

VrCKL1	CEATQQAQKKNNKSTAFASASHQVRASLAGITGLIEISSSELVDPGSELETNLKQNGCT	431
VrHK1.1	LEARRKAEYSSNYKSQLANMHSRLRTPMAAVITLXLLDILISDDCLTNEQYSTVTQIRKCS	564
VrHK1.2	LEARRKAEYSSNYKSQLANMHSRLRTPMAAVITLGLIDILISDDRLTNEQCATVTQIRKCS	533
VrCK12	LNKTIHIITEETMRAKQMLATMHSIRSPLSGVVSMAEVLN-TKLDREQRQLLDVMLSSG	418
VrHK5	LNKTIHIITEETMRAKQMLATMHSIRSPLSGVVSMAEILST-TKLDREQRQLLDNMISSG	419
VrHK2	----SRAEADVAKSQLATVSHSIRTPMNGVLGMQLMLMD-TLDDKKQMDYAQTAAHSG	640
VrHK3	----ERAAVADIKSQLATVSHSIRTPMNGVLGMQLMLMD-TLDSVQQQEYVRTAQESG	491
VrHK4.1	----VRAESAHVAKSQLATVSHSIRTPMNGILGMALLLLD-TLSTQTDYAQTAAQACG	427
VrHK4.2	----VRAESADIKSQLATVSHSIRTPMNGILGMQLLLG-TLSSTQLDYAQTAAQCG	412

VrCKL1	-----GLAREYHPHPYDYLIDCCMPIMGGLDATKWIRKIEKA-----	1013
VrHK1.1	RESLQKDRNKR-SQTEILSSRPYDLIIDCCMPKMDGYEATKIRKSEVG-----	1209
VrHK1.2	RESMMKERNTRSSQTEILSCPPYDLIIDCCMPKMDGYETTKAIRKSEAG-----	1178
VrCK12	-----RCSYDLIIDVCMFVINGLEATKLIRSFEEETGNWDAARNAG-----	908
VrHK5	-----RHTYOVILIDVFMFVINGLQTTKLIRSYVEETGNWDAARKAG-----	948
VrHK2	-----PHSFDACFHDLQMPMDGFEATREIRLMESEVNEKIIACGQ-----	1129
VrHK3	-----PHQFDACFHDIQMPMDGFGVATKQIREMEQSVNRDASMD-----	974
VrHK4.1	-----PHNFDACFHDQMPMDGFGQATSQIRHMESEKANEEMKNG-----	934
VrHK4.2	-----PHNFDACFHDQMPMDGFGQATGKIREMERKANELLMNGE-----	923

VrETR1 VALDLARREAEATIRARNDFLAVNMHEMRTPMHAVALSSLLQET-DLTAEQRLMVETIL 386
 VrERS1 VALDLARREAEAMTHARNDFLAVNMHEMRTPMHAIALSSLLLET-ELTPQRMVETIVL 387
 VrEIN4.1 RALDQAQKNAMMARKARSSFEKVMSHGMRRPMHSLGLLSLFQEDNSIRPEQKIVDSIF 413
 VrEIN4.2 RALDQAQKNAMMARKARSSFEKVMSHGMRRPMHSLGLLSMFQED-HIRPEQKIVDSIL 412
 VrERS2 RALDQAQRKNAMWASQAARNAPQKVMSDGMRRPMHSLGLLSMIOQD-NLRNEQKLTVDAML 407
 VrETR2 RALQVEKINAMKANQARAFAQKVMSSNGMRPMHSLGLLSVMQEE-NLKREQKVVDSEMF 407

VrETR1 -NGVSRVTYKGLLMHLCQDVTASSESEELRWVLSLEH---VVFMD-VCTGLDGYELAVR 678
 VrERS1 DSGSFSTRNRKRSF----- 636
 VrEIN4.1 --DYNRTVTQKLLKELGCVTA VSSGFECLSAVSASGNSSKIVL DHPMPMDGFEVTRR 700
 VrEIN4.2 --DYNRTVTQKLLKELGCVTA VSSGFECLSAVSAGNLFKII DHPMPMDGFEVAKR 699
 VrERS2 --DYNRAVTQKLLQKLGCVTPVTS SGFECLTIGPAGSSIQVIL DHPMDLDGFEVATR 697
 VrETR2 --DYNRAVTQKLLQKLGCSVTCV SGFECLSVIGGGGCSFQVIV DHPMPELDGF EVASR 701

Figure S1. Protein sequence alignment of histidine kinase and ethylene receptors. The boxes represent the conserved phosphorylation residue.

