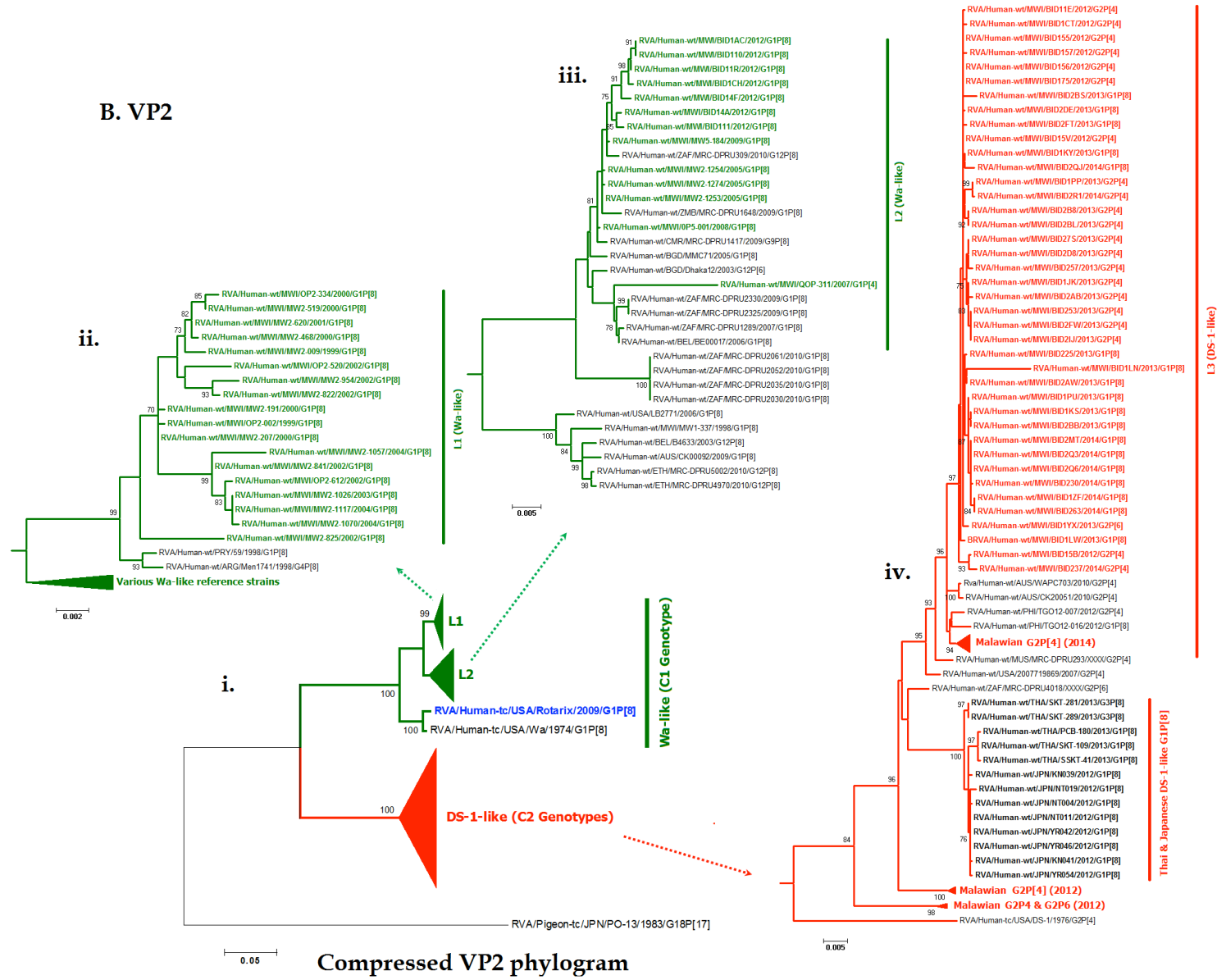


C.

