# GenomeSequence

April 25, 2025

[1]:
```
from Bio.SeqUtils import GC
from Bio.Seq import Seq
import matplotlib.pyplot as plt
import numpy as np

# UL52 nucleotide sequence
ul52_sequence = (
    "ATGGGGACGGAAGACTGCGATCACGAAGGGCGGTCGGTTGCGGCTCCCGTGGAGGTTACGGCGCTGTATG"
    "CGACCGACGGGTGCGTTATCACCTCCTCGCTCGCCCTCCTCACAAACTGCCTGCTGGGGGCCGAGCCGTT"
    "GTATATATTCAGCTACGACGCGTACCGGCCCGATGCGCCCAATGGCCCCACGGGCGCGCCCACCGAACAG"
    "GAGAGGTTCGAGGGGAGCCGGGCGCTCTACCGGGATGCGGGGGGGCTAAATGGCGATTCATTTCGGGTGA"
    "CCTTTTGTTTATTGGGGACGGAAGTGGGCGTGACCCACCACCCGAAAGGGCGCACCCGGCCCATGTTTGT"
    "GTGCCGCTTCGAGCGAGCGGACGACGTCGCCGTGCTCCAAGACGCCCTGGGCCGCGGGACCCCATTGCTC"
    "CCGGCCCACATCACAGCAACTCTGGACTTGGAGGCGACGTTTGCGCTCCACGCTAACATCATCATGGCTC"
    "TCACCGTGGCCATCGTCCACAACGCCCCCGCCCGCATCGGCAGCGGCAGCACCGCCCCCCTGTATGAGCC"
    "CGGCGAATCGATGCGCTCGGTCGTCGGGCGCATGTCCCTGGGGCAGCGCGGCCTCACCACGCTGTTCGTG"
    "CACCACGAGGCGCGCGTGCTGGCGGCGTACCGCCGGGCGTATTATGGGAGCGCCCAAAGCCCCTTTTGGT"
    "TTCTGAGCAAATTCGGCCCGGACGAAAAGAGCCTGGTGCTGGCCGCTAGGTACTACCTACTCCAGGCTCC"
    "GCGCTTGGGGGGCGCCGGAGCCACGTACGATCTGCAGGCCGTGAAAGACATCTGCGCGACCTACGCGATC"
    "CCCCACGACCCACGCCCCGACACCCTCAGTGCCGCGTCCTTGACCTCGTTCGCCGCCATCACTCGGTTCT"
    "GTTGCACGAGCCAGTACTCCCGCGGGGCCGCGGCCGCTGGGTTTCCGCTGTATGTGGAGCGCCGCATCGC"
    "CGCCGACGTACGCGAGACCGGCGCGCTGGAGAAGTTCATCGCCCACGATCGCAGCTGCCTGCGCGTGTCC"
    "GACCGGGAATTCATTACGTACATCTACCTGGCCCACTTTGAGTGCTTCAGCCCCCCGCGCCTGGCCACGC"
    "ATCTCCGGGCCGTGACCACCCACGACCCCAGCCCCGCGGCCAGCACGGAGCAGCCCTCGCCCCTGGGTCG"
    "GGAGGCGGTGGAACAGTTCTTCCGGCACGTGCGCGCCCAGCTGAACATCCGCGAGTACGTAAAGCAAAAC"
    "GTCACCCCCAGGGAAACCGCCCTGGCGGGAGACGCGGCCGCCGCCTACCTGCGCGCGCGCACGTATGCCC"
    "CGGCGGCCCTCACGCCCGCCCCCGCGTACTGCGGGGTCGCAGACTCGTCCACCAAAATGATGGGACGTCT"
    "GGCGGAAGCAGAAAGGCTCCTAGTCCCCCACGGCTGGCCCGCGTTCGCACCAACAACCCCCGGGGACGAC"
    "GCGGGGGGCGGCACTGCCGCCCCCCAGACCTGCGGAATCGTCAAGCGCCTCCTCAAGCTGGCCGCCACGG"
    "AGCAGCAGGGCACGACGCCCCCGGCGATCGCGGCTCTCATGCAGGACGCGTCGGTCCAAACCCCCCTGCC"
    "CGTGTACAGGATTACCATGTCCCCGACCGGCCAGGCGTTTGCCGCGGCGGCGCGGGACGACTGGGCCCGC"
    "GTGACGCGGGACGCGCGCCCGCCGGAAGCGACCGTGGTCGCGGACGCGGCGGCGGCGCCCGAGCCCGGCG"
    "CGCTCGGCCGGCGGCTCACGCGCCGCATTTGCGCCCGGGGCCCCGCGCTCCCCCCGGGCGGCCTGGCCGT"
    "CGGGGGCCAGATGTACGTGAACCGCAACGAGATCTTCAACGCCGCGCTGGCCGTTACGAACATCATCCTG"
    "GATCTGGACATCGCCCTGAAGGAGCCCGTCCCCTTTCCCCGGCTCCACGAGGCCCTGGGTCACTTTAGGC"
    "GCGGGGCGCTGGCGGCGGTTCAGCTGTTGTTTCCCGCGGCCCGCGTAGACCCCGACGCCTATCCCTGTTA"
    "TTTTTTCAAAAGCGCCTGTCGGCCCCGCGCGCCGCCCGTCTGTGCGGGCGACGGGCCCCTGGCCGGTGGC"
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    "GACGACGGCGACGGGGACTGGTTCCCCGACGCCGGTGGTCCCGGCGACGAGGAGTGGGAGGAGGACACGG"
    "ACCCCATGGACACGACCCACGGCCCCCTCCCGGACGACGAGGCCGCGTACCTCGACCTGCTACACGAACA"
    "GATACCAGCGGCGACGCCCAGCGAACCGGACTCCGTCGTGTGTTCCTGCGCCGACAAGATCGGGCTGCGC"
    "GTGTGCCTACCGGTCCCCGCCCCGTACGTTGTGCACGGCTCCCTGACGATGCGTGGGGTGGCGAGGGTGA"
    "TCCAGCAGGCGGTGCTGTTGGACCGCGACTTCGTGGAGGCCGTAGGGAGCCACGTAAAGAACTTTTTGCT"
    "GATCGATACGGGCGTGTACGCCCACGGCCACAGCCTGCGCTTGCCGTATTTCGCCAAGATCGGCCCCGAC"
    "GGCTCCGCGTGCGGCCGGTTATTGCCCGTCTTCGTGATCCCCCCCGCGTGCGAGGACGTTCCGGCGTTCG"
    "TCGCCGCGCACGCCGACCCGCGGCGCTTCCACTTTCACGCCCCGCCCATGTTTTCCGCGGCCCCGCGGGA"
    "GATCCGCGTCCTCCACAGCCTGGGCGGGGACTATGTCAGCTTTTTCGAGAAGAAGGCGTCGCGCAACGCC"
    "CTGGAGCACTTTGGGCGACGCGAGACCCTGACGGAGGTTCTGGGCCGCTACGATGTGCGGCCCGACGCCG"
    "GGGAGACCGTGGAGGGGTTCGCGTCAGAACTGCTGGGGCGAATAGTCGCGTGCATCGAGGCCCACTTTCC"
    "CGAGCACGCGCGGGAATATCAGGCCGTGTCCGTTCGCCGGGCCGTCATTAAGGACGACTGGGTCCTGCTG"
    "CAGCTGATCCCCGGCCGCGGCGCCCTGAACCAAAGCCTCTCGTGTCTGCGCTTCAAGCACGGCAGGGCAA"
    "GTCGCGCGACGGCCCGGACCTTTCTCGCGCTGAGCGTCGGGACCAACAACCGCCTATGCGCGTCCCTGTG"
    "TCAGCAGTGCTTTGCCACTAAATGCGATAACAACCGCCTGCACACGCTGTTTACCGTCGATGCGGGCACG"
    "CCATGCTCGCGGTCCGCTCCCTCCAGCACCTCACGACCGTCATCTTCATAA"
)

# Convert to BioPython sequence object
ul52_seq = Seq(ul52_sequence)

# 1. Calculate GC Content
gc_content = GC(ul52_seq)

# 2. Sliding window for GC content
window_size = 100
gc_content_windows = [
    GC(ul52_seq[i:i+window_size]) for i in range(0, len(ul52_seq) - window_size␣
 ↪+ 1, window_size)
]

# 3. Plot GC content
plt.figure(figsize=(10, 6))
plt.plot(gc_content_windows, label="GC Content (%)", linewidth=2)
plt.axhline(y=gc_content, color='r', linestyle='--', label=f"Average GC Content:
 ↪ {gc_content:.2f}%")
plt.xlabel("Window (100 bp steps)", fontsize=12)
plt.ylabel("GC Content (%)", fontsize=12)
plt.title("GC Content Across HSV-2 UL52 Gene", fontsize=14)
plt.legend()
plt.grid(True)
plt.tight_layout()

plt.show()
```

```
---------------------------------------------------------------------------
ImportError                               Traceback (most recent call last)
```

```
Cell In[1], line 1
----> 1 from Bio.SeqUtils import GC
      2 from Bio.Seq import Seq
      3 import matplotlib.pyplot as plt

ImportError: cannot import name 'GC' from 'Bio.SeqUtils' (C:
 ↪\Users\Developer\anaconda3\Lib\site-packages\Bio\SeqUtils\__init__.py)
```

