

Figure 1. Example of a chromatogram showing double peaks at the SAG1 allele. Type I allele is represented by nucleotide C at 267 and 291 positions while and II-III allele presents nucleotide T at 267 and 291 positions.

Table 1. Allele combination at SAG1, Alt-SAG2, SAG3 and GRA6 loci of the *T. gondii* strains.

Strain/ Num.	Genetic Marker							
	MLST genotype ^b locus background ^c							
	SAG1	Alt-SAG2	SAG3	GRA6				
GT1	I	I	I	I				
ME49	II	II	II	II				
VEG	III	III	III	III				
Pig 7 ^a	I	I	I	NA	NA			
Pig 7 ^a	I	I	u-2	NA	NA			
Pig 20	I	u-4/6	III	NA	NA			
Pig 25	I	u-4/7	NA	NA	u-3			
Pig 27	u-15	NA ^d	NA	u-3	I			
Pig 28	I	u-4	NA	NA	I			
Pig 29	I	u-8	III	NA	NA			
Pig 30	u-16	u-9	I	u-3				
Pig 35 ^a	I	u-10	NA	NA	u-5			
Pig 35 ^a	I	u-11	NA	NA	u-5			
Pig 37	u-18	u-12	I	u-6				
Pig 38 ^a	I	u-4	NA	NA	u-5			
Pig 38 ^a	u-19	u-4	NA	NA	u-7			
Pig 39	I	u-1	III	NA	NA			
Pig 40	I	u-4	I	NA	NA			
Pig 46	I	u-4	NA	NA	u-8			
Pig 50	I	u-14	NA	NA	u-8			
Pig 53	I	III	III	I				
Pig 54	I	u-15	I	NA	NA			
Pig 55	I	u-16	I	I				
Pig 58	I	I	u-4	u-4				
Pig 59	I	u-17	III	NA	NA			
Pig 60	I	u-13	I	NA	NA			
Pig 61	u-26	u-4	I	NA	NA			
Pig 62	I	u-4	I	u-1				
Pig 63	I	I	III	NA	NA			
Pig 64	I	u-15	III	NA	NA			
Pig 65	I	u-16	NA	NA	II			
Rat 1	I	NA	NA	III	I			
Rat 4	I	I	u-4	I				
Cat 1	I	u-3	III	II				

^a a and b represent the two possible allelic types for samples with double infections

^b I, II or III = allelic sequence from a type I, II or III strain, u-(n)= nonarchetypal allele

^c Red, blue or green cells = type I, II or III background

^d NA = no amplification for that locus

Table 2. MLST data at 16 loci obtained from TgCatMx6 and TgPigMx1 strains. Polymorphisms of the DNA sequences at loci A) C22-8, C29-2, HP, L358, PK1; B) SAG3, SAG1, SAG2, BTUB and C) GRA6, EF, UPRT1, UPRT7 and APICO. The published sequencing data of TgGoatUS20 was also included (Dubey *et al.*, 2011)

A)

Chromosome Ib		Chromosome III		Chr. IV	Chr. V	Chromosome VI	
Locus	C22-8	C29-2	HP	L358	PK1		
Position ^a	78 108 180 388 Allele ^b	50 69 263 373 374 407 437 Allele	215 302 304 428 Allele	188 236 358 Allele	75 92 221 269 419 506 531 607 712 783 800 825 Allele		
Consensus ^c	A A T G	C A C T C G C	C C G T	G C A	C G C G T C T G C		
GT1	. . C A I	. T . G . . T I	 I	C . . I	. A G T . . T I		
ME49	 II	T . T. . . . II	 II	. T G II	G . A. C . . II		
VEG	T G . . III	 C . III	T A A C III	. . . III	. . . - A T A . . . T . III		
TgCatMx6	 II	. . T . G C T u-1	 I/II	. . . III	G . A C . . II		
TgPigMx1	T G . . III	 C T u-2	NA ^d NA NA NA NA	. . . III	. A G T . . T I		
TgGoatUS20			 I/II				

B)

