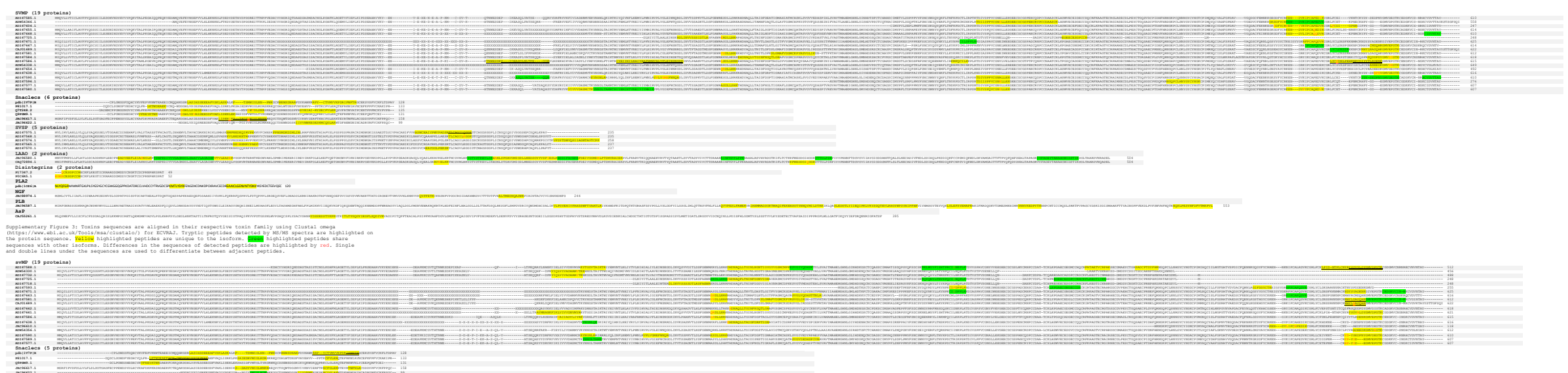


Supplementary Figure 1: Toxin sequences are aligned in their respective toxin family using Clustal omega (<https://www.ebi.ac.uk/Tools/seqservices/seqlogo/>) for ECVM. Tryptic peptides detected by MS/MS spectra are highlighted on the protein sequence. **Yellow** highlighted peptides are unique to the isoform. **Green** highlighted peptides share sequences with other isoforms. Differences in the sequences of detected peptides are highlighted by red. Single and double lines under the sequences are used to differentiate between adjacent peptides.



Supplementary Figure 2: Toxin sequences are aligned in their respective toxin family using Clustal omega (<https://www.ebi.ac.uk/Tools/seqservices/seqlogo/>) for ECVM. Tryptic peptides detected by MS/MS spectra are highlighted on the protein sequence. **Yellow** highlighted peptides are unique to the isoform. **Green** highlighted peptides share sequences with other isoforms. Differences in the sequences of detected peptides are highlighted by red. Single and double lines under the sequences are used to differentiate between adjacent peptides.



Supplementary Figure 3: Toxin sequences are aligned in their respective toxin family using Clustal omega (<https://www.ebi.ac.uk/Tools/seqservices/seqlogo/>) for ECVM. Tryptic peptides detected by MS/MS spectra are highlighted on the protein sequence. **Yellow** highlighted peptides are unique to the isoform. **Green** highlighted peptides share sequences with other isoforms. Differences in the sequences of detected peptides are highlighted by red. Single and double lines under the sequences are used to differentiate between adjacent peptides.

