

SUPPLEMENTARY METHODS AND MATERIALS

Table A. SLN, PLB and SERCA PCR-primers for different species (RT-PCR)

SERCA	Forward primer (5'→3')	Reverse primer (5'→3')	bp	T _a	#cycli
Pig	GAGATCGGCATTGCCAT	GAAC TGCTTCATGTTGTTGTA	138	55	23
Rabbit	GGCTGTCAACCAGGAYAAGA	GTGCCAGTCTTGTCA GAGCA	475	56	25
Rat	GAYGAGTTGGGAACAGCT	GAGGTGGTGATGACAGCAGG	194	58	20
Mouse	GAYGAGTTGGGAACAGCT	GAGGTGGTGATGACAGCAGG	194	58	20
PLB					
Pig	AGACAGTGATCTCATATTGGCTGG	GCAAATCAGCAAGAGGCATA	223	52	20
Rabbit	AGAACAGTCCTCTCACATCTGGG	CGATGATGCAGATCAGCAGGAGA	231	54	25
Rat	TGTGACGATCACAGAACGCC	GCAGCAGACATATCAAGATGAG	260	56	20
Mouse	ATGACGACGATTCAAATCTCTTGG	TGGGTTGCAAAGTTAGGCATAA	613	53	22
SLN					
Pig	GAGAATGGAGCGATCCACCC	ACTTGGCAGCCCTTGAGAGC	297	56	20
Rabbit	GAGAATGGAGCGATCCACCC	ACTTGGCAGCCCTTGAGAGC	297	56	20
Rat	GAGGTGGAGAGACTGAGGTCTTGG	GAAGCTCGGGGCACACAGCAG	266	58	20
Mouse	GAGGTGGAGAGACTGAGGTCTTGG	GAAGCTCGGGGCACACAGCAG	266	58	20

bp = number of base pairs; T_a = PCR annealing temperature (°C); #cycli = number of PCR cycles

Table B. Restriction enzymes for ratio-PCR of SERCA1 and SERCA2

SERCA1			SERCA2	
	Res. enzyme	bp	Res. enzyme	bp
Pig	<i>Msp</i> I	101 + 38	<i>Ava</i> II	79 + 58
Rabbit	<i>Bam</i> HI	275 + 200	<i>Eco</i> RI	300 + 175
Rat	<i>Nco</i> I	102 + 92	<i>Mse</i> I	127 + 67
Mouse	<i>Nco</i> I	102 + 92	<i>Mse</i> I	127 + 67

bp = number of base pairs; Res. enzyme = restriction enzyme

Table A. SLN, PLB and SERCA PCR-primers for different species. The primer sequence is shown in 5' → 3' order. The length of the amplified product, the annealing temperature and number of cycles for RT-PCR of each set of primers is indicated. SERCA primers were developed which allow PCR-amplification of both SERCA1 and SERCA2 with the same efficiency.

Table B. Restriction enzymes for ratio-PCR of SERCA1 and SERCA2. After co-amplification of SERCA1 and SERCA2 with RT-PCR, the amplified product was digested with restriction enzymes specific for SERCA1 or SERCA2 cleavage. The choice of restriction enzyme is dependent on the species and SERCA isoform. The length of the digested fragments is indicated in base pairs.