

Table 8. Primers used to clone RNA binding protein genes

| Internal ID | CG number | forward primer          | reverse primer         | dsRNA size (bp) |
|-------------|-----------|-------------------------|------------------------|-----------------|
| KP114       | CG1078    | TGAGGACAGCTGGCTGTATG    | GGCCTGTTAATGTCTCCGA    | 487             |
| JP126       | CG1316    | GAGATGAACGGCAAGACCAT    | ACGCTGTGTGCGTGTAGAAC   | 348             |
| KP025       | CG1434    | AAATACGCATACTGCCGGAC    | CTGCACACAGTACTTGGCGT   | 392             |
| JP061       | CG1507    | TTTGCCGGAAGATGGTAAAC    | CGAAAGCGAATCCAACATTT   | 387             |
| JP040       | CG1582    | ACCTGAAAACCACTTGCCAC    | CGGCGAACTTTCTATTAGCG   | 467             |
| KP086       | CG1646    | AATATAATCCGGGCAGTCCC    | TCATCATCTCCGTGATTGGA   | 487             |
| DSF20       | CG1658    | ATGTTTAAAATGAAACGAACG   | TTAATATAACTTCTTGATGT   | 2371            |
| JP046       | CG1666    | CGTCTTGTCTTTTGTGAGCA    | GGCACTATGTACTCGGGCAT   | 354             |
| KP034       | CG1691    | GAAGTTATGCAGCAGGAGGC    | GTGTGACATCATTGCCATC    | 343             |
| JP043       | CG1703    | ATCCAAGCCAGCTGCTAAAA    | GGACTTGTCCACTTTCTGC    | 368             |
| KP053       | CG1800    | ATGGTGACGGCGAAGAATAC    | CATGGGACATACAGCCACTG   | 401             |
| KP066       | CG1957    | GACAGGCTGCAAAGACCTTC    | GCTGGATGTGCTTGAAGTGA   | 361             |
| JP073       | CG1976    | GAGGTCAGAGCGGAAGTTTG    | TGTGTACGTCACCAGATT     | 463             |
| JP027       | CG1987    | GCAAAGTTTACGTGGGCAAT    | ATCTATAGCGTCCACCGCC    | 360             |
| KP027       | CG2050    | CTGTGTCCCAACCGAGAAAT    | TGCTTGAACGTGACAAAAGC   | 427             |
| JP094       | CG2097    | CGCGAAATGTCTATTGAGCA    | CGCACTGCATCAGTTAGGAA   | 374             |
| JP098       | CG2910    | GACGGACGGAGATACGGATA    | CCTCCGTCAGACTGTGACAA   | 371             |
| KP112       | CG2926    | ATCGTTACAGCGGCAATACC    | CATACCATCACTGGTGCAG    | 413             |
| JP135       | CG2931    | AACGCAGAAGCTGAAGAAGC    | GAAGCTCACGAAGCCAAATC   | 349             |
| KP101       | CG2950    | ATTCCACAAACGATGCTTCC    | CAAATCGTCCAAGTCACCCCT  | 461             |
| JP006       | CG3019    | GACTGCGACAAGAGGAGGAC    | GCCTTGATAGCAGCCAAAAG   | 400             |
| KP078       | CG3038    | TGCACTTACCACTCGAAACG    | TACCTGCGCAGATGAAACAC   | 472             |
| JP069       | CG3151    | GCCAACAATGTGACCAACAG    | AGAGATTGGCACCCCTTGATG  | 487             |
| KP084       | CG3158    | AATGGTCACGACCAGGAGTC    | GCCCCACACAGGAACATACT   | 495             |
| JP009       | CG3162    | CTTCTGGAATTCCGATCCA     | CCCTTGTTTCAAGTTCGTGTT  | 357             |
| DSF21       | CG3193    | ATGGAGCGGCCACAGAAGAT    | TCAGTCACCGCTATCCGTCCG  | 2109            |
| JP088       | CG3225    | AGATAGTGCCGGTGGTGAAC    | CGAACTACATAGCCCACCGT   | 333             |
| KP063       | CG3249    | CTGCCCGGTGTAGCATTAT     | TGGATTTTGATTGGTGTGTA   | 305             |
| KP048       | CG3312    | CAGGAGGAGGAGCACAAAGTC   | TTTGAATGCGATTCCAATGA   | 372             |
| KP100       | CG3506    | GCACCATTGTGTTTGTGGAG    | CGATCCTTTTCAGGGTCAAA   | 325             |
