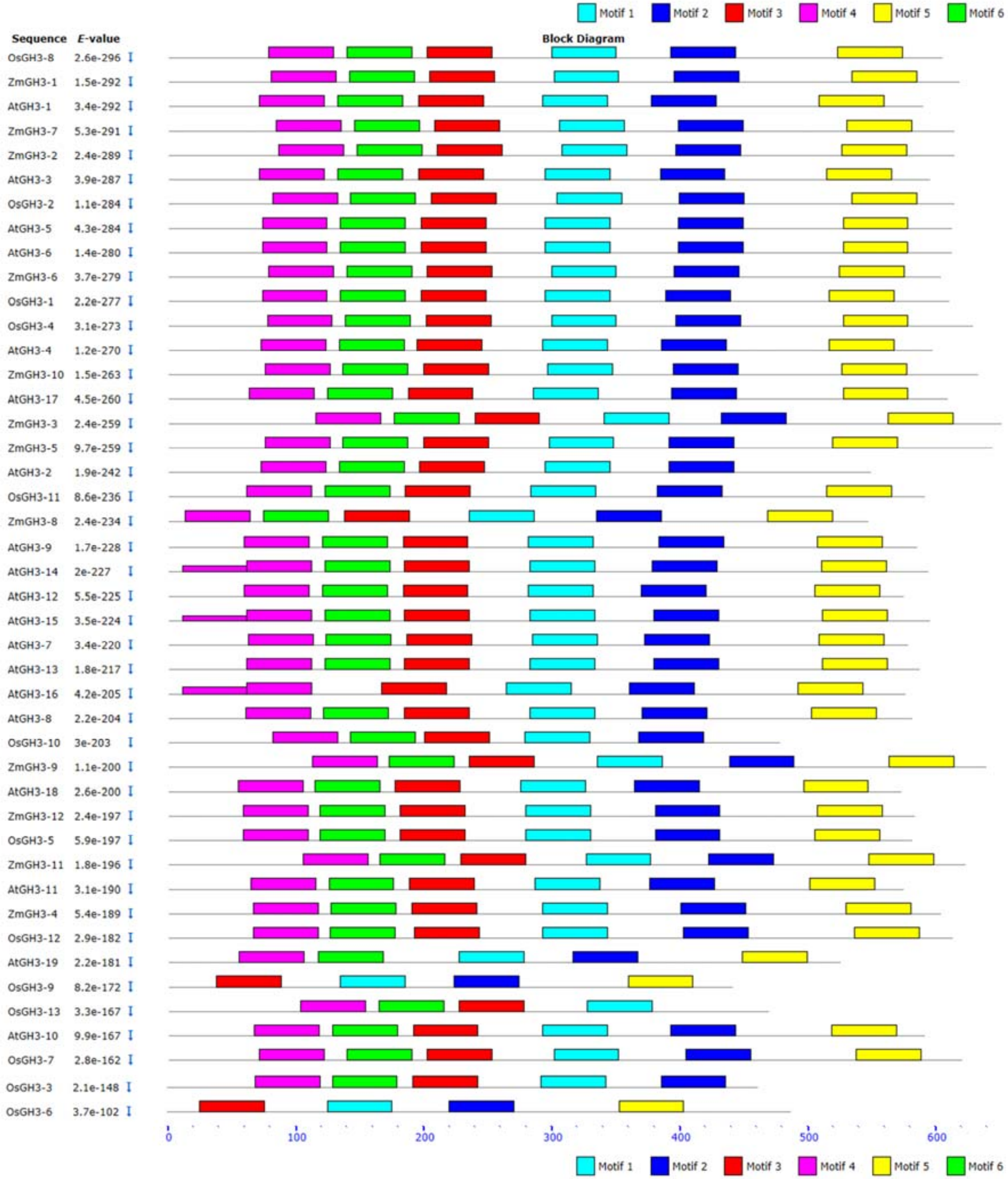
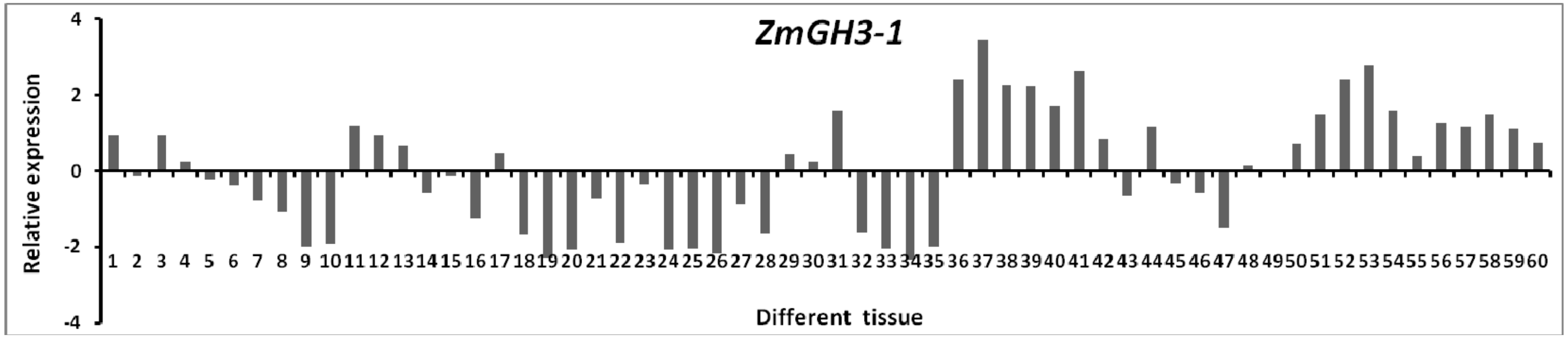
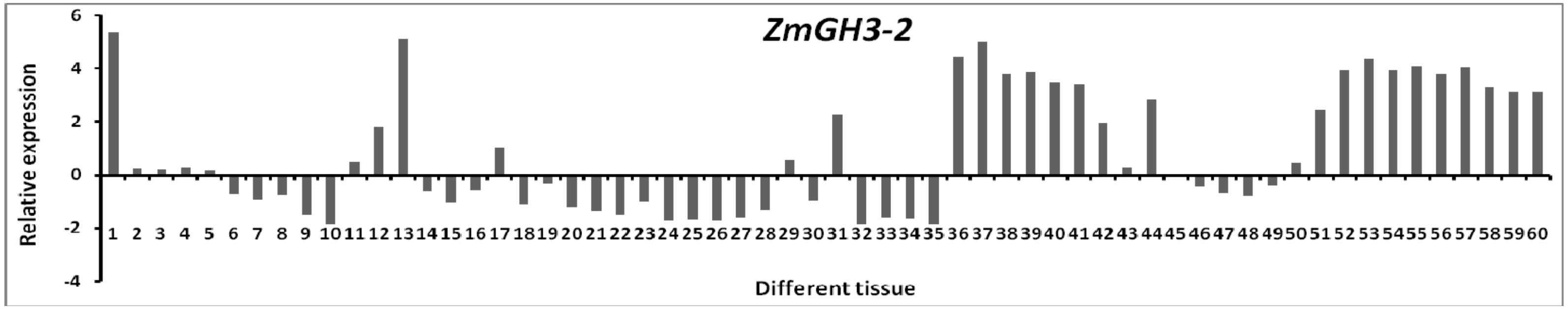
