This document contains the following supporting information:

- The Mascot search engine version 2.2.03 is used for database searching, with the following search parameters:

ESI Qtof:

```
Type of search         : MS/MS Ion Search
Enzyme                 : None
Variable modifications : Acetyl (N-term),Gln->pyro-Glu (N-term Q), Amidated
(C-term),Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 0.1 Da
Fragment Mass Tolerance: ± 0.1 Da
Max Missed Cleavages   : 1
Instrument type        : ESI-QUAD-TOF


MALDI-TOF-TOF
Type of search         : MS/MS Ion Search
Enzyme                 : None
Variable modifications : Acetyl (N-term),Gln->pyro-Glu (N-term Q), Amidated
(C-term),Oxidation (M)
Mass values            : Monoisotopic
Protein Mass           : Unrestricted
Peptide Mass Tolerance : ± 0.6 Da
Fragment Mass Tolerance: ± 0.3 Da
Max Missed Cleavages   : 1
Instrument type        : MALDI-TOF-TOF
```

- PepNovo v3 (Build 20080724) determined de novo sequences, with the following arguments:

```
Probabilistic model    : CID_IT_TRYP
Peptide Mass Tolerance : ± 0.1 Da
Fragment Mass Tolerance: ± 0.1 Da
Digestion enzyme       : none
Spectrum Charge Correct: none
PST length             : 5
Quality cut-off        : .1
```