Identification of basic/helix-loop-helix transcription factors reveals candidate genes involved in anthocyanin biosynthesis from the strawberry white-flesh mutant

Fengli Zhao<sup>1,2</sup>, Gang Li<sup>1,2</sup>, Panpan Hu<sup>1,2</sup>, Xia Zhao<sup>1,2</sup>, Liangjie Li<sup>1,2</sup>, Wei Wei<sup>3</sup>, Jiayue Feng<sup>3</sup>, Houcheng Zhou<sup>1,2\*</sup>

#### **Supplemental materials**

**Supplementary Figure 1.** Multiple sequence alignment of the bHLH domain among *FvbHLH* genes.

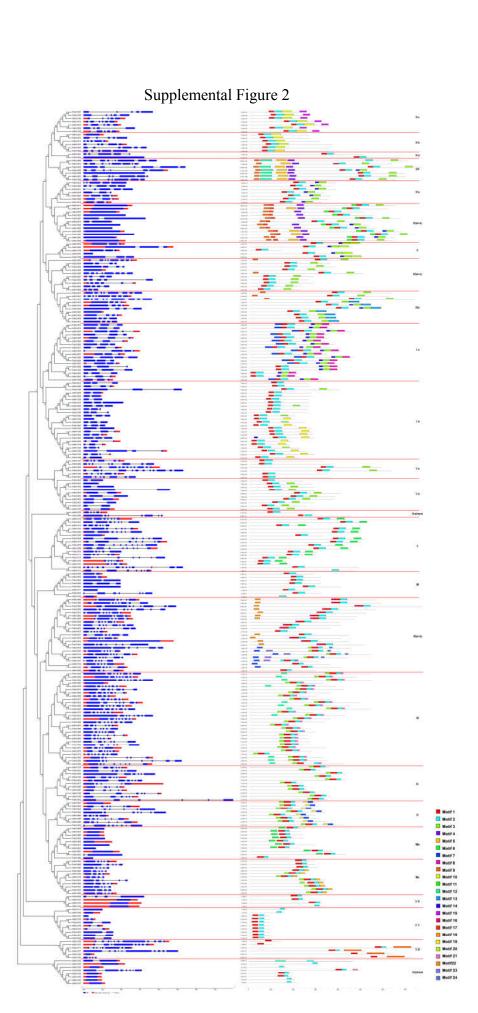
**Supplementary Figure 2.** Structural analysis of strawberry bHLH transcription factors. The gene structure is shown on the left, with exons and untranslated regions (UTRs) represented by blue-corner rectangles and red rectangles, respectively. The protein motif analysis of strawberry bHLH genes are shown on the right. 1-24 motif was denoted by rectangle with different colors on the lower right corner.

**Supplementary Figure 3.** Sequence logo of the FvbHLH domain by MEME.

**Supplementary Figure 4.** Analysis of semi-quantitative RT-PCR for expression profiles of 113 FvbHLH genes in response to ABA treatment. *FvActin*, *FvRib413* and *FvGAPDH2* were used as an internal control.

**Supplementary Figure 5.** Analysis of semi-quantitative RT-PCR for expression profiles of 113 FvbHLH genes in response to Eth treatment. *FvActin*, *FvRib413* and *FvGAPDH2* were used as an internal control.

