**Table S6:** Summary of putative pygmy rattlesnake transcripts (male/female genomic coverage<0.1, female-specific expression)

|  |
| --- |
| Pygmy rattlesnake W-linked transcripts confirmed experimentally |
| **Scaffold** | **Female FPKM** | **tblastx E-value** | **tblastx best hit** |
| C206150 | 7.03838 | 5.00E-12 | Agkistrodon contortrix clone E33DIFJ02GN6M2 microsatellite sequence |
| scaffold2801 | 16.1686 | 3.00E-11 | Xenopus (Silurana) tropicalis ubiquitin-conjugating enzyme E2M (ube2m), mRNA |
| scaffold2997 | 14.1922 | NA | No significant similarity found. |
| C235599 | 7.57759 | 0.001 | Micrurus fulvius clone FQ6DGU405FYLBQ microsatellite sequence |
| scaffold3714 | 5.86897 | 1.00E-53 | Trimeresurus flavoviridis HLP gene for HSF-like protein, partial cds, exon 1, intron 1, exon 2, L1-like LINE gene for L1-encoded reverse transcriptase-like protein, complete cds |
| scaffold7127 | 9.87032 | 1.00E-71 | Fejervarya limnocharis isolate NA0083 28S ribosomal RNA gene, partial sequence |
|  |  |  |  |
| Putative pygmy rattlesnake W-linked transcripts, not tested experimentally |
| **Scaffold** | **Female FPKM** | **tblastx E-value** | **tblastx best hit** |
| scaffold5225 | 3.85042 | NA | No significant similarity found\*\*\* |
|  |
| Parasite-derived transcript |
| **Scaffold** | **Female FPKM** | **tblastx E-value** | **tblastx best hit** |
| C216554 | 92.4672 | 2.00E-16 | Goussia balatonica strain 608 28S ribosomal RNA gene, partial sequence |
| scaffold1679 | 6.12184 | 4.00E-81 | Hepatozoon sp. BV1 18S ribosomal RNA gene, partial sequence |
| scaffold4937 | 47.4848 | 3.00E-139 | Sarcocystis rileyi 28S ribosomal RNA gene, partial sequence |
|  |  |  |  |
| Putative W-linked transcripts shown to be autosomal |
| **Scaffold** | **Female FPKM** | **tblastx E-value** | **tblastx best hit** |
| C215941 | 6.13881 | 0.046 | Trimeresurus flavoviridis vascular endothelial growth factor A190 isoform precursor, gene, complete cds |
| scaffold488 | 27.2288 | 1.00E-20 | Pantherophis guttatus HOXC13 (HoxC13) gene, complete cds; and HOXC12 (HoxC12) gene, partial cds |

\*\*\*mainly composed of CTTT repeats