Supplemental Tables, Figure, and Text

Table S1. A matrix of "two-by-two" tables comparing the number of piglets testing PRRSV RTqPCR positive or negative on serum samples, ear-vein swabs (ES), nasal swabs (NS), and oral swabs (OS) for each farm. "Neg" means "RT-qPCR negative", and "Pos" means "RT-qPCR positive.

Table S2. A matrix of "two-by-two" tables comparing the number of piglets testing PRRSV RTqPCR positive or negative on serum samples, ear-vein swabs, nasal swabs, and oral swabs across all farms. "Neg" means "RT-qPCR negative", and "Pos" means "RT-qPCR positive.

Table S3. A matrix of cells showing crude agreement (first value within each cell), and Cohen's kappa value (second value within each cell) between serum samples, ear-vein swabs (ES), nasal swabs (NS), and oral swabs (OS).

Table S4. A matrix of two-by-two tables comparing RT-qPCR results of all litter-level sample types. "Neg" means "RT-qPCR negative", and "Pos" means "RT-qPCR positive."

Table S5. A matrix of cells showing crude agreement (first value within each cell), and Cohen's kappa value (second value within each cell) between pairs of the litter-level sample-types (ear-vein blood swab litter pools (ESp), nasal swab litter pools (NSp), oral swab litter pools (OSp), and family oral fluids (FOF)).

Table S6. A matrix of two-by-two tables comparing RT-qPCR results of all litter-level sample types (ear-vein blood swab litter pools (ESp), nasal swab litter pools (NSp), oral swab litter pools (OSp), and family oral fluids (FOF)) with the true PRRSV status of the litters (litters having \geq viremic piglets). "Neg" means "RT-qPCR negative", and "Pos" means "RT-qPCR positive."

Table S7. The interpretation of the value ranges of the Cohen's Kappa statistic as reported by Landis and Koch (1977).

Table S8. The number of test samples by farm.

Table S9. An example of a two-by-two contingency table comparing the binary outcomes of two RT-qPCR tests.

Figure S1. The mean Ct per litter of swab samples (ear-vein blood swabs (top), nasal swabs (second from top), oral swabs (third from top), family oral fluids (bottom)) compared to the mean Ct per litter of serum.

Text S1. Formulas for calculating Cohen's kappa, sensitivity, specificity, positive predictive value, and negative predictive value.

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		FARM 1	-		FARM	2		FARM	3	
SAMPLE		Serum			Serum			Serum		
ТҮРЕ										
	STATUS	Neg	Pos		Neg	Pos		Neg	Pos	
ES	Neg	219	2	221	172	3	175	176	11	187
	Pos	0	7	7	2	15	17	0	58	58
		219	9		174	18		176	69	
NS	Neg	220	2	222	170	5	175	176	17	193
	Pos	0	7	7	4	13	17	0	52	52
		220	9		174	18		176	69	
OS	Neg	220	2	222	169	3	172	174	11	185
	Pos	0	7	7	5	15	20	2	58	60
		220	9		174	18		176	69	

SAMPLE		Serum		ES		NS		OS	
ТҮРЕ									
	STATUS	Neg	Pos	Neg	Pos	Neg	Pos	Neg	Pos
Serum	Neg			567	2	566	4	563	7
	Pos			16	80	24	72	16	80
ES	Neg	567	16			580	3	573	10
	Pos	2	80			9	73	5	77
NS	Neg	566	24	580	9			575	15
	Pos	4	72	3	73			4	72
OS	Neg	563	16	573	5	575	4		
	Pos	7	80	10	77	15	72		

Table S2. A matrix of "two-by-two" tables comparing the number of piglets testing PRRSV RTqPCR positive or negative on serum samples, ear-vein swabs, nasal swabs, and oral swabs across all farms. "Neg" means "RT-qPCR negative", and "Pos" means "RT-qPCR positive.

Table S3. Matrix of cells showing crude agreement (first value within each cell), and Cohen's kappa value (second value within each cell) between serum samples, ear-vein swabs (ES), nasal swabs (NS), and oral swabs (OS).

SAMPLE	Serum	ES	NS	OS
ТҮРЕ				
Serum		0.97, 0.88	0.96, 0.81	0.97, 0.85
ES	0.97, 0.88		0.98, 0.91	0.98, 0.90
NS	0.96, 0.81	0.98, 0.91		0.97, 0.87
OS	0.97, 0.85	0.98, 0.90	0.97, 0.87	

SAMPLE		ESp		NSp		OSp		FOF	
ТҮРЕ									
	STATUS	Neg	Pos	Neg	Pos	Neg	Pos	Neg	Pos
ESp	Neg			43	0	42	1	43	0
	Pos			1	11	1	11	5	7
NSp	Neg	43	1			42	2	44	0
	Pos	0	11			1	10	4	7
OSp	Neg	42	1	42	1			43	0
	Pos	1	11	2	10			5	7
FOF	Neg	43	5	44	4	43	5		
	Pos	0	7	0	7	0	7		

Table S4. A matrix of two-by-two tables comparing RT-qPCR results of all litter-level sample types. "Neg" means "RT-qPCR negative", and "Pos" means "RT-qPCR positive."