| KP050       | CG3561    | GCTTCGAGCAGTTCAAAAAC    | GCTTCTTCTGAGGCGTATG    | 382             |
| DSF5        | CG3582    | ATGGCCGAGTACTTGGCATC    | TTAATACCGTCCACCACCACCA | 790             |
| KP038       | CG3584    | ACTGCACTGGTCTGATTCCC    | GTCCGTGAATGTTTTTGGCT   | 453             |
| JP125       | CG3594    | CAGTGATTCTGGCAGCGATTATG | AGGTCTGCTTTTGTGGTTTCG  | 384             |
| KP116       | CG3606    | CGTGATGGTGACTGGAAATG    | ATCGTTTCTCATCGGTCCAC   | 351             |
| KP003       | CG3660    | ACGGAGCGAGTGGAAAGTCTA   | ACCGAGCCGTGATAAACAC    | 336             |
| KP028       | CG3733    | TGAAAGCGAGGACAGTGATG    | GCGTCTGGAGTTTGCTTTTC   | 435             |
| KP051       | CG3753    | CACTTGCAGTTCATCCGAGA    | AGCCACCGGTTTCTCCTTAT   | 418             |
| KP067       | CG3780    | GATTTCGTGAGTTCCTCAGC    | AGGCATAGGACACGGAAATG   | 363             |
| JP030       | CG3808    | CCTTGGAGATCCTGAATGGA    | GTAGCAGCCCAATCTGAAGC   | 404             |
| JP109       | CG3884    | TCCTCCTCCATCGTTCCTC     | CGGCATCGGGAGAGTAATAA   | 254             |
| DSF39       | CG3931    | ACTCGTCCGCTCCCTCAGA     | ATGTCCACCAACGCGGCGAT   | 894             |
| DSF42       | CG4043    | ATGGACGTGGAAAGGATAA     | CGTCTCATTGACGTCTCTCC   | 681             |
| KP098       | CG4049    | GACCGGGTCATTAATCCCTT    | CTGCTGTTCGAATCGTCAAA   | 428             |
| KP019       | CG4078    | GCACACTAGCTCCCTCAAG     | CAGACCTTCGGAGACTTTGC   | 449             |
| JP110       | CG4119    | AGCGCGACGATTCTCTGTAT    | GCTCTTCTGTGCTGCTTCT    | 332             |
| KP017       | CG4170    | ACGTGAATTTGGTAGCGGTC    | TCGTCCAAGGTCAGCTCTTT   | 495             |
| JP047       | CG4261    | GTCAACGCAGAAAAGCTTCC    | ATCCACCCAAGTGCCTGTAG   | 336             |
| KP018       | CG4266    | ATGGACAAGGATCTGTTCGC    | TGGAAGTTCTGCAGCGTATG   | 455             |

| Internal ID | CG number | forward primer           | reverse primer           | dsRNA size (bp) |
|-------------|-----------|--------------------------|--------------------------|-----------------|
| KP021       | CG4279    | CCTCCTGGAAGAGGTTGACA     | TGGCAGTTTCTGCTCCTTTT     | 232             |
| JP003       | CG4329    | TTTCAGATCAACGACAAGCG     | ACCGACTTGTATCGGTCCAG     | 380             |
| JP010       | CG4396    | AACCGATCACCGTCAAGTTC     | CGTAGTTGGTCATGGTCACG     | 372             |
| JP015       | CG4429    | GTCGGTACGGCAGTTTCAAT     | CTGCAGCTCCTTCAGCTTCT     | 404             |
| JP071       | CG4476    | TGACCGTGCTCAAAGATCAG     | GTTTGCATAACCTGCCAGT      | 443             |
| DSF3        | CG4528    | ATGGAGATGCTACCCAACCA     | TCACTTCTTGGCGAACGTTA     | 660             |
| KP083       | CG4548    | TAGCAAGGCAAGCAAGGAAT     | CCTCACTTTCGCTTTTGGAG     | 314             |
| DSF16       | CG4602    | ATGGCTGGCGGCAACACCCC     | CTAGGGCGAGTTGGAGATGT     | 1543            |
| JP023       | CG4612    | GAAGGTGAATGGGATGCTGT     | AAGAACTTGTGTGCGCCAG      | 309             |
| JP026       | CG4760    | CTGATCTAACC CGTCTTC      | GCCAAATGGTGGGTACATTC     | 411             |
| JP119       | CG4787    | GCTGACCTTTGACGAGGTCT     | GTACCAAGTATCCGGCCACCT    | 400             |
| JP083       | CG4792    | TGATCCCAGATCTCAAGTTCC    | ACCAGTCGCGCAAATATACC     | 367             |
