

Table III. Insertional mutants of *Arabidopsis* CDPKs^a

Name	Insertional mutagen	Clone Name(s) ^b	Hit ^c	Source ^d	Ref ^e
CPK1	T-DNA	SALK_010530, 007698	Exon	A	
	T-DNA	SALK_007911, 007917, 007918, 007919	Intron	A	
	T-DNA	Garlic_346_B04	Promoter	B	
CPK2	T-DNA	SALK_014870	300-3'	A	
	T-DNA	SALK_036166, 059237	Exon	A	
	T-DNA	Garlic_1288_C10	Exon	B	
CPK3	T-DNA	Garlic_234_B06	300-5'	B	
CPK4	T-DNA	SALK_000685	Intron	A	
	T-DNA	SALK_065975, 066735	300-5'	A	
	T-DNA	SALK_066872	Exon	A	
	T-DNA	--	?	D	1
CPK6	T-DNA	SALK_034106, 033392, 033739	300-5'	A	
	T-DNA	Garlic_690_H07	Exon	B	
	T-DNA	--	?	D	1
CPK7	T-DNA	SALK_035601	Exon	A	
CPK8	T-DNA	SALK_036581	Exon	A	
CPK9	T-DNA	SALK_034324	300-5'	A	
	T-DNA	--	?	D	1, 2
CPK10	T-DNA	SALK_015994	300-3'	A	
	T-DNA	SALK_032021	Intron	A	
	T-DNA	SALK_003484	Exon	A	
	T-DNA	--	?	D	1, 2
CPK11	T-DNA	SALK_054495	Exon	A	
	T-DNA	SALK_007814	Intron	A	
	T-DNA	--	?	D	1, 2
CPK12	T-DNA	Garlic_839_H10	Intron	B	
CPK13	T-DNA	SALK_057893, 058713	300-5'	A	
	T-DNA	SALK_050944	300-3'	A	
CPK15	T-DNA	Garlic_1284_H09	Promoter	B	
	Transposon	GT1712	300-5'	C	
CPK16	T-DNA	SALK_052257	Intron	A	
CPK17	T-DNA	SALK_001818	300-3'	A	
	T-DNA	SALK_057146	Intron	A	
CPK18	T-DNA	SALK_061352	Exon	A	
	T-DNA	SALK_069578	Intron	A	
CPK19	T-DNA	SALK_001691, 001685, 049735, 057587	Exon	A	
	T-DNA	SALK_052737	300-5'	A	
	T-DNA	Garlic_1215_F07	Exon	B	
	Transposon	ET1931	Exon	C	
CPK20	T-DNA	SALK_045192	300-3'	A	
	T-DNA	SALK_044320	Intron	A	
	T-DNA	SALK_073448	Exon	A	
	T-DNA	Garlic_377_G02	Promoter	B	
CPK21	T-DNA	SALK_029412	Exon	A	
	T-DNA	SALK_072624	Intron	A	
	T-DNA	SALK_043765	300-5'	A	
CPK22	Transposon	ET9246	Exon	C	
	Transposon	ET6769	Intron	C	
CPK23	T-DNA	SALK_007958	Intron	A	
CPK24	T-DNA	Garlic_754_E09	Intron	B	
	T-DNA	SALK_015986	Exon	A	
CPK27	T-DNA	SALK_035333	300-3'	A	
	T-DNA	Garlic_61_A09	300-5'	B	
CPK28	T-DNA	SALK_075400	300-3'	A	
CPK29	T-DNA	SALK_013734	300-3'	A	
CPK30	T-DNA	SALK_042171	300-5'	A	
	T-DNA	Garlic_337_G01	Promoter	B	
CPK32	Transposon	ET5772	Exon	C	
CPK33	T-DNA	SALK_059467	Exon	A	

^a The insertional mutants listed are all Columbia ecotype. This list last updated June 5, 2002. ^b The criteria used to determine insertional mutants from Torrey Mesa Research Institute/Syngenta and Genetrap after BLAST search are an E value less than 1e-04 and a score greater than 460. ^c 300-3'(5') indicates that insertion is within 300 nucleotides in the 3' (5') of the open reading frame, while insertion between 300 and 1000 nucleotides in the 5' of the open reading frame is listed as an insertion in the promoter. ^d A, Salk Institute Genomic Analysis Laboratory (<http://signal.salk.edu>); B, TMRI/Syngenta (<http://www.tmri.org>); C, Genetrap (Cold Spring Harbor Laboratory; <http://genetrap.cshl.org>); D, Wisconsin Arabidopsis Knockout Facility (<http://www.biotech.wisc.edu>). ^e 1, Satterlee and Sussman, 1998; 2, Krysan et al., 1996.