

Methylobacteriaceae

Fig. S1 (full caption at base of figure)

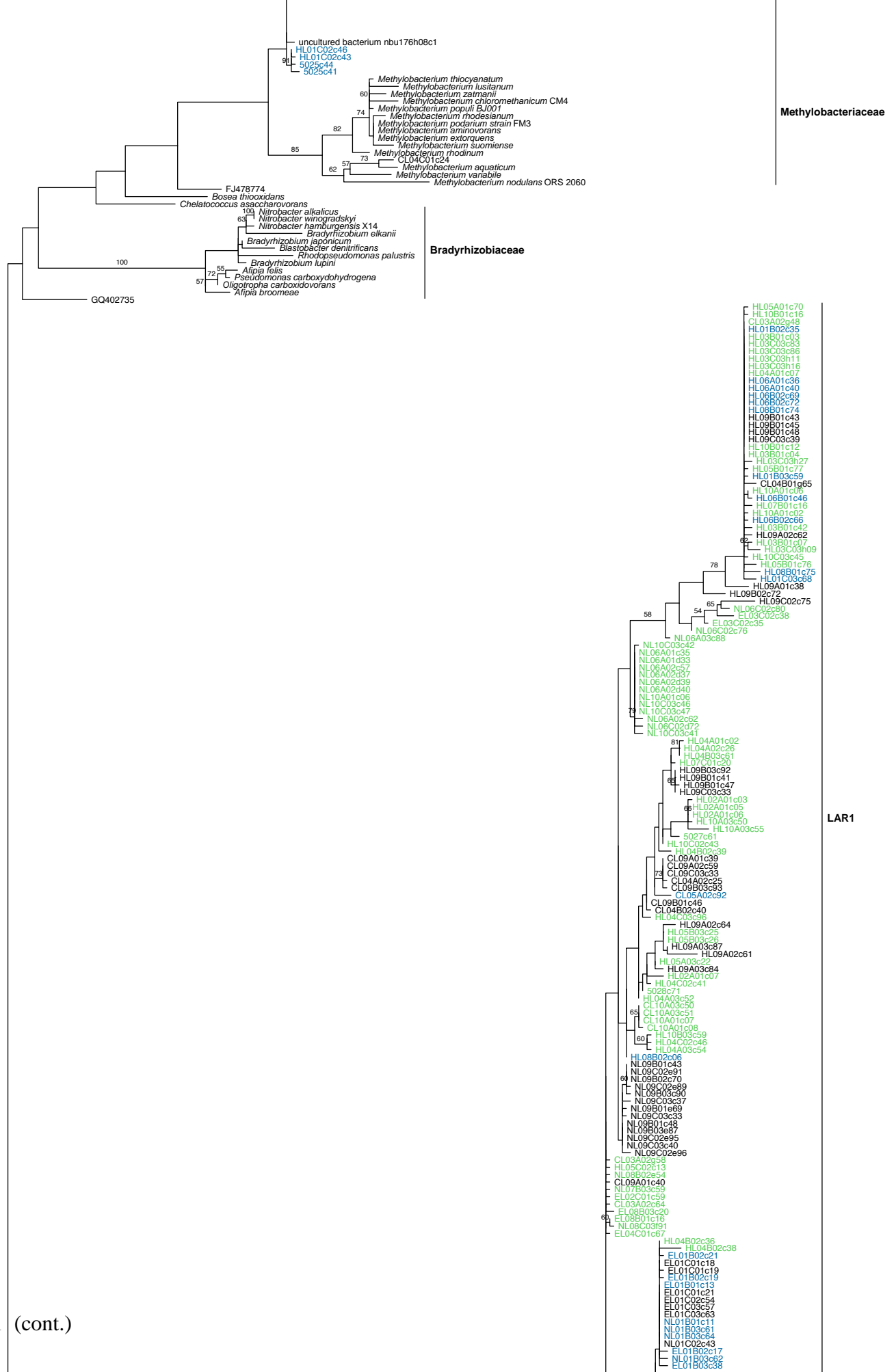


Fig. S1 (cont.)

