Oligonucleotides

In the table below, each oligonucleotide is used, and is separated by a horizontal line. The sequence is listed on the last line of text for each oligonucleotide, and is right justified. "HH" is an abbreviation for "hammerhead"; A. tumefaciens refers to *Agrobacterium tumefaciens* str. C58 (also called 1303); A. caulinodans refers to *Azhorhizobium caulinodans* ORS571.

name	template	template (detail)	Forward/Rev
			sequence
JP_077_HH_Atu-a-F	A. tumefaciens	tandem HH and flanking sequence in what is presumably a prophage	For
			TAATACGACTCACTATAGGCCGCAGCTATCGGCACG
JP_078_HH_Atu-b-F	A. tumefaciens	tandem HH and flanking sequence in what is presumably a prophage	For
			TAATACGACTCACTATAGGCAGTCACTCAACACATTC
JP_079_HH_Atu-c-F	A. tumefaciens	tandem HH and flanking sequence in what is presumably a prophage	For
			TAATACGACTCACTATAGGAAGAGCTGGGAAACAAC
JP_080_HH_Atu-a-R	A. tumefaciens	tandem HH and flanking sequence in what is presumably a prophage	Rev
			CCCATACCGGGCCAACATG
JP_081_HH_Atu-b-R	A. tumefaciens	tandem HH and flanking sequence in what is presumably a prophage	Rev
			GACCGGAGGCCAGCCGAAG
JP_082_HH_Atu-c-R	A. tumefaciens	tandem HH and flanking sequence in what is presumably a prophage	Rev
			ACTCGCATCGATCCACCGACC
JP_085_HH_Atu-d-R	A. tumefaciens	tandem HH and flanking sequence in what is presumably a prophage	Rev
			AGGCCGTGTTGTCCAGCCC
JP_088_antiHH1-1	pairs with HH1 cugauga from A. tumefaciens		Rev
			CTATTCCGCTAGCTCATCAGGCCCTAGGCGCGACCCTAGGAC
JP_089_antiHH1-2	pairs with HH2 cugauga from A. tumefaciens		Rev
			TTTCGTGCGCTGCTCATCAGGCCCTAGGCGCGACCCTAGGAC
JP_090_antiHH1-3	pairs with HH3 cugauga from A. tumefaciens		Rev
			GGGAATGGCAACCATCATCAGGCGGGGCATGCCAAGCCCCAC
JP_091_HH1_mutant-R	HH1 cugauga–>cuAauga from A. tumefaciens		Rev
			CTATTCCGCTAGCTCATTAGGCCCTAGGCGCGACC
JP_092_HH2_mutant-R	HH2 cugauga–>cuAauga from A. tumefaciens		Rev
			TTTCGTGCGCTGCTCATTAGGCCCTAGGCGCGACC
JP_093_HH3_mutant-R	HH3 cugauga–>cuAauga from A. tumefaciens		Rev
			GGAATGGCAACCATCATTAGGCGGGGCATGCCAAG
JP_094_HH1_mutant-F	HH1 cugauga–>cuAauga from A. tumefaciens		For
			GGTCGCGCCTAGGGCCTAATGAGCTAGCGGAATAG

Name	Description	Notes	Direction	Sequence
JP_095_HH2_mutant-F	HH2 cugauga–>cuAauga from A. tumefaciens		For	
				GGTCGCGCCTAGGGCCTAATGAGCAGCGCACGAAA
JP_096_HH3_mutant-F	HH3 cugauga–>cuAauga from A. tumefaciens		For	
				CTTGGCATGCCCCGCCTAATGATGGTTGCCATTCC
JP_097_HH1-2_small-F	shorten 3HH from A. tumefaciens (940->384)		For	
				GAGAGATGGTCGACCTAGATCAATCCACATGTGGAAAG
JP_098_HH1-2_small-R	shorten 3HH from A. tumefaciens (940->384)		Rev	
				TTGATCTAGGTCGACCATCTCTCACTCCTTCGCTATCG
