









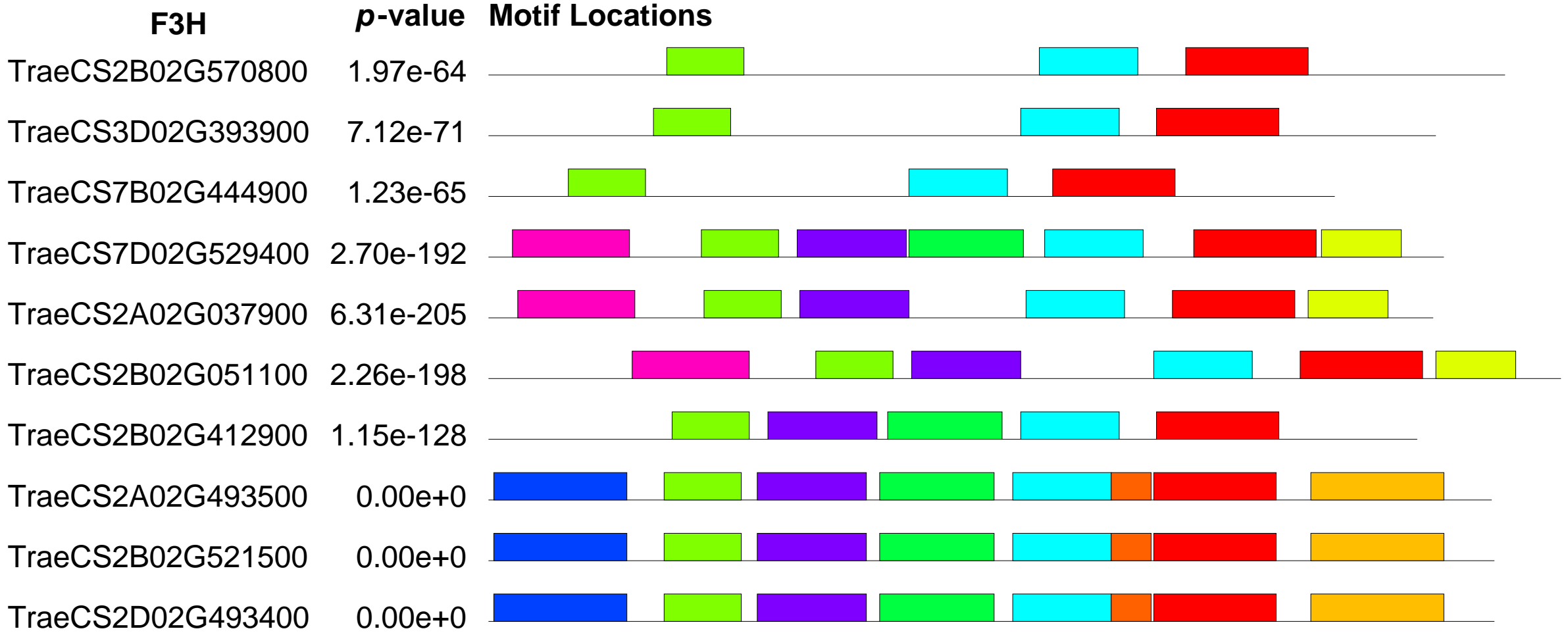




Motif	Symbol	Motif Consensus
1.		WNSVFWIAHPGGPAILDMVEAKVNLNKERMTRATHVLSEYGNMSSACVLF
2.		DYQLTKMLGLRPSVKRLMMYQQGCFAGGTVLRLAKDLAENNRGARVLVVC
3.		NCVYQADYPDYYFKITKSDHMADLKEKFKRMCDKSQIRKRYMHLTEEILQ
4.		ERPLFQLVSASQTILPDSEGAIDGHLREVGLTFHLLKDVPGLISKNIERA
5.		PNMCAYMAPSLDARQDIVVVEVPKLGKAAAQKAKEWGQPRSKITHLVFC
6.		IMDEMRKRSAEDGHATTGEGMDWGVLFGFPGPLTVETVVLH
7.		SEITAVTFRGPHESHLDLVLGQALFGDGAAAVIIGADPDES
8.		ATMTVEEVKRAQRAEGPATVLAIGTATPA
9.		EDAFKPLGIDD
10.		TTSGVDMP



