

TaAnn6-AMASLSVFPVLTSFRHDAIALHRAFKFGG...CDSTTVINILAR...DAVQRLIMQYRAYIYH...DLYHRLTSL	70						
TaAnn6-BMASLSVFPVLTSFRHDAIALHRAFKFGG...CDSTTVINILAR...DAVQRALIMQYRAYIYH...DLYHRLTSL	70						
TaAnn1-AMASLSVFPVLTPPRDVALHKAFAKFGG...CDSTTVINILAR...DSAQRALILHEYKAIYH...DLYHRLTSL	70						
TaAnn1-DMASLSVFPVLTPPRDVALHKAFAKFGG...CDSTTVINILAR...DSAQRALILHEYKAIYH...DLYHRLTSL	70						
TaAnn9-BMASLTPFAPFNQGDIDLHKAFAKFGG...CDSTTVINILAR...DSMQRTIQOQYPTMYS...ELSRITSL	70						
TaAnn9-DMASLTPFAPFNQGDIDLHKAFAKFGG...CDSTTVINILAR...DSMQRTIQOQYPTMYS...ELSRITSL	70						
TaAnn7-BMATIATVPTPLSPAADASLRNVAQVGG...TDEKALVILGR...TAQARAIIRRAYASLYK...SLLRITSL	70						
TaAnn7-DMATIATVPTPLSPAADASLRNVAQVGG...TDEKALVILGR...TAQARAIIRRAYASLYK...SLLRITSL	70						
TaAnn5-BMSAIVVSPVPSFSDAEGIRKALQVGR...ADKEALVIRLAG...PLMSFRQR...PLLRITSL	58						
TaAnn2-A	MCGGCGCLDCHNIPPLMLPLHFS...SAARTGRGEGEGARTLSPMASISVDPASSPTEDEASIRKAVQVGG...TDENALIEILGR...TAQARAIIRRAYASLYK...PLLRITSL	113						
TaAnn2-B	MCGGCGCLDCHNIPPLMLPLHFS...LSSSAASAGGEGAAAAVPMASISVVPASSPTEDEASIRKAVQVGG...TDENALIEILGR...TAQARAIIRRAYASLYK...PLLRITSL	112						
OsAnn2	MCGGCGCLDCHNIPPLMLPLHFS...LSSSAASAGGEGAAAAVPMASISVVPASSPTEDEASIRKAVQVGG...TDENALIEILGR...TAQARAIIRRAYASLYK...PLLRITSL	119						
TaAnn11-AMATLSVPAAVPAVADCCQLRKAFAKFGG...TNERLIVSILAR...DAQRAIRRAYAYEAGE...ELLRAIGSEH	70						
TaAnn11-DMATLSVPAAVPAVADCCQLRKAFAKFGG...TNERLIVSILAR...DAQRAIRRAYAYEAGE...ELLRAIGSEH	70						
TaAnn1-BMATLSVPAAVPAVADCCQLRKAFAKFGG...TNERLIVSILAR...DAQRAIRRAYAYEAGE...ELLRAIGSEH	70						
TaAnn12-AMATLKVPSNVPAADCCQLRKAFAKFGG...TNEALISILGR...DAQRAIRRAYAYEAGE...ELLRAIGSEH	70						
TaAnn12-DMATLKVPSNVPAADCCQLRKAFAKFGG...TNEALISILGR...DAQRAIRRAYAYEAGE...ELLRAIGSEH	70						
TaAnn4-AMTTITVQVPSVPEDEALIMKFAQVGG...TDEQAVIYLAR...DAQRKLIRQAYEKEVNE...LLRITSL	70						
TaAnn4-DMTTITVQVPSVPEDEALIMKFAQVGG...TDEQAVIYLAR...DAQRKLIRQAYEKEVNE...LLRITSL	70						
TaAnn8-DMQQFLAAQPSNGST...AAAAPFSPSPSPLRSRPFRRDQOQS...IKEATMADEHQETKAFSGMGLVEETALVSAIGMWRKQPEKRAQFRRCQFPFAAAGAGAGAEIRSD...VYRHLTEFA	128						
TaAnn3-AMADEVALTKAFSGMGLGVDPTMVAALANWRKQPEKRSGRFRKFFGLFK...EHGV...IERCEDE...YMLHLAASF	72						
TaAnn3-BMADEVALTKAFSGMGLGVDPTMVAALANWRKQPEKRSGRFRKFFGLFK...EHGV...IERCEDE...YMLHLAASF	72						
TaAnn10-AMAARS...PAAGFENCEIRHGACDEPR...RLSRLARR...SASERQIKATYRAMFGE...DLAQLRHLIT	64						
TaAnn10-DMAARS...PAAGFENCEIRHGACDEPR...RLSRLARR...SASERQIKATYRAMFGE...DLAQLRHLIT	64						
TaAnn10-BMAARS...PAAGFENCEIRHGACDEPR...RLSRLARR...SASERQIKATYRAMFGE...DLAQLRHLIT	64						
ConsensusMAARS...PAAGFENCEIRHGACDEPR...RLSRLARR...SASERQIKATYRAMFGE...DLAQLRHLIT	64						
	a	1	Repeat 1					
TaAnn6-A	GMHK.....KAMLWLDVPGRTATLNQSLNGDI...TDLRAATV...SFPDQIQIMKQYARFQCYLEDITER...TYGDHKLILLAYLIGFRYGEPEVDPAARADARELYRAGE...KRLGTDER	188						
