

Supplementary Materials:

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

NtNHX7	MASTMEVTPPFRTIARQTDNSAEGGSWNPTDAVTFVAISLVICTASRILITRCRTRPVYPTVATIVTGTATGCFYGTGTSIRLCKTGCTRWSNTPFRTIAY	100
Sequencing_result	MASIMEVLPFFRILAEGLSNSAEGGSWNPTDAVTFVAISLVICTASRILITRCRTRPVYPTVALLVIGIALGSLEYGTSIRLKGKIGDGIRLWSNIDPELLNV	100
Consensus	masimelvlgprflaegtsnsaeggswnptdavtfvalsvlgiashrlrgtrtrpvylvalvialgslsleyglshrlgkigdgirlwsnidpel11av	
NtNHX7	FIPALIPLLSSMSEVHQIKRCLVCMVLLAGPGVILSTFLLGAVKLAFFPYDNWKTSLILGGGLSATEFWAVVALLKELGASKKLSTVIEGESIMNDGTA	200
Sequencing_result	FIPALIPLLSSMSEVHQIKRCLVCMVLLAGPGVILSTFLLGAVKLAFFPYDNWKTSLILGGGLSATEFWAVVALLKELGASKKLSTVIEGESIMNDGTA	200
Consensus	fipallfesstsemvhqikrclvqmvlagpgvlistflgaavklafpydnwktstllgglsatdpavvalkelgaskklistviegesimndgta	
NtNHX7	IVYYQLEFLQMLAKRIFTWLAVVVAELAKVSLGNVGMLAEGFIAASVLWLGFIFENDIVIEISLTLAVSYIAYTAQCGAIIISGVLTWILQMEYAAFAARTAFK	300
Sequencing_result	IVYYQLEFLQMLAKRIFTWLAVVVAELAKVSLGNVGMLAEGFIAASVLWLGFIFENDIVIEISLTLAVSYIAYTAQCGAIIISGVLTWILQMEYAAFAARTAFK	300
Consensus	ivyyqlflqmalqktftwdavaflakvslgavmqlaqfiasvlwlqifindtvicisltlavveyayitaqcadiegtwtmwlqmfaafartafk	
NtNHX7	GESOKSHHNFMEMVAYVANTLITFLSGVVIAPGLLSSENIFKNHCFLWVCGYLILLYFLVFLAREIVVAVLFLPFLRYFCYGLWVKFLAGLAWGLRCAVALS	400
Sequencing_result	GESOKSHHNFMEMVAYVANTLITFLSGVVIAPGLLSSENIFKNHCFLWVCGYLILLYFLVFLAREIVVAVLFLPFLRYFCYGLWVKFLAGLAWGLRCAVALS	400
Consensus	gesokshhnfmewvayvan1iflsgvviiaeqlssdnifknhngawgylillyifvlvarfiivtflpflryfcyglwvkflaglawglrcavals	
NtNHX7	LSLSVKRS9CGTSIDTSETGIGWVFETGIGIVFLLTWNGTTTQVVLHMLGLDKLSAAKPRRLDLYTKYEMLNKALETGDLGLDDEELGPALWPTVKKYTIS	500
Sequencing_result	LSLSVKRS9CGTSIDTSETGIGWVFETGIGIVFLLTWNGTTTQVVLHMLGLDKLSAAKPRRLDLYTKYEMLNKALETGDLGLDDEELGPALWPTVKKYTIS	500
Consensus	lslsvkrs9gtsidtsetgtwvfifggtfltlwngtltqyvlmglgdklsaaqr1ldyt1kyemlnkaletfglgddeeelpwtvkkylts	
NtNHX7	I N E F L I C G T H P I N T S C S P N M D T I N K D T R T R I I N C V C A A Y W C M T I F C R T N C T A S S I U M C S V D P A T D I A P T E P I C W K G I K A V N F S Y Y R T I O C I T F P R K	600
Sequencing_result	I N D E L E G T H P I N T S C S P N M D T I N L K D I R I R I L L N G V C A A Y W G M L L E G R I N Q T A A S I L M G S V D E A I T G D L G L D E E L G T A D W P T V K K Y T I S	600
Consensus	indelgeghhpintscspnmldtinkdrirrlngvcaywgmldegrinlast1mgsvdeat1aplep1cdwkg1kayvnfyssy11qgl1prk	
NtNHX7	I V T Y F T V E R L E S A C Y C A A F I R A H R I A C Q C O L H E F I G E S A T A S T V I E E S Q A E G E F A K K F L E I D V R V T F C Q V L R V V K T R C V T Y S V I N H I E Y V V N L E K V G I L E	700
Sequencing_result	I V T Y F T V E R L E S A C Y C A A F I R A H R I A C Q C O L H E F I G E S A T A S T V I E E S Q A E G E F A K K F L E I D V R V T F C Q V L R V V K T R C V T Y S V I N H I E Y V V N L E K V G I L E	700
Consensus	itytfwerlesacycaafirahriacq1hdfigdsaisastvleesqaegeekfkleovtvtifpgv1rvvkrtrgvtsvlnhleyvknekvgle	
NtNHX7	EKEMIHLHQLQDQLKLLRNPNFLVKVVKIGESISVHPFMGALPSD1RQFFEGSTKEVWLRGITYLKEGSKASGVWLVSSGVVKWTSKSLRNRRHSIHFV	800
Sequencing_result	EKEMIHLHQLQDQLKLLRNPNFLVKVVKIGESISVHPFMGALPSD1RQFFEGSTKEVWLRGITYLKEGSKASGVWLVSSGVVKWTSKSLRNRRHSIHFV	800
Consensus	okcmuh1hdv1ord1kllrnpt1kvsk1qcsisvphpmqalpsdirgcrgstckwmklr1qitlykoqskasqgv1vssqvkvtsks1mrnhs1hc	
NtNHX7	FTHGSTLIGLYEVVLLGKPYICLIVTISVALCFFIDKDLSSALRADPATEEFLWQESAIVLARLLLPQWFEMK1MDLRLVALVERSMMITFLRGETIEVER	900
Sequencing_result	FTHGSTLIGLYEVVLLGKPYICLIVTISVALCFFIDKDLSSALRADPAEEFLWQESAIVLARLLLPQWFEMK1MDLRLVALVERSMMITFLRGETIEVER	900
Consensus	fthgstl1glyev1lgkpyic1divt1davalcf1ffidkdl1salradpaee1flwqesa1vlar11lpqwfemk1md1rlvalversmmttflrget1evr	
NtNHX7	I S T G T I I E C F T K T H V Q E P T I T S P A A T F F C Q N T S I T S M D A S T K V S W S F S H Q G S C Y Q V M T R A R V T I F D I A A F T T K T I M R R C S S T I S H S C D Q P M K S I S R F I I	1000
Sequencing_result	I S I G I L L E G F I K T H V Q E P T I T S P A A T F F C Q N T S I T S M D A S T K V S W S F S H Q G S C Y Q V M T R A R V T I F D I A A F T T K T I M R R C S S T I S H S C D Q P M K S I S R F I I	1000
Consensus	hsig11leg1tkuhvgce11lspaa11pggn1s1sdas1ksvs1shgsgcyqvelarv11fdiaafelek1lmrgs1ishsgdp1hks1areh	
NtNHX7	GGIMSWPENFFIAKCHCNCPGKTYAKTNLSAKAM1LSTFGSTTEIKVRGFSFNGNOAGAGVYFYSRACSYHGYPLPTSGRPAGAGTCARAAGATG	1100
Sequencing_result	GGIMSWPENFFIAKCHCNCPGKTYAKTNLSAKAM1LSTFGSTTEIKVRGFSFNGNOAGAGVYFYSRACSYHGYPLPTSGRPAGAGTCARAAGATG	1100
Consensus	ggimswpenffia1akchcn1cp1gktyaktnlsakam1sifgstddkvrpgsf1smgqjagagv1sysra1qsy1gyp1pltsgrpag1tgara1agatg	
NtNHX7	GATTKAARRLQFESKSAGQMSPPPLPPRNGINEGHGQERDHSSLESQGDLLFIV1DSFESTLSFQ	1162
Sequencing_result	GATTKAARRLQFESKSAGQMSPPPLPPRNGINEGHGQERDHSSLESQGDLLFIV1DSFESTLSFQ	1162
Consensus	gattkakr1qfsqagsqmspp1prqtnqchccordhssdsgddffiv1dsctstlsfq	

