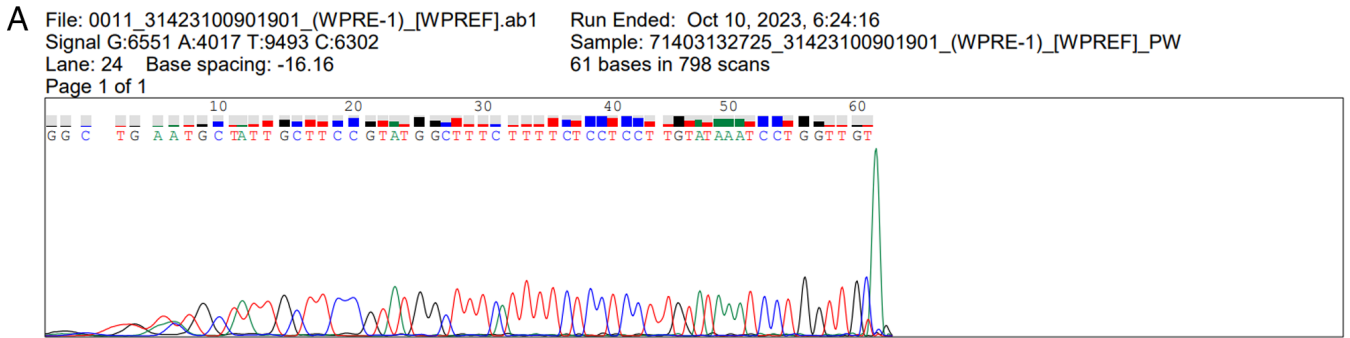Figure S1. (A) Raw sequencing results of the WPRE PCR product. (B) Basic Local Alignment Search Tool analysis. The sequenced product was highly similar to the target sequence of WPRE (J04514.1) in the National Center for Biotechnology Information gene library, indicating successful PCR amplification. WPRE, wooduck hepatitis virus posttranscriptional element.

A File: 0011_31423100901901_(WPRE-1)_[WPREF].ab1   Run Ended: Oct 10, 2023, 6:24:16
Signal G:6551 A:4017 T:9493 C:6302   Sample: 71403132725_31423100901901_(WPRE-1)_[WPREF]_PW
Lane: 24   Base spacing: -16.16   61 bases in 798 scans
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G G C   T G A A T G C TAT T G C T T C C G TAT G G C T T T C T T T T CT CCT CCT TGTATAAAT C CT G G T T G T

B

Sequence ID: gi|336146|J04514.1 Length: 3323 Number of Matches: 1

Range 1: 1196 to 1251 GenBank Graphics   ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
86.0 bits(94)	8e-14	54/56(96%)	2/56(3%)	Plus/Plus

Query   7   ATGCTATTGCTTCC-GTATGGCTTTC-TTTTCTCCTCCTTGTATAAATCCTGGTTG   60
             |||||||||||||| |||||||||||| |||||||||||||||||||||||||||||
Sbjct   1196 ATGCTATTGCTTCCCGTATGGCTTTCATTTTCTCCTCCTTGTATAAATCCTGGTTG   1251

Figure S2. (A) Raw sequencing results of the sh-Salusin-β_1 PCR product. (B) Basic Local Alignment Search Tool analysis. The sequencing results were compared and analyzed with the DNA sequence of the pLKO.1-sh-Salusin-β_1 recombinant plasmid using SnapGene v6.0.2 software. It was found that the PCR product sample showed a high similarity to the target fragment sequence of the sh-Salusin-β_1 amplification primers, indicating successful PCR amplification. sh, short hairpin RNA.

Figure S3. (A) Raw sequencing results of the sh-Salusin-β_2 PCR product. (B) Basic Local Alignment Search Tool analysis. The sequencing results were compared and analyzed with the DNA sequence of the pLKO.1-sh-Salusin-β_2 recombinant plasmid using SnapGene v6.0.2 software. It was found that the PCR product sample showed a high similarity to the target fragment sequence of the sh-Salusin-β_2 amplification primers, indicating successful PCR amplification. sh, short hairpin RNA.

