

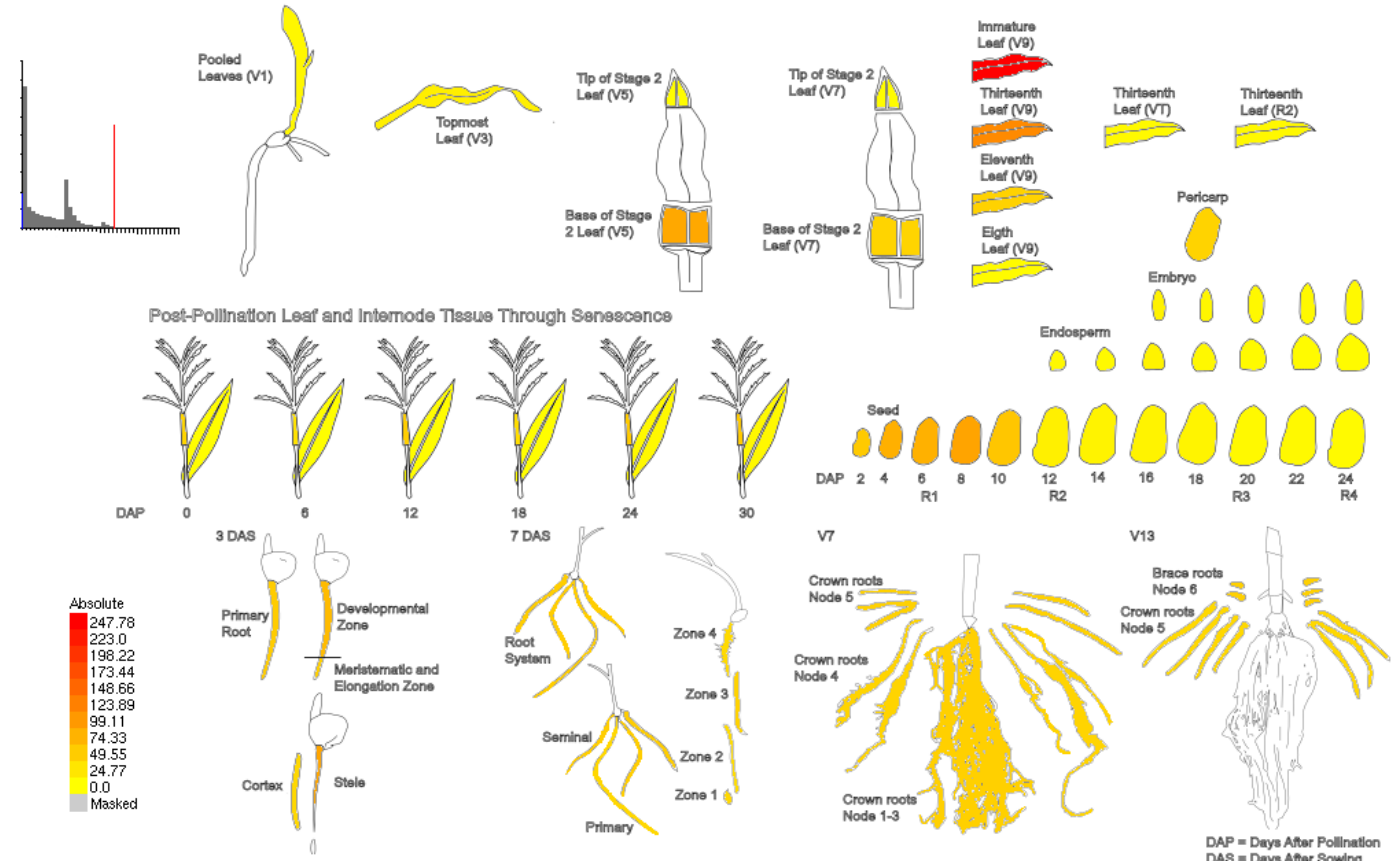
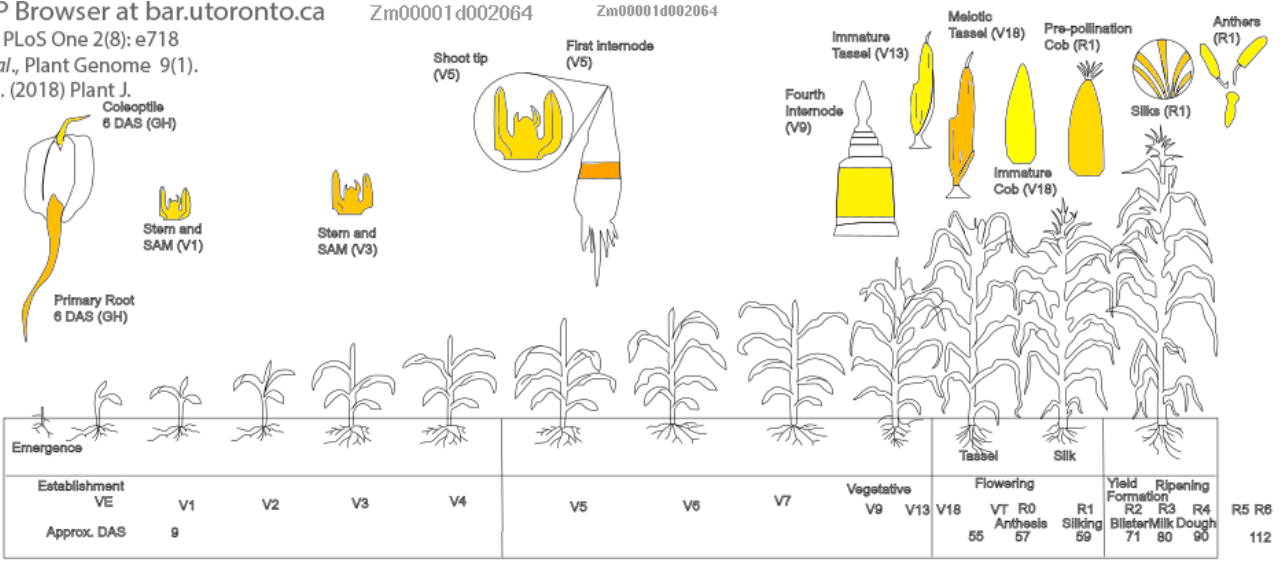
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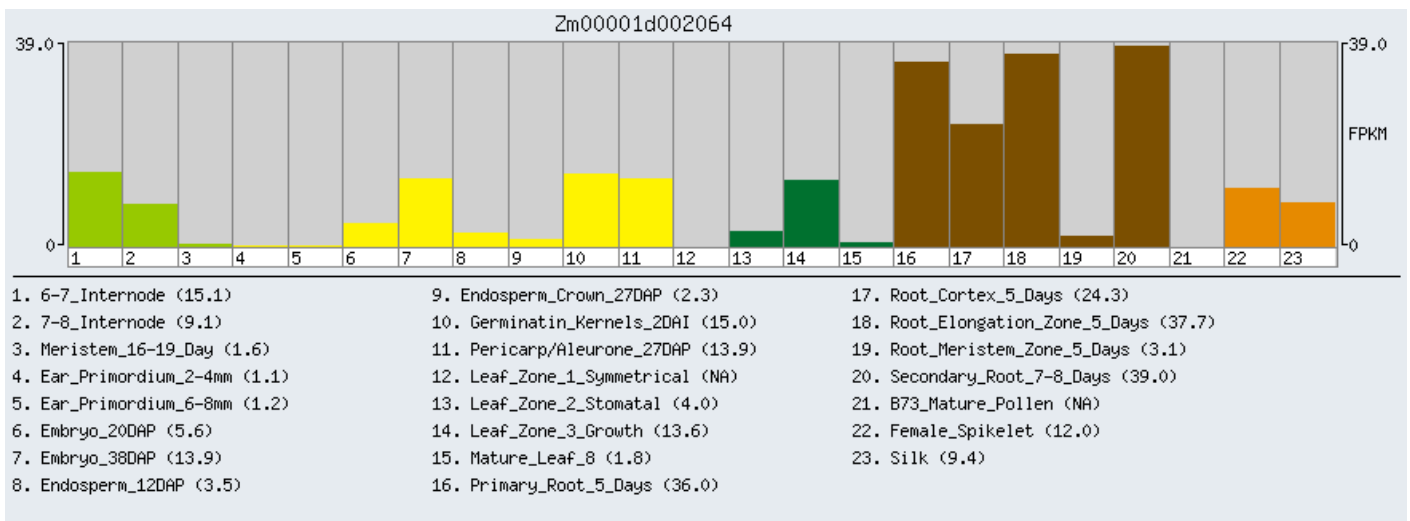
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Zm00001d002064

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



# Zm00001d004822

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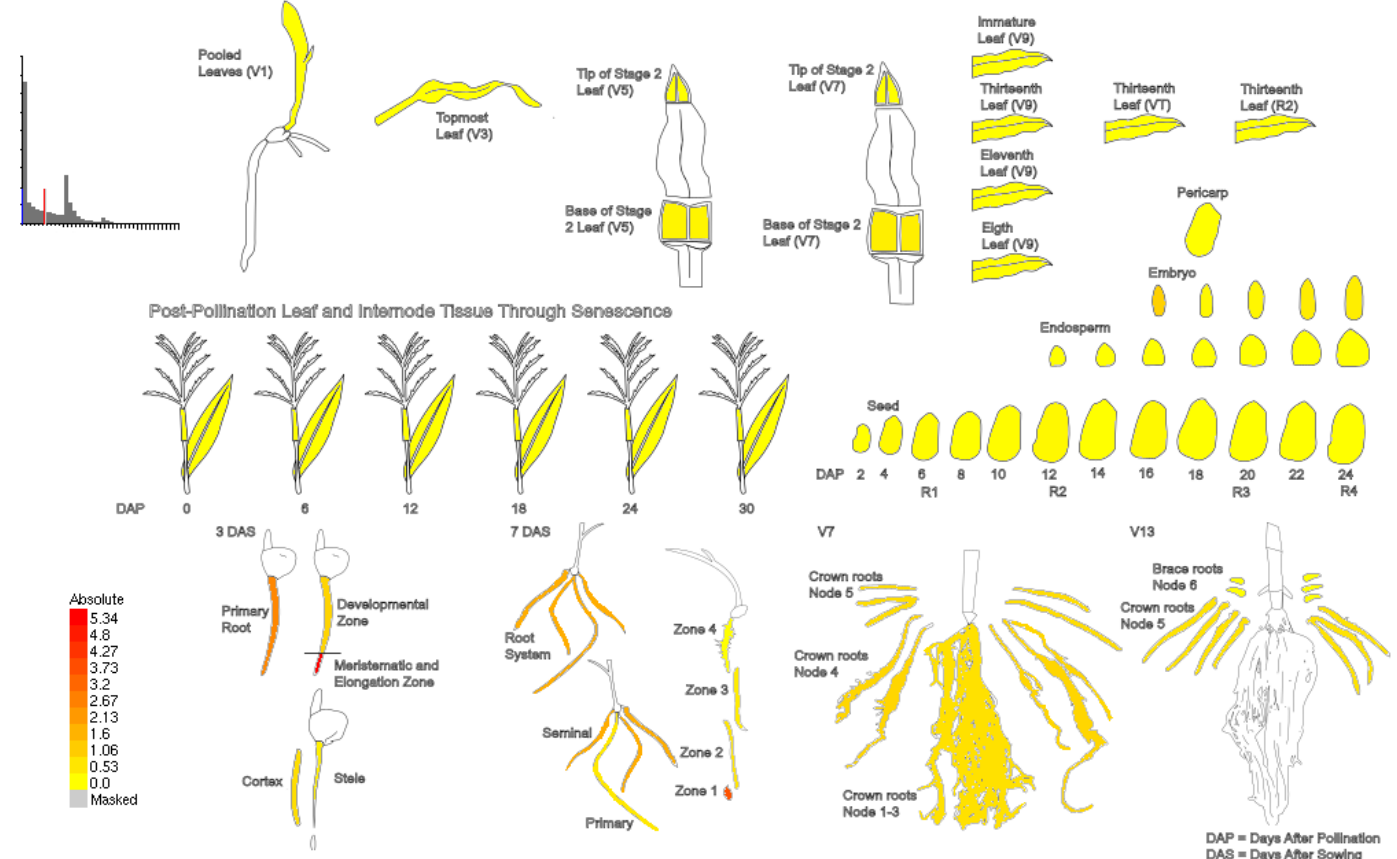
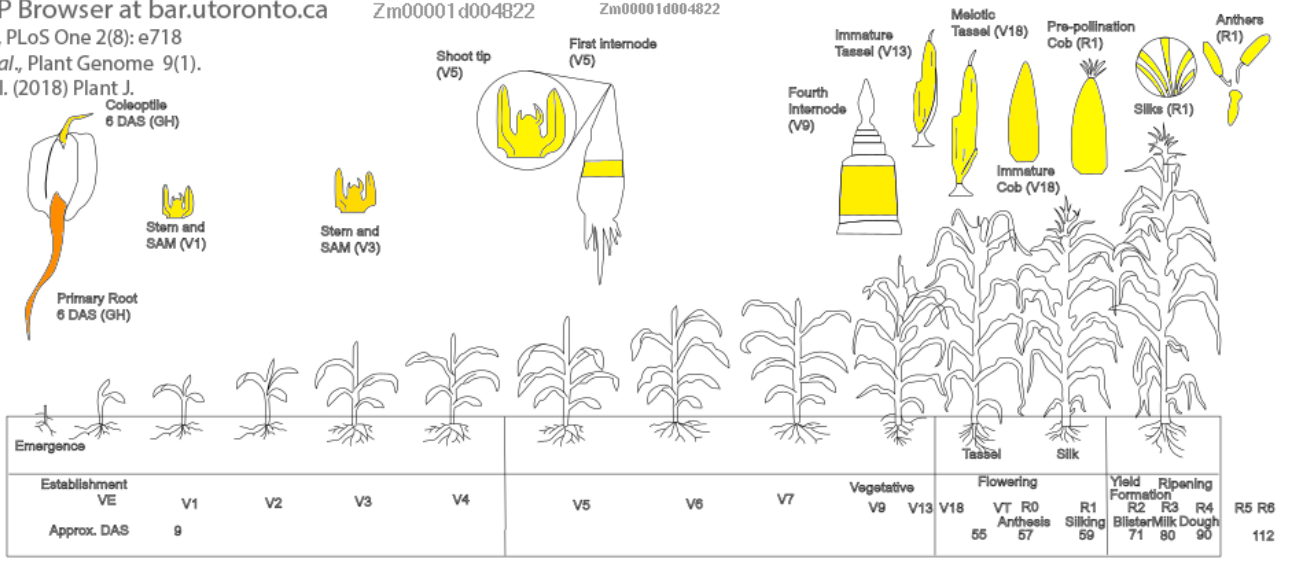
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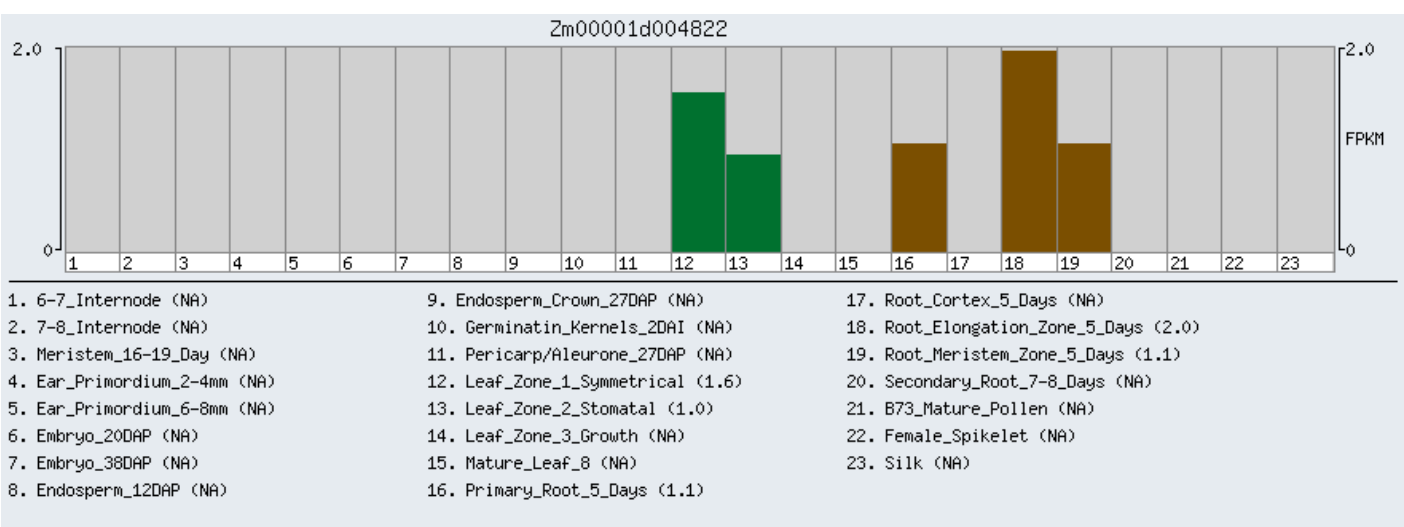
Winter *et al.*, PLoS One 2(8): e718

Stelplflug *et al.*, Plant Genome 9(1).

Hoopes *et al.* (2018) Plant J.



