

1 AAGAATTTCTAACCGAAGTTTACCTCCCTCCCTTCTGCTTTCATAGGCAGCTTCTGCTTTTGTATTTT  
76 GTGCTTTCAGTCATCGTCTTGAAGTGTGCTTCCCTTCCCTCCAGGGAGCTGGTGGAGAATGACTTCCCGAG  
151 GAGAGCGTCCCTTTCTCAGCTTAGGAAAGCCGAGACACACCTGGAGAGCAGATCCTACGGAACAAAAGTCTAC  
226 ACCTTGCTGAGCTGCGTGGTGGACCACCTGAGAAGTACAGTAAGTACTACAGACTCGGTAAGATGGTGAAGT  
301 TGGTATGCATTGCTGCTGCAAGGTTTTTAAACCATCCAGAATTCAGCAGTGGAGATGAATCCGCATCCACGAC  
1 M N P H **P R**  
376 GCATCCGCTTAAAGCCATGGCTGGTAGCACAGGTGGACAGTGGGAATTATCCAGGCCTACACTGGGAAGATAGGG  
7 **R I R L** K P **W** L V A Q V D S G N Y P G L H **W** E D R  
451 AACACAAGCTATTCGCCATTCCATGGCGTCATGCAACACGTCACATACCAATGCAAGATGATGAGAACCACATAT  
32 **E H K L F R I P W R H A T R H I P M Q D D E N T I**  
526 TTAAGCCTGGGCAAAGGAAACAGGCAAATACCAAGAGGGGTAGATGAACCTGACCCTGCAAAGTGGGAAGCAA  
57 F K A **W** A K E T G K Y Q E G V D E P D P A K **W** K A  
601 ATTTGCGTGTGCTCTGAACAAGAGTCGAGAGTTTAAATTGTTGTATGATGGCACTAAGGAAACCCWCAATGCGC  
82 N L R C A L N K S R E F K L L Y D G T K E T P M Q  
676 CATTCAAGATCTACCAGTATGTGACCTCTCTGGGCAGAATGAAGATTCTTTACCTGTGGAAGCCTTGCATGATG  
107 P F K I Y Q L C D L S G Q N E D S L P V E A L H D  
751 AACCTATAAGCGATGATAAAAAGATATCAACCATATGTTCCCAATGCTTCAAATTCAGATGCACCTTCTCCTT  
132 E P I S D D E K D I N H M F P M L E I Q D A L P P  
826 ATACCTGGCCAAAGGCTGAACCTGTTTTAGTTCCTGTCAAATCTTATACGCCCAACCGTGCACCTAGCCGATT  
157 Y T W P K A E P V F S S C S N L I Q P N R A L A D  
901 CTGTGCCCTCGCATCTCCCGTAGCATACACTGGTGTGGAGCTGTACCACAAGGCTGGTACCACAACCTGTAG  
182 S V P S A S P V A Y T G V E L S P Q G L V P Q P V  
976 TAATCCCCATCCAGAGCTGGTTCACAACAGGCTGGAGACCACCCAGAATGCAGAGCTTCTATACCAGGAG  
207 V I P H P E L V A P T G L E T T Q N A E L P I P G  
1051 TAATGCCTACACTGTGAGCAGGGGATCCAGGCTTACTATTAGTCCACAGATGCTGCCATTGACTGACCTGG  
232 V M P T P V E Q G I P G L L I S P Q M L P L T D L  
1126 AAATAAAGTTTCTATATAGAGGGAAGCAAGTTGGAATGATGACTGTTAGTAAACCCTCATGGTGCAGCTTTACT  
257 E I K F L Y R G K Q V G M M T V S N P H G C R L Y  
1201 ACAGTAACCTTGAGCCAACCCAGAGCAAGTGGAGCTTTGGCCCAACAACACTGGAACAAGTTCGATTCTCTG  
282 Y S N L E P T P E Q V E L F G P T T L E Q V R F P  
1276 GAACAGATGAGATTGGAATGAGAAACAGAAGTTCTACACTAACCATCTTCTGGATGTAATGGACCGGGGCTGA  
307 G T D E I G N E K Q K F Y T N H L L D V M D R G L  
1351 TCCTTTGCCTACAAGGCCAGGATATATGCCATTGCTGTGTCAGTCAAAGTCTTCTGGTCTGGGCCATGTG  
332 I L C L Q G Q D I Y A I R L C Q C K V F W S G P C  
1426 CCCCTAATGTAGTGGACCCCAACCTATAGAAAGGGAGAAGAGAATCAAACCTATTACGCCTTGAGACGTTCTTGA  
357 A P N V G G P N P I E R E K R I K L F S L E T F L  
1501 ATGAGCTCATTGCTGCCAGAAAGTCAAACAAATGCATTGCCTTCATATGAAATATCTTCTGTTTTGGTGAAG  
382 N E L I A C Q K G Q T N A L P S Y E I F F C F G E  
1576 AATGCCCGACCAAAAACCAAGGGAGAAAAACTAATACCGTACAGGTTATTCTGTGGCTGCCGTTTGGTTT  
407 E W P D Q K P R E K K L I T V Q V I P V A A R L L  
1651 CTGAAATCTTCTCAGGGGAGCTGTGCTGGTCTGCAGATAGTATAAACTCCAGATATCACATCCAGATCTAAAGG  
432 S E I F S G E L S W S A D S I K L Q I S H P D L K  
1726 ACAAAATGGTGAACAGTTCAAAGAACTCCATCAACTGTGGCAGAGCCAGCAGACCAAGCACTGTCTCCACAAG  
457 D K M V E Q F K E L H Q L W Q S Q Q T Q A L A P Q  
1801 GTGCAGAACTAATCCAGGGTAGATGTGGCATCCGGTCCCTGGCCATGCACACTGAAAGCATGCAATAAACCC  
482 G A G T N P G V D V A S G P W P M H T E S M Q \*  
1876 TGTATGATCACCTGTGTTACTTCACTGACTGTAGACCGCACATTAGTTCATTCCCATTTGGACTGGGGTTGAC  
1951 TTGTTAAGCTGCTTCCCACTGCCTCACCTGGTTGTATAGAGAACCCAGCAATCTATTGAATAGTCAAGA  
2026 TGTATTAAGGATAAACATACGTCTGTCAAGCTTGAGAACAGACTTAAAAAAAAAAAAAAAAAAAA

