

**Supplemental Information for
Development of Universal Mass Exclusion List (UMEL) for RNA modification mapping**

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Supplemental Tables S1-S6, Supplemental Figures S1-S4

Supplemental Table S1. Universal Mass Exclusion List (UMEL): predicted average masses and deprotonated m/z values for RNase T1 oligonucleotide digestion products (3–12 nt). “—” indicates charge states not included because the corresponding ions fall outside the instrument m/z acquisition range (600–2000). Because sequence order does not matter for the UMEL values, each digestion product is represented in [] where the nucleotide order within the bracket may vary in the experimental data.

Length (nt)	Digestion product	Average mass	m/z ($z = -1$)	m/z ($z = -2$)	m/z ($z = -3$)	m/z ($z = -4$)
3	[AU]]Gp	998.60	997.59	-	-	-
3	[AC]Gp	997.62	996.61	-	-	-
3	[UC]Gp	974.58	973.57	-	-	-
3	[AA]Gp	1021.64	1020.63	-	-	-
3	[CC]Gp	973.59	972.58	-	-	-
3	[UU]Gp	975.56	974.55	-	-	-

4	[AAA]Gp	1350.85	1349.84	674.42	-	-
4	[UUU]Gp	1281.73	1280.72	639.86	-	-
4	[CCC]Gp	1278.78	1277.77	638.38	-	-
4	[AUC]Gp	1303.79	1302.78	650.89	-	-
4	[AUU]Gp	1304.77	1303.76	651.38	-	-
4	[ACC]Gp	1302.80	1301.79	650.39	-	-
4	[UUC]Gp	1280.75	1279.74	639.37	-	-
4	[AAC]Gp	1326.83	1325.82	662.41	-	-
4	[UCC]Gp	1279.76	1278.75	638.87	-	-
4	[AUA]Gp	1327.81	1326.80	662.90	-	-
5	[AAAA]Gp	1680.06	1679.05	839.02	-	-
5	[UUUU]Gp	1587.90	1586.89	792.94	-	-
5	[CCCC]Gp	1583.96	1582.95	790.97	-	-
5	[AUUU]Gp	1610.94	1609.93	804.46	-	-
5	[ACCC]Gp	1607.99	1606.98	802.99	-	-
5	[UCCC]Gp	1584.95	1583.94	791.47	-	-
5	[CAAA]Gp	1656.04	1655.03	827.01	-	-
5	[CUUU]Gp	1586.92	1585.91	792.45	-	-
5	[UAAA]Gp	1657.02	1656.01	827.50	-	-
5	[AAUU]Gp	1633.98	1632.97	815.98	-	-
5	[AACC]Gp	1632.01	1631.00	815.00	-	-
5	[UUCC]Gp	1585.93	1584.92	791.96	-	-
5	[AACU]Gp	1633.00	1631.99	815.49	-	-
5	[AUUC]Gp	1609.96	1608.95	803.97	-	-
5	[AUCC]Gp	1608.97	1607.96	803.48	-	-
6	[AAAAA]Gp	2009.27	-	1003.63	668.75	-
6	[UUUUU]Gp	1894.07	-	946.03	630.35	-
6	[CCCCC]Gp	1889.15	-	943.57	628.71	-
6	[AAAAU]Gp	1986.23	-	992.11	661.07	-
6	[AAAUU]Gp	1963.19	-	980.59	653.39	-
6	[AAUUU]Gp	1940.15	-	969.07	645.71	-
6	[AUUUU]Gp	1917.11	-	957.55	638.03	-
6	[AAAAC]Gp	1985.25	-	991.62	660.74	-
6	[AAACC]Gp	1961.22	-	979.60	652.73	-

6	[AACCC]Gp	1937.20	-	967.59	644.72	-
6	[ACCCC]Gp	1913.17	-	955.58	636.71	-
6	[UUUUC]Gp	1893.09	-	945.54	630.02	-
6	[UUUCC]Gp	1892.10	-	945.04	629.69	-
6	[UUCCC]Gp	1891.12	-	944.55	629.36	-
6	[UCCCC]Gp	1890.13	-	944.06	629.03	-
6	[AAAUC]Gp	1962.21	-	980.10	653.06	-
6	[AAUUC]Gp	1939.17	-	968.58	645.38	-
6	[AUUUC]Gp	1916.13	-	957.06	637.70	-
6	[AAUCC]Gp	1938.18	-	968.08	645.05	-
6	[AUCCC]Gp	1914.16	-	956.07	637.04	-
6	[AUUCC]Gp	1915.14	-	956.56	637.37	-
7	[AAAAAA]Gp	2338.48	-	1168.23	778.48	-
7	[UUUUUU]Gp	2200.24	-	1099.11	732.40	-
7	[CCCCC]Gp	2194.33	-	1096.16	730.43	-
7	[AAAAAU]Gp	2315.44	-	1156.71	770.80	-
7	[AAAAUU]Gp	2292.40	-	1145.19	763.12	-
7	[AAAUUU]Gp	2269.36	-	1133.67	755.44	-
7	[AAUUUU]Gp	2246.32	-	1122.15	747.76	-
7	[AUUUUU]Gp	2223.28	-	1110.63	740.08	-
7	[AAAAAC]Gp	2314.46	-	1156.22	770.48	-
7	[AAAACC]Gp	2290.43	-	1144.21	762.47	-
7	[AAACCC]Gp	2266.41	-	1132.20	754.46	-
7	[AACCCC]Gp	2242.38	-	1120.18	746.45	-
7	[ACCCCC]Gp	2218.36	-	1108.17	738.44	-
7	[UUUUUC]Gp	2199.26	-	1098.62	732.08	-
7	[UUUUCC]Gp	2198.27	-	1098.13	731.75	-
7	[UUUCCC]Gp	2197.29	-	1097.64	731.42	-
7	[UUCCCC]Gp	2196.30	-	1097.14	731.09	-
7	[UCCCCC]Gp	2195.32	-	1096.65	730.76	-
7	[AAAAUC]Gp	2291.42	-	1144.70	762.80	-
7	[AAAUUC]Gp	2268.38	-	1133.18	755.12	-
7	[AAUUUC]Gp	2245.34	-	1121.66	747.44	-
7	[AUUUUC]Gp	2222.30	-	1110.14	739.76	-

7	[AAAUCC]Gp	2267.39	-	1132.69	754.79	-
7	[AAUCCC]Gp	2243.37	-	1120.68	746.78	-
7	[AUCCCC]Gp	2219.34	-	1108.66	738.77	-
7	[AUUCCC]Gp	2220.33	-	1109.16	739.10	-
7	[AAUUCC]Gp	2244.35	-	1121.17	747.11	-
7	[AUUUCC]Gp	2221.31	-	1109.65	739.43	-
8	[AAAAAAA]Gp	2667.69	-	1332.84	888.22	-
8	[UUUUUUU]Gp	2506.41	-	1252.20	834.46	-
8	[CCCCCCC]Gp	2499.51	-	1248.75	832.16	-
8	[AAAAAAU]Gp	2644.65	-	1321.32	880.54	-
8	[AAAAAUU]Gp	2621.61	-	1309.80	872.86	-
8	[AAAAUUU]Gp	2598.61	-	1298.30	865.19	-
8	[AAAUUUU]Gp	2575.53	-	1286.76	857.50	-
8	[AAUUUUU]Gp	2552.49	-	1275.24	849.82	-
8	[AUUUUUU]Gp	2529.45	-	1263.72	842.14	-
8	[AAAAAAC]Gp	2643.66	-	1320.82	880.21	-
8	[AAAAACC]Gp	2619.64	-	1308.81	872.20	-
8	[AAAACCC]Gp	2595.61	-	1296.80	864.19	-
8	[AAACCCC]Gp	2571.59	-	1284.79	856.19	-
8	[AACCCCC]Gp	2547.56	-	1272.77	848.18	-
8	[ACCCCCC]Gp	2523.54	-	1260.76	840.17	-
8	[UUUUUUC]Gp	2505.42	-	1251.70	834.13	-
8	[UUUUUCC]Gp	2504.44	-	1251.21	833.80	-
8	[UUUUCCC]Gp	2503.45	-	1250.72	833.47	-
8	[UUUCCCC]Gp	2502.47	-	1250.23	833.15	-
8	[UUCCCCC]Gp	2501.48	-	1249.73	832.82	-
8	[UCCCCCC]Gp	2500.50	-	1249.24	832.49	-
8	[AAAAAUC]Gp	2620.62	-	1309.30	872.53	-
8	[AAAAUUC]Gp	2597.58	-	1297.78	864.85	-
8	[AAAUUUC]Gp	2574.54	-	1286.26	857.17	-
8	[AAUUUUC]Gp	2551.50	-	1274.74	849.49	-
8	[AUUUUUC]Gp	2528.46	-	1263.22	841.81	-
8	[AAAAUCC]Gp	2596.60	-	1297.29	864.52	-
8	[AAAUCCC]Gp	2572.57	-	1285.28	856.51	-

8	[AAUCCCC]Gp	2548.55	-	1273.27	848.51	-
8	[AUCCCCC]Gp	2524.52	-	1261.25	840.50	-
8	[AUUCCCC]Gp	2525.51	-	1261.75	840.83	-
8	[AUUUCCC]Gp	2526.49	-	1262.24	841.15	-
8	[AUUUUCC]Gp	2527.51	-	1262.75	841.49	-
8	[AAUUCCC]Gp	2549.53	-	1273.76	848.83	-
8	[AAAUUCC]Gp	2573.56	-	1285.77	856.84	-
8	[AAUUUCC]Gp	2550.52	-	1274.25	849.16	-
9	[AAAAAAA]Gp	2996.90	-	1497.44	997.96	-
9	[UUUUUUUU]Gp	2812.58	-	1405.28	936.52	-
9	[CCCCCCC]Gp	2804.70	-	1401.34	933.89	-
9	[AAAAAAU]Gp	2973.86	-	1485.92	990.28	-
9	[AAAAAAU]Gp	2950.82	-	1474.40	982.60	-
9	[AAAAUUU]Gp	2927.78	-	1462.88	974.92	-
9	[AAAAUUU]Gp	2904.74	-	1451.36	967.24	-
9	[AAAUUUU]Gp	2881.70	-	1439.84	959.56	-
9	[AAUUUUU]Gp	2858.66	-	1428.32	951.88	-
9	[AUUUUUU]Gp	2835.62	-	1416.80	944.20	-
9	[AAAAAAC]Gp	2972.87	-	1485.43	989.95	-
9	[AAAAACC]Gp	2948.85	-	1473.42	981.94	-
9	[AAAAACC]Gp	2924.82	-	1461.40	973.93	-
9	[AAAACCC]Gp	2900.80	-	1449.39	965.92	-
9	[AAACCCC]Gp	2876.77	-	1437.38	957.91	-
9	[AACCCCC]Gp	2852.75	-	1425.37	949.91	-
9	[ACCCCCC]Gp	2828.72	-	1413.35	941.90	-
9	[UUUUUUUC]Gp	2811.59	-	1404.79	936.19	-
9	[UUUUUUCC]Gp	2810.61	-	1404.30	935.86	-
9	[UUUUUCCC]Gp	2809.62	-	1403.80	935.53	-
9	[UUUUUCCC]Gp	2808.64	-	1403.31	935.20	-
9	[UUUCCCCC]Gp	2807.65	-	1402.82	934.87	-
9	[UUCCCCC]Gp	2806.67	-	1402.33	934.55	-
9	[UCCCCCC]Gp	2805.68	-	1401.83	934.22	-
9	[AAAAAAUC]Gp	2949.83	-	1473.91	982.27	-
9	[AAAAAUUC]Gp	2926.79	-	1462.39	974.59	-

9	[AAAAUUUC]Gp	2903.75	-	1450.87	966.91	-
9	[AAAUUUUC]Gp	2880.71	-	1439.35	959.23	-
9	[AAUUUUUC]Gp	2857.67	-	1427.83	951.55	-
9	[AUUUUUUC]Gp	2834.63	-	1416.31	943.87	-
9	[AAAAAUCC]Gp	2925.81	-	1461.90	974.26	-
9	[AAAAUCCC]Gp	2901.78	-	1449.88	966.25	-
9	[AAAUCCCC]Gp	2877.76	-	1437.87	958.24	-
9	[AAUCCCCC]Gp	2853.73	-	1425.86	950.23	-
9	[AUCCCCCC]Gp	2829.71	-	1413.85	942.23	-
9	[AUUCCCCC]Gp	2830.69	-	1414.34	942.55	-
9	[AUUUCCCC]Gp	2831.68	-	1414.83	942.88	-
9	[AUUUUCCC]Gp	2832.66	-	1415.32	943.21	-
9	[AUUUUUCC]Gp	2833.65	-	1415.82	943.54	-
9	[AAUUCCCC]Gp	2854.72	-	1426.35	950.56	-
9	[AAAAUUCC]Gp	2879.73	-	1438.86	958.90	-
9	[AAAUUCCC]Gp	2878.74	-	1438.36	958.57	-
9	[AAUUUCCC]Gp	2855.70	-	1426.84	950.89	-
9	[AAAAUUC]Gp	2902.77	-	1450.38	966.58	-
9	[AAUUUUCC]Gp	2856.69	-	1427.34	951.22	-
10	[AAAAAAAA]Gp	3326.11	-	1662.05	1107.69	830.52
10	[UUUUUUUU]Gp	3118.75	-	1558.37	1038.57	778.68
10	[CCCCCCCC]Gp	3109.88	-	1553.93	1035.62	776.46
10	[AAAAAAAAU]Gp	3303.07	-	1650.53	1100.01	824.76
10	[AAAAAAAAUU]Gp	3280.03	-	1639.01	1092.33	819.00
10	[AAAAAUUU]Gp	3256.99	-	1627.49	1084.65	813.24
10	[AAAAUUUU]Gp	3233.95	-	1615.97	1076.97	807.48
10	[AAAAUUUUU]Gp	3210.91	-	1604.45	1069.29	801.72
10	[AAAUUUUUU]Gp	3187.87	-	1592.93	1061.61	795.96
10	[AAUUUUUUU]Gp	3164.83	-	1581.41	1053.93	790.20
10	[AUUUUUUUU]Gp	3141.79	-	1569.89	1046.25	784.44
10	[AAAAAAAAC]Gp	3302.08	-	1650.03	1099.68	824.51
10	[AAAAAAACC]Gp	3278.06	-	1638.02	1091.68	818.51
10	[AAAAAACCC]Gp	3254.03	-	1626.01	1083.67	812.50
10	[AAAAACCCC]Gp	3230.00	-	1613.99	1075.66	806.49

10	[AAAACCCCC]Gp	3205.98	-	1601.98	1067.65	800.49
10	[AAACCCCCC]Gp	3181.96	-	1589.97	1059.64	794.48
10	[AACCCCCCC]Gp	3157.93	-	1577.96	1051.63	788.47
10	[ACCCCCCCC]Gp	3133.91	-	1565.95	1043.63	782.47
10	[UUUUUUUUC]Gp	3117.76	-	1557.87	1038.24	778.43
10	[UUUUUUUCC]Gp	3116.78	-	1557.38	1037.92	778.19
10	[UUUUUUCCC]Gp	3115.79	-	1556.89	1037.59	777.94
10	[UUUUUCCCC]Gp	3114.81	-	1556.40	1037.26	777.69
10	[UUUUCCCCC]Gp	3113.82	-	1555.90	1036.93	777.45
10	[UUUCCCCCC]Gp	3112.84	-	1555.41	1036.60	777.20
10	[UUCCCCCCC]Gp	3111.85	-	1554.92	1036.27	776.95
10	[UCCCCCCCC]Gp	3110.87	-	1554.43	1035.95	776.71
10	[AAAAAAUUC]Gp	3279.04	-	1638.51	1092.00	818.75
10	[AAAAAAUUC]Gp	3256.00	-	1626.99	1084.32	812.99
10	[AAAAAUUUC]Gp	3232.96	-	1615.47	1076.64	807.23
10	[AAAAUUUUC]Gp	3209.92	-	1603.95	1068.96	801.47
10	[AAAUUUUUC]Gp	3186.88	-	1592.43	1061.28	795.71
10	[AAUUUUUUC]Gp	3163.84	-	1580.91	1053.60	789.95
10	[AUUUUUUUC]Gp	3140.80	-	1569.39	1045.92	784.19
10	[AAAAAAUCC]Gp	3255.02	-	1626.50	1084.00	812.75
10	[AAAAAUCCC]Gp	3230.99	-	1614.49	1075.99	806.74
10	[AAAAUCCCC]Gp	3206.97	-	1602.48	1067.98	800.73
10	[AAAUCCCCC]Gp	3182.94	-	1590.46	1059.97	794.73
10	[AAUCCCCCC]Gp	3158.92	-	1578.45	1051.96	788.72
10	[AUCCCCCCC]Gp	3134.89	-	1566.44	1043.95	782.71
10	[AUUCCCCCC]Gp	3135.88	-	1566.93	1044.28	782.96
10	[AUUUCCCCC]Gp	3136.86	-	1567.42	1044.61	783.21
10	[AUUUUCCCC]Gp	3137.85	-	1567.92	1044.94	783.45
10	[AUUUUUCCC]Gp	3138.83	-	1568.41	1045.27	783.70
10	[AUUUUUUCC]Gp	3139.82	-	1568.90	1045.60	783.95
10	[AAUUCCCCC]Gp	3159.90	-	1578.94	1052.29	788.97
10	[AAAUUCCCC]Gp	3184.91	-	1591.45	1060.63	795.22
10	[AAUUUUUCC]Gp	3162.86	-	1580.42	1053.28	789.71
10	[AAAAAUUCC]Gp	3231.98	-	1614.98	1076.32	806.99

