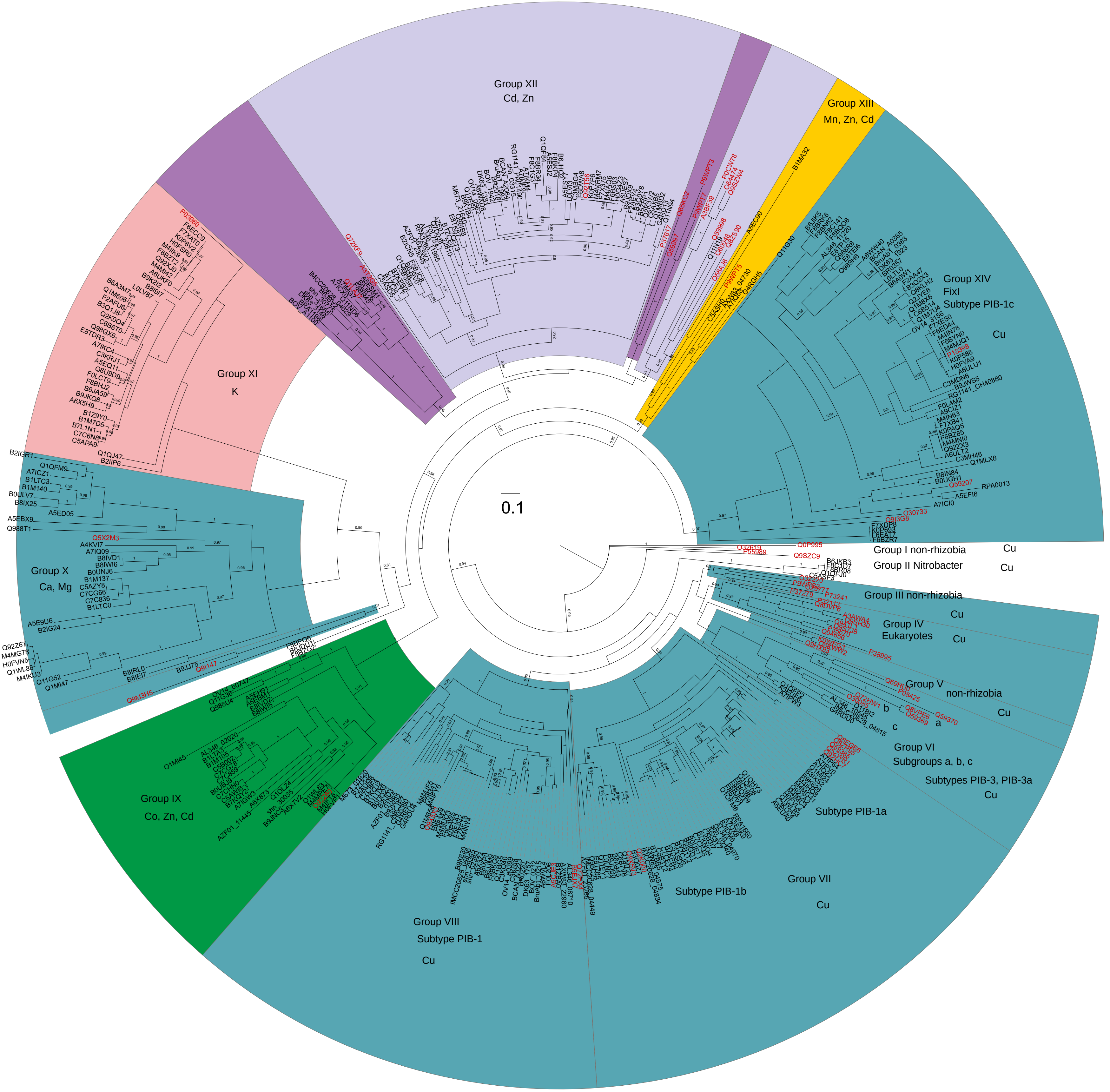

Fig S5. Diversity of P_{IB}-type ATPases revealed by ML-Phylogeny. The ML phylogeny was built by using a 410 P_{IB}-ATPase protein alignment. The fourteen monophyletic groups and their subtypes with a branch support (SH-like) p value ≥ 0.9 are indicated by Roman numbers (I to XIV). Rhizobial Cu-ATPases and their subtypes were distributed in four subfamilies (VI, VII, VIII, XIV). Argüello´s subtypes PIB-1 and PIB-3 are grouped in monophyletic groups VI, VII and VIII. Novel subtypes were distributed in three monophyletic groups (VII, VIII and XIV). The evolutionary relationships of Cu-ATPases with PIB-ATPases for Zn, Cd, Co, Mn and Mg are also shown. The P-ATPases for potassium (K) was used as outgroup.