Supplementary Information

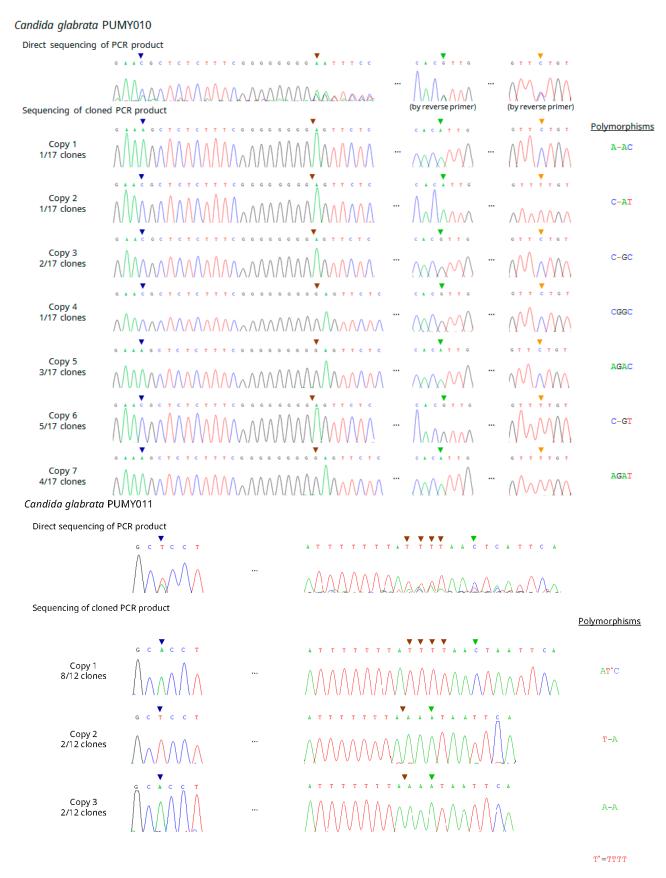


Figure S1. Cont.

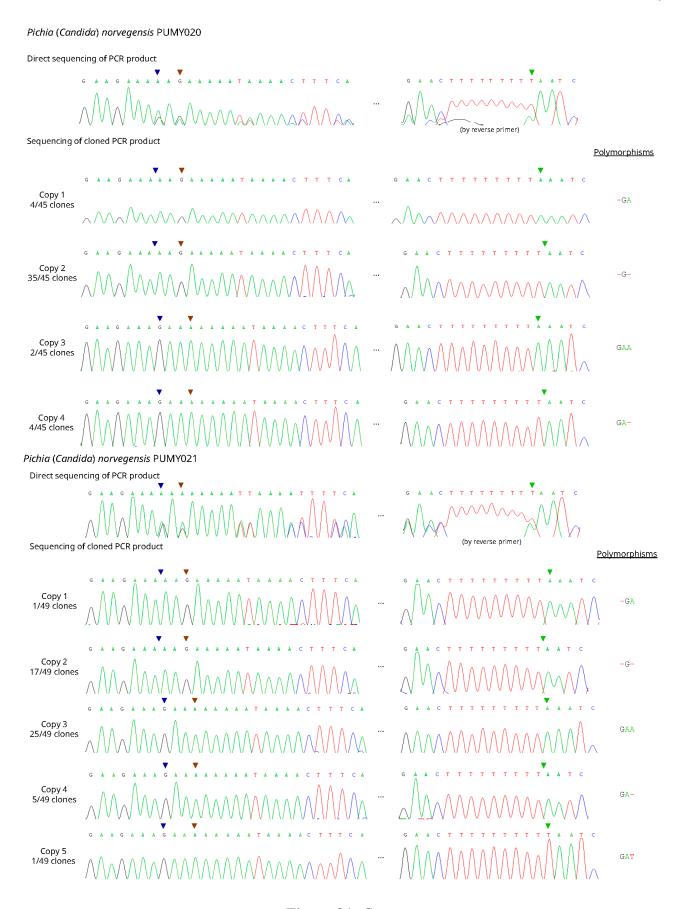


Figure S1. Cont.

Candida tropicalis PUMY040

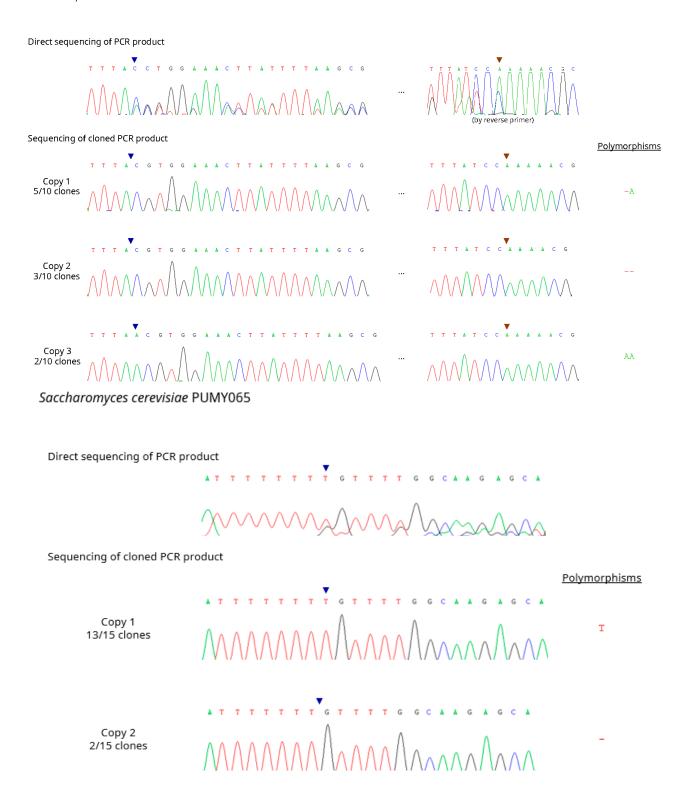


Figure S1. Sequencing electropherograms of the directly purified and cloned PCR products for the six yeast strains. The intra-genomic polymorphic sites are indicated by inverted arrowheads in different colors, and each color refers to a single polymorphic site.

