**Supplementary Document 1. The DNA sequences involved in the construction of Red Light/Green Light vectors.**

***A. EcoRI-AscI DsRed.T4.NLS cassette with Hsp70 promoter and polyadenylation signal***

GAATTCCATTAACGCTTACAATTTACGCCTTAAGATACATTGATGAGTTTGGACAAACCACAACTAGAATGCAGTGAAAAAAATGCTTTATTTGTGAAATTTGTGATGCTATTGCTTTATTTGTAACCATTATAAGCTGCAATAAACAAGTTAACAACAACAATTGCATTCATTTTATGTTTCAGGTTCAGGGGGAGGTGTGGGAGGTTTTTTAAAGCAAGTAAAACCTCTACAAATGTGGTATGGCTGATTATGATCTAGAGTCGCGGCCGGCCGCTGTACAAGTAGCGTCTTCGTTCACTGCTGCGACTTCGGCTCCGTTGACGGCGTTTTCGTTCACTGCTGCGACTTCGGCTGCGATTGCGGCTCCTAGAGCGCTGGCGATGCCTTCTGTGCCTGCTCTTGTACAGGAACAGGTGGTGGCGGCCCTCGGCGCGCTCGTACTGCTCCACGATGGTGTAGTCCTCGTTGTGGGAGGTGATGTCCAGCTTGGAGTCCACGTAGTAGTAGCCGGGCAGCTGCACGGGCTTCTTGGCCATGTAGATGGACTTGAACTCCACCAGGTAGTGGCCGCCGTCCTTCAGCTTCAGGGCCTTGTGGATCTCGCCCTTCAGCACGCCGTCGCGGGGGTACAGGCGCTCGGTGGAGGGCTCCCAGCCCATAGTCTTCTTCTGCATTACGGGGCCGTCGGAGGGGAAGTTCACGCCGATGAACTTCACCTTGTAGATGAAGCAGCCGTCCTGCAGTGAGGAGTCCTGGGTCACGGTCACCACGCCGCCGTCCTCGAAGTTCATCACGCGCTCCCACTTGAAGCCCTCGGGGAAGGACAGCTTCTTGTAGTCGGGGATGTCGGCGGGGTGCTTCACGTACACCTTGGAGCCGTACTGGAACTGGGGGGACAGGATGTCCCAGGCGAAGGGCAGGGGGCCGCCCTTGGTCACCTTCAGCTTGGCGGTCTGGGTGCCCTCGTAGGGGCGGCCCTCGCCCTCGCCCTCGATCTCGAACTCGTGGCCGTTCACGGAGCCCTCCATGCGCACCTTGAAGCGCATGAACTCCTTGATGACGTCCTCGGAGGAGGCCATGGTGGCGACGGGTGAAGGGCGAATTAAACAGGCCTCTCTCGACTCTAGCGCGTACCCTAGAGGATCAGCTTGGCTGCAGATTGTTTAGCTTGTTCAGCTGCGCTTGTTTATTTGCTTAGCTTTCGCTTAGCGACGTGTTCACTTTGCTTGTTTGAATTGAATTGTCGCTCCGTAGACGAAGCGCCTCTATTTATACTCCGGCGCTCGGCGCGCC

***B. AscI-AgeI cassette with dimorphic element core, 1kb spacer, and Hsp70 promoter***

GGCGCGCCCCGCGGCTCTTTCTCTTTGCCATTTTAACTTTTATTACTCTTAATATAAAAAAGCTGGCTAGATGCGGGCCAGCTGTAAAAATGCACGCGGTCATAAAAAGTTGCAGGAGGCATGTTGCCAGTTGCCTGCAACCGGCAACATTCGCAGAACAGCAGCAACATCGTAAAATAACTTCTTGCTCTGCGGTCTGAGTTTGGCCGCAACAATGTTGCTGCATTTATTCGTATTATTATTACATTTTAATGAATAATTCTAATTATATGCAACTTGAATAAGCCCGCCGATGCCAATAAAAAGCGGCGTGGCAAAGTGGAGTGGACTGGGTTTGTGTGGCGCCCCTGCTAGTGGCACATAAAAATTGGCGCAAGTTAATTGTGGTAGTTATTTGCTGTTTTGCCATTTGGTCATTTTACAATTTTACCATTTCAGCCACAACTTTTCGCACTGCTCCCCCCCTTTCCCAGCACAACAATGTTGCGGCATTCTCGCACTTTACGAGGCGTTTTTTTTTTATATCACTTACTTTACTTAGTTGATTAAGGGCGTGGCCGATGGGCCAGATACATGCTTAGATTTGCTCCAGCAGTGGGCTGCATTTTACGACCCTCAAAACCCGATCCAAATGGAAAATATGAAAATACGGCTAATCCGCTTATGAGCACAACAAATTGGTTCACACACGCTAGCCCTGCAGGACCACTAGCAACTGGCTCGACGATCATCGGCCCACACCGAACCGATGAATGTCAGATTAGGACAGAGTAATAGAAACTTTTGTGCGGGCAATGAGTTACAGAGACTGAGGCATCCACGACTCCTGATGCCGAGATAGAGCGTAAGAGGGAGAGTTCCATCTCCTATGACGCTAACTCTGTCAGAGTGTGTGTGTCAGTGTAACTCTAATCCTGTAACACTGTCACAGAGAGTGTGAGGAACTAAGACTTATGAACTATAATACATATACACAGAAAGACACACTACCACTCAGGCAGCGAGCTAGTGTCGACACCGCTCTGTGCGGGGAATAACAAGTACTTAGGTTCACGACTGGCATCCCCCGTCGTGCAACCCCAAACGGCCCCACAGGATACCTCGCAAGCACTAACCAGAATGACCCCGTACTGTAACTAAACGCGTTGGCCCAGCATCTTGCAGTTTCATTCGCACAGCGCAACAACGCAGCTGGGTAGCGGCCATTATACGTGTTCCGACAGAATCTTTTGCGAACAGCGCGGAGTGCATACATATCTGACTATGCGCGAACAAACTTGCAAGGGTTCCTTTGCGAAAGGGCAGGATTTAACTAAGTACTGTCCAGGTCAAATATTGAGTTTGTGGGTGTATTGCAAAATATCTCGGAGCCAGGATCGCAGAAGTACTCTCGGGGCCTTAAAGCCCCTATGAGCACTTCAGACTGAATACTGCTCCGACTACGCTGGCATAGCTCAGCACGTCTCTCTACTAGGGCAGCCACAAACAACTATGAACACGCTAGTAGACTTACTTGTATATATAGAGATAAGTACGAATCTCGGAGCCCGAGAATTTAAATCTCGGAATCCGAATACGCGCGATACCCAGAGAGATGCGCGCGCGCGCGCGCGCGGACGCGCGTGTGGGATACTGGTACTGGAATACTGGCATATTATGCGCGTCAATTGAAGAGGGAATCAATGATACACCTAGTAAAACCCTCTTACTCAGTTACACCCACATTCCTACATTGAGCGTGACGTACGCTTACAGAAACATAGACAAGGGCACTGTCATTGGATGATAGTAAATAAAAGATCTGGATCCGAGCGCCGGAGTATAAATAGAGGCGCTTCGTCTACGGAGCGACAATTCAATTCAAACAAGCAAAGTGAACACGTCGCTAAGCGAAAGCTAAGCAAATAAACAAGCGCAGCTGAACAAGCTAAACAATCTGCAGCCAAGCTGATCCTCTAGGGTACGCGCTAGAGTCGAGAGCTCGAGAGCCCTGTTTAATTCGCCCTTCACCGGT

***C. StuI-AgeI cassette with Hsp70 promoter flanked by StuI and BamHI sites, 2kb spacer flanked by BamHI-BglII sites, dimorphic element core flanked by AscI and SacII sites on one side and NheI and SbfI sites on the other, and a second Hsp70 promoter flanked by XhoI and AgeI sites.***

AGGCCTCTCGACTCTAGCGCGTACCCTAGAGGATCAGCTTGGCTGCAGATTGTTTAGCTTGTTCAGCTGCGCTTGTTTATTTGCTTAGCTTTCGCTTAGCGACGTGTTCACTTTGCTTGTTTGAATTGAATTGTCGCTCCGTAGACGAAGCGCCTCTATTTATACTCCGGCGCTCGGATCCAGTTACAGAGACTGAGGCATCCACGACTCCTGATGCCGAGATAGAGCGTAAGAGGGAGAGTTCCATCTCCTATGACGCTAACTCTGTCAGAGTGTGTGTGTCAGTGTAACTCTAATCCTGTAACACTGTCACAGAGAGTGTGAGGAACTAAGCATTAGTAACTATAATACATATACACAGAAAGACACACTACCACTCAGGCAGCGAGCTAGTGTCGACACCGCTCTGTGCGGGGAATAACAAGTACTTAGGTTCACGACTGGCATCCCCCGTCGTGCAACCCCAAACGGCCCCACAGGATACCTCTCTAGCACTAACCAGAATGACCCCGTACTGTAACTAAACGCGTTGGCCCAGCATCTTGCAGTTTCATTCGCACAGCGCAACAACGCAGCTGGGTAGCGGCCATTATACGTGTTCCGACAGAATCTTTTGCGAACAGCGCGGAGTGCATACATATCTGACTATGCGCGAACAAACTTGCAAGGGTACCTTTGCGAAAGGGCAGGATTTAACTAAGTACTGTCCAGGTCAAATATTGAGTTTGTGGGTGTATTGCAAAATATCTCGGAGCCAGGATCGCAGAAGTACTCTCGGGGCCTTAAAGCCCCTATGAGCACTTCAGACTGAATACTGCTCCGACTACGCTGGCATAGCTCAGCACGTCTCTCTACTAGGGCAGCCACAAACAACTATGAACACGCTAGTAGACTTACTTGTATATATAGAGATAAGTACGAATCTCGGAGCCCGAGAATTTAAATCTCGGAATCCGAATACGCGCGATACCCAGAGAGATGCGCGCGCGCGCGCGCGCGGACGCGCGTGTGGGATACTGGTACTGGAATACTGGCATATTATGCGCGTCAATTGAAGAGGGAATCAATGATACACCTAGTAAAACCCTCTTACTCAGTTACACCCACATTCCTACATTGAGCGTGACGTACGCTTACAGAAACATAGACAAGGGCACTGTCATTGGATGATAGTAAATAAACTGGCACTCTCAGTCTTACGAACATCAGAAGTCGTAATCTCGCTCTATGCCTCTTTCTCTGGAACGAGAAGCGTCATAGCCAGAGTGACTCTGTGTGTGTGACTGTGCCAGAGCCGAAGTGCCACAGTGACACTCTCTGTGTCTTCCAGCCTCAGGCTGCCAGCGCCGCACGCGCACACTCCCTCACACAGCAACAGACTTACTATCTAGCTGTGATCACAATAGAGTGTATTTTCCGCCAACTGCAGGCTTGGACATCAGTTACGAAAAATGATGTACCAAAACCCATTAAAACACTTCGCAAGATAGCTACAGCCAACTCCGTCAAAATGCAGTGCCAGCCCATATGGTTAAACTACGAGGTACTGGGACGGATACACTATACCACCATTCTAGTTTGCTATTAACGGCGCATGTGGAATCACTCCGAGGGGTATCCACTATATTCTGTACGCACGCGAGTCAGCGTATATCCACCCAGGTACCTTTGCAAGGGTATCCCTTTACTTCGGGCCAGCCTGCAGTGAACTTGACCAGCGGTCTGGGTGTTTGTGCGGTACCCCGCGAGATTCTAACTTCGATACTCCTGCAGAGATTTTAAGGCCCTAAAAGCGTCTACAGGACTCAGTCCGCAGTAGAATCAGCATAGTTACGCTAGACTACATGAGAGAGCAGCTTTACTAACACCCACCAGCGTCCACATAGCTGCTCAGGCAGGTGCGCGCGCTCTCGCCTGCATCCGAGATTCTAAATCTCCGGGCCCGAGATTCCGAATCCGCATATATCGCAAACTCTCTCGTATATATATATATATATATTCATATATGTGTTTCGCAGTTGCAGTTCCGCAGTTACGCGGCGTATATGTCCGGTCCTCTTTCCGACCGTCGCACAAGCTGCCCCAAAGAGGCAGACTGGCACAAACACGGAAGCACGGTCTATGTCATGCATAGGCACTCCCACGCTCACCTTTACAGTGACGGTTCGTCGCTGCCCGCCCAGATCTGGCGCGCCTCGCCTCCGCGGCTCTTTCTCTTTGCCATTTTAACTTTTATTACTCTTAATATAAAAAAGCTGGCTAGATGCGGGCCAGCTGTAAAAATGCACGCGGTCATAAAAAGTTGCAGGAGGCATGTTGCCAGTTGCCTGCAACCGGCAACATTCGCAGAACAGCAGCAACATCGTAAAATAACTTCTTGCTCTGCGGTCTGAGTTTGGCCGCAACAATGTTGCTGCATTTATTCGTATTATTATTACATTTTAATGAATAATTCTAATTATATGCAACTTGAATAAGCCCGCCGATGCCAATAAAAAGCGGCGTGGCAAAGTGGAGTGGACTGGGTTTGTGTGGCGCCCCTGCTAGTGGCACATAAAAATTGGCGCAAGTTAATTGTGGTAGTTATTTGCTGTTTTGCCATTTGGTCATTTTACAATTTTACCATTTCAGCCACAACTTTTCGCACTGCTCCCCCCCTTTCCCAGCACAACAATGTTGCGGCATTCTCGCACTTTACGAGGCGTTTTTTTTTTATATCACTTACTTTACTTAGTTGATTAAGGGCGTGGCCGATGGGCCAGATACATGCTTAGATTTGCTCCAGCAGTGGGCTGCATTTTACGACCCTCAAAACCCGATCCAAATGGAAAATATGAAAATACGGCTAATCCGCTTATGAGCACAACAAATTGGTTCACACACGCTAGCCAAGGGCCTGCAGGCTCGAGGAGCGCCGGAGTATAAATAGAGGCGCTTCGTCTACGGAGCGACAATTCAATTCAAACAAGCAAAGTGAACACGTCGCTAAGCGAAAGCTAAGCAAATAAACAAGCGCAGCTGAACAAGCTAAACAATCTGCAGCCAAGCTGATCCTCTAGGGTACGCGCTAGAGTCGAGAGCCCTGTTTAAACGATCCACCGGT