Figure S4. (A) Raw sequencing results of the sh-Salusin-β_3 PCR product. (B) Basic Local Alignment Search Tool analysis. The sequencing results were compared and analyzed with the DNA sequence of the pLKO.1-sh-Salusin-β_3 recombinant plasmid using SnapGene v6.0.2 software. It was found that the PCR product sample showed a high similarity to the target fragment sequence of the sh-Salusin-β_3 amplification primers, indicating successful PCR amplification. sh, short hairpin RNA.
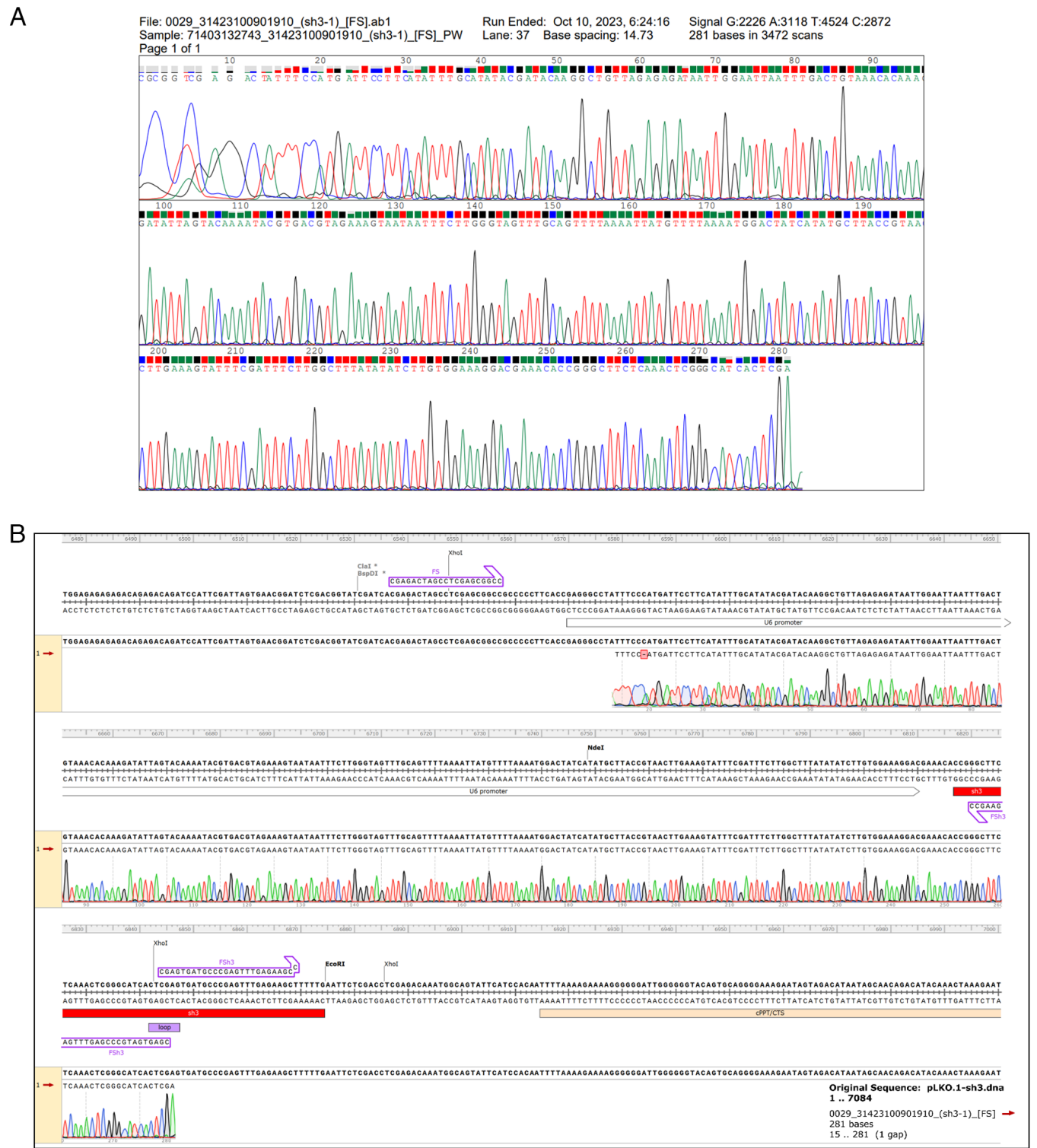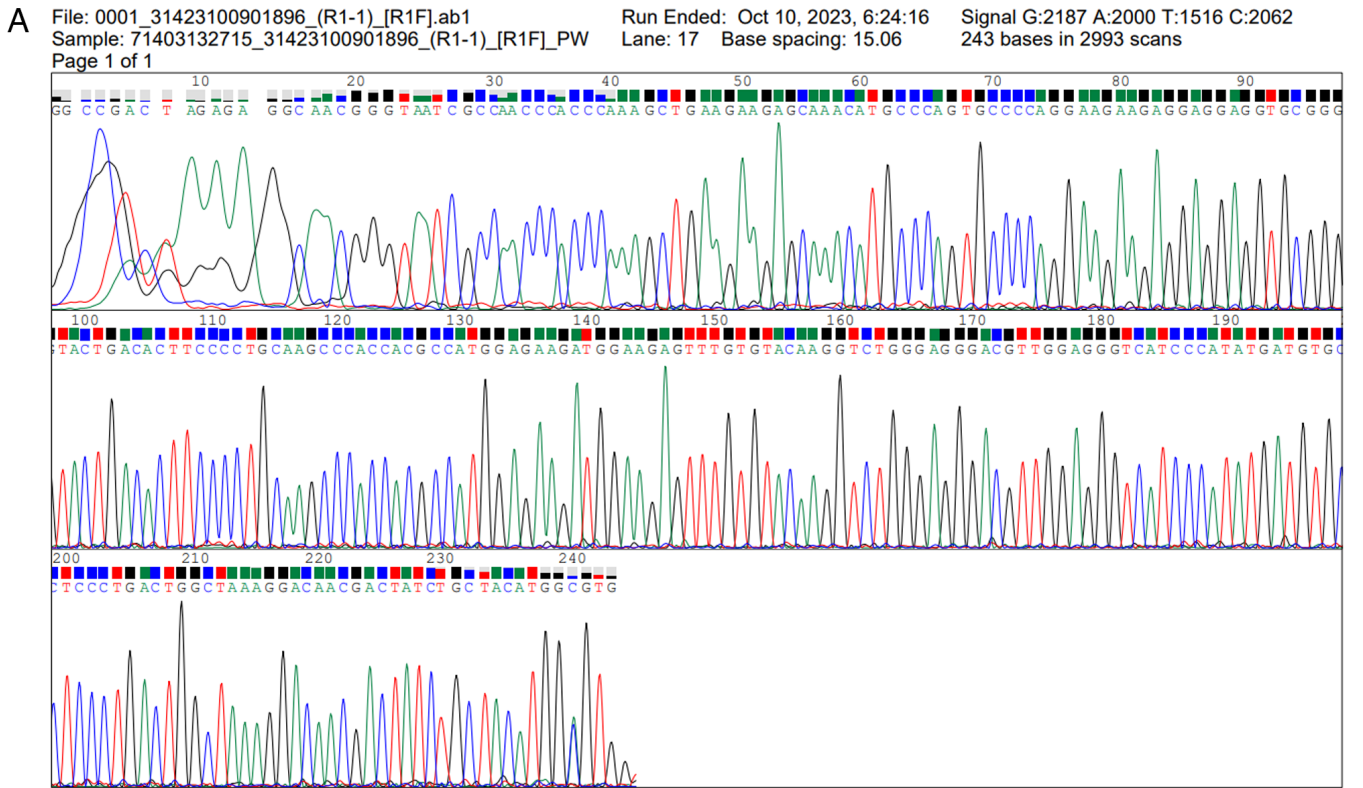
Figure S5. (A) Raw sequencing results of AdipoR1 PCR product. (B) Basic Local Alignment Search Tool analysis. The sequencing product was highly similar to the target sequence of AdipoR1 (NM_015999.6) in the National Center for Biotechnology Information gene library, indicating successful PCR amplification. AdipoR1, adiponectin receptor 1.

