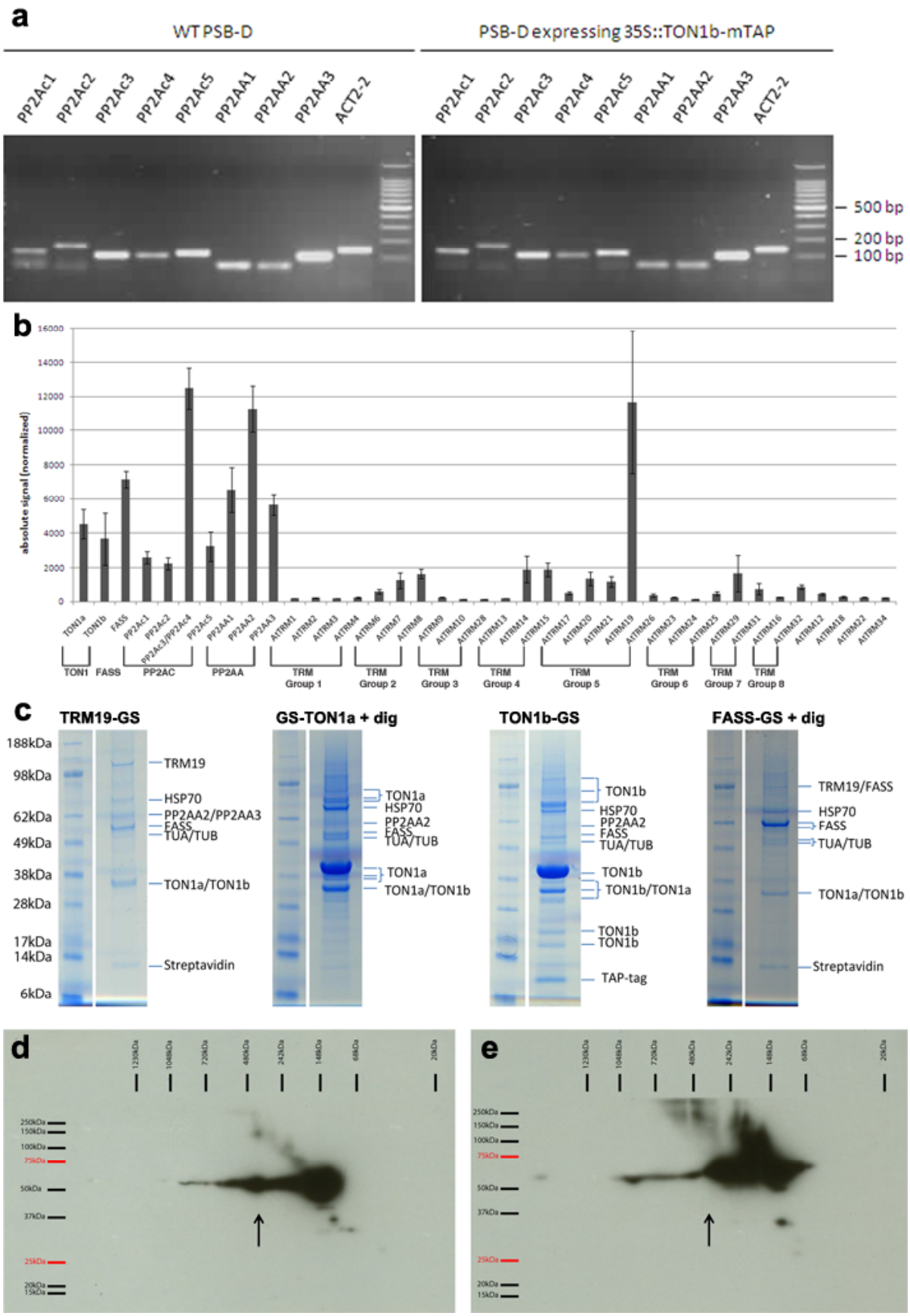
Supplementary Figure S1

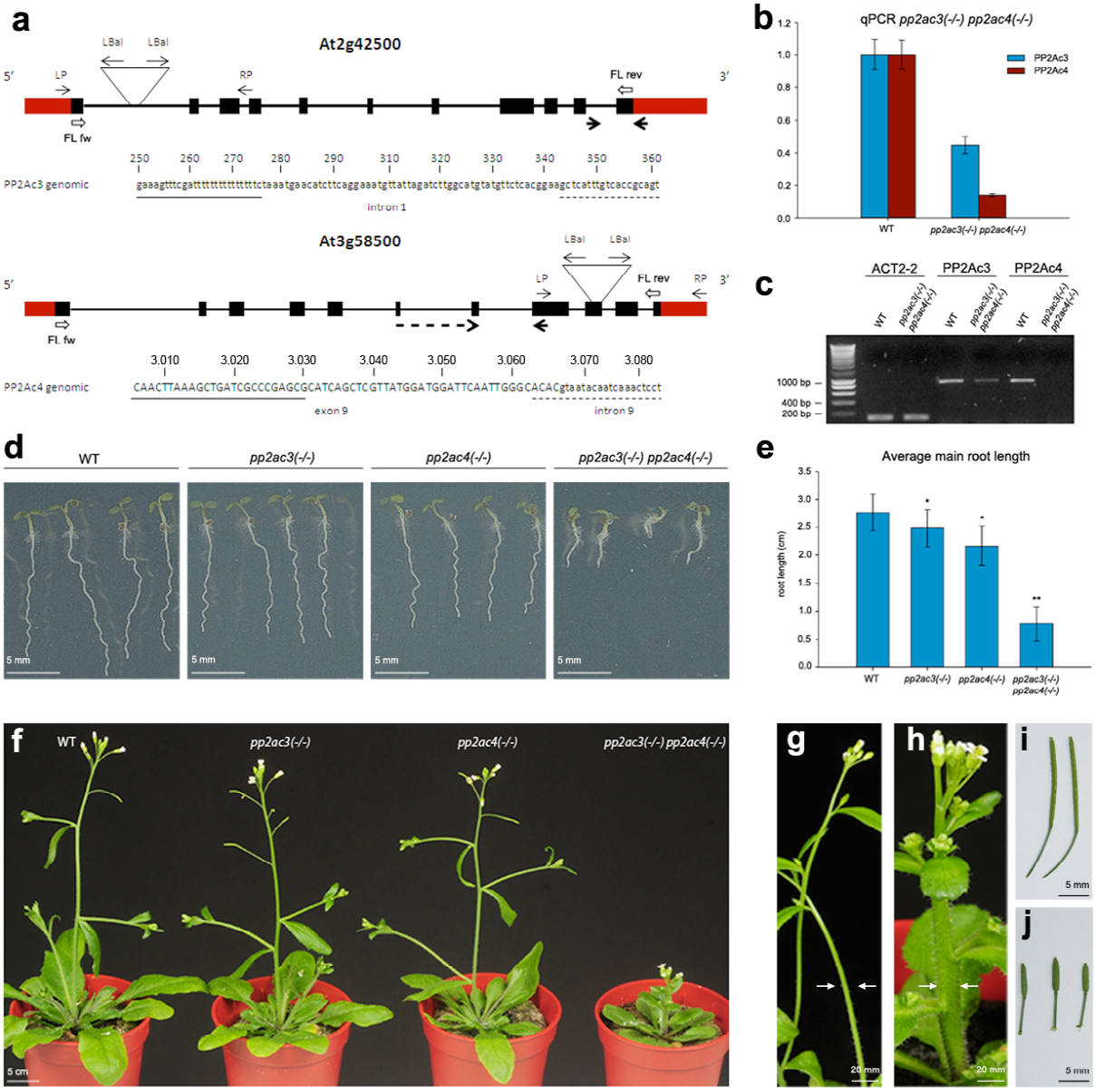


Supplementary Figure S1 : Expression and TAP analysis of TTP members in *Arabidopsis* cell culture

(**a**) RT-PCR analysis of *Arabidopsis* PP2AA and PP2AC subunits in control cells and in Pro35S:TON1b-mTAP expressing cells.
(**b**) Gene expression analysis of the TTP complex genes in *Arabidopsis* cell culture using the Genevestigator tool[61]. No Affymetrix probes are available for the *TRM5, TRM11, TRM27, TRM30* and *TRM33* genes.
(**c**) Representative Coomassie stained gels for all bait proteins used in the TAP experiments (TON1a, TON1b, FASS and TRM19) followed by MALDI TOF/TOF analysis. Proteins in the TAP eluates were separated on a 4-12% gradient NuPAGE gel (Invitrogen) and visualized with colloidal Coomassie Brilliant Blue staining. The most abundant proteins detected in each visible band on gel are indicated. In brief, the identified proteins were traced back to their gel slice number via MALDI spot numbers, making it possible to indicate the most abundant identified protein(s) in each visible band on SDS-PAGE. Some of the visible bands on SDS-PAGE correspond to non-specific co-purified proteins like HSP70, TUA/TUB, streptavidin etc... Such background proteins are not presented in the final table of interactors, as known background proteins (obtained from cultures expressing TAP-tagged mock proteins GUS, RFP and GFP) are systematically subtracted from the interactor lists as indicated in the Methods section. Identified proteins which do not give a clear visible band on SDS-PAGE or which are not the most abundant protein in a visible band on the SDS-PAGE gels are not indicated. Left lanes of each panel correspond to molecular weight standards.
(**d-e**) 2D Blue Native/SDS-PAGE on total protein extracts of PSB-D Arabidopsis cell suspension cells expressing Pro35S::TON1b-GS (**d**) or Pro35S::GS-TON1a (**e**) followed by Western blot detection using the Peroxidase Anti-Peroxidase (PAP) antibody that binds the GS-tag. The observed smear indicates incorporation of the GS-fused proteins in high molecular weight range complexes with an accumulation at an estimated size of 300-350 kDa (arrows). The strong signal at around 100kDa likely reflects the migration of uncomplexed TON1 proteins as dimers.

[61]Zimmermann, P., Hirsch-Hoffmann, M., Hennig, L., and Gruissem, W. GENEVESTIGATOR. Arabidopsis microarray database and analysis toolbox. *Plant Physiol* **136**, 2621-2632 (2004)

Supplementary Figure S2

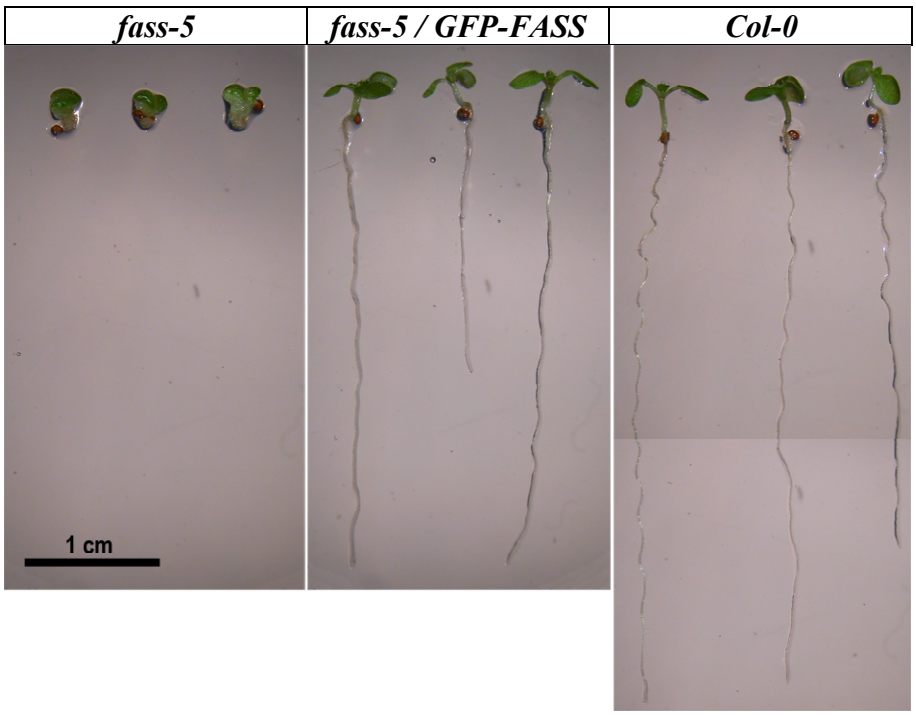


Supplementary Figure S2 : Analysis of *pp2ac3-c4* double mutant

(**a**) Gene models of *PP2AC3* and *PP2AC4* with indication of the respective T-DNA insertions and primers used for genotyping (LP, RP, LBaI), qPCR (bold arrows) and RT-PCR (FL fw and FL rev). Sequencing both the LBaI-LP and LBaI-RP PCR products allowed us to determine the exact insertion positions (underlined and dashed sequences) and to confirm the presence of tandem repeat T-DNA insertions in both lines. (**b**) Quantitative PCR (qPCR) analysis between wild type (Col-0) and the *pp2ac3-c4* double mutant showing significant reduction in *PP2AC3* and *PP2AC4* messenger levels. Expression of *PP2AC3* appears less reduced than *PP2AC4*. Both actin and eif4A were used as normalization genes. (**c**) RT-PCR analysis showing residual expression of full-length *PP2AC3* mRNA, while no full-length *PP2AC4* mRNA could be detected in the *pp2ac3-c4* double mutant. Actin (Act2-2) primers were used for normalization. (**d**) Representative images of wild type (Col-0), *pp2ac3*, *pp2ac4* and *pp2ac3-c4* double mutant seedlings showing severely affected main root growth of the *pp2ac3-c4* double mutant. (**e**) Average main root length of wild type (n=96), pp2a-c3 (n=38),

pp2a-c4 (n=35) and the *pp2ac3-ac4* double mutant (n=52). Single *pp2ac* mutants already show a statistical reduction in average main root length compared to wild type (T-test, $P<10^{-4}$ and $P<10^{-10}$ for *pp2ac3* and *pp2ac4* respectively) and the defects in main root growth are strongly enhanced (T-test, $P<10^{-60}$) in the *pp2ac3-c4* double mutant. (**f-j**) The *pp2ac3* and *pp2ac4* single mutants develop to wild type looking mature plants while the *pp2ac3-c4* double mutant are dwarfed plant with small, thick and round leaves, thick flowering stems (**g**, **h**) and shorter siliques (**i**, **j**).

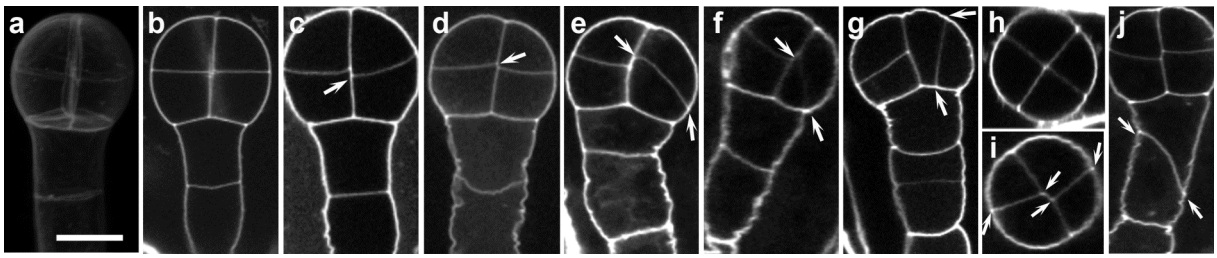
Supplementary Figure S3



Supplementary Figure S3: The GFP-FASS fusion complements the *fass* mutant phenotype

Wild-type *Arabidopsis* and heterozygous *fass-5* plants were infiltrated with *Agrobacterium* carrying the Pro35S:GFP-FASS construct. At least 20 primary transformants were obtained for each genotype. To determine whether the GFP-FASS construct complements the *fass* phenotype, the progenies were analyzed for segregation of the *fass* phenotype and of the hygromycin resistance carried by the T-DNA (GFP-FASS). No plant presenting both hygromycin resistance and the *fass* mutant phenotype was recovered indicating that the GFP-FASS construct complements the *fass* phenotype. Root growth of *fass-5* complemented plants was almost fully restored (compare one-week old seedlings in the middle panel to *fass-5* (left panel) or Col-0 (right panel)).

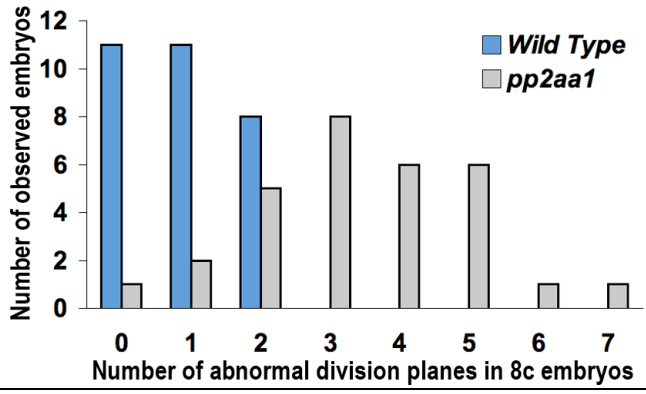
Supplementary Figure S4



k

	Wild Type	*pp2aa1*
Suspensor	0/30	13/30
First division	0/30	0/30
Second division	0/60	35/60
Third division	27/120	65/120

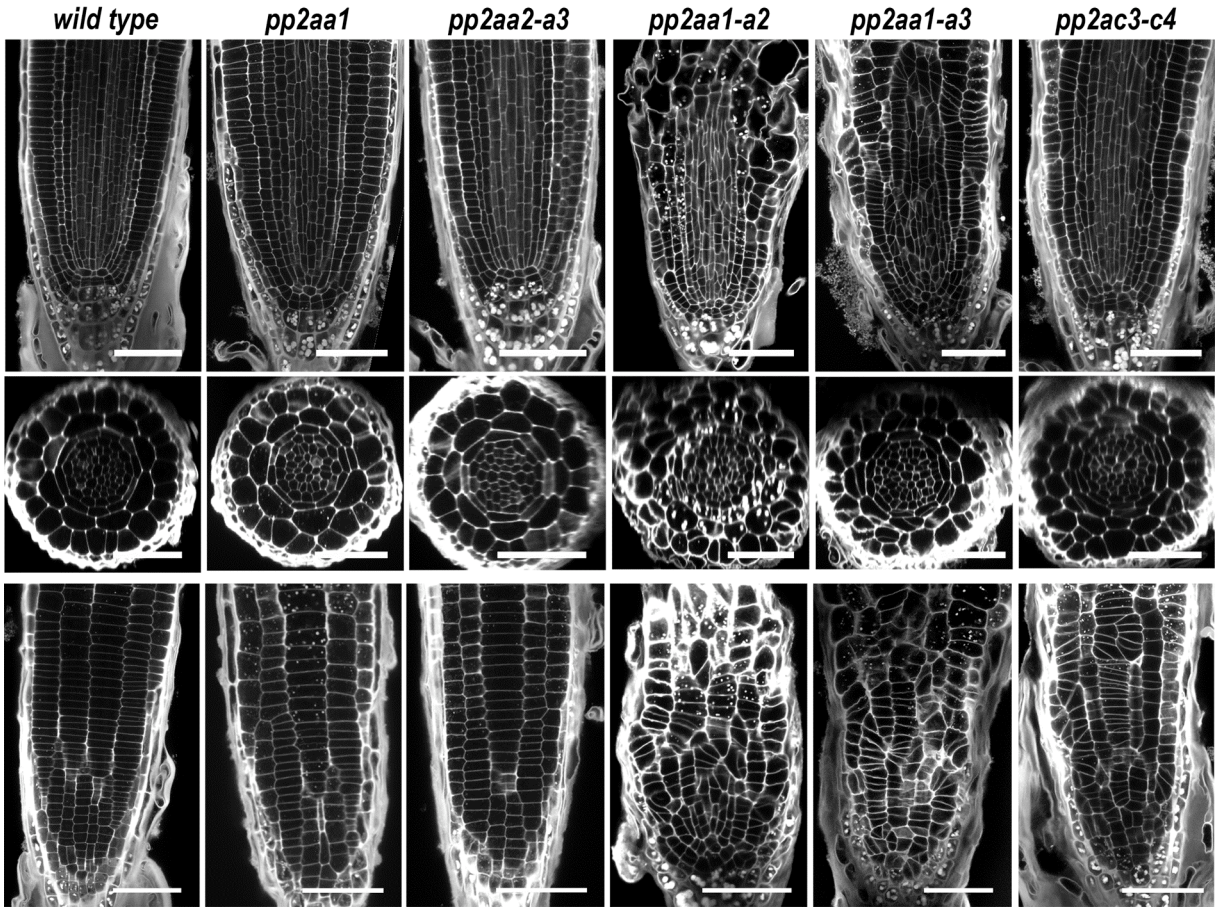
l



Supplementary Figure S4 : Cell division plane defects in 8-celled *pp2aa1* mutant embryos

(**a-j**) Propidium Iodide (PI) staining of 8-celled wild type (**a-c** and **h**) and *pp2aa1* (**d-g**, **i**, **j**) embryos. In a is shown a 3D reconstruction, in **b-g** and **j**, longitudinal views, and in **h-i** transverse sections of 8-celled embryos. 8-celled embryos result from three rounds of division (seven divisions in total, ie 1+2+4) in the embryo proper. The first division of the apical cell is longitudinal. The two-celled embryo then divides by a second longitudinal division perpendicular to the plane of the previous division. The four resulting cells then divide by transverse divisions, giving rise to the eight-celled embryo. PI imaging and 3D reconstruction of 8-celled embryos allowed to estimate division plane defects during these three rounds of division : Transverse sections enabled to follow the first and second round of division, whereas longitudinal sections revealed abnormal division plane during the third one. The table in **k** reports cell division plane defects observed in 30 embryos of *pp2aa1* compared to wild type. Abnormal division planes are visible in the second round of divisions in *pp2aa1* embryos where 35 planes were tilted (as shown in **i**) compared to wild type embryos (**h**). Defects are even more pronounced during the third round of division. At this stage, slightly tilted planes are present occasionally in wild-type embryos (27/120; as shown in **c**). Among 65 abnormal division planes observed in *pp2aa1* embryos, 35 appeared slightly tilted as in the wild type (**c-d**), while, in contrast to wild type, 15 were strongly misplaced as in **e** and 16, as in **f** or **g**. Aberrant division planes are also frequent in the suspensor of *pp2aa1* embryos (in 13/30 embryos as shown in **j**) but never observed in wild type. (**l**) Number of embryos displaying 0 to 7 abnormal division planes in wild type compared to *pp2aa1* embryos. Most *pp2aa1* embryos have more than 2 abnormal division planes. Wild type embryos reported here as having abnormal planes only have slightly tilted division planes.
Images in **a** to **j** are at the same scale (bar = 10 μm in **a**).

