











Supplementary File S1

PhyML trees of HPV-16 genomic regions

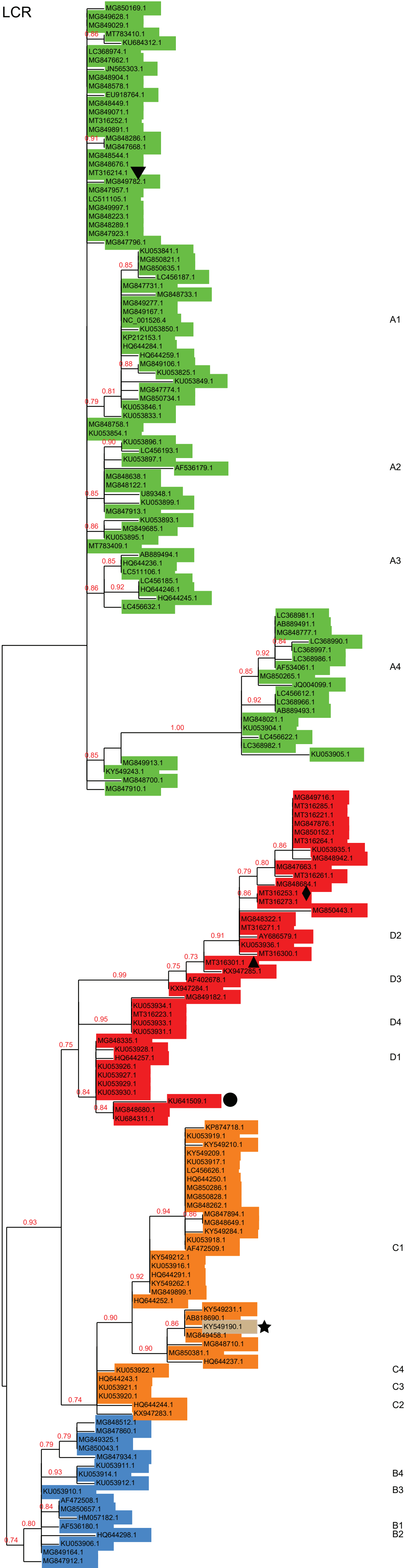
PhyML trees were computed with GTR+I+G model, aLRT, SPR on nucleotide alignments

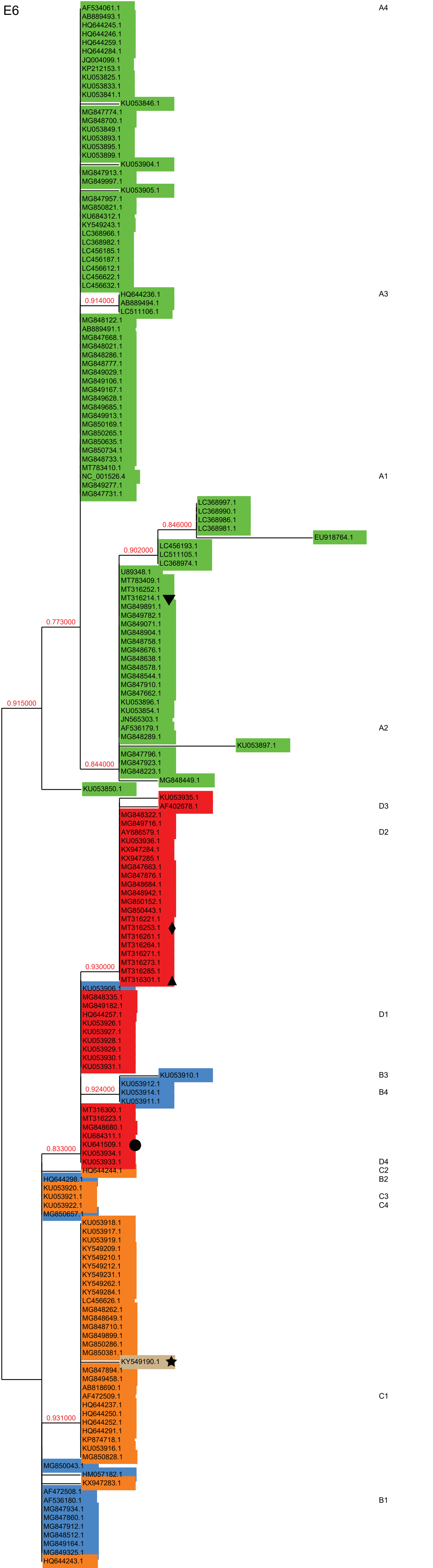
Lineage color code:

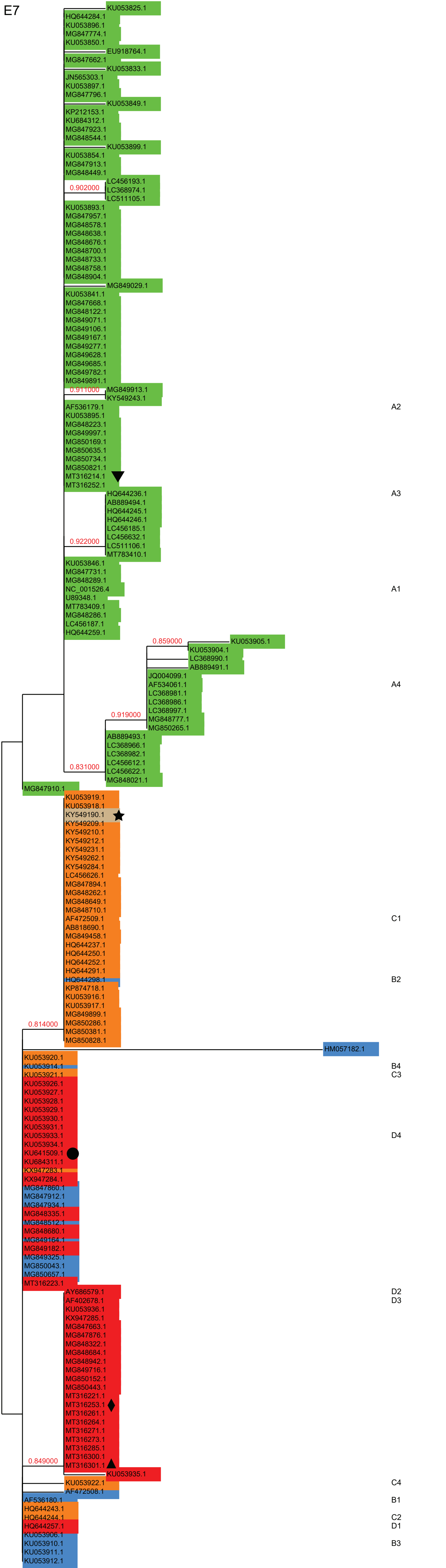
-  Group A (European lineage A)
-  Group B (African lineage 1 B)
-  Group C (African lineage 2 C)
-  Group D (American lineage D)
-  Ungrouped

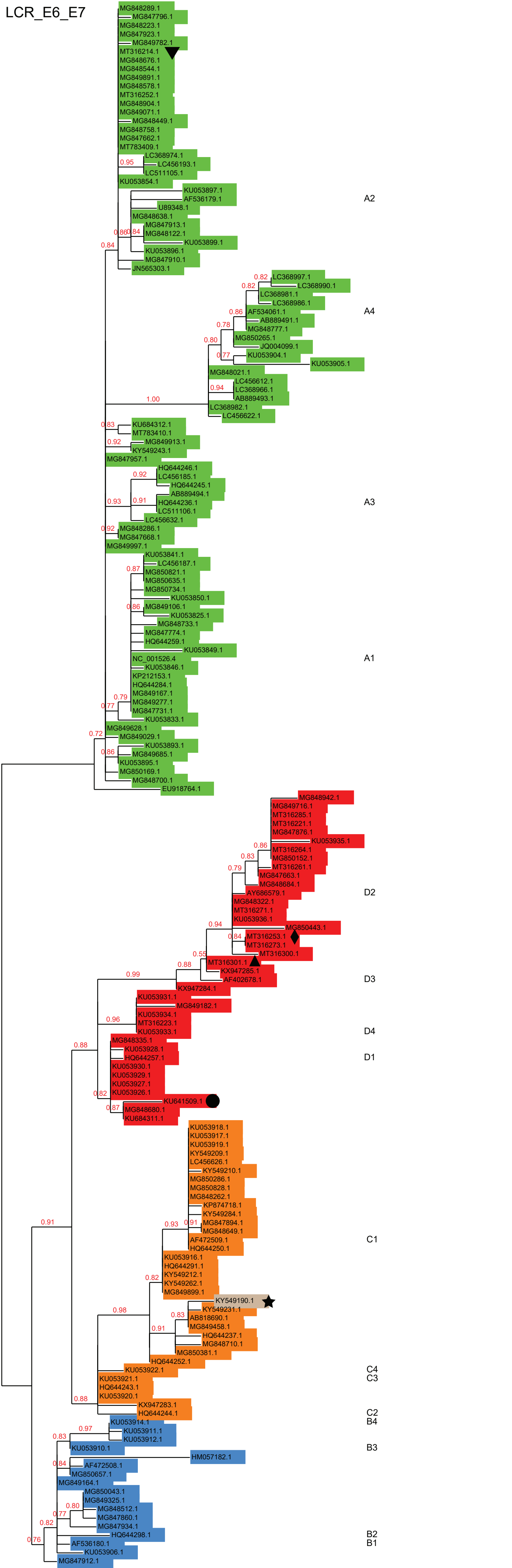
Recombinants	Inferred breakpoints
 MT316214	967-3203
 KU641509	2191-2469
 MT316301	2759-3815
 MT316253	3027-3604
 KY549190	2501-4871;5170-6218

