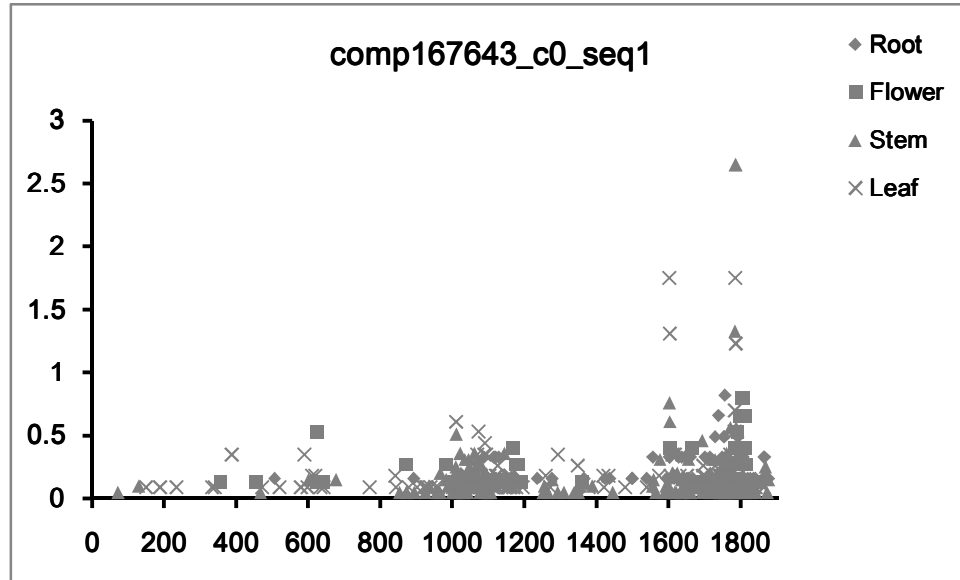


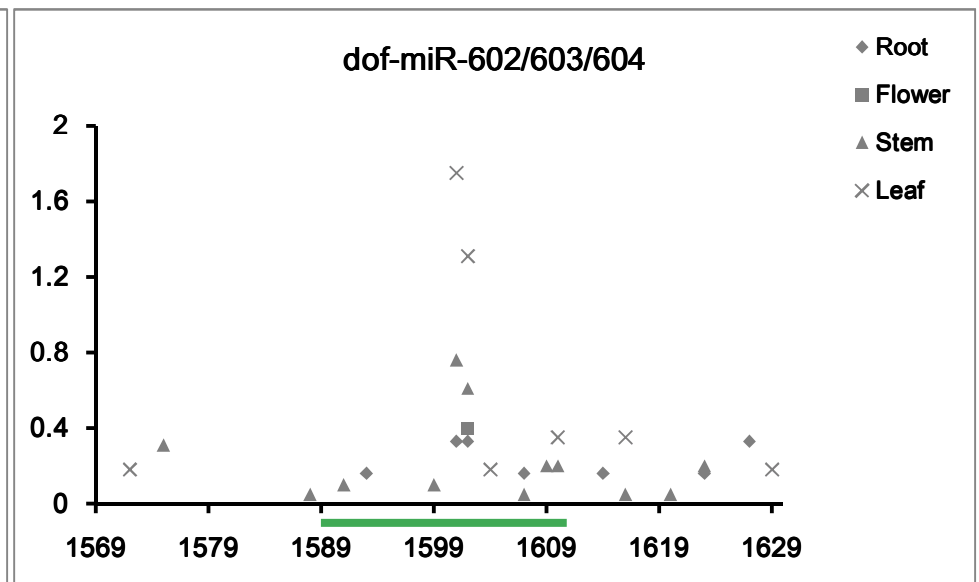
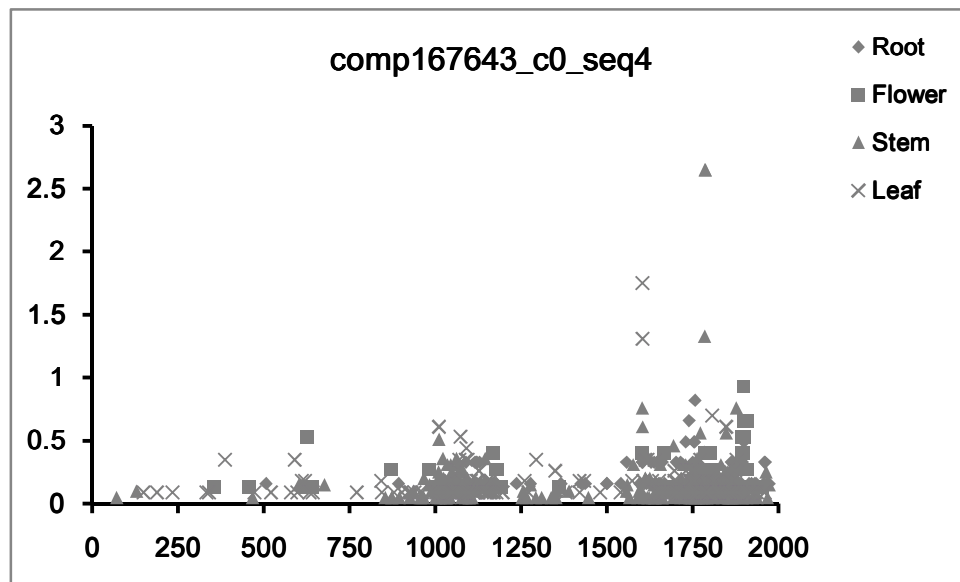
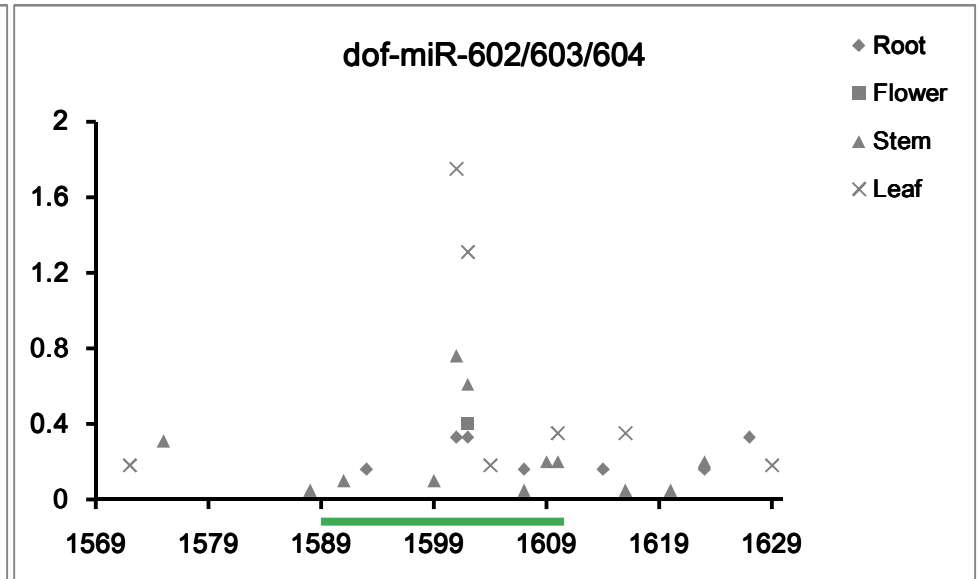
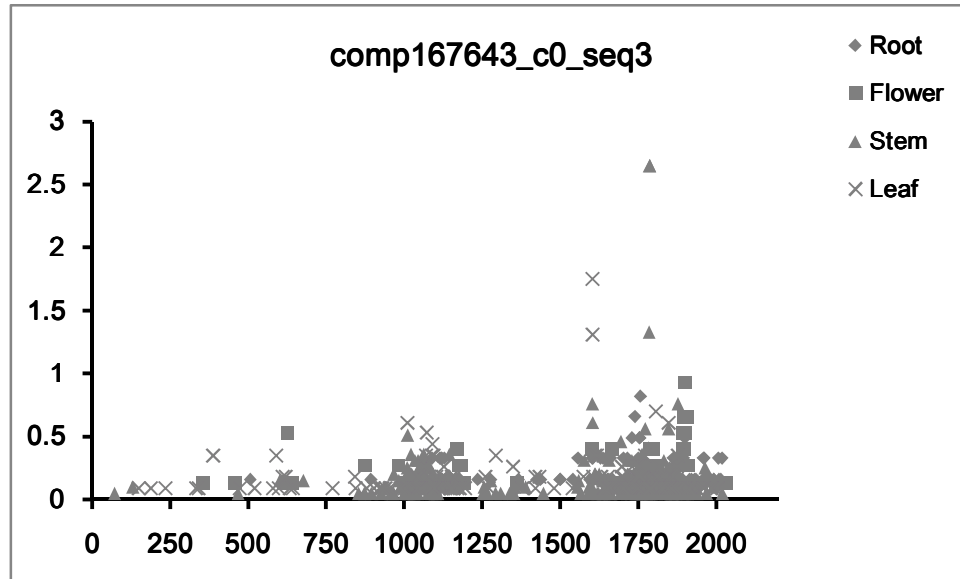


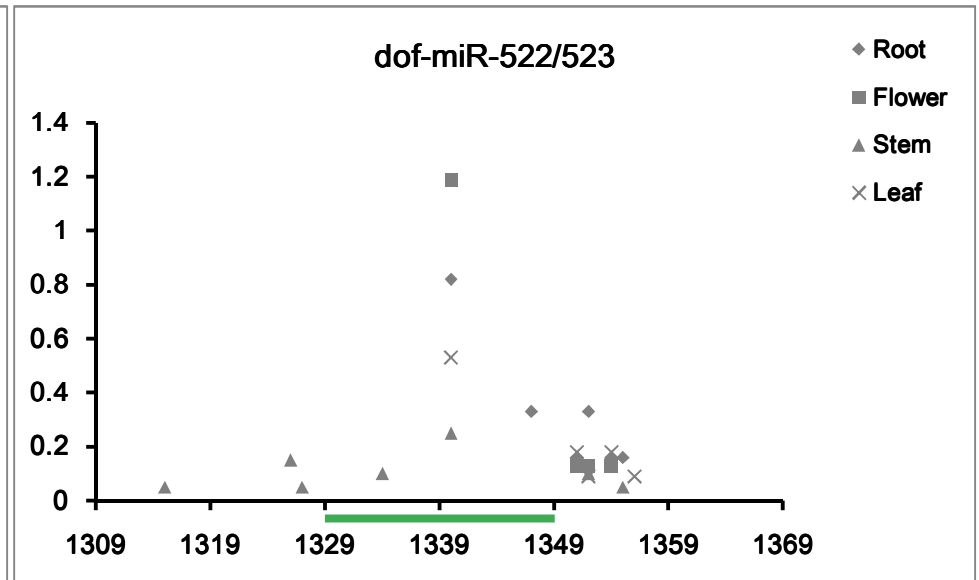
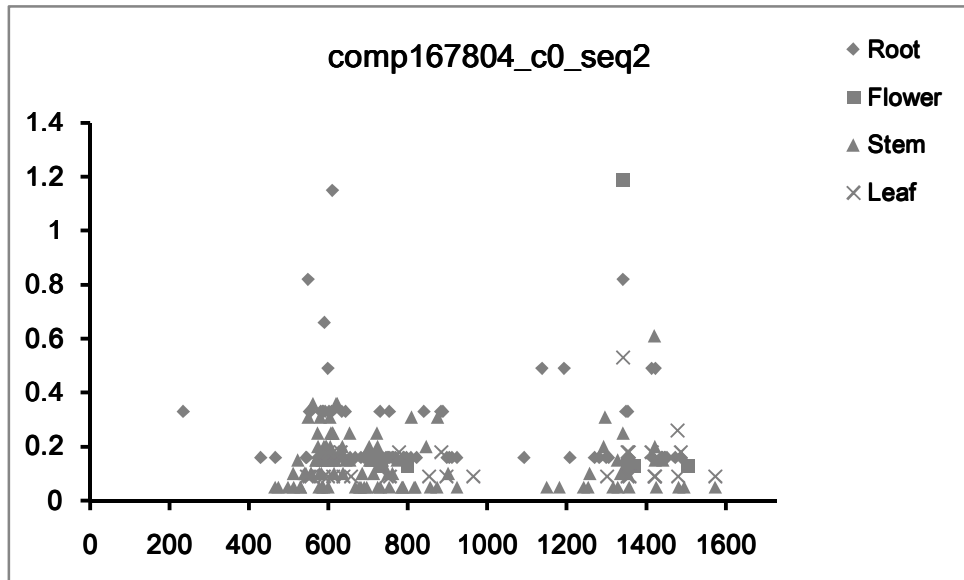
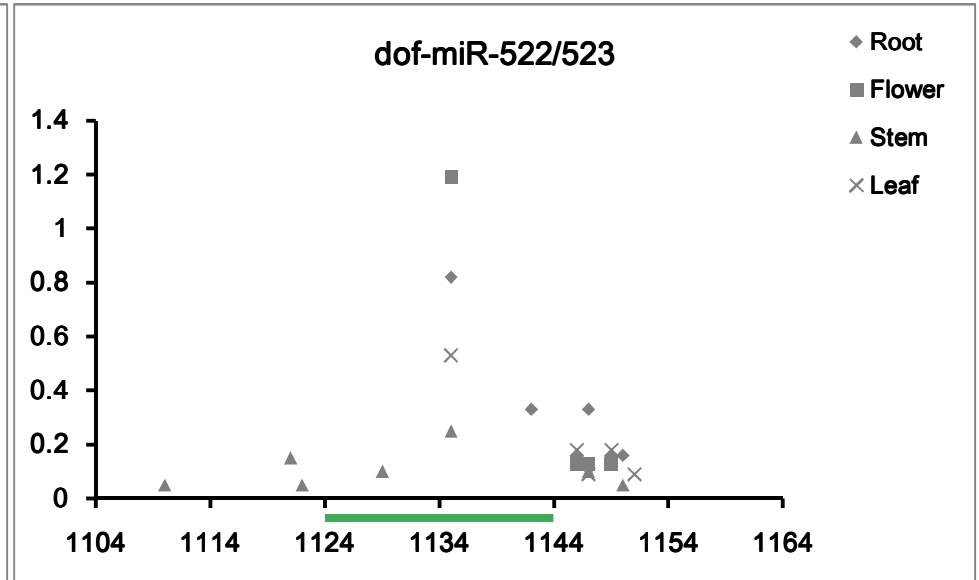
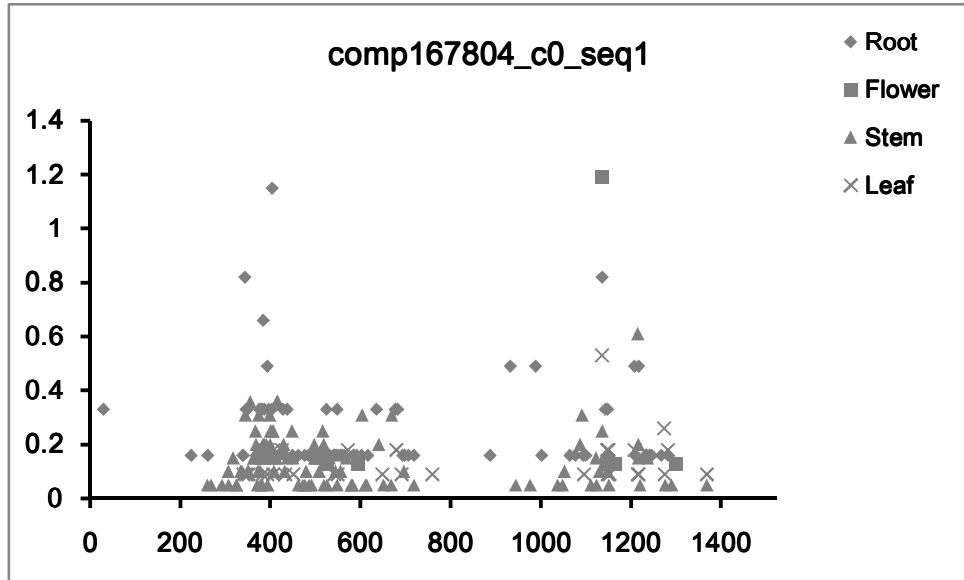


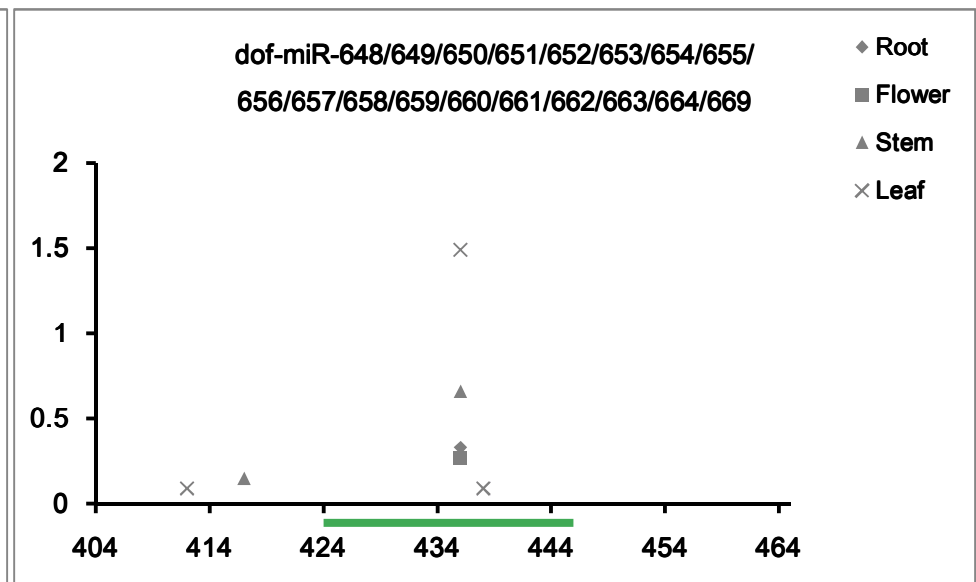
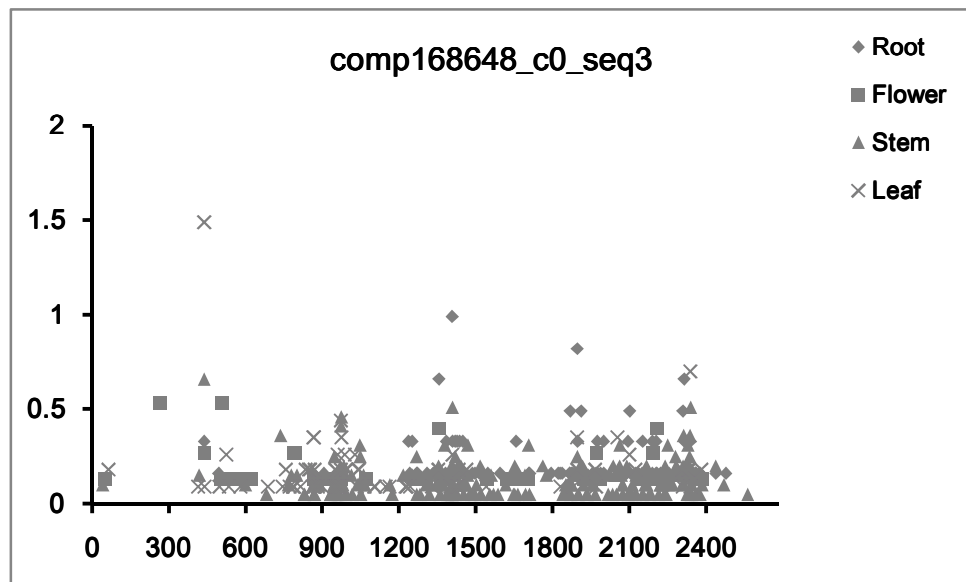
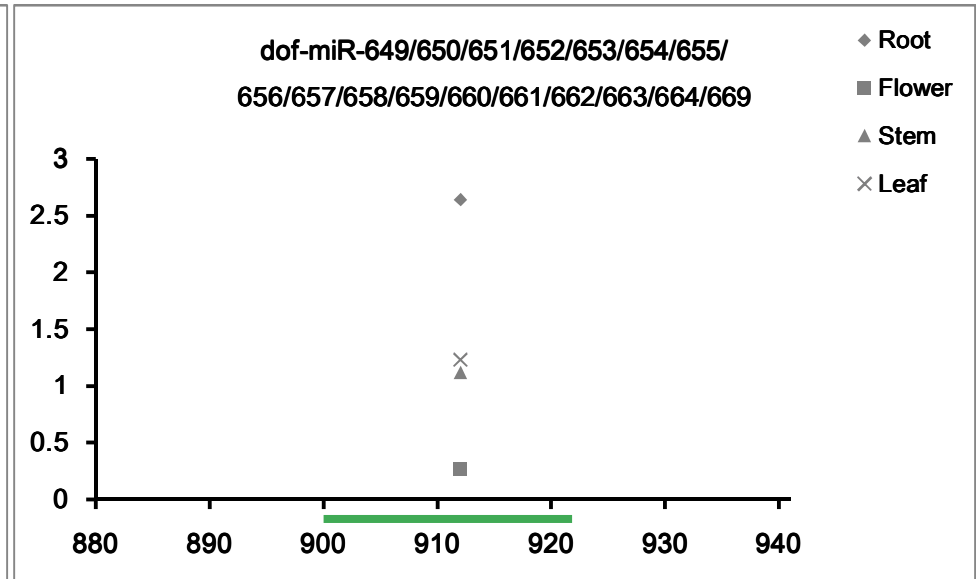
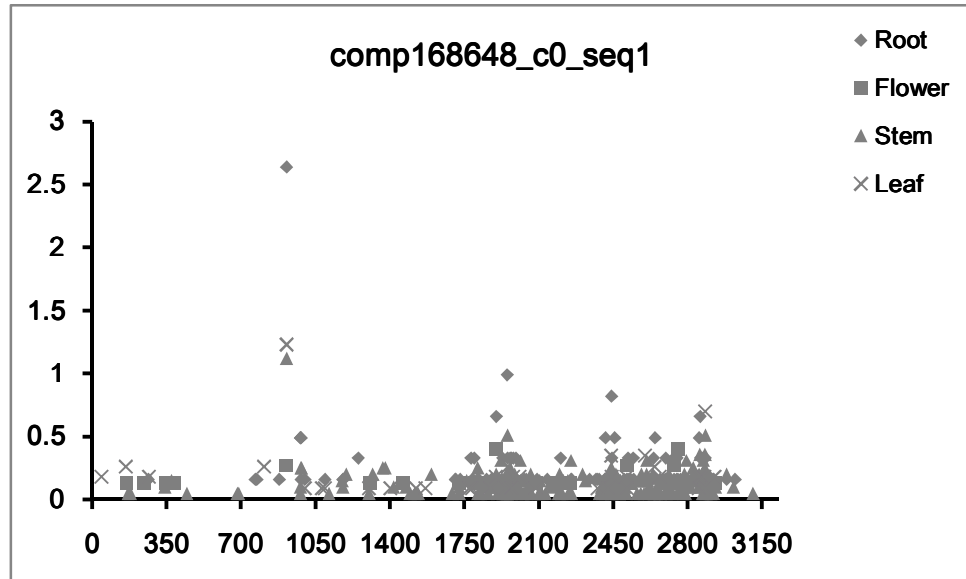


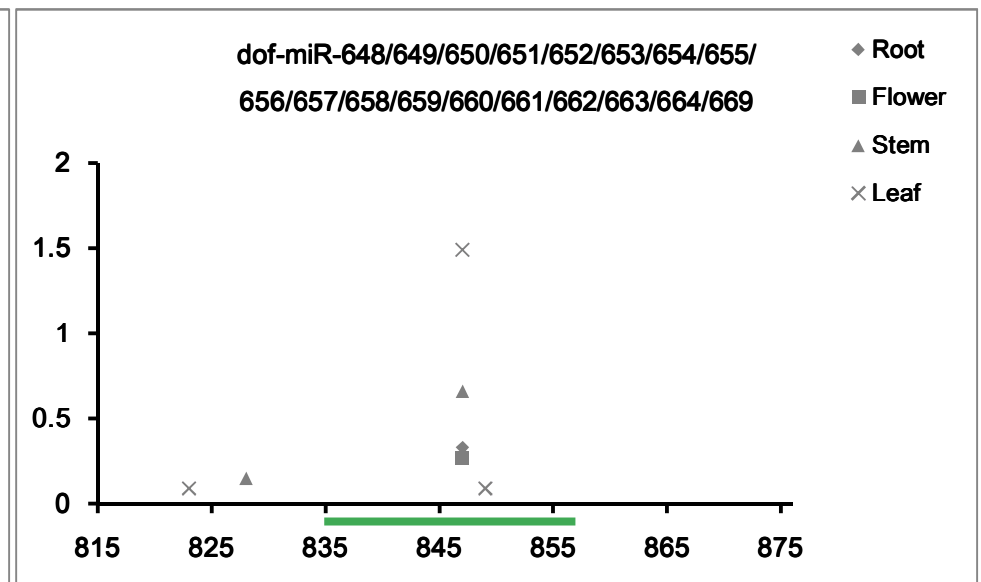
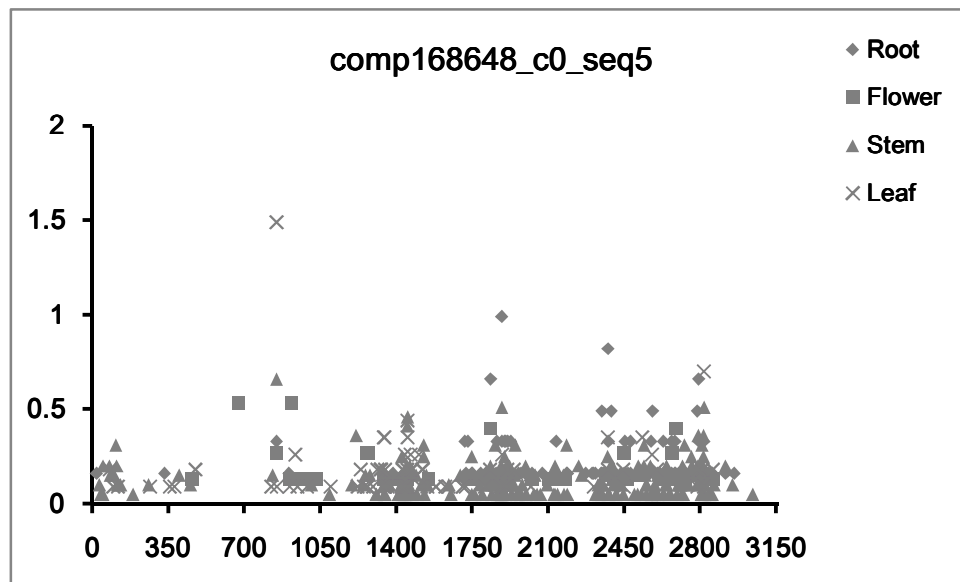
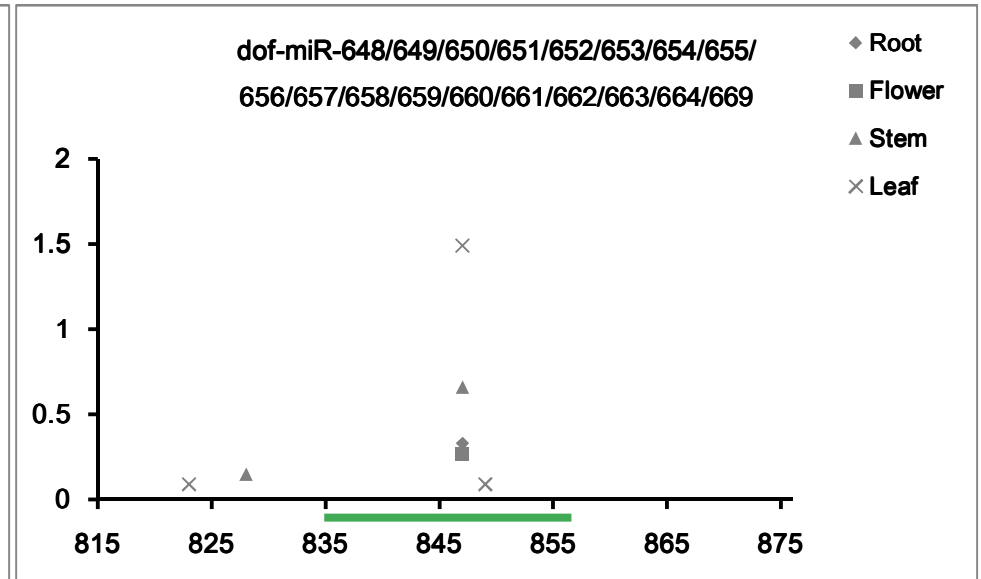
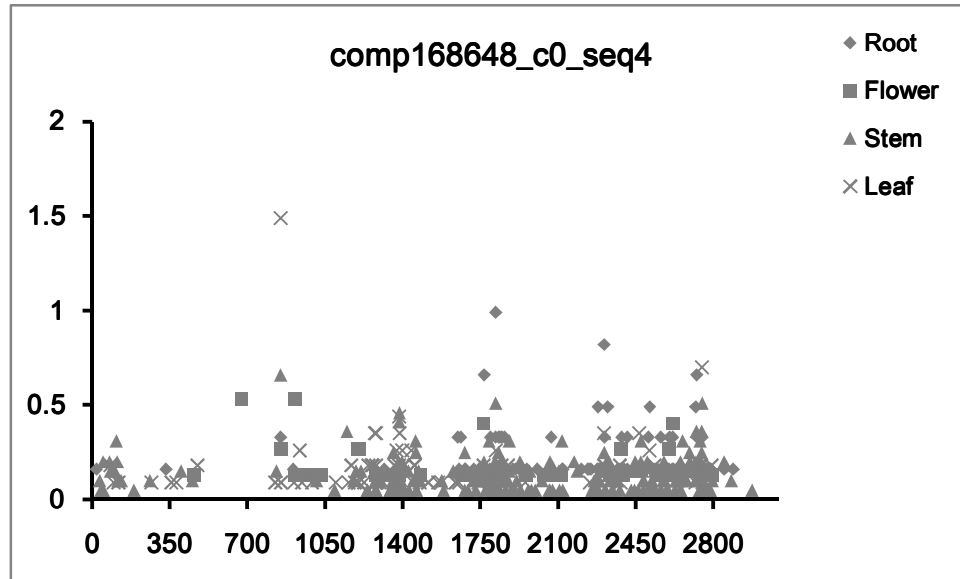


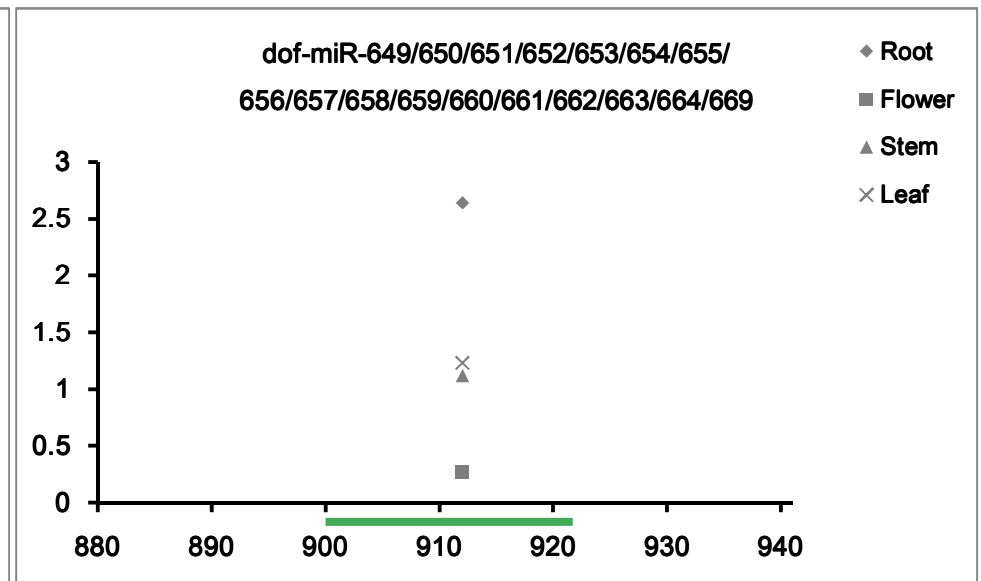
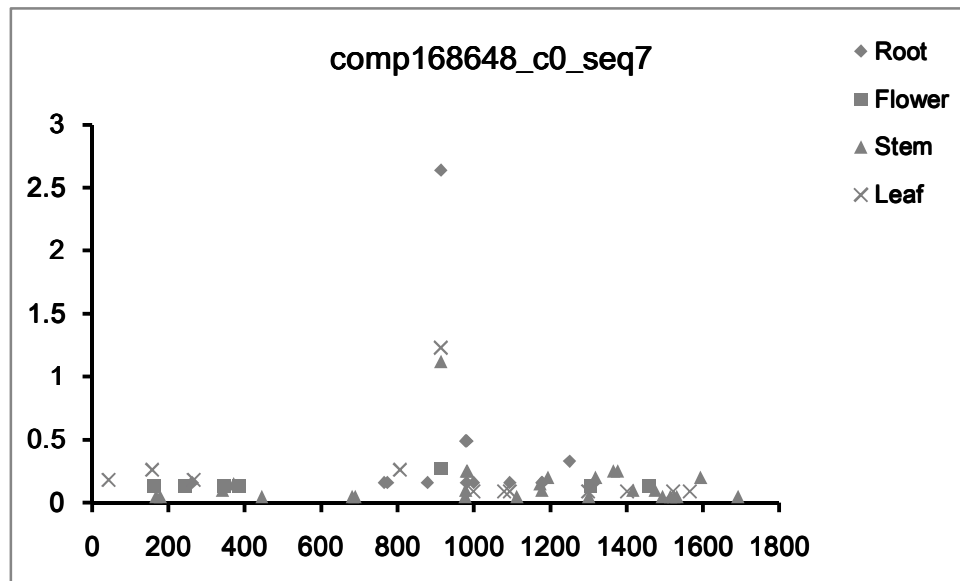
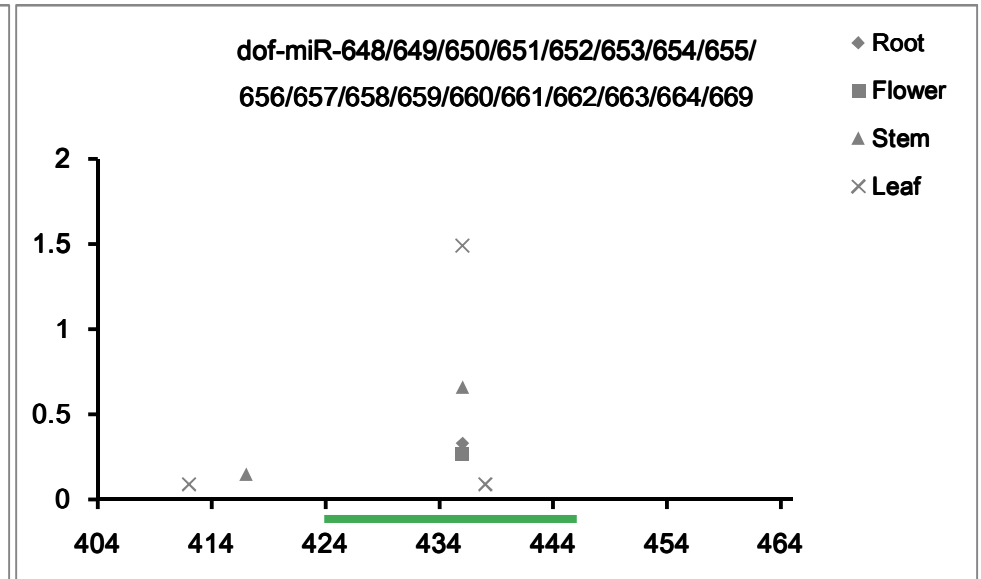
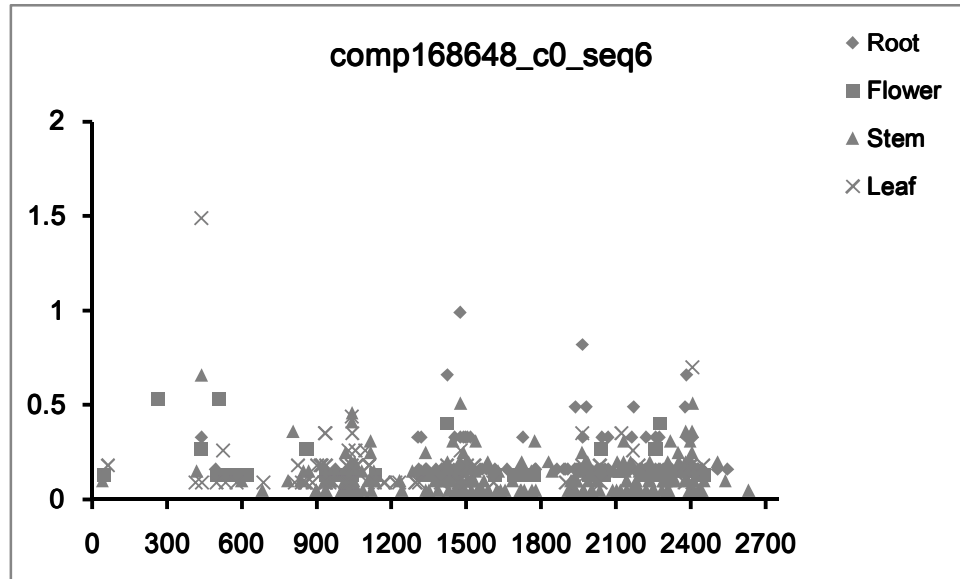


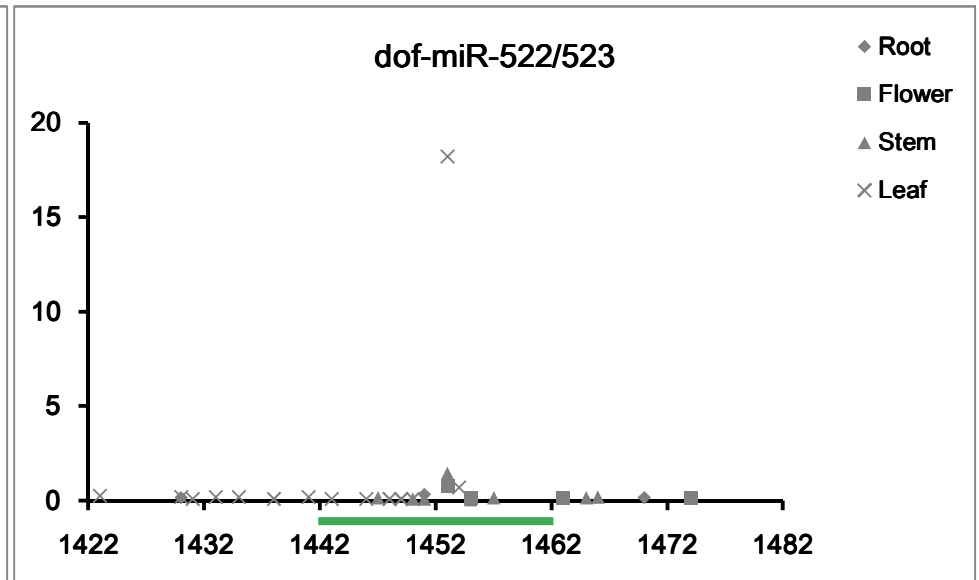
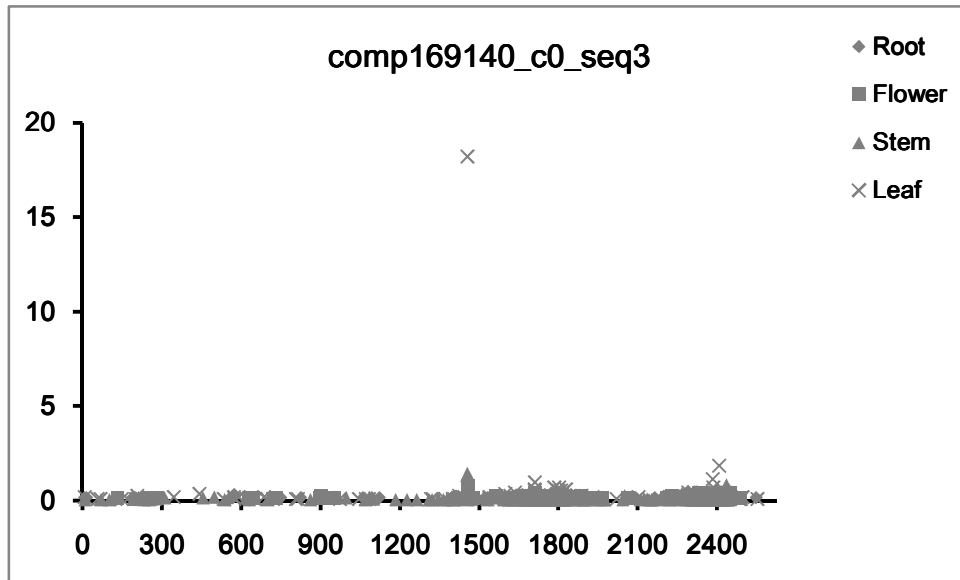
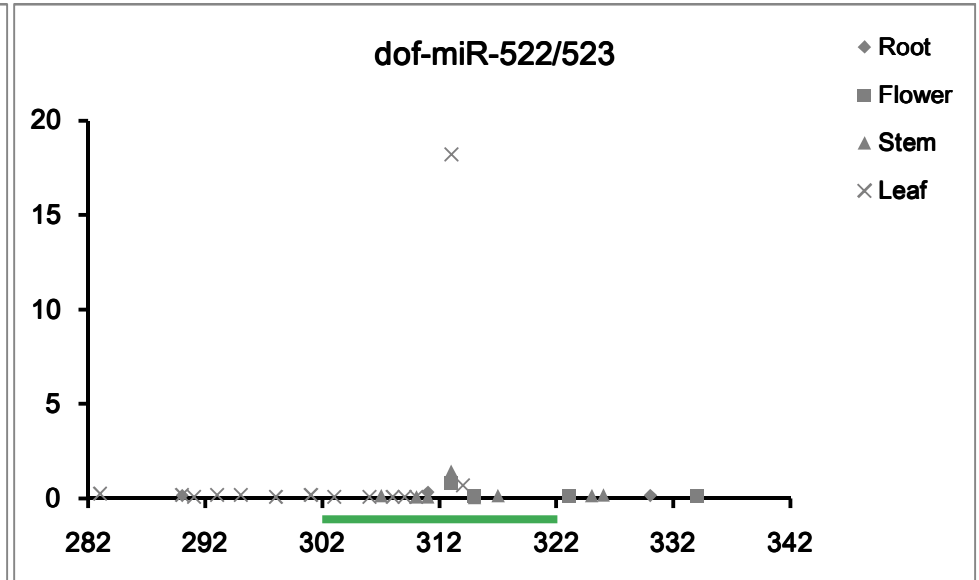
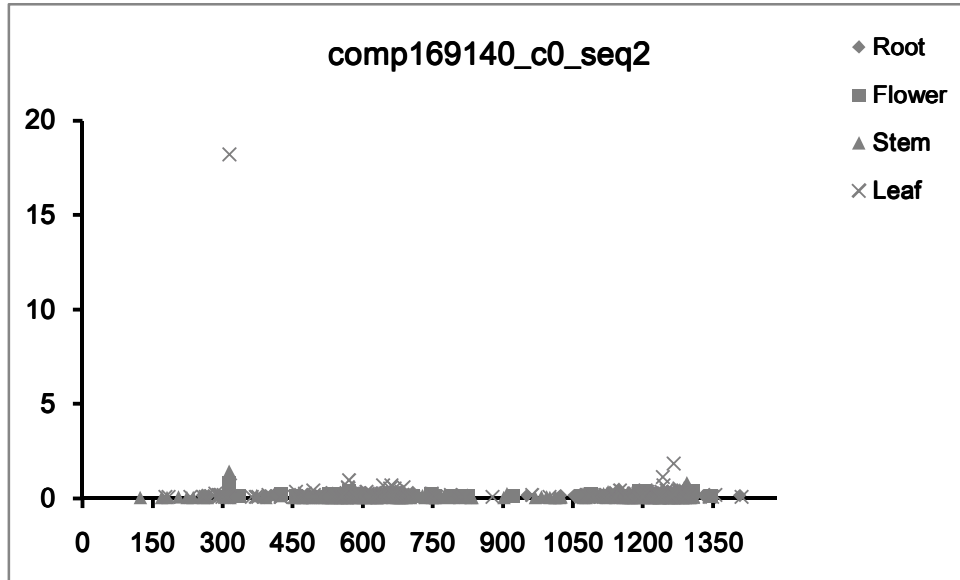


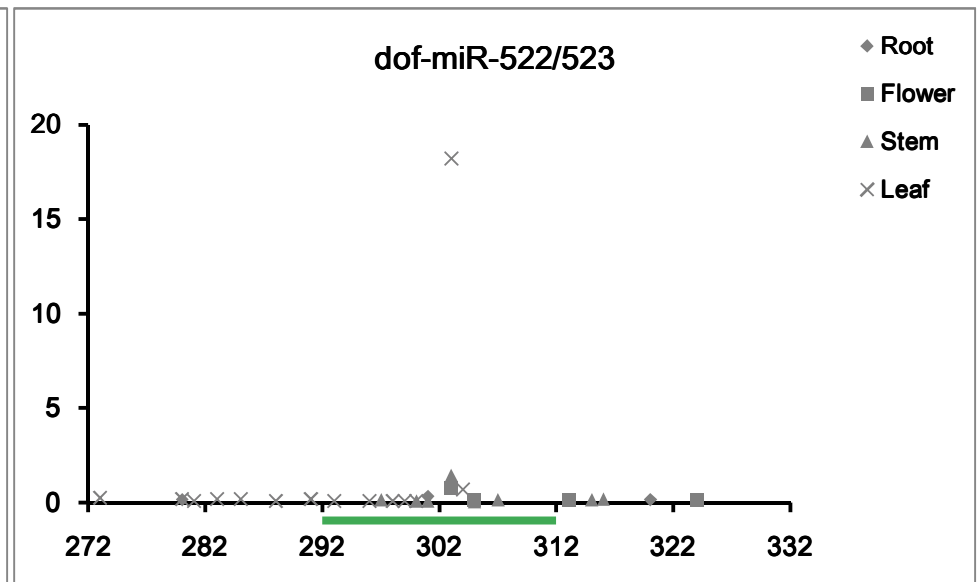
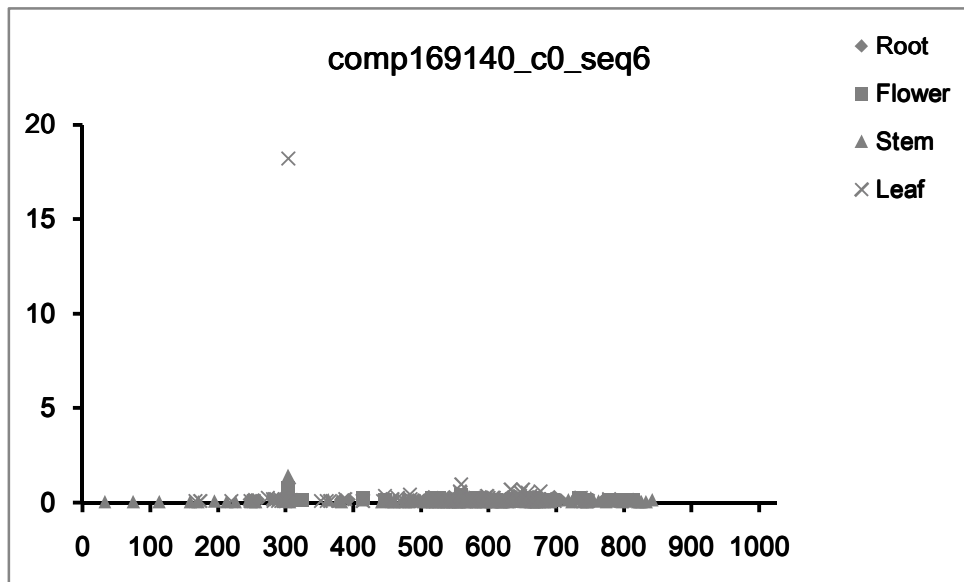
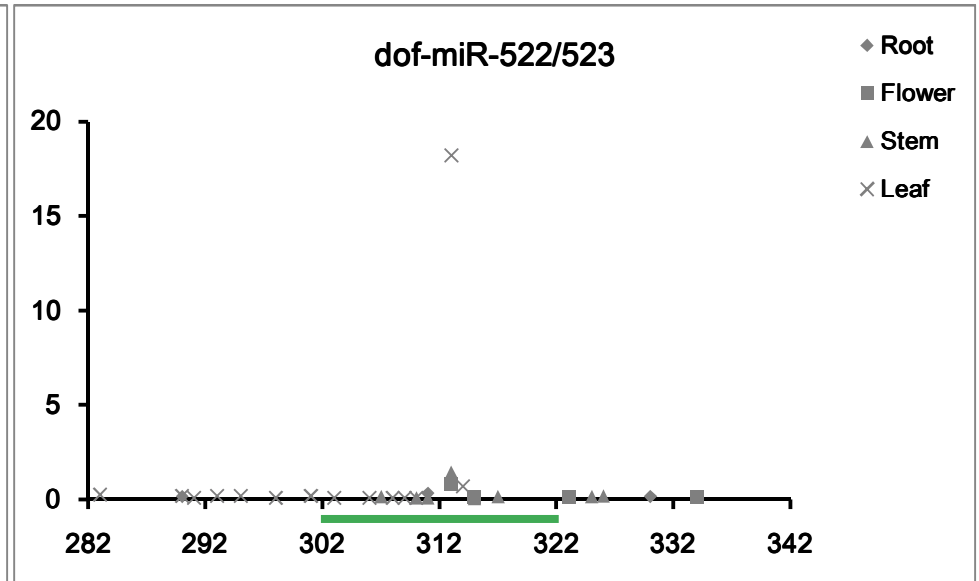
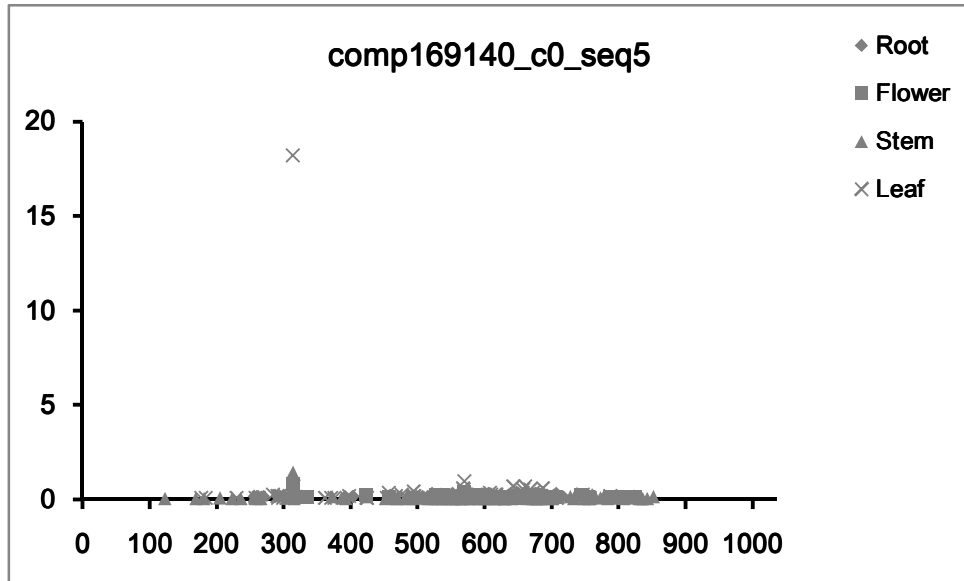


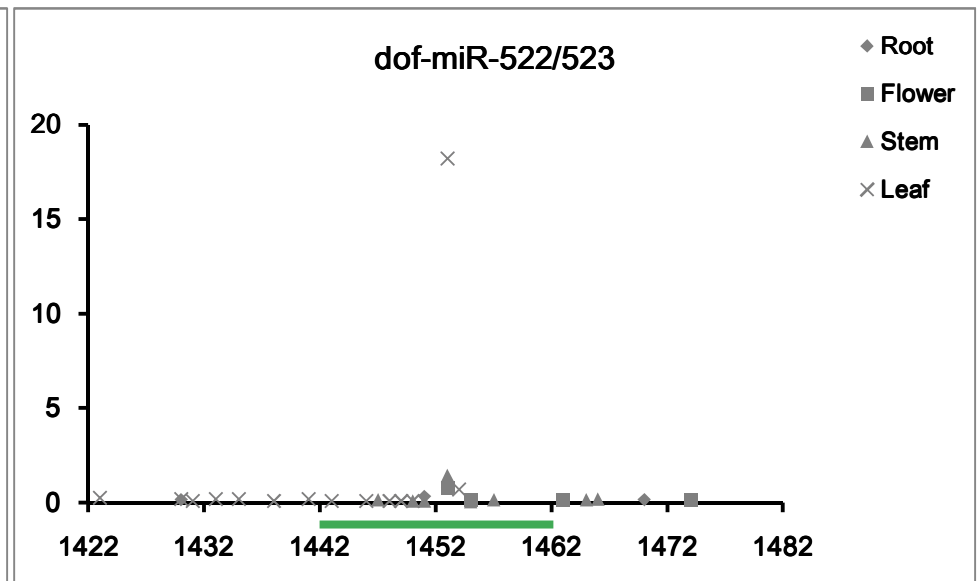
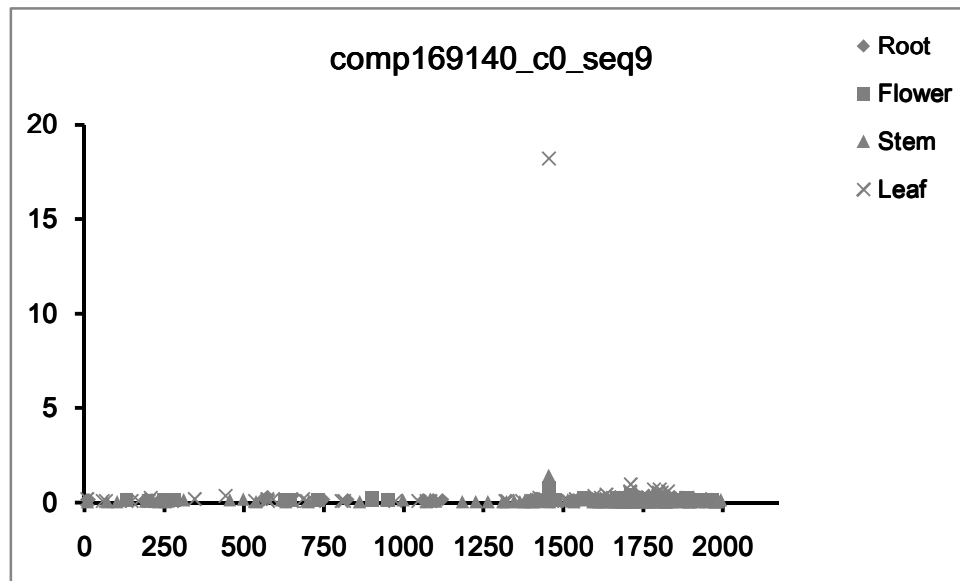
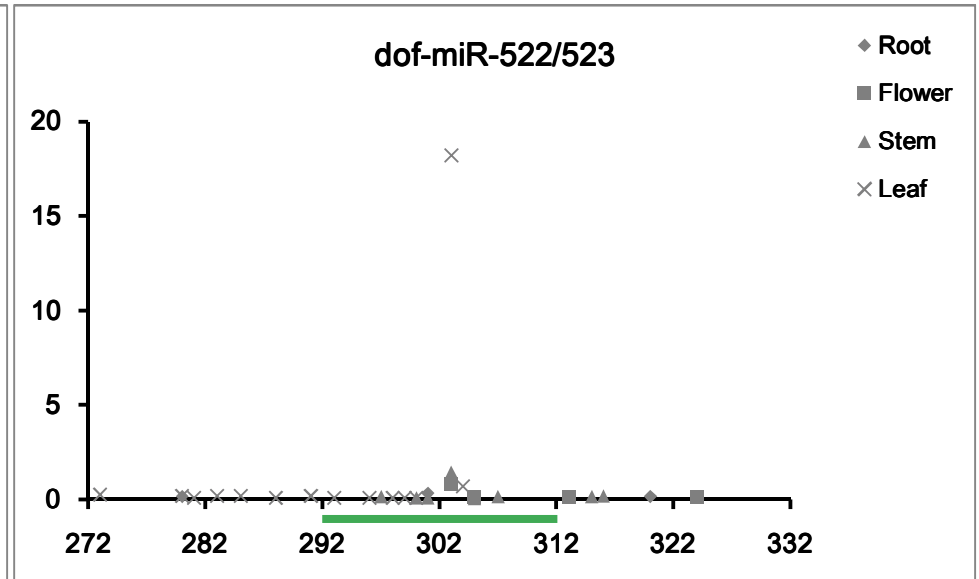
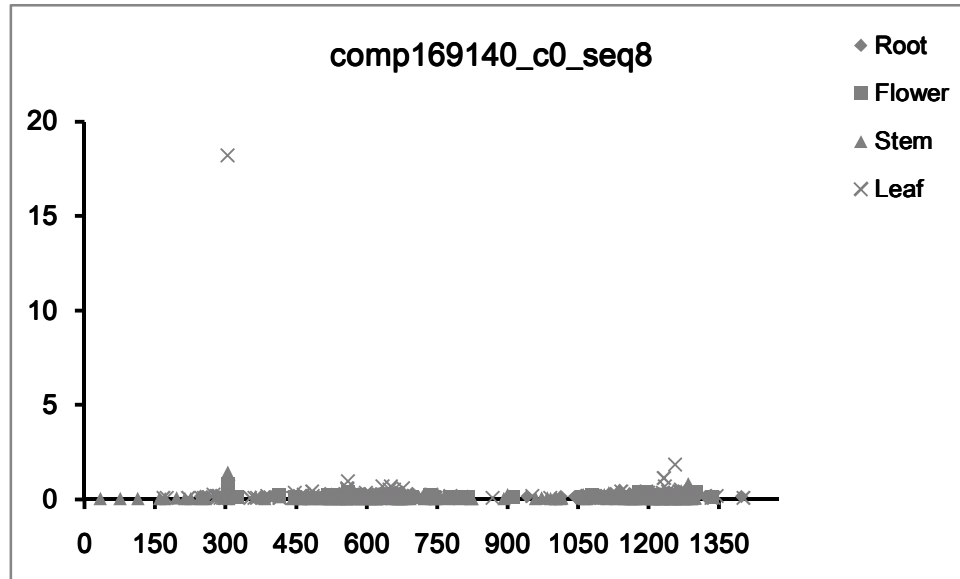


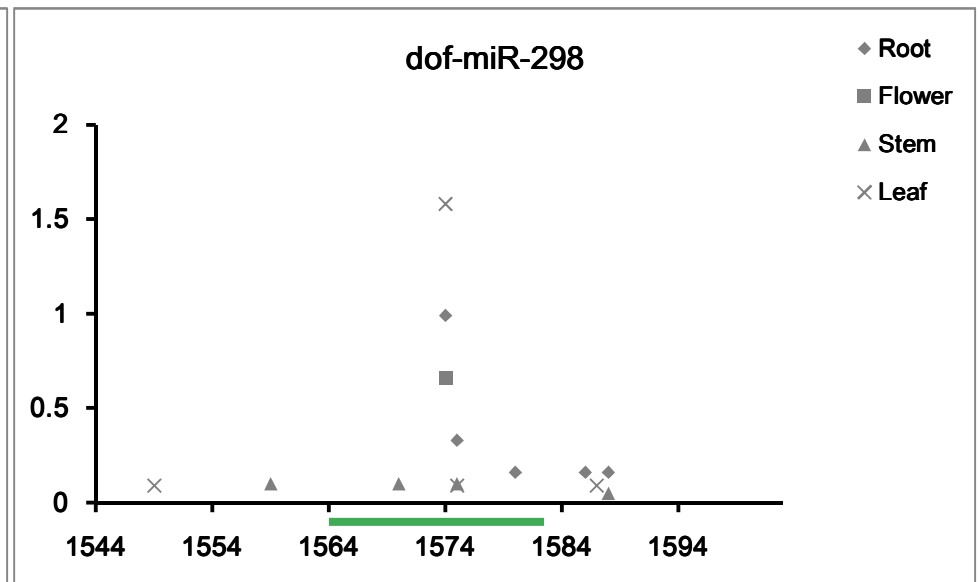
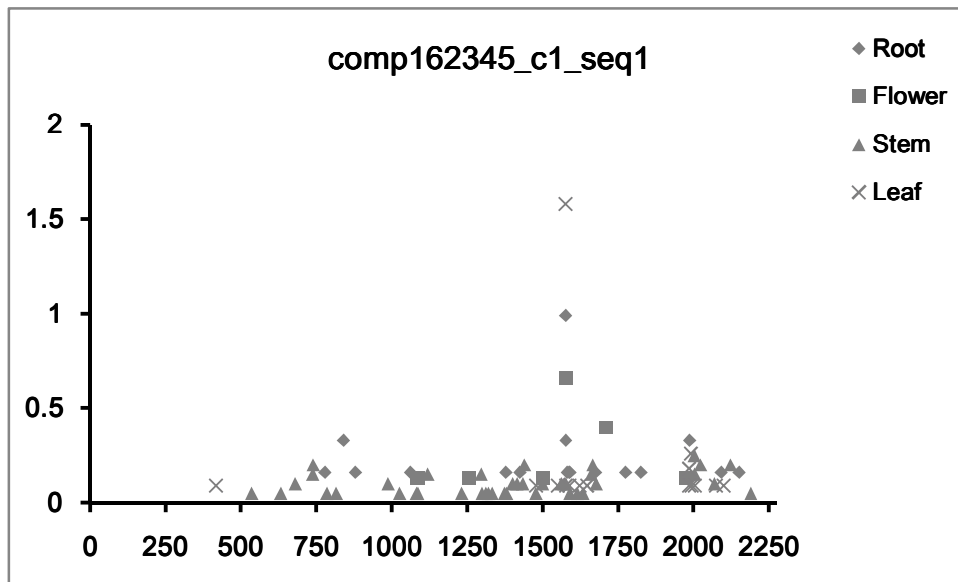
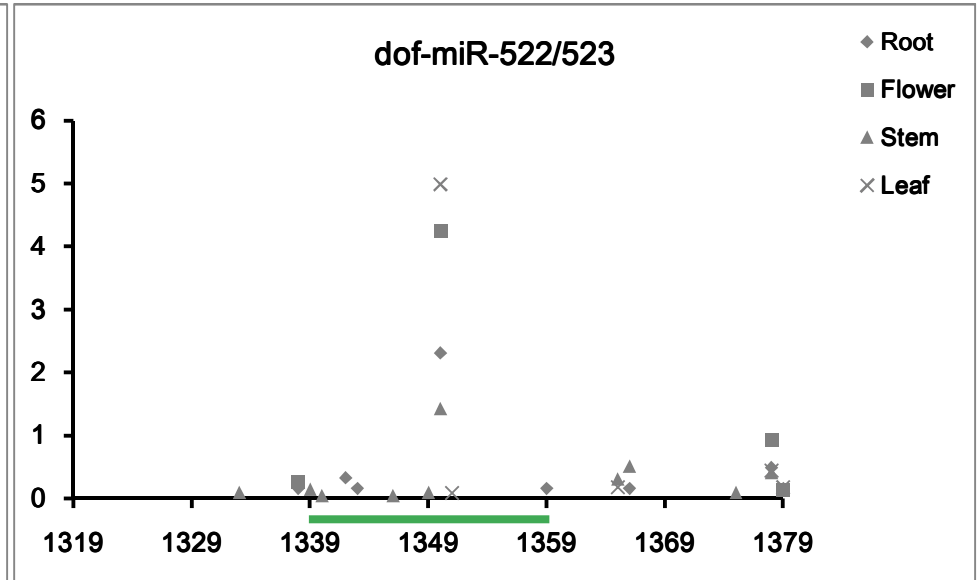
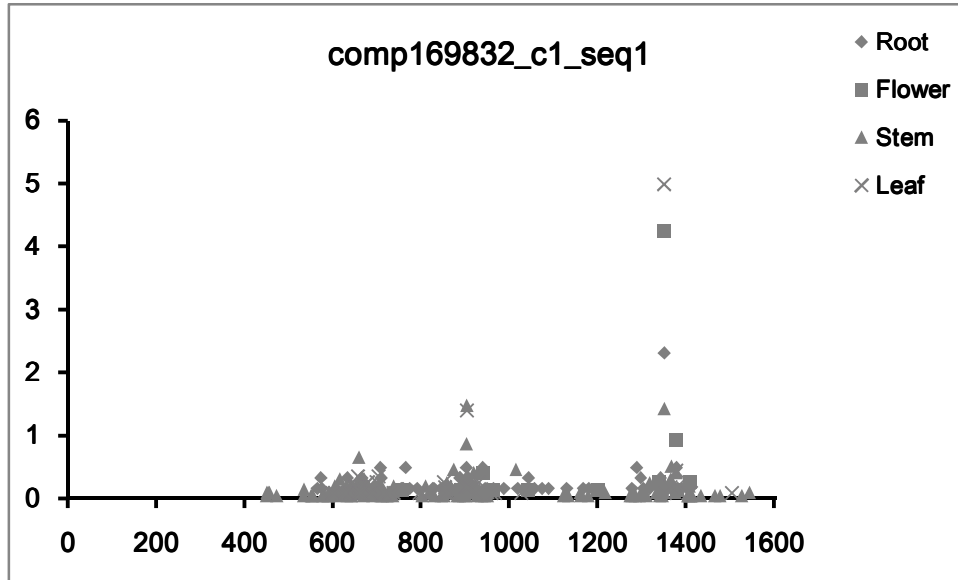


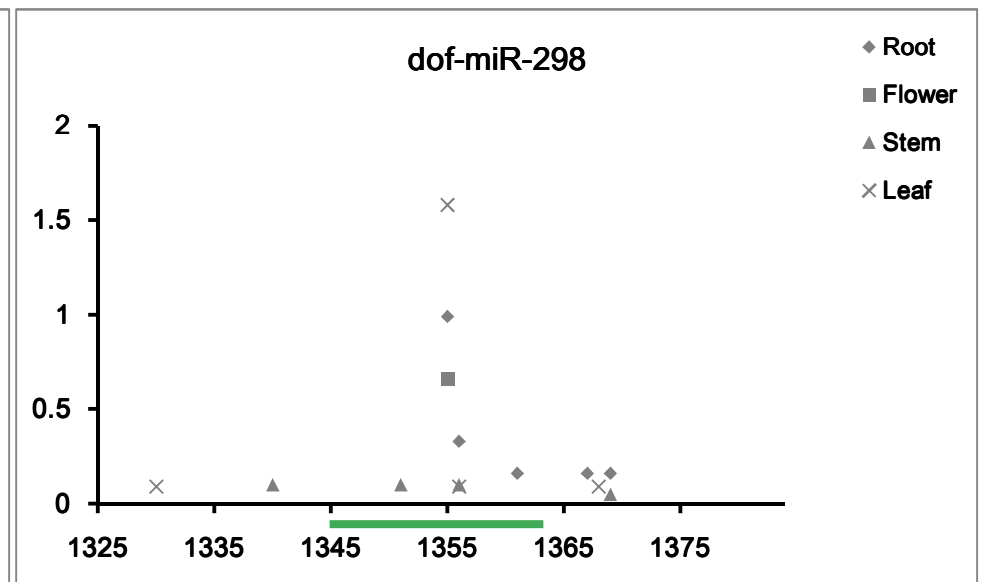
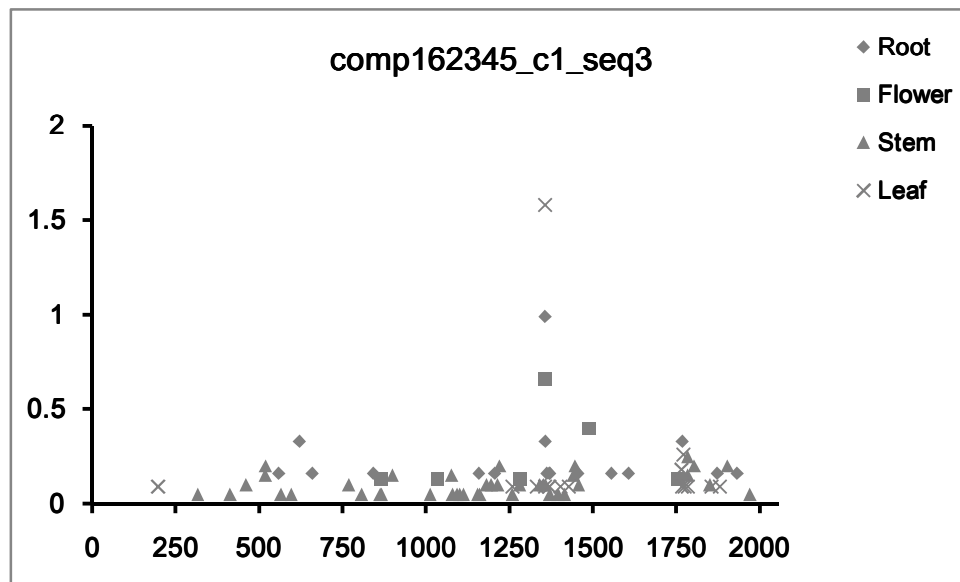
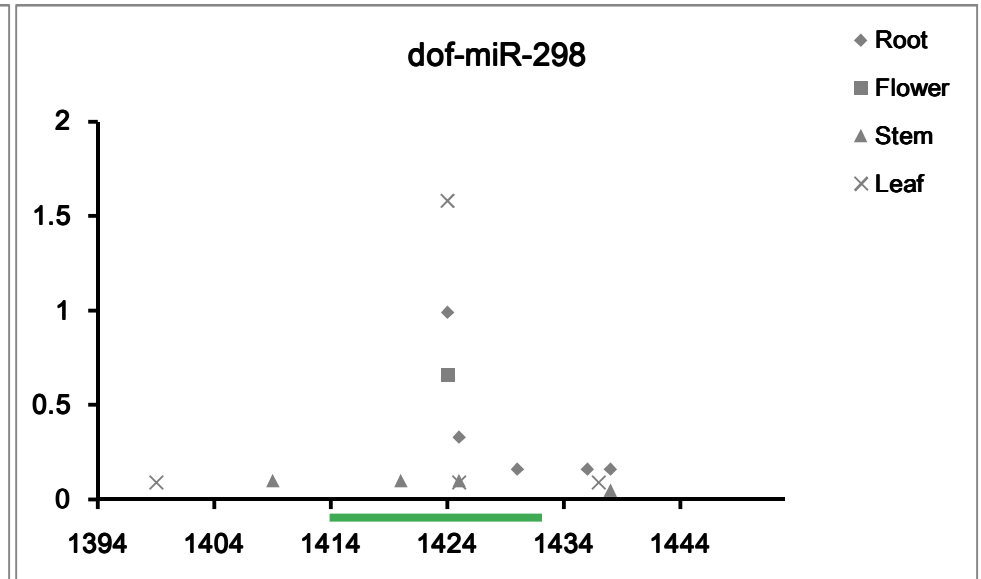
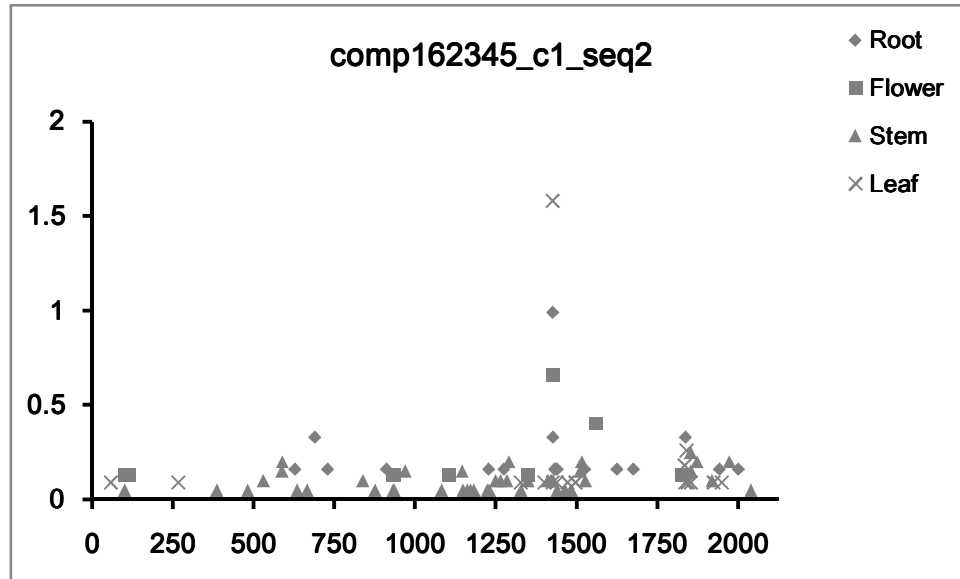


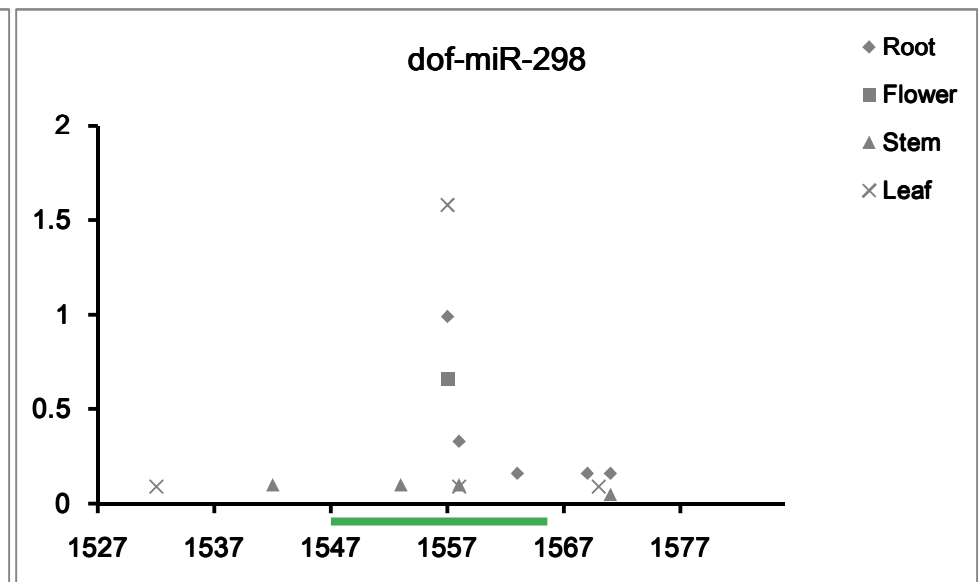
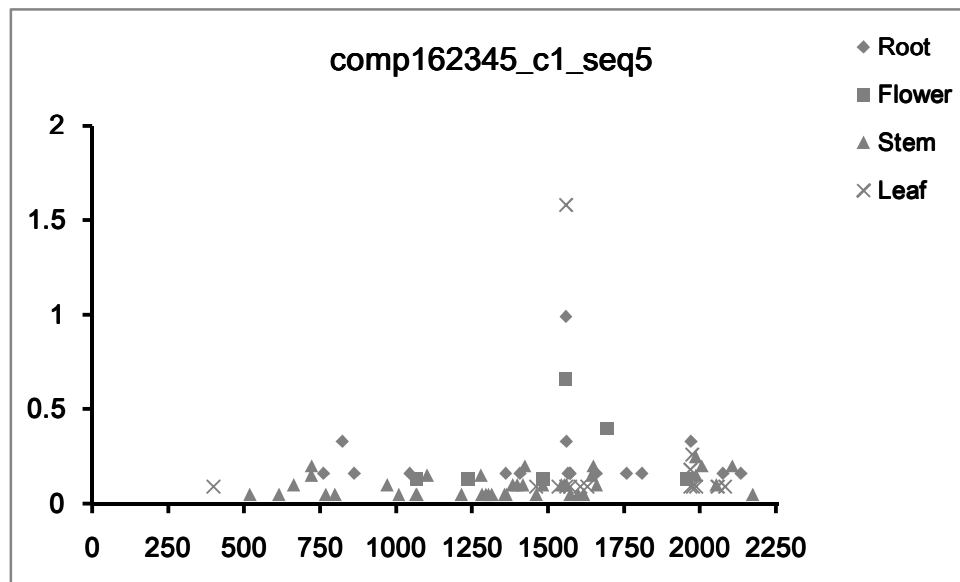
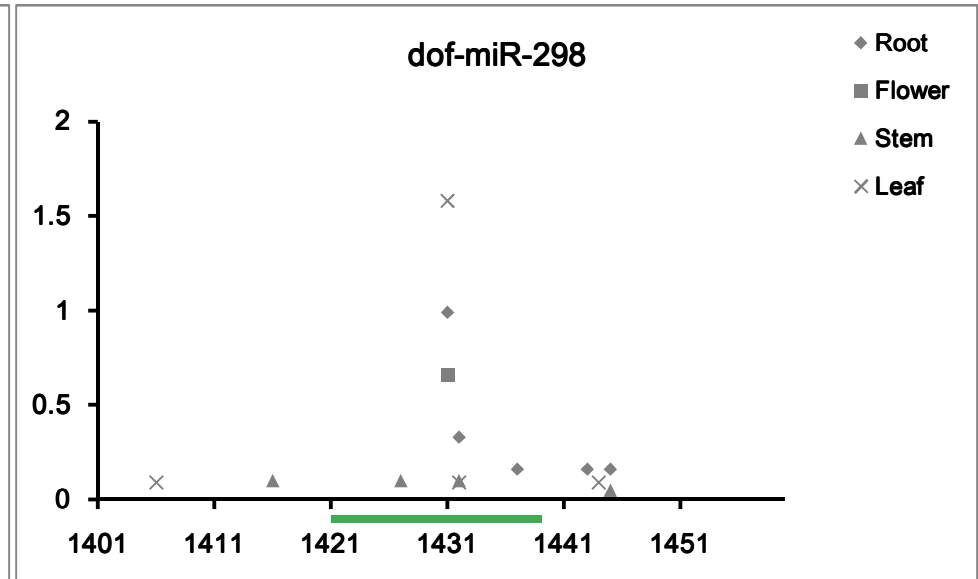
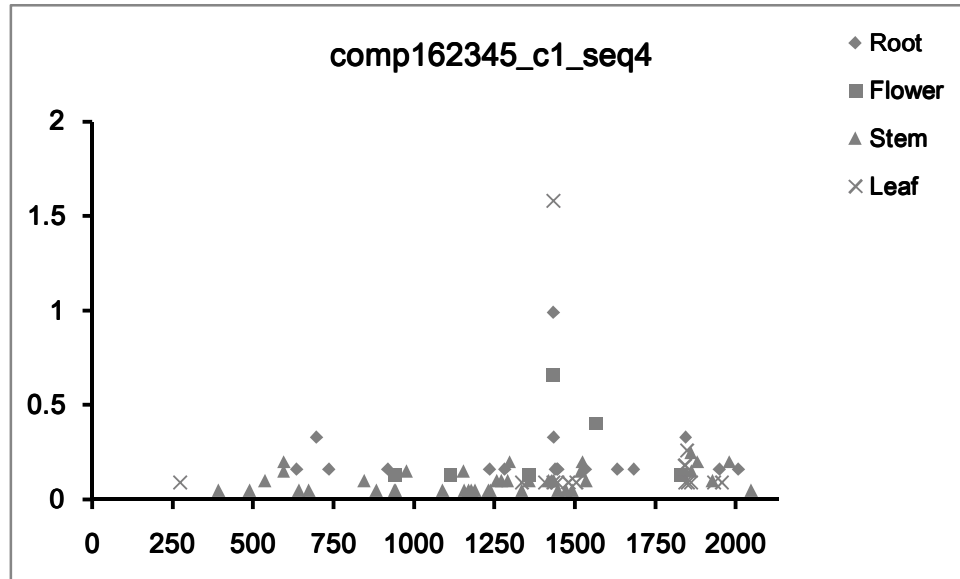


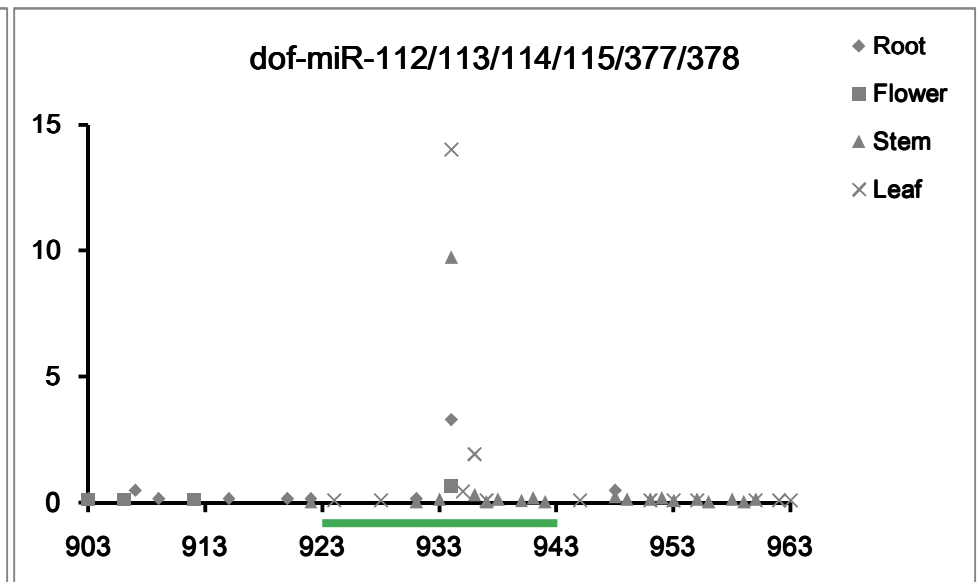
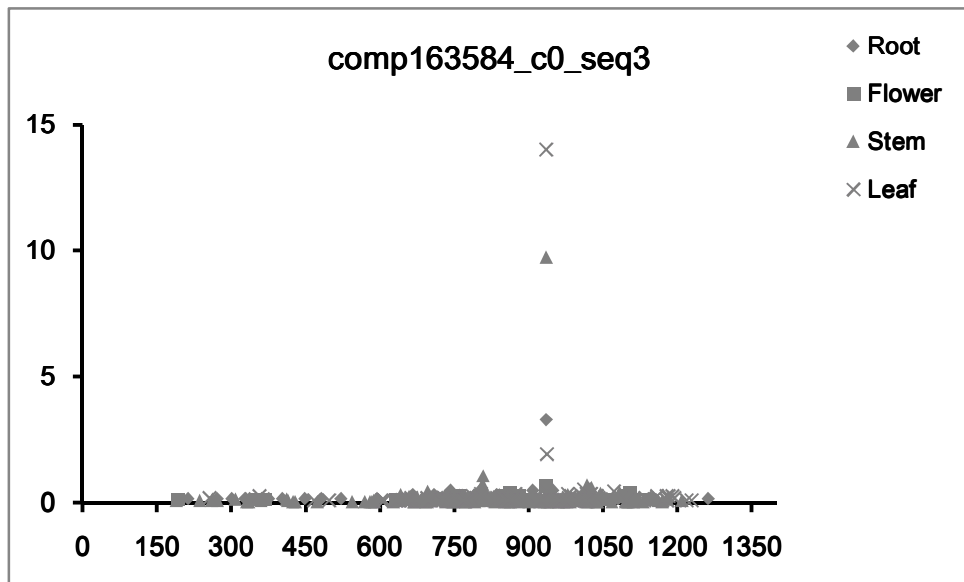
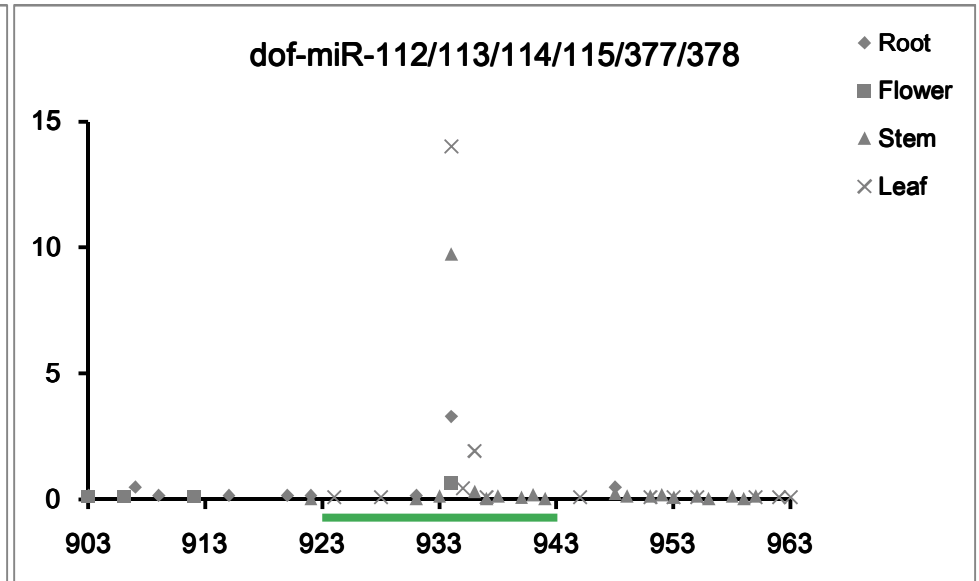
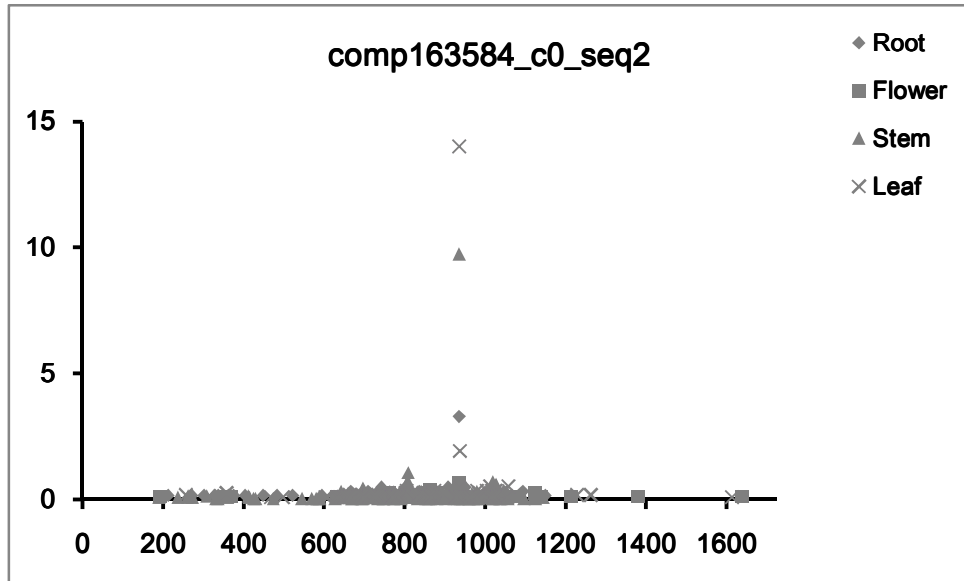


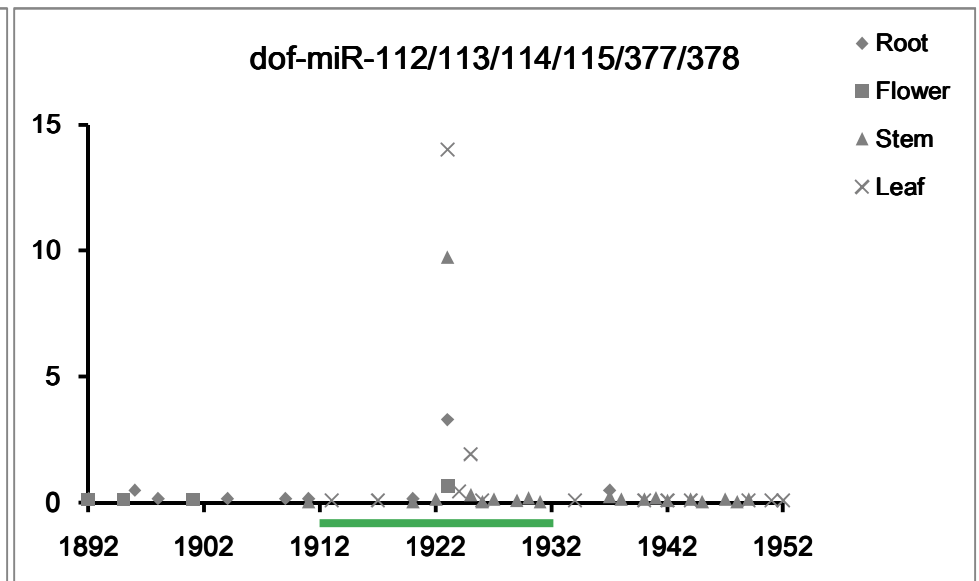
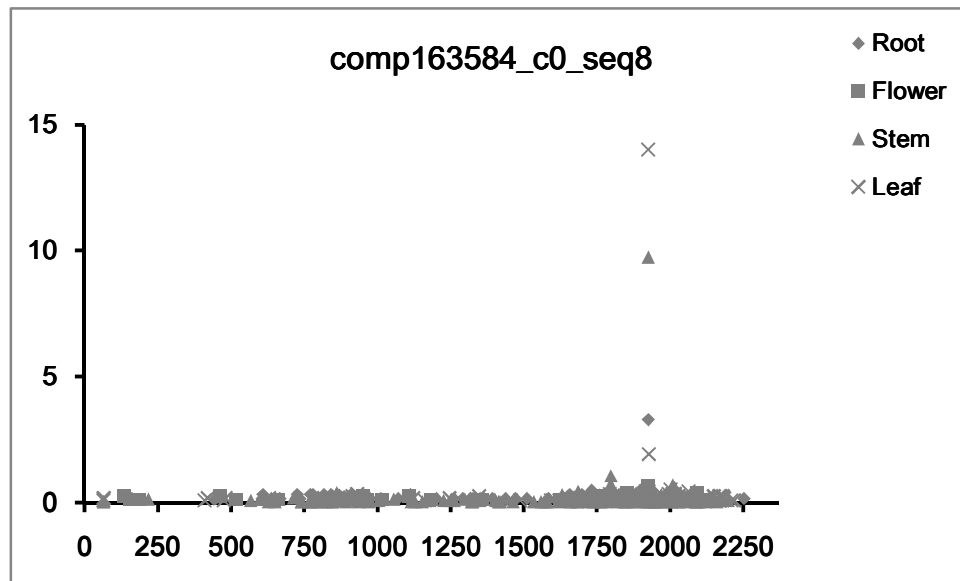
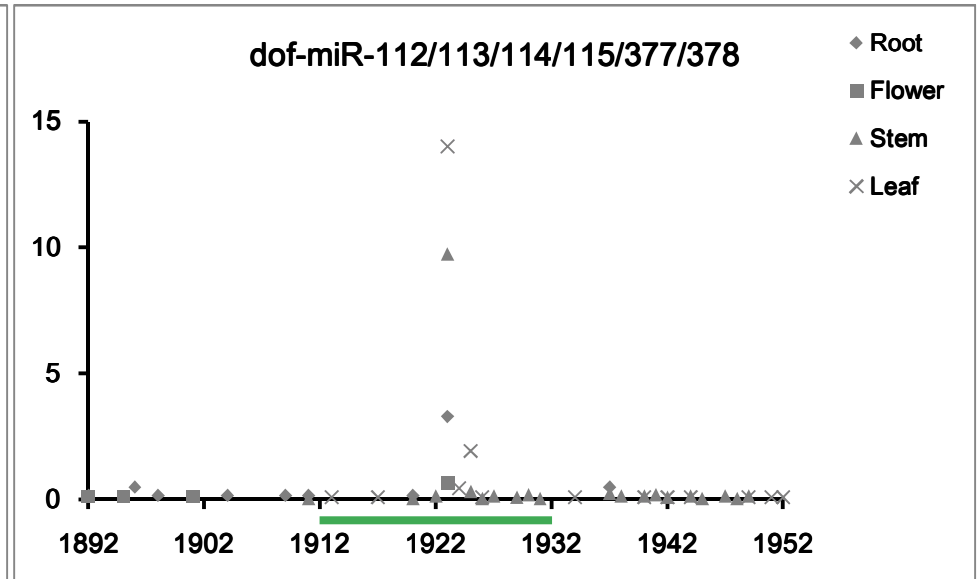
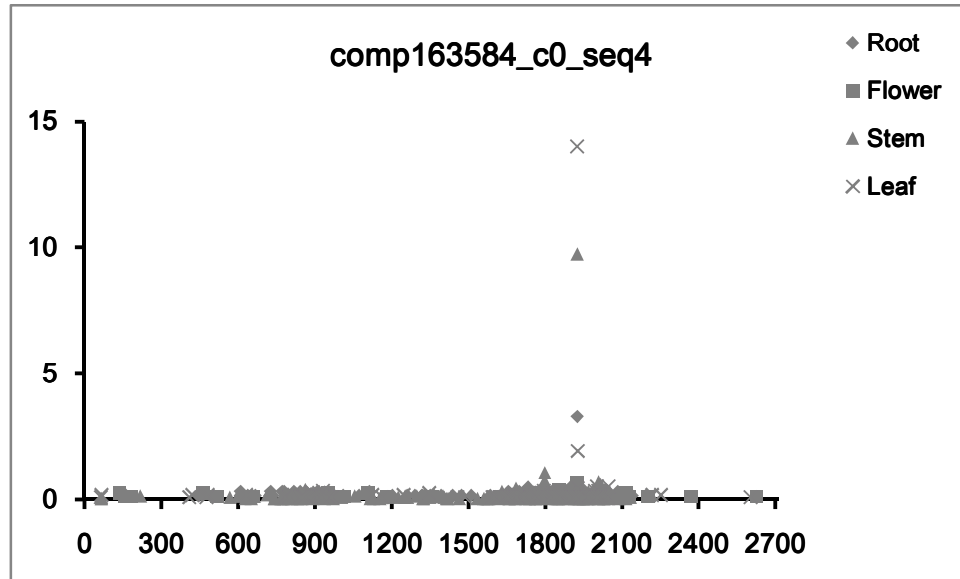


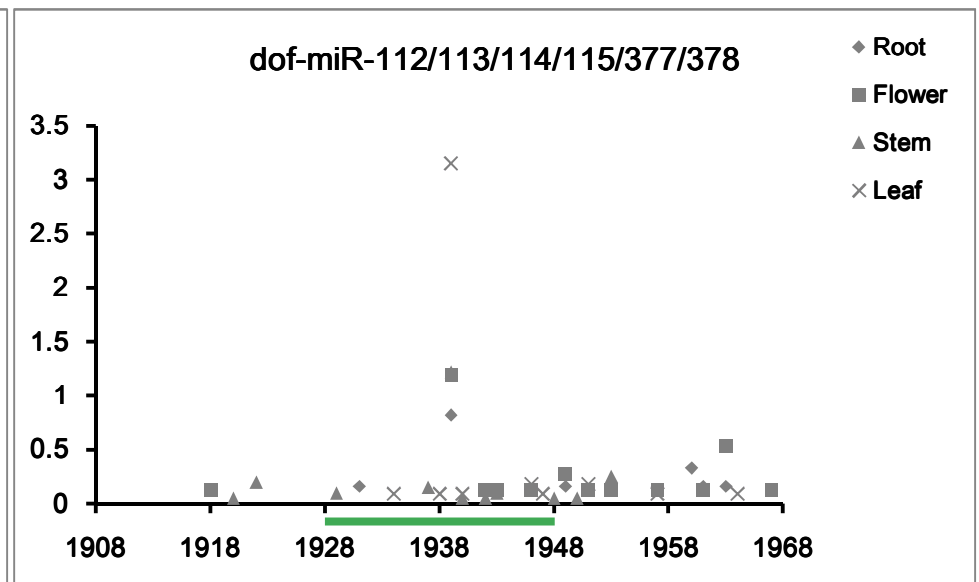
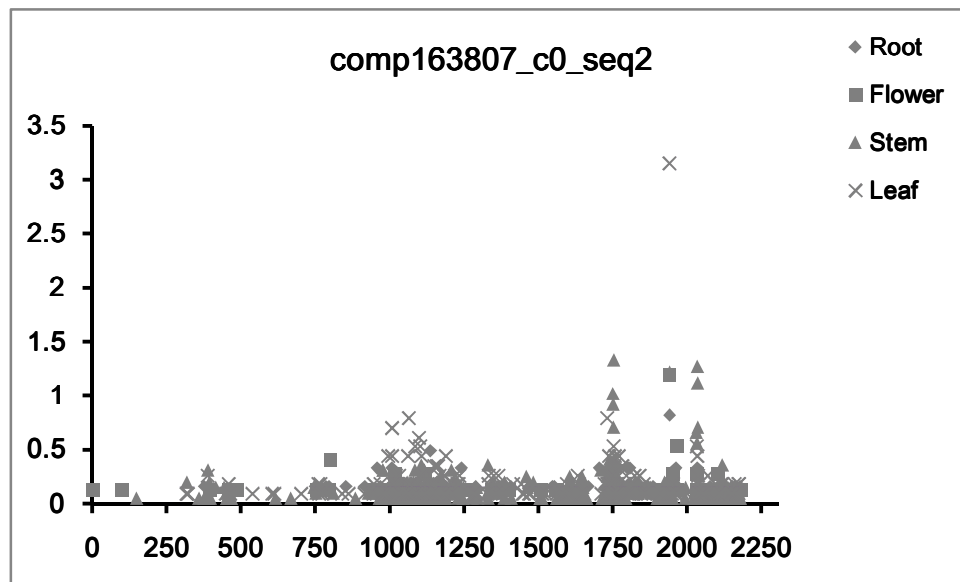
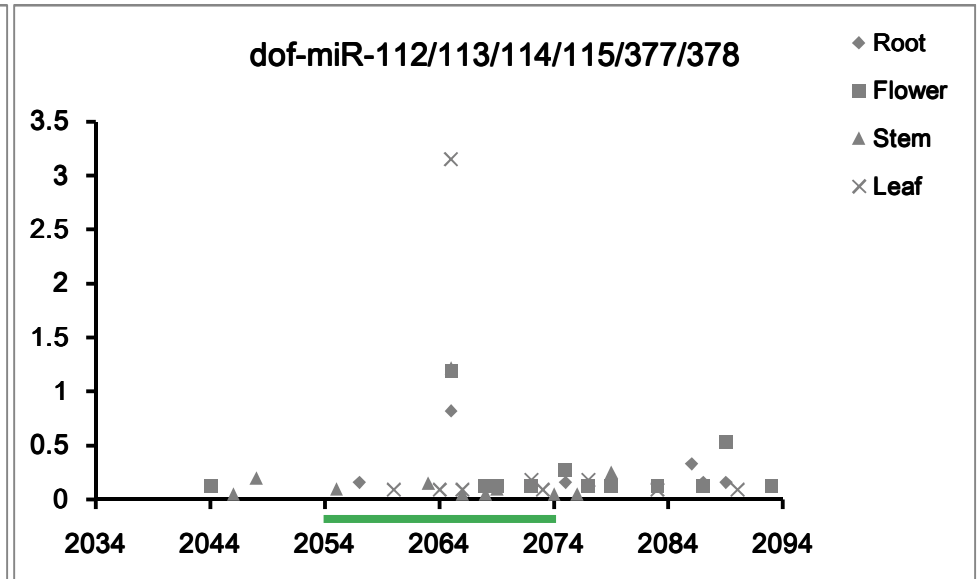
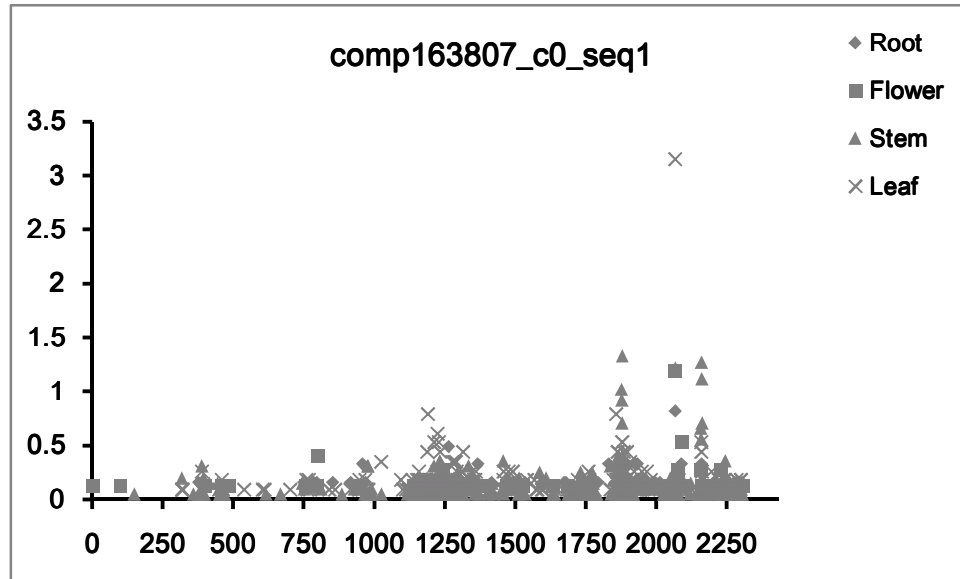


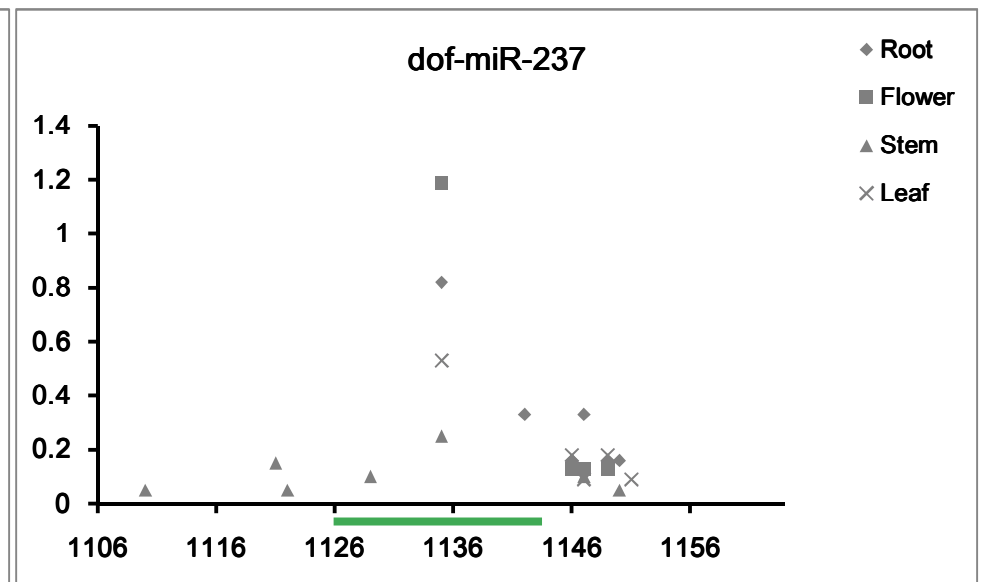
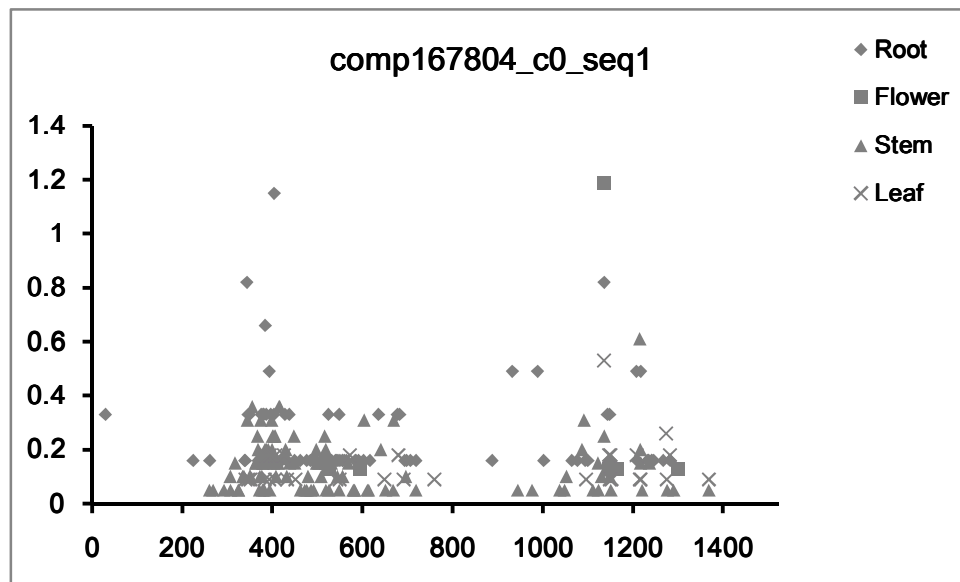
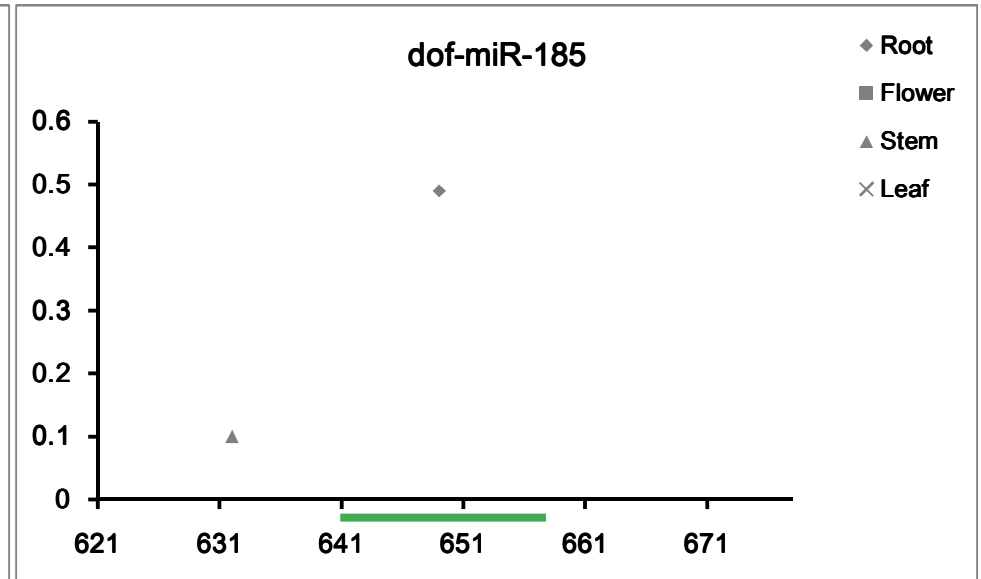
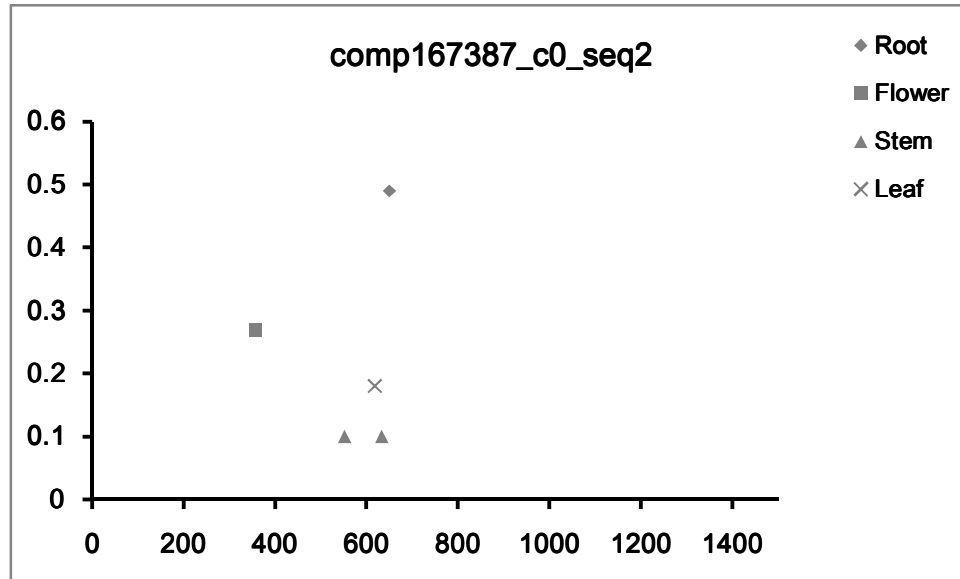


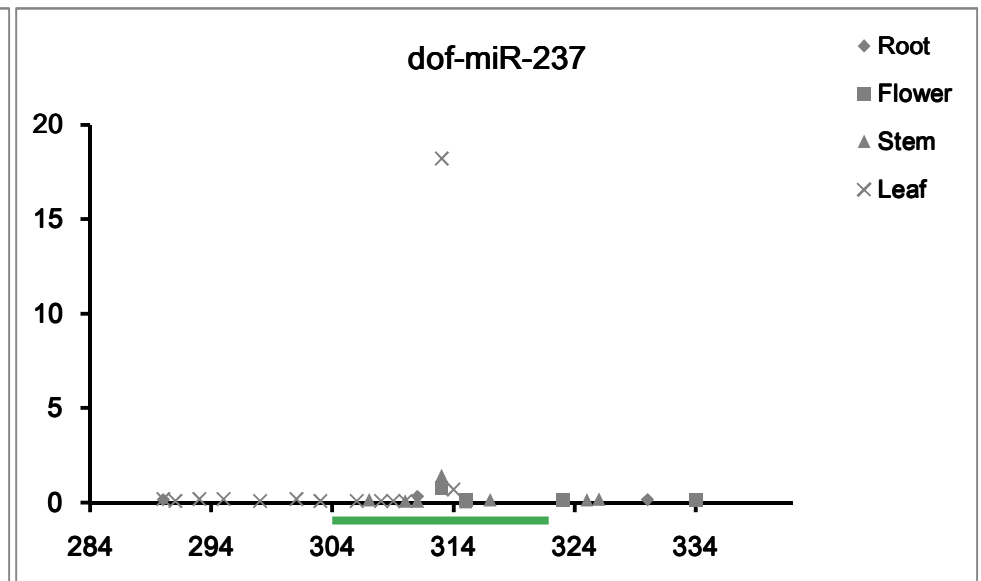
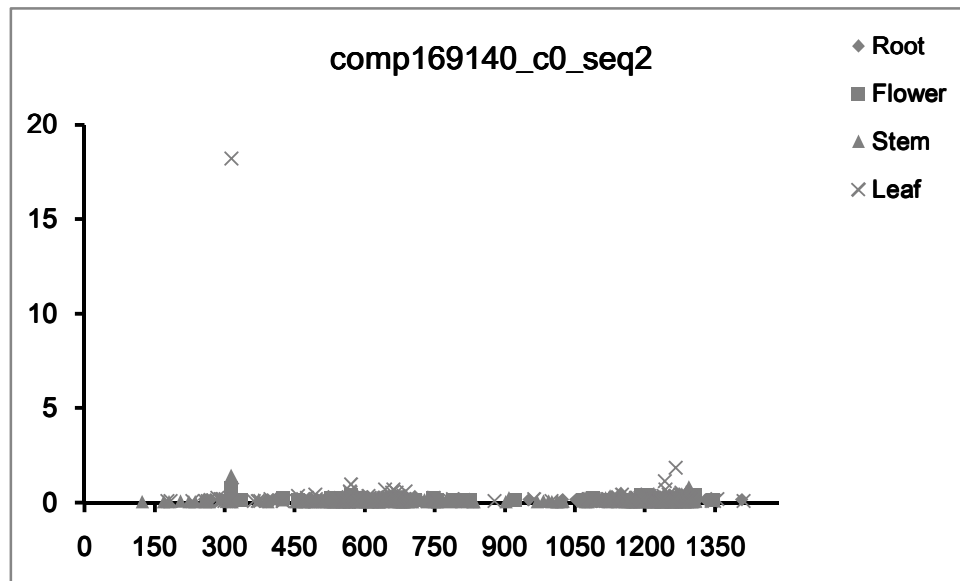
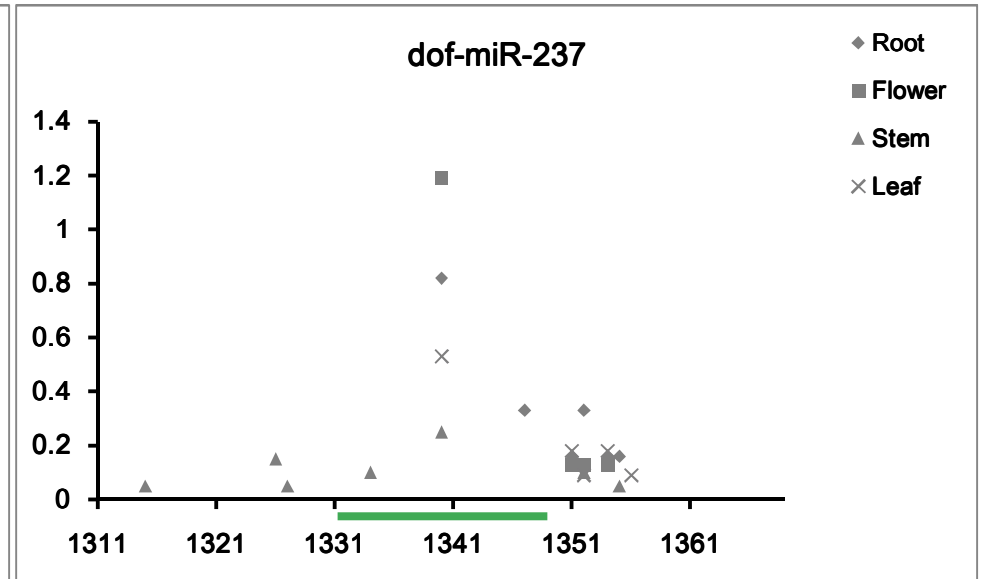
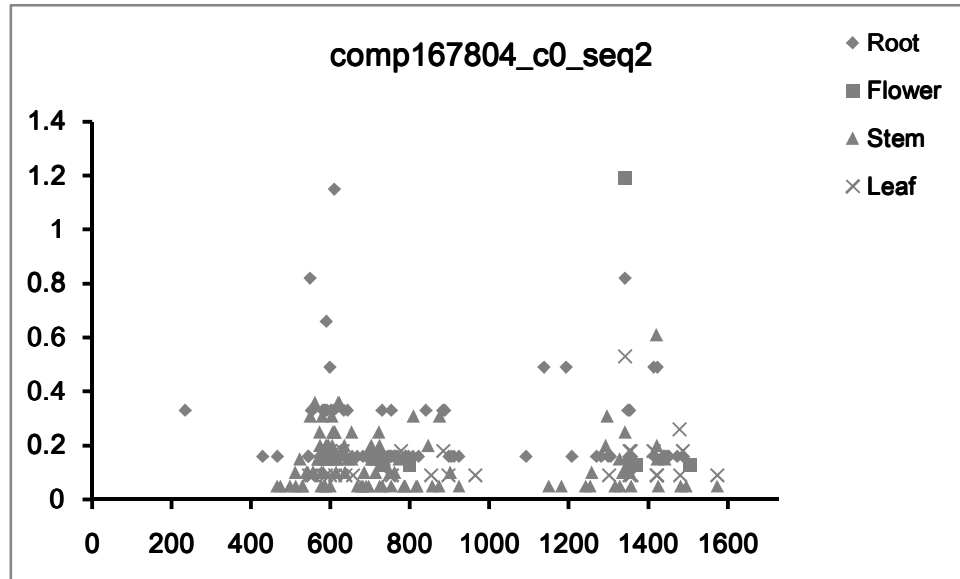


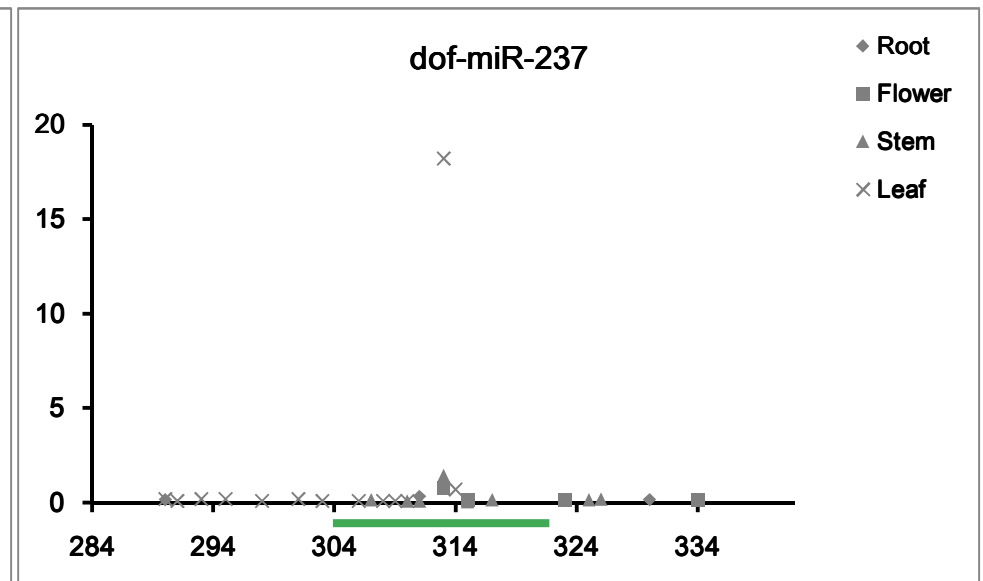
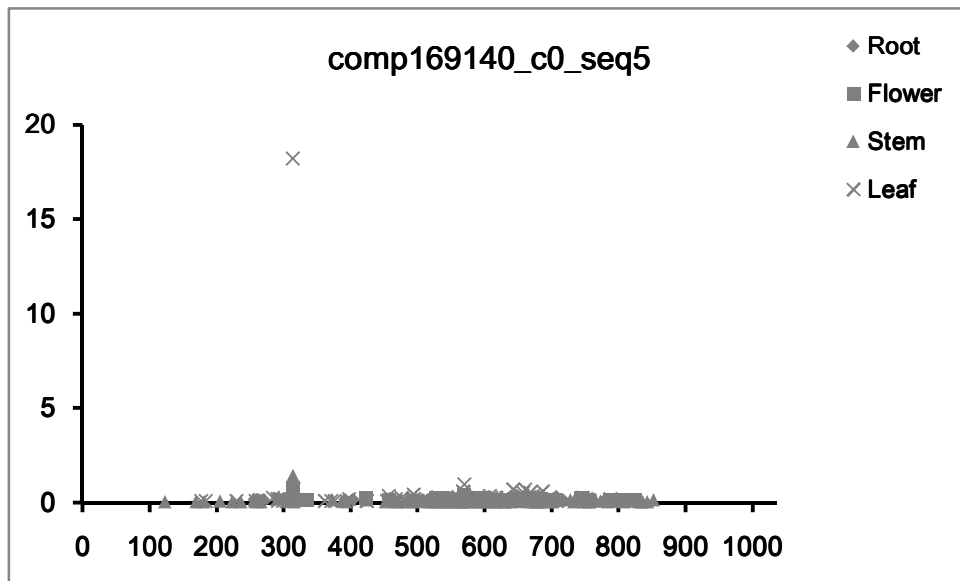
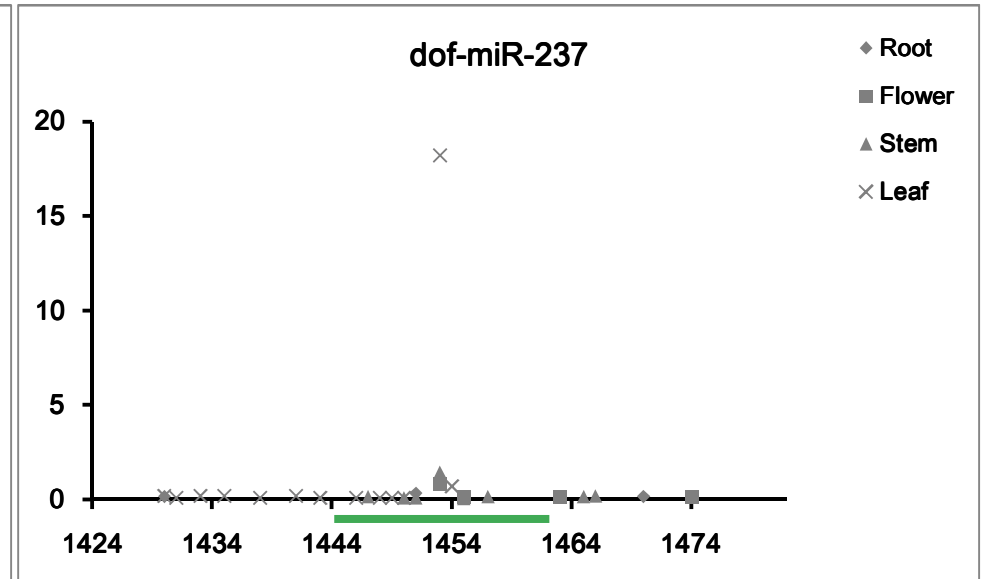
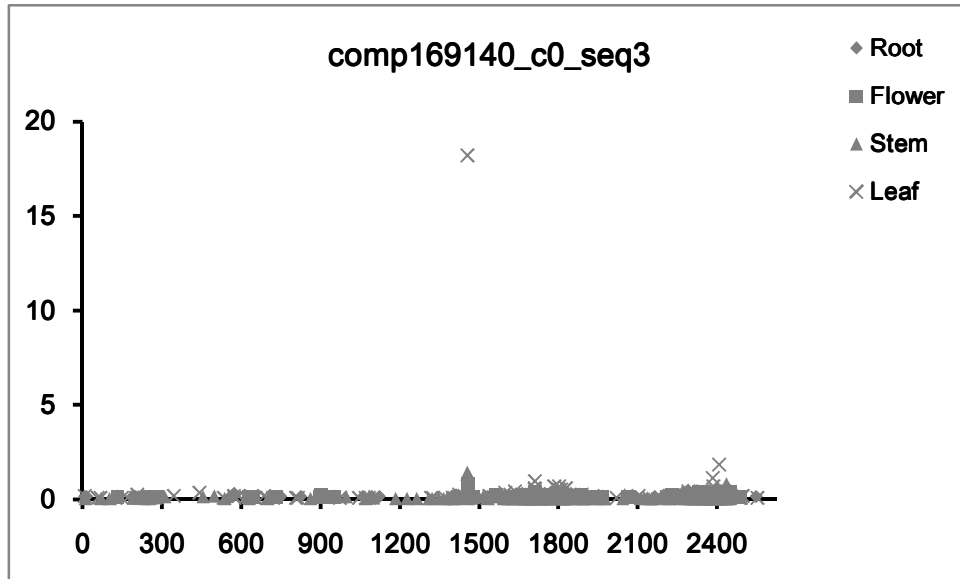


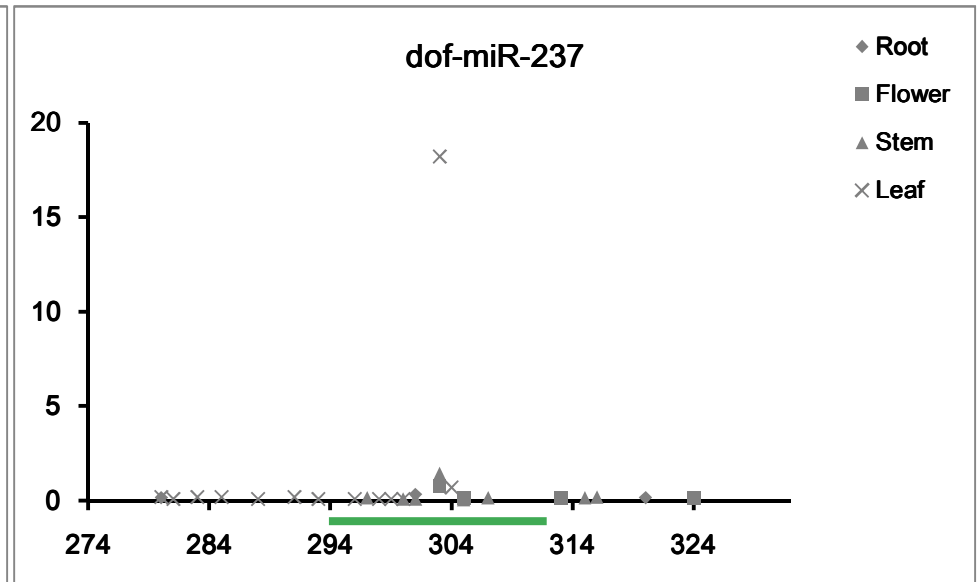
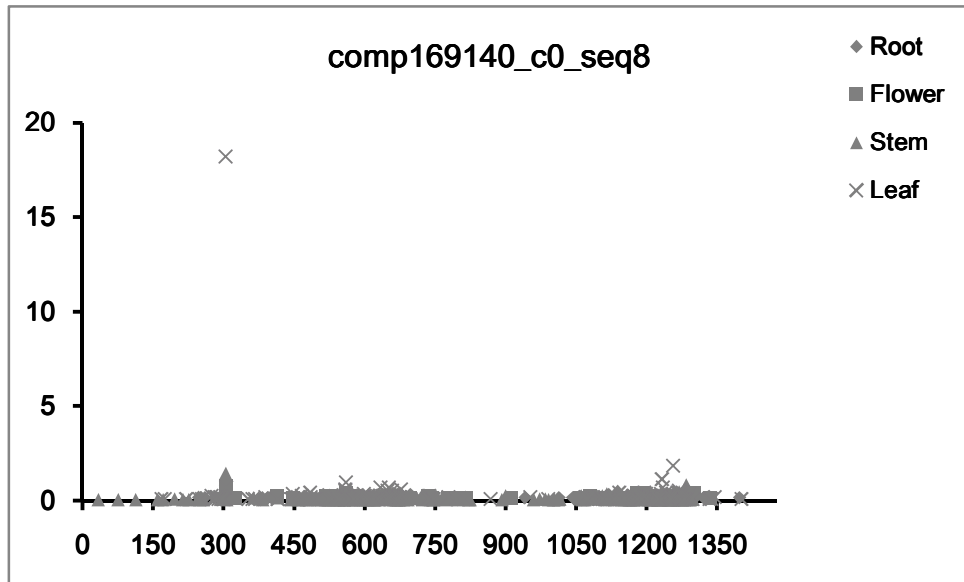
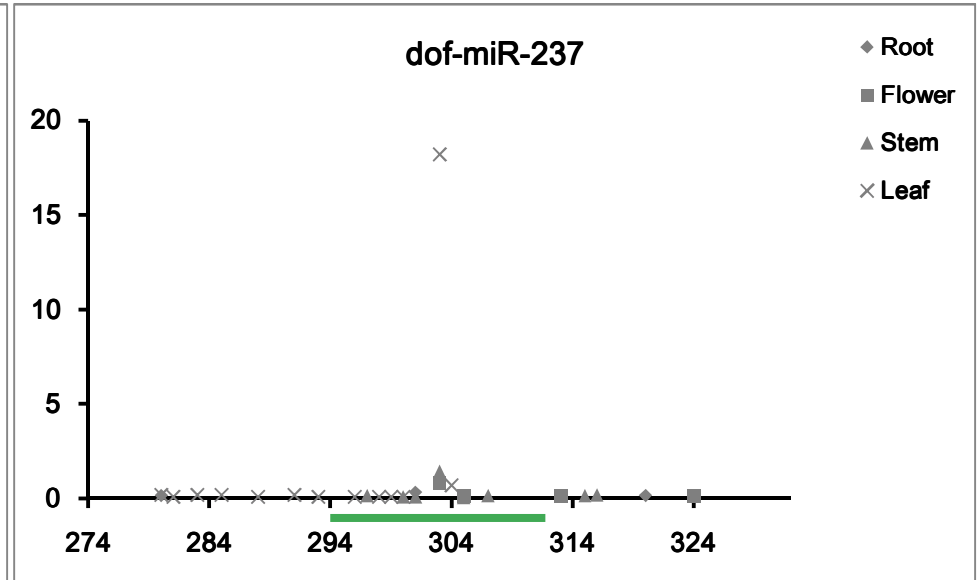
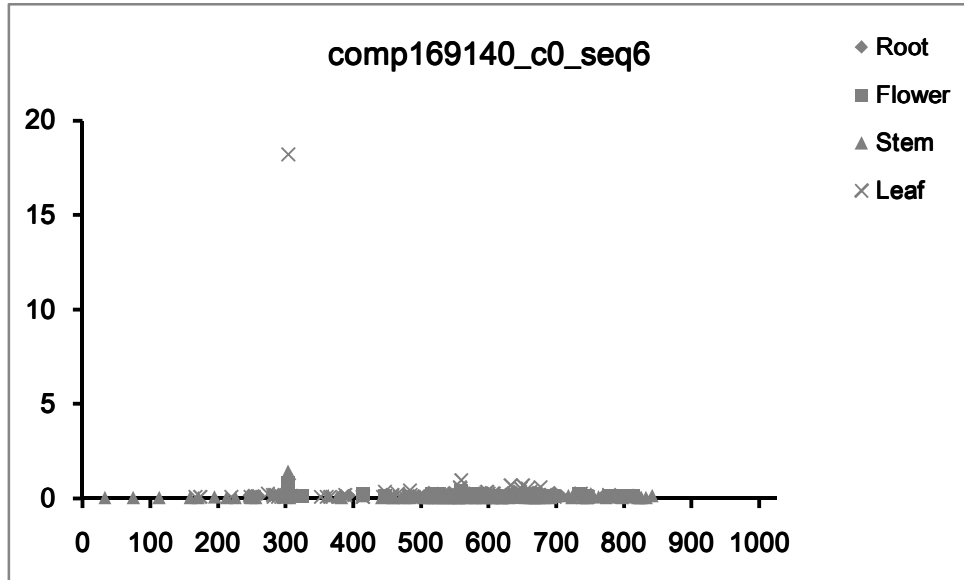


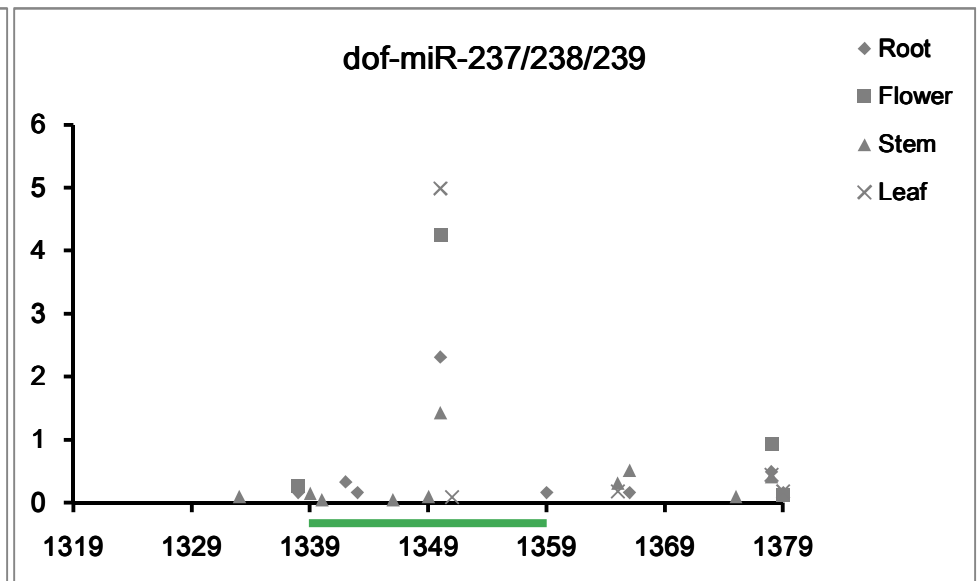
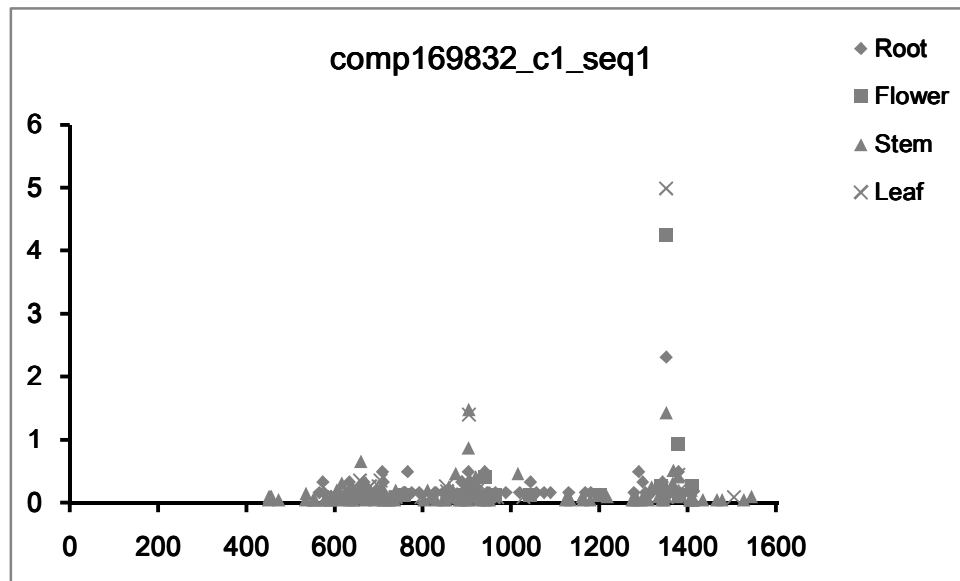
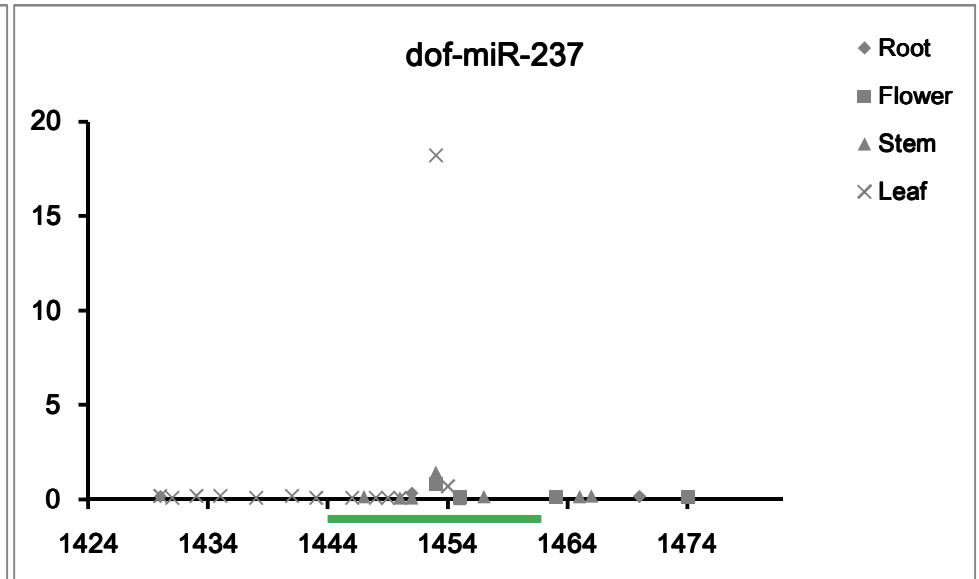
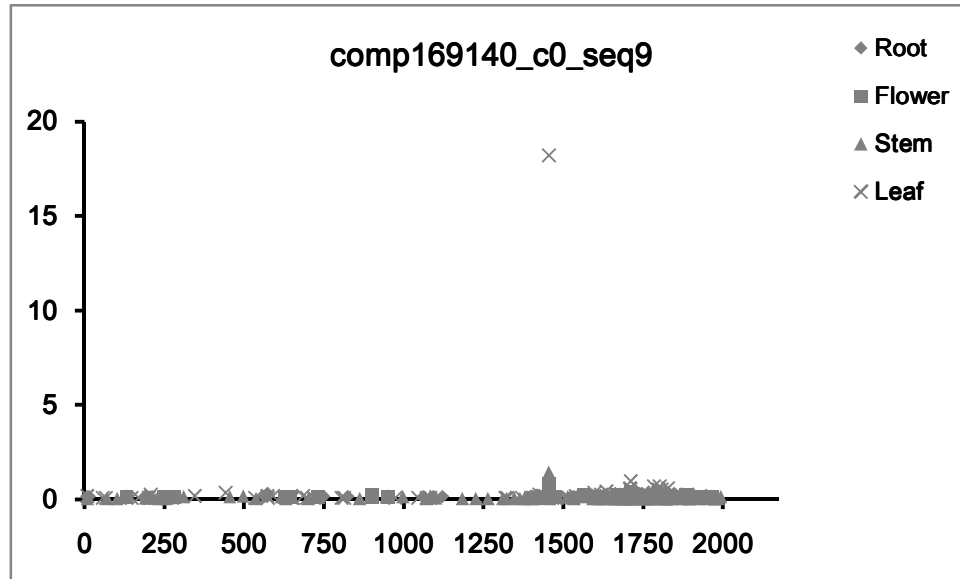


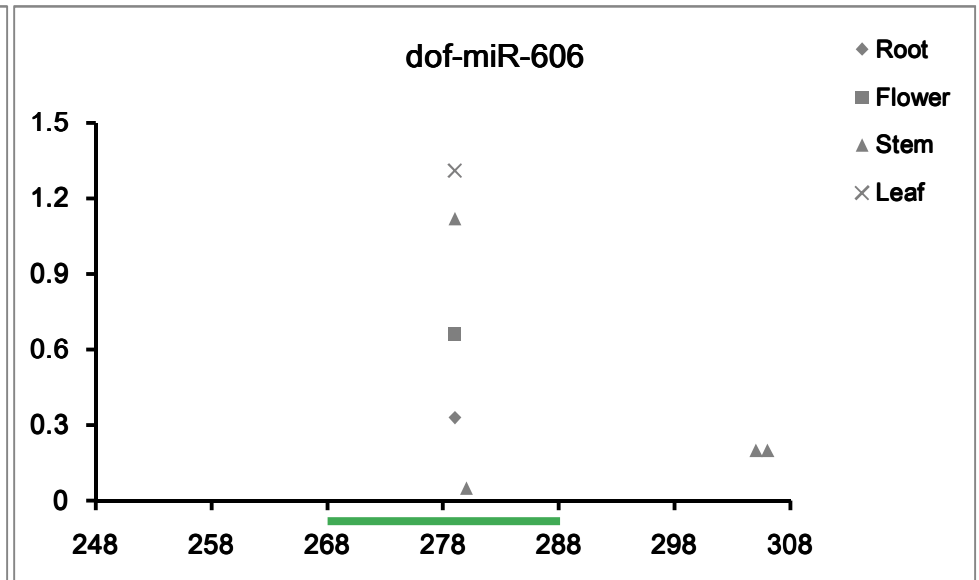
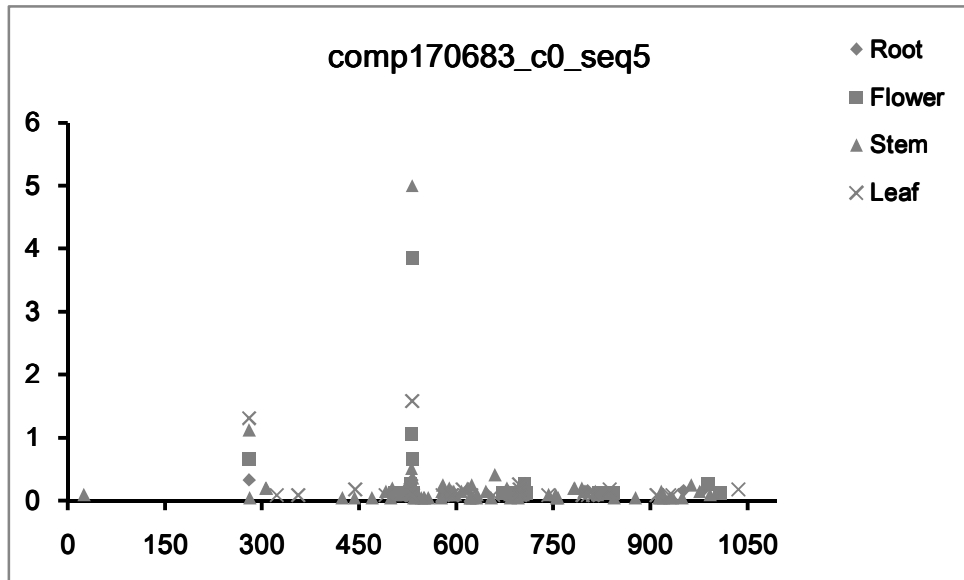
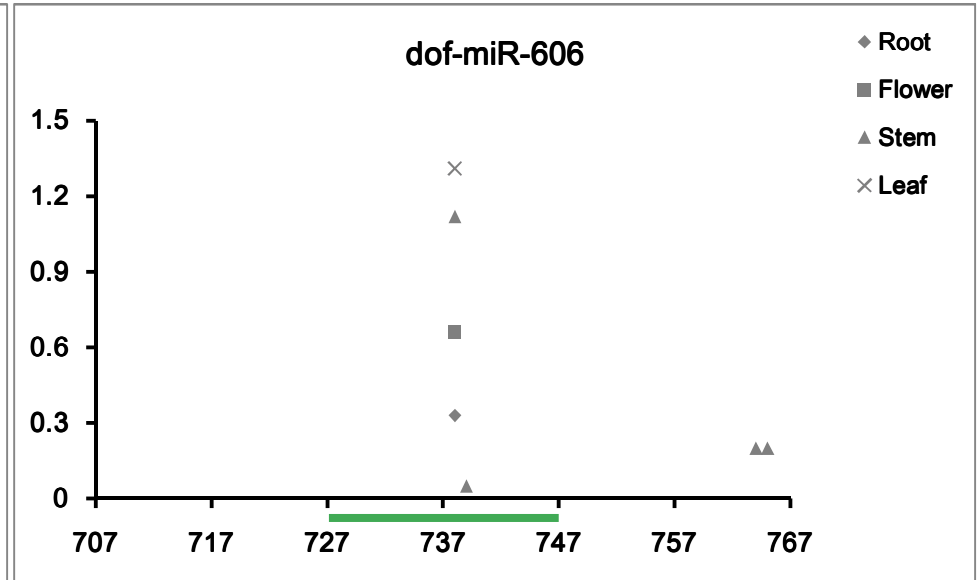
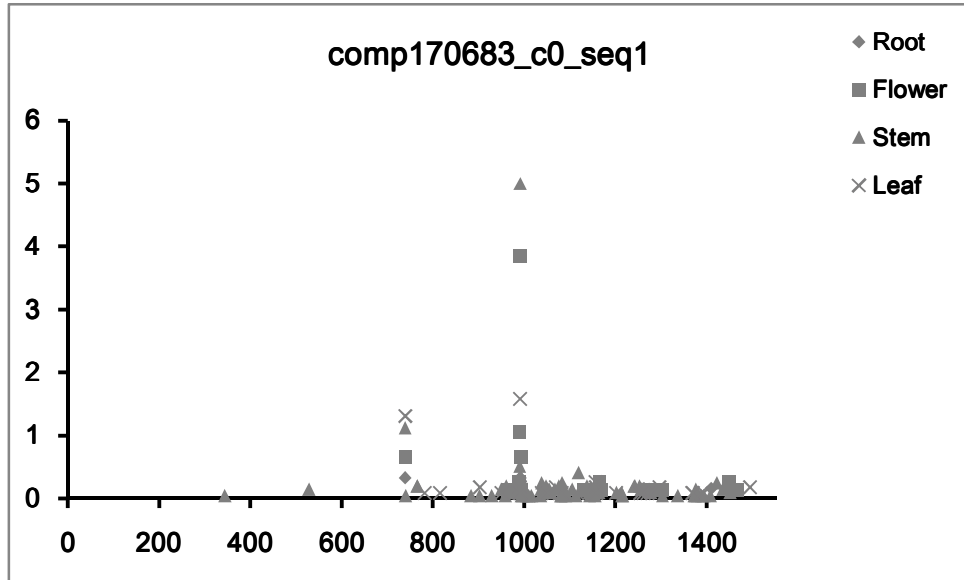


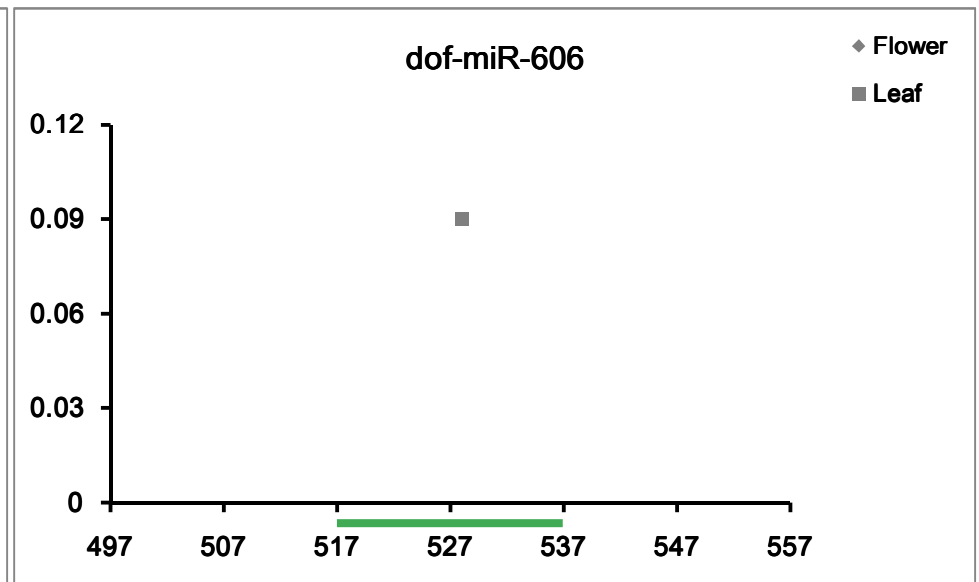
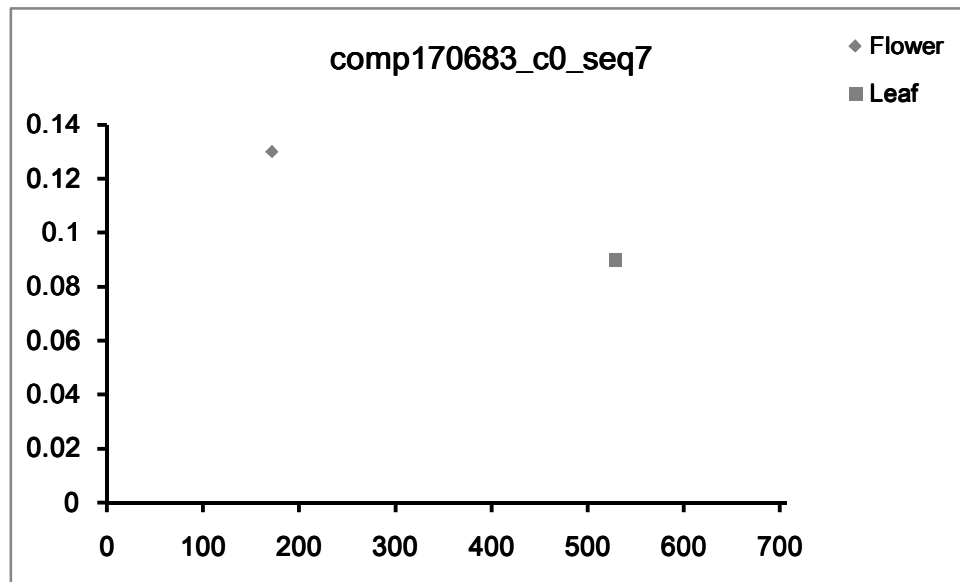
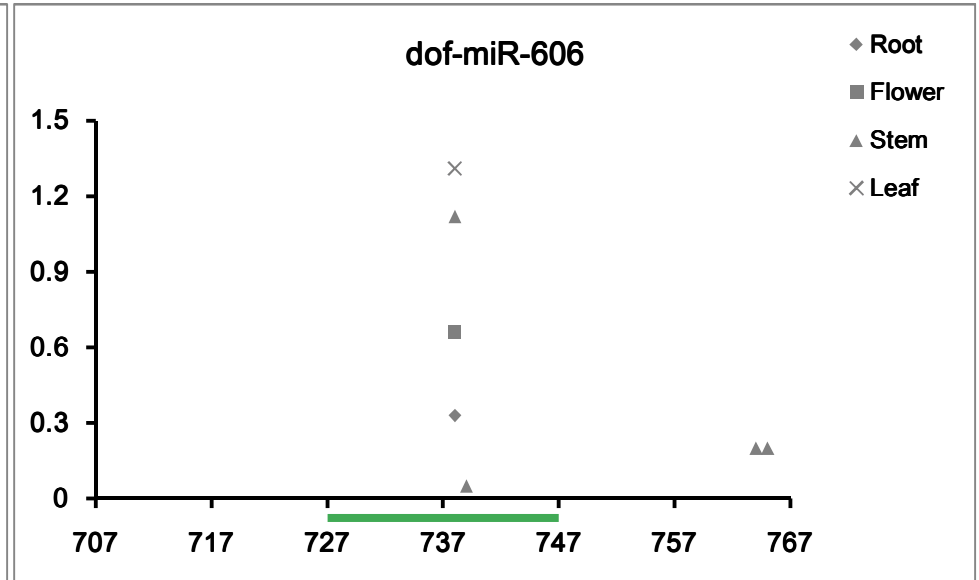
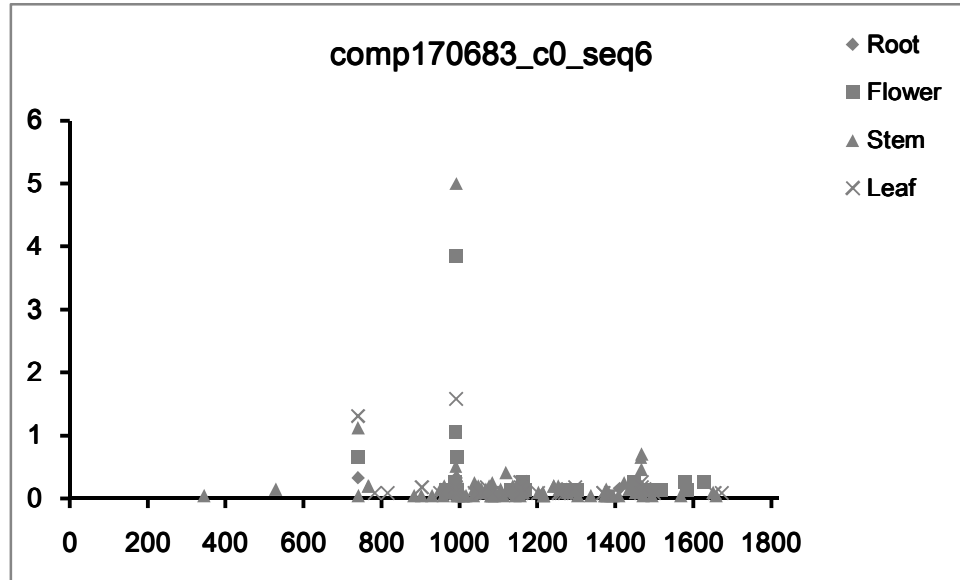


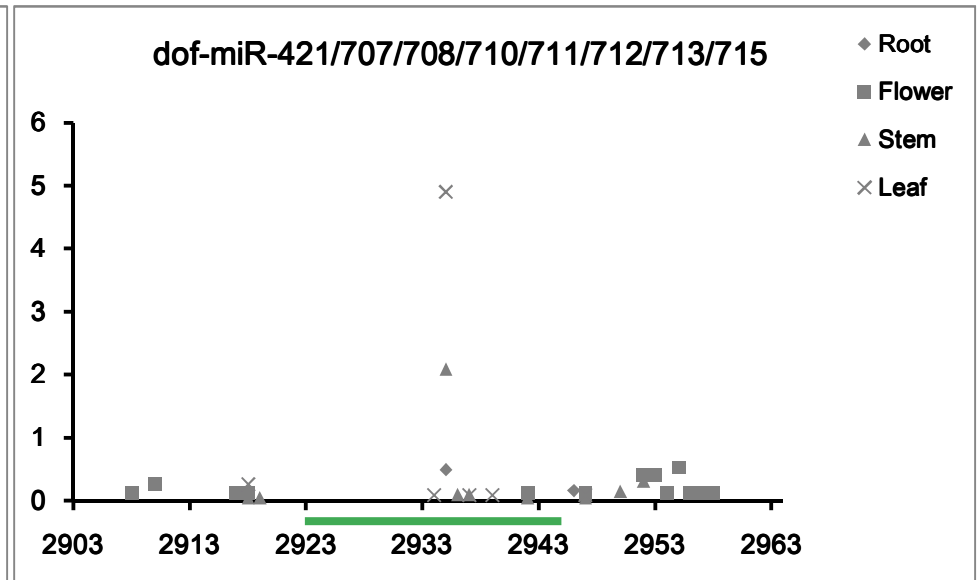
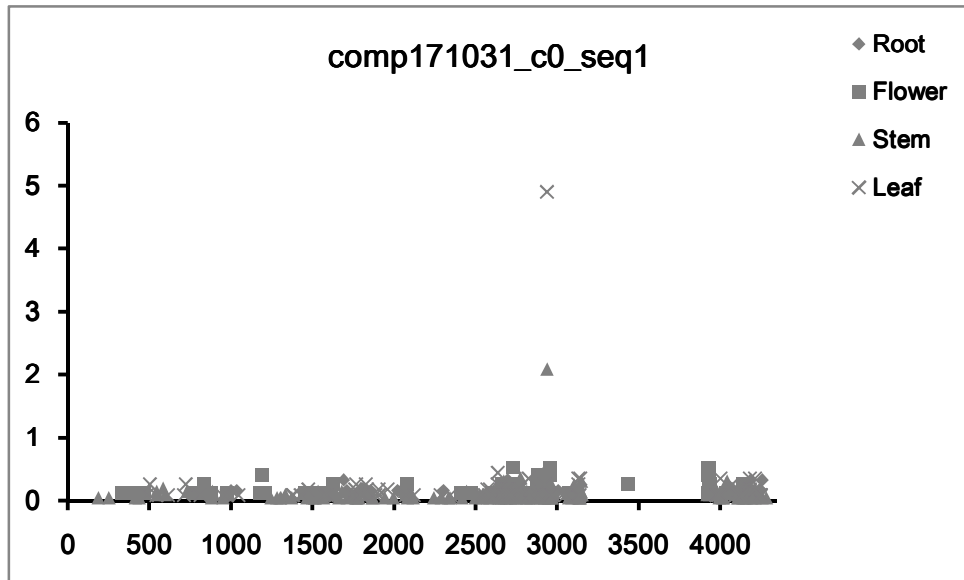
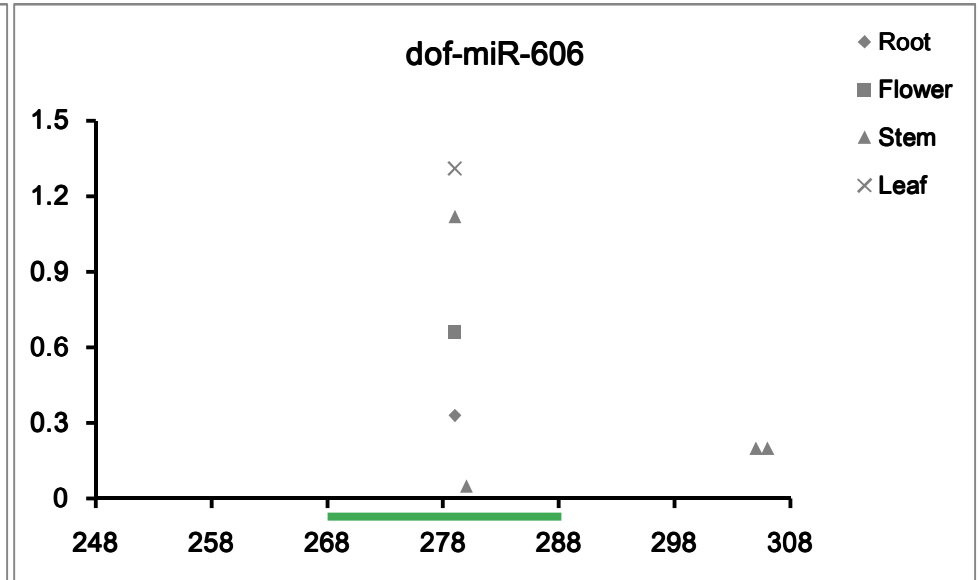
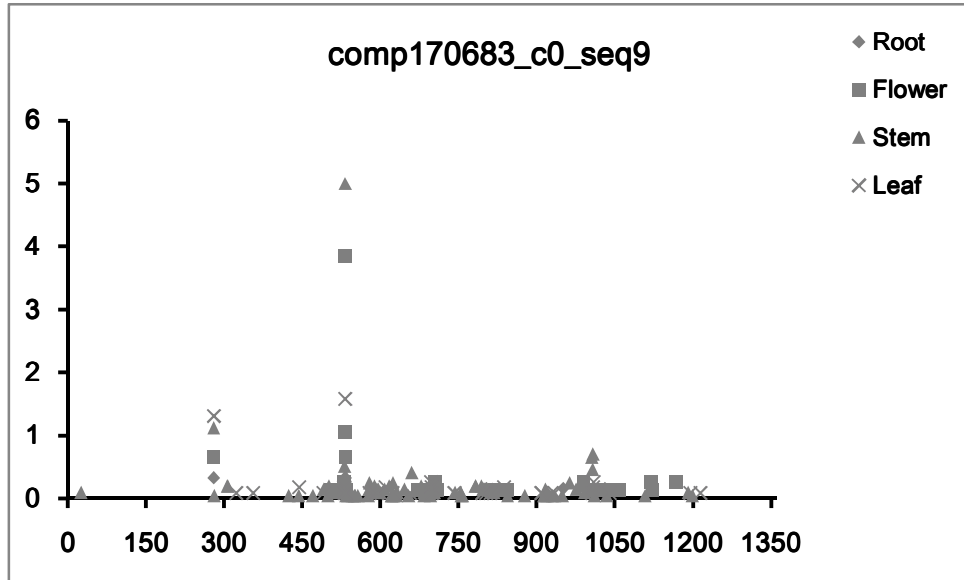


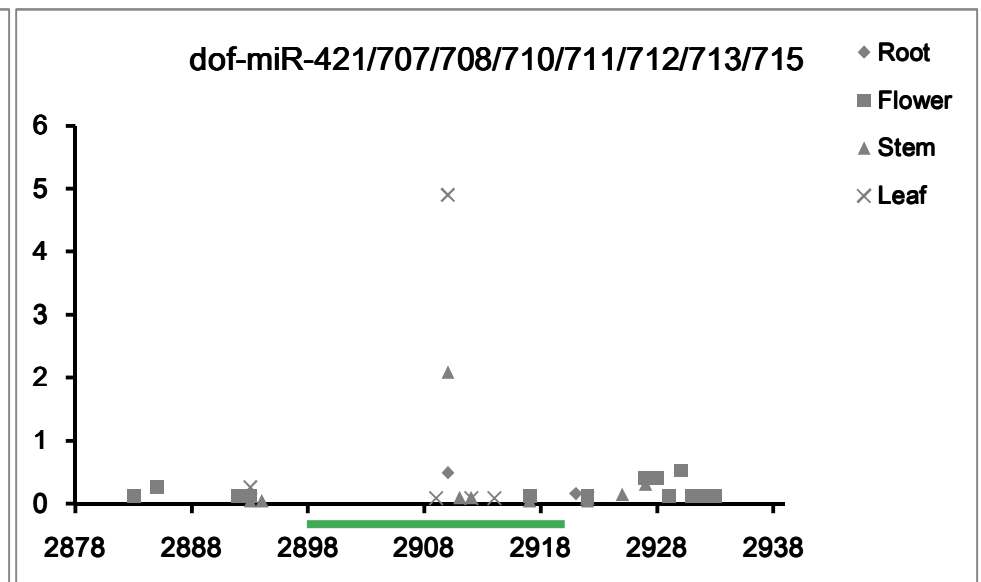
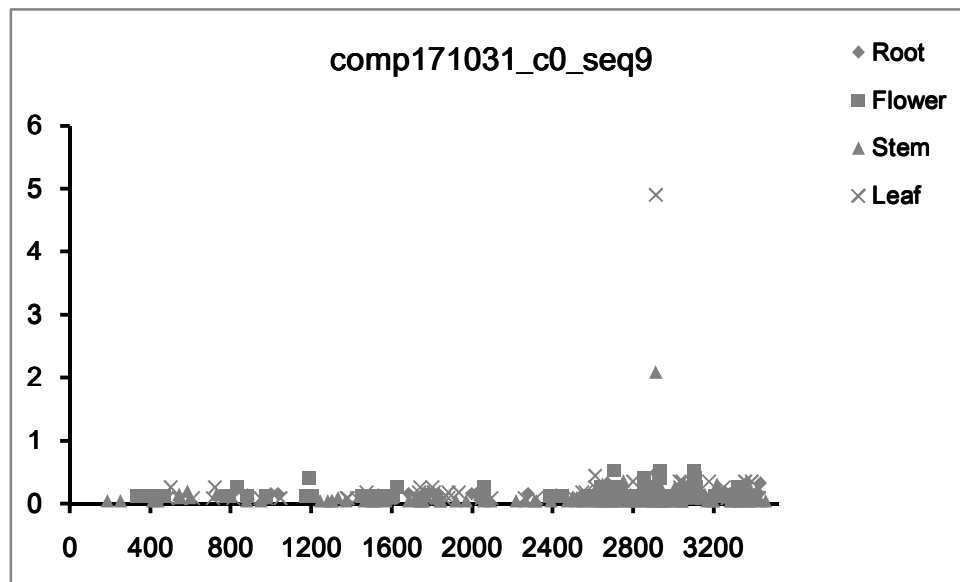
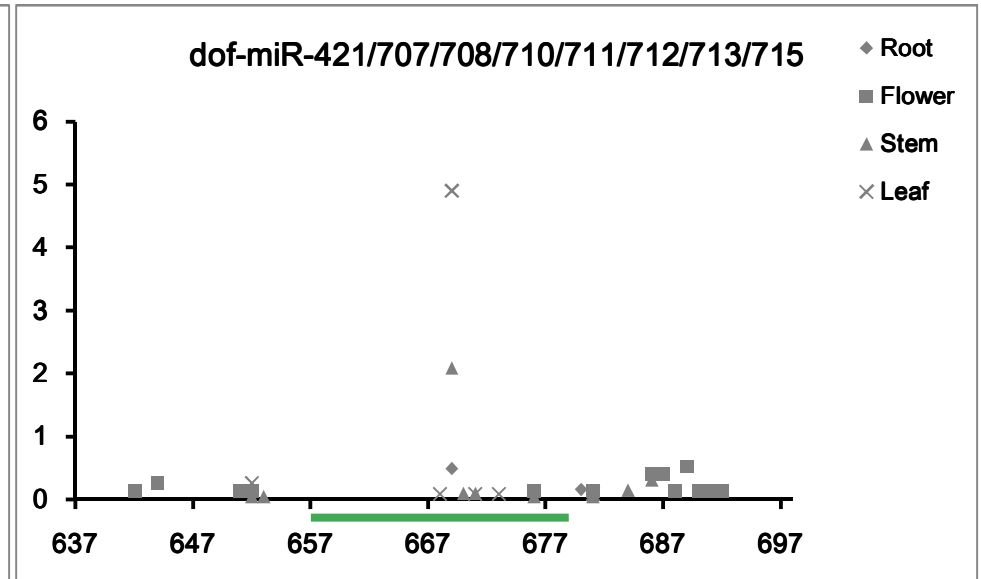
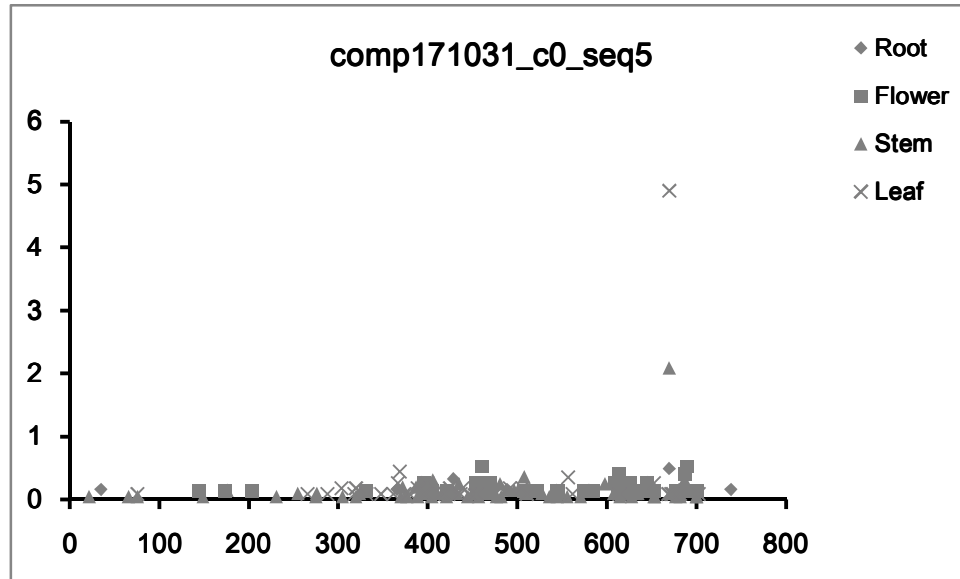


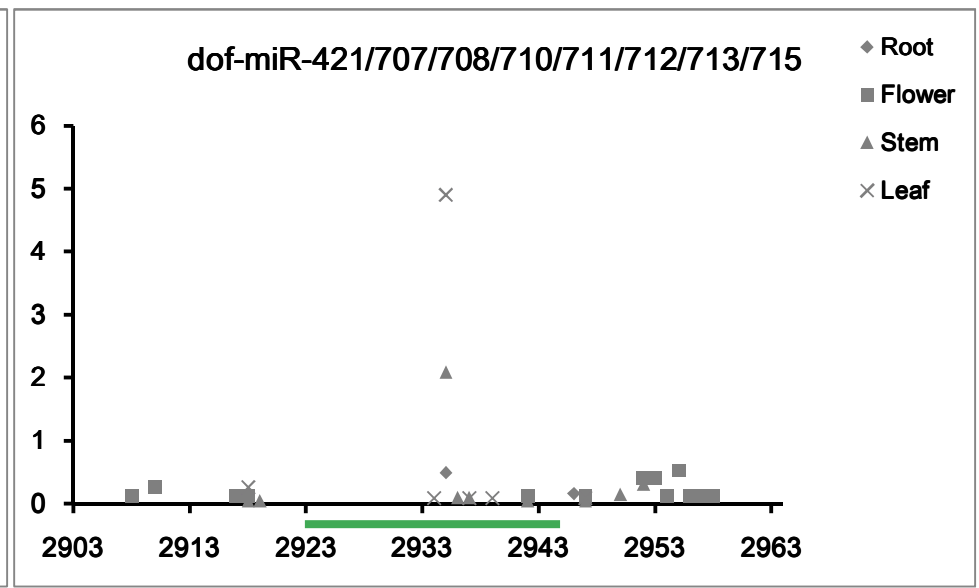
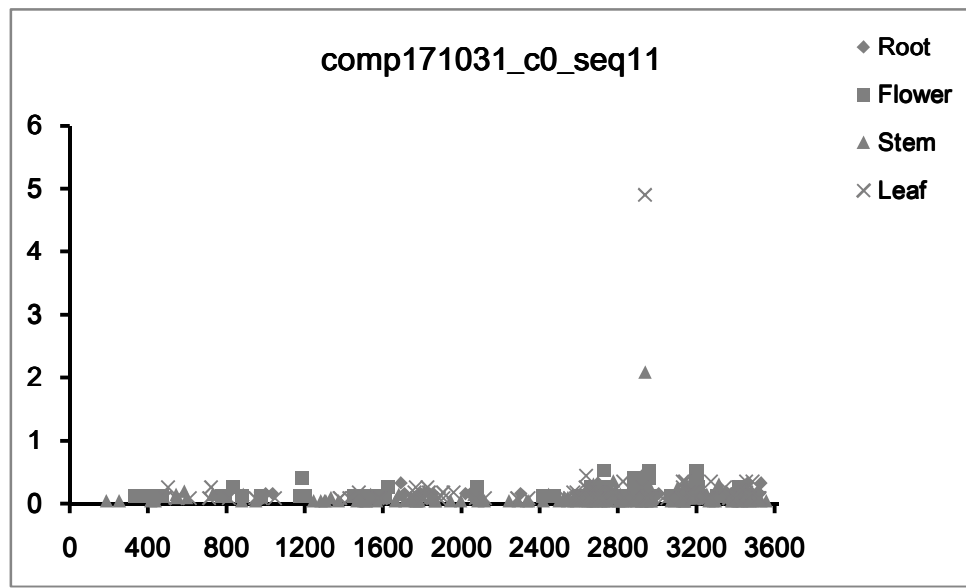
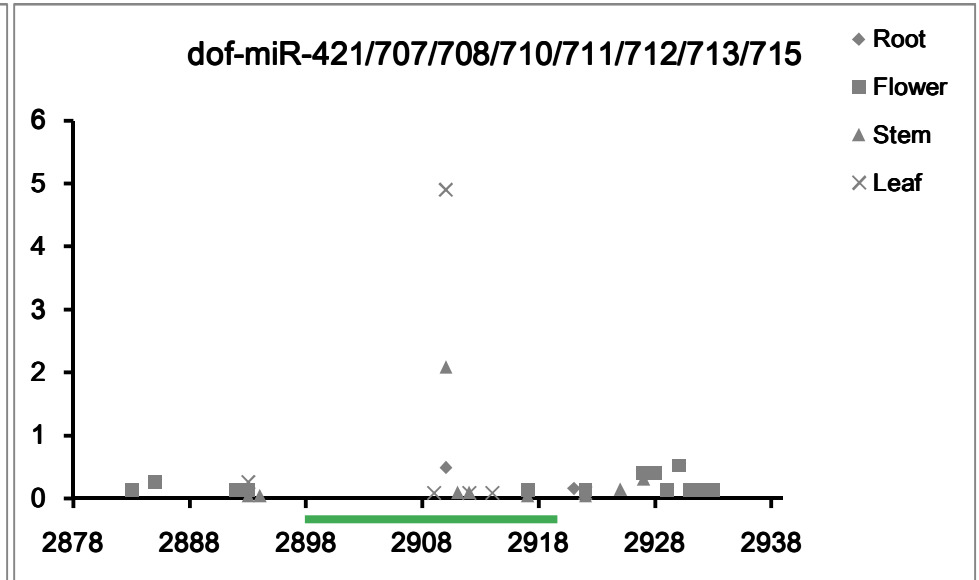
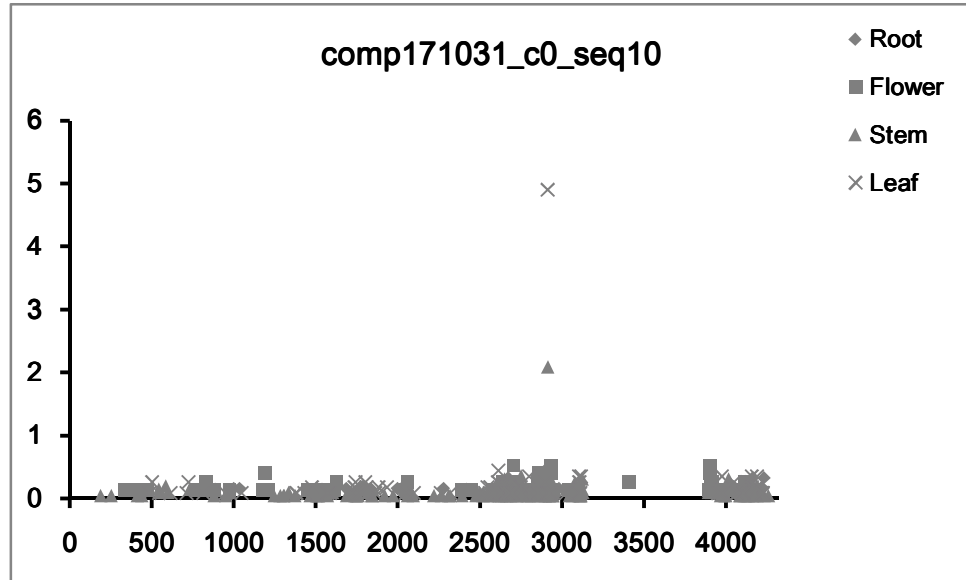


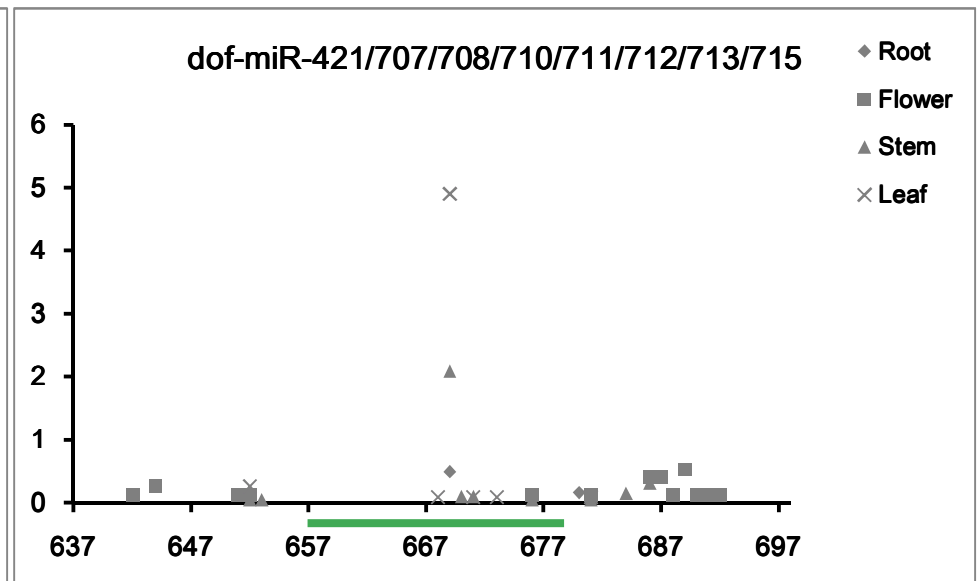
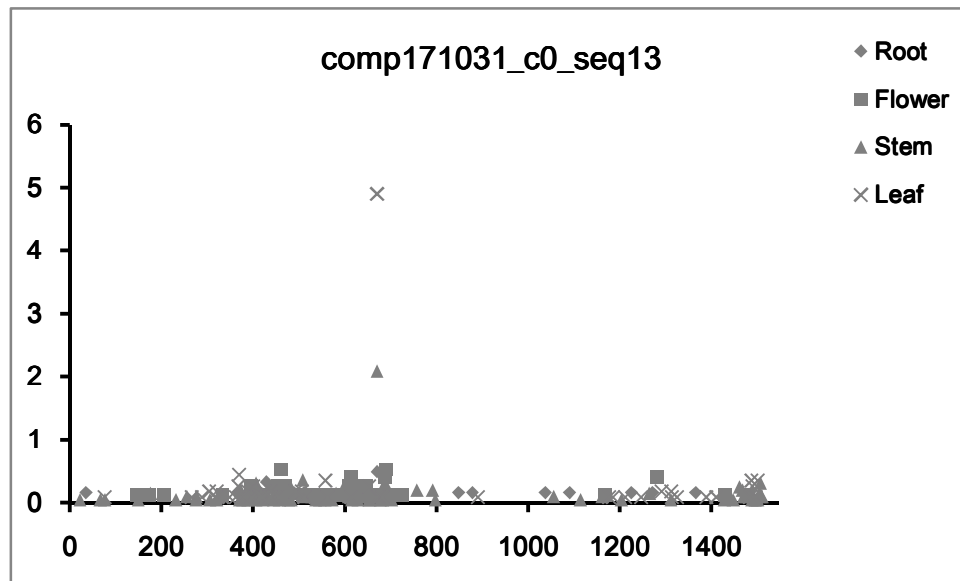
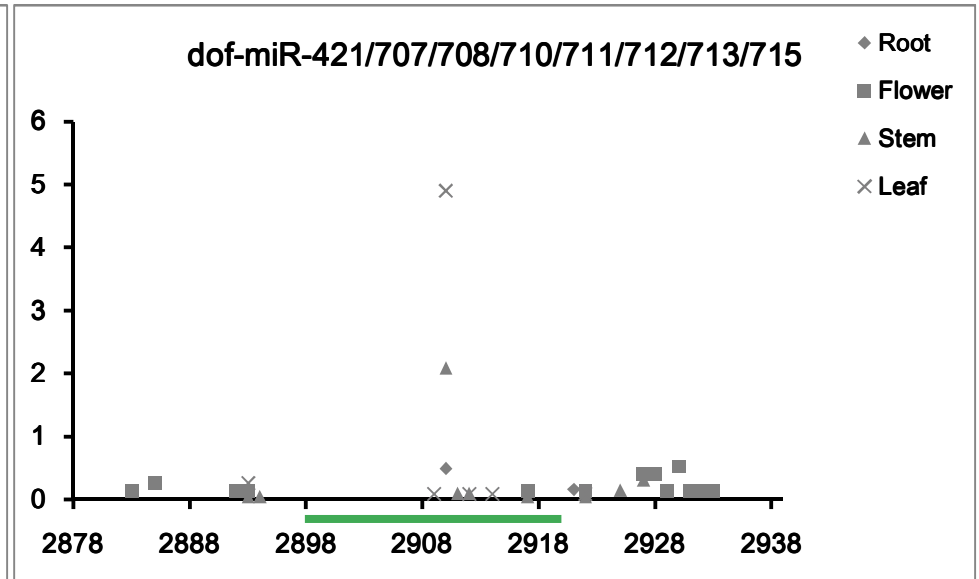
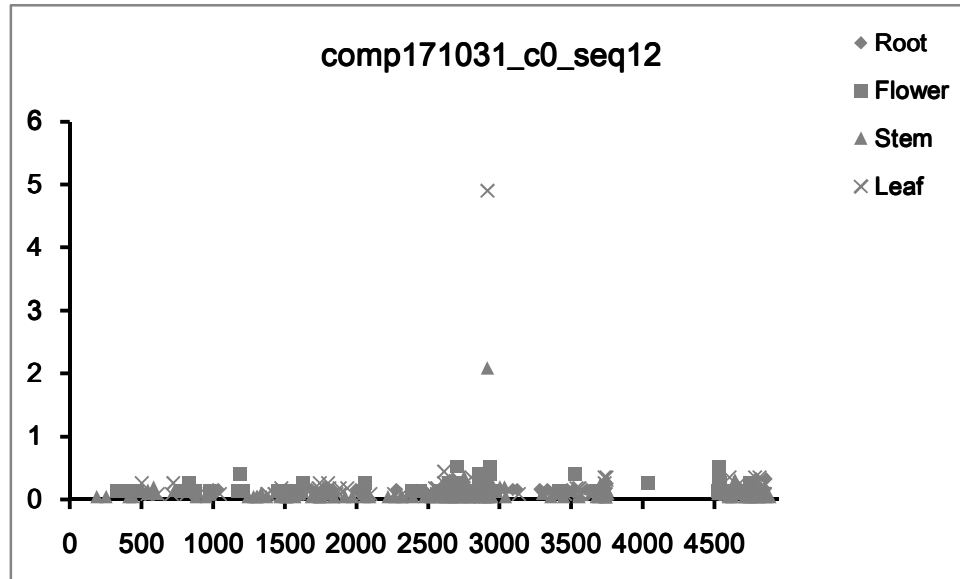


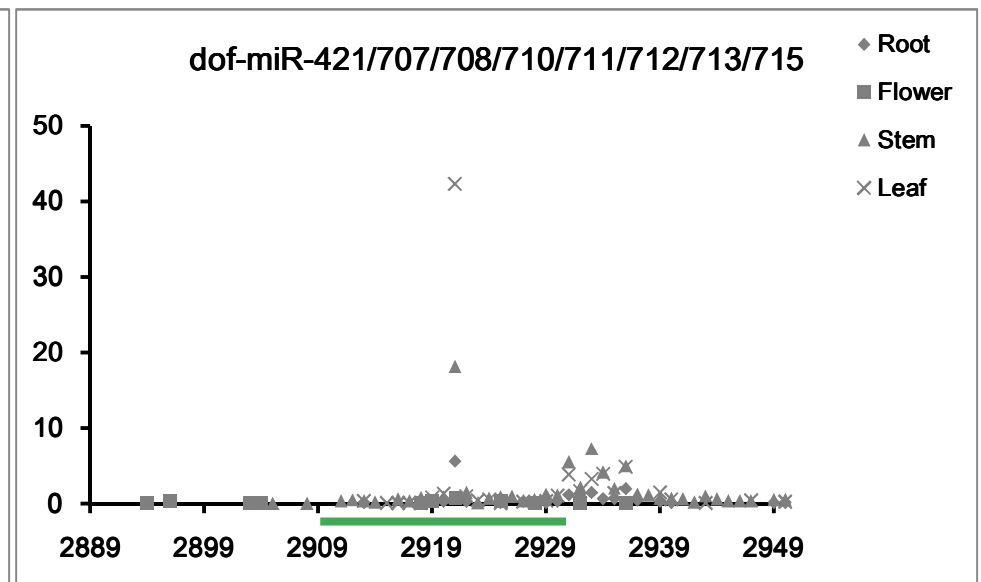
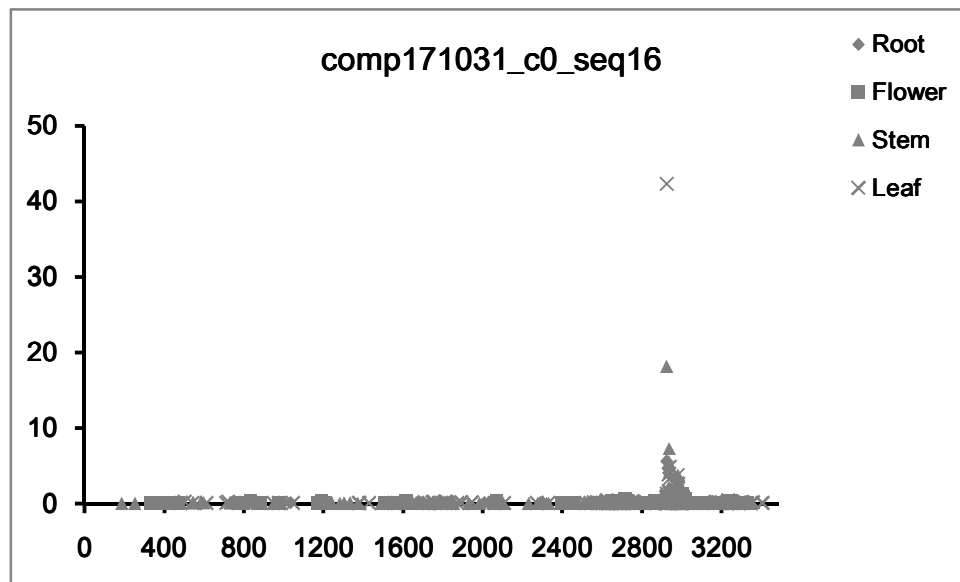
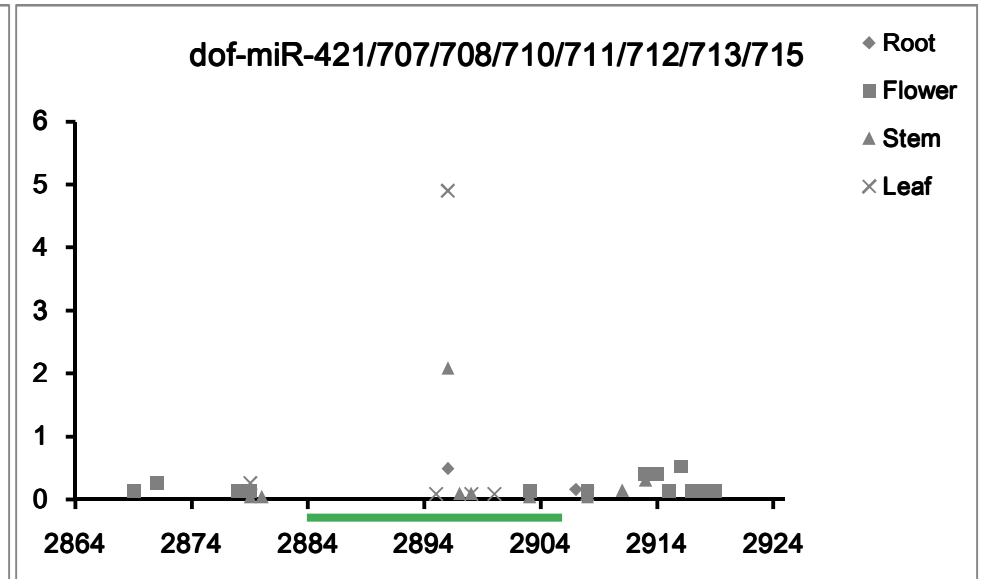
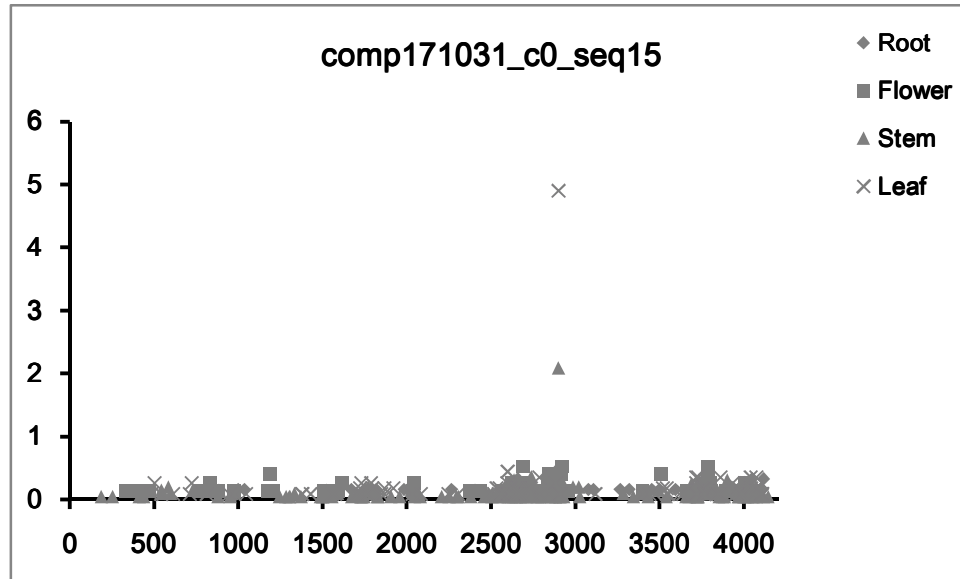


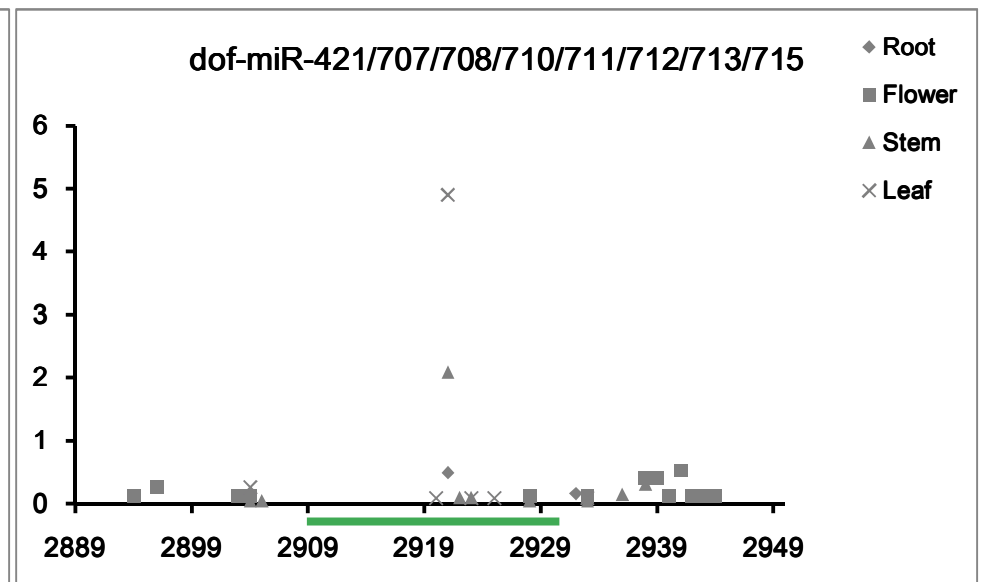
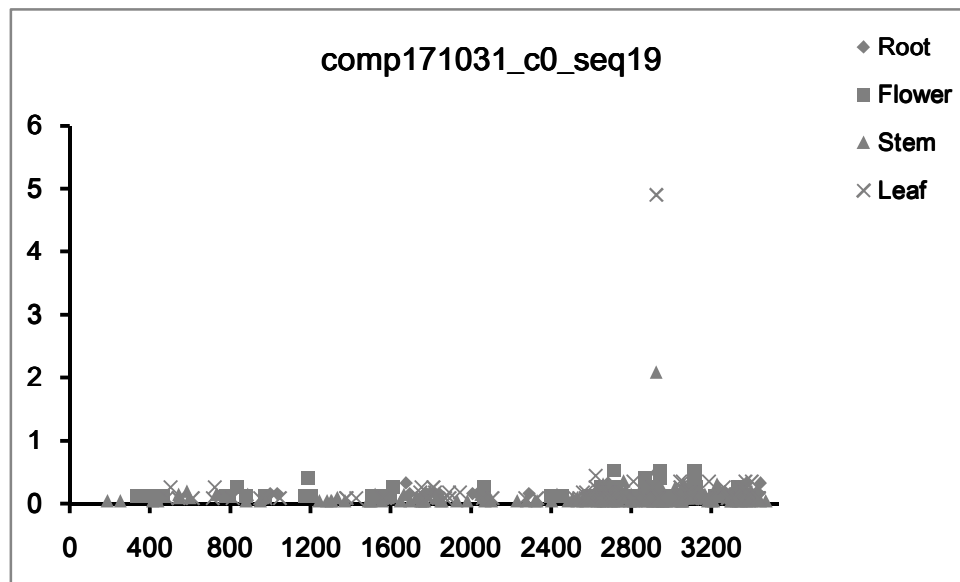
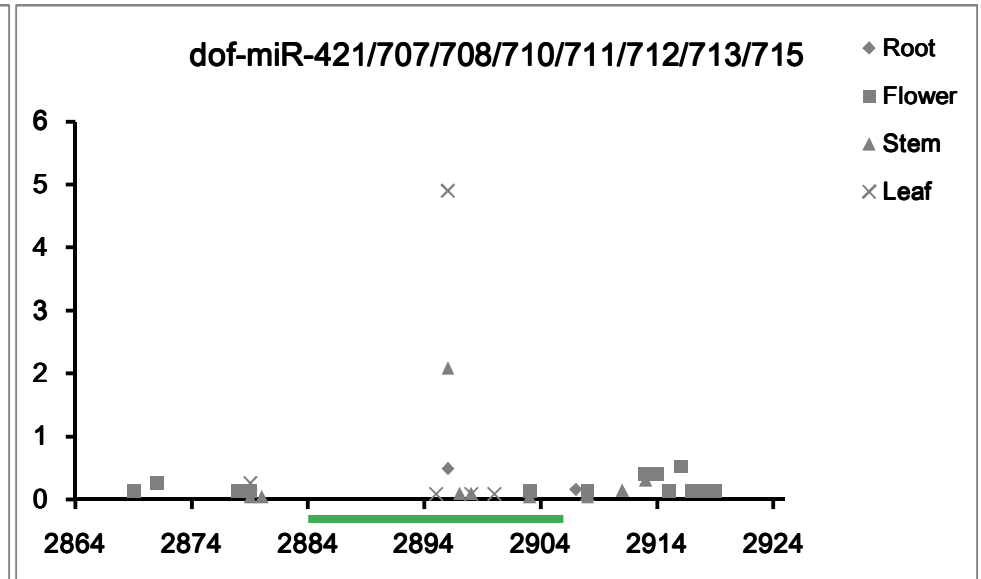
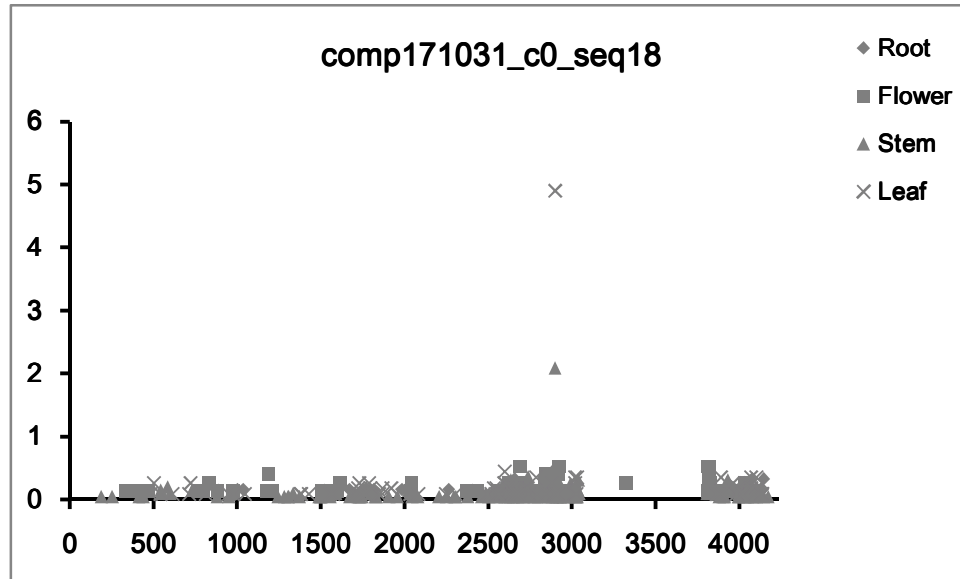


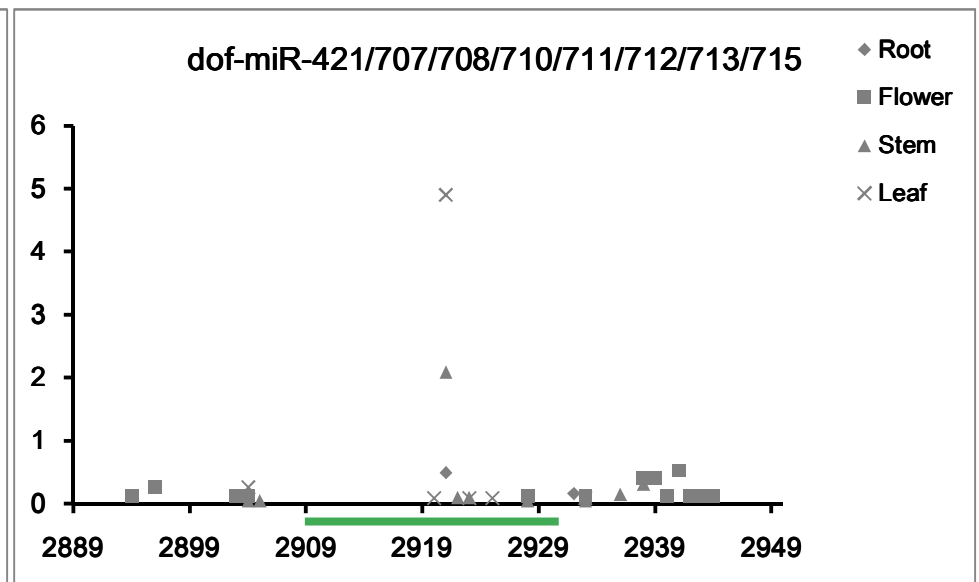
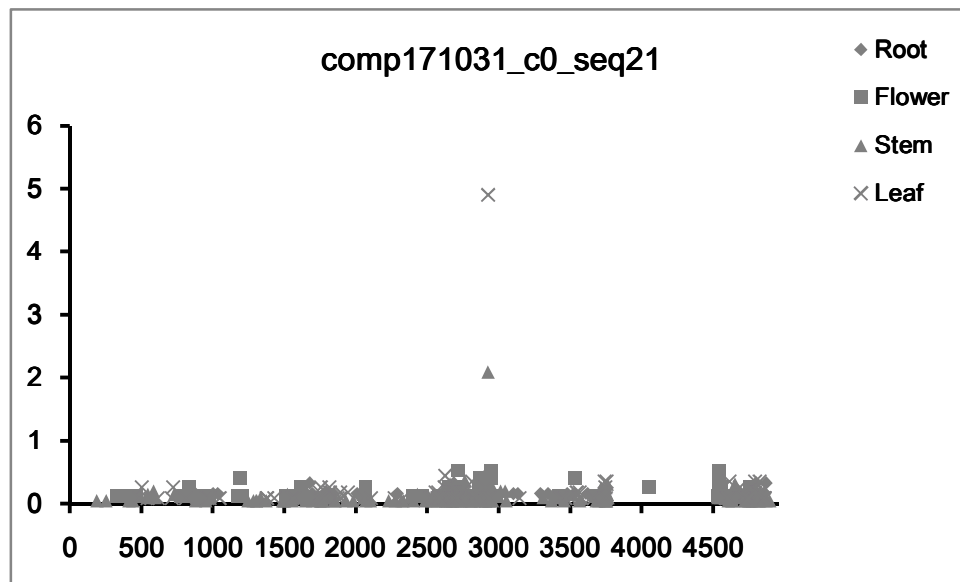
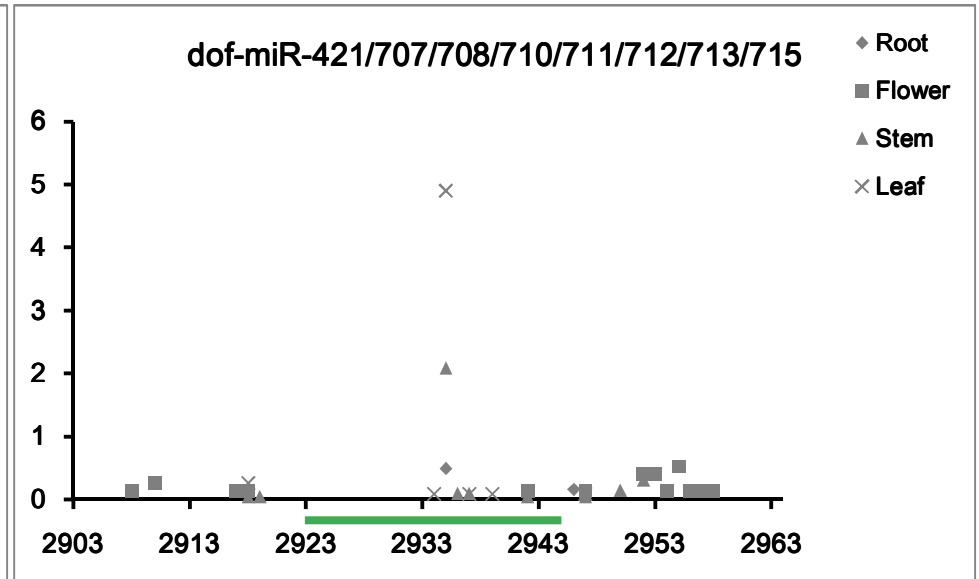
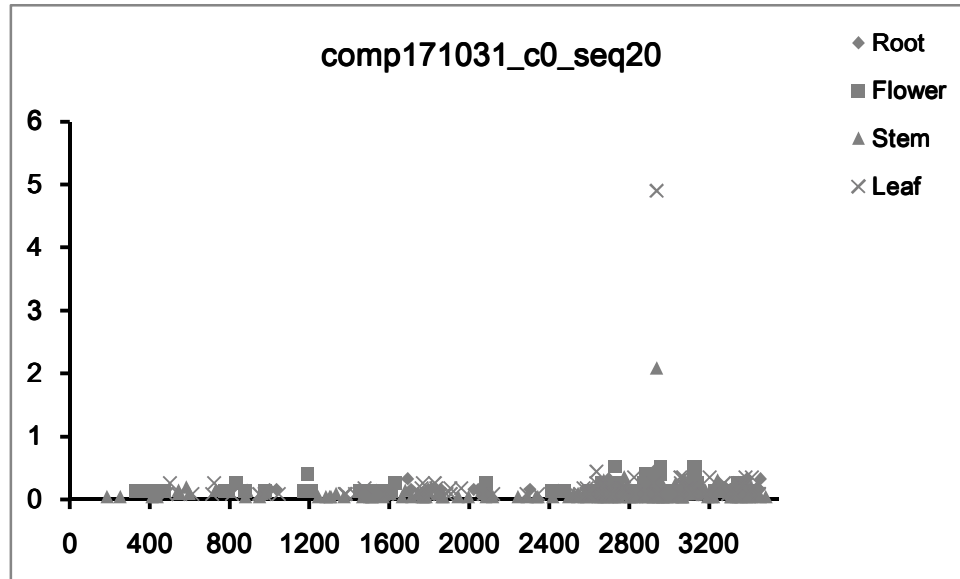


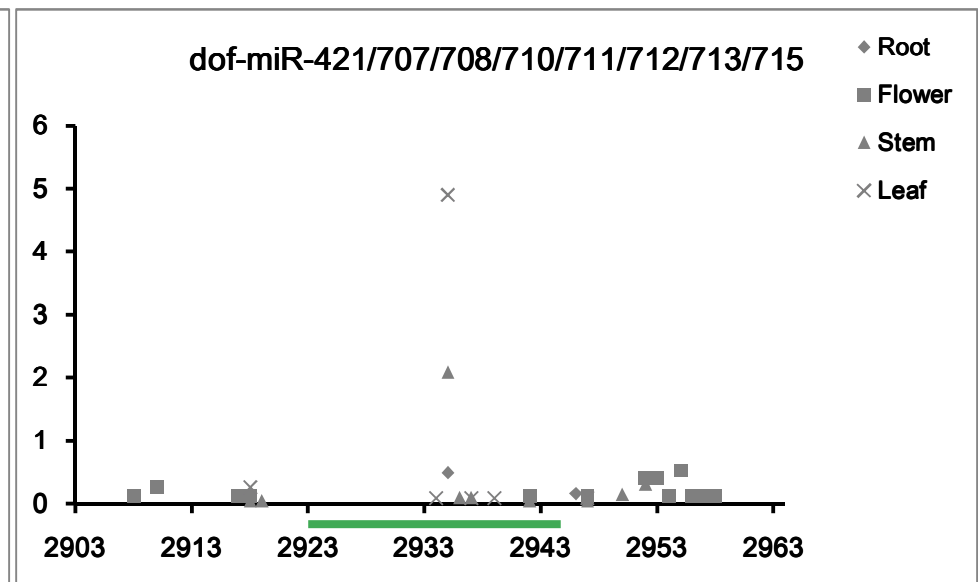
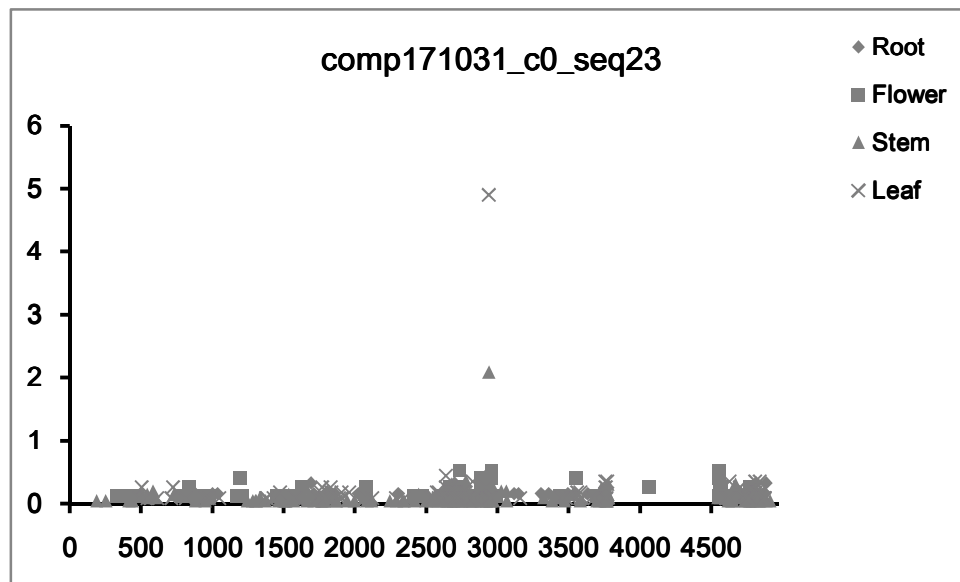
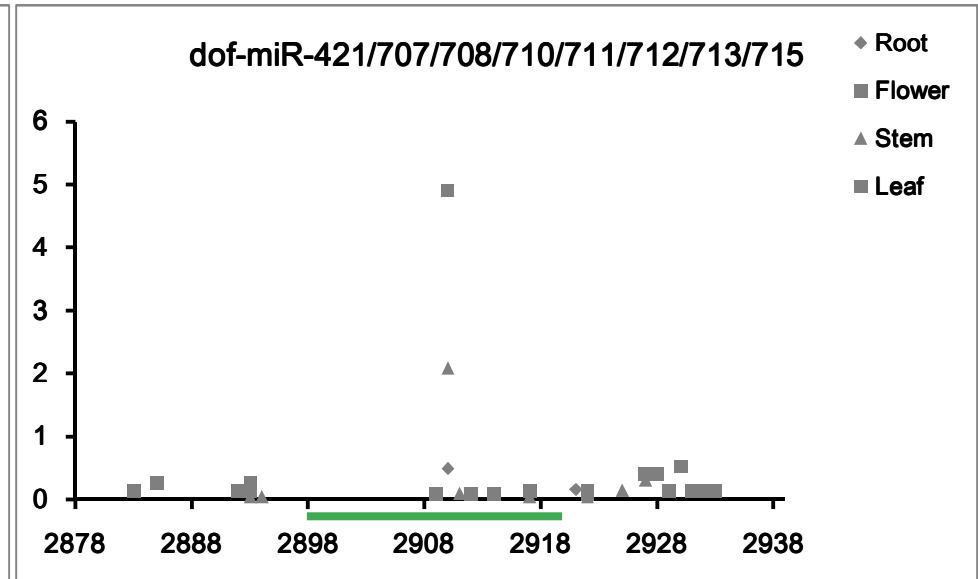
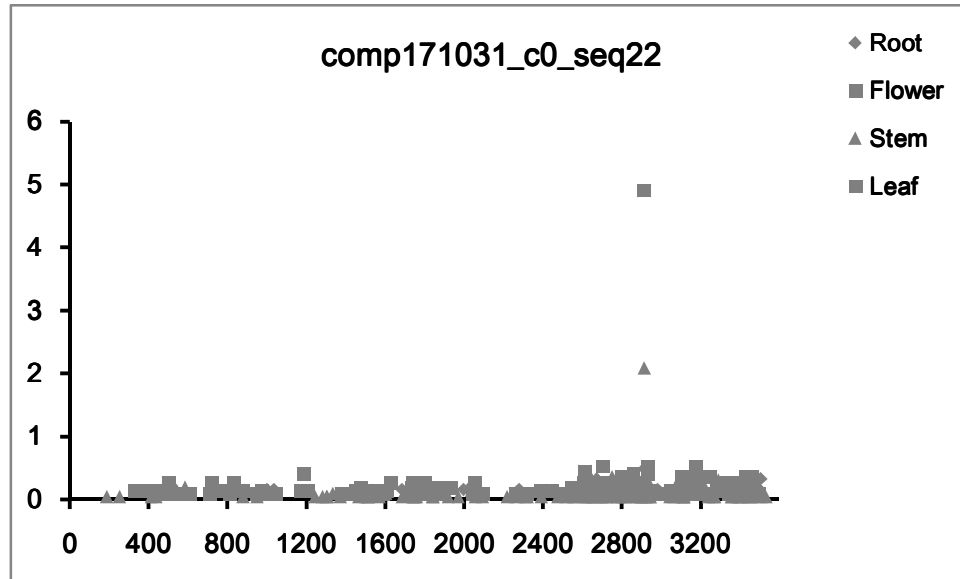


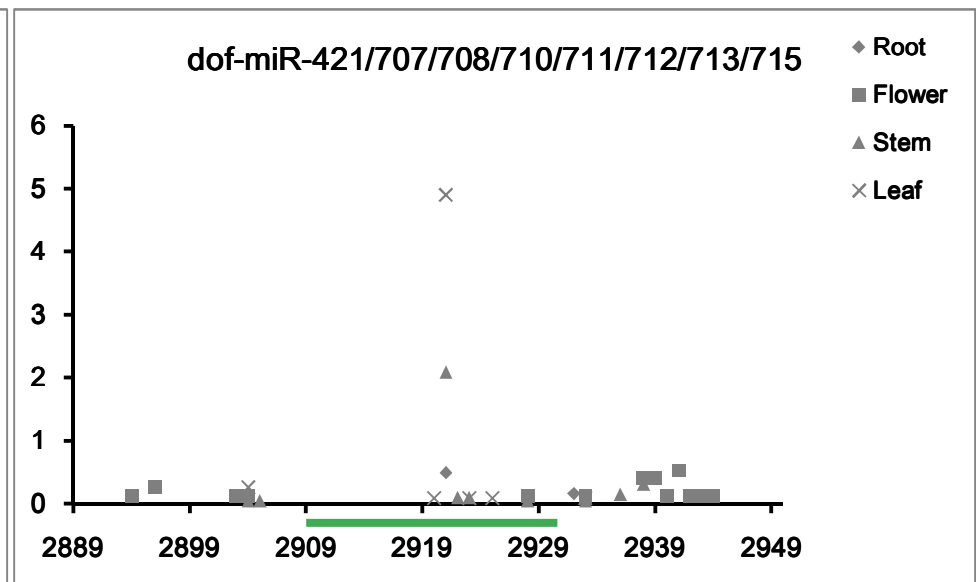
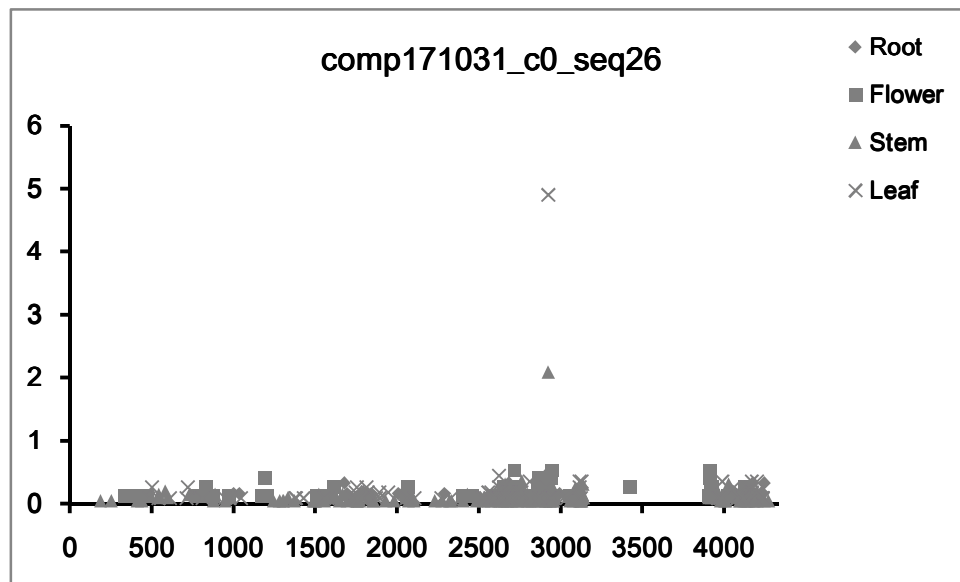
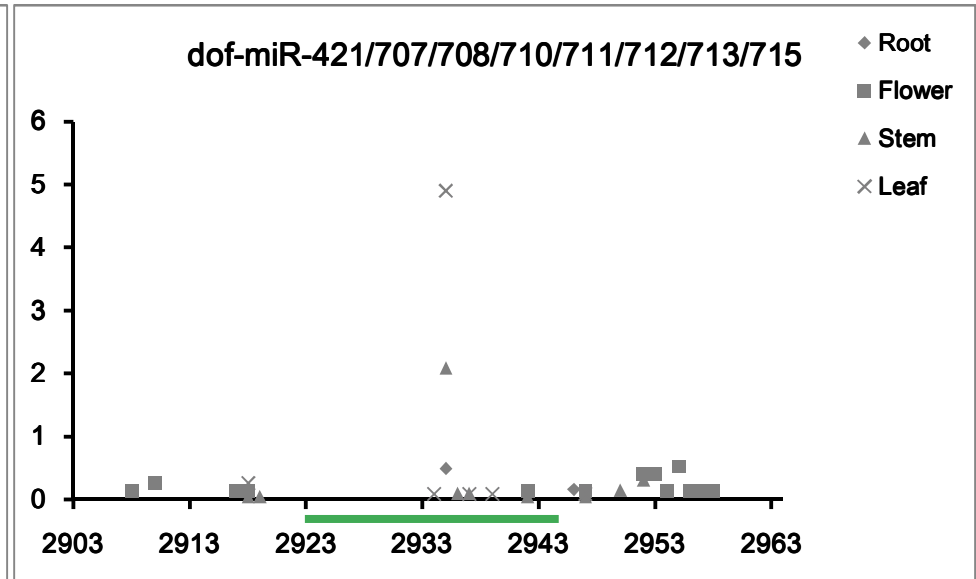
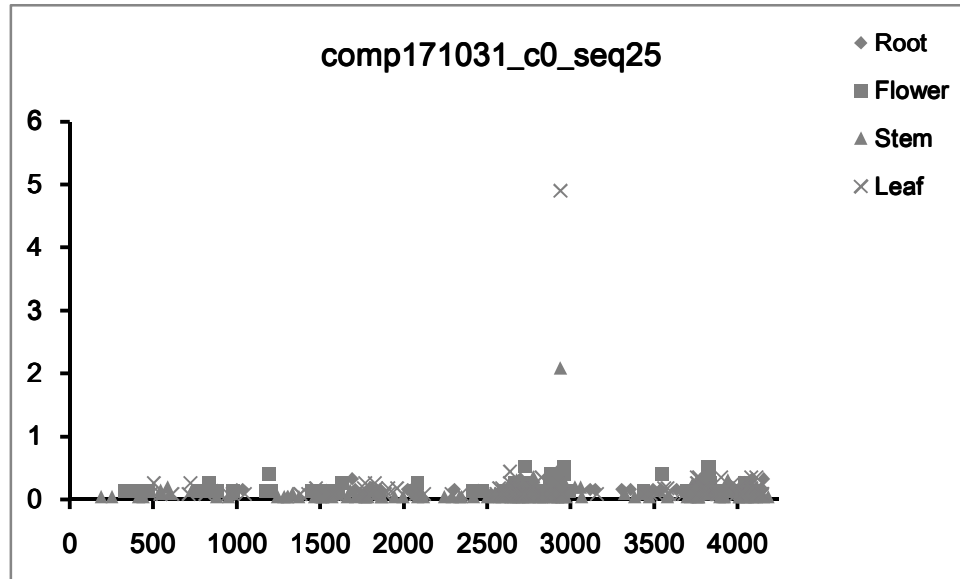


