

2 GENOME REOURCES SUMMARY ARTICLE

Table 1 (Continued)

Species (no. of individuals)	Data type	Resources	Authors
<i>Culex pipiens form molestus</i> (10), <i>Culex pipiens form pipiens</i> (10)	SNP discovery & validation	SNPs: NCBI SNP Database: dbSNP Accession nos. ss947844444–ss947844519 Annotated consensus sequence data, gene ontologies, genetic map locations, supercontig information, and validation results: Dryad: doi: 10.5061/dryad.9fg6h	
<i>Drosophila nigrosparsa</i> (2 for each of 22 developmental & physiological stages except 150 pooled for eggs and 1st instar larvae)	Transcriptome sequencing, assembly and annotation	Transcriptome sequence data: NCBI Sequence Read Archive: PRJNA232118 Sequence assembly and annotations: Dryad doi: 10.5061/dryad.0mv56	Wolfgang Arthofer, Francesco Cicconardi, Nicola Palmieri, Viola Nolte, Christian Schlötterer, Birgit C. Schlick-Steiner, Florian M. Steiner
<i>Rhinella marina</i> (5), <i>R. schneideri</i> (5)	Transcriptome sequencing, assembly and SNP discovery	Transcriptome sequence data: NCBI Sequence Read Archive: PRJNA255079, SRP044269 Sequence assembly: Dryad doi: 10.5061/dryad.3jm3n SNPs: .vcf file available on Dryad under the Accession: doi: 10.5061/dryad.3jm3n	Coralie Nourissona, Miguel Carneiro, Marcelo Vallinoto, Fernando Sequeira
<i>Sceloporus occidentalis</i> (1) and 34 other <i>Sceloporus</i> species (1 per spp.)	Partial genomic sequence assembly and annotation	Sequence data: NCBI Sequence Read Archive: SRP041983 Sequence assembly and annotations: Dryad doi: 10.5061/dryad.n2q7f	R B. Harris, B L. Banbury, A D. Leaché

Supporting Information

Additional Supporting Information may be found in the online version of this article:

Appendix S1 *De novo* transcriptome assembly of the mountain fly *Drosophila nigrosparsa* using short RNA-seq reads.

Appendix S2 Comparative genomic resources for spiny lizards (genus *Sceloporus*).

Appendix S3 Identification and assessment of single nucleotide polymorphisms (SNPs) between *Culex* complex mosquitoes.

Appendix S4 *De novo* transcriptome assembly and polymorphism detection in ecologically important widely distributed Neotropical toads from the *Rhinella marina* species complex (Anura: Bufonidae).

Appendix S5 Transcriptomic resources for three populations of *Conus miliaris* (Mollusca: Conidae) from Easter Island, American Samoa and Guam.