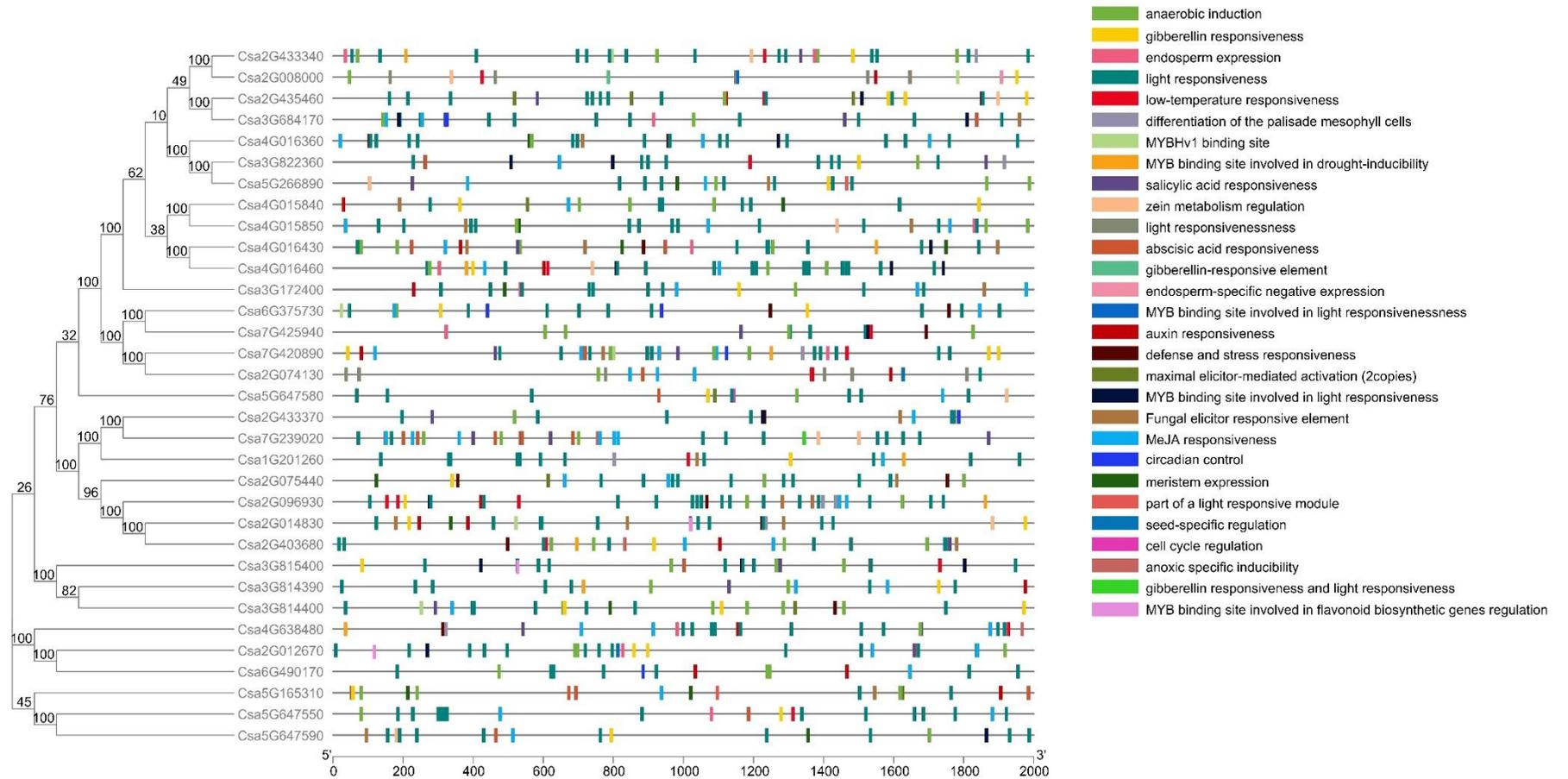


**Figure S1 The sequence logos of motifs in CsCC-NBS-LRR.**

Csa30822360	.....MAEITVYVQVETRRVYVYK.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	111
CmaCh149014850.1	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	110
Cla970070142810	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	110
XP_022145177.1	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	110
XP_00453965.1	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	109
At3G14470	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	109
XP_004245923.1	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	100
XP_00659131.1	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	119
XP_015651137.1	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	114
XP_00666515.1	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	138
Consensus	.....MAEITVAVCELEKRTASLAA.....	.....CQGLVAVLEKLESLIKRDKHDAITL.....	.....EDTRKRSKSPGNSVWVWVETV.....	.....VHACILDLIVVHRRVETVETKESVSDSSISVNS	
Csa30822360	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	249
CmaCh149014850.1	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	248
Cla970070142810	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	248
XP_022145177.1	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	248
XP_00453965.1	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	252
At3G14470	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	252
XP_004245923.1	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	285
XP_00659131.1	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	295
XP_015651137.1	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	261
XP_00666515.1	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	252
Consensus	FIFRRMARRKIRITITLNCYKASAFVGVVTV.....	TEIELALNCG.....IRITISLIDFG.....	WVGRVAVLEKLESLIKRDKHDAITL.....	.....EHHMVSIVS.....	
Csa30822360	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	391
CmaCh149014850.1	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	382
Cla970070142810	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	382
XP_022145177.1	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	382
XP_00453965.1	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	382
At3G14470	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	384
XP_004245923.1	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	389
XP_00659131.1	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	367
XP_015651137.1	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	385
XP_00666515.1	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	400
Consensus	CGSLESNKAELIGLIRREKQ.....	DNVLDVLDVWVWV.....	.....HMLDCEKGLKRLAKGKNTINM.....	.....SREKATVWEPISIVR.....	
Csa30822360	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	530
CmaCh149014850.1	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	511
Cla970070142810	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	519
XP_022145177.1	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	521
XP_00453965.1	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	521
At3G14470	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	521
XP_004245923.1	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	487
XP_00659131.1	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	528
XP_015651137.1	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	516
XP_00666515.1	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	530
Consensus	EISMTVTSVYRHSLEKRVISLKVSV.....	SNVYVLDVLDVWVWV.....	.....KCHSQCQVYRQCDLITL.....	.....KQVPOGR.....	
Csa30822360	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	634
CmaCh149014850.1	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	623
Cla970070142810	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	624
XP_022145177.1	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	624
XP_00453965.1	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	624
At3G14470	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	659
XP_004245923.1	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	729
XP_00659131.1	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	711
XP_015651137.1	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	751
XP_00666515.1	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	779
Consensus	.....SG.....	.....ESVYRRLTICN.....	.....DEVINYNDIVD.....	.....VWVGF.....	
Csa30822360	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	742
