

iB_#	OGS_# (ass. 3.0)	dsRNA sequence (5' --> 3')
iB_00105	TC000476	TCGCTGAAAAAGTATCCACACTCAGCAAATTTATGGATAAACATGGAGCTCTTGGCGAATTCTTGTTTGATAAGAACTCCTCAGTGGAGAATTG
iB_01975	TC012387	ACTGCGAGATGGAGGTGTTTCATGTCCGAGTCAGGTGGCTCAAGTACGACTGGGCCAACAGGGATAAGTACAAGTATGAA GTGCTCAAGTGCGTCAGATTTCGAAACATAGCCGCTTGGCAACTTGTGATATCAAGCGCAATCCCCGAAATTCCTGAATT TATGGAGTTAGCCAAAGACCCAGCCATTTGCAAGCTCATCGATGACGGGCTGGCGTTTGTGATCATCAAGCACTGGTACG ACCAC
iB_02774	TC008303	GCAACCATGTGAGGAAGGATCCGATGCCGATTAGTGACGATAGTGTATTATTTATATAGACAGTGTGGGTTTAAATCCGATG AAGAAAAGTGATGATAATTACTGCCAAGTTATAGACTTATCTGATAAAGCCGAGTTCAGAAAGAACGCAAGAGTGTTC AAAGAAGGAGACTAGTATCAGTCCGTTGATTCCCGAGCAGTGTGCAAAACATCACGAAGTATACCCCGACTTACC CCAAAATCGACCC
iB_03294	TC002074	GGAGAAGGATCGGGAGAGTCGCTGTGGTCACATGGAGACTTTTCTTCAAACCTTGATGGGGTTCGAGGGTGACGATGACG ATAATCTACCAATGATCGCAAAGACTTTGGCCAACATAATCCAAGACGATCACAAGTGGGTGAGCTCAAGCCGGAACAA ATGACTGACGATGAGCTGCTTGAAAGCATCAAGTTGCCACTGTTTGTCTCTTCCAAACGCT
iB_04702	TC031200	ACGTATCGAAGCGGAAAAGAGCTCCTACTTCCCGAGAACGAACACGGCGCATTTTTTGATCCGCGATTTCGGAAGCCGGC ACAACGATTACTCGTTATCAGTCCGTGATGGAGATACCGTCAAAACATTACAGAATCAGGCAACTGGATGAAGGTGGTTTC TTCATCGCGCGGCGAAGCAGCTTTAGAACGCTTCAAGAACTAGTGGAACATTACAGTAAAGACCCAGACGGTCTGTGTGT CAATCTGTGCAAAACCATGC
iB_04717	TC009877	AAGTCCCAACCACTTCTTGTCCGAAATTTACAAATGGGCCTTGGAACTCTGTGGCTAGAGTCTCTTTGGACACTAGACTT GGCTGTCTAGAACCGAACCTGTCCCAAAATTCGAATCACAGCGAATTATCAATTCCATAAACACCTTCTTCTGGAACGT GGCAGAAAGTAGAACTGAAAATGCCGTTTGGAGGGTTTACAAAAACAGAAGTTTCAAAAAATACATCGGTGCTTTGGAAG AC
iB_06359	TC031191	TAGTCTGGAGCGAAGCTACAAGAGCCCTTGTACCAGAGCGGGCCCTCACTGGCCGTTATGACCCAGTTAGCGACATCA
iB_06806	TC000393	ACGCGCAGTATTCGTAGCTTAAAGGATCCGAAAGCCGAAAGAACTTAAACTGCTTTTGAGAGAAATCTGGGAGCAGACCAA GGCCTTTGTGCAAGCCGCGCATCTCAGATATACCATAATTACGTGTCTGATCCAATTCCGACCTAACCTACAAGTTACTACA CTTTGATGATTTGGTTCCCGGAGCTTTTCTACCGGTTTGAAGAGTTCGAAAACTTCATCCGAACGAAAAAGCCACAGTG TGTG
iB_07361	TC009459	TGTAAACCGCGATGAAACAAATTTATTGTTTAAATACCGTCGTCGTTCTAATCCCGACACTCACTGCTCTTGAAATGAA GGGCAAAATCCTGATACAGCAAATTTGTGTGCGCTAGGTGGACAAAGATCAAAGATTCTGAAATAGCAAAATGGCTCA TTGCATTCTCACCAA
iB_07902	TC001275	GGACAGAAAGGTGAGGACGAAGTGATGAATCAGATTCTAATAGAATGCATGAAACATTACAACCTGATTAAAAAATACAC CAGTTTGTAGTAGCAGACTGTTTCAAAGAAATTTATAACTTTGCAGTTCGTTCCAAACGATTGTAATGATTGCAATTGCAATGT ATAAAAATATCCACGCTCGAGCCGTCGAACACGCAAGTTTGGTTTGTGCGTTTACGGAACCTCGGTGCTATAACCCAAATT TTCATTTACTGTTTTCGTTGGCAATCTGGTCACTA
