Supporting Information

\textbf{m7G-quant-seq: Quantitative Detection of RNA Internal }N^7-\textit{Methylguanosine}.\textbf{

Li-Sheng Zhang \dagger, \ddagger, *, Cheng-Wei Ju \‡, Chang Liu \dagger, \‡, Jiangbo Wei \dagger, Qing Dai \dagger, Li Chen \dagger, Chang Ye \dagger, Chuan He \dagger, *

\dagger Department of Chemistry, The University of Chicago; Howard Hughes Medical Institute, The University of Chicago; Chicago, Illinois 60637, United States.
\‡ Division of Life Science, Department of Chemistry, The Hong Kong University of Science and Technology, Clear Water Bay, 999077, Kowloon, Hong Kong SAR, China.
\‡ Pritzker School of Molecular Engineering, The University of Chicago; Chicago, Illinois 60637, United States.
* Corresponding author: chuanhe@uchicago.edu, lszhang@uchicago.edu.
* These authors contributed equally.
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**Figure S1.** (A) m^7G/A levels in synthetic RNA oligo after m^7G-seq NaBH₄ treatment and m^7G-quant-seq KBH₄ treatment, versus the untreated input, revealed by LC-MS/MS. n = 3, technically independent replicates. (B) m^7G/A levels in fragmented HeLa total RNA after m^7G-seq NaBH₄ treatment and m^7G-quant-seq KBH₄ treatment, versus the untreated input, revealed by LC-MS/MS. n = 3, biologically independent replicates. (C) The misincorporation or variation ratios at 18S rRNA m^7G1639, which were uncovered by m^7G-seq and m^7G-quant-seq with total RNA isolated from wild-type or shControl HeLa cells. (D) The variation signatures at the AP site generated from HeLa 18S rRNA m^7G1639 under m^7G-quant-seq treatment with engineered RT1306 and adjusted dNTP/dATP ratios. (E) The variation signatures at the AP site generated from HeLa 18S rRNA m^7G1639 under m^7G-quant-seq treatment with ProtoScript II RT and adjusted dNTP/dATP ratios. (F) The variation signatures at the AP site generated from HeLa 18S rRNA m^7G1639 under m^7G-quant-seq treatment with SuperScript II RT and adjusted dNTP/dATP ratios. (G) The variation signatures at the AP site generated from HeLa 18S rRNA m^7G1639 under m^7G-quant-seq treatment with SuperScript IV RT and adjusted dNTP/dATP ratios.
Figure S2. IGV plot of internal m\textsuperscript{7}G\textsubscript{46} site in representative tRNAs from HeLa cells. The upper two rows in each panel are from ‘input’ samples, n = 2, biologically independent replicates; the lower two rows in each panel are from ‘m\textsuperscript{7}G-quant-seq’ samples, n = 2, biologically independent replicates. For tRNA labeled with (+), these tRNAs locate on sense strand in human genome, in which A, C, G, and U are marked by green, blue, brown, and red colors, respectively. For tRNA labeled with (-), these tRNAs locate on antisense strand in human genome, in which A, C, G, and U are marked by red, brown, blue, and green colors, respectively.
Figure S3. (A) The variation ratios in m^7G-quant-seq, variation ratios in ‘Input’ (with any chemical treatment), and estimated m^7G methylation fraction at all guanosine sites in HeLa 18S rRNA. (B) The identified m^7G sites in tRNA from different human cell lines, for a comparison of m^7G detection in m^7G-quant-seq and TRAC-seq.
Methods

Cell culture
HeLa and HEK 293T cell lines were purchased from the American Type Culture Collection (ATCC). The HeLa cell line was grown in DMEM medium (Gibco, 11965) supplemented with 10% v/v FBS and 1% penicillin/streptomycin (Gibco). The HEK 293T cell line was maintained in DMEM (Gibco, 11995) with 10% FBS and 1% penicillin/streptomycin. Cells were cultured at 37 °C with 5.0% CO2 in a Heracell VIOS 160i incubator (Thermo Scientific).

Small RNA isolation
Cellular total RNA was isolated with TRIzol reagent (Invitrogen) following the manufacturer's protocol by isopropanol precipitation. The small RNA fraction (size < 200 nt) was further extracted from the purified total RNA using the mirVana miRNA Isolation Kit (AM1560, Invitrogen).

\( \text{m}^7 \text{G-quant-seq} \)

RNA Fragmentation:
The starting amount of RNA could be 200 ng before fragmentation. Then RNA Fragmentation Reagent (Invitrogen, AM8740) was used as 15X (add 1.0 µL buffer into 14 µL of RNA), which is originally 10X. The heating condition is 70 °C for 14 min, followed by Oligo Clean and Concentrator kit (OCC). Elute RNA to 22 µL (twice, 11 µL each time). Because we expect to capture the real methylation fraction of the internal \( \text{m}^7 \text{G} \) site in tRNA, we did not perform any AlkB demethylation treatment to erase \( \text{m}^1 \text{A} \), \( \text{m}^3 \text{C} \), or \( \text{m}^1 \text{G} \) methylations on tRNA; in this way, it is hard for HIV RT to read through the full-size tRNA. Fragmenting tRNAs into 30-50 nt will facilitate HIV RT to read through the shorter fragments generated from tRNAs, reflecting the actual \( \text{m}^7 \text{G} \) methylation fraction via variation signatures.

End repair:
Prepare the end repair reaction as follow:

| Reagents               | Volume (µL) |
|------------------------|-------------|
| RNA                    | ~200 ng     |
| 10X PNK reaction buffer | 3           |
| T4 PNK                 | 3           |
| SUPERase•In™           | 1.5         |
Prepare a stock containing RNA + 10X PNK buffer + T4 PNK + SUPERase•In™ with a final volume of 30 µL. Mix the stock well and incubate at 37 °C for 45 min. Recover RNA with Oligo Clean and Concentrator kit (OCC) and elute to 10 µL with RNase-free water.

Adaptor ligation:

Mix 1.0 µL 20 µM 3' linker (5'rApp-NNNNAGATCGGAAGAGCGTCGTG-3SpC3) with repaired 10 µL RNA fragments and incubate the mixture at 70 °C for 2 min for denaturation. Immediately move onto ice. Please pay attention to the actual adaptor sequences in Table S1. Prepare the ligation reaction as follow:

| Reagents                          | Volume (µL) |
|-----------------------------------|-------------|
| RNA and linker mixture            | 11          |
| 10X T4 RNA Ligase Reaction Buffer | 2.5         |
| 50% PEG8000                       | 7.5         |
| SUPERase•In™                      | 1           |
| T4 RNA ligase 2 truncated KQ (NEB)| 2           |
| H₂O                               | 1           |

Mix everything well before adding T4 RNA ligase 2 truncated KQ. Then add 2.0 µL T4 RNA ligase 2 truncated KQ and mix well again. Incubate the reaction at 25 °C for 2 hours, followed by 16 °C for 10 hours.

Then add 23 µL RNase-free water to dilute the reaction mixture. Add 2.0 µL 5-deadenylase, mix well/incubate at 30 °C for 30 min; then add 1.0 µL RecJf, mix well/incubate at 37 °C for another 30 min. Recover RNA with RNA Clean and Concentrator kit (RCC) and elute to 12 µL with RNase-free water.

Save 2 µL as 'input'; use the rest for the following steps. Safe stop point: -80°C for 1 week.

Reduction:

Put the eluted RNA in 10 µL RNase-free water. Prepare a fresh 1.0M KBH₄ buffer in RNase-free water. Add 40 µL KBH₄ buffer into RNA and mix well. Incubate at room temperature for 4 hours (avoid the light). Recover RNA with RNA Clean and Concentrator kit (RCC) and elute to 45 µL with RNase-free water.

Generation of RNA abasic sites:

Add 5.0 µL 1.0M NaOAc/AcOH buffer (pH 2.9) into the purified RNA and mix well. Incubate with heating for 4 hours (avoid the light). Recover RNA with Oligo Clean and Concentrator kit (OCC) and elute
to 10 µL with RNase-free water. 1.0M NaOAc/AcOH buffer was prepared with 3.3 mL 3M NaOAc (pH 5.5, Invitrogen™, AM9740) and 6.7 mL acetic acid (Fisher BioReagents, BP2401-500).

