

P5_Ins_F0	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTRGACGAGAAGACCTATARA
P5_Ins_F1	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTRGACGAGAAGACCTATARA
P5_Ins_F2	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTRGACGAGAAGACCTATARA
P5_Ins_F3	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTGTRGACGAGAAGACCTATARA
P5_Ins_F4	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTAACTRGAACGAGAAGACCTATARA
P5_Ins_R0	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTACGCTGTTATCCCTAARGTA
P5_Ins_R1	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTACGCTGTTATCCCTAARGTA
P5_Ins_R2	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTACGCTGTTATCCCTAARGTA
P5_Ins_R3	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTGCTACGCTGTTATCCCTAARGTA
P5_Ins_R4	AATGATAACGGCGACCACCGAGATCTACACTCTTCCCTACACGACGCTCTCCGATCTCGTTACGCTGTTATCCCTAARGTA

flow cell bind P5

sequ primer 1 bind

Ins_F / Ins_R (Taberlet unpub.)

N = shift (Lundberg et al. 2013)

P7_Ins_R0	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTACGCTGTTATCCCTAARGTA
P7_Ins_R1	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTACGCTGTTATCCCTAARGTA
P7_Ins_R2	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTACGCTGTTATCCCTAARGTA
P7_Ins_R3	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTGCTACGCTGTTATCCCTAARGTA
P7_Ins_R4	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTCGTTACGCTGTTATCCCTAARGTA
P7_Ins_F0	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTRGACGAGAAGACCTATARA
P7_Ins_F1	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTRGACGAGAAGACCTATARA
P7_Ins_F2	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTTRGACGAGAAGACCTATARA
P7_Ins_F3	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTGTTRGACGAGAAGACCTATARA
P7_Ins_F4	CAAGCAGAACGGCATACGAGATCGGTCTCGGCATTCCCTGCTGAACCGCTCTCCGATCTAACTRGAACGAGAAGACCTATARA

flow cell bind P7

sequ primer 2 bind

Ins_F / Ins_R (Taberlet unpub.)

N = shift (Lundberg et al. 2013)

Figure S1. 16S Fusion primers developed in this study. They include flow cell and sequencing primer binding regions for current Illumina sequencers. The amplified fragment has a size of ~157 bp and can be sequenced directly after purification (one step PCR). Up to 10 samples can be uniquely tagged from forward and reverse direction and pooled in one NextSeq run. The bases used for shifting on Ins_F and Ins_R can be used to uniquely tag samples (inline barcodes). It is recommended that all 10 primer pairs are used in the following combination to maximize sequence diversity and reduce effects of tag switching by uniquely tagging samples from both sides:

P5_Ins_R0+P7_Ins_F4, P5_Ins_R1+P7_Ins_F3, P5_Ins_R2+P7_Ins_F2, P5_Ins_R3+P7_Ins_F1, P5_Ins_R4+P7_Ins_F0,
 P5_Ins_F0+P7_Ins_R4, P5_Ins_F1+P7_Ins_R3, P5_Ins_F2+P7_Ins_R2, P5_Ins_F3+P7_Ins_R1, P5_Ins_F4+P7_Ins_R0