**Figure S2. Alignment of nucleotide sequences corresponding to *dgat2a* and *dgat2b*.**

1 50

dgat2a\_ XM\_014197366 (1) TCAAAACACGATCGACGCCGACATCACGTCACTGCAGTACCTGATAAATA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1) --------------------------------------------------

dgat2b\_EG878494rc (1) --------------------------------------------------

51 100

dgat2a\_ XM\_014197366 (51) CGTGGTTGAGAGTACTTTCAGACCACCGCAGGCTGACTTGAGAAAAATTA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1) --------------------------------------------------

dgat2b\_EG878494rc (1) --------------------------------------------------

101 150

dgat2a\_ XM\_014197366 (101) TGTTTTCGAGTAGCGCAATTTGCATCCTCTTCAGTTCTTCTACAGGAGCG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1) --------------------------------------------------

dgat2b\_EG878494rc (1) --------------------------------------------------

151 200

dgat2a\_ XM\_014197366 (151) CATCGGTTTGGACCCAGTACACCTCCCACCCTCCCTCACGTACTGACTTT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1) ------------------------------CCCCCTCCCATACTGACTGT

dgat2b\_EG878494rc (1) --------------------------------------------------

201 250

dgat2a\_ XM\_014197366 (201) GAACTGGCTCCTCCTATACGGGTTAAATGC-CGTTCAGTTATTCAATTTA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (21) GA-CTGGCTCCTCCCATACCGGTTAAATGCGCGCTCGGTGCTTCAATTCA

dgat2b\_EG878494rc (1) --------------------------------------------------

251 300

dgat2a\_ XM\_014197366 (250) AT----------GCAGTCATGATAGAGGAACTCTAGAGTTTATTAACTTT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (70) GTACAGTGGAAGGCAGTCATGATAGAGGAGCTGTAGAGTTTACAAACTTT

dgat2b\_EG878494rc (1) --------------------------------------------------

301 350

dgat2a\_ XM\_014197366 (290) ATTGTAGTAAATATTTCCAAGTATTGTAACCTGTTAATTCGCGGAGCCAC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (120) AAAGCAGCAAGTATTTCCAAGTCTTGTAATCTGTTTATTCCCGGGGCCAC

dgat2b\_EG878494rc (1) --------------------------------------------------

351 400

dgat2a\_ XM\_014197366 (340) AGTTATGAAGACAATACTTGCTGCCTACCCCGGTGTCCTAAAAGGCACCG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (170) AGTTATGAAGACCATACTTGCTGCCTACTCCGGTGCCCTAAAAGGCACAG

dgat2b\_EG878494rc (1) --------------------------------------------------

401 450

dgat2a\_ XM\_014197366 (390) GCTGCAGCATCCTCTCCGCCCTGCAGGACCTACCCTCTGCTCCTTGGCCT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (220) GCTATAGCATCCTCTCGTCCCTGCAGGACCTGCCCTCCCCTCCATGGCCT

dgat2b\_EG878494rc (1) --------------------------------------------------

451 500

dgat2a\_ XM\_014197366 (440) GCACTCCGATCCAAGATGGAGAAACACCTTCAGGTCATCTCAGTTCTGCA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (270) GCCCTTCGATCCAAGATGGAGAAACACCTTCAGGTCATCGCAGTTCTTCA

dgat2b\_EG878494rc (1) --------------------------------------------------

501 550

dgat2a\_ XM\_014197366 (490) GTGGGTCATCAGCTTCCTCGCCATGGGTGCCGCTGGCACTGTGCTCTTAA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (320) GTGGGTCATCTCCTTCCTTGCCATGGGCATCAGCTGCACTGTGCTGTTAA

dgat2b\_EG878494rc (1) --------------------------------------------------

551 600

dgat2a\_ XM\_014197366 (540) TCTACATGTTCTGCACAGACCTCTGGGTGATCGCTGCCATGTACACTGCC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (370) TCTACATGTTCTGCACAGACCTCTGGGTGATCGCTGCCATGTACACTACC