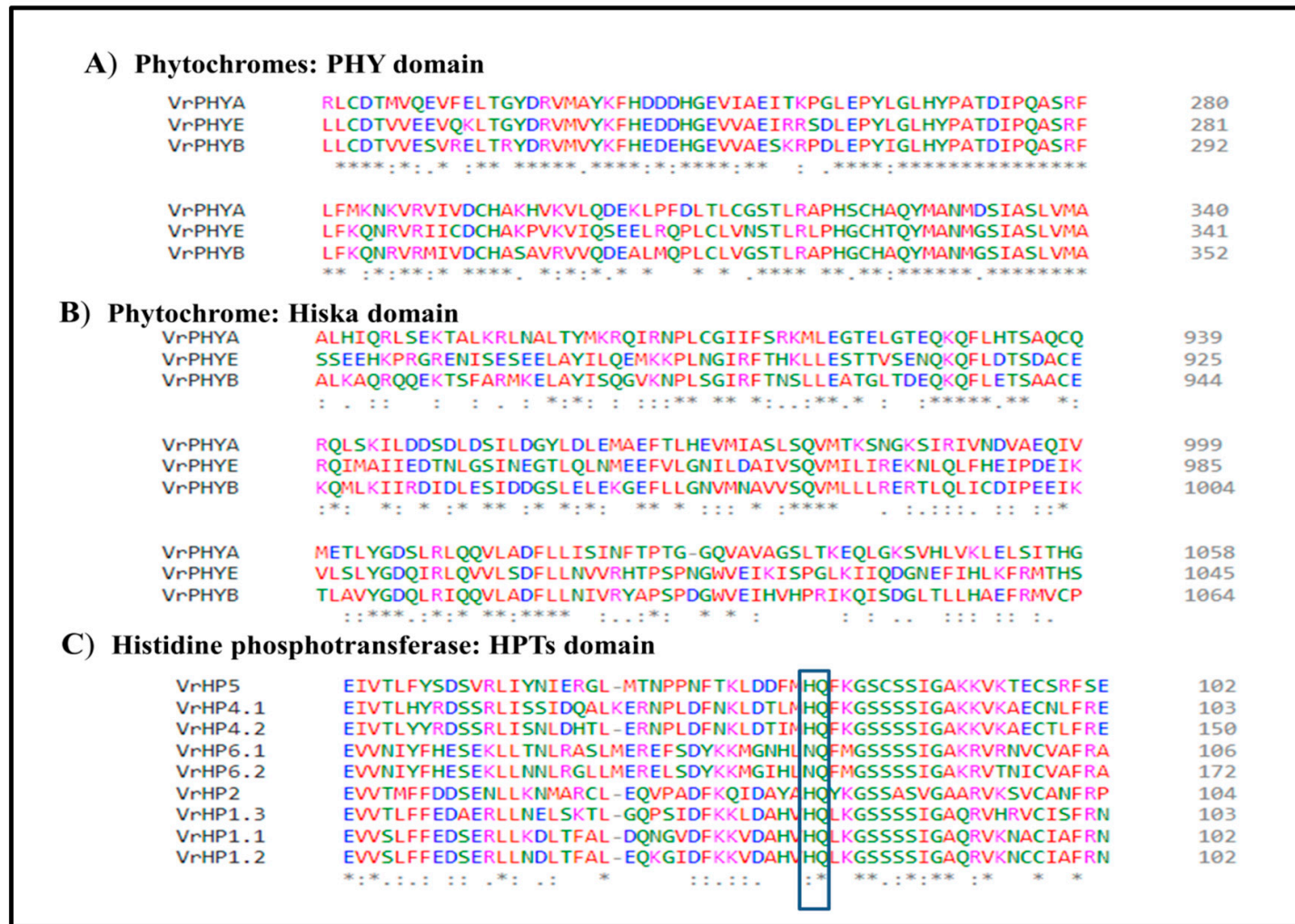


Figure S2. Protein sequence alignment of phytochrome family and histidine phosphotransferase proteins. The boxes represent the conserved phosphorylation residue.

