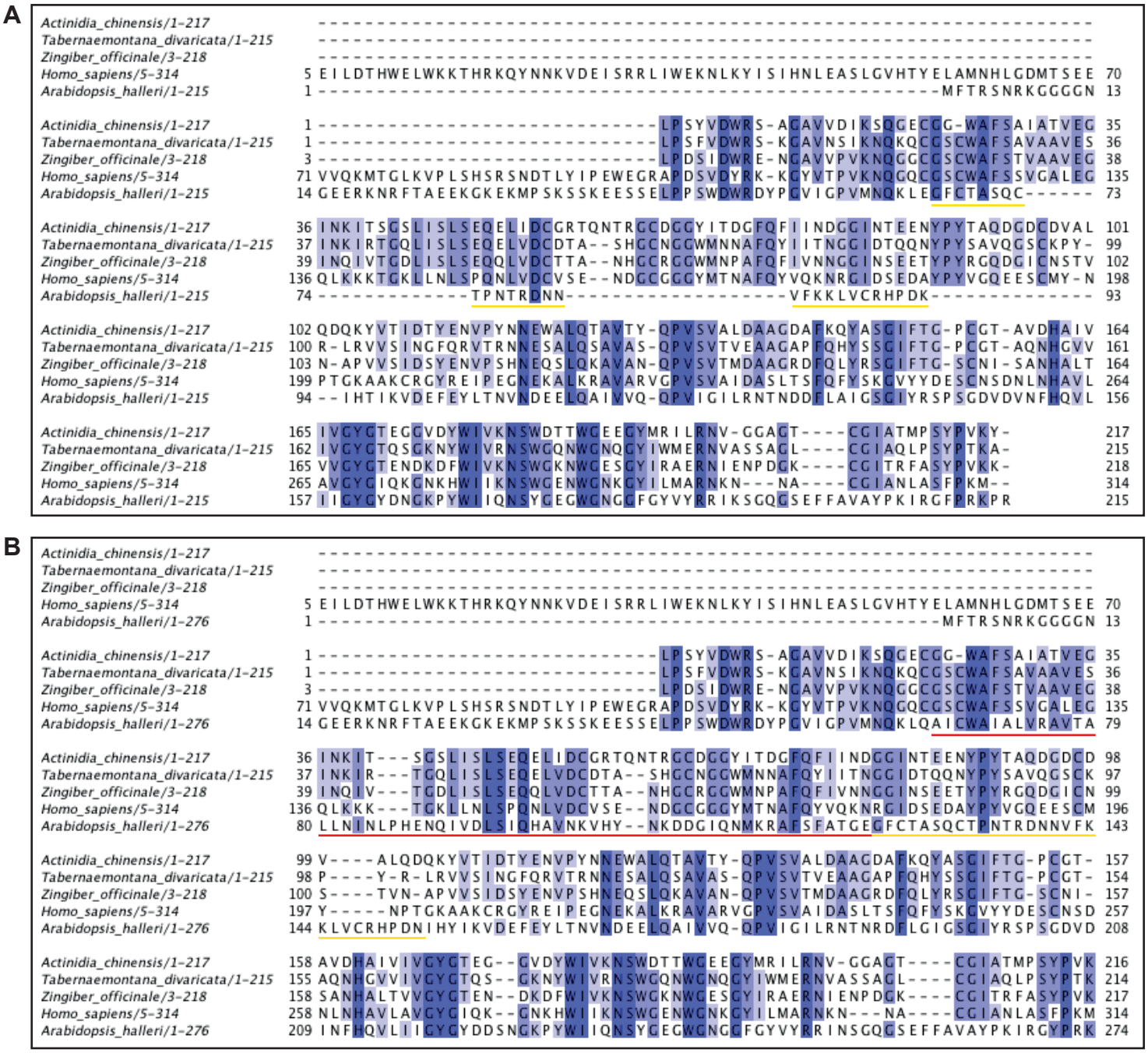

Figure S7. Multiple sequence alignment (MSA) of Papain-like cysteine proteases. Shown are *Arabidopsis halleri* (*Ah*CPL1) , *Actinidia chinensis* (PDB: 2ACT), *Tabernaemontana divaricata* (PDB: 1IWD), *Zingiber officinale* (PDB: 1CQD) and *Homo sapiens* (PDB: 1BY8). **A**, MSA showing the *Ah*CPL1 protein generated by mapping to *A. lyrata* exons. **B**, MSA showing the *Ah*CPL1 protein generated based on *A. halleri* exons. Sequence incorperated based on the genome of *A. halleri* instead of *A. lyrata* is underlined in red. Sequence repositioned based on *A. halleri* sequence data is underlined in yellow.