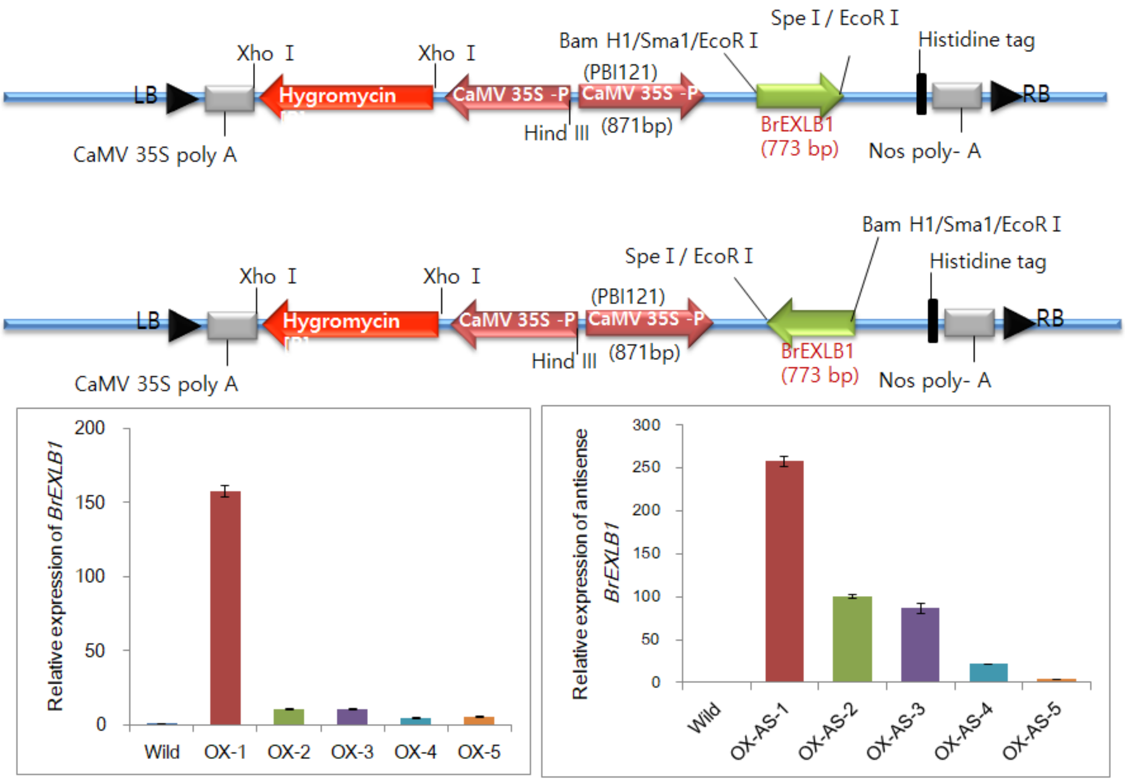

Figure S1. The simplified version of expression cassette used for Agrobacterium mediated genetic transformation and transgene (BrEXLB1) expression pattern in transgenic *Brassica rapa* lines.

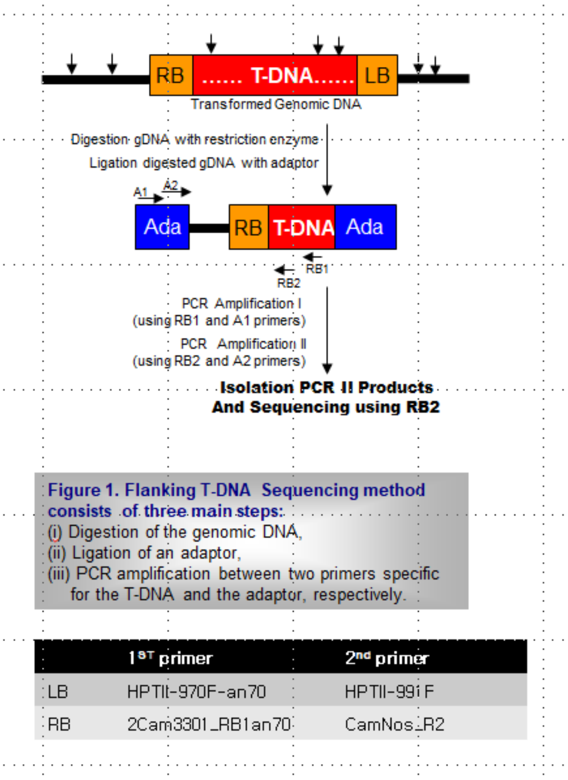

Figure 1. Flanking T-DNA Sequencing method consists of three main steps:
(i) Digestion of the genomic DNA,
(ii) Ligation of an adaptor,
(iii) PCR amplification between two primers specific for the T-DNA and the adaptor, respectively.

