

Supplementary Material

Table S1 – Details of 103 identified CBL genes.

Name	Gene ID	Gene location	CDS (bp)	Protein length	PI	MW (kDa)	Subcellular localization
<i>AtCBL1</i>	<i>AT1G64480</i>	Chr1 23948027..23949751	645	215	4.76	24.65	Mitochondrial
<i>AtCBL2</i>	<i>AT4G01420</i>	Chr4 580037..581518	612	204	4.56	23.52	Cytoplasmic
<i>AtCBL3</i>	<i>AT4G16350</i>	Chr4 9242319..9243912	681	227	5.65	26.03	Chloroplast
<i>AtCBL4</i>	<i>AT4G17615</i>	Chr4 9816451..9819312	642	214	4.49	24.56	Nuclear
<i>AtCBL5</i>	<i>AT4G26560</i>	Chr4 13406732..13407973	645	215	4.53	24.41	Nuclear
<i>AtCBL6</i>	<i>AT4G26570</i>	Chr4 13408421..13411070	693	231	4.55	26.54	Nuclear
<i>AtCBL7</i>	<i>AT4G33000</i>	Chr4 15924348..15926628	771	257	4.46	29.35	Chloroplast
<i>AtCBL8</i>	<i>AT5G24270</i>	Chr5 8238533..8243357	669	223	4.87	25.70	Cytoplasmic
<i>AtCBL9</i>	<i>AT5G47100</i>	Chr5 19129639..19132283	642	214	4.33	24.53	Nuclear
<i>AtCBL10</i>	<i>AT5G55990</i>	Chr5 22671451..22673855	681	227	4.66	25.81	Extracellular matrix
<i>ZmCBL1</i>	<i>Zm00001eb023890</i>	Chr1 96334208..96338781	642	214	4.50	24.47	Cytoplasmic
<i>ZmCBL2</i>	<i>Zm00001eb030890</i>	Chr1 171126747..171139985	678	226	4.55	25.79	Cytoplasmic
<i>ZmCBL3</i>	<i>Zm00001eb051150</i>	Chr1 260095851..260114275	762	254	4.82	29.19	Cytoplasmic
<i>ZmCBL4</i>	<i>Zm00001eb135370</i>	Chr3 116785120..116812850	678	226	4.60	25.92	Cytoplasmic
<i>ZmCBL5</i>	<i>Zm00001eb160330</i>	Chr3 226083928..226087845	963	321	5.14	35.58	Chloroplast
<i>ZmCBL6</i>	<i>Zm00001eb161280</i>	Chr3 228698970..228702491	657	219	4.60	25.06	Cytoplasmic
<i>ZmCBL7</i>	<i>Zm00001eb203330</i>	Chr4 227516915..227519211	669	223	4.54	25.47	Cytoplasmic
<i>ZmCBL8</i>	<i>Zm00001eb293130</i>	Chr6 170736802..170739618	672	224	4.51	25.24	Chloroplast
<i>ZmCBL9</i>	<i>Zm00001eb390900</i>	Chr9 119599874..119604943	642	214	4.39	24.46	Nuclear
<i>OsCBL1</i>	<i>LOC_Os01g39770</i>	Chr1 22427830..22430870	873	291	4.58	32.90	Chloroplast
<i>OsCBL2</i>	<i>LOC_Os01g41510</i>	Chr1 23498442..23502377	657	219	4.54	25.09	Mitochondrial
<i>OsCBL3</i>	<i>LOC_Os01g51420</i>	Chr1 29568546..29571484	801	267	4.61	29.92	Chromoplast
<i>OsCBL4</i>	<i>LOC_Os02g18880</i>	Chr2 11015827..11017808	642	214	4.52	24.40	Chloroplast
<i>OsCBL5</i>	<i>LOC_Os02g18930</i>	Chr2 11057895..11059975	642	214	4.66	24.49	Chloroplast
<i>OsCBL6</i>	<i>LOC_Os03g42840</i>	Chr3 23888728..23895481	678	226	4.51	25.81	Cytoplasmic

