**Supplemental Figure S1.** Design of the aphid feeding experiments. The 2nd leaf of two-week-old B73 maize plants was enclosed in a cage. At staggered intervals, 10 adult *R. maidis* aphids were added to each cage. Leaf tissue was harvested after 2 to 96 h of aphid feeding. All samples were harvested within a 4 h time frame, with two sets of control samples at the beginning and end of harvest period, respectively. Harvested tissue was used for assays of gene expression by Illumina sequencing, as well as for metabolite profiling by GC/MS, LC/MS, and HPLC.
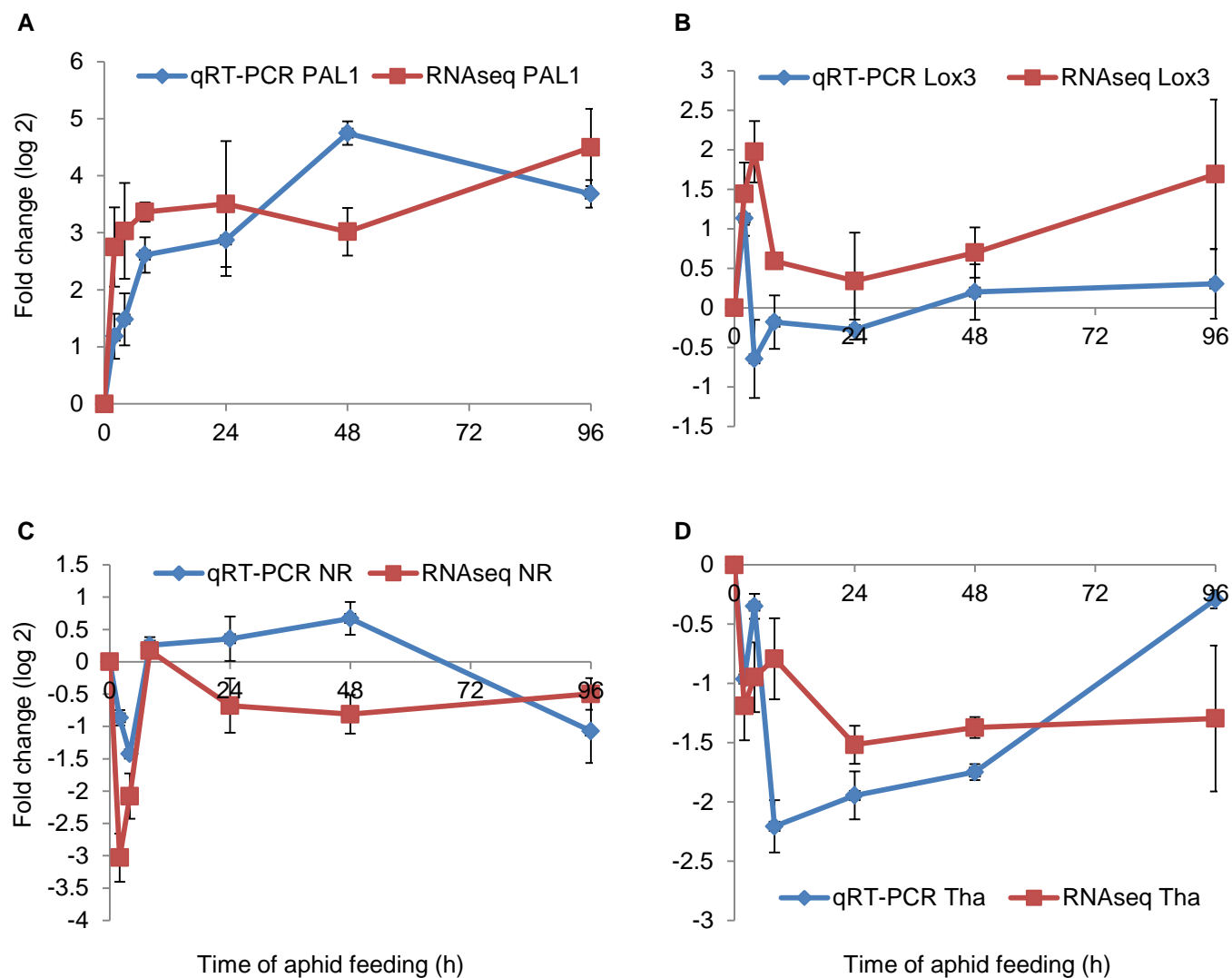
Supplemental Figure S2. Comparison of RNAseq and qRT-PCR gene expression data. The following genes were measured by qRT-PCR: A) GRMZM2G063917 Phe Ammonia-Lyase (*PAL*), B) GRMZM2G109130 Lipoxygenase3 (*Lox3*), C) GRMZM2G102959 Nitrite reductase (*NR*), and D) GRMZM2G346861 Thaumatin-like protein 1 (*Tha*). Mean +/- SE of n = 5. *$P < 0.05$ Student's t-test relative to uninfested controls, fold change in Log 2.
