

## **Abundant Protein Phosphorylation Potentially Regulates Arabidopsis Anther Development**

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### **Supplemental Figure legends.**

**Figure S1.** Mapman analysis of total identified proteins (including phosphoproteins). Only functional bins with  $P < 1.0 \times 10^{-2}$  are presented.

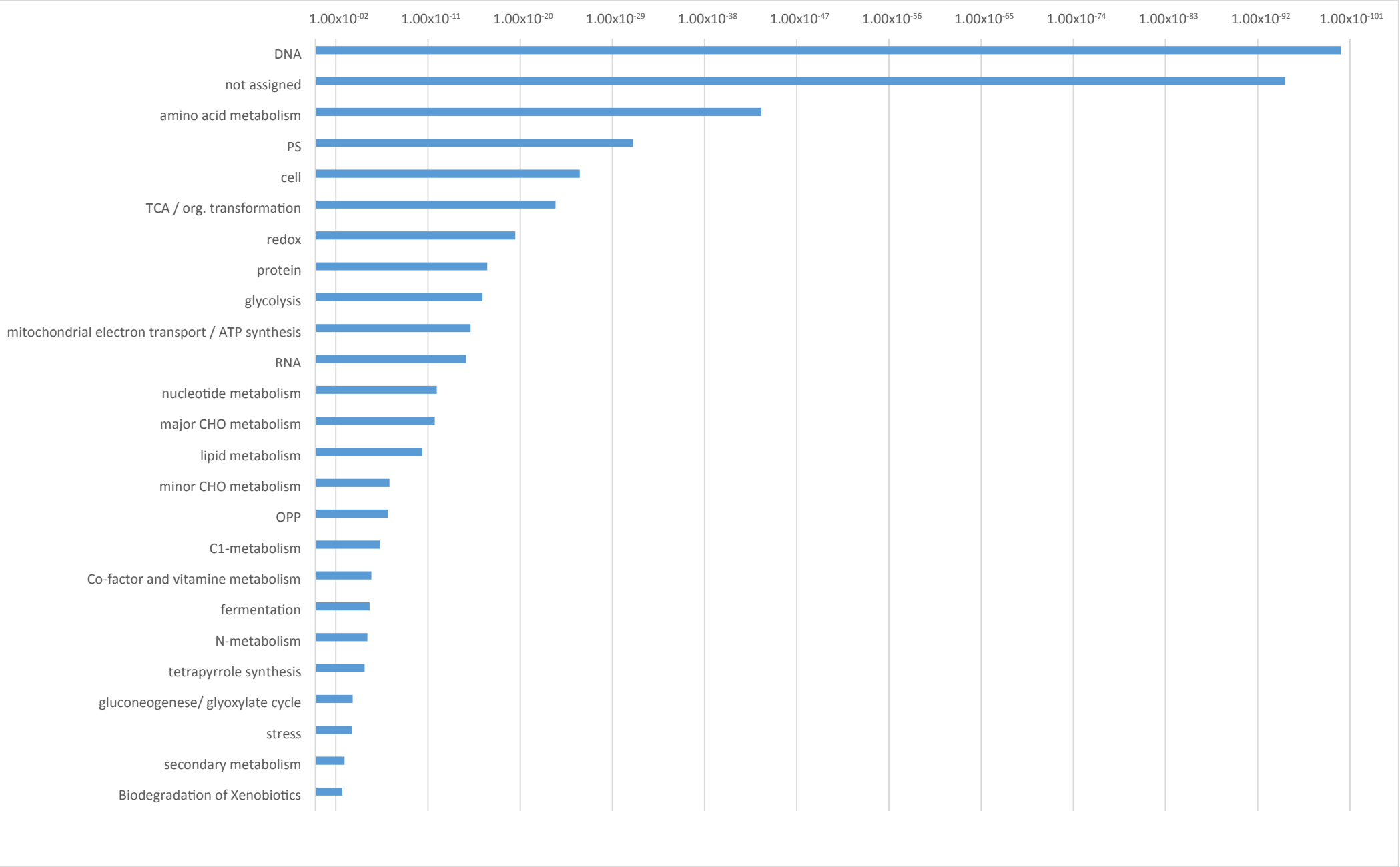
**Figure S2.** Overlap of proteomic and phosphoproteomic analyses in anther phase I and II. (a) Overlap between phosphoproteome (4-7phos) and proteome (4-7proteome) at anther stage 4-7 (phase I); (b) Overlap between phosphoproteome (8-12phos) and proteome (8-12proteome) at anther stage 8-12 (phase II).

**Figure S3.** The enriched MapMan bins (bin numbers and bin names) of identified phosphoproteins (proteins identified in proteomic analysis were set as background) for anther phase I (a) and II (b). Only functional bins with  $P < 1.0 \times 10^{-2}$  for identified proteins are presented.

