

In-silico* genome wide analysis of Mitogen Activated Protein Kinase Kinase Kinase gene family in *C. sinensis

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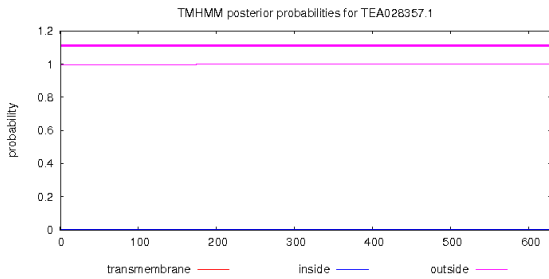
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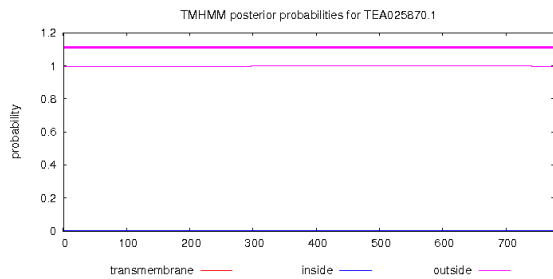
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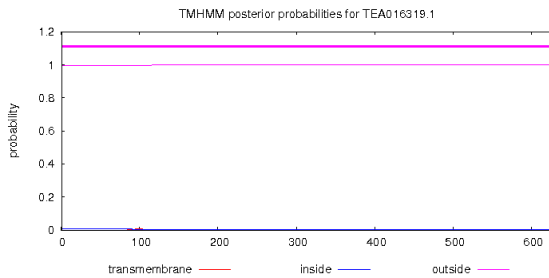
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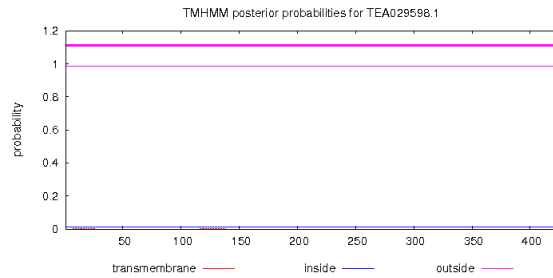
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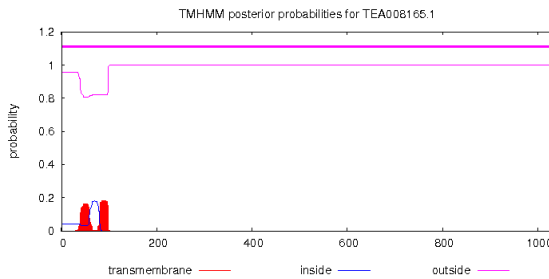
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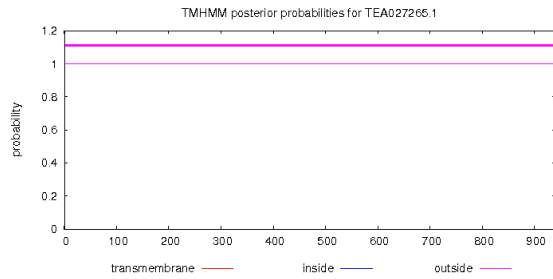
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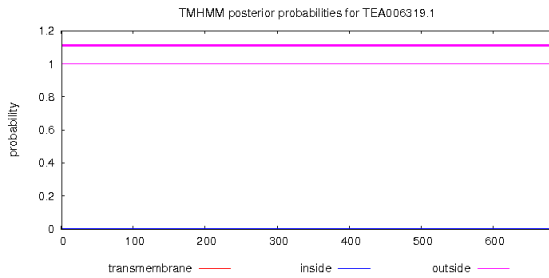
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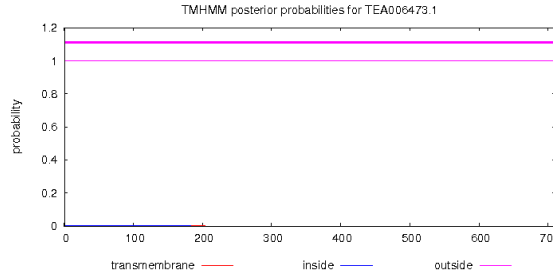
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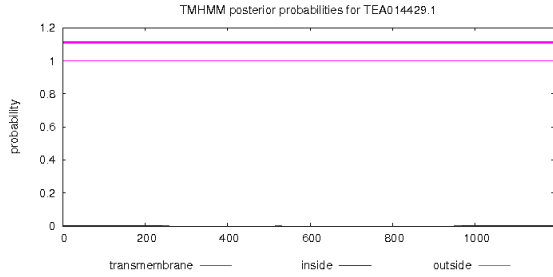
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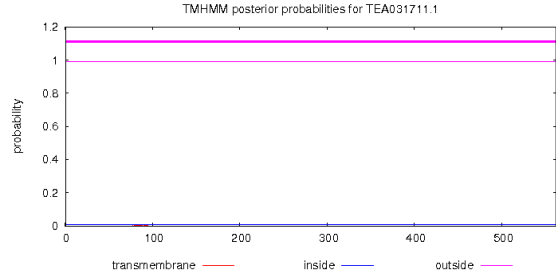
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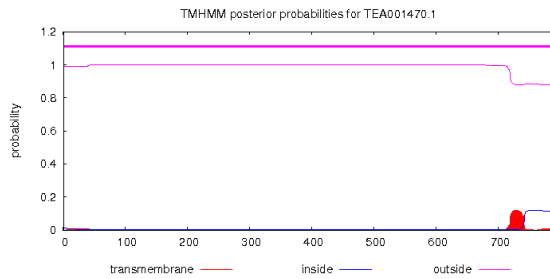
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 # TEA014429.1 Exp number of AAs in TMHs: 0.02164
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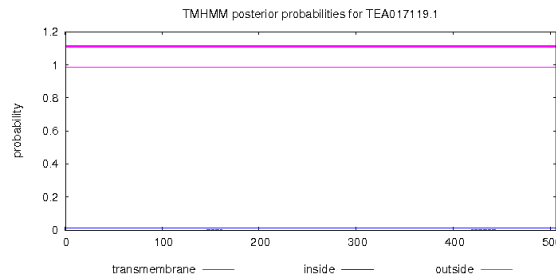
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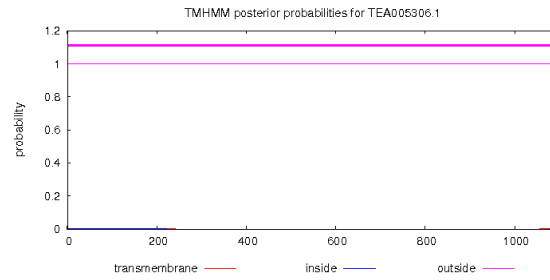
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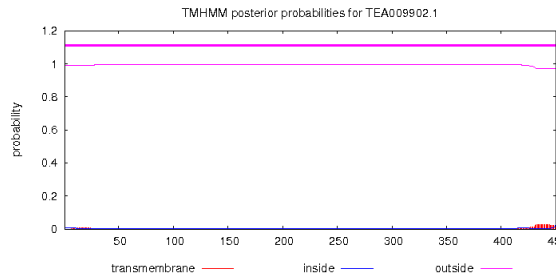
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 # TEA017119.1 Number of predicted TMHs: 0
 # TEA017119.1 Exp number of AAs in TMHs: 0.04644
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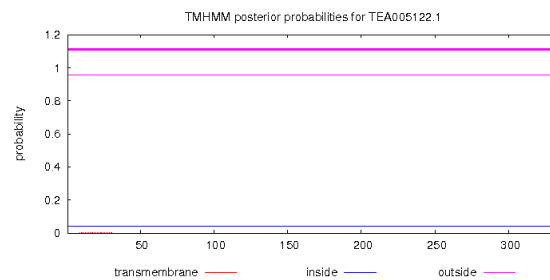
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 # TEA005306.1 Total prob of N-in: 0.00020
 TEA005306.1 TMHMM2.0 outside 1 1097



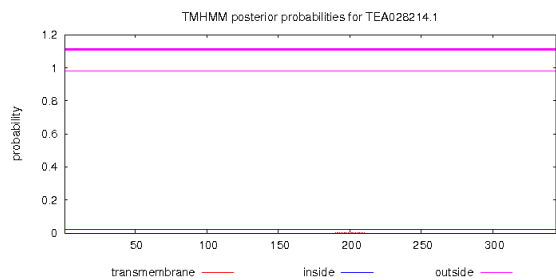
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 # TEA009902.1 Exp number of AAs in TMHs: 0.71758
 # TEA009902.1 Exp number, first 60 AAs: 0.10658
 # TEA009902.1 Total prob of N-in: 0.00748
 TEA009902.1 TMHMM2.0 outside 1 450



† **TEA005122.1** Length: 334
 # TEA005122.1 Number of predicted TMHs: 0
 # TEA005122.1 Exp number of AAs in TMHs: 0.01241
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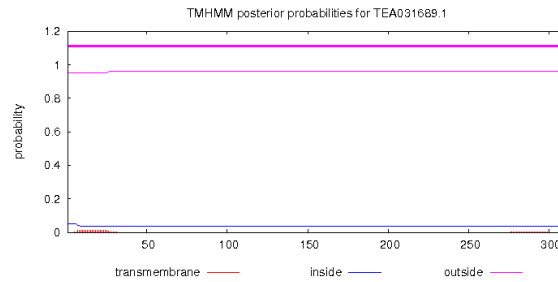
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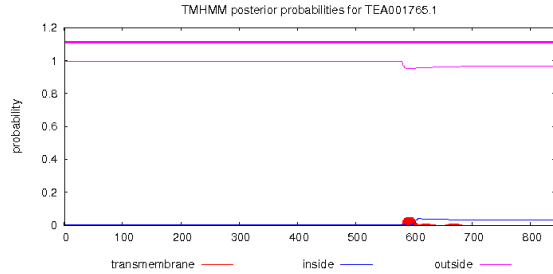
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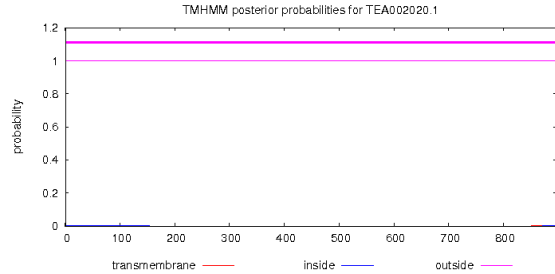


S1 Fig. Transmembrane helices of MAPKKKs of MEKK subfamily in *C. sinensis*. TMHMM Server, v.2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>), was used to predict the presence of transmembrane helices. The plot shows the posterior probabilities of inside/outside/TM helix. The plot is obtained by calculating the total probability that a residue sits in helix, inside, or outside summed over all possible paths through the model. The red peaks represent the possible transmembrane helices present. If the red peak crosses the transmembrane line (represented in pink colour), then its calculated as 1 transmembrane helix.

