SUPPLEMENTAL FIGURES AND TABLES
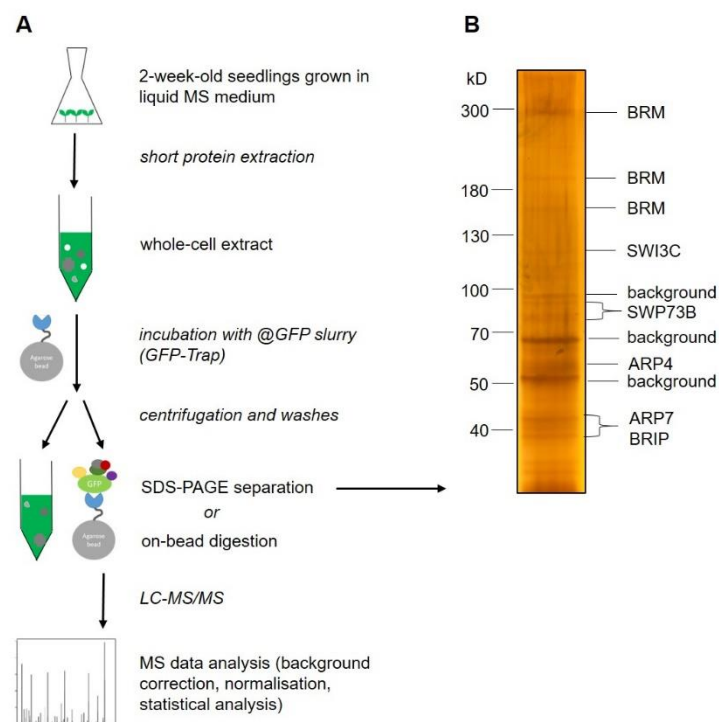
Figure S1. Isolation of SWI/SNF complexes from Arabidopsis seedlings. (**A**) Experimental setup of IP/MS analyses. (**B**) Silver-stained gel showing the proteins immunoprecipitated with BRM-GFP from the whole cell extracts of the *brm-1*/BRM-GFP line. Proteins were identified using LC-MS/MS.
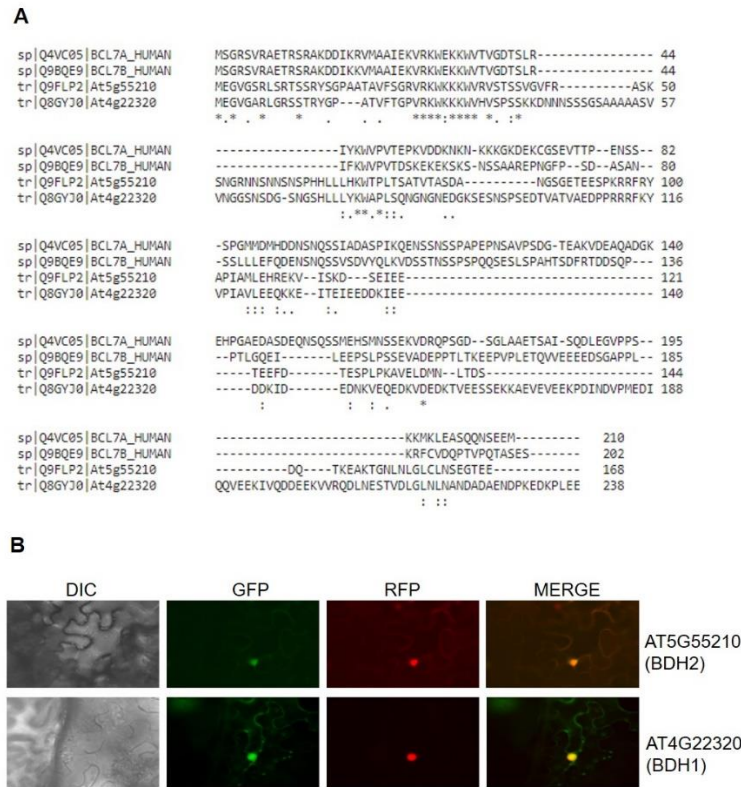
A