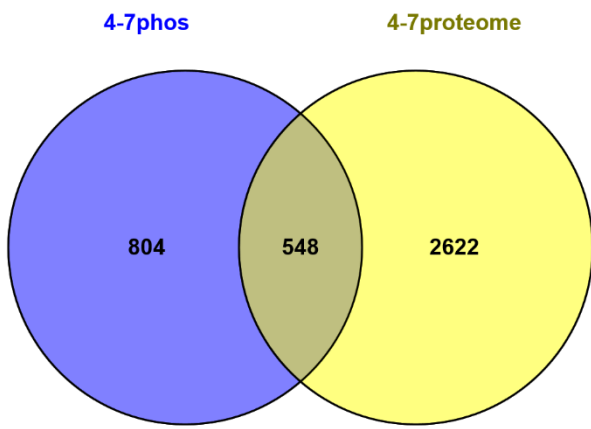
**Figure S4.** The enriched MapMan bins (bin numbers and bin names) of proteomic datasets for anther phase I and II. Only functional bins with  $P < 1.0 \times 10^{-2}$  for identified proteins are presented.

**Figure S5.** Phosphorylation motifs of phosphoSer and phosphoThr predicted by Motif-X.

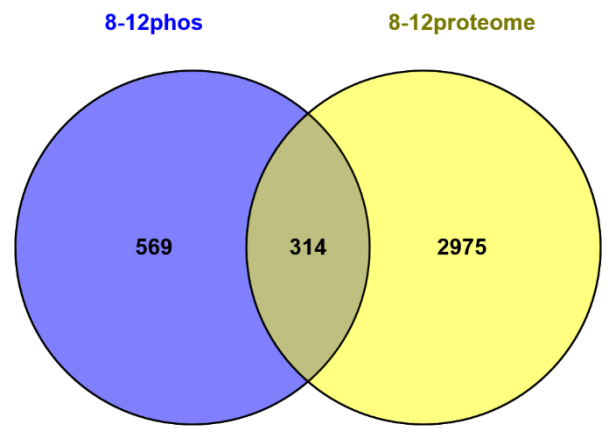
**Figure S6.** The kinase-substrate network extracted from phosphoproteome of anther phase II.