| JP136       | CG4806    | TAAGGTGACCCCTGAGCATC     | TTATCTGCTTGGGGAAGTGG     | 309             |
| KP029       | CG4816    | AACTGCTGGAAGGCGAGATA     | ACATGCAGATCGCTGTTGAG     | 319             |
| KP094       | CG4845    | TCAAGTACGTTTCGCTGATGC    | TTTCGTTGCTCTCGTTGATG     | 377             |
| JP127       | CG4887    | CGCGTGGAAATTTGTTACCTT    | CGTGGTCTCGATACTGCTCA     | 464             |
| JP054       | CG4901    | TGCCACGACGTGTTGATATT     | GTCAATCACACAACGGATGC     | 317             |
| JP060       | CG4916    | ACAGGCAAGACAGGAGCCTA     | ATCTCGTAAGGCTCGCGTAA     | 461             |
| JP105       | CG5099    | ACATTCGAAGAACCCTGCAC     | CCTTCTTGCACTCGACCTTC     | 349             |
| JP065       | CG5166    | AGCGAGTGGGAGCTACGTTA     | GTTTGGCGTTGTTGTGTTTG     | 410             |
| JP052       | CG5205    | CCTTTTCACTGAGCTCCGAC     | GAAGCTTTGGCACGTCTTTC     | 446             |
| JP004       | CG5213    | CCCTAATTTGCGGATGAAGA     | GTTTACATCCACGATGTTGC     | 370             |
| JP011       | CG5422    | CCGGTGTAAGGGGAAGTCAA     | CTGTTGCTGCGTCATCATCT     | 431             |
| DSF10       | CG5442    | ATGAGCAACGGTGGTGGTGCC    | CTAGGAGCGACTGCGACTAC     | 586             |
| DSF2        | CG5454    | ATGCCAAAGTACTATTGCGA     | TCACTTGGGTCCGTTTATGAT    | 430             |
| JP090       | CG5589    | AACAACAACCTGCAGCCACTG    | TGGTCAAAGTTGCGAGACAG     | 343             |
| DSF30       | CG5655    | ATGTCCAGCATGGGTGATCA     | TTAGAAATCGATGGTTTCCCA    | 600             |
| KP077       | CG5728    | TGCGCATCAAGAGTCAAAC      | GGGCTCTACCTCCTGCTCTT     | 320             |
| JP016       | CG5735    | ACTTTCGATTGGAAACGGTG     | GAATACCTTCCGGGAGAAGC     | 445             |
| JP092       | CG5800    | GCACGAAGAAGACTCCGAAC     | TGGGTGTCAAACCAACAGA      | 450             |
| JP095       | CG5808    | GCCAAGGGAACAAAATGAGA     | TCGATTTCTTGGCTTGCTTT     | 299             |
| KP106       | CG5821    | GGAGCATGAGAACGAACACA     | GCGATCCTTCATTGAGAAGC     | 376             |
| KP105       | CG5836    | TCAGGATCACGATCAATCCA     | GCTTGGGACTAATCTCCTCG     | 380             |
| KP121       | CG5899    | CAAGAAGCTAAGCCTGGTGG     | CTGCCTCAGTTTTTGAAGC      | 413             |
| KP049       | CG5931    | ATTTGCTGCTTCAGGCTCAT     | AGCTCAATGTTGGGGTAACG     | 382             |
| JP021       | CG5970    | AACAGCGTGCTGTACAATGC     | CTGGAACCTCACCTCGAAGC     | 384             |
| JP024       | CG6049    | TGGAGAATACAATCCCCTC      | CGGTTTCTTCTTCTGCCAAG     | 473             |
| JP099       | CG6113    | CGTTGTGTTCTGGATCATGG     | TTGAGCTGTCCAAAATGCTG     | 381             |
| KP076       | CG6197    | GTTCAAGTGGCCCAATGTCT     | GTACGTGGCAGGCCATAGAT     | 303             |
| KP002       | CG6227    | TACGATGTGCCCAACCACTA     | TCCTCCTCATCATCGGAATC     | 347             |
| DSF51       | CG6319    | CAAAAGGGGGACTGAACTAAACAC | TTATTGCTGTAGAGGCTGTGGTTG | 433             |
| KP122       | CG6375    | GAAGAAGAACCCTGTGCCAGC    | GTGTGCCATCAGCTCTTTGA     | 444             |
| KP009       | CG6418    | GATCCGATCAGGAAATCGAA     | AAAGCTGCTGTCTTACCGGA     | 397             |
