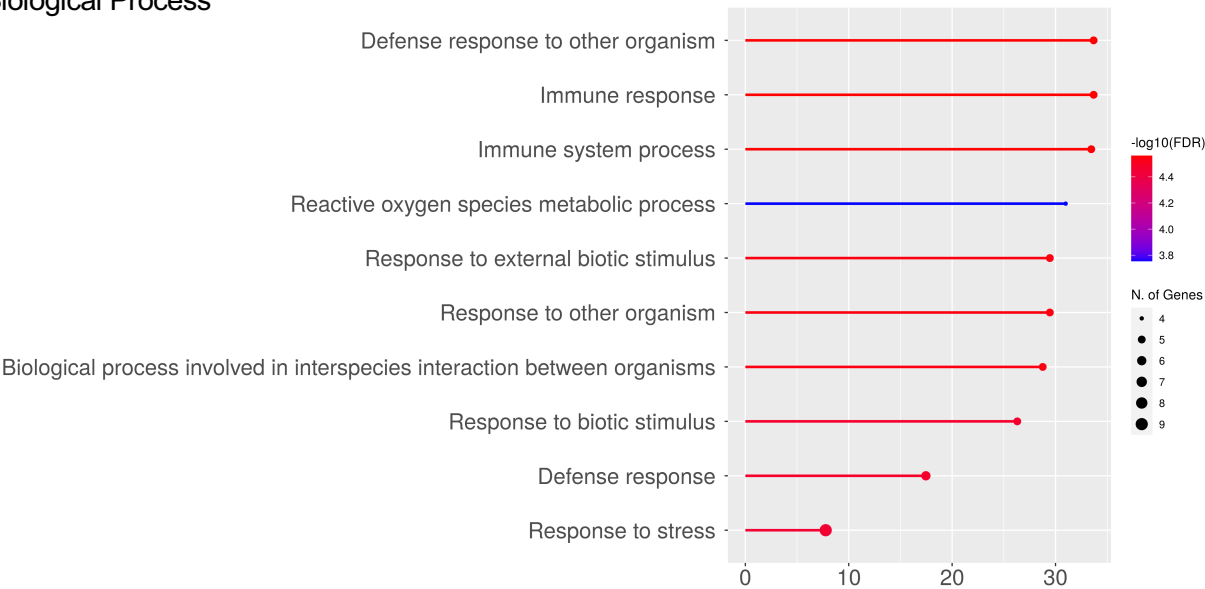
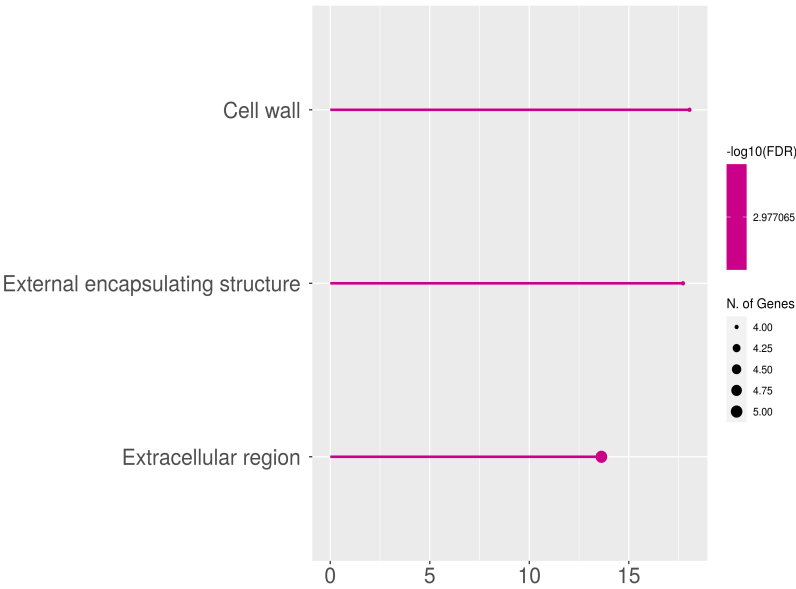


