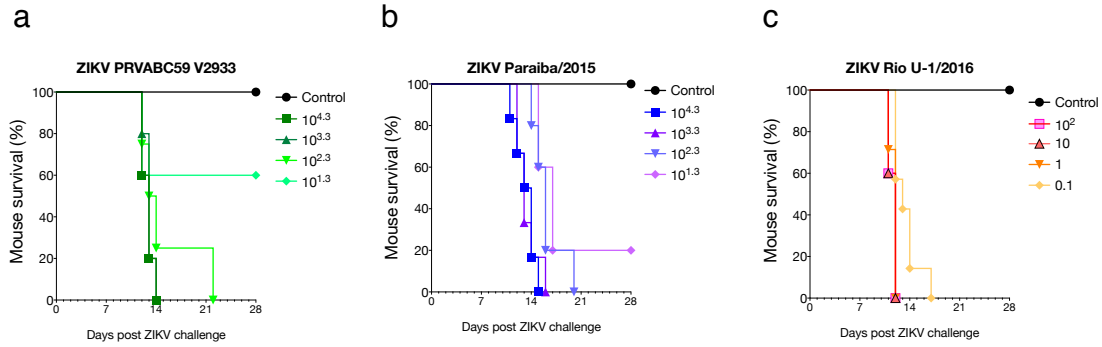


## **Supplementary information**

### **Fetal demise and failed antibody therapy during Zika virus infection of pregnant macaques**

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**Supplementary Fig. 1. ZIKV Rio U-1/2016 is pathogenic for AG129 mice.** Kaplan-Meier survival curves after challenge with different doses (PFU) of ZIKV isolates PRVABC59 (a); Paraiba/2015 (b), or Rio U-1/2016 (c). Male and female mice (groups of 5-6 animals) were inoculated with the doses (PFU) of three different ZIKV isolates and survival was followed for 28 days.

**Supplementary Table 1. Study animals**

<b>Group</b>	<b>Animal ID</b>	<b>Gestational day at day of ZIKV inoculation</b>	<b>Age at time of ZIKV inoculation</b>	<b>Weight (kg) at time of ZIKV inoculation</b>	<b>Infant ID (fetal outcome)</b>
<b>1<sup>st</sup> Trimester</b>	M01	44	14.63	6.70	F01 (deceased)
	M02	49	4.76	4.95	F02 (euthanized)
	M03	49	3.77	5.91	F03 (deceased)
<b>2<sup>nd</sup> Trimester</b>	M04	64	5.92	3.75	F04 (euthanized)
	M05	100	9.60	9.03	F05 (euthanized)
	M06	105	9.77	8.08	F06 (alive)
	M07	107	13.75	8.11	F07 (alive)
<b>3<sup>rd</sup> Trimester</b>	M08	112	8.28	8.41	F08 (euthanized)
	M09	120	6.31	8.33	F09 (alive)*
	M10	122	9.25	7.19	F10 (alive)*
	M11	124	9.34	10.18	F11 (unresponsive)
<b>Therapy experiment</b>	M12	106	14.06	6.84	F12 (euthanized)
	M13	125	8.97	6.61	F13 (euthanized)
	M14	134	5.97	8.90	F14 (euthanized)
	M15 (untreated)	139	6.82	9.07	F15 (euthanized)

\*These two animals were born alive and kept alive for 6 months.

