Cellular Component terms for the longest genes



Supplementary Figure 3A.

Cellular Component terms found associated to genes with the longest transcript length (5%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Molecular Function terms for the longest genes



Supplementary Figure 3B.

Molecular Function terms found associated to genes with the longest transcript length (5%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Cellular Component terms for the smallest genes



Supplementary Figure 3C.

Cellular Component terms found associated to genes with the smallest transcript length (5%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Molecular Function terms for the smallest genes



Supplementary Figure 3D.

Molecular Function terms found associated to genes with the smallest transcript length (5%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Biological Process terms for the top 10% longest genes



Supplementary Figure 3E.

Biological Process terms found associated to genes with the longest transcript length (10%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Cellular Component terms for the top 10% longest genes

axon cell rojection hembrane		receptor complex		or	cell leading edge		cytoplasmic region		
pa		projection		microt		cell-c	cell s	arcolemma	
postsynaptic			actin	assoc	iated	iunction		sarcolemma	
spostsvn	apt	ic	cytoskeleto	ctin	olex	cell-subs	strate	ateral plasma membrane	
specializ	zatio	on	cytos	kelet	on	site of	sarcoplasn	basal part of cell	
neuron synapse	synapse	junction	microtubule	fiber	chromatin	polarized growth		apical part of cell	

Supplementary Figure 3F.

Cellular Component terms found associated to genes with the longest transcript length (10%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Molecular Function terms for the top 10% longest genes

mo	tor		calmodulin binding		guanyl-nucleotide exchange factor activity		insulin receptor binding complex binding	Rho GTPase binding
acti	vitv	7	dynein intermedia	ate	metal ion transmembrane transporter activity	histor bindir	le _{beta-cateni} binding	cell adhesion molecule binding
	protein serine/threonine/tyrosine kinase activity activity	itinyl lase /ity	chain binding		SMAD binding	phospholipid binding	scaffold protein binding	transcription corepressor activity
ac	tin spe	ctrin	extracellula matrix structu	r Iral	PDZ	ion	protein C-terminus binding	proteoglycan binding
bind	ding	ung	constituent	t	binding	binding	promoter binding	p53 binding

Supplementary Figure 3G.

Molecular Function terms found associated to genes with the longest transcript length (10%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Biological Process terms for the top 10% smallest genes



Supplementary Figure 3H.

Biological Process terms found associated to genes with the smallest transcript length (10%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Cellular Component terms for the top 10% smallest genes



Supplementary Figure 3I.

Cellular Component terms found associated to genes with the smallest transcript length (10%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.

Molecular Function terms for the top 10% smallest genes



Supplementary Figure 3J.

Molecular Function terms found associated to genes with the smallest transcript length (10%). The significance level was p<0.05 and the FDR was set at 0.05. FDR estimation was done using the Benjamini–Hochberg method.