

Supplementary File 1:

Table 2. The list of novel proteins identified using proteogenomics approach. These proteins were not present in TAIR proteome database. The detailed information about the novel identification, its annotation from TAIR webpage and their matched peptides (highlighted in yellow) were presented following with this table.

Furthermore:

- If the spectral counts are smaller than 4, the matched spectra were also presented.
- If the novel identification shares with TAIR10 protein entry a group of peptides, then the matched TAIR10 protein entry were included, and the unique peptide(s) associated with the novel identification were specified.
- If different set of peptides (from different tissues) were associated with the novel identification, all sequence matches were listed.

[illegible]

No.1. AtChr1@30100671@30103941: Transposable_element_gene

AtChr1@30100671@30103941 (100%), 122,861.1 Da

| potential novel

13 exclusive unique peptides, 13 exclusive unique spectra, 38 total spectra, 165/1090 amino acids (15% coverage)

FYFASPLGFF	PAKDMDTNSL	MLIDNNGSFE	IDDQSHVHVD	ASHTLEPVTL
PTKRRRKKSD	VWNHFTVETV	SPGSAKACCN	HCRKSFAYIN	GQKLAGTSHL
KRHIQLGICP	MNR DDSSTLA	QIVTPTTTTD	PPKKRHRSSA	SYTPLDQDR C
YNQMAKMIIM	HDYPLHMVEH	SGFTGFVQAL	CPQFTMASFN	TIHADCVNMY
LSEKHK LSNF	ITDIPGRVNL	TVDLWTSNQS	LGAFVVTGHF	IDRDWKLTHR
LLNVAVVPSP	DSDFALNQP I	AACLSOWNLE	RR LSSITVGQ	SVVNK TSIEN
LRCCLSAR NQ	NVLNGQLLLG	NCYARLLSSM	AQDLLGAEDF	KTPIKK VRDS
VKYVKT KDSC	QERFDELKKQ	LQTPSTK DLL	IDNQTKWDT S	YDMLLAACEH
KEVFSCLGNC	DLDYKILTSP	EEWRKIEILC	SSLK ILFDAA	NVLTGSTRLT
ANDLFHEMTK	LQLDLGNSAT	SEDQDVSNLA	NTLKDKFDEY	WRECFLLMAY
AVVMDPRFKM	K LIEFSFSKA	YGEDADKWIR	SVDDAVHEL Y	HDYAEQSHSL
LDAYVVHGND	GFSETDMSQV	HFHHEYHNSN	GLSHDQIFEQ	PEDGNPLNEK
PLEGLSGEGQ	PTGTESVGGN	TTQGVQE QEGH	LGDAQTQENN	IVEGQLEESK
PMDGLTQKPL	LTEENLQSNQ	EPTTAQESRL	TDETMEETHA	NQSAEEMAHE
TQLVEEFPC E	SQPSSENVPLQ	SQSGEGNVPE	TLPMEEIVED	TQPV EEEVMQE
ETSQVSRPVE	EIPLNQVQVD	DKDITHDVQP	VEEMLEDTQP	VEGV DHEAQE
LEVHDDIQSV	EEVGHEIQPE	GELLEDTQPV	EEGAQEAQLV	EENHDDVQLV
EEAGHETHAV	EGILED TQPV	EEVAQE ARPV	EQIPENSQNP	QEYSGREGESV
QEEQQSEQHP	QSHAMPHEEE	AQHDSQSHAM	PQEEATFTIS	QEGHHVDVLL
QEGHHLEASS	QEFPLITIGD	GFSDFELYIS	EVGSHQQMK S	ELDQYLEESL
I PRSQDFEVL	GWWSLNR TKY	PTLSKMAADV	LSVPFCTVSP	DSVFDTEVKK
MDNYRSSLRH	VTLEALFCAK	DWFKHSSSNS	TSENNLKMES	

No.2. AtChr3@4967609@4969613: Transposable_element_gene

AtChr3@4967609@4969613 (100%), 76,551.7 Da

| potential novel

5 exclusive unique peptides, 5 exclusive unique spectra, 19 total spectra, 73/668 amino acids (11% coverage)

QGYKFCMMDE	SNEIILQKSK	RLTSVVWNYF	ERV RKADV CY	AVCIQCNKKL
SGSSNSGTTH	LRNHLMRCLK	RTNHDMSQLL	TPKRRKKENP	VTVATINFDD
GQAKEEYLRP	KFDQDQRRDE	VVLSRGSGGR	FSQERSQVDL	AR MIILHNP
LAMVDHVGFK	VFARNLQPLF	EAVPNSTIED	SCMEIYIREK	QRVQHTLNHL
YGKVNLSVEM	WSSRDNSNYV	CLASNYIDEE	WRLHRNVLNF	ITLDP SHTED
MLSEV IIRCL	IEWSL ENKLF	AVTFDSVSVN	EEIVLR IKDH	MSQSSQILIN
GQLFELKSAA	HLLNSLVEDC	LEAMRDVIQK	IRGSVRYVKS	SQSTQVR FNE
IAQLAGINSQ	KILVLDSIVN	SNSTFVMLET	VLEYKGAFCH	LRDHDHSFDS
SLTDEEWWT	RYVTGYLKL V	FDIASDFSAN	KCPTANVYFA	EMCDIH IQLV
EWCKNQDNFL	SSLAANMKAK	FDEYWNKCSL	VLAIAAILDP	RFKMKLVEYY
YSK IYGSTAL	DR IKEVSNQV	KELLDAYSMC	SAIVGEDSFS	GSGLGRASMD
TRDRLKGF DK	FLHETSQNQN	TTTDL DKYLS	EPIFPRSGEF	NILNYWK VHT
PR YPILSLLA	RDILGTPMSI	CAPDSTFN SG	TPVISDSQSS	LNPDIRQALF
CAHDWLSTET	EGTISNSI			

No.3. AtChr2@2859228@2863482: Transposable_element_gene

AtChr2@2859228@2863482 (100%), 158,765.0 Da

| potential novel

5 exclusive unique peptides, 5 exclusive unique spectra, 25 total spectra, 65/1418 amino acids (5% coverage)

S I A F A F M V S E	L M E H R S M E L Y	S V P S L N I S N C	V T V T L T A K N Y	I L W K S Q F E S F
L D G Q G L L G F V	T G S I P A P S Q T	S V V S D I D G S T	S A S P N P E Y Y T	W F K T D R V V K S
W L L G S F L E D I	L S V V V N C N T S	H E V W I S V A N H	F N R V S S S R L F	E L Q R R L Q N V S
K R D K S M D E Y L	K D L K T I C D Q L	A S V G S P V T E K	M K I F A A L N G L	G R E Y E P I K T T
I E N S M D A L P G	P S L E D V I P K L	T G Y D D R L Q G Y	L E E T A V S P H V	A F N I T T S D D S
N A S G Y F N A Y N	R G K G K S N R G R	N S F S T R G R G F	H Q Q I S S T N S S	S G S Q S G G T S V
V C Q I C G K M G H	P A L K C W H R F N	N S Y Q Y E E L P R	A L A A M R I T D I	T D Q H G N E W L P
D S A A T A H V T N	S P R S L Q Q S Q P	Y H G S D A V M V A	D G N F L P I T H T	G S T N L A S S S G
N V P L T D V L V C	P S I T K S L L S V	S K L T Q D Y P C T	V E F D S D G V R I	N D K A T K K L L I
M G S T C D G L Y C	L K D D S Q F K A F	F S T R Q Q S A S D	E V W H R R L G H P	H P Q V L Q Q L V K
T N S I S I N K T S	K S L C E A C Q L G	K S T R L P F V S S	S F T S N R P L E R	V H C D L W G P S P
I T S V Q G F R Y Y	A V F I D H Y S R F	S W I Y P L K L K S	D F Y N I F V A F H	K L V E N Q L N H K
I S V F Q C D G G G	E F V N H K F L Q H	L Q N H G I Q Q H I	S Y P H T P Q Q N G	L A E R K H R H L V
E L G L S M L F Q S	K V P L K F W V E A	F F T A N F L I N L	L P T S A V E D A I	S P Y E K L H Q T T
P D Y T A L R S F G	C A C F P T M R D Y	A M N K F D P R S L	K C V F L G Y N D K	Y K G Y R C L Y P P
T G R V Y I S R H V	I F D E T A Y P F S	H Y H K H L H S Q P	T T P L L A A W F K	G F E S S V S Q A P
P K V S P A Q P P Q	R K A T L P T P P L	F T A A D F P P L P	R R S P Q L S Q N S	A A A L V S Q P S T
T T I N S T H P P A	V V N E S S E R T I	N F D S A S I G D S	S H S S Q L L V D D	T V E D L M A A P V
P T Q Q A P P P T N	T H P M I T R A K V	G I T K P N P R Y V	F L S H K V T Y P E	P K T V T A A L K H
P G W T G A M T E E	M G N C S E T N T W	S L V P Y T P N M H	V L G S K W V F R T	K L H A D G T L N K
L K A R I V A K C F	L Q E E G I G Y L E	T Y S P V V R T P T	V Q L V L H L A T A	L N W E L K Q M D V
K N A F L H G D L N	E T V Y M T Q P A G	F V D K S K P T H V	C L L H K S I Y G L	K Q S P R A W F D K
F S T F L L E F G F	F C S K S D P S L F	I Y A H N N N L I L	L L L Y V D D M V I	T G N S S Q T L S S
L L A A L N K E F R	M T D M G Q L H Y F	L G I Q V Q R N Q H	G L F M S Q Q K Y A	E D L L V A S A M E
N C T P L P T P L P	V Q L D R V P H Q E	E P F T D P T Y F R	S I A G K L Q Y L T	L T R P D I H F A V
N F V C Q K M H Q P	T M S D F H L L K R	I L R Y I K G T I T	M G I S Y N Q N S P	T L L Q A Y S D S D
W G N C K L T R R S	V G G L C T F M A T	N L V S W S S K K H	P T V S R S S T E A	E Y R T L S D A A S
E I L W L S T L L R	E L G I P L P D T P	E L F C D N L S A V	Y H T A N P A F H A	M I D K A T K S T N
F R V L Y P N G D S	I L T W H E N A			

No.4. AtChr3@1247686@1249978: Transposable_element_gene

AtChr3@1247686@1249978 (100%), 86,896.1 Da

| potential novel

5 exclusive unique peptides, 5 exclusive unique spectra, 23 total spectra, 61/764 amino acids (8% coverage)

I K K I V S A M A N	R D L M L G Q N R N	I G I G Q G Q S L V	L G H S H S L G L G	Q N H V D V E L G Q
G H N M D L G L A H	H D H D H H E I D L	G N P H D D H E L D	L G N S E D Q D G E	D H H H H H H D Y
M N E N E I S V D Q	K P G H D D V D P D	L V L S S Q N H E F	S L S D N N H Q L V	V G E N H E L D D N
L E L A V D S S H E	L E I D Q H G E M V	M V S T P V Q A R A	L T A D M T Y Q L T	V G Q E F P D V K S
C R R A L R D M A I	A L H F E M Q T I K	S D K T R F T A K C	S S D G C P W R V H	A A K L P G V P T F
T I R T I H E S H S	C G G I N H L G H Q	Q A S V Q W V A S S	V E Q R L R E N P N	C K P K E I L E E I
H R V H G I T L S Y	K Q A W R G K E R I	M A T M R G S F E E	G Y R L L P Q Y C E	Q V K R T N P G S I
A S V Y G S P A D N	C F Q R L F I S F Q	A S I Y G F L N A C	R P L L G L D R T Y	L K S K Y L G T L L
L A T G F D G D G A	L F P L A F G I V D	E E N D E N W M W F	L C E L H N L L E T	N T E N M P R L T I
L S D R Q K G I V E	G V E Q N F P T A F	H G F C M R H L S E	S F R K E F N N T L	L V N Y L W E A A Q
A L T V I E F E A K	I L E I E E I S Q D	A A Y W I R R I P P	R L W A T A Y F E G	Q R F G H L T A N I
V E S L N S W I A E	A S G L P I I Q M M	E C I R R Q L M T W	F N E R R E T S M Q	W T S I L V P T A E
R R V A E A L E L A	R T Y Q V L R A N E	A E F E V I S H E G	N N I V D I R N R C	C L C R G W Q L Y G
L P C A H A V A A L	L S C R Q N V H R F	T E S C F T V A T Y	R K T Y S Q T I H P	I P D K S H W R E L
S E G D P N V N K A	A L D A I I N P P K	S L R P P G R P R K	R R V R A E D R G R	V K R V V H C S R C
N Q T G H F R T T C	A A P I			

AtChr3@1247686@1249978 (100%), 86,896.1 Da

| potential novel

6 exclusive unique peptides, 6 exclusive unique spectra, 11 total spectra, 71/764 amino acids (9% coverage)