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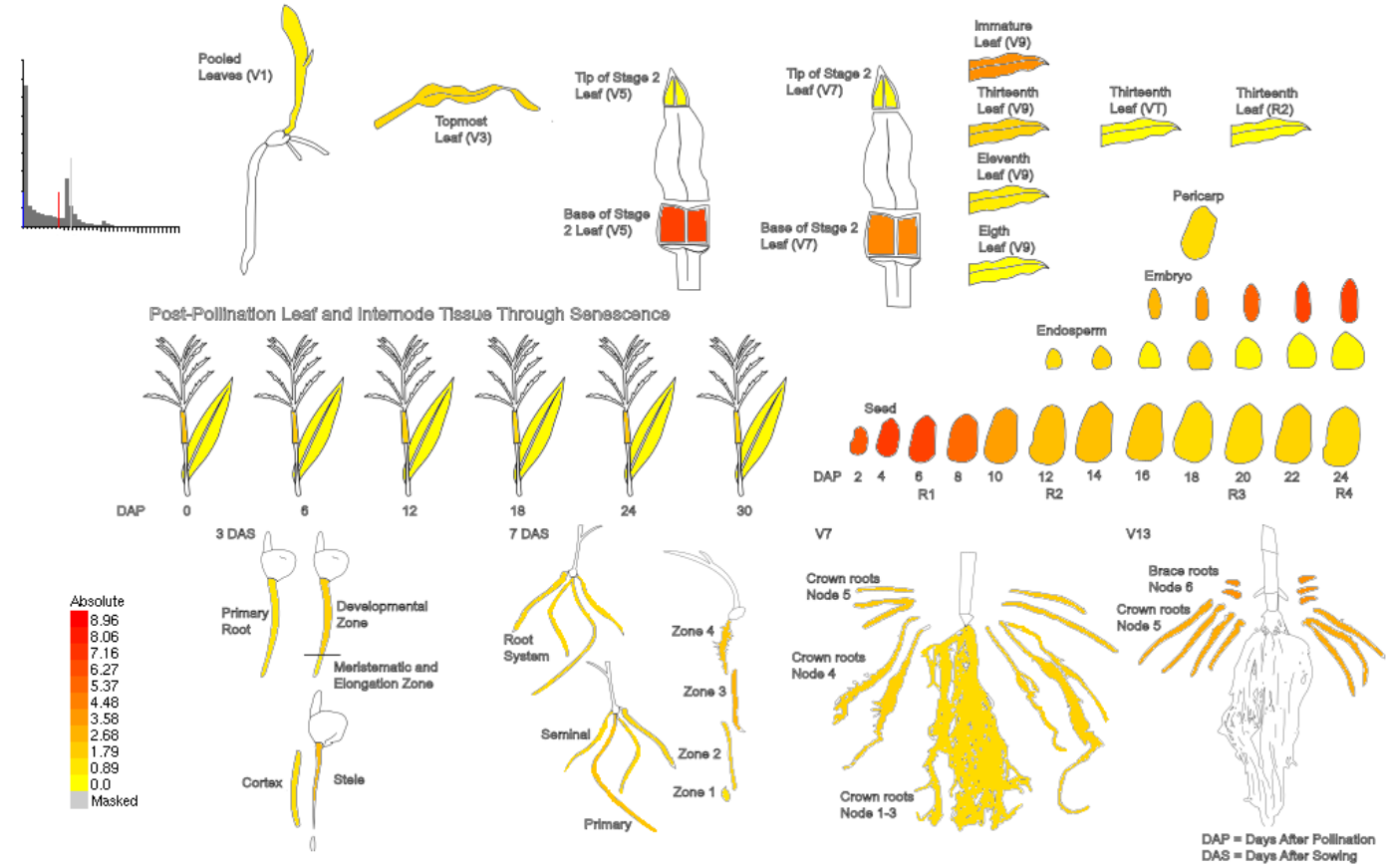
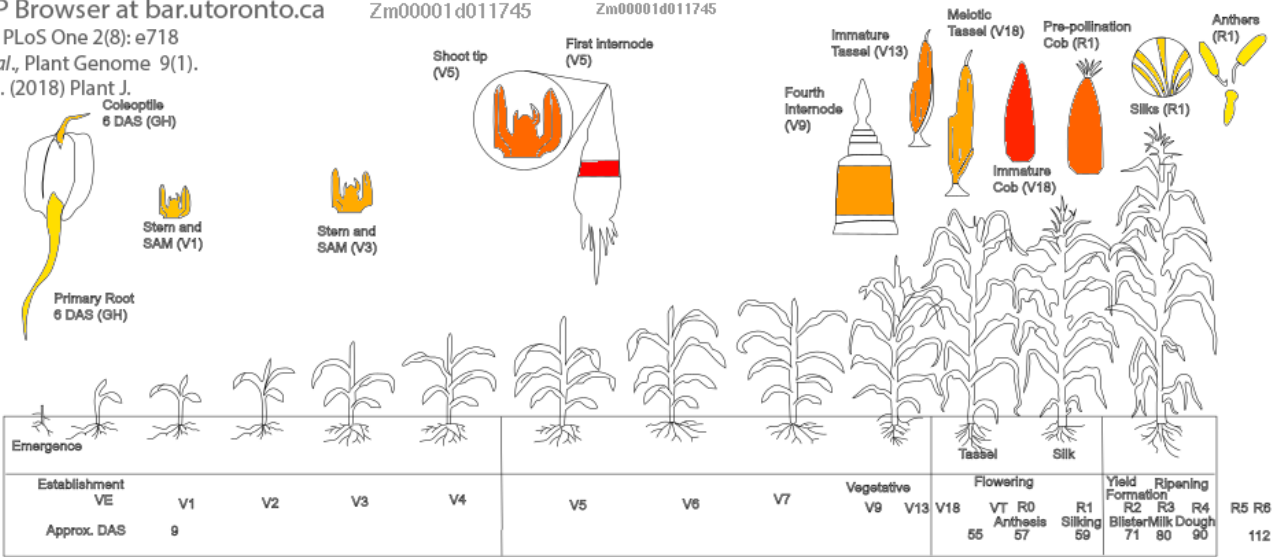
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Maize eFP Browser at bar.utoronto.ca

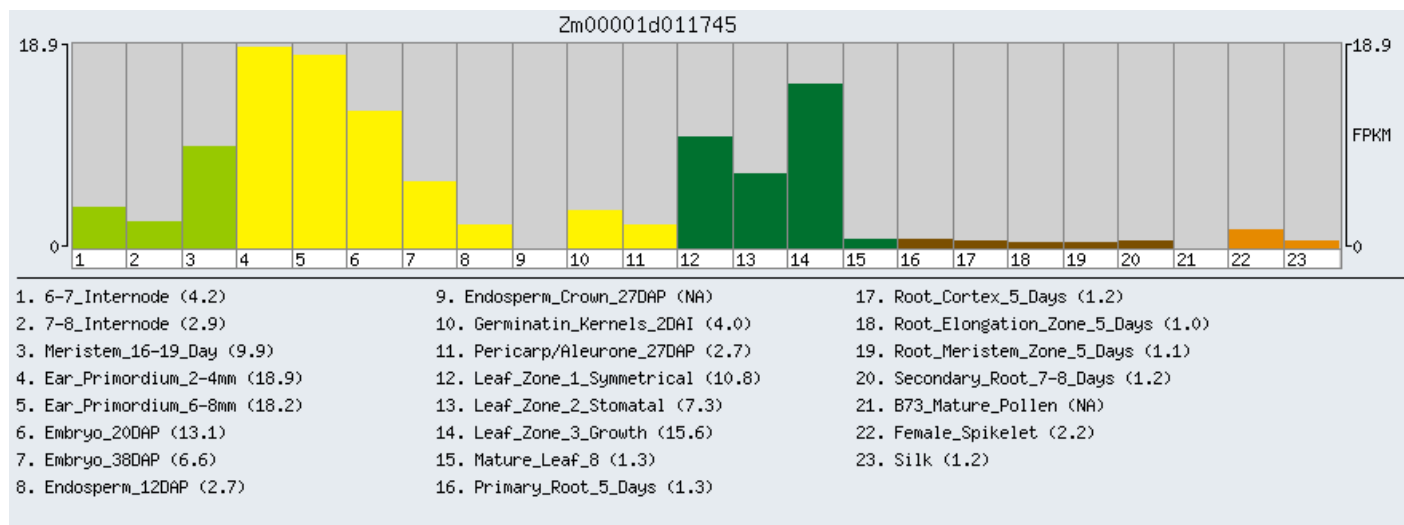
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Winter *et al.*, PLoS One 2(8): e718  
 Stelplflug *et al.*, Plant Genome 9(1).  
 Hoopes *et al.* (2018) Plant J.



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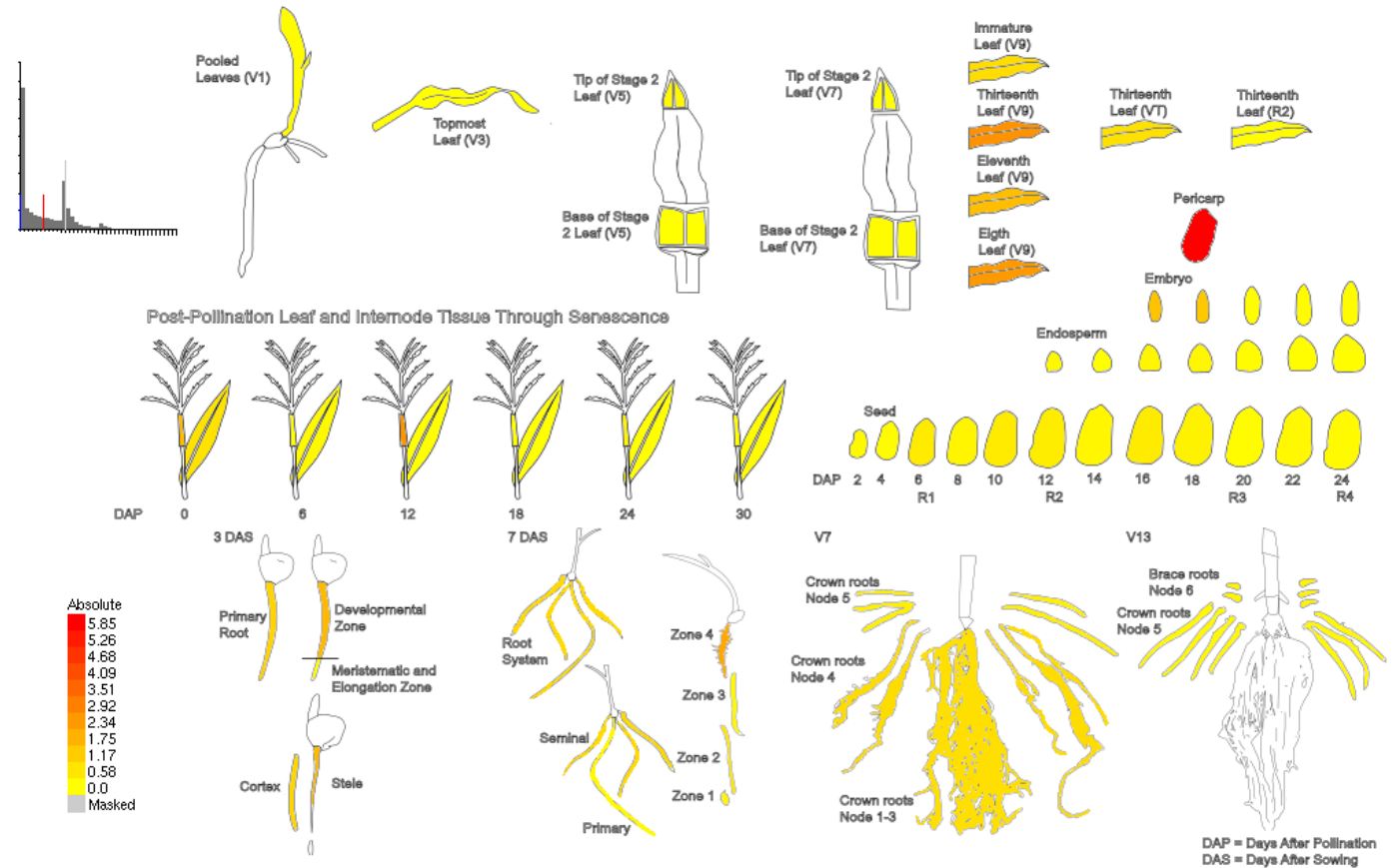
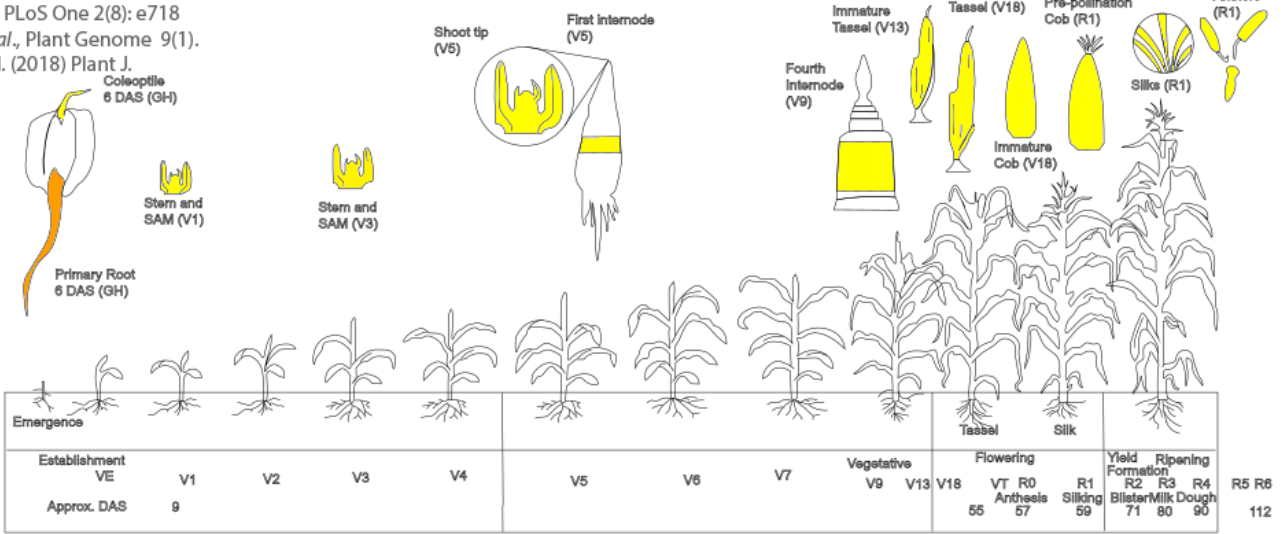
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Maize eFP Browser at bar.utoronto.ca

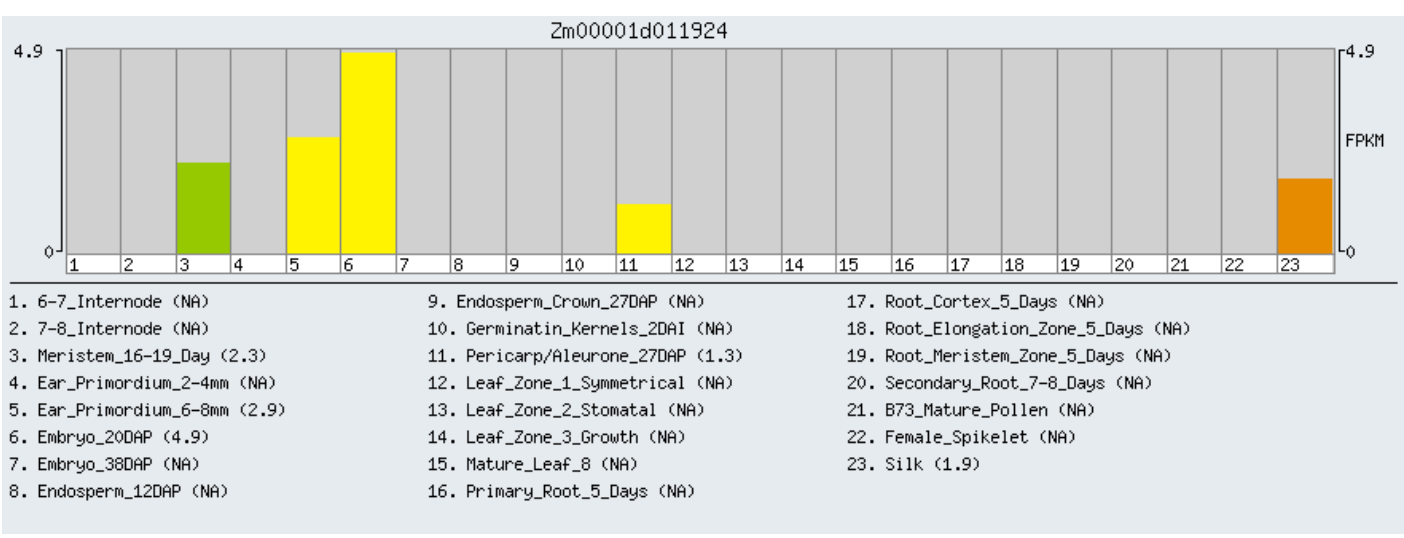
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Winter *et al.*, PLoS One 2(8): e718  
 Stelpflug *et al.*, Plant Genome 9(1).  
 Hoopes *et al.* (2018) Plant J.



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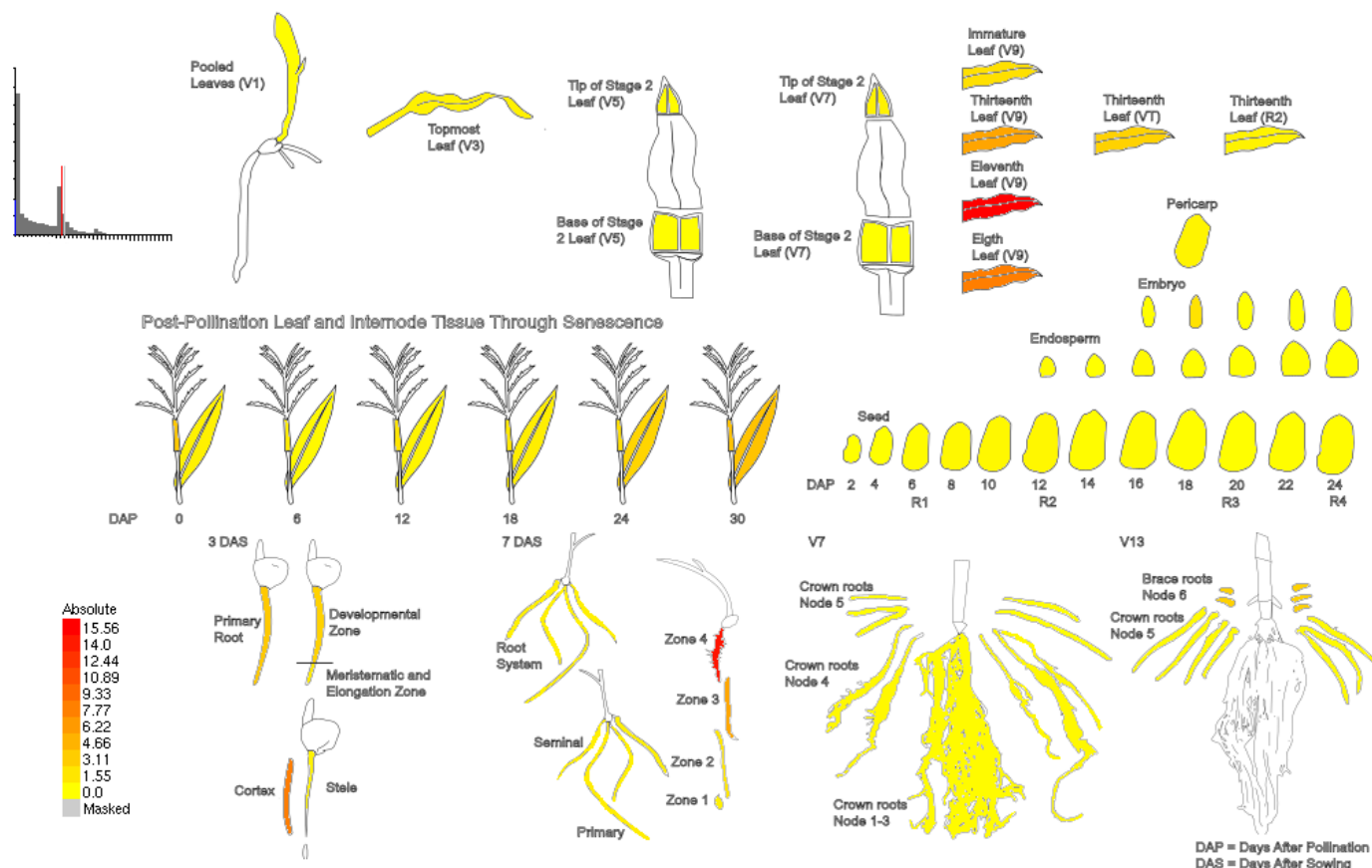
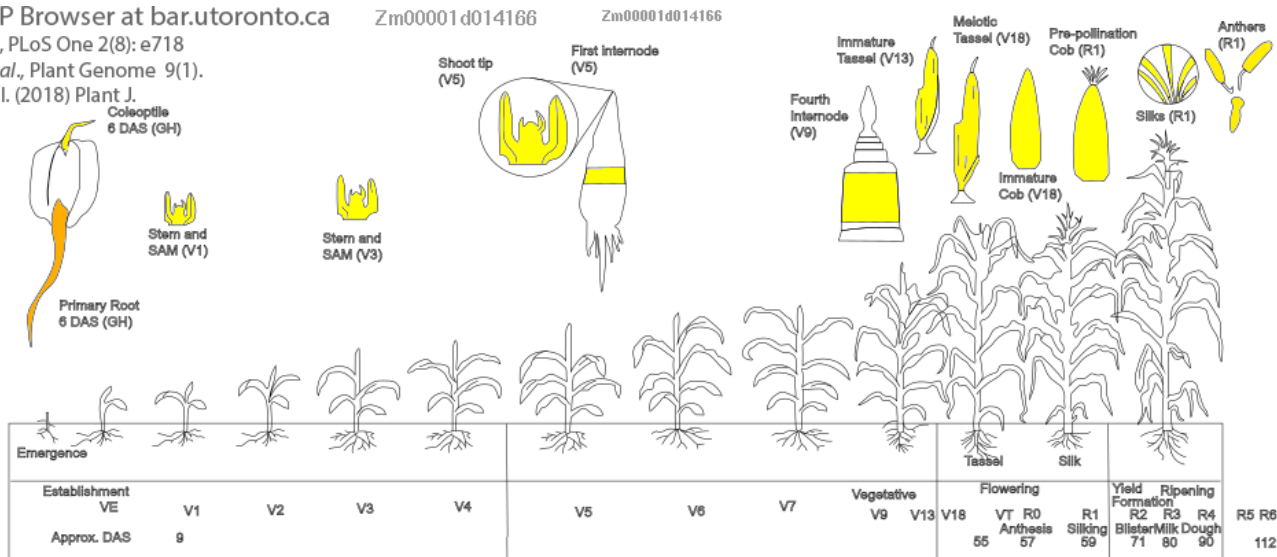
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Maize eFP Browser at bar.utoronto.ca

