

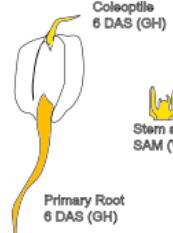
Zm00001d002064

Maize eFP Browser at bar.utoronto.ca

Winter et al., PLoS One 2(8):e718

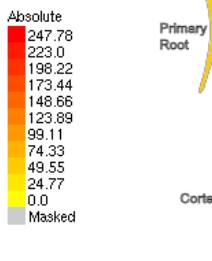
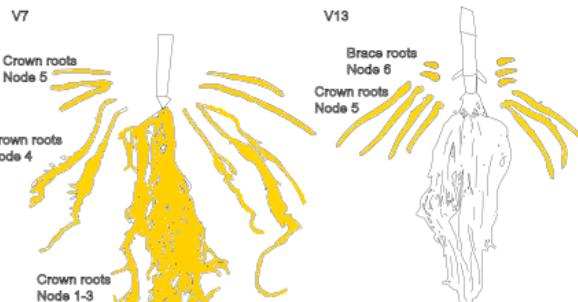
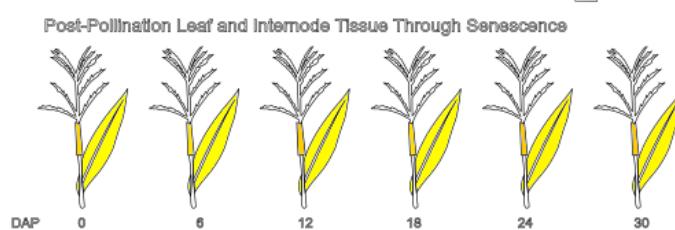
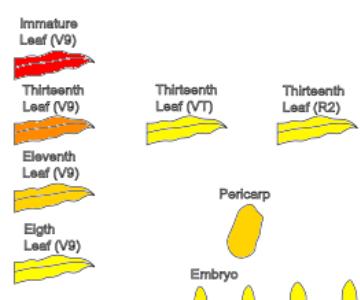
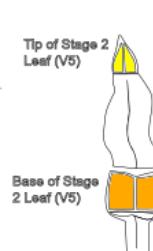
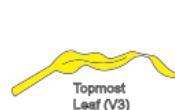
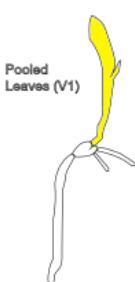
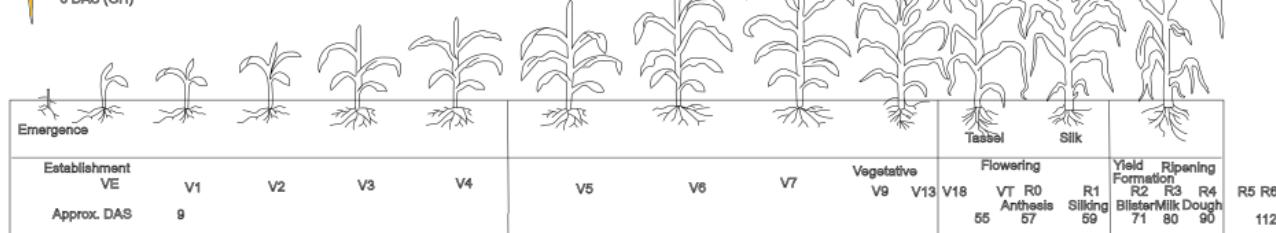
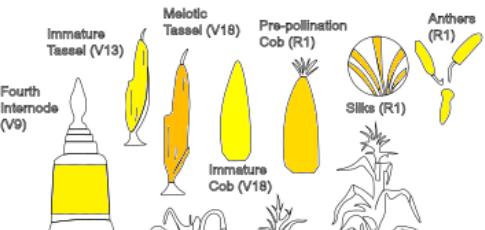
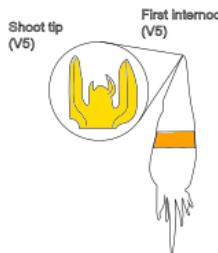
Stelpflug et al., Plant Genome 9(1)

Hoopes et al. (2018) Plant J.



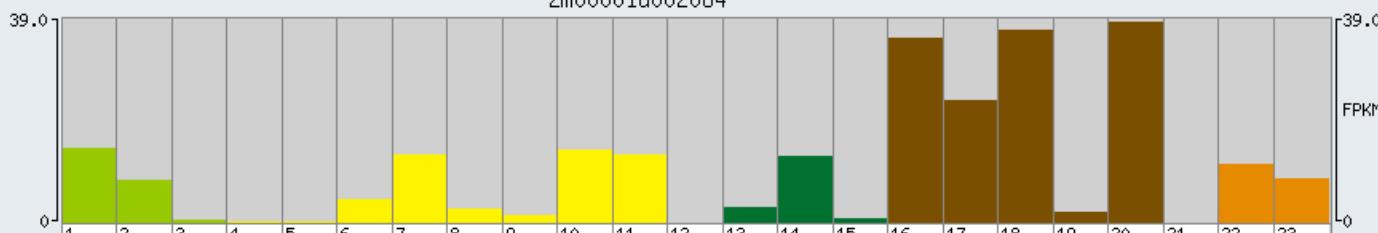
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Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

Zm00001d002064



1. 6-7_Internode (15.1)

2. 7-8_Internode (9.1)

3. Meristem_16-19_Day (1.6)

4. Ear_Primordium_2-4mm (1.1)

5. Ear_Primordium_6-8mm (1.2)

6. Embryo_20DAP (5.6)

7. Embryo_38DAP (13.9)

8. Endosperm_12DAP (3.5)

9. Endosperm_Crown_27DAP (2.3)

10. Germinatin_Kernels_2DAI (15.0)

11. Pericarp/Aleurone_27DAP (13.9)

12. Leaf_Zone_1_Symmetrical (NA)

13. Leaf_Zone_2_Stomatal (4.0)

14. Leaf_Zone_3_Growth (13.6)

15. Mature_Leaf_8 (1.8)

16. Primary_Root_5_Days (36.0)

17. Root_Cortex_5_Days (24.3)

18. Root_Elongation_Zone_5_Days (37.7)

19. Root_Meristem_Zone_5_Days (3.1)

20. Secondary_Root_7-8_Days (39.0)

21. B73_Mature_Pollen (NA)

22. Female_Spikelet (12.0)

23. Silk (9.4)

Zm00001d004822

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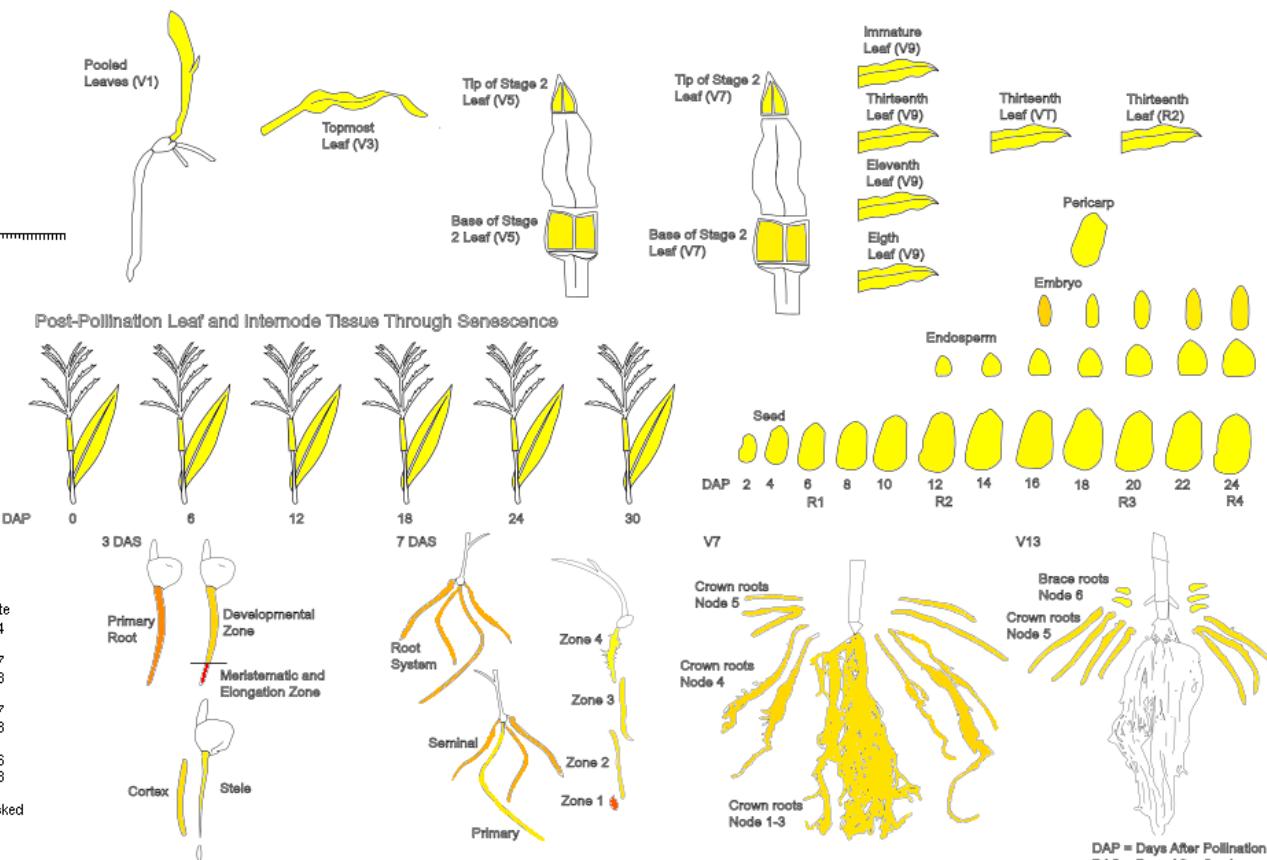
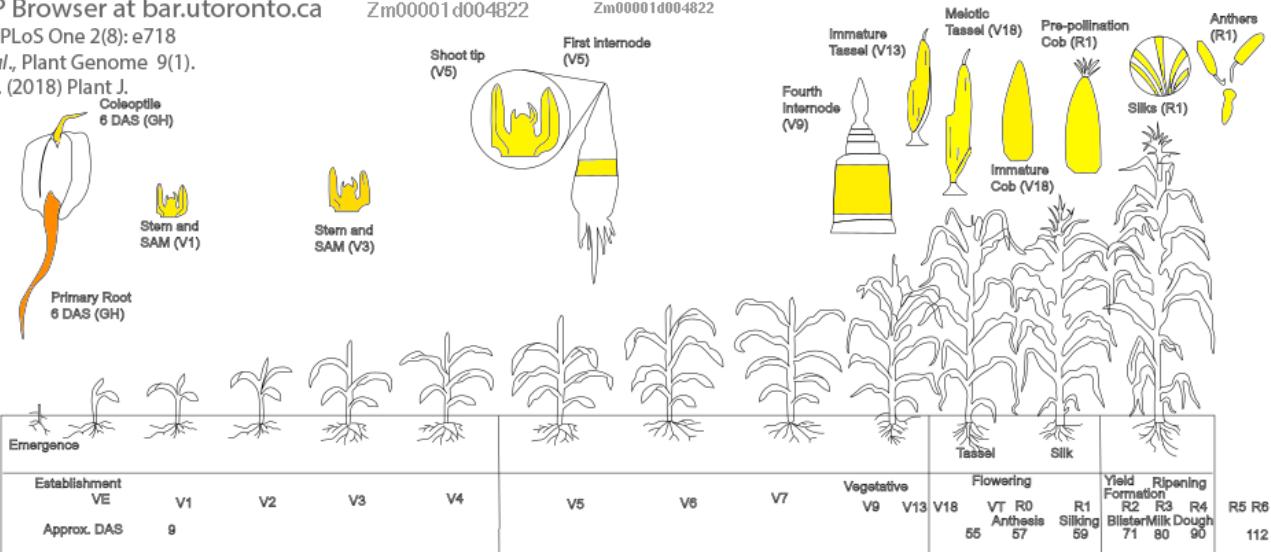
Winter et al., PLoS One 2(8):e718

Stelpflug et al., Plant Genome 9(1).

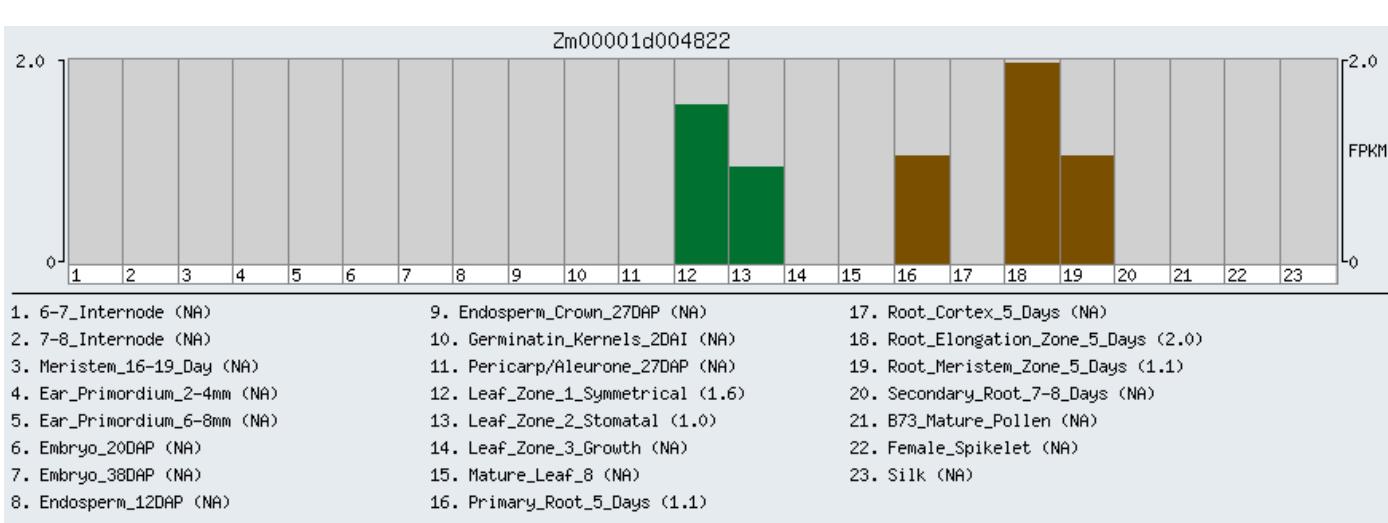
Hoopes et al. (2018) Plant J.

Zm00001d004822

Zm00001d004822



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



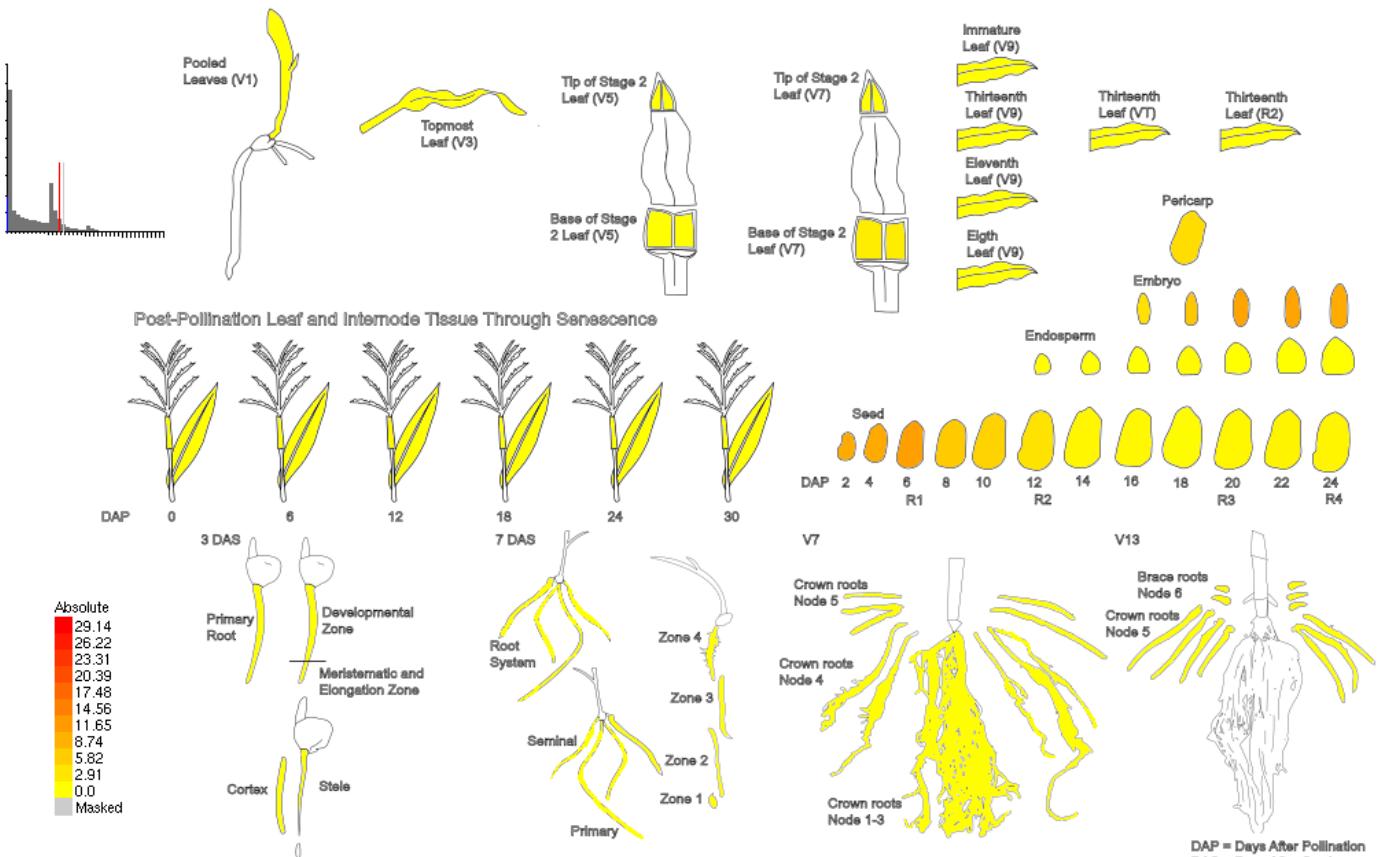
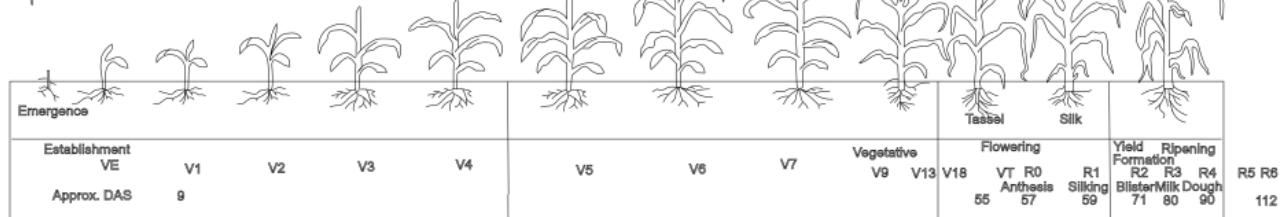
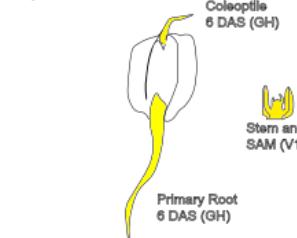
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Maize eFP Browser at bar.utoronto.ca

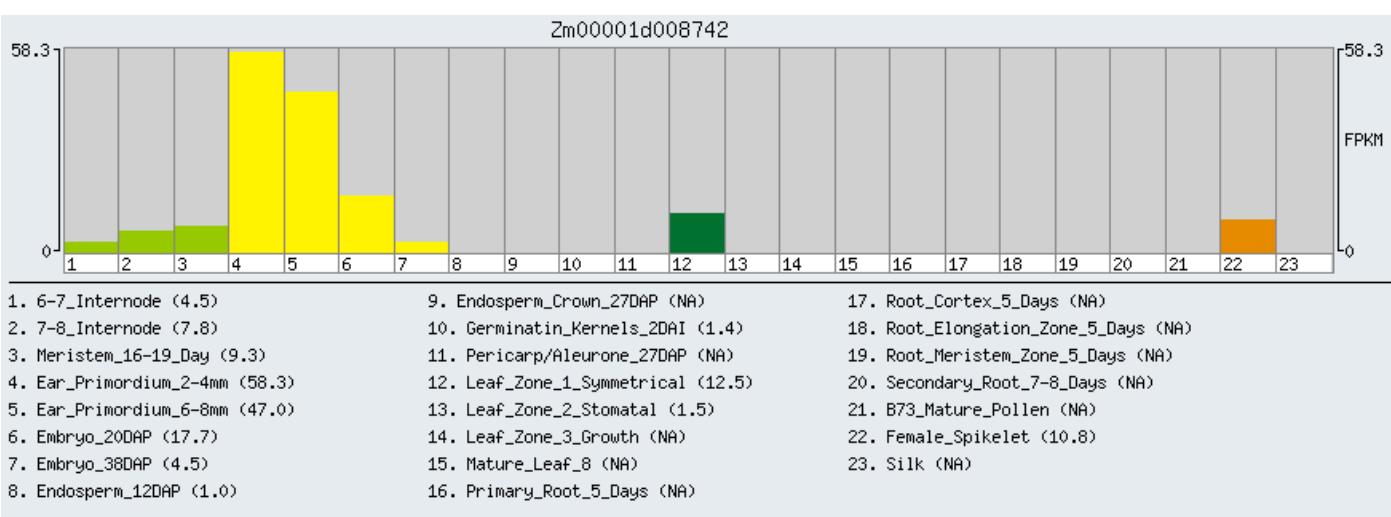
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1)

Hoopes et al. (2018) Plant J.



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPV4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPV4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



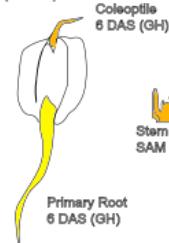
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Maize eFP Browser at bar.utoronto.ca

Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

Hoopes et al. (2018) Plant J.