	100 5313	-ma1				
PUMY010-1 PUMY010-2 PUMY010-3 PUMY010-4 PUMY010-5	AAGGATCATT AAGGATCATT	ITS1 AAAGAAATTT AAAGAAATTT AAAGAAATTT AAAGAAATTT AAAGAAATTT AAAGAAATTT	AATTGATTTG AATTGATTTG AATTGATTTG AATTGATTTG AATTGATTTG	TCTGAGCTCG TCTGAGCTCG TCTGAGCTCG TCTGAGCTCG	GAGAGAGACA GAGAGAGACA GAGAGAGACA GAGAGAGA	50 50 50 50 50
PUMY010-6 PUMY010-7	AAGGATCATT AAGGATCATT	AAAGAAATTT AAAGAAATTT	AATTGATTTG AATTGATTTG	TCTGAGCTCG TCTGAGCTCG	GAGAGAGACA GAGAGAGACA	50 50
PUMY010-1		GGACCAGTGT	AGACACTCAG	GAGGTTCCTA		100
PUMY010-2 PUMY010-3 PUMY010-4	TCTCTGGGGA	GGACCAGTGT GGACCAGTGT GGACCAGTGT	AGACACTCAG AGACACTCAG AGACACTCAG	GAGGTTCCTA GAGGTTCCTA	AAATATTTTC	100 100 100
PUMY010-5 PUMY010-6	TCTCTGGGGA	GGACCAGTGT GGACCAGTGT	AGACACTCAG AGACACTCAG	GAGGTTCCTA GAGGTTCCTA	AAATATTTTC	100 100
PUMY010-7		GGACCAGTGT	AGACACTCAG	GAGGTTCCTA		100
PUMY010-1 PUMY010-2 PUMY010-3	TCTGCTGTGA	ATGCCATTTC ATGCCATTTC ATGCCATTTC	TCCTGCCTGC TCCTGCCTGC	GCTTAAGTGC GCTTAAGTGC GCTTAAGTGC	GCGGTTGGTG GCGGTTGGTG GCGGTTGGTG	150 150 150
PUMY010-4 PUMY010-5	TCTGCTGTGA	ATGCCATTTC ATGCCATTTC	TCCTGCCTGC TCCTGCCTGC	GCTTAAGTGC GCTTAAGTGC	GCGGTTGGTG GCGGTTGGTG	150 150
PUMY010-6 PUMY010-7		ATGCCATTTC ATGCCATTTC	TCCTGCCTGC TCCTGCCTGC	GCTTAAGTGC GCTTAAGTGC	GCGGTTGGTG GCGGTTGGTG	150 150
PUMY010-1 PUMY010-2		AGTGGGGGGA AGTGGGGGGA	GGGAGCCGAC GGGAGCCGAC	AAAGACCTGG	GAGTGTGCGT GAGTGTGCGT	200 200
PUMY010-3 PUMY010-4	GGTGTTCTGC	AGTGGGGGGA	GGGAGCCGAC GGGAGCCGAC	AAAGACCTGG	GAGTGTGCGT GAGTGTGCGT	200 200
PUMY010-5	GGTGTTCTGC	AGTGGGGGGA	GGGAGCCGAC	AAAGACCTGG	GAGTGTGCGT	200
PUMY010-6 PUMY010-7			GGGAGCCGAC GGGAGCCGAC		GAGTGTGCGT GAGTGTGCGT	200 200
PUMY010-1 PUMY010-2	GGATCTCTCT GGATCTCTCT	ATTCCAAAGG ATTCCAAAGG	AGGTGTTTTA AGGTGTTTTA		CGACACTTTC CGACACTTTC	250 250
PUMY010-3	GGATCTCTCT	ATTCCAAAGG	AGGTGTTTTA		CGACACTTTC	250
PUMY010-4 PUMY010-5	GGATCTCTCT GGATCTCTCT	ATTCCAAAGG ATTCCAAAGG	AGGTGTTTTA AGGTGTTTTA		CGACACTTTC CGACACTTTC	250 250
PUMY010-6 PUMY010-7	GGATCTCTCT GGATCTCTCT	ATTCCAAAGG ATTCCAAAGG	AGGTGTTTTA AGGTGTTTTA		CGACACTTTC CGACACTTTC	250 250
PUMY010-1 PUMY010-2			GTTTACTTTA GTTTACTTTA		TTTGTTCGTT	300 300
PUMY010-3	TAATTACTAC	ACACAGTGGA	GTTTACTTTA	CTACTATTCT	TTTGTTCGTT	300
PUMY010-4 PUMY010-5			GTTTACTTTA GTTTACTTTA		TTTGTTCGTT	300 300
PUMY010-6 PUMY010-7	TAATTACTAC	ACACAGTGGA ACACAGTGGA	GTTTACTTTA GTTTACTTTA		TTTGTTCGTT TTTGTTCGTT	300 300
PUMY010-1	• GGGGGAAAGC	• TCTCTTTC-G	GGGGGGAGT	TCTCCCAGTG	GATGCAAACA	349
PUMY010-2 PUMY010-3	GGGGGAACGC GGGGGAACGC	TCTCTTTC-G TCTCTTTC-G	GGGGGGGAGT GGGGGGGAGT	TCTCCCAGTG TCTCCCAGTG	GATGCAAACA GATGCAAACA	349 349
PUMY010-4	GGGGGAACGC	TCTCTTTCGG	GGGGGGGAGT	TCTCCCAGTG	GATGCAAACA	350
PUMY010-5 PUMY010-6	GGGGGAAAGC GGGGGAACGC	TCTCTTTCGG TCTCTTTC-G	GGGGGGGAGT GGGGGGGAGT	TCTCCCAGTG TCTCCCAGTG	GATGCAAACA GATGCAAACA	350 349
PUMY010-7	GGGGGAAAGC		GGGGGGAGT	TCTCCCAGTG	GATGCAAACA	350
PUMY010-1 PUMY010-2	CAAACAAATA	TTTTTTTAAA	CTAATTCAGT CTAATTCAGT	CAACACAAGA	TTTCTTTTAG	399 399
PUMY010-3 PUMY010-4			CTAATTCAGT CTAATTCAGT			399 400
PUMY010-5	CAAACAAATA	TTTTTTTAAA	CTAATTCAGT	CAACACAAGA	TTTCTTTTAG	400
PUMY010-6 PUMY010-7			CTAATTCAGT CTAATTCAGT			399 400
PUMY010-1		CTTCAAAACT	TTCAACAATG			449
PUMY010-2 PUMY010-3			TTCAACAATG TTCAACAATG			449 449
PUMY010-4 PUMY010-5			TTCAACAATG TTCAACAATG			450 450
PUMY010-6	TAGAAAACAA	CTTCAAAACT	TTCAACAATG	${\tt GATCTCTTGG}$	TTCTCGCATC	449
PUMY010-7			TTCAACAATG GCGATACGTA			450 499
PUMY010-1 PUMY010-2	GATGAAGAAC	GCAGCGAAAT	GCGATACGTA	${\tt ATGTGAATTG}$	CAGAATTCCG	499
PUMY010-3 PUMY010-4			GCGATACGTA GCGATACGTA			499 500
PUMY010-5	GATGAAGAAC	GCAGCGAAAT	GCGATACGTA	${\tt ATGTGAATTG}$	CAGAATTCCG	500
PUMY010-6 PUMY010-7			GCGATACGTA GCGATACGTA			499 500
PUMY010-1 PUMY010-2			CGCACATTGC CGCACATTGC			549 549
PUMY010-3	TGAATCATCG	AATCTTTGAA	CGCACATTGC	GCCCTCTGGT	ATTCCGGGGG	549
PUMY010-4 PUMY010-5			CGCACATTGC CGCACATTGC			550 550
PUMY010-6	TGAATCATCG	AATCTTTGAA	CGCACATTGC	GCCCTCTGGT	ATTCCGGGGG	549
PUMY010-7	TGAATCATCG	AATCTTTGAA	CGCACATTGC	GCCCTCTGGT	ATTCCGGGGG	550

Figure S2. Cont.