	Supplemental Figure 1	
AtbHLH001	RDETGNHAVLEKKRREKINERFMTERKIIPSINKIDKVSILDDTIEYLQELERRVQELESCRESTDTETR	505
AtbHLH002	.EETGNHALSEKKRREKLNERFMTERSIIPSISKIDKVSILDDTIEYLQDLQKRVQELESCRESADTETR	469
FvbHLH066 FvbHLH029	GESLMNHVLCERKRREKLN.ERFSILKSLVFSIQKDDKVSILDDAIEYLKDLEKRVEFLETSQESTDIEA. DELSANHVLAERRREKLN.ERFIILRSLVFFVTKMDKASILGDTIEYVKQLRKKIQDLEARNVHLEDDQQ	500 542
FvbHLH098	KESTINSKSESDDVHEKLIENEKLMVIRSMVFSMIEIDKASIIDDTIKYLKELEARAEEMESCMDIVEAIA.	511
FvbHLH002	RSRTIVSERRRRGRMKDKLYAIRSLVENITKMDKASIIGDAVMYVQDIQKQAKKIKGEISGLQASIE	204
FvbHLH003 FvbHLH031	RSRTILVSERKREGRMKEKLYAIRSLVENITKMDKASIVGDAVAYVQDIQKHAKKIEVEIIGLEESIE QSKNLVAERKREKKLNEKLYKIRSLVENISKMDKASILKDAIDYVKDIQRQVKEIQDVLEDNSNGG.	204 397
FvbHLH032	QAKNIVAERKRRKKINDRIYEIRSIVENISKLDRASILGDAIEYVMEIQNQAKKIQDELDDDHDHEE	467
FvbHLH044	NHSEAERRREERINAHLSTIRGLVECTEKMDKAALLAEVIRGVKEIKKDSLESSKGFLIPIDADE	140
FvbHLH037	NHKEAEKRRRERINSHLDKIRSLLECNSKTDKASLLAKVVERVKEIKQQMSEITELETFPSEADE	154
FvbHLH055 FvbHLH043	SHSEAERRRRERINNHLAKIRSLLESITKIDKASLLAEVIQHVKE <mark>L</mark> KRQISVIAETSPVPTEIDE SLSPQSIAARERBRRITEKINEIGKLVPCGSKMNIAEMFQAAYKYIKFLQAQVAMLKIMDSVKANKGH	227
FVbHLH094	VSPQSIAARERRRKITEKTQELGKLVFGGSKMNTAEMLTAAYSYVKFLQAQMGILQFMGSFQEVK	223
FvbHLH008	AAEVHNLSEKRRRSRINEKMKALQNLIENSNKTDKASMLDEAIEYLKQLQLQVQMLSMRNGMSLHPMC	214
FvbHLH013	PSKNIMAERRERKRINDRLSMIRSIVEKISKMDRTSILGDTIDYMKELLERINKIGEEKIEENTNG.	260
FvbHLH010 FvbHLH095	ESQRITHIAVERNRRKIMN. DYLSVIRSMMEAS. YSQRGDQASIIGGAINFVKEIEQLLQSIEASRRTNQQSDL ESQRMTHIAVERNRRRQMN. DHLNVIRSLMEPS. YIQRGDQASIVGGAIDFVKEIEQHLQSIEAQKRMRRAEGF	193 273
FvbHLH099	ESCRMTHIAVERNERCOMNDHLNVIRSIMERSYIQRGDQASIVGGAIDFVKELEQHLQSIEAQKRTRRAEGF	223
FvbHLH053	MSHIAVERNREKÇMNEHLKVIRTLTECFYIKRGDQASIIGGVIEFIKEIHQVLQSIESNKRRKK	64
FvbHLH101	MAKKINHNASERERRKNINNIYSSIRSIVPADHAKRISIPATVSRVIKYIPEIQQQVEGIIQKRDELISKNF	139
FvbHLH045 FvbHLH067	RADRKTIEKNRRNOMKALYSEINSLIPHHQHSREVTSLPDQIDAAVNYIKKIQTNLEKIRAKKD.RHMGVEKLDRKTVERNRRIOMKGLCFKIASMVPPQYFKSSKSKEMMTQQSQLDLAASYIKQITERIENIKERKEKELKSQS	85
FvbHLH028	MVKKLNHNASERDREKKINNLYSSIRSLVFADHAKRLSIFATVSRVLKYIPEIQQQVEGIIQKRDELLSNMS	138
FvbHLH087	KIERRVIEKNRRNHMKILYSQINSLIPNCHSKEPVSLPEQIDEAINYIKTLESNMQKIKQKRDNLKIGRK	93
