Supplementary Figure 1

A

Thrombin-cleaved GST-SNX1 used for MS

*GSP*MASGGGGCSASERLPPPFPGLEPESEGAAGGSEPEAGDSDTEGEDIFTGAAVVSKHQ
SPKITTSLLPINNGSKENGIHEEQDQEPQDLFADATVELSLDSTQNNQKKVLAKTLISLP
PQEATNSSKPQPTYEELEEEEEQEDQFDLTVGITDPEKIGDGMNAYVAYKVTTQTSLPLFR
SKQFAVKRRFSDFLGLYEKLSEKHSQNGFIVPPPPEKSLIGMTKVKVGKEDSSSAEFLEK
RRAALERYLQRIVNHPTMLQDPDVREFLEKEELPRAVGTQTLSGAGLLKMFNKATDAVSK
MTIKMNESDIWFEEKLQEVECEEQRLRKLHAVVETLVNHRKELALNTAQFAKSLAMLGSS
EDNTALSRALSQLAEVEEKIEQLHQEQANNDFFLLAELLSDYIRLLAIVRAAFDQRMKTW
QRWQDAQATLQKKREAEARLLWANKPDKLQQAKDEILEWESRVTQYERDFERISTVVRKE
VIRFEKEKSKDFKNHVIKYLETLLYSQQQLAKYWEAFLPEAKAIS

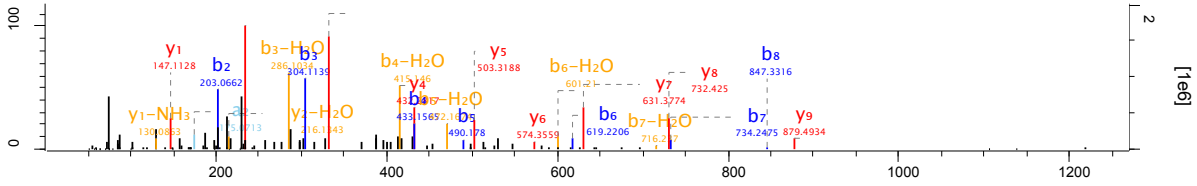
B

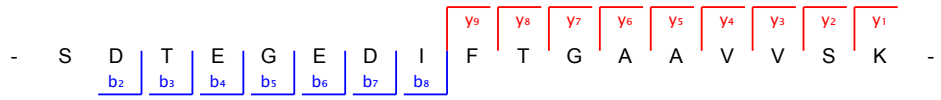
	#	Peptide sequence	SNX1 D/E ↓	cleavage window (-8,+8)	Missed cleavages	Intensity SNX1 only	Intensity SNX1+casp-10
		Cleavage following Asp	**10**		D/K/R		
	1	**SDTEGEDIFTGAAVVSK**	38	GSEPEAGD ↓ **SDTEGEDI**	2	0.00E+00	2.57E+09
	2	**LTVGITDPEK**	144	EEQEDQFD ↓ **LTVGITDP**	1	0.00E+00	4.71E+08
	3	**TEGEDIFTGAAVVSK**	40	EPEAGDSD ↓ **TEGEDIFT**	1	0.00E+00	1.91E+08
	4	**ATVELSLDSTQNNQKK**	91	EPQDLFAD ↓ **ATVELSLD**	2	0.00E+00	1.90E+08
	5	**ATVELSLDSTQNNQK**	91	EPQDLFAD ↓ **ATVELSLD**	1	0.00E+00	1.87E+08
	6	**TLISLPPQEATNSSKPQPTYEELEEEEQED**	141	**LEEEEQED** ↓ QFDLTVGI	1	0.00E+00	1.70E+08
	7	**IFTGAAVVSK**	45	DSDTEGED ↓ **IFTGAAVV**	0	0.00E+00	1.62E+08
	8	**ENGIHEEQDQEPQDLFAD**	91	**EPQDLFAD** ↓ ATVELSLD	2	0.00E+00	8.99E+07
	9	**LPPPFPGLEPESEGAAGGSEPEAGD**	38	**GSEPEAGD** ↓ SDTEGEDI	0	0.00E+00	5.58E+07
	10	**PEKIGDGMNAYVAYK**	151	DLTVGITD ↓ **PEKIGDGM**	2	0.00E+00	3.58E+07
	11	**LTVGITDPEKIGDGMNAYVAYK**	144	EEQEDQFD ↓ **LTVGITDP**	3	0.00E+00	3.53E+07
	12	**QFDLTVGITDPEK**	141	LEEEEQED ↓ **QFDLTVGI**	2	0.00E+00	2.82E+07
	13	**VREFLEKEELPR**	260	PTMLQDPD ↓ **VREFLEKE**	2	0.00E+00	2.75E+06
	14	**PDVREFLEKEELPR**	258	NHPTMLQD ↓ **PDVREFLE**	3	0.00E+00	2.36E+06
	15	**KLQQAKDEILEWESR**	444	LLWANKPD ↓ **KLQQAKDE**	3	0.00E+00	1.84E+06
		Cleavage following Glu	**6**		D/E/K/R		
	16	**AGDSDTEGEDIFTGAAVVSK**	35	AAGGSEPE ↓ **AGDSDTEG**	5	0.00E+00	5.96E+08
	17	**SEGAAGGSEPEAGDSDTEGEDIFTGAAVVSK**	24	PFPGLEPE ↓ **SEGAAGGS**	8	0.00E+00	4.41E+08
	18	**GEDIFTGAAVVSK**	42	EAGDSDTE ↓ **GEDIFTGA**	2	0.00E+00	4.17E+07
	19	**LPPPFPGLEPE**	24	**PFPGLEPE** ↓ SEGAAGGS	1	0.00E+00	4.06E+07
	20	**TLISLPPQEATNSSKPQPTYEELEEE**	137	**TYEELEEE** ↓ EQEDQFDL	6	0.00E+00	1.79E+07
	21	**LPPPFPGLEPESE**	26	**PGLEPESE** ↓ GAAGGSEP	2	0.00E+00	6.70E+06
	22	**FLEKEELPR**	263	LQDPDVRE ↓ **FLEKEELP**	4	0.00E+00	2.56E+06