| KP004       | CG6493    | TTAAGCTCCCTGAGCGTTGT     | GCACCTGCTCTTGATGTGGA     | 307             |
| JP020       | CG6512    | GATCGACAACGAGGTGAGGT     | CCTTGTTCAGCTCTTGAGG      | 257             |
| KP111       | CG6539    | GGTTCAGGAAGTGAATCGGA     | TTGAGCGTTCTGCATTGAAC     | 384             |
| KP095       | CG6610    | ATGACTGCCGTTCCACCCCC     | CTCCGCCAGCTCTCCGCCAG     | 273             |
| KP107       | CG6743    | ATTACTGGAACGGCAGGATG     | GCTCCACTTGCTCCAGAAAC     | 399             |
| KP046       | CG6779    | CATTGAGTTGTACGCCGAGA     | GGCAACATGACCTTGACCTT     | 324             |
| KP020       | CG6841    | ATGCCCTCCAAATATTTCCC     | AGCTTCGTCGAACTTTTCCA     | 389             |
| JP085       | CG6866    | AATGCCGTCAGTGGTAGTCC     | CTCCTTCTTCGATCGTCCCTG    | 426             |

| Internal ID | CG number | forward primer         | reverse primer        | dsRNA size (bp) |
|-------------|-----------|------------------------|-----------------------|-----------------|
| KP117       | CG6920    | TGCACTACTCACTGCCCAAG   | TGCAATTATCGCAAGCTGTC  | 312             |
| JP122       | CG6937    | TCGGATTTAACCAAAGCCAC   | GGAGTCCTCGTTGATGGTGT  | 300             |
| JP077       | CG6946    | TTGTGAAGCTTCGTGGTCTG   | GCACCACGATCACGTATGTC  | 316             |
| JP128       | CG6961    | TTTGACCCCAGATCCATAA    | CCAACTACGAGTCGGTTGGT  | 293             |
| DSF11       | CG6987    | ATGGGATCACGCAACGAGTG   | TTTAATAGTTAGAACGTGAGC | 769             |
| JP104       | CG6995    | GCCAACTCAAACAACAAGCA   | GTACGCTCCACCGAAATGAT  | 263             |
| JP005       | CG6999    | TCAAAGCCACCTTCAATTCC   | GGCAGGAACTTCATTTTCCA  | 328             |
| JP018       | CG7015    | TGCTGGAAACCACACACAAT   | CACGGAGAACTCCACGGTAT  | 389             |
| KP089       | CG7082    | GATCTCCACCAACAGCATT    | TGAGCGTGAGGAAATCAGTG  | 456             |
| JP012       | CG7185    | ACTCAGGACCTCCACGAATG   | GTCATGTTTCATGCCCTGTTG | 448             |
| KP108       | CG7269    | ATGGACATCCTCTGTCAGGC   | GCTCAATGTGGCAGAGAACA  | 453             |
| KP092       | CG7376    | CAATTGGACGAGCAGCTACA   | TGAATGCCGTTGAGACTGAG  | 461             |
| KP061       | CG7437    | ATCCATCGGTGACACTCACA   | TTGCCAATTAACGATCCACA  | 316             |
| KP054       | CG7483    | ATACCCACATTCAACGCCAT   | GAAGACTCGTCTGGAGTGC   | 396             |
| JP041       | CG7487    | AATACGTGTTGGCCTTGGAG   | GCAACAAGCTGTCTCCCTTC  | 450             |
| DSF4        | CG7564    | ATGAGCGCGCCGAGCAACAA   | CTAGCGGCGGTAGTTGCGCT  | 1260            |
| JP111       | CG7697    | CAGGAGACGGCTTTAAGTGC   | GAGGGTCCAAGATCCTCATA  | 352             |
| KP069       | CG7698    | CTTGGCTCCTTCTGATCTGG   | GTGGCACCCCTTCAGATTTGT | 309             |
| JP117       | CG7804    | ACGATGTCCAGATGCACGTA   | TGCACGTTCTTTTTGTGACG  | 328             |
| JP048       | CG7878    | CCACCAGGAGTACGTGTTTT   | CCAACACGGTGCACATACTC  | 440             |
| JP120       | CG7879    | GCCTACGTGGAGTTCTCTCG   | TCTTGCTCAGTGGTGGTCTG  | 284             |
| JP123       | CG7903    | CAATCAGGGACAGGGCTTTA   | GCCAGAGTTTATTGGTCCAT  | 364             |
| JP055       | CG7922    | GCTAGTGACCGAAGGACGAG   | TTGCACATCTTCTGACTGC   | 460             |
| DSF29       | CG7942    | ATGAAAATAGCTGTGGAAGG   | TTAATCTTCTTGCGCTTGGT  | 1604            |