<i>OsCBL7</i>	<i>LOC_Os05g45810</i>	Chr5 26535877..26537911	633	211	4.72	23.92	Chloroplast
<i>OsCBL8</i>	<i>LOC_Os10g41510</i>	Chr10 22298889..22308687	642	214	4.40	24.50	Chloroplast
<i>OsCBL9</i>	<i>LOC_Os12g06510</i>	Chr12 3145027..3149567	885	295	4.79	33.48	Cytoplasmic
<i>OsCBL10</i>	<i>LOC_Os12g40510</i>	Chr12 25063166..25068213	678	226	4.55	25.87	Cytoplasmic
<i>GsCBL1</i>	<i>GlysoPI483463.04</i> <i>G192800</i>	Chr4 50657900..50664524	672	224	4.44	25.26	Cytoplasmic
<i>GsCBL2</i>	<i>GlysoPI483463.05</i> <i>G060000</i>	Chr5 6754784..6764523	642	214	4.49	24.42	Nuclear
<i>GsCBL3</i>	<i>GlysoPI483463.06</i> <i>G117200</i>	Chr6 10809099..10816038	672	224	4.46	25.44	Cytoplasmic
<i>GsCBL4</i>	<i>GlysoPI483463.07</i> <i>G009700</i>	Chr7 827952..830976	792	264	4.76	30.43	Cytoplasmic
<i>GsCBL5</i>	<i>GlysoPI483463.07</i> <i>G226300</i>	Chr7 44427530..44435578	681	227	4.39	25.78	Extracellular matrix
<i>GsCBL6</i>	<i>GlysoPI483463.08</i> <i>G021700</i>	Chr8 1919783..1922344	708	236	4.58	26.73	Nuclear
<i>GsCBL7</i>	<i>GlysoPI483463.08</i> <i>G178200</i>	Chr8 15960299..15963649	786	262	4.64	30.12	Cytoplasmic
<i>GsCBL8</i>	<i>GlysoPI483463.08</i> <i>G292900</i>	Chr8 45360406..45364803	681	227	4.45	26.04	Cytoplasmic
<i>GsCBL9</i>	<i>GlysoPI483463.09</i> <i>G014800</i>	Chr9 1280304..1284347	681	227	4.64	25.93	Nuclear
<i>GsCBL10</i>	<i>GlysoPI483463.11</i> <i>G035000</i>	Chr11 2819080..2821207	639	213	4.31	24.40	Nuclear
<i>GsCBL11</i>	<i>GlysoPI483463.17</i> <i>G004000</i>	Chr17 1635199..1640348	681	227	4.40	25.80	Chloroplast
<i>GsCBL12</i>	<i>GlysoPI483463.17</i> <i>G136100</i>	Chr17 12486387..12490657	819	273	4.95	31.49	Chloroplast
<i>GsCBL13</i>	<i>GlysoPI483463.17</i> <i>G195000</i>	Chr17 5711081..5719023	777	259	4.44	29.26	Chloroplast
<i>GsCBL14</i>	<i>GlysoPI483463.18</i> <i>G067300</i>	Chr18 7128650..7133441	681	227	7.23	26.07	Cytoplasmic
<i>VuCBL1</i>	<i>Vigun02g160400</i>	Chr2 30635046..30638732	639	213	4.65	24.44	Cytoplasmic
<i>VuCBL2</i>	<i>Vigun03g035200</i>	Chr3 2707112..2710410	663	221	4.53	25.24	Chloroplast
<i>VuCBL3</i>	<i>Vigun03g297200</i>	Chr3 48352954..48357092	642	214	4.57	24.48	Nuclear
<i>VuCBL4</i>	<i>Vigun03g437100</i>	Chr3 64073888..64080875	681	227	4.50	25.84	Chloroplast
<i>VuCBL5</i>	<i>Vigun06g066300</i>	Chr6 19457635..19462125	681	227	4.45	26.04	Cytoplasmic
<i>VuCBL6</i>	<i>Vigun06g148100</i>	Chr6 27292665..27298292	684	228	4.62	26.16	Chloroplast
<i>VuCBL7</i>	<i>Vigun09g149400</i>	Chr9 31299345..31304400	897	229	5.04	34.62	Nuclear
<i>VuCBL8</i>	<i>Vigun10g174100</i>	Chr10 39276850..392801	777	259	4.53	29.45	Cytoplasmic
56							
<i>SbCBL1</i>	<i>Sobic.001G294300</i>	Chr1 57270694..57274360	642	214	4.50	24.49	Cytoplasmic
<i>SbCBL2</i>	<i>Sobic.003G196400</i>	Chr3 52152819..52157258	960	320	4.93	35.87	Endoplasmic reticulum
<i>SbCBL3</i>	<i>Sobic.003G208400</i>	Chr3 53959654..53964864	657	219	4.68	25.11	Mitochondrial
<i>SbCBL4</i>	<i>Sobic.003G275000</i>	Chr3 61123590..61127013	852	284	5.14	32.29	Chloroplast
<i>SbCBL5</i>	<i>Sobic.004G130600</i>	Chr4 16905084..16908896	642	214	4.45	24.39	Cytoplasmic

