Table S1: The quantitative PCR primers of candidate genes in *D. valens*

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| **Gene ID** | **Primer sequences（5’-3’）** | **Product length（bp）** | **Primer-pair efficiency（%）** | **R2** |
| TRINITY\_DN22243\_c0\_g1 | F:TCCATGGATGTTTGAGGCCC R:TCTGACGACTGTTGCCAGAC | 187 | 109.4 | 0.997 |
| TRINITY\_DN18757\_c0\_g2 | F:TCAACGTCGGTCTGTCTGTG  R:ACGTACTGGCCCTGTTTGAG | 208 | 105.5 | 0.997 |
| TRINITY\_DN26187\_c0\_g1 | F:GGGCGAGGACAAATCAGGAA  R:AGCCATTTCAGAGGGAAGGC | 160 | 96.7 | 0.996 |
| TRINITY\_DN21780\_c1\_g1 | F:TGGCCGAACAGACCAAAGTT  R:ATGAGCAAAGCCACCGTGTA | 235 | 94.2 | 0.998 |
| TRINITY\_DN22610\_c0\_g2 | F:TTATGACGACTGTCCACGCC  R:TGCCAGTCAATTTGCCGTTG | 171 | 99.5 | 0.998 |
| TRINITY\_DN27207\_c0\_g1 | F:GCAATGAATAAGCTGGGCGG  R:AGATCATCAGCGTGTGCCAA | 152 | 104.4 | 0.993 |
| TRINITY\_DN27539\_c3\_g1 | F:ATTGCATCCTGGGGTTGGAG  R:CGTAGTAGCTGGTGCCGTAG | 186 | 93.4 | 0.993 |
| TRINITY\_DN18927\_c0\_g1 | F:AAACTTTGGATGCGATGGCG  R:ACAGCGCTTCTTCATCACCA | 182 | 96.3 | 0.999 |
| TRINITY\_DN22377\_c1\_g1 | F:TCCACGTCGATCTGCAAACA  R:GCCATCGCAATGTCTTCGTC | 208 | 99.2 | 0.994 |
| TRINITY\_DN26090\_c0\_g1 | F:TGCAACTCTGGCGGAAATCT  R:CGATGTTGCCGTTGACGATC | 158 | 94.5 | 0.991 |
| TRINITY\_DN19691\_c0\_g1 | F:ACGCCACTGACCTGGAAAAT  R:TCCCAGATGTTGATTGCGCT | 214 | 105.9 | 0.995 |
| TRINITY\_DN25425\_c0\_g4 | F:AATGTGTGTAGCTGACGCCA  R:GCGTCTCATCAAACCTCCCA | 163 | 108.5 | 0.994 |
| TRINITY\_DN27537\_c0\_g1 | F:TTGAAGACTCACCGAACGGG  R:TGCTGGCAACCCAAATAGCT | 158 | 99.8 | 0.993 |
| TRINITY\_DN20229\_c0\_g1 | F:TGCAGTGGAGATTGGAGCAG  R:TGTTGACGCCATTAGCCACT | 237 | 96.9 | 0.999 |
| TRINITY\_DN22439\_c0\_g5 | F:CTGCGGAAATCGAATCTGGC  R:GTCTTGGGGAGTTGGGACAG | 185 | 102.3 | 0.998 |
| *TUB* | F:CTTACCACCCCCACATACGG  R:ATTGCTGACTGCCTCTGGAC | 179 | 97.8 | 1.000 |
| *PRS18* | F:CATCGCTCTGTCCTCGGTAC  R:TCGGTGTGCTTGACATCCAA | 216 | 102.3 | 0.999 |