Genetic determinants of drug resistance in *Mycobacterium tuberculosis* and their diagnostic value

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ONLINE DATA SUPPLEMENT

Supplementary Table 1: Culture, DST and fingerprinting methodology.

* INH: isoniazid, RIF: rifampicin, EMB: ethambutol, PZA: pyrazinamide, STR: streptomycin, ETH: ethionamide, CIP: ciprofloxacin, LEVO: levofloxacin, OFLX: ofloxacin, AMK: amikacin, KAN: kanamycin, CAP: capreomycin, PAS: para-aminosalicylic acid, CYS: cycloserine ** FLQ drugs tested included CIP, LEVO, OFLX, MOXI, and GATI. Spoligo: spoligotyping

Source	Culture	Colony purification	Drug Sensitivity Testing*	Finger-printing
Stellenbosch University, South Africa	BACTEC MGIT 960 system (BD Diagnostics Systems, Sparks, MD)	No	Indirect proportion method on Middlebrook 7H11 agar slants supplemented individually with: RIF (1.0 µg/ml), INH (0.2 µg/ml), EMB (7.5 µg/ml), OFLX (2.0 µg/ml), KAN (5.0 µg/ml), STR (2.0 µg/ml), AMK (5.0 µg/ml), CAP (10 µg/ml). PZA sensitivity was tested using the MGIT 960 system (100 µg/ml).	Spoligo/ RFLP
Center for Disease Control, Atlanta, USA	Middlebrook 7H9 broth supplemented with 10% (vol/vol) albumin-dextrose-catalase enrichment (Difco Laboratories) and 0.05% (vol/vol) Tween 80 (Sigma-Aldrich) at 37°C until they reached an approximate optical density at 600 nm of 1.0 (corresponding to 5 x 10^8 CFU/ml)	No	Indirect proportion method on Middlebrook 7H10 agar plates supplemented individually with: RIF (1 µg/ml), INH (0.2, 1, and 5µg/ml), EMB (5 µg/ml), OFLX (2 µg/ml), CIP (2 µg/ml), STR (2.0 µg/ml) KAN (5 µg/ml), CAP (10 µg/ml), and AMI (4 µg/ml). PZA was tested using the BACTEC 460 (100 µg/ml), MGIT (100 µg/ml), or agar proportion (25 µg/ml) method.	Spoligo
Mass State Laboratory (source country Peru, Russia), Boston, USA	Radiometric BACTEC 460 TB system (Becton-Dickinson)	No	Indirect proportion method on Middlebrook 7H10 agar plates supplemented with : INH (0.2, 1, and 5 µg/mL), RIF (1 µg/mL), EMB (5 µg/mL), STR (2 and 10 µg/mL), KAN (5 µg/mL), CAP (10 µg/mL), ETH (5 µg/mL), CYS (30 µg/mL), PAS (1 µg/mL), AMK (6 µg/mL), LEVO (1 µg/mL), OFLX (2 µg/mL), and CIP (2 µg/mL). PZA was tested using the BACTEC (100 µg/mL).	Spoligo
Public Health Research Institute, Rutgers University, Newark, NJ	Lowenstein-Jensen slant culture	No	Indirect agar proportion method on Middlebrook 7H10 agar plates containing the following drugs: RIF (1 µg/ml), INH (0.2, 1, and 5µg/ml), EMB (5 µg/ml), CIP (2 µg/ml), STR (2µg/ml), KAN (5 µg/ml), CAP (10µg/ml)	Spoligo/ RFLP
RVIM, Netherlands	MGIT and Middlebrook 7H10 solid	No	MGIT INH (0.2 µg/mL), RIF (1 µg/mL), RFB (2 µg/mL), EMB (5 µg/mL), STR (5 µg/mL), ETH (5 µg/mL), CYS (50 µg/mL), PRO (5 µg/mL), AMK (5 µg/mL), CLO (2 µg/mL), and CIP (2 µg/mL). PZA (50 µg/mL), CLARI (>16 µg/mL), PAS (1 µg/mL).	Spoligo/ MIRU-VNTR
WHO/TDR, Belgium	Dubos Agar then Lowenstein-Jensen slant culture	Yes	Indirect proportions method on two different media: On LJ for INH (0.2 µg/ml), RIF (40 µg/ml), EMB (2µg/ml),STR (4 µg/ml),PAS(0.5 µg/ml); on Middlebrook 7H11 agar for OFLX (2µg/ml), KAN (6µg/ml), CAP (10µg/ml).	

Supplementary Table 2: List of genes and non-coding regions targeted by MIPs.

Listed are the accompanying gene symbol, description, drug resistance association, the H37Rv identifier, the strand, the start and end coordinates in H37Rv genome and the length in nucleotides.

Gene	Description	Drug resistance association	ID (H37Rv)	Strand	Start	End	Length
promoter *ahpC*		Isoniazid	-	+	2726088	2726192	105
ahpC	alkyl hydroperoxide reductase C protein	Isoniazid	Rv2428	+	2726193	2726780	588
alr	alanine racemase	Cycloserine	Rv3423c	-	3840194	3841420	1227
ddl	D-alanine-D-alanine ligase ddlA	Cycloserine	Rv2981c	-	3336796	3337917	1122
embA	membrane indolylacetylinositol arabinosyltransferase A	Ethambutol	Rv3794	+	4243233	4246517	3285
embB	membrane indolylacetylinositol arabinosyltransferase B	Ethambutol, Isoniazid, Rifampicin	Rv3795	+	4246514	4249810	3297
embC	membrane indolylacetylinositol arabinosyltransferase C	Ethambutol	Rv3793	+	4239863	4243147	3285
ethA	monooxygenase	Ethionamide	Rv3854c	-	4326004	4327473	1470
gidB	glucose-inhibited division protein B	Streptomycin	Rv3919c	-	4407528	4408202	675
gyrA	DNA gyrase subunit A	Fluoroquinolones	Rv0006	+	7302	9818	2517
gyrB	DNA gyrase subunit B	Fluoroquinolones	Rv0005	+	5123	7267	2145
inhA	NADH-dependent enoyl-[acyl-carrier-protein] reductase	Ethionamide, Isoniazid	Rv1484	+	1674202	1675011	810
iniA	isoniazid inductible gene protein A	Ethambutol, Isoniazid	Rv0342	+	410838	412760	1923
iniB	isoniazid inductible gene protein B	Ethambutol, Isoniazid	Rv0341	+	409362	410801	1440
iniC	isoniazid inductible gene protein C	Ethambutol, Isoniazid	Rv0343	+	412757	414238	1482
kasA (fabF1)	3-oxoacyl-[acyl-carrier protein] synthase 1	Isoniazid	Rv2245	+	2518115	2519365	1251

katG	catalase-peroxidase-peroxynitritase T	Isoniazid	Rv1908c	-	2153889	2156111	2223
promoter *mabA*		Isoniazid	-	+	1673300	1673439	140
mabA (fabG1)	3-oxoacyl-[acyl-carrier protein] reductase (mycolic acid biosynthesis protein A)	Ethionamide, Isoniazid	Rv1483	+	1673440	1674183	744
ndh	NADH dehydrogenase	Isoniazid	Rv1854c	-	2101651	2103042	1392
oxyR'	oxidative-stress regulatory gene (pseudogene)	Isoniazid?	Rv2427Ac	-	2725571	2726087	517
pncA	pyrazinamidase/nicotinamidase	Pyrazinamide	Rv2043c	-	2288681	2289241	561
rpoB	DNA-directed RNA polymerase beta chain	Rifampicin	Rv0667	+	759807	763325	3519
rpsL	30S ribosomal protein S12	Streptomycin	Rv0682	+	781560	781934	375
rrl	ribosomal RNA 23S	Aminoglycosides	Rvnr02	+	1473658	1476795	3138
rrs	ribosomal RNA 16S	Aminoglycosides	Rvnr01	+	1471846	1473382	1537
thyA	thymidylate synthase	Para-aminosalicylic acid	Rv2764c	-	3073680	3074471	792
tlyA	cytotoxin|haemolysin	Capreomycin	Rv1694	+	1917940	1918746	807
						Total length	42367

Supplementary Table 3: Sequence and coordinates of the molecular inversion probes used for target sequence capture.

Some probes are duplicates except for one SNP in one of the arms.

