

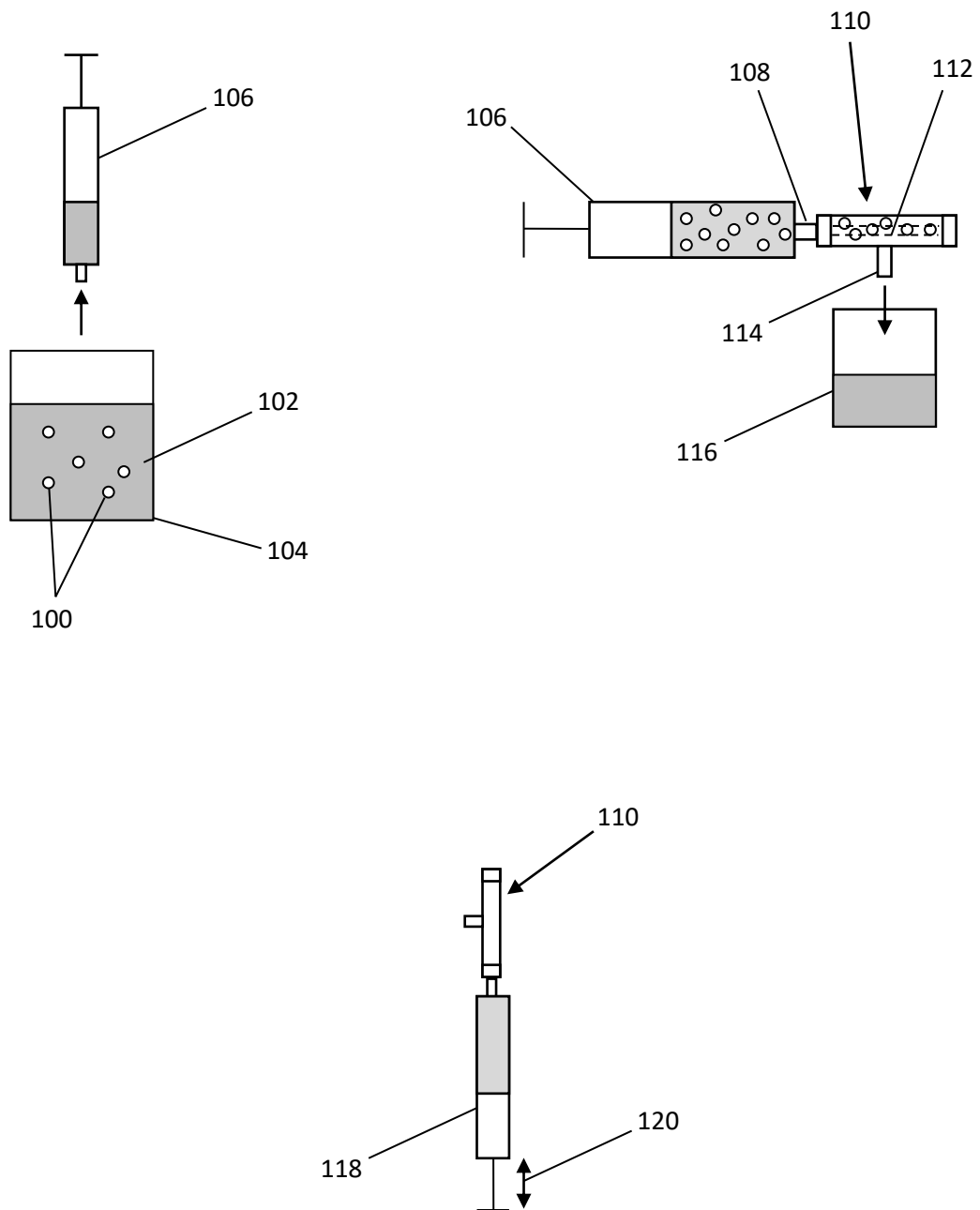


FIG. 1

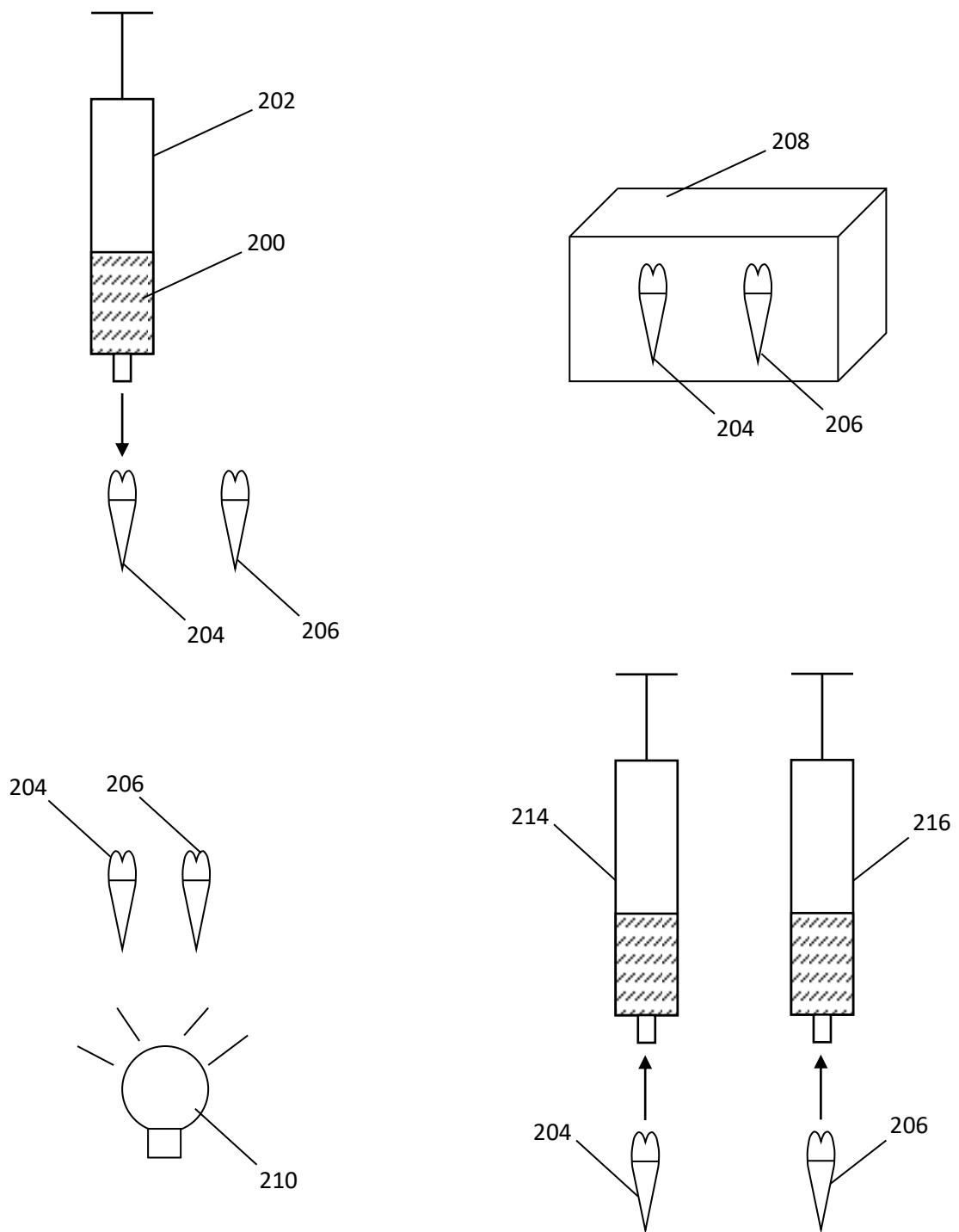


FIG. 2

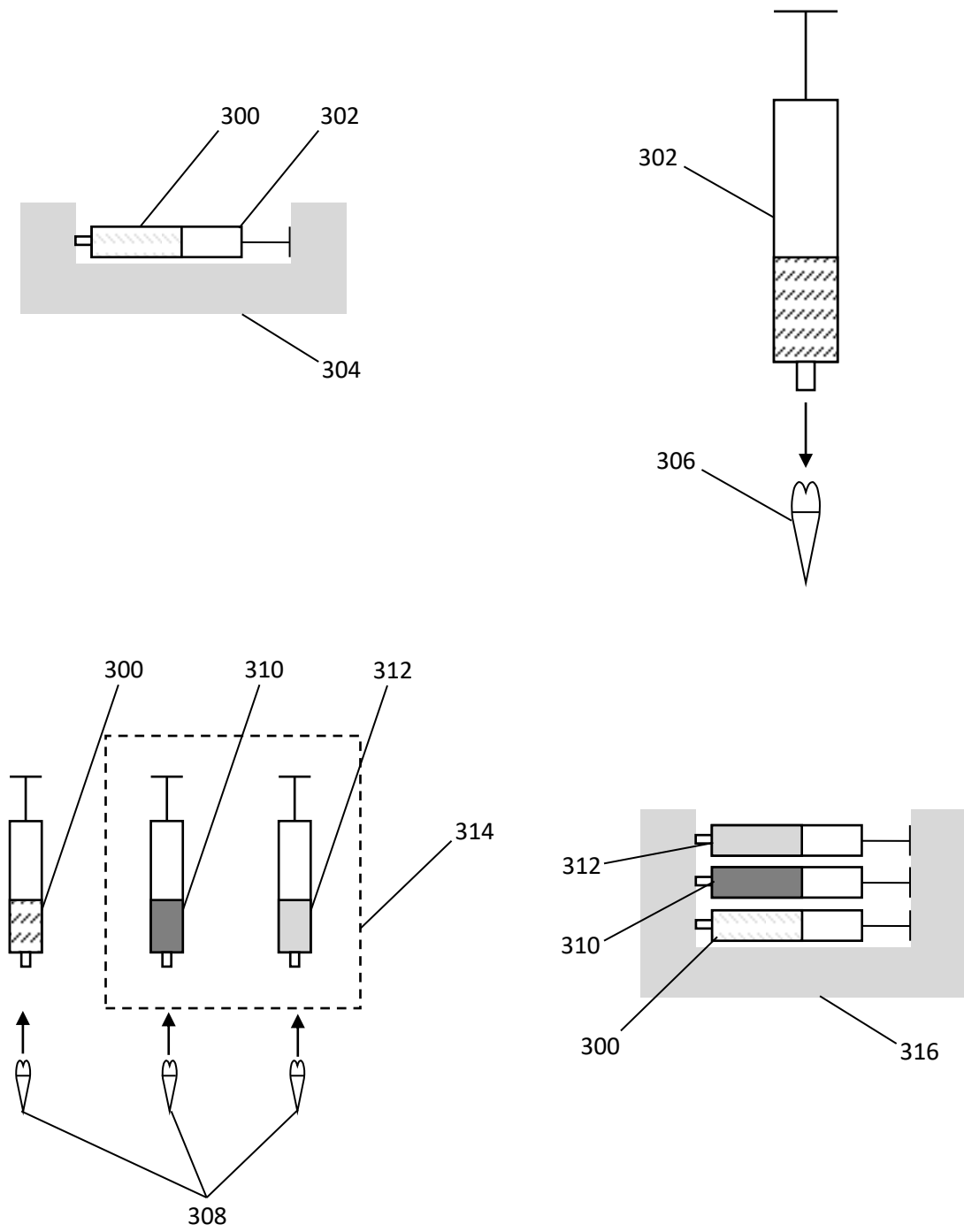


FIG. 3

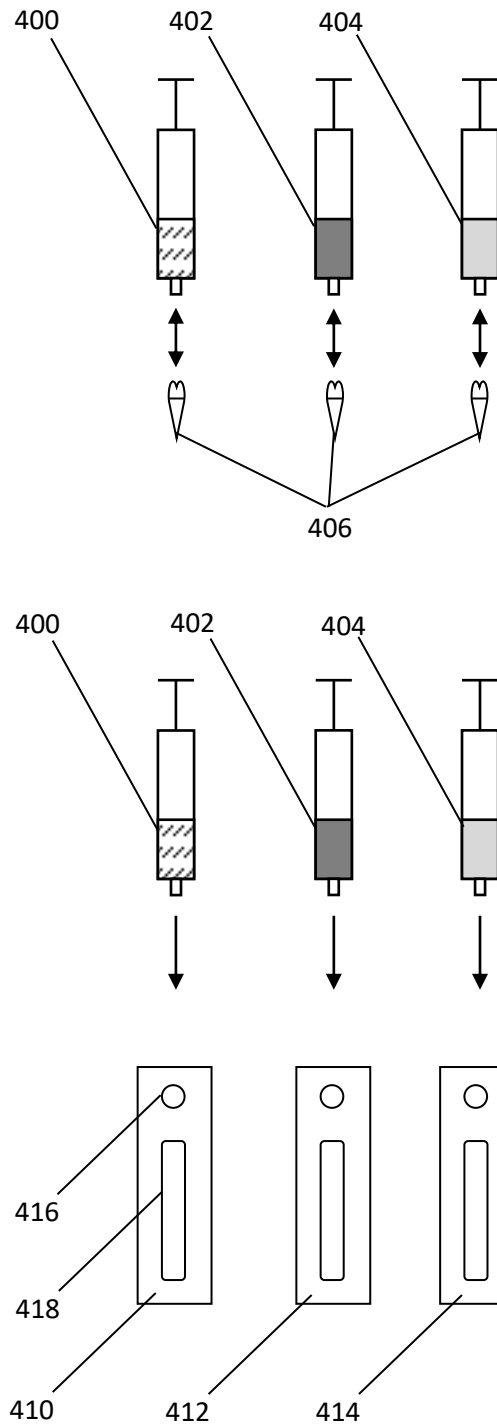


FIG. 4A

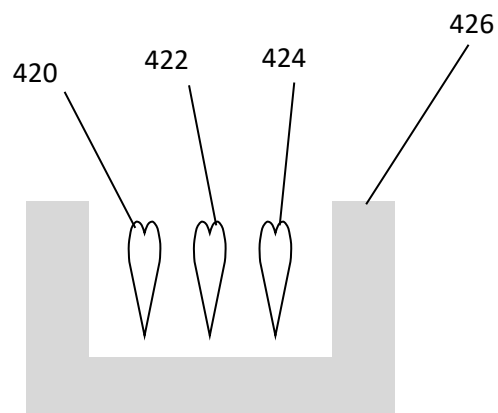


FIG. 4B

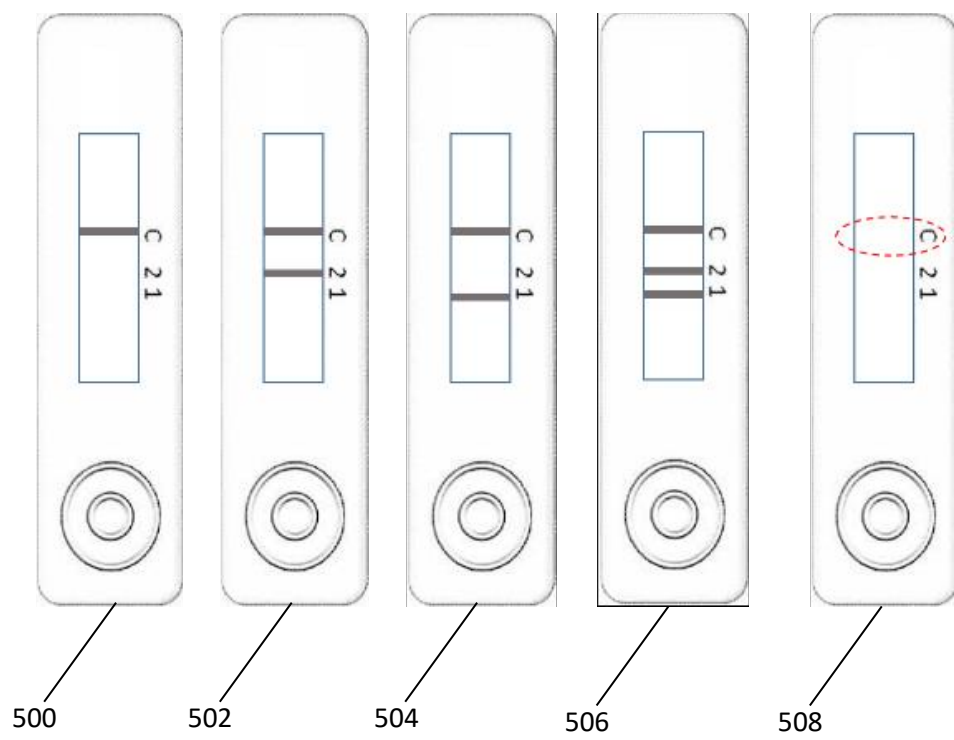


FIG. 5

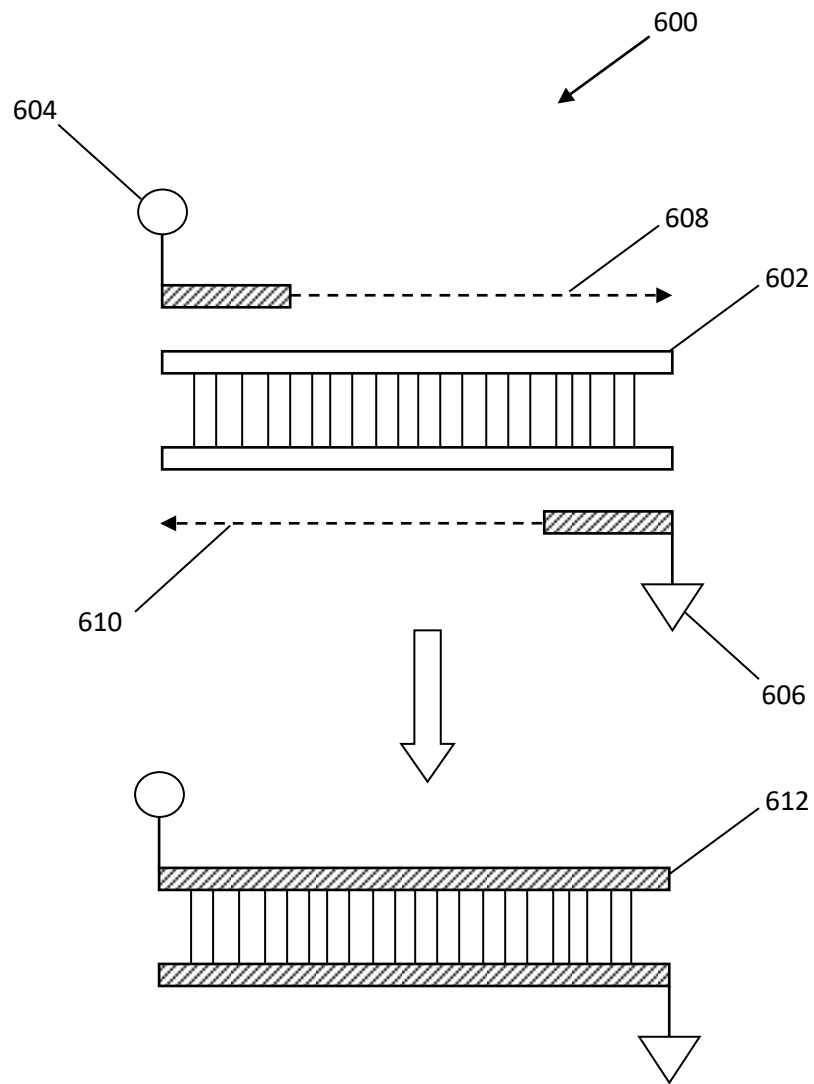


FIG. 6

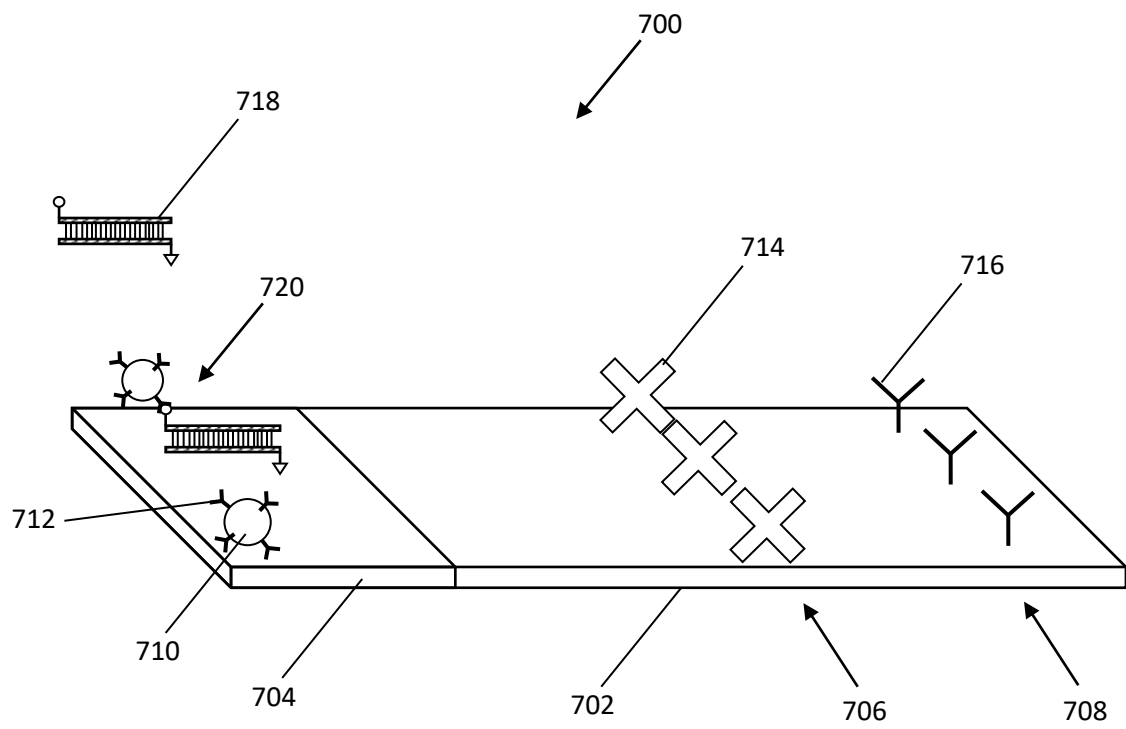


FIG. 7

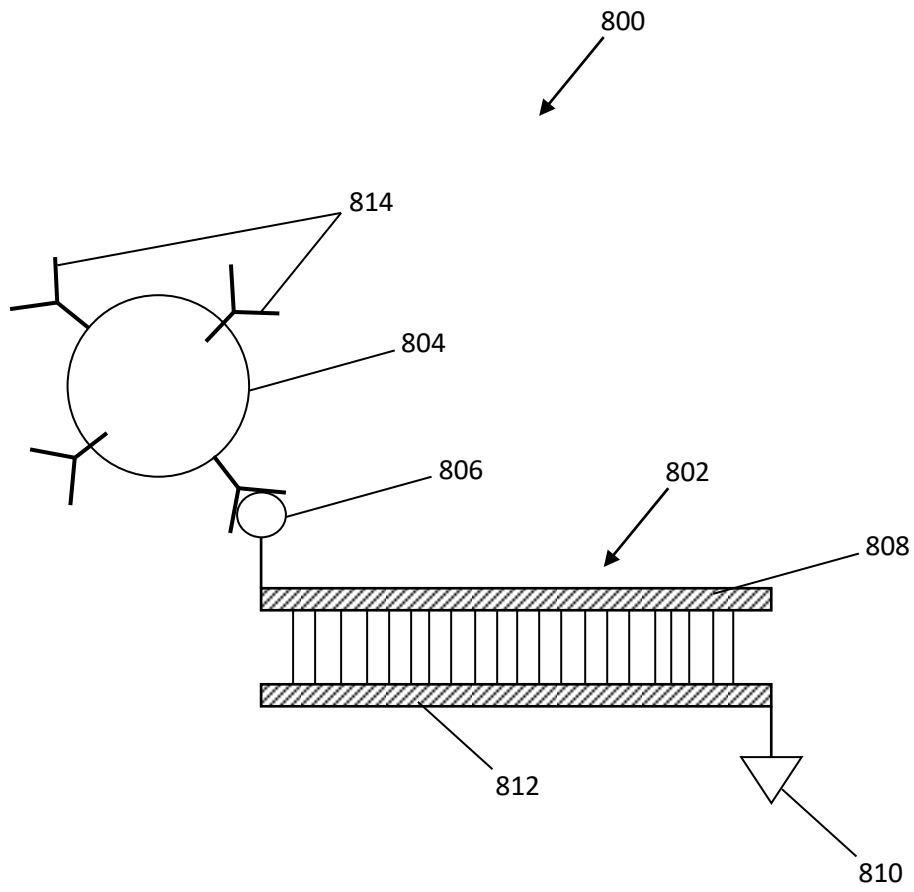


FIG. 8

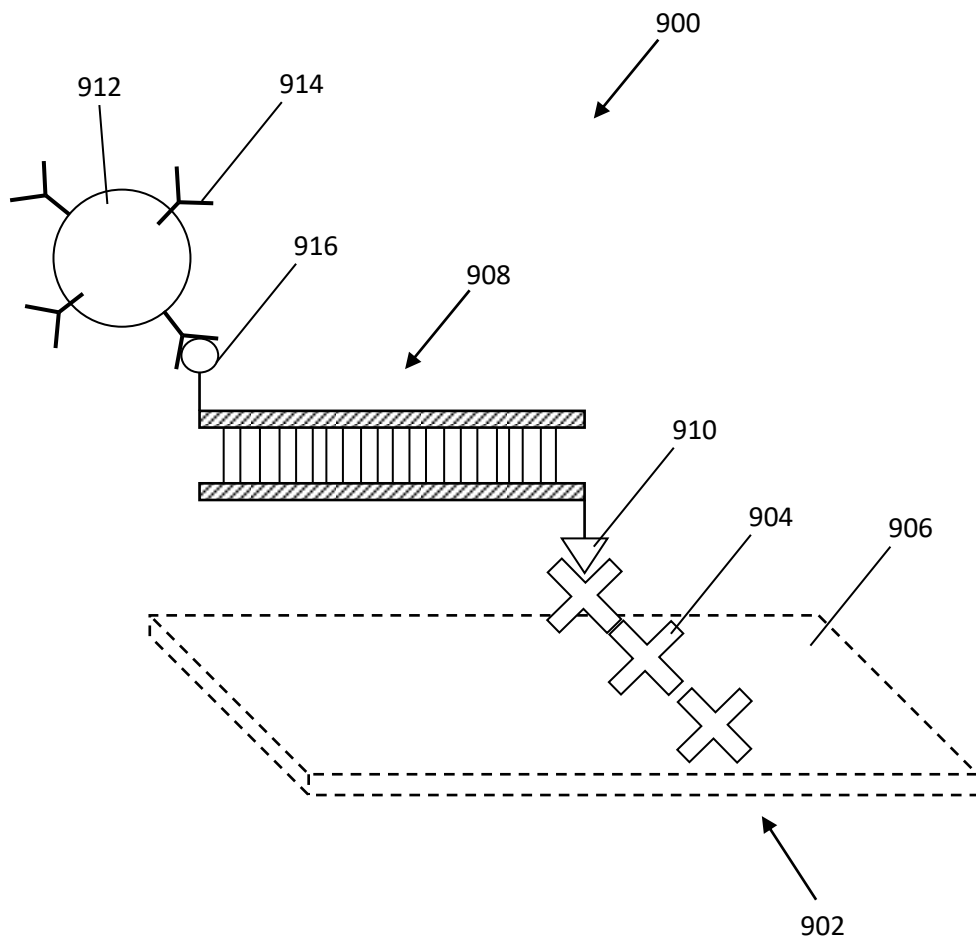


FIG. 9

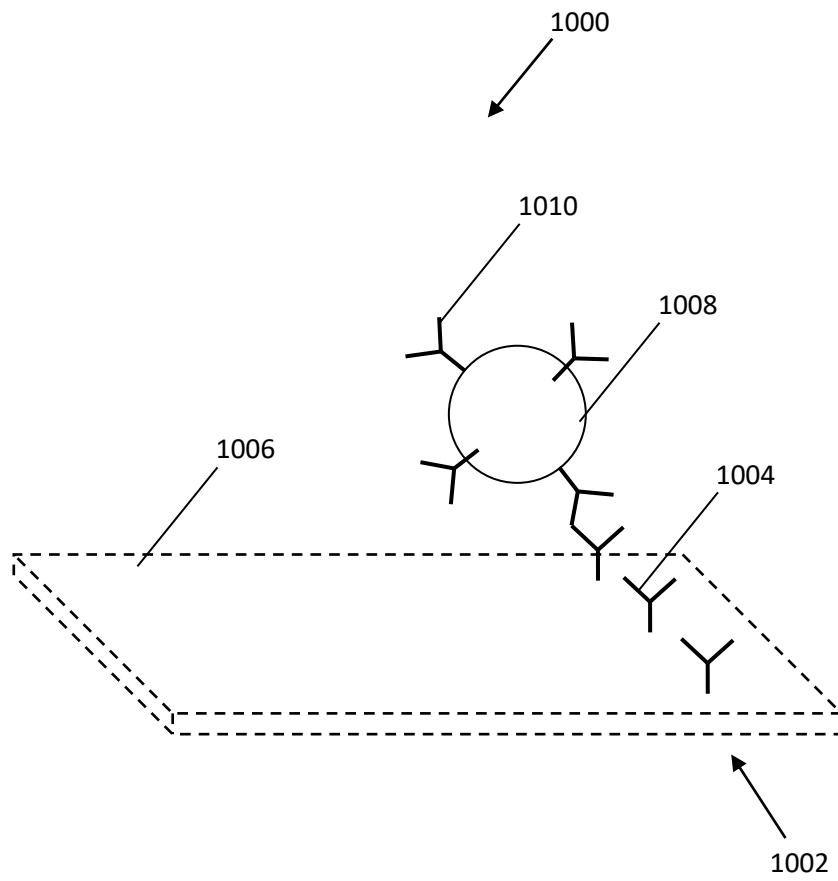


FIG. 10

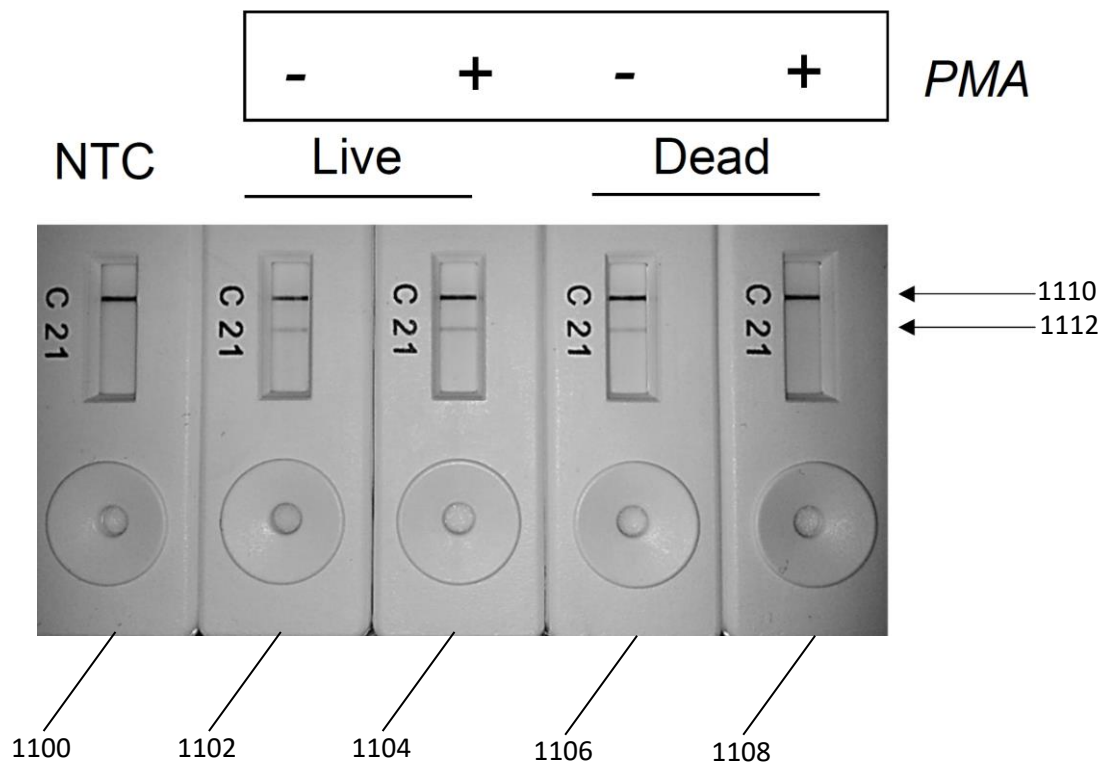


FIG. 11

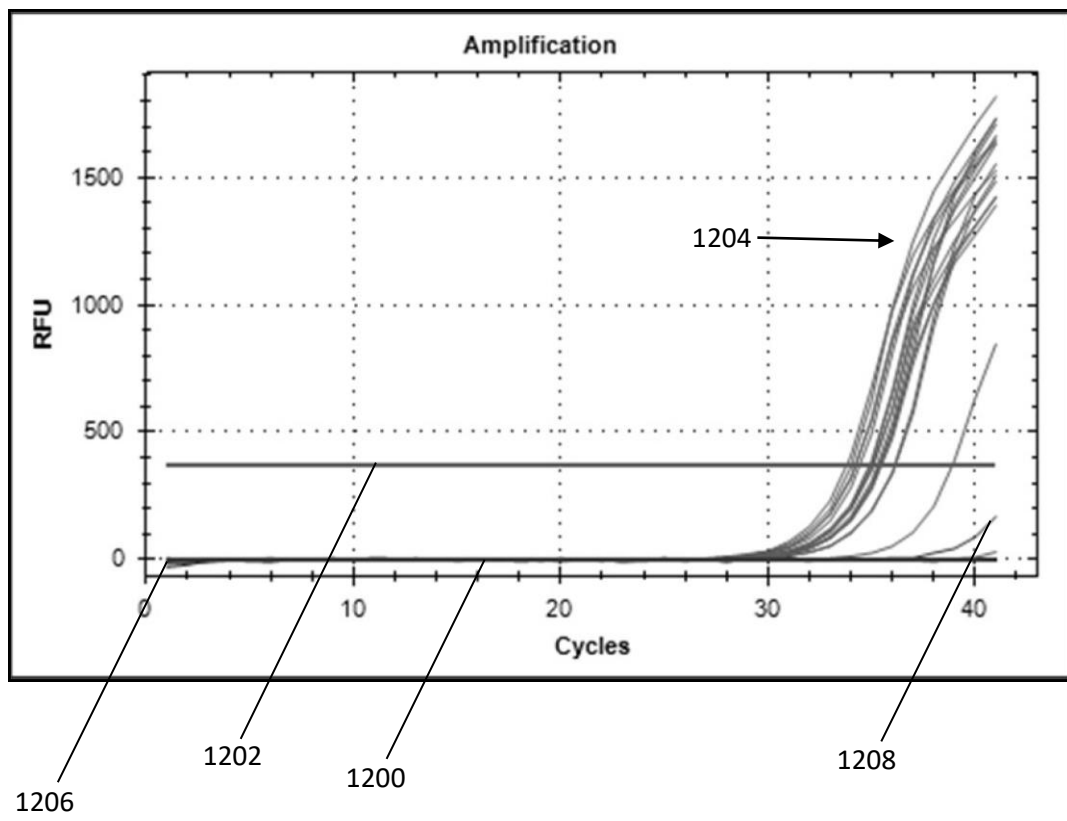


