

Group I-N	AmWRKY1	-DDGYNWRKYGQKQVKGSEYPRSYRKCT---HPNC	PVKKKVERSLDGQITEII---YKGOHNNH
	AmWRKY4	PSDGYNWRKYGQKQVKSPGFPRSYRRT---FADC	-VAKKIECCDRYNRVTDTV---YRSHNNH
	AmWRKY6	-DDGYNWRKYGQKQVKGSENPRSYRKCT---HPNC	PMRKKVEMSFAGEITEIV---YKGSNNH
	AmWRKY14	-EDGYNWRKYGQKHVKGSEFPRSYRKCT---HPNC	PVKKKVERSPEGHITEII---YKGAHNNH
	AmWRKY15	-EDGYNWRKYGQKLVKGSEFPRSYRKCT---YPNC	EVKKIFERSPSGQITEIV---YKGSDDH
	AmWRKY29	LDDGYNWRKYGQKIVKGNEFIRSYRRT---YPS	CQAKKQVERTHDGNKTDVN---YLGNNH
	AmWRKY31	-DDGYNWRKYGQKQVKGSEYPRSYRKCT---HPNC	PVKKKVERSLDGQITEII---YKGOHNNH
	AmWRKY51	--DGYNWRKYGQKHVKGSECPRSYRKCT---HLNC	PVKKKVERSSDGRVNEIT---YKGOHNNH
	AmWRKY59	-EDGYWRKYGQKQVKGSEYPRSYFKCT---NTN	CLVKKKVERSHDQITEIV---YKGSNNH
	AmWRKY63	-NDGYNWRKYGQKQVKASECPRSYRRT---HLD	CSVKKKVERSFDRGRSEIT---YKGEHNNH
	AmWRKY64	-YDGHNWRKYGQKHVKGSEYPRGYRKCT---YPNC	PVKKKVERMEDGQIAEIV---YKGEHNNH
	AmWRKY66	-DDGYNWRKYGQKQVKGSENPRSYRKCT---FPNC	PTKKKVERNLDGHITEIV---YKGSNNH
Group I-C	AmWRKY1	LDDGYRWRKYGQKVVKGNNPHPRSYRKCT---NP	CNVRKHVERAASDPKAVVTT---YEGHNNH
	AmWRKY4	--DGYRWRKYGQKVMVKGNNPHPRNYRRT---S	AGCPVRKHIETAVDNSNTSVIT---YKGGHNNH
	AmWRKY6	--DGYRWRKYGQKVVKGNNPNPRSYRKCT---S	AGCSVRKHHVERASHDAQSVITT---YEGKNNH
	AmWRKY14	LDDGYRWRKYGQKVVKGNNPNPRSYRKCT---S	AGCNVRKHVERASHDLKSVITT---YKGGHNNH
	AmWRKY15	LDDGYRWRKYGQKVVRGNPNPRSYRKCT---N	AGCPVRKHHVERASHDPKAVITT---YEGKNNH
	AmWRKY29	VNDGYRWRKYGQKFVKGNPNPRSYRCS---N	AGCPVKKHVERASHDSKVITT---YEGQHVH
	AmWRKY31	LDDGYRWRKYGQKVVKGNNPYPRSYRKCT---Y	AGCNVRKHVERAPSDPKAVITT---YEGKNNH
	AmWRKY51	LDDGFKWRKYGQKVMVKGNNPHPRSYRRT---Y	PGCNVRKQVERASADPKAVITT---YEGHDDH
	AmWRKY59	LDDGYRWRKYGQKVVKGNNPNPRSYRKCT---T	PGCPVRKHVERAANDIKSVITT---YEGKNNH
