Table S1. List of ZIKV Genbank accession numbers of sequences used in phylogenetic analysis.

Name	Genbank Accession #	Name	Genbank Accession #
Brazil/2015	KU321639	Honduras/2015	KX694534
Brazil/2015	KU527068	Honduras/2016	KX262887
Brazil/2015	KX280026	Malaysia/1966	KX377336
Brazil/2015	KX520666	Martinique/2015	KU647676
Brazil/2016	KU926310	Mexico/2015	KX247632
Brazil/2016	KU926309	Mexico/2016	KX446951
Cambodia/2010	KU955593	Micronesia/2007	EU545988
Canada/2013	KF993678	Nigeria/1968	KU963574
Central African Republic/1968	KF383115	Panama/2015	KX156775
Central African Republic/1976	KF268948	Panama/2015	KX198135
Central African Republic/1979	KF268950	Phillippines/2012	KU681082
Central African Republic/1980	KF268949	Puerto Rico/2015	KX377337
China/2016	KU761564	Samoa/2016	KX185891
Columbia/2015	KX548902	Senegal/1968	KF383116
Columbia/2016	KX247646	Senegal/1984	HQ234501
Dominican Republic/2016	KU853012	Senegal/1997	KF383117
Ecuador/2016	KX879603	Senegal/2001	KF383119
French Guiana/2015	KU758877	Singapore/2016	KX813683
French Polynesia/2013	KJ776791	Suriname/2015	KU312312
French Polynesia/2014	KX447511	Suriname/2016	KU937936
Guadeloupe/2016	KX673530	Thailand/2014	KU680181
Guatemala/2015	KU501217	Tonga/2016	KX806557
Guatemala/2016	KU870645	Uganda/1947	KU955594
Haiti/2014	KU509998	USA/2016	KX842449
Haiti/2016	KX051563	Venezuela/2016	KX702400

Table S2. Source host, isolation and passage history of ZIKV strains used in this study

Lineage	Strain	Source Host	Year	Location	Passage History	Genbank Accession
African	MR 766	Rhesus monkey	1947	Uganda	146x SM[a], 1x C6/36[b], 1x Vero[c]	HQ234498.1
Asian	PLCal_ZV	Human	2013	Canada/ Thailand	4x Vero	KF993678
Asian	PRVABC59	Human	2015	Puerto Rico	3x Vero	KU501215.1
Asian	HS-2015-BA-01	Human	2015	Brazil	3x C6/36, 1x Vero	KX520666

[a]SM = suckling mouse;
[b]C6/36 = *Aedes albopictus* cells;
[c]Vero = African green monkey kidney cells.

Table S3. Percent amino acid identity matrix of the ZIKV isolates used in this study.

	Uganda/1947	**Canada/2013**	**Puerto Rico/2015**	**Brazil/2015**
Uganda/1947	100	97.01	96.90	98.86
Canada/2013	97.01	100	99.76	99.62
Puerto Rico/2015	96.90	99.76	100	99.71
Brazil/2015	98.86	99.62	99.71	100

