

Table S1. Numbers of high-throughput sequencing reads obtained for this study. Reads labeled "5' adapter" indicate RT run off from RNA fragment ends, while reads labeled "Mod-stop" indicate reads that lacked the 5' adapter sequence.

Sample	DMS Treatment	Total reads	5' adapter reads	Mod-stop reads
Wild-type Replicate 1	None	6,572,240	1,501,392	4,314,075
	100 mM	5,213,100	1,156,426	3,680,790
<i>rpl26Δ</i> Replicate 1	None	6,318,665	1,396,911	4,233,819
	100 mM	5,438,919	958,087	4,058,273
Wild-type Replicate 2	None	7,374,336	1,941,401	4,885,646
	100 mM	5,476,710	946,597	4,048,461
<i>rpl26Δ</i> Replicate 2	None	6,645,131	1,398,804	4,649,725
	100 mM	6,961,172	1,878,217	4,685,461