

Table S1. Primer sequences used in this study

Primers	Primer sequences (5' to 3')	PCR products	Size	Reference sequence
P1	CG gaattc (<i>EcoRI</i>) ^a ACCGCTTGT ^b TGTGAAAATATGGAGGGG	upstream of <i>nanH</i>	504 bp	HAPS_RS07830
P2	<u>TTTTTATCTTGTGCAATG</u> ^c TTTAGAATCATTAAATGTCCA			
P3	<u>ATCAGAATTGGTTAATTGC</u> CTTGAATGGAATCTTCC	downstream of <i>nanH</i>	522 bp	
P4	CGggatcc (<i>BamHI</i>) ACAAGCGGTACTTTTCACTAACCGTCT			
P5	CATTGCACAAGATAAAAAA	<i>kan</i> gene	909 bp	MN913428.1
P6	CAATTAACCAATTCTGAT			
P7	CGATGTAGTTGAAGTGAA	<i>nanH</i> gene and its upstream and downstream	2500 bp	HAPS_RS07830
P8	TTATTAAACAGCGACATCC			
P9	TGCAAAAGGGCTTGGGTACC <u>ATGAAAAGAAGATTATCTAAAAAA</u> <u>TGTTAAATG</u>		2652 bp	
P10	AGGGAAACAAAAGCTGGAGCT <u>TTACCAAGTATAACTGATATCTA</u> <u>CACCTAAATT</u>	<i>nanH</i> operator for complementation		
P11	CGgaattc (<i>EcoRI</i>) GAAAAGCGATTAAACGAG	<i>nanH</i> functional region for expression in <i>E. coli</i>	2314 bp	
P12	CCGctcgag (<i>XbaI</i>) CCAAGTATAACTGATATCTACAC			
P13	ATGCCTTGCAGAGCT	internal region of <i>nanH</i> gene	594 bp	
P14	CCCCTAGCCCAGTTATCAT			
16SrRNA-F	GGCTTCGTCACCCTCTGT	16SrRNA	822 bp	NR_042879.1
16SrRNA-R	GTGATGAGGAAGGGTGGTGT			
5I-F	TAAGCTTGCGCCCGCAATT <u>CATGGTGCCCTGCTGCTG</u>	Siglec-5 gene	1665 bp	XM-003121417.4
5I-R	<u>TTTGTAGTCAGCCCAGGATC</u> <u>TTGCTTTCTGATCTGAGTA</u> 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.

1

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	GCCTTCTGGTCTTAGAG		
Siglec-3F	TCCAGTGACCACAAACAAAC	157 bp	XM-021094848.1
Siglec-3R	TCCTCTTCCACCCGAAA		
Siglec-5F	GAGGCCAGAACGTCTAC	168 bp	XM-003127386.4
Siglec-5R	TCTGCGCGTTGACTAG		
Siglec-10F	TGCAGCCAGATGAGAAGG	96 bp	XM-021094936.1
Siglec-10R	GGAGCAGGCAGAGAAGAA		
Siglec-14F	GGACCGATTCCAACACTCTC	114 bp	XM-003127392.4
Siglec-14R	CTGTGTTCTCCTCCAGC		
Siglec-15F	GGCCCAGGTGAAGATCAC	131 bp	XM-003121417.4
Siglec-15R	CGGAAGCGGAACAAGTAGA		
GAPDH-F	CACAGTCAAGGCGGAGAAC	106 bp	NM_001206359.1
GAPDH-R	CGTAGCACCAGCATCACC		
IL-1 α -F	CCTCTAAGACATCCAGGCTAA	83 bp	NM_214029.1
IL-1 α -R	CAACCGTCTCTTCTCAGAAC		
TNF- α -F	CACCACGCTCTCTGCCTAC	132 bp	NM_214022.1
TNF- α -R	ACGGGCTTATCTGAGGTTGAG		
IL-6-F	CCCTGAGGCCAAAGGGAAAGA	212 bp	NM_214399.1
IL-6-R	CGTGGACGGCATCAATCTCA		
IL-8-F	CAAGGAACGTGAGAGTGATTGAGAG	165 bp	NM_213867.1
IL-8-R	TACTGCTGTTGTTGTTGCTTCT		
IL-10-F	TCTGCCTTATTCTCTGACTCTGA	102 bp	NM_001008691.1
IL-10-R	TCGGATTAAACAGGTCTGTCACT		
IL-12-F	GATGCTGCCAGTACACC	377 bp	U08317.1
IL-12-R	TCCAGCACGACCTCAATG		

2

3

Sequence alignment of RIP-motif and Asp-box regions across four species: VC, Spn, HPS, and PM.

