

Table 1 Suppl. The primers cloning full length.

Gene	Sequences	
<i>TpSnRK2.1</i>	forward	5'-GAGGGACATAGGAAGAAAGA-3'
	reverse	5'-TTACACATCAAGCCAATCTG-3'
<i>TpSnRK2.3</i>	forward	5'-CGCAACTCTCTATATTTTCTC-3'
	reverse	5'-GTGGAATGTTTGTTTCAGTAAT-3'
<i>TpSnRK2.4</i>	forward	5'-GAGGGACATAGGAAGAAAGA-3'
	reverse	5'-TTACACATCAAGCCAATCTG-3'
<i>TpSnRK2.7</i>	forward	5'-GGGAAGAAGAAGAAGAAGAA-3'
	reverse	5'-CGAGACAAGAATGAAGAAGAA-3'
<i>TpSnRK2.8</i>	forwardF	5'-GGCGTTTTATCTTTCTCTCT-3'
	reverse	5'-CCATTATATTACAACCAGAACAG-3'

Table 2 Suppl. The primers for normalized expression.

Gene	Sequences	
<i>TpSnRK2.1</i>	forward	5'-AGGCATATTCCATAACTAT-3'
	reverse	5'-CACAAGATTGATGAACAT-3'
<i>TpSnRK2.3</i>	forward	5'-AGAAGATTGATGAGAATGTG-3'
	reverse	5'-TTGAATCGTATGATGTTAGG-3'
<i>TpSnRK2.7</i>	forward	5'-AAGATTGACGAGAATGTG-3'
	reverse	5'-CTTGAATCGGATTATGTTG-3'
<i>TpSnRK2.8</i>	forward	5'-ACCATACATCAGCAATCTT-3'
	reverse	5'-AGTCTTCAGTTCTCCATTC-3'

