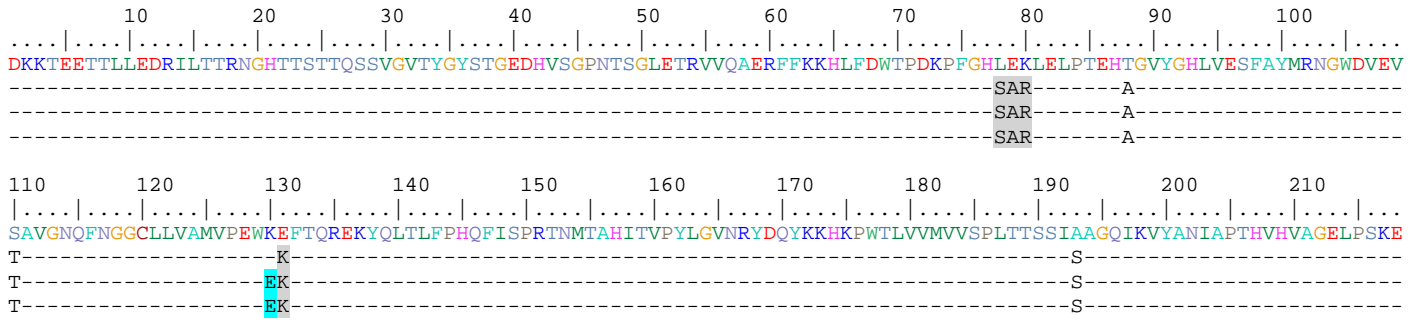
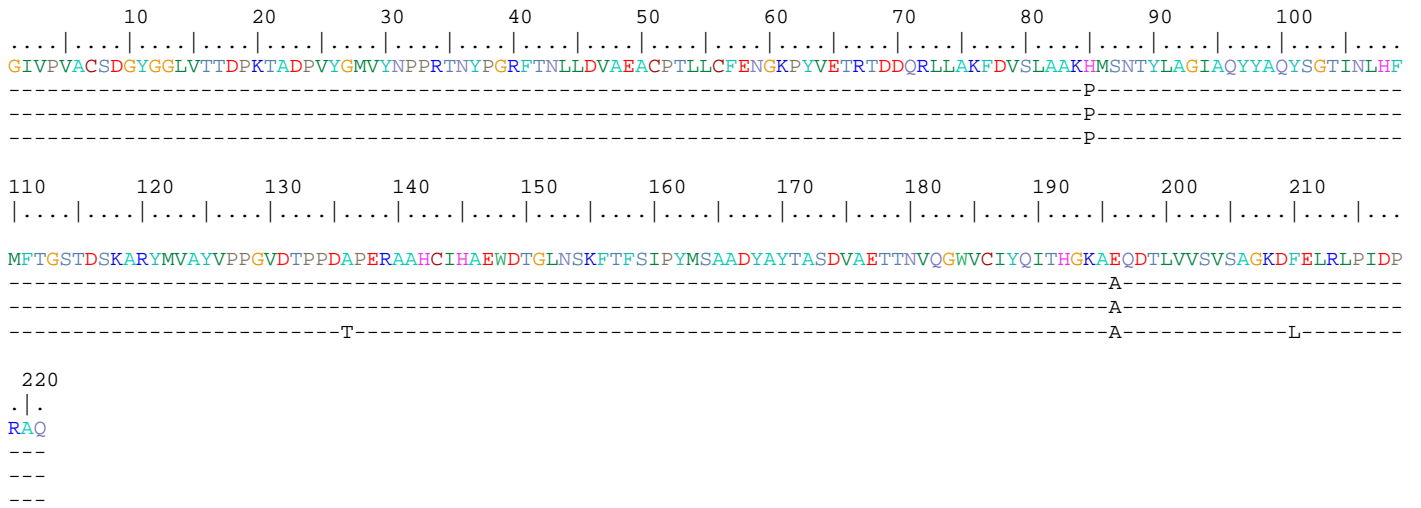


