**S1 File. Nucleotide sequence of genomic insertion site for Model I lines.**  Sequence of flanking genomic region and the predicted genome mapping insertion site of the transgene for both Model I lines.

**GenomeWalker insert sequence Model I line 1**

>GenomeWalker flanking sequence

CTTGTAGTTTTCAGAGTACAGGTCTTATGTTTCTTTAGGTAGGTTTACTCCTAGGTATTTTATTCTTTTGGATGGTGCAGTAAACAGGATTGCTTCCCTAATTTCTCTTTCTGATCTTTCATTGTTAGTGTATAGAAATGCAGTCGATTTCTGTGCCTTAACTTTGAATCCTGTGACTTTGCCAAATTCATGGATGACCTCTAACAGTTTTCTGGTAGAGTCTTTAGGATTCTCTAGGTATAGTATCATATCATCTCCAGTGATAGTTTTACTTCTTCCTTTCCAATTTGGATTCCTTTTATTTCTTTTACTCCTCTGATTTCTTTTACTCCTCTGATTGCTGCTAAGAATTTGTCCATTTCTTCTAGGTTTTCCATTTTATTGGCGTATAGTTGCATATAGTAGTCTCTTATGATCCTTTGTATTTTGGTGATGTCCATTGTTATTTCTCCTTTTTCATTTCTAATTTTATTGATTTTAGGACTTCCAAAACTATGTTGAAGTGTAGTGGCAAGAGCGGACATCCTTGTCTTGTTCCTGATCTCAGTGGGAATTCTTTCAGCTTTTCACCATTGAGAATGATATTCTCTGTGGGTTTCTTATATATGGCCTTTATGGTGTTGATGTAGCTTTCCTCTATGCCCACTTTCTGAAGGGTTTTTATCAGAAATGTGTGTTGGATTGTGTCAAATGCTTTCTCCGAGTCTATTGAGAGGATCATGTGGTTTTTATTCTTTAGTTTGTTAATGTGGTGTATCACAATGATTGATTTGCGAATATTGAAGAACTCTTGCATCTCTGGGATAAATCCTACTTGATCAAGATGTACAATCCTTTTAATGTATTTTGAATGAGGTTTGCTAATATTTTGTTGAGGATTTTTGCATTGAGTCATAANAAATTTTTCTCTACACTGAAGTCTTGATGGCATGCTTCTATATTATTTTCTAAAAGATTTAAAGTTTTGCCTTCTCCATTTAGACTTATAATTCACTGGAATTTTTTTGTGTGTATGGTATGACATATGGGTTCCCTTTTATTTTTTACATATAAATATATTTCCCTGTTTTTCTAAAAAAGAAAAAGACCATCATTTTCCCATTGTAAAATGCCATATTTTTTTCATAGGTCACTTACATATATCAATGGGCCTGTTTCTGAGCTCTACTCTATTTTA

Mapped to <http://useast.ensembl.org/Sus_scrofa/Location/View?db=core;r=1:25368175-25427711;tl=l8Jow023VfD7h62x-1889388-483094307>

**Whole Genome flanking Sequence Model I Line 2**

**Identified sequence**

> Scaffold GL896235 adjacent to human interferon-β matrix attachment regions

AGGGTCCTGGGGTGGGCGAGGCCAGGCCGTCCTGGCAGAGGAACAGCTCTGCGCAGGTCGGACACCCTTGCTGCCCCGTCCCTGTCAGTGATGCCAGGCCCGCTCACTGTCACCTGAGGGAGGGCCGCAGGTCTAAGCCAGCCATGCCACCCGCTGCCCTGTCCCTCTGCCCCCGAGGCCTCCTCCCAGAACCACTGGCCGCG

**Mapped to unassigned GL896235.1. Insertion at 400 bp location of sequence below**

>GL896235.1:14334-15134|insert\_at\_400bp\_of\_this\_fragment

GTGCATGCTCCCGTTGGCCACTCACAGCTGGCACTTTGTGTCCTCAGCTATTGCCTCTGGAGCCTCGTCCTTTGACTTCAGGGGTTCCCCATGTGCCCGGTGGCGTTGTGGTCCACTGTGGGCTTGGGGGACAGTGACCAGACAGAGCTTGGGGTGTGCGTTTCGCCCAACAGAGCCTGCAAGCCAGGAGGGAGCCGCGGCCAGTGGTTCTGGGAGGAGGCCTCGGGGGCAGAGGGACAGGGCAGCGGGTGGCATGGCTGGCTTAGACCTGCGGCCCTCCCTCAGGTGACAGTGAGCGGGCCTGGCATCACTGACAGGGACGGGGCAGCAAGGGTGTCCGACCTGCGCAGAGCTGTTCCTCTGCCAGGACGGCCTGGCCTCGCCCACCCCAGGACCCTGGTGCCGGCAGAGGGGCTTTCAGCGAGATCCGCTGGTGACTGGATGTGTGGTGGGCGGCAGAGACGGGTGGGGTGNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNGCAGAGGAGAGAGTCAGGGAGGCAGAGGGTCAGATGCCTCTCAGACACCCACCGGGAGGCGCTCAGAAGGGCCCTAGAGCAGGAGTGTCGGCCCTCCTGGTGGGAGAACCCACGGGGGGCAGAGGGGGGAATGAGTGCCGGGGGCGCCTCAGGGGAGGTGACCTGGGGCCAGAAACGAGGATGAGGGTGACCCAGGGCAGGAGGAGGCTGTGCAAAGGCCCTGAGGC