Reverse transcription:

Mix 1.0 µL 2 µM RT-primer (5'-ACACGACGCTCTTCCGATCT-3') with 10 µL depurinated RNA fragments and incubate the mixture at 65 °C for 2 min for denaturation. Immediately move onto ice. Prepare the ligation reaction as follow:

| Reagents                  | Volume (µL) |
|---------------------------|-------------|
| RNA/primer mixture        | 11          |
| 10X AMV RT Reaction Buffer| 2           |
| dNTP (10 mM)              | 2           |
| RNase Out                 | 0.5         |
| H₂O                       | 2.5         |
| HIV RT                    | 2           |

Mix everything well before adding HIV RT. Then add 2.0 µL HIV RT and mix well again. Incubate the reaction at 37 °C for 1.5 hours.

Then add 1.0 µL RNase H (NEB) into the reaction mixture. Mix well/incubate at 37 °C for 20 min. Then 70 °C for 5 min to denature.

Recover RNA with Oligo Clean and Concentrator kit (OCC) and elute to 10 µL with RNase-free water. Safe stop point: -80C for 1 week.

cDNA 3'-ligation:

Mix 1.0 µL 50 µM cDNA 3'-adapter (5'Phos-NNNNNAGATCGGAAGAGCACACGTCTG-3SpC3) with 10 µL cDNA and incubate the mixture at 75 °C for 2 min for denaturation. Immediately move onto ice. Please pay attention to the actual adaptor sequences in Table S1. Prepare the ligation reaction as follow:

| Reagents                  | Volume (µL) |
|---------------------------|-------------|
| cDNA/adapter mixture      | 11          |
| 10X T4 RNA Ligase Reaction Buffer | 3         |
| 50% PEG8000               | 15          |
Mix everything well before adding T4 RNA Ligase 1. Then add 1.0 µL T4 RNA Ligase 1 and mix well again. Add ligase enzyme to one sample followed by mixing this sample immediately. Mix each sample one by one. Do not add ligase enzyme to all samples and then start mixing everything.

Incubate the reaction at 25 °C for 12 hours.

**PCR Amplification:**

After the 12-hour cDNA ligation, heat at 65 °C for 5 min to denature. Purify the cDNA by DNA Clean & Concentrator-5. Elute cDNA with 20 µL DNase-free water. Use 4 µL per sample for each PCR amplification.

**Identification of variation signatures in m⁷G-quant-seq**

The sequencing data were all trimmed with the cutadapt tool to remove adapters and low-quality reads (lengths shorter than 20 bp). PCR duplicates were removed with the BBMap tool (https://sourceforge.net/projects/bbmap/), random barcodes at reads end were trimmed, and low-quality reads were removed using the cutadapt tool. The remaining reads were aligned to the human genome (hg38) using Tophat2 (version 2.1.1) and bowtie2 (version 2.3.5.1) allowing a maximum of three mismatches. The generated .bam files were split into positive and negative strands and sorted using Samtools. Sequence variants were identified by measuring the base composition at each position using fine-tuned bam-readcount (https://github.com/genome/bam-readcount). The generated bam-readcount output results were parsed and analyzed to calculate the misincorporation/deletion ratio at each abasic site generated from internal m⁷G site, followed by confirmation using direct visualization through IGV software (https://software.broadinstitute.org/software/igv/).

The m⁷G candidate sites must satisfy the criteria shown below:

1. variation (misincorporation and deletion) ratio above 5% in m⁷G-quant-seq libraries; (2) variation ratio below 5% in ‘Input’ libraries; (3) total reads coverage depth above 20 in both m⁷G-quant-seq and ‘Input’ libraries; (4) variation ratio in m⁷G-quant-seq libraries is > 5-fold over that in ‘input’ libraries; (5) variation ratio in m⁷G-quant-seq libraries is > 5-fold over the background in any given sequence motif (defined as the variation rates detected from RNA probes containing unmodified NNGNN after m⁷G-quant-seq treatment). Additionally, all misincorporation and deletion signatures must occur at the internal positions of the reads, instead of reads end.
Note that the estimated m\textsuperscript{7}G methylation fraction (in m\textsuperscript{7}G-quant-seq) serves as the minimum value of methylation stoichiometry at the methylated site, because the calibration curves were built with NN(AP-site)NN oligos instead of NN(m\textsuperscript{7}G)NN oligos. The actual m\textsuperscript{7}G methylation fraction could be a little higher than the estimated methylation stoichiometry in m\textsuperscript{7}G-quant-seq, due to the fact that it is hard to achieve 100% chemical conversion at m\textsuperscript{7}G site in all motif contexts.

**Calibration curves for m\textsuperscript{7}G-quant-seq**

The 31-mer RNA probe GAACGNN/irSp/NNUUCCAGUACGUGAUGCCAAU (from IDT) was used as “100% AP-site” standard. The RNA oligo GAACGNNGNUUCCAGUACGUGAUGCCAAU (from IDT) was used as “0% AP-site”. Then the “100% AP-site” and “0% AP-site” standard were mixed and generated 6 oligo mixtures with different modification fractions, as 100%, 80%, 60%, 40%, 20% and 0% AP-site.

For 200 ng of each set of mixed RNA oligos (as 100%, 80%, 60%, 40%, 20% and 0% AP-site), proceed with RNA 3’-ligation directly. Mix 1.0 µL 20 µM 3’ linker (5’rApp-NNNNAATCGGAAGGACGTCTG-3SpC3) with 10 µL RNA oligos and incubate the mixture at 70 °C for 2 min for denaturation. Immediately move onto the ice. Then add 2.5 µL 10X T4 RNA Ligase Reaction Buffer, 7.5 µL 50% PEG8000, 1 µL SUPERNase-In, and 1 µL H\textsubscript{2}O. Mix everything well before adding T4 RNA ligase 2 truncated KQ. Then add 2.0 µL T4 RNA ligase 2 truncated KQ and mix well again. Incubate the reaction at 25 °C for 2 hours, followed by 16 °C for 10 hours. Then add 23 µL RNase-free water to dilute the reaction mixture. Add 2.0 µL 5-deadenylase, mix well/incubate at 30 °C for 30 min; then add 1.0 µL RecJf, mix well/incubate at 37 °C for another 30 min. Recover RNA with RNA Clean and Concentrator kit (RCC) and elute to 10 µL with RNase-free water.

Mix 1.0 µL 2 µM RT-primer (5’-ACACGACGCTCTTCCGTCT-3’) with 2 µL ligated RNA oligos and incubate the mixture at 65 °C for 2 min for denaturation. Immediately move onto the ice. Then add 2 µL 10X AMV RT Reaction Buffer, 2 µL 10mM dNTP, 0.5 µL RNaseOut, and 10.5 µL H\textsubscript{2}O. Mix everything well before adding HIV RT. Then add 2.0 µL HIV RT and mix well again. Incubate the reaction at 37 °C for 1.5 hours. After RT, add 1.0 µL RNase H (NEB) into the reaction mixture. Mix well/incubate at 37 °C for 20 min. Then 70 °C for 5 min to denature. Recover RNA with Oligo Clean and Concentrator kit (OCC) and elute to 10 µL with RNase-free water.

Mix 1.0 µL 50 µM cDNA 3’-adapter (5’Phos-NNNNAATCGGAAGGACACGCTCTG-3SpC3) with 10 µL cRNA and incubate the mixture at 75 °C for 2 min for denaturation. Immediately move onto the ice. Then add 3 µL 10X T4 RNA Ligase Reaction Buffer, 15 µL 50% PEG8000, and 3 µL 10mM ATP. Mix everything well before adding T4 RNA Ligase 1. Then add 1.0 µL T4 RNA Ligase 1 and mix well again. Add ligase enzyme to one sample followed by mixing this sample immediately. Mix each sample one by one.
Incubate the reaction at 25 °C for 12 hours. After the 12-hour cDNA ligation, heat at 65 °C for 5 min to denature. Purify the cDNA by DNA Clean & Concentrator-5. Elute cDNA with 20 µL DNase-free water. Use 4 µL per sample for each PCR amplification.