FIG. 12

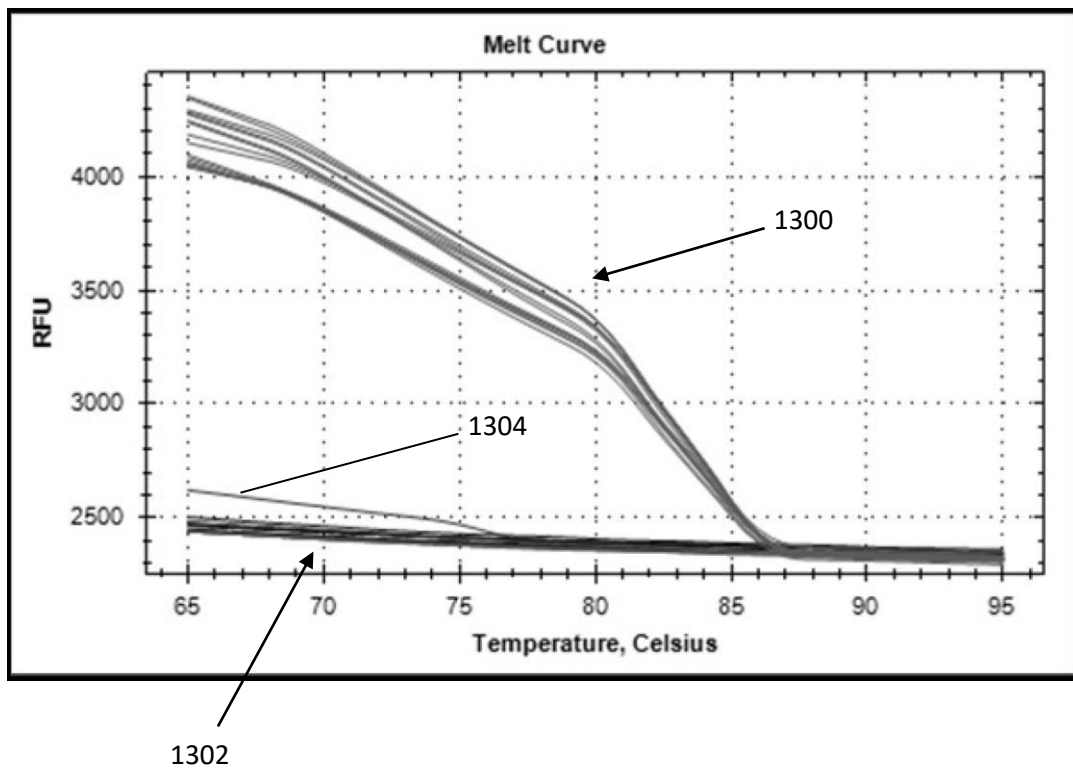


FIG. 13

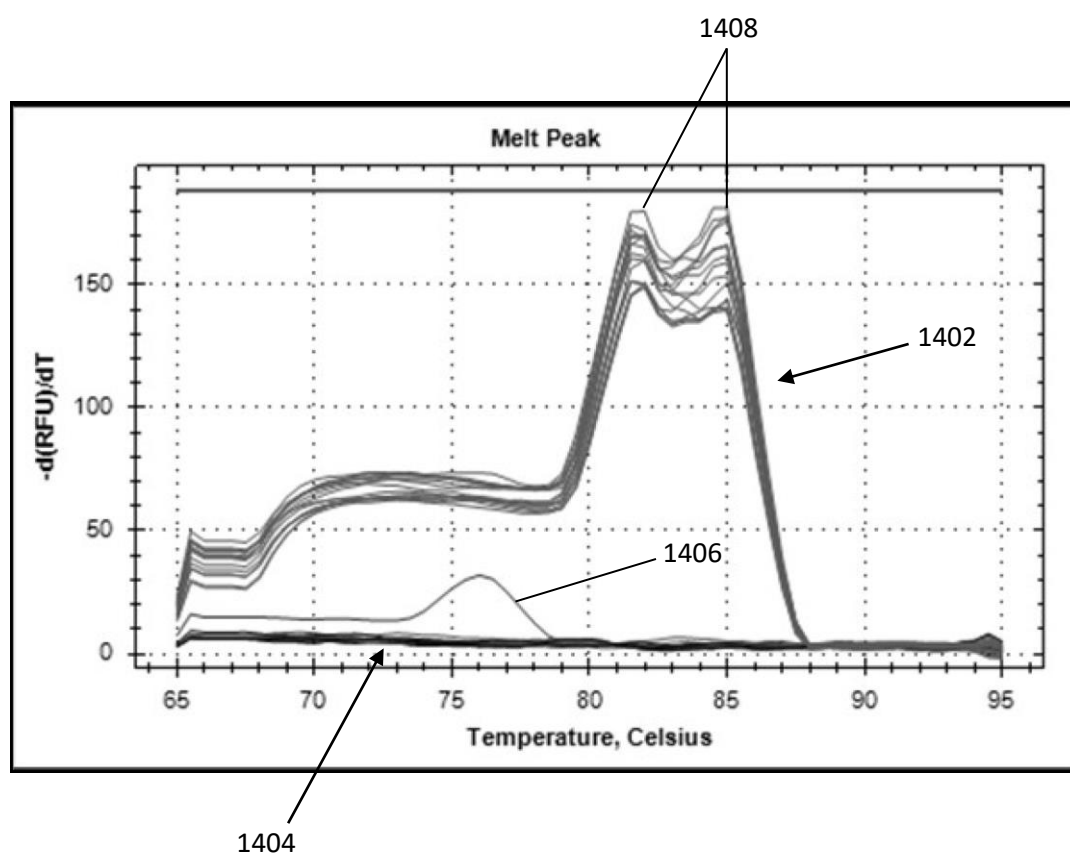


FIG. 14

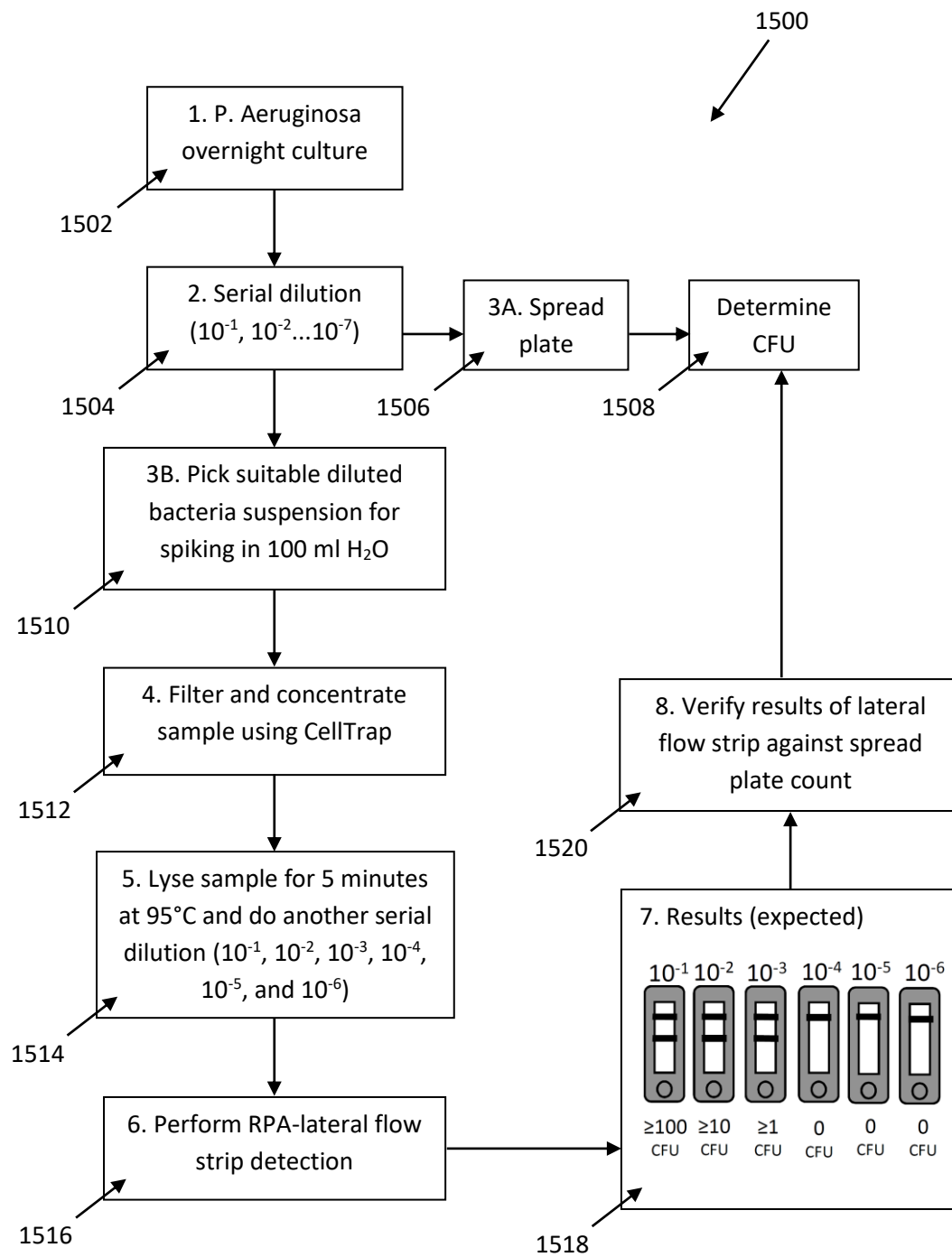


FIG. 15

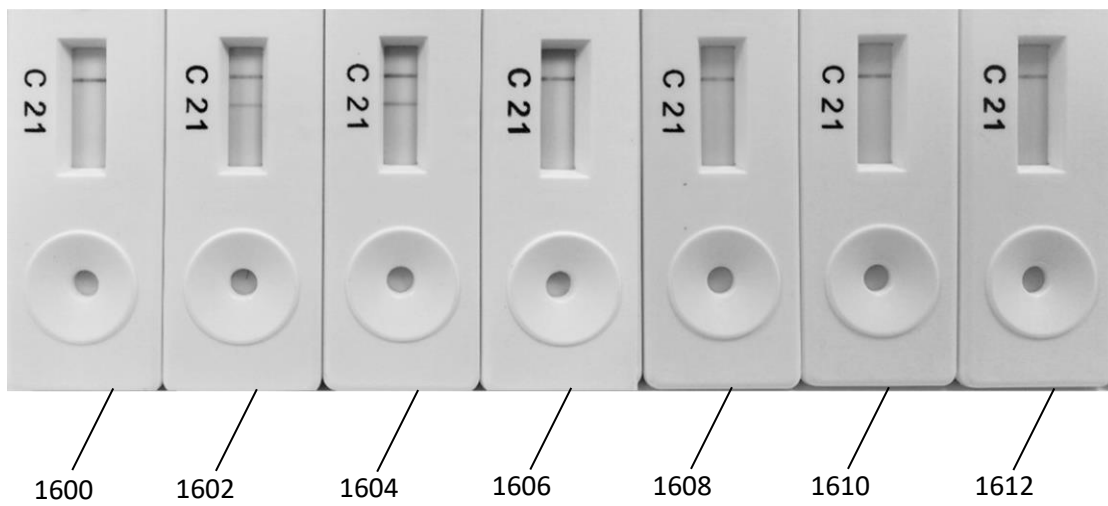


FIG. 16

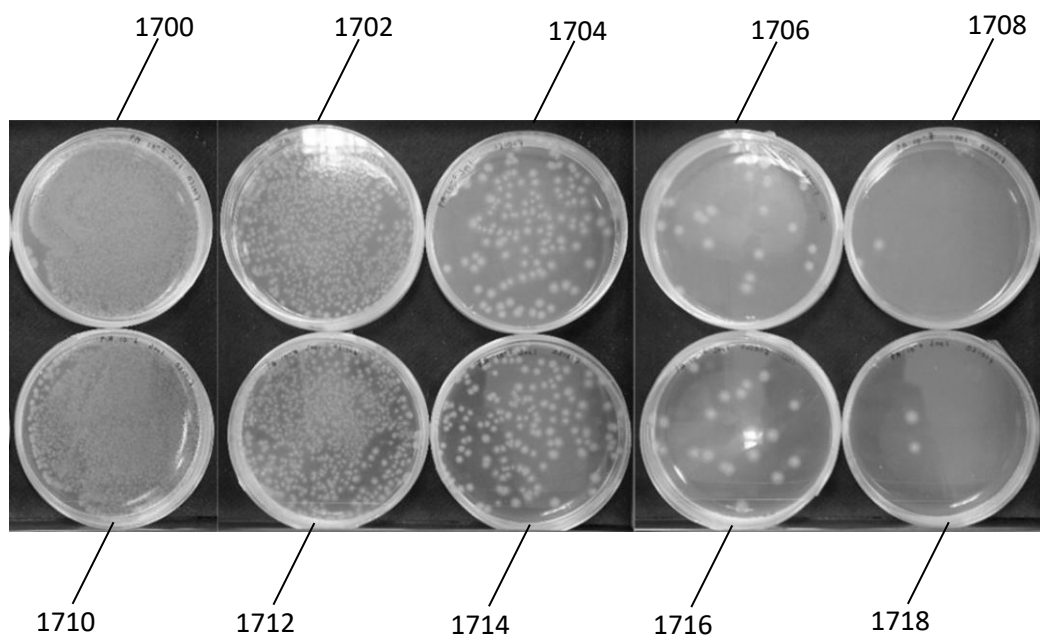


FIG. 17

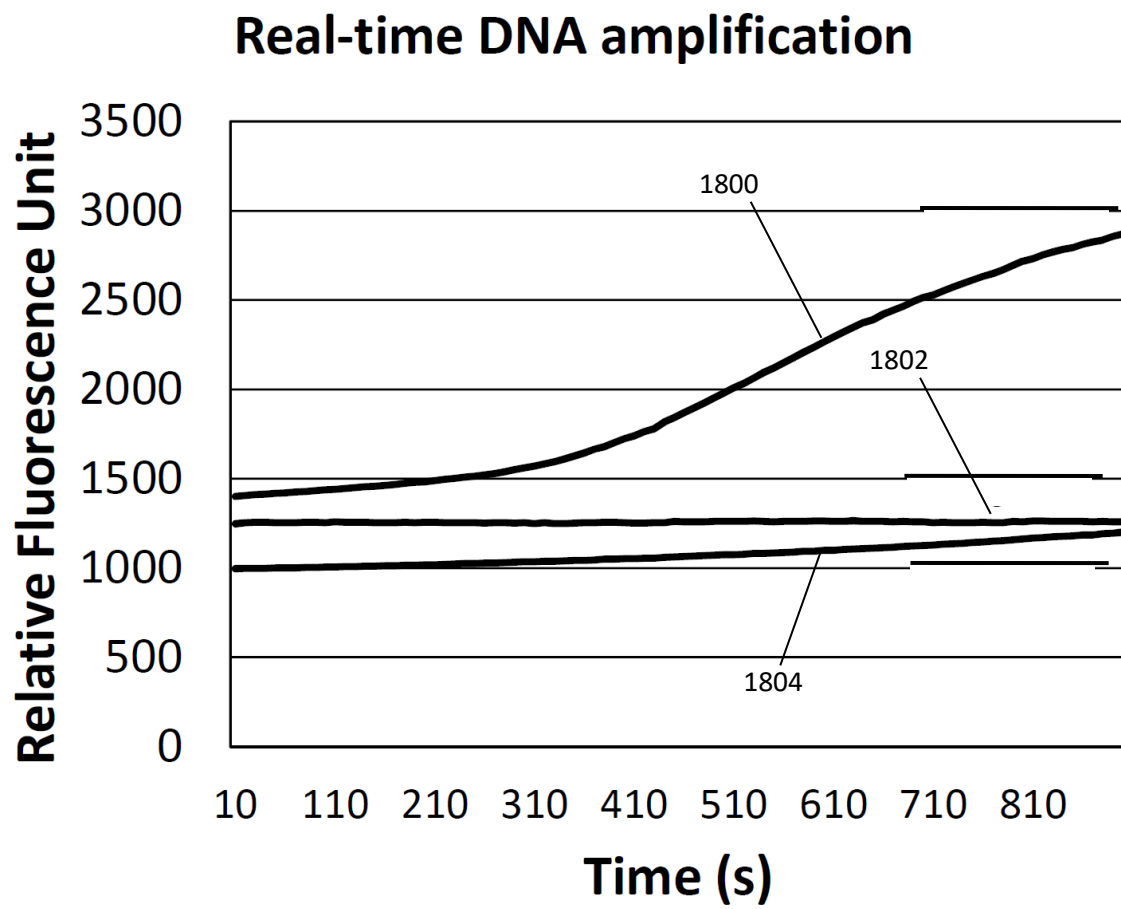


FIG. 18

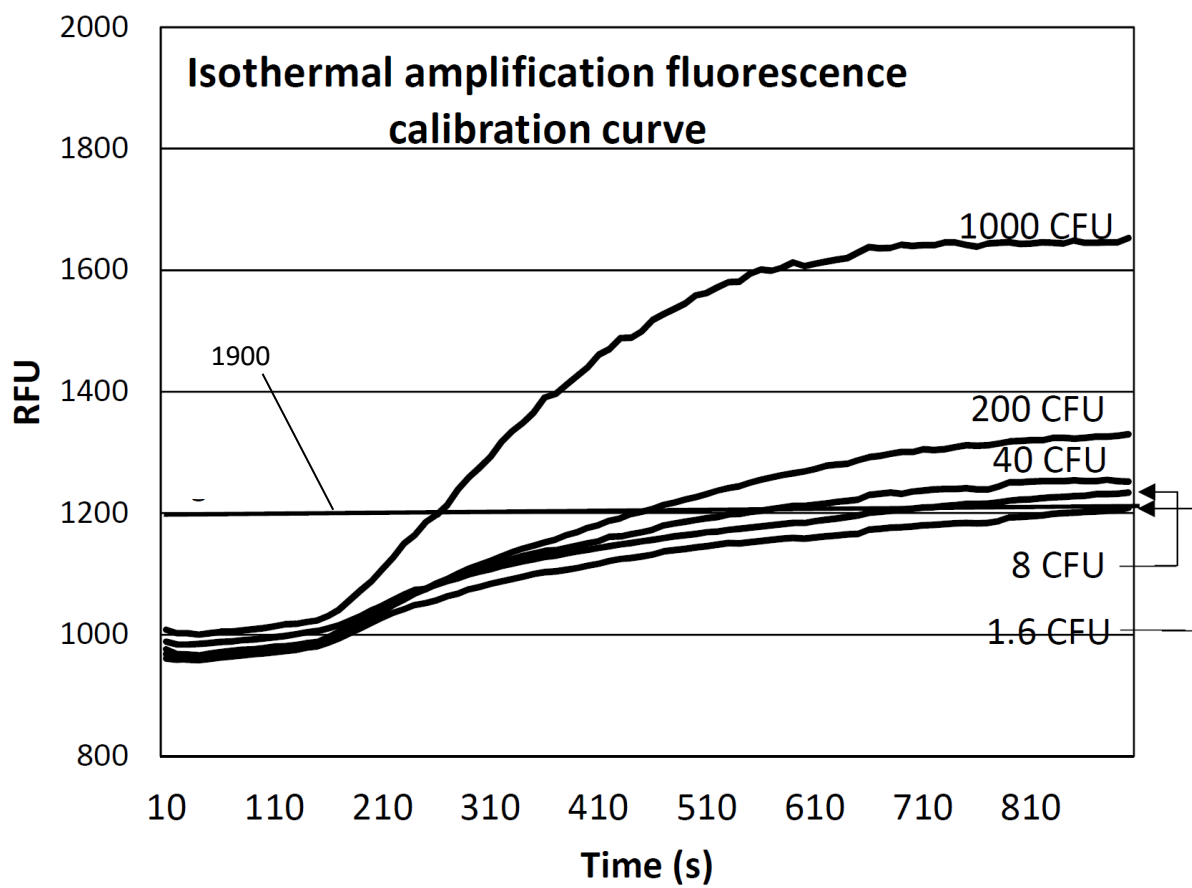


FIG. 19

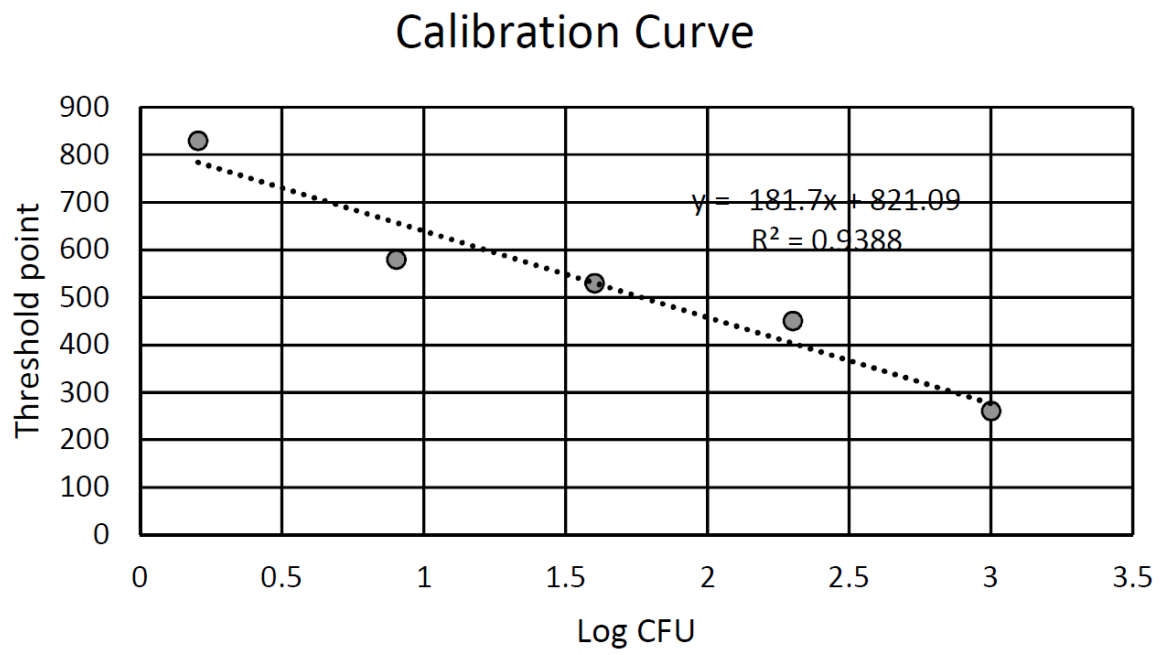


FIG. 20

Primer2	SEQ ID no. 1: 5'-TTCCCTCGCAGAGAAAAACATCCTATCACCGCG-3'	
algD_P_aeruginosa	-----0	¹ /iFluoT/
Primer1	GCGGGACAAACGGCCGGAACCTCCCTCGCAGAGAAAAACATCCTATCACCGCGATGCCTAT 180	² A to /idSp/
	-----21	³ dT-BHQ
