

Figure S1. Chromosomal locations of the *CtbHLH* genes. The 120 *CtbHLH* genes were distributed on 12 pseudo-chromosomes of *C. tinctorius* based on their physical position.

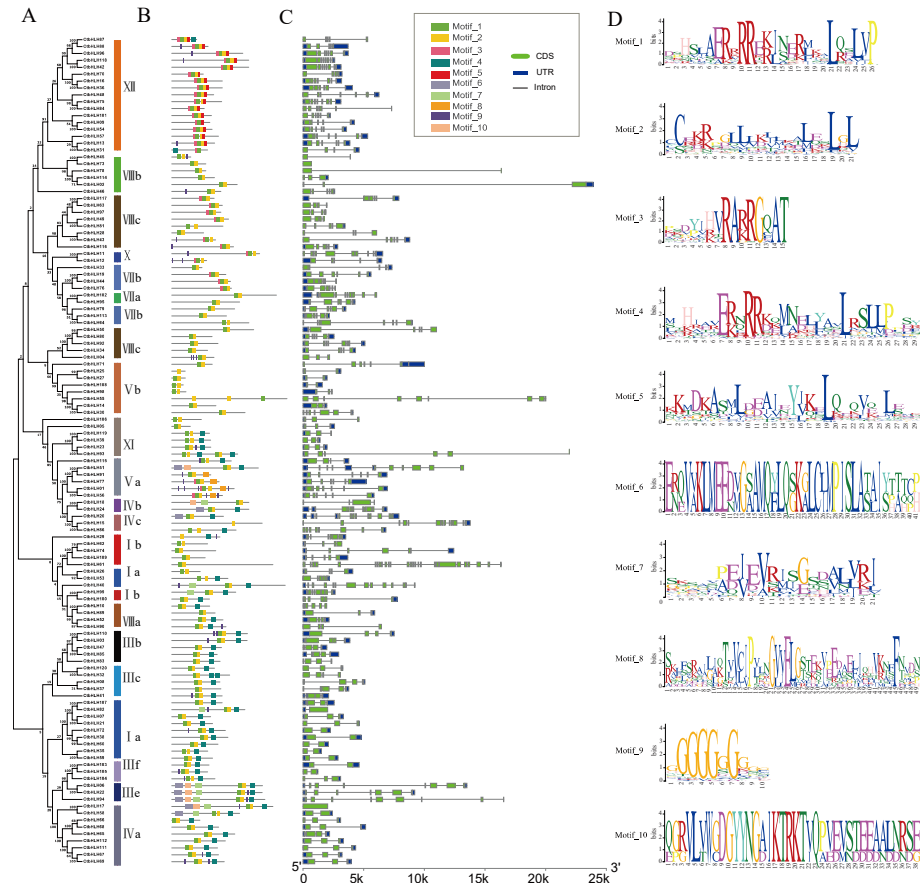


Figure S2. (A) Phylogenetic tree of *CtbHLH*s constructed using MEGA7.0 software with the neighbor joining method based on the alignments of complete predicted protein sequences of *CtbHLH* genes; (B) Conserved motif distributions of the *CtbHLH* genes of 120 proteins were identified using MEME-Suite 5.1.1, different colors represent different motifs; (C) Exon-intron structural analysis of *CtbHLH* genes

were determined using TBtools v1.130, where blue and green boxes represent untranslated regions and exons, respectively, while black lines represent introns; (D) Sequence logos for motif 1-10.

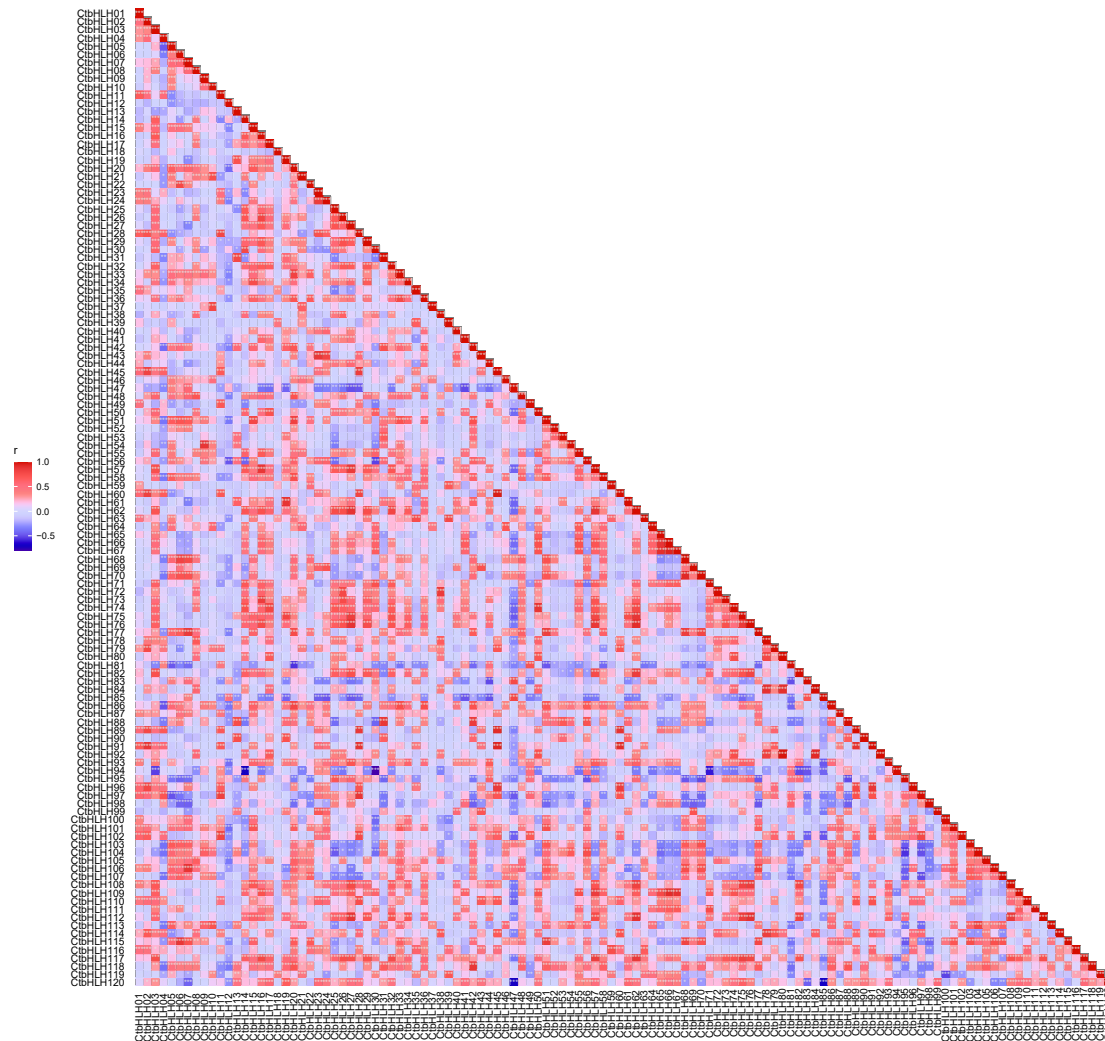


Figure S3. Co-expression analysis of *CtbHLH* genes. * $p < 0.05$.

Figure S4. Cis-regulatory elements in the promoter region of *CtbHLH* genes determined from PlantCARE database. The figure represents the number of each type of regulatory element identified in the promoter sequence of *CtbHLH* genes. The darker the red color, the higher the number of regulatory elements in the promoter regions of *CtbHLH* genes.

Figure S4. Cis-regulatory elements in the promoter region of *CtbHLH* genes determined from PlantCARE database. The figure represents the number of each type of regulatory element identified in the promoter sequence of *CtbHLH* genes. The darker the red color, the higher the number of regulatory elements in the promoter regions of *CtbHLH* genes.