Figure S1

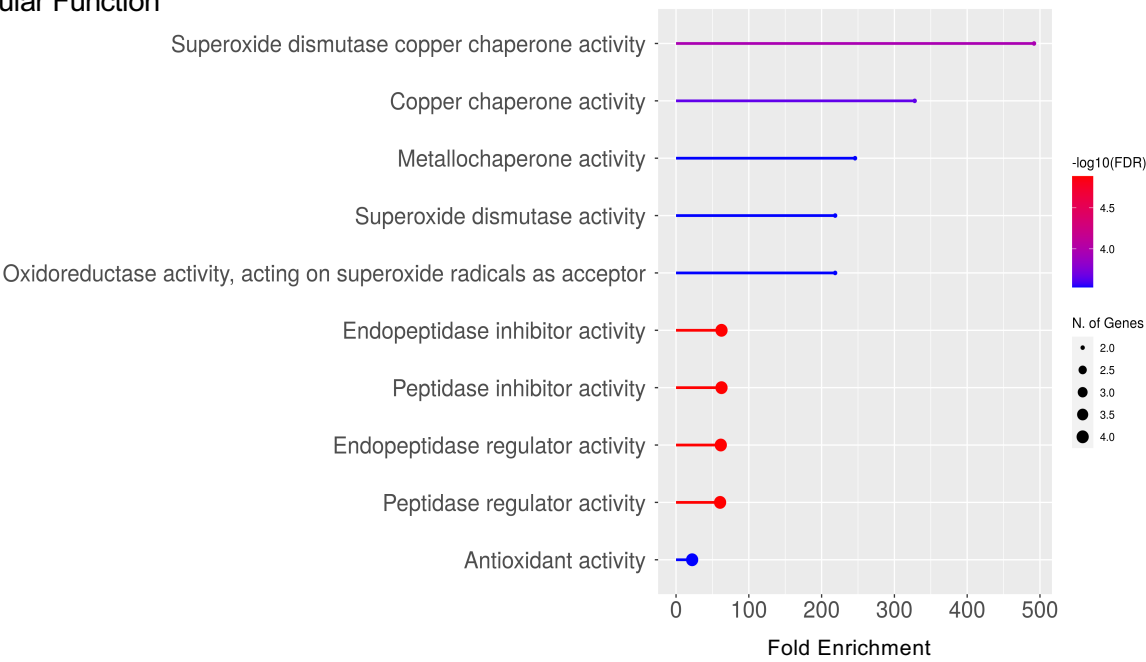
Biological Process



Cellular Component



Molecular Function




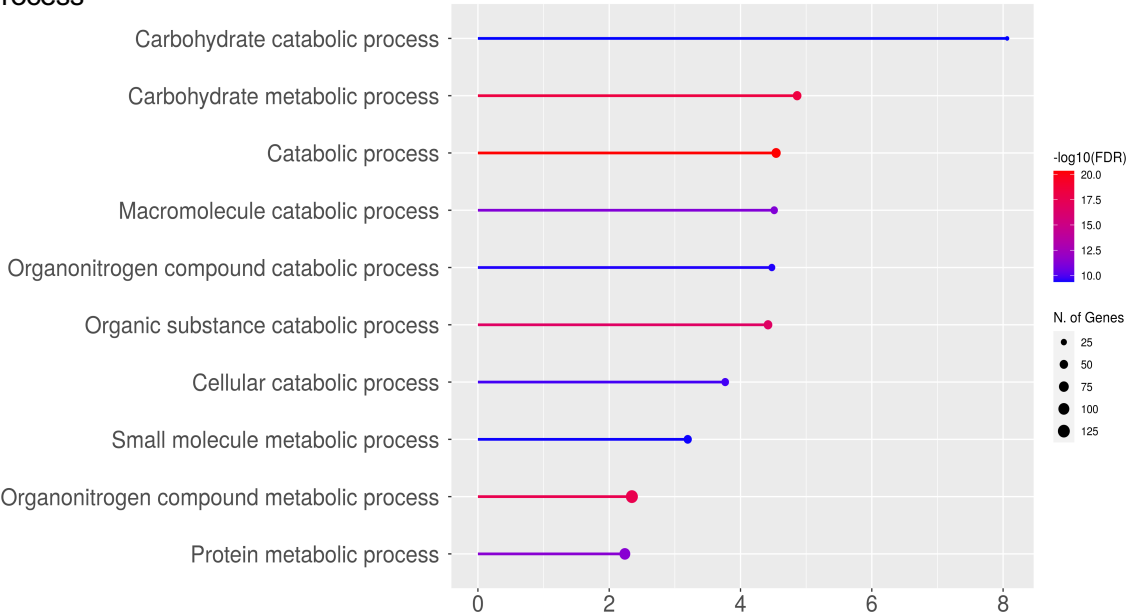