	-----21	⁴ G to /idSp/
Primer2	-----0	
algD_P_aeruginosa	CGATAGTTATGGGCAGAGCAACTTGA AACCGTCTCGAATAATCGGATTCGGTCCGAGGG 240	
Primer1	-----21	
Primer2	-----0	
algD_P_aeruginosa	ACAAACTCAACCTGTTGAAATTAAAGGCCTTTAGAACTTGAATTCATGGACCGAACTA 300	
Primer1	-----21	
Primer2	-----0	
algD_P_aeruginosa	AAACTAAGCATCCAAGTCGGGTTATGCACCGTTATTGAAACCCACCTGAAACATTAAG 360	
Primer1	-----21	
Primer2	-----0	
algD_P_aeruginosa	GGCATGAACTTATACTGCCCATTTAGAGTCCGCAACAACTAAGCACTCTATTTCGAAAC 420	
Primer1	-----21	
Primer2	-----0	
algD_P_aeruginosa	TGCCTGAAGCGGATCAAGGGCTCTGGATCGGGGCTCGTAGTAACGGCTCGCCAGATAGG 480	
Primer1	-----21	
Primer2	SEQ ID no. 5: 5'-CGGCCACCTCATTAACGGCGCGACAAACAATCGAGGT¹GA²AT³CGATGCCGAATCAG⁴-3Phos/-3'	
algD_P_aeruginosa	SEQ ID no. 4: 5'/56FAM/-CGGCCACCTCATTAACGGCGCGACAAACAATCG⁴AGTGAATCGATGC³-3Phos/-3'	
Primer2	-----0	
algD_P_aeruginosa	GAA GTGGCCATACGGCCACCTCATTAACGGCGCGACAAACAATCGAGGTGAATGGGATGC 540	
Primer1	-----21	
Primer2	-----0	
algD_P_aeruginosa	GAA TCAGCATCTTTGGTTGGGCTATGTCGGTGCAGTATGTCTGGCTGCCCTGTCGGCAC 600	
Primer1	-----21	
Primer2	SEQ ID no. 3: 3'-TCTAGCTGGACTAGTTGGTCCCGTTCCGTTCCAGCGGG-5'	
algD_P_aeruginosa	SEQ ID no. 2: 3'-TCTAGCTGGACTAGTTGGTCCCGTTCCGTTCCAGCGGG/5Biosg/-5'	
Primer2	-----21	
algD_P_aeruginosa	-----agatcgacctgatcaaccagg 21	