Motif	Symbol	Motif Consensus
1.		PPVSGALVVNIGDHLQLMSNGRFKSVEHRAVVNGEGPRLSVATFFN
2.		QKVAVNYYPACPZPDLTLGLKRHTDPGFJTLLLQDAV
3.		CETWGFFQVVNHGVPEALIADMLRAVREF
4.		KKPYDRDGGKKGRYISSSDLQGEAVABWRDILTYSYPVP
5.		EGEEPILEEPITFAEMYRRKMERDLDLAKRKKQAKDQLMQQQQLQLQQQQQ
6.		RWPEKPAGWRAVVERYSERLMGLSCKLLGVLSEAMGLESEALA
7.		PVSNETFLPTAAWGEATLRPSFVRDEDERPKVAHDRFSDAVPVISLDGID
8.		LKAFDETRAGVKGLVDAGVTAVPSIFHHPPESLDHGASRPHRFT
9.		GGLQATRDGGKTWIT
10.		APTRVLAPIVADGDEARYRSTTVEEVVRQY



Motif	Symbol	Motif Consensus
1.		PRESQEDCQVQGYDVPAGTRVLVNAWAIGRDPAYWEDAEEF
2.		DFKGNDFZFLPFGAGRRCPGMAFGLASV
3.		IKAVJLDVFAAGTDTSATTTJEWAMAELMRNPRVMQKAQAEV
4.		YGGSDIAFAPYGEYWRQLRKJAVVELLSARRVRSFRAIR
5.		VAEDDLAKLPYLKAVIKETLRLHPPAPLL
6.		GAVPTVVVSSAEAAREVLKTHDHVFASRP
7.		PPGPWALPIIGHLHLL
8.		JDMTEAFGLTVRRKEPLLLVP
9.		LPHRALRDLARRHGPLMLLRL
10.		LANLLYHFDWELPDG

