CORRECTION

Correction: Mapping of Complete Set of Ribose and Base Modifications of Yeast rRNA by RP-HPLC and Mung Bean Nuclease Assay

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In Table 1, there are missing column headers. Please see the complete, correct Table 1 here.

Table 1. RP-HPLC quantification of nucleosides in S.cerevisiae 18S and 25S rRNA.

	18S rRNA		**25S rRNA**	
Nucleosides	***Mole % (Seq)***	***Mole % (HPLC)***	***Mole % (Seq)***	***Mole %(HPLC)***
C (Cytidine)	19.1	19.5 ± 0.48	19.2	19.4 ± 0.56
U (Uridine)	27.4	27.1 ± 0.30	24.4	24.9 ± 0.39
G (Guanosine)	25.2	25.7 ± 0.12	28.2	27.5 ± 0.17
A (Adenosine)	26.3	26.6 ± 0.68	26.1	26.8 ± 0.64
	Residues/mole	*Residues/mole (HPLC)*	*Residues/mole*	*Residues/mole (HPLC)*
m^{1}A (N1-Methyladenosine)	0	0	2	1.98 ± 0.10
m^{5}C (C5-Methylcytidine)	0	0	2	1.81 ± 0.17
Cm (2'-O-Methylcytidine)	3	3.1 ± 0.26	7	6.74 ± 0.31
m^{7}G (N7-Methylguanosine)	1	0.72*± 0.16	0	0
m^{5}U (C5-Methyluridine)	0	0	0	0
Um (2'-O-Methyluridine)	2	1.89 ± 0.33	8	7.1 ± 0.31
m^{3}U (N3-Methyluridine)	0	0	2	2.1 ± 0.17
Gm (2'-O-Methylguanosine)	5	4.91 ± 0.27	10	9.3 ± 0.39
ac^{4}C (N4-Acetylcytidine)	2	2.12 ± 0.11	0	0
Am (2'-O-Methyladenosine)	8	7.33 ± 0.43	12	11.8 ± 0.48
m$^6_2$A (N6,N6-Dimethyladenosine)	2	nc	0	0

Mole % (Seq) was calculated from the number of each nucleoside in 18S and 25S rRNA sequences and as explained in Materials and Methods. Mole % (HPLC), Residues/mole (HPLC) and standard deviation values were calculated from the peak area of the respective nucleosides using their standard response factors, from nine independent runs for each 18S and 25S rRNA.

nc—not calculated

* m^{7}G has been shown to undergo partial-degradation during hydrolysis [18].

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There are several errors in Table 2. Please see the correct Table 2 here.

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Table 2. Approximate values for the extent of modifications in 18S and 25S rRNA, using RP-HPLC and its comparison with RiboMethSeq and SILNAS analyses.