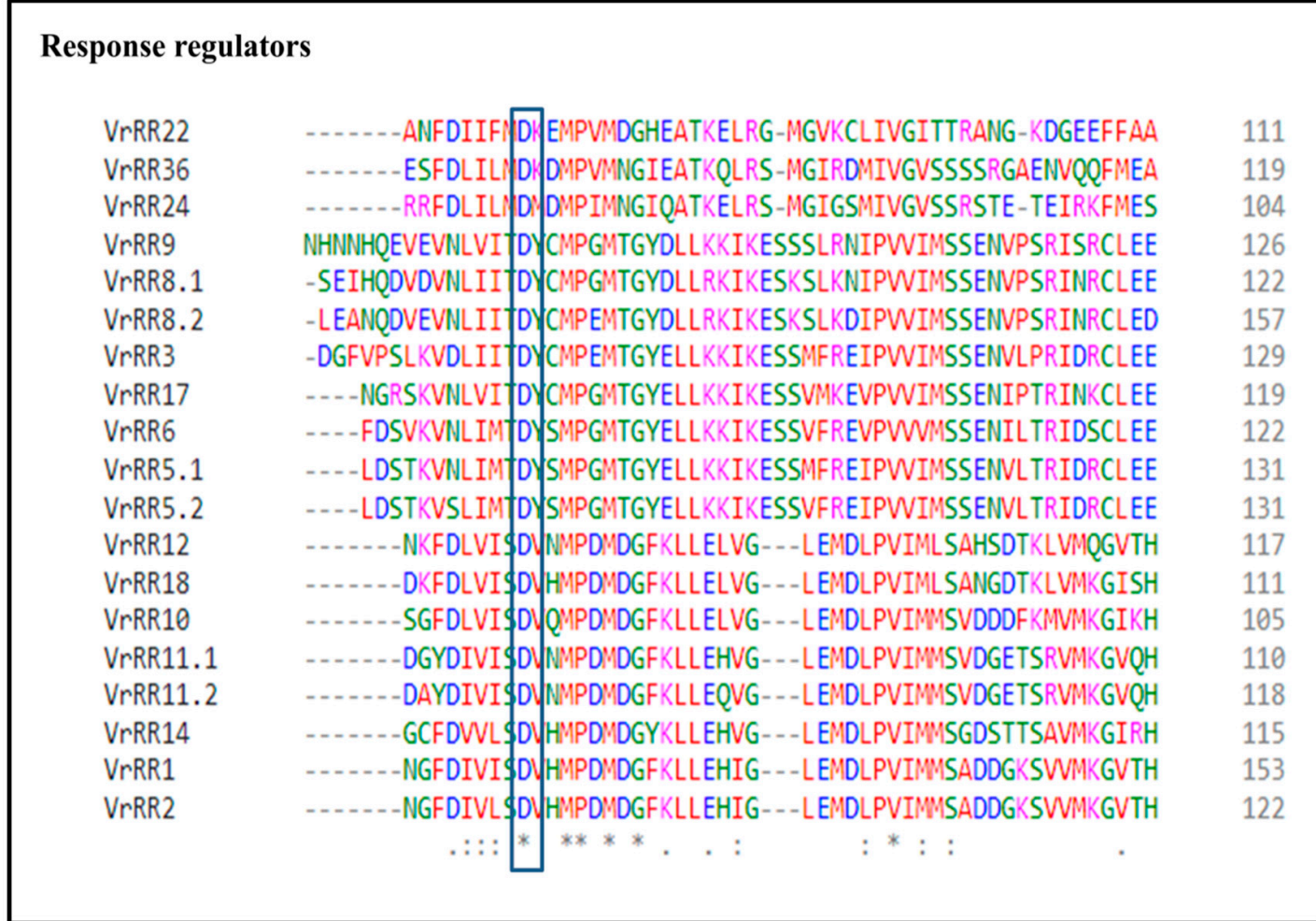


Figure S3. Sequence alignment of all types of response regulators. Showing the conserved residue in their receiver domain.




