**Figure S1.** The full-length cDNA nucleotide sequence and corresponding amino acid sequence of *PnIRF5*. The start codon (ATG) and stop codon (TAA) were formatted in bold text. The predicted DNA binding domain (DBD, 7-104 aa) was indicated by grey shade. The middle region (MR, 108-195 aa), IRF association domain (IAD, 196-327 aa) and virus activated domain (VAD, 326-479 aa) were showed by underline with line, wavy lines and double lines, respectively. The two nuclear localization signals (NLSs, 5-10 aa, 413-419 aa) in the DBD and IAD were indicated by box. The five conserved tryptophan (W) residues forming the ‘tryptophan pentad-repeat’ were formatted in bold red text.

**Table S1** The amino acid similarities (%) of *PnIRF5* and other known IRF5s

|                                      | <i>GenBank<br/>accession<br/>numbers</i> | <i>Homo sapiens</i> |       |       | <i>Mauremys mutica</i> |       |       | <i>Gallus gallus</i> |       |       | <i>Mus musculus</i> |       |       | <i>Danio rerio</i> |       |       | <i>Pelophylax<br/>nigromaculatus</i> |       |       |
|--------------------------------------|--|---------------------|-------|-------|------------------------|-------|-------|----------------------|-------|-------|---------------------|-------|-------|--------------------|-------|-------|--------------------------------------|-------|-------|
|                                      |  | All                 | DBD   | IAD   | All                    | DBD   | IAD   | All                  | DBD   | IAD   | All                 | DBD   | IAD   | All                | DBD   | IAD   | All                                  | DBD   | IAD   |
| <i>Homo sapiens</i>                  | XP_04727<br>6292.1                       | -                   | -     | -     | 63.27                  | 79.05 | 68.56 | 52.97                | 62.04 | 53.28 | 84.98               | 92.86 | 90.35 | 48.64              | 70.48 | 54.59 | 56.94                                | 73.33 | 64.19 |
| <i>Mauremys<br/>mutica</i>           | XP_04484<br>7579.1                       | 63.27               | 79.05 | 68.56 | -                      | -     | -     | 53.18                | 61.90 | 55.41 | 62.68               | 77.14 | 68.86 | 55.38              | 78.10 | 58.55 | 61.26                                | 83.81 | 66.09 |
| <i>Gallus gallus</i>                 | XP_04676<br>4556.1                       | 52.97               | 62.04 | 53.28 | 53.18                  | 61.90 | 55.41 | -                    | -     | -     | 53.18               | 61.11 | 53.07 | 48.73              | 61.90 | 51.52 | 48.73                                | 63.81 | 49.35 |
| <i>Mus musculus</i>                  | NP_0012<br>39311.1                       | 84.98               | 92.86 | 90.35 | 62.68                  | 77.14 | 68.86 | 53.18                | 61.11 | 53.07 | -                   | -     | -     | 51.58              | 69.52 | 57.46 | 56.55                                | 74.29 | 64.04 |
| <i>Danio rerio</i>                   | NP_0013<br>14746.1                       | 48.64               | 70.48 | 54.59 | 55.38                  | 78.10 | 58.55 | 48.73                | 61.90 | 51.52 | 51.58               | 69.52 | 57.46 | -                  | -     | -     | 54.00                                | 78.10 | 58.80 |
| <i>Pelophylax<br/>nigromaculatus</i> | OP03910<br>1                             | 56.94               | 73.33 | 64.19 | 61.26                  | 83.81 | 66.09 | 48.73                | 63.81 | 49.35 | 56.55               | 74.29 | 64.04 | 54.00              | 78.10 | 58.80 | -                                    | -     | -     |