

**Supplemental Table 1**

Peptide analysis of systemically translocated BQCmPP tracer proteins.

Spot Series	Identity	Observed Mass(m/z) <sup>c</sup>	Theoretical Mass(m/z) <sup>c</sup>	Assigned Peptide
BQCmPP16	CmPP16-2	779.47 <sup>f</sup>	570.33	122-125 <b>IYFK</b>
		1068.65	1068.58	15- 24 <b>GLQALDPLNK</b>
		1911.77	1911.99	106-121 GWSELPPRMYQVLAHK
		1240.61	1240.60	46- 56 <b>NAGPDPIWNEK</b>
		1306.46	1306.67	25- 35 PIDPYAEINFK
		1728.51	1728.71 <sup>a</sup>	2-14 (N-biotin)GMGMMEVHLISGK
		1877.93	1877.82	76- 92 VMDHDAIDGDDYIGDVK
		1925.63	1925.98	59- 75 FLVEYPGSGGDFHILFK
		2540.80	2540.50 <sup>a</sup>	57- 75 <b>FK(-biotin)FLVEYPGSGGDFHILFK</b>
BQCmPP19	CmPP16-1	1092.60	1092.58	15- 24 GLQAHDP <span style="text-decoration: underline;">LN</span> K
		1240.89	1240.60	46- 56 <b>NAGPNPLWDEK</b>
		1306.59	1306.67	25- 35 PIDPYAEINFK
		1562.90	1562.60 <sup>b</sup>	136-150 <b>LQGGGGC(-CAM)GGC(-CAM)NPWEN</b>
		1728.96	1728.71 <sup>a</sup>	2-14 (N-biotin)GMGMMEVHLISGK
		1793.96	1793.87 <sup>a</sup>	93-105 IDVK(-biotin)NLLAEGVRK
		1877.99	1877.82	76- 92 VMDHDAIDGDDYIGDVK
		1897.98	1897.95	59-75 FLAEYPGSGGDFHILFK
		2512.06	2512.11 <sup>a</sup>	57-75 <b>FK(-biotin)FLAEYPGSGGDFHILFK</b>
BQCmPP48	SLW1 ortholog	1470.77	1470.77 <sup>d</sup>	216-228 <sup>e</sup> <b>TYGHLFHSGLPNK</b>
		2375.99	2376.30 <sup>d</sup>	229-249 <sup>e</sup> <b>AINAELAMDAALKPIQLNFYK</b>
		2822.18	2821.46 <sup>d</sup>	44- 69 <sup>e</sup> <b>EDLVGAHVREVLDPVSTENG</b> GPLI <span style="text-decoration: underline;">IK</span>
		2936.31	2936.43 <sup>b d</sup>	189-215 <sup>e</sup> <b>GGPLYWVDTADSQPC(-CAM)IGTGGTIPWF<span style="text-decoration: underline;">IK</span></b>

Underlined bold letters indicate amino acid sequences obtained by Edman sequencing.  
 Double-underlined letters indicate amino acid substitution from database sequences (accession number Q9ZT47 and Q9ZT46 for CmPP16-1 and CmPP16-2, respectively).

<sup>a</sup> predicted mass of biotinylated peptide. Biotinylation adds m/z=339 to theoretical mass.

<sup>b</sup> predicted mass of cysteine-modified peptide. <sup>c</sup> monoisotopic mass value. <sup>d</sup> predicted

mass values based on actual sequences.<sup>e</sup> corresponding region of *Cucurbita pepo* SLW1 (AAG25896).<sup>f</sup> modification and/or amino acid substitution was unidentified. Abbreviations of modification: (N-biotin), N-terminal biotinylation; (-biotin), biotinylation; C(-CAM), carboxymethyl cystein.