Supplemental Figure Captions

Figure S1. *Bembidion* sp. nr. *transversale* genome size estimates (in Mb) from GenomeScope and CovEST at different values of K. Values of K not connected by letters are significantly different (p-value > 0.05) based on a Tukey-Kramer HSD test.

Figure S2. *Chlaenius sericeus* genome size estimates (in Mb) from GenomeScope and CovEST at different values of K. Values of K not connected by letters are significantly different (p-value > 0.05) based on a Tukey-Kramer HSD test.

Figure S3. *Lionepha tuulukwa* genome size estimates (in Mb) from GenomeScope and CovEST at different values of K. Values of K not connected by letters are significantly different (p-value > 0.05) based on a Tukey-Kramer HSD test.

Figure S4. *Pterostichus melanarius* genome size estimates (in Mb) from CovEST at different values of K. Values of K not connected by letters are significantly different (p-value > 0.05) based on a Tukey-Kramer HSD test.

Figure S5. Average per-base read coverage for the first 200 bases in loci of the Regier set for four specimens (*Bembidion* sp. nr. *transversale* DNA2544, *Chlaenius sericeus* DNA4821, *Lionepha* *tuulukwa* DNA3782, and *Pterostichus* *melanarius* DNA3787). The blue line indicates 75 base positions from the start of the locus. Based on the decrease in coverage in the bases closer to the start, this value was chosen as the cut-off for calculating coverage values: the coverage values used in genome size estimates were calculated after removing 75 base positions from the start and end of each fragment.

Figure S6. Relative red fluorescence and the number of nuclei counted at each level fluorescence level of representative *Chlaenius sericeus, Lionepha tuulukwa,* and *Pterostichus melanarius*. Bars around each peak represent statistical gates that provide the total nuclei in that peak, average channel number of nuclei in the peak and the coefficient of variation (CV). *D. virilis* standard 1C=328 Mb.

Figure S7. Percent of reads inferred to contain repetitive elements as inferred by RepeatExplorer from a sample of 500,000 read pairs for each of eight beetle species, with reads classified to major group of repetitive elements.

Figure S8. Smudgeplot results for *Bembidion* sp. nr. *transversale*.