Data availability

The sequencing data listed in Table S1 are available in the Gene Expression Omnibus database under the accession number GSE209646. All other data supporting the findings of this study are available from the corresponding author upon reasonable request.
Table S1 Sample information for high-through sequencing in this study.

| Experiment | Samples/replicates | Reads#  |
|------------|-------------------|--------|
|            | HeLa Total-RNA HIV-RT 1mM-dNTP | 16141020 |
|            | HeLa Total-RNA HIV-RT 100uM-dNTP _1mM-dATP | 20634616 |
|            | HeLa Total-RNA HIV-RT 50uM-dNTP _1mM-dATP | 14878546 |
|            | HeLa Total-RNA HIV-RT 25uM-dNTP _1mM-dATP | 16306827 |
|            | HeLa Total-RNA RT1306 1mM-dNTP | 16842442 |
|            | HeLa Total-RNA RT1306 100uM-dNTP _1mM-dATP | 21461811 |
|            | HeLa Total-RNA RT1306 50uM-dNTP _1mM-dATP | 17791752 |
|            | HeLa Total-RNA RT1306 25uM-dNTP _1mM-dATP | 16306827 |
|            | HeLa Total-RNA ProtoScript-II 1mM-dNTP | 18836930 |
|            | HeLa Total-RNA ProtoScript-II 100uM-dNTP _1mM-dATP | 20122916 |
|            | HeLa Total-RNA ProtoScript-II 50uM-dNTP _1mM-dATP | 18798320 |
|            | HeLa Total-RNA ProtoScript-II 25uM-dNTP _1mM-dATP | 18842670 |
|            | CalibrationCurves_HIV-RT_0%_AP-site | 15560359 |
|            | CalibrationCurves_HIV-RT_20%_AP-site | 16465341 |
|            | CalibrationCurves_HIV-RT_40%_AP-site | 15798437 |
|            | CalibrationCurves_HIV-RT_60%_AP-site | 15521390 |
|            | CalibrationCurves_HIV-RT_80%_AP-site | 10204722 |
|            | CalibrationCurves_HIV-RT_100%_AP-site | 12452862 |
|            | Duplicates for m7G-quant-seq "Treated" | 21275083 |
|            | Duplicates for m7G-quant-seq "Input" | 24798655 |
|            | HEK293T SmallRNA HIV-RT_Treated_rep1 | 21344929 |
|            | HEK293T SmallRNA HIV-RT_Treated_rep2 | 20370688 |
|            | HEK293T SmallRNA HIV-RT_Treated_rep3 | 18618694 |
|            | HEK293T SmallRNA HIV-RT_Treated_rep4 | 21454705 |
|            | HEK293T SmallRNA HIV-RT_Treated_rep5 | 21536302 |
|            | HEK293T SmallRNA HIV-RT_Treated_rep6 | 18117600 |

"Treated" samples for m7G-quant-seq to study the variation patterns at HeLa 18S rRNA m7G1639, under five RTs and different dNTP/dATP ratios.

RNA 3'-adaptor:
5'rApp-NNNNN AGATCGGAAGAGCGTCGTG-3SpC3

cDNA 3'-adaptor:
5'Phos-NNNNN AGATCGGAAGAGCA CACGTCTG-3SpC3

Calibration curves for estimating internal m7G methylation fractions, under HIV RT and 1mM dNTP.
RNA 3'-adaptor:
5'rApp-NNNNN AGATCGGAAGAGCGTCGTG-3SpC3

cDNA 3'-adaptor:
5'Phos-NNNNN AGATCGGAAGAGCA CACGTCTG-3SpC3

Duplicates for m7G-quant-seq "Treated" and "Input" samples to reveal tRNA m7G46 methylation fractions in HeLa and HEK293T cells, under HIV RT and 1mM dNTP.

RNA 3'-adaptor:
5'rApp-NNNNN AGATCGGAAGAGCGTCGTG-3SpC3

cDNA 3'-adaptor:
5'Phos-NNNNN AGATCGGAAGAGCA CACGTCTG-3SpC3
Table S2 Variation signatures at all guanosine sites on human 18S rRNA.