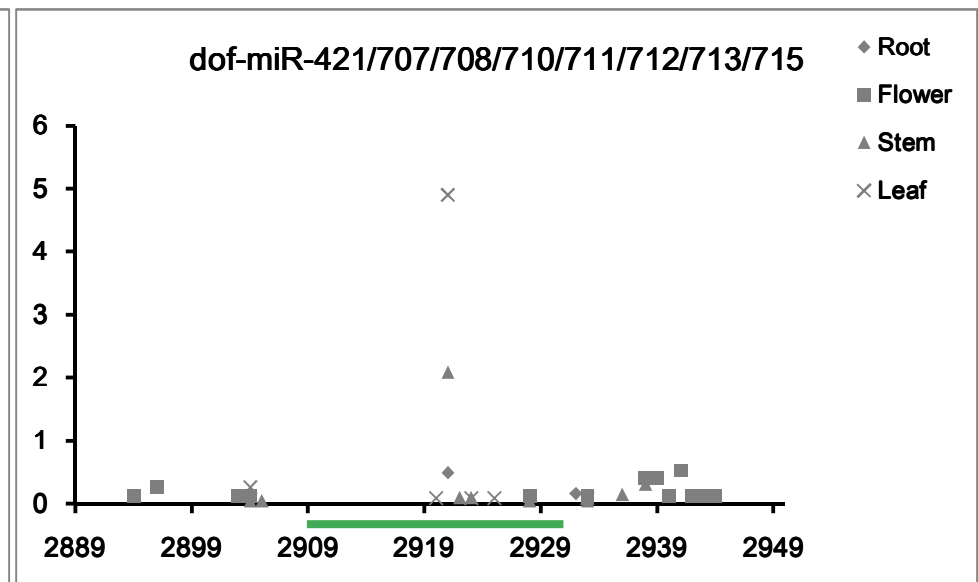
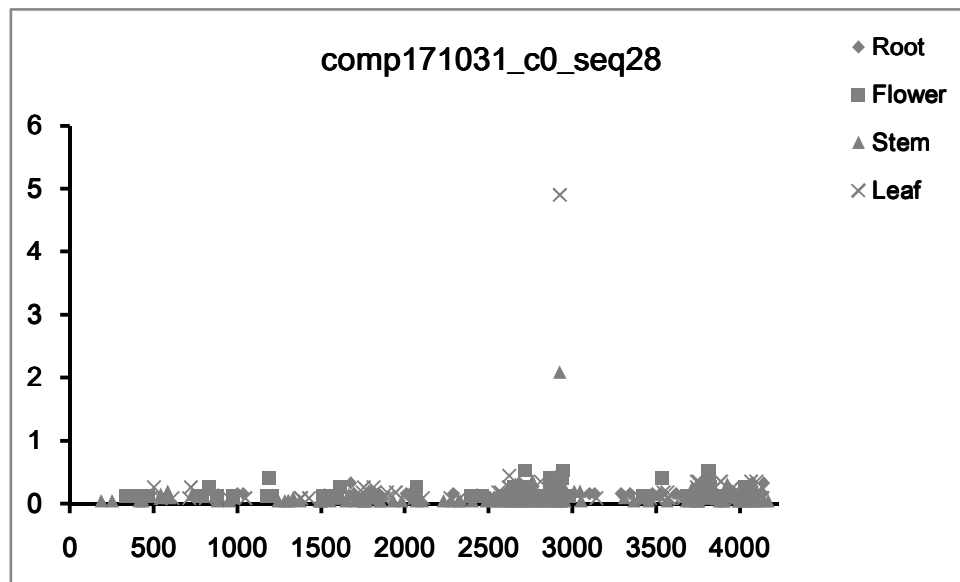
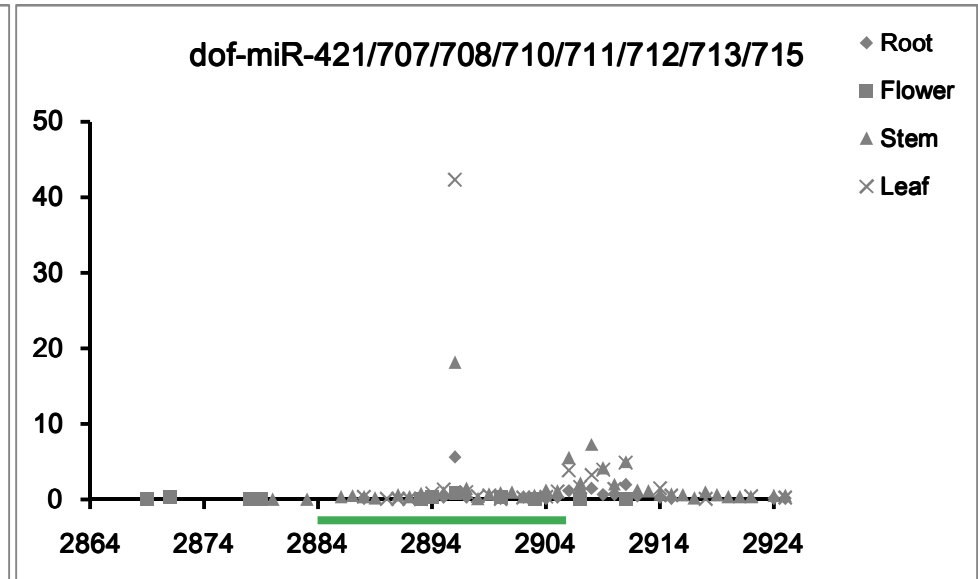
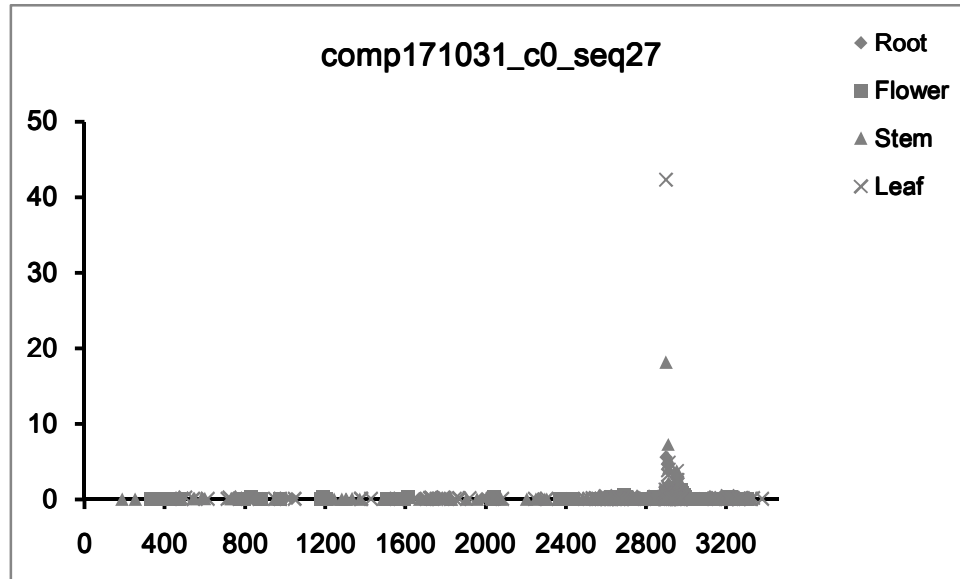


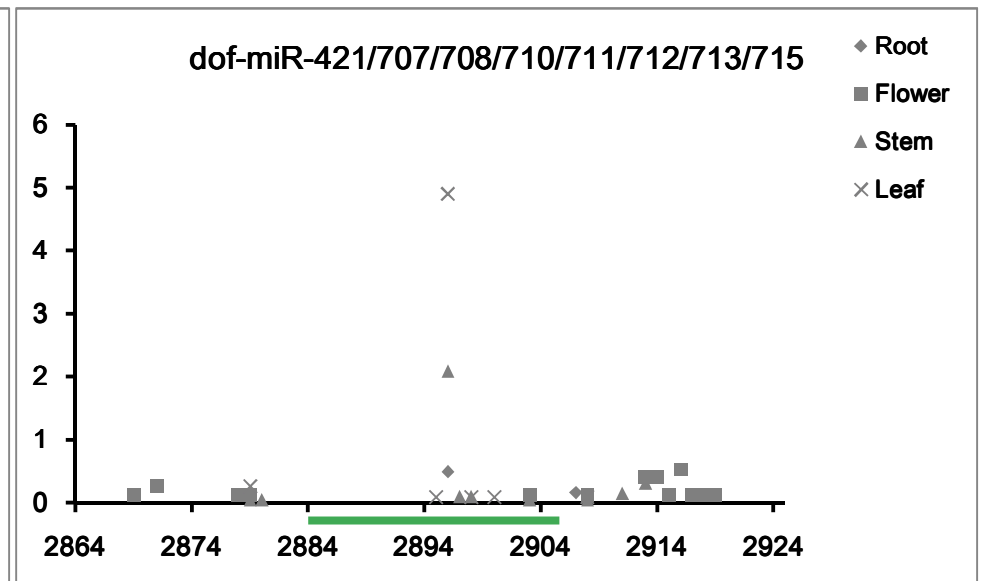
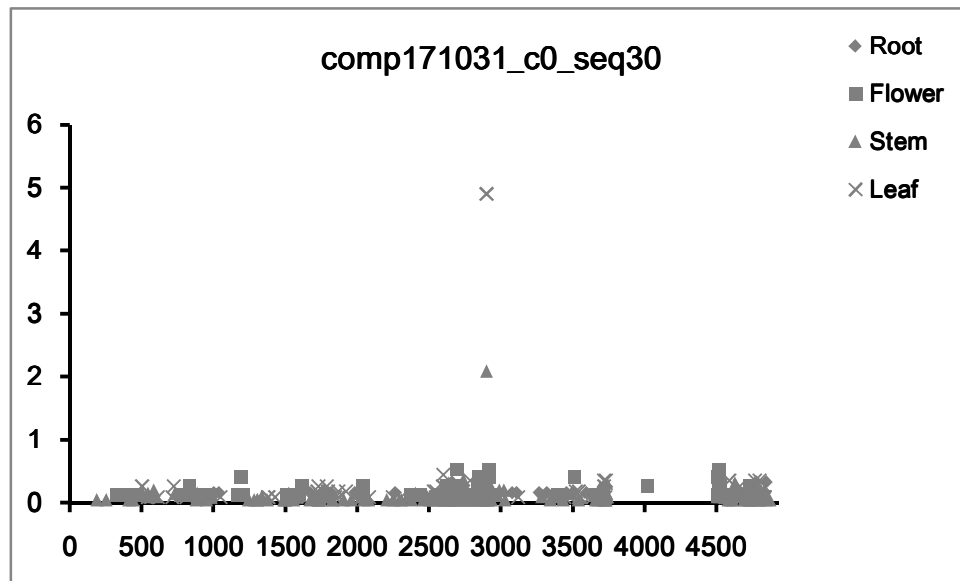
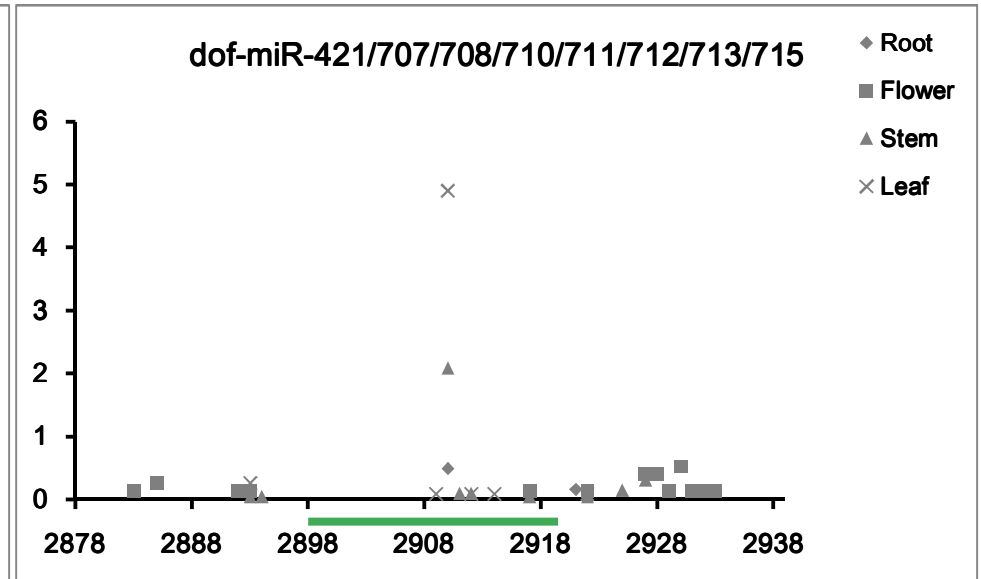
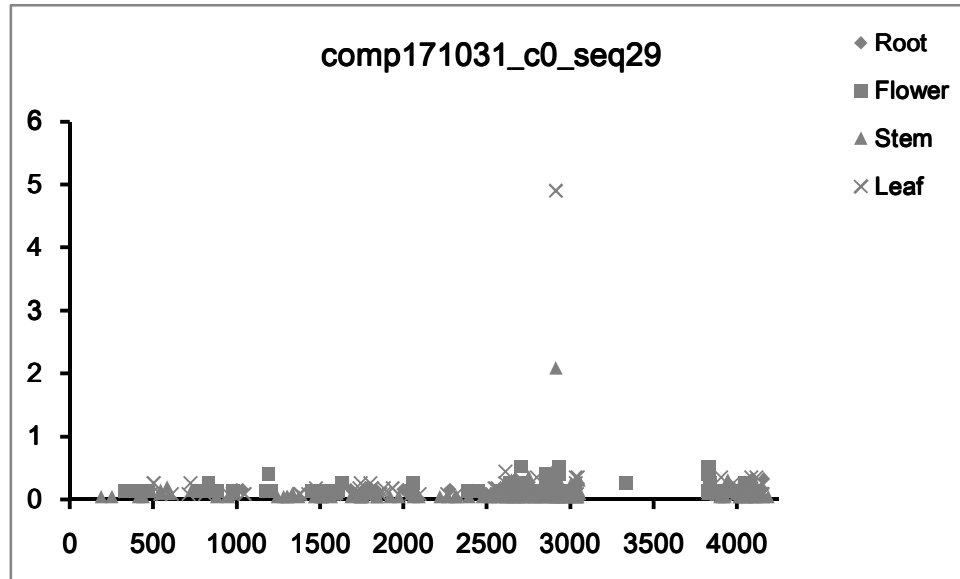


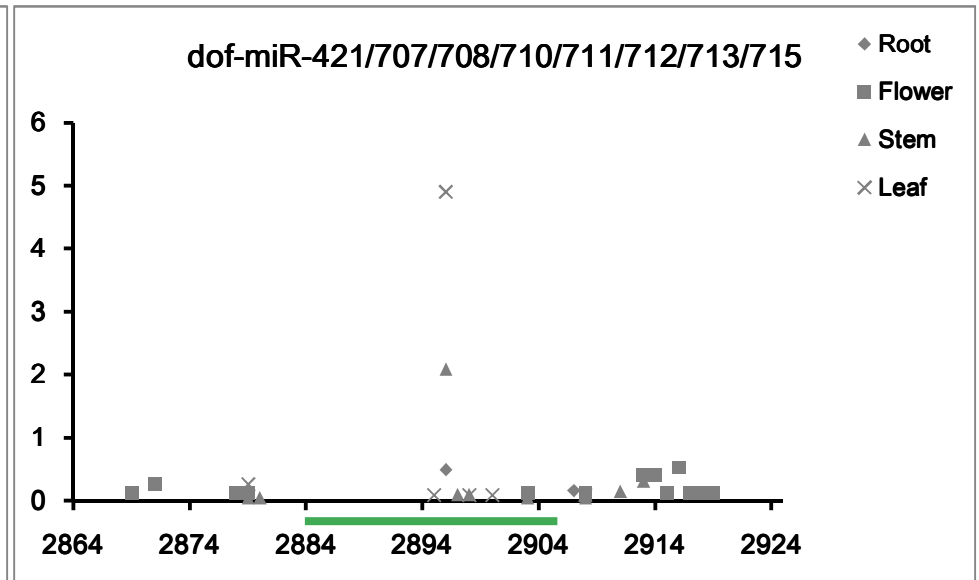
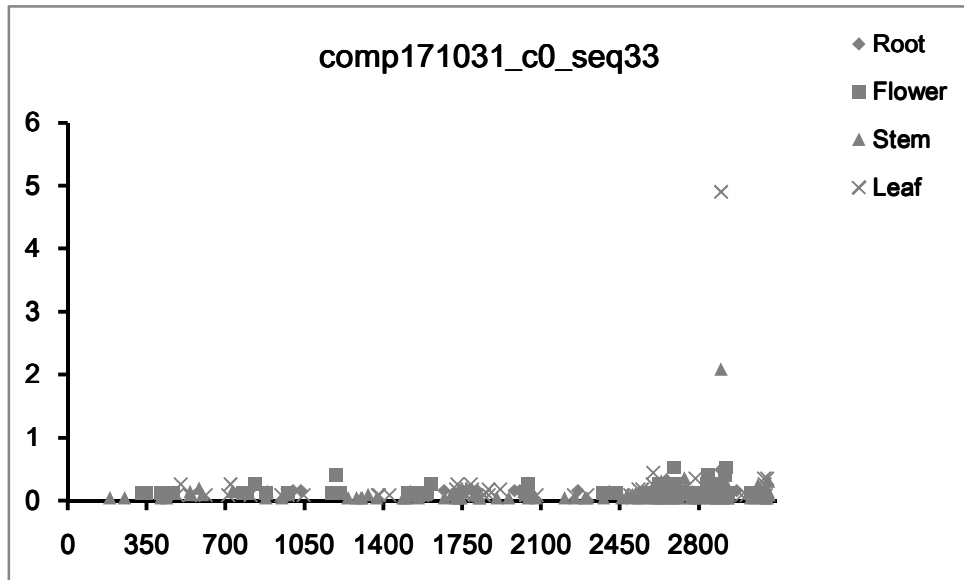
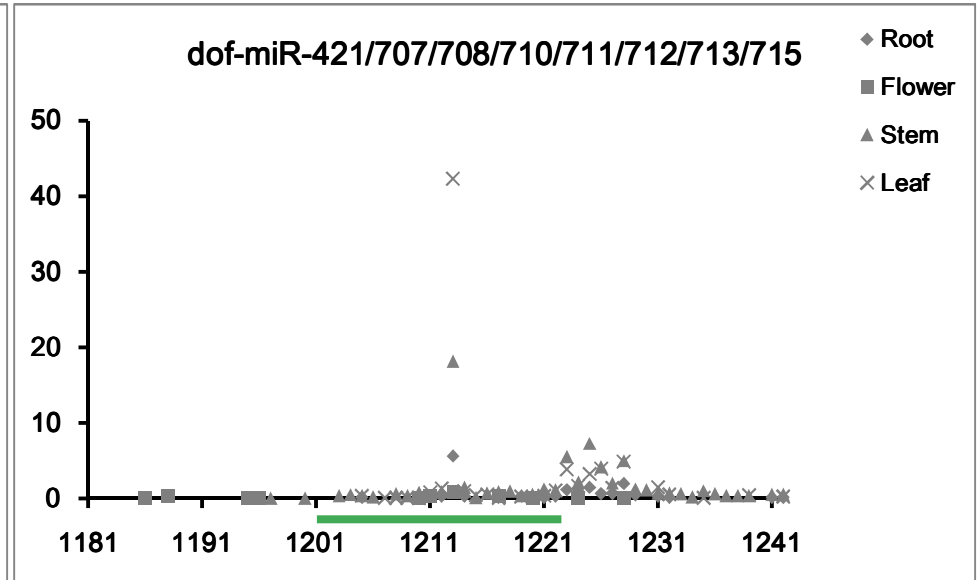
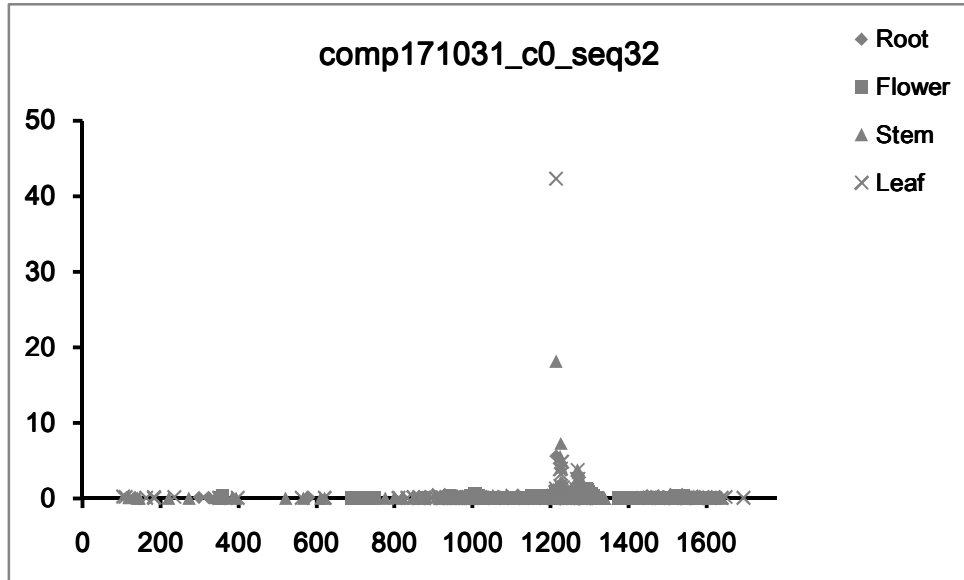


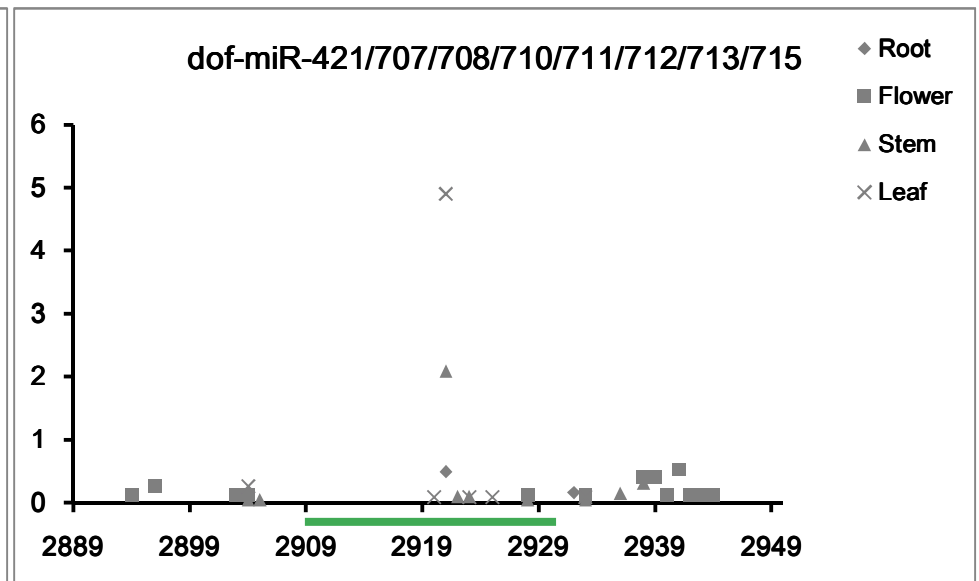
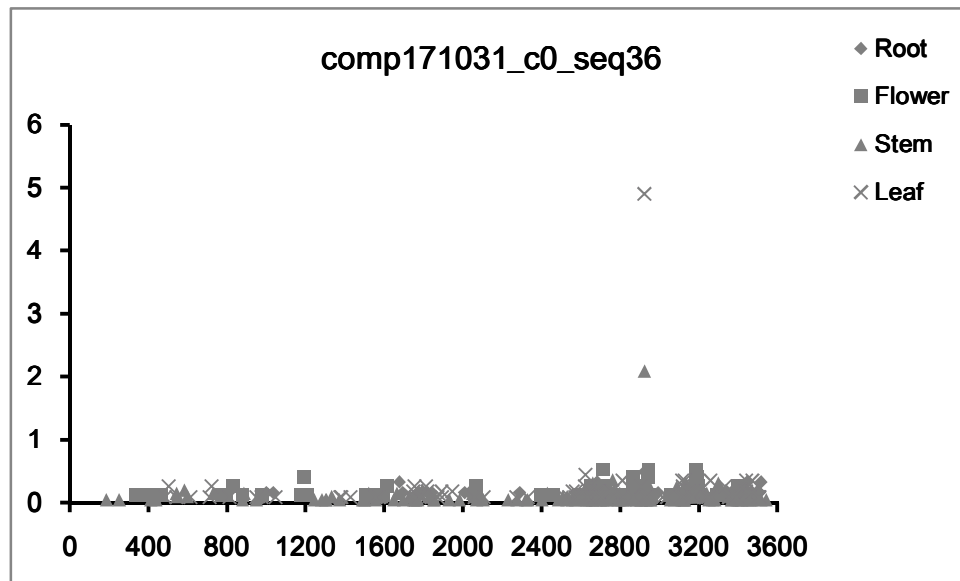
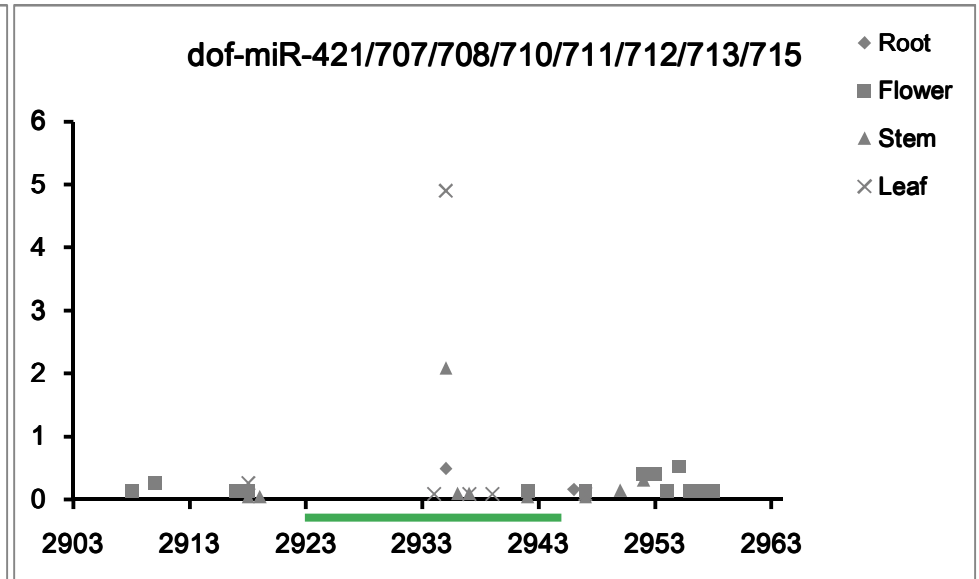
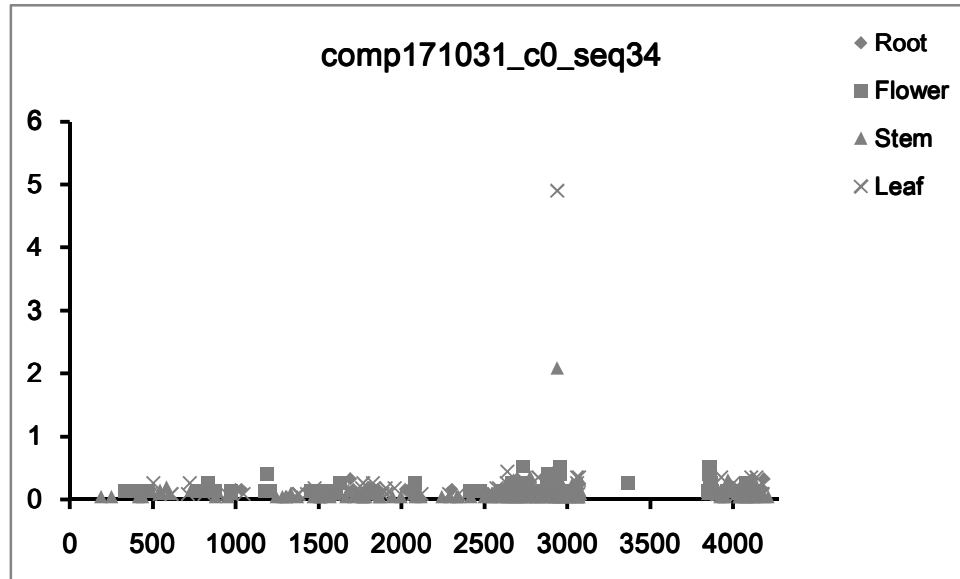


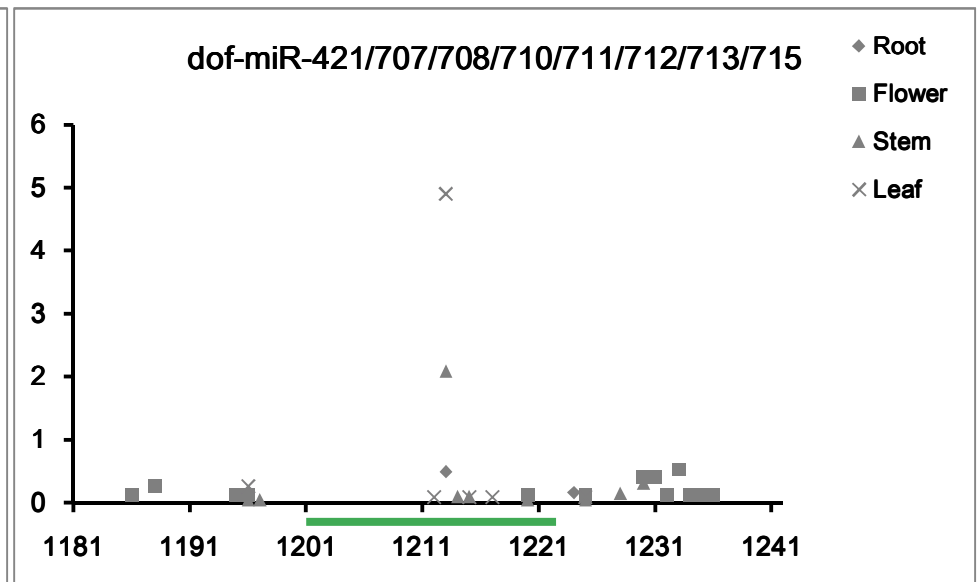
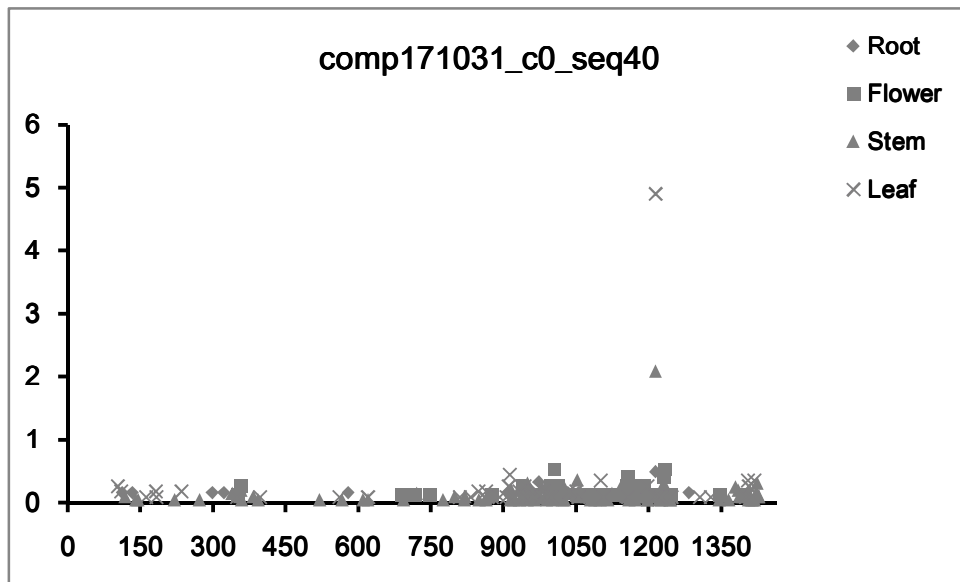
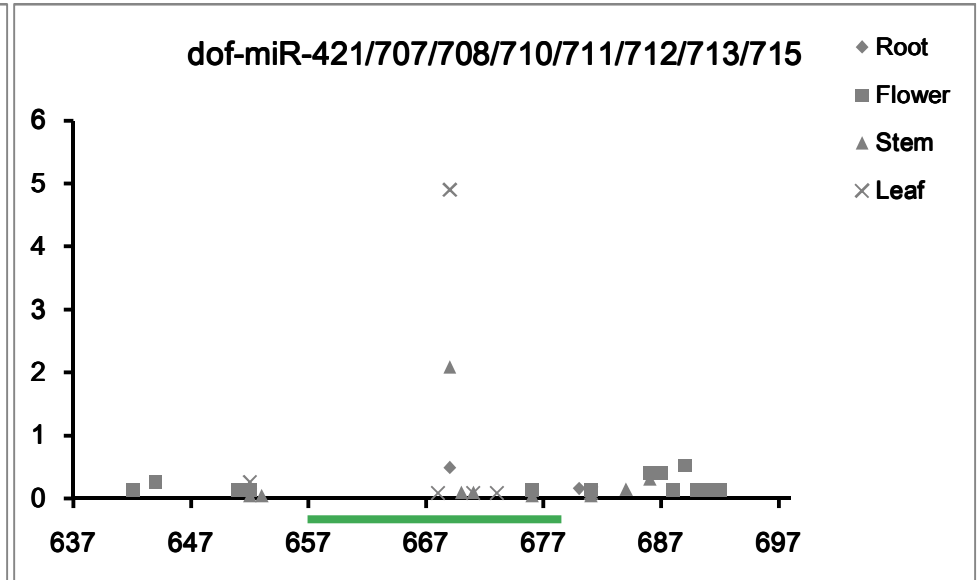
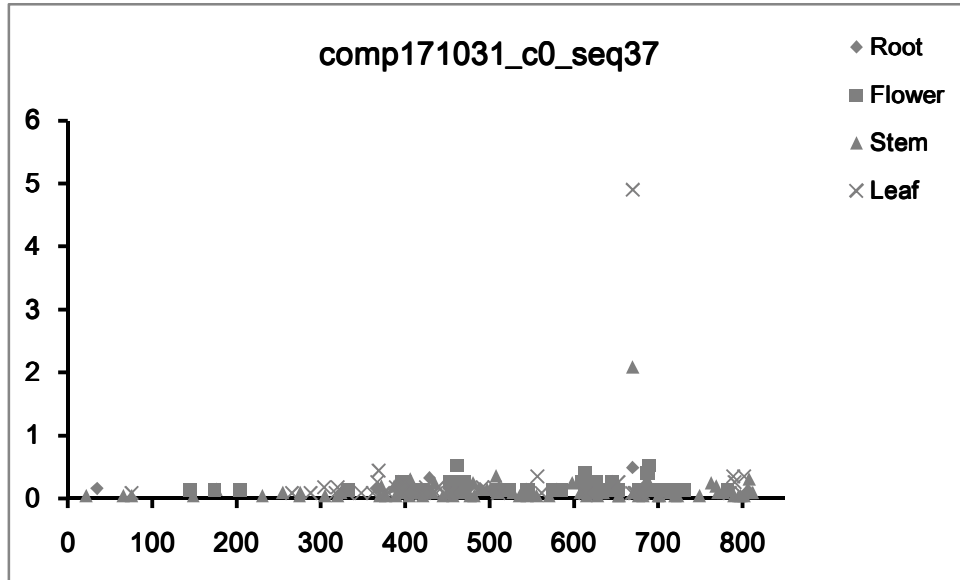


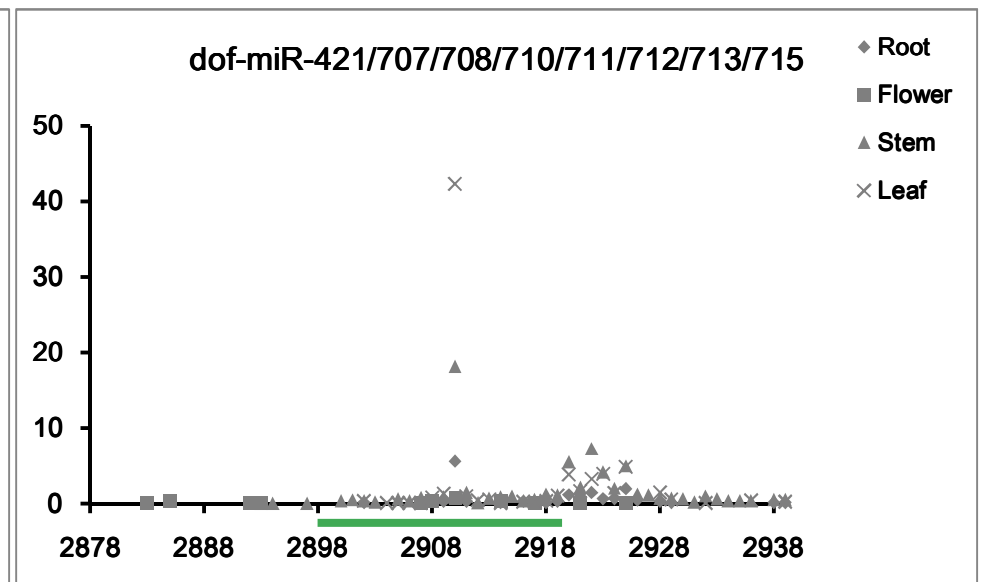
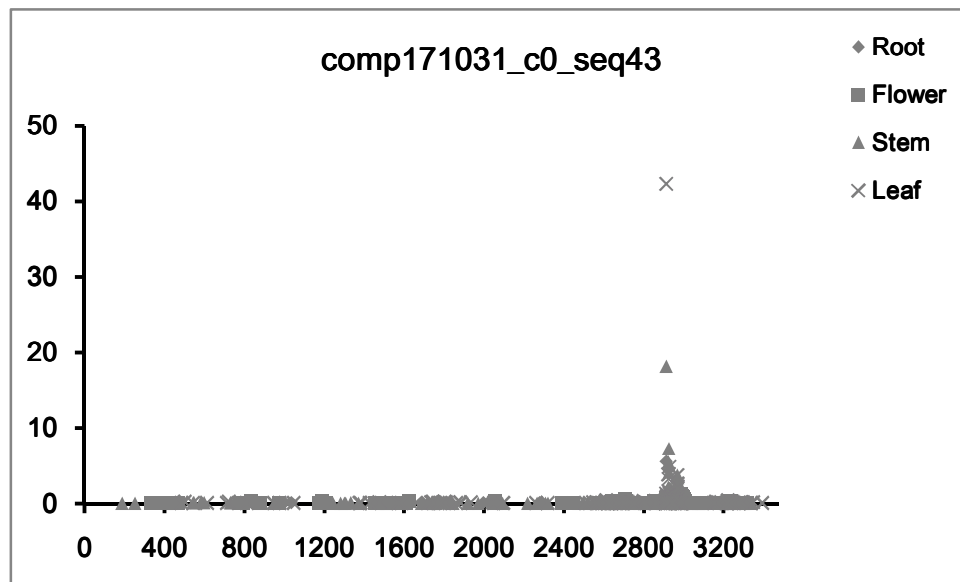
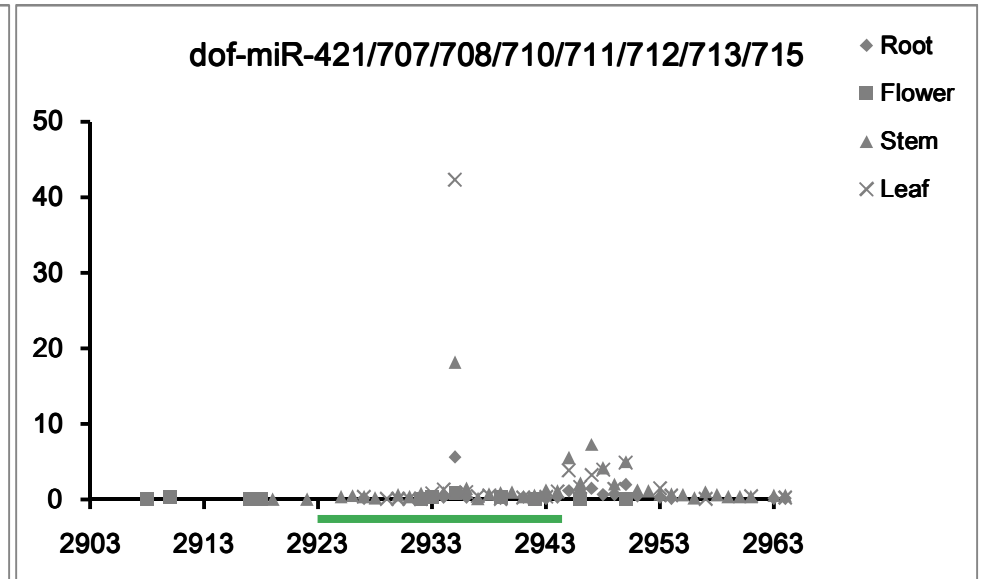
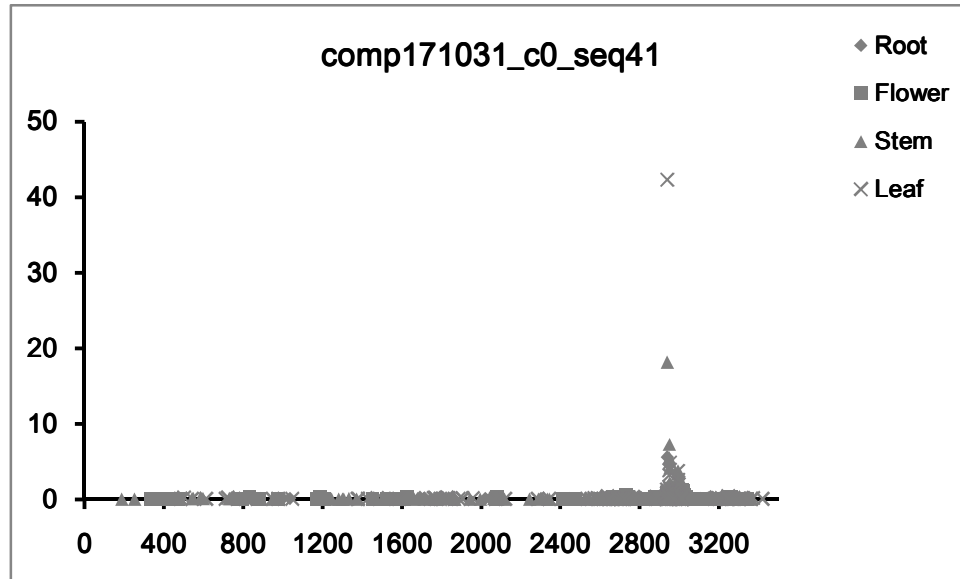


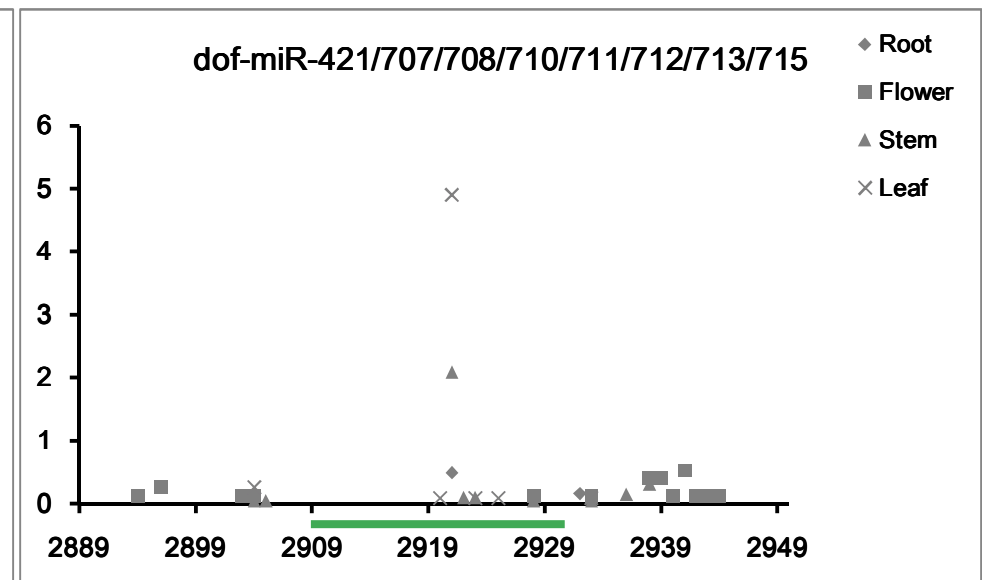
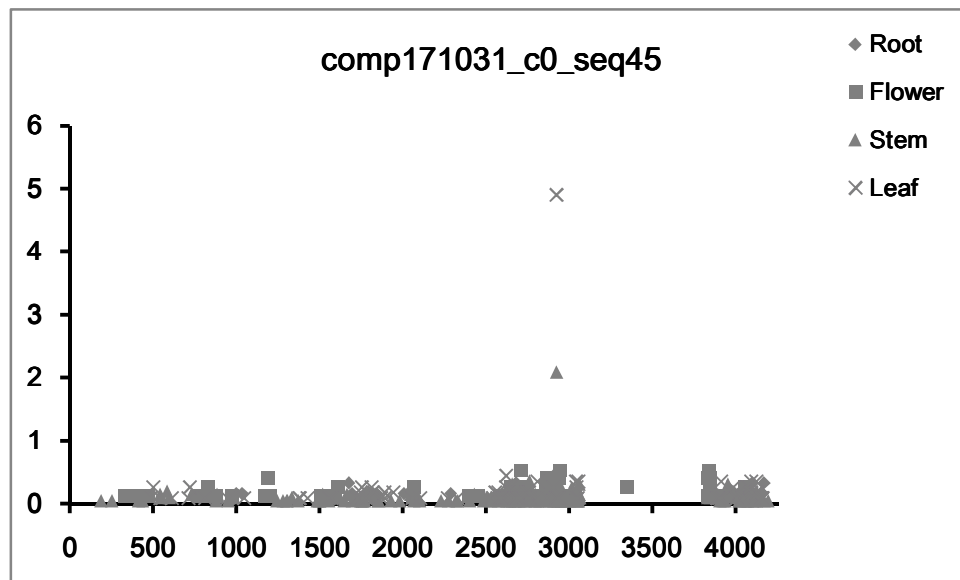
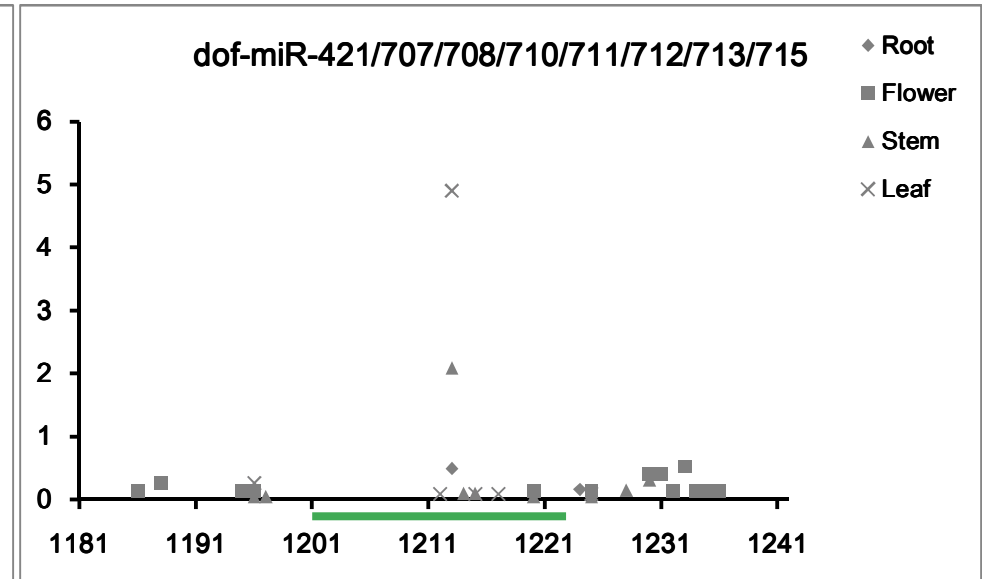
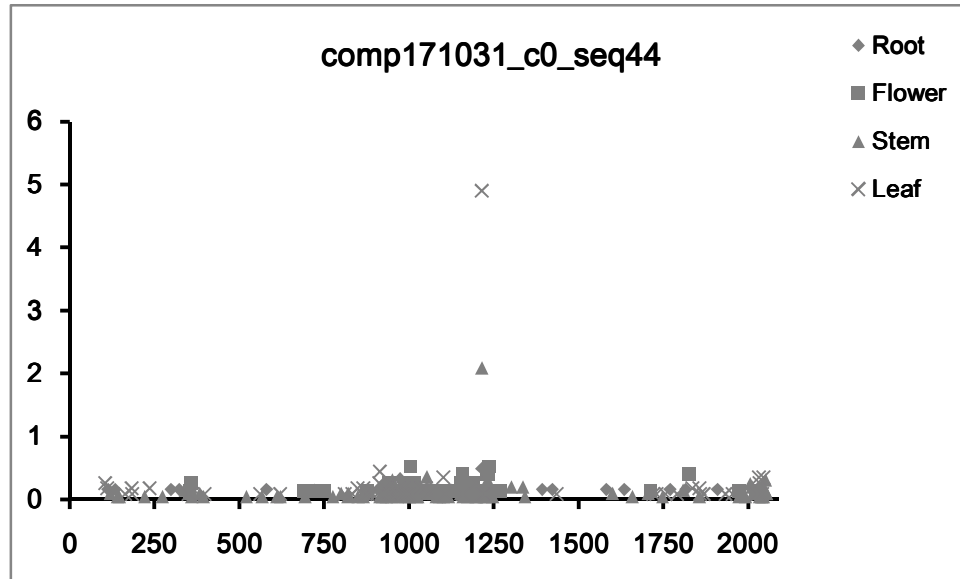


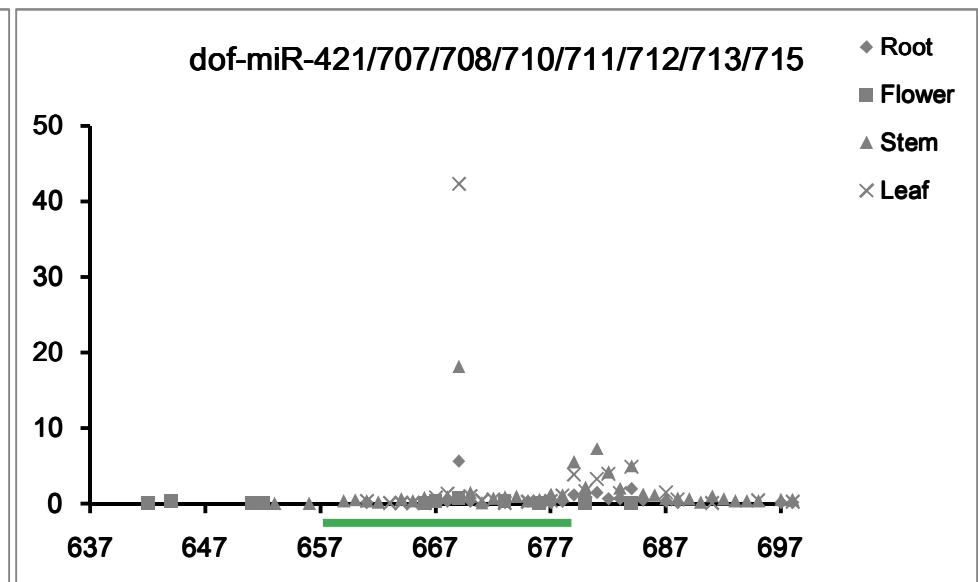
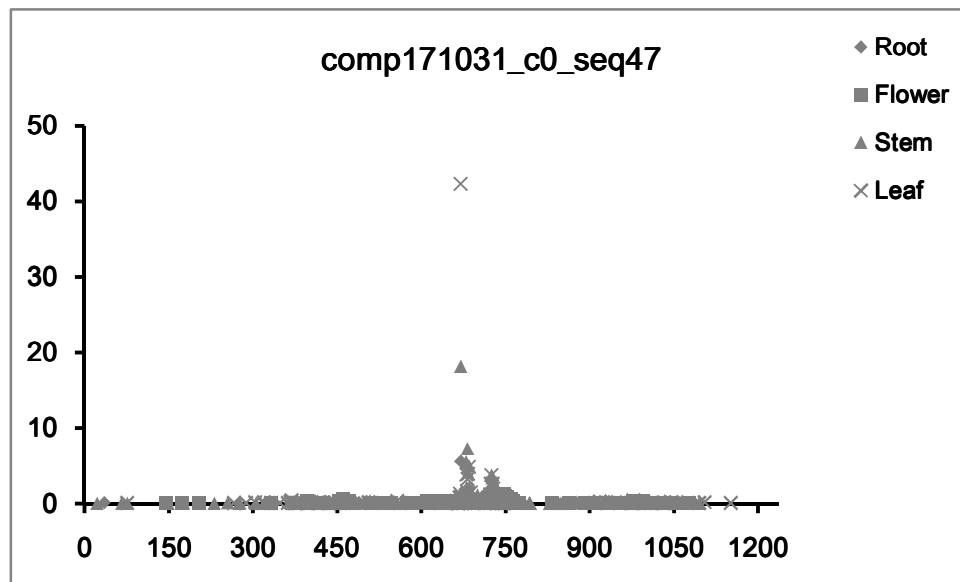
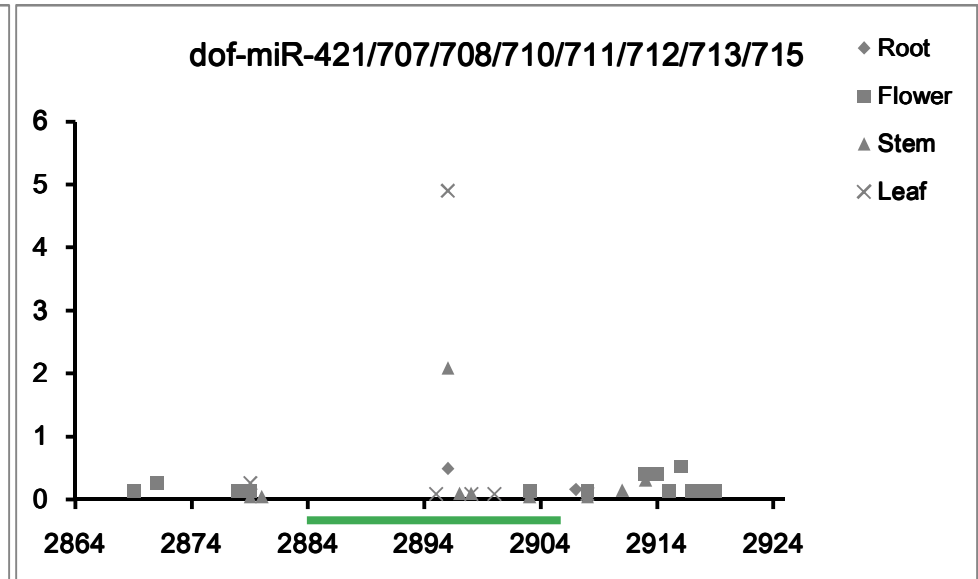
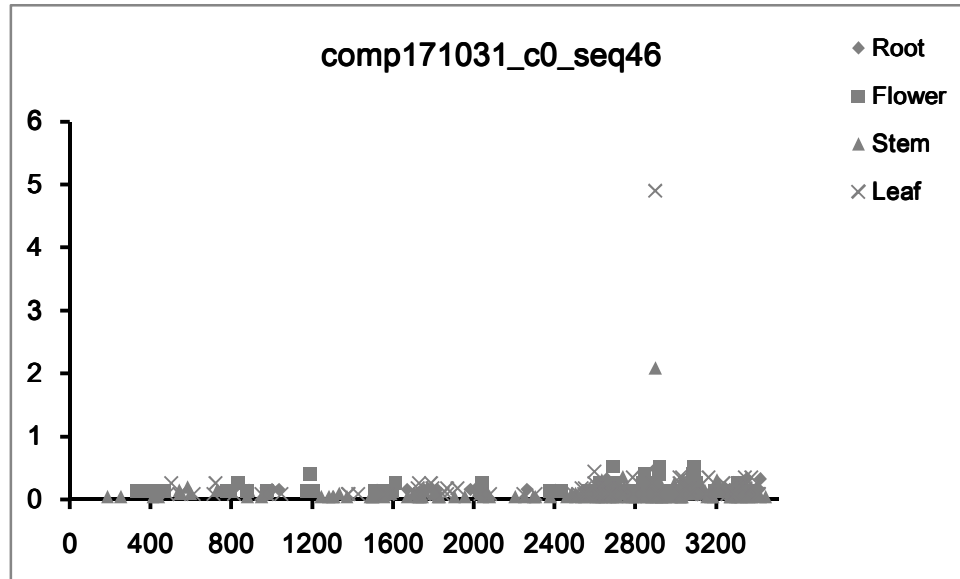


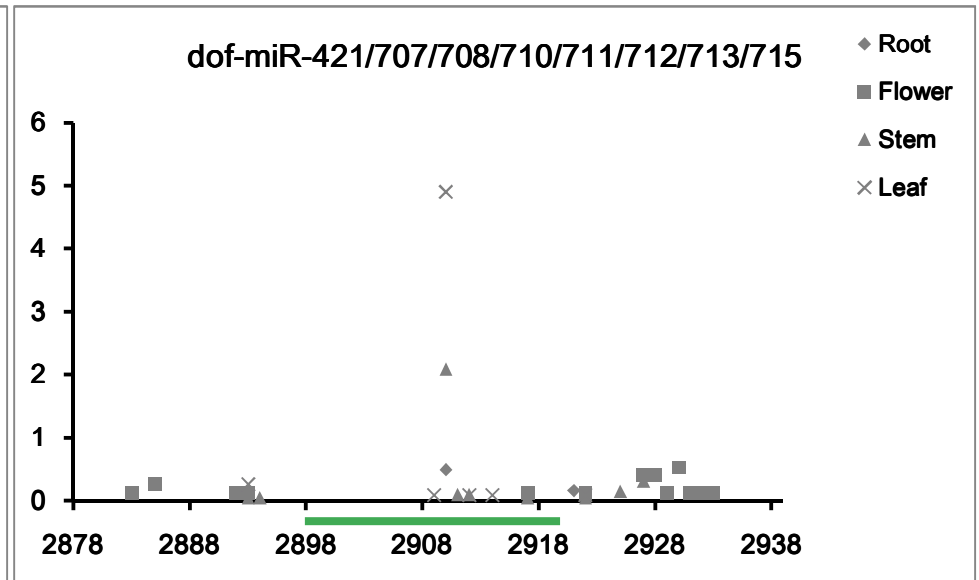
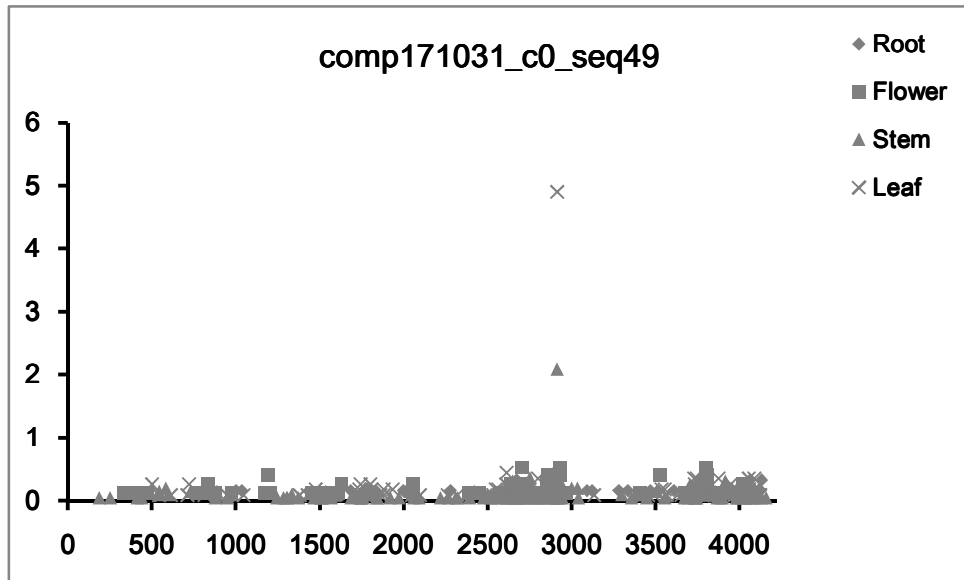
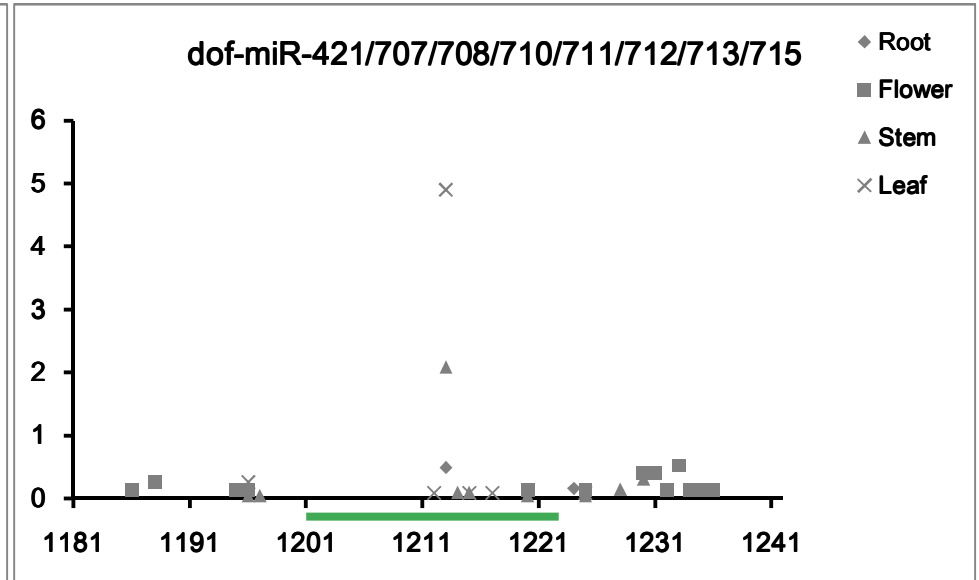
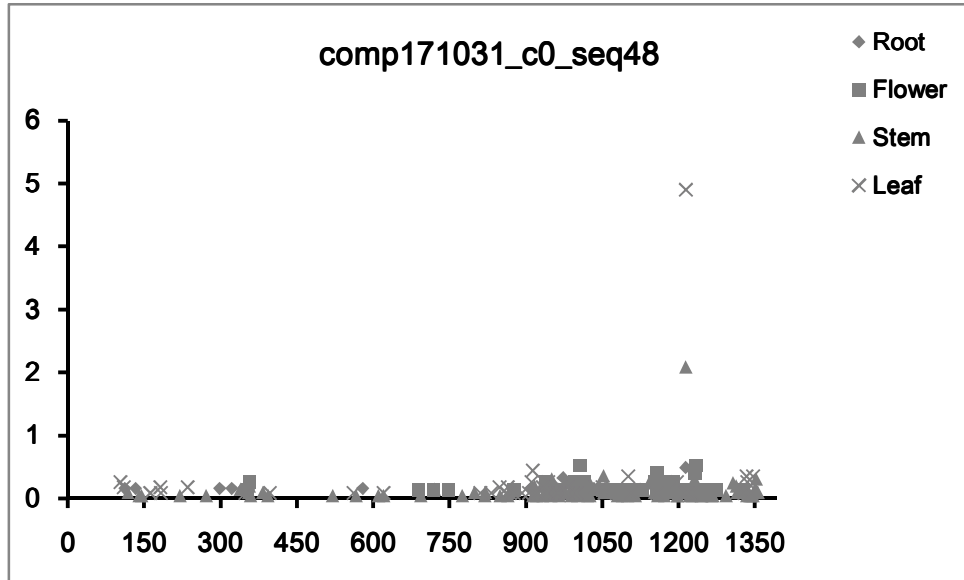


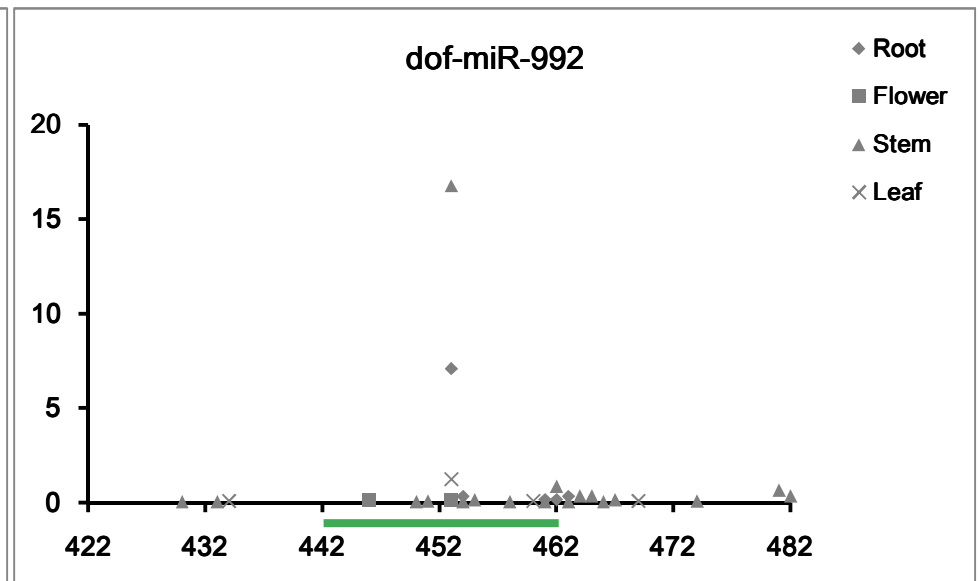
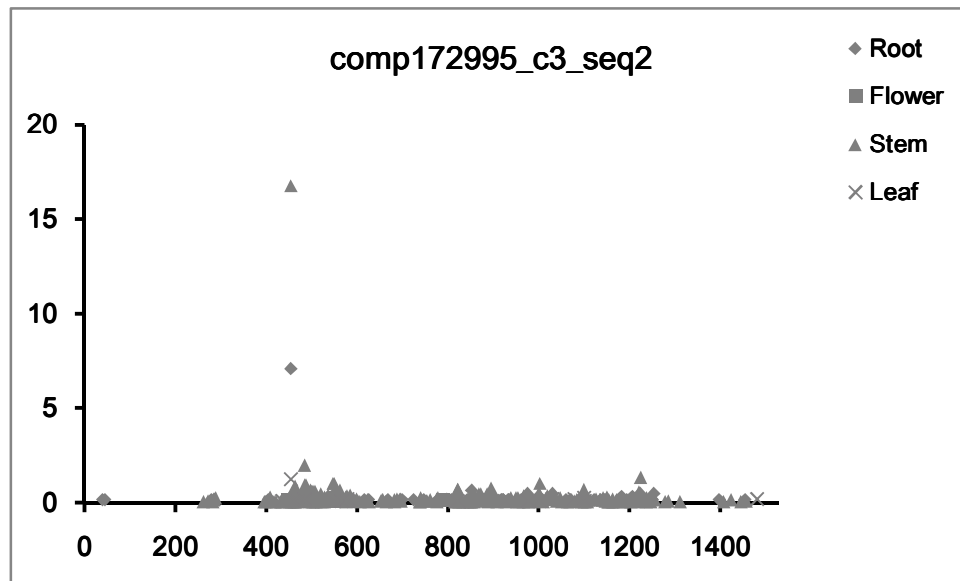
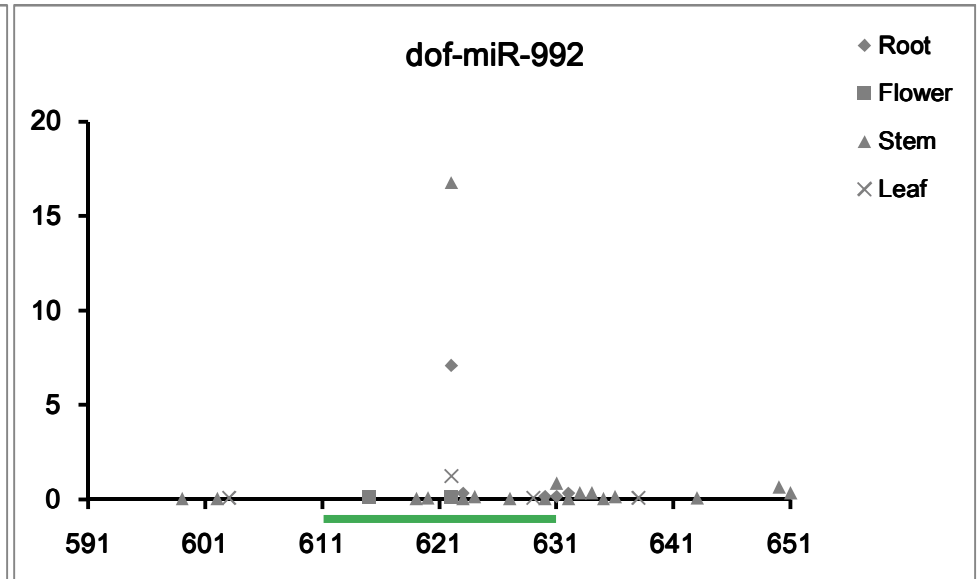
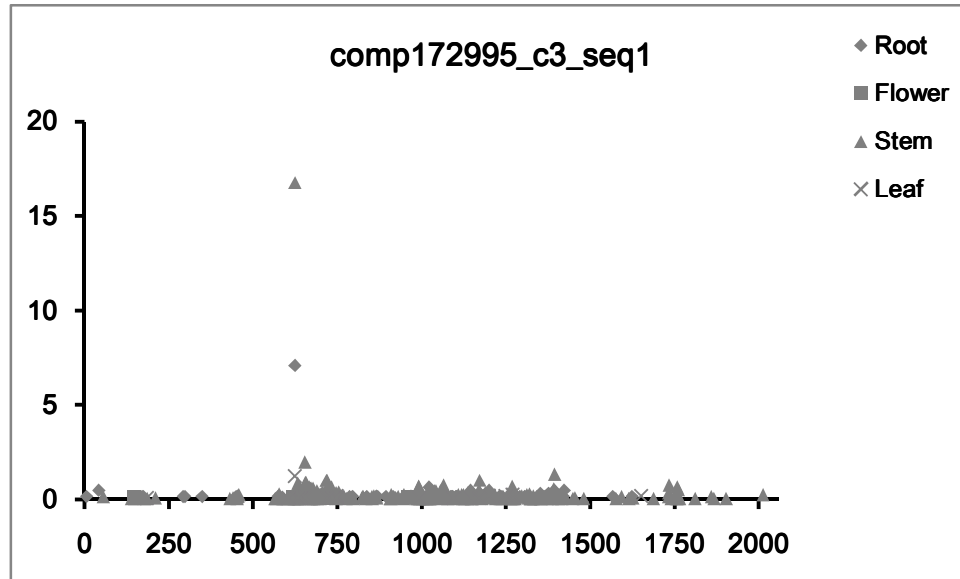


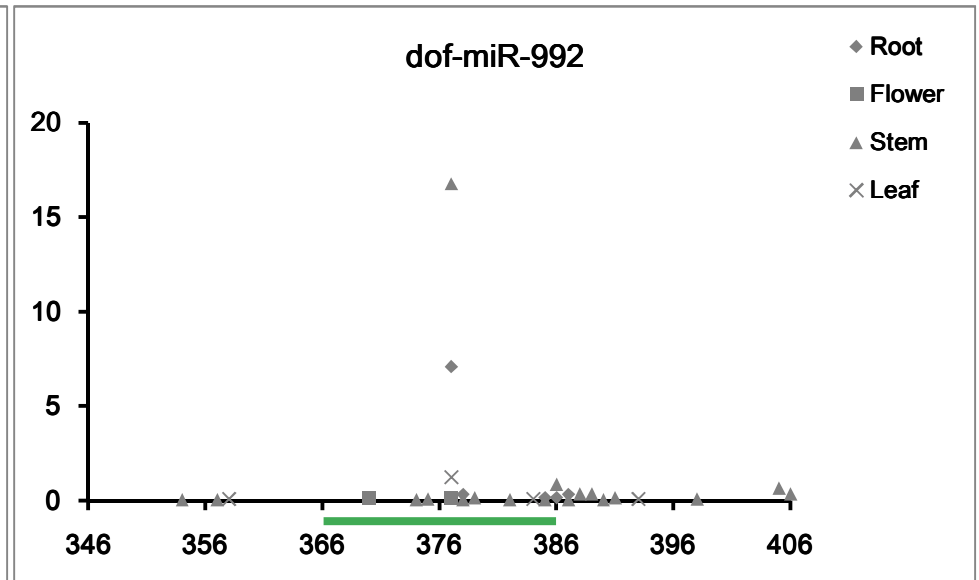
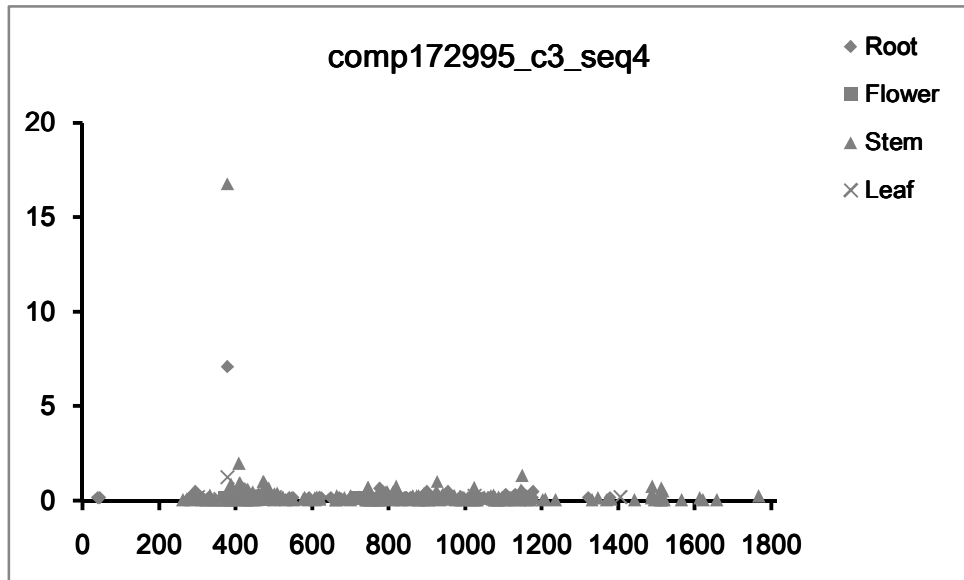
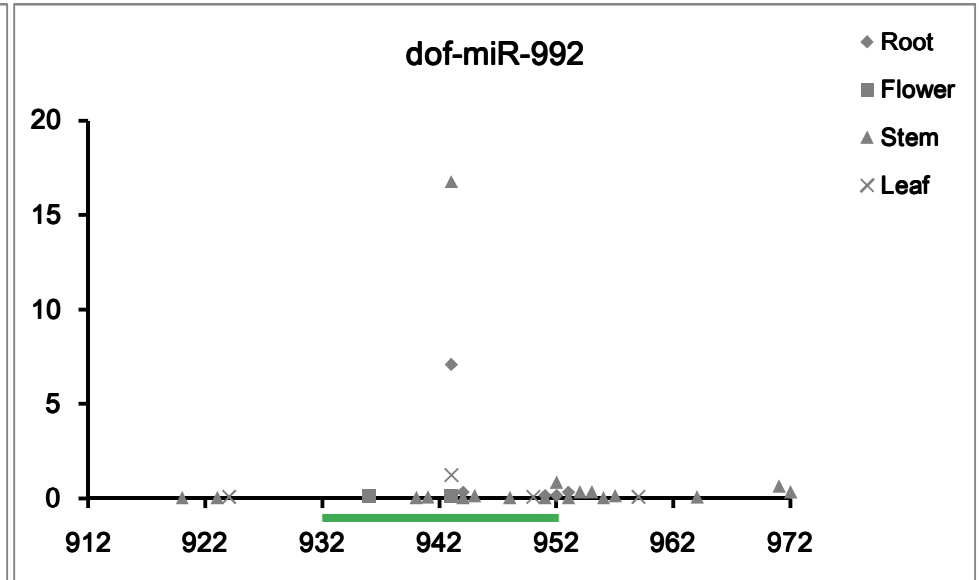
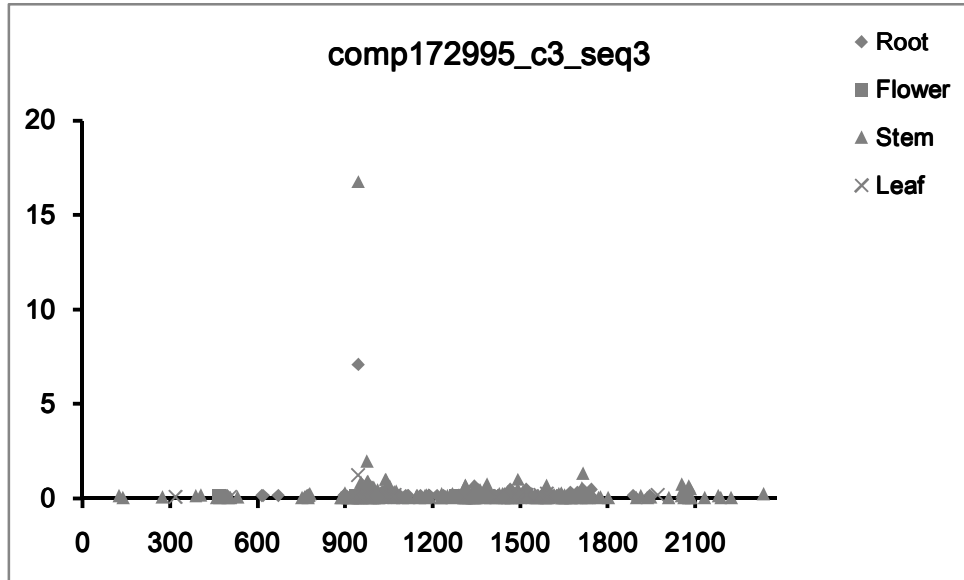


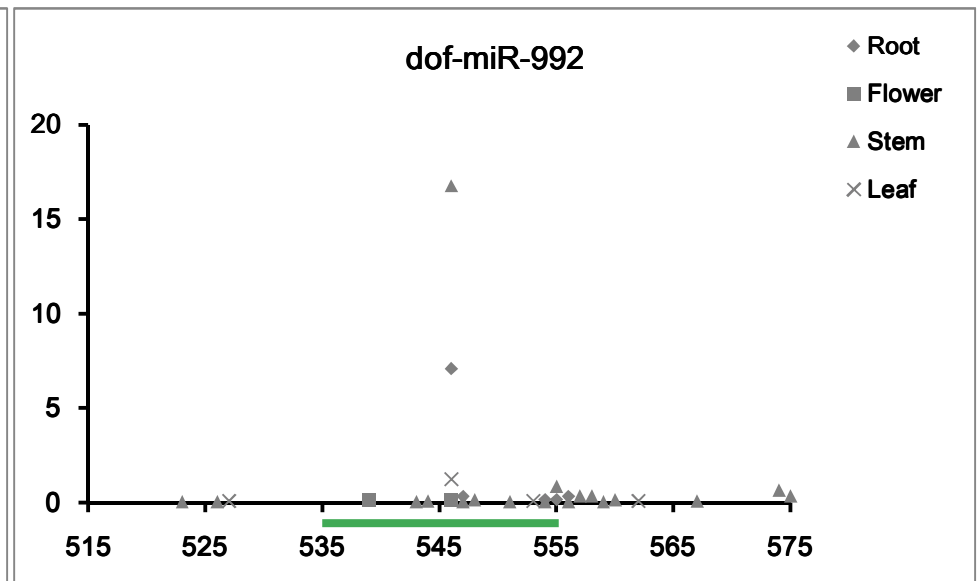
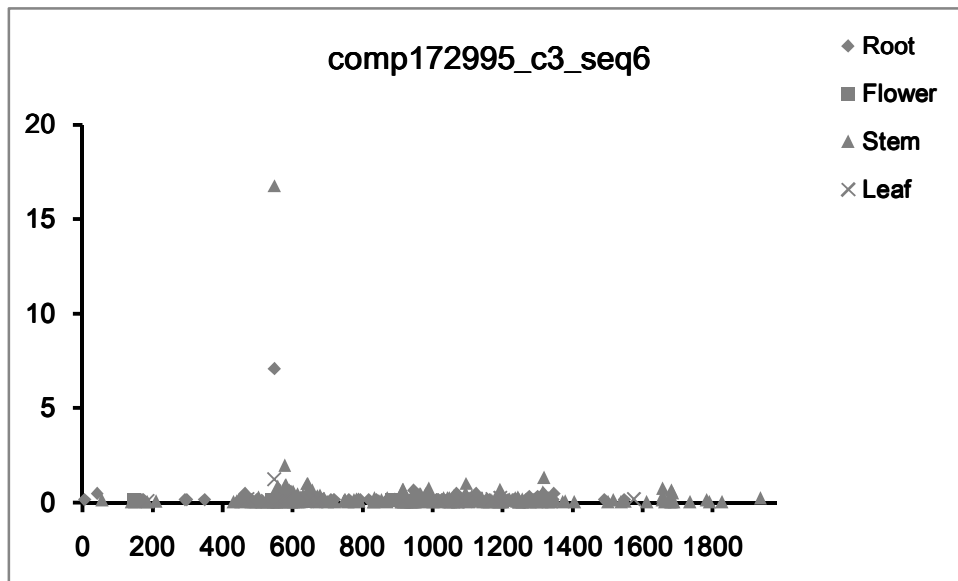
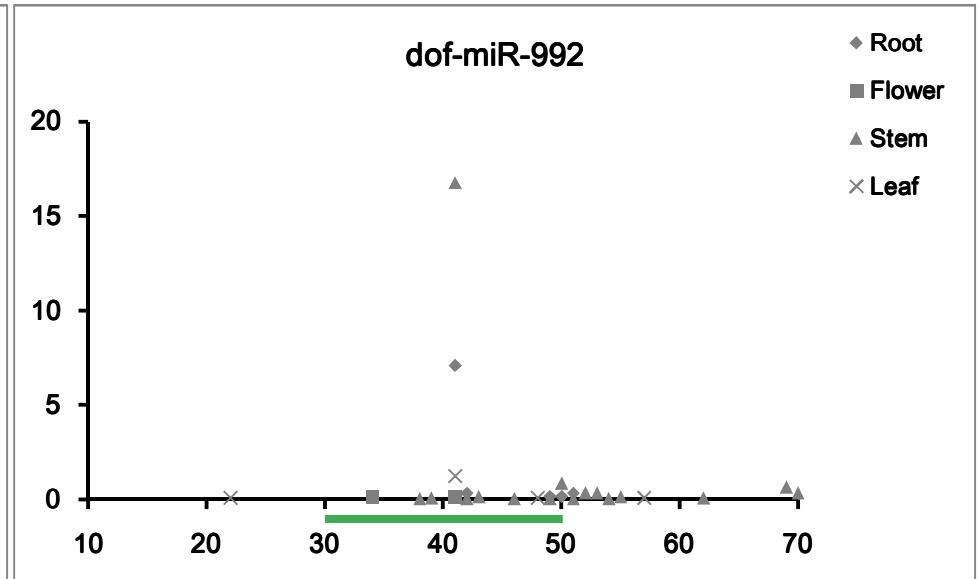
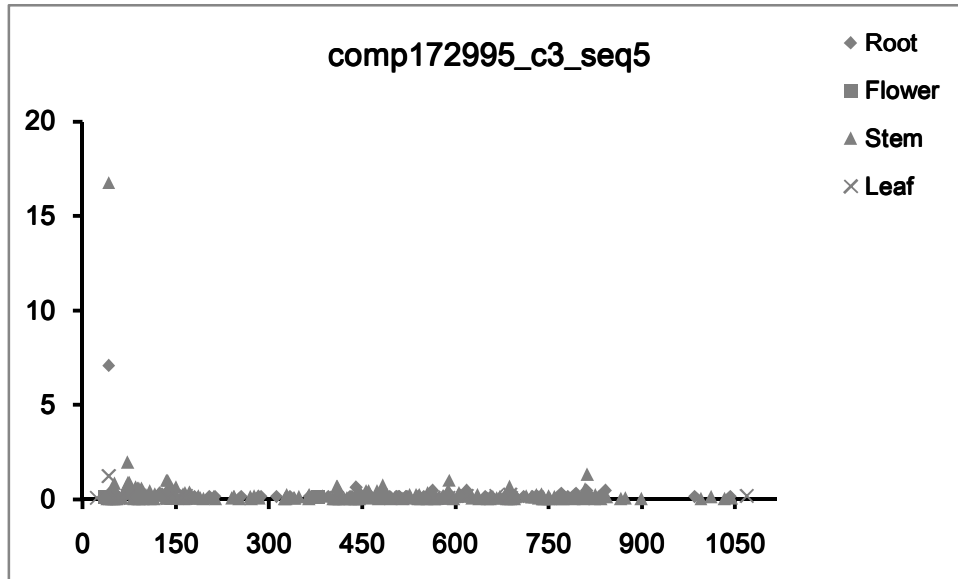


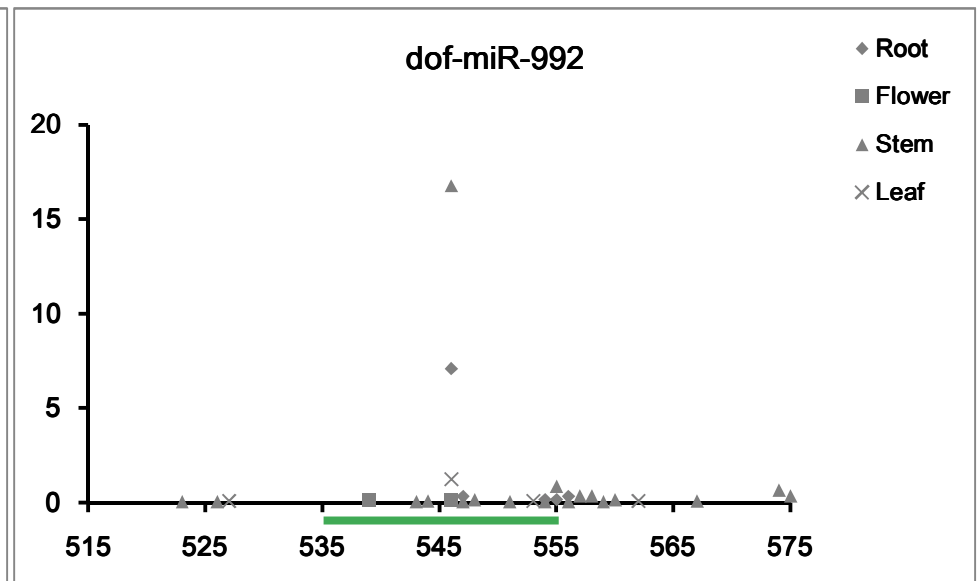
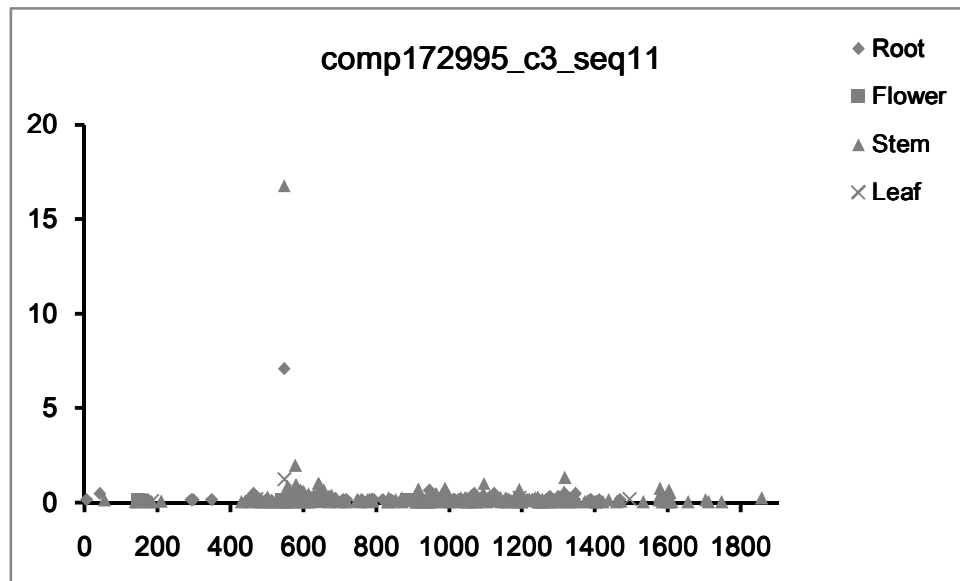
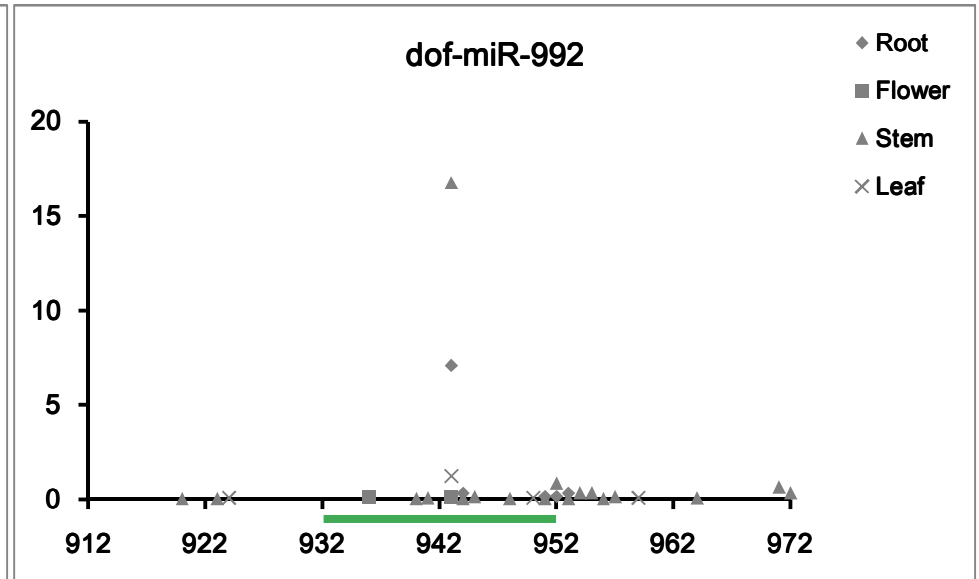
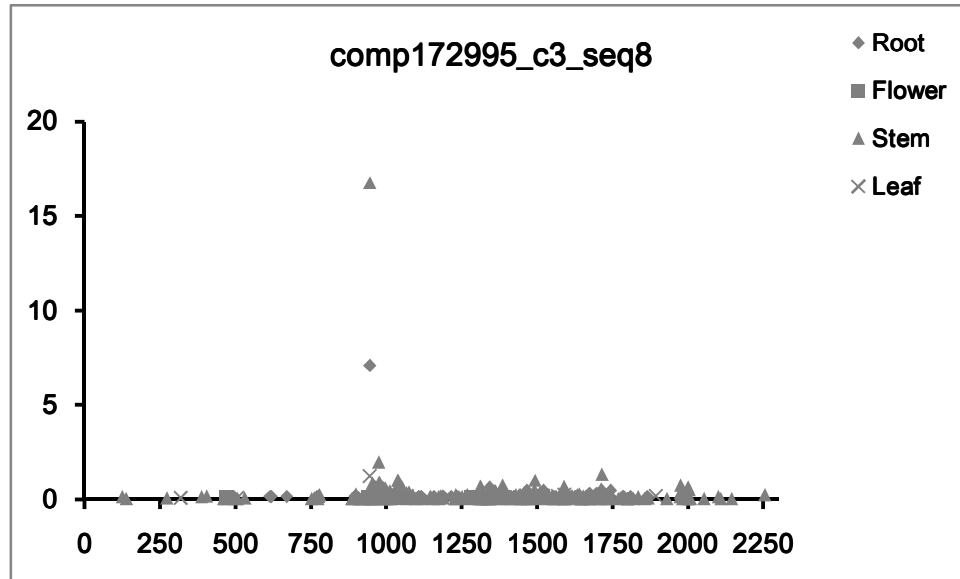


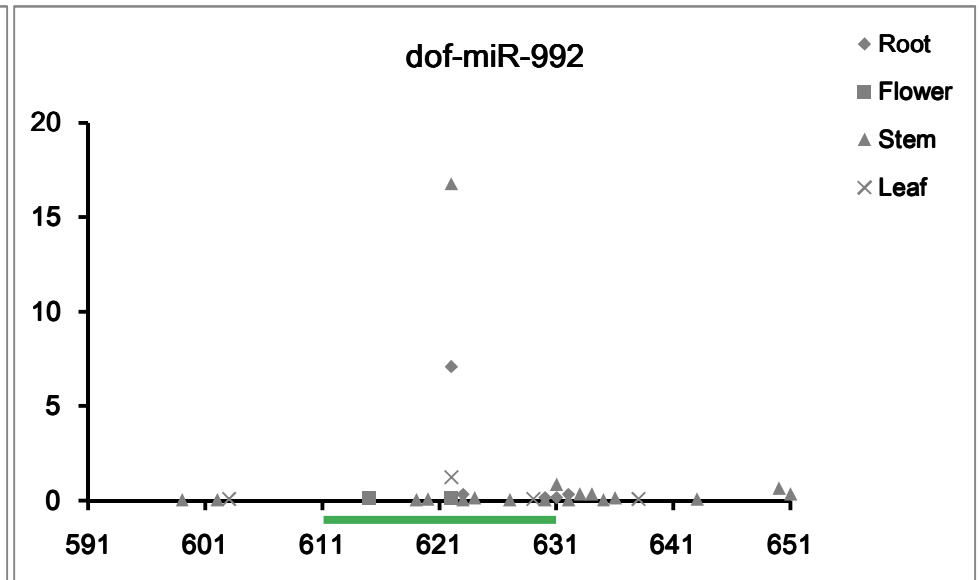
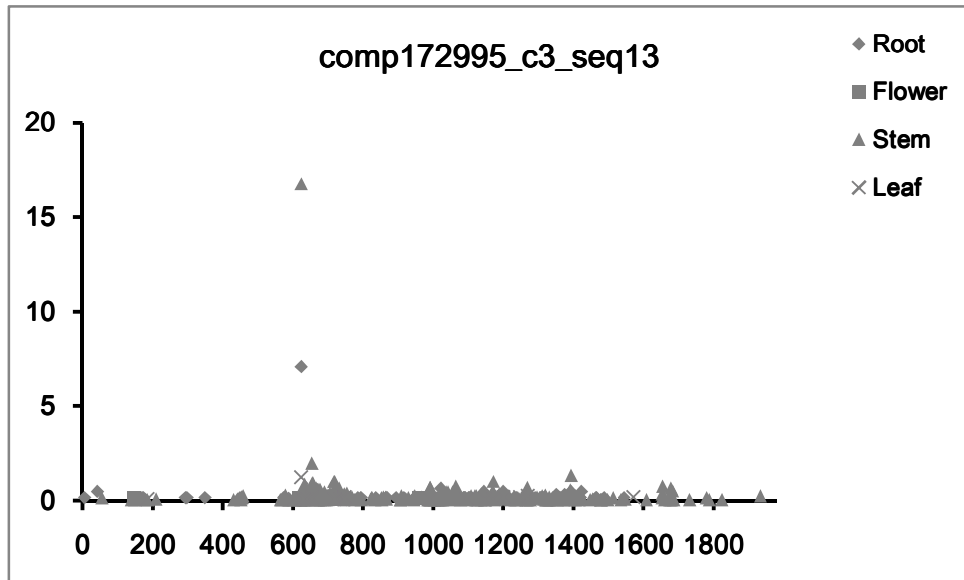
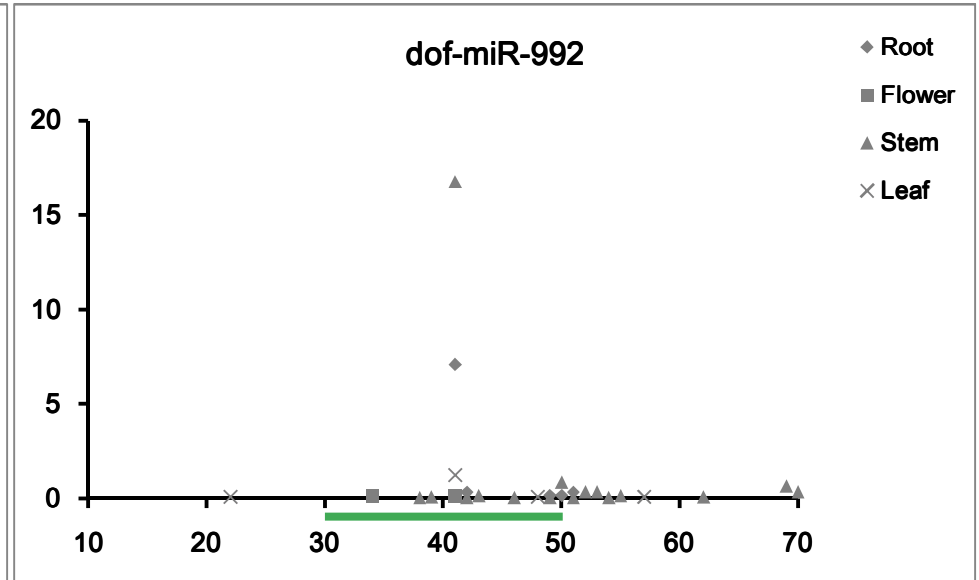
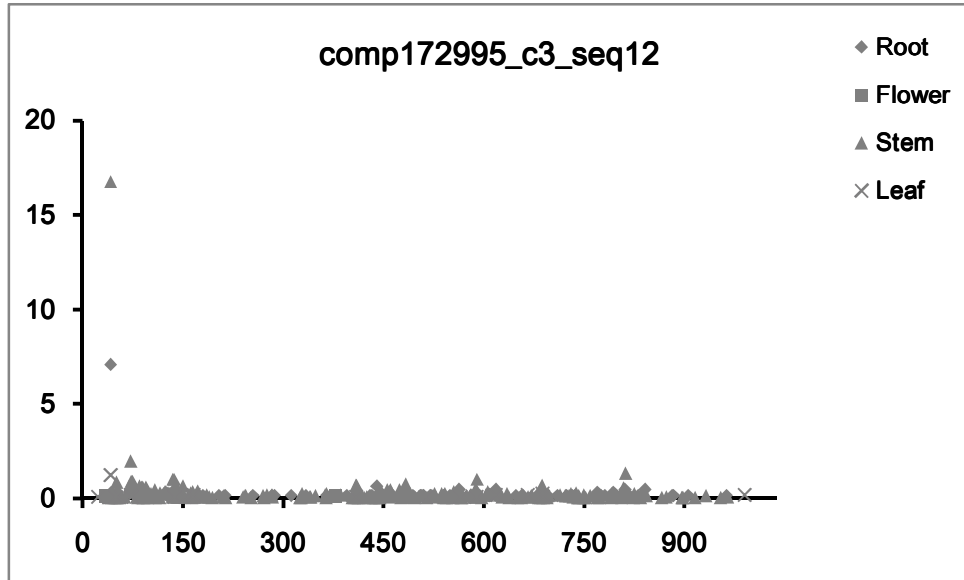


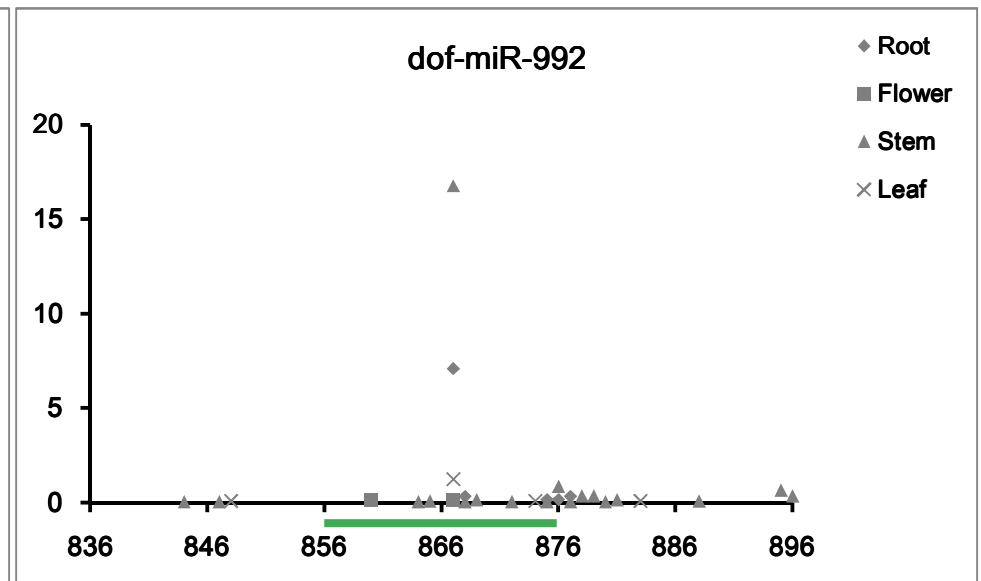
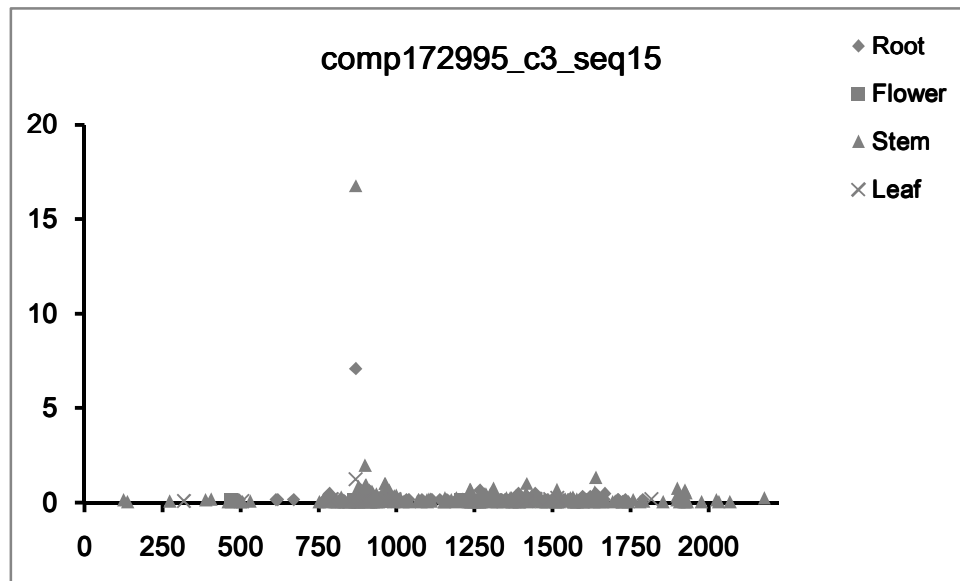
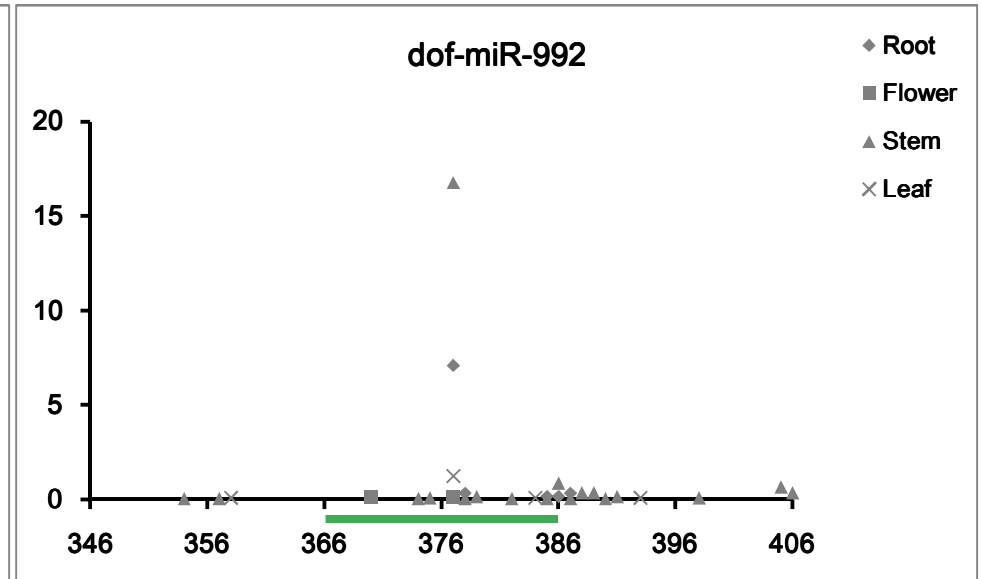
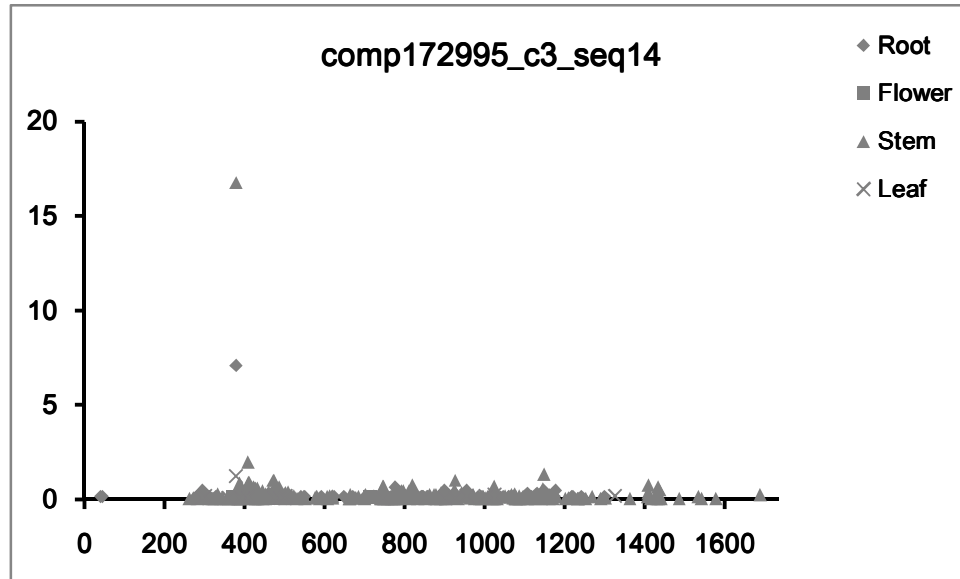


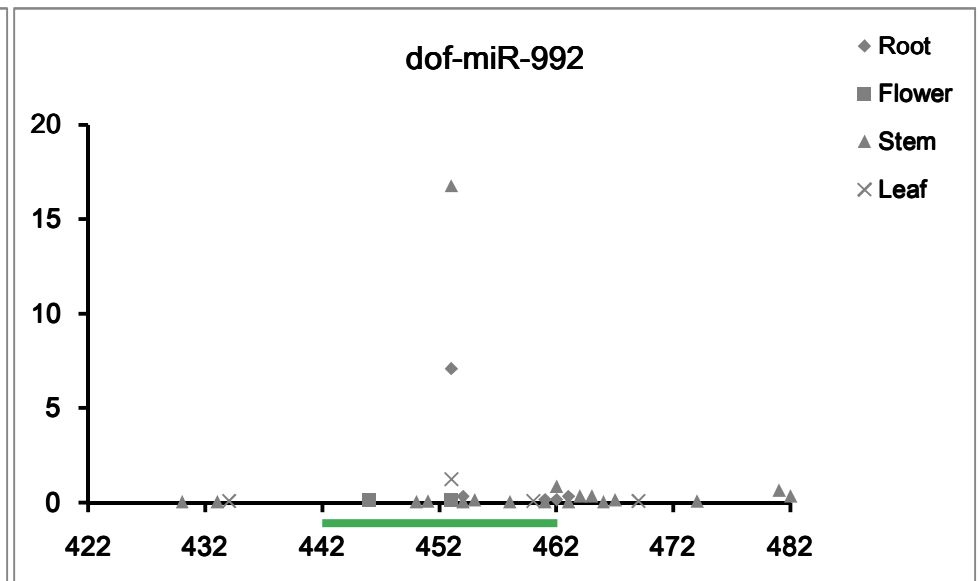
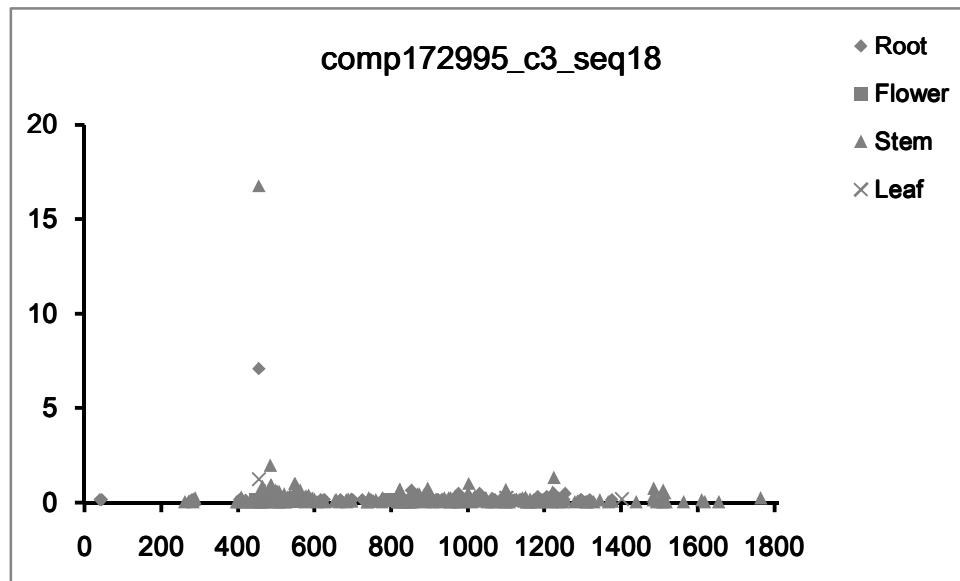
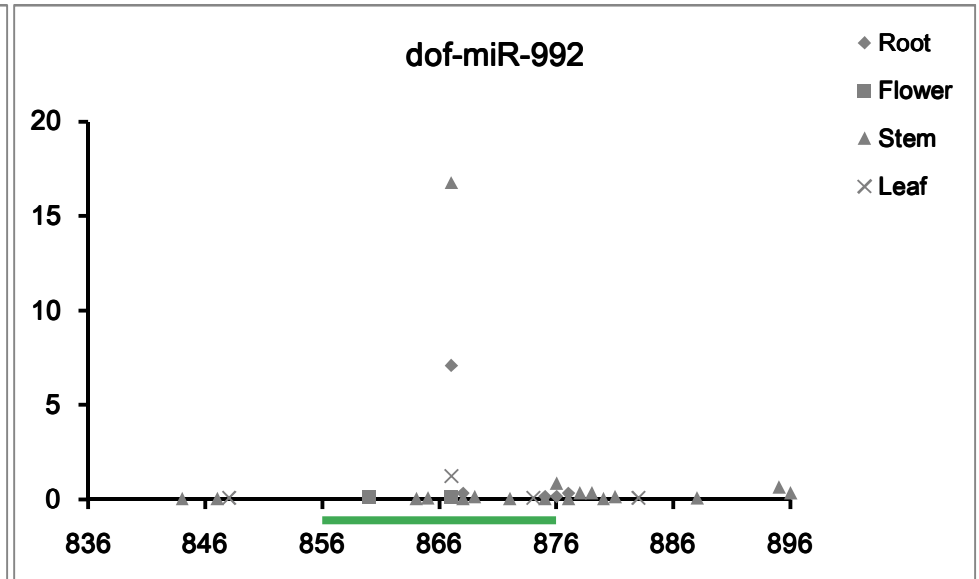
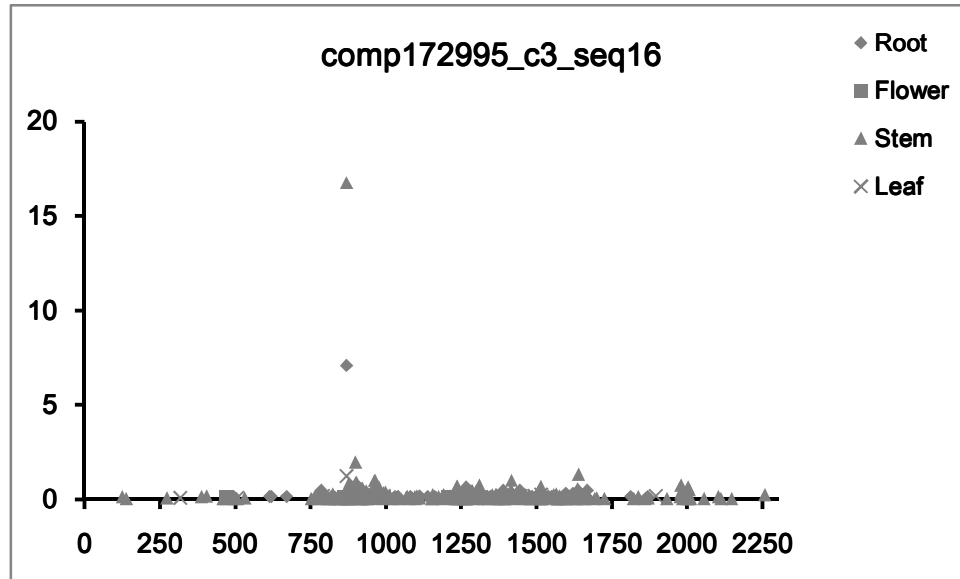


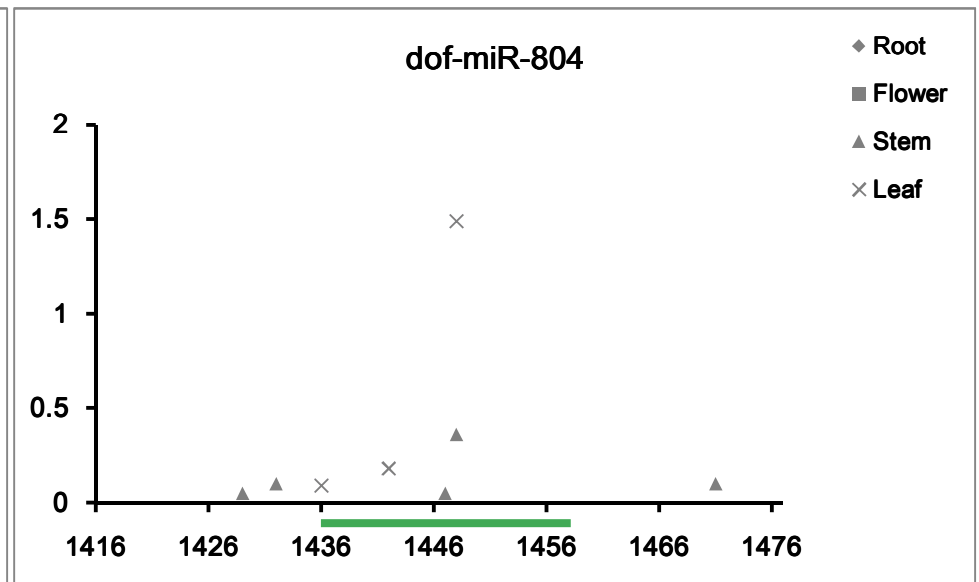
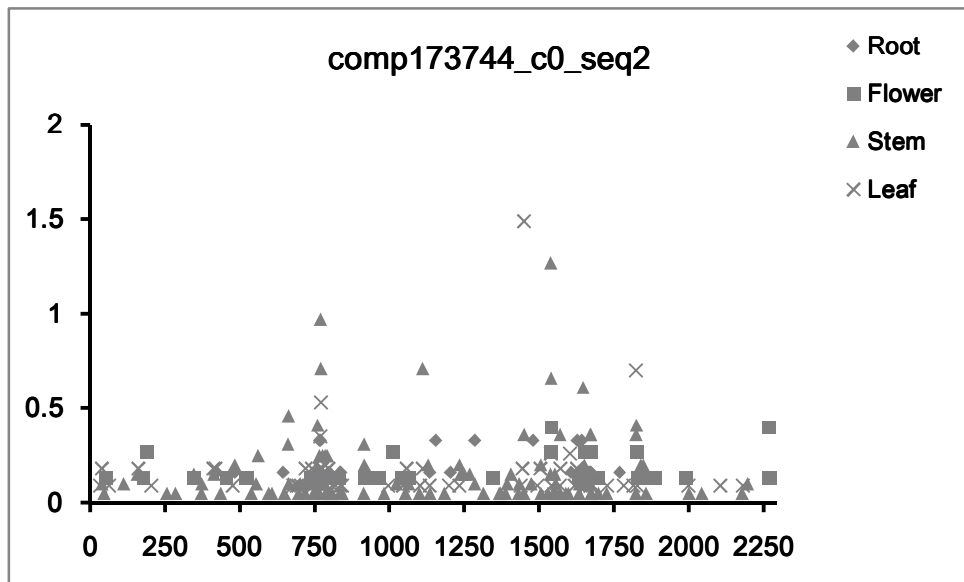
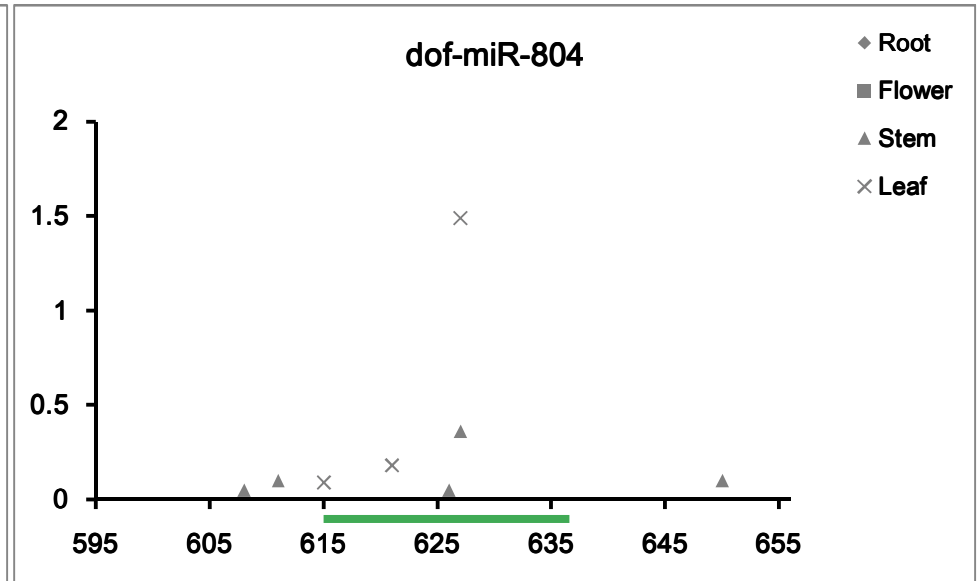
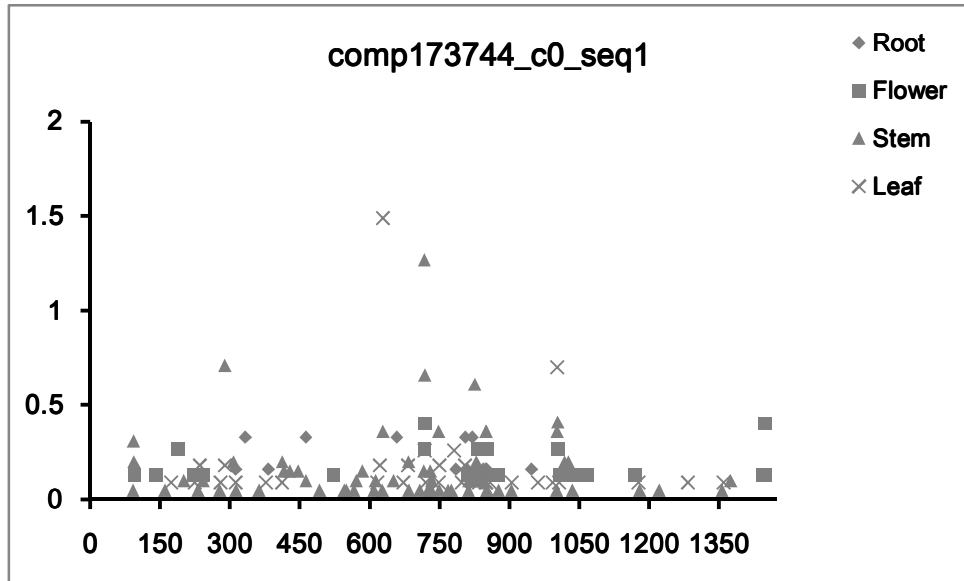


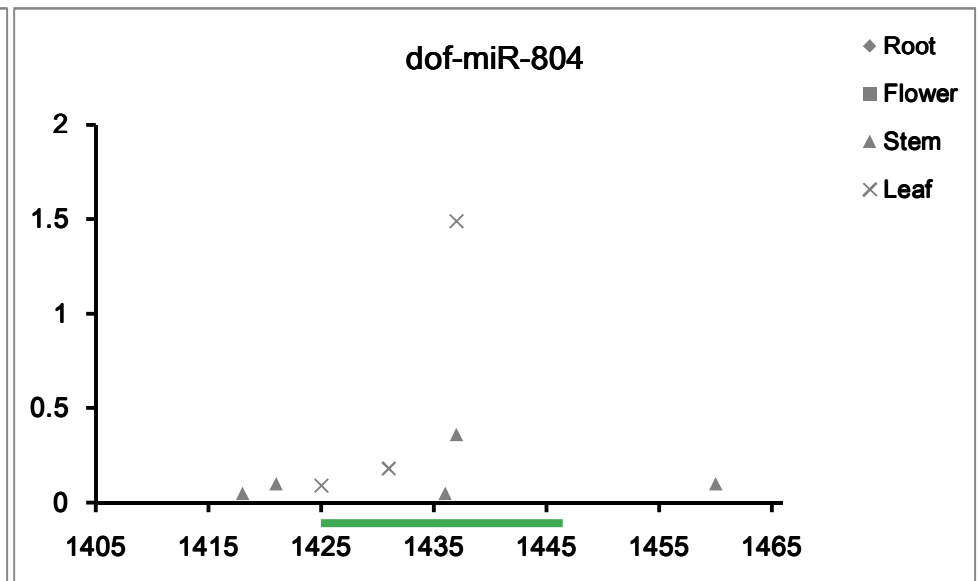
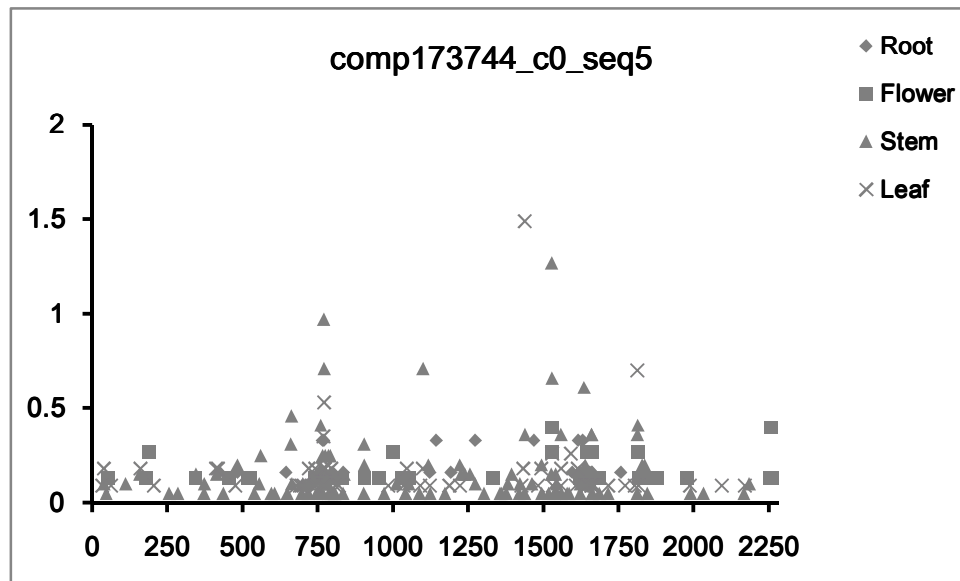
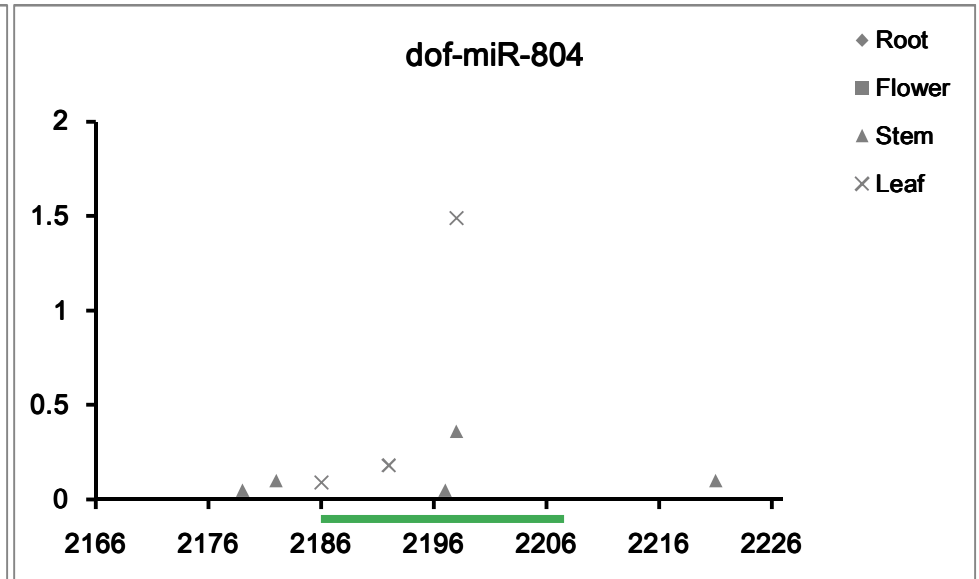
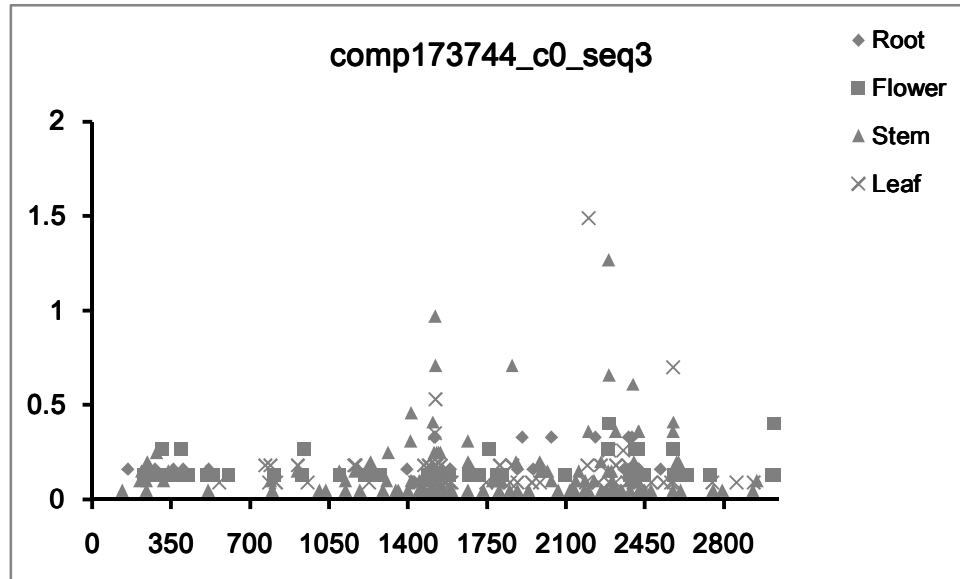


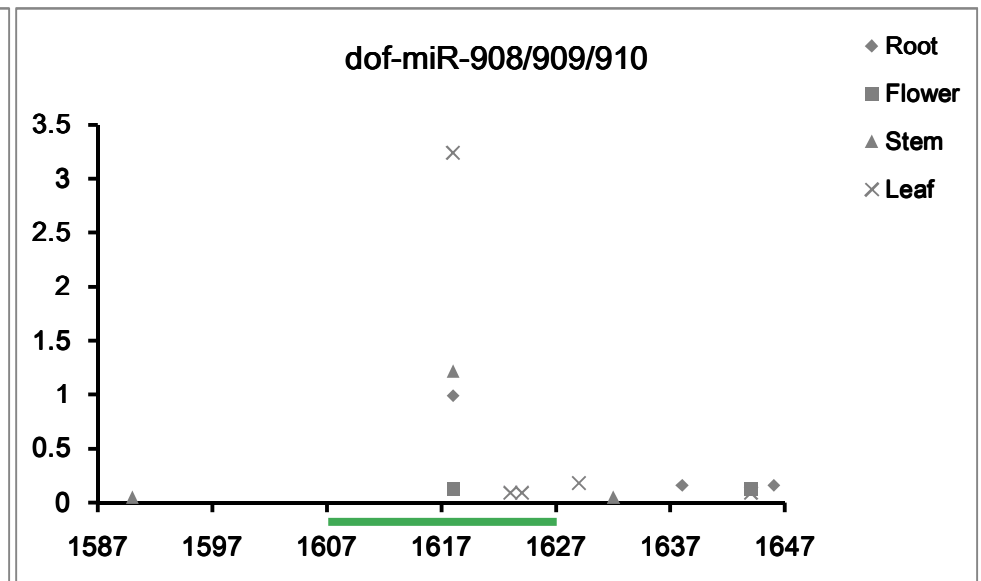
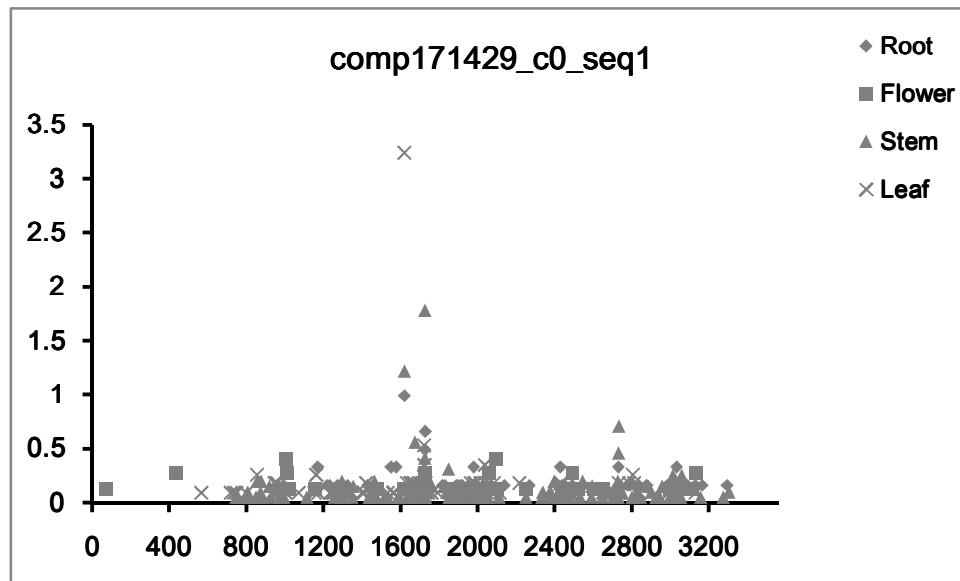
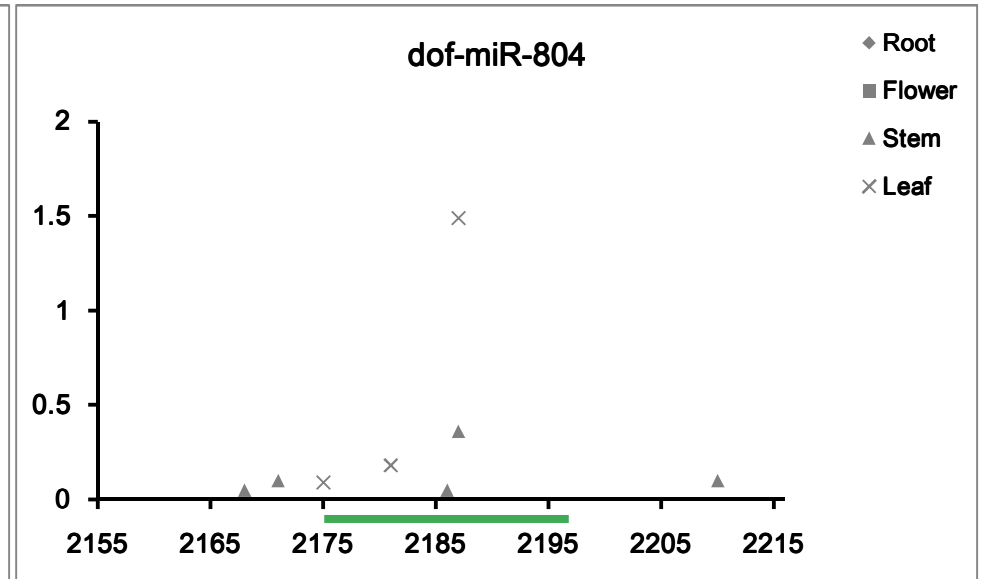
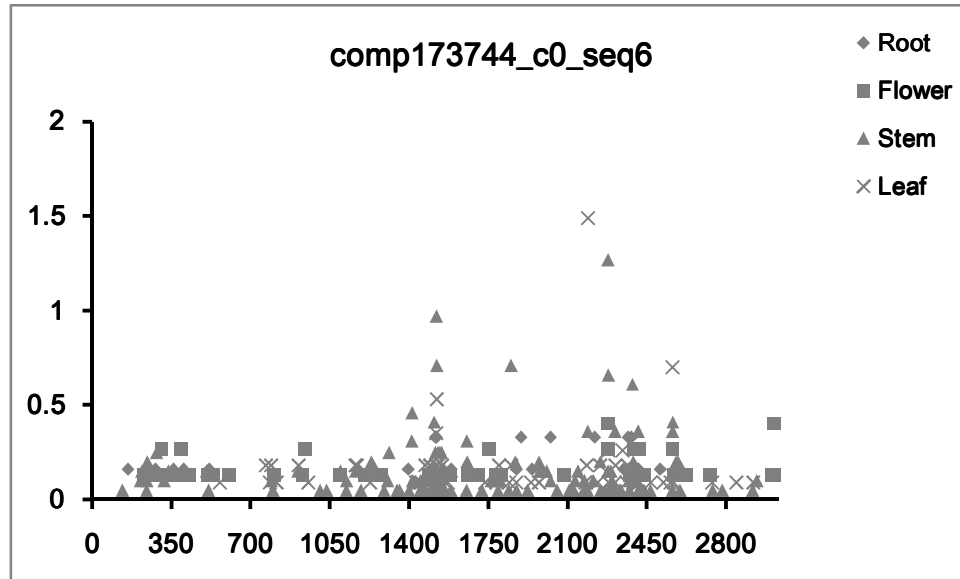


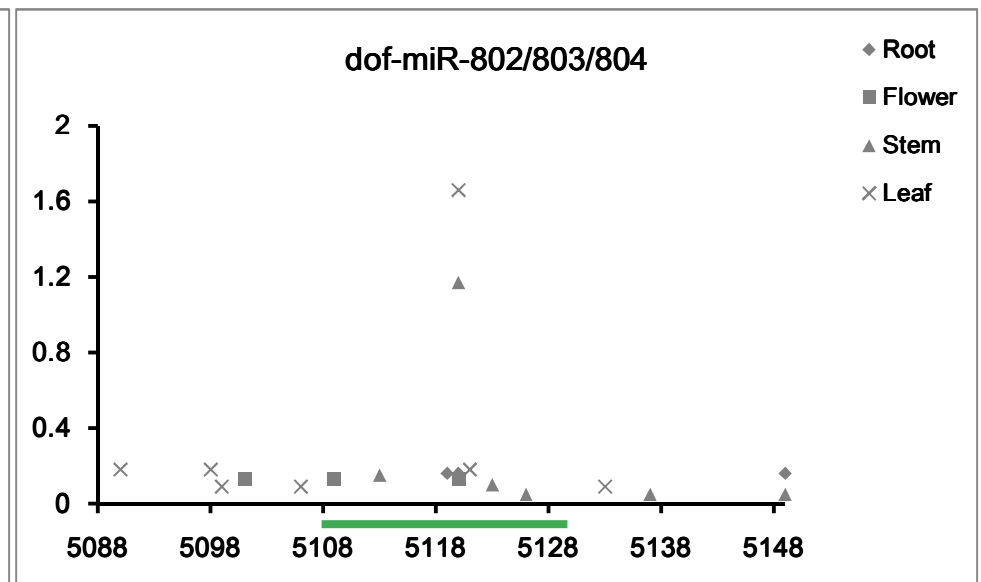
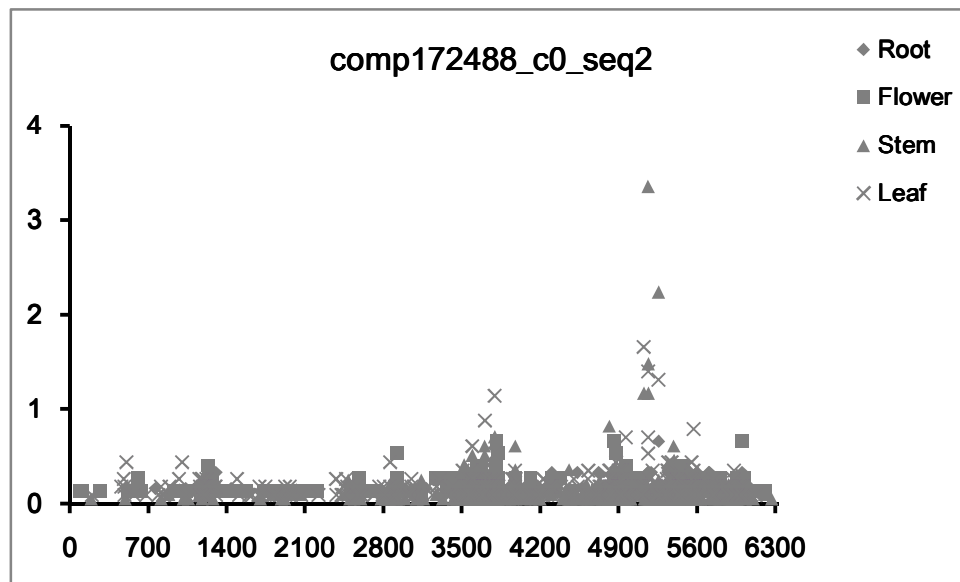
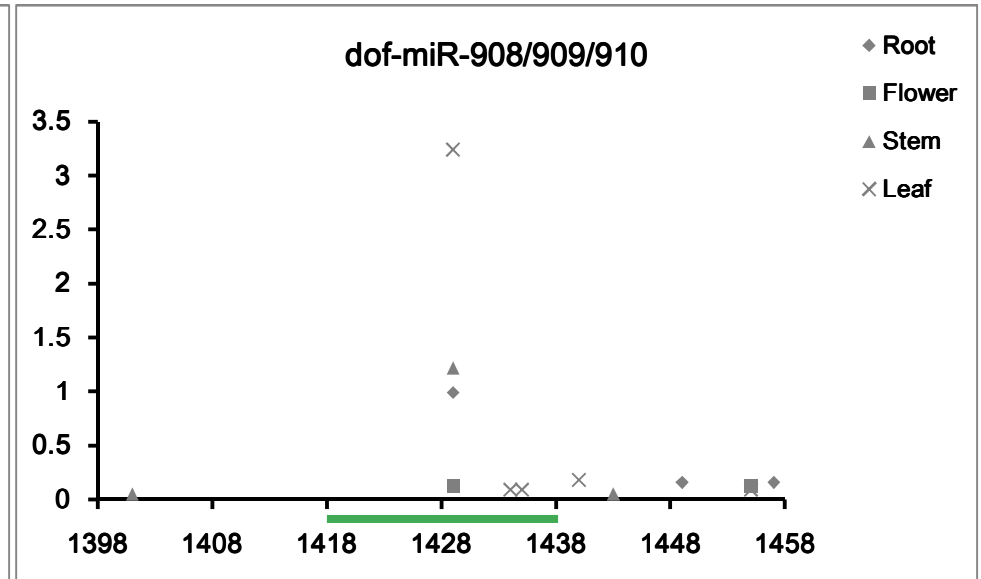
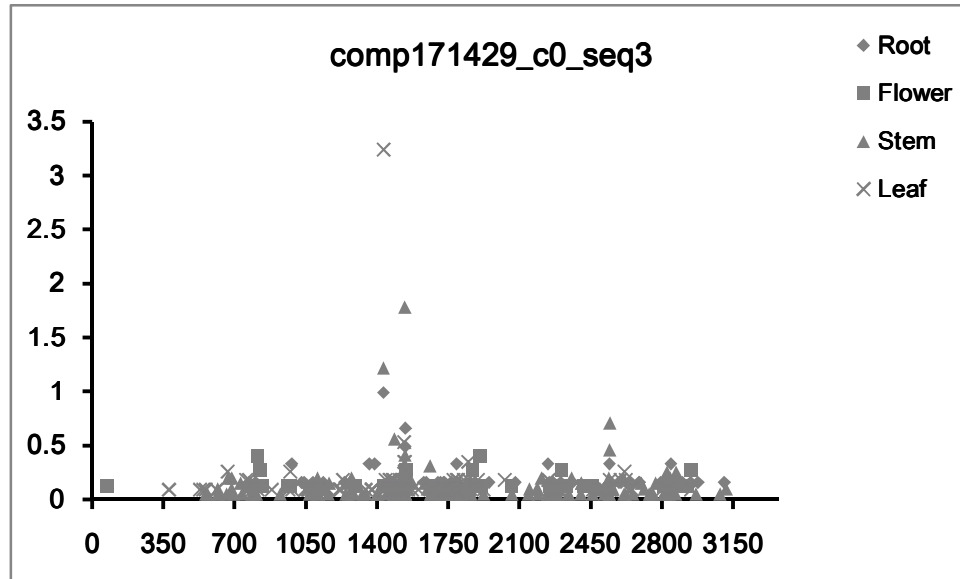


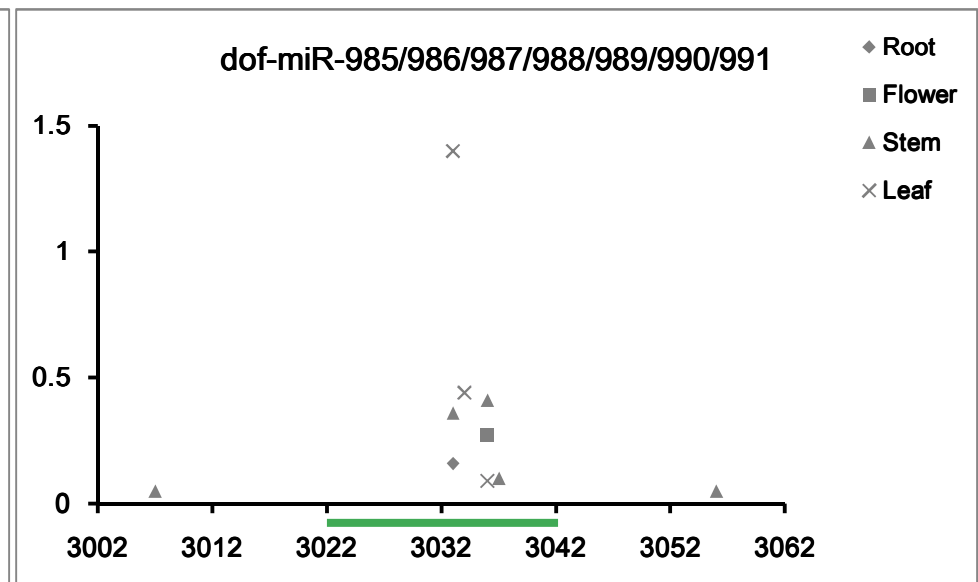
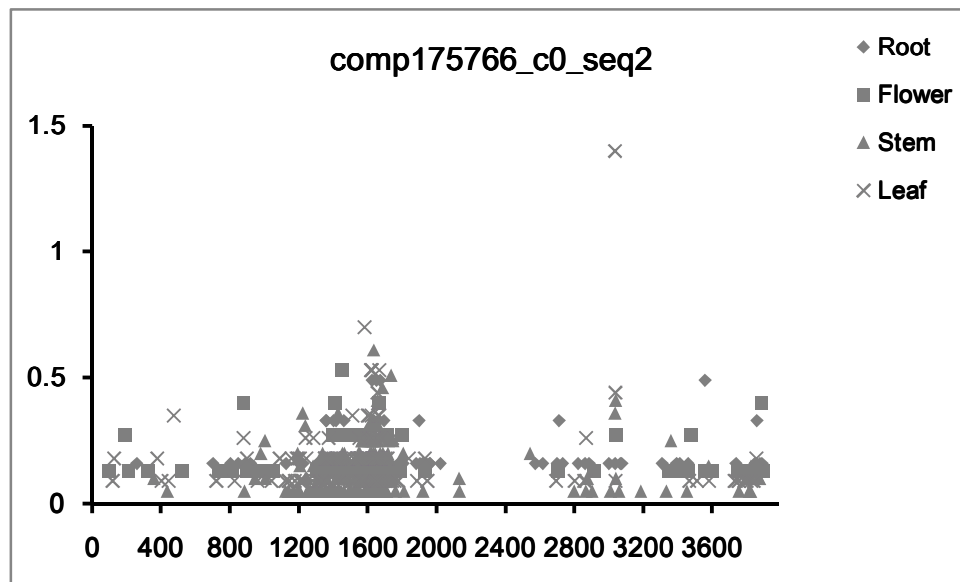
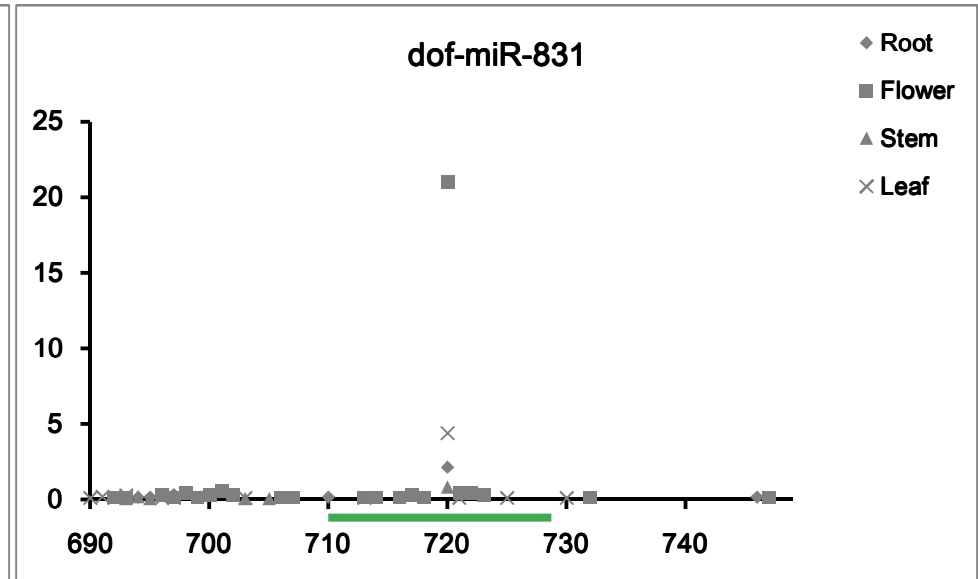
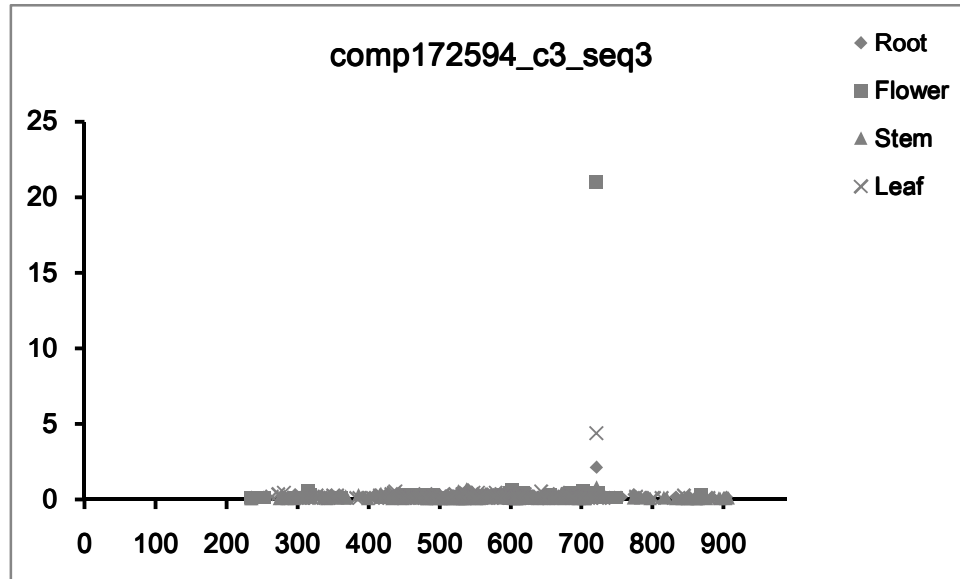


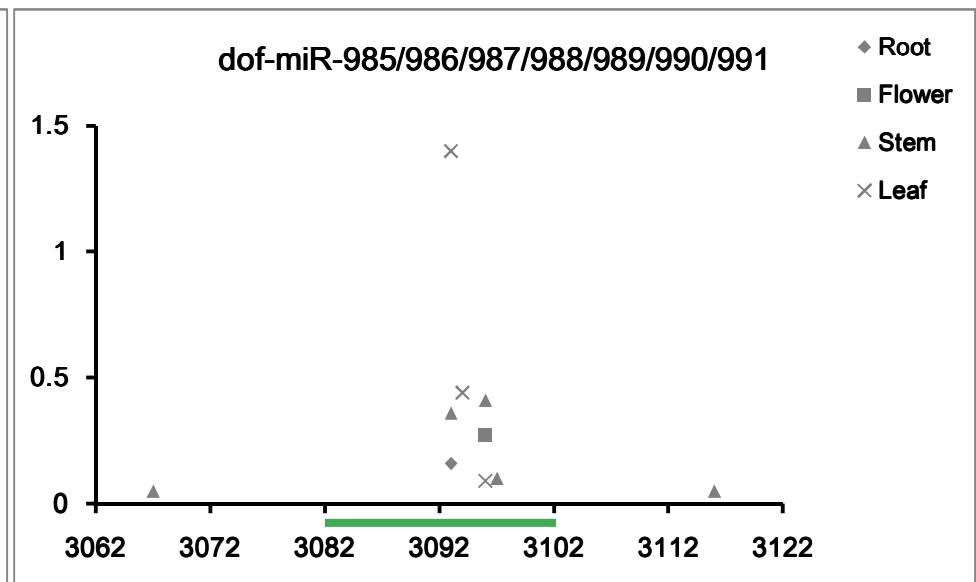
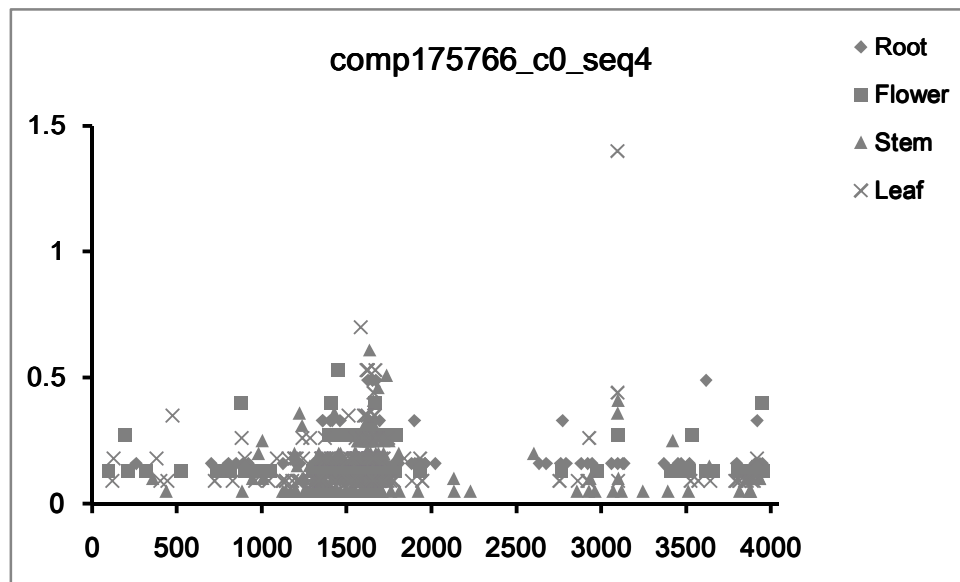
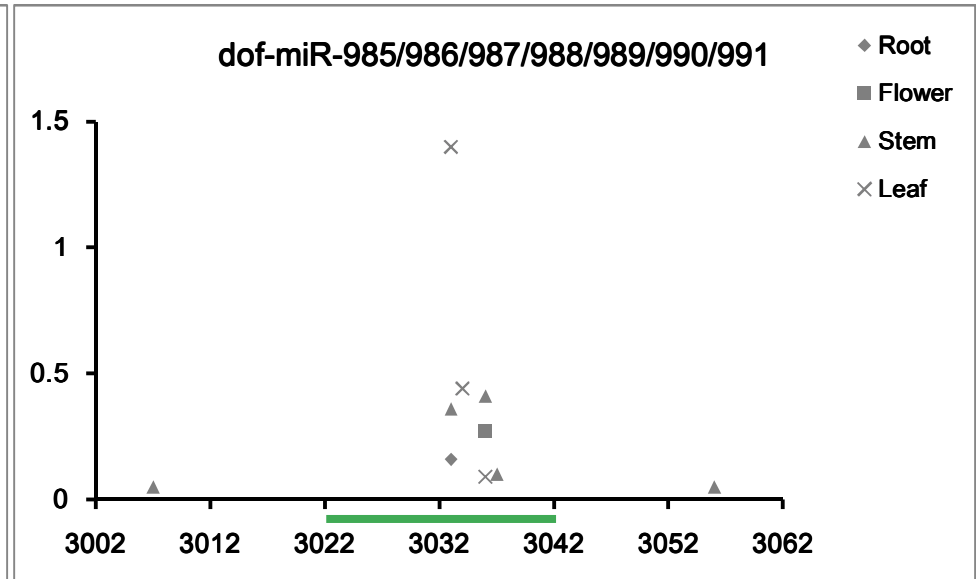
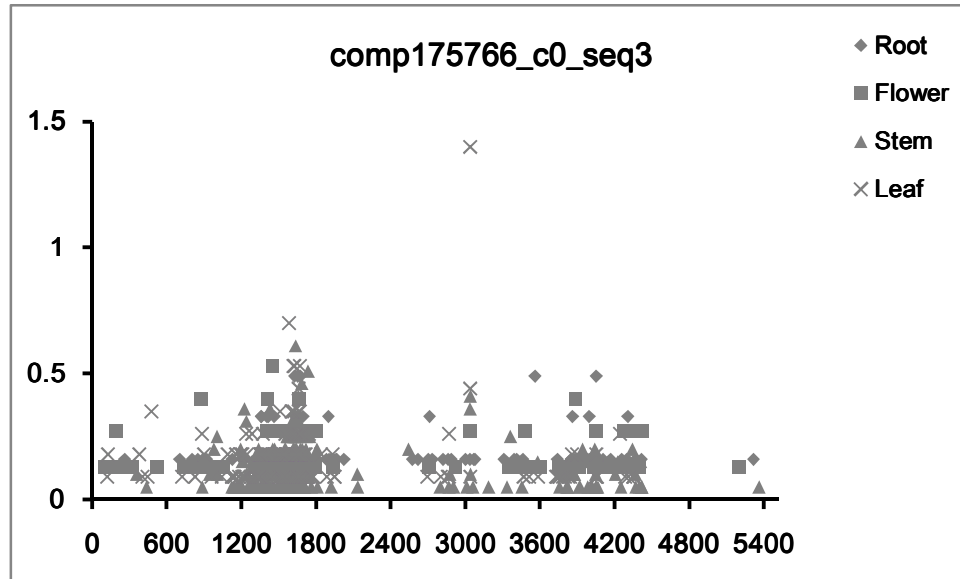


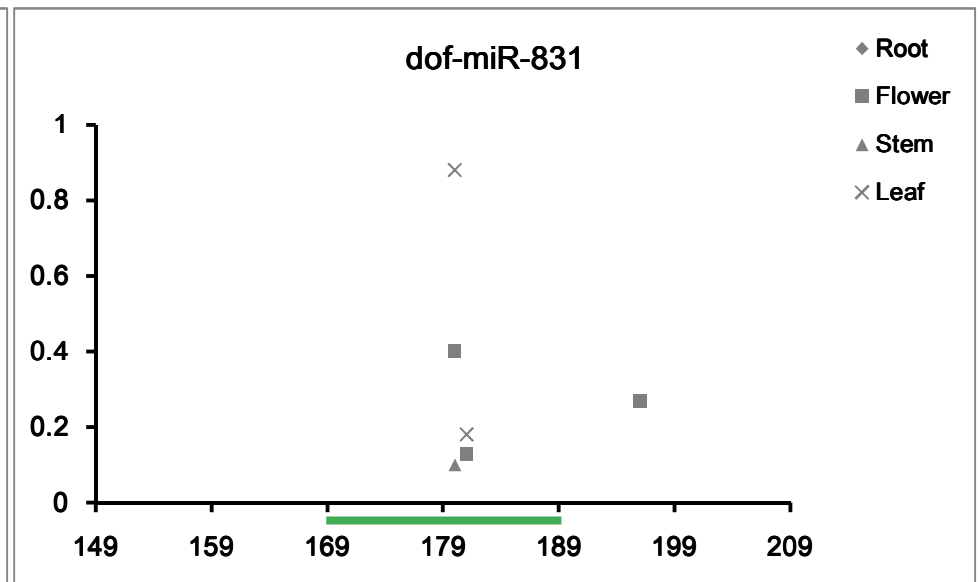
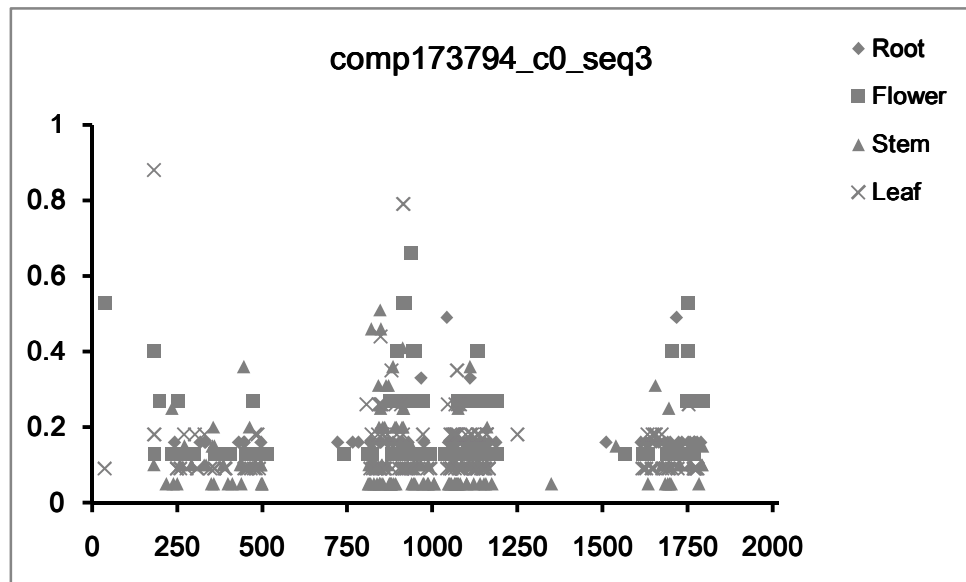
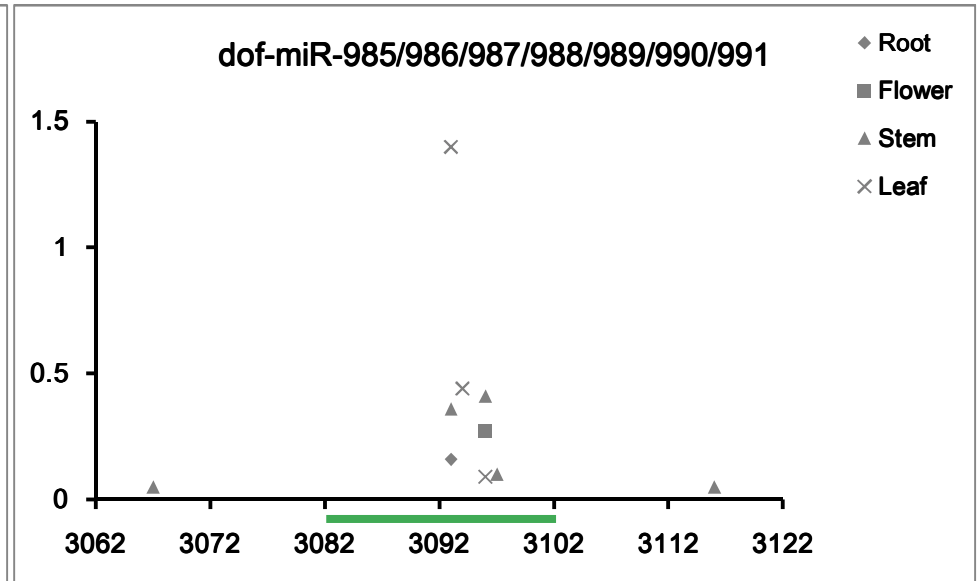
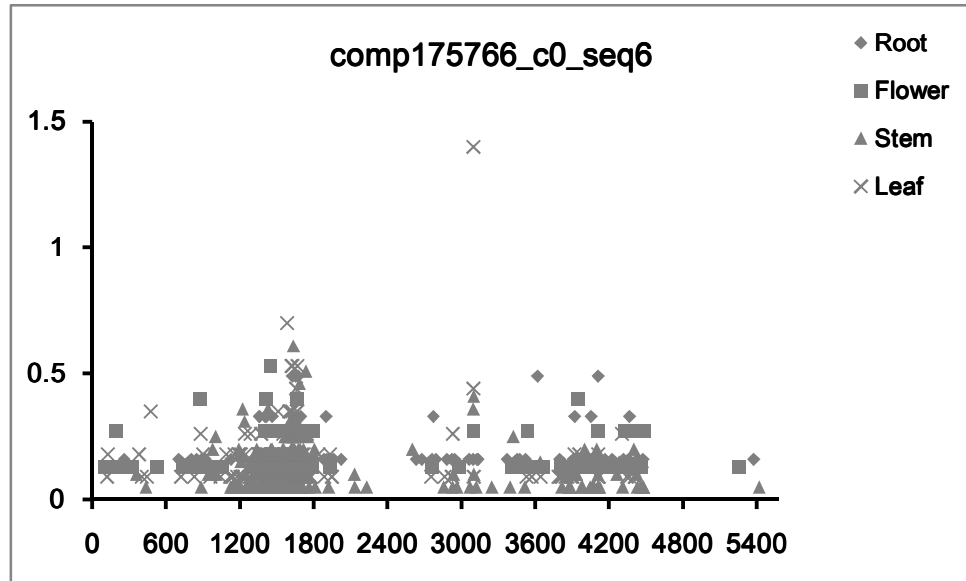


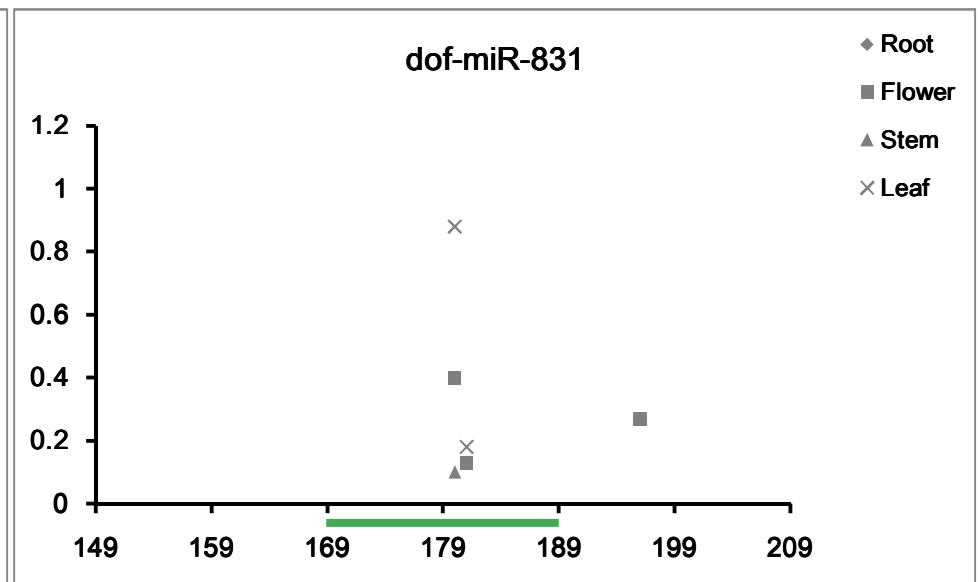
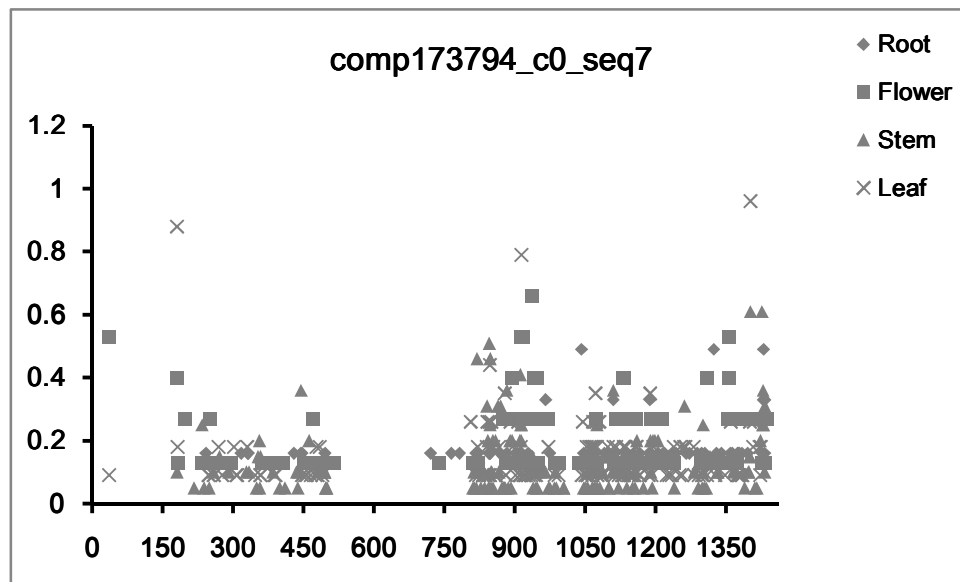
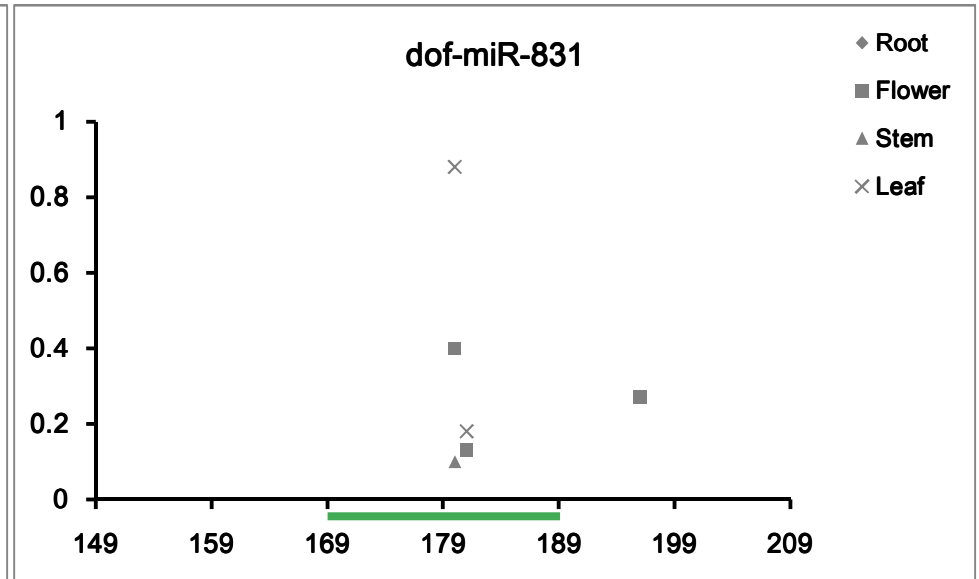
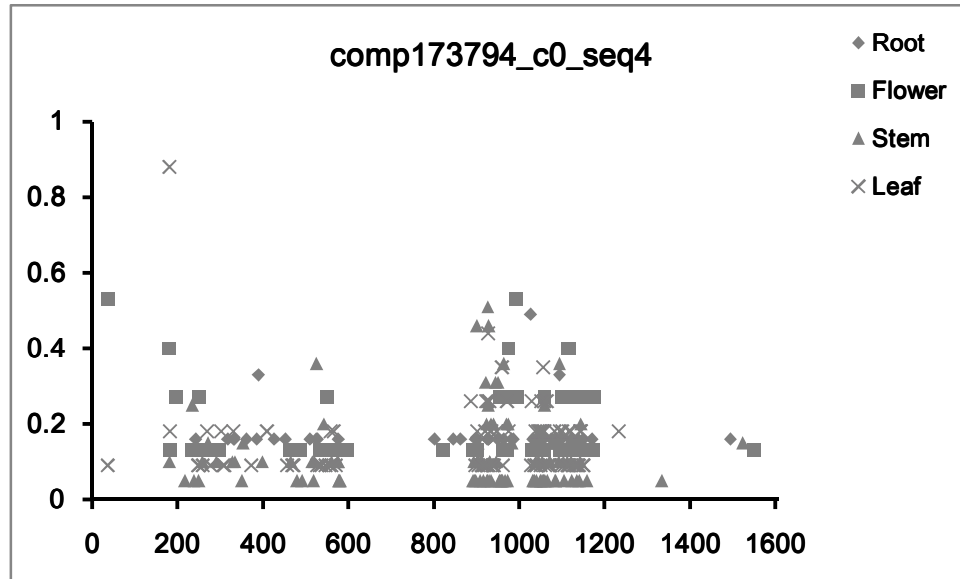


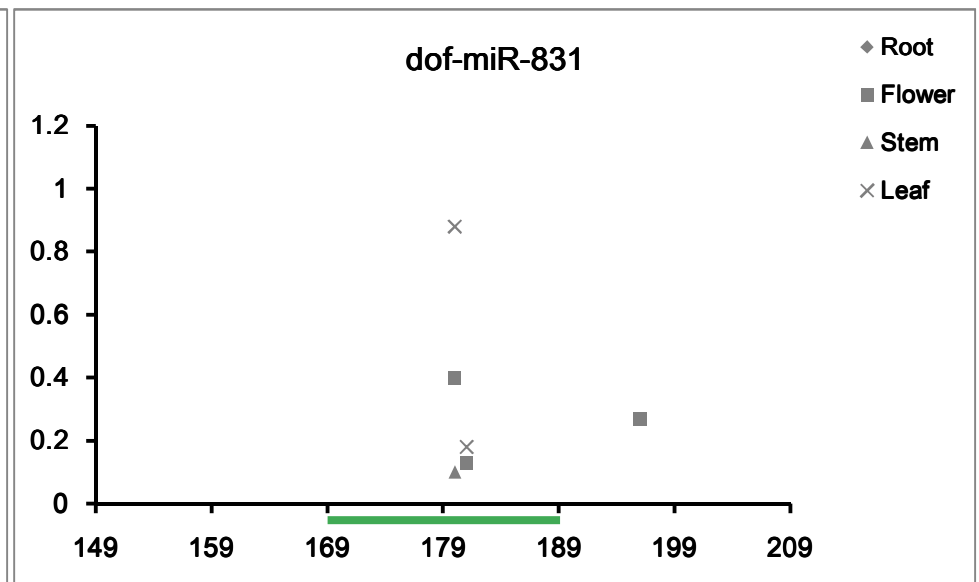
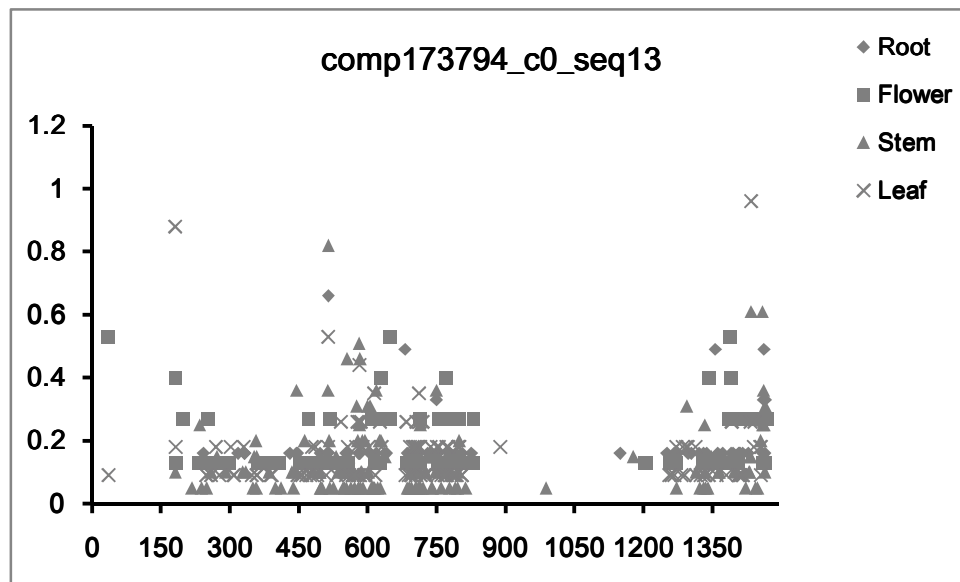
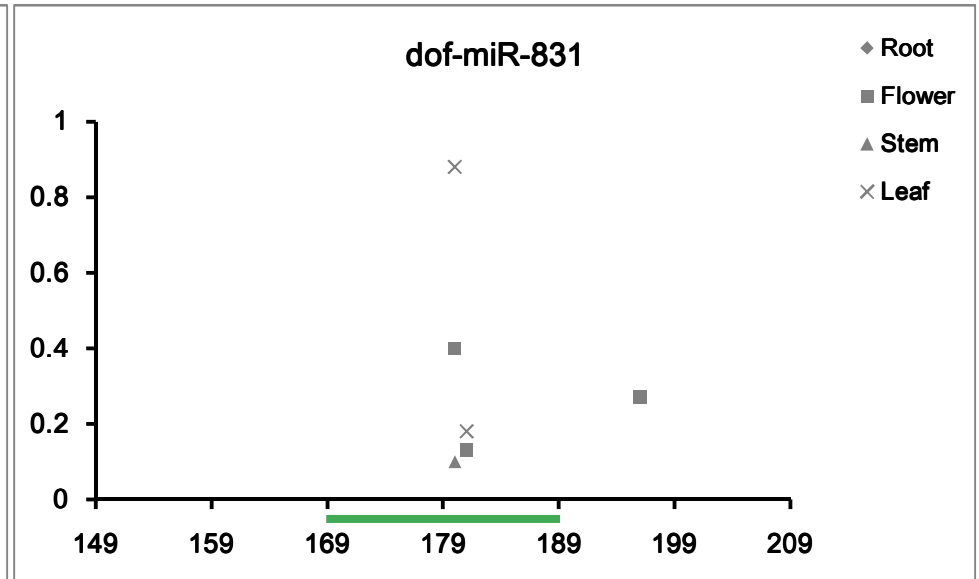
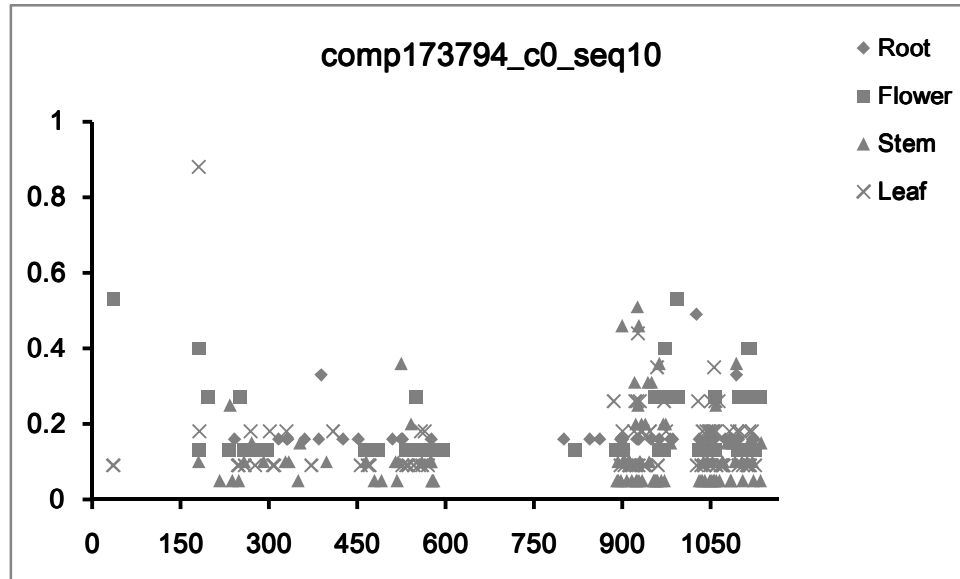


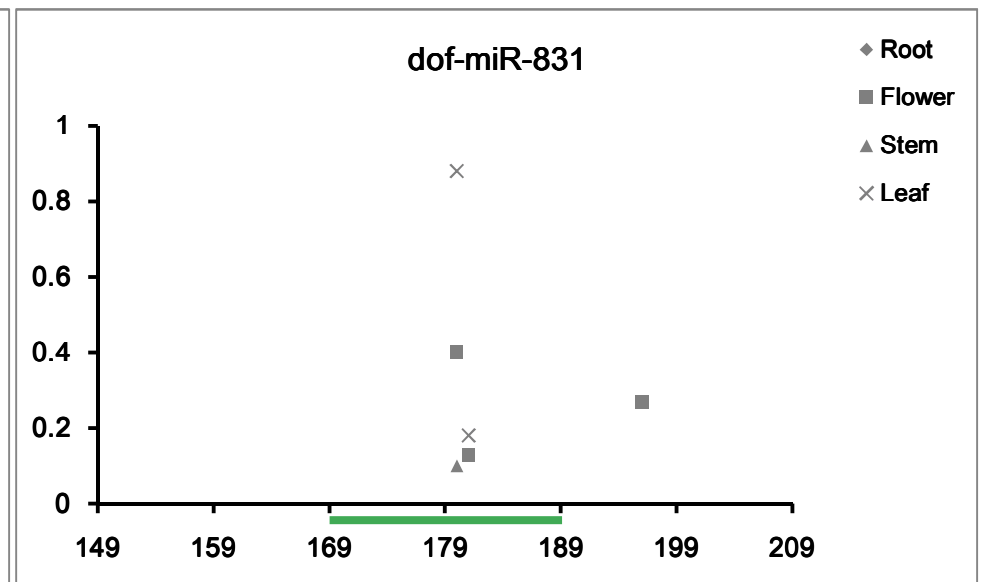
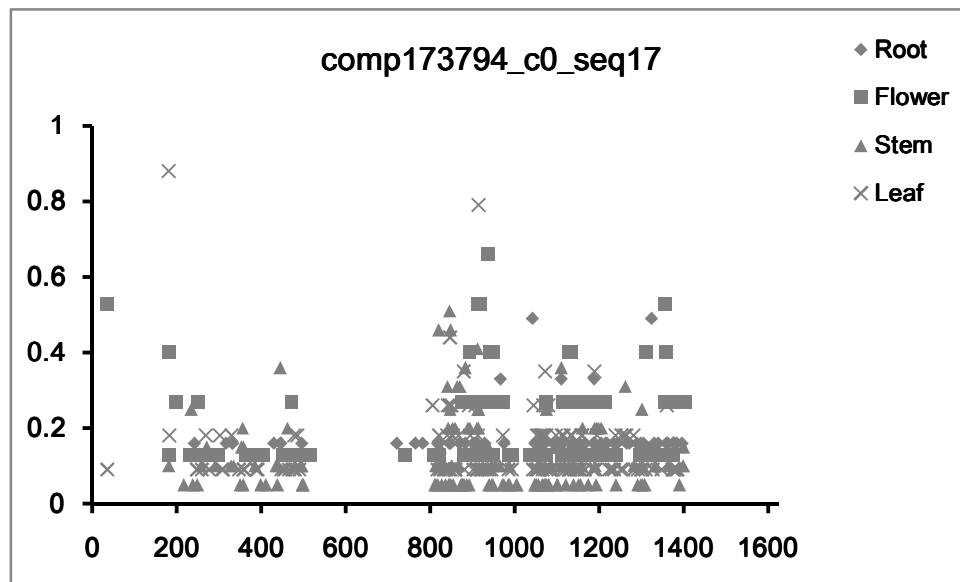
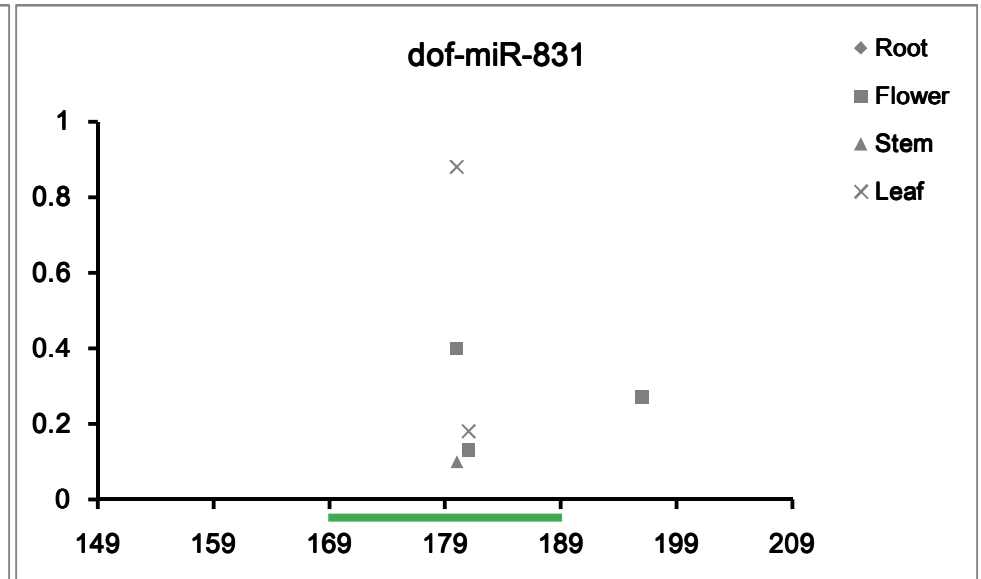
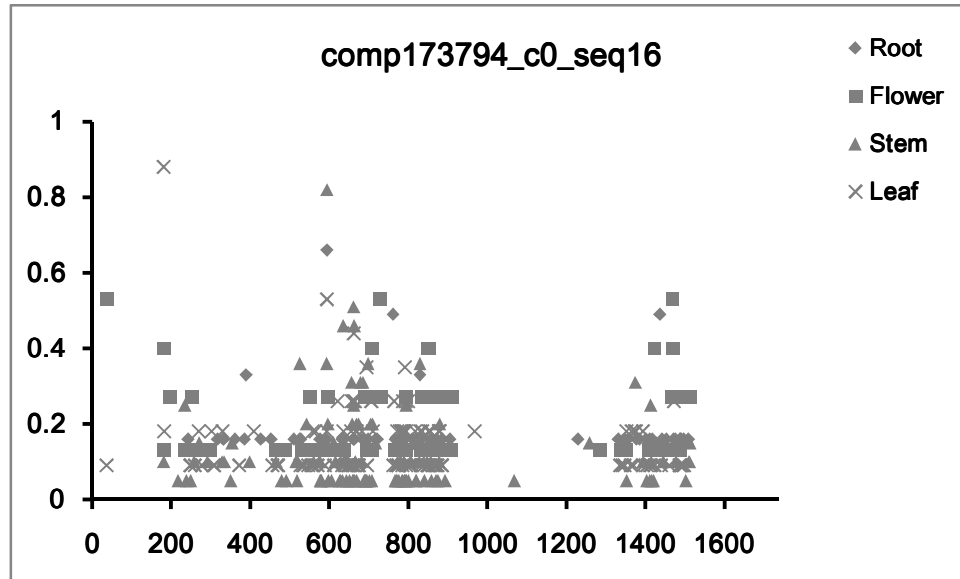


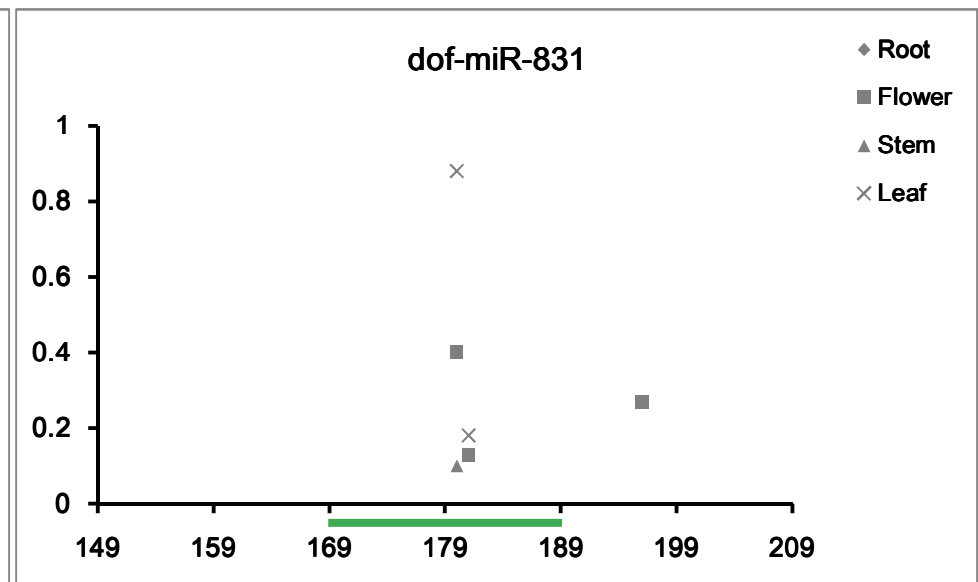
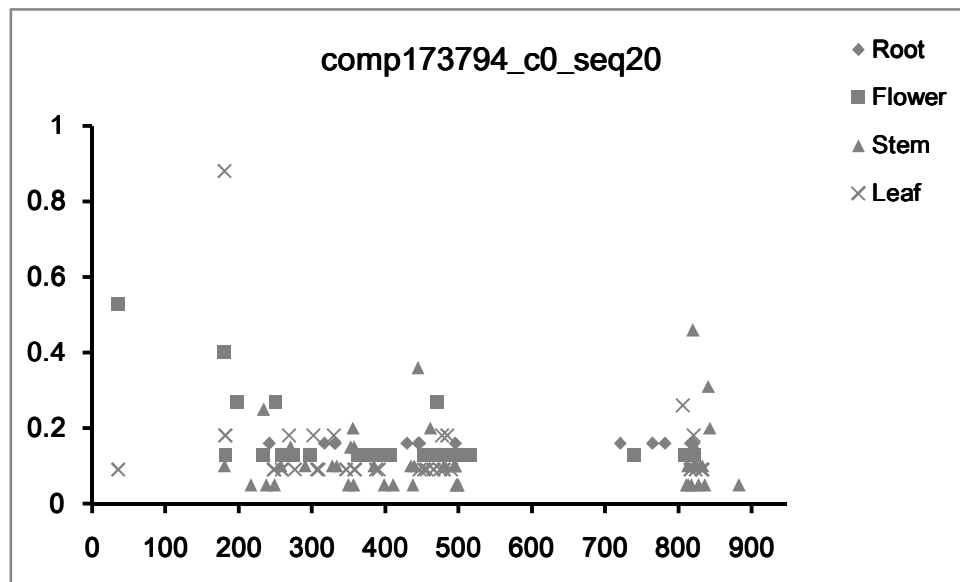
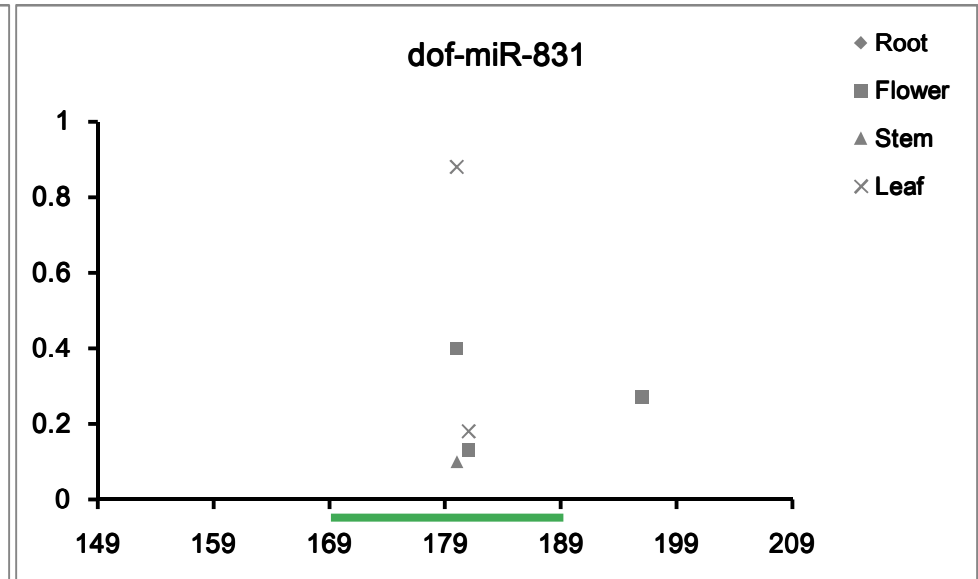
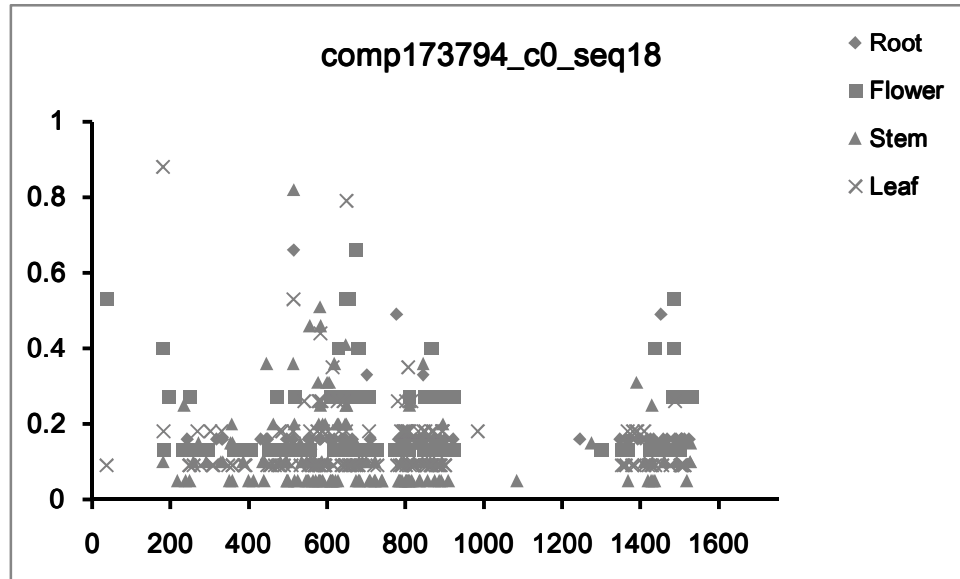


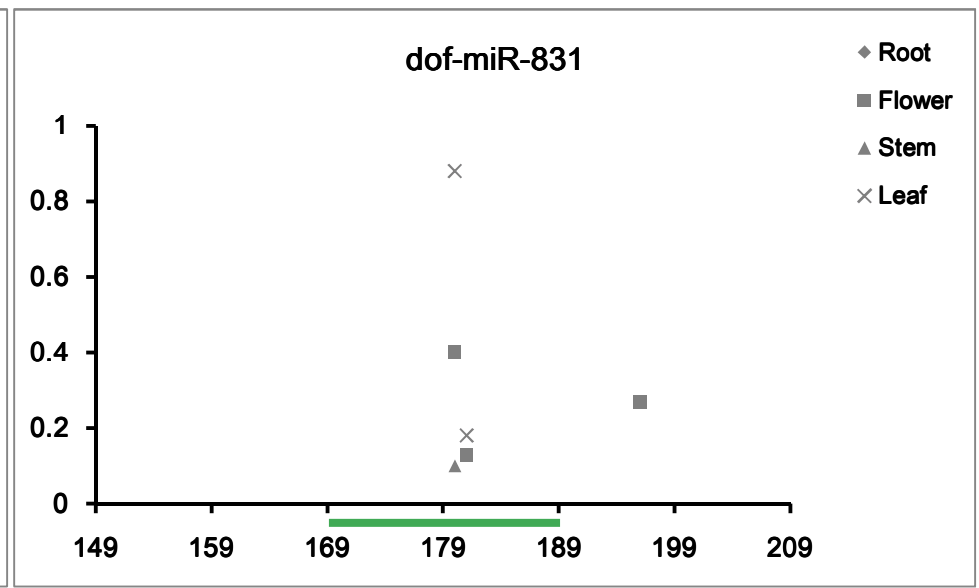
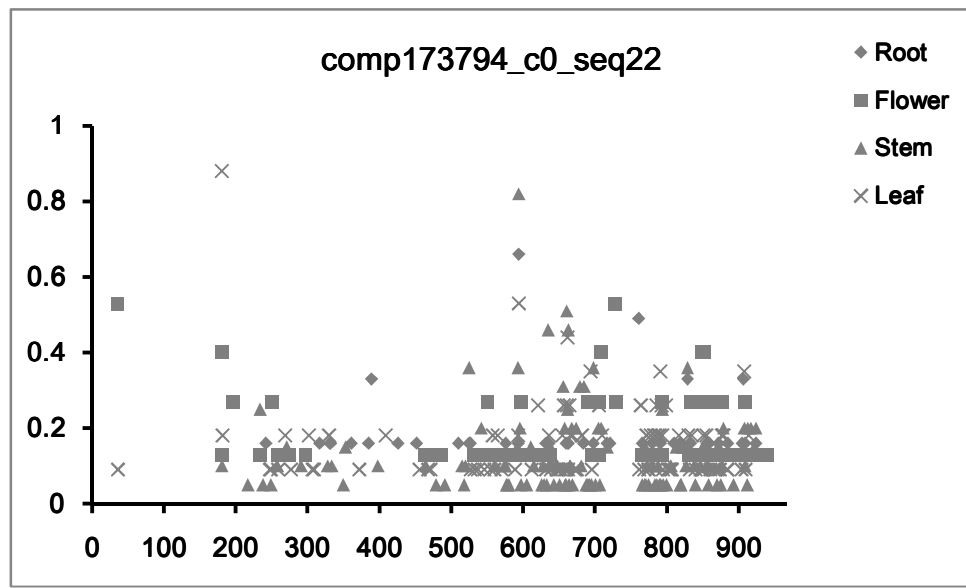
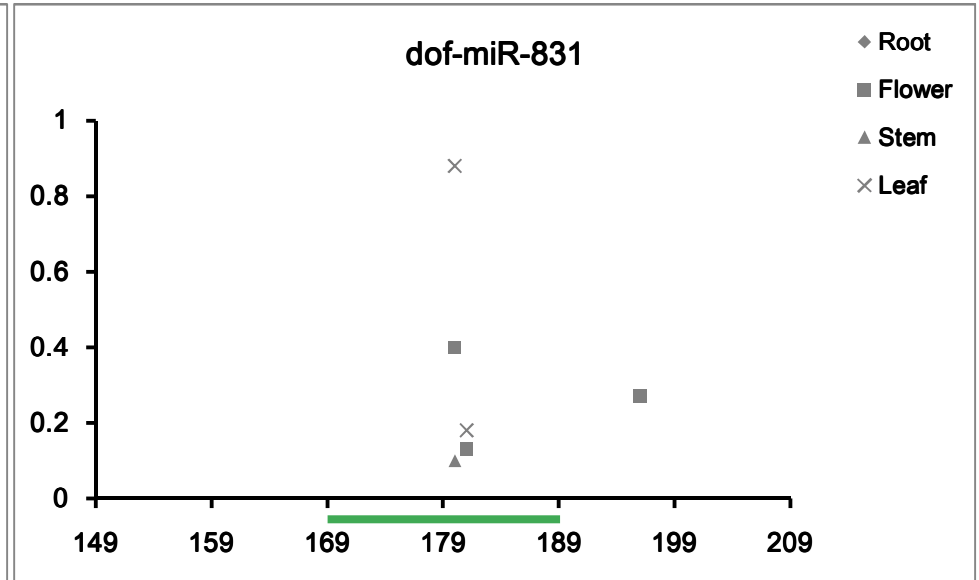
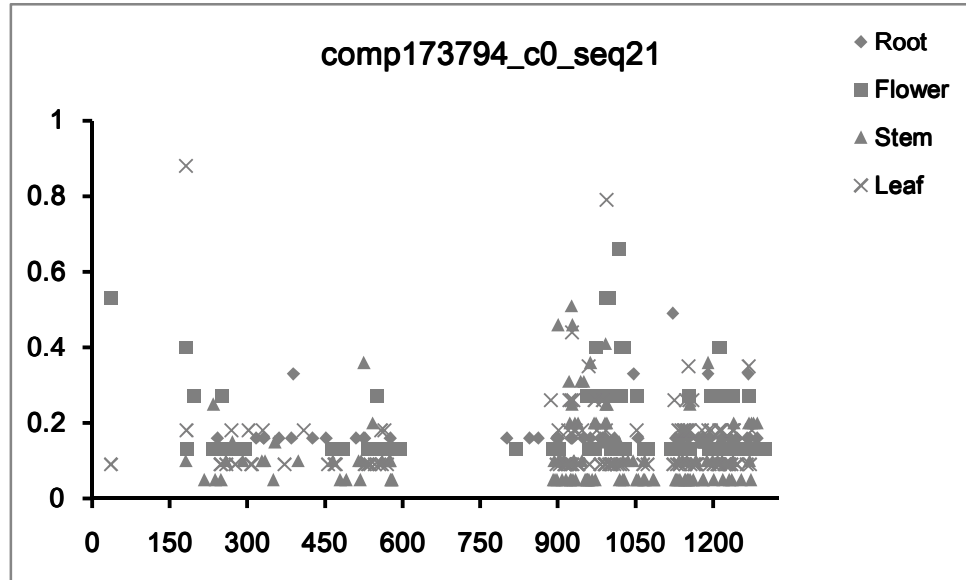


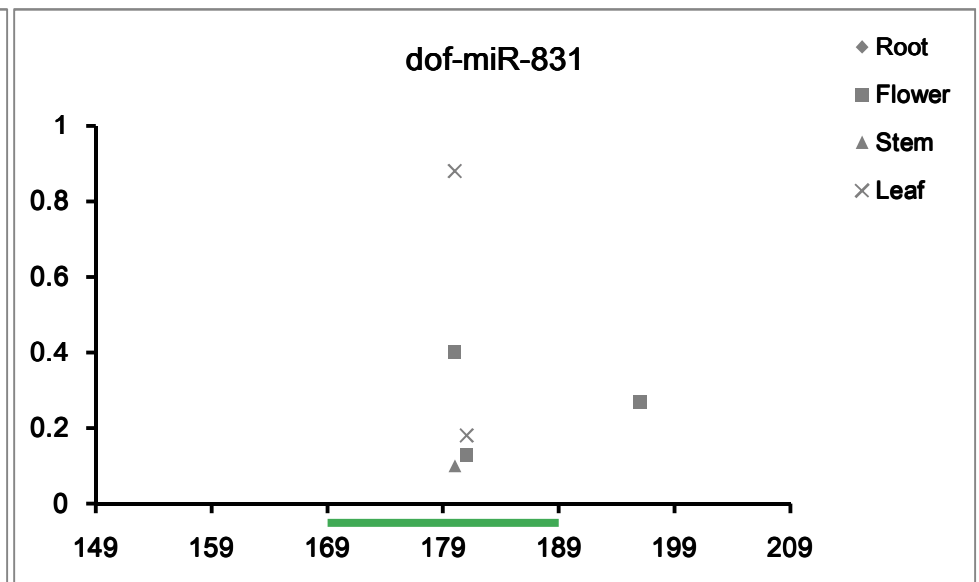
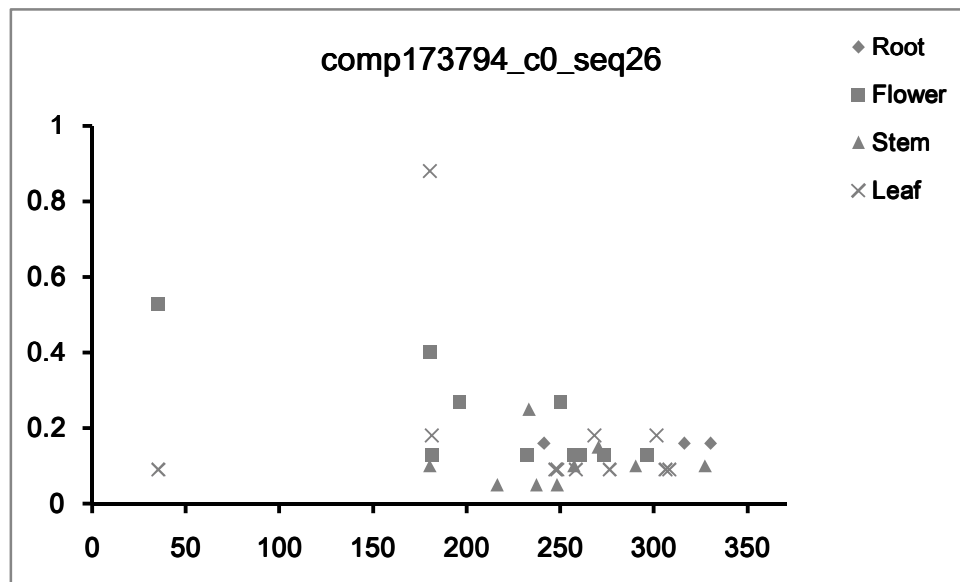
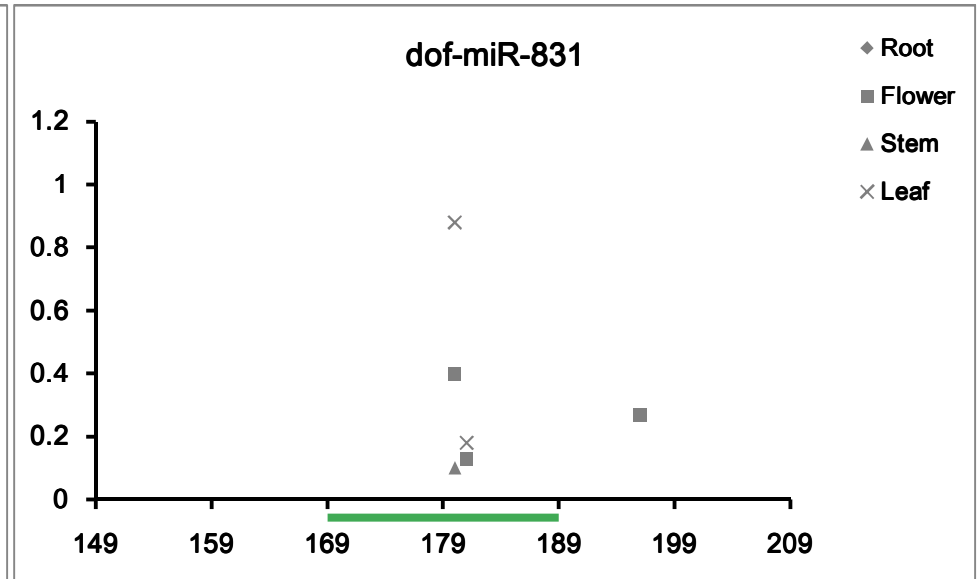
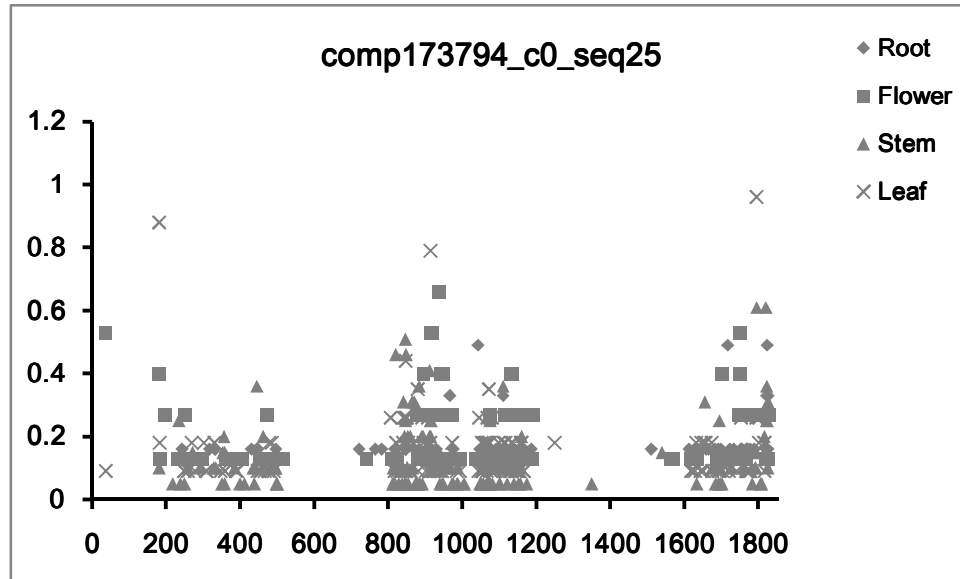


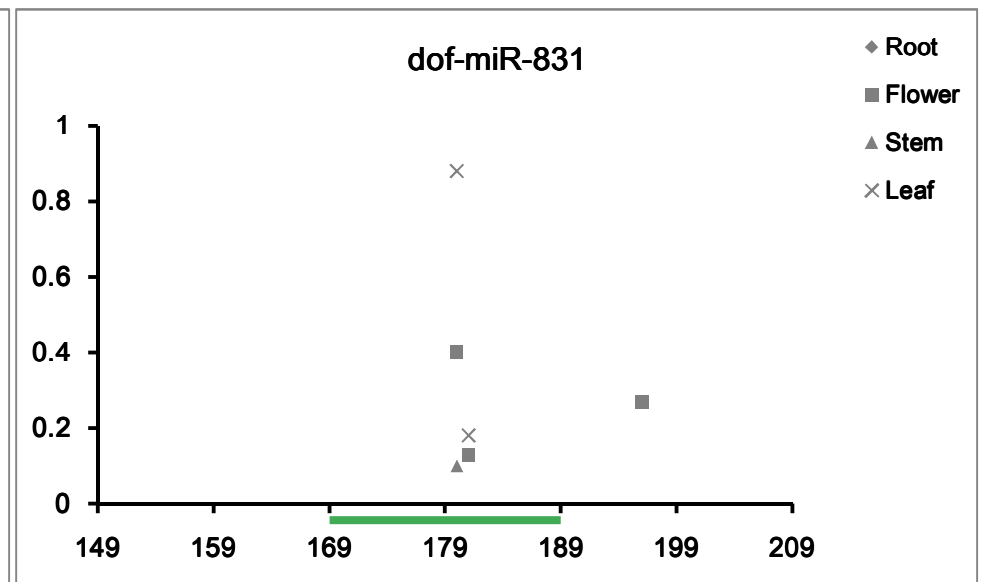
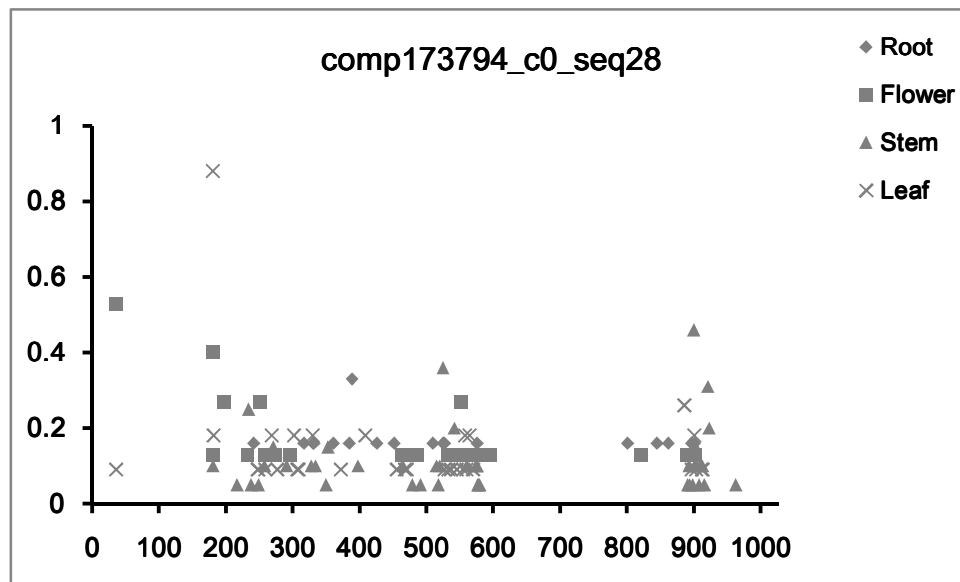
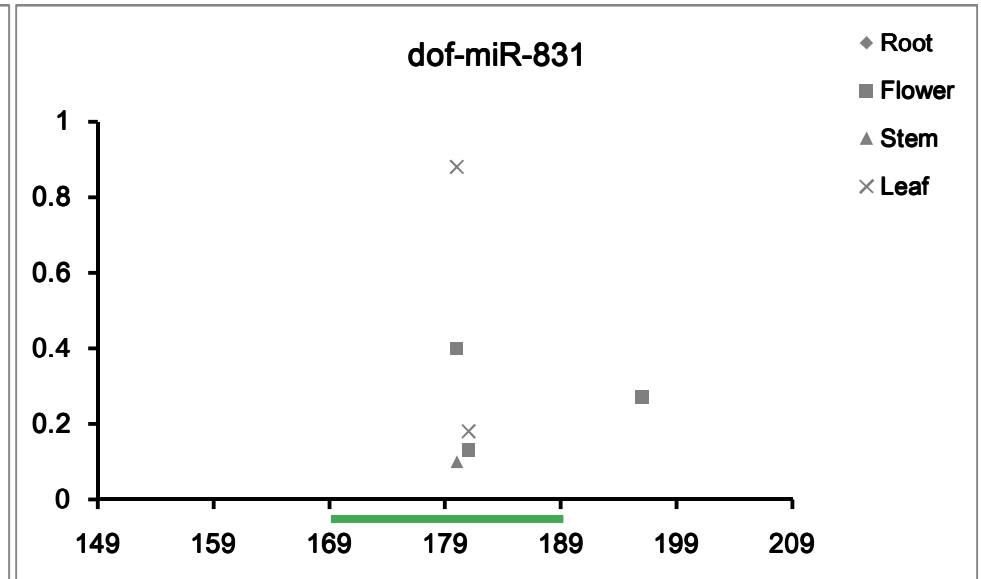
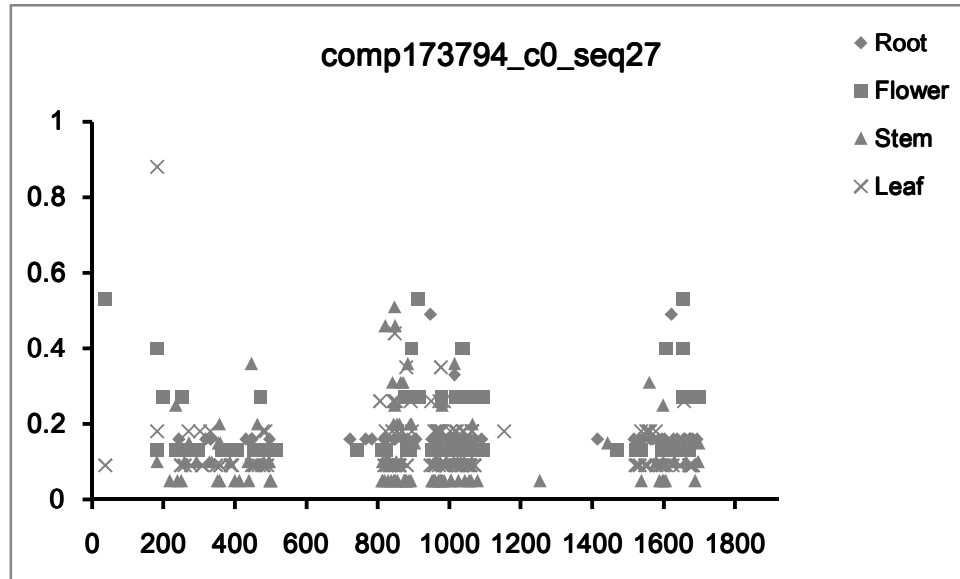


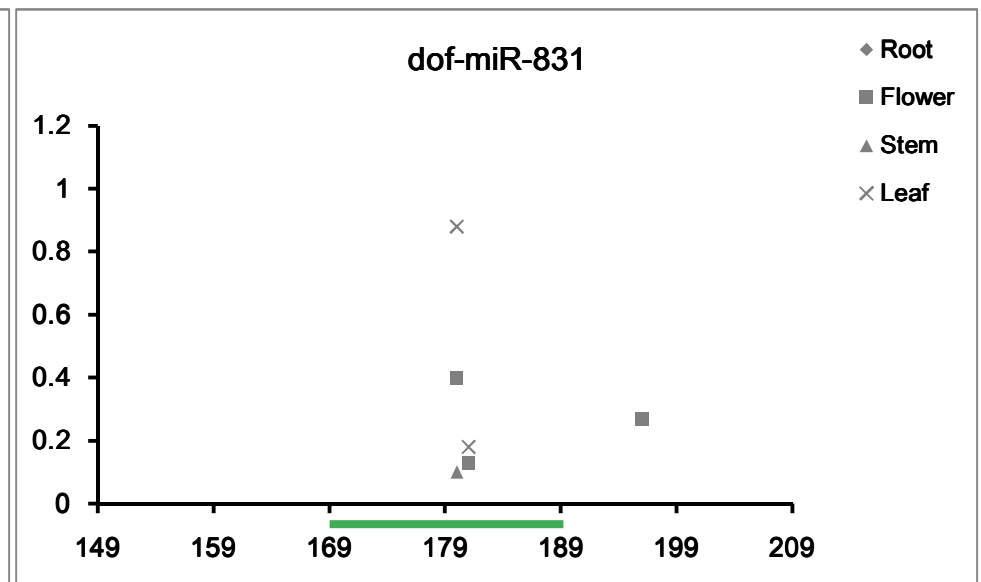
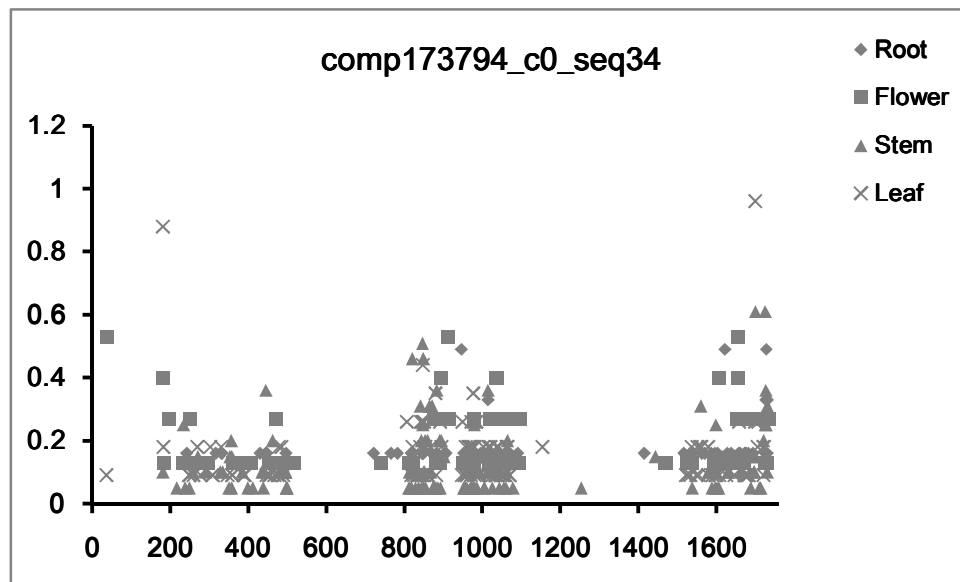
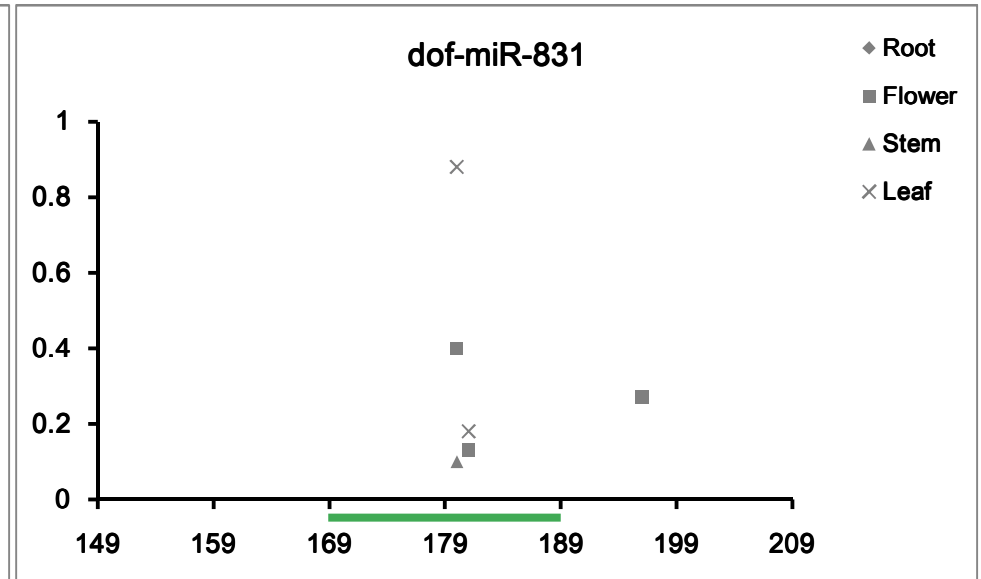
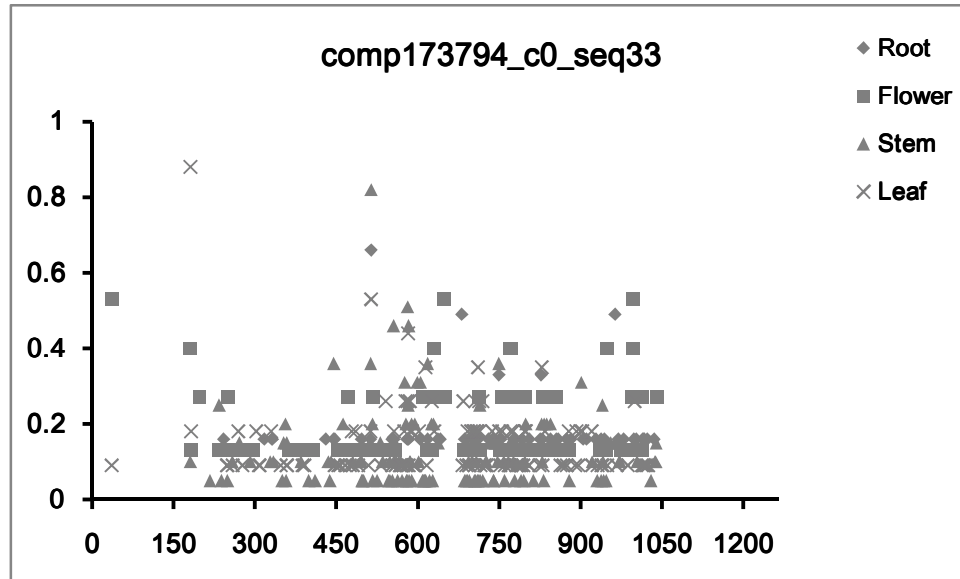