Supplementary Figure S5

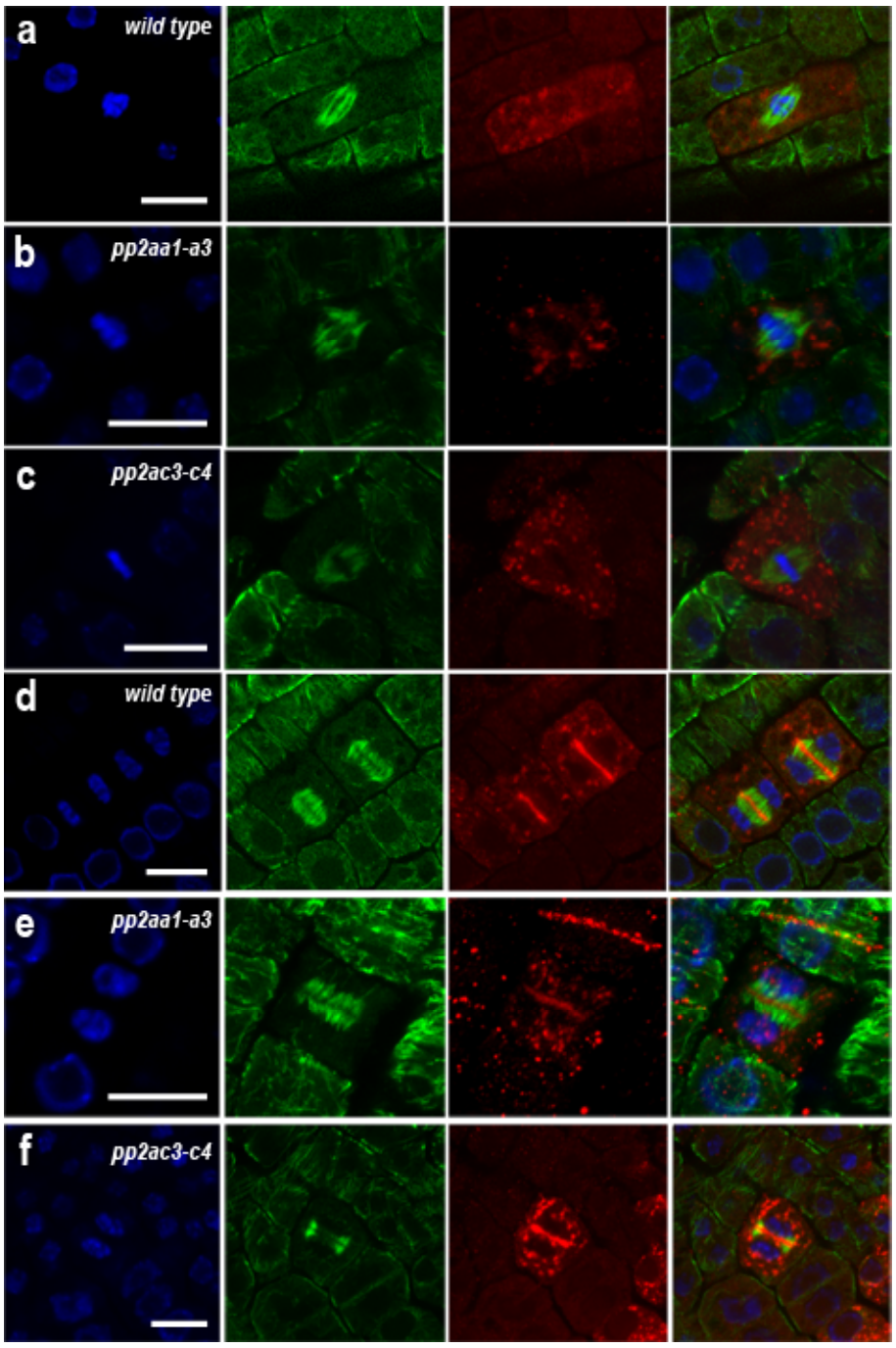


Supplementary Figure S5 : Cell division plane defects in roots of *pp2aaa and pp2ac* mutants

Longitudinal (upper panels), transverse (mid panels), and tangential views of root tips of wild-type (Col-0), *pp2aa1*, *pp2aa2-a3*, *pp2aa1-a2*, *pp2aa1-a3*, *pp2ac3-c4* three-day old seedlings stained with propidium iodide.

Bars = 50 μm in all images.

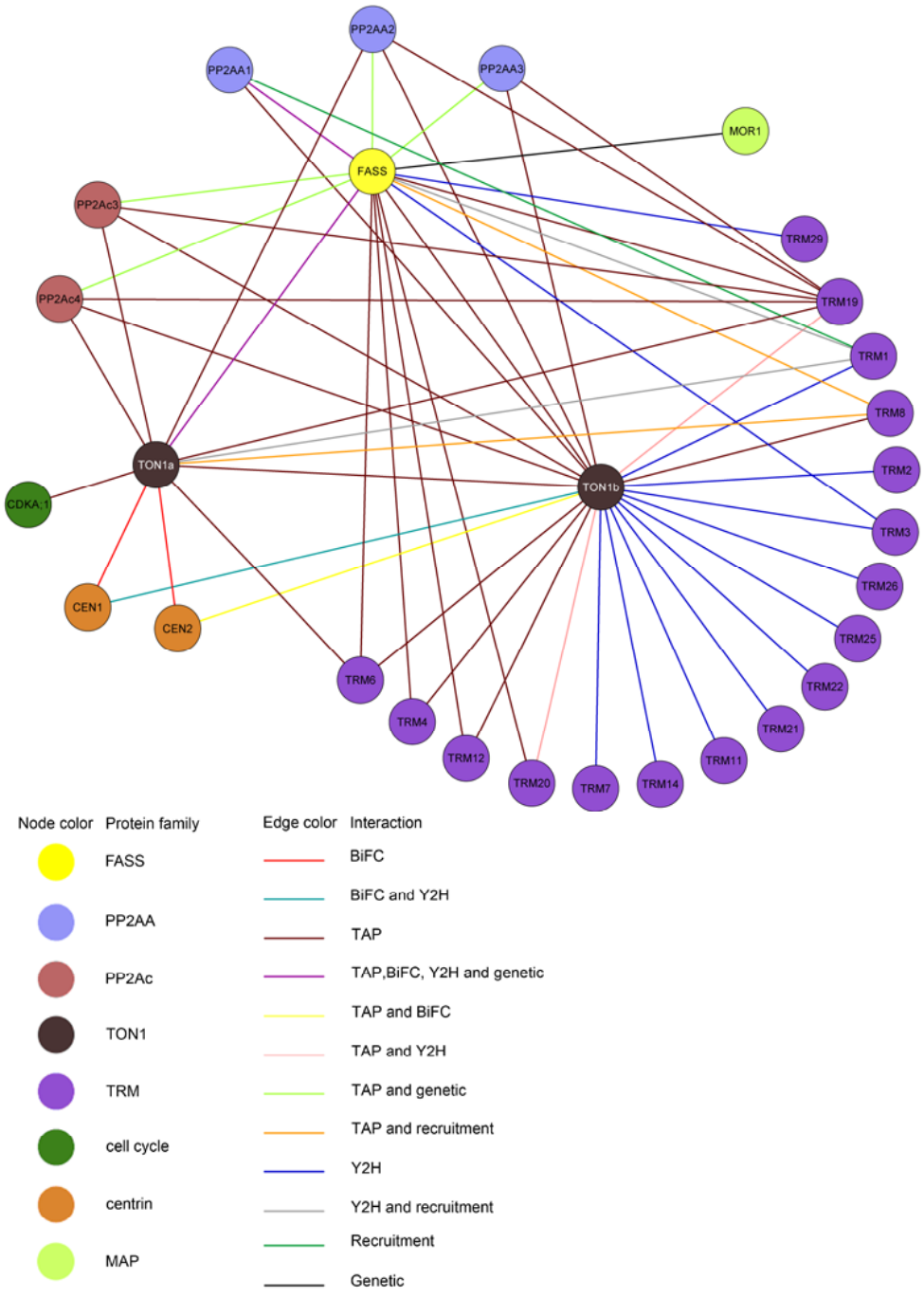
Supplementary Figure S6



Supplementary Figure S6 : *pp2aa* and *pp2ac* mutations don't affect spindle and phragmoplast

(**a-c**) Spindles and (**d-f**) phragmoplasts. Whole mount immuno-localization of α-tubulin, and KNOLLE in root tip cells of wild type (**a** and **d**), *pp2aa1-a3* (**b** and **e**), *pp2ac3-c4* (**c** and **f**) double mutants. Here are shown DAPI staining (in blue), anti-α-tubulin (in green), anti-KNOLLE (red), and overlay images. Bars = 10μm in **a-f**.

Supplementary Figure S7



Supplementary Figure S7: Interactome map overview of all TTP protein interactions

This protein-protein interaction network includes all known interactions concerning the TTP proteins. The presented data is a combination of novel data described in this paper and previously published interactions[10,11,12,15,25,43]. The nodes represent individual proteins and the node colors are indicative of the different protein families. The lines connecting the nodes indicate known interactions and are color-coded dependent on the techniques used to identify the interactions.

Supplementary Table S1 : MALDI MS/MS analysis of TAP eluates

		Prey				PMF data					MSMS data												
Bait	TAP Protocol	Prey Locus	Prey Name	# Found/ # exp	Database version	Protein Score	Expect	RMS error (ppm)	Sequence coverage %	Unique Peptides	Total Ion Score	Peptide Number	Start	End	Observed	Mr(Exp)	Mr(Calc)	Delta	Miss	Ions Score	Expect	Peptide	Variable Modification
TON1a	-dig	AT3G55005	TON1b	4/4	TAIR8	156	8,20E-12	4	42	8	106	1	237	243	863,44	862,43	862,43	0,00	0	32	2,00E-02	R.NLTSSWR.N	
												2	34	45	1394,64	1393,64	1393,64	0,00	0	52	1,00E-04	R.ASVFEAIEEEDR.V	
												3	*126*	*142*	*1958,05*	*1957,04*	*1957,05*	*-0,01*	*0*	*22*	*7,40E-02*	*R.NEDSRPLLLDVLEGFLK.F*	
TON1a	-dig	AT5G18580	FASS	4/4	TAIR8	207	6,50E-17	6	25	11	146	*1*	*244*	*252*	*1272,56*	*1271,55*	*1271,55*	*0,00*	*0*	*15*	*2,80E-01*	*K.FFFFCDPHR.R*	
												2	369	379	1311,65	1310,64	1310,65	-0,01	0	50	2,50E-04	K.DTPEGLTYLFR.C	
												3	*18*	*29*	*1384,77*	*1383,76*	*1383,77*	*-0,01*	*1*	*12*	*9,70E-01*	*R.KIPPASSMLWVR.N*	
												4	*387*	*399*	*1477,77*	*1476,76*	*1476,77*	*-0,01*	*0*	*25*	*7,20E-02*	*R.GFLTTADIHSLFR.D*	
												5	321	334	1656,81	1655,8	1655,8	0,00	0	44	7,30E-04	K.EYADGTLTEIFIER.V	
TON1a	-dig	AT3G25800	PP2AA2	1/4	TAIR8	58	5,10E-02	12	32	12	/									/			
TON1a	-dig	AT2G42500/AT3	PP2A3/PP2A4	1/4	TAIR8	68	4,60E-03	7	28	6	34	1	260	272	1589,78	1588,78	1588,77	0,01	0	34	9,40E-03	K.VVTIFSAPNYCYR.C	
TON1a	-dig	AT2G45240	MAP1A	1/4	TAIR8	*47*	*6,50E-01*	*4*	*14*	*4*	31	1	92	102	1310,69	1309,68	1309,68	0,00	0	31	1,70E-02	K.LPHFDWTGPLK.Q	
TON1a	+dig	AT3G55005	TON1b	4/4	TAIR8	441	2,60E-40	5	64	14	321	1	237	243	863,44	862,43	862,43	0,00	0	41	2,40E-03	R.NLTSSWR.N	
												2	222	233	1330,7	1329,69	1329,69	0,00	0	40	2,50E-03	R.ASTALENLQLDR.K	
												3	114	125	1441,66	1440,66	1440,66	0,00	0	83	7,40E-08	R.DFSINNGYELNR.N	
												4	187	202	1499,7	1498,7	1498,7	0,00	0	66	3,70E-06	R.SVSASQASGAATSGYR.K	
												5	126	142	1958,06	1957,05	1957,05	0,00	0	92	7,60E-09	R.NEDSRPLLLDVLEGFLK.F	
TON1a	+dig	AT5G18580	FASS	4/4	TAIR8	390	3,30E-35	4	35	16	274	*1*	*335*	*341*	*901,45*	*900,44*	*900,45*	*-0,01*	*0*	*24*	*5,30E-02*	*R.VFDEHVR.R*	
												2	457	464	1002,46	1001,45	1001,45	0,00	0	30	9,80E-03	R.GFWAHDNR.E	
												3	*19*	*29*	*1256,69*	*1255,68*	*1255,67*	*0,01*	*0*	*19*	*2,50E-01*	*K.IPPASSMLWVR.N*	
												4	244	252	1272,57	1271,57	1271,55	0,02	0	28	1,50E-02	K.FFFFCDPHR.R	
												5	*369*	*379*	*1311,66*	*1310,65*	*1310,65*	*0,00*	*0*	*25*	*7,10E-02*	*K.DTPEGLTYLFR.C*	
												6	*18*	*29*	*1384,77*	*1383,77*	*1383,77*	*0,00*	*1*	*0*	*1,40E+01*	*R.KIPPASSMLWVR.N*	
												7	387	399	1477,78	1476,78	1476,77	0,01	0	59	2,50E-05	R.GFLTTADIHSLFR.D	
												8	321	334	1656,82	1655,81	1655,8	0,01	0	52	1,30E-04	K.EYADGTLTEIFIER.V	
												9	101	119	2204,08	2203,07	2203,08	-0,01	0	36	3,90E-03	K.QSDLLLNADDLAAMWVCLR.E	
TON1a	+dig	AT3G25800	PP2AA2	2/4	TAIR8	111	2,60E-07	9	33	13	31	*1*	*279*	*287*	*1047,58*	*1046,57*	*1046,58*	*-0,01*	*0*	*1*	*2,30E+01*	*R.TELVPAYVR.L*	
												2	133	142	1121,57	1120,57	1120,57	0,00	0	30	2,80E-02	R.LAAGEWFTAR.V	
TON1a	+dig	AT2G42500/AT3	PP2A3/PP2A4	2/4	TAIR8	120	3,30E-08	4	33	8	67	1	287	298	1456,72	1455,72	1455,73	-0,01	0	66	4,20E-06	R.NHTFIQFEPAPR.R	
TON1a	+dig	AT3G06810	IBR3	1/4	TAIR8	84	1,40E-04	6	28	17	/												
TON1b	-dig	AT3G55000	TON1a	5/5	TAIR8	622	2,10E-58	10	51	15	487	*1*	*241*	*247*	*863,43*	*862,43*	*862,43*	*0,00*	*0*	*26*	*8,30E-02*	*R.NLTSSWR.N*	
												2	67	75	952,53	951,52	951,52	0,00	1	35	6,00E-03	R.KLHASPSGR.L	
												3	207	213	994,48	993,47	993,47	0,00	1	38	3,20E-03	R.KDEFNWR.Q	
												4	175	185	1144,57	1143,56	1143,55	0,01	0	33	1,00E-02	R.SSASDSLPPQR.R	
												5	226	237	1300,69	1299,68	1299,68	0,00	0	58	3,40E-05	R.ASAALENLQLDR.K	
												6	34	45	1394,68	1393,67	1393,64	0,03	0	61	1,80E-05	R.ASVFEAIEEEDR.V	
												7	114	125	1426,65	1425,65	1425,63	0,02	0	85	5,20E-08	R.DFNSNNGFELNR.N	
												8	126	142	1786,97	1785,96	1785,95	0,01	0	87	2,60E-08	R.NGDSGPLLLDVLEGFLK.F	
												9	*110*	*125*	*1911,92*	*1910,91*	*1910,89*	*0,02*	*1*	*23*	*1,00E-01*	*K.SELRDFNSNNGFELNR.N*	
TON1b	-dig	AT5G18580	FASS	5/5	TAIR8	568	5,20E-53	4	45	23	353	1	335	341	901,45	900,44	900,45	-0,01	0	33	8,50E-03	R.VFDEHVR.R	
												2	457	464	1002,46	1001,45	1001,45	0,00	0	30	9,20E-03	R.GFWAHDNR.E	
												3	156	164	1120,52	1119,51	1119,51	0,00	0	31	1,10E-02	R.FFSPSNFMK.F	Oxidation(M)
												4	*244*	*252*	*1272,57*	*1271,56*	*1271,55*	*0,01*	*0*	*21*	*7,30E-02*	*K.FFFFCDPHR.R*	
												5	369	379	1311,66	1310,65	1310,65	0,00	0	40	2,10E-03	K.DTPEGLTYLFR.C	
												6	*66*	*77*	*1327,66*	*1326,65*	*1326,65*	*0,00*	*0*	*18*	*3,20E-01*	*K.SQEAGTIPSFYK.K*	
												7	444	456	1346,71	1345,7	1345,7	0,00	0	38	4,00E-03	K.QGGTVASMLIDVR.G	
												8	18	29	1384,77	1383,77	1383,77	0,00	1	30	1,40E-02	R.KIPPASSMLWVR.N	
												9	*18*	*29*	*1400,77*	*1399,76*	*1399,76*	*0,00*	*1*	*(2)*	*1,30E+01*	*R.KIPPASSMLWVR.N*	*Oxidation(M)*
												10	387	399	1477,78	1476,77	1476,77	0,00	0	50	2,30E-04	R.GFLTTADIHSLFR.D	
												11	*173*	*184*	*1514,84*	*1513,84*	*1513,84*	*0,00*	*0*	*3*	*7,20E+00*	*R.IAILPFYLYVMR.T*	*Oxidation(M)*
												12	227	238	1529,64	1528,63	1528,63	0,00	0	28	6,20E-03	R.DMPPAFNQMYCR.I	
												13	321	334	1656,81	1655,8	1655,8	0,00	0	31	1,90E-02	K.EYADGTLTEIFIER.V	
TON1b	-dig	AT3G25800	PP2AA2	4/5	TAIR8	225	1,00E-18	6	36	15	129	*1*	*279*	*287*	*1047,58*	*1046,57*	*1046,58*	*-0,01*	*0*	*27*	*5,20E-02*	*R.TELVPAYVR.L*	
												2	133	142	1121,57	1120,57	1120,57	0,00	0	38	4,20E-03	R.LAAGEWFTAR.V	
												3	537	552	1767,02	1766,01	1766,02	-0,01	0	23	2,20E-02	K.VLQSLIPIVDQSVVEK.T	
												4	310	325	1858,06	1857,06	1857,05	0,01	0	30	6,70E-03	R.ILNPEIAIQHILPCVK.E	
												5	*259*	*278*	*2340,11*	*2339,1*	*2339,09*	*0,01*	*0*	*11*	*1,40E+00*	*R.YMVANQLYELCEAVGPEPTR.T*	
TON1b	-dig	AT2G42500/AT3	PP2A3/PP2A4	3/5	TAIR8	218	5,20E-18	5	45	11	131	1	287	298	1456,72	1455,71	1455,73	-0,02	0	34	7,20E-03	R.NHTFIQFEPAPR.R	
												2	260	272	1589,78	1588,77	1588,77	0,00	0	42	1,30E-03	K.VVTIFSAPNYCYR.C	
												3	219	239	2341,09	2340,08	2340,08	0,00	0	35	3,80E-03	R.GAGYTFGQDISEQFNHTNNLK.L	
												4	*54*	*74*	*2412,18*	*2411,17*	*2411,17*	*0,00*	*0*	*20*	*1,60E-01*	*K.SPVTICGDIHGQFHDLAELFR.I*	
TON1b	-dig	AT1G13320	PP2AA3	1/5	TAIR8	74	1,40E-03	10	13	6	50	1	133	142	1137,58	1136,57	1136,56	0,01	0	34	1,20E-02	R.LSAGEWFTAR.V	
												2	*259*	*278*	*2340,11*	*2339,1*	*2339,09*	*0,01*	*0*	*16*	*3,70E-01*	*R.YMVANQLYELCEAVGPEPTR.T*	
												3	*259*	*278*	*2356,1*	*2355,1*	*2355,09*	*0,01*	*0*	*(10)*	*1,50E+00*	*R.YMVANQLYELCEAVGPEPTR.T*	*Oxidation(M)*
TON1b	-dig	AT3G06810	IBR3	1/4	TAIR8	73	1,60E-03	7	16	9	39	1	18	25	1020,5	1019,49	1019,48	0,01	0	28	4,20E-02	R.FDHDALFR.F	

