

**Supplementary materials.**

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>PCV2 Chile Rancagua2007 Cap gene
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GATATACTATCAAGCGAACCACAGTCAAAACGCCCTCCTGGGCGGTGGACATG
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TCTGTGCCCTTTGAATACTACAGAATAAGAAAGGTTAAGGTTGAATTCTGGCCC
TGCTCCCCGATCACCCAGGGTGACAGGGGAGTGGGCTCCAGTGCTGTTATTCTA
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TACTCCTCCCGCCATAACCATAACCCAGCCCTTCTCCTACCACTCCCGCTACTTTA
CCCCCAAACCTGTCCTAGATTCCACTATTGATTACTTCCAACCAAACAACAAAA
GAAATCAGCTGTGGCTGAGACTACAAACTGCTGGAAATGTAGACCACGTAGGC
CTCGGCACTGCGTTCGAAAACAGTATATACGACCAGGAATACAATATCCGTGT
AACCATGTATGTACAATTCAGAGAATTTAATCTTAAAGACCCCCCACTTAACCC
TAA

>PCV2 Chile Rancagua2007 Cap protein
MTYPRRRYRRRRHRPRSHLGQILRRRPWLVHPRHRYRWRRKNGIFNTRLSRTFGY
TIKRTTVKTPSWAVDMMRFNINDFLPPGGGSNPRSVPFYRIRKVKVEFWPCSPIT
QGDRGVGSSAVILDDNFVTKATALTYDPYVNYSSRHITQPFSYHSRYFTP KPVL D
STIDYFQPNNKRNLWLRLQTAGNVDHVGLGTAFENSIYDQEYNIRVTMYVQFRE
FNLKDPPLNP*
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**Figure S1.** Sequence of a viral isolate of a representative Chilean strain. Up: nucleotide sequence of the gene, "PCV2 Chile Rancagua2007 Cap gene ". Down: amino acid sequence of the Cap protein, "PCV2 Chile Rancagua2007 Cap protein"

**Table S1.** Sequences of porcine circovirus type 2 (PCV2) included in this study. Genbank accession numbers (GAN) and genotypes (G) according to Franzo *et al.* (2015). Asterisk (\*) indicates that both capsid and replicase gene sequences were obtained from the same Genbank entry and used in the concatenated data set.