BRIDGE = AGATCGGAAGAGCGTCGTGTAGGGAAAGCTGAGCAAATGTTATCGAGGTC

#	Probe name	Start	End	Sequence
1.	embA-embB_W_1_1	4243003	4243142	TCCGGCGCCGTTGCGCCGCG-(BRIDGE)-CTACCTCAAAGACGACTGGTTTAGGGACTG
2.	embA-embB_W_2_2	4243143	4243282	CGGATCGCACGCCTAGCAGC-(BRIDGE)-GCTAGAAGTGCCGTGGCCACC
3.	embA-embB_W_3_1	4243283	4243422	CCCAGATCACCGCCCCTCTGGTAT-(BRIDGE)-CGTCGTCTCGGGAATCGCGGG
4.	embA-embB_W_4_2	4243423	4243562	GGCTGTTCGTCCGCGCCAAC-(BRIDGE)-CCGGGGCGCCACGCGCGCTG
5.	embA-embB_W_5_1	4243563	4243702	GGGCGCTGATTTTATGGGTATACCCGG-(BRIDGE)-CAGGACACGGTCGTCGTGGC
6.	embA-embB_W_6_2	4243703	4243842	GACGCCCGGCGCGCTCAAGA-(BRIDGE)-CGGCGCCGGGACCCTGCCGC
7.	embA-embB_W_7_1	4243843	4243982	TGCGGGTCGGATTCGCCAGC-(BRIDGE)-AGGCCGTGATGCTCCTCGGC
8.	embA-embB_W_8_2	4243983	4244122	CCGGCTATGTAGCCAACTACTACCGGTATTT-(BRIDGE)-CGGCTCGCTGACGCAGCGGT
9.	embA-embB_W_9_1	4244123	4244262	GCTGATCGTCAGCCGTTTCGTGC-(BRIDGE)-CGGCACGACGGAGGCGCCGT
10.	embA-embB_W_10_2	4244263	4244402	TGATCGCGCTGGGTGTGCTG-(BRIDGE)-TGCGGCGGCTGGGACCGGGC
11.	embA-embB_W_11_1	4244403	4244542	CCGCTGCTGACTGGTGCGCG-(BRIDGE)-GTCACGTGGGTGTTGGTGGAACG
12.	embA-embB_W_12_2	4244543	4244682	CACGGTGGCCGAATCGGCAC-(BRIDGE)-CGCCATCGCCCAGAGGATCCG
13.	embA-embB_W_13_1	4244683	4244822	GTGTTGCTGTTCTGCCTGTTCGGG-(BRIDGE)-GCATCAAGTACAAGGTCGGCCCG
14.	embA-embB_W_14_2	4244823	4244962	GCCGTGCAGTTCGGCGCATT-(BRIDGE)-GTGCTGTTCGTGCTGCTGCGG
15.	embA-embB_W_15_1	4244963	4245102	GCAACCTCGGGCATCAACGGGT-(BRIDGE)-CGCCGGGCTGGCCGGGGTGT
16.	embA-embB_W_15_1a	4244963	4245102	GCAACCTCGGGCATCAACGGCT-(BRIDGE)-CGCCGGGCTGGCCGGGGTGT
17.	embA-embB_W_16_2	4245103	4245242	GCCTGGTATCACTTCCGGATGGACTAC-(BRIDGE)-GGTTCTACGTCGGCAACTACGGGG
18.	embA-embB_W_17_1	4245243	4245382	CGGTGTTCCGTTACCCGCTTTACAC-(BRIDGE)-GCCGGGCACACCGAAGTCAAA
19.	embA-embB_W_18_2	4245383	4245522	GTTCGGACCGGACGGACCGC-(BRIDGE)-CACCGCCAAGGCCAACCTGAC
20.	embA-embB_W_19_1	4245523	4245662	CCGCCATCACCGACTCCGCG-(BRIDGE)-TGGGCGGTATCAGTCCCGTCG
21.	embA-embB_W_20_2	4245663	4245802	ACGGCCACCTCGGCCTGGTA-(BRIDGE)-GGCACCGCCGGAGGGAAGGG
22.	embA-embB_W_21_1	4245803	4245942	CGTCACCGGCCCGGACGGCC-(BRIDGE)-CCAGTTACCGCCCCGCAGCC
23.	embA-embB_W_22_2	4245943	4246082	GCCTATGACCCGAACCTGAGCCCT-(BRIDGE)-GCATCCAGCCACTGGGGCAG
24.	embA-embB_W_23_1	4246083	4246222	CCAGCGACCGTTTTCCGAGCATCT-(BRIDGE)-GAGCAATGGTTCGCCTTCACCCC
25.	embA-embB_W_24_2	4246223	4246362	GCGCACCTCGACGATCGCCA-(BRIDGE)-CGGCATTGCCGAGCTTCCGC
26.	embA-embB_W_25_1	4246363	4246502	GGGGTCGGCCAGGACCGATC-(BRIDGE)-CGTACCTGCGTGGGGACTGGT
27.	embA-embB_W_26_2	4246503	4246642	TGGCTTTGTGTTGTCGGTGGCG-(BRIDGE)-AGGGCGCTGCCATGACACAGT
28.	embA-embB_W_27_1	4246643	4246782	CCGTGCGACGTGGTGCGCGC-(BRIDGE)-ACGCCGCTGCTGCCCGTCGT
29.	embA-embB_W_28_2	4246783	4246922	GTGGTGATCTTGTCCGTGCCGC-(BRIDGE)-CATGCCACCCGCGGGCGGGG
30.	embA-embB_W_29_1	4246923	4247062	CCGACCCCAACCTGCGCCCG-(BRIDGE)-GCGAGCAGGTGACGTCCCCG
31.	embA-embB_W_30_2	4247063	4247202	GGGGCGATCGTGGCCACCGT-(BRIDGE)-CAGATTGTCGGGGTGTTCACCGACC
32.	embA-embB_W_31_1	4247203	4247342	GGCAAGCTGGCGCACCTTCA-(BRIDGE)-CGTCGCACTGATCGCGTTGTGG
33.	embA-embB_W_32_2	4247343	4247482	GGCTACATGTCCAACTATTTCCGCTGGTTC-(BRIDGE)-CCCTGACCGACGCCGTGGTG
34.	embA-embB_W_33_1	4247483	4247622	GCTGCTGTCGCGTGAGGTGCT-(BRIDGE)-GGCAGCCCGGAGGATCCCTT
35.	embA-embB_W_33_1a	4247483	4247622	GCTGCTGTCGCGTGAGGTGCT-(BRIDGE)-GGCAGCCCGGAGGGTCCCTT
36.	embA-embB_W_33_1b	4247483	4247622	GCTGCTGTCGCGTGAGGTGCT-(BRIDGE)-GGCAGCCCGGAGGATCCCTC
37.	embA-embB_W_34_2	4247623	4247762	GCTCGGCTCGCTGGTCACCTATG-(BRIDGE)-GCCCCGCCTCGGGCCGGCGG
38.	embA-embB_W_35_1	4247763	4247902	CCGGCGGCCGCCCGATGCTG-(BRIDGE)-TGCTGATCGAGCGGTCCATGCG
39.	embA-embB_W_35_1a	4247763	4247902	CAGGCGGCCGCCCGATGCTG-(BRIDGE)-TGCTGATCGAGCGGTCCATGCG
40.	embA-embB_W_36_2	4247903	4248042	GAAGCCACCAGGGTTCGCGC-(BRIDGE)-CGGATCTTGGTGCGCCGTCATC
41.	embA-embB_W_37_1	4248043	4248182	GCCTGTTCACCGCGGTGTTCATCA-(BRIDGE)-CAAAATCGGGCCGAGCCAGGC
42.	embA-embB_W_38_2	4248183	4248322	GGCTGTTCGCCGCCGTAGGG-(BRIDGE)-TGTTGCGGCGCAAGCGAATTCC
43.	embA-embB_W_38_2a	4248183	4248322	GGCTGTTCGCCGCCGTAAGG-(BRIDGE)-TGTTGCGGCGCAAGCGAATTCC
44.	embA-embB_W_39_1	4248323	4248462	CCACCAACGGCTGGTGGTATGTCTC-(BRIDGE)-GCGGCGATGGCCGCGCTGAC
45.	embA-embB_W_40_2	4248463	4248602	CCGCGGCGCCGGCGAAGGGC-(BRIDGE)-CAGCTACGGTGTGCCGTTCAACAG
46.	embA-embB_W_41_1	4248603	4248742	GGTCCAACGTGCGGGCGTTT-(BRIDGE)-GGCTGATCCGCGCGCTGACG
47.	embA-embB_W_42_2	4248743	4248882	AACCCGGTCGGCTTCACGCC-(BRIDGE)-GTCGGCGGCTGCGGACTGGC
48.	embA-embB_W_43_1	4248883	4249022	GGTGCCGCTGCCCTATGGGC-(BRIDGE)-CAACGGCGTACCGGAACACACG
49.	embA-embB_W_44_2	4249023	4249162	TGACCGCCGCGGGCAAGATC-(BRIDGE)-TCGATCCCGCCCGGGTACCG
50.	embA-embB_W_45_1	4249163	4249302	GAGCAGCCCAAGGCGTGGCG-(BRIDGE)-GCCGGCAACAGCGTGCTGCA
51.	embA-embB_W_46_2	4249303	4249442	GGACCTGCGCTCACTGCAGGAAT-(BRIDGE)-CAACCTGCGCTTCGCCCGAG
52.	embA-embB_W_47_1	4249443	4249582	CACCGGACTACTCGGCTAAGAAGCTG-(BRIDGE)-ATGTGGGCTCGACGCAGCCG
53.	embA-embB_W_48_2	4249583	4249722	CCCTGCGCAAGTTCGACACCCT-(BRIDGE)-GACACCGACACGTGGGAAGACGG
54.	embA-embB_W_48_2a	4249583	4249722	CCCTGCGCAAGTTCGACACCCT-(BRIDGE)-AACACCGACACGTGGGAAGACGG
55.	embA-embB_W_49_1	4249723	4249862	CGATGTTCGTCATTAGACGGCCCCA-(BRIDGE)-GGTCGATGCCCCTCCCGCCC
56.	embA-embB_W_50_2	4249863	4250002	GCAGGGGTGTTGGGCGCGTC-(BRIDGE)-TCAGTTAGGCCTCCTATGCTGCTCGG
57.	embA-embB_C_1_2	4243053	4243192	GGGCGTCGGGGTAGTAAGGCG-(BRIDGE)-TGCGGGGCCGCGGAGGTTGT
58.	embA-embB_C_2_1	4243193	4243332	CGCGGTTAAGGGCGGTGAGGA-(BRIDGE)-GCAGCGGAACGATGCCGCAC
59.	embA-embB_C_3_2	4243333	4243472	GCGGTGGTTTGGTTCACCGGAA-(BRIDGE)-GGCGATGGCCGAGCAGGGGA