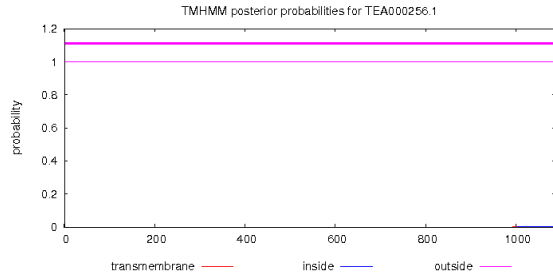
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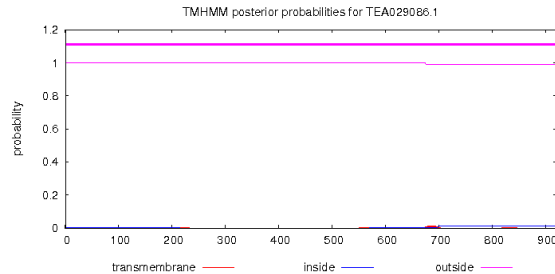
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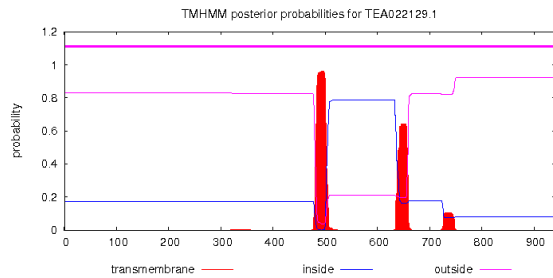
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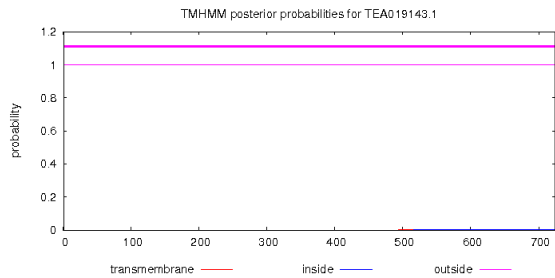
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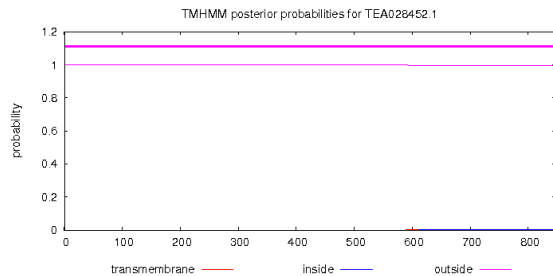
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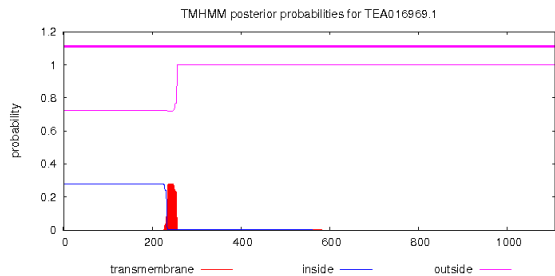
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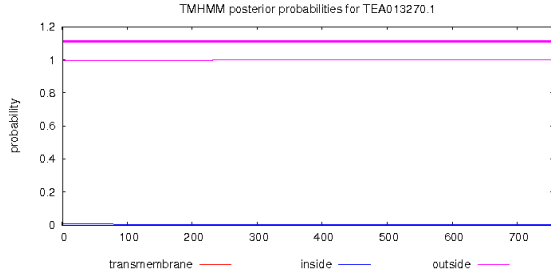
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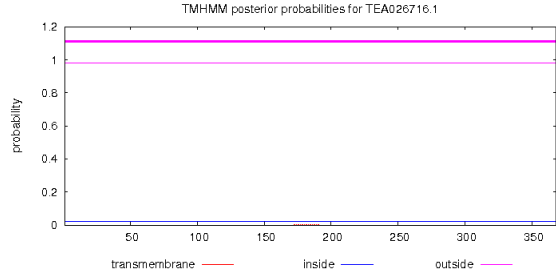
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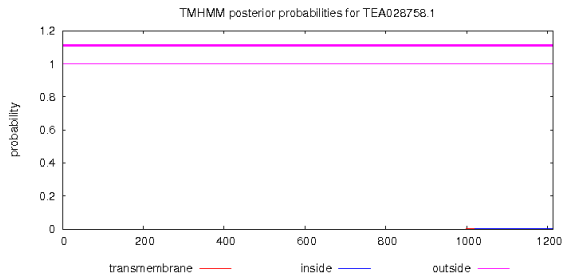
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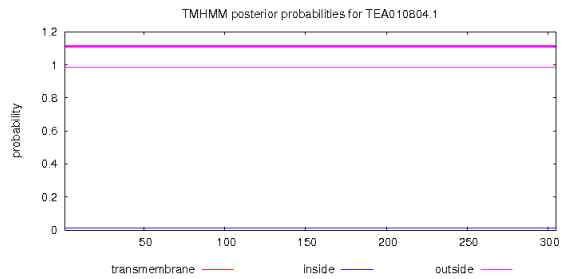
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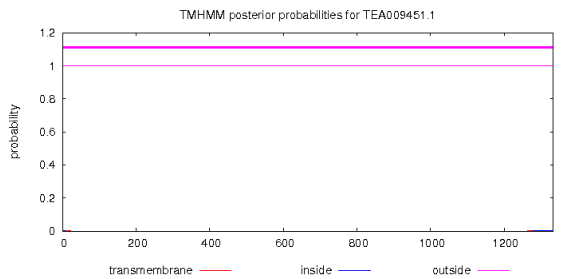
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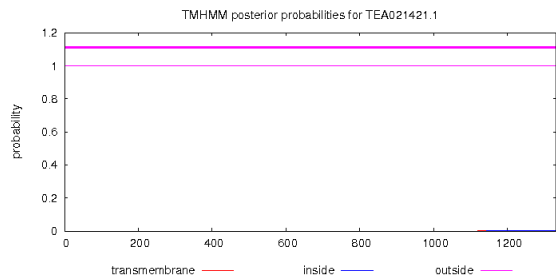
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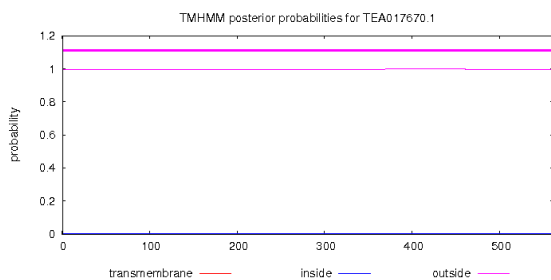
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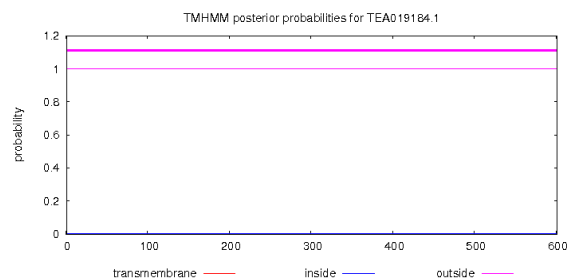
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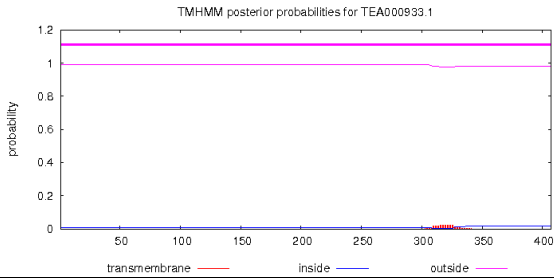
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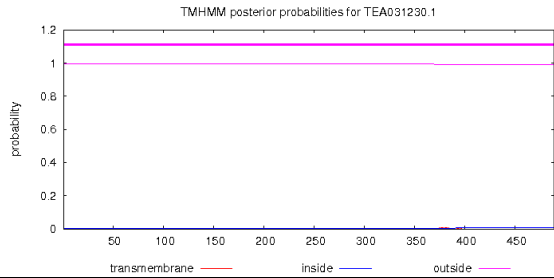
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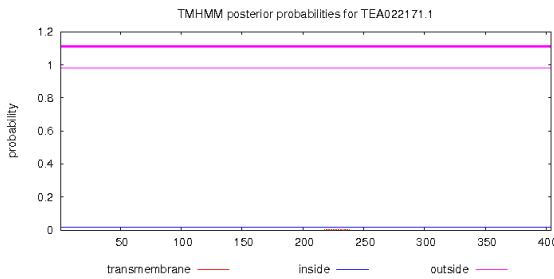
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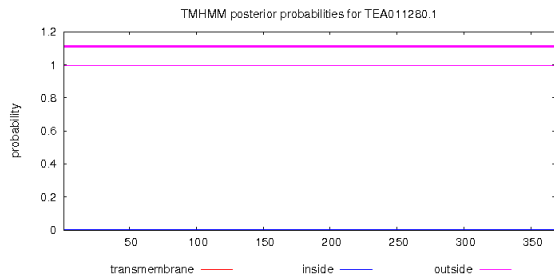
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 # TEA031230.1 Exp number of AAs in TMHs: 0.13166
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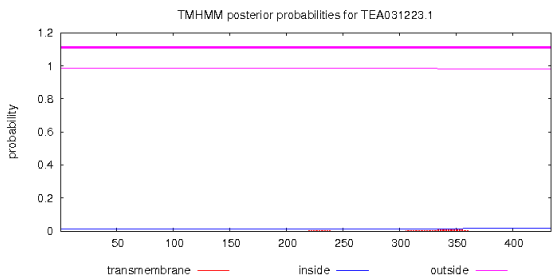
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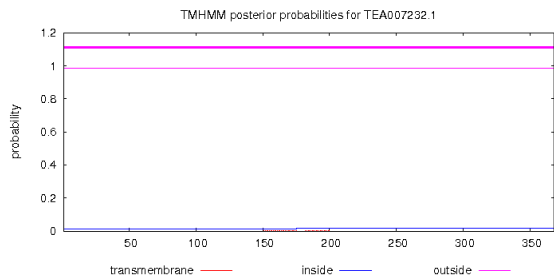
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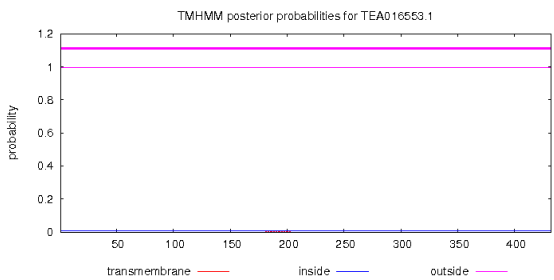
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 # TEA031223.1 Exp number of AAs in TMHs: 0.27035
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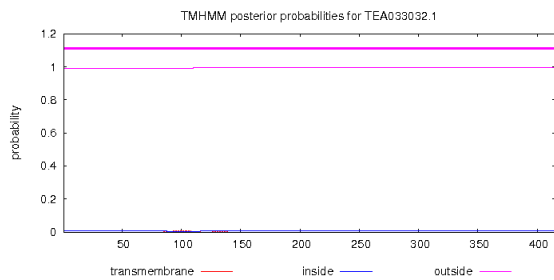
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 # TEA007232.1 Exp number of AAs in TMHs: 0.04776
 # TEA007232.1 Exp number, first 60 AAs: 0
 # TEA007232.1 Total prob of N-in: 0.01435
 TEA007232.1 TMHMM2.0 outside 1 368