Table S1. Information for the bHLH transcription factor family in *C.tinctorius*

Gene Locus	Gene Name	protein			Instability Index	Sucellular Location
		Length(aa)	MW(Da)	pI		
<i>CtAH01G0020600</i>	<i>CtbHLH01</i>	429	47997.41	6.15	58.15	nucleus
<i>CtAH01G0029900</i>	<i>CtbHLH02</i>	127	14205.52	10.14	63.2	cytosol
<i>CtAH01G0038500</i>	<i>CtbHLH03</i>	341	38402.87	4.96	55.61	nucleus
<i>CtAH01G0040800</i>	<i>CtbHLH04</i>	328	35938.09	6.18	56.51	nucleus
<i>CtAH02G0016800</i>	<i>CtbHLH05</i>	578	65695.27	4.93	49.28	nucleus
<i>CtAH02G0038900</i>	<i>CtbHLH06</i>	674	73666.67	5.82	40.56	nucleus
<i>CtAH02G0039700</i>	<i>CtbHLH07</i>	358	39900.96	6.27	55.71	nucleus
<i>CtAH02G0066300</i>	<i>CtbHLH08</i>	427	47957.88	8.19	42.46	cytosol
<i>CtAH02G0119600</i>	<i>CtbHLH09</i>	286	30609.83	6.98	59.3	nucleus
<i>CtAH02G0126300</i>	<i>CtbHLH10</i>	90	10050.45	8.93	55.51	mitochondria
<i>CtAH02G0149400</i>	<i>CtbHLH11</i>	342	38328.59	9.18	57.75	nucleus
<i>CtAH02G0150000</i>	<i>CtbHLH12</i>	213	23745.1	6.5	69.52	nucleus
<i>CtAH02G0153300</i>	<i>CtbHLH13</i>	254	28398.47	6.11	40.41	nucleus
<i>CtAH02G0158200</i>	<i>CtbHLH14</i>	358	39842.52	6.01	63.32	nucleus
<i>CtAH03G0001000</i>	<i>CtbHLH15</i>	1465	161456.2	6.21	42.53	nucleus
<i>CtAH03G0067400</i>	<i>CtbHLH16</i>	338	38125.37	8.39	42.49	nucleus
<i>CtAH03G0094800</i>	<i>CtbHLH17</i>	336	37392.52	7.21	50.96	nucleus
<i>CtAH03G0142200</i>	<i>CtbHLH18</i>	240	26998.19	5.83	44.65	nucleus
<i>CtAH03G0167300</i>	<i>CtbHLH19</i>	452	48981.62	9.13	54.15	nucleus
<i>CtAH03G0189300</i>	<i>CtbHLH20</i>	224	25305.7	6.15	50.02	nucleus
<i>CtAH03G0257900</i>	<i>CtbHLH21</i>	306	34336.97	6.76	60.44	nucleus
<i>CtAH03G0265000</i>	<i>CtbHLH22</i>	452	50694.98	5.99	62.72	nucleus
<i>CtAH03G0305900</i>	<i>CtbHLH23</i>	261	28418.81	4.69	59.28	nucleus
<i>CtAH04G0015500</i>	<i>CtbHLH24</i>	294	32749.16	5.93	67.22	nucleus
<i>CtAH04G0048700</i>	<i>CtbHLH25</i>	273	30783.98	8.31	55.28	nucleus
<i>CtAH04G0141400</i>	<i>CtbHLH26</i>	198	21950.98	9.07	49.97	nucleus
<i>CtAH04G0149100</i>	<i>CtbHLH27</i>	249	27766.58	9.15	37.79	nucleus
<i>CtAH04G0155900</i>	<i>CtbHLH28</i>	413	45807.21	6.35	68.32	nucleus
<i>CtAH04G0167000</i>	<i>CtbHLH29</i>	397	45255.72	5.64	42.2	nucleus
<i>CtAH04G0222200</i>	<i>CtbHLH30</i>	375	42123.27	6.37	69.08	nucleus
<i>CtAH04G0226500</i>	<i>CtbHLH31</i>	269	30529.58	5.99	40.16	nucleus
<i>CtAH05G0045700</i>	<i>CtbHLH32</i>	252	28880.56	4.9	64.2	nucleus
<i>CtAH05G0059100</i>	<i>CtbHLH33</i>	698	76626.45	6.31	59.42	nucleus
<i>CtAH05G0088900</i>	<i>CtbHLH34</i>	283	31696.5	5.59	52.8	nucleus
<i>CtAH05G0094600</i>	<i>CtbHLH35</i>	260	29349.19	6.46	43.94	nucleus
<i>CtAH05G0102400</i>	<i>CtbHLH36</i>	337	37724	5.81	49.89	nucleus
<i>CtAH05G0151900</i>	<i>CtbHLH37</i>	757	85427.54	5.09	47.05	nucleus
<i>CtAH05G0184800</i>	<i>CtbHLH38</i>	188	20996.41	9.07	75.37	chloroplast
<i>CtAH05G0245200</i>	<i>CtbHLH39</i>	417	43305.13	6.25	50.51	nucleus
<i>CtAH05G0277500</i>	<i>CtbHLH40</i>	489	55480.57	7.09	67.24	nucleus

Table S1. *Cont.*

Gene Locus	Gene Name	protein			Instability Index	Sucellular Location
		Length(aa)	MW(Da)	pI		
<i>CtAH06G0053200</i>	<i>CtbHLH41</i>	375	41702.87	5.89	44.15	nucleus
<i>CtAH06G0071400</i>	<i>CtbHLH42</i>	513	56099.86	5.61	42.63	nucleus
<i>CtAH06G0125600</i>	<i>CtbHLH43</i>	586	65573.53	6.35	62.06	nucleus
<i>CtAH06G0176400</i>	<i>CtbHLH44</i>	420	46605.52	9	54.95	nucleus
<i>CtAH06G0257600</i>	<i>CtbHLH45</i>	285	31634.02	7.28	45.39	nucleus
<i>CtAH06G0264200</i>	<i>CtbHLH46</i>	282	30877.64	5.92	50.13	nucleus
<i>CtAH06G0272000</i>	<i>CtbHLH47</i>	505	54784.7	5.58	54.49	nucleus
<i>CtAH06G0273300</i>	<i>CtbHLH48</i>	280	31694.09	9.23	35.69	chloroplast
<i>CtAH06G0287100</i>	<i>CtbHLH49</i>	233	25393.33	5.28	55.85	nucleus
<i>CtAH06G0292900</i>	<i>CtbHLH50</i>	328	37051.15	4.89	53.36	nucleus
<i>CtAH06G0313000</i>	<i>CtbHLH51</i>	515	56186.75	8.07	58.65	nucleus
<i>CtAH06G0321500</i>	<i>CtbHLH52</i>	77	8726.93	8.66	62.91	nucleus
<i>CtAH07G0013900</i>	<i>CtbHLH53</i>	124	14092.12	9.46	71.65	nucleus
<i>CtAH07G0018800</i>	<i>CtbHLH54</i>	239	26258.5	5.64	66.31	nucleus
<i>CtAH07G0053100</i>	<i>CtbHLH55</i>	309	34072.28	8.39	57.54	nucleus
<i>CtAH07G0058200</i>	<i>CtbHLH56</i>	321	34675.18	4.93	49.59	nucleus
<i>CtAH07G0073400</i>	<i>CtbHLH57</i>	265	29739.53	6.36	47.94	nucleus
<i>CtAH07G0199100</i>	<i>CtbHLH58</i>	336	37338.69	7.72	47.03	nucleus
<i>CtAH07G0211100</i>	<i>CtbHLH59</i>	272	30690.71	5.72	40.18	nucleus
<i>CtAH08G0007100</i>	<i>CtbHLH60</i>	313	34517.06	5.5	57.21	nucleus
<i>CtAH08G0015700</i>	<i>CtbHLH61</i>	252	28124.63	8.86	73.21	nucleus
<i>CtAH08G0016000</i>	<i>CtbHLH62</i>	261	29123.84	7.1	47.31	nucleus
<i>CtAH08G0104800</i>	<i>CtbHLH63</i>	392	43630.32	6.09	57.66	nucleus
<i>CtAH08G0144200</i>	<i>CtbHLH64</i>	308	33963.01	5.86	78.17	nucleus
<i>CtAH08G0151700</i>	<i>CtbHLH65</i>	387	43051.17	9.29	40.52	nucleus
<i>CtAH08G0151900</i>	<i>CtbHLH66</i>	321	36144.41	9.4	53.83	nucleus
<i>CtAH08G0152100</i>	<i>CtbHLH67</i>	332	36982.17	9.07	41.03	nucleus
<i>CtAH08G0152200</i>	<i>CtbHLH68</i>	328	37356.38	6.03	57.46	nucleus
<i>CtAH08G0152400</i>	<i>CtbHLH69</i>	303	34166.63	5.73	56.74	nucleus
<i>CtAH08G0160000</i>	<i>CtbHLH70</i>	211	24110.44	7.78	62.23	nucleus
<i>CtAH08G0181900</i>	<i>CtbHLH71</i>	240	26842.88	8.65	53.91	cytosol
<i>CtAH08G0237000</i>	<i>CtbHLH72</i>	421	47405.97	5.2	55.6	nucleus
<i>CtAH09G0014100</i>	<i>CtbHLH73</i>	437	48931.58	5.99	56.83	nucleus
<i>CtAH09G0028000</i>	<i>CtbHLH74</i>	440	49469.61	8.7	52.82	nucleus
<i>CtAH09G0039600</i>	<i>CtbHLH75</i>	333	37601.28	7.02	47.48	nucleus
<i>CtAH09G0067900</i>	<i>CtbHLH76</i>	365	40934.77	8.61	74	nucleus
<i>CtAH09G0072800</i>	<i>CtbHLH77</i>	603	67139.13	5.81	58.7	nucleus
<i>CtAH09G0091200</i>	<i>CtbHLH78</i>	228	25637.09	6.38	59.48	nucleus
<i>CtAH09G0091700</i>	<i>CtbHLH79</i>	269	29795.14	7.13	58.12	nucleus
<i>CtAH09G0096600</i>	<i>CtbHLH80</i>	379	42457.71	5.18	51.34	nucleus
<i>CtAH09G0102800</i>	<i>CtbHLH81</i>	202	22396.12	4.94	54.62	chloroplast