<i>SbCBL6</i>	<i>Sobic.008G046500</i>	Chr8 4578265..4582802	672	224	4.68	25.68	Chloroplast
<i>SbCBL7</i>	<i>Sobic.008G152800</i>	Chr8 58517447..58523171	678	226	4.61	25.85	Nuclear
<i>SbCBL8</i>	<i>Sobic.009G210300</i>	Chr9 55662844..55665067	639	213	4.39	24.05	Chloroplast
<i>PvCBL1</i>	<i>Phvul.001G034600</i>	Chr1 3265192..3270335	810	270	4.51	30.13	Cytoplasmic
<i>PvCBL2</i>	<i>Phvul.002G002300</i>	Chr2 192377..193630	429	143	4.43	20.55	Cytoplasmic
<i>PvCBL3</i>	<i>Phvul.002G299300</i>	Chr2 46727451..46730153	762	242	4.62	27.65	Nuclear
<i>PvCBL4</i>	<i>Phvul.002G299400</i>	Chr2 46731777..46733742	645	215	4.74	24.54	Mitochondrial
<i>PvCBL5</i>	<i>Phvul.003G088500</i>	Chr3 17036118..17042866	681	227	4.50	25.85	Chloroplast
<i>PvCBL6</i>	<i>Phvul.003G225900</i>	Chr3 45718718..45722898	642	214	4.57	24.54	Mitochondrial
<i>PvCBL7</i>	<i>Phvul.006G059266</i>	Chr6 16722421..16726237	681	227	4.45	26.08	Cytoplasmic
<i>PvCBL8</i>	<i>Phvul.006G135900</i>	Chr6 24357014..24361952	684	228	4.88	26.10	Cytoplasmic
<i>PvCBL9</i>	<i>Phvul.009G052700</i>	Chr9 10154081..10158087	672	224	4.47	25.67	Cytoplasmic
<i>PvCBL10</i>	<i>Phvul.010G139700</i>	Chr10 42201713..42205147	795	265	4.63	30.16	Cytoplasmic
<i>TaCBL1</i>	<i>Traes_1AL_021B94 DEB</i>	Chr1A 0..4771	588	196	4.45	22.32	Cytoplasmic
<i>TaCBL2</i>	<i>Traes_1AL_4AB2B F02A</i>	Chr1A 2683..7530	648	216	4.57	24.67	Cytoplasmic
<i>TaCBL3</i>	<i>Traes_1AL_746797 AE4</i>	Chr1A 5628..8192	642	214	4.59	24.52	Mitochondrial
<i>TaCBL4</i>	<i>Traes_1BL_3BF7C 2841</i>	Chr1B 22236..24893	675	225	4.66	25.78	Mitochondrial
<i>TaCBL5</i>	<i>Traes_1BL_AE5EA 0313</i>	Chr1B 1506..3179	612	204	4.40	23.05	Mitochondrial
<i>TaCBL6</i>	<i>Traes_1BL_DA652 B828</i>	Chr1B 2..3639	615	205	4.41	23.28	Mitochondrial
<i>TaCBL7</i>	<i>Traes_1DL_2154C A1B7</i>	Chr1D 2464..5776	642	214	4.59	24.49	Chloroplast
<i>TaCBL8</i>	<i>Traes_1DL_5F63C A08I</i>	Chr1D 1034..2868	621	207	4.41	23.55	Mitochondrial
<i>TaCBL9</i>	<i>Traes_1DL_69F530 041</i>	Chr1D 7..1666	249	83	4.02	9.39	Cytoplasmic
<i>TaCBL10</i>	<i>Traes_1DL_771752 3DF</i>	Chr1D 75..2114	582	194	4.69	22.32	Mitochondrial
<i>TaCBL11</i>	<i>Traes_1DL_E3D49 237I</i>	Chr1D 3173..4974	258	86	3.86	9.51	Nuclear
<i>TaCBL12</i>	<i>Traes_3AL_8456B7 FB8</i>	Chr3A 1840..5048	918	306	5.03	34.80	Cytoplasmic
<i>TaCBL13</i>	<i>Traes_3DL_42B337 576</i>	Chr3D 0..1263	246	82	4.07	9.43	Cytoplasmic
<i>TaCBL14</i>	<i>Traes_4AL_212D76 6F6</i>	Chr4A 3612..7099	309	103	4.91	11.92	Nuclear
<i>TaCBL15</i>	<i>Traes_4BS_EBA462 C3F</i>	Chr4B 3651..8333	783	261	5.80	29.51	Chloroplast
<i>TaCBL16</i>	<i>Traes_4DL_FBF95 B5AF</i>	Chr4D 582..4852	651	217	4.58	24.60	Cytoplasmic
<i>TaCBL17</i>	<i>Traes_4DS_C7F4F 974B</i>	Chr4D 2634..7773	678	226	4.57	25.73	Cytoplasmic
<i>TaCBL18</i>	<i>Traes_5AL_F2D4A CCA3</i>	Chr5A 408..4091	585	195	4.30	22.24	Extracellular
<i>TaCBL19</i>	<i>Traes_5BS_F12838 5EB</i>	Chr5B 0..5084	678	226	4.62	25.89	Cytoplasmic

Table S2 – Collinear gene pairs of CBLs in eight species.

