Table S3: Deep sequence data for position 3192, a homopolymeric region of either 5 or 6 As in the M-G intergenic region.

RABV ID	Read depth coverage	4 As	5 A's Clade 1	6 A's Clade 2
RV2975D*	445	5	**440**	0
RV1124F^	216	0	23	**193**
RV1126F*	255	0	**255**	0
RV2977F^	180	0	0	**180**
RV1127F*	1,089	0	**1,089**	0
RV1128F*	157	0	**157**	0
RV2984F*	613	0	**613**	0
RV2976F^	214	0	24	**190**
RV2979F^	539	0	37	**502**
RV2980F^	110	0	0	**110**
RV2981F^	758	0	53	**705**
RV2982F^	546	0	47	**499**
RV2983F*	916	0	**916**	0
RV3162F^	662	0	7	**655**
RV3163D^	283	0	4	**279**
sub5790F^	580	0	4	**576**
sub5791D^	2009	0	18	**1991**
sub5792F^	368	0	2	**366**
RV3160F^	722	0	3	**719**
RV3161D^	164	0	0	**164**
RV3166F*	127	2	**125**	0
RV1145F	133	0	**133**	0
RV1144F	356	2	**354**	0

RV1129F	89	0	**89**	0
RV1136D	289	1	**288**	0
RV1137D	356	0	**356**	0
RV1142D	1,078	3	**1,075**	0
RV1133D	2,833	8	**2,825**	0
RV1134D	1,451	4	**1,447**	0
RV201RD	1904	6	**1898**	0

For each sequence the read depth at position 3192 is shown alongside the number of reads that have 5As and 6As. Colour coded as Table 1, clade 1(*) and clade 2(^) and bold denotes the majority (consensus) population.