Chromosome VII										Chromosome VIII										Chromosome IX																	
Locus		SAG3								SAG1					Alt-SAG2			3' + 5' SAG2				BTUB															
Position		44	64	68	100	107	109	116	124	139	Allele	33	51	86	103	196	284	Allele	15	258	398	409	418	Allele	26	170	190	60	Allele	22	52	117	154	156	317	Allele	
Consensus		C	G	A	T	G	G	C	C	A		G	T	C	G	G	C		T	T	C	C	G		C	C	T	T		C	C	C	C	G	C		
GT1		.	.	.	.	.	.	A	G	.	I	A	C	T	C	A	T	I	.	.	.	.	.	I	.	.	.	.	I	A	.	.	.	.	T	I	
ME49		T	A	G	.	A	.	.	.	G	II	.	.	.	.	.	.	II	.	G	A	G	C	II	T	G	C	.	II	.	G	G	G	C	.	II	
VEG		.	.	.	C	.	A	.	.	.	III	.	.	.	.	.	.	III	C	.	.	.	.	III	.	.	.	C	III	.	.	.	.	.	.	III	
TgCatMx6		.	.	.	C	.	A	.	.	.	III	A	C	T	C	A	T	I	.	.	.	G	C	u-3	.	.	.	C	u-1	.	.	G	G	C	.	u-1	
TgPigMx1		.	.	.	C	.	A	.	.	.	III	A	C	T	C	A	T	I	C	.	.	.	.	III	.	.	.	C	III	.	.	.	.	.	.	III	

C)

Chromosome X										Chromosome XI										Apicoplast				
Locus		GRA6					EF					UPRT1					UPRT7					Apico		
Position	113 143 178 234 243 Allele	145 254 349 427 487 574 Allele	57 111 132 136 142 269 Allele	136 164 294 368 469 573 Allele	115 492 Allele																			
Consensus	C T C G A	C T G T C G	G C T G G C	T A T C A A	T C																			
GT1	. G . . . I	. . . C . . I	. A C . C T I	G G C . G G I	. . I																			
ME49	T . . . G II	A C A . T A II	 II	 II	C . II																			
VEG	. . T A . III	 III	 III	 III	. T III																			
TgCatMx6	T . . . G II	 III	C A C C C . u-1	. G . T . . u-1	. . I																			
TgPigMX1	. G . . . I	NA NA NA NA NA NA NA	NA NA NA NA NA NA NA	 II/III	. T II																			
TgGoatUS20	T . . . G II	. . . C . NA I	C A C C C . u-1	. G . T . . u-1																				

^a Numerical positions refer to the variable sites identified in the alignment in MEGA 6.06

^b I, II or III = allelic sequence from a type I, II or III strain, u-(n)= nonarchetypal allele

^c . = identity to the consensus sequence, grey cells= SNP not shared by the archetypal types I, II or III alleles