dgat2b\_EG878494rc (1) --------------------------------------------------

601 650

dgat2a\_ XM\_014197366 (590) TGGCTCATCTTCGACTGGAACACCCCCAAACAAGGTGGCAGGAGGTCCTC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (420) TGGCTAATCTTCGACTGGAACACCCCCAAACAAGGTGGCAGGAGGTCCTC

dgat2b\_EG878494rc (1) --------------------------------------------------

651 700

**C103R066**

dgat2a\_ XM\_014197366 (640) TTGGGTGAGGAACTGGACCATGTGGACTTACTTCAGAGACTACTTCCCCA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (470) TTGGGTGAGGAACTGGACTGTGTGGACTTACTTCAGAGATTACTTTCCCA

dgat2b\_EG878494rc (1) --------------------------------------------------

701 750

dgat2a\_ XM\_014197366 (690) TCAGGCTCATCAAGACACACAACCTGCTGCCCAGCCGAAACTACATCTTT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (520) TCAGGCTCATCAAGACACACAACCTGCTGCCCAGCCGAAACTACATCTTT

dgat2b\_EG878494rc (1) --------------------------------------------------

751 800

dgat2a\_ XM\_014197366 (740) GGCTACCACCCCCATGGGATCTTCTCTTTTGGAGCCTTCTGTAACTTCGG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (570) GGGTACCACCCCCATGGGATCTTCTCTTTCGGAGCCTTCTGTAACTTCGG

dgat2b\_EG878494rc (1) --------------------------------------------------

801 850

dgat2a\_ XM\_014197366 (790) AACAGAGGCCACCGGCTTCTCTAAGAAGTTCCCGGGCATCAAGCCTTCCC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (620) TACTGAGGCCACTGGATTCTCCAAGAAGTTCCCGGGCATCAAGCCTTCTC

dgat2b\_EG878494rc (1) --------------------------------------------------

851 900

dgat2a\_ XM\_014197366 (840) TGGCCACCCTGGCTGGAAACTTCCGGATGCCAGTCTTTAGAGACTATCTC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (670) TTGCCACCCTGGCTGGAAACTTCCGGATGCCAGTCCTTAGAGACTATCTC

dgat2b\_EG878494rc (1) --------------------------------------------------

901 950

dgat2a\_ XM\_014197366 (890) ATGTCTGGAGGTATCTGCCCAGTGAACCGTAACTCCATTGACTACCTCCT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (720) ATGTCTGGGGGTATCTGCCCAGTGAACCGTAACTCCATCGACTACCTCCT

dgat2b\_EG878494rc (1) --------------------------------------------------

951 1000

dgat2a\_ XM\_014197366 (940) CTCTCAGAATGGAACTGGCAATGCAGTGGTCATTGTTGTCGGGGGAGCAG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (770) CTCTCAGAATGGAACTGGCAACGCAGTGGTCATCGTTGTCGGGGGAGCAG

dgat2b\_EG878494rc (1) --------------------------------------------------

1001 1050

dgat2a\_ XM\_014197366 (990) CTGAATCTTTGAACTGTGCGCCAGGAAAGAATTCTGTCACCCTGAATAAC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (820) CAGAATCTCTGGACTGTGCTCCAGGCATGAATTCTGTCACCCTGAATAAC

dgat2b\_EG878494rc (1) --------------------------------------------------

1051 1100

dgat2a\_ XM\_014197366 (1040) CGCAAGGGCTTTGTGAGGTTGGCCCTCCAGCAAGGGTCTGACCTGGTACC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (870) CGCAAGGGCTTTGTGAGGCTGGCCCTCCAGCAAGGATCTGACCTGGTGCC

dgat2b\_EG878494rc (1) --------------------------------------------------

1101 1150

dgat2a\_ XM\_014197366 (1090) AGTCTACTCCTTTGGGGAGAACGATGTGTACAAACAGGTGATCTTCGAGG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (920) GGTCTACTCCTTTGGGGAGAACAATGTGTACAAGCAGGTGATCTTTGAGG

dgat2b\_EG878494rc (1) --------------------------------------------------

1151 1200

dgat2a\_ XM\_014197366 (1140) AGAGAACCTGGTGGCGGCTGGCTCAAAAGCGATTGCAGAAGATTATTGGT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (970) AGGGAACCTGGTGTCGGCTAGCTCAGAAGCGGCTGCAGAAGATTCTGGGC