#	Probe name	Start	End	Sequence
60.	embA-embB_C_3_2a	4243333	4243472	GCGGTGGTCTGGTTCACCGGAA-(BRIDGE)-GGCGATGGCCGAGCAGGGGA
61.	embA-embB_C_3_2b	4243333	4243472	GCGGTGGTTTGGTTCACCGGAA-(BRIDGE)-GGCGATGGCCGAACAGGGGA
62.	embA-embB_C_4_1	4243473	4243612	CCGCCGTTGGCGGGCAGCGT-(BRIDGE)-GCCGCCACCGCGGCCACCGA
63.	embA-embB_C_5_2	4243613	4243752	CCGCTGCGATCGTGGAGCGG-(BRIDGE)-AGATGCCGCCAACCTGTGGCT
64.	embA-embB_C_6_1	4243753	4243892	GCTCCGACCTTCAGGTCGGTGA-(BRIDGE)-CCCCACCATGGCTACCAGGACC
65.	embA-embB_C_7_2	4243893	4244032	AGCCGGTCCAGCGCGGCCAG-(BRIDGE)-ATGACATGCCAGAGCAACAAGGTCGC
66.	embA-embB_C_8_1	4244033	4244172	CATCGGACGAGGTGGCGCCG-(BRIDGE)-GCTGGGCAAGCACCGATGTATACCA
67.	embA-embB_C_9_2	4244173	4244312	GGCGGTGCTCACCGCCGCCA-(BRIDGE)-AGCGACCCGGTTGGACGCCA
68.	embA-embB_C_10_1	4244313	4244452	ACCGCACCAGCGGTGAACAC-(BRIDGE)-GGGGCCAGCCGTCCGAGCGC
69.	embA-embB_C_11_2	4244453	4244592	CGATGATGGCTACCGCGGCC-(BRIDGE)-CCAGCAGTCCATCGGTCGCCC
70.	embA-embB_C_12_1	4244593	4244732	GGCCAGCACCGCCAGCGGCG-(BRIDGE)-CAGGAAGTCCTGGTACCAGGCGATG
71.	embA-embB_C_13_2	4244733	4244872	GCTCTCCACGGTAAGGAAGTAGTAGCG-(BRIDGE)-CCGCTGGCCAGCCCCGCCAC
72.	embA-embB_C_14_1	4244873	4245012	CGATCAGTCGCCAGGCCGGG-(BRIDGE)-GGGCAAAGGTGAACGCGGTGA
73.	embA-embB_C_15_2	4245013	4245152	GGTTGCGTCGACTATGTAGACCGATGC-(BRIDGE)-GACGGGCTGGATGTCATACCACGG
74.	embA-embB_C_16_1	4245153	4245292	GTCACCGGGTGGCTGGCGAT-(BRIDGE)-GAGGCCAAGATGCGGTTGCGC
75.	embA-embB_C_17_2	4245293	4245432	GCGACCACCAGCAGTGGCGTA-(BRIDGE)-CACAGCTGGACAGCCCGGTGC
76.	embA-embB_C_18_1	4245433	4245572	CAGCACGTCGTCGGCCATCG-(BRIDGE)-GTCCTCGCCCACGCCCTCGG
77.	embA-embB_C_19_2	4245573	4245712	GAGACCACCGGGTCGGACTTGAG-(BRIDGE)-GCCGCGTGCGACCCGTTGAT
78.	embA-embB_C_20_1	4245713	4245852	GGGTCCAATCCGAACGGCAGC-(BRIDGE)-CCGCGGAAACCACCACCAGC
79.	embA-embB_C_21_2	4245853	4245992	TGTAGGACCAGATGGCGCCGG-(BRIDGE)-GGGTTGCGGTCCGATGTCGATCG
80.	embA-embB_C_22_1	4245993	4246132	AACCGCAGATTGCGCCACGC-(BRIDGE)-AGAGATTCCAGCACCGGAACCCG
81.	embA-embB_C_23_2	4246133	4246272	GCTGACCCGATCAACCGCTGC-(BRIDGE)-TCTGCTTGTGGTCCGGCAGGA
82.	embA-embB_C_24_1	4246273	4246412	TAGGTTCGACGACGCCGCCG-(BRIDGE)-GTACTGCTCCACCGATCCCCAGTC
83.	embA-embB_C_25_2	4246413	4246552	TCGGCCGGCACCAGCCGGTG-(BRIDGE)-ATTTGGGGTGCTTTTGCGTCTGCT
84.	embA-embB_C_26_1	4246553	4246692	GCAAAAGCCCCCAAAATCGCCCG-(BRIDGE)-TGTGGCCAGTCGAGCATCGCG
85.	embA-embB_C_27_2	4246693	4246832	CGCTGCCCAGTTGCCCCCGC-(BRIDGE)-TGCCTTGCTTGGGTGCGGTG
86.	embA-embB_C_28_1	4246833	4246972	AACGCCTGCAAATTGGCGTCCT-(BRIDGE)-GGTAGAGGTGACCTCGATGCGTTGA
87.	embA-embB_C_29_2	4246973	4247112	TTGGCGAAGGTGCCGGCGTG-(BRIDGE)-AGCCCGGGCGGCGCGGGCCC
88.	embA-embB_C_29_2a	4246973	4247112	TTGGCGAAGGTGCCGGCGTG-(BRIDGE)-AGGCCGGGCGGCGCGGGCCC
89.	embA-embB_C_30_1	4247113	4247252	CGATGGTCGCCGAGACCGCC-(BRIDGE)-AGCCCCGCCCGTCCAACTGG
90.	embA-embB_C_31_2	4247253	4247392	GCCTGAGGAGGAGCTGGGCAATTG-(BRIDGE)-GATGACATGCCAGAGCAGGAAGCCG
91.	embA-embB_C_32_1	4247393	4247532	TCGTCCGACGAATTCGCGCC-(BRIDGE)-ATCAGCGCCAGCAGGTTGTAATACCA
92.	embA-embB_C_33_2	4247533	4247672	CTGGCGTCGCTGACATGGGTC-(BRIDGE)-CCGCCCAGTAGGCGGGTTTG
93.	embA-embB_C_33_2a	4247533	4247672	ATGGCGTCGCTGACATGGGTC-(BRIDGE)-CCGCCCAGTAGGCGGGTTTG
94.	embA-embB_C_34_1	4247673	4247812	CGGTCAGCAAGACCATGGCCG-(BRIDGE)-CAGCGCCGCCGGTGTGAGCC
95.	embA-embB_C_35_2	4247813	4247952	AATGCGGCGGTAACGACGGC-(BRIDGE)-GACACCAACGGCAACGTGCCG
96.	embA-embB_C_36_1	4247953	4248092	TGCCGGCGGCCAGCATCGGC-(BRIDGE)-AGTAGTAACGCAGGTTCTCGGTATACCACG
97.	embA-embB_C_37_2	4248093	4248232	CGACGGTGGGCAGGATGAGGT-(BRIDGE)-CCGCCACGCCGGTCCGCGGG
98.	embA-embB_C_37_2a	4248093	4248232	CGACGGTGGGCAGGATGAGGT-(BRIDGE)-CCGCCACGCGGGTCCGCGGG
99.	embA-embB_C_38_1	4248233	4248372	GTGCCGAAGATGACGCCCATCAG-(BRIDGE)-CGCAGCACCGATGGGGATACCA
100.	embA-embB_C_39_2	4248373	4248512	CCATCCGGTTGCGCGACCAG-(BRIDGE)-TGATCCCGTCGATCTTCGGCATCG
101.	embA-embB_C_40_1	4248513	4248652	ACAGGGCGAAAAAGATTGTGCTGACTG-(BRIDGE)-GAAACCGGCCACGATCGGTACCG
102.	embA-embB_C_41_2	4248653	4248792	GCGACGAACACCGCCGCCAT-(BRIDGE)-TTGGTATCAGGCTCGACGAGTACGTCG
103.	embA-embB_C_42_1	4248793	4248932	CAGCGGCTTCATGAAACCCGCA-(BRIDGE)-TGGGTTTCATCACGATCGCCTCGG
104.	embA-embB_C_43_2	4248933	4249072	GTAGTCGGTGCCGGGCTGGT-(BRIDGE)-CTGTGCGCCGGTGGTGTAGG
105.	embA-embB_C_44_1	4249073	4249212	GCCGAGACGAGTGTGCTCTGTTG-(BRIDGE)-AGCACCACAGTCTGCCCGGG
106.	embA-embB_C_45_2	4249213	4249352	GGTCCCGGCATGGCGTATTCG-(BRIDGE)-GGACCGCGACGGCATCGGCG
107.	embA-embB_C_46_1	4249353	4249492	ACAGATCCTCGGCCACCACCC-(BRIDGE)-GGCCAAACCGACCGCCCAGT
108.	embA-embB_C_47_2	4249493	4249632	ATCGGCTGCTGGCACGGGAA-(BRIDGE)-GTGATCCCGAGCAGGCCGCC
109.	embA-embB_C_48_1	4249633	4249772	GGGCCCGCAGCAACAGGTCG-(BRIDGE)-CGCTGCGGGTCGCGGTGCCC
110.	embA-embB_C_49_2	4249773	4249912	CTTGCCCGGTGACCACAGGC-(BRIDGE)-CCAACATGGCCGGCCTGGTG
111.	gyrB-gyrA_W_1_1	4973	5112	CAGGAAGAAAGATGTCCGACGCACG-(BRIDGE)-GGGTCCGCGCGACACCTACG
112.	gyrB-gyrA_W_2_2	5113	5252	TTCGGATCGTGGCTGCCCAGA-(BRIDGE)-GCGCGGTTAGATGGGTAAAAACGAGG
113.	gyrB-gyrA_W_3_1	5253	5392	ACCATCTCATTTGGGAGGTGGTCGAC-(BRIDGE)-AAAAGAAGGCCCAAGACGAATACGGCG
114.	gyrB-gyrA_W_4_2	5393	5532	CGGCATACCGACCGTCGACGT-(BRIDGE)-AACGCGGTCGACGAGGCGAT
115.	gyrB-gyrA_W_4_2a	5393	5532	CGGCATACTGACCGTCGACGT-(BRIDGE)-AACGCGGTCGACGAGGCGAT
116.	gyrB-gyrA_W_5_1	5533	5672	CGAGATCAAGCGCGACGGGTACG-(BRIDGE)-GGTGATGACACAACTACATGCCGGC
117.	gyrB-gyrA_W_6_2	5673	5812	GGAATACGACTTCGAAACCGTCGCC-(BRIDGE)-AGTGGTCTCAGGTTTATGAGAAGTCGGAACC
118.	gyrB-gyrA_W_7_1	5813	5952	TCGGCAAGTGAACGCGCAGC-(BRIDGE)-CGCCGGCTGCAAGAGATGGC
119.	gyrB-gyrA_W_8_2	5953	6092	TTCCGGCAAGGGCACCGGGC-(BRIDGE)-CGAATCCACTGCACCGCACAAAGT
120.	gyrB-gyrA_W_9_1	6093	6232	GCTGACGTCGGTGGTGAACAAGTAC-(BRIDGE)-ACGAGGTGGAGATCGCGATGCA
121.	gyrB-gyrA_W_10_2	6233	6372	CAGACCAAGACCAAGTTGGGCAACAC-(BRIDGE)-GCCAAGGACCGCAAGCTACTGAAG
122.	gyrB-gyrA_W_10_2a	6233	6372	CAGACCAAGACCAAGTTGGGCAACAC-(BRIDGE)-GCCAAGGACCGCAAGCTATTGAAG
123.	gyrB-gyrA_W_11_1	6373	6512	CGCGGCACGTAAGGCACGAG-(BRIDGE)-CGAGGTCAAATCGTTTGTGCAGAAGGTC
124.	gyrB-gyrA_W_12_2	6513	6652	CGGTTCTGCAAAAAGCGGTCGC-(BRIDGE)-AGTTGGTGCGGCGTAAGAGCG
125.	gyrB-gyrA_W_13_1	6653	6792	CCGGGATCCACGACGAGTTCGA-(BRIDGE)-GATTCGATGTTCCAGGCGATACTTCCGC

