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Differential transcript usage analysis

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We use this protocol and it's working

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Abstract

Differential transcript usage analysis from Kilfeather, Khoo et al., 2024



Protocol

- 1 Differential transcript usage was performed using DRIMSeq (v1.24.0). To consider only genes containing more than 1 isoform, with a minimum level of expression, the following parameters were used: $\text{min_samps_gene_expr} = n * 0.75$, $\text{min_gene_expr} = 10$, $\text{min_samps_feature_expr} = 10$, $\text{min_feature_expr} = 10$, $\text{min_samps_feature_prop} = 10$, $\text{min_feature_prop} = 0.1$.