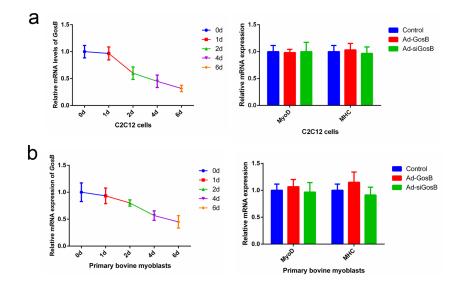
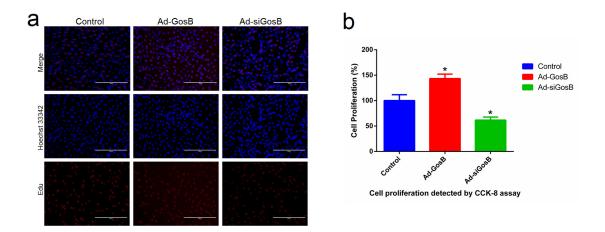
Developmental transcriptome profiling of bovine muscle tissue reveals an abundant GosB that regulates myoblast proliferation and apoptosis

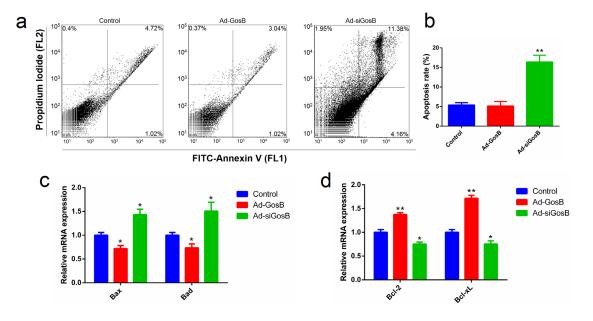
SUPPLEMENTARY FIGURES AND TABLES



Supplementary Figure 1: GosB in myoblasts differentiation.



Supplementary Figure 2: Effects of GosB on primary bovine myoblasts proliferation.



Supplementary Figure 3: Effects of GosB on cell apoptosis in primary bovine myoblasts.

Gene	Primer sequence ¹ (5'-3')	Product length (bp)	Efficiency ²
GosB	F: ACCCACCCTCATCTCTTCCAT	130	2.14
	R: GCCACTGCTGTAGCCACTCA		
GAPDH ³	F: GCAAGTTCCACGGCACAG	249	2.16
	R: GGTTCACACCAATCACAA		
<i>GAPDH</i> ^₄	F: AGGACACTTGTCATCTCATTC	169	2.18
	R: TTGGAGTCAGGTTCTCTCTTGTA		
MYOG	F: CAAATCCACTCCCTGAAA	93	2.13
	R: GCATAGGAAGAGATGAACA		
MYOD ³	F: GGAAGGGAAGAGCAGAAG	82	1.98
	R: AAGGACTACAACAACAACAAC		
MYOD⁴	F: CCGCTCCGCGACGTAGACTTGA	92	2.03
	R: GAGTCGAAACACGGGTCATCATA		
MHC ³	F: CAATAAACTGCGGGCAAAGAC	75	2.01
	R: CTTGCTCACTCCTCGCTTTCA		
MHC ⁴	F: TGCTCATCTCACCAAGTTCC	150	1.99
	R: CACTCTTCACTCTCATGGACC		
IGFBP3	F: GCGCCCTTACCTGCTACCGT	175	2.16
	R: GCTGTCCTTGGCATGACCTTTCT		
P53	F: TGAACCGCCGACCTATCC	95	2.1
	R: GCAGGCACAAACACGAACC		
Bcl-xL	F: TCGGGATGGAGTAAACTGGG	65	2.2
	R: CCACGCACAGTGCCCC		
Bad	F: GCAGCCACCAACAGTCATCAT	202	1.87
	R: CAAACTCATCGCTCATCCTTCG		
cyclinD1	F: TCTACACTGACAACTCTATCCG	304	1.76
	R: TAGCAGGAGAGGAAGTTGTTGG		
Caspase-3	F: TGTCATCTCGCTCTGGTACG	201	2.02
	R: AAATGACCCCTTCATCACCA		
Bcl-2	F: GGTGGTGGAGGAACTCTTCA	160	2.23
	R: CAGATGCCGGTTCAGGTACT		
Bax	F: GAAGCTGAGCGAGTGTCTCC	229	1.98
	R: GATCAGCTCGGGGCACTTTAG		

Supplementary Table 1: Primers designed for quantitative real time PCR (qPCR)

 ${}^{1}F$ = forward primer; R = reverse primer.

²The PCR efficiency was determined by $[10^{(-1/slope)}]$; the slope was obtained by the 7-point standard curve (with a minimum R² of 0.99).

³ Primers for real-time PCR of mouse.

⁴ Primers for real-time PCR of cattle.

Supplementary Table 2: List of differentially expressed genes identified in bovine skeletal muscle at two developmental stages

See Supplementary File 1

Supplementary Table 3: 157 terms that were found to be significantly enriched in the category 'molecular function' according to Gene Ontology analysis

See Supplementary File 2

Supplementary Table 4: 153 terms that were significantly enriched in the category 'cellular component' according to Gene Ontology analysis

See Supplementary File 3

Supplementary Table 5: 287 terms that were significantly enriched in the category 'biological processes' according to Gene Ontology analysis

See Supplementary File 4

Supplementary Table 6: 46 genes related to muscle cell proliferation and differentiation that were significantly differentially expressed in two developmental stages of bovine muscle tissue

See Supplementary File 5