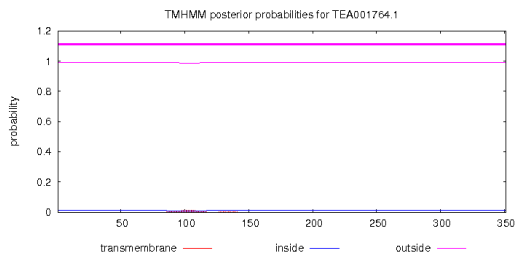
† **TEA016553.1** Length: 432
 # TEA016553.1 Number of predicted TMHs: 0
 # TEA016553.1 Exp number of AAs in TMHs: 0.01056
 # TEA016553.1 Exp number, first 60 AAs: 0
 # TEA016553.1 Total prob of N-in: 0.00632
 TEA016553.1 TMHMM2.0 outside 1 432



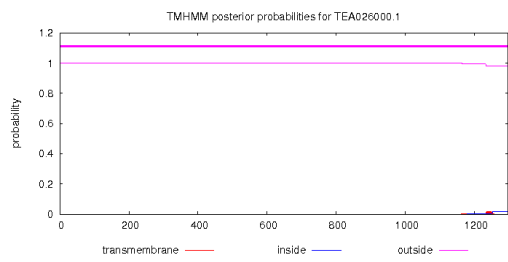
† **TEA033032.1** Length: 415
 # TEA033032.1 Number of predicted TMHs: 0
 # TEA033032.1 Exp number of AAs in TMHs: 0.16877
 # TEA033032.1 Exp number, first 60 AAs: 8e-05
 # TEA033032.1 Total prob of N-in: 0.00767
 TEA033032.1 TMHMM2.0 outside 1 415



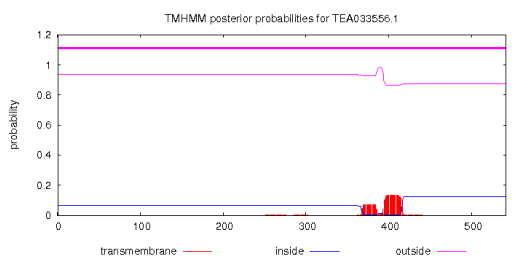
† **TEA001764.1** Length: 351
 # TEA001764.1 Number of predicted TMHs: 0
 # TEA001764.1 Exp number of AAs in TMHs: 0.22163
 # TEA001764.1 Exp number, first 60 AAs: 0.00043
 # TEA001764.1 Total prob of N-in: 0.01088
 TEA001764.1 TMHMM2.0 outside 1 351



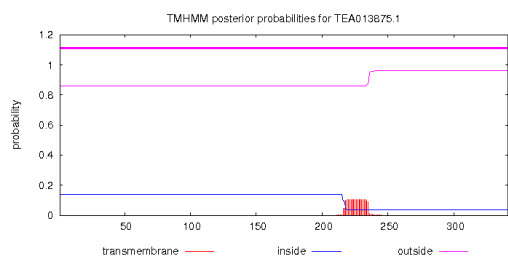
† **TEA026000.1** Length: 1296
 # TEA026000.1 Number of predicted TMHs: 0
 # TEA026000.1 Exp number of AAs in TMHs: 0.3705
 # TEA026000.1 Exp number, first 60 AAs: 0
 # TEA026000.1 Total prob of N-in: 0.00000
 TEA026000.1 TMHMM2.0 outside 1 1296



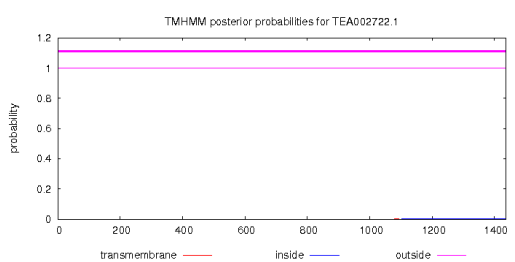
TEA033556.1 Length: 541
 # TEA033556.1 Number of predicted TMHs: 0
 # TEA033556.1 Exp number of AAs in TMHs: 4.33922
 # TEA033556.1 Exp number, first 60 AAs: 0.00021
 # TEA033556.1 Total prob of N-in: 0.06460
 TEA033556.1 TMHMM2.0 outside 1 541



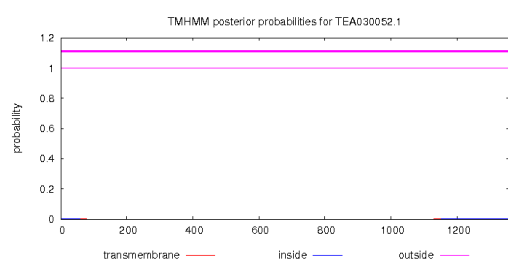
TEA013875.1 Length: 341
 # TEA013875.1 Number of predicted TMHs: 0
 # TEA013875.1 Exp number of AAs in TMHs: 1.96914
 # TEA013875.1 Exp number, first 60 AAs: 0.00196
 # TEA013875.1 Total prob of N-in: 0.13897
 TEA013875.1 TMHMM2.0 outside 1 341



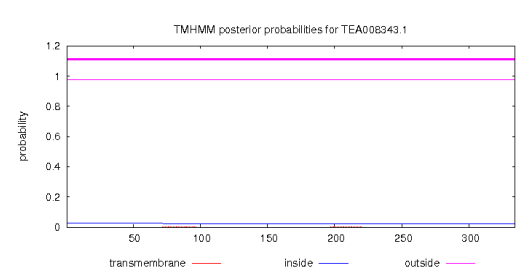
† **TEA002722.1** Length: 1436
 # TEA002722.1 Number of predicted TMHs: 0
 # TEA002722.1 Exp number of AAs in TMHs: 0.01114
 # TEA002722.1 Exp number, first 60 AAs: 6e-05
 # TEA002722.1 Total prob of N-in: 0.00001
 TEA002722.1 TMHMM2.0 outside 1 1436



† **TEA030052.1** Length: 1357
 # TEA030052.1 Number of predicted TMHs: 0
 # TEA030052.1 Exp number of AAs in TMHs: 0.02427
 # TEA030052.1 Exp number, first 60 AAs: 0.00401
 # TEA030052.1 Total prob of N-in: 0.00064
 TEA030052.1 TMHMM2.0 outside 1 1357