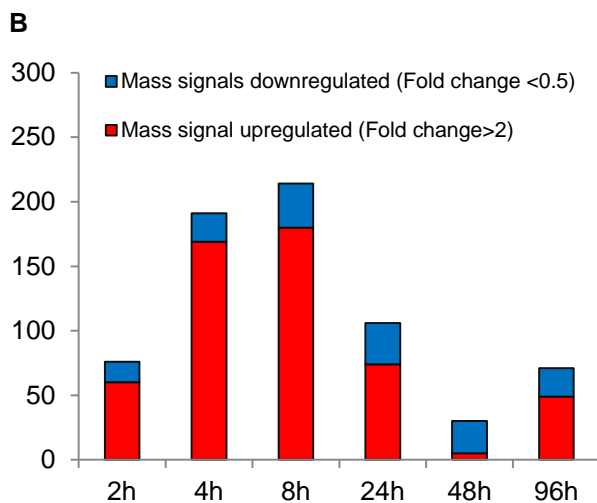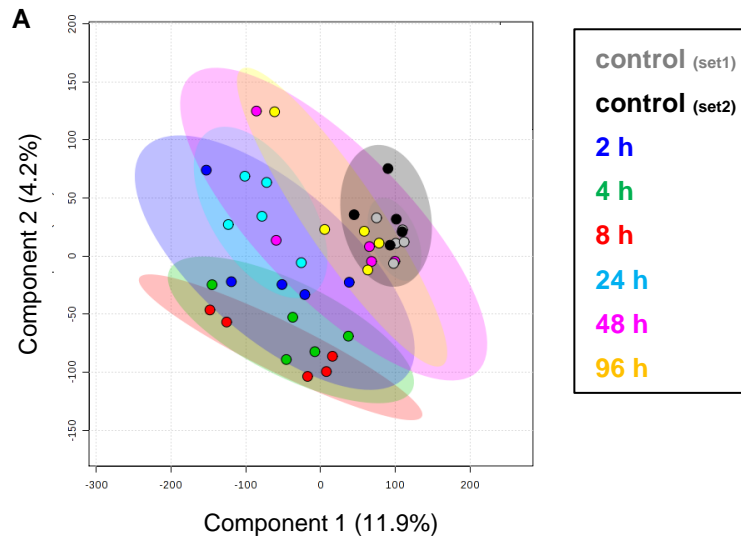
Supplemental Figure S3. Metabolites overview of aphids feeding on maize foliage. Partial least squares Discriminant Analysis (PLS-DA) plots of metabolites in maize inbred line B73 leaves infested with aphids for a time course of 0 to 96 hours. A) PLS-DA of 334 mass signals (positive ion mode). Ovals indicate 95% confidence intervals. B) Number of mass signals significantly different from aphid-free controls. $P < 0.05$ FDR and fold change > 2 or < 0.5.
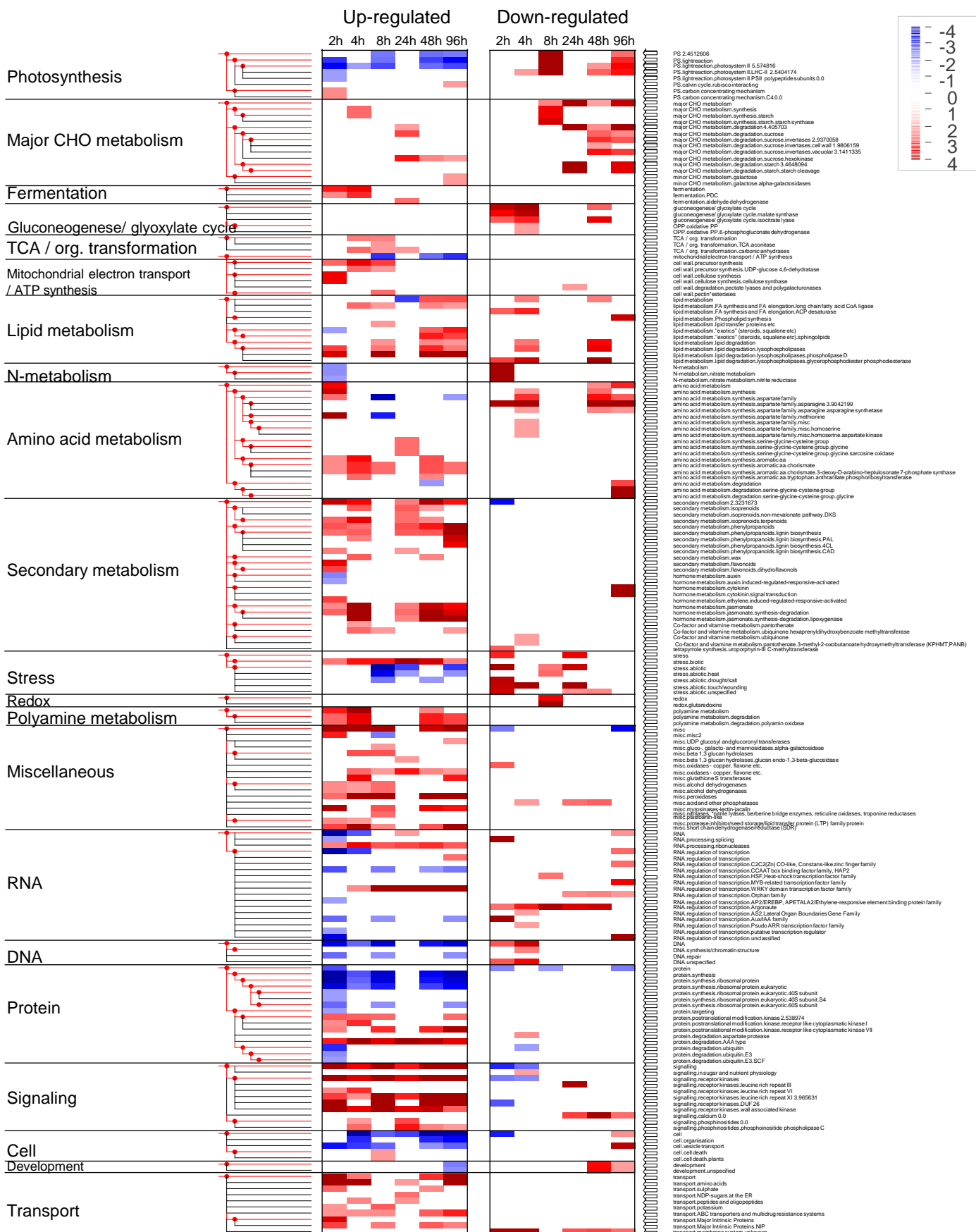
Supplemental Figure S4. Enriched terms of MapMan categories of significant differential genes altered by aphid feeding. Enrichment of each category was tested with Fisher's exact test. Red and blue boxes indicate categories that are overrepresented or underrepresented, respectively (α = 0.05). The figure was created with PageMan software and subsequently modified.