10	[AAAAUUUCC]Gp	3208.94	-	1603.46	1068.64	801.23
10	[AAAAUUUCC]Gp	3185.90	-	1591.94	1060.96	795.47
10	[AAAAUUCCC]Gp	3207.95	-	1602.97	1068.31	800.98
10	[AAUUUUCCC]Gp	3161.87	-	1579.93	1052.95	789.46
10	[AAAUUCCCC]Gp	3183.93	-	1590.96	1060.30	794.97
10	[AAUUUCCCC]Gp	3160.89	-	1579.44	1052.62	789.21
11	[AAAAAAAAA]Gp	3655.32	-	1826.65	1217.43	912.82
11	[UUUUUUUUUpG	3424.92	-	1711.45	1140.63	855.22
11	[CCCCCCCCC]Gp	3415.07	-	1706.53	1137.35	852.76
11	[AAAAAAAAAU]Gp	3632.28	-	1815.13	1209.75	907.06
11	[AAAAAAAAUU]Gp	3609.24	-	1803.61	1202.07	901.30
11	[AAAAAAAAUUU]Gp	3586.20	-	1792.09	1194.39	895.54
11	[AAAAAAAAUUUU]Gp	3563.16	-	1780.57	1186.71	889.78
11	[AAAAAUUUUU]Gp	3540.16	-	1769.07	1179.04	884.03
11	[AAAAUUUUUU]Gp	3517.08	-	1757.53	1171.35	878.26
11	[AAAUUUUUUU]Gp	3494.04	-	1746.01	1163.67	872.50
11	[AAUUUUUUUU]Gp	3471.00	-	1734.49	1155.99	866.74
11	[AUUUUUUUUU]Gp	3447.96	-	1722.97	1148.31	860.98
11	[AAAAAAAAAC]Gp	3631.29	-	1814.64	1209.42	906.81
11	[AAAAAAAAACC]Gp	3607.27	-	1802.63	1201.41	900.81
11	[AAAAAAACCC]Gp	3583.24	-	1790.61	1193.40	894.80
11	[AAAAAACCCC]Gp	3559.22	-	1778.60	1185.40	888.80
11	[AAAAACCCCC]Gp	3535.19	-	1766.59	1177.39	882.79
11	[AAAACCCCCC]Gp	3511.17	-	1754.58	1169.38	876.78
11	[AAACCCCCCC]Gp	3487.14	-	1742.56	1161.37	870.78
11	[AACCCCCCCC]Gp	3463.12	-	1730.55	1153.36	864.77
11	[ACCCCCCCCC]Gp	3439.09	-	1718.54	1145.35	858.76
11	[UUUUUUUUUC]Gp	3423.93	-	1710.96	1140.30	854.97
11	[UUUUUUUUCC]Gp	3422.95	-	1710.47	1139.97	854.73
11	[UUUUUUUCCC]Gp	3421.96	-	1709.97	1139.64	854.48
11	[UUUUUUCCCC]Gp	3420.98	-	1709.48	1139.32	854.24
11	[UUUUUCCCCC]Gp	3419.99	-	1708.99	1138.99	853.99
11	[UUUUCCCCCC]Gp	3419.00	-	1708.49	1138.66	853.74
11	[UUUCCCCCCC]Gp	3418.02	-	1708.00	1138.33	853.50

11	[UUCCCCCCCC]Gp	3417.04	-	1707.51	1138.00	853.25
11	[UCCCCCCCCC]Gp	3416.05	-	1707.02	1137.67	853.00
11	[AAAAAAAAAUC]Gp	3608.25	-	1803.12	1201.74	901.05
11	[AAAAAAAUUC]Gp	3585.21	-	1791.60	1194.06	895.29
11	[AAAAAAUUUC]Gp	3562.17	-	1780.08	1186.38	889.53
11	[AAAAAUUUUC]Gp	3539.13	-	1768.56	1178.70	883.77
11	[AAAAUUUUUC]Gp	3516.09	-	1757.04	1171.02	878.01
11	[AAAUUUUUUC]Gp	3493.05	-	1745.52	1163.34	872.25
11	[AAUUUUUUUC]Gp	3470.01	-	1734.00	1155.66	866.49
11	[AUUUUUUUUC]Gp	3446.97	-	1722.48	1147.98	860.73
11	[AAAAAAAUCC]Gp	3584.23	-	1791.11	1193.73	895.05
11	[AAAAAAUCCC]Gp	3560.20	-	1779.09	1185.72	889.04
11	[AAAAAUCCCC]Gp	3536.18	-	1767.08	1177.72	883.04
11	[AAAAUCCCCC]Gp	3512.15	-	1755.07	1169.71	877.03
11	[AAAUCCCCC]Gp	3488.13	-	1743.06	1161.70	871.02
11	[AAUCCCCCCC]Gp	3464.10	-	1731.04	1153.69	865.02
11	[AUCCCCCCCC]Gp	3440.08	-	1719.03	1145.68	859.01
11	[AAUCCCCCCC]Gp	3465.09	-	1731.54	1154.02	865.26
11	[AAUUUUUUUCC]Gp	3469.03	-	1733.51	1155.33	866.25
11	[AAAAAAAUCC]Gp	3561.19	-	1779.59	1186.05	889.29
11	[AAAUUUUCCCC]Gp	3490.10	-	1744.04	1162.36	871.52
11	[AAAUUUUCCC]Gp	3491.08	-	1744.53	1162.68	871.76
11	[AAAAUUUCCCC]Gp	3514.12	-	1756.05	1170.36	877.52
11	[AAAAAUUUCC]Gp	3538.15	-	1768.07	1178.37	883.53
11	[AAAAAUUCCC]Gp	3537.16	-	1767.57	1178.04	883.28
11	[AAAUUUUUUCC]Gp	3492.07	-	1745.03	1163.01	872.01
11	[AAUUUUUCCCC]Gp	3468.07	-	1733.03	1155.01	866.01
11	[AAAUUCCCCC]Gp	3468.04	-	1733.01	1155.00	866.00
11	[AAUUUCCCCC]Gp	3466.07	-	1732.03	1154.35	865.51
11	[AAAAAUUCCCC]Gp	3513.14	-	1755.56	1170.04	877.28
11	[AAAAAUUUUCC]Gp	3467.06	-	1732.52	1154.68	865.76
11	[AAUUUUUCCCC]Gp	3515.11	-	1756.55	1170.69	877.77
11	[AUUCCCCCCC]Gp	3441.06	-	1719.52	1146.01	859.26
11	[AUUCCCCCCC]Gp	3442.05	-	1720.02	1146.34	859.50

11	[AUUUUCCCC]Gp	3443.03	-	1720.51	1146.67	859.75
11	[AUUUUUCCCC]Gp	3444.02	-	1721.00	1147.00	860.00
11	[AUUUUUUCCC]Gp	3445.00	-	1721.49	1147.32	860.24
11	[AUUUUUUUCC]Gp	3445.99	-	1721.99	1147.65	860.49
12	[AAAAAAAAAAA]Gp	3984.52	-	1991.25	1327.17	995.12
12	[UUUUUUUUUUU]Gp	3731.08	-	1864.53	1242.69	931.76
12	[CCCCCCCCCCC]Gp	3720.25	-	1859.12	1239.07	929.05
12	[AAAAAAAAAUC]Gp	3937.46	-	1967.72	1311.48	983.36
12	[AAAAAAAAAUUC]Gp	3914.42	-	1956.20	1303.80	977.60
12	[AAAAAAAUUUC]Gp	3891.38	-	1944.68	1296.12	971.84
12	[AAAAAAUUUUC]Gp	3868.34	-	1933.16	1288.44	966.08
12	[AAAAAUUUUUC]Gp	3845.30	-	1921.64	1280.76	960.32
12	[AAAAUUUUUUC]Gp	3822.26	-	1910.12	1273.08	954.56
12	[AAAUUUUUUUC]Gp	3799.22	-	1898.60	1265.40	948.80
12	[AAUUUUUUUUC]Gp	3776.18	-	1887.08	1257.72	943.04
12	[AUUUUUUUUUC]Gp	3753.14	-	1875.56	1250.04	937.28
12	[AAAAAAAAAAU]Gp	3961.49	-	1979.74	1319.49	989.36
12	[AAAAAAAAAAUU]Gp	3938.45	-	1968.22	1311.81	983.60
12	[AAAAAAAAAUUU]Gp	3915.41	-	1956.70	1304.13	977.84
12	[AAAAAAAUUUU]Gp	3892.37	-	1945.18	1296.45	972.08
12	[AAAAAAUUUUU]Gp	3869.33	-	1933.66	1288.77	966.32
12	[AAAAAUUUUUU]Gp	3846.29	-	1922.14	1281.09	960.56
12	[AAAAUUUUUUU]Gp	3823.25	-	1910.62	1273.41	954.80
12	[AAAUUUUUUUU]Gp	3800.21	-	1899.10	1265.73	949.04
12	[AAUUUUUUUUU]Gp	3777.17	-	1887.58	1258.05	943.28
12	[AUUUUUUUUUU]Gp	3754.13	-	1876.06	1250.37	937.52
12	[UUUUUUUUUUC]Gp	3730.02	-	1864.00	1242.33	931.50
12	[UUUUUUUUUCC]Gp	3729.12	-	1863.55	1242.03	931.27
12	[UUUUUUUUUCCC]Gp	3728.13	-	1863.06	1241.70	931.02
12	[UUUUUUUCCCC]Gp	3727.15	-	1862.57	1241.37	930.78
12	[UUUUUUCCCCC]Gp	3726.16	-	1862.07	1241.04	930.53
12	[UUUUUCCCCCC]Gp	3725.18	-	1861.58	1240.72	930.29
12	[UUUUCCCCCCC]Gp	3724.19	-	1861.09	1240.39	930.04
12	[UUUCCCCCCCC]Gp	3723.21	-	1860.60	1240.06	929.79

12	[UCCCCCCCCC]Gp	3722.22	-	1860.10	1239.73	929.55
12	[UCCCCCCCCC]Gp	3721.24	-	1859.61	1239.40	929.30
12	[AAAAAAAAAAC]Gp	3960.50	-	1979.24	1319.16	989.12
12	[AAAAAAAAAAC]Gp	3936.48	-	1967.23	1311.15	983.11
12	[AAAAAAAAACC]Gp	3912.45	-	1955.22	1303.14	977.10
12	[AAAAAAAAACC]Gp	3888.43	-	1943.21	1295.13	971.10
12	[AAAAAACCCCC]Gp	3864.40	-	1931.19	1287.12	965.09
12	[AAAAACCCCC]Gp	3840.38	-	1919.18	1279.12	959.09
12	[AAAACCCCCC]Gp	3816.35	-	1907.17	1271.11	953.08
12	[AAACCCCCCC]Gp	3792.33	-	1895.16	1263.10	947.07
12	[AACCCCCCCC]Gp	3768.30	-	1883.14	1255.09	941.07
12	[ACCCCCCCCC]Gp	3744.28	-	1871.13	1247.08	935.06
12	[AAAAAAAAAUCC]Gp	3913.44	-	1955.71	1303.47	977.35
12	[AAAAAAAUCCC]Gp	3889.41	-	1943.70	1295.46	971.34
12	[AAAAAAUCCCC]Gp	3865.39	-	1931.69	1287.45	965.34
12	[AAAAAUCCCCC]Gp	3841.36	-	1919.67	1279.44	959.33
12	[AAAAUCCCCC]Gp	3817.34	-	1907.66	1271.44	953.33
12	[AAAUCCCCC]Gp	3793.31	-	1895.65	1263.43	947.32
12	[AAUCCCCCCC]Gp	3769.29	-	1883.64	1255.42	941.31
12	[AUCCCCCCCC]Gp	3745.26	-	1871.62	1247.41	935.31
12	[AUUCCCCCCC]Gp	3746.25	-	1872.12	1247.74	935.55
12	[AUUUCCCCC]Gp	3747.23	-	1872.61	1248.07	935.80
12	[AUUUUCCCCC]Gp	3748.22	-	1873.10	1248.40	936.05
12	[AUUUUUCCCC]Gp	3749.20	-	1873.59	1248.72	936.29
12	[AUUUUUUCCCC]Gp	3750.19	-	1874.09	1249.05	936.54
12	[AUUUUUUUCCC]Gp	3751.17	-	1874.58	1249.38	936.78
12	[AUUUUUUUUCC]Gp	3752.16	-	1875.07	1249.71	937.03
12	[AAUCCCCCCC]Gp	3770.27	-	1884.13	1255.75	941.56
12	[AAUUUUUUUCC]Gp	3775.20	-	1886.59	1257.39	942.79
12	[AAAAAAAUUCC]Gp	3890.40	-	1944.19	1295.79	971.59
12	[AAAUUCCCCC]Gp	3794.30	-	1896.14	1263.76	947.57
12	[AAUUUCCCCC]Gp	3771.26	-	1884.62	1256.08	941.81
12	[AAAAAAUUUCC]Gp	3867.36	-	1932.67	1288.11	965.83
12	[AAAAAAUUCCC]Gp	3866.37	-	1932.18	1287.78	965.58

12	[AAAUUUUUUCC]Gp	3798.24	-	1898.11	1265.07	948.55
12	[AAUUUUUUUCCC]Gp	3774.21	-	1886.10	1257.06	942.54
12	[AAAAUUCCCC]Gp	3818.32	-	1908.15	1271.76	953.57
12	[AAAAUUUUUCC]Gp	3821.28	-	1909.63	1272.75	954.31
12	[AAUUUUCCCC]Gp	3772.24	-	1885.11	1256.40	942.05
12	[AAAAUUUUUCC]Gp	3844.32	-	1921.15	1280.43	960.07
12	[AAAAUUCCCC]Gp	3842.35	-	1920.17	1279.77	959.58
12	[AAUUUUUCCCC]Gp	3773.23	-	1885.61	1256.73	942.30
12	[AAAAUUUCCCC]Gp	3843.33	-	1920.66	1280.10	959.82
12	[AAAUUUUUCCC]Gp	3797.25	-	1897.62	1264.74	948.30
12	[AAAUUUCCCC]Gp	3795.28	-	1896.63	1264.08	947.81
12	[AAAAUUUUCCC]Gp	3820.29	-	1909.14	1272.42	954.06
12	[AAAUUUUCCCC]Gp	3796.27	-	1897.13	1264.41	948.06
12	[AAAAUUUCCCC]Gp	3819.31	-	1908.65	1272.09	953.82

Supplemental Table S2. The 73 predicted post-transcriptionally modified RNase T1 digestion products ($n > 3$) of *E. coli* total tRNAs from the Modomics Database and their detection by DDA and UMEL.

Predicted digestion products	Standard DDA	UMEL
[m7G][acp3U]CGp	✓	✓
[m7G]UCUCAGp	✓	✓
AC[s2C]U[mnm5U]CU[t6A]AGp	✗	✓
ACUQUU[t6A]APCCGp	✓	✓
UAU[m7G]UCACUGp	✓	✓
DDAGp	✓	✓
[m7G]UCGp	✓	✓
U[s4U]AACAAAGp	✓	✓
DDAUGp	✗	✓
CA[ms2i6A]APCCGp	✓	✓
UA[s4U]CGp	✓	✓
U[Um]U[cmnm5s2U]UGp	✓	✓
[m2A]PACCGp	✓	✓
A[Um]UCUGp	✓	✓
[m2A]PPCCGp	✓	✓
CCCU[mnm5s2U]UC[m2A]CGp	✗	✓
AA[s4U]AGp	✓	✓
CUA[s4U]AGp	✓	✓
AUUQUGp	✓	✓

[m2A]PPCCAGp	✓	✓
UU[m7G]UCGp	✓	✓
AU[t6A]AGp	✓	✓
CCCCU[s4U]AGp	✗	✓
ACU[k2C]AU[t6A]APCGp	✓	✓
[m5U]PCAAGp	✓	✓
AADD[Gm]Gp	✓	✓
AADC[Gm]Gp	✓	✓
APU[cmnm5Um]AA[ms2i6A]APCCCUCGp	✓	✓
AAADC[Gm]Gp	✗	✓
APU[Cm]AA[ms2i6A]APCAACCGp	✓	✓
ACU[mnm5s2U]UU[t6A]APCAAUUGp	✓	✓
DD[Gm]Gp	✓	✓
CACAUCACU[ac4C]AU[t6A]APGp	✓	✓
[m7G][acp3U]CACAGp	✗	✓
A[s4U]AGp	✓	✓
AA[ms2i6A]APCCCCGp	✓	✓
U[m7G][acp3U]CCUUGp	✓	✓
[m5U]PCGp	✓	✓
[m1G]ACGp	✓	✓
U[Cm]U[cmo5U]Gp	✓	✓
A[ms2i6A]AACCGp	✓	✓
CUU[cmo5U]Gp	✓	✓
[m7G]UCUGp	✓	✓
[m7G]UCAGp	✓	✓
[m5U]PCAAAUCCCCUCUCUCCGp	✓	✓
CUCCC[s2C]UGp	✓	✓
CU[t6A]AGp	✓	✓
U[m6t6A]AGp	✓	✓
[m7G]UCCCCAGp	✓	✓
U[Cm]UCCA[ms2i6A]AACCGp	✓	✓
U[m7G]UUGp	✓	✓
ACUQUA[ms2i6A]AUCUGp	✓	✓
[s4U][s4U]CCCGp	✓	✓
AU[s4U]AGp	✓	✓
CACCUCCCU[cmo5U]AC[m6A]AGp	✓	✓
UUCA[s4U]AGp	✓	✓
[m5U]PCAAAUCCGp	✓	✓
UCCCCU[s4U]CGp	✗	✓
AAADD[Gm]Gp	✓	✓
AUU[cmo5U]AGp	✓	✓

[m1G]PUCUGp	✓	✓
A[Cm]U[cmo5U]Gp	✗	✓
U[t6A]AUCAGp	✓	✓
[m7G]UCACCAGp	✓	✓
CUU[k2C]CCAAGp	✓	✓
ACUUCA[i6A]AUCCAGp	✓	✓
[s2C]UICGp	✓	✓
[m2A]ACCGp	✓	✓
CC[s2C]UCCGp	✓	✓
CCU[oQ]UC[m2A]CGp	✓	✓
UUCAADDGp	✓	✓
[Cm]UCAUAACCCGp	✓	✓
CCU[mnm5U]CCAAGp	✓	✓

Supplemental Table S3. Modified nucleosides from total tRNAs detected using LC-MS/MS.