C

#1

Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	57235	FTMS; HCD	97.9	863.41	SNX1





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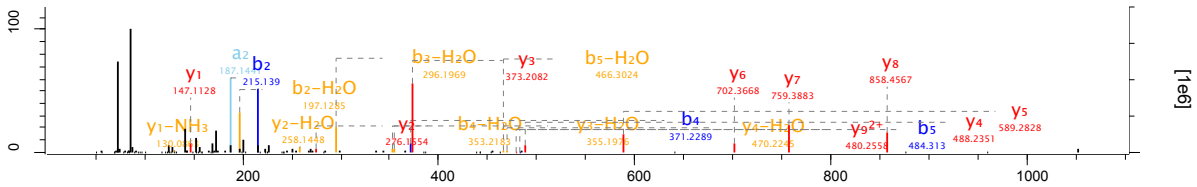
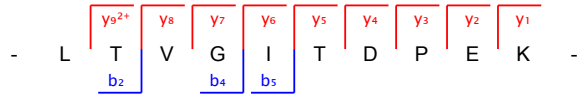
242Catherine_Caspase10	35111	FTMS; HCD	108.47	536.8	SNX1





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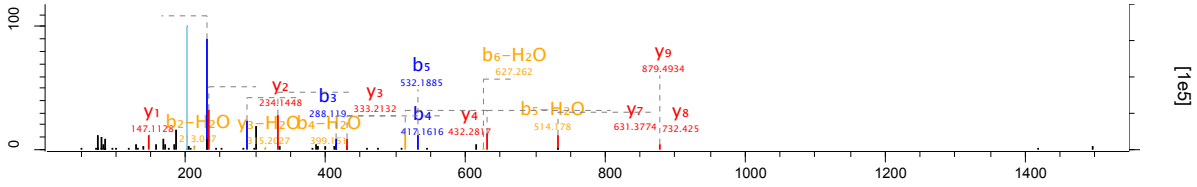
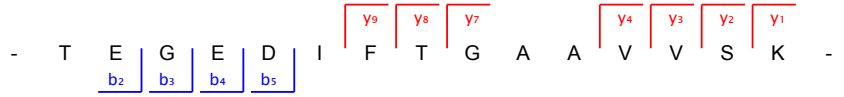
242Catherine_Caspase10	54273	FTMS; HCD	59.71	762.38	SNX1





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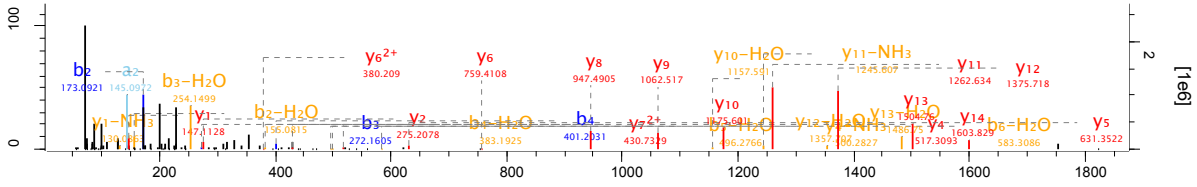
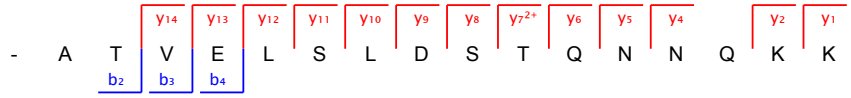
Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	25593	FTMS; HCD	123.29	592.64	SNX1





C (continued)