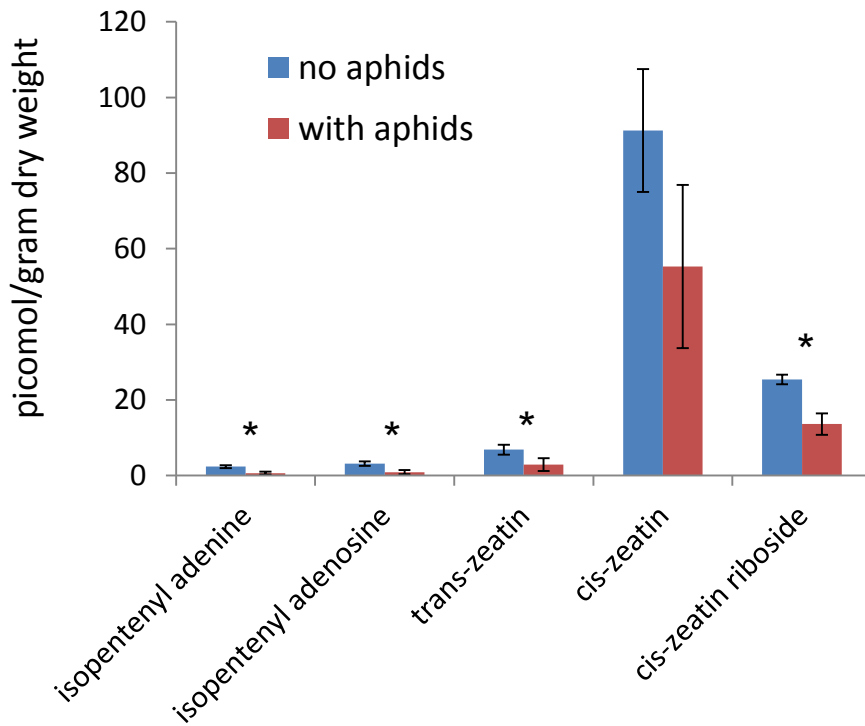
Supplemental Figure S5. Cytokinin content in maize leaves with or without ten days of aphid feeding. Mean +/- s.e. of n = 4, *$P < 0.05$, Student *t*-test.
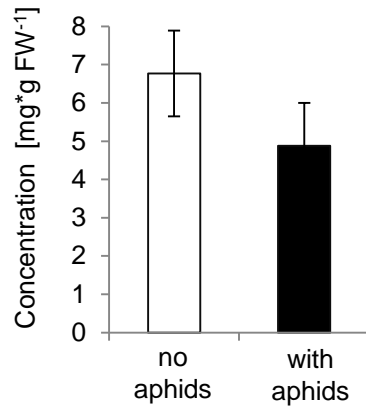
Supplemental Figure S6. DIMBOA-Glc content of wildtype W22, with and without aphid feeding for 7 days. Mean +/- s.e. of n = 4. No significant difference, $P > 0.05$.

Supplemental Figure S7. Comparison of TPS2 and TPS3 from B73 and W22 A) amino acid sequence. B) Genomic DNA sequence. Start = green highlights, exons = yellow highlights, stop = red highlights. Blue font = Ds insertion GSS name B.S08.0585_JSR05 flanking sequence.

A   **CLUSTAL 2.1 multiple sequence alignment - protein**

```
B73_TPS3      MYSLPGATMSAAPARVISSSSSSSFVEPLLLAAAS----SAAANSHHQVRQRGHLVRTLA 56
W22_TPS2/3    MYSLPGATMSAAPARVISSSSSS-FVEPLLLAAASPAA-AAAANSHHQVRQRGHLVRTLA 58
B73_TPS2      MYSLPGATMSAAPASIIS---SSSFVEPLLLAAASPAAAAAAANSHHQVRQRGHLVRTLA 57
              ************** :**    ** **********    :*******************


B73_TPS3      ASSSSNTLLRSDFDLQEGLTTDVKRMLRQRQKKSGGGREMLVTIDNLKRLCIDHFFEEEI 116
W22_TPS2/3    ASSSSNTLLRSDFDLQEGLTTDVKRMLRQR---SGGGREMLVTIDNLKRLCIDHYFEEEI 115
B73_TPS2      ASSSSNTLLRSDFDLQEGLTTDVKRMLRQRQKKSGGGREMLVTIDNLKRLCIDHYFEEEI 117
              *****************************    **********************:*****


B73_TPS3      EGAMATGACTRLLHSDDLFDATLAFRLLREAGHDVSAKEDVLRRFIDGVSGDFKLSLNND 176
W22_TPS2/3    EGAMATAACTGLLHSDDLFDATLAFRLLREAGHDVSAKDDVLRRFIDGVSGDFKISLSND 175
B73_TPS2      EGAMATGACTRLLHSDDLFDATLAFRLLREAGHDVSAKDDVLRRFIDGASGDFKLSLSND 177
              ******.*** ***************************:*********.*****:**.**


B73_TPS3      VRGLLGLHDMSHLDVGGEEAALLHRAKEFSSSHLASAVRYQDNPSLAEYVRQSLDHPYHL 236
W22_TPS2/3    VRGLLSLHDMSHLDVGG-EAALLHRAKEFSSRHLASAVRYLDDPSLAEYVRQSLDHPYHL 234
B73_TPS2      VRGLLSLHDMSHLDVGG-EAALLHRAKEFSSRHLASAVRYLDDPSLAEYVRQSLDHPYHL 236
              *****.*********** ************* ******** *:*****************


B73_TPS3      SLTQYKARHHLRYLQSLPSSCR-DAAVERLAVAEFQLNKSLHQREMREIKRWWMDLGLAE 295
W22_TPS2/3    SLTQYKARHHLRYLQSLPCSCRVDAAVERLAVAEFQLNKSLHQREMREIKRWWMDLGLAE 294
B73_TPS2      SLTQYKARHHLRYLQSLPS--R-DAAVERLAVAEFQLNKSLHQGEMREIKRWWMDLGLAE 293
              ******************.   * ********************* ***************


B73_TPS3      EIPVVRDQVMKWYMWSMAALQGSSFSRYR--------VYVVDDIFDLVGTLEELSAFTE 346
W22_TPS2/3    EIPVVRDQVMKWYMWSMAALQGSSFSRYRVEITKIISLVYVVDDIFDLVGTLEELSAFTE 354
B73_TPS2      EIPVVRDQVMKWYMWSMAALQGSSFSRYRVEITKIISLVYVVDDIFDLVGTLEELSAFTE 353
              ****************************            *********************


B73_TPS3      AVKMWDTAAADSLPSCMRSCYKALHTVTNEIAEIAHKEHGSNPINRLRKAWVVLFDGFMV 406
W22_TPS2/3    AVKMWDTVAADSLPSCMRSCYKALHTVTNEIAEIAHKEHGSDPINRLRKAWAVLFDGFMV 414
B73_TPS2      AVKMWDTVAADSLPSCMRSCYKALHTVTNEIAEIAQKEHGSNHVNRLRKAWAVLFDGFMV 413
              *******.***************************:*****: :*******.********


B73_TPS3      EARWLATDQVPTAEDYLRNGVVTSGVPLTFLHIFSMLGYDDP-STEEEEEAIIDHMPSII 465
W22_TPS2/3    EARWLATDQVPMAEDYLRNGVITSGVPLTFLHIFSMLGYDDDRSTEEEEEAIIDHMPSII 474
B73_TPS2      EARWLATDQVPTAEDYLRNGVITSGVPLTFMHIFSMLGYDDP-STEEEEEAIIDHMPSII 472
              *********** ********:********:*********    *****************


B73_TPS3      SCPAKILRLWDDMGSAE--DEAQEGFDGSYRDFYLMENPSRSPGEAEAHMRGLIAREWVE 523
W22_TPS2/3    SCPAKILRLWDDMGSAEVVDEAQEGFDGSYRDFYLMENPSRSPGEAEAHMRSLIMREWVE 534