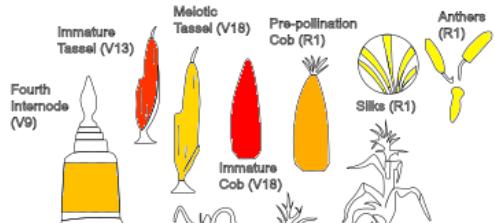
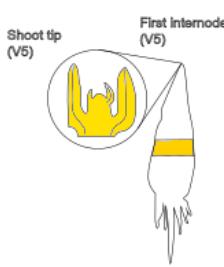


Emergence

V1 V2 V3 V4

Approx. DAS
9

Zm00001d008966



R5 R6
112

V5 V6 V7

Vegetative
Flowering

V9 V13

V18 VT

R0 R1

R2 R3

R4 R5

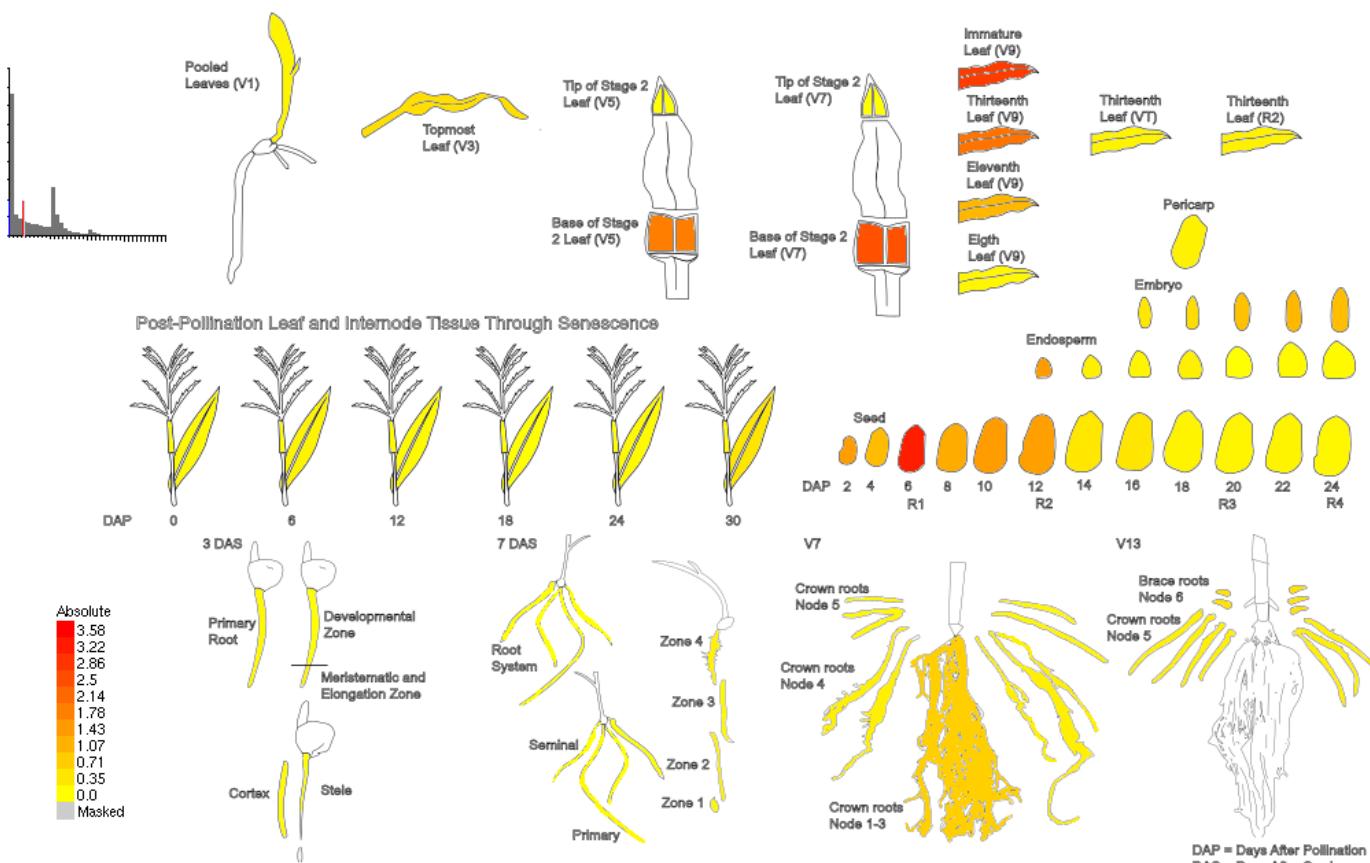
Bilster Milk Dough

Silking 59

Blister 71

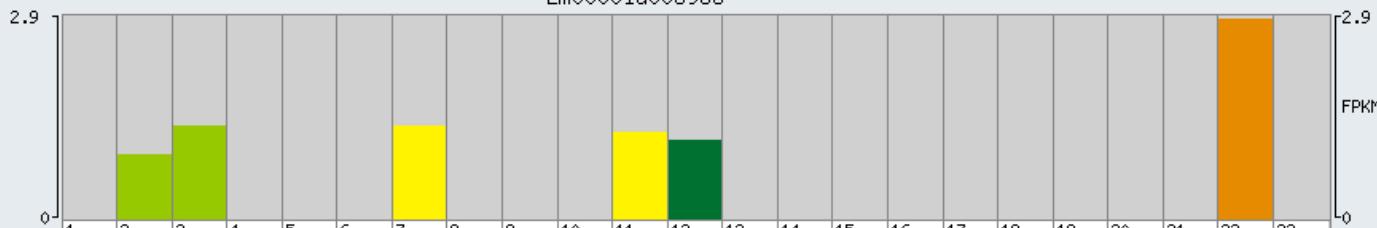
Milk 80

Dough 90



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

Zm00001d008966



1. 6-7_Internode (NA)
2. 7-8_Internode (1.0)
3. Meristem_16-19_Day (1.4)
4. Ear_Primordium_2-4mm (NA)
5. Ear_Primordium_6-8mm (NA)
6. Embryo_20DAP (NA)
7. Embryo_38DAP (1.4)
8. Endosperm_12DAP (NA)

9. Endosperm_Crown_27DAP (NA)
10. Germinatin_Kernels_20AI (NA)
11. Pericarp/Aleurone_27DAP (1.3)
12. Leaf_Zone_1_Symmetrical (1.2)
13. Leaf_Zone_2_Stomatal (NA)
14. Leaf_Zone_3_Growth (NA)
15. Mature_Leaf_8 (NA)
16. Primary_Root_5_Days (NA)

17. Root_Cortex_5_Days (NA)
18. Root_Elongation_Zone_5_Days (NA)
19. Root_Meristem_Zone_5_Days (NA)
20. Secondary_Root_7-8_Days (NA)
21. B73_Mature_Pollen (NA)
22. Female_Spikelet (2.9)
23. Silk (NA)

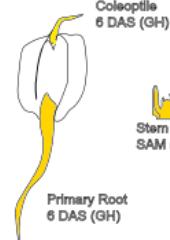
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Winter et al., PLoS One 2(8): e718

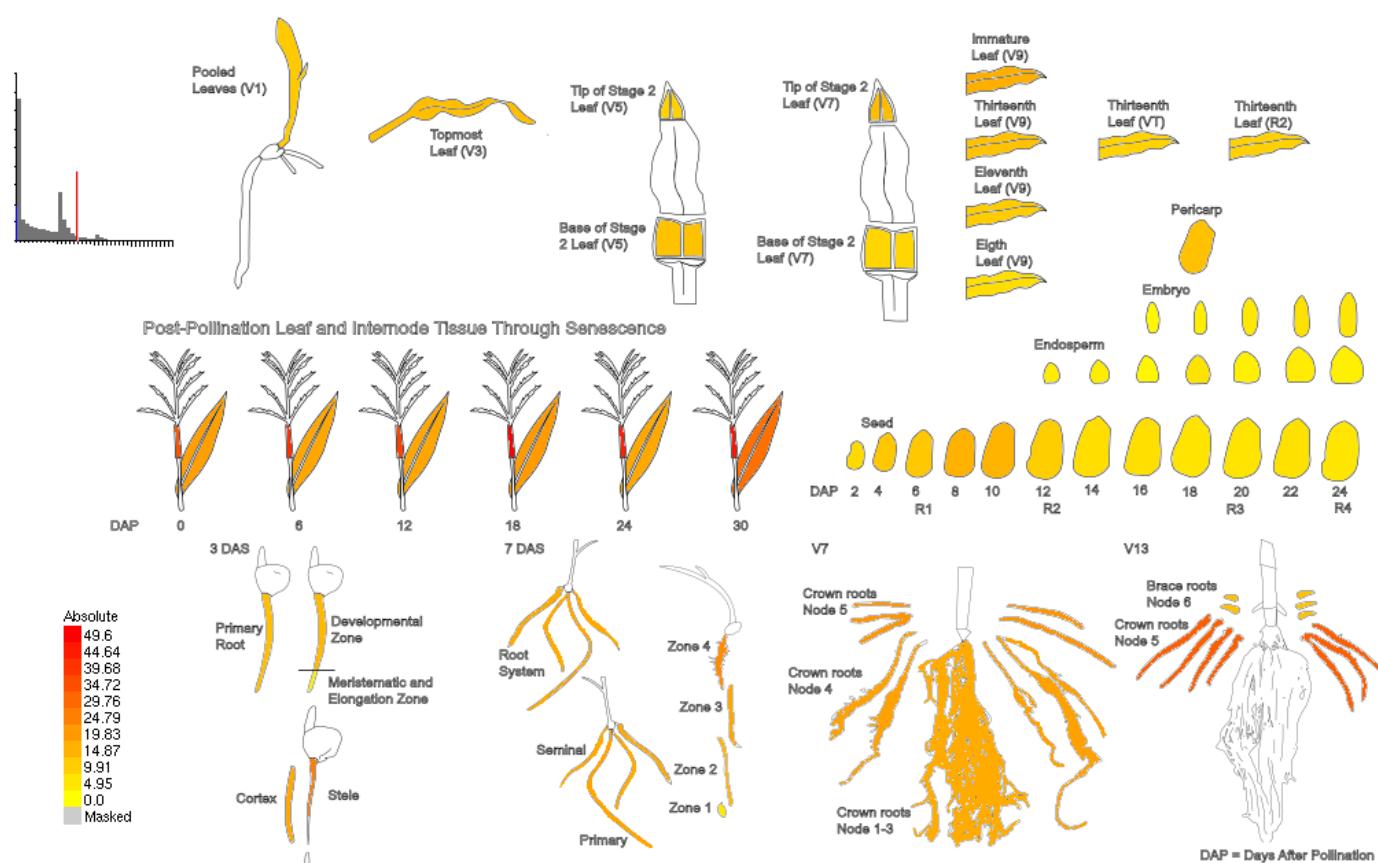
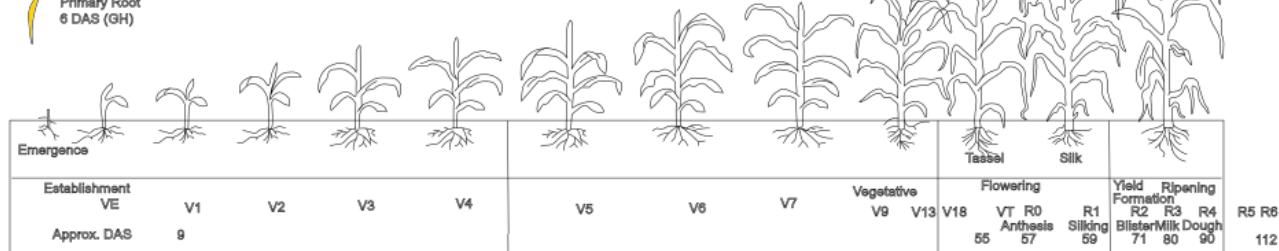
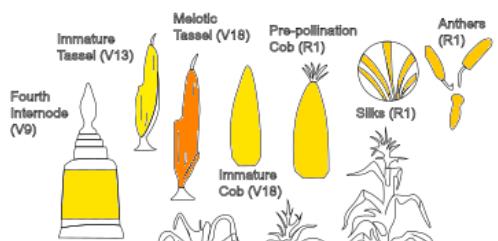
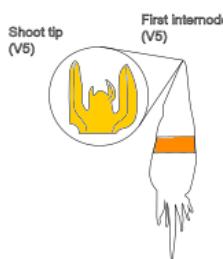
Stelpflug et al., Plant Genome 9(1).

Hoopes et al. (2018) Plant J.

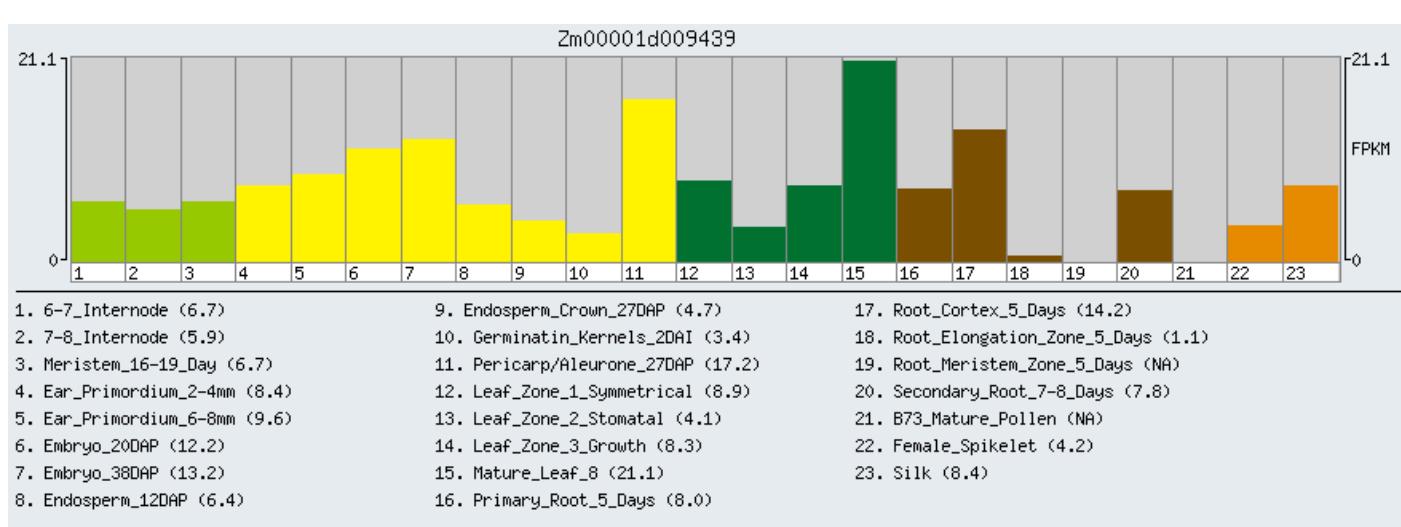


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Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



Zm00001d010366

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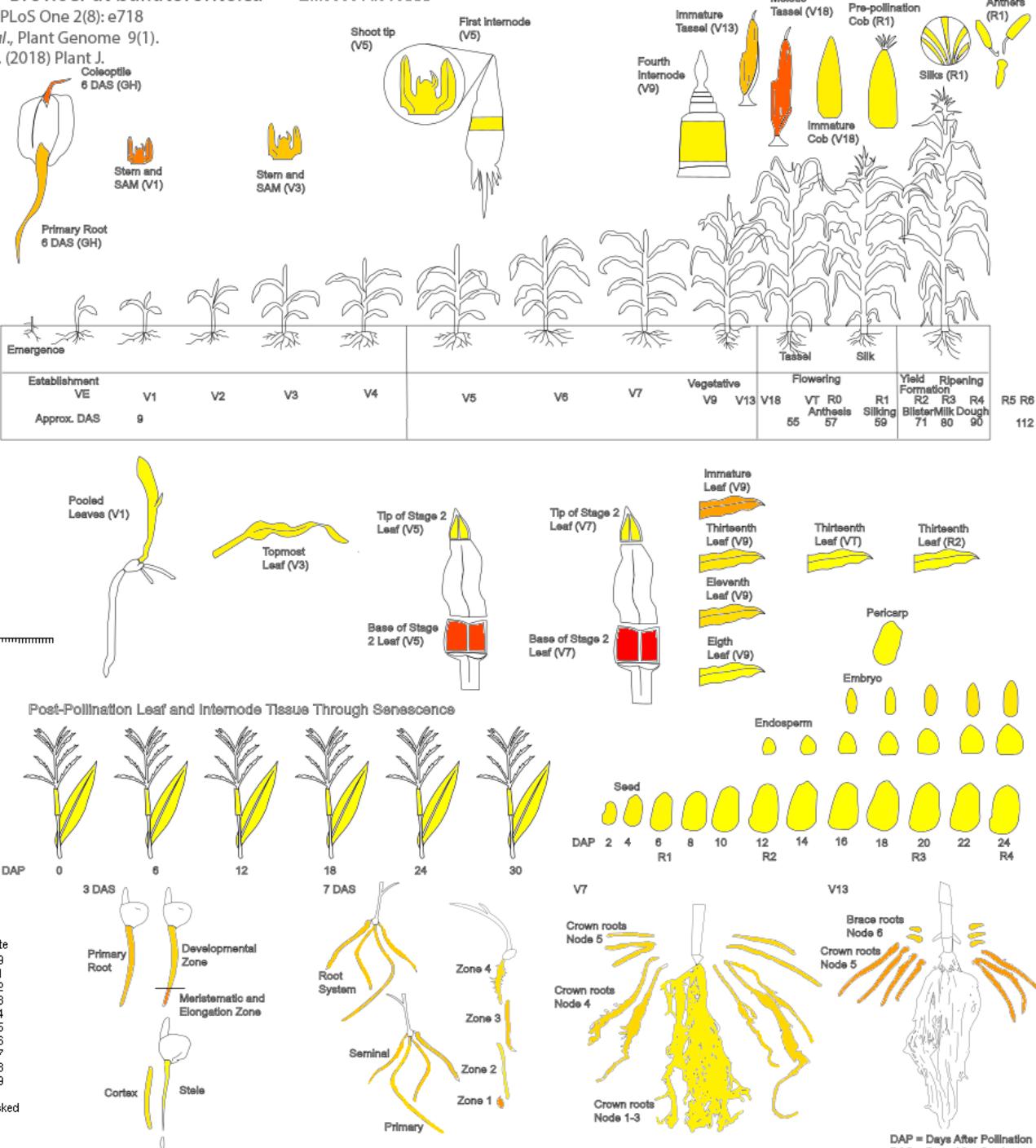
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

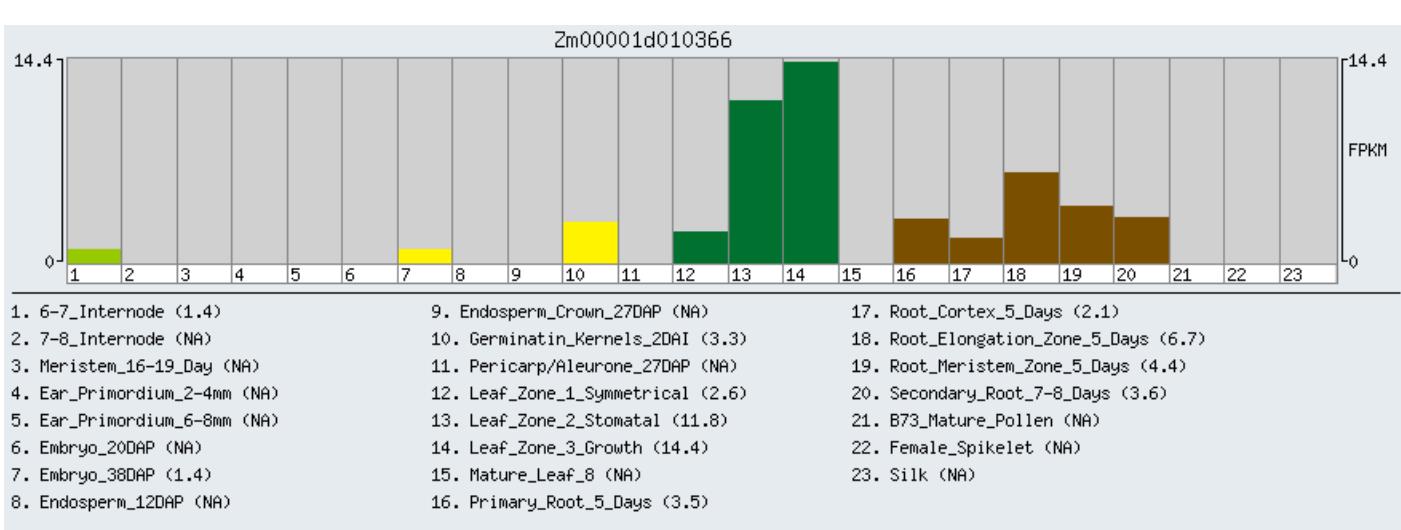
Hoopes et al. (2018) Plant J.

Zm00001d010366

Zm00001d010366



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



Zm00001d011745

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Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

Hoopes et al. (2018) Plant J.

