

Supplementary Material

1 Supplementary Tables

Table S1: Nucleotide sequences of primers and dsRNAs used

| | Sequence (5'-3') | Usage |
|-----------------------------|------------------------|-------------------------|
| ILPR-F | ACAACAAGAGCCATTAAGC | cDNA fragment cloning |
| ILPR-R | GCAAGTTATGTCCGAGTATT | |
| ILPR 3'-F | TGCTTACTTGTTGGTCATAC | 3'-RACE |
| ILPR 3'-R | CGCAATCAACAAGCAGAG | |
| ILPR 5'-F | GCCATTAGAAGCACAGACA | 5'-RACE |
| ILPR 5'-R | TCTTACAGACGGCACCAT | |
| RT-ILPR-F | GGTGGAGATCACTGACTATC | Real-time PCR |
| RT-ILPR-R | CTCCACGCTGAATAACTGT | |
| RT-Vg1-F | CACCTGCGACTGAACCTAAA | qPCR for <i>Vg1</i> |
| RT-Vg1-R | CAAGACGCTCAAGCAACATG | |
| RT-Vg2-F | GAGTCAGGCTTGCTATGG | qPCR for <i>Vg2</i> |
| RT-Vg2-R | GTGGATTCACTACGGTCTAAG | |
| RT-CtsL1-like-F | GTATCTACTTACATACGCTGAC | qPCR for CtsL1-like |
| RT-CtsL1-like-R | AGTCCGAATAATGAGATGCT | |
| RT- FS-F | CTTGTCGTATGCGTGGAA | qPCR for FS |
| RT- FS-R | ATATAGGCGATACTGACTGAC | |
| RT- β -actin F | GCCAGTTGCTCGTTACAG | qPCR for β -actin |
| RT- β -actin R | GCCAACAATAGATGGGAAT | |
| negative control- sense | UUCUUCGAACGUGUCACGUTT | RNA interference |
| negative control- antisense | ACGUGACACGUUCGGAGAATT | |
| SjILPR siRNA1- sense | GCAAGUUAUGUCCGAGUAUTT | RNA interference |
| SjILPR siRNA1- antisense | AUACUCGGACAUAACUUGCTT | |
| SjILPR siRNA2- sense | GCUGGCUACAUGAAGAUATT | RNA interference |
| SjILPR siRNA2- antisense | UAUCUUCAAUGUAGCCAGCTT | |

Table S2. Accession numbers to the sequences in Multiple sequence alignment

| Gene | Species | Accession numbers |
|---------------|----------------------------------|-------------------|
| <i>SjILPR</i> | <i>Sepiella japonica</i> | MK611806 |
| <i>ObILPR</i> | <i>Octopus bimaculoides</i> | XP014780880.1 |
| <i>LsMIPR</i> | <i>Lymnaea stagnalis</i> | CAA59353.1 |
| <i>BgIR</i> | <i>Biomphalaria glabrata</i> | AAF31166.1 |
| <i>PfIRR</i> | <i>Pinctada fucata</i> | AGA94627.1 |
| <i>AaIR</i> | <i>Aedes aegypti</i> | AAB17094.1 |
| <i>BiILPR</i> | <i>Branchiostoma lanceolatum</i> | AAB50848.1 |
| <i>HsINS</i> | <i>Homo sapiens</i> | AAA59174.1 |

Table S3. List of accession numbers and identity of IRs from other species with *SjILPR*

| Species | Accession numbers | Identities (%) |
|----------------------------------|-------------------|----------------|
| <i>Sepiella japonica</i> | MK611806 | 100 |
| <i>Octopus bimaculoides</i> | XP014780880.1 | 67.3 |
| <i>Lymnaea stagnalis</i> | CAA59353.1 | 39.2 |
| <i>Biomphalaria glabrata</i> | AAF31166.1 | 36.6 |
| <i>Pinctada fucata</i> | AGA94627.1 | 46.7 |
| <i>Aedes aegypti</i> | AAB17094.1 | 35.6 |
| <i>Branchiostoma lanceolatum</i> | AAB50848.1 | 41.6 |
| <i>Homo sapiens</i> | AAA59174.1 | 40.7 |

Table S4. Summary of functional annotation of unigenes.