#	Probe name	Start	End	Sequence
126.	gyrB-gyrA_W_14_2	6793	6932	CGAGAACGGGCATGTGTTTTTGGCAC-(BRIDGE)-TATCGGCAAGCTGCGCTACCACA
127.	gyrB-gyrA_W_15_1	6933	7072	GGAAGACGGCATTCAGCGGTACAAG-(BRIDGE)-AACCGCCGCTGTACAAACTCAAGTG
128.	gyrB-gyrA_W_16_2	7073	7212	ATGGGCGAGGACGTCGACGC-(BRIDGE)-GGTCTAGGTGAAATGGACGCTAAGGAGTTG
129.	gyrB-gyrA_W_17_1	7213	7352	TCGCTCGACCGGATCGAACCG-(BRIDGE)-GCGGCGCAGCTTTATCACCCG
130.	gyrB-gyrA_W_17_1a	7213	7352	TCGCTCGACCGGATCGAACCG-(BRIDGE)-GCGGCGCAGTTTTATCACCCG
131.	gyrB-gyrA_W_18_2	7353	7492	TGCTCTATGCAATGTTCGATTCCGGCTT-(BRIDGE)-GTTGACATCGAGCAGGAGATGCAGC
132.	gyrB-gyrA_W_18_2a	7353	7492	TGCTCTATGCAATGTTCGATTCCGGCTT-(BRIDGE)-GTTGACATCCAGCAGGAGATGCAGC
133.	gyrB-gyrA_W_19_1	7493	7632	GCTGCGCTACCCGCTGGTGG-(BRIDGE)-CCGCCCGGACCGCAGCCACG
134.	gyrB-gyrA_W_20_2	7633	7772	AGGAGACAGTCGATTTCATCCCTAACTACGAC-(BRIDGE)-ACGGCCAGGGCAACTTCGGC
135.	gyrB-gyrA_W_21_1	7773	7912	GCCGACGCGGTGTTCTGGGC-(BRIDGE)-GGCCGGGTGCAAGAGCCGAC
136.	gyrB-gyrA_W_22_2	7913	8052	CAAAACTGGCCGCGGCTCCA-(BRIDGE)-GCTGGAGAATCACGACGCCGAC
137.	gyrB-gyrA_W_22_2a	7913	8052	CAAAACTAGCCGCGGCTCCA-(BRIDGE)-GCTGGAGAATCACGACGCCGAC
138.	gyrB-gyrA_W_23_1	8053	8192	TCCGAGACGGCAAGCTGGCC-(BRIDGE)-TTCGAATGCGCGGAGTTGTTGAGG
139.	gyrB-gyrA_W_23_1a	8053	8192	TCGGAGACGGCAAGCTGGCC-(BRIDGE)-TTCGAATGCGCGGAGTTGTTGAGG
140.	gyrB-gyrA_W_24_2	8193	8332	GCAGACCAGCTTTGGCGCCAA-(BRIDGE)-GGCATTTCCAACATTGAGGACCAGTCTAGC
141.	gyrB-gyrA_W_24_2a	8193	8332	GCAGACCAGCTTCGGCGCCAA-(BRIDGE)-GGCATTTCCAACATTGAGGACCAGTCTAGC
142.	gyrB-gyrA_W_25_1	8333	8472	GGCAAACGAGCGAGCCCACATTC-(BRIDGE)-CATGCTAGCGATCGTCGACGGGG
143.	gyrB-gyrA_W_26_2	8473	8612	CCAGGCCCAGGCAATCCTGGAC-(BRIDGE)-TGCGCGGCCTGGTTAAAGCG
144.	gyrB-gyrA_W_27_1	8613	8752	ATCGTGCGCGACGAACTCGC-(BRIDGE)-ATGCAGTTGCGGCGCCTGGC
145.	gyrB-gyrA_W_28_2	8753	8892	GGGATACGCCAAGCGCACCAAGA-(BRIDGE)-CGAAATCGTGGACAGGCACGGC
146.	gyrB-gyrA_W_29_1	8893	9032	CTTCACCACCCAGGGACGGGTTTAT-(BRIDGE)-CCGATCTGTATCGCAGCCAGAAACG
147.	gyrB-gyrA_W_29_1a	8893	9032	CTTCACCACCCAGGGACGGGTTTAT-(BRIDGE)-CCGACCTGTATCGCAGCCAGAAACG
148.	gyrB-gyrA_W_30_2	9033	9172	ACCGACGCCCCGTACCTGGT-(BRIDGE)-CGGGCCAAGGCCTACGACTTGC
149.	gyrB-gyrA_W_31_1	9173	9312	GTGTTCGGCCGGCGACGACC-(BRIDGE)-GCTGGCCACTCGCAACGGGC
150.	gyrB-gyrA_W_31_1a	9173	9312	GTGTTCGGCCGACGACGACC-(BRIDGE)-GCTGGCCACTCGCAACGGGC
151.	gyrB-gyrA_W_32_2	9313	9452	GCTGCTGTCGCTGAACGTCGTG-(BRIDGE)-TGCTGCTGGTCTCGGCCAACG
152.	gyrB-gyrA_W_33_1	9453	9592	CGGCGCGGCAGGTTGGTTGG-(BRIDGE)-CGTGAAGGCACCTATCTGCTGGTGG
153.	gyrB-gyrA_W_34_2	9593	9732	TGAATCTGGGCGAGGGCGACA-(BRIDGE)-GGCGTTGATTGTCGACGACGACA
154.	gyrB-gyrA_W_35_1	9733	9872	CGTAGCGATCTGAGGAGGAATCGGG-(BRIDGE)-CACTGTTGGCCATCGCGCGC
155.	gyrB-gyrA_W_36_2	9873	10012	CACATCGGGCAGCGACCGGG-(BRIDGE)-CAGCTAGGCTCGGCAGCCGG
156.	gyrB-gyrA_C_1_2	5023	5162	TCTCAGGCCGGGACCGGAGC-(BRIDGE)-CGGGCGCCAGGGCCGATCTT
157.	gyrB-gyrA_C_2_1	5163	5302	GGTCGCACACCACTGTACCGTGAT-(BRIDGE)-TTCGAGAATGGTGATAGACGCAGCGC
158.	gyrB-gyrA_C_3_2	5303	5442	TTGCGGACGGCCTCCAGCCC-(BRIDGE)-ACTACGTTCACTGTGGTTGCATAACCGG
159.	gyrB-gyrA_C_4_1	5443	5582	GACACCGCCATCCTCAAGCAGC-(BRIDGE)-CATACGCGTCCGAGTCGAACTTGC
160.	gyrB-gyrA_C_5_2	5583	5722	CGCCGTGCAGACCACCAGATATCG-(BRIDGE)-CCCTTGCTTGAGGCCCAGGGG
161.	gyrB-gyrA_C_6_1	5723	5862	CCCGTCTTCTTGGTCGGCGC-(BRIDGE)-AGGTTGATGGTCAGCCCCTTGTTGA
162.	gyrB-gyrA_C_7_2	5863	6002	CTTGGGTCACCCTCTCGTCGGTC-(BRIDGE)-CCGGATAGTGAAAGGTGCGGCTCT
163.	gyrB-gyrA_C_8_1	6003	6142	GTTTCACGAAGTCCACCAGGCCAC-(BRIDGE)-CACCGACTCCGAATACCCGGCG
164.	gyrB-gyrA_C_9_2	6143	6282	TGTTGATGGTGTTGGCGAAGGTGTG-(BRIDGE)-TCACCGGTGAGGTTGGGGTCC
165.	gyrB-gyrA_C_10_1	6283	6422	GGCCAGGCCTTCCCGGATATCG-(BRIDGE)-AGTGGGTCAGCTGTTCGTTACAGACC
166.	gyrB-gyrA_C_11_2	6423	6562	GTCGGTGGGGTTGGCTTCAAACC-(BRIDGE)-CTTGCCGGGCAATCCACCGATG
167.	gyrB-gyrA_C_12_1	6563	6702	CGTGGAACGGCAATCGGCCAG-(BRIDGE)-ACATTGATGATCTTGCCGCGCAGC
168.	gyrB-gyrA_C_13_2	6703	6842	CGGTCGATGCGCGCTTTCTCC-(BRIDGE)-CATCGGCGTCGGCCATCAGC
169.	gyrB-gyrA_C_14_1	6843	6982	CAGCGTGGAAATATGTTGGCCGTCAA-(BRIDGE)-TGCGAATTCCGGGTCACTGCG
170.	gyrB-gyrA_C_14_1a	6843	6982	CAGCGTGGAAATATGTTGGCCGTCAA-(BRIDGE)-TGCGAATTCCGGGTCGCTGCG
171.	gyrB-gyrA_C_15_2	6983	7122	TCGCGCTCGCGGTCGGAGTA-(BRIDGE)-GGATCCATGGTGGTCTCCCACAACTC
172.	gyrB-gyrA_C_16_1	7123	7262	ACTTGACGCAACACACGAACCGAG-(BRIDGE)-CATCCAGGAACCGAACATCCTTGGCG
173.	gyrB-gyrA_C_17_2	7263	7402	CAATCGAACGCAGGGTTGCGTTAGA-(BRIDGE)-CTCATCGCATAGTCGATGTAGCTGCGC
174.	gyrB-gyrA_C_18_1	7403	7542	GCGCGCGGCCGACGATCACG-(BRIDGE)-TGGTCTCGGCAACCGACCGG
175.	gyrB-gyrA_C_19_2	7543	7682	CGTGCGGGTGGTAGTTGCCCA-(BRIDGE)-CATCGCCGCCGGTGGGTCAT
176.	gyrB-gyrA_C_19_2a	7543	7682	CGTGCGGGTGGTAGTTGCCCA-(BRIDGE)-CATCCCCGCCGGTGGGTCAT
177.	gyrB-gyrA_C_19_2b	7543	7682	CGTGCGGGTGGTAGTTGCCCA-(BRIDGE)-CATCGTCGCCGGTGGGTCAT
178.	gyrB-gyrA_C_20_1	7683	7822	CAGCCGGGCTTCGGTGTACCT-(BRIDGE)-AGCAGGTTGGGGAACCGGCT
179.	gyrB-gyrA_C_21_2	7823	7962	TGCCGCCTGACCCGTTGGCC-(BRIDGE)-CCATGACCGCGGCCAGGGTC
180.	gyrB-gyrA_C_22_1	7963	8102	GTCCGGGCCTTTAACCCGCC-(BRIDGE)-GGTACGACCGCGGGAATCCTCT
181.	gyrB-gyrA_C_23_2	8103	8242	GGCAACTCGGTGATCACCAGCGA-(BRIDGE)-ATGCGTAAACCGACCCGATCGCT
182.	gyrB-gyrA_C_24_1	8243	8382	GCATCGCGCTTGATCTCGATGACG-(BRIDGE)-GCTGGTCCAGCCGCAGCGTG
183.	gyrB-gyrA_C_25_2	8383	8522	AGTTGGTGGTCAACGTAATAGCGGATCA-(BRIDGE)-CAGTGCAATGACCTCGTCCAGCG
184.	gyrB-gyrA_C_26_1	8523	8662	ACGGTCTCCGACGCCCGGAT-(BRIDGE)-TCGTCGATGATGCGCTGGCG
185.	gyrB-gyrA_C_27_2	8663	8802	CTCGGCCTCGATTTTGGCCAGG-(BRIDGE)-CCGCGATGATCCGGGTACGC
186.	gyrB-gyrA_C_28_1	8803	8942	CGTCGCTGACGTCTCCGTCGG-(BRIDGE)-CGCACCCTGCACGCCCTTGC
187.	gyrB-gyrA_C_28_1a	8803	8942	CGTCGCTGACGTCTCCGTCGG-(BRIDGE)-CGCACCCTGCAC**T**CCCTTGC
188.	gyrB-gyrA_C_29_2	8943	9082	CGACGATGTCGTCCTGCTTCAACCC-(BRIDGE)-TGCCCGCGCGCCGTCCGGGA
189.	gyrB-gyrA_C_30_1	9083	9222	GGCTAACAGGTTGGCCACGTGC-(BRIDGE)-CGAAGTCGGTCAGCTTGGACTTTTTCAC
190.	gyrB-gyrA_C_31_2	9223	9362	TCCGCCCGAGCGATTGGAGT-(BRIDGE)-GTCGGTCGCCGAGAACCTGATGG
191.	gyrB-gyrA_C_32_1	9363	9502	CCCATTGGCCGCAGCGCCTC-(BRIDGE)-CGTTTCGCATAGCCCCCTGACG