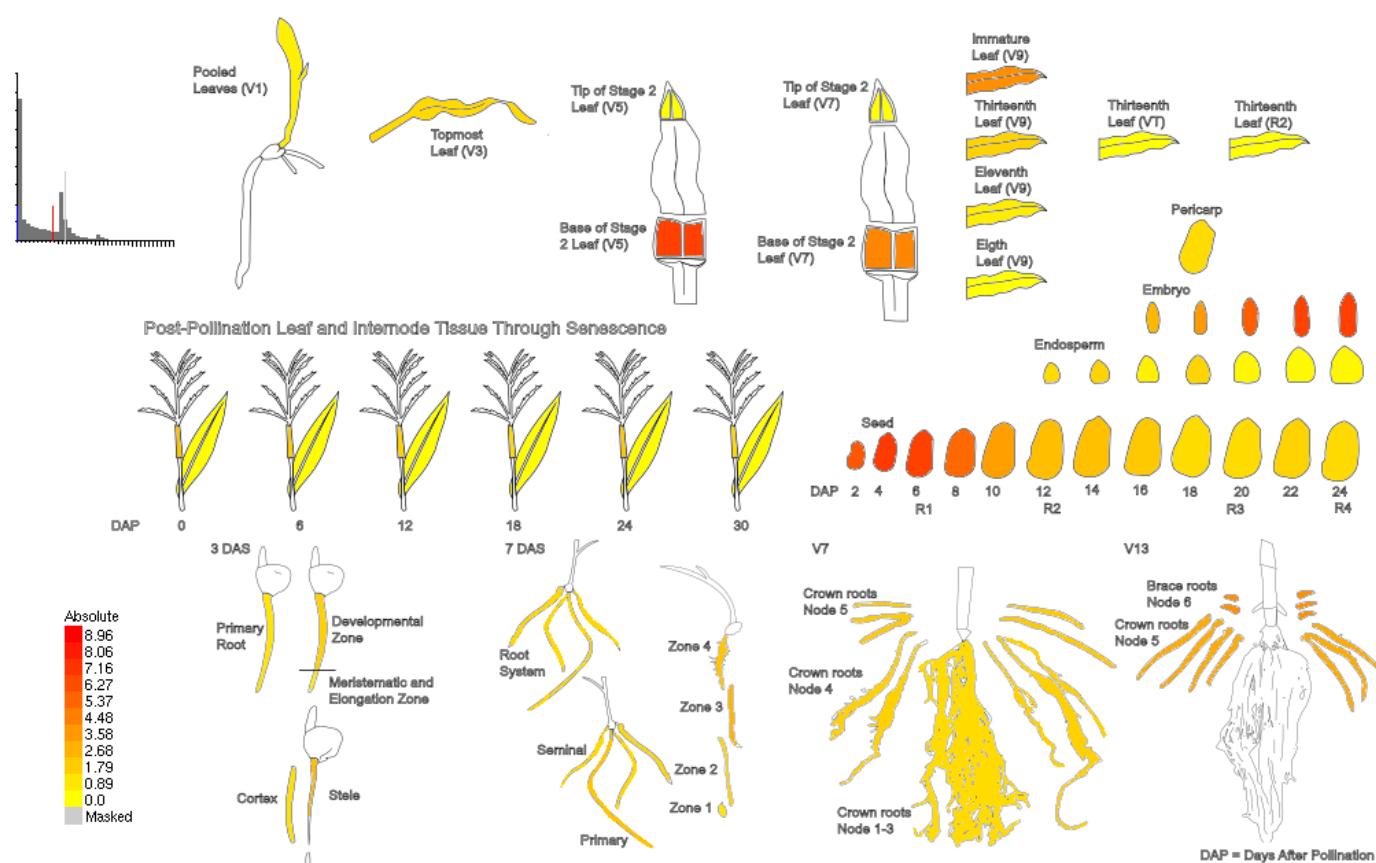
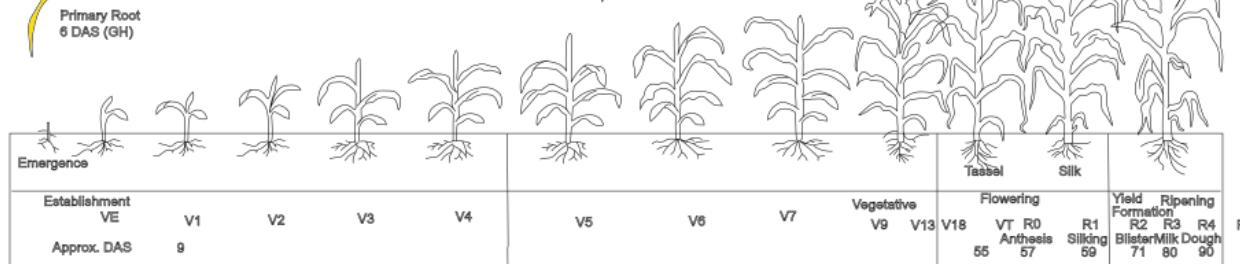
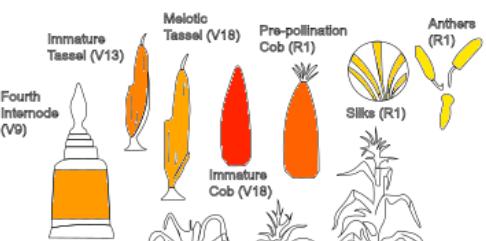
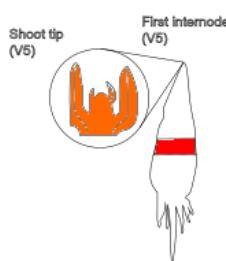
Coleoptile 6 DAS (GH)

Primary Root 6 DAS (GH)

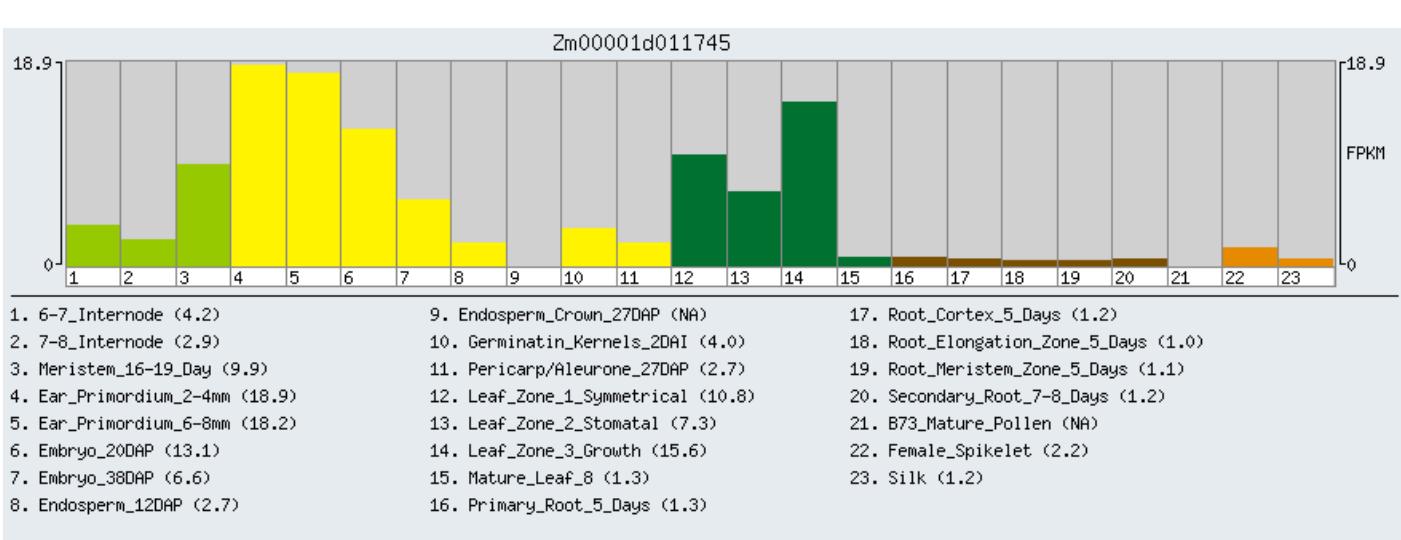
Stern and SAM (V1)

Stern and SAM (V3)

Zm00001d011745



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



Zm00001d011924

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Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1)

Hoopes et al. (2018) Plant J.

Coleoptile
6 DAS (GH)

Primary Root
6 DAS (GH)

Stem and SAM (V1)

Stem and SAM (V3)

Zm00001d011924

Shoot tip (V5)

First Internode (V5)

Zm00001d011924

Fourth Internode (V9)

Immature Tassel (V13)

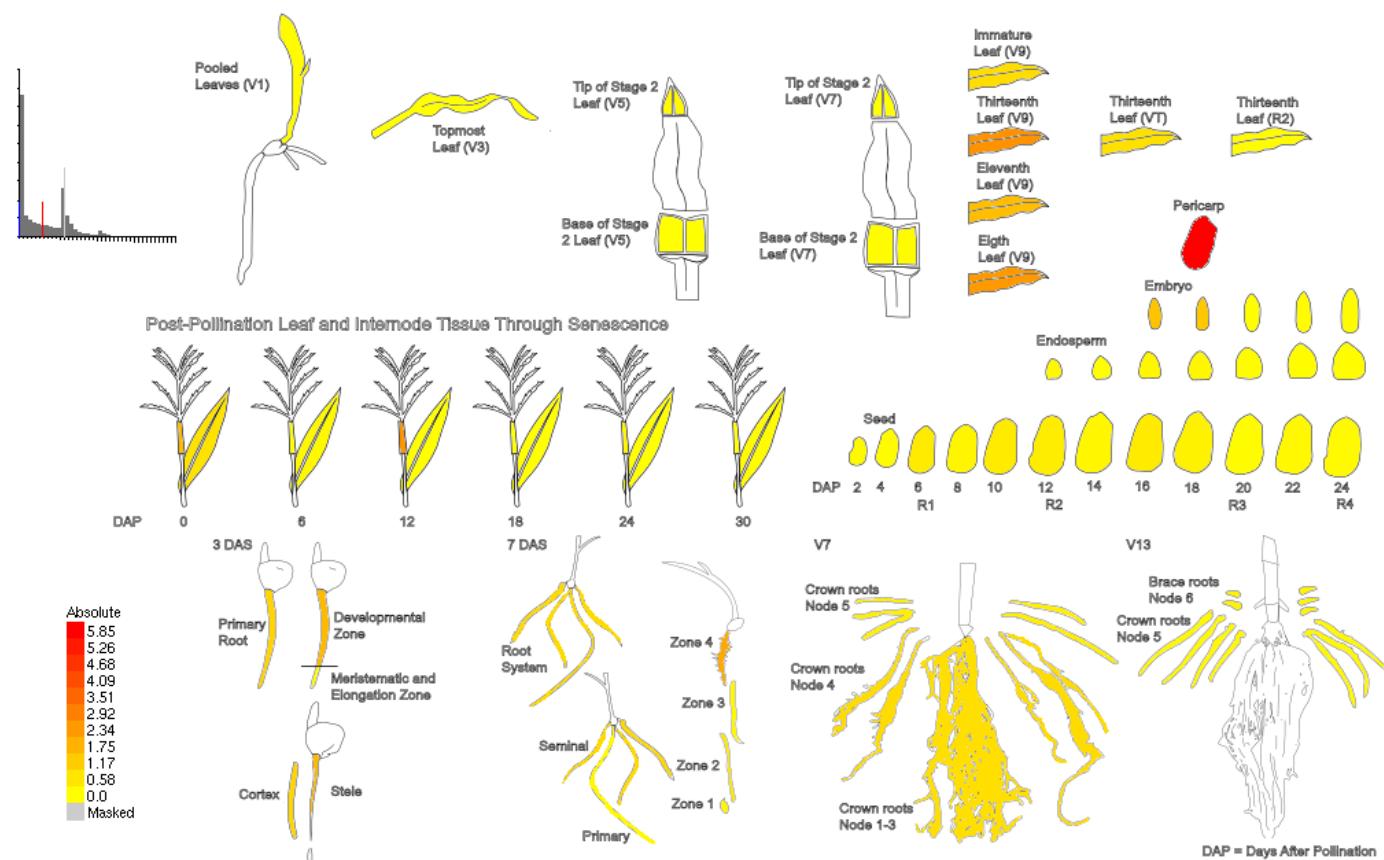
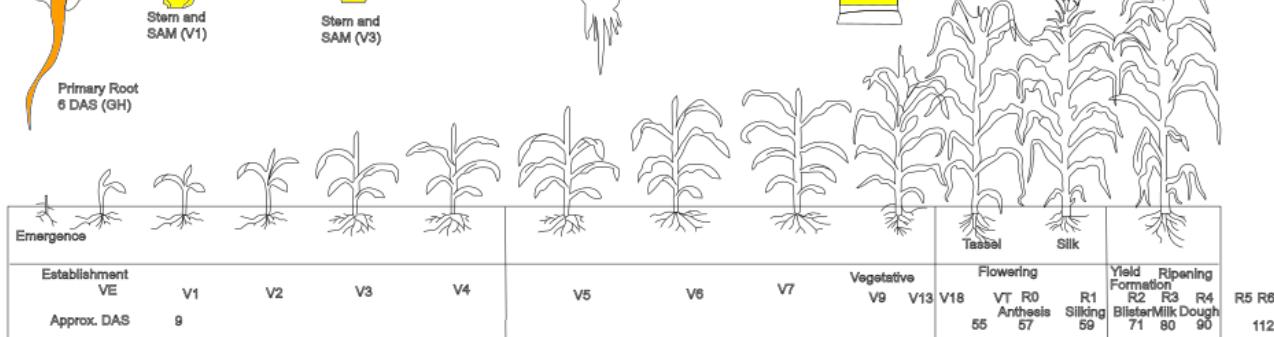
Meliotic Tassel (V18)

Pre-pollination Cob (R1)

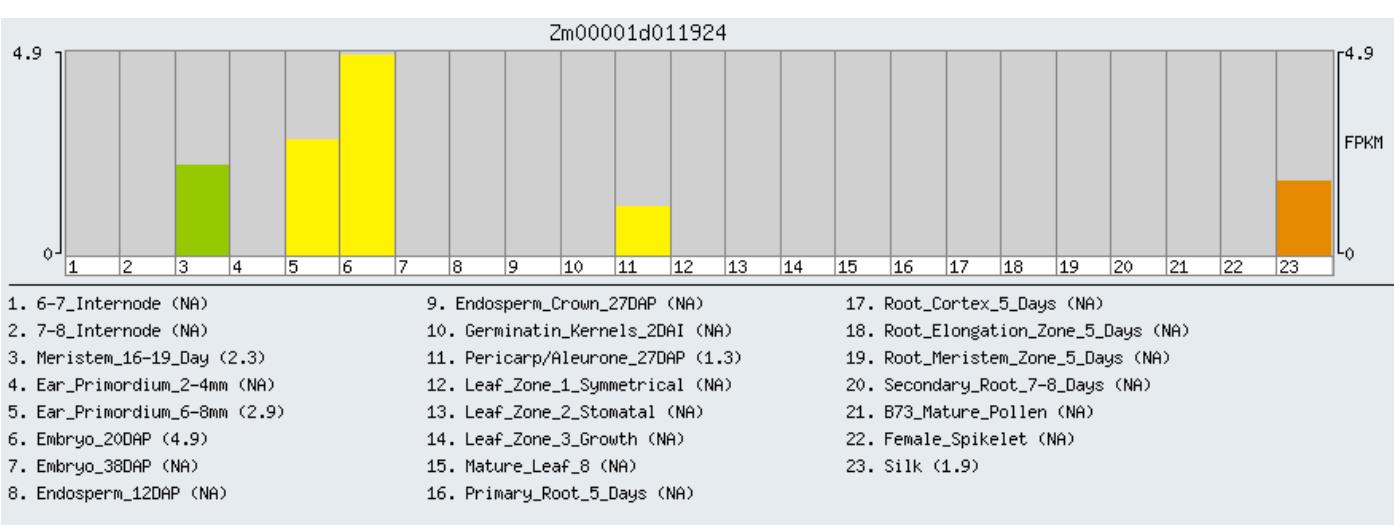
Immature Cob (V18)

Silks (R1)

Anthers (R1)



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



Zm00001d014166

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Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1)

Hoopes et al. (2018) Plant J.

Coleoptile
6 DAS (GH)



Primary Root
6 DAS (GH)



Zm00001d014166

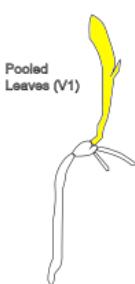
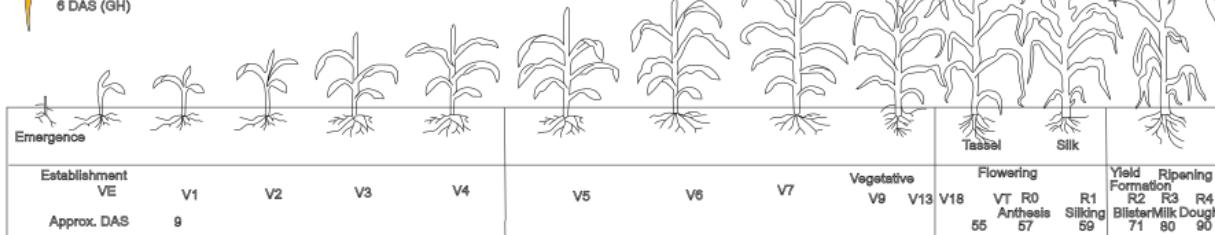
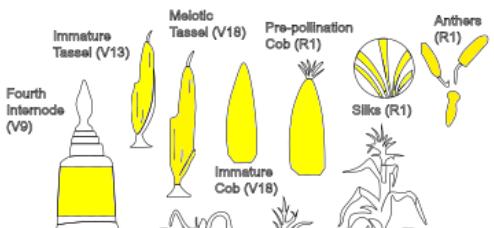
Shoot tip (V5)



First Internode (V5)



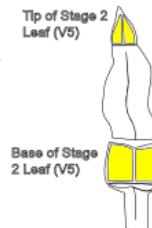
Stem and SAM (V3)



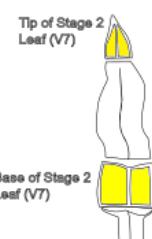
Pooled Leaves (V1)



Topmost Leaf (V3)



Tip of Stage 2 Leaf (V5)



Tip of Stage 2 Leaf (V7)



Immature Leaf (V9)



Thirteenth Leaf (VT)



Eleventh Leaf (V9)



Eighth Leaf (V9)



Thirteenth Leaf (VT)



Thirteenth Leaf (V2)



Pericarp

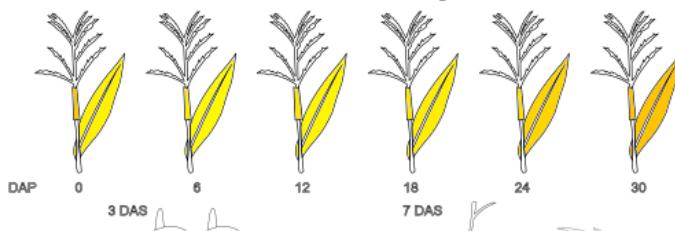


Embryo



Endosperm

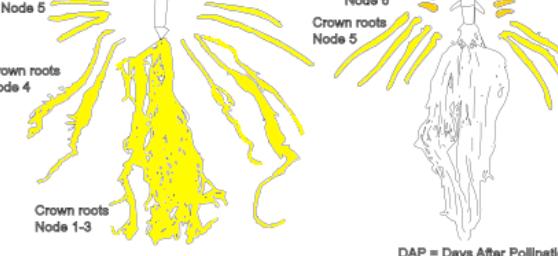
Post-Pollination Leaf and Internode Tissue Through Senescence



DAP 2 4 6 8 10 12 14 16 18 20 22 24

R1 R2 R3 R4

V7 V13



DAP = Days After Pollination

DAS = Days After Sowing

Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

Zm00001d014166



1. 6-7_Internode (NA)
2. 7-8_Internode (NA)
3. Meristem_16-19_Day (NA)
4. Ear_Primordium_2-4mm (1.5)
5. Ear_Primordium_6-8mm (2.0)
6. Embryo_20DAP (5.9)
7. Embryo_38DAP (NA)
8. Endosperm_12DAP (NA)

9. Endosperm_Crown_27DAP (NA)
10. Germinatin_Kernels_2DAI (NA)
11. Pericarp/Aleurone_27DAP (NA)
12. Leaf_Zone_1_Symmetrical (NA)
13. Leaf_Zone_2_Stomatal (NA)
14. Leaf_Zone_3_Growth (NA)
15. Mature_Leaf_8 (NA)
16. Primary_Root_5_Days (1.9)

17. Root_Cortex_5_Days (3.2)
18. Root_Elongation_Zone_5_Days (1.4)
19. Root_Meristem_Zone_5_Days (NA)
20. Secondary_Root_7-8_Days (1.9)
21. B73_Mature_Pollen (NA)
22. Female_Spikelet (NA)
23. Silk (26.9)

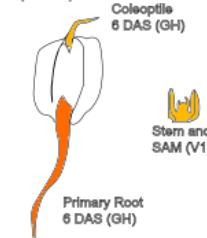
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Winter et al., PLoS One 2(8): e718