***D. 1,000 bp bab1 1st intron sequence prior to mutagenesis (for first 2 kb spacer)***

ATTGAAATATAATTATGAAGCAAAGCCGCATTAGGACTATAGATATCTTCATATGTATATTGCAAGCGCATCTTAAGATCAATATTTAATATTTTTTTTTTAATTTTCAATATCAGCATTTCAAAATTTAAAATATATTTTTATGCAATCATAATGATTCAATCTCAGAAAGAGAAAAATACATAAAAAATCCAAATAATGAATCTATCGATTTTAGCCCCAGATATTTTCTGTGCAGACCCATTCCGTCGTTGCCCTAATTGAAGCACACTTAGGGAACCACAACAAGTCACAAAATGCTCCATAGATCGAAATCAACCGCAGGCCACAGGAATTTCAATCACCTCTTGGTCACCGAAGCGTTCCGGTGCCTGCTCCCCGAGAACCCAAGAATCGGTGGATCTGACCTGAGAAGGGGTACTAAATACTATGTGGAGCAAATCTCTGCGGGAAGAAAGAGCGGCCGAGGAGAGCAAACAATGGAACGTGGAACGTGGAGCACGTGAATGCTGTCAATCATTCCGGGCAATGGCCACTCTGGCGGTGGGGTGGGGAGTTCCACAGAGCGCTGCGACCGTAGCTCCGCATTCCGCGCTGTGACGTCACGACACGAGGCGAAATGCCGCCGGCAGAATTCGCAGCCGAAGATTGAAGATCGCCGAAAGGCGCGCGAATCGTGAATCAAAACAAACCGAGGCAAAAGATCGGATAATGAATGGGAGAGAGATATAGACGGAAGCAGCGCTGCGACAGCGCAGTGACAGCGCTGCAGCAGCAGAAGAGAGCTCCACCGCGCGCTTCTCTCTCTCTCTCTCTCTGCCTCTCTTTTTGTAGAATTGGAATTGCAGAATTGAAGAGTCTTCTCTTAACTGGCATATGTACTAACTTAGAAAACGATTCACAACATATGAATAATTGAAAACAAAAGTACGAAAGTTATCTTTAAGGAAGATGAAATACAAAGATAAACGTGAAATTTAAGTTGCTTAGATTCACTCAC

***E. bab1 1st intron sequence with even base pair mutagenesis***

AgTtAcAgAgAcTgAgGcAtCcAcGaCtCcTgAtGcCgAgAtAgAgCgTaAgAgGgAgAgTtCcAtCtCcTaTgAcGcTaAcTcTgTcAgAgTgTgTgTgTcAgTgTaAcTcTaAtCcTgTaAcAcTgTcAcAgAgAgTgTgAgGaAcTaAgAcTtAgTaAcTaTaAtAcAtAtAcAcAgAaAgAcAcAcTaCcAcTcAgGcAgCgAgCtAgTgTcGaCaCcGcTcTgTgCgGgGaAtAaCaAgTaCtTaGgTtCaCgAcTgGcAtCcCcCgTcGtGcAaCcCcAaAcGgCcCcAcAgGaTaCcTcGcTaGcAcTaAcCaGaAtGaCcCcGtAcTgTaAcTaAaCgCgTtGgCcCaGcAtCtTgCaGtTtCaTtCgCaCaGcGcAaCaAcGcAgCtGgGtAgCgGcCaTtAtAcGtGtTcCgAcAgAaTcTtTtGcGaAcAgCgCgGaGtGcAtAcAtAtCtGaCtAtGcGcGaAcAaAcTtGcAaGgGtAcCtTtGcGaAaGgGcAgGaTtTaAcTaAgTaCtGtCcAgGtCaAaTaTtGaGtTtGtGgGtGtAtTgCaAaAtAtCtCgGaGcCaGgAtCgCaGaAgTaCtCtCgGgGcCtTaAaGcCcCtAtGaGcAcTtCaGaCtGaAtAcTgCtCcGaCtAcGcTgGcAtAgCtCaGcAcGtCtCtCtAcTaGgGcAgCcAcAaAcAaCtAtGaAcAcGcTaGtAgAcTtAcTtGtAtAtAtAgAgAtAaGtAcGaAtCtCgGaGcCcGaGaAtTtAaAtCtCgGaAtCcGaAtAcGcGcGaTaCcCaGaGaGaTgCgCgCgCgCgCgCgCgCgGaCgCgCgTgTgGgAtAcTgGtAcTgGaAtAcTgGcAtAtTaTgCgCgTcAaTtGaAgAgGgAaTcAaTgAtAcAcCtAgTaAaAcCcTcTtAcTcAgTtAcAcCcAcAtTcCtAcAtTgAgCgTgAcGtAcGcTtAcAgAaAcAtAgAcAaGgGcAcTgTcAtTgGaTgAtAgTaAaTaAa

***F. bab1 1st intron sequence with odd base pair mutagenesis***

cTgGcAcTcTcAgTcTtAcGaAcAtCaGaAgTcGtAaTcTcGcTcTaTgCcTcTtTcTcTgGaAcGaGaAgCgTcAtAgCcAgAgTgAcTcTgTgTgTgTgAcTgTgCcAgAgCcGaAgTgCcAcAgTgAcAcTcTcTgTgTcTtCcAgCcTcAgGcTgCcAgCgCcGcAcGcGcAcAcTcCcTcAcAcAgCaAcAgAcTtAcTaTcTaGcTgTgAtCaCaAtAgAgTgTaTtTtCcGcCaCcTgCaGgCtTgGaCaTcAgTtAcGaAaAaTgAtGtAcCaAaAcCcAtTaAaAcAcTtCgCaAgAtAgCtAcAgCcAaCtCcGtCaAaAtGcAgTgCcAgCcCaTaTgGtTaAaCtAcGaGgTaCtGgGaCgGaTaCaCtAtAcCaCcAtAcTaGtTtGcTaTtAaCgGcGcAtGtGgAaTcAcTcCgAgGgGtAtCcAcTaTaTtCtGtAcGcAcGcGaGtCaGcGtAtAtCcAcCcAgGtAcCtTtGcAaGgGtAtCcCtTtAcTtCgGgCcAgCcTgCaGtGaAcTtGaCcCgCgGtCtGgGtGtTtGtGcGgTaCcCcGcGaGaTtCtAaCtTcGaTaCtCcTgCaGaGaTtTtAaGgCcCtAaAaGcGtCtAcAgGaCtCaGtCcGcAgTaGaAtCaGcAtAgTtAcGcTaGaCtAcAtGaGaGaGcAgCtTtAcTaAcAcCcAcCaGcGtCcAcAtAgCtGcTcAgGcAgGtGcGcGcGcTcTcGcCtGcAtCcGaGaTtCtAaAtCtCcGgGcCcGaGaTtCcGaAtCcGcAtAtAtCgCaAaCtCtCtCgTaTaTaTaTaTaTaTaTaTtCaTaTaTgTgTtTcGcAgTtGcAgTtCcGcAgTtAcGcGgCgTaTaTgAcCgGtCcTcTtTcCgAcCgTcGcAcAaGcTgCcCcAaAgAgGcAgAcTgGcAcAaAcAcGgAaGcAcGgTcTaTgTcAtGcAtAgGcAcTcCcAcGcTcAcCtTtAcAgTgAcGgTtCgTcGcTgCcCgCcC

***G. tandem duplicate bab1 1st intron sequence with odd and even base pair mutagenesis***

AgTtAcAgAgAcTgAgGcAtCcAcGaCtCcTgAtGcCgAgAtAgAgCgTaAgAgGgAgAgTtCcAtCtCcTaTgAcGcTaAcTcTgTcAgAgTgTgTgTgTcAgTgTaAcTcTaAtCcTgTaAcAcTgTcAcAgAgAgTgTgAgGaAcTaAgAcTtAgTaAcTaTaAtAcAtAtAcAcAgAaAgAcAcAcTaCcAcTcAgGcAgCgAgCtAgTgTcGaCaCcGcTcTgTgCgGgGaAtAaCaAgTaCtTaGgTtCaCgAcTgGcAtCcCcCgTcGtGcAaCcCcAaAcGgCcCcAcAgGaTaCcTcGcTaGcAcTaAcCaGaAtGaCcCcGtAcTgTaAcTaAaCgCgTtGgCcCaGcAtCtTgCaGtTtCaTtCgCaCaGcGcAaCaAcGcAgCtGgGtAgCgGcCaTtAtAcGtGtTcCgAcAgAaTcTtTtGcGaAcAgCgCgGaGtGcAtAcAtAtCtGaCtAtGcGcGaAcAaAcTtGcAaGgGtAcCtTtGcGaAaGgGcAgGaTtTaAcTaAgTaCtGtCcAgGtCaAaTaTtGaGtTtGtGgGtGtAtTgCaAaAtAtCtCgGaGcCaGgAtCgCaGaAgTaCtCtCgGgGcCtTaAaGcCcCtAtGaGcAcTtCaGaCtGaAtAcTgCtCcGaCtAcGcTgGcAtAgCtCaGcAcGtCtCtCtAcTaGgGcAgCcAcAaAcAaCtAtGaAcAcGcTaGtAgAcTtAcTtGtAtAtAtAgAgAtAaGtAcGaAtCtCgGaGcCcGaGaAtTtAaAtCtCgGaAtCcGaAtAcGcGcGaTaCcCaGaGaGaTgCgCgCgCgCgCgCgCgCgGaCgCgCgTgTgGgAtAcTgGtAcTgGaAtAcTgGcAtAtTaTgCgCgTcAaTtGaAgAgGgAaTcAaTgAtAcAcCtAgTaAaAcCcTcTtAcTcAgTtAcAcCcAcAtTcCtAcAtTgAgCgTgAcGtAcGcTtAcAgAaAcAtAgAcAaGgGcAcTgTcAtTgGaTgAtAgTaAaTaAacTgGcAcTcTcAgTcTtAcGaAcAtCaGaAgTcGtAaTcTcGcTcTaTgCcTcTtTcTcTgGaAcGaGaAgCgTcAtAgCcAgAgTgAcTcTgTgTgTgTgAcTgTgCcAgAgCcGaAgTgCcAcAgTgAcAcTcTcTgTgTcTtCcAgCcTcAgGcTgCcAgCgCcGcAcGcGcAcAcTcCcTcAcAcAgCaAcAgAcTtAcTaTcTaGcTgTgAtCaCaAtAgAgTgTaTtTtCcGcCaCcTgCaGgCtTgGaCaTcAgTtAcGaAaAaTgAtGtAcCaAaAcCcAtTaAaAcAcTtCgCaAgAtAgCtAcAgCcAaCtCcGtCaAaAtGcAgTgCcAgCcCaTaTgGtTaAaCtAcGaGgTaCtGgGaCgGaTaCaCtAtAcCaCcAtAcTaGtTtGcTaTtAaCgGcGcAtGtGgAaTcAcTcCgAgGgGtAtCcAcTaTaTtCtGtAcGcAcGcGaGtCaGcGtAtAtCcAcCcAgGtAcCtTtGcAaGgGtAtCcCtTtAcTtCgGgCcAgCcTgCaGtGaAcTtGaCcCgCgGtCtGgGtGtTtGtGcGgTaCcCcGcGaGaTtCtAaCtTcGaTaCtCcTgCaGaGaTtTtAaGgCcCtAaAaGcGtCtAcAgGaCtCaGtCcGcAgTaGaAtCaGcAtAgTtAcGcTaGaCtAcAtGaGaGaGcAgCtTtAcTaAcAcCcAcCaGcGtCcAcAtAgCtGcTcAgGcAgGtGcGcGcGcTcTcGcCtGcAtCcGaGaTtCtAaAtCtCcGgGcCcGaGaTtCcGaAtCcGcAtAtAtCgCaAaCtCtCtCgTaTaTaTaTaTaTaTaTaTtCaTaTaTgTgTtTcGcAgTtGcAgTtCcGcAgTtAcGcGgCgTaTaTgAcCgGtCcTcTtTcCgAcCgTcGcAcAaGcTgCcCcAaAgAgGcAgAcTgGcAcAaAcAcGgAaGcAcGgTcTaTgTcAtGcAtAgGcAcTcCcAcGcTcAcCtTtAcAgTgAcGgTtCgTcGcTgCcCgCcC

***H. tandem duplicate bab1 1st intron sequence with odd and even base pair mutagenesis, and NheI, SbfI, SpeI, SacII, and AgeI sites removed by base pair substitutions***

AgTtAcAgAgAcTgAgGcAtCcAcGaCtCcTgAtGcCgAgAtAgAgCgTaAgAgGgAgAgTtCcAtCtCcTaTgAcGcTaAcTcTgTcAgAgTgTgTgTgTcAgTgTaAcTcTaAtCcTgTaAcAcTgTcAcAgAgAgTgTgAgGaAcTaAgAcTtAgTaAcTaTaAtAcAtAtAcAcAgAaAgAcAcAcTaCcAcTcAgGcAgCgAgCtAgTgTcGaCaCcGcTcTgTgCgGgGaAtAaCaAgTaCtTaGgTtCaCgAcTgGcAtCcCcCgTcGtGcAaCcCcAaAcGgCcCcAcAgGaTaCcTctcTaGcAcTaAcCaGaAtGaCcCcGtAcTgTaAcTaAaCgCgTtGgCcCaGcAtCtTgCaGtTtCaTtCgCaCaGcGcAaCaAcGcAgCtGgGtAgCgGcCaTtAtAcGtGtTcCgAcAgAaTcTtTtGcGaAcAgCgCgGaGtGcAtAcAtAtCtGaCtAtGcGcGaAcAaAcTtGcAaGgGtAcCtTtGcGaAaGgGcAgGaTtTaAcTaAgTaCtGtCcAgGtCaAaTaTtGaGtTtGtGgGtGtAtTgCaAaAtAtCtCgGaGcCaGgAtCgCaGaAgTaCtCtCgGgGcCtTaAaGcCcCtAtGaGcAcTtCaGaCtGaAtAcTgCtCcGaCtAcGcTgGcAtAgCtCaGcAcGtCtCtCtAcTaGgGcAgCcAcAaAcAaCtAtGaAcAcGcTaGtAgAcTtAcTtGtAtAtAtAgAgAtAaGtAcGaAtCtCgGaGcCcGaGaAtTtAaAtCtCgGaAtCcGaAtAcGcGcGaTaCcCaGaGaGaTgCgCgCgCgCgCgCgCgCgGaCgCgCgTgTgGgAtAcTgGtAcTgGaAtAcTgGcAtAtTaTgCgCgTcAaTtGaAgAgGgAaTcAaTgAtAcAcCtAgTaAaAcCcTcTtAcTcAgTtAcAcCcAcAtTcCtAcAtTgAgCgTgAcGtAcGcTtAcAgAaAcAtAgAcAaGgGcAcTgTcAtTgGaTgAtAgTaAaTaAacTgGcAcTcTcAgTcTtAcGaAcAtCaGaAgTcGtAaTcTcGcTcTaTgCcTcTtTcTcTgGaAcGaGaAgCgTcAtAgCcAgAgTgAcTcTgTgTgTgTgAcTgTgCcAgAgCcGaAgTgCcAcAgTgAcAcTcTcTgTgTcTtCcAgCcTcAgGcTgCcAgCgCcGcAcGcGcAcAcTcCcTcAcAcAgCaAcAgAcTtAcTaTcTaGcTgTgAtCaCaAtAgAgTgTaTtTtCcGcCaacTgCaGgCtTgGaCaTcAgTtAcGaAaAaTgAtGtAcCaAaAcCcAtTaAaAcAcTtCgCaAgAtAgCtAcAgCcAaCtCcGtCaAaAtGcAgTgCcAgCcCaTaTgGtTaAaCtAcGaGgTaCtGgGaCgGaTaCaCtAtAcCaCcAttcTaGtTtGcTaTtAaCgGcGcAtGtGgAaTcAcTcCgAgGgGtAtCcAcTaTaTtCtGtAcGcAcGcGaGtCaGcGtAtAtCcAcCcAgGtAcCtTtGcAaGgGtAtCcCtTtAcTtCgGgCcAgCcTgCaGtGaAcTtGaCcagCgGtCtGgGtGtTtGtGcGgTaCcCcGcGaGaTtCtAaCtTcGaTaCtCcTgCaGaGaTtTtAaGgCcCtAaAaGcGtCtAcAgGaCtCaGtCcGcAgTaGaAtCaGcAtAgTtAcGcTaGaCtAcAtGaGaGaGcAgCtTtAcTaAcAcCcAcCaGcGtCcAcAtAgCtGcTcAgGcAgGtGcGcGcGcTcTcGcCtGcAtCcGaGaTtCtAaAtCtCcGgGcCcGaGaTtCcGaAtCcGcAtAtAtCgCaAaCtCtCtCgTaTaTaTaTaTaTaTaTaTtCaTaTaTgTgTtTcGcAgTtGcAgTtCcGcAgTtAcGcGgCgTaTaTgtcCgGtCcTcTtTcCgAcCgTcGcAcAaGcTgCcCcAaAgAgGcAgAcTgGcAcAaAcAcGgAaGcAcGgTcTaTgTcAtGcAtAgGcAcTcCcAcGcTcAcCtTtAcAgTgAcGgTtCgTcGcTgCcCgCcC