Prokaryotic Organism						Eukaryotic Organism		
<i>T. thermophilus</i>			<i>C. koseri</i>			<i>S. pombe</i>		
RT (Min)	MH+	Nucleoside	RT (Min)	MH+	Nucleoside	RT (Min)	MH+	Nucleoside
1.69	247	D	1.69	247	D	1.54	247	D
1.76	245	Ψ	1.76	245	Ψ	1.6	245	Ψ
2.4	288	mnm ⁵ U	2.4	288	mnm ⁵ U	3.03	302	ncm ⁵ U
5.32	282	m ¹ A	2.84	319	cmo ⁵ U	3.48	274	nm ⁵ U
5.69	258	m ⁵ C	3.29	346	acp ³ U	4.28	282	m ¹ A
8.24	258	Cm	4.35	260	s ² C	7.29	258	Cm
9.4	298	m ⁷ G	6.22	304	mnm ⁵ s ² U	7.57	298	m ⁷ G
9.52	269	I	8.24	258	Cm	8.48	269	I
9.8	259	m ⁵ U	9.4	298	m ⁷ G	8.76	259	m ⁵ U
12.05	261	s ⁴ U	9.52	269	I	13.59	259	Um
15.22	259	Um	9.8	259	m ⁵ U	19.39	298	Gm
21.16	298	Gm	12.05	261	s ⁴ U	19.9	410	Q
21.98	298	m ¹ G	21.16	298	Gm	20.05	298	m ¹ G
23.83	298	m ² G	21.19	372	k ² C	21.05	286	ac ⁴ C
24.37	317	mcm ⁵ U	21.44	410	Q	21.94	298	m ² G

31.39	275	m ⁵ s ² U	21.98	298	m ¹ G	22.52	317	mcm ⁵ U
33.21	352	io ⁶ A	23.96	286	ac ⁴ C	29.68	312	m ^{2,2} G
33.76	296	m ^{6,6} A	37.02	282	m ² A	29.74	282	Am
36.52	398	ms ² io ⁶ A	38.39	413	t ⁶ A	31.17	333	mcm ⁵ s ² U
36.75	336	i ⁶ A	41.01	382	ms ² i ⁶ A	31.35	413	t ⁶ A
37.02	282	m ² A				34.94	377	yW
41.01	382	ms ² i ⁶ A				36.7	336	i ⁶ A
						37.02	282	m ² A
						41.01	382	ms ² i ⁶ A
Total 22			Total 20			Total 24		

Supplemental Table S4. Predicted post-transcriptionally modified RNase T1 digestion products (n > 3) from *T. thermophilus* total tRNAs and their detection by DDA and UMEL.

Predicted digestion products	Modification position in tRNA sequence	Standard DDA	UMEL
U[Gm]Gp	9	✓	✓
DD[Gm]Gp	16 17 18	✗	✓
[m7G]UCAGp	46	✓	✓
[m5s2U]UCGp	54	✓	✓
[m1A]AUCCCCUGp	58	✓	✓
C[t6A]UUGp	37	✓	✓
[s4U]AGp	8	✓	✓
A[Gm]Gp	17	✓	✓
[m7G]UCCGp	46	✓	✓
CU[Gm]Gp	18	✓	✓
[m1G]AUCAGp	37	✓	✓
[m7G]UCGp	46	✓	✓
[m1A]AUCCUCCCGp	58	✓	✓
[m1G]AGp	37	✓	✓
CA[Gm]Gp	18	✓	✓
UUCCU[t6A]AGp	37	✓	✓
[m7G]CCGp	46	✓	✓
CCU[mnm5s2U]CUAAGp	34	✓	✓
[m1A]AUCCUCCCGp	58	✓	✓
UU[t6A]ACCGp	37	✓	✓

UU[Gm]Gp	17	✓	✓
DDAACACACCCGp	20 21	✓	✓
CA[ms2i6A]AACCUCCAUCGp	37	✓	✓
[m1A]AUCCGp	58	✓	✓
CA[m2G]p	26	✓	✓
U[Cm]UGp	32	✓	✓
[s4U]CGp	8	✓	✓
[m1G]AUCCGp	37	✓	✓
[m1A]AUCCACGp	58	✓	✓
A[Cm]U[mnm5s2U]UGp	32 34	✓	✓
CCCCA[s4U]CGp	8	✓	✓
DDAGp	20 21	✓	✓
[m1A]UUCCCCUGp	58	✓	✓
[m1A]AUCCCCUGp	58	✓	✓
CCU[mnm5s2U]UCAAGp	34	✓	✓
[m5U]UCGp	54	✓	✓
[m5s2U]UCA[m1A]Gp	54 58	✓	✓
CUU[Gm]Gp	19	✓	✓
CCU[mnm5s2U]CCAGp	34	✓	✓
[m1A]AUCCCGp	58	✓	✓
AU[s4U]AGp	8	✓	✓
AU[t6A]AGp	37	✓	✓
U[s4U]AGp	8	✓	✓
CUCAAC[Gm]Gp	17	✓	✓
[m1A]AUCCUGp	58	✓	✓
U[m1G]Gp	9	✓	✓
ACU[Cm]AA[ms2io6A]AUCUGp	34 37	✓	✓
ACU[Cm]AA[ms2i6A]AUCUGp	34 37	✓	✓
AAUU[Gm]Gp	17	✓	✓
AUU[Cm]AGp	34	✓	✓
AACU[Gm]Gp	17	✓	✓
AAC[Gm]Gp	17	✓	✓
ACU[mnm5U]AA[ms2i6A]AUCCGp	34 37	✓	✓
A[s4U]Gp	8	✓	✓
AADC[Gm]Gp	16 18	✓	✓
[m1G]AUCCGp	37	✓	✓
C[s4U]AGp	8	✓	✓
CUCAACU[Gm]Gp	18	✓	✓
ACUCUU[t6A]AUCGp	37	✓	✓
[m7G]UUACAGp	46	✓	✓
ACU[mnm5s2U]UU[ms2io6A]AUCGp	34 37	✓	✓

CCU[Gm]Gp	17	✓	✓
ACUCAU[t6A]AUCGp	37	✓	✓
U[m7G]UCGp	46	✓	✓
AA[ms2i6A]AUCGp	37	✓	✓
[m1A]UUCCGp	58	✓	✓
CCC[Gm]Gp	18	✓	✓
[m5s2U]UCA[m1A]AUCCAGp	54 58	✓	✓
[m5s2U]UCA[m1A]AUCCGp	54 58	✓	✓
A[ms2i6A]AACCGp	37	✓	✓
A[ms2io6A]AACCGp	37	✓	✓
CU[t6A]AGp	37	✓	✓
CC[Cm]CAUCGp	32	×	✓
U[m7G]CCGp	46	✓	✓
A[ms2i6A]AUCGp	37	✓	✓
A[ms2io6A]AUCGp	37	✓	✓
A[i6A]AUCGp	37	✓	✓
A[ms2i6A]ACCGp	37	✓	✓
A[ms2io6A]ACCGp	37	✓	✓
U[t6A]AGp	37	✓	✓
CUCAACC[Gm]Gp	18	✓	✓
U[t6A]AUCGp	37	✓	✓
[m5s2U]UCA[m1A]CUCCCCUGp	54 58	✓	✓
U[Cm]UCCA[ms2i6A]AACCGp	32 37	✓	✓
U[Cm]UCCA[i6A]AACCGp	32 37	✓	✓
UA[ms2i6A]AACCGp	37	✓	✓
UA[ms2io6A]AACCGp	37	✓	✓
UA[i6A]AACCGp	37	✓	✓
[m1A]AUCCAGp	58	✓	✓
[Cm]UCAUAACCCGp	32	✓	✓
C[Cm]UUGp	32	×	✓
A[Cm]UACGp	32	×	✓
C[Cm]UGp	32	×	✓
CC[m1A]AGp	37	×	✓
C[m7G]CCGp	46	✓	✓
C[m7G]CAGp	46	×	✓
C[Cm]UCACACGp	32	✓	✓
CACUACC[Um]UGp	32	✓	✓

Supplemental Table S5. Predicted potential post-transcriptionally modified RNase T1 digestion products (n > 3) of *C. koseri* total tRNAs and their detection by DDA and UMEL.

Predicted digestion products	Modification position on tRNA sequence	Standard DDA	UMEL
CUA[s4U]AGp	8	✓	✓
[m7G]UCAGp	46	✓	✓
[m1A]UCCCGp	58	✓	✓
CU[Gm]Gp	18	✓	✓
[s4U]AGp	8	✓	✓
[m7G][acp3U]CGp	46 47	✓	✓
[m6A]ACCGp	37	✓	✓
CC[s2C]UCCGp	32	✓	✓
[m5U]UCGp	54	✓	✓
CCCU[s4U]AGp	8	✓	✓
DDGp	16 17	✓	✓
ACUQUU[t6A]AUCCGp	34 37	✓	✓
UAU[m7G]UCACUGp	46	✓	✓
DDAGp	16 17	✓	✓
CCUQUC[m2A]CGp	34 37	✓	✓
[m7G]UCGp	46	✓	✓
U[s4U]AGp	8	✓	✓
CA[ms2i6A]AUCCGp	37	✓	✓
[m1A]CUCCGp	58	✓	✓
UA[s4U]CGp	8	✓	✓
C[Gm]Gp	18	✓	✓
[m2A]UUCCGp	37	✓	✓
[m2A]UACCGp	37	✓	✓
UUU[mnm5s2U]UGp	37	✓	✓
CUU[ac4C]CCAAGp	34	✓	✓
AA[s4U]AGp	8	✓	✓
CA[s4U]CGp	8	✓	✓
CCU[mnm5U]CCAAGp	34	✓	✓
UU[m7G]UCGp	46	✓	✓
AUUQUGp	34	✓	✓
[m2A]UUCCAGp	37	✓	✓
AU[t6A]AGp	37	✓	✓
[m7G][acp3U]CGp	46 47	✓	✓
[m5U]UCAAGp	54	✓	✓
CCCCU[s4U]AGp	8	✓	✓
U[Gm]Gp	18	✓	✓
ACU[k2C]AU[t6A]AUCGp	37	✓	✓

U[m1G]Gp	37	✓	✓
AAADC[Gm]Gp	16 18	✓	✓
AUU[Cm]AA[ms2i6A]AUCAACCGp	34 37	✓	✓
AAADD[Gm]Gp	16 17 18	✓	✓
[m1G]UGp	37	✓	✓
AADD[Gm]Gp	16 17 18	✓	✓
AADC[Gm]Gp	16 18	✓	✓
A[s4U]Gp	8	✓	✓
AUU[cmo5U]AGp	34	✓	✓
[m1G]UUCUGp	37	✓	✓
ACU[mnm5s2U]UU[t6A]AUCAAUUGp	34 37	✓	✓
[m7G][acp3U]CACAGp	46 47	✓	✓
A[s4U]AGp	8	✓	✓
AA[ms2i6A]AUCCCCGp	37	✓	✓
[m1A]UUCCGp	58	✓	✓
U[m7G][acp3U]CCUUGp	46 47	✓	✓
AU[s4U]Gp	8	✓	✓
[m1G]ACGp	37	✓	✓
U[m5U]CAAAUCCUCUGp	54	✓	✓
[m1G]ACCAGp	37	✓	✓
UU[cmo5U]Gp	34	✓	✓
A[ms2i6A]AACCGp	37	✓	✓
CUCCC[s2C]UGp	32	✓	✓
AUA[s4U]AGp	8	✓	✓
AUA[s4U]Gp	8	✓	✓
[m7G]UCCCCAGp	46	✓	✓
[m1A]CUCUGp	58	✓	✓
ACU[s4U]AGp	8	✓	✓
[m7G]UACCAGp	46	✓	✓
A[Cm]U[cmo5U]Gp	32 34	✓	✓
U[t6A]AUCAGp	37	✓	✓
UUCAADDGp	16 17	✓	✓
U[m7G]UUGp	46	✓	✓
U[Cm]UCCA[ms2i6A]AACCGp	32 37	✓	✓
ACUQUA[ms2i6A]AUCUGp	34 37	✓	✓
UAA[t6A]Gp	37	✓	✓
UUCA[s4U]AGp	8	✓	✓
AU[s4U]AGp	8	✓	✓
CACCUCCCU[cmo5U]AC[m6A]AGp	34 37	✓	✓
[m1A]UCCCGp	58	✓	✓
[m5U]UCAAAUCCCGp	54	✓	✓

[m5U]UCAAUCUGp	54	✓	✓
[m7G]UCUCAGp	46	✓	✓
[m7G]UCUGp	46	✓	✓
CACAUCACU[ac4C]AU[t6A]AUGp	34 37	×	✓
CUU[cmo5U]Gp	34	×	✓
DDAUGp	16 17	×	✓
UCCCCU[s4U]CGp	8	×	✓
CACCC[s2C]UGp	32	×	✓
CUU[ac4C]AGp	34	×	✓
UCU[cmo5U]Gp	34	×	✓
CU[t6A]AGp	37	×	✓
[s4U][s4U]CCCGp	8 9	×	✓
CCCCUCCU[t6A]AGp	37	✓	✓

Supplemental Table S6. Predicted potential post-transcriptionally modified RNase T1 digestion products ($n > 3$) of *S. pombe* total tRNAs and their detection by DDA and UMEL.

Predicted digestion products	Modification position on tRNA sequence	Standard DDA	UMEL
C[m1A]UGp	37	✓	✓
U[m5C]CCAGp	48	✓	✓
A[m5U]UCGp	54	✓	✓
U[m5C]CCGp	48	✓	✓
CUU[ncm5U]Gp	34	✓	✓
U[m5C]CUGp	48	✓	✓
U[m1G]Gp	9	×	✓
DDAAGp	19 20	✓	✓
C[m22G]CUUGp	26	✓	✓
[m1G]AUCAAGp	37	✓	✓
AUU[m5C]CAGp	48	✓	✓
[m1A]CUCCUGp	58	✓	✓
[m1G]UGp	37	✓	✓
ACU[m5C]CAGp	48	✓	✓
AU[m5C]Gp	48	✓	✓
CUUAAUD[Gm]Gp	17 18	×	✓
DDAGp	20 21	✓	✓
U[m1A]Gp	9	✓	✓
UUU[mcm5U]CGp	34	✓	✓
ACU[mcm5U]CUAAUCAAGp	34	✓	✓
UA[m2G]p	10	✓	✓
UU[t6A]AUGp	37	✓	✓
DDGp	16 17	✓	✓

DDAUUGp	20 21	✓	✓
ACUQUU[t6A]AUCGp	34 37	✓	✓
[m7G]U[m5C]Gp	46 48	✓	✓
UC[i6A]CGp	37	✗	✓
[m5C]CCGp	48	✓	✓
[m1A]AUCCCGp	58	✓	✓
[m7G]U[m5C]ACUGp	46 48	✓	✓
TPCA[m1A]AICCGp	54 58	✓	✓
UAU[m1G]Gp	9	✓	✓
A[m5C]CUGp	48	✓	✓
AUU[mcm5s2U]UGp	34	✓	✓
[m2A]UUCUCGp	37	✓	✓
AU[m5C]UGp	48	✓	✓
CU[mcm5s2U]UCACCGp	34	✓	✓
U[m5C]Gp	48	✓	✓
CU[m5C]CGp	48	✓	✓
[m1A]CUCCCGp	58	✓	✓
A[m5C]CCGp	48	✓	✓
[m1A]UUCCCGp	58	✓	✓
CCU[mcm5U]CCAAGp	34	✓	✓
[m1G]CAUAAGp	37	✓	✓
CUCACAU[m1G]Gp	9	✓	✓
A[m5C]CCAGp	48	✓	✓
DDAUCAUGp	20 21	✗	✓
[m1A]ACCUGp	58	✗	✓
[m1A]ACCCGp	58	✓	✓
AU[t6A]AGp	37	✓	✓
AAAU[m5C]Gp	48	✓	✓
[m1A]UCCUCGp	58	✓	✓
UC[ac4C]Gp	12	✓	✓
DDAUGp	19 20	✓	✓
[m1G]CACUAGp	37	✓	✓
CU[m5C]Gp	48	✓	✓
C[ac4C]Gp	12	✓	✓
C[Gm]Gp	17	✗	✓
C[m22G]CAGp	27	✓	✓
[m1A]AUCCCUCACUGp	58	✓	✓
[m1A]ACCCACCUUCGp	58	✓	✓
CC[ac4C]Gp	12	✓	✓
[m1A]ACCUCUCUGp	58	✓	✓
U[Gm]Gp	17	✓	✓

CUU[ncm5U]AGp	34	✓	✓
DDDAGp	16 17 18	✓	✓
CCUUUU[t6A]AGp	37	×	✓
[m1A]AUCUCGp	58	✓	✓
UAADDGp	16 17	×	✓
[m5U]UCAAGp	54	✓	✓
DDAAAGp	18 19	✓	✓
CA[m22G]AGp	27	✓	✓
UA[m1G]Gp	9	✓	✓
[m1A]AACCUgP	58	×	✓
CAAU[m1G]Gp	9	✓	✓
U[m5C]AUCGp	48	✓	✓
AU[m5C]CCUGp	48	✓	✓
[m1A]AUCCUGp	58	✓	✓
U[m5C]ACGp	48	✓	✓
[m5U]UCAAUCCCCGp	54	✓	✓
[m7G]UCAGp	46	✓	✓
UUUAAUU[Gm]Gp	17	×	✓
[m22G]ACAGp	26	✓	✓
A[i6A]AUCUGp	37	✓	✓
U[Um]Gp	44	✓	✓
[m5U]UCA[m1A]AUCCUGp	54	✓	✓
A[m3C]UCGp	32	✓	✓
DDDUAAAGp	19 20 21	✓	✓
DDUAAGp	16 17	✓	✓
A[m3C]UUGp	32	✓	✓
A[m6A]UCCUGp	37	✓	✓
U[t6A]AGp	37	✓	✓
[m7G]CCCAGp	46	×	✓
C[m5C]CAGp	48	✓	✓
[m5U]UCA[m1A]Gp	54 58	✓	✓
U[m5C]CAGp	48	✓	✓
CA[m3C]U[ncm5U]Gp	32 34	✓	✓
U[t6A]AUGp	37	✓	✓
AU[m5C]CUUGp	48	✓	✓
[m1A]UUCCGp	58	×	✓
AU[m1G]Gp	9	✓	✓
DDAUCACACCCGp	16 17	×	✓
[m7G]UCGp	46	×	✓
[m1A]UUCUGp	58	×	✓
DDAUCACAUCCGp	16 17	×	✓

DDAUAAUUUCUGp	16 17	✓	✓
UC[m5C]CAAGp	49	✗	✓
[m1A]UCCCCGp	58	✓	✓
CUU[ncm5U]ACACGp	34	✓	✓
UC[m5C]CAGp	49	✓	✓
[m1A]UCCCUGp	58	✓	✓
AU[Gm]Gp	18	✓	✓
[m5U]UCGp	54	✓	✓
C[m1A]AAUCUCGp	58	✓	✓
UCUCCUUU[m1A]Gp	9	✓	✓
A[Um]UCUGp	32	✓	✓
UCCAA[Cm]Gp	16	✓	✓
[m1A]UUCCUGp	58	✓	✓
DDAUCAU[m22G]UCGp	26	✓	✓
UCAU[m5C]AGp	39	✓	✓
CDDAGp	16 17	✓	✓
[m1A]UCCCCGp	58	✓	✓
A[m5U]UCCCUUUGp	54	✓	✓

