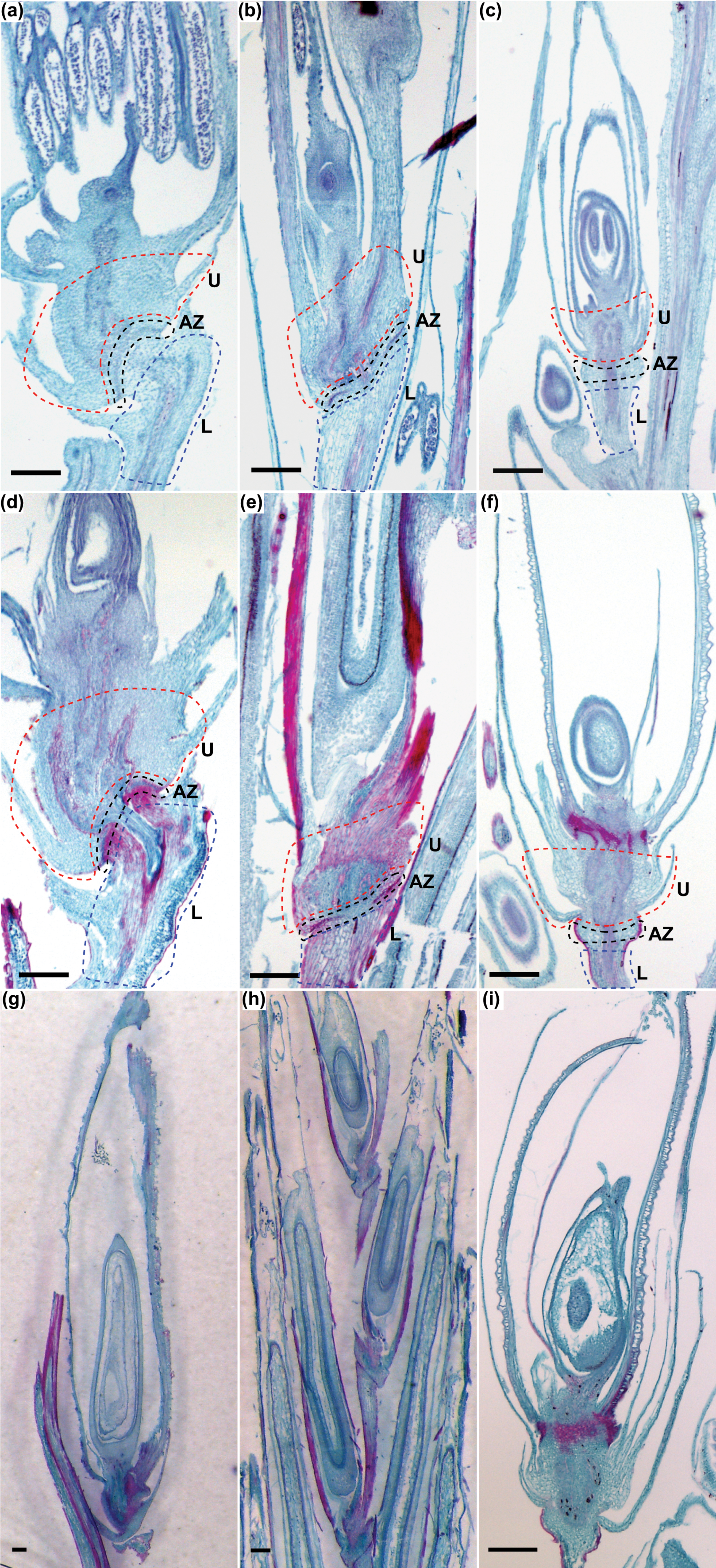
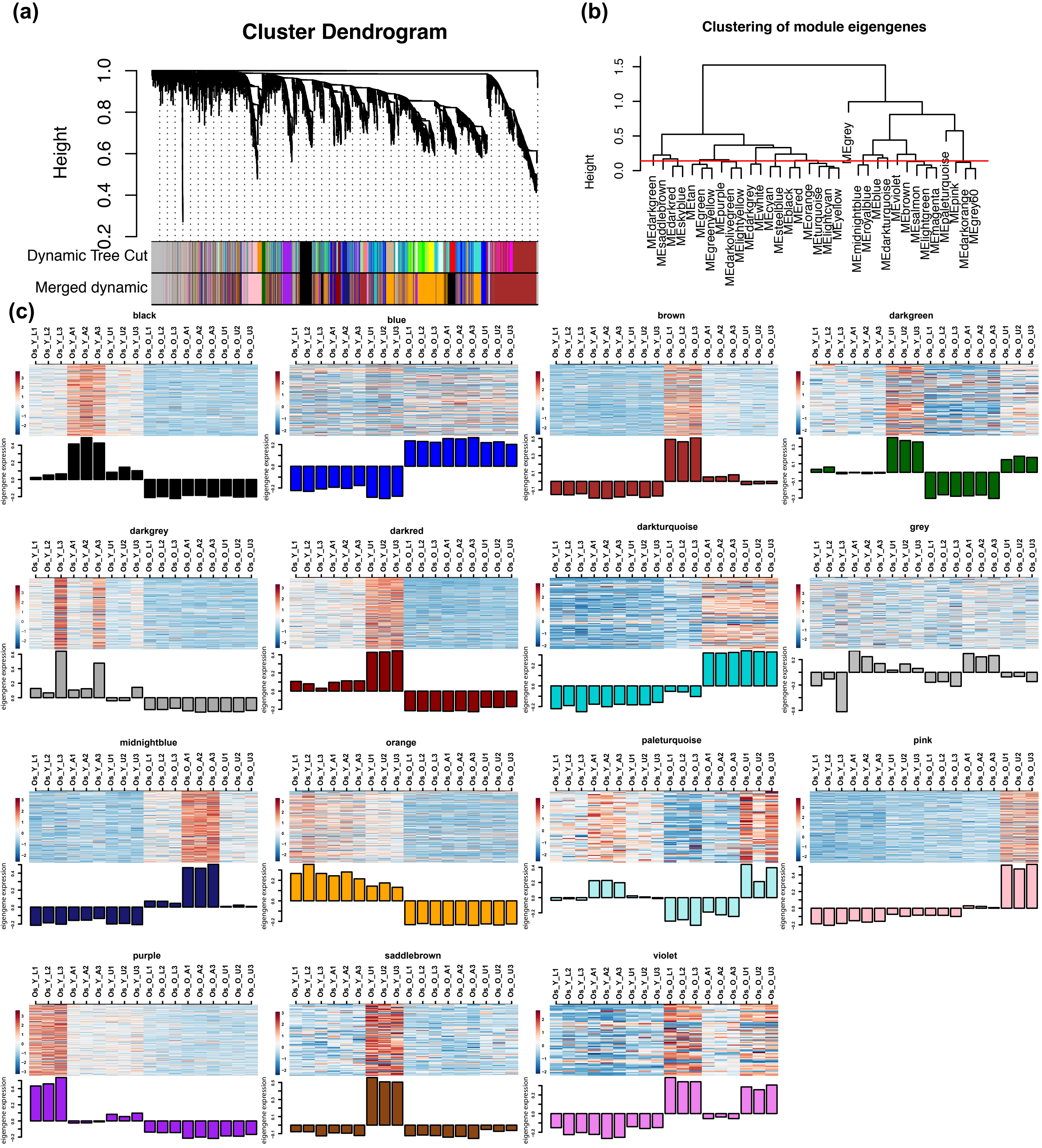
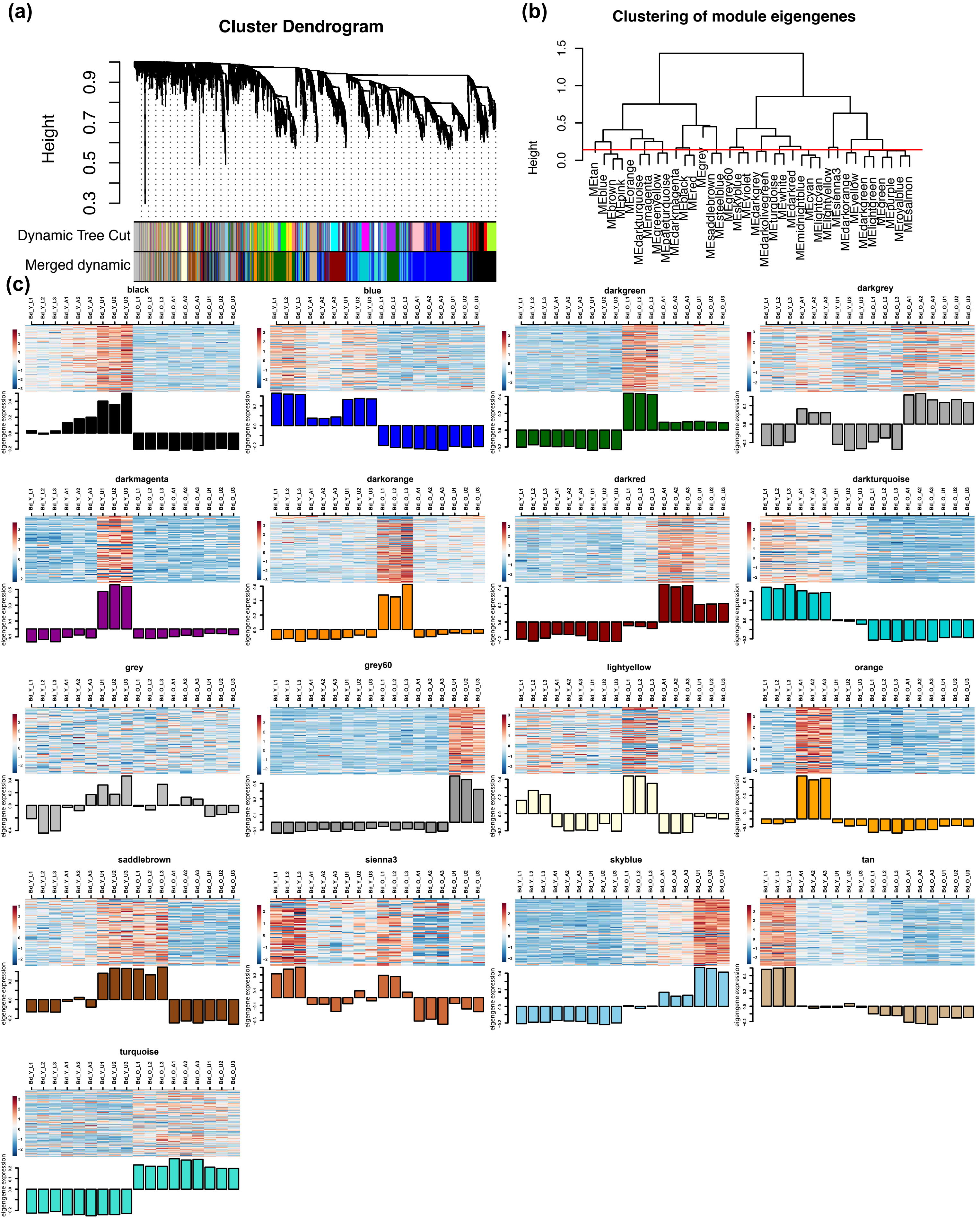
Supporting Information Figure S1. The abscission zones (AZs) have different cell wall components at different developmental stages in rice, Brachypodium and Setaria. Fast green/safranin O staining of (a-c) young and (d-i) old stage used for RNA-Seq in (a, d, g) rice, (b, e, h) Brachypodium and (c, f, i) Setaria. (a-f) The AZ, upper region (U) and lower region (L) collected for RNA-Seq are marked with dotted lines in black, red and blue, respectively. The ovary size relative to the whole spikelet is shown in (g-i). Scale bar = 200 μm.