I K K I V S A M A N	R D L M L G Q N R N	I G I G Q G Q S L V	L G H S H S L G L G	Q N H V D V E L G Q
G H N M D L G L A H	H D H D H H E I D L	G N P H D D H E L D	L G N S E D Q D G E	D H H H H H H H D Y
M N E N E I S V D Q	K P G H D D V D P D	L V L S S Q N H E F	S L S D N N H Q L V	V G E N H E L D D N
L E L A V D S S H E	L E I D Q H G E M V	M V S T P V Q A R A	L T A D M T Y Q L T	V G Q E F P D V K S
C R R A L R D M A I	A L H F E M Q T I K	S D K T R F T A K C	S S D G C P W R V H	A A K L P G V P T F
T I R T I H E S H S	C G G I N H L G H Q	Q A S V Q W V A S S	V E Q R L R E N P N	C K P K E I L E E I
H R V H G I T L S Y	K Q A W R G K E R I	M A T M R G S F E E	G Y R L L P Q Y C E	Q V K R T N P G S I
A S V Y G S P A D N	C F Q R L F I S F Q	A S I Y G F L N A C	R P L L G L D R T Y	L K S K Y L G T L L
L A T G F D G D G A	L F P L A F G I V D	E E N D E N W M W F	L C E L H N L L E T	N T E N M P R L T I
L S D R Q K G I V E	G V E Q N F P T A F	H G F C M R H L S E	S F R K E F N N T L	L V N Y L W E A A Q
A L T V I E F E A K	I L E I E E I S Q D	A A Y W I R R I P P	R L W A T A Y F E G	Q R F G H L T A N I
V E S L N S W I A E	A S G L P I I Q M M	E C I R R Q L M T W	F N E R R E T S M Q	W T S I L V P T A E
R R V A E A L E L A	R T Y Q V L R A N E	A E F E V I S H E G	N N I V D I R N R C	C L C R G W Q L Y G
L P C A H A V A A L	L S C R Q N V H R F	T E S C F T V A T Y	R K T Y S Q T I H P	I P D K S H W R E L
S E G D P N V N K A	A L D A I I N P P K	S L R P P G R P R K	R R V R A E D R G R	V K R V V H C S R C
N Q T G H F R T T C	A A P I			

No.5. AtChr3@22515146@22515965: Transposable_element_gene

AtChr3@22515146@22515965 (100%), 30,005.7 Da

| potential novel

4 exclusive unique peptides, 5 exclusive unique spectra, 9 total spectra, 92/273 amino acids (34% coverage)

R D G E F W V V V V	R N L L V P E V M L	I S F S N C N F P F	A E R T L K F L E P	I P D D F L S A F H
A L S A R K C D W L	K H F S R E R V E C	A L R L L H G V S C	P T S S E S S D H R	T Q F F V D M Q S T
K L T L R E V Y A K	K K E D K E R R L A	E E R L L V N T G L	I S P R A D P E A T	Q D G N V I P D A T
A P Q T A P E A S R	D G V N P Y T A G P	V D A A P A E A Q G	A E P S A A A P E A	V L A L P A I D K A
A G K R I R V D D V	S S K K K K K K K K	A S G S E V E K I L	P I F E D R T A S A	N L L G G C V G P L
L P P P D T L L E S	R K Y A E T A S H F	L R V		

No.6. AtChr5@19854556@19856566: Transposable_element_gene

AtChr5@19854556@19856566 (100%), 76,200.0 Da

| potential novel

7 exclusive unique peptides, 7 exclusive unique spectra, 17 total spectra, 86/670 amino acids (13% coverage)

V C V L V L R P N G	L S T L F M I V M T	D V W I S V F D R S	S R T T A S E A V V	P V V S A G D I V V
G D D M I A N D F Q	I E M G I M P E E S	S P L P C N F V L T	D E K Q H I K A A Q	Q W E N A I T G V D
Q R F N S F T E F R	D A L H K Y S I A H	G F T Y K Y K K N D	S H R V S V K C K A	Q G C P W R I T A S
R L S T T Q L I C I	K K M N T R H T C E	R A V V K A G Y R A	S R G W V G S I I K	E K L K A F P D Y K
P K D I A E D I K R	E Y G I Q L N Y S Q	A W R A K E I A R E	Q L Q G S Y K K A Y	S Q L P S F C K K I
R E T N P G S I A I	F M T K E D S S F H	R L F I S F Y A S I	S G F R Q G C R P L	L F L D T A D L N S
K Y Q G V M L V A T	A P D A E D G I F P	V A F A V V D A E T	E D N W V W F L E H	L K L A L A D P R T
I T F V A D F Q N G	L K T A L P L V F E	K Q H H H A Y C L R	H L A E K L N M D L	Q A Q F S H E A R R
F I L N D F Y A A A	Y A T Q P D A Y Y R	S L E N I K S I S P	D A Y T W V I E S E	P L H W A N A L F E
G E R Y N H M N S I	F G L D F Y S W V S	E A H E L P I T Q M	I D E L R A K L M Q	S I Y T H Q V Q S R
E W I V S T L T P T	N E E K L Q K E I E	L A R S L Q V S A P	H N S L F E V H G E	T I N L V D I N Q C
D C D C K V W R L T	G L P C S H A V A V	V E C I G K S P Y E	Y C S R Y F T S E S	Y R L T Y A E S I N
P V P N T T M T M M	I L E E P P V E G V	V S V T P P P T R L	T P P G R P K S K Q	V E P L D M F K R Q
L Q C S N C K G L G	H N K K T C K A V S			

No. 7 AtChr5@7082385@7083282: Transposable_element_gene

AtChr5@7082385@7083282 (100%), 33,959.3 Da

| potential novel

5 exclusive unique peptides, 5 exclusive unique spectra, 9 total spectra, 63/299 amino acids (21% coverage)

R N K T C I E K E G	F F V E E K F V R S	L L S N S S S M A A	I Q I L D Q V D D S	A D S L I E S M R G
V Q N T M A L L H S	T V G E L L N S M S	E T L N S M A E M K	S A L L Q Q P T A T	A T S E S T K V T V
D H D L P V A P P P	P T K Q S T A A E D	N S I D T H P H R M	S R Y I Q L M K P K	I E M P V F E G P N
V N S W L T R A E R	Y F E F G S F T D A	E K I Q L V Y M S V	E G R A L C W F N L	E N R N P F V D W N
D F K A R V L Q R F	G D P R S A M E R L	L T L K Q V D S V I	S Y L G E F E D L S	T Q C L D D L D T V
L E V V F V K G L K	E E I Q E M L R V F	Q P K G L S D I I M	M A R R L E N S P F	C R L I K N S Q V

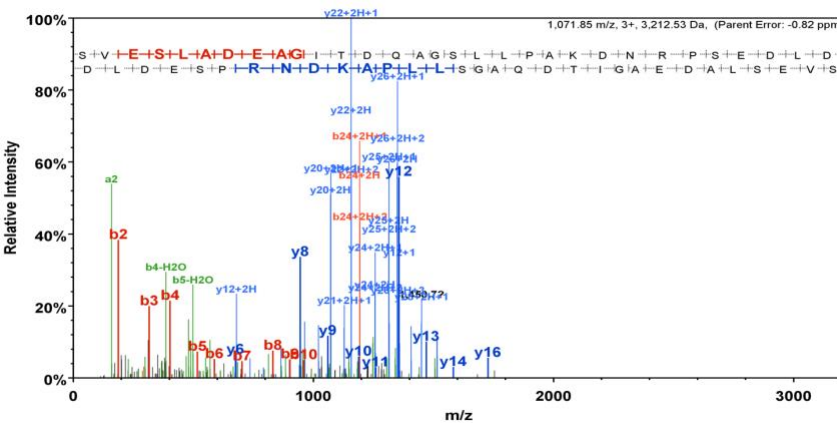
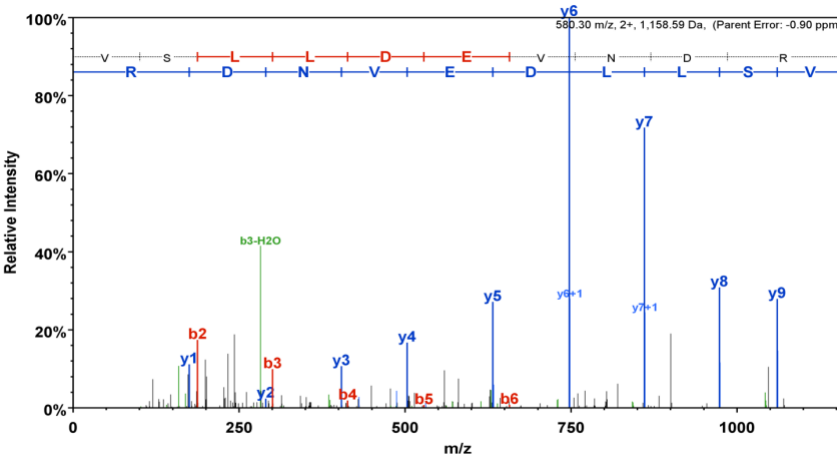
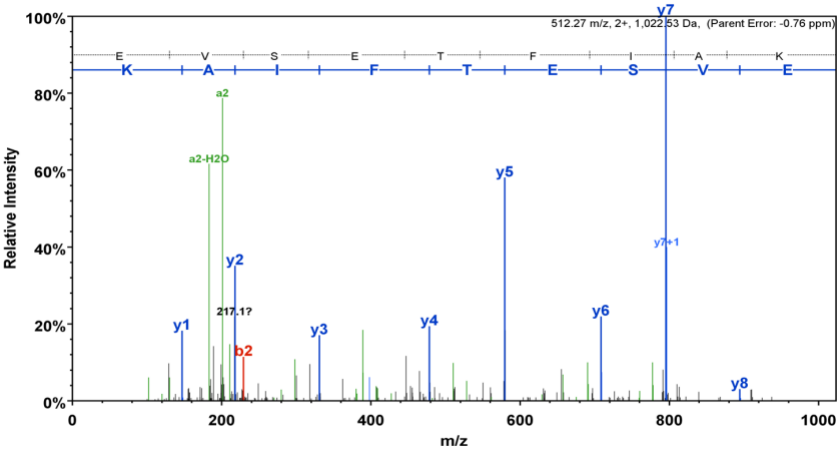
No. 8. AtChr3@22515868@22516741: Transposable_element_gene

AtChr3@22515868@22516741 (100%), 32,149.4 Da

| potential novel

3 exclusive unique peptides, 3 exclusive unique spectra, 7 total spectra, 50/291 amino acids (17% coverage)

S	A	R	G	M	C	W	S	L	A	S	S	R	Y	S	S	G	I	S	E	V	C	R	D	G	I	S	L	S	A	G	M	N	S	V	A	Y	N	L	S	W	C	Y	H	Y	K	A	N	F											
S	L	F	Q	A	V	A	S	M	N	R	M	V	H	S	Y	D	S	A	M	R	S	N	M	E	V	A	G	K	L	A	E	A	E	S	R	I	Q	A	I	E	R	E	K	N	E	A	L	S	E										
A	A	A	A	K	L	E	K	E	E	V	E	T	F	I	A	K	M	K	N	A	E	H	K	V	S	L	L	D	E	V	N	D	R	F	M	Y	L	S	Q	A	R	A	N	A	K	D	D	L	K	A	P	A	P	E					
D	S	E	V	A	R	A	V	Q	T	T	R	R	E	V	S	E	T	F	I	A	K	M	K	N	A	E	H	K	V	S	L	L	D	E	V	N	D	R	F	M	Y	L	S	Q	A	R	A	N	A	K	D	D	L	K	A	P	A	P	E
Q	L	I	E	A	L	E	G	G	G	V	L	E	S	E	K	E	Q	V	D	E	W	L	K	D	F	A	D	A	E	V	N	L	N	R	F	M	S	E	L	K	D	D	L	K	A	P	A	P	E										
P	A	P	L	S	P	G	G	H	R	S	V	E	S	L	A	D	E	A	G	I	T	D	Q	A	G	S	L	L	P	A	K	D	N	R	P	S	E	D	L	D																			



No. 9. AtChr1@26346412@26348515: Transposable_element_gene

AtChr1@26346412@26348515 (100%), 81,381.4 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 4 total spectra, 23/701 amino acids (3% coverage)