***I. 1,000 bp bab1 1st exon sequence that was template for non-complementary transversion mutations and for the making of a second 2 kb spacer***

TGCTGGGCCGAGGGGAAAACGGGAATCTCCAGCAGGCGATGCCGGGTGGTGGGCTGATCCGGCGGTCTGGGAGGGATGTGGGGCGGGTGATGCGTGATGGTGCGGATGCAGGGGCAGGGGCAAAGGAAGCTGACCCTGCTGCTGTGCCTGCTGCTGCTGGGGGCTCTGCGAGTGAGGTCTCGACGATCGGGACAGAGGTCCTGGCGTGGCAGCCGGCGATGGCATGTCCAGGGCGTGGATGGCGGTCTCCAGGCGCCTCGTGGCTCCCACTGTGGAGCCACTGCTCATTGGTGGTTTGGGTGGGGGTGTCATCAGCGAACAGTCCCTCTGTCTCTCTCTTTCCTTTTGCTCCAGCTCCATCCTTTCGGCCGCAATCAGGCTGCTCAGTGGACTGGGTGGTGCGGGTGGATTGAATATTGTGTCCGCCGATGGCCACCGGCGCTTTCTTACATTCCTGCCCTGCTGCCGCTCCAGTGGGGAGAGCCTCAGCTCAGCGGGATCCCAGTCCGAAGTGCGTAGCTTCTTCTCGGGCTGCATGAAGGCCAGCAGCTCCTCGGCCTCCCGTTCCCTGTCGTGTTCAGTTCTGGAAGTTGAAGTGCTCTCCTTGGGCGAGGAGGGCATTCTCTCCGACGAAGCGGCAGCCGCTGCTGCCGTGGCCGCCTCCATATGGGTCACATCCGCCAGACCACGCACTTTCAACATCTCAGCTATCCTGAGCAGAGGACCTATCTGGTCCTGGCTCACGTTGATCTCGCCGCGATACATGAACTCCACAATGGCCTTGAGATCCGACCAATTTACGTCCCGCATGATCACAATGGGATGCTGGCAGGGCGTTTCGGCCAGAAGTGTTTGGAAGTAGGGCGAGCAGGCGGACAGGACCATCTTGTGGGCCTTCATGGACCGACCATCGCATGCCAAGGTCACGTCCACGAAGCACTCGTTCTGGAGCAGCTGGTCAAAGATGGTGGTCAGGTTCGTCTGATAGTTGTTCCAGCGC

***J. 1,000 bp bab1 1st exon sequence with non-complementary transversion mutations at odd base pairs***

gGaTtGtCaGcGtGtAcAcCtGtAcTaTaCcGaAtGaGcTtCaGtGgGtTtGtCgGcTaCtGaGtTaTtGtAtGtAgGgGtGtCtGtTtAgGaGgGcTtGgGaGtAgGaAtGtGaAtGtGaAcAtGcAtCgGcCaCgGaTtCgGgGaCgGaTtCgGaTtGtGtCgCgGaGcGgGcGtTaTaGcCtAgCtGtAaAtAtGgCaTtGaGgGtCcGaCtGaGcTtGaAgGgCaAtGtCtTtGcTtGaGtTaTaCcGtCtCaTaGgGtCgCaCcCgGgGtAtCaAaTtCgCcTgGtTtGgTgGtGgGtGtGgGgCcTaAtCtAcCcGgCaCgCgGgCgCgCgCgTgCaTgTgGaTaCcGaTaCcTaCgTgCtGaCtCcAgCcGtCgGaTaAtTtGcCgGtGgGtTtCtGtTtGcTgGcAgAgTtTtTaCtCaGcTtGaCcCaGtCtCgTgCgTcCcTgCaTtCaCgGaTtCaGaTaCcGgGtGtAtAtCaTaAtCgCcGaGtGcTaCaAtTaCtAcGgGaGgAtCgTaTgCgCtGtCgGaAgGcAtGaCcGaAtCgCaTaGtCaTaCaGgTaCaTtTaGgGgTaAtTgCgGtAcGgTtAcGgGaTaTaCgTtGtCtAtGcGtGaAgTaTaTaCtAaGcAtCtGaAtCaGaTtCgGaCtTtGaCtCaTaCcTcTtGtTaAaAgCaGaCcGcCaAaGaAaTgTaAcCcTaTaAtCgAgCaTtAtCcGcGtAaCgAgCgGtTaCgGtCgCcCtTgGcTaTaGaCtCtAgAaAgGcAaTaCcCcAgGtCaTgGcGcTaCtAaCcAgTgAaGgCaCtCcTtAgCcCcAgGtGcTtCgGtCcGtGaGgTgCtGaCcGcAtTtTgTtGcAtTcGtGaGcGaAtGaGtAaAtGcCaAgCgTtTtGtCaTgCcTtGcCaGcCaAgCtCcTtCaAcGtTaAaGgCaAaGcAtCcCgCtTgCgGtAtCcGaTtGgCcAcGcTtGgGtTaAtGgTaGgCgGcTcGgTtTgCaAtCtC

***K. 1,000 bp bab1 1st exon sequence with non-complementary transversion mutations at even base pairs***

TtCgGtGaCtAtGtGcAcAaGtGcAgCgCaAtCcGtCtAgGaCtGtTtGgGtGaTtAgCaGtCtGgCgGtGcGtGcTtTtGtGaGtGgGcTtCtTtAgGtTtCtGcTtCcGtGtCcGtGtCcAcGtAcGaTtAaCaTtCgGaTtTtCaTtCgGaTtCgGtGtGaTaTtCtAtTtAtGgCgCtAaGcTaGtGcCcGcGtTaCgGtCtTtGaAtCaGtCtAgGtCcTtTaCcGtGaGgGtAgGtCtGgCgCaAtGaGaCgCtTtGaTaCaAaTtTtGcGaCcCgGaTaAgTtGgGtTgTtGtTtGtGtTtTaAgCcGaGcAaAtTaCaTaTtTaTaTaTaTgTaCgTgTtCgCaAtCgCaAgCaTgTaGtCaGaAcTaAtGaTtCgCcGgGtAaTtGtTtGgGaGtGgGtAgTtAcTcTgGgGgCaGaCtAgGtCaAaCtGaGaTgTaTgAaAgTaCgGaCaTtCgGaCtCgCaAtTtGtGcGcGaCgCcGaTaAtCtGtAgCaCcGgCaGcAtTtCtTcGaTgCgTaTaGtGaTtCcTtAcGtCaAtCcGaTaCgCtGaCgCaCtTgCaCgGgCtTtTgCcGgTaTtGcAtTgGcAtTtCgCgCaTgGtGaGcGtAtGtCcTgCgCgCaGcCtAcGaGtCcGaCtCgGaTtCaGgGtCaGaCgCaAgAgGtGgCcCcTaCtCaAtAaCcCtCcCgTgCcAaAgCgCcGaTcTaCgGcGaAtAtGcCaTcTaTtGgCaTtGaTaAaGgTtAgCgCtCaGaGcTcCcTtAcCgCaAaAcTtGaCgTtAtAgCaGcCaAcTgTcCtTaCaGaAgGcTaAaAcTtGtAgGaTtGaAtGtCtTgTaGtCaAtAcGgGgTgGtAcGgAtGtCtAtCcGtCtGcCcGtAaCcTaTgGgGtGaCgTaAgGtAaCtAaCcTaGaAgGaCcAtGgCcCtTaCcCtAcGaAaTaGgTaTtGcGaAtCgGtTaAcAtAgGtTtGgCcGtTgCtTaTtAgAtTgGgTaCcGaGa

***L. 2,012 bp spacer piece with flanking BglII sites***

AGATCTGGATTGTCAGCGTGTACACCTGTACTATACCGAATGAGCTTCAGTGGGTTTGTCGGCTACTGAGTTATTGTATGTAGGGGTGTCTGTTTAGGAGGGCTTGGGAGTAGGAATGTGAATGTGAACATGCATCGGCCACGGATTCGGGGACGGATTCGGATTGTGTCGCGGAGCGGGCGTTATAGCCTAGCTGTAAATATGGCATTGAGGGTCCGACTGAGCTTGAAGGGCAATGTCTTTGCTTGAGTTATACCGTCTCATAGGGTCGCACCCGGGGTATCAAATTCGCCTGGTTTGGTGGTGGGTGTGGGGCCTAATCTACCCGGCACGCGGGCGCGCGCGTGCATGTGGATACCGATACCTACGTGCTGACTCCAGCCGTCGGATAATTTGCCGGTGGGTTTCTGTTTGCTGGCAGAGTTTTTACTCAGCTTGACCCAGTCTCGTGCGTCCCTGCATTCACGGATTCAGATACCGGGTGTATATCATAATCGCCGAGTGCTACAATTACTACGGGAGGATCGTATGCGCTGTCGGAAGGCATGACCGAATCGCATAGTCATACAGGTACATTTAGGGGTAATTGCGGTACGGTTACGGGATATACGTTGTCTATGCGTGAAGTATATACTAAGCATCTGAATCAGATTCGGACTTTGACTCATACCTCTTGTTAAAAGCAGACCGCCAAAGAAATGTAACCCTATAATCGAGCATTATCCGCGTAACGAGCGGTTACGGTCGCCCTTGGCTATAGACTCTAGAAAGGCAATACCCCAGGTCATGGCGCTACTAACCAGTGAAGGCACTCCTTAGCCCCAGGTGCTTCGGTCCGTGAGGTGCTGACCGCATTTTGTTGCATTCGTGAGCGAATGAGTAAATGCCAAGCGTTTTGTCATGCCTTGCCAGCCAAGCTCCTTCAACGTTAAAGGCAAAGCATCCCGCTTGCGGTATCCGATTGGCCACGCTTGGGTTAATGGTAGGCGGCTCGGTTTGCAATCTCTTCGGTGACTATGTGCACAAGTGCAGCGCAATCCGTCTAGGACTGTTTGGGTGATTAGCAGTCTGGCGGTGCGTGCTTTTGTGAGTGGGCTTCTTTAGGTTTCTGCTTCCGTGTCCGTGTCCACGTACGATTAACATTCGGATTTTCATTCGGATTCGGTGTGATATTCTATTTATGGCGCTAAGCTAGTGCCCGCGTTACGGTCTTTGAATCAGTCTAGGTCCTTTACCGTGAGGGTAGGTCTGGCGCAATGAGACGCTTTGATACAAATTTTGCGACCCGGATAAGTTGGGTTGTTGTTTGTGTTTTAAGCCGAGCAAATTACATATTTATATATATGTACGTGTTCGCAATCGCAAGCATGTAGTCAGAACTAATGATTCGCCGGGTAATTGTTTGGGAGTGGGTAGTTACTCTGGGGGCAGACTAGGTCAAACTGAGATGTATGAAAGTACGGACATTCGGACTCGCAATTTGTGCGCGACGCCGATAATCTGTAGCACCGGCAGCATTTCTTCGATGCGTATAGTGATTCCTTACGTCAATCCGATACGCTGACGCACTTGCACGGGCTTTTGCCGGTATTGCATTGGCATTTCGCGCATGGTGAGCGTATGTCCTGCGCGCAGCCTACGAGTCCGACTCGGATTCAGGGTCAGACGCAAGAGGTGGCCCCTACTCAATAACCCTCCCGTGCCAAAGCGCCGATCTACGGCGAATATGCCATCTATTGGCATTGATAAAGGTTAGCGCTCAGAGCTCCCTTACCGCAAAACTTGACGTTATAGCAGCCAACTGTCCTTACAGAAGGCTAAAACTTGTAGGATTGAATGTCTTGTAGTCAATACGGGGTGGTACGGATGTCTATCCGTCTGCCCGTAACCTATGGGGTGACGTAAGGTAACTAACCTAGAAGGACCATGGCCCTTACCCTACGAAATAGGTATTGCGAATCGGTTAACATAGGTTTGGCCGTTGCTTATTAGATTGGGTACCGAGAAGATCT

***M. 2,012 bp spacer piece with flanking BglII sites and Abd-B TTTAT binding motifs mutagenized to TTGGG, called 4k.final.bglII.TTGGG, which was cloned into pRLGL2+DEcore BglII site to make pRLGL4+DEcore***