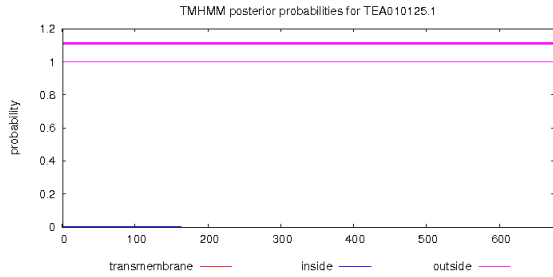


TEA008343.1 Length: 334
 # TEA008343.1 Number of predicted TMHs: 0
 # TEA008343.1 Exp number of AAs in TMHs: 0.097979999
 # TEA008343.1 Exp number, first 60 AAs: 0
 # TEA008343.1 Total prob of N-in: 0.02590
 TEA008343.1 TMHMM2.0 outside 1 334

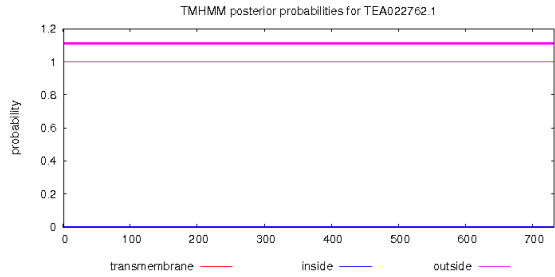


S2 Fig. Transmembrane helices of MAPKKKs of Raf subfamily in *C. sinensis*. TMHMM Server, v.2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>), was used to predict the presence of transmembrane helices. The plot shows the posterior probabilities of inside/outside/TM helix. The plot is obtained by calculating the total probability that a residue sits in helix, inside, or outside summed over all possible paths through the model. The red peaks represent the possible transmembrane helices present. If the red peak crosses the transmembrane line (represented in pink colour), then its calculated as 1 transmembrane helix.

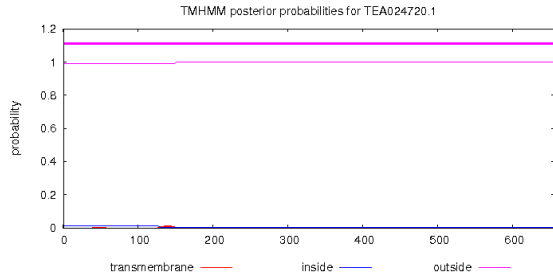
† **TEA010125.1** Length: 675
 # TEA010125.1 Number of predicted TMHs: 0
 # TEA010125.1 Exp number of AAs in TMHs: 0.00052
 # TEA010125.1 Exp number, first 60 AAs: 0
 # TEA010125.1 Total prob of N-in: 0.00014
 TEA010125.1 TMHMM2.0 outside 1 675



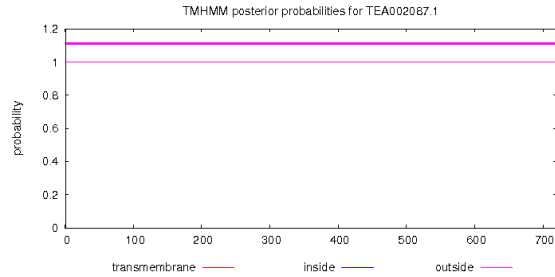
TEA022762.1 Length: 732
 # TEA022762.1 Number of predicted TMHs: 0
 # TEA022762.1 Exp number of AAs in TMHs: 0.01389
 # TEA022762.1 Exp number, first 60 AAs: 0.01054
 # TEA022762.1 Total prob of N-in: 0.00094
 TEA022762.1 TMHMM2.0 outside 1 732



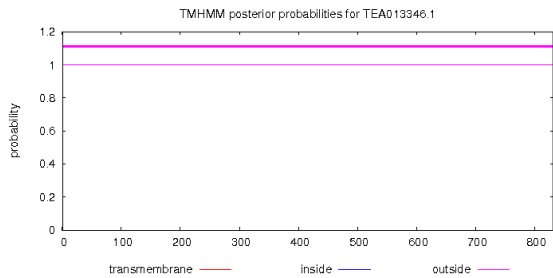
TEA024720.1 Length: 655
 # TEA024720.1 Number of predicted TMHs: 0
 # TEA024720.1 Exp number of AAs in TMHs: 0.20568
 # TEA024720.1 Exp number, first 60 AAs: 0.00353
 # TEA024720.1 Total prob of N-in: 0.01086
 TEA024720.1 TMHMM2.0 outside 1 655



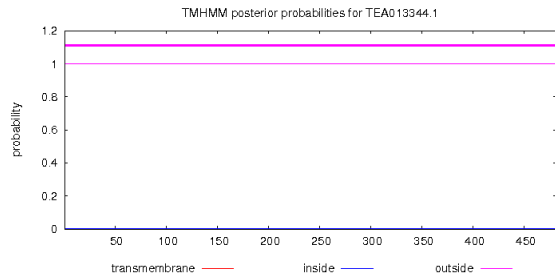
TEA002087.1 Length: 719
 # TEA002087.1 Number of predicted TMHs: 0
 # TEA002087.1 Exp number of AAs in TMHs: 0.00067
 # TEA002087.1 Exp number, first 60 AAs: 0
 # TEA002087.1 Total prob of N-in: 0.00011
 TEA002087.1 TMHMM2.0 outside 1 719



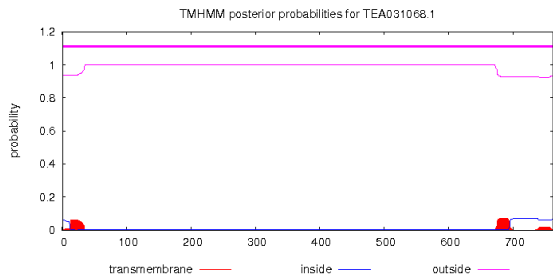
† **TEA013346.1** Length: 831
 # TEA013346.1 Number of predicted TMHs: 0
 # TEA013346.1 Exp number of AAs in TMHs: 0.00018
 # TEA013346.1 Exp number, first 60 AAs: 0
 # TEA013346.1 Total prob of N-in: 0.00002
 TEA013346.1 TMHMM2.0 outside 1 831



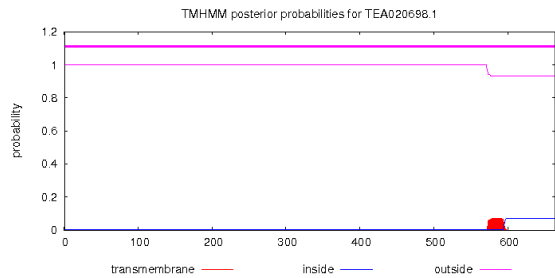
† **TEA013344.1** Length: 481
 # TEA013344.1 Number of predicted TMHs: 0
 # TEA013344.1 Exp number of AAs in TMHs: 0.00164
 # TEA013344.1 Exp number, first 60 AAs: 0
 # TEA013344.1 Total prob of N-in: 0.00069
 TEA013344.1 TMHMM2.0 outside 1 481



TEA031068.1 Length: 762
 # TEA031068.1 Number of predicted TMHs: 0
 # TEA031068.1 Exp number of AAs in TMHs: 3.06785
 # TEA031068.1 Exp number, first 60 AAs: 1.30494
 # TEA031068.1 Total prob of N-in: 0.06089
 TEA031068.1 TMHMM2.0 outside 1 762



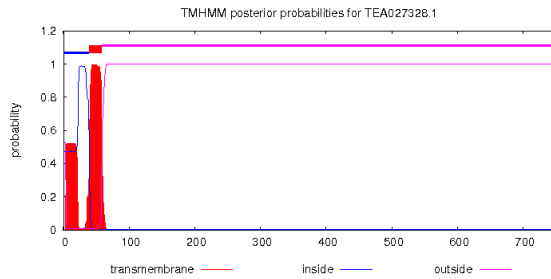
TEA020698.1 Length: 664
 # TEA020698.1 Number of predicted TMHs: 0
 # TEA020698.1 Exp number of AAs in TMHs: 1.53983
 # TEA020698.1 Exp number, first 60 AAs: 0.00118
 # TEA020698.1 Total prob of N-in: 0.00060
 TEA020698.1 TMHMM2.0 outside 1 664



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# TEA027328.1 Length: 748
# TEA027328.1 Number of predicted TMHs: 1
# TEA027328.1 Exp number of AAs in TMHs: 30.33445
# TEA027328.1 Exp number, first 60 AAs: 29.76268
# TEA027328.1 Total prob of N-in: 0.47196
# TEA027328.1 POSSIBLE N-term signal sequence
TEA027328.1 TMHMM2.0 inside 1 39
TEA027328.1 TMHMM2.0 TMhelix 40 58
TEA027328.1 TMHMM2.0 outside 59 748

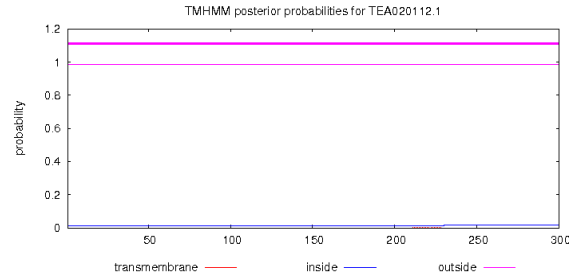
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# TEA020112.1 Length: 300
# TEA020112.1 Number of predicted TMHs: 0
# TEA020112.1 Exp number of AAs in TMHs: 0.00508
# TEA020112.1 Exp number, first 60 AAs: 0
# TEA020112.1 Total prob of N-in: 0.01462
TEA020112.1 TMHMM2.0 outside 1 300