	1ST primer	2nd primer
LB	HPTII-970F-an70	HPTII-99i F
RB	2Cam3301_RB1an70	CamNos_R2

Figure S2. The methodology followed in T-DNA flanking sequencing and the list of primers used during this study for identification of transgene integration site.

Flanking T-DNA Sequencing method consists of two main steps: first, restriction digestion of the genomic DNA and ligation of an adaptor, and second PCR amplification between two primers specific for the T-DNA and the adaptor, respectively. 500 ng genomic DNA were digested and ligated with 2U restriction enzyme and 5U T4 DNA ligase (Takara, Shiga, Japan) in a 20ul reaction volume. The reaction mixture contained T4 DNA ligase buffer and 50 pmol of the adaptors was incubated at 37 °C for 1hr. The first PCR was conducted in a 20 uL reaction containing PCR pre-mixture, 0.5 pmol each primer (Ada1 and LB1 or RB1), and 1 uL digestion/ligation product. PCR were performed in a PTC-200 thermal cycler (MJ Research, Waltham, MA, USA) and conducted as the follows(Ada2 and LB2 or RB2): first denaturation step at 95 °C for 5 min, 20 cycles of 30 s at 94 °C and 1 min at 72 °C, followed by a final elongation step at 72 °C for 10 min. Second PCR were conducted with 5ul of first PCR product under the conditions of first denaturation step at 94 °C for 5 min, 40 cycles of 30 s at 94 °C, 30 s at 60 °C, and 1 min at 72 °C, followed by a final elongation step at 72 °C for 10 min. Amplified products were loaded on a 1% agarose gel and the PCR products were purified by HiYield™ Gel/PCR DNA Extraction Kit (RBC Bioscience, Taipei, Taiwan) and sequenced by ABI3730XL using LB2 or RB2 primer.

The list of primers used for T-DNA Flanking sequencing in this study

S.No	Primer Name	Sequences
1.	CAMBIA-RB-an70(2Cam3301-RBan70)	tgaattacaggtgaccagctcgaatttcc
2.	Tnos149F (CamNos-R2)	TGATTAGAGTCCCGCAATTA
3.	HPT_991F	CTCGCCGATAGTGGAAACC
4.	HPT_970F_an70	CCGTCTGGACCGATGGCTGTGTAGAAG

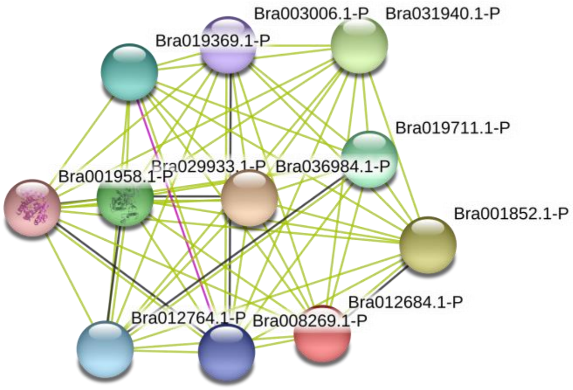

Figure S3. The BrEXLB1 protein-protein interacting prediction network obtained from String-db tools and the list of primers designed for expression profiling of BrEXLB1 interacting genes

Details of interacting proteins and their corresponding gene names from the network

>**Bra001852**.1-P=AT3G22120 CWLP | CWLP (CELL WALL-PLASMA MEMBRANE LINKER PROTEIN); lipid binding

>**Bra003006**.1-P=Uncharacterized protein; AT5G54170 INVOLVED IN: response to wounding

>**Bra001958**.1-P=Uncharacterized protein; AT2G16060 - GLB1, AHB1, ARATH GLB1, NSHB1, ATGLB1 | AHB1 (ARABIDOPSIS HEMOGLOBIN 1); oxygen binding/ oxygen transporter; Belongs to the globin family

>**Bra008269**.1-P=Uncharacterized protein; AT1G76640| calmodulin-related protein, putative

>Bra012684.1-P= Uncharacterized protein; AT4G17030, ATEXLB1, (ARABIDOPSIS THALIANA EXPANSIN-LIKE B1

>**Bra012764**.1-P=Uncharacterized protein; AT4G15800, RALFL33 | RALFL33 (ralf-like 33); signal transducer

>**Bra019369**.1-P=Uncharacterized protein; AT4G22620 | auxin-responsive family protein

>**Bra019711**.1-P=Uncharacterized protein; AT1G66700, PXMT1 | PXMT1; S-adenosylmethionine-dependent methyltransferase