Table S1. *Cont.*

Gene Locus	Gene Name	protein			Instability	Sucellular
		Length(aa)	MW(Da)	pI	Index	Location
<i>CtAH09G0112700</i>	<i>CtbHLH82</i>	312	34294.77	7.05	64.73	nucleus
<i>CtAH09G0118900</i>	<i>CtbHLH83</i>	290	32993.03	5.4	56.69	nucleus
<i>CtAH09G0132000</i>	<i>CtbHLH84</i>	217	24851.03	8.93	69.53	nucleus
<i>CtAH09G0132200</i>	<i>CtbHLH85</i>	503	53943.14	6.09	47.8	nucleus
<i>CtAH09G0142600</i>	<i>CtbHLH86</i>	191	20719.65	6.74	47.61	nucleus
<i>CtAH09G0160300</i>	<i>CtbHLH87</i>	167	18224.66	9.8	64.87	nucleus
<i>CtAH09G0160500</i>	<i>CtbHLH88</i>	242	26400.44	7.83	62.5	nucleus
<i>CtAH09G0161900</i>	<i>CtbHLH89</i>	91	10409.58	6.56	79.36	mitochondria
<i>CtAH09G0162200</i>	<i>CtbHLH90</i>	96	10707.09	9.1	77.95	nucleus
<i>CtAH09G0174600</i>	<i>CtbHLH91</i>	345	38457.98	6.9	61.44	nucleus
<i>CtAH09G0192500</i>	<i>CtbHLH92</i>	337	37534.59	4.79	60.95	nucleus
<i>CtAH09G0233200</i>	<i>CtbHLH93</i>	316	33550.52	6.12	51.36	nucleus
<i>CtAH09G0235800</i>	<i>CtbHLH94</i>	488	54381.4	6.85	51.53	nucleus
<i>CtAH09G0248300</i>	<i>CtbHLH95</i>	515	56316.34	5.61	66.58	nucleus
<i>CtAH09G0257900</i>	<i>CtbHLH96</i>	474	51930.85	6.34	51	nucleus
<i>CtAH09G0294100</i>	<i>CtbHLH97</i>	361	39704.52	6.31	47.77	nucleus
<i>CtAH10G0023000</i>	<i>CtbHLH98</i>	241	27228.02	8.86	71.7	chloroplast
<i>CtAH10G0025700</i>	<i>CtbHLH99</i>	768	86969.85	8.55	44.1	cytosol
<i>CtAH10G0025800</i>	<i>CtbHLH100</i>	295	33306.65	8.45	49.32	nucleus
<i>CtAH10G0036500</i>	<i>CtbHLH101</i>	312	34562.73	5.27	61.54	nucleus
<i>CtAH10G0079000</i>	<i>CtbHLH102</i>	547	59451.14	5.61	78.63	nucleus
<i>CtAH10G0094800</i>	<i>CtbHLH103</i>	605	67639.94	5.28	61.18	nucleus
<i>CtAH10G0094900</i>	<i>CtbHLH104</i>	622	69042.01	5	58.66	nucleus
<i>CtAH10G0095000</i>	<i>CtbHLH105</i>	603	67262.5	5.61	58.79	nucleus
<i>CtAH10G0115000</i>	<i>CtbHLH106</i>	270	30465.24	5.83	47.86	cytosol
<i>CtAH10G0181500</i>	<i>CtbHLH107</i>	351	38746.55	5.53	57.16	nucleus
<i>CtAH10G0208800</i>	<i>CtbHLH108</i>	289	32435.72	7.63	33.88	nucleus
<i>CtAH10G0227500</i>	<i>CtbHLH109</i>	260	28902.54	5.55	39.51	cytosol
<i>CtAH11G0019900</i>	<i>CtbHLH110</i>	362	41301.55	5.92	61.35	nucleus
<i>CtAH11G0020900</i>	<i>CtbHLH111</i>	323	35947.29	5.16	51.41	nucleus
<i>CtAH11G0021000</i>	<i>CtbHLH112</i>	285	31697.7	5.09	43.65	nucleus
<i>CtAH11G0034700</i>	<i>CtbHLH113</i>	240	26585.87	5.33	71.12	nucleus
<i>CtAH11G0035400</i>	<i>CtbHLH114</i>	228	25343.93	9.39	64.89	nucleus
<i>CtAH11G0094100</i>	<i>CtbHLH115</i>	515	58133.39	7.11	54.22	nucleus
<i>CtAH11G0138700</i>	<i>CtbHLH116</i>	292	31329.72	8.84	60.82	nucleus
<i>CtAH11G0244400</i>	<i>CtbHLH117</i>	398	44597.03	5.61	61.12	nucleus
<i>CtAH11G0257000</i>	<i>CtbHLH118</i>	513	56397.27	6.15	46.6	nucleus
<i>CtAH12G0137000</i>	<i>CtbHLH119</i>	339	35179.14	5.76	60.36	nucleus
<i>CtAH12G0153400</i>	<i>CtbHLH120</i>	253	29178.37	9.19	51.69	nucleus

Table S2. String interaction analysis of *CtbHLH* gene family

#node1	node2	node1_string_id	node2_string_id	coexpression	combined_score
CtbHLH04	CtbHLH92	AT1G66470.1	AT4G33880.1	0.406	0.568
CtbHLH04	CtbHLH39	AT1G66470.1	AT2G24260.1	0.181	0.405
CtbHLH04	CtbHLH89	AT1G66470.1	AT1G74500.1	0.447	0.497
CtbHLH04	CtbHLH32	AT1G66470.1	AT4G29930.3	0.171	0.408
CtbHLH04	CtbHLH05	AT1G66470.1	AT1G63650.3	0	0.63
CtbHLH05	CtbHLH92	AT1G63650.3	AT4G33880.1	0	0.548
CtbHLH08	CtbHLH31	AT1G10610.1	AT1G25330.1	0	0.457
CtbHLH08	CtbHLH114	AT1G10610.1	AT5G67060.1	0	0.61
CtbHLH08	CtbHLH78	AT1G10610.1	AT3G50330.1	0	0.61
CtbHLH10	CtbHLH57	AT1G26945.1	AT1G18400.1	0.111	0.503
CtbHLH10	CtbHLH33	AT1G26945.1	AT1G09530.2	0	0.543
CtbHLH04	CtbHLH92	AT1G66470.1	AT4G33880.1	0.406	0.568
CtbHLH10	CtbHLH48	AT1G26945.1	AT1G68920.1	0	0.587
CtbHLH100	CtbHLH41	AT3G56970.1	AT2G28160.1	0	0.977

Table S2. Cont.