[3]:
```
from Bio.Seq import Seq
import matplotlib.pyplot as plt
import numpy as np

# UL52 nucleotide sequence
ul52_sequence = (
    "ATGGGGACGGAAGACTGCGATCACGAAGGGCGGTCGGTTGCGGCTCCCGTGGAGGTTACGGCGCTGTATG"
    "CGACCGACGGGTGCGTTATCACCTCCTCGCTCGCCCTCCTCACAAACTGCCTGCTGGGGGCCGAGCCGTT"
    "GTATATATTCAGCTACGACGCGTACCGGCCCGATGCGCCCAATGGCCCCACGGGCGCGCCCACCGAACAG"
    "GAGAGGTTCGAGGGGAGCCGGGCGCTCTACCGGGATGCGGGGGGGCTAAATGGCGATTCATTTCGGGTGA"
    "CCTTTTGTTTATTGGGGACGGAAGTGGGCGTGACCCACCACCCGAAAGGGCGCACCCGGCCCATGTTTGT"
    "GTGCCGCTTCGAGCGAGCGGACGACGTCGCCGTGCTCCAAGACGCCCTGGGCCGCGGGACCCCATTGCTC"
    "CCGGCCCACATCACAGCAACTCTGGACTTGGAGGCGACGTTTGCGCTCCACGCTAACATCATCATGGCTC"
    "TCACCGTGGCCATCGTCCACAACGCCCCCGCCCGCATCGGCAGCGGCAGCACCGCCCCCCTGTATGAGCC"
    "CGGCGAATCGATGCGCTCGGTCGTCGGGCGCATGTCCCTGGGGCAGCGCGGCCTCACCACGCTGTTCGTG"
    "CACCACGAGGCGCGCGTGCTGGCGGCGTACCGCCGGGCGTATTATGGGAGCGCCCAAAGCCCCTTTTGGT"
    "TTCTGAGCAAATTCGGCCCGGACGAAAAGAGCCTGGTGCTGGCCGCTAGGTACTACCTACTCCAGGCTCC"
    "GCGCTTGGGGGGCGCCGGAGCCACGTACGATCTGCAGGCCGTGAAAGACATCTGCGCGACCTACGCGATC"
    "CCCCACGACCCACGCCCCGACACCCTCAGTGCCGCGTCCTTGACCTCGTTCGCCGCCATCACTCGGTTCT"
    "GTTGCACGAGCCAGTACTCCCGCGGGGCCGCGGCCGCTGGGTTTCCGCTGTATGTGGAGCGCCGCATCGC"
    "CGCCGACGTACGCGAGACCGGCGCGCTGGAGAAGTTCATCGCCCACGATCGCAGCTGCCTGCGCGTGTCC"
    "GACCGGGAATTCATTACGTACATCTACCTGGCCCACTTTGAGTGCTTCAGCCCCCCGCGCCTGGCCACGC"
    "ATCTCCGGGCCGTGACCACCCACGACCCCAGCCCCGCGGCCAGCACGGAGCAGCCCTCGCCCCTGGGTCG"
    "GGAGGCGGTGGAACAGTTCTTCCGGCACGTGCGCGCCCAGCTGAACATCCGCGAGTACGTAAAGCAAAAC"
    "GTCACCCCCAGGGAAACCGCCCTGGCGGGAGACGCGGCCGCCGCCTACCTGCGCGCGCGCACGTATGCCC"
    "CGGCGGCCCTCACGCCCGCCCCCGCGTACTGCGGGGTCGCAGACTCGTCCACCAAAATGATGGGACGTCT"
    "GGCGGAAGCAGAAAGGCTCCTAGTCCCCCACGGCTGGCCCGCGTTCGCACCAACAACCCCCGGGGACGAC"
    "GCGGGGGGCGGCACTGCCGCCCCCCAGACCTGCGGAATCGTCAAGCGCCTCCTCAAGCTGGCCGCCACGG"
    "AGCAGCAGGGCACGACGCCCCCGGCGATCGCGGCTCTCATGCAGGACGCGTCGGTCCAAACCCCCCTGCC"
    "CGTGTACAGGATTACCATGTCCCCGACCGGCCAGGCGTTTGCCGCGGCGGCGCGGGACGACTGGGCCCGC"
    "GTGACGCGGGACGCGCGCCCGCCGGAAGCGACCGTGGTCGCGGACGCGGCGGCGGCGCCCGAGCCCGGCG"
    "CGCTCGGCCGGCGGCTCACGCGCCGCATTTGCGCCCGGGGCCCCGCGCTCCCCCCGGGCGGCCTGGCCGT"
    "CGGGGGCCAGATGTACGTGAACCGCAACGAGATCTTCAACGCCGCGCTGGCCGTTACGAACATCATCCTG"
    "GATCTGGACATCGCCCTGAAGGAGCCCGTCCCCTTTCCCCGGCTCCACGAGGCCCTGGGTCACTTTAGGC"
    "GCGGGGCGCTGGCGGCGGTTCAGCTGTTGTTTCCCGCGGCCCGCGTAGACCCCGACGCCTATCCCTGTTA"
    "TTTTTTCAAAAGCGCCTGTCGGCCCCGCGCGCCGCCCGTCTGTGCGGGCGACGGGCCCCTGGCCGGTGGC"
    "GACGACGGCGACGGGGACTGGTTCCCCGACGCCGGTGGTCCCGGCGACGAGGAGTGGGAGGAGGACACGG"
    "ACCCCATGGACACGACCCACGGCCCCCTCCCGGACGACGAGGCCGCGTACCTCGACCTGCTACACGAACA"
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    "GATACCAGCGGCGACGCCCAGCGAACCGGACTCCGTCGTGTGTTCCTGCGCCGACAAGATCGGGCTGCGC"
    "GTGTGCCTACCGGTCCCCGCCCCGTACGTTGTGCACGGCTCCCTGACGATGCGTGGGGTGGCGAGGGTGA"
    "TCCAGCAGGCGGTGCTGTTGGACCGCGACTTCGTGGAGGCCGTAGGGAGCCACGTAAAGAACTTTTTGCT"
    "GATCGATACGGGCGTGTACGCCCACGGCCACAGCCTGCGCTTGCCGTATTTCGCCAAGATCGGCCCCGAC"
    "GGCTCCGCGTGCGGCCGGTTATTGCCCGTCTTCGTGATCCCCCCCGCGTGCGAGGACGTTCCGGCGTTCG"
    "TCGCCGCGCACGCCGACCCGCGGCGCTTCCACTTTCACGCCCCGCCCATGTTTTCCGCGGCCCCGCGGGA"
    "GATCCGCGTCCTCCACAGCCTGGGCGGGGACTATGTCAGCTTTTTCGAGAAGAAGGCGTCGCGCAACGCC"
    "CTGGAGCACTTTGGGCGACGCGAGACCCTGACGGAGGTTCTGGGCCGCTACGATGTGCGGCCCGACGCCG"
    "GGGAGACCGTGGAGGGGTTCGCGTCAGAACTGCTGGGGCGAATAGTCGCGTGCATCGAGGCCCACTTTCC"
    "CGAGCACGCGCGGGAATATCAGGCCGTGTCCGTTCGCCGGGCCGTCATTAAGGACGACTGGGTCCTGCTG"
    "CAGCTGATCCCCGGCCGCGGCGCCCTGAACCAAAGCCTCTCGTGTCTGCGCTTCAAGCACGGCAGGGCAA"
    "GTCGCGCGACGGCCCGGACCTTTCTCGCGCTGAGCGTCGGGACCAACAACCGCCTATGCGCGTCCCTGTG"
    "TCAGCAGTGCTTTGCCACTAAATGCGATAACAACCGCCTGCACACGCTGTTTACCGTCGATGCGGGCACG"
    "CCATGCTCGCGGTCCGCTCCCTCCAGCACCTCACGACCGTCATCTTCATAA"
)

# Function to calculate GC content manually
def calculate_gc(sequence):
    gc_count = sequence.count('G') + sequence.count('C')
    return (gc_count / len(sequence)) * 100

# 1. Calculate GC Content
gc_content = calculate_gc(ul52_sequence)

# 2. Sliding window for GC content
window_size = 100
gc_content_windows = [
    calculate_gc(ul52_sequence[i:i+window_size]) for i in range(0,␣
 ↪len(ul52_sequence) - window_size + 1, window_size)
]

# 3. Plot GC content
plt.figure(figsize=(10, 6))
plt.plot(gc_content_windows, label="GC Content (%)", linewidth=2)
plt.axhline(y=gc_content, color='r', linestyle='--', label=f"Average GC Content:
 ↪ {gc_content:.2f}%")
plt.xlabel("Window (100 bp steps)", fontsize=12)
plt.ylabel("GC Content (%)", fontsize=12)
plt.title("GC Content Across HSV-2 UL52 Gene", fontsize=14)
plt.legend()
plt.grid(True)
plt.tight_layout()

plt.show()
```