| rRNA | Position | Motif   | Variation rate in m7G-quant-seq (%) | Variation rate in 'Input' (%) | Background variation rate (%) in a specific motif from NNGNN, after m7G-quant-seq treatment |
|------|----------|---------|------------------------------------|-------------------------------|----------------------------------------------------------------------------------|
| 18S  | 6        | CTGGT   | 6.402                              | 1.307                         | 0.338                                                                            |
| 18S  | 7        | TGGTT   | 8.857                              | 1.162                         | 1.856                                                                            |
| 18S  | 10       | TTGAT   | 9.775                              | 3.233                         | 2.577                                                                            |
| 18S  | 16       | CTGCC   | 2.852                              | 2.819                         | 6.599                                                                            |
| 18S  | 20       | CAGTA   | 0.113                              | 0.767                         | 4.176                                                                            |
| 18S  | 23       | TAGCA   | 0.263                              | 1.806                         | 2.183                                                                            |
| 18S  | 29       | ATGCT   | 0.125                              | 1.587                         | 4.854                                                                            |
| 18S  | 33       | TGGTC   | 0.719                              | 1.972                         | 2.079                                                                            |
| 18S  | 41       | AAGAT   | 3.003                              | 1.024                         | 3.643                                                                            |
| 18S  | 47       | AAGCC   | 3.271                              | 1.813                         | 4.412                                                                            |
| 18S  | 52       | ATGCA   | 2.759                              | 2.295                         | 3.876                                                                            |
| 18S  | 56       | ATGCT   | 1.262                              | 2.491                         | 5.270                                                                            |
| 18S  | 62       | GAGTA   | 3.167                              | 16.276                        | 2.726                                                                            |
| 18S  | 66       | ACGCA   | 2.881                              | 6.781                         | 10.722                                                                           |
| 18S  | 70       | ACGGC   | 3.471                              | 2.704                         | 2.500                                                                            |
| 18S  | 71       | CGGCC   | 2.872                              | 2.634                         | 0.813                                                                            |
| 18S  | 74       | CCGGT   | 1.632                              | 2.249                         | 5.096                                                                            |
| 18S  | 75       | CGGTA   | 1.729                              | 4.099                         | 2.384                                                                            |
| 18S  | 80       | CAGTG   | 1.970                              | 0.823                         | 1.099                                                                            |
| 18S  | 82       | GTGAA   | 1.609                              | 1.964                         | 3.093                                                                            |
| 18S  | 88       | CTGCG   | 3.154                              | 1.471                         | 0.524                                                                            |
| 18S  | 90       | CGCAA   | 4.154                              | 2.236                         | 2.219                                                                            |
| 18S  | 94       | ATGCA   | 3.279                              | 1.514                         | 2.869                                                                            |
| 18S  | 95       | TGCGT   | 1.626                              | 1.516                         | 1.397                                                                            |
| 18S  | 108      | CAGTT   | 2.650                              | 2.016                         | 1.926                                                                            |
| 18S  | 113      | ATGCT   | 2.135                              | 0.296                         | 2.203                                                                            |
| 18S  | 114      | TGGTT   | 2.135                              | 0.296                         | 2.203                                                                            |
| 18S  | 122      | TTGGT   | 0.950                              | 0.400                         | 2.811                                                                            |
| 18S  | 123      | TGGTC   | 0.466                              | 0.872                         | 3.716                                                                            |
| 18S  | 126      | TCGCT   | 1.511                              | 1.540                         | 9.829                                                                            |
| 18S  | 130      | TCGCT   | 3.750                              | 1.039                         | 9.829                                                                            |
| 18S  | 145      | TTGAA   | 3.990                              | 1.329                         | 3.889                                                                            |
| 18S  | 146      | TGGAT   | 2.962                              | 3.333                         | 1.790                                                                            |
| 18S  | 153      | CTGTC   | 2.560                              | 2.081                         | 1.541                                                                            |