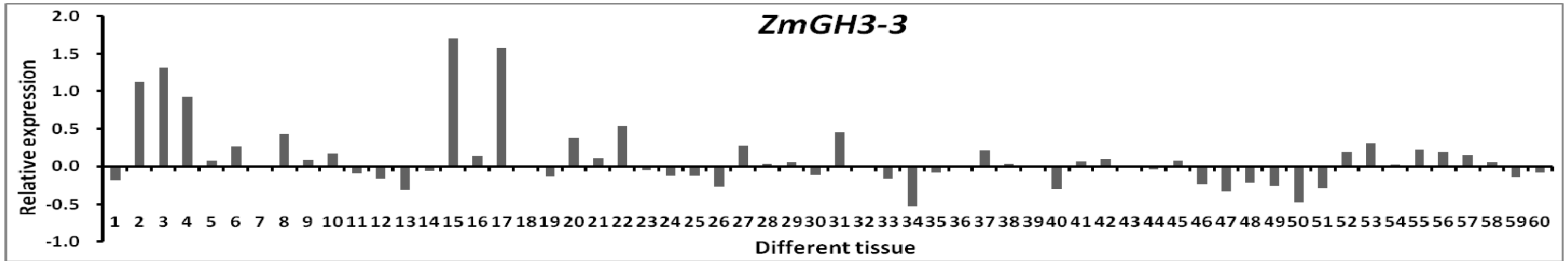
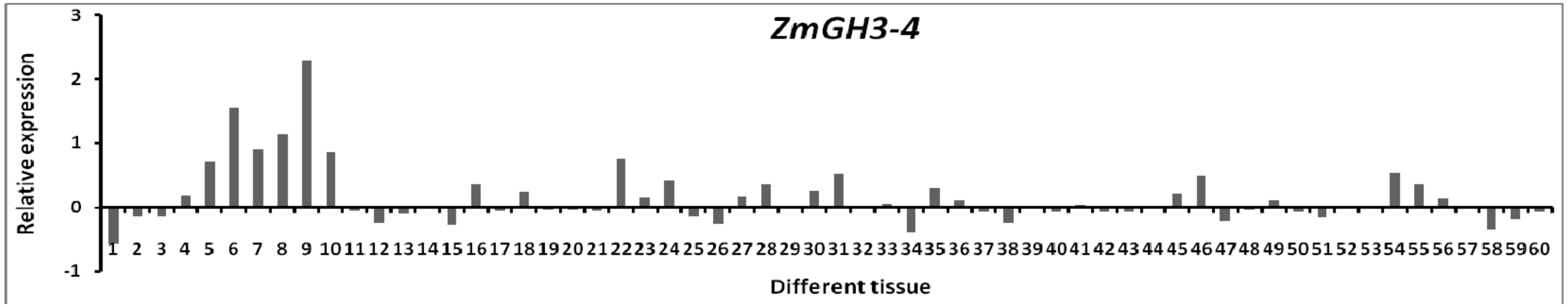

