

Y11470.1	-----
MW040324.1	-----
MW040322.1	-----
MW040323.1	-----
OL304250.1	-----
OL304248.1	-----
OL304249.1	-----
Y11471.1	-----
A7_(82708220323)	-GACTCTCGGCAACGGATATCTTGGCTCTTGCAACGATGAAGAACGCAGCGAAATGCGAT
A9_(84087220504)	CGACTCTCGGCAACGGATATCTcGGCTCTcGctACGATGAAGAACGCAGCGAAATGCGAT
A4_(82702220323)	aGACTCTCGGCAACGGATATCTTGGCTCTTGCAACGATGAAGAACGCAGCGAAATGCGAT
A3_(82701220323)	CGACTCTCGGCAACGGATATCTTGGCTCTTGCAACGATGAAGAACGCAGCGAAATGCGAT
A6_(82704220323)	CGACTCTCGGCAACGGATATCTTGGCTCTTGCAACGATGAAGAACGCAGCGAAATGCGAT
A8_(83919220502)	--ACTCTCGGCAACGGATATCTTGGCTCTTGCAACGATGAAGAACGCAGCGAAATGCGAT
A5_(82703220323)	CGACTCTCGGCAACGGATATCTTGGCTCTTGCAACGATGAAGAACGCAGCGAAATGCGAT

Y11470.1	-----cCAcgcaTCCGtG-----CaAAcCcT-----GCAAATTGtG----
MW040324.1	-----TGCAGAATTCCGtGAATCATCGAgTCTTTGAACGCAtATTGCGCCCG
MW040322.1	-----TGCAGAATTCCGtGAATCATCGAgTCTTTGAACGCAtATTGCGCnCG
MW040323.1	-----TGCAGAATTCCGtGAATCATCGAgTCTTTGAACGCAtATTGCGCCCG
OL304250.1	-----TGCAGAATTCCGtGAATCATCGAgTCTTTGAACGCAtATTGCGCCCG
OL304248.1	-----TGCAGAATTCCGtGAATCATCGAgTCTTTGAACGCAtATTGCGCCgG
OL304249.1	-----TGCAGAATTCCGtGAATCATCGAgTCTTTGAACGCAtATTGCGCCgG
Y11471.1	-----TAcAATCT-----ATTGCGC---
A7_(82708220323)	ACGTAGTGTGAATTGCAGAATTCCGCGAATCATCGAATCTTTGAACGCAAcTcGCGCCCG
A9_(84087220504)	ACGTAGTGTGAATTGCAGAATTCCGCGAATCATCGAgTCTTTGAACGCAAcTcGCGCCCG
A4_(82702220323)	ACGTAGTGTGAATTGCAGAATTCCGCGAATCATCGAATCTTTGAACGCAAcTcGCGCCCG
A3_(82701220323)	ACGTAGTGTGAATTGCAGAATTCCGCGAATCATCGAATCTTTGAACGCAAcTcGCGCCCG
A6_(82704220323)	ACGTAGTGTGAATTGCAGAATTCCGCGAATCATCGAATCTTTGAACGCAAcTcGCGCCCG
A8_(83919220502)	ACGTAGTGTGAATTGCAGAATTCCGCGAATCATCGAATCTTTGAACGCAAcTcGCGCCCG
A5_(82703220323)	ACGTAGTGTGAATTGCAGAATTCCGCGAATCATCGAATCTTTGAACGCAAcTcGCGCCCG

Y11470.1	-GaCaTCCCCaAGGaggcGaCT-----TcaAtACCCTcCtgCGCCTgtCC-
MW040324.1	AGGcTTCGgtCaAGGGCATGTCTGCCTcAGCGTCggTtgAccCtctCgtCcaaTtCCCT
MW040322.1	AGGcTTCGgtCaAGGGCATGTCTGCCTcAGCGTCggTtgAccCtctCgtCcaaTtCCCT
MW040323.1	AGGcTTCGgtCnAGGGCATGTCTGCCTcAGCGTCggTtgAccCtctCgtCcaaTtCCCT
OL304250.1	AGGcTTCGgtCaAGGGCATGTCTGCCTcAGCGTCggTtgAccCtctCgtCcaaTtCCCT
OL304248.1	AGGcTTCGgtCaAGGGCATGTCTGCCTcAGCGTCggTtgAccCtctCgtCcaaTtCCCT
OL304249.1	AGGcTTCGgtCaAGGGCATGTCTGCCTcAGCGTCggTtgAccCtctCgtCcaaTtCCCT
Y11471.1	-----CtCC
A7_(82708220323)	AGGgCTCGCCtGAGGaCATGTtTGCCTGAGCGTCCTTACAAAtCCTACGCCGCTCCCC
A9_(84087220504)	AGGgCTCGCCCGAGGGCATGTCTGCCTGAGCGTCCTTACAAAtCCTACGCCGCTCCCC
A4_(82702220323)	AGGgCTCGCCCGAGGGCATGTCTGCCTGAGCGTCCTTACAAAtCCTACGCCGCTCCCC
A3_(82701220323)	AGGgCTCGCCCGAGGGCATGTCTGCCTGAGCGTCCTTACAAAtCCTACGCCGCTCCCC
A6_(82704220323)	AGGgCTCGCCCGAGGGCATGTCTGCCTGAGCGTCCTTACAAAtCCTACGCCGCTCCCC
A8_(83919220502)	AGGgCTCGCCCGAGGGCATGTCTGCCTGAGCGTCCTTACAAAtCCTACGCCGCTCCCC
A5_(82703220323)	AGGgCTCGCCCGAGGGCATGTCTGCCTGAGCGTCCTTACAAAtCCTACGCCGCTCCCC