												2	*234*	*245*	*1441,69*	*1440,68*	*1440,7*	*-0,02*	*0*	*4*	*8,30E+00*	*R.IDNLVFHPSEDR.V*
												3	*353*	*371*	*2005,04*	*2004,03*	*2004,03*	*0,00*	*0*	*7*	*3,10E+00*	*R.NTGVQANELVESALGYIAR.E*
TON1b	+dig	AT3G55000	TON1a	4/4	TAIR8	659	4,10E-62	10	59	16	515	1	241	247	863,45	862,44	862,43	0,01	0	43	1,90E-03	R.NLTSSWR.N
												2	207	213	994,48	993,48	993,47	0,01	1	46	6,70E-04	R.KDEFNWR.Q
												3	226	237	1300,69	1299,68	1299,68	0,00	0	71	2,00E-06	R.ASAALENLQLDR.K
												4	*186*	*197*	*1329,7*	*1328,69*	*1328,69*	*0,00*	*1*	*11*	*1,80E+00*	*R.RPVSASQASDRR.A*
												5	114	125	1426,64	1425,63	1425,63	0,00	0	88	2,30E-08	R.DFNSNNGFELNR.N
												6	126	142	1786,95	1785,94	1785,95	-0,01	0	120	1,80E-11	R.NGDSGPLLLDVLEGFLK.F
												7	110	125	1911,9	1910,89	1910,89	0,00	1	67	2,70E-06	K.SELRDFNSNNGFELNR.N
												8	34	64	3427,69	3426,68	3426,6	0,08	1	71	7,70E-07	R.ASVFEAIEEEDRVIENNEGPPPALLGSCNDR.A
TON1b	+dig	AT5G18580	FASS	4/4	TAIR8	742	2,10E-70	6	43	21	557	1	335	341	901,46	900,46	900,45	0,01	0	33	9,20E-03	R.VFDEHVR.R
												2	457	464	1002,46	1001,46	1001,45	0,01	0	34	4,40E-03	R.GFWAHDNR.E
												3	244	252	1272,57	1271,56	1271,55	0,01	0	58	1,70E-05	K.FFFFCDPHR.R
												4	369	379	1311,66	1310,65	1310,65	0,00	0	48	3,80E-04	K.DTPEGLTYLFR.C
												5	444	456	1346,71	1345,7	1345,7	0,00	0	62	2,00E-05	K.QGGTVASMLIDVR.G
												6	18	29	1384,78	1383,77	1383,77	0,00	1	30	1,50E-02	R.KIPPASSMLWVR.N
												7	*244*	*253*	*1428,67*	*1427,66*	*1427,66*	*0,00*	*1*	*15*	*5,00E-01*	*K.FFFFCDPHRR.G*
												8	387	399	1477,78	1476,77	1476,77	0,00	0	82	1,40E-07	R.GFLTTADIHSLFR.D
												9	*227*	*238*	*1545,63*	*1544,62*	*1544,62*	*0,00*	*0*	*0*	*3,10E+00*	*R.DMPPAFNQMYCR.I* *Oxidation(M)*
												10	321	334	1656,81	1655,81	1655,8	0,01	0	55	6,50E-05	K.EYADGTLTEIFIER.V
												11	34	53	2082,05	2081,04	2081,05	-0,01	1	63	9,10E-06	R.YIGSGAGLGSEALMELETKR.I
												12	317	334	2155,09	2154,08	2154,08	0,00	1	67	3,50E-06	K.QELKEYADGTLTEIFIER.V
												13	*101*	*119*	*2204,08*	*2203,07*	*2203,08*	*-0,01*	*0*	*13*	*8,10E-01*	*K.QSDLLLNADDLAAMWVCLR.E*
TON1b	+dig	AT3G25800	PP2AA2	3/4	TAIR8	89	4,20E-05	9	19	9	47	1	133	142	1121,58	1120,57	1120,57	0,00	0	47	6,10E-04	R.LAAGEWFTAR.V
TON1b	+dig	AT3G53540	TRM19	2/4	TAIR8	*47*	*7,20E-01*	*15*	*6*	*5*	*39*	1	827	835	1119,65	1118,64	1118,64	0,00	1	39	1,60E-03	R.KLLFDQISR.E
TON1b	+dig	AT1G60780	mu1b (HAPLESS 13)	2/4	TAIR8	88	4,70E-05	8	40	12	/											
TON1b	+dig	AT2G42500/AT3	PP2A3/PP2A4	1/4	TAIR8	79	4,00E-04	10	31	7	33	1	260	272	1589,77	1588,76	1588,77	-0,01	0	33	9,10E-03	K.VVTIFSAPNYCYR.C
TON2	-dig	AT3G55000	TON1a	4/4	TAIR8	319	4,10E-28	7	53	13	220	*1*	*241*	*247*	*863,43*	*862,42*	*862,43*	*-0,01*	*0*	*21*	*2,80E-01*	*R.NLTSSWR.N*
												2	67	75	952,52	951,52	951,52	0,00	1	29	2,20E-02	R.KLHASPSGR.L
												3	207	213	994,47	993,47	993,47	0,00	1	28	3,40E-02	R.KDEFNWR.Q
												4	*175*	*185*	*1144,56*	*1143,55*	*1143,55*	*0,00*	*0*	*15*	*5,70E-01*	*R.SSASDSLPPQR.R*
												5	226	237	1300,68	1299,67	1299,68	-0,01	0	50	2,40E-04	R.ASAALENLQLDR.K
												6	114	125	1426,64	1425,63	1425,63	0,00	0	65	3,80E-06	R.DFNSNNGFELNR.N
												7	*46*	*64*	*2051,98*	*2050,98*	*2050,97*	*0,01*	*0*	*13*	*8,20E-01*	*R.VIENNEGPPPALLGSCNDR.A*
TON2	-dig	AT3G55005	TON1b	4/4	TAIR8	196	8,20E-16	9	43	11	113	*1*	*237*	*243*	*863,43*	*862,42*	*862,43*	*-0,01*	*0*	*14*	*1,30E+00*	*R.NLTSSWR.N*
												2	222	233	1330,69	1329,68	1329,69	-0,01	0	40	2,50E-03	R.ASTALENLQLDR.K
												3	114	125	1441,66	1440,66	1440,66	0,00	0	31	1,10E-02	R.DFSINNGYELNR.N
												4	*187*	*202*	*1499,71*	*1498,7*	*1498,7*	*0,00*	*0*	*14*	*6,40E-01*	*R.SVSASQASGAATSGYR.K*
												5	*126*	*142*	*1958,05*	*1957,04*	*1957,05*	*-0,01*	*0*	*15*	*4,30E-01*	*R.NEDSRPLLLDVLEGFLK.F*
TON2	-dig	AT2G42500/AT3	PP2A3/PP2A4	3/4	TAIR8	257	6,50E-22	5	40	11	178	1	287	298	1456,73	1455,73	1455,73	0,00	0	55	6,30E-05	R.NHTFIQFEPAPR.R
												2	260	272	1589,78	1588,77	1588,77	0,00	0	36	5,20E-03	K.VVTIFSAPNYCYR.C
												3	*94*	*108*	*1641,89*	*1640,89*	*1640,9*	*-0,01*	*0*	*12*	*8,80E-01*	*R.GYYSVETVTLLVGLK.V*
												4	*126*	*140*	*1919,93*	*1918,92*	*1918,92*	*0,00*	*1*	*25*	*6,40E-02*	*R.QITQVYGFYDECLRK.Y*
												5	219	239	2341,09	2340,08	2340,08	0,00	0	26	3,20E-02	R.GAGYTFGQDISEQFNHTNNLK.L
												6	*54*	*74*	*2412,17*	*2411,17*	*2411,17*	*0,00*	*0*	*23*	*8,10E-02*	*K.SPVTICGDIHGQFHDLAELFR.I*
TON2	-dig	AT3G53540	TRM19	1/4	TAIR8	*52*	*2,00E-01*	*3*	*0*	*2*	*52*	*1*	*828*	*835*	*991,55*	*990,55*	*990,55*	*0,00*	*0*	*13*	*1,10E+00*	*K.LLFDQISR.E*
												2	827	835	1119,65	1118,64	1118,64	0,00	1	39	1,60E-03	R.KLLFDQISR.E
TON2	-dig	AT2G45240	MAP1A	1/4	TAIR8	67	7,00E-03	19	40	11	/											
TON2	+dig	AT3G55000	TON1a	4/4	TAIR8	588	5,20E-55	7	50	13	481	*1*	*241*	*247*	*863,44*	*862,43*	*862,43*	*0,00*	*0*	*24*	*1,30E-01*	*R.NLTSSWR.N*
												2	*67*	*75*	*952,52*	*951,51*	*951,52*	*-0,01*	*1*	*22*	*1,30E-01*	*R.KLHASPSGR.L*
												3	207	213	994,48	993,47	993,47	0,00	1	55	6,20E-05	R.KDEFNWR.Q
												4	226	237	1300,69	1299,68	1299,68	0,00	0	84	9,70E-08	R.ASAALENLQLDR.K
												5	34	45	1394,65	1393,64	1393,64	0,00	0	42	1,20E-03	R.ASVFEAIEEEDR.V
												6	114	125	1426,63	1425,63	1425,63	0,00	0	84	4,50E-08	R.DFNSNNGFELNR.N
												7	126	142	1786,95	1785,94	1785,95	-0,01	0	104	6,10E-10	R.NGDSGPLLLDVLEGFLK.F
												8	46	64	2051,98	2050,97	2050,97	0,00	0	67	3,10E-06	R.VIENNEGPPPALLGSCNDR.A
TON2	+dig	AT3G55005	TON1b	4/4	TAIR8	512	2,10E-47	7	57	12	411	*1*	*237*	*243*	*863,44*	*862,43*	*862,43*	*0,00*	*0*	*21*	*2,80E-01*	*R.NLTSSWR.N*
												2	67	75	952,52	951,51	951,49	0,02	0	39	2,50E-03	R.QLHASPSGR.L
												3	222	233	1330,7	1329,69	1329,69	0,00	0	72	1,40E-06	R.ASTALENLQLDR.K
												4	34	45	1394,65	1393,64	1393,64	0,00	0	35	5,40E-03	R.ASVFEAIEEEDR.V
												5	114	125	1441,67	1440,66	1440,66	0,00	0	69	1,70E-06	R.DFSINNGYELNR.N
												6	187	202	1499,71	1498,7	1498,7	0,00	0	68	2,20E-06	R.SVSASQASGAATSGYR.K
												7	126	142	1958,06	1957,05	1957,05	0,00	0	57	2,10E-05	R.NEDSRPLLLDVLEGFLK.F
												8	46	64	2068,01	2067	2067,01	-0,01	0	49	2,00E-04	R.VIENNEGLPPALLGSCNDR.A
TON2	+dig	AT3G25800	PP2AA2	4/4	TAIR8	299	4,10E-26	7	35	14	205	*1*	*279*	*287*	*1047,58*	*1046,57*	*1046,58*	*-0,01*	*0*	*16*	*6,40E-01*	*R.TELVPAYVR.L*
												2	133	142	1121,57	1120,57	1120,57	0,00	0	37	5,60E-03	R.LAAGEWFTAR.V
												3	537	552	1767	1765,99	1766,02	-0,03	0	28	1,00E-02	K.VLQSLIPIVDQSVVEK.T
												4	310	325	1858,05	1857,04	1857,05	-0,01	0	66	2,00E-06	R.ILNPEIAIQHILPCVK.E
												5	*553*	*570*	*2010,04*	*2009,03*	*2009,04*	*-0,01*	*0*	*24*	*7,80E-02*	*K.TIRPGLVELSEDPDVDVR.F*
												6	259	278	2340,1	2339,1	2339,09	0,01	0	34	5,70E-03	R.YMVANQLYELCEAVGPEPTR.T
TON2	+dig	AT3G53540	TRM19	4/4	TAIR8	255	1,00E-21	4	14	12	224	1	828	835	991,55	990,55	990,55	0,00	0	35	7,70E-03	K.LLFDQISR.E
												2	827	835	1119,65	1118,64	1118,64	0,00	1	52	8,20E-05	R.KLLFDQISR.E
												3	310	321	1334,81	1333,8	1333,81	-0,01	0	24	1,10E-02	K.IVVLKPNLGEPR.Y
												4	*158*	*171*	*1577,81*	*1576,8*	*1576,8*	*0,00*	*0*	*16*	*6,80E-01*	*R.VNANLTQAEMAFIR.Q*
												5	*158*	*171*	*1593,8*	*1592,79*	*1592,8*	*-0,01*	*0*	*(2)*	*1,50E+01*	*R.VNANLTQAEMAFIR.Q* *Oxidation(M)*

