Additional file 2 Predicted consequences of bovine SERCA1 mutations.

Software	Prediction	p.Arg164His (Chianina)	p.Gly211Val (Romagnola)	p.Gly286Val (Romagnola)	p.Arg559Cys (Belgian Blue)
substitution on the structure and	(score of 0.903)	(score 1.000)	(score 0.994)	(score 1.000)	
function of a protein					
Net TurnP	possible changes in the formation	*	predicted beta turn not	*	*
	of Beta-turns		formed in mutant protein		
NetSurfP	surface accessibility and	*	*	changes from buried to	*
	secondary structure			exposed	
CFSSP	secondary structure of protein	*	elimination of a turn (two	elimination of a turn	*
	from the amino acid sequence		beta-sheets joined)		
PoPMuSiC	changes in stability of a given	neutral mutation	destabilizing mutation	destabilizing mutation	destabilizing
	protein or peptide under single-				mutation
	site mutations				
Phyre 2	secondary structure and disorder	*	elimination of a turn	small alpha helix extended	increased disorder in
			(two beta-sheets joined)	(1 residue)	460-472 region
TMHMM /	transmembrane helices and	*	probability decrease in	probability decrease in	*
THMpred	topology of proteins		prediction of a	prediction of a	
			transmembrane domain in the	transmembrane domain in	
			M3 subunit by ca. 20%	the M3 subunit by ca. 20%	

* no change predicted