AGATCTgGaTtGtCaGcGtGtAcAcCtGtAcTaTaCcGaAtGaGcTtCaGtGgGtTtGtCgGcTaCtGaGtTaTtGtAtGtAgGgGtGtCtGtTtAgGaGgGcTtGgGaGtAgGaAtGtGaAtGtGaAcAtGcAtCgGcCaCgGaTtCgGgGaCgGaTtCgGaTtGtGtCgCgGaGcGgGcGtTaTaGcCtAgCtTTGGGtAtGgCaTtGaGgGtCcGaCtGaGcTtGaAgGgCaAtGtCtTtGcTtGaGtTaTaCcGtCtCaTaGgGtCgCaCcCgGgGtAtCaAaTtCgCcTgGtTtGgTgGtGgGtGtGgGgCcTaAtCtAcCcGgCaCgCgGgCgCgCgCgTgCaTgTgGaTaCcGaTaCcTaCgTgCtGaCtCcAgCcGtCgGaTaAtTtGcCgGtGgGtTtCtGtTtGcTgGcAgAgTtTTGGGtCaGcTtGaCcCaGtCtCgTgCgTcCcTgCaTtCaCgGaTtCaGaTaCcGgGtGtAtAtCaTaAtCgCcGaGtGcTaCaAtTaCtAcGgGaGgAtCgTaTgCgCtGtCgGaAgGcAtGaCcGaAtCgCaTaGtCaTaCaGgTaCaTtTaGgGgTaAtTgCgGtAcGgTtAcGgGaTaTaCgTtGtCtAtGcGtGaAgTaTaTaCtAaGcAtCtGaAtCaGaTtCgGaCtTtGaCtCaTaCcTcTtGtTaAaAgCaGaCcGcCaAaGaAaTgTaAcCcTaTaAtCgAgCaTtAtCcGcGtAaCgAgCgGtTaCgGtCgCcCtTgGcTaTaGaCtCtAgAaAgGcAaTaCcCcAgGtCaTgGcGcTaCtAaCcAgTgAaGgCaCtCcTtAgCcCcAgGtGcTtCgGtCcGtGaGgTgCtGaCcGcAtTtTgTtGcAtTcGtGaGcGaAtGaTTGGGtGcCaAgCgTtTtGtCaTgCcTtGcCaGcCaAgCtCcTtCaAcGtTaAaGgCaAaGcAtCcCgCtTgCgGtAtCcGaTtGgCcAcGcTtGgGtTaAtGgTaGgCgGcTcGgTtTgCaAtCtCTtCgGtGaCtAtGtGcAcAaGtGcAgCgCaAtCcGtCtAgGaCtGtTtGgGtGaTtAgCaGtCtGgCgGtGcGtGcTtTtGtGaGtGgGcTtCtTtAgGtTtCtGcTtCcGtGtCcGtGtCcAcGtAcGaTtAaCaTtCgGaTtTtCaTtCgGaTtCgGtGtGaTaTtCtATTGGGGgCgCtAaGcTaGtGcCcGcGtTaCgGtCtTtGaAtCaGtCtAgGtCcTTGGGcGtGaGgGtAgGtCtGgCgCaAtGaGaCgCtTtGaTaCaAaTtTtGcGaCcCgGaTaAgTtGgGtTgTtGtTtGtGtTtTaAgCcGaGcAaAtTaCaTaTTGGGaTaTaTgTaCgTgTtCgCaAtCgCaAgCaTgTaGtCaGaAcTaAtGaTtCgCcGgGtAaTtGtTtGgGaGtGgGtAgTtAcTcTgGgGgCaGaCtAgGtCaAaCtGaGaTgTaTgAaAgTaCgGaCaTtCgGaCtCgCaAtTtGtGcGcGaCgCcGaTaAtCtGtAgCaCcGgCaGcAtTtCtTcGaTgCgTaTaGtGaTtCcTtAcGtCaAtCcGaTaCgCtGaCgCaCtTgCaCgGgCtTtTgCcGgTaTtGcAtTgGcAtTtCgCgCaTgGtGaGcGtAtGtCcTgCgCgCaGcCtAcGaGtCcGaCtCgGaTtCaGgGtCaGaCgCaAgAgGtGgCcCcTaCtCaAtAaCcCtCcCgTgCcAaAgCgCcGaTcTaCgGcGaAtAtGcCaTcTaTtGgCaTtGTTGGGGgTtAgCgCtCaGaGcTcCcTtAcCgCaAaAcTtGaCgTtAtAgCaGcCaAcTgTcCtTaCaGaAgGcTaAaAcTtGtAgGaTtGaAtGtCtTgTaGtCaAtAcGgGgTgGtAcGgAtGtCtAtCcGtCtGcCcGtAaCcTaTgGgGtGaCgTaAgGtAaCtAaCcTaGaAgGaCcAtGgCcCtTaCcCtAcGaAaTaGgTaTtGcGaAtCgGtTaAcAtAgGtTtGgCcGtTgCtTaTtAgAtTgGgTaCcGaGaAGATCT

***N. 4,000 bp spacer template sequence from bab1 1st intron***

AGAAGACAATTTAGCTAAAAAGTTGTAAACTTCCCACTCTGCTGTTCATTACCATTTTAAAGTATCAAGGCGAATAAAAATAGAAAACTGGACACATGTGGCAGAAATATGTGGCCCAACTGCCTGAATATCCAGACCATATCCACACCAGAAGTGGAGGATCGGGTTGCTTTTGATGATTGTGAATGCGAATTGCATTTAAATATTACACATAATAAATTCACAAGTACAACCACCATTTATATCGCACCAACCAATCTCTTTTTAACCATCTGTGAGGAGTCACCGGCTTTTGTTTTGCCTGCGATTACTATATTGAAATATTTTATTCTTTTCGTACACCGAAAATAAACGCACTATTCTTATGCCATTTGATAACCCATATTTGCCACTTAAGTGGTAAACTAAAATGAAGTGAAAATGTATATACTTAGGTAATATTTTTAAAATTTTCAATTTAAAATTGTAAACATATATTTATTTTTCGGTGTCGATTCGAATGTGGTTGTTCCATATATATTCCTAATACCGAAGCTCAAAGAGCAGCCCGAGGGCTTTTGATCCCCGTTGTGTGGCGGTTTTTCAGGGGTTGTCCAGCCCCCAACCCTTTTTCCATATTCTATAACAAGAACCCCGAGTATCTCTGTCAACTCGACGCTGGCTTATTTGCGATTTCCACCTCTCATATTTTACATATTTCACACCCCTAGCCGATGGCCCAAAGACCCCCGCCCACCTAATTACACGTGGTTACTTCTGCAGAATGGTGAGTAGAAAAATAACGCAAATTACACATAGATTTCTTAGAGTTTTGGTGCATAATCATGCAGCGGAAATGAATTAATTCTTTTTCAACCCCTTCCCCGACTTGGCATTTCCACATTGAGCTCAACTGTTGAGAGAGGGTGTAATTATTTTCCTGTTTGCAGTGGATCAGCAACTGGAGGGGATCGGGAAGTGGGCAGTCATTGGGCTTGGCTTTCTGTGTTTATTTTTTTTTTTTGTGTTGCCAGGGCATTGGGAATTCGGTTTATACCAAGTACATAATGTTTCTTGTTTCTTATTTATATTTATTGTAGATATACTATATAGGGCATTCCAAGCTTCGTTTGCGGAAACCAGTGCCATTTTCCCGATTTCAGTGGGCTTTTCCGCCGTGCCGCTTGCTGTAATTTGTTATTAGTTTTCTGCAGTTGTAGATGTAGTTATAGTTGCGGACAAAGGGCAGTATGGACTGTGCTGGGCTTCCATTGAAATCATTTGCATATGGCATATAGGAGGGAATCGGTGTGGAGGGGGAGGGTCAGGGAATTAGGTTGTGTGCAGTTTATTGCATTTACTATCGACCTCAGTAGGTGATTTGTTATTATTATTCCTGCTTCTTGGCGCCGCTGTTCATTAGTTTGCACTTCACGGAGCCCTTTGCTCAGAGTTTAATTGGCACCCCTTCGGGATTTTTCCCACTTTTTCCCCAGAAACCCCGTACTTAACCTGGCCAATTTGCACGTCAAAATTTTTAGTTGTGAGGTGTGCGGAGTTGTCGGCAATTGGCGATTATTAATACAAATGTTATGTACTTACGTTGGCCAAAGGAAAGTCACCACAGGAACTTACCTGTAACGATAAAGGGAAATGAGAAAAAGGTGTTTTAATAATGGAAAAATATGGCCGCCTATTTCTGGGCGCGAGTTTTGGGGTAGCCAAGTGTGTTTGTGTGTGTAACTACGCATTCCACGTTGCGTATACGCAATGCGAACCAAATTGCCGCCGCTGCAGTCGGTGCTTTGCTATATACTCCAGACTATAGTCTACGGGCAACTGCGGCTTGAGCTCCAGCCCCTTCCCCAGATATTCGCCCCCTCGGAGGGGGAAATCACCGGAATTTTTCGTTGCGCGCCTGCCAAAAACGAGACAGAACCCAACTCTCTCCCTCAGCTGAAGTTGCAAATTCGTGCCCAGGCAATAGGCCGAGATAAATGCATTTTCCTAACGTGAACGCTATCAAATATATGTACAGTGGAAACCATTGTGAAGAACAGCAAAGTATGGATGGGACCAGGACACTTGAATACTTTTTAAATGCTATCTTCTATGATCACAGTTTATCGAACATTCTATGTACTTTTTCCTATATTTTAATAAGTGTTCATCTTGATATTAAAAACCTCTTTTGAGAGCAGCTAGGCGTTCGTTAACTTGGATCCTCACTGTATATAGAAAACGCAGCGCCGACAACGCGTTGCTGCCGGCGACCGCAGCAGACACACGGCTCGATTTGGTTAGGCGATGGCTCCTAAACCGCCCACTCCCTTCTGGCCACCCCTTCCGCCCCCTTTTCGAATGTGCGTGTGTGTGTGGGTGTGTGTGTGTGCATTAGGTGCATGTGCAACTCGAGGCTTTTGGCAAAAGGCGCAGGAGAAGAGAAGAGAAGCTATGGAGTATCCAGGACCCGGCAATGCCTGTTGGCCATGTTCAAATAGCCTACGCTGAGGGGGTGTGCGTGTGAGGGCAGATGGCCAACACACACACACACACACAACTGCAGCCCACACACACACACTTGCAGATACAGAAGTTGCCAATAACAGGCGCAACGTTTTGTGTTCGTTCGGCTTTTTTCCTTTTGACCAGACTGGAGGAGCAGCACCCACATCACCCACTTTCCATCGGCTTTTTCCAACTTCTCGCACTAGCCAGACGCATTCATTTGTAAAGCTAAATCACATGGCCAGTGGAATGGGTTCGGGTGGCCAAAGGGCTGCAAGGTGGGGAATGTGGGTGCAGGAGGTAGGTTCGTGTCGGAGGCTTTTACTACGCACCTTTTGCTAACGTGTTAATGAAACGCATTCCAGGGCCGTAAAACATGCAGCGCTCTTCCCGCTCAACTTTCCCGACTTAAAGGTGGTGCAGCGATGCAGAAGATCTCCAAACAAAACAAAAGACCCACAATGCACAGGCATTATTTTAGATAATAAACTTATATCGAGATATTTCATTAAAAACGACATTGAATAGTTCGATCGGAAGTAGCCCAGACTTAGTCCAAGATCAGCTCGTCCTATTTCGAATAAGACGTCTGCGAAGGCGGAAAGAATGTCCATTTCCCCGTTGGAAAATTCTATTATTGGCTTATACTCTTTGTCGTTCGTTGAGAGCAGGATATACAGGATGTATGCCATCCGCCGGCATATAATTTCATTAGTATTTTTCTAAACCTGACCAGCAAAGTGCGCTCTTTTTCGAGCCGTTCTTGACCGGGCTGAATCCATATTTTTTCTTGGCCTACACAGAATGTCAGTTATTGCCCCTCCATGCATCAATGTGTGGGTGTGTATCTGTGTGCCGAGCCGGAGTGCTGAACATTCCAGCAAGTTGCTACGAGGCAATGGCAAAAACGCGGCATAGAAATCGAATTAGATTTTTCCGATTGAATTTTCTACATTTTTAATTGCTTTCGACATTTCAACTTGTCGACGAGCCGGCAGAGCAACGAGCCCCGCCACCCCAAAATAACTAACCCCCCCATATCTAACAATTCCTGGCGAATCTATGACGTGGCCTGACATTTATGGGCTTTTAAGGCCTTGACGTTTGGGGGGCGGCGAATATGAAATGCAAGTAACTAAATCAAATATGTGCGCTCCGTCTAATTTGCTTTAGTTCAGTTGCATTTTTCCAGCTGCATATTCGATGGCAACTGTATTTGCTCGTAATAGTAAGGGAAAGTCAATTACAACGATAAAGTATTTACCATTAAAGGGGAAATTGGCGAAACCAAATGGGGGTTCTTTCTAAGAAAATTAATGGGCATTAAATTAGTGTAATATTTGCGAGACCTATCGTTGCAGAATCGGATTCGCATGTCTTCTGCTGCAAGTCCAGTTTTCATATTCATATGAATATTTCGATTTCGATTAGAGTGCATGCCTGTTTCCATTCGCCACCGTCTGACGGATCTGCTGGCGAATTATTCGCATTATTTCCCCATCTTTGCACCTTC

