

PROBES

No	Name	Sequence	Length	GC %	Tm °C
1	hp1012 cwp66	TGGAGTAGTGGTTACAATATCAAATCAATC	29	31	55.5
2	hp1013 bacA1	AGGTACATCTAGGCTGGTTCTACTATA	28	39	56.9
3	hp1014 catD	CAACGGTATGGAAACAATCATAGAATG	27	37	56.4
4	hp1016 cwp66	AACAGATGAAGAGCCATTCTTGAAA	26	35	57
5	hp1018 cwp84	CAACAATACCTGTCTCAGCAGAAA	24	42	56.5
6	hp1020 cwp66	TGGTTAGTAACTATATCTAATGAATCCAGAG	31	32	55.9
7	hp1021 cwp66	TGGATTATAACTATAGATGCTGTGCTAAA	30	30	56.1
8	hp1022 ermB	ACAGTCATCTATTCAACTTATCGTCAGA	28	36	57.4
9	hp1023 cdtA	AGGCTAAAGAATGAGAAAGAAAAGATCAA	29	31	57
10	hp1026 cdtA	TTGTTACCTAATAACATTTATGCACAAGA	29	28	55.6
11	hp1027 cdtA	ACTAGTATTGGTAGTGTGAATATGAGTG	28	36	55.9
12	hp1029 cdtA	TGATTGGAGTAATAAATTAACACCTAATGAAC	32	28	56.4
13	hp1030 cdtB	AAGACATACTCACAAACAACGGATT	25	36	56.5
14	hp1031 cdtB	TGAAGATATACTCCAAACAATGGATT	27	33	55.9
15	hp1038 cdtB	GAGTTGAAGCTACTTTACAATATCTGGGA	29	34	57
16	hp1039 cdtB	AGAGTTGAAGCTACTTTACAATATTTGGA	30	30	57.1
17	hp1040 cdtB	CAGCTATAGTTTAGTCAAGCACTAGTATATC	30	37	56.4
18	hp1041 cdtB	GCCATAGTTAGTCAAGCATTAGCATA	26	38	56.6
19	hp1043 vanG	ATGGACAAAGACAAATCACATAAACTTG	28	32	56.6
20	hp1044 divIC	TGAAATACAAATAAACAGCTTAAAGAAAGATGA	33	24	56.9
21	hp1045 divIC	AATACAAATAAACGCCCTTAAAGAAAGATGA	30	27	56.3
22	hp1046 divIC	CTGAAATACAAATAAACAACTTAAAGAAAGATGA	34	24	56.2
23	hp1051 vncS	ACAGTTGAAATATTGAAAGTATCTTCTTTCC	31	29	56.5
24	hp1052 vncS	AGCTCTAATGATGAAGTTGGAGAATTAA	28	32	56.2
25	hp1055 vexP1	TGGGCAAGGTAATTCGAGTATAAAA	25	36	55.8
26	hp1059 vexP1	AGTAATTGTAGATGGATTCAATTAECTCAGA	30	30	56.1
27	hp1061 eutG	CATGCTATAGAAGCTTACGTATCTACAA	28	36	56.3
28	hp1062 eutG	CATGCTATAGAGGCTTATGTATCTACAA	28	36	55.8
29	hp1063 matE	GTGAAATCAAAGCCTATGGCATTAGATA	28	36	57.3
30	hp1071 bcrA	GAATCTTGACTTACATTGTGAATATATGGG	30	33	56.3
31	hp1072 bcrA	GAATCTTGATTTACACTGTGAATATATGGG	30	33	56.3
32	hp1073 bcrA	ATGTAAGAAAGGAAGTCAATTCGGATT	28	32	56.6
33	hp1079 spaK	TTGAAAGAAGGACTATTACGTCATCAAA	28	32	56.6
34	hp1080 spaK	GAGAGATATTGAAGAAAGGCATGCATAT	28	36	57.1
35	hp1082 sat	GAATAGTGGAAATCACTCAATGAAATCA	28	36	57.1
36	hp1083 sat	ACTAGTGGAAATCACACACTGAAATC	26	38	56.8