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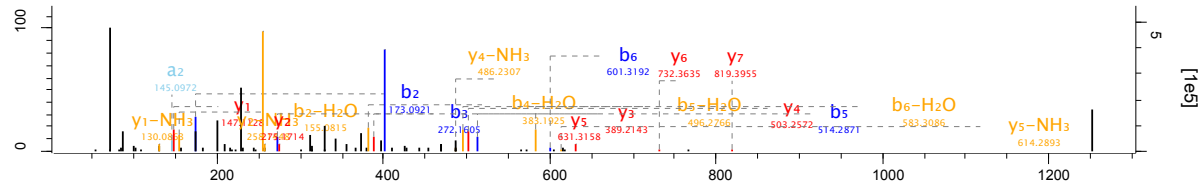
242Catherine_Caspase10	36545	FTMS; HCD	98.34	824.41	SNX1



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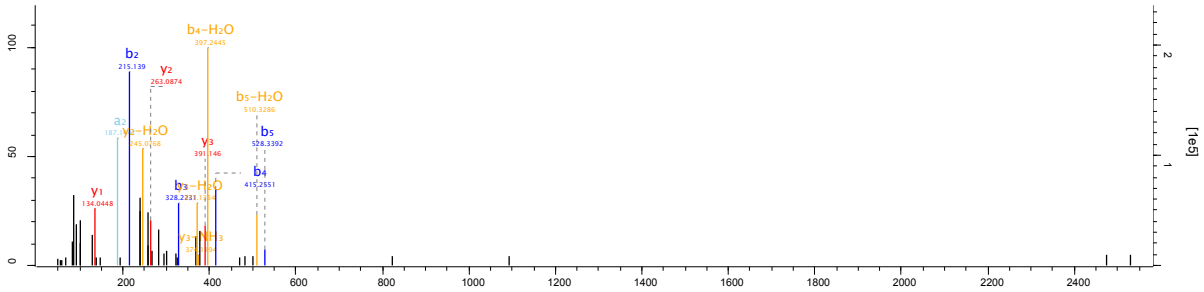
242Catherine_Caspase10	70516	FTMS; HCD	17.86	1144.87	SNX1



#7

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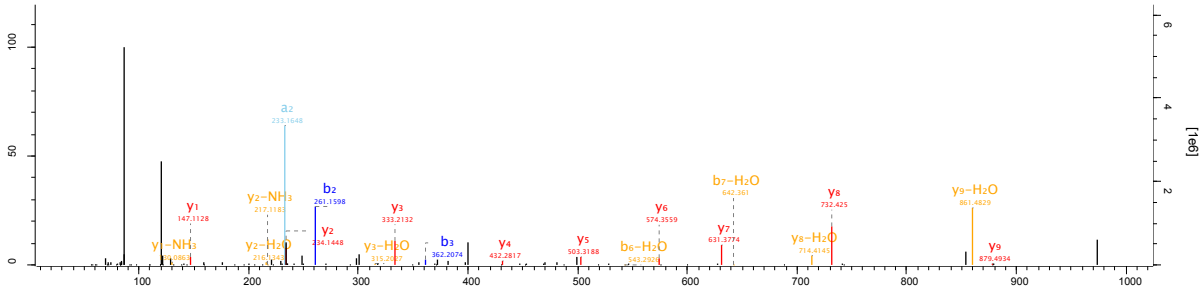
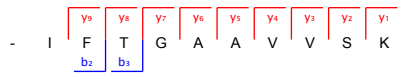
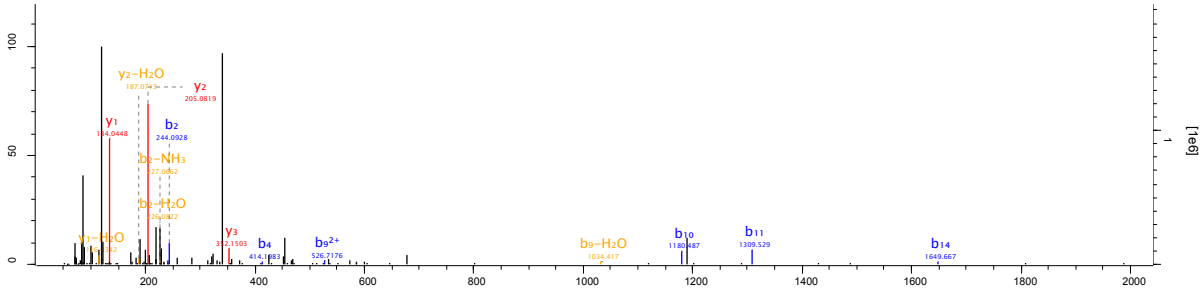
242Catherine_Caspase10	30882	FTMS; HCD	79.66	496.79	SNX1

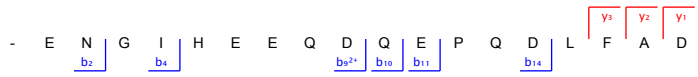




#8

Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	54922	FTMS; HCD	16.31	705.64	SNX1

