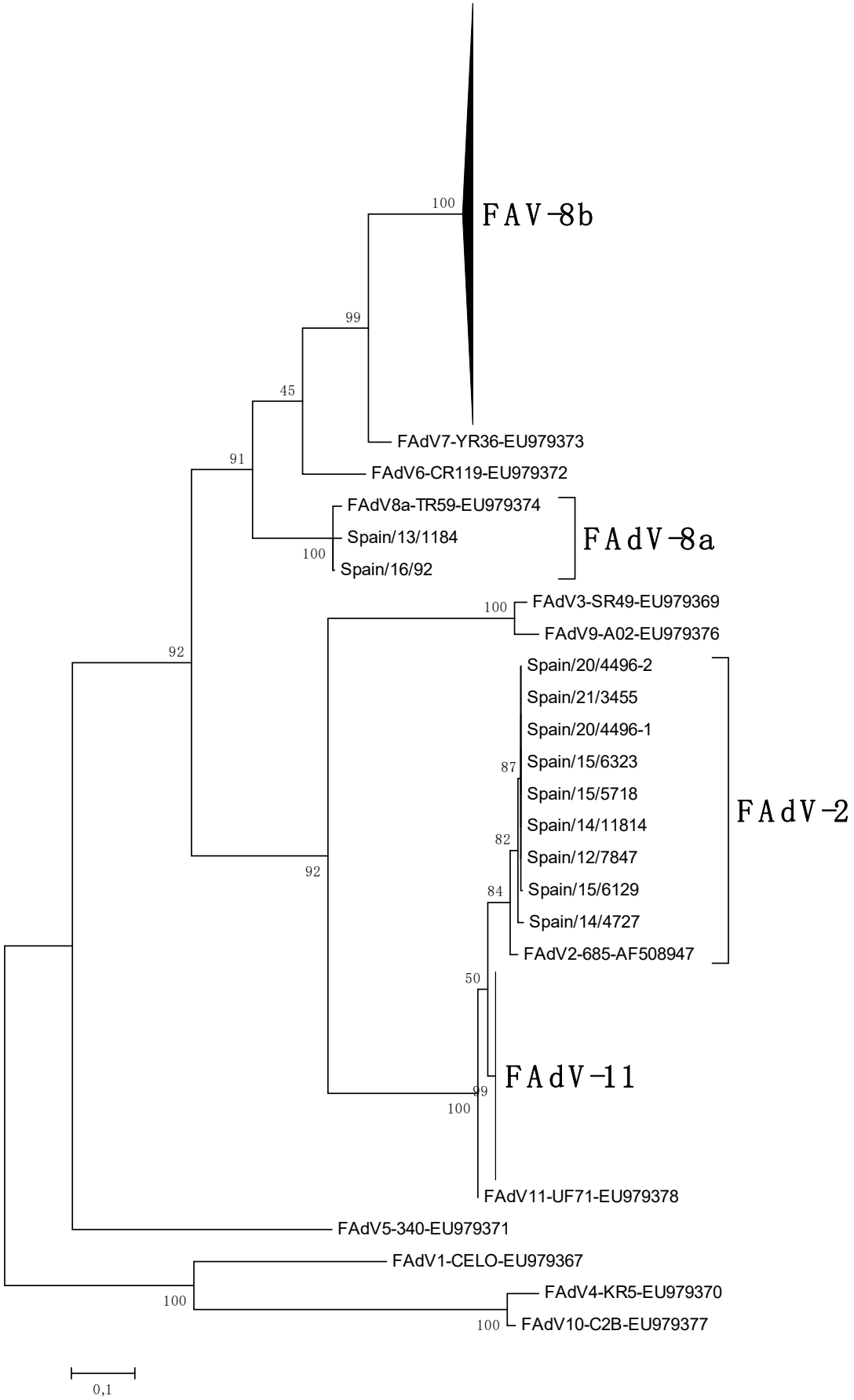
FAV-8b
100
99
45
91
FAdV7-YR36-EU979373
FAdV6-CR119-EU979372
FAdV8a-TR59-EU979374
Spain/13/1184
Spain/16/92
100
FAdV-8a
100
FAdV3-SR49-EU979369
FAdV9-A02-EU979376
92
Spain/20/4496-2
Spain/21/3455
Spain/20/4496-1
Spain/15/6323
Spain/15/5718
Spain/14/11814
Spain/12/7847
Spain/15/6129
Spain/14/4727
FAdV2-685-AF508947
87
82
84
92
FAdV-2
50
FAdV-11
99
100
FAdV11-UF71-EU979378
FAdV5-340-EU979371
FAdV1-CELO-EU979367
FAdV4-KR5-EU979370
FAdV10-C2B-EU979377
100
100
0,1

Figure S1. Maximum-likelihood phylogenetic tree. Maximum-likelihood phylogenetic tree with 1000 bootstrap replicates showing the relationships among the nucleotide partial sequences of the FAdV hexon gene (final alignment length 470 bp). FAdV strains (n=246) detected from June 2011 to May 2021 from commercial meat-type chickens in Spain and main reference FAdV serotype strains (n=12) are compared. Horizontal branches indicate the sequence distance (number of nucleotide substitutions per site) and are drawn to scale.