(a)
U
AZ
L
(b)
U
AZ
L
(c)
U
AZ
L
(d)
U
AZ
L
(e)
U
AZ
L
(f)
U
AZ
L
(g)
(h)
(i)

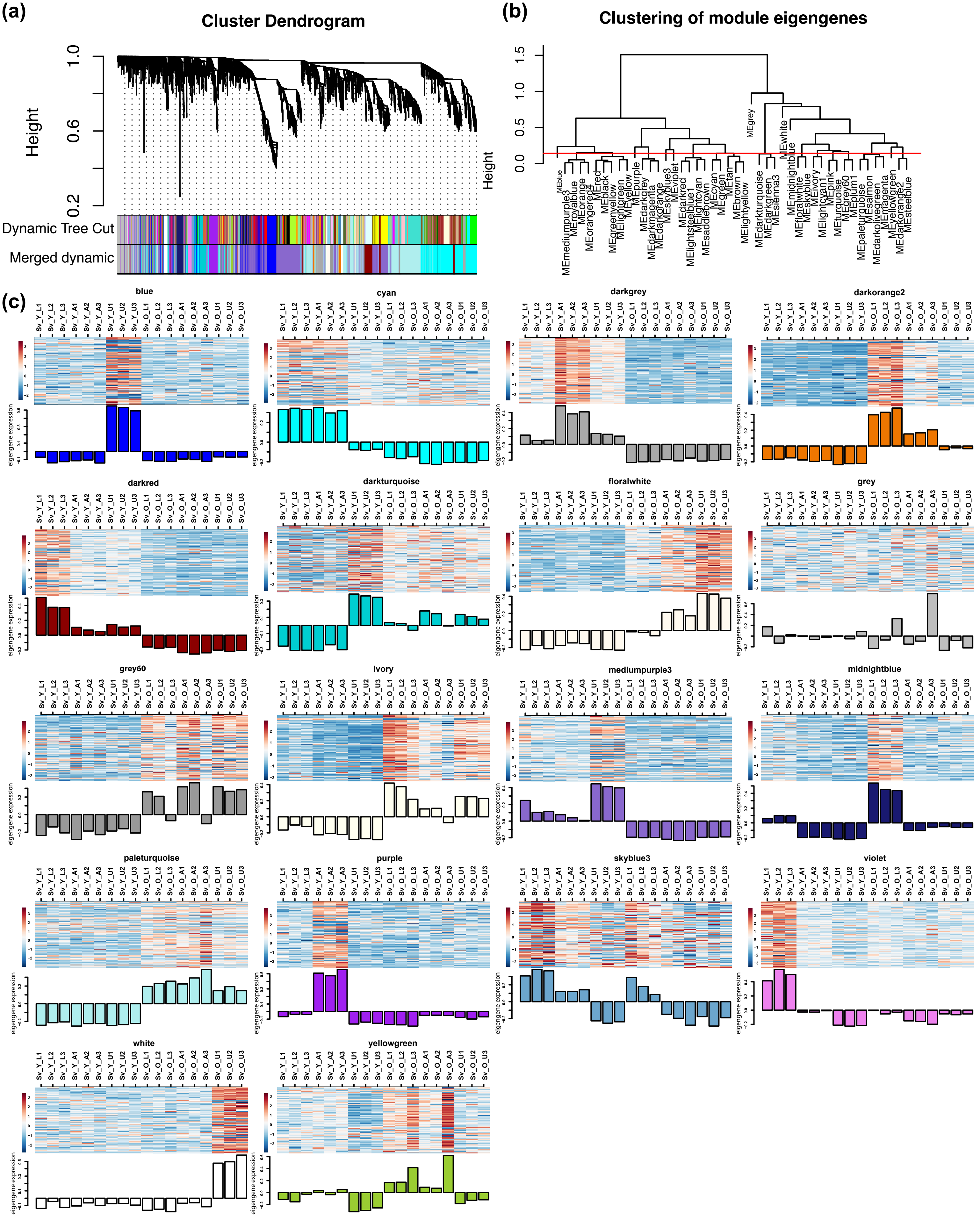
Supporting Information Figure S2. Weighted Gene Co-expression Network Analysis (WGCNA) identified 15 co-expression modules in rice. (a) Cluster dendrogram of expressed one-to-one orthologous genes in rice. Each vertical line represents a gene; assigned module colors before and after merging (cutHeight = 0.14) are shown below the dendrogram. (b) Clustering of module eigengenes with a cutHeight of 0.14 indicated by the horizontal red line. (c) Heatmap and eigengene bar graph of each module.


(a)
Cluster Dendrogram
Height
1.0
0.8
0.6
0.4
0.2
Dynamic Tree Cut
Merged dynamic
(b)
Clustering of module eigengenes
Height
1.5
1.0
0.5
0.0
MEdarkgreen
MEsaddlebrown
MEdarkred
MEskyblue
MEtan
MEgreen
MEgreenyellow
MEpurple
MEdarkolivegreen
MElightyellow
MEdarkgrey
MEwhite
MEcyan
MEsteelblue
MEblack
MEred
MEorange
MEturquoise
MElightcyan
MEyellow
MEgrey
MEmidnightblue
MEroyalblue
MEblue
MEdarkturquoise
MEviolet
MEbrown
MEsalmon
MElightgreen
MEmagenta
MEpaleturquoise
MEpink
MEdarkorange
MEgrey60
(c)
black
blue
brown
darkgreen
darkgrey
darkred
darkturquoise
grey
midnightblue
orange
paleturquoise
pink
purple
saddlebrown
violet
Os_Y_L1
Os_Y_L2
Os_Y_L3
Os_Y_A1
Os_Y_A2
Os_Y_A3
Os_Y_U1
Os_Y_U2
Os_Y_U3
Os_O_L1
Os_O_L2
Os_O_L3
Os_O_A1
Os_O_A2
Os_O_A3
Os_O_U1
Os_O_U2
Os_O_U3
eigengene expression