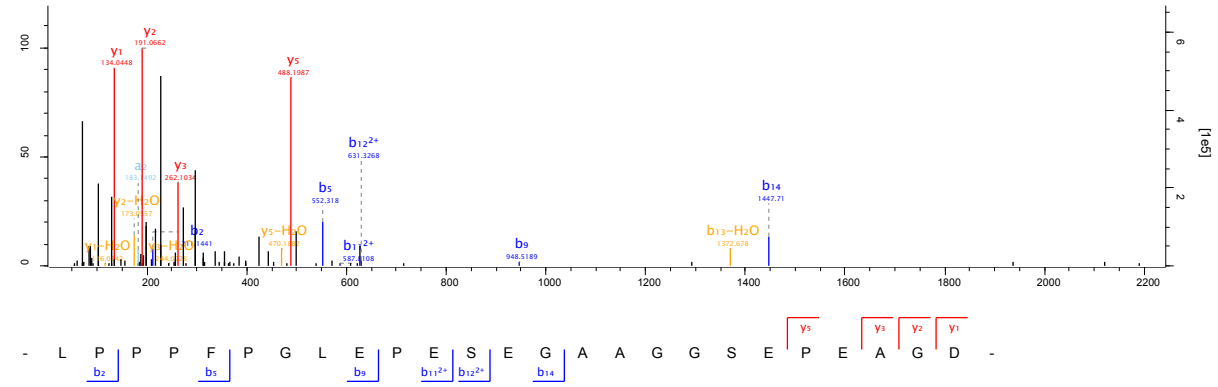




C (continued)

#9

Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	83893	FTMS; HCD	19.4	803.37	SNX1



- L P P P F P G L E P E S E G A A G G S E P E A G D -

b2 b5 b9 b11 2+ b12 2+ b14 y5 y3 y2 y1

#10

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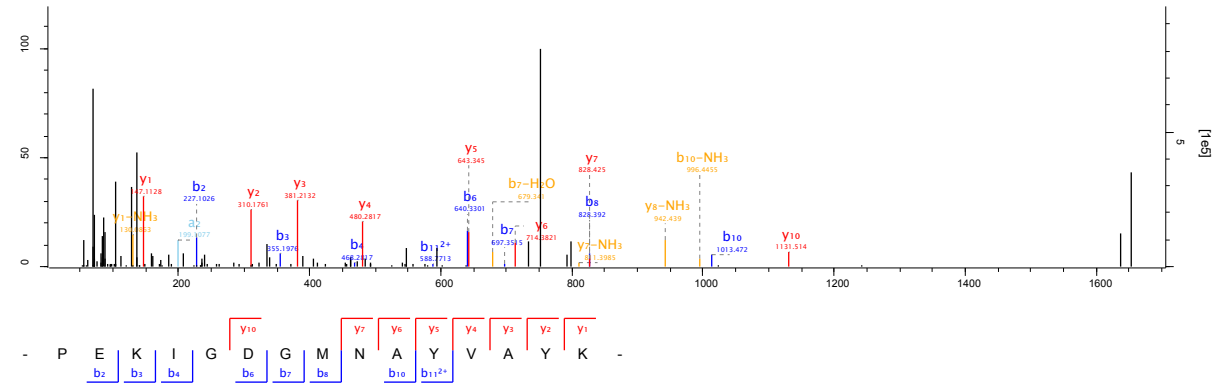
242Catherine_Caspase10	38593	FTMS; HCD	85.01	552.94	SNX1

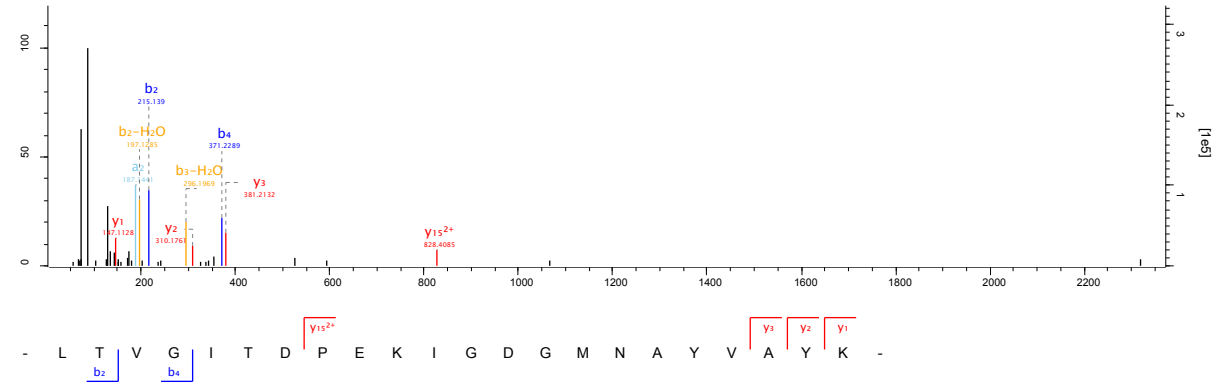


- P E K I G D G M N A Y V A Y K -

b2 b3 b4 b6 b7 b8 b10 b11 2+ y10 y7 y6 y5 y4 y3 y2 y1

#11

Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	68788	FTMS; HCD	18.32	786.07	SNX1