B73_TPS2      SCPAKILRLWDDMGSAE--DEAQEGFDGSYRDFYLMENPSRSPGEAEAHMRGLIAREWEV 530
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B73_TPS3      LNRECFCRRTFPSDIAQVCLNTARMVSVMYSYNKEQRLLVLEDYAAMMLVL 574
W22_TPS2/3    LNRECFCRRTFPSDIAQVCLNTVRMVSVMYSYNKEQRLPVLEDYATMMLVV 585
B73_TPS2      LNRECFCRRTFPSNLVQVCLNTARMVSVMYSYNKEQRLPVLEDYAAMMLVL 581
              *************::.******.************** ******:****:
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B73_TPS3     ACTCGCCCTATAAATTGGAGGGCCTGCGCTCACCTCGATGCATATCACTCAC-------- 52
W22_TPS2/3   ACTCGCCCTATAAATTGGAGGGCCTGCGCTCACCTCGATGCATATCACTCACTCACACTC 60
B73_TPS2     ACTCGCCCTATAAATTGGAGGGCCTGCGCTCACCTGGATGCATATCACTCACTCACTCAC 60
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B73_TPS3     -----TCACAAGCAGGCACAGCTAGCTGCTCACAGCTATACATCGGCGCATCGCCATTA- 106
W22_TPS2/3   ACAACTCACAAGCAGGCACAGCTAGCTGCTCACAGCTATACATCGGCGCATCGCCATTA- 119
B73_TPS2     A----ACACAAGCAGGCACAGCTAGCTGCTCACAGCTATACATCGGCGCATCGCCATTAA 116
                  ******************************************************


B73_TPS3     ---GCAGCGGCTTGCTTTGGTTT-CTGATTGATTAGCTGGTTGTTGTTCAGTTAGTTCGA 162
W22_TPS2/3   ---CCAGCGGCTTGCTTTGGTTTTCTGATTGATTAGCTGGTTGTTGTCCAGTTAGTTCGA 176
B73_TPS2     TTAGCAGCGGCTTGCTTTGGTTT-CTGATTGATTAGCTGGTTGTTGTTCAGTTAGTTCGA 175
                ******************* ********************** ***********


B73_TPS3     GTAGTAGACGATGTACTCTCTACCAGGAGCAACCATGTCTGCTGCACCTGCACGCGTCAT 222
W22_TPS2/3   GTAGTAGACGATGTACTCTCTACCAGGAGCAACCATGTCTGCTGCACCTGCACGCGTCAT 236
B73_TPS2     GTAGTAGACGATGTACTCTCTACCAGGAGCAACCATGTCTGCTGCACCTGCAAGCATCAT 235
             *************************************************** ** ****


B73_TPS3     CTCTTCCTCCTCCTCCTCCTCCTTCGTGGAGCCTCTTCTCCTTGCAGCAGCTTCGTCGG- 281
W22_TPS2/3   CTCTTCTTCCTCCTCCTCCT---TCGTGGAGCCTCTTCTCCTTGCAGCAGCTTCGCCGGC 293
B73_TPS2     CTCTTCTTCCTCCT---------TCGTGGAGCCTCTTCTCCTTGCAGCAGCTTCGCCGGC 286
             ****** *******       ************************* ***


B73_TPS3     --------CGGC---TGCAAACAGCCACCACCAAGTCCGCCAGCGCGGCCACTTGGTCCG 330
W22_TPS2/3   GGCGGCGGCGGC---TGCAAACAGCCACCACCAAGTCCGCCAGCGCGGCCACTTGGTCCG 350
B73_TPS2     GGCGGCAGCGGCAGCTGCAAACAGCCACCACCAAGTCCGCCAGCGCGGCCACTTGGTCCG 346
                  ****   *****************************************


B73_TPS3     TACTTTGGCGGCATCATCGTCGTCCAACACGCTGCTGCGGAGTGACTTCGATCTCCAGGT 390
W22_TPS2/3   TACTTTGGCGGCATCATCGTCGTCCAACACGCTGCTGCGGAGTGACTTCGATCTCCAGGT 410
B73_TPS2     TACTTTGGCGGCATCATCGTCGTCCAACACGCTGCTGCGGAGTGACTTCGATCTCCAGGT 406
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B73_TPS3     AGCTATCCTGCTGCCTAGCAAAGACATGTCCATTTATTCTTCTTCTTCTTCATACATCAC 450
W22_TPS2/3   AGCTATCCAGC---CTAGCAAAGACATGTCCATTTCTTCTTCTTCTTCTTCATACATCAC 467
B73_TPS2     AGCTATCCTGC---CTAGCAAAGACATGTCCATTTCTTCTTC--CTTCTTCGTACATCAC 461
             ******** **   ********************* ******   ******* *******


B73_TPS3     CACATGCATGC--------ATGCATGTCCTCACTCTCCATACATGAAACATACATATGTA 502
W22_TPS2/3   CACATGCATGCATGCATGCATGCATGTCCTCACTCTCCATACATGAAACATACATATGTA 527
B73_TPS2     CACATGCATGC--------ATGCATGTCCTCACTCTCCATACATGAAACATACATATGTA 513
             ***********        *****************************************


B73_TPS3     CGTACGTAGGAGGGCCTGACGACGGACGTCAAACGGATGCTGCGTCAGCGTCAGAAGAAG 562
W22_TPS2/3   CGTACGTAGGAGGGCCTGACGACGGACGTGAAACGGATGCTGCGTCAGCGT--------- 578
B73_TPS2     CGTACGTAGGAGGGCCTGACGACGGACGTCAAACGGATGCTGCGTCAGCGTCAGAAGAAG 573