	AmWRKY63	LDDGFKWRKYGQKVVKGNNPNPRSYRRT---Y	AGCNVRKHVERAAADPKSVVTT---YEGKNNH
	AmWRKY64	--DGFRWRKYGQKVVKGNNVPRSYRRT---T	PKCNVRKYVERTSEDTTSFITT---YEGRHNNH
	AmWRKY66	LDDGYRWRKYGQKVVKGNNPNPRSYRKCT---F	NGCPVRKHVERASHDLRAVITT---YEGKNNH
Group IIa	AmWRKY21	VKDGYWRKYGQKVTRDNPCCPRAYFKCS--F	APTCPVKKKVQRSIEDQSVVVAT---YEGHNNH
	AmWRKY33	VKDGYWRKYGQKVTRDNPCCPRAYFKCS--F	APTCPVKKKVQRSIEDQSIVVAT---YEGHNNH
	AmWRKY41	VKDGYWRKYGQKVTRDNPSPRAYFKCS--Y	APTCPVKKKVQRSIDQSLLVAT---YEGOHNNH
	AmWRKY49	VKDGYWRKYGQKVTRDNPSPRAYFKCS--F	APTCPVKKKVQRSVEDQSVVVAT---YEGHNNH
Group IIb	AmWRKY13	--DGCQWRKYGQKMAKGNNPCPRAYRRT--M	AVGCPVRKQVQRCADRAILTTT---YEGTHNNH
	AmWRKY16	--DGCQWRKYGQKMAKGNNPCPRAYRRT--M	AAGCPVRKQVQRCADRSILITT---YEGNNNNH
	AmWRKY17	--DGCQWRKYGQKMAKGNNPCPRAYRRT--M	RVGCPVRKQVQRCADRSVLITT---YEGTHNNH
	AmWRKY18	--DGCQWRKYGQKMAKGNNPCPRAYRRT--M	RVGCPVRKQVQRCADRSVLITT---YEGTHNNH
	AmWRKY30	-NDGCQWRKYGQKISKGNNPCPRAYRRT--I	SSSCPVRKQVQRCADHMSILTTT---YEGTHNNH
	AmWRKY46	-NDGCQWRKYGQKTAKGNPCPRAYRRT--V	APGCPVRKQVQRCLEDSILITT---YEGTHNNH
	AmWRKY50	-NDGCQWRKYGQKIAKGNNPCPRAYRRT--V	APSCPVRKQVQRCADMSILITT---YEGTHNNH
	AmWRKY53	--DGCQWRKYGQKMAKGNNPCPRAYRRT--M	AVGCPVRKQVQRCADDRGILITT---YEGTHNNH
	AmWRKY62	-NDGCQWRKYGQKISKGNNPCPRSYRRT--V	SPSCPVRKQVQRSAEDMSILTTT---YEGTHNNH
Group IIc	AmWRKY2	LDDGYKWRKYGQKAVKNSSFPFRSYRRT---S	SPSGVKKRVERSYEDSSIVITT---YEGHTHTH
	AmWRKY9	LDDGYRWRKYGQKAVKNSPFRSYRRT---S	TACGVKKRVERSCEDTSLITT---YEGHTHTH
	AmWRKY11	LEDGYRWRKYGQKAVKNSPYPRSYRRT---T	QKCGVKKRVERSFQDPSTVITT---YEGOHNNH
	AmWRKY20	LEDGYRWRKYGQKAVKNSPFRSYRRT---S	ATCNVKKRVERSFNDPSVVVTT---YEGQHTH
	AmWRKY23	LDDGYKWRKYGQKSVKNNVHPRSYRRT---H	HTCNVKKQIQRLSKDNSTVVTT---YEGHTHNNH