dgat2b\_EG878494rc (1) --------------------------------------------------

1201 1250

dgat2a\_ XM\_014197366 (1190) TTTGCTCCCTGTCTGTTCCATGGCTGTGGCTTCTTCTCCTCCGACTCCTG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1020) TTTGCTCCCTGTCTGTTCCATGGCTGTGGCCTCTTCTC---CGACTCCTG

dgat2b\_EG878494rc (1) --------------------------------------------------

1251 1300

dgat2a\_ XM\_014197366 (1240) GGGAATGGTGCCTTACAACAAACCCATCACCACCATCGTGGGTGAACCGA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1067) GGGAATGGTGCCTTACAATAAACCCATCACCACCATCGTGGGTGAACCGA

dgat2b\_EG878494rc (1) --------------------------------------------------

1301 1350

dgat2a\_ XM\_014197366 (1290) TCACAGTGCCAAAGATTGAGCAGCCTCCTCGGGATATGGTGGATCTGTAC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1117) TCACGGTACCAAAGGTTGAGGAGCCTACTCGGGTTATGGTGGAACTGTAC

dgat2b\_EG878494rc (1) --------------------------------------------------

1351 1400

dgat2a\_ XM\_014197366 (1340) CATGCCATGTACATCAATTCCCTCACGAGCCTCTTTGACAAGTATAAGAC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1167) CATGCCATGTACATCAAGTCCCTCAGGAGCCTCTTTGACAAGTATAAGAC

dgat2b\_EG878494rc (1) --------------------------------------------------

1401 1450

dgat2a\_ XM\_014197366 (1390) CTGCTTCGGCCTGAAGGAGAGTGACATCCTGCACATCCATTGAGAAAGG-

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1217) CCGCTTCGGATTGAAAGAGAGTGACATCCTGCACATCCAATGAGAAAAGA

dgat2b\_EG878494rc (1) --------------------------------------------------

1451 1500

dgat2a\_ XM\_014197366 (1439) GTCAGC------------------------TGTGGCAGCTGTCTGTTCAG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1267) GTGAGCAGGACCCCCTCGGAACCTCAGAACTGTGGCAGCTGTTTGTTCAG

dgat2b\_EG878494rc (1) --------------------------------------------------

1501 1550

dgat2a\_ XM\_014197366 (1465) CCCTGCCCCTCCATTCACGTGCCTGGCTCTGATTGATTGTCTCTGGAATT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1317) CCTCGACACCCCATTCACGTGCATGGCTCTGATTGATTGTCTCTGGAATT

dgat2b\_EG878494rc (1) --------------------------------------------------

1551 1600

dgat2a\_ XM\_014197366 (1515) CAATCGATATACATAAAGCTGTG----TCTATATAAACCCACCGCGCTCT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1367) CAATCGATATACATAAAGTTGTGGGTGTGTGTATAAACCCACCGCGCTCT

dgat2b\_EG878494rc (1) --------------------------------------------------

1601 1650

dgat2a\_ XM\_014197366 (1561) CAGCATCA--------------CTCACGTCGGTCCTTCACTCAGGATGAA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1417) CATCCTCGTCCAGTATACAAGGCTCACGTCCCTACACCACTCAGGGTGAA

dgat2b\_EG878494rc (1) --------------------------------------------------

1651 1700

dgat2a\_ XM\_014197366 (1597) AATGGCAGGTCACCTTACTATTCTCTCTGACCTAGTCACTGTCAATGGCA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1467) AATGGCAGGT----TT--TAGGCTCCCTGACCTAGTCCTTGCCAATAGCA

dgat2b\_EG878494rc (1) --------------------------------------------------

1701 1750

dgat2a\_ XM\_014197366 (1647) AAGTTGACTAACTTCCGTTTATTGAAT---ATTTCATTGAGTGTATGACA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1511) AAGTTGATTAACTTAAATGTCTCCAAATGGAGTCTCTTCAGCGTATGCCA