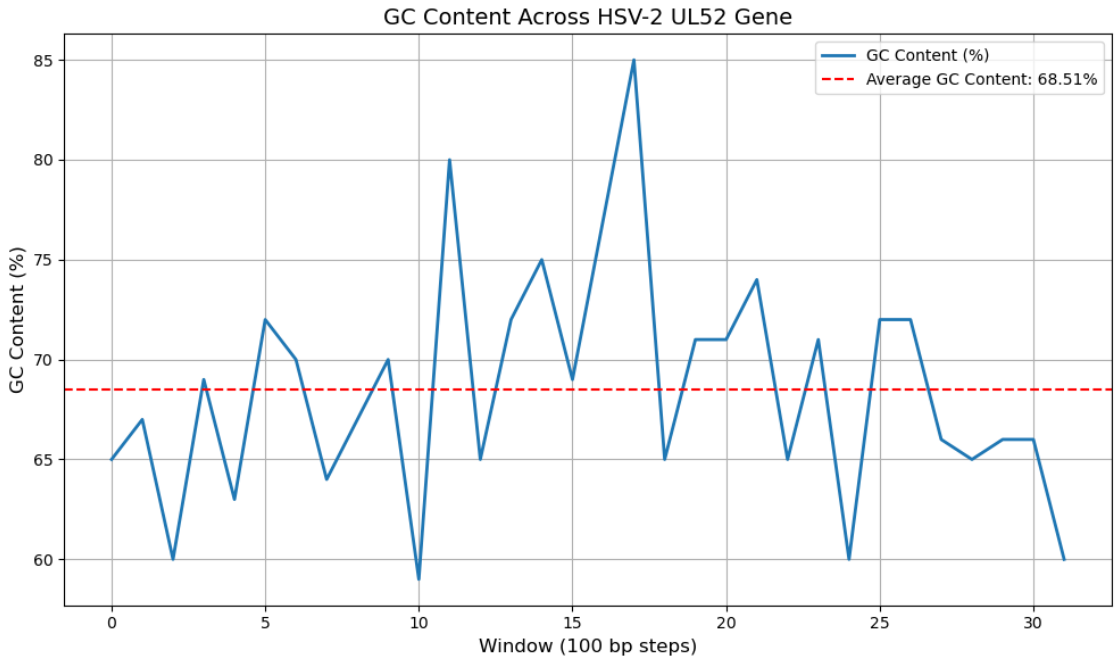


[ ]:

[5]:
```python
# Full code to handle the given sequence and fill missing nucleotides to reach a specific size.

def identify_and_fill_gaps(sequence, expected_length):
    """
    Identifies gaps in the sequence based on missing nucleotides and fills them symmetrically.

    Args:
    - sequence (str): The original nucleotide sequence.
    - expected_length (int): The expected length of the sequence after filling gaps.

    Returns:
    - filled_sequence (str): The sequence after filling the missing nucleotides.
    - gaps (list): List of identified gaps (positions and sizes).
    """
    original_length = len(sequence)
    missing_length = expected_length - original_length

    if missing_length <= 0:
        return sequence, []
```

```
    # Step 1: Analyze sequence for gaps (quantum folding rule: gaps where difference > 1)
    gaps = []
    for i in range(1, len(sequence)):
        if ord(sequence[i]) - ord(sequence[i - 1]) > 1:  # Gap detected
            gaps.append((i, ord(sequence[i]) - ord(sequence[i - 1]) - 1))

    # Step 2: Redistribute missing nucleotides symmetrically into the sequence
    filled_sequence = list(sequence)
    remaining_to_fill = missing_length

    for gap_index, gap_size in gaps:
        # Determine how many bases to fill in this gap
        fill_size = min(gap_size, remaining_to_fill)
        filler = 'N' * fill_size  # Use 'N' for missing nucleotides
        remaining_to_fill -= fill_size

        # Insert missing nucleotides symmetrically
        filled_sequence.insert(gap_index, filler)

        if remaining_to_fill <= 0:
            break

    # If there's still missing data after filling gaps, pad the end
    if remaining_to_fill > 0:
        filled_sequence.append('N' * remaining_to_fill)

    # Step 3: Combine into a complete sequence
    filled_sequence = ''.join(filled_sequence)
    return filled_sequence, gaps


# Full Input Sequence
original_sequence = (
    "ATGGGGACGGAAGACTGCGATCACGAAGGGCGGTCGGTTGCGGCTCCCGTGGAGGTTACGGCGCTGTATG"
    "CGACCGACGGGTGCGTTATCACCTCCTCGCTCGCCCTCCTCACAAACTGCCTGCTGGGGGCCGAGCCGTT"
    "GTATATATTCAGCTACGACGCGTACCGGCCCGATGCGCCCAATGGCCCCACGGGCGCGCCCACCGAACAG"
    "GAGAGGTTCGAGGGGAGCCGGGCGCTCTACCGGGATGCGGGGGGGCTAAATGGCGATTCATTTCGGGTGA"
    "CCTTTTGTTTATTGGGGACGGAAGTGGGCGTGACCCACCACCCGAAAGGGCGCACCCGGCCCATGTTTGT"
    "GTGCCGCTTCGAGCGAGCGGACGACGTCGCCGTGCTCCAAGACGCCCTGGGCCGCGGGACCCCATTGCTC"
    "CCGGCCCACATCACAGCAACTCTGGACTTGGAGGCGACGTTTGCGCTCCACGCTAACATCATCATGGCTC"
    "TCACCGTGGCCATCGTCCACAACGCCCCCGCCCGCATCGGCAGCGGCAGCACCGCCCCCCTGTATGAGCC"
    "CGGCGAATCGATGCGCTCGGTCGTCGGGCGCATGTCCCTGGGGCAGCGCGGCCTCACCACGCTGTTCGTG"
    "CACCACGAGGCGCGCGTGCTGGCGGCGTACCGCCGGGCGTATTATGGGAGCGCCCAAAGCCCCTTTTGGT"
    "TTCTGAGCAAATTCGGCCCGGACGAAAAGAGCCTGGTGCTGGCCGCTAGGTACTACCTACTCCAGGCTCC"
    "GCGCTTGGGGGGCGCCGGAGCCACGTACGATCTGCAGGCCGTGAAAGACATCTGCGCGACCTACGCGATC"
    "CCCCACGACCCACGCCCCGACACCCTCAGTGCCGCGTCCTTGACCTCGTTCGCCGCCATCACTCGGTTCT"
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    "GTTGCACGAGCCAGTACTCCCGCGGGGCCGCGGCCGCTGGGTTTCCGCTGTATGTGGAGCGCCGCATCGC"
    "CGCCGACGTACGCGAGACCGGCGCGCTGGAGAAGTTCATCGCCCACGATCGCAGCTGCCTGCGCGTGTCC"
    "GACCGGGAATTCATTACGTACATCTACCTGGCCCACTTTGAGTGCTTCAGCCCCCCGCGCCTGGCCACGC"
    "ATCTCCGGGCCGTGACCACCCACGACCCCAGCCCCGCGGCCAGCACGGAGCAGCCCTCGCCCCTGGGTCG"
    "GGAGGCGGTGGAACAGTTCTTCCGGCACGTGCGCGCCCAGCTGAACATCCGCGAGTACGTAAAGCAAAAC"
    "GTCACCCCCAGGGAAACCGCCCTGGCGGGAGACGCGGCCGCCGCCTACCTGCGCGCGCGCACGTATGCCC"
    "CGGCGGCCCTCACGCCCGCCCCCGCGTACTGCGGGGTCGCAGACTCGTCCACCAAAATGATGGGACGTCT"
    "GGCGGAAGCAGAAAGGCTCCTAGTCCCCCACGGCTGGCCCGCGTTCGCACCAACAACCCCCGGGGACGAC"
    "GCGGGGGGCGGCACTGCCGCCCCCCAGACCTGCGGAATCGTCAAGCGCCTCCTCAAGCTGGCCGCCACGG"
    "AGCAGCAGGGCACGACGCCCCCGGCGATCGCGGCTCTCATGCAGGACGCGTCGGTCCAAACCCCCCTGCC"
    "CGTGTACAGGATTACCATGTCCCCGACCGGCCAGGCGTTTGCCGCGGCGGCGCGGGACGACTGGGCCCGC"
    "GTGACGCGGGACGCGCGCCCGCCGGAAGCGACCGTGGTCGCGGACGCGGCGGCGGCGCCCGAGCCCGGCG"
    "CGCTCGGCCGGCGGCTCACGCGCCGCATTTGCGCCCGGGGCCCCGCGCTCCCCCCGGGCGGCCTGGCCGT"
    "CGGGGGCCAGATGTACGTGAACCGCAACGAGATCTTCAACGCCGCGCTGGCCGTTACGAACATCATCCTG"
    "GATCTGGACATCGCCCTGAAGGAGCCCGTCCCCTTTCCCCGGCTCCACGAGGCCCTGGGTCACTTTAGGC"
    "GCGGGGCGCTGGCGGCGGTTCAGCTGTTGTTTCCCGCGGCCCGCGTAGACCCCGACGCCTATCCCTGTTA"
    "TTTTTTCAAAAGCGCCTGTCGGCCCCGCGCGCCGCCCGTCTGTGCGGGCGACGGGCCCCTGGCCGGTGGC"
    "GACGACGGCGACGGGGACTGGTTCCCCGACGCCGGTGGTCCCGGCGACGAGGAGTGGGAGGAGGACACGG"
    "ACCCCATGGACACGACCCACGGCCCCCTCCCGGACGACGAGGCCGCGTACCTCGACCTGCTACACGAACA"
    "GATACCAGCGGCGACGCCCAGCGAACCGGACTCCGTCGTGTGTTCCTGCGCCGACAAGATCGGGCTGCGC"
    "GTGTGCCTACCGGTCCCCGCCCCGTACGTTGTGCACGGCTCCCTGACGATGCGTGGGGTGGCGAGGGTGA"
    "TCCAGCAGGCGGTGCTGTTGGACCGCGACTTCGTGGAGGCCGTAGGGAGCCACGTAAAGAACTTTTTGCT"
    "GATCGATACGGGCGTGTACGCCCACGGCCACAGCCTGCGCTTGCCGTATTTCGCCAAGATCGGCCCCGAC"
    "GGCTCCGCGTGCGGCCGGTTATTGCCCGTCTTCGTGATCCCCCCCGCGTGCGAGGACGTTCCGGCGTTCG"
    "TCGCCGCGCACGCCGACCCGCGGCGCTTCCACTTTCACGCCCCGCCCATGTTTTCCGCGGCCCCGCGGGA"
    "GATCCGCGTCCTCCACAGCCTGGGCGGGGACTATGTCAGCTTTTTCGAGAAGAAGGCGTCGCGCAACGCC"
    "CTGGAGCACTTTGGGCGACGCGAGACCCTGACGGAGGTTCTGGGCCGCTACGATGTGCGGCCCGACGCCG"
    "GGGAGACCGTGGAGGGGTTCGCGTCAGAACTGCTGGGGCGAATAGTCGCGTGCATCGAGGCCCACTTTCC"
    "CGAGCACGCGCGGGAATATCAGGCCGTGTCCGTTCGCCGGGCCGTCATTAAGGACGACTGGGTCCTGCTG"
    "CAGCTGATCCCCGGCCGCGGCGCCCTGAACCAAAGCCTCTCGTGTCTGCGCTTCAAGCACGGCAGGGCAA"
    "GTCGCGCGACGGCCCGGACCTTTCTCGCGCTGAGCGTCGGGACCAACAACCGCCTATGCGCGTCCCTGTG"
    "TCAGCAGTGCTTTGCCACTAAATGCGATAACAACCGCCTGCACACGCTGTTTACCGTCGATGCGGGCACG"
    "CCATGCTCGCGGTCCGCTCCCTCCAGCACCTCACGACCGTCATCTTCATAA"
)
expected_sequence_length = 4096

# Run the function
filled_sequence, detected_gaps = identify_and_fill_gaps(original_sequence,␣
 ↪expected_sequence_length)

# Output results
print("Original Sequence Length:", len(original_sequence))
print("Expected Sequence Length:", expected_sequence_length)
print("Filled Sequence Length:", len(filled_sequence))
print("Detected Gaps:", detected_gaps)
print("Filled Sequence (First 500 bases):", filled_sequence)
```

```
Original Sequence Length: 3201
```

