

**Table S1.** List of phospho- and nonphospho-peptides identified from immunoprecipitated SRK2E-GFP or SRK2I-GFP.

Immunoprecipitates were prepared as described in Methods, and analyzed with a nanoLC-MS/MS system. Data was analyzed and manually checked as described in Supplementary Methods, and peptides annotated as SRK2E (At4g33950) or SRK2I (At5g66880) were listed. Precursor-origin neutral loss peaks were assigned when they were one of the most intense 10 peaks in each spectrum with the m/z tolerance of 0.8Da. Phospho-peptides were marked by pink. The final evaluation of the phosphorylated site localization was performed based on PTM probability scores.

Peptide number	Peptide sequence	Modification site by Mascot	AGI code	Mascot peptide score	Observed m/z	Charge	Observed mass(Da)	Mass error(Da)	Retention time (min)	Forward residue	Backward residue	Precursor origin neutral loss peak	Phospho-site by manual confirmation	Manually-confirmed phospho-site	Ambiguous phospho-site by manual inspection	Phosphorylated positions	Phosphosite evaluation based on PTM localization probability*
1	APVTTGPLDMPIMHSDRYDFVK		AT5G66880.1	59	652.0663	4	2604.236094	0.0009	48.767	R	D						
2	APVTTGPLDMPIMHSDRYDFVK	Oxidation@M:10	AT5G66880.1	65	656.0649	4	2620.230494	0.0004	42.659	R	D						
3	APVTTGPLDMPIMHSDRYDFVK	Oxidation@M:10,Oxidation@M:13	AT5G66880.1	53	660.0644	4	2636.228494	0.0035	38.833	R	D						
4	APVTTGPLDMPIMHSDRYDFVK	Oxidation@M:13	AT5G66880.1	56	874.4177	3	2620.23127	0.0009	42.857	R	D						
5	DIGSGNFGVAR		AT3G50500.1,AT5G66880.1,AT4G33950.1	76	546.7757	2	1091.536847	0.0009	32.027	K	L						
6	ELVAVK		AT3G50500.1,AT5G66880.1	24	329.7094	2	657.404247	-0.0018	21.424	K	Y						
7	EVILTPHLAIVMEYASGGELFER		AT4G33950.1,AT4G33950.2,AT5G63650.1	23	892.4639	3	2674.36987	0.0023	93.738	K	I						
8	FFFQQLISGVSYCHAMQVCHR	Oxidation@M:16,Carbamidation@C:13,Carbamidation@C:19	AT4G33950.1,AT4G33950.2	80	658.557	4	2630.198894	0.0007	50.878	R	D						
9	FFFQQLISGVSYCHAMQVCHR	Carbamidation@C:13,Carbamidation@C:19	AT4G33950.1,AT4G33950.2	77	872.4076	3	2614.20097	-0.0021	54.712	R	D						
10	FFFQQLISGVSYCHSMQICHR	Oxidation@M:16,Carbamidation@C:13,Carbamidation@C:19	AT5G66880.1	64	887.7439	3	2660.20987	0.0011	53.497	R	D						
11	FFFQQLISGVSYCHSMQICHR	Carbamidation@C:13,Carbamidation@C:19	AT5G66880.1	63	882.4119	3	2644.21387	0	55.674	R	D						
12	FSEDEAR		AT3G50500.1,AT1G10940.1,AT1G78290.2,AT1G78290.3,AT5G66880.1,AT4G33950.1,AT4G33950.2,AT1G60940.1,AT1G60940.2	51	427.1881	2	852.361647	0.0004	19.064	R	F						
13	GDKIDENVQR		AT5G66880.1	46	587.2964	2	1172.578247	-0.0003	18.879	R	E						
14	ICDFGYSK	Carbamidation@C:2	AT3G50500.1,AT1G10940.1,AT5G08590.1,AT1G78290.2,AT1G78290.3,AT5G66880.1,AT4G33950.1,AT4G33950.2,AT1G60940.1,AT1G60940.2,AT2G23030.1,AT4G40010.1,AT5G63650.1	36	495.2235	2	988.432447	1E-04	28.114	K	S						
15	IFVADPAK		AT4G33950.1,AT4G33950.2	25	430.7481	2	859.481647	0.0014	25.865	R	R						
16	IFVADPATR		AT3G50500.1,AT5G66880.1	46	495.2741	2	988.533647	-0.0005	28.058	R	I						
17	ILNVQYAIPTYVHISPECR	Carbamidation@C:18	AT4G33950.1,AT4G33950.2	99	1144.0799	2	2286.145247	-0.0015	50.604	R	H						
18	ISIPK		AT5G66880.1	40	400.2501	2	798.485647	0.0005	35.393	R	T						
19	LENTLLDGSPAPR		AT3G50500.1,AT1G10940.1,AT5G66880.1,AT4G33950.1,AT4G33950.2,AT1G60940.1,AT1G60940.2,AT2G23030.1	95	691.8672	2	1381.719847	-0.0002	34.295	K	L						
20	NHEWFLK		AT4G33950.1,AT4G33950.2	48	487.2479	2	972.481247	-0.0005	31.362	R	N						
21	QSNELVAVK		AT4G33950.1	39	494.2769	2	986.539247	-0.0003	22.521	K	Y						
22	REIINHR		AT4G33950.1,AT4G33950.2	37	469.27	2	936.525447	0.0002	16.104	K	S						
23	RISIPK		AT4G33950.1,AT4G33950.2	50	492.3034	2	982.592247	-1E-04	30.992	K	N						