GAN	G	GAN	G	GAN	G	GAN	G	GAN	G	GAN	G
AB361566	b	AY122275*	b	AY484412*	b	DQ218419*	b	EF190943	b	EF524529*	b
AB361567	b	AY129154	a	AY484413*	b	DQ218420*	b	EF197987	b	EF524539*	d
AB361568	a	AY129155	a	AY484414*	b	DQ218421*	b	EF210106*	b	EF560608	b
AB361569	b	AY146991*	a	AY484415*	b	DQ220733*	b	EF371518	a	EF560609	b
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AB361573	a	AY180397*	a	AY536756*	b	DQ364650*	b	EF371522	a	EF565346*	b
AB361574	a	AY181945*	b	AY556473*	d	DQ397521*	a	EF371523	a	EF565347*	b
AB361576	a	AY181947*	d	AY556475*	b	DQ534442	b	EF371524	a	EF565349*	b
AB361577	a	AY181948*	a	AY556476*	d	DQ629113*	a	EF371525	a	EF565350*	b
AB361582	a	AY188355*	b	AY578327	b	DQ629114*	a	EF371528	b	EF565352*	b
AB361583	a	AY217743*	b	AY579893*	b	DQ648031*	b	EF371529	b	EF565354*	b
AB361584	b	AY256455*	a	AY596822	b	DQ861898*	b	EF371530	b	EF565355*	b
AB361585	b	AY256456*	a	AY596823*	b	DQ861900*	b	EF371531	b	EF565356*	b
AB426905*	a	AY256457*	b	AY604430*	b	DQ861901*	b	EF371532	b	EF565357*	b
AB462382	b	AY256458*	a	AY613854*	b	DQ870484*	a	EF371533	b	EF565358*	b
AB462383	a	AY256459*	a	AY613906	b	DQ910865*	b	EF371534	b	EF565359*	b
AB462384	d	AY256460*	b	AY641542*	b	DQ910866*	b	EF371535	b	EF565360*	b
AB462385	a	AY288133*	b	AY651850*	b	DQ915584*	b	EF371536	b	EF565361*	b
AB462387	b	AY288134*	b	AY672600	a	DQ915585*	b	EF371537	b	EF565362*	b
AB462388	a	AY288135*	a	AY672601	a	DQ915586*	b	EF371538	b	EF565363*	b
AB462389	b	AY291316*	b	AY678532*	b	DQ915587*	b	EF371539	b	EF565364*	b
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AF201311*	b	AY321989*	b	AY686765*	d	EF184222	a	EF394774*	a	EF675234*	b
AF264038*	a	AY321990*	b	AY691169*	b	EF184223	a	EF394775*	a	EF675235*	b
AF264039*	a	AY321991*	b	AY691679*	b	EF184224	a	EF394776*	a	EF675236*	b
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AF264042*	a	AY321996*	b	AY754022*	a	EF184227	b	EF421969*	b	EF675241*	d
AF264043*	a	AY321997*	b	AY849938*	b	EF184228	b	EF421970*	b	EF675242*	b
AF381175*	a	AY321999*	b	AY874163*	b	EF190922	b	EF421971*	b	EF675244*	b
AF381176*	a	AY322000*	b	AY874164*	a	EF190923	b	EF421973*	b	EF990645	d
AF381177*	a	AY322002*	b	AY874165*	a	EF190924	b	EF452350*	b	EU136711*	a
AF454546*	a	AY322003*	b	AY874166*	a	EF190925	b	EF467928	b	EU136712*	b
AF465211*	a	AY322004*	a	AY874168*	b	EF190926	b	EF493837*	b	EU136713*	b
AF520783*	a	AY325495*	a	AY885225	b	EF190928	b	EF493838*	b	EU136714*	b
AF544024*	a	AY424401*	a	AY916791*	b	EF190929	b	EF493839*	b	EU136715*	b
AJ623306*	b	AY424402*	a	AY943819*	d	EF190930	b	EF493840*	b	EU136716*	b
AY094619*	a	AY424403*	a	DQ104419	a	EF190932	b	EF493841*	b	EU136717*	b
AY099495*	a	AY424404*	b	DQ104421*	a	EF190933	b	EF493842*	b	EU136718*	b
AY099496*	a	AY424405*	b	DQ104422*	b	EF190934	b	EF524515*	b	EU136719*	b
AY099497*	a	AY484407*	b	DQ104423*	a	EF190935	b	EF524519*	b	EU136720*	b

