VfDgat1	(1)	1 100 TCTCTCTCTCTTTTGCTTTACGTGTACATCGACCACCACCACCACCACCACCATCTTGCGACTGTTCAATTATCCTATAAGTACCACCGCCATTCATCACCGCCAATC
VfDgat1	(101)	101 CTTAA CTCTAAT TTGC TATAC TA AACA CTTGC TT TATA TGCG CTT TTCTAT TTAC TCT TCAC TG TA ATT TCTTATTGG TA TTCAAA GTGT TTTCAAT GA C
VfDgat1	(201)	201 AATCC CTGAAAC GCCG GATAATT CCAC GGATGCTACCACCAGTGGCGGTGC TGAG TCC TCTTCCGATCTTAACCTTTCTCTTCGACGGAG GAGGACTGCT
VfDgat1	(301)	400 TCAAA CTCCGAT GGAG CTGTCGC GGAA TTGGCTTCCAA GATTGATGA GTTG GAAT CTG ATGC CGGA GGA GGCCAGGTGA TTAA GGATCCG GGAGCAG AAA
VfDgat1	(401)	401 TGGAT TCGGGGA CTTT GAAAAGTAATG GAAAAGA TTGC GGAACC GTTAAGGATAG GAT TGAA AATC GTG AGAA TC GTGGAGGAT CGGATG TTAAATT CAC
VfDgat1		501 GTATC GGCCGTC GGTG CCGGCTC ACCG GGCGCTC AA GGAGAGTCCGCTTAG CTCT GATAA TA TATT TA <mark>A</mark> AC <mark>A</mark> A A <mark>G</mark> TC <mark>ATGCA</mark> GG <mark>T</mark> C TC TTC CAAT <mark>C TC</mark> TG T
VfDgat2 VfDgat3		A GAAG G <mark>G</mark> C G <mark>ATGCA</mark> CA TGA TAC TCTC <mark>C TC T</mark> TA
Consensus	(501)	601 700
VfDgat1 VfDgat2	(33)	A TA GT AGT GC TT GTAG CG GTTTA CAGT CG GCTTA TCA TTG A A A CATAA TG A AGT ATG GTTG GT
VfDgat3 Consensus	(1) (601)	ATA AGT T TA C A G A A AAA A T G G TTAA A TGGG T G AGTT A AT
VfDgat1		701 TG <mark>A GA G</mark> AC <mark>TGGC CACT TC TTA TG TGCT G</mark> TC TTAC C <mark>C TC</mark> CCAA TA TT TT C TC TTGC TGC CTAT CT A G TTG AGAA GT T <mark>GGC</mark> C <mark>TG TC</mark> GGA A GT ATA TA TC TG C
VfDgat2		GAAGAGGTTACCATATTCAAATCTGGAGAAATATACCCAACAAACA
VfDgat3 Consensus	(701)	AGAG T C TTC AT TG G TA C C A A TT T T ATTTGGCTAT TGGC TGGC
oonbenbub	(1017	801 900
VfDgat1		A CCA CTGTTGTTTTTCTTCATA TTCTTTTTTCCCCCCAAAAGCAGTTTTATA CCCTGTTTCTGTGATATCACTTGTGATTGTGAATCTGCCGTTTTTTTT
VfDgat2 VfDqat3		TCTTCTTAGECTCTTCTTCAATCTTCCTTCCTTTCTCCAAATTTCTCCTTCGTTATTGGGTTGCTTTTGTTTTTATGGGTGATTCCCTATCAACGATC CCTGCTTCTCATCTAGGATTGTGAATTCTTCAGAGTTCAGAGACAAGGGGCATCTTCAGTGTTATAATTATTACCATGGA
Consensus		CT CTT TCTCTTCTT AT TTCTTTCTT C CASATTTCT C CASATTTCT ASTTTCASTTTT AT TTAT TT
		901 1000
VfDgat1		GCATT GATGETCTTTG CTTG TAT CGTG TGGTTGA AA TT-GGTATCTTAT-GCACA TAC AAAC TTTG ATA TGAG AGC AATTGCTAACTCAG TTGATAA GG GCAGTAAGCTTGGCCCAATGCTTGTTCAGCTATATATCTAGGCATGTTT-GCAGCTATTTTCCCATCACTCTTCATGTTGAAGATAT-A-AATGC
VfDgat2 VfDgat3		GA GTARGET TE GECRATGET TE FICA GETATATATETAGEGATETT - GEREETATETTTE - CERTERTER AUTOTTER - TEITERGREATET - A AR TGE GAA GE AAGAT TE GTGA GGTG TGGAE CA TE CTEAT TA TEAGGATTAA AA AG GAGA AAG AATE CGE CEATG TE CA AGA AA A AGTTGAAATTA TTAA - AA GG