dgat2b\_EG878494rc (1) --------------------------------------------------

1751 1800

dgat2a\_ XM\_014197366 (1694) CATCTATAGATGTGTTCCATGACAGAAAAGATGAGGGAGTATAGTT----

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1561) CATTTCTAGATATGTTCCATGACAGAAGAGATGAGGGAGTATAGTTGGAT

dgat2b\_EG878494rc (1) --------------------------------------------------

1801 1850

dgat2a\_ XM\_014197366 (1740) AAGGTATGATCCCTTGC----------AGTGGAACTCCCACTAGGTGGCA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1611) AAGATACGATCACTTGCTTTCATGTGCAGTGGAACTCCCACTAGGTGGCA

dgat2b\_EG878494rc (1) --------------------------------------------------

1851 1900

dgat2a\_ XM\_014197366 (1780) CTAGAAGGTTACACAAGACACACACAAGCACCATCTTTGTTTCCTCCATG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1661) CTAGAAGGTTATACA---CACA-ACAAGCACCATGTTTGTTTCCCTCATG

dgat2b\_EG878494rc (1) --------------------------------------------------

1901 1950

dgat2a\_ XM\_014197366 (1830) CATCCATGTAATTTTCACTGAGAATATGCCTGTACAAAGAATGTGTTAAG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1707) CATCCATGTAG---TCCCATATATTAGGCCC-TACAAA---------A-G

dgat2b\_EG878494rc (1) --------------------------------------------------

1951 2000

dgat2a\_ XM\_014197366 (1880) TGGTAAAAGGTAAATATAGGATGATGTTTTGAGACCTTACATTTTTTGTT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1743) T---------TCAATATCAGA---TGTTTTGAGGCCTT---TATTTATTT

dgat2b\_EG878494rc (1) --------------------------------------------------

2001 2050

dgat2a\_ XM\_014197366 (1930) GTTGCTAAATGCACAAACAATGCAATTGTAAGGGTGTTGCCTCACTGAGA

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1778) TTTGCTAACTGCACAAACAATGCAATTGTAATGGTATGGCCTCAATCAGA

dgat2b\_EG878494rc (1) --------------------------------------------------

2051 2100

dgat2a\_ XM\_014197366 (1980) TGTTGA---TGGTGTGGTTTATTGAGCCAAAGAGCTGATTGGTGTCCCCT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1828) AGTTTAATATAGTGTGGTA-ATTGAGCCAAAGAGTTGATGGGTGTCCCCT

dgat2b\_EG878494rc (1) --------------------------------------------------

2101 2150

dgat2a\_ XM\_014197366 (2027) CCCCACACATGAACACTTCATTGAAACTTGAAAGTGAAGGAATTCTATTG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1877) CCCAGCACACGCATACTTCATTGAAACTGGAAGGTGAAGTAATTCTA---

dgat2b\_EG878494rc (1) --------------------------------------------------

2151 2200

dgat2a\_ XM\_014197366 (2077) AATGGATTTAGATTGTGCATATTGGTAATGCAATCTG-ATTGTGTGATAG

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1924) -ATGGATTTAGATTGTGATTATATG-ATGCCACTAAGTATTGTATTATGT

dgat2b\_EG878494rc (1) --------------------------------------------TTATGT

2201 2250

dgat2a\_ XM\_014197366 (2126) CACTAAGTATTAAT-TGTATT---TTGTAAATAAGAACA---------TT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (1972) AAATAAGAAAAAACCTGTCCTCCCTTGTTGAAAGGAACAATTTTTCTTTT

dgat2b\_EG878494rc (7) AAATAAGAAAAAACCTGTCCTCCCTTGTTGAAAGGAACAATTTTTCTTTT

2251 2300

dgat2a\_ XM\_014197366 (2163) TTCAATGAAAATTAATATATTGATGCACTTTTTGTATTTGTGACAACCCT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (2022) TTAAATTAAAATTTATATATTGATGCACTTTTTGTATTTGTTACAACCCT

dgat2b\_EG878494rc (57) TTAAATTAAAATTTATATATTGATGCACTTTTTGTATTTGTTACAACCCT

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2301 2350

dgat2a\_ XM\_014197366 (2213) CTGAGGTATTTCTCTAAAACATGCCTTTGAAAGAGTCCTATGTCAAATTT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (2072) CTGAGGTATTTCTCTAAAATGTGCCTTAGGAATTTTTCAATGTCACATTT