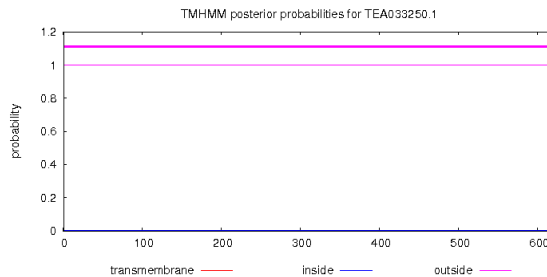
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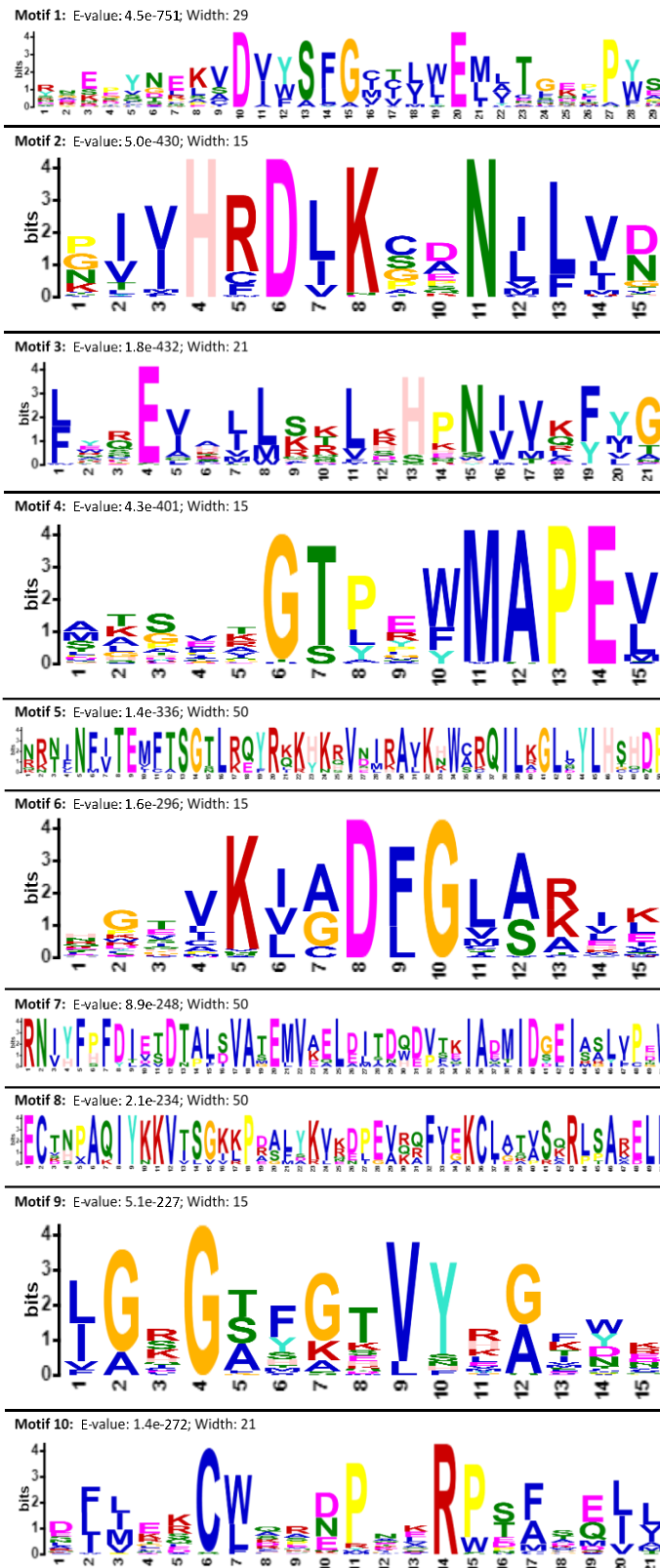
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# TEA033250.1 Length: 622
# TEA033250.1 Number of predicted TMHs: 0
# TEA033250.1 Exp number of AAs in TMHs: 0.00119
# TEA033250.1 Exp number, first 60 AAs: 0
# TEA033250.1 Total prob of N-in: 0.00024
TEA033250.1 TMHMM2.0 outside 1 622

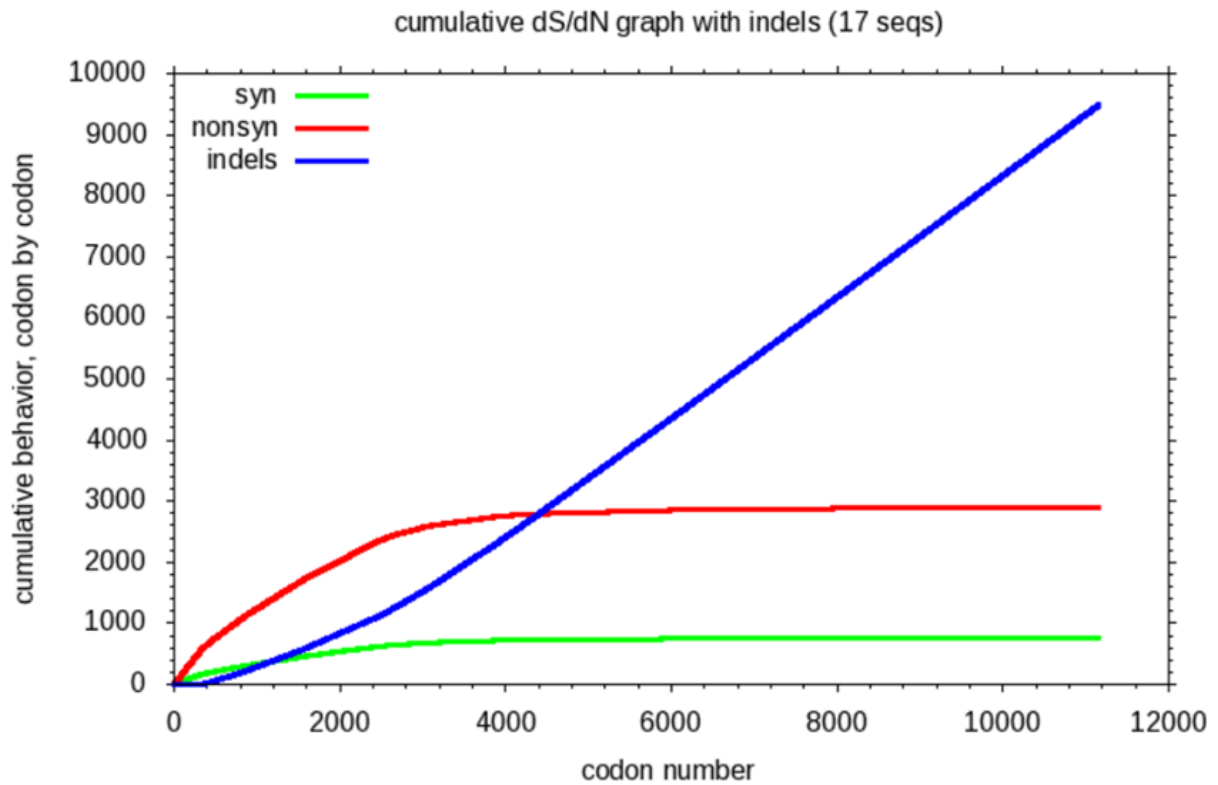
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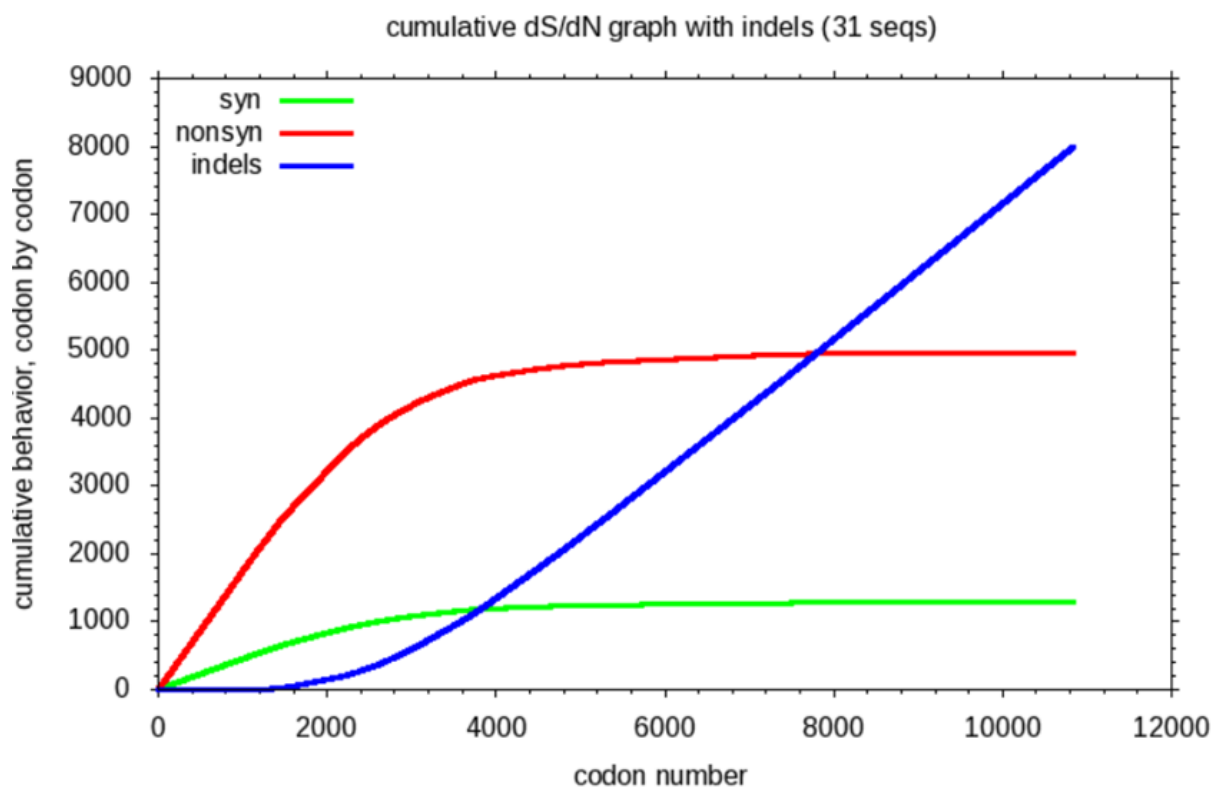
S3 Fig. Transmembrane helices of MAPKKs of ZIK subfamily in *C. sinensis*. TMHMM Server, v.2.0 (<http://www.cbs.dtu.dk/services/TMHMM/>), was used to predict the presence of transmembrane helices. The plot shows the posterior probabilities of inside/outside/TM helix. The plot is obtained by calculating the total probability that a residue sits in helix, inside, or outside summed over all possible paths through the model. The red peaks represent the possible transmembrane helices present. If the red peak crosses the transmembrane line (represented in pink colour), then its calculated as 1 transmembrane helix.