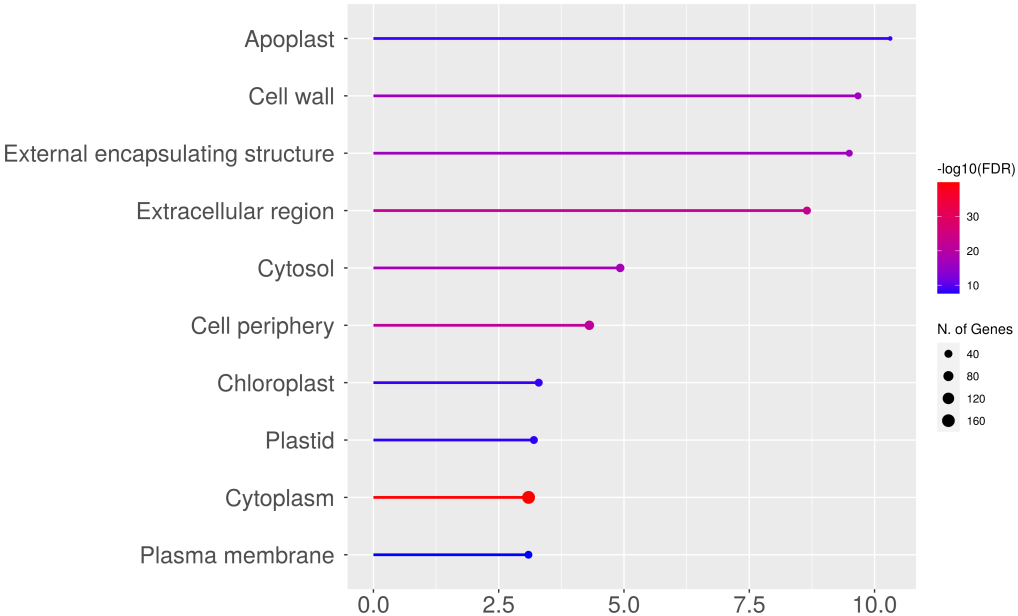
 **Figure S1.** GO analysis of the parent proteins in small-protein fractions. Ten of the top pathways are shown in each category.