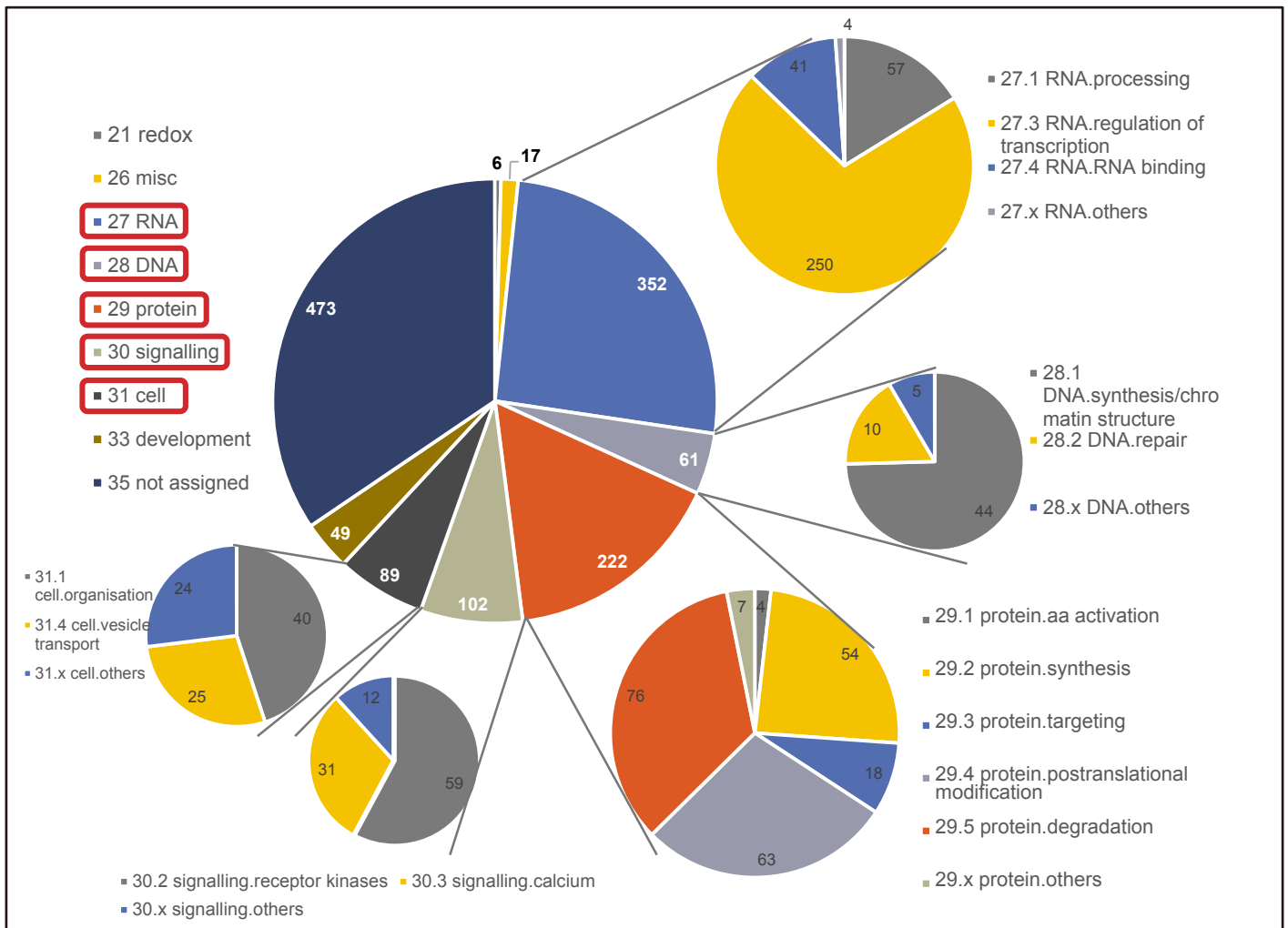
a



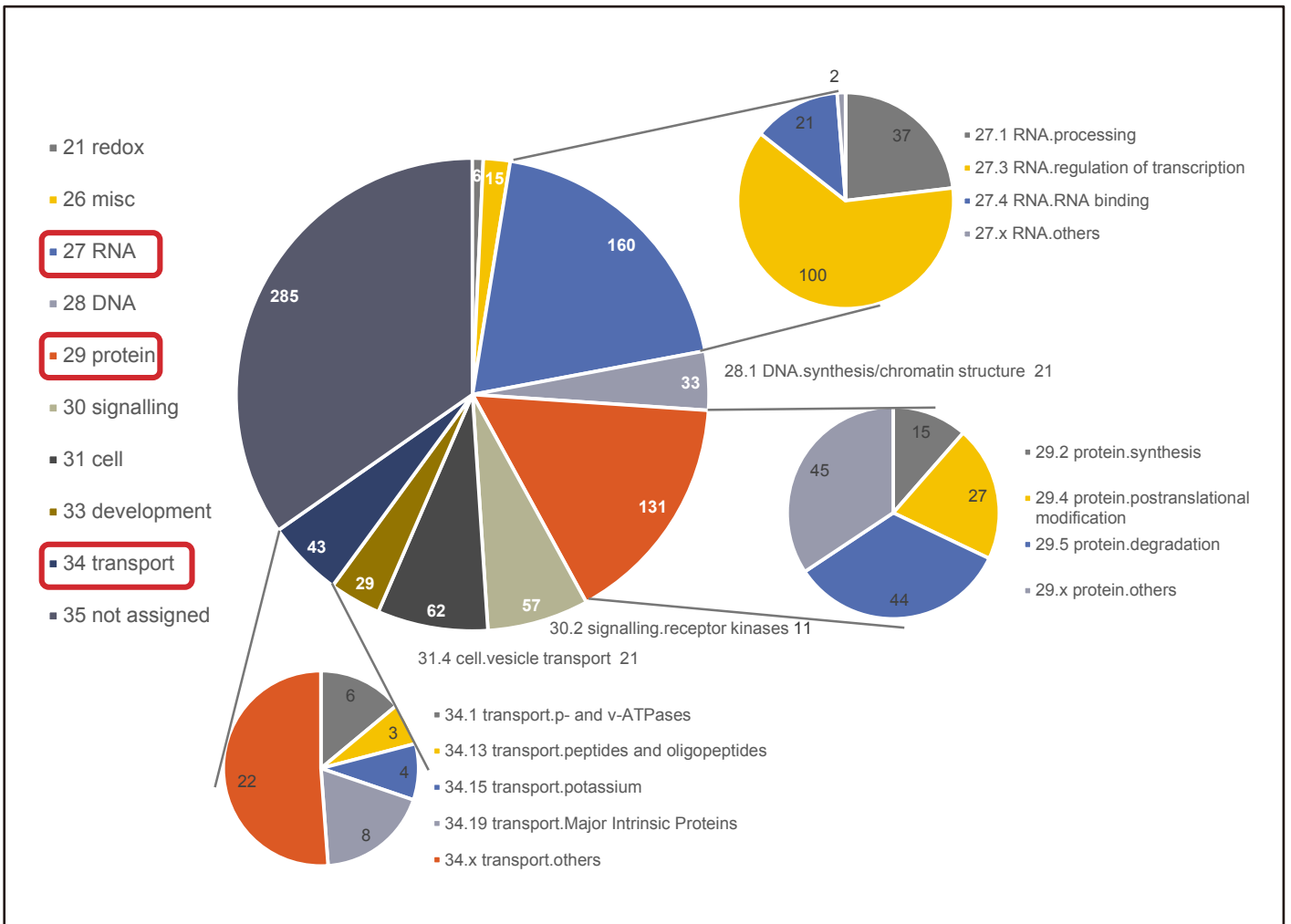
b