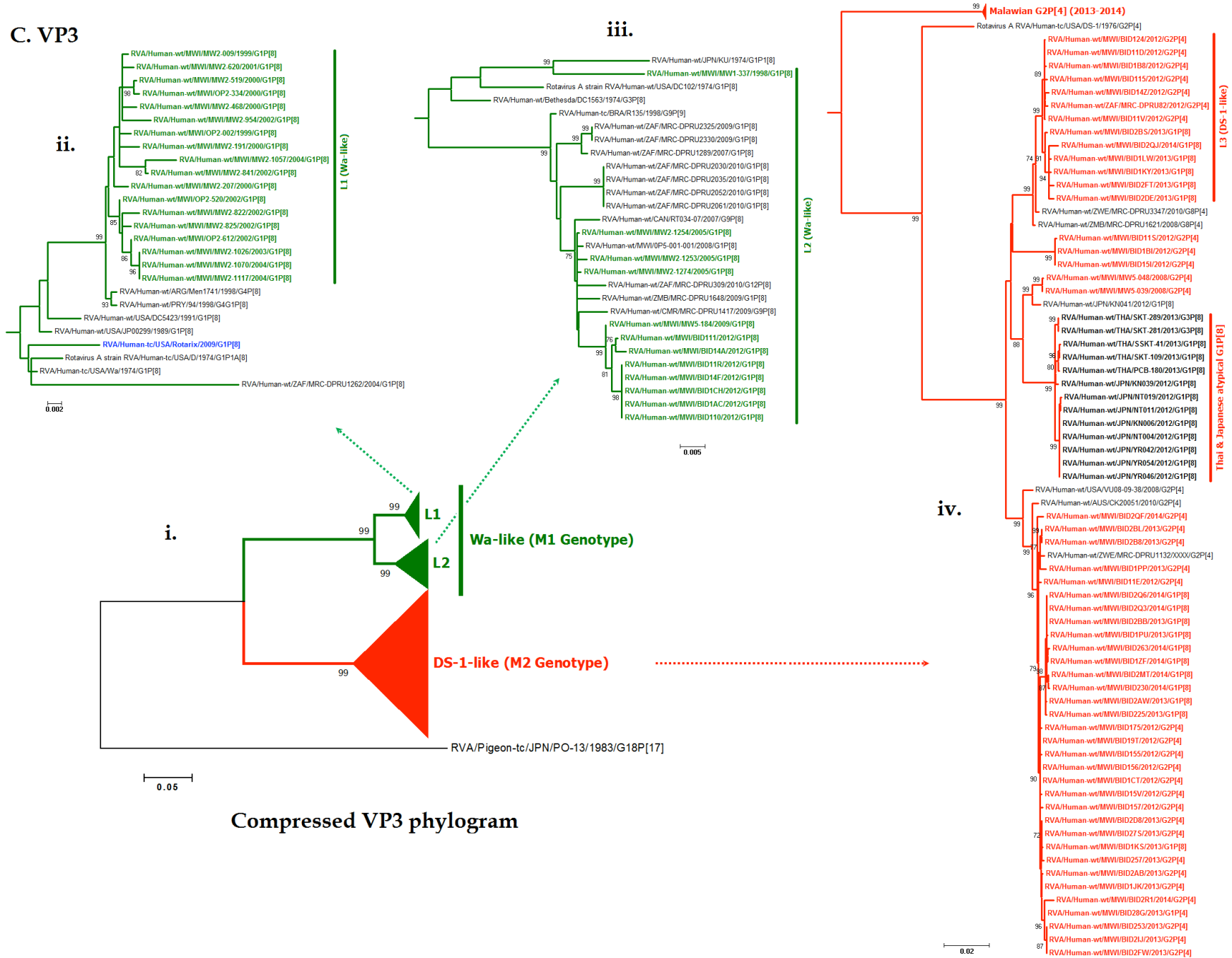
YEAR	G12P4	G12P6	G12P8	G1P4	G1P6	G1P8	G2P4	G2P6	G2P8	G3P4	G3P6	G3P8	G4P6	G4P8	G8P4	G8P6	G8P8	G9P4	G9P6	G9P8	TOTAL	TOTAL
1997	0	0	0	0	0	0	0	0	0	1	10	28	1	4	8	43	0	0	3	0	98	98
1998	0	0	0	0	0	55	0	0	0	0	2	61	2	14	22	47	0	0	0	0	203	203
1999	0	0	0	0	7	94	0	0	0	0	0	4	1	3	1	39	0	0	0	0	149	149
2000	0	0	0	0	2	78	0	0	0	0	0	0	0	0	1	36	0	0	0	0	117	117
2001	0	0	0	1	1	25	0	0	0	0	0	0	0	0	29	3	1	0	17	0	77	77
2002	0	0	0	0	3	26	0	0	0	0	0	0	0	0	3	0	0	0	11	0	43	43
2003	0	0	0	0	1	9	0	0	0	0	0	0	0	0	0	1	1	0	18	0	30	30
2004	0	0	0	0	6	54	0	0	0	0	0	0	0	0	0	1	4	0	19	3	87	87
2005	0	2	0	0	48	40	0	0	0	0	0	0	0	0	13	3	6	0	1	2	115	115
2006	0	3	0	0	26	41	0	0	0	0	0	0	0	0	2	2	13	0	0	2	89	89
2007	0	1	4	0	0	6	0	0	0	0	0	0	0	0	15	0	5	0	0	0	31	31
2008	0	27	4	0	2	31	16	3	1	0	0	0	0	0	0	1	1	0	1	6	93	93
2009	0	24	1	1	2	56	5	3	0	0	0	0	0	0	14	0	0	0	0	9	115	115
2010	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0	0
2012	1	22	9	1	1	39	56	28	2	0	0	0	0	0	0	0	0	0	0	0	159	159
2013	0	21	14	1	4	60	35	19	1	0	0	0	0	0	0	0	0	1	0	0	156	156
2014	1	17	0	2	4	20	39	3	1	0	0	0	0	0	0	0	0	0	1	0	88	88
2015	0	18	0	1	20	15	2	3	0	0	0	0	0	0	0	0	0	0	0	0	59	59

Fig. S1. G1P[8] rotavirus strains characterised from stool samples collected from Malawian infants at QECH from 1997 – 2015. (A) Proportion of rotavirus-positive samples detected in each year. (B) Proportion of G1P[8] strains detected from rotavirus-positive samples. (C) Absolute numbers of rotavirus strains characterised from 1997 – 2015.

