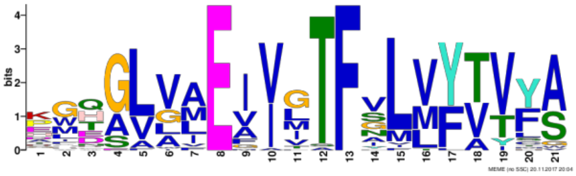
Supplementary files

1: NPA

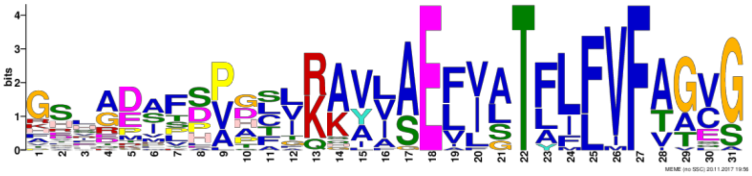
2: NPA

3: Phosphoserine

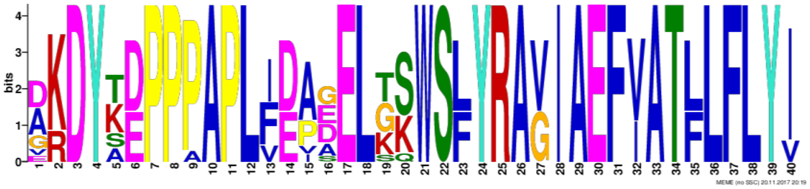
4: Amidation site



5: Casein kinase II

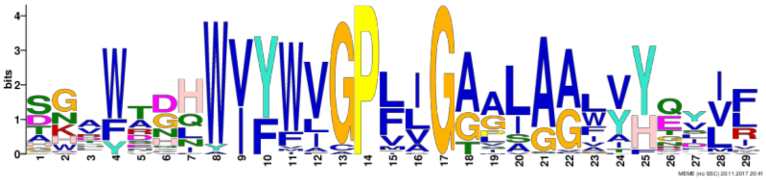


6: Novel motif

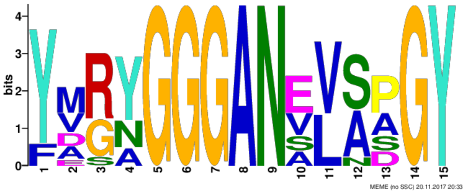


7: N-myristoylation site

8: Novel



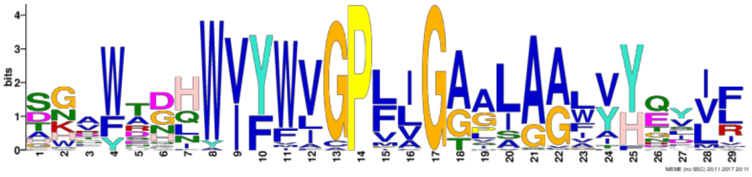
9: N-myristoylation site



10 : N-myristoylation site

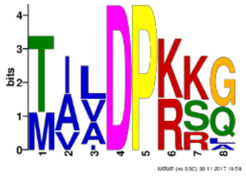
11: PKC_Phospho motif

12: N-myristoylation site



13: Novel

14: Phosphothreonine

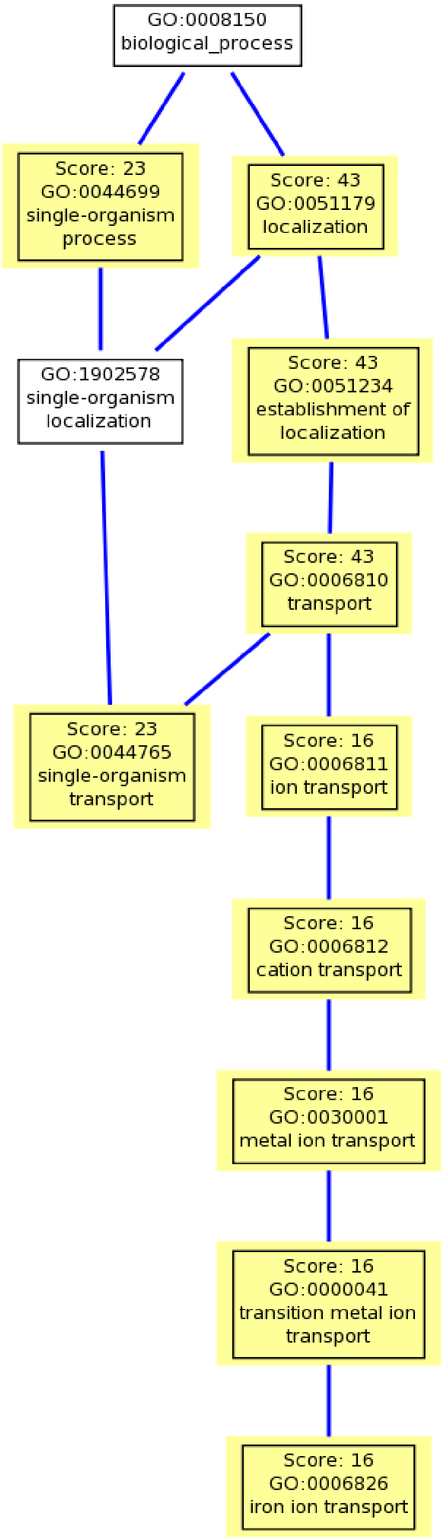


15: N-myristoylation site

Supplementary Figure: S1
Conserved motifs with their name and consensus sequences.