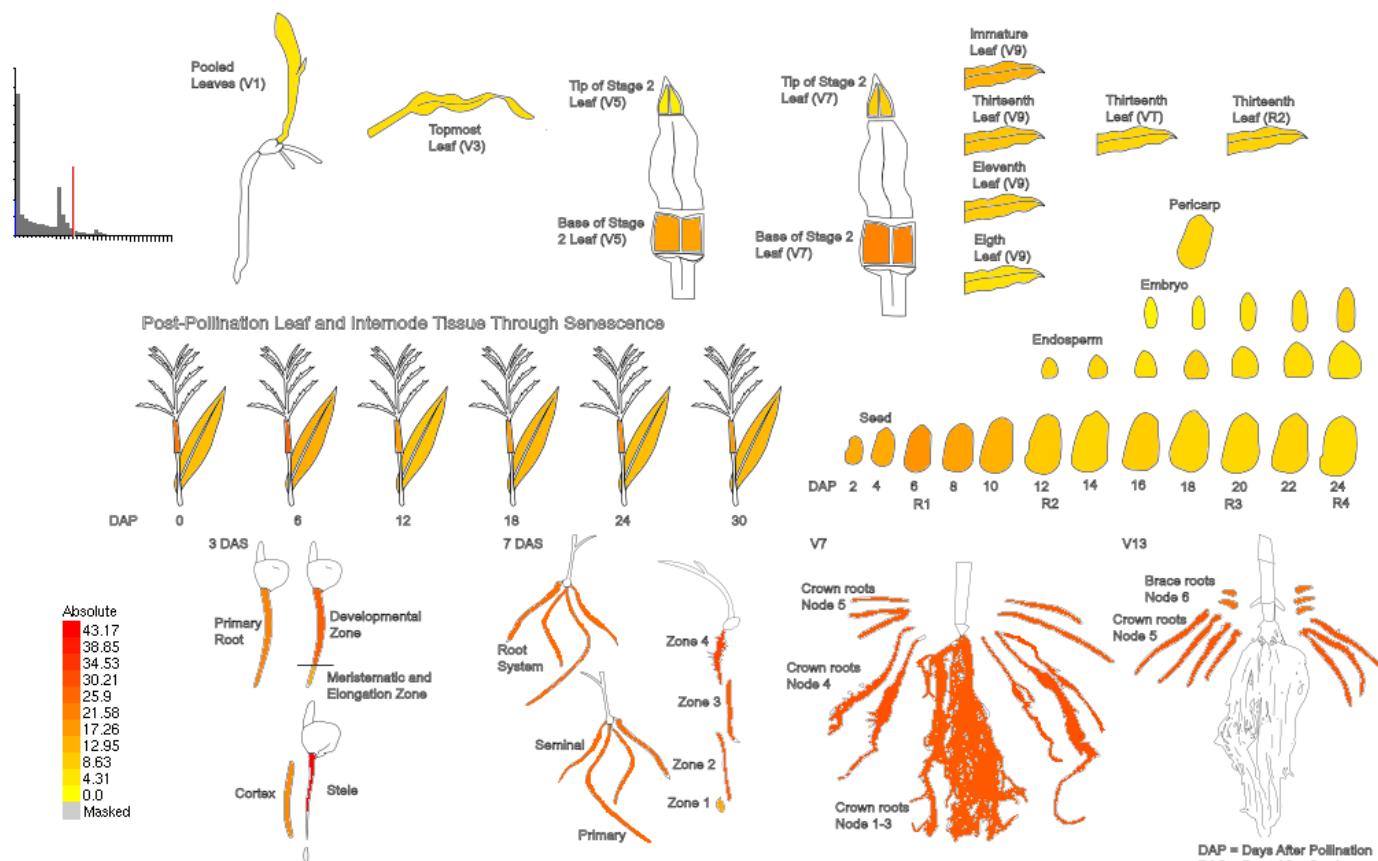
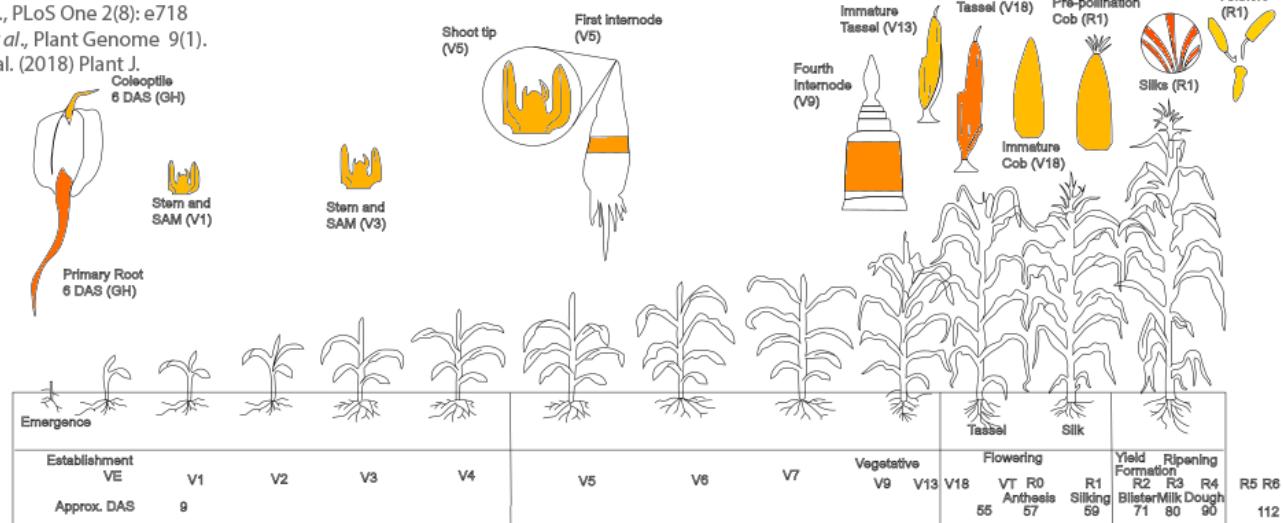
Stelpflug et al., Plant Genome 9(1).

Hoopes et al. (2018) Plant J.

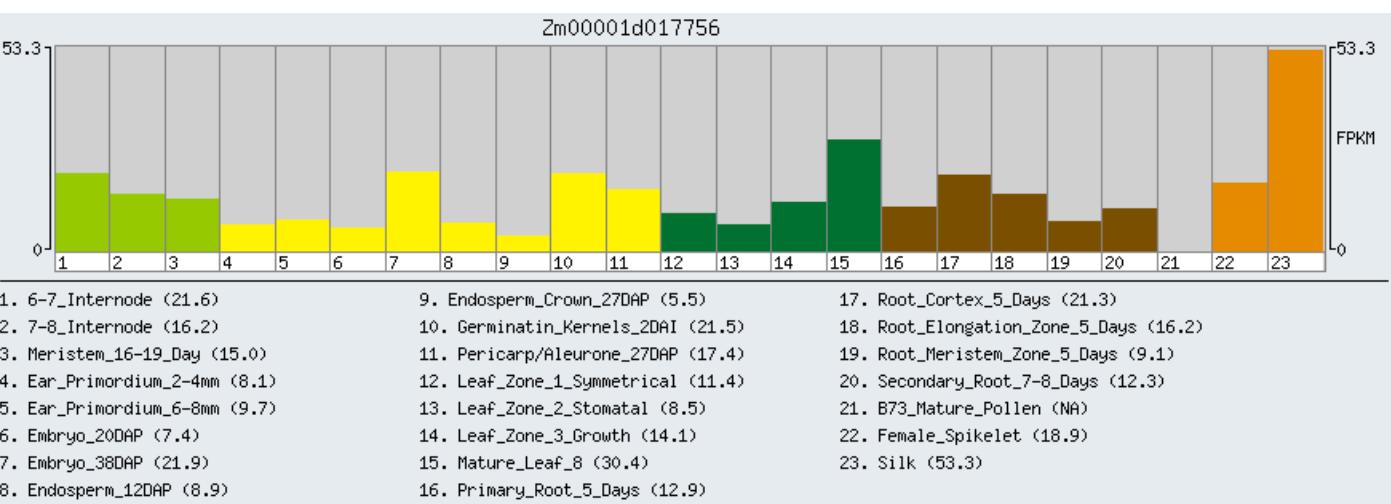


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Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



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Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

Hoopes et al. (2018) Plant J.

Coleoptile
6 DAS (GH)

Primary Root
6 DAS (GH)

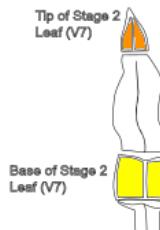
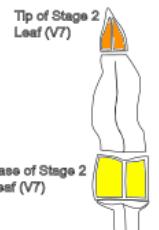
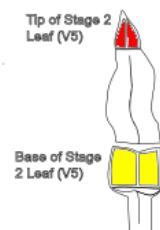
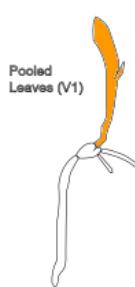
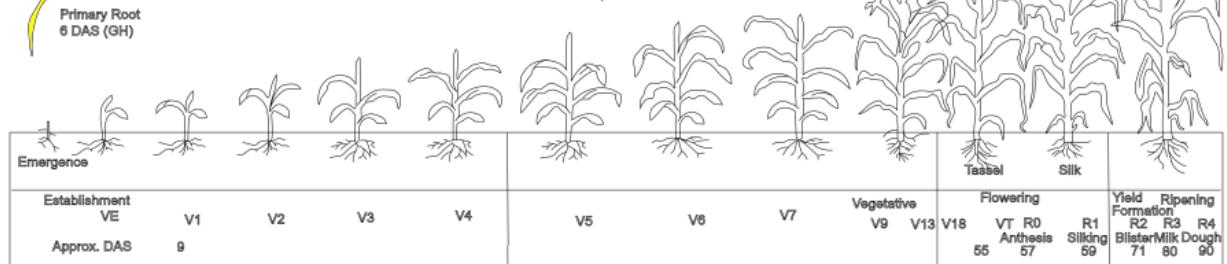
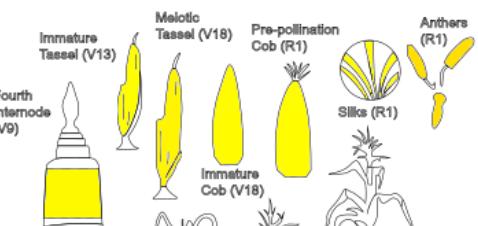
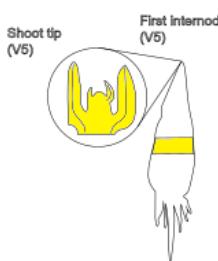
Stem and
SAM (V1)

Shoot tip
(V5)

First Internode
(V5)

Zm00001d017770

Zm00001d017770



Immature Leaf (V9)

Thirteenth Leaf (V9)

Eleventh Leaf (V9)

Eighth Leaf (V9)

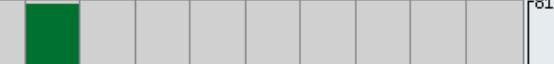
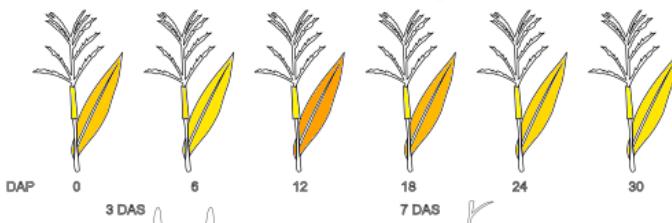


Pericarp

Embryo

Endosperm

Post-Pollination Leaf and Internode Tissue Through Senescence



Zm00001d017866

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Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

Hoopes et al. (2018) Plant J.

Coleoptile 6 DAS (GH)

Primary Root 6 DAS (GH)

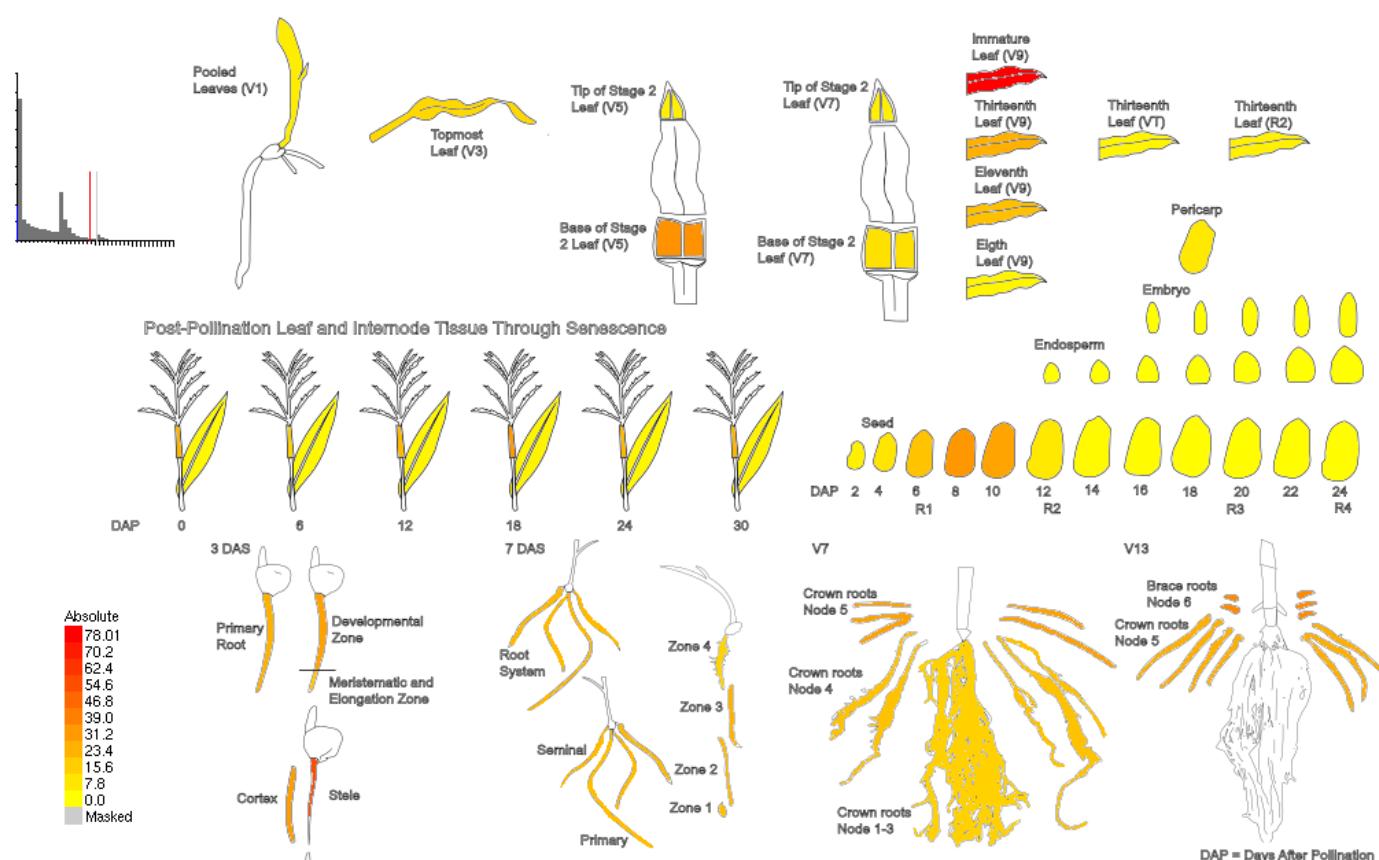
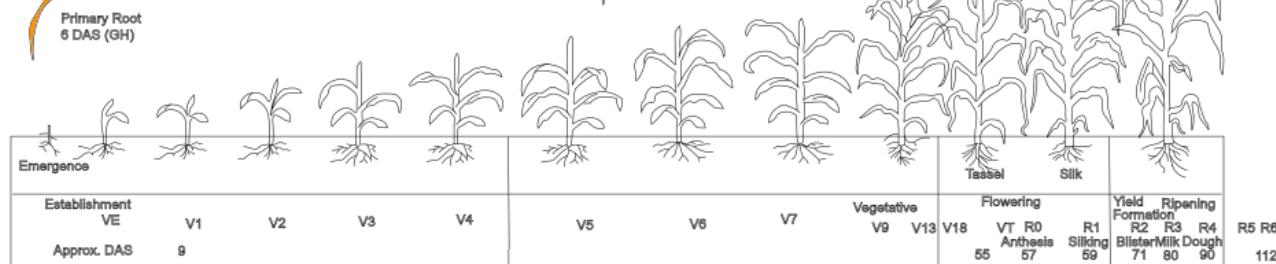
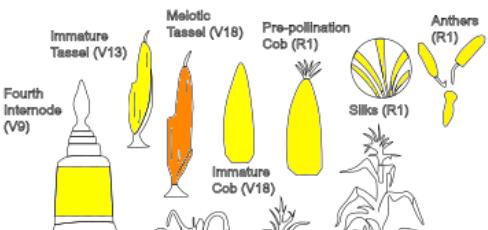
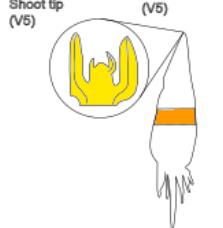
Stern and SAM (V1)

Stern and SAM (V3)

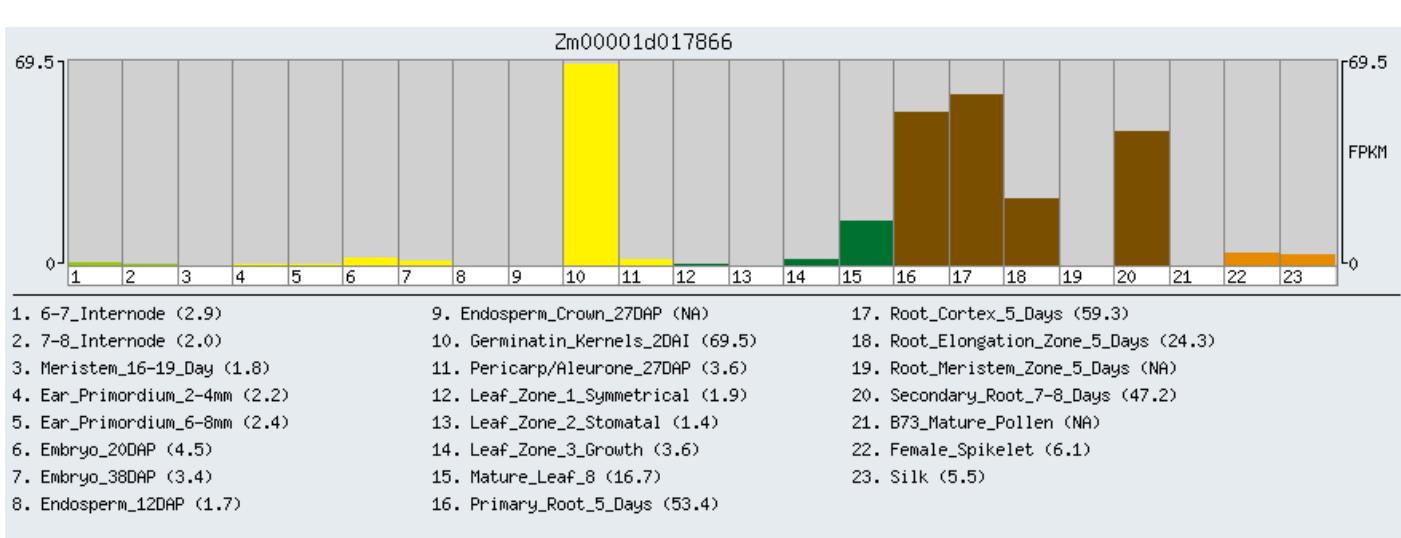
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Shoot tip (V6)

First Internode (V5)



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



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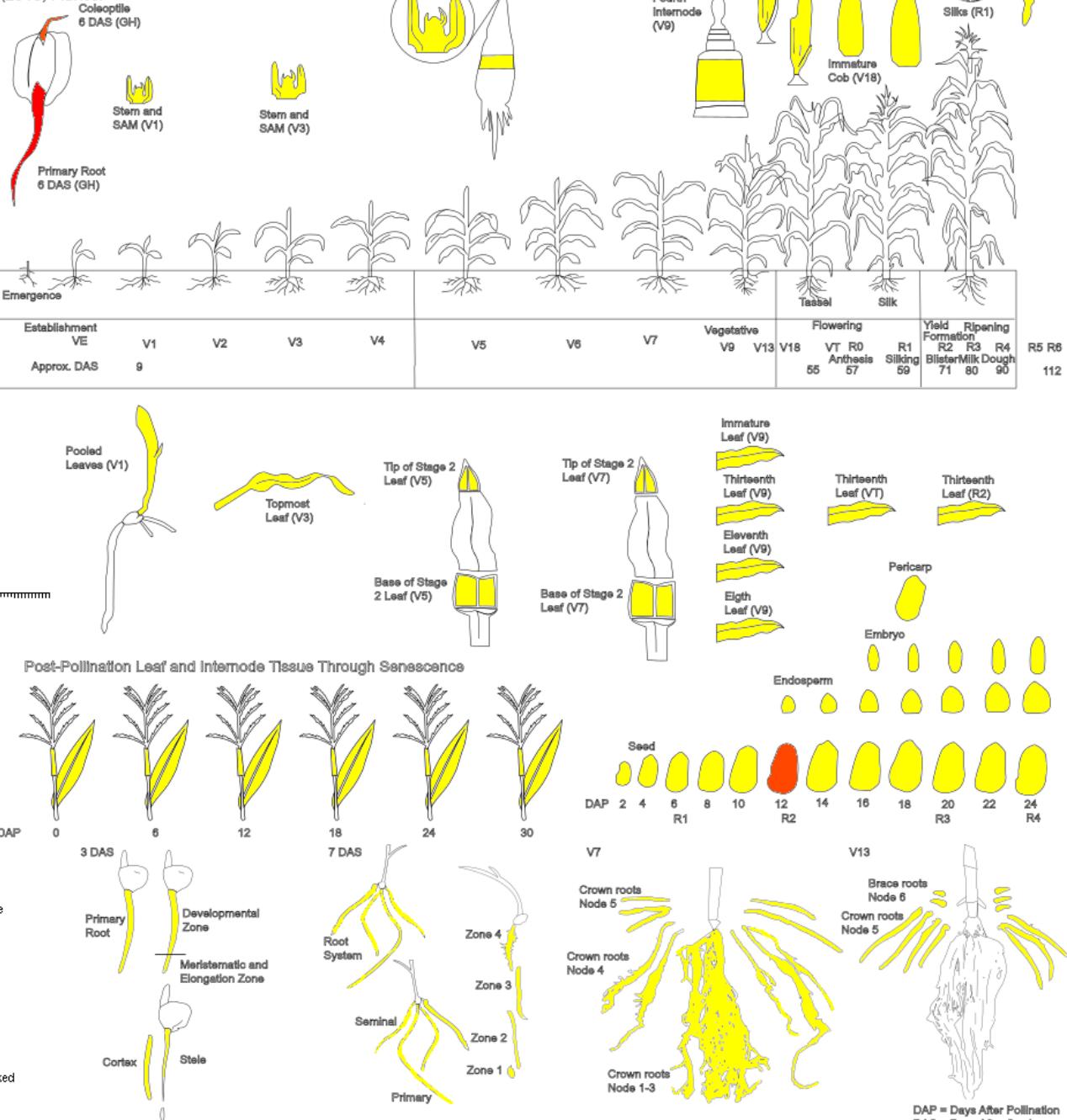
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1)

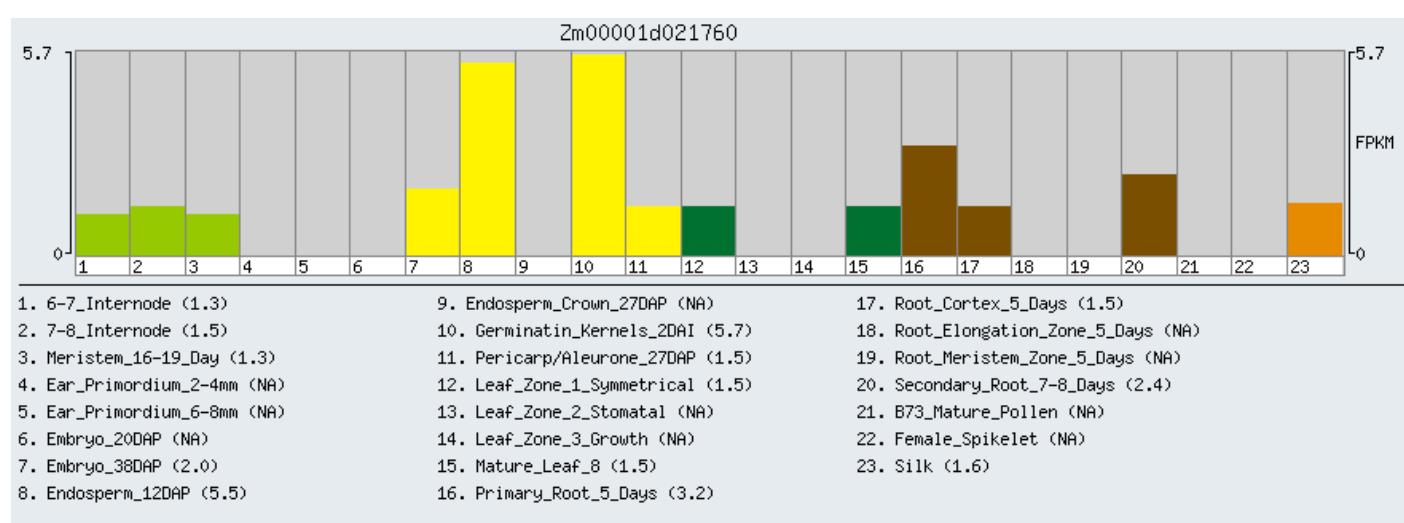
Hoopes et al. (2018) Plant J.