												6	286	300	1772,85	1771,84	1771,84	0,00	0	39	2,30E-03	R.HASYDTIDLPNEELR.K	
												7	889	904	1928,99	1927,98	1927,99	-0,01	0	58	3,00E-05	K.ELQWLSLEDDIEIIGR.E	
TON2	+dig	AT3G05750	TRM6	2/4	TAIR8	99	4,50E-06	8	12	9	73	*1*	*175*	*183*	*1088,57*	*1087,57*	*1087,57*	*0,00*	*0*	*11*	*2,30E+00*	*R.FQTETLPPR.S*	
												2	119	129	1439,7	1438,7	1438,7	0,00	1	41	1,90E-03	R.RNPDFDPYFLR.S	
												3	*134*	*149*	*1871,89*	*1870,89*	*1870,88*	*0,01*	*0*	*22*	*1,30E-01*	*K.ASTWDAYENLGYVNLR.S*	
TON2	+dig	AT5G26910	TRM8	1/4	TAIR8	75	1,00E-03	4	13	9	49	*1*	*751*	*758*	*953,48*	*952,47*	*952,48*	*-0,01*	*0*	*18*	*3,60E-01*	*K.GGFLFEQR.D*	
												2	129	141	1612,77	1611,77	1611,77	0,00	0	31	1,30E-02	R.WDAYENLGYVNLR.S	
TON2	+dig	AT2G42500/AT3	PP2A3/PP2A4	1/4	TAIR8	663	1,60E-62	3	56	13	545	*1*	*307*	*313*	*911,46*	*910,45*	*910,45*	*0,00*	*1*	*18*	*3,10E-01*	*R.RTPDYFL.-*	
												2	*141*	*148*	*951,47*	*950,46*	*950,46*	*0,00*	*0*	*28*	*5,20E-02*	*K.YGNANVWK.I*	
												3	287	298	1456,73	1455,72	1455,73	-0,01	0	82	1,30E-07	R.NHTFIQFEPAPR.R	
												4	260	272	1589,78	1588,77	1588,77	0,00	0	60	2,10E-05	K.VVTIFSAPNYCYR.C	
												5	94	108	1641,9	1640,89	1640,9	-0,01	0	58	2,30E-05	R.GYYSVETVTLLVGLK.V	
												6	79	93	1865,78	1864,77	1864,78	-0,01	0	39	4,80E-04	K.CPDTNYLFMGDYVDR.G	
												7	244	259	1910,89	1909,88	1909,89	-0,01	0	99	1,40E-09	R.AHQLVMDGFNWAHEQK.V	
												8	244	259	1926,88	1925,88	1925,88	0,00	0	(79)	1,60E-07	R.AHQLVMDGFNWAHEQK.V	Oxidation(M)
												9	219	239	2341,08	2340,07	2340,08	-0,01	0	89	1,40E-08	R.GAGYTFGQDISEQFNHTNNLK.L	
												10	54	74	2412,18	2411,17	2411,17	0,00	0	72	1,10E-06	K.SPVTICGDIHGQFHDLAELFR.I	
TON2	+dig	AT1G13320	PP2AA3	1/4	TAIR8	169	4,10E-13	6	20	8	130	1	133	142	1137,57	1136,56	1136,56	0,00	0	30	2,80E-02	R.LSAGEWFTAR.V	
												2	310	325	1858,05	1857,04	1857,05	-0,01	0	66	2,00E-06	R.ILNPELAIQHILPCVK.E	
												3	259	278	2340,1	2339,1	2339,09	0,01	0	34	5,70E-03	R.YMVANQLYELCEAVGPEPTR.T	
TON2	+dig	AT1G25490	PP2AA1	1/4	TAIR8	105	1,00E-06	8	11	4	91	*1*	*133*	*142*	*1077,55*	*1076,54*	*1076,54*	*0,00*	*0*	*25*	*9,70E-02*	*R.LAGGEWFAAR.V*	
												2	310	325	1858,05	1857,04	1857,05	-0,01	0	66	2,00E-06	R.LLNPELAIQHILPCVK.E	
TON2	+dig	AT2G45240	MAP1A	4/4	TAIR8	135	1,00E-09	10	24	7	93	1	92	102	1310,67	1309,67	1309,68	-0,02	0	49	3,10E-04	K.LPHFDWTGPLK.Q	
												2	386	398	1502,81	1501,81	1501,78	0,02	0	19	2,40E-01	R.LPSSPDVYPWLTK.-	
												3	365	385	2301,19	2300,18	2300,2	-0,02	0	25	4,20E-02	R.SAQFEHTLLVTETGVEVLTAR.L	
TIM19	-dig	AT3G55000	TON1a	2/2	TAIR9	696	8,40E-66	4	55	14	574	1	241	247	863,4374	862,4301	862,4297	0,00	0	36	8,50E-03	R.NLTSSWR.N	
												2	67	75	952,5194	951,5121	951,525	-0,01	1	53	1,10E-04	R.KLHASPSGR.L	
												3	207	213	994,4745	993,4672	993,4668	0,00	1	57	4,90E-05	R.KDEFNWR.Q	
												4	175	185	1144,5635	1143,5562	1143,552	0,00	0	52	1,20E-04	R.SSASDSLPPQR.R	
												5	226	237	1300,6829	1299,6756	1299,6782	0,00	0	87	4,20E-08	R.ASAALENLQLDR.K	
												6	34	45	1394,6445	1393,6372	1393,6361	0,00	0	92	1,10E-08	R.ASVFEAIEEEDR.V	
												7	114	125	1426,6322	1425,6249	1425,6273	0,00	0	106	3,00E-10	R.DFNSNNGFELNR.N	
												8	46	64	2051,9858	2050,9785	2050,9742	0,00	0	93	8,90E-09	R.VIENNEGPPPALLGSCNDR.A	
TIM19	-dig	AT3G55005	TON1b	2/2	TAIR9	563	1,70E-52	8	53	13	452	1	237	243	863,4374	862,4301	862,4297	0,00	0	36	8,50E-03	R.NLTSSWR.N	
												2	67	75	952,5194	951,5121	951,4886	0,02	0	53	1,10E-04	R.QLHASPSGR.L	
												3	175	185	1184,566	1183,5587	1183,5582	0,00	0	55	5,80E-05	R.SSASDSLPHQR.R	
												4	222	233	1330,697	1329,6897	1329,6888	0,00	0	55	7,20E-05	R.ASTALENLQLDR.K	
												5	34	45	1394,6445	1393,6372	1393,6361	0,00	0	92	1,10E-08	R.ASVFEAIEEEDR.V	
												6	114	125	1441,6615	1440,6542	1440,6633	-0,01	0	102	9,50E-10	R.DFSINNGYELNR.N	
												7	187	202	1499,7043	1498,697	1498,7012	0,00	0	60	1,70E-05	R.SVSASQASGAATSGYR.K	
TIM19	-dig	AT5G18580	FASS	2/2	TAIR9	1060	3,30E-102	2	55	25	832	1	54	60	875,5563	874,549	874,5528	0,00	0	53	3,00E-05	R.ILLEIFK.E	
												2	335	341	901,4531	900,4458	900,4454	0,00	0	59	2,30E-05	R.VFDEHVR.R	
												3	457	464	1002,4553	1001,448	1001,4468	0,00	0	46	2,60E-04	R.GFWAHDNR.E	
												4	434	443	1089,5973	1088,59	1088,59	0,00	0	104	1,20E-09	K.ITLGDLLGCK.Q	
												5	156	164	1120,5145	1119,5072	1119,5059	0,00	0	42	8,10E-04	R.FFSPSNFMK.F	Oxidation(M)
												6	244	252	1272,5647	1271,5574	1271,5546	0,00	0	49	1,20E-04	K.FFFFCDPHR.R	
												7	369	379	1311,6573	1310,65	1310,6507	0,00	0	67	4,70E-06	K.DTPEGLTYLFR.C	
												8	66	77	1327,656	1326,6487	1326,6456	0,00	0	49	2,50E-04	K.SQEAGTIPSFYK.K	
												9	444	456	1362,7041	1361,6968	1361,6973	0,00	0	50	3,50E-04	K.QGGTVASMLIDVR.G	Oxidation(M)
												10	*18*	*29*	*1400,7711*	*1399,7638*	*1399,7646*	*0,00*	*1*	*20*	*1,90E-01*	*R.KIPPASSMLWVR.N*	*Oxidation(M)*
												11	387	399	1477,7791	1476,7718	1476,7725	0,00	0	115	6,60E-11	R.GFLTTADIHSLFR.D	
												12	173	184	1514,8414	1513,8341	1513,8367	0,00	0	39	2,10E-03	R.IAILPFYLYVMR.T	Oxidation(M)
												13	*227*	*238*	*1561,6206*	*1560,6133*	*1560,616*	*0,00*	*0*	*13*	*1,10E-01*	*R.DMPPAFNQMYCR.I*	*2 Oxidation(M)*
												14	321	334	1656,8107	1655,8034	1655,8042	0,00	0	94	8,70E-09	K.EYADGTLTEIFIER.V	
												15	101	119	2220,0813	2219,074	2219,0715	0,00	0	33	7,80E-03	K.QSDLLLNADDLAAMWVCLR.E	Oxidation(M)
TIM19	-dig	AT3G25800	PP2AA2	2/2	TAIR9	558	5,30E-52	4	41	17	431	1	279	287	1047,5817	1046,5744	1046,576	0,00	0	52	1,80E-04	R.TELVPAYVR.L	
												2	133	142	1121,5769	1120,5696	1120,5665	0,00	0	71	2,20E-06	R.LAAGEWFTAR.V	
												3	190	200	1173,6239	1172,6166	1172,619	0,00	0	55	9,90E-05	K.FAATVESAHLK.T	
												4	119	131	1501,7883	1500,781	1500,7824	0,00	0	76	6,80E-07	R.ESDLVDHFISLVK.R	
												5	337	352	1576,8361	1575,8288	1575,8364	-0,01	0	40	2,50E-03	R.SALASVIMGMAPVLGK.D	2 Oxidation(M)
												6	537	552	1767,0187	1766,0114	1766,019	-0,01	0	42	2,90E-04	K.VLQSLIPIVDQSVVEK.T	
												7	310	325	1858,0563	1857,049	1857,0546	-0,01	0	61	5,90E-06	R.ILNPEIAIQHILPCVK.E	
												8	553	570	2010,0442	2009,0369	2009,0429	-0,01	0	34	6,40E-03	K.TIRPGLVELSEDPDVDVR.F	
TIM19	-dig	AT2G42500/AT3	PP2A3/PP2A4	2/2	TAIR9	269	4,20E-23	4	30	7	176	*1*	*307*	*313*	*911,4636*	*910,4563*	*910,4549*	*0,00*	*1*	*8*	*3,10E+00*	*R.RTPDYFL.-*	
												2	141	148	951,4745	950,4672	950,461	0,01	0	42	2,00E-03	K.YGNANVWK.I	
												3	287	298	1456,7314	1455,7241	1455,7259	0,00	0	80	1,90E-07	R.NHTFIQFEPAPR.R	
												4	260	272	1589,7764	1588,7691	1588,7708	0,00	0	46	4,90E-04	K.VVTIFSAPNYCYR.C	
TIM19	-dig	AT1G13320	PP2AA3	1/2	TAIR9	194	1,30E-15	7	27	11	130	1	133	142	1137,5729	1136,5656	1136,5614	0,00	0	29	3,70E-02	R.LSAGEWFTAR.V	
												2	337	352	1576,8361	1575,8288	1575,8364	-0,01	0	40	2,50E-03	R.SALASVIMGMAPVLGK.D	2 Oxidation(M)
												3	310	325	1858,0563	1857,049	1857,0546	-0,01	0	61	5,90E-06	R.ILNPELAIQHILPCVK.E	

Protein identification details were obtained with the 4800 MALDI TOF/TOF™ Proteomics analyzer (AB SCIEX) and the GPS explorer v3.6 (AB SCIEX) software package combined with search engine Mascot version 2.1 or 2.2 (Matrix Science)
Column headers for Protein and Peptide data are as follows :
Protein score: The score calculated by the Mascot search engine for each protein. This score is based on the probability that peptide mass matches are non-random events. If the Protein Score is equal to or greater than the Mascot® Significance Level calculated for the database search, the protein match is considered to be statistically non-random at the 95% confidence interval. Protein score = -10*Log(P), where P is the probability that the observed match is a random event. **Expect**: Protein score expectation value. **RMS error (ppm):** RMS error of the set of matched mass values, in ppm. **Sequence coverage %:** Percentage of protein sequence covered by assigned peptide matches. **Unique peptides**: The number of peptides with unique sequences matching the selected protein. **Total Ion Score**: A score calculated by weighting Ion Scores for all individual peptides matched to a given protein. **Peptide Number:** Peptide index number within the list of peptides associated with a given protein. **Start**: The starting position of the peptide in the protein. **End:** The ending position of the peptide in the protein. **Observed**: The observed monoisotopic mass of the peptide in the spectrum (m/z). **Mr (Exp)**: The experimental mass of the peptide calculated from the observed m/z value. **Mr (Calc)**: The theoretical mass of the peptide based on its sequence. **Delta (Da)**: The difference between the theoretical (Mr (Calc)) and experimental (Mr (Exp)) masses, in daltons. **Miss**: Number of missed Trypsin cleavage sites. **Ions score**: The Ions Score is calculated by the Mascot search engine for each peptide matched from MS/MS peak lists. This score is based on the probability that ion fragmentation matches are non-random events. If the Ion Score is equal to or greater than the Mascot® Significance Level calculated for the database search, the peptide match is considered to be statistically non-random at the 95% confidence interval. Ions score = -10*Log(P), where P is the probability that the observed match is a random event. **Best Ions score:** The highest individual Ion Score for a given protein identification. **Expect**: Ions score expectation value. **Peptide:** The amino acid sequence of the selected peptide. **Variable Modification**: Variable modification type on the peptide.

Supplementary Table S2: VELOS orbitrap analysis of TAP TON1b eluates

Accession	Description	Score	Coverage	# Unique Peptides	# Peptides	# AAs
AT3G55005	**TON1b**	**237,09**	**64,20**	**17**	**18**	**257**

Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
High	NEDSRPLLLDVLEGFLK		1	4,69	3	1958,06035	0,47	653,35830	28,73	0
High	NEDSRPLLLDVLeGFLK	E13(Methyl)	1	4,48	3	1972,07370	-0,69	658,02942	29,64	0
High	NEDSRPLLLDVLEGFLKFENmTQVMGGSSR	M21(Oxidation)	1	4,48	4	3398,66884	-0,95	850,42267	29,10	1
High	ASVFEAIEEEDRVIENNEGLPPALLGScNDR	C28(Carbamidomethyl)	1	4,43	4	3443,63776	-0,23	861,66490	26,02	1
High	SEIRDFSINNGYeLNR	E13(Methyl)	1	4,13	3	1940,94687	0,37	647,65381	21,77	1
High	RSVSASQASGAATSGYR		1	4,08	2	1655,80777	-1,14	828,40752	17,14	1
High	FENmTQVmGGSSR	M4(Oxidation); M8(Oxidation)	1	3,79	2	1475,62496	-0,32	738,31612	17,30	0
High	VIeNNeGLPPALLGScNDR	E3(Methyl); E6(Methyl); C16(Carbamidomethyl)	1	3,74	2	2096,04546	0,61	1048,52637	23,56	0
High	LLSALIcEYLDWAQLNHTLK	C7(Carbamidomethyl)	1	3,68	2	2401,25728	-0,51	1201,13228	27,13	0
High	YDTEDmPEEVmR	M6(Oxidation); M11(Oxidation)	1	3,65	2	1546,60247	-0,78	773,80487	18,49	0
High	ASVFEAIEEEDRVIENNeGLPPALLGScNDR	E18(Methyl); C28(Carbamidomethyl)	1	3,60	3	3457,65342	-0,22	1153,22266	27,17	1
High	ASTALENLQLDRK		1	3,58	2	1458,78997	-0,81	729,89862	20,22	1
High	FeNMTQVMGGSSR	E2(Methyl)	1	3,55	2	1457,65068	-0,38	729,32898	21,93	0
High	SEIRDFSINNGYELNR		1	3,55	3	1926,93133	0,43	642,98196	21,38	1
High	VIENNEGLPPALLGScNDR	C16(Carbamidomethyl)	1	3,54	3	2068,01265	-0,11	690,00907	22,47	0
High	ReSETESSLSLDTR	E2(Methyl)	1	3,53	2	1623,78048	-1,00	812,39388	19,08	1
High	NedSRPLLLDVLEGFLK	E2(Methyl); D3(Methyl)	1	3,48	2	1986,08820	-1,27	993,54774	29,20	0
High	ESETESSLSLDTR		1	3,46	2	1453,66570	0,25	727,33649	20,03	0
High	ASTALENLQLDR		1	3,39	2	1330,69585	-0,25	665,85156	21,68	0
High	SVSASQASGAATSGYR		1	3,39	2	1499,70744	-0,73	750,35736	18,20	0
High	eSETESSLSLDTR	E1(Methyl)	1	3,38	2	1467,68340	1,65	734,34534	20,09	0
High	FENmTQVMGGSSR	M4(Oxidation)	1	3,37	2	1459,62924	-0,87	730,31826	18,99	0
High	YDTEDmPEeVMR	M6(Oxidation); E9(Methyl)	1	3,23	2	1544,62241	-1,30	772,81485	20,28	0
High	ASTALeNLQLDR	E6(Methyl)	1	3,20	2	1344,71044	-1,03	672,85886	21,40	0
High	DFSINNGYELNR		1	3,20	2	1441,67035	-0,23	721,33881	22,28	0
High	YDTEDMPEEVMR		1	3,14	2	1514,61221	-1,09	757,80974	21,49	0
High	SSASDSLPHQR		1	3,14	2	1184,56520	-0,24	592,78624	16,35	0
High	eSeTESSLSLDTR	E1(Methyl); E3(Methyl)	1	3,13	2	1481,69475	-1,27	741,35101	21,14	0
High	YDTEDmPeeVMR	M6(Oxidation); E8(Methyl); E9(Methyl)	1	3,11	2	1558,63833	-1,12	779,82280	20,89	0
High	YDTEDmPEEVMR	M6(Oxidation)	1	2,96	2	1530,60719	-1,03	765,80723	19,74	0
High	ASVFEAIEEEdR	D11(Methyl)	1	2,96	2	1408,65850	-0,45	704,83289	24,03	0
High	ASVFEAIEEEDR		1	2,92	3	1394,64457	0,77	465,55304	23,22	0
High	ASVFEAIEeeDRVIENNEGLPPALLGScNDR	E9(Methyl); E10(Methyl); C28(Carbamidomethyl)	1	2,91	4	3471,66665	-0,92	868,67212	26,83	1
High	RSSASDSLPHQR		1	2,88	2	1340,66502	-1,18	670,83615	15,96	1
High	YDTEDmPeeVmR	M6(Oxidation); E8(Methyl); E9(Methyl); M11(Oxidation)	1	2,87	2	1574,63445	-0,34	787,82086	19,71	0
High	YDTeDmPEEVmR	E4(Methyl); M6(Oxidation); M11(Oxidation)	1	2,85	2	1560,61769	-1,05	780,81248	18,77	0
High	RESeTeSSLSLDTR	E4(Methyl); E6(Methyl)	1	2,83	3	1637,79674	-0,62	546,60376	19,58	1
High	FeNmTQVMGGSSR	E2(Methyl); M4(Oxidation)	1	2,82	2	1473,64531	-0,57	737,32629	19,37	0
High	VIENNeGLPPALLGScNDR	E6(Methyl); C16(Carbamidomethyl)	1	2,81	3	2082,02652	-0,97	694,68036	22,75	0
High	DFSINNGYeLNR	E9(Methyl)	1	2,80	2	1455,68541	-0,63	728,34634	22,51	0
High	RESETESSLSLDTR		1	2,80	2	1609,76513	-0,82	805,38620	19,23	1
High	YDTeDMPEEVMR	E4(Methyl)	1	2,52	2	1528,62847	-0,68	764,81787	22,07	0
High	ASVFEAIeeeDR	E8(Methyl); E9(Methyl); E10(Methyl)	1	2,39	2	1436,68880	-1,14	718,84804	25,31	0
AT3G55000	**TON1a**	**129,58**	**60,00**	**13**	**14**	**260**				

Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
High	ASVFEAIEEEDRVIENNEGPPPALLGScNDR	C28(Carbamidomethyl)	1	5,27	3	3427,60361	-1,06	1143,20605	25,47	1
High	LLSALIcEYLDWAQLNHTLIVYQPESNLPK	C7(Carbamidomethyl)	1	4,89	3	3541,84348	0,96	1181,28601	28,02	0
High	NGDSGPLLLDVLeGFLK	E13(Methyl)	1	4,82	2	1800,97258	-0,95	900,98993	31,08	0
High	NGDSGPLLLDVLEGFLK		1	4,53	3	1786,95831	-0,18	596,32429	30,35	0
High	SELRDFNSNNGFELNR		1	4,47	3	1911,89481	0,18	637,96979	21,01	1
High	VIeNNEGPPPALLGScNDR	E3(Methyl); C16(Carbamidomethyl)	1	4,09	2	2065,99785	0,30	1033,50256	21,50	0
High	DSETESSSSLESR		1	3,99	2	1413,59636	-0,91	707,30182	17,68	0

	High	ASVFEAIEEEDRVIeNNEGPPPALLGScNDR	E15(Methyl); C28(Carbamidomethyl)	1	3,95	3	3441,62063	-0,66	1147,87839	25,03	1
	High	RDSETESSSSLESR		1	3,33	3	1569,69815	-0,39	523,90424	16,67	1
	High	VIENNEGPPPALLGScNDR	C16(Carbamidomethyl)	1	3,32	2	2051,97952	-1,01	1026,49340	21,15	0
	High	SSASDSLPPQR		1	3,31	2	1144,55866	-0,60	572,78297	17,35	0
	High	RDSETESSSSLeSR	E12(Methyl)	1	3,31	3	1583,71410	-0,20	528,57622	16,82	1
	High	FESmTQGmGSSSR	M4(Oxidation); M8(Oxidation)	1	3,30	2	1436,57681	-0,92	718,79204	16,35	0
	High	DFNSNNGFELNR		1	3,28	2	1426,63337	-0,89	713,82032	21,74	0
	High	RSSASDSLPPQR		1	3,24	2	1300,65837	-1,61	650,83282	16,58	1
	High	dSETESSSSLESR	D1(Methyl)	1	3,09	2	1427,61283	-0,32	714,31005	17,43	0
	High	RPVSASQASDR		1	2,98	2	1173,59650	-0,53	587,30189	15,45	0
	High	ASVFEAIEEEdR	D11(Methyl)	1	2,96	2	1408,65850	-0,45	704,83289	24,03	0
	High	ASVFEAIEEEDR		1	2,92	3	1394,64457	0,77	465,55304	23,22	0
	High	FESMTQGmGSSSR	M8(Oxidation)	1	2,87	2	1420,58199	-0,87	710,79463	17,67	0
	High	QGNQDTHEeVTR	E9(Methyl)	1	2,53	2	1427,64940	-1,13	714,32834	16,28	0
	High	ASVFEAIeeeDR	E8(Methyl); E9(Methyl); E10(Methyl)	1	2,39	2	1436,68880	-1,14	718,84804	25,31	0
AT5G18580	**FASS**	**127,05**	**67,50**	**22**	**22**	**480**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	EmDFDSFLDFVLALENK	M2(Oxidation)	1	4,90	2	2048,94927	-1,45	1024,97827	30,00	0
	High	QELKEYADGTLTEIFIER		1	4,89	3	2155,09128	-0,26	719,03528	24,03	1
	High	MNYEDFcHIASVcTEQIGPK	C7(Carbamidomethyl); C13(Carbamidomethyl)	1	4,82	3	2399,04288	-1,53	800,35248	22,80	0
	High	YIGSGAGLGSEALMELETK		1	4,44	2	1925,95305	0,25	963,48016	24,17	0
	High	KKPEEGSISQR		1	4,27	3	1258,67521	0,12	420,22992	15,40	1
	High	mNYEDFcHIASVcTEQIGPK	(Oxidation); C7(Carbamidomethyl); C13(Carbamidomet	1	3,99	3	2415,03824	-1,34	805,68427	21,90	0
	High	IcDmFLALDKDmSGSLcK	domethyl); M4(Oxidation); M12(Oxidation); C17(Carba	1	3,93	2	2135,94780	-0,15	1068,47754	21,84	1
	High	QSDLLLNADDLAAMWVcLR	C17(Carbamidomethyl)	1	3,93	3	2204,08261	-0,61	735,36572	28,42	0
	High	YIGSGAGLGSEALmeLETK	M14(Oxidation); E15(Methyl)	1	3,86	2	1955,96282	-0,16	978,48505	24,45	0
	High	YIGSGAGLGSEALmELETK	M14(Oxidation)	1	3,78	2	1941,94621	-0,65	971,47675	23,73	0
	High	IDmSELDEDSDGFLHSDEMESYIGGLIPNLAQLR	M3(Oxidation)	1	3,70	3	3825,73899	-2,14	1275,91785	27,76	0
	High	IcDMFLALDKDmSGSLcK	Carbamidomethyl); M12(Oxidation); C17(Carbamidome	1	3,64	2	2119,94902	-1,97	1060,47815	23,11	1
	High	KIPPASSmLWVR	M8(Oxidation)	1	3,51	3	1400,77150	-0,32	467,59535	20,34	1
	High	ILLSNcLQELmELHQESEEEVTDTEQAENWFSLTSAQR	C6(Carbamidomethyl); M11(Oxidation)	1	3,44	4	4524,07680	-1,13	1131,77466	26,34	0
	High	WIEGGNYELcIEDVR	C10(Carbamidomethyl)	1	3,43	2	1852,85307	-0,23	926,93018	23,67	0
	High	QGGTVASmLIDVR	M8(Oxidation)	1	3,37	2	1362,70378	-0,64	681,85553	21,77	0
	High	IDmSELDEDSDGFLHSDEmESYIGGLIPNLAQLR	M3(Oxidation); M19(Oxidation)	1	3,35	3	3841,74643	1,13	1281,25366	26,33	0
	High	IAILPFYLYVmR	M11(Oxidation)	1	3,34	2	1514,84295	-0,71	757,92511	26,65	0
	High	DmPPAFNQMYcR	M2(Oxidation); C11(Carbamidomethyl)	1	3,21	2	1545,62773	-0,43	773,31750	21,30	0
	High	IAILPFYLYVMR		1	3,16	2	1498,84734	-1,18	749,92731	27,98	0
	High	DmPPAFNQmYcR	M2(Oxidation); M9(Oxidation); C11(Carbamidomethyl)	1	3,13	2	1561,62419	0,57	781,31573	19,81	0
	High	GFWAHDNRENLLQEEEEPPEEESQ		1	3,13	3	2912,25840	-0,78	971,42432	22,16	1
	High	mNYeDFcHIASVcTEQIGPK	tion); E4(Methyl); C7(Carbamidomethyl); C13(Carbami	1	3,03	3	2429,05442	-1,11	810,35632	22,33	0
	High	SQEAGTIPSFYK		1	2,99	2	1327,65325	0,26	664,33026	21,27	0
	High	IcDMFLALDK	C2(Carbamidomethyl)	1	2,92	2	1225,59514	-0,39	613,30121	24,30	0
	High	YIGSGAGLGSEALmeLeTK	M14(Oxidation); E15(Methyl); E17(Methyl)	1	2,89	2	1969,97820	-0,30	985,49274	25,07	0
	High	EYADGTLTEIFIER		1	2,89	3	1656,81076	-0,51	552,94177	24,89	0
	High	ITLGDLLGcK	C9(Carbamidomethyl)	1	2,69	2	1089,59714	-0,16	545,30221	24,73	0
	High	ILLEIFK		1	2,63	2	875,55997	-0,17	438,28362	24,56	0
	High	QGGTVASMLIDVR		1	2,61	2	1346,70891	-0,62	673,85809	23,55	0
	High	IcDmFLALDK	C2(Carbamidomethyl); M4(Oxidation)	1	2,56	2	1241,58916	-1,10	621,29822	22,61	0
	High	ENcVIDDATGAeK	C3(Carbamidomethyl); E12(Methyl)	1	2,46	2	1435,63603	-0,69	718,32166	20,31	0
	High	KPEEGSISQR		1	2,42	2	1130,57930	-0,69	565,79329	15,93	0
AT3G25800	**PP2AA2**	**98,25**	**44,63**	**10**	**16**	**587**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	LAIIEYIPLLASQLGVGFFDDK		1	5,62	3	2422,32859	0,68	808,11438	31,48	0
	High	YmVANQLYELcEAVGPEPTR	M2(Oxidation); C11(Carbamidomethyl)	1	4,92	2	2356,09331	-0,67	1178,55029	23,66	0
	High	TDVMSmFEDLTQDDQDSVR	M6(Oxidation)	1	4,57	2	2247,93486	-1,46	1124,47107	24,43	0
	High	FFANQALQSIDNVMmSS	M15(Oxidation)	1	4,40	2	1918,87187	2,30	959,93958	27,11	0
	High	FFANQALQSIDNVmmSS	M14(Oxidation); M15(Oxidation)	1	4,10	2	1934,86165	-0,37	967,93446	24,43	0
	High	SLYTQLcQDDmPmVR	C7(Carbamidomethyl); M11(Oxidation); M13(Oxidation)	1	4,07	2	1888,82247	-0,74	944,91487	21,55	0
	High	SALASVImGmAPVLGK	M8(Oxidation); M10(Oxidation)	1	4,00	3	1576,84348	-0,22	526,28601	22,87	0