F3'5'H

p-value

Motif Locations

TraesCS1D02G403300

6.50e-153



TraesCS2D02G521700











1.77e-132

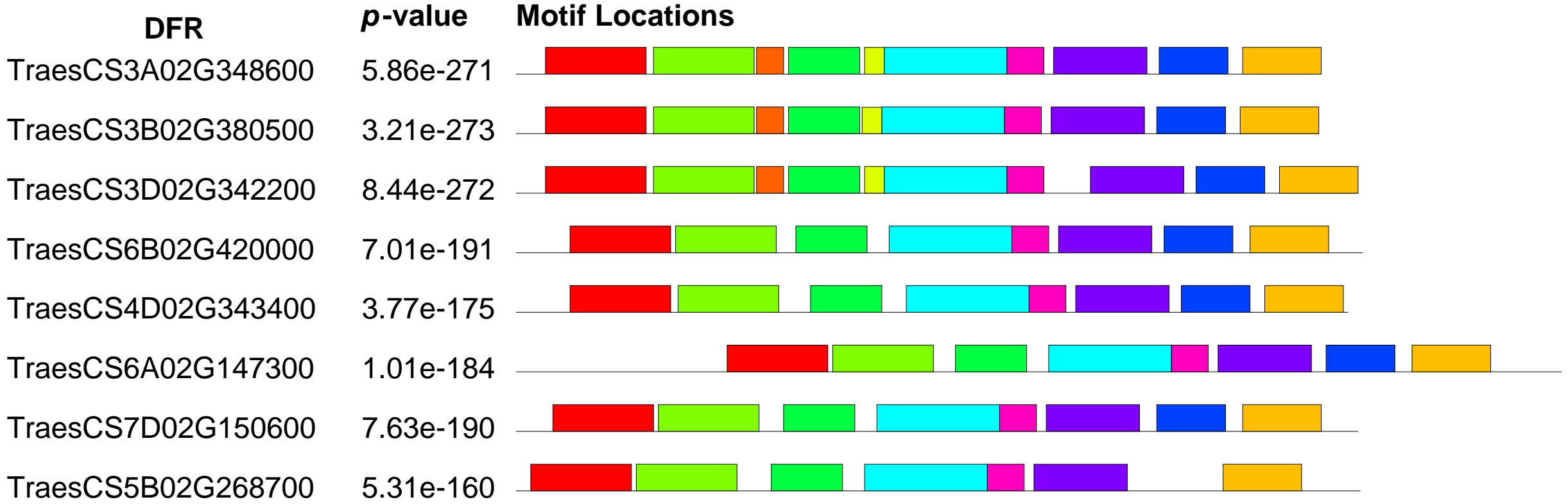


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3.32e-146



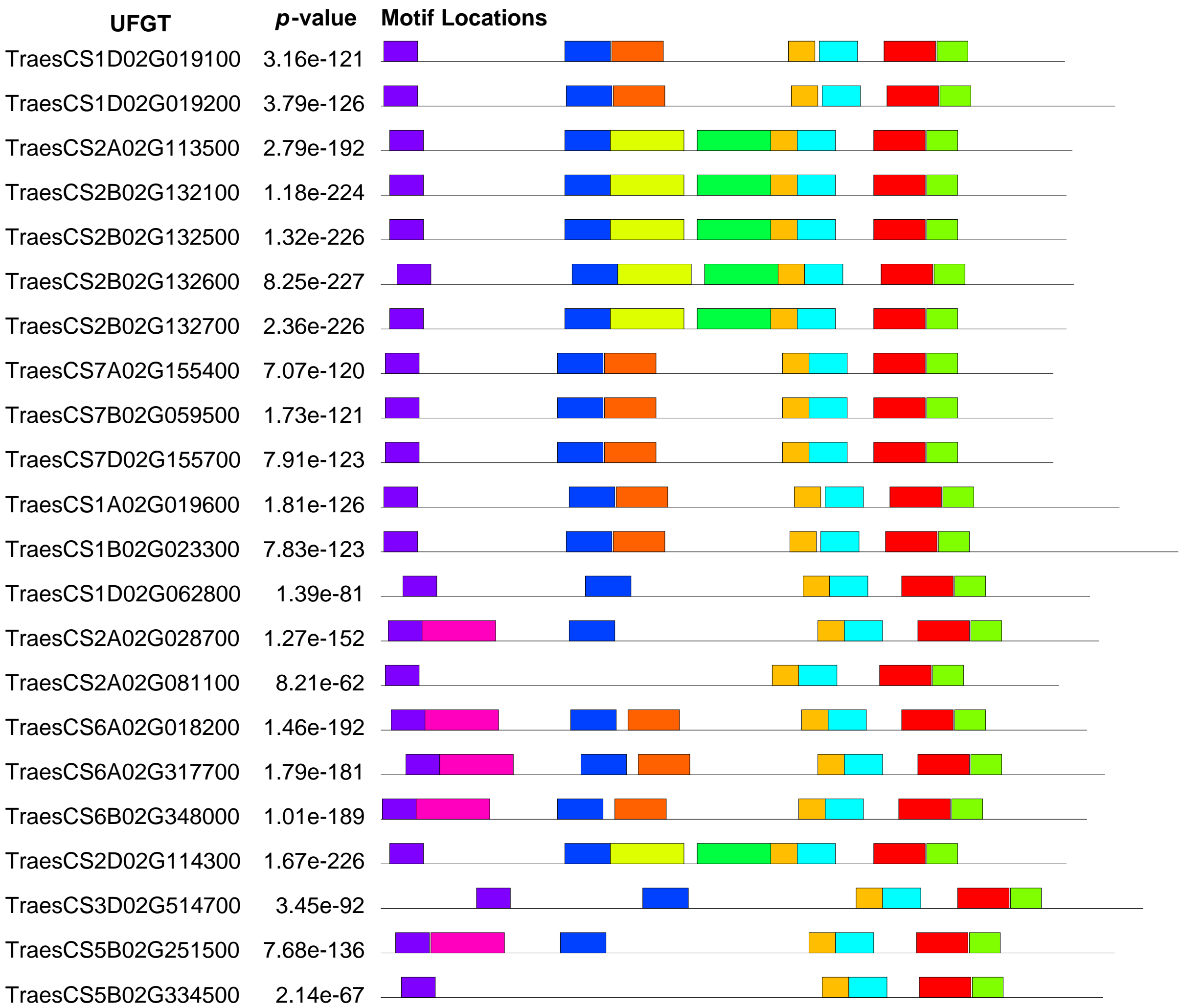
Motif	Symbol	Motif Consensus
1.		YLQAVIRETLRLHPYGPLJPPREAMEDCTVAGYDVPRGTQVIVNVWALGR
2.		IKAIVLDILIAGTDTTSATTVEWAMAELMNNPEVMRKATAELDAVVG
3.		PYGDQWRK
4.		FLPFGAGRRGCPGIALGLRFVGLALASLLQGFDW
5.		PEEFRPERF
6.		MEKCRSN
7.		DPEYWPD
8.		HQRLKNK
9.		VVSSRAAAREVLRKHDAAFAGRP
10.		IZERIEEW



