

| A | MH <sup>+</sup><br>matched | start | end | Missed<br>cleavages | Database<br>sequence |
|---|----------------------------|-------|-----|---------------------|----------------------|
|   | 832.4529                   | 82    | 88  | 0                   | VQESTLR              |
|   | 903.4536                   | 277   | 284 | 0                   | LESDGNIR             |
|   | 960.4692                   | 89    | 95  | 0                   | WVWEANR              |
|   | 1114.6148                  | 202   | 210 | 0                   | LVLYYTTNK            |
|   | 1139.5948                  | 421   | 431 | 0                   | TGDSSLVAYVK          |
|   | 1174.6220                  | 122   | 131 | 0                   | LVWQTNTANK           |
|   | 1185.5693                  | 52    | 61  | 0                   | GFVPFSDNFR           |
|   | 1242.7098                  | 201   | 210 | 1                   | KLVLYYTTNK           |
|   | 1655.7951 *                | 138   | 152 | 0                   | ILENGNMVIYDSSGK      |
|   | 2268.1552                  | 153   | 172 | 0                   | FVWQSFDSPTDTLLVGQSLK |
|   | 2287.0519                  | 32    | 51  | 0                   | VVNEGGYTDYSPIEYNPDVR |

\* Met-ox

| B | MH <sup>+</sup><br>matched | start | end | Missed<br>cleavages | Database<br>sequence |
|---|----------------------------|-------|-----|---------------------|----------------------|
|   | 903.4536                   | 277   | 284 | 0                   | LESDGNIR             |
|   | 960.4692                   | 89    | 95  | 0                   | WVWEANR              |
|   | 1185.5693                  | 52    | 61  | 0                   | GFVPFSDNFR           |
|   | 1242.7098                  | 201   | 201 | 1                   | KLVLYYTTNK           |
|   | 1244.6711                  | 78    | 88  | 1                   | IGNRAQESTLR          |
|   | 1525.8089                  | 409   | 420 | 0                   | CWLGyelKTLTK         |
|   | 1666.8110                  | 138   | 152 | 0                   | ILENGNMVIYDSSGK      |
|   | 2287.0519                  | 32    | 51  | 0                   | VVNEGGYTDYSPIEYNPDVR |

**Supplementary Figure 1. Identification of At1g78850 (A) and At1g78860 (B) by MALDI-TOF MS PMF**

Proteins have been identified in the F CWP fraction obtained by CEC (Irshad et al. 2008). PMF results have been obtained using the ProteinProspector software. The matched peptides cover respectively 26% (118/441 amino acids) and 20% (93/443 amino acids) of At1g78850 and At1g78860.