Zm00001d021760

Zm00001d021760



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

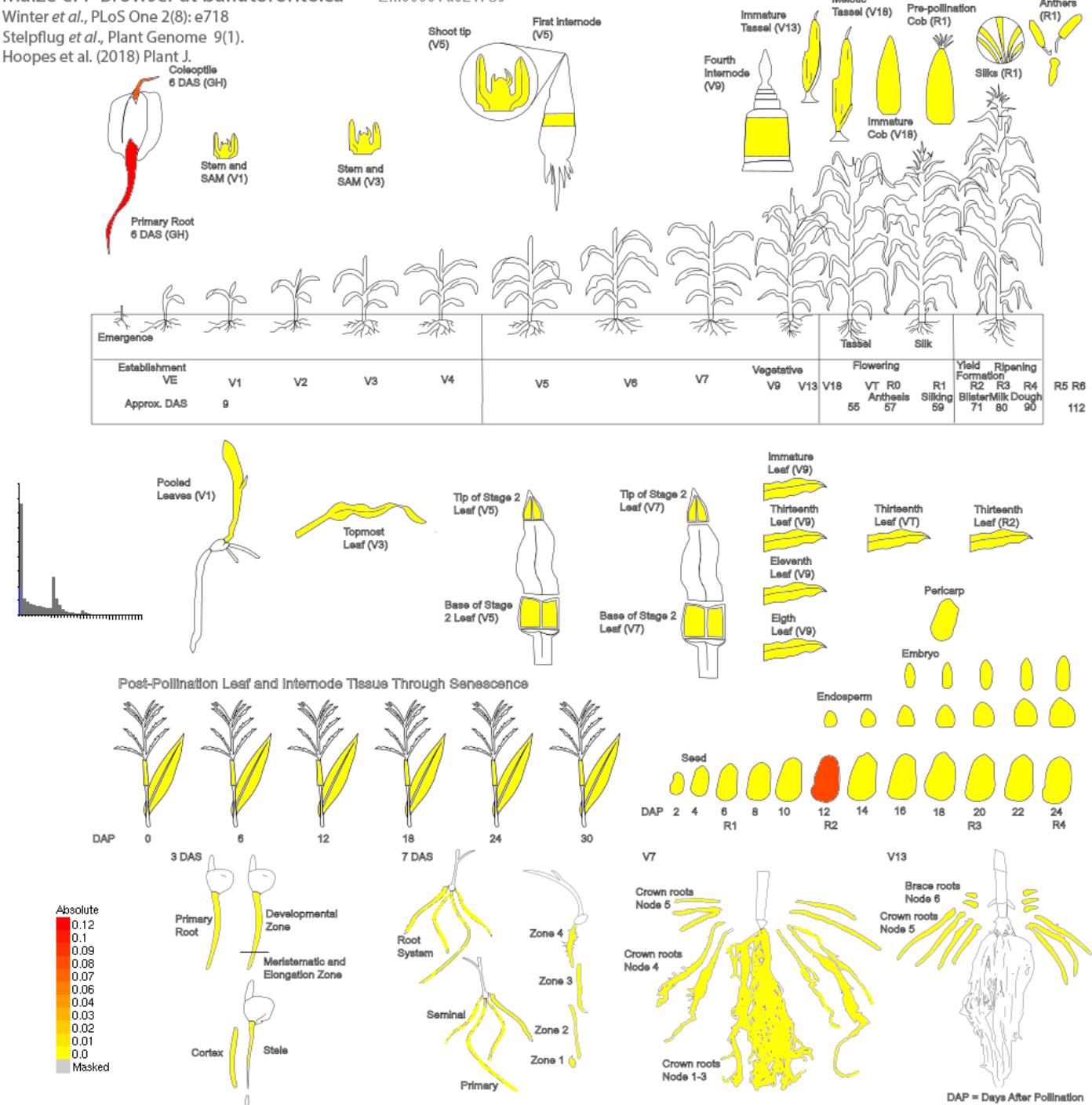


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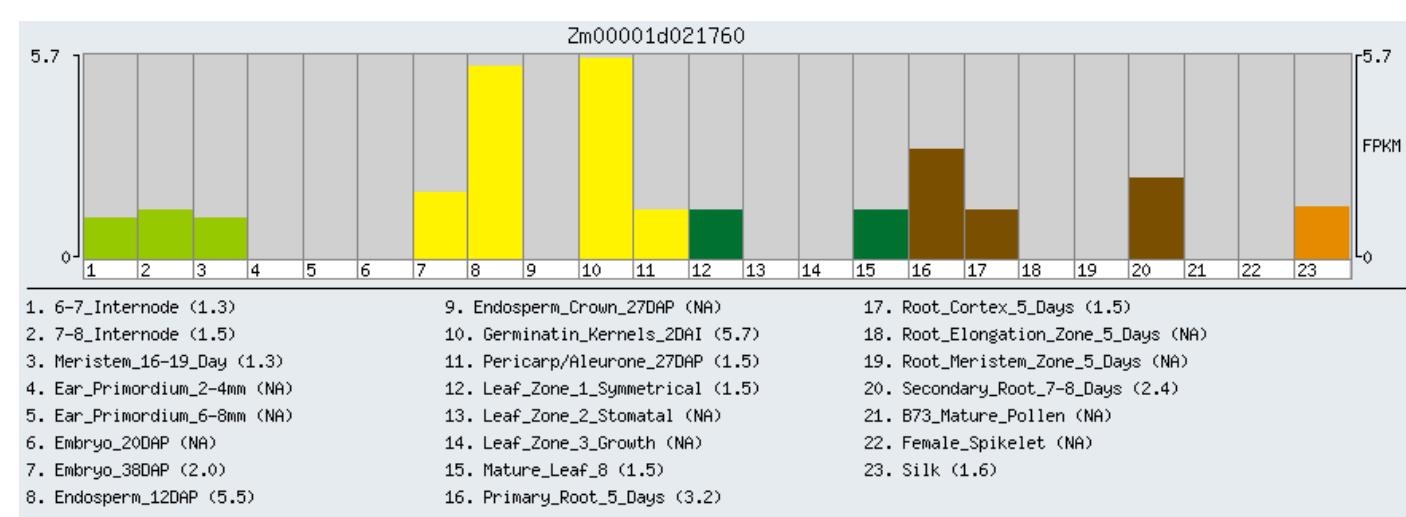
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Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPV4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPV4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



Zm00001d030812

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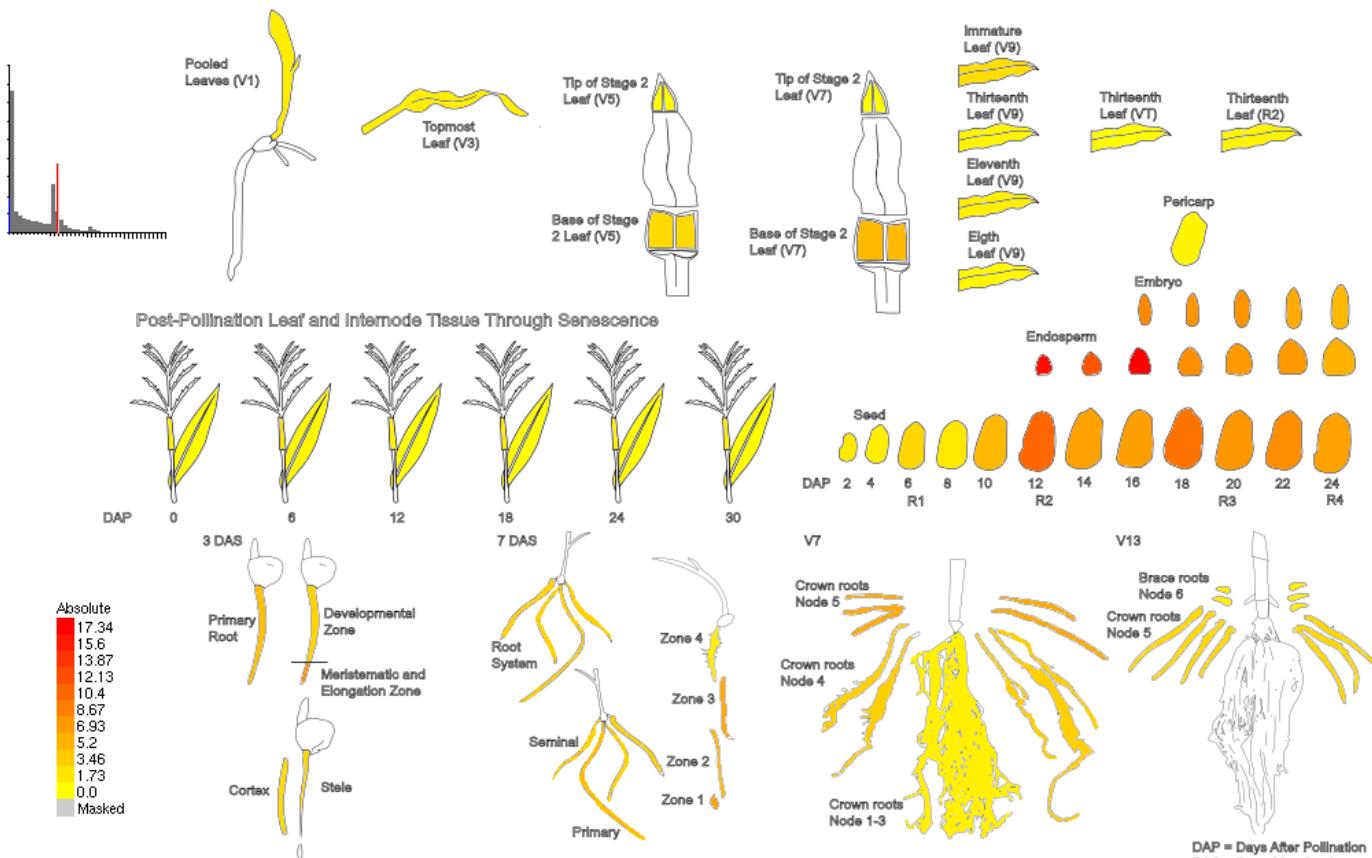
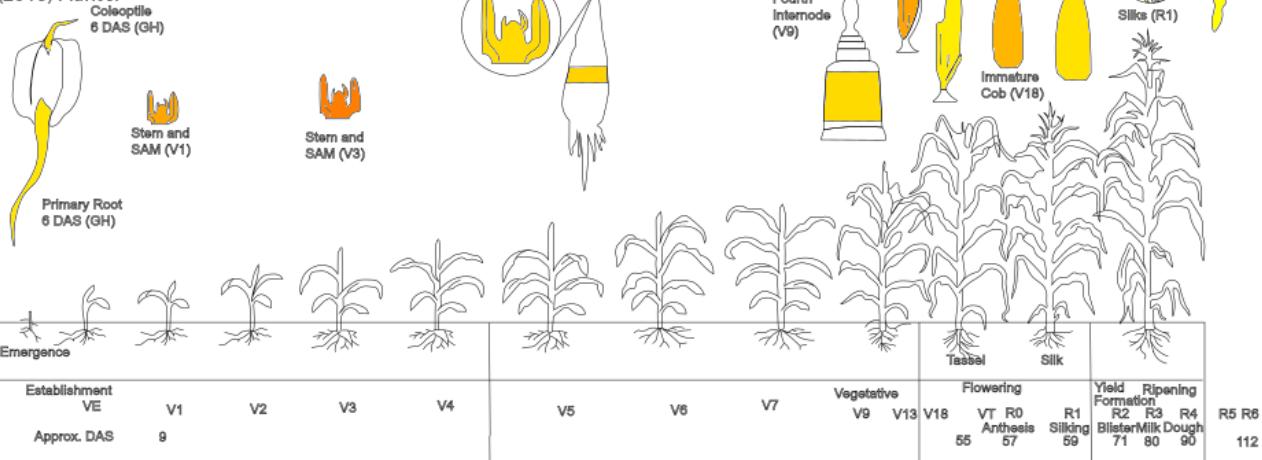
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

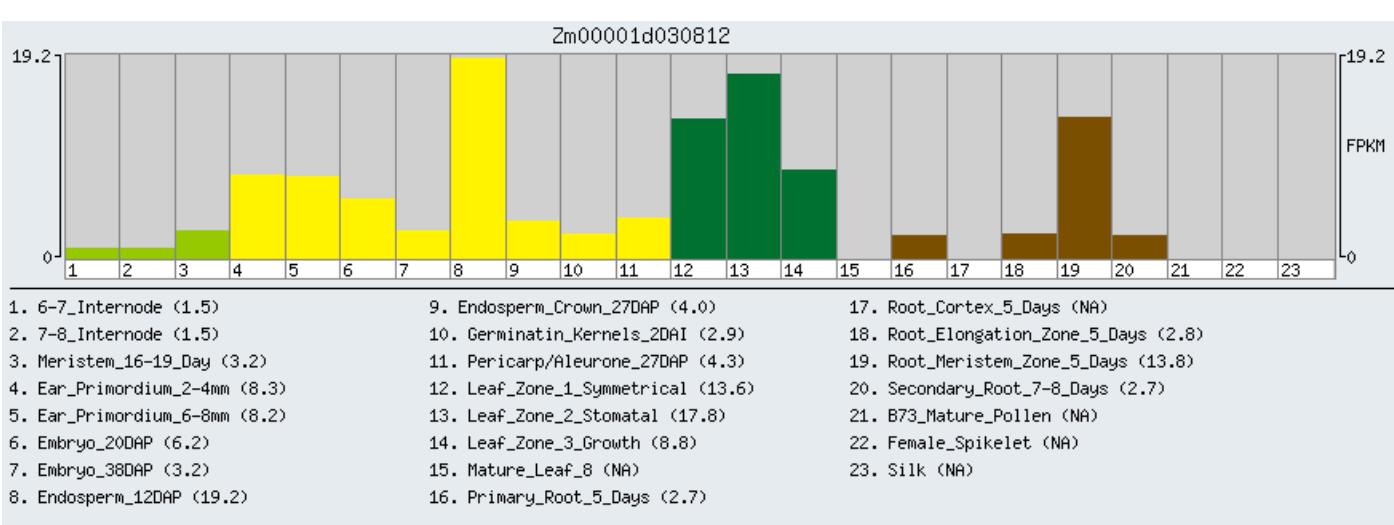
Hoopes et al. (2018) Plant J.

Zm00001d030812

Zm00001d030812



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



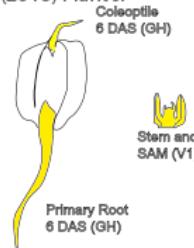
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Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

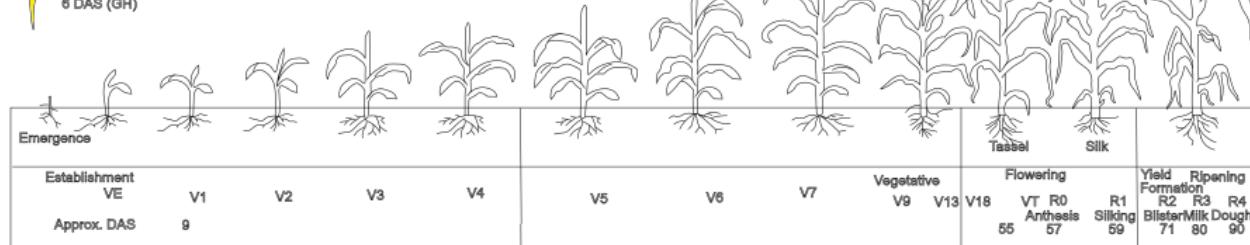
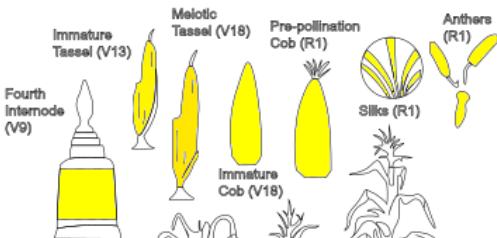
Hoopes et al. (2018) Plant J.



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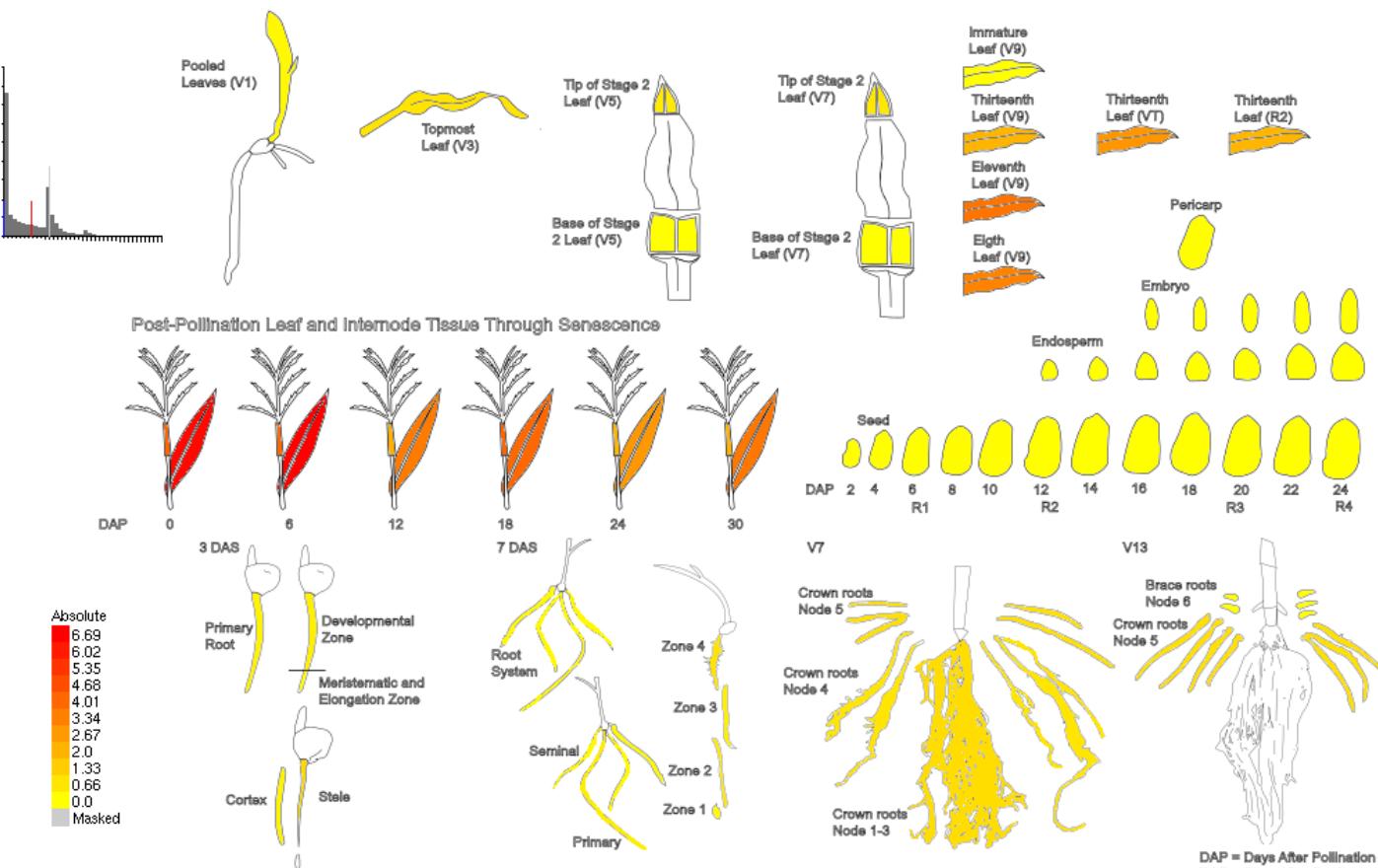
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Shoot tip (V5)