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B73_TPS3     AGCGGCGGCGGGCGGGAGATGCTGGTCACCATCGACAACCTCAAGCGCCTCTGCATCGAC 622
W22_TPS2/3   AGCGGCGGCGGGCGGGAGATGCTGGTCACCATCGACAACCTCAAGCGCCTCTGCATCGAC 638
B73_TPS2     AGCGGCGGCGGGCGGGAGATGCTGGTCACCATCGACAACCTCAAGCGCCTCTGCATCGAC 633
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B73_TPS3     CACTTCTTCGAGGAAGAGATCGAGGGCGCCATGGCGACGGGCGCCTGCACGCGTCTCCTC 682
W22_TPS2/3   CACTACTTCGAGGAAGAGATCGAGGGCGCCATGGCGACGGCCGCCTGCACGGGTCTCCTC 698
B73_TPS2     CACTACTTCGAGGAAGAGATCGAGGGCGCCATGGCGACGGGCGCCTGCACGCGTCTCCTC 693
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B73_TPS2    CACAGCGACGACCTCTTCGACGCAACCCTCGCGTTCAGGCTCCTGAGAGAGGCAGGACAC 753
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B73_TPS3    GATGTCTCAGCAAGTTAGTAGTGATAAACACCCAGTAC----TACACACAGCAGACGAAA 798
W22_TPS2/3  GATGTCTCAGCAAGTTAGTAGTGATAAAAACCAAGTACATACTACACACAGCAGACGAAA 818
B73_TPS2    GATGTCTCAGCAAGTTAGTAGTGATAAACACCCAGTAC----TACACACAGCAGACGAAA 809
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B73_TPS3    GAAGAAAGAAATTAAACATCTCGTCGTCGTCGTCGTCCATGTGCA------TCTGCAGAA 852
W22_TPS2/3  GAAGAAAGAAATTAAACATCTCGTCGTCGTCGTCGTCCATGTGCATGTGCATCTGCAGAA 878
B73_TPS2    GAAGAAAGAAATTAAACATCTCGTCGTCGTCGTCGTCCATGTGCA------TCTGCAGAA 863
            *********************************************      *********

B73_TPS3    GAGGATGTTCTACGGAGGTTCATCGACGGCGTCAGCGGCGACTTCAAGCTATCTCTGAAC 912
W22_TPS2/3  GACGATGTTCTACGGAGGTTCATCGACGGCGTCAGCGGCGACTTCAAGATATCTCTGAGC 938
B73_TPS2    GACGATGTTCTACGGCAGGTTCATCGACGGCGCCAGCGGCGACTTCAAGCTATCTCTGAGC 923
            ** ***********  **************** **************** ********* *

B73_TPS3    AACGACGTCAGAGGGCTCCTGGGCCTGCACGACATGTCCCACCTGGACGTGGGAGGGGAG 972
W22_TPS2/3  AACGACGTCAGAGGGCTCCTGAGCCTGCACGACATGTCCCACCTGGACGTGGGAGGGGAG 998
B73_TPS2    AACGACGTCAGAGGGCTCCTGAGCCTGCACGACATGTCCCACCTGGACGTGGGAGGGGAG 983
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B73_TPS3    GAGGCGGCGCTGCTCCACAGGGCCAAGGAGTTCTCGAGCAGCCACCTCGCGTCCGCCGTC 1032
W22_TPS2/3  G---CGGCGCTGCTCCACAGGGCCAAGGAGTTCTCGAGCAGGCACCTCGCGTCCGCCGTC 1055
B73_TPS2    G---CGGCGCTGCTCCACAGGGCCAAGGAGTTCTCGAGCAGGCACCTCGCGTCCGCCGTC 1040
            *      ********************************** *****************

B73_TPS3    AGGTACCAGGACAACCCTAGCCTCGCGGAGTACGTGCGGCAGTCCCTGGACCACCCCTAC 1092
W22_TPS2/3  AGGTACCTGGACGACCCTAGCCTCGCGGAGTACGTGCGGCAGTCCCTGGACCACCCCTAC 1115
B73_TPS2    AGGTACCTGGACGACCCTAGCCTCGCGGAGTACGTGCGGCAGTCCCTGGACCACCCGTAC 1100
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B73_TPS3    CACCTCAGCCTGACGCAGTACAAGGCCAGGCATCACCTCCGCTACCTGCAGAGCCTGCCC 1152
W22_TPS2/3  CACCTCAGCCTCACGCAGTACAAGGCCAGGCATCACCTCCGCTACCTGCAGAGCCTGCCC 1175
B73_TPS2    CACCTCAGCCTGACGCAGTACAAGGCCAGGCATCACCTCCGCTACCTGCAGAGCCTGCCC 1160
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B73_TPS3    TCCAGCTGCAGA---GACGCCGCCGTGGAGAGACTCGCAGTTGCCGAGTTCCAGCTCAAC 1209
W22_TPS2/3  TGCAGCTGCAGAGTCGACGCCGCCGTGGAGAGACTCGCGGTTGCCGAGTTCCAGCTCAAC 1235
B73_TPS2    TCCAG----AGA-----CGCCGCCGTGGAGAGACTCGCAGTTGCCGAGTTCCAGCTCAAC 1211
            * ***     ***     ******************** ********************

B73_TPS3    AAGTCGCTGCATCAGAGAGAGATGCGAGAGATTAAAAGGTACGTGTAAACGATCTTGTGT 1269
W22_TPS2/3  AAGTCGCTGCATCAGAGAGAGATGCGAGAGATTAAAAGGTACGTGTAAACGATCTTGTGT 1295
B73_TPS2    AAGTCGCTGCATCAGGGAGAGATGCGAGAGATTAAAAGGTACGT---------------- 1255
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W22_TPS2/3  TAGCTAGCTAGATCAGTTGACATGATATATTGTTTCGATTCTTCAGCAGTTTATGTAACT 1355
