Table S1. Primer sequences used in this study

Primers	Primer sequences (5′ to 3′)	PCR products	Size	Reference sequence
P1	CG gaattc (*EcoRI*)[a] **ACCGCTTGT**[b]TGTGAAAATATGGAGGGG	upstream of *nanH*	504 bp	HAPS_RS07830
P2	TTTTTATCTTGTGCAATG[c]TTTAGAATCATTAAATGTCCA			
P3	ATCAGAATTGGTTAATTGCCTTGAATGGAATCTTCC	downstream of *nanH*	522 bp	
P4	CGggatcc (*BamHI*) **ACAAGCGGT**ACTTTTTCACTAACCGTCT			
P5	CATTGCACAAGATAAAAA	*kan* gene	909 bp	MN913428.1
P6	CAATTAACCAATTCTGAT			
P7	CGATGTAGTTGAAGTGAA	*nanH* gene and its upstream and downstream	2500 bp	HAPS_RS07830
P8	TTATTAACAGCGACATCC			
P9	TGCAAAAGGGCTTTGGGTACCATGAAAAGAAGATTATCTAAAAA TGTTAAATG	*nanH* operator for complementation	2652 bp	
P10	AGGGAACAAAAGCTGGAGCTCTTACCAAGTATAACTGATATCTA CACCTAAATT			
P11	CGgaattc (*EcoRI*) GAAAAGCGATTTAAACGAG	*nanH* functional region for expression in *E. coli*	2314 bp	
P12	CCGctcgag (*XhoI*) CCAAGTATAACTGATATCTACAC			
P13	ATGCCTTTGCGAAGAGCT	internal region of *nanH* gene	594 bp	
P14	CCCCTAGCCCAGTTATCAT			
16SrRNA-F	GGCTTCGTCACCCTCTGT	16SrRNA	822 bp	NR_042879.1
16SrRNA-R	GTGATGAGGAAGGGTGGTGT			
5I-F	TAAGCTTGCGGCCGCGAATTCATGGTGCCCCTGCTGCTG	Siglec-5 gene	1665 bp	XM-003121417.4
5I-R	TTTGTAGTCAGCCCGGGATCCTTTGCTTTTTCTGATCTCTGAGTA CTC			

[a] Restriction enzyme sites are lowercase italic letters, and the additional 5′ sequences are in uppercase letters.

[b] The uptake signal sequence is displayed in bold.

[c] The overlapping regions for PCR are underlined.

Table S2. Quantitative RT-PCR primers used in this study

Primers	Sequence (5′ to 3′)	Size	Reference sequence
Siglec-2F	CCTGGACGGTCAATCATC	184 bp	XM-021097121.1
Siglec-2R	GCCTTCTGGTTCTTGTAGAG		
Siglec-3F	TCCAGTGACCACAAACAAC	157 bp	XM-021094848.1
Siglec-3R	TCCTCTTTCCACCCGAAA		
Siglec-5F	GAGGCCCAGAACGTCTAC	168 bp	XM-003127386.4
Siglec-5R	TCTGCGGCGTTTGACTAG		
Siglec-10F	TGCAGCCAGATGAGAAGG	96 bp	XM-021094936.1
Siglec-10R	GGAGCAGGCAGAGAAGAA		
Siglec-14F	GGACCGATTCCAACTCTC	114 bp	XM-003127392.4
Siglec-14R	CTGTGTTCTTCCTCCAGC		
Siglec-15F	GGCCCAGGTGAAGATCAC	131 bp	XM-003121417.4
Siglec-15R	CGGAAGCGGAACAAGTAGA		
GAPDH-F	CACAGTCAAGGCGGAGAAC	106 bp	NM_001206359.1
GAPDH-R	CGTAGCACCAGCATCACC		
IL-1α-F	CCTCTAAGACATCCAGGCTAA	83 bp	NM_214029.1
IL-1α-R	CAACCGTCTCTTCTTCAGAATC		
TNF-α-F	CACCACGCTCTTCTGCCTAC	132 bp	NM_214022.1
TNF-α-R	ACGGGCTTATCTGAGGTTTGAG		
IL-6-F	CCCTGAGGCAAAAGGGAAAGA	212 bp	NM_214399.1
IL-6-R	CGTGGACGGCATCAATCTCA		
IL-8-F	CAAGGAACTGAGAGTGATTGAGAG	165 bp	NM_213867.1
IL-8-R	TACTGCTGTTGTTGTTGCTTCT		
IL-10-F	TCTGCCTTATTCTTCTGACTCTGA	102 bp	NM_001008691.1
IL-10-R	TCGGATTAACAGGTCTGTCACT		
IL-12-F	GATGCTGGCCAGTACACC	377 bp	U08317.1
IL-12-R	TCCAGCACGACCTCAATG		