>**Bra029933**.1-P=Peroxidase; AT3G49120, ATPERX34, PERX34, PRXCB, ATPCB | PRXCB (PEROXIDASE CB); peroxidase; Belongs to the peroxidase family. Classical plant (class III) peroxidase subfamily

>**Bra031940**.1-P=Uncharacterized protein; AT5G64000, SAL2, ATSAL2 | SAL2; 3'(2'),5'-bisphosphate nucleotidase/ inositol or phosphatidylinositol phosphatase

>**Bra036984**.1-P=Uncharacterized protein; AT4G33710| pathogenesis-related protein, putative

Primer Name	**Sequence (5'->3')**	**Annealing temperature**	**Length (nt)**
Bra001852-FP	TGGTAAAACGCACGCGAAAG	56 °C / 30 s	20
Bra001852-RP	TTTGAAGCCAGGTGGTGGAG		20
Bra001958-FP	TGTTGTGAGTCAGCAGCACA	56 °C / 30 s	20
Bra001958-RP	CTGGCACCGCCTCCTTTATT		20
Bra003006-FP	TACGCGCTTACCAAGAGCAA	60 °C / 30 s	20
Bra003006-RP	TCCGTTGTGTGTAACGGGAG		20
GATA23-FP	GTGGTTCCTTGGAACACCCT	56 °C / 30 s	20
GATA23-RP	TCAAAAGAACCAACCTTTGTGGG		23
MAKR4-FP	GAGTGCAGCCTCCTTTTGGA	60 °C / 30 s	20
MAKR4-RP	CGCAGGCTGTCTCCTCATAG		20

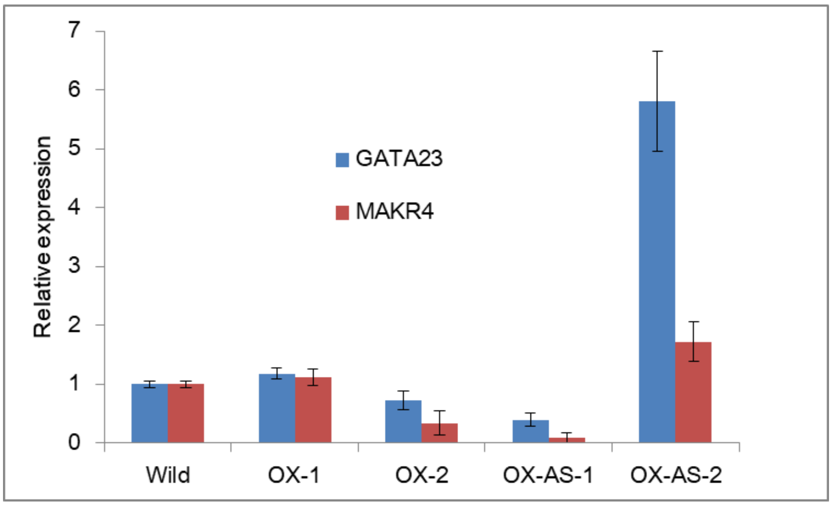

Figure S4. qRT-PCR based relative quantification of lateral root marker genes, *GATA23* and *MAKR4*.

Table S1. List of OJIP transient parameters collected from OX, OX-AS lines, and wild type *B. rapa* lines subjected to 8 days of progressive drought stress.

BrEXLB1-AS lines	Replicate 1	Replicate 2	Replicate 3	Average	SE
Bckg	260	162	162	194.6666667	32.66666667
Fo	10631	12809	9851	11097	885.119201
Fj	27211	29553	27082	27948.66667	803.0305792
Fi	45613	51660	45515	47596	2032.196923
Fm	58194	64242	56634	59690	2320.124135
Fv	47563	51433	46783	48593	1437.741284
Vj	0.349	0.326	0.368	0.347666667	0.01214267
Vi	0.735	0.755	0.762	0.750666667	0.008089774
Fm/Fo	5.474	5.015	5.749	5.412666667	0.214095254
Fv/Fo	4.474	4.015	4.749	4.412666667	0.214095254
Fv/Fm	0.817	0.801	0.826	0.814666667	0.007310571
Mo	0.67	0.632	0.673	0.658333333	0.013195117
Area	15395077	11822609	16132228	14449971.33	1330804.584
Fix Area	57153324	62947368	55591720	58564137.33	2237497.491
Sm	323.678	229.864	344.831	299.4576667	35.32855871
Ss	0.52	0.515	0.548	0.527666667	0.010268615
N	621.976	446.33	629.825	566.0436667	59.89970281
Phi_Po	0.817	0.801	0.826	0.814666667	0.007310571
Psi_o	0.651	0.674	0.632	0.652333333	0.01214267
Phi_Eo	0.532	0.54	0.522	0.531333333	0.005206833
Phi_Do	0.183	0.199	0.174	0.185333333	0.007310571
Phi_Pav	939.374	912.764	944.399	932.179	9.815282726
Pi_Abs	3.556	3.43	3.684	3.556666667	0.073324242
ABS/RC	2.351	2.425	2.211	2.329	0.062748174
TRo/RC	1.922	1.942	1.826	1.896666667	0.035801924
ETo/RC	1.252	1.31	1.154	1.238666667	0.045524108
DIo/RC	0.43	0.484	0.385	0.433	0.028618176