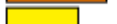
Motif	Symbol	Motif Consensus
1.		FDLIJTDVQMPMDGFELLKKIRESESLK
2.		VIMMSSEBVLSRVMKCLEHGACDFLLKPVRLNELKNJWQHVVRRK
3.		WSVELHQKFVAAVNQLGIDKAVPKKILELMNVPGLTRENVASHLQKYRLY
4.		LKVLVVDVDDPVBRRVIEKLLK
5.		LLZAKRRAEMASVARSQFLATMSHEIRTPMHGIJGLLSLLQETELDREQK
6.		VEDTGIGIPPSAIPRJFTPFMQADSSTSRKYGGTGJGLAISKCLVELMGG
7.		SLFHQGFLEQFJQLQZLQDEANPBFVEEVVTLFFEDSERL
8.		LLRLINDVLDLSKIEDGKLELEMAEFDLHSILDEVLSLFSE
9.		DAHVHQFKGSSSSIGAKRVKNVCIAFRNYCEEQNREGCLRCLQQLKHEYC
10.		PDLVIGDEKRLRQVJTNLVGNSVKFTHG
11.		PIVAMTADAIEATKEKCLQVGMDGYVTKPIELEKJASELRR
12.		VHVRMLTHEIRKSLDRHTILYTTLVELSKTLGLQNCVWMP
13.		SYKVTTVESGREALELLGLRG
14.		PELSZTNYAILVLILPSTNARSWSSHELEIVEVVADQVAVALSHAAILEE
15.		RKERCFEKKVRYQSRKRLAEQRPRVRGQF
16.		NVPFKWVLLQFIAFIVLCGATHLLNAWY
17.		RMLQDQFNVSVNHVHALAILVSTFHYYKHPSAIDQETFAEYTERTAFERP
18.		TALVSCATAJTLVTLIPLLLKVKVRELFLKKKVWELGREVG
19.		LECQKVSDFLIAIAYFSIPLELLYFVSKS
20.		FGDPFRKHEMHCYKQKPPTPWIAITTAFGFFVILLVGYI

Figure S4. Conserved motifs present in the protein sequence of *VrTCS*.

