

S2 File. Alignment of *idnT* CDS from *S. Gallinarum* strains 287/91 (SG287\_91) and 9184 (SG9184), and *S. Pullorum* strains CDC1983-67 (SPCDC) and RKS5078 (SPRKS).

```

                20                                40
SG287_91_idnT  GTGGTGGGATTTGCCGAAGGGATGGGCGCGCAAGACGTCCTGCACTCCATACAAAACGG 59
SG9184_idnT   GTGGTGGGATTTGCCGAAGGGATGGGCGCGCAAGACGTCCTGCACTCCATACAAAACGG 59
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        60                                80                                100
SG287_91_idnT  AATTGGCGGTA CTCTGGGCGGACTCGCCATGATCCTCGGTTTTGGCGCGATGCTGGGAA 118
SG9184_idnT   AATTGGCGGTA CTCTGGGCGGACTCGCCATGATCCTCGGTTTTGGCGCGATGCTGGGAA 118
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        120                                140                                160
SG287_91_idnT  GATTAATTTCCGATACCGGCGCCGCGCAGCGCATTGCGACGACGCTCATTAAATACGTTTC 177
SG9184_idnT   GATTAATTTCCGATACCGGCGCCGCGCAGCGCATTGCGACGACGCTCATTAAATACGTTTC 177
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        180                                200                                220
SG287_91_idnT  GGCAAAAACGCGTGCAATGGGCGCTGGTGATCACCGGGCTTATCGTCGGCCTGGCAAT 236
SG9184_idnT   GGCAAAAACGCGTGCAATGGGCGCTGGTGATCACCGGGCTTATCGTCGGCCTGGCAAT 236
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        240                                260                                280
SG287_91_idnT  GTTTTTTGAAGTCGGATTCGTA CTGCTGTTGCCGCTCGTTTTTACGATTGTGGCCTCAT 295
SG9184_idnT   GTTTTTTGAAGTCGGATTCGTA CTGCTGTTGCCGCTCGTTTTTACGATTGTGGCCTCAT 295
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        300                                320                                340
SG287_91_idnT  CGGGACTGCCCTTGCTGTATGTCGGGGTTCCAATGGTCGCCGCCTTATCCGTTACGCAC 354
SG9184_idnT   CGGGACTGCCCTTGCTGTATGTCGGGGTTCCAATGGTCGCCGCCTTATCCGTTACGCAC 354
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        360                                380                                400
SG287_91_idnT  TGCTTCCTGCCGCCGCA TCCCGGCCCTACCGCTATTGCGACAATTTTTGAGGCAAATCT 413
SG9184_idnT   TGCTTCCTGCCGCCGCA TCCCGGCCCTACCGCTATTGCGACAATTTTTGAGGCAAATCT 413
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        420                                440                                460
SG287_91_idnT  CGGTACGACCCTGCTGTATGGGTTAATCATTACCATACCGACCGTGATTGTTGCCGGCC 472
SG9184_idnT   CGGTACGACCCTGCTGTATGGGTTAATCATTACCATACCGACCGTGATTGTTGCCGGCC 472
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        480                                500                                520
SG287_91_idnT  CGCTGTTTTCAA AATTGCTGGCGCGCTTTGAGAAAGCGCCGCCTGAAGGATTATTTAAT 531
SG9184_idnT   CGCTGTTTTCAA AATTGCTGGCGCGCTTTGAGAAAGCGCCGCCTGAAGGATTATTTAAT 531
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

        540                                560                                580
SG287_91_idnT  CCTCATCTATT CAGTGAAGAAGAGATGCCGTCATTCTGGAACAGTATTTTTGCCGCCGT 590
SG9184_idnT   CCTCATCTATT CAGTGAAGAAGAGATGCCGTCATTCTGGAACAGTATTTTTGCCGCCGT 590
SPCDC_idnT-RC -----
SPRKS-idnT-RC -----

