

**Table S1.** Genomic organisation of porcine *FSCN3*. Coding sequences are shown in uppercase letters and non coding regions in lowercase letters

Exon	Exon size (bp)	Intron size (bp)	3' splice acceptor	5' splice donor
1	>245	1022	none (5' UTR)	CGGAGACAGgtaac
2	696	616	cccagACCTGGGAA	ATCGTCTATggcaa
3	117	2629	cagatGTTGAGGTG	CTTGTCCAGgtgag
4	160	467	tccagAGGCGCCAT	CCATTCCAGgtgag
5	171	474	ttcagGCCCCAAATG	ACTTCCAGGgtaag
6	206	1950	cccagCACAGGGAG	GAATTTTAGgtaag
7	173	none	cccagGTCCTTGGG	CACAAAAGGCCACCCC <sup>a</sup>

<sup>a</sup> The 16 bases directly upstream of the poly(A) tail are indicated; the size of the 3' UTR excluding the poly(A) tail is 138 bp.