subclass I	OSSAPK7	MERYELLKIDIGAGNFGVARLMRNKETKELVAMKYIPRGLKIDENVAREIINHRSLRHPNIIRFKFVWVET	71
	ZMSNRK2.7	MEKHELLKIDIGAGNFGVARLMRNKETKELVAMKYIPRGQKIDENVAREIINHRSLRHPNIIRFKFVWVET	71
	TASNRK2.7	MERYELLKIDIGAGNFGVARLMRNKETKELVAMKYIPRGLKIDENVAREIINHRSLRHPNIIRFKFVWVET	71
	TPSNRK2.7	MERYELLKIDIGAGNFGVARLMRNKETKELVAMKYIPRGLKIDENVAREIINHRSLRHPNIIRFKFVWVET	71
	OSSAPK1	MERYEVMRDIGSGNFGVAKLVRDVATNHLFAVKFIERGLKIDEHVQREIMNHRSLRHPNIIRFKFVWVET	71
subclass II	ZMSNRK2.1	MERYEVIRDIGSGNFGVAKLVRDVRTKELFAVKFIERGQKIDEHVQREIMNHRSLRHPNIIRFKFVWVET	71
	TASNRK2.7	MDRYEVVRDIGSGNFGVAKLVRDVRTKEHFVAVKFIERGHKIDEHVQREIMNHRSLRHPNIIRFKFVWVET	71
	TPSNRK2.1	MDRYEVVRDIGSGNFGVAKLVRDVRTKEHFVAVKFIERGHKIDEHVQREIMNHRSLRHPNIIRFKFVWVET	71
	OSSAPK3	MEERYEALKELGAGNFGVARLVRDKRKSELVAVKYIERGKKIDENVQREIINHRSLRHPNIIRFKFVWVET	72
	ZMSNRK2.3	MEERYEALKELGAGNFGVARLVRDKRKSELVAVKYIERGKKIDENVQREIINHRSLRHPNIIRFKFVWVET	72
subclass III	TASNRK2.3	MEERYEALKELDTGNFGVARLVRDKRTKELVAVKYIERGKKIDENVQREIINHRSLRHPNIIRFKFVWVET	72
	TPSNRK2.3	MEERYEALKELGTGNFGVARLVRDKSTKELVAVKYIERGKKIDENVQREIINHRSLRHPNIIRFKFVWVET	72
	ZMSNRK2.8	MAGPAPDRAALTVGPGMDMPIMHDSRYELVRDIGSGNFGVARLMRDRRTSELVAVKYIERGEKIDENVQREIINHRSLRHPNIIRFKFVWVET	95
	OSSAPK8	MAAAGAGAGAPDRAALTVGPGMDMPIMHDSRYELVRDIGSGNFGVARLMRDRRTMELVAVKYIERGEKIDENVQREIINHRSLRHPNIIRFKFVWVET	100
	TASNRK2.8	MAGAAPDRAALTVGPGMDMPIMHDSRYELVRDIGSGNFGVARLMRDRRTMELVAVKYIERGEKIDENVQREIINHRSLRHPNIIRFKFVWVET	95
subclass III	TPSNRK2.8A	MRDRRTMELVAVKYIERGEKIDENVQREIINHRSLRHPNIIRFKFVWVET	51
	TPSNRK2.8B	MINHRSLRHPNIIRFKFVWVET	23
	PHSNRK2.8	MAGAAPDRAALTVGPGMDMPIMHDSRYELVRDIGSGNFGVARLMRDRRTMELVAVKYIERGEKIDENVQREIINHRSLRHPNIIRFKFVWVET	95
	Consensus	sl hpn i rfk v t t	
subclass I	OSSAPK7	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	171
	ZMSNRK2.7	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	171
	TASNRK2.7	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	171
	TPSNRK2.7	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	171
	OSSAPK1	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	171
subclass II	ZMSNRK2.1	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	171
	TASNRK2.7	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	171
	TPSNRK2.1	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	171
	OSSAPK3	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	172
	ZMSNRK2.3	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	172
subclass III	TASNRK2.3	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	172
	TPSNRK2.3	HLAIVMEYAAAGGELFDRTICNAGRFSEDDPARVFFQQLICGVSYCHFMQICHRDLKLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	172
	ZMSNRK2.8	HLAIVMEYASGGELFERICNAGRFSEDDPARVFFQQLISGVSYCHSMQVCHRDLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	188
	OSSAPK8	HLAIVMEYASGGELFERICNAGRFSEDDPARVFFQQLISGVSYCHSMQVCHRDLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	200
	TASNRK2.8	HLAIVMEYASGGELFERICNAGRFSEDDPARVFFQQLISGVSYCHSMQVCHRDLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	195
subclass III	TPSNRK2.8A	HLAIVMEYASGGELFERICNAGRFSEDDPARVFFQQLISGVSYCHSMQVCHRDLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	151
	TPSNRK2.8B	HLAIVMEYASGGELFERICNAGRFSEDDPARVFFQQLISGVSYCHSMQVCHRDLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	123
	PHSNRK2.8	HLAIVMEYASGGELFERICNAGRFSEDDPARVFFQQLISGVSYCHSMQVCHRDLENTLLDGSAPRUKICDFGYSKSSVHSPKPKSTVGTGPAYIAPEVL	195