	High	LAIIEYIPLLASQLGVGFFDdK	D21(Methyl)	1	3,98	3	2436,33982	-1,14	812,78479	31,43	0
	High	TIRPGLVELSEDPDVDVR		1	3,82	2	2010,05022	-0,05	1005,52875	21,89	0
	High	ILNPEIAIQHILPcVK	C14(Carbamidomethyl)	1	3,78	2	1858,06035	-0,88	929,53381	24,89	0
	High	VLQSLIPIVDQSVVEK		1	3,76	3	1767,02597	-0,19	589,68018	24,53	0
	High	SALASVImGMAPVLGK	M8(Oxidation)	1	3,65	2	1560,84636	-1,63	780,92682	25,63	0
	High	TIRPGLVELSeDPDVDVR	E11(Methyl)	1	3,44	3	2024,06595	-0,01	675,36017	22,51	0
	High	LLEPQDcVQHILPVIVNFSQDK	C7(Carbamidomethyl)	1	3,32	3	2592,34824	-0,35	864,78760	25,31	0
	High	AVSLLAPVmGSEITcSK	M9(Oxidation); C15(Carbamidomethyl)	1	3,31	2	1778,90068	-1,18	889,95398	22,42	0
	High	ESDLVDHFISLVK		1	3,29	2	1501,78813	-1,08	751,39771	25,17	0
	High	LLRDNEAEVR		1	2,93	2	1214,64739	-1,20	607,82733	17,65	1
	High	VSAcGVFHIAYPSAPDmLK	C4(Carbamidomethyl); M17(Oxidation)	1	2,62	2	2079,00127	-1,26	1040,00427	22,52	0
	High	FAATVeSAHLK	E6(Methyl)	1	2,61	2	1187,64128	-0,56	594,32428	19,47	0
	High	ELSSDSSQHVR		1	2,59	2	1244,58501	-1,29	622,79614	16,21	0
AT3G06810.1	**IBR3**	**86,92**	**36,65**	**19**	**19**	**824**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	VSQFGHGQSNPTFLIEVGSGSSLKR		1	4,98	3	2632,35056	1,01	878,12170	21,69	1
	High	SGFAmTEPQVASSDATNIEcSIR	M5(Oxidation); C20(Carbamidomethyl)	1	4,74	2	2487,11235	-0,16	1244,05981	21,82	0
	High	ALASLHSADVDAIGLEK		1	4,56	2	1709,90544	-0,87	855,45636	21,30	0
	High	IADGPDEVHLGTIGK		1	4,36	2	1521,78942	-0,93	761,39835	20,50	0
	High	NTGVQANELVESALGYIAR		1	4,26	2	2005,03667	0,84	1003,02197	26,06	0
	High	NIPAEDSTGATSGLVHGDFR		1	4,14	2	2043,97295	-0,08	1022,49011	20,79	0
	High	FAADNVSGFPTNPSQFK		1	4,09	2	1826,86897	-1,04	913,93812	22,32	0
	High	YGNKEQISEWLIPLLEGR		1	3,92	3	2145,13547	0,70	715,71667	26,20	1
	High	EGLWNLFVPVDSAAR		1	3,90	2	1673,86363	-0,62	837,43545	27,07	0
	High	ELAATENKHNLSGK		1	3,76	2	1511,77995	-0,90	756,39362	16,56	1
	High	SFDQLFGEGLTNLEYGYLcEImGR	C19(Carbamidomethyl); M22(Oxidation)	1	3,76	3	2828,28916	-0,55	943,43457	28,54	0
	High	FIAQHGSFVSDLAK		1	3,76	2	1519,78874	-1,10	760,39801	21,01	0
	High	VSQFGHGQSNPTFLIEVGSGSSLK		1	3,39	3	2476,24308	-1,50	826,08588	22,61	0
	High	SVWAPQVFNcGAPDTGNmEVILR	C10(Carbamidomethyl); M18(Oxidation)	1	3,19	3	2577,21970	-1,12	859,74475	24,01	0
	High	FmETHIYPmENEFSK	M2(Oxidation); M9(Oxidation)	1	2,99	2	1934,82915	-0,44	967,91821	20,30	0
	High	LLVLEAADHLDK		1	2,98	2	1336,74687	-0,22	668,87708	22,20	0
	High	WLmGNASAGER	M3(Oxidation)	1	2,90	2	1207,55156	-0,78	604,27942	19,23	0
	High	QGDSYVINGTK		1	2,78	2	1181,57939	-0,29	591,29333	18,90	0
	High	mFELVDWLR	M1(Oxidation)	1	2,67	2	1224,60784	-0,32	612,80756	26,26	0
	High	FMETHIYPmENEFSK	M9(Oxidation)	1	2,63	2	1918,83464	-0,23	959,92096	21,06	0
AT3G53540	**TRM19**	**48,20**	**19,16**	**12**	**12**	**924**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	SHSSYNSSPEVSITPSLSK		1	4,62	2	2006,96501	-0,79	1003,98615	19,96	0
	High	EFNDALEALDSNKDLLLK		1	4,55	2	2048,05571	0,48	1024,53149	24,33	1
	High	ELQWLSLEDDIEIIGR		1	4,09	2	1928,99358	-1,51	965,00043	27,33	0
	High	VNANLTQAEMAFIR		1	3,84	2	1577,80950	-0,65	789,40839	23,49	0
	High	HASYDTIDLPNEELR		1	3,82	2	1772,84490	-0,08	886,92609	21,28	0
	High	TAmSSEALDLSTVTSVTDPDISR	M3(Oxidation)	1	3,59	2	2412,14263	-0,88	1206,57495	23,27	0
	High	LmGLDVLPSQSSSHK	M2(Oxidation)	1	3,57	2	1614,81304	-1,62	807,91016	20,74	0
	High	LTHKFEHEIEISR		1	3,28	4	1638,85903	-0,53	410,47021	18,39	1
	High	KLLFDQISR		1	2,92	3	1119,65165	-0,42	373,88873	21,21	1
	High	TFASPSSSSDEFR		1	2,87	2	1417,62322	0,10	709,31525	20,06	0
	High	FLQHPDSLFTK		1	2,74	2	1332,69646	1,31	666,85187	21,15	0
	High	FKDVFEVLDAK		1	2,62	2	1310,69878	-0,28	655,85303	23,37	1
AT1G13320	**PP2AA3**	**45,71**	**26,92**	**3**	**10**	**587**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	YmVANQLYELcEAVGPEPTR	M2(Oxidation); C11(Carbamidomethyl)	1	4,92	2	2356,09331	-0,67	1178,55029	23,66	0
	High	SALASVImGmAPVLGK	M8(Oxidation); M10(Oxidation)	1	4,00	3	1576,84348	-0,22	526,28601	22,87	0
	High	LAIIEYIPLLASQLGVGFFDEK		2	3,98	3	2436,33982	-1,14	812,78479	31,43	0
	High	SIYGQLcQDDmPmVR	C7(Carbamidomethyl); M11(Oxidation); M13(Oxidation)	1	3,84	2	1844,79436	-1,79	922,90082	21,03	0
	High	ILNPELAIQHILPcVK	C14(Carbamidomethyl)	1	3,78	2	1858,06035	-0,88	929,53381	24,89	0
	High	SALASVImGMAPVLGK	M8(Oxidation)	1	3,65	2	1560,84636	-1,63	780,92682	25,63	0
	High	YFANQALQSIDNVmmSS	M14(Oxidation); M15(Oxidation)	1	3,39	2	1950,85198	-2,71	975,92963	23,81	0
	High	AVSLLAPVmGSEITcSK	M9(Oxidation); C15(Carbamidomethyl)	1	3,31	2	1778,90068	-1,18	889,95398	22,42	0

	High	ESDLVEHFTPLAK		1	2,65	2	1485,75713	-0,89	743,38220	21,97	0
	High	ELSSDSSQHVR		1	2,59	2	1244,58501	-1,29	622,79614	16,21	0
	High	FAATIESAHLK		2	2,55	2	1187,64128	-0,56	594,32428	19,47	0
AT3G58500	**PP2A-4**	**41,53**	**45,37**	**10**	**10**	**313**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	GAGYTFGQDISEQFNHTNNLK		1	4,78	2	2341,08257	-0,80	1171,04492	22,30	0
	High	cPDTNYLFMGDYVDR	C1(Carbamidomethyl)	1	4,51	2	1865,78093	-1,30	933,39410	24,23	0
	High	GYYSVETVTLLVGLK		1	4,37	2	1641,90911	-0,45	821,45819	25,96	0
	High	SPVTIcGDIHGQFHDLAELFR	C6(Carbamidomethyl)	1	3,71	3	2412,17466	-0,80	804,72974	24,54	0
	High	cPDTNYLFmGDYVDR	C1(Carbamidomethyl); M9(Oxidation)	1	3,55	2	1881,77556	-1,45	941,39142	22,89	0
	High	AHQLVmDGFNWAHEQK	M6(Oxidation)	1	3,27	3	1926,89096	-0,34	642,96851	20,35	0
	High	cGNmASILEVDDcR	Carbamidomethyl); M4(Oxidation); C13(Carbamidomet	1	3,22	2	1655,68266	0,22	828,34497	20,96	0
	High	AKEILmDESNVQPVK	M6(Oxidation)	1	3,18	2	1716,88078	-1,73	858,94403	18,90	1
	High	NHTFIQFEPAPR		1	2,78	2	1456,73174	-1,03	728,86951	20,98	0
	High	EILmDESNVQPVK	M4(Oxidation)	1	2,56	2	1517,74986	-1,19	759,37857	19,86	0
	High	VVTIFSAPNYcYR	C11(Carbamidomethyl)	1	2,47	2	1589,77725	-0,54	795,39226	23,10	0
AT5G26910	**TRM8**	**38,62**	**21,83**	**11**	**11**	**852**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	VLSESESVSDcTSFYDK	C11(Carbamidomethyl)	1	4,33	2	1952,84294	-0,05	976,92511	21,00	0
	High	SDSSccASSVTSDDGQGTR	C5(Carbamidomethyl); C6(Carbamidomethyl)	1	4,28	2	1976,75078	-2,50	988,87903	17,47	0
	High	EYALGmATDVLPASLFDEmEGR	M6(Oxidation); M19(Oxidation)	1	4,24	2	2447,10674	-1,60	1224,05701	25,32	0
	High	GLSSDSLSSTQGIGQDTDSAVSFNIGGDSLNALLEQK		1	4,21	3	3711,77817	-1,39	1237,93091	25,68	0
	High	LmGLESLPVPNVQePR	M2(Oxidation); E14(Methyl)	1	3,76	2	1808,95256	-2,78	904,97992	23,58	0
	High	WDAYENLGYVNLR		1	3,69	2	1612,77402	-0,91	806,89065	23,68	0
	High	EmDVISFTFSSPIK	M2(Oxidation)	1	3,30	2	1616,78630	-0,87	808,89679	24,57	0
	High	EGVVSALVEPHLLSAF		1	3,19	2	1667,89958	-0,48	834,45343	26,25	0
	High	FQSETFPPR		1	2,60	2	1108,54094	-1,16	554,77411	21,18	0
	High	NPIYVmEAASR	M6(Oxidation)	1	2,56	2	1266,61394	-0,65	633,81061	19,46	0
	High	ITTSLTTPSTSK		1	2,44	2	1236,66716	-0,85	618,83722	19,02	0
AT4G28760	**TRM20**	**35,29**	**13,53**	**9**	**9**	**924**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	LLQELVEEAVIDLTR		1	4,99	2	1740,97331	-0,56	870,99030	29,93	0
	High	DSGEDmDANSLAAESLVK	M6(Oxidation)	1	4,96	2	1867,82109	-0,85	934,41418	21,79	0
	High	DASQcSSmSQLAAPSPVTLTGK	C5(Carbamidomethyl); M8(Oxidation)	1	3,87	2	2252,05107	-1,05	1126,52917	21,46	0
	High	INSIVSETTTTR		1	3,85	2	1321,69499	-0,63	661,35114	19,64	0
	High	TSSTLGEmLALTETK	M8(Oxidation)	1	3,69	2	1597,79778	-0,77	799,40253	21,60	0
	High	AVSSSQSSPR		1	3,06	2	1005,49584	-0,16	503,25156	15,45	0
	High	VSNLFFFK		1	2,70	2	1001,54588	0,36	501,27658	24,50	0
	High	LASSSQETGWGNR		1	2,61	2	1392,64812	-1,56	696,82770	18,83	0
	High	GYFDEPEDVETK		1	2,52	2	1428,61565	-0,66	714,81146	21,22	0
AT2G42500	**PP2A-3**	**28,75**	**36,74**	**1**	**8**	**313**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	GAGYTFGQDISEQFNHTNNLK		1	4,78	2	2341,08	-0,80	1171,04	22,30	0
	High	SPVTIcGDIHGQFHDLAELFR	C6(Carbamidomethyl)	1	3,71	3	2412,17	-0,80	804,73	24,54	0
	High	cGNmASILEVDDcR	Carbamidomethyl); M4(Oxidation); C13(Carbamidomet	1	3,22	2	1655,68	0,22	828,34	20,96	0
	High	AKEILmDESNVQPVK	M6(Oxidation)	1	3,18	2	1716,88	-1,73	858,94	18,90	1
	High	IGGmcPDTNYLFmGDYVDR	M4(Oxidation); C5(Carbamidomethyl); M13(Oxidation)	1	2,92	2	2255,94	-0,86	1128,47	23,08	0
	High	NHTFIQFEPAPR		1	2,78	2	1456,73	-1,03	728,87	20,98	0
	High	EILmDESNVQPVK	M4(Oxidation)	1	2,56	2	1517,75	-1,19	759,38	19,86	0
	High	VVTIFSAPNYcYR	C11(Carbamidomethyl)	1	2,47	2	1589,78	-0,54	795,39	23,10	0
AT3G05750	**TRM6**	**25,87**	**13,23**	**7**	**7**	**801**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	SDSScSTSTPTSDDGQGSK	C5(Carbamidomethyl)	1	4,16	2	1903,74394	-1,00	952,37561	16,26	0
	High	LmGLESIPVPNALEPR	M2(Oxidation)	1	3,82	2	1751,93328	-1,63	876,47028	23,88	0
	High	QNQFAETSVSNQR		1	3,31	2	1508,70842	-0,29	754,85785	18,55	0
	High	dmDVISFTFSSPIK	D1(Methyl); M2(Oxidation)	2	3,30	2	1616,78630	-0,87	808,89679	24,57	0
	High	DmDVISFTFSSPIK	M2(Oxidation)	1	3,12	2	1602,77104	-0,64	801,88916	25,04	0
	High	SKKPANGVQEAGVNSDK		1	2,98	3	1728,88565	-1,12	576,96674	15,81	1

	High	GQSPQISNGTcNNK	C11(Carbamidomethyl)	1	2,63	2	1504,68108	0,09	752,84418	16,73	0
	High	FSSSDSSSSLPmK	M12(Oxidation)	1	2,55	2	1375,60356	-0,79	688,30542	18,19	0
AT1G74160	**TRM4**	**23,22**	**9,37**	**7**	**7**	**1025**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	SLQQVDDQLSQASNESR		1	4,73	2	1904,89250	-1,05	952,94989	20,71	0
	High	SGNWADFSGEmSGLVLDVER	M11(Oxidation)	1	3,99	2	2184,98296	-1,73	1092,99512	24,41	0
	High	YISEILLASGLLLR		1	3,44	2	1560,93437	-1,06	780,97083	27,60	0
	High	LSESFSEScSSSSK	C9(Carbamidomethyl)	1	3,29	2	1521,63555	-1,22	761,32141	18,69	0
	High	ELcSAIETQQK	C3(Carbamidomethyl)	1	2,85	2	1306,62993	-0,66	653,81860	19,09	0
	High	SPSVIEAAK		1	2,54	2	901,49932	0,38	451,25330	18,43	0
	High	QQQSTNFAVQR		1	2,38	2	1306,64934	-0,41	653,82831	18,56	0
AT1G25490	**PP2AA1**	**17,70**	**13,10**	**1**	**5**	**588**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	LLNPELAIQHILPcVK	C14(Carbamidomethyl)	1	3,78	2	1858,06035	-0,88	929,53381	24,89	0
	High	LAIIEYVPLLASQLGIGFFDdK	D21(Methyl)	4	2,94	3	2436,33982	-1,14	812,78479	31,43	0
	High	LLRDNEAEVR		1	2,93	2	1214,64739	-1,20	607,82733	17,65	1
	High	ELSSDSSQHVR		1	2,59	2	1244,58501	-1,29	622,79614	16,21	0
	High	YFANQALNSIDGSTAAQS		1	2,54	2	1857,86443	1,62	929,43585	23,14	0
AT5G57580	**Calmodulin-binding protein**	**11,50**	**6,96**	**3**	**3**	**647**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	EGVGTLGELVFTDNSSWIR		1	4,41	2	2080,03520	0,26	1040,52124	26,17	0
	High	LTAEGINTVEDFLR		1	3,87	2	1577,81584	-0,76	789,41156	24,82	0
	High	NLDGNDDDQPER		1	3,22	2	1387,57158	-0,38	694,28943	17,51	0
AT1G63670	**TRM12**	**5,77**	**3,92**	**2**	**2**	**689**					
	Peptide confidence	Sequence	Modifications	Rank	XCorr	Charge	MH+ [Da]	ΔM [ppm]	m/z [Da]	RT [min]	# Missed Cleavages
	High	IGLSFDDPNIDLIEK		1	2,91	2	1688,87175	-1,47	844,93951	24,77	0
	High	TSDVSTSTVGHR		1	2,85	2	1246,60198	-0,23	623,80463	16,47	0