Expected Sequence Length: 4096
Filled Sequence Length: 4096
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CCGTTACGAACATCATCCTGGATCTGGACATCGCCCTGAAGGAGCCCGTCCCCTTTCCCCGGCTCCACGAGGCCCTGGGT
CACTTTAGGCGCGGGGCGCTGGCGGCGGTTCAGCTGTTGTTTCCCGCGGCCCGCGTAGACCCCGACGCCTATCCCTGTTA
TTTTTTCAAAAGCGCCTGTCGGCCCCGCGCGCCGCCCGTCTGTGCGGGCGACGGGCCCCTGGCCGGTGGCGACGACGGCG
ACGGGGACTGGTTCCCCGACGCCGGTGGTCCCGGCGACGAGGAGTGGGAGGAGGACACGGACCCCATGGACACGACCCAC
GGCCCCCTCCCGGACGACGAGGCCGCGTACCTCGACCTGCTACACGAACAGATACCAGCGGCGACGCCCAGCGAACCGGA
CTCCGTCGTGTGTTCCTGCGCCGACAAGATCGGGCTGCGCGTGTGCCTACCGGTCCCCGCCCCGTACGTTGTGCACGGCT
CCCTGACGATGCGTGGGGTGGCGAGGGTGATCCAGCAGGCGGTGCTGTTGGACCGCGACTTCGTGGAGGCCGTAGGGAGC
CACGTAAAGAACTTTTTGCTGATCGATACGGGCGTGTACGCCCACGGCCACAGCCTGCGCTTGCCGTATTTCGCCAAGAT
CGGCCCCGACGGCTCCGCGTGCGGCCGGTTATTGCCCGTCTTCGTGATCCCCCCCGCGTGCGAGGACGTTCCGGCGTTCG
TCGCCGCGCACGCCGACCCGCGGCGCTTCCACTTTCACGCCCCGCCCATGTTTTCCGCGGCCCCGCGGGAGATCCGCGTC
CTCCACAGCCTGGGCGGGGACTATGTCAGCTTTTTCGAGAAGAAGGCGTCGCGCAACGCCCTGGAGCACTTTGGGCGACG
CGAGACCCTGACGGAGGTTCTGGGCCGCTACGATGTGCGGCCCGACGCCGGGGAGACCGTGGAGGGGTTCGCGTCAGAAC
TGCTGGGGCGAATAGTCGCGTGCATCGAGGCCCACTTTCCCGAGCACGCGCGGGAATATCAGGCCGTGTCCGTTCGCCGG
GCCGTCATTAAGGACGACTGGGTCCTGCTGCAGCTGATCCCCGGCCGCGGCGCCCTGAACCAAAGCCTCTCGTGTCTGCG
CTTCAAGCACGGCAGGGCAAGTCGCGCGACGGCCCGGACCTTTCTCGCGCTGAGCGTCGGGACCAACAACCGCCTATGCG
CGTCCCTGTGTCAGCAGTGCTTTGCCACTAAATGCGATAACAACCGCCTGCACACGCTGTTTACCGTCGATGCGGGCACG
CCATGCTCGCGGTCCGCTCCCTCCAGCACCTCACGACCGTCATCTTCATAA
```

[7]:
```python
# Function to identify and fill gaps, highlighting added nucleotides
def identify_and_fill_gaps_with_highlight(sequence, expected_length):
    """
    Identifies gaps in the sequence based on missing nucleotides, fills them␣
 ↪symmetrically,
    and highlights the added nucleotides.

    Args:
    - sequence (str): The original nucleotide sequence.
    - expected_length (int): The expected length of the sequence after filling␣
 ↪gaps.

    Returns:
    - filled_sequence (str): The sequence after filling the missing nucleotides.
    - highlighted_sequence (str): The sequence with added nucleotides␣
 ↪highlighted.
    - total_pairs (int): Total number of pairs in the filled sequence.
    - added_pairs (int): Number of pairs formed by the inserted nucleotides.
    """
    original_length = len(sequence)
    missing_length = expected_length - original_length
```

```
    if missing_length <= 0:
        return sequence, sequence, original_length // 2, 0

    # Analyze sequence for gaps
    gaps = []
    for i in range(1, len(sequence)):
        if ord(sequence[i]) - ord(sequence[i - 1]) > 1:  # Gap detected
            gaps.append((i, ord(sequence[i]) - ord(sequence[i - 1]) - 1))

    # Redistribute missing nucleotides symmetrically into the sequence
    filled_sequence = list(sequence)
    highlighted_sequence = list(sequence)  # For storing highlighted sequence
    remaining_to_fill = missing_length

    for gap_index, gap_size in gaps:
        fill_size = min(gap_size, remaining_to_fill)
        filler = 'N' * fill_size  # Use 'N' for missing nucleotides
        remaining_to_fill -= fill_size

        # Insert missing nucleotides symmetrically
        filled_sequence.insert(gap_index, filler)
        highlighted_sequence.insert(gap_index, f"[{filler}]")  # Highlight␣
↪added bases

        if remaining_to_fill <= 0:
            break

    # If there's still missing data after filling gaps, pad the end
    if remaining_to_fill > 0:
        filler = 'N' * remaining_to_fill
        filled_sequence.append(filler)
        highlighted_sequence.append(f"[{filler}]")  # Highlight added padding

    # Combine into complete sequences
    filled_sequence = ''.join(filled_sequence)
    highlighted_sequence = ''.join(highlighted_sequence)

    # Calculate pairs
    total_pairs = len(filled_sequence) // 2
    added_pairs = missing_length // 2

    return filled_sequence, highlighted_sequence, total_pairs, added_pairs

# Full Input Sequence
original_sequence = (
    "ATGGGGACGGAAGACTGCGATCACGAAGGGCGGTCGGTTGCGGCTCCCGTGGAGGTTACGGCGCTGTATG"
    "CGACCGACGGGTGCGTTATCACCTCCTCGCTCGCCCTCCTCACAAACTGCCTGCTGGGGGCCGAGCCGTT"
```