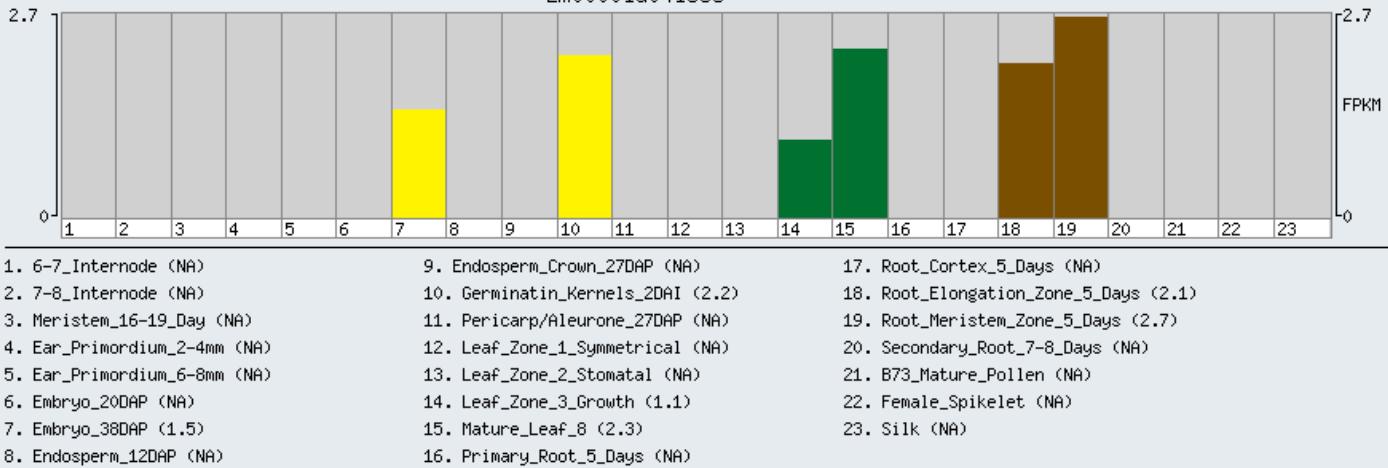
R5 R6

112



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

Zm00001d041358



Zm00001d042191

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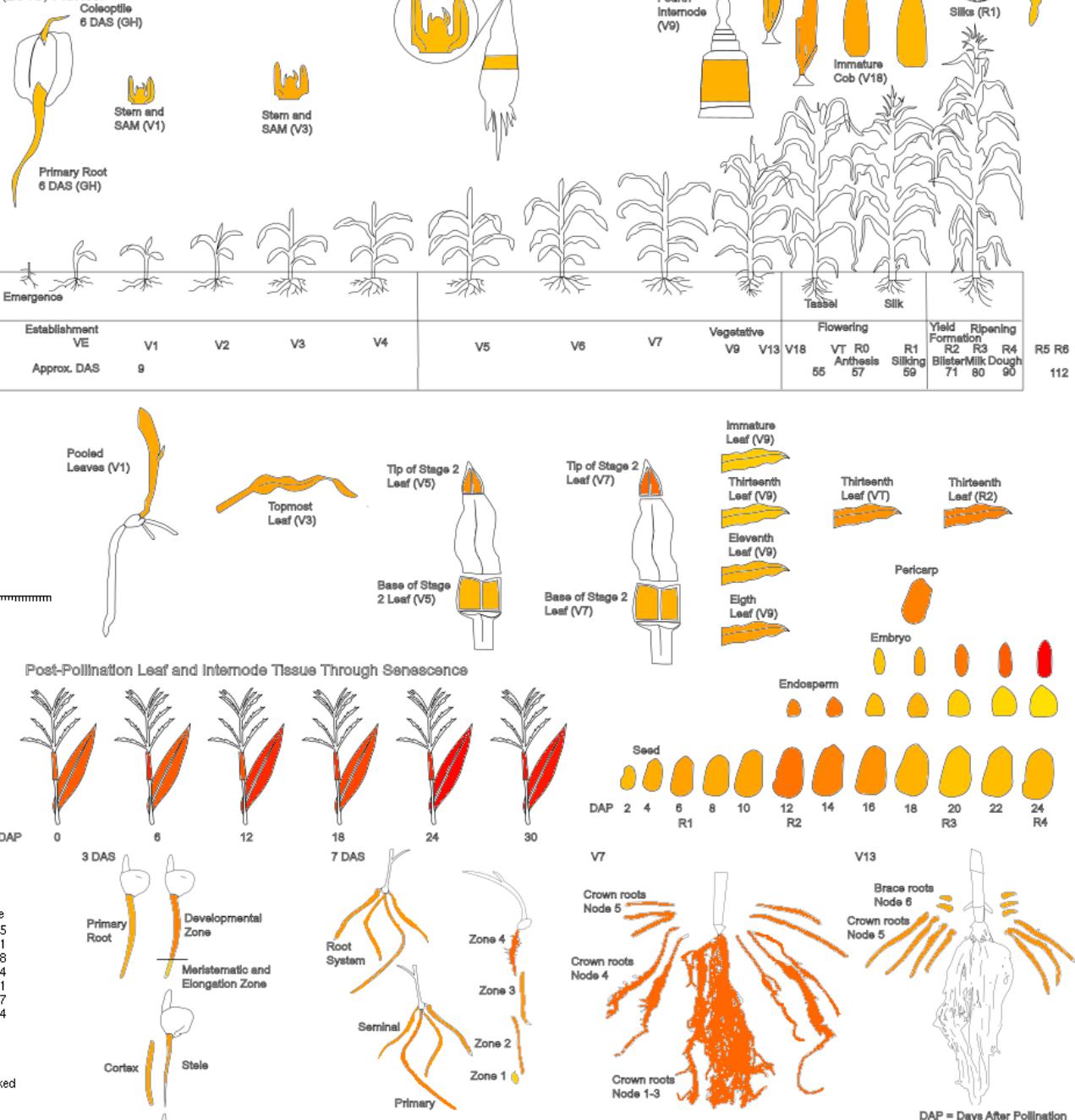
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1)

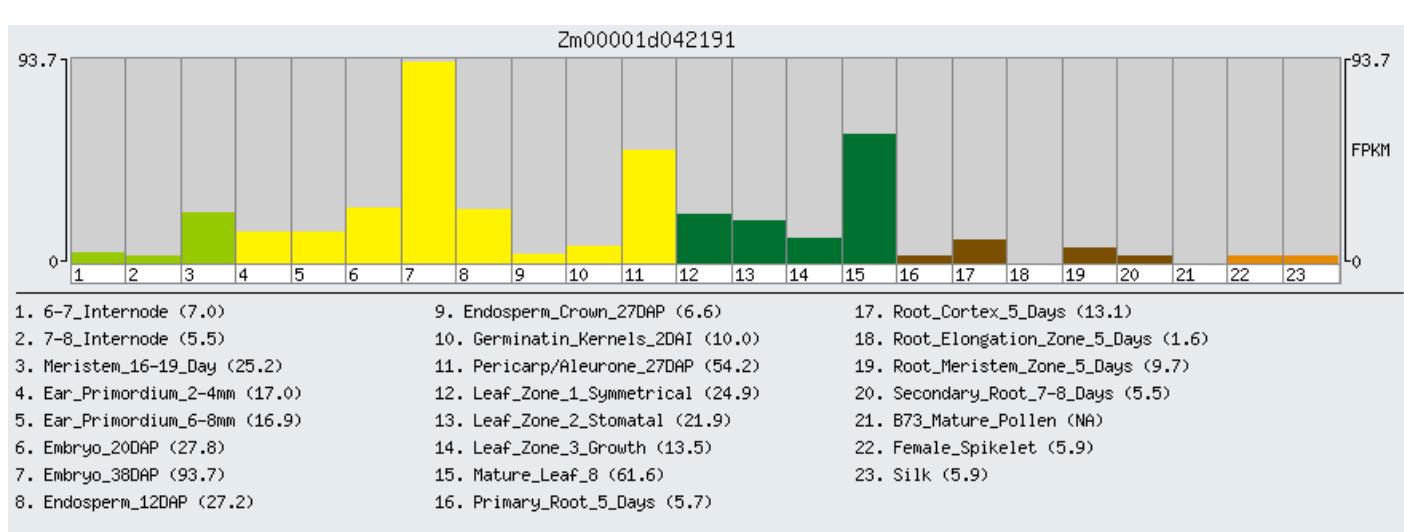
Hoopes et al. (2018) Plant J.

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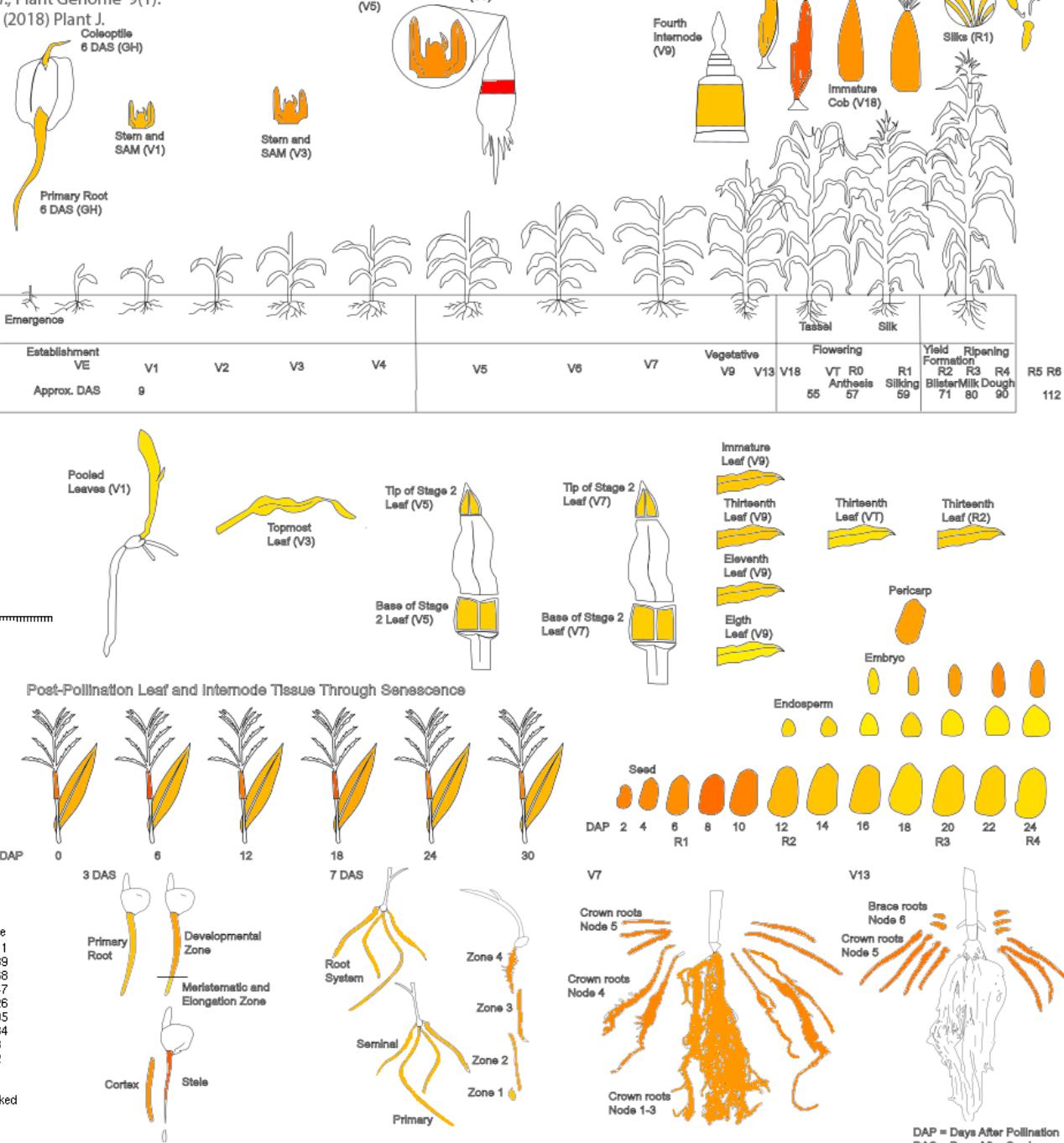
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

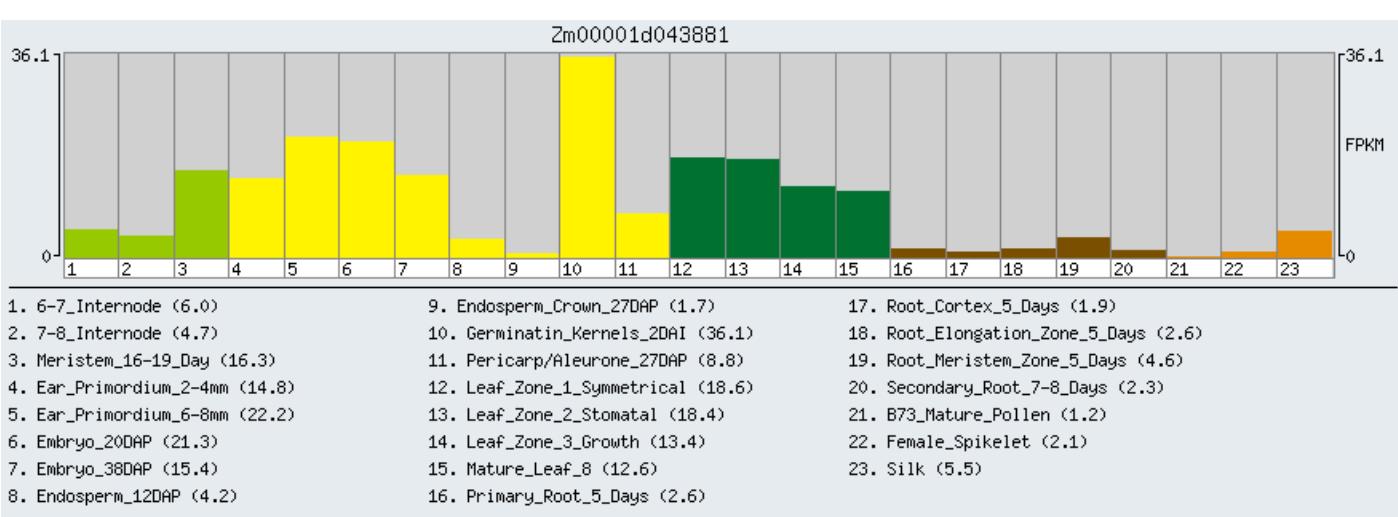
Hoopes et al. (2018) Plant J.

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Zm00001d043881



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



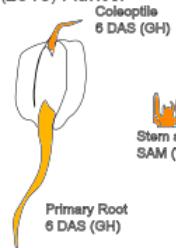
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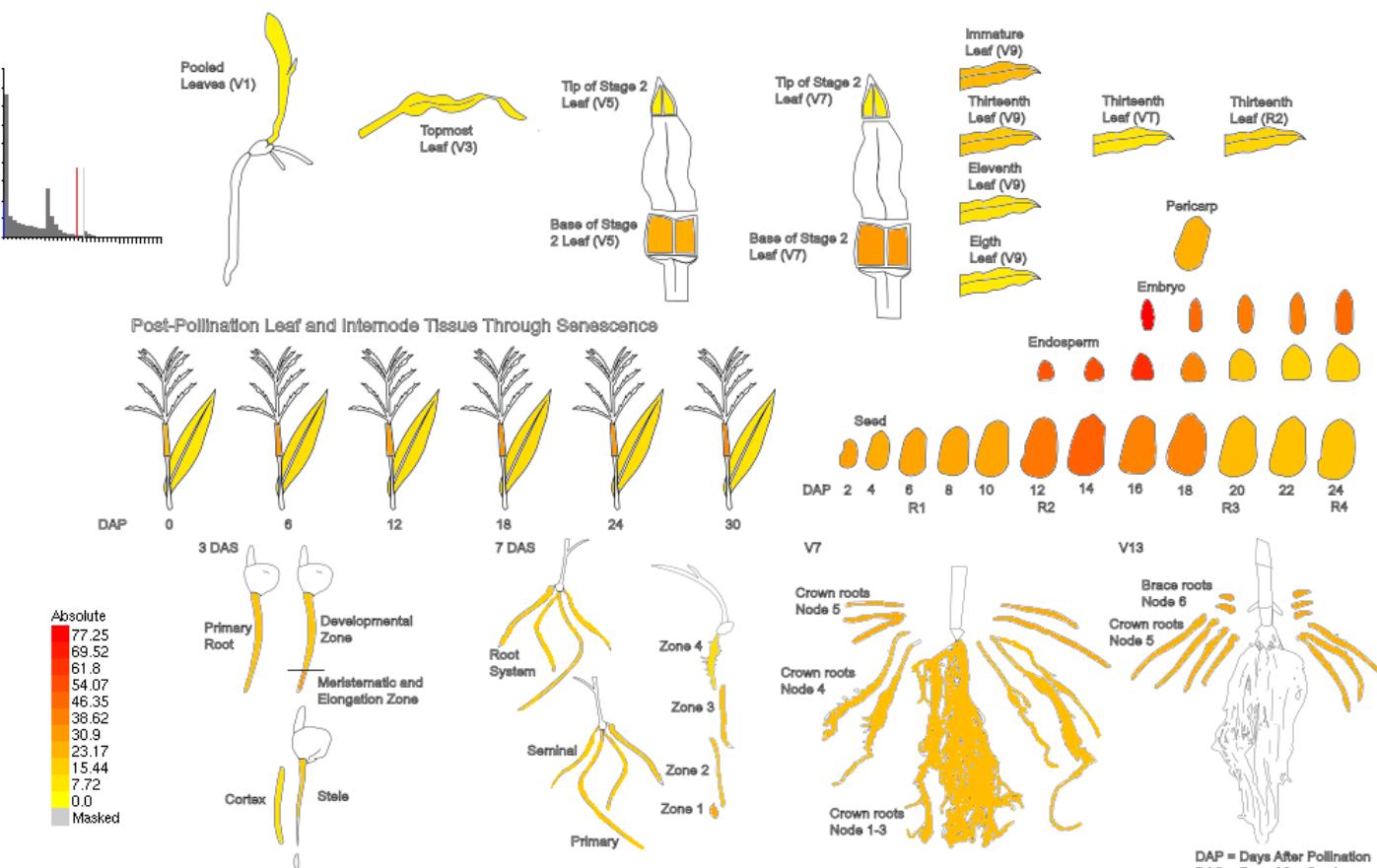
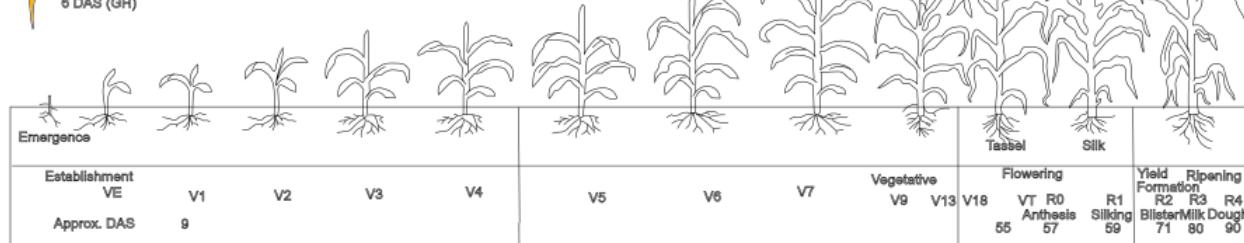
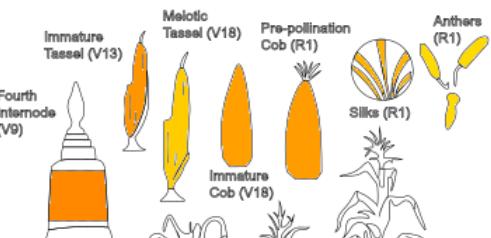
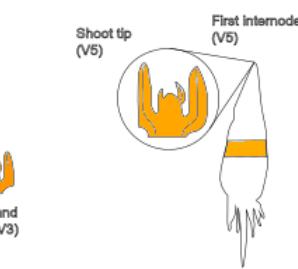
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

Hoopes et al. (2018) Plant J.