Figure S1

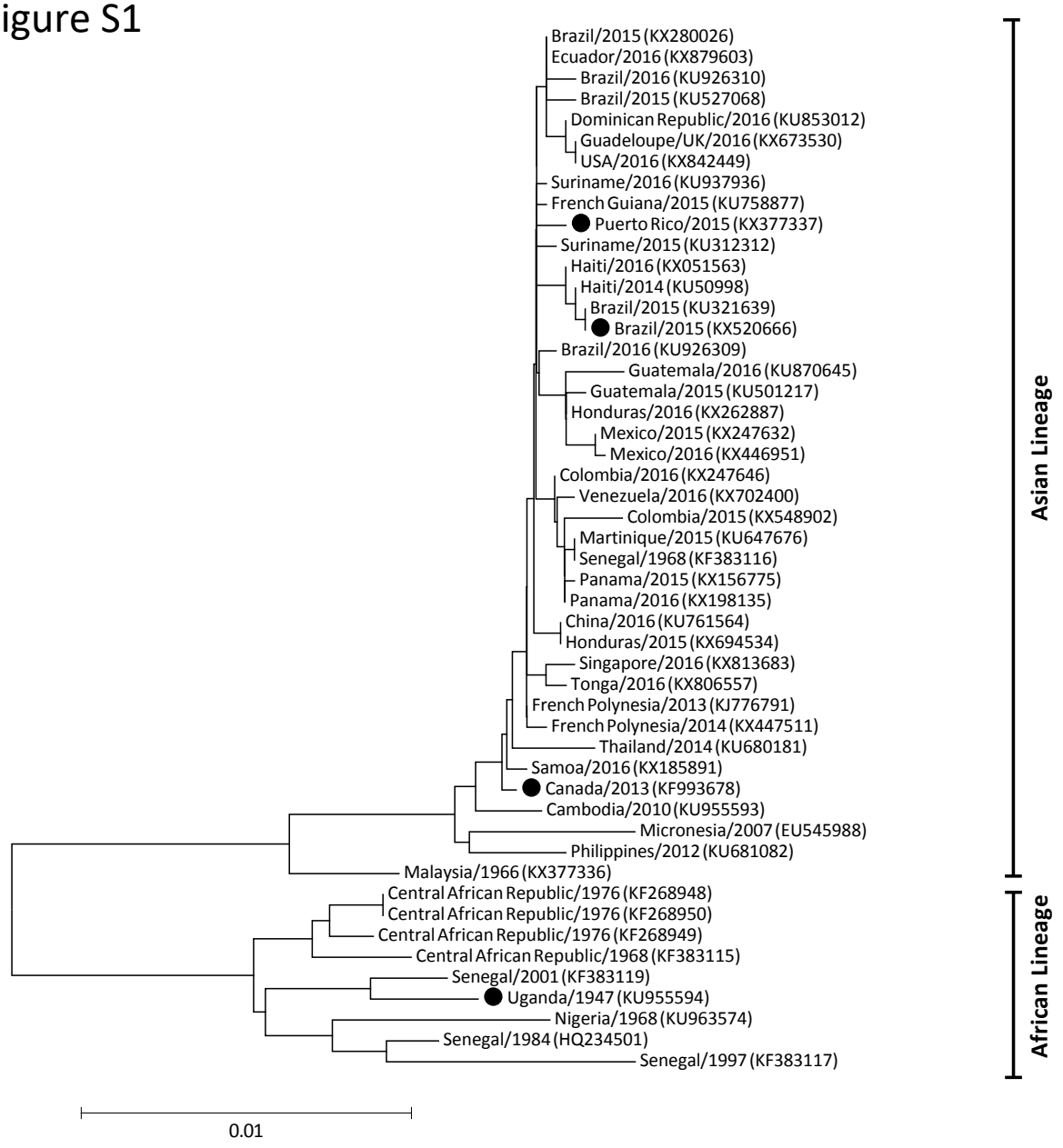


Figure S1. Phylogenetic analysis of selected ZIKV strains. Neighbor joining phylogenetic tree showing the position of the viral isolates used in this study (indicated by black circles) in the global ZIKV diversity. African and Asian lineages are indicated as well as country of origin, year of isolation, and GenBank accession number.