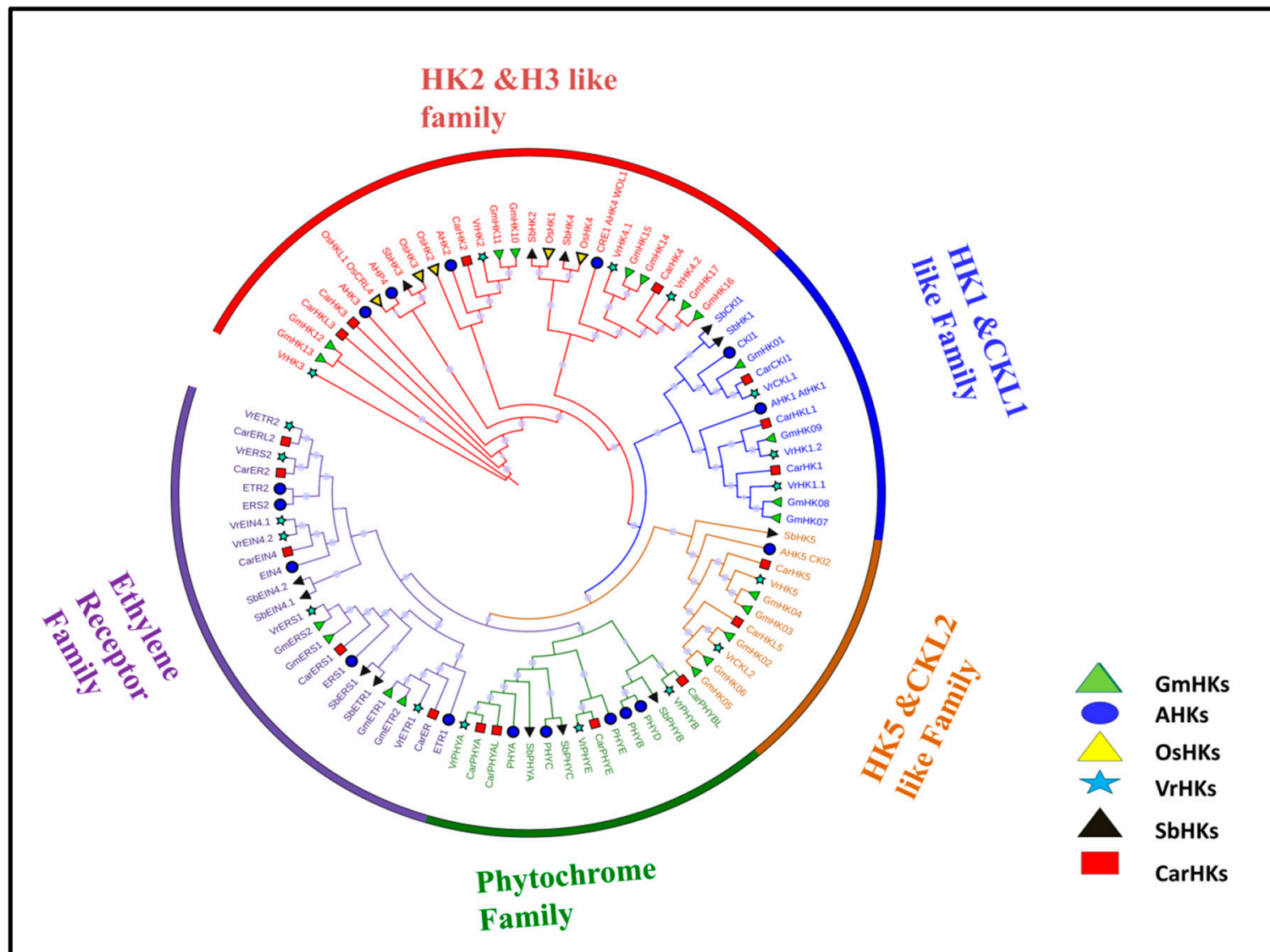


Figure S5. Phylogenetic tree of histidine kinase protein with different species and different symbols representing the different species HKs. HK1 family, HK2 family, HK5 family, Ethylene receptor, and phytochromes were represented by blue, red, brown, purple, and green colors.