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.

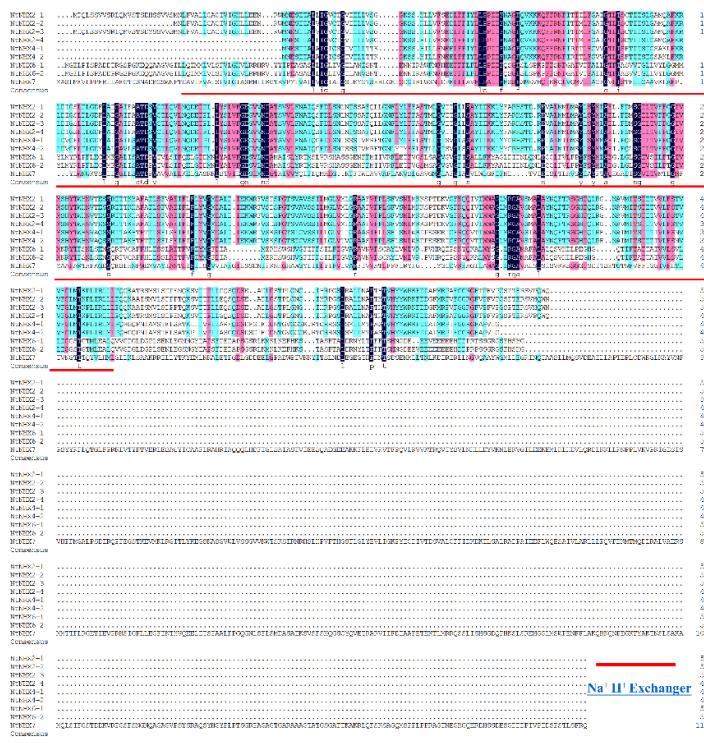


Figure S2: The amino acid multiple fragment alignments of NtNHXs