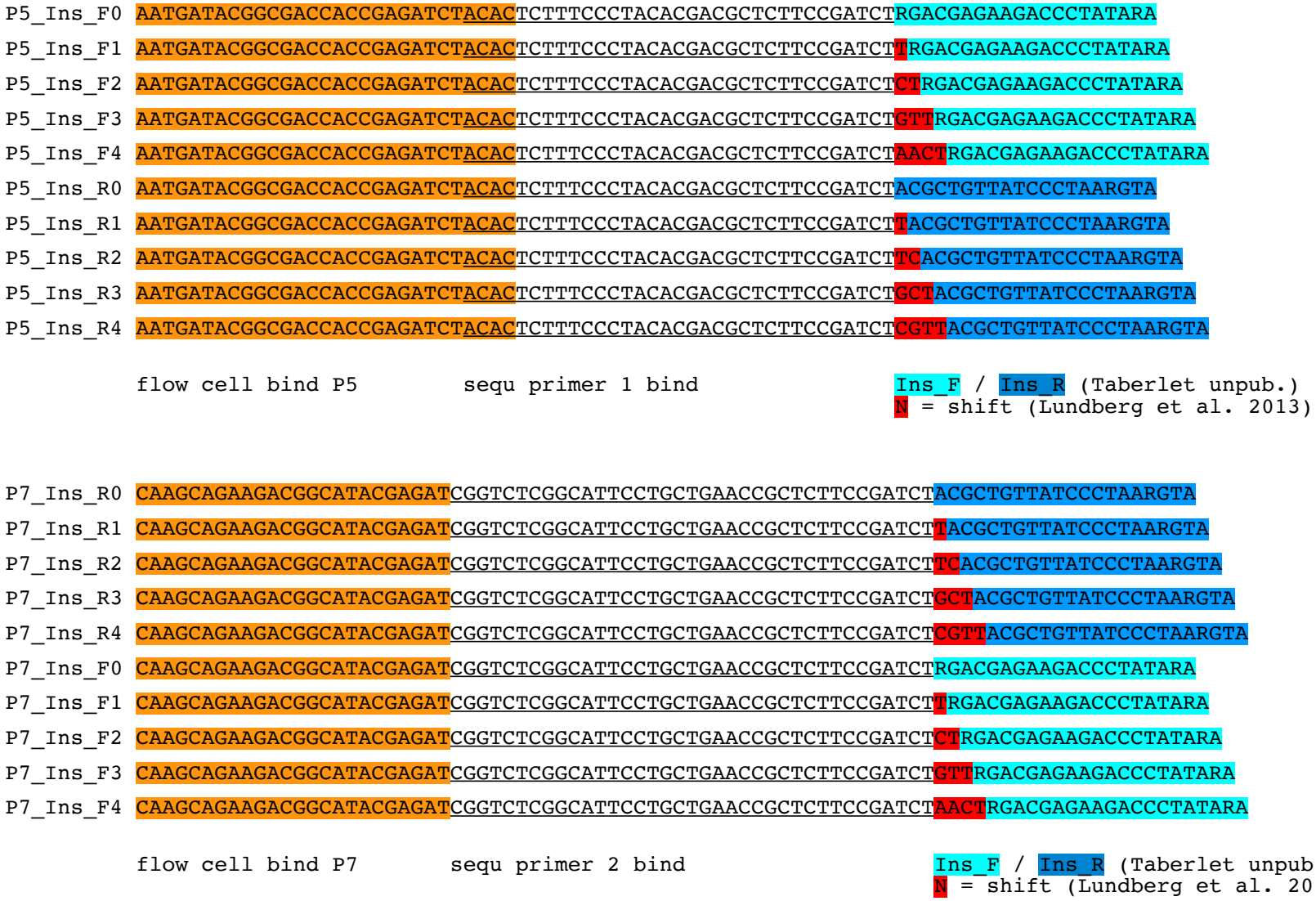

Figure S1. 16S Fusion primers developed in this study. They include flow cell and sequencing primer binding regions for current Illumina sequencers. The amplified fragment has a size fo ~157 bp and can be sequenced directly after purification (one step PCR). Up to 10 samples can be uniquely tagged from 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