TaAnn6-B	GMHK.....KAMLWLDVPGRTATLNQSLNGDI...TDLRAATV...SFPDQIQIMKQYARFQCYLEDITER...TYGDHKLILLAYLIGFRYGEPEVDPAARADARELYRAGE...KRLGTDER	188						
TaAnn1-A	GMHKSRENPAWMLQNALWLDVPGRTATLNQSLNGDI...TDLRAATV...SFPDQIQIMKQYARFQCYLEDITER...TYGDHKLILLAYLIG...LYQAGE...KRVGTDER	180						
TaAnn1-D	GMHK.....KAMLWLDVPGRTATLNQSLNGDI...TDLRAATV...SFPDQIQIMKQYARFQCYLEDITER...TYGDHKLILLAYLIGFRYGEPEVDPAARADARELYRAGE...KRLGTDER	188						
TaAnn9-B	GMHK.....KAMSLWLDVPGRTATLNQSLNGDI...LDLKAATDI...SFPDQIQIMKQYARFQCYLEDITER...ASGDQRKILLAYLIGFRYGEPEVDPTVTHDKADLYRAGE...KRLGTDER	188						
TaAnn9-D	GMHK.....KAMSLWLDVPGRTATLNQSLNGDI...LDLKAATDI...SFPDQIQIMKQYARFQCYLEDITER...ASGDQRKILLAYLIGFRYGEPEVDPTVTHDKADLYRAGE...KRLGTDER	188						
TaAnn7-B	GHFK.....AMVLLTADPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	192						
TaAnn7-D	GHFK.....AMVLLTADPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	192						
TaAnn5-B	VDFK.....AIIWLTADPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	179						
TaAnn2-A	SHFK.....AMTLMWMDPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	234						
TaAnn2-B	SHFK.....AMTLMWMDPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	235						
OsAnn2	GDPRS.....AMTLMWMDPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	244						
TaAnn11-A	GKFER.....AVIWTADPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	187						
TaAnn11-D	GKFER.....AVIWTADPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	187						
TaAnn12-A	GKFER.....AVIWTADPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	187						
TaAnn12-D	GKFER.....AVIWTADPAERAKLAREALGR...GDDRDWLV...RAPPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	187						
TaAnn4-A	GLQT.....AMGYWLDPTDTEROAVIANATKCID...EYYPV...RANSPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	188						
TaAnn4-D	GLQT.....AMGYWLDPTDTEROAVIANATKCID...EYYPV...RANSPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	188						
TaAnn8-A	RFTK.....LMVLMAMHPWERARLHHVLRHQA...PAAD...RANSPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	244						
TaAnn8-D	RFTK.....LMVLMAMHPWERARLHHVLRHQA...PAAD...RANSPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	240						
TaAnn3-A	RFTK.....LMVLMAMHPWERARLHHVLRHQA...PAAD...RANSPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	192						
TaAnn3-B	RFTK.....LMVLMAMHPWERARLHHVLRHQA...PAAD...RANSPDHLVAVRVAIRYRSLHSGSLEEDVAACSAFQPLKRLVLSVRSYRCAESVDMVAKLEAQLAERIR...KKQPHAG	192						
TaAnn10-A	ANQDNE.....LNCNLWLDLAEARIMARDAIESG...AAADYRAL...FTFRKQDLFFTKQAYLARFKKLEQDMVTD...PSPYORLLVALATSHKSHDEPSHQIAKCDARLYDAKNG...GGTGSVDEA	189						
TaAnn10-D	ANQDNE.....LNCNLWLDLAEARIMARDAIESG...AAADYRAL...FTFRKQDLFFTKQAYLARFKKLEQDMVTD...PSPYORLLVALATSHKSHDEPSHQIAKCDARLYDAKNG...GGTGSVDEA	197						