Motif 1
Motif 2
Motif 3
Motif 4
Motif 5
Motif 6
Sequence
E-value
Block Diagram
OsGH3-8 2.6e-296
ZmGH3-1 1.5e-292
AtGH3-1 3.4e-292
ZmGH3-7 5.3e-291
ZmGH3-2 2.4e-289
AtGH3-3 3.9e-287
OsGH3-2 1.1e-284
AtGH3-5 4.3e-284
AtGH3-6 1.4e-280
ZmGH3-6 3.7e-279
OsGH3-1 2.2e-277
OsGH3-4 3.1e-273
AtGH3-4 1.2e-270
ZmGH3-10 1.5e-263
AtGH3-17 4.5e-260
ZmGH3-3 2.4e-259
ZmGH3-5 9.7e-259
AtGH3-2 1.9e-242
OsGH3-11 8.6e-236
ZmGH3-8 2.4e-234
AtGH3-9 1.7e-228
AtGH3-14 2e-227
AtGH3-12 5.5e-225
AtGH3-15 3.5e-224
AtGH3-7 3.4e-220
AtGH3-13 1.8e-217
AtGH3-16 4.2e-205
AtGH3-8 2.2e-204
OsGH3-10 3e-203
ZmGH3-9 1.1e-200
AtGH3-18 2.6e-200
ZmGH3-12 2.4e-197
OsGH3-5 5.9e-197
ZmGH3-11 1.8e-196
AtGH3-11 3.1e-190
ZmGH3-4 5.4e-189
OsGH3-12 2.9e-182
AtGH3-19 2.2e-181
OsGH3-9 8.2e-172
OsGH3-13 3.3e-167
AtGH3-10 9.9e-167
OsGH3-7 2.8e-162
OsGH3-3 2.1e-148
OsGH3-6 3.7e-102
0
100
200
300
400
500
600
Motif 1
Motif 2
Motif 3
Motif 4
Motif 5
Motif 6