#	Probe name	Start	End	Sequence
192.	gyrB-gyrA_C_33_2	9503	9642	ACCGGGTATTCCTCGATCGCGGTA-(BRIDGE)-CGCCGGAAGTGACGGCATACAG
193.	gyrB-gyrA_C_34_1	9643	9782	CGCGGTGCGGATCACGCCAC-(BRIDGE)-GGCATTATCGTCGCCACTTTCTTCGG
194.	gyrB-gyrA_C_35_2	9783	9922	TCTGCGCCGTTGGCGTCCAC-(BRIDGE)-TGCAGTCACCCCGACTCCTAACAC
195.	rpoB_W_1_1	759637	759776	ACCGCTCCTCTAAGGGCTCTCGT-(BRIDGE)-GTGGTCTTAGTCTGAGCCCAGTTTGCG
196.	rpoB_W_2_2	759777	759916	GCCAAACCGGGTCTCCTTCGCTAA-(BRIDGE)-TGGTCGCATGAAGTGCTGGAAGGA
197.	rpoB_W_3_1	759917	760056	TGGGTGGCCTGGAAGAGGTGC-(BRIDGE)-GCTGCGCGAACCACTTGAGGT
198.	rpoB_W_4_2	760057	760196	GCGGCTCCACTGTTCGTCACC-(BRIDGE)-TCTACGAGCTGTCTCCGATCGAGGA
199.	rpoB_W_4_2a	760057	760196	GCGGCTCCGCTGTTCGTCACC-(BRIDGE)-TCTACGAGCTGTCTCCGATCGAGGA
200.	rpoB_W_4_2b	760057	760196	GCGGCCCCACTGTTCGTCACC-(BRIDGE)-TCTACGAGCTGTCTCCGATCGAGGA
201.	rpoB_W_5_1	760197	760336	AGCCAGCTGGTGCGGTCGCC-(BRIDGE)-GCCGAGTTCATCAACAACAACACCGG
202.	rpoB_W_6_2	760337	760476	CGTGCGCATCGACCGCAAAC-(BRIDGE)-CGGGGTGTACTTCGACGAGACCAT
203.	rpoB_W_6_2a	760337	760476	GGTGCGCATCGACCGCAAAC-(BRIDGE)-CGGGGTGTACTTCGACGAGACCAT
204.	rpoB_W_7_1	760477	760616	CCGACGAGGCGCTGTTGGAC-(BRIDGE)-GCCGGCAACCGGTCACCGTG
205.	rpoB_W_7_1a	760477	760616	CCGACGAGGCGCTGCTGGAC-(BRIDGE)-GCCGGCAACCGGTCACCGTG
206.	rpoB_W_8_2	760617	760756	GGTCAACAAGAAGCTCGGGCTGCA-(BRIDGE)-ATCTACCGCAAGCTGCGTCCGG
207.	rpoB_W_9_1	760757	760896	TGCCGGTGGAAACCGACGACA-(BRIDGE)-TGTCGGCGAGCCCATCACGT
208.	rpoB_W_10_2	760897	761036	GAGGCGATCACACCGCAGACG-(BRIDGE)-TCGACCACTTCGGCAACCGCC
209.	rpoB_W_10_2a	760897	761036	GAGGCGATCACACCGC**G**GACG-(BRIDGE)-TCGACCACTTCGGCAACCGCC
210.	rpoB_W_11_1	761037	761176	GCGCTGGGGCCCGGCGGTCT-(BRIDGE)-TTGATCAACATCCGGCCGGTGGT
211.	rpoB_W_11_1a	761037	761176	GCGC**C**GGGGCCCGGCGGTCT-(BRIDGE)-TTGATCAACATCCGGCCGGTGGT
212.	rpoB_W_12_2	761177	761316	CGCGCGGGTCAACCCGTTCG-(BRIDGE)-GTCACGTGAGCGTGCCGGGC
213.	rpoB_W_13_1	761317	761456	GCGGACGGTCGCTTCGTCGAG-(BRIDGE)-GGTTCATCGAAACGCCGTACCGC
214.	rpoB_W_13_1a	761317	761456	GCGGACGGTCGCTTCGTCGAG-(BRIDGE)-GGTTCATCGAAACGCCGTACC**C**C
215.	rpoB_W_14_2	761457	761596	CCTGGAGCACGACGACGCCAA-(BRIDGE)-CCGCGCGTGCTGGTCCGCCG
216.	rpoB_W_15_1	761597	761736	CGCCGAAGAAAGCGGCGTCA-(BRIDGE)-CCGTGCCCTCATGGGGGCAA
217.	rpoB_W_16_2	761737	761876	TGGACGCGGGCGACCGAGTC-(BRIDGE)-TCGAGGAGGTGTCGGCCGAC
218.	rpoB_W_17_1	761877	762016	CCTGTCCAACCGCCTGGTCGA-(BRIDGE)-GAGGCCGGTCAGGTGATCGCC
219.	rpoB_W_17_1a	761877	762016	CCCGTCCAACCGCCTGGTCGA-(BRIDGE)-GAGGCCGGTCAGGTGATCGCC
220.	rpoB_W_17_1b	761877	762016	CCTCTCCAACCGCCTGGTCGA-(BRIDGE)-GAGGCCGGTCAGGTGATCGCC
221.	rpoB_W_18_2	762017	762156	ACCTGGATGAGCGGGGCATCG-(BRIDGE)-AGAGGACGTGCTCACCTCGATCCA
222.	rpoB_W_18_2a	762017	762156	ACCTGGATGAGCGGGGCATCG-(BRIDGE)-AGAGGACGTGCTGACCTCGATCCA
223.	rpoB_W_19_1	762157	762296	GCGAGGTGCGCGACACTTCG-(BRIDGE)-TGCGCATCGGTGCCGAGGTT
224.	rpoB_W_20_2	762297	762436	AGAAACGCAAGATCTCCGACGGTGA-(BRIDGE)-CTGAAGGTGCCGCACGGCGA
225.	rpoB_W_20_2a	762297	762436	AGAAACGCAAGATCTCCGACGGCGA-(BRIDGE)-CTGAAGGTGCCGCACGGCGA
226.	rpoB_W_21_1	762437	762576	CGCGACGGATGAACATCGGCC-(BRIDGE)-CAAGCTGGCCGGCCGGCACG
227.	rpoB_W_22_2	762577	762716	GCCATTGTGTCGACGCCGGTG-(BRIDGE)-AGATTTTGGAGACCCACCTGGGTTGG
228.	rpoB_W_23_1	762717	762856	GAGCCGTTCCCGTACCCGGT-(BRIDGE)-TTCGACGGCGCCCAGGAGGC
229.	rpoB_W_24_2	762857	762996	CGGTGGCCAGCGGTTCGGGG-(BRIDGE)-CACGGTTGGCTACATGTACATCATGAAGC
230.	rpoB_W_24_2a	762857	762996	CGGTGGGCAGCGGTTCGGGG-(BRIDGE)-CACGGTTGGCTACATGTACATCATGAAGC
231.	rpoB_W_25_1	762997	763136	AGAACATCCCGGAGCCGGGC-(BRIDGE)-AGATGGAGTGCTGGGCCATGCA
232.	rpoB_W_25_1a	762997	763136	AGAACACCCCGGAGCCGGGC-(BRIDGE)-AGATGGAGTGCTGGGCCATGCA
233.	rpoB_W_26_2	763137	763276	CGGGCCGCGGCCAACCTGGG-(BRIDGE)-ATCCCCGAGTCGTTCAAGGTGCTG
234.	rpoB_W_27_1	763277	763416	CGATGAACTCCGCATCGGTCTTGCTAC-(BRIDGE)-AATCAATCTGTCCCGCAACGAATCCGC
235.	rpoB_C_1_2	759687	759826	GGCGAACGATCTGTCCGGATCTCA-(BRIDGE)-CTCTGGCGGGAATCTGCCAAGATGC
236.	rpoB_C_2_1	759827	759966	TCGGACTAGGACTAGCGGCTGTTTTG-(BRIDGE)-AATCGGTCTGGACGTCAAGGAGTCC
237.	rpoB_C_3_2	759967	760106	CGAACCGATCAGCCACTCGAACG-(BRIDGE)-CGACAACGACATCGACCCGGAGA
238.	rpoB_C_4_1	760107	760246	GACATCGTCGAAACGAGGGTCAGAGAA-(BRIDGE)-AACACCGTCTGACTCTTGATCTCACCG
239.	rpoB_C_4_1a	760107	760246	GACATCGTCGAAACGAGGATCAGAGAA-(BRIDGE)-AACACCGTCTGACTCTTGATCTCACCG
240.	rpoB_C_5_2	760247	760386	CGGTCATCATCGGGAAGTCACCCATG-(BRIDGE)-GCAGCGTCTTGTCGGTGGACTTG
241.	rpoB_C_6_1	760387	760526	GCTCGGGATCACCTTGACGCTGT-(BRIDGE)-CTCGCTGGTCCAGCCCAGCG
242.	rpoB_C_6_1a	760387	760526	GCCCGGGATCACCTTGACGCTGT-(BRIDGE)-CTCGCTGGTCCAGCCCAGCG
243.	rpoB_C_6_1b	760387	760526	GCTGGGGATCACCTTGACGCTGT-(BRIDGE)-CTCGCTGGTCCAGCCCAGCG
244.	rpoB_C_7_2	760527	760666	GAACCCGAACCGCTCGACAATCTG-(BRIDGE)-TGCGCTGACTCTTTGGTCGGGG
245.	rpoB_C_7_2a	760527	760666	GAACCCGAACCGCTCGACAATCTG-(BRIDGE)-TGCGCTGACTCTTTGGTCGGCG
246.	rpoB_C_8_1	760667	760806	TCCTTGAAGAACAAGTTTTCCAACAGCGTC-(BRIDGE)-CCACGACGTCTTCTTCGGTCAGCG
247.	rpoB_C_9_2	760807	760946	GCAAGCGGACCAGATATTCGATGGTGG-(BRIDGE)-TTGGATCAGCTCGCCGACCGT
248.	rpoB_C_10_1	760947	761086	ACATGCCGACCCGGATCTGGTT-(BRIDGE)-GTGCCGAAGAACTCCTTGATCGCG
249.	rpoB_C_10_1a	760947	761086	ACATGCCGACCCGGATCTGGTT-(BRIDGE)-GTGCCGAAGAACGCCTTGATCGCG
250.	rpoB_C_11_2	761087	761226	GTCCATGAATTGGCTCAGCTGGCTG-(BRIDGE)-AGTGCGACGGGTGCACGTCG
251.	rpoB_C_11_2a	761087	761226	GTCCATGAATTGGCTC**G**GCTGGCTG-(BRIDGE)-AGTGCGACGGGTGCACGTCG
252.	rpoB_C_11_2b	761087	761226	GT**A**CATGAATTGGCTCAGCTGGCTG-(BRIDGE)-AGTGCGACGGGTGCACGTCG
253.	rpoB_C_11_2c	761087	761226	G**C**CCATGAATTGGCTCAGCTGGCTG-(BRIDGE)-AGTGCGACGGGTGCACGTCG
254.	rpoB_C_11_2d	761087	761226	G**A**CCATGAATTGGCTCAGCTGGCTG-(BRIDGE)-AGTGCGACGGGTGCACGTCG
255.	rpoB_C_11_2e	761087	761226	GTCCATGAATTGGCTCAGCTGGCTG-(BRIDGE)-AGTGCGACG**C**GTGCACGTCG
256.	rpoB_C_12_1	761227	761366	GATCGGGCACATCCGGCCGT-(BRIDGE)-GTCGCTAACCACGCCGTCGAC
257.	rpoB_C_12_1a	761227	761366	GATCGGGCACATCCGGCCGT-(BRIDGE)-GTCGCTAACCACG**A**CGTCGAC