	Consensus	hlaivmeyaaggelfic rfsede r ffqql g chrdlk ntlldgs pr kiedfgysks l s p kstvgtpayiapevl	
subclass I	OSSAPK7	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	271
	ZMSNRK2.7	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	271
	TASNRK2.7	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	271
	TPSNRK2.7	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	271
	OSSAPK1	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	271
subclass II	ZMSNRK2.1	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	271
	TASNRK2.7	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	271
	TPSNRK2.1	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	271
	OSSAPK3	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	272
	ZMSNRK2.3	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	272
subclass III	TASNRK2.3	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	272
	TPSNRK2.3	SRREYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	272
	ZMSNRK2.8	LKKEYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	288
	OSSAPK8	LKKEYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	300
	TASNRK2.8	LKKEYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	295
subclass III	TPSNRK2.8A	LKKEYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	215
	TPSNRK2.8B	LKKEYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	223
	PHSNRK2.8	LKKEYDGKADVWSCGVTLVYMLVGAYPFEDPDEERNFRKTTIRILSVQVSPDYVRVMSDCRLLSRIFVGNPERRITITPEIKKHFWFLKLPLEMTDE	295
	Consensus	eydgk advwscgvtlvym g yppe p p nfrkti ri qy p v	
subclass I	OSSAPK7	AQAMYYKKNASAPTYSVQSVVEEIMKIVEEARTPPRSSTPVAGFGWAEDEQEDSKKPEEEEEEDEADEYDKQVKVQHASGEFQLS	359
	ZMSNRK2.7	AQAMYYKKNASAPTYSVQSVVEEIMKIVEEARTPPRSSTPVAGFGWAEDEQEDSKKPEEEEEEDEADEYDKQVKVQHASGEFHLSC...	356
	TASNRK2.7	AQAMYYKKNASAPTYSVQSVVEEIMKIVEEAKPPPPSTTPVAGFGWAEDEQEDGKKPEEEVEEEDDEEYDKQVQNEVRASGEFHIS...	357
	TPSNRK2.7	AQAMYYKKNASAPTYSVQSVVEEIMKIVEEAKPPPPSTTPVAGFGWAEDEQEDGKKPEEEVEEEDDEEYDKQVQNEVRASGEFHIS...	357
	OSSAPK1	YQSMQLADMTNTPQSLEEVMAIQEARKPGDAMNLAGQVACLGSMDDLDIDIDIDIDTENSQDFVCAV.....	342
subclass II	ZMSNRK2.1	YQSMQLADMTNTPQSLEEVMAIQEARKPGDAMNLAGQVACLGSMDDLDIDIDIDIDTENSQDFVCAV.....	342
	TASNRK2.7	YQSMQLADMTNTPQSLEEVMAIQEARKPGDAMNLAGQVACLGSMDDLDIDIDIDIDTENSQDFVCAV.....	342
	TPSNRK2.1	YQSMQLADMTNTPQSLEEVMAIQEARKPGDAMNLAGQVACLGSMDDLDIDIDIDIDTENSQDFVCAV.....	342
	OSSAPK3	EKADYKDTDAAPPTQAVEEIMRIQ.....EAKTPGDMMAADPALLAELAEKLSDEEEAADDYTY.....	334
	ZMSNRK2.3	EKADYKDTDAAPPTQAVEEIMRIQ.....EAKTPGDMMAADPALLAELAEKLSDEEEAADDYTY.....	333
subclass III	TASNRK2.3	DRANFKPEPTETGTAATAAQVVEEI.....MRIQEKAPGEMSKSSADAALLAELAEKLSQDDEEGGPAEGET	341
	TPSNRK2.3	DRANFKPEPTETGTAATAAQVVEEI.....MRIQEKAPGEMSKSSADAALLAELAEKLSQDDEEGGPAEGET	341
	ZMSNRK2.8	DSMSQYEEPDQPMQTMDEINQILTEATIPACSRINHLTDGLDMDMDLSDSDIDVDSGGEIVYAM.....	359
	OSSAPK8	DSMSQYEEPDQPMQTMDEINQILTEATIPACSRINHLTDGLDMDMDLSDSDIDVDSGGEIVYAM.....	371
	TASNRK2.8	DSMSQYEEPDQPMQTMDEINQILTEATIPACSRINHLTDGLDMDMDLSDSDIDVDSGGEIVYAM.....	366
subclass III	TPSNRK2.8A	DSMSQYEEPDQPMQTMDEINQILTEATIPACSRINHLTDGLDMDMDLSDSDIDVDSGGEIVYAM.....	215
	TPSNRK2.8B	DSMSQYEEPDQPMQTMDEINQILTEATIPACSRINHLTDGLDMDMDLSDSDIDVDSGGEIVYAM.....	294
	PHSNRK2.8	DSMSQYEEPDQPMQTMDEINQILTEATIPACSRINHLTDGLDMDMDLSDSDIDVDSGGEIVYAM.....	366
	Consensus		

Fig. 1 Suppl. The sequences alignment of 18 SnRK2s. TpSnRK2s were highlighted in frames, respectively.