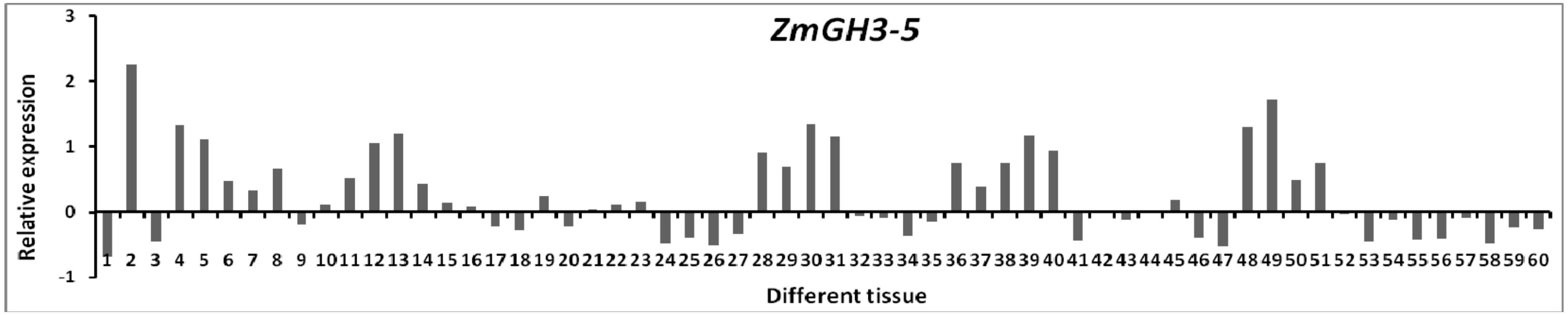
Appendix A Identification of conserved motifs in the predicted domain of the *ZmGH3* family members. The online software MEME was used to predict functional motifs and possible functional sites in this protein family from maize, rice, and *Arabidopsis*. Parameters were set as following: 0 or 1 single motif per sequence, motif length range from 40 to 50 residues; the other parameters were set to default values.

