

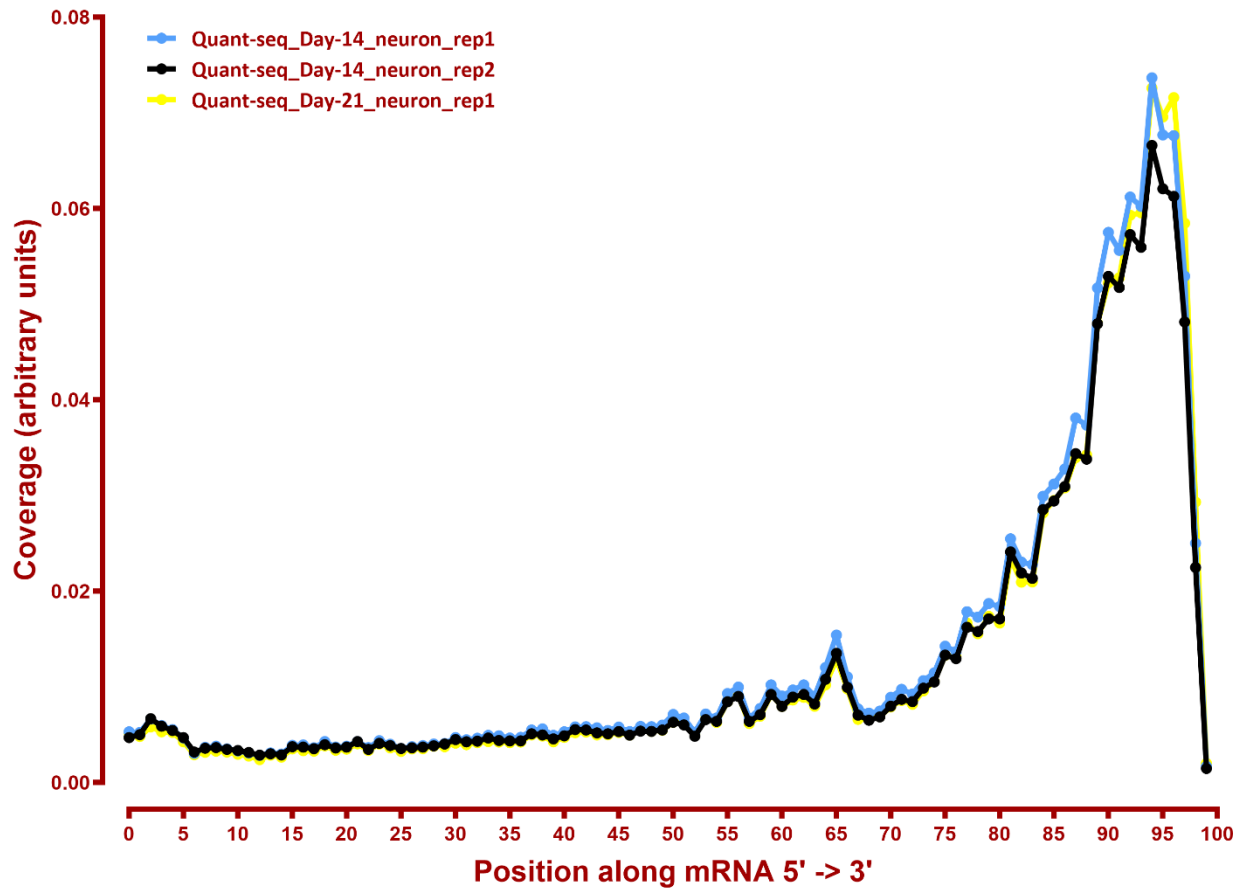
MAPPING STATS

Library	Read Length	Mapping	Species	Raw fragments	Complexity	Unique	Unique Splices	Multi	Multi Splices	Fraction mapped
Quant-seq_Day-14_neuron_rep1	1x51	STAR-2.5.3a	hg38	3,578,694	0.39	2,780,943	110,585	599,195	28,144	0.49
Quant-seq_Day-14_neuron_rep2	1x51	STAR-2.5.3a	hg38	4,548,052	0.39	3,548,413	138,511	745,294	35,461	0.49
Quant-seq_Day-21_neuron_rep1	1x51	STAR-2.5.3a	hg38	3,052,244	0.41	2,395,716	81,444	495,970	20,017	0.49
Quant-seq_Day-21_neuron_rep2	1x51	STAR-2.5.3a	hg38	3,408,820	0.45	2,717,466	78,958	528,284	24,492	0.49
Quant-seq_Day-28_neuron_rep1	1x51	STAR-2.5.3a	hg38	2,966,742	0.47	2,271,150	77,811	524,158	17,618	0.49
Quant-seq_Day-28_neuron_rep2	1x51	STAR-2.5.3a	hg38	4,215,500	0.38	3,353,922	110,360	657,837	25,860	0.49

