

Table S3. Ribosomal RNA positions with increased DMS-dependent modification in the *rpl26Δ* strain. The number of sequence reads indicating modification at each site are shown (RT stops), as are the total number for the gene (Total RT stops). The enrichment ratio is the relative enrichment of RT stops at each position in RNA from DMS treated culture as compared to untreated culture. The results of statistical analysis are given, including both raw (CMH) and Benjamini-Hochberg corrected (B-H) p-values.

Gene	Position	100 mM DMS <i>rpl26Δ</i> 1		100 mM DMS Wild-type 1		100 mM DMS <i>rpl26Δ</i> 2		100 mM DMS Wild-type 2		Enrichment Ratio (DMS /)	CMH P-values	B-H adjusted P-values
		RT stops	Total RT stops	RT stops	Total RT stops	RT stops	Total RT stops	RT stops	Total RT stops			
RDN58	48	750	92250	258	60230	542	119805	337	103487	1.625	0	0
RDN58	52	640	92250	197	60230	396	119805	241	103487	1.755	0	0
RDN58	88	5261	92250	601	60230	6964	119805	1646	103487	4.256	0	0
RDN58	89	8451	92250	1510	60230	9229	119805	2827	103487	3.131	0	0
RDN18	152	43	1001699	12	769580	27	771956	19	672446	1.845	0.0057	0.03664
RDN18	337	73	1001699	31	769580	100	771956	59	672446	1.595	0.0003743	0.004432
RDN18	596	102	1001699	36	769580	63	771956	45	672446	1.658	0.0002278	0.00306
RDN18	753	231	1001699	108	769580	72	771956	50	672446	1.525	1.91E-05	0.0003689
RDN18	764	141	1001699	51	769580	57	771956	54	672446	1.522	0.0006218	0.006432
RDN18	770	202	1001699	82	769580	146	771956	105	672446	1.52	4.51E-06	0.000104
RDN18	777	181	1001699	59	769580	82	771956	73	672446	1.614	8.65E-06	0.000177
RDN18	1198	36	1001699	14	769580	37	771956	15	672446	2.063	0.001068	0.009812
RDN18	1228	87	1001699	37	769580	24	771956	15	672446	1.692	0.002059	0.0167
RDN18	1242	123	1001699	42	769580	65	771956	41	672446	1.833	4.46E-06	0.0001043
RDN18	1485	40	1001699	15	769580	54	771956	33	672446	1.628	0.007334	0.04357
RDN25	202	41	1712976	17	1496002	80	1512478	45	1370868	1.749	0.0003864	0.002884
RDN25	211	297	1712976	140	1496002	221	1512478	160	1370868	1.535	3.42E-09	9.68E-08
RDN25	221	2892	1712976	395	1496002	1615	1512478	413	1370868	4.95	0	0
RDN25	319	166	1712976	78	1496002	60	1512478	47	1370868	1.598	2.86E-05	0.0003161
RDN25	336	141	1712976	38	1496002	72	1512478	52	1370868	2.102	2.31E-09	6.82E-08
RDN25	351	829	1712976	176	1496002	197	1512478	106	1370868	3.21	0	0
RDN25	373	456	1712976	223	1496002	169	1512478	115	1370868	1.633	2.86E-13	1.47E-11
RDN25	375	84	1712976	40	1496002	57	1512478	38	1370868	1.605	0.0009207	0.00599
RDN25	376	587	1712976	289	1496002	228	1512478	161	1370868	1.6	8.88E-16	6.03E-14
RDN25	394	1587	1712976	723	1496002	613	1512478	405	1370868	1.723	0	0
RDN25	684	21	1712976	9	1496002	15	1512478	5	1370868	2.278	0.01081	0.04543
RDN25	1228	35	1712976	21	1496002	52	1512478	25	1370868	1.687	0.00485	0.02418
RDN25	1335	85	1712976	33	1496002	238	1512478	153	1370868	1.561	1.36E-06	2.22E-05
RDN25	1336	135	1712976	85	1496002	296	1512478	165	1370868	1.544	4.55E-08	1.04E-06
RDN25	1343	49	1712976	17	1496002	42	1512478	32	1370868	1.655	0.005343	0.026
RDN25	1345	128	1712976	63	1496002	120	1512478	81	1370868	1.533	4.94E-05	0.0005117
RDN25	1390	128	1712976	59	1496002	119	1512478	65	1370868	1.772	1.82E-07	3.74E-06
RDN25	1413	109	1712976	46	1496002	85	1512478	69	1370868	1.502	0.0006339	0.004402
RDN25	1895	348	1712976	172	1496002	194	1512478	145	1370868	1.516	3.97E-09	1.11E-07
RDN25	1897	43	1712976	19	1496002	26	1512478	13	1370868	1.911	0.002883	0.01582
RDN25	1901	103	1712976	41	1496002	59	1512478	49	1370868	1.598	0.0004133	0.003071
RDN25	1904	39	1712976	17	1496002	18	1512478	10	1370868	1.867	0.009161	0.03963
RDN25	1938	36	1712976	10	1496002	35	1512478	26	1370868	1.761	0.006911	0.03155
RDN25	2924	18	1712976	3	1496002	51	1512478	32	1370868	1.775	0.006917	0.03153
RDN25	3161	49	1712976	24	1496002	107	1512478	65	1370868	1.572	0.0007609	0.005087
RDN25	3265	88	1712976	45	1496002	52	1512478	33	1370868	1.591	0.001172	0.007425
RDN25	3302	106	1712976	38	1496002	63	1512478	51	1370868	1.687	7.17E-05	0.0006934