

## **Supplemental legends**

### **Supplemental table S1, S2, S3 and S4.**

Lists of positive PSMs at < 1% FDR when search was done against protein dataset without any PTMs (Table S1: COMBI scoring, S2: OMSSA using CID data, S3: OMSSA using ETD data, S4: OMSSA using merged CID+ETD spectral data).

### **Supplemental table S5, S6, S7 and S8.**

Lists of positive PSMs at < 1% FDR when search was done against protein dataset with variable PTMs (Table S5: COMBI scoring, S6: OMSSA using CID data, S7: OMSSA using ETD data, S8: OMSSA using merged CID+ETD spectral data).

Types of PTMs and location are indicated in the peptide sequence as follows. [Ctm\_amidation] : peptide C-terminal amidation, [pyro-glu\_Q] : Pyroglutamylation from Q of peptide-N-terminus, [pyro-glu\_E] : Pyroglutamylation from E of peptide-N-terminus, [oxidation] : Oxidation, [sulfation] : Sulfation, [hydroxyPro] : Hydroxylation, [bromination] : Bromination, [dioxidation] : Dioxidation, [acetyl] : Acetylation at peptide-N-terminus [Cation-Na\_Ctm] : Cation-Na at peptide C-termini, [Cation-Na\_D] : Cation-Na at D, [Cation-Na\_E] : Cation-Na at E, [deamidation\_N] : Deamidation at N, [deamidation\_Q] : Deamidation at Q, [Formylation\_Ntm] : Formylation at peptide N-termini, [Phosphorylation\_S] : phosphorylation at S, [Phosphorylation\_T] : phosphorylation at T, [Phosphorylation\_Y] : phosphorylation at Y

### **Supplemental table S9, S10, S11 and S12.**

Lists of positive PSMs at < 1% FDR when search was done against 6 frame translated genome sequence (Table S9: COMBI scoring, S10: OMSSA using CID data, S11: OMSSA using ETD data, S12: OMSSA using merged CID+ETD spectral data). “Chromosome number” column indicates the chromosome where peptide detected by MSMS search.