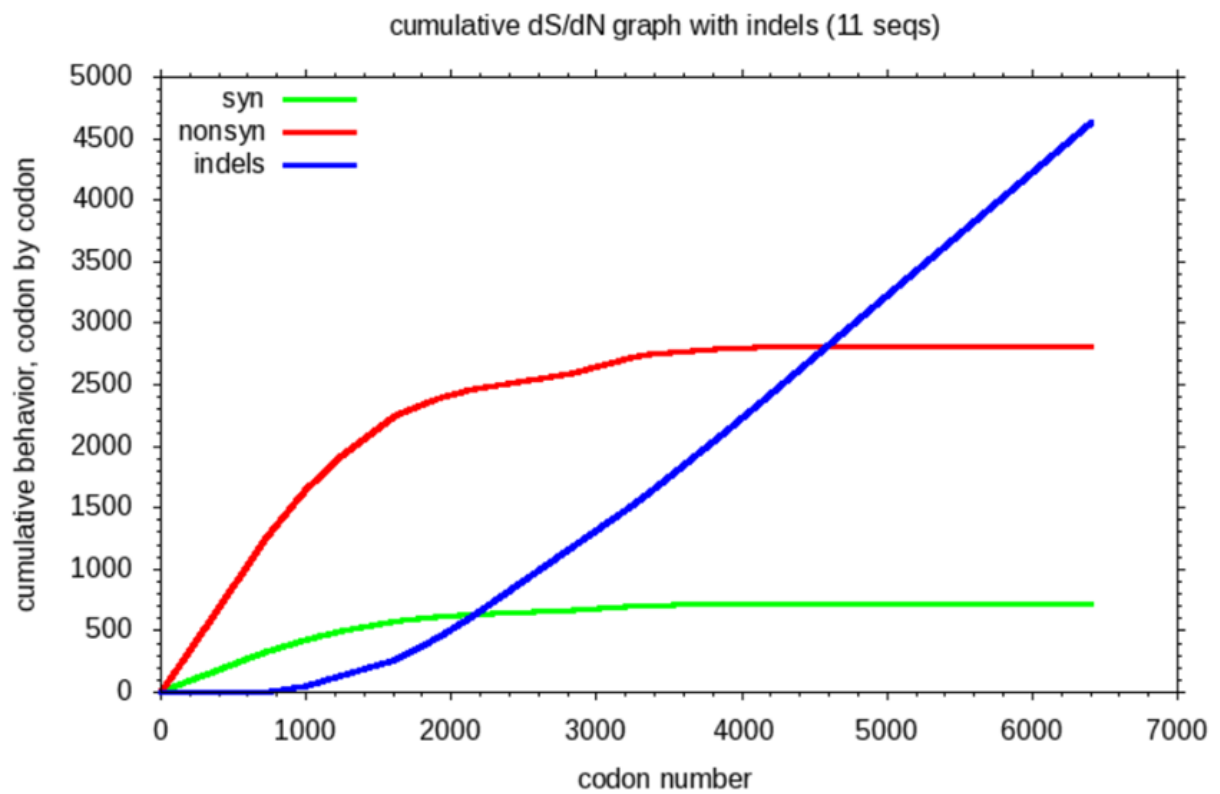
S4 Fig. Motif logos of the 10 identified motifs in 59 MAPKKKs of *C. sinensis*. The motif logos were generated by MEME suite.



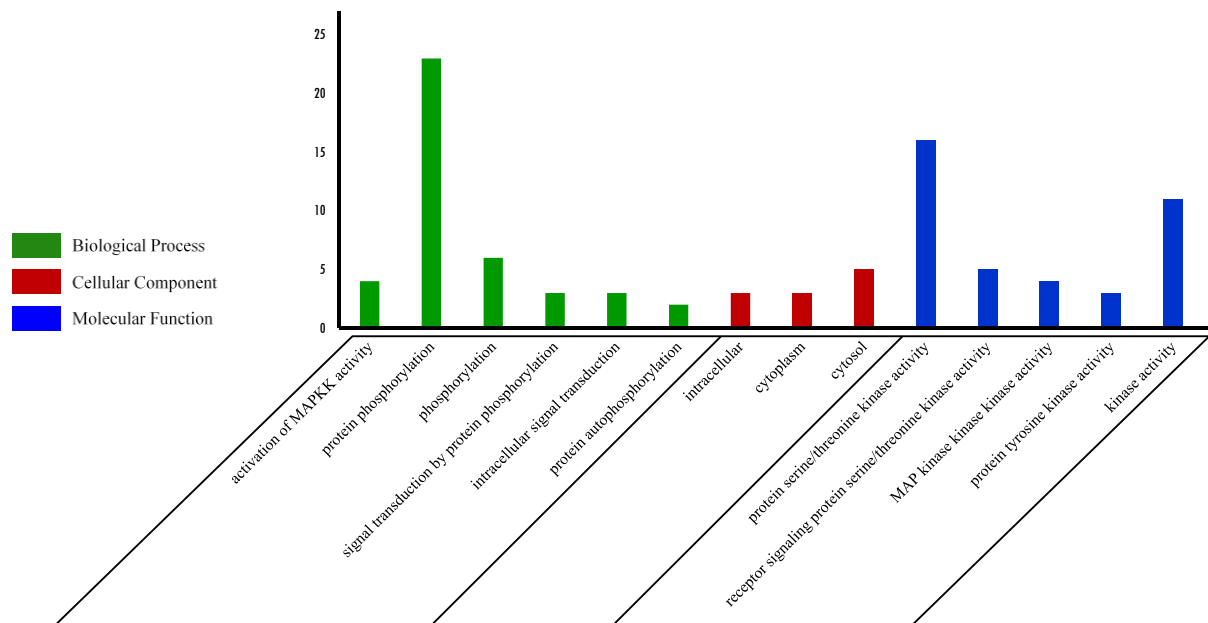
S5 Fig. The ds/dn cumulative graph of MAPKKKs of MEKK subfamily in *C. sinensis*. SNAP server (<https://www.hiv.lanl.gov/content/sequence/SNAP/SNAP.html>) has been used to generate the graph.