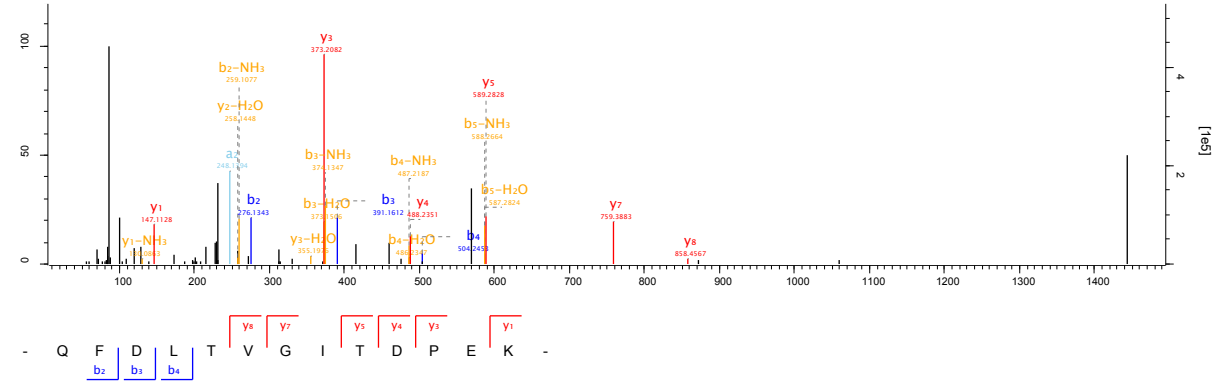


- L T V G I T D P E K I G D G M N A Y V A Y K -

b2 b4 y15 2+ y3 y2 y1

#12

Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	64586	FTMS; HCD	68	731.38	SNX1



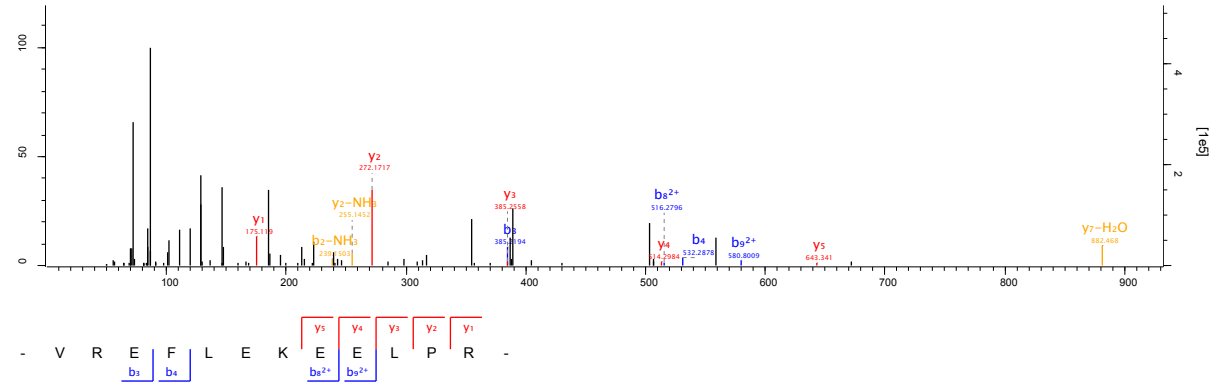
- Q F D L T V G I T D P E K -

b2 b3 b4 y8 y7 y5 y4 y3 y1

C (continued)

#13

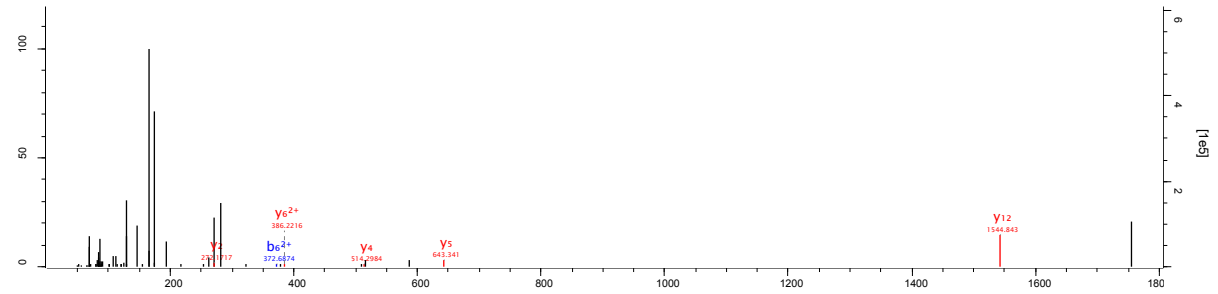
Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	30481	FTMS; HCD	25.98	387.72	SNX1