#node1	node2	node1_string_id	node2_string_id	coexpression	combined_score
CtbHLH100	CtbHLH99	AT3G56970.1	AT3G56980.1	0.487	0.498
CtbHLH100	CtbHLH82	AT3G56970.1	AT1G22490.1	0	0.532
CtbHLH100	CtbHLH76	AT3G56970.1	AT4G00050.1	0	0.453
CtbHLH100	CtbHLH84	AT3G56970.1	AT5G50915.1	0	0.591
CtbHLH100	CtbHLH69	AT3G56970.1	AT4G37850.1	0	0.594
CtbHLH100	CtbHLH20	AT3G56970.1	AT4G14410.1	0	0.914
CtbHLH100	CtbHLH86	AT3G56970.1	AT5G54680.1	0	0.929
CtbHLH101	CtbHLH71	AT2G42300.1	AT1G68810.1	0	0.584
CtbHLH101	CtbHLH98	AT2G42300.1	AT2G41130.1	0	0.6
CtbHLH101	CtbHLH94	AT2G42300.1	AT4G16430.1	0	0.598
CtbHLH101	CtbHLH74	AT2G42300.1	AT5G51780.1	0	0.615
CtbHLH101	CtbHLH83	AT2G42300.1	AT5G65640.1	0	0.626
CtbHLH101	CtbHLH40	AT2G42300.1	AT5G56960.1	0	0.695
CtbHLH105	CtbHLH84	AT4G09820.1	AT5G50915.1	0	0.494
CtbHLH108	CtbHLH91	AT2G40200.1	AT1G69010.1	0	0.627
CtbHLH108	CtbHLH34	AT2G40200.1	AT2G14760.3	0	0.543
CtbHLH108	CtbHLH78	AT2G40200.1	AT3G50330.1	0	0.429
CtbHLH108	CtbHLH96	AT2G40200.1	AT3G07340.1	0	0.463
CtbHLH108	CtbHLH69	AT2G40200.1	AT4G37850.1	0	0.497
CtbHLH108	CtbHLH36	AT2G40200.1	AT4G34530.1	0	0.514
CtbHLH108	CtbHLH93	AT2G40200.1	AT4G02590.1	0	0.519
CtbHLH108	CtbHLH21	AT2G40200.1	AT5G46690.1	0	0.615
CtbHLH108	CtbHLH109	AT2G40200.1	AT5G51790.1	0	0.616
CtbHLH108	CtbHLH92	AT2G40200.1	AT4G33880.1	0	0.619
CtbHLH108	CtbHLH86	AT2G40200.1	AT5G54680.1	0	0.62
CtbHLH108	CtbHLH114	AT2G40200.1	AT5G67060.1	0	0.637

Table S2. *Cont.*

#node1	node2	node1_string_id	node2_string_id	coexpression	combined_score
CtbHLH21	CtbHLH95	AT5G46690.1	AT2G20180.2	0.115	0
CtbHLH21	CtbHLH76	AT5G46690.1	AT4G00050.1	0.06	0
CtbHLH21	CtbHLH33	AT5G46690.1	AT1G09530.2	0	0
CtbHLH21	CtbHLH49	AT5G46690.1	AT1G35460.1	0	0
CtbHLH21	CtbHLH88	AT5G46690.1	AT1G59640.2	0	0
CtbHLH21	CtbHLH91	AT5G46690.1	AT1G69010.1	0	0
CtbHLH21	CtbHLH34	AT5G46690.1	AT2G14760.3	0	0
CtbHLH21	CtbHLH39	AT5G46690.1	AT2G24260.1	0	0
CtbHLH21	CtbHLH97	AT5G46690.1	AT2G42280.1	0	0
CtbHLH21	CtbHLH78	AT5G46690.1	AT3G50330.1	0	0
CtbHLH21	CtbHLH94	AT5G46690.1	AT4G16430.1	0	0
CtbHLH21	CtbHLH92	AT5G46690.1	AT4G33880.1	0	0
CtbHLH21	CtbHLH36	AT5G46690.1	AT4G34530.1	0	0
CtbHLH21	CtbHLH77	AT5G46690.1	AT5G08130.5	0	0
CtbHLH21	CtbHLH54	AT5G46690.1	AT5G62610.1	0	0
CtbHLH22	CtbHLH84	AT1G32640.1	AT5G50915.1	0	0
CtbHLH24	CtbHLH88	AT3G19860.2	AT1G59640.2	0	0
CtbHLH24	CtbHLH98	AT3G19860.2	AT2G41130.1	0	0
CtbHLH24	CtbHLH54	AT3G19860.2	AT5G62610.1	0	0
CtbHLH24	CtbHLH36	AT3G19860.2	AT4G34530.1	0	0
CtbHLH26	CtbHLH96	AT4G20970.1	AT3G07340.1	0	0
CtbHLH26	CtbHLH60	AT4G20970.1	AT5G53210.1	0	0
CtbHLH29	CtbHLH71	AT2G31220.1	AT1G68810.1	0	0.115
CtbHLH29	CtbHLH37	AT2G31220.1	AT2G16910.1	0	0
CtbHLH29	CtbHLH77	AT2G31220.1	AT5G08130.5	0	0
CtbHLH29	CtbHLH40	AT2G31220.1	AT5G56960.1	0	0
CtbHLH31	CtbHLH57	AT1G25330.1	AT1G18400.1	0	0.597
CtbHLH32	CtbHLH69	AT4G29930.3	AT4G37850.1	0.047	0.49
CtbHLH32	CtbHLH36	AT4G29930.3	AT4G34530.1	0	0.115
CtbHLH32	CtbHLH92	AT4G29930.3	AT4G33880.1	0.118	0
CtbHLH32	CtbHLH82	AT4G29930.3	AT1G22490.1	0.086	0
CtbHLH32	CtbHLH39	AT4G29930.3	AT2G24260.1	0.074	0
CtbHLH32	CtbHLH34	AT4G29930.3	AT2G14760.3	0.059	0
CtbHLH32	CtbHLH91	AT4G29930.3	AT1G69010.1	0.058	0
CtbHLH32	CtbHLH78	AT4G29930.3	AT3G50330.1	0	0
CtbHLH32	CtbHLH84	AT4G29930.3	AT5G50915.1	0	0
CtbHLH33	CtbHLH95	AT1G09530.2	AT2G20180.2	0	0.501
CtbHLH33	CtbHLH38	AT1G09530.2	AT3G06120.1	0	0
CtbHLH33	CtbHLH60	AT1G09530.2	AT5G53210.1	0	0
CtbHLH34	CtbHLH71	AT2G14760.3	AT1G68810.1	0	0
CtbHLH34	CtbHLH90	AT2G14760.3	AT3G28857.1	0	0

Table S2. *Cont.*

#node1	node2	node1_string_id	node2_string_id	coexpression	combined_score
CtbHLH34	CtbHLH86	AT2G14760.3	AT5G54680.1	0	0
CtbHLH36	CtbHLH96	AT4G34530.1	AT3G07340.1	0	0.499
CtbHLH36	CtbHLH98	AT4G34530.1	AT2G41130.1	0	0
CtbHLH36	CtbHLH60	AT4G34530.1	AT5G53210.1	0	0
CtbHLH36	CtbHLH69	AT4G34530.1	AT4G37850.1	0	0
CtbHLH38	CtbHLH85	AT3G06120.1	AT3G26744.1	0.08	0.5
CtbHLH38	CtbHLH76	AT3G06120.1	AT4G00050.1	0	0
CtbHLH38	CtbHLH83	AT3G06120.1	AT5G65640.1	0	0
CtbHLH38	CtbHLH84	AT3G06120.1	AT5G50915.1	0	0
CtbHLH40	CtbHLH71	AT5G56960.1	AT1G68810.1	0	0
CtbHLH40	CtbHLH41	AT5G56960.1	AT2G28160.1	0	0
CtbHLH40	CtbHLH98	AT5G56960.1	AT2G41130.1	0	0
CtbHLH40	CtbHLH79	AT5G56960.1	AT4G36930.1	0	0
CtbHLH40	CtbHLH84	AT5G56960.1	AT5G50915.1	0	0
CtbHLH40	CtbHLH74	AT5G56960.1	AT5G51780.1	0	0
CtbHLH40	CtbHLH83	AT5G56960.1	AT5G65640.1	0	0
CtbHLH40	CtbHLH54	AT5G56960.1	AT5G62610.1	0	0
CtbHLH41	CtbHLH99	AT2G28160.1	AT3G56980.1	0	0.605
CtbHLH41	CtbHLH90	AT2G28160.1	AT3G28857.1	0	0
CtbHLH41	CtbHLH86	AT2G28160.1	AT5G54680.1	0	0
CtbHLH46	CtbHLH94	AT2G34820.1	AT4G16430.1	0	0
CtbHLH48	CtbHLH71	AT1G68920.1	AT1G68810.1	0	0
CtbHLH48	CtbHLH77	AT1G68920.1	AT5G08130.5	0	0
CtbHLH48	CtbHLH69	AT1G68920.1	AT4G37850.1	0	0
CtbHLH48	CtbHLH89	AT1G68920.1	AT1G74500.1	0	0
CtbHLH54	CtbHLH71	AT5G62610.1	AT1G68810.1	0	0
CtbHLH54	CtbHLH98	AT5G62610.1	AT2G41130.1	0	0
CtbHLH54	CtbHLH94	AT5G62610.1	AT4G16430.1	0	0
CtbHLH54	CtbHLH74	AT5G62610.1	AT5G51780.1	0	0
CtbHLH54	CtbHLH60	AT5G62610.1	AT5G53210.1	0	0
CtbHLH54	CtbHLH83	AT5G62610.1	AT5G65640.1	0	0
CtbHLH57	CtbHLH83	AT1G18400.1	AT5G65640.1	0	0
CtbHLH57	CtbHLH86	AT1G18400.1	AT5G54680.1	0	0
CtbHLH57	CtbHLH77	AT1G18400.1	AT5G08130.5	0	0
CtbHLH60	CtbHLH85	AT5G53210.1	AT3G26744.1	0.087	0.5
CtbHLH60	CtbHLH76	AT5G53210.1	AT4G00050.1	0.058	0
CtbHLH60	CtbHLH88	AT5G53210.1	AT1G59640.2	0	0
CtbHLH60	CtbHLH96	AT5G53210.1	AT3G07340.1	0	0
CtbHLH60	CtbHLH99	AT5G53210.1	AT3G56980.1	0	0
CtbHLH60	CtbHLH84	AT5G53210.1	AT5G50915.1	0	0
CtbHLH60	CtbHLH83	AT5G53210.1	AT5G65640.1	0	0