FvbHLH105 FvbHLH106	RKIMRRDNERÇRRÇIMAIRTASIRSILPLESIKGKRSISEHINEAVNYIKÇ <mark>i</mark> KEKIÇEİNAKREELRRV KKMMHRDTERKRRÇEMATIYASIRSTIPPQSMKGKRSIADHMNEAVNYIKLIQTRIKEIGSRRDDIKIÇRS	139
FVbHLH107	KMMIHRENERORRODMATLYSSERSLEPLEFVKGKRSISUHMNEAVNYIKHEGNRIKTEDAKRDELKKFPK	146
FvbHLH065	KVKKIMHRDIERCRRCEMTTLYASLRSHLFLEYLKGKRSISDHVHCAANYIKHLCKDLEELREKKDELKN	155
FvbHLH090	RLKHSETEQRRRSKINERFQKIREIIFENDQKRDKASFLLEVIEYIQFIHEKINLYEGSYQKWSPEPT	100
FvbHLH051 FvbHLH058	srqssgstpsikddqiielvskirqlvfeirdrrsdkvsaskvlqetcsyirnLhrevddlserls srqssgstpsikddqiielvskirqlvfeirdrrsdkvsaskvlqetcsyirnLhrevddlserls	72
FVbHLH040	SSQSSGS.FSIRDDQIIELVSKIRQIVFETRDRRSDQVSASKVLQETCSYIRNIQREVEDLSERLS	71
FvbHLH073	SRCSGGSRISDDCINDLVTKLOCLLFEIRNSRRSDKVSASTVLCETCNYIRN HREVDDLSERLS	72
FybHLH023	AARKMQKADREKLRADRIN.EHFME <mark>IGNVLDPDRPKNDKATILACTIQVLKDL</mark> SSEVDKLKTDCTSLTEESR SSATSSKACREKLRADRIN.DKFLE <mark>I</mark> GSILEPGRPPKTDKAAILIDAVRMVNQLRGEAQK <mark>L</mark> KDSNSSLQEKIK	113
FvbHLH047 FvbHLH109	SSATSSKACREKIRRDRINDKFLEIGSILEPGRPPKIUKAAILIDAVMVNQLKGEAQKIKUSNSSLQEKIK CNVSSSKACREKMRRDRINDKFLEISTILEPGRPPKIDKAAILVDAVRMVNQLKGEAQNIKDSSESLQEKIT	148
FvbHLH006	SARKVQKADREKLRRDKINEHFLEIGHTLDFDRPKNDKATILTDTIQVLKDLISDVNKLKSECATINDESR	112
FvbHLH041	ETPSPLPTFKVRMEKLGDRITALOCIVSPFGKTDTASVLHEAIEYIKFLHDQVGVLSTP.YMNNGAPI	429
FvbHLH046 FvbHLH049	etsstlpafkvrrekmgdritalqqivspfgktdtasvlseaieyikflheqvsvlsnp.ymksgaai wcgsgakacrekirrerindkfldisavlepgrpaktdkpailddairvltqlraeaqeitqineklleeik	395 143
FVbHLH049 FvbHLH068	LKKSELHNQSERNERNAIKDKIHILGGLVENCTKRIYHFQTDQASILSDVVDHMKALLVQRQMLSMTGHPMWLAGV	265
FvbHLH007	PVVAFRGSRLARERECTLSDKTRCLCKLLPWENKMDTAAMLETAHRYVRFLCACVAALHAMPIVASDCSP	280
FvbHLH108	DHELHIYTEREREKKMRNMFANLHALLEGIPSKADKSTIVDEAVTYIKRLEITLGSLGGGKRERMRSLP	192
FVbHLH102 FVbHLH097	DNRKLQVPVRRSQKLSDKITA <mark>I</mark> CKLVSPYGKIDTASVLQEASVYIVL <mark>L</mark> QQQIQNLHRIFSSSYINAV .EEPLNHVEAERCRREKLNQRFYALRAVV <mark>F</mark> NISKMDKASLLGDAIEYIQDLQRKLKD <mark>M</mark> ESERESAGGISR	237 511
FvbHLH096	.DTPLNHVEAERCRREKLNHRFYALRAVVPNVSRMDKASLLSDAVSYINELKAKVDELESÇLÇRESKKVK	373
FvbHLH011	DHVLAERKRREKLSQRFIALSALVEGLKKMDKASVLGDAIKYVKQLQERMKILEEQAAKKTVESV	239
FvbHLH022	VHIMAERKRREKLSQQFIALSAMVPGLKKTDKASVLGDAIKYIKQLQEKLKILEEQTRVKKMETV	225
