Table 1. Muscle histological, gene expression. protein abundance, and DNA methylation analysis of the skeletal muscle of piglets from sows fed with (MET) or without (CON) a methylation blend supplemented diet. Mean values ± standard error (SE).

Item	**Treatments**		***P – value*[1]**
	CON	**MET**	
	Muscle histology		
Fiber number, 40X magnification	701 ± 57.7	713 ± 59.9	0.876
Fiber size, µm	55.5 ± 2.4	60.5 ± 2.5	0.093
	***Gene expression*[2]**		
MyoG	7.67 ± 0.25	7.88 ± 0.26	0.497
MyoD	7.43 ± 0.18	7.58 ± 0.19	0.564
MRF4	8.11 ± 0.14	8.39 ± 0.15	0.115
IGFIR	7.14 ± 0.20	7.14 ± 0.20	0.988
IGF2R	7.04 ± 0.13	7.23 ± 0.14	0.180
MSTN	7.90 ± 0.26	7.64 ± 0.28	0.486
	***Protein abundance*[3]**		
PDGFRα	0.20 ± 0.06	0.12 ± 0.06	0.405
DLK1	0.47 ± 0.13	0.22 ± 0.14	0.185
PAX7	0.34 ± 0.11	0.06 ± 0.11	0.058
	DNA methylation		
5-methyl-2′-deoxycitidine	8.50 ± 0.90	10.8 ± 0.92	0.061

[1] Significances were declared at p-value ≤ 0.05 and trends when $0.05 < p < 0.10$.

[2] RT-qPCR analysis was used to determine gene expression of the markers myogenin (*MyoG),* myogenic differentiation 1 (*MyoD*), muscle-specific regulatory factor 4 (*MRF4*), insulin like growth factor 1 receptor (*IGF1R*), insulin like growth factor 2 receptor (*IGF2R*), and myostatin (*MSTN*). Results are expressed relative to 18S gene (arbitrary units).

[3] Western Blotting analysis was used to determine protein abundance of the markers plated derived growth factor receptor alpha (PDGFRα), protein delta homolog 1 (DLK1), and paired box 7 (PAX7). The housekeeping protein used to normalize the abundance of target protein was α-tubulin.