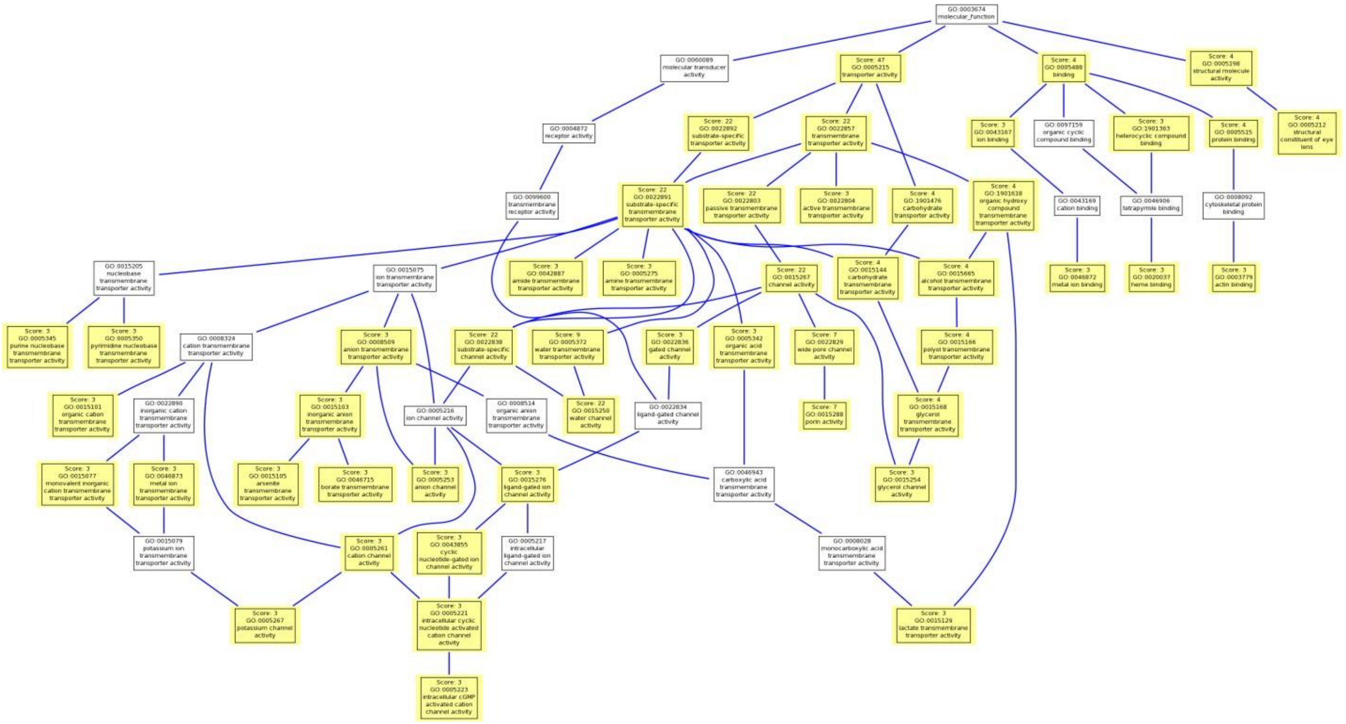
Supplementary Figure : S2

Multiple sequence alignment of 41 ZmAQPs performed through MAFFT online tool. Important conserved location are indicated with red boxes including Trans-membrane domains (TMD), ar/R filter regions (H=helix), NPA motif and Loop E (LE1 and LE2).