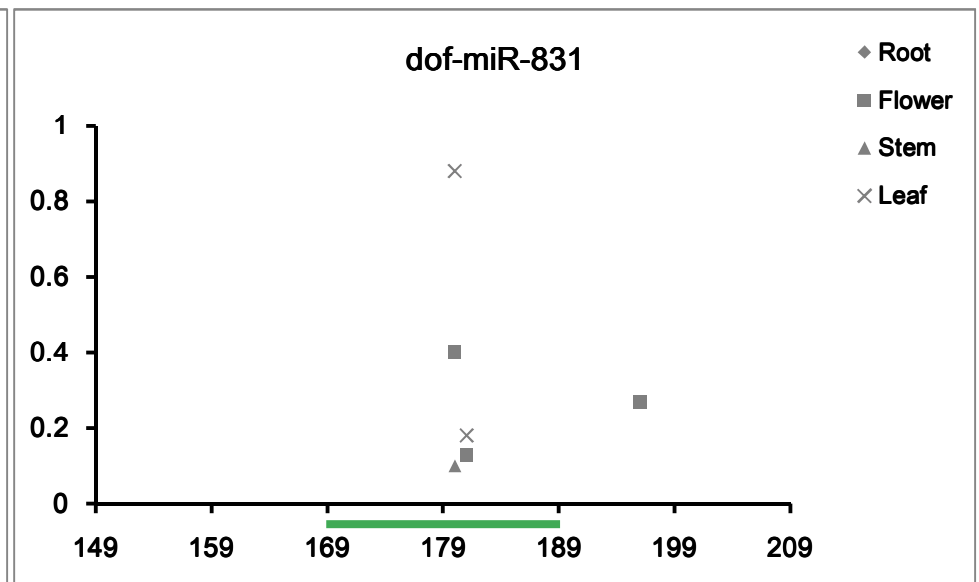
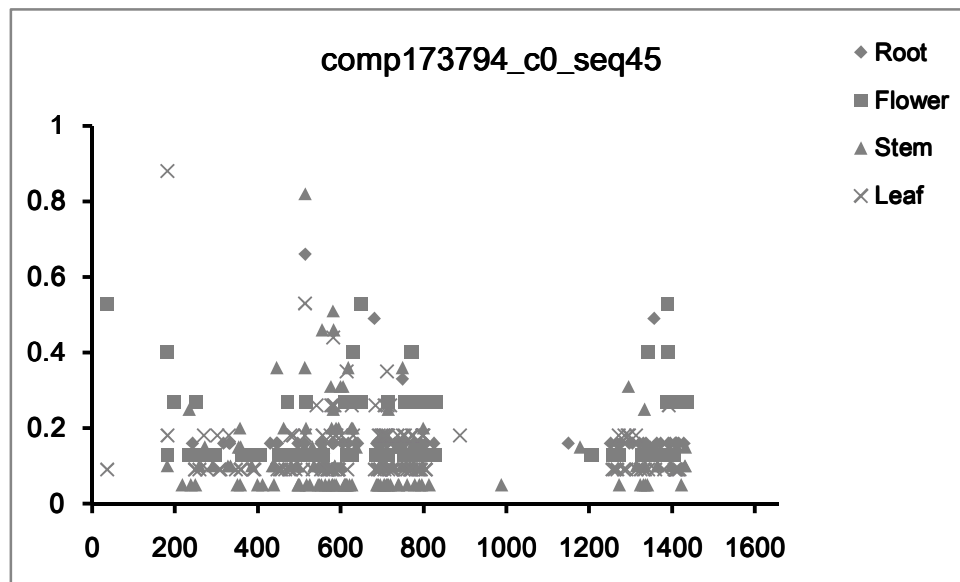
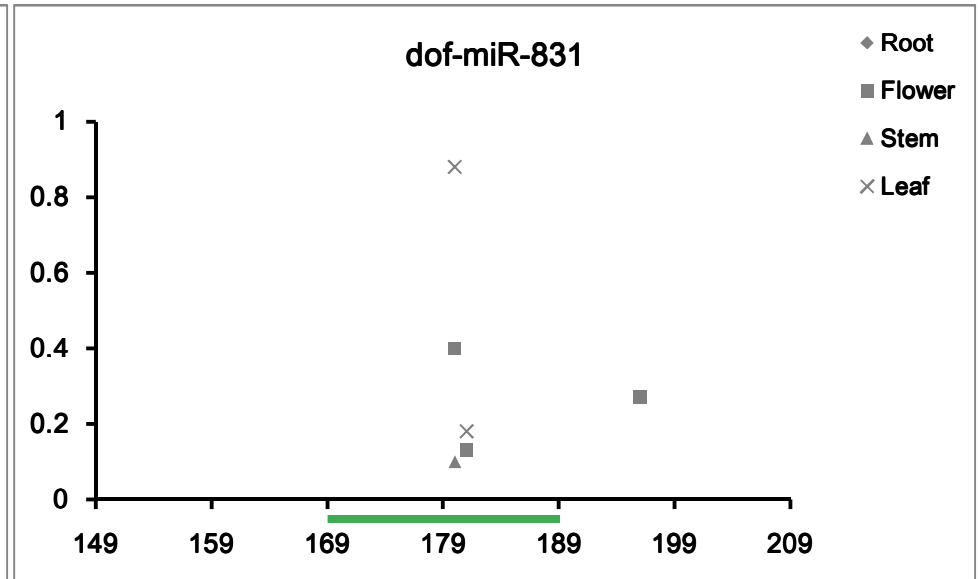
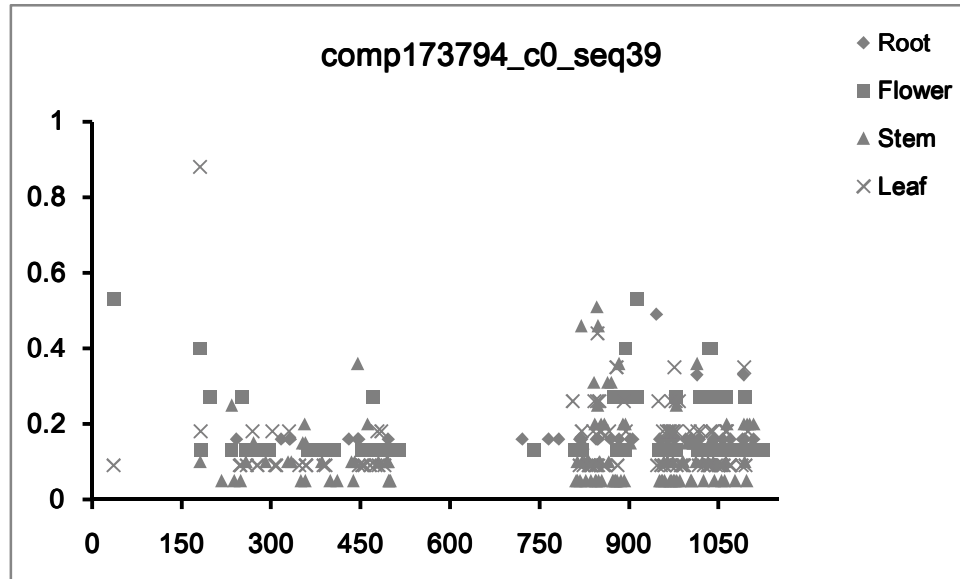


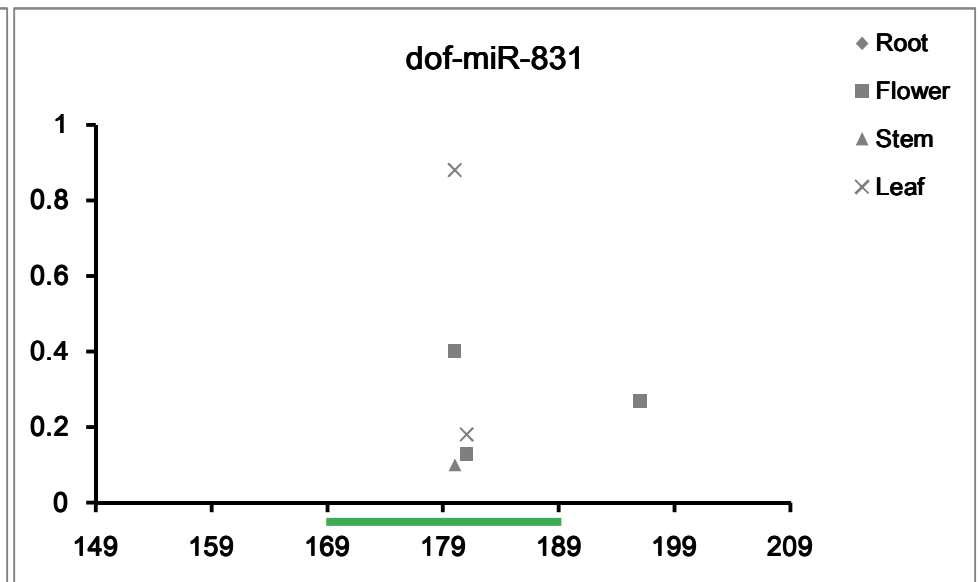
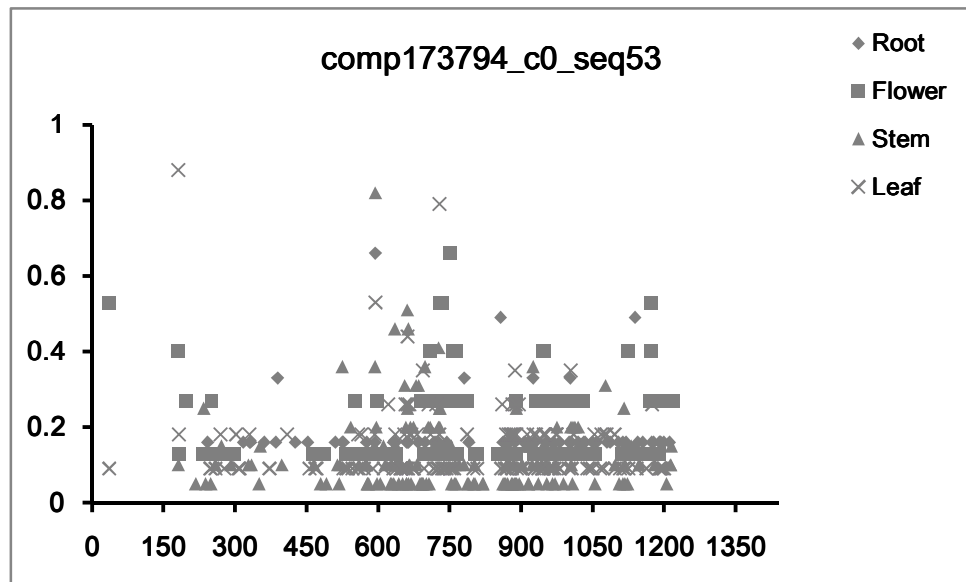
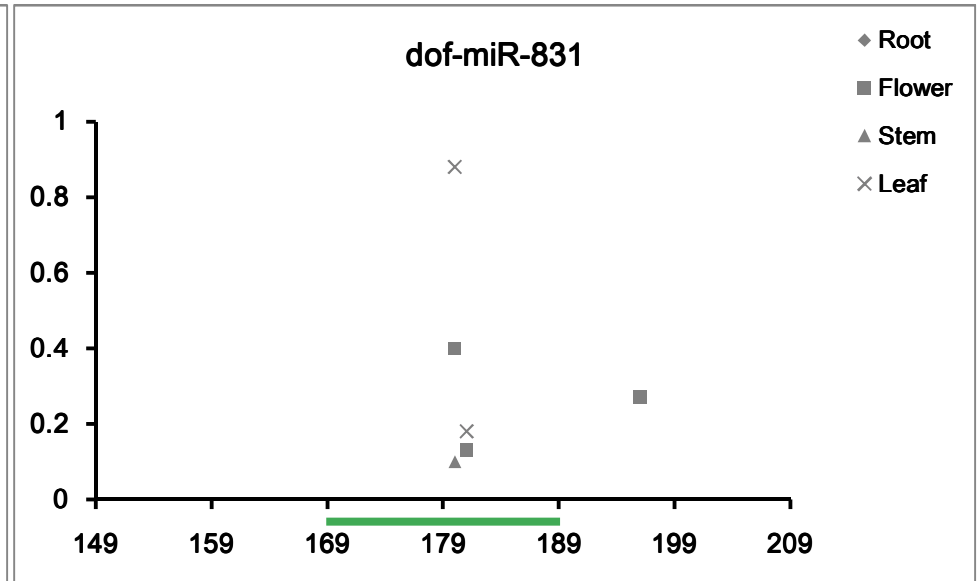
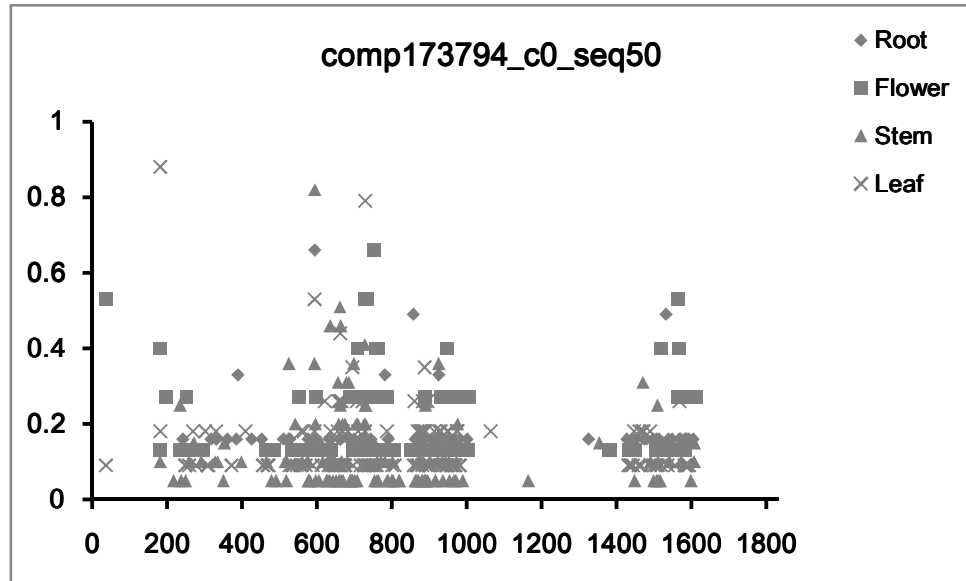


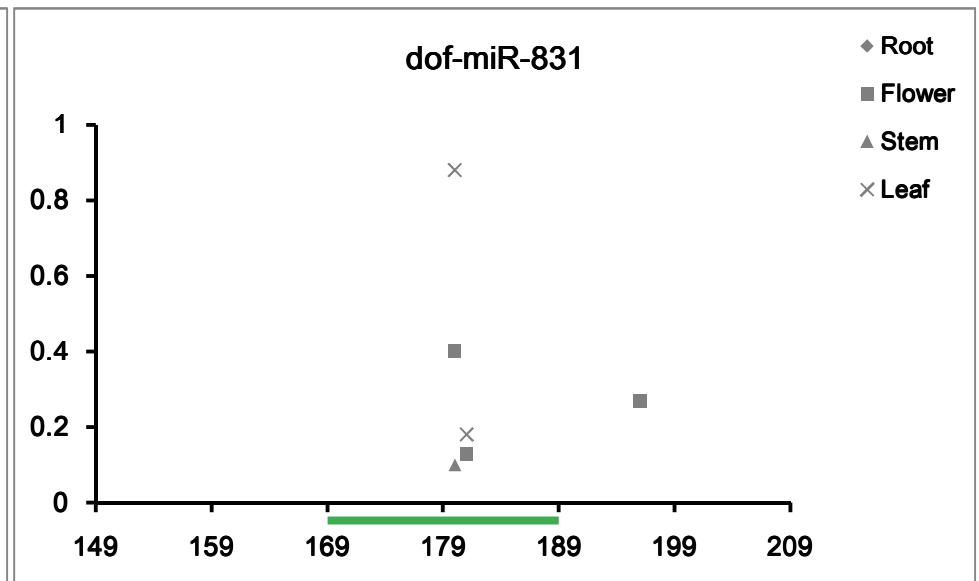
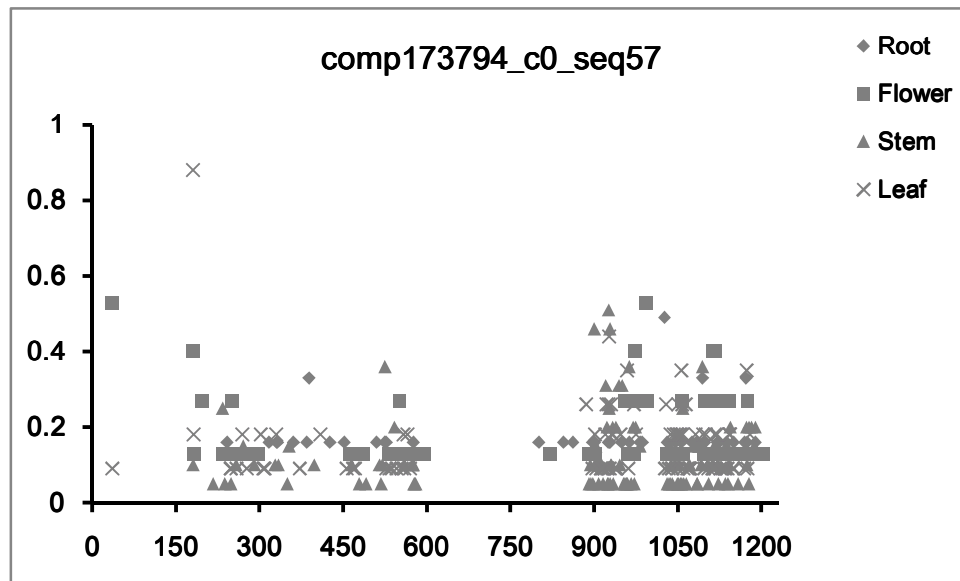
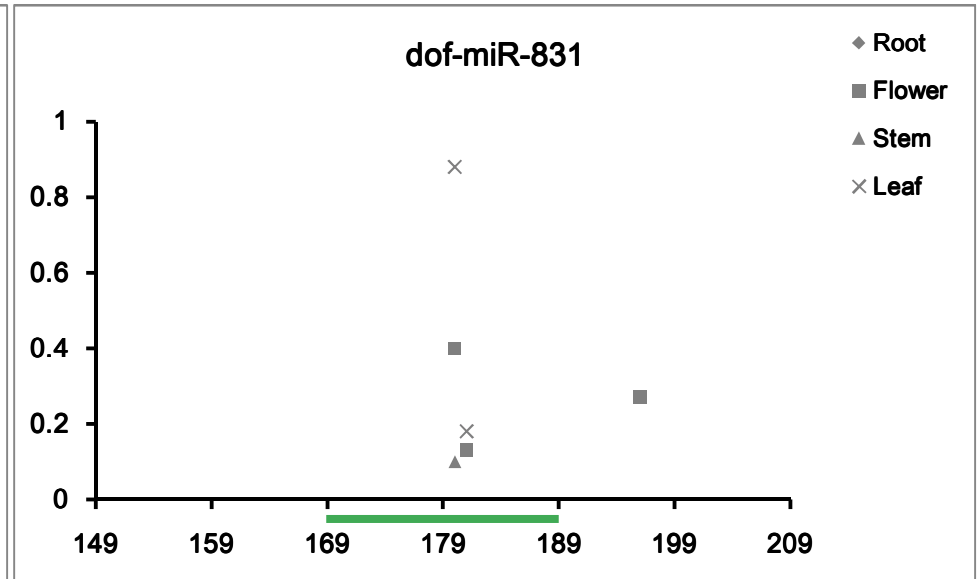
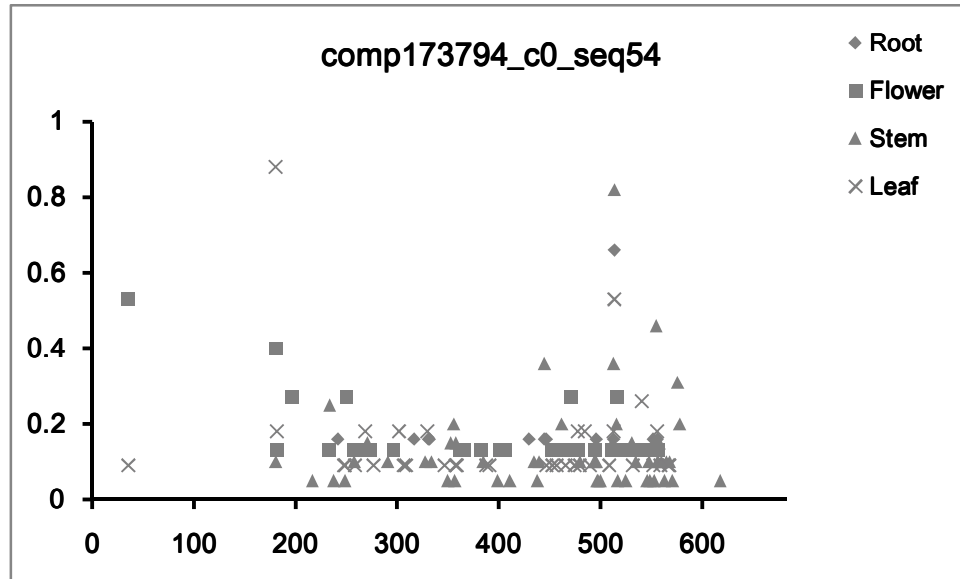


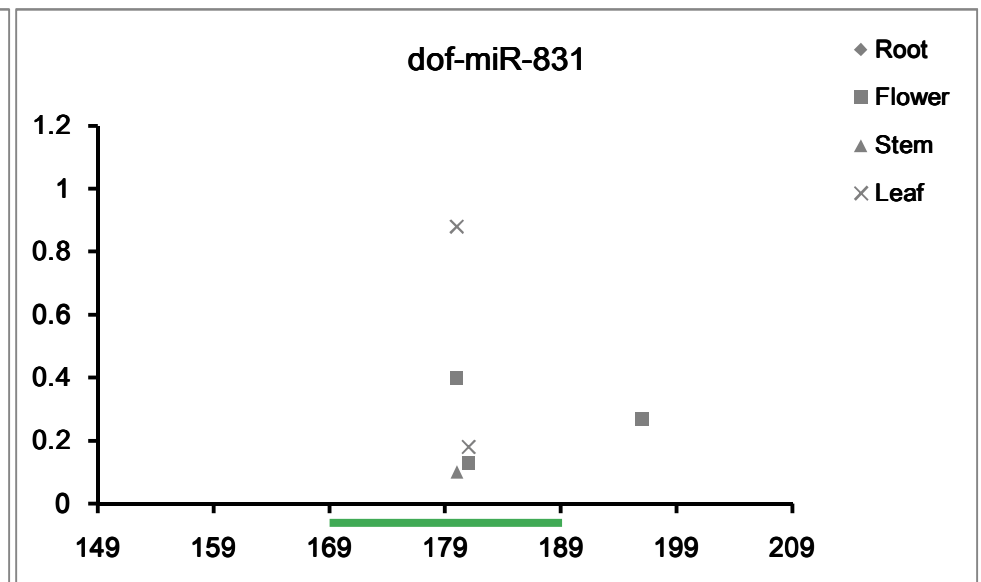
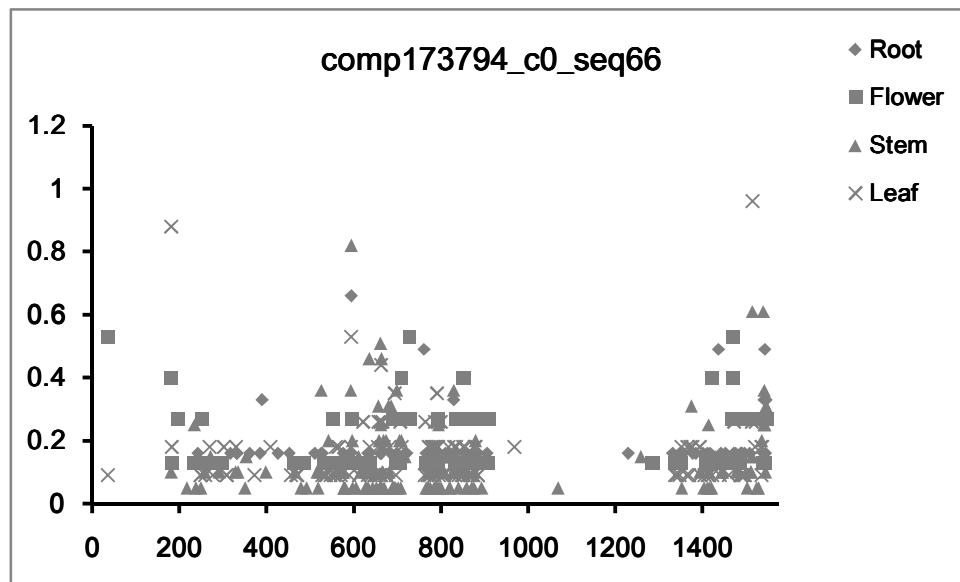
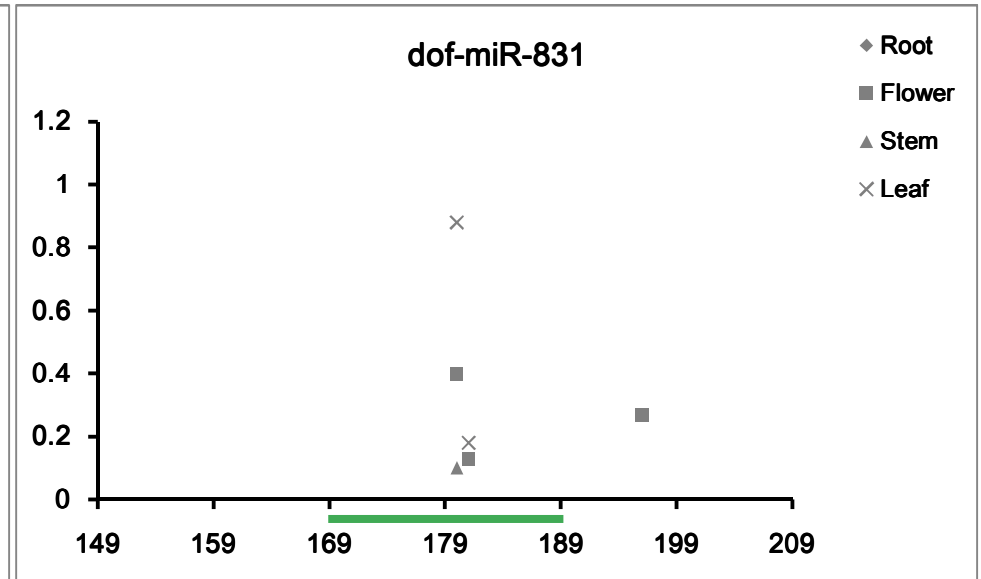
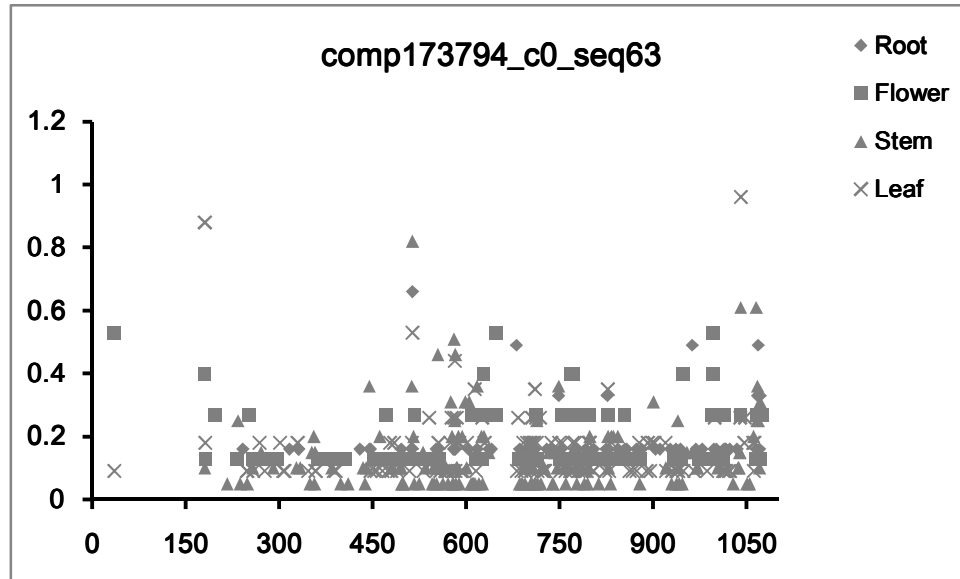


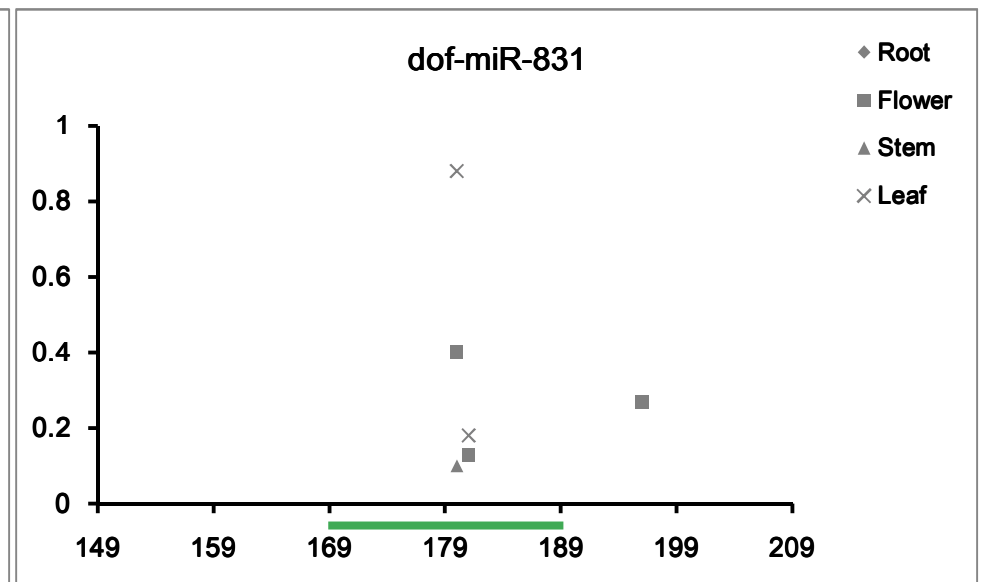
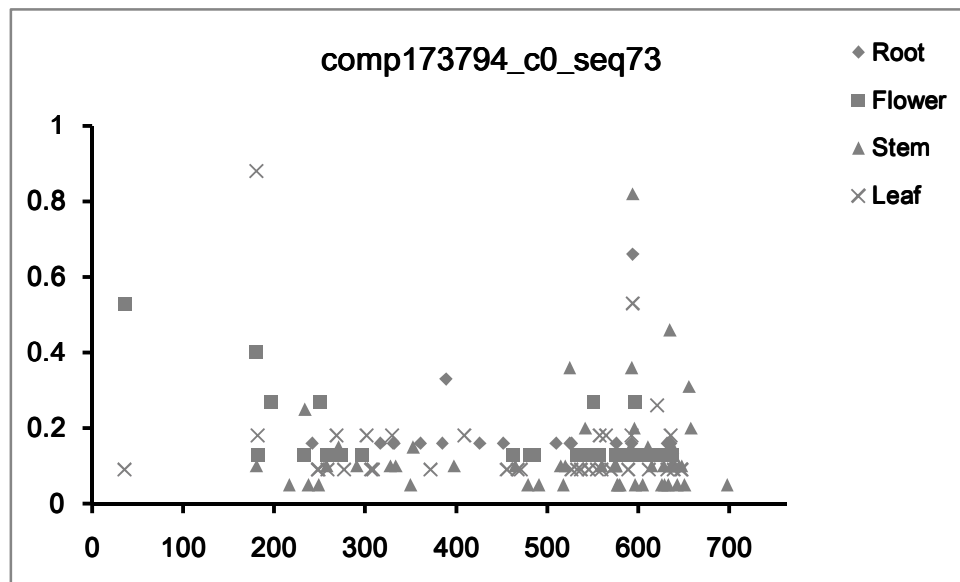
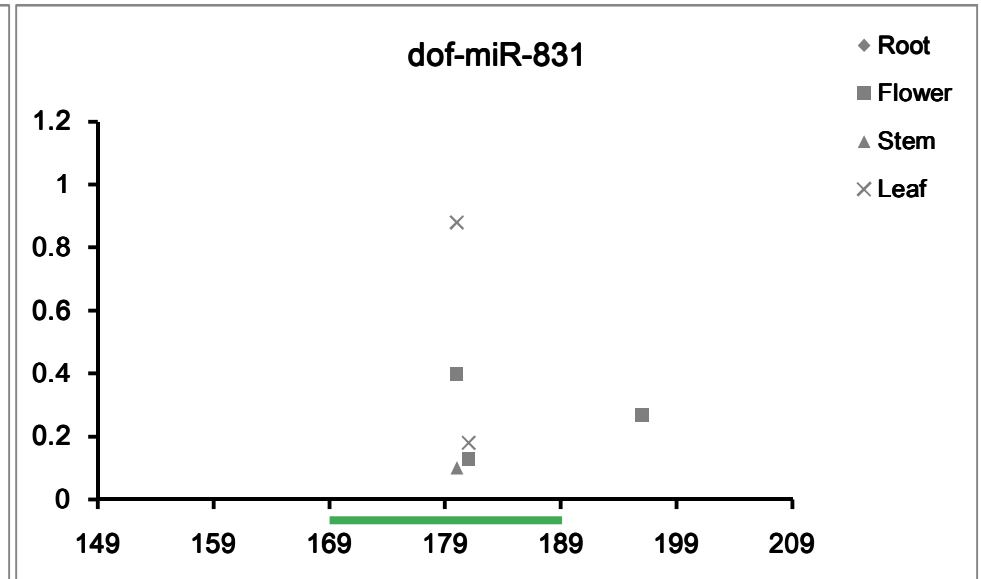
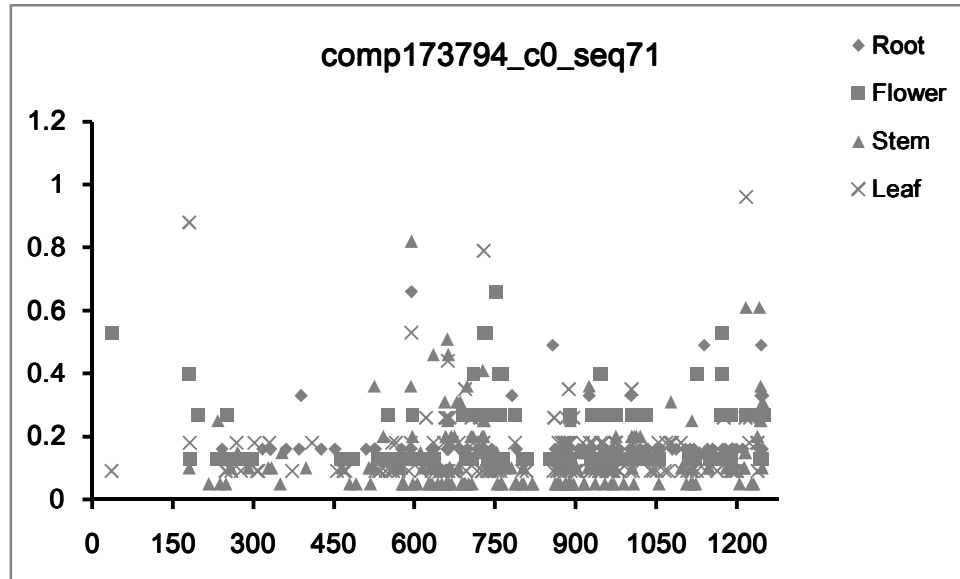


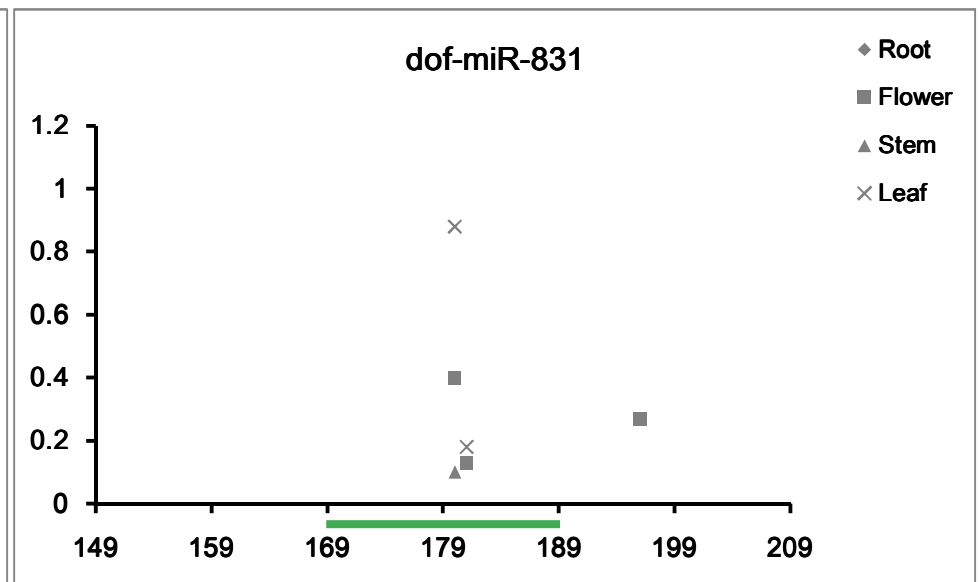
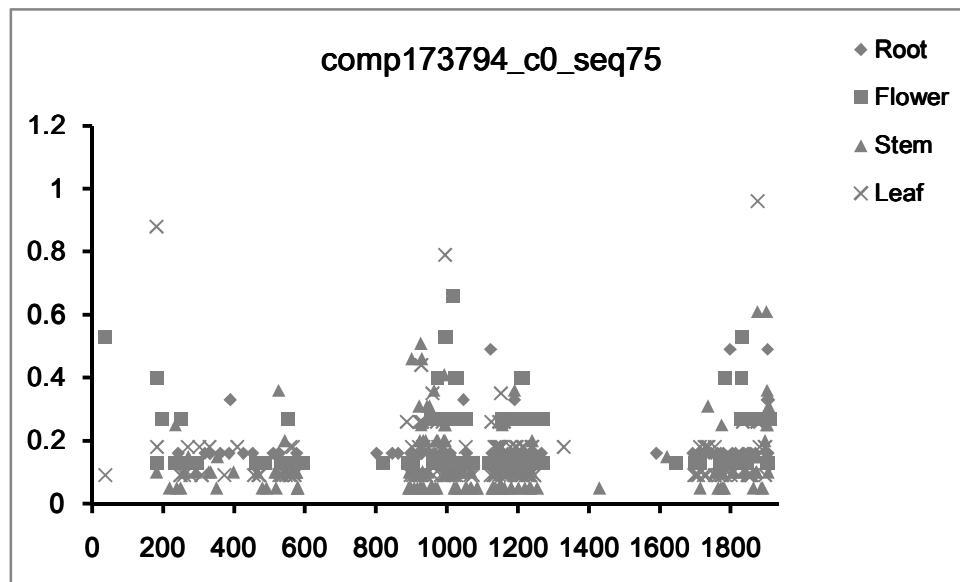
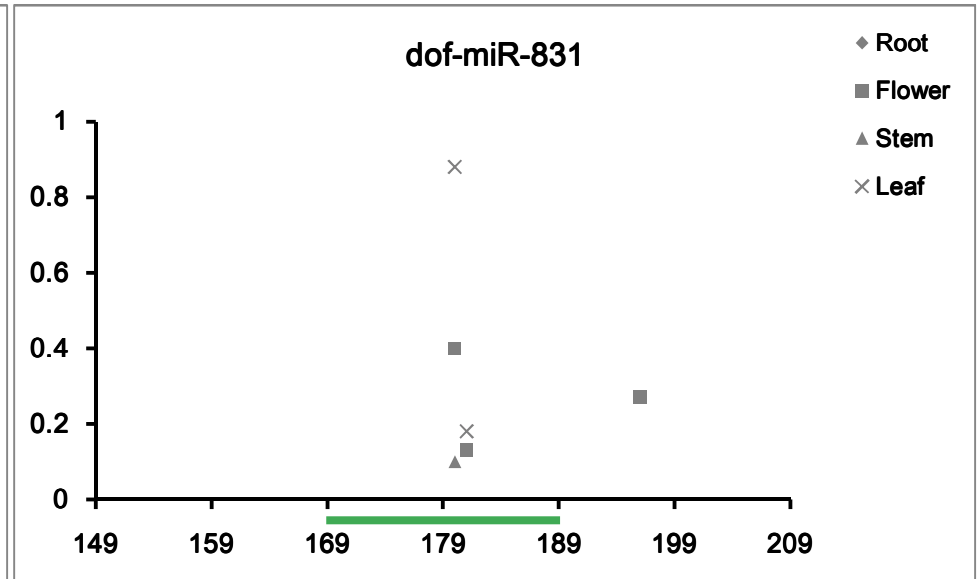
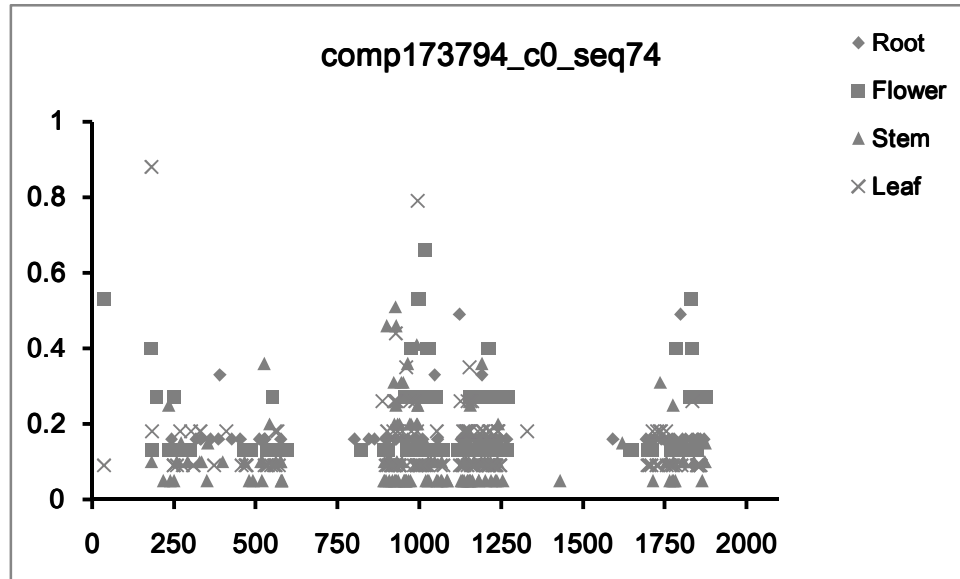


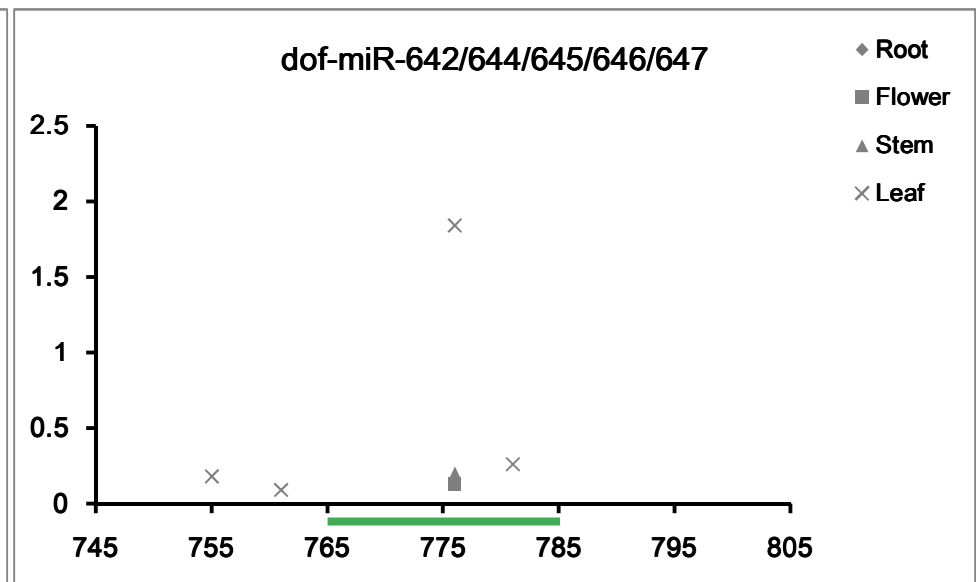
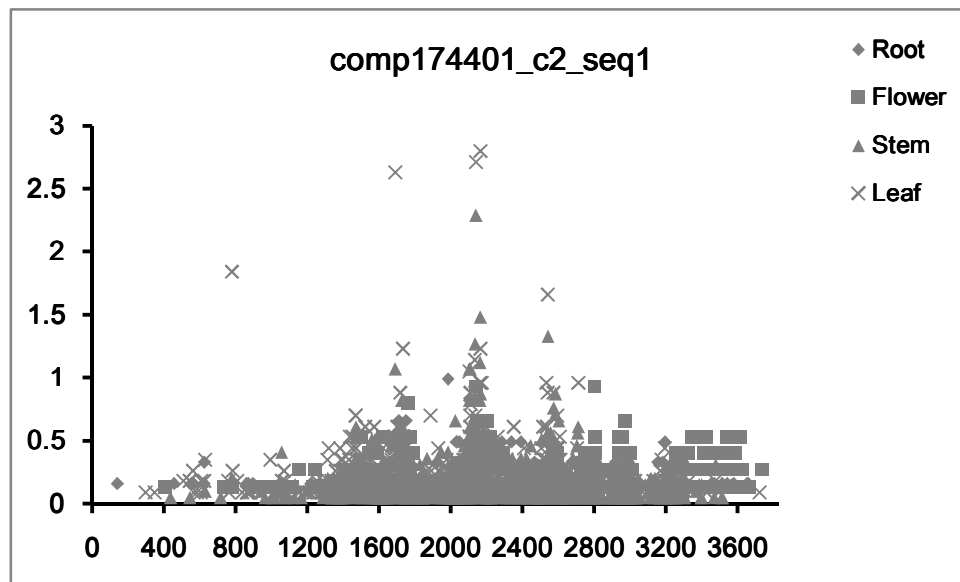
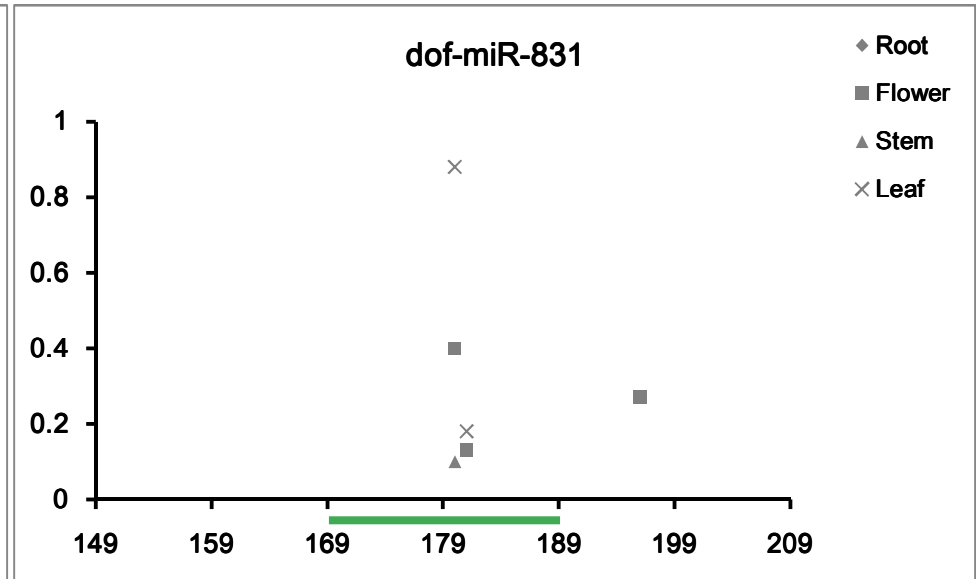
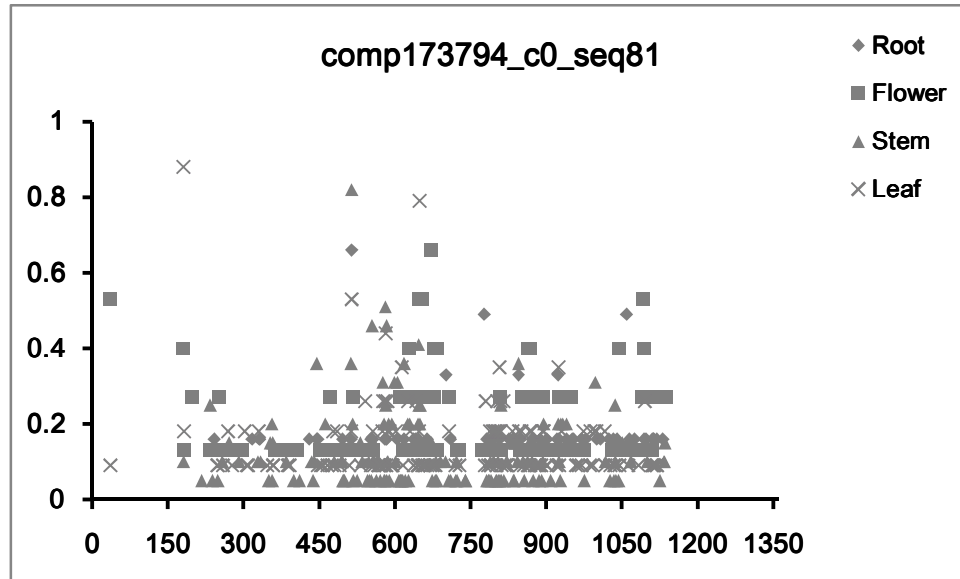


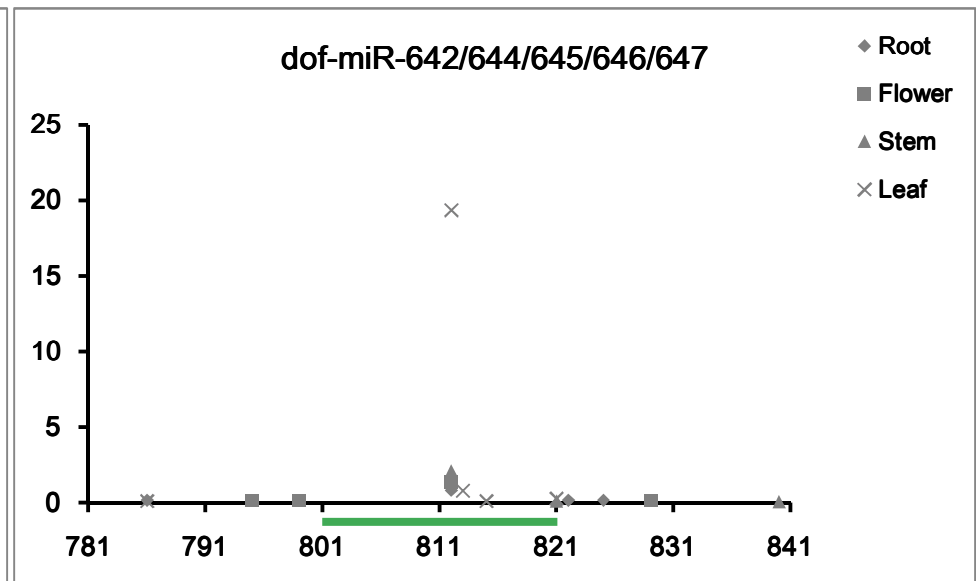
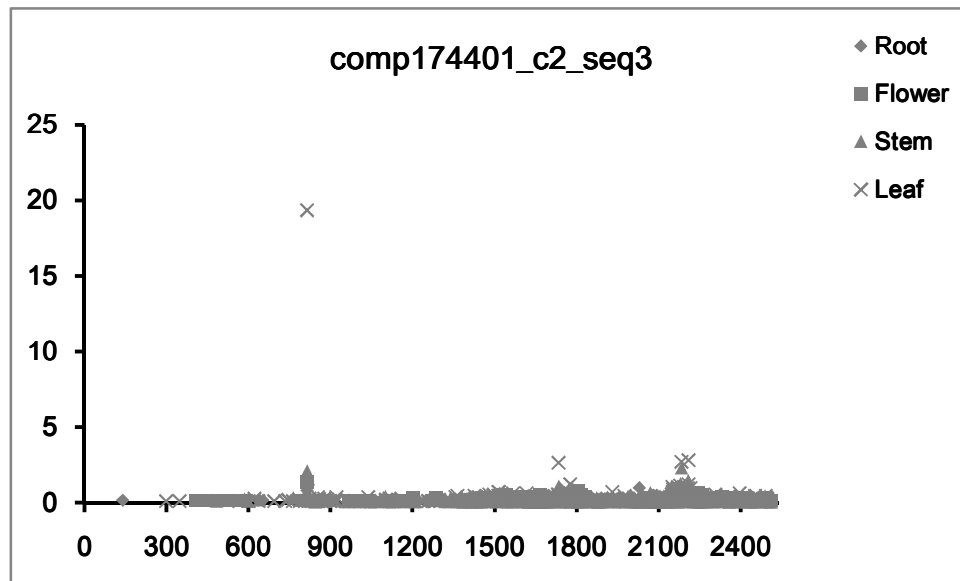
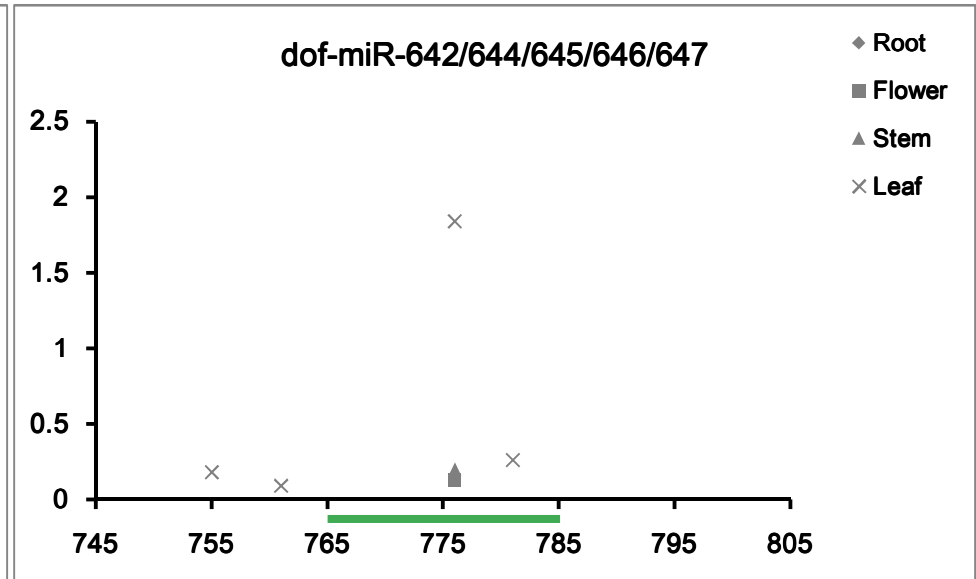
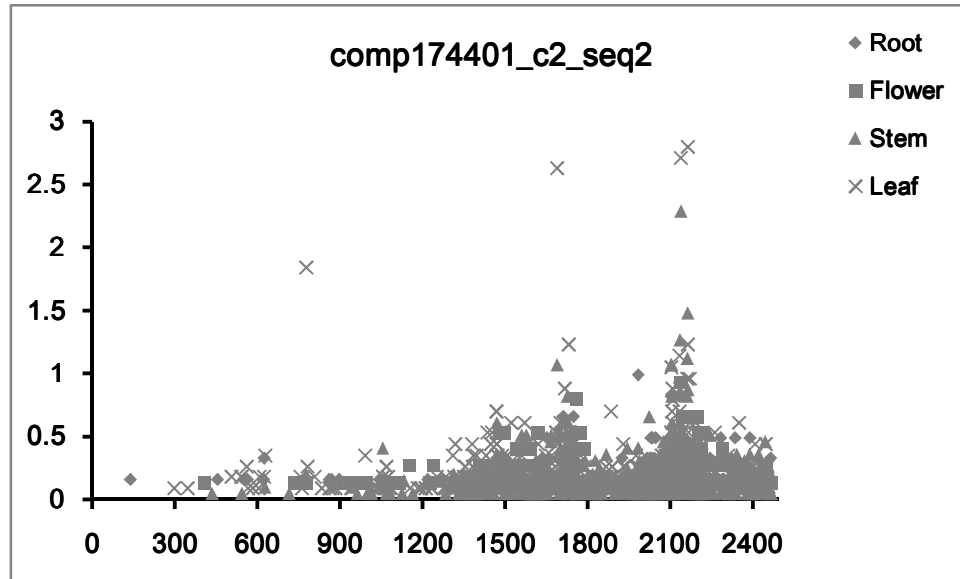


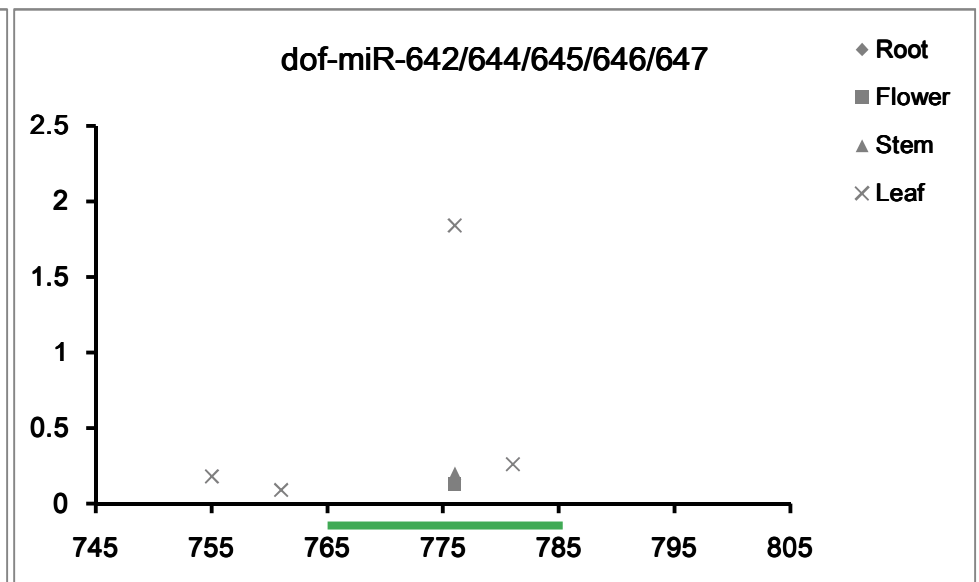
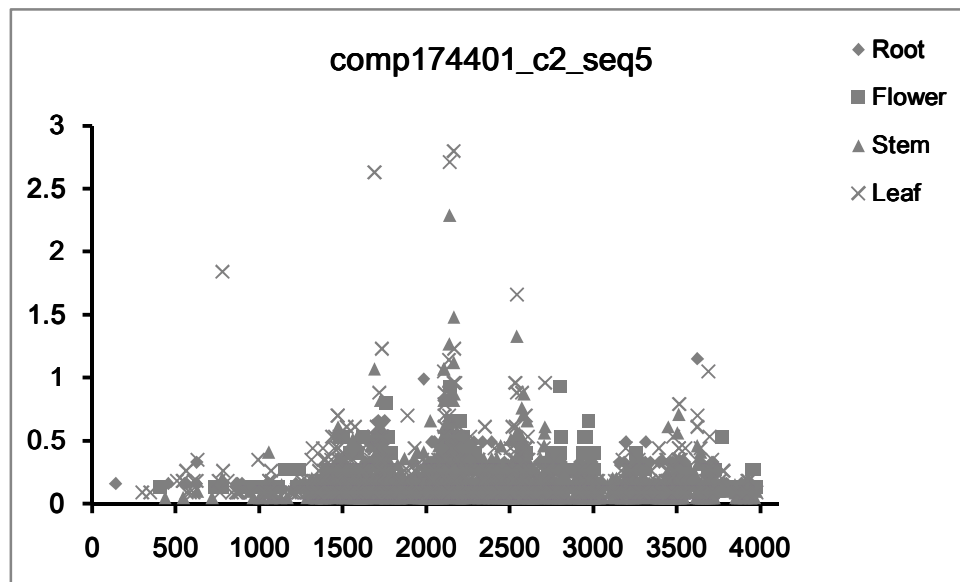
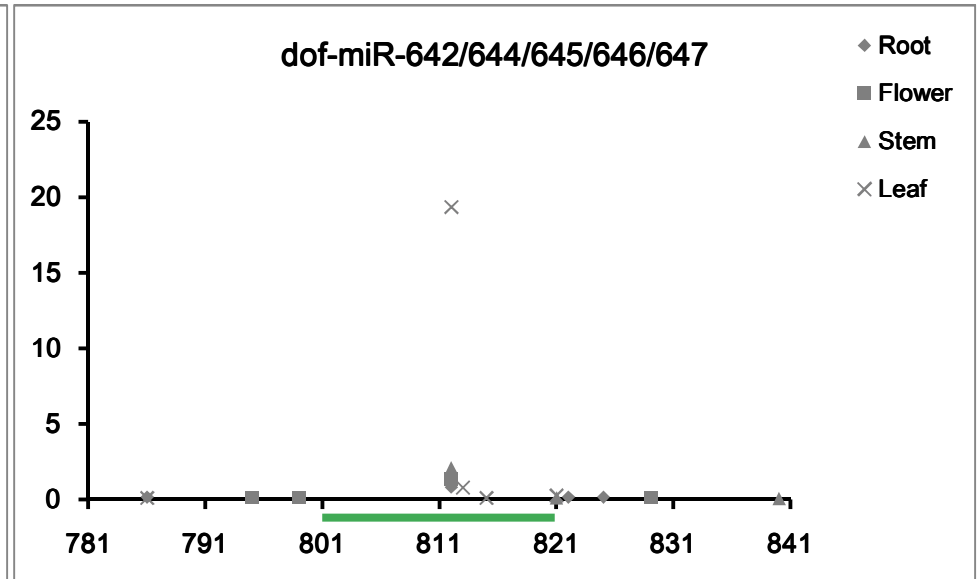
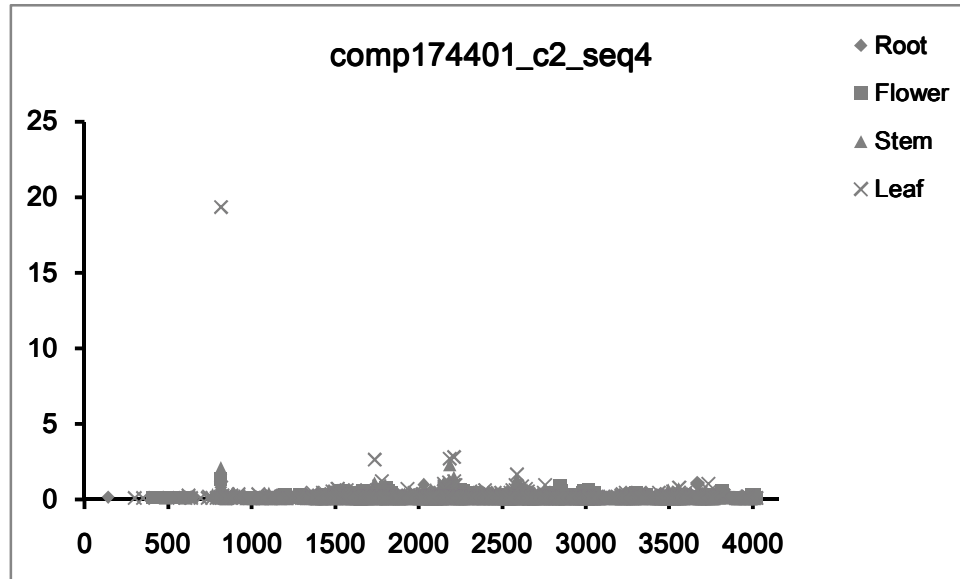


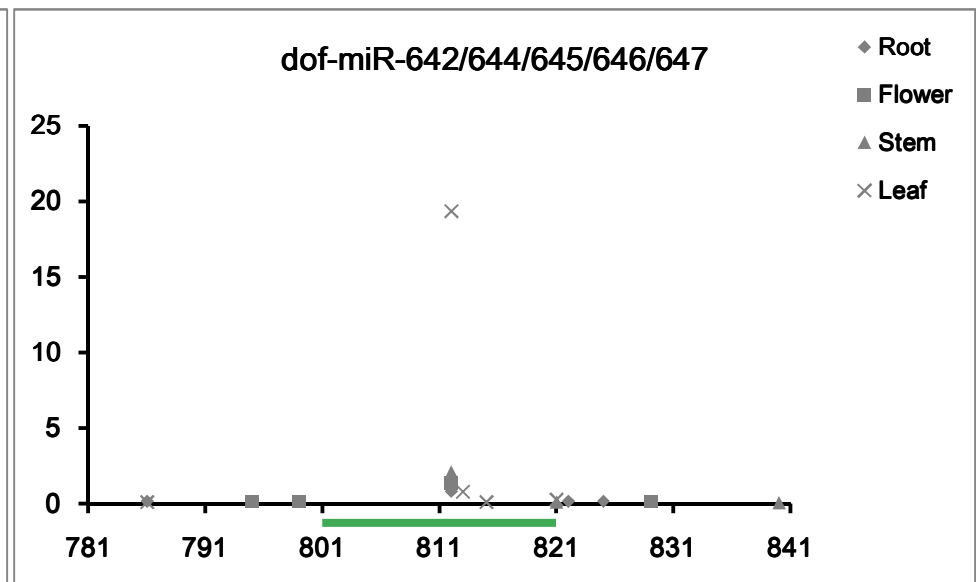
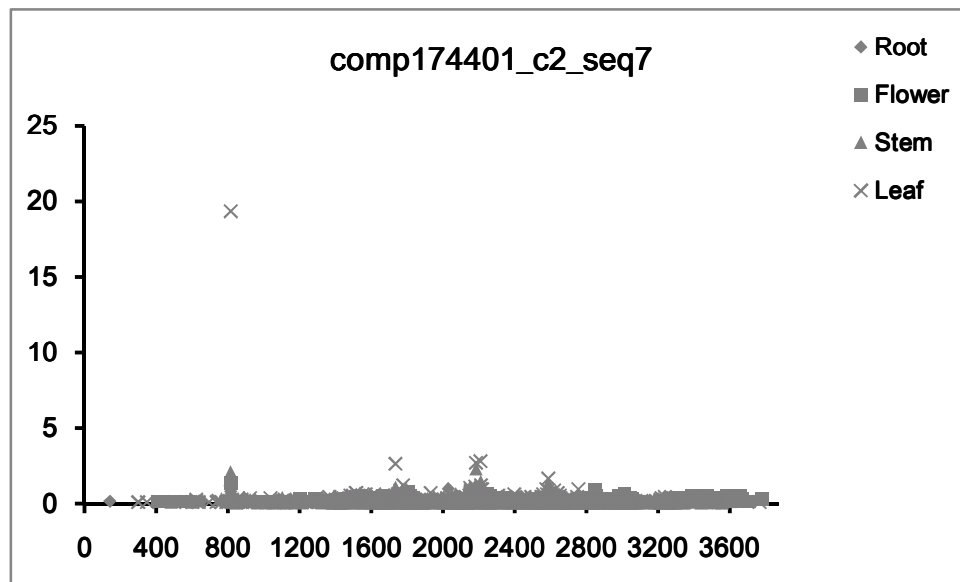
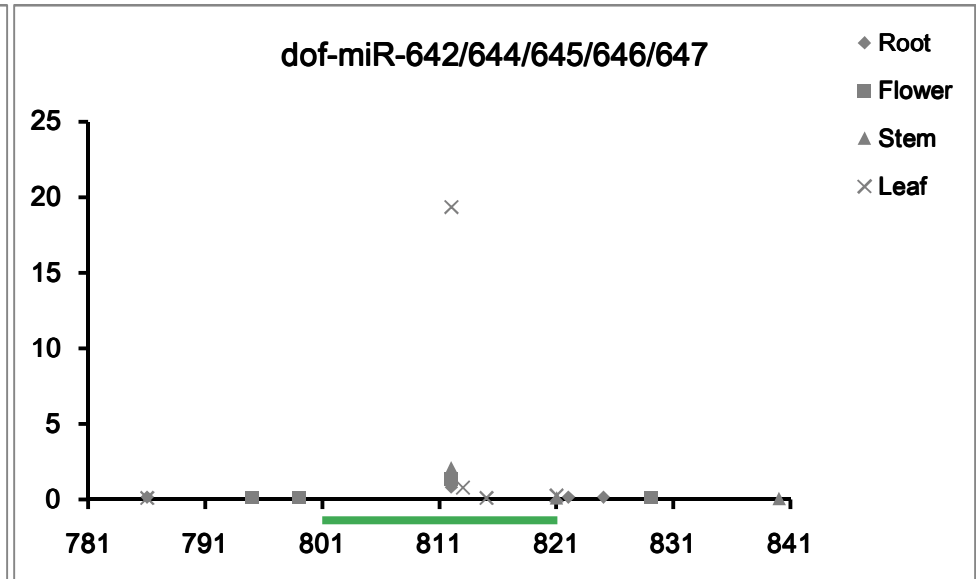
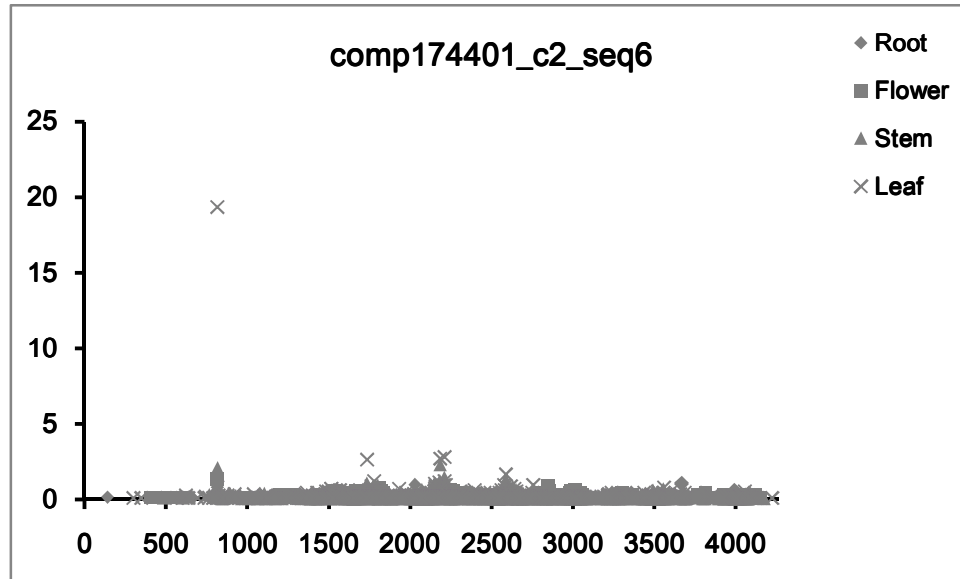












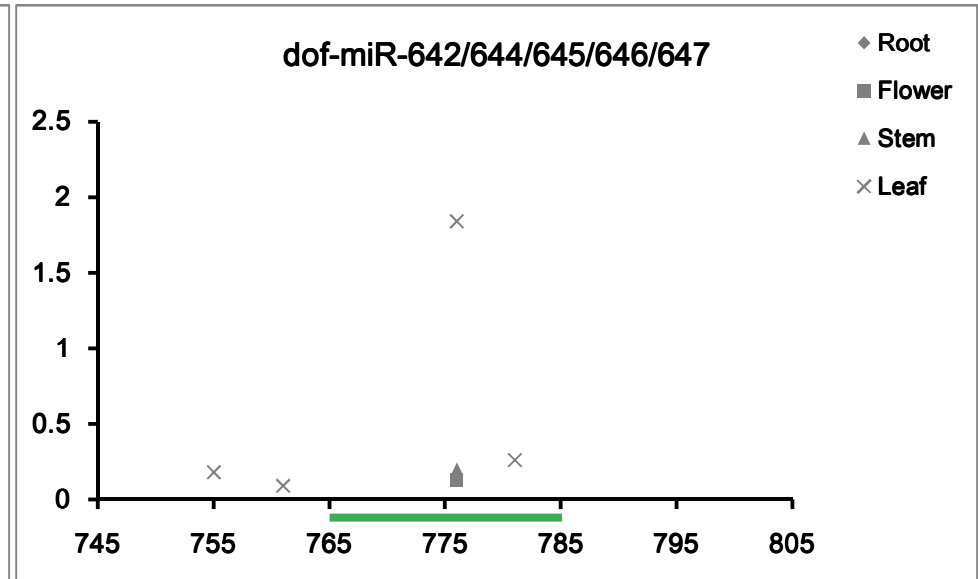
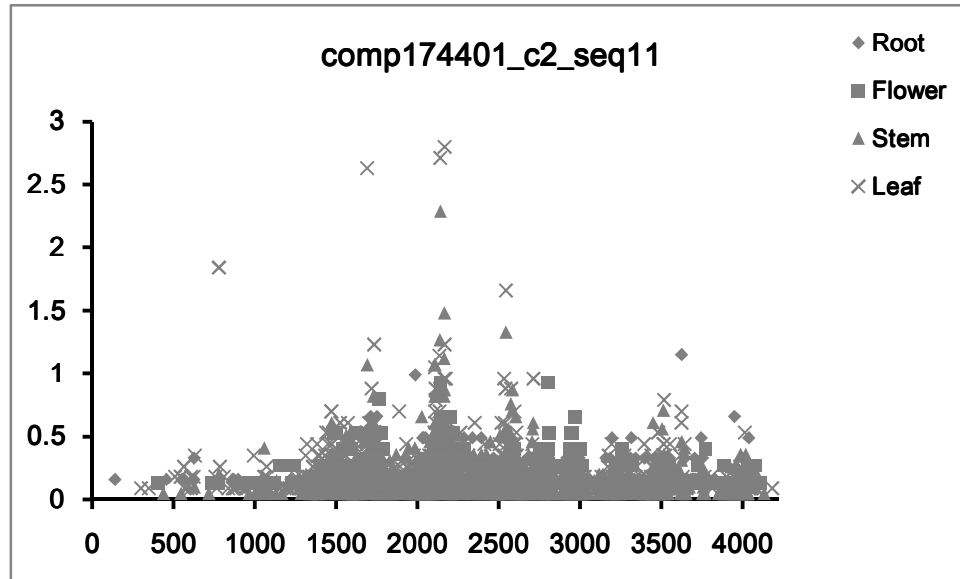
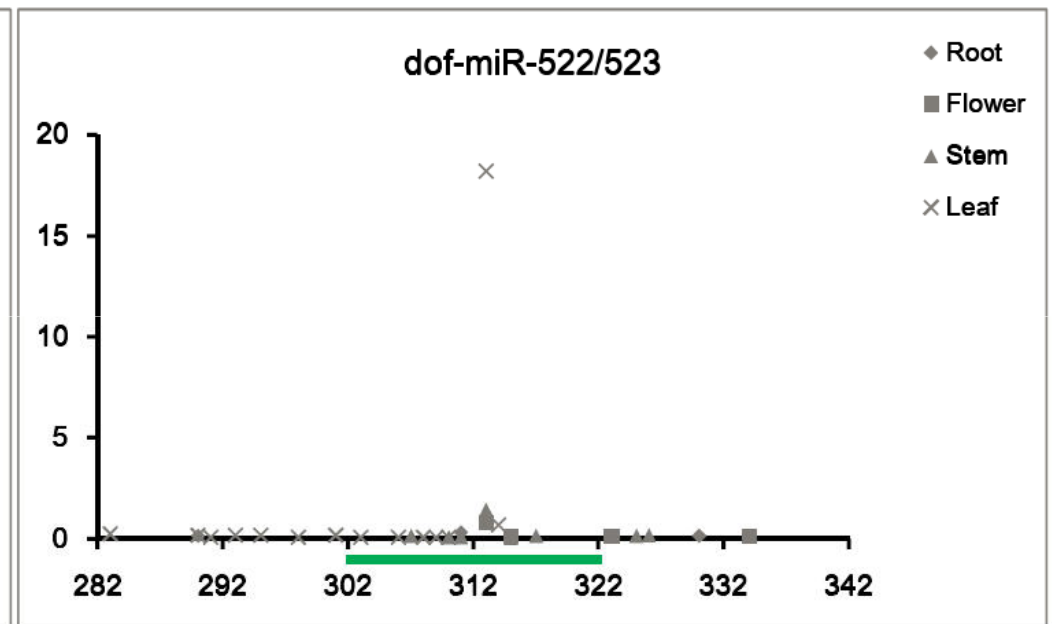
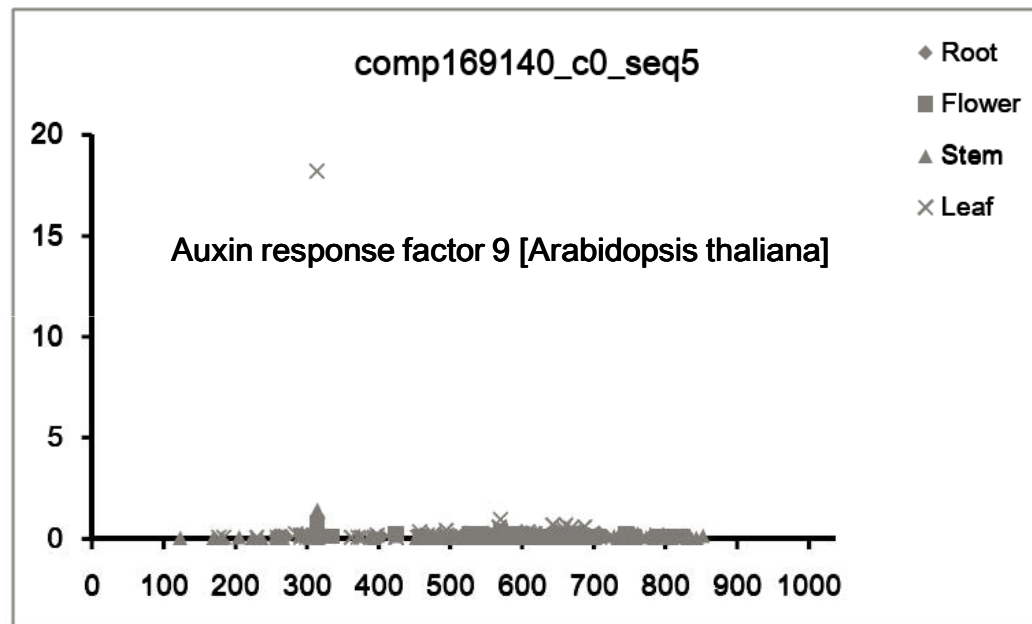
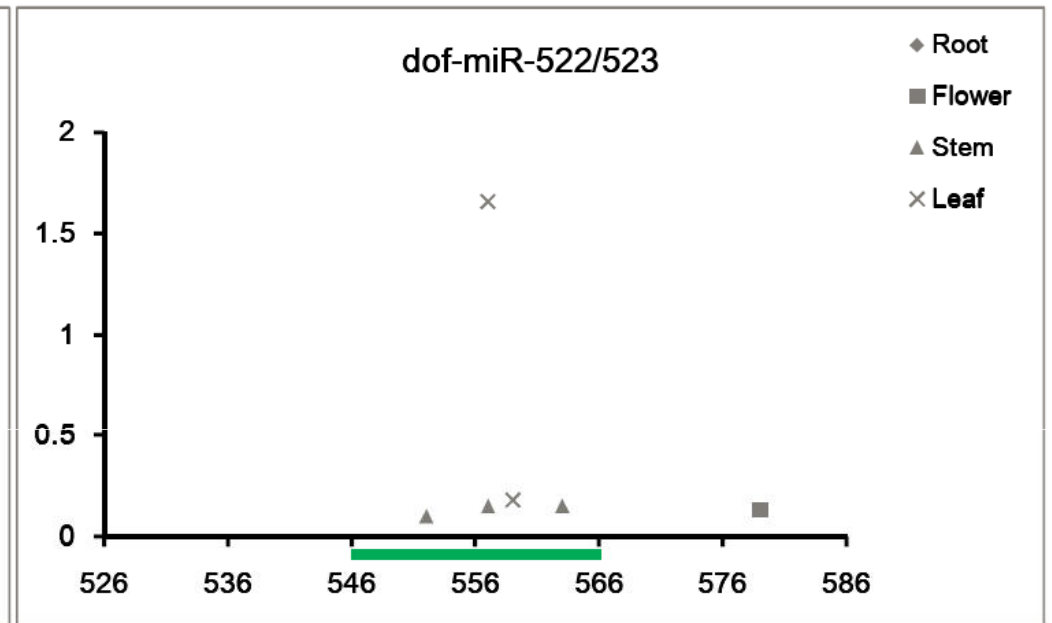
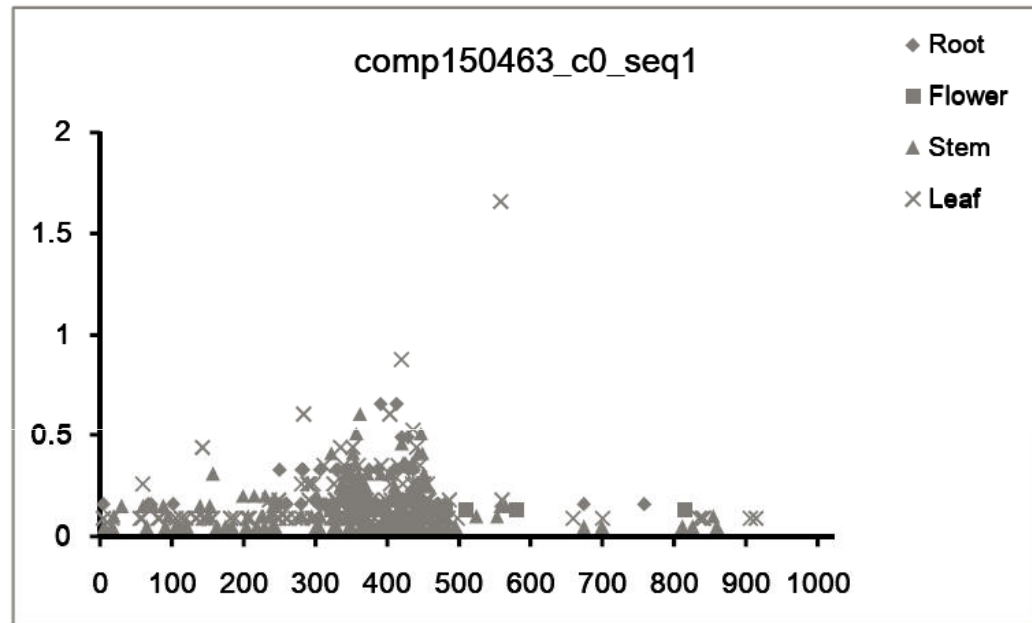
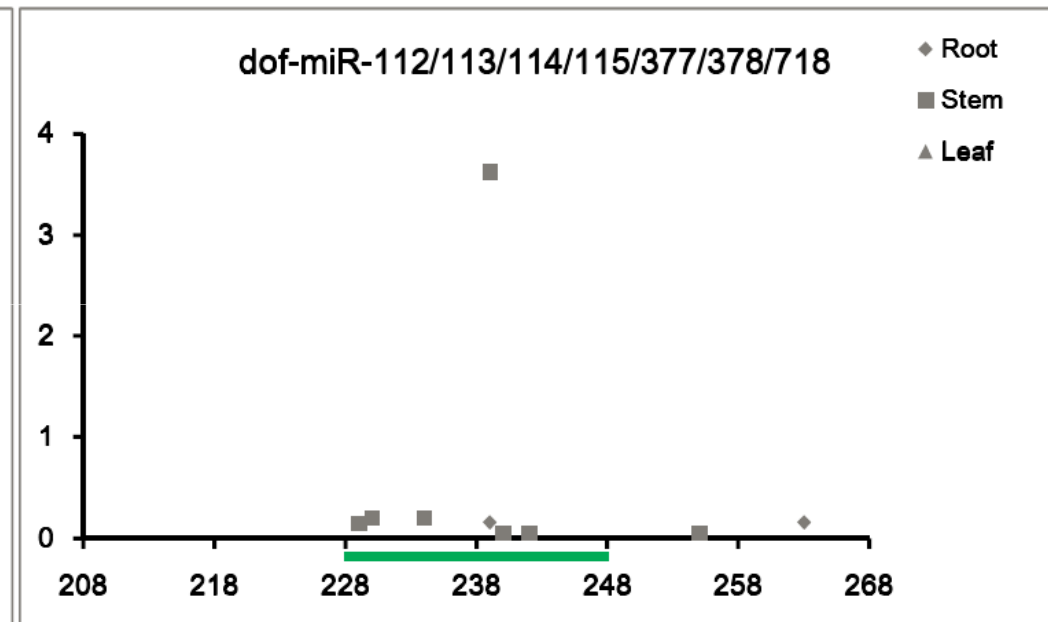
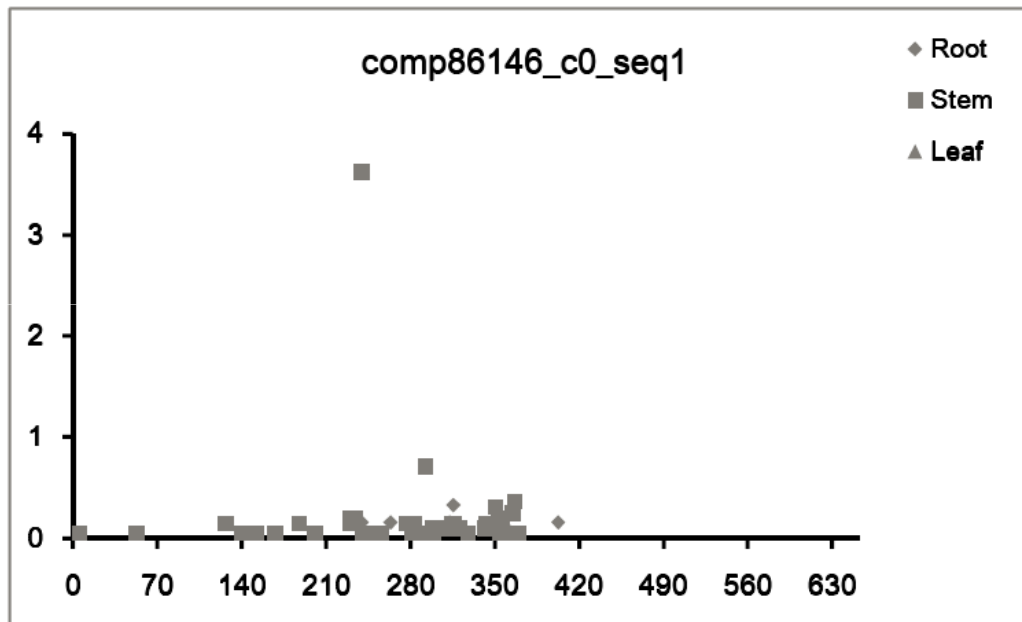
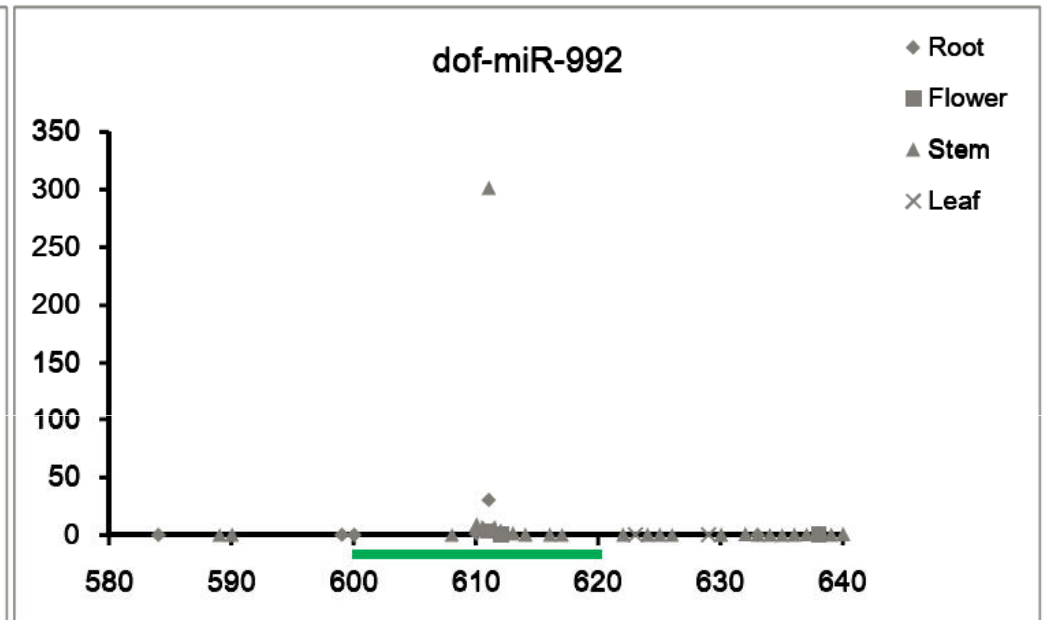
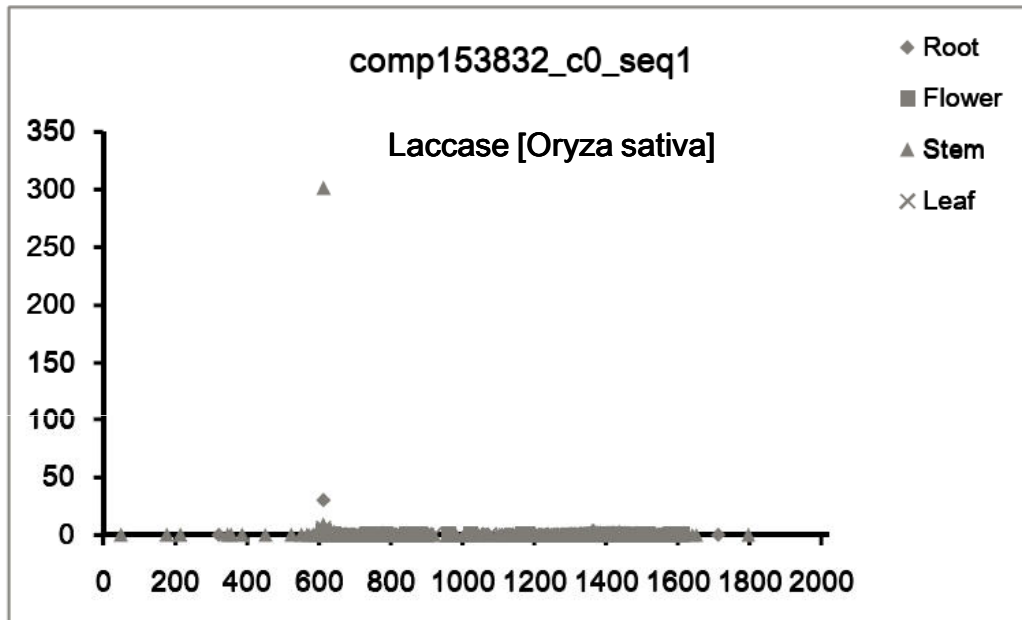


Figure S6 Examples of miRNA--target pairs showing organ-specific regulation.

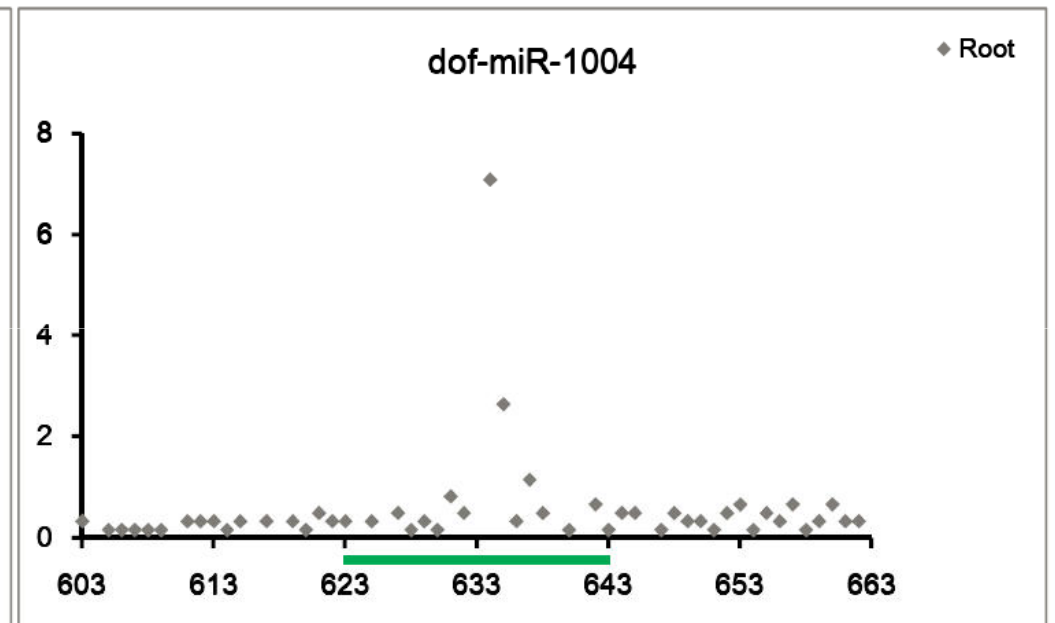
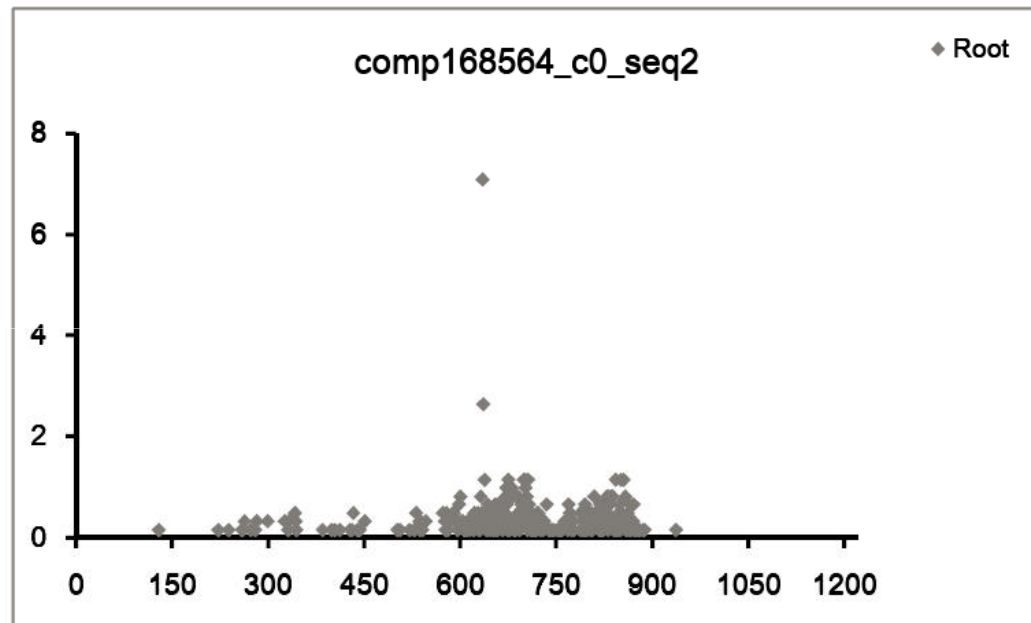
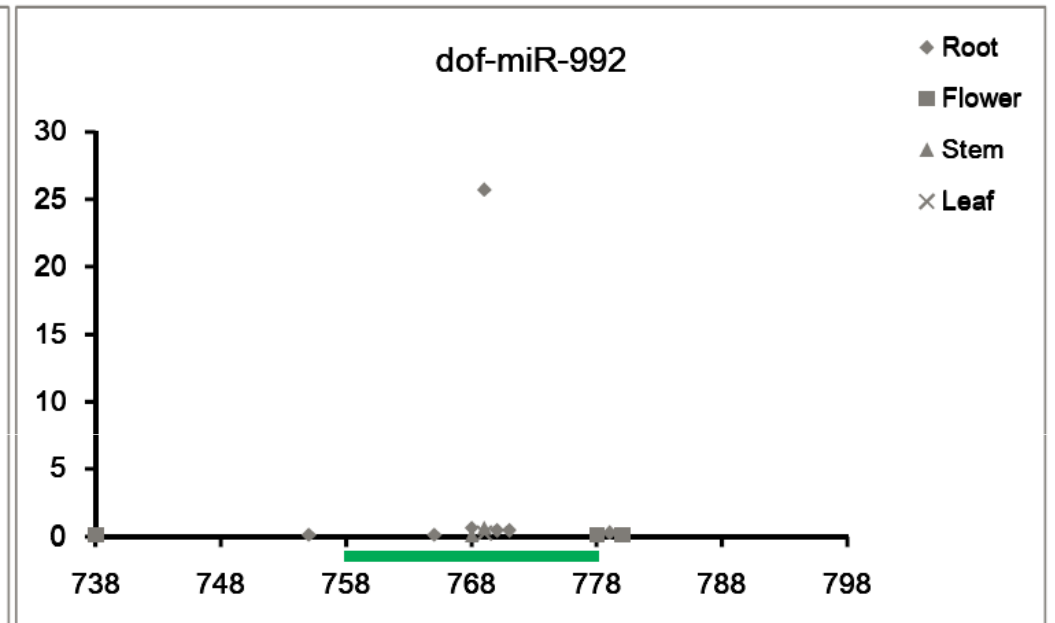
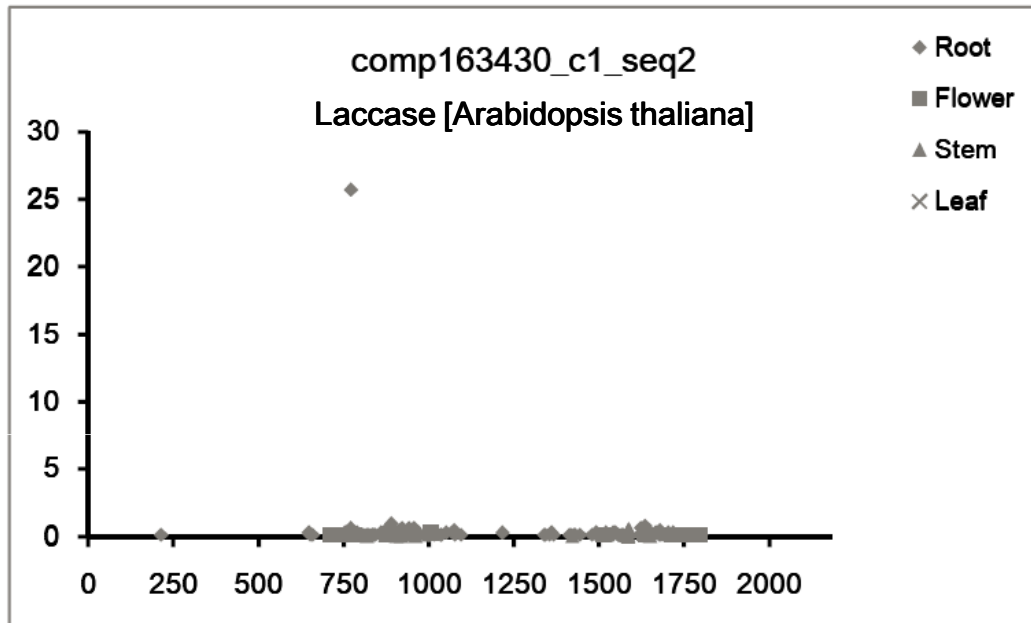
Leaf-specific regulation



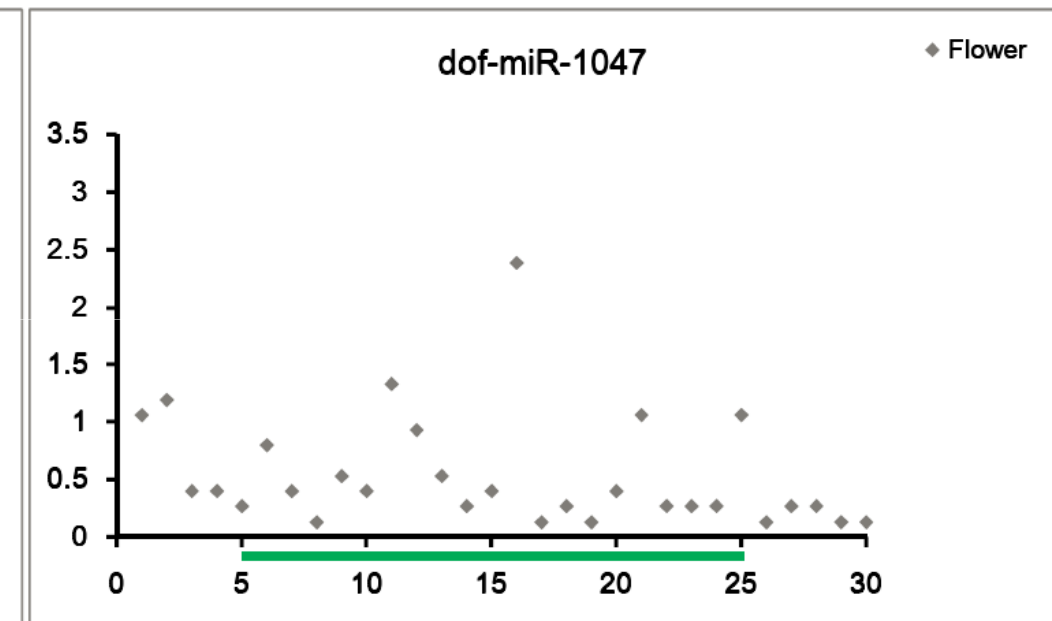
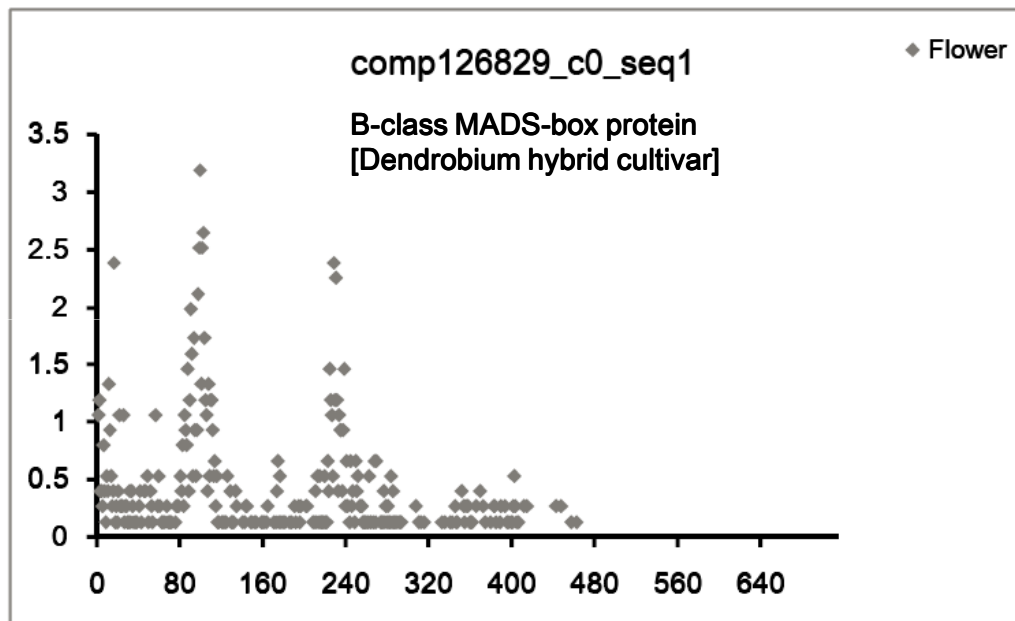
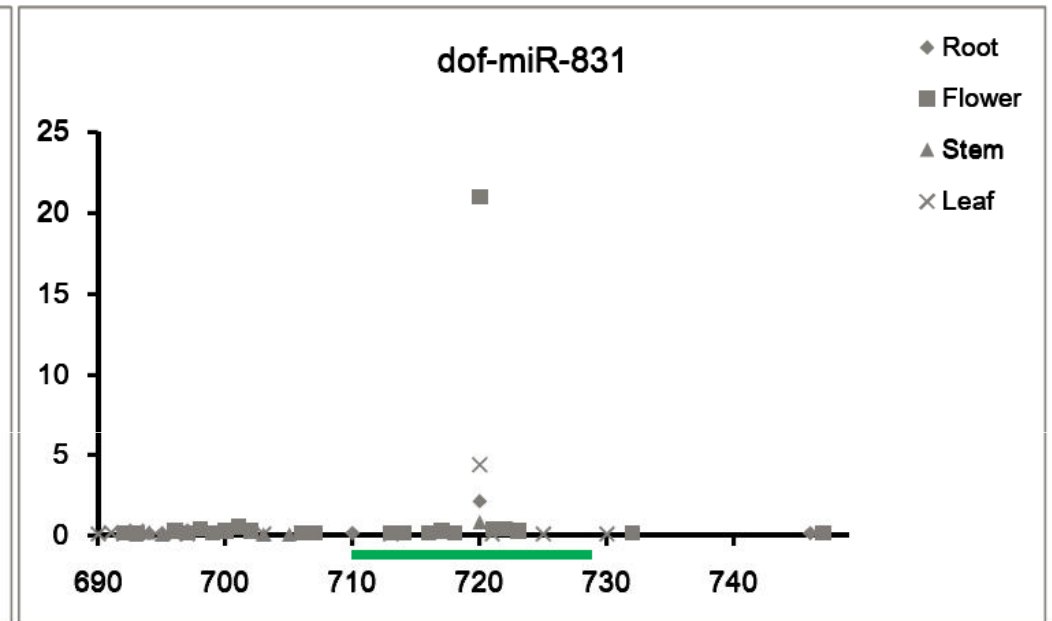
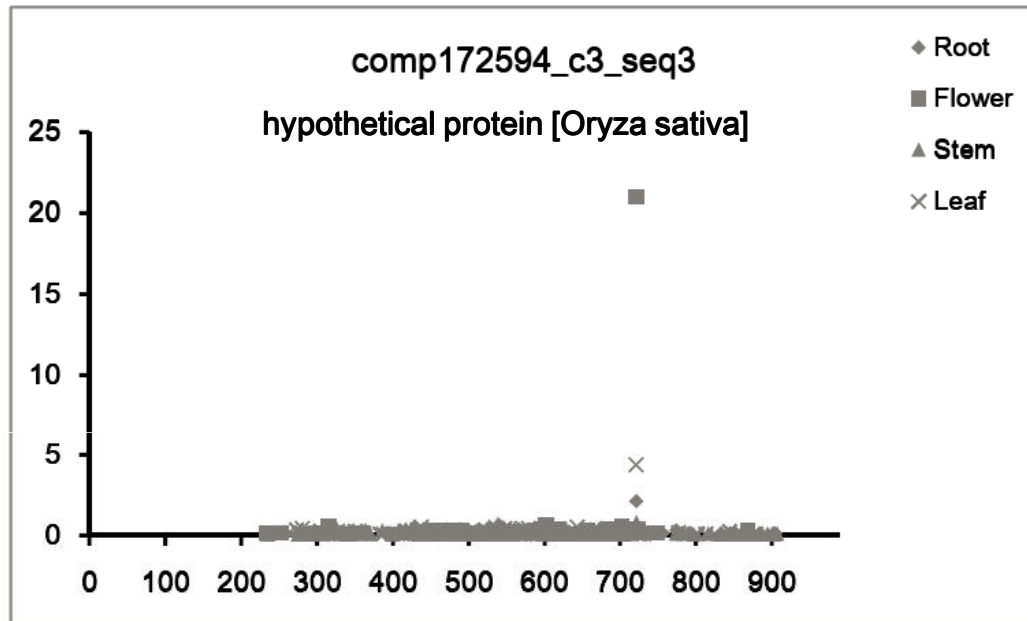
Stem-specific regulation



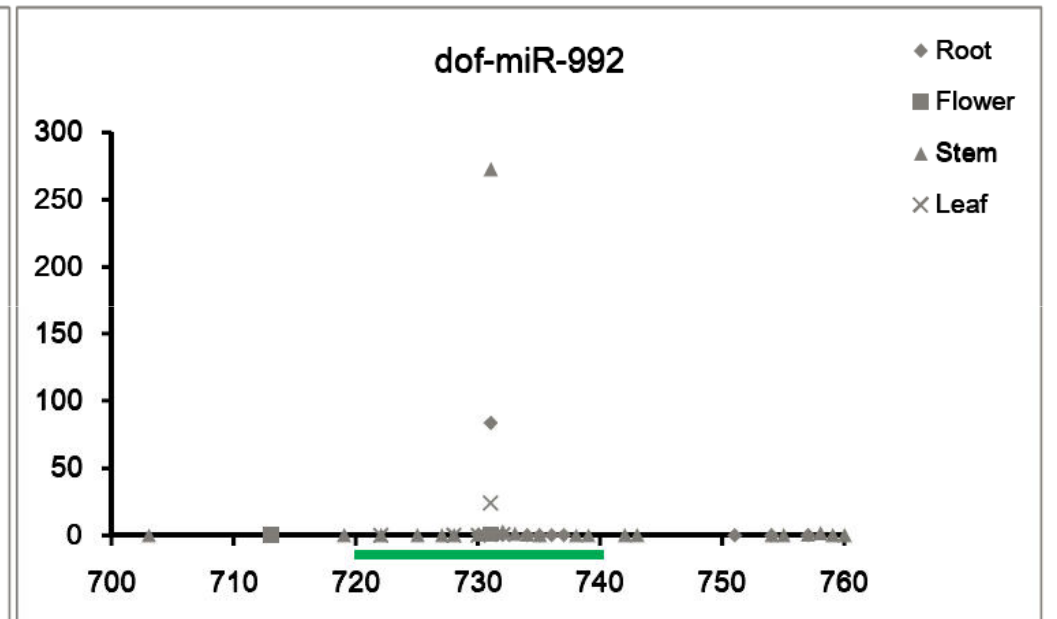
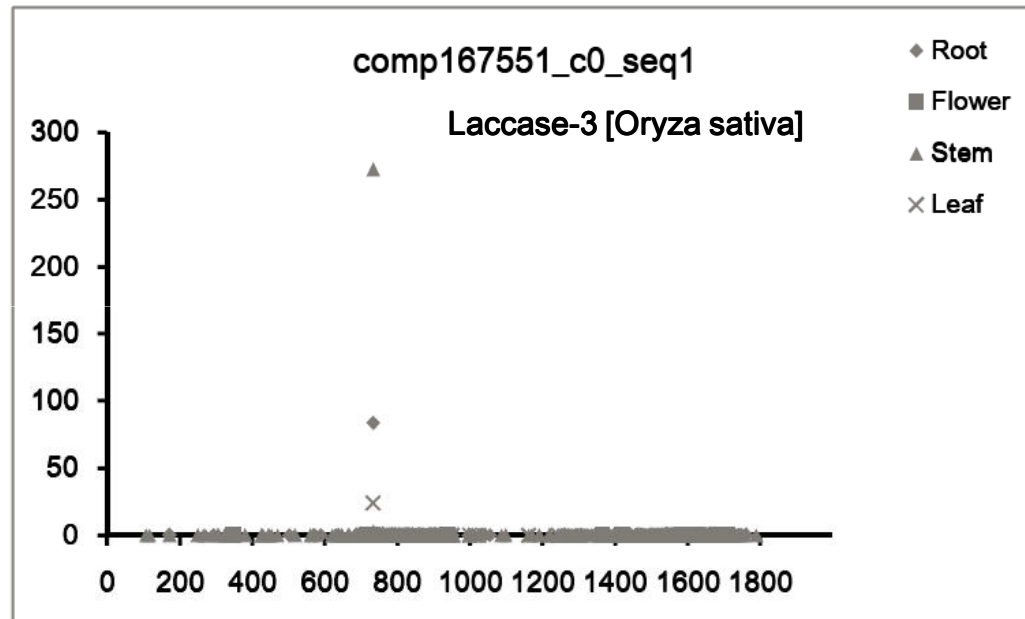
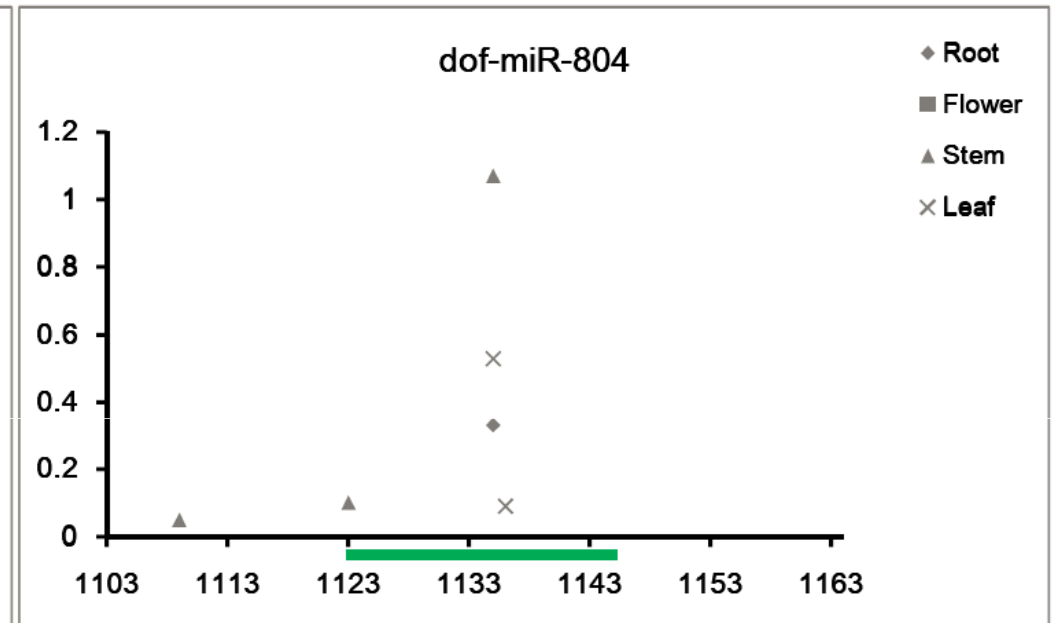
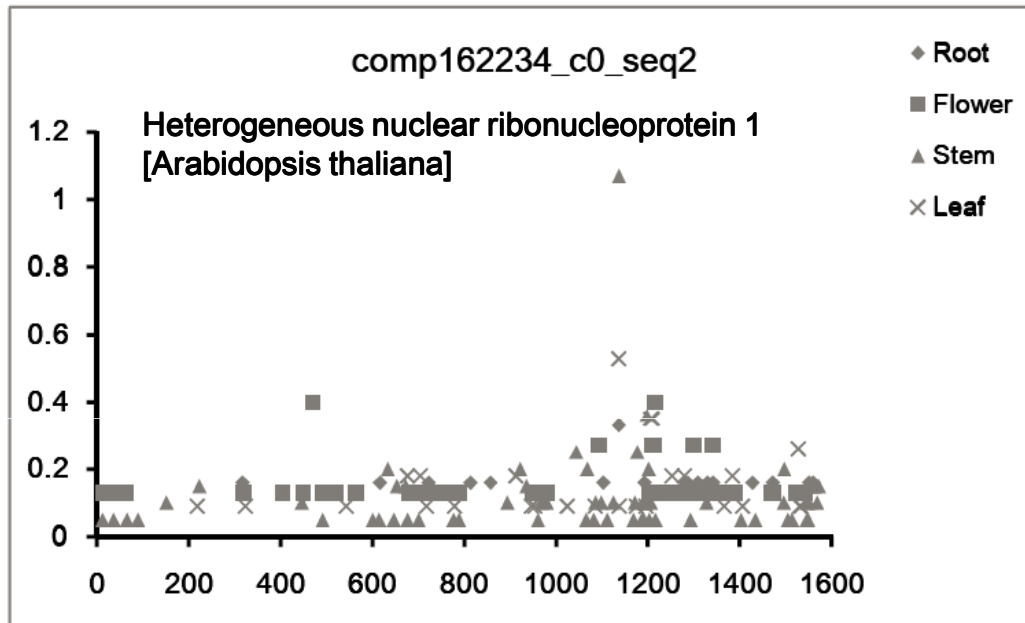
Root-specific regulation



Flower-specific regulation



Vegetative organ-specific regulation



Leaf-stem Homogeneity

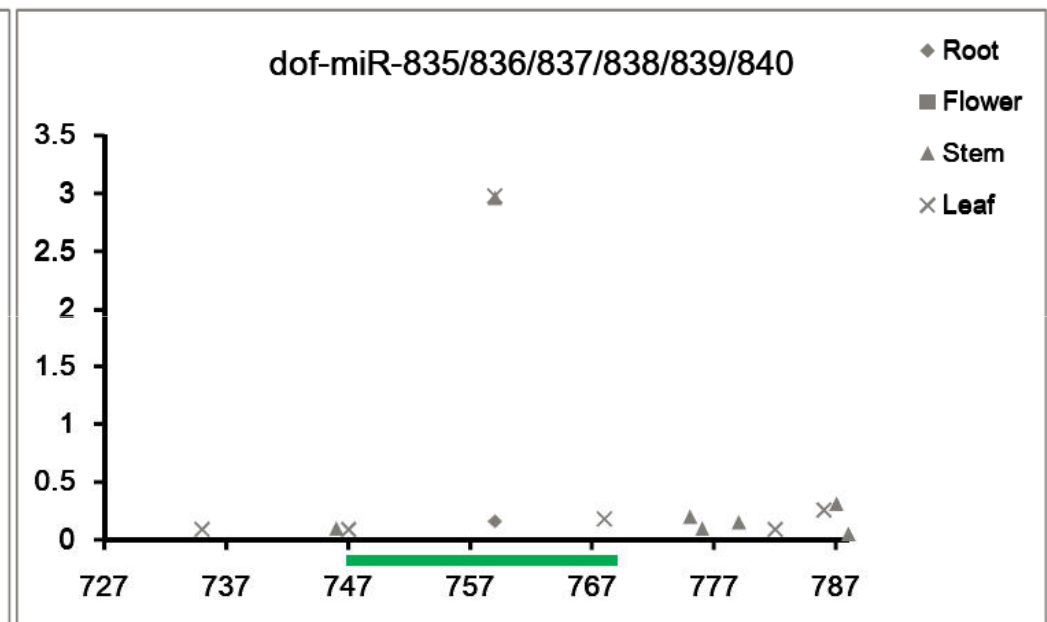
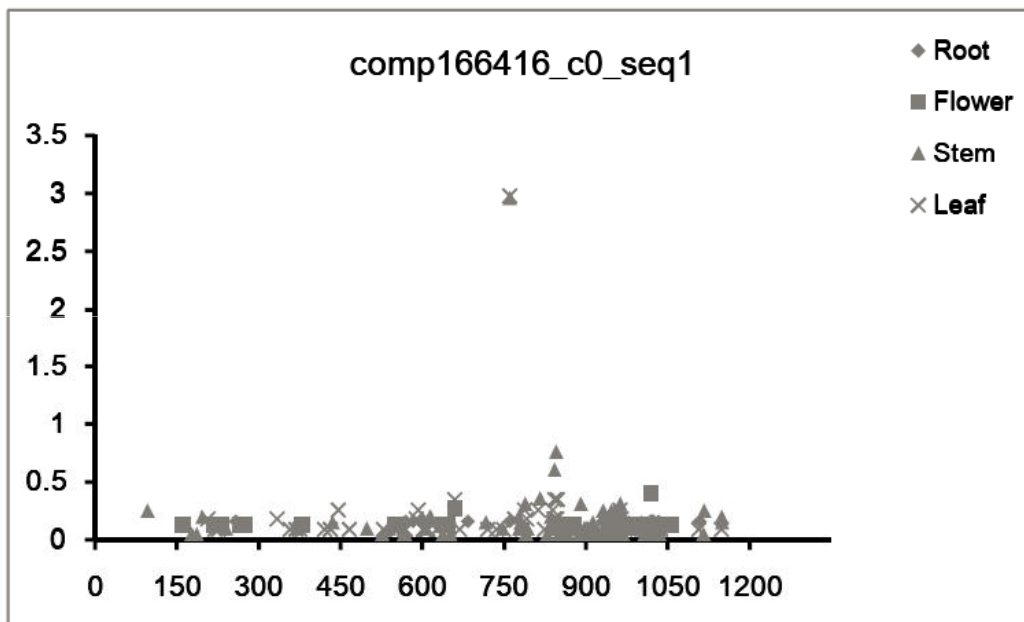
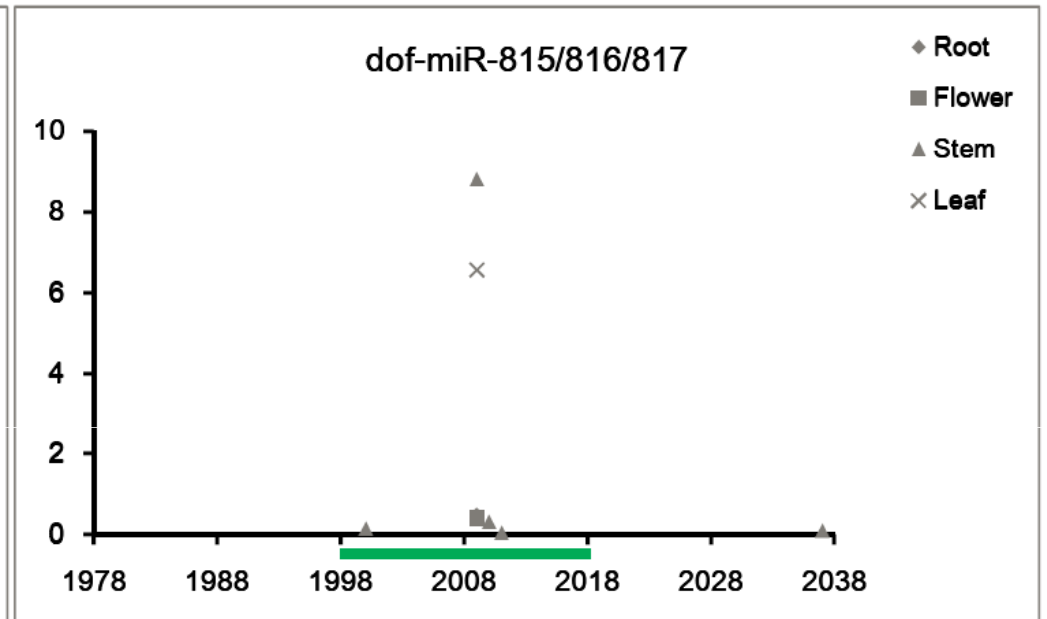
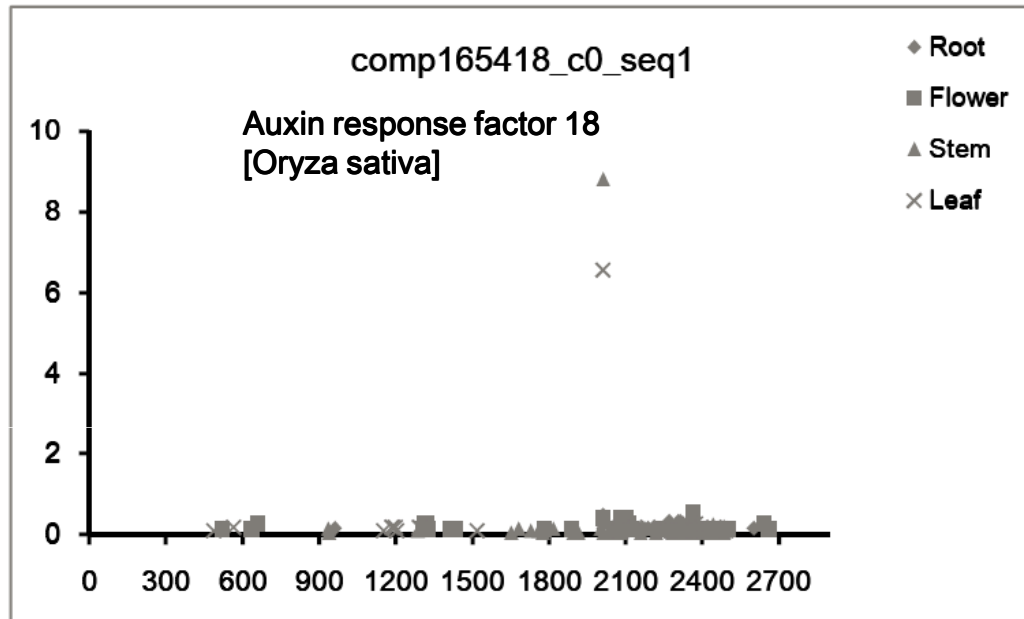


Table S1-1 Statistical result of the raw RNA-seq data.

Samples	Raw data		Valid data		Valid read ratio
	Read	Base	Read	Base	
Root-1	54,469,054	5,446,905,400	54,433,348	5,443,334,800	99.93%
Root-2	71,462,678	7,146,267,800	71,358,490	7,135,849,000	99.85%
Stem-1	50,076,260	5,007,626,000	50,076,260	5,007,626,000	100%
Stem-2	64,920,086	6,492,008,600	64,826,004	6,482,600,400	99.86%
Leaf-1	73,647,052	7,364,705,200	73,534,024	7,353,402,400	99.85%
Leaf-2	53,904,216	5,390,421,600	53,862,708	5,386,270,800	99.92%
Flower-1	38,776,952	3,877,695,200	38,736,660	3,873,666,000	99.9%
Flower-2	38,669,310	3,866,931,000	38,602,508	3,860,250,800	99.83%

Table S1-2 Statistical result of the assembled transcripts and unique genes.

	No. of transcripts /unique genes	Minimum length	Median length	Mean length	N50	Maximum length
Transcripts	536,558	201	463	931	1,731	21,555
Unique genes	299,107	201	333	660	1,192	21,555

Table S2 List of the transcripts highly accumulated in specific organs (root, flower, stem or leaf; highlighted) of *Dendrobium officinale*. The transcript IDs along with their expression levels (normalized in RPKM and rescaled by log10) in four organs are included in this table. For each organ, there are two biological replicates (“Root1” and “Root2”, for example). ND: not detected.

Transcript ID	Root1 (RPKM_log10)	Root2 (RPKM_log10)	Flower1 (RPKM_log10)	Flower2 (RPKM_log10)	Stem1 (RPKM_log10)	Stem2 (RPKM_log10)	Leaf1 (RPKM_log10)	Leaf2 (RPKM_log10)
comp100062_c0_seq1	ND	ND	0.705608898	0.642922407	ND	ND	ND	ND
comp100156_c0_seq1	-0.894770946	-0.983027335	0.307487518	0.279129056	ND	ND	ND	ND
comp100311_c0_seq1	ND	-1.327997686	0.171776788	0.2351887	ND	ND	-1.098811249	-0.381505255
comp100722_c0_seq1	ND	ND	0.419671258	0.403162069	-0.804156567	-1.467773955	-1.292565716	-0.575259722
comp100781_c1_seq1	ND	ND	0.463576743	0.50383223	ND	ND	ND	ND
comp100850_c0_seq1	ND	ND	0.226271043	0.242582976	ND	ND	ND	ND
comp101251_c0_seq1	ND	ND	0.72288165	0.66767523	ND	ND	ND	ND
comp101378_c0_seq1	ND	-0.998756835	-0.002432554	0.087308297	-0.582191244	-1.120869895	ND	-0.897362444
comp101455_c0_seq1	ND	ND	0.100615056	0.093445894	ND	ND	ND	ND
comp101476_c0_seq1	ND	ND	0.033821863	0.09359949	ND	ND	ND	ND
comp101736_c0_seq1	ND	ND	0.254578547	0.317990459	ND	ND	ND	ND
comp101775_c0_seq1	-0.660261952	-0.690526394	0.277769164	0.248323607	-0.523838276	-0.636548195	-0.665459939	-0.492221989
comp102949_c0_seq1	-0.290503443	ND	0.931958407	0.883396559	ND	ND	-0.994671435	ND
comp102949_c0_seq2	-1.137679451	ND	0.639986809	0.708318409	ND	ND	-1.297779398	ND
comp103765_c0_seq1	-0.716179162	-0.707525538	0.464890002	0.45772084	-0.445861907	-0.507419303	ND	-1.004071155
comp103898_c0_seq2	ND	ND	0.351928215	0.364064208	ND	ND	ND	ND
comp103965_c0_seq1	-1.035948961	-1.12420535	0.291248239	0.355434985	ND	-0.769197155	ND	-1.022810958
comp104594_c0_seq1	ND	ND	0.100937672	0.048011019	ND	ND	ND	ND
comp104812_c1_seq1	ND	-0.97663382	-0.008338262	0.02588526	ND	-0.922655621	-1.048477378	ND
comp105124_c0_seq1	ND	ND	0.567198732	0.619423221	ND	ND	ND	ND
comp105424_c0_seq1	ND	ND	0.069429724	0.027498455	ND	ND	ND	ND
comp105470_c0_seq1	ND	ND	0.368938546	0.378802723	ND	ND	ND	ND
comp105735_c0_seq1	ND	ND	0.593836759	0.576367639	ND	ND	ND	ND
comp105857_c0_seq1	ND	-0.664419657	0.206965887	0.141804778	ND	ND	-0.736263216	ND
comp105922_c0_seq1	-0.341540231	ND	0.371007851	0.337509749	-0.536109774	-0.59766717	-0.598550191	ND
comp106085_c1_seq1	ND	ND	0.174694197	0.138561339	ND	ND	ND	ND

comp106264_c0_seq1	ND	ND	0.716756259	0.780650452	-1.090246213	-0.549743618	ND	-0.627266162
comp107141_c0_seq1	ND	ND	1.242317499	1.226505374	ND	ND	ND	ND
comp107441_c0_seq1	ND	-1.367897949	0.641790293	0.618534311	ND	-0.614949746	ND	ND
comp108850_c0_seq1	ND	ND	0.643267027	0.65957896	ND	-1.128382828	ND	ND
comp109949_c0_seq1	ND	ND	1.219486763	1.168979584	ND	ND	ND	ND
comp110240_c0_seq1	ND	ND	0.124648927	0.168632287	ND	ND	ND	ND
comp110466_c0_seq1	ND	ND	0.076772011	0.023845358	ND	ND	ND	ND
comp111039_c0_seq1	-0.934870391	-1.500248034	0.04783112	0.017180861	-1.384712439	-0.969148581	-0.970031601	-0.921732388
comp111775_c0_seq1	ND	-0.953484861	0.696051934	0.702246733	ND	-1.501566653	ND	-1.153120465
comp111971_c0_seq1	-0.043446653	-0.270005739	0.709013683	0.732513341	ND	-0.216027541	ND	ND
comp111987_c0_seq1	ND	ND	0.056810362	-0.008350747	ND	-1.061626979	-0.710327481	ND
comp112394_c0_seq1	ND	-0.911574272	0.561871264	0.597736733	ND	-0.255536082	ND	-0.889361127
comp112619_c0_seq1	ND	-1.302691821	1.592974099	1.569058979	ND	ND	ND	-0.599237439
comp112628_c0_seq1	ND	ND	0.583068848	0.522214827	ND	ND	-1.090538723	ND
comp112712_c0_seq1	-0.782245724	ND	1.025505907	1.018336744	ND	ND	-0.305523573	-0.702160932
comp112712_c0_seq2	-0.739047891	-1.304425534	1.129252875	1.110019201	-1.188889939	-0.949417339	-0.200177833	-0.902001147
comp112990_c0_seq1	-1.247859188	-0.595752887	0.661563759	0.584052211	-0.304126033	-0.098867534	-0.036891273	-0.632661194
comp113103_c0_seq1	ND	-1.099266154	0.316187434	0.338981495	ND	ND	-0.870079717	ND
comp113219_c0_seq1	ND	-0.638292982	1.106080817	1.066567098	ND	-1.128382828	-1.254204585	-0.15154771
comp113411_c0_seq1	ND	ND	0.173464434	0.189776367	ND	-0.99612543	ND	-0.647679242
comp113485_c0_seq2	-0.708590027	-0.574997666	0.317577178	0.330611401	ND	ND	-0.567659978	-1.172573279
comp113635_c0_seq1	-0.5119771	-0.998173498	0.526424561	0.468102875	-1.183667898	-0.944195299	-1.070017056	ND
comp114874_c0_seq1	-0.922005609	-1.487383252	0.759665906	0.716781192	-1.070817661	-1.433405053	-1.082105556	-1.084958865
comp115195_c0_seq1	ND	ND	0.039974744	0.064990265	ND	-1.289315962	ND	ND
comp115336_c0_seq4	ND	ND	0.826883116	0.869880563	ND	-1.078660318	-1.204482075	ND
comp115519_c0_seq1	-0.297619421	ND	0.541991091	0.501821668	ND	ND	-1.110931882	ND
comp116270_c0_seq1	-0.642975163	-0.634321539	0.179072059	0.196036576	-0.615695957	-0.80219209	-0.560037062	-0.629837161
comp117054_c0_seq1	ND	ND	0.459400803	0.460504166	ND	ND	-0.819620402	-1.424533703
comp117315_c0_seq2	ND	ND	0.249438908	0.272232968	ND	ND	ND	ND
comp117397_c0_seq1	ND	ND	0.163480213	0.15631105	ND	ND	ND	ND
comp117454_c0_seq2	ND	ND	0.652330546	0.597736733	ND	ND	ND	ND

comp117552_c1_seq1	ND	ND	0.035030588	0.085853372	ND	ND	ND	ND
comp117641_c0_seq1	ND	ND	1.233415884	1.262291825	ND	ND	ND	ND
comp117912_c0_seq1	-1.421261309	-0.468125012	0.393276312	0.3437033	-0.916860847	ND	ND	ND
comp117914_c0_seq2	ND	ND	0.250630388	0.197703735	-0.90315957	ND	ND	ND
comp118193_c1_seq1	ND	0.067007458	0.868609531	0.920923883	-1.02157693	ND	-1.208956083	ND
comp118346_c0_seq1	ND	ND	0.725828565	0.707378392	-1.320055996	ND	ND	ND
comp118699_c1_seq1	ND	-0.825136055	0.465378798	0.391262845	-1.010630455	ND	ND	-1.024771659
comp118815_c0_seq1	-1.058290855	-1.146547244	0.326898292	0.370881652	-0.553890394	-1.092569045	-0.519420798	-1.045152853
comp118843_c0_seq2	ND	ND	0.837911448	0.84146615	ND	ND	ND	ND
comp119247_c0_seq2	ND	ND	0.186815322	0.241794066	-0.682977979	ND	-0.967267146	-0.617937937
comp119829_c0_seq1	ND	ND	0.367415372	0.320737668	-1.148102422	ND	-0.733421584	-0.560183634
comp119973_c0_seq1	-0.992586683	ND	0.188482482	0.222706004	ND	ND	ND	ND
comp120258_c0_seq1	-0.841801289	0.149123568	2.029906887	1.997679704	ND	-0.575049483	-0.70087124	-0.828663287
comp120574_c0_seq4	ND	ND	0.418121476	0.402178389	ND	ND	ND	ND
comp120574_c0_seq5	ND	ND	0.666121062	0.658951899	ND	ND	ND	ND
comp120944_c0_seq1	ND	ND	0.300740186	0.293571024	ND	ND	ND	ND
comp120967_c0_seq1	0.249246665	0.200498817	1.016581553	0.987418097	0.233060178	0.123198102	0.410380099	0.144285355
comp120994_c0_seq1	-1.403082728	-1.014217862	1.831449041	1.807845153	ND	ND	ND	-0.435702217
comp121694_c0_seq1	ND	ND	0.673429074	0.696223135	ND	ND	ND	ND
comp121722_c0_seq1	ND	ND	0.114264655	0.16261282	ND	ND	ND	-0.794029196
comp121773_c0_seq1	ND	ND	0.659885833	0.67315783	-1.412982217	-1.474539614	ND	ND
comp121911_c0_seq1	ND	ND	0.3038759	0.274430343	ND	ND	ND	ND
comp122050_c0_seq1	-0.053284523	-0.141540912	0.604905896	0.664683523	-0.327035312	0.0093473	ND	-0.943236508
comp122138_c0_seq1	-0.226428547	0.241617565	0.918428445	0.871750741	0.14327334	0.216414518	-0.006317253	-0.009170562
comp122268_c1_seq1	ND	-1.265534502	0.304821046	0.297651884	ND	ND	ND	ND
comp122268_c2_seq1	ND	ND	0.152386136	0.186609659	ND	ND	ND	-0.71451503
comp122426_c0_seq1	-0.284473299	-0.321577165	0.599169994	0.546641959	-0.792307294	-0.619781485	-1.523754492	-1.049486547
comp122478_c0_seq1	ND	-1.413954335	1.615793702	1.577366845	ND	ND	ND	-1.312559944
comp122568_c0_seq1	ND	ND	0.858210083	0.831146092	ND	ND	ND	ND
comp122650_c0_seq1	-1.591923816	ND	1.76174828	1.734570264	ND	ND	ND	ND
comp122670_c0_seq1	ND	ND	0.219999533	0.16707288	ND	ND	-1.121169578	ND

comp122716_c0_seq1	-0.925398551	ND	0.209913122	0.151591437	ND	ND	ND	ND
comp122990_c1_seq1	-0.857888109	ND	0.252599981	0.161109933	-0.654517643	ND	ND	-0.668658847
comp123286_c0_seq1	ND	ND	0.270568718	0.298161662	ND	ND	ND	-0.97654369
comp123968_c0_seq1	ND	-1.176593419	0.649034635	0.641865472	-0.362087819	-0.520555229	-0.947406982	ND
comp124031_c0_seq1	ND	-0.720163514	0.093230083	0.116024144	ND	-0.791124052	-0.792007073	-0.919799119
comp124166_c0_seq1	-0.690106621	-0.03800032	1.172203781	1.16953512	0.182270626	0.253338795	-0.248146577	-0.199847364
comp124442_c0_seq2	ND	-0.978470163	0.069006641	0.061837478	ND	ND	ND	ND
comp124473_c0_seq1	-0.614109154	-1.304425534	0.923941412	0.926213805	ND	-0.949417339	ND	-0.902001147
comp124605_c0_seq1	ND	ND	0.424677905	0.433595562	-1.453387923	ND	ND	-1.166499131
comp124609_c0_seq1	ND	-1.517005719	1.760494019	1.749256995	-1.702500119	-1.161997524	ND	-0.762398814
comp124722_c0_seq2	ND	ND	0.291466642	0.319059586	ND	ND	ND	ND
comp124826_c0_seq2	ND	ND	0.020991394	0.013822232	ND	ND	ND	-1.076358693
comp125050_c0_seq4	ND	ND	0.210310919	0.148784094	ND	ND	ND	ND
comp125616_c1_seq1	-1.253452754	ND	0.206370011	0.150896169	ND	-1.287730944	-1.112522706	ND
comp125666_c0_seq1	ND	-1.166014681	0.249438908	0.300261692	-1.050479086	ND	ND	-0.587499035
comp125713_c0_seq1	-0.39149072	-0.655838367	1.060645217	0.999893226	0.003765272	0.000199823	0.012680764	-0.378352717
comp125854_c0_seq2	0.339306629	0.160389176	1.765029322	1.710587084	-0.040899491	-0.102456888	-0.079858813	-0.372461107
comp125902_c0_seq1	-0.736444719	-0.903882354	0.465813745	0.407492059	ND	ND	ND	-1.501457967
comp125909_c1_seq1	ND	ND	0.644414437	0.617041889	ND	-1.214385594	ND	-0.865939406
comp125914_c0_seq1	ND	ND	0.529941134	0.522771972	ND	ND	ND	-0.592232537
comp125931_c0_seq2	-0.640946694	-1.331263074	1.278506594	1.311104558	-0.516757474	ND	ND	-1.229868683
comp126018_c0_seq1	ND	ND	0.98476481	1.005624371	-1.521207666	ND	ND	ND
comp126060_c0_seq1	ND	ND	1.231254938	1.178288697	ND	ND	ND	ND
comp126086_c0_seq1	ND	-0.663474511	0.259063556	0.251894393	ND	ND	ND	ND
comp126197_c0_seq1	-0.213192815	-0.000419208	0.702561906	0.717669138	ND	ND	-0.917360807	-1.045152853
comp126304_c0_seq1	ND	ND	0.030455223	0.02328606	ND	ND	ND	ND
comp126393_c0_seq1	ND	-0.640483748	1.124848404	1.179981126	-1.303099403	ND	ND	ND
comp126446_c1_seq1	ND	-0.339675387	0.656648894	0.58102235	-0.877352306	-0.336849711	-1.06473146	-0.493553501
comp126675_c0_seq1	ND	-0.528001103	1.075778201	1.015188655	0.078896186	-0.432630219	-0.395724679	-0.385214027
comp126694_c0_seq1	-0.498489991	-0.665927626	2.23055888	2.291710441	ND	-1.009889435	ND	-1.263503239
comp126713_c0_seq1	ND	ND	0.470769315	0.443078485	ND	ND	-0.905161903	-1.032953949

comp126829_c0_seq1	ND	ND	1.388789494	1.387327306	-1.342492263	ND	ND	-1.055603472
comp126833_c0_seq2	ND	-0.714311527	0.468827878	0.472124149	-0.820624681	-0.317910647	-0.281005107	-0.834765886
comp126969_c0_seq1	-0.729867696	-0.450147299	0.27511021	0.23408278	-1.480739739	-1.065175881	-0.521990857	-0.649782903
comp127026_c0_seq1	ND	ND	0.122821222	0.068227409	ND	ND	ND	-1.507507938
comp127121_c0_seq1	-1.278893422	ND	1.066528599	1.062323915	ND	ND	ND	ND
comp127121_c0_seq2	-1.38878603	-1.477042419	0.941502247	0.949466828	-1.361506823	-1.42306422	ND	ND
comp127189_c1_seq1	ND	-1.242211074	0.231234462	0.166073352	ND	ND	ND	ND
comp127199_c0_seq2	ND	ND	0.102650348	0.141238676	ND	ND	ND	ND
comp127398_c0_seq1	-0.576792225	-0.841139873	1.55122021	1.578624371	ND	-1.389221665	-1.214013427	-0.739745482
comp127540_c0_seq2	ND	-1.40029615	0.522241917	0.485109531	ND	ND	ND	ND
comp127585_c0_seq1	ND	ND	0.059939621	0.052770458	ND	-0.933558984	-0.758350746	-0.585112796
comp127594_c0_seq3	-0.975761755	-0.25783817	0.319250762	0.223444112	-0.744362566	-0.277646185	-0.931741719	-0.339374462
comp127720_c0_seq1	ND	-1.035889086	0.254625766	0.30544855	-1.221383487	ND	-0.806702649	-0.934494695
comp127818_c0_seq1	ND	ND	1.039777023	0.998749593	ND	ND	ND	ND
comp127884_c0_seq5	ND	-1.643928444	1.078715449	1.05756064	-1.051271594	-1.112828991	ND	-1.241504058
comp127927_c0_seq1	ND	-1.092976985	1.039671428	1.01116421	ND	-0.641058778	-1.164820544	ND
comp128139_c0_seq1	-0.394370031	-0.482626419	0.771975877	0.764806714	-0.242152087	-0.905769475	ND	-0.557323287
comp128365_c0_seq1	ND	ND	1.065597151	1.072536242	ND	-1.175056069	ND	ND
comp128479_c0_seq1	ND	ND	0.790950453	0.758597744	-1.214097854	ND	ND	ND
comp128517_c0_seq1	ND	-0.962608021	0.452845568	0.445676405	-0.670981167	ND	-0.557330325	-0.560183634
comp128706_c0_seq1	-0.308440455	-1.47587809	0.854145304	0.910129942	ND	-0.944778636	ND	-1.374483698
comp128712_c0_seq1	-0.793647213	-0.404782347	0.365145557	0.334495299	-1.067398002	-0.952864139	ND	-1.382569202
comp128791_c0_seq1	-1.121846793	-1.511133178	0.590701288	0.529174463	-0.793537591	ND	-1.28194674	-0.932617532
comp128947_c0_seq1	-0.337469962	-0.726756347	0.531573822	0.46481897	-0.912250747	-0.496686889	ND	-0.625361955
comp128947_c0_seq3	-0.702280553	-0.614445682	0.499977911	0.449343055	-0.578091333	-0.639648729	-0.8623805	-0.814081287
comp129096_c0_seq1	ND	ND	0.2118487	0.183490238	ND	ND	ND	ND
comp129096_c1_seq1	ND	ND	0.170919192	0.163750029	ND	ND	ND	ND
comp129156_c0_seq1	ND	ND	0.502286765	0.434419762	ND	ND	ND	-1.027372233
comp129275_c0_seq1	ND	ND	0.294535874	0.253508444	-1.160284079	ND	-1.347663233	-0.873395288
comp129414_c0_seq1	ND	ND	0.027114479	0.04990854	ND	ND	ND	ND
comp129509_c0_seq1	-0.643864697	-0.652939839	0.78762447	0.755344587	-0.361312985	-0.054893596	-0.502934648	-0.375454189

comp129587_c0_seq1	-1.367335029	-1.455591418	0.569608991	0.573720839	-1.641085818	-0.526551955	-0.828464972	-1.354197026
comp129590_c0_seq1	-0.830595745	-1.316792143	1.485287789	1.425371191	ND	ND	-1.388635701	-0.817457743
comp129769_c0_seq1	-0.788852568	-0.223896443	0.925819207	0.881054032	-0.498331927	-0.186308661	-0.279945734	-0.599623307
comp129799_c0_seq1	ND	ND	0.916007946	0.928143939	ND	ND	ND	-0.691255909
comp129821_c0_seq1	ND	ND	0.544457989	0.555772232	ND	ND	ND	ND
comp130001_c0_seq3	ND	ND	0.715640025	0.756775542	ND	ND	ND	ND
comp130262_c1_seq2	-0.544849206	ND	0.30522674	0.298057577	ND	ND	ND	ND
comp130375_c0_seq1	ND	ND	0.12628862	0.158627999	ND	ND	ND	ND
comp130473_c0_seq2	-0.472913077	ND	0.854284123	0.825925661	-0.922755126	-0.382252531	ND	-0.93689633
comp130561_c0_seq1	ND	ND	0.743064478	0.788885735	-1.050875521	-0.987494181	ND	ND
comp130612_c0_seq1	-0.573999904	-0.705721987	0.598717186	0.55871417	-1.391818738	-1.152346138	ND	-0.979991209
comp130642_c0_seq1	-0.772543734	-0.617762074	0.14888812	0.141718957	-0.870203264	-0.505791928	-0.631613686	-0.759405732
comp130659_c0_seq1	ND	-1.446331056	0.203205738	0.262983365	-1.029765465	-1.091322862	ND	ND
comp130670_c0_seq1	-1.050759548	-0.661894682	0.56167338	0.600261708	ND	ND	ND	-0.435561554
comp130849_c0_seq2	0.39519155	0.349224223	1.101600058	1.042910171	0.210381844	0.473335539	-0.232269814	-0.758001869
comp131128_c0_seq2	-0.601825259	ND	0.05636516	0.116142787	ND	ND	-0.761925206	-0.889717252
comp131222_c0_seq1	-1.029348614	-1.418634998	1.441755162	1.402229963	ND	-0.519558759	ND	-1.016210611
comp131256_c0_seq1	ND	-1.133921515	0.214585284	0.207416122	ND	ND	ND	ND
comp131314_c0_seq2	-0.991136616	-0.426180491	0.512151843	0.449935114	ND	-0.548293552	ND	-1.27902861
comp131320_c0_seq2	-0.774342058	-0.862598446	0.467424947	0.529891713	-0.747062851	ND	-0.934442005	-0.585112796
comp131416_c0_seq1	ND	-0.974789679	0.28354049	0.338519234	-0.762344071	-0.619781485	-1.347663233	-0.873395288
comp131454_c1_seq1	ND	ND	0.017786254	0.010617092	ND	ND	ND	ND
comp131673_c0_seq1	-0.132465769	-0.016602175	0.650663387	0.674902688	ND	-0.564683968	ND	-0.642206512
comp131861_c0_seq1	ND	ND	0.079203991	0.072034829	ND	-1.215324609	ND	ND
comp132603_c0_seq1	-0.356597281	-0.282126372	2.462325344	2.440363964	-0.592559509	-0.955146901	-0.353969931	-0.685881959
comp132723_c0_seq1	ND	ND	1.027867334	0.996224402	ND	ND	ND	ND
comp132740_c0_seq1	ND	-1.276742724	2.023587111	2.018837422	-0.860177133	ND	ND	ND
comp132749_c0_seq1	-1.335009364	-0.610352396	0.188482482	0.150644499	-0.705670166	-0.892166299	-0.381165958	-0.844750106
comp132856_c0_seq2	-1.20610444	-0.449262789	0.921907995	0.865422653	-0.365911877	-0.587170116	-1.065174391	-1.317905174
comp132936_c0_seq1	ND	ND	0.25811841	0.199796725	ND	ND	ND	ND
comp133048_c0_seq2	ND	-0.488957355	0.449374979	0.398740123	-0.628694265	-0.787161674	-0.259770917	-1.040775477

comp133216_c0_seq1	ND	ND	0.140558929	0.151118534	-0.791382279	ND	ND	-0.805523483
comp133273_c0_seq2	-1.314805978	-0.734055585	0.246474429	0.268463495	-0.650704673	-0.747024176	-0.537053831	-0.737396545
comp133298_c0_seq1	ND	ND	1.766235983	1.740355857	ND	-1.447370709	ND	ND
comp133298_c0_seq2	ND	ND	0.629664148	0.596166046	-1.231695986	ND	ND	ND
comp133517_c0_seq1	-0.558827706	-0.647084095	0.611246074	0.636261595	ND	-1.195165887	ND	ND
comp133818_c0_seq2	0.684664072	0.284096677	1.702803423	1.636715324	0.597999926	0.38154057	-0.163410495	-0.416141278
comp133870_c0_seq1	-1.493645945	-1.581902334	1.993633728	1.957634031	-1.165336743	-1.527924135	ND	-0.878447951
comp133938_c0_seq1	-1.076566812	-1.1648232	1.210012537	1.18011856	-1.350317601	-1.110845002	-1.236666759	-1.063428809
comp134180_c0_seq1	-0.125013441	-0.671907679	1.172894383	1.188217987	-0.079250829	-0.089655703	ND	-0.628505234
comp134220_c0_seq2	-0.233848474	ND	0.826398521	0.873104739	ND	ND	-0.938016465	ND
comp134281_c0_seq3	ND	ND	1.893517209	1.8591958	ND	ND	ND	ND
comp134312_c0_seq3	ND	ND	0.074539129	0.067369967	-0.857402079	ND	ND	ND
comp134389_c0_seq1	-0.567260874	-0.433668513	0.591531896	0.536058054	-1.017102922	-0.68072031	-0.727360821	-0.73021413
comp134506_c0_seq1	ND	ND	0.914391596	0.863557933	ND	-1.361653598	ND	-1.615267402
comp134506_c0_seq3	ND	-1.684708864	0.711721488	0.720462327	ND	-1.329700669	-1.455522426	-1.583314473
comp134661_c0_seq3	-0.848912703	-0.217009788	0.712367704	0.657425759	-0.309750135	0.127532973	-0.707982654	0.067315287
comp134723_c0_seq2	-0.46268124	-0.806210134	1.065175411	1.000014301	-0.275701191	-0.019838175	-0.497842451	-0.50069576
comp134727_c0_seq1	0.650865994	0.667344955	1.516181906	1.56393063	0.502053941	0.756085261	-0.425687902	-0.20129743
comp134807_c0_seq1	-0.458299922	-0.386855468	0.440624591	0.45155365	ND	-0.367639375	-0.794491128	-0.496314442
comp134926_c0_seq1	-0.163381602	-0.21384943	0.675264882	0.668095719	ND	ND	-1.063844239	-1.191636285
comp135074_c0_seq2	ND	ND	0.167920323	0.16075116	ND	ND	ND	-0.740373529
comp135095_c0_seq1	0.183504576	-0.237966492	2.150157772	2.132442593	-1.236374249	-0.25653896	-0.645602152	-0.209122768
comp135147_c0_seq2	ND	ND	0.068507165	0.061338002	ND	ND	ND	ND
comp135167_c0_seq1	-0.369611597	-0.245259893	0.672583053	0.652639602	-0.621085991	-0.779553401	-0.604345163	ND
comp135203_c0_seq2	0.346365729	0.587627874	1.537619821	1.554234398	0.215576781	0.449720547	0.20780546	0.10716566
comp135365_c0_seq2	-0.848912703	-0.937169091	0.493524464	0.542471243	-1.122663492	-0.142828203	-1.00901265	-1.136804696
comp135675_c0_seq1	ND	ND	2.191412672	2.139180779	-1.201676765	ND	ND	ND
comp135726_c0_seq1	-0.776728297	-0.864984686	0.501250881	0.494081718	-0.573357831	-0.157793973	-0.936828244	-0.28646904
comp135759_c0_seq2	ND	-0.649603374	0.538052133	0.559846666	-0.601014568	-0.741753211	ND	-1.393307023
comp135972_c0_seq3	-1.058290855	-1.447577239	0.236721662	0.305940845	-0.854920389	-1.092569045	ND	-0.346182848
comp136186_c0_seq1	ND	ND	0.192234509	0.185065346	ND	ND	ND	ND

comp136257_c0_seq1	-1.402519806	-1.490776195	0.176489367	0.133108032	-0.773180608	-0.737827992	ND	-0.787321812
comp136458_c0_seq1	-1.212694771	ND	0.399738158	0.35914524	ND	ND	-1.071764722	ND
comp136606_c0_seq1	0.092957966	-0.559569853	0.723996139	0.640438631	-0.921155512	-0.079622922	-0.02935342	-0.333236725
comp136658_c1_seq2	ND	ND	0.342052249	0.399823893	ND	ND	ND	ND
comp136704_c0_seq2	ND	ND	0.032135281	-0.033025829	ND	ND	ND	-0.737855873
comp136738_c0_seq1	-0.639860957	-0.506268596	0.178030305	0.218285792	-1.089703005	-0.850230406	-0.675022168	-0.92775295
comp136751_c0_seq1	ND	-1.35525752	0.50513264	0.536987585	-0.813753193	-1.47737058	ND	ND
comp136787_c0_seq1	-0.757260859	-0.669425989	0.326898292	0.346058068	ND	-0.791539049	-0.616330811	-0.744122857
comp136843_c0_seq1	ND	-1.24750338	0.383550009	0.376380847	ND	ND	ND	-1.322200248
comp136986_c0_seq1	ND	-1.520701864	1.576961289	1.567205108	ND	-1.068783657	ND	-1.021367464
comp137012_c0_seq1	0.38709846	0.102547426	1.677019541	1.624547885	-0.149893764	0.038426313	-0.38842544	-0.21518749
comp137022_c0_seq1	-1.043095329	-1.307442977	0.610242587	0.551310509	ND	ND	-0.300105289	-0.393135229
comp137025_c0_seq1	ND	ND	1.920999245	1.860577886	ND	-1.745366562	-1.269128327	ND
comp137082_c1_seq1	ND	ND	0.134124819	0.126955657	ND	ND	ND	ND
comp137107_c0_seq1	ND	-0.743600903	1.769754239	1.731275642	ND	ND	ND	-0.563025266
comp137129_c0_seq2	-0.567003819	-0.75217022	0.061223377	0.112046161	ND	ND	ND	-1.252835821
comp137319_c0_seq1	ND	-1.767777109	0.293940134	0.351711778	ND	-1.71379891	ND	-1.189261463
comp137324_c0_seq2	ND	ND	1.112195666	1.090628682	-0.704352124	-1.066939516	ND	-1.320553319
comp137324_c0_seq3	ND	-1.645114502	1.119755389	1.086863904	-1.228548911	-0.892166299	ND	ND
comp137324_c0_seq5	-0.924129302	-1.313415687	1.302262841	1.264711049	-0.896850096	-0.657377496	ND	-1.212021295
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comp137441_c0_seq1	ND	-0.687019629	0.184365915	0.145012069	-1.416582074	ND	ND	ND
comp137464_c0_seq1	ND	-0.471778179	1.181362741	1.132800893	-1.055212588	0.263441258	-0.242591741	-0.370383787
comp137530_c0_seq1	ND	-0.701326146	0.61721743	0.617735096	ND	ND	-0.472139708	-0.257509074
comp137601_c0_seq3	0.256086089	0.495188635	1.288986676	1.278944552	0.255336572	0.397899158	0.067957419	-0.194533201
comp137654_c0_seq1	-0.701573808	-0.090860192	0.609829125	0.676446177	-0.021082088	-1.036881993	0.041416232	ND
comp137728_c0_seq1	-0.796498795	-0.759816447	1.62051944	1.628227661	-0.433427487	-0.040726512	-1.433719997	-0.716414003
comp137750_c0_seq1	-0.549425019	-0.968674627	0.324784606	0.274458526	-0.999267067	-1.157734477	-1.584586229	-0.934227025
comp137809_c0_seq2	ND	-0.830751079	0.604905896	0.644480137	ND	-1.253894135	ND	ND
comp138007_c0_seq1	ND	-1.162430387	0.943641131	0.959064482	0.200259823	0.170301412	-1.109335209	-1.061035996
comp138023_c0_seq5	-0.874161528	-0.661387921	0.482998896	0.492863072	-0.846882321	-0.829258471	ND	-0.71489549

comp138159_c0_seq1	ND	-1.536195582	0.335189963	0.294162533	ND	-0.783247378	-1.307009144	-0.832741199
comp138208_c0_seq1	-0.388979782	0.08703526	1.201458853	1.190892324	ND	-0.997289239	-0.521051005	-0.437989686
comp138323_c0_seq1	-1.499091715	ND	1.002123735	0.988675507	ND	ND	ND	-1.008832458
comp138461_c0_seq2	ND	ND	0.664205041	0.612832216	-0.105885347	-0.167442744	-0.089144518	-0.393027823
comp138484_c0_seq4	ND	-1.415296823	0.251968739	0.244799576	ND	ND	-0.708989131	-1.012872436
comp138500_c0_seq2	ND	ND	0.004738258	-0.002430904	ND	ND	ND	ND
comp138501_c0_seq1	ND	-0.99904821	0.701641107	0.647819924	ND	ND	ND	-1.198683814
comp138534_c0_seq2	-0.976363271	-1.365649655	0.158948403	0.197536731	-1.25011406	-0.533520206	-0.835433222	-1.264255264
comp138541_c0_seq1	ND	-1.55651426	0.189932548	0.137005895	-1.139948669	-1.201506065	-0.725267831	ND
comp138627_c0_seq1	ND	-0.82695809	0.141337468	0.16759206	-0.632241249	-0.517707386	-1.296741657	ND
comp138670_c0_seq1	0.098454396	0.293129781	0.969538723	1.026203114	0.359816809	-0.034955266	0.230429602	-0.147239917
comp138722_c0_seq1	ND	-0.912438641	1.830478142	1.826425193	-1.164879831	-0.557430447	ND	-1.355112294
comp138756_c0_seq1	ND	ND	0.113341213	0.055019528	-0.994691254	-1.05624865	ND	ND
comp138834_c0_seq2	-1.57160769	-0.705621569	0.670159315	0.681473558	-1.243298488	-0.82773463	-1.430677642	-0.859499683
comp138837_c0_seq1	ND	ND	1.760816811	1.719027207	ND	ND	-0.490297134	ND
comp138882_c0_seq4	-0.844524147	-1.108871795	0.230491625	0.232465841	-1.595396191	-0.811855548	-1.180715354	-1.3085074
comp138887_c0_seq1	0.251715688	0.356065647	2.404082282	2.412907725	-0.877352306	-0.035819715	-0.541852714	-1.067584769
comp138965_c0_seq1	ND	ND	0.442178599	0.393616751	-1.05403404	-0.638470182	ND	ND
comp139069_c0_seq1	ND	ND	1.380818587	1.326692189	ND	ND	ND	ND
comp139089_c0_seq2	-1.558827706	-1.346054099	1.496143056	1.488392897	ND	-1.115984641	ND	ND
comp139089_c0_seq3	-1.589550117	-1.200685251	1.48361365	1.453581604	-1.261240915	-0.845677057	ND	-1.275382119
comp139089_c0_seq4	ND	-1.589597174	1.699260064	1.672124705	ND	-1.058497721	ND	ND
comp139123_c0_seq1	-1.27362005	-1.236937702	1.74419508	1.695464541	-0.878364058	-1.483989499	-0.910841252	-1.737603302
comp139258_c0_seq1	ND	-0.856574848	1.125961149	1.121584886	ND	ND	ND	-0.755180457
comp139258_c0_seq2	ND	-0.451030012	1.157888932	1.149298183	ND	ND	ND	-0.796793652
comp139262_c1_seq1	ND	ND	0.754878405	0.698021458	ND	ND	-1.455522426	ND
comp139287_c0_seq1	-0.404299896	-0.969677539	0.453462878	0.406422203	-0.757231931	ND	-0.564399843	ND
comp139301_c0_seq1	-1.096390404	-0.620375362	0.660635949	0.714331696	-0.944172461	-1.005729857	ND	-0.518980971
comp139349_c0_seq1	ND	ND	0.654879871	0.647710708	ND	ND	ND	ND
comp139353_c0_seq1	-0.352859595	-0.299786831	0.622751236	0.604724146	-0.962402486	-1.501081137	-0.626902894	-0.75469494
comp139353_c0_seq2	-0.393987224	-0.637145572	0.477278021	0.433125292	-1.366708017	-1.127235418	ND	-1.380849221

comp139414_c0_seq1	-1.480196349	-1.091331483	1.398102158	1.413862956	0.219180715	0.571885292	-0.436176314	-0.320930311
comp139428_c0_seq3	ND	ND	0.298662218	0.291493056	ND	ND	ND	ND
comp139479_c0_seq1	ND	ND	0.713028386	0.748611204	ND	ND	ND	ND
comp139640_c1_seq1	-1.316869138	-1.405125527	0.119472531	0.179250158	-0.812468677	-1.050117332	-1.17593909	-0.458633096
comp139644_c0_seq1	ND	ND	0.658151408	0.633948906	-0.366543854	-0.574229286	ND	-0.271540588
comp139728_c0_seq1	ND	-1.400989358	1.514249471	1.489555963	-0.984423767	-1.347011159	-1.472832916	ND
comp139824_c0_seq1	-0.342187948	-0.068716501	0.914428178	0.921617165	0.216570175	-0.121193633	ND	-1.329049946
comp139845_c0_seq1	ND	ND	0.402856099	0.422015875	ND	ND	ND	ND
comp139869_c0_seq2	ND	ND	0.259063556	0.299319043	-0.832578495	-1.070227151	-1.196048908	-1.022810958
comp139899_c0_seq1	-1.072370697	-1.160627086	0.585819722	0.606679283	ND	-0.629527632	ND	ND
comp140048_c0_seq2	ND	-1.640749697	0.467424947	0.529891713	ND	ND	ND	-1.539355305
comp140067_c0_seq1	-0.23700126	ND	0.680021475	0.698659576	ND	ND	ND	ND
comp140160_c0_seq1	ND	-0.950074791	0.319250762	0.249933692	-0.466562411	ND	-0.595949617	-1.325801655
comp140224_c0_seq1	ND	ND	0.581093657	0.557534078	ND	ND	ND	ND
comp140235_c0_seq1	-0.393581531	-0.297313493	0.454665804	0.508910942	-0.216540004	-0.658308642	-0.227827898	-0.569499764
comp140250_c0_seq1	ND	-1.070589437	0.277917362	0.232959638	ND	-1.016611238	ND	-0.969195046
comp140256_c0_seq1	ND	-1.245195927	0.065522311	0.096141709	ND	ND	ND	ND
comp140264_c0_seq2	ND	ND	0.551660384	0.53112726	ND	ND	ND	ND
comp140341_c0_seq1	-0.501182409	-0.564615214	0.44066391	0.455105896	ND	ND	ND	ND
comp140438_c1_seq1	-0.147669561	1.248373889	2.234455167	2.28838478	-0.069237832	-0.784007742	0.131563186	0.625136286
comp140455_c0_seq1	ND	ND	2.107594772	2.057319728	-0.547938916	-0.785587571	-1.036348065	ND
comp140493_c0_seq9	ND	ND	0.338399658	0.282538572	ND	-1.696491632	ND	-1.047015448
comp140582_c0_seq1	-0.12138584	0.360233079	1.180727017	1.24284586	-1.240234669	-0.699732074	-1.126583827	-1.254375873
comp140610_c0_seq2	-0.952687331	-0.217034978	1.239811296	1.271721317	ND	-1.464086775	ND	ND
comp140650_c0_seq1	ND	-1.543739972	2.128362651	2.11791708	ND	ND	ND	-1.442345581
comp140680_c0_seq1	-1.607132386	ND	1.005300543	0.996519896	ND	ND	ND	-1.593994383
comp140692_c0_seq3	ND	ND	0.141485919	0.192308703	ND	ND	ND	ND
comp140756_c0_seq1	-0.155378603	0.115386951	1.034898564	0.996245004	-0.274227432	-0.636814824	-0.257486603	-0.510217386
comp140812_c0_seq1	ND	-1.352684678	1.355183224	1.388038208	ND	ND	-1.123498241	-0.510927597
comp140820_c1_seq1	0.453945789	0.496457681	1.501382134	1.477945358	-1.086976728	-0.847504129	-0.070235899	-0.322966682
comp140895_c0_seq1	ND	ND	1.619408339	1.639822697	ND	-0.381268851	ND	-0.845736019

comp140916_c0_seq1	ND	-1.563716655	0.640107349	0.662227563	ND	ND	ND	-1.462322264
comp140923_c0_seq1	-0.505211794	-0.181287735	1.376272616	1.343855298	-0.858143829	-0.715581243	-1.142432996	-0.872285033
comp140923_c0_seq4	-0.272186038	-0.01365494	1.509735066	1.480225834	-1.500179336	-1.561736733	-1.386528494	-1.213290545
comp140926_c0_seq1	ND	ND	0.78630542	0.838721947	ND	ND	ND	-1.214134655
comp140927_c0_seq2	-0.19124377	-0.008433386	1.3784002	1.350633017	-0.298663137	-0.059190538	-0.080276945	-0.208068991
comp140942_c0_seq2	ND	-1.788413248	0.748084034	0.70927159	ND	ND	ND	-1.084958865
comp140942_c0_seq3	ND	ND	0.748360878	0.741191716	ND	-1.466986476	ND	-1.243479025
comp140949_c0_seq1	ND	ND	1.269817513	1.243831205	ND	ND	ND	ND
comp141002_c0_seq1	-0.478623387	-0.742971034	1.63996367	1.704727511	-0.45134418	-0.346570155	-0.61069461	-0.600183958
comp141109_c0_seq1	0.245986684	0.657417378	1.425315187	1.385558657	-0.045492872	0.175496322	-0.011023276	-0.059634076
comp141112_c0_seq3	0.16331711	0.260392637	0.913722421	0.93576053	-0.455667337	-0.341133474	ND	-0.615936577
comp141156_c0_seq1	0.108519445	0.248742385	1.112661364	1.134617827	-0.434076657	0.331365765	-0.46655385	-0.293315901
comp141267_c0_seq2	ND	-0.866963252	0.597338905	0.650465644	-1.529578907	ND	ND	-1.543720111
comp141319_c1_seq1	ND	-1.209565356	0.466300378	0.467564383	ND	-1.456617153	ND	ND
comp141400_c0_seq1	-0.905516925	-0.419742046	0.354733486	0.299791541	-1.003176455	-0.39572707	-1.065616872	-1.193408918
comp141422_c0_seq1	ND	ND	0.269496197	0.262327034	-0.560987371	ND	ND	-0.575128575
comp141491_c1_seq1	ND	-1.182361027	0.291084509	0.310244285	-0.765795436	-0.827352832	ND	-0.77993664
comp141510_c0_seq1	ND	-1.648653363	2.152534139	2.091780859	ND	ND	ND	ND
comp141602_c0_seq1	ND	ND	0.427020029	0.404056599	ND	ND	ND	ND
comp141749_c0_seq1	0.123506647	-0.354720821	1.804669918	1.831479784	-0.736509867	-0.342135307	-0.865897073	-1.118627856
comp141777_c1_seq1	0.424347366	0.555585821	1.848342777	1.864466347	0.447696279	0.679199948	0.305284271	0.108165733
comp142060_c1_seq1	-0.880953413	-0.890028556	0.254358261	0.301546761	-0.552644211	-0.468073572	-0.325050016	-1.566785415
comp142111_c0_seq1	ND	ND	0.440182074	0.433012911	-1.07533572	-1.136893116	ND	ND
comp142151_c0_seq2	-0.563129623	-0.873234761	0.149418459	0.115920357	ND	-0.995347821	ND	ND
comp142153_c0_seq10	ND	ND	0.232100586	0.1949682	ND	ND	ND	ND
comp142272_c0_seq1	-1.076328123	-0.749611164	0.34529029	0.402923248	-0.571927662	-0.663448281	-1.032308087	-0.483406524
comp142309_c0_seq2	-0.463522561	-0.27095234	0.717546604	0.688101046	-0.347302271	-0.054893596	-0.409742688	-0.792807239
comp142412_c0_seq1	ND	ND	0.658237835	0.673345067	ND	-1.738953108	-1.563744869	-1.39050692
comp142512_c0_seq1	ND	ND	0.472806784	0.425520398	-0.6104021	ND	ND	ND
comp142592_c0_seq1	ND	ND	0.130254569	0.123085406	-1.385263225	-1.446820621	-1.271612383	-1.399404429
comp142676_c0_seq1	-1.042450497	-0.711577578	0.942246463	0.943526876	-1.140110027	-1.377758682	ND	-1.154251231

comp142678_c0_seq1	-1.312732969	-0.923868103	0.667676745	0.617041889	ND	ND	ND	-0.998564971
comp142726_c0_seq1	ND	-1.486246355	0.214442963	0.25303129	-1.370710759	-0.955146901	ND	-0.606700713
comp142836_c1_seq1	ND	-0.983027335	0.553469947	0.580159052	-0.867491739	-0.531109127	-0.577749638	-0.705541684
comp142957_c0_seq1	ND	ND	1.238170266	1.187844186	ND	-1.624560059	ND	-1.276113871
comp142957_c0_seq2	ND	ND	1.012733591	1.019208309	-1.591305475	ND	ND	ND
comp142988_c0_seq1	ND	0.618432451	1.932469731	1.89019391	-0.599387614	-0.857239656	ND	-1.177800249
comp143124_c0_seq1	0.306484823	0.472682287	1.176094463	1.203687407	0.341063268	0.584139991	-1.323437141	-0.5481392
comp143130_c1_seq1	ND	-0.99773548	0.188044022	0.193839836	-0.639161836	-0.943757281	ND	ND
comp143142_c0_seq1	ND	ND	1.255531808	1.319681271	ND	ND	ND	-1.460174059
comp143205_c0_seq2	-1.13716089	0.17252273	1.117626624	1.05792841	-1.41091168	-0.472469076	-1.297260838	-0.345871638
comp143235_c0_seq1	ND	ND	0.094477459	0.02931635	-0.962402486	ND	-0.848751644	-0.97654369
comp143259_c0_seq1	ND	-1.457420029	0.243269289	0.30988634	-0.496786393	-1.102411834	ND	-0.45293565
comp143270_c0_seq1	-0.697943486	-0.699049699	1.555007686	1.50398524	-0.022846797	-0.841366145	-0.469863262	-0.147686299
comp143284_c0_seq1	-0.956898704	-1.045155093	1.021207055	1.016341847	ND	-0.468298149	ND	ND
comp143284_c0_seq2	-1.331043176	ND	0.566029332	0.606284819	ND	ND	ND	ND
comp143389_c0_seq1	0.688654554	0.790729864	1.46356338	1.439471512	0.135063069	0.491649067	0.306705858	0.230066334
comp143445_c0_seq1	ND	-1.506811804	0.063543745	0.056374582	ND	ND	ND	ND
comp143544_c0_seq1	0.498901411	0.465610515	1.515610826	1.476063384	0.438647298	0.519588714	-0.118116404	-0.442203096
comp143550_c0_seq1	-1.487205019	-0.534068723	1.063080003	1.019133443	-1.459925812	-0.822513205	-1.34627497	-0.57097703
comp143651_c0_seq1	-0.922431179	-0.408627576	0.269361851	0.217610556	-1.020090709	-0.382678101	-0.538463082	-0.812383163
comp143735_c0_seq1	-0.883442213	-1.448819857	0.411570303	0.466549047	ND	ND	ND	-1.04639547
comp143892_c0_seq1	ND	ND	0.781186969	0.811624464	ND	-1.733013462	ND	-1.685597269
comp143892_c0_seq3	ND	-1.755704212	0.794654708	0.726560266	ND	ND	ND	-1.353279825
comp143893_c0_seq2	ND	ND	0.535145296	0.514296436	-0.729234372	ND	-1.138462276	-1.743375576
comp143916_c0_seq1	0.881699746	-0.653714674	1.958428194	1.923992251	-1.237149083	-0.453608439	ND	-0.950260291
comp143946_c0_seq3	ND	ND	1.363875331	1.324306363	ND	-1.51985794	ND	-1.472441748
comp143946_c0_seq4	ND	ND	1.51368663	1.478432081	ND	ND	ND	ND
comp143947_c0_seq1	ND	ND	1.245817236	1.241706498	ND	-0.819256562	-0.20471563	-0.118627856
comp143955_c0_seq1	-1.438709447	-1.049844581	0.365609008	0.358439845	-0.809370249	-0.359044284	-0.820658143	-0.823511453
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comp144105_c1_seq4	-0.619269149	-0.707525538	0.446406597	0.508873362	-0.224013157	-1.130668594	-0.65443036	-0.48119241

comp144216_c0_seq1	-0.578360643	-0.745798278	1.023214358	1.007719806	-1.630262683	-1.089760088	-0.194392546	-0.282676051
comp144216_c0_seq2	-1.201505548	-0.687701946	0.95269147	0.905206322	-1.174226342	-1.110845002	-0.307247833	-0.551545448
comp144228_c0_seq1	ND	-0.692920184	1.519899885	1.494548298	ND	ND	ND	-1.290495797
comp144354_c1_seq1	ND	ND	0.993946116	1.033773516	ND	ND	-0.766352303	-0.593114354
comp144364_c0_seq1	-1.545660214	-0.679674093	0.762513749	0.78660228	-0.673282967	-0.061424463	-0.705760161	-0.30207329
comp144411_c0_seq1	-0.241665086	-0.305097891	0.809325702	0.766243984	-0.541744814	-0.251119692	-0.289791274	-0.504733495
comp144418_c0_seq1	-0.916003418	-0.87932107	2.091896126	2.117535163	ND	-1.029462853	-1.553224619	-0.53488863
comp144432_c0_seq2	-1.641271886	-1.25240702	0.31064929	0.256903985	-0.383543758	-0.675550076	ND	-1.026073892
comp144446_c0_seq4	ND	ND	0.408379343	0.364487373	ND	-1.07413974	ND	-1.026723548
comp144477_c0_seq3	ND	-0.909073186	0.263342354	0.256173191	ND	-0.679003728	-0.679886749	-0.631587536
comp144581_c0_seq1	-0.914562014	ND	0.479581976	0.42566941	ND	ND	-1.25075322	ND
comp144625_c0_seq1	-0.750678139	-0.139964524	1.49061655	1.490478752	-1.024428928	-0.646653631	-0.813868073	-0.862478873
comp144672_c0_seq1	ND	-0.653908167	0.676115227	0.696384313	-0.295334523	-0.503019955	ND	-0.853543771
comp144724_c1_seq1	-1.046944345	-0.290102694	1.855110563	1.818037149	0.442732859	0.731690822	-0.303954305	0.007586342
comp144747_c2_seq1	ND	-0.47555411	0.161748228	0.111113372	-1.314261024	-0.773758429	-0.598550191	ND
comp144868_c0_seq2	ND	-1.468232898	1.114959876	1.061095221	-1.352697303	-1.414254699	-1.239046461	ND
comp144876_c0_seq3	0.588008354	0.630085734	1.745885856	1.697919152	0.447796474	0.621916026	0.308722	0.371998368
comp145011_c0_seq1	-1.261060645	-0.872195779	0.601249757	0.605979818	-0.932751442	-0.81821758	-1.120130596	-0.770801387
comp145027_c0_seq2	-0.815136129	-0.692539152	0.666963032	0.657071011	-0.991976905	-0.548384323	-0.623053558	-0.801998126
comp145077_c1_seq1	ND	-0.563444456	0.222510894	0.17583319	ND	-0.509466257	-1.179356058	-0.528996854
comp145085_c0_seq1	-0.813007096	-0.822082239	1.666478449	1.620964294	-0.370754541	-0.76810404	-0.76898706	-1.197809102
comp145154_c0_seq1	-1.378788288	ND	0.200220885	0.193051722	ND	-1.413066478	-1.23785824	ND
comp145349_c0_seq1	ND	-0.810547693	0.206965887	0.257788672	-1.393982102	-0.677388248	-0.803210005	-0.366730621
comp145373_c0_seq2	ND	ND	2.375066266	2.343661154	ND	ND	ND	ND
comp145373_c0_seq3	ND	ND	1.436910663	1.472983157	-1.46038906	ND	ND	ND
comp145409_c0_seq2	ND	ND	0.846059801	0.895209001	ND	ND	ND	ND
comp145436_c1_seq1	ND	ND	0.770253266	0.702386263	ND	ND	ND	ND
comp145442_c0_seq2	-0.089496696	0.072124389	0.985519076	1.002317069	-0.238308748	0.083350607	-0.358741112	-0.252449952
comp145469_c0_seq2	-0.921437532	-1.486815175	0.273872072	0.293855155	ND	-0.955715722	ND	ND
comp145495_c0_seq1	0.287616984	0.597300604	1.729635787	1.672721865	0.659391881	0.33631303	0.461547293	0.354439846
comp145506_c1_seq1	ND	ND	1.24161357	1.26493373	-0.953569073	-0.714096474	ND	-1.268740273

comp145556_c0_seq1	ND	-1.70855022	1.15295209	1.173742225	-1.29198463	-1.654572022	ND	-1.306125834
comp145556_c0_seq3	ND	ND	1.106991748	1.045464923	-1.556000733	-1.617558129	ND	-1.269111941
comp145556_c0_seq4	ND	-1.371248716	1.123386119	1.064093943	ND	-0.919330509	-1.142062279	-0.871914316
comp145582_c0_seq2	-0.01962725	-0.195033815	1.474925652	1.460014849	-0.141646126	-0.289118151	-0.505116539	-0.445821942
comp145597_c0_seq1	-0.784978372	-0.918992252	0.724470396	0.754409614	-1.155639174	-0.740075316	-1.041988332	-0.567720387
comp145599_c0_seq2	ND	ND	1.35236222	1.364570002	-0.744262232	-1.282940883	-0.806702649	-0.758403436
comp145634_c0_seq1	ND	-0.474515749	1.578713384	1.604985613	0.477765812	0.992202917	-0.819360579	-0.704114576
comp145661_c0_seq2	0.319566713	0.200276091	1.209476636	1.254651179	-0.130275335	-0.177109475	-0.575932504	-0.70372455
comp145779_c0_seq3	ND	-0.882475418	0.297626951	0.354126868	-1.009977871	-1.071535268	-0.72023577	-0.72308908
comp145806_c0_seq1	-0.492837236	-0.176523037	1.166465334	1.167002486	-0.465558029	-0.193900746	-1.465850539	-0.748544545
comp145827_c0_seq2	0.139038315	0.639053633	1.814957501	1.824403886	0.432019555	0.620799446	0.279968364	0.215228063
comp145843_c0_seq1	-1.392836774	-0.401911917	0.80942169	0.814486983	-0.175225869	0.158345766	-1.251906725	ND
comp145874_c0_seq2	-0.533333147	-0.54240829	2.032089432	1.98789687	-0.392110588	-0.526218652	ND	-0.675097105
comp145874_c0_seq3	-0.935421177	ND	1.499712441	1.467648528	ND	ND	ND	ND
comp145893_c0_seq2	-0.775006218	-0.863262607	0.661335452	0.60900413	-0.856871481	-0.587435658	-1.588318679	-0.871012685
comp145893_c0_seq3	-1.065999515	-1.154255903	0.652888745	0.609644217	-1.163659045	-0.748095186	ND	-0.809823464
comp145893_c0_seq4	-1.140777879	-1.162087478	0.614322553	0.642360699	-0.715558664	-0.652177324	-1.079029077	-0.951548618
comp145911_c0_seq1	-1.074973069	-0.52640736	0.778193954	0.794991947	0.0066638	-0.224644677	0.190895716	-0.141016312
comp145934_c0_seq1	0.01915172	-0.139685743	1.486901854	1.460223451	0.046430927	0.16096479	0.876085113	0.479447754
comp145941_c1_seq1	ND	ND	0.227589084	0.287366711	-1.005382119	ND	ND	ND
comp145944_c0_seq1	ND	ND	0.142724991	0.186708351	ND	ND	-1.277625367	ND
comp145985_c0_seq2	ND	ND	0.820505696	0.769132871	ND	ND	ND	ND
comp146092_c0_seq1	-1.634556281	-1.421782674	1.351673786	1.375667837	-1.209337065	-0.969864466	ND	-1.922448274
comp146112_c0_seq1	-0.49676617	0.001243165	2.016741454	2.038456857	-0.314585004	-0.421899891	ND	-1.152634949
comp146147_c1_seq1	0.298697165	0.665447717	1.225969763	1.241408391	-0.304728801	0.47313471	0.566869905	0.241797301
comp146179_c1_seq1	ND	-0.687701946	1.238041261	1.187238301	ND	-0.633723747	ND	ND
comp146180_c0_seq1	-0.29677192	-0.686058304	2.452865617	2.485386611	-0.871552704	-0.359078833	-0.456871867	-0.408572654
comp146183_c0_seq1	-0.169811871	0.267357675	0.867168203	0.903972978	-0.469891598	-0.589440942	-0.782209489	-1.086092794
comp146216_c0_seq1	-1.858216995	-1.469352129	0.616582926	0.566103009	-1.266666358	-1.466526453	-1.194408202	-1.322200248
comp146216_c0_seq2	-1.271035409	-1.213163762	0.785095019	0.840883691	-1.398658162	-1.402223612	-1.431135356	-1.002624901
comp146311_c0_seq3	-0.419910469	-0.110226849	1.256008717	1.279843836	-0.216540004	-0.296580806	-0.403919157	-0.355619944

comp146322_c2_seq3	-1.481137399	-0.791242538	0.962382855	0.923211524	-1.152828197	ND		-0.298814666	-0.291908138
comp146369_c0_seq2	-0.350596222	-0.347082237	0.787544742	0.802369873	-0.298493431		-0.314293337	-0.293987059	-0.56790714
comp146470_c0_seq2	ND	-0.907996867	1.80066138	1.815808091	-1.394521263		-0.978957405	ND	-0.931541213
comp146487_c0_seq1	ND	-1.70684107	1.241002862	1.204650179	-0.989245484		-1.351832876	ND	-1.304416684
comp146487_c0_seq5	ND	-1.37714254	1.354581011	1.340619963	-0.7175389		-0.925224333	ND	-1.576778145
comp146487_c0_seq7	ND	-1.496372851	0.922171815	0.902504107	ND		ND	ND	-1.093948464
comp146487_c0_seq9	ND	ND	0.834050893	0.894407966	ND		ND	ND	-1.363264046
comp146569_c0_seq1	-1.035293422	-0.278451771	0.708068607	0.740666571	-0.610074207		-0.140152686	-0.894363373	-0.721125424
comp146585_c0_seq1	-1.527035872	-0.501348908	0.654033293	0.60110664	-1.02263541		-0.163374053	-0.431863314	-0.171475188
comp146615_c0_seq2	-0.758193156	-0.272418277	1.118576529	1.102566461	-0.730913949		-0.917410082	-0.617263107	-0.949175136
comp146616_c3_seq4	ND	ND	0.095937274	0.088768111	ND		ND	ND	ND
comp146694_c1_seq1	ND	-0.561807665	2.524156833	2.503054052	-1.145242074		-0.393886114	-0.554469978	-0.205140769
comp146729_c1_seq1	ND	ND	1.523035511	1.537646123	ND		ND	ND	ND
comp146741_c1_seq1	ND	-1.022354504	1.005882941	1.050034404	-0.651546404		-0.463226327	-1.492138071	-0.443838858
comp146788_c0_seq1	0.178615656	0.269173385	1.499920032	1.519777246	0.237493849		0.480759437	0.175053432	-0.170794375
comp146795_c0_seq1	-1.368554958	-1.456811347	2.126802867	2.110481363	-1.341275751		-0.925711893	ND	-1.05438696
comp146864_c1_seq13	-1.219615945	-0.608902329	0.24020682	0.130375316	-1.192336738		-0.55492413	-0.379715892	ND
comp146864_c1_seq7	-0.937069355	-1.326355739	0.30469765	0.316011893	ND		-1.272377541	-1.097169302	ND
comp146864_c1_seq8	ND	-0.861400392	0.263242367	0.338608092	-0.678918007		-0.983513452	-0.7113952	-1.538157251
comp146894_c0_seq2	ND	-0.738172152	2.064634938	2.000277477	-1.467734596		-1.529291993	-1.354083754	-1.180845805
comp146939_c0_seq1	-0.471800927	-0.197509282	1.238519998	1.300366077	0.250655295		0.419994777	-0.692598715	-0.706447408
comp146956_c0_seq3	ND	ND	0.612679053	0.576785739	ND		-1.699578315	ND	ND
comp147016_c0_seq1	ND	-1.361876439	1.206302191	1.16391602	ND		ND	ND	-1.561512043
comp147064_c0_seq1	-1.18229529	-0.571581674	0.347727423	0.285335469	ND		-1.392664739	ND	ND
comp147077_c0_seq1	ND	ND	0.381842693	0.44267061	-1.542799276		ND	-1.429148434	ND
comp147110_c0_seq1	-0.493515448	-0.296536108	0.490815688	0.445414127	-0.121002583		-0.383887062	-0.569294509	-0.171660621
comp147131_c0_seq2	ND	ND	0.972096628	1.039561083	ND		ND	ND	ND
comp147140_c0_seq2	0.377491499	0.430761985	2.553872121	2.496763211	0.226895894		0.265453651	0.055311008	-0.115946732
comp147166_c0_seq11	ND	ND	0.786846327	0.736797168	ND		-1.195656893	-1.32147865	-1.148240701
comp147166_c0_seq13	ND	ND	0.756337512	0.77121849	ND		-1.441281076	ND	ND
comp147199_c0_seq3	ND	-0.763374932	0.665173955	0.607925928	-0.890877386		-0.952434782	-1.379286535	-0.90501859

comp147215_c0_seq1	ND	ND	0.484372838	0.492443642	ND	ND	ND	ND
comp147269_c1_seq1	-1.649323553	-0.959428692	0.876137885	0.899324794	ND	-1.683601743	ND	-1.335155555
comp147307_c0_seq1	-1.333030798	-1.120257191	0.228249609	0.272232968	-1.305751591	-0.765248996	-0.891070753	-0.620922791
comp147413_c0_seq1	-1.442664641	-0.894098932	1.29390203	1.260580149	0.244213878	0.322397719	-1.778855847	-0.952405383
comp147432_c1_seq4	ND	-0.710931786	0.224571258	0.265706775	-0.858637626	-0.619165027	-1.523138034	-1.65093008
comp147557_c0_seq1	ND	-0.695388774	0.294096082	0.326435461	ND	-0.641410576	ND	-0.383141018
comp147578_c0_seq2	-0.425077753	-0.101891663	0.746750755	0.710617896	-0.500460889	-0.562018285	-1.562901306	-1.690693352
comp147603_c0_seq2	ND	-1.20305895	1.46246595	1.462217962	ND	ND	ND	-0.499604567
comp147603_c1_seq1	ND	ND	0.966633732	0.923252397	ND	ND	ND	-1.20129743
comp147671_c0_seq1	0.207598866	0.409907039	1.025490128	1.091360841	0.213688773	0.365206202	0.394286405	0.054864775
comp147689_c0_seq1	0.461660326	0.656335711	1.431099906	1.407012816	0.421992743	0.496853901	0.155432343	-0.118487739
comp147774_c0_seq1	1.063645365	1.183905325	1.879589988	1.815375479	0.652432719	0.562230141	0.349258209	0.298632117
comp147885_c0_seq2	0.119046587	0.131160743	1.407325721	1.459672644	0.171631659	0.243130889	0.697727198	0.149217929
comp147889_c1_seq1	ND	-0.914768933	0.633310221	0.564871401	-1.577384588	-0.434822002	ND	ND
comp147918_c0_seq1	ND	ND	1.335928559	1.272643455	-1.415556585	-0.632015941	-0.301905743	-0.429697789
comp147935_c0_seq1	0.604509889	0.636486942	2.087170274	2.038234357	0.763230759	0.815403877	0.804833589	0.632371148
comp147947_c1_seq2	-0.359909902	-0.295556128	0.71849692	0.693598991	-0.196410949	-0.241577929	-0.293613472	0.007942955
comp147947_c1_seq3	-0.323492157	-0.249021248	0.66437344	0.675302499	-0.258424389	-0.302253019	-0.320864806	-0.061712228
comp147965_c0_seq1	0.240316374	0.56021916	1.547486009	1.531724409	0.586354344	0.40233283	0.28947605	0.142088447
comp147966_c0_seq1	-1.100361772	-1.012526902	1.855953652	1.890442069	-0.294931315	-0.481427448	-0.959431724	-0.786193774
comp148000_c0_seq2	-0.723637955	ND	0.286734983	0.27956582	ND	ND	ND	ND
comp148044_c0_seq2	ND	ND	0.398810808	0.456582452	-1.246340844	-0.830776985	ND	-1.260482048
comp148091_c0_seq2	-0.609761826	-0.3223546	1.536273714	1.469934057	0.690518653	-0.003061958	0.807055183	0.60749616
comp148130_c0_seq1	-1.2943399	-1.382596289	1.631022247	1.578530106	-0.966030698	ND	-1.153409852	ND
comp148152_c1_seq10	-1.409781491	-1.020916625	0.202651438	0.241239766	-1.382502284	-0.841999689	-1.268851442	-1.396643488
comp148157_c0_seq1	0.910697663	-0.204616959	2.507915685	2.469038885	-0.193816714	-0.36734787	-0.007615205	-0.596138089
comp148157_c0_seq2	0.279371865	-0.746736617	1.357221542	1.352165739	-1.108322277	ND	-0.994671435	-0.821433485
comp148188_c0_seq2	-0.621613812	-1.215020179	1.550958313	1.536813503	-1.196394597	ND	-1.207682491	-1.812595792
comp148208_c0_seq1	-0.369276789	-0.264926831	0.603205557	0.597666019	-0.212038044	-0.019990095	-0.907572687	-0.558243478
comp148323_c0_seq1	ND	-1.213316226	0.462549508	0.429051406	-1.398810626	-0.418975338	ND	-1.111921835
comp148365_c0_seq1	-1.494102377	-1.582358765	1.52202289	1.573559387	-1.46682317	ND	ND	-0.878904383

comp148438_c0_seq2	-0.476163645	-0.369845368	0.951703718	0.899489607	-0.395638926	-0.218957157	-0.073712142	-0.569480973
comp148451_c1_seq1	-1.491356565	-0.676522966	0.738930623	0.799814733	-0.464077358	-0.411691402	-1.350426516	-0.779248558
comp148474_c0_seq1	-0.753929725	-0.92136736	1.065628696	1.048359207	ND	-1.26532917	ND	ND
comp148484_c0_seq1	-1.74283787	-0.600645338	0.848164417	0.867224778	-0.761316154	-0.822873551	-0.999847831	-0.826609881
comp148569_c0_seq2	ND	ND	0.659324671	0.652155508	ND	-1.267829913	ND	ND
comp148687_c0_seq2	-1.595128956	-1.382355349	0.91227607	0.873237272	-0.337400828	-0.04583056	ND	-1.017719523
comp148687_c0_seq4	-1.181827384	-1.270083773	0.803153893	0.790262718	-0.485541397	-0.096629733	-1.51801859	-1.101742592
comp148782_c0_seq3	-0.055377513	-0.222815147	0.631343995	0.595643744	-0.982340816	-0.780656777	-0.94787122	-1.075663266
comp148788_c1_seq1	ND	-0.904317301	0.421913104	0.491377998	-1.48775171	ND	ND	-0.723741664
comp148802_c0_seq1	-0.101731152	0.078857771	1.229875167	1.213842544	-0.266337472	-0.106046119	-0.261831099	-0.535751181
comp148865_c0_seq1	-1.595731056	-1.382957449	1.398919098	1.36064157	ND	-0.851857995	ND	-0.679503066
comp148870_c0_seq4	ND	ND	0.350833929	0.311480083	ND	ND	ND	ND
comp148870_c0_seq7	ND	ND	0.055890781	0.008292961	ND	ND	ND	ND
comp148945_c1_seq1	-0.80550004	ND	0.028781639	-0.029540046	-0.778220833	-0.839778229	-0.965599987	ND
comp148978_c0_seq1	-1.588450173	-1.199585307	1.187011542	1.177626586	ND	ND	-1.146490129	-0.621069661
comp149042_c1_seq1	0.459667905	0.415615179	1.672145534	1.674960592	0.564833888	0.980397746	-1.147590073	ND
comp149131_c0_seq2	ND	ND	0.673955811	0.706295189	ND	ND	ND	ND
comp149131_c0_seq3	ND	ND	2.752985704	2.731028212	0.232574118	0.69894813	ND	0.412622395
comp149131_c0_seq4	ND	ND	1.403022395	1.365815967	0.586059807	0.741552277	ND	0.510504302
comp149144_c0_seq2	-0.656487395	-0.443713788	1.070900049	1.072617017	-1.670600874	-0.690765585	ND	-1.684742078
comp149174_c0_seq2	-1.077460729	-1.068807104	0.823767739	0.779936591	-0.16087982	-0.537707651	-0.283318166	-0.587201472
comp149192_c0_seq4	ND	ND	0.460305206	0.506381555	ND	ND	-0.719712996	-1.546475047
comp149192_c0_seq5	ND	-1.1212476	0.208775793	0.172317254	ND	-1.192208138	-0.539878645	-1.320883205
comp149262_c1_seq1	-0.364680034	-0.045451096	0.561116625	0.531671068	-0.990613342	-0.540287377	ND	-0.828663287
comp149276_c0_seq1	-1.06015345	-1.449439835	0.619226268	0.676039416	-1.33390424	-1.09443164	-1.220253398	-1.047015448
comp149276_c0_seq3	-0.469466596	-0.427389216	1.850063163	1.832671077	-1.743217385	-1.327653527	-0.851415293	-1.280237334
comp149276_c0_seq6	-0.960030649	-1.224378297	1.01807511	0.989601129	ND	ND	ND	ND
comp149276_c0_seq8	-1.116438324	-1.204694713	1.091980448	1.028273289	ND	-1.150716514	ND	-0.802270326
comp149284_c0_seq1	-1.213275767	-0.363680062	2.054390483	2.106027843	-0.583936569	-1.025705207	-0.771315723	-0.899107769
comp149333_c0_seq3	-1.335009364	-0.578167712	0.684908892	0.638231188	-0.830608902	ND	ND	ND
comp149400_c0_seq2	-0.138462442	-0.334352709	1.082069207	1.108395442	0.244515857	0.205701587	-0.178952486	-0.290950265

comp149400_c0_seq4	-0.373029858	-0.195018357	1.119793168	1.10190014	0.20775895	0.046950324	-0.533129805	-0.473835207
comp149420_c0_seq1	ND	ND	0.430018552	0.43724721	-1.673161412	ND	ND	ND
comp149420_c0_seq2	ND	ND	0.560167606	0.496621977	ND	-1.715877588	ND	ND
comp149430_c0_seq1	ND	-1.421287186	2.203106573	2.168228138	ND	ND	-1.192100749	ND
comp149435_c1_seq2	-0.434543521	-0.30095116	0.570434385	0.623963063	-0.407264314	-0.205580276	-0.071764722	-0.597496777
comp149499_c0_seq1	-1.570078483	-0.357304876	0.846519129	0.839349966	ND	-1.002296681	ND	-1.079819226
comp149515_c0_seq1	-1.103176393	ND	1.865707338	1.866777309	-1.376927182	-1.26239332	-0.610063826	-0.993128378
comp149551_c0_seq3	-1.458959944	-0.592973823	0.874397565	0.882257393	-1.431680737	-1.493238134	ND	-1.144791946
comp149595_c1_seq1	-1.104297154	-0.891523547	1.579199131	1.541627546	ND	-1.439605339	-0.963367105	-1.392189147
comp149595_c1_seq2	ND	-0.454980166	1.08541216	1.111810345	-1.117595821	-0.878123221	-0.304974974	-0.830707029
comp149670_c0_seq2	ND	ND	0.358413432	0.409236216	-0.941504562	ND	-0.526823724	ND
comp149690_c0_seq4	-0.046683586	0.133905338	0.975668416	0.942170314	0.006402884	0.300724151	-1.118828363	-0.820651677
comp149690_c0_seq5	0.019470547	0.178661326	0.916244673	0.898500862	-0.04822576	0.245604502	-1.110666177	-0.812489491
comp149690_c0_seq8	-0.048956524	0.39021346	1.309725073	1.293347908	0.176690336	0.378374375	-1.186780076	ND
comp149703_c0_seq1	ND	ND	1.647293529	1.61297212	-0.34952146	ND	-1.190113128	-1.317905174
comp149799_c0_seq1	-1.648365198	-1.560530328	1.054495616	1.005541747	-1.621085991	-1.682643388	ND	-1.033167204
comp149802_c0_seq1	-1.314116074	ND	2.242616705	2.229741536	-0.985806871	ND	ND	-1.47706933
comp149812_c0_seq1	-0.296422467	-0.148589667	1.49684168	1.50756625	0.156825472	-0.054494245	ND	-0.392428934
comp150057_c0_seq4	-0.560135823	-0.727573458	0.567057961	0.516854166	ND	-1.673595259	ND	ND
comp150057_c0_seq7	-0.434543521	-0.858592011	0.673974977	0.678491572	ND	ND	ND	ND
comp150075_c0_seq1	ND	-0.97663382	0.715937607	0.762643825	ND	ND	ND	ND
comp150076_c0_seq1	-0.631227183	-0.482122656	1.409907618	1.353760127	-0.566159415	-0.384678763	-0.628599832	-0.814383826
comp150077_c0_seq2	-0.377298426	-0.13819588	2.195367376	2.177942323	-0.077017947	0.223152492	-0.48624585	-0.337831485
comp150083_c1_seq3	ND	ND	0.749149788	0.787738116	ND	ND	ND	ND
comp150083_c1_seq4	ND	ND	0.726873393	0.730985241	ND	ND	ND	ND
comp150083_c1_seq5	ND	ND	0.981356989	0.976375712	ND	ND	ND	ND
comp150083_c1_seq8	ND	ND	0.831464086	0.844038982	ND	ND	ND	ND
comp150083_c2_seq1	ND	ND	0.764312073	0.771267553	ND	ND	ND	-0.884344468
comp150091_c0_seq3	-0.424173792	-0.100249733	1.793324638	1.813559764	-0.630977792	0.328654111	-0.172093291	0.095243694
comp150093_c0_seq1	0.644913206	0.559189154	1.466887858	1.41832601	0.720229669	0.759655948	-0.191880351	-0.232522221
comp150105_c0_seq1	-1.543222633	-1.631479022	1.223307261	1.219509095	-0.913883435	-1.577500823	ND	-1.052963376

comp150149_c0_seq2	-1.702139296	-1.790395684	1.011684248	0.953203335	ND	ND	ND	-1.689001293
comp150149_c0_seq3	-0.975234744	ND	0.629080294	0.630029022	-0.771864278	-1.31054293	-0.959243432	-1.087035478
comp150171_c0_seq1	-0.611602675	-0.375347972	0.46032202	0.494545543	-0.216346683	-0.486180022	-0.470672626	-0.707609142
comp150184_c0_seq2	-0.74077471	-0.669330256	0.042354446	0.05291405	-0.927375323	-0.729295409	-0.813724481	-1.204757962
comp150184_c0_seq3	-0.76083292	-0.737115549	0.148828716	0.112037086	-1.009760125	-0.645348789	-1.248291801	-1.133045799
comp150213_c0_seq2	ND	ND	0.840455923	0.880283323	-0.556372083	-0.918959475	ND	ND
comp150225_c0_seq1	-0.962106134	-0.749332527	0.96972848	0.957389084	-0.031736941	0.216690501	0.133066424	0.298186483
comp150245_c0_seq1	ND	-1.228003913	0.518442895	0.552666418	ND	ND	ND	ND
comp150255_c0_seq1	ND	-1.113372296	2.270564241	2.251332133	ND	-1.235485357	ND	-1.48909916
comp150255_c0_seq3	-1.541998693	-1.630255081	2.054878199	2.050036808	ND	ND	-1.401068644	-1.051739435
comp150295_c0_seq1	-1.363962446	-0.497976325	1.139326013	1.084095405	-0.938743231	-0.921119381	-1.524062393	-1.350824444
comp150295_c0_seq2	-1.028386885	-0.307457789	1.429909361	1.416321304	-0.411282143	-0.655179748	-0.887456836	-1.015248882
comp150300_c0_seq1	ND	-1.762385798	1.826462205	1.779665573	-1.646850202	-1.708407599	ND	-1.660991406
comp150300_c0_seq2	ND	-1.657568244	1.536553305	1.488816916	ND	-1.603590045	-1.428381806	ND
comp150300_c0_seq3	-1.635380838	ND	1.92061988	1.869743944	-1.608101632	ND	ND	-1.622242836
comp150300_c0_seq4	ND	-1.607612983	1.730640182	1.685143129	ND	-1.553634784	ND	ND
comp150366_c0_seq1	-1.593922246	-1.381148639	0.961895264	0.939813238	ND	-1.628200436	ND	-1.279754248
comp150386_c0_seq2	-1.360563468	ND	0.200716938	0.244700298	ND	ND	-0.918603424	ND
comp150408_c0_seq1	ND	-1.629027682	0.681690556	0.678451687	ND	ND	ND	-1.050512036
comp150472_c0_seq11	-1.149186307	-0.760321441	0.463246622	0.400377309	-1.121907101	-0.37055114	-1.008256259	-1.738108296
comp150478_c0_seq1	-0.728983185	-0.37790688	1.965303579	1.90128285	-1.30376397	ND	ND	-1.317905174
comp150504_c0_seq1	-0.775138928	-0.863395317	1.174321649	1.208320788	-0.571768463	-0.587568369	-1.41236013	-1.239122181
comp150504_c0_seq5	ND	ND	0.217825727	0.174444392	-1.33390424	ND	-0.919223402	-1.348045444
comp150506_c0_seq1	ND	-1.589597174	0.604007665	0.564653819	ND	-1.23458898	-0.281229491	ND
comp150513_c0_seq10	ND	-1.415966514	1.125200646	1.129491106	0.041991762	-0.10671581	-0.145387391	-0.469474082
comp150513_c0_seq3	-1.127188736	ND	1.399254159	1.45410217	0.155362976	0.190715592	0.269013818	-0.034869488
comp150513_c0_seq4	-0.760154789	-1.626562428	1.105161123	1.112715218	-0.431845586	-0.016281728	-0.075156696	-0.182745356
comp150513_c0_seq9	-1.161378703	-0.705567048	0.133633814	0.126464651	-1.435129492	-0.651588849	-0.622508646	-0.671119446
comp150524_c0_seq8	-0.918585949	-0.27984361	1.088558018	1.070448869	ND	-1.429985394	-1.254777155	-1.081539206
comp150808_c0_seq5	ND	-0.850220398	1.036105497	1.035185283	-1.132624811	-1.194182207	-1.018973969	-0.845736019
comp150877_c5_seq6	ND	-1.355000921	0.746833545	0.799250072	-1.540495321	-0.488109365	ND	-1.25360653

comp150910_c0_seq9	-0.304732683	-0.171140323	0.565546648	0.568137323	-0.231695986	-0.214072137	-1.118045144	-0.291594681
comp150937_c0_seq1	-1.846487599	-1.031654001	1.074944255	1.023768791	-1.342087138	ND	-1.006587546	-0.791956912
comp150986_c0_seq1	-0.128249285	-0.517535669	0.450759888	0.471619449	-0.402000074	-0.338618734	ND	-0.893262533
comp150988_c0_seq3	ND	-1.443199864	1.917440849	1.897413344	ND	-1.08819167	-1.214013427	-0.563654223
comp150988_c1_seq3	ND	-1.256451513	1.406449244	1.465097365	ND	-1.50350331	ND	-1.456087117
comp151026_c0_seq1	ND	-0.494222677	0.106096096	0.036779026	-0.922755126	-1.285342518	-1.110134279	ND
comp151031_c0_seq4	ND	ND	0.384002293	0.318841183	ND	ND	ND	ND
comp151095_c0_seq12	-0.631688547	-0.768249615	0.588690352	0.611762717	-1.406041686	-1.099622298	-1.468482103	-0.897304145
comp151105_c1_seq1	-1.234382114	-0.720578512	1.566823105	1.608369536	ND	-0.72459226	-0.695512057	-1.045152853
comp151167_c0_seq3	-0.966593675	-1.054850064	1.581298533	1.542907488	-1.182352517	-0.891727396	ND	ND
comp151237_c0_seq2	-0.985875919	-1.773102312	1.083934206	1.019253777	-1.657566717	-1.242002859	-0.844945871	-1.194586666
comp151256_c0_seq4	-1.070358208	-0.614546552	0.502821422	0.468405344	-0.565957746	-0.435629616	-0.666186724	-0.881128946
comp151256_c0_seq6	-1.203662706	-0.638706581	0.635417855	0.583021152	-0.54799457	-0.271799163	-0.664792649	-0.947486655
comp151256_c0_seq7	-0.874034745	-0.518593634	0.647258136	0.617464354	-0.800998048	-0.306252943	-0.60816596	-0.735958006
comp151295_c0_seq1	-0.606137438	-0.292693669	0.292385136	0.277916735	-0.317336777	-0.554985433	-0.428995217	-0.875546026
comp151303_c0_seq2	-0.109142341	-0.14909405	1.500442745	1.436368731	0.67891402	0.772258584	-0.022569954	-1.025423264
comp151306_c0_seq1	0.516864528	0.437948166	1.360828332	1.334074135	0.600164301	0.614548859	-0.30599325	-0.609876555
comp151352_c1_seq14	-0.96184724	-0.65216362	1.388013944	1.348773329	ND	-0.695095435	-1.121947187	-0.208346548
comp151385_c0_seq1	ND	-1.766883192	0.226718231	0.194243203	-0.372593996	-0.712904993	-1.236666759	ND
comp151451_c0_seq1	ND	-1.742655757	1.238477025	1.202547672	ND	ND	ND	ND
comp151456_c0_seq2	-0.344983614	-0.609331262	0.438145541	0.416253122	-0.539553157	-0.513960378	-0.601993575	-0.808966867
comp151463_c0_seq4	ND	ND	0.570783356	0.597037949	ND	ND	ND	ND
comp151463_c1_seq3	ND	ND	0.993505878	0.976197084	ND	ND	ND	-1.288368636
comp151480_c0_seq2	ND	-1.161229019	1.194456365	1.250146484	-0.686671481	-0.590621024	-1.17508063	-1.001842681
comp151537_c1_seq1	-0.626055138	-1.015341523	0.701142062	0.644754876	ND	-0.961363324	ND	-0.612917136
comp151593_c0_seq2	0.079326993	0.32790543	1.248006568	1.216424347	0.1066062	0.51762243	-0.307169332	-0.509594996
comp151625_c1_seq2	0.097941745	0.204418726	1.266253679	1.226084257	0.095665708	0.216273719	0.233119465	0.099497875
comp151626_c0_seq5	-0.889602522	-0.852920174	0.405409995	0.351244269	-0.225501218	-0.622850716	-0.748672474	ND
comp151667_c0_seq2	ND	ND	1.464730567	1.407532542	ND	ND	ND	ND
comp151748_c0_seq1	ND	ND	1.025854622	1.009034074	ND	ND	ND	ND
comp151754_c0_seq1	0.118210984	-0.43802328	2.117562211	2.057525873	-0.748456417	-0.685075077	-1.713986821	-0.841778867

comp151757_c0_seq1	ND	ND	0.888626256	0.823213891	-1.055800664	-0.765175543	-0.845239809	-0.893850609
comp151757_c0_seq2	-1.40448685	ND	0.890525667	0.862834837	-0.833139599	-0.961643785	-1.263556802	-0.993408839
comp151763_c0_seq1	-0.707576503	-0.129655401	1.465523731	1.455530535	-0.680297297	-0.504493777	ND	ND
comp151799_c0_seq1	-1.474029311	-0.78413445	1.709853632	1.655077228	0.044611589	0.029511594	0.378707966	0.528113307
comp151805_c1_seq3	-0.669661086	-0.21384943	0.672776081	0.701519474	-1.068350611	-0.761931222	-0.477578515	-1.258583074
comp151836_c0_seq14	-0.581325122	-0.643252572	0.641136728	0.680710968	-0.226686981	-0.138482057	-0.56533381	-0.693125856
comp151836_c0_seq2	-0.460687745	-0.402816098	0.834324772	0.838693523	-0.121654677	0.036512982	-0.775689652	-0.903481698
comp151846_c0_seq1	-0.327487009	-0.512653411	0.3764609	0.369291738	-0.476299062	-0.391728423	-1.36264822	ND
comp151847_c0_seq2	-0.124380266	-0.107901304	1.21873708	1.168745623	0.065626238	0.004068842	-0.095423977	-0.210626896
comp151849_c0_seq1	-0.253032221	-0.173797522	2.744395236	2.74195725	-0.3100739	-1.040638077	-0.138431111	-0.51610063
comp151890_c0_seq1	-0.517168242	0.406809825	1.552401343	1.50072049	-0.614827772	-0.129372744	0.614354338	0.27926065
comp151890_c0_seq5	-0.700156859	0.314850194	1.488839674	1.439019131	-0.672877652	-0.257313794	0.463049584	0.204489258
comp151914_c0_seq3	-0.923365968	-0.3988385	0.322161185	0.279917811	-1.197116757	-1.355584167	-0.82819341	-0.955985456
comp151914_c0_seq4	-0.91513915	-0.423611942	0.355835126	0.352182537	-1.285799952	-1.104319299	-0.929111061	-0.822819901
comp151928_c1_seq1	ND	-1.163628442	0.059939621	0.052770458	ND	ND	ND	ND
comp151934_c0_seq5	0.023207584	0.019272081	1.099541398	1.085741657	-0.141398735	0.12155496	-0.504869148	-0.632661194
comp151955_c0_seq1	-0.3689424	-0.00722978	1.266278417	1.254926611	-0.178935896	-0.444613275	-0.19022379	-1.397197082
comp152013_c0_seq1	-0.975109171	ND	1.274145855	1.270672838	ND	ND	-1.612330373	ND
comp152041_c1_seq3	-1.162114172	-1.551400557	0.994386801	1.001902595	ND	-1.196392362	-1.623244115	-0.796793652
comp152095_c0_seq4	-0.427510258	-0.072069147	1.334610517	1.359173601	-0.313080875	-0.269902921	0.303245326	-0.254671412
comp152173_c1_seq1	-0.935008153	-0.370052028	1.566726478	1.52892646	-1.208758942	-1.270316338	-0.919016841	-0.824960137
comp152197_c0_seq1	-1.614800706	-0.447784589	1.566268459	1.579874784	-0.63327899	ND	ND	-0.756564663
comp152251_c0_seq4	-0.885916833	-0.451294476	0.928620788	0.890043161	-1.034728885	-0.49422629	-1.222108039	-0.3085074
comp152301_c0_seq1	ND	-0.233810532	0.423695193	0.375133345	-0.294366196	-0.355923592	-0.657836608	-0.387688646
comp152326_c0_seq2	-1.576163269	-0.851506301	2.198579553	2.132143632	-1.849914058	-1.911471454	-0.736263216	-0.864055262
comp152347_c0_seq1	ND	ND	0.766998758	0.799596722	-1.25011406	ND	ND	-0.963225268
comp152389_c0_seq1	-0.138401262	-0.101718914	0.72281105	0.684302135	-0.085567951	-0.172679451	0.096798704	-0.529833847
comp152402_c0_seq10	-0.722830466	-0.37972309	0.922131688	0.86100266	-0.440278754	-0.526659734	-0.377780434	0.285942731
comp152510_c0_seq1	-1.141394921	-0.814677962	1.320252614	1.302484758	-0.967987679	-0.728515079	-0.143132376	-0.872984413
comp152510_c0_seq3	ND	ND	1.17476445	1.181531065	ND	-0.770287526	ND	ND
comp152510_c0_seq4	-1.669584954	-1.757841342	0.926457559	0.888130414	ND	-1.402833148	ND	ND

comp152510_c0_seq5	-0.350803631	-0.791242538	0.63189788	0.701362774	-0.976736938	-0.640354326	0.040003891	-0.291908138
comp152510_c0_seq8	-1.312732969	-0.975020625	1.220518714	1.222894869	-1.762575017	-0.824132414	-0.444804192	-0.697534975
comp152517_c0_seq2	ND	ND	1.560868386	1.516888436	ND	ND	ND	ND
comp152527_c0_seq2	0.309943468	0.206447113	1.424813982	1.462354554	0.321982708	-0.010641461	0.134603554	-0.486104014
comp152533_c0_seq1	-1.24137706	-0.93169344	1.352991868	1.319912768	-1.515127849	ND	ND	-1.529269054
comp152550_c0_seq5	-0.366723777	-0.30885213	0.822945559	0.761418734	-1.038414575	-0.622850716	-0.623733737	-1.052555779
comp152563_c0_seq1	-1.359631839	-1.271796968	0.932027036	0.934842094	ND	-1.393910028	ND	-1.170402577
comp152567_c0_seq3	0.154397625	0.075901074	0.909498057	0.843207442	-0.98465459	-0.347241982	ND	-1.475917049
comp152586_c0_seq6	-1.218326599	ND	0.99415103	1.008651847	ND	ND	ND	-1.205188596
comp152619_c0_seq2	-1.31732629	-1.280643942	0.142496475	0.178793006	-1.767168338	-1.226665744	-1.653517496	-1.304188288
comp152657_c0_seq1	ND	-1.174848094	0.909057975	0.869063671	-0.382618889	-0.191450969	-1.547721648	-0.374483698
comp152680_c1_seq1	-0.756371094	-0.212604268	1.321539108	1.329826897	0.283142569	-0.0675456	-0.858479094	-0.474387779
comp152767_c0_seq1	0.08190894	0.437644388	0.970692588	1.051983296	-0.246690517	0.102853541	0.215414971	-0.032352393
comp152767_c0_seq4	-0.063240134	0.200685996	0.899584406	0.913433594	-0.206657154	-0.086794458	0.156871161	-0.189764124
comp152771_c0_seq5	-1.177278114	-1.140595766	0.730789779	0.777179208	-0.083052117	-0.387647563	-1.036348065	-1.164140111
comp152784_c0_seq1	-0.262358985	0.047324635	1.652108089	1.676836947	-0.002507163	-0.185486722	-0.723488928	-0.851280974
comp152784_c0_seq3	0.044515789	0.174315161	1.719073312	1.733482931	0.062249677	-0.019051777	-0.574222007	-0.760006001
comp152807_c0_seq1	-0.693001928	-0.781258317	0.05626896	0.082958065	-0.711480212	-1.125220127	-1.552071879	-0.980893921
comp152829_c0_seq6	ND	ND	0.106295725	0.150279085	ND	ND	-0.535903382	ND
comp152867_c1_seq1	-0.00288664	0.231076267	2.10493643	2.064220115	-0.227419406	0.076778523	-0.384835336	-0.433446136
comp152892_c0_seq5	-0.705150052	0.456262187	1.63774766	1.5928527	-0.837571688	-0.163175514	0.572256646	0.219350463
comp152921_c5_seq1	ND	-1.039088323	0.07533527	0.139522016	-0.622522732	-0.985110125	-0.712991873	ND
comp152922_c0_seq1	-0.158236858	-0.708891245	1.226952289	1.230872098	ND	-1.35388305	ND	-1.306466858
comp152922_c0_seq3	-0.261178836	-1.089797914	1.01837673	1.044514749	ND	-1.336849711	ND	-1.590463514
comp152948_c0_seq1	-0.009469513	0.146985731	2.235753974	2.204540808	-0.70529399	-0.532768181	-0.834681197	-1.263503239
comp152990_c1_seq1	ND	ND	0.574096652	0.60471605	ND	-0.478523405	ND	-0.857075945
comp152995_c0_seq1	-0.297431882	0.069604547	1.107270632	1.109912188	-0.296481614	0.000133872	-0.646588065	-0.639681537
comp152995_c0_seq2	-0.313791033	-0.030436352	1.061710846	1.046300555	-0.340869489	-0.10139689	-0.750097392	-0.628011965
comp153093_c1_seq1	ND	-1.066119815	0.244598424	0.196036576	-0.649554224	ND	ND	ND
comp153169_c0_seq1	0.271459747	0.17234543	1.051899764	1.04741974	0.182645624	0.186029034	-0.265646302	-0.544706024
comp153204_c0_seq1	ND	-1.716661793	0.642568872	0.700830635	-1.601126198	ND	ND	-0.712177415