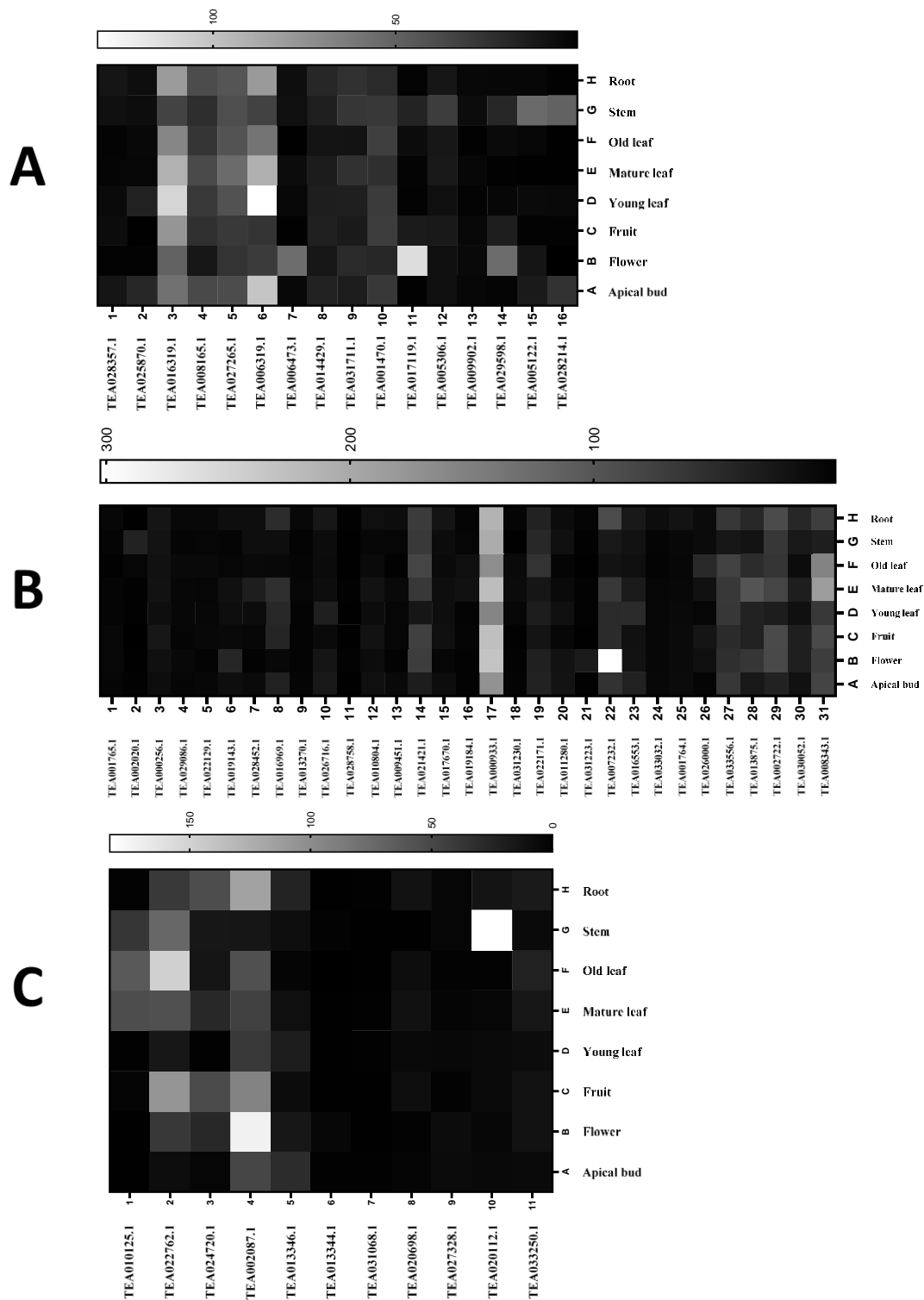
S6 Fig. The ds/dn cumulative graph of MAPKKKs of Raf subfamily in *C. sinensis*. SNAP server (<https://www.hiv.lanl.gov/content/sequence/SNAP/SNAP.html>) has been used to generate the graph.



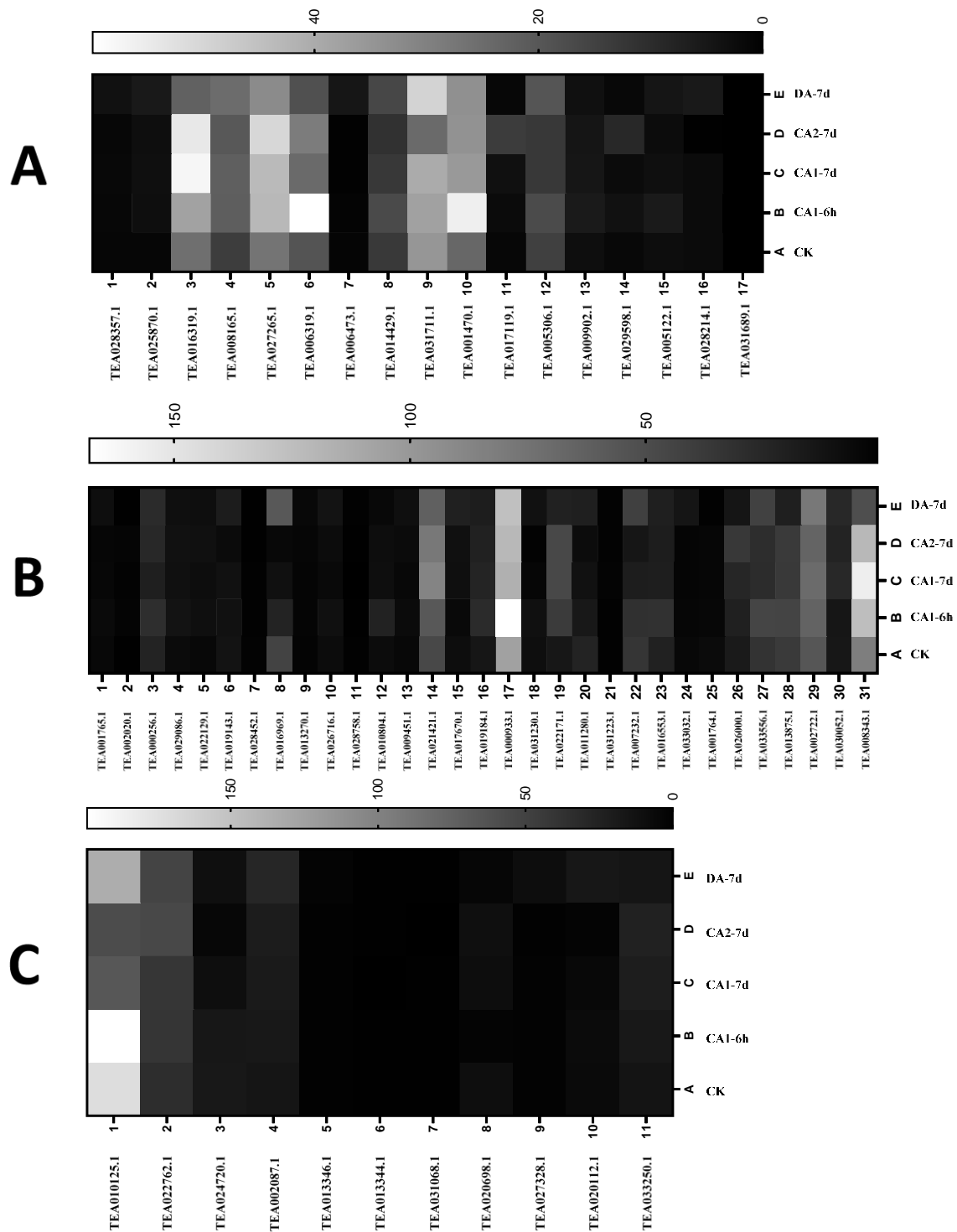
S7 Fig. The ds/dn cumulative graph of MAPKKKs of ZIK subfamily in *C. sinensis*. SNAP server (<https://www.hiv.lanl.gov/content/sequence/SNAP/SNAP.html>) has been used to generate the graph.



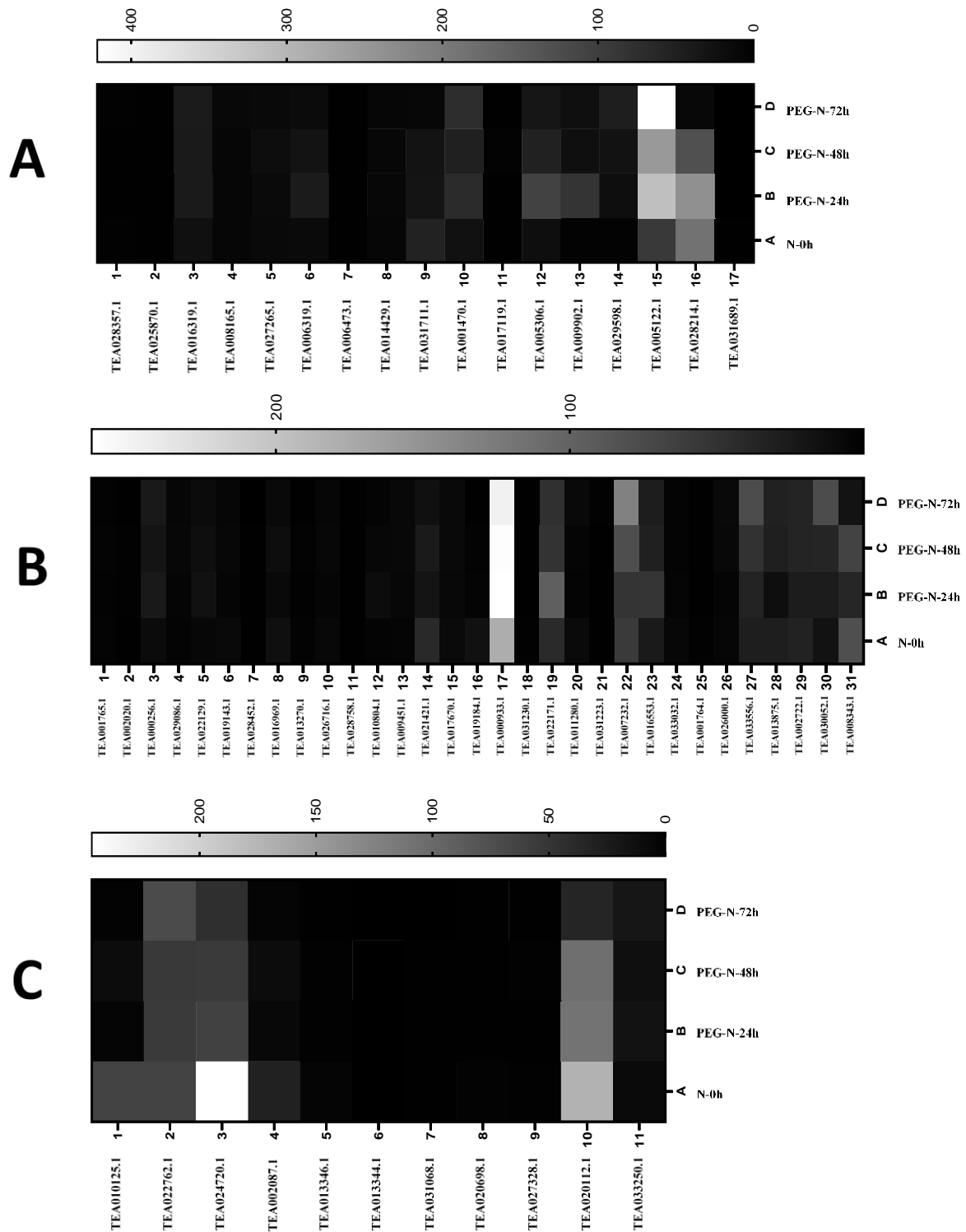
S8 Fig. GO analysis of all the 59 MAPKKs in *C. sinensis*. The results have been grouped into three main categories: Biological Process, Cellular Component and Molecular function. The y-axis represents the frequency of genes while the x-axis represents the putative functions.