Protein identification details were obtained with the LTQ Orbitrap Velos (Thermo Fisher Scientific) and the Proteome Discoverer software package version 1.3 (Thermo Fisher Scientific) combined with search engine SEQUEST.
Proteins and peptides headers generated by the software package and used in the table are listed below.
Score: Displays the protein score, which is the sum of the scores of the individual peptides. For SEQUEST results, the score is the sum of all peptide Xcorr values above the specified score threshold. The score threshold is calculated as follows: 0.8 + peptide_charge x peptide_relevance_factor where peptide_relevance_factor is an advanced parameter of the SEQUEST node in the "Protein Scoring Option" category with a default value of 0.4. For each spectrum, only the highest-scoring match is used. For each spectrum and sequence, the Proteome Discoverer application uses only the highest scored peptide. When it performs a search using dynamic modifications, one spectrum might have multiple matches because of permutations of the modification site. **Coverage**: Displays by default the percentage of the protein sequence covered by identified peptides. **# Unique Peptides**: Displays the number of peptide sequences unique to a protein group. **# Peptides**: Displays the number of distinct peptide sequences in the protein group. **# AAs**: Shows by default the sequence length of the protein. **Peptide Confidence**: Indicates a confidence level associated with the peptide sequence: high confidence (>99%), medium confidence (>95%, <99%), low confidence (<95%). **Sequence**: Displays the sequence of amino acids that compose the peptide. **Modifications**: Displays the static and dynamic modifications identified in the peptide. **XCorr (search-dependent)**: Scores the number of fragment ions that are common to two different peptides with the same precursor mass and calculates the cross-correlation score for all candidate peptides queried from the database (SEQUEST searches only). **Rank**: Displays the ordering of peptides by rank. **# Missed Cleavages**: Displays the number of cleavage sites in a peptide sequence that a cleavage reagent (enzyme) did not cleave. This number excludes cases where an amino acid such as proline inhibits the cleaving enzyme. For example, if proline resides next to lysine or arginine, trypsin does not cleave the lysine or arginine. The # of Missed Cleavages value is 0 for a complete digest of all peptides. **Charge**: Displays the charge state of the peptide. **m/z [Da]**: Displays the mass-to-charge ratio of the precursor ion, in daltons. **MH+ [Da]**: Displays the protonated monoisotopic mass of the peptides, in daltons. **ΔM [ppm]**: Displays the difference between the theoretical mass of the peptide and the experimental mass of the precursor ion. **RT [min]**: Displays the retention time when the peptide was observed, in minutes.

Supplementary Table S3: VELOS orbitrap analysis of TAP TON1a and FASS eluates

Bait	Accession	Description	Score	Coverage %	Unique Peptide	# Peptides	# AAs					
TON1A	AT3G55000	TON1a	13660	67,7	19	21	260					
TON1A	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
TON1A	High	NGDSGPLLLDVLEGFLK		1	139,44	5,60E-13	2	1785,951	1785,951	1E-04	893,983	0
TON1A	High	VIENNEGPPPALLGSCNDR	E3(Methyl); C16(Carbamidomethyl)	1	128,48	8,30E-12	2	2064,988	2064,99	-0,002	1033,501	0
TON1A	High	FESMTQGMGSSSR		1	115,98	2,00E-11	2	1403,579	1403,581	-0,002	702,797	0
TON1A	High	RDSETESSSSLESR	E4(Methyl)	1	114,44	1,20E-10	2	1582,705	1582,707	-0,002	792,36	1
TON1A	High	ASAALENLQLDR		1	103,4	2,30E-09	2	1299,678	1299,678	-2E-04	650,8463	0
TON1A	High	ASVFEAIEEEDR	E9(Methyl)	1	100,06	4,80E-09	2	1407,651	1407,652	-6E-04	704,8329	0
TON1A	High	ASAALENLQLDRK		1	95,28	1,20E-08	2	1427,772	1427,773	-0,001	714,8933	1
TON1A	High	DSETESSSSLESR		1	94,03	5,30E-09	2	1412,591	1412,59	3E-04	707,3026	0
TON1A	High	ASVFEAIEEEDRVIENNEGPPPALLGSCNDR	C28(Carbamidomethyl)	1	92,36	2,00E-08	3	3426,594	3426,6	-0,006	1143,205	1
TON1A	High	SSASDSLPPQR		1	86,84	7,40E-08	2	1143,552	1143,552	-2E-04	572,7832	0
TON1A	High	DFNSNNGFELNR		1	78,36	3,50E-07	2	1425,622	1425,627	-0,005	713,8183	0
TON1A	High	AGLSTSGYR		1	76,86	8,20E-07	2	910,4507	910,4508	-2E-04	456,2326	0
TON1A	High	QGNQDTHEEVTR	E8(Methyl)	1	73,14	1,60E-06	2	1426,641	1426,644	-0,003	714,3278	0
TON1A	High	RPVSASQASDR		1	71,07	4,20E-06	2	1172,586	1172,59	-0,003	587,3005	1
TON1A	High	RSSASDSLPPQR		1	55,55	1,30E-04	2	1299,652	1299,653	-0,001	650,8332	1
TON1A	High	DFNSNNGFELNRNGDSGPLLLDVLEGFLK		1	53,23	2,20E-04	3	3194,542	3193,568	0,974	1065,855	1
TON1A	High	KLHASPSGR		1	51,22	2,00E-04	2	951,5245	951,525	-5E-04	476,7695	1
TON1A	High	RAGLSTSGYR		1	50,03	4,90E-04	2	1066,551	1066,552	-6E-04	534,283	1
TON1A	High	KDEFNWR		1	48,19	7,20E-04	2	993,4675	993,4668	7E-04	497,741	1
TON1A	High	DGTNEEEGR		1	40,85	2,70E-04	2	1005,4	1005,4	4E-04	503,7074	0
TON1A	High	EMMDLK	M2(Oxidation)	1	34,9	5,30E-03	2	781,3349	781,335	-1E-04	391,6747	0
TON1A												
TON1A	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
TON1A	AT3G55005	TON1b	3596	62,3	11	13	257					
TON1A	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
TON1A	High	SVSASQASGAATSGYR		1	137,32	7,30E-13	2	1498,695	1498,701	-0,006	750,3547	0
TON1A	High	PLLLDVLEGFLK		1	109,56	1,10E-10	2	1355,806	1355,806	-4E-04	678,9103	0
TON1A	High	FENMTQVMGGSSR		1	105,35	5,60E-10	2	1442,627	1442,628	-0,002	722,3206	0
TON1A	High	VIENNEGLPPALLGSCNDR	C16(Carbamidomethyl)	1	105,33	1,80E-09	2	2067,005	2067,006	-2E-04	1034,51	0
TON1A	High	ASVFEAIEEEDR	M9(Methyl)	1	100,06	4,80E-09	2	1407,651	1407,652	-6E-04	704,8329	0
TON1A	High	SSASDSLPHQR		1	90,07	3,50E-08	2	1183,558	1183,558	-2E-04	592,7862	0
TON1A	High	NEDSRPLLLDVLEGFLK		1	88,36	4,30E-08	3	1957,052	1957,052	-5E-04	653,3578	1
TON1A	High	ASTALENLQLDR		1	87,7	1,00E-07	2	1329,689	1329,689	1E-04	665,8517	0
TON1A	High	YDTEDMPEEVMR		1	74,45	1,70E-07	2	1513,605	1513,607	-0,002	757,8096	0
TON1A	High	DFSINNGYELNR		1	70,46	3,20E-06	2	1440,65	1440,663	-0,014	721,3321	0
TON1A	High	LLSALICEYLDWAQLNHTLK	C7(Carbamidomethyl)	1	57,52	7,20E-05	3	2400,252	2400,251	4E-04	801,0911	0
TON1A	High	VYQPECNSAK	C6(Carbamidomethyl)	1	56,03	7,80E-05	2	1194,533	1194,534	-8E-04	598,2738	0
TON1A	High	EMMDLK	M2(Oxidation)	1	34,9	5,30E-03	2	781,3349	781,335	-1E-04	391,6747	0
TON1A												
TON1A	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
TON1A	AT5G18580	FASS	1323	51,5	20	20	480					
TON1A	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
TON1A	High	YIGSGAGLGSEALMELETK		1	144,7	2,10E-13	2	1924,943	1924,945	-0,002	963,479	0
TON1A	High	QSDLLLNADDLAAMWVCLR	M14(Oxidation); C17(Carbamidomethyl)	1	131,18	4,50E-12	2	2219,071	2219,072	0	1110,543	0
TON1A	High	EMDFDSFLDFVLALENK	M2(Oxidation)	1	115,01	1,40E-10	2	2047,946	2047,945	0,002	1024,981	0
TON1A	High	ENLLQEEEEPPEEESQ		1	108,71	1,80E-10	2	1927,815	1927,817	-0,002	964,9149	0
TON1A	High	EYADGTLTEIFIER		1	105,95	1,30E-09	2	1655,806	1655,804	0,001	828,91	0
TON1A	High	QGGTVASMLIDVR		1	103,75	2,90E-09	2	1345,702	1345,702	-9E-04	673,858	0
TON1A	High	SQEAGTIPSFYK		1	94,53	1,60E-08	2	1326,646	1326,646	-1E-04	664,33	0
TON1A	High	GFLTTADIHSLFR		1	88,06	1,00E-07	2	1476,772	1476,773	-5E-04	739,3933	0
TON1A	High	MNYEDFCHIASVCTEQIGPK	M1(Oxidation); C7(Carbamidomethyl); C13(Carbamidomethyl)	1	84,05	5,10E-08	3	2414,032	2414,034	-0,003	805,6845	0
TON1A	High	DTPEGLTYLFR		1	80,13	5,10E-07	2	1310,651	1310,651	1E-04	656,3326	0
TON1A	High	ITLGDLLGCK	C9(Carbamidomethyl)	1	73,21	3,20E-06	2	1088,59	1088,59	2E-04	545,3024	0
TON1A	High	ICDMFLALDK	C2(Carbamidomethyl)	1	71,4	3,80E-06	2	1224,589	1224,588	6E-04	613,3017	0
TON1A	High	ENCVIDDATGAEK	C3(Carbamidomethyl)	1	70,28	1,70E-06	2	1420,61	1420,614	-0,004	711,3122	0
TON1A	High	DMPPAFNQMYCR	M2(Oxidation); C11(Carbamidomethyl)	1	54,97	1,40E-05	2	1544,62	1544,621	-0,001	773,3171	0
TON1A	High	ILLEIFK		1	53,31	1,40E-05	2	874,5528	874,5528	1E-04	438,2837	0
TON1A	High	FFFFCDPHR	C5(Carbamidomethyl)	1	44,26	7,60E-04	2	1271,554	1271,555	-7E-04	636,7843	0
TON1A	High	CLDLQGR	C1(Carbamidomethyl)	1	43,46	2,50E-03	2	860,4177	860,4174	3E-04	431,2161	0
TON1A	High	VFDEHVR		1	41,56	2,00E-03	2	900,4455	900,4454	2E-04	451,23	0
TON1A	High	GFWAHDNR		1	39,82	1,50E-03	2	1001,446	1001,447	-5E-04	501,7304	0
TON1A	High	KPEEGSISQR		1	37,23	8,80E-03	2	1129,572	1129,573	-9E-04	565,7932	1
TON1A												
TON1A	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
TON1A	AT3G25800	PP2AA2	475	29	8	11	587					
TON1A	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
TON1A	High	TDVMSMFEDLTQDDQDSVR		1	139,42	1,10E-13	2	2230,937	2230,936	0,001	1116,476	0
TON1A	High	ESDLVDHFISLVK		1	85,81	1,50E-07	2	1500,782	1500,782	-5E-04	751,3982	0
TON1A	High	SALASVIMGMAPVLGK		1	77,81	6,90E-07	2	1543,846	1543,847	-3E-04	772,9304	0
TON1A	High	FFANQALQSIDNVMMSS	M15(Oxidation)	1	71,83	1,80E-06	2	1917,86	1917,86	-1E-04	959,9373	0
TON1A	High	LAAGEWFTAR		1	67,55	1,20E-05	2	1120,56	1120,567	-0,006	561,2874	0
TON1A	High	TIRPGLVELSEDPDVDVR		1	58,51	6,40E-05	2	2009,042	2009,043	-0,001	1005,528	1
TON1A	High	ELSSDSSQHVR		1	56,62	6,90E-05	2	1243,579	1243,579	-3E-04	622,7967	0
TON1A	High	AVSLLAPVMGSEITCSK	C15(Carbamidomethyl)	1	56,53	1,50E-04	2	1761,901	1761,901	1E-04	881,9576	0
TON1A	High	VLQSLIPIVDQSVVEK		1	56,33	2,00E-05	2	1766,018	1766,019	-0,001	884,0162	0
TON1A	High	LLEPQDCVQHILPVIVNFSQDK	C7(Carbamidomethyl)	1	52,79	2,10E-04	3	2591,34	2591,342	-0,002	864,7874	0
TON1A	High	FAATVESAHLK		1	52,37	3,50E-04	2	1172,617	1172,619	-0,002	587,316	0
TON1A												

TON1A	Accession	Description	Score	Coverage %I	Unique Peptide	# Peptides	# AAs						
TON1A	AT5G57580	Calmodulin-binding protein	313	14,8	7	8	647						
TON1A	Peptide confidence	Sequence	Modifications	Rank	Peptide score	Expect	Charge	Mr(Exp)	Mr(Calc)	ΔM [Da]	m/z [Da]	# Missed Cleavages	
TON1A	High	LTAEGINTVEDFLR		1	105,31	2,20E-09	2	1576,809	1576,81	-3E-04	789,412	0	
TON1A	High	EGVGTLGELVFTDNSSWIR		1	91,18	4,80E-08	2	2079,028	2079,027	4E-04	1040,521	0	
TON1A	High	LYIYYAEDSR		1	78,34	7,10E-07	2	1291,61	1291,608	0,002	646,8123	0	
TON1A	High	MWDALVEHAK		1	68,57	5,60E-06	2	1198,58	1198,581	0	600,2975	0	
TON1A	High	LCSSLEPILR	C2(Carbamidomethyl)	1	59,75	6,50E-05	2	1186,638	1186,638	-3E-04	594,3261	0	
TON1A	High	AVVYGPEASAK		1	51,35	5,10E-04	2	1090,565	1090,566	-8E-04	546,2898	0	
TON1A	High	LSLPLFTGGK		1	44,04	8,10E-04	2	1031,601	1031,602	-1E-04	516,808	0	
TON1A	High	HYPPALNDDVWR		1	38,77	7,20E-03	2	1481,704	1481,705	-0,001	741,8592	0	
TON1A													
TON1A	Accession	Description	Score	Coverage %I	Unique Peptide	# Peptides	# AAs						
TON1A	AT3G53540	TRM19	307	11,8	9	9	924						
TON1A	Peptide confidence	Sequence	Modifications	Rank	Peptide score	Expect	Charge	Mr(Exp)	Mr(Calc)	ΔM [Da]	m/z [Da]	# Missed Cleavages	
TON1A	High	SHSSYNSSPEVSITPSLSK		1	141,16	4,30E-13	2	2005,959	2005,959	2E-04	1003,987	0	
TON1A	High	ELQWLSLEDDIEIIGR		1	105,19	1,50E-09	2	1927,988	1927,989	-0,001	965,0011	0	
TON1A	High	LLFDQISR		1	57,35	7,70E-05	2	990,5495	990,5498	-3E-04	496,282	0	
TON1A	High	EGDQPSPVSVLEASFDDDVSSGSECFESVSADLR	C25(Carbamidomethyl)	1	54,53	5,40E-05	3	3617,568	3616,564	1,005	1206,863	0	
TON1A	High	MQLQLLK		1	54,28	2,10E-04	2	872,5149	872,5153	-4E-04	437,2647	0	
TON1A	High	KLLFDQISR		1	47,98	3,90E-04	2	1118,644	1118,645	-3E-04	560,3295	1	
TON1A	High	LPCTTTHGR	C3(Carbamidomethyl)	1	45,24	8,50E-04	2	1041,502	1041,503	-6E-04	521,7583	0	
TON1A	High	IQETLR		1	39,35	7,20E-03	2	758,4288	758,4286	2E-04	380,2217	0	
TON1A	High	FEHEIEISR		1	36,28	9,20E-03	2	1158,567	1158,567	-4E-04	580,2905	0	
TON1A													
TON1A	Accession	Description	Score	Coverage %I	Unique Peptide	# Peptides	# AAs						
TON1A	\T2G42500/AT3G5850	PP2A3/PP2A4	203	31	8	8	313						
TON1A	Peptide confidence	Sequence	Modifications	Rank	Peptide score	Expect	Charge	Mr(Exp)	Mr(Calc)	ΔM [Da]	m/z [Da]	# Missed Cleavages	
TON1A	High	QITQVYGFYDECLR	C12(Carbamidomethyl)	1	86,57	1,00E-07	2	1790,828	1790,83	-0,002	896,4212	0	
TON1A	High	NHTFIQFEPAPR		1	64,52	1,80E-05	2	1455,726	1455,726	-4E-04	728,87	0	
TON1A	High	VVTIFSAPNYCYR	C11(Carbamidomethyl)	1	63,31	2,60E-05	2	1588,77	1588,771	-0,001	795,3921	0	
TON1A	High	EILMDESNVQPVK	M4(Oxidation)	1	47,99	9,40E-04	2	1516,744	1516,744	-8E-04	759,379	0	
TON1A	High	YGNANVWK		1	45,9	1,40E-03	2	950,4602	950,461	-8E-04	476,2374	0	
TON1A	High	RGEPDVTR		1	41,29	2,00E-03	2	928,4738	928,4726	0,001	465,2442	1	
TON1A	High	GAGYTFGQDISEQFNHTNNLK		1	40,63	3,50E-03	3	2340,075	2340,077	-0,002	781,0324	0	
TON1A	High	PLSEQQVR		1	40,4	2,60E-03	2	955,5088	955,5087	1E-04	478,7617	0	
TON1A													
TON1A	Accession	Description	Score	Coverage %I	Unique Peptide	# Peptides	# AAs						
TON1A	AT3G05750	TRM6	179	6,4	4	4	801						
TON1A	Peptide confidence	Sequence	Modifications	Rank	Peptide score	Expect	Charge	Mr(Exp)	Mr(Calc)	ΔM [Da]	m/z [Da]	# Missed Cleavages	
TON1A	High	EFSLGMATDILPLSLFDETEGK		1	101,6	4,10E-09	2	2412,175	2412,177	-0,002	1207,095	0	
TON1A	High	QNQFAETSVSNQR		1	83,53	2,10E-07	2	1507,7	1507,702	-0,002	754,8571	0	
TON1A	High	QDIFLER		1	66,95	1,60E-05	2	919,4759	919,4763	-4E-04	460,7452	0	
TON1A	High	EILADQVLK		1	36,03	6,30E-03	2	1027,591	1027,591	-5E-04	514,8027	0	
TON1A													
TON1A	Accession	Description	Score	Coverage %I	Unique Peptide	# Peptides	# AAs						
TON1A	AT5G26910	TRM8	86	4,6	2	2	853						
TON1A	Peptide confidence	Sequence	Modifications	Rank	Peptide score	Expect	Charge	Mr(Exp)	Mr(Calc)	ΔM [Da]	m/z [Da]	# Missed Cleavages	
TON1A	High	ETYEEGIDIEGEIVSTLVDDLVNDLVSGTQR		1	78,91	5,00E-07	3	3407,643	3407,647	-0,003	1136,888	0	
TON1A	High	TLFDFVNK		1	37,73	5,20E-03	2	982,5128	982,5124	4E-04	492,2637	0	
TON1A													
TON1A	Accession	Description	Score	Coverage %I	Unique Peptide	# Peptides	# AAs						
TON1A	AT2G45240	MAP1A	50	5,3	2	2	398						
TON1A	Peptide confidence	Sequence	Modifications	Rank	Peptide score	Expect	Charge	Mr(Exp)	Mr(Calc)	ΔM [Da]	m/z [Da]	# Missed Cleavages	
TON1A	High	HATMSGLSVVR	M4(Oxidation)	1	41,17	4,30E-03	2	1172,595	1172,597	-0,002	587,3049	0	
TON1A	High	AIAIVKPGVR		1	35,45	4,00E-04	2	1022,66	1022,66	-2E-04	512,3372	1	