TaAnn10-B	ANQDNE.....LNCNLWLDLAEARIMARDAIESG...AAADYRAL...FTFRKQDLFFTKQAYLARFKKLEQDMVTD...PSPYORLLVALATSHKSHDEPSHQIAKCDARLYDAKNG...GGTGSVDEA	197						
Consensus	ANQDNE.....LNCNLWLDLAEARIMARDAIESG...AAADYRAL...FTFRKQDLFFTKQAYLARFKKLEQDMVTD...PSPYORLLVALATSHKSHDEPSHQIAKCDARLYDAKNG...GGTGSVDEA	197						
	r	a	y	d	1	Repeat II	Repeat III	Repeat IV
TaAnn6-A	AFIRFTFERSWAHLAAVAGAYHHLVARSLEKAVKESGT...FEFGLLTL...AESPA...FAKALHKAMG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	316						
TaAnn6-B	AFIRFTFERSWAHLAAVAGAYHHLVARSLEKAVKESGT...FEFGLLTL...AESPA...FAKALHKAMG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	316						
TaAnn1-A	AFIRFTFERSWAHLAAVAGAYHHLVARSLEKAVKESGT...FEFGLLTL...AESPA...FAKALHKAMG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	308						
TaAnn1-D	AFIRFTFERSWAHLAAVAGAYHHLVARSLEKAVKESGT...FEFGLLTL...AESPA...FAKALHKAMG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	316						
TaAnn9-B	TFIRFTFERSWAHLAAVAGAYHHLVARSLEKAVKESGT...FEVALLTL...AEMPAK...FAKALHKAMG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	315						
TaAnn9-D	TFIRFTFERSWAHLAAVAGAYHHLVARSLEKAVKESGT...FEVALLTL...AEMPAK...FAKALHKAMG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	315						
TaAnn7-B	EVWRVSTRSKPQLATFRCYKQHGSDIEMDMK...FARMKI...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	319						
TaAnn7-D	EVWRVSTRSKPQLATFRCYKQHGSDIEMDMK...FARMKI...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	319						
TaAnn5-B	EVVQLGTRSKPQLATFRCYKQHGSDIEMDMK...FARMKI...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	308						
TaAnn2-A	DVWRVSTRSKPQLATFRCYKQHGSDIEMDMK...FARMKI...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	362						
TaAnn2-B	DVWRVSTRSKPQLATFRCYKQHGSDIEMDMK...FARMKI...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	361						
OsAnn2	DVWRVSTRSKPQLATFRCYKQHGSDIEMDMK...FARMKI...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	372						
TaAnn11-A	EIVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	315						
TaAnn11-D	EIVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	315						
TaAnn11-B	EIVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	315						
TaAnn12-A	EIVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	314						
TaAnn12-D	EIVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	314						
TaAnn4-A	EIVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	286						
TaAnn4-D	EIVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	315						
TaAnn8-A	LVVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	367						
TaAnn8-D	LVVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	363						
TaAnn3-A	EVVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	315						
