

SEQUENCE LISTING

<110> F. Hoffmann-La Roche AG
Roche Diagnostics GmbH
Roche Molecular Systems, Inc.

<120> NON-REPLICATIVE TRANSDUCTION PARTICLES AND TRANSDUCTION
PARTICLE-BASED REPORTER SYSTEMS FOR DETECTION OF ACINETOBACTER
BAUMANNII

<130> P35222-WO-HS

<150> 62/785,510

<151> 2018-12-27

<150> 62/899,985

<151> 2019-09-13

<160> 6

<170> PatentIn version 3.5

<210> 1

<211> 1618

<212> DNA

<213> Bacteriophage Abi 33

<220>

<221> misc_feature

<222> (1)..(1618)

<223> terSL region deleted: terS (full), terL until 150 bp before 3'
stop codon

<400> 1

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acccctcaac aggtagctaa tgctgtcaag caagaattta acattgagat tgatcgaaaa 120

caggtacaac tttatgaccc gacaaaagcg gcaggaaaga atttaagtaa gaaatataaa 180

gacctttttc ataaaacccg agaggacttt aaaaagaatg tttatgacat cccttttagct 240

aataaagcct atcggtctaa agaacttcag aagatctatg aagactggaa gaacaacagg 300

cttatgaagc aaggggttat taaacagggt aggggaagaaa tgcagggtta tgacctcatg 360

cttttaaatac ttgagttaaa gcaacttgag attgaaaagt taagagaggg tgaaggtgat 420

gaagatccaa caccagtcaa ggtaactatt caagttgtag atgcgagtaa aaaagatgcc 480

gaacatcaat ccgacactga atgtacctca ggctaatttt ttgcagatgg aaaagaagtt	540
ccgcgcattt gtcgctggct ttggatcggg aaagacttgg gttggatgct ccagtttatg	600
caacaaagct tgggaattcc caaaagtacc tttgggttat tttgctcaa cttacccgca	660
gattcgcgac attttctttc caactattga agaggttgct ttcgattggg ggcttaaaac	720
taaggtttat gaaaccaata aagagggtga tatctattat ggtcggcaat atcgaactac	780
aatcatttgc cggctctatgg agaaaccagc aaccattgta ggttttaaaa ttggccacgc	840
cttgattgat gagcttgatg ttatggccaa ggtcaaagct caacaggctt ggcgtaagat	900
catcgctcgt atgcgttata agcaagctgg tttgctcaac ggtattgatg tggccacaac	960
accagaaggt ttttaagtta catacgagca atttgttaaa gaggcaaata aatcagaggc	1020
taagcgtaag ctctatggaa tgattcaagc ttcaacttat gacaatgaag ctaatcttcc	1080
agatgactac atatcatcac tttatgagtc ttatccgccg caattaattt cagcttattt	1140
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cagtgaatct gatcatgcaa tcttaaagaa aaatggattc aaagttgaag ttaatggtgt	1500
gaatcccggg attaaagatc gtatcactgc agttaatgca caaattctga atgctgaggg	1560
tgaacgacac ttaaaaagtga acacaaacaa gtgtcctaac tttacggcta ctttagaa	1618

<210> 2
 <211> 1842
 <212> DNA
 <213> Bacteriophage Abi 49

<220>
 <221> misc_feature
 <222> (1)..(1842)
 <223> terSL region deleted: 58 bp upstream of terS, terS (full), and

terL until 92 bp before 3' stop codon

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ggcgacacta aaagagcctg tgaaaatctt tatagttcag tctcttgctt gtcgtgatac	120
acctcaagaa gtggctgaac tcgtaaaaca agaatttggc gttgatatag atcgtgttca	180
agttgcaaca tatgacccta caaaagttgc tggtaagaac ttaagcaaaa agtatgtcga	240
actatttgaa aaaaccagag atgagtttga taaaggctta attgatattc ctattgctaa	300
taagtactac cgattgaagc aataccaaag acaacttgag aagactagaa acgttaaaac	360
agccttaaaa attcttgagc aagccgctaa agacattggg ggtcaattta ctaatcgcca	420
agaaaattaca ggcaaagacg gcggaccagt ccaaacagtt aattctgaaa ttcaagttcc	480
aatggaagat tacttaaaag cacggaggga agtccttagat gagtactgat gcggctcggg	540
ataaagccat ccggatcgag gcgcaagaag atttatatatt cttcacaagg tacatgttta	600
aggagcgccg tggttataaa tggatgcaaa attggcacca cttagaaatc tgcgaagctt	660
taatgaaagt ttatcgcgga gagataaagc ggtaattat taacgttcca ccacgatatt	720
ctaaaactga aattgctgta attaatttca tggcttggtg ttttggttaag aatccagact	780
gtgagtttat tcatatcagt tactcggcaa tgcttgccgc aaataatgcc ttccagattc	840
gaacactcgt acaagaggag gcgtataaaa aggtctttcc tgatcttaca ttgctgtatg	900
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caggcggtag gattactggg tttggcgcag gtaaacttcg tgatggggtt ggtggatgca	1020
tcattatcga tgaccacac aaagcgcag aagcttcttc taaaacaatt cgagaagggg	1080
taattgattg gttccaaaac acccttgagt cgctactaa ctcaccagat acgccgatca	1140
ttgtgattat gcagcgactt catgaagatg atttggctgg ttggttggtta ggcatagaa	1200
aagatggcgt tcctgtagct ggtggtaacg gtgaggtagt ggaacatctt tgtctttctg	1260
ctattcagga agacggatcc gcactatggc cagcaaaaaca caatatccaa aagttaaggc	1320
aaatggagca agctgcgccg tatgtatttg cagggaata ccgacaaatg ccatcaccgc	1380
cagcaggcgg tttttttaag cctgacaata ttcaaattgt tgatgctttg cctgcggatg	1440

