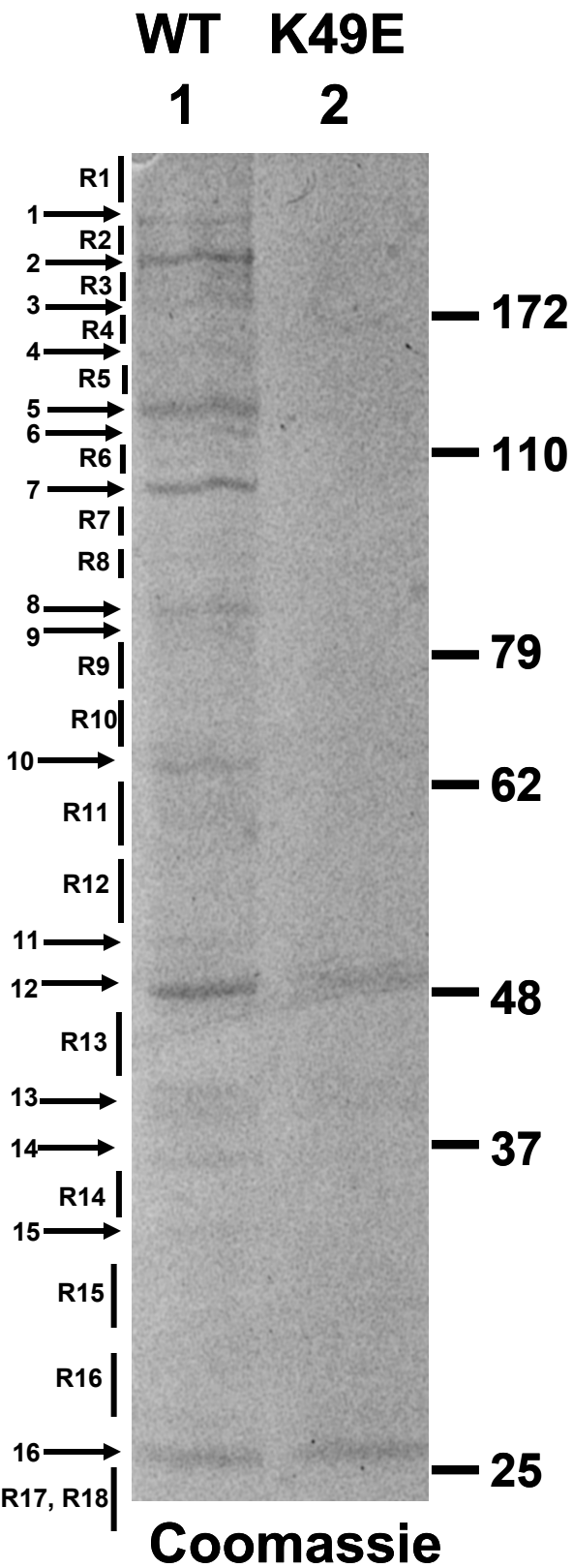


Ballif *et al.* Supplemetary Figure 1



**Supplementary Figure 1** Coomassie stained gel enlarged from Fig 1B, indicating the numbered bands (1-16) and gel regions (R1-R18) that were cut from lane 1 and subjected to in-gel digestion and LC-MS/MS analysis. Molecular weight markers are indicated. See Supplementary Table 1 for the identified proteins and phosphopeptides in each gel band or region.

## Ballif *et al.* Supplementary Figure 2

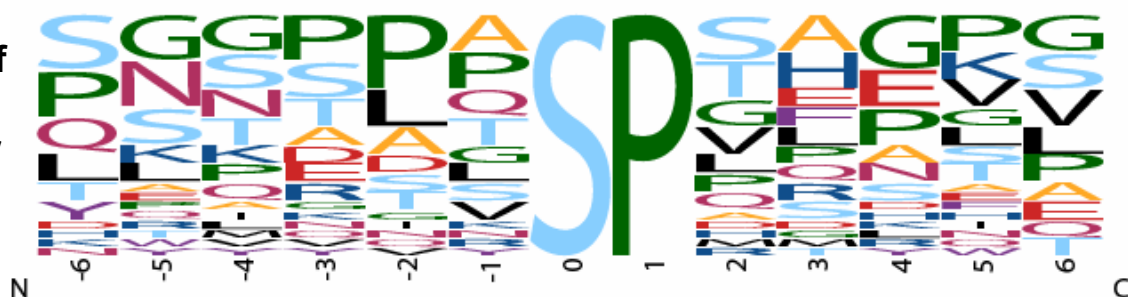
**A**

All 62 serine phosphorylation sites



**B**

26 (pS)P motif sites--5.9 fold increase over background.



**Supplementary Figure 2** (A) Amino acid frequency plot indicating the relative abundance of amino acids surrounding the phosphorylated serine residue for all of the 60 unambiguously identified phosphorylation sites identified among the 14-3-3- $\epsilon$ -interacting proteins. (B) Amino acid frequency plot for the 26 phosphopeptides that harbored a (pS)P motif. This motif was present in the phosphorylated peptides 5.9 fold higher than in the mouse proteome. Note that these peptides showed a preference for proline at the -3 and -2 positions, rather than for arginine.