Table S2. *Cont.*

#node1	node2	node1_string_id	node2_string_id	coexpression	combined_score
CtbHLH69	CtbHLH99	AT4G37850.1	AT3G56980.1	0	0
CtbHLH69	CtbHLH93	AT4G37850.1	AT4G02590.1	0	0
CtbHLH69	CtbHLH86	AT4G37850.1	AT5G54680.1	0	0
CtbHLH71	CtbHLH84	AT1G68810.1	AT5G50915.1	0	0
CtbHLH71	CtbHLH74	AT1G68810.1	AT5G51780.1	0	0
CtbHLH71	CtbHLH91	AT1G68810.1	AT1G69010.1	0	0
CtbHLH72	CtbHLH83	AT3G24140.1	AT5G65640.1	0	0.759
CtbHLH72	CtbHLH85	AT3G24140.1	AT3G26744.1	0.087	0.5
CtbHLH74	CtbHLH84	AT5G51780.1	AT5G50915.1	0	0.115
CtbHLH74	CtbHLH89	AT5G51780.1	AT1G74500.1	0.212	0
CtbHLH74	CtbHLH82	AT5G51780.1	AT1G22490.1	0	0
CtbHLH74	CtbHLH98	AT5G51780.1	AT2G41130.1	0	0
CtbHLH74	CtbHLH83	AT5G51780.1	AT5G65640.1	0	0
CtbHLH76	CtbHLH86	AT4G00050.1	AT5G54680.1	0	0
CtbHLH77	CtbHLH91	AT5G08130.5	AT1G69010.1	0.069	0.491
CtbHLH77	CtbHLH89	AT5G08130.5	AT1G74500.1	0	0
CtbHLH77	CtbHLH94	AT5G08130.5	AT4G16430.1	0	0
CtbHLH77	CtbHLH86	AT5G08130.5	AT5G54680.1	0	0
CtbHLH78	CtbHLH79	AT3G50330.1	AT4G36930.1	0.073	0.5
CtbHLH82	CtbHLH84	AT1G22490.1	AT5G50915.1	0	0
CtbHLH83	CtbHLH98	AT5G65640.1	AT2G41130.1	0	0
CtbHLH83	CtbHLH97	AT5G65640.1	AT2G42280.1	0	0
CtbHLH83	CtbHLH84	AT5G65640.1	AT5G50915.1	0	0
CtbHLH84	CtbHLH98	AT5G50915.1	AT2G41130.1	0	0
CtbHLH84	CtbHLH85	AT5G50915.1	AT3G26744.1	0	0
CtbHLH84	CtbHLH90	AT5G50915.1	AT3G28857.1	0	0
CtbHLH84	CtbHLH99	AT5G50915.1	AT3G56980.1	0	0
CtbHLH85	CtbHLH86	AT3G26744.1	AT5G54680.1	0	0
CtbHLH86	CtbHLH91	AT5G54680.1	AT1G69010.1	0	0
CtbHLH86	CtbHLH99	AT5G54680.1	AT3G56980.1	0	0
CtbHLH86	CtbHLH93	AT5G54680.1	AT4G02590.1	0	0
CtbHLH89	CtbHLH97	AT1G74500.1	AT2G42280.1	0	0

Table S3. The FPKM values of *CtbHLHs*

Gene	White	Yellow	LightRed	DeepRed	1DAG	3DAG	5DAG	7DAG	10DAG	DAF0	DAF10	DAF20	HL_DAF10	HL_DAF20	LL_DAF10	LL_DAF20	SBS	MBS	IFS	PFS	DFS
CtbHLH01	7.86	7.76	5.61	6.33	18.16	6.39	5.52	7.91	11.42	8.74	7.72	9.02	8.79	7.63	12.85	3.81	7.08	7.39	8.13	6.54	7.11
CtbHLH02	0.43	5.47	1.10	0.81	123.68	31.19	13.8	5.82	3.33	11.83	2.07	4.96	2.11	3.1	3.38	0.06	29.99	31.85	16.31	9.27	8.14
CtbHLH03	0.04	0.19	0.1	0.05	8.8	5.82	6.68	8.72	11.02	3.94	2.77	0.51	3.3	2.2	1.09	0.39	2.16	1.52	1.6	0.56	0.95
CtbHLH04	0	0	0	0	1.45	0.52	0.29	0.21	0.02	0	0.23	0.47	0.24	0.42	0.03	0.5	0	0	0	0	0
CtbHLH05	0.05	0.41	0.14	1.95	0.09	0.45	0.73	2.81	2.03	3.19	0.3	0.29	3.52	0.54	1.93	0.08	3.89	3.2	1.75	1.26	0.62
CtbHLH06	36.81	65.37	88.88	64.49	8.98	13.02	15.84	8.54	36.63	282.18	13.63	8.92	21.14	12.04	30.88	4.58	36.77	29.85	92.82	84.63	226.45
CtbHLH07	0.05	0	0.08	0.04	51.96	35.82	48.47	6.91	9.29	94.85	25	8.16	28.13	18.25	34.87	6.97	34.99	31.42	33.43	0.04	6.65
CtbHLH08	0.01	0	0	0	1.49	7.14	4.45	2.52	0.58	3.01	0.69	0.68	0.63	0.59	0.85	0.14	2.09	1.76	1.08	0.13	0.11
CtbHLH09	4.95	9.37	8.07	54.89	28.31	17.74	14.47	26.22	23.1	50.91	5.11	26.84	6.44	7.8	9.26	6.99	153.25	324.8	70.72	14.45	19.49
CtbHLH10	0.09	0.48	5.5	0.65	0	0.02	2.01	1.45	3.79	1.01	0	0	0	0	0	0	31.12	9.16	0.52	0.55	0.04
CtbHLH11	0.04	0.03	0	0.02	16.6	0.07	0.07	0.08	0.01	0	0	4.94	0.02	0.65	0	0.04	0	0	0	0	0
CtbHLH12	0	0	0	0	0.04	0.11	0.13	0.06	0	0	1.75	0.2	0.89	0.72	0	0.12	0.02	0.05	0.03	0	0
CtbHLH13	10.28	16.07	13.9	7.32	0.02	0	0	0.26	0	0.13	0	0	0.01	0	0.03	0	2.73	4	3.4	15.74	1.56
CtbHLH14	0	0.02	0.04	0	0.32	4.36	5.02	4.1	4.6	1.01	2.25	0.26	1.64	1.44	1.06	0.89	2.24	1.7	0.45	0.08	0.04
CtbHLH15	2.43	2.79	1.82	3.54	7.2	2.6	3.04	3.34	14.11	7.27	1.98	3.03	4.72	2.96	3.25	1.65	4.5	4.33	4.83	4.62	3.51
CtbHLH16	0.33	0.05	0.19	0.19	0.13	6.44	27.5	22.03	21.87	2.79	0	0	0	0	0	0	2.9	2	1.62	1.17	0.51
CtbHLH17	0.50	0.51	0.61	0.32	0.34	0.89	1.36	1.1	0.96	0.38	0.06	0.16	0.09	0.2	0.13	0.02	0.11	0.09	0.29	1.04	0.23
CtbHLH18	0.00	0.00	0.00	0.00	0	0	0	0	0	0.02	0.01	0.03	0.09	0.05	0.12	0	0.09	0.02	0	0.02	0
CtbHLH19	53.19	46.94	34.31	27.34	0.05	1.04	7.68	6.24	26.58	0.06	0.34	0.69	0.38	0.46	0.28	0.25	0.69	2.55	9.84	36.29	1.85
CtbHLH20	13.51	14.69	13.82	13.81	23.53	17.8	17.39	21.6	25.52	24.03	4.43	2.29	7.75	4.7	12.83	2.3	18.69	21.73	19.38	16.24	23.56
CtbHLH21	0.02	0	0.02	0	0.01	3.46	4.34	1.77	0.9	1.49	0.88	0.01	2.89	0.13	3.29	0.04	8.27	2.76	1.63	0.02	0.02
CtbHLH22	0.64	1.44	2.69	0.53	0.76	0.04	0.1	0.09	0.04	79.96	0.1	1.5	0.45	0.16	3.98	0.02	34.93	14.45	29.56	8.42	162.4
CtbHLH23	43.11	66.67	73.67	112.47	118.28	33.64	22.29	37.23	49.26	28.55	18.27	42.05	26.96	32.26	37.32	21.17	40.3	31.16	37.56	60.24	132.7