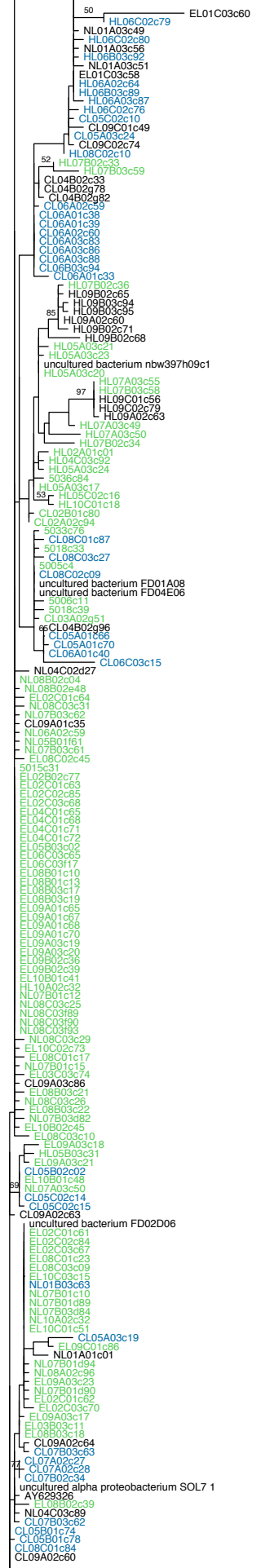
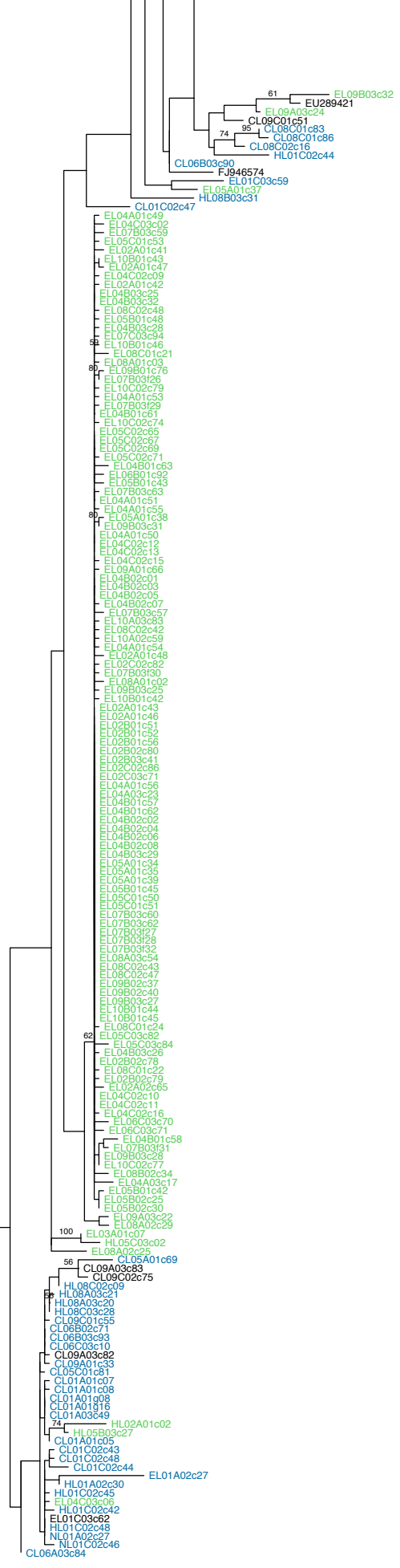


Fig. S1 (cont.)





LAR1

Fig. S1 (cont.)