	AmWRKY24	LDDGYRWRKYGQKAVKNKFPFRSYRRT---H	HTCNVKKQVQRLSKDNSIVVTT---YEGTHNNH
	AmWRKY25	LDDGYKWRKYGQKVVKNLSLHPRSYRRT---H	SNCRVKKRVERLSEDCRMVITT---YEGRHNNH
	AmWRKY28	LEDGYRWRKYGQKAVKNSPFRSYRRT---S	QKCNVKKRIERSFEDPSVVIITT---YEGQHHNNH
	AmWRKY34	LDDGYRWRKYGQKAVKNKFPFRSYRRT---H	QGCNVKKQVQRLSKDEGIIVTT---YDGVHNNH
	AmWRKY35	LDDGYKWRKYGQKVVKNLTHPRSYRRT---Q	DNCRVKKRVERLAEDPRMVITT---YEGRHNNH
	AmWRKY38	LDDGYKWRKYGQKSVKNVHPRSYRRT---H	HTCNVKKQIQRLSKDTSIVVTT---YEGHTHNNH
	AmWRKY42	LDDGFKWRKYGQKVMKNSPNPRNYRCS---A	EGCPVKKRVERDNDADRYVTT---YEGVHNNH
	AmWRKY43	LDDGYRWRKYGQKAVKNSPFRSYRRT---S	TACGVKKRVERSNEDPTTVVTT---YEGHTHTH
	AmWRKY45	LEDGYRWRKYGQKAVKNSPFRSYRRT---N	SKCMVKKRVERSCEDPVVIITT---YEGQHCH
	AmWRKY48	LDDGYRWRKYGQKAVKNKFPFRSYRRT---H	QGCNVKKQVQRLSKDEGIIVTT---YEGMHSH
	AmWRKY56	LEDGYRWRKYGQKAVKNSPYPRSYRRT---T	QKCAVKKRVERSFQDPVVIITT---YEGOHNNH
	AmWRKY60	LDDGYKWRKYGQKVVKNLTHPRSYRRT---Q	DNCRVKKRVERLAEDPRMVITT---YEGRHNNH
	AmWRKY61	LDDGYRWRKYGQKAVKNDRFPRGYRRT---H	NGCNVKKQVQRLSGDEGIIVTT---YEGTHSH
Group IIId	AmWRKY7	-PDDFSWRKYGQKPIKGSPPHPRGYRKCS--S	VRGCPARKHVERALDDPAMLIVT---YEGHNNH
	AmWRKY22	PSDEYSWRKYGQKPIKGSPPYPRGYRKCS--T	VRGCPARKHVERATDDPTMLIVT---YEGHRRH
	AmWRKY27	PPDEYSWRKYGQKPIKGSPPHPRGYRKCS--S	MRGCPARKHVERCLEEFSMLIVT---YEGEHHNNH
	AmWRKY40	PADEYSWRKYGQKPIKGSPPYPRGYRKCS--T	MRGCPARKHVERATDDPTMLIVT---YEGEHNNH
	AmWRKY44	-PDDYSWRKYGQKPIKGSPPHPRGYRKCS--S	VRGCPARKHVERALDDPTMLIVT---YEGHNNH
	AmWRKY52	-PDDYSWRKYGQKPIKGSPPHPRGYRKCS--S	VRGCPARKHVERALDDPTMLIVT---YEGEHHNNH
Group IIe	AmWRKY8	PPDSWTWRKYGQKPIKGSPPYPRGYRKCS--S	SKGCPARKQVERSRHDPPTLLIT Y ITNC H HTH
	AmWRKY10	PSDLAWWRKYGQKPIKGSPPYPRGYRKCS--S	SKGCSARKQVERSRTDPNMLVIT---YTSEHNNH
