



TGGE band number	nt	Closest sequence match (accession number)	Division/subdivision	Score (% sequence similarity)	E value
1	143	<i>Pantoea</i> sp. enrichment culture clone YFZ27 16S (GQ273907)	Gammaproteobacteria	259 (98)	4e-66
2	137	Uncultured bacterium (<i>Enterobacter</i> sp.) clone P4-12 (AY119386)	Gammaproteobacteria	239 (98)	4e-60
3	157	Uncultured <i>Enterobacter</i> sp. clone F4apr.28 (GQ418069)	Gammaproteobacteria	268 (97)	7e-69
4	169	Uncultured soil bacterium (<i>Clostridium</i> sp.) clone CRS5546T-1 (GU365991.1)	Firmicutes	294 (98)	1e-76
5	153	Uncultured <i>Megasphaera</i> sp. clone MANPL08H07 (GU480445.1)	Firmicutes	180 (88)	4e-42
6	117	Uncultured <i>Megasphaera</i> sp. clone MANPL08H07 (GU480445.1)	Firmicutes	206 (98)	7e-50