^d NA= no amplification for that locus

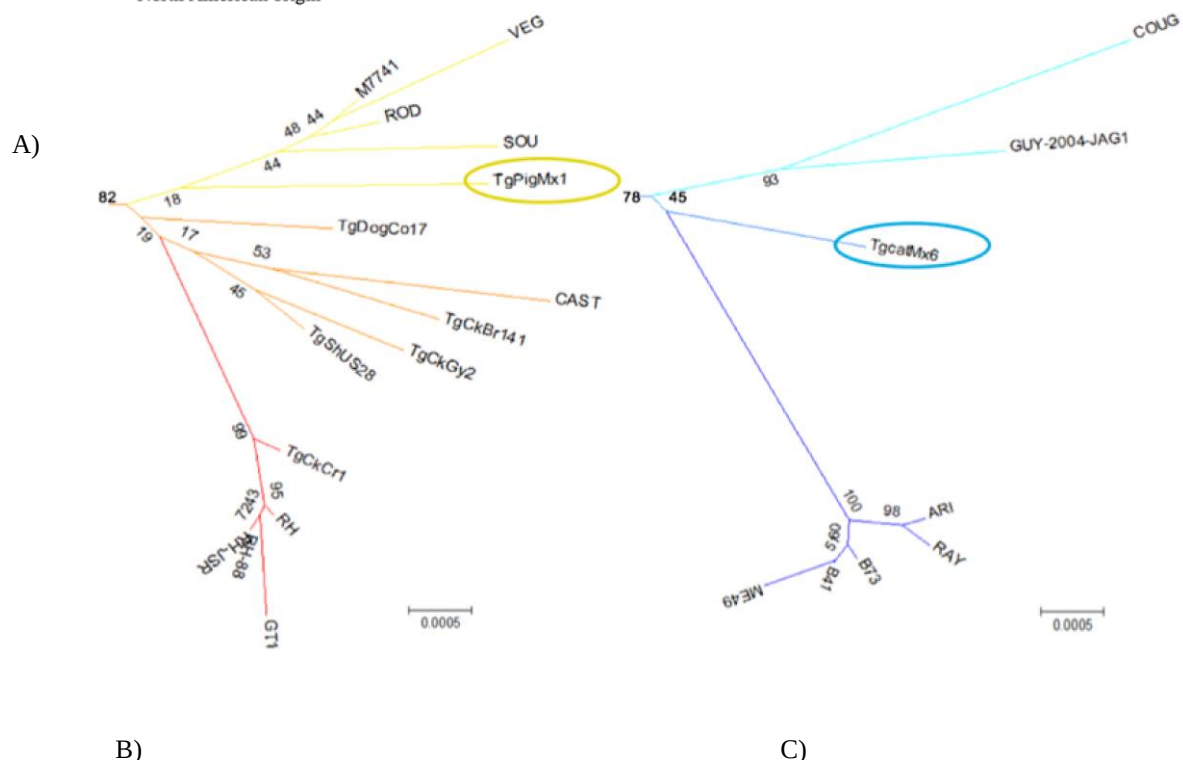
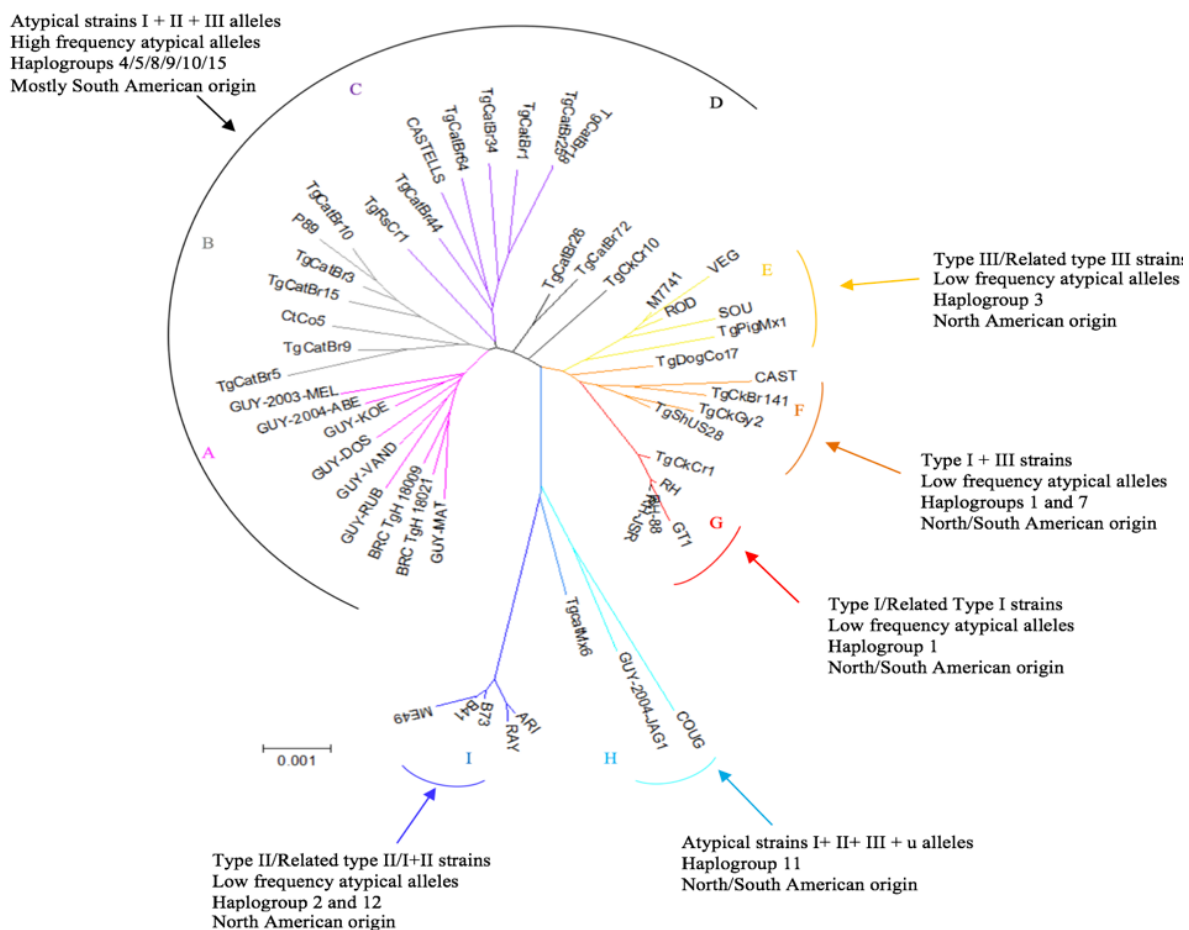