TaAnn3-B	EVVRLITRSKQALLATFNNSYDQSHPIKDKL...PKME...FLSTR...VTSPEK...FAVIRYSILG...LSDSDTL...VVVTRAEVDMQV...KAEYHKYKRSGLADAH...NRYTFLSLVGRDR...	315						
TaAnn10-A	AVLEMFKRSI...PQLR...LALCSYKH...YGHDF...TKALK...N...L...D...FEES...R...V...V...V...Y...T...P...S...K...C...K...L...Q...R...S...M...Q...R...P...E...A...D...K...R...L...V...A...I...L...G...S...D...D...V...G...I...N...E...I...K...L...A...F...K...S...N...F...G...K...N...L...A...D...F...H...S...L...P...S...D...Y...R...F...L...M...W...Q...G...G...C...L...V...A...S...322	322						
TaAnn10-D	AVLEMFKRSI...PQLR...LALCSYKH...YGHDF...TKALK...N...L...D...FEES...R...V...V...V...Y...T...P...S...K...C...K...L...Q...R...S...M...Q...R...P...E...A...D...K...R...L...V...A...I...L...G...S...D...D...V...G...I...N...E...I...K...L...A...F...K...S...N...F...G...K...N...L...A...D...F...H...S...L...P...S...D...Y...R...F...L...M...W...Q...G...G...C...L...V...A...S...330	330						
TaAnn10-B	AVLEMFKRSI...PQLR...LALCSYKH...YGHDF...TKALK...N...L...D...FEES...R...V...V...V...Y...T...P...S...K...C...K...L...Q...R...S...M...Q...R...P...E...A...D...K...R...L...V...A...I...L...G...S...D...D...V...G...I...N...E...I...K...L...A...F...K...S...N...F...G...K...N...L...A...D...F...H...S...L...P...S...D...Y...R...F...L...M...W...Q...G...G...C...L...V...A...S...330	330						
Consensus	AVLEMFKRSI...PQLR...LALCSYKH...YGHDF...TKALK...N...L...D...FEES...R...V...V...V...Y...T...P...S...K...C...K...L...Q...R...S...M...Q...R...P...E...A...D...K...R...L...V...A...I...L...G...S...D...D...V...G...I...N...E...I...K...L...A...F...K...S...N...F...G...K...N...L...A...D...F...H...S...L...P...S...D...Y...R...F...L...M...W...Q...G...G...C...L...V...A...S...330	330						

Additional file 3: Figure S1. Multiple sequence alignment of deduced amino acid sequences of 25 wheat annexin genes with rice annexin *OsAnn2* (*Os05g31760*) obtained by ClustalW. The conserved annexin repeats (Repeat 1 to Repeat 4) are shown beneath the deduced sequence alignments. The sequences highlighted are as follows; olive the two Cys and two His residues represented in bold in Zinc finger C2H2 type domain signature in *OsAnn2*, *TaAnn2-A* and *TaAnn2-B*; yellow conserved His residue; blue salt bridges suggested to be involved in ion channel function; pink conserved residues in S3 cluster that are involved in regulating redox reactions; green IRI motif involved in F-actin binding; red putative GTP binding motifs; the type-II calcium binding motifs are boxed in blue; Light grey and letters indicates the conserved

residues in all the 25 deduced sequences. Point indicate the sequence gaps to optimize the alignment (color figure online).