***O. 4,000 bp spacer template sequence from bab1 1st intron with nucleotides shuffled***

TCGTGCGTCATTCGGAAGAAAAAAGATCGCTAGCGTTGATACTTATTTTTACTGGGGGTTACACTGATACATCTCAACAGTGGTTGAAAATTTCTGTCATGACCTTTCGTCCAGGGGCTCTTTCCCGGTGTGTTAACTCAGCCTAAGTATGAGGACCTTAGGTGTGAGTTAACTTTTTGGATCACATCCTAAATCCGGTGGAACTAGGTCTCGAAGCTTAGACTTTTGCTCTTCGCTCGGCCTTAATCTACTGCTGTCCCACGTAACCACAATGGCTTTATGAGTTTCGAGTCGGAGAGTGCATGGATACAATGTTTTCCGACGGTATTGGATTAACTCTGCACATTCTGTATTATCACCGTAAATGAGAAATCACTGAAGATCTAGTGTAACGTCGCACAGGTATCTATGCGTTAACTGTTCATCACATAGAGGTAGGGGATACGACTGTGCACATGAGTGAATTCGTAACCCGTTCTGTTGTCGCTGCAATTCACAGTCTGCTGTCCCTTAACCGGTTATAGTCACGCTATACGGGACAACTTACCATCGCAGTCATCAAACATCTCTCTGCGGTTCACGGACGTTAAGCCACCACCTTGTCATAACAGAATAAACCGGACTACCCTTTGCTTTTTCTTGATTGGTGTTGGATTCAGGGAGCGTTCAACGTGTCATCATTCGTATGATAATGTCTCGTTACTTCCAAACAACAATGACAGAAGCAATGCCAAGGACGAGCTTTACCGATGCCGGTCTCTCGGTCTTGGTTACTTTAAATTGTCAGTTCATTATTTCCGTTGCTGGTAGTTGGCACCAGATAGTTAGGCCAACAAGTTACAGAGAGCTCTCCAAGCACGAACACATATGATAGTAGGTTAAATATATCGAGTGGCGGAATCTTGCCGAGTCGATGCTTGACATAGACTAGTTGGCATGGCATTCGTCGGTAATAGACCTTACGTAAACTTGGAGGTCTAAGTAGTGGAACAATATAGCTGTGGATCTGAGTAACTAAATGTAGAAACCCTGGTCTGGATAGAGTCCGCCCCGGGAGGATATCACTCAGTAGGAAGCGCTTTTTGAACTGTATGACAACCATGTCGTCGGCGGACAAAGAGGGGGGCCGCAACGTCAGCGAGCCTTCAATGTTATCTGGTGCCAGTAGTTTCTAATCGACCAATTCAGAGCAGTATGATGCGTTTATATTATTTCTGCTACGGCCACGTCATAACTCACCTGCTAAGTAGCCGCAAATGTCCATAAAGCACATTCTTCAACTATAAAGTTCAAGGGACTATTATTAAATAATGTACTCCTTATGCTCGCTGCAGTGATATCCGTCCGTAGGGTCTTCTTAGAGGTGCGCTTTCGCTAACTAGACAGATAATAGGCAATGAAAGGAACTGATTTAAAAGGGTCCGTTATCTTCGCGCCGGATTATTTCGCCTAATAGGATCCTAACATTACCAATAGAAACAGTCAATTGGTCTGAGGGCCGCTCTTTCTCAGGGCCTGGAGGCTTCTTCCGCTAGAACAAACACATGATAAACAAAATATTTGTGTGAACTACTAACGGGGAAATACATTCTTGCAGCCGGTGTATCACCTTCTATCAAAGACAAATATTTGAATAGCTATAGATTATTAGTTCTTCAGAGACAACTTACACTGCGAATCAAACGACTACTTGTACAGGGGCCACAATTTATTTCACGAAGTTGCAAGATTTCCGTGATGAGAAACGCTAAGTCAGATGGATCGCCGCCGTGAGTCATATGTTATTCACTAGTCTCCCGCGATTCGACGGGGTGTAAGGTCTGGAACGTGTTTTCGTAACACGCGGAAGCGTCAGCAAAATCTAATTTGCATTATATAAGTTCGTGTCGGACGCCTAACTGGAGGTGAACATTGACTAGTGCATATCACCGGACATTGGACGCCCCTTTTTACTCCTCGGAAATAAGTGATAGTTTGCGAGTATCTTTTCAGGGAGAAAGATCTTATCTTCGTGACTCGTGGTTGTCCTAGACTTAGCTTGGGTGCGTGTAGAAGTAGGGCCGTAATTTTGATGTTTTTTACTGGTGGTACGATTATGCCTCGAAGGACTTATCGCACTACTACCATTAACGTTGCGCATATTACATACACAATTGGCACCTTTGCGCACTGATTAACACCCAGCAGGCGCGTATGAGGCACCTTTGTCTTGGTAGAAGGAGTACAACCAAAGTACGCTAGTATGCAAGTATTGAAAGGCCTGATTATACGTAGTCTTCTACTAGTGGTTAGTTTGGCCTTACGGCTTCGTTTCTCGTATGATTTAGCATGCTGTTATTTGATTGATTAATCAACTCACAGAAATGGCTTGGATCACCATTAAAACCCGAATCGGACAATTGCGGAATTATTCTCTAATTTTAACGCTCTGACTTAACCTGATCTTCCTTGCCGTCCGGTACGGCTACTTGTAATTAAGAAGGATAATGCACCCAACAGAGGACTTGAAAGCTCGCTTTGGCGATTTTGAATGTACAGTTGACACCCATTACGCGATCTCCATAGTGTCGATTTAATATAGAGATCACAATGCACCTCCGCATCAGACTTTGCATGCAGTCCTTATACGGAAGTTATGGTTCGTTAATGGCATCATTAGGTATGCAAACTGGCATTATGAATCATCACTGAGAAAACCCGGTCAATATGTCTCGAATATAGTGAATGTTGTGGCCTTATCACCATCTGCCTGCCTGGGTATCTAGCTTTATTAACCACAAAAGCGACTGTTTTATTTAGTGACGCACGGCTCTGCCCCTCTGCATCATTTGGCTTAAAACTCTTCATTTCCACTGCTTCGACCTAAACTTGCCACCTTCTAGACGTTGTTGCGAGAGGGCTTTTCGGCGGGGTGCGCCTGGGACCGCCATCAGAACGACAAATTACCGTGTCTTCGTAACCTAGTATTATGTAAGTTAGGTGTCACCTGACACACCCTGTTGAGCACGGACGTTAAATGCATAGTCTGATCCATGATCGTCTCGAGAGCTTGCTACGGCTCGCTGTACACATGCATGTGAGCTTCCGTAGTGATGAGTGGTCGTATTTCGGTAACTGATGTGGACTTACAGATATCTGACTAGTAGCACTTGCTTAACCTAACTATTGGCTAAGCCTTTATTAGAGAAGACATTGCCCTCCTCTAAGACTTGTGGGTATTTCTGAAAAGACAATTATCTCTACTGATTTCCGTAGCAAACTTTAGATGATCAATTACGTATATCGTGCGCTAAAGATCCCCGATCATGTTTTTATCTTATATGTTCAGGAGTAGAACCTGTATGCCTGTATCATCATAAATTGATCATTTGCACTAGGTACATATGCATATGTAATAACTTTCCTTTGATTATTACCCGGAATGCGCTGATCTAAGTTCCAAAACCCGGACCAGAAAATAAGGCTGTAGTGGCGTTGTCGTTTGGTTAGGATAGCGGATGCTGTTCAGTAATTCCACCTTATTAATCAGTCTGCTTCCCATCAAGGTATACGTGCCAGACCTTTCATTCCGTAATCACGTGACAGCTTTGATACCCATTATGGATTGATCAGTTTTCTTTTGTGAGAGGTACTAAGCCGCCACTCTTATTTAAATGTTAGTTCACTAGAGGACAAGTTGTCCTTAGGATGGACTAGTCATTGTAGGAGACCAACCAGATCATGCATAATAGCACGATCCCACGATGAATTGCTAACTTCACACCCGAACCAATGCTTGTGCTTCGAAGACATCGTCAGTTTCTACAAGTATAGCCCGATTTCCGTTTTTTGCAGCCGACTTGCTTGTGCATGCTACCCCCCTGACAATAACAGGCTCCTTCGGTTGCCGGTCTCCTTTTTACTTGCTTCGGTACTCAGACACATTTAACTATTGAGTCGATCACATGATATAGTGGCGAGACGGTTATAGGGAGACATAGTACCTAGTTTGTGGCAATTA

***P. 4,000 bp spacer template sequence from bab1 1st intron with nucleotides shuffled and non-complementary transversions substituted at odd base pairs***

gCtTtCtTaAgTaGtAcGcAcAcAtAgCtCgAtCtTgGcTcCgTcTgTgTcCgGtGtGgTcCcCgGcTcCcTaTaAcCcGgGtTgGcAcAgTgCgGgCcTtAaCgTgCtTaCcGtGtCgCgTgCaCtGgGgGgTcAaTaAtCaTcAtTcTtAtGcCaTgAtGgGgGcGgTcAaTgTgTtGcTaAaAgCaTcAcTaCtGgGtAcCgAtGgCgCtAcGaTgAtAaTgTgGaTaTgCtCgCtGaCgTcAgCgAaTtCgGgCaCcCtTcAaCcCcAgGtCgTgAgGcGgTgCtAtTaGtAtAtTtCcTtGcTcCcAgGgTgTaCtAaGtTcTgGtAgTcAaTaTtCcCcTgCgGgAgTcTaAaCtTcAcTtAtAcAgCcCgGcAtAgCgAtTtTcAaGgCtCcCcGtTcTaTcTtCtTgAcCgGgTaAgCcCcTcGcGtTcGtGtAgAaGcCgGgGaAaAgGcGgGcAgTaGgAcCaCtTgCgGgTtTaGaTtCcAgTaAaAtTaTtCgGgCaCgTcAaCtGgTcTcGgCcCtCgAgAaGtGcCcAaTgAaCcTaGaAtTaAgCcAcCcTaTaTaTtCtGgTaAaGtAaGgTcAtCaAaCcCaTgGgCcTcAaAtAcTcAcCaGtAaTcCaCgTgGaTgTgTaTgGcTgGtTtTgGtAgTaAtGtAtCtTgCcAaGgGgCcTaAgTaGgAgGcTcAgGgCgCtTgAaTgCaAcAaAcCcAgGcCcGcAtCcAgGaCcAtGcCtAtCgTgAaCtAgGaCtGgCgCgCtGgCgTtGgTcCgTgAcAgTtTaAtTgCcTgAgTgCaGgTtCgGtTcGgTtGaAaCcGcTcGgTcGtCaAcCcAtTgAaAtAtAtCgCgCaAcGaAaGcAaAaAgAgGcTcGgAtGgTcAcTcTcTaGcGgGtCtGcAgCgTtCaGcGgCtAgGaTgGcCcTcGcCgAtTgGtCcTtGaAgTaGgCtGgAcTcGcCaTgAaGgAcAaTgGtAtGgCgAcGgAtTtGcAaAcTcTcGaTtTtGcTaTtAtTcAaTcAcTtTcGcAcCaCgGtTaTtGcTcGcGgCaGaCaCtGtAtGcTcTaAaTaAtTcGtAcGaGaTgTgTtAcCgGgAgGcCcAaCcTtTaGgCtGaGtAaAcAtAtGtGtGaCtCcAaGgCcGaGcGaCgTaAcTtTgAgCgGtTtCaAtTcGgTgCgAcTaGcCaAcTgCcGcGaAtTcTtAgGaGgTgAgAgTcTgTaTtCgAaGtCaAaGgCcTcAaTaAaCgGaTcAtTcGaCtCcAcTtTaCcTcAcGaAaAgTaTgCcAaTcTcAcGgTaAcGtGcCgAgTcTgAcAgAcTtTcCgCaTgAgGaTaGaTtCcGgGcTcTaCtTaCtTcGtGgCgTaTgAtAtGgGaGaTgTaGaTcAaTcGcCcGcTcAgAtGaAcTtAcAtGcAaTtAgTgAcAcGtGgCaGgTcTaTgCtCtCaGtAgTcTgTaGaCgAcTcGtAgCaTcAaAgTcCaAcTcGcAcCcGgCcAgTtGgCgGcGtGaCtCgCgTgCgCcGtGaCgGtAtGaTgCgTaCtCgAtAcCcAcCcCcTtAgAcAaAcAcTcTgTtTtTtAcCgAaTcAaGtGtAcAgAaAgTaTgGaAtCaGtTtTcTaAaCgTaTcTaAcAtAaAcAgAgTgGcAgAtCgAgAtAgTcTgAtTgCgTaAtAtAaAcCgTcCcCgGaGcAgCcAcCtAaTcCgTtTcCcGtGtCaAaAcTgTcTgTaAaGcAtTgGaAcGcTgTaCtTtAgGcGcAcCtCgAcGgCcGcTtGcTaGaCtCaGgGcGgCcTcTtTgAgTaAaTcGgCgCaCtCtAgTaGcCtGtGgGgAcGtTaTtGcAaGgGgTgTaGgAcCcCtCtGcAtCtTaAtCcAcAgCgAcTgTtCcTgAgAgAcGgTaGgGgCtGcCtCaTcAaTtGcGtTtAcCcTgGcCgAtTtCcTcTaAaCtGcCcTgGtAaGaCaCgTgTgAaTaCgCtGcAcTcAtTtAgAtTgTtCtAtTcTaTgTgCcGtGcGcAcGcTaTgAgCgTaGgGcCgCtTtGgTtTaCgAtAaTgAtCgTtGtTtCtTtTcGcAtTcGtGaCtTcAgTgTtAgGgTgTgTcCgGtTtGgAaGcTgAgGaCgCtAcGtAaTgAgCtCcCgAaTcCaAgTcAaGgTtCtCcTcTgAaAgAaAaAcTgGtCcCaTgTtCtCcCgGcTgAcCcCaCcGaAtGaGaGgAgGcGtCcCaTgTtTaTgGtTcGcAtGcGgAaAcCaAcAtTcCtCgAtTcTtCcAtTcTgGcAcGtCaTtAgTcTcCtTcGgCgTaTcCgAtTtGgTcGgTgGtCaTgAaGtCgTaGgTgCgCtTcTtAgTgAtCcTtCgGgTcTgTtAgTtAgTcAgCcAaTaAaAtAcAgGtCgTtGcTaAaCcTgAcAcCaCtAcTaGtAaAcTgGaGtAcTgAgTaTaTcAgTgTcAaGaTaTtAaTgAcCaTtAgCgTaCgTtCaGgCaGtTcCtGaTcCgTtTcAgTcAtAcGtAgAcTtCcCaCcAaAtAtGcCgTtAcAtCgCtCgTgGtCtAgTgTtAcTtTcCcGgTtAaAaCaAgTcCtCtAgCgCaAgAtTtTaGcTgTcAgAgAtAtAgCcCcAgGaAaCgCaGaAgCcGcCgTgGaAgGaAtTaCgTcTcCtGcAtTgAgGtTgCtTgAcTtGaAgCcTgAtGgAgGaAcAaTtGaAgTcTtAcTaAgCcCgGcGcAcAaCaGtTaAcTcTtTaTaGcAgAgAtTtAcTtTgGgGtCaTgAgCcCaAgCgGaCgGaCgGtGgAgCgAtCgTgAgTcAaCcCcAcAtCtAaTtTgTgAgTgAtTtAaGaAaGtCgCgGaCaCgCgGaAgCcTgTtGaTgAcAcCgCgTaAgTgCaAaTtCgTaGcCaTcAcCgTtCaAaCgTaTcGcCtTgGgTtCtAtAtGtCgTgTaGtCtGtGgGaGaCgGtGcCaGaCcTaAtAcCtAaAcAgTcCaGgGgCgTaGgAcCaTcGgAgTcTtTcAtTgAtGgGgCcCaTtAaAaAaCaTtTgGcGaAaGtAaGgTcAcTtCcTcGgCgGcTaCcTtAgCtTaTaGcGcGaTgGaTcCtGaTaGaTtTcCcCcTtCcTtTtAtCgTaCtTcGgGcTtAtTtGgCtTcTgTaGtTcAaTtAgGgGtAaTgAaAtAgAgCgGcCgAtTcGaAaTgGaTgAcCaTcAaTcTgGtCgAcGaCgTgAgTcGcGcAtAaAgTtCaCgCaTaTcAtAaTgGgGtGgAgTgCgGcAcAtAaAcTgAgCgCgAaTtAgTgCaGgAtCcAcCgTgAtAgGcTaAcTgAaGgAgAgCtTtCtCgAcAtAgCaCaGcTaAgGgTgTgAgCgTcTcTtTgCcGtAtTcGcAaCgGgAgGaCgGgAgCcTaAgAcAgTtAgCcTgTtCcCgAtGgAaAgAgGaAgAgGgAcTcAaTgTaCgTgGcTgAgTcCaCtGcAgGaGaTtAgCgAcGgTaCcAcAaCaGtAaCcGcAcAgAcGtCgGgAtTtGaGgTtTaGgTgGtTgAtGcTcGaGtAgGaTtTgCcGgAcTgCaAaCgTcTgAcTaAtTaTtCgTaCaAgCcAtGgAgAaGgGaCcGcCaTgTaAgTaCtTcAgCcCtTtAaAtCgTgGcTcCaCcTgAgGtAgTtAgCcGgTgTaTgTgGgGcGcGtTcCgAcGaCtCaAaTaTgAgTgAcAgGgTcGgTaAaTcGcGtAaAcGgTtTaCgTcGtAgGtAaTcGgCcTgGgAtGcGcCaAcCaAtAgCcTtCcTcAgAtCcCtAgCaCcCtAgGcAgTtCgAcCgTaAaAaCaGcAaCcAgGaTgGgGaTgCtAcGcCcTaGgCcGgTgCgAaAcGgAgAtCaCtAgTgCaGgTgTgTtCcGaCtAaTgGaTgGgGaAgGaTcCaCaCaTtAaAcTcAaAtGaTaCgTaGtTgGaCtGgCgCaTgTgTcCgTtCgTaGtTcCgCcGcCcCcTgTcAaTcTgGcGgCtAgCcCcTtAgAgAtTtGaGcGcCtGgTcTcGtGcGcCcTcGgAaCgAtTgTtTtGaAcTgA