Figure S2

Biological Process



Cellular Component



Molecular Function

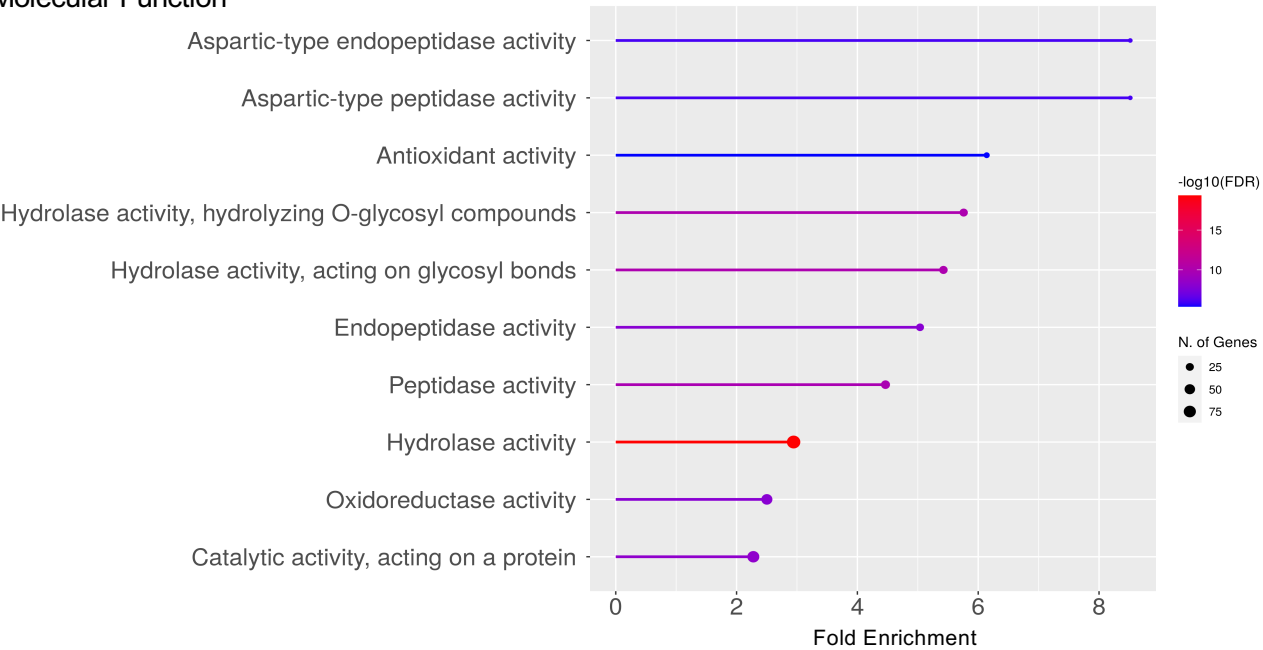
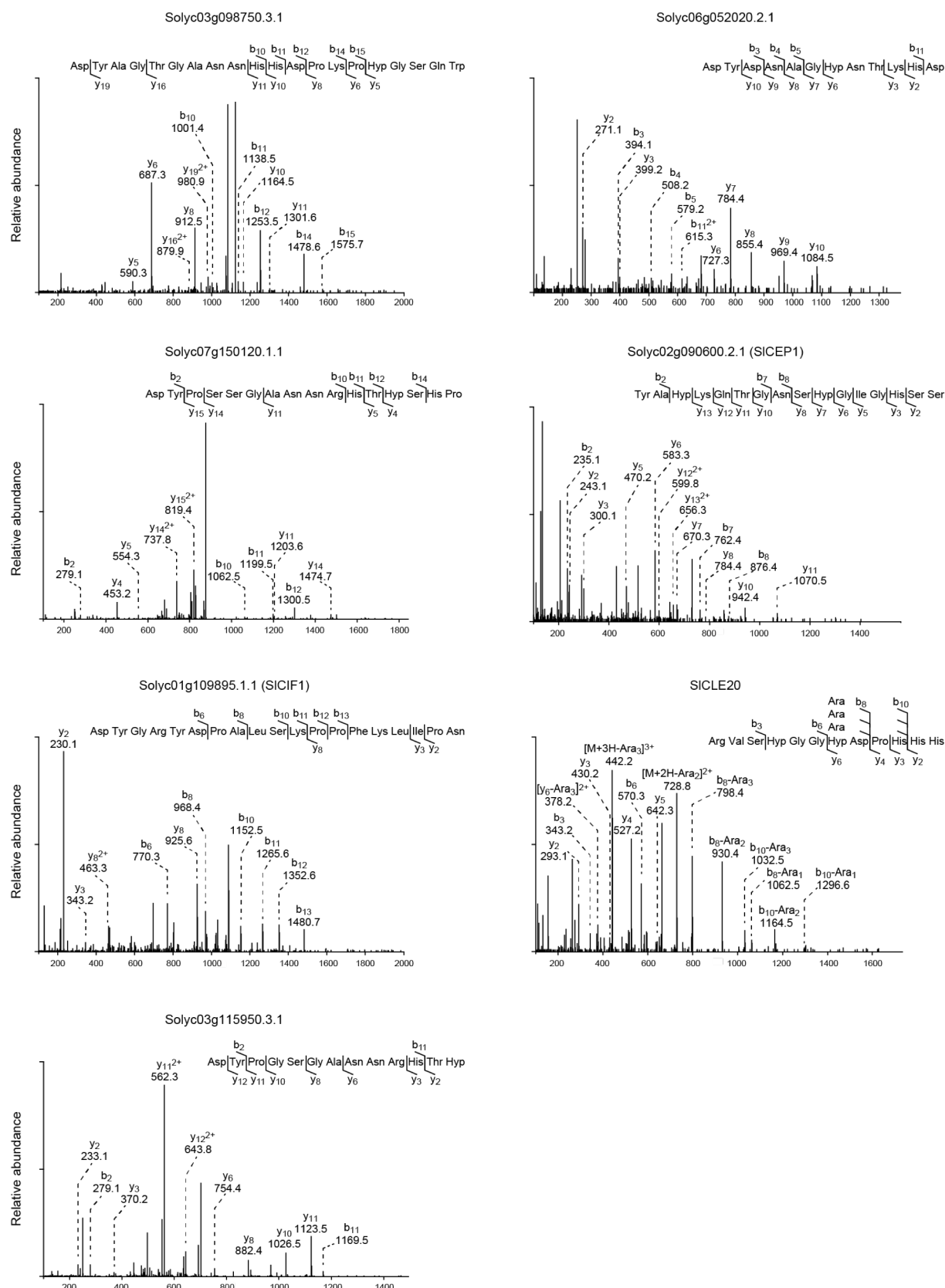