Number	Gene 1	Gene 2
1	<i>GmCBL2</i>	<i>ZmCBL1</i>
2	<i>GmCBL2</i>	<i>ZmCBL9</i>
3	<i>GmCBL5</i>	<i>ZmCBL5</i>
4	<i>GmCBL8</i>	<i>ZmCBL5</i>
5	<i>GmCBL11</i>	<i>ZmCBL1</i>
6	<i>GmCBL11</i>	<i>ZmCBL9</i>
7	<i>GmCBL13</i>	<i>ZmCBL1</i>
8	<i>GmCBL13</i>	<i>ZmCBL9</i>
9	<i>GmCBL1</i>	<i>OsCBL4</i>
10	<i>GmCBL2</i>	<i>OsCBL8</i>
11	<i>GmCBL4</i>	<i>OsCBL4</i>
12	<i>GmCBL5</i>	<i>OsCBL3</i>
13	<i>GmCBL8</i>	<i>OsCBL3</i>
14	<i>GmCBL11</i>	<i>OsCBL8</i>
15	<i>GmCBL13</i>	<i>OsCBL8</i>
16	<i>GmCBL1</i>	<i>PvCBL3</i>
17	<i>GmCBL1</i>	<i>PvCBL9</i>
18	<i>GmCBL2</i>	<i>PvCBL2</i>
19	<i>GmCBL2</i>	<i>PvCBL6</i>
20	<i>GmCBL3</i>	<i>PvCBL3</i>
21	<i>GmCBL4</i>	<i>PvCBL3</i>
22	<i>GmCBL4</i>	<i>PvCBL9</i>
23	<i>GmCBL5</i>	<i>PvCBL1</i>
24	<i>GmCBL5</i>	<i>PvCBL10</i>
25	<i>GmCBL6</i>	<i>PvCBL5</i>
26	<i>GmCBL6</i>	<i>PvCBL8</i>
27	<i>GmCBL7</i>	<i>PvCBL3</i>
28	<i>GmCBL8</i>	<i>PvCBL10</i>
29	<i>GmCBL9</i>	<i>PvCBL7</i>
30	<i>GmCBL9</i>	<i>PvCBL8</i>
31	<i>GmCBL10</i>	<i>PvCBL5</i>
32	<i>GmCBL10</i>	<i>PvCBL7</i>
33	<i>GmCBL10</i>	<i>PvCBL8</i>
34	<i>GmCBL11</i>	<i>PvCBL2</i>
35	<i>GmCBL11</i>	<i>PvCBL6</i>
36	<i>GmCBL12</i>	<i>PvCBL5</i>
37	<i>GmCBL12</i>	<i>PvCBL8</i>
38	<i>GmCBL12</i>	<i>PvCBL7</i>
39	<i>GmCBL13</i>	<i>PvCBL2</i>
40	<i>GmCBL13</i>	<i>PvCBL6</i>
41	<i>GmCBL14</i>	<i>PvCBL1</i>
42	<i>GmCBL15</i>	<i>PvCBL8</i>

43	<i>GmCBL15</i>	<i>PvCBL7</i>
44	<i>GmCBL1</i>	<i>SbCBL5</i>
45	<i>GmCBL2</i>	<i>SbCBL1</i>
46	<i>GmCBL13</i>	<i>SbCBL1</i>
47	<i>GmCBL4</i>	<i>SbCBL5</i>
48	<i>GmCBL5</i>	<i>SbCBL4</i>
49	<i>GmCBL5</i>	<i>SbCBL2</i>
50	<i>GmCBL8</i>	<i>SbCBL4</i>
51	<i>GmCBL8</i>	<i>SbCBL2</i>
52	<i>GmCBL11</i>	<i>SbCBL1</i>
53	<i>GmCBL1</i>	<i>GsCBL1</i>
54	<i>GmCBL1</i>	<i>GsCBL3</i>
55	<i>GmCBL2</i>	<i>GsCBL2</i>
56	<i>GmCBL2</i>	<i>GsCBL10</i>
57	<i>GmCBL2</i>	<i>GsCBL12</i>
58	<i>GmCBL3</i>	<i>GsCBL1</i>
59	<i>GmCBL3</i>	<i>GsCBL3</i>
60	<i>GmCBL3</i>	<i>GsCBL6</i>
61	<i>GmCBL4</i>	<i>GsCBL1</i>
62	<i>GmCBL4</i>	<i>GsCBL3</i>
63	<i>GmCBL5</i>	<i>GsCBL4</i>
64	<i>GmCBL5</i>	<i>GsCBL7</i>
65	<i>GmCBL5</i>	<i>GsCBL13</i>
66	<i>GmCBL6</i>	<i>GsCBL5</i>
67	<i>GmCBL6</i>	<i>GsCBL9</i>
68	<i>GmCBL6</i>	<i>GsCBL11</i>
69	<i>GmCBL7</i>	<i>GsCBL1</i>
70	<i>GmCBL7</i>	<i>GsCBL3</i>
71	<i>GmCBL7</i>	<i>GsCBL6</i>
72	<i>GmCBL8</i>	<i>GsCBL4</i>
73	<i>GmCBL8</i>	<i>GsCBL7</i>
74	<i>GmCBL9</i>	<i>GsCBL8</i>
75	<i>GmCBL9</i>	<i>GsCBL9</i>
76	<i>GmCBL9</i>	<i>GsCBL14</i>
77	<i>GmCBL10</i>	<i>GsCBL5</i>
78	<i>GmCBL10</i>	<i>GsCBL8</i>
79	<i>GmCBL10</i>	<i>GsCBL9</i>
80	<i>GmCBL10</i>	<i>GsCBL11</i>
81	<i>GmCBL10</i>	<i>GsCBL14</i>
82	<i>GmCBL11</i>	<i>GsCBL2</i>
83	<i>GmCBL11</i>	<i>GsCBL10</i>
84	<i>GmCBL11</i>	<i>GsCBL12</i>
85	<i>GmCBL12</i>	<i>GsCBL5</i>
86	<i>GmCBL12</i>	<i>GsCBL8</i>