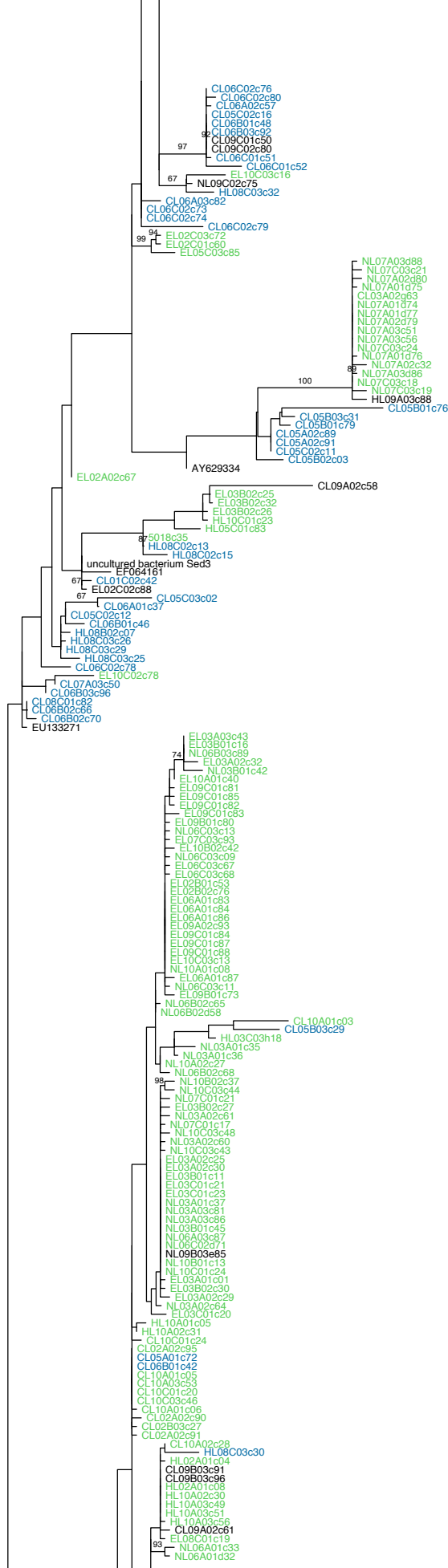
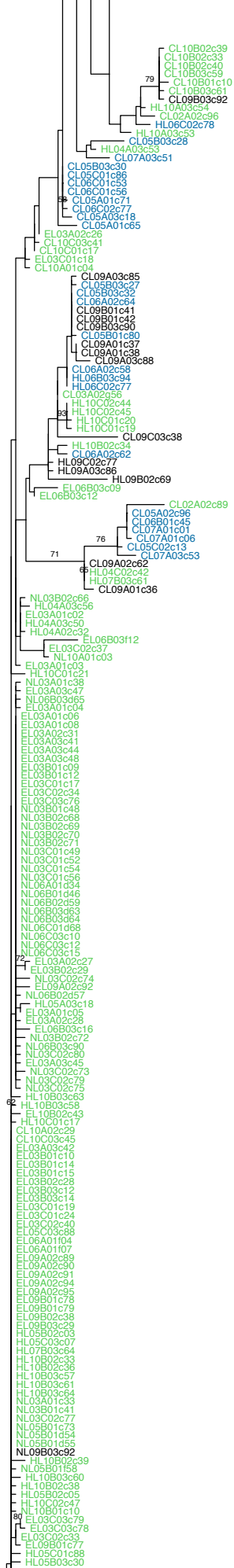


Fig. S1 (cont.)



LAR1

Fig. S1 (cont.)

