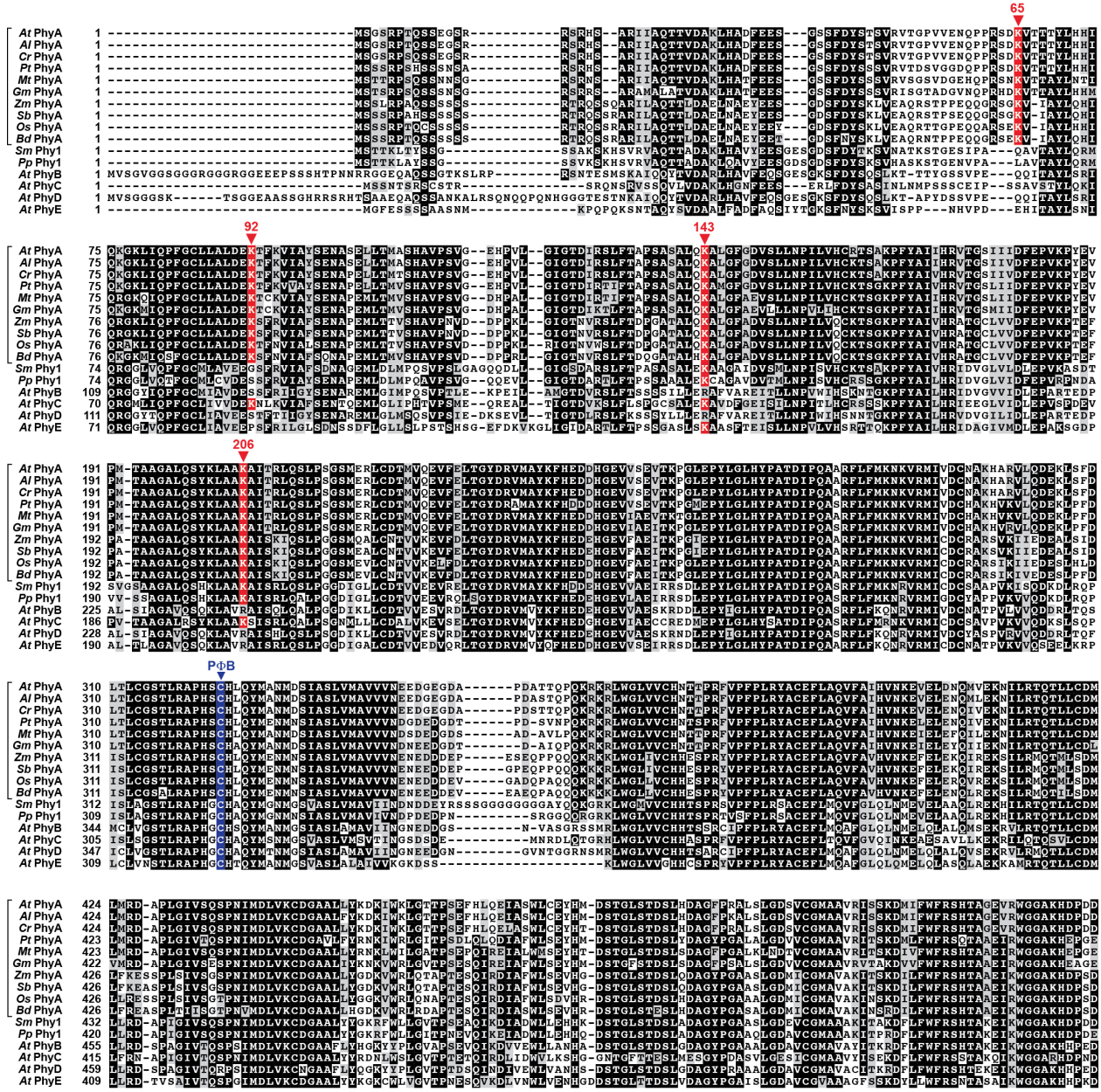
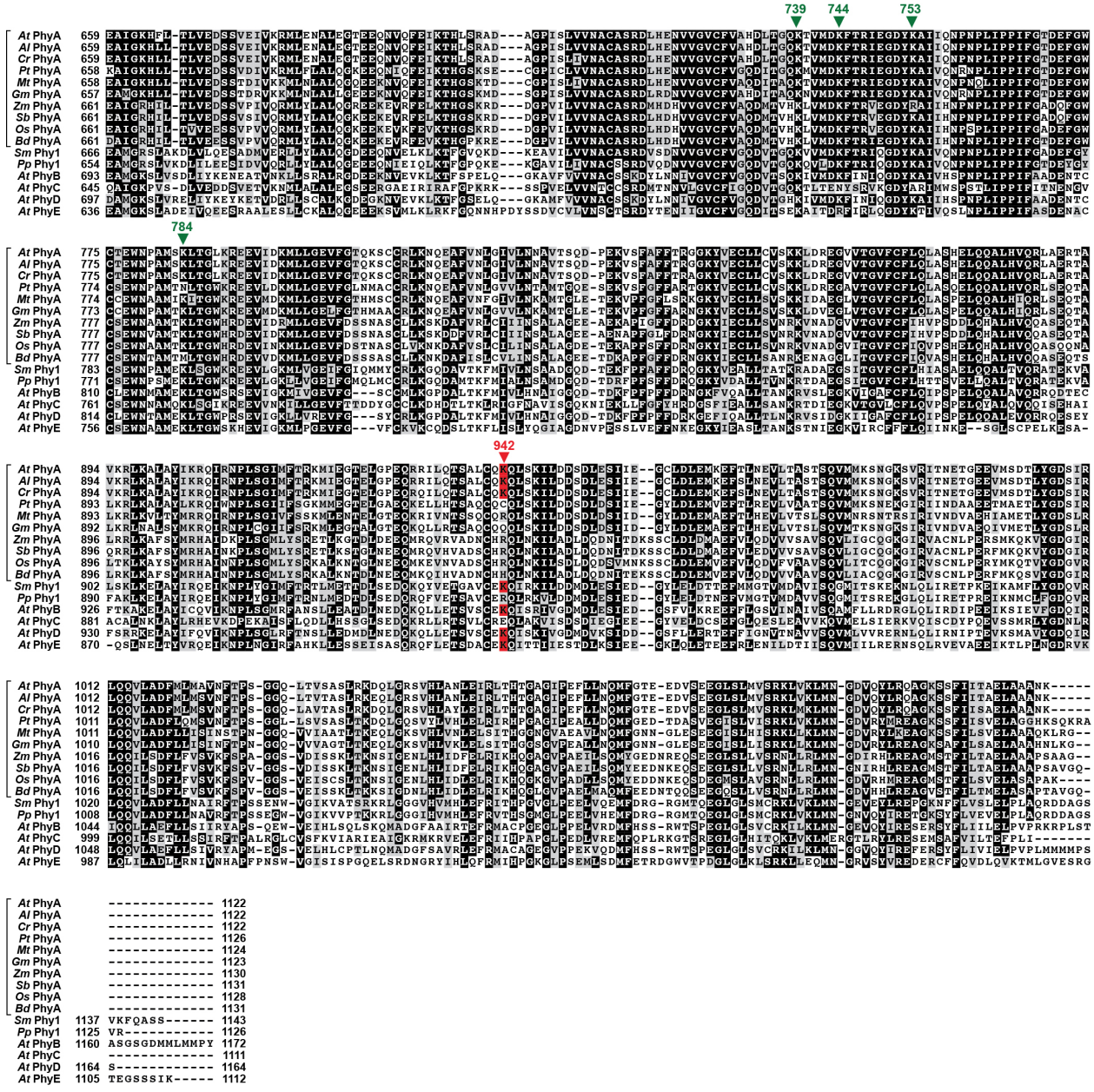