| 18S  | 155      | GTGGT   | 3.677                              | 2.703                         | 1.974                                                                            |
| 18S  | 156      | TGCGA   | 3.605                              | 5.788                         | 1.994                                                                            |
| 18S  | 165      | TAGAG   | 2.663                              | 3.451                         | 0.606                                                                            |
| 18S  | 167      | GAGCT   | 1.969                              | 4.988                         | 1.250                                                                            |
| 18S  | 177      | ATGCC   | 2.246                              | 3.389                         | 8.696                                                                            |
| 18S  | 180      | CCGAC   | 2.050                              | 2.765                         | 4.167                                                                            |
| 18S  | 183      | ACGGC   | 1.950                              | 0.969                         | 2.791                                                                            |
| 18S  | 184      | CGGCC   | 1.033                              | 1.170                         | 3.486                                                                            |
| 18S  | 185      | GGGCG   | 1.318                              | 1.244                         | 2.020                                                                            |
| 18S  | 187      | CGCGT   | 1.758                              | 1.116                         | 2.963                                                                            |
| 18S  | 190      | CTGAC   | 2.310                              | 1.225                         | 2.013                                                                            |
| 18S  | 200      | TCGCG   | 3.932                              | 2.841                         | 1.815                                                                            |
| 18S  | 202      | GCGGG   | 3.603                              | 1.443                         | 5.556                                                                            |
| 18S | 203 | CGGGG | 2.831 | 0.517 | 5.217 |
| 18S | 204 | GGGGG | 2.446 | 0.516 | 6.000 |
| 18S | 205 | GGGGG | 1.655 | 0.469 | 6.000 |
| 18S | 206 | GGGGG | 1.552 | 0.374 | 6.000 |
| 18S | 207 | GGGGA | 1.018 | 0.280 | 0.769 |
| 18S | 208 | GGGAT | 0.938 | 0.837 | 1.140 |
| 18S | 211 | ATGCG | 2.331 | 1.372 | 1.871 |
| 18S | 213 | GGGTG | 2.451 | 1.519 | 5.096 |
| 18S | 215 | GTGCA | 1.162 | 2.414 | 2.222 |
| 18S | 225 | CAGAT | 3.152 | 5.958 | 2.605 |
| 18S | 240 | CAGCC | 1.857 | 1.054 | 4.555 |
| 18S | 241 | CGGCC | 8.977 | 2.906 | 0.813 |
| 18S | 245 | CAGCC | 1.857 | 1.054 | 4.555 |
| 18S | 255 | CAGCT | 3.633 | 2.941 | 1.214 |
| 18S | 256 | CGGCC | 1.523 | 1.779 | 2.092 |
| 18S | 265 | CGGCC | 4.477 | 4.283 | 2.588 |
| 18S | 266 | CGGCC | 4.352 | 2.840 | 0.813 |
| 18S | 267 | GGGGC | 2.640 | 2.012 | 2.020 |
| 18S | 268 | GGGGG | 1.552 | 1.328 | 5.769 |
| 18S | 269 | GGGGC | 2.640 | 2.012 | 2.020 |
| 18S | 270 | GGGGC | 2.857 | 1.569 | 2.646 |
| 18S | 272 | GGGGC | 4.477 | 4.283 | 2.588 |
| 18S | 273 | GGGGC | 4.352 | 2.840 | 0.813 |
| 18S | 274 | GGGGC | 3.976 | 1.328 | 5.769 |
| 18S | 276 | GGGGC | 3.976 | 1.328 | 5.769 |
| 18S | 279 | CCGCT | 1.178 | 0.918 | 3.486 |
| 18S | 280 | CCGCT | 1.040 | 1.797 | 2.020 |
| 18S | 281 | CCGCT | 1.040 | 1.797 | 2.020 |
| 18S | 282 | CCGCT | 3.633 | 2.941 | 1.214 |
| 18S | 283 | CCGCT | 3.633 | 2.941 | 1.214 |
| 18S | 284 | CCGCT | 4.080 | 2.447 | 2.811 |
| 18S | 285 | CCGCT | 4.080 | 2.447 | 2.811 |
| 18S | 288 | TGGGT | 3.294 | 4.355 | 1.026 |
| 18S | 291 | GTGAC | 2.236 | 7.393 | 1.079 |
| 18S | 298 | TAGAT | 4.354 | 4.669 | 4.277 |
| 18S | 307 | TCGGG | 5.403 | 1.387 | 2.326 |
| 18S | 308 | CCGGC | 4.154 | 2.594 | 3.486 |
| 18S | 309 | CCGGC | 4.154 | 2.594 | 3.486 |
| 18S | 312 | CCGAT | 1.800 | 1.143 | 2.350 |
| 18S | 316 | TGGCA | 1.812 | 1.575 | 3.226 |
| 18S | 320 | AGGCC | 4.173 | 2.082 | 7.292 |
| 18S | 327 | CCGTG | 5.103 | 1.690 | 4.623 |
| 18S | 329 | GTGAC | 1.717 | 1.222 | 2.092 |
| 18S | 330 | TGGCG | 2.952 | 1.415 | 1.301 |
| 18S | 332 | CCGGT | 3.501 | 1.738 | 1.227 |
| 18S | 333 | CCGGC | 5.869 | 1.807 | 1.391 |
| 18S | 335 | CCGAC | 7.649 | 1.558 | 1.871 |
| 18S | 338 | ACGAC | 3.303 | 4.718 | 4.878 |
| 18S | 347 | TCGAA | 2.192 | 4.751 | 5.213 |
| 18S | 351 | ACGTC | 2.239 | 0.898 | 4.000 |
| 18S | 355 | CTCGC | 3.096 | 1.072 | 6.599 |
| 18S | 370 | TCGAT | 2.985 | 1.945 | 5.839 |
|   |   |   |   |
|---|---|---|---|
| **18S** | 373 | ATGGT | 4.082 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
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| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
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| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
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| **18S** | 383 | CCGTG | 2.492 |
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| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
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| **18S** | 377 | TAGTC | 2.742 |
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| **18S** | 383 | CCGTG | 2.492 |
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| **18S** | 394 | ATGGT | 3.747 |
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| **18S** | 374 | TGGTA | 3.809 |
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| **18S** | 374 | TGGTA | 3.809 |
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| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| **18S** | 374 | TGGTA | 3.809 |
| **18S** | 377 | TAGTC | 2.742 |
| **18S** | 380 | TCGCC | 2.097 |
| **18S** | 383 | CCGTG | 2.492 |
| **18S** | 385 | GTGCC | 2.649 |
| **18S** | 394 | ATGGT | 3.747 |
| **18S** | 395 | TGGTG | 3.596 |
| 18S | 535 | AGGAC   | 2.307 | 5.935 | 2.128 |
| 18S | 544 | TCGAG   | 2.180 | 3.362 | 3.052 |
| 18S | 546 | GAGGC   | 1.145 | 4.394 | 4.038 |
| 18S | 547 | AGGCC   | 1.538 | 7.066 | 5.797 |
| 18S | 552 | CTGTA   | 3.253 | 5.362 | 1.339 |
| 18S | 558 | TTGGA   | 1.903 | 1.039 | 3.889 |
| 18S | 559 | TGGAA   | 2.072 | 1.270 | 2.944 |
| 18S | 563 | ATGAG   | 1.440 | 0.848 | 1.457 |
