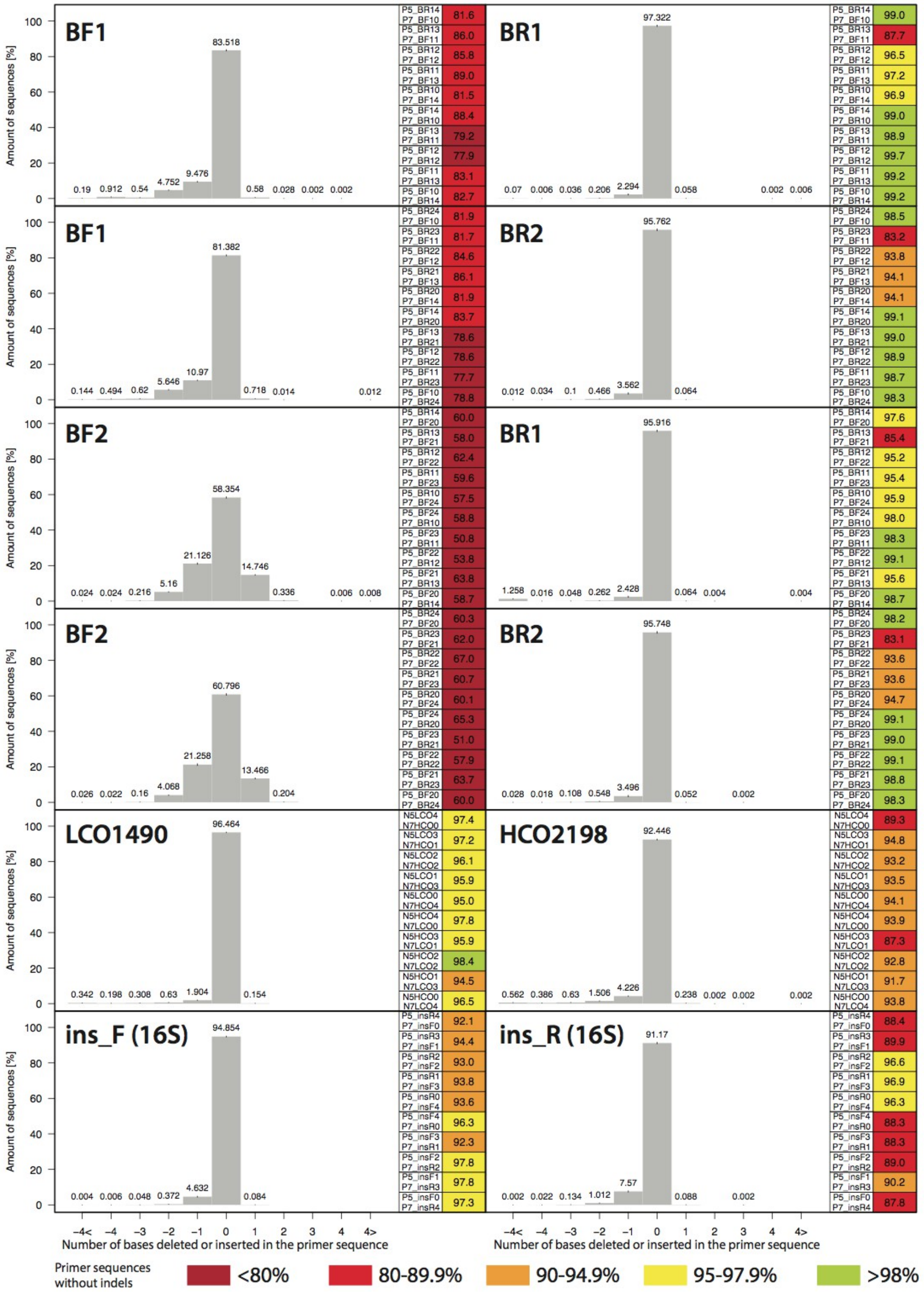

	BF1	BR1
P5_BR14 P7_BF10	81.6	99.0
P5_BR13 P7_BF11	86.0	87.7
P5_BR12 P7_BF12	85.8	96.5
P5_BR11 P7_BF13	89.0	97.2
P5_BR10 P7_BF14	81.5	96.9
P5_BF14 P7_BR10	88.4	99.0
P5_BF13 P7_BR11	79.2	98.9
P5_BF12 P7_BR12	77.9	99.7
P5_BF11 P7_BR13	83.1	99.2
P5_BF10 P7_BR14	82.7	99.2