	AmWRKY12	PSDSWAWRKYGQKPIKGSPPYPRAYRCS--S	SKGCPARKQVERSVDPNMLVVTT---YACEHNNH
	AmWRKY19	PSDRWSWRKYGQKPIKGSPPYPRGYRKCS--T	SKGCSAKKQVERCKTDASMLIIT---YTSIHNNH
	AmWRKY32	--DMWSWRKYGQKPIKGSPPYPRGYRKCS--T	SKGCLARKQVERNRSDFGMFIVT---YTAEHNNH
	AmWRKY37	--DMWAWRKYGQKPIKGSPPYPRSYRCS--S	SKSCLARKQVEQSYMDFGKFIIIT---YTAEHNNH
	AmWRKY54	PSDLAWWRKYGQKPIKGSPPYPR ---	--- QVERSRTPDNMLVIT---YTSEHNNH
	AmWRKY55	--DSWAWRKYGQKPIKGSPPYPR --- NYRCS--T	SKGCAARKQVERSPNDPLIFVVS---YTGEHTH
Group III	AmWRKY3	-EDGHAWRKYGQKMILNTEYPRNYFRCTHK	FDQCKATKHVQKIQDDPPLFRTT---YIGHHTC
	AmWRKY5	--DEHAWRKYGQKDILGSTYPRSYRRTCV	HGVSGCQARKQVHQSDDDPSKWWIT---YNNQHTC
	AmWRKY26	VDDGYNWRKYGQKDILGANHPRAYRRTY	RNTQCLANKQVQRTDEDPSILEVI---YIGKHS
	AmWRKY36	LDDGYAWRKYGQKDILGAKHPRGYRRTY	RNVQCLATKQVQRSDDDPTIFEIT---YRGHTC
	AmWRKY39	-DDGYSWRKYGQKDILGAKYPRSYRRTY	RLVQDCWATKQVQRSDDDPTIFEIT---YKGAHTC
	AmWRKY47	LNDGYSWRKYGQKDILGANHPRAYRRTT	HRNTQCLATKQVQQTDDDPISFEVI---YRGKHS
	AmWRKY57	-EDGRAWRKYGQKEILNSEYPRCYRRTCH	KYECATKQVQRKEKPLLYQTT---YFNHHTC
	AmWRKY58	PEDGFTWRKYGQKEILGSRYPRSYRRTT	HQFYCPARKQVQRLDDDPFTFEVTT---YRGHTC
	AmWRKY67	-EDGHAWRKYGQKVILNAIHPRNYFRCTH	KYDQCCATKQVQKIQDD--LFRTT---YHSHHTC
	AmWRKY65	-DDGYKWRKYGQKSIKNSPNPRSYRRT---N	PRCSAKKQVERSIDDPTTLIIT---YEGHLH

Figure S1. Multiple sequence alignment of WRKY domains amino acid sequences in snapdragon. The highly conserved WRKYGQK sequence and the zinc-finger motif were highlighted by blue and yellow background, respectively. The mutated amino acids were marked in red letter. The vertical line in red indicates the intron position.

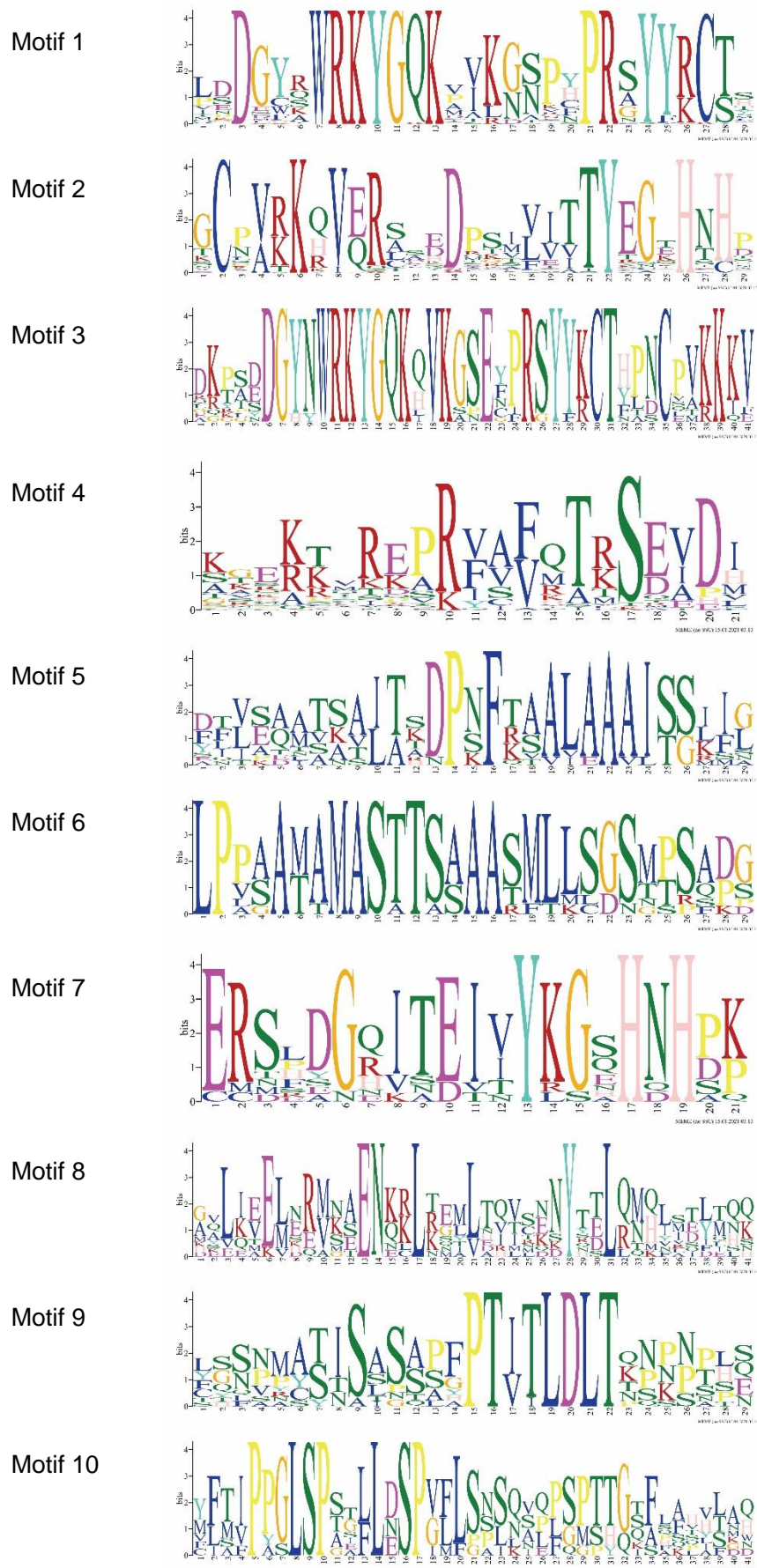


Figure S2. Conserved motifs in snapdragon WRKY proteins.