| JP087       | CG7972    | GACAGCTTCTTTTCCAACGC   | GGCCAGTAGCTTCTCTGGTG  | 414             |
| JP106       | CG7981    | AATGGACACCAGCGAGTACC   | TACGACGCTCCAGAAGACCT  | 270             |
| KP096       | CG8019    | GATCACGGAAATCGACCACT   | GCTTCAAGACCAGCTTGACC  | 307             |
| KP043       | CG8021    | TACAAATTGTTCTGTCGGCAA  | ACTCGTCCATCGAGGAAATG  | 209             |
| JP019       | CG8037    | CGCCTTCAAGTAATGGTGGT   | ACTGTTGCTTCTCGGATGCT  | 380             |
| JP031       | CG8097    | CCTGGAGTTGATGGAGCATT   | TCAACAGTCAATGAGCTGGC  | 456             |
| KP075       | CG8103    | GCAAGTCCAAGCTCAAGGTC   | GCTCTCGAGTCTTGTCCACC  | 403             |
| KP012       | CG8144    | ATGTCCAAGTCTGAAACCG    | CGCTCTGTGTCTGTTTTGA   | 444             |
| JP129       | CG8205    | CGACCAGGACATTGCCAAGTTC | TCCGCTCGTTTTGCGAATAGC | 447             |
| JP091       | CG8241    | ATGGACGAGCTGCAGAAGTT   | TGTAGGTGTCATTGGGCAAA  | 340             |
| JP058       | CG8273    | TGAAGGCACATGAGCTGAAC   | CCGTTAATCTCGACCGAAAA  | 484             |
| KP013       | CG8280    | CGTTGGTGTGAACAAGATGG   | CTTCAGCACACCAGTCTCCA  | 373             |
| DSF40       | CG8395    | ATGCGTTTTCCAGGATGACTT  | ATTTAAGAAAATCCTACTATT | 844             |
| JP059       | CG8611    | CGAGTTCAGCCGTTAAGGAG   | ATCCTTGCCCTGGAGAAGTTC | 416             |
| KP103       | CG8625    | GCAGTAGGCGCTTTGATTTC   | AATAAGGCAGACGGCTCTGA  | 500             |
| JP063       | CG8730    | CCAGTCAAGGCTACCACCAT   | GACTTCGTTTTTCGCTCTTGG | 443             |
| DSF1        | CG8749    | ATGACCCAATATCTGCCGCCG  | CTACTGACGCCACCAACTCG  | 1340            |
| JP038       | CG8781    | CCGATGTGTTGGACATTGAC   | CGAGAGCGTATCCCTTTGAG  | 351             |
| KP047       | CG8912    | CGTTATCATGTTGCGTGGTC   | ATCTGCTTGGCGTGCTCTAT  | 333             |
| JP093       | CG8915    | TGGACACAGACTTCTGCTG    | AGGTACACAATCACCCTCC   | 382             |
| KP006       | CG9054    | GGTGGAGTGAGTTGGAAGA    | CTTCGAATGATTGCCTGGAT  | 471             |
| KP082       | CG9075    | GATGAGGCCGATGAGATGTT   | CATCTCTGGGTCAGTTGGT   | 333             |
| DSF18       | CG9085    | ATGCTGCTATCACTAGCCGC   | TTAGACGAACTCCTCCTGC   | 2640            |
| KP030       | CG9143    | GATCACATGCAGAAGCGAAA   | CGTCAGTGGCTATCAGCAAA  | 397             |
| JP049       | CG9218    | AGGTGATCAACCCGTTCTTG   | TGCACTTCATGATAGCCAGC  | 306             |
| KP042       | CG9253    | CTTCTGTTTCAAGTGGACCA   | GCTCTTGCTGTTCTTCCAC   | 468             |
| KP070       | CG9323    | CCGAAACGTGCGTGACTATT   | CGCTTTAGCAGTTCCACTCC  | 367             |

| Internal ID | CG number | forward primer        | reverse primer           | dsRNA size (bp) |
|-------------|-----------|-----------------------|--------------------------|-----------------|
| JP057       | CG9373    | ATACGACTACCGTTGGCAGG  | CAAAAACGAAAGCAGAAAGCC    | 469             |
| JP107       | CG9412    | AGATCCACAACCGAATCCAG  | ATCGTGCTCCTCATCGTTCT     | 281             |
| KP057       | CG9594    | ACGTTTCGAAGGAAGAGCAA  | CCTTCGAGGAAGTGTTCGAG     | 457             |
| KP090       | CG9680    | CGGCCAAGAAGAAGAAAGTG  | ACTTTACAATCCACCCGCTG     | 346             |