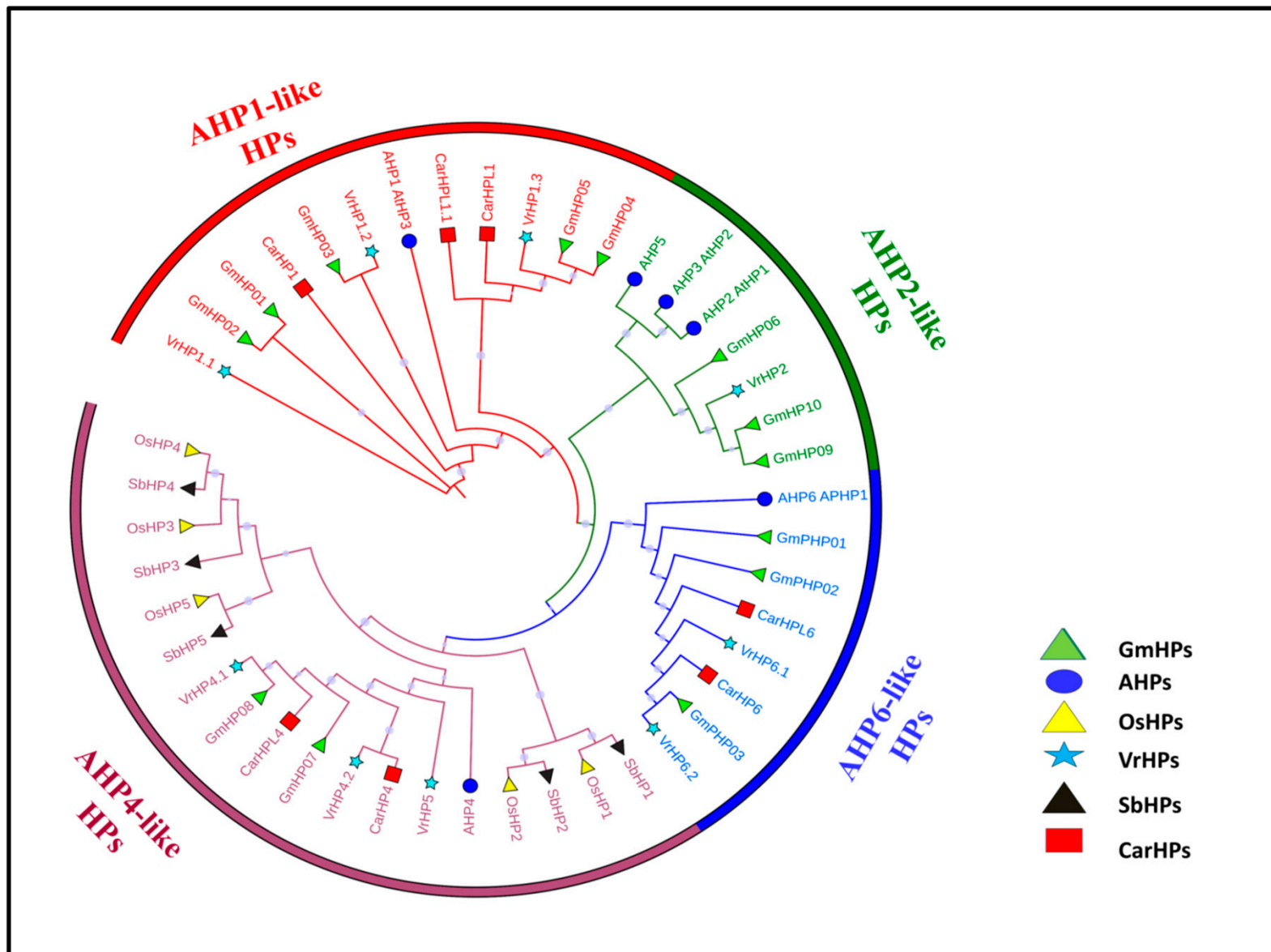


Figure S6. Phylogenetic tree of Histidine phosphotransferase proteins with other species. *AHP1*-like proteins were grouped in a separate clade and represented by red color, *AHP2* protein represent by green color whereas blue and purple colored clade show *AHP6*-like and AHP4-like proteins respectively.