- V R E F L E K E E L P R -

#14

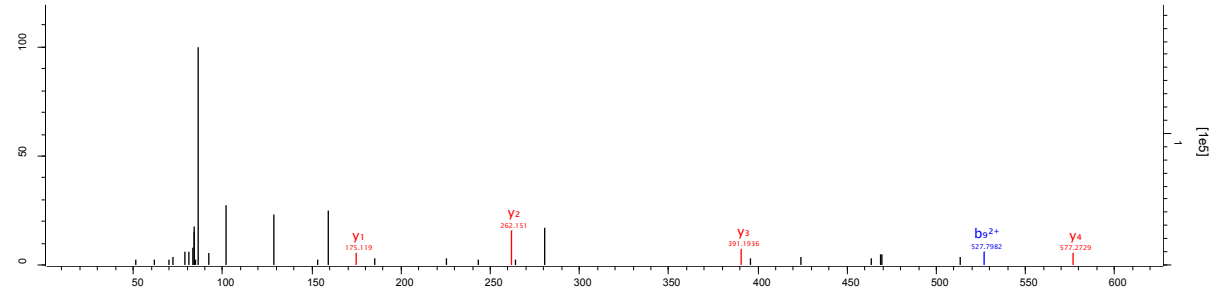
Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	55807	FTMS; HCD	18.82	586.98	SNX1



- P D V R E F L E K E E L P R -

#15

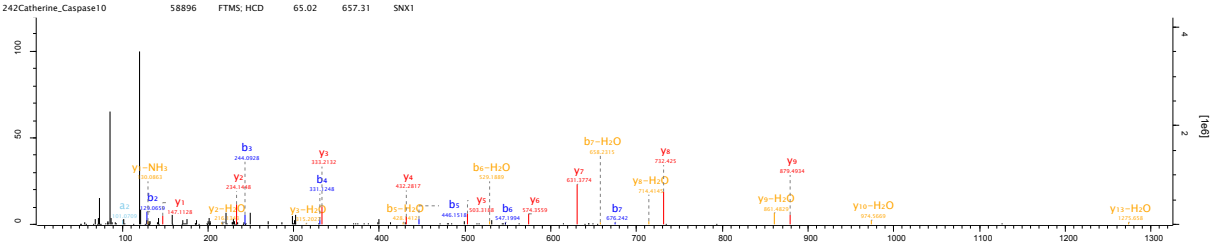
Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	43791	FTMS; HCD	12.2	469.25	SNX1



- K L Q Q A K D E I L E W E S R -

#16

Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	58896	FTMS; HCD	65.02	657.31	SNX1

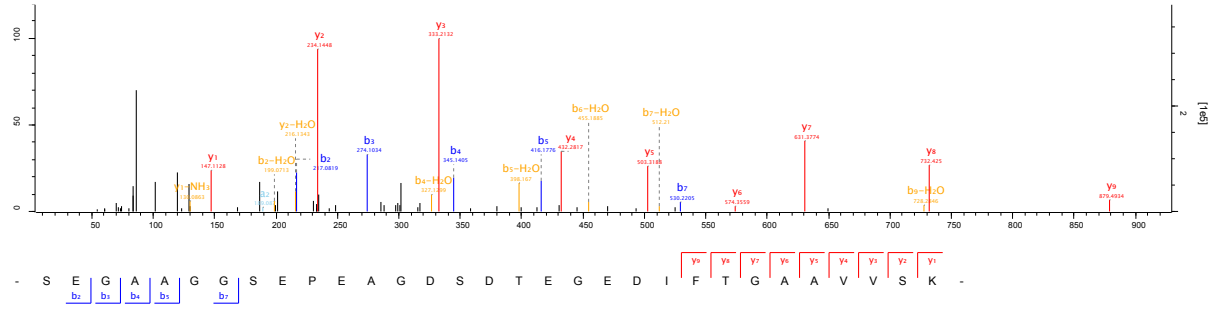


- A G D S D T E G E D I F T G A A V V S K -

C (continued)

#17

Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	61362	FTMS; HCD	40.85	981.1	SNX1



#18

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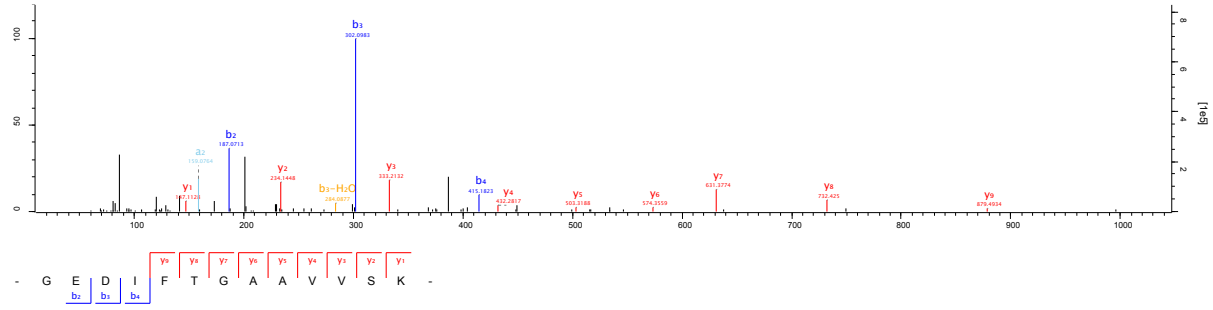
242Catherine_Caspase10	50066	FTMS; HCD	64.1	647.84	SNX1