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sp|Q9BQE9|BCL7B_HUMAN  MSGRSVRAETRSRAKDDIKKVMAAIEKVRKWEKKWVTVGDTSLR---------------  44
tr|Q9FLP2|At5g55210    MEGVGSRLSRTSSRYSGPAATAVFSGRVRKWKKKWVRVSTSSVGFR----------ASK  50
tr|Q8GYJ0|At4g22320    MEGVGARLGRSSTRYGP---ATVFTGPVRKWKKKWVHVSPSSKKDNNNSSSGSAAAAASV 57
                       *.*.*     *     .   .    ****.:****  *  .:*

sp|Q4VC05|BCL7A_HUMAN  -----------------IYKWVPVTEPKVDDKNKN-KKKGKDEKCGSEVTTP--ENSS--  82
sp|Q9BQE9|BCL7B_HUMAN  -----------------IFKWVPVTDSKEKEKSKS-NSSAAREPNGFP--SD--ASAN--  80
tr|Q9FLP2|At5g55210    SNGRNNSNNSNSPHHLLLHKWTPLTSATVTASDA----------NGSGETEESPKRRFRY 100
tr|Q8GYJ0|At4g22320    VNGGSNSDG-SNGSHLLLYKWAPLSQNGNGNEDGKSESNSPSEDTVATVAEDPPRRRFKY 116
                                       :.**.*::.       ..

sp|Q4VC05|BCL7A_HUMAN  -SPGMMDMHDDNSNQSSIADASPIKQENSSNSSPAPEPNSAVPSDG-TEAKVDEAQADGK 140
sp|Q9BQE9|BCL7B_HUMAN  -SSLLLEFQDENSNQSSVSDVYQLKVDSSTNSSPSPQQSESLSPAHTSDFRTDDSQP--- 136
tr|Q9FLP2|At5g55210    APIAMLEHREKV--ISKD---SEIEE------------------------------- 121
tr|Q8GYJ0|At4g22320    VPIAVLEEQKKE--ITEIEEDDKIEE------------------------------- 140
                       :::.. :.          ::

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sp|Q9BQE9|BCL7B_HUMAN  --PTLGQEI-------LEEPSLPSSEVADEPPTLTKEEPVPLETQVVEEEEDSGAPPL-- 185
tr|Q9FLP2|At5g55210    -----TEEFD-------TESPLPKAVELDMN--LTDS--------------------- 144
tr|Q8GYJ0|At4g22320    -----DDKID-------EDNKVEQEDKVDEDKTVEESSEKKAEVEVEEKPDINDVPMEDI 188
                            :          :  : :.     *

sp|Q4VC05|BCL7A_HUMAN  -------------------------KKMKLEASQQNSEEM---------  210
sp|Q9BQE9|BCL7B_HUMAN  -------------------------KRFCVDQPTVPQTASES-------  202
tr|Q9FLP2|At5g55210    ----------DQ----TKEAKTGNLNLGLCLNSEGTEE-----------  168
tr|Q8GYJ0|At4g22320    QQVEEKIVQDDEEKVVRQDLNESTVDLGLNLNANDADAENDPKEDKPLEE 238
                             : ::
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B