JP_099_HH_Atu-C1-R	A. tumefaciens	tandem HH and flanking sequence in what is presumably a prophage(to probe first fragment, before HH1)	Rev	
				CACCAGCCAGACCGTTGAACCGCTGGCC
JP_109_HH_Aca-a-F	A. caulinodans	prophage (near tandem HH)	For	
				taatacgactcactataggAACGGTGCAGTGACTGCAC
JP_110_HH_Aca-a-R	A. caulinodans	prophage (near tandem HH)	Rev	
				gcctcgggagagcgatcagcgttggcg
JP_111_HH_Aca-b-R	A. caulinodans	prophage (near tandem HH)	Rev	
				gggcctcgacttctccccggagacgttcg
JP_112_HH_Aca-c-R	A. caulinodans	prophage (near tandem HH)	Rev	
				caacctcttcctcgatcaccgccaccagatc
JP_113_HH_Aca-c2-R	A. caulinodans	prophage (near tandem HH)	Rev	
				caggggcgcggcgtctggcctcatcctcgg
JP_123_HH_Aca-a2-F	A. caulinodans	prophage (near tandem HH)	For	
				CGGTCACAGTCCCTCGCTA
JP_124_HH_Aca-c3-R	A. caulinodans	prophage (middle tandem HH)	Rev	
				GATACCCCTCGCGCCA
JP_125_HH_Aca-b-F	A. caulinodans	prophage (middle tandem HH)	For	
				GCTTGCGGCCAACTGGTCCGCG
JP_126_HH_PaP3-R		entire HH		
				CATGGTCGTTTCATCCTTTAGGAATCATCAGCCGGGACACACATCCCGATACGACAAccTATAGTGAGTCGTATTA
JP_127_HH_Aca-a2-F-T7	PCR from A. caulinodans prophage			
				TAATACGACTCACTATAggCGGTCACAGTCCCTCGCTA
JP_128_HH_Atu_HH1mut-gaaa-F	HH1 gaaa –> gCaa from A. caulinodans		For	
				CATCGCATAACTAAGCGcAACCGGGGGGCGTCCT
JP_129_HH_Atu_HH2mut-gaaa-F	HH2 gaaa –> gCaa from A. caulinodans		For	
				CATGTGGAAAGTAATGCGcAACCGGGTGTCGCTTC
JP_130_HH_Atu_HH3mut-gaaa-F	HH3 gaaa –> gCaa from A. caulinodans		For	
				CAATCCAACTGATACCGcAACCGGCTCCCTAGGG
JP_131_HH_Atu_HH1mut-gaaa-R	HH1 gaaa –> gCaa from A. caulinodans		Rev	
				AGGACGCCCCCGGTTgCGCTTAGTTATGCGATG
JP_132_HH_Atu_HH2mut-gaaa-R	HH2 gaaa –> gCaa from A. caulinodans		Rev	
				GAAGCGACACCCGGTTgCGCATTACTTTCCACATG
JP_133_HH_Atu_HH3mut-gaaa-R	HH3 gaaa –> gCaa from A. caulinodans		Rev	
				CCCTAGGGAGCCGGTTgGGGTATCAGTTGGATTG

Name	Description	Dir	Sequence
JP_134_HH_Aca_HH1good-F	A. caulinodans		For GCCCGCGAGGGCCGAAACGATAGAGGAGCTAG
JP_135_HH_Aca_HH1good-F	A. caulinodans		Rev CTAGCTCCTCTATCGTTTCGGCCCTCGCGGGC
JP_136_HH_Aca_anti-HH1	pairs with HH1 cugauga from A. tumefaciens	Rev	CTCGCGGGCCTCGTCAGGCCGGGACCCTCCCCG
JP_137_HH_Aca_anti-HH2	pairs with HH2 cugauga from A. tumefaciens	Rev	CTGCCATGGGCTCATCAGTGGACCGGCATCAGGTC
JP_138_HH_Atu_HH1-and-2_3'fragment	A. tumefaciens	Tandem HH and flanking sequence in what is presumably a prophage	For TAATACGACTCACTATAgGTCCTAGGGTCGCGCC
JP_139_HH_Atu_HH3_3'fragment	A. tumefaciens		For TAATACGACTCACTATAgGTGGGGCTTGGCATG
JP_140_T7-term-F	T7 terminator for annealing		For GctagcataaccccttgggggcctctaaacgggtcttgaggggtttttttgA