Table S3. *Cont.*

Gene	White	Yellow	LightRred	DeepRred	1DAG	3DAG	5DAG	7DAG	10DAG	DAF0	DAF10	DAF20	HL_DAF10	HL_DAF20	LL_DAF10	LL_DAF20	SBS	MBS	IFS	PFS	DFS
CtbHLH24	12.1	11	6.03	16.01	10.54	4.67	4.75	3.39	8.94	5.64	2.5	4.98	2.74	2.58	3.12	3.7	5.03	3.65	4.2	5.2	13.17
CtbHLH25	0.55	0.53	0.13	0.22	2.37	8.07	8.44	7.39	11.08	3.48	4.16	4.91	5.15	4.67	1.7	1.59	3.32	2.02	2.14	1.97	1.96
CtbHLH26	0.04	0.04	0	0	0.02	8.87	24.61	4.18	16.23	0	0.03	0	0.04	0	0.19	0	0.78	0.03	0.06	0.16	0
CtbHLH27	0.71	1.59	2.74	1.91	0.16	1.77	3.53	4.93	12.12	0.44	0.25	2.32	0.44	1.76	0.57	1.09	0.7	0.26	0.48	1.67	0.23
CtbHLH28	20.88	17.12	30.33	14.75	83.54	9.88	9.69	18.49	25.24	1.15	1.44	16.21	1.08	6.65	0.32	1.52	1.29	1.26	3.6	8.64	18.2
CtbHLH29	0.82	0.5	0.34	0.25	0.18	0.52	1.4	0.57	1.78	0.53	0.23	0.3	0.45	0.52	0.91	0.24	0.59	0.6	0.32	0.08	0.02
CtbHLH30	0.47	0.37	0.76	0.48	2.23	3.86	4.44	6.17	2.56	1.56	2.92	0.52	2.91	1.64	2.56	2.01	2.54	0.65	0.54	0.63	0.22
CtbHLH31	10.85	21.36	24.08	6.18	0	0	0	0	0	5.3	0	0.01	0	0	0.01	0	4	5.94	12.66	20.78	0.88
CtbHLH32	4.56	3.32	0.59	0.73	1.3	4.81	5.95	3.88	10.24	1.64	0.08	0.11	0.14	0.07	1.21	0.24	3.45	2.42	1.27	2.15	0.98
CtbHLH33	3.34	3.56	3.24	1.77	18.66	15.15	18.55	10.48	23.76	21.36	1.95	2.51	3.9	2.2	4.88	1.59	25.13	32.08	18.27	5.92	23.56
CtbHLH34	1.97	2.29	2.01	2.58	1.67	3.2	3.1	3	9.04	4.45	1.86	2.63	3.16	2.51	2.85	2.08	3.65	3.61	1.99	2.19	2.17
CtbHLH35	0	0	0	0	1.73	0	0	0.02	0	0.51	0.33	0.03	0.59	0.05	2.64	0.07	0.2	0.23	0.24	0.05	0
CtbHLH36	6.19	5.04	15.03	6.72	10.5	14.47	22.03	18.56	57.08	19.19	0.31	0.18	0.33	0.08	1.09	0.12	7.14	14.9	21.23	9.98	38.27
CtbHLH37	0	0.01	0.01	0	0.01	0.01	0	0	0	0	0.01	0.03	0.01	0.01	0	0.01	6.93	0	0	0	0.07
CtbHLH38	0	0.01	0.01	0	0.26	3.01	2.95	0.02	0	0.05	0.31	0.14	0.11	0.29	0.22	0.07	0.07	0	0	0	0
CtbHLH39	0.64	3.47	0.51	1.3	0.47	3.21	3.75	9.01	2.1	2.69	1.32	0.47	22.38	9.44	44.41	5.26	6.27	3.72	2.65	2.74	4.46
CtbHLH40	0	0.02	0	0	0	0	0	0	0.06	0	0	0	0	0	0	0	0	0	0	0.01	0.07
CtbHLH41	2.01	0	1.69	0.33	0.46	0.65	3.06	4.36	1.17	0.59	0.27	1.69	0.14	0.12	0.1	0.1	0.63	0.68	1.09	1.57	0.2
CtbHLH42	111.02	81.65	80.39	50.09	10.05	15.39	21.57	16.06	61.83	58.52	1.02	1.37	3.62	2.48	5.91	1.1	22.49	25.62	83.19	113.93	38.81
CtbHLH43	7.31	10.59	22.47	13.36	17.62	2.11	2.09	5.25	4.35	1.81	0.15	0.39	0.68	0.41	0.84	0.05	0.3	0.3	0.91	2.18	29.52
CtbHLH44	3.82	3.49	2.03	0.62	1.3	0.3	9.02	1.05	16.28	1.05	0.31	8.72	0.26	3.77	0.04	1.15	0.29	0.83	1.04	2.2	8.87
CtbHLH45	0	0.11	0.08	0.05	18.54	2.39	2.61	1.44	0.56	0.01	0.28	0.33	0.32	0.28	0.26	0.08	0.5	0.01	0.02	0	0.07
CtbHLH46	0	0	0	0	0	0.01	0	0.09	0	0.06	0	0	0	0.01	0	0	0.21	0.02	0.02	0	0.05