Figure S2. Analysis of the BCL7-like proteins AT4G22320 (BDH1) and AT5G55210 (BDH2). (**A**) Multiple sequence alignment of amino acid sequences of AT5G55210 and AT4G22320, as well as human BCL7A and BCL7B. Identical amino acids in all aligned sequences are marked with asterisks. (**B**) Nuclear localization of transiently expressed AT5G55210-GFP and AT4G22320-GFP fusions in tobacco epidermal cells examined by laser scanning confocal microscopy. Cells were co-transformed with H2B-RFP to visualize nuclei. DIC, differential interference contrast.
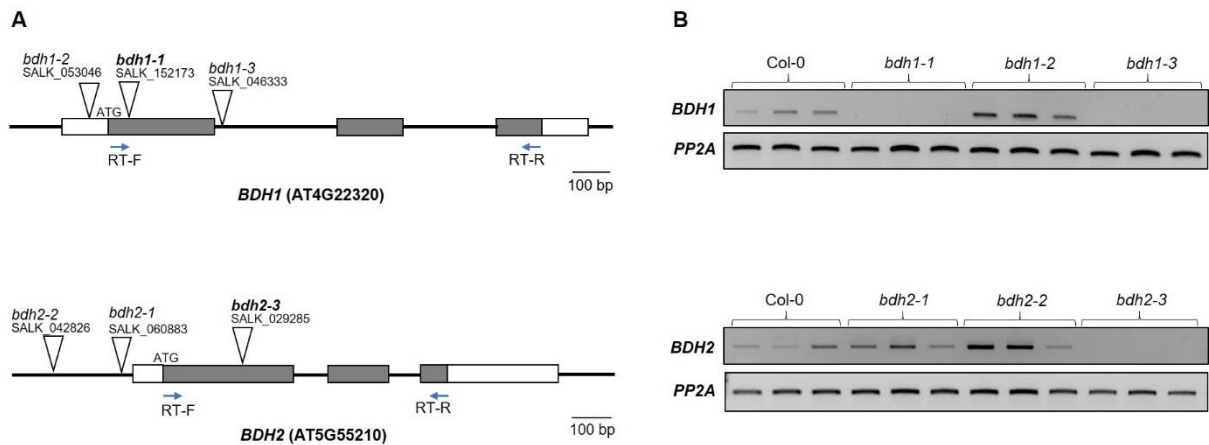

Figure S3. *BDH1* and *BDH2* mutant alleles. (**A**) Positions of T-DNA insertions in the *BDH1* and *BDH2* genes of mutant Arabidopsis lines. Arrows indicate positions of the primers used for RT-PCR. The mutant alleles used to generate double *bdh* mutants are bolded. (**B**) Full-length *BDH1* and *BDH2* transcripts detected by RT–PCR in wild-type and *bdh* mutants. Total RNA was isolated from 15-day-old seedlings grown under LD conditions, and the housekeeping gene *PP2A* was used as a control. Three biological replicates are shown for each line.
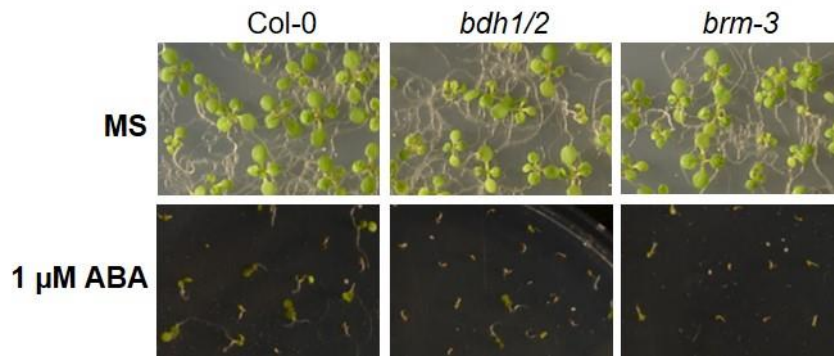
Figure S4. The *bdh1/2* double mutant shows hypersensitivity to ABA. Seedlings grown for x days on MS medium or in the presence of 1 μM ABA are shown. Bar = 10 mm.
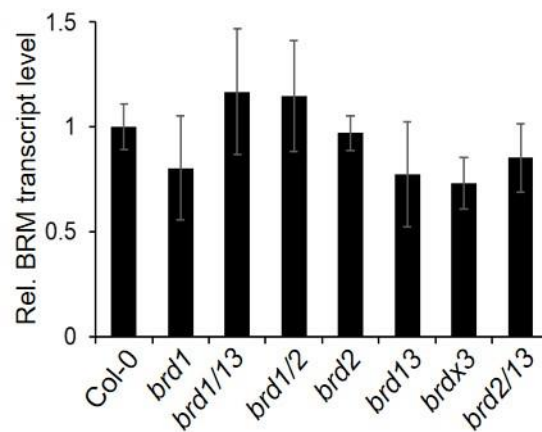