FvbHLH012 FvbHLH001	DHIMAERKRREKLSQRFIALSAIVEGLKKMDKASVLGDAIKYVKQLQESVKVLEEQTKKRTVESVAAAIHNQSERKREDKINQRMKTLQKLVENSSKTDKASMLDEVIEYLKQLQAQVHVISRMNMPAMM	340
FvbHLH019	AAAIHNQSERKRRDKINQRMKTIQKIVENSSKTDKASMLDEVIEYLKQIQAQVHVISRMNMPAMM	340
FvbHLH074	ATDSHSLAERARREKISERMKIIQDIVFGCNKVIGKALVLDEIINYIQSIQRQVEFLSLKLEAVNSRVN	220
FvbHLH063	ATDSHSLAERARREKISERMKIIQDLVPGCNKVIGKALVLDEIINYIQSLQRQVEFLSMKLEAVNTR	221 335
FvbHLH034 FvbHLH060	ATNSHSLAERVRREKISERMRLIQELVEGCNKITGKAVMLDEIINYVQSLQQQVEFISMKLATVNPE ATDSHSLAERVRREKISERMKMIQRLVEGCDKVTGRAVMLDEIINYVQSLQNQVEFISMKLASVNP	238
FvbHLH083	ATDPHSIAERIRBERIAERMKAIQELVESCNKTD.RAAMLDEIVDYVKFIRLQVKVISMSRLGGAGAVA	250
FvbHLH005	ATDPHSIAERIRREKIADRMKNIQELVPKSNKTD.KASMLDEIIEYVKFIQQQVKVISARRIGATGAKG	316
FvbHLH048 FvbHLH093	ATHPRSIAERVERTRISERMRKIQELVENMDKQINTADMLDLAVDYIKNLQTEVQILSEARAKCICS ATHPRSIAERMRRTRISERMRKIQDLFENMDKQINTAEMLELAVEYIKDLQKEVKIIKDIKAKCSCS	427
FvbHLH077	ATHPRSIAERVERTRISDRIRKECELVENMDKQTNTADMLDEAVEYVKFEQKQIQEESEYQRRCKCM	221
FvbHLH036	SKDPQSVAARHREERISERIRITQRIVEGGTKMDTASMLDEAIHYVKFTKSQVQTTERAAVNNNNRV	201
FvbHLH033	AIDPQSIYARKRRERINERLRVIQNIVFNGTKVDISTMLEEAVHYVKFLQLQIKLISSDD	356 343
FvbHLH062 FvbHLH052	EHFRSKNINAERKRENRIKEGELAIRALVEKITKMDRASIPADAIEYIKELQQQVKELEEELREMEEEDSATHPRSIAERERETRISGKLKKIQDLVENMDKÇISYADMIDLAVQHIKGLQNQVQNIYKDLEGCTCG	345
FvbHLH014	SDDPGSVAARHRRERISEKIRILORIVEGGTKMDTASMLEEAIRYVKFLKRQIRLLQQSS.HHHPQFC	214
FvbHLH086	stdpgsvaarerrhriserfkilgslvpggnkmdtvsmleeaigyvkflkngirlhgtminfarddac	98
FvbHLH071 FvbHLH009	vaaihngserkredringkmkaigrivenanktdkasmldeviryleligagvommnsmrngmofhmn .skdposvaarhrreriseririigriveggtkmdtasmldeaihyvkfikkgvotieragadr	257
FvbHLH076	ATDAQSVYARRRERINERLKVIQNLVENGRKVDISTMLEEAVNYVKFIQLQIKMISSDD	301
FvbHLH021	ASDPQSLYARKEREKINERLRVIQNLVPNGIKVDISTMLEEAVHYVKFIQLQIKLISSDD	323
FvbHLH103	askshsqaekrerdrinaqlatirklipqsdkmdkaallgsvidevkdikrranevskalmvptefdd	135
FvbHLH026 FvbHLH089	AAEVHNLSERRRRDRINEKMRT <mark>L</mark> QELIFRCNKSDKASMLEEAIEYLKSLQLQVQMMSMGCGMVFMMFP AAEVHNLSERRRRDRINEKMRA <mark>L</mark> QELIFHSNKTDKASMLDEAIEYLKSLQLQLQV <mark>M</mark> WMGGGMTFMMFP	374
FvbHLH020	ELAIDPQRTYAKKRROKINSRLRILQNLVFNGTKVDISTMLEETVEYVKFLQLQIKLLSSDELWMYAP	255
FvbHLH092	ATDSHSLAERARBEKINARMKLIQELVEGCNKISGTALVLDEIINHVQSIQRQVEFISMRLATVDPRID	261