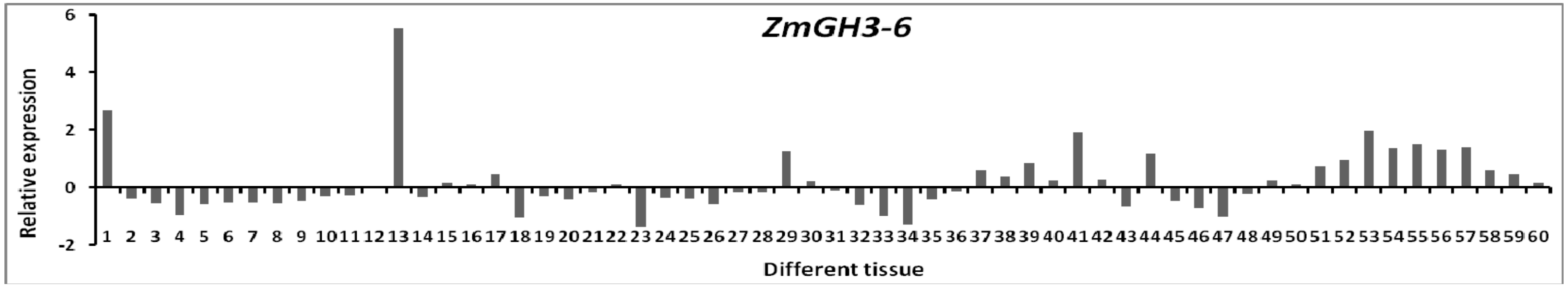


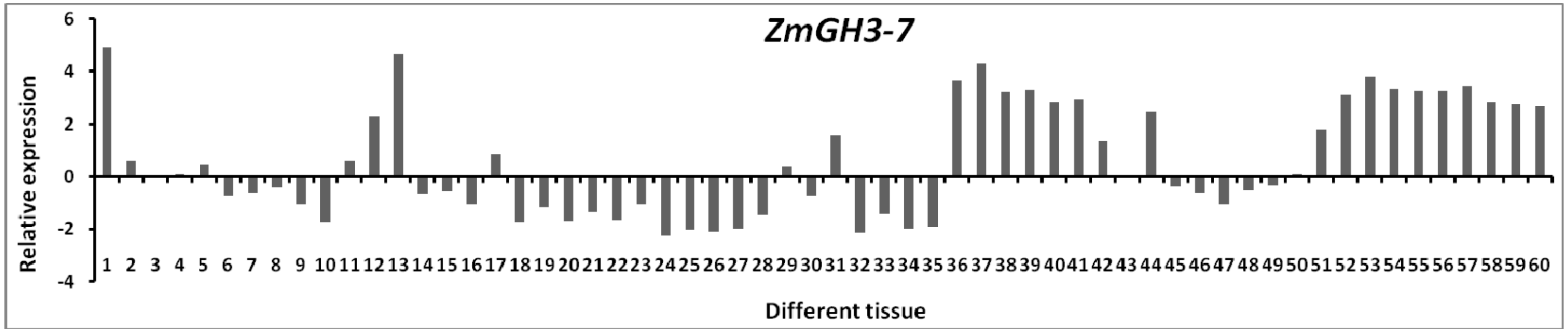


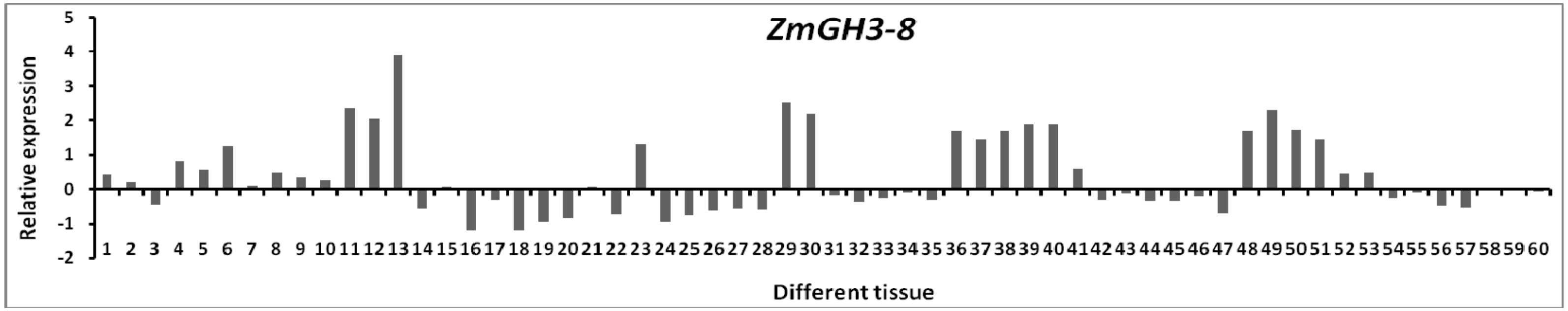


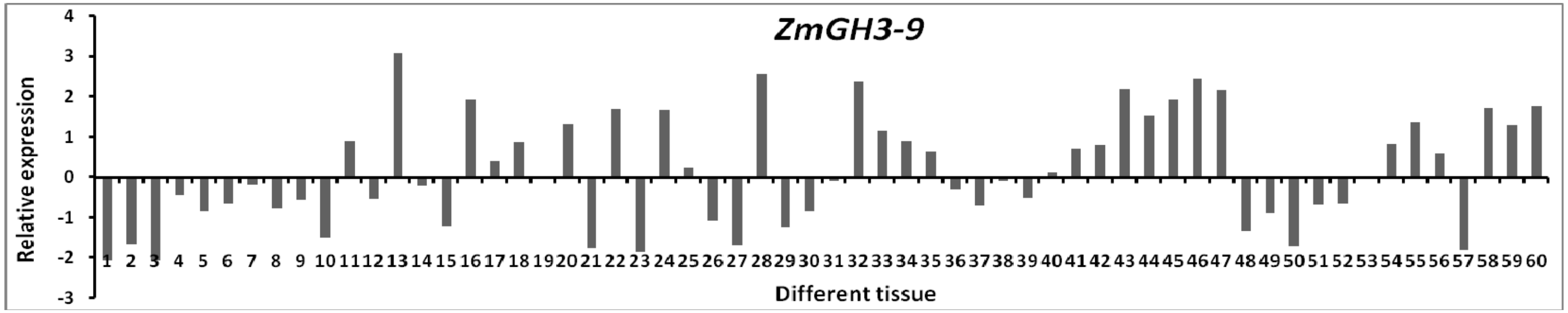

ZmGH3-4
Relative expression
3
2
1
0
-1
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
Different tissue