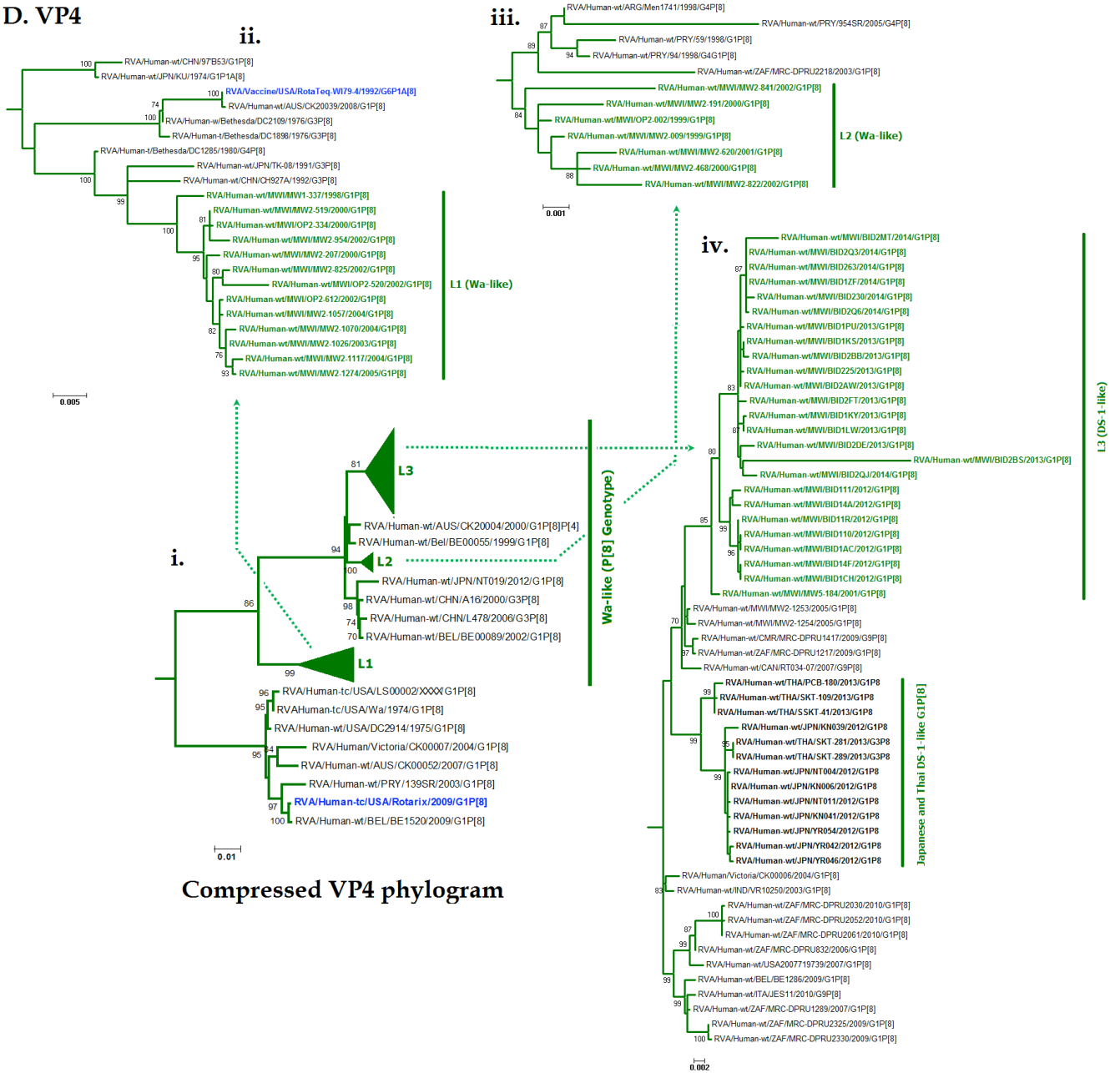
B. VP2



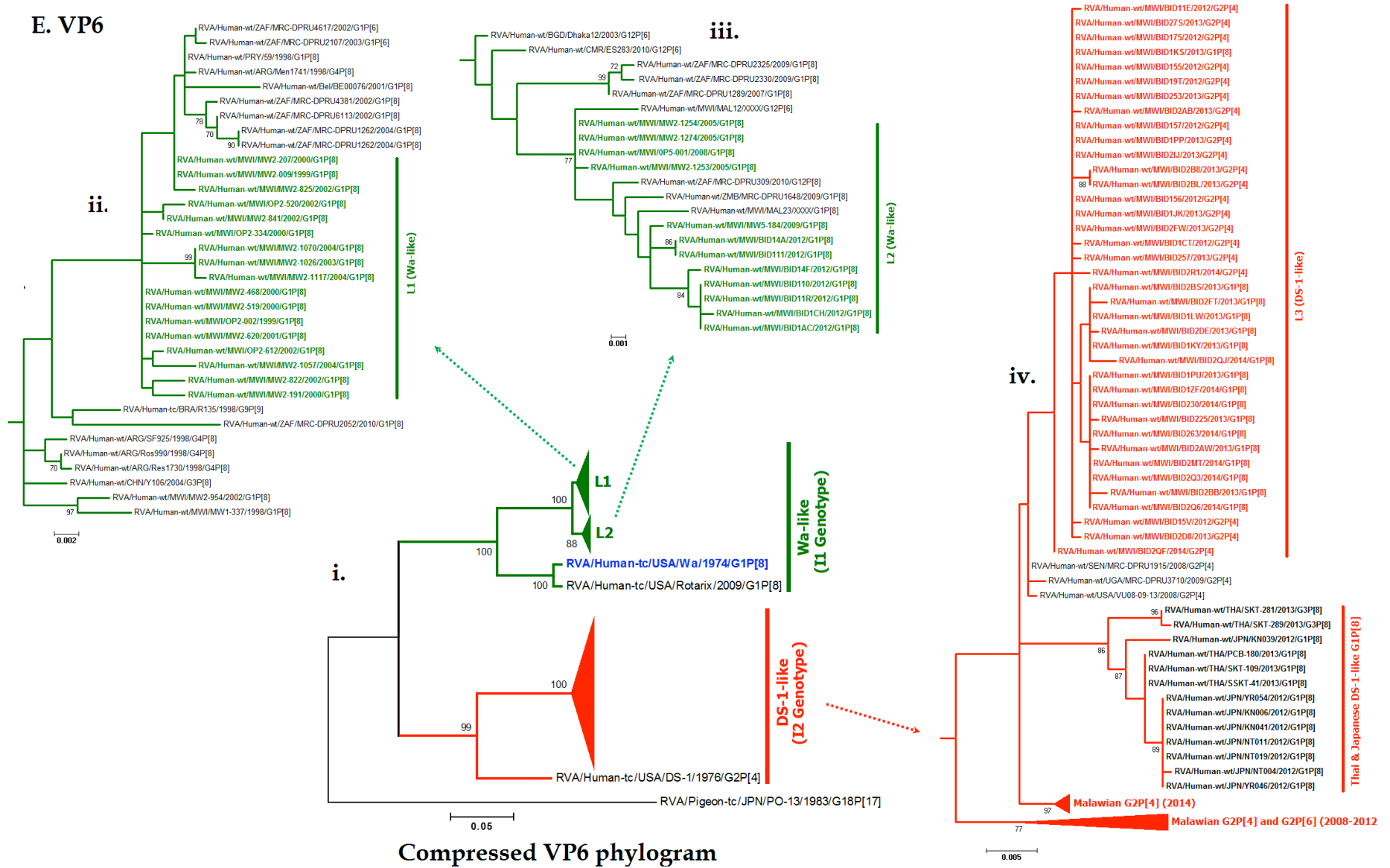
C. VP3



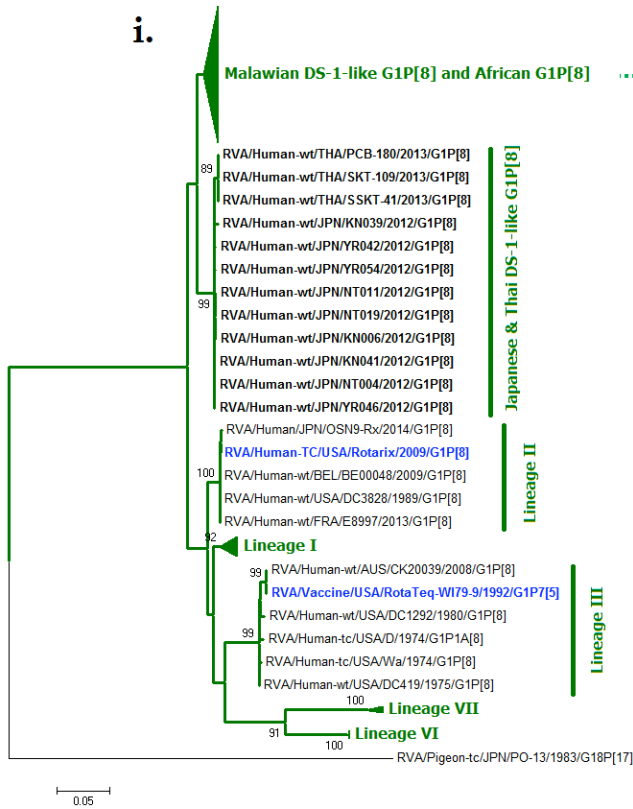