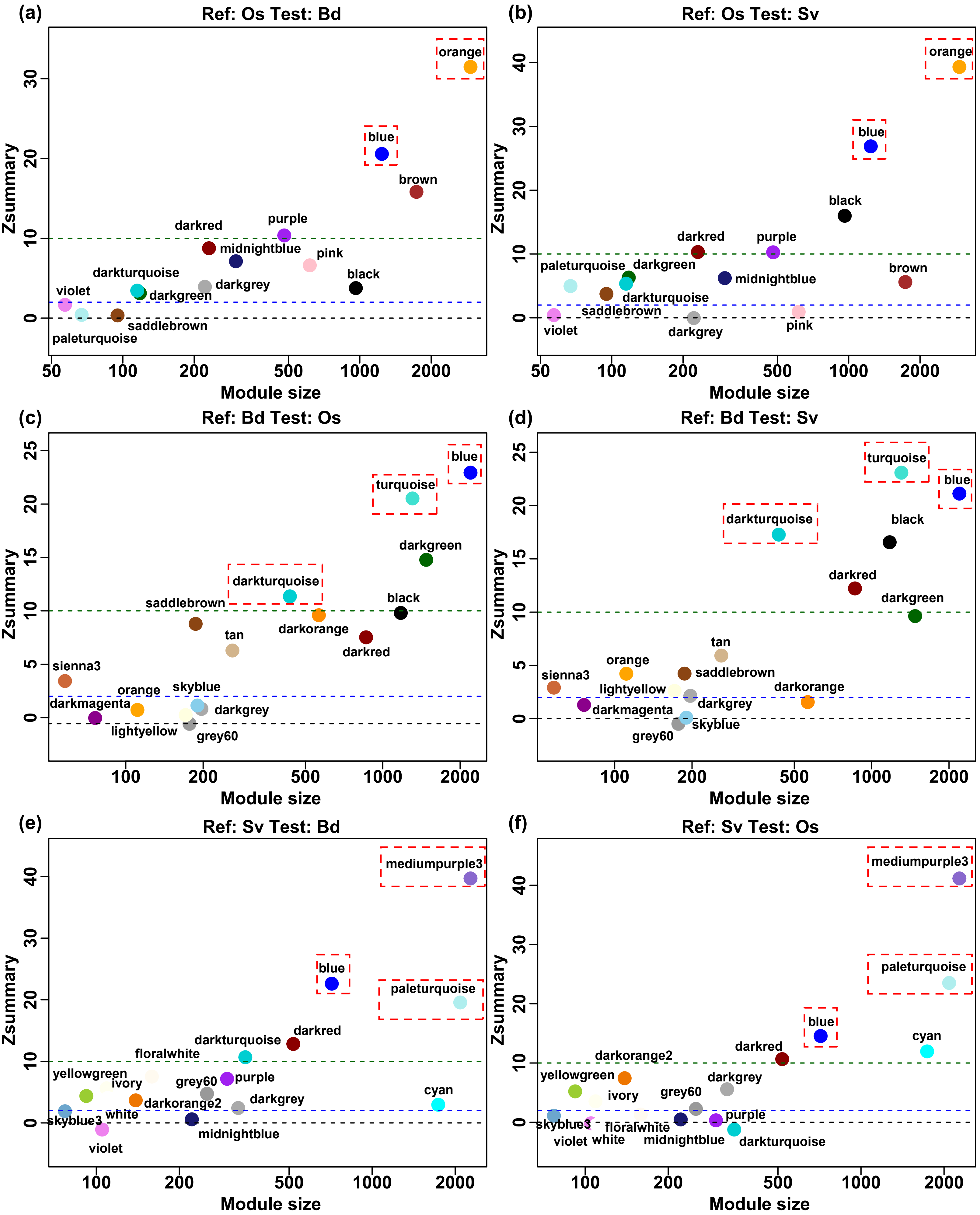
Supporting Information Figure S3. Weighted Gene Co-expression Network Analysis (WGCNA) identified 17 co-expression modules in Brachypodium. (a) Cluster dendrogram of expressed one-to-one orthologous genes in Brachypodium. Each vertical line represents a gene; assigned module colors before and after merging (cutHeight = 0.14) are shown below the dendrogram. (b) Clustering of module eigengenes with a cutHeight of 0.14 indicated by the horizontal red line. (c) Heatmap and eigengene bar graph of each module.


(a)
Cluster Dendrogram
Height
0.3
0.5
0.7
0.9
Dynamic Tree Cut
Merged dynamic
(b)
Clustering of module eigengenes
Height
0.0
0.5
1.0
1.5
MEtan
MEblue
MEbrown
MEpink
MEorange
MEdarkturquoise
MEmagenta
MEgreenyellow
MEpaleturquoise
MEdarkmagenta
MEblack
MEred
MEgrey
MEsaddlebrown
MEsteelblue
MEgrey60
MEskyblue
MEviolet
MEdarkgrey
MEdarkolivegreen
MEturquoise
MEwhite
MEdarkred
MEmidnightblue
MEcyan
MElightcyan
MElightyellow
MEsienna3
MEdarkorange
MEyellow
MEdarkgreen
MElightgreen
MEgreen
MEpurple
MEroyalblue
MEsalmon
(c)
black
blue
darkgreen
darkgrey
darkmagenta
darkorange
darkred
darkturquoise
grey
grey60
lightyellow
orange
saddlebrown
sienna3
skyblue
tan
turquoise
Bd_Y_L1
Bd_Y_L2
Bd_Y_L3
Bd_Y_A1
Bd_Y_A2
Bd_Y_A3
Bd_Y_U1
Bd_Y_U2
Bd_Y_U3
Bd_O_L1
Bd_O_L2
Bd_O_L3
Bd_O_A1
Bd_O_A2
Bd_O_A3
Bd_O_U1
Bd_O_U2
Bd_O_U3
eigengene expression

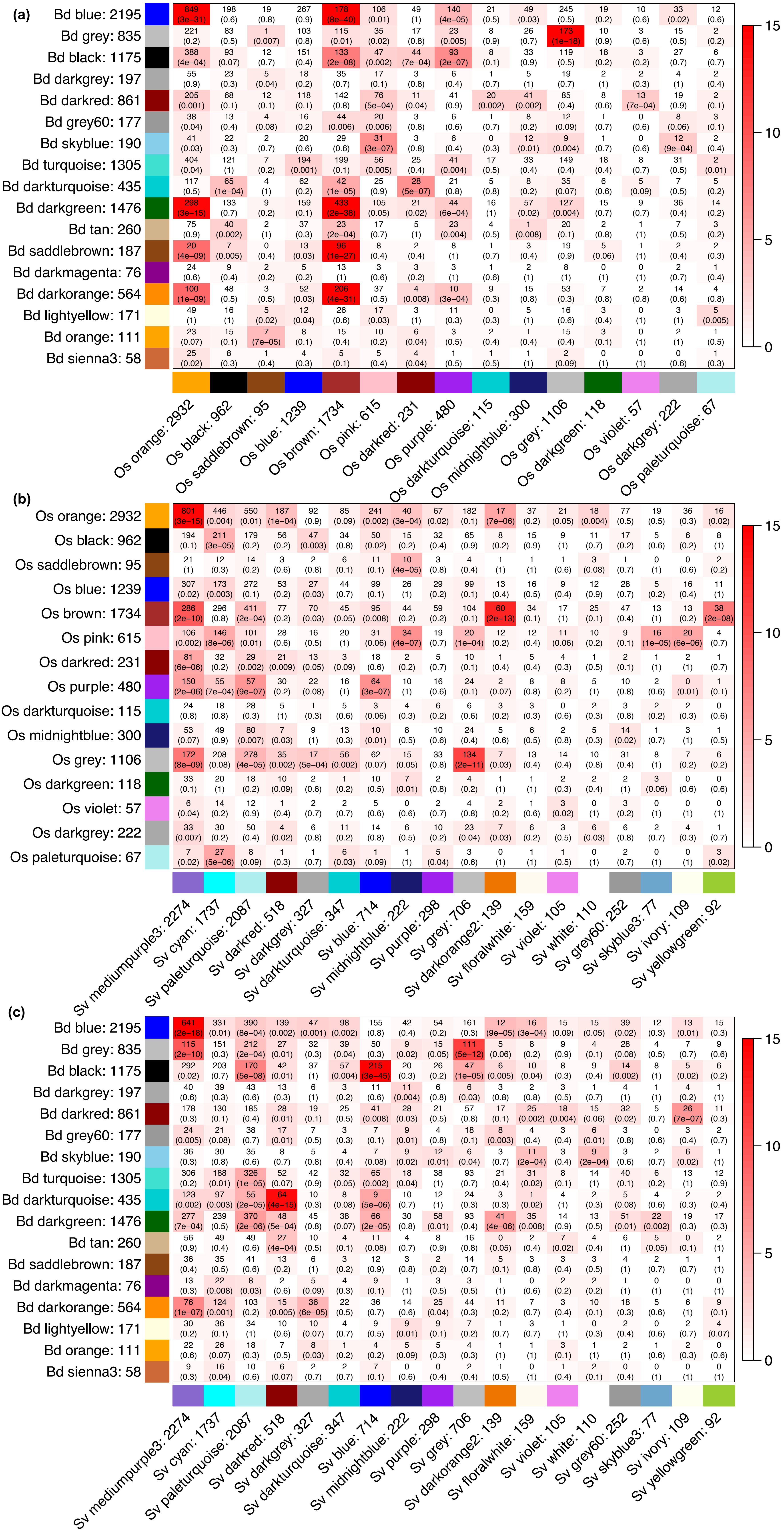
Supporting Information Figure S4. Weighted Gene Co-expression Network Analysis (WGCNA) identified 18 co-expression modules in Setaria. (a) Cluster dendrogram of expressed one-to-one orthologous genes in Setaria. Each vertical line represents a gene; assigned module colors before and after merging (cutHeight = 0.14) are shown below the dendrogram. (b) Clustering of module eigengenes with a cutHeight of 0.14 indicated by the horizontal red line. (c) Heatmap and eigengene bar graph of each module.