65
92
143
206
PΦB
603



Supplemental Figure 4. The Full Amino Acid Sequence Alignment of Plant Phys Illustrating the Conservation of the Lysine Ub-Attachment Sites Mapped to *Arabidopsis* PhyA.

The alignment includes sequences from representative PhyA isoforms from *A. thaliana* (*At*, NP_172428), *A. lyrata* (*Al*, XP_002892510), *Capsella rubella* (*Cr*, XP_006306617), *Populus trichocarpa* (*Pt*, XP_002318913), *Medicago truncatula* (*Mt*, XP_003591274), *Glycine max* (*Gm*, NP_001241532), *Zea mays* (*Zm*, XP_008665307), *Sorghum bicolor* (*Sb*, AAR30889), *Oryza sativa* (*Os*, CAA32375), and *Brachypodium distachyon* (*Bd*, XP_003560548) (see brackets), PhyA proteins from the bryophytes *Selaginella moellendorffii* (*Sm*, XP_002991119) and *Physcomitrella patens* (*Pp*, XP_001778155), and the PhyB (NP_179469), PhyC (NP_198433),

PhyD (NP_193360) and PhyE (NP_193547) isoforms *from A. thaliana*. Identical and similar amino acids are highlighted in black and grey boxes, respectively. Dashes denote gaps. The modified lysines are highlighted by the red boxes with the residue number indicated above the arrowheads. The cysteine (C323) that binds phytochromobilin (PΦB) is highlighted in blue. The lysines (K739, K744, K753, and K784) previously tested by arginine substitutions for a role in potato PhyA degradation in transgenic tobacco (Clough et al., 1999) are highlighted by the green arrowheads. For the K65, K142, K206 and K603, the ubiquitylation site was determined by direct MS detection of the KGG footprint. In case of K92 and K942, the MS-identified peptides contained multiple lysines; the most likely ubiquitylation site was then determined using the PTM localization filter implemented in MaxQuant program. Brackets locate members of the PhyA subfamily.