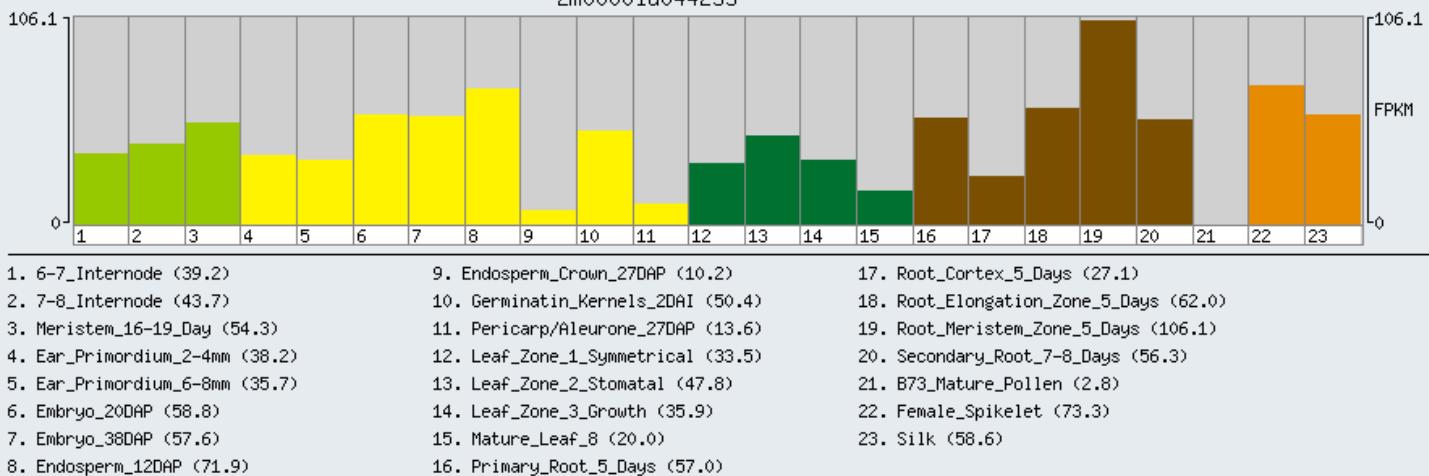


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Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

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Zm00001d052047

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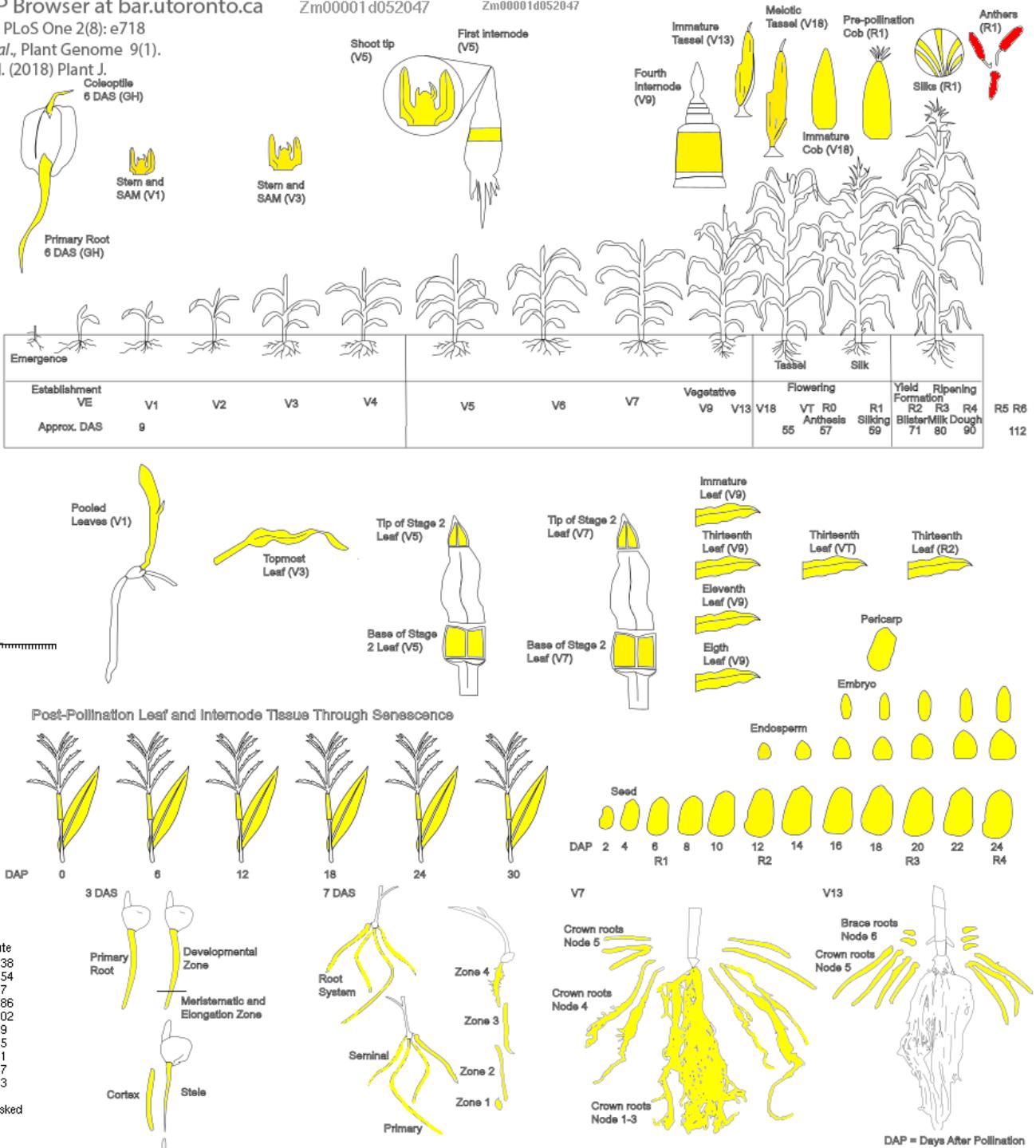
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

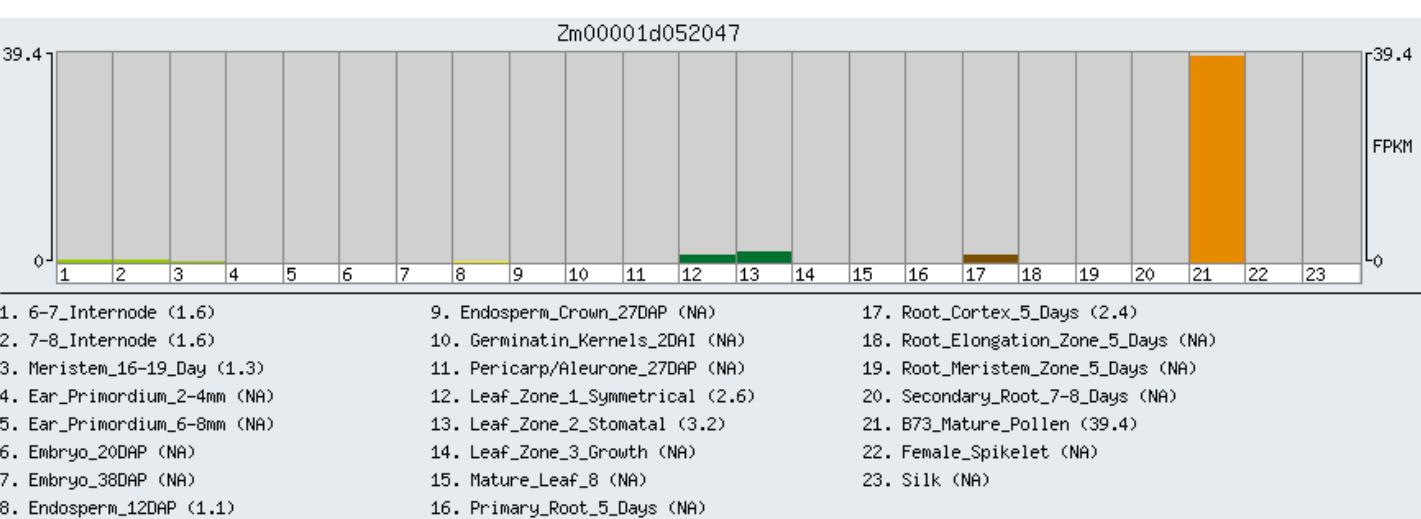
Hoopes et al. (2018) Plant J.

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Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



Zm00001d052416

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Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1)

Hoopes et al. (2018) Plant J.

Coleoptile 6 DAS (GH)



Primary Root 6 DAS (GH)

Stem and SAM (V1)

Zm00001d052416

Shoot tip (V5)

First internode (V5)

Zm00001d052416

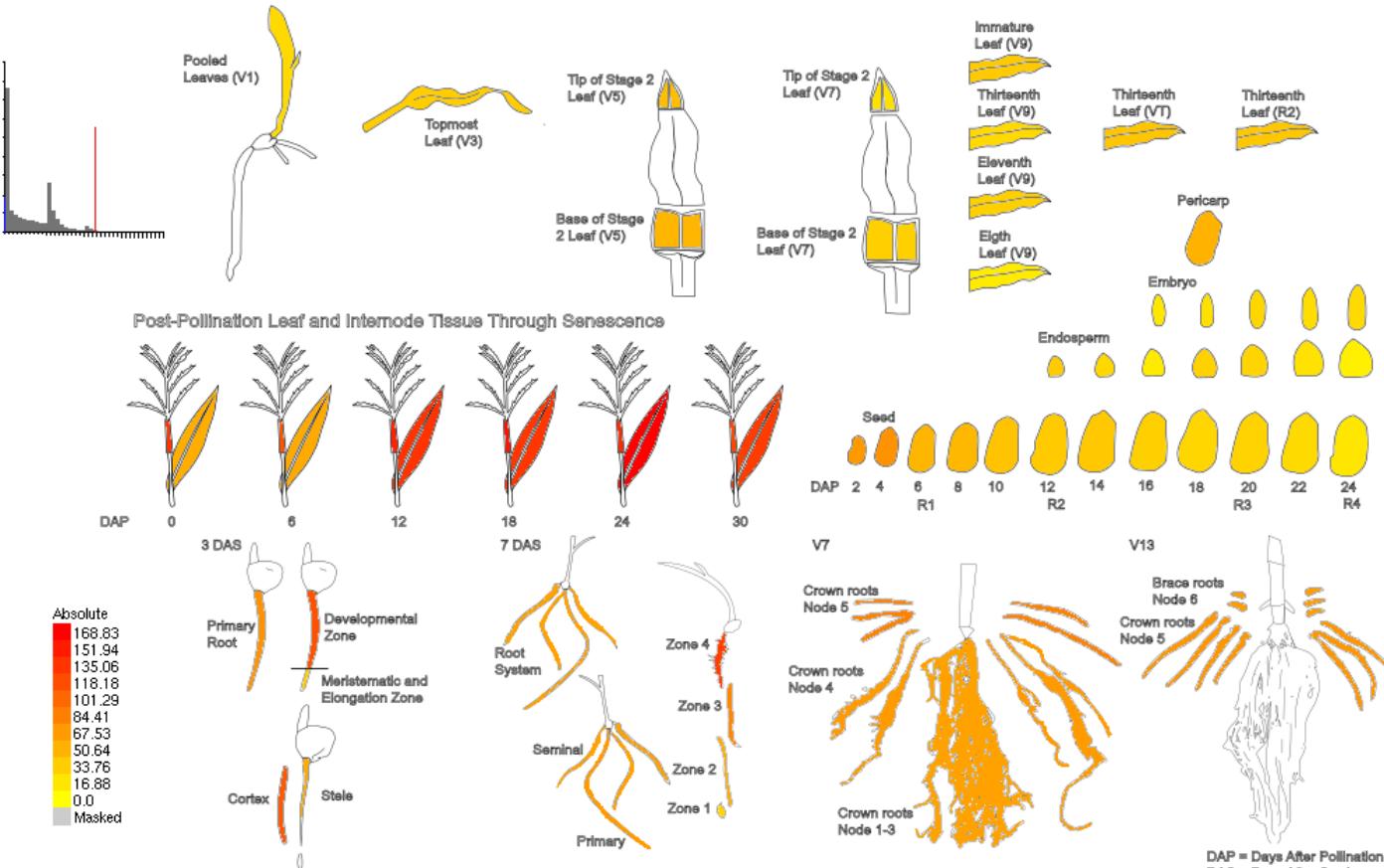
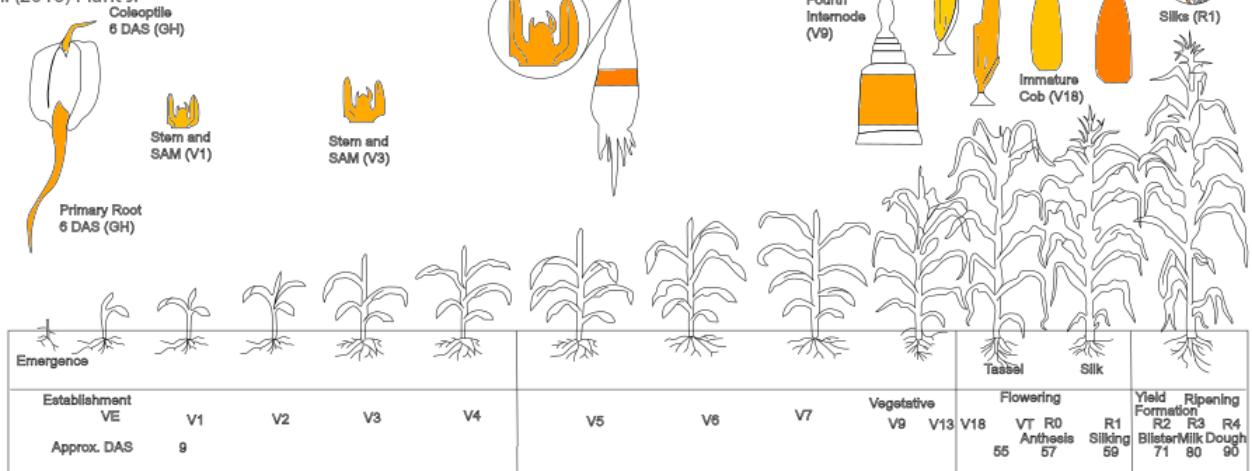
Fourth Internode (V9)

Immature Tassel (V13)

Meliotic Tassel (V18)

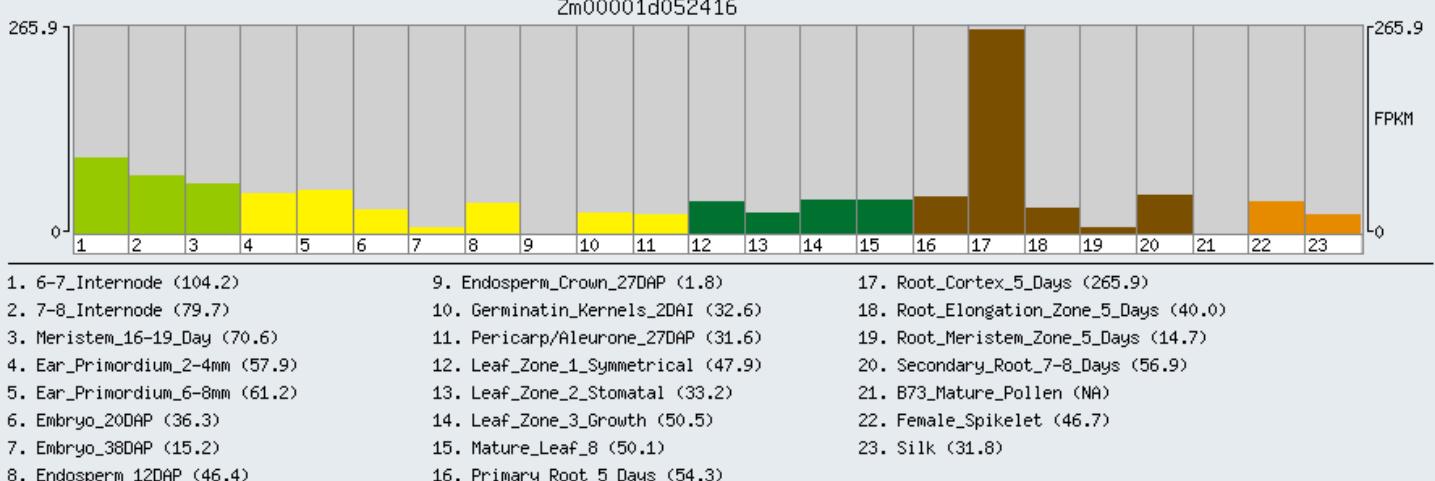
Pre-pollination Cob (R1)

Anthers (R1)



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.9) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

Zm00001d052416



Zm00001d052992

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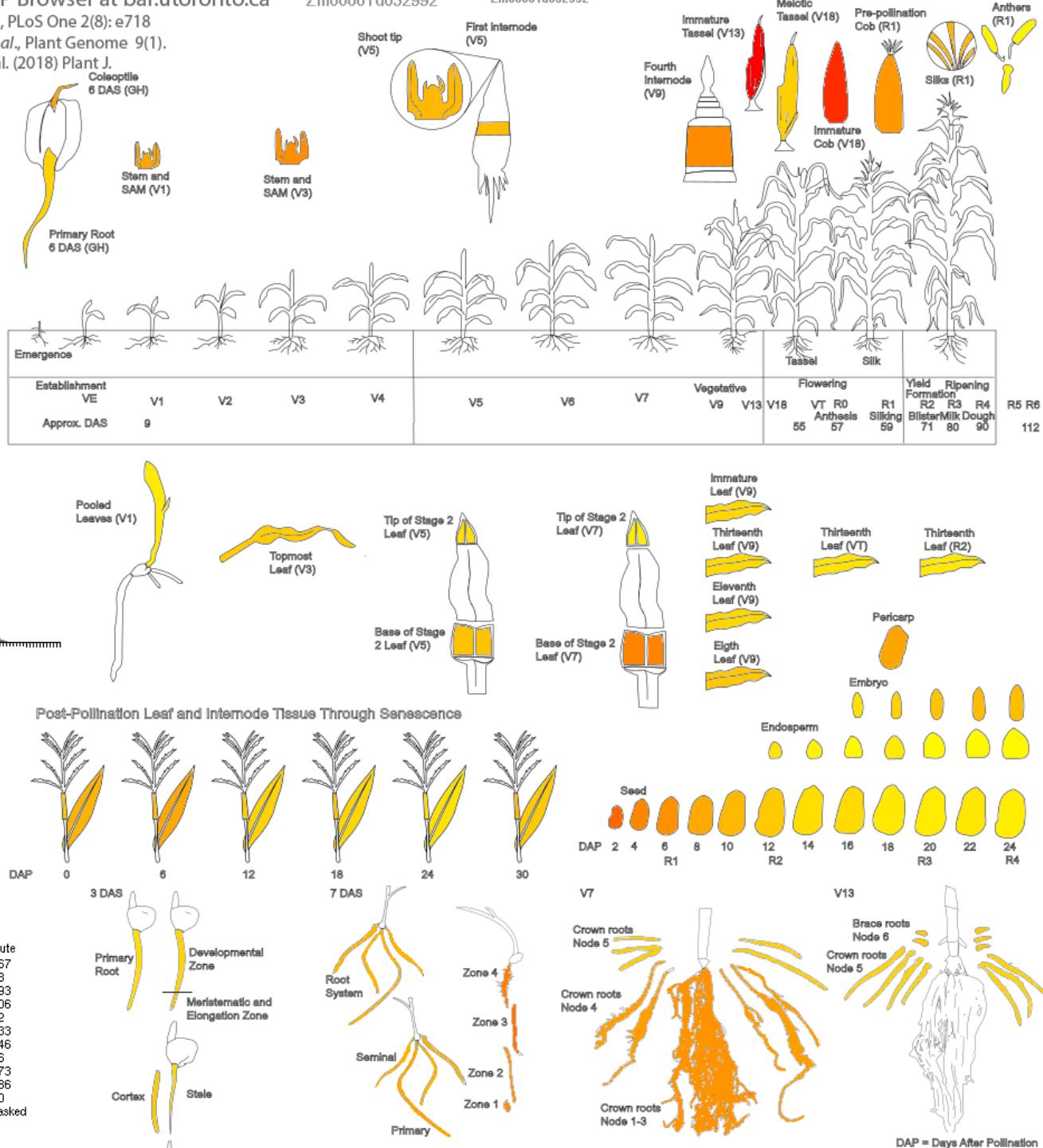
Winter et al., PLoS One 2(8): e718

Stelpflug et al., Plant Genome 9(1).

Hoopes et al. (2018) Plant J.