(a)
Cluster Dendrogram
Height
1.0
0.6
0.2
Dynamic Tree Cut
Merged dynamic
(b)
Clustering of module eigengenes
Height
1.5
1.0
0.5
0.0
MEblue
MEmediumpurple3
MEroyalblue
MEorange
MEorangered4
MEred
MEblack
MEgreenyellow
MElightgreen
MEyellow
MEpurple
MEdarkgrey
MEdarkmagenta
MEdarkorange
MEskyblue3
MEviolet
MEdarkred
MElightsteelblue1
MElightcyan
MEsaddlebrown
MEcyan
MEgreen
MEtan
MEbrown
MElightyellow
MEgrey
MEdarkturquoise
MEdarkgreen
MEsienna3
MEwhite
MEmidnightblue
MEfloralwhite
MEskyblue
MEivory
MElightcyan1
MEpink
MEturquoise
MEgrey60
MEplum1
MEpaleturquoise
MEsalmon
MEdarkolivegreen
MEmagenta
MEyellowgreen
MEdarkorange2
MEsteelblue
(c)
blue
cyan
darkgrey
darkorange2
darkred
darkturquoise
floralwhite
grey
grey60
ivory
mediumpurple3
midnightblue
paleturquoise
purple
skyblue3
violet
white
yellowgreen
Sv_Y_L1
Sv_Y_L2
Sv_Y_L3
Sv_Y_A1
Sv_Y_A2
Sv_Y_A3
Sv_Y_U1
Sv_Y_U2
Sv_Y_U3
Sv_O_L1
Sv_O_L2
Sv_O_L3
Sv_O_A1
Sv_O_A2
Sv_O_A3
Sv_O_U1
Sv_O_U2
Sv_O_U3
eigengene expression

Supporting Information Figure S5. Weighted Gene Co-expression Network Analysis (WGCNA) modules in one species are moderately preserved in the other two species. $Z_{summary}$ of the WGCNA modules in reference species (a, b) rice, (c, d) Brachypodium and (e, f) Setaria versus the test species (a, e) Brachypodium, (c, f) rice and (b, d) Setaria. Modules preserved in both the other two species are marked with dotted red rectangles. $Z_{summary}<2$, no preservation; $2< Z_{summary}<10$, weak to moderate preservation; $Z_{summary}>10$, high preservation.


(a)
Ref: Os Test: Bd
Zsummary
Module size
orange
blue
brown
purple
darkred
midnightblue
pink
darkturquoise
black
violet
darkgrey
darkgreen
saddlebrown
paleturquoise
0
10
20
30
50
100
200
500
1000
2000
(b)
Ref: Os Test: Sv
Zsummary
Module size
orange
blue
black
darkred
purple
paleturquoise
darkgreen
brown
midnightblue
darkturquoise
saddlebrown
pink
violet
darkgrey
0
10
20
30
40
50
100
200
500
1000
2000
(c)
Ref: Bd Test: Os
Zsummary
Module size
blue
turquoise
darkgreen
darkturquoise
saddlebrown
black
darkorange
tan
darkred
sienna3
skyblue
orange
darkmagenta
darkgrey
lightyellow
grey60
0
5
10
15
20
25
100
200
500
1000
2000
(d)
Ref: Bd Test: Sv
Zsummary
Module size
turquoise
blue
darkturquoise
black
darkred
darkgreen
tan
orange
sienna3
saddlebrown
lightyellow
darkorange
darkgrey
darkmagenta
skyblue
grey60
0
5
10
15
20
25
100
200
500
1000
2000
(e)
Ref: Sv Test: Bd
Zsummary
Module size
mediumpurple3
blue
paleturquoise
darkred
darkturquoise
floralwhite
yellowgreen
ivory
grey60
purple
darkorange2
darkgrey
cyan
white
skyblue3
midnightblue
violet
0
10
20
30
40
100
200
500
1000
2000
(f)
Ref: Sv Test: Os
Zsummary
Module size
mediumpurple3
paleturquoise
blue
cyan
darkred
darkorange2
yellowgreen
darkgrey
ivory
grey60
purple
skyblue3
floralwhite
violet
white
midnightblue
darkturquoise
0
10
20
30
40
100
200
500
1000
2000

Supporting Information Figure S6. Numbers of overlapping genes in pairwise comparisons of modules between species. The number of overlapping genes and p values shown in parentheses (Fisher's exact test) between modules in (a) rice and Brachypodium, (b) rice and Setaria and (c) Brachypodium and Setaria. White to red color key indicates $-\log_{10}$(p value).



(a)

	Os orange: 2932	Os black: 962	Os saddlebrown: 95	Os blue: 1239	Os brown: 1734	Os pink: 615	Os darkred: 231	Os purple: 480	Os darkturquoise: 115	Os midnightblue: 300	Os grey: 1106	Os darkgreen: 118	Os violet: 57	Os darkgrey: 222	Os paleturquoise: 67
Bd blue: 2195	849 (3e−31)	198 (0.6)	19 (0.8)	267 (0.9)	178 (8e−40)	106 (0.01)	49 (1)	140 (4e−05)	21 (0.5)	49 (0.03)	245 (0.5)	19 (0.2)	10 (0.6)	33 (0.02)	12 (0.6)
Bd grey: 835	221 (0.2)	83 (0.5)	1 (0.007)	103 (0.8)	115 (0.01)	35 (0.02)	17 (0.8)	23 (0.005)	8 (0.9)	26 (0.7)	173 (1e−18)	10 (0.9)	3 (0.6)	15 (0.5)	2 (0.2)
Bd black: 1175	388 (4e−04)	93 (0.07)	12 (0.7)	151 (0.4)	133 (2e−08)	47 (0.002)	44 (7e−04)	93 (2e−07)	8 (0.1)	33 (0.9)	119 (0.5)	18 (0.2)	3 (0.2)	27 (0.7)	6 (0.7)
Bd darkgrey: 197	55 (0.9)	23 (0.3)	5 (0.04)	18 (0.2)	35 (0.7)	17 (0.1)	3 (0.8)	6 (0.4)	1 (0.7)	5 (1)	19 (0.7)	2 (1)	2 (0.3)	4 (1)	2 (0.4)
Bd darkred: 861	205 (0.001)	68 (0.1)	12 (0.1)	118 (0.1)	142 (0.8)	76 (5e−04)	11 (0.04)	41 (0.9)	20 (0.002)	41 (0.002)	85 (0.4)	8 (0.6)	13 (7e−04)	19 (0.9)	2 (0.1)
Bd grey60: 177	38 (0.04)	13 (0.4)	4 (0.08)	16 (0.2)	44 (0.006)	20 (0.006)	3 (0.8)	6 (0.6)	1 (0.7)	8 (0.2)	12 (0.09)	1 (0.7)	0 (0.6)	8 (0.06)	3 (0.1)
Bd skyblue: 190	41 (0.03)	22 (0.3)	2 (0.7)	20 (0.6)	29 (0.6)	31 (3e−07)	3 (0.8)	6 (0.4)	0 (0.3)	12 (0.01)	9 (0.004)	1 (0.7)	0 (0.6)	12 (9e−04)	2 (0.4)
Bd turquoise: 1305	404 (0.04)	121 (1)	7 (0.2)	194 (0.001)	199 (0.1)	56 (0.005)	25 (0.4)	41 (0.004)	17 (0.5)	33 (0.4)	149 (0.4)	18 (0.4)	8 (0.7)	31 (0.5)	2 (0.01)
Bd darkturquoise: 435	117 (0.5)	65 (1e−04)	4 (1)	62 (0.2)	42 (1e−05)	25 (0.9)	28 (5e−07)	21 (0.8)	5 (0.8)	8 (0.2)	35 (0.07)	6 (0.6)	5 (0.09)	7 (0.5)	5 (0.2)
Bd darkgreen: 1476	298 (3e−15)	133 (0.7)	9 (0.2)	159 (0.1)	433 (2e−38)	105 (0.05)	21 (0.02)	44 (6e−04)	16 (1)	57 (0.02)	127 (0.004)	15 (0.7)	9 (0.7)	36 (0.4)	14 (0.2)
Bd tan: 260	75 (0.9)	40 (0.002)	2 (1)	37 (0.3)	23 (2e−04)	17 (0.7)	5 (1)	23 (0.004)	4 (0.5)	1 (0.008)	20 (0.1)	2 (0.8)	1 (1)	7 (0.5)	3 (0.2)
Bd saddlebrown: 187	20 (4e−09)	7 (0.005)	0 (0.4)	13 (0.03)	96 (1e−27)	8 (0.4)	2 (0.4)	8 (1)	1 (0.7)	3 (0.4)	19 (0.9)	5 (0.06)	1 (1)	2 (0.4)	2 (0.3)
Bd darkmagenta: 76	24 (0.6)	9 (0.4)	2 (0.2)	5 (0.2)	13 (1)	3 (0.6)	3 (0.2)	3 (1)	1 (0.6)	2 (1)	8 (1)	0 (1)	0 (1)	2 (0.7)	1 (0.4)
Bd darkorange: 564	100 (1e−09)	48 (0.5)	3 (0.5)	52 (0.03)	206 (4e−31)	37 (0.5)	4 (0.008)	10 (3e−04)	9 (0.3)	15 (0.8)	53 (0.3)	7 (0.8)	2 (0.8)	14 (0.6)	4 (0.8)
Bd lightyellow: 171	49 (1)	16 (1)	5 (0.02)	12 (0.04)	26 (0.6)	17 (0.03)	3 (1)	11 (0.3)	0 (0.3)	5 (1)	16 (0.6)	3 (0.4)	0 (1)	3 (1)	5 (0.005)
Bd orange: 111	23 (0.07)	15 (0.1)	7 (7e−05)	8 (0.1)	15 (0.4)	10 (0.2)	6 (0.04)	3 (0.5)	2 (0.4)	1 (0.4)	15 (0.4)	3 (0.1)	0 (1)	2 (1)	1 (0.5)
Bd sienna3: 58	25 (0.02)	8 (0.3)	1 (0.4)	4 (0.3)	5 (0.1)	5 (0.4)	4 (0.04)	1 (0.5)	1 (0.5)	1 (1)	2 (0.09)	0 (1)	0 (1)	0 (0.6)	1 (0.3)