DFRFCVTWFR	CLNSNYLVKI	LLFVYMCRRQ	KKLMINNEMD	LSDAVIVKSG
RLKSVVWNDF	DRVRKGETYI	AICRHCKKRL	SGSSASGTSH	LRNHLIRCR
RTNGNNNGVA	QYFVKGKKKE	LANERIKDEE	VL SVVNVRYE	HEKEEHEDVN
VVSMGLDQRR	CRFDLARMII	LHGYP L SMVE	DVGFRMFIGN	LQPLFELVAF
ERVESDCMEI	YAKEKHKIFE	ALDKLP GKIS	ISVDVWSGSG	DSDEF LCLAA
HYIDEGWELK	KRVLNFFMVD	PSHSGEMLAE	VIMTCLMEWD	IDRKLFSMAS
SHAPPFSENV	ASKIRDRLSQ	NKFLYCYGQL	FDVSCGVNVI	NEMVQDSLEA
CCDTINIIRE	SIRYVKSSSES	IQDRFNQWIV	ETGAVSERNL	CIDDPMRWDS
TCTMLENALE	QKSAFSLMNE	HDPDSVLCPS	DLEWERLGTI	VEFLKVFVEV
INAF TKSSCL	PANMYFPEVC	DIHLRL IEWS	KNPDDFISSL	VVNMRRKFDD
FWDKNYLVLA	IATILDP RFK	MKLVEYYYPL	FYGTSA SELI	EDISECIKLL
YDEHSVGSLL	ASSNQALDWQ	NHHHRSNGVA	HGKEPDDRLT	EFDRYINETT
TTPGQDSKSD	LEKYLEEPLF	PRNSDFDILN	WWKVHTPKYP	ILSMMARNVL
AVPMLNV SSE	EDAFETCQRR	RVSETWRS LR	PSTVQALMCA	QDWIQSELES
S				

AtChr1@26346412@26348515 (100%), 81,381.4 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 5 total spectra, 20/701 amino acids (3% coverage)

DFRFCVTWFR	CLNSNYLVKI	LLFVYMCRRQ	KKLMINNEMD	LSDAVIVKSG
RLKSVVWNDF	DRVRKGETYI	AICRHCKKRL	SGSSASGTSH	LRNHLIRCR
RTNGNNNGVA	QYFVKGKKKE	LANERIKDEE	VL SVVNVRYE	HEKEEHEDVN
VVSMGLDQRR	CRFDLARMII	LHGYP L SMVE	DVGFRMFIGN	LQPLFELVAF
ERVESDCMEI	YAKEKHKIFE	ALDKLP GKIS	ISVDVWSGSG	DSDEF LCLAA
HYIDEGWELK	KRVLNFFMVD	PSHSGEMLAE	VIMTCLMEWD	IDRKLFSMAS
SHAPPFSENV	ASKIRDRLSQ	NKFLYCYGQL	FDVSCGVNVI	NEMVQDSLEA
CCDTINIIRE	SIRYVKSSSES	IQDRFNQWIV	ETGAVSERNL	CIDDPMRWDS
TCTMLENALE	QKSAFSLMNE	HDPDSVLCPS	DLEWERLGTI	VEFLKVFVEV
INAF TKSSCL	PANMYFPEVC	DIHLRL IEWS	KNPDDFISSL	VVNMRRKFDD
FWDKNYLVLA	IATILDP RFK	MKLVEYYYPL	FYGTSA SELI	EDISECIKLL
YDEHSVGSLL	ASSNQALDWQ	NHHHRSNGVA	HGKEPDDRLT	EFDRYINETT
TTPGQDSKSD	LEKYLEEPLF	PRNSDFDILN	WWKVHTPKYP	ILSMMARNVL
AVPMLNV SSE	EDAFETCQRR	RVSETWRS LR	PSTVQALMCA	QDWIQSELES
S				

AtChr1@26346412@26348515 (100%), 81,381.4 Da

| potential novel

3 exclusive unique peptides, 3 exclusive unique spectra, 4 total spectra, 34/701 amino acids (5% coverage)

DFRFCVTWFR	CLNSNYLVKI	LLFVYMCRRQ	KKLMINNEMD	LSDAVIVKSG
RLKSVVWNDF	DRVRKGETYI	AICRHCKKRL	SGSSASGTSH	LRNHLIRCR
RTNGNNNGVA	QYFVKGKKKE	LANERIKDEE	VL SVVNVRYE	HEKEEHEDVN
VVSMGLDQRR	CRFDLARMII	LHGYP L SMVE	DVGFRMFIGN	LQPLFELVAF
ERVESDCMEI	YAKEKHKIFE	ALDKLP GKIS	ISVDVWSGSG	DSDEF LCLAA
HYIDEGWELK	KRVLNFFMVD	PSHSGEMLAE	VIMTCLMEWD	IDRKLFSMAS
SHAPPFSENV	ASKIRDRLSQ	NKFLYCYGQL	FDVSCGVNVI	NEMVQDSLEA
CCDTINIIRE	SIRYVKSSSES	IQDRFNQWIV	ETGAVSERNL	CIDDPMRWDS
TCTMLENALE	QKSAFSLMNE	HDPDSVLCPS	DLEWERLGTI	VEFLKVFVEV
INAF TKSSCL	PANMYFPEVC	DIHLRL IEWS	KNPDDFISSL	VVNMRRKFDD
FWDKNYLVLA	IATILDP RFK	MKLVEYYYPL	FYGTSA SELI	EDISECIKLL
YDEHSVGSLL	ASSNQALDWQ	NHHHRSNGVA	HGKEPDDRLT	EFDRYINETT
TTPGQDSKSD	LEKYLEEPLF	PRNSDFDILN	WWKVHTPKYP	ILSMMARNVL
AVPMLNV SSE	EDAFETCQRR	RVSETWRS LR	PSTVQALMCA	QDWIQSELES
S				

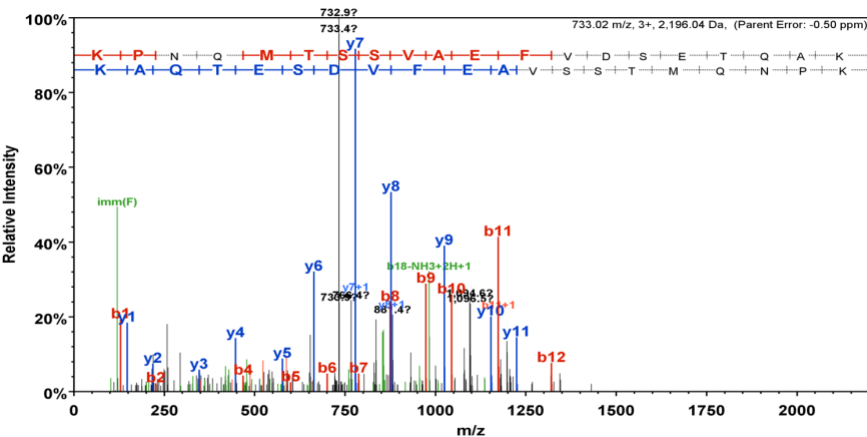
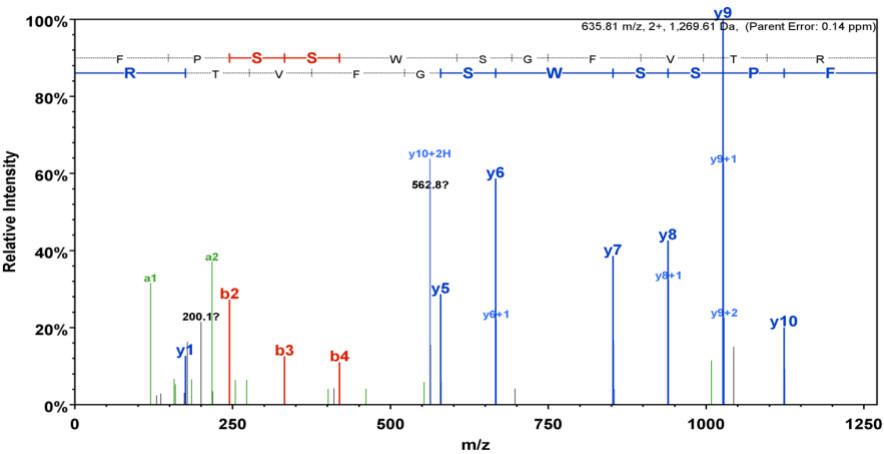
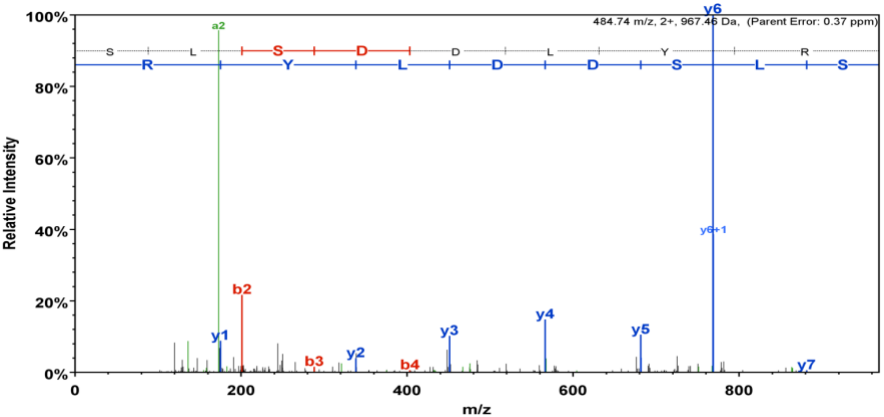
No.10. AtChr3@15403874@15404801: Transposable_element_gene

AtChr3@15403874@15404801 (100%), 35,653.2 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 28/309 amino acids (9% coverage)

A F P V K E Y V R M	L P Y S C S P F G V	L Y S L D R I S C C	R T P N G N A C E A	L D T R S S S T H G
F S L I E T W R F D	G R S Y L S W A S E	M E L F L K Q M K L	A Y V L S E P Y P G	I G S G S S Q D W L
R D D Y L C H N H L	M K S L S D D L Y R	Q Y L K R F K H A K	E L W E E L K W V Y	R R E E S N S K M V
Q V R K Y I D F K M	V E E R P V L E Q V	Q E F I K I A D S I	V G A G M V L D E T	F Y V S T I I S K F
P S S W S G F V T R	L M E E E F L T V C	M L V E R L K A E E	E F L R S G K K R V	T V S A A T G S S Q
I E M R P S L G T M	H T G S Q S V S S K	R K E P E R D I I P	E E K A P K K P N Q	M T S S V A E F V D
S E T Q A K N Q H				



No. 11. AtChr5@13104627@13107087: Transposable_element_gene

AtChr5@13104627@13107087 (100%), 91,881.4 Da

| potential novel

4 exclusive unique peptides, 4 exclusive unique spectra, 5 total spectra, 66/820 amino acids (8% coverage)

SISVFNCRSY	NIAIGTETTP	VAYGNVANVP	IQVITGTPEE	NNLADINLSS
RKVAPR VTSE	SSGLIDIPVT	ISTIPVGPAK	STSKKFKTKG	KNSLVSNIITN
LTPKSLKQTF	IGSNPGSKSS	PPTSLSVVCG	VTTSSPRSVS	KRRRVMEERI
ILLQDENVTD	TRRRSLRNRG	EIRKPVIEDT	DDDVDADVD	SDEDDSDVD
ADNVEDDDDK	DYVQDIETYY	PETEDLDYER	EINYSISEAN	DGSVESLVAS
WKRCITGVGQ	GFESVVEFRD	ALQKYAVACR	FGYRLRKNES	NRACGVCLVG
GCPWK IYASW	VPSESVER IK	KFNRRHTCGG	ESWKSAPPK K	NWVVGIIKER
LQENPNQKTK	NIADSFQDF	GIELSYCTIR	RGIDEAKGGL	HTSFKEAYKY
LPHFVNKVVE	ANPGSMVNLV	VGEDRRFQRL	FLSFQSCIHG	FQTGCRPLLF
LDAIPFKSRY	HEILLTASAL	DGDDCVLPVA	LALVDVETDE	TWRWFLEQLK
VALSSLRPLT	FVSDREKGLV	TSVLEIFENA	HHGYSIHYLM	EDFMRSRLR GP
FLGDGKPSLT	YYLLAAAR AD	RLDGFKVYTE	QIRRVSPRAY	DWVMQIESKH
WACALFEGEP	YSHITSDVAE	IYSKWIIEIQ	ETSIQKLVA	FVNKIVELVN
SSQEKSKPWF	SQLVPSKEES	LVEECKKAGS	LKVFFCSDTL	FEVHDGSVQL
VDISNQTCS	FGWKPTGLPC	QHAIAVLNTK	GRNLYDYCSS	FFTVDSYRLT
YSVALGAVAI	DLALVENEGS	GKEEDEQVLP	PLFSRVQGVE	KRIKDRKRGR
SVCCTKCGGV	GHNKATCKDD			

AtChr5@13104627@13107087 (100%), 91,881.4 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 37/820 amino acids (5% coverage)