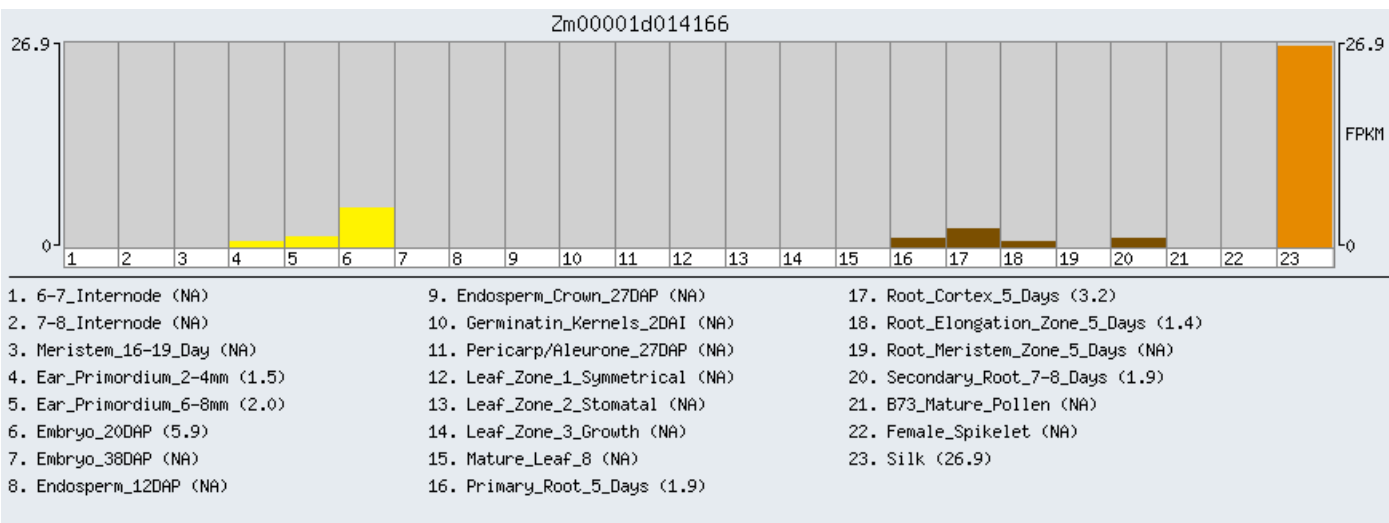
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Winter *et al.*, PLoS One 2(8): e718  
 Stelplflug *et al.*, Plant Genome 9(1).  
 Hoopes *et al.* (2018) Plant J.



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- 1. 6-7\_Internode (NA)
- 2. 7-8\_Internode (NA)
- 3. Meristem\_16-19\_Day (NA)
- 4. Ear\_Primary\_2-4mm (1.5)
- 5. Ear\_Primary\_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)



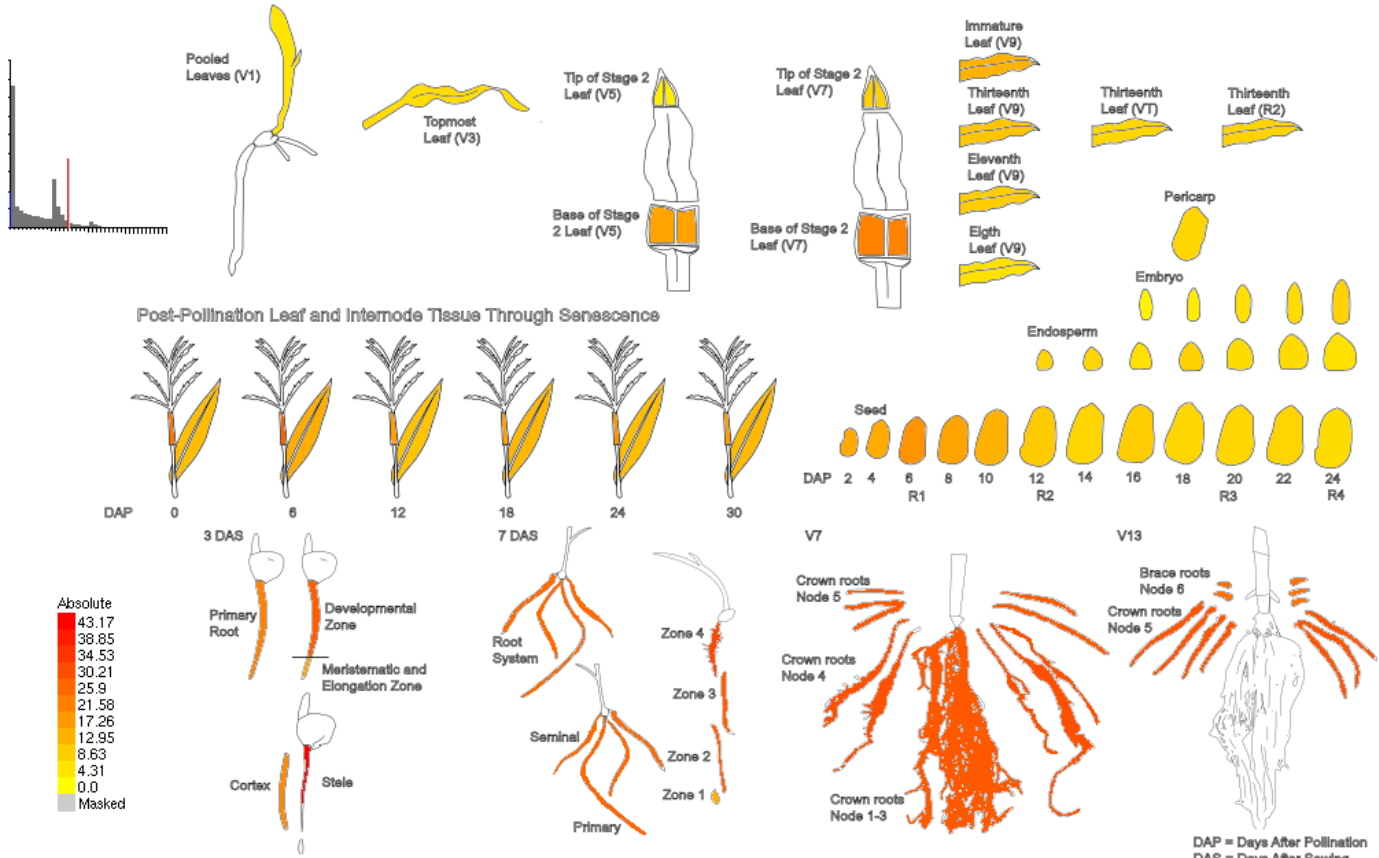
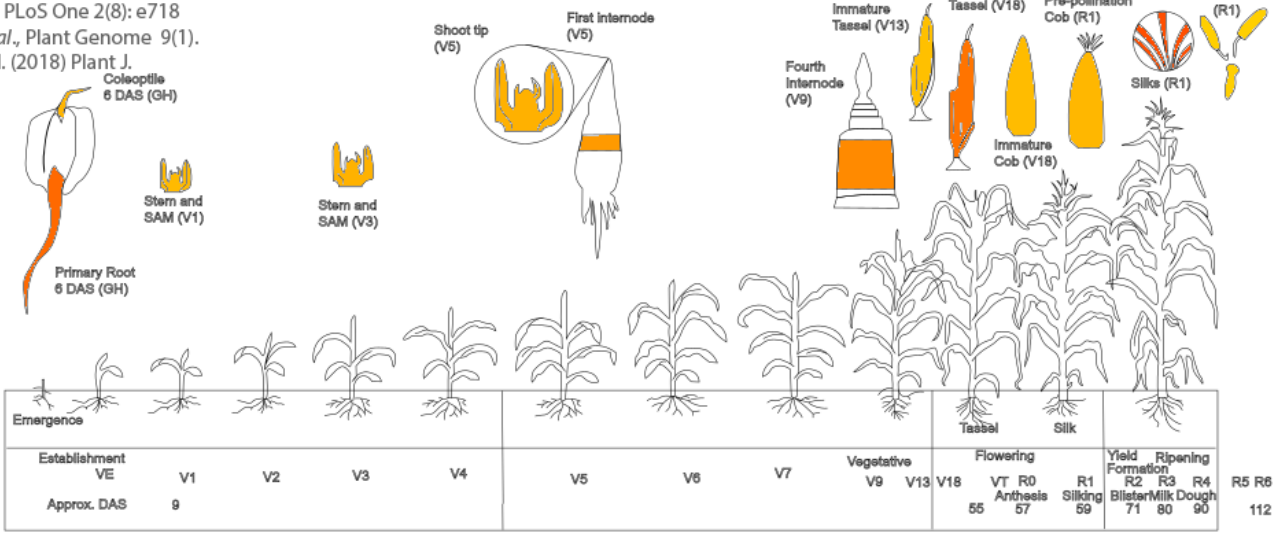
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Maize eFP Browser at bar.utoronto.ca

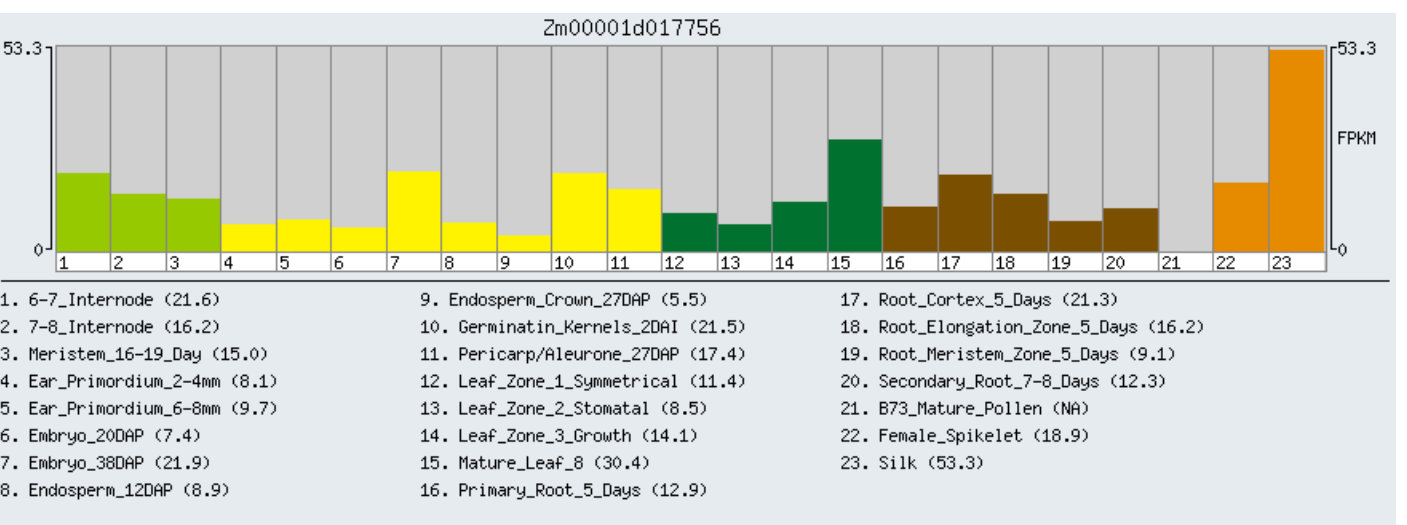
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Winter *et al.*, *PLoS One* 2(8): e718  
 Stelplflug *et al.*, *Plant Genome* 9(1).  
 Hoopes *et al.* (2018) *Plant J.*



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).



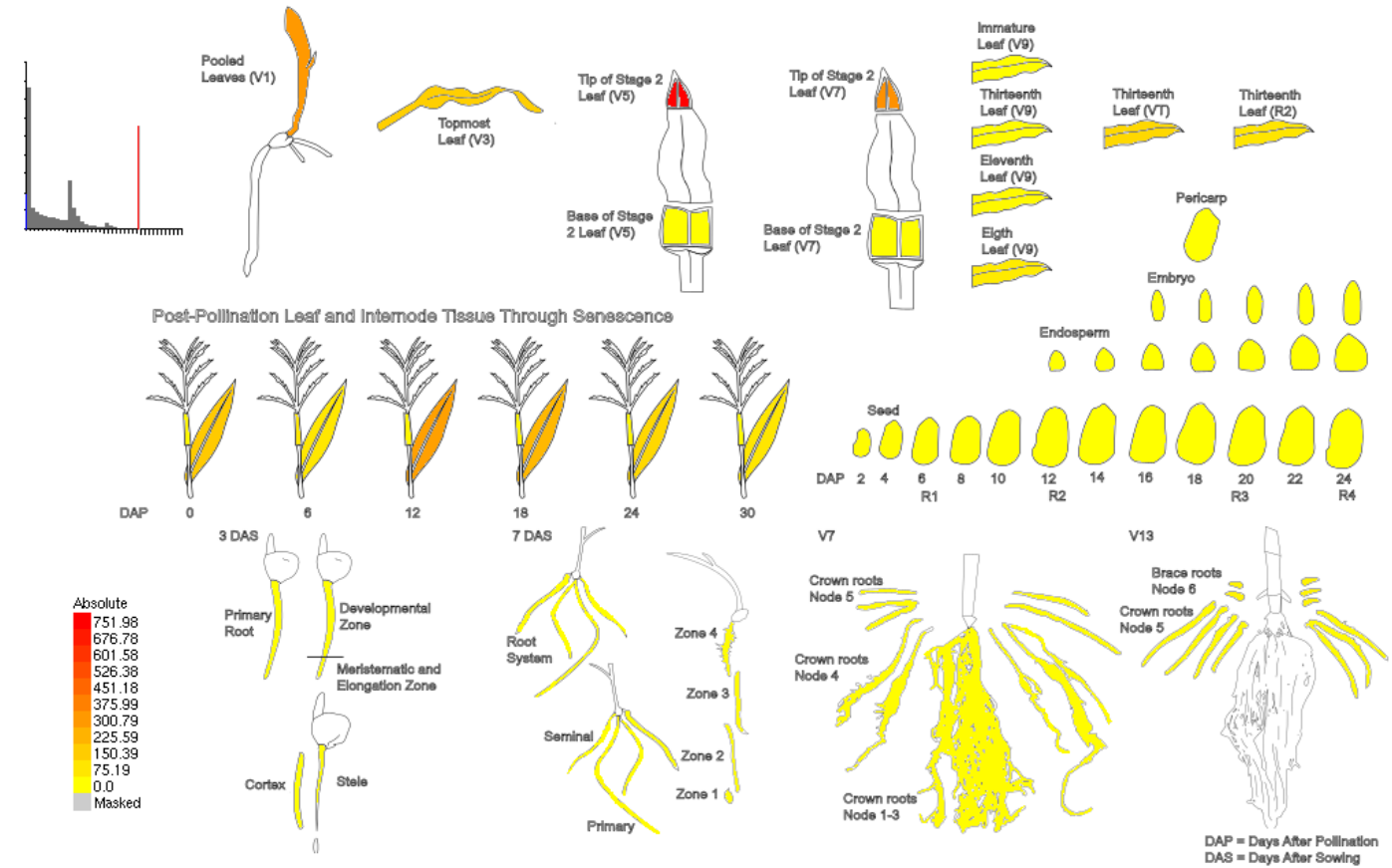
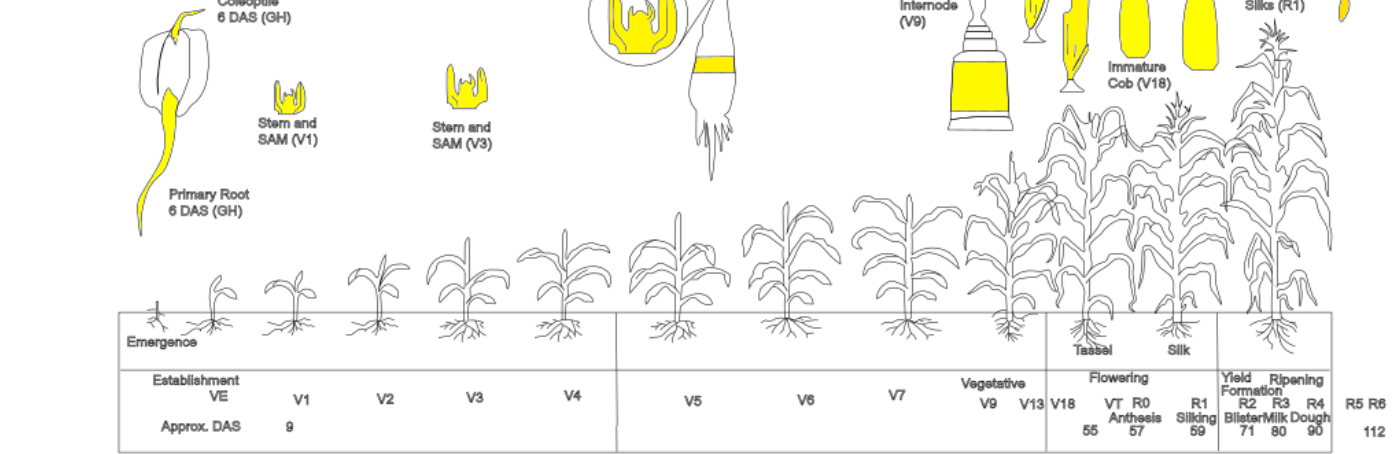
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Maize eFP Browser at bar.utoronto.ca

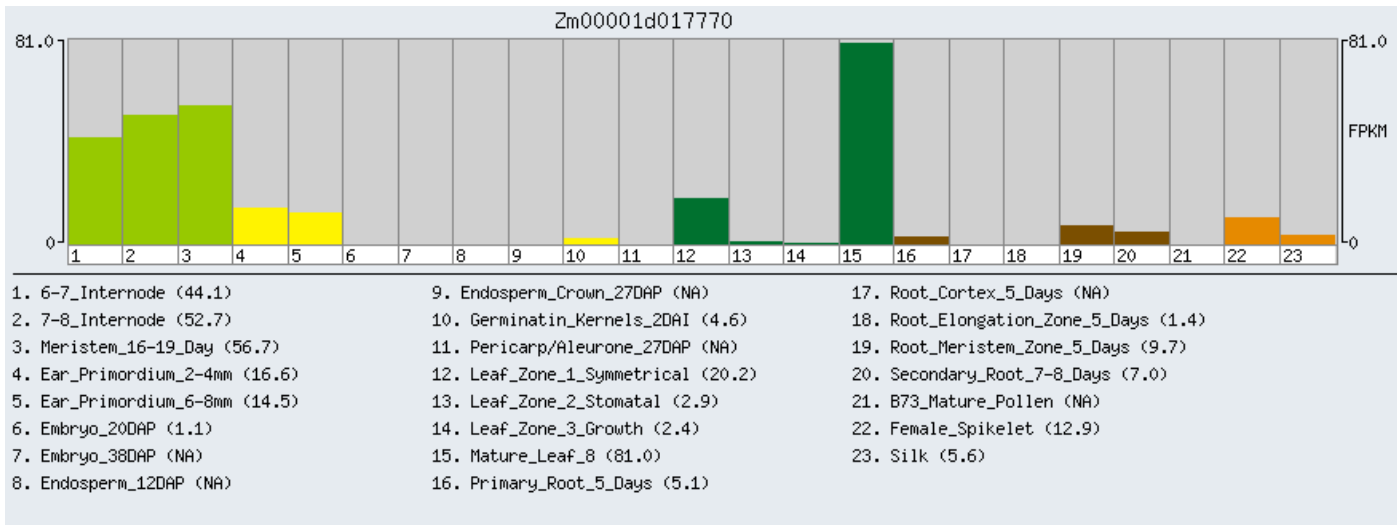
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Winter et al., PLoS One 2(8): e718  
 Stelpflug et al., Plant Genome 9(1).  
 Hoopes et al. (2018) Plant J.