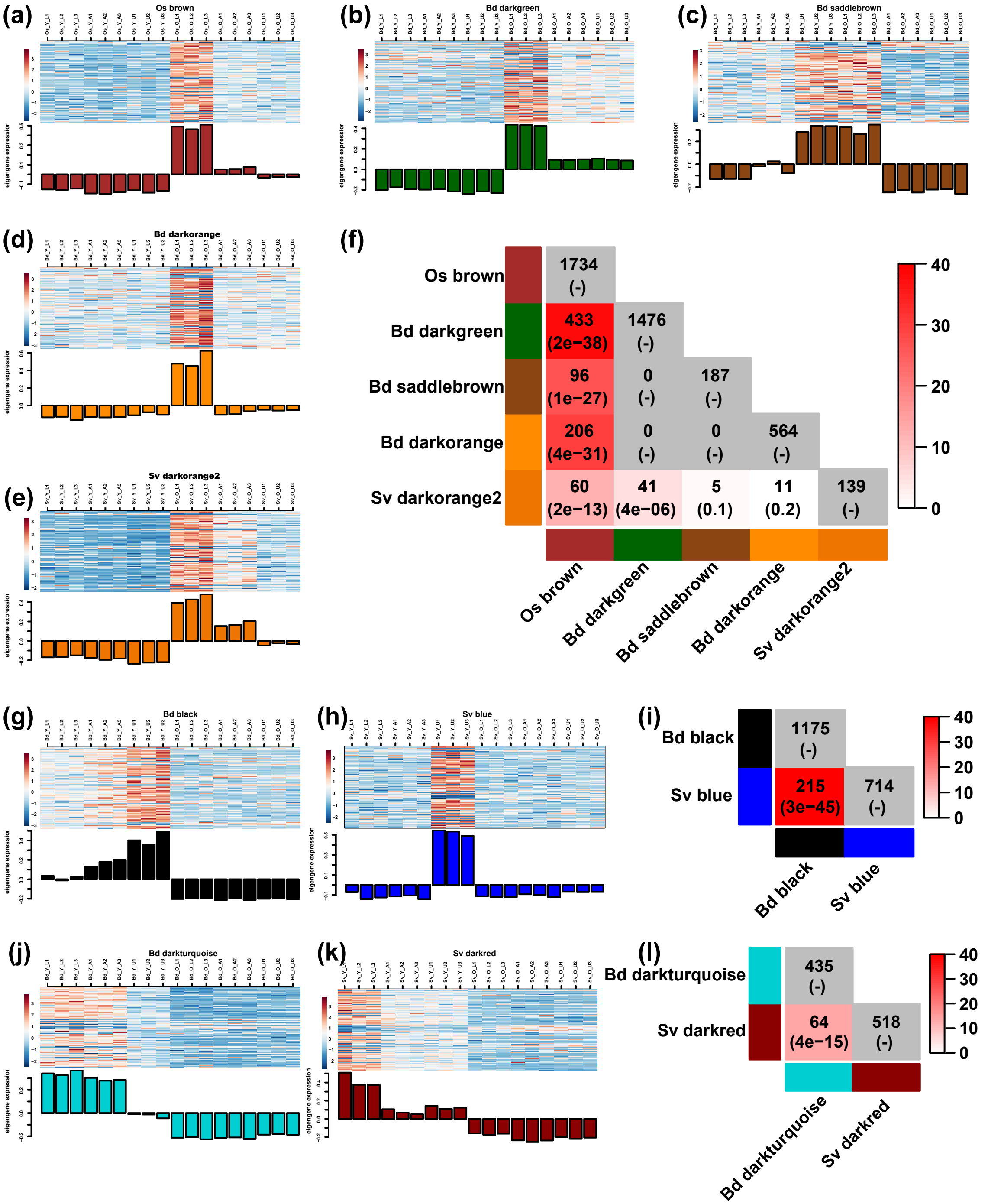
(b)

	Sv mediumpurple3: 2274	Sv cyan: 1737	Sv paleturquoise: 2087	Sv darkred: 518	Sv darkgrey: 327	Sv darkturquoise: 347	Sv blue: 714	Sv midnightblue: 222	Sv purple: 298	Sv grey: 706	Sv darkorange2: 139	Sv floralwhite: 159	Sv violet: 105	Sv white: 110	Sv grey60: 252	Sv skyblue3: 77	Sv ivory: 109	Sv yellowgreen: 92
Os orange: 2932	801 (3e−15)	446 (0.004)	550 (0.01)	187 (1e−04)	92 (0.9)	85 (0.09)	241 (0.002)	40 (3e−04)	67 (0.02)	182 (0.1)	17 (7e−06)	37 (0.2)	21 (0.05)	18 (0.004)	77 (0.5)	19 (0.5)	36 (0.3)	16 (0.02)
Os black: 962	194 (0.1)	211 (3e−05)	179 (0.2)	56 (0.2)	47 (0.003)	34 (0.8)	50 (0.02)	15 (0.2)	32 (0.4)	65 (0.9)	8 (0.2)	15 (0.9)	9 (1)	11 (0.7)	17 (0.2)	5 (0.6)	6 (0.2)	8 (1)
Os saddlebrown: 95	21 (1)	12 (0.3)	14 (0.2)	3 (0.6)	2 (0.8)	6 (0.1)	11 (0.1)	10 (4e−05)	3 (0.8)	4 (0.4)	1 (1)	1 (1)	1 (0.6)	3 (0.08)	1 (0.7)	0 (1)	0 (0.6)	2 (0.2)
Os blue: 1239	307 (0.02)	173 (0.003)	272 (0.1)	53 (0.2)	27 (0.03)	44 (0.7)	99 (0.1)	26 (1)	29 (0.2)	99 (0.1)	13 (0.4)	16 (0.5)	9 (0.4)	12 (0.9)	28 (0.7)	5 (0.2)	16 (0.4)	11 (1)
Os brown: 1734	286 (2e−10)	296 (0.8)	411 (2e−04)	77 (0.2)	70 (0.03)	45 (0.05)	95 (0.008)	44 (0.2)	59 (0.2)	104 (0.1)	60 (2e−13)	34 (0.1)	17 (1)	25 (0.1)	47 (0.4)	13 (1)	13 (0.2)	38 (2e−08)
Os pink: 615	106 (0.002)	146 (8e−06)	101 (0.01)	28 (0.6)	16 (0.5)	20 (1)	31 (0.06)	34 (4e−07)	19 (0.7)	20 (1e−04)	12 (0.2)	12 (0.4)	11 (0.06)	10 (0.2)	9 (0.1)	16 (1e−05)	20 (6e−06)	4 (0.7)
Os darkred: 231	81 (6e−06)	32 (0.2)	29 (0.002)	21 (0.009)	13 (0.05)	3 (0.09)	18 (0.6)	2 (0.2)	5 (0.7)	10 (0.1)	1 (0.4)	5 (0.4)	4 (0.3)	1 (0.5)	2 (0.1)	1 (1)	2 (1)	1 (0.7)
Os purple: 480	150 (2e−06)	55 (7e−04)	57 (9e−07)	30 (0.2)	22 (0.08)	16 (1)	64 (3e−07)	10 (1)	16 (0.6)	24 (0.1)	2 (0.07)	8 (0.8)	8 (0.2)	5 (1)	10 (0.8)	2 (0.6)	0 (0.01)	1 (0.1)
Os darkturquoise: 115	24 (0.8)	18 (0.8)	28 (0.3)	5 (1)	1 (0.3)	5 (0.6)	3 (0.06)	4 (0.3)	6 (0.2)	6 (0.6)	3 (0.2)	3 (0.3)	0 (0.6)	2 (0.3)	3 (0.8)	2 (0.2)	2 (0.3)	0 (0.6)
Os midnightblue: 300	53 (0.07)	49 (0.9)	80 (0.007)	7 (0.03)	9 (1)	13 (0.3)	10 (0.01)	8 (0.5)	10 (0.6)	24 (0.4)	5 (0.6)	6 (0.5)	2 (0.8)	5 (0.3)	14 (0.02)	1 (0.7)	3 (1)	1 (0.5)
Os grey: 1106	172 (8e−09)	208 (0.08)	278 (4e−05)	35 (0.002)	17 (5e−04)	56 (0.002)	62 (0.07)	15 (0.05)	33 (0.8)	134 (2e−11)	7 (0.03)	13 (0.4)	14 (0.4)	10 (0.8)	31 (0.4)	8 (1)	7 (0.2)	6 (0.2)
Os darkgreen: 118	33 (0.1)	20 (1)	18 (0.2)	10 (0.09)	2 (0.6)	1 (0.2)	10 (0.5)	7 (0.01)	2 (0.8)	4 (0.2)	1 (1)	1 (1)	2 (0.3)	2 (0.4)	2 (1)	3 (0.06)	0 (0.6)	0 (0.6)
Os violet: 57	6 (0.04)	14 (0.2)	12 (0.9)	1 (0.4)	2 (0.7)	2 (0.7)	5 (0.6)	0 (0.6)	2 (0.7)	4 (0.8)	2 (0.2)	1 (0.6)	3 (0.02)	0 (1)	3 (0.2)	0 (1)	0 (1)	0 (1)
Os darkgrey: 222	33 (0.007)	30 (0.2)	50 (0.4)	4 (0.02)	6 (0.8)	11 (0.2)	14 (0.8)	6 (0.5)	10 (0.2)	23 (0.04)	7 (0.03)	6 (0.2)	3 (0.5)	6 (0.03)	6 (0.8)	2 (0.7)	4 (0.3)	1 (0.7)
Os paleturquoise: 67	7 (0.02)	27 (5e−06)	8 (0.09)	1 (0.3)	1 (0.7)	6 (0.03)	1 (0.09)	1 (1)	5 (0.04)	3 (0.6)	0 (1)	1 (1)	1 (0.5)	0 (1)	2 (0.7)	0 (1)	0 (1)	3 (0.02)