D. VP4



E. VP6



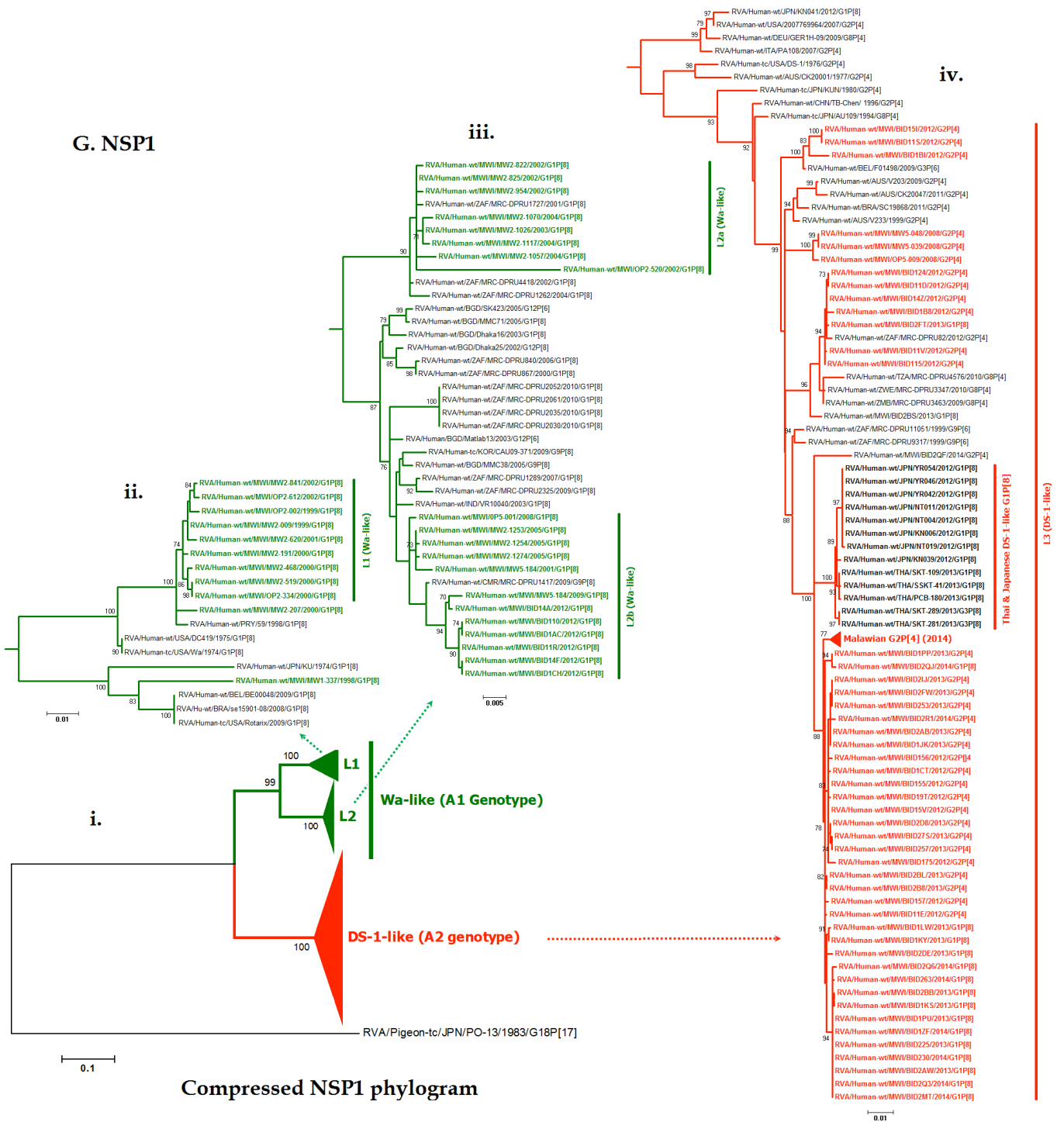
F. VP7



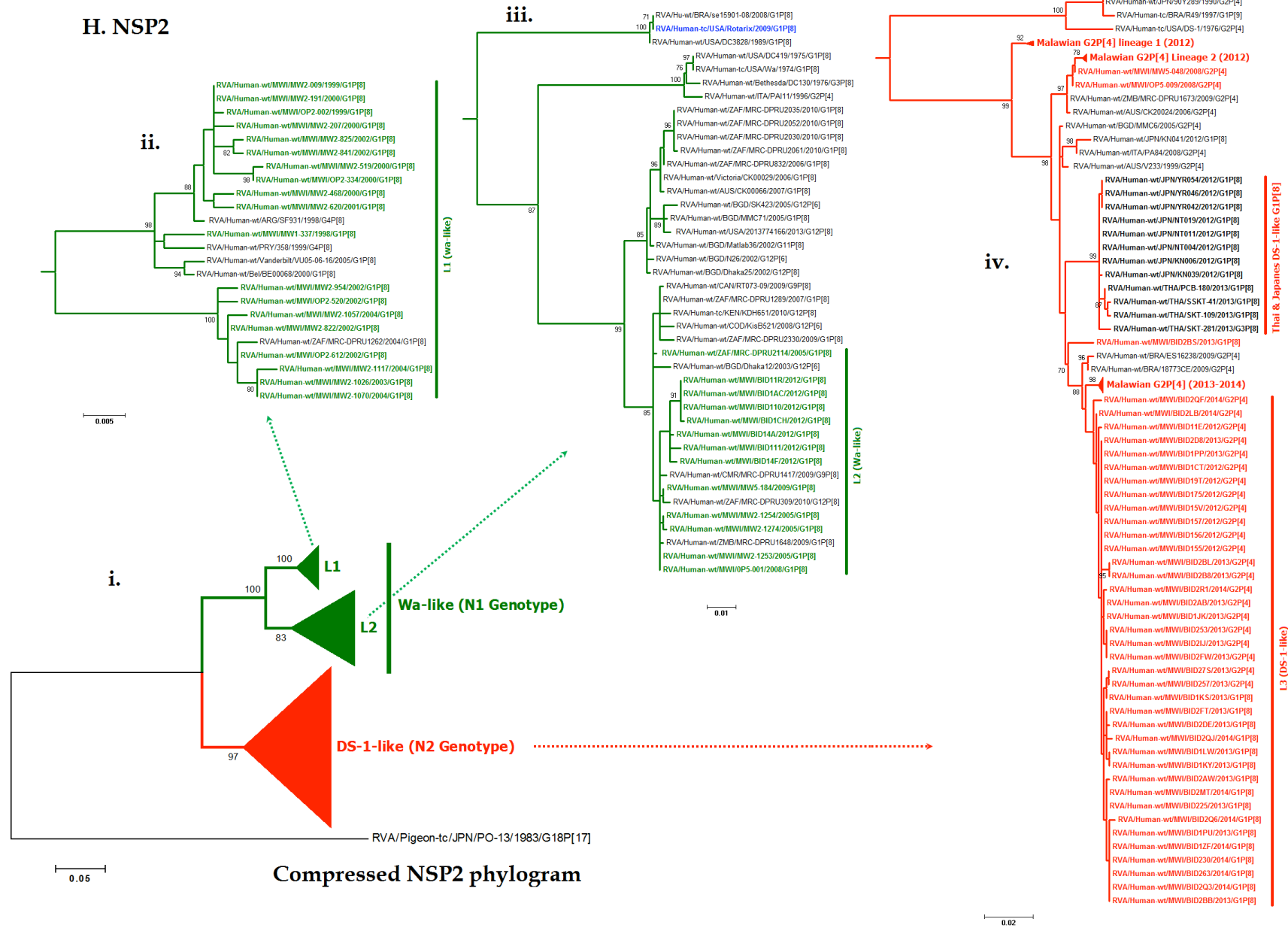
Compressed VP7 phylogram

ii.