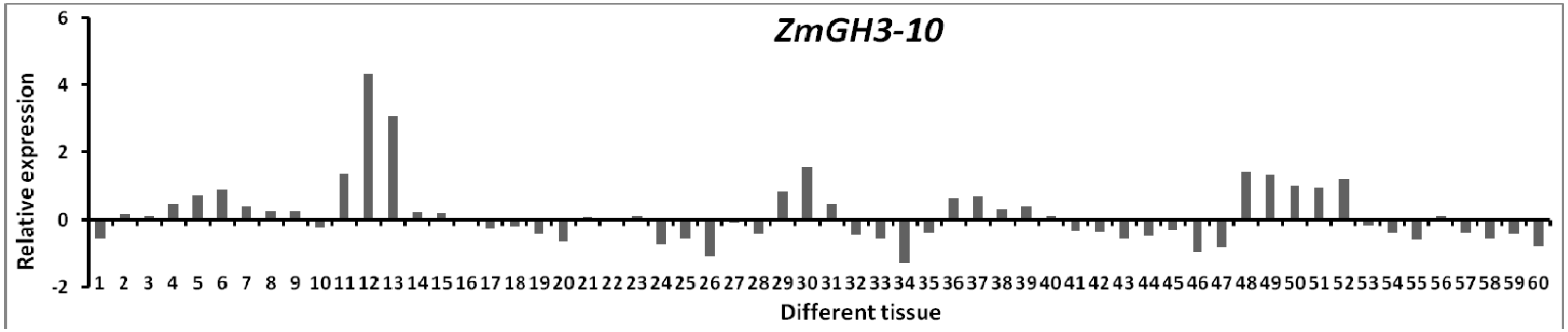

ZmGH3-5
Relative expression
3
2
1
0
-1
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
Different tissue

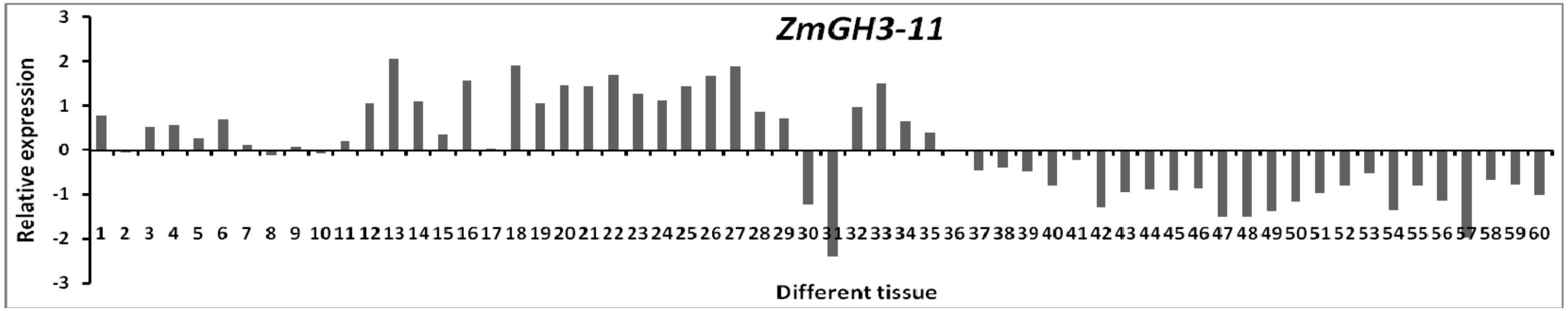

ZmGH3-6
Relative expression
6
4
2
0
-2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
Different tissue

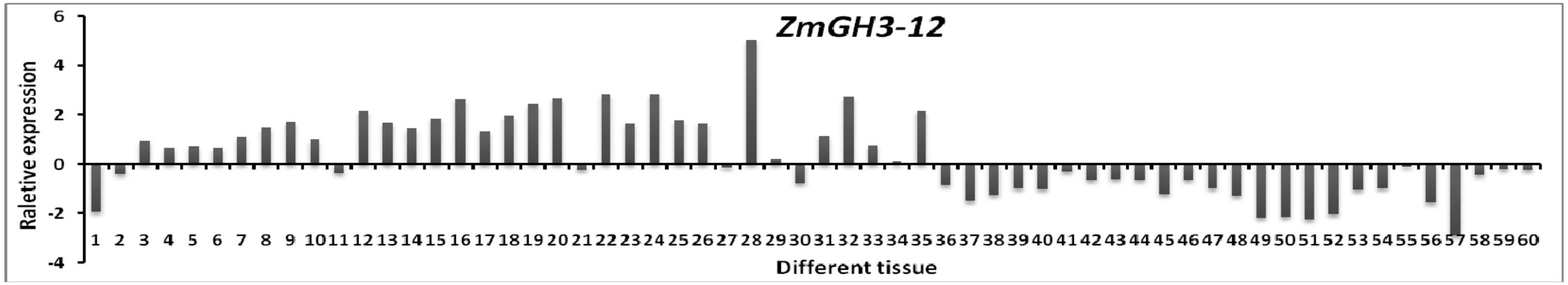

ZmGH3-7
Relative expression
6
4
2
0
-2
-4
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
Different tissue


ZmGH3-8
Relative expression
5
4
3
2
1
0
-1
-2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
Different tissue


ZmGH3-9
Relative expression
4
3
2
1
0
-1
-2
-3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
Different tissue