24	RISVPEIRNHEWFLK		AT4G33950.1,AT4G33950.2	36	485.273	4	1937.062894	-0.0008	42.732	K	N							
25	SLRHPNIVR		AT3G50500.1,AT5G66880.1,AT4G33950.1,AT4G33950.2	26	364.5527	3	1090.63627	0.0003	19.603	R	F							
26	SSVLHSQPK		AT3G50500.1,AT5G66880.1,AT4G33950.1,AT4G33950.2,AT4G40010.1	55	491.7695	2	981.524447	0.0002	16.684	K	S							
27	SSVLHSQPK	Phosphorylation@S:6	AT3G50500.1,AT5G66880.1,AT4G33950.1,AT4G33950.2,AT4G40010.1	48	531.7525	2	1061.490447	-0.0003	18.018	K	S	+		@S:6		AT3G50500.1;S173,AT5G66880.1;S172,AT4G33950.1;S171,AT4G33950.2;S123,AT4G40010.1;S154	not passed (< 0.75 for @S:6)	
28	SSVLHSQPKSTVGTPAYIAPEVLLK	Phosphorylation@S:6,Phosphorylation@S:10	AT4G33950.1,AT4G33950.2	30	928.1314	3	2781.37237	-0.0031	48.028	K	K	+		@S:6,@S:10		AT4G33950.1;S171,AT4G33950.1;S175,AT4G33950.2;S123,AT4G33950.2;S127	not passed (< 0.75 for @S:6 and @S:10)	
29	SSVLHSQPKSTVGTPAYIAPEVLLKK	Phosphorylation@S:1,Phosphorylation@S:10	AT4G33950.1,AT4G33950.2	65	970.8304	3	2909.46937	-0.001	43.913	K	E	+		@S:1,@S:10		AT4G33950.1;S166,AT4G33950.1;S175,AT4G33950.2;S118,AT4G33950.2;S127	not passed (< 0.75 for @S:1 and @S:10)	
30	SSVLHSQPKSTVGTPAYIAPEVLLKK	Phosphorylation@S:2,Phosphorylation@S:6	AT4G33950.1,AT4G33950.2	28	728.375	4	2909.470894	0.0004	43.455	K	E	+	ambiguous	@S:6	@S:1orS:2	AT4G33950.1;S171,AT4G33950.1;S166orS167,AT4G33950.2;S123,AT4G33950.2;S118orS119	not passed (< 0.75 for @S:6 , @S:1 and S:2)	
31	SSVLHSQPKSTVGTPAYIAPEVLLKK	Phosphorylation@S:6,Phosphorylation@S:10	AT4G33950.1,AT4G33950.2	39	970.8303	3	2909.46907	-0.0014	43.741	K	E	+		@S:6,@S:10		AT4G33950.1;S171,AT4G33950.1;S175,AT4G33950.2;S123,AT4G33950.2;S127	not passed (< 0.75 for @S:6 and @S:10)	
32	SSVLHSQPKSTVGTPAYIAPEVLLR	Phosphorylation@S:2,Phosphorylation@S:10	AT5G66880.1	43	937.4681	3	2809.38247	0.0009	49.419	K	Q	+	ambiguous	@S:10	@S:1orS:2	AT5G66880.1;S176,AT5G66880.1;S167orS168	not passed (< 0.75 for @S:10, @S:1 and S:2)	
33	SSVLHSQPKSTVGTPAYIAPEVLLR	Phosphorylation@S:6,Phosphorylation@T:11	AT5G66880.1	30	937.4685	3	2809.38367	0.0021	49.96	K	Q	+	ambiguous	@S:6	@S:10orT:11	AT5G66880.1;S172,AT5G66880.1;S176orT177	not passed (< 0.75 for @S:6, @S:10 and T:11)	
34	STVGTPAYIAPEVLLK		AT4G33950.1,AT4G33950.2	20	829.9714	2	1657.928247	-0.0009	46.679	K	K							
35	STVGTPAYIAPEVLLKK		AT4G33950.1,AT4G33950.2	56	894.0183	2	1786.022047	-0.0019	41.815	K	E							
36	STVGTPAYIAPEVLLR		AT5G66880.1	71	843.9761	2	1685.937647	0.0025	47.597	K	Q							
37	STVGTPAYIAPEVLLR	Phosphorylation@T:2	AT5G66880.1	42	883.9588	2	1765.903047	0.0016	55.563	K	Q	+	ambiguous		@S:1orT:2	AT5G66880.1;S176orT177	not passed (<0.75 for @S:1 and @T:2)	
38	STVGTPAYIAPEVLLRQEYDQK		AT5G66880.1	61	1204.128	2	2406.241447	-0.0017	48.044	K	I							
39	THSWFLK		AT5G66880.1	35	459.7451	2	917.475647	-0.0003	30.332	K	N							
40	TIHRILNVQYAIPTYVHISPECR	Carbamidation@C:22	AT4G33950.1,AT4G33950.2	55	699.3672	4	2793.439694	0.0013	45.528	K	H							
41	YDFVK		AT3G50500.1,AT5G66880.1,AT5G61450.1	26	336.1738	2	670.333047	0.0004	25.866	R	D							
42	YELVK		AT1G10940.1,AT4G33950.1,AT1G60940.1,AT1G60940.2	30	326.1895	2	650.364447	0.0005	22.448	R	D							
43	YIERGDKIDENVQR		AT5G66880.1	34	578.9637	3	1733.86927	-0.0005	21.807	K	E							
44	YSIPDDIR		AT5G66880.1	50	489.7479	2	977.481247	-0.0005	34.366	K	I							