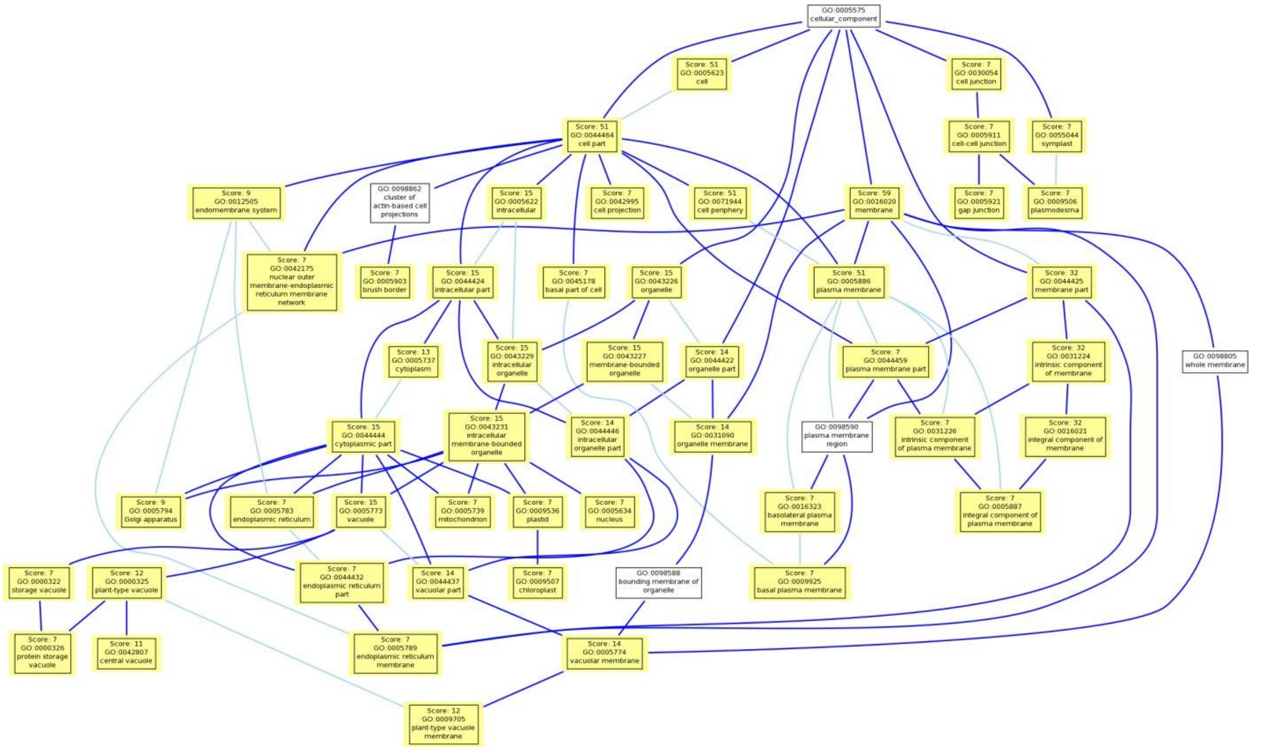
Supplementary Figure : S3

Gene ontology : Biological process of ZmAQPs.



Supplementary Figure : S4

Gene ontology : Molecular functions of ZmAQPs.



Supplementary Figure : S5

Gene ontology : Cellular component of ZmAQPs.