

S3 Table. Serotypes of German invasive *S. suis* isolates based on *cps* typing in collection A (1996-2004) and collection B (2015-2016), respectively, grouped by origin of isolation

<i>cps</i> type	Collection A			Collection B		
	CNS ^b	joint	other ^c	CNS ^b	joint	other ^c
1 and 14	4*	3	1	4*†††	17†††	3
2 and 1/2	25***	5	1	56***	17	10
3	2	0	0	14†	0†	1
4	1	0	1	27††	1††	5
5	1	0	1	6	1	0
6	0	0	0	0	0	0
7	3	1	1	36	14	4
8	0	0	0	8	2	0
9	12	1	5	57	13	9
10	0	0	0	3	0	0
11	0	0	0	1	1	2
12	0	0	0	0	0	0
13	0	0	0	1	0	0
15	0	0	0	3	0	0
16	0	0	0	1	1	1
17	0	0	0	0	0	0
18	0	0	0	4	1	0
19	0	0	0	3	0	0
20	0	0	0	0	0	0
21	0	0	0	0	1	0
22	0	0	0	0	0	0
23	0	0	0	3	0	0
24	0	0	0	1	0	1
25	0	0	0	0	0	0
26	0	0	0	0	0	0
27	0	0	0	0	0	0
28	0	0	0	4	0	1
29	0	0	0	0	0	0
30	0	0	0	1	0	0
31	0	0	0	5	0	2
32	0	0	0	0	0	0
33	0	0	0	0	0	0
34	0	0	0	0	0	0
nt ^a	0	2	0	3	2	3
Σ	48	12	10	241	71	41

^a nt: genetically non-typable by PCR

^b CNS: central nervous system

^c Other: internal organs other than lungs

* $0.01 < p \leq 0.05$ significant difference between collection A and B or [†] within collection B between CNS and joint isolates

^{††} $0.001 < p \leq 0.01$ very significant difference within collection B between CNS and joint isolates

^{***} $p \leq 0.001$ highly significant difference between collection A and B or ^{†††} within collection B between CNS and joint isolates