RIP-motif:

	1	10	20	30	40	50	60										
VC	RIP	SIV	ASSV	T P G	V V T A F	A E K	R V G G	G D	P G A L S N T	N D	I I	I T R I	S R D G C	I	I W D	T E L N L	T E Q I N
Spn	RIP	ALL	KTD	K G	T L I A G	A D E R R	L H S S	S D	W G D . . .	I G M V	I R R	S E D	D N G K	T	G D R V T I	T I N L R D	
HPS	RIP	AMT	I T D	D N	K M V M V	M Y D	L R W N S A	S D	Q D R	I D P	G V S I	S E D	D G G N	T	W L S K T A W	T F . N D	
PM	RIP	AMT	I T D	D N	K M V V M F D	L R W K T A	S D	Q N R	I D P G A A I	S E D	D G C H	H S W K	R I T A W	N F . N D			

Asp-box:

	70	80	90	100	110		
VC	V S D E . . .	F D P S	D P R P I Y	D P S S N	T V L V S Y A R	W P T	D A A Q N G D R I K P W M P N C I F Y S V Y D
Spn	N P K A S D P S	I G S P V N I	D M V L V Q D	P E T K R I F S I	Y D M F P E G K G . . .		
HPS	S K . . .	M P L R R A M D P T I L Y N S I D G	S I Y A M H G T	W A T G N G . . .			
PM	S K . . .	I S L R R A M D P T L L F N S F D G	G S L Y V M H G T	W A A G T Q . . .			

240 - 290:

	240	250	260	270	280	290
VC	F V D G Q Q I T T W A G E	V S Q E N N I Q F G N A D A Q I D G R L H V Q K I V L T Q Q G H N L V E F D A F Y L A	A Q Q T P			
Spn	Y . . . K G N O L L G N I Y F T T N K T S P F R I A K D S Y L W M S Y . . .			
HPS	F . . . Q N N I W A T T I Y K . . .			
PM	E . . . Q N Q I W A T T I Y K . . .			

300 - 340:

	300	310	320	330	340
VC	E V E K D I E K L G W T K . . .	I T K T G N T M S L Y G N A S V N P C P C H C I T L T R Q Q N I S C S Q		
Spn	. . . S D D D G K T W S A P Q D I T P M V K A D W M K F L G V C P C G T C I V L R N C P H . . .		
HPS	. . . S I D G G K T W E K N A E F S K L S N P D V F S K V S K G P N N P V V S F L G C V G C S C I V M R N C T . . .		
PM	. . . S T D G G L S W Q K N T E F S N T V N R D V F M K V Q K G V G N P T I G F I C G V C C C I V M K D C T . . .		

Asp-box:

	350	360	370	380	390
VC	N G R L I Y P A I V L D . . .	R F F L N V M S I Y S D D G C S N W Q T G S T L P I P F R W K S S S I L E T . . .			
Spn	K G R L I P P V Y T T N N V S H L N G S O S S R I I Y S D D H C K T W H A G E A V N D N R Q V D G Q K I H S S T M N N R				
HPS	. . . L V F P I Q T A H N N G I A A T I M Y S K D N G K T W E M P E T T D L P A P N Q I . . .		
PM	. . . L V F P I Q T A H R E G I A T T I M Y S K D N G R I T W D M P T I N N A L A P N P S . . .		

400 - 450:

	400	410	420	430	440	450
VC	. . . L E P S E A D M V E L O N G D L L I Z T A R I D D F N Q I V N G V N Y S P R Q Q F I L S K D G C I T W S D I L E A N N A N V F					
Spn	R A Q N T E S T V V Q L N N G D V K Y F M R G . . .	L T G D I Q V A I T S K D G C V I T W E K D I K R Y		
HPS	. . . S L E N M V F . . .	E M G D K L I M V G . . .	R E A R V R G T Q A D K R W A Y Y T E D D M C K R S W H A Y E P A S F		
PM	. . . S L E N M V F . . .	E I D N K L V M T G . . .	R E D N G K K T R W A Y Y T E D D L G O T W H V Y E P V N . . .		

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

Porcine Siglec-5

Signal peptide

1 **MVPLLLLLLWLGGSLQQDQGFWLQVQESVTQECLGVHVTCSFSFSWSYWFSP**

EYLFIYWFRREGDNTRLGEPVATNNPHRPVNPQTRDRFQLSGDPQNKCDSLIRDAR

MSDTGVYVLRLEEEHRIKHTYTDKKLVQVTALTEKPD^{Ig-D1}IRFPLESGRPTNLTCSP

PVCDGGRLVHF^{Ig-D2}SWAGAALDAVDPEALGSSVLTTPRQDHGTNLTCQVKLQGAQVT

TERTIQLNVSYAPWNLTINVSFRNVTVLKILQNTSSLFILEDQALQLLCVADGNPPAQL

SWFRGSPAPNATPISSTTILELPGVGTVPGEVTCRAQNPLGSQNLSLLV^{Ig-D3}VSPPQLL

GPSCSWEDRGLHCSCSSRAQPAPSLHWRLGEGLLDGNFSNASIKVTSSSTGPWAN

SSSLGEGLSSSLRLSCEAQNVYGSQGATVLLPGTSGSLTGAVPGTMALGGAGAMAVL

SLCLCLIFFCLVKR^{ITIM}RRRQAARTPKGMDEDPMGTVAWGSRQKPRPDSPADQAPSP

AEDAEPGEQEE^{*}LHYASL^{*}SFQEMKSREPGDQEATS^{*}TEYSEIRKSK 555

ITIM ITIM-like

15

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.

23