Table S4: Deep sequence data for position 5348, a homopolymeric region of either 7 or 8 As in the G-L intergenic region.

RABV ID	Read depth coverage	7 A’s	8 A’s	9 As
RV2984F*	833	**814**	19	0
RV1127F*	1,0156	**995**	21	0
RV2981F^	1,399	**1,372**	27	0
RV2979F^	493	**347**	146	0
RV2982F^	592	**563**	29	0
sub5791D^	2,359	**2,312**	47	0
sub5792F^	434	6	**373**	55
RV3162F^	887	**876**	11	0
RV3160F^	942	8	**838**	104
RV1142D	1,417	**1,402**	15	0
RV1133D	3,812	**3,772**	40	0
RV1134D	1,831	**1,811**	20	0

For each sequence where heterogeneity was observed in the sub-consensus data the read depth at position 5348 is shown alongside the number of reads that have 7-9As. Colour coded as Table 1, clade 1(*) and clade 2(^) and bold denotes the majority (consensus) population.