

Supplementary Material

GENOME-WIDE CHARACTERIZATION AND EXPRESSION ANALYSIS OF THE BCCP GENE FAMILY IN SOYBEAN: IMPLICATIONS FOR FATTY ACID BIOSYNTHESIS UNDER SALT STRESS AND MELATONIN TREATMENT

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Physiochemical Properties of BCCP Genes

Phytozome ID	Gene name	PAC	Chrom. #	Chromo Length	Location		Strand	Size (AA)		Mol. W	Number of Amino Acids	pi	Gravy	Instability Index (II)	Aliphatic Index (AI)	Intron : Exon
					Start location	End location		mRNA (CDS)	Protein length							
GlymaLee.08G026100	GmBCCP1	41237192	8	48715292	2249563	2257269	Reverse	1620	540	58807.6	539	7.22	-0.139	40.68	87.98	15:16
GlymaLee.04G096200	GmBCCP2	41244766	4	53163752	10219041	10234566	Forward	6783	2261	252370.5	2260	6	-0.229	40.9	93.99	30:31
GlymaLee.10G026700	GmBCCP3	41256885	10	53126121	2520819	2527612	Reverse	2196	732	80283.4	731	6.69	-0.203	39.45	89.78	13:14
GlymaLee.06G097300	GmBCCP4	41262203	6	52368333	8747215	8762730	Forward	6783	2261	252170	2260	5.92	-0.231	42.53	93.81	30:31
GlymaLee.17G112600	GmBCCP5	41267218	17	42603825	9858068	9870097	Reverse	2829	943	105970.7	942	5.5	-0.285	38.35	88	12:13
GlymaLee.14G093100	GmBCCP6	41270843	14	50809644	10724519	10728569	Reverse	678	335	36960.81	334	6.08	-0.16	28.7	82.54	7:8
GlymaLee.19G045700	GmBCCP7	41278069	19	52038378	9538919	9541986	Forward	2457	819	92160.95	818	9.12	0.045	37.01	94.88	0
GlymaLee.19G019500	GmBCCP8	41278814	19	52038378	2444805	2448983	Reverse	2316	772	90846.79	771	4.9	-0.685	46.06	72.19	4:5
GlymaLee.02G129100	GmBCCP9	41282864	2	51931201	15813629	15820117	Forward	2208	736	81097.43	735	6.66	-0.2	39.96	91.28	14:15
GlymaLee.05G191600	GmBCCP10	41284349	5	43063349	41324502	41333560	Reverse	1620	540	58888.72	539	7.22	-0.152	41.13	88.35	15:16
GlymaLee.20G128000	GmBCCP11	41293039	20	49591883	41994630	42011247	Forward	2382	794	90124.76	793	5.69	-0.314	41.63	91.85	10:11

Cis- Regulatory Elements' counts:

	GmBCCP1	GmBCCP2	GmBCCP3	GmBCCP4	GmBCCP5	GmBCCP6	GmBCCP7	GmBCCP8	GmBCCP9	GmBCCP10	GmBCCP11
4cl-CMA2b	0	1	0	0	0	0	0	0	0	0	0
AAAC-motif	0	0	0	0	0	0	1	0	0	0	0
AACA_motif	0	1	0	0	0	0	0	0	0	0	0
AAGAA-motif	2	0	0	0	1	1	2	1	0	2	1
ABRE	1	9	0	6	0	1	0	0	0	2	2
ABRE3a	0	1	0	0	0	0	0	0	0	1	0
ABRE4	0	1	0	0	0	0	0	0	0	1	0
ACE	0	0	0	0	1	0	0	0	0	0	0
AE-box	2	0	0	0	0	2	1	2	0	1	0
AP-1	0	0	0	0	0	0	0	1	0	0	0
ARE	1	6	1	3	0	1	2	5	1	1	0
AT-rich element	1	0	0	0	0	1	0	0	2	0	1
AT-rich sequence	0	0	0	0	1	1	0	0	0	0	0
AT1-motif	1	0	0	2	0	0	0	0	0	0	0
ATCT-motif	0	1	0	0	0	0	1	0	0	0	0
AT~TATA-box	6	2	2	5	4	0	2	3	4	4	2
AuxRR-core	0	1	0	1	0	1	0	0	0	0	0
Box 4	3	2	3	3	3	3	4	6	2	3	0
Box II	0	0	0	0	0	1	0	0	0	0	0
Box II -like sequence	0	1	0	0	0	0	0	0	0	0	0
Box III	0	1	0	0	0	0	0	0	0	0	0
CAAT-box	50	59	34	57	32	39	51	46	24	41	37

