pDAP101 construct used in SAIL lines

Left border primers (LB1 is proximal, LB3 is distal and was used for sequencing):

LB1: 5'-GCCTTTTCAGAAATGGATAAATAGCCTTGCTTCC-3'

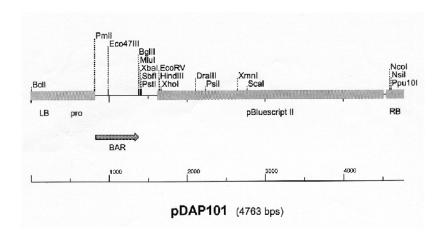
LB2: 5'-GCTTCCTATTATATCTTCCCAAATTACCAATACA-3'

LB3: 5'-TAGCATCTGAATTTCATAACCAATCTCGATACAC-3'

Right border primers:

RB1: 5' - ATT AGG CAC CCC AGG CTT TAC ACT TTA TG - 3'
RB2: 5' - GTA TGT TGT GTG GAA TTG TGA GCG GAT AAC - 3'
RB3: 5' - TAA CAA TTT CAC ACA GGA AAC AGC TAT GAC - 3'

pDAP101 is described in a paper by John McElver et al in Genetics 159: 1751 (2001).



pDAP101 T-DNA

GGATCCTGATCACAGGCAGCAACGCTCTGTCATCGTTACAATCAACATGCTACCCTCCGC GAGATCATCCGTGTTTCAAACCCGGCAGCTTAGTTGCCGTTCTTCCGAATAGCATCGGTA ACATGAGCAAAGTCTGCCGCCTTACAACGGCTCTCCCGCTGACGCCGTCCCGGACTGATG GGCTGCCTGTATCGAGTGGTGATTTTGTGCCGAGCTGCCGGTCGGGGAGCTGTTGGCTGG CTGGTGGCAGGATATATTGTGGTGTAAACAAATTGACGCTTAGACAACTTAATAACACAT TGCGGACGTTTTTAATGTACTGAATTAACGCCGAATTGAATTCGATTTGGTGTATCGAGA TTGGTTATGAAATTCAGATGCTAGTGTAATGTATTGGTAATTTGGGAAGATATAATAGGA ATTCCGTTCTTGCTGTAAAGCGTTGTTTGGTACACTTTTGACTAGCGAGGCTTGGCGTGT CAGCGTATCTATTCAAAAGTCGTTAATGGCTGCGGATCAAGAAAAGTTGGAATAGAAAC AGAATACCCGCGAAATTCAGGCCCGGTTGCCATGTCCTACACGCCGAAATAAACGACCAA ATTAGTAGAAAAATAAAAACTGACTCGGATACTTACGTCACGTCTTGCGCACTGATTTGA AAAATCTCAATATAAACAAAGACGGCCACAAGAAAAAACCAAAAACACCGATATTCATTAA TCTTATCTAGTTTCTCAAAAAAATTCATATCTTCCACACGTGGATCCATGAGCCCAGAAC GACGCCGGCCGACATCCGCCGTGCCACCGAGGCGGACATGCCGGCGGTCTGCACCATCG TCAACCACTACATCGAGACAAGCACGGTCAACTTCCGTACCGAGCCGCAGGAACCGCAGG AGTGGACGGACGTCCGTCCGTCTGCGGGAGCGCTATCCCTGGCTCGTCGCCGAGGTGG ACGGCGAGGTCGCCGCCATCGCCTACGCGGGCCCCTGGAAGGCACGCAACGCCTACGACT GGACGGCCGAGTCGACCGTGTACGTCTCCCCCCGCCACCAGCGGACGGGACTGGGCTCCA CGCTCTACACCCACCTGCTGAAGTCCCTGGAGGCACAGGGCTTCAAGAGCGTGGTCGCTG TCATCGGGCTGCCCAACGACCCGAGCGTGCGCATGCACGAGGCGCTCGGATATGCCCCCC GCGGCATGCTGCGGGCCGGCTTCAAGCACGGGAACTGGCATGACGTGGGTTTCTGGC AGCTGGACTTCAGCCTGCCGGTACCGCCCCGTCCGGTCCTGCCCGTCACCGAGATCTGAT CTCACGCGTCTAGGATCCTCTAGAGTCGACCTGCAGGCATGCCGCTGAAATCACCAGTCT CTCTCTACAAATCTATCTCTCTCTATAATAATGTGTGAGTAGTTCCCAGATAAGGGAATT GTATTTGTAAAATACTTCTATCAATAAAATTTCTAATTCCTAAAACCAAAATCCAGTGGG TACCGAGCTCGAATTCGATATCAAGCTTATCGATACCGTCGACCTCGAGGGGGGGCCCGG TACCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGCCGTCGTTTTACAAC GTCGTGACTGGGAAAACCCTGGCGTTACCCAACTTAATCGCCTTGCAGCACATCCCCCTT