**Figure S6. Alignment of nucleotide sequences corresponding to *gadd45ba* and *gadd45bb*.**

 1 50

 gadd45ba\_BT047350 (1) GGGGGAGAAACAACTGAGCCACAGTCAGAGCTAATAGAAGGACTTTGCAA

gadd45bb\_EG900267rc (1) --------------------------------------------------

 51 100

 gadd45ba\_BT047350 (51) TTCAACAGCGAGCGAGTTTACGCTGAAACATTGCAAGGGAACCTATACCG

gadd45bb\_EG900267rc (1) --------------------------------------------------

 101 150

 gadd45ba\_BT047350 (101) TATTGGATTACTGATTTGCCGGACGCGCTGGAAACCTCGATTCGGGAATA

gadd45bb\_EG900267rc (1) --------------------------------------------------

 151 200

 gadd45ba\_BT047350 (151) TACTCATTGGAGATTATCCTTGTGGATTATACAATTAACGAACTTCAATA

gadd45bb\_EG900267rc (1) --------------------------------------------------

 201 250

 gadd45ba\_BT047350 (201) TGACTCTGGAAGAACTGGGATGCAATATCACTGAGAAAAAGATGGAGACC

gadd45bb\_EG900267rc (1) --------------------------------------------------

 251 300

 gadd45ba\_BT047350 (251) GTGAGTCAAGCTCTAGAAGAGCTGCTGGTGGCAGCGCAGCAACAAGACTG

gadd45bb\_EG900267rc (1) --------------------------------------------------

 301 350

 gadd45ba\_BT047350 (301) CCTGACTTTGGGAGTCTACGAGTCTGCAAAACTGATGAATGTTGATCCTG

gadd45bb\_EG900267rc (1) --------------------------------------------------

 351 400

 gadd45ba\_BT047350 (351) ATAGTGTAGTCTTGTGTGTTCTGGCGACTGATGAGGAAGACGAGGATGAC

gadd45bb\_EG900267rc (1) --------------------------------------------------

 401 450

 gadd45ba\_BT047350 (401) ATCGCACTGCAGATTCACTTCACGCTCATCCAAGCCTTCTGCTGCGACAA

gadd45bb\_EG900267rc (1) --------------------------------------------------

 451 500

 gadd45ba\_BT047350 (451) CGACATCAACATACTGAGAGTCTCGGGCATCAGGCGCCTCGCTCAGGTTC

gadd45bb\_EG900267rc (1) --------------------------------------------------

 501 550

 gadd45ba\_BT047350 (501) TTGGCGAGCCAAGCACCGCTGACAGCAACGGCAACGAGCCCAAAGATCTG

gadd45bb\_EG900267rc (1) --------------------------------------------------

 551 600

 gadd45ba\_BT047350 (551) CACTGCATCCTTGTCACTAACACCCAGTGCCAATCTCTGAAATGCCAAGC

gadd45bb\_EG900267rc (1) --------------------------------------------------

 601 650

 gadd45ba\_BT047350 (601) GTTGCAGGACGTGGGCAACTACTGCGAGGAGAGCCGCTGCAAGAACCAGT

gadd45bb\_EG900267rc (1) --------------------------------------------------

 651 700

 gadd45ba\_BT047350 (651) GGGTGCCTTATCTGGCCCTGCAGGAGCGCTGAACTAACGACCCTCACTGA

gadd45bb\_EG900267rc (1) --------------------------------------------------

 701 750

 gadd45ba\_BT047350 (701) GAAGCGTGAAATAAACAAGTCGTGAAACTAAACAAGTCGTCATTCTTCAA

gadd45bb\_EG900267rc (1) -----------AAAGCGATTCAAATAAGTAAACAAGTCGTCATTCTTGAA