| 18S | 565 | GAGTC   | 1.326 | 0.734 | 1.766 |
| 18S | 586 | ACGAG   | 2.391 | 3.457 | 3.346 |
| 18S | 588 | GAGGA   | 1.827 | 2.878 | 3.213 |
| 18S | 589 | AGGAT   | 2.482 | 2.533 | 2.935 |
| 18S | 597 | TTGGA   | 2.917 | 4.180 | 3.889 |
| 18S | 600 | GAGGG   | 0.977 | 2.458 | 4.667 |
| 18S | 601 | AGGGC   | 0.946 | 1.093 | 0.915 |
| 18S | 602 | GGGCA   | 1.048 | 3.116 | 3.060 |
| 18S | 606 | AAGTC   | 1.783 | 1.885 | 3.763 |
| 18S | 610 | CTGGT   | 1.704 | 1.732 | 0.338 |
| 18S | 611 | TGCTG   | 1.185 | 3.529 | 1.026 |
| 18S | 613 | GTGCC   | 0.873 | 3.224 | 3.390 |
| 18S | 617 | CAGCA   | 1.512 | 3.761 | 2.936 |
| 18S | 620 | CAGCC   | 1.653 | 1.160 | 4.555 |
| 18S | 623 | CGCCG   | 2.563 | 0.859 | 1.667 |
| 18S | 625 | CGCTG   | 1.839 | 0.357 | 1.364 |
| 18S | 626 | CAGTA   | 0.963 | 0.596 | 2.384 |
| 18S | 635 | CAGCT   | 3.189 | 1.177 | 4.023 |
| 18S | 644 | TAGCG   | 2.944 | 1.203 | 1.416 |
| 18S | 646 | GCCTA   | 2.346 | 1.947 | 2.982 |
| 18S | 656 | AAGTT   | 4.432 | 1.243 | 2.556 |
| 18S | 659 | TTGCT   | 4.311 | 5.902 | 3.071 |
| 18S | 662 | CTGCA   | 3.110 | 9.356 | 1.826 |
| 18S | 665 | CAGTT   | 2.067 | 4.259 | 1.926 |
| 18S | 673 | AAGCT   | 2.177 | 4.550 | 3.448 |
| 18S | 677 | TCGTA   | 2.735 | 12.441 | 2.104 |
| 18S | 680 | TAGTT   | 4.086 | 5.772 | 1.348 |
| 18S | 683 | TTGGA   | 1.425 | 3.857 | 3.889 |
| 18S | 684 | TGGAT   | 1.533 | 4.394 | 1.790 |
| 18S | 690 | TTGGG   | 3.235 | 3.859 | 0.935 |
| 18S | 691 | TTGGG   | 3.097 | 4.348 | 1.542 |
| 18S | 692 | GGGAG   | 2.840 | 4.130 | 4.040 |
| 18S | 694 | GAGCG   | 3.597 | 1.844 | 4.595 |
| 18S | 696 | CGGCG   | 3.496 | 1.655 | 5.556 |
| 18S | 697 | CGGTC   | 2.967 | 0.989 | 3.486 |
| 18S | 698 | GGCGG   | 1.864 | 0.675 | 2.020 |
| 18S | 700 | GGCGG   | 1.939 | 1.134 | 5.556 |
| 18S | 701 | CGGCG   | 2.775 | 1.186 | 3.486 |
| 18S | 702 | GGCGG   | 3.124 | 1.955 | 2.020 |
| 18S | 704 | CGGCG   | 2.160 | 2.740 | 1.364 |
| 18S | 705 | CGGTC   | 2.834 | 4.725 | 5.469 |
| 18S | 709 | CGGCC   | 3.536 | 4.306 | 8.589 |
| 18S | 712 | CGGCC   | 4.408 | 5.183 | 1.667 |
| 18S | 714 | GCGAG | 2.374 | 6.317 | 3.970 |
| 18S | 716 | GAGGC | 4.466 | 4.226 | 4.038 |
| 18S | 717 | AGGCC | 4.027 | 3.538 | 1.796 |
| 18S | 719 | GCGAG | 4.932 | 6.427 | 3.970 |
| 18S | 721 | GAGCC | 6.241 | 7.016 | 4.918 |
| 18S | 727 | CCGCC | 5.246 | 1.634 | 8.589 |
| 18S | 731 | CGGCT | 2.333 | 1.121 | 3.694 |
| 18S | 737 | CGGCC | 2.158 | 1.399 | 8.589 |
| 18S | 744 | TTGCC | 2.127 | 2.287 | 2.743 |
| 18S | 751 | TCGGC | 4.616 | 1.049 | 2.504 |
| 18S | 752 | CGGCC | 3.006 | 3.263 | 1.391 |
| 18S | 754 | GCGCC | 2.532 | 1.174 | 3.614 |
| 18S | 762 | TCGAT | 3.563 | 2.092 | 5.839 |
| 18S | 765 | ATGCT | 4.541 | 2.945 | 4.854 |
| 18S | 772 | TAGCT | 4.541 | 2.945 | 4.770 |
| 18S | 775 | CTGAG | 3.378 | 3.672 | 2.726 |
| 18S | 777 | GAGTG | 3.558 | 3.145 | 2.174 |
| 18S | 779 | GTGTC | 3.436 | 4.656 | 1.511 |
| 18S | 784 | CCGCC | 4.655 | 2.041 | 1.667 |
| 18S | 786 | GCGGG | 2.133 | 0.319 | 5.556 |
| 18S | 787 | CCGGG | 1.493 | 1.163 | 5.217 |
| 18S | 788 | GGGGC | 0.974 | 1.681 | 2.646 |
| 18S | 789 | GGGCC | 0.731 | 1.569 | 4.167 |
| 18S | 793 | CCGAA | 2.047 | 2.149 | 4.430 |
| 18S | 796 | AAGCG | 2.356 | 0.910 | 0.974 |
| 18S | 798 | GCGTT | 4.297 | 0.927 | 1.471 |
| 18S | 807 | TTGAA | 3.100 | 5.529 | 5.033 |
| 18S | 817 | TAGAG | 1.401 | 4.496 | 0.606 |
| 18S | 819 | GAGTG | 3.506 | 7.856 | 2.174 |
| 18S | 821 | GTGCT | 2.896 | 6.080 | 1.323 |
| 18S | 828 | AAGCA | 2.685 | 2.760 | 3.790 |
| 18S | 831 | CAGGC | 2.337 | 3.073 | 3.797 |
| 18S | 832 | AGGCC | 2.802 | 4.247 | 5.797 |
| 18S | 836 | CCGAG | 2.911 | 5.043 | 6.192 |
| 18S | 838 | GAGCC | 3.721 | 2.480 | 4.918 |
| 18S | 841 | CGGCC | 4.777 | 4.610 | 8.589 |
| 18S | 845 | CTGGA | 3.414 | 2.029 | 1.197 |
| 18S | 846 | TGGAT | 2.744 | 2.693 | 1.790 |
| 18S | 852 | CCGCA | 3.714 | 3.779 | 2.484 |
| 18S | 855 | CAGCT | 2.857 | 2.109 | 4.023 |
| 18S | 859 | TAGGA | 3.491 | 0.708 | 4.368 |
| 18S | 860 | AGGAA | 3.556 | 0.775 | 4.787 |
| 18S | 867 | ATGGA | 1.876 | 0.962 | 2.826 |
| 18S | 868 | TGAGA | 2.366 | 3.538 | 2.944 |
| 18S | 873 | TAGGA | 3.158 | 1.645 | 4.368 |
| 18S | 874 | AGGAC | 2.652 | 2.194 | 2.128 |
| 18S | 878 | CCAGC | 1.211 | 0.687 | 1.667 |
| 18S | 880 | GCGGT | 1.548 | 1.028 | 1.364 |
| 18S | 881 | CGGTT | 1.328 | 2.429 | 2.116 |
| 18S | 891 | TTGTT | 6.349 | 2.567 | 1.619 |
| 18S | 894 | TTGTT | 3.001 | 3.590 | 2.811 |
| 18S | 895 | TGGTT | 1.906 | 7.224 | 1.856 |
| 18S  | 901 | TCGGA  | 2.294 | 1.100 | 2.703 |
| 18S  | 902 | CGGAA  | 1.734 | 1.913 | 1.050 |
| 18S  | 907 | CTGAG  | 3.119 | 0.669 | 2.726 |
| 18S  | 909 | GAGGC  | 2.309 | 1.647 | 4.038 |
| 18S  | 910 | AGGCC  | 2.127 | 2.609 | 5.797 |
| 18S  | 915 | ATGAT  | 2.002 | 4.084 | 5.227 |
| 18S  | 921 | AAGAG  | 3.816 | 4.153 | 1.693 |
| 18S  | 923 | GAGGG  | 3.164 | 2.354 | 4.667 |
| 18S  | 924 | AGGGA  | 3.504 | 2.544 | 1.667 |
| 18S  | 925 | GGGAC  | 2.781 | 4.158 | 1.575 |
| 18S  | 928 | ACCTG  | 3.587 | 2.610 | 2.104 |
| 18S  | 929 | CCGCC  | 2.248 | 5.178 | 0.813 |
| 18S  | 932 | CCGGG  | 2.102 | 0.893 | 5.769 |
| 18S  | 933 | CGGGG  | 1.871 | 0.998 | 5.217 |
| 18S  | 934 | CGGGG  | 1.259 | 1.870 | 6.000 |
| 18S  | 935 | GGAGG  | 0.803 | 4.541 | 2.646 |
| 18S  | 936 | GGAGG  | 0.728 | 9.199 | 3.060 |
| 18S  | 942 | TCGTA  | 3.587 | 2.610 | 2.104 |
| 18S  | 947 | TTGCG  | 4.909 | 2.849 | 1.813 |
| 18S  | 949 | GCGCC  | 3.415 | 2.479 | 3.614 |
| 18S  | 952 | CCCTA  | 3.651 | 2.484 | 3.141 |
| 18S  | 956 | TACCT  | 3.593 | 1.995 | 0.606 |
| 18S  | 958 | GAGGT  | 1.772 | 1.014 | 2.459 |
| 18S  | 959 | AGGTG  | 1.762 | 2.246 | 0.951 |
| 18S  | 961 | GTGAA  | 1.772 | 3.836 | 3.093 |
| 18S  | 970 | TTGGA  | 6.425 | 10.886 | 3.889 |
| 18S  | 971 | TGGAC  | 5.374 | 12.426 | 1.958 |
| 18S  | 975 | CCGCT  | 2.438 | 4.062 | 2.588 |
| 18S  | 976 | CGGCC  | 3.102 | 4.118 | 1.391 |
| 18S  | 978 | CCCTG  | 9.967 | 4.538 | 2.507 |
| 18S  | 982 | CCGAG  | 2.382 | 3.259 | 2.307 |
| 18S  | 985 | ACMGC  | 3.058 | 4.035 | 3.125 |
| 18S  | 986 | CCGAC  | 2.008 | 3.257 | 1.775 |
| 18S  | 991 | CAGAC  | 1.600 | 0.941 | 1.225 |
| 18S  | 993 | GACGT  | 2.950 | 0.297 | 4.595 |
| 18S  | 995 | GCGCA  | 2.962 | 0.618 | 2.219 |
| 18S  | 999 | AAGCA  | 2.602 | 0.591 | 3.790 |
| 18S  | 1005 | TTGCC  | 3.279 | 0.554 | 2.743 |
| 18S  | 1010 | AAGAA  | 1.163 | 0.542 | 4.916 |
| 18S  | 1014 | GCTCG  | 3.636 | 0.611 | 2.422 |
| 18S  | 1029 | AAGAA  | 1.404 | 3.238 | 4.916 |
| 18S  | 1033 | GCGAG  | 5.622 | 1.592 | 5.925 |