Figure S2. GO analysis of the parent proteins in peptide fractions. Ten of the top pathways are shown in each category.

**Figure S3**



**Figure S3.** MS/MS spectra of the seven tomato xylem exudate-associated oligopeptides.

Figure S4

Solyc03g098750.3.1	----- <u>MEKKVSFLSLLLLIFVGFSLLISTIAVPSSR</u> ---SIKTN-----
Glyma.19G117800.1 (GmXAP1)	-----MLRKLMLLLLLLMFFLCFSYVLSVSAIPATRTQNLKGEEEFSALPSLT
Potri.013G066600.1	-----MAGSLRLLALLLALSFLVSSVAVPATR---SLKSNDEIPSEVQDLL
AT3G47510.1	-----MANKALIHLLVIFFLALSHIFFFPASHASRLGSLMEKPKIVR-----
LOC_Os01g59970.1	MKMEQVSQRKAPLLVLVLILCGLLLLLPLVSSVPLSRVSRLRNHQASVS-----
	* : : . : * . : .
Solyc03g098750.3.1	-TENQVSHDKVVLMDLE- --KKRELLVERD <b>DYAGTGANNHHDPKPPGSQWSNLN</b>
Glyma.19G117800.1 (GmXAP1)	RLDHVVGNGEVVLVDMNEGFMERRVDLETQDYEFTGANKDHDPKSPGGA-----
Potri.013G066600.1	PQDAVISTDGEMLIDAGEGYIEGRMDLESTDYPGTGANNHHDPKTPGKA-----
AT3G47510.1	PQDQTLMDVKKEVEER-----MVMELNDYPGSGANNRHLPRQRCVVD- --
LOC_Os01g59970.1	ALEAPVQVAAAAEERDLDEVAARMVIEVNDYPGSGANNRHDPKSPGRA-----
	: : : : * ** * : * : *
Solyc03g115950.3.1	----- <u>MAAPFFRLFISFLCFSYTINSFINAVPVTRSKSLVLLDISQEHNVLS</u>
Potri.015G062300.1	-----MAGMLFRLLVSFLLISNLVYWSNISISTRRTGSQVHGHDQVPILDD
Solyc07g150120.1.1	----- <u>MATTLFLAFLCFSQVIYLN</u> ---TIPITRCSNLVYKAQQHENTRTM
LOC_Os01g59970.1	MKMEQVSQRKAPLLVLVLILCGLLLLLPLVSSVPLSRVSRLRNHQASVSALEAP
Glyma.03G007400.1	MRFKSPLQLLIILLVFSFVLSSAALQTTRRLLPNKEKTPTQITSDKFQGVVEEL
AT1G74458.1	---MARRQLFYHRMFLVLALLYLMISWKPLLTARPEKSTDFETKGQELNRQI
	: . : : : :
Solyc03g115950.3.1	ENIILMDKTR---REVLEAEEIIN-- <b>DYPGSGANNRHTPRPQLGRGCVEC</b>
Potri.015G062300.1	THLVLSQSKKDHDEHIAHGRKIVELNDYPGSGANNRHTPRPQFGR-CVDC
Solyc07g150120.1.1	ENIEAENMKLG---DVVIRMDVEVN <b>DYPSSGANNRHTPSHP</b> -----