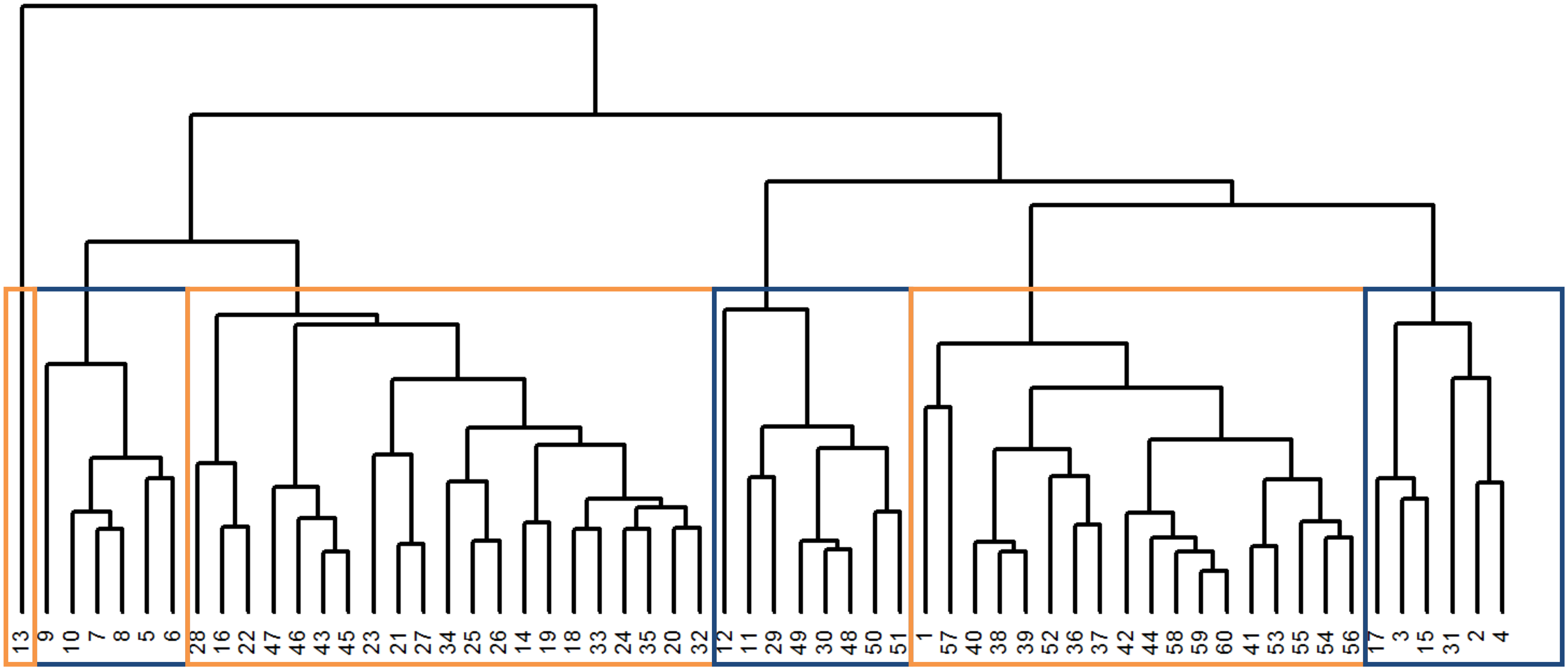

ZmGH3-10
Relative expression
6
4
2
0
-2
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
Different tissue


ZmGH3-11
Relative expression
3
2
1
0
-1
-2
-3
1 2 3 4 5 6 7 8 9 10 11 12 13 14 15 16 17 18 19 20 21 22 23 24 25 26 27 28 29 30 31 32 33 34 35 36 37 38 39 40 41 42 43 44 45 46 47 48 49 50 51 52 53 54 55 56 57 58 59 60
Different tissue



Appendix B Column diagrams of the expression level of these 12 *ZmGH3* genes in 60 different kinds of tissues. The relative expression level of these 12 *ZmGH3* genes in 60 different kinds of tissues were collected from the microarray data. The value above zero indicates the expression level of the gene is higher than that of the control, the value below zero indicates the expression level of the gene is lower than that of the control.