comp153395_c0_seq7	ND	ND	0.575482504	0.568313342	-0.666443542	-0.631090926	ND	-0.981614742
comp153420_c0_seq1	ND	ND	1.517183904	1.519560059	ND	-1.43055721	ND	-0.684171014
comp153449_c0_seq1	ND	ND	1.816106883	1.779023079	ND	ND	ND	ND
comp153473_c0_seq3	ND	-1.253056676	0.688366736	0.690340952	ND	-1.199078477	ND	ND
comp153488_c0_seq1	ND	ND	1.513815012	1.479797274	-1.534291009	ND	ND	-1.548432213
comp153488_c1_seq2	ND	ND	1.550836296	1.522075523	ND	ND	-1.543915875	-0.893556671
comp153489_c0_seq2	ND	-1.730340192	0.580378046	0.54041637	-1.438713338	-1.132293949	-1.802183751	-0.975733287
comp153489_c0_seq3	ND	-1.338521646	0.504835174	0.536418601	-1.524016047	-1.108452189	-0.808305213	-1.237127255
comp153489_c0_seq4	ND	ND	0.166930515	0.192761612	-1.867673035	-1.32717044	-0.908924153	-1.580784244
comp153515_c0_seq1	-0.270184322	0.047324635	1.172688214	1.192059769	-0.037143186	-0.037646617	0.365069011	0.163958993
comp153535_c0_seq1	-1.201878237	-1.415073363	1.223468048	1.16444982	-0.143190567	0.0702686	-0.708765671	-0.343642195
comp153535_c0_seq10	-1.181046419	-1.269302808	1.290057357	1.260611799	-0.023433444	0.04593826	-0.363422761	-0.126515732
comp153535_c0_seq13	-1.039731697	-1.349836835	1.411783376	1.404147982	-0.088173204	0.176410116	-0.518590407	-0.082111022
comp153535_c0_seq6	-1.159657749	-1.151004125	1.365312128	1.355676777	-0.132378543	0.123082162	-0.541606446	-0.146519747
comp153540_c2_seq13	ND	ND	0.203205738	0.196036576	ND	-0.887202879	ND	ND
comp153540_c2_seq5	ND	ND	0.211160072	0.15568623	ND	ND	ND	-0.536554686
comp153548_c0_seq3	ND	-1.399601834	1.473949772	1.532800409	ND	-1.345623635	-1.170415397	-0.997177447
comp153557_c0_seq6	-0.369085148	0.024424623	1.240223346	1.189671	0.359956963	0.561641001	-0.464244288	-0.944218853
comp153568_c0_seq1	-0.774693798	-1.248301068	1.897572211	1.890403048	ND	0.259432167	-1.864212671	-1.293034713
comp153568_c0_seq2	-0.633525347	-1.566879775	1.962755724	1.954711208	ND	0.366003026	-1.212754601	-1.164455389
comp153587_c0_seq1	-0.779945935	-0.935149113	1.33417644	1.398889284	-1.597764768	ND	ND	-0.912935968
comp153587_c0_seq4	-1.67952072	-1.466747113	1.38803917	1.4176233	-1.652241513	-1.71379891	ND	-1.365352722
comp153594_c1_seq1	ND	ND	-0.018214924	0.03260786	ND	ND	ND	ND
comp153662_c7_seq11	-0.448277297	ND	0.255670613	0.289894135	ND	ND	-0.784468503	ND
comp153673_c1_seq3	ND	ND	0.527051754	0.481678239	ND	ND	ND	ND
comp153690_c0_seq1	-1.502684658	-0.891971042	0.808718275	0.847306603	-1.475405451	-1.536962848	ND	-0.489546656
comp153690_c0_seq2	-0.588016095	-0.149463445	1.469165894	1.401220112	-0.371680652	-0.132208053	-0.585388745	-0.713180791
comp153762_c2_seq7	ND	ND	0.235936437	0.180462595	ND	-0.559194514	ND	ND
comp153787_c0_seq2	-0.293375337	-0.557722985	1.216752547	1.189444621	0.377356546	0.328764127	-0.726476556	-0.478604988
comp153797_c1_seq2	ND	ND	1.734989307	1.727435983	ND	ND	ND	-1.185374464
comp153812_c2_seq2	-0.822961466	ND	0.136258949	0.129089786	ND	-0.857239656	ND	ND

comp153816_c0_seq1	ND	-0.714311527	0.25398403	0.201057377	ND	ND	ND	ND
comp153849_c0_seq1	-0.288653259	-0.304358981	1.165943276	1.204636748	-0.649554224	-0.887202879	-0.8880859	-1.015877946
comp153849_c0_seq2	-0.222680643	-0.649755589	1.358494591	1.313733248	-0.534219993	-0.433050092	ND	-0.890783878
comp153911_c0_seq2	ND	ND	0.867830096	0.934333085	ND	ND	ND	ND
comp153912_c0_seq2	-1.254245987	-0.798434331	1.502588158	1.50736498	-1.050875521	-0.443426136	-0.460103424	-0.396009944
comp153968_c0_seq1	-0.544172207	-0.410579846	1.652536092	1.624631238	ND	ND	ND	-1.00815546
comp153971_c0_seq2	0.221575238	0.531258858	1.266179684	1.202381661	-0.244061077	0.40759197	0.076715258	0.12997789
comp153992_c0_seq2	-0.579923417	0.12019061	1.527635188	1.493953336	-0.318561005	-0.255179665	-0.682031417	-0.508793468
comp154072_c2_seq3	-1.374903964	-1.287069093	0.84557932	0.892417723	ND	-1.710212149	-1.535003911	-1.662795957
comp154072_c2_seq8	-1.538306039	ND	0.827454556	0.842419839	ND	ND	ND	ND
comp154080_c0_seq10	0.018821333	-0.264009721	1.35959134	1.34398901	ND	-1.571759358	ND	-1.047221911
comp154080_c0_seq11	0.016414561	0.092968421	1.459508649	1.510407565	-1.547370839	-1.30789824	ND	-1.084390789
comp154080_c0_seq12	-0.271974754	-0.263321129	1.49361409	1.533707121	-1.323876793	ND	ND	-1.338017997
comp154080_c0_seq13	0.032817897	0.049296859	1.459175346	1.453126943	ND	-0.866761719	-1.168674735	-0.898526773
comp154080_c0_seq14	0.085225268	-0.260595423	1.364117788	1.386911849	-1.166249127	ND	ND	-1.180390331
comp154097_c0_seq16	-0.162920847	-0.091476393	0.867817921	0.907994994	-1.08988415	-0.628562801	ND	ND
comp154097_c0_seq23	-0.668365025	-0.677440167	0.415794127	0.429814263	ND	-0.623461968	ND	-1.354197026
comp154097_c0_seq25	-0.605098851	-0.099728416	0.682135049	0.619210654	-1.089703005	-0.639377041	ND	-1.705904201
comp154097_c0_seq27	-0.341881255	0.054536749	0.927790229	0.893709261	ND	-0.424464125	-1.178674812	ND
comp154097_c0_seq8	-0.17117287	-0.009551785	0.777189617	0.770020455	-0.876287423	-0.460723565	ND	ND
comp154131_c0_seq4	-0.503230972	-0.70063183	0.647874969	0.703198255	-0.828134283	-0.190721675	-0.617573428	-0.402942794
comp154161_c0_seq3	-0.560788407	-0.535101443	0.724084479	0.688658556	-0.931449209	-1.294036601	-1.419858358	-1.07052915
comp154169_c0_seq2	-0.517391349	-0.605647738	0.891278894	0.863634145	-1.444354652	-1.028790794	-1.029673814	ND
comp154169_c1_seq6	-0.680808694	-0.592973823	0.98456031	0.986781664	ND	-0.590148147	ND	ND
comp154172_c0_seq1	-0.547029247	-0.518780067	0.956259212	0.976820391	-0.271965557	-0.082466933	-0.088678787	-0.346804601
comp154194_c0_seq1	-0.615835973	-0.499972379	0.870584561	0.867694196	-0.317489994	-0.05535341	-0.395724679	-0.548340308
comp154196_c0_seq1	ND	ND	0.987603746	0.944900036	-0.044181909	ND	ND	-0.926085138
comp154196_c0_seq2	ND	ND	0.966931977	0.968616236	-0.045584043	ND	ND	-0.912061696
comp154220_c1_seq15	-1.108197195	-0.953415535	1.578021948	1.562632455	-0.360758685	-0.630592023	-0.870357133	-0.374899889
comp154232_c0_seq9	ND	-0.116346928	0.675857371	0.606540301	-0.109955802	-0.414551247	-0.142432996	-0.492073791
comp154239_c1_seq5	0.621669587	0.580837848	1.395513181	1.390896197	0.539326815	0.723868047	0.311414115	-0.081195754

comp154270_c0_seq3	-0.033979368	0.117524582	0.879060061	0.916162894	0.205907931	0.190807936	-0.995711661	-0.998564971
comp154281_c1_seq1	-0.498740811	-0.763088458	0.628452973	0.679958074	-1.124674118	-0.311170251	-0.533902021	-0.418656019
comp154352_c0_seq1	-0.47824052	0.093555029	0.945866693	0.899779464	0.181061901	0.126683089	0.072863994	-0.043028829
comp154352_c0_seq2	-0.318981918	0.165532308	1.057866612	1.049492748	0.191667492	0.09119203	0.231072306	-0.024119075
comp154401_c1_seq4	ND	-1.542741593	0.188981958	0.224564776	-0.649054748	ND	-0.836433901	-0.839287211
comp154423_c0_seq1	ND	-0.87807213	2.106420781	2.053633571	ND	-1.903275177	ND	-1.077707734
comp154424_c0_seq1	-0.423950447	-0.658334871	1.535269968	1.595933007	-0.542799276	0.319922614	ND	-0.954880489
comp154424_c1_seq3	ND	-0.938175568	0.445093338	0.437924175	ND	ND	ND	ND
comp154447_c0_seq1	-0.331943465	0.153831414	1.298493885	1.303283524	0.529211077	0.599920078	-0.17577345	-0.318805463
comp154464_c0_seq1	-0.508763853	ND	0.343246592	0.280560102	ND	ND	-1.270923791	ND
comp154610_c0_seq10	-1.508901659	-1.421066788	0.184050867	0.24478194	-0.828409938	-0.844209844	-0.30727377	-0.842551142
comp154610_c0_seq11	-1.212112997	-0.99933939	0.115084204	0.137878264	-0.883803794	-0.820422454	-0.645214216	-0.773006262
comp154610_c0_seq2	ND	-0.84176792	0.197590993	0.222020817	-0.534346798	-0.96388098	-0.663734005	-0.580672686
comp154610_c0_seq5	-1.256617027	-0.566722165	0.253510857	0.259705656	-0.530367816	-0.370076463	-0.446680197	-0.441846678
comp154614_c0_seq13	-0.544087508	-0.359342625	0.720663404	0.713494241	-0.215778306	-0.420757845	0.036175234	-0.303705724
comp154655_c0_seq7	ND	-0.948114091	0.663634143	0.615072296	ND	ND	ND	ND
comp154663_c1_seq6	-1.00366349	-1.216858615	1.623398857	1.602403782	-0.87947427	ND	ND	-1.291555483
comp154760_c0_seq5	0.128591905	0.19712162	2.241074717	2.202264844	0.835535961	1.320296844	0.399155811	0.194975419
comp154760_c0_seq6	0.086594563	0.310092036	2.388237659	2.359138291	1.143257547	1.414987303	0.445008556	0.53109633
comp154760_c0_seq9	0.452117293	0.433898771	2.622803108	2.659591821	1.265615372	1.651786571	0.910065443	0.782273397
comp154796_c0_seq2	-0.650976682	-0.599054367	2.141714651	2.123429483	-1.343856778	-1.530352911	ND	-1.960057974
comp154796_c0_seq4	ND	-1.003395538	1.383201311	1.416368706	ND	-1.250447335	ND	-1.504061138
comp154796_c0_seq5	-0.988952398	-0.813967352	1.716296445	1.667106299	-1.739824442	ND	-1.325143604	-1.45293565
comp154821_c0_seq1	-0.277017417	-0.541365064	1.617962102	1.667120753	-1.328919456	-1.089446857	-1.215268614	ND
comp154821_c1_seq1	-0.252127473	0.146282711	1.80284329	1.839802866	-0.446697016	-0.617398882	-1.287288683	ND
comp154823_c0_seq1	-1.093244365	-1.084590741	0.818203268	0.836530493	-0.764935163	-1.127522555	-1.554374308	-1.205045099
comp154823_c0_seq2	-1.145893303	-1.535179688	0.742746037	0.754326311	-0.817584101	-0.879141497	ND	-1.734815292
comp154839_c4_seq7	-0.072077145	0.14622895	0.910624365	0.922377955	0.196646367	0.21639391	-1.045090449	-0.419554829
comp154839_c4_seq8	-0.001252862	0.216541547	0.982510494	1.004561536	0.23140698	0.275483165	-0.794821264	-0.922613311
comp154856_c0_seq1	-0.769126449	-0.334504092	0.466300378	0.404773553	-0.741847242	-0.678465902	ND	ND
comp154859_c0_seq3	ND	-0.759816447	0.861691624	0.824559238	-0.945310848	-0.705838249	-0.354538751	-0.959452052

comp154859_c0_seq8	-0.155615469	-0.209109752	1.350250413	1.306924939	-0.137479642	-0.199037038	-0.297986649	-0.568446199
comp154860_c0_seq2	0.174395619	0.452765176	1.488586969	1.475822953	0.374607566	0.457362969	0.291057093	0.306531165
comp154895_c0_seq11	-1.101602453	-0.441670815	0.980379779	0.934428928	-0.49453965	-0.255067051	-1.182521154	-1.48640446
comp154895_c0_seq18	-0.859857702	-0.620755156	0.930004837	0.882244024	-0.589540447	-0.541953374	-0.923047636	-1.749809686
comp154895_c0_seq6	-0.830735863	-0.511506925	1.089817741	1.053563605	-0.435479871	-0.175803886	-1.343018328	-1.470810374
comp154947_c0_seq26	-1.82869972	ND	0.373558744	0.308988109	-0.847178004	-0.501250074	ND	ND
comp154947_c0_seq36	-1.925736392	ND	0.462158648	0.394291645	-0.995367199	-0.598286746	-1.784806344	-1.611568394
comp154947_c1_seq1	-1.517199141	ND	1.364573741	1.329721768	0.309420615	0.473828534	-1.075239097	-1.504061138
comp155004_c0_seq2	0.339441804	0.259785587	1.627947074	1.62168128	0.4336678	0.414629664	0.060155449	-0.210727596
comp155008_c0_seq1	-0.536930382	-0.120036793	1.09541338	1.158978906	-1.083682443	-1.048329827	ND	-1.097823647
comp155061_c0_seq9	-0.375803435	-0.221021775	0.481959339	0.497066571	-0.473462965	-0.313171612	-0.325050016	-0.487604169
comp155065_c0_seq2	ND	ND	1.89486946	1.860732521	ND	ND	ND	ND
comp155065_c0_seq3	ND	ND	2.025665445	2.009244045	ND	-1.397316277	ND	ND
comp155097_c0_seq4	0.394072315	0.562778296	1.208432709	1.195912828	0.413664693	0.374771282	0.284277487	0.294788139
comp155153_c1_seq4	-1.623522802	-1.535687932	0.729272816	0.710245047	-1.897273591	ND	ND	-1.43429354
comp155210_c1_seq5	-1.479253256	-0.789358394	0.178937164	0.141804778	-1.150944053	-0.735380195	ND	ND
comp155222_c0_seq2	ND	ND	0.915101416	0.890488363	ND	-1.103019664	ND	ND
comp155230_c0_seq1	-1.656287608	ND	1.367390796	1.301515973	ND	-1.389535802	ND	ND
comp155230_c0_seq2	ND	ND	1.71459666	1.673206298	ND	-1.502051628	ND	ND
comp155230_c0_seq3	ND	ND	1.669783696	1.697760462	ND	-1.564264157	ND	ND
comp155230_c0_seq5	ND	-1.738854468	1.023231474	1.075970138	ND	ND	ND	ND
comp155230_c0_seq7	ND	ND	0.461483754	0.528948209	ND	ND	ND	ND
comp155230_c0_seq8	ND	ND	1.157480524	1.164128894	ND	-1.724384811	ND	ND
comp155232_c0_seq12	-1.005072394	-0.653996089	0.079086757	0.071917594	-0.977793188	-0.942440571	ND	-1.593994383
comp155232_c0_seq7	-0.840041822	-0.694215005	0.129397758	0.11200943	-1.055800664	-1.242296797	ND	ND
comp155232_c0_seq9	-0.857888109	-0.512488937	0.159324253	0.186917196	-0.897555692	-0.834174352	-1.5620561	ND
comp155255_c0_seq6	-0.700156859	-0.533140743	0.104161596	0.15498438	-0.894726402	-0.588307013	-1.258196815	-1.084958865
comp155318_c1_seq9	-0.670801466	ND	-0.012611046	0.025977281	-1.120643514	-0.705079655	-0.705962676	ND
comp155352_c0_seq1	-0.552891926	-0.641148315	1.326422815	1.261986133	-0.00819687	-0.098149638	-0.411961877	-0.61893517
comp155352_c0_seq3	-0.627015967	-0.532341672	1.348773549	1.297649484	-0.115776081	-0.085886361	-0.465882533	-0.760006001
comp155354_c0_seq1	-0.219209196	0.129784158	0.793696077	0.783147174	-0.868623599	-0.490848302	-0.879911494	-0.785854791

comp155354_c0_seq3	0.001540278	0.271540555	1.056445615	0.993498812	-0.868196354	-0.503785019	-1.009818018	-1.234520077
comp155387_c1_seq1	ND	ND	1.304188981	1.301792333	ND	ND	ND	ND
comp155388_c0_seq6	-1.046091951	ND	0.775127254	0.781020564	-1.194904004	ND	ND	ND
comp155396_c2_seq3	-1.329713024	-1.116939417	0.431139737	0.477655434	-0.457335777	-0.585839963	-0.711661721	-0.362332512
comp155409_c0_seq7	-1.177593391	-1.742971034	1.272988718	1.207605178	-1.326405443	-1.688992836	ND	-1.340546648
comp155442_c0_seq1	-0.747953295	-0.524455822	0.972191969	0.936491718	-0.013103912	-0.030183037	-0.328269645	-0.303451528
comp155464_c1_seq3	-1.091806778	ND	0.680326993	0.626161268	ND	ND	ND	ND
comp155485_c1_seq1	-0.91398411	-1.178331758	1.240212908	1.291997159	-0.886704904	-0.647232305	-0.773054062	-0.775907371
comp155491_c0_seq10	-0.909216069	-0.851344421	0.915305772	0.923648776	-0.325634361	-0.244524254	-0.263136042	-0.339775565
comp155491_c0_seq13	-0.068538959	0.223415894	1.026344058	1.00845103	0.104868284	0.053530052	0.086631529	-0.25376861
comp155491_c0_seq2	-0.824029842	-0.400402869	0.561159305	0.553990143	-0.658447937	-0.557278036	-0.243767099	-0.713981826
comp155491_c0_seq21	-0.52157476	-0.785922408	0.945801143	0.947892341	-0.494295554	-0.488906161	-0.283734699	-0.985558013
comp155491_c0_seq25	-0.68008862	-0.530984093	0.57017757	0.552789242	-0.791112111	-0.477005894	-0.580551256	-1.106283311
comp155491_c0_seq8	-0.614580786	-0.702837175	0.857534153	0.848340304	-0.783596225	-0.41149806	-0.284594501	-0.528892116
comp155518_c0_seq13	-1.271340284	-0.882475418	0.500793488	0.555772232	-1.244061077	-1.004588478	ND	-1.258202281
comp155531_c0_seq1	-1.039645106	-0.75992471	0.971798841	0.96248501	-0.711335904	-0.772893301	-1.375836313	-1.026507104
comp155588_c0_seq2	-1.066671372	-0.950807778	0.440733654	0.399484701	-0.960210919	-0.384946218	-0.846560077	-0.548383391
comp155610_c3_seq1	ND	ND	0.89874436	0.906188353	ND	ND	-1.561350504	-1.513051291
comp155617_c0_seq3	-1.60537054	ND	0.895844911	0.869559458	-0.799940083	-1.639648729	ND	-1.115111282
comp155617_c1_seq2	-1.605723481	-1.392949874	1.412934122	1.346327771	-1.277414279	-1.162880416	ND	-0.814434228
comp155625_c0_seq2	-0.321645402	-0.034238177	0.875411868	0.940390688	ND	-0.259013579	-0.384835336	ND
comp155697_c1_seq2	ND	ND	0.966633732	1.031467231	ND	ND	ND	ND
comp155751_c0_seq2	-1.661283143	-1.14747954	0.325965996	0.305008549	-0.788905896	-0.917410082	-0.82138309	-0.502017104
comp155751_c0_seq3	-1.289739023	-0.95202668	0.500568717	0.456257746	-0.894483032	-0.801138468	-0.926960225	-0.291324278
comp155758_c0_seq1	-0.054427404	0.143282456	0.958860272	0.985222444	0.085273982	0.280678954	0.086502644	-0.104958481
comp155759_c0_seq7	-0.105844217	0.215702509	0.894768883	0.873190525	0.027599726	-0.220642003	0.130657494	0.002865448
comp155772_c0_seq2	0.652401509	1.123746673	1.989817874	2.003243494	-1.02788946	-1.390476853	-0.738147359	-0.388818151
comp155793_c1_seq1	-0.187871187	-0.261887137	0.67141276	0.726391504	-0.523769883	0.033123128	-0.268789888	-0.373100838
comp155799_c0_seq5	-0.962364874	-1.226712522	0.690973043	0.656100349	-1.111176926	-1.172734323	-1.122464821	-0.949226871
comp155819_c0_seq1	ND	ND	0.451167485	0.443998323	ND	ND	ND	ND
comp155828_c0_seq1	-1.229795188	-1.054810142	0.881543626	0.819166077	-0.638244551	-1.741194632	-1.168046385	-0.880865083

comp155852_c0_seq1	0.210338541	0.294569287	1.573676124	1.541502945	0.520320362	0.343694983	-0.316543433	-0.497580991
comp155972_c0_seq3	-0.365610201	-0.152836594	1.134848969	1.18019688	0.227731344	0.388022697	-1.266072837	-0.995924875
comp155972_c1_seq1	ND	-1.112924339	0.110643723	0.052322038	ND	ND	ND	ND
comp155978_c1_seq1	ND	ND	1.613006821	1.631851091	ND	ND	ND	-0.706447408
comp155984_c1_seq3	0.052736296	-0.399601834	0.579417589	0.640705807	-1.488186222	-1.549743618	-1.37453538	-0.657229386
comp155986_c0_seq3	0.086594563	-0.090602909	0.980874171	1.042648558	-0.442428731	-0.337654706	0.063332576	-0.428541212
comp155987_c0_seq6	-1.285580723	-0.896715857	0.611491785	0.541531793	-1.258301516	-0.842737658	ND	-1.27244272
comp155993_c1_seq13	ND	ND	0.541690489	0.566120312	ND	ND	ND	ND
comp155993_c1_seq2	ND	ND	0.377802006	0.336774576	ND	ND	ND	ND
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comp156008_c1_seq6	0.11643372	0.045210671	1.158439505	1.101908728	-0.777105827	-0.502871122	-0.010242471	-0.569398282
comp156046_c0_seq2	-0.918340655	-0.509272402	0.352128921	0.397233042	-0.435129492	-0.518963283	-0.367236141	-0.796058183
comp156046_c0_seq4	-0.821430641	-0.487613342	0.525264348	0.566176807	-0.360495874	-0.311640787	-0.349507374	-0.875239429
comp156059_c0_seq1	-1.227272657	-1.08144584	0.856886494	0.868685171	-2.045091491	-0.744921051	-1.028350662	-1.281081444
comp156059_c0_seq3	-1.761964009	-1.005122358	0.846428942	0.838447254	-1.257563548	-0.66590843	-1.076965916	-2.049856002
comp156063_c0_seq1	-0.110226181	0.250150147	1.327835469	1.382432584	0.119878538	0.214517572	-0.048477378	0.13092088
comp156071_c0_seq9	-0.555869957	-0.291943828	0.695237074	0.706166133	-0.28552702	-0.046080103	-0.715969904	-0.667670691
comp156074_c0_seq6	-1.058290855	-0.845517248	0.150807033	0.129849586	-1.031011648	-1.092569045	-0.616330811	-0.823304103
comp156101_c0_seq1	-0.861165819	-0.441266719	0.80022974	0.785002935	-0.34097109	-0.594414013	-0.82938024	-0.848027816
comp156101_c0_seq3	-1.490437422	-0.335655762	0.8879123	0.853724295	-0.195986487	-0.348624353	-0.609144684	-0.824086906
comp156111_c0_seq5	ND	ND	0.795590208	0.837639068	ND	ND	ND	-0.946372222
comp156111_c0_seq6	ND	-1.028603453	1.497199306	1.443067952	-1.214097854	ND	-1.100447012	-0.751117803
comp156111_c0_seq7	ND	ND	1.087742509	1.032447278	-0.920353491	-1.282940883	ND	-0.934494695
comp156168_c0_seq1	-0.111215946	0.019022773	1.36584299	1.370344631	-0.653812047	0.525892347	0.347134515	0.395433728
comp156190_c0_seq1	ND	ND	1.721725405	1.727643319	ND	ND	-1.735885404	-1.86367745
comp156190_c0_seq10	ND	ND	0.855058957	0.801644606	ND	ND	ND	ND
comp156190_c0_seq11	ND	ND	1.300309446	1.311467664	ND	ND	ND	ND
comp156190_c0_seq2	ND	ND	1.709481474	1.694946753	ND	ND	ND	-1.202742671
comp156190_c0_seq9	ND	ND	1.805700598	1.77754978	ND	-1.891375954	ND	-1.843959761
comp156207_c0_seq3	-1.155946865	-0.767081999	0.347341594	0.360375818	-1.128667659	-0.7131038	ND	-0.841778867
comp156209_c2_seq1	-1.589000493	-0.747837956	0.940373534	0.91935326	-0.632302361	-0.392829762	-1.74910044	-0.598138885

comp156217_c1_seq1	ND	-1.887249182	0.62262562	0.630179714	ND	ND	-1.18094149	-0.882764804
comp156256_c1_seq3	-0.693722749	-0.480949142	0.730384464	0.72937561	-0.967473538	-1.029030934	ND	-1.282644738
comp156256_c1_seq5	-1.054541527	-0.21337899	0.711988367	0.699142071	-0.726232325	-0.611698462	ND	-1.041403524
comp156256_c1_seq6	0.094339109	0.136042259	0.964159113	0.959053111	-0.131638898	-0.272377541	-0.921078043	-0.82702134
comp156315_c0_seq1	-1.828488538	-1.314684936	1.801286946	1.773870237	ND	ND	ND	-1.815350536
comp156316_c0_seq1	0.453658005	0.37107875	1.515089391	1.463582138	0.262881451	0.29189389	0.274079705	0.000955764
comp156318_c0_seq3	-1.471153178	-1.559409567	0.333165276	0.374844681	-0.32993062	-0.391488016	-1.33022313	-0.281923917
comp156329_c0_seq4	-0.718226116	-1.1075125	1.665943959	1.686761007	ND	-1.053534301	-0.78141605	-1.131056845
comp156382_c0_seq6	ND	ND	0.504235734	0.444678502	ND	ND	ND	ND
comp156382_c0_seq9	ND	-1.735981506	0.339524021	0.304326135	ND	-1.380973312	ND	ND
comp156405_c0_seq1	0.374260597	0.51324799	1.661105977	1.651269149	0.582131564	0.656018312	-0.249596643	-0.418781374
comp156445_c0_seq12	-1.142831285	-0.988049625	1.426516743	1.379860185	-1.115552078	-0.737776781	-0.373512306	-0.585625238
comp156488_c0_seq1	ND	ND	0.560615227	0.595643744	-1.283370811	-0.742868216	-1.169719969	-0.820390761
comp156510_c0_seq2	-0.234118071	-0.120729096	1.632692832	1.579630483	-0.005193501	0.221689971	0.39689821	0.22898894
comp156524_c0_seq3	ND	-0.813236831	0.570032074	0.625010818	-0.220579981	-0.282137378	0.018009597	-1.012872436
comp156530_c0_seq4	-0.275530615	-0.014151674	1.125095503	1.11861515	-0.651943746	-0.527864565	-0.237262908	-0.519956914
comp156576_c0_seq1	ND	-0.904751812	1.376003202	1.317240654	0.324727135	0.004543592	0.632643205	0.257340419
comp156588_c0_seq3	0.086289902	0.205946485	1.647887659	1.613556017	0.330822107	0.3492153	-0.227624909	-0.124968034
comp156601_c0_seq1	-0.131662835	-0.219919224	0.768347414	0.746286696	-0.732772559	-0.743177433	ND	-1.172882495
comp156630_c0_seq2	ND	-1.742655757	0.938289502	0.871683152	ND	-1.387647563	ND	-1.641261366
comp156659_c0_seq7	-0.4599481	0.644123969	1.702097827	1.64080861	0.16156576	0.713754113	-0.620048047	-0.388818151
comp156682_c0_seq5	ND	-0.702941912	0.7424749	0.715561679	ND	-0.72814496	-0.95087673	-1.379698772
comp156725_c0_seq12	-1.329713024	-0.514879426	0.690205231	0.670261781	-0.825312563	-0.761931222	-0.109601729	-0.71451503
comp156725_c1_seq2	ND	-0.951051832	0.573546226	0.515224541	-0.659424978	-0.897073633	ND	ND
comp156735_c0_seq7	-0.36221478	-0.149441173	0.994945644	0.940945332	-0.732875582	-0.041105312	-0.283432638	-0.110194689
comp156769_c2_seq1	-1.318239153	-1.105465546	0.695338924	0.640990683	ND	-1.352517343	-0.70018785	-0.606131147
comp156769_c3_seq2	0.195614966	0.138767042	1.673897327	1.615027636	-0.148716897	-0.161969614	0.302686748	0.208752969
comp156769_c3_seq3	0.59759486	0.755113105	1.932411457	1.937214417	0.485609476	0.680499942	0.900290313	0.66824413
comp156769_c3_seq5	0.686787765	0.725137273	2.110894979	2.085997049	0.406303594	0.714657482	0.803679573	0.679404101
comp156769_c3_seq6	0.457936803	0.467503771	1.698310242	1.690342744	0.14096086	0.385454261	0.681841087	0.299531175
comp156771_c1_seq2	ND	ND	0.420381469	0.413212307	ND	ND	ND	ND

comp156809_c0_seq3	-0.384462331	-0.247409438	1.006121848	1.061743516	0.089974907	0.002863406	-0.29904961	-0.407536501
comp156821_c0_seq2	-0.948434719	-1.191593068	1.259576073	1.228063264	-0.966913003	-0.941320224	-1.80750467	-1.458175462
comp156821_c0_seq3	-1.177088837	-0.818187195	1.248009916	1.270043998	-1.003681595	-0.67988811	-1.258007538	-1.163950835
comp156821_c0_seq6	-1.203707224	-0.876990265	1.305333564	1.32005286	-1.574368026	-0.823012066	-1.76174718	-1.287479235
comp156825_c1_seq2	ND	ND	0.776600211	0.740785867	ND	ND	ND	ND
comp156863_c0_seq1	-0.991136616	-0.477333014	0.884537747	0.938638241	-0.662827414	-0.481346762	-0.975145304	-0.801907355
comp156883_c0_seq2	ND	-1.536702639	0.545536271	0.503605002	-1.421167043	-0.880664449	-0.161388166	-0.958186993
comp156900_c0_seq1	ND	ND	0.445495648	0.438326486	ND	ND	ND	ND
comp156907_c1_seq5	ND	ND	0.770503624	0.772289303	ND	ND	ND	ND
comp156910_c0_seq1	-0.367008187	-0.310581781	1.473070115	1.462566195	-0.32974476	-0.278879977	-0.461606585	-0.811247381
comp156910_c0_seq3	-0.233135931	-0.207448968	1.43648395	1.418849353	-0.321250143	-0.253173682	-0.548137838	-0.742876674
comp156929_c0_seq18	-0.452062939	-0.257772737	0.435154815	0.390843844	ND	-0.662432387	-1.390314136	-0.518106182
comp157049_c0_seq2	-1.042880491	-0.432166876	1.339130323	1.346745175	0.393768186	0.5918481	ND	-1.506863744
comp157061_c1_seq11	-0.389367026	-0.15540412	1.003889743	1.058690825	-0.215959784	-0.081222535	-0.771315723	-0.774169032
comp157061_c1_seq2	-0.680561303	-0.115605178	0.889673946	0.891278708	-0.255342088	-0.112779501	-0.84066125	-1.093392033
comp157061_c1_seq6	-0.77831187	-0.365965908	0.889423867	0.90073811	-0.206964619	-0.085591332	-0.570435032	-0.765173868
comp157077_c1_seq2	ND	-1.180638773	0.431109461	0.413956078	ND	-1.42769057	ND	ND
comp157078_c0_seq1	-0.024111222	0.478312835	1.103647314	1.142996894	0.017891241	0.070277197	-0.605216482	-0.774401213
comp157186_c0_seq1	-0.258670226	-0.323445519	1.493525216	1.443503553	0.382568195	0.954888516	0.089385315	-0.270355807
comp157186_c0_seq18	-0.664684541	-0.305782898	1.510261539	1.444722727	-0.132255356	0.61490449	-0.018604514	-0.748456551
comp157282_c0_seq4	-0.96648388	-0.577619014	0.585653146	0.529635416	-1.240234669	-0.602822061	-0.825553832	-0.476224623
comp157318_c0_seq4	-1.005072394	-0.634690934	0.996362455	0.972455403	-0.465909827	-0.71199165	-0.725839648	-0.71893312
comp157318_c0_seq5	-0.693426085	-0.321935315	1.097927392	1.076747515	-0.449437769	-0.727704275	-0.552496037	-0.680288083
comp157318_c0_seq6	-0.880391462	-0.491526596	0.887265007	0.873292136	-0.55208226	-0.68422073	-0.625518061	-0.753310107
comp157331_c0_seq6	-1.344340056	-0.654445194	0.427793715	0.405517134	-0.515428503	-0.776558255	-1.379501267	-1.507293313
comp157334_c0_seq4	-0.722830466	-0.731905608	1.062464752	1.042134143	-1.093491268	-1.45607866	ND	ND
comp157357_c0_seq11	-0.492579069	-0.434707422	0.632972767	0.573415535	-0.796293082	-0.401918522	-0.828770275	-0.701289816
comp157357_c0_seq13	-0.57641496	-0.460551366	0.31505367	0.302207375	-1.248105758	-0.672841057	-1.134454916	-1.262246962
comp157357_c0_seq8	-0.367001725	-0.25361275	0.56154987	0.564846141	-1.080085208	-0.513253675	-0.614251848	-0.997316399
comp157383_c0_seq1	0.317993194	0.305826974	1.555588787	1.504939697	0.289474973	0.435525887	0.37040197	0.121431336
comp157421_c1_seq4	ND	-1.537714981	0.600842292	0.575699759	-1.422179385	-1.182706786	-0.609558539	-0.737350585

comp157449_c0_seq1	-0.283151245	-0.058143181	1.149729893	1.123381897	0.057392414	-0.035422676	0.523225774	0.289722434
comp157450_c1_seq12	ND	-1.219671868	0.629437281	0.685937198	-1.104136273	ND	ND	ND
comp157450_c1_seq2	ND	ND	1.153048266	1.103026604	-1.17392796	ND	ND	-1.188069164
comp157450_c1_seq4	ND	ND	1.007788513	0.997634497	ND	-1.070881702	ND	-1.023465509
comp157450_c1_seq7	ND	-1.446331056	1.188482482	1.151283235	ND	ND	ND	ND
comp157487_c0_seq7	ND	ND	0.710892985	0.67315783	-1.154704202	ND	-1.342083356	-0.770905398
comp157487_c1_seq1	ND	-1.571269793	0.96050685	0.948565172	-0.853674206	-1.216261599	-1.04105336	-0.624777362
comp157561_c1_seq1	0.229262067	0.531436085	1.882878734	1.862554556	-0.151864169	-0.118635246	-0.236023836	-0.199005633
comp157561_c1_seq10	0.237977299	0.303182423	1.345238944	1.345170122	-0.214750438	-0.111954978	-0.385096252	-0.465463648
comp157561_c1_seq2	-1.519786802	-1.130921936	1.511928598	1.497968623	-1.492507595	ND	-1.378856753	ND
comp157561_c1_seq4	-1.156112468	-0.298244238	1.873248471	1.899362378	-1.003894525	-0.889360663	-0.751940985	-1.222155712
comp157617_c0_seq2	-0.417830987	-0.602997389	1.36746423	1.337373784	-0.487461794	-0.397751515	-0.640078841	-0.802632993
comp157629_c0_seq4	-0.05283471	-0.111127875	0.615574874	0.678228634	-0.268593552	-0.119297583	0.038877316	-0.583764752
comp157675_c0_seq1	-0.123407602	0.082735426	0.881570304	0.857288832	-0.302888474	-0.29598849	-0.459598808	-0.424663556
comp157692_c0_seq3	-0.28809825	-0.447710547	1.118749958	1.072295771	-1.177272992	-0.799497695	-0.147168201	-0.752081502
comp157705_c1_seq1	-0.941253167	-0.983752065	0.853775212	0.837112896	-0.69212521	-0.514800518	-1.277444373	ND
comp157766_c0_seq3	0.105682625	0.234910181	1.08436552	1.059539678	-0.213825654	0.141442302	-0.401204808	-0.638141323
comp157771_c0_seq1	-1.159780901	-0.380275265	0.880126115	0.816892826	-0.121777829	-0.032691088	-0.524000831	-0.458668278
comp157801_c0_seq1	0.334396402	0.631490894	1.294555832	1.25426297	0.231059739	-0.109251259	-0.207044292	-0.061835066
comp157827_c0_seq1	-1.816712517	-1.302908914	0.944140244	0.90496219	-1.488403315	-1.152020702	-1.675782468	-1.10460451
comp157827_c0_seq10	-0.080009058	-0.484535409	1.109953819	1.168051388	0.041174651	-0.622442736	-0.146204502	-0.415325701
comp157827_c0_seq11	ND	ND	1.054717373	1.069037126	-0.761830417	-0.698449077	-1.602422084	-1.429184135
comp157827_c0_seq13	ND	-0.608580351	0.456625219	0.466489396	-0.794074752	-0.281600881	ND	ND
comp157827_c0_seq5	-1.098664202	-0.982800608	1.10934659	1.045582676	-0.656411648	-0.553158795	-1.355674162	-1.182436213
comp157827_c0_seq8	ND	-1.127728262	1.274497061	1.296394744	-0.296189323	-0.082523988	-1.296481834	-1.42427388
comp157827_c0_seq9	-0.279233645	-0.118848107	1.064562817	1.070757616	-0.552984434	0.051635661	-0.526483767	-0.462390287
comp157865_c0_seq1	-0.085541133	-0.474827518	0.776769268	0.7511167	-0.395504095	0.013719585	-0.865429839	-0.868283148
comp157939_c0_seq3	0.103280606	0.24841088	1.068033509	1.009883584	-0.154079767	0.287497524	0.171659987	-0.081070795
comp157971_c1_seq1	0.610648666	0.783494326	1.520729303	1.51356014	0.51688418	0.68026661	0.638221851	0.444751029
comp157978_c0_seq2	0.013741445	0.238635685	1.501134462	1.479144334	0.129658139	0.459307368	0.438995796	0.122147513
comp158030_c0_seq11	ND	-2.178563012	0.258079876	0.229721414	-1.585906162	-1.823554817	ND	-2.077168621

comp158030_c0_seq18	-1.960134659	-1.446331056	0.229534677	0.218086717	ND	-1.517291594	ND	ND
comp158030_c0_seq24	-2.060525013	-1.370630151	0.332731756	0.358887657	-1.431185815	-1.316651952	ND	-1.570265756
comp158030_c0_seq41	-2.088801268	-1.876027661	0.259585231	0.252416068	-1.760492066	-1.424109454	ND	-2.075663266
comp158030_c0_seq48	-1.670801466	-2.06008785	0.200463779	0.146551213	-1.467431	-1.307139647	ND	ND
comp158030_c0_seq49	-2.084370843	-1.57056724	0.252034359	0.223068067	-1.756061641	-1.817619037	ND	ND
comp158030_c0_seq6	ND	-1.456963597	0.368664457	0.303503347	-1.244517989	-1.402985398	ND	ND
comp158030_c0_seq69	ND	-1.868657639	0.242652719	0.229189323	-2.054152039	-1.513649444	ND	-1.767263247
comp158085_c0_seq7	-0.844863308	-0.154968446	0.697933693	0.735576875	0.111834825	-0.277081506	-0.30599325	-0.178512791
comp158085_c2_seq1	-0.077996197	-0.2419733	0.875394674	0.907478811	-0.846597008	-0.130003154	0.183507783	-0.031434439
comp158087_c0_seq18	-1.012548727	-0.79977512	0.020457902	0.070431625	-0.93951203	-0.959676741	-1.825861188	-1.476531979
comp158119_c0_seq1	ND	ND	1.707643174	1.729229183	ND	ND	ND	ND
comp158162_c1_seq4	-1.115166597	-1.078484249	1.189754209	1.186378035	-0.58728504	-0.973353528	-1.752387799	-1.880179845
comp158162_c1_seq5	-1.287052909	-1.278399285	1.110182158	1.095019619	-1.016735654	-1.14523984	ND	-1.398853643
comp158171_c1_seq2	-0.696832555	-0.785088943	0.551183399	0.524990999	-0.447704599	-1.509261995	-1.033023761	-0.984724548
comp158173_c0_seq2	-0.70096711	-0.272593703	0.405856026	0.360228612	-0.564543434	-0.237920659	-0.259007066	-0.491534462
comp158194_c0_seq4	-0.786144264	-0.698309394	0.72432278	0.749483574	-1.018502368	-0.674294418	-0.690971706	-0.869916275
comp158194_c0_seq5	-0.103940124	-0.245715768	0.795787152	0.73079787	-0.614480012	-0.073977417	-0.44013133	-0.514677864
comp158236_c0_seq4	-0.406498186	-0.154216037	0.637043115	0.680710968	-0.379218979	-0.484242069	-0.98572744	-0.812489491
comp158263_c0_seq8	-1.066915426	-0.854141819	0.068396248	0.061227085	ND	ND	-0.925985378	-0.752747428
comp158302_c1_seq7	ND	-1.615714931	0.479685424	0.424592709	-0.801209332	-0.783585482	ND	-1.213290545
comp158306_c0_seq4	0.169938194	-0.12917156	2.161730882	2.14923448	0.514637812	0.523460381	-0.363742416	0.069132844
comp158306_c1_seq1	-0.209733049	0.07236705	1.401460808	1.355373579	-0.07891325	-0.227620822	-0.307685089	-0.465440359
comp158306_c1_seq2	-0.423183819	-0.453448261	1.684007207	1.716186672	0.915849248	0.738832636	-0.386989121	-0.233954558
comp158332_c1_seq1	0.314806716	0.278579327	1.997308622	1.973135985	0.372575245	0.484648509	0.317434066	0.155783753
comp158385_c1_seq5	ND	ND	0.193778821	0.145216974	ND	ND	ND	ND
comp158391_c0_seq1	-0.427510258	0.508855828	1.286100969	1.268181394	0.025737681	0.229882318	-0.21963342	-0.131825665
comp158429_c0_seq9	0.079048156	0.141772306	0.875393378	0.868224215	0.031998619	0.112413299	-0.34920056	-0.45926384
comp158429_c1_seq2	-1.138714719	-1.403062366	1.451159531	1.386079093	ND	-0.871962913	-1.474905925	-1.602697971
comp158429_c1_seq8	ND	-1.351909844	1.371243486	1.325219895	-1.236374249	-1.172992908	-1.599844661	-1.125576716
comp158462_c0_seq13	-0.534581719	-1.224898099	0.29969996	0.338288288	-1.109362503	ND	ND	-0.822473712
comp158469_c0_seq1	-0.216169145	0.27861122	2.096518684	2.061436862	-0.454204382	-0.151062703	-1.01724715	-0.571007928

comp158513_c1_seq1	-1.88892915	-1.977185538	1.157836075	1.125076946	ND	ND	ND	-1.574761152
comp158532_c1_seq19	ND	-0.899288917	0.02324915	0.103230163	-0.783753321	-0.544280722	ND	-0.49686453
comp158640_c0_seq2	-1.636368246	-1.122564643	1.47564995	1.489354791	ND	ND	ND	ND
comp158656_c1_seq12	-0.818661486	-0.781979138	0.528739101	0.531329775	-0.490352283	-0.48496289	-0.677731437	-0.981614742
comp158679_c0_seq3	ND	-1.460450707	0.388658443	0.435174139	-0.742855121	-0.127718907	-0.930234274	-0.513958276
comp158680_c1_seq1	ND	ND	2.413690541	2.368456637	-1.275646696	-0.638234088	ND	-0.590817896
comp158685_c0_seq1	0.089298585	0.172112654	1.466934594	1.470117469	0.326277651	0.452960403	0.207163329	-0.116923362
comp158685_c0_seq2	-0.02090407	0.172984193	1.392782782	1.38453059	0.203508998	0.325798326	0.071177411	-0.056614635
comp158685_c2_seq1	ND	ND	0.896407329	0.832510541	ND	-0.407076114	ND	-0.961719913
comp158704_c1_seq1	0.671621215	0.890735	1.571021072	1.502267473	0.702082081	0.83218372	0.471404045	0.204432823
comp158731_c0_seq11	ND	ND	0.391581795	0.358083694	ND	ND	ND	ND
comp158743_c0_seq8	-0.31102948	-0.078950718	1.16310075	1.095635686	-0.723082967	-0.06448106	0.3199868	-0.038254167
comp158759_c1_seq2	ND	ND	0.810881048	0.758899541	ND	-1.589157737	ND	ND
comp158777_c0_seq1	-0.740487383	-0.4405636	0.998222633	0.934014969	-0.667450686	-0.552916823	-0.553799844	-0.83649385
comp158795_c0_seq13	-0.35563758	-0.360919734	0.421739247	0.402831681	-0.376663053	-0.270729362	-0.414279886	-0.241041937
comp158795_c0_seq27	-1.551495159	-1.463660288	0.5909951	0.55942095	-1.223185957	-1.40968209	ND	-1.839387152
comp158795_c0_seq30	ND	ND	0.619940668	0.605632257	ND	ND	ND	ND
comp158830_c1_seq4	ND	-1.330856241	2.119025253	2.118256485	ND	-1.276878042	ND	-1.229461849
comp158918_c1_seq7	-1.275887912	-0.58599305	0.396542947	0.41652603	-0.248608705	-0.611196097	-1.134957863	-1.262749909
comp158921_c0_seq5	-0.798200801	-0.71036593	0.036080878	0.004088131	-0.895860331	-0.589440942	ND	-1.38712279
comp158940_c0_seq2	-0.265061218	-0.164261371	0.861386996	0.814389369	-0.37608471	0.114112767	-0.104826014	-0.51516465
comp158944_c0_seq3	-0.0373624	0.016487973	0.7363252	0.715829359	-0.152491339	-0.066995684	-0.07252361	-0.320609488
comp158945_c0_seq6	-0.585503295	-1.275819675	0.561707602	0.47769841	ND	-0.443690226	ND	-0.697304029
comp158970_c0_seq1	-0.583432887	-0.268669741	0.993527724	0.954410744	-0.230300101	-0.224910708	-0.631559074	-0.119502568
comp158970_c0_seq2	-0.852724968	-0.861800111	0.220438799	0.224265021	-0.621325779	-0.506791916	-0.808704932	-0.58431446
comp159055_c0_seq4	ND	ND	0.325083356	0.334304609	-1.24367995	ND	ND	-1.257821154
comp159070_c0_seq10	-1.522786381	ND	0.813618821	0.781447389	ND	-1.256034575	-1.080826337	-1.208618383
comp159070_c0_seq9	-0.363654545	-0.116118832	0.978782622	0.995882034	-0.637405334	-0.574023994	-0.699845751	-0.827637797
comp159092_c0_seq3	-0.156167655	-0.150743001	0.69562827	0.639447026	-0.35613223	-0.460441607	-1.270510112	-1.398302158
comp159094_c0_seq9	ND	ND	0.454236717	0.479252238	-0.415556585	ND	-1.000875747	-0.827637797
comp159122_c0_seq1	-0.425021457	-1.513277846	1.195380401	1.249937807	-1.397742251	-1.158269652	-1.284091409	-1.110853459

comp159139_c0_seq5	ND		-0.702365543	0.956126095	0.974764196	ND		-0.472296085	ND	ND	
comp159218_c1_seq3		0.050619343	-0.902938472	1.148142456	1.098922087		-0.404186125	-0.246900282		-1.752933281	-0.579695331
comp159231_c0_seq1	ND	ND		0.86735909	0.898381545	ND		ND	ND	ND	ND
comp159231_c0_seq10		-1.38017423	-0.866370628	1.36159843	1.360752138		-0.926926291	-0.988483688		-0.373942756	-0.501734802
comp159231_c0_seq13		-1.856107806	-1.643334199	0.871504022	0.845422097	ND		-1.890385996	ND		-1.842969803
comp159231_c0_seq15		-1.561960592	-1.650216981	0.846995277	0.899741139	ND		ND	ND		-1.54882259
comp159231_c0_seq17		-0.999154589	-0.891116332	1.367820817	1.350836672		-0.971875382	-1.100379568		-0.472873659	-0.600665705
comp159231_c0_seq2		-1.005223078	-0.984334997	1.372140732	1.348474844		-0.781649226	-0.884599308		-0.563263033	-0.79579043
comp159231_c0_seq5		-1.085034395	-0.997199524	1.343189385	1.375920485		-0.794513753	-0.818282589		-0.324315588	-1.004949603
comp159231_c0_seq8		-1.850120195	-1.938376584	0.836098948	0.866605234	ND		ND		-1.709190146	-1.535952197
comp159231_c3_seq2		-0.67683343	-0.844271065	1.361568231	1.36825018		-1.126675478	-0.21050927		-0.615084628	-0.663695428
comp159250_c8_seq4		-1.097528791	-0.708663925	0.651742098	0.607850128		-1.070249584	-0.654685726		-0.655568747	ND
comp159426_c0_seq1		-1.634391181	-1.421617574	1.760461283	1.693628346	ND		ND		-0.794491128	-0.922283174
comp159470_c1_seq3		-0.26995276	-0.067163374	0.585727063	0.548296295		-0.630853725	-0.30423095		-0.626347353	-0.997177447
comp159479_c0_seq2	ND	ND		0.121535692	0.165519052		-0.935344253	ND	ND	ND	ND
comp159484_c2_seq1		-0.354314519	-0.141540912	0.736578015	0.729408853		-0.327035312	-0.250290011		-0.21338447	-0.290023994
comp159508_c0_seq4	ND	ND		1.297109163	1.249090976	ND		ND	ND	ND	ND
comp159508_c0_seq8	ND	ND		1.165200193	1.150411634	ND		ND	ND		-1.364458805
comp159519_c0_seq23		-0.320966286	-1.409222675	1.502567398	1.517575691		0.44667561	0.22453912		0.142183057	-0.608858279
comp159529_c1_seq2		0.856884615	0.923279077	2.145281407	2.131991148		0.41696973	0.186620313		-0.126288087	-0.254080133
comp159616_c1_seq5	ND	ND		0.80936933	0.802200168	ND		ND	ND	ND	ND
comp159631_c0_seq3		-0.413092519	-0.270899987	0.888550576	0.874750835		-0.607662062	0.057779269		0.246351469	-0.169505596
comp159684_c1_seq10		-1.37430328	-0.293767648	1.327249418	1.304746701		-0.802956029	-0.159383112		-0.932343235	-1.008982759
comp159684_c1_seq12		-0.970005413	-0.067035726	1.634309625	1.617529586		-0.319476916	0.236265645		-1.227015373	-0.61444473
comp159684_c1_seq13		-0.699304465	-0.185500863	1.543970508	1.523813559		-0.672025259	0.129740205		-1.558374417	-0.841068423
comp159700_c1_seq1		-1.898742079	-1.384938476	1.929318623	1.928756305		-1.394341617	-1.154869018	ND		-0.563384781
comp159705_c0_seq17	ND	ND		0.925346908	0.903976115	ND		ND	ND	ND	ND
comp159720_c0_seq1		-0.010249891	0.150345704	1.080011859	1.137474787		0.150085942	0.260579827		-0.271376417	-0.341176516
comp159725_c1_seq1		-1.185711281	ND	1.413659175	1.373794994		-0.857402079	-1.219989471		-1.044781233	-0.695452024
comp159725_c1_seq15		-0.444419619	-0.460125341	1.628744148	1.569472354		-1.458533098	-0.918030503	ND		-0.627576262
comp159725_c1_seq18		-0.714122515	-0.688435551	1.774870353	1.733241759		-0.841745268	-0.845310718		-1.272162471	-0.524893254

comp159725_c1_seq2	-0.659520455	-0.596509169	1.72340083	1.702370029	-1.01245249	-0.927881851	-1.597771653	-0.54947244
comp159725_c1_seq9	-0.40969626	-0.435804742	0.971296773	0.99268307	-0.292240423	-0.654827815	-0.236581528	-0.51050161
comp159725_c2_seq2	-1.105042724	-0.629027682	0.640297871	0.681641135	-0.952824781	-1.616442168	ND	-1.26799598
comp159755_c0_seq2	-0.470350861	-0.479426003	0.415440637	0.471940554	-0.41504293	-0.218322312	-0.16308939	-0.633304117
comp159764_c1_seq4	ND	ND	0.08582014	0.078650977	ND	ND	ND	-0.860262273
comp159767_c1_seq1	-0.934870391	-0.655149994	1.015822229	1.03025227	-0.907591184	-0.902201791	-1.094970338	-0.585940287
comp159767_c1_seq4	-1.122652286	-0.858726156	1.074404984	1.059847888	-0.85233503	-0.758990467	-0.583782228	-0.410544279
comp159784_c2_seq18	-1.007527033	-0.618662167	0.759002861	0.811057688	-0.804156567	-0.467773955	-0.447467676	-0.392329039
comp159794_c0_seq12	-0.092094677	0.062686983	0.8152941	0.776410524	-0.098673737	0.003960902	0.037839988	-0.149537748
comp159794_c0_seq16	-0.319093224	0.120924165	0.822208814	0.796814831	-0.240661494	-0.142518048	-0.303101912	-0.363947168
comp159794_c0_seq7	-0.170054471	-0.133372123	0.867772346	0.874750835	-0.122571878	0.075508036	-0.008921036	-0.303044504
comp159796_c0_seq1	ND	-1.991467476	1.689477783	1.668281348	-1.574901885	-1.636459282	ND	-1.890073085
comp159806_c2_seq6	-0.765071382	-0.289056341	0.518660124	0.544491221	-0.515943426	-0.072350844	-1.101262589	-1.229054635
comp159808_c0_seq3	-1.391105365	ND	0.112183094	0.105013931	-0.664856154	-0.647232305	ND	-1.076937367
comp159810_c2_seq2	-0.716081447	-0.327216581	0.737160973	0.688267476	-1.53390028	-0.896487673	-0.306306086	-0.84907148
comp159812_c0_seq1	0.214173396	0.30925876	1.487743455	1.474505137	0.132308133	0.188581385	-0.494403714	-0.01244894
comp159863_c0_seq3	0.055186099	-0.158009026	0.691100123	0.644059449	-0.289145764	-0.089790388	-0.451701334	-0.75558464
comp159863_c0_seq7	-0.494242721	-0.105377854	1.22221795	1.24966106	0.508998245	0.447440849	-1.467256024	-0.81689682
comp159873_c3_seq1	-0.735573516	-0.34670865	0.445495648	0.423603229	-1.185415564	-1.246972961	-0.770734727	-1.199556768
comp159897_c1_seq9	ND	-0.633105595	0.23827995	0.17311884	ND	ND	ND	-0.531711203
comp159902_c0_seq4	-0.874161528	-0.962417916	0.332213502	0.33316223	ND	-1.607409722	ND	ND
comp159904_c1_seq11	-1.128381672	-0.688364283	0.631040134	0.604826341	-0.962799767	-0.634386084	-0.89054161	-0.976940971
comp159904_c1_seq12	-0.405467041	0.001126592	0.628386992	0.605705663	-0.327035312	-0.087562713	-0.690505725	-0.596449022
comp159904_c1_seq43	-0.866101036	-0.574146183	0.589125977	0.550008998	-0.567755058	-0.433017809	-0.558839566	-0.728024297
comp159919_c1_seq4	ND	-1.418967409	1.1746406	1.182640423	ND	-1.188897951	ND	-1.016543022
comp159946_c0_seq1	0.352915907	0.510172187	1.207927071	1.267178599	0.249426834	0.36785574	0.286237646	-0.031886099
comp159946_c0_seq2	-0.724980443	-0.512206836	0.923450139	0.89607759	-0.133429806	-0.157198641	-0.459111657	ND
comp159949_c0_seq1	ND	-1.477623415	1.414951429	1.408815072	ND	-1.423645216	-0.549466973	-0.899107769
comp159949_c0_seq5	ND	-1.63229307	0.991140923	0.939493488	ND	ND	-1.403106632	ND
comp159954_c3_seq19	-1.26054022	ND	0.464596989	0.404721476	-1.233261013	-0.993788414	-1.119610171	-0.946372222
comp159954_c3_seq22	-1.144194848	-0.755329982	0.398602153	0.337913734	-1.2930069	-0.752504305	-0.276266071	-0.528996854

comp159954_c3_seq9	-1.563518601	-1.350744994	0.571793073	0.508008492	-1.536239395	-0.752698751	-0.246497294	-0.508987914
comp159968_c0_seq1	0.288205892	0.553792806	1.533216336	1.506888874	0.374878751	0.582166667	0.520013989	0.347475616
comp159979_c0_seq2	0.356287394	0.316335685	1.299902735	1.318438973	-1.068731071	-1.005349731	-0.955080229	ND
comp159987_c0_seq13	-0.400072009	-0.421381608	0.593910512	0.618926032	-0.673822798	-0.25825894	-0.338323207	-0.085904011
comp159987_c0_seq15	-1.135601483	-1.524887867	0.335502293	0.339328514	-1.409352272	-0.868849677	-0.994671435	-0.645342226
comp160017_c0_seq1	-0.497444699	-0.132580109	1.715098086	1.716444774	-0.229133426	0.246428362	-0.41651258	-0.444189473
comp160038_c0_seq4	-0.08461271	0.152010508	0.794023245	0.772566791	-0.125449323	-0.11194204	0.034777661	-0.071474707
comp160065_c0_seq8	-0.075003773	0.001550087	0.944753065	0.937583902	-0.082486673	0.043946413	-0.394804563	-0.397657872
comp160065_c0_seq9	-0.200339734	0.039586119	0.915878998	0.877524967	-0.051638365	0.044872394	-0.198588861	-0.435525377
comp160069_c0_seq1	-0.171662795	0.03609001	1.492312793	1.457169635	-0.208841578	-0.124270939	-0.289010762	-0.416802808
comp160089_c0_seq2	0.395490392	0.193290651	2.285655486	2.273837909	-0.126902323	0.311102404	0.050866018	-0.182436213
comp160089_c1_seq2	-0.684257448	ND	1.383302441	1.400800162	-0.958008238	ND	ND	ND
comp160091_c1_seq1	-1.309255813	-1.397512202	0.2867867	0.244855431	ND	ND	ND	-1.29611781
comp160152_c0_seq1	-0.74099008	-0.43130646	0.315140348	0.288227127	-0.678948767	-0.599177011	-0.378211282	-1.10806332
comp160152_c0_seq7	-0.745217061	-0.698774876	0.431885916	0.432613235	-0.717937854	-0.440676694	-0.604287012	-1.171411752
comp160244_c0_seq2	-1.023910973	-1.316287345	0.784907983	0.809786423	-1.297661762	-1.007036641	-0.973157555	-1.369794914
comp160254_c3_seq6	-0.370085531	-0.180377228	1.420467643	1.385564093	0.064027397	-0.034252806	0.032722389	-0.263043026
comp160316_c2_seq1	-1.012395076	ND	0.071764075	0.115747435	ND	ND	ND	ND
comp160397_c0_seq1	ND	-1.286768855	0.480867252	0.437785533	ND	ND	ND	ND
comp160397_c0_seq3	ND	-1.897636558	0.841511011	0.86006417	-1.304979708	-1.190445845	ND	-1.398302158
comp160422_c0_seq1	-0.414090898	0.168067257	1.431876539	1.400109811	-0.197755455	-0.058398009	-0.61558353	-0.743375576
comp160462_c0_seq3	0.262214019	0.368532295	1.110939126	1.097638645	0.194937118	0.188427288	0.314417504	0.124477551
comp160462_c0_seq4	-0.734075948	-0.252457028	1.13845362	1.157018879	-0.375803522	-0.122090484	-0.04030393	-0.08891473
comp160462_c0_seq5	-0.099635055	-0.037354289	1.387399323	1.370302997	0.086867486	0.121359261	0.282556785	0.046128513
comp160501_c0_seq1	ND	ND	1.433438718	1.389239588	ND	-1.099971971	ND	-0.575434524
comp160521_c0_seq38	-1.675933959	-1.065220344	0.449617877	0.40105603	-0.949684748	-1.233090894	-0.932943919	-0.817697917
comp160634_c1_seq3	-0.222609617	-0.481562232	0.428281564	0.473082035	-0.184606544	-0.955857811	-0.984769555	-0.449803769
comp160634_c1_seq8	-0.726763995	ND	0.725371941	0.677584928	-0.046272275	-0.636103449	ND	-0.491777243
comp160654_c0_seq2	0.43780535	0.369910244	1.254358261	1.224065299	0.350445776	0.198711749	0.362638977	0.016791171
comp160660_c0_seq3	-1.461426132	-0.77153127	0.321703024	0.355926547	-0.95702567	-0.796734317	-0.718436092	-0.749318125
comp160709_c0_seq4	ND	-0.706155523	0.554396106	0.597393553	ND	-1.351147328	-0.874909094	ND

comp160713_c0_seq12	-0.253595236	-1.154764982	0.569405432	0.562236269	-1.817380637	-0.975848046	-1.101669803	-1.530491845
comp160713_c0_seq16	-0.079828666	-0.571104589	0.663671695	0.693598991	-1.686017915	-0.969424061	-1.572367073	-1.223037864
comp160713_c0_seq2	-0.037989503	0.174784104	0.945643971	0.998382635	-0.253748345	0.294441079	0.251593557	0.248740247
comp160713_c0_seq21	-0.188766874	-0.985538585	0.691272295	0.662819411	ND	-0.931560386	ND	-1.537356708
comp160713_c0_seq35	0.023001416	-0.702077071	0.81848101	0.827251048	-1.665722721	-0.727280118	-0.950011888	-1.077803934
comp160713_c0_seq40	-0.109777112	-0.965719317	0.780727491	0.793761714	-1.394251766	-0.642895806	-1.104509665	-1.107362975
comp160732_c0_seq14	ND	ND	0.245520983	0.203589714	ND	ND	ND	ND
comp160732_c0_seq8	-1.558827706	-1.346054099	0.910043188	0.898373524	-0.929488508	-1.593105896	-0.940776403	-0.700591664
comp160772_c0_seq6	-0.817218645	-0.127323784	1.120993389	1.133624555	ND	-1.027588094	ND	ND
comp160776_c1_seq34	0.131130409	0.302205382	1.029142949	1.00522206	0.014721443	0.302498722	0.000585705	-0.11592533
comp160796_c0_seq18	-0.271035409	-0.04966163	1.01178083	0.976216295	-0.319476916	-0.02201237	-0.272772864	-0.479746156
comp160796_c0_seq2	-1.673224314	-1.460450707	0.753357518	0.763126777	ND	-1.105442513	-0.930234274	-1.660086312
comp160796_c0_seq7	-0.705797126	-0.510056859	0.88246677	0.825451234	-0.67851792	-0.422654904	-0.356591135	-0.576153555
comp160796_c0_seq9	-0.368877308	-0.064333327	1.348155783	1.312561099	-0.492865776	0.151725416	-0.254276198	-0.68309824
comp160804_c0_seq3	0.599552011	0.848018403	1.614197463	1.561299012	0.631991212	0.669390782	0.945034391	0.759558955
comp160824_c1_seq9	0.917866556	0.997654784	2.439351094	2.408496398	1.667159366	1.462044858	0.880812991	1.383968155
comp160866_c0_seq1	-0.119417024	0.030412536	0.784755825	0.774970422	-0.31169477	-0.271794526	-0.476797529	-0.604589575
comp160902_c0_seq7	ND	ND	0.60846085	0.558539707	ND	ND	ND	ND
comp160916_c0_seq5	0.534389211	0.586100549	1.676779182	1.692404316	0.599711771	0.570539147	-0.999847831	-0.650518622
comp160945_c0_seq3	ND	ND	0.470377467	0.426485497	ND	-1.313171612	-0.836933377	-0.964725424
comp160945_c1_seq3	ND	-1.233131416	0.784382164	0.807176225	ND	-1.179153217	ND	ND
comp160999_c0_seq15	-0.617555954	-0.529721083	2.317172858	2.272848212	-0.988216756	-0.697591634	-0.272505922	-0.458289916
comp161031_c0_seq3	0.054146751	0.187739112	1.151270879	1.167414709	0.186161308	0.249542648	0.038290695	-0.150199191
comp161059_c0_seq12	ND	ND	1.175826648	1.233598292	0.508398601	ND	ND	0.527257657
comp161068_c1_seq2	-0.680313771	0.288969161	1.35808789	1.407841215	-0.079003297	-0.451350526	0.471340143	0.059822959
comp161130_c0_seq3	0.206598082	0.215251706	1.148233322	1.167181917	0.033873872	0.452160589	-0.877781151	-0.449270696
comp161132_c0_seq13	-0.610828531	-0.352297434	0.408389813	0.421742318	-0.496399149	-0.201409222	-0.220021009	-0.405805003
comp161132_c1_seq5	-0.838373533	-1.403751176	0.843297982	0.792903666	-0.032943076	0.112625021	-0.271474752	-0.098236802
comp161170_c0_seq13	0.038962137	0.297936167	0.899051079	0.91711774	-0.146833481	0.305713943	-0.047905896	0.034001918
comp161261_c1_seq1	ND	ND	1.216725725	1.199796725	-0.590276747	-0.174712889	ND	-0.905447947
comp161264_c2_seq1	-0.35849046	-1.224898099	0.29969996	0.267707213	-0.808332508	-1.1709199	ND	-1.123503707

comp161275_c0_seq1	-0.157929948	-0.1212476	1.525566336	1.523825925	-0.063703952	0.108821857	0.213449022	-0.159515203
comp161275_c0_seq3	-0.375803435	-0.163029828	1.30586808	1.317048967	-0.245861886	0.090520726	0.012281229	-0.123783343
comp161297_c0_seq1	0.042404795	0.004901944	1.376469459	1.316504393	0.00808793	0.153227939	0.207759443	-0.068201181
comp161305_c0_seq1	0.069296168	0.135941739	1.364838635	1.369167712	0.205719844	0.208805282	0.118455843	-0.044808521
comp161305_c0_seq5	0.197816608	0.159118999	1.447601585	1.41785573	0.210537095	0.200132221	0.243028125	-0.049116777
comp161305_c1_seq4	0.117257415	0.405629383	1.716814604	1.702587413	0.207092126	0.321625988	0.310019102	0.142459929
comp161322_c1_seq2	-0.891433703	-0.757841342	0.470525603	0.491086782	-1.040245756	-0.858765103	-0.829684901	-0.878295701
comp161332_c1_seq3	ND	ND	1.015239065	0.971173667	ND	ND	ND	ND
comp161332_c1_seq4	ND	ND	0.489512477	0.465309975	ND	ND	ND	ND
comp161344_c3_seq1	-1.148428596	-0.634624994	1.051756859	1.091797331	-1.422179385	-0.580646795	-0.132437284	-0.394927904
comp161365_c0_seq3	-1.103923888	-0.669301532	0.461359261	0.401290913	-0.854795932	-0.978501235	-1.218266345	-1.56790714
comp161365_c0_seq6	-0.910135952	-0.725391069	0.049084463	0.10886209	-0.831704223	-0.505081448	-0.769205904	-1.198027945
comp161365_c0_seq8	-0.95358161	-0.757841342	0.414574198	0.396409651	-0.625272408	-0.925711893	-1.023504927	-1.753356964
comp161371_c0_seq7	ND	-1.047766613	0.17580145	0.117479765	ND	-0.993788414	-0.818580175	ND
comp161375_c0_seq1	-1.536447871	-1.448613001	0.896259514	0.841572113	-1.111228656	-0.871756057	-1.696547818	-0.921249877
comp161375_c1_seq1	ND	ND	0.911785064	0.936800585	ND	ND	ND	-0.972149442
comp161439_c0_seq16	-0.890213774	-0.744386957	1.129704481	1.136398526	-1.282063875	-1.945681263	-1.117260511	-1.722173812
comp161439_c0_seq17	-0.628907382	-0.637982525	0.664431551	0.648796341	-1.057560131	-0.850272215	-0.145554653	-0.555071539
comp161439_c0_seq27	-0.547450645	-0.60574381	1.082619127	1.073237933	-1.240330742	-1.204978125	-0.853678628	-1.04361858
comp161439_c0_seq28	-0.714671907	-0.65680026	1.697611905	1.665784139	-1.386362705	-1.748950097	-1.272711863	-1.0025639
comp161439_c0_seq29	-0.602148756	-0.430767834	1.290344155	1.244688321	-1.014202243	-1.075759639	-0.38866804	-0.516460086
comp161439_c0_seq30	-0.517729691	-0.596226242	1.114707177	1.100144091	-1.288805121	-1.417309307	-0.978859634	-1.545984374
comp161439_c0_seq33	-0.464568298	-0.579153625	1.784249812	1.806446043	-0.889586762	-1.729295409	-1.253057175	-1.681879217
comp161439_c0_seq4	-0.848336524	-0.827448443	1.366156396	1.375058386	-1.365125362	-1.426682758	-0.552504516	-1.282356553
comp161439_c0_seq40	-0.664598974	-0.928946622	1.115199919	1.1179459	-1.494652264	-1.653119673	-0.966028074	-1.730642218
comp161447_c0_seq1	-0.736879666	-0.649044796	0.776627958	0.715773937	-1.010630455	-0.373217847	ND	-0.422711668
comp161448_c0_seq5	-0.319052592	-0.106278985	0.982277047	0.962380396	-0.057690179	0.095301936	-0.655243798	-0.849982633
comp161536_c1_seq1	ND	ND	0.136972662	0.17556099	ND	ND	ND	-0.985201009
comp161576_c1_seq16	ND	-0.082157125	0.488198423	0.553579928	-1.008014215	-0.46751162	-0.593333378	ND
comp161633_c0_seq2	0.661304947	-0.191738731	2.03792785	1.993284605	-0.515535829	0.640390718	ND	-1.131737025
comp161644_c0_seq1	0.184317101	0.066676935	1.026198568	0.988749525	0.261393776	0.084442961	-0.185622688	-0.451717432

comp161798_c0_seq2	-0.519786802	-0.219863019	1.189913437	1.156236724	-0.492507595	-0.554064992	-1.333099263	ND	
comp161798_c0_seq5	-0.805818087	-0.182870015	1.239422998	1.195081732	-0.544455675	-0.907043067	ND		-1.637778125
comp161812_c1_seq1	ND	ND	0.314494876	0.353083204	ND	ND	ND	ND	ND
comp161816_c1_seq2	-0.577778749	-0.210103182	0.830074383	0.871597144	-0.550499542	-0.156124983	-0.4368487		-0.807678795
comp161823_c4_seq6	-1.353369373	-0.964504507	1.367403031	1.316074967	-0.928150157	-0.989707554	-0.911409328		-0.863110116
comp161860_c0_seq5	-0.173970248	0.49285931	1.745277845	1.719375344	0.898766833	1.127313208	0.597983488		0.385369928
comp161913_c0_seq1	-0.053536215	0.238418638	1.147894232	1.087911763	0.247900841	0.157698263	0.332906501		0.093140696
comp161913_c0_seq2	0.127103171	0.335760212	1.083583549	1.06527802	0.384349018	0.322791621	0.395015699		0.194116555
comp161924_c1_seq7	-0.359607924	-0.141301829	0.730083716	0.700348725	-0.476235293	-0.192559032	-0.137644625		-0.205140769
comp161932_c0_seq2	-0.062302628	-0.191303985	1.15660911	1.155340779	0.147501947	0.016863632	0.127613881		-0.082847739
comp161933_c0_seq1	ND	ND	0.756294629	0.740692299	ND	ND	ND	ND	ND
comp161933_c0_seq15	ND	ND	1.095512951	1.031550999	ND	ND	-1.435987859	ND	ND
comp161933_c0_seq16	-1.317212047	ND	0.810800388	0.865288126	-0.988902845	ND	ND		-0.906134036
comp161933_c0_seq3	-1.725248443	ND	0.798243402	0.802759998	-1.396939241	-1.759526633	ND		-0.632929194
comp161933_c0_seq5	ND	-1.775740626	0.834029042	0.771973073	ND	ND	-1.069432934	ND	ND
comp161933_c0_seq9	ND	-1.628617777	0.783722577	0.788874651	ND	ND	ND	ND	ND
comp161938_c1_seq1	ND	ND	0.228911139	0.191778753	ND	ND	ND	ND	ND
comp161940_c2_seq11	-0.419846039	-0.106045852	0.92044646	0.916134508	-0.081317671	-0.06034018	-0.370686363		-0.649746085
comp161940_c2_seq2	-0.71289915	-0.476644447	0.636143384	0.657514783	-0.5259191	-0.286446501	-0.651150347		-0.913640967
comp161940_c2_seq9	-0.818970043	-0.606196436	0.669289426	0.654406126	-0.432668894	-0.228524257	-0.648076771		-0.65093008
comp161963_c0_seq1	-1.056420237	-0.792494108	0.662468023	0.694396721	-0.552019776	-0.738515909	ND	ND	ND
comp161963_c0_seq13	-0.633755597	-0.493532657	0.824305322	0.868680822	-0.875321703	-0.459757844	ND		-1.734560947
comp162027_c0_seq7	-0.021039315	-0.152047684	0.895429119	0.933268017	-0.294790104	-0.083346229	-0.106505644		-0.471658606
comp162029_c0_seq1	-0.258125109	0.269042455	0.913800676	0.963698445	0.079138936	-0.04936525	0.155806211		0.244033371
comp162056_c0_seq2	-1.323676401	-0.56683475	1.064218639	1.023409869	-0.857064501	-0.813886547	-0.423078508		-0.736507131
comp162110_c3_seq3	ND	ND	0.587610711	0.587503403	ND	ND	ND	ND	ND
comp162111_c0_seq1	ND	-1.040281987	0.814504295	0.86036366	-1.225776388	-0.986303789	ND		-0.695849548
comp162111_c1_seq1	-1.218326599	-1.607612983	0.775655922	0.715241248	ND	-1.252604789	ND		-0.807248588
comp162134_c0_seq1	-0.51498261	-0.411353473	0.550693135	0.613159901	-0.487703404	-0.424322064	-0.152203812		-0.309959082
comp162134_c0_seq22	ND	-1.408202006	2.192145718	2.169399903	ND	-0.956283798	-1.179015569		-0.82968636
comp162166_c1_seq4	ND	ND	0.625109282	0.617940119	ND	ND	ND	ND	ND

comp162305_c0_seq4	ND	ND	0.109301236	0.044140126	ND	ND	ND	ND
comp162324_c2_seq12	ND	ND	0.85418881	0.866042884	ND	ND	ND	ND
comp162329_c1_seq3	ND	ND	1.298736261	1.246670449	ND	ND	ND	ND
comp162329_c2_seq1	ND	-1.491901311	1.117868357	1.053556308	ND	-1.437923112	ND	-0.913385665
comp162372_c1_seq1	-0.205107208	0.070718145	0.711361227	0.683750904	-0.603796733	-0.012141616	-0.013024637	-0.617937937
comp162397_c1_seq11	ND	-1.058566677	0.252151562	0.333923482	-0.398963037	-0.828497219	-0.653288981	-0.303959772
comp162408_c0_seq3	0.158837693	0.152573527	1.477491119	1.478059241	0.367812036	0.146553797	-0.224995148	-0.413485034
comp162437_c0_seq1	-0.55863749	-0.691097541	1.659215059	1.62400001	-0.379267301	-0.251768461	-0.285819845	-0.638921173
comp162444_c0_seq1	-0.387964475	0.09610394	1.827355561	1.80797555	-0.279380328	-0.29096375	-0.523240838	-0.675856468
comp162460_c0_seq1	-0.108717921	-0.124423643	1.481720714	1.480661304	-0.115652815	0.082782932	-0.071328465	-0.129794019
comp162502_c0_seq1	-0.465298819	-0.594947893	1.089351009	1.032696483	-0.701261047	-0.364878435	-0.365761455	-1.192523506
comp162502_c0_seq5	0.208782031	0.116447729	1.383308028	1.345409743	0.057935808	0.259063415	0.139872237	-0.091460401
comp162537_c0_seq4	-0.7730177	0.152228382	0.964988435	0.914520391	-0.007458755	-0.122261663	-0.632087651	0.051271813
comp162582_c0_seq13	-0.554631592	-0.267224366	0.729813628	0.739430883	-0.585344332	-0.201965157	-0.202848178	-0.666432326
comp162582_c0_seq16	-0.549391549	-0.273566196	0.830678154	0.785876455	-0.550141066	-0.44536704	-0.382132561	-0.509924607
comp162582_c0_seq23	-0.775006218	-0.45577728	0.906665297	0.861291782	-0.660576836	-0.383315676	-0.226590843	-0.602167373
comp162582_c0_seq25	-1.071940234	-0.829203403	0.096539803	0.056202277	-0.889759067	-0.650286468	-0.873018238	-0.903900271
comp162582_c0_seq28	-0.894688514	-0.769065082	0.008415959	0.023148638	-1.306742001	-0.928966703	-0.892061163	-0.84376195
comp162593_c0_seq8	ND	ND	0.995278913	0.965068447	ND	ND	ND	ND
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comp162700_c1_seq7	-1.474029311	ND	0.897371551	0.861238693	ND	ND	ND	ND
comp162736_c0_seq11	-1.65281954	ND	1.254976834	1.294135156	-1.625540333	-1.386067734	-1.210859495	-1.162560282
comp162736_c0_seq3	ND	-1.45620181	1.231425034	1.249999376	-1.164574956	-1.703253607	ND	-1.17871616
comp162777_c0_seq2	-0.97736395	-1.065620339	0.80936933	0.76863282	-0.950084743	-0.488763394	-1.01252516	-0.964225947
comp162784_c1_seq2	-1.598250798	-0.043054511	2.604255763	2.545111711	0.546299704	0.453830842	-0.855260759	0.637603675
comp162786_c0_seq7	-0.168677942	0.405823501	0.91548121	0.987493293	-0.363247485	-0.056828096	0.118380142	-0.155539939
comp162815_c0_seq4	ND	-1.060846443	0.50404621	0.456582452	ND	ND	-1.433719997	ND
comp162815_c0_seq5	-1.509562518	-0.995758915	0.463898336	0.467111209	-1.783313307	-1.367749449	ND	-1.496424515
comp162853_c0_seq2	-0.19278198	-0.085641954	1.14897394	1.130756946	-0.553682945	-0.05759949	0.037089152	-0.12412665
comp162868_c0_seq2	-0.413092519	0.177877038	0.847157891	0.815165145	-0.385813313	0.189451388	0.052348621	0.043742982
comp162907_c0_seq1	-0.381080797	-0.556487361	1.421353514	1.378536231	-0.654831586	-0.553661685	-0.45223966	-0.649667635

comp162908_c0_seq2	ND	ND	0.589448945	0.649226572	-1.120643514	ND	-1.006992672	-0.833754722
comp162909_c1_seq4	ND	ND	0.138403617	0.198181244	ND	ND	-0.679886749	ND
comp162915_c1_seq11	ND	ND	0.103972402	0.096803239	ND	-0.764587466	-0.890409223	-0.541080015
comp162920_c1_seq1	ND	ND	0.65009157	0.715473075	ND	ND	ND	ND
comp162920_c1_seq4	-1.526189294	ND	2.254217004	2.242103259	ND	ND	ND	-1.513051291
comp162923_c0_seq3	-1.741549544	-0.71586258	0.825125894	0.784532976	-1.413240342	-1.298706479	-0.370170574	-1.728411542
comp162923_c0_seq9	-0.618889023	-0.360357925	0.945396894	0.921952497	-0.846882321	-0.218243638	-0.228081501	-1.162053521
comp162932_c1_seq10	-0.870533635	-0.958790023	0.500867228	0.449494403	-0.843254428	-0.904811824	-1.030633582	-0.556365636
comp162938_c0_seq1	-0.355885206	0.144130112	0.851512897	0.809794466	-0.210506687	0.218629978	0.160708457	0.032916411
comp162967_c1_seq10	-0.761641937	-0.557301498	0.280915683	0.264456445	-0.433332735	-0.447465482	-0.756931636	-0.801749447
comp162967_c1_seq19	-0.764527835	-0.585177983	0.25469051	0.265810133	-0.496514534	-0.417256432	-1.05496155	-0.840330916
comp162967_c1_seq23	-0.876743451	-0.674435278	0.27214103	0.255970623	-0.518471025	-0.52567076	-0.802760192	-1.009733484
comp162967_c1_seq3	-0.905782197	-0.554705891	0.248414821	0.24584141	-0.588468379	-0.500727693	-0.951938791	-0.963225268
comp162967_c1_seq30	-0.922364011	-0.483194027	0.258705153	0.251535991	-0.582773799	-0.57263797	-0.981006318	-0.957530688
comp162967_c1_seq32	-0.823147459	-0.671071693	0.27494747	0.249096094	-0.458626084	-0.419812936	-0.897817211	-0.870707297
comp162967_c1_seq4	-0.932567902	-0.560093452	0.258046581	0.306205881	-0.497803369	-0.429726907	-0.791637853	-0.970582422
comp162967_c1_seq41	-1.148658345	-0.579337415	0.234056183	0.231822238	-0.455201648	-0.53413314	-0.706698301	-0.875883032
comp162977_c0_seq1	-0.699019962	-0.282126372	0.436291712	0.500185905	-0.467620773	-0.955146901	-0.411961877	-0.606700713
comp163039_c0_seq2	-0.884681286	-0.370877683	0.57514148	0.519667638	-0.255342088	-0.918959475	-0.743751237	-0.026445243
comp163057_c1_seq1	0.430057549	0.499938103	1.878408126	1.863716609	-0.094925768	0.019608095	0.265879689	0.076569605
comp163057_c2_seq4	-0.234145022	-0.32240141	1.205629824	1.216872819	-0.808925806	-0.436827642	-0.142432996	-0.034696595
comp163077_c0_seq1	0.336303411	0.502381526	1.562201455	1.518968904	0.328468998	0.62764449	0.256787924	0.060880058
comp163081_c2_seq1	-0.868290869	-0.111449218	1.10981489	1.102645727	-0.318132917	-0.338297629	-0.426330825	-0.332274122
comp163085_c0_seq1	-0.169028745	-0.191467849	0.621925748	0.624344049	-0.840719543	-0.236099448	-0.306063388	-0.433855434
comp163085_c0_seq11	1.289946214	1.362904814	2.087260149	2.107142014	0.822498621	1.163172109	1.514471607	1.199467779
comp163085_c0_seq7	0.3087419	0.48777823	1.344085795	1.370931431	0.02134723	0.333014954	0.525482198	0.256794643
comp163085_c0_seq9	1.329676087	1.457227363	2.207099016	2.202111146	0.918491189	1.251520159	1.533998481	1.259175813
comp163157_c0_seq4	1.296966982	0.847103044	2.533206863	2.475057315	ND	ND	ND	-1.247402217
comp163176_c0_seq3	-0.169732238	0.512172749	1.339015078	1.329606454	-1.64760301	-1.408130411	-0.579709658	-0.883592964
comp163180_c0_seq7	ND	ND	0.019340083	0.01217092	-0.979547915	ND	ND	ND
comp163227_c0_seq12	ND	ND	1.207665798	1.255799444	ND	-1.217196571	-1.041988332	ND

comp163228_c0_seq1	ND	ND	0.907655872	0.84809864	ND	ND	ND	ND
comp163234_c0_seq17	-0.650279798	-0.960384937	0.485031875	0.496748057	-1.020940601	-0.538429953	-0.50934975	-0.637141796
comp163234_c0_seq25	-1.162195814	-0.949422207	0.046902074	0.011704187	ND	-0.828497219	ND	-1.626179067
comp163267_c0_seq2	-0.066354557	0.149343603	1.339604484	1.329980683	0.270669878	0.434969251	0.681014961	0.52315593
comp163320_c0_seq1	0.333974084	0.582220009	1.396221436	1.358546386	0.433448416	0.590204109	0.539202777	0.303403158
comp163349_c0_seq1	0.266626305	0.55974705	1.232335765	1.202017644	-0.156063497	-0.003741074	-0.402564103	-0.319502784
comp163391_c0_seq10	-1.941162642	ND	1.212572115	1.148664572	ND	ND	ND	-1.928024639
comp163391_c0_seq15	ND	ND	1.452399903	1.404469827	ND	ND	ND	ND
comp163391_c0_seq2	ND	ND	0.329351089	0.30694196	ND	ND	ND	ND
comp163391_c0_seq24	ND	ND	0.95414802	0.928495452	ND	ND	ND	ND
comp163391_c0_seq27	ND	ND	1.275707391	1.222836779	ND	-1.874643115	ND	-1.827226923
comp163391_c0_seq28	ND	ND	1.400975727	1.385878048	ND	ND	ND	-1.764778515
comp163391_c0_seq29	ND	ND	0.939428316	0.924141263	ND	ND	ND	-2.002289291
comp163391_c0_seq31	ND	ND	1.053258846	1.021779754	ND	ND	ND	ND
comp163391_c0_seq5	ND	ND	1.099568825	1.090172506	ND	ND	ND	ND
comp163411_c0_seq22	ND	ND	0.006911093	0.057733878	ND	ND	ND	ND
comp163418_c0_seq15	-1.150086624	-0.937313017	0.353201836	0.390902943	-1.268935453	-0.799013932	-0.775073369	-0.902865415
comp163418_c0_seq16	-1.05968855	-0.937091573	0.448739549	0.387212724	-1.032409343	-0.792936744	-0.918758501	-1.046550547
comp163418_c0_seq17	-1.171723385	-0.958949778	0.432591653	0.419925018	-1.320535438	-0.808061567	-0.963846547	-1.091638593
comp163418_c0_seq18	-1.128954881	-0.967333797	0.26222463	0.260964327	-0.941974832	-0.913355598	-0.766176083	-0.990878142
comp163418_c0_seq24	-1.284251475	-0.691266626	0.433376132	0.381010221	-1.478821018	-0.813379687	-0.666200172	-1.06699349
comp163418_c0_seq33	-1.211821817	-0.914727324	0.23809266	0.266199258	-1.075398141	-0.915106788	-0.915989808	-1.002389169
comp163418_c0_seq39	-1.365743981	-0.755030365	0.359393228	0.334495299	-0.996042093	-0.667628411	-1.020693949	-0.972394736
comp163423_c1_seq10	-0.067727951	0.115082432	1.202067777	1.245000848	0.333688349	0.56700064	0.229549298	0.070348788
comp163426_c4_seq1	-0.73948024	0.126505881	0.803316761	0.857665636	ND	-0.229690385	-0.899580187	-0.550250978
comp163446_c0_seq4	-1.330378609	ND	0.129444156	0.144551388	ND	-1.364656799	ND	-0.840119352
comp163446_c0_seq6	-1.323676401	-0.934811535	0.319790761	0.248163609	ND	-0.7558946	ND	-0.708478407
comp163446_c0_seq9	ND	ND	0.656555607	0.713055525	ND	ND	ND	ND
comp163465_c1_seq2	-0.031279083	0.000439846	0.702237058	0.759239631	-0.103384508	0.117064854	-0.002322794	-0.170232063
comp163479_c1_seq2	0.070785164	0.272834906	1.05819978	1.047709037	-0.774356797	-0.497095636	-1.224977385	-0.75070944
comp163500_c0_seq2	-0.172521281	-0.087326507	0.838728134	0.864160404	-0.107453514	-0.002679488	-0.118741408	-0.331544244

comp163500_c0_seq3	-0.274672483	-0.046293803	0.838919941	0.887416558	-0.152606957	-0.002656437	-0.093313777	-0.427160306
comp163512_c1_seq2	0.408235184	0.421005375	1.314359921	1.299330011	0.279626518	0.246714303	0.461631912	0.113394331
comp163512_c1_seq5	0.323721579	0.322615366	1.196461509	1.16576581	0.252075481	0.148114236	0.312041464	0.043798515
comp163540_c1_seq4	ND	-1.366400381	0.380046427	0.400905988	ND	ND	-1.137213943	-1.265005989
comp163541_c0_seq2	ND	ND	0.679500395	0.662625924	ND	ND	ND	-1.746109342
comp163542_c0_seq3	-0.550895166	-0.338121559	0.283386512	0.276217349	ND	ND	ND	ND
comp163570_c1_seq5	-0.617899134	-0.214793829	1.727820247	1.742392084	-0.386499945	-0.271966082	-1.476969085	-1.00270114
comp163619_c0_seq13	-0.533888511	-0.430259373	0.757396133	0.723195479	-0.381670568	-0.408465858	-1.046170976	-0.571903031
comp163619_c0_seq2	-0.613951829	-0.513151982	1.150006746	1.108505089	-0.349311707	-0.14555466	-0.560171957	-0.739116525
comp163619_c0_seq5	-0.279127354	-0.132171031	1.317436834	1.281160128	-0.177214529	0.073539081	-0.151985589	-0.373199321
comp163619_c0_seq9	-0.420103704	-0.40897546	1.145805107	1.08652323	-0.220889198	-0.029966989	-0.443030458	-0.65000375
comp163696_c0_seq1	-1.421261309	-0.907457706	1.71017271	1.690156585	-0.439739592	-0.075328257	-0.678271269	-0.931002051
comp163696_c0_seq11	-0.879265374	-1.122423722	1.489042411	1.424002224	-0.025911364	-0.290294273	-0.960184075	-1.389006116
comp163696_c0_seq24	-0.735573516	-1.159622007	1.559181946	1.518064163	0.05857593	-0.112943047	-0.86348878	-1.137408862
comp163696_c0_seq28	-0.587913292	-0.748720347	1.656171501	1.604303048	0.103573813	-0.028564658	-0.861956591	-0.910567391
comp163696_c0_seq4	-0.565167884	-0.711141622	1.388589635	1.367454816	0.115323836	-0.298416078	-1.327327823	ND
comp163696_c0_seq7	-0.480196349	-0.665362751	1.749573513	1.68581514	0.257482324	0.195924927	-0.737206309	-0.944179601
comp163702_c1_seq7	-0.444884354	0.040890525	0.985383168	1.019050259	0.021727547	-0.03982985	-0.604984301	-0.033806343
comp163727_c0_seq2	-1.337633508	-0.647738646	0.185858338	0.251239842	-1.009324305	-0.330519012	ND	-0.84737425
comp163731_c2_seq11	-1.10597289	-1.79628927	1.537494272	1.545771588	-1.078693684	ND	-0.612860323	-0.74065237
comp163769_c0_seq4	1.78489796	1.196927803	2.690456923	2.704884252	0.144724214	0.763113585	0.367519525	0.239727479
comp163822_c2_seq9	-1.044382128	ND	0.516898278	0.518683958	-1.017102922	ND	ND	ND
comp163885_c0_seq2	-0.485114269	-0.573370657	2.189935459	2.149871379	-0.758865058	-0.308539093	-0.946244211	-0.333673568
comp163926_c0_seq3	ND	ND	1.469521028	1.415643775	ND	ND	ND	ND
comp163937_c0_seq3	ND	-1.332075599	1.575739211	1.522257549	ND	ND	ND	ND
comp163961_c0_seq3	-0.614800706	-0.799967108	1.243875411	1.27510264	-0.888551495	-1.3480489	-0.359927305	-0.560270018
comp163961_c0_seq6	ND	-1.342502375	1.215742784	1.256113749	ND	-1.112432917	-0.937224679	-1.54213798
comp163963_c0_seq1	-1.115712079	-0.796483141	1.00929106	1.065840887	0.018022459	0.452069723	0.428910307	0.178711861
comp163977_c0_seq10	-1.091086197	-0.906341313	1.20808228	1.173160049	-1.267926973	-0.949273127	-0.552216139	-0.389973574
comp163977_c0_seq7	-0.015475767	0.074058888	2.017427066	2.004688558	-0.091540683	0.110732229	-0.004624094	-0.118843333
comp163984_c1_seq2	ND	ND	1.938417483	1.926723257	ND	ND	ND	ND

comp163984_c3_seq2	ND	-1.552134783	1.813753209	1.789926076	ND	ND	ND	ND
comp163984_c3_seq3	ND	ND	2.053489171	2.006239468	ND	ND	ND	ND
comp163991_c0_seq5	ND	-0.885209705	1.220439964	1.206893382	ND	ND	ND	ND
comp164043_c0_seq8	-0.706497037	-0.220722158	0.986455488	0.972552943	-0.980247826	-1.342835218	-1.16762698	ND
comp164106_c0_seq1	-0.452016403	-0.716364051	0.354593849	0.38394152	-0.555070965	-0.349456633	-0.295292087	-0.490030923
comp164106_c0_seq11	-0.492273765	-0.677440167	0.340073413	0.344384068	-0.540715273	-0.43313027	-0.406861045	-0.534653091
comp164106_c0_seq18	-0.475301504	-0.660467906	0.45653311	0.444193714	-0.54493231	-0.305459711	-0.29297877	-0.305816301
comp164106_c0_seq28	-1.107642186	-0.593838583	0.535824977	0.528655814	-0.779332983	ND	-0.06362215	-0.395534179
comp164106_c0_seq3	-0.620168124	-0.540020082	0.286468814	0.335676117	-0.491431276	-0.470801917	-0.310833645	-0.524055886
comp164106_c0_seq41	-0.594991216	-0.449164398	0.400579221	0.408977836	-0.45856754	-0.446338722	-0.361307114	-0.456914477
comp164106_c0_seq50	-0.461816036	-0.535349168	0.286238908	0.314143957	-0.595904832	-0.481370969	-0.351920222	-0.53086479
comp164106_c0_seq8	-1.160887698	-0.896961568	0.250630388	0.203344002	-0.890570442	-0.718044633	-0.475889605	-1.050839682
comp164106_c0_seq9	-0.637249817	-0.541861808	0.340612708	0.329778592	-0.526996375	-0.671528006	-0.312675371	-0.541137579
comp164139_c0_seq2	-0.383962922	-0.354119999	1.963314268	1.950368092	-0.218381017	-0.159963097	0.561447316	0.124025102
comp164139_c1_seq1	-0.621996282	-0.756010161	1.73313269	1.757919597	-0.515535829	-0.334055177	0.109998374	-0.146460282
comp164179_c0_seq7	-0.846892725	-0.759057854	0.495544442	0.517338975	-1.120643514	-0.483230906	ND	ND
comp164205_c0_seq3	ND	-0.771039152	1.486547998	1.479378836	ND	ND	ND	ND
comp164205_c1_seq3	-0.271816223	-0.02012455	1.802390269	1.734991676	ND	ND	ND	ND
comp164237_c3_seq12	ND	ND	0.532683334	0.511273733	ND	-1.174025714	ND	-1.126609522
comp164244_c1_seq28	-0.237571371	0.205168876	2.03579462	1.99795179	-0.519594686	-0.240250575	-0.616797209	-0.834765886
comp164244_c1_seq42	-0.242916311	0.135090628	2.011667549	1.9812775	-0.550090855	-0.328347023	-0.630260039	-0.786080809
comp164261_c0_seq12	-1.356824899	-0.967960033	0.505485503	0.557437793	-0.551394442	-0.215011829	-0.613834859	-0.741626905
comp164261_c0_seq15	ND	ND	0.090746028	0.040111171	ND	ND	-0.794491128	-1.399404429
comp164268_c0_seq9	-1.318922544	-0.930057678	0.694655533	0.718300318	-0.337400828	-0.450110747	-0.8769625	-0.527633291
comp164342_c0_seq6	-0.119746879	0.200932125	0.972684798	1.015756731	0.064655747	0.284294101	-0.051367498	-0.493553501
comp164342_c0_seq7	-0.617899134	0.106757834	0.979810538	0.952200215	-0.192679919	0.292305348	-0.115241249	-0.458633096
comp164344_c1_seq4	-1.536240916	-0.925527301	0.752038218	0.727564197	-0.605871723	-0.456575754	-0.140038363	-0.200883619
comp164354_c0_seq14	-0.210899773	-0.186116648	0.871789684	0.863145835	0.019029722	0.216004091	-0.094103404	-0.303565496
comp164359_c2_seq5	-1.090653273	-1.002818403	0.505389239	0.545644727	-0.887282807	-0.647810208	-0.949723224	-1.378545266
comp164459_c0_seq1	-0.41062115	-0.456125558	1.148783251	1.128250127	-1.544709946	-1.208327333	-1.033119095	-1.859881145
comp164459_c0_seq2	0.544302777	0.601308864	1.647520293	1.595377401	0.568544947	0.745869639	0.721505523	0.411312744

comp164459_c0_seq6	-0.116106928	-0.044299503	1.34072413	1.29594831	-0.149525562	-0.042290938	-0.100115616	-0.359186577
comp164473_c1_seq2	ND	-0.196638429	0.606289735	0.63954923	-1.160284079	-0.045750217	-0.005240552	-0.572365292
comp164513_c0_seq2	ND	-1.486246355	1.635559192	1.621628054	ND	-1.256176897	-1.080968658	-1.083821968
comp164513_c0_seq5	-1.608186073	-1.09438247	1.317176075	1.294067711	ND	ND	ND	-1.117926816
comp164565_c0_seq17	-0.231990447	-0.234332207	1.058825955	1.01882294	0.244381291	0.392934241	0.390561358	0.200276863
comp164611_c0_seq14	-0.984796438	-0.772022831	0.150515235	0.126955657	-0.832578495	-0.894135892	ND	ND
comp164612_c0_seq3	ND	-1.936160277	0.51643512	0.566545362	-1.644533422	-1.882182078	-1.706973839	-1.834765886
comp164612_c0_seq5	ND	-2.230472671	0.556048781	0.556728527	-1.512877084	ND	-2.001286233	ND
comp164646_c0_seq1	-1.436631479	-0.334556169	0.733442301	0.754301862	-0.330171026	-0.625811629	-0.994671435	-1.423493476
comp164646_c0_seq2	ND	-0.677963414	0.494452127	0.538435486	-0.930404604	-0.92501521	-1.594905012	-0.944545808
comp164646_c0_seq4	-1.004485906	-0.528470864	0.574523267	0.64653535	-0.340384602	-0.816915346	-1.340677112	-0.565379171
comp164670_c0_seq1	0.999680867	1.088381729	1.804988885	1.851231526	0.723321695	1.073099979	0.872136954	0.785737593
comp164672_c0_seq14	-1.125273197	-0.657227085	0.390249718	0.345291995	-0.4747447	-0.516098711	-0.838215113	-1.811105199
comp164672_c0_seq19	ND	ND	1.184218687	1.1705743	ND	ND	ND	-1.658573616
comp164672_c0_seq26	-1.836027108	-0.669010992	0.382468554	0.333508088	-0.553475397	-0.527882617	-0.916945809	-1.52185911
comp164690_c0_seq2	ND	-1.293917897	0.121535692	0.172358476	ND	ND	-1.06473146	-0.89149351
comp164701_c1_seq2	-0.662174719	-1.000308581	2.046846404	1.993526092	-0.215766205	0.090653184	ND	-0.649036717
comp164701_c3_seq1	-0.773697362	-1.498775848	1.683303009	1.635342456	-0.684270249	-0.278466228	ND	-1.029404672
comp164701_c3_seq2	-0.869573867	-1.258860252	1.715986915	1.670375344	-0.49987198	-0.31278745	ND	-0.902193355
comp164701_c3_seq6	-1.351789544	ND	1.3192381	1.297781646	-0.847389083	-0.908946479	ND	-0.560500291
comp164708_c0_seq10	0.214142694	0.167850807	1.687660564	1.688442823	0.609398686	0.61285702	-0.182746352	-0.13444714
comp164708_c0_seq11	0.460071923	0.414313764	1.874445654	1.859860652	0.81014987	0.780225321	0.062979887	0.134022228
comp164708_c0_seq12	0.071988813	0.074302259	1.525807411	1.532846182	0.495947375	0.461312622	-0.163532232	-0.151662284
comp164708_c0_seq13	-0.245439714	-0.198033501	1.416594044	1.385332197	0.21853209	0.272544619	-0.435502884	-0.430669365
comp164708_c0_seq15	0.444908032	0.386614866	1.43709718	1.451544982	0.616093814	0.498132386	0.104821782	-0.000107381
comp164708_c0_seq16	0.290328678	0.285919829	1.284929412	1.256231042	0.488304112	0.437470581	0.010618828	-0.030987071
comp164708_c0_seq2	0.656276536	0.628472693	1.752944234	1.727589392	0.933785585	0.744107793	0.36556072	0.115362274
comp164722_c0_seq10	-0.171549321	-0.112752659	1.053848946	1.0144951	0.007378688	0.098431455	0.16861179	-0.076001102
comp164722_c0_seq5	0.020877292	-0.245762152	1.03175788	0.965241716	-0.054505843	0.098780609	0.184083736	-0.024630218
comp164734_c1_seq6	ND	ND	1.304466376	1.261969251	ND	ND	ND	ND
comp164741_c0_seq11	-1.242192637	-0.853327771	0.808108247	0.800939084	-0.068785395	-0.276470827	-0.323111338	-0.75193338

comp164753_c0_seq3	-0.502237162	-0.089891201	0.693072441	0.768572852	-0.139165854	-0.314666603	0.036632895	-0.966220415
comp164756_c1_seq4	0.101824985	0.213492464	1.695806784	1.693771186	0.436764766	0.337418809	0.364340128	0.215863483
comp164770_c0_seq1	-0.878136358	-0.422324702	0.545970855	0.526212565	-0.306789107	-0.611384552	-0.339266301	-0.864998355
comp164786_c2_seq11	-1.018574865	-0.277527481	0.854900535	0.867132366	-1.292325654	-1.35388305	-0.634606768	-0.762398814
comp164786_c2_seq14	-0.796323853	-0.28252025	0.901229834	0.847964021	-0.314786275	0.009697114	-0.593245898	-0.317345606
comp164786_c2_seq8	-1.052969703	-0.597158047	0.707883058	0.717527394	-0.451659229	-0.045855208	-0.611009659	-0.52794834
comp164815_c0_seq1	-0.593438622	-1.158816265	0.826512631	0.843702815	-1.04328067	-0.104838067	-0.452508573	ND
comp164882_c1_seq1	0.427044023	0.710565709	1.764615743	1.732019543	0.412261885	0.085002455	0.246422409	-0.168611348
comp164895_c0_seq1	-0.005003885	0.258295105	0.883967105	0.886631445	-0.688124144	-0.603553505	-0.796322052	-0.463383259
comp164907_c0_seq16	ND	ND	1.419090296	1.361438302	ND	ND	ND	-1.611568394
comp164907_c0_seq18	ND	ND	1.2807504	1.272523272	ND	ND	ND	ND
comp164907_c0_seq19	ND	ND	1.494952563	1.43292087	ND	ND	ND	ND
comp164907_c0_seq21	ND	ND	1.489125233	1.451466748	ND	ND	-1.600619496	-1.728411542
comp164907_c0_seq22	ND	ND	1.089225752	1.147466052	ND	ND	ND	ND
comp164907_c0_seq5	-1.76023719	ND	1.553091664	1.497881499	ND	-1.794515379	ND	ND
comp164919_c0_seq3	-0.014835237	-0.040943719	0.866316082	0.807299637	-0.022318137	0.071629195	0.103231928	-0.048693797
comp165001_c0_seq9	ND	ND	0.869723719	0.831885737	ND	ND	ND	ND
comp165048_c1_seq1	ND	-1.60502275	1.468442236	1.483208443	ND	-0.94898456	ND	-0.725477108
comp165048_c1_seq6	ND	-1.304425534	1.218964472	1.159127981	ND	-1.250447335	ND	-0.658963098
comp165048_c1_seq8	-1.636368246	ND	1.521509256	1.482507664	ND	-1.36961644	-1.194408202	-1.322200248
comp165055_c1_seq10	-0.113685479	-0.032010917	2.01978726	2.029551671	-0.138324071	0.094199668	-0.011100422	-0.16647599
comp165062_c1_seq1	ND	-1.099266154	0.829658711	0.867612569	ND	-1.52240921	ND	-0.997871763
comp165062_c1_seq10	ND	-1.67116466	1.436380115	1.486966463	ND	ND	ND	ND
comp165062_c1_seq13	ND	-1.699239859	1.03990771	1.086662998	ND	ND	ND	-1.296815472
comp165062_c1_seq14	ND	ND	1.337668942	1.323089836	-1.542032648	ND	-1.428381806	-1.255143857
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comp165062_c1_seq8	ND	ND	1.197551148	1.232731384	ND	-1.587170116	ND	ND
comp165086_c2_seq6	-0.58457828	-0.797773405	0.316650188	0.367472973	ND	-0.521946456	-0.346738218	-0.474530264
comp165090_c1_seq4	ND	ND	0.817941589	0.780487622	ND	ND	ND	-1.158425628
comp165090_c1_seq8	ND	ND	0.213306065	0.251894393	ND	ND	ND	ND
comp165090_c1_seq9	ND	ND	1.009059632	1.00474768	ND	ND	-1.211492117	ND

comp165091_c1_seq5	ND	ND	1.768266078	1.723308355	ND	ND	ND	ND
comp165104_c1_seq1	-0.483948377	0.676993592	1.543767116	1.469908676	0.584723515	0.34211144	0.810796536	0.667492324
comp165108_c0_seq5	-0.728651029	-0.28863364	0.536099883	0.501200378	-0.525280563	-0.234655441	-0.212057366	-0.363330508
comp165152_c0_seq5	ND	ND	0.446993217	0.387117704	ND	ND	ND	ND
comp165211_c2_seq15	ND	ND	0.596562122	0.651540866	ND	ND	ND	ND
comp165211_c2_seq16	-0.849919179	-0.637145572	0.609903586	0.676163341	-0.822639973	-0.70810611	-0.612079118	ND
comp165211_c2_seq22	ND	ND	1.111746521	1.073457558	ND	ND	ND	ND
comp165215_c2_seq21	-0.593136083	-0.29817572	0.383813099	0.334091585	-0.690795613	-0.326384277	-0.686289241	ND
comp165215_c2_seq3	-1.111787567	-0.523350346	0.312319646	0.286127246	-1.08450836	-0.845035761	-1.57291751	-1.223588301
comp165215_c2_seq7	-1.030676732	-0.554661691	0.258731907	0.210170059	-0.827306267	-0.843106173	-1.366867939	-1.318568726
comp165268_c0_seq6	ND	ND	0.37371712	0.366547957	ND	ND	ND	ND
comp165283_c0_seq1	ND	-1.249798637	0.807223484	0.75795297	-0.289165002	-0.019729179	-1.497733455	-0.28310282
comp165311_c1_seq15	-1.527035872	-1.314262265	0.131154547	0.178343047	-0.596666678	-0.658224075	-0.784045832	-1.513897869
comp165311_c1_seq19	ND	-1.649044796	0.211345365	0.144590512	-1.232479205	-0.595066597	-1.419858358	-1.246620409
comp165315_c1_seq14	-0.968783768	-0.102797647	0.803350003	0.807176225	-0.941504562	-0.702031962	0.01724432	0.158297587
comp165329_c0_seq8	ND	ND	0.207938068	0.175214801	ND	ND	-0.774209101	ND
comp165378_c0_seq2	-1.67683343	ND	2.261403926	2.220358018	ND	-1.109051629	-1.535903382	ND
comp165378_c0_seq5	ND	-1.502446998	2.389817524	2.35133043	ND	-0.971347545	ND	ND
comp165378_c1_seq1	ND	-1.399601834	2.317501728	2.306599352	ND	-0.743563644	ND	ND
comp165383_c0_seq8	ND	-1.232110747	0.398942642	0.362484104	-1.417605147	-1.002041289	-1.303954305	-0.390353666
comp165431_c1_seq3	ND	ND	1.511547184	1.444923052	ND	-0.547566699	ND	ND
comp165431_c1_seq4	ND	ND	1.168511401	1.231923312	ND	ND	ND	ND
comp165431_c1_seq8	ND	ND	1.333307551	1.323684741	ND	-0.390875471	ND	-0.907730709
comp165462_c0_seq5	0.129329429	0.76651794	1.522966657	1.463311903	0.368415447	0.920199052	0.027221429	-0.059177932
comp165473_c1_seq3	-1.264815189	-1.052041582	0.991800937	0.960237336	-0.839595973	-0.219912133	-0.521825149	-0.43876383
comp165498_c1_seq6	-0.730309276	-0.420625656	0.701992416	0.726137316	-0.879121329	-0.843768712	-0.464440491	-0.893262533
comp165531_c5_seq7	ND	-1.596275335	0.846236487	0.844858003	ND	ND	ND	ND
comp165552_c1_seq1	-0.870533635	-0.782698764	0.632754825	0.645789048	-0.542224432	-1.20584182	-0.331663577	-0.255335641
comp165554_c0_seq15	ND	ND	0.456576419	0.479896579	ND	ND	ND	ND
comp165554_c0_seq19	ND	ND	1.239635004	1.1929573	ND	ND	ND	ND
comp165554_c0_seq24	ND	ND	0.783526963	0.727272366	ND	ND	ND	ND

comp165554_c0_seq27	ND	ND	0.72016552	0.781852137	ND	ND	ND	ND
comp165554_c0_seq44	-1.795588324	ND	0.886540102	0.894185521	ND	ND	ND	ND
comp165587_c0_seq2	ND	ND	0.328858188	0.351652249	ND	ND	ND	ND
comp165589_c1_seq1	0.824482634	1.22227932	2.412158329	2.398752396	1.554773911	1.755583319	0.993793775	1.102806142
comp165672_c0_seq1	-1.025473941	-1.335579079	0.797069334	0.818671914	-1.396134743	ND	-0.805362646	-1.234184688
comp165672_c0_seq11	-1.123456287	-0.637681408	0.984469587	0.960267085	-0.698237071	-0.645851116	-0.186646221	-0.481929354
comp165672_c0_seq8	-0.918340655	-0.550665088	1.050087762	1.023245164	-0.590031452	-0.47549759	-0.191144882	-0.258938998
comp165672_c0_seq9	-1.125059837	-0.611256235	1.033732932	0.977236017	-0.796750635	-0.496580196	-0.139031749	-0.412951831
comp165683_c0_seq2	-0.466247405	-0.302691821	1.230979239	1.222390039	-1.187156226	-0.345623635	-1.471445393	-0.395117456
comp165708_c0_seq3	ND	ND	0.132890443	0.190662087	ND	-1.096697351	-1.097580371	-0.681304373
comp165727_c0_seq6	-0.732071122	-0.882475418	1.702497585	1.69790489	-0.55866388	-0.863259325	-0.812989823	-0.664575458
comp165731_c0_seq1	ND	ND	0.84225214	0.867267661	ND	ND	ND	ND
comp165792_c0_seq1	-1.692135361	-1.780391749	1.3188805	1.346868616	-1.664856154	-1.726413551	-1.551205312	-1.377967363
comp165792_c0_seq2	ND	-1.738217673	1.143891737	1.147188008	-1.020622086	-1.082179482	-1.20800124	-1.636823282
comp165792_c3_seq2	-1.758503477	-1.369638611	1.511056158	1.471920249	-1.430194275	-1.315660412	-0.918603424	-1.143305483
comp165807_c1_seq10	0.696678013	0.86150762	1.645552667	1.663602441	0.415503206	0.418747931	0.121113712	-0.30770833
comp165807_c1_seq5	0.865100484	1.026167268	1.749987232	1.767519903	0.480937212	0.659140154	0.446168222	0.198766272
comp165808_c1_seq4	-0.577420272	ND	3.605228777	3.575673888	-0.300263592	0.115300266	1.32693777	1.137573423
comp165826_c0_seq17	0.508463625	0.732288578	1.675426647	1.659851523	0.540197173	0.630428501	0.666943313	0.312981144
comp165830_c0_seq1	-0.800272012	ND	0.107795881	0.126955657	ND	ND	-1.136463218	ND
comp165849_c0_seq4	ND	ND	-0.011089873	0.048687754	-0.943031082	-0.703558482	ND	ND
comp165866_c2_seq1	-1.575785457	-1.119973801	1.780795521	1.730534343	ND	-1.212123638	ND	-1.562647454
comp165866_c2_seq2	ND	-1.733733766	1.687880131	1.663555275	ND	-0.565812215	ND	-1.030279384
comp165886_c0_seq5	-1.842006097	-1.231292481	1.584822424	1.615873189	ND	ND	ND	-1.828868094
comp165886_c0_seq6	-0.330156861	-0.032211644	0.996005072	0.996031485	-0.024124053	0.039257287	-1.365318071	-1.794140113
comp165906_c0_seq6	-0.15454157	0.117817727	1.128517133	1.059588347	-0.078957683	0.065031159	0.300007602	-0.010124653
comp165912_c1_seq3	-1.429279281	-1.216505674	0.944914482	0.972507426	-1.100970078	-0.861497479	-1.288349232	ND
comp165969_c0_seq3	-0.818481392	-0.906737781	0.096319883	0.115086454	-0.791202186	-0.890548143	-0.97858134	-0.80534339
comp165969_c0_seq4	-0.523781655	-0.318307286	0.359143203	0.296848734	-0.611895867	-0.530031121	-0.780791615	-0.686734911
comp165985_c1_seq2	-0.860699086	-0.31693226	0.253423289	0.319361224	-1.076457928	-0.359864074	-0.962807086	-1.215537869
comp165985_c1_seq20	-0.882199596	-0.42638794	0.313110008	0.346058068	-0.67882913	-0.439356531	-0.820450794	-1.170091589

comp165985_c1_seq25	-1.196404967	-0.615654575	0.352640982	0.386864505	-1.044187024	-0.59386106	ND	-1.66038822
comp165985_c1_seq3	-0.512253516	-0.675143523	0.241320397	0.234151234	-0.684546664	-0.679157271	-0.804979028	-1.175809123
comp166029_c0_seq1	ND	ND	1.29229635	1.308821853	ND	ND	ND	ND
comp166083_c0_seq3	-1.834987877	-0.279791589	1.048511824	1.056582628	-0.962610631	-0.437902303	-1.216936574	-1.043698624
comp166110_c0_seq5	0.411427474	0.698386279	1.45488528	1.400201533	0.354385794	0.640390718	0.224998588	0.018025296
comp166155_c0_seq3	-1.29482138	-1.161229019	0.46982437	0.466415357	-0.899565388	-0.764828139	-1.153891331	-0.758804632
comp166155_c0_seq6	-1.198512466	-0.742700811	0.541864709	0.506866452	-0.819050742	-0.720907295	-0.814544369	-1.088464451
comp166177_c3_seq3	ND	ND	0.145447849	0.08028674	ND	ND	ND	ND
comp166194_c0_seq2	0.731206905	0.735264778	1.584536008	1.616099672	0.57081298	0.708209726	0.898017473	0.556671776
comp166210_c1_seq1	-1.272861457	ND	0.482238975	0.508493568	-1.546612246	-1.608169642	-1.131931408	-1.259723454
comp166210_c1_seq2	ND	-1.635130281	0.629830467	0.68772395	-1.519594686	-1.280122087	-1.104913848	-1.53373589
comp166247_c1_seq1	-1.777679134	-1.263875531	1.420005578	1.454267099	ND	-1.811957323	ND	-1.764541131
comp166269_c1_seq1	-1.708868331	-1.01897347	0.028503334	0.021334171	-0.640196439	-0.788904012	-0.965878291	ND
comp166269_c1_seq20	-1.299980834	-1.002886341	0.630382841	0.567897227	-0.795580372	-0.588292456	-1.049906315	-1.830910875
comp166269_c1_seq25	-1.515682521	-0.950726396	0.19686556	0.170100842	-0.675489958	-0.771809461	-0.976812464	-1.32645326
comp166269_c1_seq64	ND	-0.99933939	0.269986164	0.269995586	-0.96298504	-0.644331195	-0.946244211	ND
comp166298_c0_seq3	0.854471562	0.997179884	1.879697716	1.879382697	0.781676232	0.969132385	0.444981292	0.258918994
comp166298_c0_seq8	-0.693362488	-0.643316179	0.103130629	0.157231123	-1.092052014	-0.630730665	ND	-1.106193218
comp166301_c1_seq15	-0.932660236	-1.020916625	1.368434162	1.321625713	-0.192170586	0.010785179	-0.393790179	-0.583730132
comp166301_c1_seq17	-0.482148563	-0.605167058	1.469772613	1.447626295	-0.012510208	0.140481907	-0.09343403	-0.737855873
comp166301_c1_seq19	-0.926411287	-0.567509644	1.411812318	1.407055908	-0.12098083	0.209572239	-0.254002321	-0.767145249
comp166301_c1_seq2	-1.00766688	-0.949795233	1.215583879	1.223137974	-0.264384329	-0.016639204	-0.611464326	-1.09143889
comp166301_c1_seq7	ND	ND	0.611946549	0.573963439	-1.104136273	ND	ND	ND
comp166313_c4_seq1	-0.948434719	-1.036691108	0.639174626	0.680310143	-0.921155512	0.017287091	-0.330383416	-0.537356708
comp166341_c0_seq3	ND	-1.464658438	0.417450972	0.38856256	ND	-0.565582199	-0.45732075	-0.585112796
comp166344_c0_seq1	-0.614109154	-0.827304279	0.442021274	0.389094621	ND	-0.347357348	-1.075239097	-0.725909888
comp166351_c1_seq1	0.138266661	0.200165798	1.507836343	1.450812542	0.26621603	0.505688629	0.598710111	0.369460425
comp166356_c0_seq2	-1.020615406	-0.63175054	1.177487097	1.121767544	0.0066638	0.059049756	ND	-1.007477404
comp166361_c1_seq2	-1.258975193	-1.046201586	0.177366477	0.170197314	-1.231695986	-1.293253383	-1.118045144	-0.944807195
comp166386_c0_seq14	0.752742536	0.532729461	1.342178486	1.38721724	0.213035963	0.564141832	0.545530045	0.435466766
comp166388_c0_seq3	ND	ND	0.690631742	0.742899767	ND	ND	-1.224568637	ND

comp166401_c0_seq8	ND		-0.763088458	0.566934935	0.513308371	-0.311760761	-0.256812589	-0.466955232	-0.439845318
comp166419_c0_seq4		-0.355100572	-0.142326965	0.767976645	0.790770706	-0.452760102	-0.088348767	0.058830748	-0.245052557
comp166425_c0_seq2		-0.14584908	0.152354722	0.940663977	0.873148962	0.011063985	0.27768883	0.213136729	0.107621078
comp166439_c1_seq3		0.015579411	0.019093396	0.970521028	1.004353471	0.002741395	-0.103019664	-0.333576772	-0.724610253
comp166457_c0_seq4		0.181868813	-0.007414154	0.86911103	0.90795475	-0.284678928	-0.535292561	-0.146204502	-0.131329045
comp166464_c1_seq4		-0.731191093	-0.819447481	0.419914848	0.396951419	ND	-0.640530546	ND	-0.496204341
comp166472_c0_seq18		-1.632073172	-0.817239574	0.478414918	0.433921432	-0.759695926	-0.967381358	-1.491143124	-1.016875178
comp166472_c0_seq2		-0.738506848	-0.451099623	0.94601251	0.900590051	-1.614317629	-0.721632516	-1.801696782	-1.327428837
comp166472_c0_seq29		-1.122061737	-0.654015625	0.79620007	0.762801383	ND	-0.813917246	ND	-1.330772484
comp166472_c0_seq3		-1.32468835	-0.713974734	0.507173854	0.548181656	-1.297409143	-0.580815289	-1.484788297	-1.436489084
comp166504_c0_seq3	ND	ND		1.169308474	1.205173943	ND	ND	ND	ND
comp166504_c1_seq8		-0.633399263	ND	0.89791792	0.965382375	ND	ND	ND	ND
comp166504_c1_seq9	ND	ND		0.765919998	0.833384454	ND	ND	ND	ND
comp166516_c0_seq15		-0.606332433	-0.258860252	1.380916706	1.336407402	-0.319415915	0.016966697	-0.807825065	-0.355833514
comp166547_c0_seq1		-0.992586683	ND	1.086109573	1.105592605	-0.488186222	-0.213951516	0.102585875	-0.581508672
comp166547_c0_seq10	ND	ND		0.977015768	1.024405376	-0.979547915	-0.300742622	-0.321829029	-1.294719115
comp166547_c1_seq1	ND		-1.394006981	0.924536595	0.947330656	ND	-0.737968791	-0.386669293	-0.991582594
comp166555_c0_seq5	ND		-0.780969653	0.369169492	0.350418457	-1.364404062	-0.823901467	ND	ND
comp166555_c1_seq4		-0.51763149	-0.36284983	0.441588925	0.443374605	-1.092412275	-0.55190968	-0.802670174	-0.93046222
comp166570_c2_seq8	ND	ND		1.325028465	1.289943221	ND	ND	ND	ND
comp166573_c0_seq1		-1.188947125	-0.976173518	0.446966899	0.408198751	-1.462697914	-0.825285306	-0.394804563	-0.698687868
comp166609_c0_seq1	ND	ND		0.423393704	0.386261318	ND	ND	ND	ND
comp166627_c3_seq20		0.474892926	0.775621703	1.406675093	1.370216554	0.536251922	0.72354651	0.817721497	0.441287525
comp166629_c0_seq4		-0.557984688	-0.491339117	0.334288937	0.314885318	-0.773743531	-0.835300927	-0.563182676	-0.486854739
comp166633_c2_seq1		-1.021067561	-0.331172699	0.591365368	0.629953695	-0.356966257	-0.833497001	-0.45416878	-0.162831519
comp166651_c1_seq17	ND		-0.957830256	0.156593337	0.149424175	ND	ND	ND	ND
comp166657_c0_seq2	ND	ND		0.695197819	0.636876133	ND	ND	ND	ND
comp166709_c3_seq7	ND	ND		0.08582014	0.027498455	ND	ND	ND	ND
comp166713_c0_seq6	ND	ND		0.665603736	0.721486319	ND	ND	ND	ND
comp166713_c0_seq8	ND	ND		0.948994984	0.950734738	ND	ND	ND	ND
comp166729_c1_seq1	ND	ND		0.73831894	0.760308006	ND	ND	ND	ND

comp166775_c1_seq3	-0.114255935	-0.248269814	0.536635246	0.536765322	-0.346614039	-0.546474133	-0.973325886	-1.101117932
comp166781_c0_seq10	-0.880953413	-0.492088547	1.462480986	1.420051387	-1.029765465	-0.790292866	-1.217144619	ND
comp166781_c0_seq20	0.206000811	-0.113959082	0.997402493	0.943792449	-0.5533044	-0.590038213	-0.126034435	-0.567445604
comp166781_c0_seq22	-1.240355431	-1.231701807	0.924114472	0.884152796	-1.51410622	-1.876693612	-1.400455378	-1.051126169
comp166806_c1_seq1	-0.218517855	0.114646861	1.343264917	1.289500665	-1.048571145	-1.50806855	-1.633890307	-0.858592366
comp166839_c2_seq1	0.615627892	0.737646504	1.613866545	1.567679145	0.500072591	0.695639705	0.860326163	0.591113926
comp166894_c0_seq10	-0.523213206	-0.746168169	0.163005937	0.182165713	-0.768935272	-0.779340146	-0.516981731	-0.731923953
comp166902_c1_seq5	-1.498414717	-0.44054307	0.464409822	0.523674402	-0.429742825	-0.418749554	-0.211356632	-1.00815546
comp166944_c0_seq9	0.319101381	0.618512116	1.858204332	1.865626502	-0.540110138	-0.139269536	-0.046248054	0.201623514
comp166954_c0_seq10	-0.513288509	-0.487601545	0.871900638	0.812899837	ND	-0.547566699	-1.37235846	-1.023029252
comp166954_c0_seq4	-0.503727025	-0.591983414	0.552403403	0.590991731	-0.652539077	-1.316156465	-0.839918231	-0.791619018
comp166955_c1_seq1	-0.363859837	-0.08413944	0.959181404	0.958231361	0.018807028	-0.21250145	0.145046997	-0.146601852
comp166961_c1_seq12	-0.946024198	-0.357586977	0.84517258	0.827212937	-1.043683728	-0.804211128	-1.106124145	ND
comp166961_c1_seq13	-0.060398314	0.126361861	0.942047255	0.891652938	-0.110285062	-0.184076915	-0.853966717	-0.835630727
comp166972_c0_seq19	-1.244468137	-0.990301845	0.819694386	0.792754725	-1.217188931	-1.132618292	-0.761115408	-1.453178885
comp166972_c0_seq4	-1.666375302	-1.101419177	0.696537451	0.695045421	-0.898733406	-1.302713483	-0.712531897	-1.176116045
comp166980_c0_seq7	ND	ND	0.730454169	0.763402229	ND	ND	ND	ND
comp167025_c0_seq14	-0.790302181	-0.786788196	0.450352674	0.401122166	-0.714718295	-0.975848046	-0.925578544	-1.0076131
comp167025_c0_seq17	-0.972590054	-1.060846443	0.330694988	0.331643716	-1.070249584	-1.608928236	-0.831660006	-1.260482048
comp167025_c0_seq18	-0.895073064	-0.615352667	0.179942708	0.123924978	-0.566763862	-1.105442513	-0.49090158	-0.881935061
comp167025_c0_seq21	-1.265973823	-0.986253426	0.406457035	0.417576658	-0.937664621	-1.476343272	-1.000105038	-1.252835821
comp167025_c0_seq27	-1.406724045	-1.097040425	0.506738879	0.507538646	-0.902323584	-1.043062226	-1.390732733	-1.150547994
comp167025_c0_seq28	-0.729381438	-0.796448527	0.299876844	0.307841424	-0.799012244	-0.985508377	-0.986391398	-1.41521344
comp167025_c0_seq31	-1.06446869	-0.70902758	0.494796425	0.442990532	-1.037189484	-1.011596704	-0.974691164	-1.306603193
comp167025_c0_seq38	-0.925918198	-0.680959908	0.431242226	0.3770765	-1.012582344	-1.032747055	-0.784988149	-1.123633561
comp167025_c0_seq4	-1.146655446	-0.882729317	0.419125461	0.411956298	-1.244314976	-0.937895587	-1.607785389	ND
comp167025_c0_seq5	-1.744891276	-1.833147665	0.533087901	0.575136761	-1.416582074	-1.177109475	-1.603961227	-1.430723278
comp167033_c0_seq28	-1.292892251	ND	0.53162959	0.579977756	-1.265613044	ND	ND	ND
comp167037_c3_seq4	0.206734417	0.282334831	1.171945195	1.114366529	0.057922364	0.499815161	0.32918106	0.015752437
comp167055_c2_seq1	ND	ND	0.445982662	0.407405035	ND	ND	ND	-1.05438696
comp167080_c4_seq12	ND	ND	0.649156885	0.692292841	ND	ND	ND	-1.274649132

comp167116_c1_seq1	ND		0.280736059	2.044197138	2.066692349	-1.768081202	-1.227578607	ND		-0.879132419
comp167151_c0_seq3		-0.00549083	0.39021346	1.008695077	0.956779587	-0.124339659	-0.03976902		0.155642604	0.241730378
comp167216_c0_seq5		-0.71861492	-0.748879362	1.513606767	1.453108163	-1.360342494	-0.75289311		-0.609869555	-0.675513694
comp167224_c0_seq19		-0.698986479	-0.695472494	1.091739859	1.036856291	-0.370677276	-0.2233509		-0.466286057	-0.573874717
comp167224_c0_seq38		-0.738181899	-0.583400239	1.003690267	0.956692641	-0.346820951	-0.244186312		-0.421160592	-0.783035844
comp167260_c1_seq6	ND		-1.324156775	1.425175721	1.43722834	ND	-1.747299831	ND		-1.398853643
comp167260_c1_seq7	ND		-1.764190348	1.506436138	1.536188681		-1.648654753	ND		-0.884644706
comp167265_c0_seq16	ND	ND		0.511206755	0.486419487	ND	ND		-2.043480114	-1.694150905
comp167265_c0_seq18		-1.896038431	-1.808203561	0.48506	0.483336607	ND	-2.231346617	ND		-2.183930424
comp167272_c3_seq3	ND	ND		0.497228572	0.54393479	ND	-0.965273397	ND		ND
comp167280_c0_seq13		-0.450972694	-0.212893222	0.721322546	0.749868936	-0.208849639	-0.127316037		-0.561854618	-0.344413006
comp167280_c0_seq15		-0.573131532	-0.707145411	0.511027619	0.452026818	-0.846882321	-1.130288467		-0.830141492	-1.258963534
comp167280_c0_seq5		-0.284952162	-0.48235302	0.345566831	0.376662168	-0.68903672	-0.546474133		-0.621143368	-1.101117932
comp167280_c0_seq9		-0.843028688	-0.727165094	0.338040476	0.275353986	-0.736568236	-1.275246887		-1.401068644	-1.051739435
comp167290_c1_seq1		1.432852099	1.501788368	2.248926948	2.258836318	1.419513454	1.397976941		1.357073037	1.133474961
comp167315_c0_seq1	ND	ND		0.999098847	0.958809525	ND	-1.672614541	ND		-1.625198349
comp167325_c0_seq3	ND		-1.651386011	2.058848624	1.996019061	ND	-1.296377817		-1.121169578	-1.54999162
comp167325_c0_seq8	ND	ND		1.220590373	1.188773776	ND	ND	ND		ND
comp167347_c0_seq2		-0.199984375	-0.15354219	1.109953819	1.114366529	0.024784235	-0.028500635		0.00221533	-0.228239058
comp167347_c0_seq5		-0.034237339	0.17425747	1.232353249	1.232121846	0.204549784	0.158412746		0.403443907	-0.047428275
comp167422_c0_seq1		0.081143096	0.094344349	0.891943679	0.898841964	-0.142302574	-0.386790654		0.010266334	-0.319171076
comp167422_c0_seq3		-0.135662742	-0.153338056	1.275103319	1.255721204	-0.409413531	-0.470970927		-0.079053579	-0.273792415
comp167426_c0_seq13	ND	ND		0.162396913	0.213219698	ND	ND	ND		ND
comp167433_c1_seq2		-0.466626261	-0.05220729	0.978401588	0.903927159	-0.201986138	0.156672869		0.151425042	-0.264432022
comp167435_c1_seq11		-0.701573808	-0.391890188	0.35455662	0.317424234	-0.674294601	ND	ND		ND
comp167435_c1_seq19		-0.340360082	-0.147789861	0.515319741	0.464245093	-1.053443565	-1.115000961		-0.939792723	ND
comp167461_c1_seq2		-0.704193082	-0.382275006	1.234922415	1.173612142	-0.37588388	-0.407478053		-0.563263033	-0.58191061
comp167465_c0_seq1	ND	ND		0.47333658	0.50451241	ND	ND	ND		-1.507507938
comp167465_c1_seq1	ND	ND		0.516933482	0.532932184	ND	-1.260706737	ND		-1.213290545
comp167541_c0_seq10		-0.081313247	-0.391418385	1.658464488	1.691741756	-1.230125299	-0.513531445		-1.116474457	-1.244266503
comp167541_c0_seq6	ND	ND		1.252851848	1.281806218	ND	ND	ND		ND

comp167549_c0_seq13	-1.151060862	-0.625358036	0.25474274	0.198930399	-1.078024165	-1.025638209	-0.584162081	-1.092165369
comp167549_c0_seq17	-1.141120788	-0.581559695	0.278830465	0.202388345	-1.068084091	-0.549857891	-0.612010568	-1.003044049
comp167549_c0_seq20	-1.020162781	-0.807389174	0.373981209	0.320068643	-0.729642139	-0.628472238	-0.426935061	-0.882086042
comp167549_c0_seq27	-1.218584774	-1.10272118	0.886763676	0.88371108	-1.191305568	-0.910440283	-1.299503475	-1.603386781
comp167549_c0_seq3	-1.098916113	-0.819195716	0.353219824	0.332928984	-0.849788157	-0.656073048	-0.766100538	-0.863929361
comp167549_c0_seq34	-1.000541255	-0.829160334	0.372131334	0.313809649	-1.236503484	-0.696000889	-0.578784597	-1.028795938
comp167549_c0_seq39	-0.888009229	-0.697512017	0.173873528	0.130988813	-0.714601987	-0.968044909	-0.446049185	-0.971781239
comp167568_c0_seq2	ND	ND	1.172014367	1.152070916	ND	-0.882182078	ND	ND
comp167584_c1_seq1	ND	-0.968272812	0.672120603	0.67409482	-0.551707221	-0.738203354	-0.438056379	-0.213665907
comp167604_c0_seq2	-0.09910011	0.123581786	1.16281746	1.122224542	-0.340666215	0.365462205	-1.771083418	-1.597845468
comp167604_c0_seq28	-1.291439759	-0.953727416	0.882330166	0.815272111	-1.042311803	-0.802839204	ND	-1.755423012
comp167604_c0_seq29	-0.155045291	0.096646382	1.14875159	1.090046083	-0.310696768	0.250009213	ND	-1.102989222
comp167604_c0_seq3	ND	ND	0.965268025	0.941839951	ND	ND	ND	ND
comp167604_c0_seq34	-0.93438788	-1.448613001	0.776560589	0.725588219	-0.96510062	-0.96866607	ND	ND
comp167604_c0_seq43	-1.520645941	-0.955689816	0.852153617	0.800930385	-0.753004045	-0.70982609	ND	ND
comp167607_c0_seq4	-0.330339486	-0.535101443	0.549699683	0.557594267	-1.5335092	-0.640824087	-0.305915006	-0.401522369
comp167644_c1_seq1	ND	ND	1.511052155	1.496821138	ND	ND	ND	-0.750300692
comp167644_c1_seq2	ND	-0.823829905	1.727664427	1.73168904	ND	ND	ND	0.180654473
comp167644_c1_seq3	ND	ND	1.439323372	1.432154209	ND	ND	ND	-0.553755603
comp167644_c1_seq7	ND	-1.645114502	1.68866904	1.647236674	ND	-1.591136303	ND	-1.543720111
comp167649_c1_seq5	0.491446566	0.68474182	2.023850845	1.964850044	0.950371638	1.218489419	0.395015699	0.447679717
comp167655_c1_seq3	-1.203440048	-0.893756428	0.038326957	-0.029540046	ND	-0.936688242	ND	-0.792362037
comp167684_c0_seq20	-0.890213774	-0.715228728	0.820200178	0.781996781	-0.862934568	-0.799553227	-1.527434976	-0.956257018
comp167684_c0_seq21	-0.770737933	-0.528001103	0.800761638	0.762184011	-1.111435512	-0.394841658	-0.77593592	-1.602697971
comp167691_c0_seq5	-0.819201317	-0.555275188	0.32800958	0.28411761	-0.548884062	-0.455539498	-0.50218001	-0.32894206
comp167709_c0_seq2	-1.284842754	-0.674129139	0.218445705	0.231479928	-0.780442293	-0.841999689	-0.84288271	-0.970674756
comp167721_c0_seq1	-1.161869154	-0.773004288	0.550678927	0.580232572	ND	ND	-1.020939106	ND
comp167727_c0_seq3	-1.084839338	-0.872065731	0.867081838	0.84493552	ND	-1.119117528	ND	ND
comp167727_c0_seq9	0.273780941	0.343977063	1.545229252	1.503845988	0.160727084	0.340284658	-0.249995811	-0.348824161
comp167738_c0_seq5	-0.142216282	0.103981081	1.651848539	1.6545192	-0.609787097	-0.51373664	-1.223134983	-1.350927029
comp167775_c1_seq2	ND	ND	1.149458374	1.188046702	ND	ND	ND	ND

comp167784_c1_seq12	-1.132203435	-0.646428556	0.764869073	0.71609838	-0.292010872	-0.68936037	-0.894363373	-0.108341567
comp167788_c0_seq4	-0.981096094	-1.245443742	0.474900264	0.497438028	-0.886870098	-0.471306239	-0.53913605	-0.423890047
comp167802_c0_seq4	-1.122652286	-1.210908674	2.418110102	2.401592664	-1.69743307	-0.190788743	-1.583782228	-1.711574274
comp167814_c0_seq1	0.119703234	0.196963455	1.036634586	1.079886195	0.260581251	0.017731402	0.182346567	0.158906727
comp167820_c0_seq2	-1.280388413	-1.067614806	0.581921989	0.526980045	-1.253109206	ND	-0.537398373	ND
comp167820_c2_seq1	-0.935421177	-0.479609521	0.342558001	0.335388838	-0.607111974	-0.668669371	ND	-1.22331317
comp167893_c1_seq11	ND	ND	0.520072669	0.508707392	-1.173629373	ND	ND	-1.664891832
comp167898_c1_seq11	ND	ND	0.504036104	0.535619531	ND	-0.984312522	ND	-1.538956321
comp167898_c1_seq9	ND	-1.398558275	0.590926582	0.595991876	ND	-1.645610071	ND	-1.598193879
comp167920_c1_seq10	0.036021486	0.120222072	1.097189355	1.079153208	-0.517569999	-0.438948692	-0.646957206	-0.950840511
comp167920_c1_seq9	-0.204047029	0.046515139	1.00008744	0.998498155	-0.196971208	-0.501566653	-1.104509665	-1.533331707
comp167920_c2_seq2	0.612961636	0.687070482	1.710309241	1.662694295	0.163119588	0.046044864	-0.276071538	-0.851021616
comp167920_c2_seq9	0.067080547	-0.091213708	1.267133346	1.20032646	-0.463794752	-0.736205514	-0.862027271	-1.290849313
comp167926_c1_seq16	-0.691556687	-0.353844344	0.283457995	0.276288832	-0.577127305	-0.424804881	-0.659771108	-0.518717842
comp167926_c1_seq23	-0.375014525	-0.310660751	0.372399078	0.395193139	-0.848337669	-0.290106307	-0.336746819	-0.561448878
comp167926_c1_seq25	-0.74077471	-0.421545772	0.285392495	0.249734794	-0.822639973	-0.314322061	-0.599844661	-0.903727966
comp167985_c1_seq8	-0.076797676	-0.112347714	1.156977839	1.118958232	-0.611461238	-0.64819505	0.071081232	-0.424687599
comp167989_c0_seq3	-0.279392324	-0.543739972	1.368050102	1.302747643	-0.428204377	-0.887701782	-0.035799934	-0.840285589
comp168003_c2_seq1	-0.104297154	-0.016462283	1.522376214	1.489558597	-0.474957956	-1.138575344	ND	ND
comp168021_c0_seq4	ND	ND	0.326483691	0.354076635	ND	ND	ND	ND
comp168045_c0_seq4	-1.106530035	ND	0.472479138	0.498733731	-0.602129574	-0.66368697	-0.363539995	-0.616270778
comp168056_c1_seq4	-0.769875382	-0.472780889	1.098212859	1.05654723	-0.774780859	-0.671528006	-0.59898211	-0.58064612
comp168095_c0_seq7	-0.802146398	-0.346334742	1.146078633	1.14627057	-0.146478261	-0.438484579	-0.564306336	-0.010857145
comp168095_c0_seq9	-0.215129748	-0.002356141	1.283166765	1.232003088	-0.154426786	-0.392075442	-0.241690787	-0.094781776
comp168111_c0_seq2	-0.596134349	-0.075990569	1.019127869	1.069127346	0.140215188	0.042228526	-0.117451498	0.067368324
comp168121_c0_seq5	ND	-1.712624944	1.438085265	1.427478398	ND	-0.880495495	ND	-1.611230553
comp168121_c0_seq7	-1.344125325	ND	1.52491846	1.491114017	-1.015816122	-0.776343523	ND	-1.632017318
comp168207_c2_seq8	0.449050746	0.114811928	1.126376176	1.155119569	-0.031173931	0.022662091	-0.000497324	-0.17659405
comp168213_c0_seq1	-1.575785457	-1.186920591	1.505650836	1.516144882	ND	-1.309033651	-1.133825413	ND
comp168213_c0_seq12	ND	-1.538220268	1.280108547	1.296807725	ND	ND	ND	ND
comp168230_c0_seq3	-1.937891105	-0.594783729	1.386817295	1.359206972	-1.308551907	-1.49504804	-1.796961056	-1.924753102

comp168247_c1_seq7	0.156093187	0.117524582	0.919018956	0.93533089	0.096222218	-0.095668947	-0.075362669	-0.235339398
comp168247_c2_seq1	ND	-0.315529046	0.703919034	0.751107534	0.127365484	-0.562580843	-0.211281345	-0.075831957
comp168270_c4_seq1	-0.092382384	-0.098452017	1.17385839	1.19266807	-0.366133173	-0.126660574	-0.101214656	-0.614357583
comp168270_c4_seq10	-0.465230635	-0.521302341	1.05826121	1.03877081	-0.706796741	-0.383003256	-0.961122684	-0.867065981
comp168270_c4_seq15	-0.077142418	-0.451705545	1.199035951	1.174689061	-0.470868524	-0.573818605	-0.620459116	-0.572159904
comp168270_c4_seq5	-0.854253824	-1.118601472	1.01553171	1.060008867	-1.605125868	-1.18956201	-1.491475026	-1.318237077
comp168272_c0_seq3	0.51076137	0.729333387	1.365317184	1.318238415	0.518947635	0.688412864	0.454060482	0.193905681
comp168321_c0_seq6	ND	ND	0.616684095	0.631234182	-0.526110478	-1.189727866	-1.315549623	-1.142311674
comp168363_c1_seq3	ND	ND	0.311015148	0.354998508	ND	-1.108452189	ND	-0.760006001
comp168368_c0_seq6	-0.481393696	-0.355770265	0.622070611	0.610155013	-0.216753574	0.011137153	-0.235728297	-0.430467133
comp168374_c0_seq15	-0.356824899	-0.445081287	0.451610122	0.468353117	-0.824395714	-0.466823802	-0.710744872	-1.741626905
comp168387_c2_seq11	0.295957601	0.544536039	1.766364834	1.786548552	0.108121441	0.154469442	0.210491272	0.02142957
comp168388_c0_seq13	-0.894468618	-0.614748221	1.087088506	1.068894576	-0.35530605	-0.283652184	-0.054568565	-0.369447254
comp168388_c0_seq18	-0.5358881	-0.499205752	1.004102465	0.986244629	-0.36018906	-0.388746197	-0.224261824	-0.592386025
comp168388_c0_seq35	-0.579767393	-0.571113768	1.076003552	1.071253864	-0.42754945	-0.371007534	0.056012677	-0.323591342
comp168388_c0_seq8	-0.842597221	-0.532913601	1.039848018	1.042172008	-0.417378006	-0.478935402	-0.111841638	-0.377161548
comp168433_c1_seq1	-0.526189294	-0.262263164	0.801007907	0.844991266	ND	-0.208284965	-0.142221196	-0.513051291
comp168447_c0_seq1	-0.944140054	-0.448819857	1.129023713	1.062268861	-1.217890843	-1.05759949	-0.405269997	-1.10709331
comp168447_c0_seq4	-0.922856333	-0.533991467	1.215660481	1.173596136	-1.196607122	-0.890187733	-0.162137526	-0.733627071
comp168465_c0_seq5	ND	ND	0.503851912	0.553978153	ND	ND	ND	ND
comp168465_c0_seq6	ND	ND	0.51573176	0.495198635	ND	ND	-0.644981288	-0.772773334
comp168470_c0_seq4	0.43149381	0.43844097	1.459178997	1.409372795	0.328119796	0.530065221	0.28398299	0.048815497
comp168470_c1_seq2	0.318704471	0.293916703	1.508287346	1.444636828	0.250174539	0.55462612	0.268972015	-0.028125301
comp168479_c0_seq2	ND	-0.661170556	1.235813406	1.175843543	-0.691762997	-0.276199138	0.241431781	-0.325692959
comp168515_c0_seq3	ND	-0.857544256	1.696888327	1.661810561	-0.96385741	-0.657438021	-0.482229783	-1.455119869
comp168537_c3_seq1	-1.528443179	-0.646662791	0.695332725	0.658294048	-0.774165244	-0.717623328	-1.262574393	-1.992426431
comp168537_c3_seq16	-1.217177291	-0.879464947	0.661411812	0.622616257	-0.821921299	-0.853515472	-1.076247242	-1.681160543
comp168537_c3_seq25	-0.814941596	-0.469542423	0.41865662	0.453379619	-0.354006828	-0.351895145	-0.674011547	-0.947931629
comp168537_c3_seq9	-1.035730558	-0.726046938	0.362822551	0.333146047	-0.640474566	-0.505737317	-0.526823724	-0.846501296
comp168554_c3_seq1	0.553382921	0.557799493	1.330140895	1.277926784	0.111892948	0.119051364	0.023898426	-0.124097006
comp168565_c4_seq3	-0.508732046	-0.06747911	1.14045713	1.131008201	-0.391276209	-0.295225752	-1.180715354	-1.3085074

comp168569_c0_seq11	-0.973347325	-1.404026394	0.351020585	0.34100358	ND	ND	ND	ND
comp168569_c0_seq30	-1.157081164	-1.136193083	0.315610528	0.324009142	ND	ND	ND	ND
comp168569_c0_seq41	ND	-0.94217831	0.441090595	0.38692487	ND	ND	ND	ND
comp168569_c0_seq43	-1.157364277	-1.391748701	0.366127569	0.329800177	ND	ND	ND	ND
comp168569_c0_seq48	-0.779945935	-0.509180381	0.577214489	0.553177401	ND	-1.358292169	ND	-1.310875977
comp168569_c0_seq71	-0.81066588	-0.864160163	0.148554535	0.116561788	-1.084416669	-0.924125316	ND	-1.177739119
comp168569_c0_seq73	-0.969929161	-0.815147501	0.114229991	0.170112574	-1.845739941	-0.953054828	ND	-1.55885115
comp168569_c0_seq76	-1.385576584	-1.075892964	0.333311676	0.344625919	ND	ND	ND	ND
comp168574_c4_seq1	ND	0.004167718	1.429840472	1.479398934	-0.005235423	-0.418975338	-0.06767584	-0.973619137
comp168604_c2_seq2	-0.517871498	-0.41424236	0.939404079	0.939832098	-0.365653555	-0.904332206	-0.486085919	-0.458976005
comp168604_c2_seq3	0.282982867	0.160646689	2.230997738	2.213475923	0.142288705	-0.013173195	-0.069914033	0.140046724
comp168617_c0_seq3	ND	-1.60502275	1.71429566	1.648802648	ND	ND	ND	-0.725477108
comp168617_c0_seq4	ND	ND	1.455518231	1.457322414	ND	ND	ND	ND
comp168617_c1_seq1	-1.326705201	ND	1.920316944	1.879813562	ND	ND	-1.486805148	-1.012537203
comp168634_c0_seq3	1.13834917	0.952361537	1.79962808	1.737739041	0.687411801	0.77712208	0.743070696	0.609601517
comp168688_c0_seq10	-1.831015963	-1.220302347	0.600473204	0.560367983	-0.599616773	-0.719166117	-0.19872422	-0.29936402
comp168716_c0_seq10	-1.30610239	-1.269420042	0.766132405	0.78337331	-0.40376192	-0.114210457	-1.943323592	-1.116873129
comp168716_c0_seq5	-1.603365102	-1.323644705	0.781824045	0.750469498	-0.496904649	-0.132493313	-1.337496317	-1.025955669
comp168744_c0_seq1	-0.309707369	-0.031815584	1.48539005	1.42543436	-0.245705355	0.200082485	-0.23785824	-0.271745783
comp168750_c1_seq1	-0.808827983	-1.198114367	1.261542884	1.278885871	-0.781548776	ND	-0.96892793	-0.79568998
comp168765_c0_seq2	ND	ND	0.18727778	0.180108618	ND	ND	ND	ND
comp168783_c0_seq3	-1.223035604	-0.466193953	0.259063556	0.273083692	-0.797816389	-0.956283798	-0.538037511	-0.811957593
comp168819_c3_seq1	-0.636039359	-0.032624982	0.773344597	0.709099399	-0.733698889	0.021353216	ND	-1.003112599
comp168851_c2_seq8	-0.268473643	-0.463940001	0.936362243	0.993562447	0.128716849	0.037196229	-0.486565537	-0.079244382
comp168880_c1_seq16	-1.644187712	-1.431414106	0.068360369	0.097914013	-1.616908506	-1.377435907	-1.202227668	-1.330019714
comp168880_c1_seq18	ND	ND	0.103158354	0.167682416	ND	ND	ND	ND
comp168880_c1_seq39	ND	-1.68686596	0.073821287	0.052411685	ND	ND	ND	ND
comp168880_c1_seq7	ND	-1.21438198	0.397366254	0.462747759	ND	ND	ND	ND
comp168880_c1_seq8	ND	ND	0.219767759	0.20325857	-1.305090061	-0.713434944	ND	-1.319231265
comp168899_c0_seq2	-0.911664775	-0.086107312	0.489512477	0.531748171	-0.680265586	-0.414464048	-0.323576695	-0.296466781
comp168909_c0_seq1	0.338239788	0.515764576	1.7892485	1.771928844	0.20321602	0.421838481	-0.375369759	-0.470977122

comp168909_c0_seq3	-0.038982373	-0.025249223	1.285469016	1.224614994	-0.066060828	-0.157581448	-0.730561237	-0.603080778
comp168924_c3_seq5	ND	0.02375377	1.616385714	1.608129455	ND	-0.297931645	ND	ND
comp168948_c1_seq1	0.564134617	0.848316982	1.809451218	1.789613281	0.744217738	0.84207798	-0.487014699	-0.165714214
comp168948_c1_seq11	0.597238852	0.929095451	1.965739201	1.937117621	0.814182125	0.910522983	-0.200833642	0.015156288
comp168948_c1_seq13	0.485354769	0.363018591	1.444575184	1.412100156	0.829750792	0.519192399	-1.097991052	-0.380685058
comp168948_c1_seq6	ND	-0.375624118	0.780997155	0.777830735	ND	-0.76880395	ND	ND
comp168960_c0_seq12	0.038788882	-0.161441267	2.33349759	2.287571786	-0.674294601	-0.735851998	ND	0.051926884
comp168960_c0_seq18	-0.426623037	-0.353511423	0.5837499	0.544890695	-0.700373826	-0.284809968	-0.180182804	-0.484066109
comp168960_c0_seq19	-0.491544866	-0.25705201	0.529823455	0.467867486	-0.402117753	-0.35345967	-0.278921593	-0.638107707
comp168960_c0_seq21	-0.358074668	-0.30645197	0.593846508	0.599728913	-0.473462965	-0.258813949	-0.336331027	-0.645966661
comp168960_c0_seq42	-0.359770719	-0.379762276	0.629207531	0.614787875	-0.424805773	-0.35857659	-0.492998519	-0.571572543
comp168960_c0_seq65	-0.502720921	-0.44317569	0.644172625	0.599907005	-0.463859842	-0.406230831	-0.306743306	-0.756754647
comp168960_c0_seq72	-0.383757116	-0.43062082	0.478553286	0.427632615	-0.51137987	-0.376642621	-0.385494571	-0.65461577
comp168960_c0_seq74	-0.485114269	-0.330332609	0.608632347	0.580084195	-0.524781852	-0.285309252	-0.429614415	-0.538923056
comp168960_c0_seq95	-0.426089833	-0.3480148	0.525012692	0.527566946	-0.483821416	-0.423384457	-0.304903843	-0.651190996
comp168966_c0_seq10	ND	-0.820327511	0.823135136	0.757099314	ND	ND	-0.591141074	-0.895024379
comp168966_c0_seq12	-0.499992742	-1.065370385	0.824611648	0.835275263	-1.250864785	-0.572059492	-0.076516103	-0.452092633
comp168968_c1_seq8	-0.443348838	-0.553881622	1.435385489	1.4329817	-0.717099628	-0.875567037	-0.904478781	ND
comp168972_c1_seq3	-0.918776638	-1.007033027	0.719669723	0.691815961	-1.067588691	-1.606267342	-1.130029108	-0.956791158
comp168976_c0_seq12	-0.275729149	0.029358719	0.66001017	0.694964213	-0.129263535	-0.190820931	-0.267424666	-0.240314752
comp168985_c0_seq6	-1.034167334	-0.926129077	0.466156647	0.506822233	-0.772804921	-0.959301054	-1.437305329	-0.911884862
comp169014_c2_seq12	0.52771464	0.309318321	1.335344123	1.291883108	-0.348096141	0.000520928	-0.301392089	-0.508365381
comp169016_c0_seq2	-1.829438047	-1.440573181	0.693065642	0.705244645	-1.80215884	-1.863716237	ND	-1.640208785
comp169016_c0_seq3	-2.117090908	-1.728226042	0.697446712	0.668532402	ND	-1.850339102	-1.976160859	-1.404982901
comp169077_c0_seq14	ND	-0.281118168	0.666655722	0.689916515	-1.103434666	-0.411664396	-1.466905079	-0.895727121
comp169106_c2_seq2	-1.217464903	-0.953538774	1.03823788	0.970325159	-1.014094437	-1.251743093	-0.637202161	-0.42617565
comp169130_c1_seq10	ND	ND	0.584068585	0.557594267	ND	-0.993006605	ND	ND
comp169130_c1_seq2	-1.567774528	ND	0.303490717	0.278223332	-1.540495321	-1.602052718	ND	-1.25360653
comp169145_c0_seq15	ND	ND	0.241118083	0.220584959	ND	ND	ND	ND
comp169145_c0_seq25	-0.410575558	-0.508377265	0.44817989	0.416536958	-0.412585728	-0.215516977	-0.65364974	-1.060195387
comp169145_c0_seq41	-1.094677208	-0.784993588	0.563513211	0.549044809	-0.590276747	-0.253894135	-1.254777155	-0.905447947

comp169145_c0_seq69	-0.308634727	-0.008710944	0.590289786	0.554475442	-0.332508042	-0.15102739	-1.121947187	ND
comp169145_c0_seq70	-0.514347233	-0.39079681	0.499230845	0.495695967	-0.349894833	-0.217632203	-0.803541876	-0.814828353
comp169145_c0_seq9	ND	ND	0.390902679	0.357404578	ND	ND	ND	ND
comp169153_c1_seq1	0.714573255	0.858726488	1.598035077	1.61445665	0.731224035	0.901379548	0.836978396	0.474533577
comp169153_c1_seq3	0.497680694	0.711449248	1.552480969	1.565866265	0.62425397	0.828237388	0.663766229	0.30908277
comp169175_c0_seq4	-0.223602939	-0.487950586	0.988200843	0.950297063	-1.372414991	-1.132942392	ND	ND
comp169186_c0_seq3	-0.667906666	-0.332917181	0.379449837	0.403620427	-0.765566196	-0.304244847	-1.225946622	-1.177647409
comp169186_c0_seq5	-0.508113608	-0.463744432	0.424454612	0.411752961	-0.585569752	-0.281979653	-1.513311595	-1.641103641
comp169212_c1_seq10	-1.128954881	-0.518241266	0.639451018	0.609216551	-0.198585688	-0.385081821	-0.385964841	-1.291908138
comp169215_c1_seq1	-1.811252368	-1.054410717	1.673876262	1.607913473	-1.783973162	-1.243470567	-0.591141074	-1.099144362
comp169228_c0_seq3	ND	-1.031045603	1.124770675	1.066801359	-0.175147318	-0.323854891	0.312084186	-0.116737855
comp169244_c0_seq3	ND	-0.617401514	0.845048637	0.864862964	0.003284059	-0.221000634	-1.087185081	-0.612917136
comp169257_c0_seq12	-1.879828783	-0.968085171	0.549213648	0.568229068	-0.852549576	-0.499133625	ND	ND
comp169257_c0_seq13	-1.66205853	-1.273193664	0.693651827	0.646974123	-0.935809319	-0.599426707	-1.822158477	-1.472829269
comp169257_c0_seq20	-1.131064818	-0.234044464	0.481368111	0.524755321	-0.539514181	-0.074262539	ND	-1.59504807
comp169257_c0_seq6	-1.012987431	-0.800213824	0.566021742	0.55885258	-0.432866255	-0.530635825	ND	-1.844947468
comp169272_c0_seq1	1.052658849	1.188458556	1.978245226	1.91917566	1.015657068	0.88992385	0.650901759	0.433378284
comp169311_c1_seq1	ND	ND	0.066410386	0.059241223	-1.366133173	-0.825630578	-0.775361076	-1.079244382
comp169319_c0_seq5	ND	-1.348796608	0.367686976	0.344723546	-0.534291009	-1.29481841	ND	-1.247402217
comp169341_c0_seq1	-0.619269149	-0.477076616	1.557215814	1.536902086	-1.194049934	-0.592849499	ND	-1.430039888
comp169349_c0_seq14	-1.244630218	-1.031856611	0.668832706	0.7181449	-0.819411003	-0.880968399	-1.103700169	-1.231492215
comp169356_c0_seq2	-1.168540049	-0.897774495	0.481298296	0.488641516	-0.262083013	-0.468132682	-0.696616781	-0.569136322
comp169356_c0_seq3	-1.098286062	-0.910336038	0.571020363	0.536344779	-0.199174562	-0.387836756	-0.656326017	-0.576992571
comp169362_c3_seq5	-0.159329174	-0.109282864	1.796864787	1.763404646	-0.211231213	-0.343369684	-0.222519108	-0.681304373
comp169368_c0_seq15	-0.746552549	-0.322925576	0.860824508	0.8516164	-0.66812082	-0.507829466	-0.6056225	-0.937534529
comp169368_c0_seq8	-0.789161016	-0.462444057	0.851300636	0.804694734	-0.647938457	-0.592990285	-0.949260963	-1.173963022
comp169380_c0_seq2	0.52329607	0.59984993	1.58868122	1.583686797	0.550575276	0.47198454	0.575588631	0.351909645
comp169398_c0_seq7	-0.045082415	0.053155215	1.57316056	1.536748994	0.058075402	0.221669391	0.382834552	0.157111823
comp169398_c0_seq8	-0.130918304	0.039267859	1.584288589	1.526576831	0.098687512	0.111290561	0.320483296	0.178450811
comp169490_c0_seq21	ND	ND	0.738955439	0.731786276	-0.204884993	0.101534396	ND	-0.343964934
comp169524_c1_seq1	-1.198512466	ND	0.186676681	0.205836457	-1.17123326	-0.931760661	ND	ND

comp169529_c0_seq8	-0.929100425	-0.674934133	0.834032102	0.79134224	-0.021007626	-0.300620783	0.175617451	-0.167774396
comp169546_c0_seq7	-0.342167069	-0.330720545	1.356566143	1.331153931	-0.72706831	-0.160236777	-0.391568719	-1.343269506
comp169563_c1_seq1	ND	ND	0.532802379	0.5578179	ND	-0.796488328	ND	-1.050102131
comp169568_c1_seq5	-0.689622187	-0.409901791	0.412265731	0.356110108	-0.575192805	-0.564199534	-0.423753402	-0.329696699
comp169586_c1_seq6	-1.089496696	-0.70063183	0.237700504	0.260494565	-1.062217489	-0.521714894	-0.948566647	ND
comp169623_c1_seq8	ND	ND	0.851614061	0.807928064	ND	ND	ND	ND
comp169679_c0_seq3	-0.27770952	0.194129581	0.955019817	0.90299419	-0.250430313	-0.289711315	0.015830692	-0.221105823
comp169679_c1_seq3	ND	ND	1.077921063	1.054010426	-1.452445852	-0.610913261	ND	-0.989465801
comp169703_c0_seq5	-0.67458125	-1.063867634	1.124536011	1.101378743	-0.77224078	-1.009889435	-0.436741188	-0.86556323
comp169809_c0_seq3	-0.201654662	-0.745843007	0.871509105	0.844401612	-0.998284197	-0.423019496	-0.320361924	-0.711395405
comp169848_c0_seq1	0.178656997	0.116207872	1.127411979	1.093724683	0.354589215	0.323414447	-0.592457784	-0.352273044
comp169848_c0_seq3	-1.08833703	-1.176593419	0.17191338	0.164744218	ND	-0.821585225	ND	-1.075199028
comp169851_c0_seq1	0.470448111	0.704183697	2.628386019	2.635428068	ND	-0.677773432	0.014064603	0.557968476
comp169912_c1_seq10	ND	ND	0.215012529	0.207843366	-0.893019938	ND	ND	-0.907161142
comp169912_c1_seq5	-1.155200868	ND	0.927598988	0.946838841	-0.332041644	-0.83729654	-0.917360807	-1.443092861
comp169932_c1_seq13	ND	ND	0.172494376	0.216477736	ND	ND	ND	ND
comp169932_c1_seq6	ND	ND	1.171967394	1.160739374	ND	ND	ND	ND
comp169982_c1_seq16	ND	ND	0.119766669	0.14256073	-0.879121329	-0.940678725	ND	-0.717171274
comp170023_c1_seq1	-1.173953809	-0.484058948	1.770917579	1.743455957	-0.406311913	-1.03214074	0.197425161	-0.119423122
comp170064_c0_seq10	ND	-0.985738859	0.86337029	0.844619255	ND	ND	ND	ND
comp170081_c0_seq2	0.115702876	0.289324359	1.05604904	1.045214923	0.209500785	0.285544669	0.086490998	-0.15746586
comp170090_c0_seq13	-1.094562755	-0.978699161	0.909980639	0.844260232	-0.56213357	-0.526780953	-0.237629362	-0.780394757
comp170090_c0_seq19	0.235960829	0.320831221	1.16220042	1.113239954	0.368923973	0.406356216	0.402698141	0.270709981
comp170090_c0_seq23	-0.111739027	-0.140409726	0.81200907	0.795499881	-0.059636237	0.046779736	0.13118056	-0.152958687
comp170090_c0_seq3	-0.93022993	-0.807632954	0.811642236	0.817701339	-0.851798201	-0.469658099	-0.29444986	-0.519151919
comp170090_c0_seq6	0.01114119	0.030790198	0.999085756	0.998810301	0.119453647	0.163949643	-0.058782127	-0.151812067
comp170118_c1_seq3	-0.347974341	0.254770345	1.196535855	1.135749321	-0.171756121	-0.144891615	-1.549466973	-1.200137764
comp170118_c1_seq5	0.482728771	0.545740058	1.730744725	1.676091253	0.929137285	0.670299331	-0.279431167	-0.185374464
comp170173_c2_seq1	-0.838201433	-0.715604456	1.392570188	1.361004434	-0.868914173	-0.775569609	0.71139249	0.395698224
comp170173_c2_seq5	-0.540771293	-0.072725181	0.740668416	0.7914912	-0.735340836	-0.972989492	-0.019630003	-0.226603295
comp170177_c0_seq1	-0.214435432	0.215047284	0.885403923	0.839605358	-0.287271379	-0.275042561	-0.400864318	-0.556685088

comp170185_c2_seq3	ND	ND	1.052940724	1.058785104	-1.043683728	-1.281332383	ND	ND
comp170185_c2_seq6	-1.842824363	-1.931080751	1.120717426	1.153897285	-1.116575152	-1.576072557	ND	-1.528656364
comp170185_c2_seq7	ND	ND	1.164484553	1.150049458	-1.208758942	-0.969286343	-1.220046837	-1.222900146
comp170185_c3_seq1	-0.635490661	-0.802928296	1.421603795	1.486169722	-0.541264665	-0.049980093	ND	-1.400503909
comp170187_c3_seq5	-1.527035872	-1.138171006	0.649668487	0.60110664	ND	-0.482132816	-0.483015836	0.017581048
comp170215_c0_seq1	-0.224735389	-0.659779264	0.536117372	0.48064353	-0.457093493	-0.281289974	-0.154386415	-0.512627382
comp170235_c0_seq9	-0.565577368	-1.068807104	0.705668427	0.679070713	-0.220877749	ND	-0.584348162	-0.520254682
comp170256_c0_seq1	-1.265201744	-0.575306882	1.350436325	1.358947366	-0.538952533	-0.396389947	-0.823241699	-0.553093737
comp170275_c0_seq11	ND	ND	1.632241145	1.608236755	-0.941504562	ND	ND	ND
comp170281_c0_seq6	-0.977263986	-1.162430387	0.921475682	0.915967303	-1.046894792	-1.409482184	-0.632213954	-1.663095988
comp170295_c0_seq1	-0.073529775	0.114731682	1.165928375	1.155039323	-0.005821911	0.182498165	0.056676408	-0.005722676
comp170303_c0_seq4	-0.651279326	-0.584633755	0.477083488	0.455673886	-0.991976905	ND	-0.753387326	-1.182209368
comp170307_c1_seq4	ND	ND	0.816456301	0.802108554	ND	ND	ND	ND
comp170326_c1_seq10	-0.0893914	0.428342497	1.002593089	1.054263278	-0.094904706	-0.182791042	-0.144755996	-0.401642739
comp170393_c1_seq7	ND	ND	0.373585136	0.325798122	ND	ND	ND	ND
comp170393_c1_seq9	ND	ND	0.135630174	0.102132073	ND	ND	-0.833927867	-1.262749909
comp170406_c2_seq3	-1.144620085	-1.35781521	1.373408865	1.315960886	-1.020430865	-1.303837011	-1.128628773	-0.955390823
comp170406_c2_seq4	ND	-1.816708002	1.47131805	1.455324023	-0.746929897	-0.762729803	-1.286491569	-0.93716236
comp170419_c0_seq2	-0.082900975	0.262994817	0.921131784	0.90680769	-0.065167087	-0.072366821	-1.303698763	-0.431490809
comp170424_c2_seq2	-0.452314145	-0.053903961	1.519274747	1.475424158	-0.010061591	-0.049899737	0.193765882	-0.314237406
comp170433_c0_seq11	-0.765697709	-0.763777467	0.70626182	0.679865214	-0.676270595	-0.591699956	-0.340771004	-0.611230553
comp170433_c0_seq18	-0.372127199	-0.460383588	0.705957804	0.646870842	-1.299090502	-0.883526644	-0.884409665	ND
comp170433_c0_seq21	-0.753511531	-0.493313274	0.799335707	0.796403598	-0.609726756	-0.646460568	-0.40430554	-0.678225622
comp170433_c0_seq4	-0.698960043	-0.743750737	0.959230377	0.90883606	-0.671680836	-0.669569153	-0.535753599	-0.760455658
comp170436_c1_seq2	-0.922572943	-0.357616818	0.703061442	0.634543811	-0.559501635	-0.243640689	-0.217371464	-0.386556195
comp170436_c1_seq6	-0.666339899	-0.277475033	0.588306634	0.624065672	-0.673822798	-0.434350199	-0.147991509	-0.488391648
comp170445_c0_seq4	0.461394768	0.607761417	1.396363165	1.327514511	0.521937651	0.641116419	0.59907166	0.3699938
comp170454_c0_seq12	-0.772743916	-0.639151555	0.01038524	0.0543686	-1.046494705	-1.28414336	-1.409965118	-1.236727168
comp170454_c0_seq8	-0.674957425	-0.763213814	0.0179951	0.043010621	-0.772616955	ND	-1.437117364	-1.263879414
comp170457_c1_seq4	ND	ND	1.443754987	1.403704598	ND	ND	ND	-0.706447408
comp170483_c0_seq3	-1.55448275	-1.642739139	1.333304197	1.348582041	ND	ND	ND	-1.541344748

comp170483_c0_seq5	-1.856107806	-1.643334199	1.726706441	1.756334545	-1.828828599	ND		-1.715177757	-1.143999799
comp170496_c2_seq14	0.628237343	0.537492154	1.64869476	1.600491981	0.564766845		0.647586295	0.169582019	0.000397288
comp170496_c2_seq20	0.368029003	0.325052596	1.710630706	1.695157381	0.473693315		0.653463022	0.10622016	-0.021571886
comp170496_c2_seq21	-0.287420177	-0.472586579	1.121535692	1.078210218	-0.084049711		-0.104214423	-0.970398869	-0.429184135
comp170509_c0_seq4	-0.375572979	-0.146408955	1.119687628	1.102684962	-0.300869122		-0.233759909	-0.131102338	-0.415680488
comp170509_c0_seq5	-0.472871058	-0.172428095	1.033130055	1.024877864	-0.627435439		-0.453464389	-0.20415443	-0.624543304
comp170509_c0_seq9	-0.7555152	-0.258310859	0.956393743	0.934920175	-0.566867991		-0.860374464	-1.01252516	-2.043407193
comp170513_c0_seq1	-0.289982394	0.700942463	1.495852655	1.449174951	0.619536661		0.592193365	0.538922275	0.098819223
comp170513_c0_seq4	0.806359233	0.653343941	1.694961708	1.751779906	0.739539404		0.71166512	0.884707297	0.688881366
comp170526_c0_seq10	-0.787307035	-1.176593419	0.39376213	0.364316572	ND		-1.12261522	ND	-0.598077773
comp170557_c2_seq16	-1.494102377	-0.883388761	0.686966788	0.638839018	-0.767853166		-1.051259312	-0.575021078	-1.003843119
comp170577_c1_seq6	-0.918585949	-0.705812342	0.376426567	0.416682055	-0.414185488		-0.77677288	-0.233587856	-0.428326692
comp170600_c0_seq5	-0.85936614	-0.248652525	0.764966012	0.721074042	-0.589048885		-0.153281641	-0.475398043	-0.603190089
comp170602_c1_seq2	-0.130686866	0.52444589	1.502286765	1.532414157	0.214012753		0.645370878	-0.802670174	-0.754370961
comp170619_c0_seq6	ND	ND	1.626425432	1.57619	ND	ND	ND	ND	ND
comp170653_c4_seq14	ND	ND	0.550270641	0.524618072	ND	ND	ND	ND	ND
comp170654_c0_seq3	-1.636532596	-2.02581898	1.571886177	1.532783205	-0.071434294		-0.07421369	0.705794577	0.540958263
comp170683_c0_seq9	-0.158280842	0.125423936	0.962790393	0.920456813	0.058877908		0.298350507	-0.304592504	-0.205140769
comp170719_c1_seq2	-1.209631724	-1.297888113	0.960442056	0.920916857	ND	ND		-1.369731671	-0.895463726
comp170735_c0_seq1	-0.904631513	ND	1.612897386	1.576764527	ND	ND		-0.763701464	ND
comp170748_c1_seq8	-1.522359136	-1.008555533	0.330807886	0.367544209	-1.017958675		-1.079516071	-1.381429088	-1.509221134
comp170750_c0_seq1	-1.081313247	ND	1.125061783	1.12601051	-1.05403404	ND		-0.940383198	ND
comp170779_c0_seq3	ND	-0.844271065	0.58642249	0.63536927	-0.72873547		-0.790292866	ND	-0.19880863
comp170816_c0_seq14	-0.269813764	-0.255407811	0.567673054	0.527335528	-0.228294118		-0.237145164	-0.174641206	-0.353585774
comp170816_c2_seq10	-0.514015362	-0.4975364	0.938120575	0.923843324	-0.625038853		-0.651834143	-0.511388011	-0.740637698
comp170816_c2_seq9	-0.6932904	-0.334388757	0.733291432	0.70071769	-0.063951202		-0.125508599	-0.251330356	-0.299941156
comp170849_c0_seq6	-0.711167449	-0.354487267	0.376852123	0.361927496	-0.487593598		-0.661124754	-0.394146142	-0.698029447
comp170861_c0_seq1	ND	ND	0.625931032	0.558064029	ND	ND	ND	ND	ND
comp170861_c0_seq2	ND	ND	0.78574359	0.753750844	ND	ND	ND	ND	ND
comp170869_c0_seq4	ND	ND	0.153720375	0.121727629	-1.255342088	ND	ND	ND	-0.570513287
comp170938_c1_seq4	-1.317143487	-1.405399876	1.132971387	1.136423459	-1.687804289		-1.272240431	-1.176213439	-0.798855506

comp170938_c1_seq6	-1.529004827	-1.24928443	1.048263685	1.068686988	-1.50172562	-0.999011586	ND	-0.714234478
comp170946_c0_seq1	0.239822939	0.163148423	1.578438713	1.592466627	0.518444357	0.348306144	0.356619308	0.031112192
comp170963_c0_seq1	-0.63107594	-0.719332329	0.203205738	0.196036576	ND	ND	ND	-0.918967933
comp170995_c0_seq4	2.109412567	2.078546829	3.025088314	2.989247618	2.165898808	2.193845064	1.498227155	1.396163216
comp170995_c0_seq9	2.0351967	1.953717739	2.927193014	2.878307943	2.147224846	2.147566271	1.47043806	1.318957171
comp171042_c2_seq4	0.308443313	0.058818922	1.1309182	1.07302376	0.049415781	0.316917103	0.06615661	-0.02687333
comp171068_c0_seq1	ND	-0.967333797	0.603021752	0.573576195	ND	-0.913355598	ND	-0.865939406
comp171068_c1_seq11	-0.725936828	-0.316868576	0.596806031	0.613588999	-0.589513152	-0.544615218	-0.283976784	-0.460986853
comp171068_c1_seq16	-1.526612789	-0.453501175	1.151386024	1.153792245	-1.499333582	-1.16295097	-0.195351042	-0.70056143
comp171068_c1_seq9	-1.827219289	-1.313415687	0.546974474	0.516942428	-1.498910087	-1.384376224	-0.572345888	-1.035930036
comp171077_c0_seq1	0.231122003	0.399990124	1.08000319	1.035371636	-0.457602134	0.10408976	-0.741891301	-1.170713342
comp171084_c0_seq31	-1.551295253	-1.162430387	-0.008498253	0.020544757	-1.524016047	-0.983513452	-1.109335209	ND
comp171098_c2_seq5	ND	-1.676339293	2.080407471	2.06163351	ND	ND	ND	-0.671854915
comp171123_c1_seq2	-0.057460464	-0.446746848	0.725668692	0.680710968	-0.206272516	-0.024791864	0.083469585	-0.123503707
comp171129_c1_seq1	ND	-1.10301605	1.549611821	1.537278573	-0.878335986	-0.894135892	0.119921437	-0.014210787
comp171129_c1_seq12	ND	-1.631886236	1.519109225	1.54434874	-0.641289378	-0.577908037	0.260058033	-0.123951665
comp171129_c1_seq3	ND	ND	1.524887129	1.483338262	-1.30376397	-0.763261375	-0.148720443	-0.61893517
comp171184_c1_seq12	-0.642300059	-0.38649182	1.214700126	1.154849233	-0.404167487	-0.181728227	-0.049072339	-0.269010609
comp171184_c1_seq14	-0.475036771	-0.363720805	1.195052871	1.130226995	-0.350847551	-0.393519604	-0.003918498	-0.232871434
comp171184_c1_seq2	-0.43851847	-0.32122862	1.217762959	1.180083603	-0.36777357	-0.289152263	-0.187175938	-0.264801375
comp171184_c1_seq6	-0.603465139	-0.321365041	1.198460503	1.180357475	-0.300963201	-0.253376128	-0.020175942	-0.096815466
comp171201_c0_seq5	ND	ND	0.756996879	0.787616277	ND	ND	ND	ND
comp171257_c0_seq3	-1.163500003	-1.029907642	1.554127604	1.572296066	ND	-1.072839456	-1.022569954	-0.397034334
comp171257_c0_seq8	ND	-1.06461966	0.872158846	0.825925661	-1.25011406	-0.709611465	-1.136463218	-0.486104014
comp171279_c2_seq10	-0.47167753	-0.10301605	1.236200673	1.193584165	-0.46460171	-0.132375057	0.051105707	-0.147749695
comp171298_c0_seq3	0.188544801	0.71873882	1.639934399	1.584460556	0.454063173	0.839663808	0.402346622	0.103727556
comp171322_c0_seq1	-0.947097193	-0.245303108	1.21245683	1.190590637	-0.250811205	-0.55540665	-0.186378386	-0.193596501
comp171339_c0_seq1	ND	-1.20505738	0.199930775	0.159761352	-1.265613044	-1.32717044	-1.452992198	-1.580784244
comp171404_c2_seq5	ND	-1.414626097	1.641095917	1.583528177	-0.600120498	-1.18455664	-0.18543966	-0.711171715
comp171426_c2_seq10	-0.349474496	-0.221021775	0.823862218	0.832022688	-0.251614215	0.149226386	-0.26290211	-0.151812067
comp171448_c1_seq17	-1.853921922	-1.641148315	0.937807406	0.902041443	-1.826642715	-1.587170116	-1.411961877	-1.539753924

comp171448_c1_seq4	-1.569503639	-1.958790023	0.941979299	0.894430974	-1.542224432	-1.603781829	-1.127543595	-1.255335641
comp171448_c1_seq5	-1.859857702	-1.647084095	0.897552813	0.907328367	-1.355457241	-1.049037852	-1.417897658	-1.068568449
comp171453_c0_seq6	ND	-1.258283372	1.958279789	1.945781793	-1.540687785	-1.301215186	-1.728066939	-1.077707734
comp171466_c0_seq4	-0.902966484	-0.703981161	0.651474498	0.604632631	-1.23470922	-0.965273397	-0.886975172	-1.315797213
comp171482_c0_seq19	ND	ND	1.876519697	1.89305997	ND	-1.152074959	-1.578926711	-1.405688762
comp171482_c0_seq20	ND	ND	1.187636728	1.221629304	ND	-1.561736733	-1.085498499	ND
comp171497_c0_seq2	-0.088046629	0.16776161	0.891788241	0.923126075	0.064171314	-0.040138063	0.070612186	-0.040146521
comp171517_c1_seq2	-0.869253473	-0.781418603	0.396987301	0.365344369	-0.841974266	-0.982712909	-1.02935342	-1.634266721
comp171521_c3_seq1	-0.417876299	-0.388033376	1.854199968	1.794693529	ND	-0.656274472	ND	-0.404738297
comp171522_c3_seq1	-1.747189811	-0.794053515	1.706185197	1.715853026	-1.117850614	-0.605376742	-0.907289759	-0.271653811
comp171544_c1_seq16	-1.325473794	-1.890851438	1.493418531	1.427065418	-1.076345838	-1.836873239	-0.457545018	-1.488427051
comp171544_c1_seq9	ND	ND	1.590970118	1.525809008	-1.056974434	ND	ND	ND
comp171550_c1_seq2	-0.342813511	-0.292120449	0.650621004	0.617465487	-0.30847245	0.073106911	-0.095118695	-0.344153332
comp171581_c0_seq4	ND	ND	0.551130433	0.550800695	-0.498910087	-0.46355747	ND	-0.637990028
comp171605_c1_seq2	-0.538031256	-0.450196386	1.163739734	1.19816161	ND	-0.447370709	-0.397101207	-0.700984513
comp171624_c1_seq2	ND	-1.0865954	0.224122838	0.17556099	ND	ND	ND	ND
comp171624_c2_seq10	ND	ND	0.250630388	0.192308703	ND	ND	ND	ND
comp171646_c0_seq11	-1.024369055	-0.987686708	0.834914892	0.895992154	-1.349272367	-0.933708509	ND	-1.965473562
comp171646_c0_seq7	-1.266128074	-0.907226432	0.881552077	0.919765042	-1.238848868	-0.768927347	-1.125198026	-1.474838821
comp171667_c3_seq13	ND	ND	0.604905896	0.543379071	-0.779332983	-0.10052769	-0.966712137	ND
comp171675_c0_seq9	0.158198711	-0.13417766	0.933107537	0.97307677	-0.212462091	0.354369442	-0.047658727	-0.226603295
comp171709_c0_seq1	0.187252924	0.232335814	1.033433825	0.983107746	-0.477704491	-1.051145249	-0.398815756	-0.491845695
comp171731_c0_seq2	-1.229375782	-0.919692162	0.559148405	0.597736733	-1.503126571	-1.564683968	ND	-0.286818854
comp171731_c0_seq5	-1.166258468	-0.777393602	0.293564298	0.319395395	-0.661858006	-0.598476666	-0.548207164	-0.675999211
comp171732_c0_seq8	-1.439615441	-1.430961816	1.205719658	1.162419355	-1.111306238	-0.899862363	ND	ND
comp171744_c0_seq15	-0.053445881	0.11542224	1.119190116	1.121010552	0.456487069	0.370429345	-0.299460457	-0.224832305
comp171747_c0_seq2	-0.215399461	-0.172726749	1.108337207	1.069962204	-0.135184179	-0.042552158	-0.288349232	-0.42950524
comp171748_c3_seq1	0.256107196	0.474557935	1.510605277	1.516741581	0.481754056	0.803413411	-0.141353667	0.233529646
comp171755_c1_seq10	ND	ND	1.032667179	1.089167096	ND	ND	ND	-0.510927597
comp171755_c1_seq2	ND	ND	1.055795967	0.991130911	ND	-1.557491396	ND	ND
comp171755_c1_seq7	ND	ND	1.010225992	1.044586106	ND	-1.666019206	ND	-1.618603013

comp171755_c1_seq8	ND	-1.557964326	1.065469666	1.038645815	ND	ND	-1.027747893	-0.97944868
comp171756_c0_seq2	-0.668517703	-0.513736043	1.303188423	1.334686071	ND	-1.003825889	ND	-1.257439692
comp171757_c0_seq2	0.254567932	0.597371711	1.348850956	1.357404578	0.220329101	0.504614044	-0.073505384	0.206187897
comp171761_c0_seq6	ND	ND	1.292880516	1.301028111	ND	ND	ND	-1.642206512
comp171775_c0_seq1	-0.837167398	-0.381355742	0.354625632	0.397430445	-0.566850142	-0.359562226	-0.219116094	-0.580991346
comp171786_c0_seq8	-1.39341238	-0.741306079	1.250054783	1.27741727	-0.968193164	-0.825630578	-0.252482331	-0.727061864
comp171798_c0_seq11	0.276382114	0.225373783	1.101198492	1.121136961	-0.568170973	0.156391811	-0.028551399	-0.281282181
comp171798_c0_seq17	-0.048682684	-0.064388406	1.050035187	1.085990694	-1.062796163	-0.311440203	-1.250175317	-1.377967363
comp171805_c0_seq6	-0.089959696	0.278149948	1.300624483	1.217479214	0.458457594	0.636184597	-0.103931608	0.2616348
comp171820_c0_seq4	-1.43611043	-1.047245564	1.119707081	1.08997209	-0.107801227	0.3988431	-1.295180381	-0.276844391
comp171851_c0_seq10	-0.663223089	-0.230892529	0.702985464	0.615738678	-0.552969647	-0.06776986	-0.037618647	-0.24759745
comp171851_c0_seq5	-0.784978372	-1.174264757	1.477077839	1.443917491	-1.058729161	-0.819256562	-0.246108315	-1.072870366
comp171886_c1_seq1	-0.456313816	-0.544570204	1.0592091	1.125826151	-0.14272787	0.111467986	-0.12974719	-0.540085826
comp171886_c1_seq3	-0.887148874	ND	0.335312975	0.286751127	-1.035960927	-0.44430581	-0.524370076	-0.874010872
comp171917_c1_seq4	-1.533749737	ND	1.337515508	1.313171172	ND	ND	ND	ND
comp171922_c0_seq12	ND	-1.658334871	0.82583453	0.870993248	-1.24176928	ND	ND	-1.55694048
comp171927_c0_seq13	-0.76078824	-0.640768687	0.464700064	0.469430124	-1.069301136	-0.829828537	-1.733801544	-1.384472336
comp171927_c0_seq15	-1.442835791	-1.105123448	0.431373834	0.460768832	-1.193707835	-0.87505399	ND	-1.429697789
comp171927_c0_seq16	-0.311731314	-0.354230212	0.832863344	0.828310421	-0.124751264	-0.35824396	-0.208589826	-0.392497814
comp171927_c0_seq21	-1.905339987	-0.73832387	0.52614918	0.501556126	-1.03296274	-1.094520136	-1.764409938	ND
comp171927_c0_seq6	-0.635124477	-0.547289607	0.380577294	0.444871022	-0.960027789	-0.970432663	-0.795224424	-1.03216094
comp171950_c0_seq1	ND	-1.242211074	0.458478244	0.467103348	ND	-1.489262871	-0.615084628	-0.964725424
comp171971_c0_seq1	0.515550631	0.554069322	1.272120758	1.324001904	0.428395479	0.624234282	0.560795757	0.341413207
comp171983_c0_seq13	-1.563907232	-0.87401237	0.506463635	0.470330777	-0.723714668	-0.668766496	-0.577879143	-0.737855873
comp171983_c0_seq16	ND	-1.91164552	1.090073793	1.031752107	-1.495079929	ND	ND	-1.810251129
comp171983_c0_seq17	ND	-1.677256882	0.602792537	0.608151968	-1.862751282	ND	-1.74910044	-1.876892486
comp171983_c0_seq18	ND	-1.575461408	1.134773228	1.084634991	ND	-1.822513205	ND	-1.474067017
comp171983_c0_seq2	ND	ND	0.732550526	0.699827259	ND	ND	-0.851656634	-0.377388689
comp171983_c0_seq24	ND	ND	0.617680184	0.578663654	-1.832774964	-1.894332361	ND	-1.545886173
comp171983_c0_seq9	ND	ND	0.613287197	0.573448917	ND	-1.918030503	-1.742822264	-1.569584315
comp171983_c2_seq2	ND	-0.914768933	1.312004269	1.315870406	-0.431256553	-0.38366948	-0.317605711	-0.813374542

comp172025_c0_seq4	ND	-1.240209713	1.429653829	1.451698957	ND	-1.186231514	ND	-0.740875313
comp172029_c0_seq2	ND	ND	1.314877118	1.275120588	-1.661080919	ND	ND	-0.720979614
comp172029_c0_seq7	ND	ND	1.001296696	0.988137169	ND	-1.077373519	ND	-0.485889282
comp172088_c3_seq2	-0.254949868	-0.256056081	0.980476959	0.973307797	-0.482943166	-1.243470567	-0.767232333	-1.196054375
comp172110_c0_seq9	ND	ND	0.729844633	0.664683523	ND	ND	ND	ND
comp172150_c1_seq2	-0.716862552	-0.805118941	0.531153402	0.523984239	-1.166704601	ND	-0.575932504	-0.879815809
comp172157_c0_seq4	0.486386577	0.645110422	1.368269886	1.314524582	0.494780439	0.748493478	0.703406794	0.289824719
comp172163_c0_seq11	0.064977598	0.254685901	1.029161433	1.043651331	-1.370141193	ND	ND	-0.907161142
comp172182_c0_seq1	0.133425712	0.137226833	1.760358437	1.818466056	0.043735112	-0.076943737	-0.151612972	-0.368346101
comp172227_c1_seq6	-0.430337246	-0.372465599	0.98118084	0.998835261	0.102091939	0.3549285	-0.034134692	-0.161926738
comp172231_c2_seq19	ND	-1.40029615	0.877629575	0.92631823	-0.983730559	ND	-0.870079717	-0.821780504
comp172231_c2_seq20	-1.268281859	ND	0.770119802	0.829897429	ND	ND	ND	ND
comp172231_c2_seq24	-1.869573867	ND	0.98910225	0.944807571	ND	ND	-1.728643819	ND
comp172231_c2_seq30	ND	-1.880413346	0.812158081	0.793362751	-1.76487775	ND	-1.350196913	ND
comp172231_c3_seq7	-1.109305089	-1.197561478	1.105187831	1.044598284	-1.082025883	ND	-0.570435032	-0.920075828
comp172234_c0_seq1	0.122806736	0.219327785	1.150849945	1.10995741	0.308265612	0.132307471	0.148915182	-0.077935082
comp172256_c0_seq3	-0.665966024	-0.833403659	0.979989938	0.96150711	-1.416838068	-1.77942546	-0.3737683	-0.732009268
comp172258_c1_seq5	-0.472380527	-0.083515661	0.573990063	0.560190322	-0.445101321	-0.381719981	-0.055244067	-0.334303788
comp172262_c0_seq17	-0.754764907	-1.144051292	0.851593874	0.825675275	-1.630575688	ND	-1.21589485	-1.644716892
comp172262_c0_seq21	-0.885145028	-0.730363368	0.92812827	0.88535207	-1.061985804	-1.220453213	-0.948334962	-1.297975757
comp172262_c0_seq34	-1.333691322	-0.944826456	0.679886755	0.629083796	-1.306412115	-0.714756998	-0.648693229	-1.14446206
comp172314_c1_seq20	-1.458712553	-0.893756428	0.290558335	0.240232256	-1.732463342	-0.538748234	ND	ND
comp172314_c1_seq26	-1.134297686	-0.921524079	0.295969836	0.236882874	-0.408048475	-0.503464139	ND	-1.547128416
comp172314_c1_seq3	-0.983997368	-0.251067874	0.556432899	0.506920735	-0.206595635	-0.197089676	ND	ND
comp172319_c0_seq8	-0.630520931	-0.567509644	0.270707537	0.256589514	-0.641030285	-0.702587682	-0.364652146	-0.582620822
comp172341_c3_seq11	-1.146401547	-0.836717927	0.870358189	0.837058169	-0.943031082	-0.527467223	-1.005471499	ND
comp172369_c0_seq4	-1.201654662	-0.988881055	1.369465999	1.365820543	-0.998284197	-1.059841593	-0.282573363	-0.644448616
comp172373_c0_seq1	-0.001876759	0.037730142	0.901025293	0.884854886	0.06286484	0.103213504	0.207673663	-0.084671728
comp172381_c2_seq10	-0.723805993	-0.392933074	1.004422293	0.960303786	-0.423525514	-0.848260813	0.132082165	-0.08871317
comp172381_c2_seq8	-0.520741296	-0.307967689	0.908846047	0.940711628	-0.157669987	ND	0.228239108	-0.100117967
comp172388_c0_seq1	ND	ND	1.246069114	1.257834706	ND	ND	ND	-1.670824909

comp172451_c1_seq11	-0.300320365	-0.008365512	0.897782139	0.852824415	-0.335189065	0.102094043	0.095882189	-0.048300273
comp172451_c1_seq2	-0.203192516	-0.069600155	0.808963974	0.879787836	-0.476943305	0.160469302	0.213943944	-0.030353671
comp172461_c1_seq8	-0.358170655	-0.238151101	0.848834244	0.825637635	0.002323231	0.02508672	-0.1550927	-0.13675671
comp172485_c0_seq16	-0.618215675	-0.373257385	0.440136213	0.46704684	-0.500759838	-0.404709381	-0.591228979	-0.815931038
comp172485_c0_seq60	-0.959510224	-0.483495182	0.515289697	0.536609072	-0.865284228	-0.3405759	-0.818580175	-1.025553468
comp172494_c1_seq6	-1.049491534	-0.739807914	1.058434339	1.088196295	ND	0.030173628	ND	-1.337383527
comp172502_c1_seq1	-0.83283222	-0.108175252	1.15891742	1.183573011	-0.88473426	-0.992049147	0.424816235	0.096759731
comp172512_c0_seq2	ND	-1.213468637	1.494060105	1.509370865	ND	-1.527467223	ND	-1.002929776
comp172525_c0_seq2	0.056081108	0.215918639	0.849760446	0.89643771	0.046218506	0.214196688	0.045149777	0.024251964
comp172530_c0_seq12	-1.070559877	-0.85778627	0.629023228	0.58046138	ND	-0.627716812	ND	-0.756391879
comp172540_c0_seq1	0.033406325	0.287572617	1.454311024	1.397237569	0.072919988	0.423543039	-0.165611688	-0.155101036
comp172550_c0_seq21	-1.11657436	-0.375526976	0.495858569	0.465989516	-0.412601543	-0.337939193	-0.517006462	-0.393742487
comp172550_c0_seq36	-0.932861625	-0.399752867	0.469265944	0.437691795	-0.344915112	-0.300962324	-0.754143015	-0.392914583
comp172550_c0_seq47	-0.966553753	-0.591052849	0.525305244	0.525789046	-0.367883375	-0.242884079	-0.486805148	-0.563444672
comp172550_c0_seq54	-0.899679412	-0.766087051	0.508990831	0.469197193	-0.464914879	-0.254731656	-0.457719368	-0.363662665
comp172550_c0_seq59	-0.912100595	-0.436085553	0.540035342	0.525040841	-0.372938028	-0.122470044	-0.294049292	-0.409942115
comp172550_c0_seq67	-0.884681286	-0.405639789	0.502590813	0.47412844	-0.358561575	-0.194053737	-0.477483348	-0.394422028
comp172550_c0_seq86	-1.185446063	-0.45604266	0.546724408	0.512571756	-0.369796441	-0.279492458	-0.442456023	-0.449204377
comp172590_c1_seq4	ND	-1.168387881	0.920481608	0.926277422	ND	ND	ND	-1.06699349
comp172590_c2_seq2	ND	-1.938979073	1.128306124	1.165786557	ND	-1.583970879	-1.709792636	-0.758403436
comp172608_c0_seq1	ND	-1.076478266	0.75315253	0.776742731	-1.438063926	-1.499621322	-1.324413084	ND
comp172676_c0_seq1	0.307924287	0.279603001	1.162704329	1.1378408	0.290094688	0.366250317	0.252837817	0.086700779
comp172694_c0_seq4	-0.642029723	-0.467044677	0.459858195	0.425816886	-0.351509082	-0.250339181	-0.376160938	-0.293099619
comp172728_c0_seq13	-0.493726527	-0.164071826	1.078069998	1.052868926	0.160436255	0.202967456	0.333208549	-0.053026049
comp172728_c0_seq3	-0.423675403	-0.107361204	1.090091115	1.066033526	0.242988118	0.25633317	0.472543013	0.062855982
comp172728_c0_seq9	-0.440142238	-0.642341979	1.950854181	1.89351	-0.03544469	0.03488551	0.177909066	-0.198524907
comp172729_c0_seq3	-1.070156445	-1.033474097	0.939142834	0.900780152	-1.042877238	ND	-1.406347651	ND
comp172760_c0_seq14	0.135581024	0.376383354	1.094801439	1.072909019	0.217217893	0.443725515	0.0035098	0.014020452
comp172761_c0_seq6	-0.637681306	-0.549846436	0.584780543	0.536218695	-0.171069406	-0.232626802	-0.019630003	-0.323513308
comp172800_c1_seq2	0.28667993	0.389338576	1.382554864	1.369288295	0.546531751	0.133453367	0.59762709	0.276588091
comp172800_c1_seq3	0.204965394	0.299639689	1.32922276	1.305844459	0.447844401	0.103740415	0.515037842	0.174637703

comp172823_c0_seq8	-0.349795285	-0.646327616	1.626657277	1.605175894	-0.54782536	-0.776873844	-0.141918447	-0.561966564
comp172840_c0_seq10	-0.245885119	-0.115852569	0.963489655	0.900576635	0.116503873	0.046673951	-0.238848649	-0.475785165
comp172840_c0_seq16	-0.075222477	-0.152755	2.084369573	2.056763373	0.816122609	0.523967789	0.107100257	-0.051360609
comp172840_c0_seq18	-0.242722588	-0.31077559	2.018847083	2.006028669	0.718413334	0.44870348	0.012680764	-0.177666786
comp172840_c0_seq19	-0.338287073	-0.142546806	2.003804363	1.991940706	0.717281773	0.467733894	-0.021265766	-0.177829554
comp172840_c0_seq22	0.674210746	0.685500768	2.118835603	2.095802358	0.966484624	0.803992728	0.596332626	0.32876248
comp172840_c0_seq8	-0.078060691	-0.018090999	1.073308061	1.020468976	0.315087071	0.05632836	-0.310042645	-0.373376702
comp172869_c0_seq5	-0.836205013	-0.924461402	0.778519713	0.820976552	ND	-1.238459988	-1.239343009	-1.066105059
comp172869_c1_seq1	-1.122383954	-1.210640343	0.563835189	0.528637302	ND	-1.45769214	ND	ND
comp172872_c1_seq6	-0.423055916	-0.511312305	0.442259996	0.379233015	-0.872897964	-1.235485357	-0.884185859	-0.53485665
comp172895_c1_seq5	ND	-0.681349235	0.043908274	0.078131796	ND	ND	-0.519109587	-1.124022888
comp172930_c0_seq5	0.400717171	0.522300625	1.23572937	1.197553006	0.328611746	0.598047568	0.438106628	0.314470541
comp172975_c0_seq13	0.909201071	1.048622975	2.334201665	2.274818885	0.529646556	0.953451543	0.612263164	0.324174126
comp172977_c1_seq13	-0.278212175	-0.310951236	0.687539107	0.714633148	-0.690265663	-0.063848439	-0.224432302	-0.653254344
comp172996_c1_seq11	-1.280388413	-0.404856974	0.416554595	0.395938709	-0.629859916	-0.273273917	-0.282125868	-0.623797734
comp172996_c1_seq16	ND	ND	0.756981261	0.726949215	ND	ND	-0.874222462	-0.700984513
comp173008_c0_seq1	-0.981838689	-0.592973823	0.892370936	0.902460779	-0.52859075	-1.016116879	ND	-1.445821942
comp173008_c0_seq6	-0.728244715	-0.491990012	0.8310204	0.815695233	-0.223844253	-0.762522904	ND	-1.669349221
comp173008_c0_seq7	-1.110226181	-0.420331319	0.803236744	0.765529514	-0.38397697	-0.58023294	ND	ND
comp173015_c2_seq2	-1.130362644	-0.373520993	1.184245429	1.183416444	0.219135857	-1.164640834	0.124510757	0.462558955
comp173030_c0_seq24	-0.542361701	-0.232678081	0.628947626	0.619303844	-0.25184106	-0.061060385	-0.615311473	-0.529223699
comp173030_c0_seq25	-0.416298645	-0.537555294	0.761581072	0.72115885	-0.120989703	-0.109118182	-0.331849953	-0.392695209
comp173042_c0_seq12	-0.502734351	-0.183505413	0.543636239	0.480351135	-0.350516408	-0.537012541	-0.617076808	-0.744868854
comp173173_c0_seq2	-0.360563468	-0.361669681	1.257198294	1.209342043	-0.986496775	-0.747024176	-0.21963342	-1.301667975
comp173190_c0_seq10	-0.012649041	0.244328228	0.986753762	0.946726069	-0.295354673	-0.008769529	0.006286651	-0.528339117
comp173190_c0_seq7	-0.03295457	0.142030476	0.917327757	0.930995905	-0.174588038	0.068429842	-0.040087057	-0.468909099
comp173196_c0_seq8	ND	ND	0.157993159	0.223374664	-0.435129492	ND	ND	-0.574209433
comp173249_c0_seq1	ND	ND	0.588437782	0.569034162	ND	ND	ND	-0.53373589
comp173266_c0_seq4	-0.497736661	-0.006209453	0.957490353	0.916712589	-0.324329419	-0.452833605	0.266442678	0.046880258
comp173275_c0_seq11	ND	-1.759361451	1.585145957	1.56949349	-1.643825855	-1.404353256	-1.053053759	-0.958997055
comp173289_c0_seq13	ND	ND	0.55488456	0.587586909	-1.013878746	-0.097712537	ND	ND

comp173306_c0_seq1	ND	ND	0.422565688	0.369639034	-0.254103016	-1.093811662	ND	-0.444335479
comp173320_c0_seq4	-1.284103529	-0.770299927	1.195818712	1.153432541	-1.557854318	ND	ND	ND
comp173320_c2_seq1	-0.828845862	-0.117231751	1.97856367	1.953086189	0.339762497	0.740603099	-1.023707916	-0.725531229
comp173320_c2_seq3	-1.307156077	-0.918291211	0.979990607	1.035044939	-1.45596813	-1.517525526	-1.643347283	ND
comp173320_c2_seq4	-0.891433703	-0.979690092	2.192604794	2.208351111	-0.973298966	-1.034856363	-0.558618128	-0.98744017
comp173320_c2_seq6	-0.97905983	-0.487532622	0.395133933	0.425289093	-0.446630645	-0.369885344	-0.361008527	-0.710649323
comp173381_c0_seq11	-1.536861485	-1.023057882	1.550542721	1.544987039	ND	ND	-1.696961432	-1.523723482
comp173384_c3_seq11	ND	-0.717108024	0.464262359	0.499290876	ND	-0.839221084	ND	-0.791804892
comp173429_c0_seq4	ND	-1.128766624	0.602956927	0.564753531	-1.013231029	ND	ND	-1.027372233
comp173440_c2_seq5	0.604778187	0.890193233	1.642917514	1.618347477	0.602768018	0.602347365	0.995438165	0.813996209
comp173441_c2_seq50	ND	ND	0.257848745	0.229490284	ND	-0.677657912	ND	-0.755180457
comp173443_c0_seq7	0.096945177	0.096576306	1.098663821	1.06493563	0.128264361	0.234680334	0.053589488	-0.061968102
comp173449_c2_seq5	ND	ND	0.062339044	0.055169881	ND	ND	ND	ND
comp173456_c1_seq14	-0.99654958	-0.142797916	0.932707612	0.955501672	ND	-0.678645252	-0.503437013	-0.983411577
comp173456_c1_seq5	-1.021067561	-0.244022524	0.861857296	0.871610838	-1.470909609	-0.578224496	ND	ND
comp173456_c2_seq1	ND	ND	0.324979379	0.317810216	ND	ND	ND	ND
comp173493_c1_seq13	-0.649004337	-0.574533428	0.743525174	0.753015924	-0.62172513	-0.683282526	-0.403338937	-0.563315667
comp173493_c1_seq8	-0.538129413	-0.542064916	0.711655564	0.653995409	-0.753888255	-0.542444379	-0.288054895	-0.716876937
comp173522_c3_seq13	ND	ND	0.036821957	0.061837478	-1.355850089	-1.417407486	-1.117260511	-0.642992566
comp173522_c3_seq14	ND	ND	0.187619073	0.146766797	-1.491215692	-1.376681829	-0.900443595	-0.484167597
comp173522_c3_seq2	-1.707754041	-1.494980434	0.163511204	0.128903793	-1.379444838	-1.742032231	-1.089702737	-0.740373529
comp173522_c3_seq4	-1.525977391	-1.438142521	0.132213028	0.117744627	ND	ND	-0.987107334	-0.583420463
comp173556_c0_seq5	-0.50802922	-0.305474779	0.754738846	0.68561484	-0.065000447	-0.272685879	-0.155469587	-0.438163593
comp173559_c3_seq13	-0.832334005	-0.221620389	1.319214868	1.271714217	-0.650152838	-0.16764219	0.065557995	-0.132815125
comp173562_c0_seq7	0.044160226	0.433025092	1.649556175	1.616000236	0.663133908	0.82967421	0.639791352	0.583442361
comp173598_c2_seq1	ND	-0.720993112	1.460820202	1.398495774	ND	ND	-1.093866667	-0.443507462
comp173614_c0_seq3	-0.708769598	-0.697323074	0.852510808	0.8304976	-0.681490392	-0.449079647	-0.627837479	-0.724595292
comp173677_c1_seq6	-0.598944929	-0.622260511	1.073937613	1.017586542	-0.299599423	-0.305040877	-0.098118226	-0.142670169
comp173752_c3_seq2	-0.636696883	-0.369565614	1.219539371	1.165251292	-0.6393809	-0.73312298	-0.256884746	-0.457227459
comp173752_c3_seq3	-0.108501253	0.063929112	1.522220461	1.494421297	-0.220401223	-0.142779443	-0.126494439	-0.215657083
comp173785_c0_seq3	0.025896723	-0.751569833	1.229094202	1.263914224	-0.988216756	-1.049774152	0.014735789	-0.490474599

comp173828_c1_seq1	ND		-0.630663445	0.08582014	0.136642924	-0.913067858	-0.798533996	ND		-0.751117803
comp173930_c0_seq7		-0.8149243	-0.928004272	0.699704085	0.729015648	-0.681189762	-0.706534986		-0.514293408	-0.594660804
comp173983_c0_seq2	ND		-0.95202668	1.099054248	1.073557704	-1.13752108	-0.721957222	ND		-0.373511034
comp174001_c1_seq1	ND	ND		1.218189408	1.252086516	ND	ND	ND		ND
comp174071_c1_seq20	ND		-0.788058287	0.231389793	0.204476572	-0.973552687	-0.938200071		-1.461961837	-1.112632628
comp174080_c0_seq19	ND		-0.791242538	0.467087631	0.425156362	ND	-0.640354326		-0.686994837	ND
comp174080_c0_seq7		-1.162848398	-0.406006747	0.631004623	0.567354104	-1.135569192	-0.720005333		-0.544797095	-0.672589141
comp174114_c0_seq8		0.780904326	0.679846752	1.772105573	1.737586105	0.762626224	0.718717533		0.920932413	0.605149884
comp174165_c1_seq10		-0.702473102	-0.53109218	0.783556352	0.74600456	-0.675193895	-0.778143977		0.137426951	-0.500278863
comp174165_c1_seq5		-1.123456287	-1.211712675	0.26173286	0.240775413	-1.397207076	ND		-1.283556234	-1.110318284
comp174168_c0_seq2		-1.709285454	-2.098571839	0.719756977	0.684722636	ND	-2.04459364	ND		ND
comp174176_c0_seq5		-0.565974074	-0.478139204	0.600371833	0.607925928	-0.362603609	-0.475313528		-1.203195276	-1.330987322
comp174183_c0_seq14	ND		-0.70063183	0.42602622	0.475338413	ND	-1.345623635	ND		-0.520056193
comp174209_c0_seq11		-0.161215096	-0.182524695	1.300887435	1.307885358	-0.707967157	-0.827516501		0.585379068	0.046899509
comp174209_c0_seq5		-0.657035789	-0.13495966	1.243237135	1.241140083	-0.743699934	-1.02710608		0.452736278	0.171577787
comp174219_c0_seq8	ND	ND		0.611246074	0.621805678	ND	-0.285342518	ND		ND
comp174305_c0_seq8		-1.407560031	ND	0.188482482	0.16427998	-1.380280824	-1.441838221	ND		ND
comp174354_c0_seq1		0.111666127	0.572949856	1.382285083	1.342110158	-0.043618392	-0.064138937		-0.373230538	-0.824328974
comp174354_c0_seq4		0.143047367	0.617189438	1.415960321	1.370548552	0.03234498	-0.119117528		-0.466788034	-0.957757983
comp174354_c0_seq6		0.218082073	0.656455027	1.432821122	1.373421591	0.02129107	-0.029270942		-0.456122695	-0.718613315
comp174362_c1_seq1	ND		-1.519649029	0.497864552	0.534899051	-1.404113433	ND	ND		ND
comp174362_c1_seq3		-1.419639796	ND	0.501792058	0.486653965	-0.915239335	-1.453917986		-1.278709748	-0.929380539
comp174362_c1_seq7	ND		-1.557481509	0.609471136	0.585488474	-0.964824659	-1.202473314		-1.328295071	-1.456087117
comp174362_c2_seq1	ND	ND		0.291084509	0.255886623	ND	ND	ND		-0.77993664
comp174384_c1_seq1		-0.585297906	-0.481668768	0.590918756	0.531986678	-1.512261209	-0.494637359		-1.398610367	-1.225372417
comp174384_c1_seq6		-0.810421276	-0.738976822	1.408516867	1.427520525	-1.260263324	-1.321820721		-1.021673746	-1.149465792
comp174399_c0_seq2		-0.028887932	0.243128591	0.957315972	0.937403759	0.163201523	0.266935321		0.07728001	-0.205413996
comp174399_c4_seq2	ND	ND		0.768381906	0.738695675	-2.062101662	-1.424689054	ND		-1.231144826
comp174415_c2_seq5		0.102230341	0.183725033	0.993453676	0.98873125	0.204474309	0.067952151		0.363352691	0.102594055
comp174482_c0_seq13	ND		-1.497760818	0.861469847	0.913614686	-1.382225222	-1.142752623		-1.569604376	-1.095336431
comp174482_c0_seq17	ND	ND		0.699231914	0.742268066	ND	ND		-1.65053737	ND

comp174482_c0_seq2	ND	-1.829031099	0.824109821	0.8833744	ND	-1.076082895	-1.599844661	-1.125576716
comp174482_c0_seq21	ND	-0.860370851	0.900316396	0.929599503	ND	-1.651490692	-1.175252458	-0.700984513
comp174482_c0_seq29	ND	-1.537462116	0.773256122	0.783499761	-0.877858477	-1.085543909	ND	-1.737097721
comp174482_c0_seq31	ND	-1.917799809	1.259474266	1.257109886	ND	-1.86382161	ND	-1.117435413
comp174482_c0_seq32	ND	ND	0.691740552	0.699678807	-1.515127849	ND	ND	-1.529269054
comp174482_c0_seq35	ND	-1.641745557	1.262560796	1.237411175	ND	-1.411676099	ND	-1.364259907
comp174482_c0_seq8	ND	ND	0.753204525	0.77766821	-1.752767951	-1.513295352	ND	ND
comp174482_c0_seq9	ND	-0.969677539	0.91243187	0.872262448	-1.456201936	ND	-0.643581089	-1.169313144
comp174500_c0_seq16	-0.688651697	-1.378968077	0.452650341	0.381498868	-1.564462477	-0.780921833	-0.848751644	ND
comp174557_c2_seq2	-0.529004827	-0.395412466	0.546010945	0.519956438	-0.735808826	-0.43834428	-0.14503673	-0.272828776
comp174560_c3_seq1	-0.831435774	-0.919692162	0.44071386	0.421645474	-0.67921783	-0.342835218	-0.866596984	-0.99438903
comp174583_c3_seq4	0.397556088	0.659379092	1.344002215	1.301395211	0.29355638	0.551778415	0.443930029	0.162909607
comp174583_c3_seq5	-1.075671051	-1.16392744	0.578885083	0.560626949	-1.650451836	-0.632827986	-0.758649743	-1.062533049
comp174606_c2_seq11	ND	ND	0.92396932	0.872596495	ND	ND	ND	ND
comp174606_c2_seq14	-1.974103277	-0.506057165	1.492973009	1.502127653	-0.624604776	-0.42859787	ND	-1.006722765
comp174606_c2_seq7	ND	-0.557822377	1.374816017	1.383441122	-0.769645716	-0.516809155	ND	-1.084816916
comp174639_c0_seq5	1.971250006	1.911723324	2.948552374	2.93849999	2.024651623	2.058395861	1.355587147	1.242092369
comp174639_c0_seq7	2.024422929	1.95735245	3.02146107	3.003568721	2.077876117	2.122642904	1.41877074	1.313423849
comp174673_c0_seq2	0.717107187	0.628850798	1.412497293	1.4514096	0.410356138	0.848196391	0.567472673	0.117461333
comp174677_c0_seq3	-0.086785977	0.250926367	0.939381228	0.990204012	0.195765735	0.165242572	-0.008003835	-0.295496724
comp174680_c0_seq2	-0.68838664	-0.450058929	0.658115715	0.66335581	-0.340772283	-0.684876269	-0.486186935	-0.892732582
comp174680_c0_seq4	-0.685460296	-0.333189232	0.701370798	0.735594321	-0.460691686	-0.615003135	-0.631680423	-0.713714979
comp174680_c0_seq7	-0.582109468	-0.396658988	0.677257332	0.678844403	-0.375222429	-0.595703059	-0.622599512	-0.750391558
comp174680_c0_seq8	-0.613676374	-0.400902767	0.687143414	0.71858612	-0.396065469	-0.596802042	-0.556292377	-0.787625015
comp174694_c0_seq1	ND	-1.1075125	1.514822012	1.517987207	-1.058923694	-0.898632341	-1.246302848	-0.319737232
comp174707_c0_seq2	-0.556858113	-0.946144498	0.226271043	0.161109933	ND	-0.892166299	ND	ND
comp174712_c0_seq3	ND	ND	0.880153247	0.834525833	-1.044488722	ND	ND	ND
comp174720_c1_seq5	-1.698450395	-0.640578748	0.327716809	0.373076698	-0.415898683	-0.954577335	-0.712422307	-1.685312393
comp174721_c0_seq4	-0.382529542	-0.545419549	0.71011772	0.679934194	-0.253792694	-0.353138652	-0.140141852	0.092217549
comp174727_c1_seq1	-1.061125917	-1.994480346	0.923205219	0.938848888	-1.87894475	-1.940502147	ND	-0.746957919
comp174730_c0_seq8	-1.207430531	-0.596716915	0.119766669	0.14256073	-0.70303007	-0.940678725	ND	ND

comp174780_c0_seq7	-0.326705201	-0.113931594	1.144398575	1.164212902	-0.424364731	-0.485922127	-0.009683893	ND
comp174815_c1_seq2	ND	ND	1.783060316	1.801856716	ND	ND	ND	ND
comp174832_c0_seq7	ND	-0.522799909	0.731802387	0.767385205	ND	-0.042852978	-0.469704731	ND
comp174870_c2_seq2	-1.699872914	-1.186069311	1.327533363	1.289604837	-1.371563711	-1.433121108	-1.558942865	ND
comp174870_c2_seq20	-0.688651697	-1.077938081	1.491330372	1.443094939	-1.263432481	ND	ND	ND
comp174870_c2_seq5	ND	ND	0.742030047	0.724876663	ND	ND	ND	ND
comp174870_c2_seq7	ND	-1.314684936	1.283020221	1.230772683	ND	ND	ND	ND
comp174878_c0_seq13	ND	-0.639818162	0.532597378	0.525428215	ND	ND	ND	-0.71451503
comp174882_c1_seq1	-0.487050493	-0.207330097	1.260259694	1.230917553	-0.459771287	-0.185536581	-0.010328343	-1.252063741
comp174894_c0_seq11	ND	ND	0.797762569	0.829289043	ND	-1.562158993	ND	-1.5147428
comp174894_c0_seq16	ND	ND	0.850455409	0.807419346	-1.819208393	-1.403644534	ND	-0.988251557
comp174894_c0_seq2	ND	ND	0.712290199	0.661215551	ND	ND	ND	ND
comp174894_c0_seq5	ND	ND	0.840588512	0.852210394	ND	-1.843106173	-1.366867939	ND
comp174894_c0_seq6	ND	ND	0.812342928	0.758661636	ND	ND	ND	ND
comp174905_c0_seq2	-0.783878196	-0.872134584	0.70330049	0.671456246	-0.572074563	-0.061833573	-1.396275814	-0.887245762
comp174905_c0_seq22	-1.067321879	-0.905700794	0.693530882	0.692665089	-0.313043944	-0.002764134	-1.278574348	-1.054183876
comp174905_c0_seq27	-0.984215442	-1.113864516	0.676599121	0.661509474	-0.466850004	-0.055564944	-1.282618088	-1.167372085
comp174915_c0_seq27	-1.418826764	-1.067750459	0.813394923	0.788496993	-0.380823692	-0.072893713	-1.578926711	-1.530627499
comp174915_c0_seq29	-1.536516834	-1.323743227	0.792743527	0.824903889	-0.454879965	-0.13943126	-1.87270804	-1.523378832
comp174915_c0_seq34	-0.930299557	-1.097737192	0.798954218	0.751006504	-0.425899096	-0.052532917	-1.3914295	-1.394282809
comp174915_c0_seq6	-0.811444637	-0.825067408	0.937826251	0.949323857	-0.49692372	-0.020459032	-1.573604576	-1.701396622
comp174926_c0_seq33	0.338406536	0.467741074	1.301143525	1.328197307	0.55908186	0.289770196	0.627477576	0.303032112
comp174926_c0_seq4	0.477311768	0.516683255	1.420970969	1.45764456	0.603116468	0.318993073	0.690169542	0.426638695
comp174928_c0_seq23	0.054494877	0.155994072	1.157571017	1.102264662	0.364579259	0.20611185	0.32773726	0.096404622
comp174933_c0_seq26	ND	-0.230404283	1.277803359	1.325482864	0.061222571	ND	-0.779369096	ND
comp174933_c0_seq8	1.296386414	1.49172638	2.697458201	2.653487928	1.799674013	1.836528321	1.124456703	1.074129322
comp174970_c0_seq10	-0.73948024	-1.128766624	0.043648916	0.036479754	ND	-1.074788425	-0.899580187	-1.027372233
comp174975_c0_seq1	ND	ND	0.454305169	0.47516473	ND	ND	ND	ND
comp175009_c1_seq12	-0.673224314	-0.615352667	0.800100922	0.792931759	-1.344915112	ND	ND	-0.756996325
comp175009_c1_seq2	-0.55182813	-0.40120243	0.984628692	0.97745953	ND	-1.762197579	ND	ND
comp175020_c0_seq5	0.017963499	0.144550959	1.654790867	1.621292766	-0.875576048	-0.183805778	0.175926887	-0.162718524