87	<i>GmCBL12</i>	<i>GsCBL9</i>
88	<i>GmCBL12</i>	<i>GsCBL11</i>
89	<i>GmCBL12</i>	<i>GsCBL14</i>
90	<i>GmCBL13</i>	<i>GsCBL2</i>
91	<i>GmCBL13</i>	<i>GsCBL10</i>
92	<i>GmCBL13</i>	<i>GsCBL12</i>
93	<i>GmCBL14</i>	<i>GsCBL13</i>
94	<i>GmCBL15</i>	<i>GsCBL8</i>
95	<i>GmCBL15</i>	<i>GsCBL9</i>
96	<i>GmCBL15</i>	<i>GsCBL14</i>
97	<i>GmCBL1</i>	<i>AtCBL8</i>
98	<i>GmCBL2</i>	<i>AtCBL9</i>
99	<i>GmCBL3</i>	<i>AtCBL1</i>
100	<i>GmCBL4</i>	<i>AtCBL8</i>
101	<i>GmCBL6</i>	<i>AtCBL3</i>
102	<i>GmCBL7</i>	<i>AtCBL1</i>
103	<i>GmCBL9</i>	<i>AtCBL5</i>
104	<i>GmCBL9</i>	<i>AtCBL10</i>
105	<i>GmCBL10</i>	<i>AtCBL3</i>
106	<i>GmCBL10</i>	<i>AtCBL10</i>
107	<i>GmCBL11</i>	<i>AtCBL9</i>
108	<i>GmCBL11</i>	<i>AtCBL4</i>
109	<i>GmCBL12</i>	<i>AtCBL3</i>
110	<i>GmCBL13</i>	<i>AtCBL9</i>
111	<i>GmCBL13</i>	<i>AtCBL4</i>
112	<i>GmCBL14</i>	<i>AtCBL7</i>
113	<i>GmCBL15</i>	<i>AtCBL5</i>
114	<i>GmCBL15</i>	<i>AtCBL10</i>
115	<i>GmCBL1</i>	<i>VuCBL2</i>
116	<i>GmCBL1</i>	<i>VuCBL7</i>
117	<i>GmCBL2</i>	<i>VuCBL1</i>
118	<i>GmCBL2</i>	<i>VuCBL3</i>
119	<i>GmCBL3</i>	<i>VuCBL2</i>
120	<i>GmCBL3</i>	<i>VuCBL7</i>
121	<i>GmCBL4</i>	<i>VuCBL2</i>
122	<i>GmCBL4</i>	<i>VuCBL7</i>
123	<i>GmCBL5</i>	<i>VuCBL8</i>
124	<i>GmCBL6</i>	<i>VuCBL4</i>
125	<i>GmCBL6</i>	<i>VuCBL5</i>
126	<i>GmCBL6</i>	<i>VuCBL6</i>
127	<i>GmCBL7</i>	<i>VuCBL2</i>
128	<i>GmCBL7</i>	<i>VuCBL7</i>
129	<i>GmCBL8</i>	<i>VuCBL8</i>
130	<i>GmCBL9</i>	<i>VuCBL4</i>