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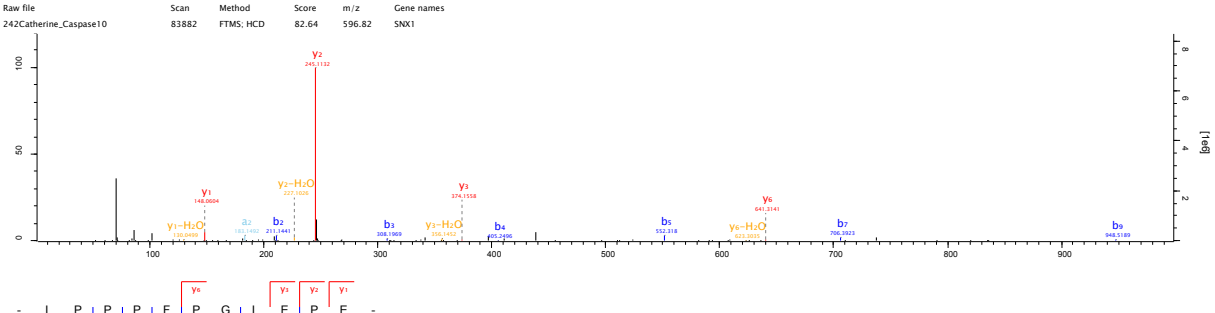
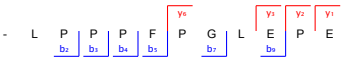
Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	83882	FTMS; HCD	82.64	596.82	SNX1





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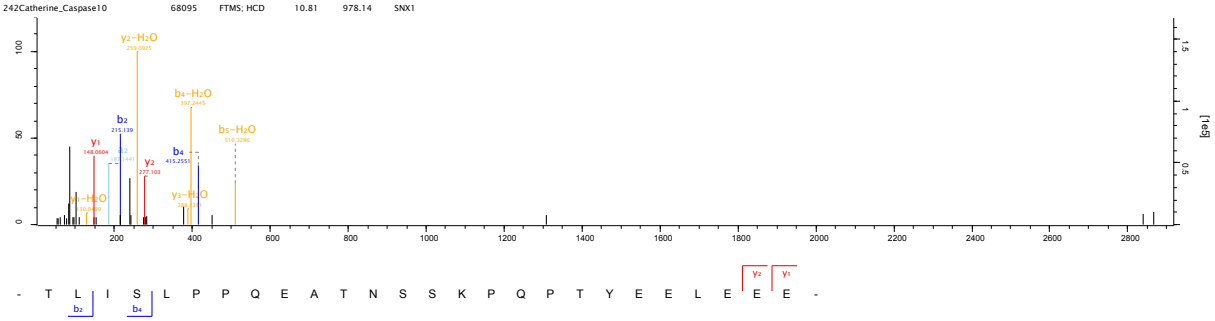
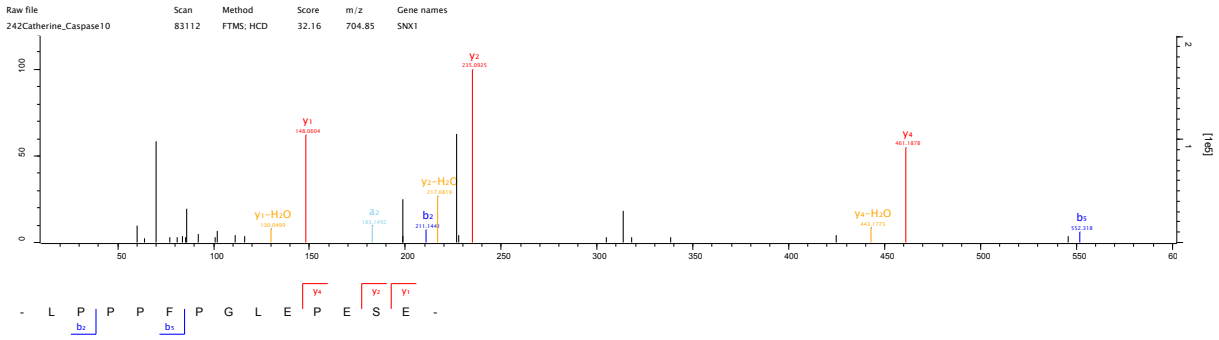
Raw file	Scan	Method	Score	m/z	Gene names
242Catherine_Caspase10	68095	FTMS; HCD	10.81	978.14	SNX1



C (continued)