***Q. 4,000 bp spacer template sequence from bab1 1st intron with nucleotides shuffled, non-complementary transversions substituted at odd base pairs, and restriction sites for KpnI, EcoRI, XhoI, StuI, SpeI, BamHI, NheI, and SacII removed by base pair substitutions***

gCtTtCtTaAgTaGtAcGcAcAcAtAgCtCgAtCtTgGcTcCgTcTgTgTcCgGtGtGgTcCcCgGcTcCcTaTaAcCcGgGtTgGcAcAgTgCgGgCcTtAaCgTgCtTaCcGtGtCgCgTgCaCtGgGgGgTcAaTaAtCaTcAtTcTtAtGcCaTgAtGgGgGcGgTcAaTgTgTtGcTaAaAgCaTcAcTaCtGgGgggggAtGgCgCtAcGaTgAtAaTgTgGaTaTgCtCgCtGaCgTcAgCgggggggGgCaCcCtTcAaCcCcAgGtCgTgAgGcGgTgCtAtTaGtAtAtTtCcTtGcTcCcAgGgTgTaCtAaGtTcTgGtAgTcAaTaTtCcCcTgCgGgAgTcTaAaCtTcAcTtAtAcAgCcCgGcAtAgCgAtTtTcAaGgCtCcCcGtTcTaTcTtCtTgAcCgGgTaAgCcCcTcGcGtTcGtGtAgAaGcCgGgGaAaAgGcGgGcAgTaGgAcCaCtTgCgGgTtTaGaTtCcAgTaAaAtTaTtCgGgCaCgTcAaCtGgTcTcGgCcggggggAaGtGcCcAaTgAaCcTaGaAtTaAgCcAcCcTaTaTaTtCtGgTaAaGtAaGgTcAtCaAaCcCaTgGgCcTcAaAtAcTcAcCaGtAaTcCaCgTgGaTgTgTaTgGcTgGtTtTgGtAgTaAtGtAtCtTgCcAaGgGgCcTaAgTaGgAgGcTcAgGgCgCtTgAaTgCaAcAaAcCcAgGcCcGcAtCcAgGaCcAtGcCtAtCgTgAaCtAgGaCtGgCgCgCtGgCgTtGgTcCgTgAcAgTtTaAtTgCcTgAgTgCaGgTtCgGtTcGgTtGaAaCcGcTcGgTcGtCaAcCcAtTgAaAtAtAtCgCgCaAcGaAaGcAaAaAgAgGcTcGgAtGgTcAcTcTcTaGcGgGtCtGcAgCgTtCaGcGgCtAgGaTgGcCcTcGcCgAtTgGtCcTtGaAgTaGgCtGgAcTcGcCaTgAaGgAcAaTgGtAtGgCgAcGgAtTtGcAaAcTcTcGaTtTtGcTaTtAtTcAaTcAcTtTcGcAcCaCgGtTaTtGcTcGcGgCaGaCaCtGtAtGcTcTaAaTaAtTcGtAcGaGaTgTgTtAcCgGgAgGcCcAaCcTtTaGgCtGaGtAaAcAtAtGtGtGaCtCcAaGgCcGaGcGaCgTaAcTtTgAgCgGtTtCaAtTcGgTgCgAcTaGcCaAcTgggggggggggTtAgGaGgTgAgAgTcTgTaTtCgAaGtCaAggggggcAaTaAaCgGaTcAtTcGaCtCcAcTtTaCcTcAcGaAaAgTaTgCcAaTcTcAcGgTaAcGtGcCgAgTcTgAcAgAcTtTcCgCaTgAgGaTaGaTtCcGgGcTcTaCtTaCtTcGtGgCgTaTgAtAtGgGaGaTgTaGaTcAaTcGcCcGcTcAgAtGaAcTtAcAtGcAaTtAgTgAcAcGtGgCaGgTcTaTgCtCtCaGtAgTcTgTaGaCgAcTcGtAgCaTcAaAgTcCaAcTcGcAcCcGgCcAgTtGgCgGcGtGaCtCgCgTgCgCcGtGaCgGtAtGaTgCgTaCtCgAtAcCcAcCcCcTtAgAcAaAcAcTcTgTtTtTtAcCgAaTcAaGtGtAcAgAaAgTaTgGaAtCaGtTtTcTaAaCgTaTcTaAcAtAaAcAgAgTgGcAgAtCgAgAtAgTcTgAtTgCgTaAtAtAaAcCgTcCcCgGaGcAgCcAcCtAaTcCgTtTcCcGtGtCaAaAcTgTcTgTaAaGcAtTgGaAcGcTgTaCtTtAgGcGcAcCtCgAcGgCcGcTtGcTaGaCtCaGgGcGgCcTcTtTgAgTaAaTcGgCgCaCtCtAgTaGcCtGtGgGgAcGtTaTtGcAaGgGgTgTaGgAcCcCtCtGcAtCtTaAtCcAcAgCgAcTgTtCcTgAgAgAcGgTaGgGgCtGcCtCaTcAaTtGcGtTtAcCcTgGcCgAtTtCcTcTaAaCtGcCcTgGtAaGaCaCgTgTgAaTaCgCtGcAcTcAtTtAgAtTgTtCtAtTcTaTgTgCcGtGcGcAcGcTaTgAgCgTaGgGcCgCtTtGgTtTaCgAtAaTgAtCgTtGtTtCtTtTcGcAtTcGtGaCtTcAgTgTtAgGgTgTgTcCgGtTtGgAaGcTgAgGaCgCtAcGtAaTgAgCtCcCgAaTcCaAgTcAaGgTtCtCcTcTgAaAgAaAaAcTgGtCcCaTgTtCtCcCgGcTgAcCcCaCcGaAtGaGaGgAgGcGtCcCaTgTtTaTgGtTcGcAtGcGgAaAcCaAcAtTcCtCgAtTcTtCcAtTcTgGcAcGtCaTtAgTcTcCtTcGgCgTaTcCgAtTtGgTcGgTgGtCaTgAaGtCgTaGgTgCgCtTcTtAgTgAtCcTtCgGgTcTgTtAgTtAgTcAgCcAaTaAaAtAcAgGtCgTtGcTaAaCcTgAcAcCaCtggggggAaAcTgGaGtAcTgAgTaTaTcAgTgTcAaGaTaTtAaTgAcCaTtAgCgTaCgTtCaGgCaGtTcCtGaTcCgTtTcAgTcAtAcGtAgAcTtCcCaCcAaAtAtGcCgTtAcAtCgCtCgTgGtCtAgTgTtAcTtTcCcGgTtAaAaCaAgTcCtCtAgCgCaAgAtTtTaGcTgTcAgAgAtAtAgCcCcAgGaAaCgCaGaAgCcGcCgTgGaAgGaAtTaCgTcTcCtGcAtTgAgGtTgCtTgAcTtGaAgCcTgAtGgAgGaAcAaTtGaAgTcTtAcTaAgCcCgGcGcAcAaCaGtTaAcTcTtTaTaGcAgAgAtTtAcTtTgGgGtCaTgAgCcCaAgCgGaCgGaCgGtGgAgCgAtCgTgAgTcAaCcCcAcAtCtAaTtTgTgAgTgAtTtAaGaAaGtCgCgGaCaCgCgGaAgCcTgTtGaTgAcAcCgCgTaAgTgCaAaTtCgTaGcCaTcAcCgTtCaAaCgTaTcGcCtTgGgTtCtAtAtGtCgTgTaGtCtGtGgGaGaCgGtGcCaGaCcTaAtAcCtAaAcAgTcCaGgGgCgTaGgAcCaTcGgAgTcTtTcAtTgAtGgGgCcCaTtAaAaAaCaTtTgGcGaAaGtAaGgTcAcTtCcTcGgCgGcTaCcTtAgCtTaTaGcGcGaTggggggtGaTaGaTtTcCcCcTtCcTtTtAtCgTaCtTcGgGcTtAtTtGgCtTcTgTaGtTcAaTtAgGgGtAaTgAaAtAgAgCgGcCgAtTcGaAaTgGaTgAcCaTcAaTcTgGtCgAcGaCgTgAgTcGcGcAtAaAgTtCaCgCaTaTcAtAaTgGgGtGgAgTgCgGcAcAtAaAcTgAgCgCgAaTtAgTgCaggggggAcCgTgAtAgGcTaAcTgAaGgAgAgCtTtCtCgAcAtAgCaCaGcTaAgGgTgTgAgCgTcTcTtTgCcGtAtTcGcAaCgGgAgGaCgGgAgCcTaAgAcAgTtAgCcTgTtCcCgAtGgAaAgAgGaAgAgGgAcTcAaTgTaCgTgGcTgAgTcCaCtGcAgGaGaTtAgCgAcGgggggAcAaCaGtAaCcGcAcAgAcGtCgGgAtTtGaGgTtTaGgTgGtTgAtGggggggtAgGaTtTgCcGgAcTgCaAaCgTcTgAcTaAtTaTtCgTaCaAgCcAtGgAgAaGgGaCcGcCaTgTaAgTaCtTcAgCcCtTtAaAtCgTgGcTcCaCcTgAgGtAgTtAgCcGgTgTaTgTgGgGcGcGtTcCgAcGaCtCaAaTaTgAgTgAcAgGgTcGgTaAaTcGcGtAaAcGgTtTaCgTcGtAgGtAaTcGgCcTgGgAtGcGcCaAcCaAtAgCcTtCcTcAgAtCcCtAgCaCcCtAgGcAgTtCgAcCgTaAaAaCaGcAaCcAgGaTgGgGaTgCtAcGcCcTaGgCcGgTgCgAaAcGgAgAtCgggggggCaGgTgTgTtCcGaCtAaTgGaTgGgGaAggggggaCaCaTtAaAcTcAaAtGaTaCgTaGtTgGaCtGgCgCaTgTgTcCgTtCgTaGtTcCgCcGcCcCcTgTcAaTcTgGcGggggggcCcTtAgAgAtTtGaGcGcCtGgTcTcGtGcGcCcTcGgAaCgAtTgTtTtGaAcTgA