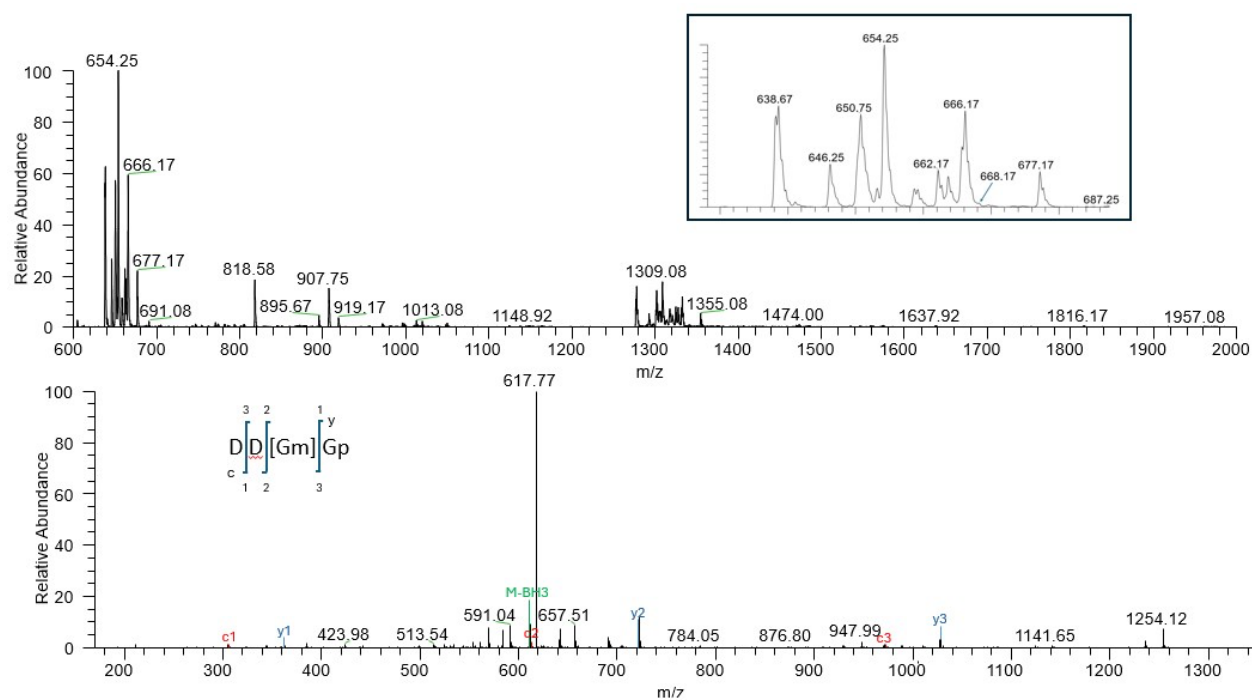


Figure S1. Mass spectrum from LC-MS/MS analysis of RNase T1-digested *T. Thermophilus* total tRNAs, showing the modified oligonucleotide DD[Gm]Gp co-eluting with other highly abundant unmodified digestion products. MS/MS annotation confirms the sequence DD[Gm]Gp. Inset shows a closer view of the 600–700 region.

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ala-GGC-1-1 (tRNAscan-SE ID: chr.trna9)
Ala (GGC) 76 bp mature sequence Sc: 75.0 chr:377442-377517 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ala-GGC-1-2 (tRNAscan-SE ID: chr.trna10)
Ala (GGC) 76 bp mature sequence Sc: 75.0 chr:377557-377632 (+)

GGGGCUA [s4U] AGCUCAGCUGGGAGAGCGCUUGCAUGGCAUGCAAGAG [m7G] UCAGCGG [m5U] UCG [m1A] UCC
CGCUUAGCUCCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ala-TGC-1-1 (tRNAscan-SE ID: chr.trna58)
Ala (TGC) 76 bp mature sequence Sc: 78.1 chr:2799058-2799133 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ala-TGC-1-2 (tRNAscan-SE ID: chr.trna56)
Ala (TGC) 76 bp mature sequence Sc: 78.1 chr:2929637-2929712 (-)

GGGGCUA [s4U] AGCUCAGCU [Gm] GGAGAGCGCCUGCUU [cmo5U] GCACGCAGGAG [m7G] UCUGCGG [m5U] UC
G [m1A] UCCCCGAUAGCUCCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Arg-ACG-1-1 (tRNAscan-SE ID: chr.trna50)
Arg (ACG) 77 bp mature sequence Sc: 85.1 chr:3760364-3760440 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Arg-ACG-1-2 (tRNAscan-SE ID: chr.trna49)
Arg (ACG) 77 bp mature sequence Sc: 85.1 chr:3760634-3760710 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Arg-ACG-1-3 (tRNAscan-SE ID: chr.trna48)
Arg (ACG) 77 bp mature sequence Sc: 85.1 chr:3760904-3760980 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Arg-ACG-1-4 (tRNAscan-SE ID: chr.trna47)
Arg (ACG) 77 bp mature sequence Sc: 85.1 chr:3761043-3761119 (-)

GCAUCCG [s4U] AGCUCAGCU [Gm] GADAGAGUACUCGCUACG [m2A] ACCGAGCG [m7G] [acp3U] CGGAGG [m
5U] UCGAAUCCUCCCGGAUGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Arg-CCG-1-1 (tRNAscan-SE ID: chr.trna4)
Arg (CCG) 77 bp mature sequence Sc: 82.9 chr:135992-136068 (+)

GCGCCCC [s4U] AGCUCAGCUGGAUAGAGCGCUGCC [s2C] UCCGAGGCAGAG [m7G] UCUCAGG [m5U] UCGAAU
CCUGUCGGGCGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Arg-CCT-1-1 (tRNAscan-SE ID: chr.trna80)
Arg (CCT) 75 bp mature sequence Sc: 64.4 chr:426987-427061 (-)

GUCUCCUUAGUAAAUGGAUUAUAACGAGCCCCUCCU [t6A] AGGGCUAGUUGCAGG [m5U] UCGAUUCCUGCAGGGG
ACACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Arg-TCT-1-1 (tRNAscan-SE ID: chr.trna67)
Arg (TCT) 77 bp mature sequence Sc: 93.7 chr:2423926-2424002 (-)

GCGCCCU [s4U] AGCUCAGDDGGAUAGAGCAACGGCCUUCUAAGCCGUGGGUCGCAGG [m5U] UCGAAUCCUGCAGG
GCGCGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Asn-GTT-1-1 (tRNAscan-SE ID: chr.trna78)
Asn (GTT) 76 bp mature sequence Sc: 79.7 chr:800572-800647 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Asn-GTT-1-2 (tRNAscan-SE ID: chr.trna11)
Asn (GTT) 76 bp mature sequence Sc: 79.7 chr:802386-802461 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Asn-GTT-1-3 (tRNAscan-SE ID: chr.trna77)
Asn (GTT) 76 bp mature sequence Sc: 79.7 chr:953771-953846 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Asn-GTT-1-4 (tRNAscan-SE ID: chr.trna76)
Asn (GTT) 76 bp mature sequence Sc: 79.7 chr:956181-956256 (-)

UCCUCUG [s4U] AGUUCAGUCGGUAGAACGGCGGACQUU [t6A] AUCCGUAU [m7G] UCACUGG [m5U] UCGAGUCC
AGUCAGAGGAGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Asp-GTC-1-1 (tRNAscan-SE ID: chr.trna2)
 Asp (GTC) 77 bp mature sequence Sc: 87.4 chr:98854-98930 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Asp-GTC-1-2 (tRNAscan-SE ID: chr.trna65)
 Asp (GTC) 77 bp mature sequence Sc: 87.4 chr:2749262-2749338 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Asp-GTC-1-3 (tRNAscan-SE ID: chr.trna64)
 Asp (GTC) 77 bp mature sequence Sc: 87.4 chr:2757583-2757659 (-)

GGAGCGG [s4U] AGUUCAGDDGGDDAGAAUACCUGCCQGUC [m2A] CGCAGGGG [m7G] UCGCGGG [m5U] UCGAGU
 CCGGUCCGUUCCGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Cys-GCA-1-1 (tRNAscan-SE ID: chr.trna14)
 Cys (GCA) 74 bp mature sequence Sc: 63.1 chr:1023310-1023383 (+)

GGCGCGU [s4U] AGCAAAGCGGDDAUGUAGCGGAUUGCA [ms2i6A] AUCCGUCUAGUCCGG [m5U] UCG [m1A] CU
 CCGGAACGCGCCUCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gln-CTG-1-1 (tRNAscan-SE ID:
 chr.trna27) Gln (CTG) 75 bp mature sequence Sc: 70.8 chr:2307895-2307969 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gln-CTG-1-2 (tRNAscan-SE ID: chr.trna28)
 Gln (CTG) 75 bp mature sequence Sc: 70.8 chr:2308012-2308086 (+)

UGGGGUA [s4U] CGCCAAGC [Gm] GUAAGGCACCGGAUUCUG [m2A] UUCCGGCAUUCGAGG [m5U] UCGAAUCCU
 CGUACCCAGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gln-TTG-1-1 (tRNAscan-SE ID: chr.trna24)
 Gln (TTG) 75 bp mature sequence Sc: 70.4 chr:2307610-2307684 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gln-TTG-1-2 (tRNAscan-SE ID: chr.trna25)
 Gln (TTG) 75 bp mature sequence Sc: 70.4 chr:2307721-2307795 (+)

UGGGGUA [s4U] GCCAAGC [Gm] GUAAGGCACCGGUUU [mnm5s2U] UG [m2A] UACCGGCAUUCGUGG [m5U] UC
 GAAUCCAGGUACCCAGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Glu-TTC-1-1 (tRNAscan-SE ID: chr.trna1)
 Glu (TTC) 76 bp mature sequence Sc: 66.6 chr:95422-95497 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Glu-TTC-1-2 (tRNAscan-SE ID: chr.trna8)
 Glu (TTC) 76 bp mature sequence Sc: 66.6 chr:185385-185460 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Glu-TTC-1-3 (tRNAscan-SE ID: chr.trna63)
 Glu (TTC) 76 bp mature sequence Sc: 66.6 chr:2761015-2761090 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Glu-TTC-1-4 (tRNAscan-SE ID: chr.trna51)
 Glu (TTC) 76 bp mature sequence Sc: 66.6 chr:3644874-3644949 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Glu-TTC-1-5 (tRNAscan-SE ID: chr.trna41)
 Glu (TTC) 76 bp mature sequence Sc: 66.6 chr:4325412-4325487 (-)

GUCCCCU [s4U] CGUCUAGAGGCCAGGACACCGCCCUUUCACGCGGUAACAGGGG [m5U] UCGAAUCCCCUAGGG
 GACGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gly-CCC-1-1 (tRNAscan-SE ID: chr.trna45)
 Gly (CCC) 74 bp mature sequence Sc: 81.1 chr:3940649-3940722 (-)

GCGGGCG [s4U] AGUUCAUGGUAGAACGAGAGCUU [ac4C] CCAAGCUCUAUACGAGGG [m5U] UCGAUUCCCUUC
 GCCCGCUCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gly-GCC-1-1 (tRNAscan-SE ID: chr.trna13)
 Gly (GCC) 76 bp mature sequence Sc: 88.4 chr:1023182-1023257 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gly-GCC-1-2 (tRNAscan-SE ID: chr.trna53)
 Gly (GCC) 76 bp mature sequence Sc: 88.4 chr:3411303-3411378 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gly-GCC-1-3 (tRNAscan-SE ID: chr.trna52)
 Gly (GCC) 76 bp mature sequence Sc: 88.4 chr:3411447-3411522 (-)
 GCGGGAA [s4U] AGCUCAGDDGGUAGAGCACGACCUUGCCAAGGUCGGG [m7G] UCGCGAG [m5U] UCGAGUCUCGU
 UCCCCGCUCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Gly-TCC-1-1 (tRNAscan-SE ID: chr.trna61)
 Gly (TCC) 75 bp mature sequence Sc: 70.6 chr:2791768-2791842 (-)
 GCGGGCA [s4U] CGUAUAAUGGCUAUUACCUCAGCCU [mnm5U] CCAAGCUGAUGAUGCGGG [m5U] UCGAUUCCCG
 CUGCCCCGCUCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-His-GTG-1-1 (tRNAscan-SE ID: chr.trna5)
 His (GTG) 76 bp mature sequence Sc: 78.7 chr:136123-136198 (+)
 GUGGCUA [s4U] AGCUCAGDDGGUAGAGCCCUGGAUUG [m2A] UUCCAGUU [m7G] GUCCUGGG [m5U] UCGAAU
 CCCAUUAGCCACCCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ile-GAT-1-1 (tRNAscan-SE ID: chr.trna57)
 Ile (GAT) 77 bp mature sequence Sc: 75.8 chr:2799247-2799323 (-)
 >Citrobacter_koseri_ATCC_BAA-895_tRNA-Ile-GAT-1-2 (tRNAscan-SE ID: chr.trna55)
 Ile (GAT) 77 bp mature sequence Sc: 75.8 chr:2929826-2929902 (-)
 AGGCUUG [s4U] AGCUCAGGUGGUUAGAGCGCACCC [s2C] UGAU [t6A] AGGGUGAG [m7G] [acp3U] CGGUGG [
 m5U] UCAAGUCCACUCAGGCCUACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ile2-CAT-1-1 (tRNAscan-SE ID:
 chr.trna38) Ile2 (CAT) 76 bp mature sequence Sc: 85.1 chr:4133781-4133856 (+)
 GGCCCCU [s4U] AGCUCAGU [Gm] GDDAGAGCAGGCGACU [k2C] AU [t6A] AUCGCUUGGUCGCUGG [m5U] UCAA
 GUCCAGCAGGGGCCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Leu-CAA-1-1 (tRNAscan-SE ID: chr.trna54)
 Leu (CAA) 85 bp mature sequence Sc: 79.3 chr:3291772-3291856 (-)
 GCCGAAGUGGCGAAAD [Gm] GUAGACGCAGUUGAUU [Cm] AA [ms2i6A] AUCAACCGUAGAAUACGUGCCGG [m
 5U] UCGAGUCCGGCCUUCGGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Leu-CAG-1-1 (tRNAscan-SE ID: chr.trna6)
 Leu (CAG) 87 bp mature sequence Sc: 67.1 chr:136218-136304 (+)
 >Citrobacter_koseri_ATCC_BAA-895_tRNA-Leu-CAG-1-2 (tRNAscan-SE ID: chr.trna29)
 Leu (CAG) 87 bp mature sequence Sc: 67.1 chr:3192511-3192597 (+)
 >Citrobacter_koseri_ATCC_BAA-895_tRNA-Leu-CAG-1-3 (tRNAscan-SE ID: chr.trna31)
 Leu (CAG) 87 bp mature sequence Sc: 67.1 chr:3192744-3192830 (+)
 >Citrobacter_koseri_ATCC_BAA-895_tRNA-Leu-CAG-2-1 (tRNAscan-SE ID: chr.trna30)
 Leu (CAG) 87 bp mature sequence Sc: 65.0 chr:3192625-3192711 (+)
 GCGAAGGUGGCGGAADD [Gm] GUAGACGCGCUAGCUU [ac4C] AG [m1G] UGUUAGUGUCCUACGGACGUGGGG [
 m5U] UCAAGUCCCCCCCCUCGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Leu-GAG-1-1 (tRNAscan-SE ID: chr.trna43)
 Leu (GAG) 87 bp mature sequence Sc: 64.5 chr:4225456-4225542 (-)
 GCCGAGGUGGUGGAADD [Gm] GUAGACACGCUACCUUGAG [m1G] UGGUAGUGCCCAUAGGGCUUACGGG [m5U] U
 CAAGUCCCGUCCUCGGUACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Leu-TAA-1-1 (tRNAscan-SE ID: chr.trna15)
 Leu (TAA) 87 bp mature sequence Sc: 70.2 chr:1023396-1023482 (+)
 GCCCGGA [s4U] GGUGGAAD [Gm] GUAGACACAAGGAUUUAAAUCCUCGGCGUUCGCGCUGUGUGGG [m5U] U
 CAAGUCCACUCCGGGUACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Leu-TAG-1-1 (tRNAscan-SE ID: chr.trna23)
 Leu (TAG) 85 bp mature sequence Sc: 74.1 chr:2307502-2307586 (+)
 GCGGGAGUGGCGAAADD [Gm] GUAGAGCGACCAGAUU [cmo5U] AG [m1G] UUCUGGCGCCGCAAGGUGUGCGAG [m5U] UCAAGUCUCGCCUCCCGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Lys-TTT-1-1 (tRNAscan-SE ID: chr.trna84)
 Lys (TTT) 76 bp mature sequence Sc: 94.9 chr:374318-374393 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Lys-TTT-1-2 (tRNAscan-SE ID: chr.trna72)
 Lys (TTT) 76 bp mature sequence Sc: 94.9 chr:2217686-2217761 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Lys-TTT-1-3 (tRNAscan-SE ID: chr.trna71)
 Lys (TTT) 76 bp mature sequence Sc: 94.9 chr:2217894-2217969 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Lys-TTT-1-4 (tRNAscan-SE ID: chr.trna70)
 Lys (TTT) 76 bp mature sequence Sc: 94.9 chr:2218115-2218190 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Lys-TTT-1-5 (tRNAscan-SE ID: chr.trna68)
 Lys (TTT) 76 bp mature sequence Sc: 94.9 chr:2218306-2218381 (-)
 GGGUCGU [s4U] AGCUCAGDDGGUAGAGCAGUUGACU [mnm5s2U] UU [t6A] AUCAAUUG [m7G] [acp3U] CGCAGG [m5U] UCGAAUCCUGCAGCACCCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Met-CAT-1-1 (tRNAscan-SE ID: chr.trna22)
 Met (CAT) 77 bp mature sequence Sc: 84.4 chr:2307417-2307493 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Met-CAT-1-2 (tRNAscan-SE ID: chr.trna26)
 Met (CAT) 77 bp mature sequence Sc: 84.4 chr:2307812-2307888 (+)
 GGCUACG [s4U] AGCUCAGDDGGUAGAGCACAUACACU [ac4C] AU [t6A] AUGAUGGG [m7G] [acp3U] CACAGG [m5U] UCGAAUCCCGUCGUAGCCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Phe-GAA-1-1 (tRNAscan-SE ID: chr.trna32)
 Phe (GAA) 76 bp mature sequence Sc: 75.3 chr:3440370-3440445 (+)
 GCCCGGA [s4U] AGCUCAGUCGGUAGAGCAGGGGAUUGAA [ms2i6A] AUCCCCGU [m7G] [acp3U] CUUGG [m5U] UCG [m1A] UUCCGAGUCCGGGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Pro-CGG-1-1 (tRNAscan-SE ID: chr.trna40)
 Pro (CGG) 77 bp mature sequence Sc: 76.0 chr:4587550-4587626 (-)
 CGGUGAU [s4U] GGCGCAGCCUGGUAGCGCACUUCGUUCGG [m1G] ACGAAGGG [m7G] UCGGAGG [m5U] UCGAAU CCUCUAUACCGACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Pro-GGG-1-1 (tRNAscan-SE ID: chr.trna79)
 Pro (GGG) 77 bp mature sequence Sc: 67.3 chr:566485-566561 (-)
 CGGCACG [s4U] AGCGCAGCCUGGUAGCGCACCGUCAUGGG [m1G] UGUCGGGGGUC [m7G] GAGGU [m5U] CAAAU CCUCUCGUGCCGACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Pro-TGG-1-1 (tRNAscan-SE ID: chr.trna7)
 Pro (TGG) 77 bp mature sequence Sc: 82.4 chr:136348-136424 (+)
 CGGCGAG [s4U] AGCGCAGCUUGGUAGCGCAACUGGUU [cmo5U] GG [m1G] ACCAGUGG [m7G] UCGGAGG [m5U] UCGAAUCCUCUCUGCCGACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ser-CGA-1-1 (tRNAscan-SE ID: chr.trna12)
 Ser (CGA) 90 bp mature sequence Sc: 90.4 chr:957248-957337 (+)
 GGAGAGA [s4U] GCCGGAGC [Gm] GCUGAACGGACCGGUCUCGA [ms2i6A] AACCGGAGUAGGGGCAACUCUACCG GGGGUUCAAUCCCCCUCUCUCCGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ser-GCT-1-1 (tRNAscan-SE ID: chr.trna46)
 Ser (GCT) 93 bp mature sequence Sc: 83.4 chr:3761123-3761215 (-)