			ITS2	•		
PUMY010-1	GCATGCCTGT	TTGAGCGTCA	TTTCCTTCTC	AAACACATTG	TGTTTGGTAG	599
PUMY010-2	GCATGCCTGT	TTGAGCGTCA	TTTCCTTCTC	AAACACATTG	TGTTTGGTAG	599
PUMY010-3	GCATGCCTGT	TTGAGCGTCA	TTTCCTTCTC	AAACACGTTG	TGTTTGGTAG	599
PUMY010-4	GCATGCCTGT	TTGAGCGTCA	TTTCCTTCTC	AAACACGTTG	TGTTTGGTAG	600
PUMY010-5	GCATGCCTGT	TTGAGCGTCA	TTTCCTTCTC	AAACACATTG	TGTTTGGTAG	600
PUMY010-6	GCATGCCTGT	TTGAGCGTCA	TTTCCTTCTC	AAACACGTTG	TGTTTGGTAG	599
PUMY010-7	GCATGCCTGT	TTGAGCGTCA	TTTCCTTCTC	AAACACATTG	TGTTTGGTAG	600
PUMY010-1	TGAGTGATAC	TCTCGTTTTT	GAGTTAACTT	GAAATTGTAG	GCCATATCAG	649
PUMY010-2	TGAGTGATAC	TCTCGTTTTT	GAGTTAACTT	GAAATTGTAG	GCCATATCAG	649
PUMY010-3	TGAGTGATAC	TCTCGTTTTT	GAGTTAACTT	GAAATTGTAG	GCCATATCAG	649
PUMY010-4		TCTCGTTTTT	GAGTTAACTT	GAAATTGTAG	GCCATATCAG	650
PUMY010-5	TGAGTGATAC	TCTCGTTTTT	GAGTTAACTT	GAAATTGTAG	GCCATATCAG	650
PUMY010-6		TCTCGTTTTT	GAGTTAACTT	GAAATTGTAG	GCCATATCAG	649
PUMY010-7	TGAGTGATAC	TCTCGTTTTT	GAGTTAACTT	GAAATTGTAG	GCCATATCAG	650
PUMY010-1		ACGAGCGCAA	GCTTCTCTAT		CTCGTTTGCG	699
PUMY010-2		ACGAGCGCAA	GCTTCTCTAT		CTCGTTTGCG	699
PUMY010-3		ACGAGCGCAA			CTCGTTTGCG	699
PUMY010-4		ACGAGCGCAA			CTCGTTTGCG	700
PUMY010-5		ACGAGCGCAA			CTCGTTTGCG	700
PUMY010-6		ACGAGCGCAA			CTCGTTTGCG	699
PUMY010-7	TATGTGGGAC	ACGAGCGCAA	GCTTCTCTAT	TAATCTGCTG	CTCGTTTGCG	700
PUMY010-1	CGAGCGGCGG	GGGTTAATAC	TGTATTAGGT	TTTACCAACT	CGGTGTTGAT	749
PUMY010-2	CGAGCGGCGG	GGGTTAATAC	TGTATTAGGT	TTTACCAACT	CGGTGTTGAT	749
PUMY010-3	CGAGCGGCGG		TGTATTAGGT	TTTACCAACT	CGGTGTTGAT	749
PUMY010-4	CGAGCGGCGG	GGGTTAATAC	TGTATTAGGT	TTTACCAACT	CGGTGTTGAT	750
PUMY010-5	CGAGCGGCGG	GGGTTAATAC	TGTATTAGGT	TTTACCAACT	CGGTGTTGAT	750
PUMY010-6	CGAGCGGCGG	GGGTTAATAC	TGTATTAGGT	TTTACCAACT	CGGTGTTGAT	749
PUMY010-7	CGAGCGGCGG	GGGTTAATAC	TGTATTAGGT	TTTACCAACT	CGGTGTTGAT	750
1011010	002100000000	000117211710	•	111210021101	00010110211	100
PUMY010-1	CTAGGGAGGG	ATAAGTGAGT	GTTCTGTGCG	TGCTGGGCAG	ACAGACGTCT	799
PUMY010-2	CTAGGGAGGG	ATAAGTGAGT	GTTTTGTGCG	TGCTGGGCAG	ACAGACGTCT	799
PUMY010-3	CTAGGGAGGG	ATAAGTGAGT	GTTCTGTGCG	TGCTGGGCAG	ACAGACGTCT	799
PUMY010-4	CTAGGGAGGG	ATAAGTGAGT	GTTCTGTGCG	TGCTGGGCAG	ACAGACGTCT	800
PUMY010-5	CTAGGGAGGG	ATAAGTGAGT	GTTCTGTGCG	TGCTGGGCAG	ACAGACGTCT	800
PUMY010-6	CTAGGGAGGG	ATAAGTGAGT	GTTTTGTGCG	TGCTGGGCAG	ACAGACGTCT	799
PUMY010-7	CTAGGGAGGG	ATAAGTGAGT	GTTTTGTGCG	TGCTGGGCAG	ACAGACGTCT	800
	25S nrI	ONA				
PUMY010-1	TTAAGTTTGA	CCTCAAATCA	GGTAGGGTTA	CCCGCTGAAC	TTAA	843
PUMY010-2	TTAAGTTTGA	CCTCAAATCA	GGTAGGGTTA	CCCGCTGAAC	TTAA	843
PUMY010-3	TTAAGTTTGA	CCTCAAATCA	GGTAGGGTTA	CCCGCTGAAC	TTAA	843
PUMY010-4	TTAAGTTTGA	CCTCAAATCA	GGTAGGGTTA	CCCGCTGAAC	TTAA	844
PUMY010-5	TTAAGTTTGA	CCTCAAATCA	GGTAGGGTTA	CCCGCTGAAC	TTAA	844
PUMY010-6	TTAAGTTTGA	CCTCAAATCA	GGTAGGGTTA	CCCGCTGAAC	TTAA	843
PUMY010-7	TTAAGTTTGA	CCTCAAATCA	GGTAGGGTTA	CCCGCTGAAC	TTAA	844

Figure S2. Cont.