| KP010       | CG9696    | CTGTGCCCTTCCTGCTAAAG  | GGTCCAACCTACGCGTTTTA     | 314             |
| KP037       | CG9748    | ATCCCGTCACTAGCATCCAC  | TTTGACGGTAATCCCTGGAG     | 420             |
| JP108       | CG9809    | CAACAAGCAGCCGTCAGTAA  | CCATGGGCAAAGAAGATTGT     | 395             |
| KP041       | CG9946    | TACATCGATCTGTGGAAGCG  | CTCGTAACCGTAGCAGGAGC     | 363             |
| KP039       | CG9983    | AACTACGGAACCCAGAATGG  | TTGTTGCCACCGTTATTGAA     | 401             |
| DSF7        | CG9998    | ATGGGATATGATGACCGTGA  | CTAAAACCTCGCGTCTGTGGTA   | 1245            |
| JP064       | CG10077   | CAGAGACCTTCCTCACCAGC  | TGCTGGGCCAACTCTCTAGT     | 328             |
| JP100       | CG10084   | GAACGAACGCGAGAAAATC   | ACTGGAGCGGAATTAGGTT      | 258             |
| KP113       | CG10110   | TCATGTTGGTCTACGGCAA   | TGCTGTATCCGCTGAACTG      | 393             |
| DSF33       | CG10128   | AGTGGATGGTCGCCGTATTC  | TTAATAGCGCGATGAAGTTCGACG | 309             |
| DSF13       | CG10203   | ATGTCGCGCCATCCGAGCGA  | CTAGTCCCTTGAAACGGAT      | 775             |
| JP066       | CG10210   | ACAAAGCCGTGGAGTATTGG  | TTGAGCTGGTTTTAGCTCGGT    | 481             |
| KP056       | CG10223   | CCCCTTAGGGGTAAAATTC   | CAGCTCCTCGTTTTTCTTGG     | 310             |
| KP035       | CG10236   | ACGATGTACGGAACGAGGTC  | GTGTACGTCTCGACGGGATT     | 472             |
| KP026       | CG10279   | CATCTACGACACCAGCGAGA  | CTTGGTGAAGAAGGCGAAAG     | 343             |
| KP014       | CG10293   | TCCTGATAACCGTCGAGGAC  | CAGCATATTCCGTGAGCAGA     | 477             |
| JP121       | CG10327   | GTTAAGGTGCCCAACTCGAA  | TGTGGGTGGTATGAGTGCAT     | 344             |
| JP051       | CG10328   | AACTGATGACGACCTACGGG  | CGTCATGTGCGTTGTTCCACC    | 446             |
| KP015       | CG10333   | TTCCCAAGGAGATCATCGAC  | CAGTTCGTATGCCCAAAGGT     | 306             |
| KP071       | CG10418   | TCCTTCTTCAAGTCTGCTGGT | GCTCACAACAGCCTCCTTTC     | 267             |
| DSF28       | CG10419   | ATGCAGCATGAGCCGAAGA   | CTATATGTAATCCTTGAAT      | 737             |
| KP008       | CG10445   | GTGCAGCATTCAAGACCAGA  | GGTCCACCAGTTCGAGTTA      | 443             |
| KP059       | CG10630   | GAAGAAGGCATTGATCCCAA  | TGGTGGTTAGGATTTCTCTGC    | 494             |
| KP052       | CG10689   | AGCCTCCTGCAGGTCTACAA  | AGCAACCACTTGCTCTCGAT     | 392             |
| KP044       | CG10777   | CTGTGCTGCGAGACTATGGA  | CCGAATCTTGATGGGAGAA      | 480             |
| KP093       | CG10851   | CATCAAAAATGGCTACGGCT  | AGCTCGGTGTATCCAACCTT     | 426             |
| JP081       | CG10881   | GAGGTGGATGCGGACTATGT  | GTTTCCATCACGGTTTTGCT     | 410             |
| KP118       | CG10922   | CCTCGTGGAGATTAGCGAAG  | CGATCTTCTCCTGTTTCGAGG    | 302             |
| KP005       | CG11023   | TGTGCGTCTAAGCCAGAATG  | GCCGCTCTTGCTTTAAATFG     | 333             |
| KP104       | CG11107   | GTTTCGTGATTGATCCAGGCT | AAACTCGGACATAACGGCAC     | 394             |
| JP045       | CG11123   | CAAGCAGGAAGAGCCAAAAC  | CTTCGATTTCTCCTTGTGCG     | 385             |
| JP007       | CG11266   | ACACGCAGGCTGAGAAGAAT  | GTGTCCAGCGAGGTGGTATT     | 340             |
| KP085       | CG11337   | GGCTGCTTTAGATAGCGGTG  | GTAATCTTCGATGCCCAGGA     | 391             |