1 Germinating Seed 24h.
2 Coleoptile 6 DAS GH.
3 Coleoptile 6 DAS Primary Root.
4 Stem and SAM (V1).
5 Stem and SAM (V3).
6 Stem and SAM (V4).
7 Shoot tip (V5).
8 First Internode (V5).
9 First Internode (V7).
10 Fourth Internode (V9).
11 Immature Tassel (V13).
12 Meiotic Tassel (V18).
13 Anthers (R1).
14 Whole Seedling (VE).
15 Primary Root (VE).
16 Pooled Leaves (V1).
17 Primary Root (V1).
18 Topmost Leaf (V3).
19 First Leaf (V3).
20 Tip of Stage 2 leaf (V5).
21 Base of Stage 2 leaf (V5).
22 Tip of Stage 2 leaf (V7).
23 Base of Stage 2 leaf (V7).
24 Eighth Leaf (V9).
25 Eleventh Leaf (V9).
26 Thirteenth Leaf (V9).
27 Immature Leaf (V9).
28 Thirteenth Leaf (VT).
29 Immature Cob (V18).
30 Pre-pollination Cob (R1).
31 Silks (R1).
32 Thirteenth Leaf (R2).
33 Innermost Husk (R1).
34 Innermost Husk (R2).
35 Outer Husk (R2).
36 Embryo 16DAP.
37 Embryo 18DAP.
38 Embryo 20DAP.
39 Embryo 22DAP.
40 Embryo 24DAP.
41 Endosperm 12DAP.
42 Endosperm 14DAP.
43 Endosperm 16DAP.
44 Endosperm 18DAP.
45 Endosperm 20DAP.
46 Endosperm 22DAP.
47 Endosperm 24DAP.
48 Seed 2DAP.
49 Seed 4DAP.
50 Seed 6DAP.
51 Seed 8DAP.
52 Seed 10DAP.
53 Seed 12DAP.
54 Seed 14DAP.
55 Seed 16DAP.
56 Seed 18DAP.
57 Pericarp 18DAP.
58 Seed 20DAP.
59 Seed 22DAP.
60 Seed 24DAP.



Appendix C Clustering analysis of these 60 tissues based on the expression relationship among these *ZmGH3* genes. The 60 tissues were divided into six classes according to the expression levels of the *ZmGH*s. From the left to right, the brackets indicate the tissue pattern Ⅰ, Ⅱ, Ⅲ, Ⅳ, Ⅴ, and Ⅵ.

1 Germinating Seed 24h. 2 Coleoptile 6 DAS GH. 3 Coleoptile 6 DAS Primary Root. 4 Stem and SAM (V1). 5 Stem and SAM (V3).
6 Stem and SAM (V4). 7 Shoot tip (V5). 8 First Internode (V5). 9 First Internode (V7). 10 Fourth Internode (V9).
11 Immature Tassel (V13). 12 Meiotic Tassel (V18). 13 Anthers (R1). 14 Whole Seedling (VE). 15 Primary Root (VE).
16 Pooled Leaves (V1). 17 Primary Root (V1). 18 Topmost Leaf (V3). 19 First Leaf (V3). 20 Tip of Stage 2 leaf (V5).
21 Base of Stage 2 leaf (V5). 22 Tip of Stage 2 leaf (V7). 23 Base of Stage 2 leaf (V7). 24 Eighth Leaf (V9). 25 Eleventh Leaf (V9).
26 Thirteenth Leaf (V9). 27 Immature Leaf (V9). 28 Thirteenth Leaf (VT). 29 Immature Cob (V18). 30 Pre-pollination Cob (R1).

31 Silks (R1).
32 Thirteenth Leaf (R2).
33 Innermost Husk (R1).
34 Innermost Husk (R2).
35 Outer Husk (R2).
36 Embryo 16DAP.
37 Embryo 18DAP.
38 Embryo 20DAP.
39 Embryo 22DAP.
40 Embryo 24DAP.
41 Endosperm 12DAP.
42 Endosperm 14DAP.
43 Endosperm 16DAP.
44 Endosperm 18DAP.
45 Endosperm 20DAP.
46 Endosperm 22DAP.
47 Endosperm 24DAP.
48 Seed 2DAP.
49 Seed 4DAP.
50 Seed 6DAP.
51 Seed 8DAP.
52 Seed 10DAP.
53 Seed 12DAP.
54 Seed 14DAP.
55 Seed 16DAP.
56 Seed 18DAP.
57 Pericarp 18DAP.
58 Seed 20DAP.
59 Seed 22DAP.
60 Seed 24DAP.