JP_141_T7-term-R	T7 terminator for annealing		Rev catgTCAAAAAACCCCTCAAGACCCGTTTAGAGGCCCCAAGGGGTTATGCTAGCtgca
JP_142_T7-term-screen-F	clones with T7-term		For gctaGCATAACCCCTTGG
JP_144_pUC19(836-821)	pUC19(836-821)		Rev CTGGCCTTTTGCTGGC
JP_147_T7-term-screen-R	clones with T7-term		Rev AACCCCTCAAGACCCGTT
JP_148_rz-JCVI_SCAF_1101668476676/866	elongation		Rev ggGGCGTTTCGACTTTGTCCTATAGTGAGTCGTATTA
JP_149_rz-NC_008536.1/7550346	elongation		Rev gGCCGGTTATCGACTTACCTATAGTGAGTCGTATTA
JP_150_rz-NC_010168.1/3000116	elongation		Rev gGTGGTGCAGCGTTTCGCAGCGGAGTCCTATAGTGAGTCGTATTA
JP_151_rz-NZ_ABED02000017.1/64984	elongation		Rev gGCACGTCCTTGCTTTTTAGGTAATTTTAAACCTATAGTGAGTCGTATTA
JP_152_rz-NZ_ABFY02000014.1/30371	elongation		Rev gGCCCGTTTCGGCTCTCCTATAGTGAGTCGTATTA
JP_153_rz-NZ_ABLC01000053.1/26585	elongation		Rev gGCGGCGTTGCTGCGTGACCTATAGTGAGTCGTATTA
JP_154_rz-NC_007497.1/12160	elongation		Rev ggCGCCGTTTCGACCTATTACCTATAGTGAGTCGTATTA
JP_155_rz-JCVI_SCAF_1096626868593/854	elongation		Rev ggGGCGTTTCGTTCTTCCTATAGTGAGTCGTATTA
JP_156_s-JCVI_SCAF_1101668476676/866	elongation		Rev TTGGTAGCCTGTCTCATTCAGTGTCGGTAGGCCACGTCCGACAGACGCCCCTATAGTGAGTCGTATTA
JP_157_s-NC_008536.1/7550346	elongation		Rev TCTTGGGCCTGTCTCTTCAGGCGTGGTGGGCCAGATCCACGCGACCGGCCTATAGTGAGTCGTATTA
JP_158_s-NC_010168.1/3000116	elongation		Rev TACCTTGTCTTGACTGATCAGATCGGCCCGTTGTGACTGATCCCAACCCGAAACGCTGCACCACcTATAGTGAGTCGTATTA
JP_159_s-NZ_ABED02000017.1/64984	elongation		Rev

			TCACAACACTAAAAGCCTGTTCAGTTAAAGAATGTTCTATAAGCAAGGACGTGCcTATAGTGAGTCGTATTA
JP_160_s-NZ_ABFY02000014.1/30371	elongation		Rev
			GTTCTGACCTGCCTTGTCAATGCGTGGGCGGTCATCCCACACAGACGGGCCTATAGTGAGTCGTATTA
JP_161_s-NZ_ABLC01000053.1/26585	elongation		Rev
			TTTTCGACCTGCGTCGTCAGGCGTTCGATGTCCACATCGGCCGCGACGCCGCCTATAGTGAGTCGTATTA
JP_162_s-NC_007497.1/12160	elongation		Rev
			CGATGGCGCTGATCTCAGCAGTACACGCATAACGTGCAGACAGCGCCTATAGTGAGTCGTATTA
JP_163_s-JCVI_SCAF_1096626868593/854	elongation		Rev
			TTCTTGAGCTATCTCATCAGTTAGAACTTCAGCTCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA
JP_164_Azo-other-phage-F	Azorhizobium caulinodans	prophage head gene (2467000-2467500)	For
			GCGCTCTACTGGAACCTCTG
JP_165_Azo-other-phage-R	Azorhizobium caulinodans	prophage head gene (2467000-2467500)	Rev
			GCTGGTCTTGGCGTCCTC
JP_166_Bce-HH-F	Bacillus cereus ATCC 14579	>gi|30018278:2631880-2634325	For
			TAAAACGATTAATTCCTTTGGTTC
JP_167_Bce-HH-R	Bacillus cereus ATCC 14579	>gi|30018278:2631880-2634325	Rev
			ATCTTTCAGCCCCCCTAAA
JP_168_Bce-HH-F	Bacillus cereus ATCC 14579	>gi|30018278:2631880-2634325	For
			TAATACGACTCACTATAggTAAAACGATTAATTCCTTTGG
JP_178_rz8-mut_C->U	use with substrate JP_163_s-JCVI_SCAF_1096626868593/854 (or other)		Rev