B73_TPS2    ------------------ACGTG-------------------------------------T 1261
                              ** **                                    *

B73_TPS3    AAAAAGAAAAAAAA---TACTCCCTTCGCACCAAAATAATATATAGTATGTTATAGGGTG 1386
W22_TPS2/3  AAAAAGAAAAAAAAAGATACTCCTTTCGCACCAAAATAATATATAGTATGTTATAGGGTG 1415
B73_TPS2    AAAG-------------------------------------------------------- 1265
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B73_TPS3    TTAATAGTAGCTAGATTCATACAATATTTAATATATATACGTGTCTATATATTTATCGTC 1446
W22_TPS2/3  TTAATAGTAGCTACATTCATACAATATTTAATATATGTACGTGTCTATATATTTATCGTC 1475
B73_TPS2    ---------------------------------------------------------GTC 1268
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B73_TPS3     ATCTATTTGAATCTGGACACAAAAA-TTCGGAGCTAGAACGAACAATAAAAAAATTATTT 1505
W22_TPS2/3   ATCTATTTGAATCTGGACATAAAAA-TTTGGAGCTAGAACGAACAATAAAAAAATTATTT 1534
B73_TPS2     ATCTATTTGAATCTGGACACAAAAAATTTGGAGCTAGAACGAACAATAA----------- 1317
             ******************* ***** ** *******************


B73_TPS3     GCCAAGCGTGAGTGGCGTATTTTTTTCTTCTTCTCTTCTTTTGTTTGAGTTACAAAATGG 1565
W22_TPS2/3   GCCAAGCGTGAGTGGCGTATTTTTTTCTTCTTCTCTTCTTTTGTTTGAGTTACAAAATAG 1594
B73_TPS2     ------------------------------------------------------------


B73_TPS3     TGAGTGGCATATATT-TTTTTCTTCTTCTTTTGTTTATGAGTTACAAAATGGTGAGATAT 1624
W22_TPS2/3   TGAGTGGCATATATTATTTTTCTTCTTCTTTTGTTTATGAGTTACAAAATGGTGAGATAT 1654
B73_TPS2     -------------TTTTTTTTCTTCTTCTTCTGTTTATGAGTTACATAATGGTGAGATAT 1364
                          ** ************* *************** ************


B73_TPS3     TTGATCAACAAATATATATAATGTGATCGATGCAGGTGGTGGATGGACCTAGGGTTGGCT 1684
W22_TPS2/3   TTGATCAACAAATATATATAATGTGATCGATGCAGGTGGTGGATGGACCTAGGGTTGGCT 1714
B73_TPS2     TTGATCAACAAATATATATAATGTGATCGATGCAGGTGGTGGATGGACCTAGGGTTGGCT 1424
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B73_TPS3     GAAGAAATACCTGTGGTACGGGATCAGGTGATGAAATGGTACATGTGGTCCATGGCAGCA 1744
W22_TPS2/3   GAAGAAATACCTGTGGTGCGGGATCAGGTGATGAAATGGTACATGTGGTCCATGGCAGCC 1774
B73_TPS2     GAAGAAATACCTGTGGTGCGGGATCAGGTGATGAAATGGTACATGTGGTCCATGGCAGCC 1484
             ***************** ******************************************


B73_TPS3     CTCCAAGGATCTTCTTTCTCCAGATACCGGGTC-------------------------- 1777
W22_TPS2/3   CTCCAAGGATCTTCCTTCTCCAGATACCGGGTCGAGATCACCAAGATAATCTCGCTTGTT 1834
B73_TPS2     CTCCAAGGATCTTCCTTCTCCAGATACCGGGTCGAGATCACCAAGATAATCTCGCTTGTT 1544
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B73_TPS3     TACGTCGTGGACGACATATTCGATCTCGTTGGCACCCTGGAGGAGCTCTCCGCCTTCACC 1837
W22_TPS2/3   TACGTCGTCGACGACATATTCGACCTAGTTGGCACCTTGGAGGAGCTCTCCGCCTTCACC 1894
B73_TPS2     TACGTCGTCGACGACATATTCGACCTCGTTGGCACCCTGGAGGAGCTCTCCGCCTTCACC 1604
             ******** ************** ** ********* ********* *********************


B73_TPS3     GAGGCAGTCAAAATGTAAGTAGTAGTAAATTTAAACTATATATATGTGTCTAGAAATTAA 1897
W22_TPS2/3   GAGGCAGTCAAAATGTAAGTAGTAGTAAATTTAGACTATATATATGTGTCTAGAAATTAA 1954
B73_TPS2     GAGGCAGTCAAAATGTAAGTAGTAGTAAATTTAGACTATATATATGTGTCTAGAAATTAA 1664
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B73_TPS3     TTAAAAGCTATACAACCACAATTAACATAGTAGTAAATATTGTTTTAGAGTGAAGGGGAA 1957
W22_TPS2/3   TTAAAAGCTATACAACCACAATTAACATAGTAGTAAATATTGTTTTAGAGTGAAGGGGAA 2014
B73_TPS2     TTAAAAGCTATACAACCACAATTAACATAGTAGTAAATATTGTTTTAGAGTGAAGGGGAA 1724
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B73_TPS3     ATAGCTAGTAAA----------------------------------------CAATGCTAA 1978