AmVQ1	RAPTTVLTTDTANFRQMVQEFTGIPAVP
AmVQ2	THSPKVIHANASDFMSLVQKLTGLNRSE
AmVQ3	TATTTFLNASITNFRALVQQHTGCHSTN
AmVQ4	GRATTHVNNANTHNFQALVQQFTGCDHSI
AmVQ5	PYPPTTFVQADTNSFKQVVQMLTGSSDTV
AmVQ6	ISSPMKVKTSASKERSLVQELTGKNSDI
AmVQ7	IVAPEIIRTDEHERELVQRLTGKPEER
AmVQ8	RNPTTLLNTDTTNFRAMVQQFTGGPTAH
AmVQ9	TLRPKVYITDSSNEKNLVQQLTGNGTNP
AmVQ10	IINTQYVETDAVSEKSVVQRLTGKGSSE
AmVQ11	THPTTFVQADTSSEKQVVQMLTGASKTA
AmVQ12	RTPTTLLNTDAANFRAMVQHFTGGPSSM
AmVQ13	RATTTFITADPANFRQMVQQVTGVRFNG
AmVQ14	ITNPIKFKTSASEFRALVQELTGQDADM
AmVQ15	IFAPEIIKTDAANRELVRRLTGKPTDD
AmVQ16	ISSPMKVKTSASKERSLVQRLTGKNSDI
AmVQ17	KARTMFVQADSTCFRDLVQRLTGPGVNE
AmVQ18	AVSPKVIHTTVTDFMNLVQRLTGNTTGD
AmVQ19	TVSPKIIHANPNEFMSLVQRLTGPNSSC
AmVQ20	TRSPKIIHAQAQDFMALVQKLTGLNESK
AmVQ21	QHQP HVYNINKNDFERNVVQQLTGSPARD
AmVQ22	QHQP HVYNINKNDFERNVVQQLTGSPARD
AmVQ23	IIEPQIIMTDVVNERDLVQKLTGKPASE
AmVQ24	IIEPQIITTDVENFLDLVQKLTKKPAPPE
AmVQ25	IVEPQIITTDVENFREIVQKLTGKHAE
AmVQ26	RAPTTVLTTDTTNFRQMVQEFTGIPAAP
AmVQ27	SQQPPVYNINKNDFREVVQKLTGSPAHE
AmVQ28	IPNTTFVQADPTTFRAVVQKLTGAGKPN
AmVQ29	PIPPKVYKVPVDFRDVVQKLTGAPEYI
AmVQ30	PNPTTFIQADTSSEKQVVQMLTGSTDAT
AmVQ31	KAPTTLLTANADNFRALVQQFTGCHSTF
AmVQ32	RAPTTVLTTDTNFRAMVQEFTGIPAPP

Figure S3. Multiple sequence alignment of VQ-motif in snapdragon. The highly conserved amino acids in the FxxhVQxhTG structure were highlighted by green background. The mutated amino acids were marked in red letter.