Figure 2. Clustering of *T. gondii* strains using sequencing data from 16 loci. 1: phylogenetic tree constructed using the Neighbour-Joining method. The length of the branches was drawn to a scale of evolutionary distance (number of base substitutions per site). The evolutionary distance was calculated using the Maximum Composite Likelihood Method. Colour and letters A) Illustrate the segregation in clusters. B) and C) Detail of the E, F, G, H, I branch. The number on the branches indicate the bootstrap value (1000 replicates). Blue and yellow circles shown the position of TgCatMx6 and TgPigMx53 in the tree.

SUPPLEMENTARY MATERIALS

S1. Description of the allelic variants for SAG1, Alt-SAG2, SAG3 and GRA6 loci. Polymorphisms of the DNA sequences at loci

A) SAG1, B) SAG2, C) SAG3 and D) GRA6.

A)

Position ^a	29	33	37	46	49	51	56	70	84	86	98	103	112	114	128	133	147	150	154	182	186	191	196	211	212	239	250	260	271	284	289	300	322	340	342	352	Allele ^b
Consensus ^c	T	G	T	A	G	T	A	T	C	C	C	G	T	T	T	G	T	T	T	C	T	T	G	A	A	G	G	T	T	C	G	C	G	A	A	G	
GT1	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	I
ME49	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	II
VEG	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	III
Pig (n) ^d Rat 1-4 Cat 1	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	I
Pig 48b ^e	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	II-III
Rat 5	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	C	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-1
Pig 1	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	G	.	.	.	.	T	.	.	.	.	.	.	u-2
Pig 3	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	C	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-3
Pig 5	.	A	.	.	.	C	G	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-4
Pig 8	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	A	.	.	.	.	.	u-5
Pig 11	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	T	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-6
Pig 14	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	T	.	.	.	.	.	T	.	.	.	.	.	.	u-7
Pig 15b	C	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-8
Pig 16b	.	A	.	.	.	C	.	.	T	.	C	C	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	T	.	.	.	.	u-9
Pig 19a ^f	.	A	.	.	.	C	.	A	.	T	.	C	.	.	.	.	.	.	.	.	.	.	A	.	.	.	R	W	.	T	.	.	.	.	.	.	u-10
Pig 19b	.	A	.	.	.	C	.	A	.	T	.	C	.	.	.	.	.	.	.	.	.	.	A	.	.	.	R	W	.	T	.	.	.	.	.	.	u-11
Pig 22	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	C	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-12
Pig 23	.	A	.	.	.	C	.	.	T	T	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-13
Pig 24	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	C	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-14
Pig 27	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-15
Pig 30	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	T	.	.	u-16
Pig 33	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	C	T	.	.	.	.	.	.	u-17
Pig 37	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	A	.	.	A	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-18
Pig 38a	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-19
Pig 38b	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	G	.	u-20
Pig 41,51	.	A	.	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	C	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-21
Pig 42	.	A	.	.	.	C	.	.	T	T	C	.	.	.	.	C	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-22
Pig 44	.	A	A	.	.	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-23
Pig 52a ^f	.	A	.	.	.	C	.	.	T	.	C	.	.	Y	.	.	.	.	.	.	.	.	A	.	.	.	.	.	T	.	.	.	.	.	.	S	u-23
Pig 52b	.	A	.	.	.	C	.	.	T	.	C	.	Y	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	T	.	.	.	.	.	.	S	u-24
Pig 57	.	A	.	G	C	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	A	.	.	.	u-25
Pig 61	.	A	.	G	C	C	.	.	T	.	C	.	.	.	.	.	.	.	.	.	.	.	A	.	.	.	.	.	.	T	.	.	.	.	.	.	u-26