#	Probe name	Start	End	Sequence
258.	rpoB_C_12_1b	761227	761366	GATCGGGCACATCCGGCCGT-(BRIDGE)-GTCGCTAACCACGC**A**GTCGAC
259.	rpoB_C_13_2	761367	761506	TCGGCGGTCAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTACTCCACCTCGC
260.	rpoB_C_13_2a	761367	761506	TCGGCGGTCAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTAC**G**CCACCTCGC
261.	rpoB_C_13_2b	761367	761506	TCGGCGGTCAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTACTCCACCTCGC
262.	rpoB_C_13_2c	761367	761506	TCGGCGGTCAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTACTCCACCTCGC
263.	rpoB_C_13_2d	761367	761506	TCGGCGG**C**CAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTACTCCACCTCGC
264.	rpoB_C_13_2e	761367	761506	TCGGCGG**A**CAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTACTCCACCTCGC
265.	rpoB_C_13_2f	761367	761506	TCGGCGGTCAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTACTCCA**T**CTCGC
266.	rpoB_C_13_2g	761367	761506	TCGGCG**C**TCAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTACTCCACCTCGC
267.	rpoB_C_13_2h	761367	761506	TCGGCG**A**TCAGGTACACGATCTC-(BRIDGE)-GAGGGCACGTACTCCACCTCGC
268.	rpoB_C_14_1	761507	761646	CGAGACGTCCATGTAGTCCACCTCAGAC-(BRIDGE)-GGACCAGCGGCACCGCCTGG
269.	rpoB_C_15_2	761647	761786	CACCAGCGGGGCCTCGCTAC-(BRIDGE)-GGTGCCGTTGTCGTGCATCACA
270.	rpoB_C_16_1	761787	761926	GCGCATCCGGTAGGTACGCCG-(BRIDGE)-ATCTCGCCGTCGTCAGTACAGGG
271.	rpoB_C_17_2	761927	762066	GCAGGTTCTTGCCCAGCGCC-(BRIDGE)-GAGCATCGATCTCATGCTCCTCGATGT
272.	rpoB_C_18_1	762067	762206	CGCACCCAGCTTGGTGTCGC-(BRIDGE)-GACCTTGCCGACCAGGATGTCCC
273.	rpoB_C_18_1a	762067	762206	CGCACCCAGCTTGGTGTCGC-(BRIDGE)-GACCTTGCCGACCAGGATGTCGC
274.	rpoB_C_19_2	762207	762346	GCTCGGTCTCACCCTTCGGGGT-(BRIDGE)-AACACCCGAATGCCGATCACCTTGC
275.	rpoB_C_20_1	762347	762486	CGTCCTCGTCCTCGCGGGAA-(BRIDGE)-GCAGGATCTTGCCGATCACGCC
276.	rpoB_C_21_2	762487	762626	CAAGGAACGGCATGTCCTCAACCG-(BRIDGE)-GACCTTCCAGCCGCTGTGGGC
277.	rpoB_C_22_1	762627	762766	GGAACCCCCTTGGCGGCGTC-(BRIDGE)-AGCGTGCACGACAACAGGCC
278.	rpoB_C_23_2	762767	762906	CGTCACCGTCGCGGTTGGGC-(BRIDGE)-TGTCGTCCACCAGGTGGTGCA
279.	rpoB_C_24_1	762907	763046	GGTGGAGCGGGCGTGGATCT-(BRIDGE)-CTGCAGGGTGTAGGCAGCACCG
280.	rpoB_C_24_1a	762907	763046	GGTGGAGCGGGCGTGGATCT-(BRIDGE)-CTGCAGGGTGTAGGCGGCACCG
281.	rpoB_C_24_1b	762907	763046	GGTGGAACGGGCGTGGATCT-(BRIDGE)-CTGCAGGGTGTAGGCAGCACCG
282.	rpoB_C_25_2	763047	763186	TGTCATCGGACTTGATGGTCAACAGCTC-(BRIDGE)-AGGCACAGCGACTGCAGTTCTTTG
283.	rpoB_C_25_2a	763047	763186	TGTCGTCGGACTTGATGGTCAACAGCTC-(BRIDGE)-AGGCACAGCGACTGCAGTTCTTTG
284.	rpoB_C_26_1	763187	763326	CGTCACTCGATAGCACCTCGACGTTG-(BRIDGE)-TTTACGCAAGATCCTCGACACTTGCGG
285.	rpoB_C_27_2	763327	763466	CCCTAACGGGTTTAGTAATTTTGCGACAGC-(BRIDGE)-TCTCCGGCTTTTTGACCTCGCCA
286.	mabA_inhA_W_1_1	1673100	1673239	CGCGACATACCTGCTGCGCAA-(BRIDGE)-AAGGCAGAAGCCGAGTAGCCGG
287.	mabA_inhA_W_2_2	1673240	1673379	CCCGCCGGAAATCGCAGCCA-(BRIDGE)-TTCGTAGGGCGTCAATACACCCGC
288.	mabA_inhA_W_3_1	1673380	1673519	GGTTACCGGAGGAAACCGGGGGAT-(BRIDGE)-CGTTACGCTCGTGGACATACCGATTTC
289.	mabA_inhA_W_4_2	1673520	1673659	CGTCGATCGCGCCTTCACGG-(BRIDGE)-CGGGCTGGCGATCGCACAGC
290.	mabA_inhA_W_5_1	1673660	1673799	CCGGGGCGTTCCGGGTGGCT-(BRIDGE)-CGGTAGAAGAGCACCAGGGTCCG
291.	mabA_inhA_W_6_2	1673800	1673939	TGATTGGCATGGCCCGCTCGAT-(BRIDGE)-CAACGGGCATCGCGCAGCAT
292.	mabA_inhA_W_7_1	1673940	1674079	AGCGAAGCGGGTCGGCACCC-(BRIDGE)-CGCCCGCGAGCTGTCGAAGG
293.	mabA_inhA_W_8_2	1674080	1674219	CGCACATGACAGGACTGCTGGAC-(BRIDGE)-CCGCCGAGGTCGCCGGGGTG
294.	mabA_inhA_W_9_1	1674220	1674359	CTGATTCAGCGCATCACCGACCG-(BRIDGE)-GGCAAACGGATTCTGGTTAGCGGAATC
295.	mabA_inhA_W_10_2	1674360	1674499	TGCATTCGATTGGGTTCATGCCGC-(BRIDGE)-GCTGCCGGCAAAGGCCCCGC
296.	mabA_inhA_W_11_1	1674500	1674639	CCCGGAGGTTCCATCGTCGGC-(BRIDGE)-AGACCGGGATGGGCATCAACCC
297.	mabA_inhA_W_12_2	1674640	1674779	AATCTCGTTGCCGCAGGCCC-(BRIDGE)-ATGGACTTCGACCCGAGCCGG
298.	mabA_inhA_W_13_1	1674780	1674919	GGATGCGACGCCGGTCGCCA-(BRIDGE)-TATCCGGACGCTGGCGATGAGTG
299.	mabA_inhA_W_14_2	1674920	1675059	GCTGTCGTTCGGCGGACCGG-(BRIDGE)-AGACGGTGTGCGCGCTGCTG
300.	mabA_inhA_W_15_1	1675060	1675199	ACCGATCAATGGCATTAATCGCACACTG-(BRIDGE)-AAGGGCCCGAGCAGGTGCGG
301.	mabA_inhA_C_1_2	1673150	1673289	AATTGCGTGCAAAAGCGCTGTGG-(BRIDGE)-CCTTTCTGGGCAGCGAGGCC
302.	mabA_inhA_C_2_1	1673290	1673429	TCAGCACACTTCGACCATGACGGATC-(BRIDGE)-TATCGTCTCGCCGCGGCCGG
303.	mabA_inhA_C_2_1a	1673290	1673429	TCAGCACACTTCGACCATGACGGATC-(BRIDGE)-TATCATCTCGCCGCGGCCGG
304.	mabA_inhA_C_3_2	1673430	1673569	TGTGGCAGTCACCCCGACAACC-(BRIDGE)-CGGCCACCTTGTGGCCGTCG
305.	mabA_inhA_C_3_2a	1673430	1673569	TGTGGCAGTCACCCCGACATCC-(BRIDGE)-CGGCCACCTTGTGGCCGTCG
306.	mabA_inhA_C_4_1	1673570	1673709	GCTCCGGATCCACGGTGGGTGA-(BRIDGE)-GCCGGCGTTGGACACCAGCA
307.	mabA_inhA_C_5_2	1673710	1673849	GCATGAGGAATGCGTCCGCGGATAG-(BRIDGE)-AATATCATTCGACCGAATTTGTTGCGCTGC
308.	mabA_inhA_C_6_1	1673850	1673989	AGCTGCCGGAGACCGAACCTATG-(BRIDGE)-CCGGGGCCACCACATTCGCG
309.	mabA_inhA_C_7_2	1673990	1674129	GCGGGTCATATCGGTGTCGATGTAGC-(BRIDGE)-GCTCGCATCCTCGGAAGCCAGG
310.	mabA_inhA_C_8_1	1674130	1674269	CCGGGATGACCGCACCGGAGATATA-(BRIDGE)-AACGCGATCGACGAGTCGGTGA
311.	mabA_inhA_C_8_1a	1674130	1674269	CCGGGATGACCGCACCGGAGATATA-(BRIDGE)-AACGCGGTCGACGAGTCGGTGA
312.	mabA_inhA_C_9_2	1674270	1674409	TGGGCTACCCGTGCGATGTGA-(BRIDGE)-GCTCCTCGTTTTGCACGTCGAGTT
313.	mabA_inhA_C_10_1	1674410	1674549	GCCGGCCAAGCTGGCCAGGT-(BRIDGE)-CACATCCGCGTAGGGCGCGT
314.	mabA_inhA_C_11_2	1674550	1674689	GCCGAGATGTGGATGCCCTTGGA-(BRIDGE)-ACCGTCATCCAGTTGTAGGCCGG
315.	mabA_inhA_C_12_1	1674690	1674829	ACTCCAACGCGCTCTTGGCG-(BRIDGE)-CCTCGCCGAGCGCACCGCCG
316.	mabA_inhA_C_13_2	1674830	1674969	CTGGATCTGGGCGCCGGCCT-(BRIDGE)-GTCACCCGTGGTCGCCGGCA
317.	mabA_inhA_C_14_1	1674970	1675109	GCCGCCGTCGGCGTAGATGAT-(BRIDGE)-GCGGCCCCGGGTAACGTTCT
318.	katG_W_1_1	2156311	2156171	GGGGTCTATGTCCTGATTGTTCGATATCCG-(BRIDGE)-CCGGTCTTGCGGGGTTATCGC
319.	katG_W_2_2	2156171	2156031	GCTGTCCCGTCGTGGGTCATATGAA-(BRIDGE)-ACACTTCGCGATCACATCCGTGATCA
320.	katG_W_3_1	2156031	2155891	GAGGTCGCGACCATCGACGTTG-(BRIDGE)-ATACCCCGTCGAGGGCGGCG
321.	katG_W_4_2	2155891	2155751	GCATCCACGACGGCCGCGGC-(BRIDGE)-ACGCCCTGACGCGGGACATC
322.	katG_W_5_1	2155751	2155611	GCTCTCATGGGCGGACCTGATTGTTTT-(BRIDGE)-GGCGCCGGGGGCGGCATGCA
323.	katG_W_6_2	2155611	2155471	GCGATGAGCGTTACAGCGGTAAGC-(BRIDGE)-CGCCGGCAACTGCGCGCTGG