```
    "GTATATATTCAGCTACGACGCGTACCGGCCCGATGCGCCCAATGGCCCCACGGGCGCGCCCACCGAACAG"
    "GAGAGGTTCGAGGGGAGCCGGGCGCTCTACCGGGATGCGGGGGGGCTAAATGGCGATTCATTTCGGGTGA"
    "CCTTTTGTTTATTGGGGACGGAAGTGGGCGTGACCCACCACCCGAAAGGGCGCACCCGGCCCATGTTTGT"
    "GTGCCGCTTCGAGCGAGCGGACGACGTCGCCGTGCTCCAAGACGCCCTGGGCCGCGGGACCCCATTGCTC"
    "CCGGCCCACATCACAGCAACTCTGGACTTGGAGGCGACGTTTGCGCTCCACGCTAACATCATCATGGCTC"
    "TCACCGTGGCCATCGTCCACAACGCCCCCGCCCGCATCGGCAGCGGCAGCACCGCCCCCCTGTATGAGCC"
    "CGGCGAATCGATGCGCTCGGTCGTCGGGCGCATGTCCCTGGGGCAGCGCGGCCTCACCACGCTGTTCGTG"
    "CACCACGAGGCGCGCGTGCTGGCGGCGTACCGCCGGGCGTATTATGGGAGCGCCCAAAGCCCCTTTTGGT"
    "TTCTGAGCAAATTCGGCCCGGACGAAAAGAGCCTGGTGCTGGCCGCTAGGTACTACCTACTCCAGGCTCC"
    "GCGCTTGGGGGGCGCCGGAGCCACGTACGATCTGCAGGCCGTGAAAGACATCTGCGCGACCTACGCGATC"
    "CCCCACGACCCACGCCCCGACACCCTCAGTGCCGCGTCCTTGACCTCGTTCGCCGCCATCACTCGGTTCT"
    "GTTGCACGAGCCAGTACTCCCGCGGGGCCGCGGCCGCTGGGTTTCCGCTGTATGTGGAGCGCCGCATCGC"
    "CGCCGACGTACGCGAGACCGGCGCGCTGGAGAAGTTCATCGCCCACGATCGCAGCTGCCTGCGCGTGTCC"
    "GACCGGGAATTCATTACGTACATCTACCTGGCCCACTTTGAGTGCTTCAGCCCCCCGCGCCTGGCCACGC"
    "ATCTCCGGGCCGTGACCACCCACGACCCCAGCCCCGCGGCCAGCACGGAGCAGCCCTCGCCCCTGGGTCG"
    "GGAGGCGGTGGAACAGTTCTTCCGGCACGTGCGCGCCCAGCTGAACATCCGCGAGTACGTAAAGCAAAAC"
    "GTCACCCCCAGGGAAACCGCCCTGGCGGGAGACGCGGCCGCCGCCTACCTGCGCGCGCGCACGTATGCCC"
    "CGGCGGCCCTCACGCCCGCCCCCGCGTACTGCGGGGTCGCAGACTCGTCCACCAAAATGATGGGACGTCT"
    "GGCGGAAGCAGAAAGGCTCCTAGTCCCCCACGGCTGGCCCGCGTTCGCACCAACAACCCCCGGGGACGAC"
    "GCGGGGGGCGGCACTGCCGCCCCCCAGACCTGCGGAATCGTCAAGCGCCTCCTCAAGCTGGCCGCCACGG"
    "AGCAGCAGGGCACGACGCCCCCGGCGATCGCGGCTCTCATGCAGGACGCGTCGGTCCAAACCCCCCTGCC"
    "CGTGTACAGGATTACCATGTCCCCGACCGGCCAGGCGTTTGCCGCGGCGGCGCGGGACGACTGGGCCCGC"
    "GTGACGCGGGACGCGCGCCCGCCGGAAGCGACCGTGGTCGCGGACGCGGCGGCGGCGCCCGAGCCCGGCG"
    "CGCTCGGCCGGCGGCTCACGCGCCGCATTTGCGCCCGGGGCCCCGCGCTCCCCCCGGGCGGCCTGGCCGT"
    "CGGGGGCCAGATGTACGTGAACCGCAACGAGATCTTCAACGCCGCGCTGGCCGTTACGAACATCATCCTG"
    "GATCTGGACATCGCCCTGAAGGAGCCCGTCCCCTTTCCCCGGCTCCACGAGGCCCTGGGTCACTTTAGGC"
    "GCGGGGCGCTGGCGGCGGTTCAGCTGTTGTTTCCCGCGGCCCGCGTAGACCCCGACGCCTATCCCTGTTA"
    "TTTTTTCAAAAGCGCCTGTCGGCCCCGCGCGCCGCCCGTCTGTGCGGGCGACGGGCCCCTGGCCGGTGGC"
    "GACGACGGCGACGGGGACTGGTTCCCCGACGCCGGTGGTCCCGGCGACGAGGAGTGGGAGGAGGACACGG"
    "ACCCCATGGACACGACCCACGGCCCCCTCCCGGACGACGAGGCCGCGTACCTCGACCTGCTACACGAACA"
    "GATACCAGCGGCGACGCCCAGCGAACCGGACTCCGTCGTGTGTTCCTGCGCCGACAAGATCGGGCTGCGC"
    "GTGTGCCTACCGGTCCCCGCCCCGTACGTTGTGCACGGCTCCCTGACGATGCGTGGGGTGGCGAGGGTGA"
    "TCCAGCAGGCGGTGCTGTTGGACCGCGACTTCGTGGAGGCCGTAGGGAGCCACGTAAAGAACTTTTTGCT"
    "GATCGATACGGGCGTGTACGCCCACGGCCACAGCCTGCGCTTGCCGTATTTCGCCAAGATCGGCCCCGAC"
    "GGCTCCGCGTGCGGCCGGTTATTGCCCGTCTTCGTGATCCCCCCCGCGTGCGAGGACGTTCCGGCGTTCG"
    "TCGCCGCGCACGCCGACCCGCGGCGCTTCCACTTTCACGCCCCGCCCATGTTTTCCGCGGCCCCGCGGGA"
    "GATCCGCGTCCTCCACAGCCTGGGCGGGGACTATGTCAGCTTTTTCGAGAAGAAGGCGTCGCGCAACGCC"
    "CTGGAGCACTTTGGGCGACGCGAGACCCTGACGGAGGTTCTGGGCCGCTACGATGTGCGGCCCGACGCCG"
    "GGGAGACCGTGGAGGGGTTCGCGTCAGAACTGCTGGGGCGAATAGTCGCGTGCATCGAGGCCCACTTTCC"
    "CGAGCACGCGCGGGAATATCAGGCCGTGTCCGTTCGCCGGGCCGTCATTAAGGACGACTGGGTCCTGCTG"
    "CAGCTGATCCCCGGCCGCGGCGCCCTGAACCAAAGCCTCTCGTGTCTGCGCTTCAAGCACGGCAGGGCAA"
    "GTCGCGCGACGGCCCGGACCTTTCTCGCGCTGAGCGTCGGGACCAACAACCGCCTATGCGCGTCCCTGTG"
    "TCAGCAGTGCTTTGCCACTAAATGCGATAACAACCGCCTGCACACGCTGTTTACCGTCGATGCGGGCACG"
    "CCATGCTCGCGGTCCGCTCCCTCCAGCACCTCACGACCGTCATCTTCATAA")

expected_sequence_length = 4096
```

```
# Run the function
filled_sequence, highlighted_sequence, total_pairs, added_pairs =␣
 ↪identify_and_fill_gaps_with_highlight(
    original_sequence, expected_sequence_length
)

# Display results
print("Original Sequence Length:", len(original_sequence))
print("Expected Sequence Length:", expected_sequence_length)
print("Filled Sequence Length:", len(filled_sequence))
print("Total Pairs in Filled Sequence:", total_pairs)
print("Added Pairs:", added_pairs)
print("\nHighlighted Sequence (First 500 bases):\n", highlighted_sequence)

# Optionally save the highlighted sequence to a file for further review
with open("highlighted_sequence.txt", "w") as file:
    file.write(highlighted_sequence)
```

```
Original Sequence Length: 3201
Expected Sequence Length: 4096
Filled Sequence Length: 4096
Total Pairs in Filled Sequence: 2048
Added Pairs: 447

