

Table 1 Rates of RNAPII elongation through various regions of different genes

Gene	Region	Length (kb)	Time to transcribe (min)	Elongation rate (kb min ⁻¹)
Utrophin	Ex1-Ex2	111	30	3.70
Utrophin	Ex2-Ex50	174	40	4.35
Utrophin	Ex50-Ex51	101	25	4.04
Utrophin	Ex51-Ex74	173	40	4.33
Utrophin	Ex1-Ex74	561	140	4.01
<i>ITPR1</i>	Ex1-Ex5	133	40	3.33
<i>ITPR1</i>	Ex5-Ex40	105	25	4.20
<i>ITPR1</i>	Ex1-Ex40	238	65	3.66
<i>EFNA5</i>	Ex1-Ex2	243	70	3.47
<i>BCL2</i>	Ex2-Ex3	189	50	3.78
<i>OPA1</i>	Ex1-Ex29	104	25	4.16
<i>IFT80</i>	Ex1-Ex20	142	35	4.06
<i>CTNNBL1</i>	Ex1-Ex16	178	45	3.96
<i>KIFAP3</i>	Ex1-Ex20	153	45	3.40
<i>SLC9A9</i>	Ex1-Ex16	583	160	3.64
Average elongation rate of all genes				3.79 ± 0.26

The elongation rates for full-length genes are shown in bold, and these values were used to compute the average and s.d. of the elongation rate for all the genes. Ex, exon.