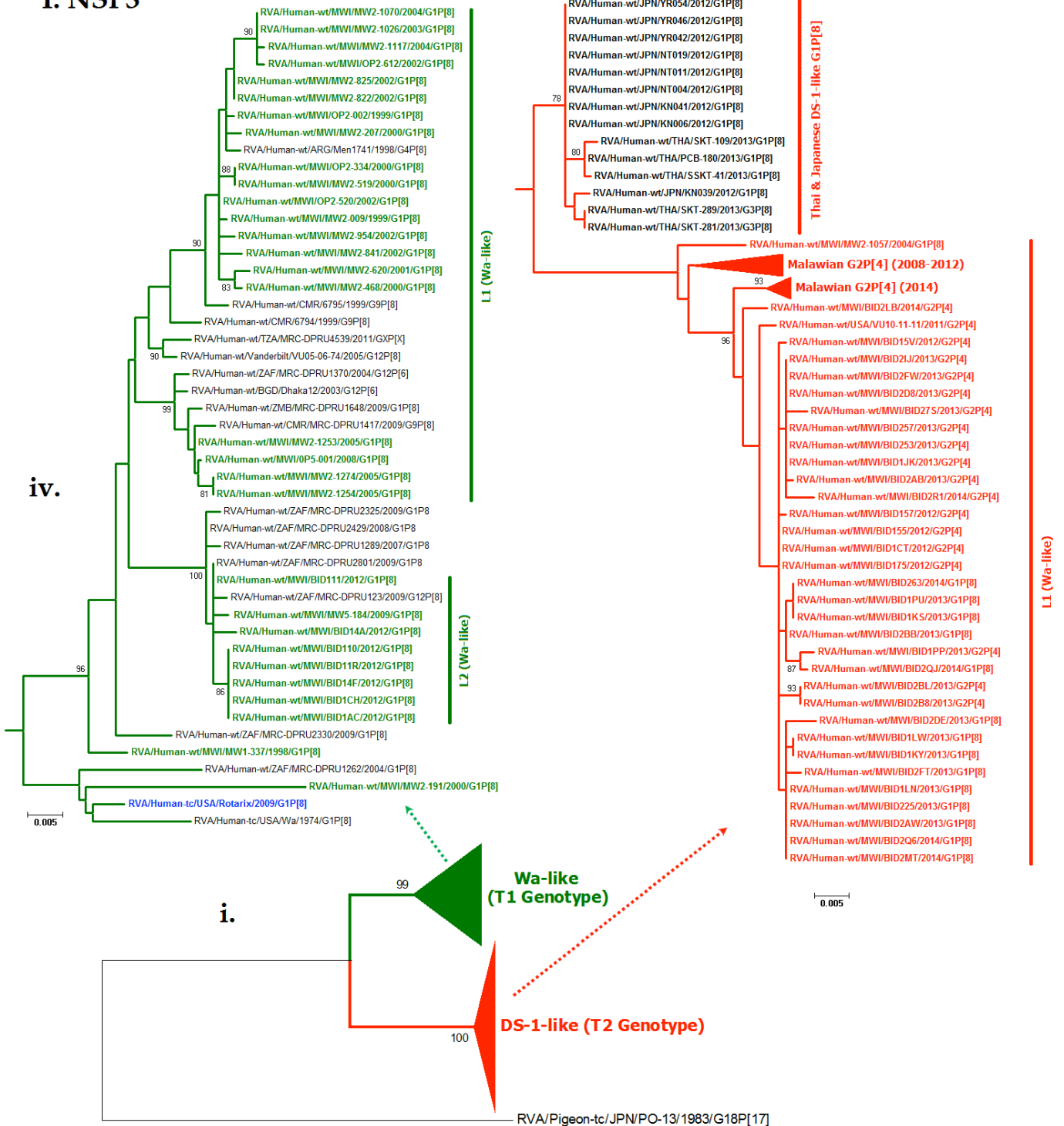
H. NSP2



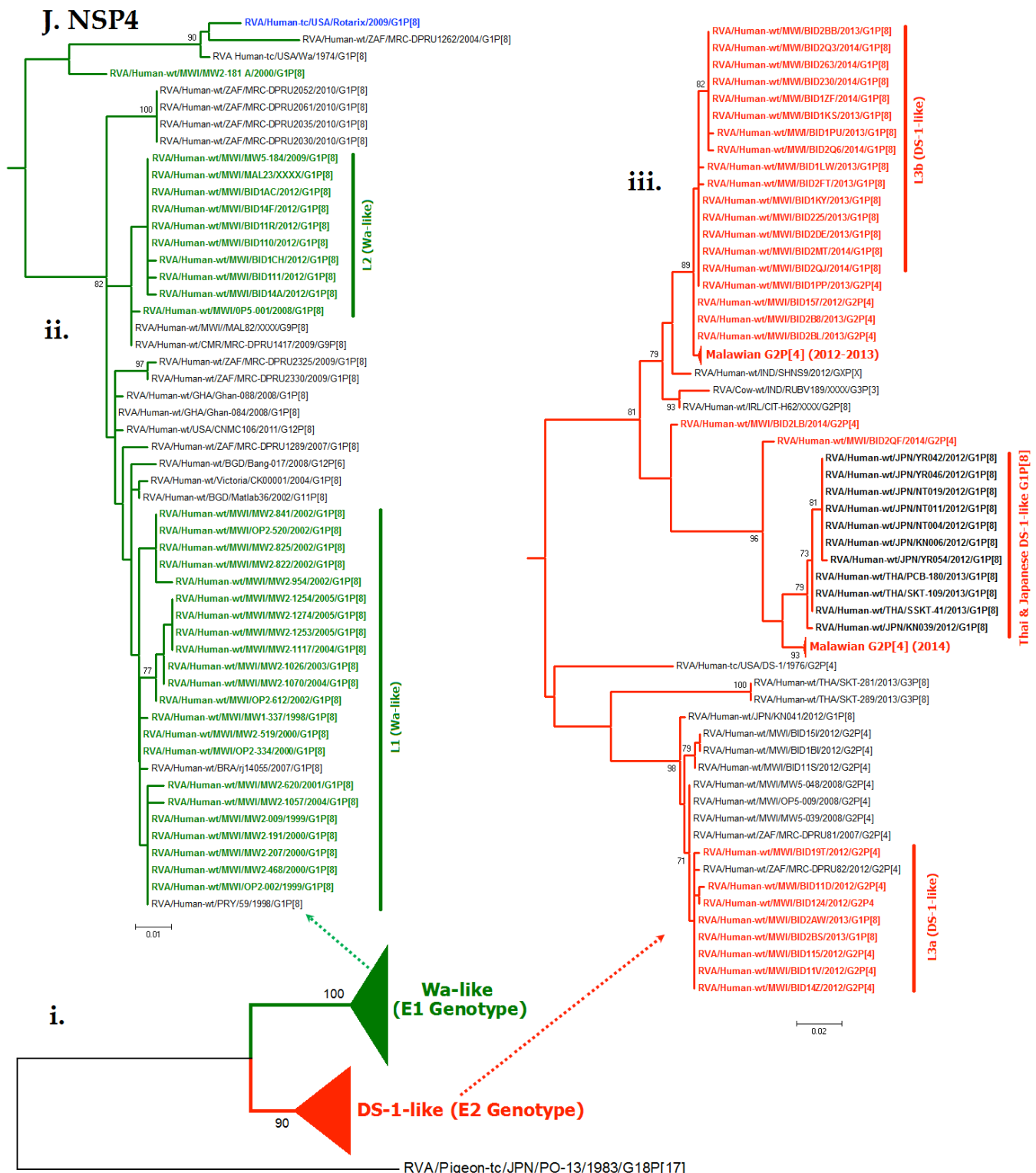
I. NSP3

ii.

iii.