PIMYO11-1 AAGGARCATT AAAGAAATTT AATTGATTG TCTGAGCTGG GAGAGAGACA 50 PIMYO11-3 AAGGARCATT AAAGAAATTT AATTGATTG TCTGAGCTCG GAGAGAGACA 50 PIMYO11-1 CTCTGGSGA GACCAGTTA AAAGAAATTT AATTGATTG TCTGAGCTCG GAGAGAGACA 50 PIMYO11-1 TCTCTGGSGA GACCAGTTA AAACAATTT CTCTGAGCTCG GAGAGAGACA 50 PIMYO11-1 TCTCTGGSGA GACCAGTGT AAACATTTC 100 PIMYO11-1 TCTCTGGSGA GACCAGTGT AGACACTCAG GAGGCACCTA AAACATTTC 100 PIMYO11-2 TCTCTGTGGA ATGCTATTC TCCTGCCTGC GCTTAAGTGC GCGGTTGGTG 150 PIMYO11-2 TCTGCTGTGA ATGCTATTC TCCTGCCTGC GCTTAAGTGC GCGGTTGGTG 150 PIMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGGCGT 150 PIMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGGCGT 150 PIMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGCGT 200 PIMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGCGT 200 PIMYO11-2 GGTGTTCTGC AGTGGGGGGA GAGAGCCGAC AAAGACCTGG GAGTGCGCT 200 PIMYO11-2 GGATCTCTC ATTCCAAAGG AGTGTTTTA TCACACGACT GGACCTTTC 250 PIMYO11-2 GGATCTCTC ATTCCAAAGG AGTGTTTTA TCACACGACT GGACCTTTC 250 PIMYO11-2 GGATCTCTC ATTCCAAAGG AGTGTTTTA TCACACGACT GACACTTTC 250 PIMYO11-2 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACACTACT TTTGTGTT 300 PIMYO11-1 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACACTACT TTTGTGTT 300 PIMYO11-1 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACACTACT TTTGTGTT 300 PIMYO11-1 GGGGGGAAAGC TCCTTTCTGG GAGGGAGTC TCCCAGTGGA TGCAAACCAC 350 PIMYO11-2 GGGGGAAAGC TCCTTTCTGG GAGGGAGTC TCCCAGTGGA TGCAAACCAC 350 PIMYO11-1 AACAAATATT TTTTTA	PIMYO11-1 AAGGATCATT AÀAGAAATTT AATTGATTTG TCTGAGCTCG GAGAGACACA PIMYO11-3 AAGGATCATT AAAGAAATTT AATTGATTTG TCTGAGCTCG GAGAGACACA 50 PUMYO11-3 AAGGATCATT AAAGAAATTT AATTGATTTG TCTGAGCTCG GAGAGACAC 50 PUMYO11-1 TCTCTGGGGA GACCAGTGT AAACACTCAG GAGCACCTA AAATATTTTC 100 PUMYO11-2 TCTCTGGGGA GACCAGTGT AGACCTCAG GAGCACCTA AAATATTTTC 100 PUMYO11-3 TCTGCTGTGGA GAGCACGTGT AGACCTCAG GAGCACCTA AAATATTTTC 100 PUMYO11-1 TCTGCTGTGA ATGCTATTTC TCCTGCGTGC GCTTAAGTGC GCGGTTGGTG 150 PUMYO11-2 TCTGCTGTGA ATGCTATTTC TCCTGCGTGC GCTTAAGTGC GCGGTTGGTG 150 PUMYO11-1 TCTGCTGTGA ATGCTATTTC TCCTGCGTG GCTTAAGTGC GCGGTTGGTG 150 PUMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMYO11-3 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMYO11-2 GGTGTCTCT ATTCCAAAGG AGTGTTTTA TCACACGACT CGACCTTTC 250 PUMYO11-2 GGATCTCTC ATTCCAAAGG AGTGTTTA TCACACGACT CGACCTTTC 250 PUMYO11-2 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACACTATTCT TTTGTTGGTT 300 PUMYO11-3 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACACTATTCT TTTGTTGGTT 300 PUMYO11-3 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACACTATCT TTTGTTGGTT 300 PUMYO11-3 GGGGGAAAGC TCCTTTTCGG GAGGGGGTTC TCCCAGTGGA TGCAAACACCA 350 PUMYO11-3 GGGGGAAAGC TCCTTTTCGG GAGGGGGTTC TCCCAGTGGA TGCAAACACCA 350 PUMYO11-3 AACAAATATT TTTTTA		100	TMC1				
PIMYO11-3 AAGGATCATT AAAGAAATTT AATTGATTTG TCTGAGCTCG GAGAGAGACA 50 PIMYO11-1 TCTCTGGGGA GACCAGTGT AAAGAATTT TAATTGATTTG TCTGAGCTCG GAGAGAGACA 50 PIMYO11-1 TCTCTGGGGA GACCAGTGT AAACACTCAG GAGCACCTA AAATATTTTC 100 PIMYO11-2 TCTCTGGGGA GACCAGTGT AAACACTCAG GAGCACCTA AAATATTTTC 100 PIMYO11-3 TCTCTGGGGA GACCAGTGT AAACACTCAG GAGCACCTA AAATATTTTC 100 PIMYO11-3 TCTGCTGTGA ATGCTATTTC TCTGCCTGC GCTTAAGTGC GCGTTGGTG 150 PIMYO11-2 TCTGCTGTGA ATGCTATTTC TCCTGCCTGC GCTTAAGTGC GCGTTGGTG 150 PIMYO11-3 TCTGCTGTGA ATGCTATTTC TCCTGCCTGC GCTTAAGTGC GCGTTGGTG 150 PIMYO11-1 GGTGTTCTGC AGTGGGGGGA GGGASCCGAC AAAGACCTGG GAGTGTGGT 150 PIMYO11-2 GGTGTTCTGC AGTGGGGGGA GGGASCCGAC AAAGACCTGG GAGTGTGGT 150 PIMYO11-3 GGTGTTCTGC AGTGGGGGGA GGGASCCGAC AAAGACCTGG GAGTGTGCGT PIMYO11-3 GGTGTTCTGC AGTGGGGGGA GGGASCCGAC AAAGACCTGG GAGTGTCCGT PIMYO11-1 GGTGTCTCTG AGTGGGGGGA GGGASCCGAC AAAGACCTGG GAGTGTCCGT PIMYO11-2 GATCTCTC ATTCCAAAGG AGGTGTTTTA TCACACACACT CGACACTTTC 250 PIMYO11-3 GATCTCTCT ATTCCAAAGG AGGTGTTTTA TCACACACACT CGACACTTTC 250 PIMYO11-1 TAATTACTAC ACACAGTGGA GTTTACTTA TCACACACAC CGACACTTTC 250 PIMYO11-1 TAATTACTAC ACACAGTGGA GTTTACTTA CTACACACAC CGACACTTTC 250 PIMYO11-1 TAATTACTAC ACACAGTGGA GTTTACTTA CTACATGTCT TTTGTTCGTT 300 PIMYO11-1 GAGGGAAAGC TCTCTTTGG GAGGGAGTC TCCCAGTGGA TGCAAACACA 350 PIMYO11-1 GAGGGAAAGC TCCTCTTGG GAGGGAGTC TCCCAGTGGA TGCAAACACA 350 PIMYO11-1 AACAAATATT TTTTTA	PUMY011-3 AAGGATCATT AAAGAAATT AATTGATTTG TCTGAGCTCG GAGAGACACA AAGACATT AAAGAAATT AATTGATTTG TCTGAGCTCG GAGAGACACA 50 PUMY011-1 TCTCTGGGGA GAGACAGTGT AAACACTCAG GAGGACACTA AAATATTTC 100 PUMY011-2 TCTCTGGGGA GAGCCAGTGT AAACACTCAG GAGGACCTA AAATATTTTC 100 PUMY011-3 TCTCTGGGGA GAGCCAGTGT AAACACTCAG GAGGACCTA AAATATTTTC 100 PUMY011-1 TCTCTGGGGA GAGCCAGTGT AGACACTCAG GAGGACCTA AAATATTTTC 100 PUMY011-1 TCTCTGTGTGA ATGCTATTTC TCCTGCCTGC GCTTAAGTGC GCGGTTGGTG 150 PUMY011-2 TCTGCTGTGA ATGCTATTTC TCCTGCCTGC GCTTAAGTGC GCGGTTGGTG 150 PUMY011-2 GGTGTTCTGC AGTGGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMY011-3 GGTGTTCTGC AGTGGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMY011-3 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMY011-3 GGTGTTCTGC AGTGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT 200 PUMY011-3 GGATCTCTC ATTCCAAAGG AGGTGTTTTA TCACAGGACT CGACACTTTC 250 PUMY011-3 GGATCTCTC ATTCCAAAGG AGGTGTTTTA TCACAGGACT CGACACTTTC 250 PUMY011-3 GGATCTCTC ATTCCAAAGG AGGTGTTTTA TCACAGGACT CGACACTTTC 250 PUMY011-1 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACAGGACT CGACACTTTC 250 PUMY011-1 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACATATTCT TTTGTTCGTT 300 PUMY011-1 GGGGGGAAGC CTCTTTCTGG GAGGGGATC TCCCAGTGGA TGCAAACACAC 350 PUMY011-1 GGGGGGAAGC TCTCTTTCGG GAGGGGATTC TCCCAGTGGA TGCAAACACAC 350 PUMY011-1 GGGGGGAAGC TCTCTTTCGG GAGGGGATTC TCCCAGTGGA TGCAAACACAC 350 PUMY011-1 AGACAAATATT TTTTAT	DIMV011_1	18S nrDNA	ITS1	<u>አ</u> ልጥጥሮልጥጥጥሮ	тстс <u>а</u> сстсс	GAGAGAGACA	50
PIMYO11-1 PIMYO11-2 PIMYO11-2 PIMYO11-3 PIMYO11-1 PIMYO11-2 PIMYO11-2 PIMYO11-3 PIMYO11-2 PIMYO11-3 PIMYO1	PINYO11-1 TCCTCGGGA GGACCAGTGT AGACACTCAG GAGGCACCTA AAANATTTCC PINYO11-2 TCCTCGGGA GGACCAGTGT AGACCACTCAG GAGGCACCTA AAANATTTC PINYO11-3 TCTCCTGGGA GACCAGTGT AGACCACTCAG GAGGCACCTA AAANATTTC 100 PINYO11-1 TCTCCTGGGA GACCAGTGT AGACCACTCAG GAGGCACCTA AAANATTTTC 100 PINYO11-2 TCTCCTGTGA ATGCTATTTC TCCTGCCTGC GCTTAAGTGC GCGGTTGGTG PINYO11-2 TCTGCTGTGA ATGCTATTTC TCCTGCCTGC GCTTAAGTGC GCGGTTGGTG PINYO11-3 GGTGTTCTGC AGTGGGGGGG GGGAGCCGAC AAAGACCTGG GAGTGTGCGT PINYO11-3 GGTGTTCTGC AGTGGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT PINYO11-3 GGTGTTCTGC AGTGGGGGGGA GGGAGCCGAC AAAGACCTGG GAGTGTGCGT PINYO11-3 GGATCTCTC ATTCCAAAGG AGGTGTTTTA TCACAGGACT CGACACTTTC 250 PINYO11-1 GGATCTCTC ATTCCAAAGG AGGTGTTTTA TCACACGACT CGACACTTTC 250 PINYO11-2 GGATCTCTC ATTCCAAAGG AGGTGTTTTA TCACACGACT CGACACTTTC 250 PINYO11-3 GGATCTCTCT ATTCCAAAGG AGGTGTTTTA TCACACGACT CGACACTTTC 250 PINYO11-1 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACATATTCT TTTGTTCGTT 300 PINYO11-1 TAATTACTAC ACACAGTGGA GTTTACTTTA CTACATATTCT TTTGTTCGTT 300 PINYO11-1 GGGGGAAAGC TCCTCTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA PINYO11-3 GGGGGAAAGC TCCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA PINYO11-3 GGGGGAAAGC TCCTTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA PINYO11-1 AGCACAATATT TTTTATTTT ACTCAACAC TGCA GATTCTTTT 300 PINYO11-1 AGCACAATATT TTTTTATTT ACTCAACACACAG GATTTCTTTT 301 PINYO11-1 AGCACAATATT TTTTTATTT ACTCAACACACAG GATTTCTTTT 302 PINYO11-1 AGCACAATATT TTTTTAT							
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PUMY011-1 GGGGGAAAGC TCTCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA 350 PUMY011-2 GGGGGAAAGC TCTCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA 350 PUMY011-3 GGGGGAAAGC TCTCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA 350 PUMY011-1 AACAAATATT TTTTATATTT AACTAATCA GTCAACACAA GATTTCTTTT 396 PUMY011-2 AACAAATATT TTTTTATTTT AACTAATCA GTCAACACAA GATTTCTTTT 396 PUMY011-2 AACAAATATT TTTTTA AAATAATTCA GTCAACACAA GATTTCTTTT 396 PUMY011-2 AACAAATAAT TTTTTA AAATAATTCA GTCAACACAA GATTCTTCTTT 396 PUMY011-2 AACAAAACAA CACTTCAAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA 446 PUMY011-2 AAGTAGAAACA AACTTCAAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA 446 PUMY011-2 TCGATGAAGA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC 496 PUMY011-3 TCGATGAAGA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC 496 PUMY011-2 CGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG 546 PUMY011-3 CGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG 546 PUMY011-3 GGGCATGCCT GTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT 596 PUMY011-3 GGGCATGCCT GTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT 596 PUMY011-3 GGGCATGCCT GTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT 596 PUMY011-3 AGTAGGTGAT ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC 646 PUMY011-3 AGTAGGTGAT ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC 646 PUMY011-3 AGTAGTGGG ACACGAGGCC AAGCTTCCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-3 AGTAGTGGG ACACGAGGCC AGGCTTCAT ATTAATCTGC TGCTCGTTTG 696 PUMY011-3 AGTAGTGGG ACACGAGGCC AGGCTTAAT ACTGTATTAG GTTTT	PUMY011-1 GGGGGAAAGC TCTCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA 350 PUMY011-2 GGGGAAAGC TCTCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA 350 PUMY011-3 GGGGGAAAGC TCTCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA 350 PUMY011-1 AACAAATATT TTTTTATTTT AACTAATCA GTCAACACAA GATTTCTTTT 396 PUMY011-2 AACAAATATT TTTTTATTT AACAAATATCA GTCAACACAA GATTTCTTTT 396 