

Table S1. The sequences of NTSs and their characteristics.

Species	Variety	Code	Sequence	Length, bp	GenBank
<i>E. angustifolia</i>		Eang34	TTTTCTTGCAATTATTTGTAGTTCGATCAACCGAATCAAACAAACATCATCACCCCTTAAT TTTTTCGATAATCTCTTCTGAGCCATTCATTTCACTATTATTGCTTCCTTATTTATAA CTTCTCGAACGTACTAAGTATATCTTTTCATTCGCAAAAATAACAAGTTTCGTTATCTAA TTATATTTAGATGTCCAATTTCTAAT	207	MW288958
		Eang38	CATTTCTTGCAATTATATGTAGTTCGATCACCCGAATCAAACAAACATCATCACCCCTTAAT TTTTTGGATAATCTCTTCTGAGCCATTCATTTCACTATTATTGCTTCCTTATTCATAA TTTCTCGAACGTATTAAGTATATCTTTTCATTCGCAAAAATAACAAGTTTCGTTATCTAA TTATATTTAGATGTCCAATTTCTAAT	207	MW288959
		Eang39	TTTTCTTGCAATTATTTGTAGTTCGATCAACCGAATCAAACAAACATCATCACCCCTTAAT TTTTTCGATAATCTCTTTGAGCCATTCATTTCACTATTATTGCTTCCTTATTTATAA CTTCTCGAACGTACTAAGTATATCTTTTCACTCGCAAAAATAACAAGTTTCGTTATCTAA TTATATTTAGATGTCCAATTTCTAAT	207	MW288960
		Eang41	TTTTCTTGCAATTATTTGTAGTTCGATTCCCGAATCAAACAAACATCATTACCCTTAATT TTTGGGATAATCTCTTCTGAGCCATTCATTTCACTTTTATTGCTTCCTTATTTACAAC TTCTCGAACGTACTAAGTATATCTTTTCATTCGCAAAAATAACAAGTTTCGTTATCTAAT TATATTTAGATGTCCAATTTCTAATT	207	MW288961
		Eang42	CTTTTCTTGCAATTATATGTAGTTCGATCACCCGAATCAAACAAACATCATCACCCCTTAAT TTTTTGGATAATCTCTTCTGAGCCATTCATTTCACTATTATTGCTTCCTTATTTATAA CTTCTCGAACGTACTAAGTATATCTTTTCATTCGCAAAAATAACAAGTTTCGTTATCTAA TTATATTTAGATGTCCAATTTCTAAA	207	MW288962
		Eang43	TTTTCTTGCAATTATATGTAGTTCGATCAACCGAATCAAACAAACATCATCACCCCTTAAT TTTTTCGATAATCTCTTCTGAGCCATTCATTTCACTATTATTGCTTCCTTATTTATAA CTTCTCGAACGTACTAAGTATATCTTTTCATTCGCAAAAATAACAAGTTTCGTTATCTAA TTATATTTAGATGTCCAATTTCTAAT	207	MW288963
<i>E. commutata</i>		Ecom45	ATTTTTGCTCTATTTTATTCTAATCCGATAAACCGAATTGTTTAAATCCAATAAATCATA ATTTTTGCGATAACATATTCAAACCGTTCAATCTATACTTCAATTACTTCCATAACTAC AATTTATCGAAAGTAACTTGTATATGTTTACGCACGCATGAAATACTTTACCCGTACAAA TCTTATAATTAGATGTCGAAAGTTGTGAT	209	MW288964
		Ecom47	ATTTTTGCTCTATTTTATTCTAATCCGATAAACCGAATTGTTTAAATCCAATAAATCATA ATTTTTGCGATAACATATTCAAACCGTTCAATCTATACTTCAATTACTTCCATAACTAC	209	MW288965