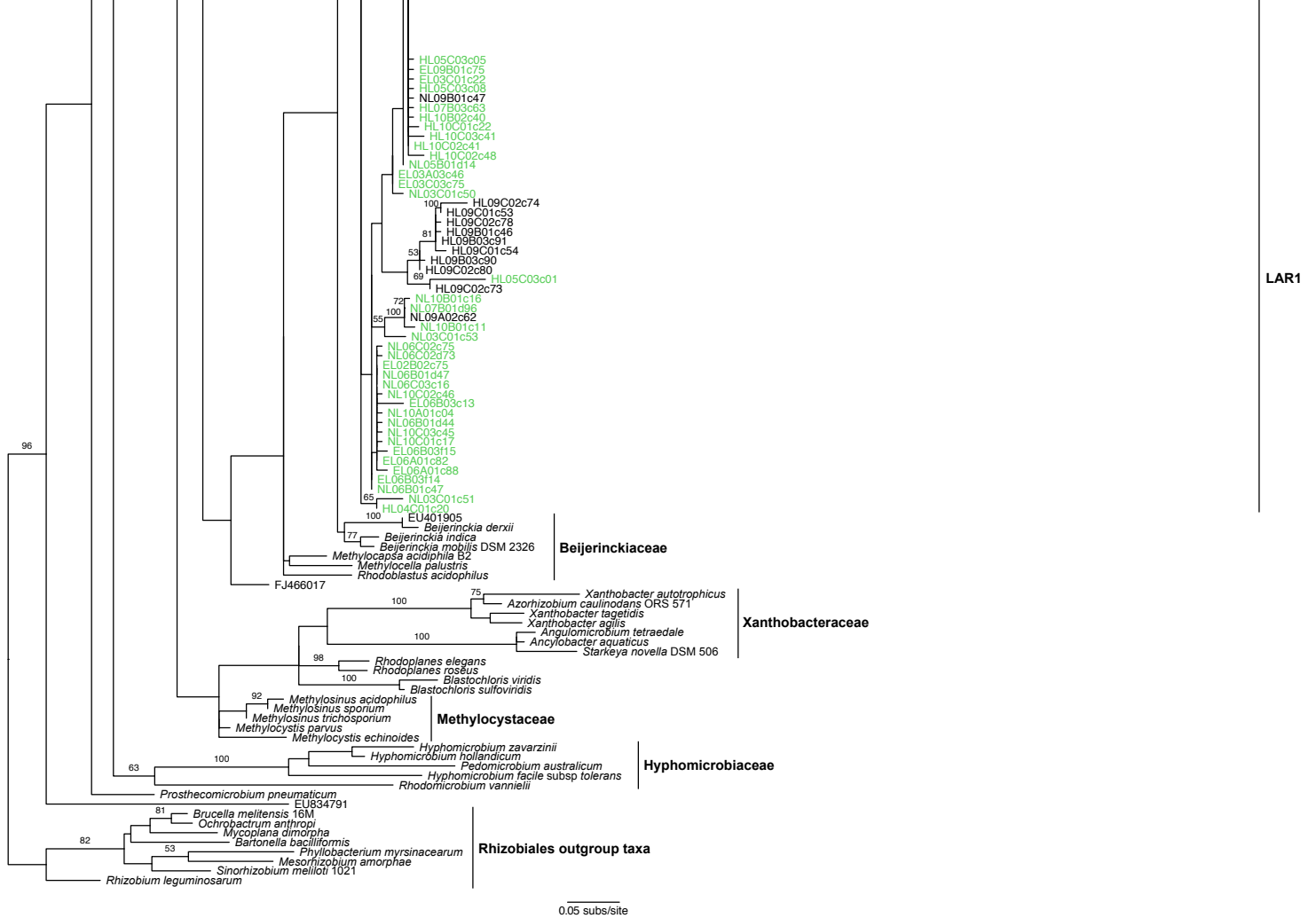


Fig. S1. Maximum likelihood (ML) phylogeny of cloned sequences generated as part of this study (10-digit alpha-numeric codes) with closest BLAST hits (8-digit accession numbers), sequences from cultured reference strains (organism names; GenInfo Identifiers are listed by Hodkinson & Lutzoni [2009]), and lichen-associated cloned sequences generated by Hodkinson & Lutzoni (2009; 6- or 7-digit alpha-numeric codes). Numbers above branches represent ML bootstrap proportions (BP) >50%. Identical sequences that were removed pre-analysis were re-inserted using a script described in the supplementary documentation. Sequence identifiers in light green are derived from chlorolichens, while those in dark blue are derived from cyanolichens (identifiers for those derived from tripartite lichens remain in black text). The 10-digit alpha-numeric codes used to identify sequences generated as part of this study encode detailed information about the origin of each sequence; this information is conveyed in the following order: site identifier (C [Cerro de la Muerte, Costa Rica], E [Eagle Summit, Alaska], H [Highlands, North Carolina], or N [Nome, Alaska]), sample type (L [lichen]), two-digit site-specific mycobiont-type identifier (01-10; see Table 2 for mycobiont-types correlated with each of the numbers at each site), cluster within the site (A, B, or C), two-digit sample-specific subsample number (01-03), and a subsample-specific 3-digit alpha-numeric clone identifier (e.g., c35). The LAR1 lineage accounts for 87% (1034/1190) of all cloned sequences generated as part of this study, while sequences from bacteria scattered throughout the genus *Methylobacterium* account for the other 13% (156/1190).