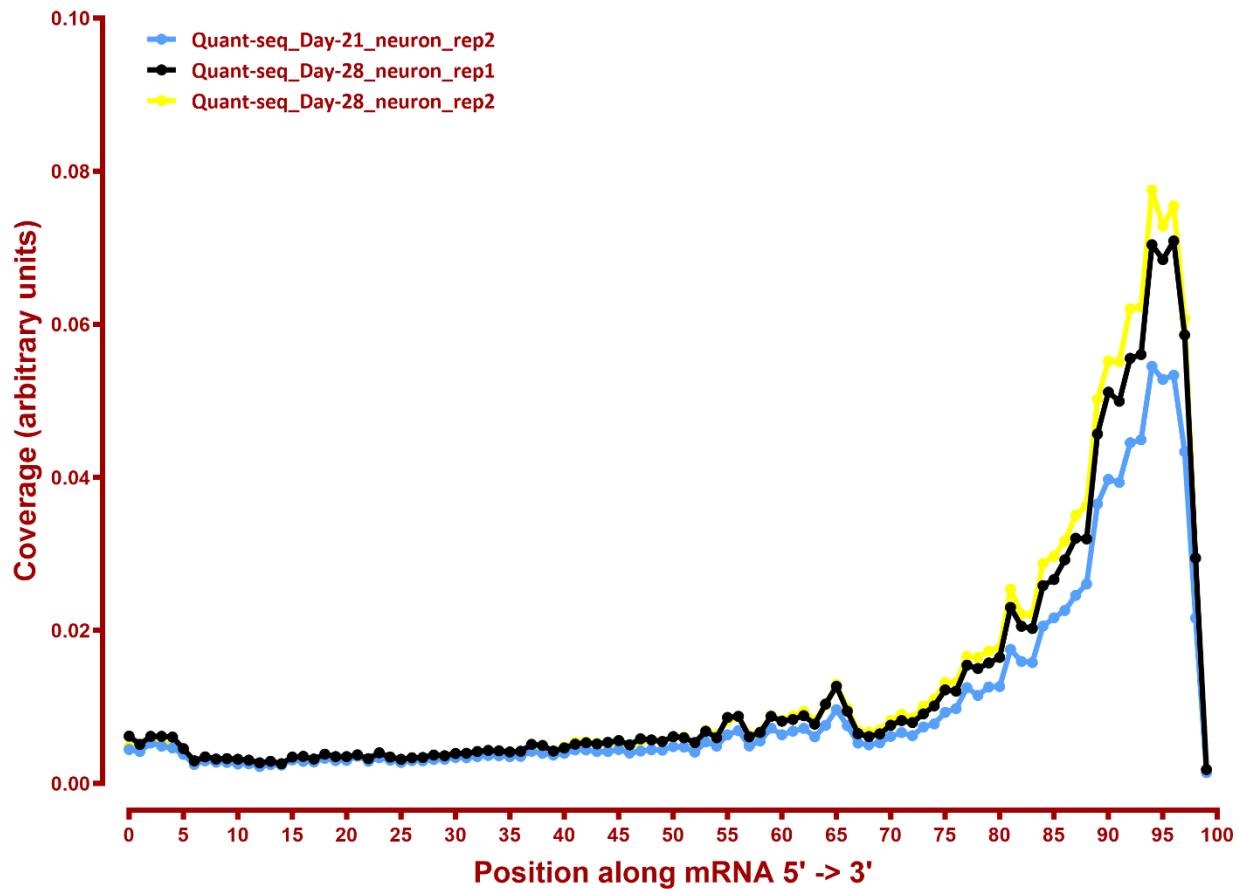
#	Exonic:	Intergenic:	Intronic:
Quant-seq_Day-14_neuron_rep1	0.75	0.09	0.16
Quant-seq_Day-14_neuron_rep2	0.70	0.09	0.21
Quant-seq_Day-21_neuron_rep1	0.72	0.10	0.17
Quant-seq_Day-21_neuron_rep2	0.57	0.11	0.32
Quant-seq_Day-28_neuron_rep1	0.70	0.11	0.19
Quant-seq_Day-28_neuron_rep2	0.74	0.10	0.16

COVERAGE

Coverage of genes; >1000bp, sacCer3



Coverage of genes; >1000bp, sacCer3



QUANTIFICATION:

-- ran Stringtie on artificial GTF files containing the last 300 bp of each gene/transcript