	BF1	BR2
P5_BR24 P7_BF10	81.9	98.5
P5_BR23 P7_BF11	81.7	83.2
P5_BR22 P7_BF12	84.6	93.8
P5_BR21 P7_BF13	86.1	94.1
P5_BR20 P7_BF14	81.9	94.1
P5_BF14 P7_BR20	83.7	99.1
P5_BF13 P7_BR21	78.6	99.0
P5_BF12 P7_BR22	78.6	98.9
P5_BF11 P7_BR23	77.7	98.7
P5_BF10 P7_BR24	78.8	98.3

	BF2	BR1
P5_BR14 P7_BF20	60.0	97.6
P5_BR13 P7_BF21	58.0	85.4
P5_BR12 P7_BF22	62.4	95.2
P5_BR11 P7_BF23	59.6	95.4
P5_BR10 P7_BF24	57.5	95.9
P5_BF24 P7_BR10	58.8	98.0
P5_BF23 P7_BR11	50.8	98.3
P5_BF22 P7_BR12	53.8	99.1
P5_BF21 P7_BR13	63.8	95.6
P5_BF20 P7_BR14	58.7	98.7

	BF2	BR2
P5_BR24 P7_BF20	60.3	98.2
P5_BR23 P7_BF21	62.0	83.1
P5_BR22 P7_BF22	67.0	93.6
P5_BR21 P7_BF23	60.7	93.6
P5_BR20 P7_BF24	60.1	94.7
P5_BF24 P7_BR20	65.3	99.1
P5_BF23 P7_BR21	51.0	99.0
P5_BF22 P7_BR22	57.9	99.1
P5_BF21 P7_BR23	63.7	98.8
P5_BF20 P7_BR24	60.0	98.3

	LCO1490	HCO2198
N5LCO4 N7HCO0	97.4	89.3
N5LCO3 N7HCO1	97.2	94.8
N5LCO2 N7HCO2	96.1	93.2
N5LCO1 N7HCO3	95.9	93.5
N5LCO0 N7HCO4	95.0	94.1
N5HCO4 N7LCO0	97.8	93.9
N5HCO3 N7LCO1	95.9	87.3
N5HCO2 N7LCO2	98.4	92.8
N5HCO1 N7LCO3	94.5	91.7
N5HCO0 N7LCO4	96.5	93.8

	ins_F (16S)	ins_R (16S)
P5_insR4 P7_insF0	92.1	88.4
P5_insR3 P7_insF1	94.4	89.9
P5_insR2 P7_insF2	93.0	96.6
P5_insR1 P7_insF3	93.8	96.9
P5_insR0 P7_insF4	93.6	96.3
P5_insF4 P7_insR0	96.3	88.3
P5_insF3 P7_insR1	92.3	88.3
P5_insF2 P7_insR2	97.8	89.0
P5_insF1 P7_insR3	97.8	90.2
P5_insF0 P7_insR4	97.3	87.8

Figure S6: Overview of “missing” base pairs at the primer 3' end for sequencing datasets from this study as well as Elbrecht & Leese 2015 and Elbrecht et al. 2016. After library demultiplexing a random subset of 5.000 reads was extracted from each sample and sequences aligned in Geneious 8 using MAFFT. The primer sequence + 10 bp (5 bp for 16S) was extracted from each alignment and the mean deviation from the expected primer length plotted for each sample. The proportion of sequences with the expected length is given for each sample on the right of each plot. The error bars show the standard deviation (N=10).