Figure S5. Quantitative RT-PCR analysis of BRM transcript levels in Col-0 wild-type and *brd* mutant lines. The *PP2A* housekeeping gene was used as normalization control. Means ± SD from 3 biological replicates are shown. The transcript level in Col-0 is set to 1.
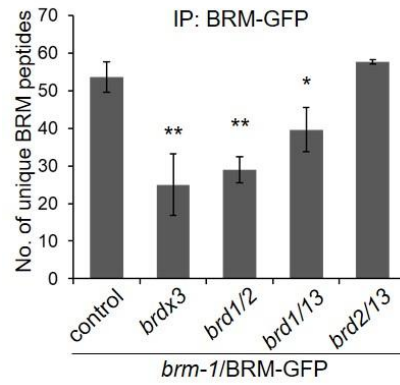
Figure S6. Mean number of BRM-derived peptides recovered by immunoprecipitation of BRM-GFP in the control and *brd* mutant lines. Means ± SD are shown. Asterisks indicate significant differences from the control line (Student's t test, *P < 0.05, **P < 0.01).
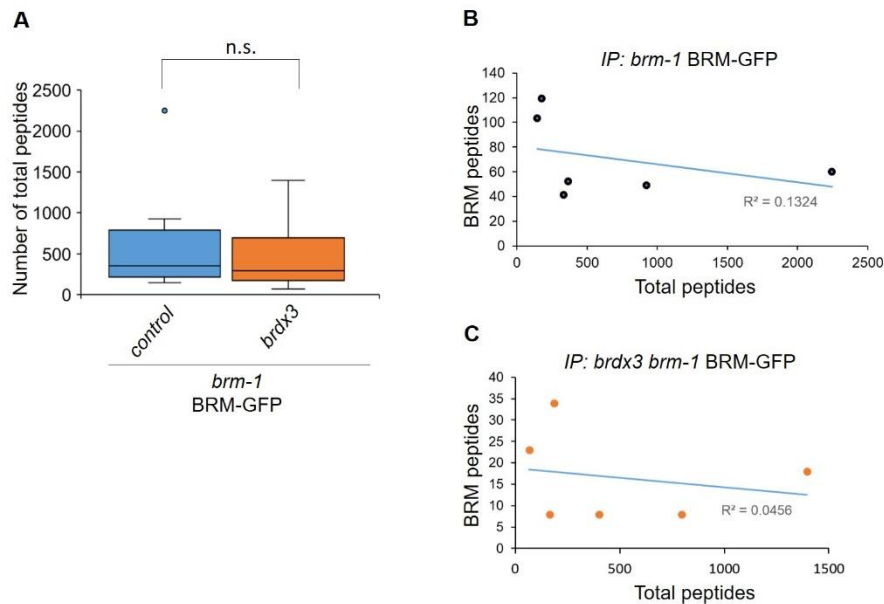

Figure S7. Comparison of total peptides and BRM-derived peptides detected in IP/MS experiments in the control line and *brdx3* mutant. (**A**) Mean number of total peptides. n.s., not significant (Student's t test). (**B, C**) The number of BRM-derived peptides does not correlate with the number of total peptides detected in the same experiments.
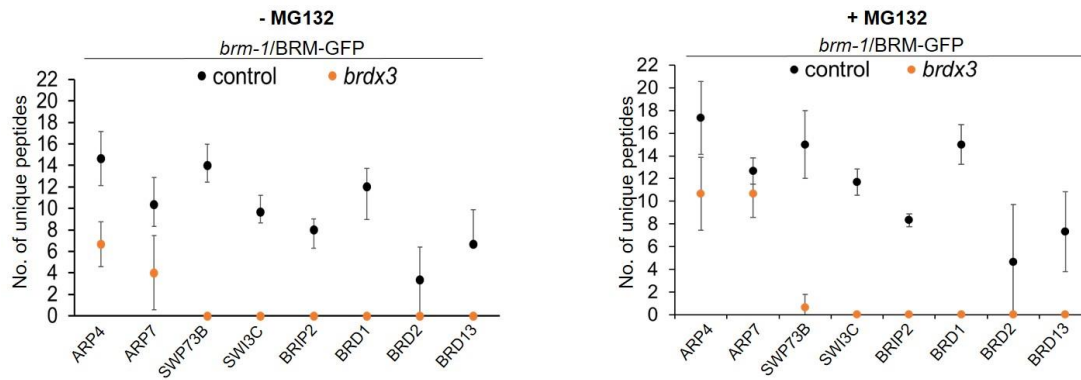
Figure S8. Peptides corresponding to the major subunits of the BRM complex identified in IP/MS experiments in the control and *brdx3* mutant. (**left**) Number of unique peptides recovered by immunoprecipitation of BRM-GFP in the control and *brdx3* mutant. (**right**) Number of unique peptides recovered by immunoprecipitation of BRM-GFP in the control and *brdx3* mutant after treatment with proteasome inhibitor MG132. Means ± SD are shown.
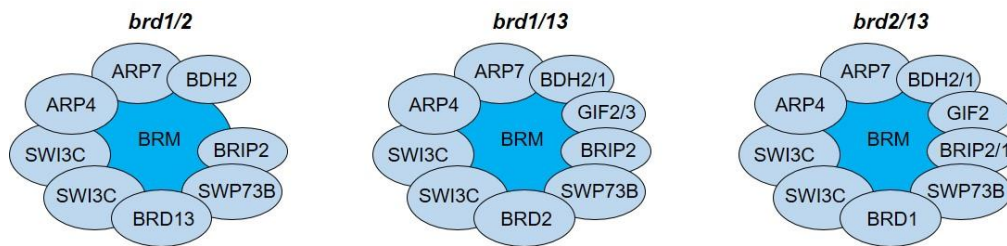