37	hp1084 CD0456	CCTTGATAGAGCATGATAAAGAGTGT	28	36	56.6
38	hp1087 eme	TGTCAAACAATTTATCAACATTAATTTCTTCA	32	22	55.9
39	hp1096 lmrB	AGCGATTAATAGTACACTTCGTCAGATA	28	36	57.3
40	hp1097 lmrB	GCAATTAATAACACACTCCGTCAGATA	27	37	57
41	hp1098 ydiC	AACAGAGGAAAGGCACCTAGGAATT	24	42	57.2
42	hp1103 hly3	GAGACCCAATAAGCAGTTAACTCAT	26	38	56.6
43	hp1105 tetM	ACCGTTATCTTTATCAACAAGATCGAC	27	37	57
44	hp1108 tetM	TGATTTAACTTTCTTTACAAATGGACGT	28	29	55.9
45	hp1109 tetM	ACTTTAACTCTATATACAAATGGCAAGC	29	34	57.4
46	hp1110 tetM	GAGTAAACCTGAACAGAGAGAAATGTT	27	37	56.8
47	hp1112 tetM	CAAACCTCAACAAAGGAAATGTTA	25	36	55.7
48	hp1113 tcdE	TGTGGATTACCAGTACCTAAGAGATTAA	28	36	56.6
49	hp1117 tcdC	GAAATAGAAACTTTAAATAGCAAATGTCTGA	32	25	55.8
50	hp1118 tcdBp1	CTGATTCAGTAAAGACAGCTGTAGATTG	28	39	57.5
51	hp1119 tcdBp1	TCTATAGAGAAACCTAGTTCAGTAACAGT	29	34	56.4
52	hp1121 tcdBp4	AGCTATAGAATGGCAAACATTAGATGAT	28	32	56.4
53	hp1122 tcdBp4	GGAGCTGTAGAATGGAAAGAATTAGATG	28	39	57.3
54	hp1124 tcdBp2	GAACTTATATTACGAGCTGAGGCAAA	26	38	56.8
55	hp1126 tcdBp2	TGAGCTTATCCTAAGAGATAAAGCAAC	27	37	56.3
56	hp1127 tcdBp2	TGATAAGTATAGAATTCCTGATAGAATCTCTG	32	31	56
57	hp1129 tcdBp3	AGAATTAAGTGAAAGTGTATGTTGGATT	28	29	55.6
58	hp1130 tcdBp3	CATFGATGGCAAATTCAAATCTGTGTT	27	33	56.3
59	hp1132 tcdAp1	GTTGATATGCTTCCAGGTATTCACCT	26	42	57.1
60	hp1134 tcdAp2	AGTGATTGTGTAGTGAATAAGGTGT	26	35	56
61	hp1135 tcdAp3	ACTTTATGCCTGATACTGCTATGG	24	42	55.7
62	hp1141 fliC	AGCAAACAATCAAATGGGAAGAAAC	25	36	56.5
63	hp1142 fliC	AGCAAATAACCAAATGGGAAGAAAC	25	36	56
64	hp1144 fliC	ATCAAGTTC AACAGAGTTTAAACGGTAA	27	33	56.7
65	hp1145 fliC	CAGACTCTACTAAATTC AATGGTGAGAA	28	36	56.5
66	hp1147 fliC	CAGGTATAACAAGTTCTACAATAGCAAG	28	36	55.7
67	hp1149 CD2797	GCATTTATGTATGCTTCTGGATTACATG	28	36	56.8
68	hp1150 slpA	CAAATGATCAAGCTCGACTATTG	24	42	56.4
69	hp1151 slpA	AGATTTCTTAATAAATCTCCAGGTCAAG	29	34	56.7
70	hp1153 slpA	TTCTTAATAAGCTCTCCAGCAGAGG	25	44	57.4

PROBES

No	Name	Sequence	Length	GC %	Tm °C
71	hp1154 slpA	AACTGATGAAGCTGAATCTGGTTTAG	26	38	56.9
72	hp1155 slpA	ACATATGCATCATCTAACTATAAGCCAG	28	36	56.5
73	hp1156 slpA	CAAGGTTTCTCAACTTATAGAGCTACAA	28	36	56.7
