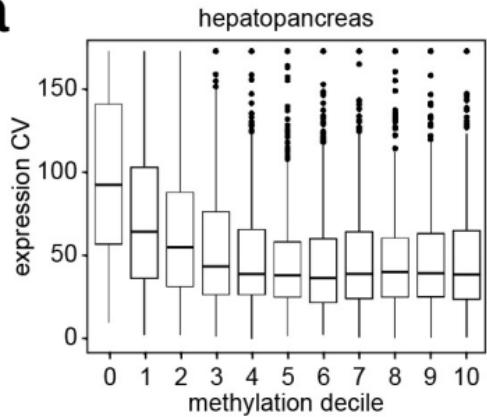


**a****abdominal musculature**

This box plot shows the coefficient of variation (CV) of gene expression across ten methylation deciles for the abdominal musculature. The y-axis ranges from 0 to 150. Median CV values are generally higher than in the hepatopancreas, with most deciles showing medians between 50 and 100.

methylation decile	median expression CV
0	~100
1	~80
2	~90
3	~70
4	~70
5	~80
6	~80
7	~70
8	~80
9	~90
10	~85

expression CV

methylation decile

**b**

*EIF3E* homolog (high-methylated)

Genomic tracks for the *EIF3E* homolog. Top: Schematic of the gene structure with exons in purple and a 1 kbp scale bar. Bottom: Bisulfite sequencing tracks for hepatopancreas (hep.) and muscle (musc.) samples, showing high levels of methylation across the entire region.

methylation

hep.

musc.

1 kbp

expression

Bar chart showing expression levels ( $\log_{10}$  TPM) for the *EIF3E* homolog. Hepatopancreas (hep.) has higher expression (~2.2) compared to muscle (musc.) (~2.0).

tissue	expression ( $\log_{10}$ TPM)
hep.	~2.2
musc.	~2.0

$\log_{10}$  TPM

hep.

musc.

*VMO1* homolog (low-methylated)

Genomic tracks for the *VMO1* homolog. Top: Schematic of the gene structure with exons in purple and a 500 bp scale bar. Bottom: Bisulfite sequencing tracks for hepatopancreas (hep.) and muscle (musc.) samples, showing low levels of methylation.

methylation

hep.

musc.

500 bp

expression

Bar chart showing expression levels ( $\log_{10}$  TPM) for the *VMO1* homolog. Hepatopancreas (hep.) has very low expression (~0.1), while muscle (musc.) has moderate expression (~1.8).

tissue	expression ( $\log_{10}$ TPM)
hep.	~0.1
musc.	~1.8

$\log_{10}$  TPM

hep.

musc.