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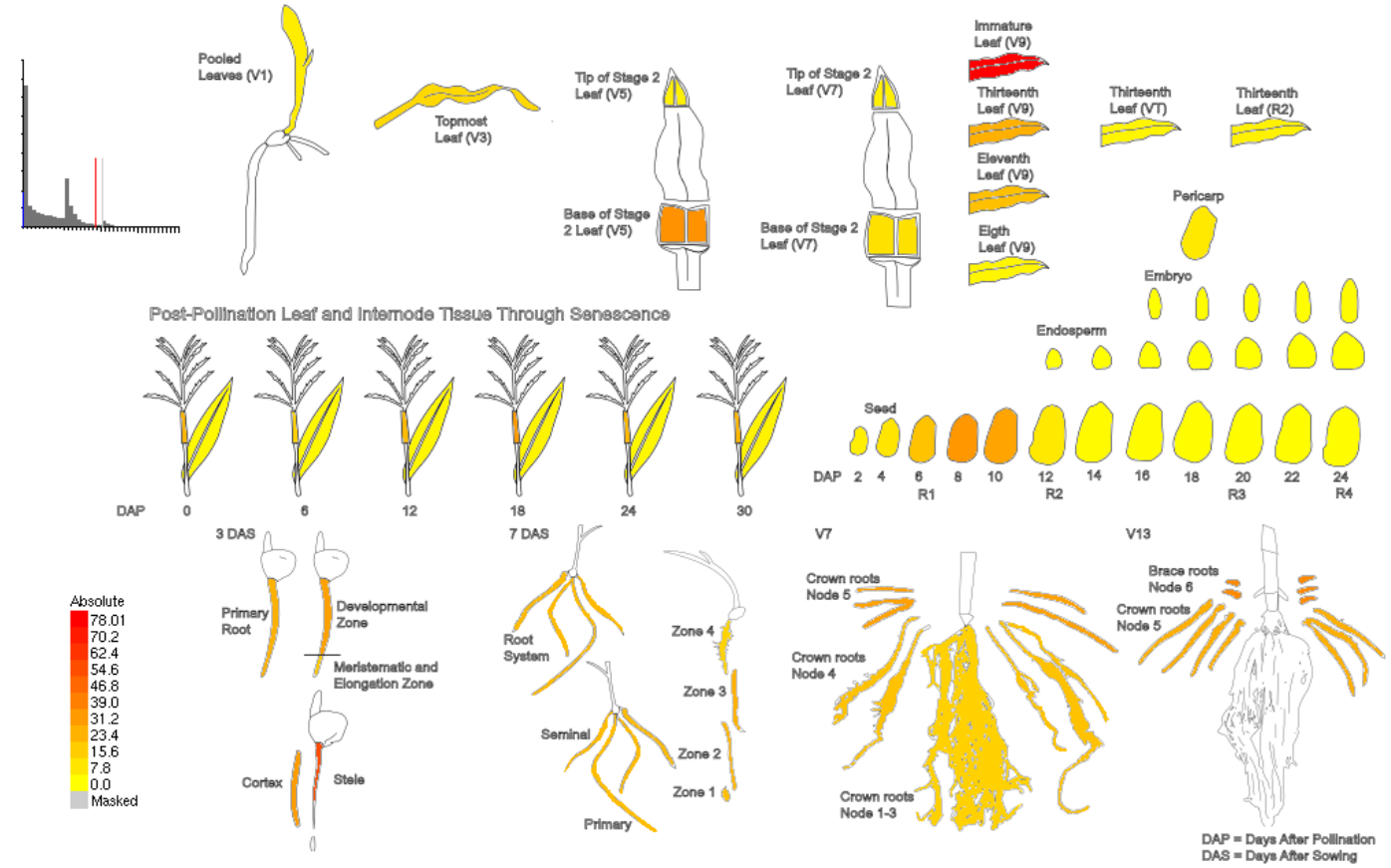
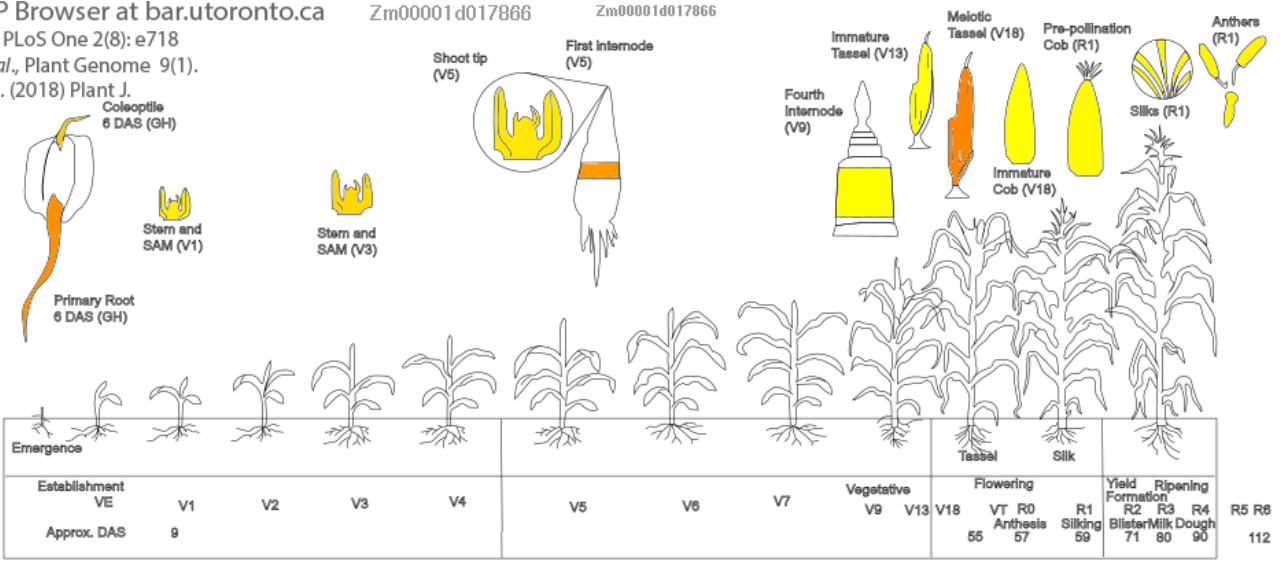
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Maize eFP Browser at bar.utoronto.ca

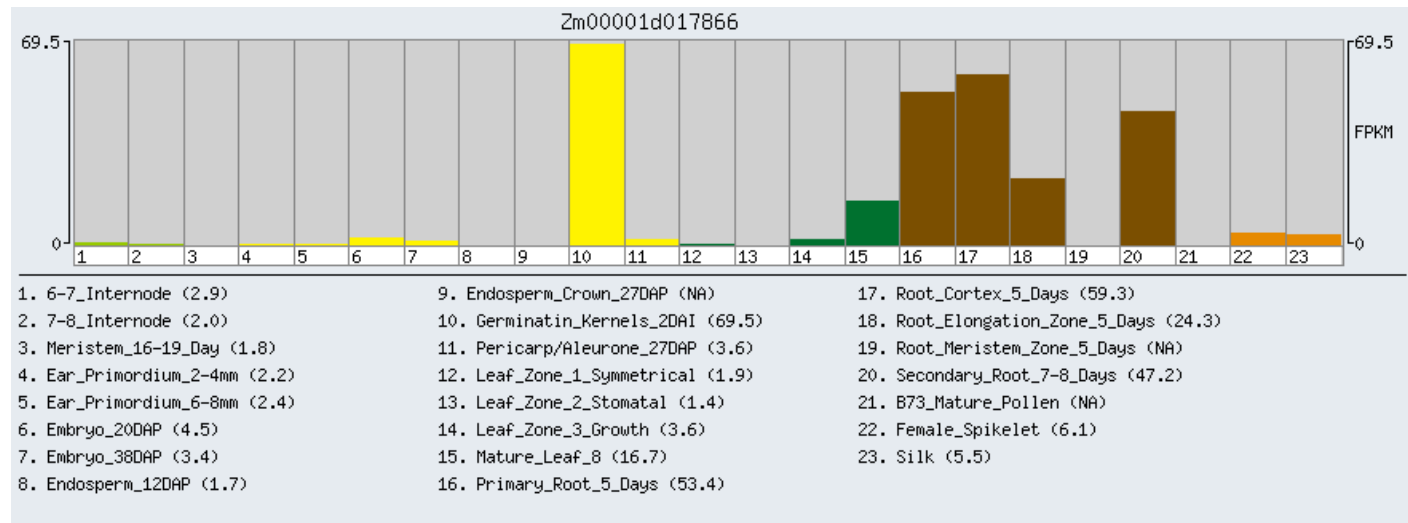
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Winter *et al.*, PLoS One 2(8): e718  
 Stelplflug *et al.*, Plant Genome 9(1).  
 Hoopes *et al.* (2018) Plant J.



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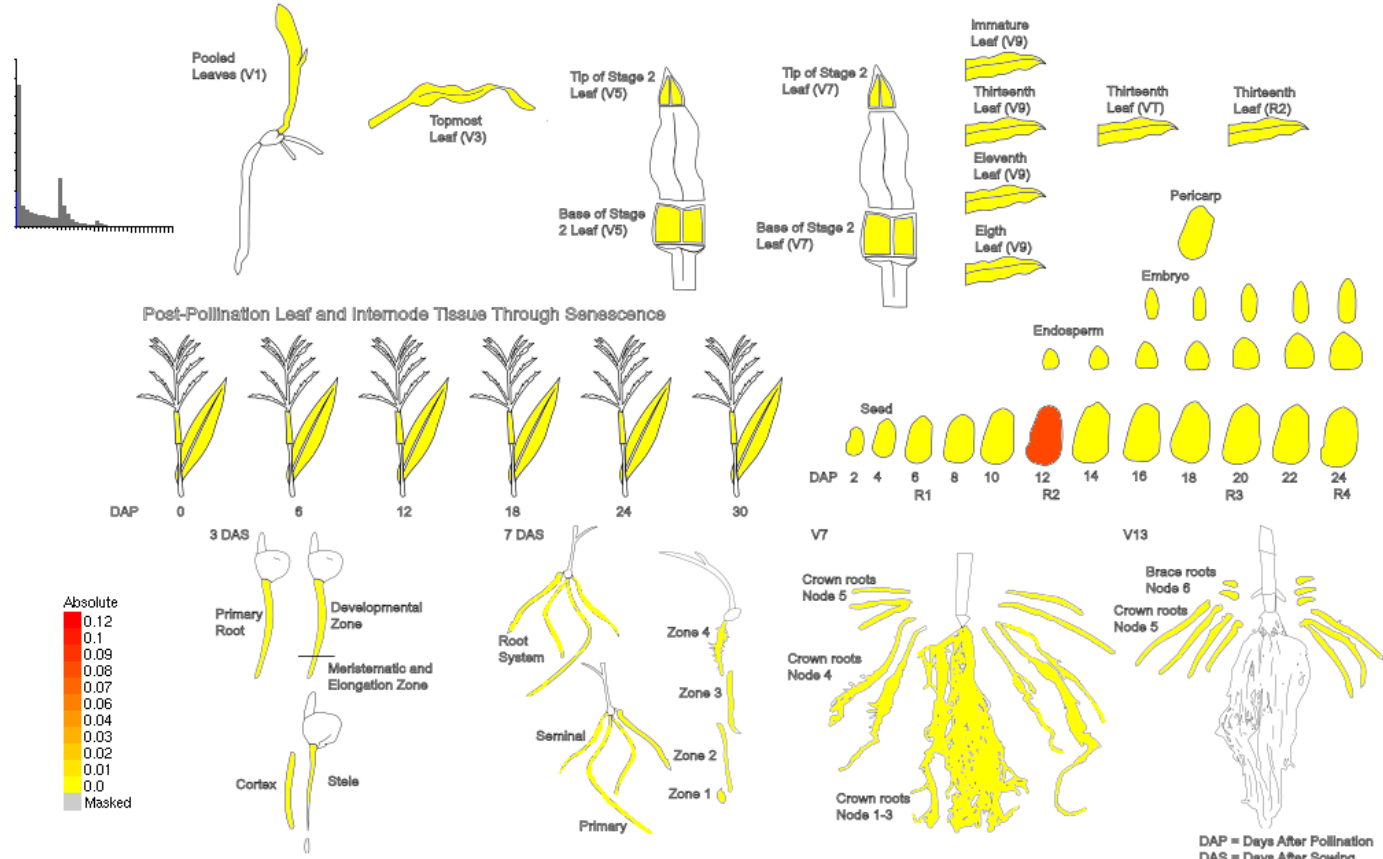
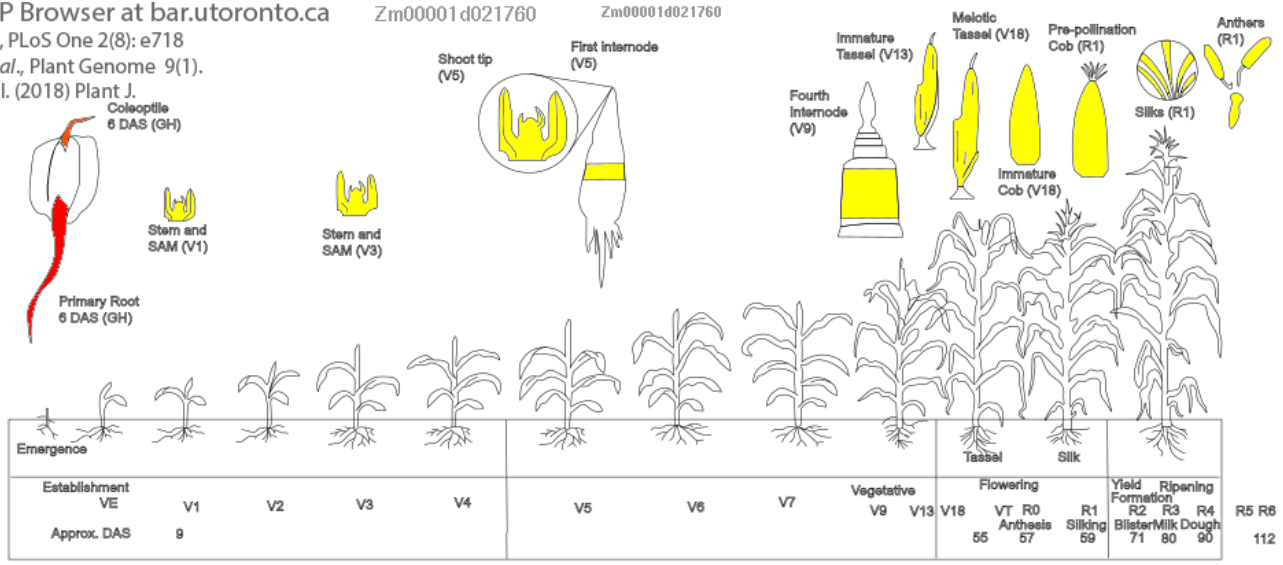


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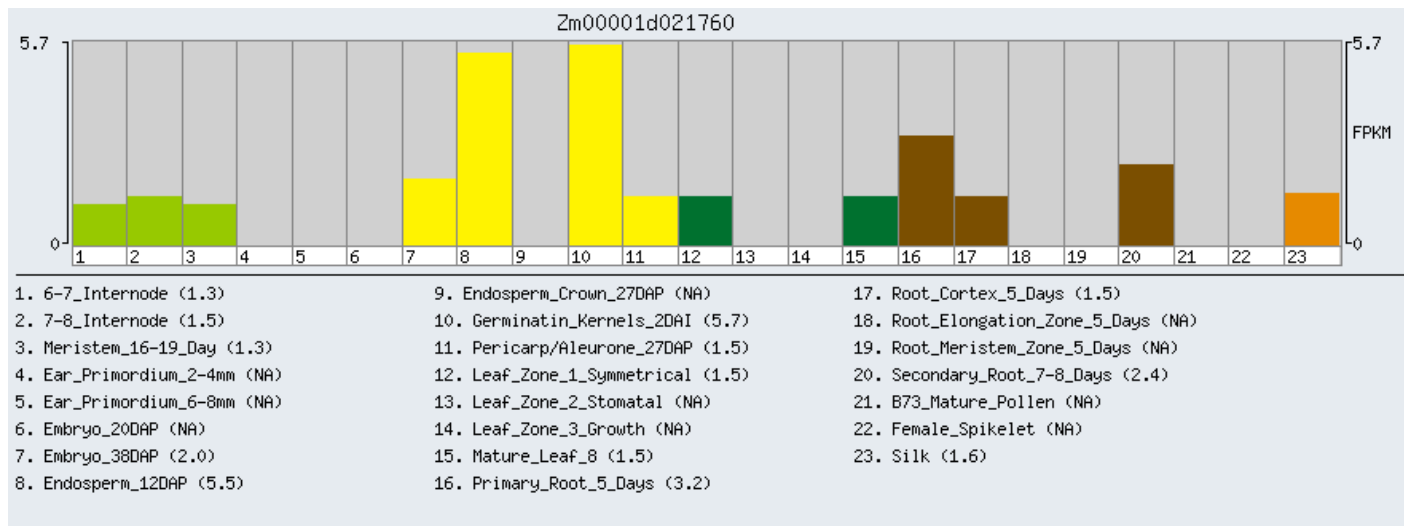
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Zm00001d021760 Zm00001d021760

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).



