

S2 Table. Evaluation of the mismatches between the RT-RPA primer and probe set binding regions to rabies-related lyssaviruses

Virus ^a	Forward primer				Reverse primer				Probe				Combined ^b	RPA result	Time delay ^c
	5'	Internal	3'	Total %	5'	Internal	3'	Total %	5'	Internal	3'	Total %			
ARAV	2	3	1	19	4	1	1	20	1	2	1	8	15	Pos	5
DUVV	3	2	3	26	4	1	1	20	1	2	2	10	18	Neg	N/A
EBLV-1	1	3	2	19	2	0	2	13	2	1	2	10	14	Neg	N/A
EBLV-2	3	4	1	25	3	1	1	17	1	1	3	10	17	Pos	15
IKOV	2	3	3	25	4	2	1	23	1	1	3	10	19	Neg	N/A
IRKV	2	2	2	19	3	1	2	20	2	1	1	8	15	Pos	13
KHUV	4	3	0	23	4	2	2	27	1	1	3	10	19	Pos	15
LBV A	0	2	2	13	2	0	3	17	0	2	1	6	11	Pos	12
LBV C	1	1	3	16	3	1	0	13	1	2	3	13	14	Pos	16
LBV D	1	2	1	13	2	1	1	13	2	3	2	15	14	Pos	12
MOKV	1	3	2	19	2	2	2	20	2	1	1	8	15	Pos	2
SHIBV	2	3	3	26	4	1	1	20	1	0	2	6	16	Neg	N/A

WCBV	1	4	1	19	1	1	3	17	0	0	1	2	11	Pos	12
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^a Genbank accession numbers can be found in Fig 5

^b Total percentage of mismatches across primer and probe binding sites (n=108)

^c Estimated additional time required for a positive RT-RPA result (based on qRT-PCR quantification)