SISVFNCRSY	NIAIGTETTP	VAYGNVANVP	IQVITGTPEE	NNLADINLSS
RKVAPR VTSE	SSGLIDIPVT	ISTIPVGPAK	STSKKFKTKG	KNSLVSNIITN
LTPK SLKQTF	IGSNPGSKSS	PPTSLSVVCG	VTTSSPRSVS	KRRRVMEERI
ILLQDENVTD	TRRRSLRNRG	EIRKPVIEDT	DDDVDADVD	SDEDDSDVD
ADNVEDDDDK	DYVQDIETYY	PETEDLDYER	EINYSISEAN	DGSVESLVAS
WKRCITGVGQ	GFESVVEFRD	ALQKYAVACR	FGYRLRKNES	NRACGVCLVG
GCPWK IYASW	VPSESVER IK	KFNRRHTCGG	ESWKSAPPK K	NWVVGIIKER
LQENPNQKTK	NIADSFQDF	GIELSYCTIR	RGIDEAKGGL	HTSFKEAYKY
LPHFVNKVVE	ANPGSMVNLV	VGEDRRFQRL	FLSFQSCIHG	FQTGCRPLLF
LDAIPFKSRY	HEILLTASAL	DGDDCVLPVA	LALVDVETDE	TWRWFLEQLK
VALSSLRPLT	FVSDREKGLV	TSVLEIFENA	HHGYSIHYLM	EDFMRSRLRGP
FLGDGKPSLT	YYLLAAAR AD	RLDGFKVYTE	QIRRVSPRAY	DWVMQIESKH
WACALFEGEP	YSHITSDVAE	IYSKWIIEIQ	ETSIQKLVA	FVNKIVELVN
SSQEKSKPWF	SQLVPSKEES	LVEECKKAGS	LKVFFCSDTL	FEVHDGSVQL
VDISNQTCS	FGWKPTGLPC	QHAIAVLNTK	GRNLYDYCSS	FFTVDSYRLT
YSVALGAVAI	DLALVENEGS	GKEEDEQVLP	PLFSRVQGVE	KRIKDRKRGR
SVCCTKCGGV	GHNKATCKDD			

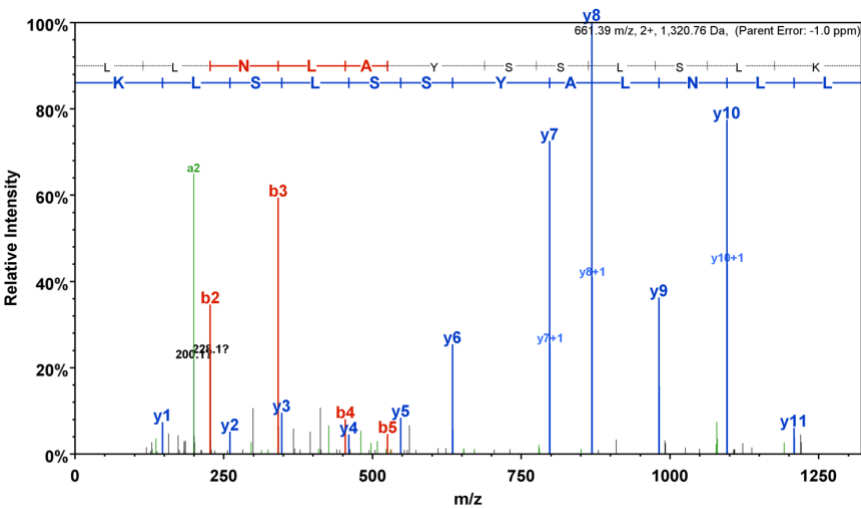
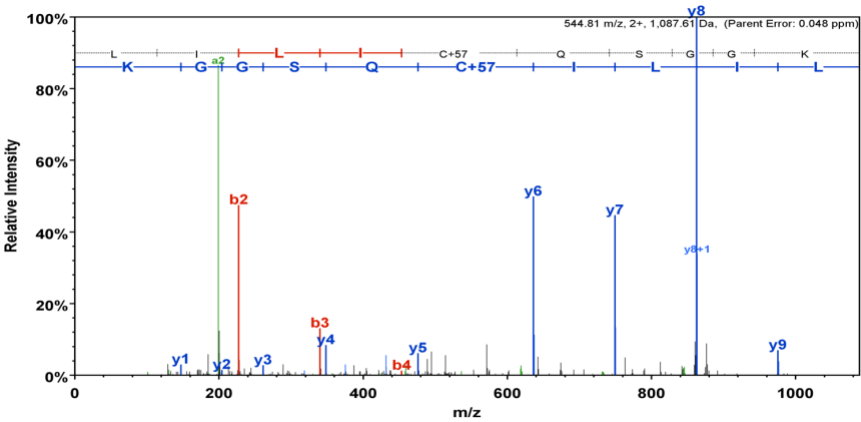
No. 12. AtChr5@13103632@13104208: Transposable_element_gene

AtChr5@13103632@13104208 (100%), 21,974.1 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 5 total spectra, 22/192 amino acids (11% coverage)

CNFFLPFRVP	QVSVGMGKGK	LILICQSGGK	FVTDDDGTMT	YTGGEAEAID
INHETTFDDF	KLKLAKLLNL	AYSSLSLK YF	LPGNRRTLIT	MKQEKDMKRM
YDFHLSSVTA	EVFITGQYGF	QSEAVLSPGT	RYSLLFNHVS	CRNFFSLYRF
RSFLFYFNLS	LPENVVDVSV	LHHLRNNNVM	ITDNLLSHLF	ES



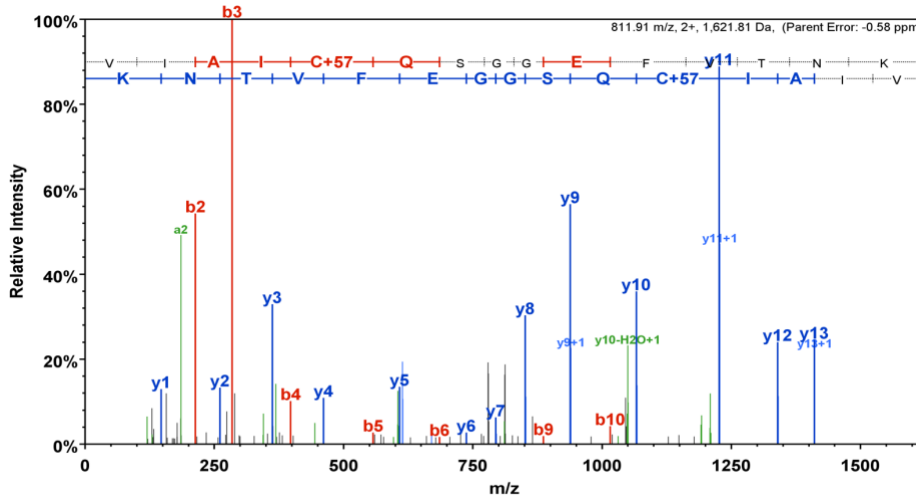
No. 13. AtChr3@18791524@18795901: Transposable_element_gene

AtChr5@19854197@19854566 (100%), 13,673.0 Da

| potential novel

1 exclusive unique peptides, 1 exclusive unique spectra, 2 total spectra, 15/123 amino acids (12% coverage)

RFLVMATKK**V** **IAICQSGGEF** **VTNK**DGSLAY SGGDAYAIDI DQDTCMSDFK
SELAENFGFS WENMTLKYFL PGNKKTLLITI SKDKDFQRMV SFSADAPNVE
IFVLPEEAEA RNVSNMPASR CVF



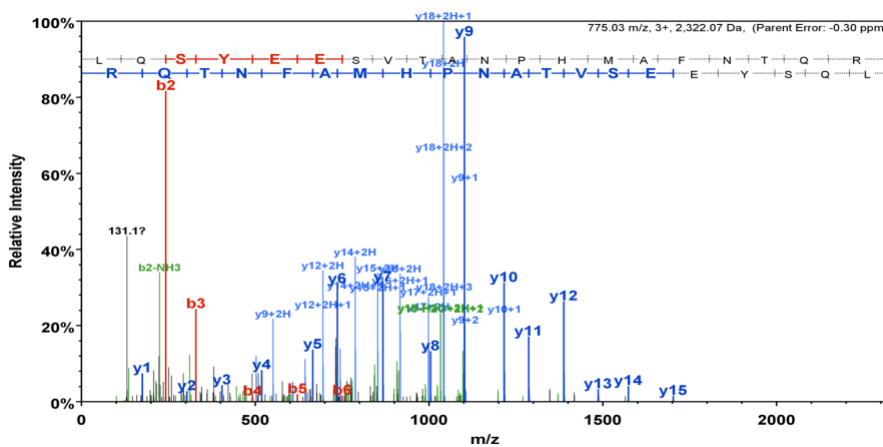
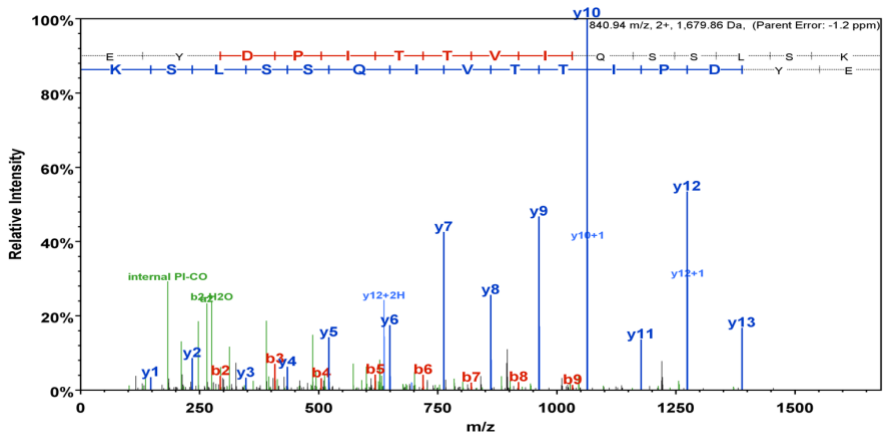
No. 14. AtChr3@18791524@18795901: Transposable_element_gene

AtChr3@18791524@18795901 (100%), 164,046.9 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 4 total spectra, 35/1459 amino acids (2% coverage)

[illegible]



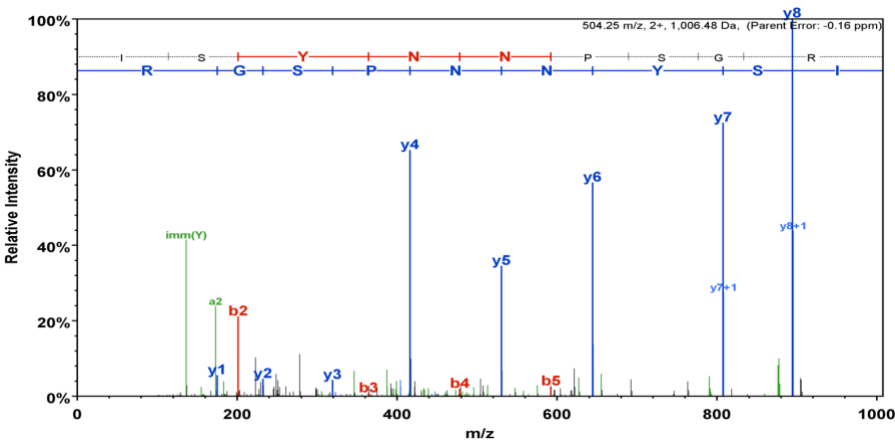
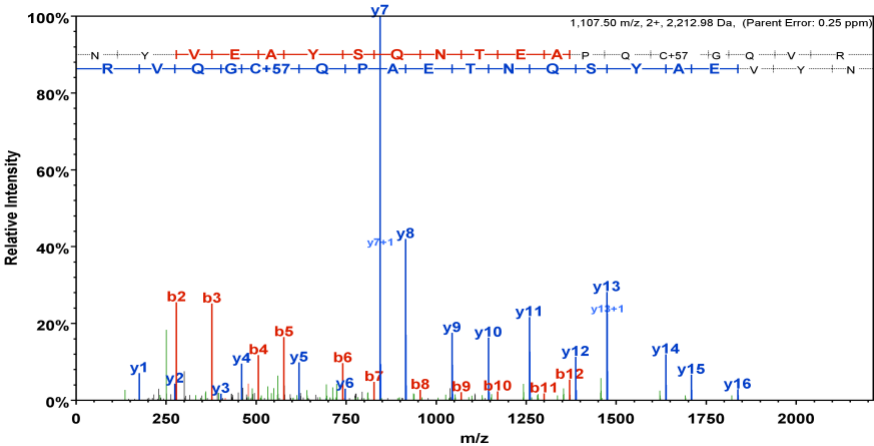
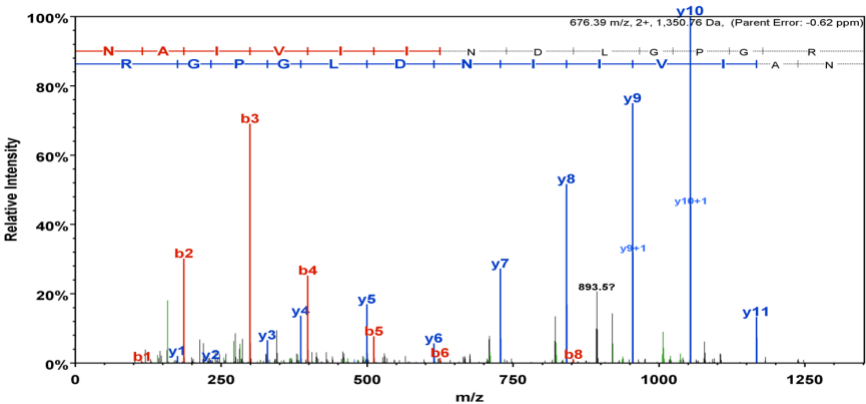
No. 15. AtChr4@7689781@7690192@0: Novel_transcribed_region