Compressed NSP3 phylogram



Compressed NSP4 phylogram

K. NSP5

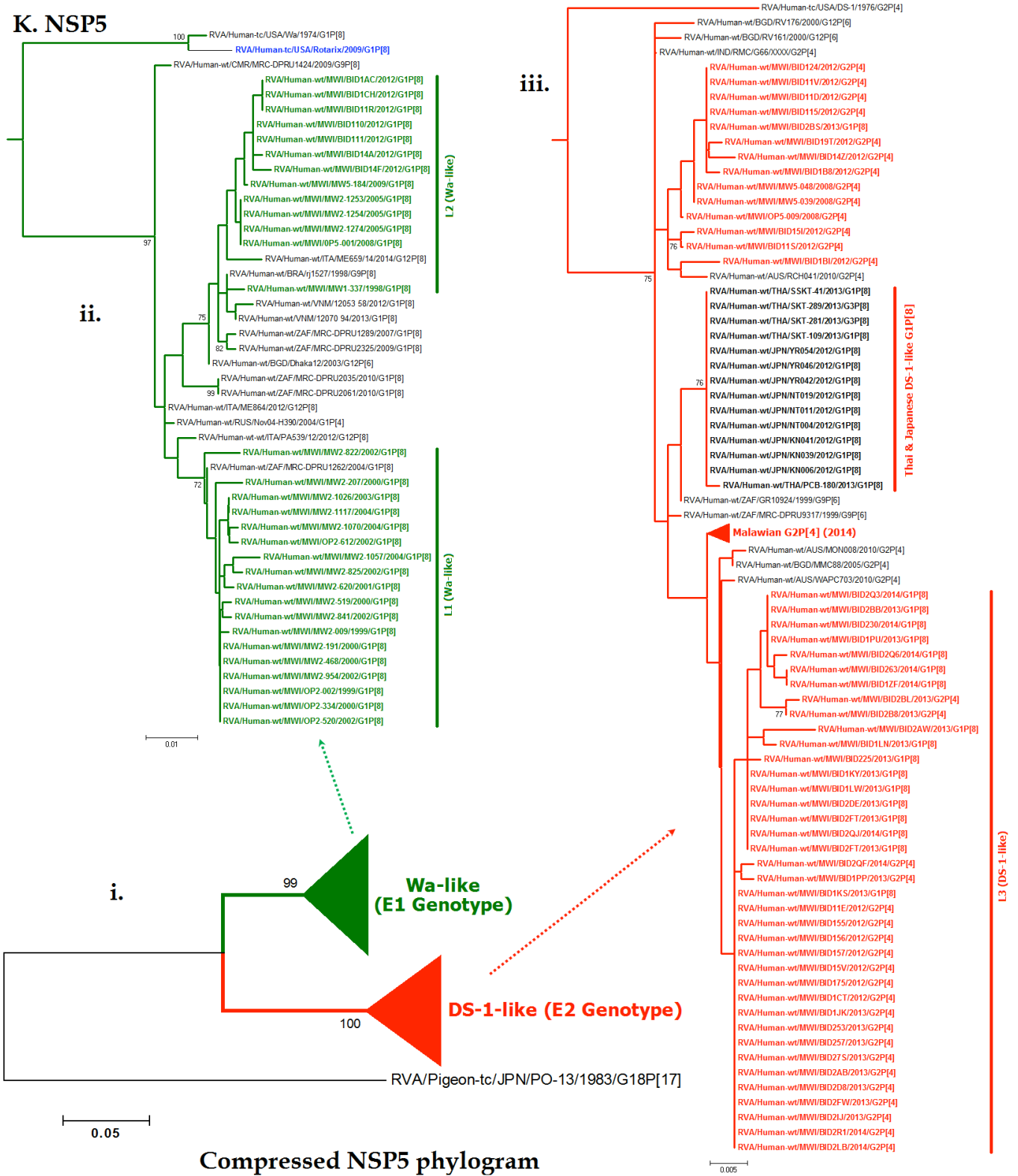


Fig. S2. Phylogenetic analysis of complete ORFs for individual 11 genome segments of Malawian G1P[8] strains compared to reference strains from elsewhere using Maximum-Likelihood method. Tree with the highest log likelihood are shown. The percentage of trees in which the associated taxa clustered together is shown next to the branches. Initial tree(s) for the heuristic search were obtained automatically by applying Neighbor-Joining and BioNJ algorithms to a matrix of pairwise distances estimated using the Maximum Composite Likelihood (MCL) approach, and then selecting the topology with superior log likelihood value. **(A – F)** Phylogenetic trees for genome segments 1 – 4, 6 and 9 that encodes rotavirus structural proteins (VP1 – VP4, VP6 and VP7), respectively. **(H–K)** Phylogenetic trees for genome segments 5, 8, 7, 10 and 11 that encodes rotavirus non-structural proteins (NSP1 – NSP5), respectively. All rotavirus strains are named according