LOC_Os01g59970.1	VQVAAAAAER-DLDEVAARMVIEVNDYPGSGANNRHDPKSPGRA-----
Glyma.03G007400.1	KNGEE--MFDMAEEFMVERRIDLESNDYPGTGANNRHDPKTPGGP-----
AT1G74458.1	SHLGRIENDPERRKGTRMMTVEDINDYPGSGANNRHTPHCSDC-----
	: : ***. : ***** *
Solyc01g109895.1.1 (SlCIF1)	- <u>MGGLMLIKKISLFFLLISASLSTSFAGRQSSFLSNFHQEELS</u> --ATHE
Glyma.13G201100.1 (GmXAP3)	-MGTLMLLKKFTLLFLLISGSLLSTSFAGRVRNSIKNFAKDVN--AIEE
Potri.009G119900.2	--MGLMLLKKISLFFLLISASLSTSFAGRRSKSVNKLAEVEVSAATYE
AT2G16385.1 (CIF1)	MGMSPLTVKKLGFIFMIVSASALSVSFAGRPSIFVHKKINLREE-----
LOC_Os11g21804.1	-MSSRRVNRASVFVILLIVASALSVF TAGGRELVAQETNQKKYSSAALGE
	: : : : : . * : * . * :
Solyc01g109895.1.1 (SlCIF1)	-----EEQLRHERVLKMNTK <b>DYGRYDPTPALS</b> <b>KPPFKLIPN</b>
Glyma.13G201100.1 (GmXAP3)	GTPRKPLNKEEVRTIHERLLRANTKDYGRYDPSPLSKPPFKLIPN
Potri.009G119900.2	EISSKPSHNNEATTIHERLLKANTKDYGNYPAPALVRPPFKLIPN
AT2G16385.1 (CIF1)	-----MVERSMHEHERLLRMNTKDYGNNSPSPRLERPPFKLIPN
LOC_Os11g21804.1	G-----ATSSGEVHPRNLMVKTNDYGRYDPSPAFSKPRFKIIPN
	* * * : * : * . * : * : * : * * : *
Solyc06g052020.2.1	----- <u>MRPRRIKALILLLLFLIFFSS</u> -- <b>GHVEG</b> -----VN
AT5G53486.1	-----MPLRIEPLSLLFLILII CSSSLAIVEGSIQLDGAKMHES
Potri.012G017400.2	-----MALTLGMIKTFLLVSLLLAPFSS--GFVEG-----FDEGMN-
Glyma.04G233800.3 (GmXAP5)	-----MALKINTFLVLVLLILILPLSS--GLAEG-----FGENMHP
LOC_Os05g46470.1	MPSVSVASSMSKLKFLVTVVLVILLFFDSSSSGQAE-----AYT
	: : : : : * . . *
Solyc06g052020.2.1	RAYKLHKHVGIGENPRKLLQLDTVL <b>DYDNAGPNTKHD</b> PRGKKGGSSGNHP
AT5G53486.1	MLYKSEEVGVKKMGHRKLMFHSTADYDDAGPNPKHDPRRRPGGKG----
Potri.012G017400.2	SYP SLHKDGIQVNRKLLLVLD-ELDYDDAGANRRHDPGRPGVGGYKNP
Glyma.04G233800.3 (GmXAP5)	THGLLYKDGIKMNSRKLLVHDFVLDYDEAGPNPRHTTK--PGKGP----
LOC_Os05g46470.1	NYEVT SKVKERIQKHSRRVLTVDQDYDYGGPNRHEPRKKPGNGH----
	: : *** . * . * : * :