#21



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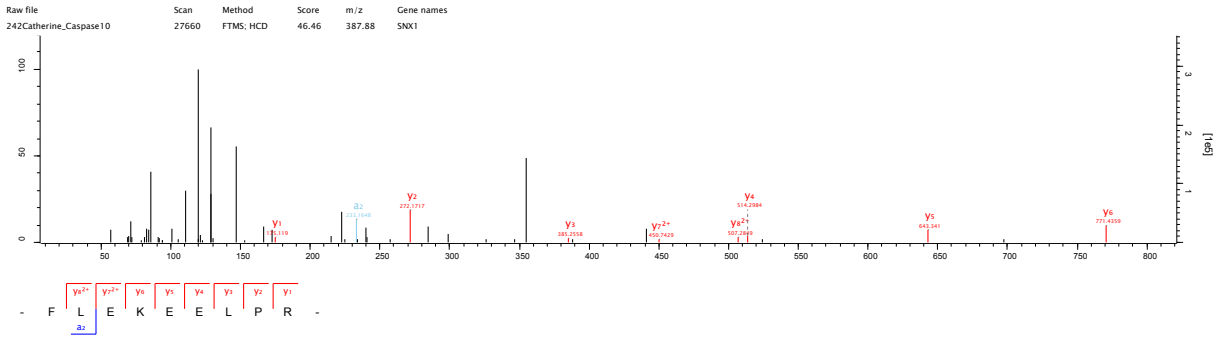
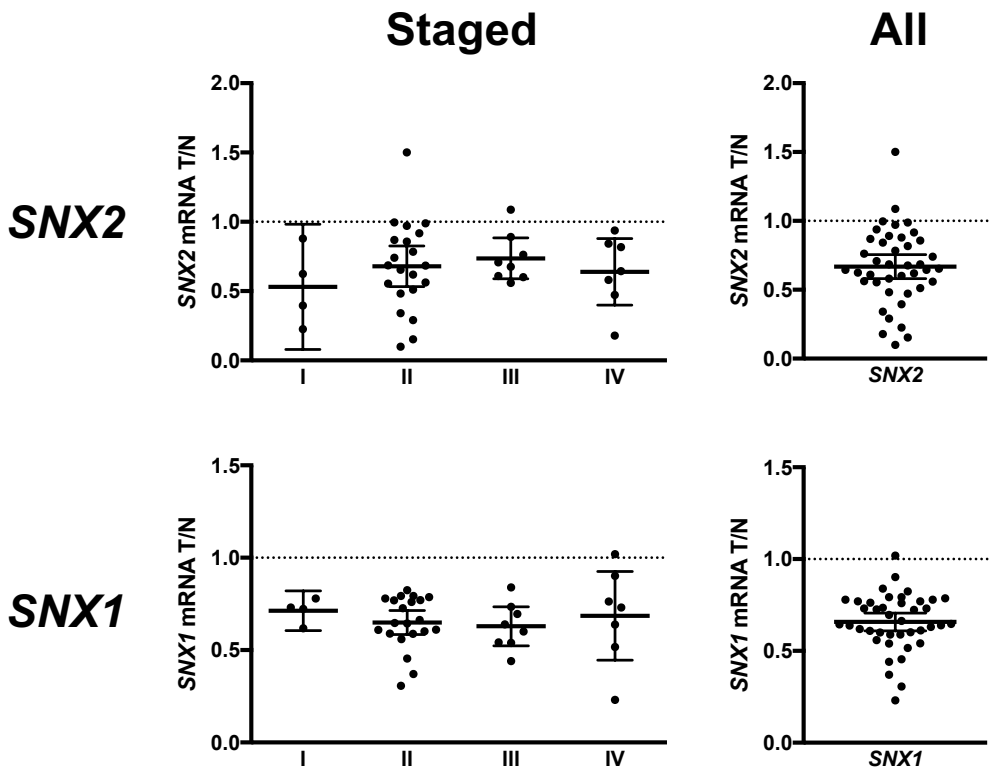


Supplementary Figure 1 Spectrometric analysis of SNX1 cleavage sites. (**a**) Primary structure of the human SNX1 protein used for the identification of cleavage sites. Peptide coverage (387/525, 73.4%) is shown in gray; aspartate and glutamate residues are in bold typeface; cleaved Asp and cleaved Glu sites are underlined and green and red typeface, respectively. The previously reported cleavage site is boxed and corresponds to Asp_{91}. The N-terminal GSP residues are from the fusion protein used to purify SNX1. (**b**) List of peptides identified that reveal cleavage sites. Cleaved aspartate/glutamate residues are identified (Uniprot: Q13596) along with [-8,+8] sequence window with cleavage site, missed Asp/Glu/Lys/Arg cleavages and peak intensities in the control and caspase-10-cleaved samples. Cleavage sites at $Asp_{38,91,141}$ and at Glu_{24} were identified by both N- and C-terminal peptides (brackets). (**c**) Peptide ion trap CID fragmentation for the peptides identified in **b**. Spectra are shown as matched to peptide sequences and annotated by MaxQuant 1.5.2.8.

Supplementary Figure 2



Supplementary Figure 2 *SNX2* gene expression is decreased in CRC tumors. *SNX2* and *SNX1* mRNA level tumor/normal ratios (staged, *left panel*; all stages, *right panel*) in CRC tumors from patients. Accompanies Figure 7.