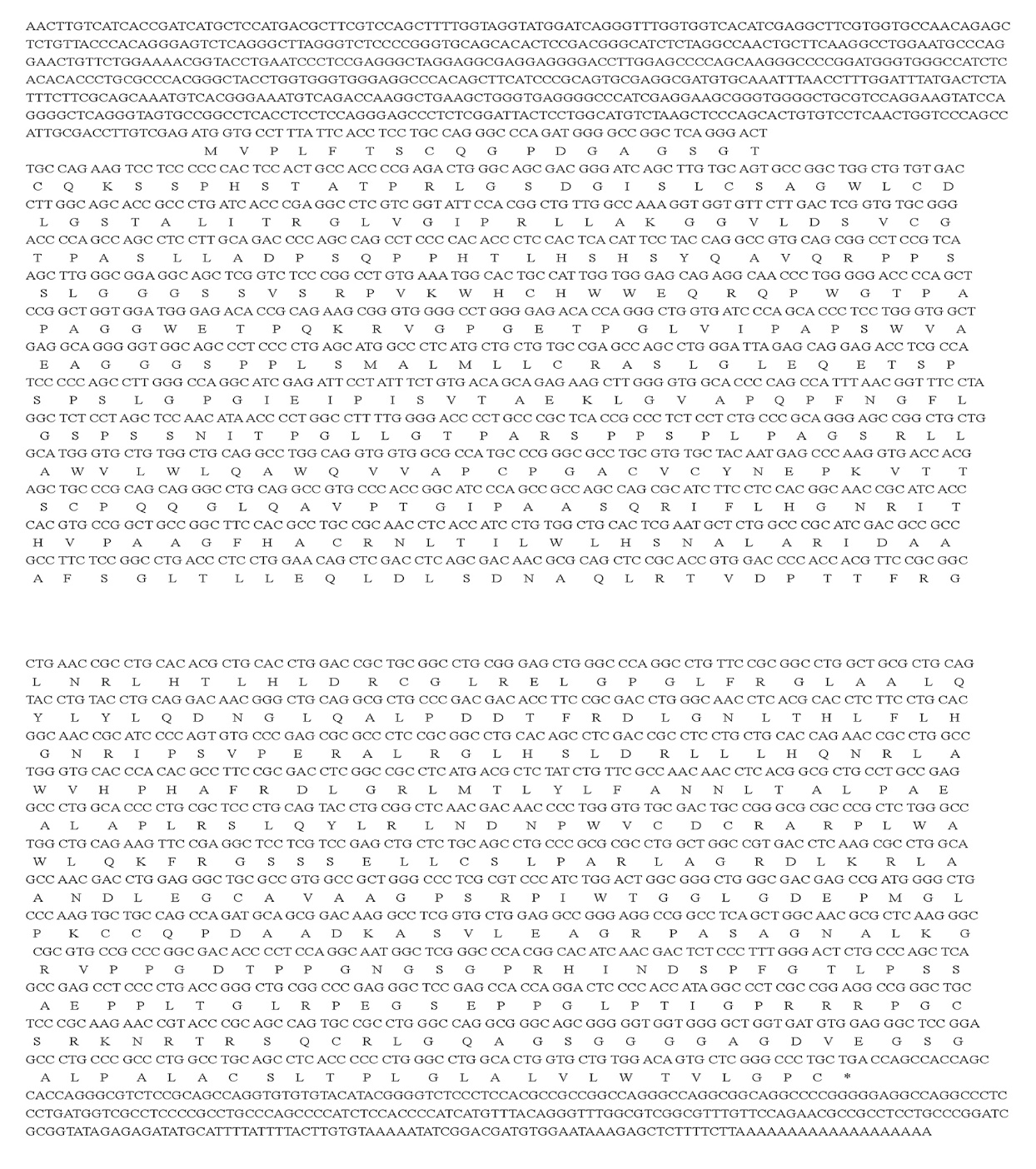
Supplementary Table 1. Primer design for the *tsNgR*1.

|  |  |  |
| --- | --- | --- |
| Primers | Sequence (5’ to 3’) | Groups |
| RTN4R-1F | ATGGTGCCTTTATTCACCTCCT | Intermediate sequence |
| RTN4R-224R | CACACCGAGTCAAGAACACCA | amplification primers |
| RTN4R-728F | GACGGGATCAGCTTGTGCAGTG |  |
| RTN4R-1456R | CTGCAGCCACAGCACCCATG |  |
| RTN4R-1371F | GCACAGCCTCGACCGCCTC |  |
| RTN4R-1777R | CATCTGGCTGGCAGCACTT |  |
| RTN4R-1597F | AAGTTCCGAGGCTCCTCGTCCGA |  |
| RTN4R-2045R | CACTGGCTGCGGGTACGGTTCTT |  |
| RTN4R-1913F | GGACTCTGCCCAGCTCAGCCGA |  |
| RTN4R-2365R | ACGCCGACGCCAAACCCTGTA |  |
| RTN4R-F1 | TGCTCGGGCCCTGCTGACCA | 3’RACE specific primer |
| RTN4R-F2 | TCCGCAGCCAGGTGTGTGTACATAC |  |
| RTN4R-R4 | CACTGCACAAGCTGATCCCGTCG | 5’RACE specific primer |
| RTN4R-R3 | GATCAGGGCGGTGCTGCCAA |  |
| RTN4R-RT4 | TCCCCCAGGGTTGCCTCT |  |
| RTN4R-RT3 | GCTTCTGCGGTGTCTCCCAT |  |

Supplementary Table 2. RT-qPCR primer sequences.

|  |  |
| --- | --- |
| Primer | Sequence |
| *NgR*1-F | 5’-TGGTGCTGTGGACAGTGCTC-3’ |
| *NgR1-*R | 5’-CACACCTGGCTGCGGAGA-3’ |
| Probe | 5’FAM-CCAGCCACCAGCCACCAGGGCG-3’TAMRA |
| *GAPDH-* F | 5’-CTTCAACTCTGGCAAGGT-3’ |
| *GAPDH-* R | 5’-AAGATGGTGATGGACTTCC-3’ |
| Probe | 5’ FAM-ACCACAGTCCACGCCATCACTGCCACC-3’TAMRA |

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Supplementary Fig. 1. Nucleotide sequences and corresponding amino acids of NgR1.



Supplementary Fig. 2. Comparison of NgR1 amino acids sequence between the tree shrew and other species. The conserved domain is marked with a black box.



Supplementary Fig. 3. Phylogenetic analysis of NgR1in the tree shrew. A phylogenetic tree with 1000 bootstrap repeats was constructed according to the Neighbor-joining (NJ) method.