Bait	Accession	Description	Score	Coverage %I	Unique Peptide	# Peptides	# AAs						
FASS	AT5G18580	FASS	3906	81	32	32	480						
FASS	Peptide confidence	Sequence	Modifications	Rank	Peptide score	Expect	Charge	Mr(Exp)	Mr(Calc)	ΔM [Da]	m/z [Da]	# Missed Cleavages	
FASS	High	YIGSGAGLGSEALMELETK		1	157,28	1,20E-14	2	1924,945	1924,945	2E-04	963,48	0	
FASS	High	QSDLLLNADDLAAMWVCLR	C17(Carbamidomethyl)	1	146,63	1,40E-13	2	2203,08	2203,077	0,004	1102,547	0	
FASS	High	MNYEDFCHIASVCTEQIGPK	M2(Oxidation); C7(Carbamidomethyl); C13(Carbamidomethyl)	1	130,67	1,10E-12	2	2414,032	2414,034	-0,002	1208,023	0	
FASS	High	EMDFDSFLDFVLALENK		1	123	2,60E-11	2	2031,951	2031,95	7E-04	1016,983	0	
FASS	High	SQEAGTIPSFYK		1	114,05	1,90E-10	2	1326,645	1326,646	-0,001	664,3296	0	
FASS	High	QGGTVASMLIDVR		1	107,68	1,20E-09	2	1345,702	1345,702	-2E-04	673,8584	0	
FASS	High	ICDMFLALDKDMSGSLCK	C2(Carbamidomethyl); M12(Oxidation); C17(Carbamidomethyl)	1	107,63	4,80E-10	2	2118,946	2118,946	0	1060,48	1	
FASS	High	GFLTTADIHSLFR		1	100,06	6,00E-09	2	1476,772	1476,773	-2E-04	739,3934	0	
FASS	High	EYADGTLTEIFIER		1	99,64	5,70E-09	2	1655,804	1655,804	-8E-04	828,909	0	
FASS	High	ENCVIDDATGAEK	C3(Carbamidomethyl); E12(Methyl)	1	89,89	2,50E-08	2	1434,629	1434,63	-0,001	718,3215	0	
FASS	High	WIEGGNYELCIEDVR	E8(Methyl); C10(Carbamidomethyl)	1	87,5	7,90E-08	2	1865,861	1865,862	-8E-04	933,9378	0	
FASS	High	DTPEGLTYLFR	E4(Methyl)	1	84,2	2,00E-07	2	1324,669	1324,666	0,003	663,342	0	
FASS	High	ITLGDLLGCK	C9(Carbamidomethyl)	1	79,08	8,30E-07	2	1088,59	1088,59	-2E-04	545,3022	0	
FASS	High	WIEGGNYELCIEDVRDEIWDMVK	C10(Carbamidomethyl)	1	75,28	1,10E-06	3	2868,31	2868,31	4E-04	957,1107	1	
FASS	High	_SNCLQELMELHQESEEEVTDTEQAENWFSLTSA(	C6(Carbamidomethyl); M11(Oxidation)	1	72,75	1,20E-06	3	4523,093	4523,074	0,019	1508,705	0	
FASS	High	ICDMFLALDK	C2(Carbamidomethyl)	1	71,65	3,60E-06	2	1224,588	1224,588	-2E-04	613,3013	0	
FASS	High	IPPASSMLWVR	M7(Oxidation)	1	69,56	5,80E-06	2	1271,67	1271,67	1E-04	636,8421	0	
FASS	High	KPEEGSISQR		1	67,63	8,40E-06	2	1129,573	1129,573	0	565,7936	1	
FASS	High	IDMSELDEDSDGFLHSDEMESYIGGLIPNLAQLR	M19(Oxidation)	1	67,21	4,60E-06	3	3824,738	3824,74	-0,002	1275,92	0	
FASS	High	IAILPFYLYVMR	M11(Oxidation)	1	59,31	4,00E-05	2	1513,836	1513,837	-5E-04	757,9254	0	
FASS	High	DEIWDMVKPSDPLK		1	55,9	1,40E-04	2	1671,818	1671,818	-2E-04	836,9161	1	
FASS	High	FFFFCDPHR	C5(Carbamidomethyl)	1	52,39	1,20E-04	2	1271,554	1271,555	-4E-04	636,7844	0	
FASS	High	VFDEHVR		1	52,06	1,80E-04	2	900,4445	900,4454	-8E-04	451,2295	0	
FASS	High	ILLEIFK		1	50,34	2,90E-05	2	874,5529	874,5528	2E-04	438,2837	0	
FASS	High	DMPPAFNQMYCR	C11(Carbamidomethyl)	1	48,04	1,10E-04	2	1528,626	1528,626	-3E-04	765,3202	0	
FASS	High	FFSPSNFMK		1	44,83	1,10E-03	2	1103,511	1103,511	1E-04	552,7628	0	

FASS	High	GFWAHDNR		1	44,77	5,00E-04	2	1001,447	1001,447	1E-04	501,7307	0	
FASS	High	TVSLTQAR		1	44,65	2,70E-03	2	874,4873	874,4872	0	438,2509	0	
FASS	High	KIPPASSMLWVR	M8(Oxidation)	1	44,64	1,50E-03	2	1399,764	1399,765	-0,001	700,889	1	
FASS	High	CLDLQGR	C1(Carbamidomethyl)	1	43,5	2,50E-03	2	860,4179	860,4174	4E-04	431,2162	0	
FASS	High	DMSGSLCK	C7(Carbamidomethyl)	1	40,97	9,60E-04	2	896,3733	896,3732	1E-04	449,1939	0	
FASS	High	FEKDEAGR		1	40,95	3,80E-03	2	950,4455	950,4457	-2E-04	476,2301	1	
FASS													
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**						
FASS	AT3G55000	TON1A	1540	60,8	15	16	260						
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**	
FASS	High	NGDSGPLLLDVLEGFLK		1	146,46	1,20E-13	2	1785,951	1785,951	-1E-04	893,9828	0	
FASS	High	VIENNEGPPPALLGSCNDR	C16(Carbamidomethyl)	1	112,98	2,90E-10	2	2050,971	2050,974	-0,003	1026,493	0	
FASS	High	DSETESSSSLESR	E11(Methyl)	1	97,46	3,00E-09	2	1426,605	1426,606	-9E-04	714,3098	0	
FASS	High	ASAALENLQLDR		1	90,73	4,00E-08	2	1299,678	1299,678	1E-04	650,8464	0	
FASS	High	FESMTQGMGSSSR	M4(Oxidation)	1	87,95	1,00E-08	2	1419,575	1419,576	-7E-04	710,7949	0	
FASS	High	ASVFEAIEEEDR		1	86,91	9,00E-08	2	1393,636	1393,636	0	697,8253	0	
FASS	High	RDSETESSSSLESR		1	75,52	7,30E-07	2	1568,691	1568,691	-2E-04	785,3529	1	
FASS	High	DFNSNNGFELNRNGDSGPLLLDVLEGFLK		1	74,46	1,70E-06	3	3194,544	3193,568	0,976	1065,855	1	
FASS	High	RPVSASQASDR		1	73,76	2,00E-06	2	1172,589	1172,59	-4E-04	587,302	1	
FASS	High	DFNSNNGFELNR		1	72,79	1,30E-06	2	1425,625	1425,627	-0,002	713,8198	0	
FASS	High	SSASDSLPPQR		1	64,13	1,40E-05	2	1143,553	1143,552	0,001	572,7838	0	
FASS	High	AGLSTSGYR		1	49,7	4,30E-04	2	910,4509	910,4508	1E-04	456,2327	0	
FASS	High	ASVFEAIEEEDRVIENNEGPPPALLGSCNDR	C28(Carbamidomethyl)	1	48,3	5,10E-04	3	3426,597	3426,6	-0,003	1143,206	1	
FASS	High	QGNQDTHEEVTR	E8(Methyl)	1	46,2	8,30E-04	2	1426,644	1426,644	-2E-04	714,329	0	
FASS	High	KDEFNWR		1	42,62	2,60E-03	2	993,4677	993,4668	9E-04	497,7411	1	
FASS	High	KLHASPSGR		1	35,75	7,20E-03	2	951,5244	951,525	-6E-04	476,7695	1	
FASS													
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**						
FASS	AT3G55005	TON1b	1096	55,6	11	12	257						
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**	
FASS	High	SVSASQASGAATSGYR		1	128,43	5,70E-12	2	1498,701	1498,701	-7E-04	750,3575	0	
FASS	High	PLLLDVLEGFLK		1	115,16	2,90E-11	2	1355,806	1355,806	-3E-04	678,9103	0	
FASS	High	FENMTQVMGGSSR	M4(Oxidation)	1	104	6,60E-10	2	1458,623	1458,623	-4E-04	730,3187	0	
FASS	High	VIENNEGLPPALLGSCNDR	C16(Carbamidomethyl)	1	94,86	2,00E-08	2	2067,005	2067,006	-8E-04	1034,51	0	
FASS	High	ASVFEAIEEEDR		1	86,91	9,00E-08	2	1393,636	1393,636	0	697,8253	0	
FASS	High	NEDSRPLLLDVLEGFLK		1	84,31	1,20E-07	2	1957,052	1957,052	3E-04	979,5335	1	
FASS	High	SSASDSLPHQR		1	78,87	4,50E-07	2	1183,558	1183,558	-5E-04	592,7861	0	
FASS	High	ASTALENLQLDR		1	74,85	2,00E-06	2	1329,688	1329,689	-8E-04	665,8513	0	
FASS	High	YDTEDMPEEVMR	M6(Oxidation); E8(Methyl); M11(Oxidation)	1	69,58	3,20E-07	2	1559,611	1559,612	-6E-04	780,813	0	
FASS	High	DFSINNGYELNR		1	67,6	7,00E-06	2	1440,66	1440,663	-0,004	721,3371	0	
FASS	High	VYQPECNSAK	C6(Carbamidomethyl)	1	53,83	1,30E-04	2	1194,533	1194,534	-8E-04	598,2738	0	
FASS	High	QLHASPSGR		1	44,3	1,80E-03	2	951,4883	951,4886	-3E-04	476,7514	0	
FASS													
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**						
FASS	AT3G25800	PP2AA2	1076	43,6	11	17	587						
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**	
FASS	High	YMVANQLYELCEAVGPEPTR	M2(Oxidation); C11(Carbamidomethyl)	1	138,34	6,20E-13	2	2355,087	2355,088	-4E-04	1178,551	0	
FASS	High	TDVMSMFEDLTQDDQDSVR	M4(Oxidation); M6(Oxidation)	1	132,03	2,90E-13	2	2262,925	2262,926	-8E-04	1132,47	0	
FASS	High	FFANQALQSIDNVMMSS	M14(Oxidation); M15(Oxidation)	1	109,61	2,40E-10	2	1933,855	1933,855	-3E-04	967,9346	0	
FASS	High	ESDLVDHFISLVK		1	94,85	1,90E-08	2	1500,781	1500,782	-0,002	751,3975	0	
FASS	High	ILNPEIAIQHILPCVK	C14(Carbamidomethyl)	1	89,37	1,40E-08	2	1857,054	1857,055	-9E-04	929,5341	0	
FASS	High	AVSLLAPVMGSEITCSK	C15(Carbamidomethyl)	1	87,06	1,40E-07	2	1761,901	1761,901	3E-04	881,9576	0	
FASS	High	LDQVNQVIGIDLLSQSLLPAIVELAEDR		1	85,5	3,40E-08	3	3060,67	3060,671	-4E-04	1021,231	0	
FASS	High	SLYTQLCQDDMPMVR	C7(Carbamidomethyl); M11(Oxidation); M13(Oxidation)	1	77,52	3,40E-07	2	1887,815	1887,817	-0,001	944,9149	0	
FASS	High	SALASVIMGMAPVLGK	M8(Oxidation)	1	76,94	9,30E-07	2	1559,842	1559,842	3E-04	780,9282	0	
FASS	High	PGLVELSEDPDVDVR		1	76,52	1,40E-06	2	1638,81	1638,81	3E-04	820,4125	0	
FASS	High	VLQSLIPIVDQSVVEK		1	70,37	8,10E-07	2	1766,018	1766,019	-7E-04	884,0164	0	
FASS	High	LAAGEWFTAR		1	70,01	6,30E-06	2	1120,567	1120,567	1E-04	561,2906	0	
FASS	High	ELSSDSSQHVR		1	61,6	2,20E-05	2	1243,578	1243,579	-0,001	622,7964	0	
FASS	High	LLEPQDCVQHILPVIVNFSQDK	C7(Carbamidomethyl)	1	55,14	1,30E-04	3	2591,34	2591,342	-0,002	864,7873	0	
FASS	High	FAATVESAHLK		1	54,88	1,90E-04	2	1172,618	1172,619	-0,001	587,3162	0	
FASS	High	NDDIQLR		1	52,64	1,80E-04	2	872,4355	872,4352	3E-04	437,225	0	
FASS	High	TIRPGLVELSEDPDVDVR		1	51,26	3,30E-04	2	2009,042	2009,043	-7E-04	1005,528	1	
FASS													
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**						
FASS	AT3G53540	TRM19	876	25,8	17	17	924						
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**	
FASS	High	SHSSYNSSPEVSITPSLSK		1	154,42	2,00E-14	2	2005,958	2005,959	-0,002	1003,986	0	
FASS	High	TAMSSEALDLSTVTSVTDPDISR	M3(Oxidation)	1	148,1	8,20E-14	2	2411,136	2411,137	-0,001	1206,575	0	
FASS	High	SSFSGDANSDTEDSSASDDIK		1	133,68	1,20E-13	2	2133,847	2133,846	0,001	1067,931	0	
FASS	High	HASYDTIDLPNEELR		1	112,37	2,70E-10	2	1771,837	1771,838	-6E-04	886,9258	0	
FASS	High	PASFNGLSFEDGISK		1	106,28	1,30E-09	2	1567,748	1567,752	-0,004	784,8813	0	
FASS	High	ELQWLSLEDDIEIIGR		1	104,2	1,90E-09	2	1927,989	1927,989	-4E-04	965,0016	0	
FASS	High	EFNDALEALDSNK		1	97,02	8,10E-09	2	1464,673	1464,673	-3E-04	733,3437	0	
FASS	High	TFASPSSSSDEFR		1	74,08	6,40E-07	2	1416,615	1416,616	-8E-04	709,3147	0	
FASS	High	SGTLAEMLATSDR		1	64,42	2,10E-05	2	1350,645	1350,645	-1E-04	676,3297	0	
FASS	High	LLFDQISR		1	63,55	1,80E-05	2	990,5501	990,5498	3E-04	496,2823	0	
FASS	High	AMSFETSGFR		1	51,24	1,20E-04	2	1131,501	1131,502	-0,001	566,7576	0	
FASS	High	MQLQLLK		1	50,94	4,50E-04	2	872,5149	872,5153	-4E-04	437,2647	0	
FASS	High	LPCTTTHGR	C3(Carbamidomethyl)	1	46,37	6,40E-04	2	1041,502	1041,503	-3E-04	521,7584	0	
FASS	High	FEHEIEISR		1	41,34	3,30E-03	2	1158,567	1158,567	0	580,2907	0	
FASS	High	FENNIQWPELPEPVGISSR		1	40,7	4,90E-03	2	2211,092	2211,096	-0,004	1106,553	0	
FASS	High	TIMNQESAGGYTIVLPK	M3(Oxidation); E6(Methyl)	1	40,33	5,40E-03	2	1850,943	1850,945	-0,002	926,4789	0	
FASS	High	FKDVFEVLDAK		1	37,39	7,90E-03	2	1309,685	1309,692	-0,007	655,8497	1	
FASS													
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**						
FASS	AT1G13320	PP2AA3	665	32,2	7	12	587						
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**	