| Database | Number.of.Unigenes | Percentage (%) |
|------------------------------------|--------------------|----------------|
| Annotated in NR | 25602 | 24.82 |
| Annotated in NT | 8201 | 7.95 |
| Annotated in KO | 12276 | 11.9 |
| Annotated in SwissProt | 17718 | 17.18 |
| Annotated in PFAM | 28190 | 27.33 |
| Annotated in GO | 28190 | 27.33 |
| Annotated in KOG | 6637 | 6.43 |
| Annotated in all Databases | 2013 | 1.95 |
| Annotated in at least one Database | 37171 | 36.04 |
| Total Unigenes | 103117 | 100 |

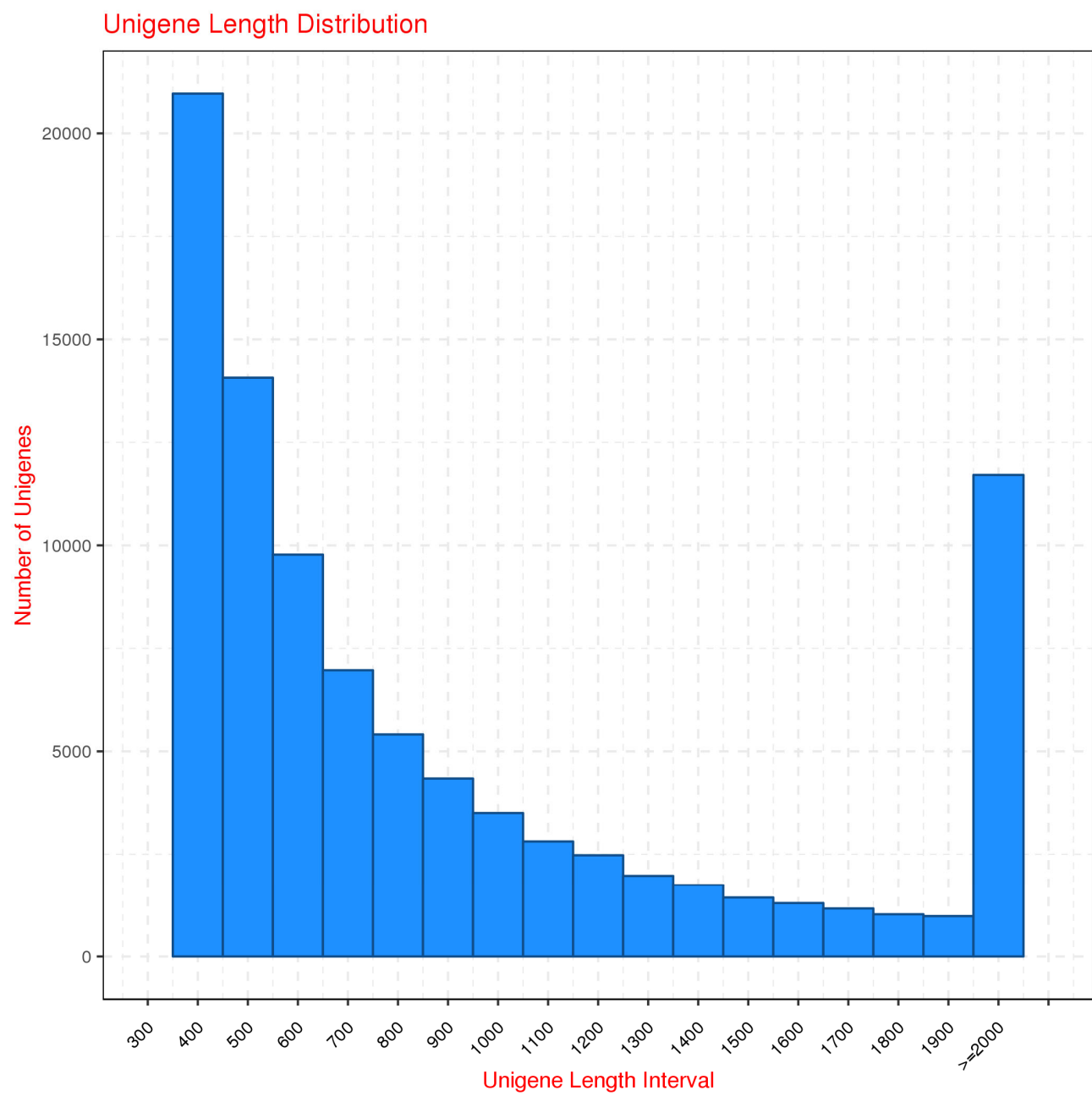


Figure S1. Length distribution of all-unigenes.