

## Supplementary Materials:

Figure S1: title, Table S1: title, Video S1: title.

NtNHX7	MASTMEVTPPFRTIARQTDNSAEGGSWNPTDAVTFVAISLVICTASRILITRCRTRPVYPTVATIVTGTATGCFYGTGTSIRLCKTGCTRIWSNTDPFRILAV	100
Sequencing_result	MASIMEVLPFFRILAEGLSNSAEGGSWNPTDAVTFVAISLVICTASRILITRCRTRPVYPTVALLVIGIALGSLEYGTSHRLGKIGDGIRLWSNIDPEILLNV	100
Consensus	masimelvlgprifilaegtsnsadeqswptdavtfvalsvlgiashrlrgtrtrpvylvalvialgslsleyglshrlgkigdgirlwsnidpeillav	
NtNHX7	FIPALIPLLFSSESSMSEVHQIKRCLVCMVLLAGPGVILSTFLLGAAVKIAFPYDWNWKTSLILGGGLSATEFWAVVALLKELGASKKLSTVIEGESIMNDGTA	200
Sequencing_result	FIPALIPLLFSSESSMSEVHQIKRCLVCMVLLAGPGVILSTFLLGAAVKIAFPYDWNWKTSLILGGGLSATEFWAVVALLKELGASKKLSTVIEGESIMNDGTA	200
Consensus	fipallfesstsemvnqikrc1vgmvlagpgvlistflgaavklafpydwnwktsslgglsatdpavvalkelgaskklistviegesimndgta	
NtNHX7	IVYYQLFELQMALGKTFIWLAVALVAFELAKVSLGVNGMGLAEGFIAASVLWLGFIFENDIVIEISLTLAVSYIAYTAQCGAIIISGVLTWILQMEYAAFAARTAFK	300
Sequencing_result	IVYYQLFELQMALGKTFIWLAVALVAFELAKVSLGVNGMGLAEGFIAASVLWLGFIFENDIVIEISLTLAVSYIAYTAQCGAIIISGVLTWILQMEYAAFAARTAFK	300
Consensus	ivyyqlflqmalqktftwdavaflakvslgvngmqlaqfiasvlwlqifindtvicisltlavveyayitaqcadiegtwtmtlqmfyaaafartafk	
NtNHX7	GESOKSHHNFMEMVAYVAYANTLITFLSGVVIAPGLLSSDNFKNCHEAWCYILILYEVILAREIVVAVILPFLTRYFCGYLWKFLAGLAWACLRCAVALS	400
Sequencing_result	GESOKSHHNFMEMVAYVAYANTLITFLSGVVIAPGLLSSDNFKNCHEAWCYILILYEVILAREIVVAVILPFLTRYFCGYLWKFLAGLAWACLRCAVALS	400
Consensus	gesgeslhnhfmewayvayantliflsgvviiaeqlssdnfkncnghawgylilyifvlvarfiivatlpfplryfcgyldvkeagilawaglrgavals	
NtNHX7	LSLSVKRS9CGTSIDTSETGIGWVFETGIGIVFLLTWNGTTTQVYLHMLGLDKLSAAKPRRLLDYTKYEMLNKALETGDLGLDDEELGPALWPTVKKYITIS	500
Sequencing_result	LSLSVKRS9CGTSIDTSETGIGWVFETGIGIVFLLTWNGTTTQVYLHMLGLDKLSAAKPRRLLDYTKYEMLNKALETGDLGLDDEELGPALWPTVKKYITIS	500
Consensus	lslsvkrs9gtsidtsetgtwvfifggtfltlwngtltqyvlmglgdklsaaqrlldytkyemlnkaletfglgddeeelpatvkkylts	
NtNHX7	IENFLJCGTIPINTSDSPNMDITNKKDTTRILINCVCAAYWGMJLDFCRTRCTAASLIMCSVDPAFLAPTEPFLCWNKGKIAVNVNFPSYYRTIOTCITIPRK	600
Sequencing_result	IENFLJCGTIPINTSDSPNMDITNKKDTTRILINCVCAAYWGMJLDFCRTRCTAASLIMCSVDPAFLAPTEPFLCWNKGKIAVNVNFPSYYRTIOTCITIPRK	600
Consensus	indledegihphtmdssemmlnlkdriplngvqaywgmndegrinlaalmsvdealdaplep1cdwkg1kayvnfpsyyrlqgliprk	
NtNHX7	IVTYFTVERLESACYCAAFIRAFRIAQQHLFIGESATASTVIEEQAEGEEAKKFLEIRVRFTEQVLRVVKTRCVTVSVINHILEYVNLKLEVKGILE	700
Sequencing_result	IVTYFTVERLESACYCAAFIRAFRIAQQHLFIGESATASTVIEEQAEGEEAKKFLEIRVRFTEQVLRVVKTRCVTVSVINHILEYVNLKLEVKGILE	700
Consensus	itytftverlesacycaafirahiqpp1hdfigdsaisastvileesqaeegeakkfleovtvtifpgv.lrvvkrtrgvtysvlmhileyvknekvgle	
NtNHX7	EKEMFLHLHVQDOLKLLRNPNFLVKVVKIGESISVHPFMGALPSDTRQFFEGSTKEVWLRGITYLKEGSKASGVWLVSSGVVKWTSKSLRNRRHSIHFV	800
Sequencing_result	EKEMFLHLHVQDOLKLLRNPNFLVKVVKIGESISVHPFMGALPSDTRQFFEGSTKEVWLRGITYLKEGSKASGVWLVSSGVVKWTSKSLRNRRHSIHFV	800
Consensus	okcmuh.lhdv1ordikllrnpnflvkvsklgcsisvhpfmqalpsdirgcrogstckwmkrlqitlykoqskasqgvwlvssgvvkwtsksirnrhsihcv	
NtNHX7	FTHGSTLIGLYEVVLLGKPYICLIVTISVALCFIDKDLSSALRADPATEEFLWQESAVILARLLLPQWFEMK1MQDLRALVAERSMMTIFLREGETIEVER	900
Sequencing_result	FTHGSTLIGLYEVVLLGKPYICLIVTISVALCFIDKDLSSALRADPATEEFLWQESAVILARLLLPQWFEMK1MQDLRALVAERSMMTIFLREGETIEVER	900
Consensus	fthgstlglgelyevlqkpyicdivtdavalcfidkdlssalradpaeeflfwqesavilarlllpqwfekmtmqd1ralvaersmmttflrgetievr	
NtNHX7	PISTGTTIICGTTKTHVQEPITTSFPAATIIFCQONITSIISMDASATKSVSFSHQGSCYQVNTRARVTTFDIAAFTTRKTTMRRCSSTTSHSQCDPINKSTSRFH	1000
Sequencing_result	PISTGTTIICGTTKTHVQEPITTSFPAATIIFCQONITSIISMDASATKSVSFSHQGSCYQVNTRARVTTFDIAAFTTRKTTMRRCSSTTSHSQCDPINKSTSRFH	1000
Consensus	hsigtttlegfikthvggee11lspaa1tpegggn1tsmdasatksvsfshqgscyqvelarvttfdiaafelekt1mrgs1ishsgdpdhkhs1reh	
NtNHX7	GGIMSWPENFFIAKCHCNCPGKTYAKTNLSAKAMLISFGSTTLKVRGFSFNGNOAGAGVYFYSRACSYHGYPLPTSGRPAGAGTCARAAAGATGSG	1100
Sequencing_result	GGIMSWPENFFIAKCHCNCPGKTYAKTNLSAKAMLISFGSTTLKVRGFSFNGNOAGAGVYFYSRACSYHGYPLPTSGRPAGAGTCARAAAGATGSG	1100
Consensus	ggimswpennflakqkqnppegtkyaktnlsakamj1sifgstddkvrpgsfsmngqagavfsysraqsylygplptsgrpagagtgaraaagatgs	
NtNHX7	GATTKARRLQFESKSAGQMSPPPLPPRNGINEGHGQERDHSSLESGDLLFIVIDSFESTLSFQ	1162
Sequencing_result	GATTKARRLQFESKSAGQMSPPPLPPRNGINEGHGQERDHSSLESGDLLFIVIDSFESTLSFQ	1162
Consensus	gattkakrlqfesksagqmsppplpprqtncqhcocrdhssdsgddffiv idscststlsfq	

