

**Structural and functional insights into the LBD family involved in
abiotic stress and flavonoid synthases in *Camellia sinensis***

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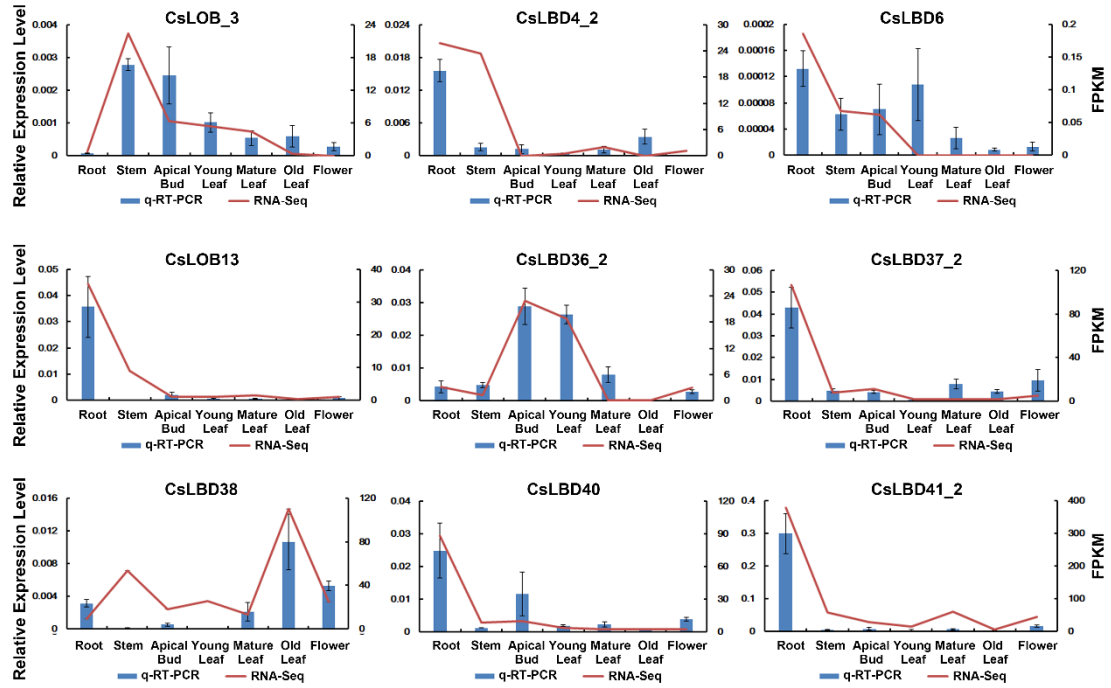
These authors contributed equally to this work

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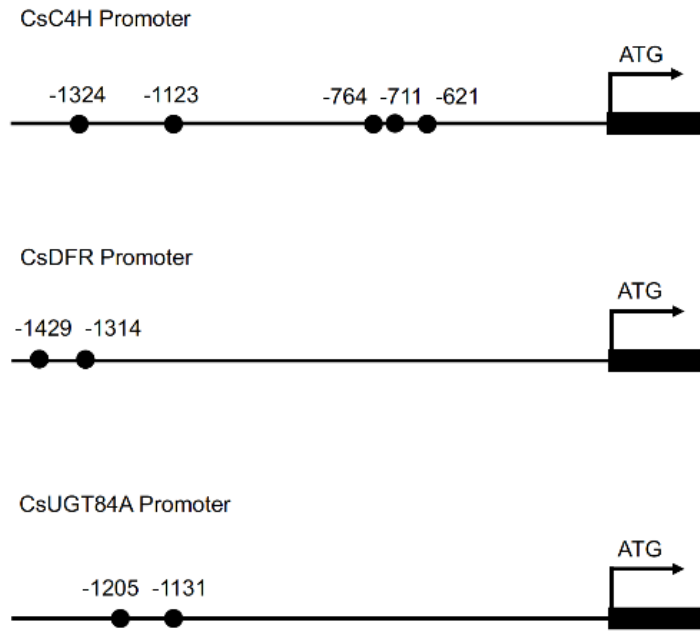
Supplementary Figures