AY099498*	a	AY484408*	b	DQ195679*	b	EF190937	b	EF524521*	b	EU148503*	c
AY099499*	a	AY484410*	d	DQ201641*	b	EF190939	b	EF524525*	b	EU148504*	c
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GAN	G	GAN	G	GAN	G	GAN	G	GAN	G	GAN	G
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EU257512*	b	EU909686*	d	FJ667588*	d	GU247988*	b	HM142895*	d	HQ395032*	d
EU257513*	b	EU909688*	b	FJ667589*	b	GU247989*	b	HM142896*	d	HQ395033*	d
EU257514*	b	EU980089	b	FJ667590*	d	GU247990*	b	HM142899*	d	HQ395036*	b
EU257515*	b	EU980090	b	FJ667591*	b	GU247991*	b	HM161710*	d	HQ395037*	d
EU283329*	b	EU980094	b	FJ667592*	b	GU247992*	b	HM161711*	d	HQ395038*	d
EU3469794	b	FJ158603*	b	FJ667593*	b	GU252370*	d	HM535639	b	HQ395039*	b
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EU366324*	b	FJ158607*	d	FJ667596*	b	GU325763*	d	HM565923	b	HQ395043*	d
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EU366326*	b	FJ233908*	a	FJ712216*	d	GU325766*	b	HM623764*	a	HQ395046*	b
EU408780*	b	FJ384965	b	FJ716703*	b	GU325767*	d	HM641752*	b	HQ395048*	d
EU418627*	b	FJ384966	b	FJ716704*	b	GU325768*	d	HM755880	d	HQ395050*	d
EU503031*	b	FJ384967	b	FJ755686	b	GU325769*	d	HM755881	d	HQ395052*	d
EU503032*	b	FJ384968	b	FJ870967*	a	GU325770*	d	HM776437*	d	HQ395053*	d
EU503033*	b	FJ384969	b	FJ870968*	a	GU370064*	a	HM776438*	b	HQ395054*	a
EU503034*	b	FJ426398*	d	FJ870969*	b	GU574204	d	HM776439*	d	HQ395055*	d
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JF317568*	b	JN006445	d	JN660055*	d	JX948781*	d
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JF317575*	b	JN006452	b	JN662684	b	JX948784*	b
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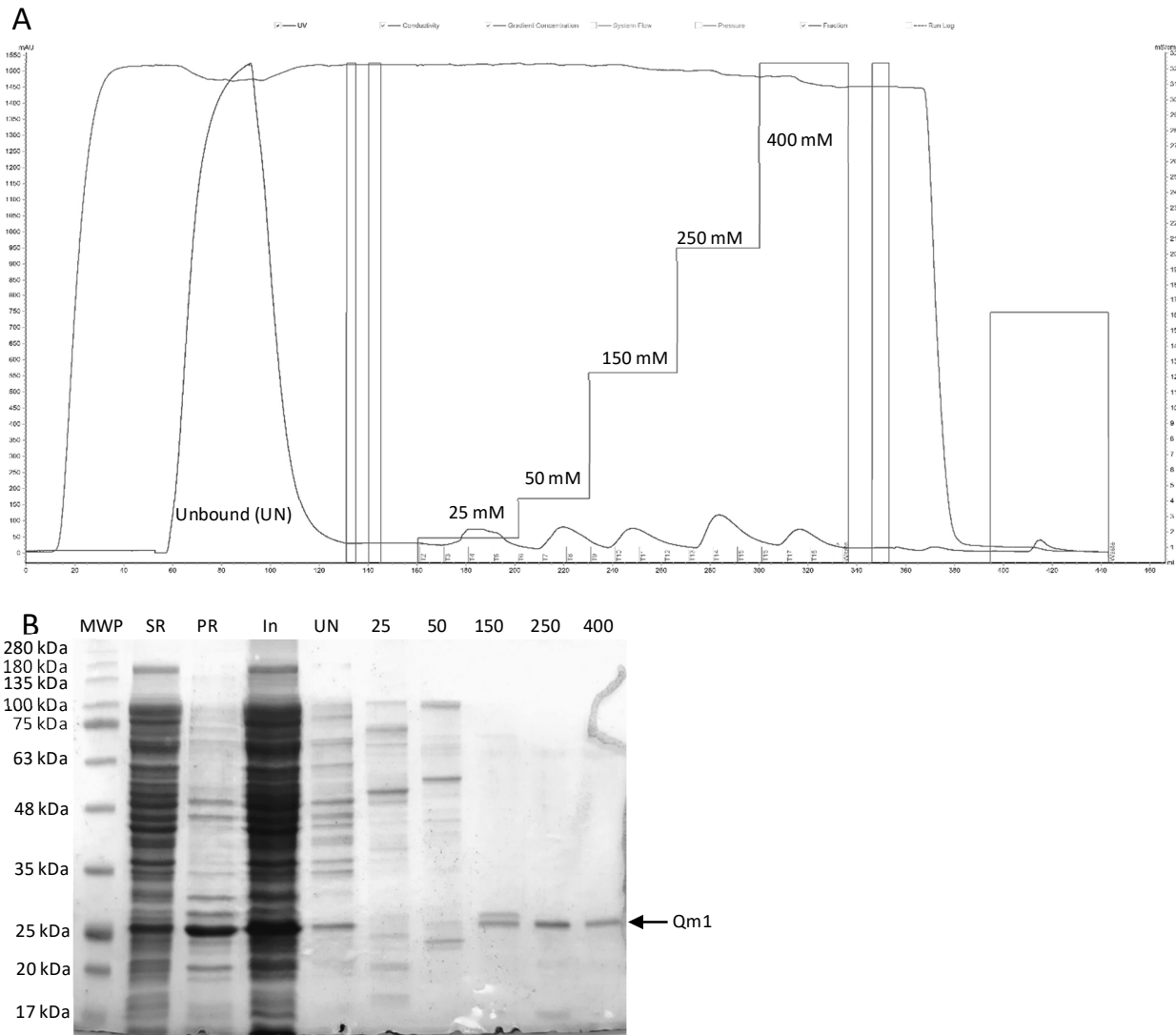
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JF927981	b	JN382188	d	JX679498*	d		