Y11470.1	-----GtCcGAC-----aTCCaGggGtCaActtCtGccCTCCgatgGAGCAc
MW040324.1	CGnGGAaGcA--GACGGACcTGGnaGTCCCGCTGGCGAcAGCGGGTCTgCTGCAGAAcAG
MW040322.1	CGtGGAaGcA--GACGGACcTGGCaGTCCCGCTGGCGAcAGCGGGTCTgCTGCAGAAcAG
MW040323.1	CGtGGAaGcA--GACGGACcTGGCaGTCCCGCTGGCGAcAGCGGGTCTgCTGCAGAAcAG
OL304250.1	CGtGGAaGcA--GACGGACcTGGCaGTCCCGCTGGCGAcAGCGGGTCTgCTGCAGAAcAG
OL304248.1	CG-GGAaGcA--GACGGACcTGGCaGTCCCGCTGGCGAcAGCGGGTCTgCTGCAGAAcAG
OL304249.1	CGaGGAaGcA--GACGGACcTGGCaGTCCCGCTGGCGAcAGCGGGTCTgCTGCAGAAcAG
Y11471.1	CGtaGAGGGAGCGAC-aACGTGGtCGTC-----GCaA-----CTCCTcCAGAG-gc
A7_(82708220323)	CaCcGgGGGAGCGgCGGAtGTGGtCGTCC-----GCGAA-----CTCCTcCAGAGCac
A9_(84087220504)	CGCGGgGGGAGCGgCGGACGTGGCCGTCC-----GCGAA-----CTCCTcCgGAGCgc
A4_(82702220323)	CGCGGgGGGAGCGgCGGACGTGGCCGTCC-----GCGAA-----CTCCTcCgGAGCgc
A3_(82701220323)	CGCGGgGGGAGCGgCGGACGTGGCCGTCC-----GCGAA-----CTCCTcCgGAGCgt
A6_(82704220323)	CGCGGgGGGAGCGgCGGACGTGGCCGTCC-----GCGAA-----CTCCTcCgGAGCgt
A8_(83919220502)	CGCGGgGGGAGCGgCGGACGTGGCCGTCC-----GCGAA-----CTCCTcCgGAGCgt
A5_(82703220323)	CGCGGgGGGAGCGgCGGACGTGGCCGTCC-----GCGAA-----CTCCTcCgGAGCgt

Y11470.1	tCttC-AaTgcGCTGAgActC-----CcaCATaG
MW040324.1	ACGACGAnCAGCcGcAgcGCCGCTCGATtGGTAGGTTTCTCCGGAAGACAtGcCgTCG
MW040322.1	ACGACGAGcCAGCcGcAgcGCCGCTCGATtGGnAGGTTTCTCCGGAAGACAtGcCgTCG
MW040323.1	ACGACGAGcCAGCcGcAgcGCCGCTCGATtGGTAGGTTTCTCCGGAAGACAtGcCgTCG
OL304250.1	ACGACGAGcCAGCcGcAgcGCCGCTCGATtGGaAGGTTTCTCCGGAAGACAtGcCgTCG
OL304248.1	ACGACGAGcCAGCcGcAgcGCCGCTCGATtGG-AGGTTTCTCCGGAAGACAtGcCgTCG
OL304249.1	ACGACGAGcCAGCcGcAgcGCCGCTCGATtGGTAGGTTTCTCCGGAAGACAtGcCgTCG
Y11471.1	ACG----GTtAGtTGAAATaC-----ATCGa-----CGaActG
A7_(82708220323)	gCG----GTtgaCTGAAATGC-----ATCGG-----CGGCATCG
A9_(84087220504)	gCG----GTCgGCTGAAATGC-----ATCGG-----CGGCACCG
A4_(82702220323)	gCG----GTCgGCTGAAATGC-----ATCGG-----CGGCACCG
A3_(82701220323)	gCG----GTCgGCTGAAATGC-----ATCGG-----CGGCACCG
A6_(82704220323)	gCG----GTCgGCTGAAATGC-----ATCGG-----CGGCACCG
A8_(83919220502)	gCG----GTCgGCTGAAATGC-----ATCGG-----CGGCACCG
A5_(82703220323)	gCG----GTCgGCTGAAATGC-----ATCGG-----CGGCACCG