B)

Position	15	30	41	42	62	86	109	126	151	175	220	225	227	229	258	281	317	365	387	394	395	398	409	418	437	459	465	466	Allele
Consensus	T	A	T	T	T	T	C	T	T	G	C	T	A	T	T	T	G	A	T	T	T	C	C	G	A	T	G	A	
GT1	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	I
ME49	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	A	G	C	.	.	.	.	II
VEG	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	III
Rat 4 Pig 4,7,58,63	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	I
Pig 53	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	III
Cat 1 Rat 5 Pig 10,14,39,52,57	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	C	.	.	.	.	u-1
Pig 2	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	C	.	.	.	.	u-2
Pig 5	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	G	C	.	.	.	.	u-3
Pig 15,20a,25a,28, 38a,40,44,46,61,62,66	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	C	.	.	G	.	u-4
Pig 19	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	C	.	.	.	.	u-5
Pig 20b	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	C	.	.	G	.	u-6
Pig 25b,38b	.	.	.	.	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	C	.	.	G	.	u-7
Pig 29	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.	.	.	.	.	.	.	.	.	u-8
Pig 30	.	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	u-9
Pig 35a ^f	.	.	.	.	.	.	.	A	.	.	C	R	.	.	.	.	.	.	.	.	.	.	G	C	.	.	W	.	u-10
Pig 35b	.	.	.	.	.	.	.	A	.	.	C	R	.	.	.	.	.	.	.	.	.	.	G	C	.	.	W	.	u-11
Pig 37	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	.	.	.	.	.	u-12
Pig 47,60,65	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	.	.	u-13
Pig 50	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	.	.	.	G	C	G	.	.	.	u-14
Pig 54	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	C	.	.	.	u-15
Pig 55	.	.	.	.	.	.	.	.	A	.	.	.	A	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	u-16
Pig 59	.	.	.	C	C	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	.	G	C	.	.	.	.	u-17
Pig 64	.	.	.	.	.	.	.	.	.	T	.	.	.	.	.	.	.	C	.	C	.	.	G	C	.	.	.	.	u-18

C)

Position	44	56	64	68	100	107	109	116	119	124	139	141	185	Allele
Consensus	C	A	G	A	T	G	G	C	G	C	A	A	G	
GT1	.	.	.	.	.	.	.	A	.	G	.	.	.	I
ME49	T	.	A	G	.	A	.	.	.	.	G	.	.	II
VEG	.	.	.	.	C	.	A	.	.	.	.	.	.	III
Pig 7a,30,37,40,41,54,55,60-62	.	.	.	.	.	.	.	A	.	G	.	.	.	I
Cat 1 Rat 1 Pig 20,29,39,53,56,59,63,64	.	.	.	.	C	.	A	.	.	.	.	.	.	III
Rat 4	.	.	.	.	C	.	A	.	.	.	.	.	C	u-1
Pig 7b	.	.	.	.	.	.	.	A	.	G	G	.	.	u-2
Pig 27	.	G	.	.	C	.	A	.	.	.	.	.	.	u-3
Pig 58	.	.	.	.	.	.	.	A	.	G	.	G	.	u-4

