

Table S1. Summary of alleles for *bps2* and *bps3*

Allele	Seed stock number	Mutation region
<i>bps2-1</i>	GABI-kat (#256H03)	A T-DNA at 96th amino acid
<i>bps2-2</i>	CS93151	Trp63Stop
<i>bps2-3</i>	CS87009	Trp96Stop
<i>bps2-4</i>	CS85964	Glu44Lys
<i>bps2-5</i>	CS94070	Cys72Tyr
<i>bps2-6</i>	CS91921	Leu85Phe
<i>bps2-7</i>	CS88898	Ala146Thr
<i>bps2-8</i>	CS93786	Pro162Leu
<i>bps2-9</i>	CS88601	Arg168Cys
<i>bps2-10</i>	CS85987	Arg168His
<i>bps2-11</i>	CS92177	Ser217Phe
<i>bps2-12</i>	CS94096	Ala233Val
<i>bps2-13</i>	CS86727	Glu261Lys
<i>bps3-2</i>	CS86632	Trp178Stop
<i>bps3-3</i>	CS86149	Pro71Ser
<i>bps3-4</i>	CS85730	His94Tyr
<i>bps3-5</i>	CS90483	Asp103Asn
<i>bps3-6</i>	CS91116	Glu105Lys
<i>bps3-7</i>	CS91333	Val108Ile
<i>bps3-8</i>	CS93018	Leu128Phe
<i>bps3-9</i>	CS91380	Ser151Asn
<i>bps3-10</i>	CS86938	Gly199Arg
<i>bps3-11</i>	CS93801	Pro245Leu
<i>bps3-12</i>	CS89879	Met258Ile
<i>bps3-13</i>	CS86288	Pro266Leu
<i>bps3-14</i>	CS88899	Asp282Asn
<i>bps3-15</i>	CS91030	Ala285Thr
<i>bps3-16</i>	CS88922	Ser301Leu

Table S2. Primers

Genotyping primers			
Gene name	Mutant allele	Primers	Enzyme; expected size
BPS2	<i>bps2-2</i>	bps2-2-F3: agtcacagcaaatcggtt bps2-2-R4: caacgctctccagctctt	<i>EcoRII</i> ; wild type (271, 206, 181, 156, 66 bp) and bps2-2 (452, 206, 156, 66 bp)
BPS3	<i>bps3-2</i>	bps3-2-F3: tcgtgaaggatttagaggtt bps3-2-R4: aatgtcactcttagctcttc	<i>DdeI</i> ; wild type (673, 102 bp) and bps3-2 (541, 132, 102 bp)
Q-RT PCR primers			
Gene name	ID	Primers	
BPS1	At1g01550	BPS1-qrt-F: tcttgtggacgagccattctga BPS1-qrt-R: cgtcttcctggaaattttgtccac	
BPS2	At2g46080	BPS2-qrt-F: gcgacttaaaacggtgtcttagcaa BPS2-qrt-R: ccatggcgataaatctgatccctt	
BPS3	At4g01360	BPS3-qrt-F: gaagtaagcggttaacatttggaga BPS3-qrt-R: agcttggcgataatcgagcattg	
IAA1	At4g14560	IAA1-qrt-F: ctccctctgaaaaacacaaaatc IAA1-qrt-R: atatggagctccgtccatactca	
IAA5	At1g15580	IAA5-qrt-F: cccaaagttcgtacgtgaaagt IAA5-qrt-R: tatagcatccgaacagaatttg	
IAA17	At1g04250	IAA17-qrt-F: tccggccaaggcacaagtt IAA17-qrt-R : tccgtccattgtacccatcacgaa	
GH3-5	At4g27260	GH3-5-qrt-F: atgcccgttatcacctacgaag GH3-5-qrt-R: atgtcccagagcttgtgaggaa	
GH3-like	At3g03400	GH3-like-qrt-F: tgtccctcagcttggaaacaac GH3-like-qrt-R:tctgttaagccgtgataatcgaa	
LBD29	At3g58190	LBD29-qrt-F: aagttgcctctcatctccatt LBD29-qrt-R: aaattcacaacctgttgtggaga	
SAUR9	At4g34760	SAUR9-qrt-F: atggcgataaagaagtgcacaa SAUR9-qrt-R: gcacgtcggtgaagttagcaatta	
SAUR15	At4g38850	SAUR15-qrt-F: tgaggagttcttgggtgtaag SAUR15-qrt-R: cggcaccacatatcttcttct	