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gCtTtCtTaAgTaGtAcGcAcAcAtAgCtCgAtCtTgGcTcCgTcTgTgTcCgGtGtGgTcCcCgGcTcCcTaTaAcCcGgGtTgGcAcAgTgCgGgCcTtAaCgTgCtTaCcGtGtCgCgTgCaCtGgGgGgTcAaTaAtCaTcAtTcTtAtGcCaTgAtGgGgGcGgTcAaTgTgTtGcTaAaAgCaTcAcTaCtGgGgggggAtGgCgCtAcGaTgAtAaTgTgGaTaTgCtCgCtGaCgTcAgCgggggggGgCaCcCtTcAaCcCcAgGtCgTgAgGcGgTgCtAtTaGtAtAtTtCcTtGcTcCcAgGgTgTaCtAaGtTcTgGtAgTcAaTaTtCcCcTgCgGgAgTcTaAaCtTcAcTtAtAcAgCcCgGcAtAgCgAtTtTcAaGgCtCcCcGtTcTaTcTtCtTgAcCgGgTaAgCcCcTcGcGtTcGtGtAgAaGcCgGgGaAaAgGcGgGcAgTaGgAcCaCtTgCgGgTtTaGaTtCcAgTaAaAtTaTtCgGgCaCgTcAaCtGgTcTcGgCcggggggAaGtGccAaTgAaCcTaGagccgAgCcAcCcTaTaTaTtCtGgTaAaGtAaGgTcAtCaAaCcCaTgGgCcTcAaAtAcTcAcCaGtAaTcCaCgTgGaTgTgTaTgGcTgGtTtTgGtAgTaAtGtAtCtTgCcAaGgGgCcTaAgTaGgAgGcTcAgGgCgCtTgAaTgCaAcAaAcCcAgGcCcGcAtCcAgGaCcAtGcCtAtCgTgAaCtAgGaCtGgCgCgCtGgCgTtGgTcCgTgAcAgTtgccgTgCcTgAgTgCaGgTtCgGtTcGgTtGaAaCcGcTcGgTcGtCaAcCcAtTgAaAtAtAtCgCgCaAcGaAaGcAaAaAgAgGcTcGgAtGgTcAcTcTcTaGcGgGtCtGcAgCgTtCaGcGgCtAgGaTgGcCcTcGcCgAtTgGtCcTtGaAgTaGgCtGgAcTcGcCaTgAaGgAcAaTgGtAtGgCgAcGgAtTtGcAaAcTcTcGaTtTtGcTaTtAtTcAaTcAcTtTcGcAcCaCgGtTaTtGcTcGcGgCaGaCaCtGtAtGcTcTaAaTaAtTcGtAcGaGaTgTgTtAcCgGgAgGcCcAaCcTtTaGgCtGaGtAaAcAtAtGtGtGaCtCcAaGgCcGaGcGaCgTaAcTtTgAgCgGtTtCaAtTcGgTgCgAcTaGcCaAcTgggggggggggTtAgGaGgTgAgAgTcTgTaTtCgAaGtCaAggggggcAgccgaCgGaTcAtTcGaCtCcAcTtTaCcTcAcGaAaAgTaTgCcAaTcTcAcGgTaAcGtGcCgAgTcTgAcAgAcTtTcCgCaTgAgGaTaGaTtCcGgGcTcTaCtTaCtTcGtGgCgTaTgAtAtGgGaGaTgTaGaTcAaTcGcCcGcTcAgAtGaAcTtAcAtGcAgccggTgAcAcGtGgCaGgTcTaTgCtCtCaGtAgTcTgTaGaCgAcTcGtAgCaTcAaAgTcCaAcTcGcAcCcGgCcAgTtGgCgGcGtGaCtCgCgTgCgCcGtGaCgGtAtGaTgCgTaCtCgAtAcCcAcCcCcTtAgAcAaAcAcTcTgTtTtTtAcCgAaTcAaGtGtAcAgAaAgTaTgGaAtCaGtTtTcTaAaCgTaTcTaAcgccgAcAgAgTgGcAgAtCgAgAtAgTcTgAtTgCgTaAtgccgAcCgTcCcCgGaGcAgCcAcCtAaTcCgTtTcCcGtGtCaAaAcTgTcTgTaAaGcAtTgGaAcGcTgTaCtTtAgGcGcAcCtCgAcGgCcGcTtGcTaGaCtCaGgGcGgCcTcTtTgAgTaAaTcGgCgCaCtCtAgTaGcCtGtGgGgAcGtTaTtGcAaGgGgTgTaGgAcCcCtCtGcAtCtTaAtCcAcAgCgAcTgTtCcTgAgAgAcGgTaGgGgCtGcCtCaTcAaTtGcGtTtAcCcTgGcCgAtTtCcTcTaAaCtGcCcTgGtAaGaCaCgTgTgAaTaCgCtGcAcTcAtTtAgAtTgTtCtAtTcTaTgTgCcGtGcGcAcGcTaTgAgCgTaGgGcCgCtTtGgTtTaCgAtAaTgAtCgTtGtTtCtTtTcGcAtTcGtGaCtTcAgTgTtAgGgTgTgTcCgGtTtGgAaGcTgAgGaCgCtAcGtAaTgAgCtCcCgAaTcCaAgTcAaGgTtCtCcTcTgAaAgAaAaAcTgGtCcCaTgTtCtCcCgGcTgAcCcCaCcGaAtGaGaGgAgGcGtCcCaTgTgccggGtTcGcAtGcGgAaAcCaAcAtTcCtCgAtTcTtCcAtTcTgGcAcGtCgccggTcTcCtTcGgCgTaTcCgAtTtGgTcGgTgGtCaTgAaGtCgTaGgTgCgCtTcTtAgTgAtCcTtCgGgTcTgTtAgTtAgTcAgCcAgccgaAtAcAgGtCgTtGcTaAaCcTgAcAcCaCtggggggAaAcTgGaGtAcTgAgTaTaTcAgTgTcAaGaTaTgccggAcCgccggCgTaCgTtCaGgCaGtTcCtGaTcCgTtTcAgTcAtAcGtAgAcTtCcCaCcAaAtAtGcCgTtAcAtCgCtCgTgGtCtAgTgTtAcTtTcCcGgTtAaAaCaAgTcCtCtAgCgCaAgAtTtTaGcTgTcAgAgtAtAgCcCcAgGaAaCgCaGaAgCcGcCgTgGaAgGaAtTaCgTcTcCtGcAtTgAgGtTgCtTgAcTtGaAgCcTgAtGgAgGaAcAaTtGaAgTcTtAcTaAgCcCgGcGcAcAaCaGtTaAcTcTgccgaGcAgAgAtTtAcTtTgGgGtCaTgAgCcCaAgCgGaCgGaCgGtGgAgCgAtCgTgAgTcAaCcCcAcAtCtAaTtTgTgAgTgAtTtAaGaAaGtCgCgGaCaCgCgGaAgCcTgTtGaTgAcAcCgCgTaAgTgCaAaTtCgTaGcCaTcAcCgTtCaAaCgTaTcGcCtTgGgTtCtAtAtGtCgTgTaGtCtGtGgGaGaCgGtGcCaGaCcTaAtAcCtAaAcAgTcCaGgGgCgTaGgAcCaTcGgAgTcTtTcAtTgAtGgGgCcCgccgaAaAaCaTtTgGcGaAaGtAaGgTcAcTtCcTcGgCgGcTaCcTtAgCtTaTaGcGcGaTggggggtGaTaGaTtTcCcCcTtCcTtgccgCgTaCtTcGgGcTtAtTtGgCtTcTgTaGtTcAgccggGgGtAaTgAaAtAgAgCgGcCgAtTcGaAaTgGaTgAcCaTcAaTcTgGtCgAcGaCgTgAgTcGcGcgccgAgTtCaCgCaTaTcAtAaTgGgGtGgAgTgCgGcAcgccgAcTgAgCgCgAgccggTgCaggggggAcCgTgAtAgGcTaAcTgAaGgAgAgCtTtCtCgAcAtAgCaCaGcTaAgGgTgTgAgCgTcTcTtTgCcGtAtTcGcAaCgGgAgGaCgGgAgCcTaAgAcAgTtAgCcTgTtCcCgAtGgAaAgAgGaAgAgGgAcTcAaTgTaCgTgGcTgAgTcCaCtGcAgGaGaTtAgCgAcGgggggAcAaCaGtAaCcGcAcAgAcGtCgGgAtTtGaGgTtTaGgTgGtTgAtGggggggtAgGaTtTgCcGgAcTgCaAaCgTcTgAcgccgTaTtCgTaCaAgCcAtGgAgAaGgGaCcGcCaTgTaAgTaCtTcAgCcCtTtAaAtCgTgGcTcCaCcTgAgGtAgTtAgCcGgTgTaTgTgGgGcGcGtTcCgAcGaCtCaAaTaTgAgTgAcAgGgTcGgTaAaTcGcGtAaAcGgTtTaCgTcGtAgGtAaTcGgCcTgGgAtGcGcCaAcCaAtAgCcTtCcTcAgAtCcCtAgCaCcCtAgGcAgTtCgAcCgTaAaAaCaGcAaCcAgGaTgGgGaTgCtAcGcCcTaGgCcGgTgCgAaAcGgAgAtCgggggggCaGgTgTgTtCcGaCgccggGaTgGgGaAggggggaCaCaTtAaAcTcAaAtGaTaCgTaGtTgGaCtGgCgCaTgTgTcCgTtCgTaGtTcCgCcGcCcCcTgTcAaTcTgGcGggggggcCcTtAgAgAtTtGaGcGcCtGgTcTcGtGcGcCcTcGgAaCgAtTgTtTtGaAcTgA

***S. GenScript synthesized 4,000 bp spacer template sequence from bab1 1st intron with nucleotides shuffled, non-complementary transversions substituted at odd base pairs, restriction sites for KpnI, EcoRI, XhoI, StuI, SpeI, BamHI, NheI, and SacII removed by base pair substitutions, Hox-like binding motifs (YTAATKV and TTTAT) mutated, added Hsp70 promoter flanked by StuI and BamHI sites, and an added terminal BglII site***

AGGCCTCTCGACTCTAGCGCGTACCCTAGAGGATCAGCTTGGCTGCAGATTGTTTAGCTTGTTCAGCTGCGCTTGTTTATTTGCTTAGCTTTCGCTTAGCGACGTGTTCACTTTGCTTGTTTGAATTGAATTGTCGCTCCGTAGACGAAGCGCCTCTATTTATACTCCGGCGCTCGGATCCgCtTtCtTaAgTaGtAcGcAcAcAtAgCtCgAtCtTgGcTcCgTcTgTgTcCgGtGtGgTcCcCgGcTcCcTaTaAcCcGgGtTgGcAcAgTgCgGgCcTtAaCgTgCtTaCcGtGtCgCgTgCaCtGgGgGgTcAaTaAtCaTcAtTcTtAtGcCaTgAtGgGgGcGgTcAaTgTgTtGcTaAaAgCaTcAcTaCtGgGgggggAtGgCgCtAcGaTgAtAaTgTgGaTaTgCtCgCtGaCgTcAgCgggggggGgCaCcCtTcAaCcCcAgGtCgTgAgGcGgTgCtAtTaGtAtAtTtCcTtGcTcCcAgGgTgTaCtAaGtTcTgGtAgTcAaTaTtCcCcTgCgGgAgTcTaAaCtTcAcTtAtAcAgCcCgGcAtAgCgAtTtTcAaGgCtCcCcGtTcTaTcTtCtTgAcCgGgTaAgCcCcTcGcGtTcGtGtAgAaGcCgGgGaAaAgGcGgGcAgTaGgAcCaCtTgCgGgTtTaGaTtCcAgTaAaAtTaTtCgGgCaCgTcAaCtGgTcTcGgCcggggggAaGtGcCcAaTgAaCcTaGagccgAgCcAcCcTaTaTaTtCtGgTaAaGtAaGgTcAtCaAaCcCaTgGgCcTcAaAtAcTcAcCaGtAaTcCaCgTgGaTgTgTaTgGcTgGtTtTgGtAgTaAtGtAtCtTgCcAaGgGgCcTaAgTaGgAgGcTcAgGgCgCtTgAaTgCaAcAaAcCcAgGcCcGcAtCcAgGaCcAtGcCtAtCgTgAaCtAgGaCtGgCgCgCtGgCgTtGgTcCgTgAcAgTtgccgTgCcTgAgTgCaGgTtCgGtTcGgTtGaAaCcGcTcGgTcGtCaAcCcAtTgAaAtAtAtCgCgCaAcGaAaGcAaAaAgAgGcTcGgAtGgTcAcTcTcTaGcGgGtCtGcAgCgTtCaGcGgCtAgGaTgGcCcTcGcCgAtTgGtCcTtGaAgTaGgCtGgAcTcGcCaTgAaGgAcAaTgGtAtGgCgAcGgAtTtGcAaAcTcTcGaTtTtGcTaTtAtTcAaTcAcTtTcGcAcCaCgGtTaTtGcTcGcGgCaGaCaCtGtAtGcTcTaAaTaAtTcGtAcGaGaTgTgTtAcCgGgAgGcCcAaCcTtTaGgCtGaGtAaAcAtAtGtGtGaCtCcAaGgCcGaGcGaCgTaAcTtTgAgCgGtTtCaAtTcGgTgCgAcTaGcCaAcTgggggggggggTtAgGaGgTgAgAgTcTgTaTtCgAaGtCaAggggggcAgccgaCgGaTcAtTcGaCtCcAcTtTaCcTcAcGaAaAgTaTgCcAaTcTcAcGgTaAcGtGcCgAgTcTgAcAgAcTtTcCgCaTgAgGaTaGaTtCcGgGcTcTaCtTaCtTcGtGgCgTaTgAtAtGgGaGaTgTaGaTcAaTcGcCcGcTcAgAtGaAcTtAcAtGcAgccggTgAcAcGtGgCaGgTcTaTgCtCtCaGtAgTcTgTaGaCgAcTcGtAgCaTcAaAgTcCaAcTcGcAcCcGgCcAgTtGgCgGcGtGaCtCgCgTgCgCcGtGaCgGtAtGaTgCgTaCtCgAtAcCcAcCcCcTtAgAcAaAcAcTcTgTtTtTtAcCgAaTcAaGtGtAcAgAaAgTaTgGaAtCaGtTtTcTaAaCgTaTcTaAcgccgAcAgAgTgGcAgAtCgAgAtAgTcTgAtTgCgTaAtgccgAcCgTcCcCgGaGcAgCcAcCtAaTcCgTtTcCcGtGtCaAaAcTgTcTgTaAaGcAtTgGaAcGcTgTaCtTtAgGcGcAcCtCgAcGgCcGcTtGcTaGaCtCaGgGcGgCcTcTtTgAgTaAaTcGgCgCaCtCtAgTaGcCtGtGgGgAcGtTaTtGcAaGgGgTgTaGgAcCcCtCtGcAtCtTaAtCcAcAgCgAcTgTtCcTgAgAgAcGgTaGgGgCtGcCtCaTcAaTtGcGtTtAcCcTgGcCgAtTtCcTcTaAaCtGcCcTgGtAaGaCaCgTgTgAaTaCgCtGcAcTcAtTtAgAtTgTtCtAtTcTaTgTgCcGtGcGcAcGcTaTgAgCgTaGgGcCgCtTtGgTtTaCgAtAaTgAtCgTtGtTtCtTtTcGcAtTcGtGaCtTcAgTgTtAgGgTgTgTcCgGtTtGgAaGcTgAgGaCgCtAcGtAaTgAgCtCcCgAaTcCaAgTcAaGgTtCtCcTcTgAaAgAaAaAcTgGtCcCaTgTtCtCcCgGcTgAcCcCaCcGaAtGaGaGgAgGcGtCcCaTgTgccggGtTcGcAtGcGgAaAcCaAcAtTcCtCgAtTcTtCcAtTcTgGcAcGtCgccggTcTcCtTcGgCgTaTcCgAtTtGgTcGgTgGtCaTgAaGtCgTaGgTgCgCtTcTtAgTgAtCcTtCgGgTcTgTtAgTtAgTcAgCcAgccgaAtAcAgGtCgTtGcTaAaCcTgAcAcCaCtggggggAaAcTgGaGtAcTgAgTaTaTcAgTgTcAaGaTaTgccggAcCgccggCgTaCgTtCaGgCaGtTcCtGaTcCgTtTcAgTcAtAcGtAgAcTtCcCaCcAaAtAtGcCgTtAcAtCgCtCgTgGtCtAgTgTtAcTtTcCcGgTtAaAaCaAgTcCtCtAgCgCaAgAtTtTaGcTgTcAgAgAtAtAgCcCcAgGaAaCgCaGaAgCcGcCgTgGaAgGaAtTaCgTcTcCtGcAtTgAgGtTgCtTgAcTtGaAgCcTgAtGgAgGaAcAaTtGaAgTcTtAcTaAgCcCgGcGcAcAaCaGtTaAcTcTgccgaGcAgAgAtTtAcTtTgGgGtCaTgAgCcCaAgCgGaCgGaCgGtGgAgCgAtCgTgAgTcAaCcCcAcAtCtAaTtTgTgAgTgAtTtAaGaAaGtCgCgGaCaCgCgGaAgCcTgTtGaTgAcAcCgCgTaAgTgCaAaTtCgTaGcCaTcAcCgTtCaAaCgTaTcGcCtTgGgTtCtAtAtGtCgTgTaGtCtGtGgGaGaCgGtGcCaGaCcTaAtAcCtAaAcAgTcCaGgGgCgTaGgAcCaTcGgAgTcTtTcAtTgAtGgGgCcCgccgaAaAaCaTtTgGcGaAaGtAaGgTcAcTtCcTcGgCgGcTaCcTtAgCtTaTaGcGcGaTggggggtGaTaGaTtTcCcCcTtCcTtgccgCgTaCtTcGgGcTtAtTtGgCtTcTgTaGtTcAgccggGgGtAaTgAaAtAgAgCgGcCgAtTcGaAaTgGaTgAcCaTcAaTcTgGtCgAcGaCgTgAgTcGcGcgccgAgTtCaCgCaTaTcAtAaTgGgGtGgAgTgCgGcAcgccgAcTgAgCgCgAgccggTgCaggggggAcCgTgAtAgGcTaAcTgAaGgAgAgCtTtCtCgAcAtAgCaCaGcTaAgGgTgTgAgCgTcTcTtTgCcGtAtTcGcAaCgGgAgGaCgGgAgCcTaAgAcAgTtAgCcTgTtCcCgAtGgAaAgAgGaAgAgGgAcTcAaTgTaCgTgGcTgAgTcCaCtGcAgGaGaTtAgCgAcGgggggAcAaCaGtAaCcGcAcAgAcGtCgGgAtTtGaGgTtTaGgTgGtTgAtGggggggtAgGaTtTgCcGgAcTgCaAaCgTcTgAcgccgTaTtCgTaCaAgCcAtGgAgAaGgGaCcGcCaTgTaAgTaCtTcAgCcCtTtAaAtCgTgGcTcCaCcTgAgGtAgTtAgCcGgTgTaTgTgGgGcGcGtTcCgAcGaCtCaAaTaTgAgTgAcAgGgTcGgTaAaTcGcGtAaAcGgTtTaCgTcGtAgGtAaTcGgCcTgGgAtGcGcCaAcCaAtAgCcTtCcTcAgAtCcCtAgCaCcCtAgGcAgTtCgAcCgTaAaAaCaGcAaCcAgGaTgGgGaTgCtAcGcCcTaGgCcGgTgCgAaAcGgAgAtCgggggggCaGgTgTgTtCcGaCgccggGaTgGgGaAggggggaCaCaTtAaAcTcAaAtGaTaCgTaGtTgGaCtGgCgCaTgTgTcCgTtCgTaGtTcCgCcGcCcCcTgTcAaTcTgGcGggggggcCcTtAgAgAtTtGaGcGcCtGgTcTcGtGcGcCcTcGgAaCgAtTgTtTtGaAcTgAagatct