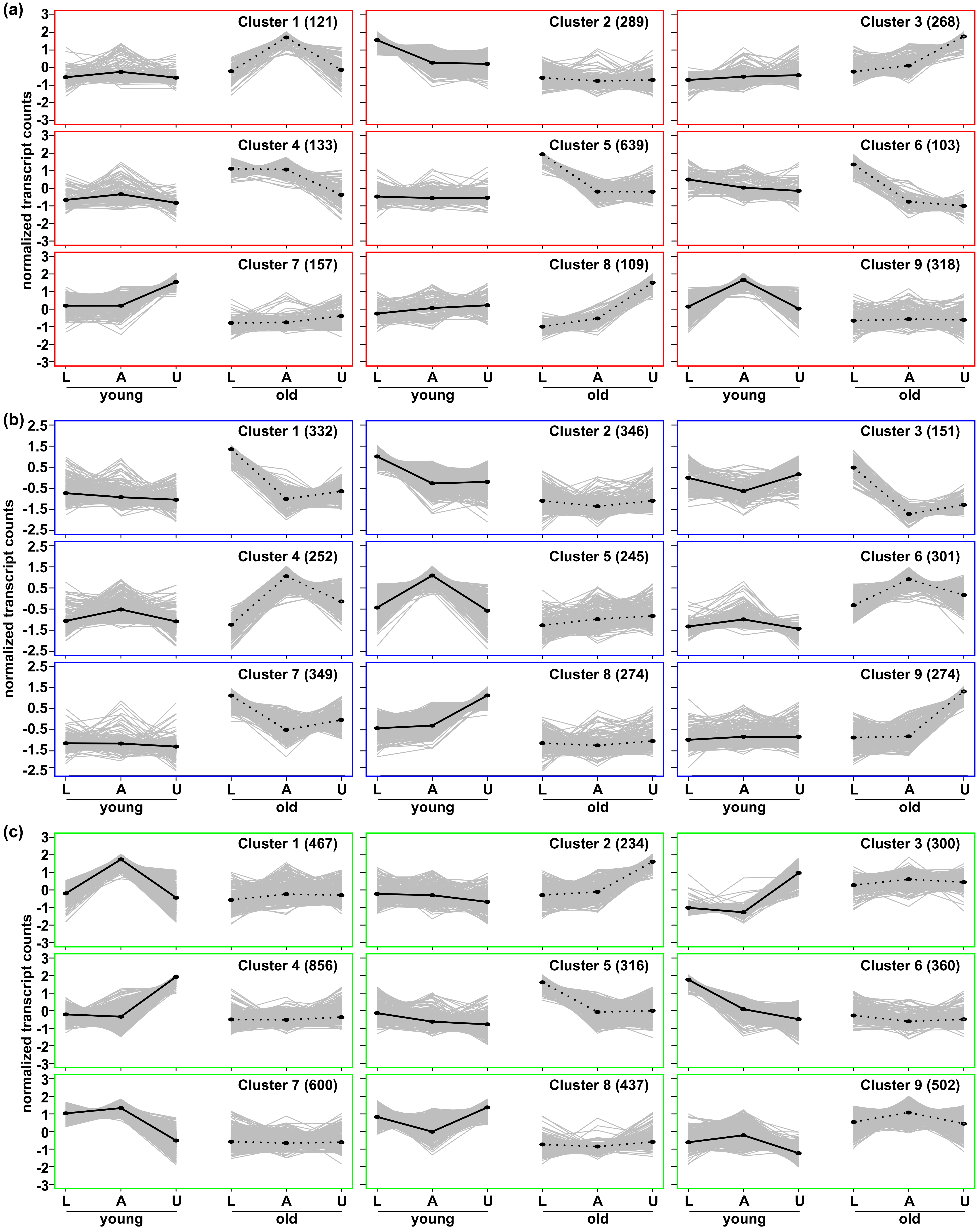
(c)