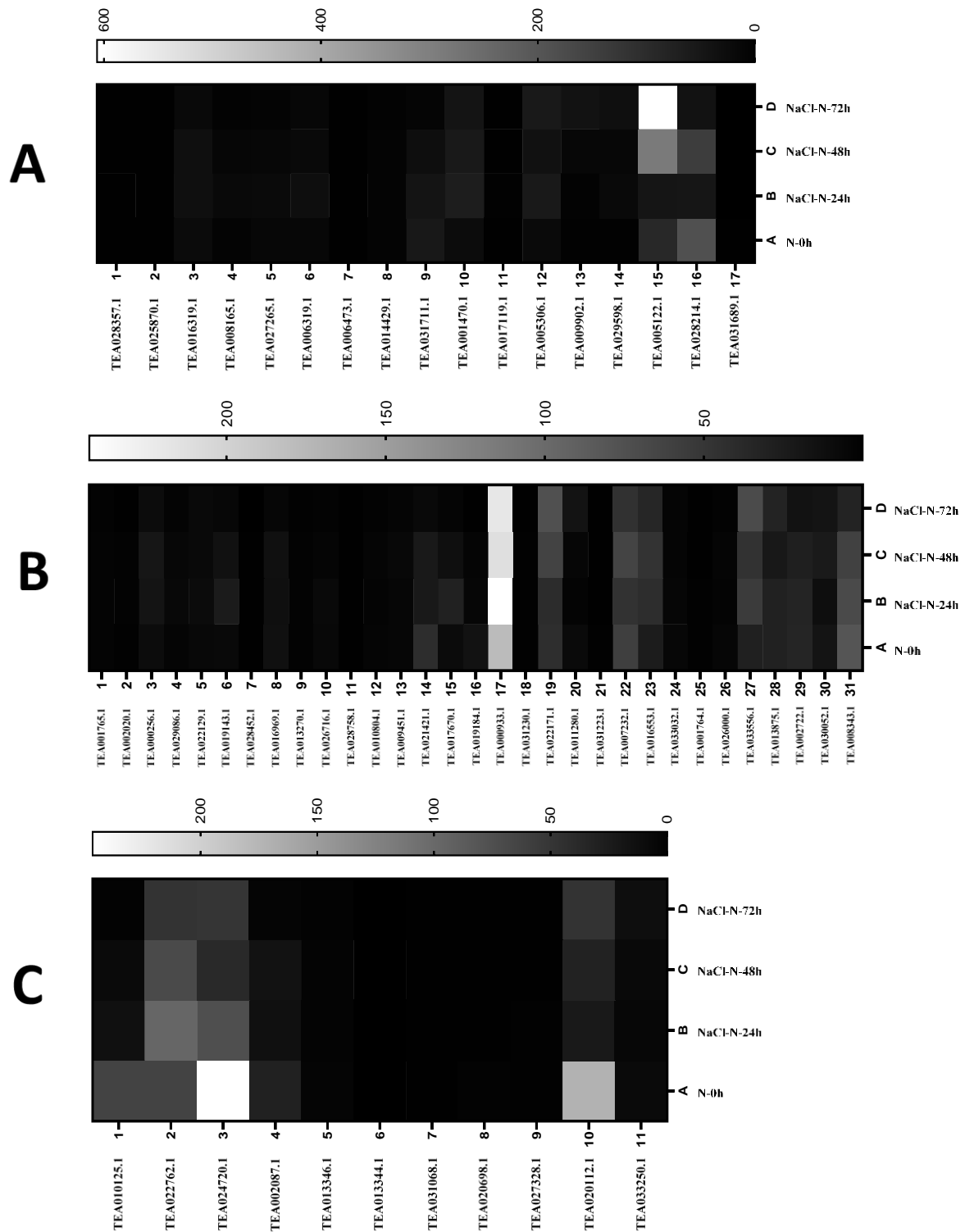
S9 Fig. Heat maps for tissue-specific expression patterns of A) MEKK; B) Raf and; C) ZIK genes in *C. sinensis*. The relative expression of these genes were analysed in different tissues, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The 8 different tissues are represented on the right and the tea genes are marked below.



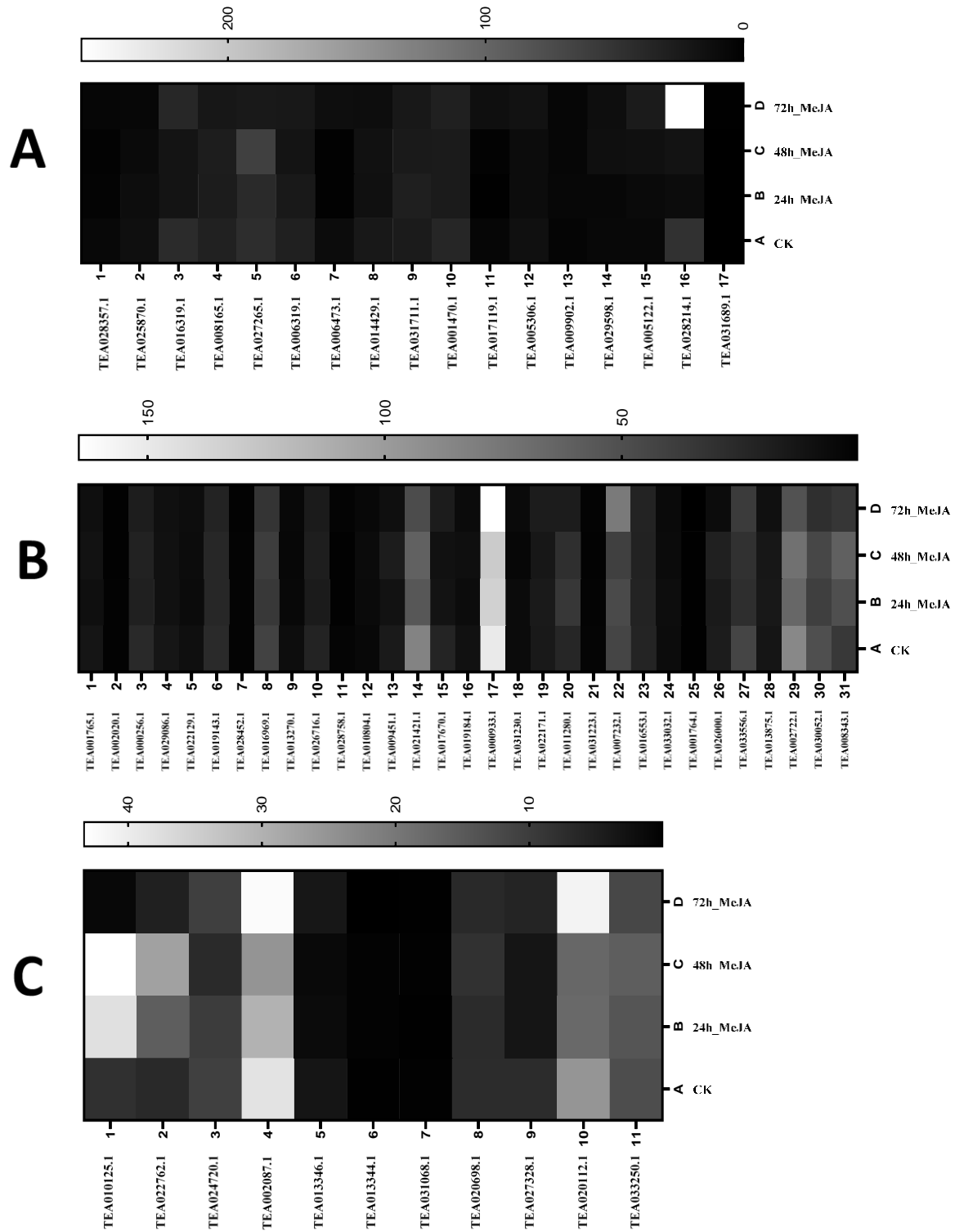
S10 Fig. Heat maps for cold stress expression patterns of A) MEKK; B) Raf and; C) ZIK genes in *C. sinensis*. The relative expression of these genes were analysed in different stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The different stages are represented on the right and the tea genes are marked below.



S11 Fig. Heat maps for drought stress expression patterns of A) MEKK; B) Raf and; C) ZIK genes in *C. sinensis*. The relative expression of these genes were analysed in different stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The different stages are represented on the right and the tea genes are marked below.



S12 Fig. Heat maps for salt stress expression patterns of (A) MEKK (B) Raf and (C) ZIK genes in *C. sinensis*. The relative expression of these genes were analysed in different stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The different stages are represented on the right and the tea genes are marked below.



S13 Fig. Heat maps for MeJA treatment expression patterns of (A) MEKK (B) Raf and (C) ZIK genes in *C. sinensis*. The relative expression of these genes were analysed in different stages, by using GraphPad Prism 8 software. The level of expression was in transcript per million (TPM). The different stages are represented on the right and the tea genes are marked below.