Figure S2

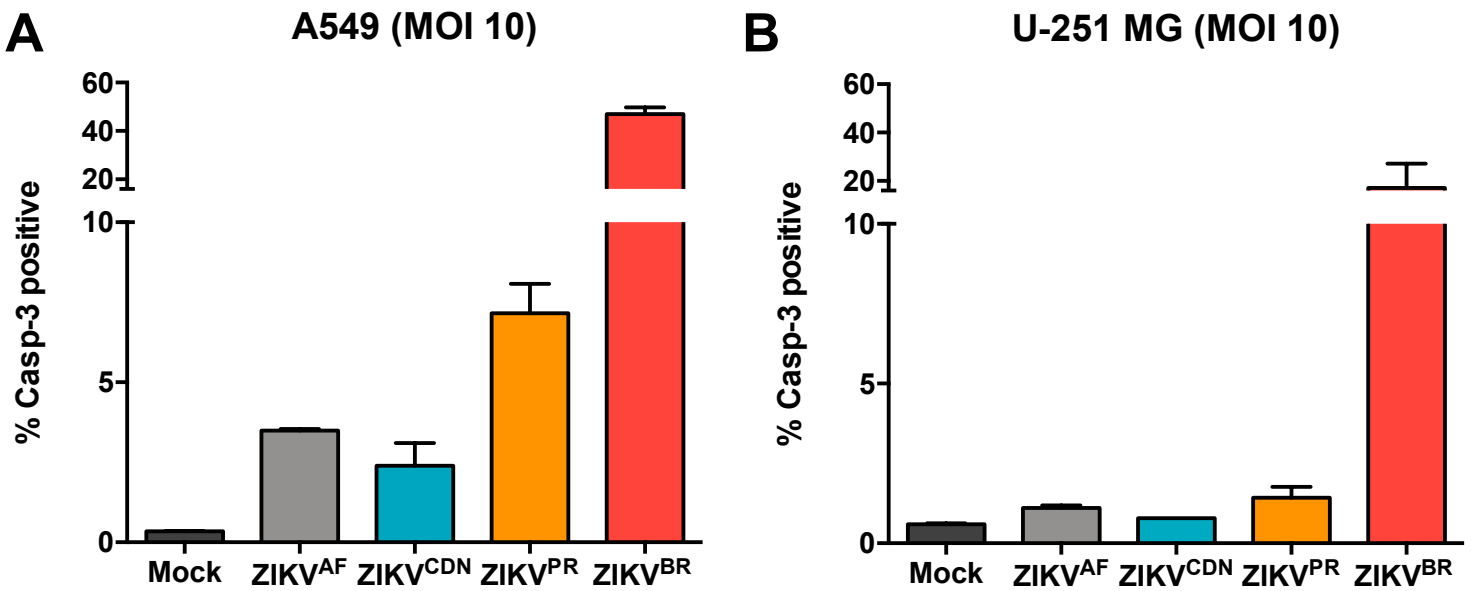


Figure S2. ZIKV isolates differentially induce apoptosis. (A) A549 cells and (B) U-251 MG cells were infected with ZIKV at MOI = 10 and 24 h post-infection the percentage of cells positive for cleaved caspase-3 was determined by flow cytometry. Values represent mean ± SD of two independent experiments.