```

	600	620	640	
SG287_91_idnT	GATCCCGGTCATTCTGATGGCCATCGCAGCGGTATGTGAAATCACGCTGCCAAAAACGA	649		
SG9184_idnT	GATCCCGGTCATTCTGATGGCCATCGCAGCGGTATGTGAAATCACGCTGCCAAAAACGA	649		
SPCDC_idnT-RC	-----CGCAGCGGTATGTGAAATCACGCTGCCAAAAACGA	35		
SPRKS_idnT-RC	-----CGCAGCGGTATGTGAAATCACGCTGCCAAAAACGA	35		
	660	680	700	
SG287_91_idnT	ATGCCGTGCGGGTTTTCTTCGAATTTATCGGTAATCCAGCAGTGGCGTTGTTTATTGCC	708		
SG9184_idnT	ATGCCGTGCGGGTTTTCTTCGAATTTATCGGTAATCCAGCAGTGGCGTTGTTTATTGCC	708		
SPCDC_idnT-RC	ATGCCGTGCGGGTTTTCTTCGAATTTATCGGTAATCCAGCAGTGGCGTTGTTTATTGCC	94		
SPRKS_idnT-RC	ATGCCGTGCGGGTTTTCTTCGAATTTATCGGTAATCCAGCAGTGGCGTTGTTTATTGCC	94		
	720	740	760	
SG287_91_idnT	ATTATCATCGCCATTTTTACGCTGGGCCGACGCAACGGACGTACGGTTGAGCAGGTGAT	767		
SG9184_idnT	ATTATCATCGCCATTTTTACGCTGGGCCGACGCAACGGACGTACGGTTGAGCAGGTGAT	767		
SPCDC_idnT-RC	ATTATCATCGCCATTTTTACGCTGGGCCGACGCAACGGACGTACGGTTGAGCAGGTGAT	153		
SPRKS_idnT-RC	ATTATCATCGCCATTTTTACGCTGGGCCGACGCAACGGACGTACGGTTGAGCAGGTGAT	153		
	780	800	820	
SG287_91_idnT	GGATATCGTTCGGCGAGTCCATTGGCGCTATTGCGATGATTGTTTTATCATCGCGGGCG	826		
SG9184_idnT	GGATATCGTTCGGCGAGTCCATTGGCGCTATTGCGATGATTGTTTTATCATCGCGGGCG	826		
SPCDC_idnT-RC	GGATATCGTTCGGCGAGTCCATTGGCGCTATTGCGATGATTGTTTTATCATCGCGGGCG	212		
SPRKS_idnT-RC	GGATATCGTTCGGCGAGTCCATTGGCGCTATTGCGATGATTGTTTTATCATCGCGGGCG	212		
	840	860	880	
SG287_91_idnT	GCGGCGCGTTTTAAACAAGTGCTGGTGGATAGCGGCGTGGGCCAATATATCTCGCAATTA	885		
SG9184_idnT	GCGGCGCGTTTTAAACAAGTGCTGGTGGATAGCGGCGTGGGCCAATATATCTCGCAATTA	885		
SPCDC_idnT-RC	GCGGCGCGTTTTAAACAAGTGCTGGTGGATAGCGGCGTGGGCCAATATATCTCGCAATTA	271		
SPRKS_idnT-RC	GCGGCGCGTTTTAAACAAGTGCTGGTGGATAGCGGCGTGGGCCAATATATCTCGCAATTA	271		
	900	920	940	
SG287_91_idnT	ATGACCGGCACCTCGCTATCTCCGTTATTAATGTGCTGGACGGTAGCCGCCGTGCTGCG	944		
SG9184_idnT	ATGACCGGCACCTCGCTATCTCCGTTATTAATGTGCTGGACGGTAGCCGCCGTGCTGCG	944		
SPCDC_idnT-RC	ATGACCGGCACCTCGCTATCTCCGTTATTAATGTGCTGGACGGTAGCCGCCGTGCTGCG	330		
SPRKS_idnT-RC	ATGACCGGCACCTCGCTATCTCCGTTATTAATGTGCTGGACGGTAGCCGCCGTGCTGCG	330		
	960	980	1,000	
SG287_91_idnT	TATTGCGTTAGGTTCCGCGACCGTGGCCGCGATAACCACAGCGGGCGTCGTATTGCCGA	1003		
SG9184_idnT	TATTGCGTTAGGTTCCGCGACCGTGGCCGCGATAACCACAGCGGGCGTCGTATTGCCGA	1003		
SPCDC_idnT-RC	TATTGCGTTAGGTTCCGCGACCGTGGCCGCGATAACCACAGCGGGCGTCGTATTGCCGA	389		
SPRKS_idnT-RC	TATTGCGTTAGGTTCCGCGACCGTGGCCGCGATAACCACAGCGGGCGTCGTATTGCCGA	389		
	1,020	1,040	1,060	
SG287_91_idnT	TTATTAACGTAACCCACGCCGATCCGGCGTTAATGGTACTGGCGACAGGCGCGGGAAGC	1062		
SG9184_idnT	TTATTAACGTAACCCACGCCGATCCGGCGTTAATGGTACTGGCGACAGGCGCGGGAAGC	1062		
SPCDC_idnT-RC	TTATTAACGTAACCCACGCCGATCCGGCGTTAATGGTACTGGCGACAGGCGCGGGAAGC	448		
SPRKS_idnT-RC	TTATTAACGTAACCCACGCCGATCCGGCGTTAATGGTACTGGCGACAGGCGCGGGAAGC	448		
	1,080	1,100	1,120	
SG287_91_idnT	GTTATTGCATCACATGTTAACGATCCCGTTTTTGGCTGTTTAAAGGGTATTTTAATCT	1121		
SG9184_idnT	GTTATTGCATCACATGTTAACGATCCCGTTTTTGGCTGTTTAAAGGGTATTTTAATCT	1121		
SPCDC_idnT-RC	GTTATTGCATCACATGTTAACGATCCCGTTTTTGGCTGTTTAAAGGGTATTTTAATCT	507		
SPRKS_idnT-RC	GTTATTGCATCACATGTTAACGATCCCGTTTTTGGCTGTTTAAAGGGTATTTTAATCT	507		
	1,140	1,160	1,180	
SG287_91_idnT	TAGCGTTCGGGGAAACCCTACGTACCTGGACCGTTATGGAAACATTGATTTCTGTCATGG	1180		
SG9184_idnT	TAGCGTTCGGGGAAACCCTACGTACCTGGACCGTTATGGAAACATTGATTTCTGTCATGG	1180		
SPCDC_idnT-RC	TAGCGTTCGGGGAAACCCTACGTACCTGGACCGTTATGGAAACATTGATTTCTGTCATGG	566		
SPRKS_idnT-RC	TAGCGTTCGGGGAAACCCTACGTACCTGGACCGTTATGGAAACATTGATTTCTGTCATGG	566		
	1,200	1,220		
SG287_91_idnT	GGTACTGGGCGTACTGGCGCTGAATGCGGTTCTGCATTAA	1221		
SG9184_idnT	GGTACTGGGCGTACTGGCGCTGAATGCGGTTCTGCATTAA	1221		
SPCDC_idnT-RC	GGTACTGGGCGTACTGGCGCTGAATGCGGTTCTGCATTAA	607		
SPRKS_idnT-RC	GGTACTGGGCGTACTGGCGCTGAATGCGGTTCTGCATTAA	607		