AtChr4@7689781@7690192@0 (100%), 16,144.3 Da

| potential novel

1 exclusive unique peptides, 1 exclusive unique spectra, 9 total spectra, 41/137 amino acids (30% coverage)

I R E M L R L I F F I L V T A I C S T K T E A C E K **N A I V** **I I N D L G P G R** I L Q Y H C R Y T K K
D L G V Q H L N F H A I K T I H L Q D E G K N I T K W H C L F K Q G L N M R Y R **N Y V E A Y S Q N T**
E A P Q C G Q V R V W T A R M S G I W F K **I S Y N N P S G R** Y I R G W K Y



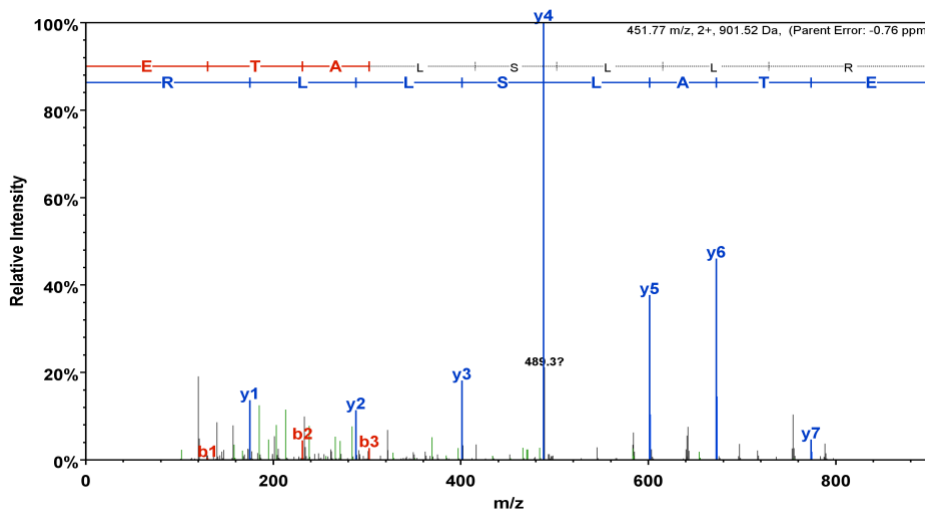
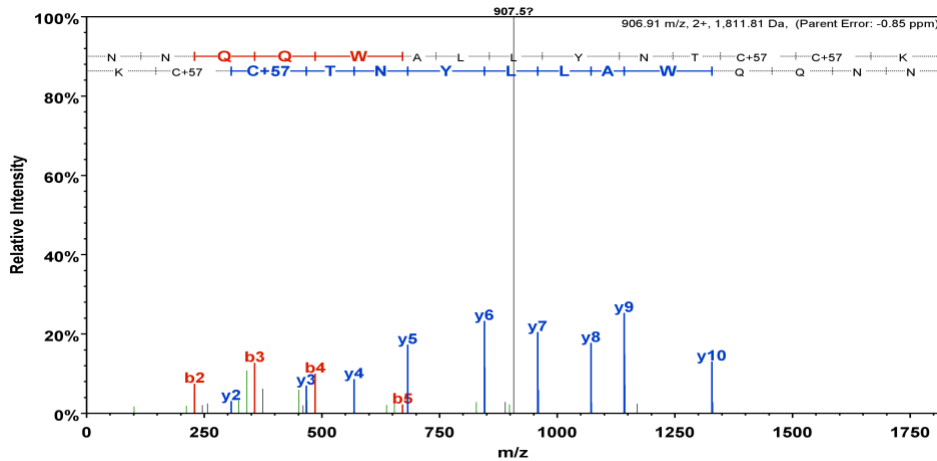
No. 16. AtChr5@10277623@10277968: Novel_transcribed_region

AtChr5@10277623@10277968 (100%), 13,016.9 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 4 total spectra, 22/115 amino acids (19% coverage)

NKTISYSITL SFLIATNLFM LNMKTIPLMF IALIILSISF LAPIKAQGIV
GCDVELDKCV VMR**NNQQWAL** **LYNTCCK**KFK KPGPQPCMCL FFKYPTPK**ET**
ALSLLRYCKA PIPKC



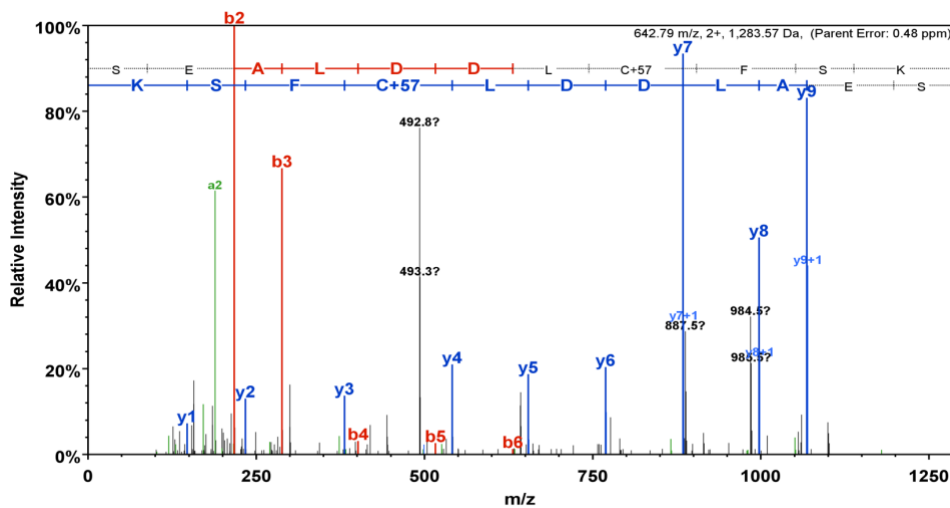
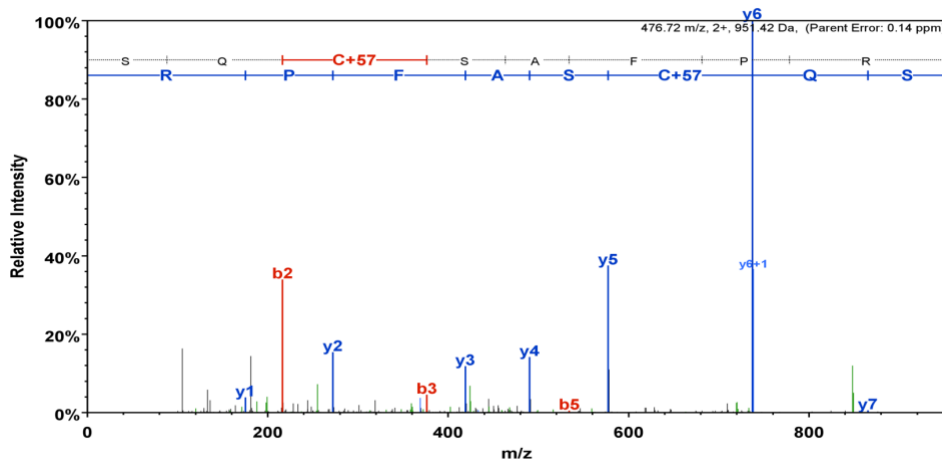
No.17. AtChr1@10428741@10429146: Antisense_long_noncoding_rna

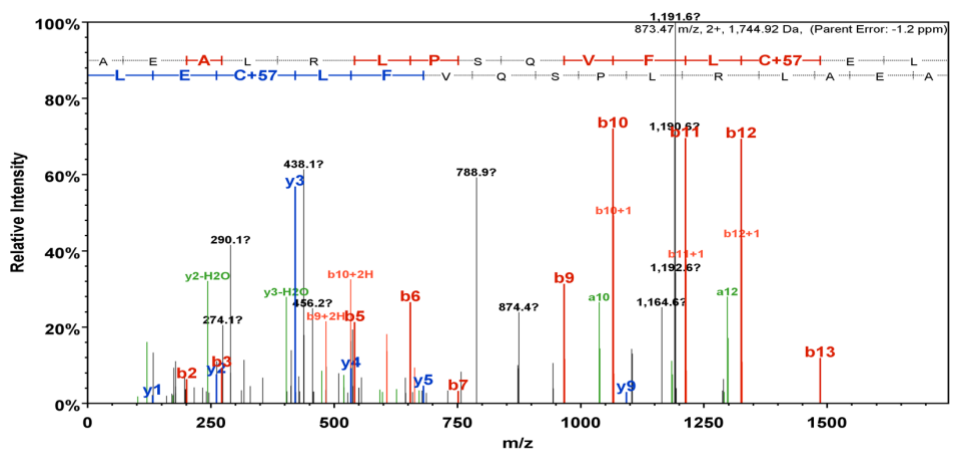
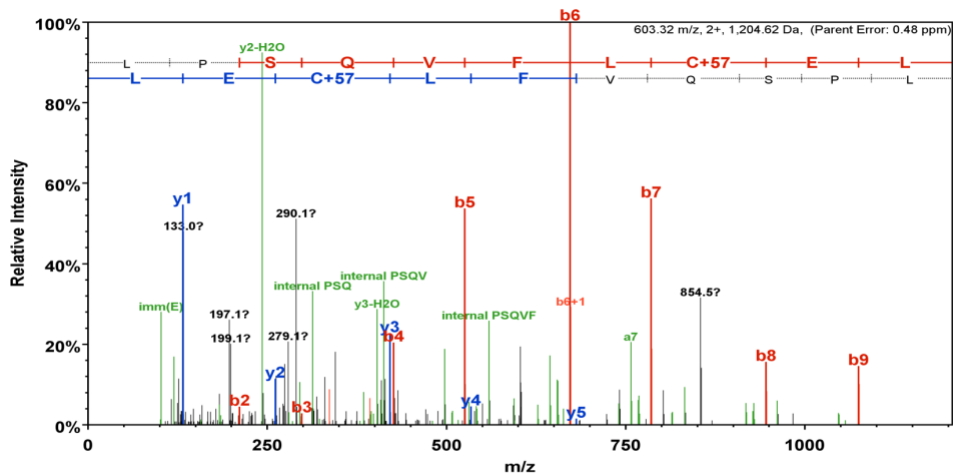
AtChr1@10428741@10429146 (100%), 15,336.7 Da

| potential novel

3 exclusive unique peptides, 3 exclusive unique spectra, 3 total spectra, 29/135 amino acids (21% coverage)

ANSRKILTLF PFSLSSTQKKR QLSKNTDSTV SMPESSSSSFS SLFLLLIIF
 LLLLSPSLSS PESEVHVLDR ELLEIQTNPK PGKTNRKLC CEMRSR **SQCS**
AFPR CRWCR **S** **EALDDLCFSK** AEALR **LPSQV** **FLCEL**





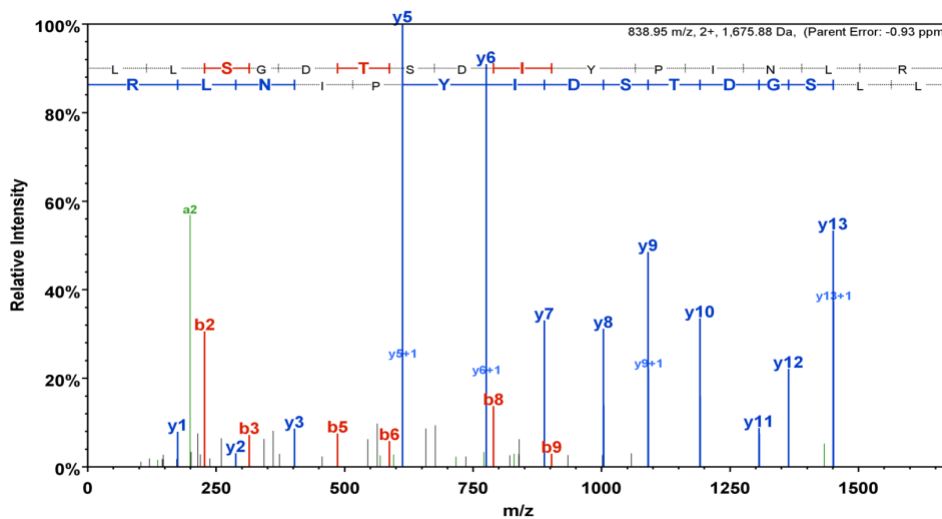
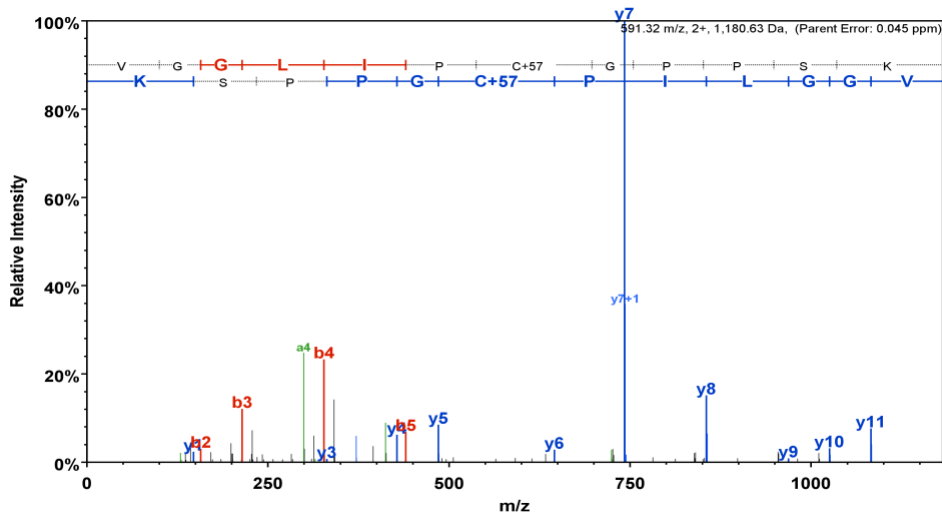
No. 18. AtChr4@9188288@9188534: Long_noncoding_rna