GGUGAGGUGGCCGAGAGGCUGAAGGCGCUGCC [s2C] UGCU [t6A] AGGGAGUAUGCGGUCAAAAGCUGCAUCCGGG
G [m5U] UCGAAUCCCCGCCUCACCGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ser-GGA-1-1 (tRNAscan-SE ID: chr.trna20)
Ser (GGA) 88 bp mature sequence Sc: 76.9 chr:1889176-1889263 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ser-GGA-1-2 (tRNAscan-SE ID: chr.trna21)
Ser (GGA) 88 bp mature sequence Sc: 76.9 chr:2036117-2036204 (+)

GGUGAGGUGUCCGAGU [Gm] GCUGAAGGAGCACGCCUGGAAAGUGUGUAUACGGCAACGUAUCGGGGG [m5U] UCGA
AUCCCCCCCUCACCGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Ser-TGA-1-1 (tRNAscan-SE ID: chr.trna73)
Ser (TGA) 88 bp mature sequence Sc: 83.5 chr:1937267-1937354 (-)

GAAGUGUGGCCGAGCGGUUGAAGGCACCGGUCU [cmo5U] GA [ms2i6A] AACCGGCGACCCGAAAGGGUCCAGA
G [m5U] UCGAAUCUCUGCGCUCCGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Thr-CGT-1-1 (tRNAscan-SE ID: chr.trna66)
Thr (CGT) 76 bp mature sequence Sc: 85.1 chr:2733970-2734045 (-)

GCCGAUA [s4U] AGCUCAGUUGGUAGAGCAGCGCAUUCGUAAUGCGAAG [m7G] UCGUAGG [m5U] UCGACUCCUAU
UAUCGGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Thr-GGT-1-1 (tRNAscan-SE ID: chr.trna62)
Thr (GGT) 76 bp mature sequence Sc: 79.8 chr:2791687-2791762 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Thr-GGT-1-2 (tRNAscan-SE ID: chr.trna42)
Thr (GGT) 76 bp mature sequence Sc: 79.8 chr:4322020-4322095 (-)

GCUGAUA [s4U] GGCUCAGUUGGUAGAGCGACCCUUGGUAAGGGUGAG [m7G] UCCCCAG [m5U] UCG [m1A] CUC
UGGGUAUCAGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Thr-TGT-1-1 (tRNAscan-SE ID: chr.trna17)
Thr (TGT) 76 bp mature sequence Sc: 81.3 chr:1336961-1337036 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Thr-TGT-1-2 (tRNAscan-SE ID: chr.trna59)
Thr (TGT) 76 bp mature sequence Sc: 81.3 chr:2792053-2792128 (-)

GCCGAC [s4U] UAGCUCAGUAGGUAGAGCAACUGA [Cm] U [cmo5U] GU [t6A] AUCAGUAG [m7G] UCACCAG [m5
U] UCGAUUCCGGUAGUCGGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Trp-CCA-1-1 (tRNAscan-SE ID: chr.trna3)
Trp (CCA) 76 bp mature sequence Sc: 79.9 chr:98939-99014 (+)

AGGGGCGUAGUUCAAADDGUAGAGCACCGGU [Cm] UCCA [ms2i6A] AACCGGGU [m7G] UUGGGAG [m5U] UCGAG
UCUCUCCGCCCCUGCCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Tyr-GTA-1-1 (tRNAscan-SE ID: chr.trna75)
Tyr (GTA) 85 bp mature sequence Sc: 73.2 chr:1277983-1278067 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Tyr-GTA-1-2 (tRNAscan-SE ID: chr.trna74)
Tyr (GTA) 85 bp mature sequence Sc: 73.2 chr:1278104-1278188 (-)

GGUGGGG [s4U] [s4U] CCCGAGUGGCCAAAGGGAGCAGACUQUA [ms2i6A] AUCUGCCGUCAUCGACUUCGAAGG [m5U] UCGAAUCCUCCCCCACCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Tyr-GTA-2-1 (tRNAscan-SE ID: chr.trna60)
Tyr (GTA) 85 bp mature sequence Sc: 73.0 chr:2791960-2792044 (-)

GGUGGGG [s4U] [s4U] CCCGAGUGGCCAAAGGGAGCAGACUQUA [ms2i6A] AUCUGCCGUCAUCGACUUCGAAGG
[m5U] UCGAAUCCUCCCCCACCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Val-GAC-1-1 (tRNAscan-SE ID: chr.trna19)
Val (GAC) 77 bp mature sequence Sc: 85.6 chr:1612528-1612604 (+)

GCGUCUG [s4U] AGCUCAGDDGGDDAGAGCACCACCUUGACAUGGUGGGGGUCGAUGG [m5U] UCGAGUCCAUCAG
ACGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Val-GAC-2-1 (tRNAscan-SE ID: chr.trna18)
Val (GAC) 77 bp mature sequence Sc: 82.5 chr:1612447-1612523 (+)

GCGUUUG [s4U] AGCUCAGDDGGDDAGAGCACCACCUUGACAUGGUGGGGGUCGUUGG [m5U] UCGAGUCCAUCAGA
CGCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Val-TAC-1-1 (tRNAscan-SE ID: chr.trna83)
Val (TAC) 76 bp mature sequence Sc: 84.6 chr:374398-374473 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Val-TAC-1-2 (tRNAscan-SE ID: chr.trna82)
Val (TAC) 76 bp mature sequence Sc: 84.6 chr:374520-374595 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Val-TAC-1-3 (tRNAscan-SE ID: chr.trna81)
Val (TAC) 76 bp mature sequence Sc: 84.6 chr:374640-374715 (-)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-Val-TAC-1-4 (tRNAscan-SE ID: chr.trna69)
Val (TAC) 76 bp mature sequence Sc: 84.6 chr:2218194-2218269 (-)

GGGUGAU [s4U] AGCUCAGCUGGGAGAGCACCUCUU [cmo5U] AC [m6A] AGGAGGGG [m7G] UCGGCGG [m5U] U
CGAUCCGUAUCACCCACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-fMet-CAT-1-1 (tRNAscan-SE ID:
chr.trna35) fMet (CAT) 77 bp mature sequence Sc: 77.5 chr:3882519-3882595 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-fMet-CAT-1-2 (tRNAscan-SE ID:
chr.trna36) fMet (CAT) 77 bp mature sequence Sc: 77.5 chr:3882747-3882823 (+)

>Citrobacter_koseri_ATCC_BAA-895_tRNA-fMet-CAT-1-3 (tRNAscan-SE ID:
chr.trna44) fMet (CAT) 77 bp mature sequence Sc: 77.5 chr:4223484-4223560 (-)

CGCGGGGUGGAGCAGCCUGGUAGCUCGUCGGGCUCAUAACCCGAAG [m7G] UCGUCGG [m5U] UCAAAUCCGCCCC
CGCAACCA

>Citrobacter_koseri_ATCC_BAA-895_tRNA-fMet-CAT-2-1 (tRNAscan-SE ID:
chr.trna34) fMet (CAT) 77 bp mature sequence Sc: 75.3 chr:3882291-3882367 (+)

CGCGGGGUGGAGCAGCCUGGUAGCUCGUCGGGCUCAUAACCCGAAG [m7G] UCGUCAG [m5U] UCAAAUCUGCCCCC
GCAACCA

Supplemental Figure S2. RNase T1 modification mapping results for *C. koseri* tRNAs. Identified RNase T1 digestion products are shown in blue, and non-identified regions are shown in black. Modifications are annotated at their corresponding positions and color-coded by base identity: adenosine modifications (green), uridine modifications (red), cytidine modifications (orange), and guanosine modifications (purple).

>Thermus_thermophilus_HB27_tRNA-Ala-CGC-1-1 (tRNAscan-SE ID: chr.trna24) Ala (CGC) 76 bp mature sequence Sc: 84.3 chr:1831791-1831866 (+)

GGGGCCGU [Gm] GCGCAGDD [Gm] GGAGCGCGCCUGAAUCGCACUCAGGAG [m7G] UCAGGGG [m5s2U] UCG [m1A] AUCCCCUCGGCUCCACCA

>Thermus_thermophilus_HB27_tRNA-Ala-GGC-1-1 (tRNAscan-SE ID: chr.trna36) Ala (GGC) 76 bp mature sequence Sc: 81.7 chr:1347714-1347789 (-)

GGGGCCGUGGCGCAGDD [Gm] GGAGCGCGCCUCA AUGGC [t6A] UUGAGGAGGUCAGGGG [m5s2U] UCG [m1A] AUCCCCUCGGCUCCACCA

>Thermus_thermophilus_HB27_tRNA-Ala-TGC-1-1 (tRNAscan-SE ID: chr.trna6) Ala (TGC) 75 bp mature sequence Sc: 85.8 chr:493891-493965 (+)

GGGGCGG [s4U] AGCUCAGA [Gm] GGAGAGCAGCCGC [Cm] UUGCAAGCGGGAG [m7G] UCCGGGG [m5U] UCA [m1A] AUCCCCGCGCGCUCCACCA

>Thermus_thermophilus_HB27_tRNA-Arg-ACG-1-1 (tRNAscan-SE ID: chr.trna32) Arg (ACG) 77 bp mature sequence Sc: 86.3 chr:1482686-1482762 (-)

GGGCCCUGAGCUCAGCU [Gm] GAUAGAGCGGCUGACUACG [m1G] AUCAGCAG [m7G] UCGGGGG [m5s2U] UCG [m1A] AUCCUCCGGGCCCGCCA

>Thermus_thermophilus_HB27_tRNA-Arg-CCG-1-1 (tRNAscan-SE ID: chr.trna16) Arg (CCG) 77 bp mature sequence Sc: 86.9 chr:1553520-1553596 (+)

GCGCCCUGAGCUCAGCU [Gm] GAUAGAGCGUCGGCCUCCG [m1G] AGCCGAAGGUCAGAGG [m5s2U] UCGAGUCCU CUCGGGCGCGCCA

>Thermus_thermophilus_HB27_tRNA-Arg-CCT-1-1 (tRNAscan-SE ID: chr.trna27) Arg (CCT) 77 bp mature sequence Sc: 84.9 chr:1804494-1804570 (-)

GCGCCCUGAGCUCAGCA [Gm] GAUAGAGCGGGGGCUUCCU [t6A] AGCCCUAG [m7G] CCGGGGG [m5s2U] UCG [m1A] AUCCUCCGGGGCGCACCA

>Thermus_thermophilus_HB27_tRNA-Arg-TCT-1-1 (tRNAscan-SE ID: chr.trna47) Arg (TCT) 76 bp mature sequence Sc: 90.6 chr:253421-253496 (-)

GGGCCCUGAGCUCAGU [Gm] GACAGAGCAGCCGCCU [mnm5s2U] CUAAGCGGUAGGUCGGGGG [m5s2U] UCG [m1A] AUCCUCCGGGCCCGCCA

>Thermus_thermophilus_HB27_tRNA-Asn-GTT-1-1 (tRNAscan-SE ID: chr.trna21) Asn (GTT) 76 bp mature sequence Sc: 86.4 chr:1653337-1653412 (+)

UCCGCGGUAGCUCAGCAGGUAGAGCAGCCGGCUGUU [t6A] ACCGGUAGGUCGCAGG [m5s2U] UCGAGUCCUGCCC GCGGAGCCA

>Thermus_thermophilus_HB27_tRNA-Asp-GTC-1-1 (tRNAscan-SE ID: chr.trna8) Asp (GTC) 77 bp mature sequence Sc: 82.5 chr:987923-987999 (+)

GGCCCCGUGGUGUAGUU [Gm] GDDAACACACCCGC [Cm] UGUCACGUGGGAGAUCGCGGG [m5s2U] UCGAGUCCCG UCGGGGCCGCCA

>Thermus_thermophilus_HB27_tRNA-Cys-GCA-1-1 (tRNAscan-SE ID: chr.trna1) Cys (GCA) 75 bp mature sequence Sc: 84.2 chr:107423-107497 (+)

GGCGCCGUAGCCAAGU [Gm] GUAAGGCA [m2G] AGGU [Cm] UGCA [ms2i6A] AACCUCAUUCGCCGG [m5s2U] UCG [m1A] AUCCGGCCGGCGCCUCCA

>Thermus_thermophilus_HB27_tRNA-Gln-CTG-1-1 (tRNAscan-SE ID: chr.trna33) Gln (CTG) 74 bp mature sequence Sc: 64.6 chr:1477443-1477516 (-)

UGGGGUG [s4U] CGUCUAAGGGUAGGACAGCGGACUCUG [m1G] AUCCGCCGGUCGUGG [m5s2U] UCG [m1A] AUC
CACGCACCCCAGCCA

>Thermus_thermophilus_HB27_tRNA-Gln-TTG-1-1 (tRNAscan-SE ID: chr.trna41) Gln
(TTG) 74 bp mature sequence Sc: 68.9 chr:804744-804817 (-)

UGGGGCGUCGUCUAACGGCAGGACAGCGGA [Cm] U [mnm5s2U] UGGAUCCGCCGGUGGUGG [m5s2U] UCGAGUCC
ACCCGCCCCAGCCA

>Thermus_thermophilus_HB27_tRNA-Glu-CTC-1-1 (tRNAscan-SE ID: chr.trna30) Glu
(CTC) 75 bp mature sequence Sc: 74.4 chr:1582356-1582430 (-)

GGCCCCA [s4U] CGUCUAGCGGDDAGGACGCGGCCCUCUCAAGGCCGAAACGGGG [m5s2U] UCG [m1A] UUUCCC
CUGGGGUCACCA

>Thermus_thermophilus_HB27_tRNA-Glu-CTC-2-1 (tRNAscan-SE ID: chr.trna35) Glu
(CTC) 76 bp mature sequence Sc: 72.7 chr:1477266-1477341 (-)

GGCCCCA [s4U] CGUCUAGAGGCCUAGGACAGGCCCUCUCAAGCCGAGACGGGG [m5s2U] UCG [m1A] AUCCC
CCUGGGGUCACCA

>Thermus_thermophilus_HB27_tRNA-Glu-TTC-1-1 (tRNAscan-SE ID: chr.trna34) Glu
(TTC) 75 bp mature sequence Sc: 78.9 chr:1477362-1477436 (-)

GGCCCCA [s4U] CGACUAGCGGDDAGGUCACCGCCU [mnm5s2U] UCAAGCCGGCGGCGGGG [m5s2U] UCGAGU
CCCCUGGGGUCACCA

>Thermus_thermophilus_HB27_tRNA-Gly-CCC-1-1 (tRNAscan-SE ID: chr.trna19) Gly
(CCC) 76 bp mature sequence Sc: 96.3 chr:1649701-1649776 (+)

GCGGGAG [s4U] AGCUCAGDD [Gm] GUAGAGCAUCGGCUUCCCAAGCCGAGG [m7G] UCGCGGG [m5s2U] UCGAGUC
CCGUCUCCCGCUCCA

>Thermus_thermophilus_HB27_tRNA-Gly-GCC-1-1 (tRNAscan-SE ID: chr.trna15) Gly
(GCC) 76 bp mature sequence Sc: 88.6 chr:1537593-1537668 (+)

>Thermus_thermophilus_HB27_tRNA-Gly-GCC-1-2 (tRNAscan-SE ID: chr.trna25) Gly
(GCC) 76 bp mature sequence Sc: 88.6 chr:1891638-1891713 (-)

GCGGGAG [s4U] AGCUCAGUCGGUAGAGCACGACCUUGCC [m1A] AGGUCGGGGUCGCGG [m5s2U] UCA [m1A] G
UCCCGUCUCCCGCUCCA

>Thermus_thermophilus_HB27_tRNA-Gly-TCC-1-1 (tRNAscan-SE ID: chr.trna46) Gly
(TCC) 77 bp mature sequence Sc: 95.0 chr:253532-253608 (-)

GCGGGAG [s4U] AGCUCAGCUU [Gm] GUAGAGCAUCGGCCU [mnm5s2U] CCAAGCCGAGGGUCGCGG [m5s2U] U
CG [m1A] AUCCCGUCUCCCGCUCCA

>Thermus_thermophilus_HB27_tRNA-His-GTG-1-1 (tRNAscan-SE ID: chr.trna3) His
(GTG) 77 bp mature sequence Sc: 82.8 chr:236743-236819 (+)

GUGAGCG [s4U] AGCUCAGCU [Gm] GDDAGAGACCGGACUGUG [m1G] AUCCGGGG [m7G] UCGUGG [m5s2U] U
CA [m1A] GUCCCAUCGCUCACCCCA

>Thermus_thermophilus_HB27_tRNA-Ile-GAT-1-1 (tRNAscan-SE ID: chr.trna22) Ile
(GAT) 77 bp mature sequence Sc: 87.8 chr:1778425-1778501 (+)