LCR

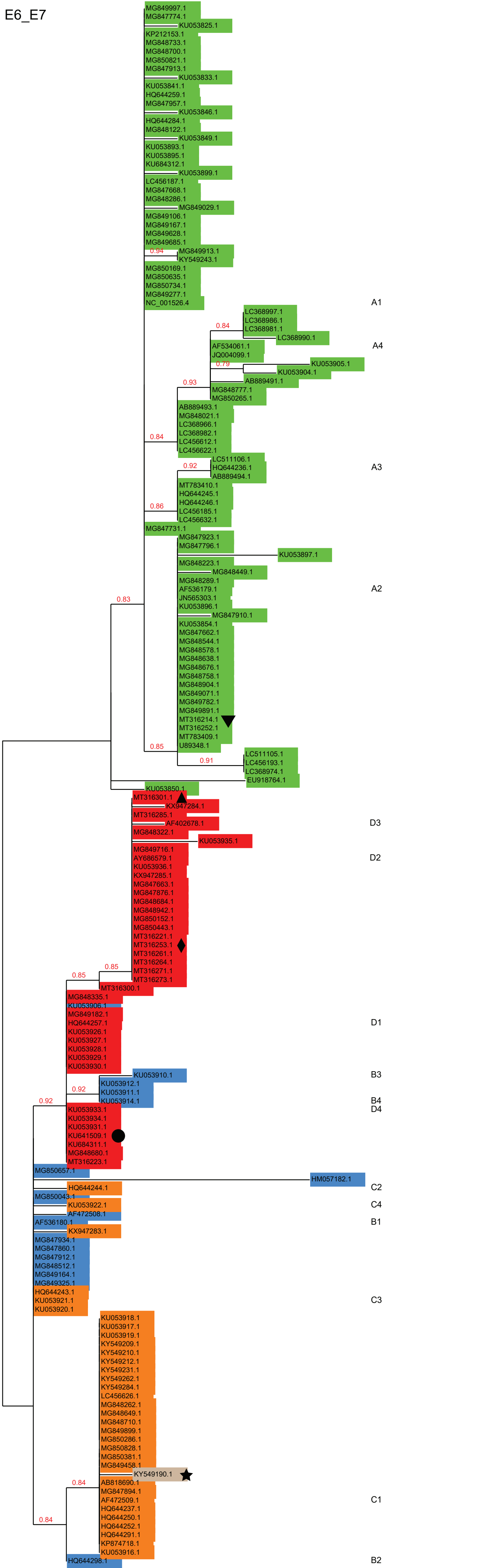


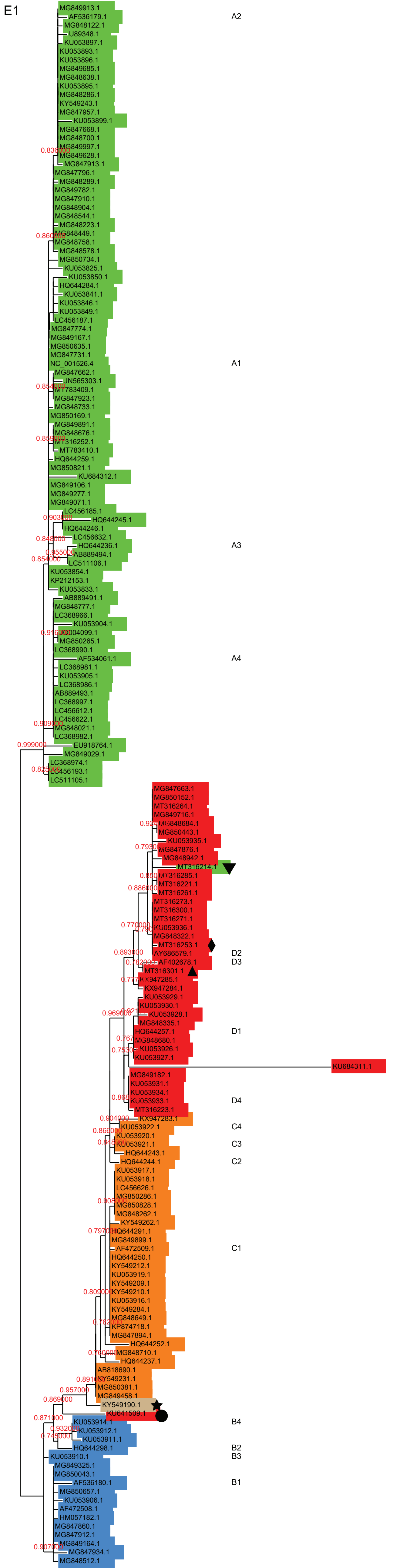