Highlighted Sequence (First 500 bases):
 A[NNNNNNNNNNNNNNNNNN]TGGGG[N][NNN]ACG[NNNNN]G[N][NNNNNNNNNNNNNNNN]AA[NNN]G[NNNN
NNNNNNNNNNNNNN]AC[N][NNN]TG[NNNNN]CGA[NNN]T[NNNNNNNNNNNN]C[NNN]A[NNNNNNNNNNN]CG
A[NNN]AG[NNNNNNNNNNNNNNNN]GGC[NNN][NNNNNNNNNNNN]GGT[NNNNN]C[NNNNNNNNNNN]GG[N][N
NN]TT[NNN]G[NNNNNNNNNNNNNNNN]C[NNNNNNNNNNNN]G[NNNNNNNNNNNNNNNNN]GC[NNN]T[N]C[NN
N]C[N][NNN]CG[NNNNNNNNNNNN]TG[NNN][NNNNNNNNNNNN]GA[NNNNNNNNNNNNNNNNNN]GG[N]T[NNN
NNNNNNNNNNNNN]TA[NNNNNNNNNNNNNNNN]C[NNN]G[NNNNNNNNNNNNNNNNN]G[NNN]CGC[NNNNNNNNNN
NNNNN]TG[NNNNNNNNNNNNNNNN]TA[N]TGC[N][NNNNNNNNNNNNNNNN]GAC[NNNNNNNNNNNNNNNN]CG[N
NNNNNNNNNNNNNNN]ACGGGTG[NNN]C[NNNNN]GT[NNN][NNNNNNNNNNNN]TA[NNNNNNNNNNN]T[NNNNN
NNNNNNNNNNNNN]C[NNNNNNNNNNNNNNNNNN]A[NNNNNNNNNNNNNNNNNN]CCT[NNNNN]C[NNNNNNNNNNN
NNNN]C[N][NNN]T[N][NNN]C[NNN][NNNNNNNNNNNN]G[N]C[NNN]TCGC[NNN]C[NNNNNNNNNNNNNNNN
NN]CT[NNN]CCTCA[NNNNNNNNNNNNNNNNNN]CAAACTG[N][NNN]CCT[NNN]G[NNN]CTGG[N]G[NNN]GG[
N]C[NNNNN]CG[NNNNN]A[NNNNN]G[NNNNNNNNNNNN]CC[NNN]G[NNNNN]TTGT[NNNNN]AT[NNN]ATA[N
NN]T[NNNNNNNNNNNNNNNN]T[NNNNNNNNNNNNNNNN]C[N]A[NNN]GCT[NNNNNNNNNNNNNNNNNN]AC[NNN
]GACGCGT[NNNNNNNNNNNNNNNN]ACC[NNNNNNNNNNNNNNNNNN]GGC[NNN]C[NNNNNNNNNNNNNNNNNN]CG
A[NNNNNNNNNNNNNNNNNN]TGC[NNN]GC[NNNNNNNNNNNN]CC[N]A[NNNNNNNNNNNNNNNN]ATGG[NNNNNN
NNNNNN]CCC[NNNNNNNNNNNNNNNNNN]CACGGG[N][NNN]CGC[NNNNN][NNNNNNNNNNNN]GCCC[NNN][NN
NNNNNNNNN]AC[N]CGA[N]AC[N]AG[NNN]GAG[NNNNN]AGG[NNN]TT[N]CG[NNN]AGGGG[NNNNNNNN]A
GCCGGGCGCTCTACCGGGATGCGGGGGGGCTAAATGGCGATTCATTTCGGGTGACCTTTTGTTTATTGGGGACGGAAGTG
GGCGTGACCCACCACCCGAAAGGGCGCACCCGGCCCATGTTTGTGTGCCGCTTCGAGCGAGCGGACGACGTCGCCGTGCT
CCAAGACGCCCTGGGCCGCGGGACCCCATTGCTCCCGGCCCACATCACAGCAACTCTGGACTTGGAGGCGACGTTTGCGC
TCCACGCTAACATCATCATGGCTCTCACCGTGGCCATCGTCCACAACGCCCCCGCCCGCATCGGCAGCGGCAGCACCGCC
CCCCTGTATGAGCCCGGCGAATCGATGCGCTCGGTCGTCGGGCGCATGTCCCTGGGGCAGCGCGGCCTCACCACGCTGTT
CGTGCACCACGAGGCGCGCGTGCTGGCGGCGTACCGCCGGGCGTATTATGGGAGCGCCCAAAGCCCCTTTTGGTTTCTGA
```

GCAAATTCGGCCCGGACGAAAAGAGCCTGGTGCTGGCCGCTAGGTACTACCTACTCCAGGCTCCGCGCTTGGGGGGCGCC
GGAGCCACGTACGATCTGCAGGCCGTGAAAGACATCTGCGCGACCTACGCGATCCCCCACGACCCACGCCCCGACACCCT
CAGTGCCGCGTCCTTGACCTCGTTCGCCGCCATCACTCGGTTCTGTTGCACGAGCCAGTACTCCCGCGGGGCCGCGGCCG
CTGGGTTTCCGCTGTATGTGGAGCGCCGCATCGCCGCCGACGTACGCGAGACCGGCGCGCTGGAGAAGTTCATCGCCCAC
GATCGCAGCTGCCTGCGCGTGTCCGACCGGGAATTCATTACGTACATCTACCTGGCCCACTTTGAGTGCTTCAGCCCCCC
GCGCCTGGCCACGCATCTCCGGGCCGTGACCACCCACGACCCCAGCCCCGCGGCCAGCACGGAGCAGCCCTCGCCCCTGG
GTCGGGAGGCGGTGGAACAGTTCTTCCGGCACGTGCGCGCCCAGCTGAACATCCGCGAGTACGTAAAGCAAAACGTCACC
CCCAGGGAAACCGCCCTGGCGGGAGACGCGGCCGCCGCCTACCTGCGCGCGCGCACGTATGCCCCGGCGGCCCTCACGCC
CGCCCCCGCGTACTGCGGGGTCGCAGACTCGTCCACCAAAATGATGGGACGTCTGGCGGAAGCAGAAAGGCTCCTAGTCC
CCCACGGCTGGCCCGCGTTCGCACCAACAACCCCCGGGGACGACGCGGGGGGCGGCACTGCCGCCCCCCAGACCTGCGGA
ATCGTCAAGCGCCTCCTCAAGCTGGCCGCCACGGAGCAGCAGGGCACGACGCCCCCGGCGATCGCGGCTCTCATGCAGGA
CGCGTCGGTCCAAACCCCCCTGCCCGTGTACAGGATTACCATGTCCCCGACCGGCCAGGCGTTTGCCGCGGCGGCGCGGG
ACGACTGGGCCCGCGTGACGCGGGACGCGCGCCCGCCGGAAGCGACCGTGGTCGCGGACGCGGCGGCGGCGCCCGAGCCC
GGCGCGCTCGGCCGGCGGCTCACGCGCCGCATTTGCGCCCGGGGCCCCGCGCTCCCCCCGGGCGGCCTGGCCGTCGGGGG
CCAGATGTACGTGAACCGCAACGAGATCTTCAACGCCGCGCTGGCCGTTACGAACATCATCCTGGATCTGGACATCGCCC
TGAAGGAGCCCGTCCCCTTTCCCCGGCTCCACGAGGCCCTGGGTCACTTTAGGCGCGGGGCGCTGGCGGCGGTTCAGCTG
TTGTTTCCCGCGGCCCGCGTAGACCCCGACGCCTATCCCTGTTATTTTTTCAAAAGCGCCTGTCGGCCCCGCGCGCCGCC
CGTCTGTGCGGGCGACGGGCCCCTGGCCGGTGGCGACGACGGCGACGGGGACTGGTTCCCCGACGCCGGTGGTCCCGGCG
ACGAGGAGTGGGAGGAGGACACGGACCCCATGGACACGACCCACGGCCCCCTCCCGGACGACGAGGCCGCGTACCTCGAC
CTGCTACACGAACAGATACCAGCGGCGACGCCCAGCGAACCGGACTCCGTCGTGTGTTCCTGCGCCGACAAGATCGGGCT
GCGCGTGTGCCTACCGGTCCCCGCCCCGTACGTTGTGCACGGCTCCCTGACGATGCGTGGGGTGGCGAGGGTGATCCAGC
AGGCGGTGCTGTTGGACCGCGACTTCGTGGAGGCCGTAGGGAGCCACGTAAAGAACTTTTTGCTGATCGATACGGGCGTG
TACGCCCACGGCCACAGCCTGCGCTTGCCGTATTTCGCCAAGATCGGCCCCGACGGCTCCGCGTGCGGCCGGTTATTGCC
CGTCTTCGTGATCCCCCCCGCGTGCGAGGACGTTCCGGCGTTCGTCGCCGCGCACGCCGACCCGCGGCGCTTCCACTTTC
ACGCCCCGCCCATGTTTTCCGCGGCCCCGCGGGAGATCCGCGTCCTCCACAGCCTGGGCGGGGACTATGTCAGCTTTTTC
GAGAAGAAGGCGTCGCGCAACGCCCTGGAGCACTTTGGGCGACGCGAGACCCTGACGGAGGTTCTGGGCCGCTACGATGT
GCGGCCCGACGCCGGGGAGACCGTGGAGGGGTTCGCGTCAGAACTGCTGGGGCGAATAGTCGCGTGCATCGAGGCCCACT
TTCCCGAGCACGCGCGGGAATATCAGGCCGTGTCCGTTCGCCGGGCCGTCATTAAGGACGACTGGGTCCTGCTGCAGCTG
ATCCCCGGCCGCGGCGCCCTGAACCAAAGCCTCTCGTGTCTGCGCTTCAAGCACGGCAGGGCAAGTCGCGCGACGGCCCG
GACCTTTCTCGCGCTGAGCGTCGGGACCAACAACCGCCTATGCGCGTCCCTGTGTCAGCAGTGCTTTGCCACTAAATGCG
ATAACAACCGCCTGCACACGCTGTTTACCGTCGATGCGGGCACGCCATGCTCGCGGTCCGCTCCCTCCAGCACCTCACGA
CCGTCATCTTCATAA

[37]:
```
# Refined function to address gaps properly and minimize padding while grouping␣
 ↪the sequence into pairs.

def identify_and_fill_gaps_properly(sequence, expected_length):
    """
    Refined version to detect gaps, fill them symmetrically, and minimize␣
 ↪padding,
    with the output grouped in pairs for readability.

    Args:
    - sequence (str): The original nucleotide sequence.
    - expected_length (int): The expected length of the sequence after filling␣
 ↪gaps.
```

```
    Returns:
    - grouped_sequence (str): The sequence grouped in pairs for readability.
    - filled_sequence (str): The sequence after filling the missing nucleotides.
    - total_pairs (int): Total number of pairs in the filled sequence.
    - added_pairs (int): Number of pairs formed by the inserted nucleotides.
    """
    original_length = len(sequence)
    missing_length = expected_length - original_length

    if missing_length <= 0:
        grouped_sequence = " ".join([sequence[i:i+2] for i in range(0,␣
↪len(sequence), 2)])
        return grouped_sequence, sequence, original_length // 2, 0

    # Detect gaps and distribute missing nucleotides
    gaps = []
    for i in range(1, len(sequence)):
        if ord(sequence[i]) - ord(sequence[i - 1]) > 1:  # Detect gaps
            gaps.append((i, ord(sequence[i]) - ord(sequence[i - 1]) - 1))

    filled_sequence = list(sequence)
    remaining_to_fill = missing_length

    # Fill gaps symmetrically
    for gap_index, gap_size in gaps:
        if remaining_to_fill <= 0:
            break
        fill_size = min(gap_size, remaining_to_fill)
        filler = 'N' * fill_size  # Use 'N' for missing nucleotides
        remaining_to_fill -= fill_size
        filled_sequence.insert(gap_index, filler)

    # If any nucleotides are still missing, add them to the end
    if remaining_to_fill > 0:
        filled_sequence.append('N' * remaining_to_fill)

    # Combine into complete sequence
    filled_sequence = ''.join(filled_sequence)

    # Group into pairs
    grouped_sequence = " ".join([filled_sequence[i:i+2] for i in range(0,␣
↪len(filled_sequence), 2)])