AtChr4@9188288@9188534 (100%), 9,087.1 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 5 total spectra, 27/82 amino acids (33% coverage)

F D I V G F E S E K I P C C S L V G K V G G L I P C G P P S K V C M D R S K Y V F W D P Y H P T E A
A N I I I I A R R L L S G D T S D I Y P I N L R Q L A N L K I Y A



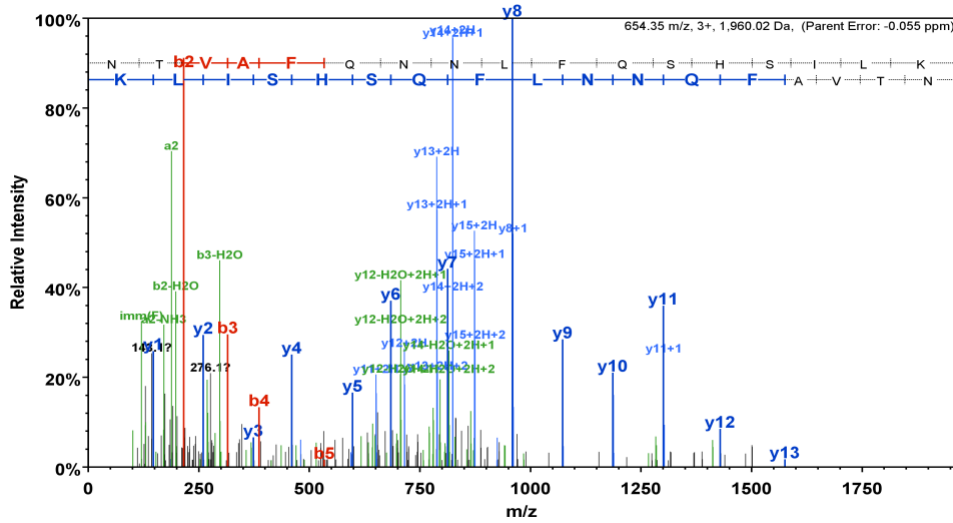
No. 19. AtChr3@3253541@3253958: Long_noncoding_rna

AtChr3@3253541@3253958 (100%), 16,526.7 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 3 total spectra, 27/139 amino acids (19% coverage)

FKIMNLVFSF LFFIFVLCCV SKEDKCHKNT VAFQNNLFQS HSILKVHCKS
R SDDLGEHFV KFQDTAYNFS FHDNLLFTTI FKCNLWKGAR MEYHRNITAY
EGDLLYRCGA LYSWDIRDDA IYLSENDNPE KLMYSWIKG



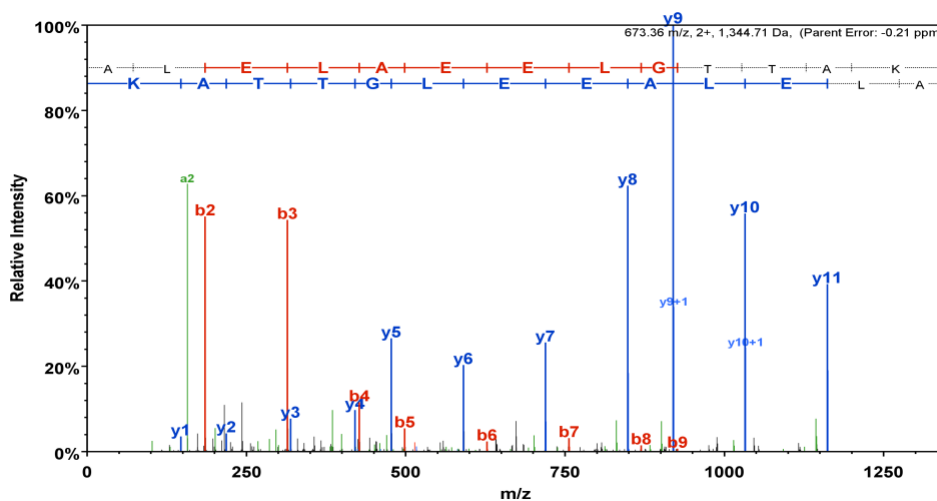
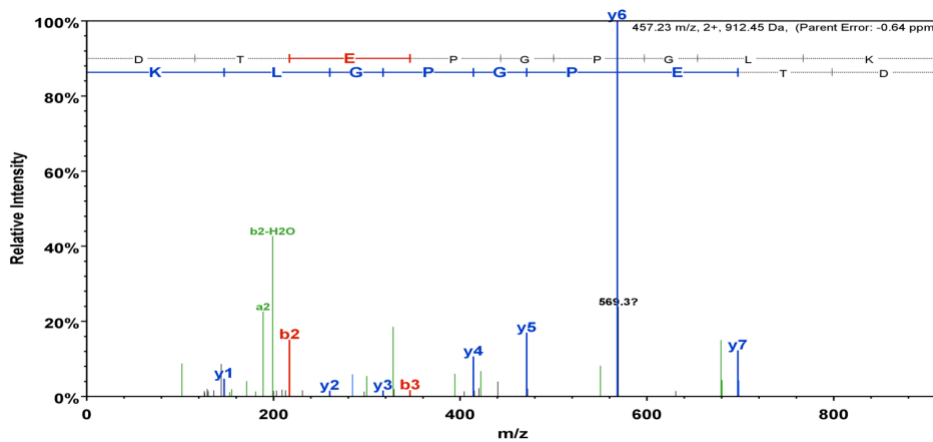
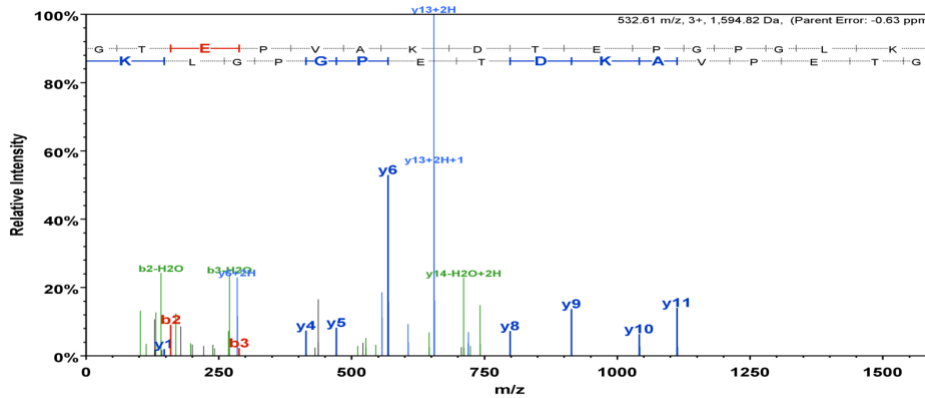
No. 20. AtChr5@26518786@26519188: Arabidopsis thaliana drought-induced 8

AtChr5@26518786@26519188 (100%), 14,782.2 Da

| potential novel

3 exclusive unique peptides, 3 exclusive unique spectra, 8 total spectra, 29/134 amino acids (22% coverage)

LSSKCLLKTR RTWRLTRTVQ EVRPLTSTET RSSSSMTSTE IRWEEEDTEL
VVVEELQVAK DTEQVAKGTD QVAK**GTEPVA** **KDTEPGPGLK** **ALELAEEELGT**
TAKSNSTRKV VVAWEECFTA PDLDPALARY VSSV



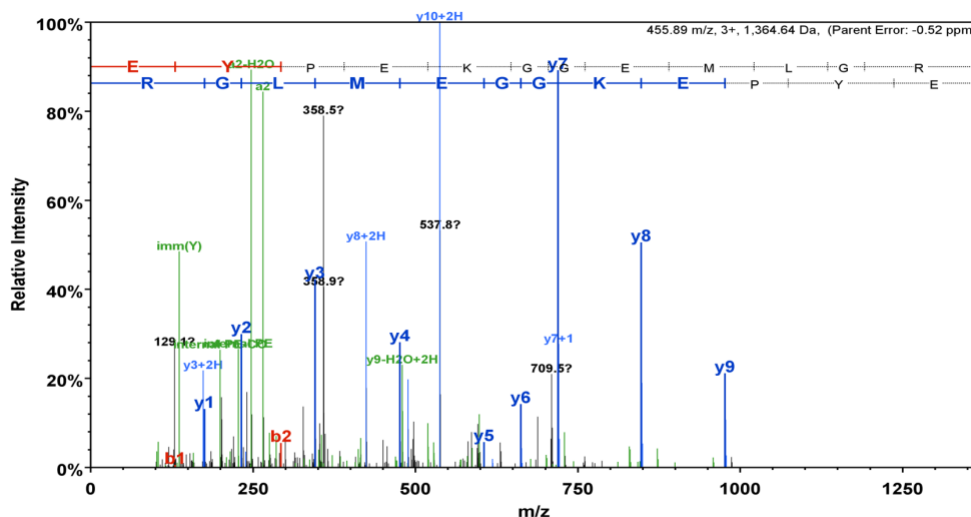
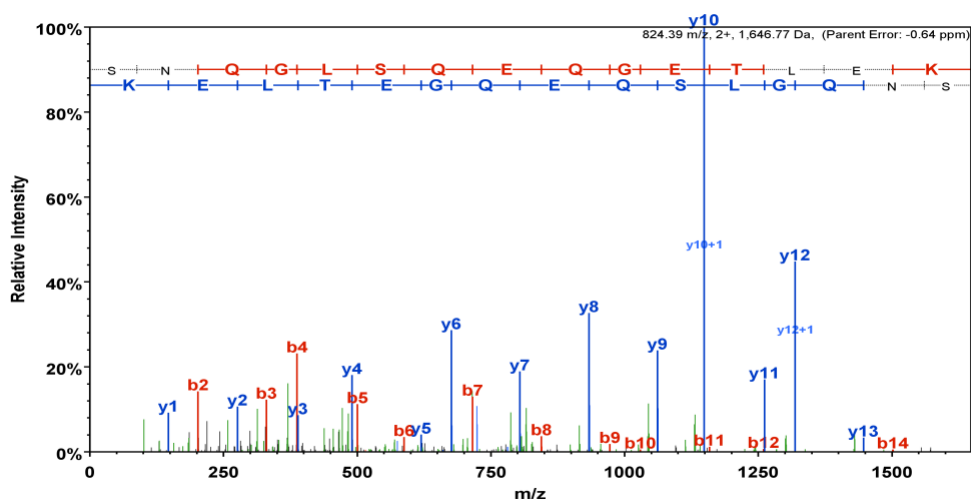
No. 21. AtChr2@17714928@17715315: Late embryogenesis abundant 25

AtChr2@17714928@17715315 (100%), 14,747.1 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 4 total spectra, 27/129 amino acids (21% coverage)

L I V V W W C F V L L K K L C F G F V L R E V R K K S N Q G L S Q E Q G E T L E K S T G K K E G V R
 K M S T A M E Q K E Y P E K G G E M L G R Q S T E E G V R K M S S D M D Q K A R S K K Q G E T L E K
 N T E E E E A V R D M L K K K G L E R E G C L G Q S A R L