FvbHLH064 FvbHLH042	.YYGSGNGLVMPDSYSSSNSARSFTDVISFNSRLGKPLIDHVHHAQKPSNFKSSINLSDNTCKKQGLQTSSPVKMSGRGQ .IYKSKNLNAERKRRAKLSDRLKKRSLVFIITNMNKATIVDDAITYIYELQKEVNMLQEQLFEMEALSS	374 109
FVbHLH059	KGLPAKNIMAERRRKKIN. DRIYMIRSVVEKISKMDRASILGDAIEYIKEILQRINNIHNELESIPPGSA	412
FvbHLH084	SRAAEVHNLSERRRODRINEKMRAICELIPNCNKVDKASMLDEAIEYLKTICLQVQIMSMGAGLYMPQMM	506
FvbHLH079	PPSSAQPTFKVRKEKIGDRITALHQLVSPFGKTDTASVLLEAIGYIRFLQNQIEALSLPYLGSGSPNM	301
FvbHLH038 FvbHLH050	.LESRIPCPPLKVRKEKLGDRIATIQQLVAPFGKTDTASVLMEAIGYIKFLQNQVETLSVPYMKSSRDNK .MASKNIVSERNRRKKLNERLFAIRAVVENISKMDKASIIKDAIDYIQEIHDQERRIQAEIMDLESGKS	116
FvbHLH100	KGTKHFATERÇREVÇINDKFSA <mark>I</mark> RELV <mark>E</mark> NFTKPDRASVVGDAIDYIÇE <mark>I</mark> KRTVSE <b>I</b> KLLVEKKRCGRE	323
FvbHLH030	.SAKGQKTLVTDRQARRIRIAERLTELEKLLPHSVEGGQEFVLDDVIDHIKFLQLQIKDLSRSRLGGEAVAE	238
FVbHLH004	TTSQLHHMISERKBREKLNESFHSLKSLLFPGTKKDKASVLTTARDYLTSLQAQVDELSKRNQQLEAAAR ENQRMTHIAVERNBRKQMNEYLSALRSIMFDSYVQRGDQASIIGGAINFVKELENQVQFLGAQNFNRNSSDL	485 199
FvbHLH091	ATHPRSIAERVERTRISERMRKIQELVENMDKQTNTADMLDLAVDYIKEIQKQFKSISDVRANCKCL	308
FvbHLH016	AKKHSESERREMRINSQYAALRKILENLIKMDKASVLAETVRQVRELKKVVTDIDAACRGSGSECV	113
FVbHLH072	SNYMTVEKNELREDTSALETÇIER ÇSELÇERVFQSKPDLNVPPVEVAAHETGNCLG PAÇESALQQSP.	171
FvbHLH111	.PNKETQSFSKRCRNDDQSDQLKFYAENYSQHFDLLQTDSSTTTTEGGGFRLISENPPKAKK_KSSSDQKSTTPS KKRAKPGESTRPRFKDRQQIQDRMKDLRGMIFNGGKQCSIDALLDRTIKYMIFLQGVTKHADKLKQPHESKLT	270 631
FVbHLH081	ETCRMTHIAVERNERKOMNEHLAILRSLMEESYAQRGDQASIVGGAIEFVKELEHLLQSLEAQKLQLLPSNV	177
FvbHLH104	GCCRMSHITVERNRRKCMNEHLTVIRSIMFCFYVKRGDCASIIGGVVEYINEICCVLCSIEAKKCRKAYSEV	171
FvbHLH110 FvbHLH024	DLSMSTKERKEKLGERIVALQQLVSPYGKTDTASVLLEAMDYIRFLHEQVKVLSAP.YLQST	204
FVbHLH024 FVbHLH069	ATDPHSIAERLRRERIAERIRA <mark>I</mark> ÇELV <mark>E</mark> SVNKID.RAAMLDEIMDYVKFIRLQVKVISMSRIGGAGAVA ATDSHSIAERVRREKINDRIRC <mark>I</mark> QNLVEGCYKIMGMAVMLDVVISYVQSIQNQIEFISMKLSAASAYYD	230
FvbHLH082	atdshslaervregkinermrclcdivegcsktmgmavmldeiinyvcslcncveflsmkltaassfhd	250
FvbHLH027	ATDSHSLAERVRBEKISERMKLIQDLVFGCNKVTGKALMLDEIINYVQSLQRQVEFLSMKLSSVNTR	430
FVbHLH018	ATDSHSLAERVEREKISERMKFIQDLVFGCNKVIGKAVMLDEIINYVQSIQRQVEFISMKLATVNPR DKPAAGKKR.EKIGERILAIQQLVSPFGKTDTASVLHEALGYIRFIHDQVQVLCSP.YLQRLPSL	424 216
