1 Additional File 4

2

— LC088128 EU486959 FU486960 P[30] OFJ169856 P[35] P[38] LC088110 - KT873811 — K18/3811 NIE13_A_1038_pigeon_KX815053 NIE13_A_1023_pigeon_KX815055 NIE13_A_1026_pigeon_KX815055 NIE13_A_1022_pigeon_KX815050 NIE13_A_1025_pigeon_KX815050 NIE13_A_1020_chicken_KX815056 NIE13_A_1020_chicken_KX815056 NIE13 A 1072 pigeon KX815052 - AB009632 — KU372527 EU486962

NIE11.A. 441. chicken_KU372529

NIE13.A. 1008_guinea_fowl_KU372530

NIE13.A. 1107_chicken_KU372531

NIE13.A. 1009_guinea_fowl_KU372530

NIE13.A. 1091_guinea_fowl_KU372531

NIE13.A. 1091_guinea_fowl_KU372531

NIE13.A. 1094_guinea_fowl_KU372534

NIE13.A. 1149_guinea_fowl_KU372535

NIE11.A. 249_chicken_KU372540

NIE11.A. 249_chicken_KU372540

NIE11.A. 256_chicken_KU372541

NIE11.A. 256_chicken_KU372542

NIE11.A. 256_chicken_KU372542

NIE11.A. 256_chicken_KU372543

NIE11.A. 256_chicken_KU372543

NIE11.A. 256_chicken_KU372543 — EU486962 NIST1 A 251 _chicken_KU372547 , NIST1 A 242 _chicken_KU372551 , NIST1 A 252 _chicken_KU372551 , NIST1 A 254 _chicken_KU372549 , NIST1 A 255 _chicken_KU372554 , NIST1 A 256 _chicken_KU3725510 , NIST1 A 295 _chicken_KU372551 NIE11_A_299_chicken_KU372536 NIE11_A_298_chicken_KU372535 KM254181
NIE13_A_1145_guinea_fowl_KU372521
NIE13_A_1142_guinea_fowl_KU372512
NIE13_A_1143_guinea_fowl_KU372513
NIE13_A_1143_chicken_KU372526
NIE13_A_1138_chicken_KU372524
NIE13_A_1152_guinea_fowl_KU372520 NIELS A. 1152_guinea_fowl_KU372522
NIELS A. 1144_guinea_fowl_KU372523
NIELS A. 1104_guinea_fowl_KU372523
NIELS A. 1104_chicken_KU372515
NIELS A. 1106_chicken_KU372515
NIELS A. 1106_chicken_KU372516
NIELS A. 366_chicken_KU372516
NIELS A. 366_chicken_KU372516
NIELS A. 366_chicken_KU372517

- 4 Maximum clade credibility tree of partial VP4 gene sequences of Rotavirus group A
- 5 (RVA). Bayesian analyses of alignments (424 bp) comprising sequences of all available
- 6 VP4 sequences that are available in Genbank
- 7 (http://www.ncbi.nlm.nih.gov/Genbank/index.html), as well as all long sequences identified
- 8 in this study. Tree topology was tested by posterior probability (pp) and only the well
- 9 supported values are shown (pp>0.7). The RVA strains are represented by their GenBank
- accession numbers and study sequences are in red. Genotypes were assigned using the
- 11 nucleotide cut-off values defined before (1).

3

12 References

19

Matthijnssens J, Ciarlet M, McDonald SM, Attoui H, Banyai K, Brister JR,
 Buesa J, Esona MD, Estes MK, Gentsch JR, Iturriza-Gomara M, Johne R,
 Kirkwood CD, Martella V, Mertens PP, Nakagomi O, Parreno V, Rahman M,
 Ruggeri FM, Saif LJ, Santos N, Steyer A, Taniguchi K, Patton JT, Desselberger
 U, Van Ranst M. 2011. Uniformity of rotavirus strain nomenclature proposed by the
 Rotavirus Classification Working Group (RCWG). Arch Virol 156:1397-1413.