PUMY011-2 AACAAATATT TTTTTAT AAATAATTCA GTCAACACAA GATTTCTTTT 396 PUMY011-2 AACAAATATT TTTTTA AAATAATTCA GTCAACACAA GATTTCTTTT 396 PUMY011-1 AGTAGAAAA CAACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA 450 PUMY011-2 AGTAGAAAAC AACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA 446 PUMY011-2 AGTAGAAAAC AACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA 446 PUMY011-1 TCGATGAAGA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC 496 PUMY011-1 TCGATGAAGA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC 496 PUMY011-2 CGTGAATCAT CGAACTCTTG AACGCACATT GCGCCCTCTG GTATTCCGGG 546 PUMY011-2 CGTGAATCAT CGAACTCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG 546 PUMY011-2 CGTGAATCAT CGAACTCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG 546 PUMY011-2 CGGGAATCCT GTTTGAGCGT CATTTCCTC TCAAACACGT TGTGTTTGGT 596 PUMY011-2 CGGGATGCCT GTTTGAGCGT CATTTCCTC TCAAACACGT TGTGTTTTGGT 596 PUMY011-2 CGGGATGCCT GTTTGAGCGT CATTTCCTC TCAAACACGT TGTGTTTTGGT 596 PUMY011-2 AGTGAGTGAT ACTCTCGTTT TTGAGTTAC TTGAAATTGT AGGCCATATC 646 PUMY011-2 AGTAGGGAGGA CACGAGGCG AAGCTTCCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-2 AGTAGGGGG CACGGAGCGC AAGCTTCCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-2 AGTAGGGGG CACGGAGCGC AAGCTTCCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-3 AGTAGGGGG CACGAGGCG AAGCTTCCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-3 AGTAGGGGG GGGGTTAAT ACTCTGTTT TTGAGGTT ACTGCGGG AGCAGACGT 796 PUMY011-3 ACTAGGGGG GGGGTTAAT ACTGTATTAG GTTTTACCAA CTGGTGTTG 746 PUMY011-3 ACTAGGGGG GGGGTTAAT ACTGTATTAG GTTTTACCAA CTGG	PUMY011-1	TAATTACTAC	ACACAGTGGA	GTTTACTTTA	CTACTATTCT	TTTGTTCGTT	300
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PUMY011-2 GGGGGAAAGC TCTCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA S50 PUMY011-1 AACAAATATT TTTTTATTTT AACTAATTCA GTCAACACAA GATTTCTTTT AACAAATATT TTTTTAT AAATAATTCA GTCAACACAA GATTTCTTTT S6.8S nrDNA ACAAATATT TTTTTA AAATAATTCA GTCAACACAA GATTTCTTTT AACAACACAT TTTTTA AAATAATTCA GTCAACACAA GATTTCTTTT S6.8S nrDNA AGTAGAAACA ACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA AGTAGAAACA ACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA AGTAGAAACA ACTTCAACAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA AGTAGAAAAC AACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA AGGAGAAACA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC CGAGGAAGA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC ACGAGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG S50 PUMY011-1 CGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG S46 FUMY011-2 CGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG S46 FUMY011-3 CGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG S46 FUMY011-1 GGGCATGCCT GTTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT S96 FUMY011-2 GGCATGCCT GTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT S96 FUMY011-1 AGTGAGGTAT ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC AGTGAGTGAT ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC AGTGAGTGAT ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC GAGTGATA ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC GAGTGGTA ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC GAGTGGTA ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC GAGTGGGA CACGAGCGC AAGCTTCCT ATTAATCTGC TGCTCGTTTG PUMY011-1 AGTATGTGGG ACACGAGCGC AAGCTTCTCT ATTAATCTGC TGCTCGTTTG PUMY011-1 AGTATGTGGG ACACGAGCGC AAGCTTCTCT ATTAATCTGC TGCTCGTTTG GCCGAGCGCC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG GCCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG GCCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG GCCGAGCGGC GGGGGTTAAT ACTGTATTAG GTT	PUMY011-2 GGGGGAAAGC TCTCTTTCGG GAGGGAGTTC TCCCAGTGGA TGCAAACACA 350 PUMY011-1 AACAAATATT TTTTTATTTT AACTAATTCA GTCAACACA GATTTCTTTT 396 PUMY011-2 AACAAATATT TTTTTA AAATAATTCA GTCAACACA GATTTCTTTT 396 PUMY011-3 AACAAATATT TTTTTA AAATAATTCA GTCAACACA GATTTCTTTT 396 PUMY011-1 AACAAATATT TTTTTA AAATAATTCA GTCAACACAA GATTTCTTTT 396 PUMY011-1 AGTAGAAAC AACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA 450 PUMY011-2 AGTAGAAAAC AACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA 446 PUMY011-3 AGTAGAAAAC AACTTCAAAA CTTTCAACAA TGGATCTCTT GGTTCTCGCA 446 PUMY011-1 TCGATGAAGA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC 496 PUMY011-2 TCGATGAAGA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC 496 PUMY011-3 TCGATGAAGA ACGCAGCGAA ATGCGATACG TAATGTGAAT TGCAGAATTC 496 PUMY011-1 CGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG 546 PUMY011-2 CGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG 546 PUMY011-3 CGTGAATCAT CGAATCTTTG AACGCACATT GCGCCCTCTG GTATTCCGGG 546 PUMY011-1 GGGCATGCCT GTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT 596 PUMY011-1 GGGCATGCCT GTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT 596 PUMY011-2 GGGCATGCCT GTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT 596 PUMY011-3 GGGCATGCCT GTTTGAGCGT CATTTCCTTC TCAAACACGT TGTGTTTGGT 596 PUMY011-1 AGTGAGTGAT ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC 646 PUMY011-1 AGTGAGTGAT ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC 646 PUMY011-1 AGTAGTGGG ACACGAGCCC AGTCTCTCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-2 AGTAGTGGG ACACGAGCCC AAGCTTCTCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-1 AGTATGTGGG ACACGAGCCC AAGCTTCTCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-1 CGCGAGCGGC GGGGGTTAAT ACTCTCGTTT TTGAGTTAAC TTGAAATTGT AGGCCATATC 646 PUMY011-1 AGTATGTGGG ACACGAGCCC AAGCTTCTC ATTAATCTGC TGCTCGTTTG 696 PUMY011-2 AGTATGTGGG ACACGAGCCC AAGCTTCTC ATTAATCTGC TGCTCGTTTG 696 PUMY011-1 AGTATGTGGG ACACGAGCCC AGCTTCTC ATTAATCTGC TGCTCGTTTG 696 PUMY011-1 AGTATGTGGG ACACGAGCCC AGCTTCTC ATTAATCTGC TGCTCGTTTG 696 PUMY011-1 CGCGAGCGGC GGGGTTAAT ACTCTGTTTT TTGAGTTACA CTCGGTGTTG 746 PUMY011-1 CTAAGGTG GGGGATAAGTGA GTGTTTTTGTG CGT	PUMY011-3	TAATTACTAC	ACACAGTGGA	GTTTACTTTA	CTACTATTCT	TTTGTTCGTT	300
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PUMY011-3 AGTATGTGGG ACACGAGCGC AAGCTTCTCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-1 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 750 PUMY011-2 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.88 nrDNA	PUMY011-3 AGTATGTGGG ACACGAGCGC AAGCTTCTCT ATTAATCTGC TGCTCGTTTG 696 PUMY011-1 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 750 PUMY011-2 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.88 nrDNA PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846 PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842	PUMY011-1	AGTATGTGGG	ACACGAGCGC	AAGCTTCTCT	ATTAATCTGC	TGCTCGTTTG	700
PUMY011-1 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 750 PUMY011-2 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.88 nrDNA	PUMY011-1 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG PUMY011-2 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT PUMY011-3 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846 PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 847							
PUMY011-2 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 S.8S nrDNA	PUMY011-2 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.8S nrDNA PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846 PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842	PUMY011-3	AGTATGTGGG	ACACGAGCGC	AAGCTTCTCT	ATTAATCTGC	TGCTCGTTTG	696
PUMY011-2 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 S.8S nrDNA	PUMY011-2 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.8S nrDNA PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846 PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842	PIMY∩11_1	CGCGAGCGGC	GGGGGTTAAT	ልሮሞሬሞልሞሞልሬ	GTTTTTACCAA	СТСССТСТТС	750
PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.88 nrDNA	PUMY011-3 CGCGAGCGGC GGGGGTTAAT ACTGTATTAG GTTTTACCAA CTCGGTGTTG 746 PUMY011-1 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.8S nrDNA PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846 PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842							
PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.8S nrDNA	PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.8S nrDNA PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846 PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842							
PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.8S nrDNA	PUMY011-2 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.8S nrDNA PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846 PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842							
PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 7965.8S nrDNA	PUMY011-3 ATCTAGGGAG GGATAAGTGA GTGTTTTGTG CGTGCTGGGC AGACAGACGT 796 5.8S nrDNA PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846 PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842							
5.8S nrDNA	5.8S nrDNA PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 846							
	PUMY011-1 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA PUMY011-2 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842	I 0111011_2			2101111010	201201300	21021GHOACGI	120
		PUMY011-1			CAGGTAGGGT	TACCCGCTGA	ACTTAA	846
	PUMY011-3 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842							
PUMY011-3 CTTTAAGTTT GACCTCAAAT CAGGTAGGGT TACCCGCTGA ACTTAA 842		PUMY011-3	CTTTAAGTTT	GACCTCAAAT	CAGGTAGGGT	TACCCGCTGA	ACTTAA	842