131	<i>GmCBL9</i>	<i>VuCBL5</i>
132	<i>GmCBL9</i>	<i>VuCBL6</i>
133	<i>GmCBL10</i>	<i>VuCBL4</i>
134	<i>GmCBL10</i>	<i>VuCBL5</i>
135	<i>GmCBL10</i>	<i>VuCBL6</i>
136	<i>GmCBL11</i>	<i>VuCBL1</i>
137	<i>GmCBL11</i>	<i>VuCBL3</i>
138	<i>GmCBL12</i>	<i>VuCBL4</i>
139	<i>GmCBL12</i>	<i>VuCBL6</i>
140	<i>GmCBL12</i>	<i>VuCBL5</i>
141	<i>GmCBL13</i>	<i>VuCBL1</i>
142	<i>GmCBL13</i>	<i>VuCBL3</i>
143	<i>GmCBL15</i>	<i>VuCBL4</i>
144	<i>GmCBL15</i>	<i>VuCBL6</i>
145	<i>GmCBL15</i>	<i>VuCBL5</i>
146	<i>GmCBL1</i>	<i>GmCBL4</i>
147	<i>GmCBL2</i>	<i>GmCBL11</i>
148	<i>GmCBL2</i>	<i>GmCBL13</i>
149	<i>GmCBL3</i>	<i>GmCBL7</i>
150	<i>GmCBL5</i>	<i>GmCBL8</i>
151	<i>GmCBL6</i>	<i>GmCBL10</i>
152	<i>GmCBL6</i>	<i>GmCBL12</i>
153	<i>GmCBL9</i>	<i>GmCBL10</i>
154	<i>GmCBL9</i>	<i>GmCBL15</i>
155	<i>GmCBL10</i>	<i>GmCBL12</i>
156	<i>GmCBL10</i>	<i>GmCBL15</i>
157	<i>GmCBL11</i>	<i>GmCBL12</i>
158	<i>GmCBL12</i>	<i>GmCBL15</i>

Table S3 – Primers used in this study.

Primer names	Sequence (5' – 3')	Description
GmCBL1-F	attgattagagatcttctagaATGGGCTGCTACTGCTCAACTT	Gene cloning
GmCBL1-R	gcccttgctcaccatgagctcCATCTCTGACTCTTCAATATCTGTTCTTAT	Gene cloning
GmACTIN4-qF	GTGTCAGCCATACTGTCCCCATTT	qRT-PCR
GmACTIN4-qR	GTTTCAAGCTCTTGCTCGTAATCA	qRT-PCR
GmCBL1-qF	ATGGGCTGCTACTGCTCAA	qRT-PCR
GmCBL1-qR	AATGACCCCATTCGCTTGA	qRT-PCR
GmCBL2-qF	AAGTCAGCGAGGCAGTTTCC	qRT-PCR
GmCBL2-qR	CGTCATCGACAACAGAACTGC	qRT-PCR
GmCBL3-qF	ACCAAACAGCGAGTCGATCA	qRT-PCR
GmCBL3-qR	TAACCCCGTCGTGGATGATG	qRT-PCR
GmCBL4-qF	TCCAGCTGGCACTATTCAGG	qRT-PCR
GmCBL4-qR	CCCAAACCTCAATGACCCCGT	qRT-PCR
GmCBL5-qF	GCTGTGCTCGGTGTTTCATTC	qRT-PCR
GmCBL5-qR	GGCGAGGGTGAGAATGTCAT	qRT-PCR
GmCBL6-qF	TCTTGCAAGAGAGACCGTGT	qRT-PCR
GmCBL6-qR	AAGACAGAGAGAGCACGTGC	qRT-PCR
GmCBL7-qF	GCGCCACAAACACAAAAAGC	qRT-PCR
GmCBL7-qR	TCCGTCTCCTTTTGAGTCTGC	qRT-PCR
GmCBL8-qF	CTGTGCGCAGTGTTTCATTC	qRT-PCR
GmCBL8-qR	TTGAACAACCTACGCAAGGC	qRT-PCR
GmCBL9-qF	AGCACTCTACGAGCTCTTCA	qRT-PCR
GmCBL9-qR	GGAAAACGGAGAGAGCACGA	qRT-PCR
GmCBL10-qF	TGTCTTTCATCCCAGCGCAT	qRT-PCR
GmCBL10-qR	TTCAGCTAGAGTGGCAACCA	qRT-PCR
GmCBL11-qF	GAGCATCAGTAGGTCCGTCG	qRT-PCR
GmCBL11-qR	AGCGCTCTAACGAAGTCACC	qRT-PCR
GmCBL12-qF	TTGCACGAGCTCTCTGTGC	qRT-PCR
GmCBL12-qR	TTCAGAAGGGATGGATGCCG	qRT-PCR
GmCBL13-qF	ATGGGCTGCATGAACTCGAA	qRT-PCR
GmCBL13-qR	TCCTTGCTTAGCAGTCCATCA	qRT-PCR
GmCBL14-qF	GTTCCACCATAGCCACGGAT	qRT-PCR
GmCBL14-qR	TCAAAACCTCAACCACCGCT	qRT-PCR
GmCBL15-qF	ATGTTGCGGTGCTTAGAGGG	qRT-PCR
GmCBL15-qR	TCGTCGATTACAGCACTGCT	qRT-PCR
GmCPA1-qF	GGGATTGCTTGTAGGCACCT	qRT-PCR
GmCPA1-qR	CCCAGCCGATGATGAGTACC	qRT-PCR
GmAPX1-qF	AGAAAGGGCTTCTTCGCTCC	qRT-PCR
GmAPX1-qR	GATTTTGCGAAGTCCTGGCG	qRT-PCR
GmCAT1-qF	GCGCTAGTGCAAAGGGTTTC	qRT-PCR
GmCAT1-qR	AAGGTTTCAGGGCTACCACG	qRT-PCR
GmGSH1-qF	TGAGGAACAGGCCGTACAAC	qRT-PCR
GmGSH1-qR	AAAAACCCGGTCTGGAAGCC	qRT-PCR

Primer names	Sequence (5' – 3')	Description
GmSOD1-qF	AGGAAGGGCTGTTGTTGTCC	qRT-PCR
GmSOD1-qR	CACAAGCTACTCTGCCACCA	qRT-PCR

Table S4 – Motif sequences identified by MEME tool.