iB_08398	TC033206	CCCCAAACGTTGATATTGCACGTGATAAGTTTCTAAGCGAGTTGCGGAGCGCTGAAGCGAAAAAAACGAAAGTTCGCT CCACAACCTCGTCTCCCTTGTCTCGCAGCTTTCCAAACCCCAACCACCAAGAGTTACCAGGTCCGAGCCGGAAGTGA ACCTACCGGATAATCTAACCTTTGTCTAACGCCTAACAGAAGACAAAGCTAAAATGCTACCCCGGTTTGTGTGTCAGT
iB_08760	TC033755	GACGGTTCTCGGTTGAGAGAGACCCCTCAAGCTCGATTTGAAGAATTCGGGGCTTTGTTAGAGCGCTTGACACAGACTGCAG GACATAGCATTTTGGTTTCGTATATTGACCCGAGCGATCAGGATTGCTGCCAATCAACAATGATGATAACCTTCGAAG GGCCTTAGCAAATGCAAAACCCCTCTGAGGGTCATAATCCAAGAAAAGGTGATAGTCTTGAAGTGAATGGATACGGGA
iB_09043	TC016314	GTCTGGGAATGGACTCAGGATAATTGGTTGAATGACCCGACGCCAAAGTGAAGAAAGGGGGCTCCTACCTCTGTCAATGA GTCTTACTGTTGGAGGTATCGCTGCGCTGCAAGATCTTTCAATACCAAGACAGTTCCGGCCGAAATTTAGGCTTTTCGAT GTGCCGGTGATGTCAAATAATTTGGCAGTGAATAACAAACAAACCAAGTACTTAAATCATCTGCCATCAAGTCTTCC
iB_09050	TC033022	ACGGGGTTTAGTGTGGAGTGTCAAGTGGACAGGTCTCAAGTGAAAAATCGTCAAATTTGCTTTGGCTAAGTTGAGGGCTTT GATTTTATCAACGTGATCTTTGAAGAGCAGATAGCGAGGAACGAGAATATGAGGAAGAACCAGTTAGGTGCAATTTTAGAA ACGAGAAAAATTAGGACTTATAATTTCCGCAAGACAGGATCACTGATCATAGGTTACAGGGGTGCAATGT
iB_09103	TC014482	AATGGGGGCGGGTATTATCACTATTCTTATTCCTGTTTCCGTGGTACGGGGCTGTAACCGGATTATTCGGTTCGATATTACGTCCC GGGGTGTCGCCCAACCGCTGAGGCCTCATGTATGGGATTTTGCAGCTTCA
iB_09413	TC005389	TGCTTGATTTTTTCCCTCAGCTGATTATGTCCGAAATTTGGTGATTAAGCAATCGATGAGGCAAAAAATTCGGTTGTTAT CGACTGTTACACATTTATGGTGCTGATTATACGGCAGCTACAGTCATTGAGAGTTTAAACCAAGATTTCAAAACGCGAC AACACCGCTGTTTTTTTACAATCTCAAGTCAAGTGTGAGCTCGGTTTTTGTGCGCTAAACCTGGACTATTTTCTAGTC TATTACAACGAAGATGAGTTGGATGATATGCTCAAGAAGTGGACCGAAA
iB_10104	TC013627	TGCTGAAGAAGAGGCTCAAAATTTACGCAAGAAAGTGTCCGGATAGAAGATGATAATGAATCTTTGGTTTTGCAGCTGA AGAAAAATGGCTACTCGAGCCGAGAAGTCGTAAACTAAGTCCCAACCAATAATTCAGATTGACCCAGAACCACTTCTGAG AAAGGTGACGTATCAGACGACGAAGACCCCGCAGAAATCAAATTACAGTTAGAGTTGAGCGAACAAGAAGCTTCTGTCTC TCGACGCAAA
iB_10181	TC015547	GATGTACAGAGGGGGCAAGATCTGTCTCAGCGATCACTTCAAGCCTTTGTGGGCGCGAAACGTCCCCAAGTTTGGGATCG CGCACGCCATGGCGCTCGGGTTGGGGCCGTGGCTAGCCGTGGAAATCCCCGACTTGATCGCCAAAGCGGTGGTCACGCAC AAGAGAAA
iB_10701	TC014985	TCTCGTGTGTCGTATCTCGCCAGAAATATATATTTTTATATTTTATTTATGTTTTTGAACAATAATCTTCTATTTAT CTAGTTAGGTTTCGTTAGTGTAATAAATTGCTCAGTCATTATTTGTGTTTGTGACCACACAGTCCATAAACAGGCGAGTCT GC