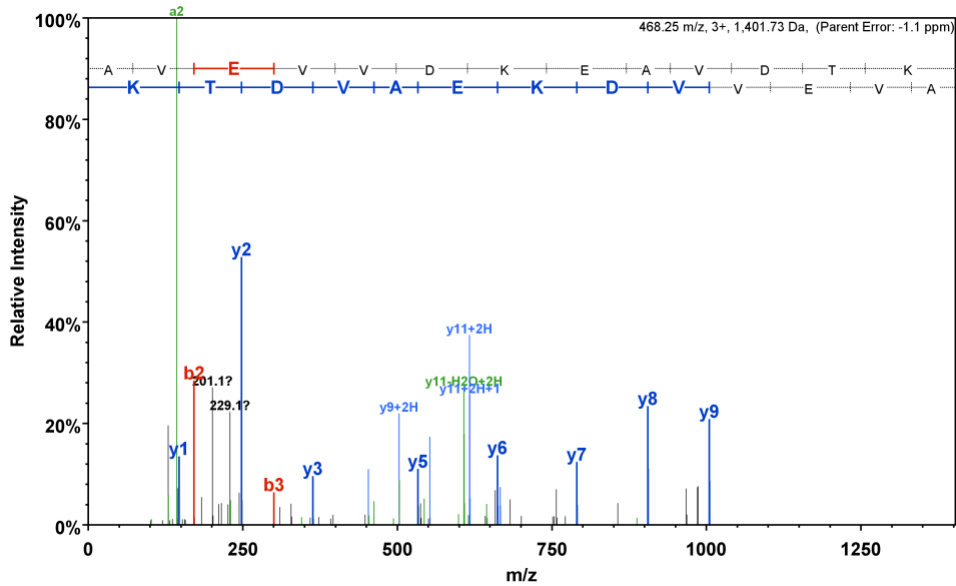
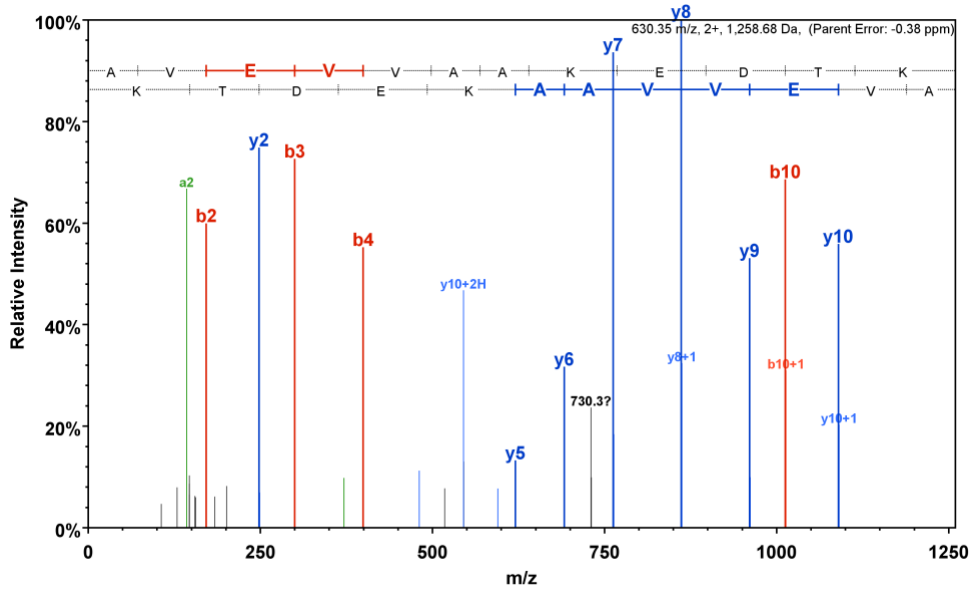
No. 22. AtChr2@2056255@2056639: Glycine-rich protein family

AtChr2@2056255@2056639 (100%), 13,590.1 Da

| potential novel

2 exclusive unique peptides, 2 exclusive unique spectra, 2 total spectra, 25/128 amino acids (20% coverage)

```
RAAVAAAKED  IRAAEVVVAK  EDTK AVEVVA  AKEDTKAVEV  VDKEAVDTKA
AVVAKEDTKA  VEEVVMLVEA  AEEVEVEVVG  VVEAEVEEVV  EVAVEVEEAV
GCRISLPILA  SFSLNAKCLR  ILNYNKVT
```



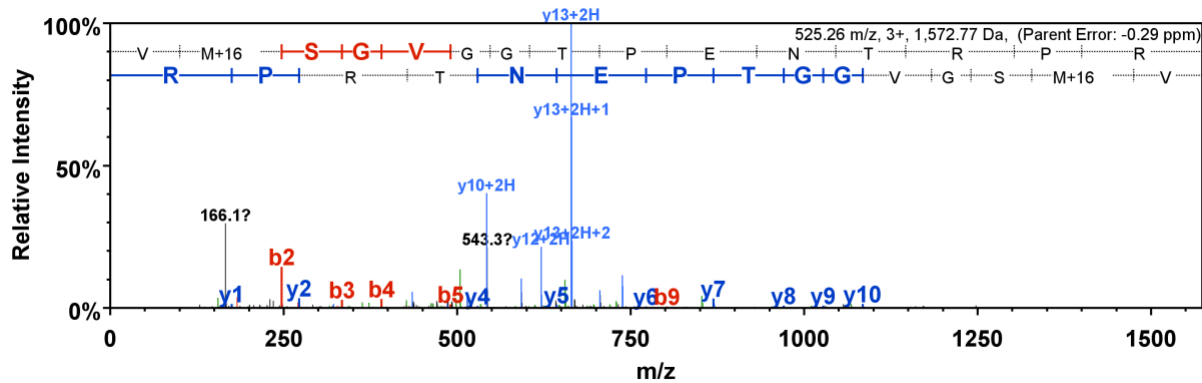
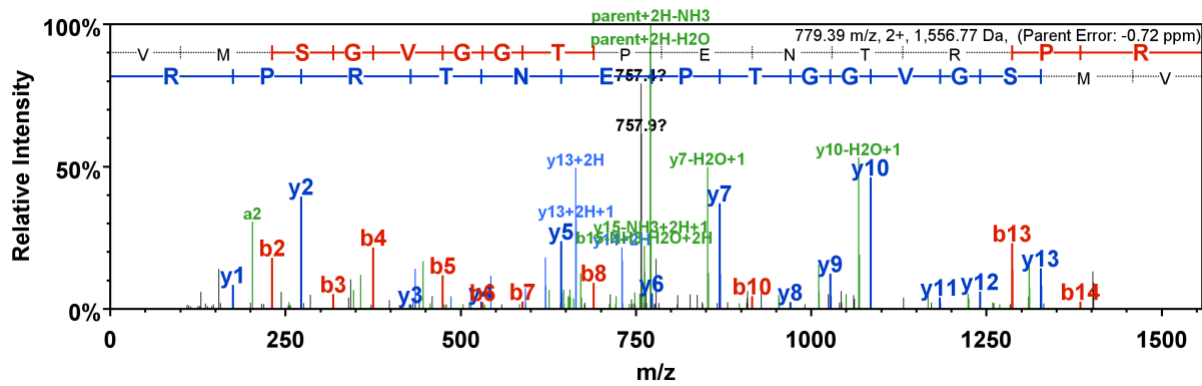
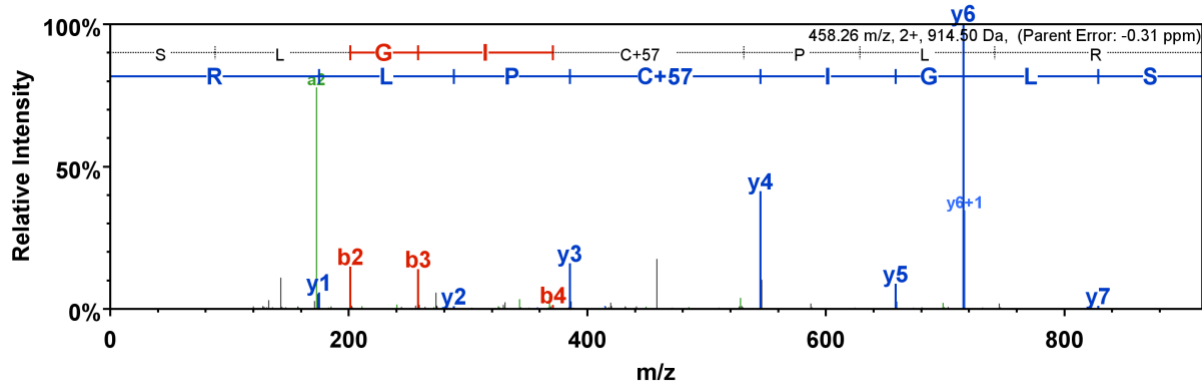
No. 23. AtChr4@6693384@6693678: Plant self-incompatibility protein S1 family

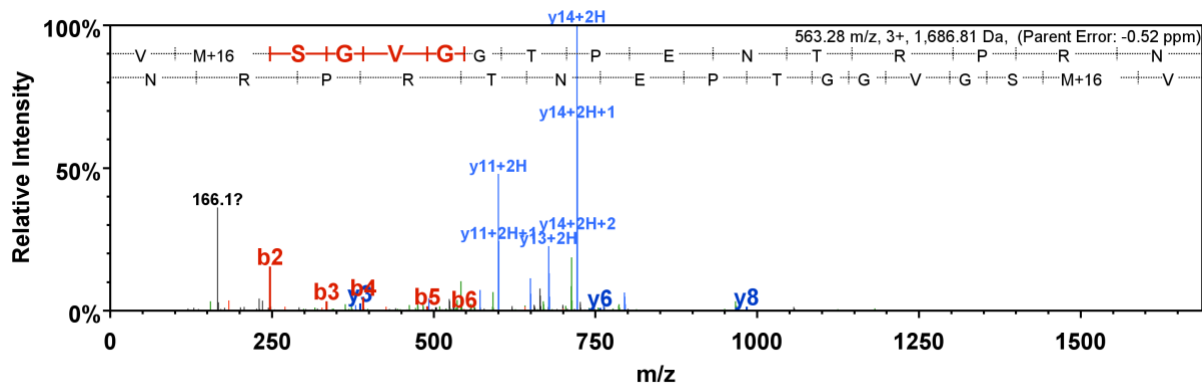
AtChr4@6693384@6693678 (100%), 10,554.5 Da

| potential novel

3 exclusive unique peptides, 5 exclusive unique spectra, 7 total spectra, 24/98 amino acids (24% coverage)

LLREIDKFTL IERYIHHRQ RREMAGPAQA AKQSSEVLGQ RKSLGICPLR
AAAVGAVIIG GIGYVVLYSK KKPEASAGDV AKVMSGVGGT PENTRPRN





No. 24. AtChr5@7534553@7534787: Arabidopsis histone deacetylase 2

Peptide (**SPNIEQYPFFDRFD**) is the novel identification, it is not in AT5G22650.1 from TAIR10 and TAIR11.

AT5G22650.1 (100%), 32,347.6 Da

| Symbols: HD2B, HDT02, HDT2, ATHD2B, HDA4, HD2, ATHD2 | histone deacetylase 2B | chr5:7534120-7536054 FORWARD L
3 exclusive unique peptides, 5 exclusive unique spectra, 52 total spectra, 98/306 amino acids (32% coverage)

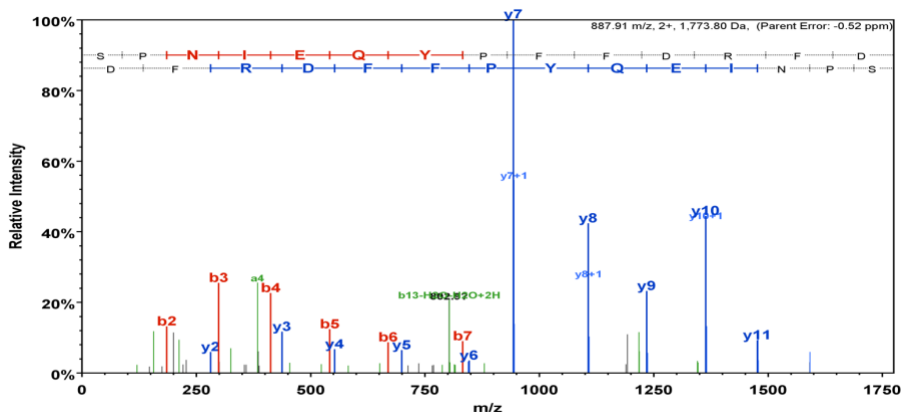
MEFWGVAVTP	KNATKVTPEE	DSLVIHSQAS	LDCTVKSGES	VVLSVTVGGA
KLVI GTLSQD	KFPQISFDLV	FDKEFELSHS	GTKANVHF IG	YKSPNIEQDD
FTSSDDEDVP	EAVPAPAPTA	VTANGNAGAA	VVKADTKPKA	KPAEVKPAEE
KPESDEEDES	DDEDESEEDD	DSEKGMVDVE	DDSDDEEED	SEDEEEETP
KKPEPINKKR	PNESVSKTPV	SGKKAKPAAA	PASTPQKTEE	KKKGGHTATP
HPAKKGGK SP	VNANQSPK SG	GQSSGGNNNK	KPFNSGKQFG	GSNNKGSNKG
KGKGRA				