GGGCGAU [s4U] AGCUCAGCU [Gm] GDDAGAGCGCACGCCUGAU [t6A] AGCGUGAG [m7G] UCGUGG [m5s2U] U
CA [m1A] GUCCACCAUCGCCACCA

>Thermus_thermophilus_HB27_tRNA-Ile2-CAT-1-1 (tRNAscan-SE ID: chr.trna49) Ile2
(CAT) 76 bp mature sequence Sc: 90.1 chr:81931-82006 (-)

GGGCCGU [s4U] AGCUCAAC [Gm] GUCAGAGCAGCCGGCUCAUAACCGUAGGUUGCAGG [m5s2U] UCG [m1A] AU
CCUGCACGCCCACCA

>Thermus_thermophilus_HB27_tRNA-Leu-CAA-1-1 (tRNAscan-SE ID: chr.trna48) Leu (CAA) 87 bp mature sequence Sc: 86.7 chr:98459-98545 (-)

GCCGGGGU [m1G] GCGGAACCGGUAGACGCGGCAGACU [Cm] AA [ms2io6A] AUCUGCUGUCCGCAAGGACGUGCGG [m5s2U] UCGAGUCCCCGCCCCCGGCACCA

>Thermus_thermophilus_HB27_tRNA-Leu-CAG-1-1 (tRNAscan-SE ID: chr.trna40) Leu (CAG) 87 bp mature sequence Sc: 77.9 chr:840876-840962 (-)

GCCGGGGUGGCGGAAUU [Gm] GUAGACGCGCAUGAUU [Cm] AGGGUCAUGUGCCCGCAAGGGCGUGCGGG [m5s2U] UCA [m1A] GUCCCCGCCCCCGGCACCA

>Thermus_thermophilus_HB27_tRNA-Leu-GAG-1-1 (tRNAscan-SE ID: chr.trna28) Leu (GAG) 87 bp mature sequence Sc: 71.2 chr:1729381-1729467 (-)

GCCGGGGUGGUGGAAAU [Gm] GUAGACACGCCAUUUAGGGGGUGGUGCCCGCAAGGGCGUGCGGG [m5s2U] UCA [m1A] GUCCCCGCCCCCGGCACCA

>Thermus_thermophilus_HB27_tRNA-Leu-TAA-1-1 (tRNAscan-SE ID: chr.trna5) Leu (TAA) 88 bp mature sequence Sc: 84.1 chr:359615-359702 (+)

GCCGGGGUGGCGGAAC [Gm] GUAGACGUGCGGACU [mnm5U] AA [ms2i6A] AUCCGUGGGGGUAGCCCCCGUACGGG [m5s2U] UCGAGUCCCCGUCCCCCGGCACCA

>Thermus_thermophilus_HB27_tRNA-Leu-TAG-1-1 (tRNAscan-SE ID: chr.trna4) Leu (TAG) 85 bp mature sequence Sc: 81.7 chr:236870-236954 (+)

GCGAGGA [s4U] GGCAGAAC [Gm] GUAGACGCGCCGACUUAG [m1G] AUCCGUGGGGGCAACCCGUGCGGG [m5s2U] UCA [m1A] GUCCCGCUCCUCGCACCA

>Thermus_thermophilus_HB27_tRNA-Lys-CTT-1-1 (tRNAscan-SE ID: chr.trna39) Lys (CTT) 76 bp mature sequence Sc: 86.5 chr:1071533-1071608 (-)

GGGCCGC [s4U] AGCUCAACU [Gm] GUAGAGCAACCGACUCUU [t6A] AUCGUGG [m7G] UUACAGG [m5s2U] UCGAGUCCUGUGCGGCCACCA

>Thermus_thermophilus_HB27_tRNA-Lys-TTT-1-1 (tRNAscan-SE ID: chr.trna29) Lys (TTT) 76 bp mature sequence Sc: 95.1 chr:1582437-1582512 (-)

GGGCCGU [s4U] AGCUCAGCU [Gm] GCAGAGCAACCGACU [mnm5s2U] UU [ms2io6A] AUCGUAG [m7G] UCGCAGG [m5s2U] UCG [m1A] AUCCUGCACGGGCCACCA

>Thermus_thermophilus_HB27_tRNA-Met-CAT-1-1 (tRNAscan-SE ID: chr.trna10) Met (CAT) 77 bp mature sequence Sc: 87.5 chr:1143997-1144073 (+)

GGCGGCG [s4U] AGCUCAGGU [Gm] GUCAGAGCACACGACUCAU [t6A] AUCGUGGU [m7G] UCGUGGG [m5s2U] UCGAGUCCACCGCCGCCACCA

>Thermus_thermophilus_HB27_tRNA-Phe-GAA-1-1 (tRNAscan-SE ID: chr.trna9) Phe (GAA) 76 bp mature sequence Sc: 87.1 chr:988001-988076 (+)

GCCGAGG [s4U] AGCUCAGUU [Gm] GUAGAGCAUGCGACUGAA [ms2i6A] AUCGCAGU [m7G] UCGGCGG [m5s2U] UCG [m1A] UCCGCCCCUCGGCACCA

>Thermus_thermophilus_HB27_tRNA-Pro-CGG-1-1 (tRNAscan-SE ID: chr.trna7) Pro (CGG) 77 bp mature sequence Sc: 80.0 chr:544999-545075 (+)

CGGGGAG [s4U] AGCGCAGCCC [Gm] GUAGCGCACCUCGUUCGGGACGAGGGGUCGCUGG [m5s2U] UCA [m1A] AUCCAGUCUCCCCGACCA

>Thermus_thermophilus_HB27_tRNA-Pro-GGG-1-1 (tRNAscan-SE ID: chr.trna26) Pro (GGG) 77 bp mature sequence Sc: 74.0 chr:1808314-1808390 (-)

CGGGGAG [s4U] AGCGCAGCCU [Gm] GUAGCGCACACGCUU [Gm] GGGUGCGUGGGGUCGUCGG [m5s2U] UCA [m1A] AUCCGCCUCCCCGACCA

>Thermus_thermophilus_HB27_tRNA-Pro-TGG-1-1 (tRNAscan-SE ID: chr.trna45) Pro (TGG) 77 bp mature sequence Sc: 75.5 chr:253610-253686 (-)
CGGGGCG [**s4U**] AGCGCAGGCCGGUAGCGCACCUGCUUUGGGAGCAGGGGGUCGCCCCGUCAAUCCGGCCGCCCG ACCA

>Thermus_thermophilus_HB27_tRNA-Ser-CGA-1-1 (tRNAscan-SE ID: chr.trna11) Ser (CGA) 92 bp mature sequence Sc: 91.7 chr:1145622-1145713 (+)
GGAGGGGUGCCGGAGCGGUUGAACGGGCCGGUCUCGA [**ms2i6A**] AACCGGUAGGCCCCUCGCGGGGCCUCGCGGG [**m5s2U**] UCGAAUCCCGCCCCUCGCGCA

>Thermus_thermophilus_HB27_tRNA-Ser-GCT-1-1 (tRNAscan-SE ID: chr.trna38) Ser (GCT) 93 bp mature sequence Sc: 98.3 chr:1278359-1278451 (-)
GGAGAGGUGGCCGAGU [**Gm**] GUCGAAGCGGCACCCUGCU [**t6A**] AGGUGUUGCACCGGGAAAACCGGU [**m7G**] CCG CGGG [**m5s2U**] UCGAAUCCCGCCCCUCGCGCA

>Thermus_thermophilus_HB27_tRNA-Ser-GGA-1-1 (tRNAscan-SE ID: chr.trna44) Ser (GGA) 94 bp mature sequence Sc: 91.4 chr:466976-467069 (-)
GGAGAGGUGCCCGAGU [**Gm**] GCUGAAGGGACACGACUGGA [**ms2i6A**] AUCGUGUAGGGGGGUUAAACCUCGCCUG CGGG [**m5s2U**] UCGAAUCCCGCCCCUCGCGCA

>Thermus_thermophilus_HB27_tRNA-Ser-TGA-1-1 (tRNAscan-SE ID: chr.trna37) Ser (TGA) 91 bp mature sequence Sc: 87.5 chr:1278459-1278549 (-)
GGAGGGUUGGCCGAGCGGUUGAAGCGCGGUCUUGA [**ms2i6A**] AACCGCUGUGGGCGCGAAGCCCACCGGGGG [**m5s2U**] UCGAAUCCCUACCCUCCGCCA

>Thermus_thermophilus_HB27_tRNA-Thr-CGT-1-1 (tRNAscan-SE ID: chr.trna12) Thr (CGT) 75 bp mature sequence Sc: 91.0 chr:1348123-1348197 (+)
GCCGGUG [**s4U**] AGCUCAGCGGUAGAGCAACCGCCUCGU [**t6A**] AGCGGUAGGCCGCCGG [**m5s2U**] UCA [**m1A**] AU CCGGCCACCGGUCCA

>Thermus_thermophilus_HB27_tRNA-Thr-GGT-1-1 (tRNAscan-SE ID: chr.trna20) Thr (GGT) 76 bp mature sequence Sc: 79.5 chr:1649780-1649855 (+)
GCCGGUG [**s4U**] AGCUCAGCGGUAGAGCAACCGCCUCGU [**t6A**] AGCGGUAGGCCGCCGG [**m5s2U**] UCA [**m1A**] AU CCGGCCACCGGUCCA

>Thermus_thermophilus_HB27_tRNA-Thr-TGT-1-1 (tRNAscan-SE ID: chr.trna17) Thr (TGT) 76 bp mature sequence Sc: 77.8 chr:1649501-1649576 (+)
GCCACCC [**s4U**] AGCUCAACC [**Gm**] GCAGAGCACCCGACUUGU [**t6A**] AUCGGGGGUUGGGGG [**m5s2U**] UCA [**m1A**] CUCCCCUGGGUGGUCCA

>Thermus_thermophilus_HB27_tRNA-Trp-CCA-1-1 (tRNAscan-SE ID: chr.trna14) Trp (CCA) 76 bp mature sequence Sc: 89.9 chr:1459528-1459603 (+)
GGGCCGU [**s4U**] AGCUCAACU [**Gm**] GCAGAGCACCGGU [**Cm**] UCCA [**ms2i6A**] AACCGGGGUUGGAGG [**m5s2U**] UCGAGUCCUUCACGGCCCCCA

>Thermus_thermophilus_HB27_tRNA-Tyr-GTA-1-1 (tRNAscan-SE ID: chr.trna18) Tyr (GTA) 86 bp mature sequence Sc: 83.0 chr:1649589-1649674 (+)
GGGCAGGUGCCCGAGCGGCCAAAGGGACGGU [**Cm**] UGUA [**ms2i6A**] AACCGUUGGCGUAUGCCUUCGCUGG [**m5s2U**] UCG [**m1A**] AUCCAGCCCUGCCCACCA

>Thermus_thermophilus_HB27_tRNA-Val-CAC-1-1 (tRNAscan-SE ID: chr.trna42) Val (CAC) 75 bp mature sequence Sc: 82.4 chr:653144-653218 (-)
GGGCGGC [**s4U**] AGCUCAGCGGAAGAGCGCUCGC [**Cm**] UCACACGCGAGAGGUAGG [**m5s2U**] UCA [**m1A**] GUC CUACGCCGCCACCA

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>Thermus_thermophilus_HB27_tRNA-Val-GAC-1-1 (tRNAscan-SE ID: chr.trna2) Val
(GAC) 77 bp mature sequence Sc: 80.4 chr:107506-107582 (+)
GGGCGCGUAGCUCAGGU [Gm] GCUAGAGCACUACC [Um] UGACACGGUAGGGGUCGGUGG [m5s2U] UCA [m1A] GU
CCACUCGCGCCACCA

>Thermus_thermophilus_HB27_tRNA-Val-TAC-1-1 (tRNAscan-SE ID: chr.trna31) Val
(TAC) 77 bp mature sequence Sc: 84.5 chr:1582278-1582354 (-)
GGGCGGC [s4U] AGCUCAGCU [Gm] GCCAGAGCACUCGCCUUACAAGCGAGGG [m7G] UCAGAGG [m5s2U] UCA [m1
A] GUCCUCUGCCGCCACCA

>Thermus_thermophilus_HB27_tRNA-fMet-CAT-1-1 (tRNAscan-SE ID: chr.trna13) fMet
(CAT) 77 bp mature sequence Sc: 82.9 chr:1371658-1371734 (+)
CGCGGGGUGGAGCAGCCU [Gm] GUAGCUCGUCGG [Cm] UCAUAACCCGAAGUCGCGGG [m5U] UCAAAUCCCGCC
CCCGCAACCA

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Supplemental Figure S3. RNase T1 modification mapping results for *T. thermophilus* tRNAs. Identified RNase T1 digestion products are shown in blue, and non-identified regions are shown in black. Modifications are annotated at their corresponding positions and color-coded by base identity: adenosine modifications (green), uridine modifications (red), cytidine modifications (orange), and guanosine modifications (purple).

>Schizosaccharomyces_pombe_972h-_tRNA-Ala-AGC-1-1 (tRNAscan-SE ID: chrI.trna54) Ala (AGC) 74 bp mature sequence Sc: 57.1 chrI:934665-934738 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Ala-AGC-1-2 (tRNAscan-SE ID: chrI.trna36) Ala (AGC) 74 bp mature sequence Sc: 57.1 chrI:3765008-3765081 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Ala-AGC-1-3 (tRNAscan-SE ID: chrI.trna24) Ala (AGC) 74 bp mature sequence Sc: 57.1 chrI:3777192-3777265 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ala-AGC-1-4 (tRNAscan-SE ID: chrII.trna2) Ala (AGC) 74 bp mature sequence Sc: 57.1 chrII:285676-285749 (+)

GGGCAUGU [m1G] GUGUAGAU [Gm] GUUAUCACGCUUCCUUAGC [m1A] UGGAAGAGGU [m5C] CCAGA [m5U] UCG AGUUCUGGCUUGUCCA

>Schizosaccharomyces_pombe_972h-_tRNA-Ala-CGC-1-1 (tRNAscan-SE ID: chrI.trna29) Ala (CGC) 72 bp mature sequence Sc: 68.5 chrI:4796977-4797059 (+)

GGGGAUGUAGUUUAGGGGUUAUAACGUUUCAUUCGCAUUGAAAAGGU [m5C] CCGGG [m5U] UCG [m1A] UUCCCGGCA UCUGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Ala-TGC-1-1 (tRNAscan-SE ID: chrI.trna53) Ala (TGC) 72 bp mature sequence Sc: 70.6 chrI:1195592-1195663 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Ala-TGC-1-2 (tRNAscan-SE ID: chrI.trna15) Ala (TGC) 72 bp mature sequence Sc: 70.6 chrI:3157430-3157501 (+)

GGGCAUGUGAUGCAGUGGUAGCAUGCUCGCUU [ncm5U] GCAUGCGAGUCGU [m5C] CUGGGUUCAAUCCCCAGCGU GUCCA

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-ACG-1-1 (tRNAscan-SE ID: chrI.trna21) Arg (ACG) 73 bp mature sequence Sc: 71.4 chrI:3736520-3736592 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-ACG-1-2 (tRNAscan-SE ID: chrI.trna32) Arg (ACG) 73 bp mature sequence Sc: 71.4 chrI:5045132-5045204 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-ACG-1-3 (tRNAscan-SE ID: chrII.trna15) Arg (ACG) 73 bp mature sequence Sc: 71.4 chrII:1602188-1602260 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-ACG-1-4 (tRNAscan-SE ID: chrII.trna43) Arg (ACG) 73 bp mature sequence Sc: 71.4 chrII:1647283-1647355 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-ACG-1-5 (tRNAscan-SE ID: chrIII.trna6) Arg (ACG) 73 bp mature sequence Sc: 71.4 chrIII:925852-925924 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-ACG-1-6 (tRNAscan-SE ID: chrIII.trna40) Arg (ACG) 73 bp mature sequence Sc: 71.4 chrIII:1068182-1068254 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-ACG-1-7 (tRNAscan-SE ID: chrIII.trna39) Arg (ACG) 73 bp mature sequence Sc: 71.4 chrIII:1092595-1092667 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-ACG-1-8 (tRNAscan-SE ID: chrIII.trna16) Arg (ACG) 73 bp mature sequence Sc: 71.4 chrIII:1106327-1106399 (+)

GGUCUCGU [m1G] GCCCAUGGDDAAGGC [m22G] CUUGACUACG [m1G] AUCAAGAGAUU [m5C] CAGG [m5U] UC G [m1A] CUCCUGGCGGGAUCG

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-CCT-1-1 (tRNAscan-SE ID: chrII.trna61) Arg (CCT) 72 bp mature sequence Sc: 56.5 chrII:1160893-1160994 (-)

UUACGCGU [m1G] GCGCAAUGGUAGCGCAUCUCAUCCUAACGAGAAGGUUGCGGG [m5U] UCGAGUCCCGUCGUGUA AG

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-TCG-1-1 (tRNAscan-SE ID: chrIII.trna41) Arg (TCG) 73 bp mature sequence Sc: 63.3 chrIII:1067092-1067164 (-)

GGGUGUGU [m1A] GCCUAAUGGDDAAGGCGUUGGUUU [mcm5U] CGGCACCAAAGACUGCAGG [m5U] UCGAGUCCU GUCACACUCG

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-TCT-1-1 (tRNAscan-SE ID: chrIII.trna3) Arg (TCT) 73 bp mature sequence Sc: 74.2 chrIII:578847-578919 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Arg-TCT-2-1 (tRNAscan-SE ID: chrII.trna64) Arg (TCT) 73 bp mature sequence Sc: 70.9 chrII:326652-326724 (-)

GCUCCCGU [m1G] GCCUAAUGGCUAGGGCAUUUGACU [mcm5U] CUAUCAAGGGAUUGUGGG [m5U] UCGAGUCCC GCCGGGAGCU

>Schizosaccharomyces_pombe_972h-_tRNA-Asn-GTT-1-1 (tRNAscan-SE ID: chrII.trna35) Asn (GTT) 74 bp mature sequence Sc: 78.5 chrII:4210053-4210126 (-)

