The protein composition of the digestive fluid from Venus flytrap shed light on the prey digestion mechanism

Supplementary Information

Supplementary Table S1: Full list of identified peptides from the 454-transcriptome.

Supplementary Table S2: Full list of identified peptides form the Illumina-transcriptome.

Supplementary Table S3: Summary of the abundance ranking of identified proteins in secreted fluid from both stimulation methods and based on both transcriptomes.

Supplementary Table S4: FASTA file of the identified ORFs from the 454-transcriptome.

Supplementary Table S5: FASTA file of the identified ORFs from the Illuminia-transcriptome.

Supplementary Table S6: Alignment overlap of contigs from the two different transcriptomes.

Supplementary Table S7: List of proteins identified by LC-MS/MS after separation on an SDS-gel and their ranking in the in-solution analysis of the magnet-based sampling. The star (*) indicates that a spectrum is included (only the highest scoring peptide (across the samples) is included, supplementary figure S4). Locus_223_Transcript_109 is a shorter version of the Locus_223_Transcript_110 sequence, and similar, Locus_52_Transcript_1 is a shorter version of Locus_52_Transcript_2. The two stars (**) indicates ranking from the filter-paper based sampling.

Supplementary figure S1: Silver-stained SDS-gel showing the protein composition of Venus flytrap-digestive fluid obtained from one trap after 48 hours. Representative gel picture from ten replicates using different plants.

Supplementary figure S2: Fragment spectra of proteins from 454-transcriptome approach with one peptide identification only. In-solution digestion.

Supplementary figure S3: Fragment spectra of proteins from Illumina-transcriptome approach with one peptide identification only. In-solution digestion.

Supplementary figure S4: Fragment spectra of proteins from Illumina-transcriptome approach with one peptide identification only. Gel-based analysis.