

# Development of Differentiating Infected from Vaccinated Animals (DIVA) Real-Time PCR for African Horse Sickness Virus Serotype 1

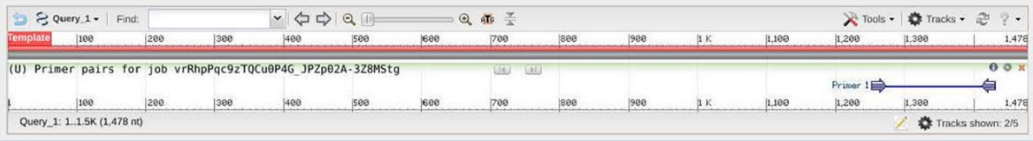
## Appendix

**A**

Primer-BLAST Results

Input PCR template ThailandAHSV1\_VP5  
Range 1 - 1478  
Specificity of primers Primer pairs are specific to input template as no other targets were found in selected database: Refseq mRNA (Organism limited to Homo sapiens)  
Other reports > Search Summary

Graphical view of primer pairs

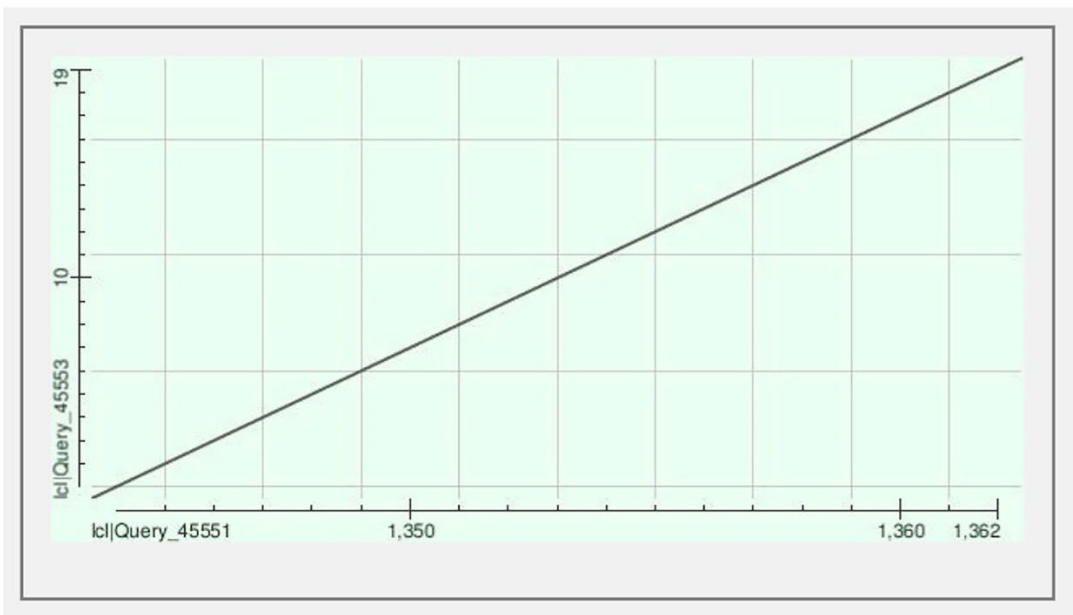


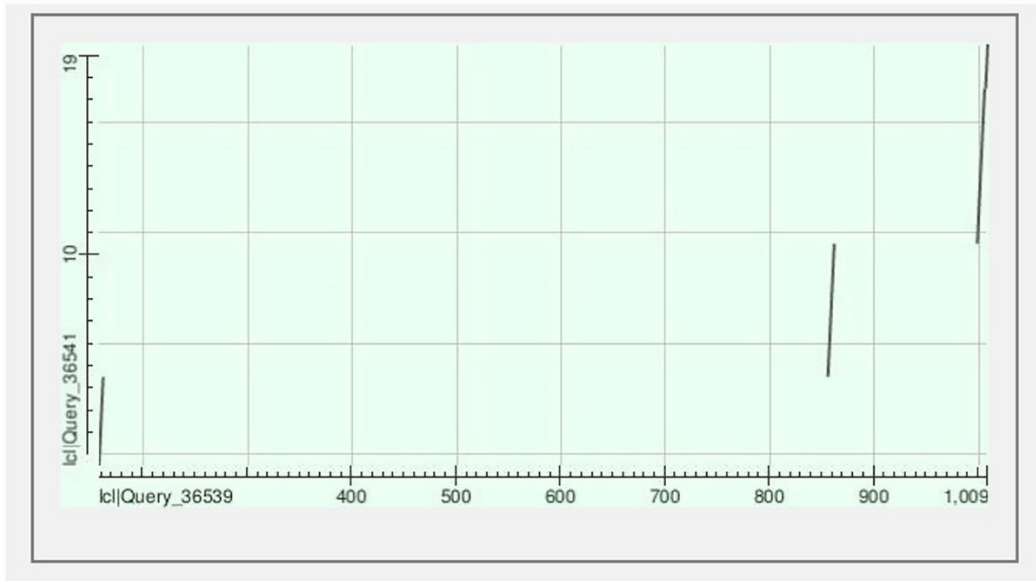
(U) Primer pairs for job vrRhpPqc9zT0Cu8P4G\_3Pz82A-3Z8HStg

Detailed primer reports

Primer pair 1									
	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AGCGTCGGATGCAAAGAAATC	Plus	21	1253	1273	59.60	47.62	5.00	2.00
Reverse primer	AAGCGGTTTCATTATCGTCC	Minus	20	1431	1412	59.07	50.00	4.00	2.00
Product length	179								

**B**



**C**

**Appendix Figure 1.** Summary of alignment plots of primers or probes to the vaccine (AHSV-1, AHSV-3 and AHSV-4) and outbreak (ThailandAHSV1) strains. These are made available from the Primer-BLAST and BLAST Global Alignment (dot plots) programs. A) Primer VP5-DIVA-P1 vs ThailandAHSV1 by Primer-BLAST; B) Primer VP5-DIVA-P1 vs ThailandAHSV1 by BLAST Global Alignment by the Needleman-Wunsch algorithm; C) VP5-DIVA-P2 vs ThailandAHSV1 by BLAST Global Alignment by the Needleman-Wunsch algorithm.