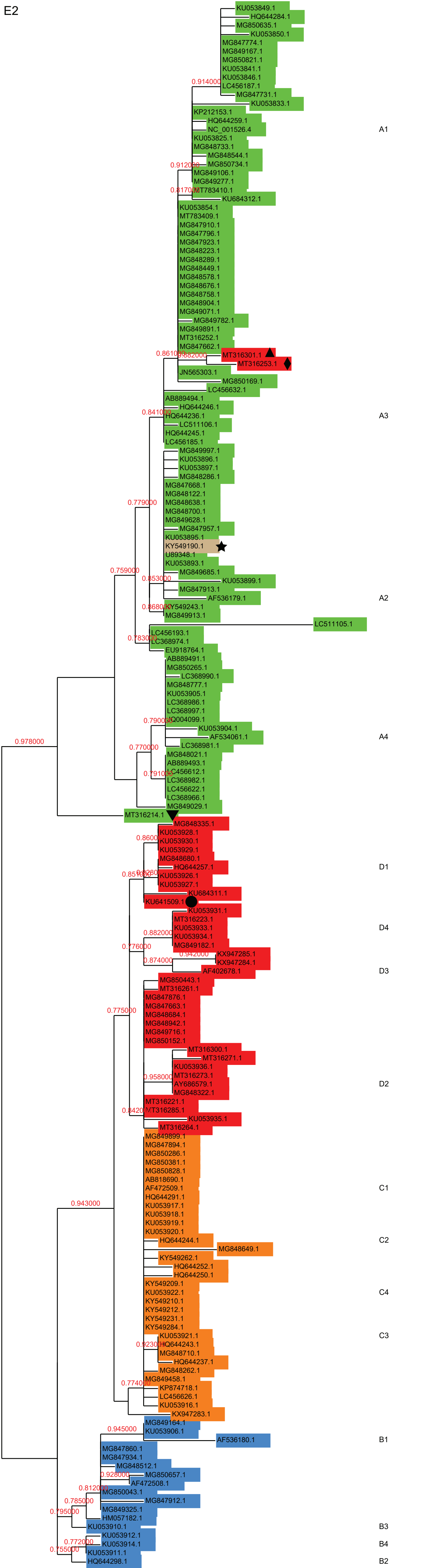


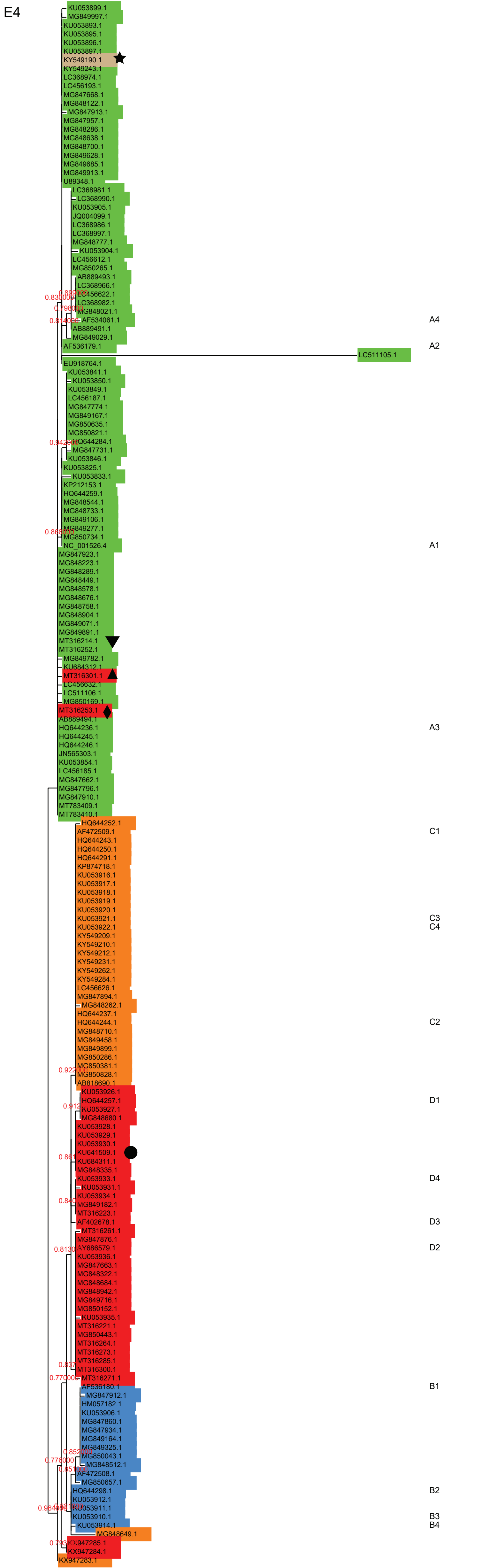