	CX2CX6CX3C	GAS block	P	LX6LX3LX6
CsLBD2_1	: AASGRHQRKKCTDKVLAFFPVNK----	SREQAVHVRVGVSNATKIVKMKKEEDRKK-AIDSLVWEPFCRIKDPILCPYG----		EYRKVVEELKIYKS : 100
CsLBD2_2	: AASGRHQRKKCTDKVLAFFPVNK----	SREQAVHVRVGVSNATKIVKMKKEEDRKK-AIDSLVWEPFCRIKDPILCPYG----		EYRKVVEELKIYKS : 100
CsLBD26_1	: AASGRHQRKKCHGGIMAHFPSSK----	TEEEAVHVRVGVSNVTKIKTKIDFARQKQ-AVNSFIWEPFWWKRFAHPLGHKIAETPNFSNEQRNYQN : 114		
CsLBD26_2	: AASGRHQRKKCHGGIMAHFPSSK----	TEEEAVHVRVGVSNVTKIKTKIDFARQKQ-AVNSFIWEPFWWKRFAHPLGHKIAETPNFSNEQRNYQN : 114		
CsLOB_1	: FAAQFLRRKQMPGIFAFVPPPEE----	PQKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 106		
CsLOB_2	: FAAQFLRRKQMPGIFAFVPPPEE----	PQKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 106		
CsLOB_3	: FAAQFLRRKQMPGIFAFVPPPEE----	PHKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 106		
CsLOB_4	: FAAQFLRRKQMPGIFAFVPPPEE----	PQKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 112		
CsLBD36_1	: FAAQFLRRKQMPGIFAFVPPPEE----	PQKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 103		
CsLBD36_2	: FAAQFLRRKQMPGIFAFVPPPEE----	PQKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 103		
CsLBD6	: FAAQFLRRKQMPGIFAFVPPPEE----	PQKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 110		
CsLBD15_1	: SAAQFLRRKQMPGIFAFVPPPEE----	PKKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 107		
CsLBD15_2	: SAAQFLRRKQMPGIFAFVPPPEE----	PKKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 153		
CsLBD15_3	: SAAQFLRRKQMPGIFAFVPPPEE----	PKKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 169		
CsLBD13	: SAAQFLRRKQMPGIFAFVPPPEE----	PKKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 145		
CsLBD1_1	: FAAQFLRRKQMPGIFAFVPPPEE----	PLKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 136		
CsLBD1_2	: FAAQFLRRKQMPGIFAFVPPPEE----	PLKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 141		
CsLBD11_1	: FAGAKLRRKQMPGIFAFVPPPEE----	LFKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 126		
CsLBD11_2	: FAGAKLRRKQMPGIFAFVPPPEE----	PLRSTIAHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 153		
CsLBD11_3	: FAGAKLRRKQMPGIFAFVPPPEE----	PLRSTIAHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 142		
CsLBD4_1	: FAAQFLRRKQMPGIFAFVPPPEE----	PHKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 112		
CsLBD4_2	: FAAQFLRRKQMPGIFAFVPPPEE----	PHKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 110		
CsLBD12_2	: FAGAKLRRKQMPGIFAFVPPPEE----	PHKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 102		
CsLBD12_3	: FAGAKLRRKQMPGIFAFVPPPEE----	PRKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 102		
CsLBD12_1	: FAGAKLRRKQMPGIFAFVPPPEE----	PHKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 102		
CsLBD16_1	: FAGAKLRRKQMPGIFAFVPPPEE----	GPASNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 107		
CsLBD16_2	: FAGAKLRRKQMPGIFAFVPPPEE----	GPASNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 93		
CsLBD17	: FAGAKLRRKQMPGIFAFVPPPEE----	SATHSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 104		
CsLBD29	: FAGAS-----	HKVSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 76		
CsLBD30	: FAGAKLRRKQMPGIFAFVPPPEE----	GAHSAVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 115		
CsLBD18	: FAGAKLRRKQMPGIFAFVPPPEE----	GAHSAVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 136		
CsLBD31	: FAGAKLRRKQMPGIFAFVPPPEE----	GTASNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 112		
CsLBD19	: FAGAKLRRKQMPGIFAFVPPPEE----	GSASNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 112		
CsLBD33	: SGAQFLRRKQMPGIFAFVPPPEE----	AAASNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 104		
CsLBD20	: FAGAKLRRKQMPGIFAFVPPPEE----	GAASNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 136		
CsLBD23	: FAAQFLRRKQMPGIFAFVPPPEE----	PEKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 93		
CsLBD24	: FAAQFLRRKQMPGIFAFVPPPEE----	PEKSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 91		
CsLBD7_1	: AQAQFLRRKQMPGIFAFVPPPEE----	HQKLNHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 139		
CsLBD22	: AQAQFLRRKQMPGIFAFVPPPEE----	HQKLNHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 129		
CsLBD7_2	: AQAQFLRRKQMPGIFAFVPPPEE----	HKHLSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 122		
CsLBD27_2	: AQAQFLRRKQMPGIFAFVPPPEE----	PKMNSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 106		
CsLBD27_3	: AQAQFLRRKQMPGIFAFVPPPEE----	PKMNSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 100		
CsLBD27_1	: AQAQFLRRKQMPGIFAFVPPPEE----	PKMNSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 153		
CsLBD34	: AQAQFLRRKQMPGIFAFVPPPEE----	PKMNSNVHRIIGASNVTKLNEILPHQED-AVNSIAYEAEAVRDPVYCVGASVLRGQVRELKQIDDA : 107		
CsLBD39_1	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 103		
CsLBD32_2	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 103		
CsLBD38_1	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 105		
CsLBD37_1	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 107		
CsLBD37_2	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 101		
CsLBD38_2	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 70		
CsLBD41_1	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 105		
CsLBD41_2	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 159		
CsLBD40	: RGVPLVLRKQMPGIFAFVPPPEE----	TIRCLQWIKTPSCANATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 120		
CsLBD42	: SNGQFLRRKQMPGIFAFVPPPEE----	ILRSCLQWIDSPSCAHATVFAAFPRAGIMSPSSPNSQPD-LFCSLFFFCGTVNPNNAVGLWTCGNWHCOAAVAVTLR : 105		

Supplementary Figure 1. Comparison of the amino acid sequences of CsLBDs.



Supplement Figure 2. Expression patterns of the nine *CsLBDs* in different tissues.



Supplementary Figure 3. Analysis of LBD binding site in the promoter region of structural genes involved in the flavonoid pathway.