**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