BrEXLB1-Sense lines	Replicate 1	Replicate 2	Replicate 3	Average	SE
Bckg	162	162	162	162	0
Fo	10143	10404	8811	9786	493.2879484
Fj	27667	27960	24481	26702.66667	1114.048822
Fi	45320	47108	42037	44821.66667	1484.925625
Fm	55301	58617	55626	56514.66667	1055.345178
Fv	45158	48213	46815	46728.66667	882.9583481
Vj	0.388	0.364	0.335	0.362333333	0.01532246
Vi	0.779	0.761	0.71	0.75	0.020663978
Fm/Fo	5.452	5.634	6.313	5.799666667	0.261988761
Fv/Fo	4.452	4.634	5.313	4.799666667	0.261988761
Fv/Fm	0.817	0.823	0.842	0.827333333	0.007535103
Mo	0.757	0.663	0.556	0.658666667	0.058064141
Area	15227274	16646788	16199915	16024659	419042.9565
Fix Area	54330196	57583580	54482664	55465480	1059964.202
Sm	337.2	345.276	346.041	342.839	2.828135251
Ss	0.512	0.549	0.603	0.554666667	0.026421792
N	658.159	629.112	574.336	620.5356667	24.57464108
Phi_Po	0.817	0.823	0.842	0.827333333	0.007535103
Psi_o	0.612	0.636	0.665	0.637666667	0.01532246
Phi_Eo	0.5	0.523	0.56	0.527666667	0.017476969
Phi_Do	0.183	0.177	0.158	0.172666667	0.007535103
Phi_Pav	944.214	941.554	934.562	940.11	2.878317101
Pi_Abs	2.937	3.653	5.355	3.981666667	0.717100024
ABS/RC	2.39	2.215	1.972	2.192333333	0.121197268
TRo/RC	1.952	1.822	1.66	1.811333333	0.084461694
ETo/RC	1.194	1.159	1.104	1.152333333	0.026193723
DIo/RC	0.438	0.393	0.312	0.381	0.036864617

Wild type lines	Replicate 1	Replicate 2	Replicate 3	Average	SE
Bckg	292	162	162	205.33333	43.333333
Fo	11704	14565	10566	12278.333	1189.593
Fj	28285	38005	29032	31774	3122.9539
Fi	45743	61413	47174	51443.333	5001.9206
Fm	57675	72305	59853	63277.667	4557.2463
Fv	45971	57740	49287	50999.333	3503.6364
Vj	0.361	0.406	0.375	0.3806667	0.0132958
Vi	0.74	0.811	0.743	0.7646667	0.0231828
Fm/Fo	4.928	4.964	5.665	5.1856667	0.2398919
Fv/Fo	3.928	3.964	4.665	4.1856667	0.2398919
Fv/Fm	0.797	0.799	0.823	0.8063333	0.0083533
Mo	0.721	0.908	0.715	0.7813333	0.063357
Area	10798650	15030871	12274413	12701311	1240242.6
Fix Area	56748832	71139952	58776652	62221812	4497329.9
Sm	234.901	260.32	249.04	248.087	7.3532883

Ss	0.5	0.447	0.524	0.4903333	0.0227474
N	469.774	582.033	475.314	509.04033	36.531356
Phi_Po	0.797	0.799	0.823	0.8063333	0.0083533
Psi_o	0.639	0.594	0.625	0.6193333	0.0132958
Phi_Eo	0.51	0.474	0.515	0.4996667	0.0129142
Phi_Do	0.203	0.201	0.177	0.1936667	0.0083533
Phi_Pav	928.637	938.004	925.345	930.662	3.7920109
Pi_Abs	2.775	2.072	3.359	2.7353333	0.3720539
ABS/RC	2.509	2.8	2.318	2.5423333	0.140136
TRo/RC	2	2.236	1.909	2.0483333	0.0974412
ETo/RC	1.279	1.328	1.194	1.267	0.039145
DIo/RC	0.509	0.564	0.409	0.494	0.0453689