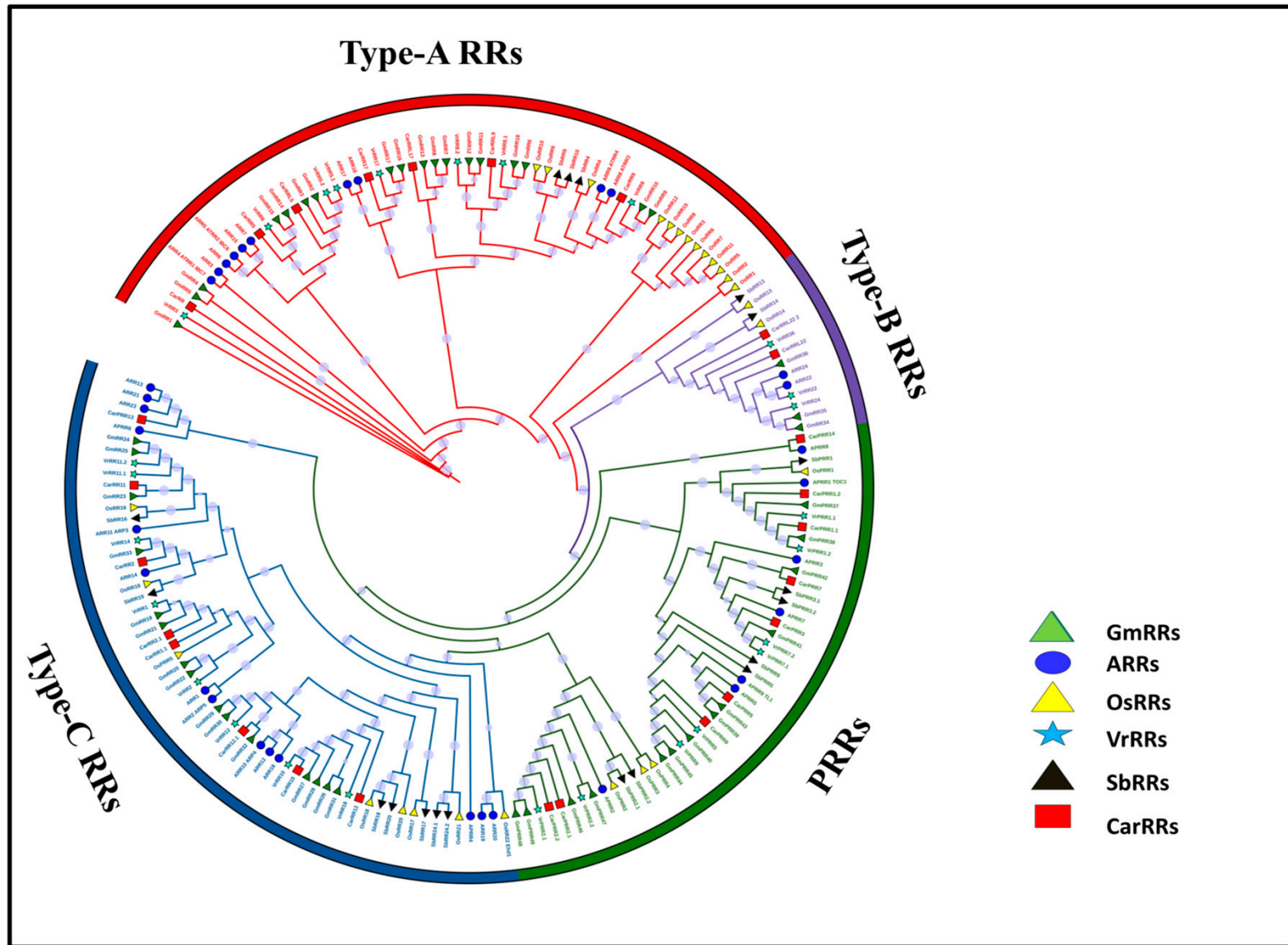


Figure S7. Phylogenetic tree of Response regulator proteins with other species. Type-A RRs-like proteins were grouped in a separate clade and represented by red color, PRRRRs-like proteins represent by green color whereas blue and purple colored clades show Type-B-like and Type-C-like proteins respectively.

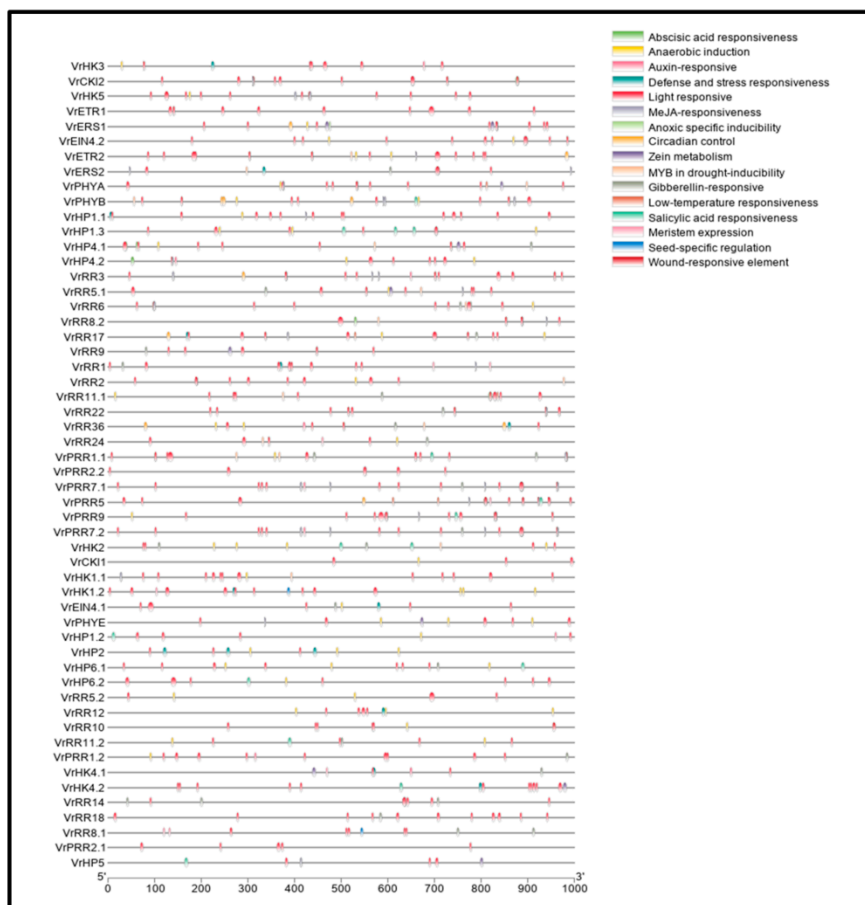


Figure S8. Representation of all the cis-regulatory identified in VrTCS promoter sequences. Various colors show a different types of switches discovered in each corresponding sequence.