**Supplemental Figures:**

**Supplemental Figure 1:** Karyotypes for *S. ariasae* (female, TG1241), *S. plummeri* (male, TG1244), and *S. streptophorus* (female, TG1247)—relative to the 17 assembled linkage groups in the *S. townsendi* genome—chromosome length bar chart and HiC contact map shown. Karyotype methods outlined in Main et al. 2012.
Supplemental Figure 2: *Sphaerodactylus* species with M/F WGS data. Comparing M/F read depth across sex chromosome linkage groups in each species LG3: *S. townsendi*, *S. nicholsi*, and *S. klauberi*; then LG1 for *S. notatus*, respectively.
Supplemental Figure 3: *Sphaerodactylus townsendi*, male nucleotide diversity calculated from RNAseq data using vcf tools. *S. townsendi* male-specific RADtags mapped to LG3 are denoted by orange ticks along the bottom of each graph. Grey horizontal line indicates the genomic mean value.
Supplemental Figure 4: *Sphaerodactylus inigoi*, comparison between M/F Fst values with RADseq (top) and RNAseq (bottom) data for *S. townsendi* LG3. Red line indicates the ‘autosomal’ mean (all other chromosomes except LG1 and LG3). Blue ribbon (top only) indicates the 95% confidence interval (μ + 2*σ).
**Supplemental Figure 5:** *Sphaerodactylus inigoi*, comparison between M/F Fst values with RADseq (top) and RNAseq (bottom) data for *S. townsendi* LG1. Red line indicates the ‘autosomal’ mean (all other chromosomes except LG1 and LG3). Blue ribbon (top only) indicates the 95% confidence interval ($\mu + 2\sigma$).
Supplemental Figure 6: *Sphaerodactylus macrolepis*, examination of M/F Fst values with RNAseq data across *S. townsendi* LG1 (top) and LG3 (bottom). Red line indicates the ‘autosomal’ mean (all other chromosomes except LG1 and LG3).
Supplemental Figure 7: Synteny of Sphaerodactylus sex chromosomes LG1 + LG3, the sex chromosomes linkage group in *Sphaerodactylus townsendii* relative to other squamates *Podarcis* and *Anolis*, and an outgroup, *Gallus*. Synteny plot generated using MCScanX and SynVisio, and silhouettes for *Podarcis*, *Anolis*, and *Gallus* were obtained from PhyloPic (*Anolis* by Sarah Werning and *Gallus* by Steven Traver).
### Supplemental Table 1: Assembly stats

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### Transcriptomes/Annotation

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**Supplemental Table 2: Comparative Lepidsaur genome information.**

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## Supplemental Table 2: Comparative Lepidosaur genome information.

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