GGUCGGGUAGCGUAGDDGGDDAUUGCGCACGACU [Q] UU [t6A] AUCGUGAG [m7G] U [m5C] GAGGG [m5U] UCGAG UCCCUCCUGACCG

>Schizosaccharomyces_pombe_972h-_tRNA-Asn-GTT-2-1 (tRNAscan-SE ID: chrII.trna59) Asn (GTT) 74 bp mature sequence Sc: 81.5 chrII:1597996-1598069 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Asn-GTT-2-2 (tRNAscan-SE ID: chrII.trna24) Asn (GTT) 74 bp mature sequence Sc: 81.5 chrII:2032160-2032233 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Asn-GTT-2-3 (tRNAscan-SE ID: chrII.trna33) Asn (GTT) 74 bp mature sequence Sc: 81.5 chrII:4031743-4031816 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Asn-GTT-2-4 (tRNAscan-SE ID: chrIII.trna7) Asn (GTT) 74 bp mature sequence Sc: 81.5 chrIII:947262-947335 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Asn-GTT-2-5 (tRNAscan-SE ID: chrIII.trna21) Asn (GTT) 74 bp mature sequence Sc: 81.5 chrIII:1701899-1701972 (+)

GGUCGGGUAGCAUAGDDGGDDAUUGCGCACGACU [Q] UU [t6A] AUCGUGAG [m7G] U [m5C] GAGGG [m5U] UCGAG UCCCUCCUGACCG

>Schizosaccharomyces_pombe_972h-_tRNA-Asp-GTC-1-1 (tRNAscan-SE ID: chrI.trna27) Asp (GTC) 71 bp mature sequence Sc: 61.0 chrI:4532857-4532927 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Asp-GTC-1-2 (tRNAscan-SE ID: chrI.trna31) Asp (GTC) 71 bp mature sequence Sc: 61.0 chrI:5232917-5232987 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Asp-GTC-1-3 (tRNAscan-SE ID: chrII.trna52) Asp (GTC) 71 bp mature sequence Sc: 61.0 chrII:1602347-1602417 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Asp-GTC-1-4 (tRNAscan-SE ID: chrII.trna32) Asp (GTC) 71 bp mature sequence Sc: 61.0 chrII:3939227-3939297 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Asp-GTC-1-5 (tRNAscan-SE ID: chrIII.trna9) Asp (GTC) 71 bp mature sequence Sc: 61.0 chrIII:1068029-1068099 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Asp-GTC-1-6 (tRNAscan-SE ID: chrIII.trna12) Asp (GTC) 71 bp mature sequence Sc: 61.0 chrIII:1092437-1092507 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Asp-GTC-1-7 (tRNAscan-SE ID: chrIII.trna34) Asp (GTC) 71 bp mature sequence Sc: 61.0 chrIII:1106487-1106557 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Asp-GTC-1-8 (tRNAscan-SE ID: chrIII.trna27) Asp (GTC) 71 bp mature sequence Sc: 61.0 chrIII:2139408-2139478 (-)

UCUCCUUU [m1A] GUAAUAGGGUAGUACACAAGCCUGUC [i6A] CGCUUGCAG [m5C] CCGGG [m5U] UCG [m1A] AUCCCGGAGGGAGAG

>Schizosaccharomyces_pombe_972h-_tRNA-Cys-GCA-1-1 (tRNAscan-SE ID: chrI.trna6) Cys (GCA) 73 bp mature sequence Sc: 68.1 chrI:1421149-1421221 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Cys-GCA-1-2 (tRNAscan-SE ID: chrI.trna19) Cys (GCA) 73 bp mature sequence Sc: 68.1 chrI:3700665-3700737 (+)
GGGGUCAUAGCUCAGUGGDDAGAGUGAGGGAUUGCAGAUCCCCAG [m7G] U [m5C] ACUGG [m5U] UCA [m1A] AUC CGGUUGGUCCCU

>Schizosaccharomyces_pombe_972h-_tRNA-Cys-GCA-2-1 (tRNAscan-SE ID: chrI.trna12) Cys (GCA) 73 bp mature sequence Sc: 65.9 chrI:2510538-2510610 (+)
GGGGUCAUAGCUCAGUGGDDAGAGUGAGGGAUUGCAGAUCCCCAG [m7G] U [m5C] ACUGG [m5U] UCA [m1A] AUC CGGUUGGUCCCU

>Schizosaccharomyces_pombe_972h-_tRNA-Gln-CTG-1-1 (tRNAscan-SE ID: chrII.trna1) Gln (CTG) 72 bp mature sequence Sc: 73.7 chrII:257454-257525 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Gln-CTG-1-2 (tRNAscan-SE ID: chrII.trna66) Gln (CTG) 72 bp mature sequence Sc: 73.7 chrII:258848-258919 (-)
GGUUGUAU [m1G] GUGUAAUGGDDAGCAGUGAGA [Um] UCUGAUUCUCGAGA [m5C] CUGGG [m5U] UCGAUUCCC AGUACGACCU

>Schizosaccharomyces_pombe_972h-_tRNA-Gln-TTG-1-1 (tRNAscan-SE ID: chrII.trna67) Gln (TTG) 72 bp mature sequence Sc: 73.7 chrII:257908-257979 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Gln-TTG-1-2 (tRNAscan-SE ID: chrII.trna4) Gln (TTG) 72 bp mature sequence Sc: 73.7 chrII:355920-355991 (+)
GGUUGUAUGGUGUAAUGGDDAGCAGUGAGAUU [mcm5s2U] UG [m2A] UUCUCGAGAC [m5C] UGGG [m5U] UCGA UUCCCAGUACGACCU

>Schizosaccharomyces_pombe_972h-_tRNA-Gln-TTG-2-1 (tRNAscan-SE ID: chrIII.trna24) Gln (TTG) 72 bp mature sequence Sc: 70.4 chrIII:1863131-1863202 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Gln-TTG-2-2 (tRNAscan-SE ID: chrIII.trna28) Gln (TTG) 72 bp mature sequence Sc: 70.4 chrIII:2074991-2075062 (-)

GGUUGUAUGGUGUAGCGGDDAGCACGCGAGAUU [mcm5s2U] UG [m2A] UUCUCGAGAU [m5C] UGGG [m5U] UCGA
CUCCCAGUACGACCU

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-CTC-1-1 (tRNAscan-SE ID:
chrI.trna35) Glu (CTC) 72 bp mature sequence Sc: 68.9 chrI:3765434-3765505 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-CTC-1-2 (tRNAscan-SE ID:
chrI.trna23) Glu (CTC) 72 bp mature sequence Sc: 68.9 chrI:3776768-3776839 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-CTC-1-3 (tRNAscan-SE ID:
chrII.trna9) Glu (CTC) 72 bp mature sequence Sc: 68.9 chrII:820491-820562 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-CTC-1-4 (tRNAscan-SE ID:
chrII.trna34) Glu (CTC) 72 bp mature sequence Sc: 68.9 chrII:4107639-4107710
(+)

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-CTC-1-5 (tRNAscan-SE ID:
chrIII.trna2) Glu (CTC) 72 bp mature sequence Sc: 68.9 chrIII:140967-141038
(+)

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-CTC-1-6 (tRNAscan-SE ID:
chrIII.trna36) Glu (CTC) 72 bp mature sequence Sc: 68.9 chrIII:1097499-1097570
(-)

UCCGUCAU [m1G] GUCCAGUGGCUAGGAUUCAUCGCUCUCACCGAUGCGGCGGGG [m5U] UCGAUUCCCCUGACGG
AG

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-TTC-1-1 (tRNAscan-SE ID:
chrI.trna55) Glu (TTC) 72 bp mature sequence Sc: 58.7 chrI:718119-718190 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-TTC-1-2 (tRNAscan-SE ID: chrI.trna3)
Glu (TTC) 72 bp mature sequence Sc: 58.7 chrI:957183-957254 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-TTC-1-3 (tRNAscan-SE ID:
chrII.trna53) Glu (TTC) 72 bp mature sequence Sc: 58.7 chrII:1601491-1601562
(-)

>Schizosaccharomyces_pombe_972h-_tRNA-Glu-TTC-1-4 (tRNAscan-SE ID:
chrII.trna44) Glu (TTC) 72 bp mature sequence Sc: 58.7 chrII:1646829-1646900
(-)

UCCGUUGU [m1G] GUCCAA [Cm] GGCUAGGAUUCGUCGCU [mcm5s2U] UCACCGACGCGGU [m5C] GGGG [m5U] U
CGACUCCCCGCAACGGAG

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-CCC-1-1 (tRNAscan-SE ID:
chrII.trna25) Gly (CCC) 71 bp mature sequence Sc: 61.2 chrII:2069487-2069557
(+)

GCAUUAGU [m1G] GUGUAGCGGUAAAUUGGAGCUUCCCAUGCUCUAGCU [m5C] CGGG [m5U] UCG [m1A] CUCCC
GGCUGAUGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-GCC-1-1 (tRNAscan-SE ID:
chrI.trna47) Gly (GCC) 71 bp mature sequence Sc: 71.4 chrI:1646292-1646362 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-GCC-1-2 (tRNAscan-SE ID:
chrI.trna44) Gly (GCC) 71 bp mature sequence Sc: 71.4 chrI:2249180-2249250 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-GCC-1-3 (tRNAscan-SE ID:
chrII.trna68) Gly (GCC) 71 bp mature sequence Sc: 71.4 chrII:180994-181064 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-GCC-1-4 (tRNAscan-SE ID:
chrII.trna6) Gly (GCC) 71 bp mature sequence Sc: 71.4 chrII:570156-570226 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-GCC-1-5 (tRNAscan-SE ID: chrII.trna56) Gly (GCC) 71 bp mature sequence Sc: 71.4 chrII:1599337-1599407 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-GCC-1-6 (tRNAscan-SE ID: chrII.trna47) Gly (GCC) 71 bp mature sequence Sc: 71.4 chrII:1644675-1644745 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-GCC-1-7 (tRNAscan-SE ID: chrIII.trna47) Gly (GCC) 71 bp mature sequence Sc: 71.4 chrIII:113716-113786 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-GCC-1-8 (tRNAscan-SE ID: chrIII.trna44) Gly (GCC) 71 bp mature sequence Sc: 71.4 chrIII:820567-820637 (-)

GCUUUGGU [m1G] GUUUAGUGGUAUAAUGAACGUUGCCAUCGAUUCGA [m5C] CCGGG [m5U] UCG [m1A] UUCCC
GGCCAAAGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-TCC-1-1 (tRNAscan-SE ID: chrIII.trna25) Gly (TCC) 71 bp mature sequence Sc: 63.4 chrIII:2037352-2037422 (+)

GCAUCAGU [m1G] GUGUAGCGGUAACAUCAAUGCCU [mcm5U] CCAAGCAUUAGCUCGCGG [m5U] UCG [m1A] CUC
CCGGUUGAUGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-TCC-2-1 (tRNAscan-SE ID: chrII.trna65) Gly (TCC) 71 bp mature sequence Sc: 64.4 chrII:285389-285459 (-)

GCAUCGAU [m1G] GUGUAGCGGUAACAUCAAUGCCU [mcm5U] CCAAGCAUUAGCUCGCGG [m5U] UCG [m1A] CUC
CCGGUUGAUGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Gly-TCC-3-1 (tRNAscan-SE ID: chrII.trna3) Gly (TCC) 71 bp mature sequence Sc: 60.5 chrII:326235-326305 (+)

GCAUCAGU [m1G] GUGUAGCGGUAACAUCAAUGCCU [mcm5U] CCAAGCAUUAGCUCGCGG [m5U] UCG [m1A] CUC
CCGGUUGAUGCA

>Schizosaccharomyces_pombe_972h-_tRNA-His-GTG-1-1 (tRNAscan-SE ID: chrII.trna5) His (GTG) 72 bp mature sequence Sc: 66.1 chrII:464238-464309 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-His-GTG-1-2 (tRNAscan-SE ID: chrII.trna10) His (GTG) 72 bp mature sequence Sc: 66.1 chrII:960729-960800 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-His-GTG-1-3 (tRNAscan-SE ID: chrIII.trna1) His (GTG) 72 bp mature sequence Sc: 66.1 chrIII:71400-71471 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-His-GTG-1-4 (tRNAscan-SE ID: chrIII.trna23) His (GTG) 72 bp mature sequence Sc: 66.1 chrIII:1844639-1844710 (+)

GCUCACAU [m1G] GUCCAGUGGDDAAGACUCAUCGUUGUGGCCGAUGCGA [m5C] CCAGG [m5U] UCG [m1A] UUCCU
GGUGUGGGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-AAT-1-1 (tRNAscan-SE ID: chrI.trna22) Ile (AAT) 74 bp mature sequence Sc: 65.0 chrI:3768290-3768363 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-AAT-1-2 (tRNAscan-SE ID: chrI.trna34) Ile (AAT) 74 bp mature sequence Sc: 65.0 chrI:3773910-3773983 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-AAT-1-3 (tRNAscan-SE ID: chrII.trna14) Ile (AAT) 74 bp mature sequence Sc: 65.0 chrII:1600086-1600159 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-AAT-1-4 (tRNAscan-SE ID: chrII.trna16) Ile (AAT) 74 bp mature sequence Sc: 65.0 chrII:1618293-1618366 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-AAT-1-5 (tRNAscan-SE ID: chrII.trna49) Ile (AAT) 74 bp mature sequence Sc: 65.0 chrII:1630049-1630122 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-AAT-1-6 (tRNAscan-SE ID: chrII.trna21) Ile (AAT) 74 bp mature sequence Sc: 65.0 chrII:1645424-1645497 (+)

GGUCGCAUGAUGUAGUCGGDDAUC AUGUCGAUCUAAUAAGUCGAAUGUCGCCAG [m5U] UCG [m1A] ACCUGGCUGU GACCA

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-AAT-2-1 (tRNAscan-SE ID: chrI.trna9) Ile (AAT) 74 bp mature sequence Sc: 61.7 chrI:1772296-1772369 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-AAT-2-2 (tRNAscan-SE ID: chrIII.trna4) Ile (AAT) 74 bp mature sequence Sc: 61.7 chrIII:817425-817498 (+)

GGUCGCAUGAUGUAGUCGGDDAUC AU [m22G] UCGAUCUAAUAAGUCGAAUGUCGCCG [m5U] UCG [m1A] ACCCG GCUGUGACCA

>Schizosaccharomyces_pombe_972h-_tRNA-Ile-TAT-1-1 (tRNAscan-SE ID: chrI.trna13) Ile (TAT) 74 bp mature sequence Sc: 57.4 chrI:2578426-2578524 (+)

GCUCCCGU [m1G] GCCAAGCUGGDDAAGCCUCAUGCUUAUAACGUGGAAAU [m5C] GCGAG [m5U] UCG [m1A] UCC UCGCCGGGAGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-AAG-1-1 (tRNAscan-SE ID: chrII.trna39) Leu (AAG) 79 bp mature sequence Sc: 53.1 chrII:2768257-2768335 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-AAG-1-2 (tRNAscan-SE ID: chrII.trna31) Leu (AAG) 79 bp mature sequence Sc: 53.1 chrII:3914043-3914121 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-AAG-1-3 (tRNAscan-SE ID: chrIII.trna10) Leu (AAG) 79 bp mature sequence Sc: 53.1 chrIII:1069166-1069244 (+)

GGAAGGUUGUC [ac4C] GAGUGGDDAUGGAGCUAGUUUAAG [m1G] CACUAGUGCGAAAGCU [m5C] GUGGG [m5U] UCGAGUCCACACCUUUCA

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-AAG-2-1 (tRNAscan-SE ID: chrI.trna33) Leu (AAG) 79 bp mature sequence Sc: 51.5 chrI:4059028-4059106 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-AAG-2-2 (tRNAscan-SE ID: chrII.trna37) Leu (AAG) 79 bp mature sequence Sc: 51.5 chrII:3209139-3209217 (-)

GGAAGGUUGUC [ac4C] GAGUGGDDAUGGAGCUAGUUUAAG [m1G] CACUAGUGCGAAAGCU [m5C] GUGGG [m5U] UCGAGUCCACACCUUUCA

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-CAA-1-1 (tRNAscan-SE ID: chrII.trna57) Leu (CAA) 82 bp mature sequence Sc: 56.5 chrII:1598745-1598845 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-CAA-1-2 (tRNAscan-SE ID: chrII.trna48) Leu (CAA) 82 bp mature sequence Sc: 56.5 chrII:1644083-1644183 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-CAA-1-3 (tRNAscan-SE ID: chrIII.trna37) Leu (CAA) 82 bp mature sequence Sc: 56.5 chrIII:1096085-1096185 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-CAA-1-4 (tRNAscan-SE ID: chrIII.trna14) Leu (CAA) 82 bp mature sequence Sc: 56.5 chrIII:1102809-1102909 (+)

GGCCAGUUGGC [ac4C] GAGC [Gm] GUCUAUGGC [m22G] CAGCACUCAAGUUGCUGUAUCGAAAGAUGCAGAGG [m5U] UCG [m1A] AUCCCUCACUGGUCA

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-CAG-1-1 (tRNAscan-SE ID: chrI.trna49) Leu (CAG) 84 bp mature sequence Sc: 67.1 chrI:1527088-1527181 (-)

GGCGAAGU [m1G] GCCGAGUGGUCUAUGGCGCUAGCUUCAGGUGCUAGUCUACGUAUGUGGCGUGGG [m5U] UCG [m1A] ACCCCACCUUCGUCA

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-TAA-1-1 (tRNAscan-SE ID: chrI.trna42) Leu (TAA) 82 bp mature sequence Sc: 47.5 chrI:2802761-2802858 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-TAA-1-2 (tRNAscan-SE ID: chrII.trna60) Leu (TAA) 82 bp mature sequence Sc: 47.5 chrII:1402444-1402541 (-)

GCGGCUAUGCC [ac4C] GAGU [Gm] GUCUAAGGGGGCAGAUUUAAGCCUGCUGUUGUAAAACGCGAGAG [m5U] UCG [m1A] ACCUCUCUGGCCGA

>Schizosaccharomyces_pombe_972h-_tRNA-Leu-TAG-1-1 (tRNAscan-SE ID: chrI.trna18) Leu (TAG) 79 bp mature sequence Sc: 46.1 chrI:3591948-3592044 (+)