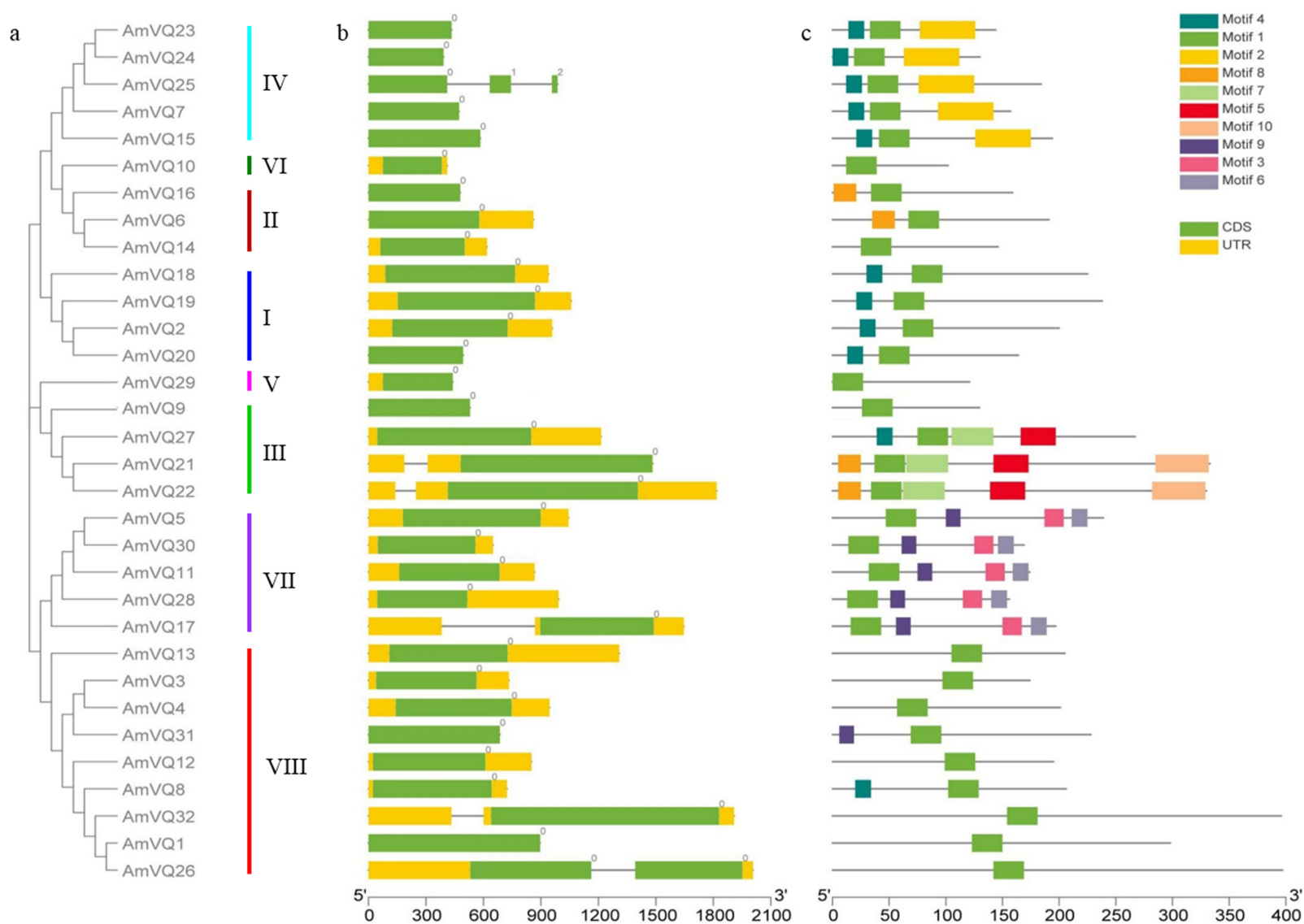


Figure S4. Structure characterization of *AmVQ* genes. (a) Phylogenetic tree of *AmVQ* proteins. (b) The exon-intron structures of *AmVQ* genes. The introns phases 0, 1 and 2 were indicated by numbers 0, 1 and 2, respectively. (c) The conserved motifs of *AmVQ* proteins.