D)

Position	43	93	113	116	120	143	152	178	179	222	223	234	243	278	Allele
Consensus	C	A	C	C	G	T	T	C	T	C	A	G	A	C	
GT1	.	.	.	.	.	G	.	.	.	.	.	.	.	.	I
ME49	.	.	T	.	.	.	.	.	.	.	.	.	G	.	II
VEG	.	.	.	.	.	.	.	T	.	.	.	A	.	.	III
Rat 1,4 Pig 22,27,28,53,55	.	.	.	.	.	G	.	.	.	.	.	.	.	.	I
Cat 1 Pig 48,49,65	.	.	T	.	.	.	.	.	.	.	.	.	G	.	II
Pig 21	T	.	T	.	.	.	.	.	.	.	.	.	G	T	u-1
Pig 23	.	.	.	.	.	G	.	.	.	.	.	G	.	.	u-2
Pig 25	.	.	.	.	.	.	.	.	.	.	.	.	G	.	u-3
Pig 30,58	.	.	T	.	.	.	.	.	A	.	.	.	G	.	u-4
Pig 35	.	G	.	.	.	G	.	.	.	.	.	.	.	.	u-5
Pig 37	.	.	.	T	.	G	C	.	.	.	.	.	.	.	u-6
Pig 38	.	.	.	.	.	G	.	.	T	.	.	.	.	.	u-7
Pig 46,50	.	.	T	.	A	.	.	.	.	.	.	G	.	.	u-8
Pig 62	.	.	.	.	.	.	.	.	.	.	.	.	.	.	u-9

^a Numerical positions refer to the variable sites identified in the alignment in MEGA 6.06

^b I, II or III = allelic sequence from a type I, II or III strain, u-(n)= nonarchetypal allele

^c . = identity to the consensus sequence, grey cells= SNP not shared by the archetypal types I, II or III alleles

^d Pig 2, 4, 6-7, 9-10, 12-13, 15a, 16a, 17-18, 20-21, 25-26, 28-29, 31-32, 34-36, 39-40, 43, 45-47, 48a, 49-50, 53-56, 58-60, 62-68

^e a and b represent the two possible allelic types for samples with double infections

^e Y= C or T, R= A or G, W= A or T, S= G or C

S2. Translated protein sequence Alt-SAG2. Blue colour highlights the samples which present the novel amino acid substitution (from lysine to glutamic acid) shared by 11 animals. Red highlights amino acid substitutions derived from the archetypal types I, II and III. Green colour highlights novel, but not shared amino acid substitutions. COLOUR PRINT

GT1	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
M49	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
VEG	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Rat 4	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Rat 5	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Cat 1	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 2	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 4	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 5	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 7	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 10	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 14	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 15	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 19	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 20	IILCVVS	RVAVLGTEL*	LCTIAV*HNL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 25	IILCVVS	RVAVLGTEL*	LCTIAV*HNL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 28	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 29	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 30	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 35	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 37	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 38	NNNNVN	RVAVLGTEL*	LCTIAV*HNL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 39	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 40	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 44	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 46	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 47	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 50	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 52	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 53	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 54	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 55	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 57	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 58	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 59	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 60	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 61	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 62	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 63	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 64	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 65	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 66	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV
Pig 72	IILCVVS	RVAVLGTEL*	LCTIAV*HLL	SRSNLCLVGT	MSFSKTTSLA	SLALTGLFVV

GT1	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
M49	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
VEG	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Rat 4	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Rat 5	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Cat 1	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 2	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 4	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 5	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 7	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 10	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 14	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 15	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 19	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 20	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 25	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 28	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 29	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 30	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 35	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS

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Pig 50	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 52	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 53	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 54	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 55	FKFALASTTE	TPAPIE S TAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 57	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 58	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
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Pig 62	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 63	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 64	FKFALASTTE	TPA S IECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 65	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 66	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS
Pig 72	FKFALASTTE	TPAPIECTAG	ATKTVDPASS	GSVVFQCGDK	LTISPSGEGD	VFYGKECTDS

GT1	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
M49	RKLTTVLPGA	VL K AKVEQPP	KGPATYTLSY	DGTPEK
VEG	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Rat 4	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Rat 5	RKLTTVLPGA	VL T ANVEQPP	KGPATYTNNN	DGNNNN
Cat 1	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 2	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 4	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 5	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 7	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 10	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 14	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 15	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 19	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 20	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 25	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 28	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 29	R L TTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 30	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 35	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPNK
Pig 37	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 38	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 39	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 40	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 44	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 46	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 47	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 50	RKLTTVLPGA	VLTAKVEQPP	KGPAT C TLSY	DGTPEK
Pig 52	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 53	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 54	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 55	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 57	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 58	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 59	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEK
Pig 60	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 61	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 62	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 63	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 64	RKLTTVLPGA	V S TAKVEQPP	KGPATYTLSY	DGTPEK
Pig 65	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK
Pig 66	RKLTTVLPGA	VLTAKVEQPP	KGPATYTLSY	DGTPEE
Pig 72	RKLTTVLPGA	VLTAKVQPPA	KGPATYTLSY	DGTPEK

S3. Origin, source and haplogroup of the 48 prototypic American isolates of *T. gondii*. Sequence data obtained from ToxoDB

(<http://toxodb.org/toxo/>).

Isolate	Country	Source	Haplogroup ^a
1. GT1	USA	Goat	1
2. ME49	USA	Sheep	2
3. VEG	USA	Human	3
4. ARI	USA	Human	12
5. B41	USA	Bear	12
6. B73	USA	Bear	2
7. CAST	USA	Human	7
8. CASTELLS	Uruguay	Sheep	16
9. COUG	Canada	Cougar	11
10. CtCo5	Colombia	Cat	15
11. GUY-KOE	French Guiana	Human	5
12. GUY-MAT	French Guiana	Human	5
13. GUY-DOS	French Guiana	Human	10
14. GUY-2003-MEL	French Guiana	Human	5
15. GUY-2004-ABE	French Guiana	Human	5
16. GUY-2004-JAG1	French Guiana	Jaguar	11
17. M7741	USA	Sheep	3
18. P89	USA	Pig	9
19. RAY	USA	Human	12
20. RH	USA	Human	1
21. RH-88	USA	Human	1
22. RH-JSR	USA	Human	1
23. ROD	USA	Human	3
24. RUB	USA	Human	5
25. SOU	USA	Human	2
26. TgCatBr1	Brazil	Cat	4
27. TgCatBr10	Brazil	Cat	8
28. TgCatBr15	Brazil	Cat	9
29. TgCatBr18	Brazil	Cat	4
30. TgCatBr25	Brazil	Cat	8
31. TgCatBr26	Brazil	Cat	6
32. TgCatBr3	Brazil	Cat	9
33. TgCatBr34	Brazil	Cat	4
34. TgCatBr44	Brazil	Cat	4
35. TgCatBr5	Brazil	Cat	8
36. TgCatBr64	Brazil	Cat	8
37. TgCatBr72	Brazil	Cat	6
38. TgCatBr9	Brazil	Cat	6
39. TgCkBr141	Brazil	Chicken	7
40. TgCkCr1	Costa Rica	Chicken	1
41. TgCkCr10	Costa Rica	Chicken	15
42. TgCkGy2	French Guiana	Chicken	3
43. TgDogCo17	Colombia	Dog	1
44. TgH18009	French Guiana	Human	10
45. TgH18021	French Guiana	Human	10
46. TgRsCr1	Costa Rica	Toucan	15
47. TgShUS28	USA	Sheep	3
48. VAND	French Guiana	Human	10

^a Haplogroup number retrieved from Lorenzi *et al.*, (2016)