***T. AgeI-EGFP-NLS-SpeI sequence that was removed from pS3aG to replace with new fluorescent reporter protein coding sequences***

The 5’ *Age*I site (blue background) and a 3’ *Spe*I site (green background) are annotated.

ACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTACGGCGTGCAGTGCTTCAGCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACTACAACAGCCACAACGTCTATATCATGGCCGACAAGCAGAAGAACGGCATCAAGGTGAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCGCCCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGAGCAGGCACAGAAGGCATCGCCAGCGCTCTAGGAGCCGCAATCGCAGCCGAAGTCGCAGCAGTGAACGAAAACGCCGTCAACGGAGCCGAAGTCGCAGCAGTGAACGAAGACGCTAACTTGTACAAGTAAAGCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAACTAGT

***U. AgeI and SpeI flanked mCherry-NLS sequence***

The following 1,142 bp sequence was synthesized in the pUC57 vector by GenScript Inc. that contains the *mCherry-NLS* coding sequence that is flanked by a 5’ *Age*I site (blue background) and a 3’ *Spe*I site (green background). The synonymous base changes that destroyed resident *Stu*I and *Sbf*I sites are indicated by the red font color.

ACCGGTCGCCACCATGGTGAGCAAGGGCGAGGAGGATAACATGGCCATCATCAAGGAGTTCATGCGCTTCAAGGTGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGAGGGCGAGGGCCGCCCCTACGAGGGCACCCAGACCGCCAAGCTGAAGGTGACCAAGGGTGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCTCAGTTCATGTACGGCTCCAAAGCCTACGTGAAGCACCCCGCCGACATCCCCGACTACTTGAAGCTGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGGACTCCTCACTGCAGGACGGCGAGTTCATCTACAAGGTGAAGCTGCGCGGCACCAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACCATGGGCTGGGAGGCTTCCTCCGAGCGGATGTACCCCGAGGACGGCGCCCTGAAGGGCGAGATCAAGCAGAGGCTGAAGCTGAAGGACGGCGGCCACTACGACGCTGAGGTCAAGACCACCTACAAGGCCAAGAAGCCCGTGCAGCTGCCCGGCGCCTACAACGTCAACATCAAGTTGGACATCACCTCCCACAACGAGGACTACACCATCGTGGAACAGTACGAACGCGCCGAGGGCCGCCACTCCACCGGCGGCATGGACGAGCTGTACAAGTCCGGAAACCTGTACAAGAGCAGGCACAGAAGGCATCGCCAGCGCTCTAGGAGCCGCAATCGCAGCCGAAGTCGCAGCAGTGAACGAAAACGCCGTCAACGGAGCCGAAGTCGCAGCAGTGAACGAAGACGCTAACTTGTACATAGGGCCGGCCGCGACTCTAGATCATAATCA

GCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATGACTAGT

***V. AgeI and SpeI site flanked E2-Crimson-NLS sequence***

The following 1,100 bp sequence was synthesized in the pUC57 vector by GenScript Inc. that contains the *E2-Crimson-NLS* coding sequence that is flanked by a 5’ *Age*I site (blue background) and a 3’ *Spe*I site (green background). The synonymous base change that destroyed resident *Sbf*I sites is indicated by the red font color.

ACCGGTCGCCACCATGGATAGCACTGAGAACGTCATCAAGCCCTTCATGCGCTTCAAGGTGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGTGGGCGAGGGCAAGCCCTACGAGGGCACCCAGACCGCCAAGCTGCAAGTGACCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCCAGTTCTTCTACGGCTCCAAGGCGTACATCAAGCACCCCGCCGACATCCCCGACTACCTCAAGCAGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGGACTCCTCACTGCAGGACGGCACCCTCATCTACCACGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACTCTGGGCTGGGAGCCCTCCACTGAGCGCAACTACCCCCGCGACGGCGTGCTGAAGGGCGAGAACCACATGGCGCTGAAGCTGAAGGGCGGCGGCCACTACCTGTGTGAGTTCAAGTCCATCTACATGGCCAAGAAGCCCGTGAAGCTGCCCGGCTACCACTACGTGGACTACAAGCTCGACATCACCTCCCACAACGAGGACTACACCGTGGTGGAGCAGTACGAGCGCGCCGAGGCCCGCCACCACCTGTTCCAGCTGTACAAGAGCAGGCACAGAAGGCATCGCCAGCGCTCTAGGAGCCGCAATCGCAGCCGAAGTCGCAGCAGTGAACGAAAACGCCGTCAACGGAGCCGAAGTCGCAGCAGTGAACGAAGACGCTAACTTGTACATAGGGCCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATGACTAGT

***W. AgeI and NotI site flanked mCerulean-NLS sequence***

The following 871 bp sequence was synthesized in the pUC57 vector by GenScript Inc. that contains the *mCerulean-NLS* coding sequence that is flanked by a 5’ *Age*I site (blue background) and a 3’ *Not*I site (yellow background).

ACCGGTGTCGCCACCATGGTGAGCAAGGGCGAGGAGCTGTTCACCGGGGTGGTGCCCATCCTGGTCGAGCTGGACGGCGACGTAAACGGCCACAAGTTCAGCGTGTCCGGCGAGGGCGAGGGCGATGCCACCTACGGCAAGCTGACCCTGAAGTTCATCTGCACCACCGGCAAGCTGCCCGTGCCCTGGCCCACCCTCGTGACCACCCTGACCTGGGGCGTGCAGTGCTTCGCCCGCTACCCCGACCACATGAAGCAGCACGACTTCTTCAAGTCCGCCATGCCCGAAGGCTACGTCCAGGAGCGCACCATCTTCTTCAAGGACGACGGCAACTACAAGACCCGCGCCGAGGTGAAGTTCGAGGGCGACACCCTGGTGAACCGCATCGAGCTGAAGGGCATCGACTTCAAGGAGGACGGCAACATCCTGGGGCACAAGCTGGAGTACAACGCCATCAGCGACAACGTCTATATCACCGCCGACAAGCAGAAGAACGGCATCAAGGCCAACTTCAAGATCCGCCACAACATCGAGGACGGCAGCGTGCAGCTCGCCGACCACTACCAGCAGAACACCCCCATCGGCGACGGCCCCGTGCTGCTGCCCGACAACCACTACCTGAGCACCCAGTCCAAGCTGAGCAAAGACCCCAACGAGAAGCGCGATCACATGGTCCTGCTGGAGTTCGTGACCGCCGCCGGGATCACTCTCGGCATGGACGAGCTGTACAAGAGCAGGCACAGAAGGCATCGCCAGCGCTCTAGGAGCCGCAATCGCAGCCGAAGTCGCAGCAGTGAACGAAAACGCCGTCAACGGAGCCGAAGTCGCAGCAGTGAACGAAGACGCTAACTTGTACAAGTAAAGCGGCCGC

***X. BamHI and EcoRI site flanked cassette with an Hsp70 promoter, E2-Crimson-NLS coding sequence, and a 3’UTR with polyA signal***

The following 1,297 bp sequence was synthesized in the pUC57 vector by GenScript Inc. that contains from 5’-3’ a *Bam*HI site (pink background), *Hsp70* gene promoter, *E2-Crimson-NLS* coding sequence, a 3’UTR containing a polyA signal sequence, and an *Eco*RI site (grey background).

GGATCCGAGCGCCGGAGTATAAATAGAGGCGCTTCGTCTACGGAGCGACAATTCAATTCAAACAAGCAAAGTGAACACGTCGCTAAGCGAAAGCTAAGCAAATAAACAAGCGCAGCTGAACAAGCTAAACAATCTGCAGCCAAGCTGATCCTCTAGGGTACGCGCTAGAGTCGAGAGGCCTGTTTAATTCGCCCTTCACCCGTCGCCACCATGGATAGCACTGAGAACGTCATCAAGCCCTTCATGCGCTTCAAGGTGCACATGGAGGGCTCCGTGAACGGCCACGAGTTCGAGATCGAGGGCGTGGGCGAGGGCAAGCCCTACGAGGGCACCCAGACCGCCAAGCTGCAAGTGCCAAGGGCGGCCCCCTGCCCTTCGCCTGGGACATCCTGTCCCCCCAGTTCTTCTACGGCTCCAAGGCGTACATCAAGCACCCCGCCGACATCCCCGACTACCTCAAGCAGTCCTTCCCCGAGGGCTTCAAGTGGGAGCGCGTGATGAACTTCGAGGACGGCGGCGTGGTGACCGTGACCCAGGACTCCTCACTGCAGGACGGCACCCTCATCTACCACGTGAAGTTCATCGGCGTGAACTTCCCCTCCGACGGCCCCGTAATGCAGAAGAAGACTCTGGGCTGGGAGCCCTCCACTGAGCGCAACTACCCCCGCGACGGCGTGCTGAAGGGCGAGAACCACATGGCGCTGAAGCTGAAGGGCGGCGGCCACTACCTGTGTGAGTTCAAGTCCATCTACATGGCCAAGAAGCCCGTGAAGCTGCCCGGCTACCACTACGTGGACTACAAGCTCGACATCACCTCCCACAACGAGGACTACACCGTGGTGGAGCAGTACGAGCGCGCCGAGGCCCGCCACCACCTGTTCCAGCTGTACAAGAGCAGGCACAGAAGGCATCGCCAGCGCTCTAGGAGCCGCAATCGCAGCCGAAGTCGCAGCAGTGAACGAAAACGCCGTCAACGGAGCCGAAGTCGCAGCAGTGAACGAAGACGCTAACTTGTACATAGGGCCGGCCGCGACTCTAGATCATAATCAGCCATACCACATTTGTAGAGGTTTTACTTGCTTTAAAAAACCTCCCACACCTCCCCCTGAACCTGAAACATAAAATGAATGCAATTGTTGTTGTTAACTTGTTTATTGCAGCTTATAATGGTTACAAATAAAGCAATAGCATCACAAATTTCACAAATAAAGCATTTTTTTCACTGCATTCTAGTTGTGGTTTGTCCAAACTCATCAATGTATCTTAAGGCGTAAATTGTAAGCGTTAATGGAATTC

***Y. 1,157 bp StuI and BamHI site flanked bab2 promoter-proximal region***

AGGCCTGCTTTGCTGTCTTTGCTGCCGCTTCTGTCGTTGTTGTTGTTGTTGTGGGTATTATTGTTGTTGTTGCTGGCTTTCAGTGGCCGTAAAAACAAACGCTGCACTCCACTCACGCCGAAAGTCAGATACGAACTGAATCTCACAGATAAACGAACTGAATTTCAAAAAATTGAATGAAACTCGACGCCGCGCTGCCGACGTCAGCTGCGCTGCCCGCTCTCTCGCGGCGAATGAGAGCGCCGGCGTGGTGTTTTCCGGTTTTTGCGGCGAATTGGGAAATCGACAGAGCGGCGGTTTAAGAGCGAAAGTAAGTGTGCTCTTTGCTTTCTTTGTTTTGAATTTTCAGAGATCTTGCTTGAAAAAAAATTGAAAATTTCGAAATTTTTAGAAATGTTAGAAATTATAATTAAAATGAAATCGTGATTGTATAAGAGGAGAACATATTTTATTAATCTGGAATGCAATTGTTTTGTTATTTTTTTATACATTTTAGTACAGATTAATAGTTTTTTATTCGAATCATATTTCTCATCATAAAAAACATACATTTCACTACGATTTTTATATAATTGTCTAAGACCCAACGTTTCTTTTTTTTTTCGTTGTCACATAAATTTGCGAAAGTAGTTTTTACTATATCAACATACTTCATTTACAATTAAAAACGAATCATATTTATTATAATTAGTTTGAATACTTATTGAAATAAGTTCTCTTATTTATATAAATGCCATGCTTACCAATAAATCGCAAAAATCTTAACAAATCGCCAAAGCAGCATGCTAAGGTCGCGAAAAAATTGCAGCCTACACCTGCAACTTGAAGAGAATAGCAACAGCAACTTGCAACCTAGCTGCAGCAGCAACAACAACAGCAACAGCAGGGGCAAGAAAGAGAAACTGGCCAATGTCCAGTAAGAAAGTGTTTCAAAATAGTTGCCAACCCTCTTTCTTCTTCTTCTGCATCATCCTTAACCTCCTTGTTGTTGCTTTTGCTGCTTAGGCACAGAAACTATGGCAAAAAAGAGCAGAGAAAAAGTGGCGACAGCAACACACTCACAACTTGGCCACGCCCCTAAAAGTGCCGTAAGAGGGCGCGAGTGCGAGTGGGACAGCAAGCTGCTTGCTCCTACACACGCACACACAAGCGGATCC