E6 E7





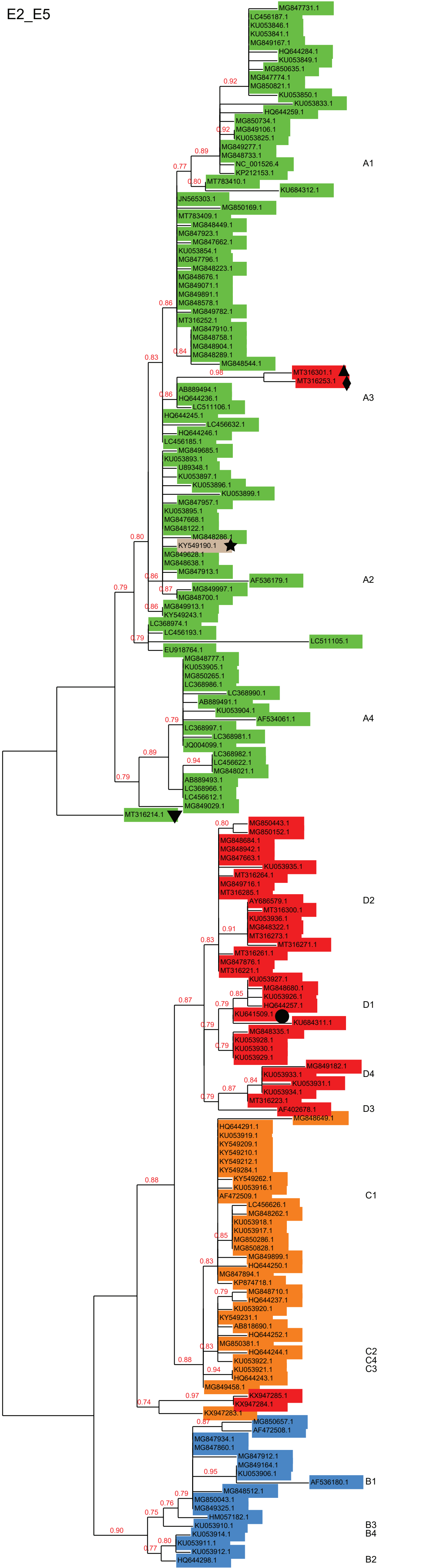




E5



E2_E5



L2