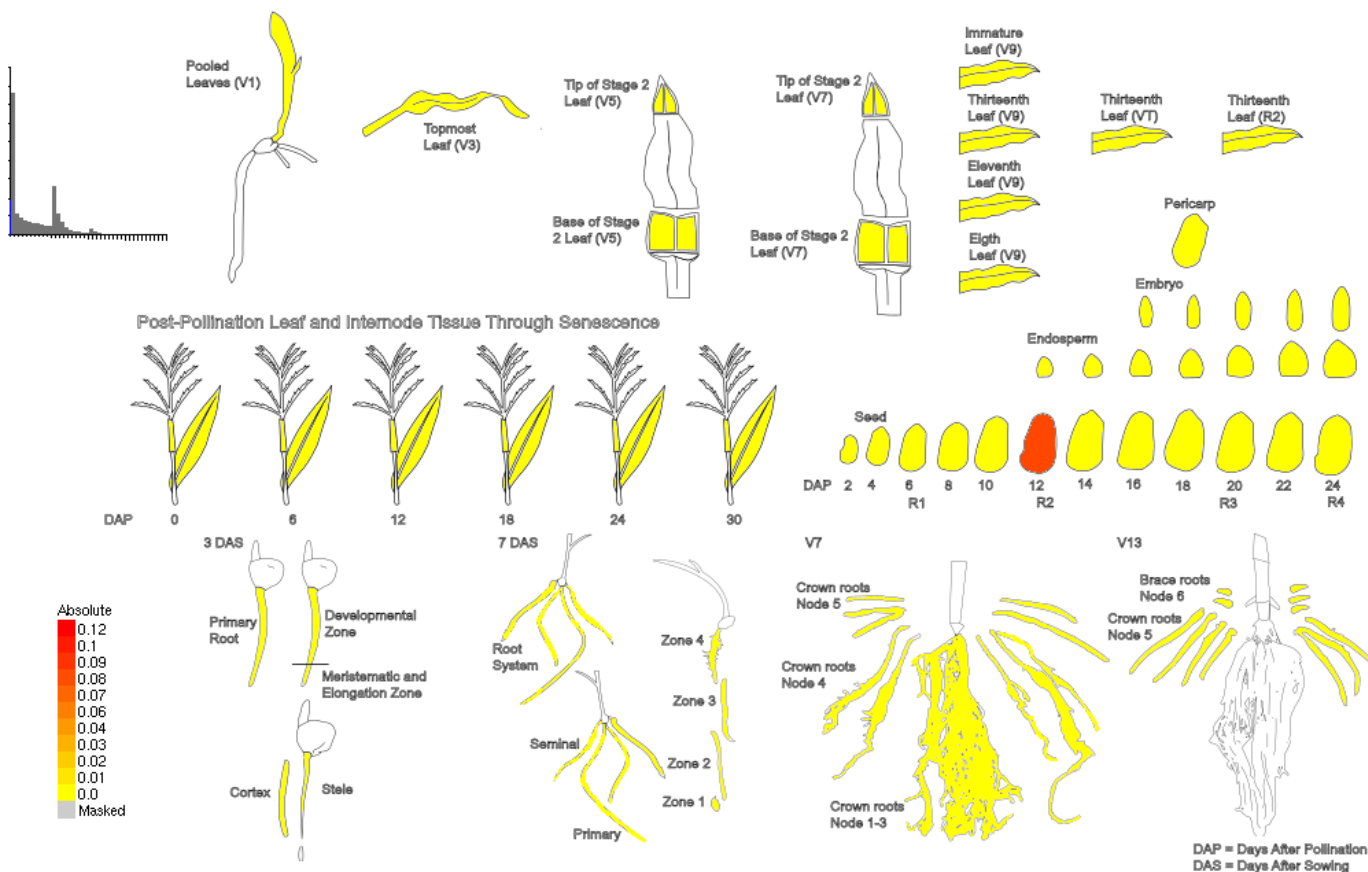
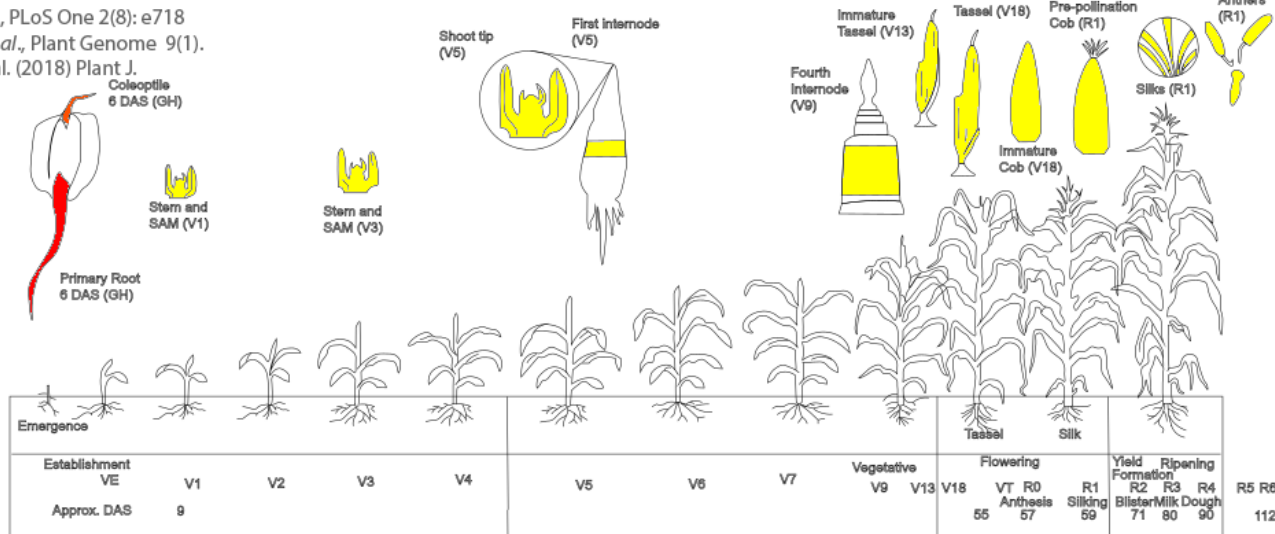
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Maize eFP Browser at bar.utoronto.ca

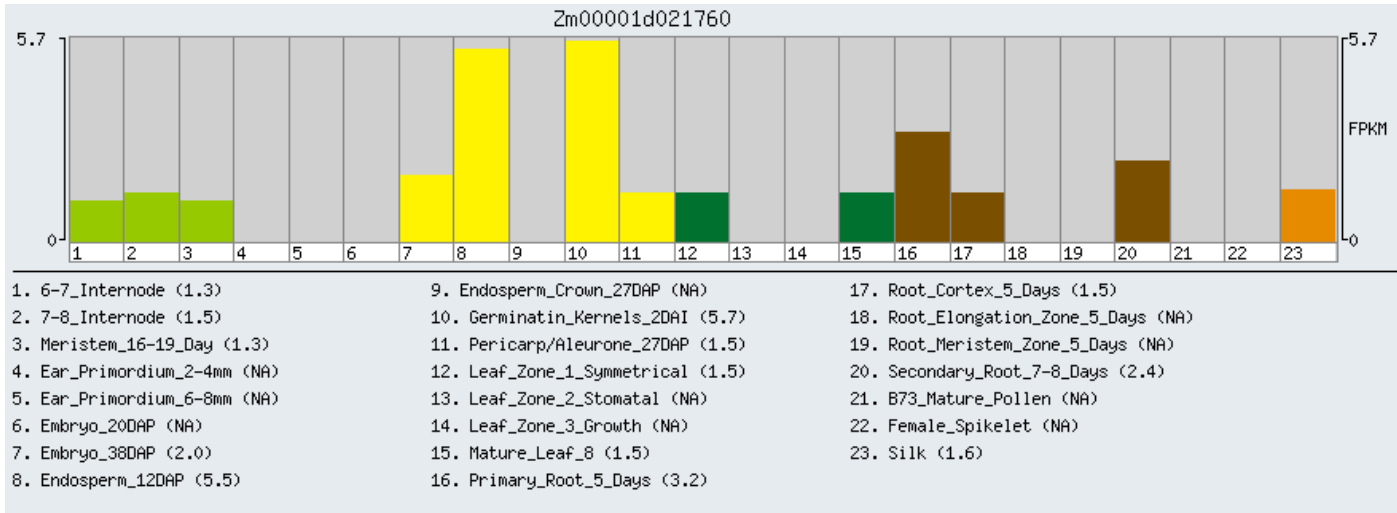
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Winter *et al.*, PLoS One 2(8): e718  
 Stelplflug *et al.*, Plant Genome 9(1).  
 Hoopes *et al.* (2018) Plant J.



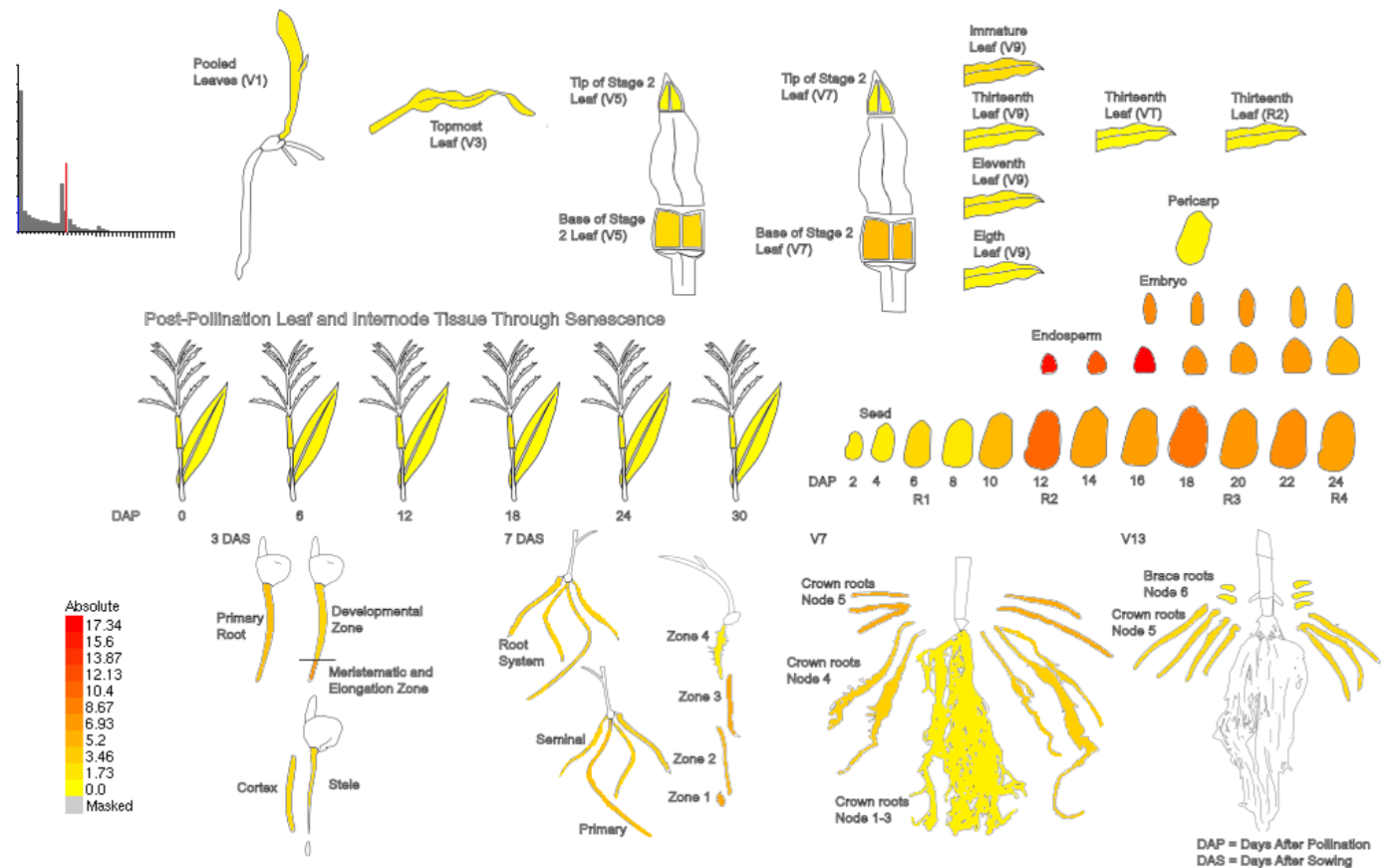
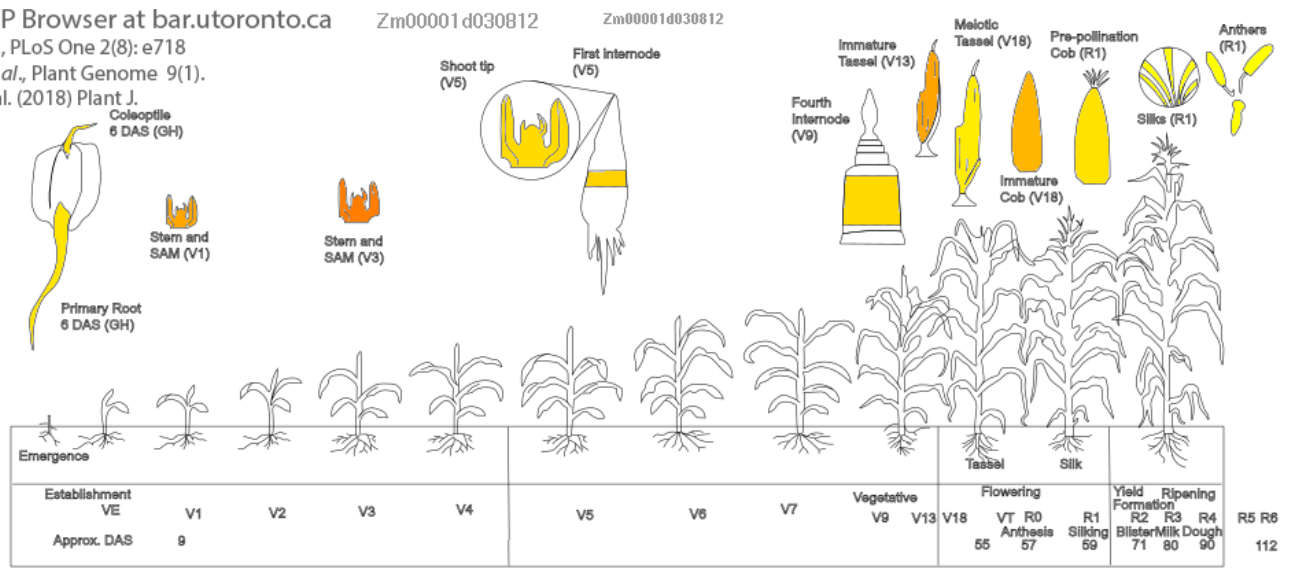
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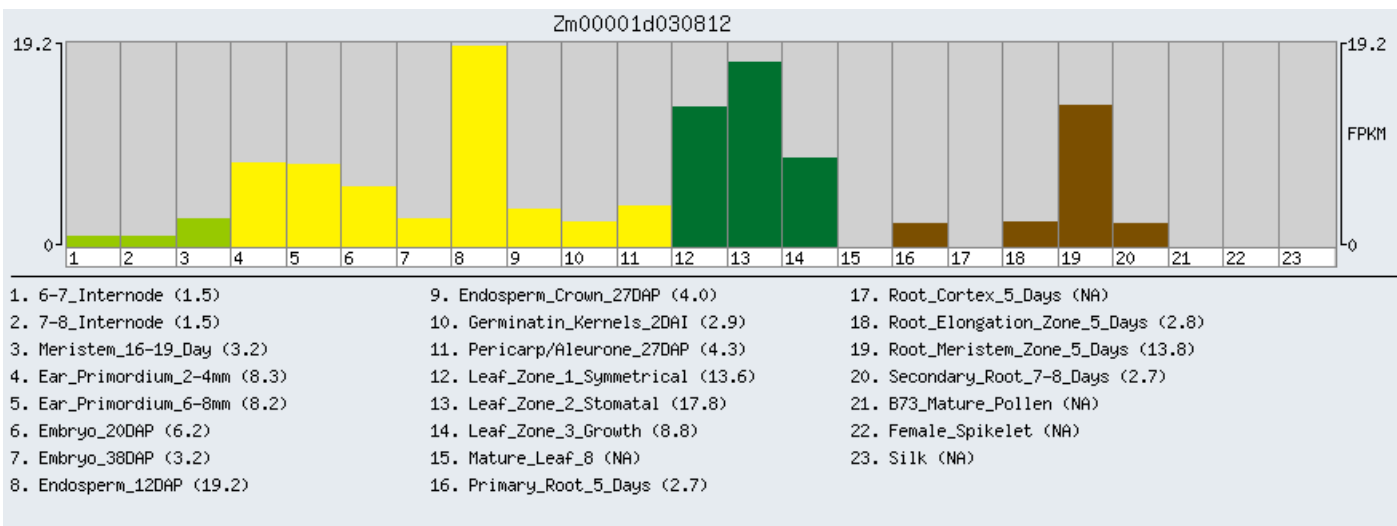
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 Winter *et al.*, PLoS One 2(8): e718  
 Stelpflug *et al.*, Plant Genome 9(1).  
 Hoopes *et al.* (2018) Plant J.

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).