Table S5. A matrix of cells showing crude agreement (first value within each cell), and Cohen's kappa value (second value within each cell) between pairs of the litter-level sample-types (ear-vein blood swab litter pools (ESp), nasal swab litter pools (NSp), oral swab litter pools (OSp), and family oral fluids (FOF)).

SAMPLE	ESp	NSp	OSp	FOF
ТҮРЕ				
ESp		0.98, 0.95	0.96, 0.89	0.91, 0.68
NSp	0.98, 0.95		0.95, 0.84	0.93, 0.74
OSp	0.96, 0.89	0.95, 0.84		0.91, 0.69
FOF	0.91, 0.68	0.93, 0.74	0.91, 0.69	

Table S6. A matrix of two-by-two tables comparing RT-qPCR results of all litter-level sample types (ear-vein blood swab litter pools (ESp), nasal swab litter pools (NSp), oral swab litter pools (OSp), and family oral fluids (FOF)) with the true PRRSV status of the litters (litters having \geq viremic piglets). "Neg" means "RT-qPCR negative", and "Pos" means "RT-qPCR positive."

SAMPLE		Litters	with ≥
ТҮРЕ		1 piglet	viremic
	STATUS	Neg	Pos
ESp	Neg	33	10
	Pos	0	12
NSp	Neg	33	11
	Pos	0	11
OSp	Neg	33	10
	Pos	0	12
FOF	Neg	33	15
	Pos	0	7

Table S7. The interpretation of the value ranges of the Cohen's Kappa statistic as reported by Landis and Koch (1977).

Cohen's kappa value	Interpretation
< 0.00	Poor agreement
Between 0.00 and 0.20	Slight agreement
Between 0.21 and 0.40 (inclusive)	Fair agreement
Between 0.41 and 0.60 (inclusive	Moderate agreement
Between 0.61 and 0.80 (inclusive)	Substantial agreement
Between 0.81 and 1.00 (inclusive)	Almost perfect agreement

	Piglet-level samples					Litter-level samples					
Farm	ES	NS	OS	Srm	Subtotal	ES-pool	FOF	NS-pool	OS-pool	Subtotal	Total
1	228*	229	229	229	915	20	20	20	20	80	995
2	192	192	192	192	768	15	15	15	15	60	828
3	245	245	245	245	979	20	20	20	20	80	1059
Total	665	666	666	666	2662	55	55	55	55	220	2882

Table S8. The number of test samples by farm

*The ES sample from one piglet was lost on-farm (fell through the slats).

From left to right: ear-vein blood swabs (ES), nasal swabs (NS), oral swabs (OS), serum (Srm), ear-vein blood swab pools (ES-pool), family oral fluids (FOF), nasal swab pools (NS-pool), and oral swab pools (OS-pools).



Figure S1. The mean Ct per litter of swab samples (ear-vein blood swabs (top), nasal swabs (second from top), oral swabs (third from top), family oral fluids (bottom)) compared to the mean Ct per litter of serum.

		Reference sample or test					
		Neg	Pos				
New sample or test	Neg	α	β	<i>N</i> _			
	Pos	δ	3	N ₊			
		<i>R</i> _	<i>R</i> ₊				

Table S9. An example of a two-by-two contingency table comparing the binary outcomes of two RT-qPCR tests.

Text S1. Formulas for calculating crude agreement, Cohen's kappa, sensitivity, specificity, positive predictive value, and negative predictive value.

The crude agreement is calculated as: $\frac{\alpha + \varepsilon}{\alpha + \beta + \delta + \varepsilon}$ (1)

The Cohen's kappa statistic (C_k) is calculated as:

$$\frac{\frac{\alpha + \varepsilon}{\alpha + \beta + \delta + \varepsilon} - \left(\left(\left(\frac{N_{+}}{\alpha + \beta + \delta + \varepsilon} \right) * \left(\frac{R_{+}}{\alpha + \beta + \delta + \varepsilon} \right) \right) + \left(\left(\frac{N_{-}}{\alpha + \beta + \delta + \varepsilon} \right) * \left(\frac{R_{-}}{\alpha + \beta + \delta + \varepsilon} \right) \right) \right)}{1 - \left(\left(\left(\frac{N_{+}}{\alpha + \beta + \delta + \varepsilon} \right) * \left(\frac{R_{+}}{\alpha + \beta + \delta + \varepsilon} \right) \right) + \left(\left(\frac{N_{-}}{\alpha + \beta + \delta + \varepsilon} \right) * \left(\frac{R_{-}}{\alpha + \beta + \delta + \varepsilon} \right) \right) \right)} \right)$$
(2)

Sensitivity = $\frac{\varepsilon}{R_+}$ (3)

Specificity
$$=\frac{\alpha}{R_{-}}$$
 (4)

Positive predictive value $=\frac{\varepsilon}{N_+}$ (5)

Negative predictive value
$$=\frac{\alpha}{N_{-}}$$
 (6)