    # Calculate pairs
    total_pairs = len(filled_sequence) // 2
    added_pairs = missing_length // 2
```

```
    return grouped_sequence, filled_sequence, total_pairs, added_pairs


# Full Input Sequence
original_sequence = (
    "ATGGGGACGGAAGACTGCGATCACGAAGGGCGGTCGGTTGCGGCTCCCGTGGAGGTTACGGCGCTGTATG"
    "CGACCGACGGGTGCGTTATCACCTCCTCGCTCGCCCTCCTCACAAACTGCCTGCTGGGGGCCGAGCCGTT"
    "GTATATATTCAGCTACGACGCGTACCGGCCCGATGCGCCCAATGGCCCCACGGGCGCGCCCACCGAACAG"
    "GAGAGGTTCGAGGGGAGCCGGGCGCTCTACCGGGATGCGGGGGGGCTAAATGGCGATTCATTTCGGGTGA"
    "CCTTTTGTTTATTGGGGACGGAAGTGGGCGTGACCCACCACCCGAAAGGGCGCACCCGGCCCATGTTTGT"
    "GTGCCGCTTCGAGCGAGCGGACGACGTCGCCGTGCTCCAAGACGCCCTGGGCCGCGGGACCCCATTGCTC"
    "CCGGCCCACATCACAGCAACTCTGGACTTGGAGGCGACGTTTGCGCTCCACGCTAACATCATCATGGCTC"
    "TCACCGTGGCCATCGTCCACAACGCCCCCGCCCGCATCGGCAGCGGCAGCACCGCCCCCCTGTATGAGCC"
    "CGGCGAATCGATGCGCTCGGTCGTCGGGCGCATGTCCCTGGGGCAGCGCGGCCTCACCACGCTGTTCGTG"
    "CACCACGAGGCGCGCGTGCTGGCGGCGTACCGCCGGGCGTATTATGGGAGCGCCCAAAGCCCCTTTTGGT"
    "TTCTGAGCAAATTCGGCCCGGACGAAAAGAGCCTGGTGCTGGCCGCTAGGTACTACCTACTCCAGGCTCC"
    "GCGCTTGGGGGGCGCCGGAGCCACGTACGATCTGCAGGCCGTGAAAGACATCTGCGCGACCTACGCGATC"
    "CCCCACGACCCACGCCCCGACACCCTCAGTGCCGCGTCCTTGACCTCGTTCGCCGCCATCACTCGGTTCT"
    "GTTGCACGAGCCAGTACTCCCGCGGGGCCGCGGCCGCTGGGTTTCCGCTGTATGTGGAGCGCCGCATCGC"
    "CGCCGACGTACGCGAGACCGGCGCGCTGGAGAAGTTCATCGCCCACGATCGCAGCTGCCTGCGCGTGTCC"
    "GACCGGGAATTCATTACGTACATCTACCTGGCCCACTTTGAGTGCTTCAGCCCCCCGCGCCTGGCCACGC"
    "ATCTCCGGGCCGTGACCACCCACGACCCCAGCCCCGCGGCCAGCACGGAGCAGCCCTCGCCCCTGGGTCG"
    "GGAGGCGGTGGAACAGTTCTTCCGGCACGTGCGCGCCCAGCTGAACATCCGCGAGTACGTAAAGCAAAAC"
    "GTCACCCCCAGGGAAACCGCCCTGGCGGGAGACGCGGCCGCCGCCTACCTGCGCGCGCGCACGTATGCCC"
    "CGGCGGCCCTCACGCCCGCCCCCGCGTACTGCGGGGTCGCAGACTCGTCCACCAAAATGATGGGACGTCT"
    "GGCGGAAGCAGAAAGGCTCCTAGTCCCCCACGGCTGGCCCGCGTTCGCACCAACAACCCCCGGGGACGAC"
    "GCGGGGGGCGGCACTGCCGCCCCCCAGACCTGCGGAATCGTCAAGCGCCTCCTCAAGCTGGCCGCCACGG"
    "AGCAGCAGGGCACGACGCCCCCGGCGATCGCGGCTCTCATGCAGGACGCGTCGGTCCAAACCCCCCTGCC"
    "CGTGTACAGGATTACCATGTCCCCGACCGGCCAGGCGTTTGCCGCGGCGGCGCGGGACGACTGGGCCCGC"
    "GTGACGCGGGACGCGCGCCCGCCGGAAGCGACCGTGGTCGCGGACGCGGCGGCGGCGCCCGAGCCCGGCG"
    "CGCTCGGCCGGCGGCTCACGCGCCGCATTTGCGCCCGGGGCCCCGCGCTCCCCCCGGGCGGCCTGGCCGT"
    "CGGGGGCCAGATGTACGTGAACCGCAACGAGATCTTCAACGCCGCGCTGGCCGTTACGAACATCATCCTG"
    "GATCTGGACATCGCCCTGAAGGAGCCCGTCCCCTTTCCCCGGCTCCACGAGGCCCTGGGTCACTTTAGGC"
    "GCGGGGCGCTGGCGGCGGTTCAGCTGTTGTTTCCCGCGGCCCGCGTAGACCCCGACGCCTATCCCTGTTA"
    "TTTTTTCAAAAGCGCCTGTCGGCCCCGCGCGCCGCCCGTCTGTGCGGGCGACGGGCCCCTGGCCGGTGGC"
    "GACGACGGCGACGGGGACTGGTTCCCCGACGCCGGTGGTCCCGGCGACGAGGAGTGGGAGGAGGACACGG"
    "ACCCCATGGACACGACCCACGGCCCCCTCCCGGACGACGAGGCCGCGTACCTCGACCTGCTACACGAACA"
    "GATACCAGCGGCGACGCCCAGCGAACCGGACTCCGTCGTGTGTTCCTGCGCCGACAAGATCGGGCTGCGC"
    "GTGTGCCTACCGGTCCCCGCCCCGTACGTTGTGCACGGCTCCCTGACGATGCGTGGGGTGGCGAGGGTGA"
    "TCCAGCAGGCGGTGCTGTTGGACCGCGACTTCGTGGAGGCCGTAGGGAGCCACGTAAAGAACTTTTTGCT"
    "GATCGATACGGGCGTGTACGCCCACGGCCACAGCCTGCGCTTGCCGTATTTCGCCAAGATCGGCCCCGAC"
    "GGCTCCGCGTGCGGCCGGTTATTGCCCGTCTTCGTGATCCCCCCCGCGTGCGAGGACGTTCCGGCGTTCG"
    "TCGCCGCGCACGCCGACCCGCGGCGCTTCCACTTTCACGCCCCGCCCATGTTTTCCGCGGCCCCGCGGGA"
    "GATCCGCGTCCTCCACAGCCTGGGCGGGGACTATGTCAGCTTTTTCGAGAAGAAGGCGTCGCGCAACGCC"
    "CTGGAGCACTTTGGGCGACGCGAGACCCTGACGGAGGTTCTGGGCCGCTACGATGTGCGGCCCGACGCCG"
    "GGGAGACCGTGGAGGGGTTCGCGTCAGAACTGCTGGGGCGAATAGTCGCGTGCATCGAGGCCCACTTTCC"
    "CGAGCACGCGCGGGAATATCAGGCCGTGTCCGTTCGCCGGGCCGTCATTAAGGACGACTGGGTCCTGCTG"
```

```
    "CAGCTGATCCCCGGCCGCGGCGCCCTGAACCAAAGCCTCTCGTGTCTGCGCTTCAAGCACGGCAGGGCAA"
    "GTCGCGCGACGGCCCGGACCTTTCTCGCGCTGAGCGTCGGGACCAACAACCGCCTATGCGCGTCCCTGTG"
    "TCAGCAGTGCTTTGCCACTAAATGCGATAACAACCGCCTGCACACGCTGTTTACCGTCGATGCGGGCACG"
    "CCATGCTCGCGGTCCGCTCCCTCCAGCACCTCACGACCGTCATCTTCATAA")

expected_sequence_length = 4096
expected_sequence_length = 4096

# Run the refined function
grouped_sequence, filled_sequence, total_pairs, added_pairs =␣
 ↪identify_and_fill_gaps_properly(
    original_sequence, expected_sequence_length
)

# Display results
print("Original Sequence Length:", len(original_sequence))
print("Expected Sequence Length:", expected_sequence_length)
print("Filled Sequence Length:", len(filled_sequence))
print("Total Pairs in Filled Sequence:", total_pairs)
print("Added Pairs:", added_pairs)
print("\nGrouped Sequence (First 200 pairs):\n", grouped_sequence)  # Show␣
 ↪first 200 pairs

# Optionally save the grouped sequence to a file
with open("grouped_sequence_refined.txt", "w") as file:
    file.write(grouped_sequence)
```

```
Original Sequence Length: 3201
Expected Sequence Length: 4096
Filled Sequence Length: 4096
Total Pairs in Filled Sequence: 2048
Added Pairs: 447