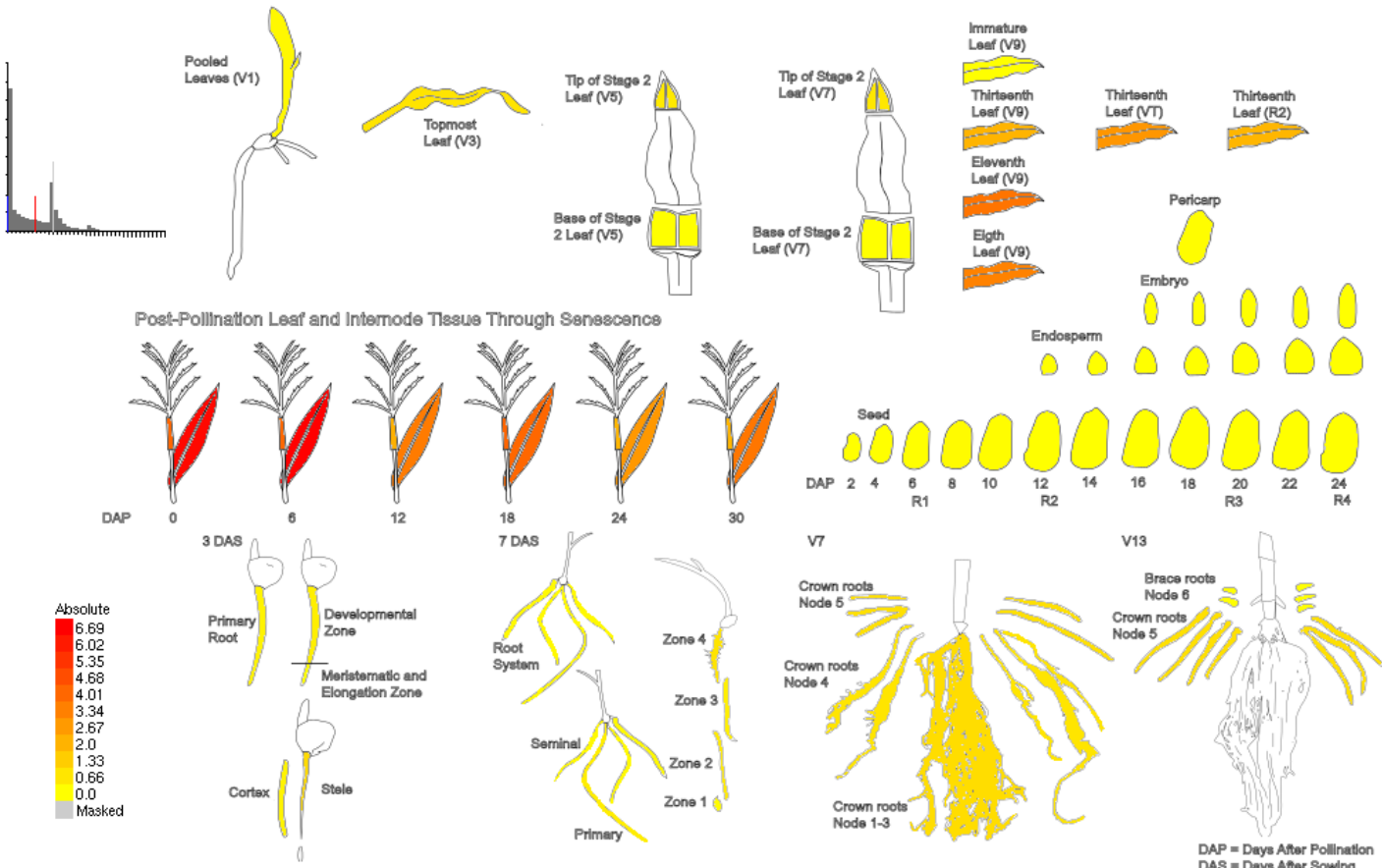
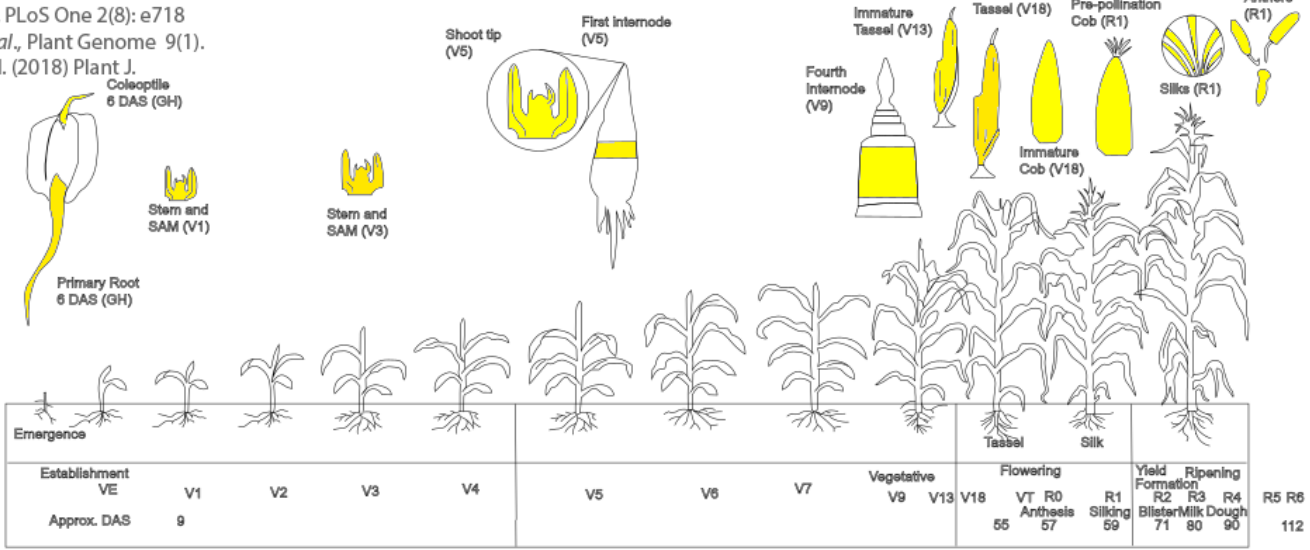
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Maize eFP Browser at bar.utoronto.ca

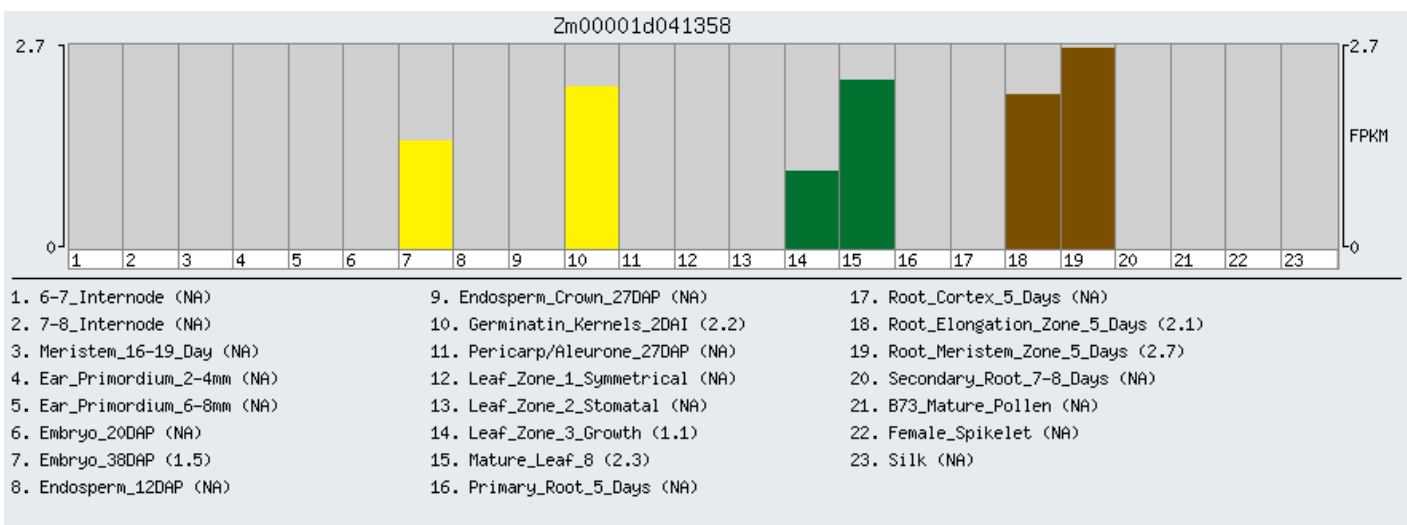
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Winter *et al.*, PLoS One 2(8): e718  
 Stelpflug *et al.*, Plant Genome 9(1).  
 Hoopes *et al.* (2018) Plant J.



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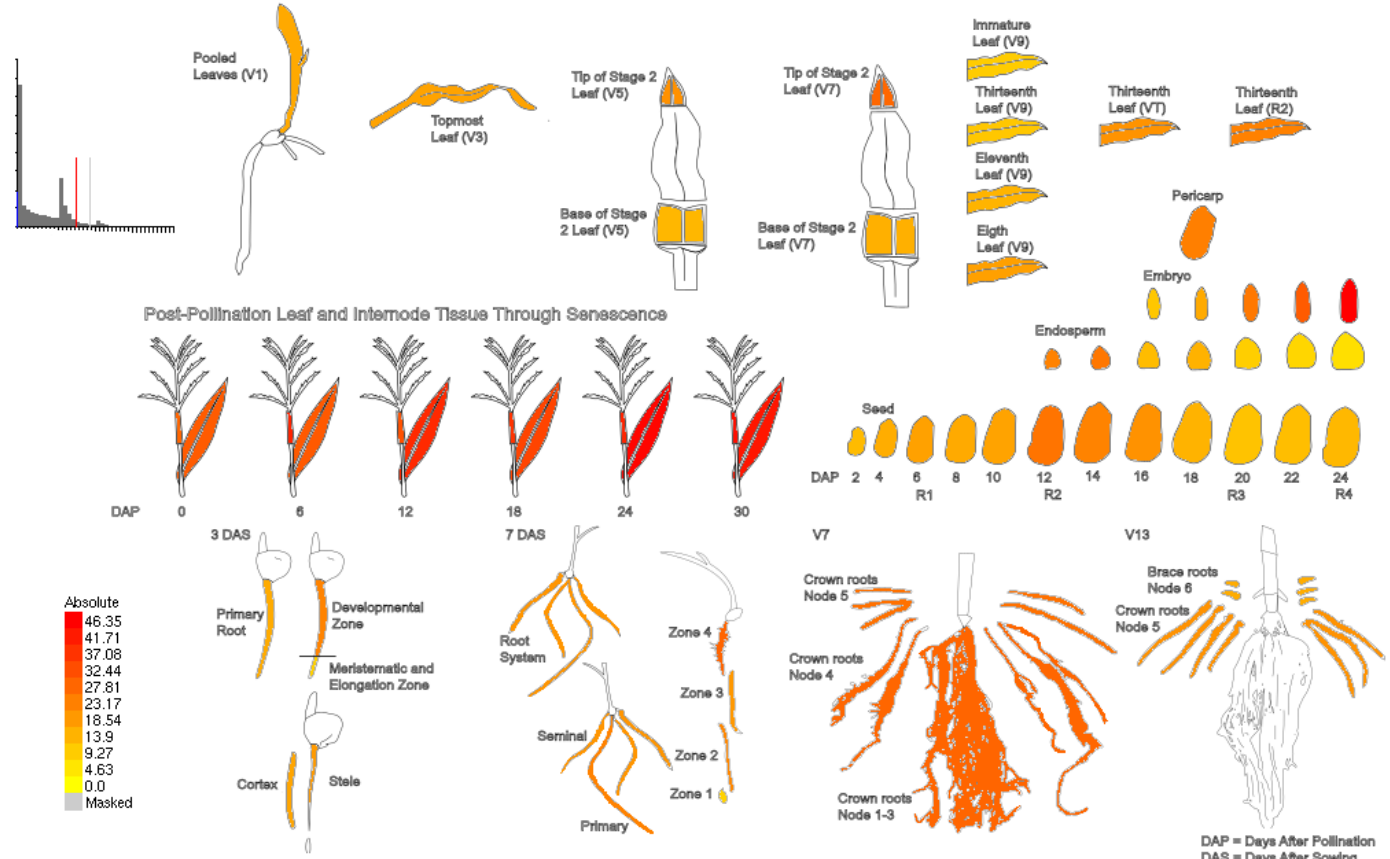
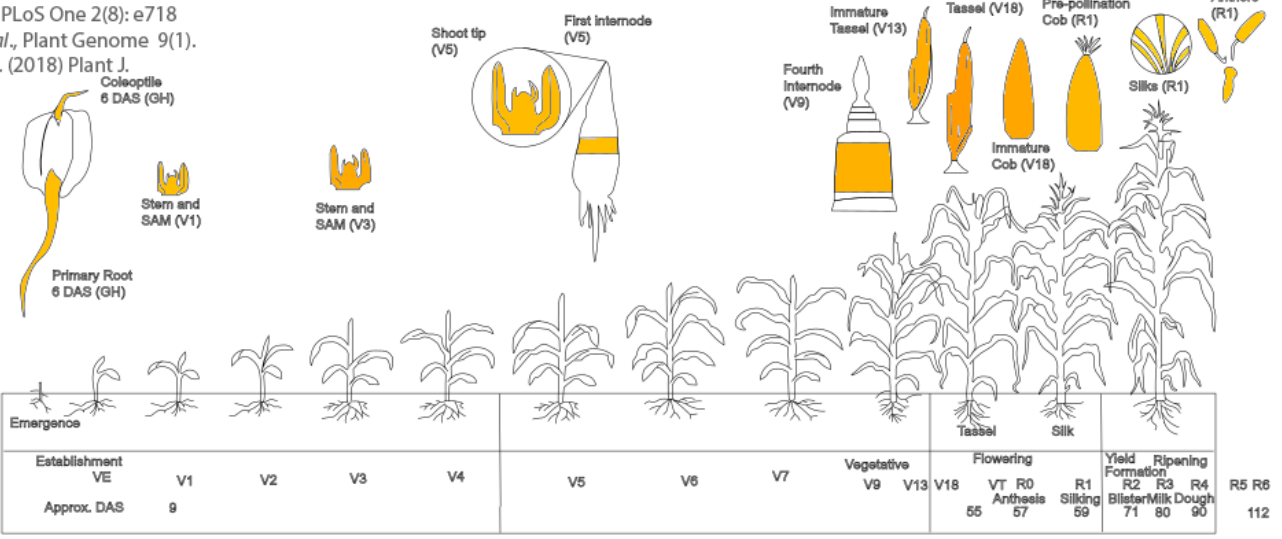
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Maize eFP Browser at bar.utoronto.ca

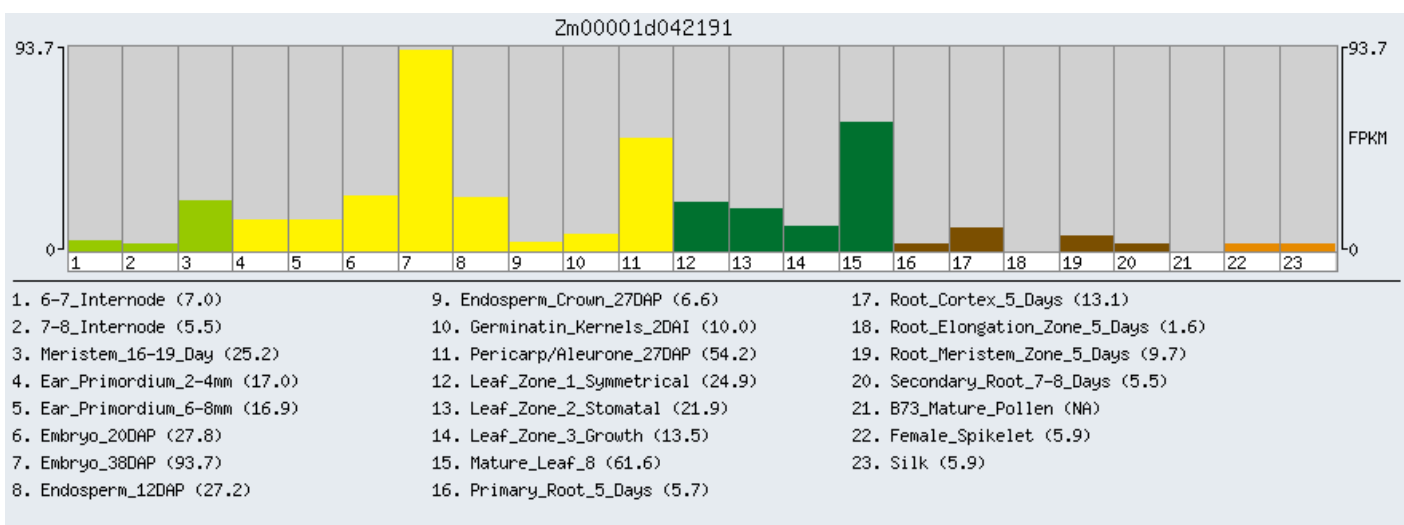
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Winter *et al.*, PLoS One 2(8): e718  
 Stelpflug *et al.*, Plant Genome 9(1).  
 Hoopes *et al.* (2018) Plant J.