74	hp1158 slpA	ATCAGCTGCACAACCTTCTAAATTA	25	36	56.3
75	hp1163 slpA	GATTAGATACTAAAGGAGCAACAGATATAGA	31	32	55.9
76	hp1164 slpA	ACTAAGAGTGCATCAACTGATATTGAAA	28	32	56.7
77	hp1166 slpA	ATCAGCAAATGATACAAATAGCTAGTCAA	28	32	56.5
78	hp1167 slpA	AAGATGGTTCTACTCCTGGTGATG	24	46	57.1
79	hp1168 slpA	AACTATAACTGCAGCTACTTCAGAG	25	40	55.7
80	hp1169 slpA	ATCAACTGGTAATGTGTCCAGGGTTAT	26	38	57.5
81	hp1170 slpA	AGCAGATAATGATATTAAGGTTCTGATTTAT	32	25	55.5
82	hp1171 slpA	TGGTTCTGAGGATGCAGATGTAAA	24	42	57.2
83	hp1173 slpA	ATCAAGATGAAAGTTAATGAAGTTGCTG	28	32	56.5
84	hp1174 slpA	TGATAAACGATAATGAGTACAAAGTAACAAA	31	26	55.9
85	hp1175 slpA	AGTTTATAACTGATGTAGTTCCAGGTGTA	29	34	57.3
86	hp1176 slpA	AGAATATGGAATAAGTGAACAAAGGTA	28	32	55.9
87	hp1177 slpA	GATACAGAGGCAGTTATATCTACTTCAA	28	36	55.7
88	hp1178 slpA	AAGATAATTCTACAGCTACAGACGTTAC	28	36	56.4
89	hp1180 slpA	ACTAAGAAATCAACTTCAACAAGTCAGA	28	32	56.7
90	hp1182 slpA	CTGTAGCTCCTTCCAAATATAAGCTTT	27	37	56.7
91	hp1183 slpA	CAGGTGATGCTGGTAAATATACATTAGA	28	36	56.4
92	hp1184 slpA	CTTATAATGCTGCAGAGACAATTCATAC	28	36	56.3
93	hp1186 slpA	AGAAATTTCACTGAGGAAGAAATAGA	28	32	56.3
94	hp1188 slpA	GAGAATAAAGAGATTGTTAAGCCAGCAT	28	36	57.4
95	hp1190 slpA	ATGCTATAAATTGCTGGAACATCTTCAG	27	37	57.3
96	hp1191 slpA	TGTAGTTACTAAAAGTTGGTACTGCAAC	27	37	56.8
97	hp1192 slpA	CAGCTAATAATGGTAAGATAATAATTGATGCA	32	28	56.4
98	hp1193 slpA	AAGGTTCTATATTCACCAGCAACAAA	26	35	56.5
99	hp1195 slpA	ATGCTAGAGGAACTAGTGAAATAGTAGT	28	36	56.5
100	hp1196 slpA	AGTTGTTGTTGCTGGTTCTACTAATTC	27	37	57.5
101	hp1197 slpA	GATAGAGATTTACTTGCCTCTGATTTCT	28	36	56.3
102	hp1198 slpA	ACAAAGGCCTTAAAGTTAAAGATGTTG	28	32	56.8
103	hp1199 slpA	ATCAAGCGCTGAAATAAGTGGATTT	25	36	57.1
104	hp1200 slpA	GACTTATTAAGCAGACCAATCACCTAA	28	36	56.9
105	hp1201 slpA	ACAAAGATAAGACAATTGCAACATATGA	28	29	55.8
106	hp1202 slpA	TTGCAACTTTAAACAATTGGTTCTGATAA	28	29	56.3
107	hp1203 slpA	GATTCTTCAACTCCAAGTGGAGATA	25	40	55.6
108	hp1204 slpA	CCTTAGCAGCTGATACTACATTTGAAA	26	38	56.5
109	hp1205 slpA	CGAAAGTAGACGGTAGTGATGTAATTG	27	41	57.3
110	hp1206 slpA	AGATGCTTCTAGTGTTAGTGCCATAA	26	38	57.3
111	hp1208 slpA	CTGTTAAAGATGCAGTAAAGGCTACT	26	38	56.7
