

附表 2 差异表达 3 倍以上的磷酸化修饰肽段具体定量信息  
Attached Table S2 Quantification information of phosphorylated peptides (fold change>3.0, P-value<0.05)

序列 Annotated sequence	类型 Phospho- type	蛋白名 Protein number	修饰的 位置 Positions	误差值 Mass error [ppm]	比值 Fold change treatment/ CK	P 值 P-value
红颊 Benihopp						
TILAKFS(phos)SNPDESQK	S	3-hydroxyisobutyryl-CoA hydrolase-like protein 3	261	0.124385	3.094	0.012
YFS(phos)KVASALGK	S	3-hydroxyisobutyryl-CoA hydrolase-like protein 3	332	0.56195	3.860	0.007
AELLHKAAS(phos)ILK	S	glyceraldehyde-3-phosphate dehydrogenase-like	86	0.334715	3.931	0.002
QGGAIS(phos)AALFLKQFVDEK	S	leucine aminopeptidase 3	526	-0.26505	4.641	0.003
VLDS(phos)LAKLK	S	eukaryotic translation initiation factor	102	0.090645	5.242	0.002
EASVIDKILEAS(phos)ADE	S	heat shock 70 kDa protein-like	11	0.2992	6.517	0.004
VAEIESFLKS(phos)IEDEK	S	U6 snRNA-associated Sm-like protein	145	0.79175	6.684	0.001
KQLAT(phos)KAAR	T	outer envelope pore protein 37	18	0.121235	7.694	0.000
TTQLS(phos)HNVAKFKQL	S	methylenetetrahydrofolate reductase 2	58	-0.26689	9.817	0.000
S(phos)IEIYKHNK	S	protein GrpE-like	189	0.114755	11.114	0.001
KY(phos)IEAGASEHAR	Y	histone H3.3-like	696	-0.094945	12.307	0.001
LVKS(phos)LEVQR	S	NADH—cytochrome b5 reductase 1	367	0.054145	12.842	0.021
LIDKHDLYGQVAY(phos)PK	Y	peptidyl-prolyl cis-trans isomerase B2-like	555	0.376955	15.374	0.005
S(phos)NYNFEKPFLYLAR	S	vacuolar membrane proton pump-like	156	0.48401	15.824	0.008
IYKT(phos)PDLETPK	T	synaptotagmin-5-like	216	-0.64225	19.681	0.000
TDKLCS(phos)LSEAR	S	probable sucrose-phosphate synthase 1	219	-0.16865	0.301	0.001
PHGGHLS(phos)HGYQDTKK	S	GTP-binding nuclear protein Ran-3-like	178	-0.36335	0.297	0.013
GTLATEYKS(phos)K	S	uncharacterized protein LOC101313543	209	0.74855	0.209	0.014
LNKQIWS(phos)R	S	eukaryotic translation initiation factor 5A	66	0.17341	0.207	0.003

续附表 2 Continuation of Attached Table S2

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MYLKENLPS(phos)R	S	serine hydroxymethyltransf erase	389	-1.38585	0.138	0.002
GGDVVLLYAS(phos)KYHDIR	S	acid phosphatase 1-like	126	0.459065	0.134	0.001
IIVT(phos)NKHGEK	T	60S ribosomal protein L31-1-like	18	-0.0409945	0.112	0.014
GLLY(phos)LHHEKHIIHR	Y	ectonucleotide pyrophosphatase family 3	194	0.161525	0.091	0.010
APEGPAGYS(phos)CKK	S	uncharacterized protein LOC101300947	38	0.147625	0.031	0.005
甜查理 Sweet charlie						
SVSLS(phos)KFK	S	mitogen-activated protein kinase kinase 2	87	0.25888	3.214	0.021
HLS(phos)AKLFHDK	S	auxin-binding protein ABP19a-like	166	0.044877	3.218	0.000
YLEKS(phos)GLQK	S	20 kDa chaperonin	489	-0.134735	4.220	0.005
HKFDADTCLVEGLVLDHGS(phos)R	S	peroxiredoxin Q	219	-0.455135	4.298	0.001
VFDKAIES(phos)R	S	sucrose synthase-like	171	-0.163155	4.421	0.000
TKFS(phos)NVYVK	S	aconitate hydratase 1-like	208	1.016	5.233	0.014
VS(phos)FEFQKTLLGVR	S	T-complex protein 1 subunit zeta-like	461	1.4561	6.235	0.021
S(phos)FLWKMFEEK	S	3-dehydroquinate synthase-like	228	0.070755	6.736	0.009
LQGNFYFFKEQLS(phos)R	S	proteasome subunit alpha type-7-like	40	-0.77795	7.238	0.000
ANKLFVDYNEPES(phos)ER	S	dormancy/auxin associated protein	447	-0.212995	7.287	0.001