Table S3. Germination and cotyledon fusion defects in *bps* multiple mutants

Parental genotype	Progeny observed								
	Total seeds (n)	Expected segregation (3:1)	Number germinated	Observed segregation (wt:mutant)	χ^2 (3:1 ratio)	Number ungerminated	χ^2 (3:1 ratio counting ungerminated seeds as triple mutants)	Germination rate* (%)	Cotyledon fusion rate† (%)
Embryogenesis and germination at 22°C									
Col	964	N.A.	961	N.A.	N.A.	3	N.A.	99.7% (961/964)	0% (0/961)
<i>bps1-2</i> ^{+/−}	942	707:236	933	701:232	0.119	9	0.157	98.3% (232/236)	1.7% (4/232)
<i>bps1-2</i> ^{+/−} <i>bps2-2</i> ^{−/−}	935	702:234	879	702:177	13.885	56	0.004	75.6% (177/234)	41% (73/177)
<i>bps1-2</i> ^{+/−} <i>bps2-2</i> ^{−/−} <i>bps3-2</i> ^{−/−}	921	691:231	759	689:70	112.218	162	0.01	30.3% (70/231)	63% (44/70)
Embryogenesis and germination at 16°C									
Col	221	N.A.	219	N.A.	N.A.	2	N.A.	99% (219/221)	0% (0/219)
<i>bps1-2</i> ^{+/−} <i>bps2-2</i> ^{−/−} <i>bps3-2</i> ^{−/−}	233	175:59	168	167:1	57.383	65	1.196	1.7% (1/59)	N.A.

Each parental genotyped plant grew at 22°C or 16°C. The progeny seeds were plated on agar plates and grown at 22°C or 16°C for phenotype analysis.

The phenotypes were observed at 9 dpi for 22°C and 11 dpi for 16°C. The critical χ^2 value at 95% confidence is 3.841 when degrees of freedom = 1.

*Number of germinated mutants / expected number of mutants based on total seed number.

†Number of mutants with at least one cotyledon fusion event/number of germinated mutants.

N.A., not applicable

Table S4. Identity and similarity of BPS gene family based on amino acid

	BPS1	BPS2	BPS3
BPS1		63%* (78%) [‡]	56%* (72%) [‡]
BPS2	63%* (78%) [‡]		42%* (64%) [‡]
BPS3	56%* (72%) [‡]	42%* (64%) [‡]	

*Identity between genes

[‡]Similarity between genes

Table S5. Segregation analysis for haploinsufficient *BPS2* in *bps1* background

	Total (n)	Phenotypes observed			χ^2
		Wild type	Typical <i>bps1</i>	More severe	
F2 progeny of <i>bps2-2</i>^{+/−} <i>bps1-2</i>^{+/−}					
Observed	687	515	48	124	
Expected if <i>BPS2</i> is haploinsufficient	687	515	43	129	0.77
Expected if <i>BPS2</i> is haplosufficient	687	515	129	43	203.5
F1 progeny of (<i>bps1-2</i>^{+/−}) × (<i>bps1-2</i>^{+/−} <i>bps2-2</i>^{−/−})					
Observed	254	192	0	62	
Expected if <i>BPS2</i> is haploinsufficient	254	190	0	64	0.08
Expected if <i>BPS2</i> is haplosufficient	254	190	64	0	64.02

The critical χ^2 value at 95% confidence is 3.841 when degrees of freedom = 1

Table S6. Frequency of abnormal phenotypes among progeny from *BPS1*⁺/*bps1-2* *bps2-2*^{-/-} *bps3-2*^{-/-} during embryogenesis

	Progeny observed				
	Globular	Transition	Heart	Torpedo	Bent-cotyledon
Total (n)	252	185	362	251	223
Wild-type-like looking	252	133	261	190	165
Abnormal patterns		52	101	61	58
Expected segregation if triple mutants show abnormal embryo development. (wild-type like:abnormal is 3:1)		139:46	271:91	188:63	167:56
χ^2		0.948	1.25	0.056	0.93

The critical χ^2 value at 95% confidence is 3.841 when degrees of freedom = 1.