comp175057_c0_seq7	-1.165772951	-0.555059336	0.82820957	0.771555044	-0.059312499	-0.086107789	-0.179744863	-0.249544962
comp175089_c0_seq14	0.758845389	0.753720037	1.587154516	1.556784089	0.763164213	0.699319044	0.936420246	0.611480231
comp175107_c1_seq1	ND	-0.582358765	0.243269289	0.184947604	-0.864763179	-0.44919932	-1.052142332	-0.878904383
comp175115_c1_seq2	-0.900714111	-0.909789253	0.622777735	0.681425857	-0.970344917	-0.730872318	-0.458754066	-0.887576108
comp175177_c0_seq5	-0.129211178	-0.781738997	1.275283125	1.28204974	ND	ND	-0.427613823	-0.37931461
comp175197_c0_seq10	-0.607132386	-0.459299586	1.181391802	1.206364768	-0.211876394	0.035283034	-0.35040698	-0.372145634
comp175197_c0_seq16	ND	ND	0.380233987	0.390793591	-1.153767213	ND	ND	ND
comp175197_c0_seq17	-0.615742807	-0.494049669	1.180679167	1.194075453	-0.259038233	-0.014102738	-0.474812758	-0.331957438
comp175197_c0_seq19	-0.889248246	-0.676474639	1.177420174	1.186597356	-0.181681248	-0.011948338	-0.373859284	-0.369534009
comp175197_c0_seq31	-0.715342444	-0.716448657	1.19000259	1.229136857	-0.179907749	-0.080613853	-0.306806155	-0.470810374
comp175208_c0_seq3	ND	ND	0.204359244	0.197190081	ND	ND	ND	ND
comp175244_c0_seq1	-0.994608676	-1.003683819	1.060362086	1.039029892	-0.387545873	-0.125796879	-0.707550592	-0.805379415
comp175244_c0_seq13	-0.82476795	-0.629027682	1.127153226	1.107927527	-0.195428752	-0.0139481	-0.593661271	-0.811629947
comp175244_c0_seq14	-0.859661144	-0.771826274	1.084086584	1.117695973	-0.252598341	-0.081025977	-0.376308415	-0.805130456
comp175244_c0_seq15	-0.720602098	-0.734224868	1.182689531	1.203420431	-0.064933961	0.141370275	-0.482762036	-0.610554082
comp175244_c0_seq3	-0.806241789	-1.029196752	1.110426275	1.112211955	-0.176902592	-0.034340005	-0.562649399	-0.82306701
comp175244_c0_seq7	-0.699778224	-0.884944626	1.022037405	1.008993638	-0.526370982	-0.219951593	-0.956788184	-0.632282559
comp175265_c0_seq37	-0.246107292	0.089238319	1.594836753	1.581424629	0.010508686	-0.194955286	0.601280783	-0.364248204
comp175299_c0_seq2	-0.471592081	-0.459178308	1.007665447	1.016358426	-0.52728711	-0.405200109	-0.650997184	-0.865939406
comp175299_c0_seq6	-0.409559855	-0.617002652	1.230901797	1.219489668	-0.666277305	-0.563024453	-0.552626463	-0.840119352
comp175316_c0_seq1	-1.112794892	-1.979202531	0.789810104	0.75424557	-1.56263694	-1.226254328	-1.750016094	-1.576778145
comp175356_c1_seq7	-1.457969534	-1.546225923	0.667582302	0.715930467	-1.430690328	-0.79327772	-1.317039486	-1.143801536
comp175418_c1_seq7	-1.431129032	ND	1.458785771	1.447778929	-1.704879821	-0.812194708	-1.290198983	-0.940869774
comp175421_c1_seq11	-0.973131097	-0.526274284	1.91950429	1.906021537	ND	-1.551477331	ND	ND
comp175421_c1_seq12	-1.271340284	-0.803294172	1.71658691	1.676346163	ND	-1.402528487	ND	ND
comp175421_c1_seq15	-1.232511496	-0.524887867	1.917274046	1.889434514	ND	-1.391728423	ND	ND
comp175421_c1_seq16	-1.262099627	-0.770572419	1.714293302	1.682210506	-1.933790425	-1.995347821	ND	ND
comp175421_c1_seq3	-0.926453433	-0.575377128	1.512294306	1.489242	-1.802264213	-1.86382161	ND	ND
comp175421_c1_seq6	-0.923196156	-0.732698944	1.688914954	1.647077573	-1.594886954	-1.65644435	ND	ND
comp175528_c1_seq4	-0.60537054	-1.061603714	1.570078632	1.506620113	-0.344008127	-0.254297848	-0.610568527	-0.437330577
comp175543_c0_seq5	-0.222562259	-0.419963117	2.014352243	1.954223431	0.682983351	0.368700639	-0.558753465	-0.686545511

comp175570_c0_seq3	-0.538946524	-0.076295444	1.113577344	1.108034755	-0.050936479	-0.043167384	-0.507160945	0.03183233
comp175570_c0_seq5	ND	-0.092272533	1.150180873	1.146692195	-1.374676947	-0.959113088	-0.5620561	0.129695789
comp175588_c0_seq3	ND	ND	1.184950307	1.1435829	-1.621085991	-0.983673384	-1.50743515	-0.790129156
comp175588_c0_seq5	-1.754138671	-1.541365064	1.279105397	1.223218446	-1.24973821	-1.135204347	-1.613208623	-0.928087312
comp175617_c1_seq7	-0.810372339	-0.694508745	0.993946116	0.980528004	-0.159843842	-0.128647185	-0.113139789	-0.320113082
comp175668_c0_seq12	ND	ND	0.789665995	0.79546181	ND	ND	ND	ND
comp175685_c0_seq2	ND	ND	0.311495297	0.274362911	ND	ND	ND	-1.032527124
comp175719_c0_seq1	ND	ND	0.394536964	0.387367801	ND	ND	ND	ND
comp175753_c0_seq14	ND	-1.474125722	0.145447849	0.101897889	-1.756530135	-1.818087532	-1.642879294	-1.77067134
comp175764_c0_seq11	-0.802258604	-1.077601636	0.347293509	0.342453009	-0.774979397	-1.096174104	-0.457208573	-0.767931302
comp175776_c0_seq9	-0.776728297	-0.864984686	1.576797842	1.551747822	-1.050479086	-0.935945223	-1.23785824	-0.086896685
comp175941_c0_seq1	1.252962405	1.343520134	2.086940487	2.057335057	1.131922931	1.017287091	1.084589932	0.797097043
comp176003_c0_seq1	ND	ND	0.94633347	0.979829734	ND	ND	ND	ND
comp176013_c0_seq1	ND	ND	0.670456239	0.719768432	-0.194538179	ND	ND	-1.053777424
comp176031_c0_seq1	-0.366723777	-0.93210142	0.698951969	0.710266212	ND	ND	ND	ND
comp176071_c0_seq1	ND	ND	0.835064417	0.816614243	ND	ND	ND	ND
comp176083_c0_seq1	-0.562740296	-0.474905425	0.940548164	0.878331435	-0.35936983	-0.898048481	ND	-0.850632289
comp176354_c0_seq1	-1.060772545	-0.370877683	0.905626455	0.94563637	ND	-1.095050734	ND	-0.746604546
comp176383_c0_seq1	ND	ND	0.32202139	0.288523289	ND	ND	ND	ND
comp176394_c0_seq1	ND	ND	0.939440994	0.982681335	ND	ND	ND	ND
comp176401_c0_seq1	ND	ND	0.536734706	0.519581323	ND	ND	ND	ND
comp176496_c0_seq1	-0.54122629	0.007339419	0.630083037	0.592245054	-0.322061557	-0.131806981	-0.877417496	-0.783360793
comp176528_c0_seq1	ND	ND	0.43776059	0.384015285	ND	ND	ND	ND
comp176585_c0_seq1	ND	ND	0.844700506	0.778825683	ND	ND	ND	ND
comp176628_c0_seq1	-1.114255935	-0.600452332	0.598292147	0.603712111	ND	-0.303436085	ND	ND
comp176643_c0_seq1	ND	ND	0.60345583	0.612677083	ND	ND	ND	ND
comp176883_c0_seq1	ND	ND	0.806765885	0.810320588	ND	-1.010641461	ND	ND
comp176960_c0_seq1	-1.028683028	-0.690970685	0.446116893	0.513193759	-0.478525076	-0.363991214	-0.364874234	-0.793696276
comp177100_c0_seq1	ND	ND	0.419474611	0.46345797	ND	-0.999992726	ND	ND
comp177104_c0_seq1	ND	ND	0.75923604	0.724914631	-0.913067858	ND	ND	ND
comp177105_c0_seq1	ND	ND	0.58921539	0.535049665	ND	ND	ND	ND

comp177186_c0_seq1	ND	ND	0.486578044	0.534631672	-1.13703393	ND	ND	-1.151175134
comp177284_c0_seq1	ND	ND	1.04423859	0.99856243	ND	ND	ND	ND
comp177362_c0_seq1	ND	ND	0.906420325	0.884143744	ND	ND	ND	ND
comp177375_c0_seq1	ND	ND	0.3849495	0.412542444	ND	ND	ND	ND
comp177518_c0_seq1	ND	-1.417969413	0.382835058	0.321308233	ND	ND	ND	ND
comp177555_c0_seq1	ND	ND	0.711361227	0.662799379	ND	ND	ND	ND
comp177681_c0_seq1	ND	-0.734055585	0.464688894	0.457519731	-0.61851999	-0.680077386	-0.504869148	-0.632661194
comp177992_c0_seq1	ND	ND	0.4274485	0.438762743	ND	ND	ND	ND
comp178070_c0_seq1	ND	ND	0.672120603	0.626322038	-0.676645958	ND	-0.739086375	ND
comp178133_c0_seq1	ND	ND	0.65036377	0.68739827	ND	ND	ND	ND
comp178295_c0_seq1	-1.166743442	-0.777878576	0.128269075	0.153284595	ND	-0.899991636	ND	ND
comp178399_c0_seq1	-0.792182474	ND	0.190519036	0.190903011	ND	ND	ND	ND
comp178466_c0_seq1	ND	ND	0.698586939	0.740404237	ND	ND	ND	ND
comp178507_c0_seq1	-1.309953475	-1.222118604	0.587119033	0.638463493	-0.805553013	-1.168140406	-0.691902171	-0.819694218
comp178560_c0_seq1	ND	ND	0.737132018	0.678810333	ND	ND	ND	ND
comp178591_c0_seq1	ND	ND	0.39759441	0.420388471	-0.504383575	ND	-0.788672742	ND
comp178603_c0_seq1	ND	ND	0.629888184	0.606924754	ND	ND	ND	ND
comp178701_c0_seq1	ND	ND	0.748054467	0.783919937	ND	ND	ND	ND
comp178704_c0_seq1	-1.081313247	ND	0.562153916	0.539744786	ND	ND	ND	ND
comp178728_c0_seq1	ND	ND	0.595908238	0.604533343	ND	-1.05080288	ND	ND
comp178857_c0_seq1	ND	ND	0.098871707	0.033710598	ND	ND	ND	-0.972149442
comp178916_c0_seq1	ND	ND	0.524401589	0.49375133	ND	ND	ND	ND
comp179104_c0_seq1	ND	ND	0.556325246	0.498003561	ND	ND	ND	ND
comp179128_c0_seq1	-1.127188736	ND	0.572394368	0.538072959	-0.25481149	-0.559406935	-0.685228692	ND
comp179262_c0_seq1	-0.235248556	ND	0.359272783	0.409142121	ND	ND	-0.737771184	ND
comp179364_c0_seq1	ND	ND	0.343384442	0.398363186	ND	ND	-0.810698027	ND
comp179718_c0_seq1	-0.670801466	-0.935149113	0.355365739	0.406188523	-1.120643514	-0.705079655	ND	-0.657663463
comp180007_c0_seq1	ND	ND	0.103852049	0.169233553	ND	ND	ND	ND
comp180254_c0_seq1	ND	ND	0.115931814	0.108762652	ND	-0.839778229	-0.664569991	-0.792362037
comp180524_c0_seq1	ND	ND	0.140558929	0.174782452	ND	ND	ND	ND
comp180603_c0_seq1	ND	ND	0.678736752	0.671567589	ND	ND	ND	ND

comp180659_c0_seq1	ND	-0.67498998	0.469396836	0.442483615	ND	-0.621011781	ND	ND
comp180717_c0_seq1	-0.851925162	-0.639151555	0.505235262	0.468102875	ND	ND	ND	-0.537757164
comp180921_c0_seq1	-0.738181899	-1.127468284	0.503585106	0.532628116	-1.011932688	-0.772460089	ND	-0.424013901
comp180953_c0_seq1	ND	-1.003395538	0.396263783	0.462880835	-0.489919934	-0.949417339	ND	-0.299941156
comp181080_c0_seq1	ND	ND	0.462914709	0.407440867	ND	ND	ND	ND
comp181102_c0_seq1	ND	-1.204694713	0.479604189	0.43767292	ND	ND	ND	ND
comp181186_c0_seq1	-0.554879547	ND	0.279402131	0.272232968	-0.828630336	-0.413066478	ND	-0.842771541
comp181429_c0_seq1	ND	ND	0.302425834	0.260494565	ND	-0.725834877	ND	ND
comp181709_c0_seq1	-1.349886132	ND	0.262546797	0.271171901	ND	ND	-1.208956083	ND
comp181871_c0_seq1	ND	ND	-0.009945487	0.034037873	ND	ND	ND	ND
comp182114_c0_seq1	ND	ND	0.469601644	0.478226748	ND	ND	ND	ND
comp182157_c0_seq1	ND	ND	0.39912301	0.440258527	ND	ND	ND	ND
comp182374_c0_seq1	ND	ND	0.362689597	0.316011893	ND	ND	ND	ND
comp182379_c0_seq1	ND	ND	0.311721433	0.329375854	ND	ND	ND	ND
comp182771_c0_seq1	ND	ND	0.132303875	0.155097936	ND	ND	ND	ND
comp182787_c0_seq1	ND	ND	0.461483754	0.477795687	ND	ND	ND	ND
comp182846_c0_seq1	-0.990409764	-0.601544898	0.36675066	0.329618274	ND	ND	-1.150509711	ND
comp182858_c0_seq1	ND	-0.917589037	0.351736516	0.344567353	ND	ND	ND	-1.117224642
comp183049_c0_seq1	ND	ND	0.547504424	0.521851856	ND	ND	ND	ND
comp183071_c0_seq1	-1.489055052	-1.57731144	0.236082157	0.241147451	ND	-1.523333241	ND	-1.475917049
comp183200_c0_seq1	ND	ND	0.44958453	0.502413297	ND	ND	ND	ND
comp183289_c0_seq1	ND	ND	0.599965064	0.615072296	ND	ND	ND	ND
comp183501_c0_seq1	ND	ND	0.269245859	0.220684011	ND	-0.987494181	ND	ND
comp183579_c0_seq1	ND	ND	0.161964349	0.103642664	ND	ND	-0.832417276	ND
comp183683_c0_seq1	-0.945217708	-1.033474097	0.332761469	0.359016062	-1.218968497	-0.678465902	ND	-0.755988447
comp184055_c0_seq1	ND	ND	0.202055289	0.16012402	-1.065678021	ND	ND	-1.079819226
comp184314_c0_seq1	-0.555672056	-0.740838457	0.193598833	0.231011803	-0.829422845	-1.112828991	-1.414742007	-0.843564049
comp184322_c0_seq1	ND	ND	0.253588137	0.220090036	-1.130650742	ND	ND	ND
comp184332_c0_seq1	ND	ND	0.423521231	0.448536752	ND	-0.604739479	ND	ND
comp184345_c0_seq1	ND	ND	0.231034832	0.178108179	ND	ND	ND	ND
comp184400_c0_seq1	-1.213565974	-0.699762371	0.222775696	0.164454011	-0.709165512	-1.247844164	ND	ND

comp184709_c0_seq1	ND	ND	0.580804113	0.573634951	ND	ND	ND	ND
comp184889_c0_seq1	ND	ND	0.135724432	0.12855527	ND	ND	ND	ND
comp184935_c0_seq1	ND	-1.046201586	0.264516652	0.215954805	-0.328605999	-0.691193391	-0.817015149	-0.643777199
comp185586_c0_seq1	ND	-0.652939839	0.190416981	0.121099912	-0.537404244	-1.201021632	-0.724783398	-0.551545448
comp185706_c0_seq1	ND	ND	0.312216517	0.379680973	ND	ND	ND	ND
comp186926_c0_seq1	-0.743352133	-0.752427275	0.081169708	0.093305701	-0.716072926	-0.698449077	-1.301392089	-1.128154139
comp187049_c0_seq1	ND	ND	0.184365915	0.2351887	ND	ND	ND	ND
comp188082_c0_seq1	-0.985287444	ND	0.15002423	0.142855067	ND	ND	ND	ND
comp188135_c0_seq1	ND	ND	0.310727314	0.285829384	ND	-1.302560049	ND	-0.653083866
comp188323_c0_seq1	ND	ND	0.492074694	0.430547869	-0.716072926	-0.652691586	-1.079543339	-0.304245398
comp188543_c0_seq1	ND	ND	0.285392495	0.22497782	ND	ND	ND	ND
comp188635_c0_seq1	ND	-0.497206163	0.284002751	0.242071482	-0.983730559	-1.045287956	ND	ND
comp188863_c0_seq1	ND	-0.673143226	0.295152332	0.354929959	ND	-0.619165027	-0.921078043	-1.349900085
comp189107_c0_seq1	ND	-1.063114305	0.461483754	0.429491007	ND	ND	ND	-0.961719913
comp189167_c0_seq1	ND	ND	0.233793397	0.238523457	ND	ND	ND	ND
comp189551_c0_seq1	ND	ND	0.49436498	0.449407257	ND	-1.101193616	-0.925985378	-1.053777424
comp189658_c0_seq1	ND	-0.876723089	0.346844974	0.406622601	-1.062217489	-0.646653631	ND	-1.076358693
comp189788_c0_seq1	ND	ND	0.147783004	0.162890236	ND	ND	ND	ND
comp189811_c0_seq1	-0.540771293	-0.930057678	0.485395911	0.478226748	ND	-0.398958224	ND	ND
comp190076_c0_seq1	ND	ND	0.32061379	0.383080555	ND	ND	ND	ND
comp190114_c0_seq1	ND	-1.566564498	0.282544652	0.329060348	ND	ND	ND	-0.687018856
comp1911751_c0_seq1	-1.122920451	-1.21117684	0.400571394	0.362733412	ND	ND	ND	-1.109782449
comp191943_c0_seq1	ND	ND	0.135546406	0.128377244	ND	ND	ND	-0.986627265
comp192160_c0_seq1	-0.864742956	ND	0.161424249	0.154255086	ND	ND	ND	ND
comp192507_c0_seq1	ND	ND	0.250630388	0.310408015	ND	ND	ND	-0.695452024
comp194028_c0_seq1	ND	ND	0.181303897	0.208896841	ND	ND	ND	ND
comp194082_c0_seq1	ND	ND	0.392261975	0.409916396	ND	-1.053534301	ND	ND
comp194397_c0_seq1	ND	ND	0.281389752	0.223068067	ND	-0.888200112	ND	ND
comp194534_c0_seq1	ND	ND	0.494533279	0.502087373	ND	ND	ND	ND
comp194603_c0_seq1	ND	ND	0.171702301	0.123140454	ND	ND	-0.608799504	-0.73659155
comp194936_c0_seq1	ND	ND	0.229794749	0.197802003	ND	ND	ND	ND

comp195001_c0_seq1	ND	-0.533140743	0.134124819	0.081198166	-1.019665139	ND	-0.906014297	-0.556685088
comp195074_c0_seq1	ND	ND	0.250630388	0.243461226	ND	ND	ND	ND
comp195219_c0_seq1	-1.17490621	-1.263162599	0.167530957	0.12932756	-1.448656999	ND	ND	-1.462798203
comp195787_c0_seq1	ND	ND	0.336545017	0.357404578	ND	ND	ND	ND
comp195918_c0_seq1	ND	ND	0.476629917	0.476409614	ND	-1.531109127	ND	-1.00657168
comp195985_c0_seq1	ND	-0.950074791	0.194312025	0.157179639	ND	ND	ND	ND
comp196742_c0_seq1	ND	ND	0.012391223	0.07216885	ND	ND	ND	ND
comp197043_c0_seq1	ND	-0.455998441	0.149119214	0.232126681	ND	-0.481201489	ND	-0.433785296
comp197203_c0_seq1	ND	ND	0.459790596	0.424592709	ND	ND	ND	ND
comp197461_c0_seq1	ND	-1.192553542	0.076772011	0.023845358	ND	-0.837545348	ND	-0.790129156
comp197542_c0_seq1	ND	ND	0.267663728	0.290457788	ND	ND	ND	-1.04639547
comp198170_c0_seq1	-0.640946694	-1.030233078	0.142182462	0.186165822	-0.437576228	-0.675224884	-0.500016645	-0.627808691
comp199524_c0_seq1	ND	ND	0.327388786	0.264103681	-1.043885116	ND	ND	-1.359056316
comp199899_c0_seq1	ND	ND	0.282012754	0.34947721	ND	ND	ND	ND
comp200257_c0_seq1	ND	-1.016182364	0.182562115	0.12103529	-1.201676765	-1.263234161	ND	ND
comp200344_c0_seq1	ND	ND	0.151297527	0.163433519	ND	ND	ND	-1.359056316
comp201028_c0_seq1	ND	ND	0.332248076	0.325078913	ND	ND	ND	ND
comp201667_c0_seq1	ND	ND	0.414574198	0.477442902	ND	ND	ND	ND
comp201730_c0_seq1	ND	ND	0.108096534	0.142320057	ND	ND	ND	ND
comp202092_c0_seq1	ND	ND	0.181303897	0.215527419	ND	ND	ND	ND
comp202276_c0_seq1	ND	-1.128766624	-0.014343031	0.036479754	ND	ND	ND	ND
comp202787_c0_seq1	ND	-0.85778627	0.189690534	0.103340125	-1.04328067	-0.405868062	-0.929629828	ND
comp203281_c0_seq1	ND	-0.705812342	0.216725725	0.209556562	-0.891306743	ND	ND	ND
comp204930_c0_seq1	ND	ND	0.343384442	0.336215279	ND	ND	ND	ND
comp20562_c0_seq1	ND	ND	-0.018643011	0.041134616	ND	-1.012141616	ND	ND
comp206292_c0_seq1	ND	-0.629027682	0.163176616	0.110249963	ND	-1.052170738	ND	-1.004754546
comp207370_c0_seq1	ND	-0.798236159	0.124301908	0.117132746	-0.983730559	-0.74425796	-0.870079717	ND
comp207730_c0_seq1	-0.649801939	-0.738058328	0.207960835	0.264460752	ND	-0.684080129	-0.633810627	-0.636663937
comp209081_c0_seq1	ND	ND	0.175517504	0.168348342	ND	ND	ND	ND
comp209106_c0_seq1	ND	-1.292141639	0.153275173	0.146106011	ND	ND	ND	ND
comp209239_c0_seq1	ND	ND	0.029389469	0.022220306	ND	ND	ND	-1.179934378

comp209722_c0_seq1	ND	ND	0.154675919	0.147506756	ND	ND	ND	ND
comp210735_c0_seq1	ND	ND	0.110307712	0.170085339	ND	ND	ND	-0.8357747
comp210794_c0_seq1	ND	ND	0.11172071	0.074588324	ND	ND	ND	ND
comp211110_c0_seq1	ND	ND	0.161498992	0.186514513	ND	ND	ND	ND
comp211232_c0_seq1	ND	ND	0.234239972	0.189282249	ND	ND	ND	ND
comp211243_c0_seq1	-1.163825439	-0.774960573	0.221363708	0.214194545	-0.835516237	-0.499133625	ND	ND
comp211843_c0_seq1	ND	ND	0.250630388	0.243461226	ND	ND	ND	ND
comp211976_c0_seq1	ND	ND	0.090127228	0.024966118	ND	ND	-0.853101875	ND
comp212072_c0_seq1	ND	ND	-0.003713144	0.030510378	ND	ND	ND	ND
comp212105_c0_seq1	ND	ND	0.194086359	0.186917196	ND	ND	ND	ND
comp212536_c0_seq1	ND	ND	0.21160628	0.153284595	ND	ND	ND	ND
comp212665_c0_seq1	ND	ND	0.207309339	0.200140176	ND	-1.049430701	ND	-1.002014508
comp213505_c0_seq1	ND	ND	0.385095408	0.343164139	ND	ND	ND	ND
comp213538_c0_seq1	ND	-1.123549811	0.291903778	0.342726563	-0.70698422	ND	ND	ND
comp214019_c0_seq1	ND	-0.757536681	0.210758876	0.157832223	-0.545091073	ND	ND	-0.957172286
comp215026_c0_seq1	ND	ND	0.233294826	0.226125663	ND	-0.911471454	ND	ND
comp215728_c0_seq1	ND	ND	0.234239972	0.181313319	ND	ND	ND	ND
comp216291_c0_seq1	ND	ND	0.236929111	0.191971387	ND	ND	-0.405269997	-1.010183297
comp216363_c0_seq1	ND	-1.161229019	0.108096534	0.055169881	ND	ND	ND	-1.059834628
comp216727_c0_seq1	ND	ND	0.069923842	0.129701469	ND	ND	ND	ND
comp217051_c0_seq1	ND	-0.439412388	0.269245859	0.220684011	-0.624906789	-0.510372926	-0.511255947	-0.462956734
comp218857_c0_seq1	-1.255828118	-1.344084506	0.323181056	0.260494565	ND	-0.591136303	-0.813868073	ND
comp219237_c0_seq1	ND	ND	0.078267002	0.071097839	ND	ND	ND	-0.867815411
comp219553_c0_seq1	ND	ND	0.235246449	0.200048563	ND	ND	ND	ND
comp219612_c0_seq1	ND	-0.675603824	0.395354075	0.313551294	-0.435129492	ND	ND	-0.750300692
comp220201_c0_seq1	ND	ND	0.172245283	0.16507612	ND	ND	ND	ND
comp220327_c0_seq1	ND	ND	0.152978625	0.09465694	ND	ND	ND	ND
comp220756_c0_seq1	ND	ND	0.326309241	0.270835398	ND	ND	ND	ND
comp220894_c0_seq1	-0.910791821	-1.300078206	0.224519853	0.263108181	-0.33944457	-0.945070011	ND	-0.897653819
comp222020_c0_seq1	ND	-0.765089819	0.048303778	0.099126563	ND	ND	-0.836933377	ND
comp222293_c0_seq1	ND	ND	0.127212825	0.120043662	-1.067969818	-0.65240596	ND	-0.781081027

comp222585_c0_seq1	ND	ND	0.128484552	0.121315389	ND	ND	ND	-0.99368912
comp222756_c0_seq1	ND	ND	0.00759234	0.000423177	-0.924348869	ND	ND	ND
comp223099_c0_seq1	ND	ND	0.279774118	0.214613008	-1.078135823	-0.838663224	ND	-1.092277027
comp223248_c0_seq1	ND	ND	0.137622512	0.130453349	ND	ND	ND	ND
comp223568_c0_seq1	ND	-0.876723089	-0.005337544	0.038645815	-1.062217489	ND	ND	ND
comp223673_c0_seq1	ND	ND	0.438359955	0.431190792	ND	ND	ND	ND
comp224554_c0_seq1	-0.846892725	-0.935149113	0.147089796	0.139920634	-1.120643514	-1.18220091	-1.006992672	ND
comp225557_c0_seq1	ND	ND	-0.030461277	0.02931635	ND	ND	ND	ND
comp227310_c0_seq1	ND	ND	0.293217832	0.253863986	ND	ND	ND	ND
comp227389_c0_seq1	ND	ND	0.123448887	0.178427631	-1.144284424	ND	-0.553512327	ND
comp230378_c0_seq1	ND	ND	0.33706732	0.36208284	ND	ND	ND	ND
comp230697_c0_seq1	ND	ND	0.09908207	0.149904855	ND	ND	ND	ND
comp230949_c0_seq1	ND	ND	0.359774858	0.398363186	ND	ND	ND	ND
comp231688_c0_seq1	ND	ND	0.055718408	0.00715656	ND	ND	ND	ND
comp232025_c0_seq1	ND	ND	0.171021055	0.129089786	ND	ND	ND	ND
comp232800_c0_seq1	ND	ND	0.316326209	0.286880651	ND	ND	ND	ND
comp233071_c0_seq1	ND	ND	-0.012611046	0.047166581	ND	ND	ND	ND
comp235381_c0_seq1	ND	ND	0.235390422	0.286213206	ND	ND	ND	ND
comp235815_c0_seq1	ND	ND	0.237174406	0.230005243	ND	ND	ND	ND
comp236054_c0_seq1	ND	ND	0.106295725	0.150279085	ND	ND	ND	ND
comp237304_c0_seq1	ND	ND	0.213306065	0.206136903	ND	ND	ND	ND
comp239110_c0_seq1	ND	ND	0.104800734	0.039639625	ND	ND	ND	ND
comp239898_c0_seq1	ND	ND	0.050472336	0.089060664	ND	ND	ND	ND
comp240457_c0_seq1	ND	ND	0.197625861	0.190456698	ND	ND	ND	ND
comp240638_c0_seq1	ND	ND	0.121535692	0.146551213	-1.146197618	-1.207755015	ND	-0.859308827
comp241426_c0_seq1	ND	ND	0.029259148	0.052053209	ND	ND	ND	ND
comp242396_c0_seq1	ND	ND	0.006911093	0.057733878	-0.991976905	ND	ND	-1.006118109
comp242444_c0_seq1	ND	ND	0.478083016	0.440950629	ND	ND	ND	ND
comp243548_c0_seq1	ND	ND	0.392157262	0.417172783	ND	ND	ND	ND
comp243615_c0_seq1	-0.645799197	ND	0.188482482	0.181313319	ND	ND	-0.805899144	ND
comp243716_c0_seq1	ND	ND	0.284101871	0.306895932	ND	ND	ND	ND

comp244082_c0_seq1	ND	ND	0.045467681	-0.007458972	ND	ND	ND	ND
comp244701_c0_seq1	ND	ND	0.164544474	0.111617821	ND	ND	ND	ND
comp246127_c0_seq1	ND	ND	0.167920323	0.180056315	ND	ND	ND	ND
comp246716_c0_seq1	ND	ND	0.352339284	0.312985438	ND	ND	ND	ND
comp246939_c0_seq1	ND	ND	0.160453758	0.095292648	ND	ND	ND	ND
comp247004_c0_seq1	ND	ND	0.130490535	0.123321372	ND	ND	ND	ND
comp247984_c0_seq1	ND	ND	0.125691652	0.067369967	ND	-0.742868216	-0.567659978	ND
comp248263_c0_seq1	ND	ND	0.011014694	0.003845531	ND	ND	ND	ND
comp249521_c0_seq1	ND	ND	0.118004823	0.11083566	ND	ND	ND	ND
comp249977_c0_seq1	ND	ND	0.061377683	0.054208521	ND	ND	ND	ND
comp253523_c0_seq1	ND	ND	0.058148713	0.11792634	ND	ND	ND	ND
comp255331_c0_seq1	ND	ND	0.228429926	0.29381143	ND	ND	-0.853101875	ND
comp255941_c0_seq1	ND	-0.548204489	0.198242319	0.236830647	ND	-0.670317549	ND	-0.622901357
comp256002_c0_seq1	ND	ND	0.107962885	0.146551213	ND	ND	ND	ND
comp256294_c0_seq1	ND	ND	0.29085539	0.283686228	ND	ND	ND	ND
comp257685_c0_seq1	ND	ND	0.166527906	0.159358743	ND	ND	ND	ND
comp258594_c0_seq1	ND	ND	0.170257662	0.163088499	ND	ND	ND	ND
comp261540_c0_seq1	ND	ND	0.267663728	0.320492495	-0.84036874	-0.533949351	ND	-1.331631198
comp265258_c0_seq1	ND	-1.072069147	0.100346393	0.09317723	ND	ND	ND	ND
comp269052_c0_seq1	ND	ND	0.130490535	0.181313319	ND	ND	ND	ND
comp271609_c0_seq1	ND	ND	0.240994299	0.268587243	ND	ND	ND	ND
comp27294_c0_seq1	ND	ND	0.519475701	0.485977599	ND	ND	ND	ND
comp274339_c0_seq1	ND	ND	0.069006641	0.016079987	ND	ND	ND	ND
comp276418_c0_seq1	ND	ND	0.043834156	0.09465694	ND	ND	ND	ND
comp276822_c0_seq1	ND	ND	0.148737975	0.192721335	ND	-0.668669371	ND	ND
comp277535_c0_seq1	ND	ND	0.170257662	0.163088499	ND	ND	ND	ND
comp281084_c0_seq1	ND	ND	0.045318925	0.038149762	ND	ND	ND	ND
comp284697_c0_seq1	ND	ND	0.130490535	0.181313319	-0.868397463	ND	ND	ND
comp284947_c0_seq1	ND	ND	0.05281988	-0.005501806	ND	ND	ND	ND
comp286910_c0_seq1	ND	ND	0.244411268	0.179250158	ND	ND	ND	ND
comp288191_c0_seq1	ND	ND	0.227853174	0.220684011	ND	ND	ND	ND

comp288554_c0_seq1	ND	ND	0.068222007	0.119044792	ND	ND	ND	ND
comp288766_c0_seq1	ND	ND	0.098871707	0.033710598	ND	ND	ND	ND
comp290626_c0_seq1	ND	ND	0.131808577	0.162427975	ND	ND	ND	ND
comp290629_c0_seq1	ND	-1.079393005	0.093022535	0.085853372	-0.96385741	ND	ND	-0.977998614
comp292782_c0_seq1	ND	ND	0.08582014	0.078650977	ND	ND	ND	ND
comp293379_c0_seq1	ND	ND	0.05070652	0.043537358	ND	ND	ND	ND
comp294051_c0_seq1	ND	ND	0.02215106	0.081928687	ND	ND	ND	ND
comp300579_c0_seq1	ND	ND	0.025453695	0.085231322	ND	ND	ND	ND
comp300676_c0_seq1	-0.857888109	ND	0.02215106	0.014981897	-0.830608902	ND	ND	ND
comp304254_c0_seq1	ND	ND	0.109301236	0.102132073	ND	ND	ND	ND
comp311451_c0_seq1	-0.976363271	-1.06461966	0.107795881	0.042634771	ND	ND	ND	ND
comp313183_c0_seq1	ND	ND	0.036194137	0.029024975	ND	ND	ND	ND
comp314912_c0_seq1	ND	ND	0.227149293	0.168827607	ND	ND	ND	ND
comp319596_c0_seq1	ND	ND	0.270152528	0.292946589	ND	ND	ND	ND
comp320584_c0_seq1	ND	ND	0.209913122	0.151591437	ND	ND	ND	ND
comp329865_c0_seq1	ND	ND	0.172688214	0.165519052	ND	ND	ND	ND
comp33706_c0_seq1	ND	ND	0.32090924	0.34592476	-0.946824071	ND	ND	-0.960965275
comp341963_c0_seq1	ND	ND	0.098708162	0.091538999	ND	ND	ND	ND
comp341983_c0_seq1	ND	ND	0.205350407	0.198181244	ND	ND	ND	ND
comp34844_c0_seq1	ND	ND	0.263055785	0.225923399	ND	ND	ND	ND
comp35333_c0_seq1	-0.957160564	ND	0.479181106	0.459777487	-1.230911353	-0.991438754	-0.33910926	-0.642992566
comp35479_c0_seq1	-0.635216052	-0.723472441	0.317930215	0.265682678	-1.0850581	-1.447645492	-0.795315999	-0.701259296
comp35777_c0_seq1	ND	-0.486436044	0.467136256	0.516083036	-0.370900449	-0.9095791	ND	-0.862162908
comp36213_c0_seq1	-0.76588543	-1.155171815	0.091877344	0.167682416	-0.562514965	-1.101193616	-1.227015373	ND
comp36740_c0_seq1	-0.753511531	ND	0.080770147	0.048777401	ND	-1.088819717	ND	-0.740373529
comp37100_c0_seq1	-1.0233213	-0.208487702	0.361867847	0.405851207	-0.695012098	-0.455539498	-0.405269997	-0.709153302
comp37137_c0_seq1	ND	ND	0.526484951	0.46345797	ND	-0.753320393	ND	-1.103844209
comp37335_c0_seq1	-0.849631852	-0.55253736	0.066122869	0.081230101	-0.764360699	-0.729008082	-1.252769848	-1.380561894
comp37469_c0_seq2	ND	ND	0.204569302	0.156007454	ND	-1.052170738	ND	ND
comp37832_c0_seq1	-0.658480228	-0.968585367	0.203830173	0.178177605	-1.330171026	-0.546630383	ND	ND
comp37887_c0_seq1	ND	-1.011112721	0.258212832	0.205286179	-0.895577126	ND	ND	-0.90971833

comp38330_c0_seq1	ND	ND	0.22038886	0.155227751	ND	ND	ND	ND
comp38521_c0_seq1	-0.585503295	-0.974789679	0.2239548	0.190456698	ND	ND	ND	ND
comp38865_c0_seq1	ND	ND	0.18727778	0.142320057	ND	ND	ND	ND
comp38946_c0_seq1	ND	ND	0.174242043	0.16707288	-0.67851792	-0.916166575	ND	-0.692659124
comp39327_c0_seq1	-1.07357373	-1.462860114	0.459677953	0.489492356	ND	ND	ND	-1.060435727
comp39539_c0_seq1	-0.757882613	-0.749228988	0.122156556	0.069229903	-0.855542143	-1.093190798	ND	ND
comp39982_c0_seq1	ND	ND	0.076399066	0.136176693	ND	ND	ND	ND
comp40354_c0_seq1	ND	ND	0.281959319	0.253600857	ND	ND	ND	ND
comp40804_c0_seq1	ND	-1.15026448	0.073303582	0.11189191	-0.733698889	-0.619165027	ND	ND
comp42048_c0_seq1	-0.985287444	ND	0.362113142	0.364703817	ND	ND	ND	ND
comp43123_c0_seq1	ND	ND	0.211345365	0.169414096	ND	ND	ND	-1.371559145
comp43223_c0_seq2	ND	ND	0.13157763	0.152437191	-1.198303587	ND	ND	ND
comp43498_c0_seq1	ND	-1.184456771	0.649140213	0.61130223	-1.54604243	-1.908629822	ND	ND
comp43612_c0_seq2	-0.714122515	-0.559340855	0.628314652	0.590111255	-0.686843308	-0.651490692	-0.272162471	-0.524893254
comp43651_c0_seq1	ND	ND	0.419034819	0.379680973	ND	ND	ND	ND
comp43858_c0_seq1	-1.320966286	-0.454980166	0.732259151	0.69491852	-0.390597093	-0.355244476	-1.003944979	-0.330104679
comp43953_c0_seq1	-0.506691504	-1.072069147	0.85046892	0.8028711	0.043466448	-0.540969694	-0.541852714	0.029325244
comp44032_c0_seq1	ND	-0.531434279	0.603192701	0.554630853	-0.591989942	-0.954577335	-0.302247841	ND
comp44145_c0_seq1	ND	ND	0.733247069	0.6913158	-1.136546233	-1.198103629	ND	ND
comp44347_c0_seq1	ND	-0.850056234	1.032053176	1.031888915	ND	-1.27319929	ND	ND
comp44373_c0_seq1	ND	ND	0.29556379	0.334152118	ND	ND	ND	ND
comp44373_c1_seq1	ND	ND	0.880677084	0.920084063	ND	ND	ND	ND
comp44471_c0_seq1	ND	ND	1.701715482	1.684024539	ND	ND	ND	-0.56428227
comp44584_c0_seq1	ND	ND	0.64974712	0.598997386	ND	ND	-1.689245073	ND
comp44605_c0_seq1	ND	-1.511670338	1.827323312	1.780275523	ND	-0.855632148	ND	ND
comp44780_c0_seq1	-0.330600245	-1.373099143	1.010169763	1.065148507	-0.780442293	-1.018090948	-0.365761455	-0.970674756
comp44867_c0_seq2	ND	ND	0.43152053	0.403162069	ND	-0.503986127	ND	ND
comp44971_c0_seq1	ND	-0.630391245	0.183002352	0.084062816	-0.690946909	ND	-0.480386054	-1.006118109
comp45067_c0_seq1	ND	ND	0.309152933	0.325464867	-1.09990953	ND	ND	ND
comp45264_c0_seq1	-0.507429473	-0.470747125	0.734337532	0.780413882	-0.480150266	-0.319858913	-0.66752942	ND
comp45280_c0_seq1	ND	ND	0.919443547	0.941481656	ND	ND	ND	ND

comp45380_c0_seq1	-1.003310548	-0.614445682	0.539486452	0.593835327	ND	-1.037588738	ND	ND
comp45785_c0_seq1	ND	-1.090860192	0.540193197	0.602659962	ND	ND	ND	ND
comp46021_c0_seq2	-1.001186855	-0.487383252	0.259063556	0.172713147	-0.973907648	ND	-0.383135551	-0.988048852
comp46066_c0_seq2	ND	ND	-0.000573755	0.06480775	ND	ND	ND	ND
comp46120_c0_seq1	-1.104297154	-0.648485498	0.366806622	0.348356449	-1.378047943	-1.138575344	-0.787275846	-0.437946637
comp46163_c0_seq1	ND	ND	0.491745359	0.532000846	-1.077017947	ND	ND	ND
comp46238_c0_seq1	ND	-1.25402934	0.65874889	0.680224908	-1.138493745	-0.421899891	ND	-0.249544962
comp46386_c0_seq1	ND	-0.344084506	0.430391025	0.486273608	-0.751427656	-0.812985053	ND	-0.941660119
comp46511_c0_seq1	-0.601825259	-0.991111643	1.026401937	1.083958104	ND	0.208994591	ND	-0.889717252
comp46570_c0_seq1	ND	ND	0.486216109	0.466457819	ND	ND	ND	ND
comp46902_c0_seq1	ND	ND	0.525425033	0.507790437	ND	-1.313171612	ND	ND
comp46927_c0_seq1	-0.529705867	-1.396113506	0.391725987	0.445826481	-1.280577911	-0.43904532	-0.865897073	-0.99368912
comp47203_c0_seq1	ND	ND	0.062709365	0.087724886	ND	ND	ND	ND
comp48093_c0_seq1	ND	ND	0.310216078	0.348804406	ND	ND	ND	ND
comp48457_c0_seq1	ND	ND	0.158197678	0.185790621	ND	ND	ND	ND
comp48859_c0_seq1	-0.660817245	ND	0.14864085	0.115142748	ND	ND	ND	ND
comp49317_c0_seq1	ND	-1.1075125	0.06490304	-0.000258069	ND	ND	ND	ND
comp51452_c0_seq1	ND	ND	0.021254683	0.051874081	-1.17392796	ND	ND	ND
comp51937_c0_seq1	ND	ND	0.2118487	0.172494854	ND	ND	ND	ND
comp52243_c0_seq1	ND	ND	1.460963329	1.447499933	ND	ND	ND	ND
comp53850_c0_seq1	-0.829332649	ND	0.254826503	0.189665393	ND	ND	ND	ND
comp5422_c0_seq1	ND	ND	0.005551798	-0.001617365	ND	ND	ND	ND
comp55077_c0_seq1	ND	ND	0.946877534	0.898179094	-1.107279552	0.233424434	-1.118567447	-1.246359493
comp55285_c0_seq1	ND	ND	0.257102855	0.282118376	ND	ND	ND	ND
comp55545_c0_seq1	ND	ND	0.092400485	0.085231322	-0.906487513	ND	ND	ND
comp55721_c0_seq1	ND	-0.938175568	0.331149985	0.278223332	ND	-0.884197369	-1.010019126	-0.836781177
comp55757_c0_seq1	ND	ND	0.177758616	0.112597507	ND	ND	ND	ND
comp55968_c0_seq1	ND	0.076888178	0.981514656	0.969749742	0.172220388	0.250841694	0.194100856	0.158079184
comp57465_c0_seq1	ND	ND	0.194964609	0.187795446	ND	ND	ND	ND
comp58363_c0_seq1	-0.735573516	-0.647738646	0.694694006	0.642446468	-0.70829431	-1.070881702	ND	ND
comp58377_c0_seq1	ND	ND	0.824661656	0.802769237	ND	ND	ND	ND

comp59112_c0_seq1	ND	ND	0.1587606	0.20274396	ND	ND	ND	ND
comp59230_c0_seq1	ND	ND	-0.016767006	0.027216354	-1.073646951	ND	ND	ND
comp60219_c0_seq1	-0.909917109	ND	0.116250096	0.109080933	-0.882637902	ND	ND	ND
comp62085_c0_seq1	ND	ND	0.186076412	0.178907249	-1.046894792	ND	ND	ND
comp62352_c0_seq1	ND	-1.004259806	0.043216997	0.070809941	ND	-0.950281607	ND	-0.726774156
comp65439_c0_seq1	-1.097528791	ND	0.197483726	0.155552457	ND	ND	ND	ND
comp69105_c0_seq1	ND	ND	0.140558929	0.133389767	ND	-0.977878412	ND	ND
comp71041_c0_seq1	-1.076566812	ND	0.058744862	0.09733319	ND	ND	ND	ND
comp72792_c0_seq1	ND	ND	0.414157639	0.358683797	ND	-0.778913321	ND	-0.731497128
comp73791_c0_seq1	0.616206691	0.36824946	2.220731787	2.23105612	ND	0.902021503	ND	-1.262749909
comp7462_c0_seq2	ND	ND	0.080143007	0.014981897	-0.976736938	ND	ND	ND
comp74827_c0_seq1	-0.825095596	-0.913351984	0.397366254	0.390197091	-0.496786393	ND	ND	-0.510927597
comp74918_c0_seq1	ND	ND	0.263342354	0.307325714	-0.793537591	ND	ND	ND
comp75317_c0_seq1	ND	ND	0.452528911	0.512306538	ND	ND	ND	ND
comp75575_c0_seq1	ND	ND	0.285392495	0.33374066	ND	ND	ND	ND
comp76010_c0_seq1	ND	ND	0.057077703	0.04990854	ND	ND	ND	ND
comp76255_c0_seq1	ND	ND	0.382713966	0.334152118	ND	ND	ND	ND
comp77092_c0_seq1	-1.277393267	ND	0.107795881	0.100626718	ND	-1.311671456	ND	ND
comp77199_c0_seq1	ND	ND	0.185391405	0.146037559	ND	ND	ND	ND
comp77380_c0_seq1	ND	-0.669114778	0.228599705	0.269735222	ND	ND	ND	ND
comp77842_c0_seq1	ND	ND	0.137499308	0.193999225	-0.817922996	ND	ND	ND
comp79793_c0_seq1	ND	ND	0.381173003	0.37400384	ND	ND	ND	ND
comp80101_c0_seq1	ND	ND	1.008831412	0.985271833	ND	ND	-0.286580209	ND
comp80328_c0_seq1	-1.035293422	ND	0.020837006	0.068025506	ND	ND	ND	ND
comp80464_c0_seq1	ND	-0.594947893	0.289801614	0.241239766	-0.604351034	-0.598961641	-0.967821447	ND
comp80557_c0_seq1	ND	ND	0.156768068	0.149598906	ND	ND	ND	ND
comp81384_c0_seq1	-1.427687485	ND	0.37663097	0.399425031	ND	-1.461965675	-0.809636181	-0.937428227
comp82426_c0_seq1	ND	ND	0.498152132	0.52877153	ND	ND	ND	ND
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comp82702_c0_seq1	ND	-1.499144363	0.150392432	0.160952036	-0.781548776	-1.445166164	ND	-0.920628717
comp83719_c1_seq1	-0.865228472	-1.254514856	0.270083202	0.30867153	-0.53691927	-0.656468613	-0.481260375	-0.675999211

comp83815_c0_seq1	ND	ND	0.367086541	0.342884039	ND	ND	ND	ND
comp84895_c0_seq1	-1.049491534	-1.137747923	0.546550978	0.555772232	ND	ND	-0.60753149	ND
comp84939_c0_seq1	-1.050759548	ND	0.635459595	0.70292405	-0.069237832	ND	ND	-0.73659155
comp85962_c0_seq1	-0.895073064	-0.381269461	0.846301344	0.827011549	-1.344915112	ND	-0.930234274	-0.881935061
comp86482_c0_seq1	ND	-1.557481509	0.698615779	0.695900958	-1.441945913	ND	-1.027265076	ND
comp86896_c0_seq1	ND	-1.336115577	0.768900548	0.809702249	-1.521609977	-0.805016123	ND	ND
comp86916_c0_seq1	-1.235624732	ND	0.790542473	0.813336534	ND	ND	ND	ND
comp87567_c0_seq1	ND	ND	0.361482664	0.412305448	ND	ND	ND	-0.952576534
comp87746_c0_seq1	-1.51763149	ND	0.395831434	0.462448486	ND	-0.648819693	-1.376701441	-0.726342237
comp87753_c0_seq1	ND	ND	0.430917762	0.458510706	ND	ND	ND	ND
comp87963_c0_seq1	-0.69386677	-0.702941912	0.319711308	0.337365729	-1.064527572	-0.582016924	ND	ND
comp88225_c0_seq2	0.013895445	0.293615841	1.175220551	1.202035886	0.317381063	0.326404741	-0.322295761	-0.325149071
comp88594_c0_seq1	ND	-0.175112988	0.515217878	0.589718761	-0.197880091	-0.68540622	-0.209167986	-0.637990028
comp89261_c0_seq1	-1.176014711	-0.699999669	0.472415871	0.407254762	-0.847705508	-0.131111654	-1.512205917	-0.794899923
comp89365_c0_seq1	-0.817940665	-1.082288312	0.164760846	0.221260763	-0.665722721	-0.551188859	-0.853101875	-0.804802662
comp89680_c0_seq1	0.014303808	-0.007005791	1.814582285	1.800987667	-0.669621446	-0.731178842	ND	-0.625770703
comp91915_c1_seq1	ND	ND	1.37847235	1.340606565	ND	ND	ND	-1.370383787
comp9193_c0_seq1	ND	ND	0.109301236	0.044140126	ND	ND	ND	ND
comp92090_c0_seq1	-0.463878394	-0.649044796	0.986703715	1.028084943	-0.094176506	-0.352028548	-0.06767584	-0.304612356
comp92236_c0_seq1	0.559499333	0.256399097	1.184689493	1.19616244	0.530297184	0.430951227	0.129038211	-0.739116525
comp92267_c0_seq1	ND	ND	0.045318925	0.096141709	ND	ND	ND	-0.666680281
comp92347_c0_seq1	-0.490130609	-0.578386998	1.00620899	1.012828112	ND	-1.001530053	-0.525291819	-0.954113861
comp92582_c1_seq1	ND	ND	0.103886987	0.082477385	ND	ND	ND	ND
comp93169_c0_seq1	ND	-0.671907679	0.266424656	0.154520142	ND	-0.492990743	-0.442721241	ND
comp93480_c0_seq2	ND	ND	0.987567639	0.942278013	ND	ND	ND	ND
comp93636_c0_seq1	-1.144364993	-1.533651377	1.960207239	1.940958975	ND	-1.178643182	ND	-1.13122699
comp93899_c0_seq2	ND	-0.897084372	1.191785117	1.240133282	ND	ND	ND	ND
comp94271_c0_seq1	ND	-1.039884464	0.00759234	0.067369967	ND	ND	ND	-0.938490073
comp94830_c0_seq1	ND	ND	0.157993159	0.109431312	ND	ND	ND	ND
comp95249_c0_seq1	ND	ND	0.225394565	0.16707288	ND	ND	-0.76898706	ND
comp95357_c1_seq1	ND	ND	0.009186083	0.00201692	ND	ND	ND	ND

comp96501_c0_seq1	ND	ND	0.633889323	0.613356199	ND	ND	ND	ND
comp96779_c0_seq1	ND	ND	0.187168428	0.13860658	ND	ND	ND	ND
comp96950_c0_seq2	ND	ND	0.036485512	0.02931635	-0.962402486	ND	ND	-0.97654369
comp97048_c0_seq2	ND	-1.191432782	0.308341693	0.371753604	-1.075897187	-0.836424587	ND	-1.090038391
comp97095_c0_seq1	ND	ND	0.38168605	0.412305448	ND	ND	ND	ND
comp97533_c0_seq1	ND	ND	0.164544474	0.157375311	ND	ND	ND	ND
comp97568_c0_seq1	ND	ND	0.457957663	0.431483345	-0.756530135	ND	ND	ND
comp97654_c0_seq2	ND	ND	0.138134954	0.205599409	ND	ND	ND	ND
comp97720_c0_seq1	ND	-0.63175054	0.27439711	0.267227948	-0.9933362	-0.577772342	ND	ND
comp97877_c0_seq1	-0.941162642	-1.02941903	0.401274525	0.443590726	-1.214913431	ND	ND	-0.75193338
comp98234_c0_seq2	-1.193983807	-0.680180205	0.19120534	0.258669796	-1.166704601	-0.751140742	-1.053053759	ND
comp98652_c0_seq1	ND	-0.751088925	0.363334669	0.403162069	-0.220579981	-0.61792948	ND	-1.047634542
comp98851_c0_seq1	ND	ND	0.77226547	0.795440323	ND	ND	ND	ND
comp99075_c0_seq2	ND	-0.959747674	0.154675919	0.205498703	ND	-0.905769475	-0.730561237	ND
comp99153_c0_seq1	ND	ND	0.333569459	0.359824052	ND	ND	ND	ND
Transcript ID	Root1 (RPKM_log10)	Root2 (RPKM_log10)	Flower1 (RPKM_log10)	Flower2 (RPKM_log10)	Stem1 (RPKM_log10)	Stem2 (RPKM_log10)	Leaf1 (RPKM_log10)	Leaf2 (RPKM_log10)
comp103083_c0_seq1	0.229262067	0.17963508	ND	ND	-0.899805928	-0.961363324	ND	-1.090038391
comp105867_c0_seq1	0.249848598	0.258502222	-1.250323475	-1.257492638	-1.404113433	ND	ND	-0.941133383
comp107869_c0_seq1	0.326746924	0.314211249	ND	ND	-0.968193164	-0.853659302	-1.155572318	ND
comp110337_c0_seq1	0.19384541	0.197359394	ND	ND	ND	ND	ND	-1.023465509
comp112828_c0_seq1	0.280414589	0.317096937	ND	ND	ND	ND	ND	ND
comp113024_c0_seq1	0.578400179	0.613670186	-1.127021382	-1.310281804	-0.643989242	ND	-0.343251757	-0.926975759
comp114042_c0_seq1	0.335931917	0.326856774	-0.579908931	ND	ND	ND	ND	ND
comp119682_c0_seq1	0.887022208	0.833527926	-0.710059878	-1.018259036	-0.386728581	-0.185044542	-0.750198994	ND
comp121651_c0_seq1	0.57819953	0.561825149	ND	ND	ND	-1.155048664	ND	-0.806602476
comp126715_c0_seq1	0.747776007	0.774474134	ND	ND	0.052421291	-0.805016123	ND	ND
comp126871_c0_seq1	0.505921322	0.460593134	ND	ND	-1.177198937	-0.812787601	-0.762518099	-0.668461396
comp127710_c0_seq1	0.268985127	0.296893551	ND	-1.432176134	-1.277766934	-1.33932433	-0.686994837	-0.893968129
comp128204_c0_seq1	1.421652971	1.422687198	ND	-0.544326114	-0.991976905	-0.354564297	0.200855183	0.224330813
comp130216_c0_seq1	0.261747821	0.304259712	ND	ND	ND	ND	-0.864493859	ND
comp134099_c0_seq1	0.680677921	0.669833756	ND	ND	ND	-0.66535413	ND	ND

comp136124_c0_seq2	0.602105749	0.581344849	-1.269903529	-1.277072692	-0.309750135	-0.443858199	-0.611072641	-0.8357747
comp137919_c0_seq1	0.709843854	0.717669461	ND	ND	-1.284066239	ND	0.005675862	-0.184264091
comp139894_c0_seq1	0.450029521	0.393957815	ND	ND	ND	-0.823130758	ND	-0.553865816
comp140803_c0_seq1	0.152535459	0.246619279	-0.426063221	ND	ND	-0.942440571	-0.369292324	-0.71893312
comp140936_c0_seq1	1.291390299	1.315421454	0.321703024	0.58170559	0.552624809	0.407385665	0.210982834	0.195164547
comp141131_c0_seq1	0.714012279	0.777404693	0.148187887	-0.762071263	-1.385813313	-0.845310718	ND	-1.098924521
comp141320_c0_seq1	0.664990636	0.604762971	-0.066790023	-0.212261884	-0.483821416	-0.244348817	-0.245231838	-0.373023884
comp141628_c0_seq1	0.534374767	0.578984483	-1.262279674	ND	-0.938948377	-0.632528988	ND	ND
comp141900_c0_seq1	-0.001186855	0.044095665	ND	ND	ND	ND	ND	ND
comp142076_c0_seq3	0.013053584	0.024500109	ND	ND	ND	-1.512586299	-0.860256806	ND
comp142575_c0_seq1	0.56860736	0.61388988	ND	ND	-0.199993451	ND	ND	-0.816194646
comp143634_c0_seq1	2.55453748	2.580901599	-0.455518201	-0.161657368	0.89584182	0.580366972	1.478239881	1.347362248
comp144100_c0_seq2	0.153285961	0.156799945	ND	ND	ND	ND	ND	-1.365054954
comp144453_c0_seq3	0.803069989	0.801963776	-0.44722461	-0.086416988	ND	-0.838663224	-0.36242499	ND
comp144543_c0_seq2	0.225259324	0.196124388	ND	ND	ND	-1.490260103	-1.014021869	-0.965722656
comp144748_c0_seq1	0.810940865	0.868393106	-0.576191695	-0.884390853	-0.377799135	-0.11484544	-0.264148293	-0.647212844
comp144830_c0_seq1	0.803433633	0.829896816	-0.084694228	-0.230166088	-0.279876871	-0.496336227	-0.865196033	-0.515866824
comp145028_c0_seq2	0.797340866	0.853628939	-0.314399635	-0.145477539	-0.028856899	-0.286708941	-0.027179817	-0.084390789
comp145150_c1_seq2	0.918855378	0.880370607	0.243831119	0.122718604	-0.4218422	-0.659490856	0.3115974	-0.236411049
comp145217_c1_seq1	-0.02466795	0.033203697	ND	ND	ND	ND	-1.184767898	ND
comp145313_c0_seq1	1.263133779	1.28501567	ND	-0.151797944	-1.29841874	-0.882854881	0.195443344	0.192590035
comp145539_c0_seq1	0.466622983	0.465100978	ND	ND	ND	-1.545378813	ND	-1.49796262
comp145539_c0_seq2	0.088107786	0.129485255	ND	ND	ND	-1.30789824	ND	-0.959452052
comp145854_c0_seq1	0.266478811	0.271339447	ND	-0.921349023	-1.368999814	-1.129527215	-0.410250932	-0.781081027
comp146819_c0_seq4	0.476394946	0.544212703	-0.813827601	-0.616876781	-0.967617559	-0.046903722	-0.552936721	-0.726486258
comp146858_c0_seq1	0.431537909	0.463575352	ND	ND	-0.736159488	-0.973808143	ND	ND
comp147826_c0_seq1	0.342115307	0.408760879	ND	ND	ND	-0.537260922	ND	-0.966965985
comp148295_c0_seq2	1.09056075	1.119597184	-0.341859538	-0.622029973	-0.080676148	-0.043102072	-0.257059918	-0.208760705
comp148808_c0_seq1	1.26446017	1.30160825	-1.222856582	-0.832085736	0.446175106	0.541799436	-0.149052345	-0.200456046
comp148876_c0_seq2	0.190416571	0.22134659	ND	-0.914437029	ND	ND	-0.947406982	-0.376229024
comp149025_c0_seq1	1.233235511	1.209682546	0.517341571	0.369993705	0.489425322	0.401889083	0.347242917	0.209231706

comp149137_c0_seq2	2.399350431	2.39423903		1.015914929	0.916743088	0.406193016	0.975340792	0.256602423	0.253749114
comp149327_c1_seq1	1.449215321	1.39370076		-0.960222977	-1.092330876	-0.017102922	-0.114872491	-0.155264053	-0.474941625
comp149351_c0_seq3	1.268136474	1.323513762	ND		-0.909179869	-0.754770669	-0.941266802	ND	ND
comp149365_c0_seq1	0.947085877	0.922846793		-1.10229388	ND	-0.955053842	-1.317641234	-0.443462991	ND
comp149463_c0_seq1	0.298303681	0.29657527		-0.478302839	-0.631600038	-1.000069583	-0.66368697	-1.06251	-0.792362037
comp149637_c0_seq2	-0.011153279	0.050976191	ND		ND	ND	-1.030708212	ND	ND
comp150067_c0_seq2	0.543837927	0.531476808		-1.272915989	-0.802963897	-1.125675951	-1.090323334	-1.313055105	-1.264755892
comp150104_c0_seq1	0.583441345	0.584863256	ND		ND	ND	ND	ND	ND
comp150374_c0_seq1	0.621918128	0.626132588	ND		ND	-0.644533422	-0.706090819	-1.008003835	-0.658674627
comp150689_c0_seq2	0.625376027	0.560857486	ND		ND	ND	ND	ND	-1.310875977
comp150837_c0_seq1	0.116922893	0.159945419		-0.807518127	-0.939626026	-0.961308085	-0.721835486	ND	-1.100388026
comp150989_c0_seq2	0.081303318	0.033164152		-1.052897953	ND	-0.984839161	-1.046396557	-0.871188319	-0.919799119
comp151041_c0_seq1	0.918669398	0.892773754	ND		ND	-0.789650295	-0.271424094	-1.374969457	-0.29864152
comp151122_c0_seq2	2.086723338	2.088289356		-1.260223838	ND	0.549774031	1.101920607	-1.300362954	ND
comp151614_c0_seq3	0.225657942	0.198099394	ND		ND	ND	ND	ND	ND
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comp152682_c0_seq4	1.015028784	1.063862319		-1.317119651	-1.148197555	-0.072969601	-0.055345751	-1.658288763	-1.007929559
comp152707_c0_seq2	1.106496461	1.097609773		-0.995735604	-0.826813507	-0.246435575	-0.432931708	-0.257723469	0.267696998
comp152707_c1_seq1	1.359798824	1.301343275		-1.187485793	-1.194654956	0.215026749	-0.361440463	-0.148443663	0.579081496
comp152730_c0_seq8	0.83883166	0.801267979		-0.320047237	-0.593484289	-0.285846713	-0.535394592	-0.48512509	-0.082859806
comp152897_c0_seq2	1.524681604	1.588453191		0.538802888	0.674843758	0.743185812	0.666494673	-0.462418161	-0.435308248
comp153510_c0_seq1	1.774774087	1.771887859		0.503825635	0.361687395	0.918880087	0.618280019	0.436054231	0.271912163
comp153574_c0_seq8	0.445087944	0.460803423		-1.460202722	ND	-1.312962684	-0.634157391	-0.655243798	-0.628133884
comp154252_c0_seq1	1.905723878	1.913415273		0.887452486	0.820285394	0.894132442	0.593323973	0.768532211	0.280688681
comp154416_c0_seq1	0.702838041	0.670193897		-1.378543885	ND	-0.687235802	-0.271671944	-0.941561746	-0.768323796
comp154428_c0_seq7	1.078269174	1.143745715	ND		ND	-0.748991215	-0.845310718	-1.272162471	-1.27501578
comp154478_c0_seq1	0.822589645	0.837732315	ND		ND	-1.595735351	-1.657292748	ND	-1.609876555
comp154629_c1_seq16	0.763894588	0.736774943		-0.512413444	-0.996703861	-0.101931971	-0.301792066	ND	ND
comp154629_c1_seq3	0.560255286	0.528903748	ND		ND	-0.333284262	-0.218750399	ND	ND
comp154664_c1_seq1	0.177845936	0.218073565	ND		-0.956462642	-1.103083438	ND	-0.767583846	-0.749247856
comp154832_c0_seq1	1.450942126	1.454094409		-0.745173497	-1.053372655	0.257383746	0.26992807	-0.132100099	-0.412502308

comp154993_c0_seq4	1.361630005	1.358236787	-0.050956038	-0.256492855	-0.176717273	-0.224910708	-0.966156418	-1.39497846
comp154993_c1_seq3	0.825901125	0.875603983	ND	-1.060896713	ND	-1.269074905	ND	ND
comp155459_c0_seq1	0.779255094	0.795409673	-0.32146638	-0.182507507	-0.372593996	-0.434151392	-1.0605755	-0.012276287
comp155724_c0_seq1	1.367157279	1.418807421	0.318093029	0.208618821	0.277007351	0.143650662	-0.785433066	-0.281201898
comp155724_c0_seq4	1.330212058	1.394714283	-0.046359629	-0.007771302	-0.02945336	-0.2780974	ND	-0.645654556
comp156337_c1_seq3	0.645454566	0.703041523	ND	ND	-1.364692726	ND	0.081396576	-0.281923917
comp156389_c2_seq15	0.683955525	0.684168856	-1.036251956	-0.821572369	-0.065103178	-0.366992729	-0.708414287	-0.778214386
comp156389_c2_seq3	0.625806377	0.617352099	-1.259450384	-0.722551502	-0.267112306	-0.28446604	-0.901649491	-1.12635155
comp156437_c0_seq2	1.187896545	1.22441079	-0.538176821	-0.334492619	-0.038754265	-0.179492908	-0.101194682	0.242060379
comp156804_c0_seq3	2.409249023	2.464112247	-0.710059878	-0.541137781	0.17754285	-0.226437228	-0.051228989	-0.179021035
comp156899_c1_seq1	1.008011931	1.028700566	-0.893704275	ND	0.128597027	-0.455839115	ND	-1.061635437
comp157125_c0_seq7	0.109841759	0.065364295	-1.528633012	ND	-0.779332983	-0.965829116	ND	-1.696564174
comp157483_c1_seq3	0.857867441	0.826993976	-0.434306995	-0.126205722	-0.287066957	-0.109742264	0.08185639	-0.062326072
comp157807_c0_seq1	0.81605389	0.762370825	-0.222821489	-0.063042772	-0.125886569	0.218049181	ND	-1.117751379
comp157887_c0_seq1	1.418524653	1.443291721	ND	ND	0.219954746	0.072685236	ND	ND
comp157887_c0_seq2	1.114570165	1.160613732	ND	ND	-0.351509082	-0.781043263	ND	-1.210748326
comp158132_c0_seq5	0.414315561	0.438032931	ND	ND	-0.663915418	-0.587170116	-0.608256523	-0.501965363
comp158132_c0_seq7	0.252011227	0.27847441	-1.501418059	ND	-0.956238013	-0.637584168	-0.696459135	-0.627956536
comp158325_c2_seq4	1.864745814	1.915668601	-0.074758953	-0.354929388	0.481850555	1.054940517	ND	-0.816721383
comp158648_c0_seq1	1.28539699	1.30352413	ND	-0.358598766	0.038848484	-0.022708913	ND	-0.218330769
comp158648_c0_seq4	0.746500545	0.706548836	ND	-1.009018379	-0.67851792	-0.740075316	-0.740958337	-0.692659124
comp158912_c0_seq3	2.98419024	3.026926854	1.239469527	1.142937782	1.86614178	1.742385818	1.841517361	1.567446352
comp159033_c0_seq1	1.232403773	1.249376057	-0.268300198	-0.301798299	0.607532311	0.375808638	-0.061766981	-0.520552246
comp159051_c1_seq14	1.094729349	1.15131989	-0.205823242	-0.186663466	-0.449789831	-0.282867899	-0.088354505	-1.276844391
comp159078_c0_seq3	0.858993485	0.917609743	-0.704230334	-0.448158062	-0.556990296	-0.794638952	-0.408577348	-1.349282751
comp159078_c0_seq4	0.912234253	0.910184741	-0.449729359	-0.088921737	-0.728458054	-0.465504359	-0.392958462	-0.918690517
comp159155_c0_seq4	1.019755686	1.04544265	-0.491896204	-0.800095363	-0.212030601	-0.649251612	ND	ND
comp159160_c0_seq4	0.688595671	0.704548534	-1.123035926	-1.607326343	-0.373735897	-0.259202034	-0.121782356	-0.489334741
comp159173_c2_seq1	0.055237896	0.091920244	ND	-1.060896713	-1.508547504	-1.269074905	-0.792836671	-1.221658713
comp159194_c0_seq10	0.243781621	0.271509126	ND	ND	-1.419135253	ND	ND	-1.433276457
comp159260_c0_seq1	1.665714513	1.658623833	0.89486983	0.828046666	0.981121627	0.856387189	0.931193971	0.724610006

comp159366_c2_seq5	0.952591417	0.997873937	ND		-1.312841275	-0.380280824	-0.479626782	-0.500713188	-0.519360765		
comp159366_c2_seq6	0.619233146	0.645931273		-1.019241625	ND		-0.872001588	-0.632528988	-0.281229491	ND	
comp159408_c0_seq3	1.073699583	1.040034097		-0.284043021		-0.615723276	-0.336375339	-0.499390376	-1.301905743	-1.128667793	
comp159539_c0_seq3	0.07733984	0.105589021	ND		ND	ND	ND		-1.196703459	-1.023465509	
comp159783_c0_seq3	0.263197058	0.266711042	ND		ND		-0.939972657	ND	ND	ND	
comp159874_c0_seq1	1.162509404	1.150100512		-0.939270034		-0.645409201	0.088783596	0.24332262	-0.044910699	-0.483951906	
comp159962_c2_seq1	3.567268996	3.515555363		0.695380126		0.568473421	ND	0.373868036	-0.962807086	0.02334422	
comp159962_c2_seq10	3.446976392	3.408219564		0.381947837		0.348449735		-0.634314257	0.082279597	-0.666791451	-0.095613493
comp160072_c0_seq1	2.390567405	2.359660917		0.749603833		0.788566392	1.179715897	0.816151464	1.623643677	1.099278045	
comp160072_c0_seq2	2.103052748	2.067024232		0.361308353		0.442776678	0.412661451	0.679363704	1.471375185	0.82128384	
comp160108_c0_seq2	0.717567488	0.689368388		-0.775305346		-1.180414517	-0.782967268	-0.309411463	-1.514414466	-1.341176516	
comp160108_c0_seq5	0.63494224	0.579171606		-1.020734561		-1.027903723	-0.697403264	-0.332991928	ND	-1.364756982	
comp160218_c0_seq1	0.459738252	0.488996582		-0.376716929		-0.660092503	-0.614827772	-0.480090524	-1.170183711	-0.599005753	
comp160423_c0_seq2	1.238743123	1.237467865		0.158549419		0.130530117	0.17170734	0.349209695	-0.646376986	-0.400588369	
comp160643_c0_seq7	0.007413317	0.074058888	ND		ND	ND	ND	ND	ND	ND	
comp160757_c1_seq8	1.46190209	1.421134437		0.236585931		0.142266592	-0.055506726	0.729582207	-0.543915875	-0.717465412	
comp160822_c0_seq1	0.840173385	0.847648462		-0.147843808		-0.439009627	-0.027475917	-0.137881881	ND	ND	
comp160860_c0_seq1	1.623415174	1.619281972		0.9329786		0.727277309	0.791509879	0.860173754	0.928801631	0.693914645	
comp160964_c0_seq1	1.522143709	1.575051937		-0.639209807		-0.64637897	0.24839292	-0.177863552	-1.281408914	-1.108170965	
comp161912_c1_seq3	0.873222987	0.817002831		-0.265854134		-0.126895261	-0.097424797	-0.202447888	-0.46089521	-0.319841944	
comp162206_c0_seq1	1.358950811	1.367914167		-0.208684761		-0.312763937	0.287508825	0.39551182	0.093598804	-0.251677186	
comp162382_c2_seq6	1.512383501	1.551084262		0.239954456		0.232785293	-0.366133173	0.593498729	0.34957766	0.163793667	
comp162514_c0_seq2	0.985694067	1.027485821		-1.061123473		-1.068292635	0.040359075	0.170687204	0.40388739	-0.18766195	
comp162536_c0_seq1	0.552428093	0.612476659		-0.523963134		-0.531132297	-0.719145777	-1.178643182	-1.003434944	-1.432256986	
comp162543_c0_seq11	0.473338684	0.503049863	ND			-1.548660967	-1.695281762	-1.279717904	-1.280600924	-1.40839297	
comp162543_c0_seq18	0.400738038	0.364869719		-1.611317396		-1.618486558	-1.765107354	ND	ND	ND	
comp162543_c0_seq4	0.534592043	0.471278076		-1.114713576		-1.121882738	-1.745624788	-1.807182185	ND	ND	
comp162543_c0_seq6	0.455177323	0.510609107		-1.548444943		-1.555614106	-1.702234901	-1.763792297	ND	ND	
comp162802_c0_seq2	0.697092034	0.658151824		-0.206552536		-0.137333353	-0.328157811	0.136254615	-0.199267002	-0.510703445	
comp162802_c1_seq1	0.678139227	0.663281117		-0.277374326		-0.390998819	-0.450469439	-0.009351476	-0.26426793	-0.630942065	
comp163485_c2_seq1	2.468156772	2.524761401		0.766432222		0.715523536	1.315753368	1.237924426	1.388371999	1.090951947	

comp163485_c2_seq14	2.718230045	2.736956457	0.732061731	0.742151574	1.683551746	1.449571915	1.567765687	1.212094747
comp163560_c1_seq3	0.379776412	0.316343607	-0.368573349	-0.579862494	-0.881385249	-0.884950699	-0.913862443	-1.740624494
comp163696_c0_seq8	0.584758421	0.538427921	ND	-1.110573297	-1.558224088	ND	ND	-1.271335297
comp163697_c0_seq6	2.133984506	2.091305084	0.664091392	0.585746638	0.617195668	0.731729531	0.312703115	-0.076610385
comp163821_c1_seq2	0.52512306	0.541200702	-0.814197721	-0.821366883	-0.699142366	-0.55242382	-0.79634489	-0.681098887
comp163922_c2_seq11	0.50847929	0.463962426	-1.188398497	-1.195567659	-0.64321845	-0.449503342	ND	ND
comp163922_c2_seq12	0.564491047	0.61679474	-0.408946755	-0.980387349	-0.303099403	-0.323264114	ND	ND
comp163922_c2_seq13	0.585443976	0.604397557	-0.710608114	-0.81468729	-0.48418683	-0.323895477	ND	ND
comp163922_c2_seq2	0.686179935	0.691436193	-0.116151638	-1.026410788	-0.474061579	-0.49422629	ND	-1.488202783
comp163922_c2_seq3	0.404027235	0.385554318	-1.452330099	-1.459499261	-0.492176704	-0.553734101	ND	ND
comp164037_c2_seq3	1.542346027	1.555775388	-0.891903466	-0.694952646	0.43718016	0.446632207	-0.55183134	-0.582713373
comp164086_c0_seq5	0.9078094	0.912974696	ND	ND	-0.939972657	-0.098440067	0.127920694	-0.476992606
comp164110_c0_seq8	1.78433369	1.795200389	-0.757642138	ND	-1.212462091	ND	ND	ND
comp164303_c0_seq3	1.495745687	1.446015076	0.287205835	0.020399362	0.370204977	0.255128325	-0.076239671	-0.160566023
comp164303_c0_seq6	1.489572847	1.497925818	-0.01210458	-0.098454989	0.448064676	0.25763825	-0.006486206	-0.156554647
comp164303_c1_seq4	1.577935115	1.566356828	0.758122463	0.678081529	0.458910066	0.28217377	-0.71870925	-1.022592555
comp164303_c1_seq5	1.782524632	1.799419386	1.014314707	0.895171784	0.683197943	0.535725917	-0.572367073	-0.922007869
comp164320_c1_seq3	0.2002028	0.141401391	-1.374602891	-1.381772054	-1.528392849	-1.28892025	-1.715772003	-1.542534053
comp164320_c1_seq4	0.62114004	0.633959591	ND	ND	-1.270658846	-1.089178193	-1.060097991	-1.28480005
comp164320_c5_seq2	-0.009155784	0.027526564	ND	ND	ND	ND	ND	ND
comp164974_c0_seq2	2.61269226	2.644480622	0.975557905	0.799596722	0.412643772	1.106629835	0.164566778	-0.118127228
comp165178_c2_seq7	0.972255258	0.910630628	-0.320377173	-0.279241656	0.18747855	-0.010298593	-0.03466271	-0.488308335
comp165178_c2_seq9	1.346633175	1.391897156	0.397053294	0.207358762	0.634336886	0.413655016	0.448684552	-0.016050046
comp165223_c0_seq2	0.510788712	0.491914871	-1.411945844	ND	ND	-1.451201939	ND	ND
comp165249_c2_seq8	1.382512179	1.440827622	0.321390148	0.356510047	0.369245554	0.360217208	0.454039656	0.101070916
comp165358_c2_seq2	2.174486115	2.235260012	-0.487389822	-0.654259828	1.255176824	0.771030436	0.030625567	-0.250750397
comp165793_c0_seq10	2.250378369	2.285415037	1.304386535	1.081198166	0.855396125	1.166750731	1.098307077	0.835425377
comp165793_c0_seq4	1.771615224	1.790877449	0.743813251	0.704192064	0.061315004	0.669601986	0.541262573	0.392785928
comp165793_c0_seq5	1.228369375	1.249078697	0.045021565	0.050086858	-0.538893085	0.160667429	0.017116905	-0.161827663
comp165793_c0_seq6	2.825787415	2.858971504	1.947433408	1.938538798	1.755510348	1.838196843	1.652297224	1.409569435
comp165793_c0_seq7	1.62461517	1.683336325	0.679905348	0.710779539	-0.035108347	0.628239995	0.416896813	0.234747105

comp165793_c0_seq8	1.458205633	1.47274144	-0.032206602	0.164744218	-0.458997832	0.408863697	0.131774264	-0.097475423
comp165793_c0_seq9	1.331985035	1.308487549	0.11729111	-0.11627443	-0.587406317	0.277607369	0.034400013	-0.093392033
comp166193_c0_seq3	2.096585347	2.152922383	0.634483936	0.969737454	1.057199865	0.809566988	0.925338039	0.502268326
comp166272_c1_seq5	0.145083131	0.153736755	ND	ND	ND	ND	ND	-1.142808863
comp166482_c1_seq5	1.060544406	1.110447123	-0.294629137	-0.602828295	0.02870216	-0.413066478	0.177115108	-0.110377781
comp166482_c1_seq8	1.42078547	1.393567011	-0.036928164	-0.027391633	0.740200959	0.314312155	0.470635049	0.277902196
comp166736_c1_seq1	2.090542722	2.091663894	1.006400859	1.033993802	0.852610901	1.308469354	0.285020506	0.060318446
comp166873_c0_seq1	0.77580473	0.814947677	ND	ND	-0.84036874	-0.424804881	ND	-0.076358693
comp167159_c0_seq1	0.4759344	0.481099697	ND	ND	ND	ND	ND	ND
comp167541_c0_seq11	2.35683211	2.381931172	-0.381281454	-1.087420622	0.2974375	1.064236669	-0.120390575	0.052847375
comp167607_c0_seq5	1.336066722	1.329115273	-0.160471066	-0.440641501	-0.677438927	-0.59766717	-0.398977836	-0.575074562
comp167661_c0_seq2	1.097219156	1.134043315	-0.243929038	-0.150428039	-0.069250752	-0.488565769	-0.344765994	-0.205386312
comp167806_c0_seq1	1.221137112	1.18802024	-0.602974236	-0.434052139	0.347039528	-0.0259299	0.195735739	0.378313715
comp167806_c0_seq5	1.150199789	1.221918662	-0.640078272	-0.148406931	0.375489646	-0.100137259	-0.140948227	0.37690029
comp167841_c2_seq4	1.83094523	1.842034916	0.522852521	0.268703124	0.563927823	0.623955522	1.002968007	0.559694908
comp167848_c0_seq10	1.225017249	1.214790861	-0.186480425	-0.330487547	-0.704352124	-0.739580582	-0.949723224	-1.320553319
comp167848_c0_seq13	1.216965138	1.173545148	-0.639085599	-0.481444513	-0.702698926	-1.065286318	-1.316046812	-1.619930117
comp167848_c0_seq14	0.959975768	0.932856123	-0.793453518	-0.97671394	-0.998395999	-1.184892132	-1.185775152	-1.438505935
comp167848_c0_seq2	1.258724803	1.242099846	-0.312965623	-0.304340518	-0.57590005	-0.880495495	-1.006317253	-1.134109299
comp167848_c0_seq3	1.239651654	1.240592652	-0.416326218	-0.44468468	-0.591305475	-1.05080288	-1.079714624	-1.304416684
comp167848_c0_seq34	1.226510456	1.216616662	-0.328510285	-0.408230115	-0.482300243	-0.703558482	-1.181562758	-1.066316755
comp167848_c0_seq37	1.23623542	1.219500564	-0.561940194	-0.514751695	-0.850428726	-0.953378808	-1.000019319	-1.428841361
comp167848_c0_seq4	1.082841799	1.033870434	-0.566035733	-0.494023649	-0.781973597	-0.843530994	-0.937168068	-1.211088149
comp167848_c0_seq47	1.200197919	1.193530587	-0.716904497	-0.72407366	-0.957844631	-0.718372031	-1.196376307	-1.22725834
comp167848_c0_seq5	1.213861322	1.194545752	-0.446905511	-0.521021463	-0.746823504	-0.808380901	-0.809263921	-1.238085963
comp167848_c0_seq52	1.048291661	0.998155736	-0.711155659	-0.4878759	-0.864945617	-1.227533009	-0.973143525	-1.180116817
comp167848_c0_seq58	1.055144193	1.046894206	-0.543743694	-0.713640154	-0.901653635	-1.118112991	-1.089032788	-1.313734847
comp167848_c0_seq59	0.960597861	0.991951376	-0.471116831	-0.60322473	-0.527996776	-0.589554172	-1.113315938	ND
comp168033_c0_seq2	0.091837619	0.117524582	ND	ND	ND	ND	ND	ND
comp168033_c1_seq4	0.357329289	0.388932111	-1.572191257	ND	-1.725981215	-0.372565263	-1.010270382	-0.837032432
comp168097_c0_seq2	0.764375268	0.825980615	0.027795726	-0.13146442	-0.728054223	-0.600555384	0.263282026	-0.203804516

comp168471_c0_seq12	2.67044393	2.729876222	0.365409726		0.292220764	1.715550063	1.592622536	0.497633997	0.501283614
comp168564_c1_seq1	1.299569791	1.308621668	-1.459877529	ND		-1.312637492	-1.073164892	-0.721865395	-0.627808691
comp168609_c1_seq1	0.045201878	0.031579108	ND	ND		-1.131638898	-1.193196294	ND	-0.844750106
comp169022_c0_seq15	0.769377806	0.742535719	ND		-0.954349283	-0.402000074	-0.259437488	ND	-1.11511282
comp169124_c1_seq1	1.200920482	1.193435747	-0.819407478		-0.173364127	-0.67216744	-0.432694841	0.094695915	-0.811247381
comp169129_c1_seq2	0.65707528	0.721988867	-0.26093163		-0.150001481	-0.664599061	-0.566455615	-0.426009483	-0.632982775
comp169282_c0_seq3	1.221986345	1.216704191	ND	ND		-1.108669296	ND	-0.995018454	-1.1228105
comp169409_c1_seq10	0.674054244	0.611698425	-0.619578372		-0.802838794	-1.852549576	-1.312046981	-0.835808747	-1.167720776
comp169409_c1_seq11	0.733468702	0.678136725	-0.593732805		-0.71484532	-1.560436119	-1.32096352	-0.492542768	-0.972517332
comp169409_c1_seq14	0.659000273	0.616501375	-0.570105028		-0.64422098	-1.870023022	-1.454459163	-0.853282193	-1.185194221
comp169562_c0_seq20	0.789556797	0.754655081	-0.067937434		-0.142053386	-1.066825432	-0.429412824	-0.95317459	-1.381996631
comp169562_c2_seq10	0.193440705	0.258272936	-1.072648162		-1.38084732	-1.305619366	-1.221048726	-1.589908532	-1.541609319
comp169562_c2_seq22	0.072811818	0.123663122	-0.959193843		-1.744514256	-1.414013796	-0.998449938	ND	-1.604246259
comp169699_c0_seq8	1.394357941	1.408605819	0.398584472		0.245287274	0.074307133	0.685912477	-0.448864123	-0.61444473
comp169922_c0_seq2	0.364015026	0.371950214	-1.53770118	ND	ND	ND	ND	-1.577840296	-1.404602346
comp170116_c0_seq1	0.562980349	0.595966551	-0.181704458		-0.732941666	-0.226349947	-0.463998602	-0.413729101	-0.717612406
comp170419_c0_seq3	0.677904318	0.648539969	0.045158164		-0.451031476	-0.229675486	0.02503708	-1.563182676	-0.845876682
comp170544_c0_seq3	0.196093703	0.192158201	ND	ND		-0.922755126	ND	ND	-0.93689633
comp170858_c0_seq13	0.508572813	0.568176444	-0.511451551		-0.569773236	-1.017424027	-0.35882212	-0.391889824	-0.679382713
comp170858_c0_seq27	0.725570814	0.69425334	-0.414932564		-0.584829024	-0.28148081	-0.162302043	-0.102889162	-0.3890437
comp170951_c1_seq3	1.055412612	1.025391541	-0.634701831	ND		-0.186431798	-0.424080453	-1.151962202	ND
comp171097_c0_seq9	1.035217657	1.043197434	ND	ND		-0.446032855	-0.155407734	ND	-0.761204055
comp171539_c0_seq3	0.381353049	0.413071978	-0.780000467		-0.78716963	-0.933790425	-0.995347821	ND	ND
comp171587_c0_seq20	1.117315057	1.103506413	0.20847911		-0.020538802	-0.132397491	0.260303484	0.013438034	-0.658422056
comp171587_c0_seq9	1.095745078	1.052070822	0.0939634		0.111617821	0.141088285	0.125288379	-0.062681285	-0.605446679
comp171735_c0_seq4	1.268285184	1.216046205	0.30703442		0.30466414	0.405827828	0.549064262	-0.043894529	-0.051711258
comp171802_c0_seq6	0.150655665	0.120391223	-0.990494466		-0.742391123	-0.940164441	-0.603781829	-1.252482331	-1.857395632
comp171996_c0_seq1	1.114039799	1.130891656	0.292691733		0.251937187	0.408523307	0.290213036	0.457933253	0.168899069
comp172652_c5_seq1	1.260698201	1.257231193	-0.595659132		-0.204888286	ND	0.064054777	ND	-0.587499035
comp172717_c0_seq1	1.076841796	1.023225126	-0.021904485		-0.00932959	-0.229379302	-0.666600313	-0.416758456	-0.709360751
comp173318_c0_seq10	0.721922347	0.711861291	-0.486174573		-0.067375004	-0.573017742	-0.576583191	-0.263072254	-0.35307574

comp173318_c0_seq9	0.209405146	0.304793154	-0.88827929	-0.497508444	-1.343099244	-0.62650539	-0.384350362	-0.658270444
comp173544_c0_seq3	0.09479084	0.12192787	-0.733685313	-0.849998945	-1.364596526	-0.789331825	-0.773824429	-0.776677739
comp173681_c0_seq1	3.671916577	3.648263839	0.631772957	0.619071306	ND	0.120858503	-1.30599325	-0.091362616
comp173797_c2_seq1	0.215805138	0.292623168	ND	-1.149370959	-0.614750516	-1.454459163	-0.927068407	-1.407042971
comp173797_c2_seq3	0.204493478	0.211808751	ND	-1.911641132	-0.643288579	-1.517759332	-1.342551094	-1.771373135
comp174253_c1_seq11	2.082063439	2.095561644	-0.202844765	-0.306923941	-0.328605999	0.878473071	0.171989467	-0.015388269
comp174253_c1_seq3	1.94222411	1.948466039	-0.236036184	-0.516206619	-0.021849357	0.896271669	0.024854696	-0.088696911
comp174253_c1_seq5	2.02793016	2.040514078	-0.148487103	-0.130832682	-0.070327984	0.96081107	0.137227361	-0.055505492
comp174780_c0_seq9	2.581584282	2.5978437	ND	ND	-0.457835062	-0.644331195	-0.946244211	-1.074036257
comp174805_c1_seq1	2.828872255	2.766992974	-0.793788751	-0.289074553	ND	-0.532014851	-0.833927867	-1.08665865
comp175298_c0_seq1	1.287641003	1.331445963	0.613608741	0.565805192	0.088455669	-0.085659137	0.425143482	0.155474277
comp176191_c0_seq1	0.036601706	-0.030465383	ND	-1.090528288	ND	-0.997676484	-0.646376986	-0.950260291
comp177866_c0_seq1	0.075165101	0.138176388	ND	ND	-0.976736938	-0.737264339	-0.863086096	ND
comp182035_c0_seq1	0.126418353	0.058365351	ND	ND	ND	ND	ND	-1.182662939
comp187502_c0_seq1	0.18592405	0.222606398	ND	ND	ND	-1.279717904	-1.104509665	-0.931271716
comp188802_c0_seq1	0.029689712	0.079736021	ND	ND	-0.846121069	ND	ND	ND
comp189731_c0_seq1	0.292557817	0.263887118	ND	ND	-0.734520639	ND	ND	ND
comp35841_c0_seq1	0.026436554	0.047324635	ND	ND	ND	ND	ND	ND
comp36142_c0_seq1	0.122806736	0.072338908	ND	ND	ND	ND	ND	ND
comp44516_c0_seq1	0.55703589	0.570010888	ND	-1.172154095	ND	-0.778272295	ND	ND
comp88516_c0_seq1	0.067709219	0.025210321	ND	ND	-0.859254084	ND	ND	-0.873395288
comp89759_c0_seq1	0.456210911	0.421200035	ND	ND	-0.702146459	ND	ND	ND
comp92950_c0_seq1	0.713641894	0.6730583	-0.28378627	-0.328743994	-1.03963622	-0.976254879	-1.403106632	-0.752747428
comp93984_c0_seq1	3.069188812	3.132496776	1.488541986	1.29495829	0.974479117	1.720144419	0.354397848	0.80063707
Transcript ID	Root1 (RPKM_log10)	Root2 (RPKM_log10)	Flower1 (RPKM_log10)	Flower2 (RPKM_log10)	Stem1 (RPKM_log10)	Stem2 (RPKM_log10)	Leaf1 (RPKM_log10)	Leaf2 (RPKM_log10)
comp101679_c0_seq1	ND	-0.648392212	ND	ND	-1.311007867	-0.895444009	0.103672971	0.072790938
comp110908_c0_seq1	ND	-1.326355739	ND	ND	-1.210820144	-0.369287554	0.28304194	0.222196683
comp122712_c0_seq1	-0.689379768	-0.777636157	ND	-1.117539757	-0.963130557	-1.325717949	0.150520285	0.101909485
comp132035_c0_seq1	ND	-0.359596673	ND	ND	ND	ND	0.381473126	0.440767723
comp132667_c0_seq1	ND	ND	-0.890698764	ND	-0.743458727	-1.106046119	0.324434625	0.321581315
comp136368_c0_seq1	-0.900177171	-0.590493551	ND	ND	-1.17392796	ND	0.229757493	0.192142077

comp137559_c0_seq1	ND	ND	ND	ND		-1.087523355	ND	0.172255523	0.199365437
comp142015_c0_seq1	ND	-1.310439599	ND	ND		-1.194904004	ND	0.094838097	0.046227297
comp149196_c1_seq12	ND	ND	ND	ND		-1.527203544	ND	0.166230895	0.174658596
comp149468_c0_seq2	ND	-1.352684678	ND	ND		ND	ND	0.052593018	0.110437549
comp152503_c0_seq5	ND	-0.640151082	ND	ND		ND	-0.71111162	0.06615661	0.005311353
comp153325_c0_seq1	ND	-1.184076478	-0.43762967	-1.222950083		-0.767510887	-0.476885765	0.124291205	0.172590418
comp153359_c0_seq4	ND	ND	ND	ND		ND	ND	0.142183057	0.169292971
comp155876_c1_seq1	-1.151953325	-1.240209713	-0.97088416	ND		-1.124674118	-0.885201519	0.030369409	0.091633599
comp156118_c0_seq20	-0.968783768	-0.534161412	-0.662775867	ND		-1.117595821	-0.525940703	0.251327526	0.200701435
comp157728_c0_seq1	-0.636039359	ND	ND	ND		ND	ND	0.06916212	0.13042631
comp158397_c0_seq5	-1.815843493	-1.205129877	-0.458683069	-0.437823509		-1.788564286	-0.736178331	0.249365842	0.25799235
comp160156_c0_seq11	ND	ND	-1.10155213	-1.108721292		-1.255342088	ND	0.113581259	0.092244544
comp160968_c0_seq11	-1.22132914	-1.610615525	0.226911752	0.156690844		0.663282563	0.771742278	1.467375614	1.491212944
comp160968_c0_seq6	-0.867923601	-1.324156775	0.28096088	0.305976401		0.885966397	0.920153122	1.641957087	1.611234204
comp160968_c0_seq9	-1.172521281	-1.26077767	-0.037209607	0.205498703		0.729819189	0.797521903	1.549333743	1.524563852
comp162420_c0_seq5	0.485522728	0.505862111	ND	ND		-0.954559483	-1.016116879	1.27966529	1.284960334
comp162798_c0_seq18	ND	ND	ND	-1.099340917		-1.546991708	-1.006489113	0.256855214	0.194741943
comp163815_c1_seq1	ND	-0.311291993	ND	ND		-0.718635143	-0.215921109	0.530678301	0.471343636
comp164089_c0_seq9	-1.040510235	-0.651645369	ND	ND		-1.013231029	ND	0.100419813	0.08657112
comp164945_c0_seq24	-1.165772951	-1.25402934	-1.160795046	-0.991872949		-1.314585004	-1.075112404	0.141488519	0.110606486
comp168953_c0_seq2	-0.92960279	-0.84176792	-0.572442367	-1.056732784		-0.726232325	-0.565940971	0.642691022	0.615014129
comp169017_c1_seq13	ND	ND	ND	ND		ND	ND	-0.008003835	0.010332154
comp169903_c0_seq2	-0.278477231	-0.525096112	0.666435718	0.584632937		0.084594077	0.231312623	1.416403234	1.362197307
comp169903_c0_seq3	-0.95637451	-1.220722158	-0.298184091	-0.356505776		-0.503126571	-0.467773955	0.78661553	0.789157252
comp170376_c0_seq5	-0.166258468	0.164614451	-0.189309286	-0.594418457		-0.087826739	0.175126956	0.770551598	0.795047896
comp171332_c1_seq2	-1.586610719	-0.528739072	-0.627390304	-0.333529471		-0.127967748	0.259924684	1.193805819	1.129818662
comp171332_c1_seq4	ND	-0.683419773	-0.51882957	-0.488210172		-0.299038865	0.056939303	0.980563605	0.9402325
comp174367_c3_seq1	ND	-0.906917874	-0.637592321	ND		ND	ND	0.167366603	0.194476517
comp174889_c2_seq12	0.006509478	0.075860943	0.731646687	0.407653261		-1.170331298	ND	1.693827939	1.745967093
comp174889_c2_seq13	0.174508512	0.444009743	1.003142588	1.011605248		-0.317737385	-0.590148147	1.950548076	1.901312841
comp174889_c2_seq15	0.106050149	0.110547814	0.078843372	0.161850839	ND		-1.250447335	0.849040189	0.900772578

comp175125_c4_seq34	ND	-1.387625396	-1.118299843	ND	-1.272089801	-1.032617202	0.072009963	0.128742343
comp175269_c0_seq7	-1.081313247	ND	-0.900244082	ND	-0.208936	-0.416621432	0.56476678	0.613065993
comp175639_c2_seq1	ND	ND	ND	ND	-0.866584122	ND	0.288459405	0.295365932
comp185013_c0_seq1	ND	ND	ND	-0.741239148	ND	-0.949417339	0.128880886	0.177180099
comp99245_c0_seq1	ND	-1.266479649	ND	ND	-0.849914058	-0.911471454	0.041888035	-0.018957222
Transcript ID	Root1 (RPKM_log10)	Root2 (RPKM_log10)	Flower1 (RPKM_log10)	Flower2 (RPKM_log10)	Stem1 (RPKM_log10)	Stem2 (RPKM_log10)	Leaf1 (RPKM_log10)	Leaf2 (RPKM_log10)
comp10084_c0_seq1	0.03737654	-0.31972516	ND	-0.90266681	1.471850479	1.525642895	ND	-0.762398814
comp127509_c0_seq1	0.769506076	0.31066843	-0.920608368	-0.25877075	1.604423437	1.53675772	ND	-0.486479539
comp127993_c0_seq1	-0.994031924	-0.684348304	-1.113992755	ND	0.054436582	0.013082572	-0.853101875	-0.679863926
comp134280_c0_seq1	-1.238099351	-0.849234485	-1.057030186	-0.763169353	0.28054155	0.204743714	-0.620048047	-0.923931353
comp139268_c0_seq2	ND	ND	ND	-0.596032937	0.724707685	0.760060302	-1.106124145	-0.279673681
comp139707_c0_seq3	-0.579173988	-0.667430376	-0.19398484	-0.627122735	1.731406448	1.741807728	-0.292115903	-0.151062637
comp144837_c0_seq1	0.350415444	0.013158059	0.046394424	-0.102103892	1.015729862	1.048531014	-0.294774688	-0.473719256
comp146627_c0_seq1	-0.154192329	0.037391979	0.167055539	-0.098391639	1.830762563	1.774642414	-0.08020907	0.336066928
comp146710_c0_seq1	-0.28970157	-0.491901311	-0.620515766	-0.530774916	0.596762138	0.539800493	-0.058594891	-0.788446928
comp147072_c0_seq2	-0.007903441	-1.210103182	-0.940777629	ND	0.676284425	0.629204852	ND	ND
comp147072_c0_seq3	0.027546006	0.010982842	-0.683479432	-0.690648595	0.89512437	0.839953772	-1.422588553	-0.508987914
comp150249_c0_seq1	0.321620119	0.424178246	0.319044886	0.280276738	1.11353059	1.173248794	-0.874909094	-0.650518622
comp150605_c0_seq1	-0.672454873	-0.310742253	-1.231748398	-1.539947556	0.257914321	0.316332241	-1.271887514	-1.700709556
comp150605_c0_seq5	-0.542134856	-0.32936125	-1.382254991	-1.213332895	0.356049654	0.300024746	-1.024454098	-1.374094894
comp152562_c0_seq1	ND	ND	-0.686578782	ND	0.822389092	0.830467624	-0.249596643	-0.155539939
comp153090_c0_seq3	-0.298286557	0.159198683	-0.782329129	-0.914437029	0.768245949	0.815236873	-0.880460192	-1.251290287
comp153459_c0_seq2	0.077994391	0.114676739	0.48809089	0.275375489	1.596245965	1.640313297	0.253686546	0.14761375
comp154068_c0_seq4	-0.880328978	-1.269615362	-0.273291081	-0.308488968	1.136696594	1.092571417	0.154547678	0.506946118
comp155674_c1_seq1	-0.034841491	0.303759889	0.247388563	0.198826715	1.146127657	1.201692746	0.146833525	0.184192752
comp158300_c0_seq4	-0.904631513	-0.992887901	ND	-0.730731511	1.474830212	1.419025145	-0.763701464	0.387260091
comp159808_c1_seq1	0.387624559	0.466859257	-0.008542684	-0.367894365	1.392627371	1.364277882	-0.249596643	-0.461709575
comp159808_c1_seq6	0.411067809	0.475579251	-0.337281952	-0.423632361	1.407470449	1.389378747	-0.280511055	-0.380274377
comp160155_c0_seq3	0.564802914	0.846903012	0.685487318	0.602483168	1.609276042	1.606036592	0.477574739	0.458534668
comp161190_c0_seq1	-0.445060503	-0.533316891	0.124869013	-0.034588494	1.108825322	1.063443822	0.065980461	0.074162451
comp161575_c0_seq6	0.071062861	0.294831852	-0.121448637	0.09323095	0.890194596	0.919207034	-0.299890451	-0.446165903

comp162571_c1_seq1	1.12251376	1.471395989	0.481915296	0.390425247	2.29419802	2.24260758	-0.135460228	-0.071366748
comp162571_c1_seq2	0.698879126	1.002272657	0.226735777	0.010306992	1.629602991	1.697130161	0.278367035	-0.296583043
comp163445_c1_seq16	-0.430948576	-0.065564806	-0.148421771	-0.305353254	0.967884553	0.920661609	-0.527379443	-0.37434488
comp163930_c0_seq1	1.356444332	1.577149311	0.606153732	0.564589731	2.15880861	2.206795176	1.384823082	1.300608244
comp164910_c0_seq13	-0.059285233	0.391534477	0.121783931	0.186496776	0.957443791	0.925968261	-0.362052684	-0.082359403
comp165301_c0_seq2	0.545709814	1.109148562	1.187359983	1.082268072	2.130911421	2.142037338	0.736275008	0.802719711
comp165358_c0_seq1	1.437109922	1.547393949	1.582792545	1.521806949	2.249397803	2.270222623	0.381909862	0.69672822
comp166591_c0_seq22	-1.21406302	-1.068236203	-0.673971913	-0.771317706	0.339186008	0.329806624	-0.441109757	-0.665811816
comp166591_c0_seq42	-1.278393946	-1.299703545	-0.796294785	-0.678525211	0.361669118	0.38774311	-0.453217149	-0.566285939
comp166591_c0_seq46	-1.368311246	-1.252447652	-1.041114046	-0.893381249	0.371617662	0.36530818	-0.463953204	-0.452083257
comp167462_c1_seq2	0.912649088	0.410094771	1.613714689	1.496817426	2.368277421	2.355041289	1.147436696	1.275521812
comp168568_c0_seq1	0.772459327	0.761076892	0.659965061	0.597614929	1.577261737	1.545066581	0.507852186	0.170800517
comp168857_c0_seq53	-0.541012234	-0.291515819	0.011668001	-0.029359429	0.904178063	0.929859555	0.01292157	0.019828098
comp169360_c0_seq3	0.461385613	0.684942257	0.553954602	0.651945528	1.34841679	1.36092826	0.590011879	0.304455955
comp170838_c1_seq1	-0.034384116	0.081479478	0.498124548	0.554489234	2.655841705	2.616886523	1.035571654	0.827653215
comp171899_c0_seq2	-0.264428289	0.698467844	0.539890165	0.440950629	1.740574522	1.749929509	0.247569621	0.515865579
comp171899_c0_seq4	-0.596452475	-0.082648872	0.324979379	0.121515571	0.993119596	0.960333942	-0.154492431	-0.407223214
comp174020_c0_seq7	-0.418555415	-0.506811804	0.415726263	0.278223332	1.169029035	1.205177792	0.058166735	-0.069625311
comp176711_c0_seq1	0.569210128	-0.322751615	-0.19172876	-0.25688987	1.528092479	1.568929778	ND	-0.660689918
comp184226_c0_seq1	ND	0.165829262	-1.027243183	-1.034412346	1.188182717	1.141224829	ND	-0.71805309
comp199478_c0_seq1	-0.341540231	ND	-0.637592321	ND	0.287798967	0.18845301	ND	-0.504493487
comp226042_c0_seq1	ND	ND	ND	-0.695673865	1.707933692	1.761728934	-0.427613823	ND
comp231923_c0_seq1	-0.834571487	-0.922827876	-0.255562314	-0.007458972	0.904514948	0.920025438	ND	ND
comp35910_c0_seq1	-0.954798122	0.118313492	-0.074758953	-0.303776865	0.929813581	0.862182037	-0.637776814	-0.397592075
comp43805_c0_seq1	0.052527885	-0.132638517	0.090929546	0.083760383	0.880524169	0.860858934	0.025966846	0.199204795
comp45349_c0_seq1	-1.228955971	-0.618242356	-0.746856811	-0.356085965	0.877504481	0.8123128	-0.008844677	-0.516847964
comp58595_c0_seq2	ND	-0.249446309	-0.014882862	-0.800203275	0.492508623	0.577079263	ND	-0.220602585
comp74633_c0_seq1	ND	-0.035085581	ND	-0.4496228	0.915639766	0.913325285	ND	ND
comp97270_c0_seq1	0.129346544	-0.102331987	-0.115553024	-0.055775397	0.83331936	0.830467624	-0.331783399	-0.408422923

Table S3 List of organ-specific transcripts potentially involved in specific organ-related biological functions.

Transcript IDs	Length	Functional annotations	GO/KOG annotations ^a	Root1 ^b	Root2 ^b	Flower1 ^b	Flower2 ^b	Stem1 ^b	Stem2 ^b	Leaf1 ^b	Leaf2 ^b	Root_ average ^c	Flower_ average ^c	Stem_ average ^c	Leaf_ average ^c
comp133870_c0_seq1	951	DROOPING LEAF	GO:0048440 (carpel development)	0.03	0.03	98.54	90.71	0.07	0.03	0.00	0.13	0.03	94.63	0.05	0.07
comp137025_c0_seq1	1569	Cytochrome P450 71A1	GO:0009835 (ripening)	0.00	0.00	83.37	72.54	0.00	0.02	0.05	0.00	0.00	77.95	0.01	0.03
comp138834_c0_seq2	1138	LOB domain-containing protein 6	GO:0048441 (petal development)	0.03	0.20	4.68	4.80	0.06	0.15	0.04	0.14	0.11	4.74	0.10	0.09
comp139349_c0_seq1	902	DROOPING LEAF	GO:0048440 (carpel development)	0.00	0.00	4.52	4.44	0.00	0.00	0.00	0.00	0.00	4.48	0.00	0.00
comp139414_c0_seq1	922	DROOPING LEAF	GO:0048440 (carpel development)	0.03	0.08	25.01	25.93	1.66	3.73	0.37	0.48	0.06	25.47	2.69	0.42
comp140455_c0_seq1	1377	Floral homeotic protein AGAMOUS		0.00	0.00	128.11	114.11	0.28	0.16	0.09	0.00	0.00	121.11	0.22	0.05
comp140923_c0_seq1	1172	MADS-box transcription factor 16	GO:0009908 (flower development)	0.31	0.66	23.78	22.07	0.14	0.19	0.07	0.13	0.49	22.93	0.17	0.10
comp140923_c0_seq4	1028	MADS-box transcription factor 16	GO:0009908 (flower development)	0.53	0.97	32.34	30.22	0.03	0.03	0.04	0.06	0.75	31.28	0.03	0.05
comp142957_c0_seq1	1188	Floral homeotic protein AGAMOUS		0.00	0.00	17.30	15.41	0.00	0.02	0.00	0.05	0.00	16.36	0.01	0.03
comp142957_c0_seq2	1268	Floral homeotic protein AGAMOUS		0.00	0.00	10.30	10.45	0.03	0.00	0.00	0.00	0.00	10.37	0.01	0.00
comp145011_c0_seq1	1670	AP2-like ethylene-responsive transcription factor	GO:0009908 (flower development)	0.05	0.13	3.99	4.04	0.12	0.15	0.08	0.17	0.09	4.01	0.13	0.12
comp145893_c0_seq2	1636	AP2-like ethylene-responsive transcription factor	GO:0009908 (flower development)	0.17	0.14	4.58	4.06	0.14	0.26	0.03	0.13	0.15	4.32	0.20	0.08
comp145893_c0_seq3	1421	AP2-like ethylene-responsive transcription factor	GO:0009908 (flower development)	0.09	0.07	4.50	4.07	0.07	0.18	0.00	0.15	0.08	4.28	0.12	0.08
comp145893_c0_seq4	2532	AP2-like ethylene-responsive transcription factor	GO:0009908 (flower development)	0.07	0.07	4.11	4.39	0.19	0.22	0.08	0.11	0.07	4.25	0.21	0.10
comp146369_c0_seq2	1163	LOB domain-containing protein 6	GO:0048441 (petal development)	0.45	0.45	6.13	6.34	0.50	0.48	0.51	0.27	0.45	6.24	0.49	0.39
comp146487_c0_seq1	1268	MADS-box transcription factor 16	GO:0009908 (flower development)	0.00	0.02	17.42	16.02	0.10	0.04	0.00	0.05	0.01	16.72	0.07	0.02
comp146487_c0_seq5	1187	MADS-box transcription	GO:0009908 (flower development)	0.00	0.04	22.62	21.91	0.19	0.12	0.00	0.03	0.02	22.27	0.16	0.01

		factor 16													
comp146487_c0_seq7	781	MADS-box transcription factor 16	GO:0009908 (flower development)	0.00	0.03	8.36	7.99	0.00	0.00	0.00	0.08	0.02	8.17	0.00	0.04
comp152995_c0_seq1	2058	Floral homeotic protein APETALA 2	GO:0010093 (specification of floral organ identity)	0.50	1.17	12.80	12.88	0.51	1.00	0.23	0.23	0.84	12.84	0.75	0.23
comp152995_c0_seq2	2137	Floral homeotic protein APETALA 2	GO:0010093 (specification of floral organ identity)	0.49	0.93	11.53	11.13	0.46	0.79	0.18	0.24	0.71	11.33	0.62	0.21
comp154859_c0_seq3	573	Protein CCA1	GO:0048574 (long-day photoperiodism, flowering)	0.00	0.17	7.27	6.68	0.11	0.20	0.44	0.11	0.09	6.97	0.16	0.28
comp154859_c0_seq8	2096	Protein CCA1	GO:0048574 (long-day photoperiodism, flowering)	0.70	0.62	22.40	20.27	0.73	0.63	0.50	0.27	0.66	21.34	0.68	0.39
comp155097_c0_seq4	702	Probable histone-arginine methyltransferase 1.3	GO:0009909 (regulation of flower development); GO:0010228 (vegetative to reproductive phase transition of meristem)	2.48	3.65	16.16	15.70	2.59	2.37	1.92	1.97	3.07	15.93	2.48	1.95
comp157450_c1_seq12	413	Floral homeotic protein AGAMOUS		0.00	0.06	4.26	4.85	0.08	0.00	0.00	0.00	0.03	4.56	0.04	0.00
comp157450_c1_seq7	1392	Floral homeotic protein AGAMOUS		0.00	0.04	15.43	14.17	0.00	0.00	0.00	0.00	0.02	14.80	0.00	0.00
comp157771_c0_seq1	3527	Leucine-rich repeat receptor protein kinase	GO:0007126 (meiosis); GO:0009556 (microsporogenesis); GO:0010234 (tapetal cell fate specification)	0.07	0.42	7.59	6.56	0.76	0.93	0.30	0.35	0.24	7.07	0.84	0.32
comp163320_c0_seq1	2659	Probable lysine-specific demethylase	GO:0009910 (negative regulation of flower development); GO:0048573 (photoperiodism, flowering)	2.16	3.82	24.90	22.83	2.71	3.89	3.46	2.01	2.99	23.87	3.30	2.74
comp164722_c0_seq10	3035	Protein LHY	GO:0048574 (long-day photoperiodism, flowering)	0.67	0.77	11.32	10.34	1.02	1.25	1.47	0.84	0.72	10.83	1.14	1.16
comp164722_c0_seq5	2763	Protein LHY	GO:0048574 (long-day photoperiodism, flowering)	1.05	0.57	10.76	9.23	0.88	1.26	1.53	0.94	0.81	9.99	1.07	1.24
comp166210_c1_seq1	1144	B3 domain-containing protein	GO:0009908 (flower development); GO:0048573 (photoperiodism, flowering)	0.05	0.00	3.04	3.22	0.03	0.02	0.07	0.05	0.03	3.13	0.03	0.06
comp166210_c1_seq2	1075	B3 domain-containing protein	GO:0009908 (flower development); GO:0048573 (photoperiodism, flowering)	0.00	0.02	4.26	4.87	0.03	0.05	0.08	0.03	0.01	4.57	0.04	0.05
comp167920_c1_seq10	2247	MADS-box transcription factor 16	GO:0009908 (flower development)	1.09	1.32	12.51	12.00	0.30	0.36	0.23	0.11	1.20	12.25	0.33	0.17

comp167920_c1_seq9	1074	MADS-box transcription factor 16	GO:0009908 (flower development)	0.63	1.11	10.00	9.97	0.64	0.32	0.08	0.03	0.87	9.98	0.48	0.05
comp167920_c2_seq2	1116	MADS-box transcription factor 16	GO:0009908 (flower development)	4.10	4.86	51.32	45.99	1.46	1.11	0.53	0.14	4.48	48.66	1.28	0.34
comp169398_c0_seq7	3724	Protein LHY	GO:0048574 (long-day photoperiodism, flowering)	0.90	1.13	37.42	34.42	1.14	1.67	2.41	1.44	1.02	35.92	1.40	1.93
comp169398_c0_seq8	3754	Protein LHY	GO:0048574 (long-day photoperiodism, flowering)	0.74	1.09	38.40	33.62	1.26	1.29	2.09	1.51	0.92	36.01	1.27	1.80
comp170023_c1_seq1	911	LOB domain-containing protein 6	GO:0048441 (petal development)	0.07	0.33	59.01	55.39	0.39	0.09	1.58	0.76	0.20	57.20	0.24	1.17
comp170445_c0_seq4	4240	Probable lysine-specific demethylase	GO:0009910 (negative regulation of flower development); GO:0048573 (photoperiodism, flowering)	2.89	4.05	24.91	21.26	3.33	4.38	3.97	2.34	3.47	23.08	3.85	3.16
comp171184_c1_seq12	3214	Protein LHY	GO:0048574 (long-day photoperiodism, flowering)	0.23	0.41	16.39	14.28	0.39	0.66	0.89	0.54	0.32	15.34	0.53	0.72
comp171184_c1_seq14	3280	Protein LHY	GO:0048574 (long-day photoperiodism, flowering)	0.33	0.43	15.67	13.50	0.45	0.40	0.99	0.58	0.38	14.58	0.42	0.79
comp171184_c1_seq2	3183	Protein LHY	GO:0048574 (long-day photoperiodism, flowering)	0.36	0.48	16.51	15.14	0.43	0.51	0.65	0.54	0.42	15.82	0.47	0.60
comp171184_c1_seq6	3184	Protein LHY	GO:0048574 (long-day photoperiodism, flowering)	0.25	0.48	15.79	15.15	0.50	0.56	0.95	0.80	0.36	15.47	0.53	0.88
comp172256_c0_seq3	1697	Protein kinase PINOID	GO:0009908 (flower development)	0.22	0.15	9.55	9.15	0.04	0.02	0.42	0.19	0.18	9.35	0.03	0.30
comp172388_c0_seq1	1474	Polygalacturonase	GO:0009835 (ripening)	0.00	0.00	17.62	18.11	0.00	0.00	0.00	0.02	0.00	17.86	0.00	0.01
comp76010_c0_seq1	203	60S ribosomal protein L8	GO:0000003 (reproduction)	0.00	0.00	1.14	1.12	0.00	0.00	0.00	0.00	0.00	1.13	0.00	0.00
comp156118_c0_seq20	852	Protein SPA1-RELATED 4	GO:0009585 (red, far-red light phototransduction)	0.03	0.30	0.24	0.46	0.74	1.82	15.62	13.48	0.16	0.35	1.28	14.55
comp158397_c0_seq5	1997	Receptor-like serine/threonine-protein kinase ALE2	GO:0048367 (shoot development)	0.00	0.21	0.30	0.32	0.50	1.14	9.56	8.71	0.10	0.31	0.82	9.14
comp171332_c1_seq2	1178	Phototropin-2	GO:0009882 (blue light photoreceptor activity)	0.02	0.06	0.35	0.36	0.02	0.18	1.78	1.81	0.04	0.36	0.10	1.79
comp171332_c1_seq4	1682	Phototropin-2	GO:0009882 (blue light photoreceptor activity)	0.11	0.29	0.22	0.00	0.08	0.30	1.78	1.59	0.20	0.11	0.19	1.69
comp148295_c0_seq2	1526	Protein SHORT-ROOT	GO:0009956 (radial pattern formation)	12.32	13.17	0.46	0.24	0.83	0.91	0.55	0.62	12.74	0.35	0.87	0.59
comp149327_c1_seq1	1690	Patatin-05	GO:0006952 (defense response)	28.13	24.76	0.11	0.08	0.96	0.77	0.70	0.34	26.45	0.10	0.86	0.52
comp153574_c0_seq8	1336	Triacylglycerol lipase 2	GO:0002213 (defense response to insect)	2.79	2.89	0.03	0.00	0.05	0.23	0.22	0.24	2.84	0.02	0.14	0.23

comp156437_c0_seq2	1279	Ethylene-responsive transcription factor 5	GO:0006952 (defense response)	15.41	16.77	0.29	0.46	0.91	0.66	0.79	1.75	16.09	0.38	0.79	1.27
comp158132_c0_seq5	1199	Triacylglycerol lipase 2	GO:0002213 (defense response to insect)	2.60	2.74	0.00	0.00	0.22	0.26	0.25	0.31	2.67	0.00	0.24	0.28
comp158132_c0_seq7	1469	Triacylglycerol lipase 2	GO:0002213 (defense response to insect)	1.79	1.90	0.03	0.00	0.11	0.23	0.20	0.24	1.84	0.02	0.17	0.22
comp159962_c2_seq10	980	Mannose-specific lectin	GO:0006952 (defense response)	2798.83	2559.88	2.41	2.23	0.23	1.21	0.22	0.80	2679.35	2.32	0.72	0.51
comp167541_c0_seq11	557	Glutathione S-transferase U17	GO:0048527 (lateral root development)	227.42	240.95	0.42	0.08	1.98	11.59	0.76	1.13	234.19	0.25	6.79	0.94
comp167806_c0_seq1	1856	Transcription factor MYC2	GO:2000068 (regulation of defense response to insect)	16.64	15.42	0.25	0.37	2.22	0.94	1.57	2.39	16.03	0.31	1.58	1.98
comp167806_c0_seq5	2628	Transcription factor MYC4	GO:0006952 (defense response)	14.13	16.67	0.23	0.71	2.37	0.79	0.72	2.38	15.40	0.47	1.58	1.55
comp169022_c0_seq15	410	Putative disease resistance protein RGA1	GO:0006952 (defense response)	5.88	5.53	0.00	0.11	0.40	0.55	0.00	0.08	5.70	0.06	0.47	0.04
comp173681_c0_seq1	854	Mannose-specific lectin	GO:0006952 (defense response)	4698.04	4449.01	4.28	4.16	0.00	1.32	0.05	0.81	4573.53	4.22	0.66	0.43
comp134280_c0_seq1	528	ABC transporter B family member 14	[Q] Secondary metabolites biosynthesis, transport and catabolism	0.00	0.06	0.14	0.09	0.17	1.91	1.60	0.24	0.12	0.10	0.13	1.76
comp161190_c0_seq1	2466	ABC transporter B family member 13	[Q] Secondary metabolites biosynthesis, transport and catabolism	0.00	0.36	0.29	1.33	0.92	12.85	11.57	1.16	1.19	0.33	1.13	12.21
comp166591_c0_seq22	3497	ABC transporter B family member 13	[Q] Secondary metabolites biosynthesis, transport and catabolism	0.00	0.06	0.09	0.21	0.17	2.18	2.14	0.36	0.22	0.07	0.19	2.16
comp166591_c0_seq42	3476	ABC transporter B family member 13	[Q] Secondary metabolites biosynthesis, transport and catabolism	0.00	0.05	0.05	0.16	0.21	2.30	2.44	0.35	0.27	0.05	0.18	2.37
comp166591_c0_seq46	3563	ABC transporter B family member 13	[Q] Secondary metabolites biosynthesis, transport and catabolism	0.00	0.04	0.06	0.09	0.13	2.35	2.32	0.34	0.35	0.05	0.11	2.34
comp168857_c0_seq53	1803	Pleiotropic drug resistance protein 6	[Q] Secondary metabolites biosynthesis, transport and catabolism	0.00	0.29	0.51	1.03	0.93	8.02	8.51	1.03	1.05	0.40	0.98	8.26
comp231923_c0_seq1	417	ABC transporter G family member 11	[Q] Secondary metabolites biosynthesis, transport and catabolism	0.00	0.15	0.12	0.56	0.98	8.03	8.32	0.00	0.00	0.13	0.77	8.17
comp35910_c0_seq1	550	Hydroquinone	[G] Carbohydrate transport and	0.00	0.11	1.31	0.84	0.50	8.51	7.28	0.23	0.40	0.71	0.67	7.89

		glucosyltransferase	metabolism; [C] Energy production and conversion												
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a: GO: Gene Ontology; KOG: eukaryotic orthologous group.

b: The expression levels (in RPKM) of each transcript in eight RNA-seq data sets (“Root1”, “Root2”, “Flower1”, “Flower2”, “Stem1”, “Stem2”, “Leaf1” and “Leaf2”) are provided in the table.

c: The average expression levels (in RPKM) of each transcript in each organ (two biological replicates for each organ) are also provided in this table.

Table S4 Organ-specific sRNAs identified in *Dendrobium officinale*. The sRNA sequences along with their accumulation levels (normalized in RPM) in sRNA-seq libraries prepared from specific organs were included in this table. Seven miRNAs were identified to be specifically accumulated in the floral organ.

Flower-specific sRNAs:

sRNA sequence	sRNA count (RPM)	sRNA HTS datasets	miRNA ID	Homologous miRNA ID	Species
GCTCTCTATGCTTCTGTCATC	40.72	Flower_2	dof-miR-376	aly-miR157d-3p	Arabidopsis lyrata
GCTCAAGAAAGCTGTGGGAGA	36.76	Flower_2	dof-miR-372	gma-miR396b-3p/gma-miR396k-3p/mtr-miR396a-3p	Glycine max/Glycine max/Medicago truncatula
TCATTGAGTGCAGCGTTGATG	30.63	Flower_2	dof-miR-600	aly-miR397a-5p/aly-miR397b-5p/ath-miR397a/bdi-miR397a/cme-miR397/csi-miR397/gma-miR397a/gma-miR397b-5p/lus-miR397b/mtr-miR397-5p/osa-miR397a/ppe-miR397/ptc-miR397a/rco-miR397/sbi-miR397-5p/ssl-miR397/tcc-miR397/vvi-miR397a	Arabidopsis lyrata/Arabidopsis lyrata/Arabidopsis thaliana/Brachypodium distachyon/Cucumis melo/Citrus sinensis/Glycine max/Glycine max/Linum usitatissimum/Medicago truncatula/Oryza sativa/Prunus persica/Populus trichocarpa/Ricinus communis/Sorghum bicolor/Salvia sclarea/Theobroma cacao/Vitis vinifera
ATGCACTGCCTCTCCCTGGC	27.03	Flower_2	dof-miR-197	ahy-miR408-3p/aly-miR408-3p/ath-miR408-3p/cme-miR408/csi-miR408/gma-miR408a-3p/gma-miR408b-3p/gma-miR408c-3p/lus-miR408a/mdm-miR408a/mes-miR408/mtr-miR408-3p/pta-miR408/ptc-miR408-3p/vun-miR408/vvi-miR408	Arachis hypogaea/Arabidopsis lyrata/Arabidopsis thaliana/Cucumis melo/Citrus sinensis/Glycine max/Glycine max/Glycine max/Linum usitatissimum/Malus domestica/Manihot esculenta/Medicago truncatula/Pinus taeda/Populus trichocarpa/Vigna unguiculata/Vitis vinifera
TATTGGCCTGGTTCACCTCAGA	22.7	Flower_2	dof-miR-568	aly-miR170-5p/aly-miR171a-5p/ath-miR170-5p/ath-miR171a-5p/gma-miR171j-5p/stu-miR171a-5p/stu-miR171c-5p	Arabidopsis lyrata/Arabidopsis lyrata/Arabidopsis thaliana/Arabidopsis thaliana/Glycine max/Solanum tuberosum/Solanum tuberosum
CGCCAAAGGAGAGTTGCCCTG	23.06	Flower_2	dof-miR-301	tcc-miR399a/vvi-miR399i	Theobroma cacao/Vitis vinifera
TTAGATGACCATCAACGAACA	19.1	Flower_2	dof-miR-927	mdm-miR827	Malus domestica
TCTAAGCATATTCTGTAGCGGACT	448.3	Flower_1	-	-	-
GCTCCCTATCATCGAAACCT	319.14	Flower_1	-	-	-
TTTTCGTGTGCGTCATTT	112.81	Flower_1	-	-	-
GTTTTCGTGTGCGTCATT	87.09	Flower_1	-	-	-
CAGAAGGATAAGAGTGAACCTT	85.25	Flower_1	-	-	-
TCGGAATTAAGTTCGGAGTGAC	77.53	Flower_1	-	-	-
GTGGAAGAAAAGCTAAAGAGC	75.14	Flower_1	-	-	-
TGTATTAAGCCAAGTAGTTCT	70.55	Flower_1	-	-	-
TCTTACTGTACGAAAGCATG	65.59	Flower_1	-	-	-
TGTTGGCGTGAAGAAAAGCT	63.39	Flower_1	-	-	-
TGAATGACAATGGACTTGGCAT	62.28	Flower_1	-	-	-
ATCAAATGGAACCTGGCATAAC	59.9	Flower_1	-	-	-

TAAGCATATTCTGTAGCGGACT	59.9	Flower_1	-	-	-
TTCTTACTGTACGAAAGCATG	53.1	Flower_1	-	-	-
AGGTGGAGAGATATGTGGGGT	49.79	Flower_1	-	-	-
CGTGAAGAAAAGCTAAAGAGC	46.85	Flower_1	-	-	-
TCGAGGATGATGACCTGGACGT	45.01	Flower_1	-	-	-
GACCGGATGCAGAGAAACATTC	45.75	Flower_1	-	-	-
CACGCCTGGAGAATTCATTGCT	45.75	Flower_1	-	-	-
ATCGGAATTAAGTTCGGAGTGAC	42.99	Flower_1	-	-	-
TTCCATCGTCGCCGAGAACA	41.71	Flower_1	-	-	-
CAAGATCCATCCCATAAGCT	40.05	Flower_1	-	-	-
TTACTGTACGAAAGCATGGGA	40.6	Flower_1	-	-	-
AGAAATGTGGCGTGAAGAA	39.13	Flower_1	-	-	-
TATTGGCTTCCAGATGATGATC	39.32	Flower_1	-	-	-
TTGTCACCATCCAGGAGAACTC	37.11	Flower_1	-	-	-
AAATGAACTGGAAGCGATTGG	37.11	Flower_1	-	-	-
CGAATGGACTCGAAAAGATAGAACT	35.83	Flower_1	-	-	-
TAAGTTCAGAACTATGAAGCCT	37.66	Flower_1	-	-	-
ATGAAATGAACTGGAAGCGAT	36.19	Flower_1	-	-	-
TAGAAGTCCAAAGCAGAACCTT	34.17	Flower_1	-	-	-
TGGAAGCGATTGGATGTAGTT	32.52	Flower_1	-	-	-
GAAACATGAGACCTTTGGCTTT	32.52	Flower_1	-	-	-
TTGGCCTCGTCGGCTTGATACC	32.7	Flower_1	-	-	-
GAAGAAAAGCTAAAGAGCACTGGC	31.23	Flower_1	-	-	-
TCTTACTGTACGAAAGCATGG	31.78	Flower_1	-	-	-
TTGGAACCTGGCATACTGATAT	33.07	Flower_1	-	-	-
AATTCTTGACTTTGATATG	30.13	Flower_1	-	-	-
ATGTTGGCGTGAAGAAAAGC	29.95	Flower_1	-	-	-
ATGGTTGGCTGAAAATTTGCT	29.4	Flower_1	-	-	-
ACGCCTGGAGAATTCATTGCTT	28.85	Flower_1	-	-	-
TGGGACAAGGAGATCTTTTCT	29.76	Flower_1	-	-	-
AAAGAGATGGGAGACGTGAAATGT	27.56	Flower_1	-	-	-

TAGTTCTGAACTTATCACGCCT	28.48	Flower_1	-	-	-
TCAACAAGAACGTCAAGAACCT	28.11	Flower_1	-	-	-
CGGCTTGGTGAACCTGGTTGCC	27.74	Flower_1	-	-	-
AGAGATGGGAGACGTGAAATGT	27.93	Flower_1	-	-	-
ACATGATCAGATGATTTAGGCT	27.93	Flower_1	-	-	-
GTCCCTCTTAATCATTACTCC	27.19	Flower_1	-	-	-
ATCTCTTTAATGACCAGTAGCCT	27.19	Flower_1	-	-	-
TGTTCAATTTGTTTTCGGCACT	27.19	Flower_1	-	-	-
TGGAGGATGATGACCTGGACGT	27.38	Flower_1	-	-	-
AATTTCCAGAAGTGAAGAGCTC	27.56	Flower_1	-	-	-
TTAGATGATATGCACATAATT	27.01	Flower_1	-	-	-
TTGCAGAGACATGAACCAAGCA	27.38	Flower_1	-	-	-
CAAATGGTTGGCTGAAAATTTGCT	26.46	Flower_1	-	-	-
AATGAGAATCGTGGGATTTGTCC	26.09	Flower_1	-	-	-
TGAAATGAACTGGAAGCGATT	26.27	Flower_1	-	-	-
GAAAAGCTAAAGAGCACTGGC	26.46	Flower_1	-	-	-
GAGAATCGTGGGATTTGTCC	25.91	Flower_1	-	-	-
TTCTCTGCGAATGGACTCGAAA	25.54	Flower_1	-	-	-
TTCAGTTAAGTCTGCCTGAACT	26.09	Flower_1	-	-	-
CCACGCCTGGAGAATTCATTGC	25.91	Flower_1	-	-	-
ACAAAGTCAATGTTGAACACTT	25.35	Flower_1	-	-	-
ATCAACGGAAGGAAGACGAAT	24.62	Flower_1	-	-	-
AGGAACGTGAATGACAATGGAC	24.44	Flower_1	-	-	-
CCGCAGAACAACCTAAACCT	24.44	Flower_1	-	-	-
GAAAGATAGAACTTTATTGGGACT	23.88	Flower_1	-	-	-
GAACGTGAATGACAATGGACTT	24.25	Flower_1	-	-	-
ATCGGAAATGAGAATCGTGGGGAT	23.88	Flower_1	-	-	-
CGACGAGAGCTCAGCCATTGCC	24.99	Flower_1	-	-	-
AAATGAACTGGAAGCGATTG	24.07	Flower_1	-	-	-
CATCCGCAGGACGAAAATTTTC	22.97	Flower_1	-	-	-
TCCTGAACTGCAGTGAGAGTGC	22.78	Flower_1	-	-	-

TTCCAAGGATTATGAACCTGCT	24.62	Flower_1	-	-	-
TGGATTACAAAGACTTGGATCT	23.7	Flower_1	-	-	-
AGGAAAAGAAAGATTGGGCCGAA	22.41	Flower_1	-	-	-
CAGAAGGAAAAAAGTGAGCTTT	23.52	Flower_1	-	-	-
TCGAGGATGATGACCTGGACGTC	22.6	Flower_1	-	-	-
AACGGAAGGAAGACGAATAGGC	22.6	Flower_1	-	-	-
AGAGGATTCAGCTGATGGAGAGT	21.86	Flower_1	-	-	-
TCACCATCCAGGAGAACTCTCT	22.23	Flower_1	-	-	-
TTAGCGACGGTGCTCTATACT	21.68	Flower_1	-	-	-
GATTCATCCATAAGCTGCC	21.31	Flower_1	-	-	-
CATATTGATATGTATTAAGCC	21.86	Flower_1	-	-	-
ACAAATTTGAGCATCTGGGAT	22.23	Flower_1	-	-	-
TCAAATTGGAACCTGGCATACT	21.5	Flower_1	-	-	-
GGTTTAGGGTTGTTCTGCGGC	20.95	Flower_1	-	-	-
ATGAACTGGAAGCGATTGGATGT	20.95	Flower_1	-	-	-
AACCGCAATGCAGACTGTCCTC	20.58	Flower_1	-	-	-
AAGCGATTGGATGTAGTTATC	20.03	Flower_1	-	-	-
TAATCGACGGTGGAGGTTCCGC	20.21	Flower_1	-	-	-
TTCTTGGACAGTGACATCTGAC	20.58	Flower_1	-	-	-
CTTGGTTAGAACAGCGAGTTGC	20.03	Flower_1	-	-	-
CAAATTGGAACCTGGCATACTG	19.84	Flower_1	-	-	-
CGGAGCTATGTCTTTGATCCCT	19.66	Flower_1	-	-	-
TCTTTAATCAGGTTGCTGACC	19.48	Flower_1	-	-	-
AGGCGAGTGATTGAGGAACCT	20.03	Flower_1	-	-	-
TCAGTCTTTGTAGTTTCGGCCT	19.66	Flower_1	-	-	-
CATCTTCGGATGGAGAAGCGCC	19.48	Flower_1	-	-	-
GGGCGATGACGAGGATGATGAT	19.48	Flower_1	-	-	-
TTATCGGCATCGAAATGAGAA	19.48	Flower_1	-	-	-
GCTGTTGTTGCTGTAGATGCCT	20.21	Flower_1	-	-	-
CTTGGCTTAATACATATCAAT	19.29	Flower_1	-	-	-
ATCGCGATTGGCGCATTGGCTC	19.48	Flower_1	-	-	-

ATTGGGGATTGCTACCTTGA	19.48	Flower_1	-	-	-
AAGATAGAACTTATTTGGGACT	19.29	Flower_1	-	-	-
ATTCCATTGTCGAGGAGTCGGA	19.11	Flower_1	-	-	-
CCTGAGTTGTTCCAGTTATCGTC	18.56	Flower_1	-	-	-
TTCCAACATCTAGAACATGAGA	19.11	Flower_1	-	-	-
TCATAGAGCTCCAATTCACCT	18.56	Flower_1	-	-	-
CGGAAATGAGAATCGTGGGGAT	19.84	Flower_1	-	-	-
TGAGACATCTGGAGAACCTTGA	18.56	Flower_1	-	-	-
TGCGGCCGAGGATTAGCATCAG	19.48	Flower_1	-	-	-
TAAACTCGGGAGTACCAATAAC	18.19	Flower_1	-	-	-
GGAAGCGATTGGATGTAGTT	19.48	Flower_1	-	-	-
ATACATGAGGAATTCATGATC	18.01	Flower_1	-	-	-
TATGGATACCAAATTTGAAAA	18.19	Flower_1	-	-	-
CTAGGAGTACAACCTGGGCAGT	18.74	Flower_1	-	-	-
TGATACGTTGATGCTCTGCCCC	18.19	Flower_1	-	-	-
TAGAGGGGAACGCGTGAGGCTGGT	17.64	Flower_1	-	-	-
TTGGCTGAAAATTTGCTGTGC	18.01	Flower_1	-	-	-
CGAGGATGATGACCTGGACGTC	18.37	Flower_1	-	-	-
TTGATATGTATTAAGCCAAGTA	17.82	Flower_1	-	-	-
AAGATATAGGTCGGATGGCTCC	18.01	Flower_1	-	-	-
TGGATTGATTTGTTGACTGGCT	18.56	Flower_1	-	-	-
CTTCCAACATCTAGAACATGA	17.64	Flower_1	-	-	-
TGCTCATGAGAATGATAGGAAC	18.01	Flower_1	-	-	-
TGAGGATAGAAGGATGAACACC	18.19	Flower_1	-	-	-
ATGAACTGGAAGCGATTGGAT	16.9	Flower_1	-	-	-
TTCAGTGAAGGCTTCTTGAAC	17.82	Flower_1	-	-	-
AAATTGGAACCTGGCATACTGA	16.54	Flower_1	-	-	-
CTGTAGATGCCTGTTCTTTGAC	17.27	Flower_1	-	-	-
CGGCAGACGAGGCCACATTGC	17.27	Flower_1	-	-	-
ATTGTGAGAATCGTCTATGTGA	16.72	Flower_1	-	-	-
TGGAGAGTGTGGACAAGTCC	16.17	Flower_1	-	-	-

ATATTGATATGTATTAAGCCAAG	15.98	Flower_1	-	-	-
AAGCGATTGGATGTAGTTATCA	16.35	Flower_1	-	-	-
TTTCCGAGACCGGTTGGCTGCC	16.54	Flower_1	-	-	-
TTAAAGTTAGTGATGTTGAGCT	16.72	Flower_1	-	-	-
TGATATGTATTAAGCCAAGTA	16.17	Flower_1	-	-	-
TGGGAGACGTGAAATGTATTTT	16.17	Flower_1	-	-	-
CTTCTCGTAGGATAGTGATGCC	15.8	Flower_1	-	-	-
GAAAGTCGAGCAAGAATGGTCAGC	15.62	Flower_1	-	-	-
CTGCGAATGGACTCGAAAGATAG	15.62	Flower_1	-	-	-
GCGATTGGATGTAGTTATCAT	15.62	Flower_1	-	-	-
GAAATGTTGGCGTGAAGAAA	15.98	Flower_1	-	-	-
TTAGAAATGTTGGCGTGAAG	15.98	Flower_1	-	-	-
ATCGAGAATCAGATGTAGATGG	16.54	Flower_1	-	-	-
CTTGGACCCCGACATATCTAC	16.17	Flower_1	-	-	-
TGACCAGTAGCCTTTCCTTGATAC	15.62	Flower_1	-	-	-
TTCCGTGAGACTGTTCTTGAGAA	15.98	Flower_1	-	-	-
TACTGTACGAAAGCATGGGAG	16.72	Flower_1	-	-	-
TATAAGGATATGAAATCTGCCT	15.25	Flower_1	-	-	-
CTGAATTGATTGACATTCTGACGAA	15.62	Flower_1	-	-	-
TTCCATGGCAACAGATTTGATC	15.43	Flower_1	-	-	-
ATACGGAAGGAAAGTATCATGC	15.43	Flower_1	-	-	-
TTCTGCTAGATACCTTGCATC	16.35	Flower_1	-	-	-
CACGGGATCAGACACTCTCTGT	15.07	Flower_1	-	-	-
TCTTCTCTGCGAATGGACTCGAAA	14.88	Flower_1	-	-	-
GTTGGCGTGAAGAAAAGCT	15.07	Flower_1	-	-	-
AAGAGGATTCAGCTGATGGA	15.25	Flower_1	-	-	-
ACACAGTTTGCGGTAGACTCCT	15.62	Flower_1	-	-	-
AATTGGAACCTGGCATACTGAT	15.25	Flower_1	-	-	-
TCCCTACAGAATCAGGAACGCC	14.88	Flower_1	-	-	-
TGAGAATCGTGGGGATTGTCC	14.88	Flower_1	-	-	-
TCGAGAATCAGATGTAGATGGT	14.88	Flower_1	-	-	-

ATCGAGATTTGTGCACTAATAG	15.25	Flower_1	-	-	-
CAAGTCATCGGGTTATAATGCT	15.07	Flower_1	-	-	-
TTCGTACAGTAAGAAGCAGCC	15.25	Flower_1	-	-	-
CATTCCATATTGTCGGATGCT	14.7	Flower_1	-	-	-
ACCTCCATCGTCGCCGAGA	14.51	Flower_1	-	-	-
CTGTTGAATCCATGAAGCTTT	14.33	Flower_1	-	-	-
CTCGTCGCACAGCAAATTTTCAGC	14.33	Flower_1	-	-	-
AACCAGCTGATTTGTGGATCTC	15.25	Flower_1	-	-	-
GTTGGTTATACTATTGAACGAGT	14.7	Flower_1	-	-	-
GAAGAGGATTCAGCTGATGGA	14.88	Flower_1	-	-	-
TAAATTTGCCGACTTGGTTGCC	14.7	Flower_1	-	-	-
ATTTTCCGATGCTGAGGAGG	14.33	Flower_1	-	-	-
TATTAGGATGCCAATTATTGAT	14.33	Flower_1	-	-	-
CGACGAGCAGGAGAAGTTTTT	14.33	Flower_1	-	-	-
TTATCGTCATAATGGGAGAAAGCT	13.96	Flower_1	-	-	-
CAAATGGTTGGCTGAAAATT	14.51	Flower_1	-	-	-
TTGTATGGTTCCAGACTCAATC	14.51	Flower_1	-	-	-
ATGATGTCGCGAGAATTCTGAT	14.88	Flower_1	-	-	-
GTTGGTTATACTATTGAACGAGTT	13.78	Flower_1	-	-	-
TGATTCATCGTTTGATTATGCT	14.51	Flower_1	-	-	-
TTGGCTTCCAGATGATGATCAC	14.88	Flower_1	-	-	-
TTACGTTGGATGCCCTGGTGAC	14.15	Flower_1	-	-	-
GCGAATGGACTCGAAAGATAGAAC	13.78	Flower_1	-	-	-
CAAAGGAATGGAGGCAGAGCCT	14.51	Flower_1	-	-	-
TTAGTTGGGCTCTAAAGGCATC	14.15	Flower_1	-	-	-
TAAAATCTATTGATCTGTGCGAA	13.96	Flower_1	-	-	-
TGAAAGCTATTGATTGGACGGC	13.41	Flower_1	-	-	-
CATCACCATGAAATGAACTGG	13.78	Flower_1	-	-	-
CGCCTGGAGAATTCATTGCTTC	14.51	Flower_1	-	-	-
TGGTACAAAAGGATGTTCCGGCC	13.96	Flower_1	-	-	-
GTTATCGGCATCGGAAATGAGAAT	13.41	Flower_1	-	-	-

TTGGGAAGAGGATTCAGCTGAT	13.23	Flower_1	-	-	-
TCGGCATCGAAATGAGAATCG	13.96	Flower_1	-	-	-
CTTCTCTGCTCGTCGCACAG	13.78	Flower_1	-	-	-
AAAAGCTAAAGAGCACTGGCT	13.96	Flower_1	-	-	-
TCACTATCGAGATTTGTGCACT	13.6	Flower_1	-	-	-
TATACTATTGAACGAGTTGGAGC	13.41	Flower_1	-	-	-
AACTGTTGACGAAAGCTTTGGCC	13.23	Flower_1	-	-	-
TGGAAGGTAAAGAGGAGGAAG	13.6	Flower_1	-	-	-
TGGTGATGGCTTATGATTAA	13.41	Flower_1	-	-	-
TACCTGAAGTTGGCTTGACCC	13.96	Flower_1	-	-	-
ATCTGGCTTTGAGGATCTCTT	13.78	Flower_1	-	-	-
ATACAGGACATTATCAGAACTAA	13.41	Flower_1	-	-	-
CGAGGATACCAATTGTGATCAT	13.6	Flower_1	-	-	-
ACAAGATCCTTGAACTTTGTTC	12.86	Flower_1	-	-	-
ATTGAGCATCTGGAGATTGTAC	13.41	Flower_1	-	-	-
GCCAAGGCCTTGAAGCACTCATGA	13.04	Flower_1	-	-	-
GAATGGACTCGAAAGATAGAACT	13.23	Flower_1	-	-	-
ACTGAGGTCCTGGAAGAAGCTCC	13.23	Flower_1	-	-	-
CTTGGCTTAATACATATCAATA	13.23	Flower_1	-	-	-
GACGATGGAAGGTAAAGAGGA	12.86	Flower_1	-	-	-
GACCACGGGATCAGACACTCTC	13.6	Flower_1	-	-	-
ATATGTATTAAGCCAAGTAGTTCT	12.86	Flower_1	-	-	-
GGAGGTTTAGGGTTGTTCTGC	13.6	Flower_1	-	-	-
GGAAGCGATTGGATGTAGTTA	12.86	Flower_1	-	-	-
ATATGTCGAGCATTGAACCTGC	13.41	Flower_1	-	-	-
AGATTCCATCCATAAGCTGC	13.41	Flower_1	-	-	-
GAACGGAAGCGATTGGATGT	12.86	Flower_1	-	-	-
AAGAATTAGAAATGTTGGCGT	12.68	Flower_1	-	-	-
TAAAGAAACGCTGGCCAGCCT	13.23	Flower_1	-	-	-
TTGAAAATACAAACCTGGAAC	12.49	Flower_1	-	-	-
ATATTGGCTTCCAGATGATGAT	13.41	Flower_1	-	-	-

CCTGGCATGTGATCTCTTTGC	13.04	Flower_1	-	-	-
TCCATGTTCCGGCGGCCCTCA	12.68	Flower_1	-	-	-
TGGGAAGACTCTACTTTTGCCCT	12.68	Flower_1	-	-	-
GTGTTCCAAGGATTATGAACCT	12.86	Flower_1	-	-	-
ACTGGAAGCGATTGGATGTAG	12.31	Flower_1	-	-	-
CGGATTTGTCAAGTTCAGTTCT	12.86	Flower_1	-	-	-
CTTTCGTACAGTAAGAAGCAGC	12.68	Flower_1	-	-	-
ATCAAGTTGTACTGCTACACCT	13.6	Flower_1	-	-	-
TACAGACCAGTAAGACAACCTAC	13.41	Flower_1	-	-	-
ACTGGAAGCGATTGGATGTA	13.04	Flower_1	-	-	-
ACAATCAAATTGGAACCTGGCA	12.49	Flower_1	-	-	-
CGCAGAGAAGAAGTCGAAATAC	13.04	Flower_1	-	-	-
TTCCAGTTATCGTCATAATG	12.49	Flower_1	-	-	-
ATCAACAGTGAATTTATGAAGC	12.49	Flower_1	-	-	-
TAAAAGCGCATGGATTCCGGAC	12.31	Flower_1	-	-	-
CTTCCTGCTAGATACCTTGCATC	11.94	Flower_1	-	-	-
CTCAAATGAGAATGACGACGGC	12.31	Flower_1	-	-	-
GAGAATGGCTTTGATTGTATCA	12.13	Flower_1	-	-	-
ATTCCATTGTCGAGGAGTCGGAA	11.94	Flower_1	-	-	-
TTCGCATTGAGGATCACTTAAC	12.31	Flower_1	-	-	-
AGAGGATTCAGCTGATGGAGA	12.68	Flower_1	-	-	-
GGAATCCTGATGATGCTGCAT	12.13	Flower_1	-	-	-
TTCTTCATGGACGCTGTCGCCT	12.13	Flower_1	-	-	-
TCGTCTCCTCCGTTGATCT	11.94	Flower_1	-	-	-
TTCTTACTGTACGAAAGCATGG	12.31	Flower_1	-	-	-
TATCAAGTTGTTACCTGTACTION	12.31	Flower_1	-	-	-
TTGAGCATCTGGAGATTGTACA	11.76	Flower_1	-	-	-
CTTGTACCAAGAGAGTTTTGAT	11.94	Flower_1	-	-	-
TGAGATGAAGCACTGTAGCACT	11.94	Flower_1	-	-	-
ATGCTCATGAGAATGATAGGAAC	11.94	Flower_1	-	-	-
TTGGAGTTCTAGTCATATCTGC	11.76	Flower_1	-	-	-

AAGCGATTGGATGTAGTTATCATC	11.57	Flower_1	-	-	-
TAATTCGAGATCTGCTATCTGC	11.76	Flower_1	-	-	-
TTCAGAAGGATAAGAGTGAACCT	12.31	Flower_1	-	-	-
CACACAGTTTGCCTGACTCC	11.94	Flower_1	-	-	-
TGACATTCTGACGATCTGTGGAGT	11.39	Flower_1	-	-	-
GGCTGCTTCTTACTGTACGAA	11.94	Flower_1	-	-	-
TCCAGGATAGGTACTTAAATGC	13.04	Flower_1	-	-	-
GTTTCAGAACTATGAAGCCACCT	11.57	Flower_1	-	-	-
CAGAGGATGATGCAAGTGCTTG	11.39	Flower_1	-	-	-
TTTGATAATGCTGGACTGGCCT	11.94	Flower_1	-	-	-
GTCCATCGAGATCTCTGGCTTA	11.76	Flower_1	-	-	-
TTGAACGCGGGCATGAGGAGGC	11.39	Flower_1	-	-	-
TTCACAAACTGTTGGAAAATCT	11.57	Flower_1	-	-	-
ATGTTGGCGTGGAAGAAAAGCT	11.57	Flower_1	-	-	-
TATCATTGATCGTTGTACGCT	11.57	Flower_1	-	-	-
TTCTGTGATGCCTTTAGAGCC	11.57	Flower_1	-	-	-
ACTTTCGTTGAGGACAGTACCT	11.21	Flower_1	-	-	-
TTATCAGAACTAGTCAACCAGAA	11.39	Flower_1	-	-	-
ATTGACTCAAAGAATTTTGCCT	11.02	Flower_1	-	-	-
CTGAGGTCCTGGAAGAACTCCA	11.21	Flower_1	-	-	-
CATATCATTGATCGTTGTACGC	11.94	Flower_1	-	-	-
TTTTTCAGACAGTCGGAAGCGGC	11.76	Flower_1	-	-	-
TAGTTTATGACTAAAGAAACCT	11.39	Flower_1	-	-	-
ATCGAGAAGCTCTAGAATTTGC	10.66	Flower_1	-	-	-
AGAATGACTGTGATTGCAACAC	11.02	Flower_1	-	-	-
CAGCATCGGAAAAATACCCCA	10.84	Flower_1	-	-	-
CGATTGGATGTAGTTATCATC	10.66	Flower_1	-	-	-
TGGAAGCGATTGGATGTAGTTATC	10.66	Flower_1	-	-	-
TGAATGACAATGGACTTGCATT	10.47	Flower_1	-	-	-
CTTCACATCATCTTGTATCTGGA	10.84	Flower_1	-	-	-
TTCGCCGTTGGCTTGACATGGGA	11.02	Flower_1	-	-	-

TCAAGGAAGTATTACAAGATT	10.84	Flower_1	-	-	-
TTTTCCGATGCTGAGGAGGTT	11.21	Flower_1	-	-	-
AGAGAGTTGGTTATACTATTGAAC	10.66	Flower_1	-	-	-
ATTCTTAAACATCTGAGACTGT	11.21	Flower_1	-	-	-
GAATGGACTCGAAAGATAGAACTT	10.66	Flower_1	-	-	-
CGATACGTTGATGCTCTGGCCC	11.02	Flower_1	-	-	-
TATTCGGATGCCAATTATTGAT	11.57	Flower_1	-	-	-
ATGAAATGAACTGGAAGCGA	11.21	Flower_1	-	-	-
ACTAGAACTCCAACGTCAGCTT	10.47	Flower_1	-	-	-
TGATATGCATTGAGAATTTTGC	10.84	Flower_1	-	-	-
TGAGGAATCCATGATCTTGT	10.29	Flower_1	-	-	-
ATAGAAGTCCAAGCAGAACCT	10.47	Flower_1	-	-	-
AGCGATTGGATGTAGTTATCA	10.47	Flower_1	-	-	-
AGAAATGTTGGCGTGAAGA	11.21	Flower_1	-	-	-
GATTGGATGTAGTTATCATC	11.02	Flower_1	-	-	-
TAACAATGTTTGAGCTGAACAT	10.47	Flower_1	-	-	-
CAGAAAGATAAGAGTGAACTTT	10.66	Flower_1	-	-	-
ATCGCCAAGTATGTCTGAGCT	10.47	Flower_1	-	-	-
AACGGCGCGGCAGTGAACCTGC	10.11	Flower_1	-	-	-
GAAATGAACTGGAAGCGATT	10.84	Flower_1	-	-	-
TGTACGAAAGCATGGGAGGGC	10.47	Flower_1	-	-	-
ATCGGAAACCTCCTCAGCATC	10.66	Flower_1	-	-	-
GGGACAATGAAAACTCTTCTT	10.84	Flower_1	-	-	-
TTGTTCTGCGGCGACGATGGA	10.29	Flower_1	-	-	-
CATCAACATCGTCGTAGGCATC	10.29	Flower_1	-	-	-
CGATCACCACATTGTAGAACCT	10.11	Flower_1	-	-	-
TTTGGAAGAGGATTCAGCTGA	10.11	Flower_1	-	-	-
GAGATGGGAGACGTGAAATGT	10.11	Flower_1	-	-	-
ATGGACGTCCAAATTACATTTT	10.29	Flower_1	-	-	-
TCTCCAAAAATATGGCCCACT	10.47	Flower_1	-	-	-
AGCGATTGGATGTAGTTATCAT	10.66	Flower_1	-	-	-

GAAATGTTGGCGTGGAAGAA	10.84	Flower_1	-	-	-
TTCCGATGCTGAGGAGTTT	10.47	Flower_1	-	-	-
ATGGTTCAGACTCAATCTTTC	10.47	Flower_1	-	-	-
AGGGTTGTTCTGCGGCGACGA	10.29	Flower_1	-	-	-
ATGTACAAAATAGTGTAGAGTCT	10.29	Flower_1	-	-	-
CATGGCCTTGAGATTCCTCGTA	10.29	Flower_1	-	-	-
GATACAAGTAGTCTGCAGCGCC	10.47	Flower_1	-	-	-
CTCGAATAGATCGTCCATGGAGA	10.29	Flower_1	-	-	-
ACCATTTGCGACCGAACGCTCT	10.66	Flower_1	-	-	-
AAGCTAAAGAGCACTGGCTGC	10.29	Flower_1	-	-	-
TCCCATACAGAATTCCTAGAA	10.29	Flower_1	-	-	-
CTAAGGTCAGTTGAGATTCGAC	10.47	Flower_1	-	-	-
ATAAGAGAGTAGATCTCATGCT	10.11	Flower_1	-	-	-
TTGGGAGAGAAAAGCTGAGCCT	10.66	Flower_1	-	-	-
TTGGCATAGGTAGAATGCTATC	10.11	Flower_1	-	-	-
ATACGGACACATCCTTTGAGGA	10.29	Flower_1	-	-	-
TATCCGGTTACGATGCTCAGT	10.11	Flower_1	-	-	-
AGAAAAGCTAAAGAGCACTGGC	10.29	Flower_1	-	-	-
ATTCATTGTGATTATGGAGCT	2195	Flower_2	-	-	-
TGTGGGTGGGTAGGGAAGATA	989.03	Flower_2	-	-	-
TGAAGGTCCAAGGTTGAGGCC	912.27	Flower_2	-	-	-
TTGTCGCAGGAGCGGTGGCACC	724.34	Flower_2	-	-	-
AGCCCTATGTCGCTCCGATTCGT	569.56	Flower_2	-	-	-
CCAGTCCGAACCCGTCGGC	432.26	Flower_2	-	-	-
GCGACCCAGGTCAGGCGGGACT	401.63	Flower_2	-	-	-
TATGTCGCTCCGATTCGT	389.2	Flower_2	-	-	-
ACTGGCTCTGATACCATGTTAGAT	353.34	Flower_2	-	-	-
TTGGCTGGATCCCTAGTTGGT	320.01	Flower_2	-	-	-
TCAGCCCCTATGTCGCTCCGATTCGT	300.55	Flower_2	-	-	-
TGCATTTGCACCTGCACCTCT	259.83	Flower_2	-	-	-
GCTCCCTATCATCGGAAACCT	257.3	Flower_2	-	-	-

TTCCGAAGCTATAATTCTTGC	238.92	Flower_2	-	-	-
ACCGTATCATTAACCTATTCTTT	224.15	Flower_2	-	-	-
CAATGAGTCTACAGTACCTGCTAC	207.03	Flower_2	-	-	-
TGGTCCAGACGGAGCTCCGAGGA	207.93	Flower_2	-	-	-
AAGTCCTCGTGTGCACCCCC	202.89	Flower_2	-	-	-
TCCCGAAGCTATAATTCTTGC	204.51	Flower_2	-	-	-
TGGGAAGTCCTCGTGTGCACCCCC	190.63	Flower_2	-	-	-
CCCAGTCCCGAACCCGTCGGCT	173.52	Flower_2	-	-	-
CGGCGGACTGCTCGAGCTGCT	163.61	Flower_2	-	-	-
ATAATTGTCAGAACACGCACC	163.61	Flower_2	-	-	-
TGTGGGAGGATTGGACAGAAC	159.1	Flower_2	-	-	-
TCCTACTCCACCCATGCATA	158.56	Flower_2	-	-	-
TTCCCAACACCTCCCATACCGT	151.53	Flower_2	-	-	-
TCCTCGTGTGCACCCCC	156.58	Flower_2	-	-	-
TCGTGCTGCTAGGCCGAAGCGG	148.83	Flower_2	-	-	-
TGAGAGACAAAAACCGTGCT	140.9	Flower_2	-	-	-
GGCAGTTCGACCGCAAATT	145.59	Flower_2	-	-	-
GTTATTCTATTCCACCTCTTAG	134.06	Flower_2	-	-	-
TTCAAATCTGGTTCCTGGCACCA	126.49	Flower_2	-	-	-
CAACGAGTCCACAGTATCTGCTAC	121.44	Flower_2	-	-	-
CCTCGTGTGCACCCCC	129.91	Flower_2	-	-	-
TGAGTTAGATGGTTAGAAAG	117.3	Flower_2	-	-	-
TCATGTTGACATCAGGATTACT	117.48	Flower_2	-	-	-
TTAGCCTGTGAACCAATTTTT	116.76	Flower_2	-	-	-
CCGATGCGGATCGCGCGGCG	115.32	Flower_2	-	-	-
AGGGTCCAGGTATTTCTTTGAAGC	109.19	Flower_2	-	-	-
ATTCATTGATGATTATGGAGCTAGT	105.95	Flower_2	-	-	-
TTTTGGACCAAGGCTCGTCT	109.19	Flower_2	-	-	-
CCTATGTCGCTCCGATTCGTA	104.87	Flower_2	-	-	-
TGAGATTCCAGCTTTGACAAAT	101.26	Flower_2	-	-	-
GTCCTCGTGTGCACCCCC	100.54	Flower_2	-	-	-

TTGTCCAACACTTCTTTCGTC	100.72	Flower_2	-	-	-
CCACGATCCACTGAGATTACAG	101.08	Flower_2	-	-	-
TTGTCCGACGAGAGATGGCAC	98.92	Flower_2	-	-	-
TCAGCTAGTAGCATTGTCTCT	98.02	Flower_2	-	-	-
CCCTATGTCGCTCCGATTCGTA	98.2	Flower_2	-	-	-
GCCGGCCGGGGACGGACTGG	95.14	Flower_2	-	-	-
GGCGGACTGCTCGAGCTGC	96.76	Flower_2	-	-	-
CGGGGGACGGACTGGGA	98.2	Flower_2	-	-	-
GACTGACTTGAGCATCGGAGGGTT	90.45	Flower_2	-	-	-
GCGACCCAGGTCAGGCGGGAC	104.69	Flower_2	-	-	-
GGTATGAGAGGGTTGGGTT	93.34	Flower_2	-	-	-
TTTGGCAGCAATGAATCTTGG	93.34	Flower_2	-	-	-
TTGGCTGGATCCCTAGTTGGTC	87.21	Flower_2	-	-	-
TTTCAAAGGATTATGAATCT	88.65	Flower_2	-	-	-
TGAGATTCCAGCTCTGCCAAC	87.75	Flower_2	-	-	-
CATAGATGTACAAGTTCTCTCT	85.95	Flower_2	-	-	-
TGAGGTTAGATGGTTAGAAGG	88.65	Flower_2	-	-	-
TCAACTGGGTACTTGGTAGAGGAT	84.15	Flower_2	-	-	-
TAGATATGTTGGCAGAGCTGG	86.13	Flower_2	-	-	-
AGGATCTTTGCTCTTGAACCGCCT	81.98	Flower_2	-	-	-
AGTTACTAATTTATGATCTGGC	83.97	Flower_2	-	-	-
CAACTAGGGATCCAGCCAATC	84.87	Flower_2	-	-	-
CTATGTCGCTCCGATTCGTA	83.97	Flower_2	-	-	-
GCGACCCAGGTCAGGCGGGACTA	78.92	Flower_2	-	-	-
ACCCGAATAGCACTGTAGCACTGT	78.2	Flower_2	-	-	-
TGTTAGTCAAAGCATGTGGGCACC	76.58	Flower_2	-	-	-
CGGATTCTGACTTAGAGGCGT	80	Flower_2	-	-	-
TCTTCTCGTCTTTTGTGCTTGACT	75.14	Flower_2	-	-	-
GCCCTATGTCGCTCCGATTCGTA	75.5	Flower_2	-	-	-
CCTGCCTGGGCGTCACGC	77.3	Flower_2	-	-	-
GTTACTAATTCATGATCTGGCC	76.58	Flower_2	-	-	-

CATTTCTGTAATTTGTGTGC	75.68	Flower_2	-	-	-
CGTTTCCCGCAATGGAACCA	74.96	Flower_2	-	-	-
TACGTAGATGCAAACCTTTGGAGGT	71.71	Flower_2	-	-	-
AGCCCTATGTCGCTCCGATTGTA	71.53	Flower_2	-	-	-
TTGTCGCAGGAGCGGTGGCAC	71.17	Flower_2	-	-	-
GGTATGAGAGGGTTGGGTTC	71.17	Flower_2	-	-	-
TTGACAAGGTTGTTGGTTGAGCCT	67.93	Flower_2	-	-	-
CCTCAACCTTGGACCTTCATT	69.55	Flower_2	-	-	-
GTTTCGTTTCCCGCAACGGAACCA	68.11	Flower_2	-	-	-
GTGTTCCGGATCGCGGCACGCGGGC	67.93	Flower_2	-	-	-
TATGTCGCTCCGATTGTA	71.17	Flower_2	-	-	-
TGTTAACGGCTGCCACCC	72.79	Flower_2	-	-	-
GATGATTGTAGCTGGTTGTGT	68.29	Flower_2	-	-	-
AAAACGACTCTCGGCAAC	71.35	Flower_2	-	-	-
GGAAGTCCTCGTGTGCACCCCC	66.31	Flower_2	-	-	-
TGTGGGACCCAGGGCTACGGTGCC	64.87	Flower_2	-	-	-
TAGTATCTGGTTGGAAGTCCC	64.69	Flower_2	-	-	-
ACCGGATTGGACTATTTTAGTCTT	62.88	Flower_2	-	-	-
TCGGCACCGCTAGGCTCAGACGCC	63.42	Flower_2	-	-	-
TACTGGAAGTCTTTGTGAGGA	64.87	Flower_2	-	-	-
TTTTCCGTTTTTCTGAAAAC	63.79	Flower_2	-	-	-
ATCTGTATTGAATCCTTGGTGT	62.34	Flower_2	-	-	-
TCCACACATCATCTAAGACAAG	64.33	Flower_2	-	-	-
TTGGATTGCACGTGACGGTCACG	61.44	Flower_2	-	-	-
TAGCGGGACCGCGGAGCTT	61.8	Flower_2	-	-	-
GGAGCGACCCGAGATCACATG	63.06	Flower_2	-	-	-
CCCCGGCGTCGAACGGTCA	61.44	Flower_2	-	-	-
GTGTGGGTGGGTAGGGAAGAT	60.36	Flower_2	-	-	-
CATTTCTGTAATTTGTGTGCA	60.54	Flower_2	-	-	-
CAGTCCCGAACCCGTCGGC	61.08	Flower_2	-	-	-
TTGAGCAAGATGTAATGAGCA	59.64	Flower_2	-	-	-

ATAGTAGTGATGTTGTTTCTC	58.02	Flower_2	-	-	-
CCGGAATCATTCTCCTGCATG	57.12	Flower_2	-	-	-
ACTTTGATGTCTTGAGAGCAGA	58.38	Flower_2	-	-	-
TCTCCCTACTCCACCCATGCCT	58.02	Flower_2	-	-	-
TAGGGTTGGGCCGGGAGGGTC	58.56	Flower_2	-	-	-
ACTTTATGGACCTTGAGAGGCACC	55.32	Flower_2	-	-	-
CTTTTTGGACCCAAGGCTCGTC	58.02	Flower_2	-	-	-
TCCAGTGTATGATGATTTCAGAAC	53.51	Flower_2	-	-	-
GCGACCCAGGTCAGGCGGGACTAC	53.15	Flower_2	-	-	-
TGTGGGTGGGTAGGGAAGATT	52.97	Flower_2	-	-	-
TGCACATCCAAATTTGGACTT	53.15	Flower_2	-	-	-
TCCGAGGACGTAGGCATTTTCGC	51.35	Flower_2	-	-	-
CGGCACTCGGTCTCCGGATT	52.43	Flower_2	-	-	-
GAAGGACGAGATACATACACGTTA	51.17	Flower_2	-	-	-
CCCAGTCCCGAACCCGTCGG	55.86	Flower_2	-	-	-
GCGAGAAGTCCACTGAACCTT	51.89	Flower_2	-	-	-
AAGTGCCGTCTGAGCTCT	53.15	Flower_2	-	-	-
CTTTTTGGACCCAAGGCTCGTCT	49.91	Flower_2	-	-	-
TGCATCAGGTAATACATGGAC	50.27	Flower_2	-	-	-
TTCAGCCTCTGTAGTGGATAGAGC	49.55	Flower_2	-	-	-
TTCTGAAAACCCCCGTTCTCT	50.45	Flower_2	-	-	-
CAATTACCAGACTCGATGAGCC	50.09	Flower_2	-	-	-
ACTGGAAGTCTTTGTGAGGAAC	49.91	Flower_2	-	-	-
GTGGATTTGAGGTTGGGTTT	49.01	Flower_2	-	-	-
GGGCTTTCTTTAGAATACTTGACT	48.47	Flower_2	-	-	-
CATCATTGTATACCTGTTGAG	51.35	Flower_2	-	-	-
TTGGATGTGCACCATTACCCT	49.37	Flower_2	-	-	-
AGTTACTAATTCATGATCTGGCCC	48.29	Flower_2	-	-	-
AGCGTCGTGCTGCTAGGCGAAGCGG	48.11	Flower_2	-	-	-
TTAGGTACCCTTGATGATCAA	48.29	Flower_2	-	-	-
TGGTTTGCCAAGAACCCTGCCT	49.37	Flower_2	-	-	-

TAATTGTCAGAACACGCACCA	48.65	Flower_2	-	-	-
CCTGGCATCGGCCTGCGAGCT	48.29	Flower_2	-	-	-
TCGTTTCCCGCAATGGAACCA	48.47	Flower_2	-	-	-
ACCGTATCATTAACTATTCTTTA	47.57	Flower_2	-	-	-
GCCGCACTAGAATTCACCACCAGG	46.49	Flower_2	-	-	-
ATACTGAGAAGTGAATGACATGTT	46.13	Flower_2	-	-	-
CCGAACCGGGACGTGGCGGCT	49.55	Flower_2	-	-	-
CTAATCGAACCGTCTAGTAGCT	48.47	Flower_2	-	-	-
ATGTTCCCTCTGAATGTTATTACT	45.77	Flower_2	-	-	-
TGCACTGTAGCGAACTGTAGCTGG	46.85	Flower_2	-	-	-
CATCATTCAATGTTCTGTTTA	46.13	Flower_2	-	-	-
CCACCCTGGAAACGGCTCAGC	45.95	Flower_2	-	-	-
GTTACTAATTCATGATCTGGCAT	45.05	Flower_2	-	-	-
ATCATCTTAGTTGGTGAATGGACC	45.41	Flower_2	-	-	-
CGCGCCCGGACCCTGTCGCACC	47.21	Flower_2	-	-	-
TAGATGTACAAGTTCTCCTCT	45.41	Flower_2	-	-	-
CAGTTGGGCACCGTAACCCGG	46.31	Flower_2	-	-	-
GTTTCGTTTCCCGCAATGGAACCA	43.96	Flower_2	-	-	-
CTCCTGGCATCGGCCTGCGAGCTCC	43.42	Flower_2	-	-	-
CAGCCCTATGTCGCTCCGATTCTGA	43.42	Flower_2	-	-	-
ATGTCGTTTTATAAATGGAAGTCT	43.42	Flower_2	-	-	-
AGGGAATGATGTTGTCTGGAACAA	43.6	Flower_2	-	-	-
TACTAAGGCCAAGTCCCTTGAACT	43.42	Flower_2	-	-	-
CCCTATGTCGCTCCGATTCTGTT	43.96	Flower_2	-	-	-
TCCCAGTCCCGAACCCGTCGGC	45.23	Flower_2	-	-	-
TAATGAAGGTCCAAGTTGAGGCT	43.24	Flower_2	-	-	-
GCCGGCCGGGGACGGACT	44.51	Flower_2	-	-	-
ATTTGTTTGTCTCAGATTC	42.7	Flower_2	-	-	-
TTTTGGACCAAGGCTCGTC	43.96	Flower_2	-	-	-
TTGGTAACTTGTTATGCTCGA	44.33	Flower_2	-	-	-
TGTTGAATAAGACCTTCTGCC	42.34	Flower_2	-	-	-

TTACTAATTCATGATCTGGC	44.87	Flower_2	-	-	-
CAACTTAATGTTTAGGACTTT	42.52	Flower_2	-	-	-
TGGTAATATATATGGTTGGTT	41.98	Flower_2	-	-	-
ACTCGAACTCGGCCCTTGGATGGC	40.9	Flower_2	-	-	-
TGTGCACCATTACCCTTACCC	41.62	Flower_2	-	-	-
CCCGGGCGTCGAACGGTCGACT	42.52	Flower_2	-	-	-
GCGGACCGATGCGGATGCGCGCGGC	40.54	Flower_2	-	-	-
TTATTCGGTACCATAATAATT	41.98	Flower_2	-	-	-
GAC TTCATGCAGACAAGCTG	40.9	Flower_2	-	-	-
CCTGTTGGCTAGGTCTAAAGGACC	40	Flower_2	-	-	-
GTTGTATTACTTATTATTACT	40.36	Flower_2	-	-	-
CAAGTGTATCTTTCCAAC	41.08	Flower_2	-	-	-
TCCATGGGCTGTGTCGGACCG	42.16	Flower_2	-	-	-
AACAAACGTGTAGAAGAATGCATT	39.82	Flower_2	-	-	-
CGAGTCATGGAAGTCTTTC	41.44	Flower_2	-	-	-
TTTTATTCACTGATTGTCGGCT	39.64	Flower_2	-	-	-
TGCAGAGATTCAACATGGACGACG	39.64	Flower_2	-	-	-
TAGCTCGACGCCAGGATAC	41.98	Flower_2	-	-	-
TCGAATGAATTCTAGGACATATT	39.28	Flower_2	-	-	-
CTGTTTAACGGCCTGCCACCC	44.69	Flower_2	-	-	-
CGCGCCACGGAATCGAGAGCT	39.64	Flower_2	-	-	-
TCCCGGGCGTCGAACGGTCGA	39.28	Flower_2	-	-	-
TAAGGAATGGAGAATGTCCTTGCT	38.56	Flower_2	-	-	-
TTTCAATGAGTCTACAGTACCTGC	38.92	Flower_2	-	-	-
TGTGCTTCTTGGGAAGCTGAGCT	38.92	Flower_2	-	-	-
CAGTCCCGAACCCGTCGGCT	40.72	Flower_2	-	-	-
GGAATAGTTGAGTAGAGCTGG	40.9	Flower_2	-	-	-
TCTTACAAGGTCAAGAAGACT	40	Flower_2	-	-	-
CTACCCGAATAGCACTGTAGCACT	37.84	Flower_2	-	-	-
TTTTTGACCCAAGGCTCGTCT	40.36	Flower_2	-	-	-
TTGTGAGCCATTGACGATTGCCTT	37.84	Flower_2	-	-	-

TCTTTAATCAGGTTGCTGACC	38.38	Flower_2	-	-	-
CGGCTGCAGTAGCAGTAGAGCACC	38.02	Flower_2	-	-	-
CCCCGGGCGTCGAACGGTCGACT	38.02	Flower_2	-	-	-
TCATGGTTTTGCGATTTTAGG	38.92	Flower_2	-	-	-
TGGCACCCTCAATTGTAAACATT	37.84	Flower_2	-	-	-
ATGTCGCTCCGATTCGTAA	40.36	Flower_2	-	-	-
TAAACAGATGCATTCTGTAGGCCT	37.3	Flower_2	-	-	-
TTCGTTTCCCGGCAATGGAACCA	37.84	Flower_2	-	-	-
CATGTGCCCGTCTTCCCCATC	38.74	Flower_2	-	-	-
GAAGTCGATCACCGAAGAAGCACC	37.12	Flower_2	-	-	-
TGTGGTGGGTAGGGAAGAT	38.2	Flower_2	-	-	-
CCGTTTCTGATTGTTAATGACATT	36.4	Flower_2	-	-	-
AGTTACTAATTCATGATCTGGCCA	36.04	Flower_2	-	-	-
CTCTTATCATGAGTTTGACT	38.74	Flower_2	-	-	-
CCCGGTGCAGGGTAAACTCGTCC	36.04	Flower_2	-	-	-
TTCCCTACTCCACCCATGCCAT	35.86	Flower_2	-	-	-
TCATGTGTTCTCAGGTCGCC	36.4	Flower_2	-	-	-
CAAATTTGGACTTCGTTTGCA	36.4	Flower_2	-	-	-
CAGTACTAATTCATGATCTGGC	36.4	Flower_2	-	-	-
TTGTCAGAGTTGTGATTCTCT	36.04	Flower_2	-	-	-
ATGGGACTGAGATCTCAAGGATCT	35.32	Flower_2	-	-	-
CCAGCCGGCGCACTGTGTGGGACC	34.96	Flower_2	-	-	-
CACCATATAGTGCATAGCACA	37.3	Flower_2	-	-	-
CGGACACCGCGCAGCTGCGG	36.58	Flower_2	-	-	-
ATTTATGGCCTGAGTCTTACT	36.22	Flower_2	-	-	-
AGTTACTAATTCATGATC	57.84	Flower_2	-	-	-
TTCTGTTTAAACGGCTGCCACCC	36.04	Flower_2	-	-	-
AGGGATGTAGCGCAGCTT	36.58	Flower_2	-	-	-
GGTCCAGACGGAGCTCCGAGGAC	34.23	Flower_2	-	-	-
CTTTGATGTCTTGAGAGCAGA	36.22	Flower_2	-	-	-
TCCCAGTCCGAACCCGTCGGCT	35.86	Flower_2	-	-	-

CGAGACATTCTTGCAAGATCATGC	34.78	Flower_2	-	-	-
TCATATCCAATTTGTATCTCAAT	34.05	Flower_2	-	-	-
AGTTACTAATTCATAATCTGGC	35.32	Flower_2	-	-	-
TTATAGTTGTTTGTATGGTAACT	34.96	Flower_2	-	-	-
ATGGACCTTGAGAGGCACCGAGTG	33.87	Flower_2	-	-	-
AACTTCATCTAGTTTTGTTGGTCT	34.23	Flower_2	-	-	-
CGCCTGCCTGGGCGTCACGC	35.14	Flower_2	-	-	-
TGTCGCTCCGATTCGTA	36.76	Flower_2	-	-	-
TGAGGTTAGATGGTTAGAAAGCCT	33.69	Flower_2	-	-	-
GCGGTCCGGATATCTACTCTCATA	33.15	Flower_2	-	-	-
CGAGGTCATGGAAGTTCTTTCT	33.87	Flower_2	-	-	-
CATTAGGATAGTCTGTAAGCCT	34.6	Flower_2	-	-	-
TGAAGGTCCAAGGTTGAGGCTT	35.14	Flower_2	-	-	-
TCGTGCTAAAGAGCGTGGAG	34.6	Flower_2	-	-	-
CCCCGGGCGTCGAACGGTCGAC	34.78	Flower_2	-	-	-
AGAGGGATTGGGTGAGTTTGGAGT	32.97	Flower_2	-	-	-
AATCGAACCGTCTAGTAGCTGGT	33.51	Flower_2	-	-	-
GCATCGGCTGCGAGCTCCCC	35.68	Flower_2	-	-	-
CTGAGATTCCCATCTCTGATGAGC	32.79	Flower_2	-	-	-
CGGTGTCCTTCAGCTAGTAGC	34.78	Flower_2	-	-	-
CACTTTCAGCAACTTCTTGC	34.42	Flower_2	-	-	-
CCGGCTTAGCTCAGTTGGC	33.69	Flower_2	-	-	-
TATAGTTTGTGTTGATGGTAACTACT	32.79	Flower_2	-	-	-
CTAGGGTTGGGCCGGGAGGGTC	33.33	Flower_2	-	-	-
TCCTGGCATCGGCTGCGAGCT	33.69	Flower_2	-	-	-
CCAGTCCCGAACCCGTCGGCTG	33.69	Flower_2	-	-	-
GTTATCTTTCTAACGGCACTG	33.15	Flower_2	-	-	-
ATTGGCTCTGAGGGCTGGGCAC	33.33	Flower_2	-	-	-
AAAACGACTCTCGGCAACGGATA	32.61	Flower_2	-	-	-
CGGTTTTGTGICTCTCATGAC	33.87	Flower_2	-	-	-
AACGACTCTCGGCAACGGAT	34.05	Flower_2	-	-	-

TTCTGGATCTGGATTTATGATC	32.97	Flower_2	-	-	-
GATTCGGTCCTATCTGTTGGC	32.97	Flower_2	-	-	-
TGAAGGGAGACTTTAGGATTT	32.79	Flower_2	-	-	-
TCATATGCATGGTTCGTGAAC	32.97	Flower_2	-	-	-
ATTTGTGGATGAAATCTCTGGGA	30.99	Flower_2	-	-	-
CGTGTCCGGGCGACGCCACCA	31.71	Flower_2	-	-	-
TTAGACCTTCGGAATTTGAAGCT	32.07	Flower_2	-	-	-
CCTGGCATCGGCCTGCGAGC	33.33	Flower_2	-	-	-
CTGGCATCGGCCTGCGAGCT	32.61	Flower_2	-	-	-
ACCTGAGTCTGATTTTACCTACTA	30.99	Flower_2	-	-	-
AGTCCCGAACCCGTCGGCTGTCGG	31.71	Flower_2	-	-	-
TCCTATTCTGTTGGCCTTCGGGATC	30.45	Flower_2	-	-	-
GGGGATTAGGGCTTGTGCAAAGC	30.99	Flower_2	-	-	-
CGCAACCGAGTTACCTGGGAT	31.89	Flower_2	-	-	-
GAGGGTTTGTGTATTATTGTATT	31.53	Flower_2	-	-	-
AAGTCCACTGAACCTTATCATT	32.07	Flower_2	-	-	-
ACAACGAGAGAGACACGCTT	31.89	Flower_2	-	-	-
TCGCACCACGAGGGCTGTCT	31.17	Flower_2	-	-	-
CCTTGGACCTTCATTATTCATTGT	30.63	Flower_2	-	-	-
ACTGCATCAACTGGGTACTIONGGTA	29.91	Flower_2	-	-	-
CAAGGGACGTTTGAACATTGCACC	30.63	Flower_2	-	-	-
TTTTCCGAAGGATTATGAAT	30.63	Flower_2	-	-	-
CATGTGTTCTCAGGTCGCCCC	31.53	Flower_2	-	-	-
TCGCAAGAGGCTGGTTTGAGG	31.53	Flower_2	-	-	-
ACTGCACGGGCTGGCGCACCCAC	29.73	Flower_2	-	-	-
ATTTCACTCGACCACTGTAGCATT	29.73	Flower_2	-	-	-
TTCCAATGACAGTATCTTGTATC	29.73	Flower_2	-	-	-
TACCGGGCTCATCGAGTCTGGTAAT	29.91	Flower_2	-	-	-
TATCGGCACCAATCCGAGTAGGAC	30.27	Flower_2	-	-	-
GGGAAGTCTCTGTTGCACCC	30.09	Flower_2	-	-	-
CTCTTATCATGAGTTGGACT	31.35	Flower_2	-	-	-

ATGAAGGTCCAAGGTTGAGGCT	32.43	Flower_2	-	-	-
CTAAAGTCTCCCTTCATGGCT	32.43	Flower_2	-	-	-
CGCTGGATTATGACTGAACGCCT	29.73	Flower_2	-	-	-
ATGGGATCCGTTGAATATTGT	30.45	Flower_2	-	-	-
TCAAACAAGGAAAGGCTT	32.25	Flower_2	-	-	-
AGTGTTATTTGGTTTAAAGACTTT	29.73	Flower_2	-	-	-
ATCTTTCTGTTTAACGGCCT	30.63	Flower_2	-	-	-
AGACTTGCTCATCGACCTTGCTCC	29.55	Flower_2	-	-	-
GAAAGTCATGAGAGAATTCCAAAT	29.01	Flower_2	-	-	-
AGACCGGTAGACTTGAAC	30.99	Flower_2	-	-	-
GCATCGGCCTGCGAGCTCCC	31.17	Flower_2	-	-	-
TCGGTCCATCGTCGATGACGTAAG	30.09	Flower_2	-	-	-
GCGAGTCGACGGGCCAGTAAACCC	29.73	Flower_2	-	-	-
CAGACCGGTAGACTTGAAC	30.63	Flower_2	-	-	-
TGATCGGAGAAGATGATGAATAGT	28.83	Flower_2	-	-	-
TAAGCCAAGTCCCTTGAAC	28.47	Flower_2	-	-	-
CAGGATTACTCAATGCATAGCCGT	28.47	Flower_2	-	-	-
AGTCCGAACCCGTCGGCTGTC	29.19	Flower_2	-	-	-
GTAGCATATGGGATGGCGTAG	29.19	Flower_2	-	-	-
CGGACCCTGTGCGACCACGAGG	30.27	Flower_2	-	-	-
TTGGCTCTGAGGGCTGGGCACGG	29.19	Flower_2	-	-	-
CTCTTTCTGTATAATTGGTGACC	28.47	Flower_2	-	-	-
AGAGGATTCATCTCTGGAAAAGTGC	28.29	Flower_2	-	-	-
CGGCACTGCATCAACTGGGTA	28.47	Flower_2	-	-	-
CCTGGCATCGGCCTGCGAGCTCC	28.29	Flower_2	-	-	-
GCGGACCGATGCGGATCGCGGCG	28.83	Flower_2	-	-	-
TAGCCTTGGACGGAATTTACC	29.19	Flower_2	-	-	-
CTATTCTGTTGGCCTTCGGGATC	28.65	Flower_2	-	-	-
CCATCCACTGTCAATGCTTTTGAG	27.93	Flower_2	-	-	-
CTAGGGTTGGGCCGGGAGGGT	29.19	Flower_2	-	-	-
GCTCGACGCCAGGATAC	30.63	Flower_2	-	-	-

GTCCCGAACCCGTCGGCTGTCGGC	28.29	Flower_2	-	-	-
TAGGGTTGGGCCGGGAGGGT	29.91	Flower_2	-	-	-
TTGGCTCTGAGGGCTGGGCACGGG	28.29	Flower_2	-	-	-
TGTAGCAGGTACTGTAGACTCGTT	27.75	Flower_2	-	-	-
GTGCTGCTAGGCGAAGCGG	30.27	Flower_2	-	-	-
CGAGGCGCGGACCGATGCG	29.01	Flower_2	-	-	-
TGAACAGTAATCGGTAATAGTAAC	27.93	Flower_2	-	-	-
ACAACACTGACTCTTTTAGTTCCT	27.39	Flower_2	-	-	-
CCGGGCGTCGAACGGTCGACT	28.11	Flower_2	-	-	-
AGCTCGACGCCAGGATAC	29.01	Flower_2	-	-	-
TTTCTCAGTCATGTGGTGCCT	28.65	Flower_2	-	-	-
TTGGGTTTTAGTCTGATGCC	28.29	Flower_2	-	-	-
TCCTGGCATCGGCCTGCGAGCTCC	27.39	Flower_2	-	-	-
TTTGGTAGTAGCTGAGATTCC	28.29	Flower_2	-	-	-
TGGGCAGATGAACGGCGACGAGAA	27.39	Flower_2	-	-	-
CCTCTTTTGGACCCAAGGCT	29.01	Flower_2	-	-	-
TTTAGACCTTCGGAATTTGAAGCT	27.93	Flower_2	-	-	-
GATTGGCTCTGAGGGCTGGGC	28.65	Flower_2	-	-	-
CCATTGGGCTGGATCCATGTTGGCA	27.21	Flower_2	-	-	-
TGCTCCTAGAACTCCTCAACAAA	27.21	Flower_2	-	-	-
CATGTTGACATCAGGATTACT	27.57	Flower_2	-	-	-
CCCGAACCCGTCGGCTGTCGGC	29.73	Flower_2	-	-	-
CAACGGATCCCATTTGTTAATG	29.01	Flower_2	-	-	-
GTTGTATTACTTATTATTACTATA	26.67	Flower_2	-	-	-
CGGGGACGGACTGGGAACGGCCCC	26.85	Flower_2	-	-	-
CCCGGGCGTCGAACGGTCGAC	27.93	Flower_2	-	-	-
TTAGCCTGTGAACCAATATT	27.21	Flower_2	-	-	-
AGGGTTGTTCTGCGGCGACGA	27.57	Flower_2	-	-	-
GTCCCGAACCCGTCGGCTGTCGGC	27.03	Flower_2	-	-	-
GAAACAAGTCGGGAAAATCCTCT	26.67	Flower_2	-	-	-
CTTTTGGACCCAAGGCTCGT	27.57	Flower_2	-	-	-

TGTCCTGGATTGGTCCATTTGAGC	26.67	Flower_2	-	-	-
CTTGGTATTTTCGGATACTGACCT	26.31	Flower_2	-	-	-
CAAATTGGTGTTCATTGGAGATG	26.85	Flower_2	-	-	-
CTTCGTTACTCGGATGTGGCCATT	26.49	Flower_2	-	-	-
CTGCACGGGCCTGGCGCACCCAC	26.49	Flower_2	-	-	-
CTCCACTGTAGCCATAGCCATAGG	27.21	Flower_2	-	-	-
ATGAGAGACACAAAACCGTGC	26.67	Flower_2	-	-	-
AGTCCCGAACCCGTCGGCTGTCGGC	26.49	Flower_2	-	-	-
TGCTGCTGTTACATGGAACCT	27.03	Flower_2	-	-	-
AGAGTCTGAAATGACGACCTGAGA	25.95	Flower_2	-	-	-
AGTTACTAATTCATGATCTGGCCT	26.13	Flower_2	-	-	-
TCCGTGAATCGGAAGCGGGCAC	27.21	Flower_2	-	-	-
TCCCCGGGCGTCGAACGGTCGAC	26.67	Flower_2	-	-	-
CGGGCTAGAGCGACGCTGCGCC	26.49	Flower_2	-	-	-
ACCCAGAAGTCAAACCTGAACAAC	25.59	Flower_2	-	-	-
GATCATGCGGCAGTTTCACC	28.11	Flower_2	-	-	-
AGGATTCGATTCAACTCCGAAAT	26.31	Flower_2	-	-	-
GTCCCGAACCCGTCGGCTGTCGG	26.67	Flower_2	-	-	-
ATGAAGGGAGACTTTAGGATT	26.67	Flower_2	-	-	-
TCGAACCGTCTAGTAGCTGGT	27.21	Flower_2	-	-	-
CCGCAGAACAACCCTAAACCT	25.95	Flower_2	-	-	-
TTTCGGTCCTATTCTGTTGGC	25.95	Flower_2	-	-	-
TGAAGGTCCAAGGTTGAGGC	31.17	Flower_2	-	-	-
TGCACGGGCCTGGCGCACCCAC	26.31	Flower_2	-	-	-
ATAGCGCGGACCGCGGAGCT	25.95	Flower_2	-	-	-
GAGGCGCGGACCGATGC	27.75	Flower_2	-	-	-
CTAGCCGACGTGGACGGTTGAGCT	25.05	Flower_2	-	-	-
CAGGAATCTGCAGACAAAAGAGTC	25.41	Flower_2	-	-	-
ATCTGCTCTGATACCATGTTGAAA	25.05	Flower_2	-	-	-
TCGACGACACTGTAGCATCGACGG	25.05	Flower_2	-	-	-
TAGCCTGTGAACCAATTTTTT	26.31	Flower_2	-	-	-

TTCGTGTCCGGGCGACGCCACCA	25.59	Flower_2	-	-	-
TCTTTCTAACGGCACTGCATC	26.13	Flower_2	-	-	-
CGACCTTGATCTTCTGAGAA	26.31	Flower_2	-	-	-
TCCCGGGCGTCGAACGGTCGACT	25.23	Flower_2	-	-	-
TTCCCGGGCGTCGAACGGTCGA	25.77	Flower_2	-	-	-
CTAGACTTGCTCATCGACCTTGCT	24.87	Flower_2	-	-	-
ACGGTTTGTGTCTCTCATGA	25.41	Flower_2	-	-	-
TTTTCGGATCCTGTGAACAGGCTC	24.87	Flower_2	-	-	-
GAAATAGGGCTGTACCTGTGGCT	24.69	Flower_2	-	-	-
TCGGCTCCCGGTAGGACCTCCA	25.59	Flower_2	-	-	-
TTGGATGTGCACCATTACCCT	25.77	Flower_2	-	-	-
CCTGTCGCACCACGAGGCGTGTCT	24.51	Flower_2	-	-	-
TCCAGGTTGGTGTATGATCTAGC	24.14	Flower_2	-	-	-
GTCCAACAAGGACTTATTGAGCCC	24.51	Flower_2	-	-	-
TTACGGATAAGTTCTTCGGGCTCC	24.69	Flower_2	-	-	-
AGAATGCATCTGTTAAGGACTGT	24.32	Flower_2	-	-	-
TAGTAGTGATGTTGTTCTCT	25.23	Flower_2	-	-	-
ATCTTCTAGGTGATTGGTCCCGGT	24.14	Flower_2	-	-	-
CCCCGAAAATGGATGGCGCTG	24.51	Flower_2	-	-	-
ATGATTGATGTAACATCGTAACCT	24.14	Flower_2	-	-	-
TAGACCTTCGGAATTTGAAGCT	24.32	Flower_2	-	-	-
TCATGTTGGTACCTGGGTTT	24.51	Flower_2	-	-	-
TTGAGATTCTCCTTTAGAAA	25.23	Flower_2	-	-	-
TCGCACCACGAGGCGTGTCTG	24.87	Flower_2	-	-	-
TTTTAATGTTAAGATTTGGGAGT	23.96	Flower_2	-	-	-
GAGGATGTAAGCAATCAGGAGC	25.23	Flower_2	-	-	-
TTTCCGAAGGATTATGAATT	25.05	Flower_2	-	-	-
CTCGAGGCGCGGACCGATGCGGATC	23.42	Flower_2	-	-	-
CTGGCATCGGCCTGCGAGC	25.59	Flower_2	-	-	-
CGGCCTGCGAGCTCCCCATTCGG	23.96	Flower_2	-	-	-
AGACCGGTAGACTTGAA	25.23	Flower_2	-	-	-

TGGGATATGATTGTAAAGAAT	23.96	Flower_2	-	-	-
CCCGAACCCGTCGGCTGTCCGG	25.77	Flower_2	-	-	-
CGAGTCGACGGGCCAGTAAACCC	23.78	Flower_2	-	-	-
GTTAATTGTATCACTGTTCCAGACT	23.6	Flower_2	-	-	-
AACAAACTTGTTCCTTTGAAACC	23.96	Flower_2	-	-	-
TCGCGAGAAGTCCACTGAACCTT	23.78	Flower_2	-	-	-
TCCATAGATGTACAAGTTCTC	23.96	Flower_2	-	-	-
AGGATTATATCAATGTTTTGGGCC	23.24	Flower_2	-	-	-
TGGTGACGTTTGATTGATCA	23.6	Flower_2	-	-	-
TGATGACAGCGTCGTAATAGT	23.96	Flower_2	-	-	-
CGAGGCGCGGACCGATGCGGATC	24.51	Flower_2	-	-	-
ACTTTTGATTGGTTGAAATCACT	23.42	Flower_2	-	-	-
CTCCTGGCATCGGCCTGCGAGCT	23.6	Flower_2	-	-	-
CTCTGAGGGCTGGGCACGGGG	23.78	Flower_2	-	-	-
CGAGCTTTCCTGTAGCTGGGACT	23.24	Flower_2	-	-	-
CGAGAGGAACCGTTGATTCCGC	23.96	Flower_2	-	-	-
TTCCCCGGGCGTCGAACGGTCG	23.78	Flower_2	-	-	-
ACCGGTAGACTTGAACCT	25.95	Flower_2	-	-	-
GGCCTGAGTTGCTGTAGTAACAGC	22.88	Flower_2	-	-	-
AGCCCGGGGCGAGTTCTATC	23.96	Flower_2	-	-	-
CTATTCTGTTGGCCTTCGGGA	23.42	Flower_2	-	-	-
GCGGACCGATGCGGATGCGGGC	25.41	Flower_2	-	-	-
ACCGTTCGACTTTATCTGCAGAGT	23.42	Flower_2	-	-	-
AGTTATTAATTCATGATCTGGC	23.6	Flower_2	-	-	-
CAGTCCCGAACCCGTCGGCTGTC	23.6	Flower_2	-	-	-
ACAAGTCTAGCCGACGTAGACGGC	22.88	Flower_2	-	-	-
TGGAAGAAATAGGGCTGTACCTGT	22.52	Flower_2	-	-	-
GGGGATTAGGACTTGTTCGAAAGC	22.88	Flower_2	-	-	-
CATTCTGTTTTCTAGGACATGCT	22.7	Flower_2	-	-	-
CGGGGGACGGACTGGGAACGGCCC	22.7	Flower_2	-	-	-
CCAAAGACAAGACTCCAGAGT	23.24	Flower_2	-	-	-

CGGGCGTCGAACGGTCGACT	23.96	Flower_2	-	-	-
AACTCCGAAATTGCTGACTTGAGC	22.7	Flower_2	-	-	-
CCCACGTTTCGAATTGTAGTC	23.42	Flower_2	-	-	-
ATGTTCCCTCTGAATGTTATTACT	22.88	Flower_2	-	-	-
CAGACGAGCAGTAGCGACAGCCAC	22.52	Flower_2	-	-	-
GAACAGTGACTGAATATTGAGAAC	22.52	Flower_2	-	-	-
CCCGGGCGTCGAACGGTCGA	24.14	Flower_2	-	-	-
TGCTCACTTCTCTCTGTGCAGC	23.06	Flower_2	-	-	-
ACGGGTTTACCCTGCACTTGGGGC	22.34	Flower_2	-	-	-
TCACCTTGCACGTTAGAACCAAAAC	22.16	Flower_2	-	-	-
TTCAACGGATCCCATTGTAA	22.7	Flower_2	-	-	-
CTGTGCGACCACGAGCGCTGTCT	21.8	Flower_2	-	-	-
CGGTTTTGTGTCTCTCATGACT	22.7	Flower_2	-	-	-
CGAAATTGCTGACTTGAGCCT	22.16	Flower_2	-	-	-
GCAGGCTGTATTCATGATCTACT	21.98	Flower_2	-	-	-
CTTCCCTACTCCACCCATGCC	23.06	Flower_2	-	-	-
AAGTGCCGCTGAGCTC	23.78	Flower_2	-	-	-
TCCGGAGGACCGAGTGCCGTC	22.34	Flower_2	-	-	-
AGGTGGAGAGATATGTGGGGT	21.98	Flower_2	-	-	-
TTTTCTGTTTAAACGGCCTGCC	21.98	Flower_2	-	-	-
ATAGTTTGTGTTGATGGTAACT	22.16	Flower_2	-	-	-
CTTACCCGATAGAACTCGCC	22.7	Flower_2	-	-	-
CGGAGCTCCGAGGACGTAGGCATT	21.62	Flower_2	-	-	-
CCGGCCGGGGACGGACTGGGA	22.16	Flower_2	-	-	-
GTCCCAATTTTCTCTGTAGAATT	21.8	Flower_2	-	-	-
AAATCCGGAGGACCGAGTGCC	22.16	Flower_2	-	-	-
GAAATTCGAGATTGGAAGTGAGCT	21.44	Flower_2	-	-	-
CGATCCACTGAGATTCAGCCCT	22.34	Flower_2	-	-	-
TCCTGGCATCGGCCTGCGAGC	22.88	Flower_2	-	-	-
ATTCTATGTACGGTCCTGTAGACT	21.26	Flower_2	-	-	-
TCTATCGTGGTGAAAGACTCCATA	21.26	Flower_2	-	-	-

TTTCTGTTTAACGGCCTGCC	22.7	Flower_2	-	-	-
CCGATGCGGATCGCGGGCGCGCC	21.62	Flower_2	-	-	-
GAGGCGCGGACCGATGCGGATC	22.16	Flower_2	-	-	-
TTTTACATGGAACTAATCAACA	21.08	Flower_2	-	-	-
CCCTGATGGTTGCGTCTTTAGAGA	21.62	Flower_2	-	-	-
GACGAACTGCCAAACGAGGACTT	21.08	Flower_2	-	-	-
CCTGATGATCTCCAACAGGAACT	21.62	Flower_2	-	-	-
TTCCCCGGGCGTGAACGGTCGACT	21.8	Flower_2	-	-	-
TCGTGTCGGGCGACGCCACCA	21.62	Flower_2	-	-	-
TTTTACCGACTCCTCCCATGCC	22.52	Flower_2	-	-	-
GAGGTTACGGTAGGTAGACATGAC	21.44	Flower_2	-	-	-
CCTATTCTGTGGCCTTCGGGATC	21.26	Flower_2	-	-	-
GTTATTCTATTCCACCTCTTAGA	20.9	Flower_2	-	-	-
ATTCTGTGGCCTTCGGGATC	21.8	Flower_2	-	-	-
CGTGCACCGAACCCCGACTTC	22.16	Flower_2	-	-	-
ACGACTCTCGGCAACGGATAT	21.44	Flower_2	-	-	-
CTCGAGGCGCGGACCGATGCG	21.62	Flower_2	-	-	-
GGCATCGGCCTGCGAGCTCC	21.62	Flower_2	-	-	-
GTTCCCGCAATGGAACCA	22.52	Flower_2	-	-	-
GCCGAGGAATTGTCGAACTTGATC	20.72	Flower_2	-	-	-
CACTGTCCCTGGGATTGGCTT	21.98	Flower_2	-	-	-
TGAGAAITCTGTTTGTGTGTTGAC	21.44	Flower_2	-	-	-
CCGCGCCACGGAATCGAGAGCT	21.44	Flower_2	-	-	-
GGCAGTTCGACCGCAAATTT	22.16	Flower_2	-	-	-
CACCTGCGCGCTCCTGGCATC	21.08	Flower_2	-	-	-
TGGGATAACATCATAGGATTT	22.16	Flower_2	-	-	-
CAAGTCCGCTCTGAGCTCT	22.16	Flower_2	-	-	-
TTTGTGTTCTCAGATTTCT	20.9	Flower_2	-	-	-
CTACTTCTGGTACTCCAGCC	20.9	Flower_2	-	-	-
CGCTGGATTATGACTGAACGCC	21.8	Flower_2	-	-	-
AGGATTGGCTCTGAGGGCTGGGCAC	20.72	Flower_2	-	-	-

TTCTCGTGATGCTCCTGATTGC	21.26	Flower_2	-	-	-
ATTCATGGITTCAGGAATCTG	21.08	Flower_2	-	-	-
TGTTACAGGTTTGACTTCTGGGTCT	20.9	Flower_2	-	-	-
CCAAATTGGACTTCGTTTGC	20.72	Flower_2	-	-	-
CGGCGGACTGCTCGAGCTGCTCC	20.54	Flower_2	-	-	-
CTTCCCCGGGCGTCGAACGGTCGA	20.72	Flower_2	-	-	-
CCGCCGAGACGAGCCTGGGTC	20.54	Flower_2	-	-	-
TCCCGAACCCGTCGGCTGTCGGCG	20.54	Flower_2	-	-	-
TGGTATTTTCGGATACTGACCT	21.08	Flower_2	-	-	-
TAGCTGAGATTCCAGCTCTGC	20.72	Flower_2	-	-	-
CAAAGCCGGGCTTTTCGTAC	20.54	Flower_2	-	-	-
CAGTTTTGTGTATGTATGCTT	20.9	Flower_2	-	-	-
CGCCCGGATCGTGGATGGCAGC	21.08	Flower_2	-	-	-
CGAGGCGGGACCGATGC	21.44	Flower_2	-	-	-
CTAAGCCAAGTCCCTTGAACCT	21.44	Flower_2	-	-	-
GCCTGCGACGTCGCGAGAA	20.72	Flower_2	-	-	-
TTCAATTGACTATTCATCTATT	20.72	Flower_2	-	-	-
GCCTGCGACGTCGCGAGAAGTC	20.54	Flower_2	-	-	-
CTCCAAC TAGGA ACTGAGCGTGGT	20	Flower_2	-	-	-
AAGGACTTATTGAGCCACAACCT	20	Flower_2	-	-	-
ATTGGCTCTGAGGGCTGGGCA	20.18	Flower_2	-	-	-
TGAGGGAGCTCCATCATGACGGGC	19.82	Flower_2	-	-	-
AGGACATAACTCTTGGCCCTGAAA	19.82	Flower_2	-	-	-
AACCGTCTAGTAGCTGGTCCCT	20.9	Flower_2	-	-	-
AATCTTGGATGGGACGGTCTCATT	20	Flower_2	-	-	-
CGGAATCGAGAGCTCCAAGTGGGC	19.64	Flower_2	-	-	-
TACCCTTTCAACCAAGACTG	20.36	Flower_2	-	-	-
CCGAACCCGTCGGCTGTCGGC	20.54	Flower_2	-	-	-
AGGGATGTAGCGCAGCTTGG	20.54	Flower_2	-	-	-
TGGCATCGGCCGTCGAGCTCCC	20.18	Flower_2	-	-	-
CCGAGGACGTAGGCATTTTCGCC	19.46	Flower_2	-	-	-

CCCGGGCGTCGAACGGTCGACTC	19.46	Flower_2	-	-	-
CGGCGGACCGGGCCCAAGTCCCC	21.08	Flower_2	-	-	-
ATCAAGTGCCGTCTGAGCTCT	20.72	Flower_2	-	-	-
TTGGACCAAGGCTCGTCTCGGCG	20	Flower_2	-	-	-
TGTAGCAGGTACTGTAGACTCGT	19.46	Flower_2	-	-	-
GAGAGCATGCCTGTCGGGACCC	19.64	Flower_2	-	-	-
TTGGTCCAGACCCATACTGAT	20.54	Flower_2	-	-	-
TGAAGGGCCAAGTTGAGGCT	24.14	Flower_2	-	-	-
CCAGTCCGAACCCGTCGGTGTGC	19.64	Flower_2	-	-	-
GGAATGAAACGGTCTCGTCAGATC	19.46	Flower_2	-	-	-
TGCCTGATTTCCTTCTCGTGAAT	19.28	Flower_2	-	-	-
CCGACCTTGATCTTCTGAGAA	20	Flower_2	-	-	-
TCGAGGCGGGACCGATGCGGATC	19.64	Flower_2	-	-	-
ATTCGTTGGAGTTAA	20.36	Flower_2	-	-	-
GTATGGATTCTTGATGCTGAAATC	19.1	Flower_2	-	-	-
GGGAATATGCGACTCCACTGG	19.64	Flower_2	-	-	-
TTTAACGGCCTGCCACCC	26.85	Flower_2	-	-	-
TCATGTTGACATCAGGATTAC	20.9	Flower_2	-	-	-
CCCCGACGTTTGAATGTAGTC	20.18	Flower_2	-	-	-
TTCCCCGGGCGTCGAACGGTCGAC	19.46	Flower_2	-	-	-
ACCTAGGAGGAACAAGCTGACACT	19.46	Flower_2	-	-	-
GCGTGTCTGACAATTATCCT	20	Flower_2	-	-	-
TGGCTCTGAGGGCTGGGCACGG	19.46	Flower_2	-	-	-
TACCCGAATAGCACTGTAGCACTG	19.1	Flower_2	-	-	-
CGGGTAGAATCCTTGCAGAC	19.82	Flower_2	-	-	-
CTACTTCCTGGTGTCCAGCC	19.64	Flower_2	-	-	-
CCTATGTCGCTCCGATTCTGAA	19.64	Flower_2	-	-	-
CCCCGACGTTTGAATGTAGT	19.82	Flower_2	-	-	-
GCAACCGTAGATATTACCACC	19.82	Flower_2	-	-	-
CCAGGAAGTAGGATAATTGTC	19.82	Flower_2	-	-	-
TGCCGGCCGGGGACGGACT	19.46	Flower_2	-	-	-

AAACCATCAGAACTCCTACTC	19.64	Flower_2	-	-	-
TGGCATCGGCCCTGCGAGCTCC	19.64	Flower_2	-	-	-
TGCGATTGAAACAAATCTGGCACT	18.92	Flower_2	-	-	-
CGGCTCCGTGATTGTCTTGGCATC	18.92	Flower_2	-	-	-
TTGCCACCGTTGAGTTTGGAAACCC	18.74	Flower_2	-	-	-
CGAGAAGTCCACTGAACCT	19.82	Flower_2	-	-	-
CCGGGCTAGAGCGACGCGTGCGCC	18.74	Flower_2	-	-	-
CTTCTGACTTAGCTGCAGCGAGCT	18.92	Flower_2	-	-	-
TGAGAATCGATCGTCCCGAC	19.28	Flower_2	-	-	-
TCGGAGGACTTATCCGTAGCGGGA	19.1	Flower_2	-	-	-
CACGGAATCGAGAGCTCCAAGT	19.1	Flower_2	-	-	-
AGGATCCAGGTATTTCTTTGAAGC	18.92	Flower_2	-	-	-
CATTTGGTAGTAGCTGAGATT	18.92	Flower_2	-	-	-
CCCCGGGCGTCGAACGGTCGACTC	18.92	Flower_2	-	-	-
CCTGTCGGGACCCGAAAGATGG	19.28	Flower_2	-	-	-
AAGGCTTTCGATTTGCATGGGACT	18.74	Flower_2	-	-	-
GTGACAGAGGATGAAGAAACATAT	18.74	Flower_2	-	-	-
AGCGTCTTGGTGGTGAATCTAGT	18.56	Flower_2	-	-	-
TCCCCGGGCGTCGAACGGTCGACTC	18.38	Flower_2	-	-	-
CGTGGCGGCTGACGGCAACGTTA	18.74	Flower_2	-	-	-
CAGTCCCGAACCCGTGCGGTGTCGG	19.1	Flower_2	-	-	-
TGGCTCTGAGGGCTGGGCACG	19.64	Flower_2	-	-	-
AATCCGGAGGACCGAGTGCCGTC	18.38	Flower_2	-	-	-
TAAATATATTGTCAAAGCTGG	19.28	Flower_2	-	-	-
GTCCCCGACGTTCGAATTGTAGTC	18.38	Flower_2	-	-	-
GATGGTTGCGTCTTTAGAGACTTA	19.1	Flower_2	-	-	-
TATCTGTTGGCCTTCGGGATC	19.64	Flower_2	-	-	-
GGTAGGAGATGCACTGTAGCAATT	18.38	Flower_2	-	-	-
TCAGGCTTTGTATCTCTAGAACC	18.38	Flower_2	-	-	-
GCCGAGAAGATGATAAATAGTAT	18.38	Flower_2	-	-	-
TTCTGTTGGCCTTCGGGATC	19.64	Flower_2	-	-	-

GGGACGGACTGGGAACGGCCCCT	18.56	Flower_2	-	-	-
AGTGCCGTCTGAGCTCT	19.82	Flower_2	-	-	-
CTTGCGTGGAGGGACTGCCCGAGA	18.56	Flower_2	-	-	-
GGCATCGGCCTGCGAGCTCCC	19.1	Flower_2	-	-	-
TTTGACCCAAAGGCTCGTCT	20.18	Flower_2	-	-	-
TTGAATAAGACCTTCTGCCATC	18.92	Flower_2	-	-	-
AGGCGCGGACCGATGCGGATC	19.28	Flower_2	-	-	-
GCGGTCCGGATATCTACTCTCATT	18.2	Flower_2	-	-	-
TTTCTAAATATTCTGAACGTATT	18.2	Flower_2	-	-	-
TCTAACCTTGTTGCAGGACC	19.82	Flower_2	-	-	-
ATTCTGTTGGCCTTCGGGATCGGA	18.56	Flower_2	-	-	-
CGCAAGCGACTGTTATTGGGGAGC	18.02	Flower_2	-	-	-
GCTACGTAGATGCAAACCTTGGAG	18.38	Flower_2	-	-	-
TAATGAAGTCCAAGTTGAGGC	18.38	Flower_2	-	-	-
AGAGGAACCGTTGATTCGCAC	19.1	Flower_2	-	-	-
GGTAGAATCCTTTCAGAC	19.64	Flower_2	-	-	-
AAATCGGGCGTAAATTCGGTC	18.74	Flower_2	-	-	-
TTCTGAACCAAAGATTGTTCTCTT	18.2	Flower_2	-	-	-
TCAAACAAGGAAAGGCT	20.54	Flower_2	-	-	-
CGGGTCCGGCGACGCCACCA	19.64	Flower_2	-	-	-
GGGGACGGACTGGGAACGGCCC	18.2	Flower_2	-	-	-
CCGTCTAGTAGCTGGTTCCTT	19.64	Flower_2	-	-	-
TAGGAGTTCTGATGGTTTTGT	18.38	Flower_2	-	-	-
TGAAGTCCAAGGGTGAGGCT	24.32	Flower_2	-	-	-
TTGCAAGTCCGAGAATATAGT	18.74	Flower_2	-	-	-
TCCCCGACGTTCGAATTGTAGTC	18.2	Flower_2	-	-	-
GAGAAGTCCACTGAACCTT	19.64	Flower_2	-	-	-
CAATTCCTACTGGATGCACCA	18.38	Flower_2	-	-	-
TACTGAGAACTGAATGACATGTT	18.38	Flower_2	-	-	-
ATATCAAGTGCCGTCTGAGCTCT	17.84	Flower_2	-	-	-
TCCCGTGAACCATCGAGTCTT	18.92	Flower_2	-	-	-

TTTTCCGAAGCTATAATTCT	18.74	Flower_2	-	-	-
CGTTTGATTCTGATTTTCAGT	18.92	Flower_2	-	-	-
CGCCACGGAATCGAGAGCTCC	18.74	Flower_2	-	-	-
GGGCTGAGTTGCTGTAGTAACAG	17.84	Flower_2	-	-	-
TCGCCGCGATCGTGGATGGCAGC	17.84	Flower_2	-	-	-
CGGGCGTGGACGGCACTCGGT	18.38	Flower_2	-	-	-
CGATGATTGTAGCTGGTTGTG	18.56	Flower_2	-	-	-
ACCGGGACGTGGCGGCTGACGGCA	17.84	Flower_2	-	-	-
ATTCTAACCTTGTGTCAGGACC	18.56	Flower_2	-	-	-
CGGATGGGGGCTGGCGATGCGCC	17.84	Flower_2	-	-	-
GAAGTCCACTGAACCTTATCAIT	18.38	Flower_2	-	-	-
ACCGGGACGTGGCGGCTGACGGC	17.84	Flower_2	-	-	-
TGACCTCTTGAACGTTGAGCCT	18.56	Flower_2	-	-	-
GGGATTTAACCTGGATGTTAT	18.56	Flower_2	-	-	-
CCAGTAAAGCTACTAGCTCAGAAC	17.84	Flower_2	-	-	-
TTGCAGGAACACATTAGAGACATG	17.66	Flower_2	-	-	-
AACCGGGACGTGGCGGCTGACGGC	17.84	Flower_2	-	-	-
GATTTGGGCCTGAGTTGCTGAGT	17.84	Flower_2	-	-	-
CTTGGCTTTTGGTTGGTAGCATC	17.84	Flower_2	-	-	-
ATCTTTCTAACGGCACTGCATC	18.2	Flower_2	-	-	-
ATAACCGTAGATATTAACCTC	18.38	Flower_2	-	-	-
GTCCGAACCCGTCGGCT	19.46	Flower_2	-	-	-
GATGACAGCGTCGTAATAGT	18.56	Flower_2	-	-	-
GGGCAGCCTGCCTGGGCGTCACGC	17.48	Flower_2	-	-	-
TGCTCAACGGGTACAATGATGAAT	17.3	Flower_2	-	-	-
GCAACCGAGGCCTGTAATAACTAC	17.66	Flower_2	-	-	-
ATGGTCCCTGCGGATGCTCAC	17.66	Flower_2	-	-	-
TTTGTTTGATGGTAACTACT	18.2	Flower_2	-	-	-
TGCTCTTTCAGATCACTCTC	18.38	Flower_2	-	-	-
TGGGTTTCGTTTATGTGTTGCA	18.2	Flower_2	-	-	-
CCGAACCCGTCGGCTGTCGGCG	19.1	Flower_2	-	-	-

TTTGGACCCAAGGCTCGTCTCGGCG	17.66	Flower_2	-	-	-
CTTTAGAGACTTATGGGACTGAGA	17.3	Flower_2	-	-	-
TTTGGACCCAAGGCTCGTCTC	19.1	Flower_2	-	-	-
TGTTAAGAACCGGTCGTTTGT	18.56	Flower_2	-	-	-
TGGCATCGGCCTGCGAGC	18.38	Flower_2	-	-	-
CCCACCCTGGAAACGGCTCAGC	17.48	Flower_2	-	-	-
TCTGTACGAGACCAGACATTGGCC	17.84	Flower_2	-	-	-
CTTCCCCGGGCGTCGAACGGTCG	17.48	Flower_2	-	-	-
CTGATGACAGCGTCGTAATAGT	17.84	Flower_2	-	-	-
AGTTACTAATTCATGATCTGGCATG	17.12	Flower_2	-	-	-
CTAATCGTAGTTTATGTGTTGGCT	17.12	Flower_2	-	-	-
GGCAGTTCGACCGGAAATTTTGG	17.3	Flower_2	-	-	-
ATCCGGAGGACCGAGTGCCGTC	18.2	Flower_2	-	-	-
ATTCCGTACCATAATAATTGA	18.02	Flower_2	-	-	-
CCCTGGGATTGGCTTTGGGCTT	17.48	Flower_2	-	-	-
AAAACGACTCTCGGCAACGGATAT	17.3	Flower_2	-	-	-
CCAAGGGCAAGAGCATTGAGGGCT	17.12	Flower_2	-	-	-
ATCGGAGTAATGATTAAC	18.74	Flower_2	-	-	-
CGCGTCGTTGCTCGGCTTGCACC	17.48	Flower_2	-	-	-
CCCGATCGTATCCAATTTTCGAAT	16.94	Flower_2	-	-	-
GAAGTCCACTGAACCTTATCAT	18.2	Flower_2	-	-	-
TGGTGACGTTTGATGTGATTA	17.66	Flower_2	-	-	-
CCCGACGGCGGTCACGTAGCAGC	17.66	Flower_2	-	-	-
TCCCTGGGATTGGCTTTGGGCT	17.48	Flower_2	-	-	-
GCTGGATTATGACTGAACGCCT	17.3	Flower_2	-	-	-
TCTGGAGTCTTGTCTTTGGGC	19.1	Flower_2	-	-	-
CGGCCGAGTCTGATTCTGATAAT	16.94	Flower_2	-	-	-
CCGTCCGTGCAGATCTGGTG	17.84	Flower_2	-	-	-
GTGAGAGCATGCCTGTCGGGACCC	16.94	Flower_2	-	-	-
CCCCGACGTTCGAATTGTAGTCT	17.66	Flower_2	-	-	-
TGGTGGTTGAGAGTGACATGAAGG	17.3	Flower_2	-	-	-

TCGGCCTGCGAGCTCCCCATTCCG	17.48	Flower_2	-	-	-
AGACCTTCGGAATTTGAAGCT	17.84	Flower_2	-	-	-
CTTGGGAGGCTCTGGATAACATGTC	16.94	Flower_2	-	-	-
TAAACTCGTCCAGGATCGCACCCC	17.48	Flower_2	-	-	-
TGATGTGGCTCTGTGGCTAAGGCT	17.48	Flower_2	-	-	-
TCAGTGTAAATTTTCGATCTAAC	17.3	Flower_2	-	-	-
CGGCCTGCGAGCTCCCCATTCCGC	16.94	Flower_2	-	-	-
TCCTATTCTGTTGGCCTTCGGGA	16.94	Flower_2	-	-	-
CACCATATAGTGCACCGCACA	18.38	Flower_2	-	-	-
TTCATCGTGGTGAAAGACTCCATA	16.76	Flower_2	-	-	-
TATAGTTTGTGGTGAAC	16.94	Flower_2	-	-	-
ATCCAGATTTTCAGATTTAGTTAC	16.76	Flower_2	-	-	-
GCCCCATCGTCTAGTGGTTCAGG	17.66	Flower_2	-	-	-
TCTCCCTACTCCACCCATGC	18.2	Flower_2	-	-	-
AGTGATAGGGTTCGAGTCTCACC	17.12	Flower_2	-	-	-
CGAGAAGTCCACTGAACCTT	17.48	Flower_2	-	-	-
GATAGCACCCATGAGGGATTGAAC	16.76	Flower_2	-	-	-
CTGGCATCGGCCTGCGAGCTCC	16.76	Flower_2	-	-	-
TTAAAGATGAAAGTGTGGCTC	16.94	Flower_2	-	-	-
TGCCGGCCGGGGACGGACTGGGA	16.58	Flower_2	-	-	-
GCACCTTATGGACATAAATTGACC	16.76	Flower_2	-	-	-
TGGACCAAGGCTCGTCTCGGCG	17.3	Flower_2	-	-	-
TGTGTTCTCAGGTCGCCCC	17.48	Flower_2	-	-	-
TAAGAAGAATGCTTGGCTGATA	17.3	Flower_2	-	-	-
GTCCGAACCCGTCGGCTGTC	16.76	Flower_2	-	-	-
GCTCGAGGCGGGACCGATGCG	18.38	Flower_2	-	-	-
GCAACCGAGGCTGTAAATAGCTAC	16.76	Flower_2	-	-	-
GGCTTTACCCGATAGAACTCGCC	16.94	Flower_2	-	-	-
TCCAGACTACAATTCGAACGTC	16.94	Flower_2	-	-	-
ATCAACTGGGTACTTGGTAGAGGA	16.58	Flower_2	-	-	-
AACTTTACGTCGAGTTTACAGCCT	16.4	Flower_2	-	-	-