112	hp1209 slpA	TGCTTCATTAAGTGCAGATGATATACAA	28	32	56.8
113	hp1210 slpA	CAGGATCTGAAGCAGGTATAGCAA	24	46	57.4
114	hp1211 slpA	TGCTAAATCATCGTTTAAATTTGATGCA	28	29	56.7
115	hp1212 CD2797	GAACAAGAAGAAGTAAATCAAGAAGAAGT	29	31	56
116	hp1214 CD0425	AAGAAATTGACAAGGATATGCAGCTAC	27	37	57.4
117	hp1220 CD0425	AGCTACTGCCATATTCAATTTATGAAA	28	32	56.9
118	hp1227 IPR007253	TGTTAATAAATGACTCTAGCATATCGGA	28	32	55.7
119	hp1228 CD0425	AAGATCTTAGATAGCAAGATTTCTGCTC	28	36	56.6
120	hp1229 CD0425	AGATTATTGATAAAGAAATGCAGGAGCT	28	32	56.7
121	hp1230 CD0425	AAGGTTATTGATAAGGAAATGCAGGAG	27	37	56.9
122	hp1231 CD0425	AAGGCTATTGATAAGAAAATGCAGAAG	27	33	55.8
123	hp1232 slpA	CAACTAACTATACTTCTGGAGCTGAATA	29	34	56.3
124	hp1233 slpA	TGCTAATAATGATACACTTGCAGATGTT	28	32	57
125	hp1234 slpA	GACTACAAGTTTTATTGTATGGTACGGTT	28	36	56.9
126	hp1236 slpA	GCTACAGCATTACTGTAACATAATCCAA	28	36	57.2
127	hp1237 slpA	CAGCTGCTAATGATCTTAAAGGATCTG	27	41	57.3
128	hp1239 slpA	ATCAGTTCTACTCTTAGAGCAAGTATA	28	36	56.5
129	hp1242 slpA	CAACTGATAAAGAGAAGGAAGTAGCAG	27	41	57
130	hp1243 slpA	AACTTAAAGGAACTAAAGGAGAAAGCAC	28	36	57.4
131	hp1244 ydc	AGGACAAGTTATAGGTATTACTATTTCTACAA	32	28	55.8
132	hp1247 tcdAp2	ACTATAAATGTACTACATAATAACAGAGG	31	32	56
133	hp1249 slpA	TGATAAAGTACTTATAAATCTGCAACAGAT	31	26	55.6
134	hp1251 spaE	TTGTATGCTGGGTTGTTCTCTTG	24	42	57
135	hp1252 spaE	TTGTATGTTGGGTTGGTTCTCTTG	24	42	56.7

PRIMERS

No	Name	Sequence	Length	GC %	Tm °C
1	lb2053-cwp66	TGTTATGTCCTCATCATTCT	22	32	50.4
2	lb2059-cwp66	TCCATCATTCTATATGCACA	22	32	50.6
3	lb2060-bacA1	TACCAAGTAATACTGCACCT	20	40	50.6
4	lb2064-cdtA	TTCTATAGGAGCCTTGTAAGT	21	38	50.4
5	lb2065-cdtA	CAGGAGAACCTTTAGGTATAGT	22	41	51.3
6	lb2067-cdtA	GCATATAATCATTACATCAGCAA	24	29	51.2
7	lb2079-vncS	AGTTCTTTATCGTCTTTAACTCT	24	29	51.3
8	lb2084-eutG	TTTCAGCTAGTGCATCTGA	19	42	51.1
9	lb2085-matE	GTGTAAGTTCACAAATAGGGA	22	36	51.3
10	lb2092-berA	CACTGTACTTTTACCTGCTC	20	45	51.1
11	lb2099-spaK	CTGGAGAACTATATCTGATACT	23	35	49.6
12	lb2100-spaK	TGGAGAACTATACTCTGATACT	22	36	49.9
13	lb2101-cwp66	ACAGCTTCTACATAACAACC	20	40	50.3