Figure S3

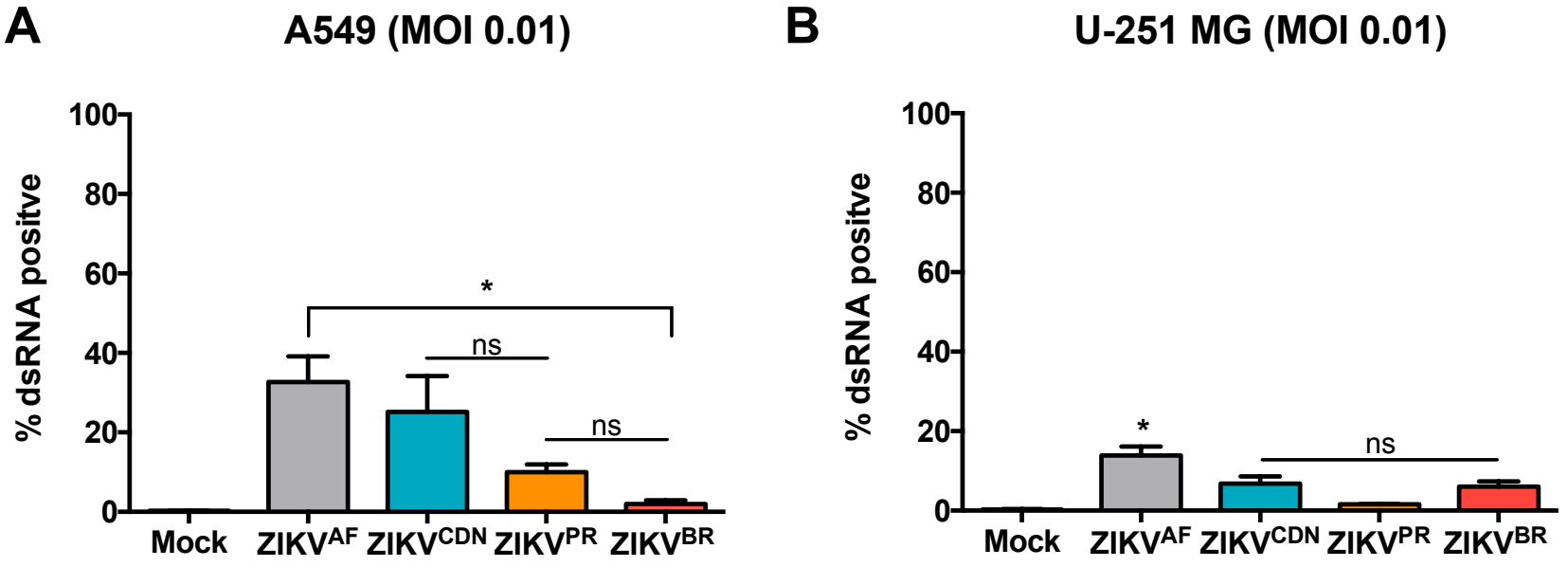