dgat2b\_EG878494rc (107) CTGAGGTATTTCTCTAAAATGTGCCTTAGGAATTTTTCAATGTCACATTT

2351 2400

dgat2a\_ XM\_014197366 (2263) GCCAATTTCTAAGAGAATCACTATGGTGCTTTTGTCATTTAACCTTGACC

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (2122) T-------------------------------------------------

dgat2b\_EG878494rc (157) T-------------------------------------------------

2401 2450

dgat2a\_ XM\_014197366 (2313) TGTGTTTTAGTTTTCTTGTACATTTCTCCACATGAGTGTATTGACTGGGT

dgat2a\_BQ036283rc (1) --------------------------------------------------

dgat2b\_XM\_014137863 (2123) --------------------------------------TATTGACTGGGC

dgat2b\_EG878494rc (158) --------------------------------------TATTGACTGGGC

2451 2500

dgat2a\_ XM\_014197366 (2363) TGCAGAG--TGTTACCTAGTGCATTGAGGCCCCATGTACTGTAGTGATGG

dgat2a\_BQ036283rc (1) -------------------------------------ACTGTAGTGATGG

dgat2b\_XM\_014137863 (2135) TGCAGAGAGTGTTGTTTAGTGCCTTGATGCCCCATGTACTGTAGT-----

dgat2b\_EG878494rc (170) TGCAGAGAGTGTTGTTTAGTGCCTTGATGCCCCATGTACTGTAGT-----

2501 2550

dgat2a\_ XM\_014197366 (2411) TGATGTAAGAACAATTTCAGGGTGAAGAACATTTCTTCCCCTACACAGAG

dgat2a\_BQ036283rc (14) TGATGTAAGAACAATTTCAGGGTGAAGAACATTTCTTCCCCTACACAGAG

dgat2b\_XM\_014137863 (2180) ---TGTT-GACTATTCTCT--------ACTAATTCTTCCCCCACACAGAG

dgat2b\_EG878494rc (215) ---TGTT-GACTATTCTCT--------ACTAATTCTTCCCCCACACAGAG

2551 2600

dgat2a\_ XM\_014197366 (2461) GGCAGATTACTGATGAATGAAATTAAGAGATTGCAAAGCATATGCCTTAT

dgat2a\_BQ036283rc (64) GGCAGATTACTGATGAATGAAATTAAGAGATTGCAAAGCATATGCCTTAT

dgat2b\_XM\_014137863 (2218) GGCAGATCAGTGATGAA--------AGGGATTGTAAAGCATATGCCTTGT

dgat2b\_EG878494rc (253) GGCAGATCAGTGATGAA--------AGGGATTGTAAAGCATATGCCTTGT

2601 2650

dgat2a\_ XM\_014197366 (2511) TTTAAAAACTACAACTCAAACCTCTTAGGGGCTTCCACTCAATTGAGTAA

dgat2a\_BQ036283rc (114) TTTAAAAACTACAACTC**AAACCTCTTAGGGGCTTCCA**CTCAATTGAGTAA

dgat2b\_XM\_014137863 (2260) ----AAAAATAAAACGCA--CTTATTGTGGGGTTCTACTCAATTGAGGAA

dgat2b\_EG878494rc (295) ----AAAAATAAAA**CGCA--CTTATTGTGGGGTTCT**ACTCAATTGAGGAA

2651 2700

dgat2a\_ XM\_014197366 (2561) AATGGCAAA-------------GGGGTTGCTATCACAGATTTGAAATAGA

dgat2a\_BQ036283rc (164) AATGGCAAA-------------GGGGTTGCTATCACAGATTTGAAATAGA

dgat2b\_XM\_014137863 (2304) AATGGCAAATGTACAGTATAAGGGTTTTTCTATCACACATTTGGATTAGA

dgat2b\_EG878494rc (339) AATGGCAAATGTACAGTATAAGGGTTTTTCTATCACACATTTGGATTAGA

