



SUPPLEMENTAL FIGURE 1. Zika virus (ZIKV) envelope (E) protein structure (PDB accession no. 5JHM) with relevant amino acid (AA) positions indicated in structural domain I (residue 169), domain I-II hinge region (residue 285), domain II (residues 120 and 227), and domain III (residues 317, 368, and 393). The red AA positions have substitutions that distinguish the Asian lineage strains—CPC-0740, SV0127-14, and PRVABC59—from the African lineage strain—41525-DAK—and might affect virulence in mice. The blue AA positions contain substitutions that are unique to the strain SV0127-14 and might contribute to its attenuated phenotype in mice. Residues 437, 438, and 495 have substitutions that distinguish African and Asian lineage ZIKV strains but are located in the stem-anchor portion of the E protein and are not pictured here. Strain SV0127-14 shares a valine at position 437 with African lineage strains. More contemporary, Asian lineage strains also share V473M and T487M substitutions in the stem-anchor region.

SUPPLEMENTAL TABLE 1  
Zika virus isolate histories and reference sequences

Isolate	Lineage	Source	Location	Year of collection	Accession number
SV0127-14	Asian	<i>Homo sapiens</i>	Thailand	2014	KU681081
CPC-0740	Asian	<i>H. sapiens</i>	Philippines	2012	KU681082
FSS13025	Asian	<i>H. sapiens</i>	Cambodia	2010	KU955593
H/PF/2013	Asian	<i>H. sapiens</i>	French Polynesia	2013	KJ776791
Micronesia	Asian	<i>H. sapiens</i>	Micronesia	2007	EU545988
Z1106033	Asian	<i>H. sapiens</i>	Suriname	2015	KU312312
PRVABC59	Asian	<i>H. sapiens</i>	Puerto Rico	2015	KU501215
P6-740	Asian	<i>Aedes aegypti</i>	Malaysia	1966	KX377336
103344	Asian	<i>H. sapiens</i>	Guatemala	2015	KU501216
MEX-InDRE-Lm	Asian	<i>H. sapiens</i>	Mexico	2016	KU922923
Haiti-0097	Asian	<i>H. sapiens</i>	Haiti	2014	KY415991
Brazil-ZKV2015	Asian	<i>H. sapiens</i>	Brazil	2015	KU497555
MR 766	Africa	<i>Macaca mulatta</i>	Uganda	1947	KU955594
ArD 41525	Africa	<i>Aedes africanus</i>	Senegal	1984	KU955591
ArD 41519	Africa	<i>A. africanus</i>	Senegal	1984	HQ234501
ArB13565	Africa	<i>A. africanus</i>	Central African Republic	1976	KF268948
IbH 30656	Africa	<i>H. sapiens</i>	Nigeria	1968	HQ234500

SUPPLEMENTAL TABLE 2

Genetic analysis of capsid (C), prM, and envelope (E) proteins of African (ArD 41525) and Asian (CPC-0740, SV0127-14, and PRVABC59) isolates

Polyprotein aa number	Protein	Protein aa number	Amino acid substitutions				
			ArD 41525 (African)	CPC-0740 (Asian)	SV0127-14 (Asian)	PRVABC59 (Asian/American)	
25	C	25	<b>N</b>	S	S	S	
27		27	<b>L</b>	F	F	F	
80		80	<b>I</b>	I	I	T	
101		101	<b>R</b>	K	K	K	
106		106	<b>A</b>	A	T	A	
110		110	<b>I</b>	V	V	V	
123		prM	1	<b>A</b>	V	A	A
125			3	<b>I</b>	V	V	V
139			17	<b>S</b>	S	S	N
143			21	<b>K</b>	E	E	E
148	26		<b>A</b>	P	P	P	
153	31		<b>V</b>	M	M	M	
157	35		<b>H</b>	Y	Y	Y	
158	36		<b>V</b>	I	I	I	
246	124		<b>K</b>	R	R	R	
260	138		<b>V</b>	A	A	A	
262	140	<b>V</b>	A	A	A		
263	141	<b>A</b>	V	A	A		
410	E	120	<b>T</b>	A	A	A	
459		169	<b>V</b>	I	I	I	
517		227	<b>A</b>	A	T	A	
550		260	<b>S</b>	S	S	S	
575		285	<b>F</b>	S	S	S	
607		317	<b>V</b>	I	I	I	
658		368	<b>S</b>	S	G	S	
683		393	<b>D</b>	E	E	E	
727		437	<b>V</b>	A	V	A	
728		438	<b>F</b>	L	L	L	
763	473	<b>V</b>	V	M	M		
777	487	<b>T</b>	T	M	M		
785	495	<b>M</b>	L	L	L		

Bold denotes mutations unique to ArD 41525 isolate.