Figure S1: The amino acid sequence comparison between predicted sequence and sequencing result of NtNHX7. The top row is the prediction result, and the second row is the sequencing result.

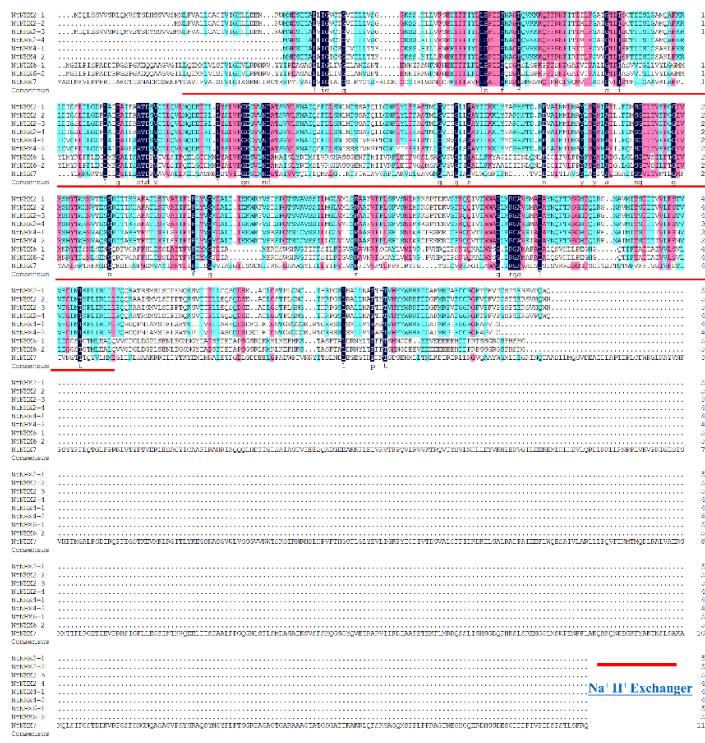


Figure S2: The amino acid multiple fragment alignments of NtNHXs