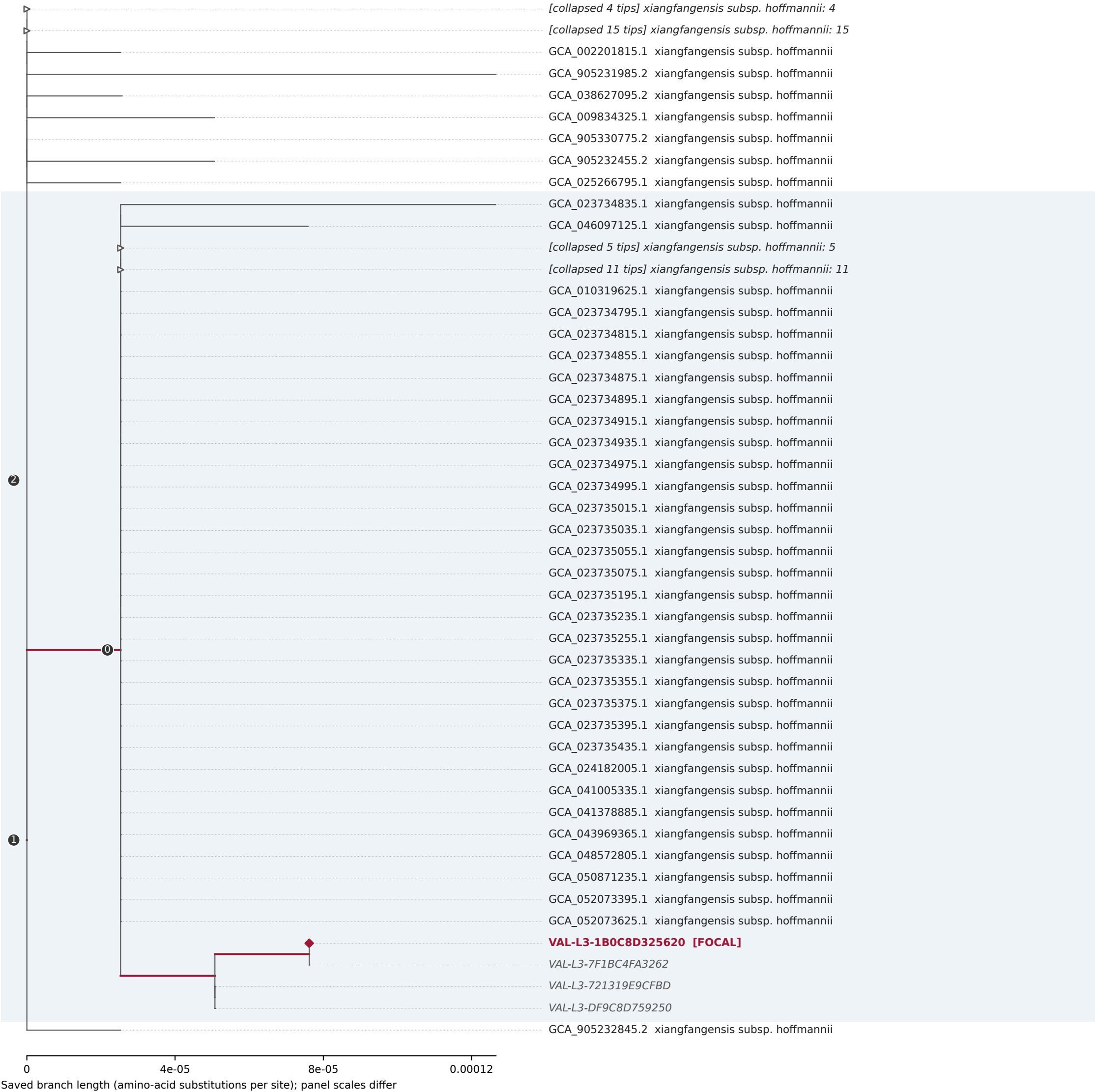


Same Klebsiella aerogenes rooting. Shading = original visible clade. 0 = original root; 1, 2 = added ancestors. Diamond / [FOCAL] = focal query.

Triangles represent collapsed clades: every tip is included in the source table. Dotted lines align labels; they are not branches. No new inference or author-decision change.

BAC120 / FastTree WAG+gamma
52 → 79 tips; +2 ancestor splits; 4 collapsed clades
FastTree support on focal path (wider root → query): 0.000, 0.819, 0.917, 0.871



VerticalI / FastME (median, first)
83 → 87 tips; +2 ancestor splits; 10 collapsed clades
Branch supports are not supplied in this saved FastME tree.