Motif	Best possible match	Number of amino acids
Motif 1	RNGVIEFEEFVRALSVFHPNAPJEDKIEFSFRLYDLKQTGFIERZEVKZM	50
Motif 2	IIDKTFEEADTKHDGKIDKEEWKNFVLRHPSLL	33
Motif 3	EIEALYELFKKJSSSIIDDGLISKEEFQLALFKTKKKENLFADRVFDLFD	50
Motif 4	NMTLPYLKDITTTFSPFVHFS	21
Motif 5	MVQCLDGLKPLFAAIINCCDADIYKQPRGLEBPVLAARETV	41
Motif 6	ALLAESGMNLSDDVI	15
Motif 7	MGCYCSKSRKTEPDP	15
Motif 8	RLSLRSSLTFGETLCAVFIPLIGIVEALVFTFTSCFDFQSP	41
Motif 9	LASETPFTVN	10
Motif 10	HWHFNGNH	8

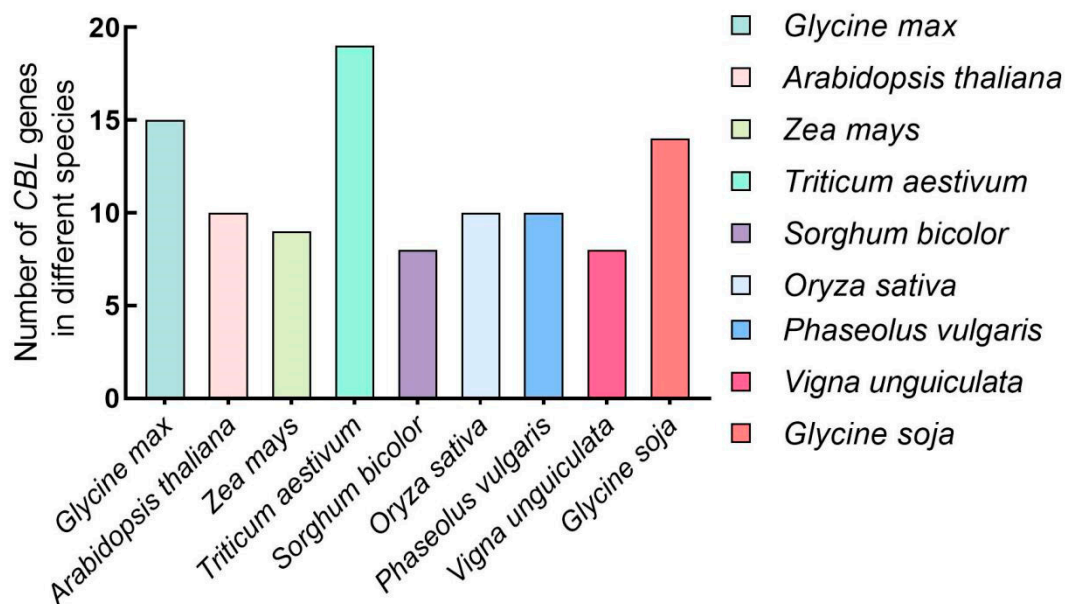


Figure. S1 – Numbers of CBL genes in nine plant species.