Continued on the next page

**Figure S4** (continued)

Solyc02g090600.2.1 (SlCEP1)	----- <u>MQQICLFSFIVAVIACHLVPFAEGRQLKELKKPKLADN</u> ---
Glyma.01G185000.1 (GmXAP6)	-----MDEFQTMHKYFTIFVALFACHGSLFAHGRQIKPLNQHSSLNTNPI
AT5G66816.1 (CEP6)	-----MKLSVYIILSILFISTVFYEQFTEARQLRKTTDDQ-----
SLOC_Os03g27680.1	MKGKRTFLSSLNKEHIKKFYVLERVVAQFYLFSSQGRPLPDDDGITSEMQIR-
	: : . . :.* :
Solyc02g090600.2.1 (SlCEP1)	-----MSANQILEKQRFRTIRDASKVVNGKIN <b>YAPKQTGN</b> SPGIGHSS
Glyma.01G185000.1 (GmXAP6)	LAPLSRTSIKVEAPIVPKFKFSDVDSGDSGADHANAFRPTTPGNSPGVGHKK
AT5G66816.1 (CEP6)	-----DHDDHHFTVGYTDDFGPTSPGNSPGIGHKM
LOC_Os03g27680.1	-----RYLLSHGNGVVEGAVSPSSEIGGPMVGASGGVRPTNPGHSPGIGHHV
	. . * . .*:***:**
Solyc02g090600.2.1 (SlCEP1)	SVPKKFNY---TPNQTN <b>SPGIGHSS</b> SVP-----KTNYQ
Glyma.01G185000.1 (GmXAP6)	FEEDKVMK---VMGALVHSPDV-----KTS
AT5G66816.1 (CEP6)	KENE-----
LOC_Os03g27680.1	AINGDVDDDDVRPTNPGHSPGIGHHAIVNGADDADDVRPTNPGHSPGIGHAVV
Solyc02g090600.2.1 (SlCEP1)	TKHTNVEKSIDDIKAGHSPGIGHSSQSEKIGPNV----
Glyma.01G185000.1 (GmXAP6)	VAEGSFENDFKPTDPGHSPGVGHPRQNKRN-----
AT5G66816.1 (CEP6)	ENAGGYKDDFEPTTPGHSPGVGHAVKNNPNA-----
LOC_Os03g27680.1	NSADDDADDVRPTNPGHSPGIGHAFVNKIDGPAGKKKL
	. . . . .*****:** .:
SlCLE20	- <u>MINTMSKFKYLS</u> CIILLSSALLEARPIR-----SIRIAREA
Glyma.13G171400.1 (GmXAP4)	----MAMLTRFLGCICLILLSAGSEARPLNPT-----IVRDVLGT
AT4G18510.1 (CLE2)	----MAKLSFTFCFLFLLLSSIAAGSRPLEGARVGVK--VRGLSPSIEA
Potri.019G091100.1	----MANLKLWVCLLLFLFTFSKSETRLLDQPYLGRKNPARMLQELNEK
LOC_Os01g55080.1	MAARTYLAVFAFCAILMLSAVARASARALRERAPEEAAVVAGRAGVAGM
	: : : *
SlCLE20	LEEQFEREKAKVG-----AHEWPQ <b>RVSPGGPD</b> PHHHFKNN
Glyma.13G171400.1 (GmXAP4)	LKWTPIQPIAEEG-----GQRGTQRLSPGGPDAAHH-----
AT4G18510.1 (CLE2)	TSPTVEDDQAAGS-----HGKSPERLSPGGPDQHH-----
Potri.019G091100.1	SKQLFEDDSVDTG-----SPYEPKRISPGGPDQHH-----
LOC_Os01g55080.1	MKVPAAGAAAGARRSGGGAVVVVGAAAHESKRLSPGGPDQHH-----
	. . .*:*****:**

**Figure S4.** Amino acid sequence alignment of the precursor polypeptides of tomato xylem exudate-associated peptides and their homologs in various plants. The predicted signal peptides are underlined (SignalP 3.0 <https://services.healthtech.dtu.dk/service.php?SignalP-3.0>). The mature peptide regions are shown in red.