**Figure S3. Alignment of nucleotide sequences corresponding to *fabp3a* and *fabp3b*.**

 1 50

fabp3a\_NM\_001123578 (1) -----------------------ATGGCTGAGGCATTCGCAGGCACATGG

 fabp3b\_BT050105 (1) CATTTCTCCACACTACTGCTAACATGGCTGAGGCATTCGCAGGCACATGG

 51 100

fabp3a\_NM\_001123578 (28) AACCTGAAGGACAGCAAGAACTTTGATGAATACATGAAGGCTCTGGGTGT

 fabp3b\_BT050105 (51) AACCTGAAGGAGAGCAAGAACTTTGATGAATACATGAAGGCCCTGGGTGT

 101 150

fabp3a\_NM\_001123578 (78) GGGCTTTGCGACACGCCAGGTTGGCGGTATGACCAAGCCCACCACCATCA

 fabp3b\_BT050105 (101) GGGCTTTGCAACCCGCCAGGTTGGCAGTATGACTA**AACCCACCACCATCA**

 151 200

fabp3a\_NM\_001123578 (128) TCGAGGTAGCTGGAGACACAGTCACTCTGAAGACACAGAGCACTTTCAAG

 fabp3b\_BT050105 (151) **TTGAG**GTAGCAGGAGACATGGTCACTCTGAAGACACAGAGCACCTTCAAG

 201 250

fabp3a\_NM\_001123578 (178) AACACCGAGATCTCCTTCAAACTAGGAGAAGAGTTCGACGAGACCACCGC

 fabp3b\_BT050105 (201) AACACAGAGATCAACTT**CAAACTGGGAGAGGAGTTCG**ACGAGACCACCGC

 251 300

fabp3a\_NM\_001123578 (228) TGACGACAGGAAAGTCAAGTCCCTAATAA**CGATAGACGGTGGTAAGATG**G

 fabp3b\_BT050105 (251) CGACGACAGGAAGGTCAAGTCCCTAATAACGGTGGACGGTGGTAAGATGG

 301 350

fabp3a\_NM\_001123578 (278) TTCACGTGCAAAAGTGGGACGGCAAGGAGACCACTCTGGTTCGCGAAGTC

 fabp3b\_BT050105 (301) TTCACGTGCAGAAGTGGGACGGCAAGGAGACCACTCTGGTCCGTGAAGTC

 351 400

fabp3a\_NM\_001123578 (328) AGCGGCAACGCCCTCGAACGTACTCTG**ACTCTGGGTGACGTCGTCTC**CAC

 fabp3b\_BT050105 (351) AGCGGCAACGCCCTCGAACTGACACTGACTCTTGGTGATGTCATCTGCAC

 401 450

fabp3a\_NM\_001123578 (378) ACGCTCCTACGTCAAGGCCGAGTGAAAGCTTATCACTATGTAACAGCCC-

 fabp3b\_BT050105 (401) ACGCTCCTACATCAAGGCCGAGTAACAACGTC-CGCCAAAAAAAACTCCA

 451 500

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (450) CTATCCTTTACCACACCTGCCAAAATAACAACAACCCTTCACCCTTAACC

 501 550

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (500) CCGATCCCCACTGTAACGACCTCTAACCCCTGTCTGACCTCTAAACCCCG

 551 600

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (550) ACCCCTTCTATGTTGTCCCGTCCTTCTCTTTGTAGTGCTTCTCCTTTGTA

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 601 650

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (600) TGAAACACTGAATAAATTCCACTGACGTTTATTTTCTTCTCTAAAGCCTT

 651 700

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (650) CCTGAGTTCTTCTCTGTCAGTCACCTCACAATCCCCATGACAACAGTCAG

 701 750

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (700) AACACCTACACCAGAGACTCTACTTTCATCAAACCACAGGGGTTTGCCAC

 751 800

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (750) TGGCCTGGAGAAAACTCAGTGAATCTACTAACTCTGTGTAGCAACCATTT

 801 850

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (800) TGTGCCAAATGGCTCATCACGTGTTACAGTTGTAGCAGCCATCTGGGTGG

 851 900

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (850) GTTATGGCAGCCATTTTGTGCCAAGTTGAGATCTGAGGCTGTTGTAGGGG

 901 950

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (900) AAGCAGCACATGTCTCCTCAGACGGATCAAAGCTGCTCTATATTCTGCTG

 951 1000

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (950) ACAGAAAAGGGTGTGTGTAGGCAGTGCGTGTGCGTATTGTTGGATTCGGG

 1001 1050

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (1000) ATAAACTTTGAACATTGAGATATTATTAAAGACATGATAGATCAGACGCA

 1051 1100

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (1050) TAGTATATAAAGGATTGAGAAGGTAATGGTTCTCTGTAGTAAGACAACTA

 1101 1150

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (1100) AGCTTGGAATGCATTGAGTGCAGGGAAAACAATAGCATGTGACAGTACTG

 1151 1200

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (1150) ATAAGGGGAGAAACCGTTGAAGGCTAATATCACTTAGTTCCCTGCTTAGC

 1201 1250

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (1200) AAGAATGATGCAATGTTTAGAGATACGGAGGAGACTCCACCAAAAGTGGG

 1251 1300

fabp3a\_NM\_001123578 (427) --------------------------------------------------

 fabp3b\_BT050105 (1250) GTATGAATACTACCACGGGGGAAGCCATGTCGGTGTCTGAATTACAGCTG

 1301 1339

fabp3a\_NM\_001123578 (427) ---------------------------------------

 fabp3b\_BT050105 (1300) AAACAACCCTTTGGGAAGAATTAAACGTAGATAAGATTC