

Supplementary Table S1. Main distribution data (mean, median, SD) of the variables analyzed across slow, medium and fast rate genes.

(A) Elongation rates of slow, medium and fast rate categories (**Figure 1D**).

Distribution statistics	mean	median	SD
WT slow	1.741578	1.82	0.6204964
WT medium	3.047892	3.06	0.1980922
WT fast	4.149014	3.7	1.098192
H1-TKO slow	1.621007	1.58	0.5870089
H1-TKO medium	3.189032	3.24	0.270798
H1-TKO fast	4.276415	3.96	0.931213

(B) RNAPII levels at TSS and transcription elongation rate categories (**Figure 2C**).

Distribution statistics	mean	median	SD
WT slow	2.078333	1.796961	1.519135
WT medium	2.910465	2.65276	1.573692
WT fast	3.096705	2.883417	1.808997
H1-TKO slow	2.268346	1.949536	1.835134
H1-TKO medium	3.173807	2.916454	1.704815
H1-TKO fast	3.373803	3.149902	1.88342

(C) CheRNA levels and transcription elongation rate categories (**Figure 2D**).

Distribution statistics	mean	median	SD
WT slow	0.6778481	0.3967252	2.671459
WT medium	1.33611	0.9492873	1.560947
WT fast	1.64832	1.23254	1.59928
H1-TKO slow	0.6964565	0.4051067	2.879507
H1-TKO medium	1.254151	0.8773069	1.424471
H1-TKO fast	1.593306	1.214152	1.542872

(D) RNAPII pausing and transcription elongation rate categories (**Figure 2E**).

Distribution statistics	mean	median	SD
WT slow	4.047321	3.601417	2.444012
WT medium	4.729108	4.440732	2.10001
WT fast	4.494256	4.269058	2.02727
H1-TKO slow	3.804525	3.476232	2.12269
H1-TKO medium	4.547046	4.330952	1.977218
H1-TKO fast	4.429188	4.234174	2.036129

(E) m6A levels on nascent RNAs and transcription elongation rate categories (**Figure 2F**).

Distribution statistics	mean	median	SD
WT slow	1.171492	0.587628	12.37888
WT medium	0.7106489	0.5421378	4.49058
WT fast	0.6123346	0.5321565	0.9104364
H1-TKO slow	0.8846519	0.5113616	11.65021
H1-TKO medium	0.8490443	0.4763778	9.28557
H1-TKO fast	0.7145619	0.4918678	6.316083

(F) H1c and H1d levels and transcription elongation rate categories (**Figure 3B**).

Distribution statistics	mean	median	SD
H1c slow	15.85641	14.51838	18.14094
H1c medium	13.59969	13.08446	4.640742
H1c fast	13.62549	13.08446	4.34269
H1d slow	17.18394	16.14409	19.29534
H1d medium	15.49293	15.14754	3.599277
H1d fast	15.50367	15.14754	3.510373

(G) METTL3 levels and transcription elongation rate categories (**Figure 3C**).

Distribution statistics	mean	median	SD
TSS slow	135.5698	125	119.8566
TSS medium	139.1475	131	60.1823
TSS fast	142.4269	134	56.43799
TTS slow	85.46481	74	73.24369
TTS medium	84.35304	73	74.21311
TTS fast	83.80666	75	44.11249