CTCGTTTGATTCTGATTTTCAGT	16.58	Flower_2	-	-	-
AGTGCCGGCGCTGGGGTAGGGCCC	16.58	Flower_2	-	-	-
GCAATGACTATTTCATGATTCC	16.76	Flower_2	-	-	-
ACTGCTCGGGCCTGGCGCACCCAC	16.4	Flower_2	-	-	-
CTTCCCTACTCCACCCATGCCA	16.94	Flower_2	-	-	-
TATCTTTCTTCTTAAATGTAGACT	16.76	Flower_2	-	-	-
ACCGGATGAGTCAGATATCTACTC	16.4	Flower_2	-	-	-
ATGTCGCTCCGATTCGTG	17.84	Flower_2	-	-	-
GATAGCGCGGACCGCGGAGCT	16.94	Flower_2	-	-	-
GGGGGACGGACTGGGAACGGCCCC	16.22	Flower_2	-	-	-
TGAGTCTACAGTACCTGTACAGT	16.58	Flower_2	-	-	-
TGGCTCTGAGGGCTGGGCAC	17.48	Flower_2	-	-	-
CATGCCTGTCGGGACCCGAA	17.48	Flower_2	-	-	-
TGCGTGTCTGACAATTATCC	17.3	Flower_2	-	-	-
CCGGACACCGCGGACGTGCG	16.76	Flower_2	-	-	-
GATGGGGCTGGCGATGCGCC	17.66	Flower_2	-	-	-
TTTAGCCTTGACGGAATTTAC	16.76	Flower_2	-	-	-
GCAATATGGGACGGAGCAATGCTC	16.4	Flower_2	-	-	-
GTCCCAGTCCGAACCCGTCGGCT	16.22	Flower_2	-	-	-
ACTAATCGAACCGTCTAGTAGCT	16.58	Flower_2	-	-	-
CGTGCTTGGGCGAGAGCAGTACT	16.58	Flower_2	-	-	-
TGCAACCGAGTTACCTGGGAT	16.58	Flower_2	-	-	-
GGAGCGACCCGAGATCACAT	17.66	Flower_2	-	-	-
GCGCCACGGAATCGAGAGCTC	16.76	Flower_2	-	-	-
TTTCCAGAAGGTCTGAGCCTTAGC	16.22	Flower_2	-	-	-
ATTTGAAACGGGACCCTGAGGGCT	16.4	Flower_2	-	-	-
GCGAGAAGTCCACTGAACC	17.48	Flower_2	-	-	-
AGGACCACGCGAGCCATTTAATGA	16.22	Flower_2	-	-	-
TTCTAACCTTGTGTCAGGACC	16.76	Flower_2	-	-	-
AGTTACTAATTCATGATCTTGC	17.66	Flower_2	-	-	-
CGGCAACGGATATCTCGGCTCTCGC	16.22	Flower_2	-	-	-

CCTGGCATCGGCCTGCGAGCTCCC	16.4	Flower_2	-	-	-
CAGAATTCCTTTACTATTGCTAGT	16.04	Flower_2	-	-	-
CCTGGAGAAAGATCCGTGCTT	16.58	Flower_2	-	-	-
ACCGGACGGACCAGATGTCTACTC	16.22	Flower_2	-	-	-
CCTGGCATCGGCCTGCGAGCTC	16.4	Flower_2	-	-	-
CCGGGCGTCGAACGGTCGACTC	16.22	Flower_2	-	-	-
AGCAGGTCCGGAGACATAGGCACA	16.04	Flower_2	-	-	-
AATCCTGAGTGTCTTGTGGACTCC	16.04	Flower_2	-	-	-
CCAAGTCCCTTGAAGTGTGCACC	16.04	Flower_2	-	-	-
TCCAGCGCCCGAAGAGCACC	16.76	Flower_2	-	-	-
ACAACCAGCTACAATCATCGC	16.58	Flower_2	-	-	-
TTGTTTGATGGTAACTACTACT	16.94	Flower_2	-	-	-
GTTGAGAACATTCGGGAAGCTGGA	15.68	Flower_2	-	-	-
GCAATGACTATTTCATGATTC	17.12	Flower_2	-	-	-
GTTGTATTACTTATTATTACTA	16.4	Flower_2	-	-	-
CTAATCGAACCGTCTAGTAGCTGGT	16.04	Flower_2	-	-	-
GCGCGGACCGATGCGGATC	16.58	Flower_2	-	-	-
GTTCCTGGGATTGGCTTTGGGCT	16.04	Flower_2	-	-	-
TATTCAACGAGTCTATAGCCT	16.4	Flower_2	-	-	-
ACTGGCTCTGATACCATGTTAGA	16.4	Flower_2	-	-	-
CAACAGTCGTCATCTGATAGT	16.76	Flower_2	-	-	-
CTGTTGGCCTTCGGGATCGGAGT	15.86	Flower_2	-	-	-
AGCTCAGCTGGTAGATGGACGAGC	15.68	Flower_2	-	-	-
TGCTCTTTCAGATCACTCTCC	16.76	Flower_2	-	-	-
AGAAATGAAATGGATCGTCCCAC	16.04	Flower_2	-	-	-
GACCGGATGCAGAGAAACATTC	16.4	Flower_2	-	-	-
GACCGGTAGACTTGAAC	16.76	Flower_2	-	-	-
CCCAGTCCCGAACCCGTCGGCTGTC	16.04	Flower_2	-	-	-
TTTGAATCCATGAGTTTAGGGACT	15.68	Flower_2	-	-	-
GTTCGGATCGCGGCGACGCGGGC	15.86	Flower_2	-	-	-
GGCGCGGACCGATGCGGATC	16.94	Flower_2	-	-	-

TGGCTCTGAGGGCTGGGCACGGGGG	16.04	Flower_2	-	-	-
ATACCCGGCCGTCGGGGCAAGCGCC	15.5	Flower_2	-	-	-
ACCGTATCATTAACTATTTCTT	17.48	Flower_2	-	-	-
ATTTCACTCGATCACTGTAGCATT	15.5	Flower_2	-	-	-
TGCTGAAGGATTAAGGGGCACC	15.5	Flower_2	-	-	-
CCGGGCTAGAGCGACGCGTGC GCC	15.5	Flower_2	-	-	-
ACTCGAACTCGGCCCTGAATGGC	16.04	Flower_2	-	-	-
ATTCTCATATGTAGAGAGAGGACT	15.5	Flower_2	-	-	-
TCCCGAACCCTCGGCTGTC	16.94	Flower_2	-	-	-
CAGGCACAGAAGACTCCTTTTGA	15.86	Flower_2	-	-	-
CCTGCTAACTAGCTATGCGGAGGGT	16.76	Flower_2	-	-	-
TGAGAGCAGATTGGCTGGATC	16.76	Flower_2	-	-	-
TATCTTTTCTGTTTAACGGCCT	16.94	Flower_2	-	-	-
GGCCGTCGGTGCAGATCTTGGTG	15.68	Flower_2	-	-	-
GTTGTATTACTTATTATTACTATT	16.04	Flower_2	-	-	-
ACCCGAAACCGAACTGAAGGCATC	15.32	Flower_2	-	-	-
CGGCGGACTGCTCGAGCTG	16.04	Flower_2	-	-	-
ATTTTACAAGTTTACCTGGAGCCT	15.32	Flower_2	-	-	-
GCCTATCGATCCTTAGACCT	16.4	Flower_2	-	-	-
TGGACCCAAGGCTCGTCTCGGC	16.58	Flower_2	-	-	-
TTTATGGCTGAGTCTTACTG	16.22	Flower_2	-	-	-
AAACGACTCTCGGCAAC	16.22	Flower_2	-	-	-
TCGGGATCGGAGTAATGATTAAC	15.5	Flower_2	-	-	-
GCTGGATTATGACTGAACGCC	16.22	Flower_2	-	-	-
GATATCAAGTGCCGCTGAGCTCT	15.32	Flower_2	-	-	-
TTTTCCGAAGGATTATGAATT	15.86	Flower_2	-	-	-
CCCTTGGACATGTCATCGACGACA	15.32	Flower_2	-	-	-
ACAAGGGGAATCCGACTGTTT	15.68	Flower_2	-	-	-
GCTCTGAGGGCTGGGCACGGGGG	15.86	Flower_2	-	-	-
TCCGGGCTAGAGCGACGCGTGC GC	15.32	Flower_2	-	-	-
CGTTCCTGCATGGGGCACCA	16.4	Flower_2	-	-	-

TCCGTTGTTTGAACCTGTTGGACC	15.14	Flower_2	-	-	-
CCGGATCGACGACACTGTAGCATC	15.32	Flower_2	-	-	-
CCTTCCCGGGCGTCGAACGGTCGA	15.32	Flower_2	-	-	-
ACCGATGCGGATCGCGGCGGGCC	15.32	Flower_2	-	-	-
CACGGTTTTGTGTCTCTCATG	15.86	Flower_2	-	-	-
ACCACACGAGTTACCTGGGCT	15.68	Flower_2	-	-	-
TCGGACCGACGACACTGTAGCACT	15.5	Flower_2	-	-	-
TTGAGAATCGATCGTCCCGCA	15.86	Flower_2	-	-	-
TGGCATCGGCCTGCGAGCTCCCC	16.22	Flower_2	-	-	-
CATCGGGGCTGGCGTTGCC	16.22	Flower_2	-	-	-
AACTCTACCCAACTATTTCTT	15.86	Flower_2	-	-	-
ACCTTGTGTCAGGACCTACGGGCC	15.32	Flower_2	-	-	-
TTCCCTGGGATTGGCTTTGGGCT	15.32	Flower_2	-	-	-
CCGCGATCGTGGATGGCAGC	16.04	Flower_2	-	-	-
TGGCATCGGCCTGCGAGCT	16.76	Flower_2	-	-	-
GGGCGACTCAACTCAAACTCAGT	16.04	Flower_2	-	-	-
AGAAGTCCACTGAACCTTATC	15.14	Flower_2	-	-	-
TGCTTGGGCGAGAGCAGTACT	15.68	Flower_2	-	-	-
GCTCTGAGGGCTGGGCACGGGG	16.04	Flower_2	-	-	-
AGTCCCGAACCCGTCGGGTGTCG	15.32	Flower_2	-	-	-
TATCAAGTGCCGTCTGAGCTCT	15.86	Flower_2	-	-	-
TGAATAAGATTGTTTGCATT	16.04	Flower_2	-	-	-
GGTCCCAGTCCCGAACCCGTCGGC	14.96	Flower_2	-	-	-
TCGAACGGTCGACTCAGAACT	15.5	Flower_2	-	-	-
AGAGTCCAGGTATTTCTTGAAGC	15.14	Flower_2	-	-	-
GTGCTCCCCCTCGTTGCATA	15.86	Flower_2	-	-	-
TAGGCACCTCCATTCTTIGACCAA	14.96	Flower_2	-	-	-
GCGAGTCGACGGGCCAGTAAACCCG	15.68	Flower_2	-	-	-
ATTCGGTCCCTATTCTGTTGGCCT	15.14	Flower_2	-	-	-
CTGAGATTCCAGCTTGCCAAC	16.04	Flower_2	-	-	-
CCGGGCTAGAGCGACGCGTGCGC	15.14	Flower_2	-	-	-

TTGTCGGACGAGAGATGGCACT	15.14	Flower_2	-	-	-
TAAGAAGAATGCTTGGCTGAT	14.96	Flower_2	-	-	-
AACCGGTAACAGTCATGTAGGACC	14.96	Flower_2	-	-	-
GCGGATATAGTCGAATGGTA	15.68	Flower_2	-	-	-
CGATTATGAAGCCTTTGATGCC	15.14	Flower_2	-	-	-
TGATCGGAGAAGACGATGAACAGT	15.14	Flower_2	-	-	-
AATAGCTCGACGCCAGGATAC	15.86	Flower_2	-	-	-
CGATAGCGCGGACCGCGGAGCT	14.96	Flower_2	-	-	-
CCCGCCTTGCATCAACTGAATT	16.22	Flower_2	-	-	-
GCCGTCTTAGCTCAGTGGTAGA	16.22	Flower_2	-	-	-
CCTGATCCAGGTCTGCCAGAGGAC	15.14	Flower_2	-	-	-
CGAACCGTCTAGTAGCTGGT	15.5	Flower_2	-	-	-
TGGTAACTTGTATGCTCGAA	15.14	Flower_2	-	-	-
TTGTTAATGGGAATATGCAACT	15.5	Flower_2	-	-	-
GCTGAATCTTTCTGTAGTTGCCT	14.78	Flower_2	-	-	-
GACAGAGGATGAAGAAACATATGT	14.78	Flower_2	-	-	-
GTCCCAGTCCCGAACCCGTCGGCTG	14.96	Flower_2	-	-	-
CCACGATCCACTGAGATTACGC	15.14	Flower_2	-	-	-
TTTTATTGGATGGACGTACGGATG	15.32	Flower_2	-	-	-
CGGATGGGGGCTGGCGATGCGCCT	14.59	Flower_2	-	-	-
TGAGCTGTTCCAACCCGAGTA	15.32	Flower_2	-	-	-
GCCCCATCGTCTAGTGGTTCAG	14.59	Flower_2	-	-	-
AACCTACCCGAATAGCACTGTAGC	14.96	Flower_2	-	-	-
TATGGCGATTTGGTAGTAGCT	15.68	Flower_2	-	-	-
CAGTACTAGGATGGGTGACCT	14.78	Flower_2	-	-	-
TCCCTAATTTGATCATTTGGACT	14.59	Flower_2	-	-	-
ACTGAGAACTGAATGACATGTTT	14.78	Flower_2	-	-	-
TGGTTGAGAGTGACATGAAGGATA	14.78	Flower_2	-	-	-
ATCCGGGCTAGAGCGACGCGTGC	15.14	Flower_2	-	-	-
TGATATCAAGTGCCGCTGAGCTCT	14.78	Flower_2	-	-	-
GAATACAATGTATCGTCAATCAT	14.96	Flower_2	-	-	-

TGCCAGATTCCTAAACTTAGAATT	15.14	Flower_2	-	-	-
TGCCGTAACATGTAACTCTT	14.96	Flower_2	-	-	-
GATCATTACTGAACATGCCGGGAA	14.78	Flower_2	-	-	-
TCGTGCACCTGCGCGCTCCTGGCA	14.59	Flower_2	-	-	-
CCCCTTCTTGGTTCTAGTGGCTCC	14.78	Flower_2	-	-	-
GGCAACCTTCTTTGATTTTGGACT	14.59	Flower_2	-	-	-
CTCGAGGCGCGGACCGATGC	14.96	Flower_2	-	-	-
TGCGAGTCGACGGGCCAGTAAACCC	14.78	Flower_2	-	-	-
TCATCGAGTCTGGTAATTGGA	14.96	Flower_2	-	-	-
TCTCTAATTCGCTTGGTGCAG	15.14	Flower_2	-	-	-
CACGTGCCGTTGGTGAAGCTCG	15.14	Flower_2	-	-	-
TTTTATGCGATGATGTAGCT	15.14	Flower_2	-	-	-
CACGGATCTTCTCCAGGCAA	14.59	Flower_2	-	-	-
CGAGGCGCGGACCGATGCGGAT	15.14	Flower_2	-	-	-
CTACGTAGATGCAAACCTTGGAGG	14.78	Flower_2	-	-	-
ATAGTTTGTTTGATGGTAACTACT	14.59	Flower_2	-	-	-
CGCACTGTAGCAATGGTGCCACT	15.14	Flower_2	-	-	-
CAAGGAAAACCCGTCTTTGGACC	14.78	Flower_2	-	-	-
CTTCTGCCGCGGATGCGCTCC	15.32	Flower_2	-	-	-
GCGCCCGGACCCTGTCGACCACGA	14.41	Flower_2	-	-	-
GCTCTGAGGGCTGGGCACGG	15.86	Flower_2	-	-	-
CGCGCCACGGAATCGAGAGCTC	14.96	Flower_2	-	-	-
GTCCCAGTCCCGAACCCGTCGGC	15.14	Flower_2	-	-	-
TCCTCAGCGGCGGACCGGGCC	14.78	Flower_2	-	-	-
TGGAGAAAAGATCCGTGCTTGT	14.78	Flower_2	-	-	-
CAAAGGAGTTTGACATGAAGGACT	14.41	Flower_2	-	-	-
CTATCGATCCITTAGACCT	14.96	Flower_2	-	-	-
ACCGGATGGACCAGATATCTACTC	14.78	Flower_2	-	-	-
TGGCAGGCTGTATTCCATGATCTA	14.41	Flower_2	-	-	-
TCCGTGAATCGGAAGCGGGGC	14.59	Flower_2	-	-	-
ATTTTGATGGAAATTGTATGTAGT	14.23	Flower_2	-	-	-

TCTTTTGGACCCAAGGCTCGTCT	14.41	Flower_2	-	-	-
CCTTTTTTGGACCCAAGGCTC	15.14	Flower_2	-	-	-
GGGTCCAGGTATTTCTTTGAAGCT	14.59	Flower_2	-	-	-
CGTATTTAGCCTTGACGGAAT	14.78	Flower_2	-	-	-
CGTTTCCCGCAACGGAACCA	14.59	Flower_2	-	-	-
TCATGCGATCCCTTAGGAATT	14.59	Flower_2	-	-	-
CCGGGGGACGGACTGGGAACGGCCC	14.41	Flower_2	-	-	-
ATGTCGCTCCGATTCGTC	16.4	Flower_2	-	-	-
TGGAAAATTAGATTTATGGCC	15.14	Flower_2	-	-	-
TATGTGATAACACTTGGCTCC	14.96	Flower_2	-	-	-
TGACTGACTTGAGCATCGGAGGGT	14.59	Flower_2	-	-	-
TGCTAACTAGCTATGCGGAGGGT	14.59	Flower_2	-	-	-
TTCAACGGATCCCATTGTTAAT	15.14	Flower_2	-	-	-
TTGCCTGATTTCCTTTCTCGTGAA	14.41	Flower_2	-	-	-
CCTATACCCGGCCGTCGGGGC	15.5	Flower_2	-	-	-
GTGAGAGCATGCCTGTCGGGACC	14.41	Flower_2	-	-	-
GATTCGGTCCTATTCTGTTGGCC	14.41	Flower_2	-	-	-
TGAGGGTTTGTGATTATTGTATT	14.23	Flower_2	-	-	-
GACCCTGCAGAAATTCACGAGAAA	14.41	Flower_2	-	-	-
CTAGCCCGGATTCTGACTTAG	14.41	Flower_2	-	-	-
TCGCACCACGAGGCGCTGTCTGC	14.05	Flower_2	-	-	-
TGGGACTAGATATCCGAGTCGTGC	14.05	Flower_2	-	-	-
AACCGGGACGTGGCGGCTGACGGCA	14.96	Flower_2	-	-	-
CGTGCCCGCCGGGGACGGACT	14.59	Flower_2	-	-	-
GTGGGTGGGTAGGGAAGATA	14.23	Flower_2	-	-	-
TTGAGAATCGATCGTCCCGAC	14.41	Flower_2	-	-	-
GCCCGTCGCTCTGACGATTCATGA	14.05	Flower_2	-	-	-
TTGTTTGATGGTAACTACT	14.96	Flower_2	-	-	-
AGAGCATGCCTGTCGGGACCCGA	14.23	Flower_2	-	-	-
TCGAGAACGCATCGACAGGAAAGA	13.87	Flower_2	-	-	-
ACCAGGCTCTGATACCA	15.32	Flower_2	-	-	-

CACGATCCACTGAGATTCAGC	14.23	Flower_2	-	-	-
ATCGGTTAAAATTCAGTACCTGC	14.05	Flower_2	-	-	-
GCCACGATCCACTGAGATTCAG	14.59	Flower_2	-	-	-
CGCTCTAGCCCGGATTCTGAC	14.59	Flower_2	-	-	-
TTGTCGTTCTTGAGTGTTAGTACT	14.59	Flower_2	-	-	-
CGGACCGATGCGGATCGCGGC	14.59	Flower_2	-	-	-
CTGGCATCGGCCTGCGAGCTCCC	14.05	Flower_2	-	-	-
TAATTTCTACTCTACCTTCCCGG	14.05	Flower_2	-	-	-
CCCGACGTTCAATTGTAGT	14.59	Flower_2	-	-	-
ATGGTCCCTGCGGATGCTCACGC	14.23	Flower_2	-	-	-
ACAGTGACTGAATACTGAGAACT	14.05	Flower_2	-	-	-
GGGACGGACTGGGAACGGCCC	14.78	Flower_2	-	-	-
TGAGATGAAGCACTGTAGCACT	16.58	Flower_2	-	-	-
ATTCCAAGTTTACTGTAAGGATT	14.05	Flower_2	-	-	-
GGGGACGGACTGGGAACGGCC	14.41	Flower_2	-	-	-
CAGTCCCGAACCCGTCGGCTGT	15.68	Flower_2	-	-	-
CCTGGTTICTCAATTGTTCTGAT	14.05	Flower_2	-	-	-
ACCTCAGCTGGTAGATGGACGAGC	13.87	Flower_2	-	-	-
TGACCTCGGGAGAATACACTTAAT	14.41	Flower_2	-	-	-
CTTGAGAATCGATCGTCCCGAC	15.14	Flower_2	-	-	-
TCGTTTCCCGCAACGGAACCA	14.05	Flower_2	-	-	-
GGTAGAATCCTTTGCAGACGA	14.05	Flower_2	-	-	-
TCATGGTTTTGCGATTCAGG	14.41	Flower_2	-	-	-
CTCCACTGGTGCGTGTCTGA	14.78	Flower_2	-	-	-
TTGTGATTTAAAATTTTATGC	15.5	Flower_2	-	-	-
CGACTCCCGGTAGGACCTCCA	14.96	Flower_2	-	-	-
AAAACAAGTCGGGAAAATCTCT	13.87	Flower_2	-	-	-
CAGGAGTGATCTGTCCATTGGATA	13.87	Flower_2	-	-	-
GAACCCGTCGGCTGTCCGC	14.59	Flower_2	-	-	-
ATCTGGTAGGGACAATGTGACAT	14.05	Flower_2	-	-	-
GTGCAGATCTGGTGGTAGTAGC	14.05	Flower_2	-	-	-

CTGAGGGCTGGGCACGGGGT	14.23	Flower_2	-	-	-
CTGCTCGGGCCTGGCGCACCCAC	14.23	Flower_2	-	-	-
CGGTCCCGTAAAACCCGGGG	14.05	Flower_2	-	-	-
CGAACCCGTCGGCTGTCGGC	15.86	Flower_2	-	-	-
CTCCCCGGGCGTCGAACGGTCGAC	13.87	Flower_2	-	-	-
GCATCTGAGGAACCAGGCAGG	14.96	Flower_2	-	-	-
CTTATGGATGGCAGAAGGTCT	14.23	Flower_2	-	-	-
TTTCGGTCTATTCTGTGGCCT	14.23	Flower_2	-	-	-
CGAGAAGTCCACTGAACCTTAT	13.87	Flower_2	-	-	-
CGCGCCACGGAATCGAGAGCTCC	14.05	Flower_2	-	-	-
GAGATTCAGCTTTGACAAT	14.96	Flower_2	-	-	-
GAAACGGGACCCTGAGGGCT	15.5	Flower_2	-	-	-
AAGAGATTTGAGGTTAATTTGATT	13.69	Flower_2	-	-	-
GATTGAAACGGGACCCTGAGGGCT	13.51	Flower_2	-	-	-
CTGGCATCGGCCTGCGAGCTCCCC	13.51	Flower_2	-	-	-
GAGAGCATGCCTGTCTGGGACC	14.05	Flower_2	-	-	-
TTATCTTTTCTGTTAACGGCCT	13.69	Flower_2	-	-	-
AGAAGTCCACTGAACCTTAT	15.14	Flower_2	-	-	-
GCTCGTTGATTCTGATTTTCAGT	13.51	Flower_2	-	-	-
CCAGGTGTCAACTGTCTATGGAGT	13.51	Flower_2	-	-	-
CTTGGCCTGCAATTGTGACTTATT	13.69	Flower_2	-	-	-
TTCTGCCGGGATGCGCTCCT	13.69	Flower_2	-	-	-
CGGGCTAGAGCGACGCGTGCGC	13.87	Flower_2	-	-	-
CACCACGAGGCGCTGTCTGCGA	13.51	Flower_2	-	-	-
GAACGAAGGAGATATAGTCCTCTT	13.51	Flower_2	-	-	-
CGGACCCTGTGACACCACGAG	14.78	Flower_2	-	-	-
CGCGAGAAGTCCACTGAACC	14.78	Flower_2	-	-	-
CCTCTAAGTCAGAATCCGGGCT	14.23	Flower_2	-	-	-
AGTCCCGAACCCGTCGGC	14.05	Flower_2	-	-	-
CACTGTTCCCTGGGATTGGCT	14.05	Flower_2	-	-	-
TTTGTTTGATGGTAACTACTACT	13.87	Flower_2	-	-	-

TGTGGGAGGATTGGACAGAACT	15.14	Flower_2	-	-	-
TTAAGAGGATTAAATGTAATTGT	13.51	Flower_2	-	-	-
TTAACGGCCTGCCACCC	20.9	Flower_2	-	-	-
TTTCGATCTGTAATCCTAAGGCC	13.69	Flower_2	-	-	-
CTTTAGACCTTCGGAATTGAAGC	13.51	Flower_2	-	-	-
TATAGAACCGTTGCTGGACCT	14.23	Flower_2	-	-	-
TCTTCGTGACCATGTTTGAAATA	13.51	Flower_2	-	-	-
ATCGGCCTGCGAGCTCCCCATTCCG	13.87	Flower_2	-	-	-
TTTGTTCCTGTTTCTGAA	13.69	Flower_2	-	-	-
TCTGGTCTGTTTAGGAATAGCCT	13.51	Flower_2	-	-	-
CGCCCGTCGCTCTGACGATTCATG	13.33	Flower_2	-	-	-
TTTGGACCCAAGGCTCGTCTC	14.41	Flower_2	-	-	-
CGCTCTAGCCCGGATTCTGACT	13.87	Flower_2	-	-	-
ATGTCCTTGGTGTGACACTGTAGC	13.51	Flower_2	-	-	-
CAACATATCTGTTGGATTCTTGCT	13.51	Flower_2	-	-	-
CTCGTGACCTGCGCGCTCCTGGCA	13.33	Flower_2	-	-	-
TGCCACCGTTGAGTTGGAACC	13.69	Flower_2	-	-	-
AGGAACCGTTGATTCCGAC	14.23	Flower_2	-	-	-
CCCGTTCCTGTCCAACATC	13.69	Flower_2	-	-	-
TCACTGTCCCTGGGATTGGCT	14.23	Flower_2	-	-	-
CACTGTCTTTGTCAACATATCTGT	13.33	Flower_2	-	-	-
TAATCGAACCGTCTAGTAGCTGGTT	13.51	Flower_2	-	-	-
TTTGGACCCAAGGCTCGTCTCGGC	13.69	Flower_2	-	-	-
GCGACCCAGGTCAGGCGGGA	14.05	Flower_2	-	-	-
TACTTGGATGGAAGGATATGGGCC	13.15	Flower_2	-	-	-
CTGGCATCGGCCTGCGAGCTC	13.33	Flower_2	-	-	-
AGCCTTGTGCTTGTGGAAGCATG	13.51	Flower_2	-	-	-
CCGATCGGCTCGAGGCGGGACC	13.69	Flower_2	-	-	-
TTAGATTCTAAGACTGTAGCGCT	13.15	Flower_2	-	-	-
TTGGCCCTGAGTTGCTGTAGTAAC	13.33	Flower_2	-	-	-
TCCTATTCTGTTGGCCTTCGGAT	13.15	Flower_2	-	-	-

CGGCTTGAGACTGATGTGGCGACT	13.33	Flower_2	-	-	-
TTCGGGTCCGGGCGACGCCACCA	13.51	Flower_2	-	-	-
CGCCCGTCGCTCTGACGATTCATGA	13.15	Flower_2	-	-	-
TAAAGGACTGCAGGTAC	14.78	Flower_2	-	-	-
TTCGTCTCCCGGTAGGACCTCCA	14.05	Flower_2	-	-	-
TGGTTCACGGGATTCTGCAAT	13.33	Flower_2	-	-	-
TGGACCTTGGGTTGGGTGGCC	13.87	Flower_2	-	-	-
GACTCTCGGCAACGGATATCTCGG	13.51	Flower_2	-	-	-
CGGCCGTCGGTGCAGATCT	13.87	Flower_2	-	-	-
CAAGTGGCAAGCCTCTGCACT	13.33	Flower_2	-	-	-
CGAAGTTAAGCGTGTGGGC	13.33	Flower_2	-	-	-
CTTGACATGGGTTAGTCGATC	13.69	Flower_2	-	-	-
GTATGAACTAATTCGGACT	14.23	Flower_2	-	-	-
CTCCCTTCATGGCTGGAGCACC	13.87	Flower_2	-	-	-
CGGACTGGGAACGGCCCTCCGGGG	12.97	Flower_2	-	-	-
TGAAACGGGACCCTGAGGGCT	13.51	Flower_2	-	-	-
TTGGGCTTTTCCTGCGCAGCTTAGG	13.69	Flower_2	-	-	-
TCTTGGTACCCCTTCTAGAACT	12.97	Flower_2	-	-	-
TTGGGTATAGGGCGAAAGACT	13.33	Flower_2	-	-	-
TTGCATATCTCTGGAGCTTC	14.05	Flower_2	-	-	-
TTGGACCTGATTGACAAAGTTACT	13.51	Flower_2	-	-	-
CCTGGCATCGGCCTGCGAGCTCCCC	12.97	Flower_2	-	-	-
TTGGTAAATTGTTATGCTCGA	13.69	Flower_2	-	-	-
TAACGGCACTGCATCAACTGG	13.69	Flower_2	-	-	-
GCGTCTGTAGTCCAACGGTTAGGA	13.15	Flower_2	-	-	-
AGGTCCATTTTGATTCTGAATCGA	13.15	Flower_2	-	-	-
GGCGGACTGCTCGAGCTGTCC	13.69	Flower_2	-	-	-
AGTGCGGCAGTTTTCCTTTGAAAC	13.15	Flower_2	-	-	-
TCCGATAGCGGGACCGCGGAGCT	13.15	Flower_2	-	-	-
ATGAGAGACACAAAACCGTGTCT	13.15	Flower_2	-	-	-
GGACGGACTGGGAACGGCCCT	13.87	Flower_2	-	-	-

CACGCCTGCCTGGGCGTCACGC	13.33	Flower_2	-	-	-
TCCGGGCTAGAGCGACGCGTGCGCC	12.97	Flower_2	-	-	-
CTTGATATCTCTGGAGCTTC	13.69	Flower_2	-	-	-
GCTCTCTATGCTTCTGTCATCC	13.33	Flower_2	-	-	-
TGGATGAGGAGATATACATGCACC	13.15	Flower_2	-	-	-
CCGGGGGACGGACTGGGAACGGCC	12.79	Flower_2	-	-	-
TTGTTTGGGTAGGATCTTGA	13.33	Flower_2	-	-	-
AGCCGTTTTGACTCGAAATTGAGC	13.15	Flower_2	-	-	-
TTATCTTTTCTGTTAACGGCC	13.51	Flower_2	-	-	-
CACACGGTTGCTGACAGAC	14.23	Flower_2	-	-	-
CTTTTCTGTTAACGGCCTGCC	14.41	Flower_2	-	-	-
AATCGAACCGTCTAGTAGCTGGTT	13.33	Flower_2	-	-	-
GCTTGTCCCGACATGTGATTGATT	12.79	Flower_2	-	-	-
GATGGGGGCTGGCGATGCGCCT	13.33	Flower_2	-	-	-
CAGCCAGATGGACAGGACTGTC	12.97	Flower_2	-	-	-
TTCATTATATCCTTTCTAAGACC	13.33	Flower_2	-	-	-
ATTACTAATTCATGATCTGGC	13.87	Flower_2	-	-	-
AGAATTACAATTCTGACAAAT	12.97	Flower_2	-	-	-
GCACGTGCCGTTGGTGAAGCTC	13.69	Flower_2	-	-	-
CCGGACCCTGTCGCACCACGAGGC	12.79	Flower_2	-	-	-
GGACCGCAGCTGTAGATTAACCGC	12.79	Flower_2	-	-	-
GCGGGTGTAGCATCATCAAGA	13.33	Flower_2	-	-	-
TGTTCCCTGGGATTGGCTTTGGGCT	12.61	Flower_2	-	-	-
CAAGTTTGTGTGACGATTGGACT	12.97	Flower_2	-	-	-
CGATCCACTGAGATTCAGCCC	13.51	Flower_2	-	-	-
TGCACCGGATTGGACTATTTTAGT	12.61	Flower_2	-	-	-
ACCATCCGAGTTACCTGGGCT	14.05	Flower_2	-	-	-
ATGTCAACGGTCACTGGTTACTGT	12.97	Flower_2	-	-	-
GTAGGATTCGAACCGCTGACTTGG	12.79	Flower_2	-	-	-
TCAAGTGCCGCTGAGCTCT	13.51	Flower_2	-	-	-
GAGGCGCGGACCGATGCG	13.87	Flower_2	-	-	-

CCCAGTCCCGAACCCGTCGGCTG	13.51	Flower_2	-	-	-
TTTGAAATTCATCGTGATGG	13.33	Flower_2	-	-	-
TCCCTGGGATTGGCTTTGGGCTT	12.61	Flower_2	-	-	-
CATGCCTGTCGGGACCCG	14.05	Flower_2	-	-	-
GACGTGAGTGGTCCAAAGACGGGT	12.61	Flower_2	-	-	-
CGGGTAGAATCCTTTGCAGACG	13.15	Flower_2	-	-	-
TACTGAGAACTGAATGACATGTTT	12.79	Flower_2	-	-	-
CTAATTTCCAGAAGGTCTGAGCCT	12.97	Flower_2	-	-	-
AGAGGGACTATGGCCGCTTAGGC	13.15	Flower_2	-	-	-
TTGACCTTGTAAGACCCCGTG	12.97	Flower_2	-	-	-
GGGCGTCGAACGGTCGACT	13.51	Flower_2	-	-	-
GTTTGTTTGATGGTAACTACTACT	12.79	Flower_2	-	-	-
GAGCGGCCGTCGGTGCAGATCT	13.51	Flower_2	-	-	-
TGCCTGCGACGTCGCGAGAAGTC	13.15	Flower_2	-	-	-
CGATGGTAGGATAGAGGCCT	13.87	Flower_2	-	-	-
ACTCTCACATATGGAGAGAGGGCT	13.15	Flower_2	-	-	-
GCCTGCGACGTCGCGAGAAGTCC	12.97	Flower_2	-	-	-
GGGTAGAATCCTTTGCAGACG	13.15	Flower_2	-	-	-
CCCGGACCCTGTCGCACCACGAGGC	12.97	Flower_2	-	-	-
ATCGAACCGTCTAGTAGCTGGTT	12.97	Flower_2	-	-	-
GGCTTTACCCGATAGAACTCGC	13.69	Flower_2	-	-	-
TCGCCACATGATCTCTACATC	13.51	Flower_2	-	-	-
AAGGTCCAGGTATTTCTTTGAAGC	13.15	Flower_2	-	-	-
AATGGAACCCAGGAATAATTCAC	12.43	Flower_2	-	-	-
TCCCCGACGTTCGAATTGTAGTCT	12.43	Flower_2	-	-	-
CTGGAAGTCTTTGTGAGGAACT	12.43	Flower_2	-	-	-
GAGATTTAAGTAACCGTGTGCAAC	12.43	Flower_2	-	-	-
TTGGATTGAAGGGAGCTCTA	13.15	Flower_2	-	-	-
CGCCCGGACCCTGTCGCACCACGA	12.79	Flower_2	-	-	-
CAATAAGAATGCTAGTTCTTACTG	12.97	Flower_2	-	-	-
AAACGGGACCCTGAGGGCT	13.87	Flower_2	-	-	-

CGAGGATTGTGGCTACGATA	12.97	Flower_2	-	-	-
AAAGGTCGACGCGGGCTTCGCC	13.87	Flower_2	-	-	-
TACGGACAAGGGGAATCCGACTGTT	12.43	Flower_2	-	-	-
CAATGCTGCTGTTTCTCTGGCAT	12.61	Flower_2	-	-	-
TACCCGGCCGTCGGGGCAAGCGCC	12.61	Flower_2	-	-	-
ACTCGAACTTGGTCCTGGATGGCC	12.79	Flower_2	-	-	-
CCCCGAAAATGGATGGCGCTGAAGC	12.43	Flower_2	-	-	-
CCGCGCCACGGAATCGAGAGC	13.51	Flower_2	-	-	-
CTCTGACGATTCATGATAACT	12.79	Flower_2	-	-	-
GTCTTGCACTGTAGTTCATTTAGT	12.43	Flower_2	-	-	-
CCTGGGATTGGCTTTGGGCT	12.79	Flower_2	-	-	-
ACTCGAACTCGGCTCTGGATGGC	12.43	Flower_2	-	-	-
CTCTTTTGGACCCAAGGCTC	13.33	Flower_2	-	-	-
CACCTGGAAACGGCTCAGC	13.15	Flower_2	-	-	-
CGTCCCCGACGTTTCAATTTGTA	12.79	Flower_2	-	-	-
AACCTTGTGTCAGGACCTACGGGCC	12.43	Flower_2	-	-	-
GAGCATGCCTGTCGGGACCCG	12.79	Flower_2	-	-	-
AGGATTGGCTCTGAGGGCTGGGCA	12.43	Flower_2	-	-	-
ACTTGTCACACTTGCACTTGAAT	12.61	Flower_2	-	-	-
AAGATGACTGAGTTGAAGAAACT	12.79	Flower_2	-	-	-
GCGCCCGGACCCTGTCGCACC	13.87	Flower_2	-	-	-
TAATACTACGCGAGCCACACT	13.87	Flower_2	-	-	-
TCAACGGATCCCATTGTTAAT	13.33	Flower_2	-	-	-
CGCGGGTAGAGCAGTTT	12.97	Flower_2	-	-	-
TAAAGTCTTCAAGTCTCTGCACC	12.43	Flower_2	-	-	-
TCCCTTCATGGCTGGAGCACC	12.97	Flower_2	-	-	-
CACCACGAGGCGCTGTCTG	12.25	Flower_2	-	-	-
CCTTGAGAGTCTACATTGGACAGT	12.25	Flower_2	-	-	-
AATCTCAGTCATTGGATGCAATCT	12.43	Flower_2	-	-	-
CTGGGAATCTTTGAATTTCCACT	12.61	Flower_2	-	-	-
CGAGAATATAGTACTTAGGT	12.61	Flower_2	-	-	-

AGTCCCGAACCCGTCGGCTGT	12.97	Flower_2	-	-	-
GTCCTATCTGTTGGCCITCGGGA	12.25	Flower_2	-	-	-
TCGGCACTGTTAGGCTCAGACGCC	12.61	Flower_2	-	-	-
TATCATGGTTACTTGTCTGTACA	12.43	Flower_2	-	-	-
TCTTGACCTTGTAAGACCCCG	12.61	Flower_2	-	-	-
GCCTGTCGGGACCCGAAAG	13.69	Flower_2	-	-	-
TCGTGCACCTGCGCGCTCCTGGC	12.43	Flower_2	-	-	-
CGCCGAGACGAGCCTTGGGTC	12.25	Flower_2	-	-	-
CCATCGTCTACGCATCTACGCGGC	12.25	Flower_2	-	-	-
TATTATGTTTCAGATTTAGTACT	12.61	Flower_2	-	-	-
CAGCTTGAGAATCGATCGTCCC	12.97	Flower_2	-	-	-
CGGCAACGGATATCTCGGCTCTCG	12.25	Flower_2	-	-	-
TTGGACTCAACCACACATCGCCTG	12.07	Flower_2	-	-	-
CAAACCATAGATATTAGCACC	12.79	Flower_2	-	-	-
AGTTTGTGATGGTAACT	13.15	Flower_2	-	-	-
CTGATGGTTGCGTCTTTAGAGACT	12.07	Flower_2	-	-	-
ACCTATACCCGGCCGTCGGGGC	13.51	Flower_2	-	-	-
AGAGCATGCCTGTCGGGACCCG	12.61	Flower_2	-	-	-
CTCTGAGGGCTGGGCACGGG	13.33	Flower_2	-	-	-
TTACTGGAGAGAACCATT	15.5	Flower_2	-	-	-
CGTCCCCGACGTTTCGAATTGTAGT	12.07	Flower_2	-	-	-
TCCATTGTCGTCCAGCGTTAGG	12.97	Flower_2	-	-	-
TTGCGATGGTCCCTGCGGATGCT	12.25	Flower_2	-	-	-
CTGGAGCCCGGGCGAGTTCTATC	12.25	Flower_2	-	-	-
GGGGAGAATGTCACGACCTGCACG	12.07	Flower_2	-	-	-
GCCGATCCGGGCGGAAGACATTGTC	12.07	Flower_2	-	-	-
AGAAGTCCACTGAACCT	13.51	Flower_2	-	-	-
GTTGCCACCGTTGAGTTTGAACCC	12.43	Flower_2	-	-	-
TTTGCCTATACCTCCCATGCC	13.33	Flower_2	-	-	-
TTTCGGCAAATGTAGACTAGC	12.07	Flower_2	-	-	-
GTGGATATTTGTGGTTGTGGCACT	12.25	Flower_2	-	-	-

CATTGCGATGGTCCCTGCGGATGCT	12.07	Flower_2	-	-	-
GGTAGAATCCTTTGCAGA	12.61	Flower_2	-	-	-
CGGCCGTCGGTGCAGATCTT	13.15	Flower_2	-	-	-
TCTTTTGGACCCAAGGCTCGTC	12.79	Flower_2	-	-	-
ATCGAACCGTCTAGTAGCTGG	12.43	Flower_2	-	-	-
ATTAGTTTGGATCCAATTATCACT	12.25	Flower_2	-	-	-
ATTGACTCGGAGTTCAAGATATCT	12.43	Flower_2	-	-	-
CCCTGTTCGACCACGAGGCGCTGTC	12.07	Flower_2	-	-	-
TCTGGTTCCTGGCACCA	12.97	Flower_2	-	-	-
TACACTTGGCGAAGAATTCAGCAT	12.61	Flower_2	-	-	-
GATGACAGCGTCGTAATAGTA	12.25	Flower_2	-	-	-
TCGCGAGAAGTCCACTGA	12.61	Flower_2	-	-	-
TCGCAGGAGAGATGGCACTAGC	12.61	Flower_2	-	-	-
TGTTCCGATCGCGGCGACGCGGGC	12.07	Flower_2	-	-	-
AGCTCGTTGATTCTGATTTTCAGT	12.25	Flower_2	-	-	-
TTGCGCTCAGGGATCACGTAGACC	12.43	Flower_2	-	-	-
CTATGTCGCTCCGATTTCGTAA	12.61	Flower_2	-	-	-
TTTTCCCTACTCCACCCATGCC	12.79	Flower_2	-	-	-
ATAGCTCGACGCCAGGATC	12.97	Flower_2	-	-	-
ACCTGACTAATTGATCTTTTCCTT	11.89	Flower_2	-	-	-
TGGAGAAAGATCCGTGCTTGT	12.25	Flower_2	-	-	-
GCGAGAAGTCCACTGAACCTTAT	12.25	Flower_2	-	-	-
AGTACAAGTGAAGAGTCTCAGCCT	12.07	Flower_2	-	-	-
GGGACGGACTGGGAACGGCC	12.25	Flower_2	-	-	-
TTCGGTCTATTCTGTTGGC	12.97	Flower_2	-	-	-
TCGACGGATCGCACGGCCACCGTG	12.07	Flower_2	-	-	-
TAGAGGGACTATGGCCGCTTAGGC	12.25	Flower_2	-	-	-
GCCTGCCTGGGGCTCACGC	12.25	Flower_2	-	-	-
TTACGCTATGGACTTGAGTTCAAG	12.07	Flower_2	-	-	-
TAAGGCCAGAAAGATAGTAGAAAC	12.07	Flower_2	-	-	-
GGGGACGGACTGGGAA	12.61	Flower_2	-	-	-

CTGCCTGCGACGTCGCGAGAA	12.07	Flower_2	-	-	-
GGTCCCAGTCCCGAACCCGTCGGCT	11.89	Flower_2	-	-	-
CGTCCCCGACGTTTCGAATTGTAGTC	12.07	Flower_2	-	-	-
AAGGTTGGTCCAGTGATATGTCTC	12.07	Flower_2	-	-	-
TTGGACCCAAGGCTCGTCTCGGC	12.79	Flower_2	-	-	-
GGGTAGAATCCTTTGCAGACGACTT	12.07	Flower_2	-	-	-
TAGGCTTGCTTTGAGCACTCT	12.25	Flower_2	-	-	-
GTCCACTGAACCTTATCATTTA	12.07	Flower_2	-	-	-
ATAGCGCGGACCGCGGAGCCTT	12.43	Flower_2	-	-	-
AATCGGAAAGCGGGCACC GCCCC	11.71	Flower_2	-	-	-
GAGGGACTATGGCCGCTTAGGC	12.43	Flower_2	-	-	-
CTAATCGAACCGTCTAGTAGC	12.25	Flower_2	-	-	-
AGATCATGCGGCAGTTTCACC	11.89	Flower_2	-	-	-
CCCTGTGCGACCACGAGGCGCT	11.89	Flower_2	-	-	-
CCCGAAAATGGATGGCGCTG	12.43	Flower_2	-	-	-
TAGTTTGTGGTATGGTAACTACT	12.07	Flower_2	-	-	-
TTTTTGACCCAAGGCTCGTCTC	11.89	Flower_2	-	-	-
ACCCTGTGCGACCACGAGGCGCT	12.07	Flower_2	-	-	-
CAACATTTAATTGCCCTGGACT	11.71	Flower_2	-	-	-
TGTCGGCGGACTGCTCGAGCT	12.25	Flower_2	-	-	-
TTAAGGAGAATGCATGAATTA	11.71	Flower_2	-	-	-
TGCGCCCGTCGCCCGTTTGCC	12.07	Flower_2	-	-	-
CCGATGCGGATCGCGGCGGC	14.59	Flower_2	-	-	-
CTGTTGGCCTTCGGGATCGGAGTA	11.89	Flower_2	-	-	-
GAGAAGTCCACTGAACCTTA	12.79	Flower_2	-	-	-
TTGGGGTACTTGTTTCATCAGAACT	12.43	Flower_2	-	-	-
TTTCTGGCACACTTTTCGAA	12.07	Flower_2	-	-	-
CACACGGCTATGCATTGAGTA	12.07	Flower_2	-	-	-
GAATCTCAGTGGATCGTGGCAGC	11.89	Flower_2	-	-	-
GCAACCGAGGCTTGTAATAACTAC	11.89	Flower_2	-	-	-
GGACAATTGGCAGGATGG	16.4	Flower_2	-	-	-

GACGGACTGGGAACGGCCCCT	12.43	Flower_2	-	-	-
AGAGATCACATTGCTGAACAACCT	11.89	Flower_2	-	-	-
CGAGTCGACGGGCCAGTAAACCCG	12.07	Flower_2	-	-	-
CGGGGGACGGACTGGGAACGGCC	12.43	Flower_2	-	-	-
CGGCCGGGGACGGACT	12.43	Flower_2	-	-	-
AGAATTCAGAGAATTGTATTGCT	11.89	Flower_2	-	-	-
GCGAGAAGTCCACTGAACCTTATC	11.53	Flower_2	-	-	-
CCGACGTTCAATTGTAGTCT	11.89	Flower_2	-	-	-
GAGGATCCTGCACATCAGAACGGT	11.53	Flower_2	-	-	-
TTTGAAACGGGACCCTGAGGGCT	11.89	Flower_2	-	-	-
TTGCCACCGTTGAGTTTGAACCT	11.53	Flower_2	-	-	-
CGGCGATGCGCTCCTGGCCTTAAC	11.53	Flower_2	-	-	-
TACCGGATCTTCTTCTCATC	11.89	Flower_2	-	-	-
TCGGCATGAAGTAGTCTTGACC	11.71	Flower_2	-	-	-
AGGTTTGGTAGAGAATTAGCGAGC	12.07	Flower_2	-	-	-
GATAGCGCGACCGCGGAGCTT	12.07	Flower_2	-	-	-
TGGTGTGTATTTGTCTGC	11.53	Flower_2	-	-	-
TCCATTGGTTCCAGGAATCTG	12.43	Flower_2	-	-	-
CGCCCGGACCCGTGTCGACCACG	12.07	Flower_2	-	-	-
TTGAATTCTGCTCATTTTAG	12.25	Flower_2	-	-	-
GGTATGAGAGGGTTGGTTCT	11.53	Flower_2	-	-	-
GGGTAGAATCCTTTGCAGACGA	12.61	Flower_2	-	-	-
CGGGATCGGAGTAATGATTAAC	11.89	Flower_2	-	-	-
CCGATCGGATCGCGGC	12.79	Flower_2	-	-	-
TATTTTCGGCATCGGACACTCGGT	11.53	Flower_2	-	-	-
TCTCGAACCTGGCACTTGACC	12.61	Flower_2	-	-	-
AGCTTCACTGTTCCCTGGGATT	11.89	Flower_2	-	-	-
TTTTGGCATGCTAGAACTAGTAAT	11.53	Flower_2	-	-	-
CCGTCCAAGGCTAAATACGGGC	11.89	Flower_2	-	-	-
TCCTAAGGCCCAGAAGATAGTAGA	11.89	Flower_2	-	-	-
CAGCCGTCCGGACATGGTACAACA	11.53	Flower_2	-	-	-

TTGGATTGGTAGGTGAGATTAAT	11.71	Flower_2	-	-	-
GCCCATAGGATTAATGTGGACCC	11.71	Flower_2	-	-	-
CGGC CGGCTGCTCCGTTGAGC	12.43	Flower_2	-	-	-
GTTATAGTTTGGTTGATGGTAACT	11.53	Flower_2	-	-	-
TTGGACCTGGGTTGGGTCGGCC	11.89	Flower_2	-	-	-
TTCCCTGGGATTGGCTTTGGGCTT	11.89	Flower_2	-	-	-
CTCTTTAGAAGACAATGAGCT	12.07	Flower_2	-	-	-
TGCCAGATTCCAAAACCTCAGAATC	11.89	Flower_2	-	-	-
AACTCGACGGATCGCACGGCCACCG	11.53	Flower_2	-	-	-
AATGATCCACCGGATATGTTCCGGG	11.89	Flower_2	-	-	-
CCCGGCCGTCGGGGCAAGCGCC	12.61	Flower_2	-	-	-
CGCTCTGACGATTCATGATAACT	11.53	Flower_2	-	-	-
TAATCGAACCGTCTAGTAGC	12.25	Flower_2	-	-	-
GAACCGTCGGCTGTCGGCG	12.25	Flower_2	-	-	-
TTCCAACCTCGTTGGAACCAACGT	11.35	Flower_2	-	-	-
GTCCCCGACGTTCGAATTGTAGT	11.53	Flower_2	-	-	-
GCTCGAGGCGCGGACCGATCGGGAT	11.35	Flower_2	-	-	-
TACCCGGCCGTCGGGGC	12.07	Flower_2	-	-	-
TCGTCTCCCGTAGGACCTCCA	11.53	Flower_2	-	-	-
TTGAAACGGGACCCTGAGGGCT	11.89	Flower_2	-	-	-
TCTTTCTTTAAATGTAGACT	11.53	Flower_2	-	-	-
GCTAAATACGGGCGAGAGACCGAT	12.07	Flower_2	-	-	-
AGGATCCCGTGGAGCGAACCCATT	11.35	Flower_2	-	-	-
TAGCGCGGACCGCGGAGCT	12.25	Flower_2	-	-	-
AAAAGGTCGACGCGGGCTTCGCC	11.71	Flower_2	-	-	-
TCCCTACTCCACCCATGCCAT	12.43	Flower_2	-	-	-
CAAACCTCGTAGCACCACTGTT	11.35	Flower_2	-	-	-
TCTCGTGATGCTCCTGATTGC	11.71	Flower_2	-	-	-
CGCACACGAGGCGCTGTCTGC	11.71	Flower_2	-	-	-
TTGTAATCCAAGACTTTATGGAT	11.53	Flower_2	-	-	-
GTCCCCGACGTTCGAATTGTAGTCT	11.71	Flower_2	-	-	-

GAGGCGCGGACCGATGCGGATCG	11.89	Flower_2	-	-	-
TTATAGTTTGTGGATGTAAC	11.71	Flower_2	-	-	-
TTCGAGGTCCATATGAGAGAGGTG	11.35	Flower_2	-	-	-
CATGGGCCGAATGATAATCTGGGT	11.35	Flower_2	-	-	-
GCGTCCTCAGCGGGGACCGGGCCC	11.35	Flower_2	-	-	-
ACCGTTTGGATTGTATAGTTCAGA	11.35	Flower_2	-	-	-
CAAGCTCACTGTAGAGCCTGCC	11.53	Flower_2	-	-	-
CTGGGAACGGCCCTCCGGGGGC	11.35	Flower_2	-	-	-
AGTTCTTCGGGCTCCTAGGGTATC	11.35	Flower_2	-	-	-
GCATCGGCTGCGAGCT	12.25	Flower_2	-	-	-
ATTGTCAGAACACGCACCAGT	12.07	Flower_2	-	-	-
TCTAAGTATAGGTGTTAGGCT	12.79	Flower_2	-	-	-
TTTATGGATGGCAGAAGGTCT	11.35	Flower_2	-	-	-
GATACACTGGCGAAGAATTCAGC	11.35	Flower_2	-	-	-
TTCCAGACGGAGCTCCGAGGA	12.07	Flower_2	-	-	-
GCCGCTATGGTAAAATCGGTAGA	11.35	Flower_2	-	-	-
TGGCAGAGTTTGTAAACGATGGAGT	11.35	Flower_2	-	-	-
CCCAGATGATCGTTACAAAAACAGC	11.53	Flower_2	-	-	-
CGGGCGTCGAACGGTCGACTC	11.89	Flower_2	-	-	-
CCGGAGGACCGAGTGCCGTC	12.07	Flower_2	-	-	-
AGTCAGAATCCGGGCTAGAGC	11.89	Flower_2	-	-	-
AATCTGTCGAAATTAC	12.61	Flower_2	-	-	-
CGTATTTAGCCTTGGACGGAATT	12.79	Flower_2	-	-	-
TCAACATGTGCAGCCTGATGT	11.35	Flower_2	-	-	-
GCAGCAGTTCAAGGACCTGGCCT	11.17	Flower_2	-	-	-
ATGTCGCTCCGATTCGTCC	12.07	Flower_2	-	-	-
ACCAAGGAGTCTGACATGTGT	11.71	Flower_2	-	-	-
GTTGTCTTTACGCTGCATAACCCT	11.17	Flower_2	-	-	-
GGCAGAGGATGAAGAAACATATGT	11.35	Flower_2	-	-	-
CCGCGGGCGAGTTCTATCGGGT	11.53	Flower_2	-	-	-
GAAGATTGAAGACACATGGCCC	12.07	Flower_2	-	-	-

CTGAGACTAGCTCCATAATCACAA	11.17	Flower_2	-	-	-
GGCATCGGCCTGCGAGC	12.07	Flower_2	-	-	-
GTGGCAGAGGATGAAGAAACATAT	11.17	Flower_2	-	-	-
CGCCCGGACCCGTGTCGACCA	11.89	Flower_2	-	-	-
GGGACGGACTGGGAACGGCCCTCC	11.53	Flower_2	-	-	-
TTTGGGCTTTTCTGCGCAGCT	11.35	Flower_2	-	-	-
CCCGAACCCGTCGGCTGTC	12.25	Flower_2	-	-	-
TGATGACAGCGTCGTAATAGTA	11.53	Flower_2	-	-	-
CTTTTGGACCCAAGGCTCGTCTC	11.53	Flower_2	-	-	-
CATTCCAATTACCAGACTCGAT	11.89	Flower_2	-	-	-
CTACTACTCGGATAACCGTAGT	11.53	Flower_2	-	-	-
GCACCACGAGGCGCTGTCTG	12.25	Flower_2	-	-	-
GGAGAGACTGCAGTTGGAACAAC	10.99	Flower_2	-	-	-
CACCGAGAAGTCGATGCAAGTGCT	10.99	Flower_2	-	-	-
ATGGTGTGAATTGCAGAATCCC	11.53	Flower_2	-	-	-
TGTTTAACGGCCTGCCACCCT	11.71	Flower_2	-	-	-
CTCTGGAGTCTTGCTTTGGGC	11.17	Flower_2	-	-	-
TCGACTCCCGGTAGGACCTCCA	11.17	Flower_2	-	-	-
ATCCCTTCGGATATATTGACTCGG	11.17	Flower_2	-	-	-
ATTCTGATGGCGACACATGGCTGT	10.99	Flower_2	-	-	-
TGGGAATATGCAACTCCACTG	11.17	Flower_2	-	-	-
GCTCGAGGCGGGACCGATG	12.61	Flower_2	-	-	-
TTAATTATGTTTTGGGCCTTGAT	11.35	Flower_2	-	-	-
GTC AAGGCACTGTAGCGGCACT	10.99	Flower_2	-	-	-
GTTCGGCTCCCGGTAGGACCTCCA	11.17	Flower_2	-	-	-
CTGTTTAACGGCCTGCCACC	11.35	Flower_2	-	-	-
GAGCCCGGGGCGAGTCTATC	11.71	Flower_2	-	-	-
CCGAGAGAGTGTGCACATGGGTGT	11.35	Flower_2	-	-	-
TGCACCGAACCCGACTTC	15.14	Flower_2	-	-	-
CTCCAAGAGGCTTGACTTAGACTC	11.17	Flower_2	-	-	-
TTTCCTACTCCACCCATGCC	11.35	Flower_2	-	-	-

CCGTGAATCGGAAGCGGGGCAC	11.17	Flower_2	-	-	-
CAACCCGACTCGGTCTAAAACCT	11.17	Flower_2	-	-	-
CTTCCAGTGCTGCTGACATGGCTT	11.35	Flower_2	-	-	-
CGTGCACCTGCGCGCTCCTGGC	12.07	Flower_2	-	-	-
CTCGTGCACCTGCGCGCTCCTGGC	11.53	Flower_2	-	-	-
TCACTGTTCCTGGGATTGG	11.17	Flower_2	-	-	-
TCTTTTGGACCCAAGGCTCGT	11.35	Flower_2	-	-	-
ACTCTTCCTCAAGGGCTTCCT	11.35	Flower_2	-	-	-
CCTATCGATCCTTTAGACCT	11.35	Flower_2	-	-	-
ATCAACGGAAGGAAGACGAAT	11.71	Flower_2	-	-	-
ATTCTGTGGCCTTCGGGATCGG	11.35	Flower_2	-	-	-
GGCATCGGCCTGCGAGCTCCCC	12.25	Flower_2	-	-	-
TCGCCCCTCGCTCTGACGA	11.35	Flower_2	-	-	-
GCAGTAGAACTACTAGGCGACGCC	11.71	Flower_2	-	-	-
GATGGTCCCTGCGGATGCTCACGC	11.17	Flower_2	-	-	-
TTTTCCGAAGGATTATGAAT	11.71	Flower_2	-	-	-
TGAGATGCAATTCATGTTGGGGAT	10.99	Flower_2	-	-	-
CAAAAAGCAAGGCGGTCTGGGACT	10.99	Flower_2	-	-	-
ACACGGTTGTCTGACAGAC	12.61	Flower_2	-	-	-
ACTTCCATGTGTTTTCAACTTT	11.17	Flower_2	-	-	-
CTTGACTGAGGGCCATTGAACATC	10.99	Flower_2	-	-	-
CTTGTTGCACCGTTGGATTGAGCT	11.17	Flower_2	-	-	-
ATTGGACCGTGGGCTTAATGAGCC	10.99	Flower_2	-	-	-
AATGAATGACTAAGATTTAATCTC	10.81	Flower_2	-	-	-
TTGGACAGAGAAATCACGGTC	10.99	Flower_2	-	-	-
CAGATCCAAGTCAGCTGCTCT	10.99	Flower_2	-	-	-
GCTCGAGGCGCGGACCGATGCGG	11.53	Flower_2	-	-	-
CCGGCCGGGGACGGACT	11.71	Flower_2	-	-	-
CCTATGTCGCTCCGATTCGTT	10.81	Flower_2	-	-	-
TCGAGTGAGAGCATGCCTGTC	10.99	Flower_2	-	-	-
CGACCTCGGCACCGCTAGGCTC	11.71	Flower_2	-	-	-

TGAGAATCAACTATTTATTG	11.35	Flower_2	-	-	-
TAATTTCTACTCTACCTCCCGGAG	11.35	Flower_2	-	-	-
ACCCGGCCGTCGGGGCAAGCGCC	10.99	Flower_2	-	-	-
CGGGCCGCTTGAAACGTAATT	11.17	Flower_2	-	-	-
GCGTGCCGGCCGGGGACGGACT	10.99	Flower_2	-	-	-
TCCGGGCTAGAGCGACGCGTG	11.53	Flower_2	-	-	-
TGCGCTGGATTATGACTGAACGC	10.99	Flower_2	-	-	-
AAAACGACTCTCGGCAACGGAT	11.17	Flower_2	-	-	-
GTTCTGTCCGGGCGACGCCACCA	10.99	Flower_2	-	-	-
CGGGTAGAATCCTTTGCAGACGA	10.99	Flower_2	-	-	-
ATCCGGGCTAGAGCGACGCGTGCG	10.81	Flower_2	-	-	-
TCTGCTTACGTAGCCTTGACT	10.99	Flower_2	-	-	-
TAAATCAGGCACCAACCCAAC	10.99	Flower_2	-	-	-
ACTGATGACAGCGTCGTAATAGT	11.17	Flower_2	-	-	-
ATGAGAATCAACTATTTATT	11.71	Flower_2	-	-	-
GCGACCCAGGTCAGGCG	11.35	Flower_2	-	-	-
GTTACTAATTCATGATCTGGCATA	10.81	Flower_2	-	-	-
CTTGGTTGAAGAGGGTATTGCC	10.99	Flower_2	-	-	-
TTTTGGACCAAGGCTCGTCTCGGC	11.35	Flower_2	-	-	-
TTTTACCGATACCTTCCATACC	10.99	Flower_2	-	-	-
CCCCGAAAATGGATGGCGCTGA	10.81	Flower_2	-	-	-
GGTAGAATCCTTTGCAGACGACTTA	10.99	Flower_2	-	-	-
ACCACGGGAGCCATTTAATGAAAC	10.99	Flower_2	-	-	-
TTCGACTCCCGGTAGGACCTCCA	10.81	Flower_2	-	-	-
GAACCGGGACGTGGCGGCTGACGGC	11.35	Flower_2	-	-	-
TAATTGAGCACGGAGAAGTCGAAT	10.99	Flower_2	-	-	-
ATGGGGCTGGCGATGCGCCT	11.53	Flower_2	-	-	-
GGACGGACTGGGAACGGCC	11.71	Flower_2	-	-	-
GAGAATGATGACAGTTTGACAATT	10.99	Flower_2	-	-	-
CTGAGATTCCAGCTTTGACAAT	12.43	Flower_2	-	-	-
CGCGCCCGACCCTGTCGCACCA	10.63	Flower_2	-	-	-

TTTACTGGAGAGAACCATT	11.89	Flower_2	-	-	-
TGTGCACCGTCTCTCGTCC	10.81	Flower_2	-	-	-
GCCCGGACCCTGTCGCACCACGA	10.63	Flower_2	-	-	-
TACCCGAAGTGTACCTGACTAATT	10.63	Flower_2	-	-	-
AATCCGGGCTAGAGCGACGCGTGC	10.81	Flower_2	-	-	-
GGCGCGGCTGCTCCGTTGAGC	11.17	Flower_2	-	-	-
CGATGGTCCCTGCGGATGCTCACGC	10.63	Flower_2	-	-	-
TCTGAACTATAACAATCCAAACGGT	10.63	Flower_2	-	-	-
GGACGGACTGGGAACGGCCCC	11.35	Flower_2	-	-	-
ATAGCACTGTTAGGCTTTCGGCCT	11.17	Flower_2	-	-	-
TCCCGACGTTTGAATTGTAG	11.53	Flower_2	-	-	-
CTATGTCGCTCCGATTTCGTTT	10.63	Flower_2	-	-	-
TTTTCTGTTTAACGGCCTGCCC	11.17	Flower_2	-	-	-
TCTTTGAACGCAAGTTGCGCCCC	10.81	Flower_2	-	-	-
TTCTGATTTTTCCATGTAGAGACA	10.81	Flower_2	-	-	-
TGGATGGCAGAAGGTCTTATT	11.17	Flower_2	-	-	-
CACCACGAGGCGCTGTCTGC	11.89	Flower_2	-	-	-
CCCTCTTTTTGGACCCAAGGCT	11.35	Flower_2	-	-	-
GAGCTTCAAAGAAATACCTGGACC	10.63	Flower_2	-	-	-
GCTGAGATTCCAACCTACCC	10.81	Flower_2	-	-	-
CATCATTCAATGTTCTGCATA	10.99	Flower_2	-	-	-
CGAGAAGTCCACTGAACC	10.99	Flower_2	-	-	-
GAAATAGTTGGGTAGAGTTGG	11.89	Flower_2	-	-	-
AATGAAGTCCAAGGTTGAGGCT	11.17	Flower_2	-	-	-
GCCCGTCGCTCTGACGATTCATG	10.81	Flower_2	-	-	-
GCTAACTAGCTATGCGGAGGGT	10.63	Flower_2	-	-	-
TCTTAAAAGATGTCAAAGCTT	11.17	Flower_2	-	-	-
CAGGTTCTGAGCTAGTAGCTTT	10.99	Flower_2	-	-	-
TAAGTATGAACTAATTCGGACT	11.17	Flower_2	-	-	-
GTAGAATCCTTTCAGACGACTT	11.35	Flower_2	-	-	-
TGAACTGGAGGGAGTATCTGAAGG	10.99	Flower_2	-	-	-

TGATGATCCATGTTAGTAGAAAATT	10.63	Flower_2	-	-	-
TTGAATGATGACATAGGAGGAG	11.35	Flower_2	-	-	-
TCCGGGCTAGAGCGACGCGTGCG	10.63	Flower_2	-	-	-
CTTGGACGGAATTTACTGCC	10.99	Flower_2	-	-	-
TAGACCTTCGGAATTTGAAGC	10.63	Flower_2	-	-	-
TCTGGAGAAGCGTCCTCAGCGGC	11.35	Flower_2	-	-	-
CAAAACTCTATAATACTTCTTGTT	10.81	Flower_2	-	-	-
GCTCTGAGGGCTGGGCACGGGGGTC	10.63	Flower_2	-	-	-
GAAGTCCACTGAACCTTATCATT	10.81	Flower_2	-	-	-
TATCCATCGATTCACTGTTTGACT	10.63	Flower_2	-	-	-
TGCTCGGGCCTGGCGACCCAC	10.63	Flower_2	-	-	-
TTTGACTCAACCACACATCGCCT	10.63	Flower_2	-	-	-
TTCCATCGTCGCCGAGAACA	10.99	Flower_2	-	-	-
CGAGTTGGGTGATATTAGTAGGCT	10.45	Flower_2	-	-	-
ATTCTCGTCGCCGTTTATCTGCC	10.45	Flower_2	-	-	-
CGCTTCTTAGAGGGACTATGGCC	10.63	Flower_2	-	-	-
TTAGCTGCAGCGAGCTTTGCCT	11.17	Flower_2	-	-	-
GACGGATCGCACGGCCACCGTG	10.99	Flower_2	-	-	-
ATGCACCTACCTAGATTCTAAAT	10.45	Flower_2	-	-	-
TCTTTGGTGCGACTGTAGCGGC	10.99	Flower_2	-	-	-
TTCGGAGTATTATCTTTGAGT	10.63	Flower_2	-	-	-
ACGAATTGTTCTAACGTTGACTGT	10.45	Flower_2	-	-	-
TGTAGTTTCTCTTATTTTCT	11.35	Flower_2	-	-	-
CGCCACGGAATCGAGAGCT	10.99	Flower_2	-	-	-
TAGCTGGTTGTGTTACGAAC	10.81	Flower_2	-	-	-
AATACTGAGAACTGAATGACATGT	10.99	Flower_2	-	-	-
GCTGAGATTCCAGCTCTACTC	11.17	Flower_2	-	-	-
ACCCTGCAGAAATTCACGAGAAAG	10.99	Flower_2	-	-	-
GAGGATGAAGAAACATATGTGAAT	10.45	Flower_2	-	-	-
GGCACGTGCCGTTGGTGAAGCTC	10.99	Flower_2	-	-	-
CTTGGTCGGGATCCCTTTTCAGA	10.45	Flower_2	-	-	-

ATGGGGCTGGCGATGCGCC	10.45	Flower_2	-	-	-
CACGGGCTGGCGCACCCAC	10.99	Flower_2	-	-	-
CATCACTAGTTTACGCTCTGA	10.81	Flower_2	-	-	-
CCGAGACTGCACAAAATGGAGAA	10.45	Flower_2	-	-	-
AGACCCTGCAGAAAATCACGAGAA	10.63	Flower_2	-	-	-
TCACCTAGAAGATACTCTGAAG	10.63	Flower_2	-	-	-
TTCACTGTTCCCTGGGATTGG	10.45	Flower_2	-	-	-
CTCGAGGCGGGACCGATGCGG	10.81	Flower_2	-	-	-
ATAGCTCGACGCCAGGATGC	11.53	Flower_2	-	-	-
TTCTCTGGATTTTTTGATGCCCT	10.27	Flower_2	-	-	-
ATGTCGCTCCGATTCGTAG	11.53	Flower_2	-	-	-
CTTCTGGCCGAGGGCACGCCT	10.63	Flower_2	-	-	-
TCTAATACCAATTGTTGGACT	11.17	Flower_2	-	-	-
GCGAGGCAAGTTGGGAACCCGAAC	10.27	Flower_2	-	-	-
ATACATCTGAATAGTCTGTAACT	10.63	Flower_2	-	-	-
GCAACTGAGGCCTGTACTAACTAC	10.27	Flower_2	-	-	-
CGGCCGTCGGTGCAGATCTGGT	10.63	Flower_2	-	-	-
AGCGGGGACCGGGCCCAAGTCCCC	10.81	Flower_2	-	-	-
GTCGGGATAGCTCAGCC	11.35	Flower_2	-	-	-
CCAAGCCCGGGCTTTTCGTACT	11.17	Flower_2	-	-	-
GAAGTCCACTGAACCTTATCA	11.53	Flower_2	-	-	-
CCGGAGGCTAAGTAGTGAGAATT	10.45	Flower_2	-	-	-
GAATCGATCGTCCCCGACGTT	10.27	Flower_2	-	-	-
CCTGGGATTGGCTTTGGGCTTTT	10.99	Flower_2	-	-	-
CCCTACTCCACCCATGCCATA	10.27	Flower_2	-	-	-
ATCTTGGTAACTTGTATGCT	10.45	Flower_2	-	-	-
ATCCGGTGTGGGCGTTAGAGC	10.99	Flower_2	-	-	-
AGCGGGACCGCGGAGCT	10.81	Flower_2	-	-	-
TTAACGGCCTGCCACCCCTGGA	10.45	Flower_2	-	-	-
CATGGGATAACATCATAGGATTT	10.45	Flower_2	-	-	-
TTAGATGATGTGTGGAGCAAG	10.81	Flower_2	-	-	-

ATATCTGTTGGATTCTTGCTTCCT	10.45	Flower_2	-	-	-
ACGGATCGCACGGCCACCGTG	10.45	Flower_2	-	-	-
ATAAAAGTACAAGTTCCTCT	11.17	Flower_2	-	-	-
CGGGCTAGAGCGACGCTGCGCCC	10.45	Flower_2	-	-	-
CGACGTCGCGAGAAGTCCACTGA	10.99	Flower_2	-	-	-
GGTTACTAATTCATGATCTGGC	11.35	Flower_2	-	-	-
GGACCCACGCTGATGTGTTGACT	10.27	Flower_2	-	-	-
CCAGGATTCCCCTAGTAACGGC	12.07	Flower_2	-	-	-
TTCCCGCATGTTCAAGTAATGATC	10.63	Flower_2	-	-	-
CTGTGCGGCGACTGCTCGAGCT	11.35	Flower_2	-	-	-
GCGAGTTCTATCGGGTAAAG	10.63	Flower_2	-	-	-
CCCTATGTCGCTCCGATTCGTAA	11.17	Flower_2	-	-	-
TTGGCAGCAATGAATCTTGGT	10.45	Flower_2	-	-	-
CGACGTTCGAATTGTAGTC	10.99	Flower_2	-	-	-
CCCAGATAATTGTCAGTGTAGAAC	10.09	Flower_2	-	-	-
ACCCAACCTCAAAATCCACCC	10.45	Flower_2	-	-	-
AGTTACTAATTCATGATCTGGT	10.63	Flower_2	-	-	-
CCGGGGGACGGACTGGGA	10.99	Flower_2	-	-	-
AGGTCATGGAAGTTCCTTCTT	10.81	Flower_2	-	-	-
CCTGCGACGTCGCGAGAAGTC	10.27	Flower_2	-	-	-
AGCTTACTCAACTATTCCT	10.63	Flower_2	-	-	-
GCTCTGAGGGCTGGGCACGGG	10.81	Flower_2	-	-	-
GTAGCTCAGCTGGTAGATGGACGA	10.09	Flower_2	-	-	-
CCGGCGATGCGCTCCTGGCCTTAAC	10.09	Flower_2	-	-	-
TCCGATAGCGCGGACCGCGGAGC	10.27	Flower_2	-	-	-
CGAGGTCTGATACCCATGAAATAT	10.09	Flower_2	-	-	-
CGAGTCCGGGCGACGCCACCA	10.27	Flower_2	-	-	-
TAGCTCGACGCCAGGATC	10.99	Flower_2	-	-	-
TTCCTTGTCTTCAGTTCTGAGC	10.09	Flower_2	-	-	-
ATTCTGTTGGCCTTCGGGA	10.45	Flower_2	-	-	-
GAACCTTACATTACAGCGGACGGC	10.63	Flower_2	-	-	-

CCCTCAAAGGCTCCAGTATT	10.45	Flower_2	-	-	-
CGTGCGAACTGGTGTAGAGAAGC	10.09	Flower_2	-	-	-
CTAACTAGCTATGCGGAGGGT	10.63	Flower_2	-	-	-
TCTGGGCAAAGAGAACAAAGTCAT	10.09	Flower_2	-	-	-
TCGGCCTGCGAGCTCCCCATTCCGC	10.09	Flower_2	-	-	-
TCAACGAGTCTATAGCCTTGGC	10.81	Flower_2	-	-	-
TCAATAACAGTGAATGATGAC	10.45	Flower_2	-	-	-
GCTTGTCTGCATGAAGTCAA	11.17	Flower_2	-	-	-
TTATGCAAGCCGGCAGGACCC	11.17	Flower_2	-	-	-
TACGAGAGGAACCGTTGATTCCG	10.27	Flower_2	-	-	-
GAACAGTGAATACTGAGAAC	10.27	Flower_2	-	-	-
CGTGCACCTGCGCGCTCCTGGCA	10.27	Flower_2	-	-	-
GCATCGGCCTGCGAGCTCC	10.99	Flower_2	-	-	-
CAATTACCAGACTCGATGAGC	10.45	Flower_2	-	-	-
GGAAGACTGGACGATGAAGAAGTC	10.09	Flower_2	-	-	-
TTTTGCGACGAAAGAAGTTGAACT	10.45	Flower_2	-	-	-
GGAATATGCAACTCCACTGG	10.45	Flower_2	-	-	-
AACCCGTCGGCTGTCGGC	11.17	Flower_2	-	-	-
ATCATGCGGCAGTTTCACCT	11.17	Flower_2	-	-	-
GCAGATGATGTGGCTCTGTGGCTA	10.27	Flower_2	-	-	-
CCACTGGACTGTTCTCTTCT	10.45	Flower_2	-	-	-
AAAAGCTCGTTTGATTCTGAT	10.45	Flower_2	-	-	-
TGACCCTAATTGAACCATCACCTTT	10.09	Flower_2	-	-	-
CTCTTTTGGACCAAGGCTCGTC	10.27	Flower_2	-	-	-
TAACCCTGGCTGTCTGAGACA	10.45	Flower_2	-	-	-
CCGTCGCGCCCGGACCCTGTC	10.45	Flower_2	-	-	-
TCACTGTCCCTGGGATTGGCIT	10.45	Flower_2	-	-	-
CAACGAGTCTATAGCCTTGGC	10.27	Flower_2	-	-	-
AGGCGGGACCGATGCGGAT	10.81	Flower_2	-	-	-
TACTAGCTGAAGGACACCGGT	10.45	Flower_2	-	-	-
CTAACCTTGTGTCAGGACC	11.35	Flower_2	-	-	-

CCTCAGGATAGCTGGAGCCCG	10.45	Flower_2	-	-	-
CTTTGGACCACTCACGTATTGGG	10.27	Flower_2	-	-	-
TTCCCCGGGCGTCGAACGG	11.17	Flower_2	-	-	-
TTTAGACCTTCGGAATTTGAAGC	10.45	Flower_2	-	-	-
TTATCTTTCTAACGGCACTGCATC	10.09	Flower_2	-	-	-
GTTAGGGAGTCCGGAGACGTCGGC	10.09	Flower_2	-	-	-
AGGAGATGCACTGTAGCAATTACT	10.09	Flower_2	-	-	-
CATCAAGGGGAATTGAATTCTGCT	10.09	Flower_2	-	-	-
TTAGTTGCCACCGTTGAGTT	12.97	Flower_2	-	-	-
TCTGACGATTCATGATAACT	10.63	Flower_2	-	-	-
TGCACCGGTCGTCTCGTCCCT	10.81	Flower_2	-	-	-
TGAAGGGAGACTTTAGGATTTT	10.45	Flower_2	-	-	-
TGAATTGCAGAATCCCGTGAAC	10.09	Flower_2	-	-	-
AATCCGGAGGACCGAGTGCCGT	10.27	Flower_2	-	-	-
CCGGACCTGTGCGACCAACGAG	10.81	Flower_2	-	-	-
GTGCGCTGGATTATGACTG	10.63	Flower_2	-	-	-
TGGACCAATTCGGGACAAACCGCT	10.09	Flower_2	-	-	-
CTTCGGAATTTGAAGCT	11.53	Flower_2	-	-	-
GAGATGGGCACCACAGAACACC	10.45	Flower_2	-	-	-
TCCATGGGCTGTGTCGAACCG	10.27	Flower_2	-	-	-
TTCCCGAAGGATTATGAATTC	10.63	Flower_2	-	-	-
CGGACCGATGCGGATCGCGCGGC	10.09	Flower_2	-	-	-
GGTAGAATCCTTTGCAGACG	10.09	Flower_2	-	-	-
CGACGTTCGAATTGTAGTCT	10.99	Flower_2	-	-	-
CATCAAATTTGGACTTCGTT	10.81	Flower_2	-	-	-
TCGGAGTAATGATTAACA	10.09	Flower_2	-	-	-
ATTTATGCGATGATTGTAGC	10.09	Flower_2	-	-	-
TACTCTCATGATCGAGAAGGGGCT	10.09	Flower_2	-	-	-
ATCGGAAGCGGGCACCGCCCC	10.27	Flower_2	-	-	-
TCCCGAACCCGTCGGCTGTGCG	10.27	Flower_2	-	-	-
CCTTGGACGGAATTTACCGCC	10.27	Flower_2	-	-	-

CGGTCTGTAGTCCAACGGTTAGG	10.09	Flower_2	-	-	-
TTCCAACCAGATACTATGGGC	10.63	Flower_2	-	-	-
CGGCCGTCGGTGCAGATCTTGG	10.27	Flower_2	-	-	-
TAAAGGTCCAAGGTTGAGGCT	10.09	Flower_2	-	-	-
CTACGCTTCTTAGAGGGACT	10.81	Flower_2	-	-	-
TTTGAGATTGATGTTATTGATA	10.27	Flower_2	-	-	-
AAAATCAGGCACCAACCCACC	10.09	Flower_2	-	-	-
AACGGTCGACTCAGAACT	10.09	Flower_2	-	-	-
ACTCCCGGTAGGACCTCCA	10.99	Flower_2	-	-	-
AACCGTCTAGTAGCTGGT	10.09	Flower_2	-	-	-
TCGCTCTAGCCCGGATTCTGA	10.09	Flower_2	-	-	-
AATTCTTGCCTCGCACGAGTTCTT	10.09	Flower_2	-	-	-
ATTCCGAAGGTCTAAAGGATC	10.27	Flower_2	-	-	-
CGGGCGAGAGACCGATAGCAAAC	10.09	Flower_2	-	-	-
GGGTAGAATCCTTTGCAGA	10.81	Flower_2	-	-	-
TGCCTCGTGCACCTGCGCGCTC	10.09	Flower_2	-	-	-
TCGAACCGTCTAGTAGCT	10.09	Flower_2	-	-	-
GGCTCTGAGGGCTGGGCACGGGG	10.45	Flower_2	-	-	-
TGGCCTATCGATCCTTTAGAC	10.09	Flower_2	-	-	-
CAATACCGGGCTCATCGAGTCTG	10.09	Flower_2	-	-	-
AATTCTAACCTTGTGTCAGGACC	10.45	Flower_2	-	-	-
GAGTCGACGGGCCAGTAAACCC	10.09	Flower_2	-	-	-
TCTGAGGGCTGGGCACGGGGGT	10.27	Flower_2	-	-	-
ACCCGGATCCTAGCAACTGTGAGT	10.09	Flower_2	-	-	-
CAGGATTCCCCTAGTAACGGC	10.63	Flower_2	-	-	-
CCGTCCAAGGCTAAATACG	10.09	Flower_2	-	-	-
ATCCGGAGGACCGAGTGCC	10.81	Flower_2	-	-	-
CATTTTAGGCTTTATGAACACC	10.09	Flower_2	-	-	-
GCCCTATGTCGCTCCGATTCTG	11.89	Flower_2	-	-	-
AGATGATGTGGCTCTGTGGCTA	10.09	Flower_2	-	-	-
CAGGCATCGCCTAGTAGCTCCT	10.27	Flower_2	-	-	-

CTCTTTTGGACCCAAGGCT	10.09	Flower_2	-	-	-
AATATTCAAATGAGAACTTT	10.27	Flower_2	-	-	-
CGGCCTGCGAGCTCCCC	10.81	Flower_2	-	-	-
TCAAGCACAGAAGATGAGAAGAAC	10.09	Flower_2	-	-	-
CAGCTTGAGAATCGATCGTCC	10.09	Flower_2	-	-	-
CGCGGGCGAGTTCTATCGGGT	10.81	Flower_2	-	-	-
GATGGTAGGATAGAGGCCT	10.63	Flower_2	-	-	-
CGAACCGGGACGTGGCGGCT	10.63	Flower_2	-	-	-
TCCACTGAACCTTATCATT	10.09	Flower_2	-	-	-
CACCCTGGAAACGGCTCAGCC	10.09	Flower_2	-	-	-
GCACGGGCTGGCGCACCCAC	10.09	Flower_2	-	-	-
GTGAATTGCAGAATCCCGTGA	10.45	Flower_2	-	-	-
CATCGGCCTGCGAGCTCCC	10.09	Flower_2	-	-	-
TACTGGAGAGAACCATT	13.69	Flower_2	-	-	-
TGGCTGTATCTTTCATCCACT	10.27	Flower_2	-	-	-
TTTTGGACCCAAGGCTCGTC	10.27	Flower_2	-	-	-
TTACAATACCCCGTCGCGTAT	10.09	Flower_2	-	-	-
ACTCAACCCCATGTGCAAT	10.09	Flower_2	-	-	-
GCCTGCGACGTGCGGAGA	10.63	Flower_2	-	-	-
ACGTGCACCGAACCCCGACTTC	10.81	Flower_2	-	-	-
AACAGACCGGTAGACTTGAACT	10.09	Flower_2	-	-	-
AATCTCAGTGGATCGTGGCAGC	10.27	Flower_2	-	-	-
ACTGGGAACGGCCCTCCGGGGG	10.09	Flower_2	-	-	-
GTGTTCGGATCGCGGCGACGGGG	10.09	Flower_2	-	-	-
GTCTCAGCGGCGGACCGGGCC	10.45	Flower_2	-	-	-
TTTTGGACCCAAGGCTCGT	10.45	Flower_2	-	-	-
TGGGAACGGCCCTCCGGGGG	10.09	Flower_2	-	-	-
TCCCGAACCCGTCGGCT	10.63	Flower_2	-	-	-
TTCCACAGCTTGAACTT	10.09	Flower_2	-	-	-
TGCTTAGTTGCCACCGTTGAGTT	10.81	Flower_2	-	-	-
CGATCGGCTCGAGGCGGGACC	10.27	Flower_2	-	-	-

TAGAATCCTTTGCAGAC	10.09	Flower_2	-	-	-
GCGACCCAGGTCAGGCGGG	15.14	Flower_2	-	-	-
TAACGGCCTGCCACCC	15.14	Flower_2	-	-	-
CCGAACCGGGACGTGGCGGC	10.09	Flower_2	-	-	-

Leaf-specific sRNAs:

sRNA sequence	sRNA count (RPM)	sRNA HTS datasets
ATCGGGTTTCGTAGGCTTGGTGCC	61.44	Leaf_1
CTATTTACGTTGTATGTAGCCT	49.75	Leaf_1
ATCCAAGAACATTCTTTGAACACT	43.74	Leaf_1
TATTTACGTTGTATGTAGCCT	27.21	Leaf_1
GTATTTTCGGATGTCGAAGCCT	25.04	Leaf_1
AACACTGTGACCAATTATTAAT	17.2	Leaf_1
CGCACTGAGAGGAGTTGGCATC	16.36	Leaf_1
AGGACAACGTCTTTCTTTGGCACC	15.53	Leaf_1
AATGACATCAGGGACCATCTGA	13.02	Leaf_1
TGATTGTGGAGGGTGGCACTCGATT	12.35	Leaf_1
AAAAGAGTTAGACTGCCT	12.02	Leaf_1
TTCGAGACAGATGACATGCATC	10.18	Leaf_1
ACCGAGACAACAGGTAGAGAACT	10.02	Leaf_1
CGGGTAGGATATCTGGCT	26.48	Leaf_2
CGATAGTAGTACTGGGA	25.08	Leaf_2
GCTTTAGTTTAGTGGTTAGAATCC	13.73	Leaf_2
AAGGGGAACATAAAATAGCCT	14.29	Leaf_2
GCTTTAGTTTAGTGGTTAGAAT	12.61	Leaf_2
GTAGTTTAGTGGTAAGAAT	11.63	Leaf_2
AGGTATGTAGCGCAGTTTGGTAGC	10.79	Leaf_2
GGTGAGGATATCTGGCT	10.09	Leaf_2

Root-specific sRNAs:

sRNA sequence	sRNA count (RPM)	sRNA HTS datasets
TAAAAGCGCAGGGAATTCGGAC	12.08	Root_1
CTTCTACAGTCCGACGATCCGGGGC	11.71	Root_2

Stem-specific sRNAs:

sRNA sequence	Srna count (RPM)	sRNA HTS datasets
TACTAACTTGGCATTGGTGAGAGC	27.23	Stem_1
GAAAATCGAGAAGACTGTCCT	18.19	Stem_1
CCACGGACGAACTATTAAGGCGCC	17.72	Stem_1
GTTTGTGATGACTTACA	16.88	Stem_1
TGTGACGGAGGAACITTCATG	14.92	Stem_1
TCGGCAAGGCTGAAACTTAA	17.81	Stem_1
GGGAGAAGGATTGGCTCTGAGGGT	13.71	Stem_1
TGTACGACAGTCTTTGGACC	14.18	Stem_1
GACCACGACTCTCGGCAA	17.44	Stem_1
AACTTGTGACGCGAATTTGTGCC	12.31	Stem_1
TTGTCTAAGAAATGGTAGATGCCT	11.75	Stem_1
TCGTACCGAGACTACAGGCCT	11.75	Stem_1
AAATGGGTTATCTCTGAAAAGCCT	11.66	Stem_1
ATTTAATTCAGTAGATCTAGCCT	10.07	Stem_1
TGACACGGACTCTCGGCAA	14.27	Stem_1
TTCGTAGGCTCATAAAGTGCT	33.49	Stem_2
TTGGGACTGAAGGGAGCTCCCT	17.22	Stem_2
TAAACCTGTAGAAATAGCAAT	14.4	Stem_2
TGACTAGAGACACAATGTATTCAT	14.4	Stem_2
TGTACGACAGTCTTTGGACC	14.29	Stem_2
TTGTCTAAGAAATGGTAGATGCCT	11.58	Stem_2
TGAAGAGATAAGGTCGTCCACC	12.1	Stem_2
TAGTTATGCTCGGTATTGCT	10.02	Stem_2
CCGAGGCCATTGATATAATCTG	10.02	Stem_2

Table S5 List of 1,047 miRNA candidates identified from *Dendrobium officinale*. The miRNA candidates from *Dendrobium officinale* along with the homologous miRNAs from other species sharing identical sequences according to miRBase (release 21) are provided. The accumulation levels of the miRNA candidates in the sRNA-seq libraries prepared from four organs are also included in this table. For each organ, there are two biological replicates (“Root1” and “Root2”, for example).

miRNA ID	Homologous miRNA ID	Species	sRNA_sequence	Root1	Root2	Flower1	Flower2	Stem1	Stem2	Leaf1	Leaf2
dof-miR-1	hsa-miR-320a	Homo sapiens	AAAAGCTGGGTTGAGAGGGCGA	0	0	0	0.36	2.7	0.63	0	0
	mmu-miR-320-3p	Mus musculus		0	0	0	0.36	2.7	0.63	0	0
	rno-miR-320-3p	Rattus norvegicus		0	0	0	0.36	2.7	0.63	0	0
	bta-miR-320a	Bos taurus		0	0	0	0.36	2.7	0.63	0	0
	chi-miR-320-3p	Capra hircus		0	0	0	0.36	2.7	0.63	0	0
	cgr-miR-320a	Cricetulus griseus		0	0	0	0.36	2.7	0.63	0	0
	ggo-miR-320a	Gorilla gorilla		0	0	0	0.36	2.7	0.63	0	0
	ppy-miR-320a	Pongo pygmaeus		0	0	0	0.36	2.7	0.63	0	0
	mml-miR-320a	Macaca mulatta		0	0	0	0.36	2.7	0.63	0	0
	cfa-miR-320	Canis familiaris		0	0	0	0.36	2.7	0.63	0	0
	ptr-miR-320a	Pan troglodytes		0	0	0	0.36	2.7	0.63	0	0
dof-miR-2	ssc-miR-320	Sus scrofa	AAAAGCTGGGTTGAGAGGGCGAA	0	0	0.37	0.36	0.37	0.21	0	0
dof-miR-3	hsa-miR-548k	Homo sapiens	AAAAGTACTTGCGGATTTTGCT	0	0	0	0	0.19	0	0	0
	ptr-miR-548k	Pan troglodytes		0	0	0	0	0.19	0	0	0
dof-miR-4	dre-miR-93	Danio rerio	AAAAGTGCTGTTTGTGCAGGTA	0	0	0.37	0.18	0	0	0	0
dof-miR-5	ssa-miR-93a-5p	Salmo salar	AAAAGTGCTGTTTGTGCAGGTAG	0	0	0.18	0.36	0	0	0.17	0
	ccr-miR-93	Cyprinus carpio		0	0	0.18	0.36	0	0	0.17	0
dof-miR-6	hsa-miR-495-3p	Homo sapiens	AAACAAACATGGTGCACTTCTT	0.2	0	0	0.18	0	0	0.17	0
	mmu-miR-495-3p	Mus musculus		0.2	0	0	0.18	0	0	0.17	0
	rno-miR-495	Rattus norvegicus		0.2	0	0	0.18	0	0	0.17	0
	chi-miR-495-3p	Capra hircus		0.2	0	0	0.18	0	0	0.17	0
	oar-miR-495-3p	Ovis aries		0.2	0	0	0.18	0	0	0.17	0
	ppy-miR-495	Pongo pygmaeus		0.2	0	0	0.18	0	0	0.17	0
	eca-miR-495	Equus caballus		0.2	0	0	0.18	0	0	0.17	0
	mml-miR-495-3p	Macaca mulatta		0.2	0	0	0.18	0	0	0.17	0
	cfa-miR-495	Canis familiaris		0.2	0	0	0.18	0	0	0.17	0
	ptr-miR-495	Pan troglodytes		0.2	0	0	0.18	0	0	0.17	0
	bta-miR-495	Bos taurus		0.2	0	0	0.18	0	0	0.17	0

dof-miR-7	efu-miR-495	Eptesicus fuscus	AAACAAACATGGTGCACCTCTTT	0	0	0	0.36	0	0	0	0
dof-miR-8	rno-miR-322-3p	Rattus norvegicus	AAACATGAAGCGCTGCAACA	0	0	0	0	0.09	0	0	0
dof-miR-9	rno-miR-543-3p	Rattus norvegicus	AAACATTCGCGGTGCACCTCT	0	0	0	0.18	0	0	0	0
	chi-miR-543-3p	Capra hircus		0	0	0	0.18	0	0	0	0
	ggo-miR-543	Gorilla gorilla		0	0	0	0.18	0	0	0	0
dof-miR-10	oar-miR-543-3p	Ovis aries	AAACATTCGCGGTGCACCTCTTT	0	0	0.18	0	0.09	0	0	0
dof-miR-11	chi-miR-451-5p	Capra hircus	AAACCGTTACCATTACTGA	0.79	2.04	0	0	0.65	0.42	0	0.84
dof-miR-12	hsa-miR-451a	Homo sapiens	AAACCGTTACCATTACTGAGTT	2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	mmu-miR-451a	Mus musculus		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	rno-miR-451-5p	Rattus norvegicus		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	dre-miR-451	Danio rerio		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	xtr-miR-451	Xenopus tropicalis		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	aca-miR-451-5p	Anolis carolinensis		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	ppy-miR-451	Pongo pygmaeus		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	ssc-miR-451	Sus scrofa		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	mml-miR-451	Macaca mulatta		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
	ptr-miR-451	Pan troglodytes		2.18	11.2	0	0.18	5.5	2.3	3.34	4.06
cfa-miR-451	Canis familiaris	2.18	11.2	0	0.18	5.5	2.3	3.34	4.06		
dof-miR-13	gga-miR-451	Gallus gallus	AAACCGTTACCATTACTGAGTTT	2.97	21.13	0.18	0	1.49	0.83	6.68	8.27
	oan-miR-451	Ornithorhynchus anatinus		2.97	21.13	0.18	0	1.49	0.83	6.68	8.27
	oha-miR-451-??	Ophiophagus hannah		2.97	21.13	0.18	0	1.49	0.83	6.68	8.27
	tgu-miR-451	Taeniopygia guttata		2.97	21.13	0.18	0	1.49	0.83	6.68	8.27
	bta-miR-451	Bos taurus		2.97	21.13	0.18	0	1.49	0.83	6.68	8.27
dof-miR-14	rgl-miR5139	Rehmannia glutinosa	AAACCTGGCTCTGATACCA	8.52	4.07	13.6	5.77	5.69	2.3	2.17	9.81
dof-miR-15	cfa-miR-106a	Canis familiaris	AAAGTGCTTACAGTGCAGGTAG	0	0	0	0	0	0.1	0	0
dof-miR-16	hsa-miR-148a-5p	Homo sapiens	AAAGTTCTGAGACACTCCGACT	0	0	0	0	0.09	0	0	0
	mmu-miR-148a-5p	Mus musculus		0	0	0	0	0.09	0	0	0
	ssc-miR-148a-5p	Sus scrofa		0	0	0	0	0.09	0	0	0
	chi-miR-148a-5p	Capra hircus		0	0	0	0	0.09	0	0	0
	mml-miR-148a-5p	Macaca mulatta		0	0	0	0	0.09	0	0	0
dof-miR-17	fru-miR-216a	Fugu rubripes	AAATCTCAGCTGGCAACTGTGA	0.4	0	0	0	0	0	0.33	0.28
	tni-miR-216a	Tetraodon nigroviridis		0.4	0	0	0	0	0	0.33	0.28
dof-miR-18	mmu-miR-216b-5p	Mus musculus	AAATCTCTGCAGGCAAATGTGA	0	0	0.18	0	0	0	0	0
	hsa-miR-216b-5p	Homo sapiens		0	0	0.18	0	0	0	0	0

	aca-miR-216b-5p	Anolis carolinensis		0	0	0.18	0	0	0	0	0	
	ppy-miR-216b	Pongo pygmaeus		0	0	0.18	0	0	0	0	0	
	rno-miR-216b-5p	Rattus norvegicus		0	0	0.18	0	0	0	0	0	
	eca-miR-216b	Equus caballus		0	0	0.18	0	0	0	0	0	
	mml-miR-216b	Macaca mulatta		0	0	0.18	0	0	0	0	0	
	cfa-miR-216b	Canis familiaris		0	0	0.18	0	0	0	0	0	
	gga-miR-216b	Gallus gallus		0	0	0.18	0	0	0	0	0	
	ptr-miR-216b	Pan troglodytes		0	0	0.18	0	0	0	0	0	
	bta-miR-216b	Bos taurus		0	0	0.18	0	0	0	0	0	
dof-miR-19	chi-miR-338-5p	Capra hircus	AACAATATCCTGGTGCTGAGT	0	0	0	0	0	0.1	0	0	
dof-miR-20	bta-miR-21-3p	Bos taurus	AACAGCAGTCGATGGGCTGTCT	0	0	0	0	0	0	0.17	0	
dof-miR-21	dre-miR-2184	Danio rerio	AACAGTAAGAGTTTATGTGCT	0	0	0	0	0	0	0.17	0	
dof-miR-22	hsa-miR-376c-3p	Homo sapiens	AACATAGAGGAAATTCACGT	0	0	0	0	0	0	0	0.14	
	chi-miR-376c-3p	Capra hircus		0	0	0	0	0	0	0	0	0.14
	tch-miR-376c-3p	Tupaia chinensis		0	0	0	0	0	0	0	0	0.14
	oar-miR-376c-3p	Ovis aries		0	0	0	0	0	0	0	0	0.14
	ppy-miR-376c	Pongo pygmaeus		0	0	0	0	0	0	0	0	0.14
	eca-miR-376c	Equus caballus		0	0	0	0	0	0	0	0	0.14
	mml-miR-376c-3p	Macaca mulatta		0	0	0	0	0	0	0	0	0.14
	ptr-miR-376c	Pan troglodytes		0	0	0	0	0	0	0	0	0.14
dof-miR-23	chi-miR-181c-5p	Capra hircus	AACATTCAACCTGTCGGTGAG	0	0	0	0	0.09	0	0	0	
dof-miR-24	hsa-miR-181c-5p	Homo sapiens	AACATTCAACCTGTCGGTGAGT	0	0	0	0	0.19	0	0	0	
	mmu-miR-181c-5p	Mus musculus		0	0	0	0	0.19	0	0	0	
	rno-miR-181c-5p	Rattus norvegicus		0	0	0	0	0.19	0	0	0	
	ssc-miR-181c	Sus scrofa		0	0	0	0	0.19	0	0	0	
	mml-miR-181c-5p	Macaca mulatta		0	0	0	0	0.19	0	0	0	
	ptr-miR-181c	Pan troglodytes		0	0	0	0	0.19	0	0	0	
	ggo-miR-181c	Gorilla gorilla		0	0	0	0	0.19	0	0	0	
	ppa-miR-181c	Pan paniscus		0	0	0	0	0.19	0	0	0	
	tch-miR-181c-5p	Tupaia chinensis		0	0	0	0	0.19	0	0	0	
	cgr-miR-181c-5p	Cricetulus griseus		0	0	0	0	0.19	0	0	0	
	ppy-miR-181c	Pongo pygmaeus		0	0	0	0	0.19	0	0	0	
dof-miR-25	cfa-miR-181c	Canis familiaris	AACATTCAACCTGTCGGTGAGTT	0	0	0.18	0	0.56	0	0	0	
dof-miR-26	ola-miR-181a-5p	Oryzias latipes	AACATTCAACGCTGTCGGT	0	0	0.18	0	0	0	0	0	

dof-miR-32	oan-miR-181b-5p	Ornithorhynchus anatinus	AACATTCATTGCTGTCGGTGG	0	0	0	0.18	0	0	0	0
	ccr-miR-181b	Cyprinus carpio		0	0	0	0.18	0	0	0	0
	cgr-miR-181b-5p	Cricetulus griseus		0	0	0	0.18	0	0	0	0
dof-miR-33	gga-miR-181b-5p	Gallus gallus	AACATTCATTGCTGTCGGTGGG	0.2	0.25	0	0	0.09	0	0.17	0
	dre-miR-181b-5p	Danio rerio		0.2	0.25	0	0	0.09	0	0.17	0
	fru-miR-181b	Fugu rubripes		0.2	0.25	0	0	0.09	0	0.17	0
	tmi-miR-181b	Tetraodon nigroviridis		0.2	0.25	0	0	0.09	0	0.17	0
	xtr-miR-181b	Xenopus tropicalis		0.2	0.25	0	0	0.09	0	0.17	0
	ssa-miR-181c-5p	Salmo salar		0.2	0.25	0	0	0.09	0	0.17	0
	ipu-miR-181b	Ictalurus punctatus		0.2	0.25	0	0	0.09	0	0.17	0
aca-miR-181b	Anolis carolinensis	0.2	0.25	0	0	0.09	0	0.17	0		
dof-miR-34	hsa-miR-181b-5p	Homo sapiens	AACATTCATTGCTGTCGGTGGGT	0	0.25	0.18	1.44	0.28	0	0.5	0
	mmu-miR-181b-5p	Mus musculus		0	0.25	0.18	1.44	0.28	0	0.5	0
	rno-miR-181b-5p	Rattus norvegicus		0	0.25	0.18	1.44	0.28	0	0.5	0
	ptr-miR-181b	Pan troglodytes		0	0.25	0.18	1.44	0.28	0	0.5	0
	ppy-miR-181b	Pongo pygmaeus		0	0.25	0.18	1.44	0.28	0	0.5	0
	mdo-miR-181b-5p	Monodelphis domestica		0	0.25	0.18	1.44	0.28	0	0.5	0
	chi-miR-181b-5p	Capra hircus		0	0.25	0.18	1.44	0.28	0	0.5	0
	tch-miR-181b-5p	Tupaia chinensis		0	0.25	0.18	1.44	0.28	0	0.5	0
	oha-miR-181b-5p	Ophiophagus hannah		0	0.25	0.18	1.44	0.28	0	0.5	0
eca-miR-181b	Equus caballus	0	0.25	0.18	1.44	0.28	0	0.5	0		
dof-miR-35	ssc-miR-181b	Sus scrofa	AACATTCATTGCTGTCGGTGGGTT	0	0	0.18	0.72	0.28	0.1	0.33	0.14
	mml-miR-181b-5p	Macaca mulatta		0	0	0.18	0.72	0.28	0.1	0.33	0.14
	ggo-miR-181b	Gorilla gorilla		0	0	0.18	0.72	0.28	0.1	0.33	0.14
	lla-miR-181b	Lagothrix lagotricha		0	0	0.18	0.72	0.28	0.1	0.33	0.14
	mne-miR-181b	Macaca nemestrina		0	0	0.18	0.72	0.28	0.1	0.33	0.14
	ppa-miR-181b	Pan paniscus		0	0	0.18	0.72	0.28	0.1	0.33	0.14
	bta-miR-181b	Bos taurus		0	0	0.18	0.72	0.28	0.1	0.33	0.14
	hhi-miR-181b	Hippoglossus hippoglossus		0	0	0.18	0.72	0.28	0.1	0.33	0.14
	ola-miR-181b-5p	Oryzias latipes		0	0	0.18	0.72	0.28	0.1	0.33	0.14
tgu-miR-181b-5p	Taeniopygia guttata	0	0	0.18	0.72	0.28	0.1	0.33	0.14		
dof-miR-36	efu-miR-181e	Eptesicus fuscus	AACATTCATTGCTGTCGGTGGGTTT	0	0.25	0	0	0.09	0	0	0
dof-miR-37	lva-miR-2003-5p	Lytechinus variegatus	AACCCGTAAGGTCTTAACCTTGT	0	0	0	0	0	0	0.17	0
dof-miR-38	mdo-miR-100-5p	Monodelphis domestica	AACCCGTAGATCCGAACCTTGT	2.77	5.09	4.41	9.73	3.17	4.07	6.68	1.82

	chi-miR-100-5p	Capra hircus		2.77	5.09	4.41	9.73	3.17	4.07	6.68	1.82
	pmi-miR-100-5p	Patiria miniata		2.77	5.09	4.41	9.73	3.17	4.07	6.68	1.82
	ccr-miR-100	Cyprinus carpio		2.77	5.09	4.41	9.73	3.17	4.07	6.68	1.82
	sha-miR-100	Sarcophilus harrisii		2.77	5.09	4.41	9.73	3.17	4.07	6.68	1.82
	cgr-miR-100-5p	Cricetulus griseus		2.77	5.09	4.41	9.73	3.17	4.07	6.68	1.82
	tgu-miR-100-5p	Taeniopygia guttata		2.77	5.09	4.41	9.73	3.17	4.07	6.68	1.82
dof-miR-39	hsa-miR-100-5p	Homo sapiens	AACCCGTAGATCCGAACITGTG	5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	mmu-miR-100-5p	Mus musculus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	rno-miR-100-5p	Rattus norvegicus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	gga-miR-100-5p	Gallus gallus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	aga-miR-100	Anopheles gambiae		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	dre-miR-100-5p	Danio rerio		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	ggo-miR-100	Gorilla gorilla		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	age-miR-100	Ateles geoffroyi		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	ppa-miR-100	Pan paniscus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	ppy-miR-100	Pongo pygmaeus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	ptr-miR-100	Pan troglodytes		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	mml-miR-100-5p	Macaca mulatta		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	sla-miR-100	Saguinus labiatus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	lla-miR-100	Lagothrix lagotricha		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	fru-miR-100	Fugu rubripes		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	tmi-miR-100	Tetraodon nigroviridis		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	xtr-miR-100	Xenopus tropicalis		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	ame-miR-100	Apis mellifera		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	oan-miR-100-5p	Ornithorhynchus anatinus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	tch-miR-100-5p	Tupaia chinensis		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	bbe-miR-100-5p	Branchiostoma belcheri		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	ssa-miR-100a-5p	Salmo salar		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	ipu-miR-100	Ictalurus punctatus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	mse-miR-100	Manduca sexta		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	pma-miR-100a-5p	Petromyzon marinus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	aca-miR-100	Anolis carolinensis		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	nvi-miR-100	Nasonia vitripennis		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	bmo-miR-100	Bombyx mori		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38

	eca-miR-100	Equus caballus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	ssc-miR-100	Sus scrofa		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	bma-miR-100b	Brugia malayi		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	aae-miR-100	Aedes aegypti		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	cqu-miR-100-5p	Culex quinquefasciatus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	bta-miR-100	Bos taurus		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	lgi-miR-100	Lottia gigantea		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
	sko-miR-100	Saccoglossus kowalevskii		5.15	4.58	7.53	10.99	14.55	24.21	9.85	2.38
dof-miR-40	isc-miR-100	Ixodes scapularis	AACCCGTAGATCCGAACCTTGTGT	0	0.51	1.65	3.6	0.75	1.88	1.5	0.42
	bfl-miR-100-5p	Branchiostoma floridae		0	0.51	1.65	3.6	0.75	1.88	1.5	0.42
	dpu-miR-100	Daphnia pulex		0	0.51	1.65	3.6	0.75	1.88	1.5	0.42
dof-miR-41	prd-miR-100-5p	Panagrellus redivivus	AACCCGTAGATCCGAACCTTGTGTT	0	0	0.18	0	0	0	0	0
	asu-miR-100a-5p	Ascaris suum		0	0	0.18	0	0	0	0	0
dof-miR-42	oar-miR-99a	Ovis aries	AACCCGTAGATCCGATCTTG	0	0	0.18	0.72	0.19	0	0	0.28
dof-miR-43	bta-miR-99a-5p	Bos taurus	AACCCGTAGATCCGATCTTGT	4.16	1.02	11.39	17.66	1.31	0.21	2.84	2.1
	oan-miR-99-5p	Ornithorhynchus anatinus		4.16	1.02	11.39	17.66	1.31	0.21	2.84	2.1
	chi-miR-99a-5p	Capra hircus		4.16	1.02	11.39	17.66	1.31	0.21	2.84	2.1
	ccr-miR-99	Cyprinus carpio		4.16	1.02	11.39	17.66	1.31	0.21	2.84	2.1
	cgr-miR-99a-5p	Cricetulus griseus		4.16	1.02	11.39	17.66	1.31	0.21	2.84	2.1
	tgu-miR-99-5p	Taeniopygia guttata		4.16	1.02	11.39	17.66	1.31	0.21	2.84	2.1
	cfa-miR-99a	Canis familiaris		4.16	1.02	11.39	17.66	1.31	0.21	2.84	2.1
dof-miR-44	hsa-miR-99a-5p	Homo sapiens	AACCCGTAGATCCGATCTTGTG	0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	mmu-miR-99a-5p	Mus musculus		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	rno-miR-99a-5p	Rattus norvegicus		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	gga-miR-99a-5p	Gallus gallus		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	dre-miR-99	Danio rerio		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	mml-miR-99a-5p	Macaca mulatta		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	ptr-miR-99a	Pan troglodytes		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	ggo-miR-99a	Gorilla gorilla		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	ppy-miR-99a	Pongo pygmaeus		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	lla-miR-99a	Lagothrix lagotricha		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	mne-miR-99a	Macaca nemestrina		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	ppa-miR-99a	Pan paniscus		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14
	xtr-miR-99	Xenopus tropicalis		0.4	0.51	4.04	5.77	0.19	0	2.17	0.14

	stu-miR390-5p	Solanum tuberosum		0	0	0	0	0	0	0	0	0.28
	nta-miR390a	Nicotiana tabacum		0	0	0	0	0	0	0	0	0.28
	gma-miR390d	Glycine max		0	0	0	0	0	0	0	0	0.28
	gma-miR390b-5p	Glycine max		0	0	0	0	0	0	0	0	0.28
dof-miR-52	ath-miR390a-5p	Arabidopsis thaliana	AAGCTCAGGAGGGATAGCGCC	220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ath-miR390b-5p	Arabidopsis thaliana		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	osa-miR390-5p	Oryza sativa		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ptc-miR390a	Populus trichocarpa		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ptc-miR390b	Populus trichocarpa		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ptc-miR390c	Populus trichocarpa		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ptc-miR390d-5p	Populus trichocarpa		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ppt-miR390a	Physcomitrella patens		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ppt-miR390b	Physcomitrella patens		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	mtr-miR390	Medicago truncatula		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ghr-miR390a	Gossypium hirsutum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ghr-miR390b	Gossypium hirsutum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ghr-miR390c	Gossypium hirsutum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	bna-miR390a	Brassica napus		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	bna-miR390b	Brassica napus		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	bna-miR390c	Brassica napus		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	vvi-miR390	Vitis vinifera		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	sly-miR390b-5p	Solanum lycopersicum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	bra-miR390-5p	Brassica rapa		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ata-miR390-5p	Aegilops tauschii		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	ppe-miR390	Prunus persica		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	cpa-miR390a	Carica papaya		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	cpa-miR390b	Carica papaya		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	atr-miR390.2	Amborella trichopoda		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	lja-miR390a-5p	Lotus japonicus		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	lja-miR390b-5p	Lotus japonicus		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	hex-miR390a	Helianthus exilis		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
	hex-miR390b	Helianthus exilis		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09	
mdm-miR390a	Malus domestica	220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09			
mdm-miR390b	Malus domestica	220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09			

	mdm-miR390c	Malus domestica		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	mdm-miR390d	Malus domestica		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	mdm-miR390e	Malus domestica		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	mdm-miR390f	Malus domestica		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	cme-miR390d	Cucumis melo		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	cme-miR390a	Cucumis melo		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	cme-miR390c	Cucumis melo		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	lus-miR390a	Linum usitatissimum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	lus-miR390b	Linum usitatissimum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	lus-miR390c	Linum usitatissimum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	lus-miR390d	Linum usitatissimum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	nta-miR390b	Nicotiana tabacum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	nta-miR390c	Nicotiana tabacum		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	gma-miR390f	Glycine max		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	gma-miR390g	Glycine max		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	tcc-miR390a	Theobroma cacao		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	tcc-miR390b	Theobroma cacao		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	bdi-miR390a-5p	Brachypodium distachyon		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	cme-miR390b	Cucumis melo		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	zma-miR390a-5p	Zea mays		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	zma-miR390b-5p	Zea mays		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	csi-miR390	Citrus sinensis		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	rco-miR390a	Ricinus communis		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	rco-miR390b	Ricinus communis		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	aly-miR390a-5p	Arabidopsis lyrata		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	aly-miR390b-5p	Arabidopsis lyrata		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	gma-miR390a-5p	Glycine max		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
	sbi-miR390	Sorghum bicolor		220.63	3.56	31.05	40.36	1.68	4.28	27.71	32.09
dof-miR-53	cca-miR390	Cynara cardunculus	AAGCTCAGGAGGGATAGCGTC	0.2	0	0	0	0	0	0	0
dof-miR-54	bta-miR-423-3p	Bos taurus	AAGCTCGGTCTGAGGCCCTCAGT	0	0	0	0	0.09	0	0	0
dof-miR-55	ola-miR-22	Oryzias latipes	AAGCTGCCAGCTGAAGAACTG	0.2	0	0.18	0	0	0	0	0.14
dof-miR-56	dre-miR-22a-3p	Danio rerio	AAGCTGCCAGCTGAAGAACTGT	0.59	1.02	0.73	3.06	0	0	1.5	0.56
	fru-miR-22a	Fugu rubripes		0.59	1.02	0.73	3.06	0	0	1.5	0.56
	tmi-miR-22a	Tetraodon nigroviridis		0.59	1.02	0.73	3.06	0	0	1.5	0.56

	ssa-miR-22a-3p	Salmo salar		0.59	1.02	0.73	3.06	0	0	1.5	0.56
	ipu-miR-22a	Ictalurus punctatus		0.59	1.02	0.73	3.06	0	0	1.5	0.56
	pol-miR-22-3p	Paralichthys olivaceus		0.59	1.02	0.73	3.06	0	0	1.5	0.56
	ccr-miR-22a	Cyprinus carpio		0.59	1.02	0.73	3.06	0	0	1.5	0.56
dof-miR-57	chi-miR-22-3p	Capra hircus	AAGCTGCCAGTTGAAGAAC	0.59	0	0	0	0.19	0.21	0	0.7
dof-miR-58	bta-miR-22-3p	Bos taurus		0	0	0	0	0.09	0	0	0
	oar-miR-22-3p	Ovis aries	AAGCTGCCAGTTGAAGAACTG	0	0	0	0	0.09	0	0	0
	ggo-miR-22	Gorilla gorilla		0	0	0	0	0.09	0	0	0
dof-miR-59	hsa-miR-22-3p	Homo sapiens		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	mmu-miR-22-3p	Mus musculus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	rno-miR-22-3p	Rattus norvegicus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	age-miR-22	Ateles geoffroyi		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	ppa-miR-22	Pan paniscus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	lca-miR-22	Lemur catta		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	mml-miR-22	Macaca mulatta		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	ppy-miR-22	Pongo pygmaeus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	ptr-miR-22	Pan troglodytes		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	sla-miR-22	Saguinus labiatus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	lla-miR-22	Lagothrix lagotricha		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	mne-miR-22	Macaca nemestrina		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	xtr-miR-22-3p	Xenopus tropicalis		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	oan-miR-22-3p	Ornithorhynchus anatinus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	gga-miR-22-3p	Gallus gallus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	tch-miR-22-3p	Tupaia chinensis		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	oha-miR-22a	Ophiophagus hannah		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	aja-miR-22	Artibeus jamaicensis		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	cgr-miR-22-3p	Cricetulus griseus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
	ssc-miR-22-3p	Sus scrofa		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4
eca-miR-22	Equus caballus		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4	
cfa-miR-22	Canis familiaris		0.4	1.02	0.18	1.98	15.11	3.34	1.34	1.4	
dof-miR-60	chi-miR-28-5p	Capra hircus		0	0	0.37	1.26	0.47	0.21	0	0
	cgr-miR-28-5p	Cricetulus griseus	AAGGAGCTCACAGTCTATTGA	0	0	0.37	1.26	0.47	0.21	0	0
dof-miR-61	cgr-miR-1839-5p	Cricetulus griseus	AAGGTAGATAGAACAGGTCTTGT	0	0	0	0	0.28	0	0	0
dof-miR-62	ipu-miR-2188	Ictalurus punctatus	AAGGTCCAACCTCACATGTCC	1.58	0.51	0	0	0	0	1.5	0.28

	dre-miR-2188-5p	Danio rerio		1.58	0.51	0	0	0	0	1.5	0.28
dof-miR-63	ssa-miR-2188-5p	Salmo salar	AAGGTCCAACCTCACATGTCCT	1.19	0.51	0	0	0	0	3.51	0.42
	gga-miR-2188-5p	Gallus gallus		1.19	0.51	0	0	0	0	3.51	0.42
	tgu-miR-2188-5p	Taeniopygia guttata		1.19	0.51	0	0	0	0	3.51	0.42
dof-miR-64	hsa-miR-369-3p	Homo sapiens	AATAATACATGGTTGATCTTT	0	0	0	0.18	0	0	0.17	0
	mmu-miR-369-3p	Mus musculus		0	0	0	0.18	0	0	0.17	0
	rno-miR-369-3p	Rattus norvegicus		0	0	0	0.18	0	0	0.17	0
	bta-miR-369-3p	Bos taurus		0	0	0	0.18	0	0	0.17	0
	chi-miR-369-3p	Capra hircus		0	0	0	0.18	0	0	0.17	0
	tch-miR-369-3p	Tupaia chinensis		0	0	0	0.18	0	0	0.17	0
	cgr-miR-369-3p	Cricetulus griseus		0	0	0	0.18	0	0	0.17	0
	oar-miR-369-3p	Ovis aries		0	0	0	0.18	0	0	0.17	0
	ssc-miR-369	Sus scrofa		0	0	0	0.18	0	0	0.17	0
	ppy-miR-369-3p	Pongo pygmaeus		0	0	0	0.18	0	0	0.17	0
	eca-miR-369-3p	Equus caballus		0	0	0	0.18	0	0	0.17	0
	mml-miR-369-3p	Macaca mulatta		0	0	0	0.18	0	0	0.17	0
	ptr-miR-369	Pan troglodytes		0	0	0	0.18	0	0	0.17	0
dof-miR-65	mmu-miR-410-3p	Mus musculus	AATATAACACAGATGGCCTGT	0	0	0	0.36	0	0.1	0	0
	hsa-miR-410-3p	Homo sapiens		0	0	0	0.36	0	0.1	0	0
	rno-miR-410-3p	Rattus norvegicus		0	0	0	0.36	0	0.1	0	0
	chi-miR-410-3p	Capra hircus		0	0	0	0.36	0	0.1	0	0
	cgr-miR-410-3p	Cricetulus griseus		0	0	0	0.36	0	0.1	0	0
	oar-miR-410-3p	Ovis aries		0	0	0	0.36	0	0.1	0	0
	ppy-miR-410	Pongo pygmaeus		0	0	0	0.36	0	0.1	0	0
	eca-miR-410	Equus caballus		0	0	0	0.36	0	0.1	0	0
	mml-miR-410-3p	Macaca mulatta		0	0	0	0.36	0	0.1	0	0
	cfa-miR-410	Canis familiaris		0	0	0	0.36	0	0.1	0	0
	ptr-miR-410	Pan troglodytes		0	0	0	0.36	0	0.1	0	0
bta-miR-410	Bos taurus	0	0	0	0.36	0	0.1	0	0		
dof-miR-66	chi-miR-34b-3p	Capra hircus	AATCACTAGTTCCTGCCCATC	0	0	0	0.36	0	0	0	0
dof-miR-67	mmu-miR-154-3p	Mus musculus	AATCATAACGGTTGACCTATT	0	0	0	0	0.09	0	0	0
	hsa-miR-154-3p	Homo sapiens		0	0	0	0	0.09	0	0	0
	rno-miR-154-3p	Rattus norvegicus		0	0	0	0	0.09	0	0	0
	cgr-miR-154-3p	Cricetulus griseus		0	0	0	0	0.09	0	0	0

	mml-miR-154-3p	Macaca mulatta		0	0	0	0	0.09	0	0	0
dof-miR-68	hsa-miR-362-5p	Homo sapiens	AATCCTTGGAACCTAGGTGTGAGT	0	0	0	0.54	0.09	0	0	0
	chi-miR-362-5p	Capra hircus		0	0	0	0.54	0.09	0	0	0
	oar-miR-362	Ovis aries		0	0	0	0.54	0.09	0	0	0
	ppy-miR-362-5p	Pongo pygmaeus		0	0	0	0.54	0.09	0	0	0
	eca-miR-362-5p	Equus caballus		0	0	0	0.54	0.09	0	0	0
	mml-miR-362-5p	Macaca mulatta		0	0	0	0.54	0.09	0	0	0
	bta-miR-362-5p	Bos taurus		0	0	0	0.54	0.09	0	0	0
	cfa-miR-362	Canis familiaris		0	0	0	0.54	0.09	0	0	0
dof-miR-69	ggo-miR-487b	Gorilla gorilla	AATCGTACAGGGTCATCCACT	0	0	0	0	0	0	0	0.14
dof-miR-70	hsa-miR-487b-3p	Homo sapiens	AATCGTACAGGGTCATCCACTT	0	0	0	0	0.09	0	0	0
	mmu-miR-487b-3p	Mus musculus		0	0	0	0	0.09	0	0	0
	rno-miR-487b-3p	Rattus norvegicus		0	0	0	0	0.09	0	0	0
	bta-miR-487b	Bos taurus		0	0	0	0	0.09	0	0	0
	chi-miR-487b-3p	Capra hircus		0	0	0	0	0.09	0	0	0
	oar-miR-487b-3p	Ovis aries		0	0	0	0	0.09	0	0	0
	ppy-miR-487b	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	eca-miR-487b	Equus caballus		0	0	0	0	0.09	0	0	0
	mml-miR-487b-3p	Macaca mulatta		0	0	0	0	0.09	0	0	0
	cfa-miR-487b	Canis familiaris		0	0	0	0	0.09	0	0	0
	ptr-miR-487b	Pan troglodytes		0	0	0	0	0.09	0	0	0
dof-miR-71	mmu-miR-425-5p	Mus musculus	AATGACACGATCACTCCCGTTGA	0	0	0	0	0.37	0	0.17	0
	hsa-miR-425-5p	Homo sapiens		0	0	0	0	0.37	0	0.17	0
	xtr-miR-425-5p	Xenopus tropicalis		0	0	0	0	0.37	0	0.17	0
	mdo-miR-425-5p	Monodelphis domestica		0	0	0	0	0.37	0	0.17	0
	rno-miR-425-5p	Rattus norvegicus		0	0	0	0	0.37	0	0.17	0
	oan-miR-425-5p	Ornithorhynchus anatinus		0	0	0	0	0.37	0	0.17	0
	chi-miR-425-5p	Capra hircus		0	0	0	0	0.37	0	0.17	0
	tch-miR-425-5p	Tupaia chinensis		0	0	0	0	0.37	0	0.17	0
	cgr-miR-425-5p	Cricetulus griseus		0	0	0	0	0.37	0	0.17	0
	ppy-miR-425	Pongo pygmaeus		0	0	0	0	0.37	0	0.17	0
	ssc-miR-425-5p	Sus scrofa		0	0	0	0	0.37	0	0.17	0
	mml-miR-425	Macaca mulatta		0	0	0	0	0.37	0	0.17	0
	cfa-miR-425	Canis familiaris		0	0	0	0	0.37	0	0.17	0

	ptr-miR-425	Pan troglodytes		0	0	0	0	0.37	0	0.17	0
dof-miR-72	ssa-miR-731-5p	Salmo salar	AATGACACGTTTTCTCCCGGATT	0.2	0	0	0.36	0	0	0.5	0.14
dof-miR-73	hsa-miR-501-3p	Homo sapiens	AATGCACCCGGGAAGGATTCT	0	0	0	0	0.47	0	0	0
	ptr-miR-501	Pan troglodytes		0	0	0	0	0.47	0	0	0
dof-miR-74	hsa-miR-502-3p	Homo sapiens	AATGCACCTGGGAAGGATTCA	0	0	0	0	0.28	0	0	0
	ggo-miR-502a	Gorilla gorilla		0	0	0	0	0.28	0	0	0
	ppy-miR-501-3p	Pongo pygmaeus		0	0	0	0	0.28	0	0	0
	ppy-miR-502-3p	Pongo pygmaeus		0	0	0	0	0.28	0	0	0
	eca-miR-502-3p	Equus caballus		0	0	0	0	0.28	0	0	0
	mml-miR-502-3p	Macaca mulatta		0	0	0	0	0.28	0	0	0
	cfa-miR-502	Canis familiaris		0	0	0	0	0.28	0	0	0
	bta-miR-502a	Bos taurus		0	0	0	0	0.28	0	0	0
dof-miR-75	hme-miR-263a	Heliconius melpomene	AATGGCACTGGAAGAATTCACGG	0	0	0	0	0	0	0.33	0
	aae-miR-263a-5p	Aedes aegypti		0	0	0	0	0	0	0.33	0
	cqu-miR-263	Culex quinquefasciatus		0	0	0	0	0	0	0.33	0
dof-miR-76	dme-miR-263a-5p	Drosophila melanogaster	AATGGCACTGGAAGAATTCACGGG	0	0	0	0	0	0	0.5	0
	mse-miR-263a	Manduca sexta		0	0	0	0	0	0	0.5	0
	dvi-miR-263a-5p	Drosophila virilis		0	0	0	0	0	0	0.5	0
	tca-miR-263a-5p	Tribolium castaneum		0	0	0	0	0	0	0.5	0
dof-miR-77	ptc-miR475a-5p	Populus trichocarpa	AATGGCCATTGTAAGAGTAGA	0	0	0.18	0	0	0	0	0
	ptc-miR475b-5p	Populus trichocarpa		0	0	0.18	0	0	0	0	0
	ptc-miR475d-5p	Populus trichocarpa		0	0	0.18	0	0	0	0	0
dof-miR-78	rno-miR-409a-3p	Rattus norvegicus	AATGTTGCTCGGTGAACCCC	0	0	0	0	0	0.1	0	0
dof-miR-79	rno-miR-363-3p	Rattus norvegicus	AATTGCACGGTATCCATCTGT	0	0	0	0	0.84	0	0.17	0
	xtr-miR-363-3p	Xenopus tropicalis		0	0	0	0	0.84	0	0.17	0
	oan-miR-363-3p	Ornithorhynchus anatinus		0	0	0	0	0.84	0	0.17	0
	aca-miR-363-3p	Anolis carolinensis		0	0	0	0	0.84	0	0.17	0
	tgu-miR-363-3p	Taeniopygia guttata		0	0	0	0	0.84	0	0.17	0
dof-miR-80	hsa-miR-363-3p	Homo sapiens	AATTGCACGGTATCCATCTGTA	0	0	0	0.18	0.47	0.1	0	0.14
	mmu-miR-363-3p	Mus musculus		0	0	0	0.18	0.47	0.1	0	0.14
	dre-miR-363-3p	Danio rerio		0	0	0	0.18	0.47	0.1	0	0.14
	tch-miR-363-3p	Tupaia chinensis		0	0	0	0.18	0.47	0.1	0	0.14
	ccr-miR-363	Cyprinus carpio		0	0	0	0.18	0.47	0.1	0	0.14
	ppy-miR-363	Pongo pygmaeus		0	0	0	0.18	0.47	0.1	0	0.14

	eca-miR-363	Equus caballus		0	0	0	0.18	0.47	0.1	0	0.14
	mml-miR-363-3p	Macaca mulatta		0	0	0	0.18	0.47	0.1	0	0.14
dof-miR-81	oha-miR-363-3p	Ophiophagus hannah	AATTGCACGGTATCCATCTGTAA	0	0.25	0	0.18	0.19	0	0.17	0
	ipu-miR-363	Ictalurus punctatus		0	0.25	0	0.18	0.19	0	0.17	0
	ggo-miR-363	Gorilla gorilla		0	0.25	0	0.18	0.19	0	0.17	0
	ssc-miR-363	Sus scrofa		0	0.25	0	0.18	0.19	0	0.17	0
	cfa-miR-363	Canis familiaris		0	0.25	0	0.18	0.19	0	0.17	0
dof-miR-82	chi-miR-125b-3p	Capra hircus	ACAAGTCAGGCTCTGGGACC	0	0	0	0	0.09	0	0	0
dof-miR-83	rno-miR-125b-2-3p	Rattus norvegicus	ACAAGTCAGGCTCTGGGACCT	0	0.25	0	0	0	0	0	0.14
	gga-miR-125b-3p	Gallus gallus		0	0.25	0	0	0	0	0	0.14
	mml-miR-125b-2-3p	Macaca mulatta		0	0.25	0	0	0	0	0	0.14
	tgu-miR-125-1-3p	Taeniopygia guttata		0	0.25	0	0	0	0	0	0.14
dof-miR-84	hsa-miR-214-3p	Homo sapiens	ACAGCAGGCACAGACAGGCAGT	0	0	0.55	0.72	0	0	0.33	0.14
	mmu-miR-214-3p	Mus musculus		0	0	0.55	0.72	0	0	0.33	0.14
	bta-miR-214	Bos taurus		0	0	0.55	0.72	0	0	0.33	0.14
	oan-miR-214-3p	Ornithorhynchus anatinus		0	0	0.55	0.72	0	0	0.33	0.14
	aja-miR-214	Artibeus jamaicensis		0	0	0.55	0.72	0	0	0.33	0.14
	aca-miR-214-3p	Anolis carolinensis		0	0	0.55	0.72	0	0	0.33	0.14
	eca-miR-214	Equus caballus		0	0	0.55	0.72	0	0	0.33	0.14
	tgu-miR-214-3p	Taeniopygia guttata		0	0	0.55	0.72	0	0	0.33	0.14
	cfa-miR-214	Canis familiaris		0	0	0.55	0.72	0	0	0.33	0.14
dof-miR-85	mdo-miR-199b-3p	Monodelphis domestica	ACAGTAGTCTGCACATTGGTT	0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	oan-miR-199-3p	Ornithorhynchus anatinus		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	chi-miR-199a-3p	Capra hircus		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	chi-miR-199b-3p	Capra hircus		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	chi-miR-199c-3p	Capra hircus		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	tch-miR-199b-3p	Tupaia chinensis		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	tch-miR-199a-3p	Tupaia chinensis		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	ssa-miR-199a-3p	Salmo salar		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	ipu-miR-199a-3p	Ictalurus punctatus		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	oar-miR-199a-3p	Ovis aries		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	ccr-miR-199-3p	Cyprinus carpio		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	sha-miR-199a	Sarcophilus harrisii		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	cgr-miR-199a-3p	Cricetulus griseus		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42

	tgu-miR-199-3p	Taeniopygia guttata		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
	cfa-miR-199	Canis familiaris		0.59	0.25	8.08	11.17	1.87	0.52	1.34	0.42
dof-miR-86	mmu-miR-199a-3p	Mus musculus	ACAGTAGTCTGCACATTGGTTA	0.4	0	1.84	5.41	1.03	0	0.33	0
	hsa-miR-199a-3p	Homo sapiens		0.4	0	1.84	5.41	1.03	0	0.33	0
	hsa-miR-199b-3p	Homo sapiens		0.4	0	1.84	5.41	1.03	0	0.33	0
	mmu-miR-199b-3p	Mus musculus		0.4	0	1.84	5.41	1.03	0	0.33	0
	rno-miR-199a-3p	Rattus norvegicus		0.4	0	1.84	5.41	1.03	0	0.33	0
	bta-miR-199a-3p	Bos taurus		0.4	0	1.84	5.41	1.03	0	0.33	0
	oha-miR-199a-3p	Ophiophagus hannah		0.4	0	1.84	5.41	1.03	0	0.33	0
	pol-miR-199a-3p	Paralichthys olivaceus		0.4	0	1.84	5.41	1.03	0	0.33	0
	ola-miR-199a-3p	Oryzias latipes		0.4	0	1.84	5.41	1.03	0	0.33	0
	ppy-miR-199a-3p	Pongo pygmaeus		0.4	0	1.84	5.41	1.03	0	0.33	0
	eca-miR-199a-3p	Equus caballus		0.4	0	1.84	5.41	1.03	0	0.33	0
	eca-miR-199b-3p	Equus caballus		0.4	0	1.84	5.41	1.03	0	0.33	0
	ssc-miR-199a-3p	Sus scrofa		0.4	0	1.84	5.41	1.03	0	0.33	0
	mml-miR-199a-3p	Macaca mulatta		0.4	0	1.84	5.41	1.03	0	0.33	0
	ptr-miR-199a-3p	Pan troglodytes		0.4	0	1.84	5.41	1.03	0	0.33	0
ptr-miR-199b	Pan troglodytes	0.4	0	1.84	5.41	1.03	0	0.33	0		
dof-miR-87	mmu-miR-669a-3p	Mus musculus	ACATAACATACACACACAGTAT	0	0	0	0	0	0	0.33	0
	mmu-miR-669o-3p	Mus musculus		0	0	0	0	0	0	0.33	0
dof-miR-88	ola-miR-140-3p	Oryzias latipes	ACCACAGGGTAGAACCACGG	0	0	0.18	0	0	0	0	0
dof-miR-89	sha-miR-140	Sarcophilus harrisii	ACCACAGGGTAGAACCACGGA	0	0	0.18	0.36	0.09	0	0.17	0
	cfa-miR-140	Canis familiaris		0	0	0.18	0.36	0.09	0	0.17	0
dof-miR-90	chi-miR-140-3p	Capra hircus	ACCACAGGGTAGAACCACGGAC	0	0.51	1.65	2.88	1.49	0.52	0.67	0.14
	ipu-miR-140	Ictalurus punctatus		0	0.51	1.65	2.88	1.49	0.52	0.67	0.14
	pol-miR-140-3p	Paralichthys olivaceus		0	0.51	1.65	2.88	1.49	0.52	0.67	0.14
	cgr-miR-140-3p	Cricetulus griseus		0	0.51	1.65	2.88	1.49	0.52	0.67	0.14
	ggo-miR-140	Gorilla gorilla		0	0.51	1.65	2.88	1.49	0.52	0.67	0.14
dof-miR-91	hsa-miR-181a-2-3p	Homo sapiens	ACCACTGACCGTTGACTGTACC	0	0	0	0	0.09	0	0	0
dof-miR-92	mmu-miR-181c-3p	Mus musculus	ACCATCGACCGTTGAGTGGACC	0	0	0	0.18	0.09	0	0	0
	rno-miR-181c-3p	Rattus norvegicus		0	0	0	0.18	0.09	0	0	0
	chi-miR-181c-3p	Capra hircus		0	0	0	0.18	0.09	0	0	0
	cgr-miR-181c-3p	Cricetulus griseus		0	0	0	0.18	0.09	0	0	0
dof-miR-93	hsa-miR-181a-3p	Homo sapiens	ACCATCGACCGTTGATTGTACC	0	0	0	0	0.19	0	0	0.14

dof-miR-111	hsa-miR-605-3p	Homo sapiens	AGAAGGCACTATGAGATTAGA	0	0	0	0	0.09	0	0	0
dof-miR-112	tcc-miR172d	Theobroma cacao	AGAATCCTGATGATGCTGCAT	0	0	0.18	1.08	0	0	0.17	0
dof-miR-113	stu-miR172c-3p	Solanum tuberosum	AGAATCTTGATGATGCTGC	0	0	0	0	0.09	0	0	0
dof-miR-114	zma-miR172a	Zea mays	AGAATCTTGATGATGCTGCA	0	1.27	0	0	0	0.21	0	0.14
	zma-miR172d-3p	Zea mays		0	1.27	0	0	0	0.21	0	0.14
	zma-miR172b-3p	Zea mays		0	1.27	0	0	0	0.21	0	0.14
	zma-miR172c-3p	Zea mays		0	1.27	0	0	0	0.21	0	0.14
	sbi-miR172c	Sorghum bicolor		0	1.27	0	0	0	0.21	0	0.14
	sbi-miR172a	Sorghum bicolor		0	1.27	0	0	0	0.21	0	0.14
	lja-miR172b	Lotus japonicus		0	1.27	0	0	0	0.21	0	0.14
	lja-miR172c	Lotus japonicus		0	1.27	0	0	0	0.21	0	0.14
	mtr-miR172d-3p	Medicago truncatula		0	1.27	0	0	0	0.21	0	0.14
	mdm-miR172a	Malus domestica		0	1.27	0	0	0	0.21	0	0.14
	mdm-miR172b	Malus domestica		0	1.27	0	0	0	0.21	0	0.14
	mdm-miR172c	Malus domestica		0	1.27	0	0	0	0.21	0	0.14
	gma-miR172f	Glycine max		0	1.27	0	0	0	0.21	0	0.14
dof-miR-115	csi-miR172a-3p	Citrus sinensis	AGAATCTTGATGATGCTGCAT	0	1.27	0	0	0	0.21	0	0.14
	sbi-miR172d	Sorghum bicolor		0	1.27	0	0	0	0.21	0	0.14
	ath-miR172a	Arabidopsis thaliana		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	ath-miR172b-3p	Arabidopsis thaliana		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	osa-miR172a	Oryza sativa		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	osa-miR172d-3p	Oryza sativa		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	gma-miR172a	Glycine max		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	gma-miR172b-3p	Glycine max		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	ptc-miR172a	Populus trichocarpa		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	ptc-miR172b-3p	Populus trichocarpa		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	ptc-miR172c	Populus trichocarpa		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	ptc-miR172f	Populus trichocarpa		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	ata-miR172b-3p	Aegilops tauschii		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	ppe-miR172a-3p	Prunus persica		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	ppe-miR172b	Prunus persica		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
mes-miR172b	Manihot esculenta	6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5		
mes-miR172d	Manihot esculenta	6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5		
stu-miR172b-3p	Solanum tuberosum	6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5		

	bdi-miR172a-3p	Brachypodium distachyon		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	mtr-miR172b	Medicago truncatula		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	mtr-miR172c-3p	Medicago truncatula		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	gma-miR172h-3p	Glycine max		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	aly-miR172a-3p	Arabidopsis lyrata		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	aly-miR172b-3p	Arabidopsis lyrata		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	sly-miR172a	Solanum lycopersicum		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	sly-miR172b	Solanum lycopersicum		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	bra-miR172a	Brassica rapa		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	bra-miR172b-3p	Brassica rapa		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	bol-miR172a	Brassica oleracea		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	bol-miR172b	Brassica oleracea		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
	aqc-miR172a	Aquilegia caerulea		6.14	13.75	2.02	74.78	6.25	15.02	10.35	3.5
dof-miR-116	osa-miR5083	Oryza sativa	AGACTACAATTATCTGATCA	0	0	0	0	0.09	0	0	0
dof-miR-117	mtr-miR319a-5p	Medicago truncatula	AGAGCTTCCTCAGTCCACTC	0.2	0	0.73	0	3.54	4.07	0.5	0.7
dof-miR-118	oar-let-7d	Ovis aries let-7d	AGAGGTAGTAGGTTGCATAG	0	0	0.18	0	0.19	0.1	0	0
dof-miR-119	mdo-let-7d	Monodelphis domestica let-7d	AGAGGTAGTAGGTTGCATAGT	0	0	0	0.18	0.28	0.1	0	0
	aca-let-7d-5p	Anolis carolinensis let-7d-5p		0	0	0	0.18	0.28	0.1	0	0
dof-miR-120	hsa-let-7d-5p	Homo sapiens let-7d-5p	AGAGGTAGTAGGTTGCATAGTT	0.2	0.25	0.92	1.44	1.49	0.1	0	0
	mmu-let-7d-5p	Mus musculus let-7d-5p		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	rno-let-7d-5p	Rattus norvegicus let-7d-5p		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	bta-let-7d	Bos taurus let-7d		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	oan-let-7d-5p	Ornithorhynchus anatinus let-7d-5p		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	chi-let-7d-5p	Capra hircus let-7d-5p		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	oha-let-7d-5p	Ophiophagus hannah let-7d-5p		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	ssc-let-7d-5p	Sus scrofa let-7d-5p		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	cgr-let-7d-5p	Cricetulus griseus let-7d-5p		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	ppy-let-7d	Pongo pygmaeus let-7d		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	eca-let-7d	Equus caballus let-7d		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	tgu-let-7d-5p	Taeniopygia guttata let-7d-5p		0.2	0.25	0.92	1.44	1.49	0.1	0	0
	mml-let-7d	Macaca mulatta let-7d		0.2	0.25	0.92	1.44	1.49	0.1	0	0
ptr-let-7d	Pan troglodytes let-7d	0.2	0.25	0.92	1.44	1.49	0.1	0	0		
dof-miR-121	hsa-miR-377-5p	Homo sapiens	AGAGGTTGCCCTTGGTGAATTC	0	0	0	0.18	0	0	0	0
	mmu-miR-377-5p	Mus musculus		0	0	0	0.18	0	0	0	0

	rno-miR-377-5p	Rattus norvegicus		0	0	0	0.18	0	0	0	0
	mml-miR-377-5p	Macaca mulatta		0	0	0	0.18	0	0	0	0
	cfa-miR-377	Canis familiaris		0	0	0	0.18	0	0	0	0
dof-miR-122	tur-miR-190-5p	Tetranychus urticae	AGATATGTTTGATATTCTTGTT	0	0	0	0	0	0.1	0	0
	bmo-miR-190-5p	Bombyx mori		0	0	0	0	0	0.1	0	0
dof-miR-123	dme-miR-190-5p	Drosophila melanogaster	AGATATGTTTGATATTCTTGTTG	0	0	0	0	0.09	0.42	0	0
	dvi-miR-190-5p	Drosophila virilis		0	0	0	0	0.09	0.42	0	0
	mse-miR-190	Manduca sexta		0	0	0	0	0.09	0.42	0	0
	api-miR-190	Acyrtosiphon pisum		0	0	0	0	0.09	0.42	0	0
	aae-miR-190	Aedes aegypti		0	0	0	0	0.09	0.42	0	0
	cqu-miR-190	Culex quinquefasciatus		0	0	0	0	0.09	0.42	0	0
	aga-miR-190	Anopheles gambiae		0	0	0	0	0.09	0.42	0	0
	dps-miR-190-5p	Drosophila pseudoobscura		0	0	0	0	0.09	0.42	0	0
	dsi-miR-190-5p	Drosophila simulans		0	0	0	0	0.09	0.42	0	0
dof-miR-124	chi-miR-3958-3p	Capra hircus	AGATATTGCACGGTTGATCTCT	0	0	0.18	0.9	0	0	0	0.14
	bta-miR-154c	Bos taurus		0	0	0.18	0.9	0	0	0	0.14
	oar-miR-3958-3p	Ovis aries		0	0	0.18	0.9	0	0	0	0.14
dof-miR-125	ptc-miR167f-3p	Populus trichocarpa	AGATCATGTGGCAGTTTCACC	0	0	0.18	5.05	0	0	0	0
	ptc-miR167g-3p	Populus trichocarpa		0	0	0.18	5.05	0	0	0	0
	ptc-miR167h-3p	Populus trichocarpa		0	0	0.18	5.05	0	0	0	0
	ahy-miR167-3p	Arachis hypogaea		0	0	0.18	5.05	0	0	0	0
dof-miR-126	hsa-miR-369-5p	Homo sapiens	AGATCGACCGTGTATATTCGC	0	0	0	0	0	0.1	0	0
	mmu-miR-369-5p	Mus musculus		0	0	0	0	0	0.1	0	0
	rno-miR-369-5p	Rattus norvegicus		0	0	0	0	0	0.1	0	0
	cgr-miR-369-5p	Cricetulus griseus		0	0	0	0	0	0.1	0	0
	ppy-miR-369-5p	Pongo pygmaeus		0	0	0	0	0	0.1	0	0
	mml-miR-369-5p	Macaca mulatta		0	0	0	0	0	0.1	0	0
dof-miR-127	oan-miR-10b-3p	Ornithorhynchus anatinus	AGATTCGATTCTAGGGGAAT	0	0.25	0	0	0	0	0	0
	aca-miR-10b-3p	Anolis carolinensis		0	0.25	0	0	0	0	0	0
	tgu-miR-10a-3p	Taeniopygia guttata		0	0.25	0	0	0	0	0	0
dof-miR-128	ipu-miR-107b	Ictalurus punctatus	AGCAGCATTGTACAGGGCT	0.2	0	0.55	0	0.84	0.63	0	0.28
dof-miR-129	chi-miR-107-3p	Capra hircus	AGCAGCATTGTACAGGGCTAT	0	0	0.55	0.36	0.47	0.21	0.33	0
	tch-miR-107	Tupaia chinensis		0	0	0.55	0.36	0.47	0.21	0.33	0
	ola-miR-103	Oryzias latipes		0	0	0.55	0.36	0.47	0.21	0.33	0

	ola-miR-107	Oryzias latipes		0	0	0.55	0.36	0.47	0.21	0.33	0
	cfa-miR-107	Canis familiaris		0	0	0.55	0.36	0.47	0.21	0.33	0
dof-miR-130	bta-miR-107	Bos taurus	AGCAGCATTGTACAGGGCTATC	0	0	0	0	0.09	0	0	0
	oan-miR-107-3p	Ornithorhynchus anatinus		0	0	0	0	0.09	0	0	0
	ssa-miR-107-3p	Salmo salar		0	0	0	0	0.09	0	0	0
	ipu-miR-107a	Ictalurus punctatus		0	0	0	0	0.09	0	0	0
	oar-miR-107	Ovis aries		0	0	0	0	0.09	0	0	0
	ccr-miR-107	Cyprinus carpio		0	0	0	0	0.09	0	0	0
	cgr-miR-107	Cricetulus griseus		0	0	0	0	0.09	0	0	0
	aca-miR-107-3p	Anolis carolinensis		0	0	0	0	0.09	0	0	0
dof-miR-131	hsa-miR-107	Homo sapiens	AGCAGCATTGTACAGGGCTATCA	0	0.25	0	0	0.19	0	0	0
	mmu-miR-107-3p	Mus musculus		0	0.25	0	0	0.19	0	0	0
	rno-miR-107-3p	Rattus norvegicus		0	0.25	0	0	0.19	0	0	0
	gga-miR-107-3p	Gallus gallus		0	0.25	0	0	0.19	0	0	0
	dre-miR-107a-3p	Danio rerio		0	0.25	0	0	0.19	0	0	0
	ssc-miR-107	Sus scrofa		0	0.25	0	0	0.19	0	0	0
	mml-miR-107-3p	Macaca mulatta		0	0.25	0	0	0.19	0	0	0
	ptr-miR-107	Pan troglodytes		0	0.25	0	0	0.19	0	0	0
	ggo-miR-107	Gorilla gorilla		0	0.25	0	0	0.19	0	0	0
	ppy-miR-107	Pongo pygmaeus		0	0.25	0	0	0.19	0	0	0
	lla-miR-107	Lagothrix lagotricha		0	0.25	0	0	0.19	0	0	0
	mne-miR-107	Macaca nemestrina		0	0.25	0	0	0.19	0	0	0
	ppa-miR-107	Pan paniscus		0	0.25	0	0	0.19	0	0	0
	tni-miR-107	Tetraodon nigroviridis		0	0.25	0	0	0.19	0	0	0
	xtr-miR-107	Xenopus tropicalis		0	0.25	0	0	0.19	0	0	0
	mdo-miR-107	Monodelphis domestica		0	0.25	0	0	0.19	0	0	0
	oha-miR-107-3p	Ophiophagus hannah		0	0.25	0	0	0.19	0	0	0
	eca-miR-107b	Equus caballus		0	0.25	0	0	0.19	0	0	0
tgu-miR-107	Taeniopygia guttata	0	0.25	0	0	0.19	0	0	0		
dof-miR-132	oar-miR-103	Ovis aries	AGCAGCATTGTACAGGGCTATG	0	0	0.37	1.26	0.56	0.1	0	0
	aca-miR-103-3p	Anolis carolinensis		0	0	0.37	1.26	0.56	0.1	0	0
dof-miR-133	hsa-miR-103a-3p	Homo sapiens	AGCAGCATTGTACAGGGCTATGA	0	0	3.67	5.59	9.05	0.94	0.5	0.42
	mmu-miR-103-3p	Mus musculus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	rno-miR-103-3p	Rattus norvegicus		0	0	3.67	5.59	9.05	0.94	0.5	0.42

	gga-miR-103-3p	Gallus gallus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	dre-miR-103	Danio rerio		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	ssc-miR-103	Sus scrofa		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	age-miR-103	Ateles geoffroyi		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	ggo-miR-103	Gorilla gorilla		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	ppa-miR-103	Pan paniscus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	ppy-miR-103	Pongo pygmaeus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	ptr-miR-103	Pan troglodytes		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	mml-miR-103-3p	Macaca mulatta		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	lla-miR-103	Lagothrix lagotricha		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	mne-miR-103	Macaca nemestrina		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	fru-miR-103	Fugu rubripes		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	tmi-miR-103	Tetraodon nigroviridis		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	fru-miR-107	Fugu rubripes		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	bta-miR-103	Bos taurus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	xtr-miR-103	Xenopus tropicalis		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	mdo-miR-103-3p	Monodelphis domestica		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	oan-miR-103-3p	Ornithorhynchus anatinus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	chi-miR-103-3p	Capra hircus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	tch-miR-103a-3p	Tupaia chinensis		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	oha-miR-103a-3p	Ophiophagus hannah		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	oha-miR-103b-3p	Ophiophagus hannah		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	ssa-miR-103-3p	Salmo salar		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	ipu-miR-103	Ictalurus punctatus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	ccr-miR-103	Cyprinus carpio		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	cgr-miR-103-3p	Cricetulus griseus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	pma-miR-103b-3p	Petromyzon marinus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	eca-miR-107a	Equus caballus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	eca-miR-103	Equus caballus		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	tgu-miR-103-3p	Taeniopygia guttata		0	0	3.67	5.59	9.05	0.94	0.5	0.42
	cfa-miR-103	Canis familiaris		0	0	3.67	5.59	9.05	0.94	0.5	0.42
dof-miR-134	hbr-miR6173	Hevea brasiliensis	AGCCGTAAACGATGGATACT	1.58	15.53	0	3.24	1.03	0.42	2	1.54
dof-miR-135	ccr-miR-222	Cyprinus carpio	AGCTACATCTGGCTACTGGG	0	0	0	0	0	0.1	0	0
dof-miR-136	hsa-miR-222-3p	Homo sapiens	AGCTACATCTGGCTACTGGGT	0	0	0	0	0.47	0	0.17	0

	mmu-miR-222-3p	Mus musculus		0	0	0	0	0.47	0	0.17	0
	rno-miR-222-3p	Rattus norvegicus		0	0	0	0	0.47	0	0.17	0
	bta-miR-222	Bos taurus		0	0	0	0	0.47	0	0.17	0
	oan-miR-222a-3p	Ornithorhynchus anatinus		0	0	0	0	0.47	0	0.17	0
	tch-miR-222-3p	Tupaia chinensis		0	0	0	0	0.47	0	0.17	0
	sha-miR-222	Sarcophilus harrisii		0	0	0	0	0.47	0	0.17	0
	ppy-miR-222	Pongo pygmaeus		0	0	0	0	0.47	0	0.17	0
	eca-miR-222	Equus caballus		0	0	0	0	0.47	0	0.17	0
	mml-miR-222-3p	Macaca mulatta		0	0	0	0	0.47	0	0.17	0
	cfa-miR-222	Canis familiaris		0	0	0	0	0.47	0	0.17	0
dof-miR-137	ssa-miR-222b-3p	Salmo salar	AGCTACATCTGGCTACTGGGTC	0	0	0	0	0.19	0	0	0
	ptr-miR-222	Pan troglodytes		0	0	0	0	0.19	0	0	0
	ggo-miR-222	Gorilla gorilla		0	0	0	0	0.19	0	0	0
	aca-miR-222a-3p	Anolis carolinensis		0	0	0	0	0.19	0	0	0
dof-miR-138	gga-miR-222a	Gallus gallus	AGCTACATCTGGCTACTGGGTCTC	0	0	0	0.18	0.37	0	0.17	0.14
	dre-miR-222a-3p	Danio rerio		0	0	0	0.18	0.37	0	0.17	0.14
	age-miR-222	Ateles geoffroyi		0	0	0	0.18	0.37	0	0.17	0.14
	fru-miR-222	Fugu rubripes		0	0	0	0.18	0.37	0	0.17	0.14
	tmi-miR-222	Tetraodon nigroviridis		0	0	0	0.18	0.37	0	0.17	0.14
	xtr-miR-222	Xenopus tropicalis		0	0	0	0.18	0.37	0	0.17	0.14
	mdo-miR-222a	Monodelphis domestica		0	0	0	0.18	0.37	0	0.17	0.14
	chi-miR-222-3p	Capra hircus		0	0	0	0.18	0.37	0	0.17	0.14
	oha-miR-222a-3p	Ophiophagus hannah		0	0	0	0.18	0.37	0	0.17	0.14
	ssa-miR-222a-3p	Salmo salar		0	0	0	0.18	0.37	0	0.17	0.14
	ssc-miR-222	Sus scrofa		0	0	0	0.18	0.37	0	0.17	0.14
	tgu-miR-222-3p	Taeniopygia guttata		0	0	0	0.18	0.37	0	0.17	0.14
dof-miR-139	cgr-miR-222-3p	Cricetulus griseus	AGCTACATCTGGCTACTGGGTCTCT	0	0	0	0.18	0.56	0.1	0.17	0
dof-miR-140	tch-miR-221-3p	Tupaia chinensis	AGCTACATTGTCTGCTGGGTT	0	0	0	0	0.28	0.31	0.17	0.14
	sha-miR-221	Sarcophilus harrisii		0	0	0	0	0.28	0.31	0.17	0.14
dof-miR-141	bta-miR-221	Bos taurus	AGCTACATTGTCTGCTGGGTTT	0	0	0.37	0	0.65	0.31	0.67	0.14
	oan-miR-221-3p	Ornithorhynchus anatinus		0	0	0.37	0	0.65	0.31	0.67	0.14
	chi-miR-221-3p	Capra hircus		0	0	0.37	0	0.65	0.31	0.67	0.14
	ssa-miR-221-5p	Salmo salar		0	0	0.37	0	0.65	0.31	0.67	0.14
	ipu-miR-221	Ictalurus punctatus		0	0	0.37	0	0.65	0.31	0.67	0.14

	oar-miR-221	Ovis aries		0	0	0.37	0	0.65	0.31	0.67	0.14
	pol-miR-221-3p	Paralichthys olivaceus		0	0	0.37	0	0.65	0.31	0.67	0.14
	aca-miR-221-3p	Anolis carolinensis		0	0	0.37	0	0.65	0.31	0.67	0.14
	cfa-miR-221	Canis familiaris		0	0	0.37	0	0.65	0.31	0.67	0.14
	ssc-miR-221-3p	Sus scrofa		0	0	0.37	0	0.65	0.31	0.67	0.14
dof-miR-142	hsa-miR-221-3p	Homo sapiens	AGCTACATTGTCTGCTGGGTTTC	0.2	0.25	0.18	0	2.33	0.1	0	0
	mmu-miR-221-3p	Mus musculus		0.2	0.25	0.18	0	2.33	0.1	0	0
	rno-miR-221-3p	Rattus norvegicus		0.2	0.25	0.18	0	2.33	0.1	0	0
	gga-miR-221-3p	Gallus gallus		0.2	0.25	0.18	0	2.33	0.1	0	0
	dre-miR-221-3p	Danio rerio		0.2	0.25	0.18	0	2.33	0.1	0	0
	mml-miR-221-3p	Macaca mulatta		0.2	0.25	0.18	0	2.33	0.1	0	0
	ggo-miR-221	Gorilla gorilla		0.2	0.25	0.18	0	2.33	0.1	0	0
	ppy-miR-221	Pongo pygmaeus		0.2	0.25	0.18	0	2.33	0.1	0	0
	ppa-miR-221	Pan paniscus		0.2	0.25	0.18	0	2.33	0.1	0	0
	fru-miR-221	Fugu rubripes		0.2	0.25	0.18	0	2.33	0.1	0	0
	tni-miR-221	Tetraodon nigroviridis		0.2	0.25	0.18	0	2.33	0.1	0	0
	xtr-miR-221	Xenopus tropicalis		0.2	0.25	0.18	0	2.33	0.1	0	0
	mdo-miR-221-3p	Monodelphis domestica		0.2	0.25	0.18	0	2.33	0.1	0	0
	oha-miR-221-3p	Ophiophagus hannah		0.2	0.25	0.18	0	2.33	0.1	0	0
	ola-miR-221	Oryzias latipes		0.2	0.25	0.18	0	2.33	0.1	0	0
	cgr-miR-221-3p	Cricetulus griseus		0.2	0.25	0.18	0	2.33	0.1	0	0
	eca-miR-221	Equus caballus		0.2	0.25	0.18	0	2.33	0.1	0	0
tgu-miR-221-3p	Taeniopygia guttata	0.2	0.25	0.18	0	2.33	0.1	0	0		
ptr-miR-221	Pan troglodytes	0.2	0.25	0.18	0	2.33	0.1	0	0		
dof-miR-143	gma-miR390e	Glycine max	AGCTCAGGAGGGATAGCGCC	1.58	0	0.37	1.26	0	0	0	0.7
dof-miR-144	hsa-miR-423-3p	Homo sapiens	AGCTCGGTCTGAGGCCCTCAGT	0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
	mmu-miR-423-3p	Mus musculus		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
	rno-miR-423-3p	Rattus norvegicus		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
	chi-miR-423-3p	Capra hircus		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
	tch-miR-423-3p	Tupaia chinensis		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
	cgr-miR-423-3p	Cricetulus griseus		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
	ppy-miR-423-3p	Pongo pygmaeus		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
	eca-miR-423-3p	Equus caballus		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
ssc-miR-423-3p	Sus scrofa	0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14		

	mml-miR-423-3p	Macaca mulatta		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
	ptr-miR-423	Pan troglodytes		0.2	0.51	0.18	1.44	1.4	0.31	0.17	0.14
dof-miR-145	ola-miR-1388-5p	Oryzias latipes	AGGACTGTCCAACCTGAGAATG	0	0	0	0	0.09	0	0	0
	dre-miR-1388-5p	Danio rerio		0	0	0	0	0.09	0	0	0
dof-miR-146	ola-miR-144	Oryzias latipes	AGGATATCATCTTATACTGTAA	0	0.25	0	0	0	0	0	0
dof-miR-147	hsa-miR-31-5p	Homo sapiens		0	0	0	0	0.09	0	0	0
	bta-miR-31	Bos taurus	AGGCAAGATGCTGGCATAGCT	0	0	0	0	0.09	0	0	0
	eca-miR-31	Equus caballus		0	0	0	0	0.09	0	0	0
dof-miR-148	pml-miR-31-5p	Patiria miniata		0	0	0	0	0	0	0.17	0
	lva-miR-31-5p	Lytechinus variegatus		0	0	0	0	0	0	0.17	0
	aca-miR-31-5p	Anolis carolinensis	AGGCAAGATGTTGGCATAGCT	0	0	0	0	0	0	0.17	0
	cte-miR-31	Capitella teleta		0	0	0	0	0	0	0.17	0
	lgi-miR-31	Lottia gigantea		0	0	0	0	0	0	0.17	0
	spu-miR-31	Strongylocentrotus purpuratus		0	0	0	0	0	0	0.17	0
dof-miR-149	gma-miR4995	Glycine max	AGGCAGTGGCTTGGTTAAGGG	0	1.02	0	0	0	0	0	0.14
dof-miR-150	mmu-miR-34c-5p	Mus musculus		0	0	2.2	1.44	0	0	0.17	0
	hsa-miR-34c-5p	Homo sapiens		0	0	2.2	1.44	0	0	0.17	0
	rno-miR-34c-5p	Rattus norvegicus		0	0	2.2	1.44	0	0	0.17	0
	gga-miR-34c-5p	Gallus gallus		0	0	2.2	1.44	0	0	0.17	0
	oan-miR-34a-5p	Ornithorhynchus anatinus		0	0	2.2	1.44	0	0	0.17	0
	chi-miR-34c-5p	Capra hircus		0	0	2.2	1.44	0	0	0.17	0
	tch-miR-34c-5p	Tupaia chinensis		0	0	2.2	1.44	0	0	0.17	0
	mdo-miR-34c-5p	Monodelphis domestica	AGGCAGTGTAGTTAGCTGATTGC	0	0	2.2	1.44	0	0	0.17	0
	cgr-miR-34c-5p	Cricetulus griseus		0	0	2.2	1.44	0	0	0.17	0
	ppy-miR-34c-5p	Pongo pygmaeus		0	0	2.2	1.44	0	0	0.17	0
	eca-miR-34c	Equus caballus		0	0	2.2	1.44	0	0	0.17	0
	ssc-miR-34c	Sus scrofa		0	0	2.2	1.44	0	0	0.17	0
	tgu-miR-34b	Taeniopygia guttata		0	0	2.2	1.44	0	0	0.17	0
	mml-miR-34c-5p	Macaca mulatta		0	0	2.2	1.44	0	0	0.17	0
	cfa-miR-34c	Canis familiaris		0	0	2.2	1.44	0	0	0.17	0
dof-miR-151	chi-miR-25-5p	Capra hircus	AGGCGGAGACTTGGGCAATTGCT	0	0	0.18	0.18	0	0	0	0
	cgr-miR-25-5p	Cricetulus griseus		0	0	0.18	0.18	0	0	0	0
dof-miR-152	mmu-miR-185-3p	Mus musculus	AGGGGCTGGCTTTCCTCTGGT	0	0	0	0	0.09	0	0	0
	cgr-miR-185-3p	Cricetulus griseus		0	0	0	0	0.09	0	0	0

	mml-miR-185-3p	Macaca mulatta		0	0	0	0	0.09	0	0	0
dof-miR-153	ssc-miR-296-3p	Sus scrofa	AGGGTTGGGCGGAGGCTTTCC	0	0	0	0.54	0	0	0	0
dof-miR-154	osa-miR171i-5p	Oryza sativa	AGGTATTGGCGTGCTCAATC	22.78	3.82	0.92	0.18	0.09	0.42	20.2	15.83
dof-miR-155	ggo-miR-409	Gorilla gorilla	AGGTTACCCGAGCAACTTTGCA	0	0	0	0	0	0	0.17	0
dof-miR-156	mmu-miR-409-5p	Mus musculus	AGGTTACCCGAGCAACTTTGCAT	0	0.25	0.37	0.54	0.09	0	0.33	0
	hsa-miR-409-5p	Homo sapiens		0	0.25	0.37	0.54	0.09	0	0.33	0
	rno-miR-409a-5p	Rattus norvegicus		0	0.25	0.37	0.54	0.09	0	0.33	0
	chi-miR-409-5p	Capra hircus		0	0.25	0.37	0.54	0.09	0	0.33	0
	oar-miR-409-5p	Ovis aries		0	0.25	0.37	0.54	0.09	0	0.33	0
	ppy-miR-409-5p	Pongo pygmaeus		0	0.25	0.37	0.54	0.09	0	0.33	0
	eca-miR-409-5p	Equus caballus		0	0.25	0.37	0.54	0.09	0	0.33	0
	mml-miR-409-5p	Macaca mulatta		0	0.25	0.37	0.54	0.09	0	0.33	0
bta-miR-409a	Bos taurus	0	0.25	0.37	0.54	0.09	0	0.33	0		
dof-miR-157	cgr-miR-409-5p	Cricetulus griseus	AGGTTACCCGAGCAACTTTGCATC	0	0	0	0	0	0	0.33	0
dof-miR-158	chi-miR-485-3p	Capra hircus	AGTCATACACGGCTCTCTCTCT	0	0	0	0.18	0	0	0	0
dof-miR-159	bta-miR-142-3p	Bos taurus	AGTGTTCCTACTTTATGGATG	0	0	0	0	0.28	0	0	0
	ssa-miR-142a-3p	Salmo salar		0	0	0	0	0.28	0	0	0
dof-miR-160	mmu-miR-669b-5p	Mus musculus	AGTTTTGTGTGCATGTGCATGT	0	0	0	0	0	0	0.17	0
dof-miR-161	mmu-miR-9-3p	Mus musculus	ATAAAGCTAGATAACCGAAAGT	0	0	0	0	0.09	0	0	0
	hsa-miR-9-3p	Homo sapiens		0	0	0	0	0.09	0	0	0
	rno-miR-9a-3p	Rattus norvegicus		0	0	0	0	0.09	0	0	0
	mdo-miR-9a-3p	Monodelphis domestica		0	0	0	0	0.09	0	0	0
	ssa-miR-9a-4-3p	Salmo salar		0	0	0	0	0.09	0	0	0
	ssa-miR-9a-5-3p	Salmo salar		0	0	0	0	0.09	0	0	0
	tgu-miR-9-3p	Taeniopygia guttata		0	0	0	0	0.09	0	0	0
dof-miR-162	chi-miR-655	Capra hircus	ATAATACATGGTTAACCTCTCT	0	0	0	0.18	0	0	0	0
	oar-miR-655-3p	Ovis aries		0	0	0	0.18	0	0	0	0
	bta-miR-655	Bos taurus		0	0	0	0.18	0	0	0	0
dof-miR-163	fru-miR-458	Fugu rubripes	ATAGCTCTTTAAATGGTACTGC	0.2	0	0	0	0	0	0	0.14
dof-miR-164	dre-miR-458-3p	Danio rerio	ATAGCTCTTTGAATGGTACTGC	0	0	0	0.18	0	0	0	0
	oan-miR-458-3p	Ornithorhynchus anatinus		0	0	0	0.18	0	0	0	0
	oha-miR-458-3p	Ophiophagus hannah		0	0	0	0.18	0	0	0	0
	ssa-miR-458-3p	Salmo salar		0	0	0	0.18	0	0	0	0
	ipu-miR-458	Ictalurus punctatus		0	0	0	0.18	0	0	0	0

	aca-miR-458	Anolis carolinensis		0	0	0	0.18	0	0	0	0
	gga-miR-458a-3p	Gallus gallus		0	0	0	0.18	0	0	0	0
dof-miR-165	chi-miR-411a-5p	Capra hircus	ATAGTAGACCGTATAGCGTAC	0	0	0.18	0.18	0	0	0	0
dof-miR-166	ggo-miR-411	Gorilla gorilla	ATAGTAGACCGTATAGCGTACC	0	0	0.18	0.54	0	0	0.17	0
	oar-miR-411a-5p	Ovis aries		0	0	0.18	0.54	0	0	0.17	0
	cfa-miR-411	Canis familiaris		0	0	0.18	0.54	0	0	0.17	0
	bta-miR-411a	Bos taurus		0	0	0.18	0.54	0	0	0.17	0
dof-miR-167	oar-miR-374b	Ovis aries	ATATAATACAACCTGCTAAGT	0	0	0.18	0.54	0.37	0	0	0
dof-miR-168	rno-miR-374-5p	Rattus norvegicus	ATATAATACAACCTGCTAAGTG	0	0	0.18	0	0.09	0.1	0	0
	mmu-miR-374b-5p	Mus musculus		0	0	0.18	0	0.09	0.1	0	0
	hsa-miR-374b-5p	Homo sapiens		0	0	0.18	0	0.09	0.1	0	0
	chi-miR-374b-5p	Capra hircus		0	0	0.18	0	0.09	0.1	0	0
	cgr-miR-374-5p	Cricetulus griseus		0	0	0.18	0	0.09	0.1	0	0
	ggo-miR-374b	Gorilla gorilla		0	0	0.18	0	0.09	0.1	0	0
	eca-miR-374b	Equus caballus		0	0	0.18	0	0.09	0.1	0	0
	ssc-miR-374b-5p	Sus scrofa		0	0	0.18	0	0.09	0.1	0	0
	mml-miR-374b-5p	Macaca mulatta		0	0	0.18	0	0.09	0.1	0	0
	cfa-miR-374b	Canis familiaris		0	0	0.18	0	0.09	0.1	0	0
	ptr-miR-374b	Pan troglodytes		0	0	0.18	0	0.09	0.1	0	0
	bta-miR-374b	Bos taurus		0	0	0.18	0	0.09	0.1	0	0
dof-miR-169	tch-miR-374b-5p	Tupaia chinensis	ATATAATACAACCTGCTAAGTGT	0	0	0.18	0	0	0	0	0
dof-miR-170	mmu-miR-467e-3p	Mus musculus	ATATACATACACACACATAT	0	0	0.18	0	0	0	0	0
dof-miR-171	ggo-miR-421	Gorilla gorilla	ATCAACAGACATTAATTGGGCG	0	0	0	0.18	0	0	0	0
	cfa-miR-421	Canis familiaris		0	0	0	0.18	0	0	0	0
dof-miR-172	hsa-miR-421	Homo sapiens	ATCAACAGACATTAATTGGGCG	0	0	0.18	0	0	0	0	0
	mmu-miR-421-3p	Mus musculus		0	0	0.18	0	0	0	0	0
	chi-miR-421-3p	Capra hircus		0	0	0.18	0	0	0	0	0
	ppy-miR-421	Pongo pygmaeus		0	0	0.18	0	0	0	0	0
	ssc-miR-421-3p	Sus scrofa		0	0	0.18	0	0	0	0	0
	mml-miR-421	Macaca mulatta		0	0	0.18	0	0	0	0	0
	ptr-miR-421	Pan troglodytes		0	0	0.18	0	0	0	0	0
	bta-miR-421	Bos taurus		0	0	0.18	0	0	0	0	0
dof-miR-173	oar-miR-23b	Ovis aries	ATCACATTGCCAGGGATT	0.2	0	0	0.18	0.09	0	0	1.4
dof-miR-174	sha-miR-23b	Sarcophilus harrisii	ATCACATTGCCAGGGATTA	0	0	0	0.18	0	0	0	0.14

	cfa-miR-23b	Canis familiaris		0	0	0	0.18	0	0	0	0.14
dof-miR-175	mmu-miR-23b-3p	Mus musculus	ATCACATTGCCAGGGATTACC	0.2	0	0.92	0.9	0.37	0	0.67	0.28
	hsa-miR-23b-3p	Homo sapiens		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	rno-miR-23b-3p	Rattus norvegicus		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	gga-miR-23b-3p	Gallus gallus		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	xtr-miR-23b	Xenopus tropicalis		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	mdo-miR-23b-3p	Monodelphis domestica		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	chi-miR-23b-3p	Capra hircus		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	ipu-miR-23b	Ictalurus punctatus		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	ccr-miR-23b	Cyprinus carpio		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	cgr-miR-23b-3p	Cricetulus griseus		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	aca-miR-23b-3p	Anolis carolinensis		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	eca-miR-23b	Equus caballus		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	tgu-miR-23-3p	Taeniopygia guttata		0.2	0	0.92	0.9	0.37	0	0.67	0.28
	mml-miR-23b-3p	Macaca mulatta		0.2	0	0.92	0.9	0.37	0	0.67	0.28
dof-miR-176	dre-miR-23b	Danio rerio	ATCACATTGCCAGGGATTACCA	0	0.25	0.18	0.36	0.37	0	0.17	0
	fru-miR-23b	Fugu rubripes		0	0.25	0.18	0.36	0.37	0	0.17	0
	tmi-miR-23b	Tetraodon nigroviridis		0	0.25	0.18	0.36	0.37	0	0.17	0
	ggo-miR-23b	Gorilla gorilla		0	0.25	0.18	0.36	0.37	0	0.17	0
	ssc-miR-23b	Sus scrofa		0	0.25	0.18	0.36	0.37	0	0.17	0
dof-miR-177	ptr-miR-23b	Pan troglodytes	ATCACATTGCCAGGGATTACCAC	0	0	0	0	0.28	0	0	0
	ppy-miR-23b	Pongo pygmaeus		0	0	0	0	0.28	0	0	0
	ppa-miR-23b	Pan paniscus		0	0	0	0	0.28	0	0	0
	bta-miR-23b-3p	Bos taurus		0	0	0	0	0.28	0	0	0
	oha-miR-23b-3p	Ophiophagus hannah		0	0	0	0	0.28	0	0	0
	ola-miR-23b	Oryzias latipes		0	0	0	0	0.28	0	0	0
	pma-miR-23b	Petromyzon marinus		0	0	0	0	0.28	0	0	0
dof-miR-178	ssa-miR-23b-3p	Salmo salar	ATCACATTGCCAGGGATTACCACC	0	0.25	0	0	0	0	0	
dof-miR-179	sha-miR-23a	Sarcophilus harrisii	ATCACATTGCCAGGGATT	0	0	0	0	0.37	0	0	0.14
	cfa-miR-23a	Canis familiaris		0	0	0	0	0.37	0	0	0.14
dof-miR-180	mdo-miR-23a-3p	Monodelphis domestica	ATCACATTGCCAGGGATTTC	0	0	0.18	0	0.28	0	0	
dof-miR-181	hsa-miR-23a-3p	Homo sapiens	ATCACATTGCCAGGGATTCC	0.59	0.51	1.1	0.18	1.03	0.21	0.83	0.28
	mmu-miR-23a-3p	Mus musculus		0.59	0.51	1.1	0.18	1.03	0.21	0.83	0.28
	rno-miR-23a-3p	Rattus norvegicus		0.59	0.51	1.1	0.18	1.03	0.21	0.83	0.28

	ppy-miR-1260b	Pongo pygmaeus		0	0	0	0	0	0	0.17	0		
	bta-miR-1260b	Bos taurus		0	0	0	0	0	0	0.17	0		
dof-miR-186	cgr-miR-1260	Cricetulus griseus	ATCCCACCGTGCCACCA	0	0	0	0.18	0.09	0	0	0		
dof-miR-187	ipu-miR-7550	Ictalurus punctatus	ATCCGGCTCGAAGGACCA	0	0	0	0	0	0	0	0.14		
	mse-miR-2779	Manduca sexta		0	0	0	0	0	0	0	0	0.14	
dof-miR-188	oan-miR-1388-3p	Ornithorhynchus anatinus	ATCTCAGGTTTCGTCAGCCCATG	0	0	0	0	0	0	0	0.17	0	
	ssa-miR-1338-3p	Salmo salar		0	0	0	0	0	0	0	0	0.17	0
	tgu-miR-1388-3p	Taeniopygia guttata		0	0	0	0	0	0	0	0	0.17	0
	dre-miR-1388-3p	Danio rerio		0	0	0	0	0	0	0	0	0.17	0
dof-miR-189	ipu-miR-1388	Ictalurus punctatus	ATCTCAGGTTTCGTCAGCCCATGA	0	0	0	0	0	0	0.33	0		
dof-miR-190	mtr-miR395a	Medicago truncatula	ATGAAGTGTTGGGGGAAGTC	0	1.02	0.18	0	1.87	3.65	0.5	0		
	sbi-miR395f	Sorghum bicolor		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395c	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395d	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395e	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395f	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395i	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395j	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395l	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395m	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395n	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	mtr-miR395o	Medicago truncatula		0	1.02	0.18	0	1.87	3.65	0.5	0		
	gma-miR395i	Glycine max		0	1.02	0.18	0	1.87	3.65	0.5	0		
	gma-miR395j	Glycine max		0	1.02	0.18	0	1.87	3.65	0.5	0		
	gma-miR395k	Glycine max		0	1.02	0.18	0	1.87	3.65	0.5	0		
	gma-miR395l	Glycine max		0	1.02	0.18	0	1.87	3.65	0.5	0		
gma-miR395m	Glycine max	0	1.02	0.18	0	1.87	3.65	0.5	0				
dof-miR-191	hsa-miR-215-5p	Homo sapiens	ATGACCTATGAATTGACAGAC	0.79	1.53	0	0	0	0	2.5	1.96		
	gga-miR-215-5p	Gallus gallus		0.79	1.53	0	0	0	0	2.5	1.96		
	mml-miR-215-5p	Macaca mulatta		0.79	1.53	0	0	0	0	2.5	1.96		
	ptr-miR-215	Pan troglodytes		0.79	1.53	0	0	0	0	2.5	1.96		
	ppy-miR-215	Pongo pygmaeus		0.79	1.53	0	0	0	0	2.5	1.96		
	ggo-miR-215	Gorilla gorilla		0.79	1.53	0	0	0	0	2.5	1.96		
	mne-miR-215	Macaca nemestrina		0.79	1.53	0	0	0	0	2.5	1.96		

	oan-miR-215-5p	Ornithorhynchus anatinus		0.79	1.53	0	0	0	0	2.5	1.96
	chi-miR-215-5p	Capra hircus		0.79	1.53	0	0	0	0	2.5	1.96
	eca-miR-215	Equus caballus		0.79	1.53	0	0	0	0	2.5	1.96
	tgu-miR-215-5p	Taeniopygia guttata		0.79	1.53	0	0	0	0	2.5	1.96
	ssc-miR-215	Sus scrofa		0.79	1.53	0	0	0	0	2.5	1.96
dof-miR-192	bta-miR-215	Bos taurus	ATGACCTATGAATTGACAGACA	1.39	2.55	0	0.18	0	0	12.86	7.29
	cgr-miR-215-5p	Cricetulus griseus		1.39	2.55	0	0.18	0	0	12.86	7.29
	mdo-miR-215	Monodelphis domestica		1.39	2.55	0	0.18	0	0	12.86	7.29
dof-miR-193	dre-miR-192	Danio rerio	ATGACCTATGAATTGACAGCC	0.4	0.76	0.18	0	0.09	0	0.33	0
	fru-miR-192	Fugu rubripes		0.4	0.76	0.18	0	0.09	0	0.33	0
	tmi-miR-192	Tetraodon nigroviridis		0.4	0.76	0.18	0	0.09	0	0.33	0
	xtr-miR-192	Xenopus tropicalis		0.4	0.76	0.18	0	0.09	0	0.33	0
	ssa-miR-192a-5p	Salmo salar		0.4	0.76	0.18	0	0.09	0	0.33	0
	ipu-miR-192	Ictalurus punctatus		0.4	0.76	0.18	0	0.09	0	0.33	0
	ccr-miR-192	Cyprinus carpio		0.4	0.76	0.18	0	0.09	0	0.33	0
dof-miR-194	chi-miR-500-3p	Capra hircus	ATGCACCTGGGCAAGGATTCT	0	0	0	0	0.09	0	0	0
	ssc-miR-500	Sus scrofa		0	0	0	0	0.09	0	0	0
	cfa-miR-500	Canis familiaris		0	0	0	0	0.09	0	0	0
dof-miR-195	hsa-miR-500a-3p	Homo sapiens	ATGCACCTGGGCAAGGATTCTG	0	0	0	0.36	0	0	0	0
dof-miR-196	ggo-miR-502b	Gorilla gorilla	ATGCACCTGGGCAAGGATTCTGA	0	0	0	0.36	0.28	0	0.33	0
	mml-miR-500a-3p	Macaca mulatta		0	0	0	0.36	0.28	0	0.33	0
dof-miR-197	ath-miR408-3p	Arabidopsis thaliana	ATGCACTGCCTCTTCCCTGGC	0	0	0	27.03	0	0	0	0
	ptc-miR408-3p	Populus trichocarpa		0	0	0	27.03	0	0	0	0
	pta-miR408	Pinus taeda		0	0	0	27.03	0	0	0	0
	vvi-miR408	Vitis vinifera		0	0	0	27.03	0	0	0	0
	mdm-miR408a	Malus domestica		0	0	0	27.03	0	0	0	0
	cme-miR408	Cucumis melo		0	0	0	27.03	0	0	0	0
	mtr-miR408-3p	Medicago truncatula		0	0	0	27.03	0	0	0	0
	vun-miR408	Vigna unguiculata		0	0	0	27.03	0	0	0	0
	mes-miR408	Manihot esculenta		0	0	0	27.03	0	0	0	0
	lus-miR408a	Linum usitatissimum		0	0	0	27.03	0	0	0	0
	gma-miR408a-3p	Glycine max		0	0	0	27.03	0	0	0	0
	gma-miR408b-3p	Glycine max		0	0	0	27.03	0	0	0	0
	gma-miR408c-3p	Glycine max		0	0	0	27.03	0	0	0	0

	ahy-miR408-3p	Arachis hypogaea		0	0	0	27.03	0	0	0	0
	csi-miR408	Citrus sinensis		0	0	0	27.03	0	0	0	0
	aly-miR408-3p	Arabidopsis lyrata		0	0	0	27.03	0	0	0	0
dof-miR-198	ssc-miR-7134-3p	Sus scrofa	ATGCGGAACCTGCGGATACGG	0.2	0	0.37	0	0	0	0	0
dof-miR-199	mmu-miR-297b-5p	Mus musculus	ATGTATGTGTGCATGAACATGT	0	0	0	0.18	0	0	0	0
dof-miR-200	oan-miR-145-3p	Ornithorhynchus anatinus	ATTCCTGGAAATACTGTCTT	0	0.25	0.55	0.54	0	0	0	0
	chi-miR-145-3p	Capra hircus		0	0.25	0.55	0.54	0	0	0	0
	ssa-miR-145-3p	Salmo salar		0	0.25	0.55	0.54	0	0	0	0
dof-miR-201	hsa-miR-576-5p	Homo sapiens	ATTCTAATTCTCCACGTCTTT	0	0	0	0	0.09	0	0	0
dof-miR-202	sly-miR397	Solanum lycopersicum	ATTGAGTGCAGCGTTGATGA	0	0	0	0.9	0	0	0	0
dof-miR-203	bdi-miR397b-5p	Brachypodium distachyon	ATTGAGTGCAGCGTTGATGAA	0	0	0	2.16	0	0	0	0
	lus-miR397a	Linum usitatissimum		0	0	0	2.16	0	0	0	0
dof-miR-204	tca-miR-92b-3p	Tribolium castaneum	ATTGCACTTGTCGGCCTG	0	0	0	0	0.09	0	0	0
dof-miR-205	oar-miR-25	Ovis aries	ATTGCACTTGTCGGTCTGA	0	0.25	0	0.18	0	0.1	0	0
dof-miR-206	cpa-miR319	Carica papaya	ATTGGACTGAAGGGAGCTCC	0	0	0.37	0.36	0	0	0	0
dof-miR-207	mmu-miR-186-5p	Mus musculus	CAAAGAATTCTCCTTTTGGGCT	0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	hsa-miR-186-5p	Homo sapiens		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	rno-miR-186-5p	Rattus norvegicus		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	bta-miR-186	Bos taurus		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	oan-miR-186-5p	Ornithorhynchus anatinus		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	chi-miR-186-5p	Capra hircus		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	tch-miR-186-5p	Tupaia chinensis		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	ppy-miR-186	Pongo pygmaeus		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	eca-miR-186	Equus caballus		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
	mml-miR-186-5p	Macaca mulatta		0.2	2.55	0.37	1.08	2.24	0.31	0.5	0.84
dof-miR-208	ssc-miR-186	Sus scrofa	CAAAGAATTCTCCTTTTGGGCTT	0	0.51	0	0.72	1.59	0	0	0
	ptr-miR-186	Pan troglodytes		0	0.51	0	0.72	1.59	0	0	0
	ggo-miR-186	Gorilla gorilla		0	0.51	0	0.72	1.59	0	0	0
	ppa-miR-186	Pan paniscus		0	0.51	0	0.72	1.59	0	0	0
	mdo-miR-186-5p	Monodelphis domestica		0	0.51	0	0.72	1.59	0	0	0
	cgr-miR-186-5p	Cricetulus griseus		0	0.51	0	0.72	1.59	0	0	0
dof-miR-209	chi-miR-330-3p	Capra hircus	CAAAGCACACGGCCTGCAGAGA	0	0	0.18	0	0.09	0	0	0
dof-miR-210	sha-miR-93	Sarcophilus harrisii	CAAAGTGTCTTCTGCAGGT	0	1.27	0.37	0	0.09	0.31	0.33	0.42

dof-miR-211	bta-miR-93	Bos taurus	CAAAGTGCTGTTCTGCAGGTA	0	0	0	0	0.75	0.31	0.17	0
dof-miR-212	hsa-miR-93-5p	Homo sapiens	CAAAGTGCTGTTCTGCAGGTAG	0	0.25	0.18	0.36	0.19	0.31	0	0
	mmu-miR-93-5p	Mus musculus		0	0.25	0.18	0.36	0.19	0.31	0	0
	rno-miR-93-5p	Rattus norvegicus		0	0.25	0.18	0.36	0.19	0.31	0	0
	chi-miR-93-5p	Capra hircus		0	0.25	0.18	0.36	0.19	0.31	0	0
	tch-miR-93-5p	Tupaia chinensis		0	0.25	0.18	0.36	0.19	0.31	0	0
	cgr-miR-93-5p	Cricetulus griseus		0	0.25	0.18	0.36	0.19	0.31	0	0
	eca-miR-93	Equus caballus		0	0.25	0.18	0.36	0.19	0.31	0	0
	cfa-miR-93	Canis familiaris		0	0.25	0.18	0.36	0.19	0.31	0	0
dof-miR-213	dre-miR-17a-5p	Danio rerio	CAAAGTGCTTACAGTGCAGGTA	0	0.25	0.18	0.36	0	0	0	0
	fru-miR-17	Fugu rubripes		0	0.25	0.18	0.36	0	0	0	0
	tui-miR-17	Tetraodon nigroviridis		0	0.25	0.18	0.36	0	0	0	0
	oar-miR-17-5p	Ovis aries		0	0.25	0.18	0.36	0	0	0	0
dof-miR-214	hsa-miR-17-5p	Homo sapiens	CAAAGTGCTTACAGTGCAGGTA	0	0	0.37	0.54	0.56	0.21	0.33	0
	mmu-miR-17-5p	Mus musculus		0	0	0.37	0.54	0.56	0.21	0.33	0
	rno-miR-17-5p	Rattus norvegicus		0	0	0.37	0.54	0.56	0.21	0.33	0
	oan-miR-17-5p	Ornithorhynchus anatinus		0	0	0.37	0.54	0.56	0.21	0.33	0
	tch-miR-17-5p	Tupaia chinensis		0	0	0.37	0.54	0.56	0.21	0.33	0
	ssa-miR-17-5p	Salmo salar		0	0	0.37	0.54	0.56	0.21	0.33	0
	ccr-miR-17-5p	Cyprinus carpio		0	0	0.37	0.54	0.56	0.21	0.33	0
	cgr-miR-17-5p	Cricetulus griseus		0	0	0.37	0.54	0.56	0.21	0.33	0
	aca-miR-17-5p	Anolis carolinensis		0	0	0.37	0.54	0.56	0.21	0.33	0
	eca-miR-17	Equus caballus		0	0	0.37	0.54	0.56	0.21	0.33	0
	eca-miR-106a	Equus caballus		0	0	0.37	0.54	0.56	0.21	0.33	0
	tgu-miR-17a-5p	Taeniopygia guttata		0	0	0.37	0.54	0.56	0.21	0.33	0
	ssc-miR-17-5p	Sus scrofa		0	0	0.37	0.54	0.56	0.21	0.33	0
dof-miR-215	gga-miR-17-5p	Gallus gallus	CAAAGTGCTTACAGTGCAGGTAGT	0	0	0	0	0.19	0.21	0.17	0
	ggo-miR-17-5p	Gorilla gorilla		0	0	0	0	0.19	0.21	0.17	0
	lca-miR-17-5p	Lemur catta		0	0	0	0	0.19	0.21	0.17	0
	age-miR-17-5p	Ateles geoffroyi		0	0	0	0	0.19	0.21	0.17	0
	ppa-miR-17-5p	Pan paniscus		0	0	0	0	0.19	0.21	0.17	0
	ppy-miR-17-5p	Pongo pygmaeus		0	0	0	0	0.19	0.21	0.17	0
	ptr-miR-17-5p	Pan troglodytes		0	0	0	0	0.19	0.21	0.17	0
	mml-miR-17-5p	Macaca mulatta		0	0	0	0	0.19	0.21	0.17	0

	sla-miR-17-5p	Saguinus labiatus		0	0	0	0	0.19	0.21	0.17	0
	lla-miR-17-5p	Lagothrix lagotricha		0	0	0	0	0.19	0.21	0.17	0
	mne-miR-17-5p	Macaca nemestrina		0	0	0	0	0.19	0.21	0.17	0
	xtr-miR-17-5p	Xenopus tropicalis		0	0	0	0	0.19	0.21	0.17	0
	bta-miR-17-5p	Bos taurus		0	0	0	0	0.19	0.21	0.17	0
	mdo-miR-17-5p	Monodelphis domestica		0	0	0	0	0.19	0.21	0.17	0
	chi-miR-17-5p	Capra hircus		0	0	0	0	0.19	0.21	0.17	0
	oha-miR-17-5p	Ophiophagus hannah		0	0	0	0	0.19	0.21	0.17	0
dof-miR-216	hsa-miR-21-3p	Homo sapiens	CAACACCAGTCGATGGGCTGT	0	0	0	0	0.47	0	0	0
dof-miR-217	chi-miR-21-3p	Capra hircus	CAACAGCAGTCGATGGGCTGT	0	0	0	0	0	0	0.17	0
dof-miR-218	gma-miR9757	Glycine max	CAACCTCCTCAGTTAGATCTC	0	0	0.18	0	0	0	0	0
dof-miR-219	ggo-miR-191	Gorilla gorilla	CAACGGAATCCCAAAAGCAGC	0.2	0	0	0	0.65	0.1	0.17	0.14
dof-miR-220	xtr-miR-191	Xenopus tropicalis	CAACGGAATCCCAAAAGCAGCT	0.99	6.11	1.29	3.06	9.33	0.63	2.67	2.24
	mdo-miR-191-5p	Monodelphis domestica		0.99	6.11	1.29	3.06	9.33	0.63	2.67	2.24
	oan-miR-191-5p	Ornithorhynchus anatinus		0.99	6.11	1.29	3.06	9.33	0.63	2.67	2.24
	chi-miR-191-5p	Capra hircus		0.99	6.11	1.29	3.06	9.33	0.63	2.67	2.24
	tch-miR-191-5p	Tupaia chinensis		0.99	6.11	1.29	3.06	9.33	0.63	2.67	2.24
	oar-miR-191	Ovis aries		0.99	6.11	1.29	3.06	9.33	0.63	2.67	2.24
	cfa-miR-191	Canis familiaris		0.99	6.11	1.29	3.06	9.33	0.63	2.67	2.24
dof-miR-221	mmu-miR-191-5p	Mus musculus	CAACGGAATCCCAAAAGCAGCTG	0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	hsa-miR-191-5p	Homo sapiens		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	rno-miR-191a-5p	Rattus norvegicus		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	bta-miR-191	Bos taurus		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	ocu-miR-191-5p	Oryctolagus cuniculus		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	oha-miR-191-5p	Ophiophagus hannah		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	cgr-miR-191-5p	Cricetulus griseus		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	aca-miR-191-5p	Anolis carolinensis		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	ppy-miR-191	Pongo pygmaeus		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	eca-miR-191a	Equus caballus		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
	ssc-miR-191	Sus scrofa		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
		mml-miR-191-5p		Macaca mulatta		0	2.29	0.55	2.52	3.64	0.83
	ptr-miR-191	Pan troglodytes		0	2.29	0.55	2.52	3.64	0.83	0.67	0.28
dof-miR-222	chi-miR-99a-3p	Capra hircus	CAAGCTCGCTTCTATGGGTCTGT	0.2	0	0	0	0	0	0	0
dof-miR-223	rno-miR-224-5p	Rattus norvegicus	CAAGTCACTAGTGGTCCGTTT	0	0	0.37	0.54	0.09	0.1	0	0

	chi-miR-224-5p	Capra hircus		0	0	0.37	0.54	0.09	0.1	0	0
	cfa-miR-224	Canis familiaris		0	0	0.37	0.54	0.09	0.1	0	0
dof-miR-224	ssa-miR-33a-3p	Salmo salar	CAATGTGTCTGCAGTGAGTA	0.2	0	0	0	0	0	0	0
dof-miR-225	gga-miR-219b	Gallus gallus	CACAAGAATTGCGTTTGACAA	0	0	0.18	0	0	0	0	0
dof-miR-226	hbr-miR396a	Hevea brasiliensis	CACAGCTTTCTTGAACCTTCT	0	0	0	0.9	0	0.1	0	0
dof-miR-227	rno-miR-323-3p	Rattus norvegicus	CACATTACACGGTCGACCTCT	0	0	0	0.9	0	0	0	0
	mmu-miR-323-3p	Mus musculus		0	0	0	0.9	0	0	0	0
	hsa-miR-323a-3p	Homo sapiens		0	0	0	0.9	0	0	0	0
	chi-miR-323a-3p	Capra hircus		0	0	0	0.9	0	0	0	0
	oar-miR-323a-3p	Ovis aries		0	0	0	0.9	0	0	0	0
	ppy-miR-323-3p	Pongo pygmaeus		0	0	0	0.9	0	0	0	0
	eca-miR-323-3p	Equus caballus		0	0	0	0.9	0	0	0	0
	mml-miR-323a-3p	Macaca mulatta		0	0	0	0.9	0	0	0	0
	cfa-miR-323	Canis familiaris		0	0	0	0.9	0	0	0	0
ptr-miR-323	Pan troglodytes	0	0	0	0.9	0	0	0	0		
dof-miR-228	hsa-miR-941	Homo sapiens	CACCCGGCTGTGTGCACATGTGC	0	0	0	0	0.28	0	0	0
dof-miR-229	mmu-miR-99b-5p	Mus musculus	CACCCGTAGAACCACCTTGCG	0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	hsa-miR-99b-5p	Homo sapiens		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	rno-miR-99b-5p	Rattus norvegicus		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	bta-miR-99b	Bos taurus		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	ssc-miR-99b	Sus scrofa		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	chi-miR-99b-5p	Capra hircus		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	tch-miR-99b-5p	Tupaia chinensis		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	eca-miR-99b	Equus caballus		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	mml-miR-99b-5p	Macaca mulatta		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
	cfa-miR-99b	Canis familiaris		0.2	0	4.59	5.77	0.84	0.21	0.5	0.14
ptr-miR-99b	Pan troglodytes	0.2	0	4.59	5.77	0.84	0.21	0.5	0.14		
dof-miR-230	ssa-miR-10d-5p	Salmo salar	CACCCGTAGAACCGAATTTGT	0	0	0.55	0.72	0	0	0.17	0
dof-miR-231	hsa-miR-574-3p	Homo sapiens	CACGCTCATGCACACCCACA	0	0	0	0	0.09	0	0	0
	mmu-miR-574-3p	Mus musculus		0	0	0	0	0.09	0	0	0
	ggo-miR-574	Gorilla gorilla		0	0	0	0	0.09	0	0	0
	ssc-miR-574	Sus scrofa		0	0	0	0	0.09	0	0	0
	cfa-miR-574	Canis familiaris		0	0	0	0	0.09	0	0	0
dof-miR-232	hsa-miR-28-3p	Homo sapiens	CACTAGATTGTGAGCTCCTGGA	0	0	0	0.36	0.28	0	0.17	0

	rno-miR-28-3p	Rattus norvegicus		0	0	0	0.36	0.28	0	0.17	0
	ssc-miR-28-3p	Sus scrofa		0	0	0	0.36	0.28	0	0.17	0
	mml-miR-28-3p	Macaca mulatta		0	0	0	0.36	0.28	0	0.17	0
	cgr-miR-28-3p	Cricetulus griseus		0	0	0	0.36	0.28	0	0.17	0
	eca-miR-28-3p	Equus caballus		0	0	0	0.36	0.28	0	0.17	0
	cfa-miR-28	Canis familiaris		0	0	0	0.36	0.28	0	0.17	0
dof-miR-233	ptc-miR1447	Populus trichocarpa	CAGAATTGCAGTGCCTTGATT	0	0	1.1	0	0	0	0.5	0
dof-miR-234	cfa-miR-3958	Canis familiaris	CAGATATTGCACGGTTGATCTCT	0	0	0.18	0	0	0	0	0
dof-miR-235	chi-miR-424-5p	Capra hircus	CAGCAGCAATTCATGTTTTGA	0	0	0.73	0.9	0	0	0	0
	tch-miR-424-5p	Tupaia chinensis		0	0	0.73	0.9	0	0	0	0
	ggo-miR-424	Gorilla gorilla		0	0	0.73	0.9	0	0	0	0
	bta-miR-424-5p	Bos taurus		0	0	0.73	0.9	0	0	0	0
dof-miR-236	hsa-miR-497-5p	Homo sapiens	CAGCAGCACACTGTGGTTTGT	0	0	0.37	0	0	0	0	0
	sha-miR-497	Sarcophilus harrisii		0	0	0.37	0	0	0	0	0
	ppy-miR-497	Pongo pygmaeus		0	0	0.37	0	0	0	0	0
	mdo-miR-497-5p	Monodelphis domestica		0	0	0.37	0	0	0	0	0
	eca-miR-497	Equus caballus		0	0	0.37	0	0	0	0	0
	ssc-miR-497	Sus scrofa		0	0	0.37	0	0	0	0	0
	mml-miR-497-5p	Macaca mulatta		0	0	0.37	0	0	0	0	0
	cfa-miR-497	Canis familiaris		0	0	0.37	0	0	0	0	0
dof-miR-237	gma-miR169v	Glycine max	CAGCCAAGGATGACTTGCC	0.2	0.25	0	0.18	0	0	0	0
dof-miR-238	ath-miR169a-5p	Arabidopsis thaliana	CAGCCAAGGATGACTTGCCGA	0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	osa-miR169a	Oryza sativa		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	zma-miR169a-5p	Zea mays		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	zma-miR169b-5p	Zea mays		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	sbi-miR169a	Sorghum bicolor		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	mtr-miR169a	Medicago truncatula		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	ptc-miR169a	Populus trichocarpa		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	ptc-miR169b-5p	Populus trichocarpa		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	ptc-miR169c	Populus trichocarpa		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	bna-miR169a	Brassica napus		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	bna-miR169b	Brassica napus		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	vvi-miR169f	Vitis vinifera		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	vvi-miR169g	Vitis vinifera		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28

	ata-miR169g-5p	Aegilops tauschii		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	ata-miR169e-5p	Aegilops tauschii		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	ata-miR169f-5p	Aegilops tauschii		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	mes-miR169g	Manihot esculenta		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	lus-miR169g	Linum usitatissimum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	lus-miR169l	Linum usitatissimum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169a	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169b	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169c	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169d	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169e	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169f	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169g	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169h	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169i	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169j	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169k	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169l	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169m	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169o	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	nta-miR169p	Nicotiana tabacum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	tcc-miR169a	Theobroma cacao		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	tcc-miR169c	Theobroma cacao		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	tcc-miR169e	Theobroma cacao		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	bdi-miR169a-5p	Brachypodium distachyon		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	aly-miR169a-5p	Arabidopsis lyrata		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	gma-miR169b	Glycine max		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
	sly-miR169c	Solanum lycopersicum		0.99	8.15	4.59	1.08	1.12	1.25	3.34	0.28
dof-miR-239	ath-miR169b-5p	Arabidopsis thaliana	CAGCCAAGGATGACTTGCCGG	0.4	0	0	0.18	0	0.1	0	0.14
	ath-miR169c	Arabidopsis thaliana		0.4	0	0	0.18	0	0.1	0	0.14
	osa-miR169b	Oryza sativa		0.4	0	0	0.18	0	0.1	0	0.14
	osa-miR169c	Oryza sativa		0.4	0	0	0.18	0	0.1	0	0.14
	sbi-miR169b	Sorghum bicolor		0.4	0	0	0.18	0	0.1	0	0.14
	gma-miR169a	Glycine max		0.4	0	0	0.18	0	0.1	0	0.14

	nta-miR169s	Nicotiana tabacum		0.4	0	0	0.18	0	0.1	0	0.14
	tcc-miR169b	Theobroma cacao		0.4	0	0	0.18	0	0.1	0	0.14
	tcc-miR169k	Theobroma cacao		0.4	0	0	0.18	0	0.1	0	0.14
	tcc-miR169l	Theobroma cacao		0.4	0	0	0.18	0	0.1	0	0.14
	gma-miR169f	Glycine max		0.4	0	0	0.18	0	0.1	0	0.14
	gma-miR169g	Glycine max		0.4	0	0	0.18	0	0.1	0	0.14
	bdi-miR169c-5p	Brachypodium distachyon		0.4	0	0	0.18	0	0.1	0	0.14
	bdi-miR169f	Brachypodium distachyon		0.4	0	0	0.18	0	0.1	0	0.14
	gma-miR169m	Glycine max		0.4	0	0	0.18	0	0.1	0	0.14
	zma-miR169r-5p	Zea mays		0.4	0	0	0.18	0	0.1	0	0.14
	rco-miR169a	Ricinus communis		0.4	0	0	0.18	0	0.1	0	0.14
	rco-miR169b	Ricinus communis		0.4	0	0	0.18	0	0.1	0	0.14
	aly-miR169b-5p	Arabidopsis lyrata		0.4	0	0	0.18	0	0.1	0	0.14
	aly-miR169c-5p	Arabidopsis lyrata		0.4	0	0	0.18	0	0.1	0	0.14
	vvi-miR169w	Vitis vinifera		0.4	0	0	0.18	0	0.1	0	0.14
	sly-miR169a	Solanum lycopersicum		0.4	0	0	0.18	0	0.1	0	0.14
	sbi-miR169k	Sorghum bicolor		0.4	0	0	0.18	0	0.1	0	0.14
	aqc-miR169c	Aquilegia caerulea		0.4	0	0	0.18	0	0.1	0	0.14
dof-miR-240	gga-miR-34b-5p	Gallus gallus	CAGGCAGTGTAGTTAGCTGATTG	0	0	0	0.18	0	0	0	0
	xtr-miR-34b	Xenopus tropicalis		0	0	0	0.18	0	0	0	0
dof-miR-241	dre-miR-456	Danio rerio	CAGGCTGGTTAGATGGTTGTCA	0	0	0	0.18	0	0	0	0
	gga-miR-456-3p	Gallus gallus		0	0	0	0.18	0	0	0	0
	oha-miR-456	Ophiophagus hannah		0	0	0	0.18	0	0	0	0
	ssa-miR-456-3p	Salmo salar		0	0	0	0.18	0	0	0	0
	ipu-miR-456	Ictalurus punctatus		0	0	0	0.18	0	0	0	0
	pma-miR-456	Petromyzon marinus		0	0	0	0.18	0	0	0	0
dof-miR-242	rno-miR-370-5p	Rattus norvegicus	CAGGTCACGTCTCTGCAGTTACAC	0	0	0	0.18	0	0	0	0
dof-miR-243	mmu-miR-431-3p	Mus musculus	CAGGTCGTCTTGCAAGGCTTCT	0	0	0.37	0	0	0	0	0
	hsa-miR-431-3p	Homo sapiens		0	0	0.37	0	0	0	0	0
dof-miR-244	hsa-miR-802	Homo sapiens	CAGTAACAAAGATTCATCCTTGT	0	0.25	0	0	0	0	0	0
	ppy-miR-802	Pongo pygmaeus		0	0.25	0	0	0	0	0	0
	eca-miR-802	Equus caballus		0	0.25	0	0	0	0	0	0
	mml-miR-802	Macaca mulatta		0	0.25	0	0	0	0	0	0
	ptr-miR-802	Pan troglodytes		0	0.25	0	0	0	0	0	0

	cfa-miR-802	Canis familiaris		0	0.25	0	0	0	0	0	0
dof-miR-245	pma-miR-199a-3p	Petromyzon marinus	CAGTAGTCTGCACATTGGTTA	0	0	0	0.36	0.09	0	0	0
	pma-miR-199b-3p	Petromyzon marinus		0	0	0	0.36	0.09	0	0	0
dof-miR-246	dre-miR-130b	Danio rerio	CAGTGCAATAATGAAAGGGCAT	0	0	0	0.18	0	0	0	0
	oha-miR-130d	Ophiophagus hannah		0	0	0	0.18	0	0	0	0
	ccr-miR-130b	Cyprinus carpio		0	0	0	0.18	0	0	0	0
dof-miR-247	mmu-miR-301a-3p	Mus musculus	CAGTGCAATAGTATTGTCAAAGC	0	0	0.18	0.36	0.19	0	0	0
	rno-miR-301a-3p	Rattus norvegicus		0	0	0.18	0.36	0.19	0	0	0
	hsa-miR-301a-3p	Homo sapiens		0	0	0.18	0.36	0.19	0	0	0
	xtr-miR-301	Xenopus tropicalis		0	0	0.18	0.36	0.19	0	0	0
	oan-miR-301-3p	Ornithorhynchus anatinus		0	0	0.18	0.36	0.19	0	0	0
	chi-miR-301a-3p	Capra hircus		0	0	0.18	0.36	0.19	0	0	0
	ssa-miR-301d-3p	Salmo salar		0	0	0.18	0.36	0.19	0	0	0
	ipu-miR-301a	Ictalurus punctatus		0	0	0.18	0.36	0.19	0	0	0
	ccr-miR-301a	Cyprinus carpio		0	0	0.18	0.36	0.19	0	0	0
	cgr-miR-301a-3p	Cricetulus griseus		0	0	0.18	0.36	0.19	0	0	0
	aca-miR-301a-3p	Anolis carolinensis		0	0	0.18	0.36	0.19	0	0	0
	mdo-miR-301-3p	Monodelphis domestica		0	0	0.18	0.36	0.19	0	0	0
	eca-miR-301a	Equus caballus		0	0	0.18	0.36	0.19	0	0	0
	tgu-miR-301-3p	Taeniopygia guttata		0	0	0.18	0.36	0.19	0	0	0
	mml-miR-301a-3p	Macaca mulatta		0	0	0.18	0.36	0.19	0	0	0
ptr-miR-301a	Pan troglodytes	0	0	0.18	0.36	0.19	0	0	0		
cfa-miR-301a	Canis familiaris	0	0	0.18	0.36	0.19	0	0	0		
dof-miR-248	oha-miR-301a-3p	Ophiophagus hannah	CAGTGCAATAGTATTGTCAAAGCA	0	0	0.18	0	0	0	0	0
	hhi-miR-301	Hippoglossus hippoglossus		0	0	0.18	0	0	0	0	0
dof-miR-249	hsa-miR-301b-3p	Homo sapiens	CAGTGCAATGATATTGTCAAAGC	0	0	0	0	0.19	0	0	0
	chi-miR-301b	Capra hircus		0	0	0	0	0.19	0	0	0
	ppy-miR-301b	Pongo pygmaeus		0	0	0	0	0.19	0	0	0
	eca-miR-301b-3p	Equus caballus		0	0	0	0	0.19	0	0	0
	mml-miR-301b	Macaca mulatta		0	0	0	0	0.19	0	0	0
	ptr-miR-301b	Pan troglodytes		0	0	0	0	0.19	0	0	0
	cfa-miR-301b	Canis familiaris		0	0	0	0	0.19	0	0	0
dof-miR-250	mmu-miR-130b-3p	Mus musculus	CAGTGCAATGATGAAAGGGCAT	0.2	0	0	0	0	0	0	0
	hsa-miR-130b-3p	Homo sapiens		0.2	0	0	0	0	0	0	0

	rno-miR-130b-3p	Rattus norvegicus		0.2	0	0	0	0	0	0	0	0
	xtr-miR-130b	Xenopus tropicalis		0.2	0	0	0	0	0	0	0	0
	chi-miR-130b-3p	Capra hircus		0.2	0	0	0	0	0	0	0	0
	cgr-miR-130b-3p	Cricetulus griseus		0.2	0	0	0	0	0	0	0	0
	ppy-miR-130b	Pongo pygmaeus		0.2	0	0	0	0	0	0	0	0
	eca-miR-130b	Equus caballus		0.2	0	0	0	0	0	0	0	0
	ssc-miR-130b	Sus scrofa		0.2	0	0	0	0	0	0	0	0
	mml-miR-130b-3p	Macaca mulatta		0.2	0	0	0	0	0	0	0	0
	cfa-miR-130b	Canis familiaris		0.2	0	0	0	0	0	0	0	0
	ptr-miR-130b	Pan troglodytes		0.2	0	0	0	0	0	0	0	0
	bta-miR-130b	Bos taurus		0.2	0	0	0	0	0	0	0	0
dof-miR-251	mml-miR-130a-3p	Macaca mulatta	CAGTGCAATGTAAAAGGGC	0	0	0.18	0.18	0	0	0	0	0.14
	ggo-miR-130a	Gorilla gorilla		0	0	0.18	0.18	0	0	0	0	0.14
	mne-miR-130a	Macaca nemestrina		0	0	0.18	0.18	0	0	0	0	0.14
	ppa-miR-130a	Pan paniscus		0	0	0.18	0.18	0	0	0	0	0.14
dof-miR-252	chi-miR-130a-3p	Capra hircus	CAGTGCAATGTAAAAGGGCA	0	0	0	0.36	0	0	0	0	0
	ssa-miR-130b-3p	Salmo salar		0	0	0	0.36	0	0	0	0	0
	aca-miR-130a-3p	Anolis carolinensis		0	0	0	0.36	0	0	0	0	0
dof-miR-253	mmu-miR-130a-3p	Mus musculus	CAGTGCAATGTAAAAGGGCAT	0	0	0.55	0	0.09	0	0	0	0.28
	hsa-miR-130a-3p	Homo sapiens		0	0	0.55	0	0.09	0	0	0	0.28
	rno-miR-130a-3p	Rattus norvegicus		0	0	0.55	0	0.09	0	0	0	0.28
	dre-miR-130a	Danio rerio		0	0	0.55	0	0.09	0	0	0	0.28
	xtr-miR-130a	Xenopus tropicalis		0	0	0.55	0	0.09	0	0	0	0.28
	oan-miR-130b-3p	Ornithorhynchus anatinus		0	0	0.55	0	0.09	0	0	0	0.28
	tch-miR-130a-3p	Tupaia chinensis		0	0	0.55	0	0.09	0	0	0	0.28
	oha-miR-130b-3p	Ophiophagus hannah		0	0	0.55	0	0.09	0	0	0	0.28
	ccr-miR-130a	Cyprinus carpio		0	0	0.55	0	0.09	0	0	0	0.28
	mdo-miR-130c-3p	Monodelphis domestica		0	0	0.55	0	0.09	0	0	0	0.28
	cgr-miR-130a-3p	Cricetulus griseus		0	0	0.55	0	0.09	0	0	0	0.28
	ppy-miR-130a	Pongo pygmaeus		0	0	0.55	0	0.09	0	0	0	0.28
	eca-miR-130a	Equus caballus		0	0	0.55	0	0.09	0	0	0	0.28
	tgu-miR-130c-3p	Taeniopygia guttata		0	0	0.55	0	0.09	0	0	0	0.28
	gga-miR-130c-3p	Gallus gallus		0	0	0.55	0	0.09	0	0	0	0.28
	cfa-miR-130a	Canis familiaris		0	0	0.55	0	0.09	0	0	0	0.28

	dvi-miR-8-5p	<i>Drosophila virilis</i>		0	0	0	0	0	0	0	0.17	0	
	lmi-miR-8-5p	<i>Locusta migratoria</i>		0	0	0	0	0	0	0	0.17	0	
dof-miR-264	hsa-miR-532-5p	<i>Homo sapiens</i>	CATGCCTTGAGTGTAGGACCGT	0	0	0.73	0.72	0.37	0	0	0	0	
	mmu-miR-532-5p	<i>Mus musculus</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
	bta-miR-532	<i>Bos taurus</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
	chi-miR-532-5p	<i>Capra hircus</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
	tch-miR-532-5p	<i>Tupaia chinensis</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
	cgr-miR-532-5p	<i>Cricetulus griseus</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
	ppy-miR-532-5p	<i>Pongo pygmaeus</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
	eca-miR-532-5p	<i>Equus caballus</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
	ssc-miR-532-5p	<i>Sus scrofa</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
	mml-miR-532-5p	<i>Macaca mulatta</i>		0	0	0.73	0.72	0.37	0	0	0	0	0
cfa-miR-532	<i>Canis familiaris</i>	0	0	0.73	0.72	0.37	0	0	0	0	0		
dof-miR-265	tgu-miR-126-5p	<i>Taeniopygia guttata</i>	CATTATTACTTTTGGTACGC	0	0	0	0.36	0.19	0	0	0	0	
dof-miR-266	mmu-miR-126a-5p	<i>Mus musculus</i>	CATTATTACTTTTGGTACGCG	0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	hsa-miR-126-5p	<i>Homo sapiens</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	rno-miR-126a-5p	<i>Rattus norvegicus</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	gga-miR-126-5p	<i>Gallus gallus</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	dre-miR-126a-5p	<i>Danio rerio</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	bta-miR-126-5p	<i>Bos taurus</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	xtr-miR-126-5p	<i>Xenopus tropicalis</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	oan-miR-126-5p	<i>Ornithorhynchus anatinus</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	ssa-miR-126-5p	<i>Salmo salar</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	ipu-miR-126b	<i>Ictalurus punctatus</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	ccr-miR-126-5p	<i>Cyprinus carpio</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	ola-miR-126-5p	<i>Oryzias latipes</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	aca-miR-126-5p	<i>Anolis carolinensis</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	ssc-miR-126-5p	<i>Sus scrofa</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	mdo-miR-126-5p	<i>Monodelphis domestica</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
	eca-miR-126-5p	<i>Equus caballus</i>		0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0	
cfa-miR-126	<i>Canis familiaris</i>	0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0			
dre-miR-126b-5p	<i>Danio rerio</i>	0.2	0.51	1.1	2.34	6.53	1.25	0.17	0	0			
dof-miR-267	chi-miR-126-5p	<i>Capra hircus</i>	CATTATTACTTTTGGTACGCGC	0	0	0	0	0.28	0	0.17	0		
dof-miR-268	sha-miR-25	<i>Sarcophilus harrisii</i>	CATTGCACTTGCTCGGTC	0.2	0.76	0	0	0.09	0.1	0	0		

dof-miR-269	hsa-miR-25-3p	Homo sapiens	CATTGCACTGTCTCGGTCTGA	0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	mmu-miR-25-3p	Mus musculus		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	rno-miR-25-3p	Rattus norvegicus		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	dre-miR-25-3p	Danio rerio		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	ggo-miR-25	Gorilla gorilla		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	ppa-miR-25	Pan paniscus		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	ppy-miR-25	Pongo pygmaeus		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	mml-miR-25	Macaca mulatta		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	lla-miR-25	Lagothrix lagotricha		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	mne-miR-25	Macaca nemestrina		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	fru-miR-25	Fugu rubripes		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	tui-miR-25	Tetraodon nigroviridis		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	xtr-miR-25	Xenopus tropicalis		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	bta-miR-25	Bos taurus		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	mdo-miR-25	Monodelphis domestica		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	chi-miR-25-3p	Capra hircus		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	tch-miR-25-3p	Tupaia chinensis		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	ssa-miR-25-3p	Salmo salar		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	aja-miR-25	Artibeus jamaicensis		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
	ipu-miR-25	Ictalurus punctatus		0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82
ccr-miR-25	Cyprinus carpio	0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82		
cgr-miR-25-3p	Cricetulus griseus	0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82		
eca-miR-25	Equus caballus	0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82		
cfa-miR-25	Canis familiaris	0.2	4.07	1.84	3.24	5.88	1.67	1.84	1.82		
dof-miR-270	chi-miR-1306-5p	Capra hircus	CCACCTCCCCTGCAAACGTCC	0	0	0	0	0	0	0.17	0
	mml-miR-1306-5p	Macaca mulatta		0	0	0	0	0	0	0.17	0
	ola-miR-1306	Oryzias latipes		0	0	0	0	0	0	0.17	0
	cgr-miR-1306-5p	Cricetulus griseus		0	0	0	0	0	0	0.17	0
	cfa-miR-1306	Canis familiaris		0	0	0	0	0	0	0.17	0
	bta-miR-1306	Bos taurus		0	0	0	0	0	0	0.17	0
dof-miR-271	hsa-miR-1306-5p	Homo sapiens	CCACCTCCCCTGCAAACGTCCA	0	0	0.37	0	0	0	0	0
	tch-miR-1306-5p	Tupaia chinensis		0	0	0.37	0	0	0	0	0
	dre-miR-1306	Danio rerio		0	0	0.37	0	0	0	0	0
	rno-miR-1306-5p	Rattus norvegicus		0	0	0.37	0	0	0	0	0