Figure S6. (A) Raw sequencing results of Salusin-β PCR product. The top image are the forward sequencing results, while the bottom image indicates the reverse sequencing results for the same Salusin-β PCR product. (B) Basic Local Alignment Search Tool analysis. The 598-657 bases of the TOR2A nucleotide sequence (NM_001134430.3) in the National Center for Biotechnology Information gene library encode Salusin-β. The forward sequencing result of a PCR amplification product sample was highly similar to the 620-657 bases of this target sequence, while the reverse sequencing result was highly similar to the 598-620 bases. This indicated successful PCR amplification, replicating the desired region of the Salusin-β target sequence. TOR2A, torsin family 2 member A.

A

File: 0003_31423101700518_(B3)_[F61].ab1   Run Ended: Oct 18, 2023, 6:09:03   Signal G:6061 A:7804 T:6652 C:7798
Sample: 71403155030_31423101700518_(B3)_[F61]_PW   Lane: 80   Base spacing: -16.16   80 bases in 1012 scans
Page 1 of 1

AAAGGG C TTC TCAGCT CG G G CAT CAT G G AA GAGC GCC TCCT CTCGAGCG GCT GATG AAGAT GAAGAT G GCA GATCCGCGA

File: 0004_31423101700518_(B3)_[F62].ab1   Run Ended: Oct 18, 2023, 6:09:03   Signal G:5970 A:12441 T:6363 C:5084
Sample: 71403155031_31423101700518_(B3)_[F62]_PW   Lane: 78   Base spacing: -16.16   52 bases in 677 scans
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CTAGATGG CG A C TT G AG AGC ATCT GATG AAGAT GAAGAT G GC G GATCCGCGA

B

Sequence ID: gi|1676319774|NM_001134430.3 **Length:** 1372 **Number of Matches:** 2

Range 1: 620 to 657 GenBank Graphics   ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
57.2 bits(62)	3e-06	36/38(95%)	1/38(2%)	Plus/Plus

```
Query    5    GGCTTCTCAG-CTCGGGCATCATGGAAGAGCGCCTCCT    41
              ||||||||||  |||||||||||||||||||||||||||
Sbjct    620  GGCTTCTCAAACTCGGGCATCATGGAAGAGCGCCTCCT    657
```

Range 2: 598 to 617 GenBank Graphics   ▼ Next Match ▲ Previous Match ⌃ First Match

Score	Expect	Identities	Gaps	Strand
37.4 bits(40)	2.7	20/20(100%)	0/20(0%)	Plus/Minus

```
Query    51    CTGATGAAGATGAAGATGGC    70
               ||||||||||||||||||||
Sbjct    617   CTGATGAAGATGAAGATGGC    598
```

Sequence ID: gi|1676319774|NM_001134430.3 **Length:** 1372 **Number of Matches:** 1