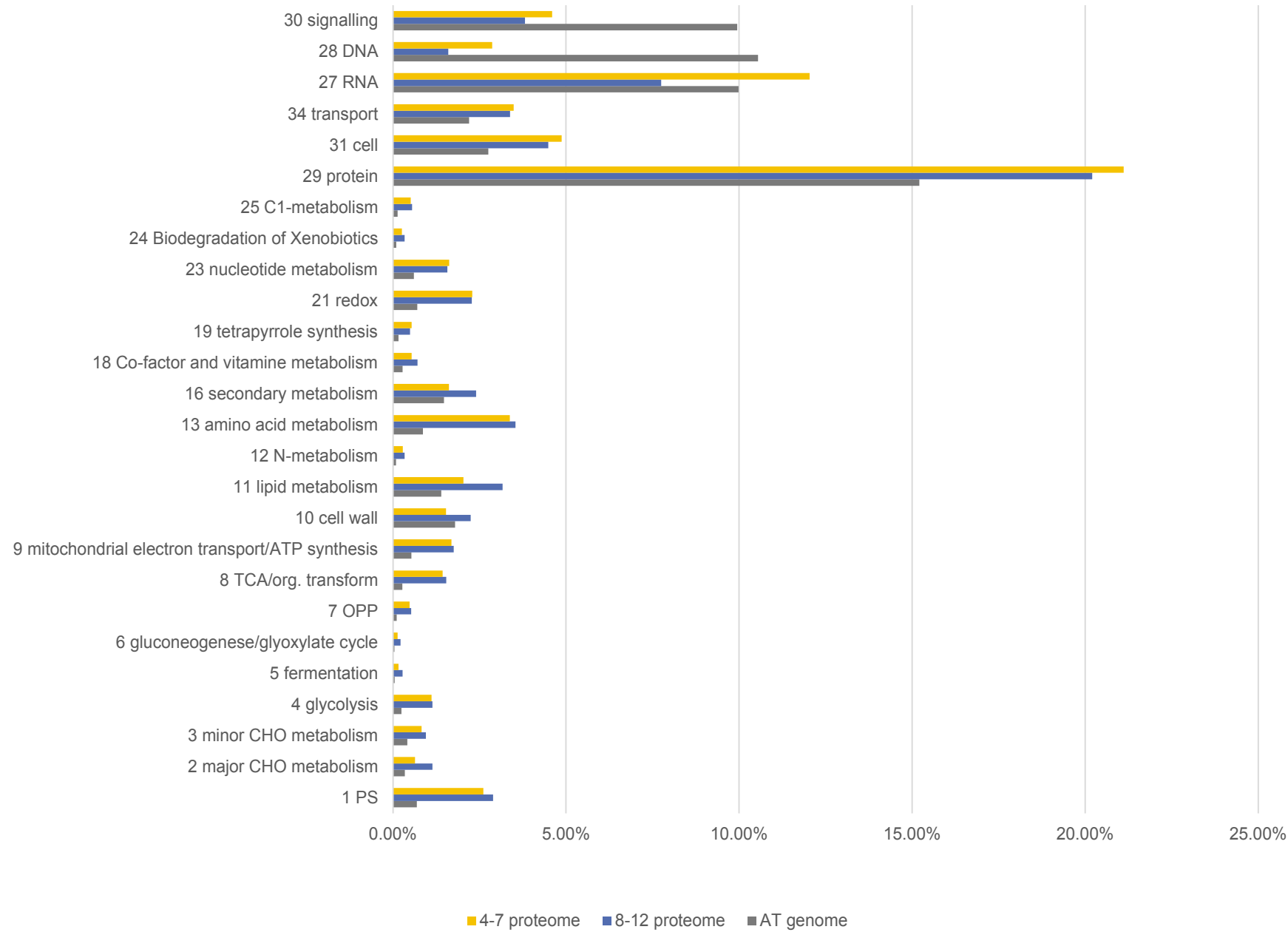


a



b





Motif 1-15

Motif 15-30

Motif 30-45