Consensus		GCAGTAAG TT GT A TTGT G CATC TTATAATTAGG AT TTA GCAGATA AATC CCAT TC AGCAA TSTTGAA TATTA AAGGC
		1001 1100
VfDgat1		AG <mark>AT</mark> G CECTAT <mark>C</mark> CAA <mark>T SCTT- CG</mark> AGTC CACGAGTC CTCTCATGATGTTAGCTTCAA GAGTTTG GTTTGAT TGAT
VfDgat2		CTTTC GTTCTGATCGTGCTTACGTGTTTGGTTAT-GAGCCACATTC-AGTTTTTCCCA-TTGGTGTGAT-GATTCTTTCTTTGGGTTTAATTCCTC TTATCAAAGGACTTGTCCGTGTTTTTCCAAATAGATCCTGATAATAGTCAAGCCAAGTTGGTGGCA-GAAGCAGCAGCAGAGAATTAATCAAAG
VfDgat3 Consensus	(1001)	
		1101 1200
VfDgat1		A A GTTATCCTCG A A COCCATC CA TTCG A A A GGTTGG C GTCGTC GTC A TTGTT A A GTTA TA - A TATTTA CA GA TTCATGGA A TTA TA TA A CA
VfDgat2 VfDqat3		TTCCTAATATAA AATTCCTTGCAAGTAGTGCTGTG-TTCTACACTCCATTTTTAAGACATATATGGTCATGGTGTGGTCTTACACCAGCAACA AACTTCAAGAGCTCAGAGCCAAAGGAGAAGGAGAAGGAG-TTGAAGAGAAACAAGAAACAAGAAAGGCCAAGGCTAAAAGCAGAAGGACAAGGATCA
Consensus		AACTTAA TAGAACT CATTGCAAAGGGT GGTG TTC ACA T ATTAAGAAAA A ATATGG CA G T ATGGGCTTAA CAAGGAACA 1201 1300
VfDgat1		ATATA TCAAT-CCTATCGTTCAGAATTCACAACATCCTTAAAAGGGGATCTCTTATAAGGGGATCTCTTATA
VfDgat2 VfDgat3		AG-GAAAAAT-TTTGTTTCCCTCCTGTCTTCTGGTTATAGTTGCATTCTGGTGGGGGTGCAGTCCAA-GAGAAATTT-TATATGAAGC-AGG AC-TATCAATGTCAATCATCCACTTCTGAATGCAGCGATGCGGATGCGGATGTGACAGTAATTTGGAGAAATGGAGTGGTGCTACGGGTGCTAGTTGAATT-ACA
Consensus		A TATCAAT TO ATC TTOTACT CTGACT CASC TGA GT CAT AT TGCCA TGAGTGT A GAA C T TAT TGAAT A
		13011400
VfDgat1		TETTECTTECTTECTECTECTECTECTECTECTECTECTE
VfDgat2 VfDgat3		A CTCT GAGATTG CTTT CCTTAAG GCAA GAAGAGGATTTATTC GAATAGCTA TG CA GAC GGGC ACAC OCTTGGTTCCTGTT-TTCTGCTTTGGTCA A CAACAATTG GAAG CAATTGG ACAT GA CACTTCA TCAAATCTTTC CAAAGCC CAGG CCAAGAG AATT GA GGTGTGTAT GGGTAACA
Consensus		ACTCTGA TTGCATGC TA GGCATGA ATTT TCAAATA CTTTGCAGA GCC GCCTTGGT ATTGAG TTCTGTAT GGT CA
776 David 1	11000	1401 AA TGCAAGGACA GTTGAGGAGTA TTGGAGAATGTGGAATATGCCTGTTCATAAGTGGA TGGTTCGCCATATCTACTTTCCATGCGCATAAAA TAC
VfDgat1 VfDgat2	(1396)	AR IGC ACACA TI CAAA IGGIGAAAACC IGAIGAA AA IG IGGA AAA IGCCI IGII CAIAAGIGAA AAA IGGI ICGCCAIACI I ICCAIGCI IGCGGCAAAAAA IAC AA IGC ACACA II CAAA IGGIGGAAACC IGAIGGAGAGIIGII CAIAAA II GC IAGAACI
VfDgat3		ACTCCAAGAA CTCTGGACGTCCTCCTTTCTTCGAAGCATTTGAGAGTCT-TCTCGGCTCTACACGCTCTC-TC-TTGCGCTCAAGTCTTGCTTCTTGCGTGCAAGTCTATCGG
Consensus	(1401)	AATGCAAG A TCT GAGGTG A TGATGGA G AT TGAGTGTTT TATG G AT G T G
WEDwot 1	114065	1501 CAAGG GGG TGG CCTTATTAATTACTTTCTTCGTTTCAGCAG TATTCATGAGTTGTG CATTGCTGTCCTTGCCACATATTCAAGCTCTGGGGCTTTTAT