Primer1	GCGGTCATGAAGTCATTGGTGTGGATGTCTCCAGCACCAGATCGACCTGATCAACCCAGG 660	
	-----21	

FIG. 21

Legion-R	SEQ ID no. 6: 5'-AGGGTTGATAGGTTAAGAGCTGATTAACCTGGA-3'		¹ /IfluorT/
Legion-F	-----	0	² G to /idSp/
Legionella	-----AGGGTTGATAGGTTAAGAGC-----	20	³ dT-BHQ
	NAGGGTTGTAAGCACTTTCAGTGGGAGGAGGGTTGATAGGTTAAGAGCTGATTAACCTG	480	⁴ G to /idSp/
Legion-R	-----	0	
Legion-F	-----	20	
Legionella	GACGTTACCCACAGAAGACCCGGCTAACTCCGTGCCAGCAGCCNCGGTAATACGGAG	540	
Legion-R	-----	0	
Legion-F	-----	20	
Legionella	NGTGCNAGCGTTAATCGGAATTACTGGCGGTAAAGGGTGCGTAGGTGGTTGATTAAGTTA	600	
Legion-R	-----	0	
Legion-F	-----	20	
Legionella	TCTGTGAAATTTCCTGGGCTTAACCTGGGACGGTCAGATAATACTGGTTGACTCGAGTATG	660	