FvbHLH018 FvbHLH075	ENGRMTHIVVERNREKOMN. EYLAVIRSLMETS YVQRGDQASIIGGAINEVKEIEGLLQSMDGSHKRISKPEQ	195
FvbHLH088	.PSKDPQSIAAKNRBERISERLKIIQELVFNGCKVDLVTMLEKAISYVKFIQLQVKVIATDEFWPVQGGK	271
FvbHLH080	.EEPLNHVEAERQRREKLNQRFYALRAVVFNVSKMDKASLLGDAISYITELKTKLQTTESDKEDMQKQVE	574
FvbHLH078 FvbHLH017	psknimaerrrrkrindrismirsivekiskmdrtsilgdtidymkelidrinniqhgieeggsdqatdshslaervrrekisermkyiqdivegcnkitgkagmldeiinyvqsiqrqvefismklaavnfr	248
FvbHLH025	.EEPLNHVEAERCRREKLNCRFYALRAVVFNISKMDKASLLGDAITYINDLQTKIRVMETEKQMG	414
FvbHLH015	KGFRHMINERMRREKCKQGYFALHSLLFNGTKSDKNWIVQVATTTIEQLERCKDELRKRNMELESILC	150
FVbHLH070	NTPRSKHSATECRRESKINDRFCMIRELIEHSDCKRDKASFLLEVIEYICYICEKVTKYEVPYCGWNCDPA	334 430
FvbHLH056 FvbHLH057	ATNSHSLAERVRREKISERMKFIQDLVEGCSKVIGKAVMLDEIINYVQSLQRQVEFLSMKLATVNFR SAIRSKHSVTEQRRESKINERFQILRDLIEHSEQKRDTASFLLEVIEYVQYLQERVNKHEGSCQGWSAEFT	115
FvbHLH035	AAEVHNLSEKRRRSKINEKMKA <mark>I</mark> QNLI <mark>E</mark> NSNKIDKASMLDEAIEYLKQ <mark>I</mark> QIQVQM <mark>I</mark> TMRNGLGLHPMC	194
FvbHLH112	ATDNHSLAERARRAKICMRMKLIQSLVFGCDKITGKAHVLDEIIKYVQFIQNQVESLAAKVAFVNL	100
FybHLH113	.MKTKCLGKKMKKKKKLKCSKEITDIRKFVEGGEAMDACSLLDEAAHYIRSISTQVQVMKRIADVYSVNFNEGNNENKETSSSLKEDSDDIDALLSLEEEEEQEEYDEEEVSTARTHGNYGSSYSDSCSSYGLKTR	171
FvbHLH039		100



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Motif 2	- KODRAZTP-BOTOTKR-PS-BXA-T-	1.1e-1670	166	29	
Motif 3	1	1.4e-451	81	29	
Motif 4	LSFFORSAGFO LANCAS TFF CAST	3.0e-188	18	28	
Motif 5	TRIEWEY LYSWEES RIGGE GLOGBOT SUGHT WESBOTTED	3.0e-168	11	41	
Motif 6	DLRSRGLCLYPYSaTesVessw9ADeWesa	4.9e-154	14	30	
Motif 7	PARREKRERIERS KNREET ENORMINIA	1.3e-162	14	29	
Motif 8	NULT-PREYL SERY KLEER COLESX PEL	2.8e-131	18	29	
Motif 9	Less Vesce Na / AVENS. S. B	4.3e-125	24	21	
	FREE PEEPEETAS ENDERBEENS KEENER GARAGE	1.2e-148	13	40	
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Motif 20	ACGO GE#YSFLFNIKU;EGS;YYASA AB;YMEYYBKOYM	3.2e-044	4	41	Motif 15 Motif 16
Motif 21	<b>₹L\$W</b> KL\$\$XN\$	7.6e-112	28	11	Motif 17 Motif 18
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Motif 24	BENFENGI CI GREES	1.8e-038	13	15	Motif 23

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<b>VEAPORE</b>		Figure 1	FIGURE 1