14	lb2102-cwp66	TCCATCTTTGGCTCTTTCA	19	42	51.2
15	lb2105-spaK	GGAGAAACAAATTCTGCTACT	21	38	51.1
16	lb2106-cwp84	TGCAGTTTCTACTCCATCT	19	42	50.3
17	lb2108-cdtB	AAATCTTTAAAGTGTTCGTCTG	22	32	50.4
18	lb2109-cdtB	AAATCTTTAAAGTGTCTCATCTG	22	32	50.1
19	lb2110-divIC	TCTTGCTATATCCTCTAAGTCT	22	36	50.2
20	lb2111-catD	AGCATTTGGCTTTCCTTC	18	44	50.5
21	lb2112-vanG	GGTACTTTAATACCTTCTGAATG	23	35	50
22	lb2113-ermB	CTTGGTGAATTAAGTGACAC	21	38	50.4
23	lb2114-cdtA	TCTGAGAATATTTGCTTATCTCT	23	30	50
24	lb2115-vexP1	TTCAAGATCAATATTTGGACCA	21	33	49.8
25	lb2116-vexP1	CCACCGGAAATCATTGAG	18	50	50.5
26	lb2117-berA	ACACATTCCAATACCTCTGA	20	40	50.9
27	lb2119-berA	GACACATTCCAATATCTCTGAT	22	36	50.7
28	lb2122-cdtB	TTGTACTAGTTTGAGCATATACA	23	30	50.3
29	lb2123-vncS	TCGTCAATTGTTCTTAATAAAGT	23	26	49.8
30	lb2124-sat	AGATAGGAAAGGTATATGTGGA	22	36	50.4
31	lb2125-sat	GATGGGAAAAGTATATGTGGA	21	38	50
32	lb2126-CD0456	ACTTCATCTGCTATGGAGAT	20	40	50.5
33	lb2128-cme	TGCATTGGAAACTATACCAAG	21	38	51.2
34	lb2132-lmrB	GCAGAACCTATAGCACCA	18	50	50.9
35	lb2133-lmrB	GCAGAACCTATAGCTCCA	18	50	50.3
36	lb2134-ydiC	CATATTTCCAATAGCAACTGC	21	38	50.7
37	lb2136-hly3	AAAAGAGATAAACAAGCACCT	21	33	50.6
38	lb2137-tetM	CTTATCCCGAACAGACTGA	19	47	50.9
39	lb2139-tetM	GTTTACAAGTAGCAATTTGAT	21	33	50.1
40	lb2140-tetM	CCAGTAGTAACATAGTACCCT	21	43	50.5
41	lb2141-tetM	GGTAGTAACATGGTACCCT	19	47	50.1
42	lb2142-tetM	GTCACTGTCCGAGATTTTC	18	50	49.9
43	lb2143-tetM	GGATCACTATCTGAGATTTCC	21	43	50.3
44	lb2144-tcdE	AGCATTCATTTTCATCTGTCTCAT	21	33	50.8
45	lb2145-tcdC	TCTTTCATTTTGAACCATGGT	21	33	51.1
46	lb2146-tcdBp1	CTTCTAACTGCATCTCTTCC	20	45	50.5
47	lb2148-tcdBp1	GCTTCTAACTTTGTCAATTTCC	21	38	50.5
48	lb2149-tcdBp1	GCTTCTAACTTTTACCATTTCCC	22	36	50.8
49	lb2152-tcdBp4	AAGCTTTACCTGTTTCTGG	19	42	50.1
50	lb2154-tcdBp4	AAAGCTCTACCTGTATCTGT	20	40	50.4
51	lb2155-tcdBp4	AAGCTTTGCCTGTTTCTG	18	44	50.8
52	lb2158-tcdBp2	GACTCAGCTAATGATATATGACT	23	35	50.3
53	lb2159-tcdBp2	GATTCAGCTAATGAAATATGGC	22	36	50.8
54	lb2160-tcdBp2	GCCATGACCAATGAATGT	18	44	50.2
55	lb2161-tcdBp2	CTTTGCCATGACCAATAAGT	20	40	51.2
56	lb2162-tcdBp3	TCTCTCACAACTATCAACA	21	33	49.8