TCGCCAGCTGGCGTAATAGCGAAGAGGCCCGCACCGATCGCCCTTCCCAACAGTTGCGCA GCCTGAATGGCGAATGGGACGCCCCTGTAGCGGCGCATTAAGCGCGGCGGGTGTGGTGG TTACGCGCAGCGTGACCGCTACACTTGCCAGCGCCCTAGCGCCCGCTCCTTTCGCTTTCT TCCCTTCCTTTCTCGCCACGTTCGCCGGCTTTCCCCGTCAAGCTCTAAATCGGGGGCTCC CTTTAGGGTTCCGATTTAGTGCTTTACGGCACCTCGACCCCAAAAAACTTGATTAGGGTG ATGGTTCACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCGCCCTTTGACGTTGGAGT CCACGTTCTTTAATAGTGGACTCTTGTTCCAAACTGGAACAACACTCAACCCTATCTCGG TCTATTCTTTTGATTTATAAGGGATTTTGCCGATTTCGGCCTATTGGTTAAAAAATGAGC TGATTTAACAAAAATTTAACGCGAATTTTAACAAAATATTAACGCTTACAATTTAGGTGG CACTTTTCGGGGAAATGTGCGCGGAACCCCTATTTGTTTATTTTTCTAAATACATTCAAA TATGTATCCGCTCATGAGACAATAACCCTGATAAATGCTTCAATAATATTGAAAAAGGAA GAGTATGAGTATTCAACATTTCCGTGTCGCCCTTATTCCCTTTTTTGCGGCATTTTGCCT TCCTGTTTTTGCTCACCCAGAAACGCTGGTGAAAGTAAAAGATGCTGAAGATCAGTTGGG TGCACGAGTGGGTTACATCGAACTGGATCTCAACAGCGGTAAGATCCTTGAGAGTTTTCG CCCCGAAGAACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCGGTATT ATCCCGTATTGACGCCGGGCAAGAGCAACTCGGTCGCCGCATACACTATTCTCAGAATGA CTTGGTTGAGTACTCACCAGTCACAGAAAAGCATCTTACGGATGGCATGACAGTAAGAGA GATCGGAGGACCGAAGGAGCTAACCGCTTTTTTGCACAACATGGGGGATCATGTAACTCG CCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAAACGACGAGCGTGACACCAC AGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTGCAGGACCACTTCT GTCTCGCGGTATCATTGCAGCACTGGGGCCAGATGGTAAGCCCTCCCGTATCGTAGTTAT CTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGCTGAGATAGG TGCCTCACTGATTAAGCATTGGTAACTGTCAGACCAAGTTTACTCATATACTTTAGAT TGATTTAAAACTTCATTTTTAATTTAAAAGGATCTAGGTGAAGATCCTTTTTGATAATCT CATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCGTAGAAAA AAAACCACCGCTACCAGCGGTGGTTTGTTTGCCGGATCAAGAGCTACCAACTCTTTTTCC GAAGGTAACTGGCTTCAGCAGAGCGCAGATACCAAATACTGTCCTTCTAGTGTAGCCGTA GTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTGCTAATCCT GTTACCAGTGGCTGCCAGTGGCGATAAGTCGTGTCTTACCGGGTTGGACTCAAGACG ATAGTTACCGGATAAGGCGCAGCGGTCGGGCTGAACGGGGGGTTCGTGCACACAGCCCAG CTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAGAAAGCGC CACGCTTCCCGAAGGGAGAAAGGCGGACAGGTATCCGGTAAGCGGCAGGGTCGGAACAGG AGAGCGCACGAGGGGGCTTCCAGGGGGGAAACGCCTGGTATCTTTATAGTCCTGTCGGGTT GAAAAACGCCAGCAACGCGGCCTTTTTACGGTTCCTGGCCTTTTGCTGGCCTTTTGCTCA CATGTTCTTTCCTGCGTTATCCCCTGATTCTGTGGATAACCGTATTACCGCCTTTGAGTG AGCTGATACCGCTCGCCGCAGCCGAACGACCGAGCGCAGCTCAGTGAGCGAGGAAGC GGAAGAGCGCCCAATACGCAAACCGCCTCTCCCCGCGCGTTGGCCGATTCATTAATGCAGCTG GCACGACAGGTTTCCCGACTGGAAAGC