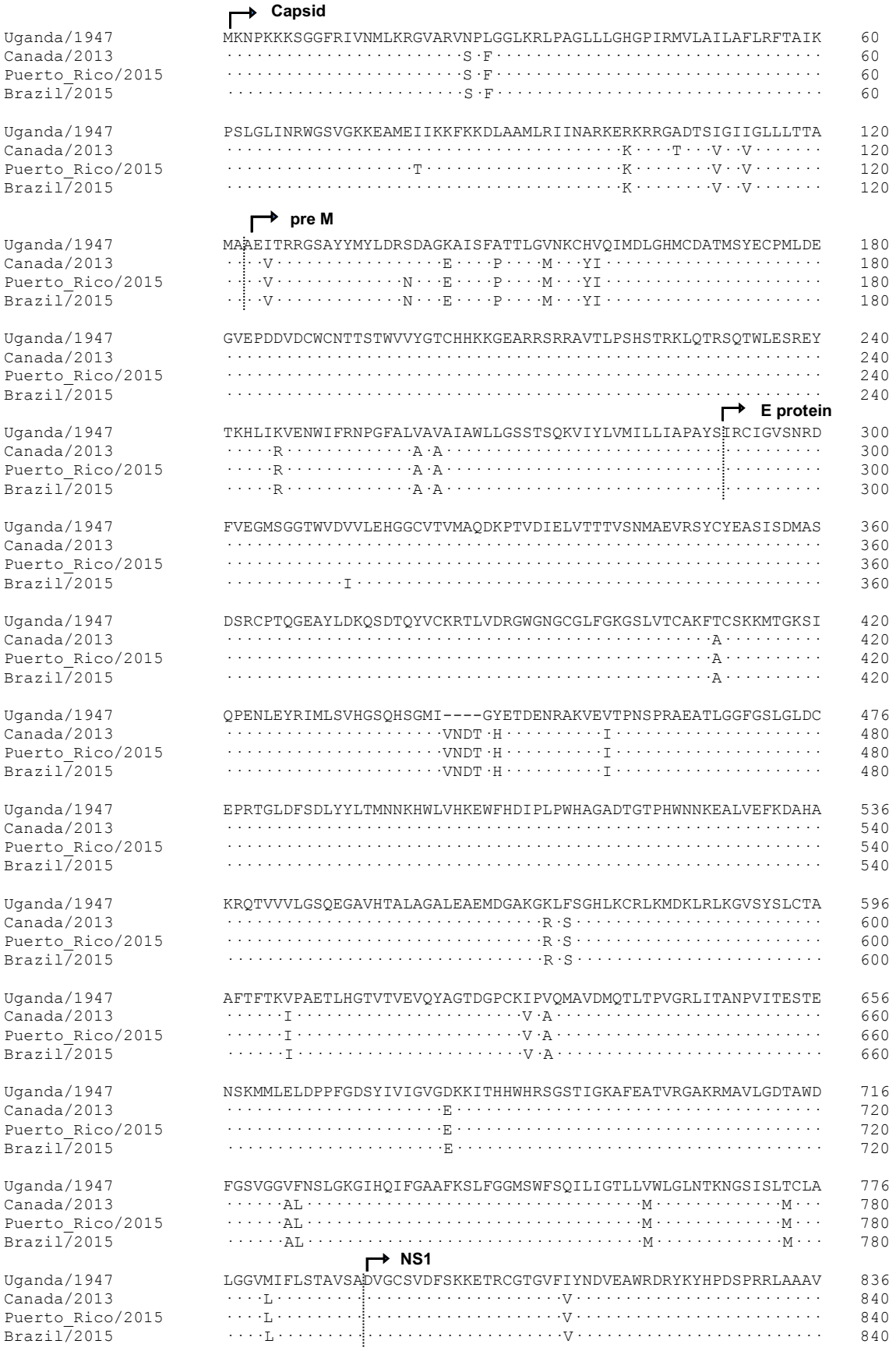
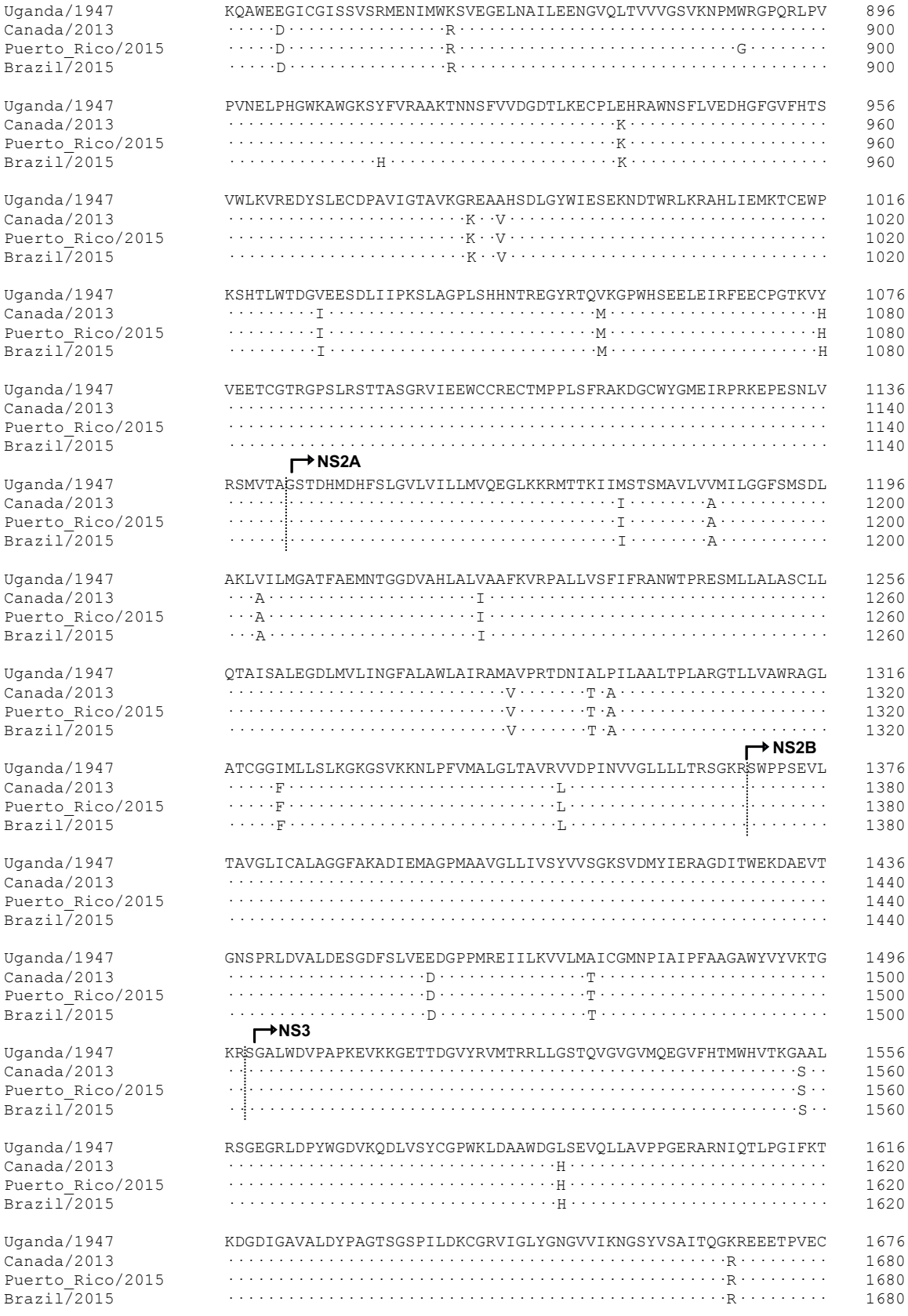