Figure S9. BRM complex assemblies purified from 2-week-old *brd* double mutants after treatment with MG132.

Table S1 Defects of floral organs in *bdh* mutants compared to WT.

	WT	*bdh1*	*bdh2*	*bdh1/2*
Mean number of stamens	6±0	5.8 ± 0.4	5.7 ± 0.7	5.2 ± 0.4
Flowers with decreased number of stamens	0 (0%)	5 (20%)	9 (36%)	19 (76%)
Flowers with increased number of stamens	0 (0%)	0 (0%)	3 (12%)	0 (0%)
N	25	25	25	25

Table S2 Identification of SWI/SNF subunits in IP/MS experiments using BRM-GFP, SWP73B-YFP, BDH2-GFP, or BRD1-GFP as baits. The numbers of identifications are shown.

Protein name	Gene	IP: BRM-GFP	IP: SWP73-YFP	IP: BDH2-GFP	IP: BRD1-GFP
BRM	AT2G46020	8/8	2/2	2/2	2/2
SWI3C	AT1G21700	8/8	2/2	2/2	2/2
SWP73B	AT5G14170	8/8	2/2	2/2	2/2
SWP73A	AT3G01890	2/8	-	2/2	-
ARP7	AT3G60830	8/8	2/2	2/2	2/2
ARP4	AT1G18450	8/8	2/2	2/2	2/2
BRIP2	AT5G17510	8/8	2/2	2/2	2/2
BRIP1	AT3G03460	2/8	-	-	-
BRD1	AT1G20670	8/8	2/2	2/2	2/2
BRD2	AT1G76380	4/8	-	2/2	-
BRD13	AT5G55040	8/8	-	2/2	-
BDH1	AT4G22320	1/8	-	-	-
BDH2	AT5G55210	4/8	-	2/2	-
GIF1	AT5G28640	-	-	-	-
GIF2	AT1G01160	1/8	-	1/2	-
GIF3	AT4G00850	1/8	-	1/2	-
SYD	AT2G28290	-	2/2	2/2	-
CHR12	AT3G06010	-	1/2	2/2	-
CHR23	AT5G19310	-	-	2/2	-
SWI3A	AT2G47620	-	1/2	2/2	-
SWI3B	AT2G33610	-	1/2	2/2	-
SWI3D	AT4G34430	-	2/2	2/2	-
BSH	AT3G17590	-	1/2	2/2	-
LFR	AT3G22990	-	-	2/2	-
TPF1	AT3G52100	-	-	2/2	-
TPF2	AT3G08020	-	-	1/2	-
OPF1	AT1G50620	-	-	2/2	-
OPF2	AT3G20280	-	-	-	-
BRD5	AT1G58025	-	-	2/2	-
PSA1	AT1G32730	-	-	2/2	-
PSA2	AT1G06500	-	-	1/2	-
SHH2	AT3G18380	-	-	-	-

Table S3. Oligonucleotides used in this study.