Modified residue	Made by	% of modification (RP-HPLC)	% of modification (Ribo-Meth Seq) (Ref.35)	% of modification (Ribo-Meth Seq) (Ref.34)	% of modification (SILNAS) (Ref.37)
18S rRNA					
Am28	snR74	90% ± 3.8%	85%	99%	>95%
Am100	snR51	73% ± 2.4%	77%	77%	80%
Cm414	U14	89% ± 3.1%	89%	96%	>95%
Am420	snR52	98% ± 1.5%	83%	90%	>95%
Am436	snR87	98% ± 1.8%	74%	89%	73%
Am541	snR41	95% ± 3.2%	87%	99%	>95%
Gm562	snrR40	100%	94%	92%	67%
Um578	snR77	95% ± 3.3%	90%	93%	>95%
Am619	snR47	98% ± 1.2%	85%	92%	100%
Am796	snR53	98% ± 1.1%	92%	97%	>95%
Am974	snR54	95% ± 3.4%	91%	96%	94%
Cm1007	snR79	100%	92%	98%	>95%
Gm1126	snR41	100%	94%	93%	89%
m^{1}acp^{3}Ψ1191	snR35-Nep1-Tsr3	nd	nd	nd	100%
Um1269	snR55	95% ± 2.1%	88%	92%	>95%
Gm1271	snR40	100%	92%	98%	>95%
ac^{4}C1280	Kre33	96% ± 1.9%	nd	nd	84%
Gm1428	snR56	100%	95%	99%	>95%
Gm1572	snR57	100%	89%	97%	100%
m^{7}G1575	Bud23	72*% ± 2.8%	nd	nd	>95%
Cm1639	snR70	92% ± 2.9%	93%	98%	79%
ac^{4}C1773	Kre33	100%	nd	nd	>95%
m$^6_2$A1781	Dim1	nc	nd	nd	90%
m$^6_2$A1782	Dim1	nc	nd	nd	90%
25S rRNA					
m^{1}A645	Rrp8	99% ± 1%	nd	nd	>95%
Am649	U18	93% ± 2.5%	88%	98%	>95%
Cm650	U18	100%	95%	98%	94%
Cm663	snR58	81% ± 4.3%	62%	91%	74%
Gm805	snR39b	90% ± 4.7%	93%	98%	>95%
Am807	snR39_snR59	98% ± 1%	94%	97%	>95%
Am817	snR60	98% ± 0.8%	92%	85%	89%
Gm867	snR50	90% ± 3.7%	95%	95%	78%
Am876	snR72	95% ± 2.2%	89%	91%	75%
Um898	snR40	94% ± 1.8%	78%	85%	94%
Gm908	snR60	95% ± 1.1%	96%	96%	100%
Am1133	snR61	98% ± 0.5%	92%	99%	88%
Gm1142	?(snr57)	absent	absent	absent	absent
Cm1437	U24	100%	92%	97%	>95%
Am1449	U24	97% ± 0.7%	67%	99%	>95%
Gm1450	U24	100%	94%	99%	>95%
Um1888	snR62	99% ± 1.3%	94%	97%	>95%
m^{1}A2142	Bmt2	99% ± 0.7%	nd	nd	>95%
Cm2197	snR76	100%	71%	86%	91%
Am2220	snR47	98% ± 3.1%	94%	99%	93%

(*Continued*)

Table 2. (*Continued*)

Modified residue	**Made by**	**% of modification (RP-HPLC)**	**% of modification (Ribo-Meth Seq) (Ref.35)**	**% of modification (Ribo-Meth Seq) (Ref.34)**	**% of modification (SILNAS) (Ref.37)**
Am2256	snR63	98% ± 2.3%	94%	95%	100%
m^5C2278	Rcm1	100%	nd	nd	100%
Am2280	snR13	99% ± 0.6%	91%	100%	100%
Am2281	snR13	99% ± 0.9%	92%	100%	100%
Gm2288	snR75	100%	95%	96%	>95%
Cm2337	snR64	100%	94%	99%	100%
Um/Ψm 2347	snR65/snR9	66% ± 3.7%	69%	61%	76.2%/12.9%
Gm2395	?snR190	absent	absent	absent	absent
Um2417	snR66	99% ± 0.1%	95%	99%	100%
Um2421	snR78	99% ± 1.5%	86%	93%	>95%
Gm2619	snR67	100%	93%	98%	87%
m^3U2634	Bmt5	100%	nd	nd	>95%
Am2640	snR68	95% ± 3.6%	90%	96%	93%
Um2724	snR67	92% ± 2.1%	92%	98%	>95%
Um2729	snR51	89% ± 4.3%	67%	94%	75%
Gm2791	snR48	95% ± 2.3%	94%	98%	86%
Gm2793	snR48	95% ± 1.9%	95%	98%	>95%
Gm2815	snR38	95% ± 2%	95%	99%	>95%
m^3U2843	Bmt6	100%	nd	nd	>95%
m^5C2870	Nop2	100%	nd	nd	>95%
Um2921	snR52	93% ± 2.2%	92%	99%	>95%
Gm2922	Spb1	97% ± 3.5%	95%	98%	>95%
Am2946	snR71	99% ± 0.6%	92%	99%	91%
Cm2948	snR69	99% ± 0.8%	77%	82%	>95
Cm2959	snR73	93% ± 4.1%	96%	95%	94%

nd—not detected; nc—not calculated.? (snRx)- predicted according to the guide sequence; lacks experimental evidence

% modification was calculated as a mean of three independent calculations ± Relative standard deviations (RSD).

m^7G has been shown to undergo partial-degradation during hydrolysis [18].

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Reference

1. Yang J, Sharma S, Watzinger P, Hartmann JD, Kötter P, Entian K-D (2016) Mapping of Complete Set of Ribose and Base Modifications of Yeast rRNA by RP-HPLC and Mung Bean Nuclease Assay. PLoS ONE 11(12): e0168873. doi: 10.1371/journal.pone.0168873 PMID: 28033325