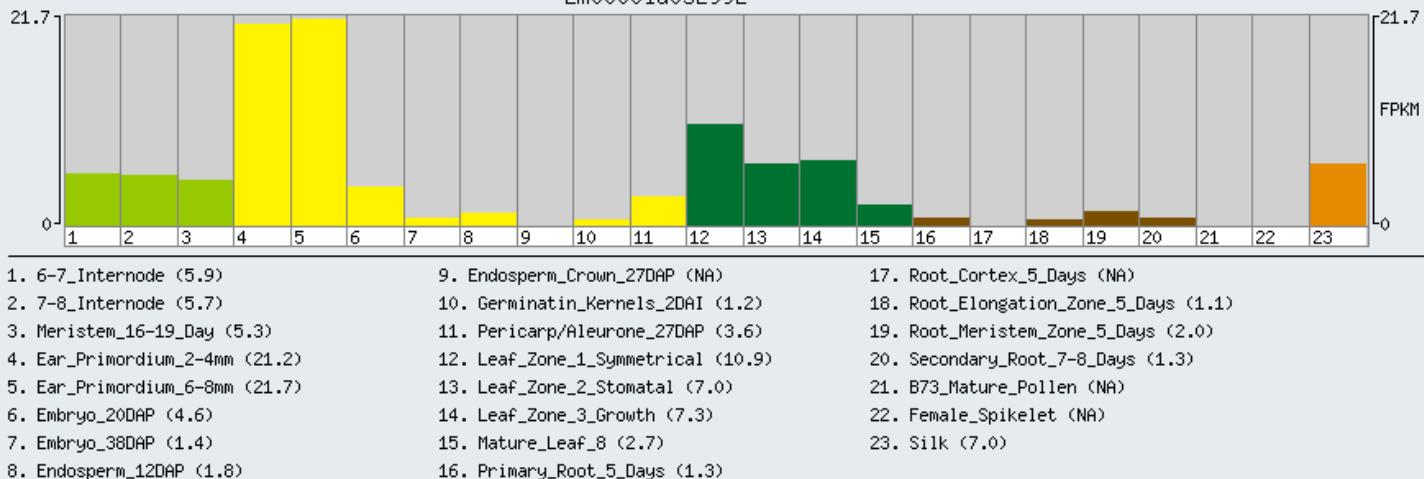
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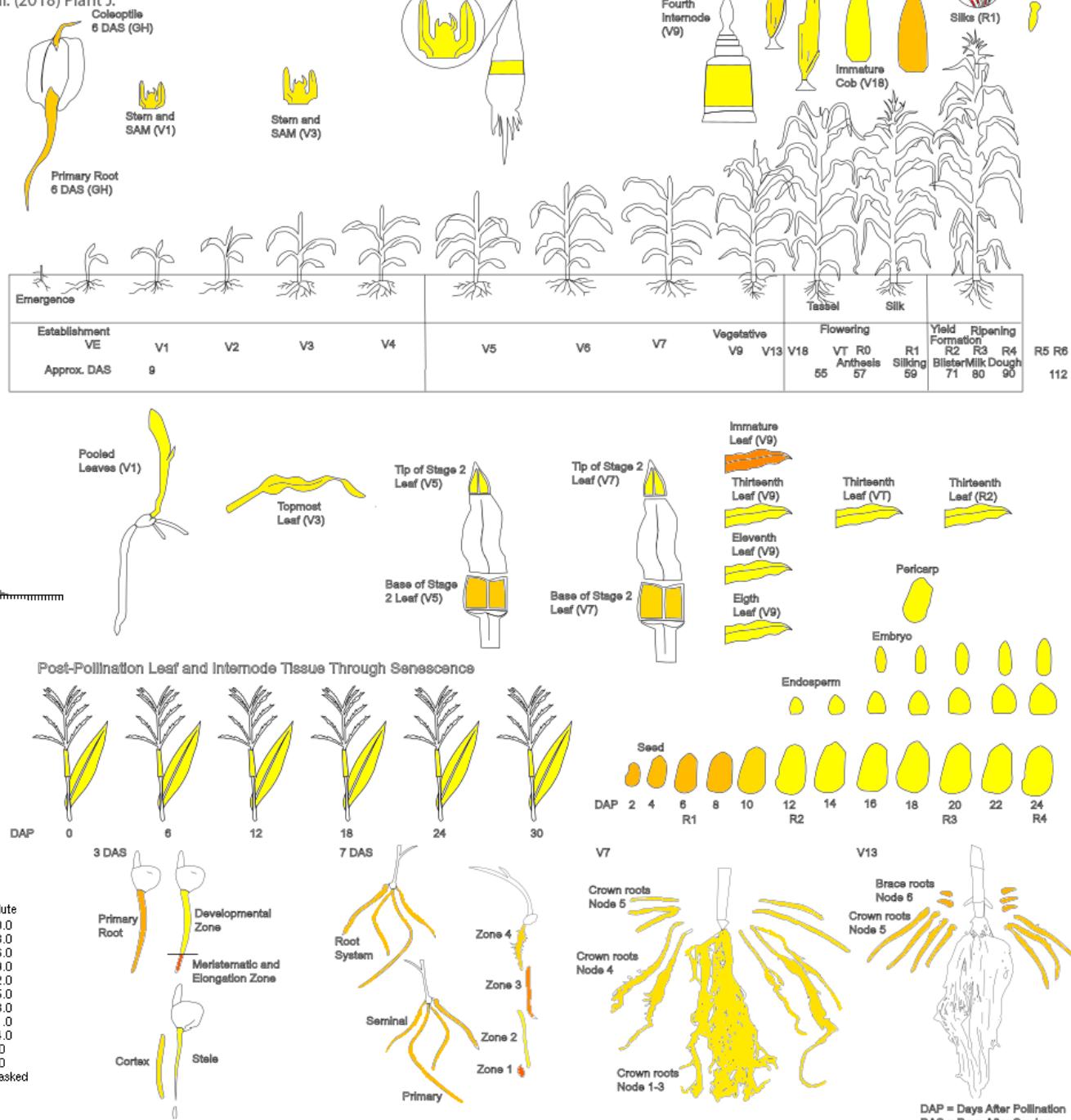
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Zm00001d052992

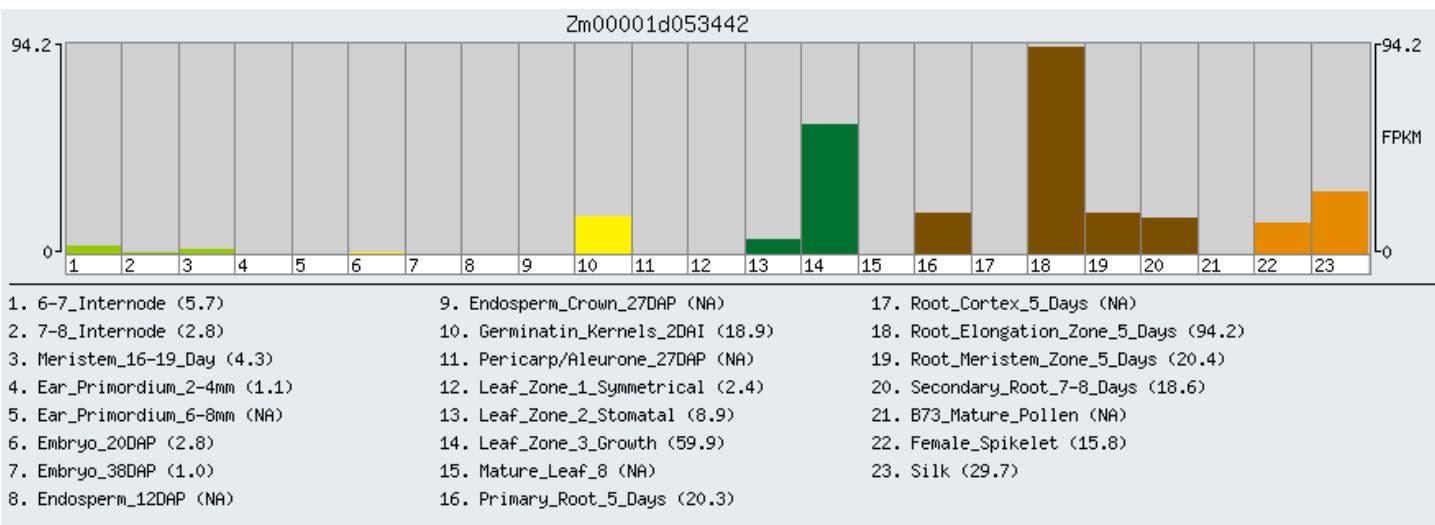


Zm00001d053442

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 Winter et al., PLoS One 2(8): e718
 Stelpflug et al., Plant Genome 9(1).
 Hoopes et al. (2018) Plant J.



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).



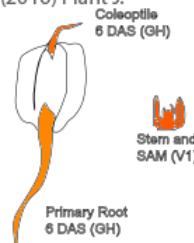
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Maize eFP Browser at bar.utoronto.ca

Winter et al., PLoS One 2(8): e718

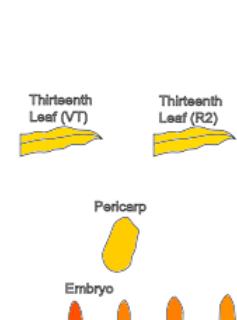
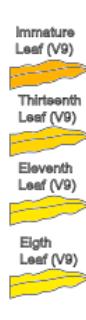
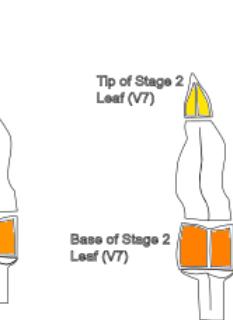
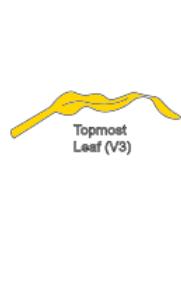
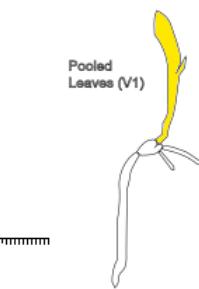
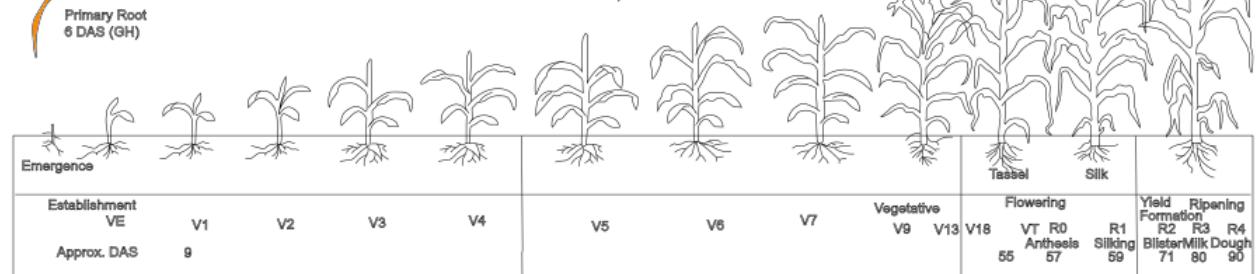
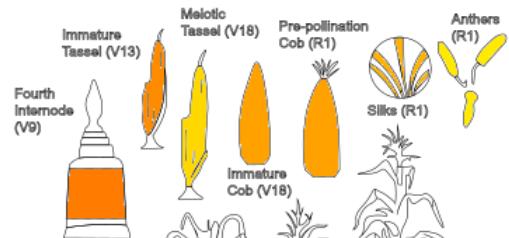
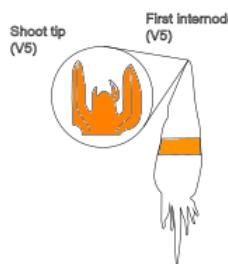
Stelpflug et al., Plant Genome 9(1)

Hoopes et al. (2018) Plant J.

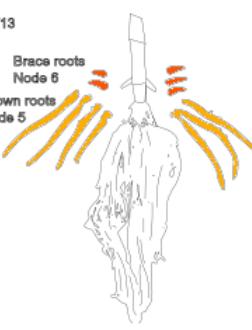
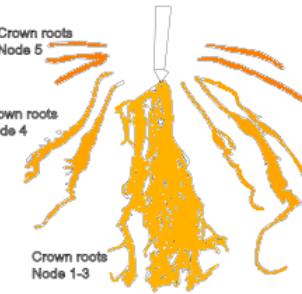
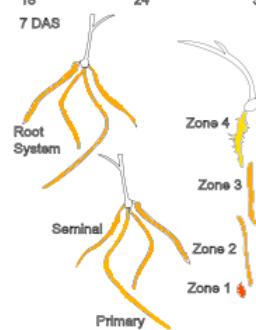
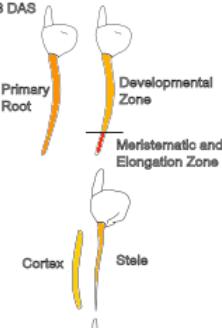
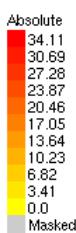
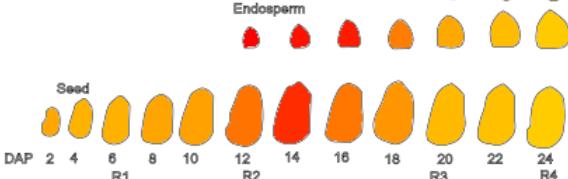
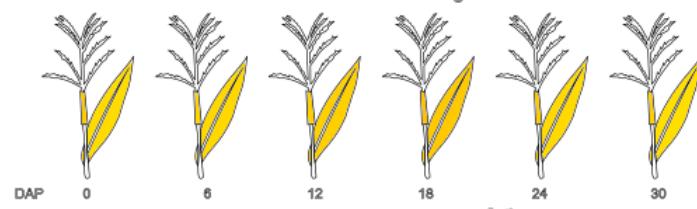


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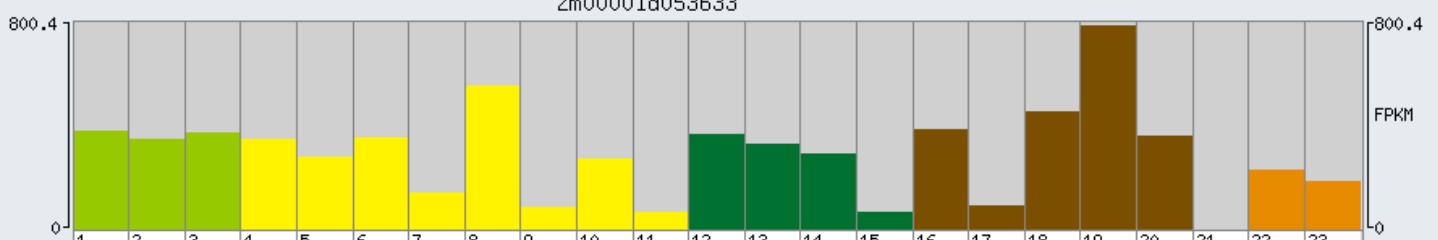
Post-Pollination Leaf and Internode Tissue Through Senescence



DAP = Days After Pollination
DAS = Days After Sowing

Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

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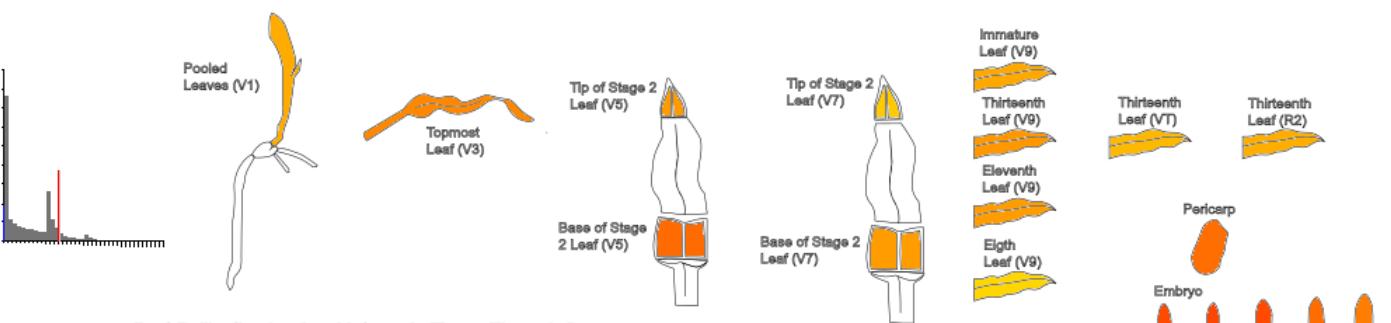
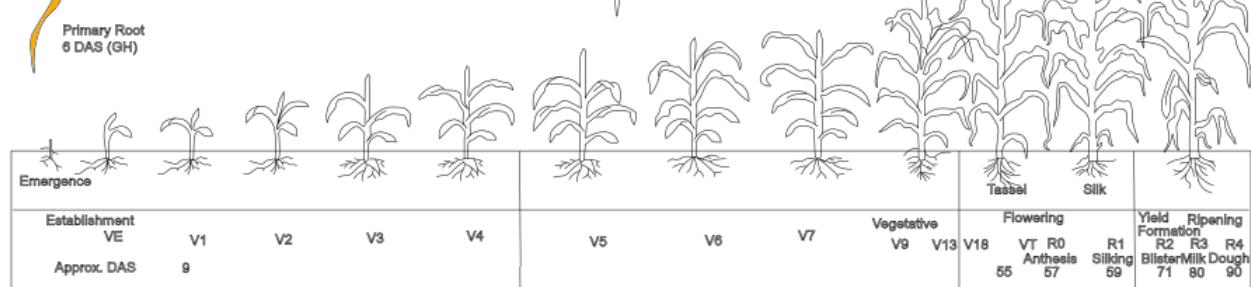
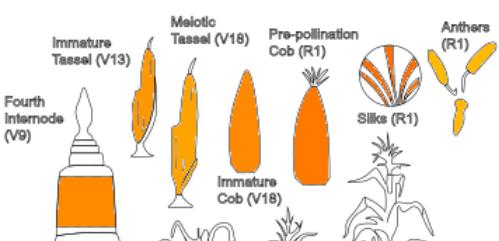
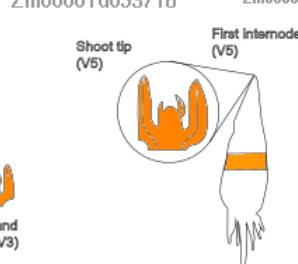
1. 6-7_Internode (397.5)
2. 7-8_Internode (370.5)
3. Meristem_16-19_Day (393.7)
4. Ear_Primordium_2-4mm (370.5)
5. Ear_Primordium_6-8mm (301.6)
6. Embryo_20DAP (375.9)
7. Embryo_38DAP (164.7)
8. Endosperm_12DAP (570.2)
9. Endosperm_Crown_27DAP (105.9)
10. Germination_Kernels_2DAI (292.5)
11. Pericarp/Aleurone_27DAP (89.1)
12. Leaf_Zone_1_Symmetrical (385.6)
13. Leaf_Zone_2_Stomatal (349.3)
14. Leaf_Zone_3_Growth (313.8)
15. Mature_Leaf_8 (89.9)
16. Primary_Root_5_Days (406.0)

17. Root_Cortex_5_Days (111.4)
18. Root_Elongation_Zone_5_Days (470.4)
19. Root_Meristem_Zone_5_Days (800.4)
20. Secondary_Root_7-8_Days (382.3)
21. B73_Mature_Pollen (2.4)
22. Female_Spikelet (247.5)
23. Silk (206.1)

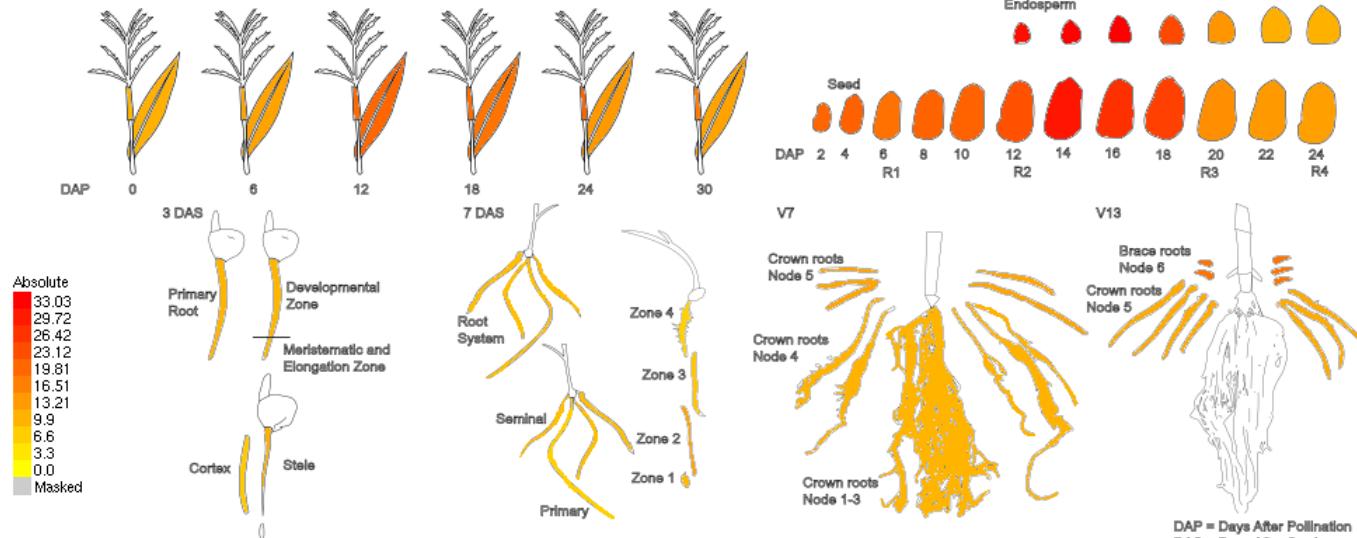
Zm00001d053716

Maize eFP Browser at bar.utoronto.ca
 Winter et al., PLoS One 2(8): e718
 Stelpflug et al., Plant Genome 9(1).
 Hoopes et al. (2018) Plant J.

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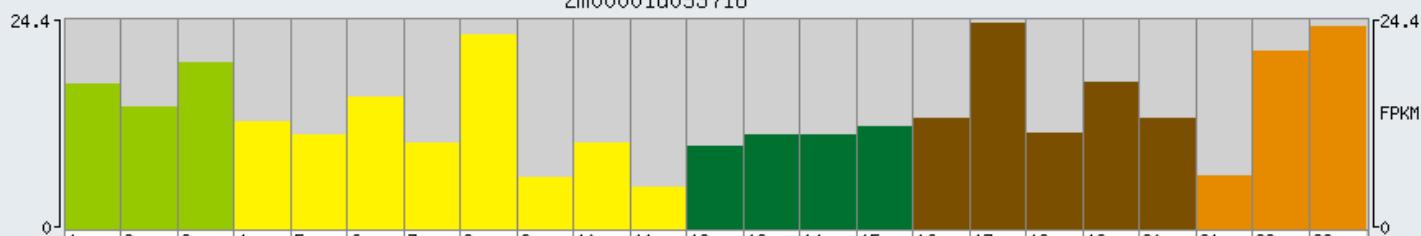


Post-Pollination Leaf and Internode Tissue Through Senescence



Adapters and low quality bases were removed using Cutadapt (v1.12) (Martin, 2011). All cleaned reads were aligned to the *Z. mays* inbred B73 AGPv4 genome assembly (Jiao et al., 2017) with Bowtie2 (v2.2.3) (Langmead and Salzberg, 2012) and TopHat2 (v2.0.14) (Kim et al., 2013). Fragments Per Kilobase of transcript per Million mapped reads (FPKM) gene expression values for *Z. mays* inbred B73 AGPv4 genes (Jiao et al., 2017) was quantified with Cufflinks (v2.2.1) (Trapnell et al., 2010).

Zm00001d053716



- 1. 6-7_Internode (17.4)
- 2. 7-8_Internode (14.9)
- 3. Meristem_16-19_Day (20.0)
- 4. Ear_Primordium_2-4mm (13.1)
- 5. Ear_Primordium_6-8mm (11.5)
- 6. Embryo_20DAP (16.0)
- 7. Embryo_38DAP (10.7)
- 8. Endosperm_12DAP (23.1)
- 9. Endosperm_Crown_27DAP (6.7)
- 10. Germinatin_Kernels_2DAI (10.7)
- 11. Pericarp/Aleurone_27DAP (5.5)
- 12. Leaf_Zone_1_Symmetrical (10.3)
- 13. Leaf_Zone_2_Stomatal (11.6)
- 14. Leaf_Zone_3_Growth (11.6)
- 15. Mature_Leaf_8 (12.6)
- 16. Primary_Root_5_Days (13.4)
- 17. Root_Cortex_5_Days (24.4)
- 18. Root_Elongation_Zone_5_Days (11.8)
- 19. Root_Meristem_Zone_5_Days (17.6)
- 20. Secondary_Root_7-8_Days (13.5)
- 21. B73_Mature_Pollen (6.8)
- 22. Female_Spikelet (21.2)
- 23. Silk (24.2)