			AATTTATCGAAAGTAACTGGTATATGTTTACGCACGCATGAAATACTTTACCCGTACAAA TCTTATAATTAGATGTCGAAAGTTGTGAT		
		Ecom48	TTTTTGCCTCTTTTATTCTAATCCGATAAACCGAATTGTTTAAATCTAATAAATCATAA TTTTTGCATAACTTATTCAAACCGTTCAATCTATACTTCAATTACTTCCTTAACTACA ATTTATCGAAAGTAACTTGTATATGTTTACGCACACATGAAAACTTTACCCGTACAAAT CTTATAATTAGATGTCGAAAGTTGTGAT	208	MW288966
		Ecom49	TTTTTGCCTCTTTTATTCTAATCCGATAAACCGAATTGTTTAAATCTAATAAATCATAA TTTTTGCATAACTTATTCAAACCGTTCAATCTATACTTCAATTACTTCCTTAACTACA ATTTATCGAAAGTAACTTGTATATGTTTACGCACACATGAAAACTTTACCCGTACAAAT CTTATAATTAGATGTCGAAAGTTGTGAT	208	MW288967
		Ecom50	TTTTTGCTCTCTTTTATTCTAATCCGATAAACCGAATTGTTTAAATCCAATAAACCATAA TTTTTGCATAACCTCTTCAAACCGTTCAATCTATACTTAAATTACTTCCTTAACTACA ATTTATCGAAAGTAACTTGTATATGTTTACGCACGCATGAAAACTCTACCCGTACAAAT CTTATAATTAGATGTCGAAAGTTGTGAT	208	MW288968
E. multiflora		Emult51	TTTTTGGCGCATTTATTGCTTTCAGAATTCAACATTCCAAATCATTCAAATTCCTGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCAGAATGTACTAAATAGACGTTACGAATGCATGTAGAACGTTATTGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288969
		Emult53	TTTTTGGCGCATTTATTGCCTTCGGAATTCAATATTCCAAATCATTCAAATTCATGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCATTA CCATAACTTTTAAATGTACTAAATAGACGTTACGCATGCATGTAGAACGATATTGAA ATCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288970
		Emult54	TTTTTGGCGCATTTATTGCTTTCAGAATTCAACATTCCAAATCATTCAAATTCCTGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCAGAATGTACTAAATAGACGTTACGAATGCATGTAGAACGTTATTGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288971
		Emult57	TTTTTGGCGCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTCGAAGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCAGAATGTACTAAATAGACGTTACGCATGCATGTAGAACGATATTGAA CACCTCTTATGATACGATGTCGAAGTTTATAAC	213	MW288972
		Emult61	TTTTTCGCGCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTCATGAC ACATATTTTTCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTT ACCATAACTTTCAGAATGTACTAAATAGACGTTACATGCATGCATGTAGAACGATATTGAA ACTCCTCTTATGATAAGATGTCGAAGTTTATAAC	214	MW288973

E. pungens	'Maculata'	Epung64	TTTTGCCGCATTTATTGACTTCAGAATTCGTTATTCCAAATCATTCAAATTTTCATGAAA TATATTTTTTGCTAAATCTTCTTTGCAACTTTTCTACTTATACTTTATTTTTATCGTTA CCATAAGTTTAAGAATGTACTAAATAGACGTTTCATGCATGCATGTAGAACGATATTGAA CTCTTCTTATGATTTGGTTTCGAAGTTTATAAC	213	MW288974
		Epung65	CTTTGCCGCATTTATTGATCTAAGGATTGCTATTCCAAATCATTCAAATTTTCATGAAA CATATTTTTTGCTAAATCATCTTTCCAACTTTCTACTTATACTTTATTTTTGTCGTTA CCATAAGTTTAAGAATGTACTAAATAGACGTTTCATGCATGCATGTAGAACGATATTGAA CTCTTCTTATGATTTGGTTTCGATGTTTATAAC	213	MW288975
		Epung72	CTTTGCCGCATTTATTGATCTCAGAATTCGATATTCCAAATCATTCAAATTTTCATGAAA CATATTTTTTGCTAAATCATGTTTCCAACTTTCTACTTACACTTTATTTTTATCGTTA CCATAAGTTTAAGAATGTACTAAATAGACGTTTCATGCATGCATGTAGAACGATATTGAA CTCTTCTTATGATTTGGTTTCGAAGTTTATAAC	213	MW288976
E. umbellata	Sweet'n'Sour	EumbSS75	TTTTGGCGCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCCAAGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCAGAATGTACTAAATAGACGTTTCACGCATGCATGTAGAACGATATTGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288989
	Fortunella	EumbF79	TTTTGGCGCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCCAAGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCAAGATATTTTAATTATTGTCGTTA CCATAACTTTCAGAATATACTAAATAGACGTTTCACACATGCATGTAGAACGATATTGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288977
		EumbF82	TTTTGGTGCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCCCTGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCATAATGTACTAAATAGACGTTTCACGCATGCATGTAGAACGATATTGAA CACCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288978
		EumbF84	TTTTGGTGCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCCCTGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCATAATGTACTAAATAGACGTTTCACGCATGCATGTAGAACGATATTGAA CACCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288979
		EumbF85	TTTTGGCGCATTTATTGCTTTTGAATTCAGAATTCCAAATCATTCAAATTTCCAACACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCAGAATGTACTAAATAGACGTTTACGCATGCATGTAGAACGATATTGAA CACCTCTTATGATAGGATGTCGAAGTTTATAAC	213	MW288980
		EumbF86	TTTTGGTGCATTTATTGCTTTCAGAATTCAATAGTCCAAATCATTCAAATTTCCAAAACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCTCTGATATTTTTATTATTGTCGTTA	213	MW288981

			CCATAACTTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTAGAACGATATT CGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC		
	Brilliant Rose	EumbBR88	TTTTTGGCGCATTTATTGCTTT CAGAATTCAATATTCCAAATCATACAAATTCCATGACA CATATTTTTTGCTACATCACCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTATAACGATATT CGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288982
		EumbBR89	ATTTTTGGCGCATTTATAGCTTT CAGAATTCAATATTCCAAATCATTCAAATTCCAAGAC CCATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTT ACCATAACTTT CAGAATGTACTAAATAAACGTTACGCGATGCATGTAGAACGATATT CGA ACTCTTCTTATGATAAGATGTCGAAGTTTATAAC	214	MW288983
		EumbBR91	TTTTTGGCGCATTTATTGCTTT CGGAATTCAATATTCCAAATCATTCAAATTCCATGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTT GAGAATGTACTAAATAGACGTTACGCGATGCATGTAGAACGATATT CGAA CACCTCTTATGATACGATGTCGAAGTTTATAAC	213	MW288984
		EumbBR92	TTTTTGGCGCATTTATTGCTTT CAGAATTCAATATTCCAAATCATTCAAATTCCAAGACA CATAATTTTTACTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTAGAACGATATT CGAA CTCTTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288985
		EumbBR98	TTTTTGGCACATTTATTGCTTT CAGAATTCAATATTCCAAATCATTCAAATTCCAAGACA CATATTTTTTGCTACATCTTAGTCCAACATTTTCACTGATATTTTTGTTATGTTTCGTTA CCATAACTTT CAGAATGTACTAAATAGACGTTACGAATGCATGTAGAACGATATT CGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288986
		EumbBR100	TTTTTGGCGCATTTATTGCTTTT AGAATTCAATATTCCAAATCATTCAAATTCCTGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTAGAACGATATT CGAA CTCTTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288987
		EumbBR101	ATTTTTGGCGCATTTATTGCTTT CAGAATTCAATATTCCGAATCATTCAAATTCCAAGAC ACATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTT ACCATAACTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTGGAACGATATT CGA ACTCCTCTTATGATAAGATGTCGAAGTTTACAAC	214	MW288988
	without variety	EumbB104	TTTTTGGCACATTTATTGCTCTTAGAATTCAATATTCCAAATCATTCAAATTCATGACA CATATTTTTTGCTACATCACCCGTCCAACATTTTCACTGATATTTTTATTATTGTCATTA CCATAACTTT CAAAATGTACTAAATAGACGTTACGCGATGCATGTAGAACGATATT CGAA CTCCTCTTATGATAAGATGTCGAAGTTTGTAAAC	213	MW288990

		EumbB109	TTTTGGCGAATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCTGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCAGAATGTACTAAATAGACGTTACGCATGCATGTATAACGATATTGGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288991
		EumbB110	TTTTGGCGCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCTATGACA CATATTTTTTGATAACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCAGAATGTACTAAATAGACGTTACGCATGCATGTAGAACGATATTCGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288992
		EumbB111	TCTTTGGCTCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCTATGACA CATATTTTTTGCTACATCATCAGTACAACATTTTCACTGATATTTTTATTATTGTCATTA CCATAACTTTCAGAATGTACTAAATAGACGTTACGCATGCATGTAGAACGATATTCGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAGC	213	MW288993
		EumbB112	TTTTGGCGCATTTATTGCTTTCACAATTCAATATTCCAAATCATTCAAATTCCTGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTAGAATGTACTAAATAGACGTTACGCATGGATGTAGAACGATATTCGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW288994
		EumbB113	TTTTGGCGCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCTATGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTCAGAATGTCCTAAATAGACGTTACGCATGCATGTAGAACGATATTCGAA CTCCTCTTATGATATGATGTCGAAGTTTATAAC	213	MW288995
		EumbB115	TCTTTGGCTCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCTATGACA CATATTTTTTGCTACATCATCAGTACAACATTTTCACTGATATTTTTATTATTGTCATTA CCATAACTTTCAGAATGTACTAAATAGACGTTACGCATGCATGTAGAACGATATTCGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAGC	213	MW288996
		EumbB116	TTTTGGCGCATTTATTGCTTTCAGAATTCAACATTCCAAATCATTCAAATTCATGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CAATAACTTTCAGAATGTATTAATAGACGTTACGCATGCATGTAGAACGATATTCGAA CTCCTCTTATGATAAGATGTCGAAGTTTGCAAC	213	MW288997
		EumbB117	TCTTTGGCTCATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCTATGACA CATATTTTTTGCTACATCATCAGTACAACATTTTCACTGATATTTTTATTATTGTCATTA CCATAACTTTCAGAATGTACTAAATAGACGTTACGCATGCATGTAGAACGATATTCGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAGC	213	MW288998
		EumbB118	TTTTGGCGAATTTATTGCTTTCAGAATTCAATATTCCAAATCATTCAAATTTCTGACA CATATTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA	213	MW288999

			CCATAACTTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTATAACGATATTGGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC		
		EumbB119	TTTTTGGCGAATTTATTGCTTT CAGAATTCAATATTCCAAATCATTCAAATTCTCTGACA CATATTTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTATAACGATATTGGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW289000
		EumbB120	TTTTTGGCGAATTTATTGCTTT CAGAATTCAATATTCCAAATCATTCAAATTCTCTGACA CATATTTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTATAACGATATTGGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW289001
		EumbB121	TTTTTGGCGCATTTATTGCTTT CACAATTCAATATTCCAAATCATTCAAATTCCTGACA CATATTTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTT AGAATGTACTAAATAGACGTTACGCGATGGATGTAGAACGATATTGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW289002
		EumbB124	TTTTTGGCGCATTTATTGCTTT CAGAATTCAATATTCCAAATCATTCAAATTCGAAGACA CATATTTTTTTGCTACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTATAACGATATTGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW289003
		EumbB125	TTTTTGGTGCATTTATTGCTTT CACAATTCAATATTCCAAATCATTCAAATTCCTGACA CATATTTTTTTGCTACATCTCCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTT CCATAACTTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTAGAACGATATTGAA CACCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW289004
		EumbB126	TTTTTGGCGCATTTATTGCTTT CAGAATTCAATATTCCAAATCATTCAAATTCATGACA CATATTTTTTTGATACATCATCAGTCCAACATTTTCACTGATATTTTTATTATTGTCGTTA CCATAACTTTT CAGAATGTACTAAATAGACGTTACGCGATGCATGTAGAACGATATTGAA CTCCTCTTATGATAAGATGTCGAAGTTTATAAC	213	MW289005
Sh. argentea		Sharg5	CACCTCCTTCCCTTTTTTTTTTTTTTTT CAGAAAACGAATACGTTAATATATGTTACAATC AATAAATAGAGTTTACATTGCTTATTCTTTCTTATACATAAACGTTGAAATCTATAAT	119	MW288952
		Sharg8	CTTTTCCCCCTTTTTTTTTTTTTTTT CAGAAAACGAATACGTTAATATATGTT ACAATCAATAAATAGAGTTTACATTGCTTATTCTTTCTTATACATAAACGTTGAAATCT ATAAT	125	MW288953
		Sharg9	CTCTTCCCCCACTTTTTTTTTTTTTTTT CAGAAAACGAATACGTTAATATATGTTACAATCAA TAAATAGAGTTTACATTGCTTATTCTTTCTTATACATAAACGTGGAAATCTATAAT	117	MW288954
		Sharg10	CTCTTCCCCCACTTTTTTTTTTTTTTTT CAGAAAACGAATACGTTAATATATGTTACAATC	119	MW288955

			AATAAATAGAGTTTACATTGCTTATTCTTTCTTATACATAAACGTTGAAATCTATAAT		
		Sharg14	CCTTTTCCCCCCCCCTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTTCAGAAAAC GAATACGTTAATATATGTTACAATCAATAAATAGAGTTTACATTGCTTATTCTTTCTTA TACATAAACGTTGAAATCTATAAT	144	MW288956
Sh. canadensis		Shcan25	TTTTTCCATCTCATTACATTTTTTTTTTCCGGTACGAAATGCCTTATTCTTGTTTATAAA AATAATGTTAATACTTCTTAACATTAATTTGAAAAATTAAAGACCGCAAAAAACAATTT ATAAGATCTCTTCTTATATGTAATAAGTGGTTCATCTGAC	160	MW288957