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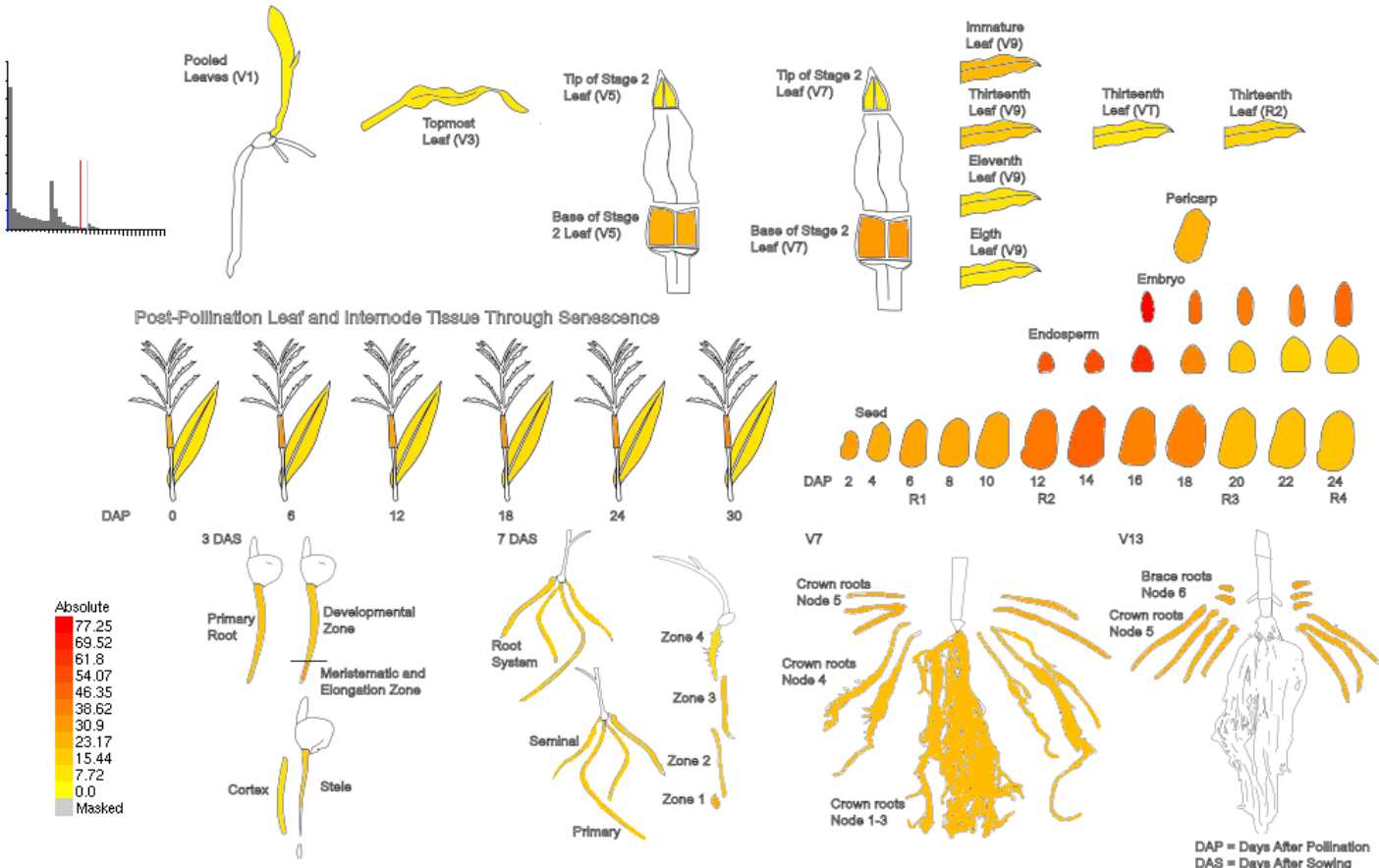
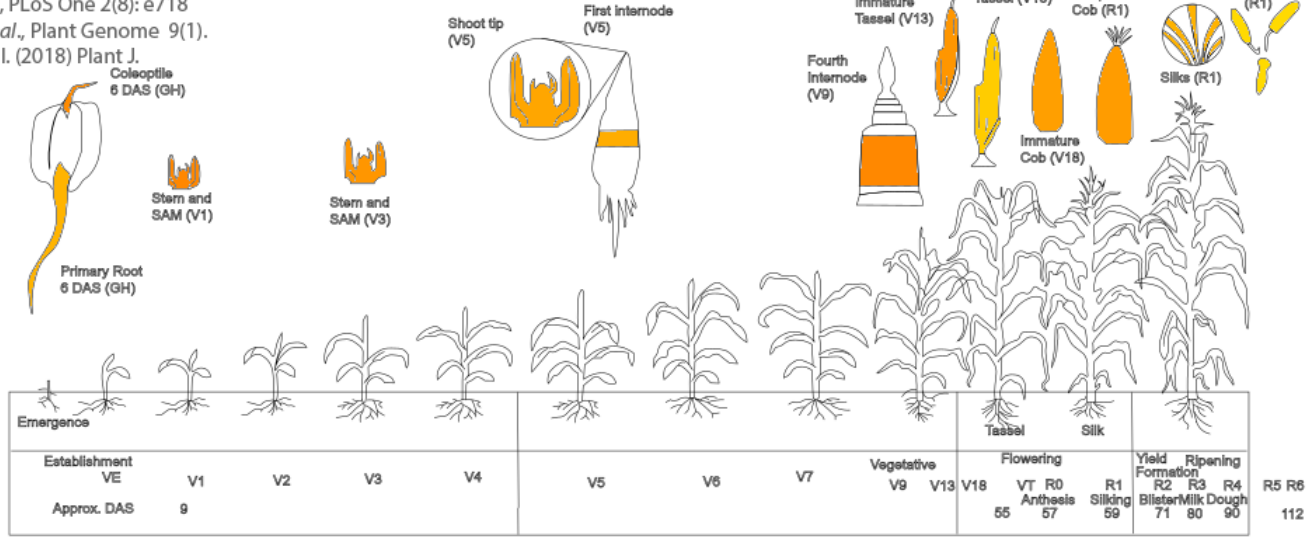
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Maize eFP Browser at bar.utoronto.ca

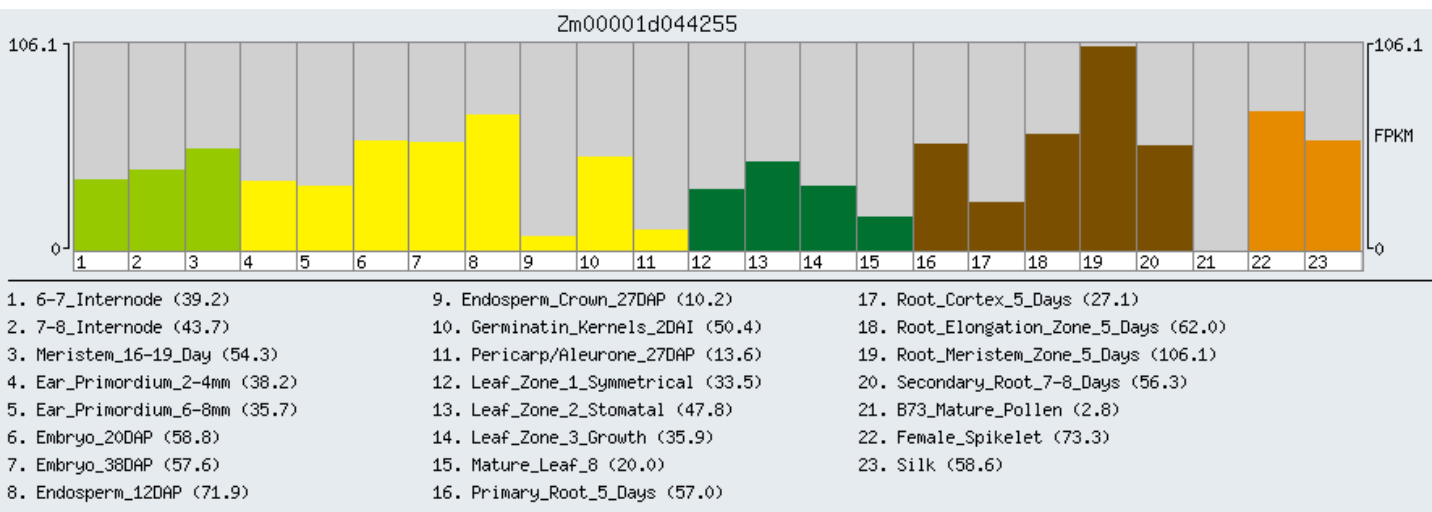
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Winter *et al.*, *PLoS One* 2(8): e718  
 Stelpflug *et al.*, *Plant Genome* 9(1).  
 Hoopes *et al.* (2018) *Plant J.*



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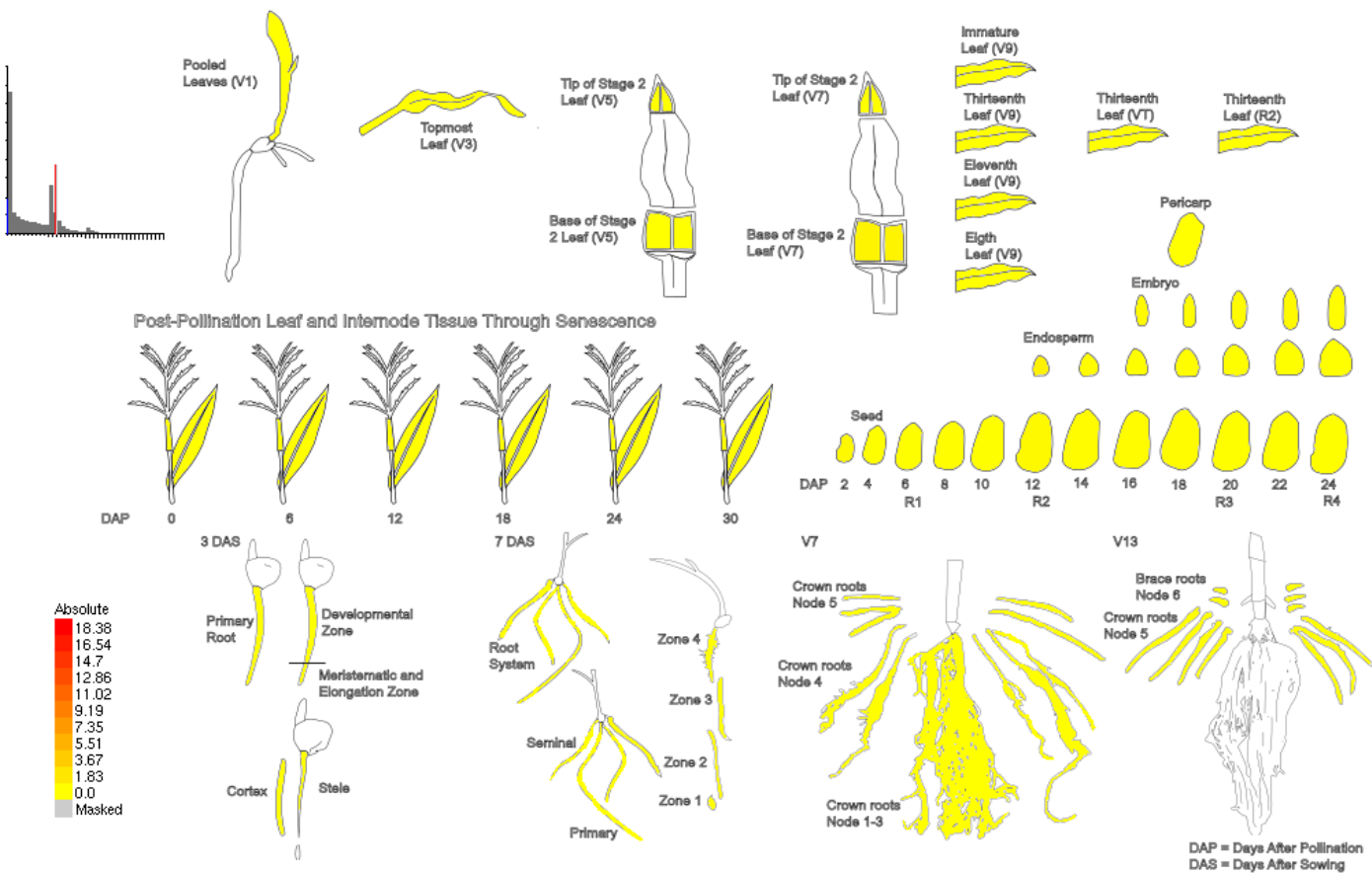
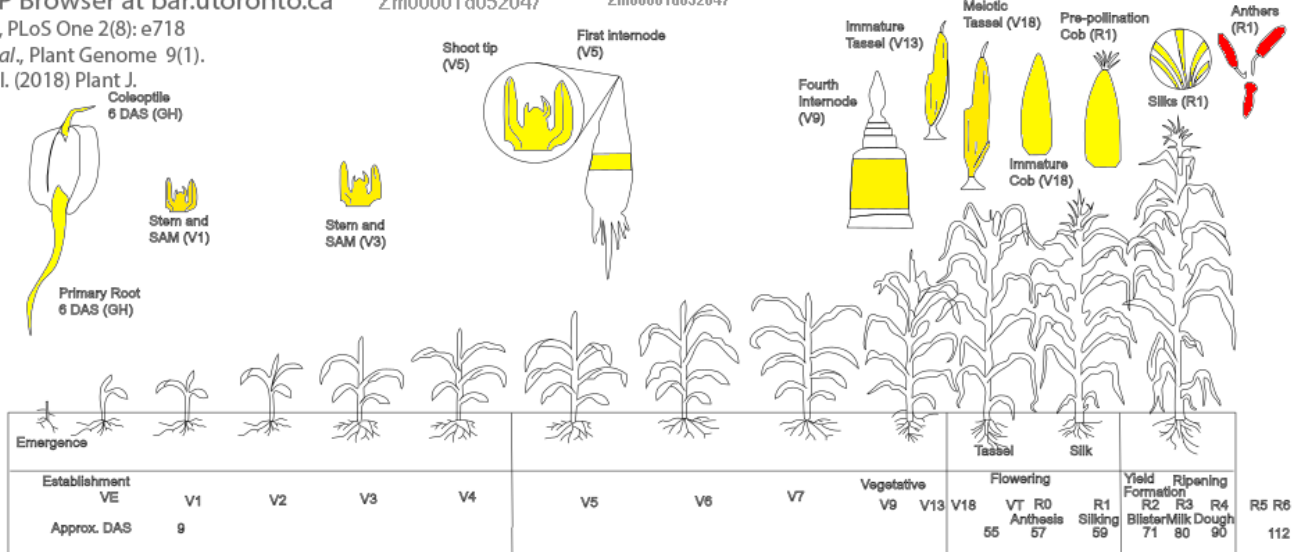
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Maize eFP Browser at bar.utoronto.ca

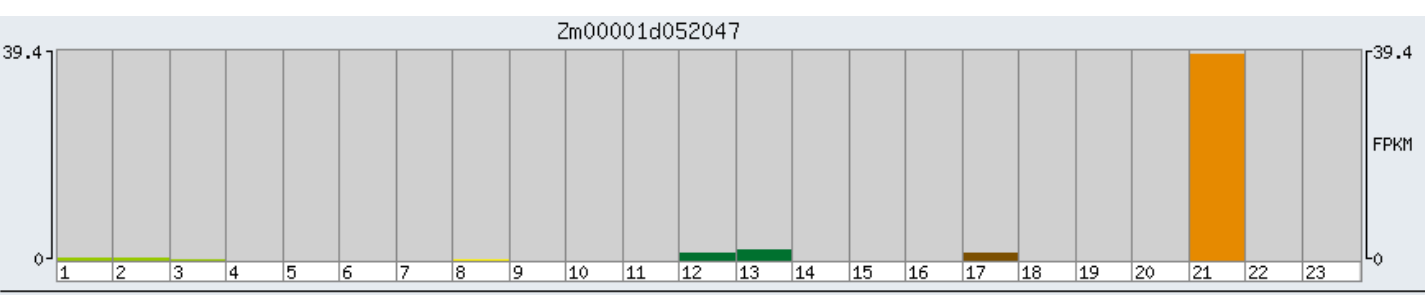
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Zm00001d052047

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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- |                              |                                   |                                      |
|------------------------------|-----------------------------------|--------------------------------------|
| 1. 6-7_Internode (1.6)       | 9. Endosperm_Crown_27DAP (NA)     | 17. Root_Cortex_5_Days (2.4)         |
| 2. 7-8_Internode (1.6)       | 10. Germinatin_Kernels_2DAI (NA)  | 18. Root_Elongation_Zone_5_Days (NA) |
| 3. Meristem_16-19_Day (1.3)  | 11. Pericarp/Aleurone_27DAP (NA)  | 19. Root_Meristem_Zone_5_Days (NA)   |
| 4. Ear_Primordium_2-4mm (NA) | 12. Leaf_Zone_1_Symmetrical (2.6) | 20. Secondary_Root_7-8_Days (NA)     |
| 5. Ear_Primordium_6-8mm (NA) | 13. Leaf_Zone_2_Stomatal (3.2)    | 21. B73_Mature_Pollen (39.4)         |
| 6. Embryo_20DAP (NA)         | 14. Leaf_Zone_3_Growth (NA)       | 22. Female_Spikelet (NA)             |
| 7. Embryo_38DAP (NA)         | 15. Mature_Leaf_8 (NA)            | 23. Silk (NA)                        |
| 8. Endosperm_12DAP (1.1)     | 16. Primary_Root_5_Days (NA)      |                                      |

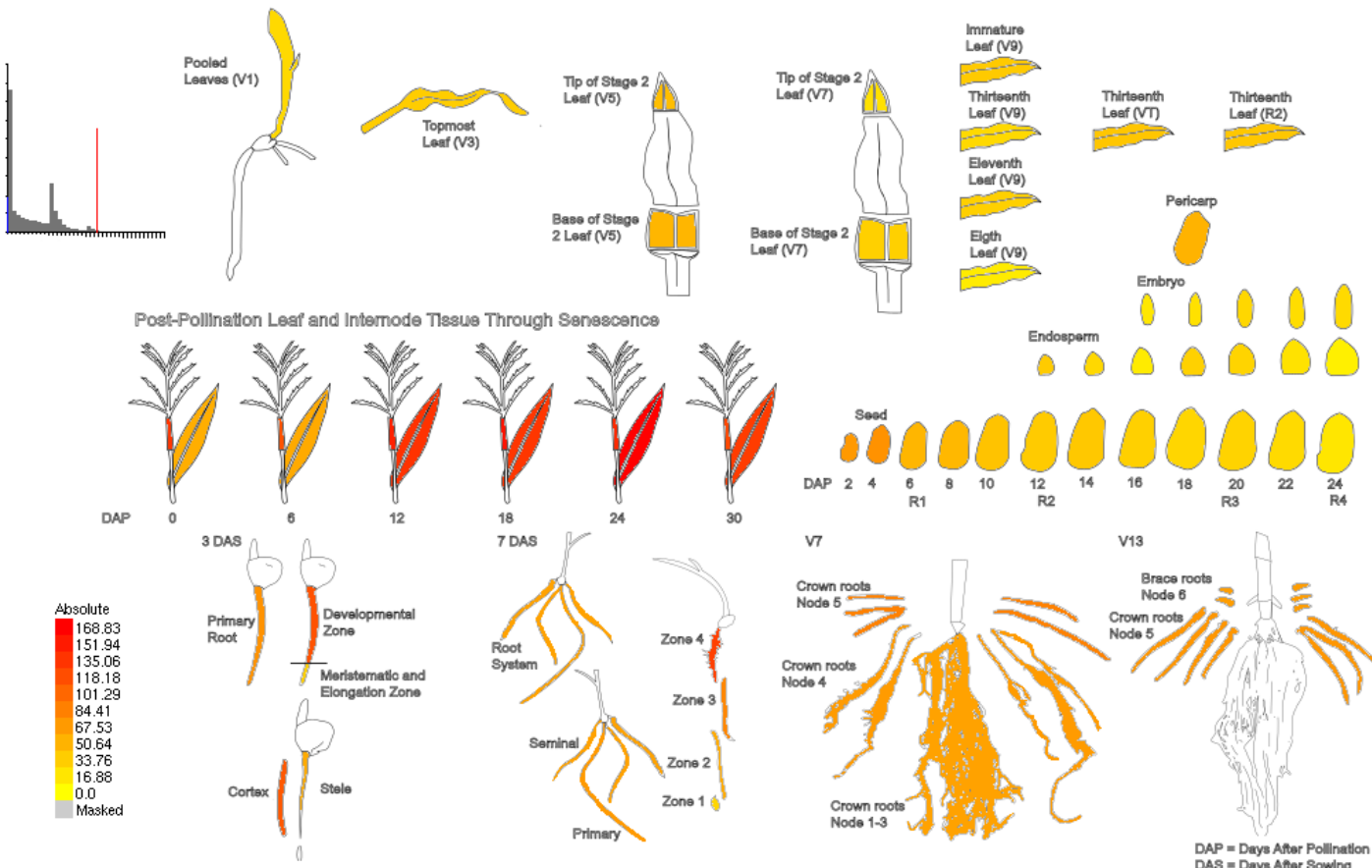
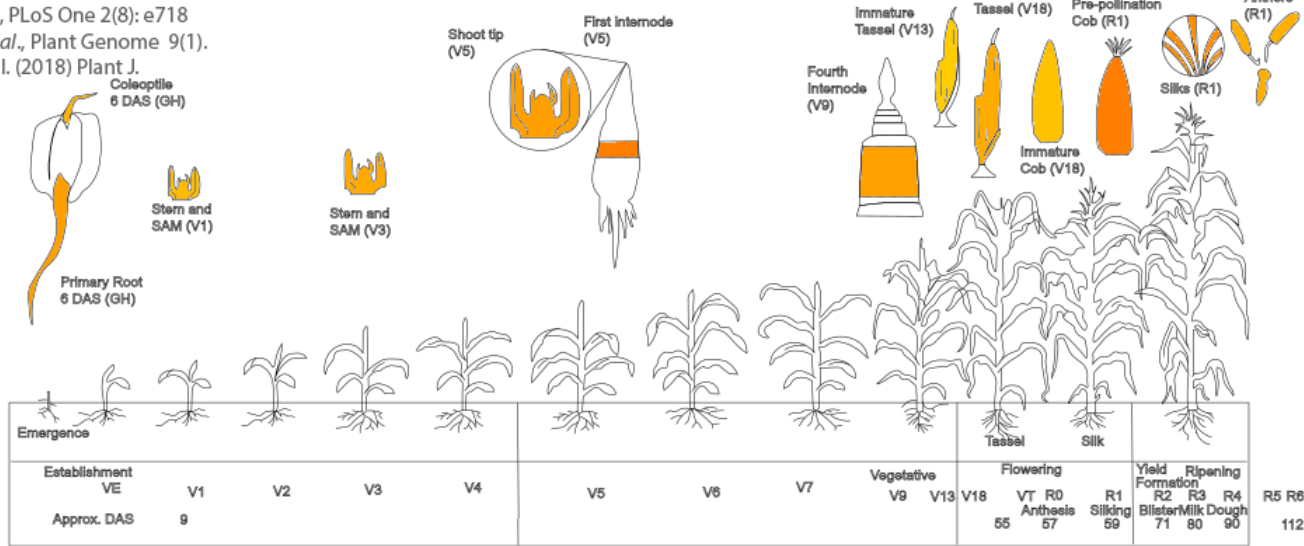
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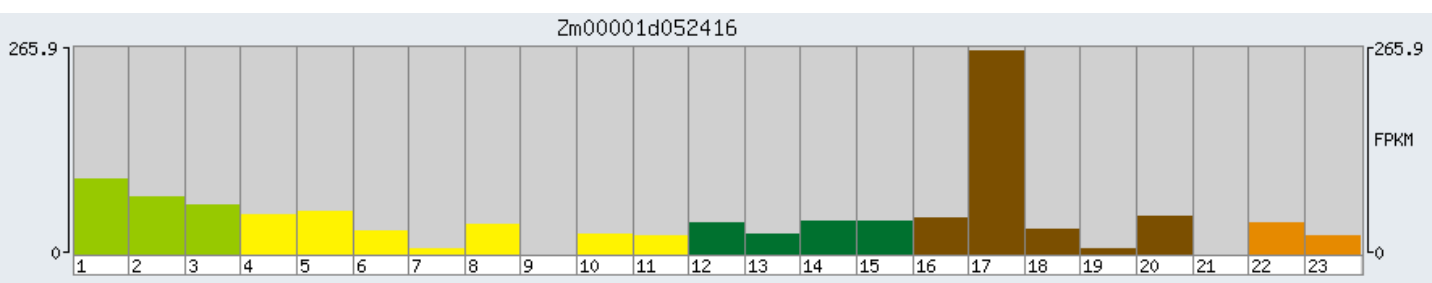
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Winter et al., PLoS One 2(8): e718  
 Stelpflug et al., Plant Genome 9(1).  
 Hoopes et al. (2018) Plant J.