Figure S3. ZIKV isolates differ in infectivity at low MOI. (A) A549 cells and (B) U-251 MG cells were infected with ZIKV at MOI = 0.01 and 72 h post-infection the percentage of dsRNA-positive cells was determined by flow cytometry. Values represent mean ± SEM of at least three independent experiments. Asterisks indicate significant differences in % infected cells: ** $p < 0.01$, *** $p < 0.001$.

File S1: Amino acid sequence alignment of the ZIKV isolates used in this study.

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Puerto_Rico/2015 ·····D··············R·····G····· 900
Brazil/2015 ·····D··············R····· 900
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Brazil/2015 ··············H·····K····· 960
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Brazil/2015 ·····I·····M·····H 1080
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Puerto_Rico/2015 ····· 1140
Brazil/2015 ····· 1140
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Puerto_Rico/2015 ···A·····I····· 1260
Brazil/2015 ···A·····I····· 1260
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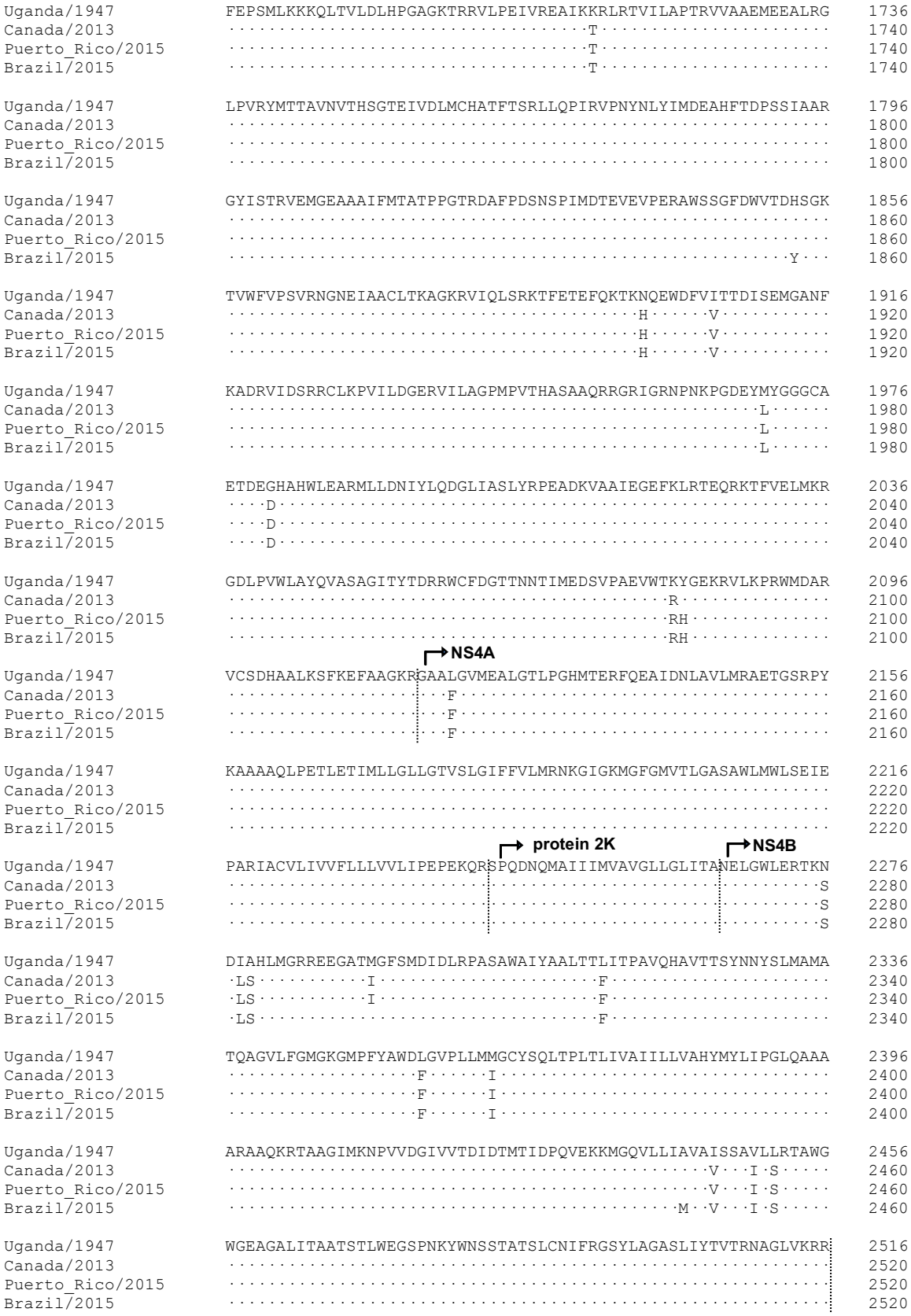
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Puerto_Rico/2015 ····· 1800
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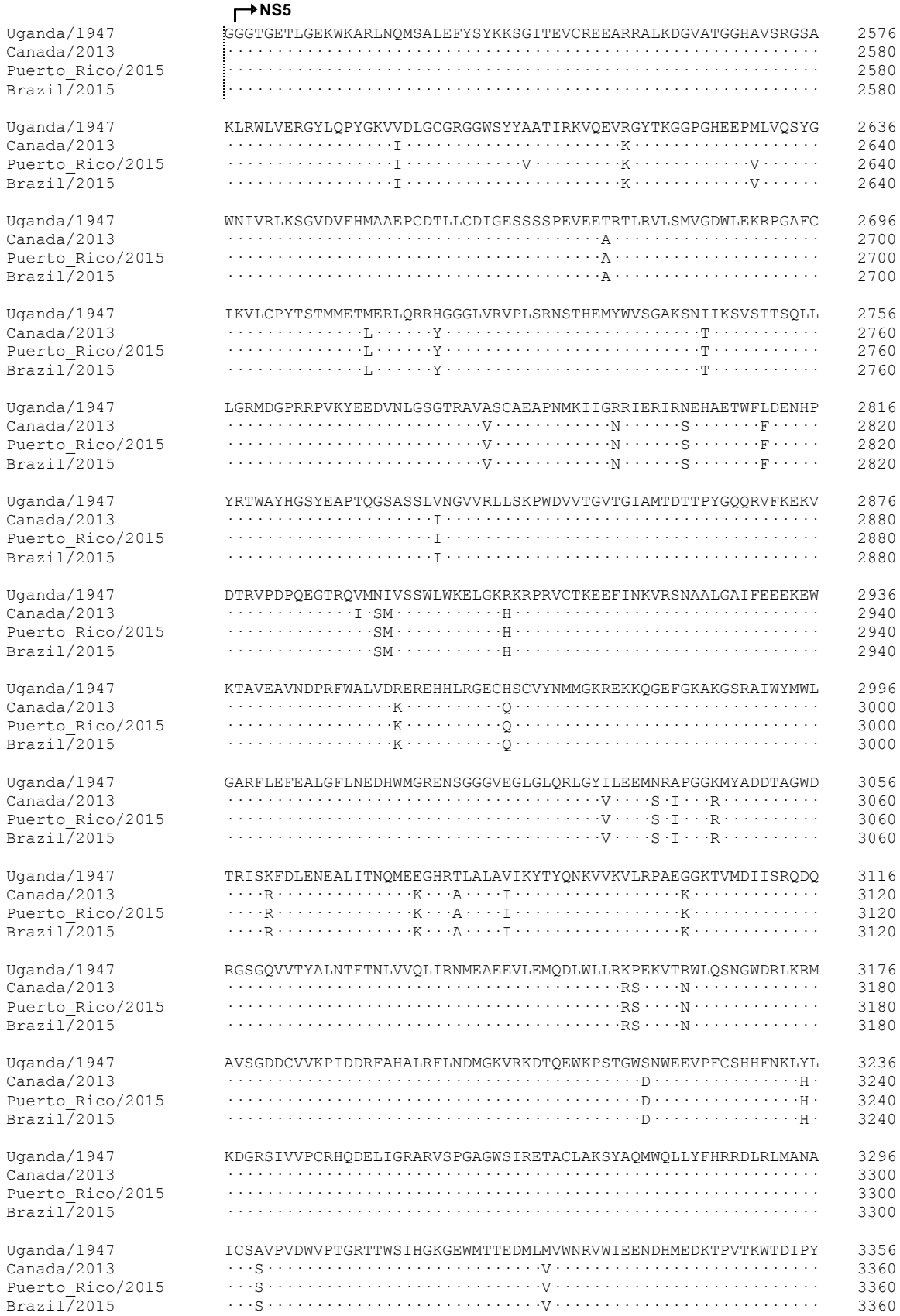
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