GGAUGGGUGUCCGAGU [Gm] GDDAUGGAGCUGGCUU [ncm5U] AGGCGCCAGUGCGAAAGCUCGCGGG [m5U] UCGAG UCCCGUCCCAUUA

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-1 (tRNAscan-SE ID: chrI.trna7) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrI:1704582-1704664 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-2 (tRNAscan-SE ID: chrI.trna43) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrI:2684683-2684765 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-3 (tRNAscan-SE ID: chrI.trna14) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrI:3086310-3086392 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-4 (tRNAscan-SE ID: chrII.trna13) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrII:1599706-1599788 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-5 (tRNAscan-SE ID: chrII.trna20) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrII:1645044-1645126 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-6 (tRNAscan-SE ID: chrII.trna29) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrII:3814134-3814216 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-7 (tRNAscan-SE ID: chrIII.trna11) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrIII:1071093-1071175 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-8 (tRNAscan-SE ID: chrIII.trna33) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrIII:1139536-1139618 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-CTT-1-9 (tRNAscan-SE ID: chrIII.trna18) Lys (CTT) 75 bp mature sequence Sc: 74.7 chrIII:1475034-1475116 (+)

UCCCGAGU [m1G] GCUCAAUCGGDDAGAGCGUCUGACUCUUAUCAGAAGGUUGCGAG [m5U] UCGAGUCUCGCCUU
GGGAG

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-TTT-1-1 (tRNAscan-SE ID:
chrI.trna46) Lys (TTT) 75 bp mature sequence Sc: 72.9 chrI:1733764-1733838 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-TTT-1-2 (tRNAscan-SE ID:
chrI.trna11) Lys (TTT) 75 bp mature sequence Sc: 72.9 chrI:2441963-2442037 (+)

UCCCGUUUAGCUCAAUCGGDDAGAGCGUCCGGCUUUUAACCGGAAGGUUGCGAG [m5U] UCG [m1A] GUCUCGCAG
UGGGAG

>Schizosaccharomyces_pombe_972h-_tRNA-Lys-TTT-2-1 (tRNAscan-SE ID:
chrII.trna63) Lys (TTT) 75 bp mature sequence Sc: 73.6 chrII:602625-602699 (-)

UCCCGUUUAGCUCAAUCGGDDAGAGCGUCCGGCUUUUAACCGGAAGGUUGCGAG [m5U] UCG [m1A] AUCUCGCAG
UGGGAG

>Schizosaccharomyces_pombe_972h-_tRNA-Met-CAT-1-1 (tRNAscan-SE ID:
chrI.trna50) Met (CAT) 74 bp mature sequence Sc: 57.1 chrI:1484979-1485061 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Met-CAT-1-2 (tRNAscan-SE ID:
chrII.trna7) Met (CAT) 74 bp mature sequence Sc: 57.2 chrII:658451-658531 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Met-CAT-1-3 (tRNAscan-SE ID:
chrII.trna58) Met (CAT) 74 bp mature sequence Sc: 57.2 chrII:1598075-1598155
(-)

UGCGAUUUAAUGUAADDGGUUAACAUCUCUGACUCAUGAUCAGUGUAUUAAAGG [m5U] UCAAGUCCUUAGGUCGCAC

>Schizosaccharomyces_pombe_972h-_tRNA-Phe-GAA-1-1 (tRNAscan-SE ID:
chrI.trna20) Phe (GAA) 73 bp mature sequence Sc: 69.0 chrI:3701556-3701628 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Phe-GAA-1-2 (tRNAscan-SE ID:
chrI.trna37) Phe (GAA) 73 bp mature sequence Sc: 69.0 chrI:3752334-3752406 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Phe-GAA-1-3 (tRNAscan-SE ID:
chrIII.trna46) Phe (GAA) 73 bp mature sequence Sc: 69.0 chrIII:331228-331300
(-)

>Schizosaccharomyces_pombe_972h-_tRNA-Phe-GAA-1-4 (tRNAscan-SE ID:
chrIII.trna32) Phe (GAA) 73 bp mature sequence Sc: 69.0 chrIII:1142192-1142264
(-)

GUCGCAAU [m1G] GUGUAGDDGGGAGCAUGACAGACUGAAGAUCUGUUGGU [m5C] AUCGG [m5U] UCG [m1A] UCC
CGGUUUGUGACA

>Schizosaccharomyces_pombe_972h-_tRNA-Phe-GAA-2-1 (tRNAscan-SE ID:
chrII.trna40) Phe (GAA) 73 bp mature sequence Sc: 70.3 chrII:2576376-2576448
(-)

GUCGCGAU [m1G] GUGUAGDDGGGAGCAUGACAGACUGAAGAUCUGUUGGU [m5C] AUCGG [m5U] UCG [m1A] UCC
CGGUUUGUGACA

>Schizosaccharomyces_pombe_972h-_tRNA-Pro-AGG-1-1 (tRNAscan-SE ID:
chrI.trna51) Pro (AGG) 72 bp mature sequence Sc: 61.8 chrI:1449398-1449469 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Pro-AGG-1-2 (tRNAscan-SE ID:
chrII.trna42) Pro (AGG) 72 bp mature sequence Sc: 61.8 chrII:1825787-1825858
(-)

>Schizosaccharomyces_pombe_972h-_tRNA-Pro-AGG-1-3 (tRNAscan-SE ID:
chrII.trna23) Pro (AGG) 72 bp mature sequence Sc: 61.8 chrII:1877221-1877292
(+)

>Schizosaccharomyces_pombe_972h-_tRNA-Pro-AGG-1-4 (tRNAscan-SE ID: chrII.trna26) Pro (AGG) 72 bp mature sequence Sc: 61.8 chrII:2319292-2319363 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Pro-AGG-1-5 (tRNAscan-SE ID: chrII.trna27) Pro (AGG) 72 bp mature sequence Sc: 61.8 chrII:2939715-2939786 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Pro-AGG-1-6 (tRNAscan-SE ID: chrIII.trna22) Pro (AGG) 72 bp mature sequence Sc: 61.8 chrIII:1788949-1789020 (+)

GGCCGUUUGGUCUAGU [Gm] GUAUGAUACCAUCUUAGGGUGAUGGUGGU [m5C] GUGGG [m5U] UCGAUUCCCACAA CAGCCC

>Schizosaccharomyces_pombe_972h-_tRNA-Pro-TGG-1-1 (tRNAscan-SE ID: chrII.trna36) Pro (TGG) 72 bp mature sequence Sc: 68.2 chrII:3360519-3360590 (-)

GGUUUCGU [m1G] GUGUAGU [Gm] GUAGCAUACUUCGUUUGGGUCGAAGUG [m7G] U [m5C] ACGGG [m5U] UCAAUC CCCGUCGAAACCC

>Schizosaccharomyces_pombe_972h-_tRNA-Pro-TGG-2-1 (tRNAscan-SE ID: chrI.trna1) Pro (TGG) 72 bp mature sequence Sc: 68.8 chrI:365155-365226 (+)

GGCUUCGU [m1G] GUGUAGU [Gm] GUAGCAUACUUCGUUUGGGUCGAAGUG [m7G] U [m5C] AGGGG [m5U] UCGAUC CCCCUCGAAGCCC

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-AGA-1-1 (tRNAscan-SE ID: chrI.trna40) Ser (AGA) 82 bp mature sequence Sc: 79.7 chrI:3047677-3047758 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-AGA-1-2 (tRNAscan-SE ID: chrI.trna30) Ser (AGA) 82 bp mature sequence Sc: 79.7 chrI:5437747-5437828 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-AGA-1-3 (tRNAscan-SE ID: chrII.trna62) Ser (AGA) 82 bp mature sequence Sc: 79.7 chrII:744754-744835 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-AGA-1-4 (tRNAscan-SE ID: chrIII.trna45) Ser (AGA) 82 bp mature sequence Sc: 79.7 chrIII:473199-473280 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-AGA-1-5 (tRNAscan-SE ID: chrIII.trna5) Ser (AGA) 82 bp mature sequence Sc: 79.7 chrIII:847701-847782 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-AGA-1-6 (tRNAscan-SE ID: chrIII.trna8) Ser (AGA) 82 bp mature sequence Sc: 79.7 chrIII:1066628-1066709 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-AGA-1-7 (tRNAscan-SE ID: chrIII.trna29) Ser (AGA) 82 bp mature sequence Sc: 79.7 chrIII:1775992-1776073 (-)

GACACUAUGCCUGAGU [Gm] GDDAAAGG [m22G] ACAGACUAGA [i6A] AUCUGU [Um] GCGGUCUCCGCGCGCAGG [m5U] UCAAAUCCUGCUGGUGUCG

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-CGA-1-1 (tRNAscan-SE ID: chrI.trna4) Ser (CGA) 82 bp mature sequence Sc: 76.5 chrI:1096369-1096466 (+)

GUCACUAUGUCCGAGU [Gm] GDDAAGGAGUUAGA [m3C] UCGAAAUCAAUGGGCUCUGCCCCGCGCAGG [m5U] UCAA AUCCUGCUGGUGACG

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-GCT-1-1 (tRNAscan-SE ID: chrII.trna28) Ser (GCT) 84 bp mature sequence Sc: 70.1 chrII:3350594-3350688 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-GCT-1-2 (tRNAscan-SE ID: chrIII.trna17) Ser (GCT) 84 bp mature sequence Sc: 70.1 chrIII:1253193-1253287 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-GCT-1-3 (tRNAscan-SE ID: chrIII.trna26) Ser (GCT) 84 bp mature sequence Sc: 70.1 chrIII:2072080-2072174 (+)

GACAACGU [m1G] GCCGAGU [Gm] GDDUAAGGCGUUCGCCUGCUAAGCGGA [m5U] UCCCUUUGGAGCGCAGG [m5U] UCG [m1A] AUCCUGCCGUUGUCG

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-TGA-1-1 (tRNAscan-SE ID: chrI.trna25) Ser (TGA) 82 bp mature sequence Sc: 77.3 chrI:4265149-4265245 (+)

GUCACUAUGUCCGAGU [Gm] GDDAAGGAGUUAGA [m3C] UUGAAAUCUAAUGGGCUCUGCCCGCGCAGG [m5U] UCA [m1A] AUCCUGCUGGUGACG

>Schizosaccharomyces_pombe_972h-_tRNA-Ser-TGA-2-1 (tRNAscan-SE ID: chrIII.trna19) Ser (TGA) 82 bp mature sequence Sc: 76.5 chrIII:1689713-1689809 (+)

GUCACUAUGUCCGAGU [Gm] GDDAAGGAGUUAGACUUGAAAUCUAAUGGGCUCUGCCCGCGCAGG [m5U] UCA [m1A] AUCCUGCUGGUGACG

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-AGT-1-1 (tRNAscan-SE ID: chrI.trna41) Thr (AGT) 72 bp mature sequence Sc: 80.6 chrI:2844674-2844745 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-AGT-2-1 (tRNAscan-SE ID: chrI.trna48) Thr (AGT) 72 bp mature sequence Sc: 79.6 chrI:1603305-1603376 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-AGT-2-2 (tRNAscan-SE ID: chrI.trna10) Thr (AGT) 72 bp mature sequence Sc: 79.6 chrI:2433048-2433119 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-AGT-2-3 (tRNAscan-SE ID: chrI.trna28) Thr (AGT) 72 bp mature sequence Sc: 79.6 chrI:4715431-4715502 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-AGT-2-4 (tRNAscan-SE ID: chrII.trna38) Thr (AGT) 72 bp mature sequence Sc: 79.6 chrII:2790375-2790446 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-AGT-2-5 (tRNAscan-SE ID: chrIII.trna38) Thr (AGT) 72 bp mature sequence Sc: 79.6 chrIII:1093083-1093154 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-AGT-2-6 (tRNAscan-SE ID: chrIII.trna15) Thr (AGT) 72 bp mature sequence Sc: 79.6 chrIII:1105840-1105911 (+)

GCUCUUGUAGCUCAGU [Gm] GUAGAGCGCUUGCCUAGU [t6A] AGCAAGAG [m7G] CCCAGUG [m5U] UCA [m1A] G UCACUGCUGGAGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-CGT-1-1 (tRNAscan-SE ID: chrI.trna16) Thr (CGT) 72 bp mature sequence Sc: 72.2 chrI:3164749-3164820 (+)

GCUCUUGUAGCUCAGU [Gm] GUAGAGCGCCUGUCUGUAAACAGGAGGU [m5C] CAGUG [m5U] UCGAGUCACUGCC GGAGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-TGT-1-1 (tRNAscan-SE ID: chrIII.trna30) Thr (TGT) 72 bp mature sequence Sc: 75.7 chrIII:1361090-1361161 (-)

GCCCCUAUGGCUUAGU [Gm] GUACAGCAUCGCA [m3C] U [ncm5U] GU [t6A] AUGCGAAGAU [m5C] CUUGG [m5U]
] UCG [m1A] UUCCGAGUGGAGGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Thr-TGT-2-1 (tRNAscan-SE ID:
chrII.trna11) Thr (TGT) 72 bp mature sequence Sc: 74.7 chrII:1503953-1504024
(+)

GCCUCUAUGGCUUAGU [Gm] GUACAGCAUCGCA [m3C] U [ncm5U] GU [t6A] AUGCGAAGAU [m5C] CUUGG [m5U]
] UCG [m1A] UUCCGAGUGGAGGCA

>Schizosaccharomyces_pombe_972h-_tRNA-Tyr-GTA-1-1 (tRNAscan-SE ID: chrI.trna8)
Tyr (GTA) 74 bp mature sequence Sc: 62.3 chrI:1746464-1746547 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-Tyr-GTA-1-2 (tRNAscan-SE ID:
chrII.trna12) Tyr (GTA) 74 bp mature sequence Sc: 62.3 chrII:1598511-1598594
(+)

>Schizosaccharomyces_pombe_972h-_tRNA-Tyr-GTA-1-3 (tRNAscan-SE ID:
chrII.trna19) Tyr (GTA) 74 bp mature sequence Sc: 62.3 chrII:1643849-1643932
(+)

CUCCUGAU [m1G] GUGUAGUUGGDDAUCACAUCGGCUGUAAACCGGUUG [m7G] UCGCUAG [m5U] UCG [m1A] UUC
UGGCUCAGGAGA

>Schizosaccharomyces_pombe_972h-_tRNA-Tyr-GTA-2-1 (tRNAscan-SE ID:
chrII.trna30) Tyr (GTA) 74 bp mature sequence Sc: 63.9 chrII:3814558-3814641
(+)

CUCCUGAU [m1G] GUGUAGUUGGDDAUCACACCCGGCUGUAAACCGGUUG [m7G] UCGCUAG [m5U] UCG [m1A] UUC
UGGCUCAGGAGA

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-1 (tRNAscan-SE ID:
chrI.trna45) Val (AAC) 74 bp mature sequence Sc: 58.6 chrI:2214733-2214814 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-2 (tRNAscan-SE ID:
chrI.trna38) Val (AAC) 74 bp mature sequence Sc: 58.5 chrI:3710739-3710821 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-3 (tRNAscan-SE ID:
chrII.trna54) Val (AAC) 74 bp mature sequence Sc: 58.5 chrII:1600967-1601049
(-)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-4 (tRNAscan-SE ID:
chrII.trna50) Val (AAC) 74 bp mature sequence Sc: 58.5 chrII:1619174-1619256
(-)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-5 (tRNAscan-SE ID:
chrII.trna17) Val (AAC) 74 bp mature sequence Sc: 58.5 chrII:1629159-1629241
(+)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-6 (tRNAscan-SE ID:
chrII.trna45) Val (AAC) 74 bp mature sequence Sc: 58.5 chrII:1646305-1646387
(-)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-7 (tRNAscan-SE ID:
chrIII.trna42) Val (AAC) 74 bp mature sequence Sc: 58.5 chrIII:1065778-1065860
(-)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-8 (tRNAscan-SE ID:
chrIII.trna13) Val (AAC) 74 bp mature sequence Sc: 58.5 chrIII:1092934-1093016
(+)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-AAC-1-9 (tRNAscan-SE ID:
chrIII.trna35) Val (AAC) 74 bp mature sequence Sc: 58.5 chrIII:1105978-1106060
(-)

GGUCGUGU [m1G] GUUUAGAUGGDDAUAAUUUCUGCUUAACACGCAGACGGUCCCAAG [m5U] UCGAGUCUUGGCACG
AUC

>Schizosaccharomyces_pombe_972h-_tRNA-Val-CAC-1-1 (tRNAscan-SE ID: chrI.trna2)
Val (CAC) 72 bp mature sequence Sc: 64.9 chrI:446000-446071 (+)

AGUCCCGUGUUCUAGUGGUAUGAUUUCUCCUUCACACGGAGAAGGU [m5C] CCGGG [m5U] UCG [m1A] UCCCGGC
GGGACUA

>Schizosaccharomyces_pombe_972h-_tRNA-Val-TAC-1-1 (tRNAscan-SE ID:
chrI.trna56) Val (TAC) 73 bp mature sequence Sc: 72.1 chrI:703075-703147 (-)

>Schizosaccharomyces_pombe_972h-_tRNA-Val-TAC-1-2 (tRNAscan-SE ID:
chrIII.trna31) Val (TAC) 73 bp mature sequence Sc: 72.1 chrIII:1206747-1206819
(-)

GCAUCUGUAGUCUAGU [Gm] GDDAUGAUUUCUGCUU [ncm5U] ACACGCAGACGGUC [m5C] CAGG [m5U] UCG [m1
A] UCCUGGUAGAUGCA

>Schizosaccharomyces_pombe_972h-_tRNA-iMet-CAT-1-1 (tRNAscan-SE ID:
chrI.trna5) iMet (CAT) 72 bp mature sequence Sc: 54.9 chrI:1096474-1096545 (+)

>Schizosaccharomyces_pombe_972h-_tRNA-iMet-CAT-1-2 (tRNAscan-SE ID:
chrI.trna26) iMet (CAT) 72 bp mature sequence Sc: 54.9 chrI:4265253-4265324
(+)

>Schizosaccharomyces_pombe_972h-_tRNA-iMet-CAT-1-3 (tRNAscan-SE ID:
chrII.trna41) iMet (CAT) 72 bp mature sequence Sc: 54.9 chrII:2434303-2434374
(-)

>Schizosaccharomyces_pombe_972h-_tRNA-iMet-CAT-1-4 (tRNAscan-SE ID:
chrIII.trna20) iMet (CAT) 72 bp mature sequence Sc: 54.9 chrIII:1689817-
1689888 (+)

UGCGCGGUA [m1G] GAGAGUGGAACUCCGACGGGCUCAU [t6A] ACCCGUAGGUCCAGGAUCG [m1A] AACCGGCC
GCGCAA

Supplemental Figure S4. RNase T1 modification mapping results for *S. pombe* tRNAs. Identified RNase T1 digestion products are shown in blue, and non-identified regions are shown in black. Modifications are annotated at their corresponding positions and color-coded by base identity: adenosine modifications (green), uridine modifications (red), cytidine modifications (orange), and guanosine modifications (purple).