Name	Sequence 5'-3'	Note
SALK_012963-F	ATCACCTCCTCAGGATCAAC	Genotyping of *brd1-2* mutant
SALK_012963-R	AAGGTGAAGACAACGACGAT	
GK219B04-02kz	TGAATTGTATTCCATTGCATTTGT	Genotyping of *brd1-5* mutant
GK219B04-03kz	TTGGAGTTGATGATGATGATCTGT	
SALK_025965-R	AATTAACGCGCCAAAATATC	Genotyping of *brd2-1* mutant
SALK_025965-F	CGCTGTTGGTTTCATTGTTTC	
SALK_208635C-F	GTCACGCTGATTCTGAGGAAG	Genotyping of *brd13-4* mutant
SALK_208635C-R	TGTATTGCATTGCATTTGAGC	
SALK_152173-F	CGACCGGAGAGATCTAAATCC	Genotyping of *bdh1-1* mutant
SALK_152173-R	ACTCCAAGGAATCAAAATGGC	
SALK_053046-F	CGACAATTAACGATTAGTTTCGG	Genotyping of *bdh1-2* mutant
SALK_053046-R	ACGACGAATCGTTTATCGTTG	
SALK_046333-F	TCCTTGGAGTAACTGGACTGG	Genotyping of *bdh1-3* mutant
SALK_046333-R	GGAGGTCAAAAAGTTCCCTTC	
SALK_060883-F	TCAACAGCAAGCATTACATGG	Genotyping of *bdh2-1* mutant
SALK_060883-R	TAACCGTCGCTGAGGTAAGTG	
SALK_042826-F	GCTGCGTTTCGACTAATCAAC	Genotyping of *bdh2-2* mutant
SALK_042826-R	CTCTGTACTTCCAGGGAAGCC	
SALK_029285-F	ACACAAGACATGTCCAAAGGC	Genotyping of *bdh2-3* mutant
SALK_029285-R	CAGTTTTTGCTTCCTGCAGAG	
Mut1L	GATTTCCCCAAATTCGATGC	Genotyping of *brm-1* mutant
Mut1R	GGGCTCTATGCAAATGCCTCA	
Lba1	TGGTTCACGTAGTGGGCCATCG	Genotyping, T-DNA primer
Lbb1	GCGTGGACCGCTTGCTGCAACT	Genotyping, T-DNA primer

BDH1-RTF	GGTAGGTCCTCGACACGGTAC	RT-PCR
BDH1-RTR	GGCTTGTCCTCTTTCGGGTCG	
BDH2-RTF	ATGGAAGGTGTAGGATCGAG	RT-PCR
BDH2-RTR	TCATTCTTCAGTCCCTTCAG	
BDH1-qF	GTGCGACAAGATTTGAACGA	RT-PCR
BDH1-qR	CTAATGGCTTGTCCTCTTTCG	
BDH2-qF	TGGTAATTTGAATCTGGGACTGT	RT-PCR
BDH2-qR	GATCTAGAAGACGTCAAAGTGGA	
PP2A-F	TATCGGATGACGATTCTTCGTGCAG	RT-qPCR
PP2A-R	GCTTGGTCGACTATCGGAATGAGAG	
BRM-qF	TATCCTCCGGGTTCTGG	RT-qPCR
BRM-qR	CTCCGTTTCCGTTTTATCGT	
BDH1cds-Fattb	GGGACAAGTTTGTACAAAAAAGCAGGCT TCATGGAAGGAGTTGGTGCACG	Cloning of BDH1 cds
BDH1cds-Rattb	GGGACCACTTTGTACAAGAAAGCTGGGT CTTCTTCTAATGGCTTGTC	
BDH2cds-Fattb	GGGACAAGTTTGTACAAAAAAGCAGGCT TCATGGAAGGTGTAGGATCGAG	Cloning of BDH2 cds
BDH2cds-Rattb	GGGACCACTTTGTACAAGAAAGCTGGGT CTTCTTCAGTCCCTTCAG	