			ggGGCGTTTCATTCTTCCTATAGTGAGTCGTATTA
JP_179_rz8-mut_C->G	use with substrate JP_163_s-JCVI_SCAF_1096626868593/854 (or other)		Rev
			ggGGCGTTTCCTTCTTCCTATAGTGAGTCGTATTA
JP_180_rz8-mut_+U-A_bp	use with substrate JP_163_s-JCVI_SCAF_1096626868593/854 (or other)		Rev
			ggGGCGTTTCGATCTTCCTATAGTGAGTCGTATTA
JP_181_s8-mut__pk-4	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other)		Rev
			TATCTCATCAGTTAGAACTTCAGCTCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA
JP_182_s8-mut_-extra	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other)		Rev
			GAGCTATCTCATCAGTTAGAACTTCAGCTCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA
JP_183_s8-mut_pk-2	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other)		Rev
			GCTATCTCATCAGTTAGAACTTCAGCTCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA
JP_184_Bce-HH-T7-R	Bacillus cereus ATCC 14579	>gi|30018278:2631880-2634325	Rev
			TAATACGACTCACTATAggATCTTTCAGCCCCCCTAAA
JP_185_s8-mut_spacer+1	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other, like JP_180 to see P2=2)		Rev
			GAGCTATTCTCATCAGTTAGAACTTCAGCTCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA
JP_186_s8-mut_P1+2bp	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other, like JP_180 to see P2=2)		Rev
			GAGCTATCTCATCAGTTAGAAC gg TT CAGCTC T cc GTTCTAAGACGCCCCTATAGTGAGTCGTATTA

Name	Source	Description	Dir	
JP_187_s8-mut_L1-5'-1	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other, like JP_180 to see P2=2)		Rev	
		GAGCTA TCTCATCAGTTAGAAC TT CAGCTC GTTCTAAGACGCCCCTATAGTGAGTCGTATTA		
JP_188_s8-mut_L1-3'-2	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other, like JP_180 to see P2=2)		Rev	
		GAGCTA TCTCATCAGTTAGAAC CAGCTC T GTTCTAAGACGCCCCTATAGTGAGTCGTATTA		
JP_189_s8-mut_spacer-1	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other)		Rev	
		GAGCTACTCATCAGTTAGAACTTCAGCTCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA		
JP_190_s8-mut_pk-6	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other)		Rev	
		TCTCATCAGTTAGAACTTCAGCTCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA		
JP_191_HH_Bcl-F	Bacillus clausii	CDS of spore germination protein KC (gerKC)	For	
		AGGAGGGAGATGATTATGTGTTG		
JP_192_HH_Bcl-R	Bacillus clausii	CDS of spore germination protein KC (gerKC)	Rev	
		GGATCATTTTCCGTAACGATTC		
JP_193_HH_Bcl-T7-F	Bacillus clausii	CDS of spore germination protein KC (gerKC)	For	
		TAATACGACTCACTATAGGAGGGAGATGATTATGTGTTG		
JP_194_PaP3-R	PaP3 phage	potential type3 HH at end of genome	Rev	
		GACGCAGCTTTTTGTCAAGA		
JP_195_PaP3-F	PaP3 phage	potential type3 HH at end of genome	For	