AtChr5@7534553@7534787 (100%), 8,603.8 Da

| potential novel

1 exclusive unique peptides, 1 exclusive unique spectra, 42 total spectra, 70/78 amino acids (90% coverage)

ASLDCTVK SG	ESVLSVTVG	GAKLVIGTLS	QDKFPQISFD	LVFDKEFELS
HSGTKANVHF	IGYKSPNIEQ	YPFFDRFD		



No. 25. AtChr1@20390129@20390324: Acyl carrier protein 3

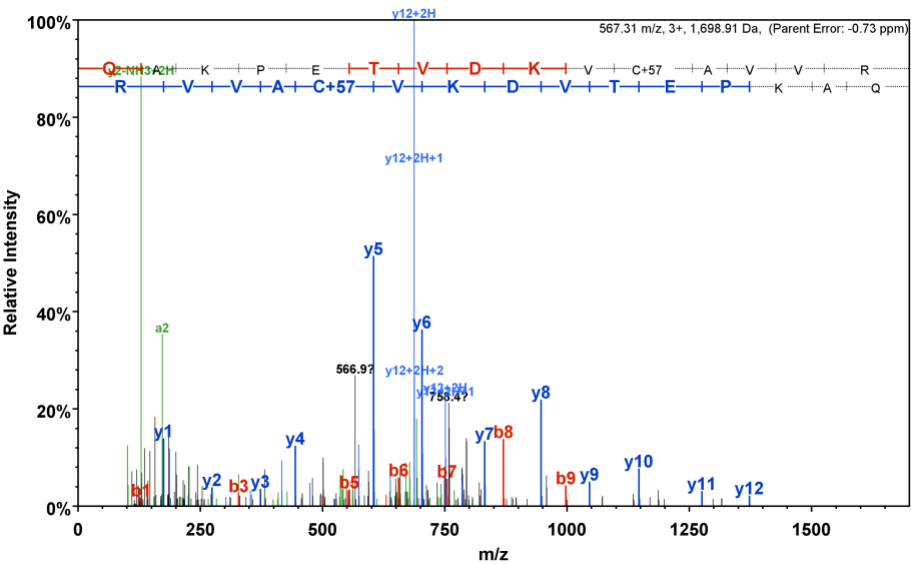
Peptide (QAKPETVDKVCVVVR) is the novel identification. It is not present in AT1G54630.1 from TAIR10 and TAIR11.

AT1G54630.1 (100%), 14,650.2 Da
| Symbols: ACP3 | acyl carrier protein 3 | chr1:20401642-20402919 REVERSE LENGTH=136
1 exclusive unique peptides, 1 exclusive unique spectra, 36 total spectra, 37/136 amino acids (27% coverage)

MAS	IATS	SAST	SLQ	ARPR	QLV	IGAK	QVK	SFS	YGSR	SNLS	SN	LRQL	PTRL	TV
YCA	AKPE	TVD	KVC	AVVR	KQL	SLKE	ADE	ITA	ATK	FAAL	GAD	SLDT	VEIV	MG
LEEE	FGIE	MA	EEL	AQSI	IATV	EQAA	ALIE	EEL	LLEK	AK				

AtChr1@20390129@20390324 (100%), 7,064.8 Da
| potential novel
1 exclusive unique peptides, 1 exclusive unique spectra, 21 total spectra, 31/65 amino acids (48% coverage)

LGSL	IIRL	GDW	LIY	ISIF	LLL	CK	QAKPETVD	KVC	AVVR	KQL	SLKE	ADE	ITA
ATK	FAAL	GAD	SLDT	V									



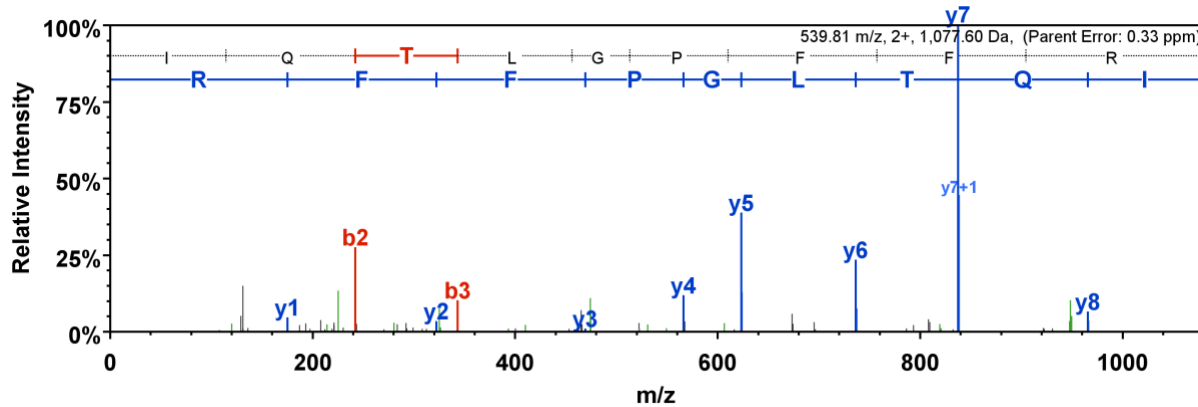
No. 26. AtChr1@18512092@18512548: DNA/RNA polymerases superfamily protein

AtChr1@18512092@18512548 (85%), 16,579.7 Da

| potential novel

1 exclusive unique peptides, 1 exclusive unique spectra, 6 total spectra, 9/152 amino acids (6% coverage)

RNPEEMKMAL SPPKLILSPS NSLGDSNSLP SMSDILTSSK ARKLDLK **IQT**
LGPFFRVTGK NADTGGEVGR AEGVVRPWFG RGLVLHLDTI RLTKETVAMD
 KSVLGVGLYV GAVAIRHGYD CGCRTAQLLA IYDSDLYHSK VSLSLHNSFY
 RN



No. 27. AtChr2@15278911@15279358: Transcriptional activator (DUF662)

Peptide (**STEDSSSCFGLR**) is the novel identification. It is not present in AT2G36410.1 from TAIR10 or TAIR11.

AT2G36410.1 (100%), 22,347.1 Da

| Symbols: | Family of unknown function (DUF662) | chr2:15279041-15280270 FORWARD LENGTH=195

2 exclusive unique peptides, 2 exclusive unique spectra, 10 total spectra, 55/195 amino acids (28% coverage)

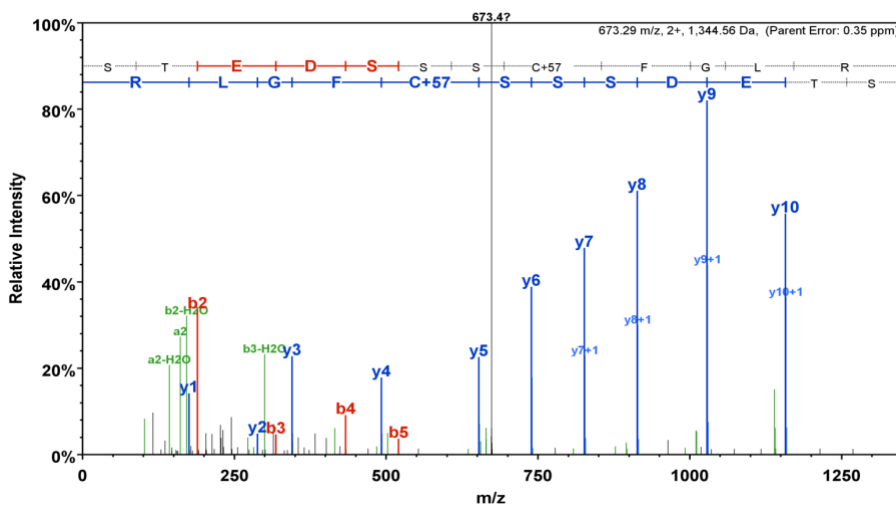
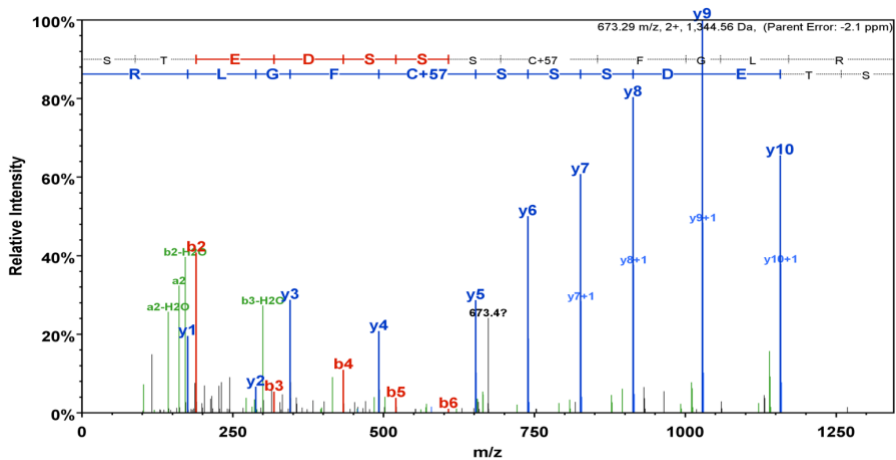
MTQSQTNDGA GAGAVTTVES VPPQPQSQPQ PQQPQQSNEM VLHTGSLSF
 SHMSREDEEM TRSALSAFRA KEDEIEKRRM EVRERIQAQL GRVEQETKRL
STIREELES **ADPMRKEVSV** VRKKIDSVNK **ELKPLGSTVQ** **KKEREYKEAL**
DTFNEKNREK VQLITK**LMEM** **EQLVGESEKL** RMIKLEELSK SIETV

AtChr2@15278911@15279358 (100%), 16,765.7 Da

| potential novel

1 exclusive unique peptides, 1 exclusive unique spectra, 4 total spectra, 25/149 amino acids (17% coverage)

NTPKSAKIGL IEEPHRK**STE** **DSSSCFGLR**K KNSKNLKEKK KSKMTQSQT
 DGAGAGAVTT VESVPPQPQS QPQPQPQQQS NEMVLHTGSL SFSSHMSRED
 EEMTRSALSA FRAKEDEIEK RRMEVRER**IQ** **AQLGRVEQET** **KRLSTIREV**



No. 28. AtChr5@21376666@21377527: DNA/RNA polymerases superfamily protein

Peptide (**IDPLIIQGLDGK**) is the novel identification. It is not present in AT5G52710.1 from TAIR10 or TAIR11.

AT5G52710.1 (100%), 48,127.5 Da

| Symbols: | Copper transport protein family | chr5:21375753-21377841 FORWARD LENGTH=423

5 exclusive unique peptides, 5 exclusive unique spectra, 13 total spectra, 131/423 amino acids (31% coverage)

MSNPHYNLKT	QEKTAEFKLD	VSDENIRRNT	MK	IVWMFPVT	FVDIKEKGIL
KVRGKFDHIE	MREILQQHID	ESVDLINPMK	KSEK	KQIPGL	ATVFNYFKTP
ATQEIVVFEF	RVLDERIIPK	AMEVIWEFPV	TSVE	IENDFY	LKVKGGEINK
EVMKTQLKDV	DKHVKIKWHG	QDVEEEPKKQ	SEAGGSKLQP		EQLSKKKNIY
EDAYGEHLKK	RQGINQAKQP	AFYDDWLLLE	AHGPFNQQQG		FKQENLLPIY
GGAHAQGLYK	QNANKVFQPP	PK	GGFAALNL	GEK	KKQAEVK
NMFGNQPPQV	KQEFRGKREN	QHAQRIDPLI	IQEF	GSSSTR	NRSSFSSSS
AMDLSQTTSS	SSVAYSSYST	TPNSSR	NSSH	SRSR	SSENLS
YTSSQSNTAS	GSK	QGQSSKK	PGK		QFQSNSTGNS

AtChr5@21376666@21377527 (100%), 32,697.2 Da

| potential novel

1 exclusive unique peptides, 1 exclusive unique spectra, 15 total spectra, 56/287 amino acids (20% coverage)

INPCLLLLLL	LLVVTSEIE	NDFYLVKVG	EINKEVMKTQ	LKDVDKHKVI
KWHGQDVEEE	PKKQSEAGGS	KLQPEQLSKK	KNIYEDAYGE	HLK
AKQPAFYDDW	LLEEAHGPFN	QQQGFKQENL	LPIYGGAHQA	GLYKQNAKV
FQPQPKGGFA	ALNLGEKKKQ	AEVK	KQNQDA	GWFGNMFGNQ
KRENQHAQRI	DPLIIQGLDG	KFHAYKEKNN	NPYARSSNGP	TSNNGTSQNL
GINKLVSVYQ	IYFYGITFKI	KFLLLFVVDL	TILAFFC	

