

gi 392514913 gb AFM77742.1 B1 hordein [Hordeum vulgare]						
MKTFLIFALL AIAATSTIAQ QQPLPQQPIP QKPQYPQQP FPPQQFFPQQ VVPCQQQPYE QQPQQFFPQQ QPFFQQPHFG						
LQ QPFFQQPF FGLQQRIL SQ QQPCTPQQ TP LPQGQLYQTL LQLQIPYVHP SILQQLNPCK VFLQQQCSPV RMPQLIARLQ						
MLQLSSCHVL QQQCCQLPQ ISEQFRHEA I RAIVY SIFLQ EQPQQSVQGV SOTQQQLQQE RYGQCSFQQP QPQQLGQPQQ						
VFQSVFLOPH QIAQL EATTS IALRTLPRMC NVNVPLYDIM PPDFWH						
Coverage: AA 28.8% (111 / 286 residues) Mass 39.1% (12808 / 32777 Da)						
Position	Mass	Peptide		Position	Mass	Peptide
60-74	1759.87	<u>FQQPQQFFPQQPF</u>	←	131-142	1388.75	<u>SILQQLNPCKVF</u>
				131-151	2428.27	<u>SILQQLNPCKVFLQQQCSPV</u>
				132-142	1301.72	<u>ILQQLNPCKVF</u>
				133-142	1188.63	<u>LQQLNPCKVF</u>
				136-142	819.43	<u>LNPKVF</u>
				136-150	1702.85	<u>LNPKVFLOQQCSPV</u>
				138-142	592.30	<u>PCKVF</u>
				141-150	1147.57	<u>VFLQQQCSPV</u>
				143-150	901.43	<u>LQQQCSPV</u>
				143-151	1057.53	<u>LQQQCSPV</u>

Supplementary Figure 1. VFLQQQCSPVR was selected as the peptide for selected reaction monitoring quantification. The VFLQQQCSPVR sequence was identified in one peptide in the untreated fraction. Fragments of this peptide, however, were also identified in nine other peptides. These data demonstrate that the selected VFLQQQCSPVR peptide can resemble neither the molar amount of the original protein nor the molar abundance of gluten epitopes occurring in the protein.