		TACGCCAATGCCAAGGTT		
JP_196_PaP3-T7-F	PaP3 phage	potential type3 HH at end of genome	For	
		TAATACGACTCACTATAGGTACGCCAATGCCAAGGTT		
JP_199_Csc_2HH-F	Clostridium scindens	tandem HH	For	
		GGTACGACGAGCATCTTGAA		
JP_200_Csc_2HH-T7-F	Clostridium scindens	tandem HH	For	
		TAATACGACTCACTATAGGTACGACGAGCATCTTGAA		
JP_201_Csc_2HH-R	Clostridium scindens	tandem HH	Rev	
		TGCCTGTATGTCTTTTCCGG		
JP_202_Bcep176-(7)cis-HH-R	elongation		Rev	
		TGGCGCTGATCTCAGCAGTACACGCATAACGTGCAGACAGCGGGCCGTTACTACGTCTTCCTCCCGCCGTTTCGACCTATTCCTATAGTGAGTCGTATTA		
JP_209_AgroH1-Rz-R	elongation		Rev	
		GGCCCGGTTTCGCTTAGTTATGCCTATAGTGAGTCGTATTA		
JP_210_AgroH1-subs-F	elongation		For	
		TAATACGACTCACTATAGGCTCGGTCGTCCTAGGGTCGCGCCTAG		
JP_222_Rz?-F	elongation		For	
		TAATACGACTCACTATAgGtCAtCtCtGAtGACCACCAAtGAtCtAtCAG		
JP_223_Rz?-R	elongation		Rev	
		GATTCAGTCACCCGAAGGCGATCTTCACAGACTGATAGATCATTGGTGGT		
JP_233_Csc2_2HH-F	Clostridium scindens	tandem HH	For	

Name	Source	Region	Direction	Sequence
				GGGAACGGGGTTCTCC
JP_234_Csc2_2HH-T7-F	Clostridium scindens	tandem HH	For	
				TAATACGACTCACTATAGGGAACGGGGTTCTCC
JP_235_Csc2_2HH-R	Clostridium scindens	tandem HH	Rev	
				GGAGTTTCCCTTGCTGC
JP_236_16S(large)-F	16S rRNA from bacteria		For	
				agagtttgatcctggctcag
JP_237_16S(large)-R	16S rRNA from bacteria		Rev	
				ggytaccttgttacgactt
JP_238_Csc-16S-F	Clostridium scindens	16S rRNA	For	
				gcaacctgccttgcact
JP_239_Csc-16S-R	Clostridium scindens	16S rRNA	Rev	
				accgaatggccttgcca
JP_240_Atu-HH1-substr-R	Agrobacterium	3HH region	Rev	
				GGCCACCCGCCTTA
JP_245_Csc-between-2HH-R	Clostridium scindens	sequence between both HH in phage	Rev	
				CGCCTCTGTTCCGGCTGAATTTACCG
JP_246_Csc-before-2HH-R	Clostridium scindens	sequence before first HH in phage	Rev	
				CTGCTGCCCCGTTTCGGCTTTTA
JP_254_Atu-HH1-T7-F	Agrobacterium	first HH of 3HHs	For	
				TAATACGACTCACTATAggCTCGGTCGTCCTAGGGTC
JP_260_Rz_JCVI_scaf_1096626965523	elongation		Rev	
				GGCAGTGAGTGAGTTTCGCCTATAGTGAGTCGTATTA
JP_261_S_JCVI_scaf_1096626965523	elongation		Rev	
				AATGACCTGGCTCTTCAGGGCAGGGAGGTCATCCCACTGCCGACTCACTCACTGCCTATAGTGAGTCGTATTA
JP_266_t3-pk13	elongation		Rev	
				GCGTGTTTCGTCCCCTCTGGACCCTACTCGTCAGGGCCACGGACGAGGTCCAGAAGGGGCCGTGGCCGACACGCCTATAGTGAGTCGTATTA
JP_267_t3-weak	elongation		Rev	
				TTCCCTTTCGTGGTAACTCATCAGGGCAGACTACCAATGCCTGCCGAGGGAAccTATAGTGAGTCGTATTA
JP_268_t3-Droso	elongation		Rev	
				TAGACTGTTTCGGAAGACACCACTCTTCCTCATCAGCGATCTTTTCTTTTTCAATAATGAAAAAGATGGTAAATCGGACAGCCTAccTATAGTGAGTCGTATTA
JP_269_t1-mouse-gut-weak	elongation		Rev	
				TTATGGTACTATCCCGACTACCCTTGTTTGGGTAGTTTCGCCGGCTCTCACCGTTGCTCATCAGGGGATTTATTCGGTAccTATAGTGAGTCGTATTA