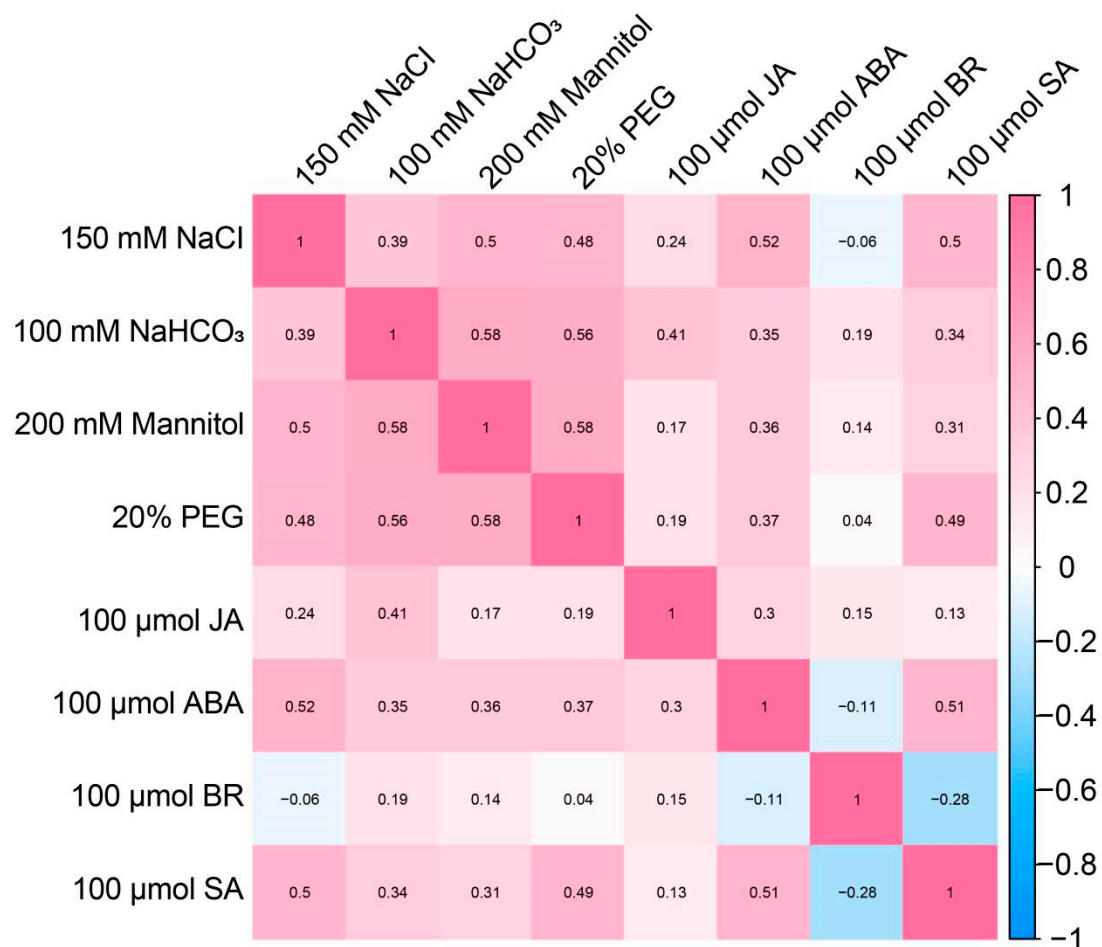


Figure. S4 – Correlation analysis of hormone stress and abiotic stress. Positive numbers represent positive correlation and negative numbers represent negative correlation. The color scale, ranging from -1.00 to 1.00 with blue representing lower values and pink representing higher values, is used to depict the normalized gene expression correlation.

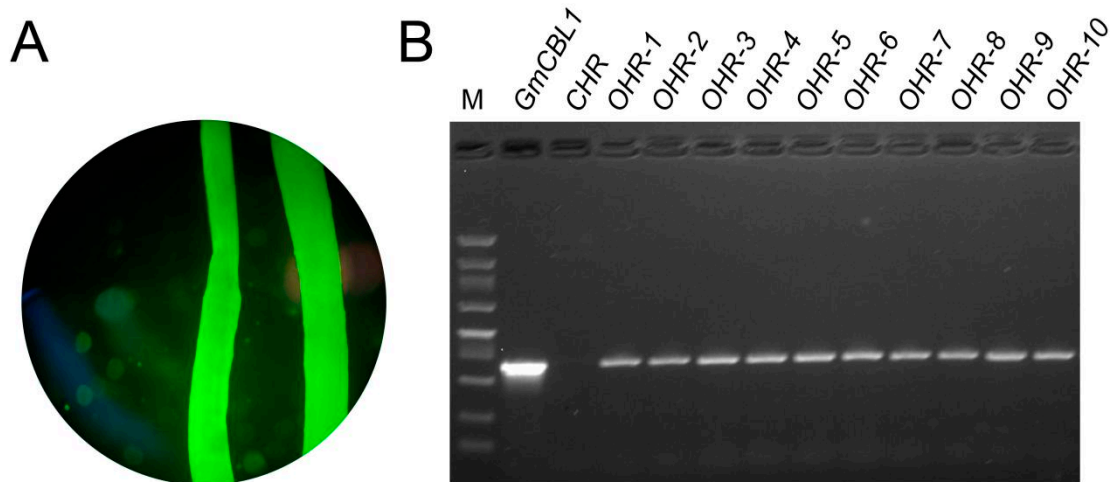


Figure. S5 – Identification of *GmCBL1* transgenic soybean hair roots.

(A) Images were captured approximately 3 weeks post-transformation to assess GFP fluorescence using a Leica stereomicroscope. (B) PCR verification of *GmCBL1* in the *35s::GmCBL1*-overexpressing hairy roots (OHR1-10). M: DNA marker; Vector: the plasmid of empty vector (*pSOY I-GFP*), as the negative control; *GmCBL1*: the recombinant expression plasmid of *pSOY I-GmCBL1::GFP*, as the positive control. M: 2K PLUS.