57	lb2163-tcdBp3	TCGCTATTCAACTCTATATAACT	24	29	50
58	lb2164-tcdBp3	CGCTGTTCAACTCTATATAACT	23	35	51.2
59	lb2165-tcdAp1	AGTCCAATAGAGCTAGGTC	19	47	49.9
60	lb2168-tcdAp2	CAAATCCATTAGAGGTACTAAAC	23	35	50
61	lb2169-tcdAp2	TCAAATCCATTAGAGCCACT	20	40	51.3
62	lb2171-tcdAp3	ACTCCATCAACACCAAGA	19	42	51.1
63	lb2175-fliC	TCCATAGACTTACTTTGTCCA	21	38	50.9
64	lb2176-fliC	CCATAGACTTACTTTGTGCA	20	40	50.3
65	lb2178-fliC	TTCTGCTCCAACTTGTAATG	20	40	50.9
66	lb2179-fliC	AGAAGTTCATCAAGTAGCT	20	40	50.9
67	lb2182-fliC	CTGCATCTGTTCCAGAAG	18	50	50.1
68	lb2183-fliC	TTGTTTAGCTGCATTTGTTTC	20	35	50.3
69	lb2185-CD2797	CATTCATAAGCCCTGGAAC	19	47	50.7
70	lb2194-IPR007253	CTTTAGACTTAGCAAATGGTG	21	38	49.9

PRIMERS

No	Name	Sequence	Length	GC %	Tm °C
71	lb2196-CD0425	ATGAACCTGCTCCATAGTT	19	42	50.6
72	lb2197-CD0425	GAACCTGCTCCATTGTATC	19	47	50.5
73	lb2198-CD0425	GGATGGATTGCTTTATATTCC	22	36	50.3
74	lb2199-CD0425	AGACGGATTAGCCTTATATTCT	22	36	51.2
75	lb2200-CD0425	AGATGGATTAGCCTTATATTCC	22	36	49.9
76	lb2201-slpA	ATCTATTCAATTCGCCTGAAG	21	38	51.1
77	lb2202-slpA	TGAAATAAAGTTCGAATGTTGT	22	27	50.7
78	lb2203-slpA	AGTTTACTTGTAGTTACTTTATCTC	25	28	49.9
79	lb2204-slpA	TGCATTCAATATTCTAAGTTAGT	24	25	49.8
80	lb2205-slpA	CCTGTTAAATCTTTCAATGCA	21	33	50
81	lb2206-slpA	TGAATTTGCTCAGTAGAACC	21	38	50.5
82	lb2208-slpA	GTATCAGCAGTTAATGTTAAGC	22	36	50.7
83	lb2210-slpA	ACTAATTTAAGAGCTGCATTTTC	22	32	50.2
84	lb2212-slpA	ATCTACTCTATCACTGTAGGT	22	36	50.1
85	lb2213-slpA	GATTATTTCCCTCAACTTACC	22	36	49.9
86	lb2215-slpA	GAAGCATTTATTTGATCTGCA	21	33	50.2
87	lb2217-slpA	TCTCCTGCTATAAAGTTTATTGTT	23	30	50.5
88	lb2218-slpA	GTCTTTACATAATCTTCATTTCCA	24	29	50.4
89	lb2219-slpA	TGTATTACCATATGCAGTTCC	21	38	50.4
90	lb2220-slpA	CCATCACTAGCATCACTAAC	20	45	50.6
91	lb2222-slpA	TTGTTGTAGAAGCAACAGG	19	42	50.5
92	lb2223-slpA	ACAGATATCTTTGCATCATCTT	22	32	50.6
93	lb2224-slpA	CTGGTGGAAATGCTTCAG	18	50	50.7
94	lb2225-slpA	ACAAAGTGGAGAATTGTCAC	20	40	51.1
95	lb2226-slpA	CATCTGCTATAGTCAATGGAG	21	43	50.7
96	lb2227-slpA	TTACTAAGTTTGAAGTAGAAAGTG	24	29	50
97	lb2228-slpA	AAGTGAACAACAATTTCTTCTTC	21	33	50.6