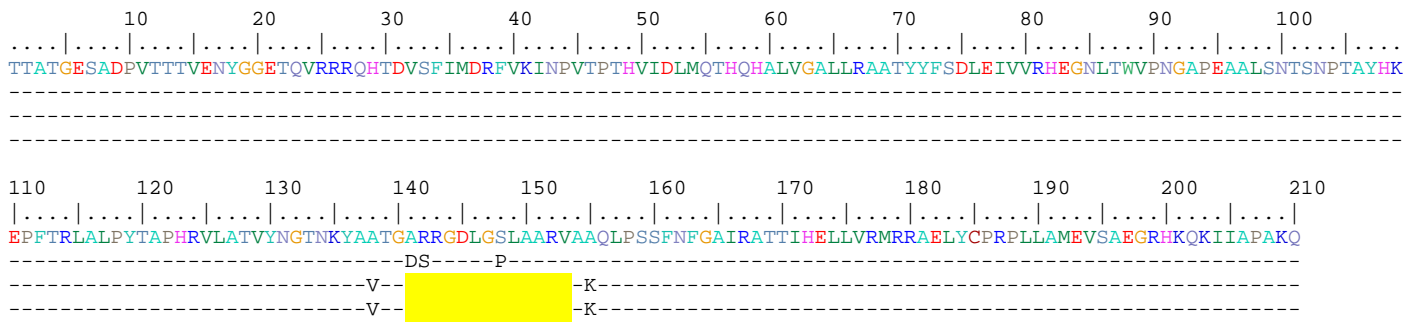
**VP2**



**VP3**

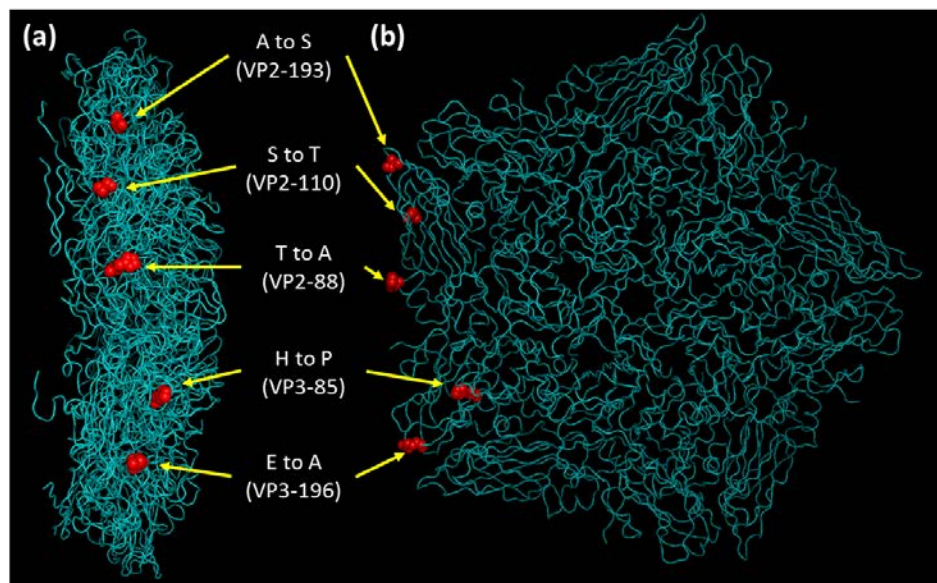


**VP1**



**Fig. S1. Capsid amino-acid sequence alignment**

Shown is the amino acid sequence of VP2, VP3 and VP1. Upper sequence, the A/IRN/2/87 field isolate; Second sequence, the A+ virus; Third sequence, the consensus sequence of the A- virus; Lower sequence, v01K/A-. A dash indicates identity with the field isolate. The region of VP1 G-H loop deleted in the A- virus and v01K/A- are highlighted by the yellow bar. VP2 residues (78-80 and 131) are indicated by grey highlights. The K to E changes at VP2 130 seen in the A- virus and v01K/A- are indicated by blue highlights. The T and L at VP3 136 and 210 respectively were only present in v01K/A-. All other changes were at residues that are either buried within VP3 (VP3 85) or at the inter-pentamer interface (VP2: 88, 110, 193 and VP3 196) where they are unlikely to directly influence receptor specificity.



**Fig. S2.** Selected residues where the amino acids of the A/IRN/2/87 field isolate are different to the A+ and A- viruses. Residue positions are shown mapped onto the crystal structure of a pentamer of a related FMDV A<sub>10</sub>61. In the virion, these residues are either located at the interface between adjacent pentamers (VP2 88, 110, 193 and VP3 196) or buried within VP3 (VP3-85). Panel (a) shows a side elevation and panel (b) a view of the outer capsid surface. Amino acids are given by the single letter code.

<b>Table S1. List of mutagenesis primer sequences</b>			
<b>vO1K/A-</b>	<b>Sequence 5'-3'</b>	<b>Site and mutation</b>	
F	AAGCCGTTTGGGCACGCAGCAGCGTTGGAAC TCCCACC	VP2 78-80	SAR → AAA
R	GGTGGGGAGTTCCAACGCTGCTGCGTGCCCAAACGGCTT		
F	AAGCCGTTTGGGCACTCAGCAGCGTTGGAAC TCCCACC		SAR → SAA
R	GGTGGGGAGTTCCAACGCTGCTGAGTGCCCAAACGGCTT		
F	AAGCCGTTTGGGCACGCAGCAAGATTGGAAC TCCCACC		SAR → AAR
R	GGTGGGGAGTTCCAATCTTGCTGCGTGCCCAAACGGCTT		
F	GCCATGGTTCTCTGAATGGGCAGCATTACTCAGCGCGAG	VP2 130-131	EK → AA
R	CTCGCGCTGAGTGAATGCTGCCATT CAGGAACCATGGC		
F	GCCATGGTTCTCTGAATGGAAAGAGTTACTCAGCGCGAG		EK → KE
R	CTCGCGCTGAGTGAAC TTTCCATT CAGGAACCATGGC		
<b>vO1k/A/TUR</b>			
F	GGTAATGGCAGAAAAGGTGCGCTGGGGCCTC	VP1 143-145	RGD → KGA
R	GAGGCC-CAGCGCACCTTTTCTGCCATTACC		
F	GCCTACCACAAGGCACCATTACGAGACTTGCG	VP1 110	Q → A
R	CGCAAGTCTCGTAAATGGTGCCTTGTTGGTAGGC		
F	GCTTTTGGACTCGGCAAGGCTGGAAC TCCC	VP2 78-80	LEK → SAR
R	GGGGAGTTCCAGCCTTGCCGAGTG TCCAAAAGC		
F	GCCATGGTACCTGAGTGGGAGAAATTTACCCCTCGTGAG	VP2 130-131	KE → EK
R	CTCACGAGGGGTAAATTTCTCCCACTCAGGTACCATGGC		
F	GCCATGGTACCTGAGTGGAAAAAATTTACCCCTCGTGAG		KE → KK
R	CTCACGAGGGGTAAATTTTTCCTACTCAGGTACCATGGC		
F: Forward primer; R: Reverse primer; Amino acids are shown using the single letter code			