Supplementary Material.

Table 1. Primers used to resequence ***CDA*** and create expression constructs[a]

Primer Name	**Primer Location**	**Primer Sequence**
Gene resequencing		
UF(-565)	5'-FR	tgtaaaacgacggccagtCCAGCAGCTGAGACACTT
UR(-67)	5'-UTR	caggaaacagctatgaccCCAGACACGATTGCAGCT
UF(-296)	5'-FR	tgtaaaacgacggccagtCCAGTAGCGTGGCACCA
I1R113	IVS 1	caggaaacagctatgaccGACAGAGCCGCGCTCTT
I1F(-223)	IVS 1	tgtaaaacgacggccagtGGTAAATTAAGACAGTGCCAGGTT
I2R238	IVS 2	caggaaacagctatgaccCCTTGTATGAGAGTTGCCT
I2F(-232)	IVS 2	tgtaaaacgacggccagtCGTTTATGGATGGCACTAATGA
I3R172	IVS 3	caggaaacagctatgaccCCAGTGACTCATGCAAGCGTA
I3F(-84)	IVS 3	tgtaaaacgacggccagtGTGGCAGAGTCAGACTCA
DR11	3'-FR	caggaaacagctatgaccCACGCTTTGATCCAGGATGTT
Site-directed mutagenesis, expression construct		
F67WT	Exon 1	CAGGAGGCCAAG**A**AGTCAGCCTACT
R91WT	Exon 1	AGTAGGCTGACT**T**CTTGGCCTCCTG

[a]Lower case letters in resequencing primers indicate the universal M13 forward sequence added to the 5'-ends of forward primers and the universal M13 reverse sequence added to the 5'-ends of reverse primers. Bold, underlined letters are mutated bases in site-directed mutagenesis primers. "F" represents forward; "R" reverse; "U" upstream; "E" exon; "I" intron; "D" downstream; "FR" flanking region; "UTR" untranslated region; "IVS" intervening sequence (intron); and "WT" wild type. The numbering scheme for primers located in exons and 5'-FR is based on the cDNA sequence, with the "A" at the translation initiation codon designated as (+1). Positions 5' and 3' to that location were assigned negative or positive numbers, respectively. Intron-based primers were numbered on the basis of nucleotide distance from splice junctions, with (+1) as the first nucleotide at the 5'-end and (-1) as the first nucleotide at the 3'-end of the intron. Primers located downstream of the cDNA sequence were assigned positive numbers with (+1) as the first nucleotide 3' to that position.

Table 2. Primers used to resequence ***DCTD*** and create expression constructs [a]

Primer Name	**Primer Location**	**Primer Sequence**
Gene resequencing		
UF(-887)	5'-FR	tgtaaaacgacggccagtCAGGCGCAGCCAAATGC
UR(-349)	5'-FR	caggaaacagctatgaccGGTCGCACGCCGCAA
UF(-417)	5'-FR	tgtaaaacgacggccagtCCGCGGGCTGCGTCACGGGGA
I1R244	IVS 1	caggaaacagctatgaccCCGGGGCACTCCAAGGGG
I1F(-131)	IVS 1	tgtaaaacgacggccagtGGGAAACCAGGCTGATTCAGCACCT
I2R129	IVS 2	caggaaacagctatgaccGGCAAGCAGAGACTGTCTACGGCA
I1F181	IVS 1	tgtaaaacgacggccagtCCAGGGTCGATTTCTC
E2R(-119)	Exon 2	caggaaacagctatgaccGCGGCAGTGCCTAAG
E2F(-41)	Exon 2	tgtaaaacgacggccagtCCACATTCCTCGCCTTT
I2R(-277)	IVS 2	caggaaacagctatgaccGCCAGCCTACAAATTGTT
I2F(-332)	IVS 2	tgtaaaacgacggccagtGCTGACTCCGCTTTGTA
I3R146	IVS 3	caggaaacagctatgaccCTAAGCTTGTAGAAACGCA
I3F105	IVS 3	tgtaaaacgacggccagtCAGGGTCGGTCTGCCTT
I4R133	IVS 4	caggaaacagctatgaccGGTAGTTCAGTAGGATACT
I4F(-283)	IVS 4	tgtaaaacgacggccagtGGTCTTGTGGAGCCGTGAA
I5R190	IVS 5	caggaaacagctatgaccCAGAGGATGCAATTAGTCTTAGA
I5F(-86)	IVS 5	tgtaaaacgacggccagtGCTGAAAGTGCTCCAGCT
I6R370	IVS 6	caggaaacagctatgaccCTGGCAGGCTACTTTCAT
I6F(-115)	IVS 6	tgtaaaacgacggccagtGCAAGTGAATCCCAGGACATA
DR904	3'-UTR	caggaaacagctatgaccCCAGCACATGTAGCAGTGAA
Site-directed mutagenesis, expression construct		
F163Mut	Exon 4	GGGATGCCA**G**ATGGGTGCAGTGAT
R186Mut	Exon 4	ATCACTGCACCCAT**C**TGGCATCCC

[a]Except for the external nested primers UF(-879) and E2R(-107), the universal M13 forward sequence was added to the 5'-ends of forward primers and the universal M13 reverse sequence was added to the 5'-ends of reverse primers used for resequencing, as indicated by lower case letters. Bold, underlined letters are mutated bases in site-directed mutagenesis primers. Abbreviations and the numbering scheme for primers are identical to those described in the legend for Table 1.