to the *Rotavirus Classification Working Group* (RCWG) guidelines where the nomenclature indicates the rotavirus group, host species, name of the country where the strain was originally isolated, the common name, year of isolation and the genotypes for genome segments encoding VP7 and VP4 (Matthijssens et al., 2011), respectively. Taxa for study strains are highlighted in Green and red, and branches for Wa- and DS-1-like strains are shown in green and red, respectively. Taxa for vaccine strains is highlighted in blue whereas atypical G1P[8] strains from Asia are in bold. The horizontal branch lengths are proportional to the genetic distance calculated by the Maximum-likelihood method. The numbers adjacent to the node represents the bootstrap value of 1,000 replicates, and values less than 70% are not shown. The scale bar shows the genetic distance expressed as nucleotide substitution per rate of the nucleotide sequences.

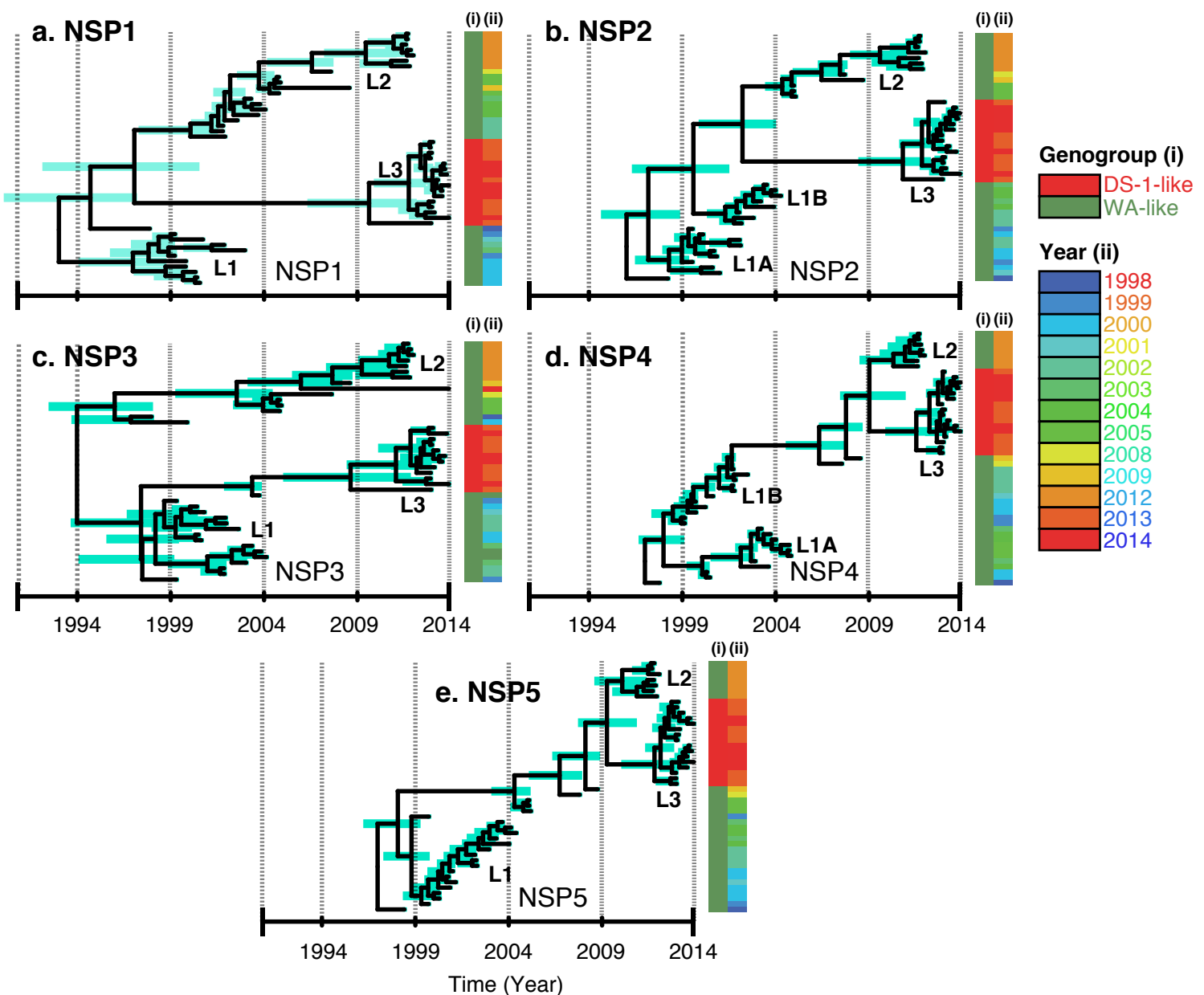
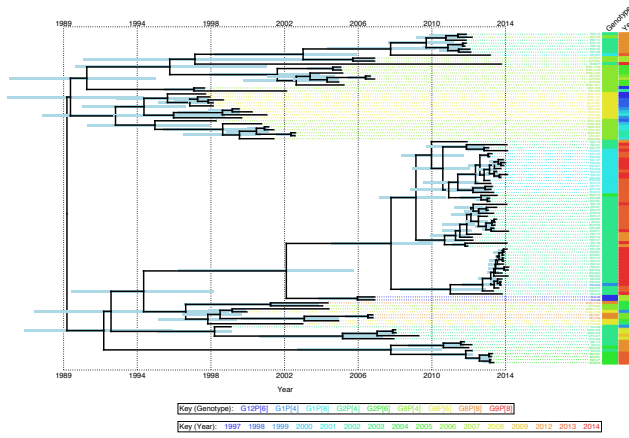
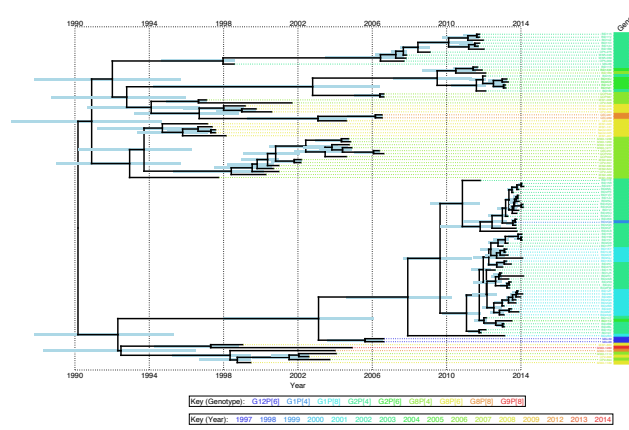