JP_270-t1-Cenarchaeum	elongation		Rev	
				AGCAATAAATGCCACAGACACGGCACCGGTGGTCTGGCGCCGTGTTTCGTCCACATAGGACTCGTCAGTATGGCTGCCGGGATAccTATAGTGAGTCGTATTA
JP_271_t1-Saltern	elongation		Rev	
				TGCGGTGGCTACCGCGACGGGGCACGAGGCCCCGTTTCGCCCGCGGCCAAGCGGGCTCGTCAGGCGGCTATGAGGTGAccTATAGTGAGTCGTATTA
JP_272_t1-Yarrowia	elongation		Rev	
				TTATGACTAGTGGCTGCCGACACCAACAGCCCCCACTGTTGATGTTTCGACGCTAGTCATGGGTTTGTTCTCATCAGGGCAGCCAGTCCCCCTATAGTGAGTCGTATTA
JP_273_t2-UAAA	elongation		Rev	
				GTGTCGGCCTGTCTCATCAGTGACGCGCGGCCATATGCGCCAGACCCCGCCGGGGCGGGGTTTAGACcTATAGTGAGTCGTATTA
JP_274_t2-CUAAAGA	elongation		Rev	
				AAAATCACGTTACAGCCTCTTTAGCACACGCCAGACGTGCGGACGCCCCGAAGGGCGTTTCGGCCTGTCAGCcTATAGTGAGTCGTATTA
JP_275_s8-mut_pk-swap	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other)		Rev	
				GtcgaATCTCATCAGTTAGAACTTCAGCTCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA

JP_276_s8-mut_pk-comp	use with Rz JP_155_rz-JCVI_SCAF_1096626868593/854 (or other)		Rev
	GtcgaATCTCATCAGTTAGAACTTCtcgaCTGTTCTAAGACGCCCCTATAGTGAGTCGTATTA		
JP_277_t1-X.phage(cugaagU)-R	elongation	NC_007024.1/490-419	Rev
	CCGCCGACCTGACCCCTGTATGGGGCCAGGTTTCGTCCGAGGTTAACTTACTCGGTCACTTCAGCGTCACGAACTTCCTATAGTGAGTCGTATTA		
JP_278_t1-Aedes(cuUacgaa)-R	elongation	NW_001810328.1/53176-53230	Rev
	CTAAATGCTTATCTCTGACAGATACGCGTATTTCGACTACAATTTGCAGTCTTCGTAAGTGTCAGCCTATAGTGAGTCGTATTA		
JP_279_t1-Aspergi(cugacUa-gaaG)-R	elongation	NT_107005.1/1253669-1253736	Rev
GTCAGAGCTACGGTGACTGTGGCCCTCCTTAAGAGCAGGCTTCAATCAGTCATATCTTCGTGATCTAGTCAGACGGTCACCGACTTGTCTTCCTATAGTGAGTCGTATTA			
JP_280_t1-Ep.viroid(-G-)-R	elongation	NC_004728.1/11-64	Rev
	TAAAGCTCTACCCCATGGCAGAACCCCATTTCGTCCTTTTGGACTCATCAGGGGTGGTACACACCTATAGTGAGTCGTATTA		
JP_281_t1-Aedes(cCgauga)-R	elongation	NZ_AAGE02023894.1/13988-14043	Rev
	AGAGTTTGTATTCTTCGACAGATACGCGTATTTCGACCTCAACTGTAAGGCCGTCTTCGGTGTCGGAAGAAGACGGTCTTACAGTTCcTATAGTGAGTCGTATTA		
JP_282_t1-Bos(Uaaa)-R	elongation	NW_001494989.2/1604723-1604611	Rev
	ATTTTCTAACCCACAAACACTCTGGAATATGGCAAGAGAGTGTTTAGCAAAAGGTAGCCAACTGCTCTTCAGTGTAAGATGTTGCTTCcTATAGTGAGTCGTATTA		
JP_283_t1-Monodelphis(UaaC)-R	elongation	NW_001581879.1/85484827-85484696	Rev
	CACCTTTGAGACGTTGCTTCACTTCTGGGATTCAGTTTCTTCATAGG		
JP_284_t1-Macaca(gaaG)-R	elongation	NW_001124105.1/14934-15038	Rev
	CCAGAGAAACCACTGGAAGCCCCAGTGTTATGGCAATGCCAGGGCTTCAGGCATTACCTTCTTCAGTCCAATGGTCCCCAACCTATAGTGAGTCGTATTA		
JP_285_t1-Yarrowia(gGaa)-R	elongation	NC_006068.1/1043901-1044007	Rev
GATATGTTTCGAACCAGTGGCTGTCTACACTACAGTTAGCAGTGTTCCGACGCTTGTCTCGGGGTCGTCTCATCAGGACAGCTAGGGGGCcTATAGTGAGTCGTATTA			
JP_286_t1-Monodelphis(UaaC)-F	elongation	NW_001581879.1/85484827-85484696	For