| KP080       | CG11360   | GAAGTTTCTGTGCCTTTGG   | TGGGTATGATATTTGCCGGT     | 310             |
| KP060       | CG11403   | TGGATCAGATCAGGAAAGGG  | AAACGGGCATCTACTGTTGG     | 425             |
| JP112       | CG11454   | TGTCACATAACCAACGCCTGT | CAATCTGCGTTTTGTTGTTGG    | 370             |
| JP017       | CG11505   | CAGTAGCTCCTCCAGTTGCC  | CTGGACCGGCACTACAATTT     | 470             |
| KP097       | CG11680   | AGTCTGTGTTTTCCACGACCC | CGAAGGCACAAAGTCTGTCA     | 335             |
| KP120       | CG11844   | ACGAGTGGAAAGGCTTTGAGA | GTCGTTGCGATAACCACCTT     | 359             |
| JP132       | CG12085   | CTTCATCGAGTACGCCAACA  | GACAGGAGTGTCTGCGACA      | 250             |
| KP074       | CG12129   | TGGAGAAGTCAAGGAGCGTT  | CTTATTGCGGTAGCGGTTGT     | 418             |
| JP074       | CG12288   | AGCCCAAAAAGAAGACGGTT  | CCTTGTTATTGGCATTGGCT     | 312             |
| KP036       | CG12493   | TAAAAACAAGACCAGAGGGG  | CATTTGCATCAGAACCATGC     | 368             |
| JP036       | CG12581   | GCGGGACAAAAGTTAACCA   | GCTGAAAGGCGTATATGGGA     | 452             |
| KP024       | CG12598   | ATGACCGTCACAATCAACGA  | CGCCTGGAGACTATTTACGC     | 422             |
| JP134       | CG12749   | CTACCGCACCACAGATGATG  | GAACCTCAATGAAGGCGAAGC    | 394             |
| KP072       | CG12759   | CGCTTCAAGTCCAACCAAAT  | TTCGCCTATAGTTTTGCGCT     | 367             |

| Internal ID | CG number | forward primer          | reverse primer            | dsRNA size (bp) |
|-------------|-----------|-------------------------|---------------------------|-----------------|
| JP124       | CG12870   | TTCAAGGACAAGGGATACGC    | TACTGGCCGAAGTGATAGCC      | 395             |
| KP064       | CG12924   | GAGATCAGGGGACATCGAAA    | CCTGGGAAGAGTGATACCCA      | 425             |
| KP007       | CG13298   | TGAACAAGCGCAACCATATC    | GCTTCAGGCGTCTTCAGATT      | 358             |
| KP062       | CG13425   | AAATACTTTGAGGAGCGCGA    | GCCATAGCCACCGTACTCAT      | 324             |
| JP130       | CG13793   | TCCCTACATGGGCCAGTTCTC   | GAGAACGGAAGGGACATGAA      | 303             |
| KP016       | CG13796   | TCCAAATCTCTGGGCATTTT    | AAACGAACCGCTCCATAAAC      | 300             |
| JP056       | CG14066   | CTTCCAGTTTGACGAGGAGC    | GCCAGTTTTTCGAAGTCTGC      | 342             |
| JP002       | CG14230   | AACAAAAAGATGCTGCGCTT    | GCCTTGTCTCCTTGCTGAC       | 461             |
| JP008       | CG14414   | CAATGCGCTACTGAACTGG     | TGATGATATGGAGCCGATGA      | 339             |
| KP011       | CG14443   | CGCCTTATGAAGGAGCTGAC    | AAGCTGATGACCTCGCAGTT      | 359             |
| JP113       | CG14506   | CAGTTCGGCAAAGCTCCTAC    | AGCGGAGATCTGACTTGGA       | 344             |
| KP099       | CG14637   | CACTACAGCAAGCACCTCCA    | CTGTTGGGTGACGTTTCATTG     | 399             |
| JP022       | CG14641   | TGTGTCAGACCTGCCTCTTG    | ATCGTTGCGTCCGTAGTACC      | 383             |
| JP025       | CG14648   | TCAGTCTGGTGTGGAAGCAG    | GTCTCGCCACCAGTGGTAAT      | 327             |
| JP118       | CG14718   | ATTACTCGGACACCAGCAG     | TCATCTGAAGATCCCGTTCC      | 369             |
| JP075       | CG14891   | ACCAACATATCCTTGAGGCG    | GGCGGAAGAGTGAATAACCA      | 387             |