	Sv mediumpurple3: 2274	Sv cyan: 1737	Sv paleturquoise: 2087	Sv darkred: 518	Sv darkgrey: 327	Sv darkturquoise: 347	Sv blue: 714	Sv midnightblue: 222	Sv purple: 298	Sv grey: 706	Sv darkorange2: 139	Sv floralwhite: 159	Sv violet: 105	Sv white: 110	Sv grey60: 252	Sv skyblue3: 77	Sv ivory: 109	Sv yellowgreen: 92
Bd blue: 2195	641 (2e−18)	331 (0.01)	390 (8e−04)	139 (0.002)	47 (0.001)	98 (0.002)	155 (0.8)	42 (0.4)	54 (0.2)	161 (0.3)	12 (9e−05)	16 (3e−04)	15 (0.09)	15 (0.05)	39 (0.02)	12 (0.3)	13 (0.01)	15 (0.3)
Bd grey: 835	115 (2e−10)	151 (0.3)	212 (2e−04)	27 (0.01)	32 (0.3)	39 (0.04)	50 (0.3)	9 (0.02)	15 (0.05)	111 (5e−12)	5 (0.06)	8 (0.2)	9 (0.9)	4 (0.1)	28 (0.08)	4 (0.5)	7 (0.7)	9 (0.6)
Bd black: 1175	292 (0.02)	203 (0.7)	170 (5e−08)	42 (0.01)	37 (1)	57 (0.004)	215 (3e−45)	20 (0.3)	26 (0.2)	47 (1e−05)	6 (0.005)	10 (0.04)	8 (0.3)	9 (0.4)	14 (0.002)	8 (1)	5 (0.02)	6 (0.2)
Bd darkgrey: 197	40 (0.6)	39 (0.3)	43 (0.6)	13 (0.3)	6 (1)	3 (0.2)	11 (0.6)	11 (0.004)	6 (0.8)	6 (0.03)	3 (0.8)	2 (0.8)	3 (0.5)	1 (0.7)	4 (1)	1 (1)	4 (0.2)	1 (1)
Bd darkred: 861	178 (0.3)	130 (0.1)	185 (0.4)	28 (0.01)	19 (0.1)	25 (0.5)	41 (0.008)	28 (0.03)	21 (0.5)	57 (0.8)	17 (0.1)	25 (0.002)	18 (0.004)	15 (0.06)	32 (0.02)	5 (0.7)	26 (7e−07)	11 (0.3)
Bd grey60: 177	24 (0.005)	21 (0.08)	38 (0.7)	17 (0.01)	7 (0.5)	3 (0.3)	7 (0.1)	9 (0.01)	4 (0.8)	18 (0.1)	8 (0.003)	4 (0.4)	3 (0.4)	6 (0.01)	3 (0.8)	0 (0.6)	3 (0.4)	2 (0.7)
Bd skyblue: 190	36 (0.3)	30 (0.8)	35 (0.6)	8 (0.7)	5 (0.8)	4 (0.4)	7 (0.08)	9 (0.02)	12 (0.01)	6 (0.04)	3 (0.7)	11 (2e−04)	3 (0.4)	9 (2e−04)	3 (0.6)	2 (0.7)	6 (0.02)	1 (1)
Bd turquoise: 1305	306 (0.2)	188 (0.01)	326 (1e−05)	52 (0.07)	42 (0.9)	32 (0.05)	65 (0.002)	18 (0.04)	38 (1)	93 (0.7)	21 (0.4)	31 (0.02)	8 (0.1)	14 (1)	40 (0.1)	6 (0.2)	13 (1)	12 (0.9)
Bd darkturquoise: 435	123 (0.002)	97 (0.003)	55 (2e−05)	64 (4e−15)	10 (0.3)	8 (0.08)	9 (5e−06)	10 (0.7)	12 (1)	24 (0.3)	3 (0.3)	1 (0.02)	4 (1)	2 (0.3)	5 (0.08)	4 (0.6)	2 (0.3)	2 (0.4)
Bd darkgreen: 1476	277 (7e−04)	239 (0.5)	370 (2e−06)	48 (5e−04)	45 (0.8)	38 (0.07)	66 (2e−05)	30 (0.8)	58 (0.01)	93 (0.4)	41 (4e−06)	35 (0.008)	14 (0.9)	13 (0.5)	51 (0.01)	22 (0.002)	19 (0.3)	17 (0.3)
Bd tan: 260	56 (0.9)	49 (0.4)	49 (0.6)	27 (4e−04)	10 (0.5)	4 (0.1)	11 (0.08)	4 (0.7)	8 (0.9)	16 (0.8)	0 (0.05)	2 (0.4)	7 (0.02)	4 (0.4)	6 (1)	5 (0.05)	0 (0.1)	2 (1)
Bd saddlebrown: 187	36 (0.4)	35 (0.5)	41 (0.6)	13 (0.2)	6 (1)	3 (0.2)	12 (0.9)	3 (0.8)	2 (0.2)	14 (0.7)	5 (0.1)	3 (0.8)	3 (0.4)	3 (0.5)	4 (1)	2 (0.7)	1 (0.7)	1 (1)
Bd darkmagenta: 76	13 (0.3)	22 (0.008)	8 (0.03)	2 (0.6)	5 (0.09)	4 (0.3)	9 (0.1)	1 (1)	3 (0.5)	3 (0.5)	1 (1)	0 (0.6)	2 (0.2)	2 (0.2)	1 (1)	0 (1)	0 (1)	0 (1)
Bd darkorange: 564	76 (1e−07)	124 (0.001)	103 (0.2)	15 (0.005)	36 (6e−05)	22 (0.5)	36 (0.7)	14 (0.6)	25 (0.04)	44 (0.3)	11 (0.2)	7 (0.7)	3 (0.4)	10 (0.1)	18 (0.3)	5 (0.6)	6 (1)	9 (0.1)
Bd lightyellow: 171	30 (0.2)	36 (0.1)	34 (1)	10 (0.6)	10 (0.07)	4 (0.7)	9 (0.5)	9 (0.01)	9 (0.1)	7 (0.2)	1 (0.7)	3 (0.7)	1 (1)	0 (0.3)	2 (0.4)	0 (0.6)	2 (0.7)	4 (0.07)
Bd orange: 111	22 (0.6)	26 (0.07)	18 (0.3)	7 (0.5)	8 (0.03)	1 (0.2)	4 (0.2)	5 (0.09)	5 (0.3)	4 (0.3)	1 (1)	1 (1)	3 (0.1)	1 (1)	2 (1)	1 (0.6)	2 (0.3)	0 (0.6)
Bd sienna3: 58	9 (0.3)	16 (0.04)	10 (0.6)	6 (0.07)	2 (0.7)	2 (0.7)	7 (0.1)	0 (0.6)	0 (0.4)	2 (0.4)	1 (0.5)	0 (1)	1 (0.4)	2 (0.1)	0 (0.4)	0 (1)	0 (1)	0 (1)

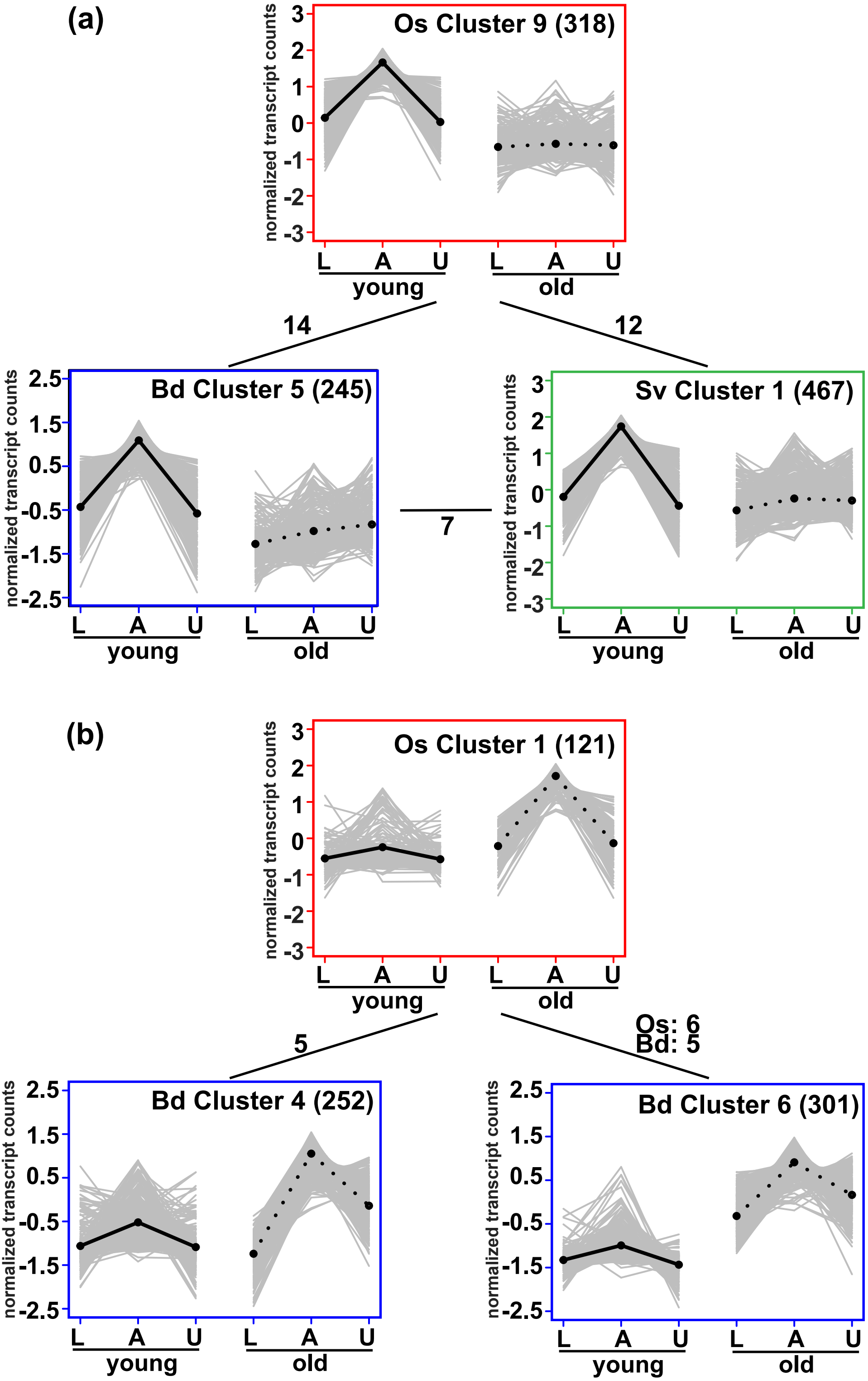
Supporting Information Figure S7. Modules with highly significant overlapping genes have similar expression patterns. Modules that have highly significant overlap (Fisher's exact test, $p < 1e\text{-}10$) are shown. (a-e) Modules that are highly expressed below the AZ (L) at old stage in (a) rice, (b-d) Brachypodium and (e) Setaria. (g-h) modules that are highly expressed above the AZ (U) at young stage in (g) Brachypodium and (h) Setaria. (j, k) Modules that are highly expressed (j) below and at the AZ in Brachypodium and (k) below the AZ in Setaria at young stage. (f, i, l) Pairwise comparisons of the number of overlapping genes between modules. The numbers in parentheses are p values from Fisher's exact test. White to red color key indicates $-\log_{10}$(p value).