Legion-R	5'-GGAGAGGGTACTGGAATTTCCGGTGTAGCGGTGAAAT ¹ GCG ² T ³ AGAGATCGGAAGGA-/3Phos/-3' (SEQ ID no. 10)		
Legion-F	5'--/5dign/-GGAGAGGGTACTGGAATTTCCGGTGTAGCGGTG ⁴ AAATGCGTAGAGATCG-/3Phos/-3' (SEQ ID no. 9)		
Legionella	-----	0	
	GGAGAGGGTAGTGGAATTTCCGGTGTAGCGGTGAAATGCGTAGAGATCGGAAGGAACACC	720	
Legion-R	-----	0	
Legion-F	-----	20	
Legionella	AGTGCGAAGCGGGCTACCTGGCCTAATACTGACACTGAGGCACGAAAGCGTGGGAGCA	780	
Legion-R	SEQ ID no. 8: 3'-ACATTTGCTACAGTTGATCGACAACCAATATA-5'		
Legion-F	SEQ ID no. 7: 3'-ACATTTGCTACAGTTGATCGACAACCAATATA/5Biosg/-5'		
Legionella	-----CGATGTCAACTAGCTGTTGG-----	20	
	AACAGGATTAGATACCCCTGGTAGTCCACGCTGTAAACGATGTCAACTAGCTGTTGTTAT	840	