Table S3. *Cont.*

Gene	White	Yellow	LightRed	DeepRed	1DAG	3DAG	5DAG	7DAG	10DAG	DAF0	DAF10	DAF20	HL_DAF10	HL_DAF20	LL_DAF10	LL_DAF20	SBS	MBS	IFS	PFS	DFS
CtbHLH47	6.2	4.47	4.07	7.94	8.32	10.84	8.08	1.41	3.13	45.9	35.98	17.6	55.79	31.91	66.65	12.23	29.57	24.7	20.49	5.91	10.47
CtbHLH48	0.45	0.35	0.12	0.59	1.86	3.1	3.27	2.39	2.08	2.51	0.06	0.14	0.16	0.14	0.3	0.15	1.23	1.16	1.12	0.49	0.21
CtbHLH49	3.71	7.21	5.25	9.53	41.74	4.28	4.91	4.65	13.08	7.64	3.77	60.47	3.99	8.03	3.85	7.7	6.6	6.74	8.76	9.93	19.27
CtbHLH50	0	0	0	0	0.27	0.5	0.48	0.85	0.15	0	0	0	0	0	0.06	0.01	0	0	0	0	0
CtbHLH51	36.37	31.16	36.88	15.2	14.35	5.4	9	8.41	31	33.01	2.01	2.01	4.32	3.08	5.69	2.91	17.42	23.98	21.65	14.3	12.05
CtbHLH52	0	0	0	0	0.1	0	0	0.06	0.02	2.13	0.04	0	0.06	0.03	0	0	0.22	0.2	5.17	0	0
CtbHLH53	7.66	3.93	2.39	0.28	0.02	0	0.02	0.02	0	0.06	0	0	0	0	0	0	0.15	0.29	1.55	0.56	0
CtbHLH54	86.07	52.72	84.45	79.96	3.44	4.63	2.92	0.93	1.03	20.16	1.08	2.51	1.85	1.11	5.03	1.39	61.26	143.22	43.71	56.27	10.31
CtbHLH55	0.02	0.02	0	0	0.2	0.37	0.62	1.28	0.4	0.25	0.14	0.01	0.25	0.16	0.08	0.08	0.47	0.71	0.18	0.16	0
CtbHLH56	15.04	18.15	18.66	18.46	17.59	8.91	9.28	10.29	13.42	17.77	6.46	13.04	10.91	9.72	17.06	7.55	21.16	22.33	20.83	25.08	27.63
CtbHLH57	0.15	0.29	1.07	0	0.61	2.65	7.72	13.13	17.35	0.05	0	0	0	0	0	0	0.01	0.02	0	0	0.51
CtbHLH58	0.7	0.92	0.82	0.4	0.66	1.58	1.26	8.59	5.19	4.66	0.81	0.18	1.01	0.68	0.71	0.23	1.91	2.61	2.85	3.45	1.77
CtbHLH59	0	0	0	0	0.17	0.01	0	0.03	0.35	0.06	0.03	0	0.1	0.1	1.39	0.1	0.02	0	0	0	0.84
CtbHLH60	0	0	0	0	16.68	3.29	1.66	0.1	0	0.05	1.03	0.63	0.96	1.27	1.5	0.71	0.02	0.01	0.01	0.03	0
CtbHLH61	0.14	0.27	2.78	7.6	5.32	18.3	21.79	18.45	67.24	5.75	12.42	9.53	14.48	11.47	3.64	1.47	6.92	5.23	32.12	84.18	31.16
CtbHLH62	0.24	0.28	0	0	0.04	2.9	3.94	3.21	10.28	0	0	0	0	0	0	0	0	0.05	0	0.01	0
CtbHLH63	5.25	7.44	4.37	5.11	12.44	1.96	6.21	3.32	10.1	6.46	0.73	1.12	9.92	4.05	27.16	1.78	5.5	5.57	5.93	6.78	5.75
CtbHLH64	0.06	0.02	0.04	0	0.13	1.05	1.11	9.53	1.12	2.19	1.68	0.11	1.87	1.17	1.24	0.35	8.67	1.36	1.05	0.47	0.54
CtbHLH65	0	0	0	0	0.78	0.25	0.25	2.7	0.25	0.01	0.29	0.32	0.18	0.45	0.38	0.03	0	0	0.02	0	0
CtbHLH66	0	0	0	0	0.33	0.27	0.33	2.05	0.59	0.01	0.13	0.16	0.04	0.14	0.09	0.07	0.24	0.15	0	0	0
CtbHLH67	0	0	0	0	0.44	0.55	0.6	5.76	0.9	0	0.46	0.25	0.31	0.47	0.23	0.05	0	0	0	0	0
CtbHLH68	2.96	6.93	7.02	7.01	1.82	6.22	7.35	0.68	0.96	27	0.96	1.9	0.84	1.11	1.67	0.45	5.63	5.91	10.61	8.63	5.41
CtbHLH69	13.24	14.74	25.96	33.48	11.47	5.95	8.32	7.88	6.28	16.56	5.01	6.68	5.13	5.86	6.36	5.35	6.16	6.75	7.63	14.65	37.96

Table S3. *Cont.*

Gene	White	Yellow	LightRred	DeepRred	1DAG	3DAG	5DAG	7DAG	10DAG	DAF0	DAF10	DAF20	HL_DAF10	HL_DAF20	LL_DAF10	LL_DAF20	SBS	MBS	IFS	PFS	DFS
CtbHLH70	30.44	41.44	37.32	7.92	0.11	0.39	0.58	0.34	0.13	28.59	0.22	0.11	0.27	0.58	1.45	0.44	8.53	7.19	18.64	8.58	2.7
CtbHLH71	0	0	0	0	0.03	1.74	1.79	3.7	2.56	0.78	1.1	0.03	0.69	0.4	0.91	0.23	0.66	0.13	0.02	0	0
CtbHLH72	0	0	0	0	0.35	1.46	2.71	0.12	0.05	0.03	0	0.05	0.02	0.02	0	0	0.05	0.01	0	0.05	0.07
CtbHLH73	0.07	0.39	0.27	0.08	0.35	2.93	6.63	1.13	4.29	0	0.03	0.02	0.06	0.08	0.13	0.02	0.71	0.22	0.12	0.18	0.05
CtbHLH74	0.12	0.06	0.02	0.02	0	1.36	1.41	1.7	1.51	0.01	0.03	0.02	0.09	0.07	0.08	0.06	0.14	0.05	0.04	0.09	0.1
CtbHLH75	1.52	16.77	3.09	0.82	5.14	9.68	9.76	11.16	46.27	1.01	0.15	0.12	0.33	0.34	0.64	0.09	1.71	1.08	7.9	19.43	2.58
CtbHLH76	1.69	2.05	3.53	4.75	0.92	2.8	17.74	6.31	43.31	0.52	0.98	1.13	0.31	0.73	0.08	0.36	0.13	0.06	0.55	1.19	0.57
CtbHLH77	40.12	28.15	17.77	22.02	10.85	7.88	6.52	5.71	6.86	22.72	0.81	0.59	1.86	0.95	3.77	0.89	6.11	5.61	10.73	10.03	5.38
CtbHLH78	0	0	0	0	59.85	185.07	69.22	8.82	19.46	0	0.19	1.66	0.44	0.76	0.08	0.09	0.03	0	0	0	0
CtbHLH79	6.18	10.13	5.83	7.12	55.98	29.14	27.25	1.53	0.4	1.91	7.57	7.9	8.23	8.35	8.98	4.68	40.61	22.78	5.22	10.28	2.67
CtbHLH80	0	0	0	0.03	0	0.89	0.71	0.16	0.08	0	0	0	0	0	0	0	0	0	0	0	0
CtbHLH81	0.11	0.22	0.15	0.57	5.04	27.63	22.53	7.78	9.05	0.82	5.85	57.54	4.4	21.58	1.23	9.58	2.53	1.6	0.76	0.47	0.35
CtbHLH82	0	0	0.04	0.06	2.28	2.96	2.72	3.23	9	1.25	2.09	0.84	1.72	2.28	2.55	0.88	1.66	0.9	0.54	0.14	1.15
CtbHLH83	0.04	0.14	0.47	0.78	8.95	8.75	1.73	19.65	0.02	20.78	19.22	0.77	30.43	8.28	27.33	2.2	10.01	6.96	8.31	1.92	0.86
CtbHLH84	0	0	0	0	1.61	8.55	3.45	0.15	0.06	0.2	0	0.02	0	0.06	1.39	0.11	0.11	0	0	0	0.04
CtbHLH85	1.81	1.57	2.43	0.93	25.82	34.11	18.7	7.15	7.21	62.33	81.59	19.55	106.29	66.53	56.78	7.79	47.7	33.64	25.48	3.6	5.1
CtbHLH86	59.34	65.01	64.49	75.21	42.18	53.25	62.77	54.99	144.98	81.37	32.03	29.93	47.37	31.36	76.98	17.68	110.1	109.94	109.18	97.73	124.54
CtbHLH87	0.38	0.23	0.33	0.86	0.81	0.22	0.38	0.33	0.18	0.59	0.02	0.25	0.12	0.14	0.09	0.26	0	0.02	0	0.1	0.18
CtbHLH88	82.75	92.39	107.15	172.82	11.48	5.21	3.99	4.2	8.22	33.27	2.43	5.76	4.86	6.17	9.25	2.37	20.48	43.62	88.19	112.09	47.58
CtbHLH89	0	0	0	0	28.81	3.17	2.83	10.24	1.98	0.07	1.55	1.78	0.52	1.99	1.34	2.38	0.03	0	0	0.02	0.19
CtbHLH90	15.91	14.35	43.41	13.64	0.07	0.07	0.24	0.16	0.12	0.11	0.02	0.02	0.02	0.01	0.05	0.02	0.03	0.05	3.01	8.32	0.07
CtbHLH91	2.51	3.07	2.68	5.78	66.93	6.17	7.95	5.42	15.72	4.56	1.27	3.76	2.96	2.5	8.1	2.59	4.57	4.2	3.97	3.23	4.24
CtbHLH92	0	0	0	0	0.03	0.56	0.43	0.13	0.06	0	0	0	0	0.01	0	0	0	0	0	0	0