FASS	High	YMVANQLYELCEAVGPEPTR	M2(Oxidation); C11(Carbamidomethyl)	1	138,34	6,20E-13	2	2355,087	2355,088	-4E-04	1178,551	0
FASS	High	ILNPELAIQHILPCVK	C14(Carbamidomethyl)	1	89,37	1,40E-08	2	1857,054	1857,055	-9E-04	929,5341	0
FASS	High	AVSLLAPVMGSEITCSK	C15(Carbamidomethyl)	1	87,06	1,40E-07	2	1761,901	1761,901	3E-04	881,9576	0
FASS	High	LDQVNQVIGIDLLSQSLLPAIVELAEDR		1	85,5	3,40E-08	3	3060,67	3060,671	-4E-04	1021,231	0
FASS	High	SALASVIMGMAPVLGK	M8(Oxidation)	1	76,94	9,30E-07	2	1559,842	1559,842	3E-04	780,9282	0
FASS	High	LLEPQDCVAHILPVIVNFSQDK	C7(Carbamidomethyl)	1	67,41	7,60E-06	3	2534,319	2534,32	-0,001	845,7803	0
FASS	High	LSAGEWFTAR		1	63,26	2,80E-05	2	1136,561	1136,561	-3E-04	569,2879	0
FASS	High	ELSSDSSQHVR		1	61,6	2,20E-05	2	1243,578	1243,579	-0,001	622,7964	0
FASS	High	ESDLVEHFTPLAK		1	56,29	1,10E-04	2	1484,751	1484,751	-4E-04	743,3827	0
FASS	High	FAATIESAHLK		1	53,26	2,90E-04	2	1186,634	1186,635	-3E-04	594,3244	0
FASS	High	SIYGQLCQDDMPMVR	C7(Carbamidomethyl); M11(Oxidation); M13(Oxidation)	1	48,29	2,30E-04	2	1843,788	1843,79	-0,002	922,9013	0
FASS	High	LLPAVITASK		1	29,37	5,30E-03	2	1011,633	1011,633	-3E-04	506,8235	0
FASS												
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
FASS	AT3G58500	PP2A4	477	40,9	2	10	313					
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
FASS	High	GAGYTFGQDISEQFNHTNNLK		1	118,69	5,40E-11	2	2340,075	2340,077	-0,002	1171,045	0
FASS	High	EILMDESNVQPVK	M4(Oxidation)	1	98,09	9,30E-09	2	1516,743	1516,744	-0,002	759,3786	0
FASS	High	CPDTNYLFMGDYVDR	C1(Carbamidomethyl); M9(Oxidation)	1	97,65	1,40E-09	2	1880,77	1880,771	-0,001	941,392	0
FASS	High	QITQVYGFYDECLR	C12(Carbamidomethyl)	1	89,96	4,60E-08	2	1790,83	1790,83	0	896,4222	0
FASS	High	VVTIFSAPNYCYR	C11(Carbamidomethyl)	1	66,82	1,20E-05	2	1588,77	1588,771	-0,001	795,3921	0
FASS	High	YGNANVWK		1	66,68	1,10E-05	2	950,4605	950,461	-5E-04	476,2375	0
FASS	High	NHTFIQFEPAPR		1	64,58	1,80E-05	2	1455,726	1455,726	-4E-04	728,87	0
FASS	High	PLSEQQVR		1	52,18	1,80E-04	2	955,5086	955,5087	-1E-04	478,7616	0
FASS	High	RGEPDVTR		1	50,65	2,60E-04	2	928,4722	928,4726	-5E-04	465,2434	1
FASS	High	AHQLVMDGFNWAHEQK	M6(Oxidation)	1	42,95	2,00E-03	3	1925,883	1925,884	-9E-04	642,9684	0
FASS												
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
FASS	AT5G26910	TRM8	366	22,3	13	13	853					
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
FASS	High	ETYEEGIDIEGEIVSTLVDDLVNDLVSGTQR		1	105,63	1,20E-09	3	3408,656	3407,647	1,009	1137,226	0
FASS	High	SDSSCCASSVTSDDGQGTR	C5(Carbamidomethyl); C6(Carbamidomethyl)	1	83,18	7,70E-09	2	1975,749	1975,748	9E-04	988,8819	0
FASS	High	EYALGMATDVLPASLFDEMEGR	M6(Oxidation); M19(Oxidation)	1	77,96	5,30E-07	2	2446,108	2446,103	0,004	1224,061	0
FASS	High	DNQPSMTSVLNQK	M6(Oxidation)	1	76,26	1,20E-06	2	1476,688	1476,688	4E-04	739,3514	0
FASS	High	EGVVSALVEPHLLSAF		1	63,41	1,60E-05	2	1666,894	1666,893	8E-04	834,4542	0
FASS	High	QLGLSTASAEK		1	54,88	2,50E-04	2	1103,582	1103,582	-8E-04	552,798	0
FASS	High	DWLAEELNR		1	47,62	7,20E-04	2	1144,551	1144,551	1E-04	573,283	0
FASS	High	VSLIEVDEIGK		1	46,62	1,30E-03	2	1200,66	1200,66	-6E-04	601,3371	0
FASS	High	GGFLFEQR		1	41,95	2,90E-03	2	952,4771	952,4767	5E-04	477,2458	0
FASS	High	CEQMFMGSCR	arbamidomethyl); M4(Oxidation); M6(Oxidation); C9(Carbamidom	1	41,54	7,00E-05	2	1336,466	1336,467	-4E-04	669,2405	0
FASS	High	ITTSLTTPSTSK		1	40,77	3,90E-03	2	1235,663	1235,661	0,002	618,8387	0
FASS	High	VPVESGSISK		1	40,69	5,40E-03	2	1001,539	1001,539	-6E-04	501,7766	0
FASS	High	QNSNDTFNLK		1	38,21	7,60E-03	2	1179,551	1179,552	-7E-04	590,7829	0
FASS												
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
FASS	AT2G45240	MAP1A	270	26,4	8	8	398					
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
FASS	High	VEPNSDLQHVVEIK		1	83,72	2,70E-07	2	1605,834	1605,836	-0,002	803,9243	0
FASS	High	LPSSPDVYPWLTK		1	79,16	7,90E-07	2	1501,781	1501,782	-4E-04	751,8979	0
FASS	High	VVPAEIEKPDWAIDGTPK		1	76,85	9,50E-07	2	1964,024	1964,026	-0,001	983,0194	1
FASS	High	SAQFEHTLLVTETGVEVLTAR		1	74,98	1,20E-06	3	2300,204	2300,201	0,003	767,7419	0
FASS	High	VIHPGVTTDEIDR		1	54,41	2,40E-04	2	1450,741	1450,742	-9E-04	726,3776	0
FASS	High	EVLDAAAR		1	52,36	2,00E-04	2	843,4437	843,445	-0,001	422,7292	0
FASS	High	EIGEIVNR		1	44,47	1,20E-03	2	928,4976	928,4978	-1E-04	465,2561	0
FASS	High	AIAIVKPGVR		1	36,16	3,40E-04	2	1022,66	1022,66	-3E-04	512,3372	1
FASS												
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
FASS	AT3G05750	TRM6	190	7,9	6	6	801					
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
FASS	High	QNQFAETSVSNQR		1	64,48	1,80E-05	2	1507,702	1507,702	3E-04	754,8582	0
FASS	High	FSSSDSSSSLPMK	M12(Oxidation)	1	58,48	2,40E-05	2	1374,596	1374,597	-9E-04	688,3055	0
FASS	High	QDIFLER		1	53,34	3,70E-04	2	919,4763	919,4763	0	460,7455	0
FASS	High	SPGFVQSR		1	46,03	2,00E-03	2	876,4449	876,4454	-4E-04	439,2298	0
FASS	High	CEQMFMGTCK	arbamidomethyl); M4(Oxidation); M6(Oxidation); C9(Carbamidom	1	40,14	9,70E-05	2	1322,476	1322,476	-3E-04	662,2453	0
FASS												
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
FASS	AT4G28760	TRM20	186	6	4	4	924					
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
FASS	High	LLQELVEEAVIDLTR		1	112,2	1,20E-10	2	1739,968	1739,967	0,001	870,9912	0
FASS	High	INSIVSETTTTR		1	90,69	5,40E-08	2	1320,687	1320,689	-0,001	661,351	0
FASS	High	VSNLFFFK		1	52,73	2,70E-04	2	1000,538	1000,538	-1E-04	501,2763	0
FASS	High	GTEEHTVQPTR		1	38,82	6,30E-03	2	1253,599	1253,6	-0,001	627,8068	0
FASS												
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
FASS	AT1G63670	TRM12	131	7,3	4	4	689					
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
FASS	High	IGLSFDDPNIDLIEK		1	72,17	3,80E-06	2	1687,865	1687,867	-0,002	844,9397	0
FASS	High	TSDVSTSTVGHR		1	66,85	9,50E-06	2	1245,595	1245,595	-1E-04	623,8047	0
FASS	High	VLNLESSLR		1	53,7	2,30E-04	2	1029,584	1029,582	0,002	515,7993	0
FASS	High	QEQEQPSPVSVLER		1	43,53	2,70E-03	2	1624,803	1624,806	-0,003	813,4088	0
FASS												
FASS	**Accession**	**Description**	**Score**	**Coverage %**	**Unique Peptide**	**# Peptides**	**# AAs**					
FASS	AT1G74160	TRM4	85	2,3	2	2	1025					
FASS	**Peptide confidence**	**Sequence**	**Modifications**	**Rank**	**Peptide score**	**Expect**	**Charge**	**Mr(Exp)**	**Mr(Calc)**	**ΔM [Da]**	**m/z [Da]**	**# Missed Cleavages**
FASS	High	SENFLLEEEDDFLK		1	81,76	2,80E-07	2	1726,795	1726,794	0,002	864,4049	0
FASS	High	SILAEDVTIR		1	39,09	6,50E-03	2	1115,62	1115,619	0,002	558,8174	0

Protein identification details were obtained with the LTQ Orbitrap Velos (Thermo Fisher Scientific) and Mascot Distiller software (version 2.3.2.0, Matrix Science) combined with the Mascot search engine (Matrix Science) using the Mascot Daemon interface (version 2.4, Matrix Science).

Proteins and peptides headers used in the table are listed below.

Score: Displays the protein score. **Coverage %**: Displays by default the percentage of the protein sequence covered by identified peptides. **# Unique Peptides**: Displays the number of peptide sequences unique to a protein group. **# Peptides**: Displays the number of distinct peptide sequences in the protein group. **# AAs**: Shows by default the sequence length of the protein. **Peptide Confidence**: Indicates a confidence level associated with the peptide sequence: high confidence (>99%), medium confidence (>95%, <99%), low confidence (<95%). **Sequence**: Displays the sequence of amino acids that compose the peptide. **Modifications**: Displays the static and dynamic modifications identified in the peptide. **Rank**: Displays the ordering of peptides by rank. **Peptide score**: Displays the peptide ions score. **Expect**: Expectation value for the peptide match. (The number of times we would expect to obtain an equal or higher score, purely by chance. The lower this value, the more significant the result.) **Charge**: Displays the charge state of the peptide. **Mr(Exp)**: experimental relative molecular mass, in daltons. **Mr(Calc)**: calculated relative molecular mass, in daltons. **ΔM [Da]**: difference (error) between the experimental and calculated masses, in daltons. **m/z [Da]**: Displays the mass-to-charge ratio of the precursor ion, in daltons. **# Missed Cleavages**: Displays the number of cleavage sites in a peptide sequence that a cleavage reagent (enzyme) did not cleave. This number excludes cases where an amino acid such as proline inhibits the cleaving enzyme. For example, if proline resides next to lysine or arginine, trypsin does not cleave the lysine or arginine. The # of Missed Cleavages value is 0 for a complete digest of all peptides.

Supplementary Table S4: List of primers used in this study

Primer name	Construct	Sequence
TON1a_fwd	Entry vectors of TON1a, TON1b, FASS and TRM19 to generate TAP constructs	published Van Leene et. al. 2007
TON1a_nostop_rev		published Van Leene et. al. 2007
TON1a_stop_rev		AGAAAGCTGGGTCTCAATCTCTCCCTTCTTCTTC
TON1b_fwd		AAAAAGCAGGCTCCACCATGGACATTATACAAGAGAG
TON1b_stop_rev		AGAAAGCTGGGTCTCAATCTTTCCCTTCTTCTTCTTC
TON1b_nostop_rev		AGAAAGCTGGGTCATCTTTCCCTTCTTCTTCTTCAC
FASS_fwd		AAAAAGCAGGCTCCACCATGTATAGCGGATCTAGCGATGG
FASS_stop_rev		AGAAAGCTGGGTCTCACTGAGACTCTTCCTCAGG
FASS_nostop_rev		AGAAAGCTGGGTCCTGAGACTCTTCCTCAGGTGG
AT3G53540_fwd		AAAAAGCAGGCTCCACCATGAACAGATTTCGACTCAGC
AT3G53540_stop_rev		AGAAAGCTGGGTCCTAGAAGATTGCACCTACCACAAGC
AT3G53540_nostop_rev		AGAAAGCTGGGTCGAAGATTGCACCTACCACAAGC
attB1-F		GGGGACAAGTTTGTACAAAAAAGCAGGCTCCACC
attB2-R		GGGGACCACTTTGTACAAGAAAGCTGGGTC
FASSGW (+1)	Entry vectors of FASS and truncated versions of FASS	GGGGACAAGTTTGTACAAAAAAGCAGGCTACAAAATGTATAGCGGATCTAG
FASSGW (-480)		GGGGACCACTTTGTACAAGAAAGCTGGGTACTGAGACTCTTCCTCAG
FASSGW (-185)		GGGGACCACTTTGTACAAGAAAGCTGGGTCCGTGCGCATCACATAAAG
FASSGW (+186)		GGGGACAAGTTTGTACAAAAAAGCAGGCTACAAAATGGTGTCGCTTACACAAGC
TRM1 (+1)	Entry vectors of TRM1 and truncated versions of TRM1	GGGGACAAGTTTGTACAAAAAAGCAGGCTACAAAATGTCTGCAAAACTTCT
TRM1 (+587)		GGGGACAAGTTTGTACAAAAAAGCAGGCTACAAAATGAGCTTGGGATCGAATGTT
TRM1 (-698)		GGGGACCACTTTGTACAAGAAAGCTGGGTATTATCCCCGGTTACTCTGAGG
TRM1 (-827)		GGGGACCACTTTGTACAAGAAAGCTGGGTATTTTTTAAGTGGATTTGC
TRM1 (-905)		GGGGACCACTTTGTACAAGAAAGCTGGGTAGCAGAAGCAAACTTCAT
TON1a (+1)	Entry vectors of TON1a and truncated versions of TON1a	GGGGACAAGTTTGTACAAAAAAGCAGGCTTGATGGACGATTATACAAG
TON1a (-107)		GGGGACCACTTTGTACAAGAAAGCTGGGTACGAATCTTTTGGCAAA
TON1a (+108)		GGGGACAAGTTTGTACAAAAAAGCAGGCTACAAAATGTGGAAGTCTGAGTTACG
TON1a (-260)		GGGGACCACTTTGTACAAGAAAGCTGGGTAATCTTTCCCTTCTTC
RCN1GW FWD	PP2AA1 entry vector	GGGGACAAGTTTGTACAAAAAAGCAGGCTACAAAATGGCTATGGTAGATGAA
RCN1GW REV		GGGGACCACTTTGTACAAGAAAGCTGGGTAGGATTGTGCTGCTGTGG
TRM8 (+1)	TRM8 entry vector	GGGGACAAGTTTGTACAAAAAAGCAGGCTACAAAATGGAGGTTGTTGAGAGG
TRM8 (-854)		GGGGACCACTTTGTACAAGAAAGCTGGGTAGAATGCCGAGAGAAGAT
R1	Genotyping of *pp2aa1* mutant	AGCACATCCTTCCTTGTGTGAAGG
R2		AACTTGCTTATGATGTTAAGGCGC
T (T-DNA)		TGTCCCGCGTCATCGGCGGGGGTC
oA2RAV	Genotyping of *pp2aa2* mutant	GCGTGCGGTGTCTCTTCTTGCACC
oA2new3'		CACATTAGTAGCAAGACAATGGACAAAACCCG
oA3leader	Genotyping of *pp2aa3* mutant	GATCGCTCGGAACTTGGAAAGCAGC
oA3DDEV		GCCAAAAGCACCTCATCGTCATCGTC
SALK_069250 RP	Genotyping of *pp2ac3* mutant	TGTTTCCTGATCTGTTTTCCG
SALK_069250 LP		TAATTGGTATCAGGGCACTGC
SALK_035009 RP	Genotyping of *pp2ac4* mutant	GTGGATTATCACCATCCATCG
SALK_035009 LP		GCTTGAAAGAACAGCATTTCG
LB-Salk2	Genotyping of *pp2aa2, pp2aa3, pp2ac3* and *pp2ac4* mutants	GCTTTCTTCCCTTCCTTTCTC
ACT2_2_FWD	RT-PCR primers for actin, eif4A, PP2Ac1-c5 and PP2AA1-A3	TTGACTACGAGCAGGAGATGG
ACT2_2_REV		ACAAACGAGGGCTGGAACAAG
eif4A-FWD		ACGGAGACATGGACCAGAAC
eif4A-REV		GCTGAGTTGGGAGATCGAAG
at3g58500_LP1		TCTGCGAAAGTATGGCAATG
at3g58500_RP1		CCACCGTGAAGGCAGAATA
at2g42500_LP2		GAACCACACCTTCATCCAGTTT
at2g42500_RP2		TGAGATGAGTCTGTGTCCAGTGA
at3g25800_fwd		CGATGCTGCTGCTAACAATC
at3g25800_rev		ATTGCCCATTCAGGACCA
at1g10430_fwd		CCAGAGAAGCTAGGAGGATTTGATC
at1g10430_rev		TTGAAAAGCCACCACCGATCC
at1g59830_fwd		TATGAGAGAAACAAAACCAAAGACG
at1g59830_rev		TCTCGTCGTCGTCTCCTTTAAC
at1g69960_fwd		ATGGACCAGAATTTCCTTCAGTTTG
at1g69960_rev		TAGTGTGTGGAATTGCAGCTTTAG
at1g13320_fwd		GACCGGAGCCAACTAGGAC
at1g13320_rev		AAAACTTGGTAACTTTTCCAGCA
at1g25490-fwd		ATCCTTGTTACCGGCCATT
at1g25490-rev		TGCAAGTCGGACTCTCCAG

Supplementary Methods for the LC-MS/MS VELOS1 analysis (related to Supplementary Table S2)

Tuning of equipment and sample analyses were performed using a standard operation procedure. Quality performance of the LC MS analyses was assessed using control standards. Nanoflow LC-MS/MS analyses were performed on a dual channel NanoLC Ultra 2D system (Eksigent, Dublin, California, USA) and connected to an LTQ Orbitrap Velos mass spectrometer (Thermo, Bremen, Germany) using a chip based nano electrospray source (Triversa Advion Biosystems, Ithaca, NY, USA) operated at 1.8 kV. Mobile phase A (CH_3CN : CHOOH : H_2O in a 2:0.1:97.9 (v/v) ratio) and mobile phase B (CH_3CN : CHOOH : H_2O in a 90:0.1:9.9 (v/v) ratio) were reconstituted from ULC/MS-grade CH_3CN, CHOOH and H_2O (Biosolve-chemicals, Valkenswaard, the Netherlands). All standards and samples were dissolved in mobile phase A. A volume of 10 µL of each sample or control standard was loaded on a C_{18} precolumn (PepMap 100, 5 µm particles, 20 mm x 200 µm ID, Dionex, Sunnyvale, California, USA) using a flow rate of 6 µL/min (100% mobile phase A). Five minutes after injection the trapping column was switched in line with an analytical C_{18} column (Acclaim Pepmap 100, 3 µm particles, 150 mm x 75 µm ID, Dionex). Effective elution of peptides was accomplished within a 45 minutes gradient flow (95% A to 50% A) at a flow rate of 350 nl/min.
MS spectra were recorded in the orbitrap FT analyzer with a resolution of 60000 (at m/z 400) and an AGC target setting of 500000. The maximum injection time was set to 500 msec and lock mass was enabled (polysiloxane ion at m/z 445.12024). Collision induced dissociation MS/MS spectra were acquired using the ion trap in data dependent mode selecting up to the 20 most abundant multiply charged precursor ions from the MS spectrum. The maximum injection time was set to 50 msec and an AGC setting of 7500. Fragmentation was accomplished by CID wideband activation at normalized collision energy of 35 eV and a 30msec activation time. After MS/MS the precursor m/z's were excluded for 30 seconds. Peak lists were generated and submitted for protein identification with Proteome Discoverer 1.3.0.339 (Thermo, Bremen, Germany). Spectrum grouping was allowed with a maximum retention time of 1 minute and a precursor mass tolerance of 2 ppm. Peak lists were generated only for MS/MS spectra containing more than 5 peaks, with a total intensity above 50. The relative signal-to-noise limit was set to 5. Peak lists were submitted for protein identification against TAIR10 containing 35386 sequence entries with search engine SEQUEST. Enzyme was set to trypsin, allowing for maximum 1 missed cleavage site. Precursor mass tolerance was set to 3 ppm and fragment mass tolerance at 0.8 Da. Fixed modifications were set to carbamidomethylation of cysteines. Variable modifications were set to methionine oxidation and methylation of aspartic acid and glutamic acid, with a maximum of 4 modifications per peptide. Peptides were validated using a decoy database search. The strict target False Discovery Rate (FDR) was set to 0.01 (or 1%), the relaxed FDR was set to 0.05 (or 5%). Only high confident (>99%) peptides were withheld. Only proteins with at least two matched high confident peptides were retained.

Supplementary Methods for the LC-MS/MS VELOS2 analysis (related to Supplementary Table S3)

The obtained peptide mixtures were introduced into an LC-MS/MS system, the Ultimate 3000 RSLC nano (Dionex, Amsterdam, The Netherlands) in-line connected to an LTQ Orbitrap Velos (Thermo Fisher Scientific, Bremen, Germany). The sample mixture was loaded on a trapping column (made in-house, 100 µm internal diameter (I.D.) x 20 mm (length), 5 µm

C18 Reprosil-HD beads, Dr. Maisch GmbH, Ammerbuch-Entringen, Germany). After back-flushing from the trapping column, the sample was loaded on a reverse-phase column (made in-house, 75 μm I.D. x 150 mm , 5 μm C18 Reprosil-HD beads, Dr. Maisch). Peptides were loaded with solvent A (0.1% trifluoroacetic acid, 2% acetonitrile), and separated with a linear gradient from 2% solvent A' (0.1% formic acid) to 50% solvent B' (0.1% formic acid and 80% acetonitrile) at a flow rate of 300 nl/min, followed by a wash step reaching 100% solvent B'.

The mass spectrometer was operated in data-dependent mode, automatically switching between MS and MS/MS acquisition for the ten most abundant peaks in a given MS spectrum. In the LTQ-Orbitrap Velos, full scan MS spectra were acquired in the Orbitrap at a target value of 1E6 with a resolution of 60,000. The ten most intense ions were then isolated for fragmentation in the linear ion trap, with a dynamic exclusion of 20 seconds. Peptides were fragmented after filling the ion trap at a target value of 1E4 ion counts.

From the MS/MS data in each LC run, Mascot Generic Files were created using the Mascot Distiller software (version 2.3.2.0, Matrix Science, www.matrixscience.com/Distiller.html). When generating these peak lists, grouping of spectra was allowed with a maximum intermediate retention time of 30 seconds and a maximum intermediate scan count of 5 was used where possible. Grouping was done with 0.005 Da precursor tolerance. A peak list was only generated when the MS/MS spectrum contained more than 10 peaks. There was no de-isotoping and the relative signal-to-noise limit was set to 2. These peak lists were then searched with the Mascot search engine (MatrixScience, www.matrixscience.com, PMID 10612281) using the Mascot Daemon interface (version 2.4, Matrix Science). Spectra were searched against the TAIR10 database containing 35386 sequence entries. Variable modifications were set to methionine oxidation and methylation of aspartic acid and glutamic acid. Fixed modifications were set to carbamidomethylation of cysteines. Mass tolerance on MS was set to 10 ppm (with Mascot's C13 option set to 1) and the MS/MS tolerance at 0.5 Da. The peptide charge was set to 1+, 2+ and 3+ and the instrument setting was set to ESI-TRAP. Trypsin was set as the protease used, allowing for 1 missed cleavage, and also cleavage was allowed when arginine or lysine is followed by proline. Only high confident peptides, ranked one and with scores above the threshold score, set at 99% confidence, were withheld. Only proteins with at least two matched high confident peptides were retained.