	ssc-miR-1306-5p	Sus scrofa		0	0	0.37	0	0	0	0	0
dof-miR-272	rno-miR-194-3p	Rattus norvegicus	CCAGTGGGGCTGCTGTATCT	0	0	0	0	0.09	0	0	0
dof-miR-273	mdo-miR-199b-2-5p	Monodelphis domestica	CCAGTGTTTCAGACTACCTGTTC	0	0	0.37	0	0	0	0.17	0
dof-miR-274	ssc-miR-7139-5p	Sus scrofa	CCATTCTTCGTCTGTGCACTAG	0	0	0	0	0	0	0.17	0
dof-miR-275	mml-miR-323b-3p	Macaca mulatta	CCCAATACACGGTCGACCTCT	0	0	0	0	0.09	0	0	0
dof-miR-276	oar-miR-323b	Ovis aries	CCCAATACACGGTCGATCTCT	0	0	0.18	0	0	0	0	0
dof-miR-277	aca-miR-199a-5p	Anolis carolinensis	CCCAGTGTTTCAGACTACCTGT	0.2	0	0.73	0.54	0	0	0	0.14
dof-miR-278	bta-miR-199a-5p	Bos taurus	CCCAGTGTTTCAGACTACCTGTT	0.59	1.27	4.59	5.95	0.37	0	1.5	0.42
	oan-miR-199-5p	Ornithorhynchus anatinus		0.59	1.27	4.59	5.95	0.37	0	1.5	0.42
	pol-miR-199a-5p	Paralichthys olivaceus		0.59	1.27	4.59	5.95	0.37	0	1.5	0.42
	ola-miR-199a-5p	Oryzias latipes		0.59	1.27	4.59	5.95	0.37	0	1.5	0.42
	tgu-miR-199-5p	Taeniopygia guttata		0.59	1.27	4.59	5.95	0.37	0	1.5	0.42
dof-miR-279	mmu-miR-199a-5p	Mus musculus	CCCAGTGTTTCAGACTACCTGTT	2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	hsa-miR-199a-5p	Homo sapiens		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	rno-miR-199a-5p	Rattus norvegicus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	gga-miR-199-5p	Gallus gallus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	dre-miR-199-5p	Danio rerio		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	ggo-miR-199a	Gorilla gorilla		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	ppa-miR-199a	Pan paniscus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	ppy-miR-199a	Pongo pygmaeus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	ptr-miR-199a-5p	Pan troglodytes		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	mml-miR-199a	Macaca mulatta		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	sla-miR-199a	Saguinus labiatus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	lla-miR-199a	Lagothrix lagotricha		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	mne-miR-199a	Macaca nemestrina		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	fru-miR-199	Fugu rubripes		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	tni-miR-199	Tetraodon nigroviridis		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	xtr-miR-199a-5p	Xenopus tropicalis		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	chi-miR-199a-5p	Capra hircus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	oha-miR-199c-5p	Ophiophagus hannah		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	ssa-miR-199a-5p	Salmo salar		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	ipu-miR-199a-5p	Ictalurus punctatus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
hhi-miR-199a	Hippoglossus hippoglossus	2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26		
ccr-miR-199-5p	Cyprinus carpio	2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26		

	pma-miR-199a-5p	Petromyzon marinus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	ppy-miR-199a-5p	Pongo pygmaeus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	eca-miR-199a-5p	Equus caballus		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	ssc-miR-199a-5p	Sus scrofa		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
	mml-miR-199a-5p	Macaca mulatta		2.77	2.55	13.41	20.9	5.78	0.52	5.34	1.26
dof-miR-280	mmu-miR-199b-5p	Mus musculus	CCCAGTGTTTAGACTACCTGTTC	0	0	0	0	0	0.1	0	0
	cgr-miR-199b	Cricetulus griseus		0	0	0	0	0	0.1	0	0
dof-miR-281	ssc-miR-199b-5p	Sus scrofa	CCCAGTGTTTAGACTATCTGTT	0	0.25	1.65	2.88	0.28	0	0	0
dof-miR-282	hsa-miR-199b-5p	Homo sapiens	CCCAGTGTTTAGACTATCTGTTC	0.2	0	1.65	2.16	0.28	0.1	0.33	0
	bta-miR-199b	Bos taurus		0.2	0	1.65	2.16	0.28	0.1	0.33	0
	mdo-miR-199b-1-5p	Monodelphis domestica		0.2	0	1.65	2.16	0.28	0.1	0.33	0
	chi-miR-199b-5p	Capra hircus		0.2	0	1.65	2.16	0.28	0.1	0.33	0
	chi-miR-199c-5p	Capra hircus		0.2	0	1.65	2.16	0.28	0.1	0.33	0
	eca-miR-199b-5p	Equus caballus		0.2	0	1.65	2.16	0.28	0.1	0.33	0
dof-miR-283	tgu-miR-142-5p	Taeniopygia guttata	CCCATAAAGTAGAAAGCACT	0	1.27	0	0	1.96	0.94	0.17	0.7
dof-miR-284	sha-miR-142	Sarcophilus harrisii	CCCATAAAGTAGAAAGCACTA	0.2	0	0	0	1.49	0.31	0.17	0
	ggo-miR-142	Gorilla gorilla		0.2	0	0	0	1.49	0.31	0.17	0
	cfa-miR-142	Canis familiaris		0.2	0	0	0	1.49	0.31	0.17	0
dof-miR-285	gga-miR-142-5p	Gallus gallus	CCCATAAAGTAGAAAGCACTAC	0	0	0	0	1.12	0.42	0.5	0
	cgr-miR-142-5p	Cricetulus griseus		0	0	0	0	1.12	0.42	0.5	0
dof-miR-286	ssc-miR-361-3p	Sus scrofa	CCCCAGGTGTGATTCTGATTGTC	0	0	0	0.18	0.09	0	0	0
dof-miR-287	ata-miR168-3p	Aegilops tauschii	CCCGCCTTGACCAAGTGAAT	0	0	0	0	0.19	0	0	0
	bdi-miR168-3p	Brachypodium distachyon		0	0	0	0	0.19	0	0	0
dof-miR-288	ath-miR168a-3p	Arabidopsis thaliana	CCCGCCTTGCATCAACTGAAT	0.2	0	4.96	161.99	0.09	0	0.83	0.14
	ptc-miR168a-3p	Populus trichocarpa		0.2	0	4.96	161.99	0.09	0	0.83	0.14
	ptc-miR168b-3p	Populus trichocarpa		0.2	0	4.96	161.99	0.09	0	0.83	0.14
	bra-miR168b-3p	Brassica rapa		0.2	0	4.96	161.99	0.09	0	0.83	0.14
	bra-miR168c-3p	Brassica rapa		0.2	0	4.96	161.99	0.09	0	0.83	0.14
	sly-miR168b-3p	Solanum lycopersicum		0.2	0	4.96	161.99	0.09	0	0.83	0.14
	mtr-miR168c-3p	Medicago truncatula		0.2	0	4.96	161.99	0.09	0	0.83	0.14
	aly-miR168a-3p	Arabidopsis lyrata		0.2	0	4.96	161.99	0.09	0	0.83	0.14
dof-miR-289	hsa-miR-6852-5p	Homo sapiens	CCCTGGGGTTCTGAGGACATG	0	0	0	0	0.09	0	0	0
dof-miR-290	ptc-miR6478	Populus trichocarpa	CCGACCTTAGCTCAGTTGGTG	0	0	0	0	0.09	0	0	0
dof-miR-291	chi-miR-106b-3p	Capra hircus	CCGCACTGTGGGTACTTGCT	0	0.25	0.18	0	0.65	0.1	0	0.28

dof-miR-292	pde-miR1314	Pinus densata	CCGGCCTCGAATGTTAGGAGAA	0	0	0.73	2.7	0	0	0	0	
dof-miR-293	eca-miR-676	Equus caballus	CCGTCTAAGGTTGTTGAGTT	0	0	0	0	0	0	0.17	0	
	mml-miR-676-3p	Macaca mulatta		0	0	0	0	0	0	0	0.17	0
	ssc-miR-676-3p	Sus scrofa		0	0	0	0	0	0	0	0.17	0
dof-miR-294	chi-miR-3431-5p	Capra hircus	CCTCAGTCAGCCTTGTGGATGT	0	0	0.55	0.54	0	0	0	0	
	bta-miR-3431	Bos taurus		0	0	0.55	0.54	0	0	0	0	
dof-miR-295	mmu-miR-326-3p	Mus musculus	CCTCTGGGCCCTTCCTCAGT	0	0	0	0.18	0.19	0	0	0	
	rno-miR-326-3p	Rattus norvegicus		0	0	0	0.18	0.19	0	0	0	
	cgr-miR-326	Cricetulus griseus		0	0	0	0.18	0.19	0	0	0	
dof-miR-296	sly-miR168a-3p	Solanum lycopersicum	CCTGCCTTGCATCAACTGAAT	294.7	357.68	673.92	259.46	176.37	408.27	259.61	359.14	
dof-miR-297	oar-miR-409-3p	Ovis aries	CGAATGTTGCTCGGTGAACCCCT	0	0	0.18	0.36	0.09	0	0	0	
dof-miR-298	ath-miR156g	Arabidopsis thaliana	CGACAGAAGAGAGTGAGCAC	0	0	0.18	0	0	0	0	0	
	smo-miR156a	Selaginella moellendorffii		0	0	0.18	0	0	0	0	0	
	aly-miR156g-5p	Arabidopsis lyrata		0	0	0.18	0	0	0	0	0	
dof-miR-299	ppe-miR171d-3p	Prunus persica	CGAGCCGAATCAATATCACTC	0	0	0.37	0.18	0	0	0	0	
	mtr-miR171g	Medicago truncatula		0	0	0.37	0.18	0	0	0	0	
	mtr-miR171h	Medicago truncatula		0	0	0.37	0.18	0	0	0	0	
	csi-miR171b	Citrus sinensis		0	0	0.37	0.18	0	0	0	0	
	gma-miR171b-3p	Glycine max		0	0	0.37	0.18	0	0	0	0	
dof-miR-300	ptc-miR399e	Populus trichocarpa	CGCCAAAGGAGAGTTGCCCTC	0	0	0	0.36	0	0	0	0	
dof-miR-301	tcc-miR399a	Theobroma cacao	CGCCAAAGGAGAGTTGCCCTG	0	0	0	23.06	0	0	0	0	
	vvi-miR399i	Vitis vinifera		0	0	0	23.06	0	0	0	0	
dof-miR-302	ptc-miR390d-3p	Populus trichocarpa	CGCTATCCATCCTGAGTTTTA	0	0	0	0.54	0	0	0	0	
	sly-miR390a-3p	Solanum lycopersicum		0	0	0	0.54	0	0	0	0	
dof-miR-303	gma-miR166m	Glycine max	CGGACCAGGCTTCATTCCCC	28.12	13.49	49.79	291.54	3.73	1.36	8.35	12.89	
dof-miR-304	mmu-miR-486b-3p	Mus musculus	CGGGGCAGCTCAGTACAGGA	0	0	0	0	0.28	0.1	0	0	
dof-miR-305	hsa-miR-486-3p	Homo sapiens	CGGGGCAGCTCAGTACAGGAT	0	0	0	0	0.19	0	0	0	
	mmu-miR-486a-3p	Mus musculus		0	0	0	0	0.19	0	0	0	
	tch-miR-486-3p	Tupaia chinensis		0	0	0	0	0.19	0	0	0	
	eca-miR-486-3p	Equus caballus		0	0	0	0	0.19	0	0	0	
	mml-miR-486-3p	Macaca mulatta		0	0	0	0	0.19	0	0	0	
dof-miR-306	bta-miR-126-3p	Bos taurus	CGTACCGTGAGTAATAATGCG	0	0	0	0	0.09	0	0.17	0	
dof-miR-307	hsa-miR-505-3p	Homo sapiens	CGTCAACACTTGCTGGTTTCCT	0.2	0	0	0	0	0	0	0	
	tch-miR-505-3p	Tupaia chinensis		0.2	0	0	0	0	0	0	0	

	ppy-miR-505	Pongo pygmaeus		0.2	0	0	0	0	0	0	0	0
	eca-miR-505	Equus caballus		0.2	0	0	0	0	0	0	0	0
	mml-miR-505-3p	Macaca mulatta		0.2	0	0	0	0	0	0	0	0
	ptr-miR-505	Pan troglodytes		0.2	0	0	0	0	0	0	0	0
	bta-miR-505	Bos taurus		0.2	0	0	0	0	0	0	0	0
dof-miR-308	ssa-miR-22b-5p	Salmo salar	CGTTCTTCACTGGCTAGCTTT	0	0	0	0	0	0	0	0.17	0
dof-miR-309	ppt-miR894	Physcomitrella patens	CGTTTCACGTCGGGTTACCC	0.2	0	50.53	7.21	2.98	2.19	2.5	1.26	
dof-miR-310	ssa-miR-144-3p	Salmo salar	CTACAGTATAGATGATGTAC	1.78	1.27	0	0	0.09	0	1	0.7	
dof-miR-311	ipu-miR-144	Ictalurus punctatus	CTACAGTATAGATGATGTACT	0.4	1.53	0	0	0	0	2	0.14	
	ccr-miR-144	Cyprinus carpio		0.4	1.53	0	0	0	0	2	0.14	
dof-miR-312	hsa-miR-151a-3p	Homo sapiens	CTAGACTGAAGCTCCTTGAGG	0	0	0.18	0	1.03	0.21	0	0	
	bta-miR-151-3p	Bos taurus		0	0	0.18	0	1.03	0.21	0	0	
	chi-miR-151-3p	Capra hircus		0	0	0.18	0	1.03	0.21	0	0	
	ppy-miR-151a-3p	Pongo pygmaeus		0	0	0.18	0	1.03	0.21	0	0	
	mml-miR-151-3p	Macaca mulatta		0	0	0.18	0	1.03	0.21	0	0	
	ptr-miR-151	Pan troglodytes		0	0	0.18	0	1.03	0.21	0	0	
dof-miR-313	ssc-miR-151-3p	Sus scrofa	CTAGACTGAAGCTCCTTGAGGA	0	0	0	0	1.03	0	0	0	
dof-miR-314	mmu-miR-151-3p	Mus musculus	CTAGACTGAGGCTCCTTGAGG	0	0	0	0	0	0	0	0	0.14
	rno-miR-151-3p	Rattus norvegicus		0	0	0	0	0	0	0	0	0.14
	cgr-miR-151-3p	Cricetulus griseus		0	0	0	0	0	0	0	0	0.14
dof-miR-315	ggo-miR-29a	Gorilla gorilla	CTAGCACCATCTGAAATCGGTT	0	0	0.18	0	0	0	0.17	0	
	age-miR-29a	Ateles geoffroyi		0	0	0.18	0	0	0	0.17	0	
	ppa-miR-29a	Pan paniscus		0	0	0.18	0	0	0	0.17	0	
	ppy-miR-29a	Pongo pygmaeus		0	0	0.18	0	0	0	0.17	0	
	ptr-miR-29a	Pan troglodytes		0	0	0.18	0	0	0	0.17	0	
	mml-miR-29a-3p	Macaca mulatta		0	0	0.18	0	0	0	0.17	0	
	sla-miR-29a	Saguinus labiatus		0	0	0.18	0	0	0	0.17	0	
	lla-miR-29a	Lagothrix lagotricha		0	0	0.18	0	0	0	0.17	0	
	mne-miR-29a	Macaca nemestrina		0	0	0.18	0	0	0	0.17	0	
dof-miR-316	chi-let-7b-3p	Capra hircus let-7b-3p	CTATAACAACCTACTGCCTTCCT	0	0	0	0.18	0	0	0	0	
dof-miR-317	ssa-let-7h-3p	Salmo salar let-7h-3p	CTATAACAACCTACTGCCTTCCT	0	0	0	0.18	0	0	0	0	
dof-miR-318	chi-let-7d-3p	Capra hircus let-7d-3p	CTATACGACCTGCTGCCTTTC	0	0	0	0	0.09	0	0	0	
dof-miR-319	hsa-let-7d-3p	Homo sapiens let-7d-3p	CTATACGACCTGCTGCCTTTC	0	0	0.18	0	0.09	0.21	0	0	
	mmu-let-7d-3p	Mus musculus let-7d-3p		0	0	0.18	0	0.09	0.21	0	0	

	rno-let-7d-3p	Rattus norvegicus let-7d-3p		0	0	0.18	0	0.09	0.21	0	0
	ssc-let-7d-3p	Sus scrofa let-7d-3p		0	0	0.18	0	0.09	0.21	0	0
	cgr-let-7d-3p	Cricetulus griseus let-7d-3p		0	0	0.18	0	0.09	0.21	0	0
dof-miR-320	hsa-let-7e-3p	Homo sapiens let-7e-3p	CTATACGGCCTCCTAGCTTTCC	0	0	0	0.36	0	0	0	0
	mmu-let-7e-3p	Mus musculus let-7e-3p		0	0	0	0.36	0	0	0	0
	rno-let-7e-3p	Rattus norvegicus let-7e-3p		0	0	0	0.36	0	0	0	0
	chi-let-7e-3p	Capra hircus let-7e-3p		0	0	0	0.36	0	0	0	0
	mml-let-7e-3p	Macaca mulatta let-7e-3p		0	0	0	0.36	0	0	0	0
dof-miR-321	ptc-miR396g-3p	Populus trichocarpa	CTCAAGAAAGCCGTGGGAAAA	0	0	0	0	0	0	0.17	0
dof-miR-322	ptc-miR396e-3p	Populus trichocarpa	CTCAAGAAAGCTGTGGGAGA	0	0	0.55	16.94	0	0	0.33	0
dof-miR-323	chi-miR-1468-5p	Capra hircus	CTCCGTTTGCCTGTTTTGTGTA	0	0	0.18	0.18	0	0	0	0
	ssc-miR-1468	Sus scrofa		0	0	0.18	0.18	0	0	0	0
	bta-miR-1468	Bos taurus		0	0	0.18	0.18	0	0	0	0
dof-miR-324	bdi-miR166e-3p	Brachypodium distachyon	CTCGGACCAGGCTTCATTCCC	287.18	90.12	275.59	108.11	153.14	106.63	173.29	245.08
dof-miR-325	ccr-miR-126-3p	Cyprinus carpio	CTCGTACCCTGAGTAATAATGC	0.4	0	0	1.8	0.09	0	1	0
dof-miR-326	mes-miR477a	Manihot esculenta	CTCTCCCTCAAGGGCTTCTG	0	0	0	0.54	0	0	0	0
	mes-miR477b	Manihot esculenta		0	0	0	0.54	0	0	0	0
	mes-miR477c	Manihot esculenta		0	0	0	0.54	0	0	0	0
	mes-miR477e	Manihot esculenta		0	0	0	0.54	0	0	0	0
dof-miR-327	ath-miR395a	Arabidopsis thaliana	CTGAAGTGTTGGGGGAAGCTC	0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ath-miR395d	Arabidopsis thaliana		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ath-miR395e	Arabidopsis thaliana		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395b	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395c	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395d	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395e	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395f	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395g	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395h	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395i	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	ptc-miR395j	Populus trichocarpa		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	vvi-miR395a	Vitis vinifera		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	vvi-miR395b	Vitis vinifera		0	1.78	0.55	0.54	0.84	0.31	0.33	0
vvi-miR395c	Vitis vinifera	0	1.78	0.55	0.54	0.84	0.31	0.33	0		

	gma-miR395a	Glycine max		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	gma-miR395b	Glycine max		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	gma-miR395c	Glycine max		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	aly-miR395g-3p	Arabidopsis lyrata		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	csi-miR395	Citrus sinensis		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	rco-miR395a	Ricinus communis		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	rco-miR395b	Ricinus communis		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	rco-miR395c	Ricinus communis		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	rco-miR395d	Ricinus communis		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	rco-miR395e	Ricinus communis		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	aly-miR395d-3p	Arabidopsis lyrata		0	1.78	0.55	0.54	0.84	0.31	0.33	0
	aly-miR395e-3p	Arabidopsis lyrata		0	1.78	0.55	0.54	0.84	0.31	0.33	0
dof-miR-328	stu-miR156f-5p	Solanum tuberosum	CTGACAGAAGAGAGTGAGCA	0	0	0.18	0	0	0	0	0
dof-miR-329	ama-miR156	Avicennia marina	CTGACAGAAGAGAGTGAGCAC	0	0	0.18	0.18	0	0.1	0.17	0.14
dof-miR-330	smo-miR156b	Selaginella moellendorffii	CTGACAGAAGATAGAGAGCAC	7.92	9.16	33.81	13.51	10.63	24.73	34.73	25.92
	mdm-miR156p	Malus domestica		7.92	9.16	33.81	13.51	10.63	24.73	34.73	25.92
	mdm-miR156q	Malus domestica		7.92	9.16	33.81	13.51	10.63	24.73	34.73	25.92
	mdm-miR156r	Malus domestica		7.92	9.16	33.81	13.51	10.63	24.73	34.73	25.92
	mdm-miR156s	Malus domestica		7.92	9.16	33.81	13.51	10.63	24.73	34.73	25.92
dof-miR-331	hsa-miR-192-5p	Homo sapiens	CTGACCTATGAATTGACAGCC	2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	mmu-miR-192-5p	Mus musculus		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	rno-miR-192-5p	Rattus norvegicus		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	oan-miR-192-5p	Ornithorhynchus anatinus		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	chi-miR-192-5p	Capra hircus		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	tch-miR-192-5p	Tupaia chinensis		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	ggo-miR-192	Gorilla gorilla		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	ppy-miR-192	Pongo pygmaeus		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	eca-miR-192	Equus caballus		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	ssc-miR-192	Sus scrofa		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	mml-miR-192-5p	Macaca mulatta		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	cfa-miR-192	Canis familiaris		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
	ptr-miR-192	Pan troglodytes		2.18	2.04	0.18	0.18	4.01	2.19	15.69	3.22
dof-miR-332	cgr-miR-192	Cricetulus griseus	CTGACCTATGAATTGACAGCCA	0.4	0.76	0	0	0.75	0.21	0.83	0.84
dof-miR-333	bta-miR-192	Bos taurus	CTGACCTATGAATTGACAGCCAG	0	0	0	0	0	0.1	0	0

dof-miR-334	mmu-let-7i-3p	Mus musculus let-7i-3p	CTGGCGCAAGCTACTGCCTTGCT	0	0	0	0	0.09	0	0	0
	hsa-let-7i-3p	Homo sapiens let-7i-3p		0	0	0	0	0.09	0	0	0
	rno-let-7i-3p	Rattus norvegicus let-7i-3p		0	0	0	0	0.09	0	0	0
	chi-let-7i-3p	Capra hircus let-7i-3p		0	0	0	0	0.09	0	0	0
	aja-let-7i	Artibeus jamaicensis let-7i		0	0	0	0	0.09	0	0	0
	tgu-let-7i-3p	Taeniopygia guttata let-7i-3p		0	0	0	0	0.09	0	0	0
dof-miR-335	hsa-miR-30c-2-3p	Homo sapiens	CTGGGAGAAGGCTGTTTACTCT	0	0	0	0.18	0	0	0	0
	mmu-miR-30c-2-3p	Mus musculus		0	0	0	0.18	0	0	0	0
	rno-miR-30c-2-3p	Rattus norvegicus		0	0	0	0.18	0	0	0	0
	ssc-miR-30c-3p	Sus scrofa		0	0	0	0.18	0	0	0	0
	oan-miR-30c-2-3p	Ornithorhynchus anatinus		0	0	0	0.18	0	0	0	0
	oha-miR-30c-1-3p	Ophiophagus hannah		0	0	0	0.18	0	0	0	0
	aca-miR-30c-3p	Anolis carolinensis		0	0	0	0.18	0	0	0	0
	tgu-miR-30c-3p	Taeniopygia guttata		0	0	0	0.18	0	0	0	0
dof-miR-336	ssa-miR-210-3p	Salmo salar	CTGTGCGTGTGACAGCGGCT	0	0	0.18	0	0	0	0	0
	ipu-miR-210	Ictalurus punctatus		0	0	0.18	0	0	0	0	0
	ccr-miR-210	Cyprinus carpio		0	0	0.18	0	0	0	0	0
dof-miR-337	dre-miR-210-3p	Danio rerio	CTGTGCGTGTGACAGCGCTAA	0.2	0	0	0	0	0	0	0
	fru-miR-210	Fugu rubripes		0.2	0	0	0	0	0	0	0
	tmi-miR-210	Tetraodon nigroviridis		0.2	0	0	0	0	0	0	0
	xtr-miR-210	Xenopus tropicalis		0.2	0	0	0	0	0	0	0
	oha-miR-210-3p	Ophiophagus hannah		0.2	0	0	0	0	0	0	0
dof-miR-338	mmu-miR-744-3p	Mus musculus	CTGTTGCCACTAACCTCAACCT	0	0	0	0	0.09	0	0	0
	hsa-miR-744-3p	Homo sapiens		0	0	0	0	0.09	0	0	0
dof-miR-339	hsa-miR-374a-3p	Homo sapiens	CTTATCAGATTGTATTGTAATT	0	0	0	0	0.28	0	0	0
	mml-miR-374a-3p	Macaca mulatta		0	0	0	0	0.28	0	0	0
dof-miR-340	ppt-miR319a	Physcomitrella patens	CTTGACTGAAGGGAGCTCC	0.79	0	2.02	1.44	5.97	5.32	1.17	0.28
	ppt-miR319b	Physcomitrella patens		0.79	0	2.02	1.44	5.97	5.32	1.17	0.28
	sly-miR319a	Solanum lycopersicum		0.79	0	2.02	1.44	5.97	5.32	1.17	0.28
dof-miR-341	ppt-miR319c	Physcomitrella patens	CTTGACTGAAGGGAGCTCCC	177.85	9.67	197.88	61.44	510.72	529.51	92.16	105.51
	ppt-miR319d-3p	Physcomitrella patens		177.85	9.67	197.88	61.44	510.72	529.51	92.16	105.51
	ppt-miR319e	Physcomitrella patens		177.85	9.67	197.88	61.44	510.72	529.51	92.16	105.51
dof-miR-342	mes-miR319h	Manihot esculenta	CTTGACTGAAGGGAGCTCCT	0	0	0.37	1.08	1.31	2.4	0	0
	vun-miR319b	Vigna unguiculata		0	0	0.37	1.08	1.31	2.4	0	0

dof-miR-343	cpa-miR159b	Carica papaya	CTTGGATTGAAGGGAGCTCC	200.83	1.53	7.17	2.52	1.4	0.94	2.34	17.94
	mdm-miR159a	Malus domestica		200.83	1.53	7.17	2.52	1.4	0.94	2.34	17.94
	mdm-miR159b	Malus domestica		200.83	1.53	7.17	2.52	1.4	0.94	2.34	17.94
dof-miR-344	pta-miR159c	Pinus taeda	CTTGGATTGAAGGGAGCTCCC	0.2	0	0.18	0.18	0.28	0	0	0.14
	smo-miR159	Selaginella moellendorffii		0.2	0	0.18	0.18	0.28	0	0	0.14
dof-miR-345	sof-miR159c	Saccharum officinarum	CTTGGATTGAAGGGAGCTCCT	6.73	0	0.37	0.9	0	0	0	0.84
	zma-miR159c-3p	Zea mays		6.73	0	0.37	0.9	0	0	0	0.84
	zma-miR159d-3p	Zea mays		6.73	0	0.37	0.9	0	0	0	0.84
	sbi-miR159b	Sorghum bicolor		6.73	0	0.37	0.9	0	0	0	0.84
	ptc-miR159d	Populus trichocarpa		6.73	0	0.37	0.9	0	0	0	0.84
dof-miR-346	bdi-miR159a-3p	Brachypodium distachyon	CTTGGATTGAAGGGAGCTCT	0.2	0	0.18	0.36	0.56	0.1	0	0
dof-miR-347	cfa-miR-1271	Canis familiaris	CTTGGCACCTAGTAAGCACT	0	0.51	0	0	0	0	0	0.42
dof-miR-348	mmu-miR-30e-3p	Mus musculus	CTTTCAGTCGGATGTTTACAGC	0	0	0.18	0	0.75	0	0	0.14
	hsa-miR-30e-3p	Homo sapiens		0	0	0.18	0	0.75	0	0	0.14
	rno-miR-30e-3p	Rattus norvegicus		0	0	0.18	0	0.75	0	0	0.14
	oan-miR-30e-3p	Ornithorhynchus anatinus		0	0	0.18	0	0.75	0	0	0.14
	oha-miR-30e-3p	Ophiophagus hannah		0	0	0.18	0	0.75	0	0	0.14
	cgr-miR-30e-3p	Cricetulus griseus		0	0	0.18	0	0.75	0	0	0.14
	aca-miR-30e-3p	Anolis carolinensis		0	0	0.18	0	0.75	0	0	0.14
	ssc-miR-30e-3p	Sus scrofa		0	0	0.18	0	0.75	0	0	0.14
	tgu-miR-30a-3p	Taeniopygia guttata		0	0	0.18	0	0.75	0	0	0.14
	cfa-miR-30e	Canis familiaris		0	0	0.18	0	0.75	0	0	0.14
dof-miR-349	hsa-miR-30a-3p	Homo sapiens	CTTTCAGTCGGATGTTTGCAGC	0.2	0.25	0	0.54	0	0	0	0.14
	mmu-miR-30a-3p	Mus musculus		0.2	0.25	0	0.54	0	0	0	0.14
	rno-miR-30a-3p	Rattus norvegicus		0.2	0.25	0	0.54	0	0	0	0.14
	gga-miR-30a-3p	Gallus gallus		0.2	0.25	0	0.54	0	0	0	0.14
	dre-miR-30e-3p	Danio rerio		0.2	0.25	0	0.54	0	0	0	0.14
	mml-miR-30a-3p	Macaca mulatta		0.2	0.25	0	0.54	0	0	0	0.14
	ptr-miR-30a-3p	Pan troglodytes		0.2	0.25	0	0.54	0	0	0	0.14
	ggo-miR-30a-3p	Gorilla gorilla		0.2	0.25	0	0.54	0	0	0	0.14
	ppy-miR-30a-3p	Pongo pygmaeus		0.2	0.25	0	0.54	0	0	0	0.14
	ppa-miR-30a-3p	Pan paniscus		0.2	0.25	0	0.54	0	0	0	0.14
	oan-miR-30a-3p	Ornithorhynchus anatinus		0.2	0.25	0	0.54	0	0	0	0.14
	oha-miR-30a-3p	Ophiophagus hannah		0.2	0.25	0	0.54	0	0	0	0.14

	ssa-miR-30c-3p	Salmo salar		0.2	0.25	0	0.54	0	0	0	0.14		
	ssa-miR-30d-3p	Salmo salar		0.2	0.25	0	0.54	0	0	0	0.14		
	ipu-miR-30e	Ictalurus punctatus		0.2	0.25	0	0.54	0	0	0	0.14		
	cgr-miR-30a-3p	Cricetulus griseus		0.2	0.25	0	0.54	0	0	0	0.14		
	aca-miR-30a-3p	Anolis carolinensis		0.2	0.25	0	0.54	0	0	0	0.14		
	ssc-miR-30a-3p	Sus scrofa		0.2	0.25	0	0.54	0	0	0	0.14		
dof-miR-350	mmu-miR-129-5p	Mus musculus	CTTTTTCGGTCTGGGCTTGC	0	0	0	0	0	0	0	0.17	0	
	hsa-miR-129-5p	Homo sapiens		0	0	0	0	0	0	0	0	0.17	0
	rno-miR-129-5p	Rattus norvegicus		0	0	0	0	0	0	0	0	0.17	0
	xtr-miR-129	Xenopus tropicalis		0	0	0	0	0	0	0	0	0.17	0
	oan-miR-129-5p	Ornithorhynchus anatinus		0	0	0	0	0	0	0	0	0.17	0
	chi-miR-129-5p	Capra hircus		0	0	0	0	0	0	0	0	0.17	0
	tch-miR-129-5p	Tupaia chinensis		0	0	0	0	0	0	0	0	0.17	0
	ssa-miR-129-5p	Salmo salar		0	0	0	0	0	0	0	0	0.17	0
	ipu-miR-129	Ictalurus punctatus		0	0	0	0	0	0	0	0	0.17	0
	ccr-miR-129	Cyprinus carpio		0	0	0	0	0	0	0	0	0.17	0
	sha-miR-129	Sarcophilus harrisii		0	0	0	0	0	0	0	0	0.17	0
	cgr-miR-129	Cricetulus griseus		0	0	0	0	0	0	0	0	0.17	0
	ssc-miR-129b	Sus scrofa		0	0	0	0	0	0	0	0	0.17	0
	aca-miR-129a-5p	Anolis carolinensis		0	0	0	0	0	0	0	0	0.17	0
	ppy-miR-129-5p	Pongo pygmaeus		0	0	0	0	0	0	0	0	0.17	0
	eca-miR-129a-5p	Equus caballus		0	0	0	0	0	0	0	0	0.17	0
	eca-miR-129b-5p	Equus caballus		0	0	0	0	0	0	0	0	0.17	0
	ssc-miR-129a-5p	Sus scrofa		0	0	0	0	0	0	0	0	0.17	0
	tgu-miR-129-5p	Taeniopygia guttata		0	0	0	0	0	0	0	0	0.17	0
	mml-miR-129-5p	Macaca mulatta		0	0	0	0	0	0	0	0	0.17	0
cfa-miR-129	Canis familiaris	0	0	0	0	0	0	0	0	0.17	0		
ptr-miR-129	Pan troglodytes	0	0	0	0	0	0	0	0	0.17	0		
dof-miR-351	chi-miR-499-3p	Capra hircus	GAACATCACAGCAAGTCTGTGC	0	0.25	0	0	0	0	0	0	0	
	cgr-miR-499-3p	Cricetulus griseus		0	0.25	0	0	0	0	0	0	0	
dof-miR-352	mmu-miR-148b-5p	Mus musculus	GAAGTTCTGTTATACACTCAGGCT	0	0	0	0	0.09	0	0	0	0	
	mml-miR-148b-5p	Macaca mulatta		0	0	0	0	0.09	0	0	0	0	
dof-miR-353	hsa-miR-382-5p	Homo sapiens	GAAGTTGTTTCGTGGTGGATTCC	0	0	0	0.36	0.09	0	0	0	0	
	mmu-miR-382-5p	Mus musculus		0	0	0	0.36	0.09	0	0	0	0	

	rno-miR-382-5p	Rattus norvegicus		0	0	0	0.36	0.09	0	0	0
	chi-miR-382-5p	Capra hircus		0	0	0	0.36	0.09	0	0	0
	cgr-miR-382	Cricetulus griseus		0	0	0	0.36	0.09	0	0	0
	oar-miR-382-5p	Ovis aries		0	0	0	0.36	0.09	0	0	0
	eca-miR-382	Equus caballus		0	0	0	0.36	0.09	0	0	0
	mml-miR-382-5p	Macaca mulatta		0	0	0	0.36	0.09	0	0	0
	ptr-miR-382	Pan troglodytes		0	0	0	0.36	0.09	0	0	0
	bta-miR-382	Bos taurus		0	0	0	0.36	0.09	0	0	0
dof-miR-354	aly-miR172e-3p	Arabidopsis lyrata	GAATCTTGATGATGCTGCAT	0	0	0	0.18	0.09	0.1	0	0.14
dof-miR-355	mmu-miR-409-3p	Mus musculus	GAATGTTGCTCGGTGAACCCCT	0	0.25	1.29	1.62	0.19	0.1	0	0
	hsa-miR-409-3p	Homo sapiens		0	0.25	1.29	1.62	0.19	0.1	0	0
	tch-miR-409-3p	Tupaia chinensis		0	0.25	1.29	1.62	0.19	0.1	0	0
	cgr-miR-409-3p	Cricetulus griseus		0	0.25	1.29	1.62	0.19	0.1	0	0
	ppy-miR-409-3p	Pongo pygmaeus		0	0.25	1.29	1.62	0.19	0.1	0	0
	eca-miR-409-3p	Equus caballus		0	0.25	1.29	1.62	0.19	0.1	0	0
	mml-miR-409-3p	Macaca mulatta		0	0.25	1.29	1.62	0.19	0.1	0	0
	ptr-miR-409	Pan troglodytes		0	0.25	1.29	1.62	0.19	0.1	0	0
dof-miR-356	api-miR-100	Acyrtosiphon pisum	GACCCGTAGATCCGAACCTTGTG	0	0.25	0	0	0	0	0	0
	nve-miR-100-5p	Nematostella vectensis		0	0.25	0	0	0	0	0	0
dof-miR-357	ssa-miR-7132b-5p	Salmo salar	GACTTGGTCAAAGTCCTCAGC	0	0	0	0	0	0	0.17	0
dof-miR-358	ppt-miR390c-5p	Physcomitrella patens	GAGCTCAGGAGGGATAGCGCC	0.2	0	0	0	0	0	0.17	0
dof-miR-359	gma-miR159e-5p	Glycine max	GAGTCCTTGAAGTCCAATT	0	0	0	0.18	0	0	0	0
dof-miR-360	hsa-miR-590-5p	Homo sapiens	GAGCTTATTCATAAAAGTGCAG	0	0	0	0	0.09	0	0	0
	mmu-miR-590-5p	Mus musculus		0	0	0	0	0.09	0	0	0
	ggo-miR-590	Gorilla gorilla		0	0	0	0	0.09	0	0	0
	ppy-miR-590-5p	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	mml-miR-590-5p	Macaca mulatta		0	0	0	0	0.09	0	0	0
dof-miR-361	ath-miR167a-3p	Arabidopsis thaliana	GATCATGTTCCGACGTTTCACC	0	0	0	0	0	0	0	0.28
	aly-miR167a-3p	Arabidopsis lyrata		0	0	0	0	0	0	0	0.28
dof-miR-362	ath-miR8175	Arabidopsis thaliana	GATCCCCGGCAACGGCGCCA	4.95	1.53	0.37	5.41	3.54	1.67	3.17	9.39
dof-miR-363	hsa-miR-330-3p	Homo sapiens	GCAAAGCACACGGCTGCAGAGA	0	0	0	0	0.19	0	0	0
	tch-miR-330-3p	Tupaia chinensis		0	0	0	0	0.19	0	0	0
	ggo-miR-330	Gorilla gorilla		0	0	0	0	0.19	0	0	0
	ppy-miR-330-3p	Pongo pygmaeus		0	0	0	0	0.19	0	0	0

	mml-miR-330-3p	Macaca mulatta		0	0	0	0	0.19	0	0	0
	ptr-miR-330	Pan troglodytes		0	0	0	0	0.19	0	0	0
	bta-miR-330	Bos taurus		0	0	0	0	0.19	0	0	0
dof-miR-364	ssc-miR-323	Sus scrofa	GCACATTACACGGTCGACCTCT	0	0	0.18	0.72	0	0	0.17	0
	bta-miR-323	Bos taurus		0	0	0.18	0.72	0	0	0.17	0
dof-miR-365	bta-miR-455-3p	Bos taurus	GCAGTCCATGGGCATATACACT	0	0	0.18	0.18	0	0	0	0
	chi-miR-455-3p	Capra hircus		0	0	0.18	0.18	0	0	0	0
	tch-miR-455-3p	Tupaia chinensis		0	0	0.18	0.18	0	0	0	0
	ssa-miR-455-3p	Salmo salar		0	0	0.18	0.18	0	0	0	0
dof-miR-366	ptc-miR160e-3p	Populus trichocarpa	GCATGAGGGGAGTCGAGCAGG	0	0	0	0.18	0	0	0	0
dof-miR-367	cgr-miR-331-3p	Cricetulus griseus	GCCCCTGGGCCTATCCTAGA	0	0	0	0.36	0	0	0	0
dof-miR-368	rno-miR-331-3p	Rattus norvegicus	GCCCCTGGGCCTATCCTAGAA	0	0	0	0.36	0	0	0	0
	mmu-miR-331-3p	Mus musculus		0	0	0	0.36	0	0	0	0
	hsa-miR-331-3p	Homo sapiens		0	0	0	0.36	0	0	0	0
	bta-miR-331-3p	Bos taurus		0	0	0	0.36	0	0	0	0
	aja-miR-331	Artibeus jamaicensis		0	0	0	0.36	0	0	0	0
	eca-miR-331	Equus caballus		0	0	0	0.36	0	0	0	0
	ssc-miR-331-3p	Sus scrofa		0	0	0	0.36	0	0	0	0
	mml-miR-331-3p	Macaca mulatta		0	0	0	0.36	0	0	0	0
	ptr-miR-331	Pan troglodytes		0	0	0	0.36	0	0	0	0
	cfa-miR-331	Canis familiaris		0	0	0	0.36	0	0	0	0
dof-miR-369	hsa-miR-370-3p	Homo sapiens	GCCTGCTGGGGTGAACCTGGT	0	0	0.55	0.9	0	0	0	0
	mmu-miR-370-3p	Mus musculus		0	0	0.55	0.9	0	0	0	0
	rno-miR-370-3p	Rattus norvegicus		0	0	0.55	0.9	0	0	0	0
	efu-miR-370	Eptesicus fuscus		0	0	0.55	0.9	0	0	0	0
	ssc-miR-370	Sus scrofa		0	0	0.55	0.9	0	0	0	0
	ppy-miR-370	Pongo pygmaeus		0	0	0.55	0.9	0	0	0	0
	eca-miR-370	Equus caballus		0	0	0.55	0.9	0	0	0	0
	mml-miR-370-3p	Macaca mulatta		0	0	0.55	0.9	0	0	0	0
	ptr-miR-370	Pan troglodytes		0	0	0.55	0.9	0	0	0	0
	bta-miR-370	Bos taurus		0	0	0.55	0.9	0	0	0	0
	cfa-miR-370	Canis familiaris		0	0	0.55	0.9	0	0	0	0
dof-miR-370	ath-miR160a-3p	Arabidopsis thaliana	GCGTATGAGGAGCCATGCATA	0	0	0.18	5.59	0	0	0	0
	ptc-miR160b-3p	Populus trichocarpa		0	0	0.18	5.59	0	0	0	0

	ptc-miR160c-3p	Populus trichocarpa		0	0	0.18	5.59	0	0	0	0
	cpa-miR160c-3p	Carica papaya		0	0	0.18	5.59	0	0	0	0
	cpa-miR160f-3p	Carica papaya		0	0	0.18	5.59	0	0	0	0
	aly-miR160a-3p	Arabidopsis lyrata		0	0	0.18	5.59	0	0	0	0
	bra-miR160a-3p	Brassica rapa		0	0	0.18	5.59	0	0	0	0
dof-miR-371	ath-miR396b-3p	Arabidopsis thaliana	GCTCAAGAAAGCTGTGGGAAA	0	0	0	0.18	0	0	0	0
	bra-miR396-3p	Brassica rapa		0	0	0	0.18	0	0	0	0
	aly-miR396b-3p	Arabidopsis lyrata		0	0	0	0.18	0	0	0	0
dof-miR-372	gma-miR396b-3p	Glycine max	GCTCAAGAAAGCTGTGGGAGA	0	0	0	36.76	0	0	0	0
	mtr-miR396a-3p	Medicago truncatula		0	0	0	36.76	0	0	0	0
	gma-miR396k-3p	Glycine max		0	0	0	36.76	0	0	0	0
dof-miR-373	ath-miR156f-3p	Arabidopsis thaliana	GCTCACTCTCTATCCGTCACC	0	0	0	0	0	0	0	0.14
dof-miR-374	bra-miR156b-3p	Brassica rapa	GCTCACTCTCTATCTGTCACC	0	0	0.18	1.62	0	0.21	0.33	5.6
	bra-miR156d-3p	Brassica rapa		0	0	0.18	1.62	0	0.21	0.33	5.6
	aly-miR156f-3p	Arabidopsis lyrata		0	0	0.18	1.62	0	0.21	0.33	5.6
dof-miR-375	osa-miR156f-3p	Oryza sativa	GCTCACTTCTTTTCTGTCAGC	0	0	0	3.6	0	0	0	0
	osa-miR156h-3p	Oryza sativa		0	0	0	3.6	0	0	0	0
	osa-miR156l-3p	Oryza sativa		0	0	0	3.6	0	0	0	0
	zma-miR156d-3p	Zea mays		0	0	0	3.6	0	0	0	0
	zma-miR156f-3p	Zea mays		0	0	0	3.6	0	0	0	0
	zma-miR156g-3p	Zea mays		0	0	0	3.6	0	0	0	0
dof-miR-376	aly-miR157d-3p	Arabidopsis lyrata	GCTCTCTATGCTTCTGTCATC	0	0	0	40.72	0	0	0	0
dof-miR-377	ptc-miR172g-3p	Populus trichocarpa	GGAATCTTGATGATGCTGCAG	0	0	0	0.18	0	0	0	0
	ptc-miR172h-3p	Populus trichocarpa		0	0	0	0.18	0	0	0	0
	vvi-miR172c	Vitis vinifera		0	0	0	0.18	0	0	0	0
	ppe-miR172d	Prunus persica		0	0	0	0.18	0	0	0	0
	mes-miR172e	Manihot esculenta		0	0	0	0.18	0	0	0	0
	mes-miR172f	Manihot esculenta		0	0	0	0.18	0	0	0	0
	stu-miR172d-3p	Solanum tuberosum		0	0	0	0.18	0	0	0	0
	mdm-miR172l	Malus domestica		0	0	0	0.18	0	0	0	0
	cme-miR172a	Cucumis melo		0	0	0	0.18	0	0	0	0
	lus-miR172e	Linum usitatissimum		0	0	0	0.18	0	0	0	0
	lus-miR172i	Linum usitatissimum		0	0	0	0.18	0	0	0	0
	rco-miR172	Ricinus communis		0	0	0	0.18	0	0	0	0

	gma-miR172c	Glycine max		0	0	0	0.18	0	0	0	0
dof-miR-378	ath-miR172e-3p	Arabidopsis thaliana	GGAATCTTGATGATGCTGCAT	0.2	0	0	0.36	0	0	0	0
	osa-miR172b	Oryza sativa		0.2	0	0	0.36	0	0	0	0
	zma-miR172e	Zea mays		0.2	0	0	0.36	0	0	0	0
	ptc-miR172d	Populus trichocarpa		0.2	0	0	0.36	0	0	0	0
	ptc-miR172e	Populus trichocarpa		0.2	0	0	0.36	0	0	0	0
	bra-miR172d-3p	Brassica rapa		0.2	0	0	0.36	0	0	0	0
	ata-miR172c-3p	Aegilops tauschii		0.2	0	0	0.36	0	0	0	0
	ppe-miR172c	Prunus persica		0.2	0	0	0.36	0	0	0	0
	mdm-miR172i	Malus domestica		0.2	0	0	0.36	0	0	0	0
	mdm-miR172j	Malus domestica		0.2	0	0	0.36	0	0	0	0
	mdm-miR172k	Malus domestica		0.2	0	0	0.36	0	0	0	0
	cme-miR172d	Cucumis melo		0.2	0	0	0.36	0	0	0	0
	gma-miR172l	Glycine max		0.2	0	0	0.36	0	0	0	0
	bnm-miR172b	Brassica napus		0.2	0	0	0.36	0	0	0	0
	bnm-miR172c	Brassica napus		0.2	0	0	0.36	0	0	0	0
	lus-miR172g	Linum usitatissimum		0.2	0	0	0.36	0	0	0	0
	nta-miR172j	Nicotiana tabacum		0.2	0	0	0.36	0	0	0	0
	tcc-miR172c	Theobroma cacao		0.2	0	0	0.36	0	0	0	0
	bdi-miR172b	Brachypodium distachyon		0.2	0	0	0.36	0	0	0	0
	gma-miR172i-3p	Glycine max		0.2	0	0	0.36	0	0	0	0
aqc-miR172b	Aquilegia caerulea	0.2	0	0	0.36	0	0	0	0		
dof-miR-379	osa-miR166h-5p	Oryza sativa	GGAATGTTGGCTGGCTCGAGG	0.2	0	0	0	0.09	0.1	0	0
	zma-miR166m-5p	Zea mays		0.2	0	0	0	0.09	0.1	0	0
	mtr-miR166e-5p	Medicago truncatula		0.2	0	0	0	0.09	0.1	0	0
dof-miR-380	ath-miR165a-5p	Arabidopsis thaliana	GGAATGTTGTCTGGATCGAGG	0	0	0	0	0	0	0	0.14
dof-miR-381	osa-miR166d-5p	Oryza sativa	GGAATGTTGTCTGGCTCGAGG	264.8	18.07	83.41	251	19.21	29.11	105.85	111.68
	zma-miR166c-5p	Zea mays		264.8	18.07	83.41	251	19.21	29.11	105.85	111.68
	gma-miR166a-5p	Glycine max		264.8	18.07	83.41	251	19.21	29.11	105.85	111.68
	mtr-miR166g-5p	Medicago truncatula		264.8	18.07	83.41	251	19.21	29.11	105.85	111.68
	stu-miR166a-5p	Solanum tuberosum		264.8	18.07	83.41	251	19.21	29.11	105.85	111.68
	gma-miR166l	Glycine max		264.8	18.07	83.41	251	19.21	29.11	105.85	111.68
	gma-miR166c-5p	Glycine max		264.8	18.07	83.41	251	19.21	29.11	105.85	111.68
	bdi-miR166e-5p	Brachypodium distachyon		264.8	18.07	83.41	251	19.21	29.11	105.85	111.68

dof-miR-392	hsa-miR-145-3p	Homo sapiens	GGATTCCTGGAAATACTGTTCT	0.4	0.25	0.55	0	0	0	1.17	0
	dre-miR-145-3p	Danio rerio		0.4	0.25	0.55	0	0	0	1.17	0
	ssc-miR-145-3p	Sus scrofa		0.4	0.25	0.55	0	0	0	1.17	0
	oha-miR-145-3p	Ophiophagus hannah		0.4	0.25	0.55	0	0	0	1.17	0
	aja-miR-145	Artibeus jamaicensis		0.4	0.25	0.55	0	0	0	1.17	0
dof-miR-393	aly-miR167b-3p	Arabidopsis lyrata	GGTCATGCTCTGACAGCCTCACT	0	0	0.18	6.49	0	0	0	0
dof-miR-394	mmu-miR-143-5p	Mus musculus	GGTGCAGTGCTGCATCTCTGG	0	0	0.18	0.18	0	0	0	0
	rno-miR-143-5p	Rattus norvegicus		0	0	0.18	0.18	0	0	0	0
	chi-miR-143-5p	Capra hircus		0	0	0.18	0.18	0	0	0	0
	aca-miR-143-5p	Anolis carolinensis		0	0	0.18	0.18	0	0	0	0
	ssc-miR-143-5p	Sus scrofa		0	0	0.18	0.18	0	0	0	0
dof-miR-395	hsa-miR-143-5p	Homo sapiens	GGTGCAGTGCTGCATCTCTGGT	0	0	0.18	0.18	0	0	0	0
	ssa-miR-143-5p	Salmo salar		0	0	0.18	0.18	0	0	0	0
dof-miR-396	chi-miR-3959-5p	Capra hircus	GGTTGATCAGAGAACATACATT	0	0	0	0.18	0	0	0	0.14
	bta-miR-411c-5p	Bos taurus		0	0	0	0.18	0	0	0	0.14
	oar-miR-3959-5p	Ovis aries		0	0	0	0.18	0	0	0	0.14
dof-miR-397	tch-miR-101	Tupaia chinensis	GTACAGTACTGTGATAACTGA	0	0	0.37	0.72	0.28	0.21	0.17	0
	ola-miR-101a-3p	Oryzias latipes		0	0	0.37	0.72	0.28	0.21	0.17	0
	sha-miR-101	Sarcophilus harrisii		0	0	0.37	0.72	0.28	0.21	0.17	0
dof-miR-398	gga-miR-101-3p	Gallus gallus	GTACAGTACTGTGATAACTGAA	0	0	0.55	0.54	0.09	0.1	0.17	0
	oha-miR-101a-3p	Ophiophagus hannah		0	0	0.55	0.54	0.09	0.1	0.17	0
	tgu-miR-101-3p	Taeniopygia guttata		0	0	0.55	0.54	0.09	0.1	0.17	0
dof-miR-399	gma-miR172b-5p	Glycine max	GTAGCATCATCAAGATTCAC	0	0	0	2.16	0	0	0	0
dof-miR-400	mtr-miR172c-5p	Medicago truncatula	GTAGCATCATCAAGATTCACA	0	0	0	0.9	0	0	0.17	0
dof-miR-401	ccr-miR-142-3p	Cyprinus carpio	GTAGTGTTCCTACTTTATGG	0	0	0	0	0.28	0	0	0
	cgr-miR-142-3p	Cricetulus griseus		0	0	0	0	0.28	0	0	0
dof-miR-402	tch-miR-142	Tupaia chinensis	GTAGTGTTCCTACTTTATGGA	0.2	0	0	0.18	0.28	0	0	0.14
	ipu-miR-142	Ictalurus punctatus		0.2	0	0	0.18	0.28	0	0	0.14
	tgu-miR-142-3p	Taeniopygia guttata		0.2	0	0	0.18	0.28	0	0	0.14
dof-miR-403	hsa-miR-485-3p	Homo sapiens	GTCATACACGGCTCTCCTCTCT	0	0	0	0.36	0.09	0	0	0
	efu-miR-485	Eptesicus fuscus		0	0	0	0.36	0.09	0	0	0
	oar-miR-485-3p	Ovis aries		0	0	0	0.36	0.09	0	0	0
	ppy-miR-485-3p	Pongo pygmaeus		0	0	0	0.36	0.09	0	0	0
	eca-miR-485-3p	Equus caballus		0	0	0	0.36	0.09	0	0	0

	mml-miR-485-3p	Macaca mulatta		0	0	0	0.36	0.09	0	0	0
	ptr-miR-485	Pan troglodytes		0	0	0	0.36	0.09	0	0	0
dof-miR-404	oan-miR-153-1-5p	Ornithorhynchus anatinus	GTCCATTTTGTGATCTGCAGCT	0	0	0	0	0	0.1	0	0
dof-miR-405	oan-miR-145-5p	Ornithorhynchus anatinus	GTCCAGTTTCCCAGGAAT	0	0	0	0.36	0	0.1	0	0
dof-miR-406	dre-miR-145-5p	Danio rerio	GTCCAGTTTCCCAGGAATCCC	0	0.25	0.73	1.26	0	0	0.33	0
	aca-miR-145-5p	Anolis carolinensis		0	0.25	0.73	1.26	0	0	0.33	0
dof-miR-407	mmu-miR-145a-5p	Mus musculus	GTCCAGTTTCCCAGGAATCCCT	0.2	0.25	1.29	0.54	0	0	0.17	0.14
	hsa-miR-145-5p	Homo sapiens		0.2	0.25	1.29	0.54	0	0	0.17	0.14
	rno-miR-145-5p	Rattus norvegicus		0.2	0.25	1.29	0.54	0	0	0.17	0.14
	bta-miR-145	Bos taurus		0.2	0.25	1.29	0.54	0	0	0.17	0.14
	mdo-miR-145-5p	Monodelphis domestica		0.2	0.25	1.29	0.54	0	0	0.17	0.14
	chi-miR-145-5p	Capra hircus		0.2	0.25	1.29	0.54	0	0	0.17	0.14
	ssa-miR-145-5p	Salmo salar		0.2	0.25	1.29	0.54	0	0	0.17	0.14
	ipu-miR-145	Ictalurus punctatus		0.2	0.25	1.29	0.54	0	0	0.17	0.14
	pma-miR-145-5p	Petromyzon marinus		0.2	0.25	1.29	0.54	0	0	0.17	0.14
	eca-miR-145	Equus caballus		0.2	0.25	1.29	0.54	0	0	0.17	0.14
cfa-miR-145	Canis familiaris	0.2	0.25	1.29	0.54	0	0	0.17	0.14		
dof-miR-408	gma-miR6300	Glycine max	GTCCGTGTAGTATAGTGG	2.18	0.51	9.74	2.34	1.59	1.67	0.83	27.6
dof-miR-409	mmu-miR-203-3p	Mus musculus	GTGAAATGTTTAGGACCACTAG	0	0	0	0	0	0	0	0.14
	hsa-miR-203a-3p	Homo sapiens		0	0	0	0	0	0	0	0.14
	rno-miR-203a-3p	Rattus norvegicus		0	0	0	0	0	0	0	0.14
	ppy-miR-203	Pongo pygmaeus		0	0	0	0	0	0	0	0.14
	mml-miR-203	Macaca mulatta		0	0	0	0	0	0	0	0.14
	ptr-miR-203	Pan troglodytes		0	0	0	0	0	0	0	0.14
	cfa-miR-203	Canis familiaris		0	0	0	0	0	0	0	0.14
dof-miR-410	ssc-miR-24-1-5p	Sus scrofa	GTGCCTACTGAGCTGAAACACAGT	0	0	0	0	0.09	0	0	0
	mdo-miR-24-5p	Monodelphis domestica		0	0	0	0	0.09	0	0	0
dof-miR-411	cgr-miR-24-5p	Cricetulus griseus	GTGCCTACTGAGCTGAAACAG	0	0	0	0	0.09	0	0	0
dof-miR-412	aly-miR172a-5p	Arabidopsis lyrata	GTGGCATCATCAAGATTCACA	0.4	0	0	0	0.37	0.31	0.83	0.14
dof-miR-413	ptc-miR6427-3p	Populus trichocarpa	GTGGGAATGAACATTATGAGA	0	0	0.55	0.18	0	0	0.33	0
dof-miR-414	osa-miR396a-3p	Oryza sativa	GTTCAATAAAGCTGTGGGAA	0	0.25	4.04	2.34	0	0.21	0.17	0.14
	osa-miR396b-3p	Oryza sativa		0	0.25	4.04	2.34	0	0.21	0.17	0.14
dof-miR-415	zma-miR396b-3p	Zea mays	GTTCAATAAAGCTGTGGGAA	10.1	4.84	37.85	8.29	4.1	7.83	2.34	4.62
	zma-miR396a-3p	Zea mays		10.1	4.84	37.85	8.29	4.1	7.83	2.34	4.62

	ata-miR396e-3p	Aegilops tauschii		10.1	4.84	37.85	8.29	4.1	7.83	2.34	4.62
	bdi-miR396d-3p	Brachypodium distachyon		10.1	4.84	37.85	8.29	4.1	7.83	2.34	4.62
	bdi-miR396c-3p	Brachypodium distachyon		10.1	4.84	37.85	8.29	4.1	7.83	2.34	4.62
dof-miR-416	ath-miR396a-3p	Arabidopsis thaliana	GTTCAATAAAGCTGTGGGAAG	0	0	0.92	77.84	0	0	0.17	0
	mtr-miR396b-3p	Medicago truncatula		0	0	0.92	77.84	0	0	0.17	0
	sly-miR396a-3p	Solanum lycopersicum		0	0	0.92	77.84	0	0	0.17	0
	gma-miR396i-3p	Glycine max		0	0	0.92	77.84	0	0	0.17	0
	aly-miR396a-3p	Arabidopsis lyrata		0	0	0.92	77.84	0	0	0.17	0
dof-miR-417	ipu-miR-737	Ictalurus punctatus	GTTTTTTTAGGTTTTGATTTTT	0.2	0	0	0.36	0	0	0	0
dof-miR-418	gga-miR-9-3p	Gallus gallus	TAAAGCTAGAGAACCGAATGT	0	0	0.18	0.18	0	0	0	0
	oan-miR-9-3p	Ornithorhynchus anatinus		0	0	0.18	0.18	0	0	0	0
dof-miR-419	dre-miR-9-4-3p	Danio rerio	TAAAGCTAGAGAACCGAATGTA	0	0	0.37	1.44	0	0	0	0
	ssa-miR-9b-3p	Salmo salar		0	0	0.37	1.44	0	0	0	0
dof-miR-420	ssa-miR-9a-1-3p	Salmo salar	TAAAGCTAGAGAACCGAATGTAT	0	0	0	0.36	0	0	0	0
dof-miR-421	sly-miR167b-5p	Solanum lycopersicum	TAAAGCTGCCAGCATGATCTGG	0	0	0	2.16	0	0	0	0
dof-miR-422	mmu-miR-106b-5p	Mus musculus	TAAAGTGCTGACAGTGCAGAT	0	0	0	0.9	0.47	0.1	0.17	0
	hsa-miR-106b-5p	Homo sapiens		0	0	0	0.9	0.47	0.1	0.17	0
	rno-miR-106b-5p	Rattus norvegicus		0	0	0	0.9	0.47	0.1	0.17	0
	ggo-miR-106b	Gorilla gorilla		0	0	0	0.9	0.47	0.1	0.17	0
	age-miR-106b	Ateles geoffroyi		0	0	0	0.9	0.47	0.1	0.17	0
	ppa-miR-106b	Pan paniscus		0	0	0	0.9	0.47	0.1	0.17	0
	ppy-miR-106b	Pongo pygmaeus		0	0	0	0.9	0.47	0.1	0.17	0
	ptr-miR-106b	Pan troglodytes		0	0	0	0.9	0.47	0.1	0.17	0
	mml-miR-106b-5p	Macaca mulatta		0	0	0	0.9	0.47	0.1	0.17	0
	sla-miR-106b	Saguinus labiatus		0	0	0	0.9	0.47	0.1	0.17	0
	lla-miR-106b	Lagothrix lagotricha		0	0	0	0.9	0.47	0.1	0.17	0
	mne-miR-106b	Macaca nemestrina		0	0	0	0.9	0.47	0.1	0.17	0
	chi-miR-106b-5p	Capra hircus		0	0	0	0.9	0.47	0.1	0.17	0
	oar-miR-106b	Ovis aries		0	0	0	0.9	0.47	0.1	0.17	0
	eca-miR-106b	Equus caballus		0	0	0	0.9	0.47	0.1	0.17	0
	cfa-miR-106b	Canis familiaris		0	0	0	0.9	0.47	0.1	0.17	0
bta-miR-106b	Bos taurus	0	0	0	0.9	0.47	0.1	0.17	0		
dof-miR-423	cgr-miR-106b-5p	Cricetulus griseus	TAAAGTGCTGACAGTGCAGATA	0	0	0	0	0.28	0	0	0
dof-miR-424	ola-miR-106a	Oryzias latipes	TAAAGTGCTTACAGTGCAGGT	0	0	0	0.54	0	0	0	0

	ame-miR-277	Apis mellifera		0	0	0	0	0	0	0.17	0
	aga-miR-277	Anopheles gambiae		0	0	0	0	0	0	0.17	0
	bmo-miR-277-3p	Bombyx mori		0	0	0	0	0	0	0.17	0
	pxy-miR-277	Plutella xylostella		0	0	0	0	0	0	0.17	0
	mse-miR-277	Manduca sexta		0	0	0	0	0	0	0.17	0
	nvi-miR-277	Nasonia vitripennis		0	0	0	0	0	0	0.17	0
	ngi-miR-277	Nasonia giraulti		0	0	0	0	0	0	0.17	0
	nlo-miR-277	Nasonia longicornis		0	0	0	0	0	0	0.17	0
	api-miR-277	Acyrtosiphon pisum		0	0	0	0	0	0	0.17	0
	tca-miR-277-3p	Tribolium castaneum		0	0	0	0	0	0	0.17	0
	dan-miR-277	Drosophila ananassae		0	0	0	0	0	0	0.17	0
	der-miR-277	Drosophila erecta		0	0	0	0	0	0	0.17	0
	dgr-miR-277	Drosophila grimshawi		0	0	0	0	0	0	0.17	0
	dmo-miR-277	Drosophila mojavensis		0	0	0	0	0	0	0.17	0
	dpe-miR-277	Drosophila persimilis		0	0	0	0	0	0	0.17	0
	dse-miR-277	Drosophila sechellia		0	0	0	0	0	0	0.17	0
	dvi-miR-277-3p	Drosophila virilis		0	0	0	0	0	0	0.17	0
	dwi-miR-277	Drosophila willistoni		0	0	0	0	0	0	0.17	0
	dya-miR-277	Drosophila yakuba		0	0	0	0	0	0	0.17	0
dof-miR-429	sha-miR-141	Sarcophilus harrisii	TAACACTGTCTGGTAAAGATG	0	0	0	0	0.09	0	4.67	0.28
dof-miR-430	mmu-miR-141-3p	Mus musculus	TAACACTGTCTGGTAAAGATGG	0	0	0	0.18	0	0	0.17	0
	hsa-miR-141-3p	Homo sapiens		0	0	0	0.18	0	0	0.17	0
	rno-miR-141-3p	Rattus norvegicus		0	0	0	0.18	0	0	0.17	0
	chi-miR-141	Capra hircus		0	0	0	0.18	0	0	0.17	0
	eca-miR-141	Equus caballus		0	0	0	0.18	0	0	0.17	0
	ptr-miR-141	Pan troglodytes		0	0	0	0.18	0	0	0.17	0
	bta-miR-141	Bos taurus		0	0	0	0.18	0	0	0.17	0
dof-miR-431	efu-miR-141	Eptesicus fuscus	TAACACTGTCTGGTAAAGATGGC	0	0	0	0	0	0	0.17	0
	tch-miR-141-3p	Tupaia chinensis		0	0	0	0	0	0	0.17	0
	cgr-miR-141	Cricetulus griseus		0	0	0	0	0	0	0.17	0
dof-miR-432	chi-miR-200a	Capra hircus	TAACACTGTCTGGTAAACGATG	0.4	0.25	0.18	1.44	0.09	0	2.84	0.7
	ipu-miR-141	Ictalurus punctatus		0.4	0.25	0.18	1.44	0.09	0	2.84	0.7
	ipu-miR-200a	Ictalurus punctatus		0.4	0.25	0.18	1.44	0.09	0	2.84	0.7
	ccr-miR-200a	Cyprinus carpio		0.4	0.25	0.18	1.44	0.09	0	2.84	0.7

	rno-miR-124-3p	Rattus norvegicus		0	0	0	0	0	0	0	0	0.14
	chi-miR-124a	Capra hircus		0	0	0	0	0	0	0	0	0.14
	ipu-miR-124a	Ictalurus punctatus		0	0	0	0	0	0	0	0	0.14
	ppy-miR-124	Pongo pygmaeus		0	0	0	0	0	0	0	0	0.14
	eca-miR-124	Equus caballus		0	0	0	0	0	0	0	0	0.14
	crm-miR-124a	Caenorhabditis remanei		0	0	0	0	0	0	0	0	0.14
	ppc-miR-124	Pristionchus pacificus		0	0	0	0	0	0	0	0	0.14
dof-miR-441	prd-miR-124-3p	Panagrellus redivivus	TAAGGCACGCGGTGAATGCCAAT	0	0	0	0	0	0	0	0	0.14
dof-miR-442	ipu-miR-18a	Ictalurus punctatus	TAAGGTGCATCTAGTGCAGA	0	0.25	0	0	0	0	0	0	0
dof-miR-443	gga-miR-18a-5p	Gallus gallus	TAAGGTGCATCTAGTGCAGATA	0	0	0	0.18	0	0	0.17	0.14	
	dre-miR-18a	Danio rerio		0	0	0	0.18	0	0	0.17	0.14	
	ssc-miR-18a	Sus scrofa		0	0	0	0.18	0	0	0.17	0.14	
	ggo-miR-18a	Gorilla gorilla		0	0	0	0.18	0	0	0.17	0.14	
	lca-miR-18	Lemur catta		0	0	0	0.18	0	0	0.17	0.14	
	age-miR-18	Ateles geoffroyi		0	0	0	0.18	0	0	0.17	0.14	
	ppa-miR-18	Pan paniscus		0	0	0	0.18	0	0	0.17	0.14	
	ppy-miR-18a	Pongo pygmaeus		0	0	0	0.18	0	0	0.17	0.14	
	ptr-miR-18a	Pan troglodytes		0	0	0	0.18	0	0	0.17	0.14	
	mml-miR-18a-5p	Macaca mulatta		0	0	0	0.18	0	0	0.17	0.14	
	sla-miR-18	Saguinus labiatus		0	0	0	0.18	0	0	0.17	0.14	
	lla-miR-18	Lagothrix lagotricha		0	0	0	0.18	0	0	0.17	0.14	
	mne-miR-18	Macaca nemestrina		0	0	0	0.18	0	0	0.17	0.14	
	fru-miR-18	Fugu rubripes		0	0	0	0.18	0	0	0.17	0.14	
	tni-miR-18	Tetraodon nigroviridis		0	0	0	0.18	0	0	0.17	0.14	
	bta-miR-18a	Bos taurus		0	0	0	0.18	0	0	0.17	0.14	
	mdo-miR-18a-5p	Monodelphis domestica		0	0	0	0.18	0	0	0.17	0.14	
	ssa-miR-18b-5p	Salmo salar		0	0	0	0.18	0	0	0.17	0.14	
	tgu-miR-18a	Taeniopygia guttata		0	0	0	0.18	0	0	0.17	0.14	
	cfa-miR-18a	Canis familiaris		0	0	0	0.18	0	0	0.17	0.14	
dof-miR-444	hsa-miR-18a-5p	Homo sapiens	TAAGGTGCATCTAGTGCAGATAG	0	0	0	0.54	0	0	0	0	
	mmu-miR-18a-5p	Mus musculus		0	0	0	0.54	0	0	0	0	
	rno-miR-18a-5p	Rattus norvegicus		0	0	0	0.54	0	0	0	0	
	xtr-miR-18a-5p	Xenopus tropicalis		0	0	0	0.54	0	0	0	0	
	chi-miR-18a-5p	Capra hircus		0	0	0	0.54	0	0	0	0	

	oha-miR-18a-5p	Ophiophagus hannah		0	0	0	0.54	0	0	0	0
	ccr-miR-18a	Cyprinus carpio		0	0	0	0.54	0	0	0	0
	ola-miR-18	Oryzias latipes		0	0	0	0.54	0	0	0	0
	cgr-miR-18a-5p	Cricetulus griseus		0	0	0	0.54	0	0	0	0
	pma-miR-18a-5p	Petromyzon marinus		0	0	0	0.54	0	0	0	0
	aca-miR-18a-5p	Anolis carolinensis		0	0	0	0.54	0	0	0	0
	eca-miR-18a	Equus caballus		0	0	0	0.54	0	0	0	0
dof-miR-445	mmu-miR-467a-5p	Mus musculus	TAAGTGCCTGCATGTATATGCG	0	0	0	0	0	0	0.17	0
dof-miR-446	mmu-miR-467c-5p	Mus musculus	TAAGTGCCTGCATGTATATGTG	0	0	0	0	0	0	0.17	0
dof-miR-447	dre-miR-430a-3p	Danio rerio	TAAGTGCTATTTGTTGGGGTAG	0	0	0.55	0.18	0	0	0	0
	hhi-miR-430a	Hippoglossus hippoglossus		0	0	0.55	0.18	0	0	0	0
	ccr-miR-430	Cyprinus carpio		0	0	0.55	0.18	0	0	0	0
dof-miR-448	rno-miR-200c-3p	Rattus norvegicus	TAATACTGCCGGGTAATGATG	0	0.25	0	0	0	0	0	0.14
dof-miR-449	mdo-miR-200c-3p	Monodelphis domestica	TAATACTGCCGGGTAATGATGG	0	0	0	0	0	0	0	0.14
	oar-miR-200c	Ovis aries		0	0	0	0	0	0	0	0
dof-miR-450	hsa-miR-200c-3p	Homo sapiens	TAATACTGCCGGGTAATGATGGA	0	0	0.37	1.08	0	0.1	0.67	0.28
	mmu-miR-200c-3p	Mus musculus		0	0	0.37	1.08	0	0.1	0.67	0.28
	bta-miR-200c	Bos taurus		0	0	0.37	1.08	0	0.1	0.67	0.28
	efu-miR-200c	Eptesicus fuscus		0	0	0.37	1.08	0	0.1	0.67	0.28
	chi-miR-200c	Capra hircus		0	0	0.37	1.08	0	0.1	0.67	0.28
	tch-miR-200c-3p	Tupaia chinensis		0	0	0.37	1.08	0	0.1	0.67	0.28
	cgr-miR-200c	Cricetulus griseus		0	0	0.37	1.08	0	0.1	0.67	0.28
	ptr-miR-200c	Pan troglodytes		0	0	0.37	1.08	0	0.1	0.67	0.28
	eca-miR-200c	Equus caballus		0	0	0.37	1.08	0	0.1	0.67	0.28
	cfa-miR-200c	Canis familiaris		0	0	0.37	1.08	0	0.1	0.67	0.28
dof-miR-451	sha-miR-200b	Sarcophilus harrisii	TAATACTGCCTGGTAATGA	0	0	0	0.18	0	0	0.17	0
dof-miR-452	bta-miR-200b	Bos taurus	TAATACTGCCTGGTAATGATG	0	0	0.37	0.72	0	0	0	0
	oar-miR-200b	Ovis aries		0	0	0.37	0.72	0	0	0	0
	ola-miR-200b	Oryzias latipes		0	0	0.37	0.72	0	0	0	0
dof-miR-453	mmu-miR-200b-3p	Mus musculus	TAATACTGCCTGGTAATGATGA	0	0	1.1	2.7	0	0	0.67	0.28
	hsa-miR-200b-3p	Homo sapiens		0	0	1.1	2.7	0	0	0.67	0.28
	dre-miR-200b-3p	Danio rerio		0	0	1.1	2.7	0	0	0.67	0.28
	fru-miR-200b	Fugu rubripes		0	0	1.1	2.7	0	0	0.67	0.28
	tmi-miR-200b	Tetraodon nigroviridis		0	0	1.1	2.7	0	0	0.67	0.28

	der-miR-8	Drosophila erecta		0	0	0	0	0	0.73	0	0
	dgr-miR-8	Drosophila grimshawi		0	0	0	0	0	0.73	0	0
	dmo-miR-8	Drosophila mojavensis		0	0	0	0	0	0.73	0	0
	dpe-miR-8	Drosophila persimilis		0	0	0	0	0	0.73	0	0
	dse-miR-8	Drosophila sechellia		0	0	0	0	0	0.73	0	0
	dsi-miR-8	Drosophila simulans		0	0	0	0	0	0.73	0	0
	dvi-miR-8-3p	Drosophila virilis		0	0	0	0	0	0.73	0	0
	dwi-miR-8	Drosophila willistoni		0	0	0	0	0	0.73	0	0
	dya-miR-8	Drosophila yakuba		0	0	0	0	0	0.73	0	0
	cte-miR-8	Capitella teleta		0	0	0	0	0	0.73	0	0
	lgi-miR-8	Lottia gigantea		0	0	0	0	0	0.73	0	0
dof-miR-460	xla-miR-429	Xenopus laevis	TAATACTGTCTGGTAATGCCG	0	0	0	0.18	0	0	0.17	0.14
	chi-miR-429	Capra hircus		0	0	0	0.18	0	0	0.17	0.14
	ssa-miR-429-3p	Salmo salar		0	0	0	0.18	0	0	0.17	0.14
	ipu-miR-429a	Ictalurus punctatus		0	0	0	0.18	0	0	0.17	0.14
	eca-miR-429	Equus caballus		0	0	0	0.18	0	0	0.17	0.14
dof-miR-461	mmu-miR-429-3p	Mus musculus	TAATACTGTCTGGTAATGCCGT	0	0	0.18	0	0	0	0	0
	rno-miR-429	Rattus norvegicus		0	0	0.18	0	0	0	0	0
	cfa-miR-429	Canis familiaris		0	0	0.18	0	0	0	0	0
	dre-miR-429a	Danio rerio		0	0	0.18	0	0	0	0	0
	fru-miR-429	Fugu rubripes		0	0	0.18	0	0	0	0	0
	tmi-miR-429	Tetraodon nigroviridis		0	0	0.18	0	0	0	0	0
	gga-miR-429-3p	Gallus gallus		0	0	0.18	0	0	0	0	0
	xtr-miR-429	Xenopus tropicalis		0	0	0.18	0	0	0	0	0
	oan-miR-429-3p	Ornithorhynchus anatinus		0	0	0.18	0	0	0	0	0
	ccr-miR-429	Cyprinus carpio		0	0	0.18	0	0	0	0	0
	cgr-miR-429	Cricetulus griseus		0	0	0.18	0	0	0	0	0
	ssc-miR-429	Sus scrofa		0	0	0.18	0	0	0	0	0
	aca-miR-429-3p	Anolis carolinensis		0	0	0.18	0	0	0	0	0
	bta-miR-429	Bos taurus		0	0	0.18	0	0	0	0	0
dof-miR-462	hsa-miR-500a-5p	Homo sapiens	TAATCCTTGCTACCTGGGTGAGA	0	0	0	0.54	0	0	0	0
	chi-miR-500-5p	Capra hircus		0	0	0	0.54	0	0	0	0
	mml-miR-500b-5p	Macaca mulatta		0	0	0	0.54	0	0	0	0
	ppy-miR-500	Pongo pygmaeus		0	0	0	0.54	0	0	0	0

	eca-miR-500	Equus caballus		0	0	0	0.54	0	0	0	0
	mml-miR-500a-5p	Macaca mulatta		0	0	0	0.54	0	0	0	0
	ptr-miR-500	Pan troglodytes		0	0	0	0.54	0	0	0	0
	bta-miR-500	Bos taurus		0	0	0	0.54	0	0	0	0
dof-miR-463	dre-miR-216b	Danio rerio	TAATCTCTGCAGGCAACTGTGA	0	0.25	0	0	0	0	0	0
	fru-miR-216b	Fugu rubripes		0	0.25	0	0	0	0	0	0
	tmi-miR-216b	Tetraodon nigroviridis		0	0.25	0	0	0	0	0	0
	ssa-miR-216a-5p	Salmo salar		0	0.25	0	0	0	0	0	0
	ipu-miR-216b	Ictalurus punctatus		0	0.25	0	0	0	0	0	0
	csa-miR-216b	Ciona savignyi		0	0.25	0	0	0	0	0	0
dof-miR-464	ptc-miR2111a	Populus trichocarpa	TAATCTGCATCCTGAGGTTTG	0	0	0	1.26	0	0	0	0
	ptc-miR2111b	Populus trichocarpa		0	0	0	1.26	0	0	0	0
dof-miR-465	hsa-miR-590-3p	Homo sapiens	TAATTTTATGTATAAGTAGT	0	0	0	0	0.09	0	0	0
	mmu-miR-590-3p	Mus musculus		0	0	0	0	0.09	0	0	0
	ppy-miR-590-3p	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	eca-miR-590-3p	Equus caballus		0	0	0	0	0.09	0	0	0
	cfa-miR-590	Canis familiaris		0	0	0	0	0.09	0	0	0
	ptr-miR-590	Pan troglodytes		0	0	0	0	0.09	0	0	0
dof-miR-466	chi-miR-214-3p	Capra hircus	TACAGCAGGCACAGACAGGC	0	0	0.18	0	0	0	0	0
dof-miR-467	dre-miR-101b	Danio rerio	TACAGTACTATGATAACTGAAG	0	0	0	0	0	0	0	0.14
	fru-miR-101b	Fugu rubripes		0	0	0	0	0	0	0	0.14
	tmi-miR-101b	Tetraodon nigroviridis		0	0	0	0	0	0	0	0.14
dof-miR-468	chi-miR-101-3p	Capra hircus	TACAGTACTGTGATAACTGA	0.2	0	0.73	0.18	0.28	0.21	0	0
	aca-miR-101-3p	Anolis carolinensis		0.2	0	0.73	0.18	0.28	0.21	0	0
	cfa-miR-101	Canis familiaris		0.2	0	0.73	0.18	0.28	0.21	0	0
dof-miR-469	hsa-miR-101-3p	Homo sapiens	TACAGTACTGTGATAACTGAA	0	0	0	0	0.37	0	0.17	0
	mmu-miR-101a-3p	Mus musculus		0	0	0	0	0.37	0	0.17	0
	rno-miR-101a-3p	Rattus norvegicus		0	0	0	0	0.37	0	0.17	0
	ppy-miR-101	Pongo pygmaeus		0	0	0	0	0.37	0	0.17	0
	bta-miR-101	Bos taurus		0	0	0	0	0.37	0	0.17	0
	eca-miR-101	Equus caballus		0	0	0	0	0.37	0	0.17	0
	ssc-miR-101	Sus scrofa		0	0	0	0	0.37	0	0.17	0
dof-miR-470	dre-miR-101a	Danio rerio	TACAGTACTGTGATAACTGAAG	0	0	0.18	0.54	1.12	0.52	0.5	0
	ggo-miR-101	Gorilla gorilla		0	0	0.18	0.54	1.12	0.52	0.5	0

	sla-miR-101	Saguinus labiatus		0	0	0.18	0.54	1.12	0.52	0.5	0
	age-miR-101	Ateles geoffroyi		0	0	0.18	0.54	1.12	0.52	0.5	0
	ppa-miR-101	Pan paniscus		0	0	0.18	0.54	1.12	0.52	0.5	0
	ptr-miR-101	Pan troglodytes		0	0	0.18	0.54	1.12	0.52	0.5	0
	mml-miR-101-3p	Macaca mulatta		0	0	0.18	0.54	1.12	0.52	0.5	0
	lla-miR-101	Lagothrix lagotricha		0	0	0.18	0.54	1.12	0.52	0.5	0
	mne-miR-101	Macaca nemestrina		0	0	0.18	0.54	1.12	0.52	0.5	0
	fru-miR-101a	Fugu rubripes		0	0	0.18	0.54	1.12	0.52	0.5	0
	tni-miR-101a	Tetraodon nigroviridis		0	0	0.18	0.54	1.12	0.52	0.5	0
	xtr-miR-101a	Xenopus tropicalis		0	0	0.18	0.54	1.12	0.52	0.5	0
	mdo-miR-101-3p	Monodelphis domestica		0	0	0.18	0.54	1.12	0.52	0.5	0
	oan-miR-101	Ornithorhynchus anatinus		0	0	0.18	0.54	1.12	0.52	0.5	0
	oha-miR-101b-3p	Ophiophagus hannah		0	0	0.18	0.54	1.12	0.52	0.5	0
	ssa-miR-101a-3p	Salmo salar		0	0	0.18	0.54	1.12	0.52	0.5	0
	ipu-miR-101a	Ictalurus punctatus		0	0	0.18	0.54	1.12	0.52	0.5	0
	ccr-miR-101a	Cyprinus carpio		0	0	0.18	0.54	1.12	0.52	0.5	0
	cgr-miR-101b-3p	Cricetulus griseus		0	0	0.18	0.54	1.12	0.52	0.5	0
dof-miR-471	dre-miR-199-3p	Danio rerio	TACAGTAGTCTGCACATTGGTT	0	0	3.67	3.24	0.19	0	0.17	0.14
	xtr-miR-199a-3p	Xenopus tropicalis		0	0	3.67	3.24	0.19	0	0.17	0.14
	oha-miR-199c-3p	Ophiophagus hannah		0	0	3.67	3.24	0.19	0	0.17	0.14
	ssc-miR-199b-3p	Sus scrofa		0	0	3.67	3.24	0.19	0	0.17	0.14
dof-miR-472	chi-miR-144-3p	Capra hircus	TACAGTATAGATGATGTAC	3.37	6.36	0.55	0	0.75	0.21	1.84	5.04
	ssc-miR-144	Sus scrofa		3.37	6.36	0.55	0	0.75	0.21	1.84	5.04
dof-miR-473	mmu-miR-144-3p	Mus musculus	TACAGTATAGATGATGTACT	0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	hsa-miR-144-3p	Homo sapiens		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	rno-miR-144-3p	Rattus norvegicus		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	dre-miR-144-3p	Danio rerio		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	fru-miR-144	Fugu rubripes		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	tni-miR-144	Tetraodon nigroviridis		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	oan-miR-144-3p	Ornithorhynchus anatinus		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	aja-miR-144	Artibeus jamaicensis		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	aca-miR-144-3p	Anolis carolinensis		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	eca-miR-144	Equus caballus		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
	tgu-miR-144-3p	Taeniopygia guttata		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4

	mml-miR-144	Macaca mulatta		0.79	3.82	0.18	0.18	0.19	0.52	0.83	1.4
dof-miR-474	mmu-miR-140-3p	Mus musculus	TACCACAGGGTAGAACACGG	0	0.25	0.18	0	0.19	0.1	0.17	0
	hsa-miR-140-3p	Homo sapiens		0	0.25	0.18	0	0.19	0.1	0.17	0
	rno-miR-140-3p	Rattus norvegicus		0	0.25	0.18	0	0.19	0.1	0.17	0
	aca-miR-140-3p	Anolis carolinensis		0	0.25	0.18	0	0.19	0.1	0.17	0
	ppy-miR-140-3p	Pongo pygmaeus		0	0.25	0.18	0	0.19	0.1	0.17	0
	eca-miR-140-3p	Equus caballus		0	0.25	0.18	0	0.19	0.1	0.17	0
	mml-miR-140-3p	Macaca mulatta		0	0.25	0.18	0	0.19	0.1	0.17	0
dof-miR-475	bta-miR-140	Bos taurus	TACCACAGGGTAGAACACGGA	0.2	0	0.18	0.9	0.93	0.1	0.17	0.14
	oan-miR-140-3p	Ornithorhynchus anatinus		0.2	0	0.18	0.9	0.93	0.1	0.17	0.14
	ssa-miR-140-3p	Salmo salar		0.2	0	0.18	0.9	0.93	0.1	0.17	0.14
	ccr-miR-140-3p	Cyprinus carpio		0.2	0	0.18	0.9	0.93	0.1	0.17	0.14
	mdo-miR-140-3p	Monodelphis domestica		0.2	0	0.18	0.9	0.93	0.1	0.17	0.14
dof-miR-476	dre-miR-140-3p	Danio rerio	TACCACAGGGTAGAACACGGAC	0.2	0.25	0.73	1.62	0.84	0	0.33	0.28
	ssc-miR-140-3p	Sus scrofa		0.2	0.25	0.73	1.62	0.84	0	0.33	0.28
	oha-miR-140-3p	Ophiophagus hannah		0.2	0.25	0.73	1.62	0.84	0	0.33	0.28
	tgu-miR-140-3p	Taeniopygia guttata		0.2	0.25	0.73	1.62	0.84	0	0.33	0.28
dof-miR-477	bta-miR-660	Bos taurus	TACCCATTGCATATCGGAGCTG	0	0	0.18	0	0	0	0	
dof-miR-478	chi-miR-660	Capra hircus	TACCCATTGCATATCGGAGCTGT	0	0	0	0.18	0	0	0	
dof-miR-479	hsa-miR-660-5p	Homo sapiens	TACCCATTGCATATCGGAGTTG	0	0	0	0	0.19	0	0	0
	ggo-miR-660	Gorilla gorilla		0	0	0	0	0.19	0	0	0
	ppy-miR-660	Pongo pygmaeus		0	0	0	0	0.19	0	0	0
	eca-miR-660	Equus caballus		0	0	0	0	0.19	0	0	0
	mml-miR-660-5p	Macaca mulatta		0	0	0	0	0.19	0	0	0
	cfa-miR-660	Canis familiaris		0	0	0	0	0.19	0	0	0
	ptr-miR-660	Pan troglodytes		0	0	0	0	0.19	0	0	0
dof-miR-480	efu-miR-660	Eptesicus fuscus	TACCCATTGCATATCGGAGTTGT	0	0	0	0	0.19	0.21	0	
dof-miR-481	gga-miR-10b-5p	Gallus gallus	TACCCGTAGAACCGAATTTGT	3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	ggo-miR-10b	Gorilla gorilla		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	mne-miR-10b	Macaca nemestrina		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	ppa-miR-10b	Pan paniscus		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	xtr-miR-10b	Xenopus tropicalis		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	oan-miR-10b-5p	Ornithorhynchus anatinus		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	chi-miR-10b-5p	Capra hircus		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8

	ssa-miR-10b-5p	Salmo salar		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	ipu-miR-10b	Ictalurus punctatus		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	ccr-miR-10b	Cyprinus carpio		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	ola-miR-10b	Oryzias latipes		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	cgr-miR-10b-5p	Cricetulus griseus		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	aca-miR-10b-5p	Anolis carolinensis		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	tgu-miR-10a-5p	Taeniopygia guttata		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
	ssc-miR-10b	Sus scrofa		3.56	5.86	3.31	5.59	0.56	0.1	8.01	2.8
dof-miR-482	mmu-miR-10b-5p	Mus musculus	TACCCTGTAGAACCGAATTTGTG	0	0.25	0.18	0.36	0	0	0	0
	hsa-miR-10b-5p	Homo sapiens		0	0.25	0.18	0.36	0	0	0	0
	dre-miR-10b-5p	Danio rerio		0	0.25	0.18	0.36	0	0	0	0
	fru-miR-10b	Fugu rubripes		0	0.25	0.18	0.36	0	0	0	0
	tmi-miR-10b	Tetraodon nigroviridis		0	0.25	0.18	0.36	0	0	0	0
	bta-miR-10b	Bos taurus		0	0.25	0.18	0.36	0	0	0	0
	tch-miR-10b-5p	Tupaia chinensis		0	0.25	0.18	0.36	0	0	0	0
	ppy-miR-10b	Pongo pygmaeus		0	0.25	0.18	0.36	0	0	0	0
	eca-miR-10b	Equus caballus		0	0.25	0.18	0.36	0	0	0	0
	mml-miR-10b-5p	Macaca mulatta		0	0.25	0.18	0.36	0	0	0	0
	ptr-miR-10b	Pan troglodytes		0	0.25	0.18	0.36	0	0	0	0
dof-miR-483	oar-miR-10a	Ovis aries	TACCCTGTAGATCCGAATTTG	0	0	0	0	0.28	0	0	0
dof-miR-484	dre-miR-10a-5p	Danio rerio	TACCCTGTAGATCCGAATTTGT	0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	oan-miR-10a-5p	Ornithorhynchus anatinus		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	chi-miR-10a-5p	Capra hircus		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	bbe-miR-10a-5p	Branchiostoma belcheri		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	pxy-miR-10-5p	Plutella xylostella		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	ipu-miR-10a	Ictalurus punctatus		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	cgr-miR-10a-5p	Cricetulus griseus		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	isc-miR-10	Ixodes scapularis		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	ssc-miR-10a-5p	Sus scrofa		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	gga-miR-10a-5p	Gallus gallus		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	cfa-miR-10a	Canis familiaris		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	tca-miR-10-5p	Tribolium castaneum		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	lgi-miR-10	Lottia gigantea		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
	lmi-miR-10-5p	Locusta migratoria		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84

	dpu-miR-10	Daphnia pulex		0.2	0.76	4.23	5.05	2.15	0.31	2.17	0.84
dof-miR-485	hsa-miR-10a-5p	Homo sapiens	TACCCTGTAGATCCGAATTTGTG	0	0	0.73	0.9	0	0.1	0.17	0
	mmu-miR-10a-5p	Mus musculus		0	0	0.73	0.9	0	0.1	0.17	0
	rno-miR-10a-5p	Rattus norvegicus		0	0	0.73	0.9	0	0.1	0.17	0
	ggo-miR-10a	Gorilla gorilla		0	0	0.73	0.9	0	0.1	0.17	0
	ppy-miR-10a	Pongo pygmaeus		0	0	0.73	0.9	0	0.1	0.17	0
	sla-miR-10a	Saguinus labiatus		0	0	0.73	0.9	0	0.1	0.17	0
	age-miR-10a	Ateles geoffroyi		0	0	0.73	0.9	0	0.1	0.17	0
	ppa-miR-10a	Pan paniscus		0	0	0.73	0.9	0	0.1	0.17	0
	xtr-miR-10a	Xenopus tropicalis		0	0	0.73	0.9	0	0.1	0.17	0
	bta-miR-10a	Bos taurus		0	0	0.73	0.9	0	0.1	0.17	0
	mdo-miR-10a-5p	Monodelphis domestica		0	0	0.73	0.9	0	0.1	0.17	0
	oha-miR-10a-5p	Ophiophagus hannah		0	0	0.73	0.9	0	0.1	0.17	0
	aca-miR-10a-5p	Anolis carolinensis		0	0	0.73	0.9	0	0.1	0.17	0
	eca-miR-10a	Equus caballus		0	0	0.73	0.9	0	0.1	0.17	0
	mml-miR-10a-5p	Macaca mulatta		0	0	0.73	0.9	0	0.1	0.17	0
	ptr-miR-10a	Pan troglodytes		0	0	0.73	0.9	0	0.1	0.17	0
	bfl-miR-10a-5p	Branchiostoma floridae		0	0	0.73	0.9	0	0.1	0.17	0
sko-miR-10	Saccoglossus kowalevskii	0	0	0.73	0.9	0	0.1	0.17	0		
dof-miR-486	dre-miR-10c-5p	Danio rerio	TACCCTGTAGATCCGGATTTGT	0.59	1.78	0.73	0.72	0	0	4.34	0.42
	fru-miR-10c	Fugu rubripes		0.59	1.78	0.73	0.72	0	0	4.34	0.42
	tmi-miR-10c	Tetraodon nigroviridis		0.59	1.78	0.73	0.72	0	0	4.34	0.42
	ssa-miR-10a-5p	Salmo salar		0.59	1.78	0.73	0.72	0	0	4.34	0.42
	ipu-miR-10c	Ictalurus punctatus		0.59	1.78	0.73	0.72	0	0	4.34	0.42
dof-miR-487	ccr-miR-10c	Cyprinus carpio	TACCCTGTAGATCCGGATTTGTG	0	0.51	0	0	0	0	0.33	0.14
dof-miR-488	ptc-miR6421-3p	Populus trichocarpa	TAGAGCAGATTGTAAGGGAAG	0	0	0.18	0	0	0	0	0
dof-miR-489	chi-miR-29a-3p	Capra hircus	TAGACCATCTGAAATCGGTT	0	0	0.18	0	4.2	0.83	0	0
	tch-miR-29a-3p	Tupaia chinensis		0	0	0.18	0	4.2	0.83	0	0
	cgr-miR-29a-3p	Cricetulus griseus		0	0	0.18	0	4.2	0.83	0	0
	oar-miR-29a	Ovis aries		0	0	0.18	0	4.2	0.83	0	0
dof-miR-490	hsa-miR-29a-3p	Homo sapiens	TAGACCATCTGAAATCGGTTA	0	0	0.37	0.54	0.56	0.1	0	0
	mmu-miR-29a-3p	Mus musculus		0	0	0.37	0.54	0.56	0.1	0	0
	rno-miR-29a-3p	Rattus norvegicus		0	0	0.37	0.54	0.56	0.1	0	0
	eca-miR-29a	Equus caballus		0	0	0.37	0.54	0.56	0.1	0	0

	cfa-miR-29a	Canis familiaris		0	0	0.37	0.54	0.56	0.1	0	0
dof-miR-491	ppy-miR-29b	Pongo pygmaeus	TAGCACCATTGAAATCAGT	0	0	0	0	0	0.1	0	0
	ptr-miR-29b	Pan troglodytes		0	0	0	0	0	0.1	0	0
	ggo-miR-29b	Gorilla gorilla		0	0	0	0	0	0.1	0	0
	lla-miR-29b	Lagothrix lagotricha		0	0	0	0	0	0.1	0	0
	age-miR-29b	Ateles geoffroyi		0	0	0	0	0	0.1	0	0
	ppa-miR-29b	Pan paniscus		0	0	0	0	0	0.1	0	0
	sla-miR-29b	Saguinus labiatus		0	0	0	0	0	0.1	0	0
	mne-miR-29b	Macaca nemestrina		0	0	0	0	0	0.1	0	0
	ame-miR-29b	Apis mellifera		0	0	0	0	0	0.1	0	0
	chi-miR-29b-3p	Capra hircus		0	0	0	0	0	0.1	0	0
	ssa-miR-29a-3p	Salmo salar		0	0	0	0	0	0.1	0	0
	nvi-miR-29b	Nasonia vitripennis		0	0	0	0	0	0.1	0	0
ngi-miR-29b	Nasonia giraulti	0	0	0	0	0	0.1	0	0		
dof-miR-492	aca-miR-29b	Anolis carolinensis	TAGCACCATTGAAATCAGTG	0	0	0	0	0.09	0	0	0
	tgu-miR-29b-3p	Taeniopygia guttata		0	0	0	0	0.09	0	0	0
	cte-miR-29b	Capitella teleta		0	0	0	0	0.09	0	0	0
dof-miR-493	dre-miR-29b	Danio rerio	TAGCACCATTGAAATCAGTGT	0	0	0	0.18	0.09	0	0	0
	fru-miR-29b	Fugu rubripes		0	0	0	0.18	0.09	0	0	0
	tmi-miR-29b	Tetraodon nigroviridis		0	0	0	0.18	0.09	0	0	0
	mdo-miR-29b-3p	Monodelphis domestica		0	0	0	0.18	0.09	0	0	0
	oan-miR-29b-3p	Ornithorhynchus anatinus		0	0	0	0.18	0.09	0	0	0
	oar-miR-29b	Ovis aries		0	0	0	0.18	0.09	0	0	0
	ola-miR-29b	Oryzias latipes		0	0	0	0.18	0.09	0	0	0
	pma-miR-29c	Petromyzon marinus		0	0	0	0.18	0.09	0	0	0
sko-miR-29b-3p	Saccoglossus kowalevskii	0	0	0	0.18	0.09	0	0	0		
dof-miR-494	hsa-miR-29b-3p	Homo sapiens	TAGCACCATTGAAATCAGTGT	0	0	0	0	0.09	0	0.33	0
	mmu-miR-29b-3p	Mus musculus		0	0	0	0	0.09	0	0.33	0
	rno-miR-29b-3p	Rattus norvegicus		0	0	0	0	0.09	0	0.33	0
	gga-miR-29b-3p	Gallus gallus		0	0	0	0	0.09	0	0.33	0
	ssc-miR-29b	Sus scrofa		0	0	0	0	0.09	0	0.33	0
	xtr-miR-29b	Xenopus tropicalis		0	0	0	0	0.09	0	0.33	0
	bta-miR-29b	Bos taurus		0	0	0	0	0.09	0	0.33	0
	tch-miR-29b-3p	Tupaia chinensis		0	0	0	0	0.09	0	0.33	0

	oha-miR-29b-3p	Ophiophagus hannah		0	0	0	0	0.09	0	0.33	0
	aja-miR-29b	Artibeus jamaicensis		0	0	0	0	0.09	0	0.33	0
	ccr-miR-29b	Cyprinus carpio		0	0	0	0	0.09	0	0.33	0
	cgr-miR-29b-3p	Cricetulus griseus		0	0	0	0	0.09	0	0.33	0
	eca-miR-29b	Equus caballus		0	0	0	0	0.09	0	0.33	0
	mml-miR-29b-3p	Macaca mulatta		0	0	0	0	0.09	0	0.33	0
	cfa-miR-29b	Canis familiaris		0	0	0	0	0.09	0	0.33	0
dof-miR-495	gga-miR-29c-3p	Gallus gallus	TAGCACCATTGAAATCGGT	0	0	0	0	0.28	0.1	0	0
	xtr-miR-29c-3p	Xenopus tropicalis		0	0	0	0	0.28	0.1	0	0
dof-miR-496	gga-miR-29a-3p	Gallus gallus	TAGCACCATTGAAATCGGT	0	0	0	0	0.65	0.1	0.17	0
	xtr-miR-29a	Xenopus tropicalis		0	0	0	0	0.65	0.1	0.17	0
	mdo-miR-29a-3p	Monodelphis domestica		0	0	0	0	0.65	0.1	0.17	0
	oan-miR-29a-3p	Ornithorhynchus anatinus		0	0	0	0	0.65	0.1	0.17	0
	tch-miR-29c-3p	Tupaia chinensis		0	0	0	0	0.65	0.1	0.17	0
	cgr-miR-29c-3p	Cricetulus griseus		0	0	0	0	0.65	0.1	0.17	0
	aca-miR-29a-3p	Anolis carolinensis		0	0	0	0	0.65	0.1	0.17	0
	tgu-miR-29a-3p	Taeniopygia guttata		0	0	0	0	0.65	0.1	0.17	0
dof-miR-497	mmu-miR-29c-3p	Mus musculus	TAGCACCATTGAAATCGGTTA	0	0	0	0.18	0.09	0	0.17	0
	hsa-miR-29c-3p	Homo sapiens		0	0	0	0.18	0.09	0	0.17	0
	rno-miR-29c-3p	Rattus norvegicus		0	0	0	0.18	0.09	0	0.17	0
	dre-miR-29a	Danio rerio		0	0	0	0.18	0.09	0	0.17	0
	ssc-miR-29c	Sus scrofa		0	0	0	0.18	0.09	0	0.17	0
	fru-miR-29a	Fugu rubripes		0	0	0	0.18	0.09	0	0.17	0
	tni-miR-29a	Tetraodon nigroviridis		0	0	0	0.18	0.09	0	0.17	0
	bta-miR-29c	Bos taurus		0	0	0	0.18	0.09	0	0.17	0
	oha-miR-29a-3p	Ophiophagus hannah		0	0	0	0.18	0.09	0	0.17	0
	ssa-miR-29b-3p	Salmo salar		0	0	0	0.18	0.09	0	0.17	0
	aja-miR-29c	Artibeus jamaicensis		0	0	0	0.18	0.09	0	0.17	0
	ccr-miR-29a	Cyprinus carpio		0	0	0	0.18	0.09	0	0.17	0
	ggo-miR-29c	Gorilla gorilla		0	0	0	0.18	0.09	0	0.17	0
	ppy-miR-29c	Pongo pygmaeus		0	0	0	0.18	0.09	0	0.17	0
	eca-miR-29c	Equus caballus		0	0	0	0.18	0.09	0	0.17	0
	mml-miR-29c-3p	Macaca mulatta		0	0	0	0.18	0.09	0	0.17	0
	cfa-miR-29c	Canis familiaris		0	0	0	0.18	0.09	0	0.17	0

	ptr-miR-29c	Pan troglodytes		0	0	0	0.18	0.09	0	0.17	0
dof-miR-498	mmu-miR-195a-5p	Mus musculus	TAGCAGCACAGAAATATTGGC	0	0	0.37	0.36	0.09	0	0	0
	hsa-miR-195-5p	Homo sapiens		0	0	0.37	0.36	0.09	0	0	0
	rno-miR-195-5p	Rattus norvegicus		0	0	0.37	0.36	0.09	0	0	0
	ggo-miR-195	Gorilla gorilla		0	0	0.37	0.36	0.09	0	0	0
	ppa-miR-195	Pan paniscus		0	0	0.37	0.36	0.09	0	0	0
	ppy-miR-195	Pongo pygmaeus		0	0	0.37	0.36	0.09	0	0	0
	eca-miR-195	Equus caballus		0	0	0.37	0.36	0.09	0	0	0
	ssc-miR-195	Sus scrofa		0	0	0.37	0.36	0.09	0	0	0
	mml-miR-195-5p	Macaca mulatta		0	0	0.37	0.36	0.09	0	0	0
	ptr-miR-195	Pan troglodytes		0	0	0.37	0.36	0.09	0	0	0
dof-miR-499	bta-miR-195	Bos taurus	TAGCAGCACAGAAATATTGGCA	0	0	0.18	0.18	0	0	0	0
	tch-miR-195-5p	Tupaia chinensis		0	0	0.18	0.18	0	0	0	0
	cgr-miR-195	Cricetulus griseus		0	0	0.18	0.18	0	0	0	0
	cfa-miR-195	Canis familiaris		0	0	0.18	0.18	0	0	0	0
dof-miR-500	dre-miR-15a-5p	Danio rerio	TAGCAGCACAGAATGGTTTGTG	0	0	0	0.18	0	0	0	0
dof-miR-501	gga-miR-15a	Gallus gallus	TAGCAGCACATAATGGTTTGT	0	0	0	0	0.75	0.21	0	0
	bta-miR-15a	Bos taurus		0	0	0	0	0.75	0.21	0	0
	oan-miR-15a-5p	Ornithorhynchus anatinus		0	0	0	0	0.75	0.21	0	0
	tgu-miR-15a-5p	Taeniopygia guttata		0	0	0	0	0.75	0.21	0	0
	cfa-miR-15a	Canis familiaris		0	0	0	0	0.75	0.21	0	0
	ssc-miR-15a	Sus scrofa		0	0	0	0	0.75	0.21	0	0
dof-miR-502	hsa-miR-15a-5p	Homo sapiens	TAGCAGCACATAATGGTTTGTG	0	0.25	0	0	0.09	0.1	0.17	0
	mmu-miR-15a-5p	Mus musculus		0	0.25	0	0	0.09	0.1	0.17	0
	age-miR-15a	Ateles geoffroyi		0	0.25	0	0	0.09	0.1	0.17	0
	ggo-miR-15a	Gorilla gorilla		0	0.25	0	0	0.09	0.1	0.17	0
	mne-miR-15a	Macaca nemestrina		0	0.25	0	0	0.09	0.1	0.17	0
	sla-miR-15a	Saguinus labiatus		0	0.25	0	0	0.09	0.1	0.17	0
	ppa-miR-15a	Pan paniscus		0	0.25	0	0	0.09	0.1	0.17	0
	lca-miR-15a	Lemur catta		0	0.25	0	0	0.09	0.1	0.17	0
	mml-miR-15a-5p	Macaca mulatta		0	0.25	0	0	0.09	0.1	0.17	0
	ppy-miR-15a	Pongo pygmaeus		0	0.25	0	0	0.09	0.1	0.17	0
	ptr-miR-15a	Pan troglodytes		0	0.25	0	0	0.09	0.1	0.17	0
	lla-miR-15a	Lagothrix lagotricha		0	0.25	0	0	0.09	0.1	0.17	0

	xtr-miR-15a	Xenopus tropicalis		0	0.25	0	0	0.09	0.1	0.17	0
	eca-miR-15a	Equus caballus		0	0.25	0	0	0.09	0.1	0.17	0
dof-miR-503	chi-miR-15a-5p	Capra hircus	TAGCAGCACATAATGGTTGTGG	0	0.25	0	0	0	0	0	0
	tch-miR-15a-5p	Tupaia chinensis		0	0.25	0	0	0	0	0	0
dof-miR-504	cgr-miR-15a-5p	Cricetulus griseus	TAGCAGCACATAATGGTTGTGGA	0	0	0	0	0	0.1	0	0
dof-miR-505	cfa-miR-15b	Canis familiaris	TAGCAGCACATCATGGTTTA	0	0	0	0.18	0	0	0	0
dof-miR-506	mmu-miR-15b-5p	Mus musculus	TAGCAGCACATCATGGTTTACA	0	0.76	0	0.36	1.4	0.42	0	0.28
	hsa-miR-15b-5p	Homo sapiens		0	0.76	0	0.36	1.4	0.42	0	0.28
	rno-miR-15b-5p	Rattus norvegicus		0	0.76	0	0.36	1.4	0.42	0	0.28
	ssc-miR-15b	Sus scrofa		0	0.76	0	0.36	1.4	0.42	0	0.28
	ggo-miR-15b	Gorilla gorilla		0	0.76	0	0.36	1.4	0.42	0	0.28
	age-miR-15b	Ateles geoffroyi		0	0.76	0	0.36	1.4	0.42	0	0.28
	ppa-miR-15b	Pan paniscus		0	0.76	0	0.36	1.4	0.42	0	0.28
	ppy-miR-15b	Pongo pygmaeus		0	0.76	0	0.36	1.4	0.42	0	0.28
	ptr-miR-15b	Pan troglodytes		0	0.76	0	0.36	1.4	0.42	0	0.28
	mml-miR-15b-5p	Macaca mulatta		0	0.76	0	0.36	1.4	0.42	0	0.28
	lla-miR-15b	Lagothrix lagotricha		0	0.76	0	0.36	1.4	0.42	0	0.28
	mne-miR-15b	Macaca nemestrina		0	0.76	0	0.36	1.4	0.42	0	0.28
	bta-miR-15b	Bos taurus		0	0.76	0	0.36	1.4	0.42	0	0.28
	efu-miR-15	Eptesicus fuscus		0	0.76	0	0.36	1.4	0.42	0	0.28
	chi-miR-15b-5p	Capra hircus		0	0.76	0	0.36	1.4	0.42	0	0.28
	tch-miR-15b-5p	Tupaia chinensis		0	0.76	0	0.36	1.4	0.42	0	0.28
	cgr-miR-15b-5p	Cricetulus griseus		0	0.76	0	0.36	1.4	0.42	0	0.28
	eca-miR-15b	Equus caballus		0	0.76	0	0.36	1.4	0.42	0	0.28
dof-miR-507	gga-miR-15b-5p	Gallus gallus	TAGCAGCACATCATGGTTTGCA	0	0	0	0	0	0	0	0.14
dof-miR-508	dre-miR-15b-5p	Danio rerio	TAGCAGCACATCATGGTTTGTA	0	0	0.37	0	0	0	0	0
	xtr-miR-15c	Xenopus tropicalis		0	0	0.37	0	0	0	0	0
	ipu-miR-15b	Ictalurus punctatus		0	0	0.37	0	0	0	0	0
	gga-miR-15c-5p	Gallus gallus		0	0	0.37	0	0	0	0	0
	xla-miR-15c	Xenopus laevis		0	0	0.37	0	0	0	0	0
dof-miR-509	fru-miR-15a	Fugu rubripes	TAGCAGCACGGAATGGTTGTG	0	0	0	0	0	0	0.17	0
	tmi-miR-15a	Tetraodon nigroviridis		0	0	0	0	0	0	0.17	0
	hhi-miR-15a	Hippoglossus hippoglossus		0	0	0	0	0	0	0.17	0
dof-miR-510	ppy-miR-16	Pongo pygmaeus	TAGCAGCACGTAATATTTGG	0	0	0.18	0	0.65	0.42	0	0

	oar-miR-16b	Ovis aries		0	0	0.18	0	0.65	0.42	0	0
	aca-miR-16a-5p	Anolis carolinensis		0	0	0.18	0	0.65	0.42	0	0
dof-miR-511	dre-miR-16b	Danio rerio	TAGCAGCACGTAAATATTGGAG	0.4	0	0	0.18	0	0	1.17	0.28
	fru-miR-16	Fugu rubripes		0.4	0	0	0.18	0	0	1.17	0.28
	tni-miR-16	Tetraodon nigroviridis		0.4	0	0	0.18	0	0	1.17	0.28
	chi-miR-16a-5p	Capra hircus		0.4	0	0	0.18	0	0	1.17	0.28
	ssa-miR-16a-5p	Salmo salar		0.4	0	0	0.18	0	0	1.17	0.28
	ipu-miR-16b	Ictalurus punctatus		0.4	0	0	0.18	0	0	1.17	0.28
	ccr-miR-16b	Cyprinus carpio		0.4	0	0	0.18	0	0	1.17	0.28
	tgu-miR-16b-5p	Taeniopygia guttata		0.4	0	0	0.18	0	0	1.17	0.28
dof-miR-512	pma-miR-16-5p	Petromyzon marinus	TAGCAGCACGTAAATATTGGAGT	0	0	0	0	0	0	0.33	0.14
dof-miR-513	bta-miR-16b	Bos taurus	TAGCAGCACGTAAATATTGGC	2.38	2.55	0	0.18	2.05	0.1	6.18	1.68
	ola-miR-16	Oryzias latipes		2.38	2.55	0	0.18	2.05	0.1	6.18	1.68
dof-miR-514	hsa-miR-16-5p	Homo sapiens	TAGCAGCACGTAAATATTGGCG	2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	mmu-miR-16-5p	Mus musculus		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	rno-miR-16-5p	Rattus norvegicus		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	age-miR-16	Ateles geoffroyi		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	ggo-miR-16	Gorilla gorilla		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	mne-miR-16	Macaca nemestrina		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	sla-miR-16	Saguinus labiatus		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	ppa-miR-16	Pan paniscus		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	mml-miR-16-5p	Macaca mulatta		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	ptr-miR-16	Pan troglodytes		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	lla-miR-16	Lagothrix lagotricha		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	mdo-miR-16-5p	Monodelphis domestica		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	oan-miR-16a-5p	Ornithorhynchus anatinus		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	ssa-miR-16c-5p	Salmo salar		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	cgr-miR-16-5p	Cricetulus griseus		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	eca-miR-16	Equus caballus		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
	cfa-miR-16	Canis familiaris		2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48
ssc-miR-16	Sus scrofa	2.18	15.53	2.02	1.98	24.34	9.39	4.84	4.48		
dof-miR-515	efu-miR-16	Eptesicus fuscus	TAGCAGCACGTAAATATTGGCGT	0.4	0.25	0.37	0	0.47	0	0.17	0.42
dof-miR-516	chi-miR-16b-5p	Capra hircus	TAGCAGCACGTAAATATTGGGG	0	0	0	0	0.09	0	0	0
dof-miR-517	gga-miR-16-5p	Gallus gallus	TAGCAGCACGTAAATATTGGTG	0	0	0	0.54	0	0.1	0	0

	dre-miR-16a	Danio rerio		0	0	0	0.54	0	0.1	0	0
	lca-miR-16	Lemur catta		0	0	0	0.54	0	0.1	0	0
	xtr-miR-16a	Xenopus tropicalis		0	0	0	0.54	0	0.1	0	0
	oan-miR-16b-5p	Ornithorhynchus anatinus		0	0	0	0.54	0	0.1	0	0
	oha-miR-16b-5p	Ophiophagus hannah		0	0	0	0.54	0	0.1	0	0
	ssa-miR-16b-5p	Salmo salar		0	0	0	0.54	0	0.1	0	0
	ccr-miR-16a	Cyprinus carpio		0	0	0	0.54	0	0.1	0	0
	tgu-miR-16a-5p	Taeniopygia guttata		0	0	0	0.54	0	0.1	0	0
	bta-miR-16a	Bos taurus		0	0	0	0.54	0	0.1	0	0
dof-miR-518	ccr-miR-16c	Cyprinus carpio	TAGCAGCATGTAAATATTGGA	0	0	0	0.36	0	0	0	0
dof-miR-519	dre-miR-16c-5p	Danio rerio	TAGCAGCATGTAAATATTGGAG	0	0	0.18	0.18	0	0	0	0
dof-miR-520	ssa-miR-15c-5p	Salmo salar	TAGCAGCGCATCATGGTTGA	0	1.02	0	0	0	0	1.34	0
dof-miR-521	bta-miR-503-5p	Bos taurus	TAGCAGCGGGAACAGTACTG	0	0	0	0.36	0	0	0	0
	cfa-miR-503	Canis familiaris		0	0	0	0.36	0	0	0	0
dof-miR-522	sbi-miR169d-5p	Sorghum bicolor	TAGCCAAGGATGACTTGCCCT	0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	stu-miR169a-5p	Solanum tuberosum		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	stu-miR169b-5p	Solanum tuberosum		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	stu-miR169c-5p	Solanum tuberosum		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	stu-miR169d-5p	Solanum tuberosum		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	stu-miR169e-5p	Solanum tuberosum		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	stu-miR169f-5p	Solanum tuberosum		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	stu-miR169g	Solanum tuberosum		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	stu-miR169h	Solanum tuberosum		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
	atr-miR169a	Amborella trichopoda		0.2	12.98	13.96	5.05	0.56	1.25	1.17	0
atr-miR169c	Amborella trichopoda	0.2	12.98	13.96	5.05	0.56	1.25	1.17	0		
dof-miR-523	cca-miR169a	Cynara cardunculus	TAGCCAAGGATGACTTGCCCT	0	0	1.1	0	0	0.21	0.17	0
	nta-miR169t	Nicotiana tabacum		0	0	1.1	0	0	0.21	0.17	0
dof-miR-524	hsa-miR-21-5p	Homo sapiens	TAGCTTATCAGACTGATGTTGA	1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	mmu-miR-21a-5p	Mus musculus		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	rno-miR-21-5p	Rattus norvegicus		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	ssc-miR-21	Sus scrofa		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	mml-miR-21-5p	Macaca mulatta		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	ptr-miR-21	Pan troglodytes		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	ggo-miR-21	Gorilla gorilla		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1

	ppy-miR-21	Pongo pygmaeus		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	mne-miR-21	Macaca nemestrina		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	age-miR-21	Ateles geoffroyi		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	ppa-miR-21	Pan paniscus		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	gga-miR-21-5p	Gallus gallus		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	mdo-miR-21-5p	Monodelphis domestica		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	cgr-miR-21-5p	Cricetulus griseus		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	oan-miR-21-5p	Ornithorhynchus anatinus		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	tch-miR-21-5p	Tupaia chinensis		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	oha-miR-21-5p	Ophiophagus hannah		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	aca-miR-21-5p	Anolis carolinensis		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	eca-miR-21	Equus caballus		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	tgu-miR-21-5p	Taeniopygia guttata		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
	cfa-miR-21	Canis familiaris		1.19	2.04	3.67	6.49	18.93	5.01	4.01	2.1
dof-miR-525	chi-miR-21-5p	Capra hircus	TAGCTTATCAGACTGATGTTGAC	0.4	1.78	6.98	6.85	39.17	4.07	3.67	0.7
	oar-miR-21	Ovis aries		0.4	1.78	6.98	6.85	39.17	4.07	3.67	0.7
dof-miR-526	bta-miR-21-5p	Bos taurus	TAGCTTATCAGACTGATGTTGACT	0	1.27	1.1	2.7	13.99	0.83	0.67	0.14
dof-miR-527	ola-miR-21	Oryzias latipes	TAGCTTATCAGACTGGTGTTG	0.4	0.76	0.18	0.9	0	0	1.5	0
dof-miR-528	pol-miR-21-5p	Paralichthys olivaceus	TAGCTTATCAGACTGGTGTTGG	2.38	1.78	1.65	0.9	0	0	6.01	0.98
dof-miR-529	dre-miR-21	Danio rerio	TAGCTTATCAGACTGGTGTTGGC	4.36	6.11	2.2	7.21	0	0	16.86	1.4
	fru-miR-21	Fugu rubripes		4.36	6.11	2.2	7.21	0	0	16.86	1.4
	tmi-miR-21	Tetraodon nigroviridis		4.36	6.11	2.2	7.21	0	0	16.86	1.4
	ssa-miR-21b-5p	Salmo salar		4.36	6.11	2.2	7.21	0	0	16.86	1.4
	ipu-miR-21	Ictalurus punctatus		4.36	6.11	2.2	7.21	0	0	16.86	1.4
	hhi-miR-21	Hippoglossus hippoglossus		4.36	6.11	2.2	7.21	0	0	16.86	1.4
	ccr-miR-21	Cyprinus carpio		4.36	6.11	2.2	7.21	0	0	16.86	1.4
dof-miR-530	dme-miR-276a-3p	Drosophila melanogaster	TAGGAACTTCATACCGTGCTCT	0.2	0	0	2.34	0	0	0	0
	dps-miR-276a	Drosophila pseudoobscura		0.2	0	0	2.34	0	0	0	0
	ame-miR-276	Apis mellifera		0.2	0	0	2.34	0	0	0	0
	aga-miR-276-3p	Anopheles gambiae		0.2	0	0	2.34	0	0	0	0
	bmo-miR-276-3p	Bombyx mori		0.2	0	0	2.34	0	0	0	0
	mse-miR-276	Manduca sexta		0.2	0	0	2.34	0	0	0	0
	nvi-miR-276	Nasonia vitripennis		0.2	0	0	2.34	0	0	0	0
	ngi-miR-276	Nasonia giraulti		0.2	0	0	2.34	0	0	0	0

	nlo-miR-276	Nasonia longicornis		0.2	0	0	2.34	0	0	0	0
	dpu-miR-276	Daphnia pulex		0.2	0	0	2.34	0	0	0	0
	api-miR-276	Acyrtosiphon pisum		0.2	0	0	2.34	0	0	0	0
	cqu-miR-276-3p	Culex quinquefasciatus		0.2	0	0	2.34	0	0	0	0
	tca-miR-276-3p	Tribolium castaneum		0.2	0	0	2.34	0	0	0	0
	dan-miR-276a	Drosophila ananassae		0.2	0	0	2.34	0	0	0	0
	der-miR-276a	Drosophila erecta		0.2	0	0	2.34	0	0	0	0
	dgr-miR-276a-3p	Drosophila grimshawi		0.2	0	0	2.34	0	0	0	0
	dmo-miR-276a	Drosophila mojavensis		0.2	0	0	2.34	0	0	0	0
	dpe-miR-276a	Drosophila persimilis		0.2	0	0	2.34	0	0	0	0
	dse-miR-276a	Drosophila sechellia		0.2	0	0	2.34	0	0	0	0
	dsi-miR-276a	Drosophila simulans		0.2	0	0	2.34	0	0	0	0
	dvi-miR-276a-3p	Drosophila virilis		0.2	0	0	2.34	0	0	0	0
	dwi-miR-276a-3p	Drosophila willistoni		0.2	0	0	2.34	0	0	0	0
	dya-miR-276a	Drosophila yakuba		0.2	0	0	2.34	0	0	0	0
	lmi-miR-276-3p	Locusta migratoria		0.2	0	0	2.34	0	0	0	0
dof-miR-531	mmu-miR-1197-3p	Mus musculus	TAGGACACATGGTCTACTTCT	0	0	0	0.36	0	0	0	0
	hsa-miR-1197	Homo sapiens		0	0	0	0.36	0	0	0	0
	chi-miR-1197-3p	Capra hircus		0	0	0	0.36	0	0	0	0
	oar-miR-1197-3p	Ovis aries		0	0	0	0.36	0	0	0	0
	ppy-miR-1197	Pongo pygmaeus		0	0	0	0.36	0	0	0	0
	eca-miR-1197	Equus caballus		0	0	0	0.36	0	0	0	0
	ptr-miR-1197	Pan troglodytes		0	0	0	0.36	0	0	0	0
	bta-miR-1197	Bos taurus		0	0	0	0.36	0	0	0	0
dof-miR-532	nta-miR6153	Nicotiana tabacum	TAGGACCATATTCACTATTG	0	0	0	0	0	0	0	0.14
dof-miR-533	osa-miR1425-5p	Oryza sativa	TAGGATTCAATCCTTGTCTGT	0	0	0	0	0.09	0.1	0	0
dof-miR-534	gga-miR-196-5p	Gallus gallus	TAGGTAGTTTCATGTTGTTGG	0	0	0	0.18	0	0	0	0
	mml-miR-196a-5p	Macaca mulatta		0	0	0	0.18	0	0	0	0
	ggo-miR-196	Gorilla gorilla		0	0	0	0.18	0	0	0	0
	ppy-miR-196	Pongo pygmaeus		0	0	0	0.18	0	0	0	0
	xtr-miR-196a	Xenopus tropicalis		0	0	0	0.18	0	0	0	0
	chi-miR-196a	Capra hircus		0	0	0	0.18	0	0	0	0
	ola-miR-196a	Oryzias latipes		0	0	0	0.18	0	0	0	0
	aca-miR-196a	Anolis carolinensis		0	0	0	0.18	0	0	0	0

dof-miR-535	hsa-miR-196a-5p	Homo sapiens	TAGGTAGTTTCATGTTGTTGGG	0	0	0	0.36	0	0	0	0
	mmu-miR-196a-5p	Mus musculus		0	0	0	0.36	0	0	0	0
	rno-miR-196a-5p	Rattus norvegicus		0	0	0	0.36	0	0	0	0
	dre-miR-196a-5p	Danio rerio		0	0	0	0.36	0	0	0	0
	ssc-miR-196a	Sus scrofa		0	0	0	0.36	0	0	0	0
	ptr-miR-196a	Pan troglodytes		0	0	0	0.36	0	0	0	0
	ppy-miR-196-2	Pongo pygmaeus		0	0	0	0.36	0	0	0	0
	lla-miR-196	Lagothrix lagotricha		0	0	0	0.36	0	0	0	0
	age-miR-196	Ateles geoffroyi		0	0	0	0.36	0	0	0	0
	ppa-miR-196	Pan paniscus		0	0	0	0.36	0	0	0	0
	fru-miR-196a	Fugu rubripes		0	0	0	0.36	0	0	0	0
	tui-miR-196a	Tetraodon nigroviridis		0	0	0	0.36	0	0	0	0
	oan-miR-196a-5p	Ornithorhynchus anatinus		0	0	0	0.36	0	0	0	0
	oha-miR-196b-5p	Ophiophagus hannah		0	0	0	0.36	0	0	0	0
	ssa-miR-196a-5p	Salmo salar		0	0	0	0.36	0	0	0	0
	ccr-miR-196a	Cyprinus carpio		0	0	0	0.36	0	0	0	0
	cgr-miR-196a-5p	Cricetulus griseus		0	0	0	0.36	0	0	0	0
	pma-miR-196a-5p	Petromyzon marinus		0	0	0	0.36	0	0	0	0
	eca-miR-196a	Equus caballus		0	0	0	0.36	0	0	0	0
	cfa-miR-196a	Canis familiaris		0	0	0	0.36	0	0	0	0
bta-miR-196a	Bos taurus	0	0	0	0.36	0	0	0	0		
dof-miR-536	efu-miR-196	Eptesicus fuscus	TAGGTAGTTTCATGTTGTTGGGA	0	0	0.18	0.54	0	0	0	0
	tch-miR-196a-5p	Tupaia chinensis		0	0	0.18	0.54	0	0	0	0
	ipu-miR-196a	Ictalurus punctatus		0	0	0.18	0.54	0	0	0	0
dof-miR-537	mdo-miR-196b	Monodelphis domestica	TAGGTAGTTTCCTGTTGTTGG	0	0	0.18	0	0	0	0	0
	oan-miR-196b-5p	Ornithorhynchus anatinus		0	0	0.18	0	0	0	0	0
	chi-miR-196b	Capra hircus		0	0	0.18	0	0	0	0	0
dof-miR-538	hsa-miR-196b-5p	Homo sapiens	TAGGTAGTTTCCTGTTGTTGGG	0	0	0	0.18	0	0	0	0
	mmu-miR-196b-5p	Mus musculus		0	0	0	0.18	0	0	0	0
	rno-miR-196b-5p	Rattus norvegicus		0	0	0	0.18	0	0	0	0
	mdo-miR-196a-5p	Monodelphis domestica		0	0	0	0.18	0	0	0	0
	cgr-miR-196b	Cricetulus griseus		0	0	0	0.18	0	0	0	0
	ppy-miR-196b	Pongo pygmaeus		0	0	0	0.18	0	0	0	0
	eca-miR-196b	Equus caballus		0	0	0	0.18	0	0	0	0

	ssc-miR-196b-5p	Sus scrofa		0	0	0	0.18	0	0	0	0
	mml-miR-196b-5p	Macaca mulatta		0	0	0	0.18	0	0	0	0
	ptr-miR-196b	Pan troglodytes		0	0	0	0.18	0	0	0	0
dof-miR-539	cfa-miR-196b	Canis familiaris	TAGGTAGTTTCCTGTTGTTGGGA	0	0	0.18	0	0	0	0	0
	bta-miR-196b	Bos taurus		0	0	0.18	0	0	0	0	0
dof-miR-540	ptc-miR476a	Populus trichocarpa	TAGTAATCCTTCTTTGCAAAG	0	0	0	0.18	0	0	0	0
dof-miR-541	mmu-miR-411-5p	Mus musculus	TAGTAGACCGTATAGCGTACG	0	0	0	0.72	0	0	0	0
	hsa-miR-411-5p	Homo sapiens		0	0	0	0.72	0	0	0	0
	rno-miR-411-5p	Rattus norvegicus		0	0	0	0.72	0	0	0	0
	tch-miR-411-5p	Tupaia chinensis		0	0	0	0.72	0	0	0	0
	ppy-miR-411	Pongo pygmaeus		0	0	0	0.72	0	0	0	0
	eca-miR-411	Equus caballus		0	0	0	0.72	0	0	0	0
	mml-miR-411-5p	Macaca mulatta		0	0	0	0.72	0	0	0	0
	ptr-miR-411	Pan troglodytes		0	0	0	0.72	0	0	0	0
dof-miR-542	dre-miR-454b	Danio rerio	TAGTGCAATATTGCTTATAGGG	0	0	0	0.18	0	0	0	0
	ppy-miR-454	Pongo pygmaeus		0	0	0	0.18	0	0	0	0
	cfa-miR-454	Canis familiaris		0	0	0	0.18	0	0	0	0
dof-miR-543	hsa-miR-454-3p	Homo sapiens	TAGTGCAATATTGCTTATAGGGT	0	0.25	0	0	0.09	0	0	0
	oan-miR-454-3p	Ornithorhynchus anatinus		0	0.25	0	0	0.09	0	0	0
	gga-miR-454-3p	Gallus gallus		0	0.25	0	0	0.09	0	0	0
	chi-miR-454-3p	Capra hircus		0	0.25	0	0	0.09	0	0	0
	ipu-miR-454b	Ictalurus punctatus		0	0.25	0	0	0.09	0	0	0
	sha-miR-454	Sarcophilus harrisii		0	0.25	0	0	0.09	0	0	0
	aca-miR-454-3p	Anolis carolinensis		0	0.25	0	0	0.09	0	0	0
	eca-miR-454	Equus caballus		0	0.25	0	0	0.09	0	0	0
	tgu-miR-454-3p	Taeniopygia guttata		0	0.25	0	0	0.09	0	0	0
	mml-miR-454-3p	Macaca mulatta		0	0.25	0	0	0.09	0	0	0
	ptr-miR-454	Pan troglodytes		0	0.25	0	0	0.09	0	0	0
	bta-miR-454	Bos taurus		0	0.25	0	0	0.09	0	0	0
dof-miR-544	hsa-miR-381-3p	Homo sapiens		TATACAAGGCAAGCTCTCTGT	0	0	0.37	0	0	0	0
	mmu-miR-381-3p	Mus musculus	0		0	0.37	0	0	0	0	0
	chi-miR-381	Capra hircus	0		0	0.37	0	0	0	0	0
	tch-miR-381-3p	Tupaia chinensis	0		0	0.37	0	0	0	0	0
	cgr-miR-381	Cricetulus griseus	0		0	0.37	0	0	0	0	0

	ppy-miR-381	Pongo pygmaeus		0	0	0.37	0	0	0	0	0
	eca-miR-381	Equus caballus		0	0	0.37	0	0	0	0	0
	mml-miR-381-3p	Macaca mulatta		0	0	0.37	0	0	0	0	0
	ptr-miR-381	Pan troglodytes		0	0	0.37	0	0	0	0	0
	bta-miR-381	Bos taurus		0	0	0.37	0	0	0	0	0
	cfa-miR-381	Canis familiaris		0	0	0.37	0	0	0	0	0
dof-miR-545	api-miR-2a	Acyrtosiphon pisum	TATCACAGCCAGCTTTGATGAGCG	0	0	0	0	0	0	0.17	0
dof-miR-546	fru-miR-135b	Fugu rubripes	TATGGCTTTTTATTCTATCTG	0	0	0.18	0.36	0	0	0	0
	tmi-miR-135b	Tetraodon nigroviridis		0	0	0.18	0.36	0	0	0	0
	dre-miR-135b-5p	Danio rerio		0	0	0.18	0.36	0	0	0	0
	ipu-miR-135b	Ictalurus punctatus		0	0	0.18	0.36	0	0	0	0
dof-miR-547	ssa-miR-135a-5p	Salmo salar	TATGGCTTTTTATTCTATCTGA	0	0	0.73	0.18	0	0	0	0
dof-miR-548	chi-miR-411a-3p	Capra hircus	TATGTAACACGGTCCACTAAC	0	0	0.18	1.08	0.09	0	0.17	0
	oar-miR-411a-3p	Ovis aries		0	0	0.18	1.08	0.09	0	0.17	0
	mml-miR-411-3p	Macaca mulatta		0	0	0.18	1.08	0.09	0	0.17	0
dof-miR-549	mmu-miR-411-3p	Mus musculus	TATGTAACACGGTCCACTAAC	0	0	0	0.18	0	0	0	0
	hsa-miR-411-3p	Homo sapiens		0	0	0	0.18	0	0	0	0
dof-miR-550	cfa-miR-380	Canis familiaris	TATGTAATATGGTCCACGTCT	0.2	0	0.18	1.26	0	0	0.17	0.56
dof-miR-551	bta-miR-380-3p	Bos taurus	TATGTAATGTGGTCCACGTCT	0	0	0.37	0	0	0	0	0
	chi-miR-380-3p	Capra hircus		0	0	0.37	0	0	0	0	0
	oar-miR-380-3p	Ovis aries		0	0	0.37	0	0	0	0	0
dof-miR-552	rno-miR-299a-3p	Rattus norvegicus	TATGTGGGACGGTAAACCGCT	0	0	0	0.18	0	0	0	0
dof-miR-553	mmu-miR-299a-3p	Mus musculus	TATGTGGGACGGTAAACCGCTT	0	0	0.37	0	0	0	0	0
	ppy-miR-299-3p	Pongo pygmaeus		0	0	0.37	0	0	0	0	0
	mml-miR-299-3p	Macaca mulatta		0	0	0.37	0	0	0	0	0
dof-miR-554	oan-miR-32-5p	Ornithorhynchus anatinus	TATTGCACATTACTAAGTTG	0	0	0	0	0.19	0	0	0
dof-miR-555	gga-miR-32-5p	Gallus gallus	TATTGCACATTACTAAGTTGC	0.2	0	0	0	0.09	0	0	0
	sse-miR-32	Sus scrofa		0.2	0	0	0	0.09	0	0	0
	mml-miR-32-5p	Macaca mulatta		0.2	0	0	0	0.09	0	0	0
	ptr-miR-32	Pan troglodytes		0.2	0	0	0	0.09	0	0	0
	ggo-miR-32	Gorilla gorilla		0.2	0	0	0	0.09	0	0	0
	ppy-miR-32	Pongo pygmaeus		0.2	0	0	0	0.09	0	0	0
	sla-miR-32	Saguinus labiatus		0.2	0	0	0	0.09	0	0	0
	mne-miR-32	Macaca nemestrina		0.2	0	0	0	0.09	0	0	0

	ppa-miR-32	Pan paniscus		0.2	0	0	0	0.09	0	0	0
	mdo-miR-32-5p	Monodelphis domestica		0.2	0	0	0	0.09	0	0	0
	cgr-miR-32-5p	Cricetulus griseus		0.2	0	0	0	0.09	0	0	0
	tgu-miR-32	Taeniopygia guttata		0.2	0	0	0	0.09	0	0	0
dof-miR-556	bma-miR-92	Brugia malayi	TATTGCACTCGTCCCGGCCT	0	0	0	0	0.09	0	0	0
dof-miR-557	xtr-miR-92b	Xenopus tropicalis	TATTGCACTCGTCCCGGCCTC	0	0	0	0	0	0	0.17	0
dof-miR-558	dre-miR-92b-3p	Danio rerio	TATTGCACTCGTCCCGGCCTCC	0	0	0	0.18	0	0	0	0
	hsa-miR-92b-3p	Homo sapiens		0	0	0	0.18	0	0	0	0
	mmu-miR-92b-3p	Mus musculus		0	0	0	0.18	0	0	0	0
	rno-miR-92b-3p	Rattus norvegicus		0	0	0	0.18	0	0	0	0
	efu-miR-92b	Eptesicus fuscus		0	0	0	0.18	0	0	0	0
	ssa-miR-92b-3p	Salmo salar		0	0	0	0.18	0	0	0	0
	ipu-miR-92b	Ictalurus punctatus		0	0	0	0.18	0	0	0	0
	ccr-miR-92b	Cyprinus carpio		0	0	0	0.18	0	0	0	0
	mdo-miR-92b-3p	Monodelphis domestica		0	0	0	0.18	0	0	0	0
	cgr-miR-92b-3p	Cricetulus griseus		0	0	0	0.18	0	0	0	0
	ptr-miR-92b	Pan troglodytes		0	0	0	0.18	0	0	0	0
	ppy-miR-92b	Pongo pygmaeus		0	0	0	0.18	0	0	0	0
	eca-miR-92b	Equus caballus		0	0	0	0.18	0	0	0	0
	ssc-miR-92b-3p	Sus scrofa		0	0	0	0.18	0	0	0	0
	mml-miR-92b-3p	Macaca mulatta		0	0	0	0.18	0	0	0	0
cfa-miR-92b	Canis familiaris	0	0	0	0.18	0	0	0	0		
bta-miR-92b	Bos taurus	0	0	0	0.18	0	0	0	0		
dof-miR-559	pmi-miR-92b-3p	Patiria miniata	TATTGCACTCGTCCCGGCCTGC	0	0	0	0	0	0	0.17	0
	lva-miR-92b-3p	Lytechinus variegatus		0	0	0	0	0	0	0.17	0
	spu-miR-92c	Strongylocentrotus purpuratus		0	0	0	0	0	0	0.17	0
dof-miR-560	oan-miR-92b	Ornithorhynchus anatinus	TATTGCACTTGTCACAGCCTGT	0	0	0	0	0.09	0	0	0
dof-miR-561	pmi-miR-92c-3p	Patiria miniata	TATTGCACTTGTCACAGCCTGC	0	0	0	0	0.09	0	0	0
dof-miR-562	ska-miR-92a	Saccoglossus kowalevskii	TATTGCACTTGTCACAGCCTAA	0	0	0	0	0.19	0	0	0
dof-miR-563	mmu-miR-92a-3p	Mus musculus	TATTGCACTTGTCACAGCCTG	0	0.25	0.37	0	1.68	1.04	0.33	0.14
	rno-miR-92a-3p	Rattus norvegicus		0	0.25	0.37	0	1.68	1.04	0.33	0.14
	gga-miR-92-3p	Gallus gallus		0	0.25	0.37	0	1.68	1.04	0.33	0.14
	xtr-miR-92a	Xenopus tropicalis		0	0.25	0.37	0	1.68	1.04	0.33	0.14
	ola-miR-92a	Oryzias latipes		0	0.25	0.37	0	1.68	1.04	0.33	0.14

	xla-miR-92a	Xenopus laevis		0	0.25	0.37	0	1.68	1.04	0.33	0.14
dof-miR-564	sko-miR-92b	Saccoglossus kowalevskii	TATTGCACTTGTCGCCGCCTGC	0	0	0.18	0.18	0	0	0	0
	spu-miR-92b-3p	Strongylocentrotus purpuratus		0	0	0.18	0.18	0	0	0	0
	hsa-miR-92a-3p	Homo sapiens		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
dof-miR-565	dre-miR-92a-3p	Danio rerio	TATTGCACTTGTCGCCGCCTGT	3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	ggo-miR-92	Gorilla gorilla		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	lca-miR-92	Lemur catta		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	age-miR-92	Ateles geoffroyi		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	ppa-miR-92	Pan paniscus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	ppy-miR-92	Pongo pygmaeus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	ptr-miR-92	Pan troglodytes		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	mml-miR-92a-3p	Macaca mulatta		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	sla-miR-92	Saguinus labiatus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	lla-miR-92	Lagothrix lagotricha		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	mne-miR-92	Macaca nemestrina		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	fru-miR-92	Fugu rubripes		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	tmi-miR-92	Tetraodon nigroviridis		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	bta-miR-92a	Bos taurus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	mdo-miR-92a-3p	Monodelphis domestica		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	oan-miR-92a-3p	Ornithorhynchus anatinus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	chi-miR-92a-3p	Capra hircus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	chi-miR-92b	Capra hircus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	tch-miR-92a-3p	Tupaia chinensis		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	oha-miR-92a-3p	Ophiophagus hannah		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	oha-miR-92a	Ophiophagus hannah		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	ssa-miR-92a-3p	Salmo salar		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	ipu-miR-92a	Ictalurus punctatus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	ccr-miR-92a	Cyprinus carpio		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	cgr-miR-92a-3p	Cricetulus griseus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	aca-miR-92a	Anolis carolinensis		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	eca-miR-92a	Equus caballus		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	ssc-miR-92a	Sus scrofa		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	tgu-miR-92-3p	Taeniopygia guttata		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31
	cfa-miR-92a	Canis familiaris		3.17	12.73	5.51	3.96	29.01	11.27	5.18	6.31

dof-miR-566	efu-miR-92a	Eptesicus fuscus	TATTGCACTGTCCCGCCTGTG	0	0	0	0	0.19	0	0	0
dof-miR-567	cin-miR-92b-3p	Ciona intestinalis	TATTGCACTGTCCCGCCTT	0	0	0	0	0.09	0	0	0
dof-miR-568	ath-miR170-5p	Arabidopsis thaliana	TATTGGCCTGGTCACTCAGA	0	0	0.18	22.7	0	0	0	0
	ath-miR171a-5p	Arabidopsis thaliana		0	0	0.18	22.7	0	0	0	0
	stu-miR171a-5p	Solanum tuberosum		0	0	0.18	22.7	0	0	0	0
	stu-miR171c-5p	Solanum tuberosum		0	0	0.18	22.7	0	0	0	0
	gma-miR171j-5p	Glycine max		0	0	0.18	22.7	0	0	0	0
	aly-miR170-5p	Arabidopsis lyrata		0	0	0.18	22.7	0	0	0	0
	aly-miR171a-5p	Arabidopsis lyrata		0	0	0.18	22.7	0	0	0	0
dof-miR-569	chi-miR-335-5p	Capra hircus	TCAAGAGCAATAACGAAAAAT	0	0.25	0.18	0.54	0.47	0	0.17	0
dof-miR-570	tch-miR-335-5p	Tupaia chinensis	TCAAGAGCAATAACGAAAAATG	0	0	0	0.18	0.09	0	0	0
	ggo-miR-335	Gorilla gorilla		0	0	0	0.18	0.09	0	0	0
	ssc-miR-335	Sus scrofa		0	0	0	0.18	0.09	0	0	0
dof-miR-571	rno-miR-335	Rattus norvegicus	TCAAGAGCAATAACGAAAAATGT	0	0	0	0.54	0.47	0	0	0.28
	hsa-miR-335-5p	Homo sapiens		0	0	0	0.54	0.47	0	0	0.28
	mmu-miR-335-5p	Mus musculus		0	0	0	0.54	0.47	0	0	0.28
	efu-miR-335	Eptesicus fuscus		0	0	0	0.54	0.47	0	0	0.28
	ppy-miR-335	Pongo pygmaeus		0	0	0	0.54	0.47	0	0	0.28
	eca-miR-335	Equus caballus		0	0	0	0.54	0.47	0	0	0.28
	mml-miR-335-5p	Macaca mulatta		0	0	0	0.54	0.47	0	0	0.28
	cfa-miR-335	Canis familiaris		0	0	0	0.54	0.47	0	0	0.28
	ptr-miR-335	Pan troglodytes		0	0	0	0.54	0.47	0	0	0.28
	bta-miR-335	Bos taurus		0	0	0	0.54	0.47	0	0	0.28
dof-miR-572	ath-miR161.2	Arabidopsis thaliana	TCAATGCATTGAAAAGTGACTA	0	0	0	0	0	0	0	0.14
	aly-miR161-5p.2	Arabidopsis lyrata		0	0	0	0	0	0	0	0.14
dof-miR-573	mse-miR-2a	Manduca sexta	TCACAGCCAGCTTTGATGAGCA	0	0	0	0	0	0.1	0.17	0
dof-miR-574	ola-miR-128	Oryzias latipes	TCACAGTGAACCGGTCTCTT	0.2	0	0	0.18	0	0.1	0	0
	ggo-miR-128	Gorilla gorilla		0.2	0	0	0.18	0	0.1	0	0
dof-miR-575	mmu-miR-128-3p	Mus musculus	TCACAGTGAACCGGTCTCTTT	0.2	1.02	0.37	0.72	0.75	0	0	0
	hsa-miR-128-3p	Homo sapiens		0.2	1.02	0.37	0.72	0.75	0	0	0
	rno-miR-128-3p	Rattus norvegicus		0.2	1.02	0.37	0.72	0.75	0	0	0
	gga-miR-128-3p	Gallus gallus		0.2	1.02	0.37	0.72	0.75	0	0	0
	ssc-miR-128	Sus scrofa		0.2	1.02	0.37	0.72	0.75	0	0	0
	ptr-miR-128	Pan troglodytes		0.2	1.02	0.37	0.72	0.75	0	0	0

	ppy-miR-128	Pongo pygmaeus		0.2	1.02	0.37	0.72	0.75	0	0	0
	bta-miR-128	Bos taurus		0.2	1.02	0.37	0.72	0.75	0	0	0
	mdo-miR-128a-3p	Monodelphis domestica		0.2	1.02	0.37	0.72	0.75	0	0	0
	oan-miR-128-3p	Ornithorhynchus anatinus		0.2	1.02	0.37	0.72	0.75	0	0	0
	chi-miR-128-3p	Capra hircus		0.2	1.02	0.37	0.72	0.75	0	0	0
	tch-miR-128	Tupaia chinensis		0.2	1.02	0.37	0.72	0.75	0	0	0
	ssa-miR-128-3p	Salmo salar		0.2	1.02	0.37	0.72	0.75	0	0	0
	mdo-miR-128b-3p	Monodelphis domestica		0.2	1.02	0.37	0.72	0.75	0	0	0
	ipu-miR-128	Ictalurus punctatus		0.2	1.02	0.37	0.72	0.75	0	0	0
	ccr-miR-128	Cyprinus carpio		0.2	1.02	0.37	0.72	0.75	0	0	0
	sha-miR-128	Sarcophilus harrisii		0.2	1.02	0.37	0.72	0.75	0	0	0
	cgr-miR-128-3p	Cricetulus griseus		0.2	1.02	0.37	0.72	0.75	0	0	0
	aca-miR-128-3p	Anolis carolinensis		0.2	1.02	0.37	0.72	0.75	0	0	0
	eca-miR-128	Equus caballus		0.2	1.02	0.37	0.72	0.75	0	0	0
	tgu-miR-128-3p	Taeniopygia guttata		0.2	1.02	0.37	0.72	0.75	0	0	0
	mml-miR-128b-3p	Macaca mulatta		0.2	1.02	0.37	0.72	0.75	0	0	0
	cfa-miR-128	Canis familiaris		0.2	1.02	0.37	0.72	0.75	0	0	0
dof-miR-576	efu-miR-128a	Eptesicus fuscus	TCACAGTGAACCGGTCTCTTTC	0.4	0	0	0.18	0	0	0.17	0
	pma-miR-128	Petromyzon marinus		0.4	0	0	0.18	0	0	0.17	0
dof-miR-577	dre-miR-128-3p	Danio rerio		0.2	0.25	0.18	0.54	0	0.1	0	0
	mml-miR-128a-3p	Macaca mulatta		0.2	0.25	0.18	0.54	0	0.1	0	0
	sla-miR-128	Saguinus labiatus		0.2	0.25	0.18	0.54	0	0.1	0	0
	age-miR-128	Ateles geoffroyi		0.2	0.25	0.18	0.54	0	0.1	0	0
	ppa-miR-128	Pan paniscus	TCACAGTGAACCGGTCTCTTTT	0.2	0.25	0.18	0.54	0	0.1	0	0
	fru-miR-128	Fugu rubripes		0.2	0.25	0.18	0.54	0	0.1	0	0
	tni-miR-128	Tetraodon nigroviridis		0.2	0.25	0.18	0.54	0	0.1	0	0
	xtr-miR-128	Xenopus tropicalis		0.2	0.25	0.18	0.54	0	0.1	0	0
	oha-miR-128-3p	Ophiophagus hannah		0.2	0.25	0.18	0.54	0	0.1	0	0
dof-miR-578	efu-miR-128b	Eptesicus fuscus	TCACAGTGAACCGGTCTTTTT	0	0	0	0.54	0	0	0	0
dof-miR-579	pab-miR950-5p	Picea abies	TCACATCTGGGCCACGATGGTT	0	0	8.45	13.33	0	0	0.33	0
dof-miR-580	pde-miR1311	Pinus densata		0	0	0.37	1.26	0	0	0.17	0
	pab-miR1311	Picea abies	TCAGAGTTTTGCCAGTCCGCC	0	0	0.37	1.26	0	0	0.17	0
	pta-miR1311	Pinus taeda		0	0	0.37	1.26	0	0	0.17	0
dof-miR-581	gra-miR167a	Gossypium raimondii	TCAGATCATCTTGCAGCTTCA	0.79	4.33	0	0	0.47	0.94	0.67	0.98

	gra-miR167b	Gossypium raimondii		0.79	4.33	0	0	0.47	0.94	0.67	0.98
dof-miR-582	ggo-miR-484	Gorilla gorilla	TCAGGCTCAGTCCCCTCCCGA	0	0	0	0	0.19	0	0	0
dof-miR-583	hsa-miR-484	Homo sapiens	TCAGGCTCAGTCCCCTCCCGAT	0	0	0.37	0.18	0	0	0	0
	mmu-miR-484	Mus musculus		0	0	0.37	0.18	0	0	0	0
	bta-miR-484	Bos taurus		0	0	0.37	0.18	0	0	0	0
	rno-miR-484	Rattus norvegicus		0	0	0.37	0.18	0	0	0	0
	cgr-miR-484	Cricetulus griseus		0	0	0.37	0.18	0	0	0	0
	ppy-miR-484	Pongo pygmaeus		0	0	0.37	0.18	0	0	0	0
	mml-miR-484	Macaca mulatta		0	0	0.37	0.18	0	0	0	0
	ptr-miR-484	Pan troglodytes		0	0	0.37	0.18	0	0	0	0
dof-miR-584	dme-miR-275-3p	Drosophila melanogaster	TCAGGTACCTGAAGTAGCGCGCG	0	0	0	0	0	0	0.17	0
	dps-miR-275	Drosophila pseudoobscura		0	0	0	0	0	0	0.17	0
	aga-miR-275	Anopheles gambiae		0	0	0	0	0	0	0.17	0
	bmo-miR-275-3p	Bombyx mori		0	0	0	0	0	0	0.17	0
	ame-miR-275	Apis mellifera		0	0	0	0	0	0	0.17	0
	mse-miR-275	Manduca sexta		0	0	0	0	0	0	0.17	0
	nvi-miR-275	Nasonia vitripennis		0	0	0	0	0	0	0.17	0
	ngi-miR-275	Nasonia giraulti		0	0	0	0	0	0	0.17	0
	nlo-miR-275	Nasonia longicornis		0	0	0	0	0	0	0.17	0
	dpu-miR-275	Daphnia pulex		0	0	0	0	0	0	0.17	0
	isc-miR-275	Ixodes scapularis		0	0	0	0	0	0	0.17	0
	tca-miR-275-3p	Tribolium castaneum		0	0	0	0	0	0	0.17	0
	dan-miR-275	Drosophila ananassae		0	0	0	0	0	0	0.17	0
	der-miR-275	Drosophila erecta		0	0	0	0	0	0	0.17	0
	dgr-miR-275	Drosophila grimshawi		0	0	0	0	0	0	0.17	0
	dmo-miR-275	Drosophila mojavensis		0	0	0	0	0	0	0.17	0
	dpe-miR-275	Drosophila persimilis		0	0	0	0	0	0	0.17	0
	dse-miR-275	Drosophila sechellia		0	0	0	0	0	0	0.17	0
	dsi-miR-275	Drosophila simulans		0	0	0	0	0	0	0.17	0
	dvi-miR-275-3p	Drosophila virilis		0	0	0	0	0	0	0.17	0
	dwi-miR-275	Drosophila willistoni		0	0	0	0	0	0	0.17	0
	dya-miR-275	Drosophila yakuba		0	0	0	0	0	0	0.17	0
dof-miR-585	dre-miR-459-5p	Danio rerio	TCAGTAACAAGGATTCATCCTG	0	0	0	0.18	0	0	0	0
	ipu-miR-459	Ictalurus punctatus		0	0	0	0.18	0	0	0	0

	ola-miR-459-5p	Oryzias latipes		0	0	0	0.18	0	0	0	0		
dof-miR-586	ssa-miR-459-5p	Salmo salar	TCAGTAACAAGGATTCATCCTGT	0	0	0	0.36	0	0	0	0		
dof-miR-587	efu-miR-452	Eptesiscus fuscus	TCAGTCTCATCTGCAAAGAAGT	0	0	0.18	0	0	0	0	0		
dof-miR-588	dme-miR-14-3p	Drosophila melanogaster	TCAGTCTTTTTCTCTCTCTAT	0	0	0	0	0	0	0	0.5	0	
	hme-miR-14	Heliconius melpomene		0	0	0	0	0	0	0	0	0.5	0
	mse-miR-14	Manduca sexta		0	0	0	0	0	0	0	0	0.5	0
	aae-miR-14	Aedes aegypti		0	0	0	0	0	0	0	0	0.5	0
	cqu-miR-14	Culex quinquefasciatus		0	0	0	0	0	0	0	0	0.5	0
	api-miR-14	Acyrtosiphon pisum		0	0	0	0	0	0	0	0	0.5	0
	tca-miR-14-3p	Tribolium castaneum		0	0	0	0	0	0	0	0	0.5	0
dof-miR-589	rno-miR-148a-3p	Rattus norvegicus	TCAGTGCACTACAGAACTTTG	0	0	0	0	0.19	0.31	0.17	0		
	ggo-miR-148a	Gorilla gorilla		0	0	0	0	0.19	0.31	0.17	0		
dof-miR-590	hsa-miR-148a-3p	Homo sapiens	TCAGTGCACTACAGAACTTTGT	1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	mmu-miR-148a-3p	Mus musculus		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	gga-miR-148a-3p	Gallus gallus		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	ssc-miR-148a-3p	Sus scrofa		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	bta-miR-148a	Bos taurus		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	xtr-miR-148a	Xenopus tropicalis		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	oan-miR-148-3p	Ornithorhynchus anatinus		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	chi-miR-148a-3p	Capra hircus		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	tch-miR-148a-3p	Tupaia chinensis		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	oar-miR-148a	Ovis aries		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	aca-miR-148a-3p	Anolis carolinensis		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	ppy-miR-148a	Pongo pygmaeus		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	mdo-miR-148-3p	Monodelphis domestica		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	eca-miR-148a	Equus caballus		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	tgu-miR-148-3p	Taeniopygia guttata		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	mml-miR-148a-3p	Macaca mulatta		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
	cfa-miR-148a	Canis familiaris		1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26		
ptr-miR-148a	Pan troglodytes	1.58	3.82	6.61	7.75	11.19	3.55	1.5	1.26				
dof-miR-591	ssa-miR-152-3p	Salmo salar	TCAGTGATAACAGAACTTTG	0	0	0.18	0.36	0	0	0	0		
dof-miR-592	fru-miR-152	Fugu rubripes	TCAGTGATAACAGAACTTTGT	0	0.76	0.18	1.8	0	0	0.33	0		
	tmi-miR-152	Tetraodon nigroviridis		0	0.76	0.18	1.8	0	0	0.33	0		
dof-miR-593	ggo-miR-148b	Gorilla gorilla	TCAGTGATCACAGAACTTTG	0	0.25	0	0	0.28	0.1	0	0.14		

dof-miR-594	rno-miR-148b-3p	Rattus norvegicus	TCAGTGCATCACAGAACTTTGT	0	0.76	0.18	0.36	0.84	0.42	0	0.56
	mmu-miR-148b-3p	Mus musculus		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	hsa-miR-148b-3p	Homo sapiens		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	xtr-miR-148b	Xenopus tropicalis		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	bta-miR-148b	Bos taurus		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	chi-miR-148b-3p	Capra hircus		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	tch-miR-148b-3p	Tupaia chinensis		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	oha-miR-148b	Ophiophagus hannah		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	cgr-miR-148b-3p	Cricetulus griseus		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	aca-miR-148b-3p	Anolis carolinensis		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	ppy-miR-148b	Pongo pygmaeus		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	eca-miR-148b-3p	Equus caballus		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	ssc-miR-148b-3p	Sus scrofa		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	mml-miR-148b-3p	Macaca mulatta		0	0.76	0.18	0.36	0.84	0.42	0	0.56
	cfa-miR-148b	Canis familiaris		0	0.76	0.18	0.36	0.84	0.42	0	0.56
ptr-miR-148b	Pan troglodytes	0	0.76	0.18	0.36	0.84	0.42	0	0.56		
dof-miR-595	efu-miR-148	Eptesicus fuscus	TCAGTGCATCACAGAACTTTGTC	0	0	0	0	0.09	0	0	0
dof-miR-596	mmu-miR-152-3p	Mus musculus	TCAGTGCATGACAGAACITGG	0.2	0	1.29	0.18	0.28	0.21	0	0.14
	hsa-miR-152-3p	Homo sapiens		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	rno-miR-152-3p	Rattus norvegicus		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	tch-miR-152	Tupaia chinensis		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	oar-miR-152	Ovis aries		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	cgr-miR-152-3p	Cricetulus griseus		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	ggo-miR-152	Gorilla gorilla		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	ppy-miR-152	Pongo pygmaeus		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	ssc-miR-152	Sus scrofa		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	mml-miR-152-3p	Macaca mulatta		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	cfa-miR-152	Canis familiaris		0.2	0	1.29	0.18	0.28	0.21	0	0.14
	ptr-miR-152	Pan troglodytes		0.2	0	1.29	0.18	0.28	0.21	0	0.14
dof-miR-597	ola-miR-148	Oryzias latipes	TCAGTGCATTACAGAACTTT	0	0	0	0.18	0	0	0	0
dof-miR-598	dre-miR-148	Danio rerio	TCAGTGCATTACAGAACTTTGT	0	0.25	0.18	0.9	0	0	0.17	0.14
	fru-miR-148	Fugu rubripes		0	0.25	0.18	0.9	0	0	0.17	0.14
	tmi-miR-148	Tetraodon nigroviridis		0	0.25	0.18	0.9	0	0	0.17	0.14
	ssa-miR-148a-3p	Salmo salar		0	0.25	0.18	0.9	0	0	0.17	0.14

	ipu-miR-148	Ictalurus punctatus		0	0.25	0.18	0.9	0	0	0.17	0.14
	ccr-miR-148	Cyprinus carpio		0	0.25	0.18	0.9	0	0	0.17	0.14
dof-miR-599	hme-miR-970	Heliconius melpomene	TCATAAGACACACGCGGCTCT	0	0	0	0.18	0	0	0	0
	mse-miR-970	Manduca sexta		0	0	0	0.18	0	0	0	0
	bmo-miR-970-3p	Bombyx mori		0	0	0	0.18	0	0	0	0
dof-miR-600	ath-miR397a	Arabidopsis thaliana	TCATTGAGTGCAGCGTTGATG	0	0	0.18	30.63	0	0	0	0
	osa-miR397a	Oryza sativa		0	0	0.18	30.63	0	0	0	0
	ptc-miR397a	Populus trichocarpa		0	0	0.18	30.63	0	0	0	0
	ppe-miR397	Prunus persica		0	0	0.18	30.63	0	0	0	0
	mtr-miR397-5p	Medicago truncatula		0	0	0.18	30.63	0	0	0	0
	cme-miR397	Cucumis melo		0	0	0.18	30.63	0	0	0	0
	ssl-miR397	Salvia sclarea		0	0	0.18	30.63	0	0	0	0
	lus-miR397b	Linum usitatissimum		0	0	0.18	30.63	0	0	0	0
	tcc-miR397	Theobroma cacao		0	0	0.18	30.63	0	0	0	0
	gma-miR397a	Glycine max		0	0	0.18	30.63	0	0	0	0
	gma-miR397b-5p	Glycine max		0	0	0.18	30.63	0	0	0	0
	csi-miR397	Citrus sinensis		0	0	0.18	30.63	0	0	0	0
	rco-miR397	Ricinus communis		0	0	0.18	30.63	0	0	0	0
	aly-miR397a-5p	Arabidopsis lyrata		0	0	0.18	30.63	0	0	0	0
	aly-miR397b-5p	Arabidopsis lyrata		0	0	0.18	30.63	0	0	0	0
	vvi-miR397a	Vitis vinifera		0	0	0.18	30.63	0	0	0	0
	sbi-miR397-5p	Sorghum bicolor		0	0	0.18	30.63	0	0	0	0
bdi-miR397a	Brachypodium distachyon	0	0	0.18	30.63	0	0	0	0		
dof-miR-601	bna-miR397a	Brassica napus	TCATTGAGTGCAGCGTTGATGT	0	0	0	1.8	0	0	0	0
	bna-miR397b	Brassica napus		0	0	0	1.8	0	0	0	0
dof-miR-602	osa-miR393a	Oryza sativa	TCCAAAGGGATCGCATTGATC	0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	sbi-miR393a	Sorghum bicolor		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	mtr-miR393a	Medicago truncatula		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	ptc-miR393a-5p	Populus trichocarpa		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	ptc-miR393b-5p	Populus trichocarpa		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	ptc-miR393c	Populus trichocarpa		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	mtr-miR393b-5p	Medicago truncatula		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	bna-miR393	Brassica napus		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	vvi-miR393b	Vitis vinifera		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12

	ppe-miR393b	Prunus persica		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	cme-miR393a	Cucumis melo		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	cme-miR393b	Cucumis melo		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	cme-miR393c	Cucumis melo		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	lus-miR393a	Linum usitatissimum		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	lus-miR393b	Linum usitatissimum		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	lus-miR393c	Linum usitatissimum		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	lus-miR393d	Linum usitatissimum		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	tcc-miR393b	Theobroma cacao		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	bdi-miR393a	Brachypodium distachyon		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	bdi-miR393b-5p	Brachypodium distachyon		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	rco-miR393	Ricinus communis		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	gma-miR393a	Glycine max		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	vvi-miR393a	Vitis vinifera		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
	sbi-miR393b	Sorghum bicolor		0	1.78	1.65	1.8	0.93	1.77	0.5	1.12
dof-miR-603	ath-miR393a-5p	Arabidopsis thaliana	TCCAAAGGGATCGCATTGATCC	0	0	0.18	0.36	0	0	0	0.14
	ath-miR393b-5p	Arabidopsis thaliana		0	0	0.18	0.36	0	0	0	0.14
	cpa-miR393	Carica papaya		0	0	0.18	0.36	0	0	0	0.14
	atr-miR393	Amborella trichopoda		0	0	0.18	0.36	0	0	0	0.14
	mes-miR393a	Manihot esculenta		0	0	0.18	0.36	0	0	0	0.14
	mes-miR393b	Manihot esculenta		0	0	0.18	0.36	0	0	0	0.14
	stu-miR393-5p	Solanum tuberosum		0	0	0.18	0.36	0	0	0	0.14
	gma-miR393e	Glycine max		0	0	0.18	0.36	0	0	0	0.14
	gma-miR393f	Glycine max		0	0	0.18	0.36	0	0	0	0.14
	gma-miR393g	Glycine max		0	0	0.18	0.36	0	0	0	0.14
	htu-miR393a	Helianthus tuberosus		0	0	0.18	0.36	0	0	0	0.14
	htu-miR393b	Helianthus tuberosus		0	0	0.18	0.36	0	0	0	0.14
	htu-miR393c	Helianthus tuberosus		0	0	0.18	0.36	0	0	0	0.14
	gma-miR393c-5p	Glycine max		0	0	0.18	0.36	0	0	0	0.14
	gma-miR393d	Glycine max		0	0	0.18	0.36	0	0	0	0.14
	tcc-miR393a	Theobroma cacao		0	0	0.18	0.36	0	0	0	0.14
	zma-miR393b-5p	Zea mays		0	0	0.18	0.36	0	0	0	0.14
	aly-miR393a-5p	Arabidopsis lyrata		0	0	0.18	0.36	0	0	0	0.14
aly-miR393b-5p	Arabidopsis lyrata	0	0	0.18	0.36	0	0	0	0.14		

dof-miR-604	osa-miR393b-5p	Oryza sativa	TCCAAAGGGATCGCATTGATCT	18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
	zma-miR393a-5p	Zea mays		18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
	mes-miR393c	Manihot esculenta		18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
	mes-miR393d	Manihot esculenta		18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
	mdm-miR393a	Malus domestica		18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
	mdm-miR393b	Malus domestica		18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
	mdm-miR393c	Malus domestica		18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
	zma-miR393c-5p	Zea mays		18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
	ghr-miR393	Gossypium hirsutum		18.82	47.1	33.81	24.87	14.08	37.77	24.21	25.64
dof-miR-605	gma-miR396h	Glycine max	TCCACAGCTTTCTTGAAGCTG	6.34	4.84	1.29	59.82	0.37	0.73	3.01	5.32
dof-miR-606	osa-miR396e-5p	Oryza sativa	TCCACAGGCTTTCTTGAAGCTG	0	0.25	0	0	0.09	0	0	0.14
	ata-miR396a-5p	Aegilops tauschii		0	0.25	0	0	0.09	0	0	0.14
	ata-miR396d-5p	Aegilops tauschii		0	0.25	0	0	0.09	0	0	0.14
	ata-miR396b-5p	Aegilops tauschii		0	0.25	0	0	0.09	0	0	0.14
	bdi-miR396a-5p	Brachypodium distachyon		0	0.25	0	0	0.09	0	0	0.14
	bdi-miR396b-5p	Brachypodium distachyon		0	0.25	0	0	0.09	0	0	0.14
	far-miR396	Festuca arundinacea		0	0.25	0	0	0.09	0	0	0.14
dof-miR-607	chi-miR-338-3p	Capra hircus	TCCAGCATCAGTGATTTTGT	0	0	0	0.18	0	0	0	0.14
	ola-miR-338-3p	Oryzias latipes		0	0	0	0.18	0	0	0	0.14
	aca-miR-338-3p	Anolis carolinensis		0	0	0	0.18	0	0	0	0.14
dof-miR-608	ola-miR-142	Oryzias latipes	TCCATAAAGTAGAAAGCACTAC	0	0	0	0.18	0	0	0	0
dof-miR-609	hsa-miR-885-5p	Homo sapiens	TCCATTACACTACCCTGCCTCT	0	0	0	0	0.09	0	0	0
	ppy-miR-885-5p	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	eca-miR-885-5p	Equus caballus		0	0	0	0	0.09	0	0	0
	ssc-miR-885-5p	Sus scrofa		0	0	0	0	0.09	0	0	0
	mml-miR-885-5p	Macaca mulatta		0	0	0	0	0.09	0	0	0
	bta-miR-885	Bos taurus		0	0	0	0	0.09	0	0	0
	cfa-miR-885	Canis familiaris		0	0	0	0	0.09	0	0	0
dof-miR-610	ath-miR158a-3p	Arabidopsis thaliana	TCCCAAATGTAGACAAAGCA	0	0	0	0	0	0	0	0.7
	aly-miR158a-3p	Arabidopsis lyrata		0	0	0	0	0	0	0	0.7
dof-miR-611	chi-miR-361-3p	Capra hircus	TCCCCCAGGTGTGATTCTGATT	0	0	0	0	0.19	0	0.17	0
dof-miR-612	hsa-miR-361-3p	Homo sapiens	TCCCCCAGGTGTGATTCTGATT	0	0	0	0	0.09	0	0	0
	ppy-miR-361-3p	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	mml-miR-361-3p	Macaca mulatta		0	0	0	0	0.09	0	0	0

	ptr-miR-361	Pan troglodytes		0	0	0	0	0.09	0	0	0
dof-miR-613	dre-miR-125c-5p	Danio rerio	TCCCTGAGACCCTAACTCGTGA	0	0	0	0.18	0	0	0	0
	ipu-miR-125c	Ictalurus punctatus		0	0	0	0.18	0	0	0	0
	ccr-miR-125c	Cyprinus carpio		0	0	0	0.18	0	0	0	0
dof-miR-614	chi-miR-125b-5p	Capra hircus	TCCCTGAGACCCTAACTTGT	0	0.25	0.92	1.26	0.19	0	0.17	0.42
dof-miR-615	oar-miR-125b	Ovis aries	TCCCTGAGACCCTAACTTGTG	0.59	1.02	2.76	2.7	0	0	1.17	0.42
	dvi-miR-125-5p	Drosophila virilis		0.59	1.02	2.76	2.7	0	0	1.17	0.42
dof-miR-616	mmu-miR-125b-5p	Mus musculus	TCCCTGAGACCCTAACTTGTGA	0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dme-miR-125-5p	Drosophila melanogaster		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	hsa-miR-125b-5p	Homo sapiens		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	rno-miR-125b-5p	Rattus norvegicus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	gga-miR-125b-5p	Gallus gallus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dps-miR-125	Drosophila pseudoobscura		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	aga-miR-125	Anopheles gambiae		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dre-miR-125b-5p	Danio rerio		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	ssc-miR-125b	Sus scrofa		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	ggo-miR-125b	Gorilla gorilla		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	age-miR-125b	Ateles geoffroyi		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	ppa-miR-125b	Pan paniscus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	ppy-miR-125b	Pongo pygmaeus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	ptr-miR-125b	Pan troglodytes		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	mml-miR-125b-5p	Macaca mulatta		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	sla-miR-125b	Saguinus labiatus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	lla-miR-125b	Lagothrix lagotricha		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	mne-miR-125b	Macaca nemestrina		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	lca-miR-125b	Lemur catta		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	fru-miR-125b	Fugu rubripes		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	tmi-miR-125b	Tetraodon nigroviridis		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	bta-miR-125b	Bos taurus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	xtr-miR-125b	Xenopus tropicalis		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	mdo-miR-125b-5p	Monodelphis domestica		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	oan-miR-125-5p	Ornithorhynchus anatinus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	tch-miR-125b-5p	Tupaia chinensis		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	bbe-miR-125a-5p	Branchiostoma belcheri		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14

	ssa-miR-125a-5p	Salmo salar		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	ipu-miR-125b	Ictalurus punctatus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	pmi-miR-125-5p	Patiria miniata		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	lva-miR-125-5p	Lytechinus variegatus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	ccr-miR-125b	Cyprinus carpio		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	ola-miR-125b	Oryzias latipes		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	sha-miR-125a	Sarcophilus harrisi		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	cgr-miR-125b-5p	Cricetulus griseus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	pma-miR-125-5p	Petromyzon marinus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	aca-miR-125b	Anolis carolinensis		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	nvi-miR-125	Nasonia vitripennis		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	nlo-miR-125	Nasonia longicornis		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	eca-miR-125b-5p	Equus caballus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	aae-miR-125-5p	Aedes aegypti		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	cqu-miR-125-5p	Culex quinquefasciatus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	tgu-miR-125-5p	Taeniopygia guttata		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	cfa-miR-125b	Canis familiaris		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	tca-miR-125-5p	Tribolium castaneum		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dan-miR-125	Drosophila ananassae		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	der-miR-125	Drosophila erecta		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dgr-miR-125	Drosophila grimshawi		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dmo-miR-125	Drosophila mojavensis		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dpe-miR-125	Drosophila persimilis		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dse-miR-125	Drosophila sechellia		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dsi-miR-125	Drosophila simulans		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dwi-miR-125	Drosophila willistoni		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	dya-miR-125	Drosophila yakuba		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	bfl-miR-125a-5p	Branchiostoma floridae		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	cte-miR-125	Capitella teleta		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	sko-miR-125a	Saccoglossus kowalevskii		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
	spu-miR-125-5p	Strongylocentrotus purpuratus		0	1.02	6.98	9.01	0.19	0.1	1.5	0.14
dof-miR-617	dre-miR-125a	Danio rerio	TCCCTGAGACCCTTAACCTGTG	0	0.76	0	0.36	0	0	0.67	0.14
	fru-miR-125a	Fugu rubripes		0	0.76	0	0.36	0	0	0.67	0.14
	tmi-miR-125a	Tetraodon nigroviridis		0	0.76	0	0.36	0	0	0.67	0.14

	xtr-miR-125a	Xenopus tropicalis		0	0.76	0	0.36	0	0	0.67	0.14
	oha-miR-125a-5p	Ophiophagus hannah		0	0.76	0	0.36	0	0	0.67	0.14
	ipu-miR-125a	Ictalurus punctatus		0	0.76	0	0.36	0	0	0.67	0.14
	ola-miR-125a-5p	Oryzias latipes		0	0.76	0	0.36	0	0	0.67	0.14
	aca-miR-125a-5p	Anolis carolinensis		0	0.76	0	0.36	0	0	0.67	0.14
dof-miR-618	ggo-miR-125a	Gorilla gorilla	TCCCTGAGACCCCTTAACTG	0	0	0.18	0	0.09	0	0	0
dof-miR-619	chi-miR-125a-5p	Capra hircus	TCCCTGAGACCCCTTAACTGT	0.2	1.27	4.78	4.5	0.37	0.1	0.33	0.14
	cfa-miR-125a	Canis familiaris		0.2	1.27	4.78	4.5	0.37	0.1	0.33	0.14
dof-miR-620	bta-miR-125a	Bos taurus	TCCCTGAGACCCCTTAACTGTG	0	0	2.02	1.44	0.19	0	0	0.14
	tch-miR-125a-5p	Tupaia chinensis		0	0	2.02	1.44	0.19	0	0	0.14
	ssc-miR-125a	Sus scrofa		0	0	2.02	1.44	0.19	0	0	0.14
dof-miR-621	mmu-miR-125a-5p	Mus musculus	TCCCTGAGACCCCTTAACTGTGA	0	0	0	0.54	0.09	0	0.17	0
	hsa-miR-125a-5p	Homo sapiens		0	0	0	0.54	0.09	0	0.17	0
	rno-miR-125a-5p	Rattus norvegicus		0	0	0	0.54	0.09	0	0.17	0
	cgr-miR-125a-5p	Cricetulus griseus		0	0	0	0.54	0.09	0	0.17	0
	ppy-miR-125a-5p	Pongo pygmaeus		0	0	0	0.54	0.09	0	0.17	0
	eca-miR-125a-5p	Equus caballus		0	0	0	0.54	0.09	0	0.17	0
	mml-miR-125a-5p	Macaca mulatta		0	0	0	0.54	0.09	0	0.17	0
dof-miR-622	mmu-miR-351-5p	Mus musculus	TCCCTGAGGAGCCCTTTGAGCCTG	0	0	0	0.18	0	0	0	0
dof-miR-623	cfa-miR-339	Canis familiaris	TCCCTGTCCTCCAGGAGCT	0.2	0	0	0	0	0	0	0
dof-miR-624	ssc-miR-4334-3p	Sus scrofa	TCCCTGTCCTCCAGGAGCTC	0.2	0.76	0.18	0.18	0.09	0	0	0.28
	bta-miR-339b	Bos taurus		0.2	0.76	0.18	0.18	0.09	0	0	0.28
dof-miR-625	ssc-miR-339	Sus scrofa	TCCCTGTCCTCCAGGAGCTCA	0	0	0.92	0	0	0.1	0	0.28
dof-miR-626	ssc-miR-339-5p	Sus scrofa	TCCCTGTCCTCCAGGAGCTCAC	0	0.51	0.55	0.18	0	0	0	0
	bta-miR-339a	Bos taurus		0	0.51	0.55	0.18	0	0	0	0
dof-miR-627	ppt-miR166j	Physcomitrella patens	TCCGGACCAGGCTTCATTCCC	0.2	0.25	0	0	0	0.1	0	0
	ppt-miR166k	Physcomitrella patens		0.2	0.25	0	0	0	0.1	0	0
	ppt-miR166l	Physcomitrella patens		0.2	0.25	0	0	0	0.1	0	0
dof-miR-628	cfa-miR-486	Canis familiaris	TCCTGTACTGAGCTGCCCGA	0.4	1.02	0.18	0.18	11.56	4.8	0.5	0
dof-miR-629	hsa-miR-486-5p	Homo sapiens	TCCTGTACTGAGCTGCCCGAG	0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	mmu-miR-486a-5p	Mus musculus		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	rno-miR-486	Rattus norvegicus		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	cgr-miR-486-5p	Cricetulus griseus		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	ggo-miR-486	Gorilla gorilla		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26

	ppy-miR-486-5p	Pongo pygmaeus		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	eca-miR-486-5p	Equus caballus		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	ssc-miR-486	Sus scrofa		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	mmu-miR-486b-5p	Mus musculus		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	mml-miR-486-5p	Macaca mulatta		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	ptr-miR-486	Pan troglodytes		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
	bta-miR-486	Bos taurus		0.79	7.13	0	0.36	21.82	9.39	1.67	1.26
dof-miR-630	cgr-miR-205	Cricetulus griseus	TCCTTCATTCCACCGGAGT	0	0	0	0	0	0	0	0.28
dof-miR-631	oan-miR-205-5p	Ornithorhynchus anatinus	TCCTTCATTCCACCGGAGTCT	0	0	0	0.18	0	0	0	0.14
	sha-miR-205	Sarcophilus harrisii		0	0	0	0.18	0	0	0	0.14
dof-miR-632	mmu-miR-205-5p	Mus musculus	TCCTTCATTCCACCGGAGTCTG	0	0	0	0.18	0	0	0.17	0
	hsa-miR-205-5p	Homo sapiens		0	0	0	0.18	0	0	0.17	0
	gga-miR-205a	Gallus gallus		0	0	0	0.18	0	0	0.17	0
	dre-miR-205-5p	Danio rerio		0	0	0	0.18	0	0	0.17	0
	ssc-miR-205	Sus scrofa		0	0	0	0.18	0	0	0.17	0
	ggo-miR-205	Gorilla gorilla		0	0	0	0.18	0	0	0.17	0
	age-miR-205	Ateles geoffroyi		0	0	0	0.18	0	0	0.17	0
	ppa-miR-205	Pan paniscus		0	0	0	0.18	0	0	0.17	0
	ptr-miR-205	Pan troglodytes		0	0	0	0.18	0	0	0.17	0
	lla-miR-205	Lagothrix lagotricha		0	0	0	0.18	0	0	0.17	0
	mne-miR-205	Macaca nemestrina		0	0	0	0.18	0	0	0.17	0
	fru-miR-205	Fugu rubripes		0	0	0	0.18	0	0	0.17	0
	tni-miR-205	Tetraodon nigroviridis		0	0	0	0.18	0	0	0.17	0
	bta-miR-205	Bos taurus		0	0	0	0.18	0	0	0.17	0
	xtr-miR-205a	Xenopus tropicalis		0	0	0	0.18	0	0	0.17	0
	ssa-miR-205b-5p	Salmo salar		0	0	0	0.18	0	0	0.17	0
	ccr-miR-205	Cyprinus carpio		0	0	0	0.18	0	0	0.17	0
	aca-miR-205a	Anolis carolinensis		0	0	0	0.18	0	0	0.17	0
	ppy-miR-205	Pongo pygmaeus		0	0	0	0.18	0	0	0.17	0
	mdo-miR-205a	Monodelphis domestica		0	0	0	0.18	0	0	0.17	0
eca-miR-205	Equus caballus	0	0	0	0.18	0	0	0.17	0		
mml-miR-205	Macaca mulatta	0	0	0	0.18	0	0	0.17	0		
xla-miR-205	Xenopus laevis	0	0	0	0.18	0	0	0.17	0		
cfa-miR-205	Canis familiaris	0	0	0	0.18	0	0	0.17	0		

dof-miR-633	rno-miR-205	Rattus norvegicus	TCCTTCATCCACGGAGTCTGT	0	0	0	1.08	0	0	0	0.14
	efu-miR-205	Eptesicus fuscus		0	0	0	1.08	0	0	0	0.14
	oha-miR-205a-5p	Ophiophagus hannah		0	0	0	1.08	0	0	0	0.14
	ipu-miR-205	Ictalurus punctatus		0	0	0	1.08	0	0	0	0.14
	pma-miR-205a-5p	Petromyzon marinus		0	0	0	1.08	0	0	0	0.14
dof-miR-634	osa-miR166e-3p	Oryza sativa	TCGAACCAGGCTTCATCCCC	6.73	3.05	1.65	14.78	0.75	0.21	0.67	6.45
dof-miR-635	hsa-miR-1307-5p	Homo sapiens	TCGACCGGACCTCGACCGGCT	0	0	0	0.36	0.09	0	0	0
dof-miR-636	ggo-miR-151a	Gorilla gorilla	TCGAGGAGCTCACAGTCTAG	0	0	0	0	0.65	0	0	0
dof-miR-637	mmu-miR-151-5p	Mus musculus	TCGAGGAGCTCACAGTCTAGT	0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	rno-miR-151-5p	Rattus norvegicus		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	hsa-miR-151a-5p	Homo sapiens		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	bta-miR-151-5p	Bos taurus		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	chi-miR-151-5p	Capra hircus		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	cgr-miR-151-5p	Cricetulus griseus		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	ppy-miR-151a-5p	Pongo pygmaeus		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	eca-miR-151-5p	Equus caballus		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	ssc-miR-151-5p	Sus scrofa		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	mml-miR-151-5p	Macaca mulatta		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
	cfa-miR-151	Canis familiaris		0.99	0.76	1.84	2.16	6.99	1.46	0	0.28
dof-miR-638	zma-miR162-3p	Zea mays	TCGATAAACCTCTGCATCCA	0	0	0.73	4.32	0.19	0.1	0	0
	gma-miR162a	Glycine max		0	0	0.73	4.32	0.19	0.1	0	0
dof-miR-639	ath-miR162a-3p	Arabidopsis thaliana	TCGATAAACCTCTGCATCCAG	0.79	0	2.02	447.22	0.19	0.42	0.67	0
	ath-miR162b-3p	Arabidopsis thaliana		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	osa-miR162a	Oryza sativa		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	mtr-miR162	Medicago truncatula		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	ptc-miR162a	Populus trichocarpa		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	ptc-miR162b	Populus trichocarpa		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	ghr-miR162a	Gossypium hirsutum		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	cpa-miR162a	Carica papaya		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	vvi-miR162	Vitis vinifera		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	bra-miR162-3p	Brassica rapa		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	ppe-miR162	Prunus persica		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	mes-miR162	Manihot esculenta		0.79	0	2.02	447.22	0.19	0.42	0.67	0
stu-miR162a-3p	Solanum tuberosum	0.79	0	2.02	447.22	0.19	0.42	0.67	0		

	stu-miR162b-3p	Solanum tuberosum		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	pde-miR162	Pinus densata		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	htu-miR162a	Helianthus tuberosus		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	hpe-miR162a	Helianthus petiolaris		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	mdm-miR162a	Malus domestica		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	mdm-miR162b	Malus domestica		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	cme-miR162	Cucumis melo		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	vun-miR162	Vigna unguiculata		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	lus-miR162a	Linum usitatissimum		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	lus-miR162b	Linum usitatissimum		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	nta-miR162a	Nicotiana tabacum		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	nta-miR162b	Nicotiana tabacum		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	tcc-miR162	Theobroma cacao		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	gma-miR162b	Glycine max		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	gma-miR162c	Glycine max		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	aau-miR162	Acacia auriculiformis		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	sbi-miR162	Sorghum bicolor		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	csi-miR162-3p	Citrus sinensis		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	rco-miR162	Ricinus communis		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	aly-miR162a-3p	Arabidopsis lyrata		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	aly-miR162b-3p	Arabidopsis lyrata		0.79	0	2.02	447.22	0.19	0.42	0.67	0
	sly-miR162	Solanum lycopersicum		0.79	0	2.02	447.22	0.19	0.42	0.67	0
dof-miR-640	bdi-miR162	Brachypodium distachyon	TCGATAAACCTCTGCATCCGG	487.81	359.97	599.69	532.98	451.97	1309.44	211.86	670.07
dof-miR-641	mdm-miR3627a	Malus domestica	TCGCAGGAGAGATGGCACTA	0	0	0	0.72	0	0	0	0
	mdm-miR3627b	Malus domestica		0	0	0	0.72	0	0	0	0
	mdm-miR3627c	Malus domestica		0	0	0	0.72	0	0	0	0
dof-miR-642	osa-miR168a-5p	Oryza sativa	TCGCTTGGTGCAGATCGGGAC	0.2	0	0	0	0.09	0	0	0
	sbi-miR168	Sorghum bicolor		0.2	0	0	0	0.09	0	0	0
	sof-miR168a	Saccharum officinarum		0.2	0	0	0	0.09	0	0	0
	zma-miR168a-5p	Zea mays		0.2	0	0	0	0.09	0	0	0
	zma-miR168b-5p	Zea mays		0.2	0	0	0	0.09	0	0	0
	ata-miR168-5p	Aegilops tauschii		0.2	0	0	0	0.09	0	0	0
	bdi-miR168-5p	Brachypodium distachyon		0.2	0	0	0	0.09	0	0	0
	ssp-miR168a	Saccharum sp.		0.2	0	0	0	0.09	0	0	0

	hvu-miR168-5p	Hordeum vulgare		0.2	0	0	0	0.09	0	0	0
dof-miR-643	bna-miR168b	Brassica napus	TCGCTTGGTGCAGGTCGAGAA	0.2	0	0.18	0.9	0	0.1	0	0.14
dof-miR-644	gma-miR168b	Glycine max	TCGCTTGGTGCAGGTCGGG	0	0	2.39	0	0.19	0	0	0.7
dof-miR-645	cme-miR168	Cucumis melo	TCGCTTGGTGCAGGTCGGGA	91.3	42.51	191.63	82.88	19.87	26.81	44.41	95.84
dof-miR-646	ath-miR168a-5p	Arabidopsis thaliana	TCGCTTGGTGCAGGTCGGGAA	130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	ath-miR168b-5p	Arabidopsis thaliana		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	gma-miR168a	Glycine max		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	ptc-miR168a-5p	Populus trichocarpa		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	ptc-miR168b-5p	Populus trichocarpa		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	bna-miR168a	Brassica napus		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	vvi-miR168	Vitis vinifera		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	bra-miR168a-5p	Brassica rapa		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	ppe-miR168	Prunus persica		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	atr-miR168	Amborella trichopoda		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	mdm-miR168a	Malus domestica		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	mdm-miR168b	Malus domestica		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	mtr-miR168c-5p	Medicago truncatula		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	vun-miR168	Vigna unguiculata		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	mes-miR168a	Manihot esculenta		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	cca-miR168a	Cynara cardunculus		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	lus-miR168a	Linum usitatissimum		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	lus-miR168b	Linum usitatissimum		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	nta-miR168d	Nicotiana tabacum		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	nta-miR168e	Nicotiana tabacum		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	tcc-miR168	Theobroma cacao		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
	mtr-miR168b	Medicago truncatula		130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48
cc1-miR168	Citrus clementina	130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48		
crt-miR168	Citrus reticulata	130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48		
rco-miR168	Ricinus communis	130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48		
aly-miR168a-5p	Arabidopsis lyrata	130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48		
aly-miR168b-5p	Arabidopsis lyrata	130.52	217.41	1243.11	3662.24	105.11	116.96	88.98	275.48		
dof-miR-647	bra-miR168b-5p	Brassica rapa	TCGCTTGGTGCAGGTCGGGAC	83.58	107.18	395.75	109.19	67.8	56.13	110.35	151.05
	bra-miR168c-5p	Brassica rapa		83.58	107.18	395.75	109.19	67.8	56.13	110.35	151.05
	sly-miR168a-5p	Solanum lycopersicum		83.58	107.18	395.75	109.19	67.8	56.13	110.35	151.05

	sly-miR168b-5p	Solanum lycopersicum		83.58	107.18	395.75	109.19	67.8	56.13	110.35	151.05
	nta-miR168a	Nicotiana tabacum		83.58	107.18	395.75	109.19	67.8	56.13	110.35	151.05
	nta-miR168b	Nicotiana tabacum		83.58	107.18	395.75	109.19	67.8	56.13	110.35	151.05
	nta-miR168c	Nicotiana tabacum		83.58	107.18	395.75	109.19	67.8	56.13	110.35	151.05
dof-miR-648	osa-miR166k-3p	Oryza sativa	TCGGACCAGGCTTCAATCCCT	0	0	0	0	0.47	0	0	0
	osa-miR166l-3p	Oryza sativa		0	0	0	0	0.47	0	0	0
	sbi-miR166e	Sorghum bicolor		0	0	0	0	0.47	0	0	0
	zma-miR166k-3p	Zea mays		0	0	0	0	0.47	0	0	0
	zma-miR166j-3p	Zea mays		0	0	0	0	0.47	0	0	0
	sbi-miR166g	Sorghum bicolor		0	0	0	0	0.47	0	0	0
	ata-miR5168-3p	Aegilops tauschii		0	0	0	0	0.47	0	0	0
	bdi-miR166h-3p	Brachypodium distachyon		0	0	0	0	0.47	0	0	0
	zma-miR166n-3p	Zea mays		0	0	0	0	0.47	0	0	0
dof-miR-649	aly-miR165a-3p	Arabidopsis lyrata	TCGGACCAGGCTTCATCCCC	0.59	0	0.37	4.86	0.37	0.21	0	0.42
	aly-miR165b-3p	Arabidopsis lyrata		0.59	0	0.37	4.86	0.37	0.21	0	0.42
dof-miR-650	ath-miR165a-3p	Arabidopsis thaliana	TCGGACCAGGCTTCATCCCC	47.73	20.11	82.68	298.02	12.78	10.33	21.54	35.73
	ath-miR165b	Arabidopsis thaliana		47.73	20.11	82.68	298.02	12.78	10.33	21.54	35.73
	bna-miR166f	Brassica napus		47.73	20.11	82.68	298.02	12.78	10.33	21.54	35.73
	lus-miR166b	Linum usitatissimum		47.73	20.11	82.68	298.02	12.78	10.33	21.54	35.73
dof-miR-651	vvi-miR166a	Vitis vinifera	TCGGACCAGGCTTCATCC	17.43	7.89	9.19	61.44	15.58	11.48	7.35	15.13
	vvi-miR166b	Vitis vinifera		17.43	7.89	9.19	61.44	15.58	11.48	7.35	15.13
	hbr-miR166a	Hevea brasiliensis		17.43	7.89	9.19	61.44	15.58	11.48	7.35	15.13
	pde-miR166a	Pinus densata		17.43	7.89	9.19	61.44	15.58	11.48	7.35	15.13
	pde-miR166b	Pinus densata		17.43	7.89	9.19	61.44	15.58	11.48	7.35	15.13
dof-miR-652	zma-miR166h-3p	Zea mays	TCGGACCAGGCTTCATCCCC	17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	zma-miR166e	Zea mays		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	zma-miR166i-3p	Zea mays		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	zma-miR166f	Zea mays		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	zma-miR166g-3p	Zea mays		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	zma-miR166b-3p	Zea mays		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	zma-miR166c-3p	Zea mays		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	zma-miR166d-3p	Zea mays		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	sbi-miR166d	Sorghum bicolor		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	sbi-miR166c	Sorghum bicolor		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55

	sbi-miR166b	Sorghum bicolor		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	sbi-miR166a	Sorghum bicolor		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	cme-miR166g	Cucumis melo		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	gma-miR166p	Glycine max		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	gma-miR166q	Glycine max		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	gma-miR166r	Glycine max		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	gma-miR166s	Glycine max		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	gma-miR166t	Glycine max		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	tcc-miR166b	Theobroma cacao		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	csi-miR166c	Citrus sinensis		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	sbi-miR166h	Sorghum bicolor		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	sbi-miR166i	Sorghum bicolor		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
	sbi-miR166j	Sorghum bicolor		17.43	6.36	24.07	117.48	13.99	10.33	8.18	15.55
dof-miR-653	ath-miR166a-3p	Arabidopsis thaliana	TCGGACCAGGCTTCATTCCCC	9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	ath-miR166b-3p	Arabidopsis thaliana		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	ath-miR166c	Arabidopsis thaliana		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	ath-miR166d	Arabidopsis thaliana		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	ath-miR166e-3p	Arabidopsis thaliana		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	ath-miR166f	Arabidopsis thaliana		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	ath-miR166g	Arabidopsis thaliana		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	osa-miR166a-3p	Oryza sativa		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	osa-miR166b-3p	Oryza sativa		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	osa-miR166c-3p	Oryza sativa		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	osa-miR166d-3p	Oryza sativa		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	osa-miR166f	Oryza sativa		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	osa-miR166j-3p	Oryza sativa		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	zma-miR166a-3p	Zea mays		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	mtr-miR166a	Medicago truncatula		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	gma-miR166a-3p	Glycine max		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	gma-miR166b	Glycine max		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	ptc-miR166a	Populus trichocarpa		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
ptc-miR166b	Populus trichocarpa	9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53		
ptc-miR166c	Populus trichocarpa	9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53		
ptc-miR166d	Populus trichocarpa	9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53		

	gma-miR166c-3p	Glycine max		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	gma-miR166d	Glycine max		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	gma-miR166e	Glycine max		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	gma-miR166f	Glycine max		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	gma-miR166g	Glycine max		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	bdi-miR166d-3p	Brachypodium distachyon		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	bdi-miR166b-3p	Brachypodium distachyon		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	bdi-miR166c-3p	Brachypodium distachyon		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	hvu-miR166c	Hordeum vulgare		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	gma-miR166i-3p	Glycine max		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	hvu-miR166a	Hordeum vulgare		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	hvu-miR166b	Hordeum vulgare		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	csi-miR166e-3p	Citrus sinensis		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	rco-miR166a	Ricinus communis		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	rco-miR166b	Ricinus communis		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	rco-miR166c	Ricinus communis		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	rco-miR166d	Ricinus communis		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	rco-miR166e	Ricinus communis		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aly-miR166a-3p	Arabidopsis lyrata		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aly-miR166b-3p	Arabidopsis lyrata		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aly-miR166c-3p	Arabidopsis lyrata		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aly-miR166d-3p	Arabidopsis lyrata		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aly-miR166e-3p	Arabidopsis lyrata		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aly-miR166f-3p	Arabidopsis lyrata		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aly-miR166g-3p	Arabidopsis lyrata		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	sly-miR166a	Solanum lycopersicum		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	sly-miR166b	Solanum lycopersicum		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	pvu-miR166a	Phaseolus vulgaris		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	bdi-miR166a-3p	Brachypodium distachyon		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aqc-miR166e	Aquilegia caerulea		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
	aqc-miR166b	Aquilegia caerulea		9666.41	4616.5	17796.83	76532.76	7029.53	4550.58	5029.88	8342.53
dof-miR-654	lus-miR166k	Linum usitatissimum	TCGGACCAGGCTTCATTCCCCC	0.4	1.02	7.17	20.9	2.8	1.88	1.17	0.42
	hbr-miR166b	Hevea brasiliensis		0.4	1.02	7.17	20.9	2.8	1.88	1.17	0.42
	lus-miR166i	Linum usitatissimum		0.4	1.02	7.17	20.9	2.8	1.88	1.17	0.42

	ctr-miR166	Citrus trifoliata		0.4	1.02	7.17	20.9	2.8	1.88	1.17	0.42
	csi-miR166a	Citrus sinensis		0.4	1.02	7.17	20.9	2.8	1.88	1.17	0.42
dof-miR-655	cpa-miR166d	Carica papaya	TCGGACCAGGCTTCATTCCCG	0.2	0	1.84	163.97	17.63	14.09	0.17	0.98
	gma-miR166j-3p	Glycine max		0.2	0	1.84	163.97	17.63	14.09	0.17	0.98
dof-miR-656	mes-miR166h	Manihot esculenta	TCGGACCAGGCTTCATTCCCGT	0	0	0	0.36	0	0.1	0	0
	crt-miR166a	Citrus reticulata		0	0	0	0.36	0	0.1	0	0
	csi-miR166b	Citrus sinensis		0	0	0	0.36	0	0.1	0	0
dof-miR-657	osa-miR166m	Oryza sativa	TCGGACCAGGCTTCATTCCCT	2.97	1.53	22.6	100.18	9.33	4.59	3.17	3.08
	csi-miR166d	Citrus sinensis		2.97	1.53	22.6	100.18	9.33	4.59	3.17	3.08
dof-miR-658	crt-miR166b	Citrus reticulata	TCGGACCAGGCTTCATTCCCTT	0	0.25	0	0.72	0	0.1	0	0
dof-miR-659	sbi-miR166k	Sorghum bicolor	TCGGACCAGGCTTCATTCCCT	0.4	0	0.73	9.37	0.47	0.42	0.33	0.28
	aqc-miR166c	Aquilegia caerulea		0.4	0	0.73	9.37	0.47	0.42	0.33	0.28
dof-miR-660	mtr-miR166b	Medicago truncatula	TCGGACCAGGCTTCATTCCCTA	0	0	0	0.18	0	0	0	0
dof-miR-661	osa-miR166g-3p	Oryza sativa	TCGGACCAGGCTTCATTCCCTC	7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	osa-miR166h-3p	Oryza sativa		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	sbi-miR166f	Sorghum bicolor		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	zma-miR166l-3p	Zea mays		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	zma-miR166m-3p	Zea mays		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	mtr-miR166c	Medicago truncatula		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	mtr-miR166f	Medicago truncatula		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	sly-miR166c-3p	Solanum lycopersicum		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	mes-miR166j	Manihot esculenta		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	stu-miR166b	Solanum tuberosum		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	cme-miR166e	Cucumis melo		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	ssl-miR166a	Salvia sclarea		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	dpr-miR166a	Digitalis purpurea		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	lus-miR166e	Linum usitatissimum		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	tcc-miR166c	Theobroma cacao		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	pab-miR166a	Picea abies		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
	aqc-miR166a	Aquilegia caerulea		7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75
aqc-miR166d	Aquilegia caerulea	7.13	3.31	17.82	70.99	1.87	1.57	5.34	5.75		
dof-miR-662	ptc-miR166n	Populus trichocarpa	TCGGACCAGGCTTCATTCCCTT	0	0	6.61	205.59	0.28	0.1	0.67	0.14
	ptc-miR166o	Populus trichocarpa		0	0	6.61	205.59	0.28	0.1	0.67	0.14
	ptc-miR166q	Populus trichocarpa		0	0	6.61	205.59	0.28	0.1	0.67	0.14

	bdi-miR166j	Brachypodium distachyon		0	0	6.61	205.59	0.28	0.1	0.67	0.14
	ata-miR166c-3p	Aegilops tauschii		0	0	6.61	205.59	0.28	0.1	0.67	0.14
	lus-miR166f	Linum usitatissimum		0	0	6.61	205.59	0.28	0.1	0.67	0.14
	pab-miR166b	Picea abies		0	0	6.61	205.59	0.28	0.1	0.67	0.14
dof-miR-663	cme-miR166i	Cucumis melo	TCGGACCAGGCTTCATTCTC	0.4	0	0	0.72	0.19	0	0.17	0
dof-miR-664	osa-miR166i-3p	Oryza sativa	TCGGATCAGGCTTCATTCCTC	0	0	0	0.18	0	0	0	0
dof-miR-665	chi-miR-127-3p	Capra hircus	TCGGATCCGTCTGAGCTTGG	0	0.25	1.1	2.16	0	0	0	0
dof-miR-666	ggo-miR-127	Gorilla gorilla	TCGGATCCGTCTGAGCTTGGC	0	0	1.29	1.8	0	0	0.33	0.14
dof-miR-667	mmu-miR-127-3p	Mus musculus	TCGGATCCGTCTGAGCTTGGCT	0.2	0.76	5.7	6.13	0.19	0	1	0.14
	hsa-miR-127-3p	Homo sapiens		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	rno-miR-127-3p	Rattus norvegicus		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	mml-miR-127-3p	Macaca mulatta		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	ptr-miR-127	Pan troglodytes		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	ppy-miR-127	Pongo pygmaeus		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	sla-miR-127	Saguinus labiatus		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	lla-miR-127	Lagothrix lagotricha		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	mne-miR-127	Macaca nemestrina		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	age-miR-127	Ateles geoffroyi		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	bta-miR-127	Bos taurus		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	tch-miR-127-3p	Tupaia chinensis		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	eca-miR-127	Equus caballus		0.2	0.76	5.7	6.13	0.19	0	1	0.14
	ssc-miR-127	Sus scrofa		0.2	0.76	5.7	6.13	0.19	0	1	0.14
cfa-miR-127	Canis familiaris	0.2	0.76	5.7	6.13	0.19	0	1	0.14		
dof-miR-668	pta-miR1314	Pinus taeda	TCGGCCTTGAATGTTAGGAGAA	0	0	1.29	1.62	0	0	0	0
dof-miR-669	mtr-miR166d	Medicago truncatula	TCGGGCCAGGCTTCATCCCC	0	0	0	0.36	0	0	0	0
dof-miR-670	sha-miR-126	Sarcophilus harrisii	TCGTACCGTGAGTAATAAT	0	0	0.18	0.72	0.19	0	0	0.14
dof-miR-671	ola-miR-126-3p	Oryzias latipes	TCGTACCGTGAGTAATAATG	0.2	0	1.29	0.18	0.28	0.1	0.33	0.28
dof-miR-672	dre-miR-126a-3p	Danio rerio	TCGTACCGTGAGTAATAATGC	1.39	3.31	9	8.11	3.26	1.04	5.01	1.12
	fru-miR-126	Fugu rubripes		1.39	3.31	9	8.11	3.26	1.04	5.01	1.12
	tmi-miR-126	Tetraodon nigroviridis		1.39	3.31	9	8.11	3.26	1.04	5.01	1.12
	xtr-miR-126-3p	Xenopus tropicalis		1.39	3.31	9	8.11	3.26	1.04	5.01	1.12
	chi-miR-126-3p	Capra hircus		1.39	3.31	9	8.11	3.26	1.04	5.01	1.12
dof-miR-673	ssa-miR-126-3p	Salmo salar	TCGTACCGTGAGTAATAATGCA	3.96	5.09	5.88	8.29	0	0	8.18	1.26
	ipu-miR-126a	Ictalurus punctatus		3.96	5.09	5.88	8.29	0	0	8.18	1.26

dof-miR-674	mmu-miR-126a-3p	Mus musculus	TCGTACCGTGAGTAATAATGCG	0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	hsa-miR-126-3p	Homo sapiens		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	rno-miR-126a-3p	Rattus norvegicus		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	oan-miR-126-3p	Ornithorhynchus anatinus		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	cgr-miR-126	Cricetulus griseus		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	aca-miR-126-3p	Anolis carolinensis		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	ppy-miR-126	Pongo pygmaeus		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	ssc-miR-126-3p	Sus scrofa		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	mdo-miR-126-3p	Monodelphis domestica		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	eca-miR-126-3p	Equus caballus		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	tgu-miR-126-3p	Taeniopygia guttata		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
	mml-miR-126	Macaca mulatta		0.2	0.51	2.39	2.34	1.4	0.52	0.33	0	
ptr-miR-126	Pan troglodytes	0.2	0.51	2.39	2.34	1.4	0.52	0.33	0			
dof-miR-675	lla-miR-139	Lagothrix lagotricha	TCTACAGTGCACGTGTCT	0	0	0.18	0	0	0	0	0	
	ppa-miR-139	Pan paniscus		0	0	0.18	0	0	0	0	0	
dof-miR-676	hsa-miR-139-5p	Homo sapiens	TCTACAGTGCACGTGTCTCCAGT	0	0	0	0.36	0	0	0	0	
	bta-miR-139	Bos taurus		0	0	0	0.36	0	0	0	0	
	tch-miR-139-5p	Tupaia chinensis		0	0	0	0.36	0	0	0	0	
dof-miR-677	oan-miR-139-5p	Ornithorhynchus anatinus	TCTACAGTGCATGTGTCTCCAG	0	0	0	0	0	0	0	0.42	
dof-miR-678	ssa-miR-139-5p	Salmo salar	TCTACAGTGCATGTGTCTCCAGT	0	0	0	0	0	0	0	0.17	0
	ipu-miR-139	Ictalurus punctatus		0	0	0	0	0	0	0	0.17	0
	ccr-miR-139	Cyprinus carpio		0	0	0	0	0	0	0	0.17	0
	sha-miR-139	Sarcophilus harrisii		0	0	0	0	0	0	0	0.17	0
	tgu-miR-139-5p	Taeniopygia guttata		0	0	0	0	0	0	0	0.17	0
dof-miR-679	ggo-miR-342	Gorilla gorilla	TCTCACACAGAAATCGCACCCG	0	0.25	0	0	0.84	0	0	0	
dof-miR-680	rno-miR-342-3p	Rattus norvegicus	TCTCACACAGAAATCGCACCCGT	0	0.76	0	0	1.4	0.21	0	0.14	
	mmu-miR-342-3p	Mus musculus		0	0.76	0	0	1.4	0.21	0	0.14	
	hsa-miR-342-3p	Homo sapiens		0	0.76	0	0	1.4	0.21	0	0.14	
	tch-miR-342-3p	Tupaia chinensis		0	0.76	0	0	1.4	0.21	0	0.14	
	ppy-miR-342-3p	Pongo pygmaeus		0	0.76	0	0	1.4	0.21	0	0.14	
	eca-miR-342-3p	Equus caballus		0	0.76	0	0	1.4	0.21	0	0.14	
	mml-miR-342-3p	Macaca mulatta		0	0.76	0	0	1.4	0.21	0	0.14	
	cfa-miR-342	Canis familiaris		0	0.76	0	0	1.4	0.21	0	0.14	
	ptr-miR-342	Pan troglodytes		0	0.76	0	0	1.4	0.21	0	0.14	

dof-miR-681	cgr-miR-342-3p	Cricetulus griseus	TCTCACACAGAAATCGCACCCGTC	0	0	0	0	0.75	0	0.17	0
dof-miR-682	mmu-miR-150-5p	Mus musculus	TCTCCCAACCCTTGTACCAGTG	0	0.25	0	0.18	2.52	0.31	0	0
	hsa-miR-150-5p	Homo sapiens		0	0.25	0	0.18	2.52	0.31	0	0
	rno-miR-150-5p	Rattus norvegicus		0	0.25	0	0.18	2.52	0.31	0	0
	chi-miR-150	Capra hircus		0	0.25	0	0.18	2.52	0.31	0	0
	oar-miR-150	Ovis aries		0	0.25	0	0.18	2.52	0.31	0	0
	ssc-miR-150	Sus scrofa		0	0.25	0	0.18	2.52	0.31	0	0
	ggo-miR-150	Gorilla gorilla		0	0.25	0	0.18	2.52	0.31	0	0
	aca-miR-150-5p	Anolis carolinensis		0	0.25	0	0.18	2.52	0.31	0	0
	ppy-miR-150	Pongo pygmaeus		0	0.25	0	0.18	2.52	0.31	0	0
	eca-miR-150	Equus caballus		0	0.25	0	0.18	2.52	0.31	0	0
	mml-miR-150-5p	Macaca mulatta		0	0.25	0	0.18	2.52	0.31	0	0
	cfa-miR-150	Canis familiaris		0	0.25	0	0.18	2.52	0.31	0	0
ptr-miR-150	Pan troglodytes	0	0.25	0	0.18	2.52	0.31	0	0		
dof-miR-683	bta-miR-150	Bos taurus	TCTCCCAACCCTTGTACCAGTGT	0	0	0	0.18	1.03	0.21	0	0
	oha-miR-150	Ophiophagus hannah		0	0	0	0.18	1.03	0.21	0	0
dof-miR-684	dre-miR-150	Danio rerio	TCTCCCAATCCTTGTACCAGTG	0	0	0	0	0	0	0.17	0
	ipu-miR-150	Ictalurus punctatus		0	0	0	0	0	0	0	0.17
dof-miR-685	gma-miR166u	Glycine max	TCTCGGACCAGGCTTCATTC	2.97	0	0.92	8.47	0.47	0.52	0.5	5.04
dof-miR-686	atr-miR166b	Amborella trichopoda	TCTCGGACCAGGCTTCATTC	1336.47	497.95	368.38	6709.15	136.82	77.31	339.24	5855.62
	gma-miR166k	Glycine max		1336.47	497.95	368.38	6709.15	136.82	77.31	339.24	5855.62
	gma-miR166h-3p	Glycine max		1336.47	497.95	368.38	6709.15	136.82	77.31	339.24	5855.62
	bdi-miR166f	Brachypodium distachyon		1336.47	497.95	368.38	6709.15	136.82	77.31	339.24	5855.62
dof-miR-687	mml-miR-4677-3p	Macaca mulatta	TCTGTGAGACCAAAGAACTACT	0	0	0	0	0.09	0	0	0
	hsa-miR-4677-3p	Homo sapiens		0	0	0	0	0.09	0	0	0
dof-miR-688	gma-miR482d-3p	Glycine max	TCTTCCCTACACCTCCCATACC	0	0	0.18	0.54	0	0	0	0
	gma-miR482b-3p	Glycine max		0	0	0.18	0.54	0	0	0	0
dof-miR-689	mes-miR482	Manihot esculenta	TCTTCCCTACTCCACCCATTC	0	0	0	2.34	0	0	0	0
dof-miR-690	pta-miR482a	Pinus taeda	TCTTCCCTACTCCTCCCATTC	0	0	1.65	1.08	0	0	0	0
	pta-miR482b	Pinus taeda		0	0	1.65	1.08	0	0	0	0
	pab-miR482a	Picea abies		0	0	1.65	1.08	0	0	0	0
dof-miR-691	ghr-miR482b	Gossypium hirsutum	TCTTGCTACTCCACCCATGCC	0	0	0	0.9	0	0	0	0
dof-miR-692	mes-miR828a	Manihot esculenta	TCTTGCTCAAATGAGTATTCCA	0	0	0	0.18	0	0	0	0
	mes-miR828b	Manihot esculenta		0	0	0	0.18	0	0	0	0

	ptc-miR828a	Populus trichocarpa		0	0	0	0.18	0	0	0	0
	ptc-miR828b-5p	Populus trichocarpa		0	0	0	0.18	0	0	0	0
	mdm-miR828a	Malus domestica		0	0	0	0.18	0	0	0	0
	mdm-miR828b	Malus domestica		0	0	0	0.18	0	0	0	0
	cme-miR828	Cucumis melo		0	0	0	0.18	0	0	0	0
	ssl-miR828	Salvia sclarea		0	0	0	0.18	0	0	0	0
	gma-miR828a	Glycine max		0	0	0	0.18	0	0	0	0
	gma-miR828b	Glycine max		0	0	0	0.18	0	0	0	0
	ppe-miR828-5p	Prunus persica		0	0	0	0.18	0	0	0	0
	vvi-miR828a	Vitis vinifera		0	0	0	0.18	0	0	0	0
dof-miR-693	tch-miR-432-5p	Tupaia chinensis	TCTTGAGTAGGTCATTGGGTG	0	0.25	0	0	0.09	0	0	0
	ggo-miR-432	Gorilla gorilla		0	0.25	0	0	0.09	0	0	0
dof-miR-694	oar-miR-432	Ovis aries	TCTTGAGTAGGTCATTGGGTGG	0	0	0	0	0.19	0	0	0
	hsa-miR-432-5p	Homo sapiens		0	0	0	0	0.19	0	0	0
	chi-miR-432-5p	Capra hircus		0	0	0	0	0.19	0	0	0
	ppy-miR-432	Pongo pygmaeus		0	0	0	0	0.19	0	0	0
	eca-miR-432	Equus caballus		0	0	0	0	0.19	0	0	0
	mml-miR-432-5p	Macaca mulatta		0	0	0	0	0.19	0	0	0
	ptr-miR-432	Pan troglodytes		0	0	0	0	0.19	0	0	0
	bta-miR-432	Bos taurus		0	0	0	0	0.19	0	0	0
	cfa-miR-432	Canis familiaris		0	0	0	0	0.19	0	0	0
dof-miR-695	ptc-miR482c-3p	Populus trichocarpa	TCTTCCGAGTCCTCCCATAACC	0	0	0	0.36	0	0	0.17	0
dof-miR-696	pde-miR482a	Pinus densata	TCTTTCCTACTCCTCCCATTCC	0	0	0.55	1.26	0	0	0	0
	pab-miR482c	Picea abies		0	0	0.55	1.26	0	0	0	0
	vvi-miR482	Vitis vinifera		0	0	0.55	1.26	0	0	0	0
dof-miR-697	sha-miR-9	Sarcophilus harrisii	TCTTTGGTTATCTAGCTGTAT	0	0	0.18	0	0	0	0	0.14
	sko-miR-9-5p	Saccoglossus kowalevskii		0	0	0.18	0	0	0	0	0.14
	tca-miR-9a-5p	Tribolium castaneum		0	0	0.18	0	0	0	0	0.14
dof-miR-698	xtr-miR-9-5p	Xenopus tropicalis	TCTTTGGTTATCTAGCTGTATG	0	0	0.18	0.36	0	0	0	0
	oan-miR-9-5p	Ornithorhynchus anatinus		0	0	0.18	0.36	0	0	0	0
	lva-miR-9-5p	Lytechinus variegatus		0	0	0.18	0.36	0	0	0	0
	ssc-miR-9	Sus scrofa		0	0	0.18	0.36	0	0	0	0
	ccr-miR-9-3p	Cyprinus carpio		0	0	0.18	0.36	0	0	0	0
	cgr-miR-9	Cricetulus griseus		0	0	0.18	0.36	0	0	0	0

	pma-miR-9a-5p	Petromyzon marinus		0	0	0.18	0.36	0	0	0	0
	bta-miR-9-5p	Bos taurus		0	0	0.18	0.36	0	0	0	0
	spu-miR-9-5p	Strongylocentrotus purpuratus		0	0	0.18	0.36	0	0	0	0
	bfl-miR-9-5p	Branchiostoma floridae		0	0	0.18	0.36	0	0	0	0
	ppc-miR-9	Pristionchus pacificus		0	0	0.18	0.36	0	0	0	0
dof-miR-699	dme-miR-9a-5p	Drosophila melanogaster	TCTTTGGTTATCTAGCTGTATGA	0	0	0	0.18	0	0	0.5	0.14
	mmu-miR-9-5p	Mus musculus		0	0	0	0.18	0	0	0.5	0.14
	hsa-miR-9-5p	Homo sapiens		0	0	0	0.18	0	0	0.5	0.14
	rno-miR-9a-5p	Rattus norvegicus		0	0	0	0.18	0	0	0.5	0.14
	gga-miR-9-5p	Gallus gallus		0	0	0	0.18	0	0	0.5	0.14
	dps-miR-9a	Drosophila pseudoobscura		0	0	0	0.18	0	0	0.5	0.14
	ame-miR-9a	Apis mellifera		0	0	0	0.18	0	0	0.5	0.14
	aga-miR-9a	Anopheles gambiae		0	0	0	0.18	0	0	0.5	0.14
	dre-miR-9-5p	Danio rerio		0	0	0	0.18	0	0	0.5	0.14
	ssc-miR-9-1	Sus scrofa		0	0	0	0.18	0	0	0.5	0.14
	ssc-miR-9-2	Sus scrofa		0	0	0	0.18	0	0	0.5	0.14
	ptr-miR-9	Pan troglodytes		0	0	0	0.18	0	0	0.5	0.14
	ggo-miR-9	Gorilla gorilla		0	0	0	0.18	0	0	0.5	0.14
	lla-miR-9	Lagothrix lagotricha		0	0	0	0.18	0	0	0.5	0.14
	mne-miR-9	Macaca nemestrina		0	0	0	0.18	0	0	0.5	0.14
	age-miR-9	Ateles geoffroyi		0	0	0	0.18	0	0	0.5	0.14
	fru-miR-9	Fugu rubripes		0	0	0	0.18	0	0	0.5	0.14
	tni-miR-9	Tetraodon nigroviridis		0	0	0	0.18	0	0	0.5	0.14
	xtr-miR-9a-5p	Xenopus tropicalis		0	0	0	0.18	0	0	0.5	0.14
	bmo-miR-9a-5p	Bombyx mori		0	0	0	0.18	0	0	0.5	0.14
	mdo-miR-9a-5p	Monodelphis domestica		0	0	0	0.18	0	0	0.5	0.14
	chi-miR-9-5p	Capra hircus		0	0	0	0.18	0	0	0.5	0.14
	tch-miR-9-5p	Tupaia chinensis		0	0	0	0.18	0	0	0.5	0.14
	bbe-miR-9-5p	Branchiostoma belcheri		0	0	0	0.18	0	0	0.5	0.14
	ssa-miR-9a-5p	Salmo salar		0	0	0	0.18	0	0	0.5	0.14
	ipu-miR-9	Ictalurus punctatus		0	0	0	0.18	0	0	0.5	0.14
	pmi-miR-9-5p	Patiria miniata		0	0	0	0.18	0	0	0.5	0.14
	pol-miR-9b-5p	Paralichthys olivaceus		0	0	0	0.18	0	0	0.5	0.14
ola-miR-9b-5p	Oryzias latipes	0	0	0	0.18	0	0	0.5	0.14		

	ola-miR-9a-5p	Oryzias latipes		0	0	0	0.18	0	0	0.5	0.14
	hco-miR-9	Haemonchus contortus		0	0	0	0.18	0	0	0.5	0.14
	asu-miR-9-5p	Ascaris suum		0	0	0	0.18	0	0	0.5	0.14
	nvi-miR-9a	Nasonia vitripennis		0	0	0	0.18	0	0	0.5	0.14
	ppy-miR-9	Pongo pygmaeus		0	0	0	0.18	0	0	0.5	0.14
	ngi-miR-9a	Nasonia giraulti		0	0	0	0.18	0	0	0.5	0.14
	nlo-miR-9a	Nasonia longicornis		0	0	0	0.18	0	0	0.5	0.14
	dpu-miR-9-5p	Daphnia pulex		0	0	0	0.18	0	0	0.5	0.14
	eca-miR-9a	Equus caballus		0	0	0	0.18	0	0	0.5	0.14
	aae-miR-9a	Aedes aegypti		0	0	0	0.18	0	0	0.5	0.14
	tgu-miR-9-5p	Taeniopygia guttata		0	0	0	0.18	0	0	0.5	0.14
	api-miR-9a	Acyrtosiphon pisum		0	0	0	0.18	0	0	0.5	0.14
	mml-miR-9-5p	Macaca mulatta		0	0	0	0.18	0	0	0.5	0.14
	cfa-miR-9	Canis familiaris		0	0	0	0.18	0	0	0.5	0.14
	dan-miR-9a	Drosophila ananassae		0	0	0	0.18	0	0	0.5	0.14
	der-miR-9a	Drosophila erecta		0	0	0	0.18	0	0	0.5	0.14
	dgr-miR-9a	Drosophila grimshawi		0	0	0	0.18	0	0	0.5	0.14
	dmo-miR-9a	Drosophila mojavensis		0	0	0	0.18	0	0	0.5	0.14
	dpe-miR-9a	Drosophila persimilis		0	0	0	0.18	0	0	0.5	0.14
	dse-miR-9a	Drosophila sechellia		0	0	0	0.18	0	0	0.5	0.14
	dsi-miR-9a	Drosophila simulans		0	0	0	0.18	0	0	0.5	0.14
	dvi-miR-9a-5p	Drosophila virilis		0	0	0	0.18	0	0	0.5	0.14
	dwi-miR-9a	Drosophila willistoni		0	0	0	0.18	0	0	0.5	0.14
	dya-miR-9a	Drosophila yakuba		0	0	0	0.18	0	0	0.5	0.14
	cte-miR-9-5p	Capitella teleta		0	0	0	0.18	0	0	0.5	0.14
	lgi-miR-9-5p	Lottia gigantea		0	0	0	0.18	0	0	0.5	0.14
	lmi-miR-9a-5p	Locusta migratoria		0	0	0	0.18	0	0	0.5	0.14
dof-miR-700	bta-miR-2284x	Bos taurus	TGAAAAGTTCGTTCCGGGTTTT	0	0	0	0.18	0	0	0	0
dof-miR-701	rno-miR-494-3p	Rattus norvegicus	TGAAACATACACGGGAAACCTCT	0	0	0.73	1.44	0.19	0.1	0	0
	efu-miR-494	Eptesicus fuscus		0	0	0.73	1.44	0.19	0.1	0	0
	chi-miR-494	Capra hircus		0	0	0.73	1.44	0.19	0.1	0	0
	oar-miR-494-3p	Ovis aries		0	0	0.73	1.44	0.19	0.1	0	0
dof-miR-702	sme-miR-71c-5p	Schmidtea mediterranea	TGAAAGACATGGGTAGTGAGAT	0	0	0	0	0	0.52	0	0
	bbe-miR-71-5p	Branchiostoma belcheri		0	0	0	0	0	0.52	0	0