Motif	Symbol	Motif Consensus
1.		VCVTGGGGFIGSWJVKLLLDRGYTVHGTVRNPQDEKNAHLL
2.		DESCWSDVEICKKTELWYCVSKTLAEKAAWEFAGEEGLELVVNPGLVLG
3.		DGADERLRLRFQADLLDPASLRAAIEGCHGVFHLASPVILDP
4.		GQKLTYENFFVGYVDVRDVAQALVLVYENPSAQGRYLC
5.		SSKKLRDLGVRFTPLDETLRETVDCLREKGEJ
6.		GTLNVLRAAKDAGVKRVVMTSSQTAVCPN
7.		HLVDFHDI LANLYPEYPIPRIQEDEQGW
8.		PTLQPAPNGSLRLLL
9.		QDPENELLPA
10.		DWPAGKVI



Motif	Symbol	Motif Consensus
1.		PGTLVVHIGDALEILSNGRYRSVLHRGLVNRQAVRVSVAVF
2.		LKLKJNYYP RCPQPELAVGVEPHTDVSALTFIL
3.		RDWEDYLYLMLHPDARRDHALWPAHPPEY
4.		LRAAGTGFFRMPJEDKZAYAN
5.		MARVEALSMSGATAIPA EYVRPQEERQGLGDAYDEAAA SWSAAGSPRIPV
6.		ETPRFEPRTFRQH LERKVLKKTNDQQEEEVVKKPPVVAQEEEKEVVKKPP
7.		VPVTKTTFGEHVSALSSRLLAILSLGLGVPADTLERRLR LRTSG
8.		VRAAAE EWGVFHVAGHGIPEDLI
9.		TNGVPGLQVLLPGDGQ TWVTA
10.		GRLEGYGSRLVGS



Motif	Symbol	Motif Consensus
1.		SWAPQERVLRHPAVGAFLTHCGWNSVLESMAAGVP
2.		SPEZLAELAWGLELSGAPFLWVLRPD
3.		VCLPFFADQPTNARLVAAEEWG
4.		EKPHVVVFPFPAQGHINPLLELA
5.		GKEPGSVVYVSFGSEATM
6.		IKTCADIERKYVDYLSQLVGKEVVPTGPLLVDSGGSEGKRDGGRIMRWLD
7.		MWWAAEAAAARGVPAVHFWTGSACAFLAYLH
8.		KVLHARGFHVTFVNTEYNHRLLRSRGPDALAGVPGFRFETIPDGLPPSD
9.		DALRKDVGDLAASRADELLTSHPGGLGGYRVRDLPD
10.		CLKNERTPSAFFPFESISLGAEEDAKYAAQLVSRDDGTAQIPERDRLPLS