**Table S2.** Structural analysis by online TopSearch software. The S score corresponds to the number of residues that have structural similarity between each alignment.  $S_q$ : indicates the percentage of homologous residues of the structure 3r0r with each of the alignments.  $S_t$ : indicates the percentage of homologous residues of each structural homolog aligned with pdb: 3r0r.

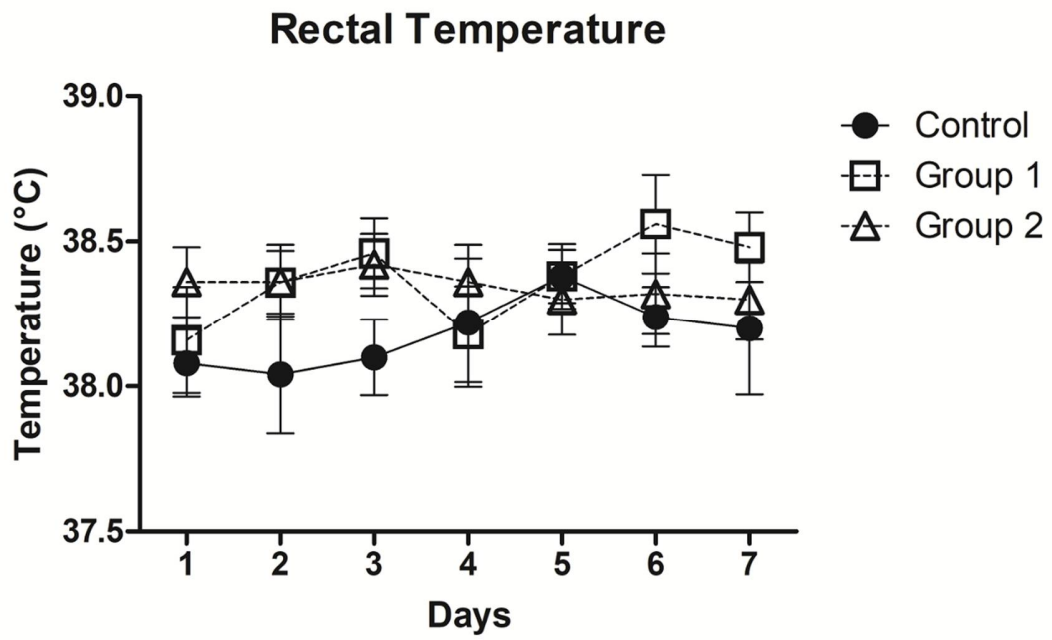
PDB ID	Alignment size	S	$S_q$	$S_t$
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1aym	114	93.6	48.2	11.6
1f2n	136	114.4	59.0	19.4