| DSF38       | CG15481   | AACTTTCGCAAAGTCAGAGGC   | ATGTCTGGTAAATACGATCTG     | 735             |
| DSF36       | CG16724   | AATGGATGCCGACAGCAGTGAAC | TCAATATGGGGGACGGGGCCCCGCG | 589             |
| DSF26       | CG16725   | ATGTCCGACGAGACGAACGC    | TTACTTCTTGGGTGTCTTTT      | 682             |
| JP032       | CG16788   | ATTCATGTGGTTCGGCTTAC    | CCTCCACGATTGTTGAACCT      | 341             |
| KP045       | CG16901   | AGGAAACTGTTTGTGCGGTGG   | ACGATATTGCCGAACGTGCC      | 323             |
| JP001       | CG16941   | GGGAGCAGCGTAACTTTCAG    | CCGCTGTCCAATAGGTTGTT      | 475             |
| KP119       | CG17136   | ATGCCGCGATATAGGGAGT     | GGAACCAGAGCGACCACTAC      | 306             |
| DSF27       | CG17454   | ATGGCGGACGACTTGCATAA    | CTAAAGACCTTTTCTATATT      | 722             |
| DSF40       | CG17540   | CAGATTGATGGATGGTCTTCGG  | TTGTGGCACCTCCCTGTTTAGC    | 505             |
| JP013       | CG17838   | GGACAGTTTCTGGAATCGAA    | TGATTATCGAGCTGTGCGAC      | 449             |
| JP096       | CG18259   | TTTGACCCCAGATCCATAA     | GGCTCCTTGGTGGTATTTGA      | 317             |
| DSF35       | CG18350   | ATGTACGGCAACAATAATCCG   | TATAAGTAAGGATAATGGTAC     | 1102            |
| JP039       | CG18426   | GCCGCCAGGTTAATTTTACA    | TTGGGAGGTCTTTTCGATTG      | 398             |
| KP001       | CG18497   | TCAGCAGCAACATCCTCAAC    | GTAGGAGTGGGTGTGCGAAT      | 438             |
| KP031       | CG18766   | TAGAACGCAATCAACGCAAG    | GCCATTGCCACATACAGATG      | 300             |
| JP072       | CG18823   | TAGAAAACGATATCCCGGCAC   | CCTCGAAGTATACTCCATCCTCA   | 305             |
| JP029       | CG30327   | CGCTGTGCATCAGTGTCTTT    | CTTTTGGCCAACCTTTTGCTC     | 445             |
| JP033       | CG31000   | GGAAGCGACGAACCTTTGAG    | GTTGTGACCTTGGTCCGTCT      | 387             |
| KP079       | CG31156   | CAGGATCATTTCGTACAGCA    | ACCAACAGGAACTCCAATCG      | 681             |
| KP022       | CG31184   | GTGATTTTGCCGGTAAAGGA    | AAACCAGGATGACTCCATCG      | 259             |
| JP089       | CG31212   | ACAAGCTGGACCAAAAACAC    | CAAAGCTGCTGGGTTCTTTC      | 304             |
| JP131       | CG31243   | GCAACGCCATAATGGAGAAT    | GCTGTATTGGGCTGTGGTTT      | 385             |
| JP014       | CG31716   | CTAGCAATAGAACGAGGGCG    | CACTTCTTGCTGGCTTTCC       | 351             |
| JP037       | CG31762   | AAACGTTGGCAACAACAACA    | AAAGCAGCAACCCTTGCTAA      | 367             |
| KP091       | CG31990   | AAAACAGCACAGAGCCATCC    | ATGTCGATTACTIONCGTCGGG    | 212             |
| JP044       | CG31992   | GGGAAAATGTCAATCCAATG    | GCCGTCAAATTTTGTTCGT       | 397             |
| JP115       | CG32062   | CAGCAACAGCAACAACAGGT    | TACAGCGAGGCATTGACAAC      | 308             |
| JP042       | CG32344   | AAGTTGCAGGAGGAAAAGCA    | CTTGTAAGGGCGTCCATGT       | 318             |
| JP116       | CG32364   | ATGTGGACCTCAAGGAATCG    | CAAGATGTTCTCCGAGTCA       | 335             |
| JP028       | CG32423   | ATGGATTCCGGTTACATGA     | TGCTAGCCTGTTTCGGAATCT     | 308             |
| JP067       | CG32533   | TTAAGCTGACCGAAAGCGAT    | CGTCACTTGAATGGGAAGGT      | 366             |
| KP023       | CG32604   | GCGAGCACAAAGACGATACA    | CTATTGGATATGCCACCGCT      | 355             |