**A**

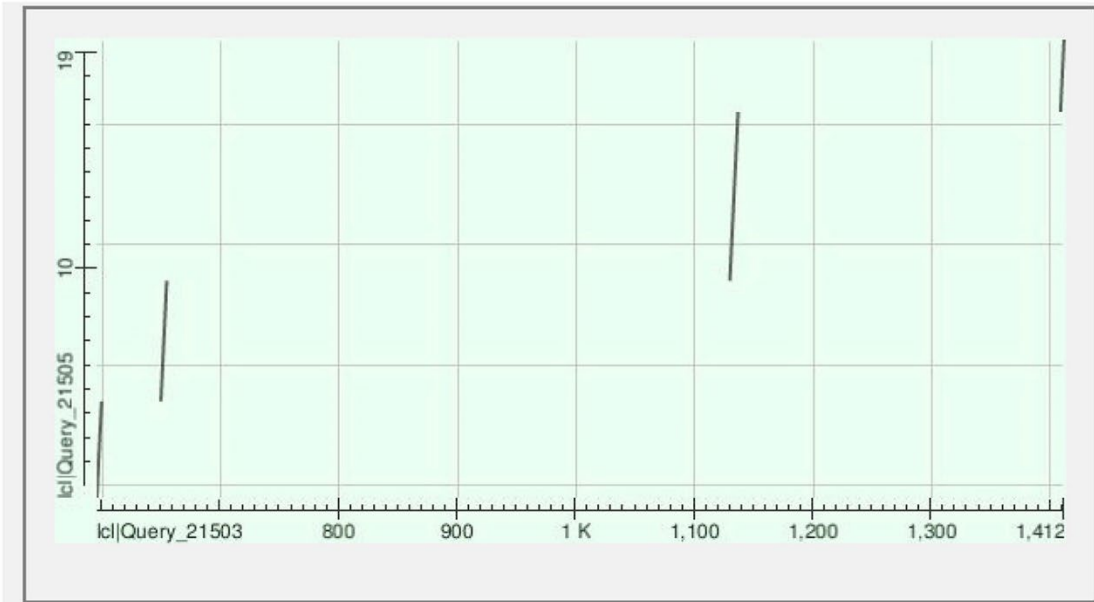
**Primer-BLAST Results**

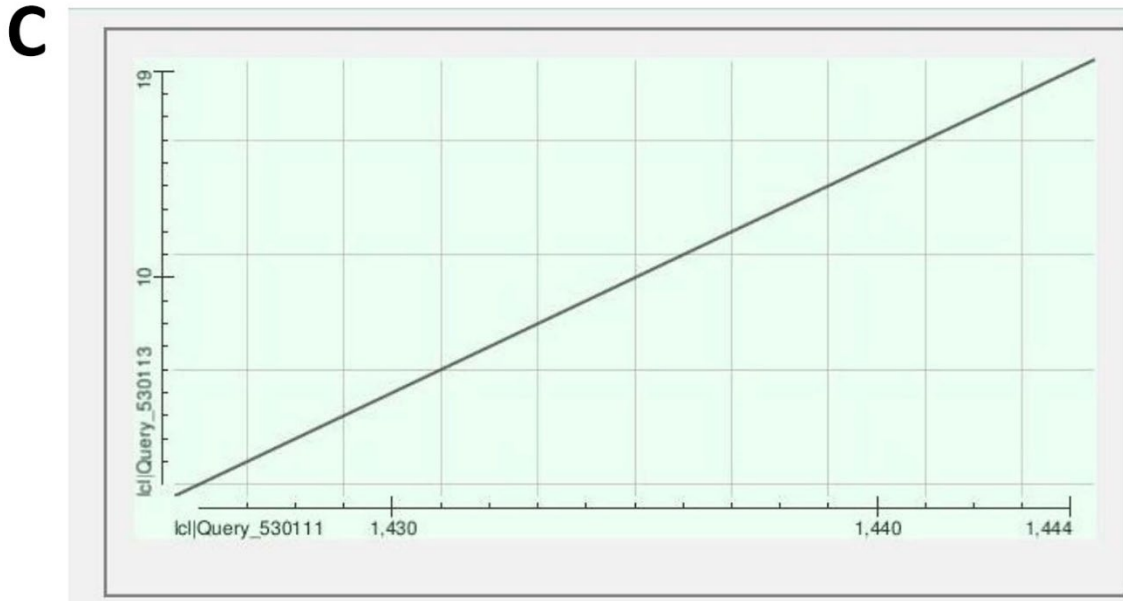
Input PCR template: KT030334\_AHSV1\_OBP\_VP5  
 Range: 1 - 1564  
 Specificity of primers: Primer pairs are specific to input template as no other targets were found in selected database: Refseq mRNA (Organism limited to Homo sapiens)  
 Other reports: [Search Summary](#)