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<u>1C8N C</u>	86	GNSTV	VSNSEL	ILNLT	Pi----	aLAYT	VQSLP	LIATQ
<u>1F2N C</u>	52	SNTW	PLHSV	EFLAD	fkrs---	stsAD	ATTYD	CVPFN
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								slarC
								YSMwK
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		70	80	90	100	110	120	
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								FVTSS
								VWY 151
		130	140	150	160	170	180	
<u>gi 340707970</u>	151	-----	Y-----	-----	HSRY	FTP	KPV	Ldsti
<u>1AYM 1</u>	175	-----	P-----	-----	FPRF	SLP	FLSI	-----
<u>1C8N C</u>	191	ailn	tdvt	ptsA	-----	IYVD	VDV	TRFD
<u>1F2N C</u>	152	-----	Gaeg	chl	sggs	sarna	VVAS	MDCsr
								-----
								vGWK
								Rvtss 185
		190	200	210	220	230		
<u>gi 340707970</u>	185	a-----	GNVD	HVGL	GTAF-	ENSI	---YD	QE-
<u>1AYM 1</u>	195	dgyd	gdty	ksry	gtvV	TNDM	GTLC	SRI-
<u>1C8N C</u>	222	taaf	aa---	ltaf	dqnq	FCP	CTV	HIGS-
<u>1F2N C</u>	186	ipss	-----	vdpn	vvt	ILP	ARL	AVRS
								IKPT---
								VSDT
								pGKLY
								VIAS
								MV--
								LrDP
								VDP 234

**Figure S2:** Sequences alignment of secondary structure information. Alignment between 3r0r and 1aym, 1c8n and 1f2n proteins. The light gray residues were eliminated from the alignment.

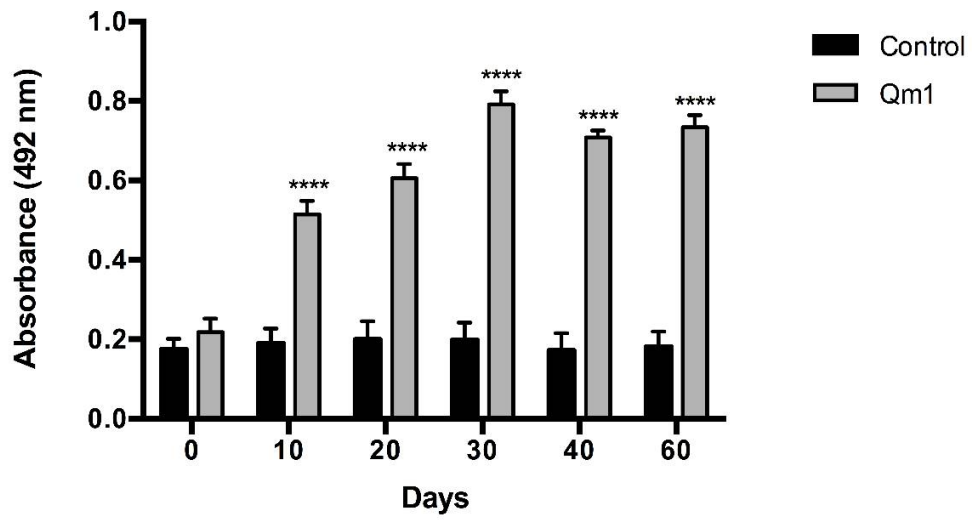


**Figure S3.** Qm1 purification by IMAC. **A)** Chromatogram resulting from the IMAC Qm1 purification. UN: unbound proteins, 25, 50, 150, 250 and 400 mM correspond to the imidazole concentration in the elution buffer respectively. **B)** SDS-PAGE Coomassie blue staining on reducing condition MWP: molecular weight pattern; SR: supernatant of rupture; PR: pellet of rupture; In: initial sample; UN: unbound protein sample; 25, 50, 150, 250 and 400: samples obtained from IMAC purification. 20  $\mu$ L per sample was used in each case in both conditions.



**Figure S4.** Rectal temperature assay. The rectal temperature was measured daily for 7 days. Values are mean  $\pm$  SEM. n=5, Two-way ANOVA and Sidak test without significance different versus control group.





**Figure S5.** Response to Qm1 vaccination in pigs. Total IgG was measured by indirect ELISA, using serum diluted 1:1000 at the indicated days. Values are mean  $\pm$  SEM. n=6, Two-way ANOVA and Sidak test \*\*\*\*p<0.0001 versus the control group