| 18S  | 1037 | TCCTG  | 2.539 | 3.485 | 3.763 |
| 18S  | 1040 | TCCTG  | 2.775 | 2.036 | 2.703 |
| 18S  | 1041 | CCGAG  | 2.771 | 2.120 | 4.478 |
| 18S  | 1043 | CCGAG  | 1.624 | 1.306 | 2.459 |
| 18S  | 1044 | CCGAG  | 2.260 | 4.256 | 2.881 |
| 18S  | 1048 | CCGAG  | 1.966 | 2.156 | 5.213 |
| 18S  | 1051 | AAGAC  | 1.841 | 0.883 | 2.307 |
| 18S  | 1054 | ACGAT  | 2.956 | 0.553 | 6.569 |
| 18S  | 1059 | CAGAT  | 2.827 | 0.547 | 2.605 |
| 18S  | 1065 | CGGTCA | 3.330 | 0.211 | 3.694 |
| 18S | 1068  | TCGTA  | 2.370 | 0.453 | 2.104 |
| 18S | 1071  | TAGTT  | 2.814 | 0.867 | 1.348 |
| 18S | 1076  | CCGAC  | 3.050 | 3.066 | 4.167 |
| 18S | 1086  | ACGAT  | 3.852 | 2.359 | 6.569 |
| 18S | 1089  | ATGCC  | 3.803 | 3.428 | 8.696 |
| 18S | 1092  | CCGAC  | 2.380 | 3.033 | 4.167 |
| 18S | 1096  | CGGCG  | 4.633 | 10.871 | 2.588 |
| 18S | 1097  | CGGCC  | 5.026 | 10.913 | 1.391 |
| 18S | 1099  | GCAGT  | 1.358 | 1.939 | 2.802 |
| 18S | 1102  | ATGCC  | 3.222 | 0.904 | 1.871 |
| 18S | 1104  | CGGCC  | 3.269 | 0.395 | 1.227 |
| 18S | 1105  | CGGCC  | 4.887 | 0.398 | 1.391 |
| 18S | 1107  | CGGCC  | 4.117 | 0.545 | 1.227 |
| 18S | 1108  | CGGCC  | 3.154 | 1.027 | 1.391 |
| 18S | 1110  | GCAGT  | 3.154 | 1.391 | 2.429 |
| 18S | 1121  | ATGCC  | 2.471 | 7.448 | 3.482 |
| 18S | 1126  | CGGCC  | 3.158 | 1.707 | 8.589 |
| 18S | 1129  | CGGCC  | 2.718 | 2.391 | 5.769 |
| 18S | 1130  | CGGCC  | 2.391 | 2.971 | 3.486 |
| 18S | 1131  | GGGCA  | 2.862 | 5.291 | 3.060 |
| 18S | 1134  | CAGCT  | 3.671 | 1.836 | 4.023 |
| 18S | 1140  | CGGGG  | 4.555 | 0.644 | 5.769 |
| 18S | 1141  | GGAGA  | 3.529 | 0.997 | 2.429 |
| 18S | 1142  | GGGAA  | 2.634 | 1.585 | 2.195 |
| 18S | 1151  | AAGTC  | 1.793 | 0.940 | 3.763 |
| 18S | 1157  | TTGGG  | 5.805 | 1.820 | 0.935 |
| 18S | 1158  | TGGGT  | 2.224 | 2.576 | 1.977 |
| 18S | 1159  | GGGTT  | 1.946 | 3.423 | 2.091 |
| 18S | 1164  | CGGCC  | 3.024 | 0.884 | 5.769 |
| 18S | 1165  | CGGCC  | 2.783 | 0.404 | 5.217 |
| 18S | 1166  | CGGCC  | 1.880 | 0.405 | 6.000 |
| 18S | 1167  | CGGCC  | 0.611 | 0.403 | 6.000 |
| 18S | 1168  | CGGCC  | 0.536 | 0.646 | 0.769 |
| 18S | 1169  | CGGCC  | 0.895 | 1.128 | 4.040 |
| 18S | 1171  | CGGCC  | 1.091 | 2.126 | 2.726 |
| 18S | 1175  | ATGCC  | 2.424 | 1.254 | 2.203 |
| 18S | 1176  | TGGTT  | 1.772 | 1.370 | 1.856 |
| 18S | 1179  | TTGGA  | 1.684 | 0.887 | 3.339 |
| 18S | 1184  | AAGTC  | 4.375 | 2.350 | 3.448 |
| 18S | 1187  | CGGTA  | 1.996 | 3.933 | 2.784 |
| 18S | 1197  | AAGTA  | 10.488 | 5.470 | 5.686 |
| 18S | 1198  | AGGG  | 9.849 | 8.096 | 4.787 |
| 18S | 1203  | CGGCC  | 2.577 | 7.759 | 3.569 |
| 18S | 1206  | CGGCC  | 2.542 | 0.878 | 3.125 |
| 18S | 1207  | CGGCC  | 2.351 | 0.449 | 1.050 |
| 18S | 1210  | AAGTA  | 2.684 | 0.283 | 1.026 |
| 18S | 1211  | AGGG  | 3.317 | 0.472 | 0.915 |
| 18S | 1212  | AGGG  | 3.354 | 0.755 | 3.060 |
| 18S | 1221  | AAGTA  | 4.697 | 0.793 | 1.282 |
| 18S | 1222  | AGGG  | 4.318 | 1.144 | 3.512 |
| 18S | 1224  | AGGG  | 4.021 | 0.213 | 2.174 |
| 18S | 1226  | GTGGA  | 5.112 | 0.228 | 3.209 |
| 18S | 1227  | TGGAG   | 4.787   | 0.166   | 2.880  |
|-----|-------|---------|---------|---------|--------|
| 18S | 1229  | GAGGC   | 2.888   | 0.352   | 4.918  |
| 18S | 1233  | CTGCG   | 2.099   | 0.373   | 0.524  |
| 18S | 1235  | GCCGC   | 2.232   | 0.275   | 1.227  |
| 18S | 1236  | CGGCT   | 2.156   | 0.442   | 1.214  |
| 18S | 1245  | TTGAC   | 2.914   | 1.224   | 3.569  |
| 18S | 1255  | ACGGG   | 4.253   | 2.086   | 2.791  |
| 18S | 1256  | CGGGA   | 2.198   | 1.498   | 2.429  |
| 18S | 1257  | GGGAA   | 2.449   | 3.434   | 2.195  |
| 18S | 1269  | CGGCG   | 3.041   | 2.623   | 2.588  |
| 18S | 1270  | CGGCC   | 3.491   | 2.207   | 0.813  |
| 18S | 1274  | CGGCA   | 1.712   | 4.774   | 2.721  |
| 18S | 1275  | CGGAC   | 1.639   | 4.743   | 1.775  |
| 18S | 1280  | CGGAC   | 2.105   | 1.828   | 1.775  |
| 18S | 1285  | CAGGA   | 3.304   | 1.005   | 1.282  |
| 18S | 1286  | AGGAT   | 2.623   | 0.534   | 2.935  |
| 18S | 1290  | TTGAC   | 5.311   | 1.842   | 3.569  |
| 18S | 1294  | CAGAT   | 2.459   | 1.140   | 2.605  |
| 18S | 1298  | TTGAT   | 3.452   | 1.115   | 2.577  |
| 18S | 1302  | TAGCT   | 1.503   | 1.543   | 4.770  |
| 18S | 1312  | TCGAT   | 2.419   | 2.839   | 5.839  |
| 18S | 1318  | CCGTG   | 2.773   | 2.765   | 4.623  |
| 18S | 1320  | GTGGG   | 1.891   | 2.670   | 0.000  |
| 18S | 1321  | TGGGT   | 1.825   | 2.502   | 1.977  |
| 18S | 1322  | GGGTG   | 1.410   | 1.948   | 0.806  |
| 18S | 1324  | GTGCT   | 1.041   | 0.697   | 1.974  |
| 18S | 1325  | TGCTG   | 1.439   | 1.487   | 1.026  |
| 18S | 1327  | GTGCT   | 1.024   | 2.081   | 1.974  |
| 18S | 1328  | TGGTG   | 0.942   | 2.291   | 1.026  |
| 18S | 1330  | GTGGA   | 2.276   | 2.913   | 3.209  |
| 18S | 1332  | CTGCT   | 3.182   | 1.623   | 2.079  |
| 18S | 1335  | TGCTG   | 2.430   | 0.950   | 0.338  |
| 18S | 1338  | CCGGT   | 1.168   | 4.683   | 2.993  |
| 18S | 1340  | TAGTT   | 3.759   | 7.136   | 1.348  |
| 18S | 1348  | TTGCT   | 4.255   | 3.912   | 2.811  |
| 18S | 1349  | TGCTG   | 3.564   | 3.255   | 1.026  |
| 18S | 1351  | GTGCA   | 1.472   | 4.113   | 2.869  |
| 18S | 1352  | TGGTC   | 3.650   | 2.155   | 2.827  |
| 18S | 1354  | GAGCG   | 1.513   | 3.480   | 4.595  |
| 18S | 1356  | GCGAT   | 1.663   | 3.033   | 2.802  |
| 18S | 1361  | TTGTC   | 3.182   | 1.623   | 2.079  |
| 18S | 1365  | CTGCT   | 2.430   | 0.950   | 0.338  |
| 18S | 1366  | TGCTG   | 3.359   | 2.516   | 1.856  |
| 18S | 1375  | CCGAT   | 2.953   | 6.210   | 2.350  |
| 18S | 1381  | ACGAA   | 3.899   | 4.902   | 5.925  |
| 18S | 1385  | ACGAG   | 1.298   | 0.688   | 3.346  |
| 18S | 1387  | GAGAC   | 1.772   | 0.990   | 1.538  |
| 18S | 1393  | CTGAC   | 1.832   | 0.598   | 2.083  |
| 18S | 1394  | TGGCA   | 2.533   | 0.441   | 3.233  |
| 18S | 1398  | ATGCT   | 2.604   | 0.913   | 4.854  |
| 18S | 1406  | TAGTT   | 5.060   | 2.923   | 1.348  |
| 18S  | 1411 | ACGCG  | 4.124 | 3.834 | 4.640 |
|------|------|--------|-------|-------|-------|
| 18S  | 1413 | GCGAC  | 5.335 | 6.462 | 1.871 |
| 18S  | 1420 | CCGAG  | 2.603 | 15.587 | 6.192 |
| 18S  | 1422 | GAGCG  | 2.437 | 6.717 | 4.595 |
| 18S  | 1424 | GCGGT  | 1.394 | 2.541 | 1.364 |
| 18S  | 1425 | CGGTC  | 3.157 | 1.958 | 5.469 |
| 18S  | 1428 | TCGGC  | 2.886 | 1.332 | 2.504 |
| 18S  | 1431 | GCGTC  | 2.258 | 1.466 | 1.455 |
| 18S  | 1437 | TAGAG  | 3.206 | 2.071 | 0.606 |
| 18S  | 1449 | GAGGG  | 1.883 | 1.786 | 4.667 |
| 18S  | 1450 | AGGGA  | 3.822 | 3.753 | 1.667 |
