

Figure S1 Effect of excess Mn on the xylem sap protein profile using label-free shotgun proteomic analyses, showing the different protein categories. The volcano scatter plot contains the 668 identified and quantified proteins (peptides assigned to a protein and used for quantification ≥ 2). CPS: conventional secretory pathway; UPS: unconventional secretory pathway; sUPS: suggested unconventional secretory pathway; InS: likely non-secretory.

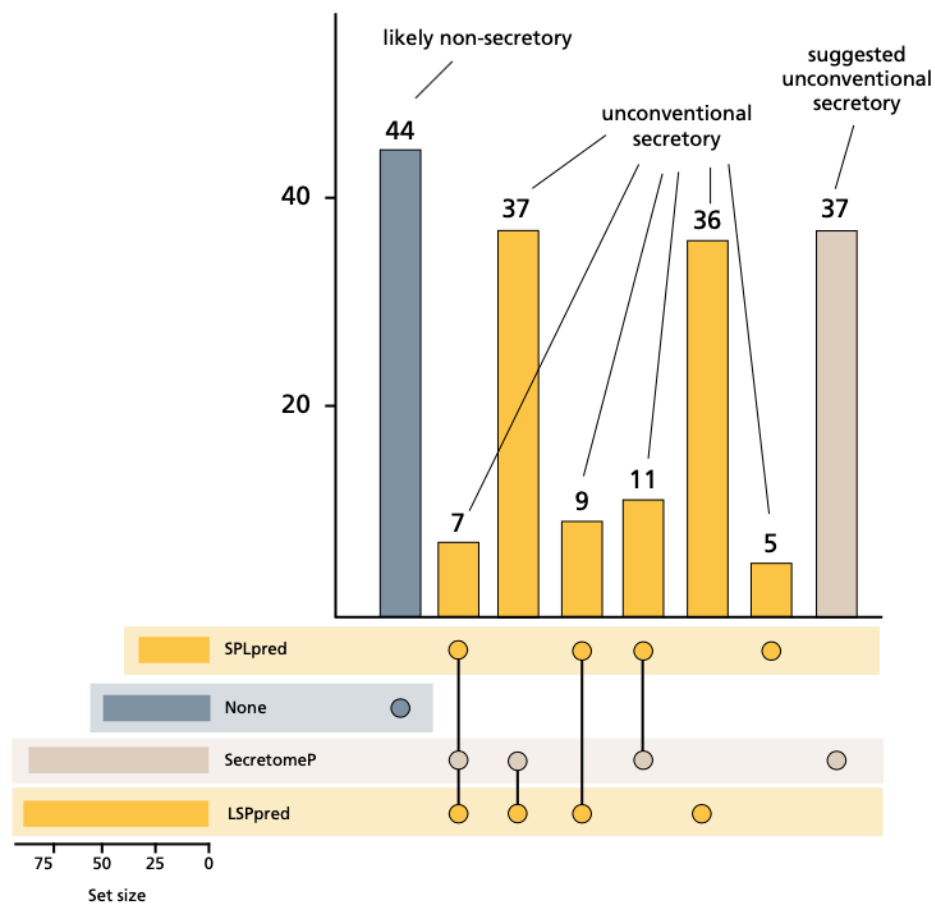


Figure S2 UpSet plot showing the number of proteins lacking a signal peptide, but predicted to be secretory by the three different prediction tools used in the study. Those predicted to be secretory by LSPpred and/or SPLpred were considered 'unconventional secretory'; those predicted to be secretory by Secretome P only were considered 'suggested unconventional secretory', and those not considered to be secretory by any tool were considered 'likely non-secretory'.