	pmi-miR-71-5p	Patiria miniata		0	0	0	0	0	0.52	0	0
	tca-miR-71-5p	Tribolium castaneum		0	0	0	0	0	0.52	0	0
	bfl-miR-71-5p	Branchiostoma floridae		0	0	0	0	0	0.52	0	0
dof-miR-703	tur-miR-71-5p	Tetranychus urticae	TGAAAGACATGGGTAGTGAGATG	0	0	0	0	0	0.1	0.17	0
	mse-miR-71	Manduca sexta		0	0	0	0	0	0.1	0.17	0
	dpu-miR-71	Daphnia pulex		0	0	0	0	0	0.1	0.17	0
	isc-miR-71	Ixodes scapularis		0	0	0	0	0	0.1	0.17	0
	api-miR-71	Acyrtosiphon pisum		0	0	0	0	0	0.1	0.17	0
	cte-miR-71	Capitella teleta		0	0	0	0	0	0.1	0.17	0
dof-miR-704	pde-miR3701	Pinus densata	TGAACAATGCCACCCCTTCATC	0	0	0.55	1.62	0	0	0	0
dof-miR-705	ame-miR-317	Apis mellifera	TGAACACAGCTGGTGGTATCTCAGT	0	0	0	0	0	0.1	0	0
	nvi-miR-317	Nasonia vitripennis		0	0	0	0	0	0.1	0	0
	ngi-miR-317	Nasonia giraulti		0	0	0	0	0	0.1	0	0
	dpu-miR-317	Daphnia pulex		0	0	0	0	0	0.1	0	0
	tca-miR-317-3p	Tribolium castaneum		0	0	0	0	0	0.1	0	0
dof-miR-706	lja-miR167a	Lotus japonicus	TGAAGCTGCCAGCATGATCT	8.52	4.33	2.94	24.87	1.77	3.65	0.5	4.9
	lja-miR167b	Lotus japonicus		8.52	4.33	2.94	24.87	1.77	3.65	0.5	4.9
	lja-miR167c	Lotus japonicus		8.52	4.33	2.94	24.87	1.77	3.65	0.5	4.9
	bna-miR167d	Brassica napus		8.52	4.33	2.94	24.87	1.77	3.65	0.5	4.9
dof-miR-707	ath-miR167a-5p	Arabidopsis thaliana	TGAAGCTGCCAGCATGATCTA	8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	ath-miR167b	Arabidopsis thaliana		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	osa-miR167a-5p	Oryza sativa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	osa-miR167b	Oryza sativa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	osa-miR167c-5p	Oryza sativa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	zma-miR167a-5p	Zea mays		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	zma-miR167b-5p	Zea mays		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	zma-miR167d-5p	Zea mays		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	zma-miR167c-5p	Zea mays		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	sbi-miR167a	Sorghum bicolor		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	sbi-miR167b	Sorghum bicolor		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	gma-miR167a	Glycine max		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	gma-miR167b	Glycine max		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	ptc-miR167a	Populus trichocarpa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	ptc-miR167b	Populus trichocarpa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01

	lus-miR167d	Linum usitatissimum		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	lus-miR167e	Linum usitatissimum		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	lus-miR167h	Linum usitatissimum		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	nta-miR167d	Nicotiana tabacum		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	nta-miR167e	Nicotiana tabacum		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	tcc-miR167a	Theobroma cacao		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	tcc-miR167b	Theobroma cacao		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	bdi-miR167b	Brachypodium distachyon		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	rco-miR167a	Ricinus communis		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	rco-miR167b	Ricinus communis		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	ghr-miR167a	Gossypium hirsutum		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	aly-miR167a-5p	Arabidopsis lyrata		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	aly-miR167b-5p	Arabidopsis lyrata		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	sly-miR167a	Solanum lycopersicum		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	gma-miR167d	Glycine max		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	bra-miR167a	Brassica rapa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	bra-miR167b	Brassica rapa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	bra-miR167c	Brassica rapa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	bra-miR167d	Brassica rapa		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	sbi-miR167i	Sorghum bicolor		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
	bdi-miR167a	Brachypodium distachyon		8.91	0	1.1	1.44	0.75	2.4	3.34	7.01
dof-miR-708	bna-miR167a	Brassica napus	TGAAGCTGCCAGCATGATCTAA	0.2	0.51	0.18	0	0.09	0.31	0	0.84
	bna-miR167b	Brassica napus		0.2	0.51	0.18	0	0.09	0.31	0	0.84
dof-miR-709	vvi-miR167c	Vitis vinifera	TGAAGCTGCCAGCATGATCTC	0	0	0	0.18	0.09	0.1	0	0
	lus-miR167a	Linum usitatissimum		0	0	0	0.18	0.09	0.1	0	0
dof-miR-710	osa-miR167d-5p	Oryza sativa	TGAAGCTGCCAGCATGATCTG	0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	osa-miR167e-5p	Oryza sativa		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	osa-miR167f	Oryza sativa		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	osa-miR167g	Oryza sativa		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	osa-miR167h-5p	Oryza sativa		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	osa-miR167i-5p	Oryza sativa		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	osa-miR167j	Oryza sativa		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	sbi-miR167d	Sorghum bicolor		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	sbi-miR167f	Sorghum bicolor		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4

	sbi-miR167g	Sorghum bicolor		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	sbi-miR167e	Sorghum bicolor		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	sbi-miR167c	Sorghum bicolor		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	sof-miR167a	Saccharum officinarum		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	sof-miR167b	Saccharum officinarum		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	zma-miR167e-5p	Zea mays		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	zma-miR167f-5p	Zea mays		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	zma-miR167g-5p	Zea mays		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	zma-miR167h-5p	Zea mays		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	zma-miR167i-5p	Zea mays		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	ptc-miR167e	Populus trichocarpa		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	vvi-miR167a	Vitis vinifera		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	atr-miR167	Amborella trichopoda		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	cme-miR167d	Cucumis melo		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	cme-miR167f	Cucumis melo		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	mtr-miR167b-5p	Medicago truncatula		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	dpr-miR167c	Digitalis purpurea		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	mes-miR167a	Manihot esculenta		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	lus-miR167f	Linum usitatissimum		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	lus-miR167g	Linum usitatissimum		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	lus-miR167i	Linum usitatissimum		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	ssp-miR167b	Saccharum sp.		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	gma-miR167j	Glycine max		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	gso-miR167a	Glycine soja		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	csi-miR167c	Citrus sinensis		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	csi-miR167a	Citrus sinensis		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	zma-miR167j-5p	Zea mays		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	gma-miR167c	Glycine max		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	lja-miR167	Lotus japonicus		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
	sbi-miR167h	Sorghum bicolor		0.79	1.53	4.04	20.54	3.45	6.57	0.83	1.4
dof-miR-711	bdi-miR167g	Brachypodium distachyon	TGAAGCTGCCAGCATGATCTGA	343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	ata-miR167b-5p	Aegilops tauschii		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	ata-miR167d-5p	Aegilops tauschii		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	ppe-miR167c	Prunus persica		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77

	cpa-miR167d	Carica papaya		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	mes-miR167d	Manihot esculenta		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	mes-miR167e	Manihot esculenta		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	mes-miR167f	Manihot esculenta		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	bdi-miR167e-5p	Brachypodium distachyon		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	bdi-miR167c-5p	Brachypodium distachyon		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	bdi-miR167d-5p	Brachypodium distachyon		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	gma-miR167g	Glycine max		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	ccl-miR167a	Citrus clementina		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	ctr-miR167	Citrus trifoliata		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
	ccl-miR167b	Citrus clementina		343.82	449.58	50.89	148.29	85.43	317.6	138.57	370.77
dof-miR-712	tae-miR167c-5p	Triticum aestivum	TGAAGCTGCCAGCATGATCTGC	0.4	0.25	0	0.72	0.19	0.52	0	0.28
	ata-miR167f-5p	Aegilops tauschii		0.4	0.25	0	0.72	0.19	0.52	0	0.28
dof-miR-713	ath-miR167d	Arabidopsis thaliana	TGAAGCTGCCAGCATGATCTGG	6.34	2.8	5.88	836.23	7.65	41	8.51	1.26
	cca-miR167	Cynara cardunculus		6.34	2.8	5.88	836.23	7.65	41	8.51	1.26
	nta-miR167a	Nicotiana tabacum		6.34	2.8	5.88	836.23	7.65	41	8.51	1.26
	nta-miR167b	Nicotiana tabacum		6.34	2.8	5.88	836.23	7.65	41	8.51	1.26
	nta-miR167c	Nicotiana tabacum		6.34	2.8	5.88	836.23	7.65	41	8.51	1.26
	rco-miR167c	Ricinus communis		6.34	2.8	5.88	836.23	7.65	41	8.51	1.26
	aly-miR167d-5p	Arabidopsis lyrata		6.34	2.8	5.88	836.23	7.65	41	8.51	1.26
dof-miR-714	ptc-miR167f-5p	Populus trichocarpa	TGAAGCTGCCAGCATGATCTT	0.2	0	0	21.44	0	0.1	0.5	0
	ptc-miR167g-5p	Populus trichocarpa		0.2	0	0	21.44	0	0.1	0.5	0
	cpa-miR167c	Carica papaya		0.2	0	0	21.44	0	0.1	0.5	0
	mes-miR167g	Manihot esculenta		0.2	0	0	21.44	0	0.1	0.5	0
	mes-miR167h	Manihot esculenta		0.2	0	0	21.44	0	0.1	0.5	0
	cme-miR167c	Cucumis melo		0.2	0	0	21.44	0	0.1	0.5	0
	lus-miR167b	Linum usitatissimum		0.2	0	0	21.44	0	0.1	0.5	0
	tcc-miR167c	Theobroma cacao		0.2	0	0	21.44	0	0.1	0.5	0
	ahy-miR167-5p	Arachis hypogaea		0.2	0	0	21.44	0	0.1	0.5	0
	csi-miR167b	Citrus sinensis		0.2	0	0	21.44	0	0.1	0.5	0
	gma-miR167e	Glycine max		0.2	0	0	21.44	0	0.1	0.5	0
	gma-miR167f	Glycine max		0.2	0	0	21.44	0	0.1	0.5	0
dof-miR-715	ppe-miR167d	Prunus persica	TGAAGCTGCCAGCATGATCTTA	0	0.25	0.37	18.74	0	0.21	0	0
	mdm-miR167h	Malus domestica		0	0.25	0.37	18.74	0	0.21	0	0

	mdm-miR167i	Malus domestica		0	0.25	0.37	18.74	0	0.21	0	0
	mdm-miR167j	Malus domestica		0	0.25	0.37	18.74	0	0.21	0	0
dof-miR-716	hsa-miR-493-3p	Homo sapiens	TGAAGGTCTACTGTGTGCCAGG	0	0	0	0.18	0	0	0	0
	chi-miR-493-3p	Capra hircus		0	0	0	0.18	0	0	0	0
	ssc-miR-493-3p	Sus scrofa		0	0	0	0.18	0	0	0	0
	oar-miR-493-3p	Ovis aries		0	0	0	0.18	0	0	0	0
	ppy-miR-493	Pongo pygmaeus		0	0	0	0.18	0	0	0	0
	mml-miR-493-3p	Macaca mulatta		0	0	0	0.18	0	0	0	0
	bta-miR-493	Bos taurus		0	0	0	0.18	0	0	0	0
dof-miR-717	bdi-miR395q	Brachypodium distachyon	TGAAGTGTGGGGGAAGTC	0	0	0	0	0	0.1	0	0
	ata-miR395e-3p	Aegilops tauschii		0	0	0	0	0	0.1	0	0
	ata-miR395a-3p	Aegilops tauschii		0	0	0	0	0	0.1	0	0
	ata-miR395d-3p	Aegilops tauschii		0	0	0	0	0	0.1	0	0
	ata-miR395f-3p	Aegilops tauschii		0	0	0	0	0	0.1	0	0
	ata-miR395c-3p	Aegilops tauschii		0	0	0	0	0	0.1	0	0
	cpa-miR395a	Carica papaya		0	0	0	0	0	0.1	0	0
	cpa-miR395b	Carica papaya		0	0	0	0	0	0.1	0	0
	cpa-miR395c	Carica papaya		0	0	0	0	0	0.1	0	0
	cpa-miR395d	Carica papaya		0	0	0	0	0	0.1	0	0
	cpa-miR395e	Carica papaya		0	0	0	0	0	0.1	0	0
	bdi-miR395o-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395a	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395b	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395c-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395m	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395e-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395f-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395g-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395h-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395j-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395k-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395l-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR395n-3p	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	tae-miR395b	Triticum aestivum		0	0	0	0	0	0.1	0	0

dof-miR-718	gma-miR172k	Glycine max	TGAATCTTGATGATGCTGCAT	0	0	6.06	1.98	0.09	0	0.17	0
dof-miR-719	ppt-miR535a	Physcomitrella patens	TGACAACGAGAGAGCAGC	1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	ppt-miR535b	Physcomitrella patens		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	ppt-miR535c	Physcomitrella patens		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	osa-miR535-5p	Oryza sativa		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	ppt-miR535d	Physcomitrella patens		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	vvi-miR535a	Vitis vinifera		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	vvi-miR535b	Vitis vinifera		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	vvi-miR535c	Vitis vinifera		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	ppe-miR535a	Prunus persica		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	cpa-miR535	Carica papaya		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	atr-miR535	Amborella trichopoda		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	mdm-miR535a	Malus domestica		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	pab-miR535	Picea abies		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
	rco-miR535	Ricinus communis		1409.75	1031.8	1317.33	1316.6	905.33	1585.41	958.29	1647.29
dof-miR-720	aqc-miR535	Aquilegia caerulea	TGACAACGAGAGAGCAGC	0	0	0	0	0	0.21	0	0
dof-miR-721	mes-miR535b	Manihot esculenta	TGACAACGAGAGAGCAGC	0	0	0.18	0	2.33	4.9	0.33	0
dof-miR-722	mes-miR535a	Manihot esculenta	TGACAACGAGAGAGCAGC	0.4	0.25	0.92	1.44	1.21	2.3	0.5	0.28
dof-miR-723	tcc-miR535	Theobroma cacao	TGACAACGATAGAGAGCAGC	0.79	0.51	0.55	0.18	0.09	0.31	0.33	1.12
dof-miR-724	mdm-miR535b	Malus domestica	TGACAAGGAGAGAGCAGC	0.2	0	0.37	0.36	0	0.1	0	0
	mdm-miR535c	Malus domestica		0.2	0	0.37	0.36	0	0.1	0	0
dof-miR-725	mdm-miR156ad	Malus domestica	TGACAGAAGAAAGTGAGCAC	0	0	0	0	0	0	0	0.28
	mdm-miR156ae	Malus domestica		0	0	0	0	0	0	0	0.28
dof-miR-726	bdi-miR156j	Brachypodium distachyon	TGACAGAAGAGAGAGCAGC	0	0	0	0	0	0	0	0.14
	hpa-miR156a	Helianthus paradoxus		0	0	0	0	0	0	0	0.14
	ath-miR156j	Arabidopsis thaliana		0	0	0	0	0	0	0	0.14
	ahy-miR156a	Arachis hypogaea		0	0	0	0	0	0	0	0.14
dof-miR-727	zma-miR156k-5p	Zea mays	TGACAGAAGAGAGCGAGCAC	0	0	0.37	0.54	0	0	0	0.14
	sbi-miR156e	Sorghum bicolor		0	0	0.37	0.54	0	0	0	0.14
dof-miR-728	har-miR156c	Helianthus argophyllus	TGACAGAAGAGAGGGAGCA	0	0	0	0	0.09	0	0	0
dof-miR-729	ptc-miR156k	Populus trichocarpa	TGACAGAAGAGAGGGAGCAC	0.4	0	1.65	0.72	0.19	0.52	0.5	0.84
	vvi-miR156a	Vitis vinifera		0.4	0	1.65	0.72	0.19	0.52	0.5	0.84
	hci-miR156b	Helianthus ciliaris		0.4	0	1.65	0.72	0.19	0.52	0.5	0.84
	cme-miR156h	Cucumis melo		0.4	0	1.65	0.72	0.19	0.52	0.5	0.84

	cme-miR156g	Cucumis melo		0.4	0	1.65	0.72	0.19	0.52	0.5	0.84
	dpr-miR156a	Digitalis purpurea		0.4	0	1.65	0.72	0.19	0.52	0.5	0.84
dof-miR-730	ath-miR156a-5p	Arabidopsis thaliana	TGACAGAAGAGAGTGAGCAC	69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	ath-miR156b-5p	Arabidopsis thaliana		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	ath-miR156c-5p	Arabidopsis thaliana		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	ath-miR156d-5p	Arabidopsis thaliana		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	ath-miR156e	Arabidopsis thaliana		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	ath-miR156f-5p	Arabidopsis thaliana		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156a	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156b-5p	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156c-5p	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156d	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156e	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156f-5p	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156g-5p	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156h-5p	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156i	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	osa-miR156j-5p	Oryza sativa		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156d-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156f-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156g-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156b-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156c	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156e-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156a-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156h-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156i-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	sbi-miR156a	Sorghum bicolor		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	sbi-miR156c	Sorghum bicolor		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	sbi-miR156b	Sorghum bicolor		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	sof-miR156	Saccharum officinarum		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	gma-miR156a	Glycine max		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
ptc-miR156a	Populus trichocarpa	69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61		
ptc-miR156b	Populus trichocarpa	69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61		

	gma-miR156h	Glycine max		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	bdi-miR156b-5p	Brachypodium distachyon		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	bdi-miR156c	Brachypodium distachyon		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	bdi-miR156d-5p	Brachypodium distachyon		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	csi-miR156	Citrus sinensis		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	zma-miR156l-5p	Zea mays		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	ctr-miR156	Citrus trifoliata		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	aly-miR156a-5p	Arabidopsis lyrata		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	aly-miR156b-5p	Arabidopsis lyrata		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	aly-miR156c-5p	Arabidopsis lyrata		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	aly-miR156d-5p	Arabidopsis lyrata		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	aly-miR156e-5p	Arabidopsis lyrata		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	aly-miR156f-5p	Arabidopsis lyrata		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	sbi-miR156f	Sorghum bicolor		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	sbi-miR156g	Sorghum bicolor		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	sbi-miR156h	Sorghum bicolor		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
	sbi-miR156i	Sorghum bicolor		69.52	49.9	181.16	63.42	13.34	37.67	76.96	239.61
dof-miR-731	bna-miR156a	Brassica napus	TGACAGAAGAGAGTGAGCAC	0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	hvu-miR156b	Hordeum vulgare		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	ssl-miR156	Salvia sclarea		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	ssp-miR156	Saccharum sp.		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	hvu-miR156a	Hordeum vulgare		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	tae-miR156	Triticum aestivum		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	rco-miR156a	Ricinus communis		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	rco-miR156b	Ricinus communis		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	rco-miR156c	Ricinus communis		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
	rco-miR156d	Ricinus communis		0	0.25	1.1	0.54	0.19	0.31	0.33	1.26
dof-miR-732	gma-miR156q	Glycine max	TGACAGAAGAGAGTGAGCACT	0.4	0.51	1.29	0.72	0.28	0.63	0.67	2.24
	gma-miR156s	Glycine max		0.4	0.51	1.29	0.72	0.28	0.63	0.67	2.24
dof-miR-733	hci-miR156a	Helianthus ciliaris	TGACAGAAGAGAGTGAGTAC	0	0	0.37	0	0	0	0	0
dof-miR-734	mtr-miR156j	Medicago truncatula	TGACAGAAGAGGGTGAGCAC	0	0	0	0	0	0	0	0.14
dof-miR-735	ath-miR157d	Arabidopsis thaliana	TGACAGAAGATAGAGAGCAC	0	0	1.29	1.26	0.28	1.04	0.5	2.38
	ppe-miR156f	Prunus persica		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	mdm-miR156x	Malus domestica		0	0	1.29	1.26	0.28	1.04	0.5	2.38

	mdm-miR156y	Malus domestica		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	mdm-miR156z	Malus domestica		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	mdm-miR156aa	Malus domestica		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	cme-miR156f	Cucumis melo		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	nta-miR156g	Nicotiana tabacum		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	nta-miR156h	Nicotiana tabacum		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	nta-miR156i	Nicotiana tabacum		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	nta-miR156j	Nicotiana tabacum		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	aly-miR157d-5p	Arabidopsis lyrata		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	aqc-miR156b	Aquilegia caerulea		0	0	1.29	1.26	0.28	1.04	0.5	2.38
	aqc-miR156a	Aquilegia caerulea		0	0	1.29	1.26	0.28	1.04	0.5	2.38
dof-miR-736	vvi-miR156e	Vitis vinifera	TGACAGAGGAGAGTGAGCAC	0	0.25	0	0	0	0	0	0.14
dof-miR-737	ola-miR-192-5p	Oryzias latipes	TGACCTATGAATTGACAGCCA	0.4	0.51	0.37	0	0.19	0	0.5	0.7
dof-miR-738	ppe-miR535b	Prunus persica	TGACGACGAGAGAGCACGC	0	0.51	0	0.18	0.56	0.21	0	0.28
	mdm-miR535d	Malus domestica		0	0.51	0	0.18	0.56	0.21	0	0.28
dof-miR-739	api-miR-279a	Acyrtosiphon pisum	TGACTAGATCCACACTCATCC	0	0	0	0	0	0	0.33	0
	cte-miR-279	Capitella teleta		0	0	0	0	0	0	0.33	0
dof-miR-740	ame-miR-279d	Apis mellifera	TGACTAGATCCACACTCATCCA	0	0	0	0	0	0	0.17	0
	hme-miR-279a	Heliconius melpomene		0	0	0	0	0	0	0.17	0
	mse-miR-279a	Manduca sexta		0	0	0	0	0	0	0.17	0
	dpu-miR-279a	Daphnia pulex		0	0	0	0	0	0	0.17	0
	isc-miR-279	Ixodes scapularis		0	0	0	0	0	0	0.17	0
	lgi-miR-279	Lottia gigantea		0	0	0	0	0	0	0.17	0
	tca-miR-279b-3p	Tribolium castaneum		0	0	0	0	0	0	0.17	0
dof-miR-741	dre-miR-146b	Danio rerio	TGAGAACTGAATTCCAAGGGTG	0	0	0	0.18	0	0	0	0
	ipu-miR-146b	Ictalurus punctatus		0	0	0	0.18	0	0	0	0
dof-miR-742	dre-miR-146a	Danio rerio	TGAGAACTGAATTCATAGATGG	16.64	15.02	2.2	7.21	0	0	25.88	3.36
	ssa-miR-146a-5p	Salmo salar		16.64	15.02	2.2	7.21	0	0	25.88	3.36
	ipu-miR-146a	Ictalurus punctatus		16.64	15.02	2.2	7.21	0	0	25.88	3.36
	ccr-miR-146a	Cyprinus carpio		16.64	15.02	2.2	7.21	0	0	25.88	3.36
dof-miR-743	aca-miR-146a-5p	Anolis carolinensis	TGAGAACTGAATTCATAGGC	0	0	0	0	1.59	0.21	0	0
	ssc-miR-146b	Sus scrofa		0	0	0	0	1.59	0.21	0	0
dof-miR-744	gga-miR-146b-5p	Gallus gallus	TGAGAACTGAATTCATAGGCG	0	0	0	0	0.09	0	0	0
	tgu-miR-146b-5p	Taeniopygia guttata		0	0	0	0	0.09	0	0	0

dof-miR-745	hsa-miR-146b-5p	Homo sapiens	TGAGAACTGAATTCATAGGCT	0	0	0.18	0	6.62	0.31	0	0
	mmu-miR-146b-5p	Mus musculus		0	0	0.18	0	6.62	0.31	0	0
	oan-miR-146b-5p	Ornithorhynchus anatinus		0	0	0.18	0	6.62	0.31	0	0
	pma-miR-146-5p	Petromyzon marinus		0	0	0.18	0	6.62	0.31	0	0
	ppy-miR-146b-5p	Pongo pygmaeus		0	0	0.18	0	6.62	0.31	0	0
	mdo-miR-146b-5p	Monodelphis domestica		0	0	0.18	0	6.62	0.31	0	0
	eca-miR-146b-5p	Equus caballus		0	0	0.18	0	6.62	0.31	0	0
	mml-miR-146b-5p	Macaca mulatta		0	0	0.18	0	6.62	0.31	0	0
	cfa-miR-146b	Canis familiaris		0	0	0.18	0	6.62	0.31	0	0
	ptr-miR-146b	Pan troglodytes		0	0	0.18	0	6.62	0.31	0	0
dof-miR-746	cgr-miR-146b-5p	Cricetulus griseus	TGAGAACTGAATTCATAGGCTG	0	0	0	0	0.93	0	0	0
dof-miR-747	rno-miR-146b-5p	Rattus norvegicus	TGAGAACTGAATTCATAGGCTGT	0	0.25	0.18	0	4.38	0.63	0.33	0.14
	chi-miR-146b-5p	Capra hircus		0	0.25	0.18	0	4.38	0.63	0.33	0.14
	ggo-miR-146b	Gorilla gorilla		0	0.25	0.18	0	4.38	0.63	0.33	0.14
	bta-miR-146b	Bos taurus		0	0.25	0.18	0	4.38	0.63	0.33	0.14
dof-miR-748	xtr-miR-146a	Xenopus tropicalis	TGAGAACTGAATTCATAGGTT	0	0	0.73	0.36	0	0	0	0
	chi-miR-146a	Capra hircus		0	0	0.73	0.36	0	0	0	0
dof-miR-749	gga-miR-146c-5p	Gallus gallus	TGAGAACTGAATTCATGGACTG	0	0	0.18	0	0	0	0	0
dof-miR-750	ggo-miR-146a	Gorilla gorilla	TGAGAACTGAATTCATGGGT	0	0	0.18	0.18	0.56	0.42	0.33	0
dof-miR-751	mmu-miR-146a-5p	Mus musculus	TGAGAACTGAATTCATGGGTT	0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	hsa-miR-146a-5p	Homo sapiens		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	rno-miR-146a-5p	Rattus norvegicus		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	gga-miR-146a-5p	Gallus gallus		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	tch-miR-146a-5p	Tupaia chinensis		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	cgr-miR-146a	Cricetulus griseus		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	ppy-miR-146a	Pongo pygmaeus		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	ssc-miR-146a-5p	Sus scrofa		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	mdo-miR-146a-5p	Monodelphis domestica		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	eca-miR-146a	Equus caballus		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	tgu-miR-146c	Taeniopygia guttata		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	mml-miR-146a-5p	Macaca mulatta		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	cfa-miR-146a	Canis familiaris		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
	ptr-miR-146a	Pan troglodytes		0.2	1.02	1.65	1.08	8.49	1.25	1.17	0.14
dof-miR-752	vvi-miR172d	Vitis vinifera	TGAGAATCTTGATGATGCTGCAT	0	0.25	0	0	0	0	0	0

	aau-miR172	Acacia auriculiformis		0	0.25	0	0	0	0	0	0
dof-miR-753	gso-miR3522a	Glycine soja	TGAGACCAAATGAGCAGCTGA	0	0	0.37	0	0	0	0	0
dof-miR-754	bta-miR-769	Bos taurus	TGAGACCTCCGGGTTCTGAGCT	0	0	0	0.36	0	0	0	0
dof-miR-755	hsa-miR-769-5p	Homo sapiens	TGAGACCTCTGGGTTCTGAGCT	0	0	0	0	0.19	0.1	0	0
dof-miR-756	mse-bantam	Manduca sexta bantam	TGAGATCATTGTGAAAGCTAAT	0.2	0	0	0	0	0	0	0
dof-miR-757	ame-bantam	Apis mellifera bantam	TGAGATCATTGTGAAAGCTGATT	0	0	0	0	0.37	0.94	0	0
	nvi-bantam	Nasonia vitripennis bantam		0	0	0	0	0.37	0.94	0	0
	isc-bantam	Ixodes scapularis bantam		0	0	0	0	0.37	0.94	0	0
	tca-bantam-3p	Tribolium castaneum bantam-3p		0	0	0	0	0.37	0.94	0	0
	dpu-bantam	Daphnia pulex bantam		0	0	0	0	0.37	0.94	0	0
dof-miR-758	ccr-miR-143	Cyprinus carpio	TGAGATGAAGCACTGTAGCT	5.35	6.36	12.68	12.61	1.21	0.83	6.18	0.7
	ola-miR-143	Oryzias latipes		5.35	6.36	12.68	12.61	1.21	0.83	6.18	0.7
dof-miR-759	mmu-miR-143-3p	Mus musculus	TGAGATGAAGCACTGTAGCTC	1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	hsa-miR-143-3p	Homo sapiens		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	dre-miR-143	Danio rerio		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	oan-miR-143-3p	Ornithorhynchus anatinus		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	ssa-miR-143-3p	Salmo salar		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	ipu-miR-143	Ictalurus punctatus		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	oar-miR-143	Ovis aries		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	cgr-miR-143	Cricetulus griseus		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	aca-miR-143-3p	Anolis carolinensis		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	eca-miR-143	Equus caballus		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	ssc-miR-143-3p	Sus scrofa		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	mml-miR-143-3p	Macaca mulatta		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
	cfa-miR-143	Canis familiaris		1.98	2.29	11.39	9.19	1.87	0.42	5.51	0.98
dof-miR-760	rno-miR-143-3p	Rattus norvegicus	TGAGATGAAGCACTGTAGCTCA	0	0	0.92	0.72	0.47	0.1	0.17	0
	ptr-miR-143	Pan troglodytes		0	0	0.92	0.72	0.47	0.1	0.17	0
	ggo-miR-143	Gorilla gorilla		0	0	0.92	0.72	0.47	0.1	0.17	0
	ppy-miR-143	Pongo pygmaeus		0	0	0.92	0.72	0.47	0.1	0.17	0
	lla-miR-143	Lagothrix lagotricha		0	0	0.92	0.72	0.47	0.1	0.17	0
	ppa-miR-143	Pan paniscus		0	0	0.92	0.72	0.47	0.1	0.17	0
	oha-miR-143-3p	Ophiophagus hannah		0	0	0.92	0.72	0.47	0.1	0.17	0
dof-miR-761	xtr-miR-143	Xenopus tropicalis	TGAGATGAAGCACTGTAGCTCG	0	0	0.73	0.36	0	0.1	0.17	0
	mdo-miR-143-3p	Monodelphis domestica		0	0	0.73	0.36	0	0.1	0.17	0

	chi-miR-143-3p	Capra hircus		0	0	0.73	0.36	0	0.1	0.17	0
	tch-miR-143-3p	Tupaia chinensis		0	0	0.73	0.36	0	0.1	0.17	0
	aja-miR-143	Artibeus jamaicensis		0	0	0.73	0.36	0	0.1	0.17	0
	bta-miR-143	Bos taurus		0	0	0.73	0.36	0	0.1	0.17	0
dof-miR-762	ata-miR171a-3p	Aegilops tauschii	TGAGCCGAACCAATATCACTC	0	0	0	0	0	0	0	0.14
	stu-miR479	Solanum tuberosum		0	0	0	0	0	0	0	0.14
	mdm-miR171i	Malus domestica		0	0	0	0	0	0	0	0.14
dof-miR-763	pte-miR473a-3p	Populus trichocarpa	TGAGGCCTTTGGGGGAGAGTGG	0	0	0.18	0	0	0	0	0
dof-miR-764	ggo-miR-423	Gorilla gorilla	TGAGGGGCAGAGAGCGAGACTT	0	0	0	0	1.21	0.21	0	0
dof-miR-765	hsa-miR-423-5p	Homo sapiens	TGAGGGGCAGAGAGCGAGACTTT	0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	mmu-miR-423-5p	Mus musculus		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	bta-miR-423-5p	Bos taurus		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	chi-miR-423-5p	Capra hircus		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	cgr-miR-423-5p	Cricetulus griseus		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	ppy-miR-423-5p	Pongo pygmaeus		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	eca-miR-423-5p	Equus caballus		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	ssc-miR-423-5p	Sus scrofa		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	mml-miR-423-5p	Macaca mulatta		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
	cfa-miR-423a	Canis familiaris		0.4	1.27	0	0.18	1.21	0.42	0.17	0.14
dof-miR-766	rno-miR-423-5p	Rattus norvegicus	TGAGGGGCAGAGAGCGAGACTTTT	0	0	0	0	0.09	0.63	0	0
	efu-miR-423	Eptesicus fuscus		0	0	0	0	0.09	0.63	0	0
dof-miR-767	bta-let-7e	Bos taurus let-7e	TGAGGTAGGAGGTTGTATAGT	0	0	0.18	0.54	0.09	0.1	0	0
	ggo-let-7e	Gorilla gorilla let-7e		0	0	0.18	0.54	0.09	0.1	0	0
dof-miR-768	hsa-let-7e-5p	Homo sapiens let-7e-5p	TGAGGTAGGAGGTTGTATAGTT	0.4	0.25	1.65	1.26	0.37	0	0	0
	mmu-let-7e-5p	Mus musculus let-7e-5p		0.4	0.25	1.65	1.26	0.37	0	0	0
	rno-let-7e-5p	Rattus norvegicus let-7e-5p		0.4	0.25	1.65	1.26	0.37	0	0	0
	chi-let-7e-5p	Capra hircus let-7e-5p		0.4	0.25	1.65	1.26	0.37	0	0	0
	tch-let-7e-5p	Tupaia chinensis let-7e-5p		0.4	0.25	1.65	1.26	0.37	0	0	0
	ppy-let-7e	Pongo pygmaeus let-7e		0.4	0.25	1.65	1.26	0.37	0	0	0
	eca-let-7e	Equus caballus let-7e		0.4	0.25	1.65	1.26	0.37	0	0	0
	ssc-let-7e	Sus scrofa let-7e		0.4	0.25	1.65	1.26	0.37	0	0	0
	mml-let-7e-5p	Macaca mulatta let-7e-5p		0.4	0.25	1.65	1.26	0.37	0	0	0
	cfa-let-7e	Canis familiaris let-7e		0.4	0.25	1.65	1.26	0.37	0	0	0
ptr-let-7e	Pan troglodytes let-7e	0.4	0.25	1.65	1.26	0.37	0	0	0		

dof-miR-769	aca-miR-98-5p	Anolis carolinensis	TGAGGTAGTAAGTTGTATTGT	0	0	0.18	0	0.28	0	0	0
dof-miR-770	hsa-miR-98-5p	Homo sapiens	TGAGGTAGTAAGTTGTATTGT	0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	mmu-miR-98-5p	Mus musculus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	rno-miR-98-5p	Rattus norvegicus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	mml-miR-98	Macaca mulatta		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	ptr-miR-98	Pan troglodytes		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	ggo-miR-98	Gorilla gorilla		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	ppy-miR-98	Pongo pygmaeus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	age-miR-98	Ateles geoffroyi		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	ppa-miR-98	Pan paniscus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	xtr-miR-98	Xenopus tropicalis		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	bta-miR-98	Bos taurus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	oan-miR-98	Ornithorhynchus anatinus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	chi-miR-98-5p	Capra hircus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	tch-miR-98-5p	Tupaia chinensis		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	oha-miR-98-5p	Ophiophagus hannah		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	cgr-miR-98	Cricetulus griseus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	eca-miR-98	Equus caballus		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
	ssc-miR-98	Sus scrofa		0.2	0.25	0.92	1.08	0.75	0	0.17	0.14
cfa-miR-98	Canis familiaris	0.2	0.25	0.92	1.08	0.75	0	0.17	0.14		
dof-miR-771	dre-let-7h	Danio rerio let-7h	TGAGGTAGTAAGTTGTGTTGTT	0	0.25	0.55	1.26	0	0	0.33	0
	fru-let-7h	Fugu rubripes let-7h		0	0.25	0.55	1.26	0	0	0.33	0
	tmi-let-7h	Tetraodon nigroviridis let-7h		0	0.25	0.55	1.26	0	0	0.33	0
	ssa-let-7h-5p	Salmo salar let-7h-5p		0	0.25	0.55	1.26	0	0	0.33	0
	ipu-let-7h	Ictalurus punctatus let-7h		0	0.25	0.55	1.26	0	0	0.33	0
dof-miR-772	gga-let-7k-5p	Gallus gallus let-7k-5p	TGAGGTAGTAGATTGAATAGTT	1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
	dre-let-7e	Danio rerio let-7e		1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
	fru-let-7e	Fugu rubripes let-7e		1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
	tmi-let-7e	Tetraodon nigroviridis let-7e		1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
	oan-let-7e-5p	Ornithorhynchus anatinus let-7e-5p		1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
	oha-let-7e-5p	Ophiophagus hannah let-7e-5p		1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
	ssa-let-7e-5p	Salmo salar let-7e-5p		1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
	ipu-let-7e	Ictalurus punctatus let-7e		1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
aca-let-7e-5p	Anolis carolinensis let-7e-5p	1.78	2.8	1.1	1.08	0.09	0	4.17	0.42		

	tgu-let-7e-5p	Taeniopygia guttata let-7e-5p		1.78	2.8	1.1	1.08	0.09	0	4.17	0.42
dof-miR-773	oar-let-7f	Ovis aries let-7f	TGAGGTTAGTAGATTGTATAGT	1.39	0.76	1.65	2.34	5.04	0.83	1	1.12
	ggo-let-7f	Gorilla gorilla let-7f		1.39	0.76	1.65	2.34	5.04	0.83	1	1.12
dof-miR-774	hsa-let-7f-5p	Homo sapiens let-7f-5p	TGAGGTTAGTAGATTGTATAGTT	1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	mmu-let-7f-5p	Mus musculus let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	rno-let-7f-5p	Rattus norvegicus let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	gga-let-7f-5p	Gallus gallus let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	dre-let-7f	Danio rerio let-7f		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	ssc-let-7f	Sus scrofa let-7f		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	bta-let-7f	Bos taurus let-7f		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	xtr-let-7f	Xenopus tropicalis let-7f		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	mdo-let-7f-5p	Monodelphis domestica let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	oan-let-7f-5p	Ornithorhynchus anatinus let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	chi-let-7f-5p	Capra hircus let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	tch-let-7f-5p	Tupaia chinensis let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	oha-let-7f-5p	Ophiophagus hannah let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	ipu-let-7f	Ictalurus punctatus let-7f		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	cgr-let-7f	Cricetulus griseus let-7f		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	aca-let-7f-5p	Anolis carolinensis let-7f-5p		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	ppy-let-7f	Pongo pygmaeus let-7f		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
	eca-let-7f	Equus caballus let-7f		1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1
tgu-let-7f-5p	Taeniopygia guttata let-7f-5p	1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1		
mml-let-7f-5p	Macaca mulatta let-7f-5p	1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1		
cfa-let-7f	Canis familiaris let-7f	1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1		
ptr-let-7f	Pan troglodytes let-7f	1.98	2.8	8.64	10.63	26.67	2.92	2.17	2.1		
dof-miR-775	pma-let-7c	Petromyzon marinus let-7c	TGAGGTTAGTAGATTGTATGGTT	0	0	0	0	0.19	0.1	0	0
dof-miR-776	ssa-let-7f-5p	Salmo salar let-7f-5p	TGAGGTTAGTAGATTGTATTGTT	0	0	0	0	0.09	0	0	0
dof-miR-777	mse-let-7a	Manduca sexta let-7a	TGAGGTTAGTAGGTTGTATAG	0	0	0.18	0.54	1.59	0.42	0.17	0
	tca-let-7-5p	Tribolium castaneum let-7-5p		0	0	0.18	0.54	1.59	0.42	0.17	0
dof-miR-778	dme-let-7-5p	Drosophila melanogaster let-7-5p	TGAGGTTAGTAGGTTGTATAGT	0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dps-let-7	Drosophila pseudoobscura let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	bmo-let-7-5p	Bombyx mori let-7-5p		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	ame-let-7	Apis mellifera let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	ola-let-7a-5p	Oryzias latipes let-7a-5p		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26

	sha-let-7a	Sarcophilus harrisii let-7a		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	ggo-let-7a	Gorilla gorilla let-7a		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	nvi-let-7	Nasonia vitripennis let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	ngi-let-7	Nasonia giraulti let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	isc-let-7	Ixodes scapularis let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dan-let-7	Drosophila ananassae let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	der-let-7	Drosophila erecta let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dgr-let-7	Drosophila grimshawi let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dmo-let-7	Drosophila mojavensis let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dpe-let-7	Drosophila persimilis let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dse-let-7	Drosophila sechellia let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dsi-let-7	Drosophila simulans let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dvi-let-7	Drosophila virilis let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dwi-let-7	Drosophila willistoni let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	dya-let-7	Drosophila yakuba let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
	cte-let-7	Capitella teleta let-7		0.79	3.56	4.96	5.23	4.29	0.83	1.67	1.26
dof-miR-779	hme-let-7	Heliconius melpomene let-7	TGAGGTAGTAGGTTGTATAGTA	0	0	0.18	0.18	0.09	0.1	0	0
dof-miR-780	cel-let-7-5p	Caenorhabditis elegans let-7-5p	TGAGGTAGTAGGTTGTATAGTT	3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	hsa-let-7a-5p	Homo sapiens let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	cbr-let-7	Caenorhabditis briggsae let-7		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	mmu-let-7a-5p	Mus musculus let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	rno-let-7a-5p	Rattus norvegicus let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	gga-let-7a-5p	Gallus gallus let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	gga-let-7j-5p	Gallus gallus let-7j-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	dre-let-7a	Danio rerio let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	fru-let-7a	Fugu rubripes let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	tni-let-7a	Tetraodon nigroviridis let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	xtr-let-7a	Xenopus tropicalis let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	bta-let-7a-5p	Bos taurus let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	mdo-let-7a-5p	Monodelphis domestica let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	chi-let-7a-5p	Capra hircus let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	oha-let-7a	Ophiophagus hannah let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	oha-let-7a-5p	Ophiophagus hannah let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
bbe-let-7a-5p	Branchiostoma belcheri let-7a-5p	3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66		

	ssa-let-7a-5p	Salmo salar let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	ipu-let-7a	Ictalurus punctatus let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	cbn-let-7	Caenorhabditis breneri let-7		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	oar-let-7a	Ovis aries let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	ccr-let-7a	Cyprinus carpio let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	ola-let-7a	Oryzias latipes let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	cgr-let-7a	Cricetulus griseus let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	pma-let-7a	Petromyzon marinus let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	asu-let-7-5p	Ascaris suum let-7-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	aca-let-7a-5p	Anolis carolinensis let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	ppy-let-7a	Pongo pygmaeus let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	eca-let-7a	Equus caballus let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	ssc-let-7a	Sus scrofa let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	bma-let-7	Brugia malayi let-7		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	tgu-let-7a-5p	Taeniopygia guttata let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	mml-let-7a-5p	Macaca mulatta let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	cfa-let-7a	Canis familiaris let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	ptr-let-7a	Pan troglodytes let-7a		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	bfl-let-7a-5p	Branchiostoma floridae let-7a-5p		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	lgi-let-7	Lottia gigantea let-7		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	sko-let-7	Saccoglossus kowalevskii let-7		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	crm-let-7	Caenorhabditis remanei let-7		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
	ppc-let-7	Pristionchus pacificus let-7		3.56	10.95	15.43	23.6	18.09	4.07	6.68	2.66
dof-miR-781	prd-let-7-5p	Panagrellus redivivus let-7-5p	TGAGGTAGTAGGTTGTATAGTTT	0.59	1.27	0.73	1.26	1.21	0	0.5	0.28
dof-miR-782	ola-let-7c	Oryzias latipes let-7c	TGAGGTAGTAGGTTGTATGGT	0	0	0.37	0.36	0	0	0.17	0
	ggo-let-7c	Gorilla gorilla let-7c		0	0	0.37	0.36	0	0	0.17	0
dof-miR-783	hsa-let-7c-5p	Homo sapiens let-7c-5p	TGAGGTAGTAGGTTGTATGGTT	0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	mmu-let-7c-5p	Mus musculus let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	rno-let-7c-5p	Rattus norvegicus let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	gga-let-7c-5p	Gallus gallus let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	dre-let-7c-5p	Danio rerio let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	ssc-let-7c	Sus scrofa let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	xtr-let-7c	Xenopus tropicalis let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
bta-let-7c	Bos taurus let-7c	0.4	0	4.41	7.93	0.65	0.1	0.5	0.14		

	chi-let-7c-5p	Capra hircus let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	oha-let-7c-5p	Ophiophagus hannah let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	ssa-let-7c-5p	Salmo salar let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	oan-let-7c-5p	Ornithorhynchus anatinus let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	ipu-let-7c	Ictalurus punctatus let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	hhi-let-7c	Hippoglossus hippoglossus let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	pol-let-7a-5p	Paralichthys olivaceus let-7a-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	aca-let-7c-5p	Anolis carolinensis let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	ppy-let-7c	Pongo pygmaeus let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	eca-let-7c	Equus caballus let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	tgu-let-7c-5p	Taeniopygia guttata let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	oar-let-7c	Ovis aries let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	mml-let-7c-5p	Macaca mulatta let-7c-5p		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	cfa-let-7c	Canis familiaris let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
	ptr-let-7c	Pan troglodytes let-7c		0.4	0	4.41	7.93	0.65	0.1	0.5	0.14
dof-miR-784	ipu-let-7b	Ictalurus punctatus let-7b	TGAGGTAGTAGGTTGTGTGGT	0.2	0.51	2.39	1.08	1.96	0.73	0	0
	ola-let-7b	Oryzias latipes let-7b		0.2	0.51	2.39	1.08	1.96	0.73	0	0
	ggo-let-7b	Gorilla gorilla let-7b		0.2	0.51	2.39	1.08	1.96	0.73	0	0
	aca-let-7b-5p	Anolis carolinensis let-7b-5p		0.2	0.51	2.39	1.08	1.96	0.73	0	0
	oar-let-7b	Ovis aries let-7b		0.2	0.51	2.39	1.08	1.96	0.73	0	0
dof-miR-785	hsa-let-7b-5p	Homo sapiens let-7b-5p	TGAGGTAGTAGGTTGTGTGGTT	0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	mmu-let-7b-5p	Mus musculus let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	rno-let-7b-5p	Rattus norvegicus let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	gga-let-7b	Gallus gallus let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	dre-let-7b	Danio rerio let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	fru-let-7b	Fugu rubripes let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	tni-let-7b	Tetraodon nigroviridis let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	mdo-let-7b	Monodelphis domestica let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	bta-let-7b	Bos taurus let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	oan-let-7b-5p	Ornithorhynchus anatinus let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	chi-let-7b-5p	Capra hircus let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	oha-let-7b-5p	Ophiophagus hannah let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	ssa-let-7b-5p	Salmo salar let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	pol-let-7b-5p	Paralichthys olivaceus let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7

	ccr-let-7b	Cyprinus carpio let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	cgr-let-7b	Cricetulus griseus let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	ppy-let-7b	Pongo pygmaeus let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	tgu-let-7b-5p	Taeniopygia guttata let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	mml-let-7b-5p	Macaca mulatta let-7b-5p		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	ptr-let-7b	Pan troglodytes let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
	cfa-let-7b	Canis familiaris let-7b		0.4	0.25	6.43	5.05	2.05	0.73	0.67	0.7
dof-miR-786	gga-let-7g-5p	Gallus gallus let-7g-5p	TGAGGTAGTAGTTTGTACAGT	0.2	1.53	0.73	0.36	4.57	0.52	0	0.42
	mdo-let-7g-5p	Monodelphis domestica let-7g-5p		0.2	1.53	0.73	0.36	4.57	0.52	0	0.42
	oar-let-7g	Ovis aries let-7g		0.2	1.53	0.73	0.36	4.57	0.52	0	0.42
	sha-let-7g	Sarcophilus harrisii let-7g		0.2	1.53	0.73	0.36	4.57	0.52	0	0.42
	ggo-let-7g	Gorilla gorilla let-7g		0.2	1.53	0.73	0.36	4.57	0.52	0	0.42
dof-miR-787	mmu-let-7g-5p	Mus musculus let-7g-5p	TGAGGTAGTAGTTTGTACAGTT	0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	hsa-let-7g-5p	Homo sapiens let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	bta-let-7g	Bos taurus let-7g		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	oan-let-7g-5p	Ornithorhynchus anatinus let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	rno-let-7g-5p	Rattus norvegicus let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	chi-let-7g-5p	Capra hircus let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	tch-let-7g-5p	Tupaia chinensis let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	oha-let-7g-5p	Ophiophagus hannah let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	cgr-let-7g-5p	Cricetulus griseus let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	aca-let-7g	Anolis carolinensis let-7g		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	ppy-let-7g	Pongo pygmaeus let-7g		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	eca-let-7g	Equus caballus let-7g		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	ssc-let-7g	Sus scrofa let-7g		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	tgu-let-7g-5p	Taeniopygia guttata let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	mml-let-7g-5p	Macaca mulatta let-7g-5p		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	cfa-let-7g	Canis familiaris let-7g		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
	ptr-let-7g	Pan troglodytes let-7g		0.99	3.31	4.23	3.06	23.04	1.67	1.67	1.4
dof-miR-788	dre-let-7g	Danio rerio let-7g	TGAGGTAGTAGTTTGTATAGTT	0.59	1.27	4.41	5.59	0	0	2.5	0.14
	fru-let-7g	Fugu rubripes let-7g		0.59	1.27	4.41	5.59	0	0	2.5	0.14
	tmi-let-7g	Tetraodon nigroviridis let-7g		0.59	1.27	4.41	5.59	0	0	2.5	0.14
	ssa-let-7g-5p	Salmo salar let-7g-5p		0.59	1.27	4.41	5.59	0	0	2.5	0.14
	ipu-let-7g	Ictalurus punctatus let-7g		0.59	1.27	4.41	5.59	0	0	2.5	0.14

	ccr-let-7g	Cyprinus carpio let-7g		0.59	1.27	4.41	5.59	0	0	2.5	0.14
dof-miR-789	ssc-let-7i	Sus scrofa let-7i	TGAGGTAGTAGTTGTGCT	0	0	0	0	0.28	0.1	0	0
dof-miR-790	gga-let-7i	Gallus gallus let-7i	TGAGGTAGTAGTTGTGCTGT	0	0.25	0.92	1.08	1.77	1.04	0	0
	xtr-let-7i	Xenopus tropicalis let-7i		0	0.25	0.92	1.08	1.77	1.04	0	0
	mdo-let-7i-5p	Monodelphis domestica let-7i-5p		0	0.25	0.92	1.08	1.77	1.04	0	0
	ccr-let-7i	Cyprinus carpio let-7i		0	0.25	0.92	1.08	1.77	1.04	0	0
	sha-let-7i	Sarcophilus harrisii let-7i		0	0.25	0.92	1.08	1.77	1.04	0	0
	ggo-let-7i	Gorilla gorilla let-7i		0	0.25	0.92	1.08	1.77	1.04	0	0
dof-miR-791	mmu-let-7i-5p	Mus musculus let-7i-5p	TGAGGTAGTAGTTGTGCTGTT	0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	hsa-let-7i-5p	Homo sapiens let-7i-5p		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	rno-let-7i-5p	Rattus norvegicus let-7i-5p		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	dre-let-7i	Danio rerio let-7i		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	fru-let-7i	Fugu rubripes let-7i		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	tmi-let-7i	Tetraodon nigroviridis let-7i		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	bta-let-7i	Bos taurus let-7i		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	chi-let-7i-5p	Capra hircus let-7i-5p		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	tch-let-7i-5p	Tupaia chinensis let-7i-5p		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	oha-let-7i-5p	Ophiophagus hannah let-7i-5p		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	ssa-let-7i-5p	Salmo salar let-7i-5p		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	ipu-let-7i	Ictalurus punctatus let-7i		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	oar-let-7i	Ovis aries let-7i		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	aca-let-7i-5p	Anolis carolinensis let-7i-5p		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	ppy-let-7i	Pongo pygmaeus let-7i		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
	tgu-let-7i-5p	Taeniopygia guttata let-7i-5p		0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12
mml-let-7i-5p	Macaca mulatta let-7i-5p	0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12		
ptr-let-7i	Pan troglodytes let-7i	0.59	2.55	3.49	5.95	7.09	1.88	1.84	1.12		
dof-miR-792	dre-let-7d-5p	Danio rerio let-7d-5p	TGAGGTAGTTGGTTGTATGGTT	0.2	0	0.18	0	0	0	1.34	0.28
	fru-let-7d	Fugu rubripes let-7d		0.2	0	0.18	0	0	0	1.34	0.28
	tmi-let-7d	Tetraodon nigroviridis let-7d		0.2	0	0.18	0	0	0	1.34	0.28
	ssa-let-7d-5p	Salmo salar let-7d-5p		0.2	0	0.18	0	0	0	1.34	0.28
	ipu-let-7d	Ictalurus punctatus let-7d		0.2	0	0.18	0	0	0	1.34	0.28
	pol-let-7d-5p	Paralichthys olivaceus let-7d-5p		0.2	0	0.18	0	0	0	1.34	0.28
dof-miR-793	dre-let-7j	Danio rerio let-7j	TGAGGTAGTTGTTTGTACAGTT	0.4	0	0.92	1.98	0	0	0.5	0
	ipu-let-7j	Ictalurus punctatus let-7j		0.4	0	0.92	1.98	0	0	0.5	0

	hhi-let-7j	Hippoglossus hippoglossus let-7j		0.4	0	0.92	1.98	0	0	0.5	0
	ccr-let-7j	Cyprinus carpio let-7j		0.4	0	0.92	1.98	0	0	0.5	0
dof-miR-794	hsa-miR-7854-3p	Homo sapiens	TGAGGTGACCGCAGATGGGAA	0	0	0	0	0.09	0	0	0
dof-miR-795	dme-miR-12-5p	Drosophila melanogaster	TGAGTATTACATCAGGTACTGGT	0	0	0	0	0.28	0	0	0
	dps-miR-12	Drosophila pseudoobscura		0	0	0	0	0.28	0	0	0
	ame-miR-12	Apis mellifera		0	0	0	0	0.28	0	0	0
	aga-miR-12	Anopheles gambiae		0	0	0	0	0.28	0	0	0
	nvi-miR-12	Nasonia vitripennis		0	0	0	0	0.28	0	0	0
	nlo-miR-12	Nasonia longicornis		0	0	0	0	0.28	0	0	0
	isc-miR-12	Ixodes scapularis		0	0	0	0	0.28	0	0	0
	aae-miR-12-5p	Aedes aegypti		0	0	0	0	0.28	0	0	0
	cqu-miR-12-3p	Culex quinquefasciatus		0	0	0	0	0.28	0	0	0
	dan-miR-12	Drosophila ananassae		0	0	0	0	0.28	0	0	0
	der-miR-12	Drosophila erecta		0	0	0	0	0.28	0	0	0
	dgr-miR-12	Drosophila grimshawi		0	0	0	0	0.28	0	0	0
	dmo-miR-12	Drosophila mojavensis		0	0	0	0	0.28	0	0	0
	dpe-miR-12	Drosophila persimilis		0	0	0	0	0.28	0	0	0
	dse-miR-12	Drosophila sechellia		0	0	0	0	0.28	0	0	0
	dsi-miR-12	Drosophila simulans		0	0	0	0	0.28	0	0	0
	dvi-miR-12-5p	Drosophila virilis		0	0	0	0	0.28	0	0	0
	dwi-miR-12	Drosophila willistoni		0	0	0	0	0.28	0	0	0
dpu-miR-12	Daphnia pulex	0	0	0	0	0.28	0	0	0		
dof-miR-796	sly-miR156e-5p	Solanum lycopersicum	TGATAGAAGAGAGTGAGCAC	0.59	0	0.18	0	0	0.1	0.17	0.28
dof-miR-797	mmu-miR-190a-5p	Mus musculus	TGATATGTTTGATATATTAGGT	0	0.25	0	0	0	0	0.33	0
	hsa-miR-190a-5p	Homo sapiens		0	0.25	0	0	0	0	0.33	0
	rno-miR-190a-5p	Rattus norvegicus		0	0.25	0	0	0	0	0.33	0
	gga-miR-190a-5p	Gallus gallus		0	0.25	0	0	0	0	0.33	0
	dre-miR-190a	Danio rerio		0	0.25	0	0	0	0	0.33	0
	mml-miR-190a-5p	Macaca mulatta		0	0.25	0	0	0	0	0.33	0
	ptr-miR-190a	Pan troglodytes		0	0.25	0	0	0	0	0.33	0
	ggo-miR-190a	Gorilla gorilla		0	0.25	0	0	0	0	0.33	0
	ppa-miR-190	Pan paniscus		0	0.25	0	0	0	0	0.33	0
	fru-miR-190	Fugu rubripes		0	0.25	0	0	0	0	0.33	0
tmi-miR-190	Tetraodon nigroviridis	0	0.25	0	0	0	0	0.33	0		

	oan-miR-190a-5p	Ornithorhynchus anatinus		0	0.25	0	0	0	0	0.33	0
	sha-miR-190	Sarcophilus harrisii		0	0.25	0	0	0	0	0.33	0
	ppy-miR-190a	Pongo pygmaeus		0	0.25	0	0	0	0	0.33	0
	mdo-miR-190a-5p	Monodelphis domestica		0	0.25	0	0	0	0	0.33	0
	eca-miR-190a	Equus caballus		0	0.25	0	0	0	0	0.33	0
	tgu-miR-190-5p	Taeniopygia guttata		0	0.25	0	0	0	0	0.33	0
	bta-miR-190a	Bos taurus		0	0.25	0	0	0	0	0.33	0
	cfa-miR-190a	Canis familiaris		0	0.25	0	0	0	0	0.33	0
dof-miR-798	hsa-miR-4772-5p	Homo sapiens	TGATCAGGCAAAATTGCAGACT	0	0	0	0	0.19	0	0	0
dof-miR-799	htu-miR171a	Helianthus tuberosus	TGATTGAGCCGTGCCAATAT	0	0	0.18	0	0	0	0	0
dof-miR-800	osa-miR171b	Oryza sativa	TGATTGAGCCGTGCCAATATC	0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	osa-miR171c-3p	Oryza sativa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	osa-miR171d-3p	Oryza sativa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	osa-miR171e-3p	Oryza sativa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	osa-miR171f-3p	Oryza sativa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	sbi-miR171b	Sorghum bicolor		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	sbi-miR171d	Sorghum bicolor		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	sbi-miR171a	Sorghum bicolor		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	zma-miR171d-3p	Zea mays		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	zma-miR171j-3p	Zea mays		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	zma-miR171e-3p	Zea mays		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	zma-miR171i-3p	Zea mays		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	ptc-miR171e	Populus trichocarpa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	ptc-miR171f	Populus trichocarpa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	ptc-miR171g-3p	Populus trichocarpa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	ptc-miR171h-3p	Populus trichocarpa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	ptc-miR171i	Populus trichocarpa		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	mtr-miR171d	Medicago truncatula		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	tae-miR171a	Triticum aestivum		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	vvi-miR171a	Vitis vinifera		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
vvi-miR171c	Vitis vinifera	0	21.64	37.3	17.3	17.44	30.26	36.9	0.56		
vvi-miR171d	Vitis vinifera	0	21.64	37.3	17.3	17.44	30.26	36.9	0.56		
vvi-miR171i	Vitis vinifera	0	21.64	37.3	17.3	17.44	30.26	36.9	0.56		
bdi-miR171e	Brachypodium distachyon	0	21.64	37.3	17.3	17.44	30.26	36.9	0.56		

	tcc-miR171f	Theobroma cacao		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	tcc-miR171g	Theobroma cacao		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	tcc-miR171h	Theobroma cacao		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	gma-miR171e	Glycine max		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	gma-miR171f	Glycine max		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	gma-miR171g	Glycine max		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	bdi-miR171b	Brachypodium distachyon		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	bdi-miR171d-3p	Brachypodium distachyon		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	gma-miR171j-3p	Glycine max		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	hvu-miR171-3p	Hordeum vulgare		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	far-miR171	Festuca arundinacea		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	crt-miR171	Citrus reticulata		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	rco-miR171c	Ricinus communis		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	rco-miR171d	Ricinus communis		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	rco-miR171e	Ricinus communis		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	rco-miR171f	Ricinus communis		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	sly-miR171a	Solanum lycopersicum		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	sbi-miR171i	Sorghum bicolor		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	sbi-miR171k	Sorghum bicolor		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	bdi-miR171c-3p	Brachypodium distachyon		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	aqc-miR171a	Aquilegia caerulea		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	aqc-miR171b	Aquilegia caerulea		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
	aqc-miR171d	Aquilegia caerulea		0	21.64	37.3	17.3	17.44	30.26	36.9	0.56
dof-miR-801	ath-miR170-3p	Arabidopsis thaliana	TGATTGAGCCGTGCAATATC	0	0	0	0	0	0.1	0	0
	stu-miR171c-3p	Solanum tuberosum		0	0	0	0	0	0.1	0	0
	aly-miR170-3p	Arabidopsis lyrata		0	0	0	0	0	0.1	0	0
dof-miR-802	gma-miR408d	Glycine max	TGCACTGCCTCTCCCTGGC	15.25	30.04	0.73	10.81	1.21	3.03	6.18	43.72
dof-miR-803	ppt-miR408b	Physcomitrella patens		322.23	2916.69	14.15	91.17	34.23	147.53	331.9	1192.73
	stu-miR408b-3p	Solanum tuberosum	TGCACTGCCTCTCCCTGGCT	322.23	2916.69	14.15	91.17	34.23	147.53	331.9	1192.73
	cca-miR408	Cynara cardunculus		322.23	2916.69	14.15	91.17	34.23	147.53	331.9	1192.73
	nta-miR408	Nicotiana tabacum		322.23	2916.69	14.15	91.17	34.23	147.53	331.9	1192.73
dof-miR-804	smo-miR408	Selaginella moellendorffii	TGCACTGCCTCTCCCTGGCTG	0.2	1.02	0	0	0	0.1	0.17	0
dof-miR-805	gga-miR-455-3p	Gallus gallus	TGCAGTCCATGGGCATATACAC	0	0	0	0	0	0	0.17	0
dof-miR-806	osa-miR444b.2	Oryza sativa	TGCAGTTGTTGTCTCAAGCTT	0	0	0	0	0	0.1	0	0

	osa-miR444c.2	Oryza sativa		0	0	0	0	0	0.1	0	0
	bdi-miR444c	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	bdi-miR444d	Brachypodium distachyon		0	0	0	0	0	0.1	0	0
	zma-miR444a	Zea mays		0	0	0	0	0	0.1	0	0
	zma-miR444b	Zea mays		0	0	0	0	0	0.1	0	0
	ssp-miR444c-3p	Saccharum sp.		0	0	0	0	0	0.1	0	0
dof-miR-807	tcc-miR530a	Theobroma cacao	TGCATTGCACCTGCACCTC	0	0	0	2.88	0	0	0	0
dof-miR-808	ptc-miR530a	Populus trichocarpa	TGCAATTGCACCTGCACCTT	0	0	0.18	0	0	0	0	0
	mes-miR530a	Manihot esculenta		0	0	0.18	0	0	0	0	0
	mes-miR530b	Manihot esculenta		0	0	0.18	0	0	0	0	0
	htu-miR530	Helianthus tuberosus		0	0	0.18	0	0	0	0	0
	cme-miR530a	Cucumis melo		0	0	0.18	0	0	0	0	0
	lus-miR530a	Linum usitatissimum		0	0	0.18	0	0	0	0	0
	lus-miR530b	Linum usitatissimum		0	0	0.18	0	0	0	0	0
	tcc-miR530b	Theobroma cacao		0	0	0.18	0	0	0	0	0
dof-miR-809	tae-miR399	Triticum aestivum	TGCCAAAGGAGAATTGCC	0.2	0	0.18	0.36	0	0	0.17	0
dof-miR-810	ssl-miR399	Salvia sclarea	TGCCAAAGGAGAATTGCCCGG	0	0	0	0.18	0	0	0	0
dof-miR-811	osa-miR399a	Oryza sativa	TGCCAAAGGAGAATTGCCCTG	0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	osa-miR399b	Oryza sativa		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	osa-miR399c	Oryza sativa		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	sbi-miR399a	Sorghum bicolor		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	sbi-miR399c	Sorghum bicolor		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	zma-miR399a-3p	Zea mays		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	zma-miR399c-3p	Zea mays		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	sbi-miR399h	Sorghum bicolor		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	ptc-miR399f	Populus trichocarpa		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	ptc-miR399g	Populus trichocarpa		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	vvi-miR399a	Vitis vinifera		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	vvi-miR399h	Vitis vinifera		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	bdi-miR399c	Brachypodium distachyon		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	gma-miR399i	Glycine max		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	ata-miR399b-3p	Aegilops tauschii		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	ata-miR399a-3p	Aegilops tauschii		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
mdm-miR399a	Malus domestica	0.2	22.15	3.31	42.16	2.33	3.13	1	3.64		

	mdm-miR399b	Malus domestica		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	mdm-miR399c	Malus domestica		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	vun-miR399b	Vigna unguiculata		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	mes-miR399a	Manihot esculenta		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	lus-miR399b	Linum usitatissimum		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	lus-miR399d	Linum usitatissimum		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	tcc-miR399g	Theobroma cacao		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	bdi-miR399b	Brachypodium distachyon		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	csi-miR399e	Citrus sinensis		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	csi-miR399c	Citrus sinensis		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	zma-miR399h-3p	Zea mays		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
	sbi-miR399j	Sorghum bicolor		0.2	22.15	3.31	42.16	2.33	3.13	1	3.64
dof-miR-812	ath-miR399b	Arabidopsis thaliana	TGCCAAAGGAGAGTTGCCCTG	0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	ath-miR399c-3p	Arabidopsis thaliana		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	osa-miR399d	Oryza sativa		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	sbi-miR399d	Sorghum bicolor		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	zma-miR399e-3p	Zea mays		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	sbi-miR399i	Sorghum bicolor		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	mtr-miR399l	Medicago truncatula		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	mtr-miR399p	Medicago truncatula		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	vvi-miR399b	Vitis vinifera		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	mes-miR399f	Manihot esculenta		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	mdm-miR399i	Malus domestica		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	mdm-miR399j	Malus domestica		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	vun-miR399a	Vigna unguiculata		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	gma-miR399a	Glycine max		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	gma-miR399b	Glycine max		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	gma-miR399c	Glycine max		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	gma-miR399h	Glycine max		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	tcc-miR399i	Theobroma cacao		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	csi-miR399d	Citrus sinensis		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
	zma-miR399i-3p	Zea mays		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14
zma-miR399j-3p	Zea mays	0	1.27	0.18	0.18	0.19	0.21	0.17	0.14		
rco-miR399a	Ricinus communis	0	1.27	0.18	0.18	0.19	0.21	0.17	0.14		

	aly-miR399b-3p	Arabidopsis lyrata		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14	
	aly-miR399c-3p	Arabidopsis lyrata		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14	
	vvi-miR399c	Vitis vinifera		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14	
	pvu-miR399a	Phaseolus vulgaris		0	1.27	0.18	0.18	0.19	0.21	0.17	0.14	
dof-miR-813	osa-miR399e	Oryza sativa	TGCCAAAGGAGATTTGCCAG	0.2	0	0	0	0	0	0	1.82	
	osa-miR399f	Oryza sativa		0.2	0	0	0	0	0	0	0	1.82
	osa-miR399g	Oryza sativa		0.2	0	0	0	0	0	0	0	1.82
	sbi-miR399e	Sorghum bicolor		0.2	0	0	0	0	0	0	0	1.82
	sbi-miR399f	Sorghum bicolor		0.2	0	0	0	0	0	0	0	1.82
	mtr-miR399a	Medicago truncatula		0.2	0	0	0	0	0	0	0	1.82
	mtr-miR399e	Medicago truncatula		0.2	0	0	0	0	0	0	0	1.82
	mtr-miR399f	Medicago truncatula		0.2	0	0	0	0	0	0	0	1.82
	mtr-miR399g	Medicago truncatula		0.2	0	0	0	0	0	0	0	1.82
	mtr-miR399s-3p	Medicago truncatula		0.2	0	0	0	0	0	0	0	1.82
	mtr-miR399t-3p	Medicago truncatula		0.2	0	0	0	0	0	0	0	1.82
	gma-miR399d	Glycine max		0.2	0	0	0	0	0	0	0	1.82
	gma-miR399e	Glycine max		0.2	0	0	0	0	0	0	0	1.82
	gma-miR399f	Glycine max		0.2	0	0	0	0	0	0	0	1.82
	gma-miR399g	Glycine max		0.2	0	0	0	0	0	0	0	1.82
	lus-miR399f	Linum usitatissimum		0.2	0	0	0	0	0	0	0	1.82
	lus-miR399g	Linum usitatissimum		0.2	0	0	0	0	0	0	0	1.82
rco-miR399e	Ricinus communis	0.2	0	0	0	0	0	0	0	1.82		
dof-miR-814	ssa-miR-24a-5p	Salmo salar	TGCCTACTGAACTGGTATCAGT	0	0	0	0	0	0	0.17	0	
dof-miR-815	osa-miR160f-5p	Oryza sativa	TGCCCTGGCTCCCTGAATGCCA	0	0	0.18	0.18	0	0	0	0	
	ptc-miR160e-5p	Populus trichocarpa		0	0	0.18	0.18	0	0	0	0	
	ptc-miR160f	Populus trichocarpa		0	0	0.18	0.18	0	0	0	0	
	mtr-miR160c	Medicago truncatula		0	0	0.18	0.18	0	0	0	0	
	cpa-miR160d	Carica papaya		0	0	0.18	0.18	0	0	0	0	
	cme-miR160d	Cucumis melo		0	0	0.18	0.18	0	0	0	0	
	tcc-miR160a	Theobroma cacao		0	0	0.18	0.18	0	0	0	0	
	bdi-miR160e-5p	Brachypodium distachyon		0	0	0.18	0.18	0	0	0	0	
	ahy-miR160-5p	Arachis hypogaea		0	0	0.18	0.18	0	0	0	0	
	rco-miR160c	Ricinus communis		0	0	0.18	0.18	0	0	0	0	
	sbi-miR160f	Sorghum bicolor		0	0	0.18	0.18	0	0	0	0	

dof-miR-816	bdi-miR160f	Brachypodium distachyon	TGCCTGGCTCCCTGTATGCC	2.18	1.27	2.76	2.16	1.68	3.03	3.17	1.4
	htu-miR160a	Helianthus tuberosus		2.18	1.27	2.76	2.16	1.68	3.03	3.17	1.4
	gma-miR160b	Glycine max		2.18	1.27	2.76	2.16	1.68	3.03	3.17	1.4
	gma-miR160c	Glycine max		2.18	1.27	2.76	2.16	1.68	3.03	3.17	1.4
	gma-miR160d	Glycine max		2.18	1.27	2.76	2.16	1.68	3.03	3.17	1.4
	gma-miR160e	Glycine max		2.18	1.27	2.76	2.16	1.68	3.03	3.17	1.4
dof-miR-817	ath-miR160a-5p	Arabidopsis thaliana	TGCCTGGCTCCCTGTATGCCA	1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	ath-miR160b	Arabidopsis thaliana		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	ath-miR160c-5p	Arabidopsis thaliana		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	osa-miR160a-5p	Oryza sativa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	osa-miR160b-5p	Oryza sativa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	osa-miR160c-5p	Oryza sativa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	osa-miR160d-5p	Oryza sativa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	zma-miR160a-5p	Zea mays		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	zma-miR160c-5p	Zea mays		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	zma-miR160d-5p	Zea mays		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	zma-miR160b-5p	Zea mays		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	zma-miR160e	Zea mays		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	sbi-miR160d	Sorghum bicolor		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	sbi-miR160a	Sorghum bicolor		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	sbi-miR160c	Sorghum bicolor		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	sbi-miR160b	Sorghum bicolor		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	sbi-miR160e	Sorghum bicolor		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	mtr-miR160a	Medicago truncatula		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	gma-miR160a-5p	Glycine max		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	ptc-miR160a	Populus trichocarpa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	ptc-miR160b-5p	Populus trichocarpa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	ptc-miR160c-5p	Populus trichocarpa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	ptc-miR160d	Populus trichocarpa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	mtr-miR160b	Medicago truncatula		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	mtr-miR160d	Medicago truncatula		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	mtr-miR160e	Medicago truncatula		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	ppt-miR160a	Physcomitrella patens		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
ppt-miR160e	Physcomitrella patens	1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76		

	bnamiR160c	Brassica napus		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	bnamiR160d	Brassica napus		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	cca-miR160b	Cynara cardunculus		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	lus-miR160a	Linum usitatissimum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	lus-miR160b	Linum usitatissimum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	lus-miR160d	Linum usitatissimum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	lus-miR160e	Linum usitatissimum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	lus-miR160f	Linum usitatissimum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	lus-miR160h	Linum usitatissimum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	lus-miR160i	Linum usitatissimum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	lus-miR160j	Linum usitatissimum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	nta-miR160a	Nicotiana tabacum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	nta-miR160b	Nicotiana tabacum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	nta-miR160c	Nicotiana tabacum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	gma-miR160f	Glycine max		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	tcc-miR160b	Theobroma cacao		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	bdi-miR160a-5p	Brachypodium distachyon		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	bdi-miR160b-5p	Brachypodium distachyon		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	bdi-miR160c-5p	Brachypodium distachyon		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	bdi-miR160d-5p	Brachypodium distachyon		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	pab-miR160a	Picea abies		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	pab-miR160b	Picea abies		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	ttu-miR160	Triticum turgidum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	far-miR160	Festuca arundinacea		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	zma-miR160g-5p	Zea mays		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	rco-miR160a	Ricinus communis		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	rco-miR160b	Ricinus communis		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	aly-miR160a-5p	Arabidopsis lyrata		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	aly-miR160b-5p	Arabidopsis lyrata		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	aly-miR160c-5p	Arabidopsis lyrata		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	sly-miR160a	Solanum lycopersicum		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	bra-miR160a-5p	Brassica rapa		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
	aqc-miR160b	Aquilegia caerulea		1.98	3.82	12.49	7.39	5.32	7.41	4.17	4.76
dof-miR-818	cgr-miR-744-5p	Cricetulus griseus	TGCGGGGCTAGGGCTAACAGC	0	0	0	0.18	0.47	0	0.17	0

dof-miR-819	mtr-miR156b-3p	Medicago truncatula	TGCTCACTCTCTATCTGTCACC	0	0.25	0	0	0	0	0.33	6.03
dof-miR-820	ssa-miR-222a-5p	Salmo salar	TGCTCAGTAGGCAGTGTAGATCCT	0	0	0	0	0	0	0.17	0
dof-miR-821	ssa-miR-222b-5p	Salmo salar	TGCTCAGTAGTCAGTGTAGATC	0	0	0	0	0	0	0.17	0
	ipu-miR-222a	Ictalurus punctatus		0	0	0	0	0	0	0	0.17
dof-miR-822	dre-miR-222a-5p	Danio rerio	TGCTCAGTAGTCAGTGTAGATCC	0	0	0	0.18	0	0	0	0
dof-miR-823	mtr-miR156c-3p	Medicago truncatula	TGCTTACTCTCTATCTGTCACC	0	0	0	0	0	0	0	0.14
dof-miR-824	ggo-miR-7	Gorilla gorilla	TGGAAGACTAGTGATTTTGT	0	0	0.18	0.18	0	0.21	0	0.14
	ppy-miR-7	Pongo pygmaeus		0	0	0.18	0.18	0	0.21	0	0.14
	sla-miR-7	Saguinus labiatus		0	0	0.18	0.18	0	0.21	0	0.14
	lla-miR-7	Lagothrix lagotricha		0	0	0.18	0.18	0	0.21	0	0.14
	mne-miR-7	Macaca nemestrina		0	0	0.18	0.18	0	0.21	0	0.14
	ppa-miR-7	Pan paniscus		0	0	0.18	0.18	0	0.21	0	0.14
	fru-miR-7	Fugu rubripes		0	0	0.18	0.18	0	0.21	0	0.14
dof-miR-825	gga-miR-7	Gallus gallus	TGGAAGACTAGTGATTTTGTG	0	0	0	0.72	0	0	0	0.28
	xtr-miR-7	Xenopus tropicalis		0	0	0	0.72	0	0	0	0.28
	mdo-miR-7	Monodelphis domestica		0	0	0	0.72	0	0	0	0.28
	odi-miR-7	Oikopleura dioica		0	0	0	0.72	0	0	0	0.28
	cin-miR-7-5p	Ciona intestinalis		0	0	0	0.72	0	0	0	0.28
	hme-miR-7	Heliconius melpomene		0	0	0	0.72	0	0	0	0.28
dof-miR-826	dme-miR-7-5p	Drosophila melanogaster	TGGAAGACTAGTGATTTTGTG	0	0	0.37	0.18	0.09	0.1	0.17	0.28
	hsa-miR-7-5p	Homo sapiens		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	rno-miR-7a-5p	Rattus norvegicus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	mmu-miR-7a-5p	Mus musculus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dps-miR-7	Drosophila pseudoobscura		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dre-miR-7a	Danio rerio		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	ame-miR-7	Apis mellifera		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	aga-miR-7	Anopheles gambiae		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	ptr-miR-7	Pan troglodytes		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	tmi-miR-7	Tetraodon nigroviridis		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	bmo-miR-7-5p	Bombyx mori		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	oan-miR-7-5p	Ornithorhynchus anatinus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	bbe-miR-7-5p	Branchiostoma belcheri		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	ssa-miR-7a-5p	Salmo salar		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	ipu-miR-7a	Ictalurus punctatus		0	0	0.37	0.18	0.09	0.1	0.17	0.28

	pmi-miR-7-5p	Patiria miniata		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	lva-miR-7-5p	Lytechinus variegatus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	cgr-miR-7a	Cricetulus griseus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	pma-miR-7a-5p	Petromyzon marinus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	aca-miR-7-5p	Anolis carolinensis		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	nvi-miR-7	Nasonia vitripennis		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	nlo-miR-7	Nasonia longicornis		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dpu-miR-7	Daphnia pulex		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	isc-miR-7	Ixodes scapularis		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	eca-miR-7	Equus caballus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	aae-miR-7	Aedes aegypti		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	cqu-miR-7	Culex quinquefasciatus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	tgu-miR-7-5p	Taeniopygia guttata		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	csa-miR-7	Ciona savignyi		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	mml-miR-7	Macaca mulatta		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	cfa-miR-7	Canis familiaris		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dan-miR-7	Drosophila ananassae		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	der-miR-7	Drosophila erecta		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dgr-miR-7	Drosophila grimshawi		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dmo-miR-7	Drosophila mojaveensis		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dpe-miR-7	Drosophila persimilis		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dse-miR-7	Drosophila sechellia		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dsi-miR-7	Drosophila simulans		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dwi-miR-7	Drosophila willistoni		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	dya-miR-7	Drosophila yakuba		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	bfl-miR-7	Branchiostoma floridae		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	sko-miR-7-5p	Saccoglossus kowalevskii		0	0	0.37	0.18	0.09	0.1	0.17	0.28
	spu-miR-7	Strongylocentrotus purpuratus		0	0	0.37	0.18	0.09	0.1	0.17	0.28
dof-miR-827	ssc-miR-7	Sus scrofa	TGGAAGACTAGTGATTTTGTGTT	0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	bta-miR-7	Bos taurus		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	chi-miR-7-5p	Capra hircus		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	tch-miR-7-5p	Tupaia chinensis		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	oha-miR-7-5p	Ophiophagus hannah		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	ccr-miR-7a	Cyprinus carpio		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56

	tur-miR-7-5p	Tetranychus urticae		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	mse-miR-7	Manduca sexta		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	api-miR-7	Acyrtosiphon pisum		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	dvi-miR-7-5p	Drosophila virilis		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
	lgi-miR-7	Lottia gigantea		0.4	1.02	0.37	0	1.03	0.52	0.83	0.56
dof-miR-828	efu-miR-7b	Eptesicus fuscus	TGGAAGACTAGTGATTTGTGTGT	0	0	0	0	0.19	0.31	0	0
dof-miR-829	mmu-miR-7b-5p	Mus musculus	TGGAAGACTTGTGATTTGTGTGT	0	0	0.37	0.9	0	0	0	0.14
	rno-miR-7b	Rattus norvegicus		0	0	0.37	0.9	0	0	0	0.14
	ipu-miR-7b	Ictalurus punctatus		0	0	0.37	0.9	0	0	0	0.14
	ccr-miR-7b	Cyprinus carpio		0	0	0.37	0.9	0	0	0	0.14
	bma-miR-7	Brugia malayi		0	0	0.37	0.9	0	0	0	0.14
dof-miR-830	cgr-miR-7b	Cricetulus griseus	TGGAAGACTTGTGATTTGTGTGT	0	0	0.37	0.36	0	0	0	0
dof-miR-831	osa-miR528-5p	Oryza sativa	TGGAAGGGGCATGCAGAGGAG	1469.16	4641.45	646.54	5.41	352.82	1246.83	991.35	4676.9
	ata-miR528-5p	Aegilops tauschii		1469.16	4641.45	646.54	5.41	352.82	1246.83	991.35	4676.9
	bdi-miR528-5p	Brachypodium distachyon		1469.16	4641.45	646.54	5.41	352.82	1246.83	991.35	4676.9
	ssp-miR528	Saccharum sp.		1469.16	4641.45	646.54	5.41	352.82	1246.83	991.35	4676.9
	zma-miR528a-5p	Zea mays		1469.16	4641.45	646.54	5.41	352.82	1246.83	991.35	4676.9
	zma-miR528b-5p	Zea mays		1469.16	4641.45	646.54	5.41	352.82	1246.83	991.35	4676.9
	sbi-miR528	Sorghum bicolor		1469.16	4641.45	646.54	5.41	352.82	1246.83	991.35	4676.9
dof-miR-832	aga-miR-184	Anopheles gambiae	TGGACGGAGAACTGATAAGGG	0	0	0	0	2.42	6.57	0.5	0
	fru-miR-184	Fugu rubripes		0	0	0	0	2.42	6.57	0.5	0
	tmi-miR-184	Tetraodon nigroviridis		0	0	0	0	2.42	6.57	0.5	0
	ola-miR-184-3p	Oryzias latipes		0	0	0	0	2.42	6.57	0.5	0
	bfl-miR-184-3p	Branchiostoma floridae		0	0	0	0	2.42	6.57	0.5	0
dof-miR-833	dme-miR-184-3p	Drosophila melanogaster	TGGACGGAGAACTGATAAGGGC	0	0	0	0	3.26	12	0.5	0
	dps-miR-184	Drosophila pseudoobscura		0	0	0	0	3.26	12	0.5	0
	ame-miR-184	Apis mellifera		0	0	0	0	3.26	12	0.5	0
	dre-miR-184	Danio rerio		0	0	0	0	3.26	12	0.5	0
	cin-miR-184	Ciona intestinalis		0	0	0	0	3.26	12	0.5	0
	bbe-miR-184-3p	Branchiostoma belcheri		0	0	0	0	3.26	12	0.5	0
	ipu-miR-184	Ictalurus punctatus		0	0	0	0	3.26	12	0.5	0
	pmi-miR-184-3p	Patiria miniata		0	0	0	0	3.26	12	0.5	0
	lva-miR-184-3p	Lytechinus variegatus		0	0	0	0	3.26	12	0.5	0
	hme-miR-184	Heliconius melpomene		0	0	0	0	3.26	12	0.5	0

	ccr-miR-184	Cyprinus carpio		0	0	0	0	3.26	12	0.5	0
	tur-miR-184-3p	Tetranychus urticae		0	0	0	0	3.26	12	0.5	0
	mse-miR-184	Manduca sexta		0	0	0	0	3.26	12	0.5	0
	nvi-miR-184	Nasonia vitripennis		0	0	0	0	3.26	12	0.5	0
	ngi-miR-184	Nasonia giraulti		0	0	0	0	3.26	12	0.5	0
	nlo-miR-184	Nasonia longicornis		0	0	0	0	3.26	12	0.5	0
	isc-miR-184	Ixodes scapularis		0	0	0	0	3.26	12	0.5	0
	api-miR-184a	Acyrtosiphon pisum		0	0	0	0	3.26	12	0.5	0
	aae-miR-184	Aedes aegypti		0	0	0	0	3.26	12	0.5	0
	cqu-miR-184	Culex quinquefasciatus		0	0	0	0	3.26	12	0.5	0
	tca-miR-184-3p	Tribolium castaneum		0	0	0	0	3.26	12	0.5	0
	dan-miR-184-3p	Drosophila ananassae		0	0	0	0	3.26	12	0.5	0
	der-miR-184-3p	Drosophila erecta		0	0	0	0	3.26	12	0.5	0
	dgr-miR-184-3p	Drosophila grimshawi		0	0	0	0	3.26	12	0.5	0
	dmo-miR-184-3p	Drosophila mojavensis		0	0	0	0	3.26	12	0.5	0
	dpe-miR-184-3p	Drosophila persimilis		0	0	0	0	3.26	12	0.5	0
	dse-miR-184-3p	Drosophila sechellia		0	0	0	0	3.26	12	0.5	0
	dsi-miR-184-3p	Drosophila simulans		0	0	0	0	3.26	12	0.5	0
	dvi-miR-184-3p	Drosophila virilis		0	0	0	0	3.26	12	0.5	0
	dwi-miR-184-3p	Drosophila willistoni		0	0	0	0	3.26	12	0.5	0
	dya-miR-184-3p	Drosophila yakuba		0	0	0	0	3.26	12	0.5	0
	cte-miR-184a	Capitella teleta		0	0	0	0	3.26	12	0.5	0
	lgi-miR-184	Lottia gigantea		0	0	0	0	3.26	12	0.5	0
	ske-miR-184-3p	Saccoglossus kowalevskii		0	0	0	0	3.26	12	0.5	0
	spu-miR-184	Strongylocentrotus purpuratus		0	0	0	0	3.26	12	0.5	0
dof-miR-834	mmu-miR-184-3p	Mus musculus	TGGACGGAGAACTGATAAGGGT	0	0	0	0	0.19	0.21	0	0
	hsa-miR-184	Homo sapiens		0	0	0	0	0.19	0.21	0	0
	rno-miR-184	Rattus norvegicus		0	0	0	0	0.19	0.21	0	0
	gga-miR-184-3p	Gallus gallus		0	0	0	0	0.19	0.21	0	0
	ssc-miR-184	Sus scrofa		0	0	0	0	0.19	0.21	0	0
	ptr-miR-184	Pan troglodytes		0	0	0	0	0.19	0.21	0	0
	ppy-miR-184	Pongo pygmaeus		0	0	0	0	0.19	0.21	0	0
	mne-miR-184	Macaca nemestrina		0	0	0	0	0.19	0.21	0	0
	mdo-miR-184-3p	Monodelphis domestica		0	0	0	0	0.19	0.21	0	0

	chi-miR-184	Capra hircus		0	0	0	0	0.19	0.21	0	0
	tch-miR-184	Tupaia chinensis		0	0	0	0	0.19	0.21	0	0
	cgr-miR-184	Cricetulus griseus		0	0	0	0	0.19	0.21	0	0
	aca-miR-184-3p	Anolis carolinensis		0	0	0	0	0.19	0.21	0	0
	eca-miR-184	Equus caballus		0	0	0	0	0.19	0.21	0	0
	tgu-miR-184	Taeniopygia guttata		0	0	0	0	0.19	0.21	0	0
	mml-miR-184	Macaca mulatta		0	0	0	0	0.19	0.21	0	0
	bta-miR-184	Bos taurus		0	0	0	0	0.19	0.21	0	0
	cfa-miR-184	Canis familiaris		0	0	0	0	0.19	0.21	0	0
dof-miR-835	gma-miR164b	Glycine max	TGGAGAAGCAGGGCACGTGC	2.97	0.51	0.37	27.03	0.75	2.4	0.17	0.56
	gma-miR164c	Glycine max		2.97	0.51	0.37	27.03	0.75	2.4	0.17	0.56
	gma-miR164d	Glycine max		2.97	0.51	0.37	27.03	0.75	2.4	0.17	0.56
dof-miR-836	ath-miR164a	Arabidopsis thaliana	TGGAGAAGCAGGGCACGTGCA	19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	ath-miR164b-5p	Arabidopsis thaliana		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	osa-miR164a	Oryza sativa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	osa-miR164b	Oryza sativa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	osa-miR164f	Oryza sativa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	zma-miR164a-5p	Zea mays		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	zma-miR164d-5p	Zea mays		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	zma-miR164b-5p	Zea mays		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	zma-miR164c-5p	Zea mays		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	sbi-miR164a	Sorghum bicolor		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	ptc-miR164a	Populus trichocarpa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	ptc-miR164b	Populus trichocarpa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	ptc-miR164c	Populus trichocarpa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	ptc-miR164d	Populus trichocarpa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	ptc-miR164e	Populus trichocarpa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	mtr-miR164a	Medicago truncatula		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	mtr-miR164b	Medicago truncatula		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	mtr-miR164c	Medicago truncatula		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	tae-miR164	Triticum aestivum		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	bnm-miR164a	Brassica napus		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	vvi-miR164a	Vitis vinifera		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	vvi-miR164c	Vitis vinifera		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08

	gma-miR164g	Glycine max		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	gma-miR164h	Glycine max		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	gma-miR164i	Glycine max		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	gma-miR164j	Glycine max		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	gma-miR164k	Glycine max		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	tcc-miR164a	Theobroma cacao		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	tcc-miR164b	Theobroma cacao		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	bdi-miR164b	Brachypodium distachyon		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	bdi-miR164a-5p	Brachypodium distachyon		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	bdi-miR164e	Brachypodium distachyon		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	zma-miR164g-5p	Zea mays		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	csi-miR164	Citrus sinensis		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	ctr-miR164	Citrus trifoliata		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	rco-miR164a	Ricinus communis		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	rco-miR164b	Ricinus communis		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	rco-miR164c	Ricinus communis		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	ghr-miR164	Gossypium hirsutum		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	aly-miR164a-5p	Arabidopsis lyrata		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	aly-miR164b-5p	Arabidopsis lyrata		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	gma-miR164a	Glycine max		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	bra-miR164a	Brassica rapa		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	sbi-miR164d	Sorghum bicolor		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
	sbi-miR164e	Sorghum bicolor		19.21	75.86	26.46	1457.69	65.57	129.27	52.59	18.08
dof-miR-837	bra-miR164e-5p	Brassica rapa	TGGAGAAGCAGGGCACGTGCAA	0	0	0	0.72	0	0.1	0	0
dof-miR-838	ath-miR164c-5p	Arabidopsis thaliana	TGGAGAAGCAGGGCACGTGCG	0	0	0.18	2.34	0.19	0.21	0	0
	bra-miR164b-5p	Brassica rapa		0	0	0.18	2.34	0.19	0.21	0	0
	bra-miR164d-5p	Brassica rapa		0	0	0.18	2.34	0.19	0.21	0	0
	bra-miR164c-5p	Brassica rapa		0	0	0.18	2.34	0.19	0.21	0	0
	cln-miR164	Cunninghamia lanceolata		0	0	0.18	2.34	0.19	0.21	0	0
	bna-miR164b	Brassica napus		0	0	0.18	2.34	0.19	0.21	0	0
	bna-miR164c	Brassica napus		0	0	0.18	2.34	0.19	0.21	0	0
	bna-miR164d	Brassica napus		0	0	0.18	2.34	0.19	0.21	0	0
	aly-miR164c-5p	Arabidopsis lyrata		0	0	0.18	2.34	0.19	0.21	0	0
dof-miR-839	osa-miR164d	Oryza sativa	TGGAGAAGCAGGGCACGTGCT	0	0	0	8.65	0.28	0.42	0.17	0

	sbi-miR164b	Sorghum bicolor		0	0	0	8.65	0.28	0.42	0.17	0
	ata-miR164a-5p	Aegilops tauschii		0	0	0	8.65	0.28	0.42	0.17	0
	bdi-miR164c-5p	Brachypodium distachyon		0	0	0	8.65	0.28	0.42	0.17	0
	cme-miR164a	Cucumis melo		0	0	0	8.65	0.28	0.42	0.17	0
	zma-miR164f-5p	Zea mays		0	0	0	8.65	0.28	0.42	0.17	0
dof-miR-840	osa-miR164c	Oryza sativa	TGGAGAAGCAGGGTACGTGCA	0	0	0	0.36	0	0	0	0
	cca-miR164	Cynara cardunculus		0	0	0	0.36	0	0	0	0
dof-miR-841	mmu-miR-185-5p	Mus musculus	TGGAGAGAAAGGCAGTTCCTGA	0	0.25	0.18	0	3.73	1.67	0.17	0
	hsa-miR-185-5p	Homo sapiens		0	0.25	0.18	0	3.73	1.67	0.17	0
	rno-miR-185-5p	Rattus norvegicus		0	0.25	0.18	0	3.73	1.67	0.17	0
	tch-miR-185-5p	Tupaia chinensis		0	0.25	0.18	0	3.73	1.67	0.17	0
	cgr-miR-185-5p	Cricetulus griseus		0	0.25	0.18	0	3.73	1.67	0.17	0
	ggo-miR-185	Gorilla gorilla		0	0.25	0.18	0	3.73	1.67	0.17	0
	ppy-miR-185	Pongo pygmaeus		0	0.25	0.18	0	3.73	1.67	0.17	0
	mml-miR-185-5p	Macaca mulatta		0	0.25	0.18	0	3.73	1.67	0.17	0
	cfa-miR-185	Canis familiaris		0	0.25	0.18	0	3.73	1.67	0.17	0
	ssc-miR-185	Sus scrofa		0	0.25	0.18	0	3.73	1.67	0.17	0
	ptr-miR-185	Pan troglodytes		0	0.25	0.18	0	3.73	1.67	0.17	0
	bta-miR-185	Bos taurus		0	0.25	0.18	0	3.73	1.67	0.17	0
dof-miR-842	efu-miR-185	Eptesicus fuscus	TGGAGAGAAAGGCAGTTCCTGAT	0	0	0.18	0	0.28	0.1	0	0
dof-miR-843	tch-miR-122-5p	Tupaia chinensis	TGGAGTGTGACAATGGTGTTT	1.98	2.04	0.37	0	13.06	6.89	0.5	2.24
	ipu-miR-122	Ictalurus punctatus		1.98	2.04	0.37	0	13.06	6.89	0.5	2.24
	ccr-miR-122	Cyprinus carpio		1.98	2.04	0.37	0	13.06	6.89	0.5	2.24
	cgr-miR-122	Cricetulus griseus		1.98	2.04	0.37	0	13.06	6.89	0.5	2.24
dof-miR-844	mmu-miR-122-5p	Mus musculus	TGGAGTGTGACAATGGTGTTTG	0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	hsa-miR-122-5p	Homo sapiens		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	rno-miR-122-5p	Rattus norvegicus		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	dre-miR-122	Danio rerio		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	fru-miR-122	Fugu rubripes		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	tmi-miR-122	Tetraodon nigroviridis		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	bta-miR-122	Bos taurus		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	oan-miR-122-5p	Ornithorhynchus anatinus		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	chi-miR-122	Capra hircus		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	ssa-miR-122-5p	Salmo salar		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98

	pol-miR-122-5p	Paralichthys olivaceus		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	ggo-miR-122	Gorilla gorilla		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	aca-miR-122-5p	Anolis carolinensis		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	ppy-miR-122	Pongo pygmaeus		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	eca-miR-122	Equus caballus		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	tgu-miR-122-5p	Taeniopygia guttata		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	mml-miR-122a-5p	Macaca mulatta		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	cfa-miR-122	Canis familiaris		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
	ptr-miR-122	Pan troglodytes		0.79	2.04	0	0.36	3.08	2.71	1.17	0.98
dof-miR-845	gga-miR-122-5p	Gallus gallus	TGGAGTGTGACAATGGTGTTTGT	1.98	4.33	0.18	0	10.45	5.63	1.5	1.82
	ssc-miR-122	Sus scrofa		1.98	4.33	0.18	0	10.45	5.63	1.5	1.82
	xtr-miR-122	Xenopus tropicalis		1.98	4.33	0.18	0	10.45	5.63	1.5	1.82
dof-miR-846	oha-miR-122-5p	Ophiophagus hannah	TGGAGTGTGACAATGGTGTTTGTAT	0	0	0	0	0	0.21	0	0
dof-miR-847	bta-miR-2320-5p	Bos taurus	TGGCACAGGGTCCAGCTGTCGGC	0	0	0.18	0	0	0	0	0
dof-miR-848	hsa-miR-449a	Homo sapiens	TGGCAGTGTATTGTTAGCTGGT	0	0	0.18	0.18	0	0	0	0
	mmu-miR-449a-5p	Mus musculus		0	0	0.18	0.18	0	0	0	0
	rno-miR-449a-5p	Rattus norvegicus		0	0	0.18	0.18	0	0	0	0
	cfa-miR-449a	Canis familiaris		0	0	0.18	0.18	0	0	0	0
	mdo-miR-449a-5p	Monodelphis domestica		0	0	0.18	0.18	0	0	0	0
	ppy-miR-449a	Pongo pygmaeus		0	0	0.18	0.18	0	0	0	0
	eca-miR-449a	Equus caballus		0	0	0.18	0.18	0	0	0	0
	mml-miR-449a-5p	Macaca mulatta		0	0	0.18	0.18	0	0	0	0
bta-miR-449a	Bos taurus	0	0	0.18	0.18	0	0	0	0	0	
dof-miR-849	hsa-miR-34a-5p	Homo sapiens	TGGCAGTGTCTTAGCTGGTTGT	0	0	0.55	0.18	0	0.1	0	0
	mmu-miR-34a-5p	Mus musculus		0	0	0.55	0.18	0	0.1	0	0
	rno-miR-34a-5p	Rattus norvegicus		0	0	0.55	0.18	0	0.1	0	0
	dre-miR-34a	Danio rerio		0	0	0.55	0.18	0	0.1	0	0
	ggo-miR-34a	Gorilla gorilla		0	0	0.55	0.18	0	0.1	0	0
	age-miR-34a	Ateles geoffroyi		0	0	0.55	0.18	0	0.1	0	0
	ppa-miR-34a	Pan paniscus		0	0	0.55	0.18	0	0.1	0	0
	ppy-miR-34a	Pongo pygmaeus		0	0	0.55	0.18	0	0.1	0	0
	ptr-miR-34a	Pan troglodytes		0	0	0.55	0.18	0	0.1	0	0
	mml-miR-34a-5p	Macaca mulatta		0	0	0.55	0.18	0	0.1	0	0
	sla-miR-34a	Saguinus labiatus		0	0	0.55	0.18	0	0.1	0	0

	lla-miR-34a	Lagothrix lagotricha		0	0	0.55	0.18	0	0.1	0	0
	mne-miR-34a	Macaca nemestrina		0	0	0.55	0.18	0	0.1	0	0
	bta-miR-34a	Bos taurus		0	0	0.55	0.18	0	0.1	0	0
	chi-miR-34a	Capra hircus		0	0	0.55	0.18	0	0.1	0	0
	ipu-miR-34a	Ictalurus punctatus		0	0	0.55	0.18	0	0.1	0	0
	ccr-miR-34	Cyprinus carpio		0	0	0.55	0.18	0	0.1	0	0
	cgr-miR-34a	Cricetulus griseus		0	0	0.55	0.18	0	0.1	0	0
	eca-miR-34a	Equus caballus		0	0	0.55	0.18	0	0.1	0	0
	tgu-miR-34a	Taeniopygia guttata		0	0	0.55	0.18	0	0.1	0	0
	cfa-miR-34a	Canis familiaris		0	0	0.55	0.18	0	0.1	0	0
	ssc-miR-34a	Sus scrofa		0	0	0.55	0.18	0	0.1	0	0
dof-miR-850	gga-miR-34a-5p	Gallus gallus	TGGCAGTGTCTTAGCTGGTTGTT	0	0	0	0.18	0	0	0	0
	xtr-miR-34a	Xenopus tropicalis		0	0	0	0.18	0	0	0	0
	mdo-miR-34a-5p	Monodelphis domestica		0	0	0	0.18	0	0	0	0
	tch-miR-34a-5p	Tupaia chinensis		0	0	0	0.18	0	0	0	0
	oha-miR-34a-5p	Ophiophagus hannah		0	0	0	0.18	0	0	0	0
dof-miR-851	sha-miR-24	Sarcophilus harrisi	TGGCTCAGTTCAGCAGGAA	0	0	0	0	0.09	0	0	0
dof-miR-852	chi-miR-24-3p	Capra hircus	TGGCTCAGTTCAGCAGGAAC	0.79	0.76	2.94	4.32	2.98	0.42	0.5	0.28
	ssa-miR-24a-3p	Salmo salar		0.79	0.76	2.94	4.32	2.98	0.42	0.5	0.28
	ipu-miR-24b	Ictalurus punctatus		0.79	0.76	2.94	4.32	2.98	0.42	0.5	0.28
dof-miR-853	hsa-miR-24-3p	Homo sapiens	TGGCTCAGTTCAGCAGGAACAG	0	0	0.55	0.18	0.47	0.31	0	0
	mmu-miR-24-3p	Mus musculus		0	0	0.55	0.18	0.47	0.31	0	0
	rno-miR-24-3p	Rattus norvegicus		0	0	0.55	0.18	0.47	0.31	0	0
	gga-miR-24-3p	Gallus gallus		0	0	0.55	0.18	0.47	0.31	0	0
	dre-miR-24	Danio rerio		0	0	0.55	0.18	0.47	0.31	0	0
	ssc-miR-24-3p	Sus scrofa		0	0	0.55	0.18	0.47	0.31	0	0
	mml-miR-24-3p	Macaca mulatta		0	0	0.55	0.18	0.47	0.31	0	0
	ppy-miR-24-3p	Pongo pygmaeus		0	0	0.55	0.18	0.47	0.31	0	0
	mne-miR-24-3p	Macaca nemestrina		0	0	0.55	0.18	0.47	0.31	0	0
	ppa-miR-24-3p	Pan paniscus		0	0	0.55	0.18	0.47	0.31	0	0
	ggo-miR-24	Gorilla gorilla		0	0	0.55	0.18	0.47	0.31	0	0
	ptr-miR-24	Pan troglodytes		0	0	0.55	0.18	0.47	0.31	0	0
	fru-miR-24-3p	Fugu rubripes		0	0	0.55	0.18	0.47	0.31	0	0
	tmi-miR-24	Tetraodon nigroviridis		0	0	0.55	0.18	0.47	0.31	0	0

	xtr-miR-24a-3p	Xenopus tropicalis		0	0	0.55	0.18	0.47	0.31	0	0
	bta-miR-24-3p	Bos taurus		0	0	0.55	0.18	0.47	0.31	0	0
	oan-miR-24-3p	Ornithorhynchus anatinus		0	0	0.55	0.18	0.47	0.31	0	0
	ccr-miR-24	Cyprinus carpio		0	0	0.55	0.18	0.47	0.31	0	0
	ola-miR-24a	Oryzias latipes		0	0	0.55	0.18	0.47	0.31	0	0
	pma-miR-24	Petromyzon marinus		0	0	0.55	0.18	0.47	0.31	0	0
	aca-miR-24-3p	Anolis carolinensis		0	0	0.55	0.18	0.47	0.31	0	0
	eca-miR-24	Equus caballus		0	0	0.55	0.18	0.47	0.31	0	0
	tgu-miR-24-3p	Taeniopygia guttata		0	0	0.55	0.18	0.47	0.31	0	0
dof-miR-854	chi-miR-144-5p	Capra hircus	TGGGATATCATCATATACTGT	0	0	0	0	0	0	0.17	0
dof-miR-855	aca-miR-193-5p	Anolis carolinensis	TGGGTCTTTGCGGGCGAGATG	0	0	0	0	0.09	0	0	0
dof-miR-856	hsa-miR-193a-5p	Homo sapiens	TGGGTCTTTGCGGGCGAGATGA	0	0	0	0	0.09	0	0	0
	bta-miR-193a-5p	Bos taurus		0	0	0	0	0.09	0	0	0
	oha-miR-193-5p	Ophiophagus hannah		0	0	0	0	0.09	0	0	0
	ppy-miR-193a-5p	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	eca-miR-193a-5p	Equus caballus		0	0	0	0	0.09	0	0	0
	ssc-miR-193a-5p	Sus scrofa		0	0	0	0	0.09	0	0	0
	tgu-miR-193b-5p	Taeniopygia guttata		0	0	0	0	0.09	0	0	0
	gga-miR-193a-5p	Gallus gallus		0	0	0	0	0.09	0	0	0
	mml-miR-193a-5p	Macaca mulatta		0	0	0	0	0.09	0	0	0
cfa-miR-193a	Canis familiaris	0	0	0	0	0.09	0	0	0		
dof-miR-857	hsa-miR-629-5p	Homo sapiens	TGGGTTTACGTTGGGAGAACT	0	0	0	0	0.09	0.1	0	0
dof-miR-858	hme-miR-2765	Heliconius melpomene	TGGTAACTCCACCACCGTTGGC	0	0	0	0	0	0	0.67	0
	ame-miR-2765-5p	Apis mellifera		0	0	0	0	0	0	0.67	0
	mse-miR-2765	Manduca sexta		0	0	0	0	0	0	0.67	0
	tca-miR-2765-5p	Tribolium castaneum		0	0	0	0	0	0	0.67	0
	bmo-miR-2765	Bombyx mori		0	0	0	0	0	0	0.67	0
	aae-miR-2765	Aedes aegypti		0	0	0	0	0	0	0.67	0
dof-miR-859	hsa-miR-379-5p	Homo sapiens	TGGTAGACTATGGAACGTAGG	0	0	0	0.18	0.09	0	0	0
	mmu-miR-379-5p	Mus musculus		0	0	0	0.18	0.09	0	0	0
	rno-miR-379-5p	Rattus norvegicus		0	0	0	0.18	0.09	0	0	0
	chi-miR-379-5p	Capra hircus		0	0	0	0.18	0.09	0	0	0
	cgr-miR-379	Cricetulus griseus		0	0	0	0.18	0.09	0	0	0
	ggo-miR-379	Gorilla gorilla		0	0	0	0.18	0.09	0	0	0

	ppy-miR-379	Pongo pygmaeus		0	0	0	0.18	0.09	0	0	0
	eca-miR-379	Equus caballus		0	0	0	0.18	0.09	0	0	0
	mml-miR-379-5p	Macaca mulatta		0	0	0	0.18	0.09	0	0	0
	cfa-miR-379	Canis familiaris		0	0	0	0.18	0.09	0	0	0
	ptr-miR-379	Pan troglodytes		0	0	0	0.18	0.09	0	0	0
	bta-miR-379	Bos taurus		0	0	0	0.18	0.09	0	0	0
dof-miR-860	hsa-miR-412-5p	Homo sapiens	TGGTCGACCAGTTGGAAAGTAAT	0	0	0	0.72	0	0	0	0
	efu-miR-412	Eptesicus fuscus		0	0	0	0.72	0	0	0	0
	chi-miR-412-5p	Capra hircus		0	0	0	0.72	0	0	0	0
	oar-miR-412-3p	Ovis aries		0	0	0	0.72	0	0	0	0
dof-miR-861	chi-miR-30f-5p	Capra hircus	TGTAACACCCCTACACTCTCAGC	0	0	0.55	0.18	0	0	0	0
	pma-miR-30f	Petromyzon marinus		0	0	0.55	0.18	0	0	0	0
dof-miR-862	bta-miR-30f	Bos taurus	TGTAACACCCCTACACTCTCAGCT	0	0	0	0.9	0	0	0	0
dof-miR-863	oar-miR-30d	Ovis aries	TGTAACATCCCCGACTGG	0	0	0	0.18	0.19	0	0	0
dof-miR-864	hsa-miR-30d-5p	Homo sapiens		0	0.25	0.55	0.36	0.75	0.1	0	0
	mmu-miR-30d-5p	Mus musculus		0	0.25	0.55	0.36	0.75	0.1	0	0
	rno-miR-30d-5p	Rattus norvegicus		0	0.25	0.55	0.36	0.75	0.1	0	0
	gga-miR-30d	Gallus gallus		0	0.25	0.55	0.36	0.75	0.1	0	0
	dre-miR-30d	Danio rerio		0	0.25	0.55	0.36	0.75	0.1	0	0
	ptr-miR-30d	Pan troglodytes		0	0.25	0.55	0.36	0.75	0.1	0	0
	ggo-miR-30d	Gorilla gorilla		0	0.25	0.55	0.36	0.75	0.1	0	0
	mne-miR-30d	Macaca nemestrina	TGTAACATCCCCGACTGGAAG	0	0.25	0.55	0.36	0.75	0.1	0	0
	ppa-miR-30d	Pan paniscus		0	0.25	0.55	0.36	0.75	0.1	0	0
	fru-miR-30d	Fugu rubripes		0	0.25	0.55	0.36	0.75	0.1	0	0
	tmi-miR-30d	Tetraodon nigroviridis		0	0.25	0.55	0.36	0.75	0.1	0	0
	xtr-miR-30d	Xenopus tropicalis		0	0.25	0.55	0.36	0.75	0.1	0	0
	aca-miR-30d-5p	Anolis carolinensis		0	0.25	0.55	0.36	0.75	0.1	0	0
	ppy-miR-30d	Pongo pygmaeus		0	0.25	0.55	0.36	0.75	0.1	0	0
	eca-miR-30d	Equus caballus		0	0.25	0.55	0.36	0.75	0.1	0	0
	mml-miR-30d-5p	Macaca mulatta		0	0.25	0.55	0.36	0.75	0.1	0	0
dof-miR-865	oan-miR-30d-5p	Ornithorhynchus anatinus		0	0.51	1.29	1.8	1.96	0.63	0.5	0.42
	ccr-miR-30d	Cyprinus carpio	TGTAACATCCCCGACTGGAAGC	0	0.51	1.29	1.8	1.96	0.63	0.5	0.42
	ola-miR-30d-5p	Oryzias latipes		0	0.51	1.29	1.8	1.96	0.63	0.5	0.42
dof-miR-866	bta-miR-30d	Bos taurus	TGTAACATCCCCGACTGGAAGCT	0.4	0.51	1.65	3.42	10.45	1.25	1.5	0.28

	oha-miR-30d-5p	Ophiophagus hannah		0.4	0.51	1.65	3.42	10.45	1.25	1.5	0.28
	ssa-miR-30b-5p	Salmo salar		0.4	0.51	1.65	3.42	10.45	1.25	1.5	0.28
	ssc-miR-30d	Sus scrofa		0.4	0.51	1.65	3.42	10.45	1.25	1.5	0.28
	tgu-miR-30d-5p	Taeniopygia guttata		0.4	0.51	1.65	3.42	10.45	1.25	1.5	0.28
	cfa-miR-30d	Canis familiaris		0.4	0.51	1.65	3.42	10.45	1.25	1.5	0.28
dof-miR-867	pma-miR-30b	Petromyzon marinus	TGTAACATCCCTGACTGGAAGCT	0	0	0	0	0.09	0	0	0
dof-miR-868	mml-miR-30b-5p	Macaca mulatta	TGTAACATCCTACTCAGC	0.2	0	0	0.9	0	0	0	0.14
	ptr-miR-30b	Pan troglodytes		0.2	0	0	0.9	0	0	0	0.14
	ggo-miR-30b	Gorilla gorilla		0.2	0	0	0.9	0	0	0	0.14
	lla-miR-30b	Lagothrix lagotricha		0.2	0	0	0.9	0	0	0	0.14
	mne-miR-30b	Macaca nemestrina		0.2	0	0	0.9	0	0	0	0.14
	age-miR-30b	Ateles geoffroyi		0.2	0	0	0.9	0	0	0	0.14
	ppa-miR-30b	Pan paniscus		0.2	0	0	0.9	0	0	0	0.14
	oar-miR-30b	Ovis aries		0.2	0	0	0.9	0	0	0	0.14
dof-miR-869	mmu-miR-30b-5p	Mus musculus	TGTAACATCCTACTCAGCT	0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	hsa-miR-30b-5p	Homo sapiens		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	rno-miR-30b-5p	Rattus norvegicus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	gga-miR-30b-5p	Gallus gallus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	dre-miR-30b	Danio rerio		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	fru-miR-30b	Fugu rubripes		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	tni-miR-30b	Tetraodon nigroviridis		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	bta-miR-30b-5p	Bos taurus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	xtr-miR-30b	Xenopus tropicalis		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	oan-miR-30b-5p	Ornithorhynchus anatinus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	chi-miR-30b-5p	Capra hircus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	tch-miR-30b-5p	Tupaia chinensis		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	oha-miR-30b-5p	Ophiophagus hannah		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	ssa-miR-30e-5p	Salmo salar		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	ipu-miR-30b	Ictalurus punctatus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	tgu-miR-30e	Taeniopygia guttata		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	ccr-miR-30b	Cyprinus carpio		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	mdo-miR-30b-5p	Monodelphis domestica		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	cgr-miR-30b-5p	Cricetulus griseus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	aca-miR-30b-5p	Anolis carolinensis		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14

	ppy-miR-30b	Pongo pygmaeus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	eca-miR-30b	Equus caballus		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	cfa-miR-30b	Canis familiaris		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
	ssc-miR-30b-5p	Sus scrofa		0.99	0.51	2.02	3.24	2.7	0.31	0.67	0.14
dof-miR-870	oar-miR-30c	Ovis aries	TGTA AACATCCTACACTCTCA	0	0.25	0	0	0	0	0.83	0.14
	aca-miR-30c-5p	Anolis carolinensis		0	0.25	0	0	0	0	0.83	0.14
dof-miR-871	dre-miR-30c-5p	Danio rerio	TGTA AACATCCTACACTCTCAG	0	0	0.18	0	0	0	0	0
dof-miR-872	hsa-miR-30c-5p	Homo sapiens	TGTA AACATCCTACACTCTCAGC	1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	mmu-miR-30c-5p	Mus musculus		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	rno-miR-30c-5p	Rattus norvegicus		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	ssc-miR-30c-5p	Sus scrofa		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	ptr-miR-30c	Pan troglodytes		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	lla-miR-30c	Lagothrix lagotricha		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	mne-miR-30c	Macaca nemestrina		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	xtr-miR-30c	Xenopus tropicalis		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	bta-miR-30c	Bos taurus		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	oan-miR-30c-5p	Ornithorhynchus anatinus		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	chi-miR-30c-5p	Capra hircus		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	tch-miR-30c-5p	Tupaia chinensis		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	ssa-miR-30a-5p	Salmo salar		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	mdo-miR-30c-5p	Monodelphis domestica		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	ola-miR-30c	Oryzias latipes		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	cgr-miR-30c	Cricetulus griseus		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	ggo-miR-30c	Gorilla gorilla		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	ppy-miR-30c	Pongo pygmaeus		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	eca-miR-30c	Equus caballus		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
	mml-miR-30c-5p	Macaca mulatta		1.19	1.02	2.76	2.7	1.31	0.31	0.83	0.14
dof-miR-873	gga-miR-30c-5p	Gallus gallus	TGTA AACATCCTACACTCTCAGCT	0.99	1.27	2.76	5.05	3.73	0.52	1.5	0.28
	oha-miR-30c-5p	Ophiophagus hannah		0.99	1.27	2.76	5.05	3.73	0.52	1.5	0.28
	ipu-miR-30c	Ictalurus punctatus		0.99	1.27	2.76	5.05	3.73	0.52	1.5	0.28
	sha-miR-30c	Sarcophilus harrisii		0.99	1.27	2.76	5.05	3.73	0.52	1.5	0.28
	tgu-miR-30c-5p	Taeniopygia guttata		0.99	1.27	2.76	5.05	3.73	0.52	1.5	0.28
	cfa-miR-30c	Canis familiaris		0.99	1.27	2.76	5.05	3.73	0.52	1.5	0.28
dof-miR-874	fru-miR-30c	Fugu rubripes	TGTA AACATCCTACACTCTCGG	0	0.25	0	0	0	0	0.67	0

	tmi-miR-30c	Tetraodon nigroviridis		0	0.25	0	0	0	0	0.67	0
dof-miR-875	tch-miR-30a-5p	Tupaia chinensis	TGTA AACATCCTCGACTGGA	0.4	0.51	2.2	2.52	0.37	0.31	0.17	0.28
dof-miR-876	hsa-miR-30a-5p	Homo sapiens	TGTA AACATCCTCGACTGGAAG	0	0.25	0.55	0.72	0	0.1	0.17	0
	mmu-miR-30a-5p	Mus musculus		0	0.25	0.55	0.72	0	0.1	0.17	0
	rno-miR-30a-5p	Rattus norvegicus		0	0.25	0.55	0.72	0	0.1	0.17	0
	gga-miR-30a-5p	Gallus gallus		0	0.25	0.55	0.72	0	0.1	0.17	0
	mml-miR-30a-5p	Macaca mulatta		0	0.25	0.55	0.72	0	0.1	0.17	0
	ptr-miR-30a-5p	Pan troglodytes		0	0.25	0.55	0.72	0	0.1	0.17	0
	ggo-miR-30a-5p	Gorilla gorilla		0	0.25	0.55	0.72	0	0.1	0.17	0
	ppy-miR-30a-5p	Pongo pygmaeus		0	0.25	0.55	0.72	0	0.1	0.17	0
	ppa-miR-30a-5p	Pan paniscus		0	0.25	0.55	0.72	0	0.1	0.17	0
	xtr-miR-30a-5p	Xenopus tropicalis		0	0.25	0.55	0.72	0	0.1	0.17	0
	mdo-miR-30a-5p	Monodelphis domestica		0	0.25	0.55	0.72	0	0.1	0.17	0
	aca-miR-30a-5p	Anolis carolinensis		0	0.25	0.55	0.72	0	0.1	0.17	0
ssc-miR-30a-5p	Sus scrofa	0	0.25	0.55	0.72	0	0.1	0.17	0		
dof-miR-877	oan-miR-30a-5p	Ornithorhynchus anatinus	TGTA AACATCCTCGACTGGAAGC	0	0	1.84	2.7	0.65	0.52	0	0
	oar-miR-30a-5p	Ovis aries		0	0	1.84	2.7	0.65	0.52	0	0
	cgr-miR-30a-5p	Cricetulus griseus		0	0	1.84	2.7	0.65	0.52	0	0
	pma-miR-30a-5p	Petromyzon marinus		0	0	1.84	2.7	0.65	0.52	0	0
	tgu-miR-30b-5p	Taeniopygia guttata		0	0	1.84	2.7	0.65	0.52	0	0
	cfa-miR-30a	Canis familiaris		0	0	1.84	2.7	0.65	0.52	0	0
dof-miR-878	bta-miR-30a-5p	Bos taurus	TGTA AACATCCTCGACTGGAAGCT	0.79	0.76	3.49	7.57	2.61	0.94	1	0.28
	chi-miR-30a-5p	Capra hircus		0.79	0.76	3.49	7.57	2.61	0.94	1	0.28
	oha-miR-30a-5p	Ophiophagus hannah		0.79	0.76	3.49	7.57	2.61	0.94	1	0.28
dof-miR-879	ssa-miR-30d-5p	Salmo salar	TGTA AACATCCTTGACTGAAAGCT	0	0	0	0	0.09	0	0	0
dof-miR-880	gga-miR-30e-5p	Gallus gallus	TGTA AACATCCTTGACTGG	0	0	0	0	0.28	0	0.17	0.14
	ola-miR-30a-5p	Oryzias latipes		0	0	0	0	0.28	0	0.17	0.14
dof-miR-881	mmu-miR-30e-5p	Mus musculus	TGTA AACATCCTTGACTGGAAG	0.2	0	0	0.54	0.09	0	0	0
	hsa-miR-30e-5p	Homo sapiens		0.2	0	0	0.54	0.09	0	0	0
	rno-miR-30e-5p	Rattus norvegicus		0.2	0	0	0.54	0.09	0	0	0
	dre-miR-30e-5p	Danio rerio		0.2	0	0	0.54	0.09	0	0	0
	xtr-miR-30e	Xenopus tropicalis		0.2	0	0	0.54	0.09	0	0	0
	ppy-miR-30e	Pongo pygmaeus		0.2	0	0	0.54	0.09	0	0	0
	eca-miR-30e	Equus caballus		0.2	0	0	0.54	0.09	0	0	0

	mml-miR-30e-5p	Macaca mulatta		0.2	0	0	0.54	0.09	0	0	0
	ptr-miR-30e	Pan troglodytes		0.2	0	0	0.54	0.09	0	0	0
dof-miR-882	oan-miR-30e-5p	Ornithorhynchus anatinus	TGTAACATCCTTGACTGGAAGC	0	0	0.92	1.8	0.37	0	0.33	0
	mdo-miR-30d-5p	Monodelphis domestica		0	0	0.92	1.8	0.37	0	0.33	0
	cgr-miR-30e-5p	Cricetulus griseus		0	0	0.92	1.8	0.37	0	0.33	0
	ggo-miR-30e	Gorilla gorilla		0	0	0.92	1.8	0.37	0	0.33	0
	aca-miR-30e-5p	Anolis carolinensis		0	0	0.92	1.8	0.37	0	0.33	0
dof-miR-883	bta-miR-30e-5p	Bos taurus	TGTAACATCCTTGACTGGAAGCT	0.99	3.31	3.67	10.63	24.06	2.71	4.01	3.64
	chi-miR-30e-5p	Capra hircus		0.99	3.31	3.67	10.63	24.06	2.71	4.01	3.64
	ssa-miR-30c-5p	Salmo salar		0.99	3.31	3.67	10.63	24.06	2.71	4.01	3.64
	ssc-miR-30e-5p	Sus scrofa		0.99	3.31	3.67	10.63	24.06	2.71	4.01	3.64
	tgu-miR-30a-5p	Taeniopygia guttata		0.99	3.31	3.67	10.63	24.06	2.71	4.01	3.64
dof-miR-884	dre-miR-194a	Danio rerio	TGTAACAGCAACTCCATGTGG	0	0	0.18	0	0	0	0	0
	fru-miR-194	Fugu rubripes		0	0	0.18	0	0	0	0	0
	tmi-miR-194	Tetraodon nigroviridis		0	0	0.18	0	0	0	0	0
	ssc-miR-194a	Sus scrofa		0	0	0.18	0	0	0	0	0
dof-miR-885	mmu-miR-194-5p	Mus musculus	TGTAACAGCAACTCCATGTGGA	0	0.25	0	0	0.37	0.1	0.5	0.14
	hsa-miR-194-5p	Homo sapiens		0	0.25	0	0	0.37	0.1	0.5	0.14
	rno-miR-194-5p	Rattus norvegicus		0	0.25	0	0	0.37	0.1	0.5	0.14
	gga-miR-194	Gallus gallus		0	0.25	0	0	0.37	0.1	0.5	0.14
	mml-miR-194-5p	Macaca mulatta		0	0.25	0	0	0.37	0.1	0.5	0.14
	ptr-miR-194	Pan troglodytes		0	0.25	0	0	0.37	0.1	0.5	0.14
	ppy-miR-194	Pongo pygmaeus		0	0.25	0	0	0.37	0.1	0.5	0.14
	ggo-miR-194	Gorilla gorilla		0	0.25	0	0	0.37	0.1	0.5	0.14
	mne-miR-194	Macaca nemestrina		0	0.25	0	0	0.37	0.1	0.5	0.14
	age-miR-194	Ateles geoffroyi		0	0.25	0	0	0.37	0.1	0.5	0.14
	xtr-miR-194	Xenopus tropicalis		0	0.25	0	0	0.37	0.1	0.5	0.14
	oan-miR-194-5p	Ornithorhynchus anatinus		0	0.25	0	0	0.37	0.1	0.5	0.14
	efu-miR-194	Eptesicus fuscus		0	0.25	0	0	0.37	0.1	0.5	0.14
	chi-miR-194	Capra hircus		0	0.25	0	0	0.37	0.1	0.5	0.14
	oha-miR-194-5p	Ophiophagus hannah		0	0.25	0	0	0.37	0.1	0.5	0.14
	ssa-miR-194a-5p	Salmo salar		0	0.25	0	0	0.37	0.1	0.5	0.14
	ipu-miR-194a	Ictalurus punctatus		0	0.25	0	0	0.37	0.1	0.5	0.14
	oar-miR-194	Ovis aries		0	0.25	0	0	0.37	0.1	0.5	0.14

	ccr-miR-194	Cyprinus carpio		0	0.25	0	0	0.37	0.1	0.5	0.14
	cgr-miR-194	Cricetulus griseus		0	0.25	0	0	0.37	0.1	0.5	0.14
	aca-miR-194-5p	Anolis carolinensis		0	0.25	0	0	0.37	0.1	0.5	0.14
	eca-miR-194	Equus caballus		0	0.25	0	0	0.37	0.1	0.5	0.14
	tgu-miR-194-5p	Taeniopygia guttata		0	0.25	0	0	0.37	0.1	0.5	0.14
	cfa-miR-194	Canis familiaris		0	0.25	0	0	0.37	0.1	0.5	0.14
	xla-miR-194	Xenopus laevis		0	0.25	0	0	0.37	0.1	0.5	0.14
	bta-miR-194	Bos taurus		0	0.25	0	0	0.37	0.1	0.5	0.14
dof-miR-886	pma-miR-194-5p	Petromyzon marinus	TGTAACAGCAACTCCATGTGGAT	0	0	0	0	0	0.1	0	0
dof-miR-887	ssc-miR-194b-5p	Sus scrofa	TGTAACAGCGACTCCATGTGGGA	0	0	0	0	0.09	0	0.33	0.28
dof-miR-888	gga-miR-142-3p	Gallus gallus	TGTAGTGTTTCCTACTTTATGG	0	0	0	0.72	0.56	0.1	0.17	0.28
	oan-miR-142-3p	Ornithorhynchus anatinus		0	0	0	0.72	0.56	0.1	0.17	0.28
	ssc-miR-142-3p	Sus scrofa		0	0	0	0.72	0.56	0.1	0.17	0.28
dof-miR-889	mmu-miR-142a-3p	Mus musculus	TGTAGTGTTTCCTACTTTATGGA	0	0	0.37	0	0	0	0.17	0.14
	hsa-miR-142-3p	Homo sapiens		0	0	0.37	0	0	0	0.17	0.14
	rno-miR-142-3p	Rattus norvegicus		0	0	0.37	0	0	0	0.17	0.14
	dre-miR-142a-3p	Danio rerio		0	0	0.37	0	0	0	0.17	0.14
	xtr-miR-142-3p	Xenopus tropicalis		0	0	0.37	0	0	0	0.17	0.14
	mdo-miR-142	Monodelphis domestica		0	0	0.37	0	0	0	0.17	0.14
	efu-miR-142	Eptesicus fuscus		0	0	0.37	0	0	0	0.17	0.14
	oha-miR-142-3p	Ophiophagus hannah		0	0	0.37	0	0	0	0.17	0.14
	aja-miR-142	Artibeus jamaicensis		0	0	0.37	0	0	0	0.17	0.14
	ppy-miR-142-3p	Pongo pygmaeus		0	0	0.37	0	0	0	0.17	0.14
	eca-miR-142-3p	Equus caballus		0	0	0.37	0	0	0	0.17	0.14
	mml-miR-142-3p	Macaca mulatta		0	0	0.37	0	0	0	0.17	0.14
	ptr-miR-142	Pan troglodytes		0	0	0.37	0	0	0	0.17	0.14
dof-miR-890	chi-miR-3959-3p	Capra hircus	TGTATGTCAACTGATCCACAGT	0	0	0.18	0	0	0	0	0
	bta-miR-411c-3p	Bos taurus		0	0	0.18	0	0	0	0	0
	oar-miR-3959-3p	Ovis aries		0	0	0.18	0	0	0	0	0
dof-miR-891	ola-miR-223	Oryzias latipes	TGTCAGTTTGTCAAATACCC	0	0	0.18	0	0.56	0	0.17	0
dof-miR-892	rno-miR-223-3p	Rattus norvegicus	TGTCAGTTTGTCAAATACCCC	0.2	0	0.18	0	0.47	0	0	0
	gga-miR-223	Gallus gallus		0.2	0	0.18	0	0.47	0	0	0
	dre-miR-223	Danio rerio		0.2	0	0.18	0	0.47	0	0	0
	mml-miR-223	Macaca mulatta		0.2	0	0.18	0	0.47	0	0	0

	ptr-miR-223	Pan troglodytes		0.2	0	0.18	0	0.47	0	0	0
	ggo-miR-223	Gorilla gorilla		0.2	0	0.18	0	0.47	0	0	0
	ppy-miR-223	Pongo pygmaeus		0.2	0	0.18	0	0.47	0	0	0
	sla-miR-223	Saguinus labiatus		0.2	0	0.18	0	0.47	0	0	0
	ppa-miR-223	Pan paniscus		0.2	0	0.18	0	0.47	0	0	0
	fru-miR-223	Fugu rubripes		0.2	0	0.18	0	0.47	0	0	0
	tni-miR-223	Tetraodon nigroviridis		0.2	0	0.18	0	0.47	0	0	0
	xtr-miR-223	Xenopus tropicalis		0.2	0	0.18	0	0.47	0	0	0
	mdo-miR-223-3p	Monodelphis domestica		0.2	0	0.18	0	0.47	0	0	0
	tgu-miR-223	Taeniopygia guttata		0.2	0	0.18	0	0.47	0	0	0
	xla-miR-223	Xenopus laevis		0.2	0	0.18	0	0.47	0	0	0
	cfa-miR-223	Canis familiaris		0.2	0	0.18	0	0.47	0	0	0
dof-miR-893	hsa-miR-223-3p	Homo sapiens	TGTCAGTTTGCAAATACCCCA	0.4	0.76	0	0	2.61	0	0	0
	mmu-miR-223-3p	Mus musculus		0.4	0.76	0	0	2.61	0	0	0
	chi-miR-223-3p	Capra hircus		0.4	0.76	0	0	2.61	0	0	0
	eca-miR-223	Equus caballus		0.4	0.76	0	0	2.61	0	0	0
	bta-miR-223	Bos taurus		0.4	0.76	0	0	2.61	0	0	0
dof-miR-894	efu-miR-223	Eptesicus fuscus	TGTCAGTTTGCAAATACCCCAA	0	0.25	0.18	0	1.68	0	0	0
dof-miR-895	oan-miR-223-3p	Ornithorhynchus anatinus	TGTCAGTTTGCAAATACCCTA	0	0	0	0	0	0	0	0.14
dof-miR-896	chi-miR-542-3p	Capra hircus	TGTGACAGATTGATAACTGA	0	0	0.18	0	0	0	0	0
dof-miR-897	mmu-miR-542-3p	Mus musculus	TGTGACAGATTGATAACTGAAA	0	0	0	0.18	0	0	0	0
	rno-miR-542-3p	Rattus norvegicus		0	0	0	0.18	0	0	0	0
	hsa-miR-542-3p	Homo sapiens		0	0	0	0.18	0	0	0	0
	tch-miR-542-3p	Tupaia chinensis		0	0	0	0.18	0	0	0	0
	ggo-miR-542	Gorilla gorilla		0	0	0	0.18	0	0	0	0
	ppy-miR-542-3p	Pongo pygmaeus		0	0	0	0.18	0	0	0	0
	eca-miR-542-3p	Equus caballus		0	0	0	0.18	0	0	0	0
	ssc-miR-542-3p	Sus scrofa		0	0	0	0.18	0	0	0	0
	mml-miR-542-3p	Macaca mulatta		0	0	0	0.18	0	0	0	0
	cfa-miR-542	Canis familiaris		0	0	0	0.18	0	0	0	0
dof-miR-898	mmu-miR-134-5p	Mus musculus	TGTGACTGGTTGACCAGAGGGG	0	0	0	0	0.09	0	0	0
	hsa-miR-134-5p	Homo sapiens		0	0	0	0	0.09	0	0	0
	rno-miR-134-5p	Rattus norvegicus		0	0	0	0	0.09	0	0	0
	chi-miR-134	Capra hircus		0	0	0	0	0.09	0	0	0

	cgr-miR-134	Cricetulus griseus		0	0	0	0	0.09	0	0	0
	eca-miR-134	Equus caballus		0	0	0	0	0.09	0	0	0
	mml-miR-134-5p	Macaca mulatta		0	0	0	0	0.09	0	0	0
	ptr-miR-134	Pan troglodytes		0	0	0	0	0.09	0	0	0
	cfa-miR-134	Canis familiaris		0	0	0	0	0.09	0	0	0
dof-miR-899	ptc-miR1711-5p	Populus trichocarpa	TGTGATATTGGTCCGGCTCATC	0	0	0.18	0.36	0	0	0	0
dof-miR-900	ola-miR-19d	Oryzias latipes	TGTGCAAACCCATGCAAAACTG	0	0	0	0.18	0	0	0.17	0
dof-miR-901	dre-miR-19d-3p	Danio rerio	TGTGCAAACCCATGCAAAACTGA	0	0.25	0.18	0.36	0	0	0.33	0
	ccr-miR-19d	Cyprinus carpio		0	0.25	0.18	0.36	0	0	0.33	0
dof-miR-902	aca-miR-19b	Anolis carolinensis	TGTGCAAATCCATGCAAAACT	0.2	0.51	0	0	0.19	0.21	1	0.84
dof-miR-903	ssa-miR-19c-3p	Salmo salar	TGTGCAAATCCATGCAAAACTG	0	0	0.92	0.9	0.37	0.1	0.17	0.14
	cfa-miR-19b	Canis familiaris		0	0	0.92	0.9	0.37	0.1	0.17	0.14
dof-miR-904	hsa-miR-19b-3p	Homo sapiens	TGTGCAAATCCATGCAAAACTGA	0	0.76	1.1	0.9	0.93	0.1	0.17	0
	mmu-miR-19b-3p	Mus musculus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	rno-miR-19b-3p	Rattus norvegicus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	gga-miR-19b-3p	Gallus gallus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	xla-miR-19b	Xenopus laevis		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	dre-miR-19b-3p	Danio rerio		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	ggo-miR-19b	Gorilla gorilla		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	lca-miR-19b	Lemur catta		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	age-miR-19b	Ateles geoffroyi		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	ppa-miR-19b	Pan paniscus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	ppy-miR-19b	Pongo pygmaeus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	ptr-miR-19b	Pan troglodytes		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	mml-miR-19b	Macaca mulatta		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	sla-miR-19b	Saguinus labiatus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	lla-miR-19b	Lagothrix lagotricha		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	mne-miR-19b	Macaca nemestrina		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	fru-miR-19b	Fugu rubripes		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	tni-miR-19b	Tetraodon nigroviridis		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	xtr-miR-19b	Xenopus tropicalis		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	mdo-miR-19b-3p	Monodelphis domestica		0	0.76	1.1	0.9	0.93	0.1	0.17	0
bta-miR-19b	Bos taurus	0	0.76	1.1	0.9	0.93	0.1	0.17	0		
oan-miR-19b-3p	Ornithorhynchus anatinus	0	0.76	1.1	0.9	0.93	0.1	0.17	0		

	chi-miR-19b-3p	Capra hircus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	tch-miR-19b-3p	Tupaia chinensis		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	oha-miR-19b-3p	Ophiophagus hannah		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	oar-miR-19b	Ovis aries		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	cgr-miR-19b-3p	Cricetulus griseus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	pma-miR-19b-3p	Petromyzon marinus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	eca-miR-19b	Equus caballus		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	ssc-miR-19b	Sus scrofa		0	0.76	1.1	0.9	0.93	0.1	0.17	0
	tgu-miR-19b-3p	Taeniopygia guttata		0	0.76	1.1	0.9	0.93	0.1	0.17	0
dof-miR-905	ssa-miR-19a-3p	Salmo salar	TGTGCAAATCTATGCAAAACTG	0	0	0.18	0.36	0.09	0	0.17	0
	aca-miR-19a-3p	Anolis carolinensis		0	0	0.18	0.36	0.09	0	0.17	0
dof-miR-906	hsa-miR-19a-3p	Homo sapiens	TGTGCAAATCTATGCAAAACTGA	0	0	0.18	0.36	0.37	0	0	0
	mmu-miR-19a-3p	Mus musculus		0	0	0.18	0.36	0.37	0	0	0
	rno-miR-19a-3p	Rattus norvegicus		0	0	0.18	0.36	0.37	0	0	0
	gga-miR-19a-3p	Gallus gallus		0	0	0.18	0.36	0.37	0	0	0
	dre-miR-19a-3p	Danio rerio		0	0	0.18	0.36	0.37	0	0	0
	ssc-miR-19a	Sus scrofa		0	0	0.18	0.36	0.37	0	0	0
	ggo-miR-19a	Gorilla gorilla		0	0	0.18	0.36	0.37	0	0	0
	lca-miR-19a	Lemur catta		0	0	0.18	0.36	0.37	0	0	0
	age-miR-19a	Ateles geoffroyi		0	0	0.18	0.36	0.37	0	0	0
	ppa-miR-19a	Pan paniscus		0	0	0.18	0.36	0.37	0	0	0
	ppy-miR-19a	Pongo pygmaeus		0	0	0.18	0.36	0.37	0	0	0
	ptr-miR-19a	Pan troglodytes		0	0	0.18	0.36	0.37	0	0	0
	mml-miR-19a-3p	Macaca mulatta		0	0	0.18	0.36	0.37	0	0	0
	sla-miR-19a	Saguinus labiatus		0	0	0.18	0.36	0.37	0	0	0
	lla-miR-19a	Lagothrix lagotricha		0	0	0.18	0.36	0.37	0	0	0
	mne-miR-19a	Macaca nemestrina		0	0	0.18	0.36	0.37	0	0	0
	fru-miR-19a	Fugu rubripes		0	0	0.18	0.36	0.37	0	0	0
	tmi-miR-19a	Tetraodon nigroviridis		0	0	0.18	0.36	0.37	0	0	0
	xtr-miR-19a	Xenopus tropicalis		0	0	0.18	0.36	0.37	0	0	0
	mdo-miR-19a-3p	Monodelphis domestica		0	0	0.18	0.36	0.37	0	0	0
	bta-miR-19a	Bos taurus		0	0	0.18	0.36	0.37	0	0	0
	oan-miR-19a-3p	Ornithorhynchus anatinus		0	0	0.18	0.36	0.37	0	0	0
	chi-miR-19a	Capra hircus		0	0	0.18	0.36	0.37	0	0	0

	tch-miR-19a-3p	Tupaia chinensis		0	0	0.18	0.36	0.37	0	0	0
	oha-miR-19a-3p	Ophiophagus hannah		0	0	0.18	0.36	0.37	0	0	0
	cgr-miR-19a	Cricetulus griseus		0	0	0.18	0.36	0.37	0	0	0
	eca-miR-19a	Equus caballus		0	0	0.18	0.36	0.37	0	0	0
	cfa-miR-19a	Canis familiaris		0	0	0.18	0.36	0.37	0	0	0
dof-miR-907	pta-miR946a-5p	Pinus taeda	TGTGGATAGAGAAGGGTTAGT	0	0	0.37	0.36	0	0	0	0
dof-miR-908	ath-miR398b-3p	Arabidopsis thaliana	TGTGTTCTCAGGTCACCCCTG	0	0	0	0.18	0	0	0	0
	ath-miR398c-3p	Arabidopsis thaliana		0	0	0	0.18	0	0	0	0
	bra-miR398-3p	Brassica rapa		0	0	0	0.18	0	0	0	0
	aly-miR398b-3p	Arabidopsis lyrata		0	0	0	0.18	0	0	0	0
dof-miR-909	ath-miR398a-3p	Arabidopsis thaliana	TGTGTTCTCAGGTCACCCCTT	0	0	0	0.54	0	0	0	0
	osa-miR398a	Oryza sativa		0	0	0	0.54	0	0	0	0
	gma-miR398a	Glycine max		0	0	0	0.54	0	0	0	0
	gma-miR398b	Glycine max		0	0	0	0.54	0	0	0	0
	ptc-miR398a	Populus trichocarpa		0	0	0	0.54	0	0	0	0
	mtr-miR398a-3p	Medicago truncatula		0	0	0	0.54	0	0	0	0
	vvi-miR398a	Vitis vinifera		0	0	0	0.54	0	0	0	0
	mdm-miR398a	Malus domestica		0	0	0	0.54	0	0	0	0
	cme-miR398b	Cucumis melo		0	0	0	0.54	0	0	0	0
	tcc-miR398b	Theobroma cacao		0	0	0	0.54	0	0	0	0
	csi-miR398	Citrus sinensis		0	0	0	0.54	0	0	0	0
	rco-miR398a	Ricinus communis		0	0	0	0.54	0	0	0	0
	gra-miR398	Gossypium raimondii		0	0	0	0.54	0	0	0	0
	ghr-miR398	Gossypium hirsutum		0	0	0	0.54	0	0	0	0
	aly-miR398a-3p	Arabidopsis lyrata		0	0	0	0.54	0	0	0	0
	bol-miR398a-3p	Brassica oleracea		0	0	0	0.54	0	0	0	0
aqc-miR398a	Aquilegia caerulea	0	0	0	0.54	0	0	0	0		
dof-miR-910	osa-miR398b	Oryza sativa	TGTGTTCTCAGGTCGCCCTG	0	0	0.37	192.44	0	0	0.17	0
	ptc-miR398b	Populus trichocarpa		0	0	0.37	192.44	0	0	0.17	0
	ptc-miR398c-3p	Populus trichocarpa		0	0	0.37	192.44	0	0	0.17	0
	mtr-miR398b	Medicago truncatula		0	0	0.37	192.44	0	0	0.17	0
	mtr-miR398c	Medicago truncatula		0	0	0.37	192.44	0	0	0.17	0
	gma-miR398d	Glycine max		0	0	0.37	192.44	0	0	0.17	0
	mdm-miR398b	Malus domestica		0	0	0.37	192.44	0	0	0.17	0

	ssc-miR-499-5p	Sus scrofa		0	0.25	0	0	0	0	0.17	0
	mml-miR-499-5p	Macaca mulatta		0	0.25	0	0	0	0	0.17	0
	cfa-miR-499	Canis familiaris		0	0.25	0	0	0	0	0.17	0
dof-miR-917	dre-miR-499-5p	Danio rerio	TTAAGACTTGCAGTGATGTTTA	0	0	0	0	0	0	0.17	0
	ssa-miR-499b-5p	Salmo salar		0	0	0	0	0	0	0.17	0
	ccr-miR-499	Cyprinus carpio		0	0	0	0	0	0	0.17	0
	cgr-miR-499-5p	Cricetulus griseus		0	0	0	0	0	0	0.17	0
	aca-miR-499-5p	Anolis carolinensis		0	0	0	0	0	0	0.17	0
dof-miR-918	hsa-miR-889-3p	Homo sapiens	TTAATATCGGACAACCATTGT	0	0	0	0	0.09	0	0	0
	ppy-miR-889	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	eca-miR-889	Equus caballus		0	0	0	0	0.09	0	0	0
	mml-miR-889-3p	Macaca mulatta		0	0	0	0	0.09	0	0	0
	ptr-miR-889	Pan troglodytes		0	0	0	0	0.09	0	0	0
dof-miR-919	tgu-miR-155-5p	Taeniopygia guttata	TTAATGCTAATCGTGATAGGG	0	0	0	0	0.19	0	0.17	0
dof-miR-920	hsa-miR-155-5p	Homo sapiens	TTAATGCTAATCGTGATAGGGTT	0	0	0.18	0	0.37	0.1	0.17	0
	oan-miR-155-5p	Ornithorhynchus anatinus		0	0	0.18	0	0.37	0.1	0.17	0
	chi-miR-155-5p	Capra hircus		0	0	0.18	0	0.37	0.1	0.17	0
	tch-miR-155-5p	Tupaia chinensis		0	0	0.18	0	0.37	0.1	0.17	0
	ssa-miR-155-5p	Salmo salar		0	0	0.18	0	0.37	0.1	0.17	0
	ppy-miR-155	Pongo pygmaeus		0	0	0.18	0	0.37	0.1	0.17	0
	eca-miR-155	Equus caballus		0	0	0.18	0	0.37	0.1	0.17	0
	mml-miR-155	Macaca mulatta		0	0	0.18	0	0.37	0.1	0.17	0
	cfa-miR-155	Canis familiaris		0	0	0.18	0	0.37	0.1	0.17	0
	ptr-miR-155	Pan troglodytes		0	0	0.18	0	0.37	0.1	0.17	0
	bta-miR-155	Bos taurus		0	0	0.18	0	0.37	0.1	0.17	0
dof-miR-921	ipu-miR-155	Ictalurus punctatus	TTAATGCTAATCGTGATAGGGTT	0	0	0	0	0.65	0	0	0
dof-miR-922	ssa-miR-7552a-5p	Salmo salar	TTACAATTAAGGATATTTCTT	0	0.25	0	0	0	0	0	0
dof-miR-923	ptc-miR475a-3p	Populus trichocarpa	TTACAGTGCCCATGATTAAG	0	0	0.37	0	0	0	0	0
	ptc-miR475b-3p	Populus trichocarpa		0	0	0.37	0	0	0	0	0
dof-miR-924	hsa-miR-582-5p	Homo sapiens	TTACAGTTGTTCAACCAGTTACT	0	0	0	0	0.09	0	0	0
	ppy-miR-582-5p	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	eca-miR-582-5p	Equus caballus		0	0	0	0	0.09	0	0	0
	mml-miR-582-5p	Macaca mulatta		0	0	0	0	0.09	0	0	0
	bta-miR-582	Bos taurus		0	0	0	0	0.09	0	0	0

dof-miR-925	ptc-miR482b-3p	Populus trichocarpa	TTACCAATACCTCTCATGCCAA	0	0	0	0.18	0	0	0	0
dof-miR-926	ptc-miR827	Populus trichocarpa	TTAGATGACCATCAACGAAAA	0	0	0	0	0	0	0.33	0
dof-miR-927	mdm-miR827	Malus domestica	TTAGATGACCATCAACGAACA	0	0	0	19.1	0	0	0	0
dof-miR-928	bdi-miR827-3p	Brachypodium distachyon	TTAGATGACCATCAGCAAAACA	16.83	105.14	72.76	26.31	38.89	19.62	24.71	40.78
	ssp-miR827	Saccharum sp.		16.83	105.14	72.76	26.31	38.89	19.62	24.71	40.78
	zma-miR827-3p	Zea mays		16.83	105.14	72.76	26.31	38.89	19.62	24.71	40.78
	osa-miR827	Oryza sativa		16.83	105.14	72.76	26.31	38.89	19.62	24.71	40.78
dof-miR-929	ath-miR403-3p	Arabidopsis thaliana	TTAGATTCACGCACAAACTCG	0	0	4.04	702.9	0.28	0	0.17	0.14
	ptc-miR403a	Populus trichocarpa		0	0	4.04	702.9	0.28	0	0.17	0.14
	ptc-miR403b	Populus trichocarpa		0	0	4.04	702.9	0.28	0	0.17	0.14
	ptc-miR403c-3p	Populus trichocarpa		0	0	4.04	702.9	0.28	0	0.17	0.14
	bra-miR403-3p	Brassica rapa		0	0	4.04	702.9	0.28	0	0.17	0.14
	aly-miR403b-3p	Arabidopsis lyrata		0	0	4.04	702.9	0.28	0	0.17	0.14
	ppe-miR403	Prunus persica		0	0	4.04	702.9	0.28	0	0.17	0.14
	mes-miR403a	Manihot esculenta		0	0	4.04	702.9	0.28	0	0.17	0.14
	mes-miR403b	Manihot esculenta		0	0	4.04	702.9	0.28	0	0.17	0.14
	ptc-miR403d	Populus trichocarpa		0	0	4.04	702.9	0.28	0	0.17	0.14
	htu-miR403a	Helianthus tuberosus		0	0	4.04	702.9	0.28	0	0.17	0.14
	htu-miR403b	Helianthus tuberosus		0	0	4.04	702.9	0.28	0	0.17	0.14
	htu-miR403c	Helianthus tuberosus		0	0	4.04	702.9	0.28	0	0.17	0.14
	htu-miR403d	Helianthus tuberosus		0	0	4.04	702.9	0.28	0	0.17	0.14
	htu-miR403e	Helianthus tuberosus		0	0	4.04	702.9	0.28	0	0.17	0.14
	har-miR403a	Helianthus argophyllus		0	0	4.04	702.9	0.28	0	0.17	0.14
	hpe-miR403a	Helianthus petiolaris		0	0	4.04	702.9	0.28	0	0.17	0.14
	mdm-miR403a	Malus domestica		0	0	4.04	702.9	0.28	0	0.17	0.14
	mdm-miR403b	Malus domestica		0	0	4.04	702.9	0.28	0	0.17	0.14
	bnm-miR403	Brassica napus		0	0	4.04	702.9	0.28	0	0.17	0.14
	tcc-miR403a	Theobroma cacao		0	0	4.04	702.9	0.28	0	0.17	0.14
	tcc-miR403b	Theobroma cacao		0	0	4.04	702.9	0.28	0	0.17	0.14
	csi-miR403	Citrus sinensis		0	0	4.04	702.9	0.28	0	0.17	0.14
	rco-miR403a	Ricinus communis		0	0	4.04	702.9	0.28	0	0.17	0.14
	rco-miR403b	Ricinus communis		0	0	4.04	702.9	0.28	0	0.17	0.14
	aly-miR403a-3p	Arabidopsis lyrata		0	0	4.04	702.9	0.28	0	0.17	0.14
	vvi-miR403a	Vitis vinifera		0	0	4.04	702.9	0.28	0	0.17	0.14

	vvi-miR403b	Vitis vinifera		0	0	4.04	702.9	0.28	0	0.17	0.14
	vvi-miR403c	Vitis vinifera		0	0	4.04	702.9	0.28	0	0.17	0.14
	vvi-miR403d	Vitis vinifera		0	0	4.04	702.9	0.28	0	0.17	0.14
	vvi-miR403e	Vitis vinifera		0	0	4.04	702.9	0.28	0	0.17	0.14
	vvi-miR403f	Vitis vinifera		0	0	4.04	702.9	0.28	0	0.17	0.14
dof-miR-930	gma-miR403a	Glycine max	TTAGATTCACGCACAAACTTG	0	0	0	1.62	0	0	0	0
	gma-miR403b	Glycine max		0	0	0	1.62	0	0	0	0
dof-miR-931	hsa-miR-4662a-5p	Homo sapiens	TTAGCCAATTGTCCATCTTTAG	0	0	0	0	0.09	0	0	0
dof-miR-932	ggo-miR-340	Gorilla gorilla	TTATAAAGCAATGAGACTGAT	0	0	0.18	0.18	0.37	0	0	0
dof-miR-933	rno-miR-340-5p	Rattus norvegicus	TTATAAAGCAATGAGACTGATT	0	0.25	0.18	0.18	1.87	0.21	0.17	0
	mmu-miR-340-5p	Mus musculus		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	hsa-miR-340-5p	Homo sapiens		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	chi-miR-340-5p	Capra hircus		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	cgr-miR-340-5p	Cricetulus griseus		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	ppy-miR-340	Pongo pygmaeus		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	eca-miR-340-5p	Equus caballus		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	ssc-miR-340	Sus scrofa		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	mml-miR-340-5p	Macaca mulatta		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	ptr-miR-340	Pan troglodytes		0	0.25	0.18	0.18	1.87	0.21	0.17	0
	cfa-miR-340	Canis familiaris		0	0.25	0.18	0.18	1.87	0.21	0.17	0
dof-miR-934	chi-miR-374a-5p	Capra hircus	TTATAATACAACCTGATAAGT	0.4	1.53	0.55	0.18	0.84	0.1	0.17	0.14
	cfa-miR-374a	Canis familiaris		0.4	1.53	0.55	0.18	0.84	0.1	0.17	0.14
dof-miR-935	hsa-miR-374a-5p	Homo sapiens	TTATAATACAACCTGATAAGTG	0	0	0.18	0.54	0.56	0.21	0	0
	bta-miR-374a	Bos taurus		0	0	0.18	0.54	0.56	0.21	0	0
	tch-miR-374a-5p	Tupaia chinensis		0	0	0.18	0.54	0.56	0.21	0	0
	oar-miR-374a	Ovis aries		0	0	0.18	0.54	0.56	0.21	0	0
	ppy-miR-374a	Pongo pygmaeus		0	0	0.18	0.54	0.56	0.21	0	0
	eca-miR-374a	Equus caballus		0	0	0.18	0.54	0.56	0.21	0	0
	ssc-miR-374a-5p	Sus scrofa		0	0	0.18	0.54	0.56	0.21	0	0
	mml-miR-374a-5p	Macaca mulatta		0	0	0.18	0.54	0.56	0.21	0	0
ptr-miR-374a	Pan troglodytes	0	0	0.18	0.54	0.56	0.21	0	0		
dof-miR-936	tch-miR-361-5p	Tupaia chinensis	TTATCAGAATCTCCAGGGGTA	0	0	0	0	0	0	0	0.14
dof-miR-937	hsa-miR-361-5p	Homo sapiens	TTATCAGAATCTCCAGGGGTAC	0.4	0	0.37	0.72	0.56	0.21	0.5	0
	mmu-miR-361-5p	Mus musculus		0.4	0	0.37	0.72	0.56	0.21	0.5	0

	rno-miR-361-5p	Rattus norvegicus		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	bta-miR-361	Bos taurus		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	efu-miR-361	Eptesicus fuscus		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	chi-miR-361-5p	Capra hircus		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	cgr-miR-361	Cricetulus griseus		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	ggo-miR-361	Gorilla gorilla		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	ppy-miR-361-5p	Pongo pygmaeus		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	eca-miR-361-5p	Equus caballus		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	ssc-miR-361-5p	Sus scrofa		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	mml-miR-361-5p	Macaca mulatta		0.4	0	0.37	0.72	0.56	0.21	0.5	0
	cfa-miR-361	Canis familiaris		0.4	0	0.37	0.72	0.56	0.21	0.5	0
dof-miR-938	ggo-miR-584	Gorilla gorilla	TTATGGTTTGCCTGGGACTGA	0	0	0	0	0.75	0	0	0
dof-miR-939	hsa-miR-95-3p	Homo sapiens	TTCAACGGGTATTTATTGAGCA	0	0	0	0	0.09	0	0	0
	ssc-miR-95	Sus scrofa		0	0	0	0	0.09	0	0	0
	ptr-miR-95	Pan troglodytes		0	0	0	0	0.09	0	0	0
	ggo-miR-95	Gorilla gorilla		0	0	0	0	0.09	0	0	0
	ppy-miR-95	Pongo pygmaeus		0	0	0	0	0.09	0	0	0
	sla-miR-95	Saguinus labiatus		0	0	0	0	0.09	0	0	0
	lla-miR-95	Lagothrix lagotricha		0	0	0	0	0.09	0	0	0
	ppa-miR-95	Pan paniscus		0	0	0	0	0.09	0	0	0
	tch-miR-95	Tupaia chinensis		0	0	0	0	0.09	0	0	0
	mml-miR-95-3p	Macaca mulatta		0	0	0	0	0.09	0	0	0
	bta-miR-95	Bos taurus		0	0	0	0	0.09	0	0	0
cfa-miR-95	Canis familiaris	0	0	0	0	0.09	0	0	0		
dof-miR-940	tch-miR-26a-2-5p	Tupaia chinensis	TTCAAGTAACCCAGGATAGGCT	0.2	0	0	0	0.09	0	0	0
dof-miR-941	cgr-miR-26a	Cricetulus griseus	TTCAAGTAATCCAGGATAGG	0.4	0.51	1.1	1.26	3.17	0.63	1.17	0.56
	aca-miR-26-5p	Anolis carolinensis		0.4	0.51	1.1	1.26	3.17	0.63	1.17	0.56
dof-miR-942	gga-miR-26a-5p	Gallus gallus	TTCAAGTAATCCAGGATAGGC	2.18	0.25	5.33	5.59	4.57	0.21	2.17	2.1
	xtr-miR-26	Xenopus tropicalis		2.18	0.25	5.33	5.59	4.57	0.21	2.17	2.1
	hhi-miR-26	Hippoglossus hippoglossus		2.18	0.25	5.33	5.59	4.57	0.21	2.17	2.1
	ola-miR-26	Oryzias latipes		2.18	0.25	5.33	5.59	4.57	0.21	2.17	2.1
	mdo-miR-26-5p	Monodelphis domestica		2.18	0.25	5.33	5.59	4.57	0.21	2.17	2.1
dof-miR-943	hsa-miR-26a-5p	Homo sapiens	TTCAAGTAATCCAGGATAGGCT	15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	mmu-miR-26a-5p	Mus musculus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81

	rno-miR-26a-5p	Rattus norvegicus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	dre-miR-26a-5p	Danio rerio		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	ssc-miR-26a	Sus scrofa		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	ptr-miR-26a	Pan troglodytes		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	ggo-miR-26a	Gorilla gorilla		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	ppy-miR-26a	Pongo pygmaeus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	lla-miR-26a	Lagothrix lagotricha		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	mne-miR-26a	Macaca nemestrina		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	mml-miR-26a-5p	Macaca mulatta		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	ppa-miR-26a	Pan paniscus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	fru-miR-26	Fugu rubripes		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	tui-miR-26	Tetraodon nigroviridis		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	bta-miR-26a	Bos taurus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	oan-miR-26-5p	Ornithorhynchus anatinus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	chi-miR-26a-5p	Capra hircus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	tch-miR-26a-5p	Tupaia chinensis		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	oha-miR-26-5p	Ophiophagus hannah		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	ssa-miR-26a-5p	Salmo salar		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	ipu-miR-26a	Ictalurus punctatus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	oar-miR-26a	Ovis aries		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	ccr-miR-26a	Cyprinus carpio		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	pma-miR-26a-5p	Petromyzon marinus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	eca-miR-26a	Equus caballus		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	tgu-miR-26-5p	Taeniopygia guttata		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
	cfa-miR-26a	Canis familiaris		15.05	24.18	30.87	57.66	65.85	8.03	32.05	9.81
dof-miR-944	dre-miR-26b	Danio rerio	TTCAAGTAATCCAGGATAGGTT	0.2	0.25	0.92	1.44	0	0	0.33	0.42
	ssa-miR-26b-5p	Salmo salar		0.2	0.25	0.92	1.44	0	0	0.33	0.42
	ipu-miR-26b	Ictalurus punctatus		0.2	0.25	0.92	1.44	0	0	0.33	0.42
	pma-miR-26b-5p	Petromyzon marinus		0.2	0.25	0.92	1.44	0	0	0.33	0.42
dof-miR-945	ssa-miR-26d-5p	Salmo salar	TTCAAGTAATCTAGGATAGGCT	0.2	0	0	0	0	0	0	
dof-miR-946	hsa-miR-26b-5p	Homo sapiens	TTCAAGTAATTCAGGATAGGT	0.2	0.25	0.55	1.26	5.69	0.52	0.33	0.28
	mmu-miR-26b-5p	Mus musculus		0.2	0.25	0.55	1.26	5.69	0.52	0.33	0.28
	rno-miR-26b-5p	Rattus norvegicus		0.2	0.25	0.55	1.26	5.69	0.52	0.33	0.28
	oar-miR-26b	Ovis aries		0.2	0.25	0.55	1.26	5.69	0.52	0.33	0.28

	ggo-miR-26b	Gorilla gorilla		0.2	0.25	0.55	1.26	5.69	0.52	0.33	0.28
	ppy-miR-26b	Pongo pygmaeus		0.2	0.25	0.55	1.26	5.69	0.52	0.33	0.28
	mml-miR-26b-5p	Macaca mulatta		0.2	0.25	0.55	1.26	5.69	0.52	0.33	0.28
	ptr-miR-26b	Pan troglodytes		0.2	0.25	0.55	1.26	5.69	0.52	0.33	0.28
dof-miR-947	bta-miR-26b	Bos taurus	TTCACAGTAATTCAGGATAGGTT	0.79	1.27	2.02	4.5	16.41	1.98	0.33	0.56
	chi-miR-26b-5p	Capra hircus		0.79	1.27	2.02	4.5	16.41	1.98	0.33	0.56
	tch-miR-26b-5p	Tupaia chinensis		0.79	1.27	2.02	4.5	16.41	1.98	0.33	0.56
	cgr-miR-26b-5p	Cricetulus griseus		0.79	1.27	2.02	4.5	16.41	1.98	0.33	0.56
	cfa-miR-26b	Canis familiaris		0.79	1.27	2.02	4.5	16.41	1.98	0.33	0.56
dof-miR-948	gma-miR396a-3p	Glycine max	TTCATAAAAGCTGTGGGAAG	0	0	0	14.96	0	0.1	0.17	0
dof-miR-949	ptc-miR1450	Populus trichocarpa	TTCATGGCTCGGTCAGGTTAC	0	0	0.18	0	0	0	0	0
dof-miR-950	ola-miR-27d-3p	Oryzias latipes	TTCACAGTGCTAAGTTC	0	0	0	0	0.19	0	0	0
dof-miR-951	ssa-miR-27c-3p	Salmo salar	TTCACAGTGGCTAAGTTCAGT	0	0	0	0	0	0	0.17	0.14
	ipu-miR-27e	Ictalurus punctatus		0	0	0	0	0	0	0.17	0.14
dof-miR-952	bta-miR-27a-3p	Bos taurus	TTCACAGTGGCTAAGTTCGG	0	0	0.18	0.18	0.84	0.21	0	0
	chi-miR-27a-3p	Capra hircus		0	0	0.18	0.18	0.84	0.21	0	0
	ola-miR-27a	Oryzias latipes		0	0	0.18	0.18	0.84	0.21	0	0
	cfa-miR-27a	Canis familiaris		0	0	0.18	0.18	0.84	0.21	0	0
dof-miR-953	hsa-miR-27a-3p	Homo sapiens	TTCACAGTGGCTAAGTTCGGC	0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	mmu-miR-27a-3p	Mus musculus		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	rno-miR-27a-3p	Rattus norvegicus		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	ssc-miR-27a	Sus scrofa		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	xtr-miR-27a	Xenopus tropicalis		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	mdo-miR-27a-3p	Monodelphis domestica		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	oan-miR-27a-3p	Ornithorhynchus anatinus		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	oar-miR-27a	Ovis aries		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	ccr-miR-27a	Cyprinus carpio		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	cgr-miR-27a-3p	Cricetulus griseus		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	aca-miR-27a-3p	Anolis carolinensis		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
	eca-miR-27a	Equus caballus		0.2	0	1.1	1.44	1.59	0.21	0.83	0.14
dof-miR-954	dre-miR-27a-3p	Danio rerio	TTCACAGTGGCTAAGTTCGGCT	0	0	0.18	0.54	0.19	0	0	0
	ssa-miR-27a-3p	Salmo salar		0	0	0.18	0.54	0.19	0	0	0
	ipu-miR-27a	Ictalurus punctatus		0	0	0.18	0.54	0.19	0	0	0
dof-miR-955	tch-miR-27a-3p	Tupaia chinensis	TTCACAGTGGCTAAGTTCGGT	0	0	0.18	0.36	0.28	0	0	0

dof-miR-956	mmu-miR-27b-3p	Mus musculus	TTCACAGTGGCTAAGTTCTGC	1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	hsa-miR-27b-3p	Homo sapiens		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	rno-miR-27b-3p	Rattus norvegicus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	gga-miR-27b-3p	Gallus gallus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	bta-miR-27b	Bos taurus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	xtr-miR-27b	Xenopus tropicalis		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	mdo-miR-27b-3p	Monodelphis domestica		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	oan-miR-27b-3p	Ornithorhynchus anatinus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	chi-miR-27b-3p	Capra hircus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	tch-miR-27b-3p	Tupaia chinensis		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	ssa-miR-27b-3p	Salmo salar		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	ipu-miR-27b	Ictalurus punctatus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	sha-miR-27b	Sarcophilus harrisii		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	cgr-miR-27b-3p	Cricetulus griseus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	ggo-miR-27b	Gorilla gorilla		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	pma-miR-27b-3p	Petromyzon marinus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	ppy-miR-27b	Pongo pygmaeus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	eca-miR-27b	Equus caballus		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	ssc-miR-27b-3p	Sus scrofa		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
	tgu-miR-27-3p	Taeniopygia guttata		1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96
mml-miR-27b-3p	Macaca mulatta	1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96		
cfa-miR-27b	Canis familiaris	1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96		
ptr-miR-27b	Pan troglodytes	1.58	4.33	9.92	13.15	7.37	1.15	4.51	1.96		
dof-miR-957	dre-miR-27b-3p	Danio rerio	TTCACAGTGGCTAAGTTCTGCA	0	0	0.18	0.54	0.19	0	0	0
	fru-miR-27b	Fugu rubripes		0	0	0.18	0.54	0.19	0	0	0
	tmi-miR-27b	Tetraodon nigroviridis		0	0	0.18	0.54	0.19	0	0	0
	oha-miR-27b-3p	Ophiophagus hannah		0	0	0.18	0.54	0.19	0	0	0
	aca-miR-27b-3p	Anolis carolinensis		0	0	0.18	0.54	0.19	0	0	0
dof-miR-958	ssa-miR-27d-3p	Salmo salar	TTCACAGTGGTTAAGTTCTG	0	0.25	0	0.18	0	0	0.17	0
	ipu-miR-27c	Ictalurus punctatus		0	0.25	0	0.18	0	0	0.17	0
	ola-miR-27c-3p	Oryzias latipes		0	0.25	0	0.18	0	0	0.17	0
dof-miR-959	dre-miR-27c-3p	Danio rerio	TTCACAGTGGTTAAGTTCTGC	0.59	0.51	0.18	0.36	0	0	0	0.14
	fru-miR-27c	Fugu rubripes		0.59	0.51	0.18	0.36	0	0	0	0.14
	tmi-miR-27c	Tetraodon nigroviridis		0.59	0.51	0.18	0.36	0	0	0	0.14

dof-miR-960	ccr-miR-27c-3p	Cyprinus carpio	TTCACAGTGGTTAAGTTCTGCC	0	0	0	0.18	0	0	0.17	0
dof-miR-961	hsa-miR-197-3p	Homo sapiens	TTCACCACCTTCCACCCAGC	0	0	0.37	0	0.19	0	0	0
	ptr-miR-197	Pan troglodytes		0	0	0.37	0	0.19	0	0	0
	ppy-miR-197	Pongo pygmaeus		0	0	0.37	0	0.19	0	0	0
	age-miR-197	Ateles geoffroyi		0	0	0.37	0	0.19	0	0	0
	ppa-miR-197	Pan paniscus		0	0	0.37	0	0.19	0	0	0
	chi-miR-197-3p	Capra hircus		0	0	0.37	0	0.19	0	0	0
	ggo-miR-197	Gorilla gorilla		0	0	0.37	0	0.19	0	0	0
	eca-miR-197	Equus caballus		0	0	0.37	0	0.19	0	0	0
	mml-miR-197-3p	Macaca mulatta		0	0	0.37	0	0.19	0	0	0
	cfa-miR-197	Canis familiaris		0	0	0.37	0	0.19	0	0	0
bta-miR-197	Bos taurus	0	0	0.37	0	0.19	0	0	0	0	
dof-miR-962	ata-miR393-5p	Aegilops tauschii	TTCCAAAGGGATCGATTGAT	0.2	1.02	6.25	7.75	1.59	1.04	0.83	0.42
dof-miR-963	gma-miR393h	Glycine max	TTCCAAAGGGATCGATTGATC	18.02	74.85	32.7	56.76	27.33	61.98	44.58	37.83
	gma-miR393i	Glycine max		18.02	74.85	32.7	56.76	27.33	61.98	44.58	37.83
	gma-miR393j	Glycine max		18.02	74.85	32.7	56.76	27.33	61.98	44.58	37.83
	gma-miR393k	Glycine max		18.02	74.85	32.7	56.76	27.33	61.98	44.58	37.83
dof-miR-964	mdm-miR396a	Malus domestica	TTCCACAGCTTTCTTGAACAG	2.38	0.51	0	0.72	0.09	0.52	0.17	0.42
dof-miR-965	ppe-miR396a	Prunus persica	TTCCACAGCTTTCTTGAACGT	0.2	0	0	1.26	0	0	0	0
dof-miR-966	vvi-miR396b	Vitis vinifera	TTCCACAGCTTTCTTGAACT	91.1	20.37	107.48	821.1	84.31	99.43	15.36	63.9
dof-miR-967	vvi-miR396a	Vitis vinifera	TTCCACAGCTTTCTTGAACTA	3.96	2.29	2.39	29.91	3.45	9.91	1.5	2.66
	pab-miR396a	Picea abies		3.96	2.29	2.39	29.91	3.45	9.91	1.5	2.66
dof-miR-968	ath-miR396a-5p	Arabidopsis thaliana	TTCCACAGCTTTCTTGAACTG	6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	osa-miR396a-5p	Oryza sativa		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	osa-miR396b-5p	Oryza sativa		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	sbi-miR396b	Sorghum bicolor		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	sbi-miR396a	Sorghum bicolor		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	sof-miR396	Saccharum officinarum		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	gma-miR396a-5p	Glycine max		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	zma-miR396b-5p	Zea mays		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	zma-miR396a-5p	Zea mays		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	ptc-miR396a	Populus trichocarpa		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	ptc-miR396b	Populus trichocarpa		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	mtr-miR396b-5p	Medicago truncatula		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94

	ghr-miR396a	Gossypium hirsutum		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	ghr-miR396b	Gossypium hirsutum		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	vvi-miR396d	Vitis vinifera		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	sly-miR396a-5p	Solanum lycopersicum		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	ata-miR396e-5p	Aegilops tauschii		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	cpa-miR396	Carica papaya		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	mes-miR396a	Manihot esculenta		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	mes-miR396b	Manihot esculenta		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	hbr-miR396b	Hevea brasiliensis		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	mdm-miR396b	Malus domestica		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	cme-miR396b	Cucumis melo		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	ssl-miR396	Salvia sclarea		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	dpr-miR396	Digitalis purpurea		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	lus-miR396a	Linum usitatissimum		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	lus-miR396c	Linum usitatissimum		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	nta-miR396a	Nicotiana tabacum		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	bgym-miR396a	Bruguiera gymnorhiza		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	bcy-miR396a	Bruguiera cylindrica		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	tcc-miR396a	Theobroma cacao		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	tcc-miR396b	Theobroma cacao		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	bdi-miR396d-5p	Brachypodium distachyon		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	bdi-miR396c-5p	Brachypodium distachyon		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	ssp-miR396	Saccharum sp.		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	gma-miR396i-5p	Glycine max		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	aau-miR396	Acacia auriculiformis		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	amg-miR396	Acacia mangium		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	csi-miR396a	Citrus sinensis		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	csi-miR396b	Citrus sinensis		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	aly-miR396a-5p	Arabidopsis lyrata		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	vvi-miR396c	Vitis vinifera		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	lja-miR396	Lotus japonicus		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
	aqc-miR396a	Aquilegia caerulea		6360.1	3143.77	831.37	12378.63	2218.04	4734.21	2528.8	2836.94
dof-miR-969	gma-miR396e	Glycine max	TTCCACAGCTTCTTGAAGTGT	1.19	1.53	0	1.8	0.56	2.61	1.17	0.42
dof-miR-970	ath-miR396b-5p	Arabidopsis thaliana	TTCCACAGCTTCTTGAAGT	31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39

	bgm-miR396b	Bruguiera gymnorhiza		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	bey-miR396b	Bruguiera cylindrica		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	tcc-miR396c	Theobroma cacao		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	tcc-miR396e	Theobroma cacao		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	bdi-miR396e-5p	Brachypodium distachyon		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	zma-miR396e-5p	Zea mays		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	zma-miR396f-5p	Zea mays		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	ccl-miR396	Citrus clementina		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	rco-miR396	Ricinus communis		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	aly-miR396b-5p	Arabidopsis lyrata		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	gma-miR396c	Glycine max		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
	aqc-miR396b	Aquilegia caerulea		31.49	7.38	26.27	4297.21	17.07	34.85	7.68	31.39
dof-miR-971	ptc-miR396f	Populus trichocarpa	TTCCACGGCTTTCTTGAAC TG	2.38	0.25	0.37	4.14	0.47	1.67	0.33	0
	mdm-miR396f	Malus domestica		2.38	0.25	0.37	4.14	0.47	1.67	0.33	0
	mdm-miR396g	Malus domestica		2.38	0.25	0.37	4.14	0.47	1.67	0.33	0
	cme-miR396e	Cucumis melo		2.38	0.25	0.37	4.14	0.47	1.67	0.33	0
dof-miR-972	ptc-miR396g-5p	Populus trichocarpa	TTCCACGGCTTTCTTGAAC TT	0	0	0.18	2.34	0	0	0.17	0
	tcc-miR396d	Theobroma cacao		0	0	0.18	2.34	0	0	0.17	0
	pab-miR396b	Picea abies		0	0	0.18	2.34	0	0	0.17	0
	pab-miR396c	Picea abies		0	0	0.18	2.34	0	0	0.17	0
dof-miR-973	hsa-miR-7977	Homo sapiens	TTCCCAGCCAACGCACCA	0	0	0	0	0	0	0	0.14
dof-miR-974	ata-miR2118b-5p	Aegilops tauschii	TTCCCGATGCCTCCCATTCCTA	0	0	0	0	0.09	0	0	0
	osa-miR2118b	Oryza sativa		0	0	0	0	0.09	0	0	0
	osa-miR2118n	Oryza sativa		0	0	0	0	0.09	0	0	0
	zma-miR2118b	Zea mays		0	0	0	0	0.09	0	0	0
dof-miR-975	mmu-miR-204-5p	Mus musculus	TTCCCTTTGTCATCCTATGCCT	0	0	0	0.18	0	0	0	0.14
	hsa-miR-204-5p	Homo sapiens		0	0	0	0.18	0	0	0	0.14
	rno-miR-204-5p	Rattus norvegicus		0	0	0	0.18	0	0	0	0.14
	gga-miR-204	Gallus gallus		0	0	0	0.18	0	0	0	0.14
	dre-miR-204-5p	Danio rerio		0	0	0	0.18	0	0	0	0.14
	ssc-miR-204	Sus scrofa		0	0	0	0.18	0	0	0	0.14
	ptr-miR-204	Pan troglodytes		0	0	0	0.18	0	0	0	0.14
	ggo-miR-204	Gorilla gorilla		0	0	0	0.18	0	0	0	0.14
	ppy-miR-204	Pongo pygmaeus		0	0	0	0.18	0	0	0	0.14

	far-miR156b	Festuca arundinacea		0.2	0	0	0	0	0	0	0
dof-miR-982	gma-miR156k	Glycine max	TTGACAGAAGAGAGTGAGCAC	1.78	8.91	7.72	7.03	2.61	3.23	7.51	1.82
	gma-miR156n	Glycine max		1.78	8.91	7.72	7.03	2.61	3.23	7.51	1.82
	gma-miR156o	Glycine max		1.78	8.91	7.72	7.03	2.61	3.23	7.51	1.82
dof-miR-983	hbr-miR156	Hevea brasiliensis	TTGACAGAAGATAGAGAGC	0	0	0	0.18	0	0	0	0
dof-miR-984	ath-miR157a-5p	Arabidopsis thaliana	TTGACAGAAGATAGAGAGC	0	0	1.29	21.62	0	0	0.17	0.14
	ath-miR157b-5p	Arabidopsis thaliana		0	0	1.29	21.62	0	0	0.17	0.14
	ath-miR157c-5p	Arabidopsis thaliana		0	0	1.29	21.62	0	0	0.17	0.14
	gma-miR156d	Glycine max		0	0	1.29	21.62	0	0	0.17	0.14
	gma-miR156e	Glycine max		0	0	1.29	21.62	0	0	0.17	0.14
	gma-miR156c	Glycine max		0	0	1.29	21.62	0	0	0.17	0.14
	ptc-miR156g	Populus trichocarpa		0	0	1.29	21.62	0	0	0.17	0.14
	ptc-miR156h	Populus trichocarpa		0	0	1.29	21.62	0	0	0.17	0.14
	ptc-miR156i	Populus trichocarpa		0	0	1.29	21.62	0	0	0.17	0.14
	ptc-miR156j	Populus trichocarpa		0	0	1.29	21.62	0	0	0.17	0.14
	mtr-miR156e	Medicago truncatula		0	0	1.29	21.62	0	0	0.17	0.14
	mtr-miR156f	Medicago truncatula		0	0	1.29	21.62	0	0	0.17	0.14
	mtr-miR156h-5p	Medicago truncatula		0	0	1.29	21.62	0	0	0.17	0.14
	gra-miR157a	Gossypium raimondii		0	0	1.29	21.62	0	0	0.17	0.14
	gra-miR157b	Gossypium raimondii		0	0	1.29	21.62	0	0	0.17	0.14
	bn-miR156b	Brassica napus		0	0	1.29	21.62	0	0	0.17	0.14
	bn-miR156c	Brassica napus		0	0	1.29	21.62	0	0	0.17	0.14
	vvi-miR156f	Vitis vinifera		0	0	1.29	21.62	0	0	0.17	0.14
	vvi-miR156g	Vitis vinifera		0	0	1.29	21.62	0	0	0.17	0.14
	vvi-miR156i	Vitis vinifera		0	0	1.29	21.62	0	0	0.17	0.14
	ppe-miR156g	Prunus persica		0	0	1.29	21.62	0	0	0.17	0.14
	ppe-miR156h	Prunus persica		0	0	1.29	21.62	0	0	0.17	0.14
	ppe-miR156i	Prunus persica		0	0	1.29	21.62	0	0	0.17	0.14
	cpa-miR156e	Carica papaya		0	0	1.29	21.62	0	0	0.17	0.14
	cpa-miR156f	Carica papaya		0	0	1.29	21.62	0	0	0.17	0.14
	lus-miR156h	Linum usitatissimum		0	0	1.29	21.62	0	0	0.17	0.14
	atr-miR156a	Amborella trichopoda		0	0	1.29	21.62	0	0	0.17	0.14
atr-miR156c	Amborella trichopoda	0	0	1.29	21.62	0	0	0.17	0.14		
mes-miR156h	Manihot esculenta	0	0	1.29	21.62	0	0	0.17	0.14		

	bra-miR157a	Brassica rapa		0	0	1.29	21.62	0	0	0.17	0.14
	bol-miR157a	Brassica oleracea		0	0	1.29	21.62	0	0	0.17	0.14
dof-miR-985	csi-miR171a	Citrus sinensis	TTGAGCCGCGCCAATATCAC	0	0	0	0	0	0	0	0.14
	sly-miR171d	Solanum lycopersicum		0	0	0	0	0	0	0	0.14
dof-miR-986	vvi-miR171f	Vitis vinifera	TTGAGCCGCGCCAATATCAC	1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
	lja-miR171d-5p	Lotus japonicus		1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
	mdm-miR171j	Malus domestica		1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
	mdm-miR171k	Malus domestica		1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
	mdm-miR171l	Malus domestica		1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
	ssl-miR171b	Salvia sclarea		1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
	nta-miR171b	Nicotiana tabacum		1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
	ppe-miR171b	Prunus persica		1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
	gma-miR171k-3p	Glycine max		1.19	0.25	0	0.18	2.24	1.15	0.17	0.98
dof-miR-987	gma-miR171m	Glycine max	TTGAGCCGCGTCAATATCTCA	0	0	0	0.9	0	0	0	0
	gma-miR171t	Glycine max		0	0	0	0.9	0	0	0	0
dof-miR-988	mdm-miR171a	Malus domestica	TTGAGCCGCGTCAATATCTCC	93.68	10.95	5.14	7.57	6.62	9.81	77.63	199.26
	mdm-miR171b	Malus domestica		93.68	10.95	5.14	7.57	6.62	9.81	77.63	199.26
	ppe-miR171h	Prunus persica		93.68	10.95	5.14	7.57	6.62	9.81	77.63	199.26
	ctr-miR171	Citrus trifoliata		93.68	10.95	5.14	7.57	6.62	9.81	77.63	199.26
dof-miR-989	sly-miR171e	Solanum lycopersicum	TTGAGCCGCGTCAATATCTCT	1.19	0	0.55	0.18	0	0.52	1.17	2.66
	stu-miR171b-3p	Solanum tuberosum		1.19	0	0.55	0.18	0	0.52	1.17	2.66
dof-miR-990	zma-miR171b-3p	Zea mays	TTGAGCCGTGCCAATATCAC	0	0	0	0.18	0	0	0	0
dof-miR-991	ath-miR171b-3p	Arabidopsis thaliana	TTGAGCCGTGCCAATATCAC	0	0	0	1.08	0	0	0	0
	ath-miR171c-3p	Arabidopsis thaliana		0	0	0	1.08	0	0	0	0
	ptc-miR171a-3p	Populus trichocarpa		0	0	0	1.08	0	0	0	0
	ptc-miR171b	Populus trichocarpa		0	0	0	1.08	0	0	0	0
	mtr-miR171f	Medicago truncatula		0	0	0	1.08	0	0	0	0
	bnm-miR171a	Brassica napus		0	0	0	1.08	0	0	0	0
	bnm-miR171b	Brassica napus		0	0	0	1.08	0	0	0	0
	bnm-miR171c	Brassica napus		0	0	0	1.08	0	0	0	0
	bnm-miR171d	Brassica napus		0	0	0	1.08	0	0	0	0
	bnm-miR171e	Brassica napus		0	0	0	1.08	0	0	0	0
	ata-miR171c-3p	Aegilops tauschii		0	0	0	1.08	0	0	0	0
	mes-miR171b	Manihot esculenta		0	0	0	1.08	0	0	0	0

dof-miR-999	mes-miR166i	Manihot esculenta	TTGGACCAGGCTTCATTCCCC	10.1	5.09	19.84	74.96	1.49	1.04	8.01	16.95
dof-miR-1000	gma-miR319c	Glycine max	TTGGACTGAAAGGAGCTCCT	0	0	0	0	0.09	0	0	0
dof-miR-1001	pta-miR319	Pinus taeda	TTGGACTGAAGGGAGCTCC	0	0	3.31	0.9	4.66	4.8	0.5	0.28
dof-miR-1002	mtr-miR319a-3p	Medicago truncatula	TTGGACTGAAGGGAGCTCCC	114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	gma-miR319a	Glycine max		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	gma-miR319b	Glycine max		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	ptc-miR319a	Populus trichocarpa		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	ptc-miR319b	Populus trichocarpa		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	ptc-miR319c	Populus trichocarpa		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	ptc-miR319d	Populus trichocarpa		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	mtr-miR319b-3p	Medicago truncatula		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	atr-miR319a	Amborella trichopoda		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	atr-miR319c	Amborella trichopoda		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	cme-miR319b	Cucumis melo		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	cme-miR319a	Cucumis melo		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	lus-miR319b	Linum usitatissimum		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	ppe-miR319a	Prunus persica		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
	gma-miR319e	Glycine max		114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74
ctr-miR319	Citrus trifoliata	114.08	12.98	299.66	93.7	634.39	802.88	66.45	64.74		
dof-miR-1003	vvi-miR319g	Vitis vinifera	TTGGACTGAAGGGAGCTCCCA	0.2	0.25	4.59	0.36	9.89	20.97	2.5	0.56
	mtr-miR319c-3p	Medicago truncatula		0.2	0.25	4.59	0.36	9.89	20.97	2.5	0.56
dof-miR-1004	ath-miR319a	Arabidopsis thaliana	TTGGACTGAAGGGAGCTCCCT	546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	ath-miR319b	Arabidopsis thaliana		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	vvi-miR319b	Vitis vinifera		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	vvi-miR319c	Vitis vinifera		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	vvi-miR319f	Vitis vinifera		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	sly-miR319b	Solanum lycopersicum		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	bra-miR319-3p	Brassica rapa		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	mes-miR319a	Manihot esculenta		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	mes-miR319b	Manihot esculenta		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	mes-miR319c	Manihot esculenta		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	mes-miR319d	Manihot esculenta		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	mes-miR319e	Manihot esculenta		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	mtr-miR319d-3p	Medicago truncatula		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83

	stu-miR319a-3p	Solanum tuberosum		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	hbr-miR319	Hevea brasiliensis		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	mdm-miR319a	Malus domestica		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	mdm-miR319b	Malus domestica		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	vun-miR319a	Vigna unguiculata		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	cca-miR319	Cynara cardunculus		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	lus-miR319a	Linum usitatissimum		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	nta-miR319a	Nicotiana tabacum		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	nta-miR319b	Nicotiana tabacum		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	gma-miR319h	Glycine max		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	gma-miR319j	Glycine max		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	gma-miR319k	Glycine max		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	gma-miR319m	Glycine max		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	aau-miR319	Acacia auriculiformis		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	amg-miR319	Acacia mangium		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	tae-miR319	Triticum aestivum		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	rco-miR319a	Ricinus communis		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	rco-miR319b	Ricinus communis		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	rco-miR319c	Ricinus communis		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	aly-miR319a-3p	Arabidopsis lyrata		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	aly-miR319b-3p	Arabidopsis lyrata		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
	aqc-miR319	Aquilegia caerulea		546.63	34.88	2277.68	762.18	4933.47	8395.52	1765.5	308.83
dof-miR-1005	ptc-miR319e	Populus trichocarpa	TTGGACTGAAGGGAGCTCCT	0.99	0.25	1.65	8.47	4.01	5.74	0.67	0.56
	ptc-miR319f	Populus trichocarpa		0.99	0.25	1.65	8.47	4.01	5.74	0.67	0.56
	ptc-miR319g	Populus trichocarpa		0.99	0.25	1.65	8.47	4.01	5.74	0.67	0.56
	ptc-miR319h	Populus trichocarpa		0.99	0.25	1.65	8.47	4.01	5.74	0.67	0.56
	stu-miR319b	Solanum tuberosum		0.99	0.25	1.65	8.47	4.01	5.74	0.67	0.56
	cme-miR319c	Cucumis melo		0.99	0.25	1.65	8.47	4.01	5.74	0.67	0.56
	cme-miR319d	Cucumis melo		0.99	0.25	1.65	8.47	4.01	5.74	0.67	0.56
dof-miR-1006	ath-miR319c	Arabidopsis thaliana	TTGGACTGAAGGGAGCTCCTT	0.2	0.25	0.55	1.08	0.56	2.19	0.83	0.14
	sly-miR319c-3p	Solanum lycopersicum		0.2	0.25	0.55	1.08	0.56	2.19	0.83	0.14
	mes-miR319f	Manihot esculenta		0.2	0.25	0.55	1.08	0.56	2.19	0.83	0.14
	mes-miR319g	Manihot esculenta		0.2	0.25	0.55	1.08	0.56	2.19	0.83	0.14
	aly-miR319d-3p	Arabidopsis lyrata		0.2	0.25	0.55	1.08	0.56	2.19	0.83	0.14

	rco-miR319d	Ricinus communis		0.2	0.25	0.55	1.08	0.56	2.19	0.83	0.14
	aly-miR319c-3p	Arabidopsis lyrata		0.2	0.25	0.55	1.08	0.56	2.19	0.83	0.14
	pvu-miR319c	Phaseolus vulgaris		0.2	0.25	0.55	1.08	0.56	2.19	0.83	0.14
dof-miR-1007	osa-miR319a-3p.2-3p	Oryza sativa	TTGGACTGAAGGGTGCTCCC	0	0	0	0	0.19	0.31	0.17	0
	osa-miR319b	Oryza sativa		0	0	0	0	0.19	0.31	0.17	0
	sbi-miR319a	Sorghum bicolor		0	0	0	0	0.19	0.31	0.17	0
	zma-miR319a-3p	Zea mays		0	0	0	0	0.19	0.31	0.17	0
	zma-miR319c-3p	Zea mays		0	0	0	0	0.19	0.31	0.17	0
	zma-miR319b-3p	Zea mays		0	0	0	0	0.19	0.31	0.17	0
	zma-miR319d-3p	Zea mays		0	0	0	0	0.19	0.31	0.17	0
	sbi-miR319b	Sorghum bicolor		0	0	0	0	0.19	0.31	0.17	0
dof-miR-1008	bdi-miR319b-3p	Brachypodium distachyon	TTGGACTGAAGGGTGCTCCCT	0	0	0.55	0.18	1.21	3.55	0.17	0.14
dof-miR-1009	ath-miR394a	Arabidopsis thaliana	TTGGCATTCTGTCCACCTCC	25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ath-miR394b-5p	Arabidopsis thaliana		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	osa-miR394	Oryza sativa		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	sbi-miR394a	Sorghum bicolor		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	zma-miR394a-5p	Zea mays		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	zma-miR394b-5p	Zea mays		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ptc-miR394a-5p	Populus trichocarpa		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ptc-miR394b-5p	Populus trichocarpa		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	vvi-miR394b	Vitis vinifera		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	sly-miR394-5p	Solanum lycopersicum		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ata-miR394-5p	Aegilops tauschii		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	stu-miR384-5p	Solanum tuberosum		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ppe-miR394b	Prunus persica		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	cpa-miR394a	Carica papaya		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	cpa-miR394b	Carica papaya		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	atr-miR394	Amborella trichopoda		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	mes-miR394b	Manihot esculenta		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	gma-miR394g	Glycine max		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	mdm-miR394a	Malus domestica		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	mdm-miR394b	Malus domestica		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
cme-miR394b	Cucumis melo	25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81		
cme-miR394a	Cucumis melo	25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81		

	ssl-miR394	Salvia sclarea		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	gma-miR394d	Glycine max		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	gma-miR394e	Glycine max		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	gma-miR394f	Glycine max		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	bnm-miR394a	Brassica napus		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	bnm-miR394b	Brassica napus		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	mes-miR394a	Manihot esculenta		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	cca-miR394	Cynara cardunculus		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	lus-miR394a	Linum usitatissimum		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	lus-miR394b	Linum usitatissimum		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	nta-miR394	Nicotiana tabacum		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ppe-miR394a	Prunus persica		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	tcc-miR394a	Theobroma cacao		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	tcc-miR394b	Theobroma cacao		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	gma-miR394c-5p	Glycine max		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	bdi-miR394	Brachypodium distachyon		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ahy-miR394	Arachis hypogaea		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	gma-miR394b-5p	Glycine max		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	gma-miR394a-5p	Glycine max		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	csi-miR394	Citrus sinensis		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ghr-miR394b	Gossypium hirsutum		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	ghr-miR394a	Gossypium hirsutum		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	aly-miR394a-5p	Arabidopsis lyrata		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	aly-miR394b-5p	Arabidopsis lyrata		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
	sbi-miR394b	Sorghum bicolor		25.75	56.52	55.85	610.1	45.05	69.49	21.04	31.81
dof-miR-1010	ptc-miR319i	Populus trichocarpa	TTGGGCTGAAGGGAGCTCC	0	0	0	0	0.09	0.31	0	0
dof-miR-1011	dme-miR-133-3p	Drosophila melanogaster	TTGGTCCCCTTCAACCAGCTGT	2.18	2.55	0.92	1.44	0	0	1.5	0.84
	gga-miR-133a-3p	Gallus gallus		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	dps-miR-133	Drosophila pseudoobscura		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	xla-miR-133a	Xenopus laevis		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	ame-miR-133	Apis mellifera		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	aga-miR-133	Anopheles gambiae		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	ggo-miR-133a	Gorilla gorilla		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	age-miR-133a	Ateles geoffroyi		2.18	2.55	0.92	1.44	0	0	1.5	0.84

	lgi-miR-133-3p	Lottia gigantea		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	ske-miR-133	Saccoglossus kowalevskii		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	cfa-miR-133a	Canis familiaris		2.18	2.55	0.92	1.44	0	0	1.5	0.84
	dpu-miR-133	Daphnia pulex		2.18	2.55	0.92	1.44	0	0	1.5	0.84
dof-miR-1012	hsa-miR-493-5p	Homo sapiens	TTGTACATGGTAGGCTTTCATT	0	0	0	0.36	0	0	0	0
	rno-miR-493-5p	Rattus norvegicus		0	0	0	0.36	0	0	0	0
	chi-miR-493-5p	Capra hircus		0	0	0	0.36	0	0	0	0
	ssc-miR-493-5p	Sus scrofa		0	0	0	0.36	0	0	0	0
	oar-miR-493-5p	Ovis aries		0	0	0	0.36	0	0	0	0
	mml-miR-493-5p	Macaca mulatta		0	0	0	0.36	0	0	0	0
dof-miR-1013	hsa-miR-218-5p	Homo sapiens	TTGTGCTTGATCTAACCATGT	0	0	0.55	0.36	0	0	0	0
	mmu-miR-218-5p	Mus musculus		0	0	0.55	0.36	0	0	0	0
	rno-miR-218a-5p	Rattus norvegicus		0	0	0.55	0.36	0	0	0	0
	gga-miR-218-5p	Gallus gallus		0	0	0.55	0.36	0	0	0	0
	ggo-miR-218	Gorilla gorilla		0	0	0.55	0.36	0	0	0	0
	age-miR-218	Ateles geoffroyi		0	0	0.55	0.36	0	0	0	0
	ppa-miR-218	Pan paniscus		0	0	0.55	0.36	0	0	0	0
	lca-miR-218	Lemur catta		0	0	0.55	0.36	0	0	0	0
	ppy-miR-218	Pongo pygmaeus		0	0	0.55	0.36	0	0	0	0
	ptr-miR-218	Pan troglodytes		0	0	0.55	0.36	0	0	0	0
	sla-miR-218	Saguinus labiatus		0	0	0.55	0.36	0	0	0	0
	lla-miR-218	Lagothrix lagotricha		0	0	0.55	0.36	0	0	0	0
	mne-miR-218	Macaca nemestrina		0	0	0.55	0.36	0	0	0	0
	mml-miR-218-5p	Macaca mulatta		0	0	0.55	0.36	0	0	0	0
	xtr-miR-218	Xenopus tropicalis		0	0	0.55	0.36	0	0	0	0
	mdo-miR-218-5p	Monodelphis domestica		0	0	0.55	0.36	0	0	0	0
	oan-miR-218-5p	Ornithorhynchus anatinus		0	0	0.55	0.36	0	0	0	0
	chi-miR-218	Capra hircus		0	0	0.55	0.36	0	0	0	0
	tch-miR-218-5p	Tupaia chinensis		0	0	0.55	0.36	0	0	0	0
	oar-miR-218a	Ovis aries		0	0	0.55	0.36	0	0	0	0
	ssc-miR-218	Sus scrofa		0	0	0.55	0.36	0	0	0	0
	ola-miR-218a	Oryzias latipes		0	0	0.55	0.36	0	0	0	0
	ssc-miR-218-5p	Sus scrofa		0	0	0.55	0.36	0	0	0	0
	eca-miR-218	Equus caballus		0	0	0.55	0.36	0	0	0	0

	tgu-miR-218-5p	Taeniopygia guttata		0	0	0.55	0.36	0	0	0	0
	cfa-miR-218	Canis familiaris		0	0	0.55	0.36	0	0	0	0
dof-miR-1014	dre-miR-218a	Danio rerio	TTGTGCTTGATCTAACCATGTG	0	0	0.18	0	0	0	0	0
	fru-miR-218a	Fugu rubripes		0	0	0.18	0	0	0	0	0
	tni-miR-218a	Tetraodon nigroviridis		0	0	0.18	0	0	0	0	0
	bta-miR-218	Bos taurus		0	0	0.18	0	0	0	0	0
	oha-miR-218-5p	Ophiophagus hannah		0	0	0.18	0	0	0	0	0
	ssa-miR-218-5p	Salmo salar		0	0	0.18	0	0	0	0	0
	ccr-miR-218a	Cyprinus carpio		0	0	0.18	0	0	0	0	0
	cgr-miR-218a	Cricetulus griseus		0	0	0.18	0	0	0	0	0
	pma-miR-218a-5p	Petromyzon marinus		0	0	0.18	0	0	0	0	0
	ssc-miR-218b	Sus scrofa		0	0	0.18	0	0	0	0	0
aca-miR-218-5p	Anolis carolinensis	0	0	0.18	0	0	0	0	0	0	
dof-miR-1015	stu-miR398b-3p	Solanum tuberosum	TTGTGTTCTCAGGTCACCCCT	0	0	0	3.42	0	0	0	0
dof-miR-1016	xtr-miR-202-5p	Xenopus tropicalis	TTTCCTATGCATATACTCTTT	0	0	2.02	2.7	0	0	0	0
dof-miR-1017	atr-miR319b	Amborella trichopoda	TTTGGACTGAAGGGAGCTCCT	0	0.76	2.39	1.62	0	0.1	0.33	0
	atr-miR319d	Amborella trichopoda		0	0.76	2.39	1.62	0	0.1	0.33	0
	atr-miR319e	Amborella trichopoda		0	0.76	2.39	1.62	0	0.1	0.33	0
	tcc-miR319	Theobroma cacao		0	0.76	2.39	1.62	0	0.1	0.33	0
	csi-miR319	Citrus sinensis		0	0.76	2.39	1.62	0	0.1	0.33	0
	vvi-miR319e	Vitis vinifera		0	0.76	2.39	1.62	0	0.1	0.33	0
dof-miR-1018	pde-miR1312	Pinus densata	TTTGGAGAGAAAATGGCGACAT	0	0	0.37	1.26	0	0	0.17	0
	pta-miR1312	Pinus taeda		0	0	0.37	1.26	0	0	0.17	0
dof-miR-1019	zma-miR159h-3p	Zea mays	TTTGGAGTGAAGGGAGCTCTG	0	0	0.37	0.36	0.19	0.52	0	0
	zma-miR159i-3p	Zea mays		0	0	0.37	0.36	0.19	0.52	0	0
dof-miR-1020	ath-miR159c	Arabidopsis thaliana	TTTGGATTGAAGGGAGCTCCT	0	0	0	1.08	0	0.1	0	0
	aly-miR159c-3p	Arabidopsis lyrata		0	0	0	1.08	0	0.1	0	0
dof-miR-1021	ath-miR159a	Arabidopsis thaliana	TTTGGATTGAAGGGAGCTCTA	0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	gma-miR159a-3p	Glycine max		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	ptc-miR159a	Populus trichocarpa		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	ptc-miR159b	Populus trichocarpa		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	bna-miR159	Brassica napus		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	vvi-miR159c	Vitis vinifera		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	ppe-miR159	Prunus persica		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7

	cpa-miR159a	Carica papaya		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	atr-miR159	Amborella trichopoda		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	mes-miR159b	Manihot esculenta		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	hbr-miR159a	Hevea brasiliensis		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	htu-miR159a	Helianthus tuberosus		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	cme-miR159a	Cucumis melo		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	mes-miR159a	Manihot esculenta		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	nta-miR159	Nicotiana tabacum		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	gma-miR159e-3p	Glycine max		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	ahy-miR159	Arachis hypogaea		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	csi-miR159	Citrus sinensis		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	rco-miR159	Ricinus communis		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	aly-miR159a-3p	Arabidopsis lyrata		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	sly-miR159	Solanum lycopersicum		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	bra-miR159a	Brassica rapa		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	mtr-miR159a	Medicago truncatula		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
	pvu-miR159a.1	Phaseolus vulgaris		0.59	0.25	6.61	718.21	2.05	4.8	2.84	0.7
dof-miR-1022	lus-miR159b	Linum usitatissimum	TTTGGATTGAAGGGAGCTCTC	0	0	0.55	0.9	0.93	1.98	0	0
dof-miR-1023	osa-miR159a.1	Oryza sativa	TTTGGATTGAAGGGAGCTCTG	289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	osa-miR159b	Oryza sativa		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	sbi-miR159a	Sorghum bicolor		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	sof-miR159a	Saccharum officinarum		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	sof-miR159b	Saccharum officinarum		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	sof-miR159d	Saccharum officinarum		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	zma-miR159a-3p	Zea mays		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	zma-miR159b-3p	Zea mays		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	tae-miR159a	Triticum aestivum		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	tae-miR159b	Triticum aestivum		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	bdi-miR159b-3p.1	Brachypodium distachyon		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	ssp-miR159a	Saccharum sp.		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	hvu-miR159b	Hordeum vulgare		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	hvu-miR159a	Hordeum vulgare		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
	far-miR159	Festuca arundinacea		289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07
zma-miR159f-3p	Zea mays	289.75	678.7	1547.54	1150.65	1814.86	2489.7	315.2	282.07		

	rno-miR-758-3p	Rattus norvegicus		0	0	0	0	0	0.1	0	0
	chi-miR-758	Capra hircus		0	0	0	0	0	0.1	0	0
	ppy-miR-758	Pongo pygmaeus		0	0	0	0	0	0.1	0	0
	eca-miR-758	Equus caballus		0	0	0	0	0	0.1	0	0
	ptr-miR-758	Pan troglodytes		0	0	0	0	0	0.1	0	0
	bta-miR-758	Bos taurus		0	0	0	0	0	0.1	0	0
	cfa-miR-758	Canis familiaris		0	0	0	0	0	0.1	0	0
dof-miR-1037	ptc-miR403c-5p	Populus trichocarpa	TTTGTGCGTGGATCTGAGGCC	0	0	0	0	0	0	0.17	0
dof-miR-1038	hsa-miR-375	Homo sapiens	TTTGTTCGTTTCGGCTCGCGTGA	0	0	0	0.18	0.09	0	0.17	0
	mmu-miR-375-3p	Mus musculus		0	0	0	0.18	0.09	0	0.17	0
	rno-miR-375-3p	Rattus norvegicus		0	0	0	0.18	0.09	0	0.17	0
	ggo-miR-375	Gorilla gorilla		0	0	0	0.18	0.09	0	0.17	0
	ppy-miR-375	Pongo pygmaeus		0	0	0	0.18	0.09	0	0.17	0
	mml-miR-375	Macaca mulatta		0	0	0	0.18	0.09	0	0.17	0
	ptr-miR-375	Pan troglodytes		0	0	0	0.18	0.09	0	0.17	0
cfa-miR-375	Canis familiaris	0	0	0	0.18	0.09	0	0.17	0		
dof-miR-1039	ptc-miR472b	Populus trichocarpa	TTTTCCCAACTCCACCCATCCC	0	0	2.57	2.7	0	0	1	0
dof-miR-1040	ptc-miR472a	Populus trichocarpa	TTTTCCCTACTCCACCCATCCC	0	0	2.94	3.96	0	0	1.5	0
dof-miR-1041	cfa-miR-450b	Canis familiaris	TTTTGCAATATGTTCTGAAT	0	0	0.18	0.72	0	0	0	0
dof-miR-1042	hsa-miR-450b-5p	Homo sapiens	TTTTGCAATATGTTCTGAATA	0.2	0	0	0	0	0	0	0
	ggo-miR-450b	Gorilla gorilla		0.2	0	0	0	0	0	0	0
	bta-miR-450b	Bos taurus		0.2	0	0	0	0	0	0	0
	ppy-miR-450b-5p	Pongo pygmaeus		0.2	0	0	0	0	0	0	0
	eca-miR-450b-5p	Equus caballus		0.2	0	0	0	0	0	0	0
	ssc-miR-450b-5p	Sus scrofa		0.2	0	0	0	0	0	0	0
	mml-miR-450b-5p	Macaca mulatta		0.2	0	0	0	0	0	0	0
dof-miR-1043	chi-miR-450-5p	Capra hircus	TTTTGCGATGTGTTCTAAT	0.2	0	0.55	0.18	0	0	0	0
dof-miR-1044	rno-miR-450b-5p	Rattus norvegicus	TTTTGCGATGTGTTCTAATA	0	0	0	0.36	0	0	0	0
	ggo-miR-450a	Gorilla gorilla		0	0	0	0.36	0	0	0	0
	ppy-miR-450a	Pongo pygmaeus		0	0	0	0.36	0	0	0	0
dof-miR-1045	ssc-miR-450c-5p	Sus scrofa	TTTTGCGATGTGTTCTAATAC	0	0	0.37	0.18	0	0	0	0
	eca-miR-450c	Equus caballus		0	0	0.37	0.18	0	0	0	0
dof-miR-1046	hsa-miR-450a-5p	Homo sapiens	TTTTGCGATGTGTTCTAATAT	0	0	1.84	0.54	0.09	0	0	0
	mmu-miR-450a-5p	Mus musculus		0	0	1.84	0.54	0.09	0	0	0

	bta-miR-450a	Bos taurus		0	0	1.84	0.54	0.09	0	0	0
	efu-miR-450	Eptesicus fuscus		0	0	1.84	0.54	0.09	0	0	0
	tch-miR-450a-5p	Tupaia chinensis		0	0	1.84	0.54	0.09	0	0	0
	cgr-miR-450a	Cricetulus griseus		0	0	1.84	0.54	0.09	0	0	0
	eca-miR-450a	Equus caballus		0	0	1.84	0.54	0.09	0	0	0
	mml-miR-450a-5p	Macaca mulatta		0	0	1.84	0.54	0.09	0	0	0
	ptr-miR-450a	Pan troglodytes		0	0	1.84	0.54	0.09	0	0	0
	ssc-miR-450a	Sus scrofa		0	0	1.84	0.54	0.09	0	0	0
dof-miR-1047	osa-miR5179	Oryza sativa	TTTTGCTCAAGACCGCAAC	7.13	5.86	18.19	6.67	12.59	16.28	30.22	12.47
	bdi-miR5179	Brachypodium distachyon		7.13	5.86	18.19	6.67	12.59	16.28	30.22	12.47

Table S6 A partial list of miRNA--target pairs identified from *Dendrobium officinale*. The miRNA IDs, target transcript IDs, target length and target annotations are included in this table. Based on the functional annotations of the target transcripts, the miRNA--target pairs were classified into four functional groups (hormone signaling-, plant development-, secondary metabolism- and Argonaute 1-related groups) for network construction.

Hormone signaling:

Regulatory miRNA IDs	Target transcript IDs	Target transcript length	Target transcript annotations	GO (Gene Ontology) term annotations of target transcripts
dof-miR-835	comp151738_c1_seq1	1151	NAC domain-containing protein	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0009734(auxin mediated signaling pathway);GO:0048527(lateral root development);GO:0010072(primary shoot apical meristem specification)
dof-miR-836				
dof-miR-837				
dof-miR-838				
dof-miR-839				
dof-miR-840				
dof-miR-835	comp151738_c1_seq2	1220	NAC domain-containing protein	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0009734(auxin mediated signaling pathway);GO:0048527(lateral root development);GO:0010072(primary shoot apical meristem specification)
dof-miR-836				
dof-miR-837				
dof-miR-838				
dof-miR-839				
dof-miR-840				
dof-miR-835	comp151738_c1_seq3	1178	NAC domain-containing protein 21/22 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0009734(auxin mediated signaling pathway);GO:0048527(lateral root development);GO:0010072(primary shoot apical meristem specification)
dof-miR-836				
dof-miR-837				
dof-miR-838				
dof-miR-839				
dof-miR-840				
dof-miR-835	comp160962_c0_seq2	1758	NAC domain-containing protein 100 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-836				
dof-miR-837				

dof-miR-838				
dof-miR-839				
dof-miR-835	comp160962_c0_seq11	1369	NAC domain-containing protein 100 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-836				
dof-miR-837				
dof-miR-838				
dof-miR-839				
dof-miR-840				
dof-miR-835	comp160962_c0_seq13	1484	NAC domain-containing protein 100 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-836				
dof-miR-837				
dof-miR-838				
dof-miR-839				
dof-miR-840				
dof-miR-815	comp165418_c0_seq1	2900	Auxin response factor 18 OS=Oryza sativa subsp. Japonica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-816				
dof-miR-817				
dof-miR-815	comp165418_c0_seq8	3366	Auxin response factor 18 OS=Oryza sativa subsp. Japonica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-816				
dof-miR-817				
dof-miR-815	comp165418_c0_seq16	2926	Auxin response factor 18 OS=Oryza sativa subsp. Japonica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-816				
dof-miR-817				
dof-miR-815	comp165418_c0_seq18	2790	Auxin response factor 18 OS=Oryza sativa subsp. Japonica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-816				
dof-miR-817				
dof-miR-815	comp165418_c0_seq20	3432	Auxin response factor 18 OS=Oryza sativa subsp. Japonica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-816				
dof-miR-817				
dof-miR-421	comp171031_c0_seq1	4351	Auxin response factor 12 OS=Oryza sativa subsp. Indica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-707				

dof-miR-708				
dof-miR-710				
dof-miR-711				
dof-miR-712				
dof-miR-713				
dof-miR-715				
dof-miR-421	comp171031_c0_seq10	4326	Auxin response factor 12 OS=Oryza sativa subsp. Indica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-707				
dof-miR-708				
dof-miR-710				
dof-miR-711				
dof-miR-712				
dof-miR-713				
dof-miR-715				
dof-miR-421	comp171031_c0_seq12	4952	Auxin response factor 12 OS=Oryza sativa subsp. Indica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-707				
dof-miR-708				
dof-miR-710				
dof-miR-711				
dof-miR-712				
dof-miR-713				
dof-miR-715				
dof-miR-421	comp171031_c0_seq23	4977	Auxin response factor 12 OS=Oryza sativa subsp. Indica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-707				
dof-miR-708				
dof-miR-710				
dof-miR-711				
dof-miR-712				
dof-miR-713				
dof-miR-715				
dof-miR-421	comp171031_c0_seq29	4254	Auxin response factor 12 OS=Oryza sativa subsp.	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin

dof-miR-707			Indica	mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-708				
dof-miR-710				
dof-miR-711				
dof-miR-712				
dof-miR-713				
dof-miR-715				
dof-miR-421	comp171031_c0_seq32	1782	Auxin response factor 12 OS=Oryza sativa subsp. Indica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-707				
dof-miR-708				
dof-miR-710				
dof-miR-711				
dof-miR-712				
dof-miR-713				
dof-miR-715				
dof-miR-421	comp171031_c0_seq34	4279	Auxin response factor 12 OS=Oryza sativa subsp. Indica	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-707				
dof-miR-708				
dof-miR-710				
dof-miR-711				
dof-miR-712				
dof-miR-713				
dof-miR-715				
dof-miR-522	comp169140_c0_seq5	1037	Auxin response factor 9 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0046983(protein dimerization activity);GO:0009734(auxin mediated signaling pathway);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-523				
dof-miR-962	comp167643_c0_seq3	2202	TRANSPORT INHIBITOR RESPONSE (TIR) 1 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0019005(SCF ubiquitin ligase complex);GO:0010011(auxin binding);GO:0000822(inositol hexakisphosphate binding);GO:0005515(protein binding);GO:0004842(ubiquitin-protein ligase activity);GO:0009734(auxin mediated signaling pathway);GO:0007049(cell cycle);GO:0016036(cellular response to phosphate starvation);GO:0006952(defense response);GO:0009873(ethylene mediated signaling pathway);GO:0010311(lateral root formation);GO:0002237(response to molecule of bacterial origin)
dof-miR-963				
dof-miR-718	comp163584_c0_seq4	2715	Ethylene-responsive transcription factor RAP2-7 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0009873(ethylene mediated signaling pathway);GO:0010228(vegetative to reproductive phase transition of meristem)
dof-miR-752				

Development:

Regulatory miRNA IDs	Target transcript IDs	Target transcript length	Target transcript annotations	GO (Gene Ontology) term annotations of target transcripts
dof-miR-718	comp163584_c0_seq3	1402	Floral homeotic protein APETALA 2 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0030154(cell differentiation);GO:0010073(meristem maintenance);GO:0048316(seed development);GO:0010093(specification of floral organ identity)
dof-miR-752				
dof-miR-718	comp163807_c0_seq1	2436	Floral homeotic protein APETALA 2 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0030154(cell differentiation);GO:0010073(meristem maintenance);GO:0048316(seed development);GO:0010093(specification of floral organ identity)
dof-miR-718	comp163807_c0_seq2	2310	Floral homeotic protein APETALA 2 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0030154(cell differentiation);GO:0010073(meristem maintenance);GO:0048316(seed development);GO:0010093(specification of floral organ identity)
dof-miR-1047	comp167920_c2_seq11	1185	MADS-box transcription factor 16 OS=Oryza sativa subsp. Japonica	GO:0005634(nucleus);GO:0043565(sequence-specific DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0030154(cell differentiation);GO:0009908(flower development)
dof-miR-1047	comp167920_c2_seq2	1116	MADS-box transcription factor 16 OS=Oryza sativa subsp. Japonica	GO:0005634(nucleus);GO:0043565(sequence-specific DNA binding);GO:0003700(sequence-specific DNA binding transcription factor activity);GO:0030154(cell differentiation);GO:0009908(flower development)
dof-miR-1001	comp166058_c0_seq4	2025	Transcription factor TCP2 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0048366(leaf development);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-1005				
dof-miR-1006				
dof-miR-1007				
dof-miR-1008				
dof-miR-1001	comp166058_c0_seq9	1802	Transcription factor TCP2 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0003677(DNA binding);GO:0048366(leaf development);GO:0006355(regulation of transcription, DNA-dependent);GO:0006351(transcription, DNA-dependent)
dof-miR-1005				
dof-miR-1006				
dof-miR-1007				
dof-miR-1008				

dof-miR-606	comp154657_c0_seq2	3067	Growth-regulating factor 6 OS=Oryza sativa subsp. Japonica	-
dof-miR-606	comp154657_c0_seq3	2463	Growth-regulating factor 6 OS=Oryza sativa subsp. Japonica	-
dof-miR-606	comp154657_c0_seq5	2996	Growth-regulating factor 6 OS=Oryza sativa subsp. Japonica	-
dof-miR-606	comp154657_c0_seq6	3600	Growth-regulating factor 6 OS=Oryza sativa subsp. Japonica	-
dof-miR-606	comp165566_c0_seq1	1689	Growth-regulating factor 4 OS=Oryza sativa subsp. Japonica	-
dof-miR-606	comp170683_c0_seq9	1362	Growth-regulating factor 5 OS=Oryza sativa subsp. Japonica	-
dof-miR-606	comp68197_c0_seq2	575	Growth-regulating factor 7 OS=Oryza sativa subsp. Japonica	-
dof-miR-985	comp156499_c0_seq2	2726	Scarecrow-like protein 6 OS=Arabidopsis thaliana	GO:0005634(nucleus);GO:0005515(protein binding);GO:0051301(cell division);GO:0007623(circadian rhythm);GO:0006355(regulation of transcription, DNA-dependent);GO:0048768(root hair cell tip growth);GO:0006351(transcription, DNA-dependent)
dof-miR-986				
dof-miR-987				
dof-miR-988				
dof-miR-989				
dof-miR-990				
dof-miR-991				
dof-miR-831	comp150481_c0_seq2	876	Expansin-like B1 OS=Oryza sativa subsp. Japonica	GO:0005576(extracellular region)
dof-miR-831	comp150481_c0_seq3	998	Expansin-like B1 OS=Oryza sativa subsp. Japonica	GO:0005576(extracellular region)

Secondary metabolism:

Regulatory miRNA IDs	Target transcript IDs	Target transcript length	Target transcript annotations	KOG (eukaryotic orthologous group) annotations of target transcripts	GO (Gene Ontology) term annotations of target transcripts
dof-miR-992	comp153832_c0_seq1	2021	Laccase-3 OS=Oryza sativa subsp. Japonica	[Q] Secondary metabolites biosynthesis, transport and catabolism	GO:0048046(apoplast);GO:0005507(copper ion binding);GO:0052716(hydroquinone:oxygen oxidoreductase activity);GO:0008471(laccase activity);GO:0046274(lignin catabolic process)
dof-miR-992	comp163430_c1_seq2	2185	Laccase-7 OS=Arabidopsis thaliana	[Q] Secondary metabolites biosynthesis, transport and catabolism	GO:0048046(apoplast);GO:0005507(copper ion binding);GO:0052716(hydroquinone:oxygen oxidoreductase activity);GO:0008471(laccase activity);GO:0046274(lignin catabolic process)
dof-miR-992	comp167551_c0_seq1	1998	Laccase-3 OS=Oryza sativa subsp. Japonica	[Q] Secondary metabolites biosynthesis, transport and catabolism	GO:0048046(apoplast);GO:0005507(copper ion binding);GO:0052716(hydroquinone:oxygen oxidoreductase activity);GO:0008471(laccase activity);GO:0046274(lignin catabolic process)
dof-miR-803	comp167551_c0_seq6	2127	Laccase-3 OS=Oryza sativa subsp. Japonica	[Q] Secondary metabolites biosynthesis, transport and catabolism	GO:0048046(apoplast);GO:0005507(copper ion binding);GO:0052716(hydroquinone:oxygen oxidoreductase activity);GO:0008471(laccase activity);GO:0046274(lignin catabolic process)
dof-miR-804					
dof-miR-992	comp172995_c3_seq3	2382	Laccase-22 OS=Oryza sativa subsp. Japonica	[Q] Secondary metabolites biosynthesis, transport and catabolism	GO:0048046(apoplast);GO:0005507(copper ion binding);GO:0052716(hydroquinone:oxygen oxidoreductase activity);GO:0008471(laccase activity);GO:0046274(lignin catabolic process)
dof-miR-992	comp172995_c3_seq8	2303	Laccase-22 OS=Oryza sativa subsp. Japonica	[Q] Secondary metabolites biosynthesis, transport and catabolism	GO:0048046(apoplast);GO:0005507(copper ion binding);GO:0052716(hydroquinone:oxygen oxidoreductase activity);GO:0008471(laccase activity);GO:0046274(lignin catabolic process)
dof-miR-992	comp172995_c3_seq15	2227	Laccase-22 OS=Oryza sativa subsp. Japonica	[Q] Secondary metabolites biosynthesis, transport and catabolism	GO:0048046(apoplast);GO:0005507(copper ion binding);GO:0052716(hydroquinone:oxygen oxidoreductase activity);GO:0008471(laccase activity);GO:0046274(lignin catabolic process)
dof-miR-992	comp172995_c3_seq16	2306	Laccase-22 OS=Oryza sativa subsp. Japonica	[Q] Secondary metabolites biosynthesis, transport and catabolism	GO:0048046(apoplast);GO:0005507(copper ion binding);GO:0052716(hydroquinone:oxygen oxidoreductase activity);GO:0008471(laccase activity);GO:0046274(lignin catabolic process)

AGO1-related:

Regulatory miRNA IDs	Target transcript IDs	Target transcript length	Target transcript annotations
dof-miR-642	comp174401_c2_seq5	4114	Protein argonaute 1B OS=Oryza sativa subsp. Japonica
dof-miR-644			
dof-miR-645			
dof-miR-646			
dof-miR-647			
dof-miR-642	comp174401_c2_seq6	4269	Protein argonaute 1B OS=Oryza sativa subsp. Japonica
dof-miR-644			
dof-miR-645			
dof-miR-646			
dof-miR-647			