

SUPPLEMENTARY FIGURE 7

Phylogeny derived from BEAST analyses of TrpA amino acid sequences for scytonemin-dedicated AAAB genes. Entries in blue type correspond to homologs found within full scytonemin operons. Those marked by a blue arrow, correspond to those found in operon remnants operons or to supernumerary copies. Bayesian posterior probabilities (BPP) at the nodes are color coded as follows: red for $BPP \geq 0.8$, pink for $0.8 \geq BPP \geq 0.5$ and white for $BPP \leq 0.5$. Red arrow marks the node corresponding to the most recent common ancestor of the oldest clade containing scytonemin-associated homologs.