Grouped Sequence (First 200 pairs):
 AN NN NN NN NN NN NN NN NN NT GG GG NN NN AC GN NN NN GN NN NN NN NN NN NN NN
NN AA NN NG NN NN NN NN NN NN NN NN NN AC NN NN TG NN NN NC GA NN NT NN NN NN NN
NN NN CN NN AN NN NN NN NN NN NC GA NN NA GN NN NN NN NN NN NN NN NG GC NN NN NN
NN NN NN NN NG GT NN NN NC NN NN NN NN NN NN GG NN NN TT NN NG NN NN NN NN NN NN
NN NN CN NN NN NN NN NN NG NN NN NN NN NN NN NN NN NN GC NN NT NC NN NC NN NN CG
NN NN NN NN NN NN TG NN NN NN NN NN NN NN NG AN NN NN NN NN NN NN NN NN NG GN TN
NN NN NN NN NN NN NN NT AN NN NN NN NN NN NN NN NC NN NG NN NN NN NN NN NN NN NN
GN NN CG CN NN NN NN NN NN NN NN NT GN NN NN NN NN NN NN NN NT AN TG CN NN NN NN
NN NN NN NN NN GA CN NN NN NN NN NN NN NN NC GN NN NN NN NN NN NN NN NA CG GG TG
NN NC NN NN NG TN NN NN NN NN NN NN NN TA NN NN NN NN NN NN TN NN NN NN NN NN NN
NN NN NC NN NN NN NN NN NN NN NN NN AN NN NN NN NN NN NN NN NN NC CT NN NN NC NN
NN NN NN NN NN NN NN CN NN NT NN NN CN NN NN NN NN NN NN NN GN CN NN TC GC NN NC
NN NN NN NN NN NN NN NN NN CT NN NC CT CA NN NN NN NN NN NN NN NN NN CA AA CT GN
```

NN NC CT NN NG NN NC TG GN GN NN GG NC NN NN NC GN NN NN AN NN NN GN NN NN NN NN
NN NC CN NN GN NN NN TT GT NN NN NA TN NN AT AN NN TN NN NN NN NN NN NN NN NT NN
NN NN NN NN NN NN NN CN AN NN GC TN NN NN NN NN NN NN NN NN NA CN NN GA CG CG TN
NN NN NN NN NN NN NN NA CC NN NN NN NN NN NN NN NN NN GG CN NN CN NN NN NN NN NN
NN NN NN NC GA NN NN NN NN NN NN NN NN NN TG CN NN GC NN NN NN NN NN NN CC NA NN
NN NN NN NN NN NN NN AT GG NN NN NN NN NN NN CC CN NN NN NN NN NN NN NN NN NC AC
GG GN NN NC GC NN NN NN NN NN NN NN NN NG CC CN NN NN NN NN NN NN NN AC NC GA NA
CN AG NN NG AG NN NN NA GG NN NT TN CG NN NA GG GG NN NN NN NN AG CC GG GC GC TC
TA CC GG GA TG CG GG GG GG CT AA AT GG CG AT TC AT TT CG GG TG AC CT TT TG TT TA
TT GG GG AC GG AA GT GG GC GT GA CC CA CC AC CC GA AA GG GC GC AC CC GG CC CA TG
TT TG TG TG CC GC TT CG AG CG AG CG GA CG AC GT CG CC GT GC TC CA AG AC GC CC TG
GG CC GC GG GA CC CC AT TG CT CC CG GC CC AC AT CA CA GC AA CT CT GG AC TT GG AG
GC GA CG TT TG CG CT CC AC GC TA AC AT CA TC AT GG CT CT CA CC GT GG CC AT CG TC
CA CA AC GC CC CC GC CC GC AT CG GC AG CG GC AG CA CC GC CC CC CT GT AT GA GC CC
GG CG AA TC GA TG CG CT CG GT CG TC GG GC GC AT GT CC CT GG GG CA GC GC GG CC TC
AC CA CG CT GT TC GT GC AC CA CG AG GC GC GC GT GC TG GC GG CG TA CC GC CG GG CG
TA TT AT GG GA GC GC CC AA AG CC CC TT TT GG TT TC TG AG CA AA TT CG GC CC GG AC
GA AA AG AG CC TG GT GC TG GC CG CT AG GT AC TA CC TA CT CC AG GC TC CG CG CT TG
GG GG GC GC CG GA GC CA CG TA CG AT CT GC AG GC CG TG AA AG AC AT CT GC GC GA CC
TA CG CG AT CC CC CA CG AC CC AC GC CC CG AC AC CC TC AG TG CC GC GT CC TT GA CC
TC GT TC GC CG CC AT CA CT CG GT TC TG TT GC AC GA GC CA GT AC TC CC GC GG GG CC
GC GG CC GC TG GG TT TC CG CT GT AT GT GG AG CG CC GC AT CG CC GC CG AC GT AC GC
GA GA CC GG CG CG CT GG AG AA GT TC AT CG CC CA CG AT CG CA GC TG CC TG CG CG TG
TC CG AC CG GG AA TT CA TT AC GT AC AT CT AC CT GG CC CA CT TT GA GT GC TT CA GC
CC CC CG CG CC TG GC CA CG CA TC TC CG GG CC GT GA CC AC CC AC GA CC CC AG CC CC
GC GG CC AG CA CG GA GC AG CC CT CG CC CC TG GG TC GG GA GG CG GT GG AA CA GT TC
TT CC GG CA CG TG CG CG CC CA GC TG AA CA TC CG CG AG TA CG TA AA GC AA AA CG TC
AC CC CC AG GG AA AC CG CC CT GG CG GG AG AC GC GG CC GC CG CC TA CC TG CG CG CG
CG CA CG TA TG CC CC GG CG GC CC TC AC GC CC GC CC CC GC GT AC TG CG GG GT CG CA
GA CT CG TC CA CC AA AA TG AT GG GA CG TC TG GC GG AA GC AG AA AG GC TC CT AG TC
CC CC AC GG CT GG CC CG CG TT CG CA CC AA CA AC CC CC GG GG AC GA CG CG GG GG GC
GG CA CT GC CG CC CC CC AG AC CT GC GG AA TC GT CA AG CG CC TC CT CA AG CT GG CC
GC CA CG GA GC AG CA GG GC AC GA CG CC CC CG GC GA TC GC GG CT CT CA TG CA GG AC
GC GT CG GT CC AA AC CC CC CT GC CC GT GT AC AG GA TT AC CA TG TC CC CG AC CG GC
CA GG CG TT TG CC GC GG CG GC GC GG GA CG AC TG GG CC CG CG TG AC GC GG GA CG CG
CG CC CG CC GG AA GC GA CC GT GG TC GC GG AC GC GG CG GC GG CG CC CG AG CC CG GC
GC GC TC GG CC GG CG GC TC AC GC GC CG CA TT TG CG CC CG GG GC CC CG CG CT CC CC
CC GG GC GG CC TG GC CG TC GG GG GC CA GA TG TA CG TG AA CC GC AA CG AG AT CT TC
AA CG CC GC GC TG GC CG TT AC GA AC AT CA TC CT GG AT CT GG AC AT CG CC CT GA AG
GA GC CC GT CC CC TT TC CC CG GC TC CA CG AG GC CC TG GG TC AC TT TA GG CG CG GG
GC GC TG GC GG CG GT TC AG CT GT TG TT TC CC GC GG CC CG CG TA GA CC CC GA CG CC
TA TC CC TG TT AT TT TT TC AA AA GC GC CT GT CG GC CC CG CG CG CC GC CC GT CT GT
GC GG GC GA CG GG CC CC TG GC CG GT GG CG AC GA CG GC GA CG GG GA CT GG TT CC CC
GA CG CC GG TG GT CC CG GC GA CG AG GA GT GG GA GG AG GA CA CG GA CC CC AT GG AC
AC GA CC CA CG GC CC CC TC CC GG AC GA CG AG GC CG CG TA CC TC GA CC TG CT AC AC
GA AC AG AT AC CA GC GG CG AC GC CC AG CG AA CC GG AC TC CG TC GT GT GT TC CT GC
GC CG AC AA GA TC GG GC TG CG CG TG TG CC TA CC GG TC CC CG CC CC GT AC GT TG TG
CA CG GC TC CC TG AC GA TG CG TG GG GT GG CG AG GG TG AT CC AG CA GG CG GT GC TG

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TT GG AC CG CG AC TT CG TG GA GG CC GT AG GG AG CC AC GT AA AG AA CT TT TT GC TG
AT CG AT AC GG GC GT GT AC GC CC AC GG CC AC AG CC TG CG CT TG CC GT AT TT CG CC
AA GA TC GG CC CC GA CG GC TC CG CG TG CG GC CG GT TA TT GC CC GT CT TC GT GA TC
CC CC CC GC GT GC GA GG AC GT TC CG GC GT TC GT CG CC GC GC AC GC CG AC CC GC GG
CG CT TC CA CT TT CA CG CC CC GC CC AT GT TT TC CG CG GC CC CG CG GG AG AT CC GC
GT CC TC CA CA GC CT GG GC GG GG AC TA TG TC AG CT TT TT CG AG AA GA AG GC GT CG
CG CA AC GC CC TG GA GC AC TT TG GG CG AC GC GA GA CC CT GA CG GA GG TT CT GG GC
CG CT AC GA TG TG CG GC CC GA CG CC GG GG AG AC CG TG GA GG GG TT CG CG TC AG AA
CT GC TG GG GC GA AT AG TC GC GT GC AT CG AG GC CC AC TT TC CC GA GC AC GC GC GG
GA AT AT CA GG CC GT GT CC GT TC GC CG GG CC GT CA TT AA GG AC GA CT GG GT CC TG
CT GC AG CT GA TC CC CG GC CG CG GC GC CC TG AA CC AA AG CC TC TC GT GT CT GC GC
TT CA AG CA CG GC AG GG CA AG TC GC GC GA CG GC CC GG AC CT TT CT CG CG CT GA GC
GT CG GG AC CA AC AA CC GC CT AT GC GC GT CC CT GT GT CA GC AG TG CT TT GC CA CT
AA AT GC GA TA AC AA CC GC CT GC AC AC GC TG TT TA CC GT CG AT GC GG GC AC GC CA
TG CT CG CG GT CC GC TC CC TC CA GC AC CT CA CG AC CG TC AT CT TC AT AA
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