**Supplementary Table 2. Summary of ZIKV sequencing**

Sample ID	Sample info				Sequencing stats			Variant site (nt, frequency, coverage depth) <sup>b</sup>								
	Time (dpi)	Type	ZIKV GE/ul RNA	CDS coverage	ZIKV reads	Ave. cov. depth	637	3053	4740	5548	5592	6472	6499	7505	8888	8963
RIO U-1/2016	0	stock	UD	100%	1,007,502	18,763	T	T	G	C	C	C (T 2%, 19316)	C	C	T	C
M12	3	serum	4,635	100%	306,288	5,327	--	--	--	--	--	--	--	--	--	--
M12	5	serum	~1	55.3%	441,201	3,951	--	?	--	?	--	?	?	--	?	?
M12	7	serum	5	91.4%	116,939	1,779	--	--	A (26%, 10081)	--	--	?	?	--	--	--
M12	10	serum	7	82.8%	429,089	6,945	A (35%, 18830)	--	--	--	--	--	?	--	--	--
M15	3	serum	6,582	98.2%	68,645	1,186	--	--	--	--	--	T (40%, 241)	--	--	--	--
M15	7	serum	13	91.9%	325,938	5,771	--	--	--	--	--	?	?	T (41%, 27176)	--	--
M15	10	serum	~1	48.2%	331,494	4,143	?	--	?	?	--	?	?	T (100%, 964)	--	--
M01	3	serum	43	93.3%	1,263,658	21,839	--	--	--	--	--	--	--	--	--	--
M01	3	serum	43	97.9%	536,471	8,997	--	--	--	--	--	?	?	--	--	--
M05	3	serum	2	83.7%	477,124	8,350	--	--	?	--	--	?	?	--	--	?
M05	20	AF	59	89.4%	91,413	1,563	--	C (94%, 668)	--	--	--	?	?	--	--	--
M05	41	AF	36	83.1%	362,283	6,377	--	C (100%, 2789)	--	A (26%, 311)	T (52%, 337)	?	?	--	--	T (100%, 2300)
M09	3	serum	3,203	99.6%	713,830	10,373	--	--	--	--	--	--	--	--	--	--
M09	28	AF	3,489	99.1%	303,059	5,234	--	--	--	--	--	--	--	--	C (55%, 822)	--
M04	3	serum	87	98.5%	934,007	13,311	--	--	--	--	--	--	--	--	--	--
M04	10	AF	2,401	98.7%	73,412	1,276	--	--	--	--	--	?	?	--	--	--
M07	3	serum	471	97.7%	217,375	3,869	--	--	--	--	--	?	?	--	--	--
M11	3	serum	330	97.9%	839,985	11,333	--	--	--	--	--	?	?	--	--	--
M06	3	serum	2,273	99.2%	383,218	6,775	--	--	--	--	--	T (40%, 1333)	--	--	?	--
M10	3	serum	625	99.4%	687,650	9,759	--	--	--	--	--	--	--	--	--	--
M08	3	serum	482	97.7%	742,999	10,292	--	--	--	--	--	?	?	--	--	--
M13	3	serum	840	98.2%	290,580	5,133	--	--	--	--	--	?	?	--	--	--
M14	3	serum	141	97.9%	391,076	6,905	--	--	--	--	--	?	?	--	--	--
M02	3	serum	1,734	99.1%	280,327	4,988	--	--	--	--	--	?	?	--	--	--
M03	3	serum	136	97.9%	609,080	10,189	--	--	--	--	--	?	?	--	--	--
Male control	3	serum	~500	100%	1,373,000	23,722	--	--	--	--	--	--	--	--	--	--
						<i>Amino acid substitution</i>	prM-M <sub>52</sub> K	silent	NS3-E <sub>45</sub> K	NS3-A <sub>312</sub> D	NS3-P <sub>327</sub> S	NS4A-A <sub>3</sub> V	NS4A-T <sub>121</sub> I	silent	silent	silent

<sup>a</sup>Percent coverage of coding sequence (CDS) at a depth of >25 nt

<sup>b</sup>Called intrahost variants must be present at >25% frequency, >100x coverage, on both forward and reverse reads, and not found in other lab stock viruses. Nucleotides sequenced from the stock virus at these sites are >99.9% in favor of the consensus, unless otherwise specified.

--, no change from ZIKV RIO U-1/2016

?, not sufficient coverage (<100x) at this position to confidently call intrahost variants