W22_TPS2/3   ATAGCTAGTAAATATTGTTGTTGTTGTTGTTGTTGTTGTTGTTAATTTAAACAATGTTAA 2074
B73_TPS2     ATAGCTAGTAAATATTGTTGTTGTTGTTGTTGTTGTTGTTGTTAATTTAAACAATGTTAA 1784
             ************                                        ***** ***


B73_TPS3     TATATATGAGAAAAAAACCCACAACATTGGCTGCAGGTGGGATACTGCGGCTGCTGATTC 2038
W22_TPS2/3   TATATATGAGAAAAA-CCCACAACACTGGCTGCAGGTGGGATACTGTGGCTGCTGATTC 2133
B73_TPS2     TATATATGAGAAAAA-CCCACAACACTGGCTGCAGGTGGGATACTGTGGCTGCTGATTC 1843
             *************** ********* *************************** ************


B73_TPS3     ACTTCCCAGTTGCATGAGATCATGCTATAAGGCCCTCCACACCGTTACGAACGAGATCGC 2098
W22_TPS2/3   ACTTCCTAGTTGCATGAGATCATGCTATAAGGCCCTCCACACCGTTACGAACGAGATCGC 2193
B73_TPS2     ACTTCCCAGTTGCATGAGATCATGCTATAAGGCCCTCCACACCGTTACGAACGAGATCGC 1903
             ****** *****************************************************


B73_TPS3     AGAGATTGCCCACAAGGAGCATGGATCTAACCCTATCAATCGTCTCAGGAAAGCAGTATG 2158
W22_TPS2/3   AGAGATTGCCCACAAGGAGCATGGATCTGACCCTATCAATCGTCTCAGGAAAGCAGTATG 2253
B73_TPS2     AGAGATTGCCCAGAAGGAGCATGGATCTAACCATGTCAATCGTCTTAGGAAAGCAGTATG 1963
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B73_TPS3    TTCATAAACACCTTTATCTTATGTATGCTTCTCTTCGGTTTGATCAAGACAAACATTCAT 2218
W22_TPS2/3  TTCATAAACACCTTTATCTTATGTATGCTTCTCTTCAGTTTGATCAAGACAAACATCCAT 2313
B73_TPS2    TTCATAAACACCTTTATCTTATGTATGCTTCTCTTCAGTTTGATCAAGACAAACATCCAT 2023
            ***********************************  ******************* ***


B73_TPS3    AAATAAATAAA---AAATATACCAGTTGATTTAAAACTGGTTAAAATGATTCATAAATAA 2275
W22_TPS2/3  AAATAAATAAA---AAATATACCAGTTGATTTAAAACTGGTTAAAACGATTCATAAATAA 2370
B73_TPS2    AAATAAATAAATAAAAATATACCAGTTGATTTAAAACTGGTTAAAATGATTCATAAATAA 2083
            **********    ********************************* ************


B73_TPS3    ATCAGTTTCCTGCTGCTAATGATCGAGCAACTGCTTACGCTAGCTAGAAATCCAACAACG 2335
W22_TPS2/3  ATCAGTTTACTGCTGCTAATGATCGAGCAACTGCTAAAGCTAGCTAGAAATTCAACAACG 2430
B73_TPS2    ATAAGTTTACTGCTGCTAATGATCGAGCAACTCCTAACGCTAGCTACAAAT-------CG 2136
            ** ***** ********************** ** * ******** ****       **


B73_TPS3    TAACTTTGTGTAGTGGGTGGTGCTGTTCGACGGTTTCATGGTTGAGGCGAGATGGCTAGC 2395
W22_TPS2/3  TAACTTTGTGCAGTGGGCGGTGCTGTGTTTGACGGTTTCATGGTTGAGGCGAGATGGCTAGC 2490
B73_TPS2    TAACTTTGTGCAGTGGGCGGTGTTGTTCGACGGTTTCATGGTTGAGGCGAGATGGCTAGC 2196
            ********** ****** **** **** ********************************


B73_TPS3    GACCGACCAGGTCCCTACGGCGGAGGACTACCTACGAAATGGCGTCGTCACATCAGGAGT 2455
W22_TPS2/3  GACCGACCAGGTCCCTATGGCGGAGGACTACCTACGAAACGGCGTCATCACATCAGGAGT 2550
B73_TPS2    GACCGACCAAGTCCCTACGGCGGAGGACTACCTACGAAACGGCGTCATCACATCAGGAGT 2256
            ********* ******* ********************** ****** ************


B73_TPS3    GCCGCTCACATTTCTGCACATATTCAGCATGCTAGGGTATGATGAC---CCAAGCACCGA 2512
W22_TPS2/3  GCCACTCACATTTCTGCACATATTCAGCATGCTAGGGTATGATGACGATCGAAGCACCGA 2610
B73_TPS2    GCCGCTCACATTTATGCACATATTCAGCATGCTAGGGTATGATGAC---CCAAGCACCGA 2313
            *** ********* ********************************   * *********


B73_TPS3    GGAAGAAGAAGAAGCGATCATCGACCACATGCCCTCGATCATCTCCTGCCCAGCCAAGAT 2572
W22_TPS2/3  GGAAGAAGAAGAAGCGATCATCGACCACATGCCCTCGATCATCTCCTGCCCGGCCAAGAT 2670
B73_TPS2    GGAAGAAGAAGAAGCGATCATCGACCACATGCCCTCAATCATCTCCTGCCCAGCCAAGAT 2373
            ************************************ ************** *******


B73_TPS3    CCTCAGGCTCTGGGATGACATGGGCAGCGCAGAGGTCGTTGTTAGTTCGTCGAACCATAC 2632
W22_TPS2/3  CCTCAGGCTCTGGGATGACATGGGCAGCGCAGAGGTCGTTGTTAGTTCGTCGAACCATAC 2730