**Graphical view of primer pairs**

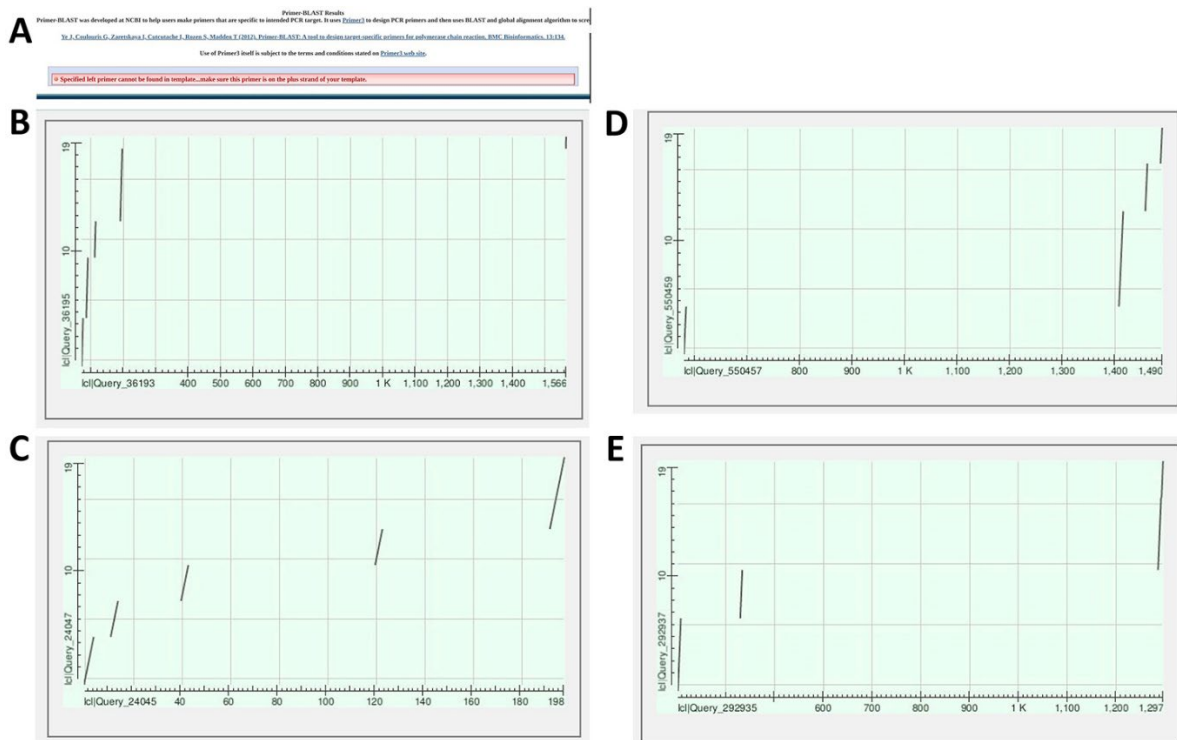
**Detailed primer reports**

Primer pair 1									
	Sequence (5'->3')	Template strand	Length	Start	Stop	Tm	GC%	Self complementarity	Self 3' complementarity
Forward primer	AGCGTCGGATGCAAAGAAATC	Plus	21	1335	1355	59.60	47.62	5.00	2.00
Reverse primer	AAGCGGTTTCATTATCGTCC	Minus	20	1513	1494	59.07	50.00	4.00	2.00
Product length	179								

**B**



**Appendix Figure 2.** Summary of alignment plots of primers or probes to the vaccine (AHSV-1, AHSV-3 and AHSV-4) and outbreak (ThailandAHSV1) strains. These are made available from the Primer-BLAST and BLAST Global Alignment (dot plots) programs. A) Primer vs AHSV\_1; B) VP5-DIVA-P1 vs AHSV\_1 by BLAST Global Alignment by the Needleman-Wunsch algorithm; C) VP5-DIVA-P2 vs AHSV1 by BLAST Global Alignment by the Needleman-Wunsch algorithm.



**Appendix Figure 3.** Summary of alignment plots of primers or probes to the vaccine (AHSV-1, AHSV-3 and AHSV-4) and outbreak (ThailandAHSV1) strains, by BLAST Global Alignment by the Needleman-Wunsch algorithm (dot plots). A) Primers vs AHSV\_3 / AHSV\_4; B) VP5-DIVA-1 vs AHSV\_3; C) VP5-DIVA-2 vs AHSV\_3; D) VP5-DIVA-1 vs AHSV\_4; E) VP5-DIVA-2 vs AHSV\_4.