H66 Mendelian Simulation of Short Tandem Repeat (STR) Genotypes From Existing Sample Data to Create Standard Truth Pedigrees for Benchmarking New Familial Inference Methods

Stephen Turner*, Signature Science, Charlottesville, VA 22911; Chris Hulme-Lowe, PhD, Signature Science LLC, Austin, TX 78759; Chris Simpson, Charlottesville, VA 22911; Carlos Acevedo, MS, Signature Science, Charlottesville, VA 22911

THIS ABSTRACT WAS NOT PRESENTED.