Supplementary Text File 1

The depicted alignment derives from a comparison of the NLGN4X and NLGN4Y exon 6 sequences from the Mongolian gerbil (Mun). Within exon 6 a length polymorphism was identified that served as a basis for a sex-typing strategy to infer the biological sex. The flanking oligonucleotides that serve as a primer pair are depicted with an underscore.

 1 80

NLGN4X\_Mun GCCTGTTCCAGAAGGCCATCATCCAGAGCGGCACCGCACTGTCCAGCTGGGCTGTCAACTACCAGCCGGCGGCGTATGCG

NLGN4Y\_Mun GCCTGTTCCAGAAGGCCATCATCCAGAGCGGCACCGCACTGTCCAGCTGGGCTGTCAACTACCAGCCGGCGGTGTATGCA

 81 160

NLGN4X\_Mun CGCATGCTCGGAGCCCGTGTAGGCTGCGGAGGAGACATGACGTCGGCGACCTCGCCCCCGGACACCATGGCGACGCCTCC

NLGN4Y\_Mun CGCATGCTCGGGGCCCGTGTGGGCTGCGGGGGAGACGTGATGTCGGCGACCCCGCTCCCGGACGCTGCGGCGACGCCACC

 161 240

NLGN4X\_Mun CTTGACGTCCTCGGTGCACGACCCGCCCTCCCCGTCAGCTGCGCTAGTGGCCTGCCTCCGCCGCCGAGGCGCCCGCGAGC

NLGN4Y\_Mun CCGGATGTCCTCGTCTCACGATCTGCCTTCCGCATCAGCTGCGCTAGTGGCCTGCCTCCGTCGCCGTGGGGCCCGCGAGC

 241 320

NLGN4X\_Mun TGACCCGGGCTGCGGGTTCGGTACCCGCGTCCGCGCCCTTCCACGTGGCCTTCGGGCCAGTGATCGATGGTGATGTGGTG

NLGN4Y\_Mun TGACCCGGGCCGCGGGTTCGGTGCCCGCGTCCTCACCATTCCATGTGGCCTTCGGGCCAGTGATCGATGGAGATGTGGTG

 321 400

NLGN4X\_Mun CCTGACGACCCGCAGATCCTCATGGAGCAGGGTGAGTTCCTCAACTACGACATCCTTCTGGGCGTCAACCAGGCGGAGGG

NLGN4Y\_Mun CCGGACGACCCGCAGATCCTCATGGAGCAGGGTGAGTTCCTCAACTACGACATCCTTCTGGGCGTCAACCAGGCGGAGGG

 401 480

NLGN4X\_Mun CGTGGCCCTGGCCGACCCCGCCCACCCGGACGGCGGCGGCGACGTCACAGCGGATGGCGAAGAGGAGGAGGAGGTGTCGG

NLGN4Y\_Mun CGTGGCCCTGGCAGACCCCGCCCACCCCGACAGCCTCGGGGATATAATGGCTGACGGTGA------GGAGGAGGTGTCGG

 481 560

NLGN4X\_Mun CTGCAGGCTTCGAACTCGCTGTTGCCGCCTTCGTGGATGCGCTGTACGGCTACCCGGGAGGGGATGTGGGCGTGGCCGGA

NLGN4Y\_Mun CTGCCGGCTTCGAACTCGCTGTTGCTGCCTTCGTGGATGCGCTGTACGGCTACCCAGGAGGGGATGTGGGCGTGGCCGG-

 561 640

NLGN4X\_Mun CTGGGCGGGGGCGTGGCCGGCTGGGGCAGTGGAGCTGGCGGGGACTCGGCCCTTCGCGAGACGGCGCGCTTCATGTACAC

NLGN4Y\_Mun --------------------CTGGAGCGGTGGAGCCGGCGGGGACTCCGCCCTTCGCGAGACGGCGCGCTTCATGTACAC

 641 720

NLGN4X\_Mun GGACTGGGCGGAGCGCGAGGGCGGGGCGGGGTCACGGCGCCGCGCCCTGGCGGCCATGATGACGGACCACCAGTGGGCGG

NLGN4Y\_Mun GGACTGGGCGGAGCGCGAGGGCGGGGCGGGGTCACGGCGCCGCGCCTTGGCGGCCATGATGACGGACCACCAGTGGGCGG

 721 800

NLGN4X\_Mun CGCCCGCCGTGGCCACCGCGGACTTGCACGCCCGGTACGGCTCGGCCACCTACTTCTACGCCTTTGCACACCCGTGTCGG

NLGN4Y\_Mun CGCCCGCCGTGGCCACGGCCGACTTGCACGCCCGGTACGGCTCGGCCACCTACTTCTACGCCTTTGCACACCCGTGTCGG

 801 880

NLGN4X\_Mun GGGGACGCGCACCCCGCCTGGGCGGCCGAAGCGGGCGCGGCTCATGGTGACGAGCTGCCCTTCGTGTTCGGGGTCCCGAT

NLGN4Y\_Mun GGGGACGCGCACCCCGCCTGGGCGGCCGAAGCGGGCGCTGCCCATGGCGACGAGCTGCCCTTCGTATTCGGGGTCCCGAT

 881 960

NLGN4X\_Mun GCTCGTGCTGGCGGCGGCCGGGGGTGGG---GTTGGAGGAGTCGGAAGCGAGGGCGCGGCCGGAAGTGACGTCGCCGTGG

NLGN4Y\_Mun GCTCGTGCTGGCGGCGGCCGGTGATGGCAGTGTCGGAGGAGTCGGAGGCGAAGGCGCAACGGGAACTGATGTCGCTGCGG

 961 1040

NLGN4X\_Mun CCACCGCCGCCAATGCTGCCGCCCTCTTCCCGTGCAACTTCACGCGTAATGACGTAATGCTCAGCGCCGTCGTCATGACG

NLGN4Y\_Mun CCACCGCCGCT---------GCCCTCTTTCCATGCAACTTCACGCGCAATGACGTGATGCTCAGCGCCGTCGTCATGACG

 1041 1066

NLGN4X\_Mun TACTGGACCAACTTCGCCAAGACGGG

NLGN4Y\_Mun TACTGGACCAACTTCGCCAAGACCGG