CARE	0	0	0	2	0	0	0	0	0	0	0
CAT-box	1	0	0	0	0	0	0	0	0	0	0
CGTCA-motif	0	3	1	2	0	2	0	0	0	1	2
DRE1	0	0	0	1	0	0	0	0	0	0	0
ERE	1	1	2	0	1	1	1	2	2	3	5
G-Box	1	4	0	3	0	1	0	0	0	1	0
G-box	0	6	0	3	0	0	1	0	1	1	4
GARE-motif	0	0	0	0	0	1	0	0	0	2	0
GATA-motif	0	0	0	0	2	0	0	0	1	0	0
GC-motif	0	0	0	0	0	1	0	0	0	0	0
GCN4_motif	0	2	0	2	0	0	0	1	0	1	0
GT1-motif	3	3	2	2	1	2	2	0	1	4	3
Gap-box	0	0	0	0	0	1	0	0	1	0	1
HD-Zip 1	1	0	0	0	0	0	0	0	0	1	1
HD-Zip 3	0	1	0	0	0	0	0	0	0	0	0
I-box	0	2	0	1	0	0	0	1	1	0	0
LS7	0	0	0	0	0	0	1	0	0	0	0
LTR	0	0	0	1	0	1	1	1	0	2	0
MBS	0	0	0	0	1	1	0	0	0	0	0
MBSI	0	1	0	1	0	0	0	0	0	0	0
MRE	0	1	0	1	0	1	1	0	0	1	0
MSA-like	0	0	0	0	0	1	0	0	0	0	0
MYB	3	4	3	6	3	2	2	2	5	6	2
MYB-like sequence	2	2	1	1	1	1	1	0	1	3	0
MYC	3	2	4	6	4	3	1	3	1	6	7
Myb	1	3	0	0	3	2	0	0	3	1	0
Myb-binding site	0	1	2	1	1	1	0	0	0	2	2
Myc	0	2	0	2	1	1	0	0	0	0	0
O2-site	0	1	0	1	0	1	0	0	0	0	1

OCT	0	0	0	0	0	2	0	0	0	0	0
P-box	0	3	1	3	0	0	0	0	0	0	0
STRE	1	4	1	5	0	1	1	1	1	1	3
Sp1	0	0	0	1	0	1	0	0	0	0	0
TATA	0	1	0	3	1	0	0	0	1	1	2
TATA-box	38	59	43	71	61	9	23	38	50	38	56
TATC-box	0	0	1	0	1	0	0	1	0	0	1
TC-rich repeats	2	0	0	0	0	0	0	0	1	1	0
TCA	0	0	1	1	1	0	0	0	0	0	0
TCA-element	0	0	1	1	1	2	0	0	1	1	2
TCCC-motif	0	0	0	0	0	0	1	0	0	0	0
TCT-motif	0	2	1	1	0	4	0	2	0	2	2
TGA-box	0	0	0	0	0	0	0	0	0	1	0
TGA-element	0	0	1	0	0	0	0	0	1	0	1
TGACG-motif	0	3	1	2	0	2	0	0	0	1	2
W box	0	0	0	1	0	2	2	2	0	0	0
WRE3	0	1	0	0	0	1	1	1	1	0	0
WUN-motif	0	1	0	2	2	2	1	1	0	1	0
as-1	0	3	1	2	0	2	0	0	0	1	2
box S	0	1	0	1	0	0	0	0	0	0	0
chs-CMA1a	0	0	0	0	1	0	1	0	0	0	0
chs-CMA2a	0	0	0	0	0	0	0	0	0	0	2
chs-Unit 1 m1	0	0	0	1	0	0	0	0	0	0	0
dOCT	0	0	0	0	0	1	0	0	0	0	0
re2f-1	0	0	0	0	1	0	0	0	0	0	0