Supplemental Table S1: Analysed motifs of anthocyanin biosynthetic genes

CHS			
	Domain ID	Motif	Function
1	Chal_sti_synt_C	WNSVFWIAHPGGPAILDMVEAKVNLNKERMTRATHVLSEYGNMSSACVLF	Catalyze the formation of (2S)-5-hydroxyflavanone from 6'-hydroxychalcone (naringenin chalcone)
2	Chal_sti_synt_N	DYQLTKMLGLRPSVKRLMMYQQGCFAGGTVLRRLAKDLAENNRGARVLVVC	
3	Chal_sti_synt_N	NCVYQADYPDYYFKITKSDHMADLKEKFKRMCDKSQIRKRYMHLTEEILQ	
4	Chal_sti_synt_C	QLVSASQTILPDSEGAIDGHLREVGLTFHLLKDVPGLISKNIER	
5	Chal_sti_synt_N	PNMCAYMAPSLDARQDIVVVEVPKLGKAAAQKAIKEWGQPRSKITHLVFC	
6	Chal_sti_synt_C	IMDEMRKRSAEDGHATTGEGMDWGVLFGFGPGLTVETVVLH	
7	Chal_sti_synt_N	SEITAVTFRGPHESHLDLVLGQALFGDGAAAVIIGADP	
8	Chal_sti_synt_N	EEVRKAQRAEGPATVLAIGTATPA	
F3H			
1	2OG-Fell_Oxy	PPVSGALVVNIGDHLQLMSNGRFKSVEHRAV-VNGEGPRLSVATFF	Role in the 3-hydroxylation of flavanone to form dihydroflavonol
2	2OG-Fell_Oxy	VAVNYYPACPZPDLTLGLKRHTDPGFJTLLQDA	
3	DIOX_N	CETWGFFQVVNHGVPEALIADMLRAVREF	
6	MbtH	WPEK---PAGWRVVER	
9	BNR	ATRDGGKTW	
F3'H			
1	p450	PRESQEDCQVQGYDVPAGTRVLVNAWAIGRDPAYWEDAEEF	Catalyze the hydroxylation step to impart purple-blue pigments
2	p450	FKGNDFZFLPFGAGRRMCPGMAFG	
3	p450	IKAVJLDVFAAGTDTSATTJEWAMAELMRNPRVMQKAQAEV	
5	p450	EDDLAKLPYLKAVIKETLRLHPPAPL	
6	p450	VPTVVVSSAEAAREVLKTHDHVFASRP	
F3'5'H			
1	p450	YLQAVIRETLRLHPYGPLJPPREAMEDCTVAGYDVPRGTQVIVNVWALGR	Catalyze the hydroxylation step to impart purple-blue pigments
2	p450	IKAIVLIDILIAGTDTSATTVEWAMAELMNNPEVMRKATAELDAVVG	
4	p450	FLPFGAGRRGCPGIALGLRFVGLALASLLQGFDW	
DFR			
1	GDP_Man_Dehyd	VTGGGGFIGSWJVKLLLDRGYTVHGTVRNPQDEK	

1	Epimerase	VCVTGGGGFIGSWJVKLLLD RGYTVHGTVRNPQDEKNA	NAD dependent epimerase/dehydratase
2	NAD_binding_4	KTELWYCVSKTLAEKAAWEFAGEEGLELVVNPGLVLG	
3	NAD_binding_10	DERLRLFQADLLDPASLRAAIEGCHGVFHLA	
3	Epimerase	DERLRLFQADLLDPASLRAAIE--GCHGVFHLAS	
6	3Beta_HSD	GTLNVLRAAKDAGVKRVVMTSSQTAVCPN	
ASN			
1	2OG-Fell_Oxy	GTLVVHIGDALEILSNGRYRSVLHRGL-VNRQAVRVSVAVF	Catalyze a remarkably diverse range of oxidative reactions
2	2OG-Fell_Oxy	KJNYYP RCPQPELAVGVEPHTDVSALTFIL	
8	DIOX_N	VRAAAEEWGVFHVAGHGIPEDLI	
UFGT			
1	UDPGT	WAPQERVLRHPAVGAFLTHCGWNSVLESMAAGVP	UDP- glycosyltransferase
2	UDPGT	VCLPFFADQPTNARLVAEEWG	