(a)
Os brown
eigengene expression
(b)
Bd darkgreen
(c)
Bd saddlebrown
(d)
Bd darkorange
(e)
Sv darkorange2
(f)
Os brown
Bd darkgreen
Bd saddlebrown
Bd darkorange
Sv darkorange2
1734 (-)
433 (2e−38)
1476 (-)
96 (1e−27)
0 (-)
187 (-)
206 (4e−31)
0 (-)
0 (-)
564 (-)
60 (2e−13)
41 (4e−06)
5 (0.1)
11 (0.2)
139 (-)
40
30
20
10
0
(g)
Bd black
(h)
Sv blue
(i)
Bd black
Sv blue
1175 (-)
215 (3e−45)
714 (-)
(j)
Bd darkturquoise
(k)
Sv darkred
(l)
Bd darkturquoise
Sv darkred
435 (-)
64 (4e−15)
518 (-)

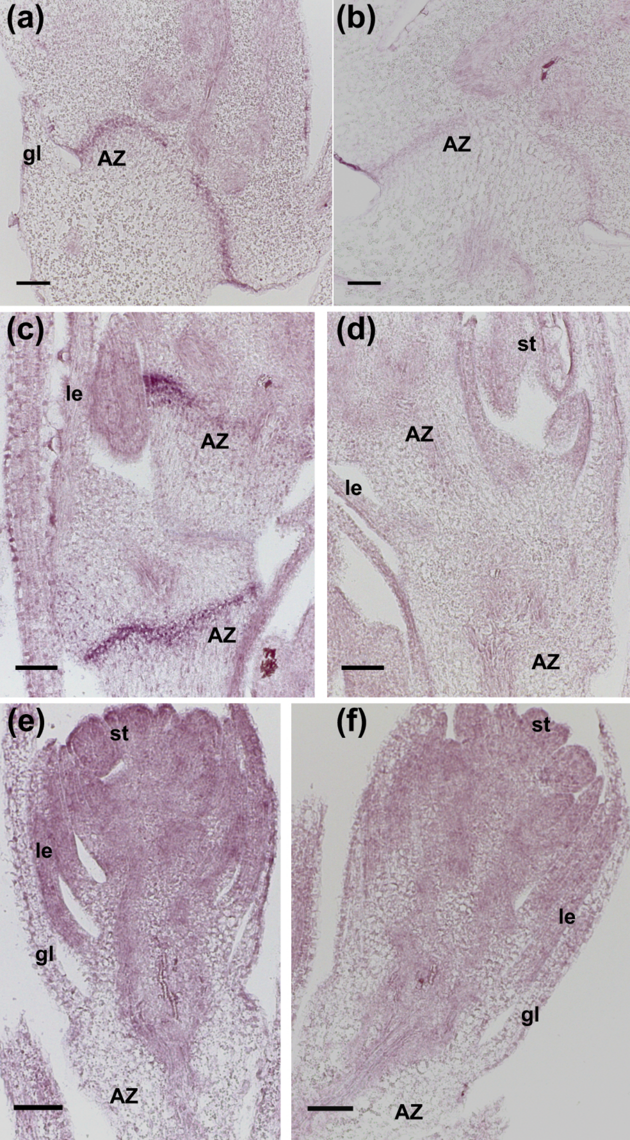
Supporting Information Figure S8. Expression patterns of Self-organizing map (SOM) clustering in rice, Brachypodium and Setaria. Genes with at least one significant differential expression in A vs. L or A vs. U comparisons at either young or old stage were used for clustering in (a) rice, (b) Brachypodium and (c) Setaria. Each grey line indicates normalized transcript abundance in one gene, and the black line indicates the average of all of the genes in the cluster.


(a)
Cluster 1 (121)
Cluster 2 (289)
Cluster 3 (268)
Cluster 4 (133)
Cluster 5 (639)
Cluster 6 (103)
Cluster 7 (157)
Cluster 8 (109)
Cluster 9 (318)
(b)
Cluster 1 (332)
Cluster 2 (346)
Cluster 3 (151)
Cluster 4 (252)
Cluster 5 (245)
Cluster 6 (301)
Cluster 7 (349)
Cluster 8 (274)
Cluster 9 (274)
(c)
Cluster 1 (467)
Cluster 2 (234)
Cluster 3 (300)
Cluster 4 (856)
Cluster 5 (316)
Cluster 6 (360)
Cluster 7 (600)
Cluster 8 (437)
Cluster 9 (502)
normalized transcript counts
3
2
1
0
-1
-2
-3
2.5
1.5
0.5
-0.5
-1.5
-2.5
L
A
U
young
old

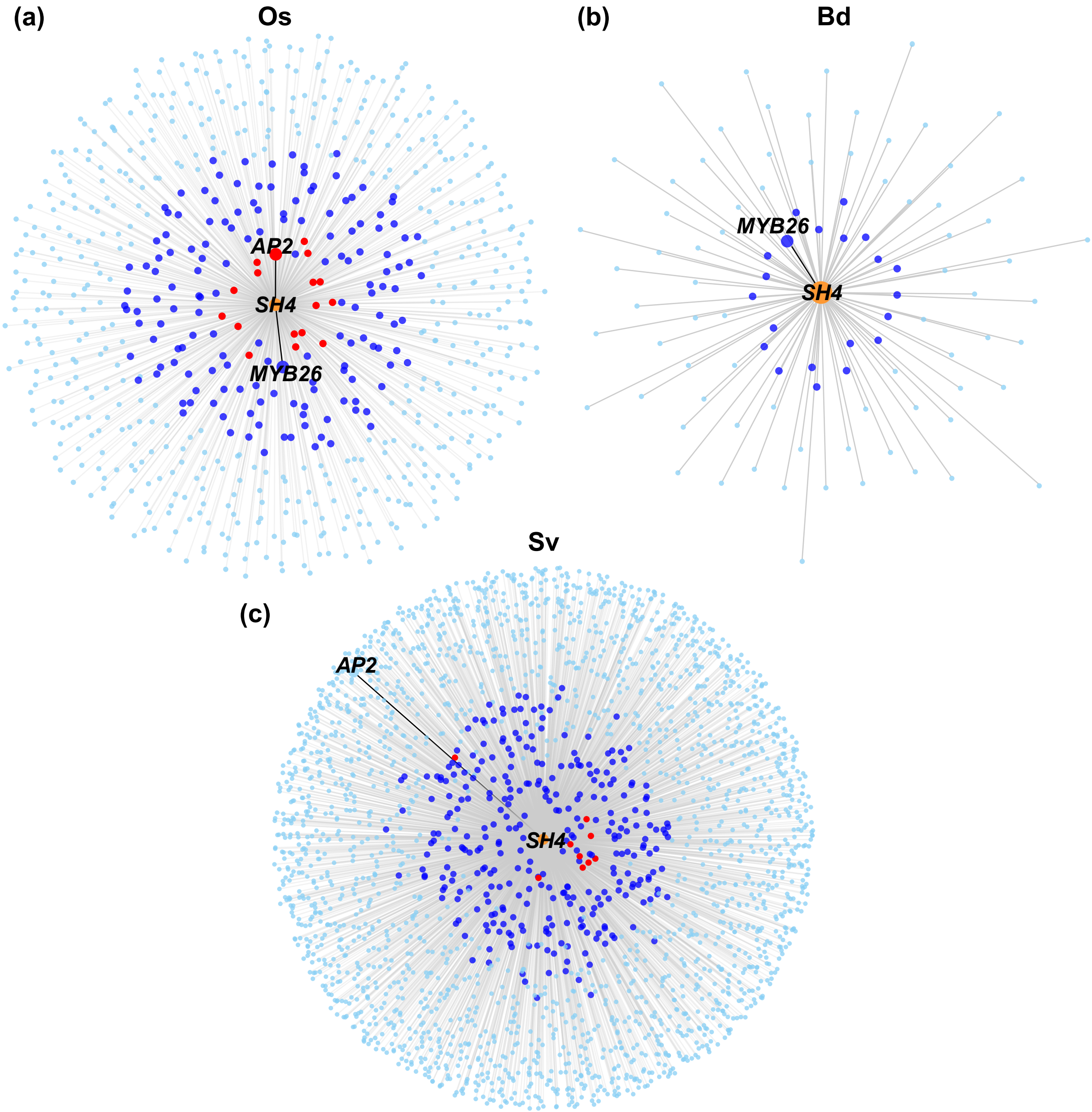
Supporting Information Figure S9. AZ clusters generated by Self-organizing map (SOM) have a limited number of overlapping genes between species. AZ clusters at (a) young and (b) old stages. Number of genes in each cluster is shown in parentheses. The number of overlapping genes is shown on the line connecting two clusters. Each grey line indicates normalized transcript abundance in one gene, and the black line indicates the average of all of the genes in the cluster.


(a)
Os Cluster 9 (318)
normalized transcript counts
3
2
1
0
-1
-2
-3
L
A
U
young
L
A
U
old
14
12
Bd Cluster 5 (245)
2.5
1.5
0.5
-0.5
-1.5
-2.5
7
Sv Cluster 1 (467)
(b)
Os Cluster 1 (121)
5
Os: 6
Bd: 5
Bd Cluster 4 (252)
Bd Cluster 6 (301)

Supporting Information Figure S10. *MYB26* is expressed in the abscission zone in rice and Brachypodium. In situ hybridization of *Myb26* in (a, b) rice, (c, d) Brachypodium and (e, f) Setaria. (a, c, e) anti-sense probes. (b, d, f) sense probes. gl, glume; le, lemma; st, stamens. Scale bar = 50 µm.


(a)
gl
AZ
(b)
AZ
(c)
le
AZ
AZ
(d)
st
AZ
le
AZ
(e)
st
le
gl
AZ
(f)
st
le
gl
AZ

Supporting Information Figure S11. *SH4* is co-expressed with *AP2* and/or *MYB26*. Co-expressed genes of *SH4* in (a) rice, (b) Brachypodium and (c) Seteria. Interaction weight ≥ 0.3 is indicated in red; 0.2 ≤ interaction weight < 0.3 is indicated in blue; 0.1 ≤ interaction weight < 0.2 is indicated in cyan.


(a)
Os
AP2
SH4
MYB26
(b)
Bd
MYB26
SH4
Sv
(c)
AP2
SH4