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).



- |                              |                                    |  |
|------------------------------|------------------------------------|--|
| 1. 6-7_Internode (104.2)     | 9. Endosperm_Crown_27DAP (1.8)     | 17. Root_Cortex_5_Days (265.9)         |
| 2. 7-8_Internode (79.7)      | 10. Germinatin_Kernels_2DAI (32.6) | 18. Root_Elongation_Zone_5_Days (40.0) |
| 3. Meristem_16-19_Day (70.6) | 11. Pericarp/Aleurone_27DAP (31.6) | 19. Root_Meristem_Zone_5_Days (14.7)   |
| 4. Ear_Primary_2-4mm (57.9)  | 12. Leaf_Zone_1_Symmetrical (47.9) | 20. Secondary_Root_7-8_Days (56.9)     |
| 5. Ear_Primary_6-8mm (61.2)  | 13. Leaf_Zone_2_Stomatal (33.2)    | 21. B73_Mature_Pollen (NA)             |
| 6. Embryo_20DAP (36.3)       | 14. Leaf_Zone_3_Growth (50.5)      | 22. Female_Spikelet (46.7)             |
| 7. Embryo_38DAP (15.2)       | 15. Mature_Leaf_8 (50.1)           | 23. Silk (31.8)                        |
| 8. Endosperm_12DAP (46.4)    | 16. Primary_Root_5_Days (54.3)     |  |



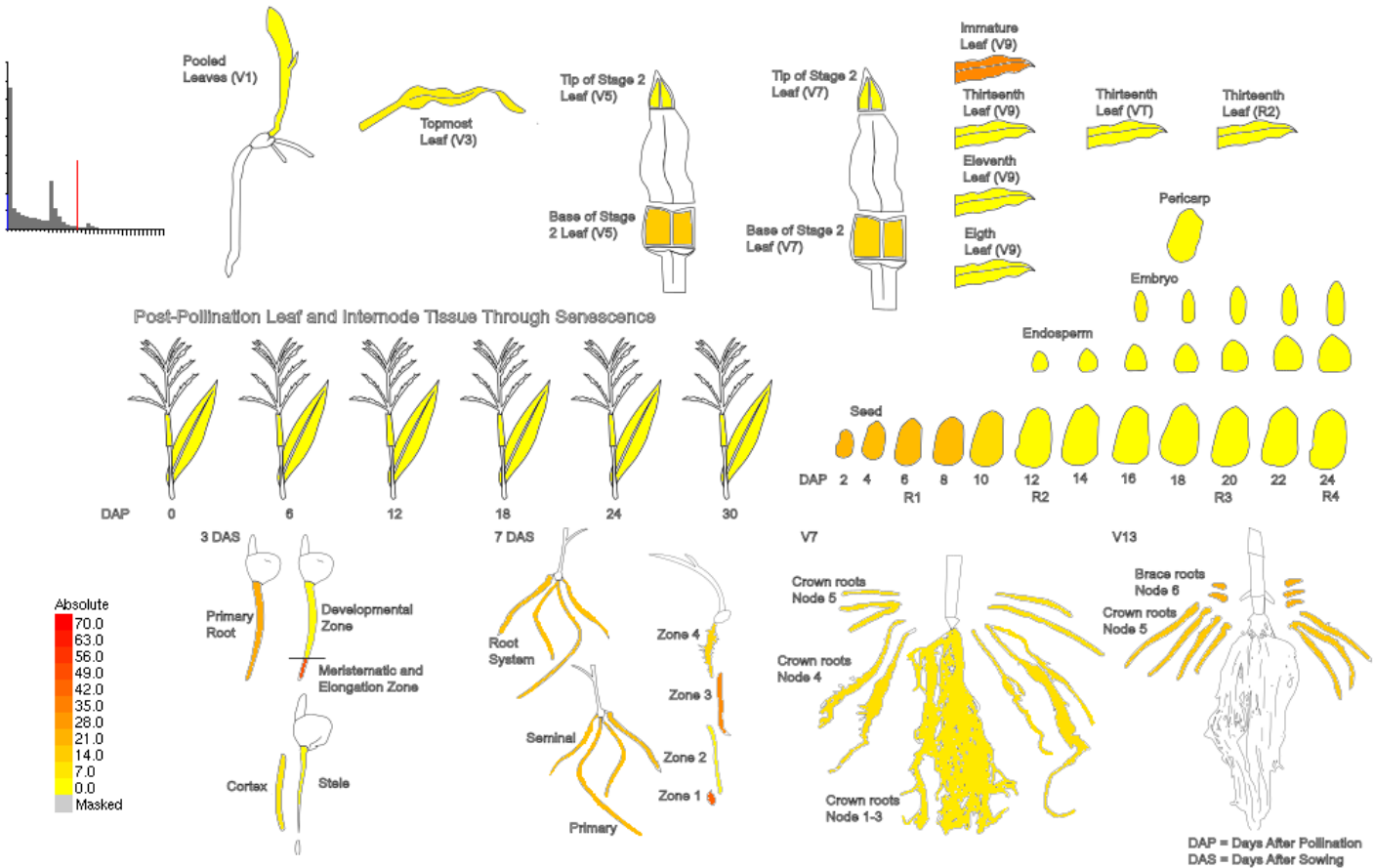
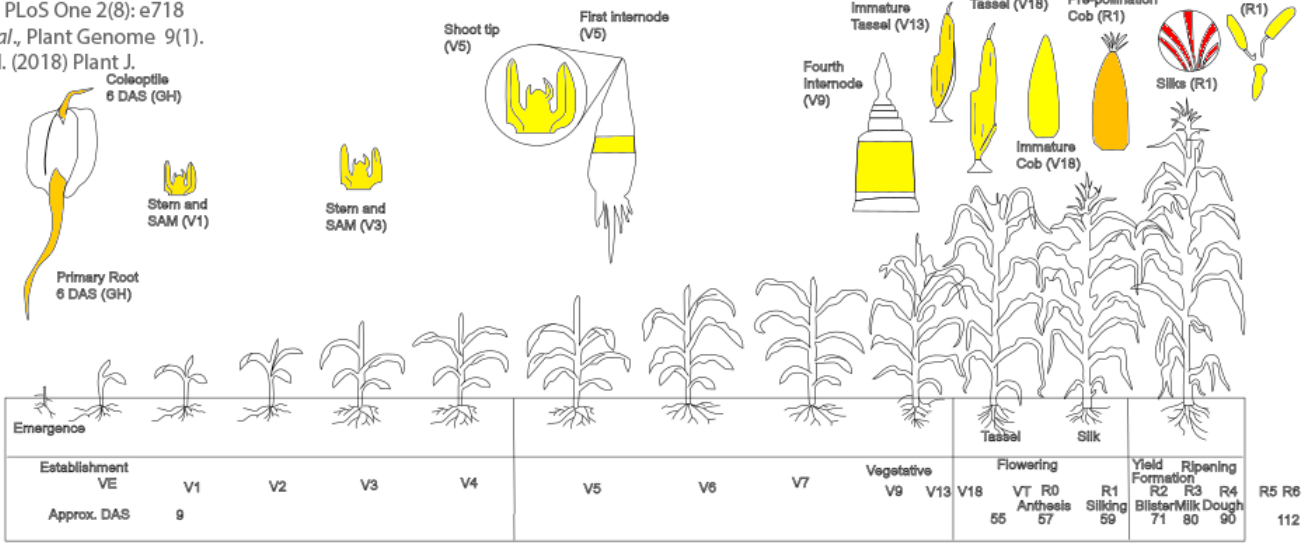
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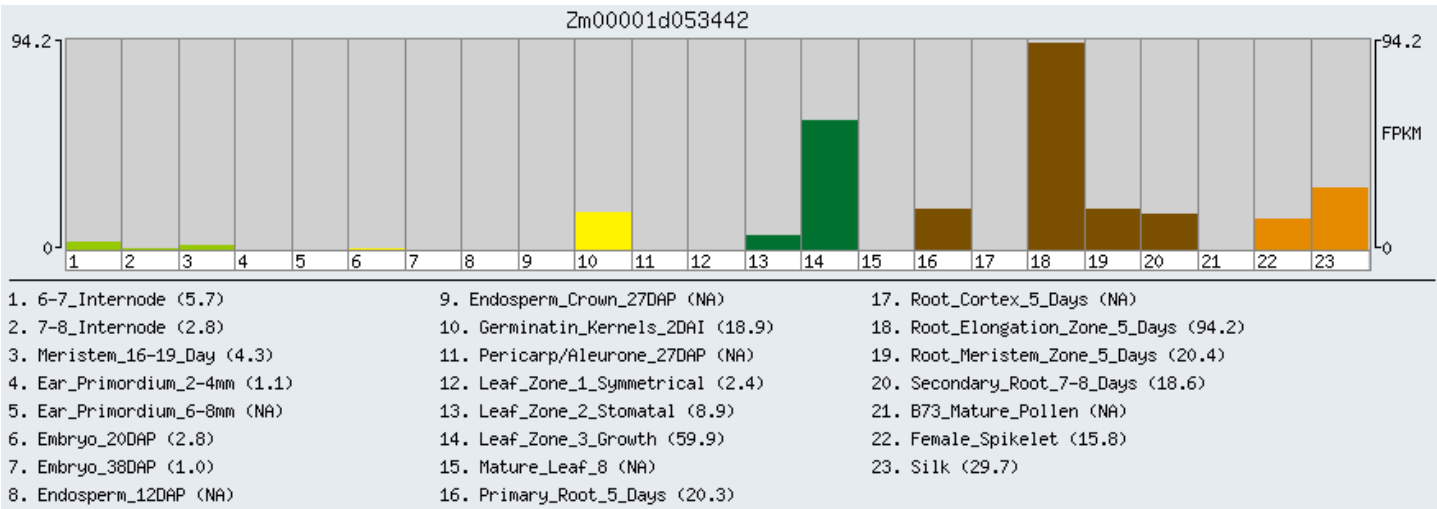
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Zm00001d053442

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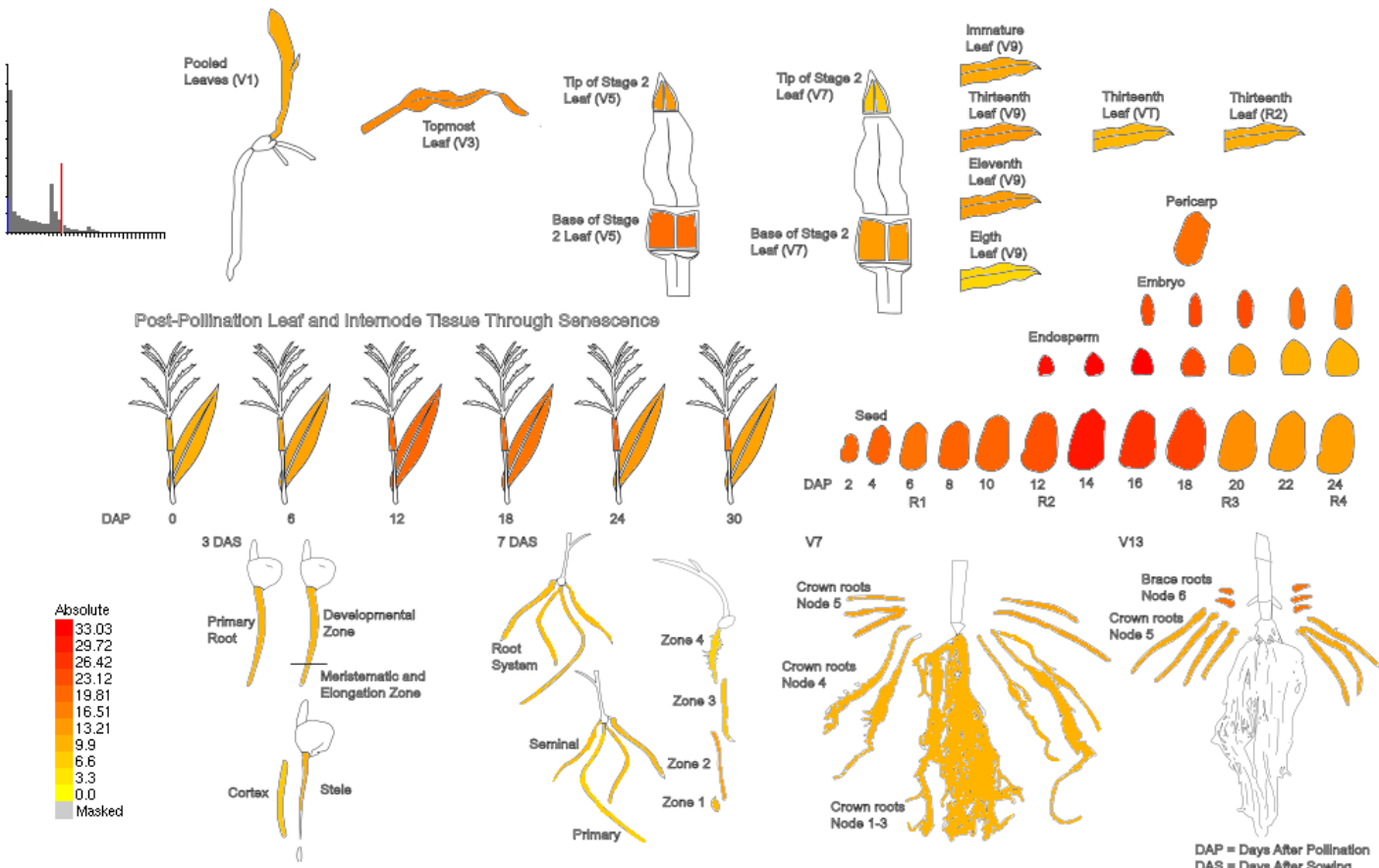
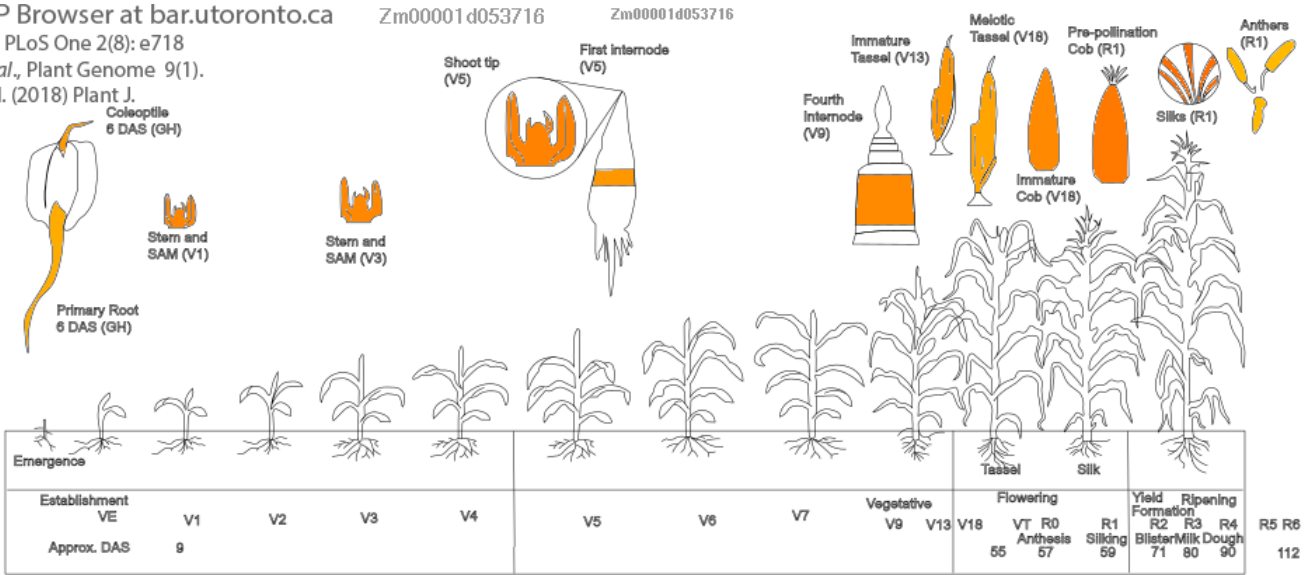
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Winter *et al.*, PLoS One 2(8): e718  
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