 751 800

 gadd45ba\_BT047350 (751) GAATGAGAAAGGCATTCAAG---GGGCATTATCGATAGGCCTGTGTCTGC

gadd45bb\_EG900267rc (40) GAATGAGAAAGGCGTTCAAGAAGGGGCATCGTCGACATGCCTGTGTTTGC

 801 850

 gadd45ba\_BT047350 (798) CTACCCCTTGCCGCTACCCAGTGACGGAGCTGGGAATGCGCATGTTCCAA

gadd45bb\_EG900267rc (90) CTGCCCTGGTCCGCTATCCAGTGACGGAGTTGAGCATGCGAAGATTCCGA

 851 900

 gadd45ba\_BT047350 (848) GGGACAATGCACATGCATCCATAACGCATCGGGCCCCAGTTCTCTTCCTC

gadd45bb\_EG900267rc (140) TGGACAATGCGCATACAACCATGACGCATCTGACCCC-GCTCTCTTCCTT

 901 950

 gadd45ba\_BT047350 (898) TGCGGAAAGGAAAAGTATCCGCTGGAGTGGGGAGTAAAAACGAACGGTAG

gadd45bb\_EG900267rc (189) CGCGGAAAGGAACAGTGTCGGCCGGAGTGGGGCGTAGGAACGAACTGTAG

 951 1000

 gadd45ba\_BT047350 (948) AGAAGACTCACTGCTGTTTGCCCAGCCATTTTGGAGCAACCGTGGGCGGC

gadd45bb\_EG900267rc (239) AGAAATCTCGCTGCTGTTTGCCCAGCCATGTTGGAACAACCGGGGGCGGC

 1001 1050

 gadd45ba\_BT047350 (998) TGCATAGCGTGGGAACTGATTTGCAGTTTCGTTTATGCAGAGGAGGGACA

gadd45bb\_EG900267rc (289) TGCATCGCGTGGGAACGCACTTGCAGTTTCGTTATTTGA**GAGGAGGGACA**

 1051 1100

 gadd45ba\_BT047350 (1048) AAGCAACAG--------AGAATACAGACTTGAAACTGGGTTTAACCCTAT

gadd45bb\_EG900267rc (339) **AAGCAACTG**TATCAATGAGAATACAGACTTGAAACTGAGTTTAACCCTAT

 1101 1150

 gadd45ba\_BT047350 (1090) GCTTTCCGACGTGGAAGTCGGGGTATTTATGATGAAATGCAATGTGAATG

gadd45bb\_EG900267rc (389) GCTTTCTGACGTGGAAGTCAGTGTGTTTATGATCAAATGCAATGTGAATG

 1151 1200

 gadd45ba\_BT047350 (1140) ACTTCAATGCTCTATGGTTGGATGTTATGAG--------CTTTGAAGAAG

gadd45bb\_EG900267rc (439) ACTGCAATGCTCTACA**GTTGGATGTTATGAGTAACAGTGCA**ATGAAGAAG

 1201 1250

 gadd45ba\_BT047350 (1182) TGTCTTCAGAGCAACAATGCCTATGGATTGTTATTATGTGAAATATATTG

gadd45bb\_EG900267rc (489) T--CTTCAGAGCAACAATGCCTATGGGTTGTTATTGTGTAAAAGATATTG

 1251 1300

 gadd45ba\_BT047350 (1232) ATCAGGTATTCTG-------------------------GCTACACTCATA

gadd45bb\_EG900267rc (537) ATAGGGTATTGTGTAAAAGATATTGATAGGGTATTGTGGTTACACTCATA

 1301 1350

 gadd45ba\_BT047350 (1257) GCC**CGATGGCTGTCAGTTAAGAGG**GTCAAAACTTTG--------CCACAA

gadd45bb\_EG900267rc (587) GCCAGGTGGCTGCCTGTTAAGAGGGTCAAAACAATGTAACAATGCCACAA

 1351 1400

 gadd45ba\_BT047350 (1299) TGTAACAATGTATT--------TGACATTGACACATCAAACTAATGTATT

gadd45bb\_EG900267rc (637) TGTAACAATGTATTCATTTATTTGACATTGACACAATTAACTAATGTATT

**C100R113**

 1401 1450

 gadd45ba\_BT047350 (1341) GTTATTATTTAAGTTGGACCGAGTAATATATGACA**GTGAACTAACTGCAT**

gadd45bb\_EG900267rc (687) GCTATTATTTAAGTTGAACAGAGTAATATATAACAGTGAAAT----GCAT

 1451 1494

 gadd45ba\_BT047350 (1391) **TGCTGAATT**TAATGTTAAACCTATTTGAATAAATTATTGAACC-

gadd45bb\_EG900267rc (733) ---TG---------TTAAACCTATTTGAATAAATTATTGAACTG