Range 1: 598 to 620 GenBank Graphics   ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
42.8 bits(46)	0.029	23/23(100%)	0/23(0%)	Plus/Minus

```
Query    20    CATCTGATGAAGATGAAGATGGC    42
               |||||||||||||||||||||||
Sbjct    620   CATCTGATGAAGATGAAGATGGC    598
```
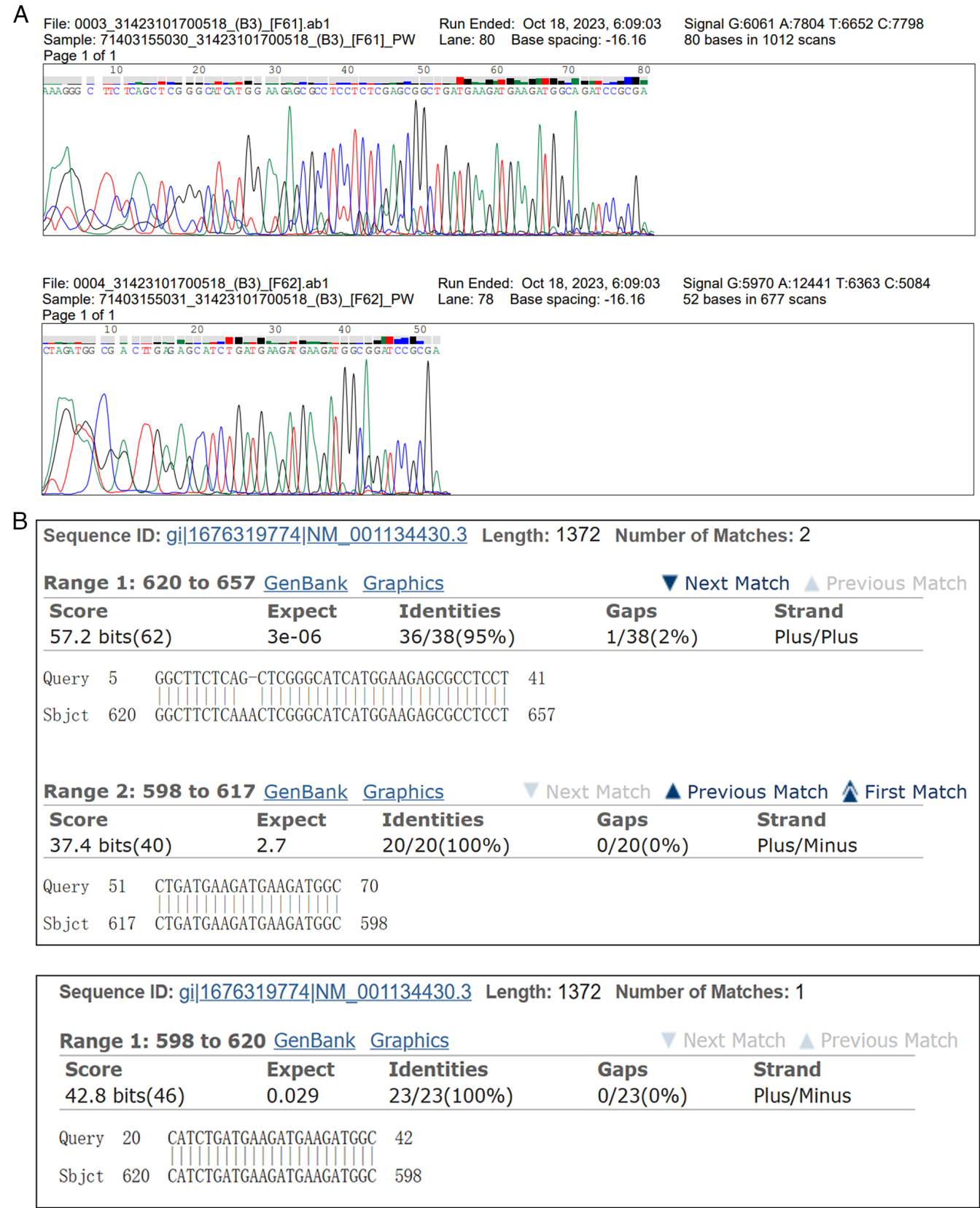
Figure S7. (A) Raw sequencing results of the GAPDH PCR product. (B) Basic Local Alignment Search Tool analysis. The sequencing product was highly similar to the target sequence of GAPDH (XM_004052561.4) in the National Center for Biotechnology Information gene library, indicating successful PCR amplification.

A

File: 0007_31423100901899_(G-1)_[GAPDHF].ab1   Run Ended: Oct 10, 2023, 6:24:16
Signal G:8125 A:6398 T:7562 C:8262   Sample: 71403132721_31423100901899_(G-1)_[GAPDHF]_PW
Lane: 28   Base spacing: -16.16   104 bases in 1230 scans
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B

Sequence ID: gi|2493335755|XM_004052561.4 Length: 1320 Number of Matches: 1

Range 1: 989 to 1090 GenBank Graphics   ▼ Next Match ▲ Previous Match

Score	Expect	Identities	Gaps	Strand
172 bits(190)	1e-38	100/102(98%)	1/102(0%)	Plus/Plus

```
Query   4    CTCC-CCTTCGACGCTGGGGCTGGCATTGCCCTCAACGACCACTTTGTCAAGCTCATTTC  62
             |||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct   989  CTCCACCTTCGACGCTGGGGCTGGCATTGCCCTCAACGACCACTTTGTCAAGCTCATTTC  1048

Query   63   CTGGTATGACAACGAATTTGGCTACAGCAACAGGGTGGTCGA  104
             |||||||||||||||||||||||||||||||||||||||| ||
Sbjct   1049 CTGGTATGACAACGAATTTGGCTACAGCAACAGGGTGGTGGA  1090
```