VfDqat2		GA GTTTTCG GA ACTC CTTTAC-CTTCAAAAA TCCAAT-GCAAT-GCAAT-GCAATG GTG GTG AG GTA AC GTAAG GTGAA ATCCACGTG AG CTACCG TG AA
VfDgat3		CAAGTGCAGGGCCCTAATGTCAGGGTCAAT-GCTGCCCATGATCCAATCACAACTCCAATCAATCAATCAA
Consensus	(1501)	CAAGTGC GGGACCTTCTTAA C TTCT AG TTCAAT GCAT TCATGAT GT CAC CT A T CCAAATTCA A CCT C CTG AT
WfDget1	(1506)	1601 T <mark>ggaa taatgtttcagattcctttggtcgggatcacaaattaccttcaaaacaag</mark> ttc <mark>agaagctcaatggtggggaacatg-atctt</mark> ctgg <mark>ttcatttt</mark>
VfDqat2		A GTT GG GAAG TACA GA GA GA GTTA TTGCAT CACTTA AAAAC TT TTTGAAAG G-CACAAAG CACG GGTC GG CTATTCA GACC TTAAACTT CAAAT
VfDgat3		C <mark>gg</mark> cg <mark>it gg tt gg ag gat</mark> gt <mark>gg tg cat cg tc gc ta atta ctttc</mark> a gg a c <mark>aag g</mark> ata <mark>a gc</mark> attte <mark>gg tc tg g</mark> c c <mark>tg c atctt</mark> ag
Consensus	(1601)	GG T GG TTT AGGAT AGTTGTC GCATCACTAATTACTTTCA ACAAGG A AAGC CA GGGTCGGG AC TG ATCTTA TT A TT
VfDqat1	(1695)	1701 CTGCA TTCTTGG TCAA CCAATGT GCTT GCTGTTG TATTACCATGA CCTAATGA AT CGA AA AG GGAC TAC CGAA TCAA GA TGACACTTAACT CATCGTG TGG
VfDgat2		TTTTGACCAGAA ATCA GAA CTTA AAAG TAGTTTTGCATGCTTTCCATTTCATTT
VfDgat3		
Consensus	(1701)	
VfDqat1	(1795)	1900 TAGAC TCTATAT ATAT ACATA GA CTTA CCAGA GA TGGGTTGCTTCCAAC AT ATTG TGC ACAA GAGGCAA TTGTTGTTCTCATC A GA A GA
VfDgat2	(1160)	ATTTG TGTTCTT AGAT AA TGA TGA AAA TGA GAAA AAAAAAAA
VfDgat3	(838)	
Consensus	(1801)	TT TA ATA A A AGA A T A A G A AAG AATTT C A A AA A A
VfDgat1	(1895)	a atta atta atg ta ca agca att ttga aagta ta atca ctggca ggga cta gtgc ccg actg tagta ct gaga tta taga ggta tta tca atcg tta gtg gg
<u></u>		2001 2090
VtDgat1	(1995)	GAAAA TTGTAAA TGTA TAAAGTT CAAT CTTTGTA TTGTTTCTTTTCT

Figure S1. Nucleotide sequence alignment of the three tung DGATs. DGAT sequence name is on the left of alignment followed by the start of the nucleotide sequence of each DGAT. The numbers at the top of the alignment are the positions of the multiple sequence alignment. The letters at the bottom of the alignment are the consensus nucleotides. Nucleotides in red on yellow represent those conserved in all three DGAT sequences at a given position, whereas those in black on blue represent nucleotides conserved in two of the three sequences at a given position. The underlined nucleotides represent the forward primers, TaqMan probes, and the complementary sequences of the reverse primers for the three DGAT assays.