Figure S2. Cont.

	18S nrDNA	ITS1				
PUMY020-1			AAACTTCTTT	CTTACACCGC	GTGAGCGCAC	50
PUMY020-2			AAACTTCTTT			50
PUMY020-3	AAGGATCATT	ACTGTGATTT	AAACTTCTTT	CTTACACCGC	GTGAGCGCAC	50
PUMY020-4			AAACTTCTTT			50
PUMY020-1	AACAACACCT	AAACACGAAT	AACCATGTCA	CCCAGAGAAA	ATCTCAAACG	100
PUMY020-2	AACAACACCT		AACCATGTCA			100
PUMY020-3			AACCATGTCA			100
PUMY020-4			AACCATGTCA	CCCAGAGAAA	ATCTCAAACG	100
	•	•	5.8S nrDNA			
PUMY020-1			AACTTTCAAC			149
PUMY020-2						149
PUMY020-3			AACTTTCAAC			150
PUMY020-4	AGAAGAAAGA	AAAAAAATAA	AACTTTCAAC	AACGGATCTC	TTGGTTCTCG	150
PUMY020-1	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	199
PUMY020-2	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	199
PUMY020-3	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	200
PUMY020-4	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	200
PUMY020-1		TCGAGTTCTT		TGCGCCCTCC		249
PUMY020-2		TCGAGTTCTT		TGCGCCCTCC		249
PUMY020-3		TCGAGTTCTT		TGCGCCCTCC		250
PUMY020-4	TCGTGAATCA	TCGAGTTCTT	GAACGCACAT ITS2	TGCGCCCTCC	GGCATTCCGG	250
PUMY020-1	GGGGCATGCC	TGTTTGAGCG		CTTGCGCAAG	CAGAGTTGGG	299
PUMY020-2			TCGTTTCCTT			299
PUMY020-3		TGTTTGAGCG		CTTGCGCAAG		300
PUMY020-4	GGGGCATGCC	TGTTTGAGCG	TCGTTTCCTT			300
PUMY020-1	GTTGCCACGG	CCCGTGCGGC	CTGTGTGTGG	CTCCCCGAA	ACGGAACGGC	349
PUMY020-2			CTGTGTGTGG			349
PUMY020-3	GTTGCCACGG	CCCGTGCGGC	CTGTGTGTGG	CTCCCCGAA	ACGGAACGGC	350
PUMY020-4	GTTGCCACGG	CCCGTGCGGC	CTGTGTGTGG	CTCCCCGAA	ACGGAACGGC	350
PUMY020-1	AGCGGGACTG	AGCGAAGTAC	ACAACACTCG	CGCTTGGCCC	GCCGAACTTT	399
PUMY020-2			ACAACACTCG			399
PUMY020-3			ACAACACTCG			400
PUMY020-4			ACAACACTCG			400
	•	25S 1	nrDNA			
PUMY020-1	TTTTTTAAAT	CTAAGCTCGA	CCTCAAATCA	GGTAGGAATA	CCCGCTGAAC	449
PUMY020-2	TTTTTT-AAT	CTAAGCTCGA	CCTCAAATCA	GGTAGGAATA	CCCGCTGAAC	448
PUMY020-3	ΤΤΤΤΤΤΤΔΑΔΤ	CTAAGCTCGA	CCTCAAATCA	GGTAGGAATA	CCCGCTGAAC	450
DIB417000 4	1111112221	011110010011				
PUMY020-4			CCTCAAATCA	GGTAGGAATA	CCCGCTGAAC	449
	TTTTTT-AAT		CCTCAAATCA	GGTAGGAATA	CCCGCTGAAC	
PUMY020-1	TTTTTT-AAT TTAA		CCTCAAATCA	GGTAGGAATA	CCCGCTGAAC	453
	TTTTTT-AAT		CCTCAAATCA	GGTAGGAATA	CCCGCTGAAC	