2701 2750

dgat2a\_ XM\_014197366 (2598) GTATAAAAGTCACAAACTCCCCTAGTAATTACCAAGAAGTGTTTGAGAGA

dgat2a\_BQ036283rc (201) GTATAAAAGTCACAAACTCCCCTAGTAATTACCAAGAAGTGTTTGAGAGA

dgat2b\_XM\_014137863 (2354) GT-TAAAAGTC--AAACTCCCCTGGTAATTACCAAGAAGTGTTTGAGATA

dgat2b\_EG878494rc (389) GT-TAAAAGTC--AAACTCCCCTGGTAATTACCAAGAAGTGTTTGAGATA

2751 2800

dgat2a\_ XM\_014197366 (2648) AATCATTTTTTCATATTGGGCATATCAAGTCCATTATCCAGCCAATGATC

dgat2a\_BQ036283rc (251) AATCATTTTTTCATATTGGGCATATCAAGTCCATT**ATCCAGCCAATGATC**

dgat2b\_XM\_014137863 (2401) AAT-------T---ACTGGGCGTATCAAGTC---TATCAAT--TATTTTT

dgat2b\_EG878494rc (436) AAT-------T---ACTGGGCGTATCAAGTC---TATCAAT--TATTT**TT**

2801 2850

dgat2a\_ XM\_014197366 (2698) CTAGGTGCAGAAATGTATGTATGTTGTATATTA-TGCAAGATAAAAG-GA

dgat2a\_BQ036283rc (301) **CTAGGT**GCAGAAATGTATGTATGTTGTATATTA-TGCAAGATAAAAG-GA

dgat2b\_XM\_014137863 (2436) CCATGTGGTGAAATGT-TG-AGGTTGGTGATGAGTGCTAAATAGAAGTGT

dgat2b\_EG878494rc (471) **CCATGTGGTGAAATGT-TG-A**GGTTGGTGATGAGTGCTAAATAGAAGTGT

2851 2900

dgat2a\_ XM\_014197366 (2746) C-TACGAGATTTCACCTCATG--GCAAAATAATTGAGATT--------GG

dgat2a\_BQ036283rc (349) C-TACGAGATTTCACCTCATG--GCAAAATAATTGAGATT--------GG

dgat2b\_XM\_014137863 (2484) CATTTGAAATGTAAATTCTTCTAGCTTCAACATTGACTTCTTGTAAAGGG

dgat2b\_EG878494rc (519) CATTTGAAATGTAAATTCTTCTAGCTTCAACATTGACTTCTTGTAAAGGG

2901 2950

dgat2a\_ XM\_014197366 (2785) TGAGAAATAGTGTGTCATTCAAAATGTAATTTCTTCTAGCTTCATCGGTG

dgat2a\_BQ036283rc (388) TGAGAAATAGTGTGTCATTCAAAATGTAATTTCTTCTAGCTTCATCGGTG

dgat2b\_XM\_014137863 (2534) GCAGTAAACATCTCACTCTCTTAATTAATGTGCAGTTAACAGCAGCCAAG

dgat2b\_EG878494rc (569) GCAGTAAACATCTCACTCTCTTAATTAATGTGCAGTTAACAGCAGCCAAG

2951 3000

dgat2a\_ XM\_014197366 (2835) ACTTTT--TGCAAA-GAGCAG--TGAACATCCCGCTCTCCTAATTCATGT

dgat2a\_BQ036283rc (438) ACTTTT--TGCAAA-GAGCAG--TGAACATCCCGCTCTCCTAATTCATGT

dgat2b\_XM\_014137863 (2584) GCCTTTGTTGTGAATGAATAGCTTGAGCAAAAT-CTGTC-TACTTAAATT

dgat2b\_EG878494rc (619) GCCTTTGTTGTGAATGAATAGCTTGAGCAAAAT-CTGTC-TACTTAAATT

3001 3045

dgat2a\_ XM\_014197366 (2880) ACAATAAATACAGCAATA-AATAGCAGCCAA--TGCATTTTTA--

dgat2a\_BQ036283rc (483) ---------------------------------------------

dgat2b\_XM\_014137863 (2632) AAACTTTTTATGTTTTTAGAATAAAACTTAACATGTCTTAGTAAA

dgat2b\_EG878494rc (667) AAACTTTTTATGTTTTTAGAATAAAACTT----------------