## Additional file 4: Table S4. Complete list of significantly expanded gene families in *Glyptelasma gigas*

| Glyptelasma gigas | Octolasmis warwicki | Eurytemora affinis | Daphnia pulex | Parhyale hawaiensis | Litopenaeus vannamei | P value  | Function annotation                                                                 |
|-------------------|---------------------|-------------------|---------------|---------------------|---------------------|---------|-------------------------------------------------------------------------------------|
| 28                | 8                   | 1                 | 0             | 1                   | 0                   | 1.40E-04 | X-ray repair cross-complementing protein 4 (XRCC4)                                  |
| 19                | 8                   | 3                 | 4             | 1                   | 0                   | 3.51E-02 | PREDICTED: uncharacterized protein LOC100568550                                   |
| 30                | 2                   | 0                 | 0             | 0                   | 0                   | 6.27E-23 | Tenascin                                                                            |
| 26                | 1                   | 0                 | 1             | 1                   | 0                   | 2.19E-34 | Titin                                                                               |
| 20                | 8                   | 0                 | 0             | 0                   | 0                   | 2.14E-02 | Circovirus capsid protein                                                          |
| 17                | 6                   | 0                 | 0             | 1                   | 1                   | 1.76E-02 | Ribosomal protein L13e                                                             |
| 17                | 0                   | 0                 | 0             | 3                   | 2                   | 5.16E-18 | Protocadherin fat 4/16/23                                                           |
| 20                | 1                   | 0                 | 0             | 0                   | 0                   | 2.91E-20 | Very short patch repair endonuclease (VSR)                                          |
| 17                | 3                   | 0                 | 0             | 0                   | 0                   | 4.69E-05 | Pro-kumamolisin, activation domain                                                |
| 15                | 4                   | 0                 | 0             | 1                   | 0                   | 4.90E-03 | Integrase core domain                                                              |
| 15                | 5                   | 0                 | 0             | 0                   | 0                   | 2.01E-02 | hypothetical protein HELRODRAFT_163242                                            |
| 15                | 4                   | 0                 | 0             | 0                   | 0                   | 4.90E-03 | PREDICTED: uncharacterized protein LOC105338248                                   |
| 14                | 5                   | 0                 | 0             | 0                   | 0                   | 3.72E-02 | RNA-directed DNA polymerase from mobile element jockey [Larimichthys crocea]       |
| 10                | 2                   | 2                 | 0             | 4                   | 0                   | 6.71E-03 | PREDICTED: RNA-directed DNA polymerase from mobile element jockey-like             |
| 14                | 4                   | 0                 | 0             | 0                   | 0                   | 1.07E-02 | PREDICTED: uncharacterized protein LOC105564550                                   |
| 14                | 1                   | 0                 | 0             | 1                   | 0                   | 5.28E-10 | RNA-directed DNA polymerase from mobile element jockey [Drosophila melanogaster]   |
| 12                | 4                   | 0                 | 0             | 0                   | 0                   | 4.33E-02 | Trehalose phosphatase                                                              |
| 11                | 1                   | 0                 | 3             | 0                   | 0                   | 2.60E-06 | hypothetical protein [Cotesia congregata]                                         |
| 11                | 0                   | 1                 | 0             | 0                   | 2                   | 2.16E-10 | PREDICTED: titin [Tribolium castaneum]                                             |
|   |   |   |   |   |   |                          |
|---|---|---|---|---|---|--------------------------------|
| 9 | 1 | 0 | 4 | 0 | 0 | 2.25E-04 hypothetical protein DAPPUDRAFT_118411 |
| 9 | 3 | 0 | 0 | 0 | 0 | 9.56E-02 -- |
| 9 | 2 | 0 | 0 | 0 | 0 | 1.90E-02 hypothetical protein N307_01365, partial |
| 8 | 1 | 0 | 0 | 1 | 0 | 1.46E-03 -- |
| 7 | 1 | 0 | 0 | 1 | 1 | 7.53E-03 Plexin-B [*Drosophila melanogaster*] |
| 8 | 1 | 0 | 0 | 0 | 0 | 1.46E-03 THAP domain |
| 7 | 1 | 0 | 0 | 0 | 0 | 7.53E-03 Nine Cysteines Domain of family 3 GPCR |