Figure S2. Cont.

	18S nrDNA	TTS1				
DIM(V/001 1			AAACTTCTTT	CTT CTCCC	CTCTCCCCTC	EΟ
PUMY021-1						50
PUMY021-2		ACTGTGATTT		CTTACACCGC		50
PUMY021-3		ACTGTGATTT		CTTACACCGC		50
PUMY021-4		ACTGTGATTT		CTTACACCGC		50
PUMY021-5	AAGGATCATT	ACTGTGATTT	AAACTTCTTT	CTTACACCGC	GTGAGCGCAC	50
PUMY021-1	AACAACACCT	AAACACGAAT	AACCATGTCA	CCCAGAGAAA	ATCTCAAACG	100
PUMY021-2	AACAACACCT	AAACACGAAT	AACCATGTCA	CCCAGAGAAA	ATCTCAAACG	100
PUMY021-3	AACAACACCT	AAACACGAAT	AACCATGTCA	CCCAGAGAAA	ATCTCAAACG	100
PUMY021-4	AACAACACCT	AAACACGAAT	AACCATGTCA	CCCAGAGAAA	ATCTCAAACG	100
PUMY021-5	AACAACACCT	AAACACGAAT	AACCATGTCA	CCCAGAGAAA	ATCTCAAACG	100
	•	•	5.8S nrDNA			
PUMY021-1	AGAAGAAA-A	AGAAAAATAA	AACTTTCAAC	AACGGATCTC	TTGGTTCTCG	149
PUMY021-2	AGAAGAAA-A	AGAAAAATAA	AACTTTCAAC	AACGGATCTC	TTGGTTCTCG	149
PUMY021-3	AGAAGAAAGA	AAAAAAATAA	AACTTTCAAC	AACGGATCTC	TTGGTTCTCG	150
PUMY021-4	AGAAGAAAGA	AAAAAAATAA		AACGGATCTC		150
PUMY021-5		AAAAAAATAA		AACGGATCTC		150
10.11021 0	21022102221021		221011102210	721000711010	1100110100	100
PUMY021-1	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	199
PUMY021-2	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	199
PUMY021-3	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	200
PUMY021-4	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	200
PUMY021-5	CATCGATGAA	GAGCGCAGCG	AAATGCGATA	CCTAGTGTGA	ATTGCAGCCA	200
PUMY021-1	TCGTGAATCA	TCGAGTTCTT	GAACGCACAT	TGCGCCCTCC	GGCATTCCGG	249
PUMY021-2	TCGTGAATCA	TCGAGTTCTT	GAACGCACAT	TGCGCCCTCC	GGCATTCCGG	249
PUMY021-3	TCGTGAATCA	TCGAGTTCTT	GAACGCACAT	TGCGCCCTCC	GGCATTCCGG	250
PUMY021-4	TCGTGAATCA	TCGAGTTCTT	GAACGCACAT	TGCGCCCTCC	GGCATTCCGG	250
PUMY021-5	TCGTGAATCA	TCGAGTTCTT	GAACGCACAT	TGCGCCCTCC	GGCATTCCGG	250
			ITS2			
PUMY021-1	GGGGCATGCC	TGTTTGAGCG	TCGTTTCCTT	CTTGCGCAAG	CAGAGTTGGG	299
PUMY021-2	GGGGCATGCC	TGTTTGAGCG	TCGTTTCCTT	CTTGCGCAAG	CAGAGTTGGG	299
PUMY021-3	GGGGCATGCC	TGTTTGAGCG	TCGTTTCCTT	CTTGCGCAAG	CAGAGTTGGG	300
PUMY021-4	GGGGCATGCC	TGTTTGAGCG	TCGTTTCCTT	CTTGCGCAAG	CAGAGTTGGG	300
PUMY021-5		TGTTTGAGCG		CTTGCGCAAG		300
10111021		10111011000	1001110011	01100001110	021021011000	000
PUMY021-1	GTTGCCACGG	CCCGTGCGGC	CTGTGTGTGG	CTCCCCCGAA	ACGGAACGGC	349
PUMY021-2	GTTGCCACGG	CCCGTGCGGC	CTGTGTGTGG	CTCCCCCGAA	ACGGAACGGC	349
PUMY021-3	GTTGCCACGG	CCCGTGCGGC	CTGTGTGTGG	CTCCCCCGAA	ACGGAACGGC	350
PUMY021-4	GTTGCCACGG	CCCGTGCGGC	CTGTGTGTGG	CTCCCCGAA	ACGGAACGGC	350
PUMY021-5	GTTGCCACGG	CCCGTGCGGC	CTGTGTGTGG	CTCCCCGAA	ACGGAACGGC	350
DIR477001 1	3.0.000.03.0m.a	3.00033.003.0	3 03 3 03 0E 00	~~~~~~	0000330mmm	200
PUMY021-1			ACAACACTCG			399
PUMY021-2			ACAACACTCG			399
PUMY021-3		AGCGAAGTAC				400
PUMY021-4		AGCGAAGTAC				400
PUMY021-5	AGCGGGACTG	AGCGAAGTAC	ACAACACTCG nrDNA	CGCTTGGCCC	GCCGAACTTT	400
PUMY021-1	$ \frac{1}{4} $	CTAAGCTCGA		GGTAGGAATA	CCCCCTGAAC	449
		CTAAGCTCGA				449
PUMY021-2						
PUMY021-3		CTAAGCTCGA				450
PUMY021-4		CTAAGCTCGA				449
PUMY021-5	TTTTTTTAAT	CTAAGCTCGA	CCTCAAATCA	GGTAGGAATA	CCCGCTGAAC	450
PUMY021-1	TTAA					453
PUMY021-2	TTAA					452
PUMY021-3	TTAA					454
PUMY021-4	TTAA					453
PUMY021-5	TTAA					454

Figure S2. Cont.