98	lb2229-slpA	GTAGATACAGTGGCATTGAT	21	38	50.7
99	lb2230-slpA	TGCTTATCAACAAGGTTAAGT	21	33	50.4
100	lb2231-slpA	CATCTACAGTTCTCCTGT	19	47	50.4
101	lb2233-slpA	TGTAGTTAACTCAGCATTGT	21	33	50.4
102	lb2234-slpA	TCAGGAACCTTAGGGATATCA	21	38	50.3
103	lb2235-slpA	AGTGTTTCTAATTTGTCAGCT	21	33	50.7
104	lb2236-slpA	GTAGAACCCTAGCTTTAGG	20	45	49.8
105	lb2237-slpA	GTAGCTTCTTGTCTCTAGC	20	45	50.6
106	lb2239-slpA	TGCTACTCCATTAGCTTGA	19	42	50.4
107	lb2240-slpA	AAGTTTGACCAGCTTGAC	18	44	50.1
108	lb2241-slpA	GCTATCTTCACAGTTAAGCA	20	40	50.4
109	lb2242-slpA	CATTTAACTTTGCTTCAGTCA	21	33	50
110	lb2243-slpA	GCTATCAACTTGTGTATCAGA	21	38	50.4
111	lb2245-slpA	AGACTCATCTGTAACTCTGA	21	38	50.7
112	lb2246-slpA	TGTATTTGCTAGTGAAGTAGC	21	38	50.7
113	lb2247-slpA	ATCAGCCATTACTAGACCAG	20	45	51.2
114	lb2248-slpA	GCTTTAAGAACTAATTTAACAGGA	24	29	50.6
115	lb2249-slpA	ACGTAGAATCTGTACCTATACT	22	36	50.3
116	lb2251-slpA	GTGTATAAGAAGCACTTAGATCT	23	35	50.7
117	lb2252-slpA	TCTGCTACAACATCAGTAT	20	40	50.7
118	lb2253-slpA	TCATTTCAACAACATATCCAGT	22	32	51
119	lb2254-slpA	AACTACTTTAGCTGGTGTATC	21	38	50
120	lb2255-slpA	GTCTTTGCAGTTATACTAAGC	21	38	49.8
121	lb2257-slpA	GAATCACTACCTGGATTGT	20	40	49.9
122	lb2259-slpA	ACCTTTACTGAACCTGGAG	19	47	51
123	lb2260-slpA	TCTTAACCGCTGAAGTATAATC	22	36	50.8
124	lb2261-slpA	TGGTTTAGCAACTACTGTG	19	42	49.9
125	lb2262-slpA	CTGGAACCACTTGAATATCAT	21	38	50.6
126	lb2264-slpA	GTAGTTGCACCACTAATAGTT	21	38	50.6
127	lb2266-slpA	TGTGAACCTTGAATCAACTCT	21	33	50.7
128	lb2267-slpA	CTTTACCTGCAGTTGCAT	18	44	50.2
129	lb2268-slpA	TTGGATCTCCAAGTATACATA	20	40	50.6
130	lb2270-slpA	CACCTAAACCTTTAAGTTGGT	21	38	50.9
131	lb2271-slpA	TCTTGATCTACAATCTTAACTGT	23	30	50.2
132	lb2272-slpA	TGTTTATCTGCCTTAAAGCAC	20	40	50.9
133	lb2273-CD0425	AGTATCATTTGCTTCTCTGTG	20	40	49.9
134	lb2274-ydiC	CCTATATCCAGCTTTAATACTCA	23	35	50.2
135	lb2275-tcdAp2	TGCACCTAAGTTTATTCCG	19	42	50
136	lb2276-bcrA	ATCCGACACATTTCAATATCT	21	33	50
137	lb2278-slpA	TGAATCACTACTTGGATTTGT	21	33	50
138	lb2280-spaE	ACATACCTTTCCATGTAGCT	20	40	51
139	lb2281-cdtB	TGGATCTCCTAAATAATTACGC	22	36	50.8
140	lb2282-cdtB	TTTGTATCTCCTAAATAATTACGC	24	29	50.4