ttttgaaaca agtgagggct tgggacttcg gagcgaccga aaacgaaggc gactttactg	1500
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gacagcttgg tccagacaat gtgaataagc gcttagaaca aaccgcaaaa atagatggga	1620
aaaaagtttc tgtgctcta ccacaagatc ccggtcaagc tggtaaatacg caagctagtt	1680
catttgtaag gcttcttgcg gggtatagcg tgatagctaa gccaatttca ggtgacaagc	1740
ttacacgtgc acaaccatctt gcggcccaag ttaacgtagg aaatgtacga atgctcaaag	1800
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<210> 3
 <211> 2679
 <212> DNA
 <213> Bacteriophage Abi 147

<220>
 <221> misc_feature
 <222> (1)..(2679)
 <223> terSL region deleted:

128 bp upstream of terS, terS (full), terL (full)

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aaaattccct ctcaaaaaa gttaaagcaa aaagttaaaa tcaagttaaa ggtagagcaa	120
tggcattaac agagaaaatg gaaaaatttg ctcttgccat tgttgacggc aagacaaata	180
aagaagcagc aatttcagca gggtatgcgg aaaaaactgc atccgccgca ggtgctaggt	240
tagcaaaaaga tcctgaaatt attgtctata ttgaaatggt aaaggcccaa aaagaagggc	300
gctctttaac atctaattca ccaaaagtta aacctaaaga tacacccgaa aatagtgggtg	360
aagatgaaaa ccctattgag gaatttcaat ttgaagggtga tgatccttta gattttttaa	420
ttaaggtcat gaacttcaat ggcaacaagc tgccacttag aatgcaagca gcaattgcag	480
cattgcctta taaacacggg aagggtgcgg aaaaaggcaa aaaagaaact aaacaagaca	540
aggcaaagga agcgaccaga acaggaaaat acgccacatt ggacaatcag ttgccaagct	600

aactattaag aggaactttg catgcaaagt ctagaatacg aaaccgtaag tggtgaaact	660
atcactattc aaaatatcaa agatggccct tgctgtcatg actctattga aaagttgcca	720
gcaacagaaa ggttggtgaa gattacttat caatgtcgca agtgcttttc cagattttcc	780
gaagaagatt atcaattgat tgttaatcaa taaaagggtt tgtatggatc cgtaggcgat	840
acggtgcgtt ggaggaagga ggaccacaac tgccaacgta ataaccgct agcagtgggc	900
gaaacagcgt agttaagca ggggttcgca acctgtcata caaatattt cgccttcgg	960
gcggtttttt catggaccat tttaatgact gcaaaactac cagactggac tacagcttgc	1020
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cccaaagtgg ctgacgtagc ggagcgtatc tttaaagagt taattcttgt tgatgtgatg	1140
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tttggcgcac atgatccaag cacaaagcgc agattaattc gtgaattcct tcttttgatt	1260
tcgaagaaga atactaaatc tacgattgcc gccggcatta tgcttactgc attaattcct	1320
aatgatcgac aatctgccga actaattatt cttgcgccta ctaaagaagt tgctgataac	1380
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gtatctgagc acacaaaaac agttacgcat ctaggtaccg gagcaacact taaagttatt	1500
gcagcagaat ctaacgctgc agctggtaag aaagcttcaa tcattttgat agatgaggtc	1560
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aagaaggttt atgacagtgg aaagcttaat aagatcggac tagatccatt gggcttaggc	2340
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attgccacat ttaacgcagt tgctttgatg tcaagcaatc ctgagcctgc caatcgcgtt	2640
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<210> 4
 <211> 9247
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> plasmid pZX058 with Abi 33 terSL region

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acccctattt gtttattttt ctaaatacat tcaaatatgt atccgctcat gagacaataa	180
ccctgataaa tgcttcaata atattgaaaa aggaagagtc gatcgaatga gtttggaat	240
atttgttttt cgtatcaacc accagggtgaa actcataagc aagtaatgga tcgctttggt	300
cggcttggtg tcgcctcaga agaggtaggg tttgatacat attggacctt agaacatcat	360
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cagttagaag acgtttttatt attagatcaa atgtcgaaa gtcgttttaa ttttgaacc	540
gttcgagggc tataccataa agattttcga gtatttggtg ttgatatgga agagtctcga	600

gcaattactc	aaaattttcta	ccagatgata	atggaaagct	tacagacagg	aaccattagc	660
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