CmaCh149014850.1	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	731
Cla970070142810	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	753
XP_022145177.1	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	733
XP_00453965.1	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	772
At3G14470	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	711
XP_004245923.1	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	772
XP_00659131.1	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	751
XP_015651137.1	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	779
XP_00666515.1	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	779
Consensus	GET.A.HSDMEN.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	
Csa30822360	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	826
CmaCh149014850.1	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	853
Cla970070142810	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	875
XP_022145177.1	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	822
XP_00453965.1	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	822
At3G14470	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	861
XP_004245923.1	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	807
XP_00659131.1	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	858
XP_015651137.1	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	843
XP_00666515.1	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	919
Consensus	LNFAEVLVETVFNKVV.....	.....IHLGSGVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	.....SREKATVWEPISIVR.....	
Csa30822360	.....	.....	.....	.....	870
CmaCh149014850.1	.....	.....	.....	.....	937
Cla970070142810	.....	.....	.....	.....	869
XP_022145177.1	.....	.....	.....	.....	880
XP_00453965.1	.....	.....	.....	.....	914
At3G14470	.....	.....	.....	.....	853
XP_004245923.1	.....	.....	.....	.....	893
XP_00659131.1	.....	.....	.....	.....	1044
XP_015651137.1	.....	.....	.....	.....	
XP_00666515.1	.....	.....	.....	.....	
Consensus	.....	.....	.....	.....	
Csa30822360	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	989
CmaCh149014850.1	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	1039
Cla970070142810	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	1057
XP_022145177.1	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	988
XP_00453965.1	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	999
At3G14470	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	981
XP_004245923.1	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	1032
XP_00659131.1	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	1019
XP_015651137.1	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	1171
XP_00666515.1	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	
Consensus	YLSRGCFMMLNVNKHRYHLEIDKRLRFGMDGTRL.....	.....ELKGGCMQYEFFS.....	.....VHLSAQVLEKLESLIKRDKHDAITL.....	.....SREKATVWEPISIVR.....	
Csa30822360	CSYCFKLEKSRKALRLTKENLDFECPHLLVGSQDQKRALSHLFSKRVHSESEYSGLL.....	.....	.....	.....	1053
CmaCh149014850.1	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1078
Cla970070142810	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1086
XP_022145177.1	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1012
XP_00453965.1	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1046
At3G14470	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1054
XP_004245923.1	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1082
XP_00659131.1	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1182
XP_015651137.1	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1110
XP_00666515.1	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	1195
Consensus	SLRVYGCQLEKSGCFQVNTSNGSIEFFVQIHTFFV.....	.....	.....	.....	
Csa30822360	.....	.....	.....	.....	1053
CmaCh149014850.1	.....	.....	.....	.....	1078
Cla970070142810	.....	.....	.....	.....	1086
XP_022145177.1	.....	.....	.....	.....	1012
XP_00453965.1	.....	.....	.....	.....	1046
At3G14470	.....	.....	.....	.....	1054
XP_004245923.1	.....	.....	.....	.....	1082
XP_00659131.1	.....	.....	.....	.....	1182
XP_015651137.1	.....	.....	.....	.....	1110
XP_00666515.1	.....	.....	.....	.....	1195
Consensus	.....	.....	.....	.....	

Figure S2 Alignment of the partial CNL proteins between cucumber and other species.



**Figure S3 The cis-element of the promoters of the CNL gene in cucumber.**