| 18S  | 1451 | GGGAC  | 2.784 | 3.678 | 1.575 |
| 18S  | 1456 | AAGTG  | 3.349 | 4.024 | 1.102 |
| 18S  | 1458 | GTGCC  | 0.949 | 4.394 | 2.092 |
| 18S  | 1459 | TGGCG  | 0.847 | 5.038 | 1.301 |
| 18S  | 1461 | GCGTT  | 0.575 | 5.204 | 1.471 |
| 18S  | 1466 | CAGCC  | 1.532 | 2.913 | 4.555 |
| 18S  | 1473 | CGGAG  | 1.746 | 1.721 | 6.192 |
| 18S  | 1475 | GAGAT  | 1.317 | 2.023 | 2.734 |
| 18S  | 1479 | TTGAG  | 3.089 | 2.115 | 1.671 |
| 18S  | 1481 | GAGCA  | 2.946 | 2.223 | 3.951 |
| 18S  | 1490 | CAGGT  | 4.417 | 0.811 | 3.125 |
| 18S  | 1491 | AGGTC  | 4.896 | 1.043 | 6.490 |
| 18S  | 1495 | CTGTG  | 3.965 | 1.557 | 1.541 |
| 18S  | 1497 | GTGAT  | 1.494 | 1.606 | 2.367 |
| 18S  | 1500 | ATGCC  | 2.038 | 2.043 | 8.696 |
| 18S  | 1507 | TAGAT  | 1.055 | 5.377 | 4.277 |
| 18S  | 1510 | ATGTC  | 3.011 | 3.574 | 5.270 |
| 18S  | 1514 | CCGGC  | 2.234 | 0.845 | 5.769 |
| 18S  | 1515 | CGGGG  | 1.638 | 1.055 | 5.217 |
| 18S  | 1516 | GGGGC  | 1.752 | 1.421 | 2.646 |
| 18S  | 1517 | GGGCT  | 1.662 | 2.120 | 1.845 |
| 18S  | 1520 | CTGCA  | 1.822 | 2.454 | 1.826 |
| 18S  | 1524 | ACGCG  | 1.904 | 2.932 | 4.640 |
| 18S  | 1526 | GCCGC  | 2.936 | 3.189 | 2.881 |
| 18S  | 1528 | GCCGT  | 3.273 | 2.337 | 2.963 |
| 18S  | 1536 | CTGAC  | 3.307 | 2.777 | 2.013 |
| 18S  | 1540 | CTGCA  | 3.482 | 1.692 | 2.083 |
| 18S  | 1541 | TGGCT  | 3.696 | 2.771 | 1.397 |
| 18S  | 1546 | CAGGC  | 3.363 | 1.115 | 1.457 |
| 18S  | 1548 | GCGTG  | 2.995 | 0.970 | 2.277 |
| 18S  | 1550 | GTGAG  | 2.479 | 1.898 | 3.030 |
| 18S  | 1552 | GTGCC  | 2.257 | 2.196 | 3.390 |
| 18S  | 1563 | ACGCC  | 1.892 | 3.354 | 7.292 |
| 18S  | 1566 | CCGGC  | 1.877 | 2.419 | 2.588 |
| 18S  | 1567 | CGCCA  | 4.031 | 4.551 | 2.367 |
| 18S  | 1570 | CAGGC  | 1.558 | 1.701 | 3.797 |
| 18S  | 1571 | AGGCC  | 2.146 | 1.542 | 1.796 |
| 18S  | 1573 | GCCGC  | 2.345 | 1.400 | 2.881 |
| 18S  | 1575 | CGCGG  | 4.710 | 1.038 | 5.556 |
| 18S  | 1576 | CGGGT  | 3.463 | 1.586 | 2.041 |
| 18S | 1577 GGGTA | 4.433 | 2.513 | 1.050 |
| 18S | 1584 CCGTT | 4.027 | 0.764 | 2.993 |
| 18S | 1587 TTGAA | 3.218 | 2.898 | 5.033 |
| 18S | 1598 TCGTG | 4.248 | 10.159 | 3.325 |
| 18S | 1600 GTGAT | 3.013 | 7.938 | 2.367 |
| 18S | 1603 ATGGG | 2.637 | 2.362 | 2.190 |
| 18S | 1604 TGGGG | 2.970 | 1.886 | 0.000 |
| 18S | 1605 GGGGA | 2.559 | 1.729 | 0.769 |
| 18S | 1606 GGGAT | 1.511 | 1.791 | 1.140 |
| 18S | 1610 TCGGG | 2.209 | 0.443 | 2.326 |
| 18S | 1611 CGGGG | 2.614 | 0.889 | 5.217 |
| 18S | 1612 GGGGA | 1.029 | 0.669 | 0.769 |
| 18S | 1613 GGGAT | 0.780 | 0.696 | 1.140 |
| 18S | 1617 TTGCA | 0.541 | 1.023 | 3.339 |
| 18S | 1632 ATGAA | 1.119 | 3.890 | 5.233 |
| 18S | 1636 ACGAG | 1.238 | 1.484 | 3.346 |
| 18S | 1638 GAGGA | 4.894 | 1.347 | 3.213 |
| 18S | 1648 CAGTA | 1.775 | 3.550 | 4.176 |
| 18S | 1652 AAGTG | 3.788 | 2.426 | 1.102 |
| 18S | 1654 GTGCC | 2.216 | 1.460 | 2.076 |
| 18S | 1656 GCAGG | 1.594 | 1.592 | 5.556 |
| 18S | 1657 CCGTG | 1.687 | 2.150 | 2.041 |
| 18S | 1658 GGGTC | 1.546 | 1.864 | 2.791 |
| 18S | 1665 AAGCT | 3.155 | 1.743 | 3.448 |
| 18S | 1669 TTGCG | 3.256 | 1.722 | 1.813 |
| 18S | 1671 GCATT | 3.486 | 1.236 | 1.471 |
| 18S | 1674 TCGAT | 3.453 | 2.268 | 2.577 |
| 18S | 1680 AAGTC | 0.715 | 2.062 | 3.763 |
| 18S | 1686 CTGCC | 1.484 | 5.946 | 6.599 |
| 18S | 1693 TTGTA | 5.278 | 22.013 | 2.550 |
| 18S | 1702 CGGCC | 4.434 | 4.870 | 8.589 |
| 18S | 1706 CCCTC | 3.571 | 0.822 | 3.694 |
| 18S | 1709 TCGCT | 3.553 | 1.322 | 9.829 |
| 18S | 1718 CCGAT | 4.117 | 5.189 | 2.350 |
| 18S | 1722 TTGGA | 3.166 | 3.539 | 3.889 |
| 18S | 1723 TGGAT | 3.469 | 2.984 | 1.790 |
| 18S | 1726 ATGGT | 2.884 | 2.999 | 2.203 |
| 18S | 1727 TGGTT | 3.037 | 5.124 | 1.856 |
| 18S | 1732 TAGTG | 5.646 | 3.072 | 1.437 |
| 18S | 1734 GTGAG | 3.042 | 2.372 | 2.821 |
| 18S | 1736 GAGGC | 1.469 | 7.174 | 4.038 |
| 18S | 1737 AGGCC | 2.454 | 10.509 | 5.797 |
| 18S | 1743 TCGGA | 4.890 | 3.154 | 2.703 |
| 18S | 1744 CCGAT | 3.114 | 1.815 | 2.100 |
| 18S | 1748 TCGGC | 3.609 | 3.919 | 2.504 |
| 18S | 1749 CGGCC | 2.210 | 3.247 | 0.813 |
| 18S | 1754 CCGCC | 6.055 | 3.221 | 8.589 |
| 18S | 1757 CGGGG | 2.329 | 2.868 | 5.769 |
| 18S | 1758 CGGGG | 2.894 | 3.202 | 5.217 |
| 18S | 1759 GGGGT | 1.958 | 2.413 | 0.000 |
| 18S | 1760 GGGTC | 2.464 | 2.085 | 2.791 |
| 18S  | Position | Sequence | 1st_row | 2nd_row | 3rd_row |
|------|----------|----------|---------|---------|---------|
| 18S  | 1763     | TCGGC    | 4.840   | 4.358   | 2.504   |
| 18S  | 1764     | CGGCC    | 3.501   | 4.655   | 0.813   |
| 18S  | 1770     | ACGGC    | 5.024   | 3.081   | 2.500   |
| 18S  | 1771     | CGGCC    | 3.932   | 3.588   | 0.813   |
| 18S  | 1776     | CTGGC    | 3.401   | 3.433   | 2.083   |
| 18S  | 1777     | TGGCG    | 4.809   | 2.891   | 1.301   |
| 18S  | 1779     | CGGGA    | 2.842   | 1.804   | 1.389   |
| 18S  | 1780     | CGGAG    | 3.234   | 2.636   | 4.478   |
| 18S  | 1782     | GAGCG    | 1.285   | 2.959   | 4.595   |
| 18S  | 1784     | GCGCT    | 2.239   | 2.413   | 2.963   |
| 18S  | 1787     | CTGAG    | 1.723   | 2.404   | 2.726   |
| 18S  | 1789     | GAGAA    | 1.453   | 2.867   | 2.304   |
| 18S  | 1792     | AAGAC    | 3.277   | 1.061   | 2.307   |
| 18S  | 1795     | ACGGT    | 3.558   | 1.114   | 3.200   |
| 18S  | 1796     | CCGTC    | 2.638   | 0.852   | 5.469   |
| 18S  | 1799     | TCGAA    | 2.370   | 2.281   | 5.213   |
| 18S  | 1805     | TTGAC    | 4.762   | 3.614   | 3.569   |
| 18S  | 1814     | TAGAG    | 2.549   | 1.746   | 0.606   |
| 18S  | 1816     | GAGGA    | 2.705   | 1.126   | 3.213   |
| 18S  | 1817     | AGGAA    | 2.373   | 1.168   | 4.787   |
| 18S  | 1820     | AAGTA    | 1.096   | 1.197   | 5.179   |
| 18S  | 1826     | AAGTC    | 3.369   | 3.938   | 3.763   |
| 18S  | 1829     | TCGTA    | 3.003   | 4.807   | 2.104   |
| 18S  | 1836     | AAGGT    | 1.251   | 0.341   | 2.528   |
| 18S  | 1837     | AGGTT    | 1.061   | 0.448   | 2.881   |
| 18S  | 1843     | CCGTA    | 1.359   | 3.798   | 7.973   |
| 18S  | 1846     | TAGGT    | 3.874   | 1.067   | 2.344   |
| 18S  | 1847     | AGGTG    | 4.589   | 0.992   | 0.951   |
| 18S  | 1849     | GTGAA    | 1.487   | 1.356   | 3.093   |
| 18S  | 1855     | CTGCG    | 0.154   | 0.061   | 0.524   |
| 18S  | 1857     | CGGGA    | 0.044   | 0.321   | 1.389   |
| 18S  | 1858     | CGGAA    | 0.178   | 0.227   | 1.050   |
| 18S  | 1861     | AAGGA    | 0.210   | 0.034   | 5.686   |
| 18S  | 1862     | AGGAT    | 0.166   | 0.176   | 2.935   |

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