Y11470.1	gaatat---GAaAtcA-----
MW040324.1	AGtaGCCTGGgGACcAactGCCCCGTCTACCAACGACGGGGGaGCGCGCAAGcCaTcCcC
MW040322.1	AGnaGCCTGGgGACcAactGCCCCGTCTACCAACGACGGGGGaGCGCGCAAGcCaTcCcC
MW040323.1	AGtaGCCTGGgGACcAactGCCCCGTCTACCAACGACGGGGGaGCGCGCAAGcnaTcCcC
OL304250.1	AGtaGCCTGGgGACcAactGCCCCGTCTACCAACGACGGGGGaGCGCGCAAGcCaTcCcC
OL304248.1	AGtaGCCTGGgGACcAactGCCCCGTCTACCAACGACGGGGGaGCGCGCAAGcCaTcCcC
OL304249.1	AGtaGCCTGGgGACcAactGCCCCGTCTACCAACGACGGGGGaGCGCGCAAGcCaTcCcC
Y11471.1	AGCGGC---aAGACGAGTtG-----taGGGGTG-----cTCCTTCAC
A7_(82708220323)	AGCGGC---aAGACGAGTCG-----CaGGGGTG-----GTCCTTCAC
A9_(84087220504)	AGCGGC---GAGACGAGTCG-----CGGGGGTG-----GTCCTTCAC
A4_(82702220323)	AGCGGC---GAGACGAGTCG-----CGGGGGTG-----GTCCTTCAC
A3_(82701220323)	AGCGGC---GAGACGAGTCG-----CGGGGGTG-----GTCCTTCAC
A6_(82704220323)	AGCGGC---GAGACGAGTCG-----CGGGGGTG-----GTCCTTCAC
A8_(83919220502)	AGCGGC---GAGACGAGTCG-----CGGGGGTG-----GTCCTTCAC
A5_(82703220323)	AGCGGC---GAGACGAGTCG-----CGGGGGTG-----GTCCTTCAC

Y11470.1	-----
MW040324.1	CtGaCTCTCA-----
MW040322.1	CtGaCTCTCA-----
MW040323.1	CtGaCTCTCA-----
OL304250.1	CtGaCTCTCA-----
OL304248.1	CtGaCTCTCA-----
OL304249.1	CtGaCTCTCA-----
Y11471.1	CCGcCttagctcgcggggcttacagtggtcacagtcatccgcctcagtgccaagctag
A7_(82708220323)	CtGtT-----
A9_(84087220504)	CCGTt-----
A4_(82702220323)	CCGTt-----
A3_(82701220323)	CCGTt-----
A6_(82704220323)	CCGTt-----
A8_(83919220502)	CCGTt-----
A5_(82703220323)	CCGTt-----

Y11470.1	-----
MW040324.1	-----TTTCGACCTGAGTTCAGGCAAGaCCACCCGCTCAACTTAA
MW040322.1	-----TTTCGACCTGAGTTCAGGCAAGaCCACCCGCTCAACTTAA
MW040323.1	-----TTTCGACCTGAGTTCAGGCAAGaCCACCCGCTCAACTTAA
OL304250.1	-----TTTCGACCTGAGTTCAGGCAAGaCCACCCGCTCAACTTAA
OL304248.1	-----TTTCGACCTGAGTTCAGGCAAGaCCACCCGCTCAACTTAA
OL304249.1	-----TTTCGACCTGAGTTCAGGCAAGaCCACCCGCTCAACTTAA
Y11471.1	agagggcTTTaGggtcGAccTtgtGCgctCCCACctaCTC-----
A7_(82708220323)	-----GCAAGCCCcCtCGcggggt-----
A9_(84087220504)	-----GCAAGCCCcCtCGcggg-----
A4_(82702220323)	-----GgAAGCCCc-----
A3_(82701220323)	-----GaAAGCCCcCtCGC-----
A6_(82704220323)	-----GCAAGCCCcCtCGC-----
A8_(83919220502)	-----GCAAGCCCcCtCGggg-----
A5_(82703220323)	-----GgAAGCCCcCtCGgg-----