Fig. S3. Bayesian Maximum Clade Credibility (MCC) time tree based on complete nucleotide sequences illustrating lineage replacement within the genome segments encoding non-structural proteins of the G1P[8] strains that circulated in Malawi from 1998 – 2014. With the exception of NSP4 genes that had L1 sub-lineages, the rest had three main G1P[8] lineages. L1, L2 and L3 represents lineage 1, 2 and 3, respectively.

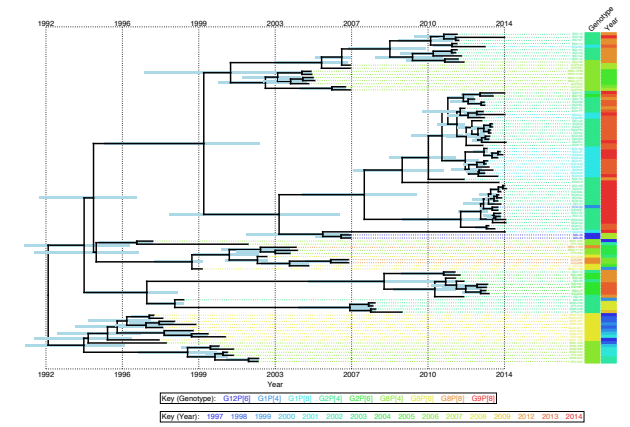
A. NSP1



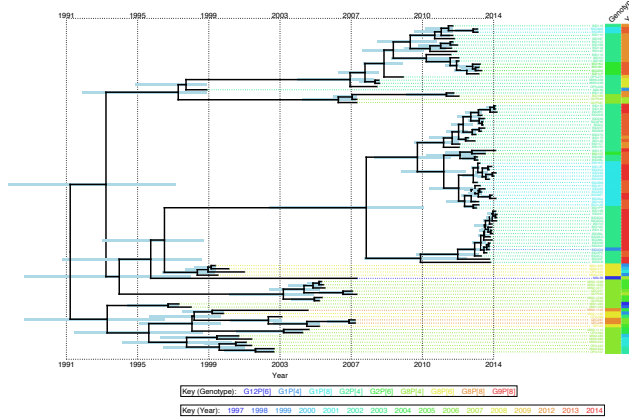
B. NSP2



C. NSP3



D. NSP4



D. NSP5

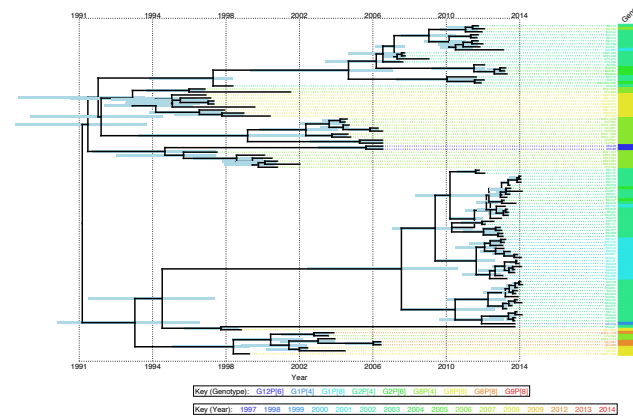


Fig. S4. Bayesian Maximum Clade Credibility (MCC) time tree based on complete nucleotide sequences of nonstructural proteins for G1P[8] strains from Malawi. Only DS-1-like genome segments for typical DS-1-like strains that were assigned G2P[4], G2P[6], G8P[4], G8P[6] and G12P[6] outer capsid genotypes from Malawi were included to calculate evolutionary dynamics for for genes encoding non-structural proteins (NSP1 – NSP5). The summary for their evolutionary rates and tMRCAs are presented in Table 2.