SUPPLEMENTAL TABLE 3

Genetic analysis of NS1, NS2A, NS2B, and NS3 proteins of African (ArD 41525) and Asian (CPC-0740, SV0127-14, and PRVABC59) isolates

Polyprotein aa number	Protein	Protein aa number	Amino acid substitutions			
			ArD 41525 (African)	CPC-0740 (Asian)	SV0127-14 (Asian)	PRVABC59 (Asian/American)
839	NS1	45	A	A	V	A
846		52	E	D	D	D
863		69	K	R	R	R
956		162	I	V	V	V
982		188	V	A	V	V
988		194	A	V	V	V
1007		213	R	K	R	K
1030		236	V	V	I	I
1058		264	V	M	M	M
1180		NS2A	34	<b>M</b>	I	I
1191	45		<b>V</b>	I	I	I
1204	58		<b>V</b>	A	A	A
1226	80		V	I	V	I
1259	113		L	L	L	L
1270	124		<b>E</b>	D	D	D
1275	129		<b>V</b>	I	I	I
1289	143		<b>A</b>	V	V	V
1297	151		<b>A</b>	T	T	T
1354	208		<b>I</b>	L	L	L
1439	NS2B	67	V	I	V	V
1461		89	<b>E</b>	D	D	D
1477		105	<b>A</b>	T	T	T
1558	NS3	56	<b>A</b>	S	S	S
1594		92	<b>L</b>	H	H	H
1617		115	I	T	I	I
1671		169	<b>K</b>	R	R	R
1676		174	<b>A</b>	T	T	T
1687		185	<b>R</b>	K	K	K
1717		215	<b>K</b>	T	T	T
1849		347	<b>S</b>	T	S	S
1862		360	<b>I</b>	V	V	V
1902		400	<b>N</b>	N	H	H
1909	407	<b>I</b>	V	V	V	
1962	460	<b>V</b>	I	I	I	
1974	472	<b>M</b>	L	L	L	
2068	566	<b>T</b>	M	M	T	
2085	583	<b>K</b>	R	R	R	
2086	584	<b>Y</b>	Y	H	H	

Bold denotes mutations unique to ArD 41525 isolate.

SUPPLEMENTAL TABLE 4

Genetic analysis of NS4A, NS4B, and NS5 proteins of African (ArD 41525) and Asian (CPC-0740, SV0127-14, and PRVABC59) isolates

Polyprotein aa number	Protein	Protein aa number	Amino acid substitutions			
			ArD 41525 (African)	CPC-0740 (Asian)	SV0127-14 (Asian)	PRVABC59 (Asian/American)
2123	NS4A	4	<b>L</b>	F	F	F
2126		7	<b>M</b>	I	M	M
2127		8	<b>D</b>	E	E	E
2197	NS4B	78	<b>I</b>	M	I	I
2282		13	<b>I</b>	L	L	L
2283		14	<b>A</b>	S	S	S
2289		20	<b>K</b>	R	R	R
2293		24	<b>T</b>	A	A	A
2295		26	<b>M</b>	T	I	I
2318		49	<b>L</b>	F	F	F
2367		98	<b>M</b>	M	I	I
2453		184	<b>V</b>	I	I	I
2455		186	<b>L</b>	S	S	S
2594	NS5	74	<b>H</b>	Y	Y	Y
2598		78	<b>V</b>	I	I	I
2621		101	<b>R</b>	K	K	K
2634		114	<b>M</b>	M	M	<b>V</b>
2679		159	<b>T</b>	A	A	A
2701		181	<b>I</b>	I	V	I
2715		195	<b>M</b>	L	L	L
2722		202	<b>H</b>	Y	Y	Y
2749		229	<b>I</b>	T	T	T
2765		245	<b>E</b>	D	D	D
2787		267	<b>A</b>	V	V	V
2800		280	<b>R</b>	N	N	N
2807		287	<b>N</b>	S	S	S
2831		311	<b>E</b>	E	E	E
2842		322	<b>V</b>	I	I	I
2896		376	<b>N</b>	S	S	S
2909		389	<b>R</b>	H	H	H
2969		449	<b>H</b>	Q	Q	Q
3039		519	<b>I</b>	V	V	V
3044		524	<b>N</b>	S	S	S
3046		526	<b>A</b>	I	I	I
3050		530	<b>K</b>	R	R	R
3065		545	<b>K</b>	R	R	R
3080		560	<b>E</b>	K	K	K
3089		569	<b>V</b>	I	I	I
3107		587	<b>G</b>	K	K	K
3154		634	<b>H</b>	Q	Q	Q
3161		641	<b>K</b>	R	R	R
3162	642	<b>P</b>	P	S	S	
3167	647	<b>R</b>	N	N	N	
3223	703	<b>S</b>	D	D	D	
3304	784	<b>A</b>	S	S	S	
3307	787	<b>I</b>	V	V	V	
3333	813	<b>M</b>	V	V	V	
3387	867	<b>D</b>	N	N	N	
3392	872	<b>V</b>	M	V	V	
3402	882	<b>F</b>	Y	Y	Y	

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