FIG. 22

ent-r Ent-f Enterococcus	SEQ ID no.11: 5' - TGCATTAGCTAGTTGGTGAAGGTAACGGCTCACCA-3'	
	-----	0
	-----tgcattagct	10
ent-r Ent-f Enterococcus	AGTTGGTGAAGGCGCTTTCGGGTGTCGCTGATGGATGGACCCGCGGTGCATTAGCT	240
	-----	0
	agttggtg-----	18
ent-r Ent-f Enterococcus	AGTTGGTGAAGGCTACCAAGGCCACGATGCATAGCCGACCTGAGAGGGTGATCG	300
	-----	0
	-----	18
ent-r Ent-f Enterococcus	-----	0
	-----	18
	GCCACATTGGGACTGAGACACGGCCCCAACTCCTACGGGAGGCAGTAGGGAATCTTC	360
ent-r Ent-f Enterococcus	-----	0
	-----	18
	GGCAATGGACGAAAGTCTGACCGAGCAACGCCGCTGAGTGAAGAGTTTTCGGATCGT	420
SEQ ID no. 15: 5'-ACTCTGTTGTAGACAAGAAACAAGGATGAGAGT ¹ AA ² CT ³ GTTTCATCCTTGACG/3Phos/-3' 5'/56FAM/-AAAACCTCTGTTGTAGAGAAGAACAAGGATGAG ⁴ AGTAACTGTTTCATCC/3Phos/-3' (SEQ ID no. 14)		
ent-r	-----	0
Ent-f	-----	18
Enterococcus	AAAACCTCTGTTGTAGAGAAGAACAAGGATGAGAGTAACTGTTTCATCCCTTGACGGTATC	480
ent-r Ent-f Enterococcus	-----	0
	-----	18
	TAACCAGAAAGCCACGGCTAACTACGTGCCAGCAGCCGCGGTAAATACGTAGTGGCAAGC	540
ent-r Ent-f Enterococcus	SEQ ID no. 13: 3'-CGCGTCCGCCAAAGAATTTCAGACTACACTTTC/-5' SEQ ID no. 12: 3'-CGCGTCCGCCAAAGAATTTCAGACTACACTTTC/5Biosg/-5'	
	-----gcgcaggcggttctcttaa-----	18
	-----	18
Enterococcus	GTTGTCGGGATTTATTGGGCGTAAAGCGAGCGCGGGTTTCTTAAGTCTGATGTGAAA	600

¹ /iFluorT/
² A to /idSp/
³ dT-BHQ
⁴ G to /idSp/

FIG. 23