A foundation for reliable spatial proteomics experiments
data analysis
Supplementary tables

Trans-localisations

<table>
<thead>
<tr>
<th>from</th>
<th>to</th>
</tr>
</thead>
<tbody>
<tr>
<td>AT5G45160 ER membrane</td>
<td>TGN</td>
</tr>
<tr>
<td>AT5G61840 Golgi</td>
<td>PM</td>
</tr>
<tr>
<td>AT1G27390 Mitochondrion</td>
<td>Plastid</td>
</tr>
<tr>
<td>AT2G47840 Plastid</td>
<td>ER</td>
</tr>
<tr>
<td>AT2G14720 TGN</td>
<td>Golgi</td>
</tr>
<tr>
<td>AT4G26690 PM</td>
<td>Vacuola</td>
</tr>
<tr>
<td>AT2G21410 vacuole</td>
<td>Mitochondrion</td>
</tr>
</tbody>
</table>

Table 1: The seven marker proteins that have been trans-localised and their destination organelles. The destination profiles have been computed by averaging the fractions of the destination organelle markers.
| AT5G45160.1 | ER membrane 0.97 |
| AT5G45160.3 | TGN 0.78 |
| AT5G61840.1 | Golgi 0.87 |
| AT5G61840.3 | PM 0.94 |
| AT1G27390.1 | Mitochondrion 0.87 |
| AT1G27390.3 | Plastid 0.94 |
| AT2G47840.1 | Plastid 0.54 |
| AT2G47840.3 | ER membrane 0.97 |
| AT2G14720.1 | TGN 0.82 |
| AT2G14720.3 | Golgi 0.92 |
| AT4G26690.1 | PM 0.93 |
| AT4G26690.3 | vacuole 0.89 |
| AT2G21410.1 | vacuole 0.72 |
| AT2G21410.3 | Mitochondrion 0.93 |

Table 2: Classification details of the 7 in silico trans-localised proteins. The rows ending with .1 show results for the first replicate and the second replicate, corresponding to the changes in localisation, are suffixed by a .3. The svm column defines the classification result and the svm.scores gives the classification posterior probability.

| AT4G11010.1 | Plastid 1.00 |
| AT4G11010.3 | Plastid 1.00 |
| AT5G22640.1 | Plastid 0.60 |
| AT5G22640.3 | Plastid 0.89 |
| AT5G27850.1 | Ribosome 0.58 |
| AT5G27850.3 | Ribosome 0.76 |
| AT1G76270.1 | Golgi 0.35 |
| AT1G76270.3 | Golgi 0.94 |
| AT2G18690.1 | vacuole 0.39 |
| AT2G18690.3 | ER lumen 0.43 |
| AT2G30930.1 | PM 0.37 |
| AT2G30930.3 | vacuole 0.89 |
| AT3G62700.1 | ER lumen 0.27 |
| AT3G62700.3 | vacuole 0.85 |
| AT4G31430.1 | PM 0.53 |
| AT4G31430.3 | Golgi 0.92 |
| AT5G50370.1 | Plastid 0.87 |
| AT5G50370.3 | Mitochondrion 0.86 |

Table 3: Details of the non-trans-localised proteins that had greater distance score than the smallest trans-localised protein. The svm column defines the classification result and the svm.scores gives the classification posterior probability. The protein identifiers ending with .1 are those of the first replicate and the .3 correspond to the second replicate after in silico trans-localisation.
## Concerted trans-localisations

<table>
<thead>
<tr>
<th>Gene</th>
<th>Localisation</th>
<th>svm.scores</th>
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</tbody>
</table>

Table 4: Classification results for the concerted trans-localisations from the mitochondrion (first replicate ending with .1) and second, in silico perturbed replicate (.3 suffix), showing the expected plastid localisation.