#	Probe name	Start	End	Sequence
324.	katG_W_7_1	2155471	2155331	GCGCATGGCCATGAACGACGTC-(BRIDGE)-GGGATCTGGAGAACCCGCTGGC
325.	katG_W_8_2	2155331	2155191	TGGAAGAGCTCGTATGGCACCGG-(BRIDGE)-GAAACAGCGGCGCTGATCGTCG
326.	katG_W_9_1	2155191	2155051	CCTGCTGGCGCTTGGCAATACA-(BRIDGE)-AACCGGTAAGGACGCGATCACCA
327.	katG_W_10_2	2155051	2154911	CGCGTCGCTGGCTGGAACAC-(BRIDGE)-CCGCCAAGGACGGCGCCGGT
328.	katG_W_11_1	2154911	2154771	CCGGTCCCTGCGGTCAGCCA-(BRIDGE)-CCCGAGGAATTGGCCGACGAGT
329.	katG_W_12_2	2154771	2154631	CAAGCGCGGCGGCGCCAACG-(BRIDGE)-CGACCTCGTCGGCGAAGCCG
330.	katG_W_13_1	2154631	2154491	GCCGGGGAACATCAAAGTGTCCTTC-(BRIDGE)-GTGGTCGCATCCGCCTGCAG
331.	katG_W_14_2	2154491	2154351	CGACGTGGAATCCTTTGCCGTGCT-(BRIDGE)-GCCGACCTCGTCGTGCTCGG
332.	katG_W_15_1	2154351	2154211	GGTAGGTGGCCTGCGCGTCC-(BRIDGE)-GGAGCCCAAGGCAGATGGCTTCC
333.	katG_W_16_2	2154211	2154071	CAGATGACGGGACCTACCAGGGC-(BRIDGE)-TCGGCGCAAACTACAAGCGCTT
334.	katG_W_17_1	2154071	2153931	CGTGCAGGACTTCGTCGCTGC-(BRIDGE)-AAGGATGGCAGTGGCAAGGTGAAGT
335.	katG_W_18_2	2153931	2153791	CTGGTGTTTGCCCGGCGCGA-(BRIDGE)-CTGGGACAAGGTGATGAACCTCGACA
336.	katG_C_1_2	2156261	2156121	GGTCCGAGGCCGTCAGACAGG-(BRIDGE)-CCAGGAGTTGGTGTTATCGGGCTGT
337.	katG_C_2_1	2156121	2155981	GTTGCTCGGGCACAGCATTCCTT-(BRIDGE)-TGAGCCGGTTGGGCCACCAG
338.	katG_C_3_2	2155981	2155841	CCGGGTTTTGGTGCAGTACCTTCAGAT-(BRIDGE)-CCACGGCTGCGAGGTGGTCA
339.	katG_C_4_1	2155841	2155701	TGGCCGTAGTCGGCGGGCCA-(BRIDGE)-TCGGGCCAGCTGTTAAGCGGC
340.	katG_C_5_2	2155701	2155561	CGCCTTGTCCAAGCTGGCGTTG-(BRIDGE)-CGAACCCGAACGTCTTGAAGCCC
341.	katG_C_6_1	2155561	2155421	CTGGTCGACCCGGCCGAAGC-(BRIDGE)-CACGTAGATCAGCCCCATCTGCACC
342.	katG_C_7_2	2155421	2155281	CCGTTCGGCCCCTCCGGGTT-(BRIDGE)-CCATGGGTCTTACCGAAAGTGTGACCG
343.	katG_C_7_2a	2155421	2155281	CCGTTCGGCCTCTCCGGGTT-(BRIDGE)-CCATGGGTCTTACCGAAAGTGTGACCG
344.	katG_C_8_1	2155281	2155141	CCAGATCGGCCGGGCCGGCG-(BRIDGE)-TGTTCGTCCATACGACCTCGATGCC
345.	katG_C_8_1a	2155281	2155141	CCAGATCGGCCGGGTCGGCG-(BRIDGE)-TGTTCGTCCATACGACCTCGATGCC
346.	katG_C_9_2	2155141	2155001	GAAACTGTTGTCCCATTTCGTCGGGG-(BRIDGE)-CCCGCCGAACGGGTCCGGGA
347.	katG_C_10_1	2155001	2154861	ATCGTCGGGGAGCGCCCTGG-(BRIDGE)-TGGATCAGCTTGTACCAGGCCTTGG
348.	katG_C_11_2	2154861	2154721	CGCAACGGGACCCATGTCTCGG-(BRIDGE)-CCCGGATCTGGCTCTTAAGGCTGG
349.	katG_C_11_2a	2154861	2154721	CGCAACGGGACCCATGTCTCGG-(BRIDGE)-CCAGGATCTGGCTCTTAAGGCTGG
350.	katG_C_12_1	2154721	2154581	AACTAGCTGTGAGACAGTCAATCCCGATG-(BRIDGE)-GGGGTCGTTGACCTCCCACCC
351.	katG_C_13_2	2154581	2154441	TGACCTTGCGCAGATCCCCGTC-(BRIDGE)-TTTGCTGCTTTCTCTATGGCGGCAC
352.	katG_C_14_1	2154441	2154301	TGATGTTGTGGCCAGCCGCC-(BRIDGE)-ACGGGTTGCCCTTTCCGAGGT
353.	katG_C_15_2	2154301	2154161	GCAGCATGTACTCGGCCGGCA-(BRIDGE)-GGAGGCCTCGGTGAACACGC
354.	katG_C_16_1	2154161	2154021	TCACGAAGAAGTCGTTGGTCAGTGACTC-(BRIDGE)-ACCAGGTCCACGCGGCTGCC
355.	katG_C_17_2	2154021	2153881	CGCAACTCCGAGTTGGACCCGAAG-(BRIDGE)-ACCCGAATCAGCGCACGTCG
356.	katG_C_18_1	2153881	2153741	TCGGCGGGCAGGGCCGATCA-(BRIDGE)-ATCCCCGTCTCGTCGTGCCTG
357.	ddl_W_1_1	3338117	3337977	TGAGCCTCGCACGGGCCGGC-(BRIDGE)-CTGGCGTCCAGCTACGACGTCG
358.	ddl_W_2_2	3337977	3337837	GCAGCAACGAGCACGCCATCTC-(BRIDGE)-ACGACCGAAAACTGCAGCTCGTG
359.	ddl_W_3_1	3337837	3337697	TGACGATCACCAACCGGGAGCTTC-(BRIDGE)-GTGTGTGTCCGCCGGCAGCA
360.	ddl_W_4_2	3337697	3337557	TCCCGGTACTGCACGGCCCG-(BRIDGE)-CTCAGGTCAAATCAGGATCGGGCACC
361.	ddl_W_5_1	3337557	3337417	CGCCGATGGACTTCCGGTGGG-(BRIDGE)-TACGGCGAGGACGGCACGAT
362.	ddl_W_6_2	3337417	3337277	CGGGTGTCGAGTTGGGATCAACTGC-(BRIDGE)-TGCGTACGCGGTGCTGCGTC
363.	ddl_W_7_1	3337277	3337137	CGCTGGGGGAGATCCGGGTG-(BRIDGE)-CCGCCGCGGTCGCGCGGGCC
364.	ddl_W_8_2	3337137	3336997	CTGGCGATCCGGGCGTTCGC-(BRIDGE)-GCCGGGGTGCGGGGACGCGA
365.	ddl_W_9_1	3336997	3336857	GGCGGCCAGCGGTGTCGACT-(BRIDGE)-GGCTATCGACTGCCGGGGTCT
366.	ddl_C_1_2	3338067	3337927	CCACCGACAGCCCTTTATGACAGACC-(BRIDGE)-GGCTACCGGGTCAGGCAGACG
367.	ddl_C_2_1	3337927	3337787	GGTCGTTAGCACTCACAACCTGCAGA-(BRIDGE)-CGAACCGCCGCGAGTCCAGG
368.	ddl_C_3_2	3337787	3337647	GGTGATACCCACCGCGATCACGT-(BRIDGE)-CGGATCGGCCGGCAGCGCCA
369.	ddl_C_4_1	3337647	3337507	ACCAACTGGCCACCACGCCG-(BRIDGE)-GGCACCCCGGCGAGTTCGAG
370.	ddl_C_5_2	3337507	3337367	GCACACCGGCGCCCACGTAG-(BRIDGE)-ACTCCTGGCGGTGCAGTGTCG
371.	ddl_C_6_1	3337367	3337227	CGGTAAGCCCAGCCGTTCGC-(BRIDGE)-CTCGACGATGACCTTAGGGTCATGCC
372.	ddl_C_7_2	3337227	3337087	TCGCGGCCGCTGATCGCGGC-(BRIDGE)-TACTTGGTTGCGAAGTCGTAGAAAGAGTCC
373.	ddl_C_8_1	3337087	3336947	CCAATTCGGCTGCGTCGTCGAGA-(BRIDGE)-CGTCGGTGAGGAAGAAGTCCACCC
374.	ddl_C_9_2	3336947	3336807	TTGATCTCGTTGATCACCGGACCGT-(BRIDGE)-CACGCCGCGGGCCAATGTCG
375.	ddl_C_9_2a	3336947	3336807	TTGATCTCGTTGATCACCGGACCGT-(BRIDGE)-CACGCCGCGGGCCAATGCCG
376.	oxyR-ahpC_W_1_1	2726940	2726800	CGCGGCCTTGAGCTTTTCTATACTCATTGATT-(BRIDGE)-CGCTGCGGCGCTGGCCAGCA
377.	oxyR-ahpC_W_2_1	2726800	2726660	GCACTCGCAGTACCTCATCGACGTT-(BRIDGE)-CCCGGCCAACCAGATCCCGG
378.	oxyR-ahpC_W_3_1	2726660	2726520	TCGCGCTTGATGTCGGAGAGCA-(BRIDGE)-GCGTCCCACCGAACCGGCGG
379.	oxyR-ahpC_W_4_1	2726520	2726380	TGCTGAACGCCGCGATCTCG-(BRIDGE)-TCGGGAAGGGTAACGTTTTGAGGTCG
380.	oxyR-ahpC_W_5_1	2726380	2726240	ACAGGTCACCGCCGATGAGAGC-(BRIDGE)-GTAGGGCACACGAACGTGAAGTCTTTC
381.	oxyR-ahpC_W_6_1	2726240	2726100	TCGCTGTCAGGCAAAGGTGATATATCACAC-(BRIDGE)-GGTGAGCTGGTAGGCGGGGAA
382.	oxyR-ahpC_W_7_1	2726100	2725960	GTCGACGTTGCGGCGAGCGG-(BRIDGE)-CATATTTATCGGCATCGCCGCCAAGAG
383.	oxyR-ahpC_W_8_1	2725960	2725820	GACCAGACGCTCGATGCTGCC-(BRIDGE)-TGGTCGGAAGCCGGTCTCGG
384.	oxyR-ahpC_W_9_1	2725820	2725680	CCGATTCGTCGCCCCTGCCC-(BRIDGE)-CAACACCCGGGCGGTGTGGC
385.	oxyR-ahpC_W_10_1	2725680	2725540	GCAACCACCCAGCCGGATCG-(BRIDGE)-GGCGCGACGAATCGGTTTGGT
386.	oxyR-ahpC_W_11_1	2725540	2725400	CGCCGCGCCCGGGTGGCCGC-(BRIDGE)-CTGCGCGGCCCGTCCGGAGC
387.	oxyR-ahpC_C_1_2	2726890	2726750	GCTCAATCACCCGCAGCAGCG-(BRIDGE)-GCTGGCGAACTCCTCAAGGCTTC
388.	oxyR-ahpC_C_2_2	2726750	2726610	AGGGCGACCCGACGCTAGAC-(BRIDGE)-CCAACAACGAGATCCAGTTCGTCTCGG
389.	oxyR-ahpC_C_3_2	2726610	2726470	ACCGCGTGACCTTTATCGTCGACC-(BRIDGE)-TTTCCAGTGGCGTGCACAGCAC