	TAATACGACTCACTATAGGCCATCTTTGATGTTCTGATGAGTGTGGGGTAAGATCTCACACTAACTTCCTTCTTTTACCTATGAAGAAACTGAATC		
JP_287_+5-Bcep176-(7)cis-HH-F	Bcep176 previous PCR		Rev
	TAATACGACTCACTATAGgcctcgtaataggtcgaaacggcgggagg		
JP_288_+5-Bcep176-(7)cis-HH-R	Bcep176 previous PCR		Rev
	GCGCTGATCTCAGCAGtac		
JP_289_manHH-t2-A-F	human genome	Chr14-pos59056349(intron of neurexin2)	For
	TATTTATAGAAGGACATTCATAG		
JP_290_manHH-t2-B-T7-F	human genome	Chr14-pos78890872(intron of neurexin2)	For
	TAATACGACTCACTATAGGACATTCATAGTGCTAGAGG		
JP_291_manHH-t2-A-R	human genome	Chr14-pos78890872(intron of neurexin2)	Rev
	CATCCTGCTTCCCTCCAAAGG		
JP_292_manHH-t2-B-R	human genome	Chr14-pos78890872(intron of neurexin2)	Rev
	GGTAATACCTGAATCATCAGC		
JP_293_manHH-t1-RECK-A-F	human genome	Chr9-36072672(intron of RECK)	For
	TCACAGTAGATTTGAGCCG		
JP_294_manHH-t1-RECK-B-T7-F	human genome	Chr9-36072672(intron of RECK)	For
	TAATACGACTCACTATAgGCCGTTACCTGCAGCTGATG		
JP_295_manHH-t1-RECK-A-R	human genome	Chr9-36072672(intron of RECK)	Rev
	TTAATACTATCTTAAGCCAGTAC		
JP_296_manHH-t1-RECK-B-R	human genome	Chr9-36072672(intron of RECK)	Rev
	GCCAGTACTGCAGGACCTAATAG		
JP_297_manHH-t1-c10-A-F	human genome	Chr10-115928020(intron in 5'UTR of c10orf118)	For
	AAATTGTTTCTTGACCAGTTGC		

JP_298_manHH-t1-c10-B-T7-F	human genome	Chr10-115928020(intron in 5'UTR of c10orf118)	For	
				TAATACGACTCACTATAggagttgcctacagctgatgagctc
JP_299_manHH-t1-c10-A-R	human genome	Chr10-115928020(intron in 5'UTR of c10orf118)	Rev	
				TGTTTCTGTTTCTGACACAGTACTAC
JP_300_manHH-t1-c10-B-R	human genome	Chr10-115928020(intron in 5'UTR of c10orf118)	Rev	
				CACAGTACTACAGGACCAATTC
JP_301_Danio-no-P2-R	elongation	Danio rerio	Rev	
				ggTCCACCCATTTCCATCAGAGCAATGCTTCATTGCcGATGGGTGGAccTATAGTGAGTCGTATTA
JP_302_chimp-no-P2-R	elongation	Pan troglodytes	Rev	
				ggATTCCATTTCTCTTCAGAGTGGAGATCCCCACTGATGGAATccTATAGTGAGTCGTATTA
JP_303_Aedes-typical-R	elongation	NW_0018112881/397739-397685	Rev	
				CTGTGACAGATACACGTATTTCGACTACTACTTGTAGTCTTCTTCAGTGTCAGTTACTCGTATCCTATAGTGAGTCGTATTA
JP_304_Nematostella-typical-R	elongation	NZ_ABAV01012423.1/13414-13365	Rev	
				aacTAACCATGGACAGCTGTTTCGTCCTTGTTAGGACTCGTCAGCATGGCATAccTATAGTGAGTCGTATTA
JP_318_t2-env-(A-U)to(U-A)	elongation	to obtain A15-U16 U16-A15 mutant	Rev	
				TTGTTAGCCAGTCTCATCAGTACGGGTAGGCTAGTTCCCGCAGTCACCCCGAAGGGTGATTCGACTTAGTTAGccTATAGTGAGTCGTATTA
ZW_093	elongation		Rev	
				TTACCTATTCCGCTAGCTCATCAGGCCCTAGGCGCGACCCT
saltern 1 trunc B	elongation	to obtain Hhmeta	For	
				TAATACGACTCACTATAGGTCTTTAGGCGCCTGACGAGGCCCGTGTGGGGCCGAAAC
saltern 2 trunc A	elongation	to obtain Hhmeta	Rev	
				TTGGCTAAGGCTACGGGGCTGACGCCCCGTTTCGGCCCCACACGGGCC