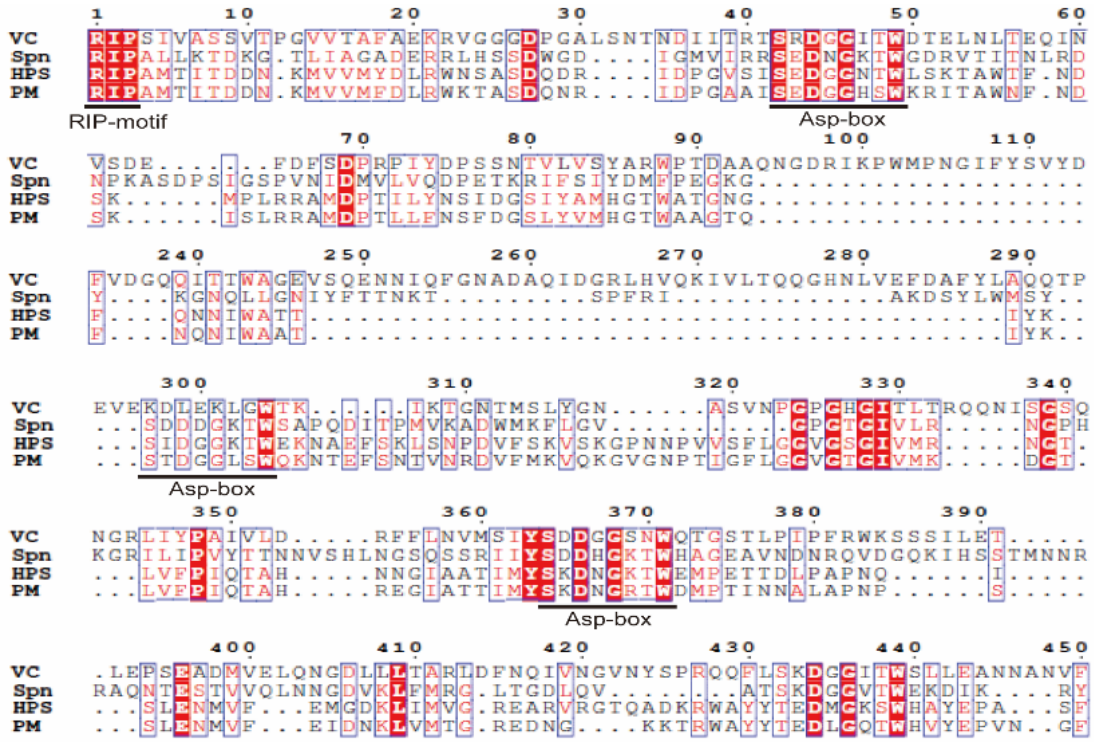

Fig. S1 The motifs of the sialidase of *Glaesserella parasuis* JS0135

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16 **Fig S2. Amino acid sequence of porcine Siglec-5.** The N-terminal is an 18-amino acid long
17 hydrophobic signal peptide (indicated in a box). There are four immunoglobulin-like domains.
18 One V-type domain is underlined using a green line, followed by three C2-type domains
19 underlined by orange, blue, and purple lines. The blue sequence indicates the transmembrane
20 region. In the putative cytoplasmic tail, there are two tyrosine residues, Y525 and Y548, marked
21 by an asterisk. Y525 is embedded in LHYASL, named ITIM motif, and Y548 is included in
22 TEYSEI, similar to ITIM-like motifs.

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