B73_TPS2    CCTCAGGCTCTGGGATGACATGGGCAGCGCAGAGGTCGTCGTTAGTTCATCGAACCATAC 2433
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B73_TPS3    ACTACATA--CTAGCTTGTTAATTAAATGCTTTTACCTTCAAATTTTGCAATCCAATCAT 2690
W22_TPS2/3  ACTACATA--CTAGCTTGTTAATTGAATGCTTTTACCTTCAAATTTTGCAATCCAATCAT 2788
B73_TPS2    ACTACATATACTAGCTTGTTAATTAAATGCTTTTACCTTTAAATTTTGCAATCCAATCGT 2493
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B73_TPS3    ACTTGATGTGTGCATGGGCTTTGCAGGATGAGGCTCAGGAAGGATTCGATGGGTCTTACA 2750
W22_TPS2/3  ACTTGATGTGTGCATGGGCTTTGCAGGATGAGGCTCAAGAAGGATTCGATGGGTCGTACA 2848
B73_TPS2    ACTTGATGTGTGCATGGGCTTTGCAGGATGAGGCTCAGGAAGGATTCGATGGGTCGTACA 2553
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B73_TPS3    GGGACTTCTACCTCATGGAGAACCCTAGCCGCAGCCCCGGCGAGGCGGAAGCGCACATGC 2810
W22_TPS2/3  GGGACTTCTACCTCATGGAGAACCCTAGCCGCAGCCCCGGCGAGGCGGAAGCGCACATGC 2908
B73_TPS2    GGGACTTCTACCTCATGGAGAACCCTAGCCGCAGCCCCGGCGAGGCGGAAGCGCACATGC 2613
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B73_TPS3    GCGGCCTGATCGCGAGGGAGTGGGTGGAGCTCAACAGGGAGTGCTTCTGCCGGAGGACCT 2870
W22_TPS2/3  GCAGCCTGATCATGAGGGAGTGGGTGGAGCTCAACAGGGAGTGCTTCTGCAGGAGGACCT 2968
B73_TPS2    GCGGCCTCATCGCGAGGGAGTGGGAGGTGCTCAACAGGGAGTGCTTCTGCAGGAGGACCT 2673
            ** **** ***  ********** * ** ******************** *********
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B73_TPS3    TCCCCTCGGACATCGCGCAGGTCTGCTTGAACACCGCCAGGATGGTCAGCGTCATGTACT 2930
W22_TPS2/3  TCCCCTCGGACATCGCGCAGGTCTGCTTGAACACCGTGAGGATGGTCAGCGTCATGTACT 3028
B73_TPS2    TCCCCTCGAACCTCGTGCAGGTCTGCTTGAACACCGCGAGGATGGTCAGCGTCATGTACT 2733
            ******** ** *** ******************* ********************

B73_TPS3    CGTACAACAAGGAGCAGAGGCTTCTCGTCCTCGAGGACTACGCGGCGATGATGTTGGTGC 2990
W22_TPS2/3  CGTACAACAAGGAGCAGAGGCTTCCCGTCCTCGAGGACTACGCGACGATGATGTTGGTGG 3088
B73_TPS2    CGTACAACAAGGAGCAGAGGCTTCCCGTCCTCGAGGACTACGCGGCGATGATGTTGGTGC 2793
            *********************** ***************** **************

B73_TPS3    TTTGATTTGAAGCATGCATGCATGCATTTGCTCTCTCCGATCCGCGGATATGAAAGTAAA 3050
W22_TPS2/3  TTTGATTTGAAGCATGCATGCATGCAAT-GCTCTCTCCGATCCGCGGATATGAAAGTAAA 3147
B73_TPS2    TTTGATTTGAAGCATGCATGCATGCATT-GCTCTCTCCGATCCGCAGATATGAAAGTAAA 2852
            ************************* * *************** **************

B73_TPS3    G---TAGTGATTAGGTTGATGATTTGTTTTGAGACCA--GTAATGTAGAGTAGCGATTAG 3105
W22_TPS2/3  GTCCTTGTCATGCAGATAATGATTTGTTTTGAGACCAGAGTAGTCTAGAGTAGAGATTAG 3207
B73_TPS2    GTCCATGTCATGCAGATGATGATTTGTTTTGAGACCA--GTAGTGTAGAGTAGATATTAG 2910
            *       ** **    * * ***************** *** * ******** *****

B73_TPS3    GTTGTGTAAAATTAGATAGCTAGGATTAGAATAACTGGGCAAACGAATA--TGGTATGTG 3163
W22_TPS2/3  GCTCTGTAAAATTAGATAGCTAGGATTAGAATAACTGGGCAAACGAATATATGGTATATG 3267
B73_TPS2    GTTGTGTAAAATTAGATAGTTGTGATTAGAATAATTGGGCAAACGAATA--TGGTAT--- 2965
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B73_TPS3    TCCATATGTAATGATGCAATATATAGCAACATATATGGTATCGGCGTTATTATCTT-TTT 3222
W22_TPS2/3  TCCATATGTAAAGATGCAATATATAGCAACATATATGGTACCGTCGTTATTATCTT-TTT 3326
B73_TPS2    -------GTAAAGATGCAATATATAGCAACATATATGGTACCGTCGTTATTATTATATTT 3018
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B73_TPS3     CTTTCAAAAAA-TGTAATAATATTCACATATGCAGTGCAATGTAATATGG 3271
W22_TPS2/3   --TTCAAAAAA-TGTAATAATATTCAAATATGCAGTGCAATGTAATATGG 3373
B73_TPS2     TTTTCAAAAAAATGTAATAATATTAAAAATATGCAATGCAATGTAATATGG 3068
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