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AVISKS(phos)FER	S	dormancy/auxin associated protein	896	0.409015	9.740	0.004
IAIIS(phos)KSGEGVEQAA PSEK	S	gamma carbonic anhydrase 1	167	-0.13948	10.240	0.014
FLT(phos)KCLVGADVSNS PK	T	aconitate hydratase 2	206	0.57885	11.247	0.000
GLLFHKS(phos)ADQEVN HGLIQH	S	aconitate hydratase 2	51	0.063715	11.753	0.008
LDHLKVFDS(phos)SEDVK	S	extensin	64	-0.154525	12.276	0.000
VDETPIS(phos)KHALR	S	allene oxide synthase	462	0.08229	14.548	0.000
HVNBGY(phos)FDR	Y	uncharacterized acetyltransferase At3g50280	388	0.207495	15.780	0.003
IDS(phos)QAKYGALSR	S	bifunctional 3-dehydroquinone dehydratase	301	-0.27071	16.285	0.038
ALDKELS(phos)SNFER	S	bifunctional 3-dehydroquinone dehydratase	70	1.05915	16.997	0.001
S(phos)VKYEFK	S	SAL1 phosphatase-like isoform 2	48	0.496995	18.594	0.012
AS(phos)YVHYVDLLKR	S	annexin D1-like	185	0.137925	20.494	0.000
GGLEKINWS(phos)K	S	inositol-3-phosp hate synthase-like	214	0.117345	25.572	0.014
YLDEKTIFHLNPS(phos)G R	S	outer membrane protein porin 2	235	0.058005	0.327	0.001
DQVEAVVS(phos)KIIEEA R	S	xyloglucan endotransglucosy lase	145	-0.014155	0.308	0.007
FATFAKS(phos)YK	S	S-adenosylmethi onine synthase 2-like isoform	211	0.289125	0.294	0.001

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IFSTFIGFLKS(phos)K	S	nitrogen regulatory protein P-II homolog	166	0.296805	0.241	0.008
DNNLLGKFELT(phos)GIPPAPR	T	protein LOC101297958 isoform 1	468	0.174735	0.213	0.018
NSQGLDIPS(phos)LLKHVK	S	glutathione S-transferase DHAR3	252	0.56685	0.155	0.000
S(phos)YHDKVIQTMK	S	glutamate dehydrogenase 1-like	621	-0.11188	0.134	0.003
WDKILYTGs(phos)AR	S	uncharacterized protein LOC101298363	259	1.0828	0.129	0.003
AAAAADQIS(phos)KLLK	S	aldehyde dehydrogenase family 3 member II	10	-0.27808	0.106	0.010
NKY(phos)GDAFIR	Y	uridylyltransferase-like isoform 1	68	-0.40997	0.101	0.009
DEAIKHLGADS(phos)FLVSR	S	uncharacterized protein LOC101304719	231	0.094945	0.085	0.004
ELAGSIEKGVs(phos)FIR	S	malate dehydrogenase, glyoxysomal-like	353	0.72935	0.057	0.000
EADVIS(phos)LHPILDKTT	S	glycerate dehydrogenase-like	241	-0.17303	0.038	0.036
YTS(phos)IKPLGDR	S	uncharacterized protein LOC101300947	57	0.0480395	0.022	0.001