Table S3. *Cont.*

Gene	White	Yellow	LightRred	DeepRred	1DAG	3DAG	5DAG	7DAG	10DAG	DAF0	DAF10	DAF20	HL_DAF10	HL_DAF20	LL_DAF10	LL_DAF20	SBS	MBS	IFS	PFS	DFS
CtbHLH93	4.18	9.39	5.58	11.52	10.29	9.98	12.09	22.66	31.96	12.83	5.61	14.49	12.72	8.5	12.66	4.53	13.9	10.11	9.82	13.92	15.67
CtbHLH94	40.17	45.77	43.46	42.02	23.34	10.3	8.15	8.94	11.97	24.95	9.94	42.03	16.43	31.94	17.91	22.42	22.11	32.59	30.27	31.14	38.51
CtbHLH95	1.02	0.68	1.36	0.53	6.41	11.71	13.84	7.28	27.31	1.34	10.68	11.83	8.64	11.12	0.59	8.87	5.82	4.43	0.88	0.7	0.89
CtbHLH96	3.33	0.35	1.14	0.45	39.47	4.42	3.3	3.09	2.61	9	2.75	3.38	5.66	3.46	2.58	1.22	4.05	3.08	5.47	0.41	0.94
CtbHLH97	0.55	1.5	1.42	1.07	54.88	17	18.04	10.18	23.38	0.97	7.16	21.54	7.38	12.46	1.67	6.88	0.69	0.77	1.36	1.91	2.83
CtbHLH98	0.03	0.03	0	0	0.45	0.88	0.93	1.61	1.14	0.26	0.71	1.49	0.51	0.56	0.73	0.65	1.37	0.74	0.51	0.12	0.04
CtbHLH99	2.03	4.19	1.71	7.37	0.01	0.24	0.29	0.28	1.32	0.05	0.03	0.01	0.04	0.01	0.05	0.03	0.14	0.02	0.7	2.64	4.64
CtbHLH100	0	0.02	0.15	0.1	22.6	4.45	3.1	1.13	22.45	26.2	5.92	20.05	7	15.6	0.01	0.02	8.48	8.51	6	4.3	6.03
CtbHLH101	25.73	15.79	27.31	26.13	48.77	10.23	18.76	9.28	34.72	36.88	7.8	21.65	10.19	9.96	12.76	6.1	34.69	31.68	20.73	19.83	23.4
CtbHLH102	7.46	6.14	6.31	3.42	25.31	8.51	6.79	1.97	8.63	3.07	0.52	10.56	0.37	1.27	0.15	3.25	10.36	7.23	5.56	3.92	2.01
CtbHLH103	0.42	2.35	0.04	0.12	0.91	0.64	0.23	0.28	0.05	6.69	0.64	1.33	4.28	1.56	2.49	0.13	5.55	4.65	3.7	3.7	1.84
CtbHLH104	0.04	3.27	0.04	0.04	1.13	0.96	0.86	0.06	0.14	6.19	1.02	1.83	2.02	2.4	1.32	0.62	11.17	10.19	8	6.53	7.12
CtbHLH105	6.09	4.7	0.73	0.54	1.99	5.92	5.89	0.27	1.13	3.41	0.06	0.54	1.78	1.03	3.53	0.35	2.96	2.23	2.52	3.68	3.17
CtbHLH106	0.25	0.14	0.13	0.23	3.29	1.29	1.8	0.81	0.24	3.75	0.85	0.9	0.77	1.24	2.36	0.2	2.58	2.11	1.72	0.3	0.66
CtbHLH107	0.75	1.07	6.05	7.13	4.16	1.87	1.72	6.52	0.28	31.06	11.18	6.54	17.08	15.43	9.94	2.76	45.73	27.22	36.26	3.99	20.39
CtbHLH108	0.03	0.11	0	0	1.3	0.14	0.4	0.28	3.14	0.09	0.01	0.08	0	0	0	0	0.04	0.02	0.02	0.04	0.34
CtbHLH109	0	0	0	0	0	0.32	0.84	4.22	2.1	0.07	0	0	0	0	0.02	0	0	0	0.02	0.07	0.01
CtbHLH110	0.51	0.86	0.53	0.34	19	1.68	1.65	10.25	9.56	1.14	1.26	1.99	0.27	0.8	0.13	1.26	1.81	0.61	0.53	0.11	12.21
CtbHLH111	0	0	0.03	0	0	0	0.11	0.95	0.09	0.14	0	0.01	0	0	0	0	0	0	0	0	0
CtbHLH112	0	0	0	0	0	0.11	0.26	0.25	1.84	0	0	0	0	0	0	0	0.14	0.11	0	0	0
CtbHLH113	4.87	12.76	15.6	8.64	0.76	0.99	0.95	2.42	0.62	7.9	0.04	0	0.23	0.63	0.25	0.04	28.97	16.98	9.46	9.89	1.73
CtbHLH114	0	0	0	0.04	33.31	34.43	18.54	0.45	0.75	0.03	1.36	1.37	0.76	1.52	0.29	0.22	0.07	0	0	0.1	0.41
CtbHLH115	21.9	21.19	20.3	17.69	33.87	14.21	11.21	11.73	18.13	60.24	9.14	11.74	12.05	12.92	20.53	6.99	31.56	37.9	28.43	17.09	30.74

Table S3. *Cont.*

Gene	White	Yellow	LightRred	DeepRred	1DAG	3DAG	5DAG	7DAG	10DAG	DAF0	DAF10	DAF20	HL_DAF10	HL_DAF20	LL_DAF10	LL_DAF20	SBS	MBS	IFS	PFS	DFS
CtbHLH116	0.75	0.41	1.55	0.81	27.13	3.65	3.32	4.39	0.94	5.27	0.21	0	10.56	3.56	22.17	2.32	0.63	0.33	1.78	0.94	17.86
CtbHLH117	11.88	11.83	7.32	5.49	10.87	14.22	19.52	16.94	29.79	5.13	2.29	2.24	8.16	4.78	11.07	2.76	3.5	5.99	7.48	9.08	4.44
CtbHLH118	34.86	21.64	32.43	22	2.04	10.07	15.31	9.36	11.69	13.2	0.93	0.98	2.43	1.5	5.53	0.75	7.38	4.79	17.12	22	5.71
CtbHLH119	41.05	37.2	13.1	16.02	1.35	2.72	3.06	9.06	1.86	1.56	3.31	1.5	5.12	2.88	10.66	1.21	7.12	4.73	3.45	6.95	2.63
CtbHLH120	9.36	16.16	11.44	10.12	8.32	6.63	7.24	12.38	10.46	1.96	1.99	4.82	2.49	3.91	2.72	2.32	6.32	4.8	6.18	12.69	9.66

Table S4. Primers used in the quantitative real-time PCR analysis

Gene Name	Forward primer sequence	Reverse primer sequence
<i>CtbHLH03</i>	CAAACCCCAGTTGTTTTAC	TCTTCGTCTTTCCGCCAT
<i>CtbHLH06</i>	CACCTACCACCACCGTACCT	TAACCGTCTCCCCAACCTAA
<i>CtbHLH12</i>	CAAGCCAATCCCACAGAAAG	TGATGTAGCAGCAACTCCCA
<i>CtbHLH20</i>	ATGTCGCATCCACCGATC	TCTCCCTCCTTTGCCTCTC
<i>CtbHLH24</i>	CACCCCCCTTCGTATCCCTA	CTTCCGCTCTCCCTTGTTT
<i>CtbHLH26</i>	GCTCCATTCTCTTGTTCTCA	CAAACATCCTTTTCTTCCGTC
<i>CtbHLH42</i>	CAACACATCATCCTACAATACTCC	TGCTGCCCTCTCCACAA
<i>CtbHLH51</i>	AACGGGTAGGGAACGACGT	TTTGGGTTTGATTGAGGCA
<i>CtbHLH70</i>	AATGCCTCATCACCTCCTTC	CTTCTTGGGGTTCACTTCTACA
<i>CtbHLH74</i>	CCGATGGGGTTGAAGATG	TCGATTGAGACCAGGAGC
<i>CtbHLH88</i>	AACAGTCAGACAAACCCTCCA	GAACCCAAGATTACCACAAAAG
<i>CtbHLH99</i>	GTGAGCGTTTTAGGCGAGA	ACAAAGGAGGGGGGGAT
<i>CtbHLH102</i>	GCAGAGCCAAAACCAGAGA	GTAATGAAGCCAAGCCGAC
<i>CtbHLH105</i>	GCCATTCTTCCAACACC	CTCAAAGTCCGACCCGTT
<i>CtbHLH119</i>	AGGTGGTGAAGCTGATGGA	AGATGGCAGTGGCAAGTGA
<i>Ct60S</i>	TGGAGCTCATCAAGAAGGG	GGTAAGGACCACAAGACCGTA