	18S nrDNA	ITS1				
PUMY040-1	AAGGATCATT	ACTGATTTGC	TTAATTGCAC	CACATGTGTT	TTTTATTGAA	50
PUMY040-2	AAGGATCATT	ACTGATTTGC	TTAATTGCAC	CACATGTGTT	TTTTATTGAA	50
PUMY040-3	AAGGATCATT	ACTGATTTGC	TTAATTGCAC	CACATGTGTT	TTTTATTGAA	50
PUMY040-1	CAAATTTCTT	TGGTGGCGGG	AGCAATCCTA	CCGCCAGAGG	TTATAACTAA	100
PUMY040-2	CAAATTTCTT	TGGTGGCGGG	AGCAATCCTA	CCGCCAGAGG	TTATAACTAA	100
PUMY040-3	CAAATTTCTT	TGGTGGCGGG	AGCAATCCTA	CCGCCAGAGG	TTATAACTAA	100
PUMY040-1	ACCAAACTTT	TTATTTACAG	TCAAACTTGA	TTTATTATTA	CAATAGTCAA	150
PUMY040-2	ACCAAACTTT	TTATTTACAG	TCAAACTTGA	TTTATTATTA	CAATAGTCAA	150
PUMY040-3	ACCAAACTTT	TTATTTACAG	TCAAACTTGA	TTTATTATTA	CAATAGTCAA	150
	5.8S nrDNA					
PUMY040-1	AACTTTCAAC			CATCGATGAA		200
PUMY040-2		AACGGATCTC		CATCGATGAA		200
PUMY040-3	AACTTTCAAC	AACGGATCTC	TTGGTTCTCG	CATCGATGAA	GAACGCAGCG	200
PUMY040-1		CGTAATATGA				250
PUMY040-2		CGTAATATGA				250
PUMY040-3	AAATGCGATA	CGTAATATGA	ATTGCAGATA	TTCGTGAATC	ATCGAATCTT	250
PUMY040-1	TGAACGCACA			AAGGGCATGC		300
PUMY040-2	TGAACGCACA			AAGGGCATGC		300
PUMY040-3	TGAACGCACA		TGGTATTCCA	AAGGGCATGC	CTGTTTGAGC	300
D.D.C.C. 0. 0. 0.	~~~~~~~~~	ITS2	~~~~~~~~		m	050
PUMY040-1	GTCATTTCTC		CCGGGTTTGG			350
PUMY040-2	GTCATTTCTC		CCGGGTTTGG	TGTTGAGCAA		350
PUMY040-3	GTCATTTCTC	CCTCAAACCC	CCGGGTTTGG	TGTTGAGCAA	TACGCTAGGT	350
D. D. C.	mm ommm oz z z	•	maa			200
PUMY040-1	TTGTTTGAAA			TTTTAAGCGA		399
PUMY040-2	TTGTTTGAAA		TGGAAACTTA			399
PUMY040-3	TTGTTTGAAA	GAATTTAACG	TGGAAACTTA	TTTTAAGCGA		400
DIRECTO 4.0. 1	•	~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~~	m3.0m0.0003.0	~3 ~3 3 mmm3 m	25S nrDNA	440
PUMY040-1	TCCAAAAACG	CTTATTTTGC	TAGTGGCCAC		TTCATAACTT	449
PUMY040-2	TCC-AAAACG	CTTATTTTGC	TAGTGGCCAC		TTCATAACTT	448
PUMY040-3	TCCAAAAACG	CTTATTTTGC	TAGTGGCCAC	CACAATTTAT	TTCATAACTT	450
PUMY040-1	TCACCTCAAA	TCAGGTAGGA	CTACCCCCTC	ል እርጥጥል <u>አ</u>		486
PUMY040-1		TCAGGTAGGA				485
PUMY040-2		TCAGGTAGGA				487
10111040-2	TONCCIONAN	MUDUITOUN	CIACCOCIG	THO I I LL		407

Figure S2. Cont.

	18S nrDNA	ITS1		•		
PUMY065-1			AATAATTTTG			50
PUMY065-2	AAGGATCATT	AAAGAAATTT	AATAATTTTG	AAAATGGA-T	TTTTTTGTTT	49
PUMY065-1		ATGAGAGCTT		AGAAGACAAG		100
PUMY065-2		ATGAGAGCTT		AGAAGACAAG		99
PUMY065-1			AGTGCGCGGT			150
PUMY065-2			AGTGCGCGGT			149
PUMY065-1 PUMY065-2			GTGAGAGATT GTGAGAGATT		TGTTATAGGA	200 199
PUMY065-1 PUMY065-2			CAACACACTG CAACACACTG			250 249
PUM1005-2	CAATTAAAAC	CGITICAATA	CAACACACIG	IGGAGIIIIC	ATAICITIGC	249
PUMY065-1			GAGCAATCGG			300
PUMY065-2	AACTTTTTCT		GAGCAATCGG			299
PUMY065-1		ATTTATTCAT		TCAAAAACAA		350
PUMY065-2	AAACAATTTT	ATTTATTCAT	5.8S nrD	TCAAAAACAA VA	GAATTTTCGT	349
PUMY065-1	AACTGGAAAT	TTTAAAATAT	TAAAAACTTT	CAACAACGGA	TCTCTTGGTT	400
PUMY065-2	AACTGGAAAT	TTTAAAATAT	TAAAAACTTT	CAACAACGGA	TCTCTTGGTT	399
PUMY065-1			AGCGAAATGC			450
PUMY065-2	CTCGCATCGA	TGAAGAACGC	AGCGAAATGC	GATACGTAAT	GTGAATTGCA	449
PUMY065-1			TCTTTGAACG			500
PUMY065-2			TCTTTGAACG ITS	52		499
PUMY065-1			GAGCGTCATT			550 549
PUMY065-2			GAGCGTCATT			
PUMY065-1 PUMY065-2			TGGAGTTAAC TGGAGTTAAC			600 599
PUMY065-1	ATTGGATGTT		AGAGAGGTTT			650
PUMY065-2	ATTGGATGTT		AGAGAGGTTT			649
PUMY065-1	ATGCAAGTAC		GGTTTTACCA			700
PUMY065-2			GGTTTTACCA			699
PUMY065-1			TATCGATAAG			750
PUMY065-2	TACTGAGCGT	ATTGGAACGT 28S ni	TATCGATAAG rDNA	AAGAGAGCGT	CTAGGCGAAC	749
PUMY065-1			TCAAATCAGG			800
PUMY065-2	AATGTTCTTA	AAGTTTGACC	TCAAATCAGG	TAGGAGTACC	CGCTGAACTT	799
PUMY065-1	AA					802
PUMY065-2	AA					801

Figure S2. Multiple alignments of ITS sequences of the six yeast strains. The internal transcribed spacer regions ITS1 and ITS2 are highlighted in gray, and the intra-genomic polymorphic sites are indicated by solid black dots above the corresponding nucleotides.