#	Probe name	Start	End	Sequence
390.	oxyR-ahpC_C_4_2	2726470	2726330	TCGATTGACAGCGAATTCGCGCA-(BRIDGE)-TGGCGGGTGGTGTTCTTTTGGC
391.	oxyR-ahpC_C_5_2	2726330	2726190	ACCAGTGACGAACACCCAGGCAAG-(BRIDGE)-TCATGCCACTGCTAACCATTGGCG
392.	oxyR-ahpC_C_6_2	2726190	2726050	TGCATTGTCCGCTTTGATGATGAGGAGAG-(BRIDGE)-GCCCGGCCACGGCCGGCTAG
393.	oxyR-ahpC_C_7_2	2726050	2725910	CACCGCGGCGAACGCGCGAA-(BRIDGE)-CTTGCCGGAAAGACATGCCCTGG
394.	oxyR-ahpC_C_8_2	2725910	2725770	GCGGTCAGCGGCACCCGCTG-(BRIDGE)-CGCCGGTCACGCACTGCACG
395.	oxyR-ahpC_C_9_2	2725770	2725630	CGGAATCAGTGTCACCCCCAGCC-(BRIDGE)-ACTTCTCGCGGCCGCCGAAA
396.	oxyR-ahpC_C_9_2a	2725770	2725630	CGGAATCAGTGTCCCCCCCAGCC-(BRIDGE)-ACTTCTCGCGGCCGCCGAAA
397.	oxyR-ahpC_C_10_2	2725630	2725490	TCCCGGCAAGACGCTGGTAGG-(BRIDGE)-CGGGCTTGCGCTGGCCAGGT
398.	embC_W_1_1	4239643	4239782	CGGTGGACCTACGGACCGCC-(BRIDGE)-TGGACAAGCTGCCCTGGCAGC
399.	embC_W_2_1	4239783	4239922	GGCTACCATCTACCTCCGTGCGC-(BRIDGE)-CTCTTCGCCGACCCGCGTTT
400.	embC_W_3_1	4239923	4240062	TGGCCCCAAAACGGCACGTT-(BRIDGE)-GACGCGGGAGCAAACTACCGG
401.	embC_W_4_1	4240063	4240202	AACGGTGCCCAAGCAGGCGC-(BRIDGE)-CGCCAGTGTCGAGGCACCGC
402.	embC_W_5_1	4240203	4240342	GCGGTTGACATTCACCGCGCAC-(BRIDGE)-CTAAGGCCGTCGATCGCGGGC
403.	embC_W_6_1	4240343	4240482	TTCACCGACCTGGCCGGGCC-(BRIDGE)-GCCGATCGGGTCGCCGCCGA
404.	embC_W_7_1	4240483	4240622	CGCTGCACATCCTGGACACCG-(BRIDGE)-GGCGCCACCGGGTCTGAGCT
405.	embC_W_8_1	4240623	4240762	CGACGACGGCTACATCCTGACCATG-(BRIDGE)-CCGACGGCATGCGGCACCGG
406.	embC_W_9_1	4240763	4240902	GGCCAGTATCTGGATGCGCCTACC-(BRIDGE)-GCCCGGGTGTCCGAGCATGC
407.	embC_W_10_1	4240903	4241042	TGTCTGGCTGCCGCTGGACA-(BRIDGE)-CACCCTGGCGATGGCGCTCA
408.	embC_W_11_1	4241043	4241182	TGACCCTGTTCTCCGGGCCG-(BRIDGE)-ACGGCCTTCGGCCCGAGCCG
409.	embC_W_12_1	4241183	4241322	ACCGTCACCGCGATCCCGAT-(BRIDGE)-ACGGGCATCGCCTCGATCGG
410.	embC_W_13_1	4241323	4241462	CGACGGCTCGATCGCCCGCC-(BRIDGE)-CTTTCGTGATCAGACCTTCGCGGGC
411.	embC_W_14_1	4241463	4241602	CACGATCATTTCCTTCCTCGCGATGATG-(BRIDGE)-GCTTCGCCGTGCTGGCCTTG
412.	embC_W_15_1	4241603	4241742	GTGTTCGCCGCCGTGGTGGT-(BRIDGE)-TTCACCCCGACAAAGTGGACCCAT
413.	embC_W_16_1	4241743	4241882	GCTGACGGTGCTGGTGCTGC-(BRIDGE)-CTTCGTGTTGGCCCTGTCGTTCG
414.	embC_W_17_1	4241883	4242022	TGGTTGCTGGTGCTTTTCGAGGTG-(BRIDGE)-TGCTAGCGGCATGGTTCCACTTCG
415.	embC_W_18_1	4242023	4242162	CCCAACGCAGGCATGCTGGC-(BRIDGE)-GTATCGCTGACCCAGGCGATGATTTCC
416.	embC_W_19_1	4242163	4242302	CAGTTTCCTCAACGACGACGGGC-(BRIDGE)-GCCGGTGACCGCGCCGTTGG
417.	embC_W_19_1a	4242163	4242302	CAGTTTCCTCAACGACGACGGGC-(BRIDGE)-GCCGGTGACCGCGCCGTTGT
418.	embC_W_20_1	4242303	4242442	GGCGAGCCGGCGTGCAGGTG-(BRIDGE)-TGATCACCGGCAGCGAACCCG
419.	embC_W_21_1	4242443	4242582	GCCACCGACGAGCAAGCGGC-(BRIDGE)-CCCGCCATGCTGCGGTCGGG
420.	embC_W_22_1	4242583	4242722	CCGACGACCAGGATCTGGCGC-(BRIDGE)-CGCCGGACACCACGGTGGGT
421.	embC_W_23_1	4242723	4242862	AACGCCCGTTCGGCCACCAA-(BRIDGE)-CGCAGCACTGGATCGCCCTC
422.	embC_W_24_1	4242863	4243002	CGCGCAACCACGGTGGCCAG-(BRIDGE)-TACGGCGTCGACGAGACACCC
423.	embC_C_1_2	4239693	4239832	CCGCAGGGTGTAGCTGTTATGTGC-(BRIDGE)-AGCACGAACGGGCCAATGTCCT
424.	embC_C_2_2	4239833	4239972	CCTGCGGCTTGCGGATGGCC-(BRIDGE)-CCCGCCACCACAGCGACGTA
425.	embC_C_3_2	4239973	4240112	GCCAGCACAGCGCCTAGCAGA-(BRIDGE)-TGTTCAAGTCGGTGGCCACGTAGC
426.	embC_C_4_2	4240113	4240252	GGCCTGGCAGGGGACGGTGA-(BRIDGE)-CAGGTCGTCGTTGGCCCGTTG
427.	embC_C_5_2	4240253	4240392	CGGGACATTACGCACCACAAGCAC-(BRIDGE)-GCATTGGGTCCCTGCACCAGTCC
428.	embC_C_6_2	4240393	4240532	GCGGTGCACCGGGGTGCTCA-(BRIDGE)-TGCTGTAGCGGGTATCCACGCT
429.	embC_C_7_2	4240533	4240672	CTTCAGCGGCGTGGGGCTGC-(BRIDGE)-GGTCGACCACCAGCGCGCGG
430.	embC_C_8_2	4240673	4240812	ACCAGGGTGTCCAGACCGCC-(BRIDGE)-AACCAGCGGTAGTAGTTGGCCATATAGC
431.	embC_C_9_2	4240813	4240952	AAGGCGCCTCGGGTGTGCCG-(BRIDGE)-TGACCTCACGGCTGATTACCCACC
432.	embC_C_10_2	4240953	4241092	GGCGTGCCCCAGCCGGGGAA-(BRIDGE)-CCAGGTCAGCAGGATGCCCAGG
433.	embC_C_11_2	4241093	4241232	ACCGCCCGCTCCACCGAGCA-(BRIDGE)-CGTAGCGGCCCGATCGCGAC
434.	embC_C_12_2	4241233	4241372	GAACGCCGGTGCAGGATGGTC-(BRIDGE)-GCTTGAGGAGGTTGGCCTGGATCT
435.	embC_C_13_2	4241373	4241512	CAGGCTGGGCCCTACGGCAC-(BRIDGE)-CATTGCCACCGATACCGCGAGC
436.	embC_C_14_2	4241513	4241652	TGGAATGCGGCCCTTACGTAACGA-(BRIDGE)-GCCAACCCCGCGAACACCCC
437.	embC_C_15_2	4241653	4241792	CAAGCGCCCCCAGCGACCCG-(BRIDGE)-ACACGTACCACCAGCCGTTGACA
438.	embC_C_16_2	4241793	4241932	CGACCATGGCACACCGAAGTTGG-(BRIDGE)-TGTTCGGCGCCCGTCACCGT
439.	embC_C_17_2	4241933	4242072	CCCTAAACCGGGTTGGCCTGGC-(BRIDGE)-CCAACCGACCACGCCGGGTA
440.	embC_C_18_2	4242073	4242212	GGCCAAAGCCTGTAGGTTAGACCGG-(BRIDGE)-CTTCAGACAGGCCGGCTCCCA
441.	embC_C_19_2	4242213	4242352	GGGAATGCCGTTGGGTGTGAAGG-(BRIDGE)-CGGTGCGGCCGTGGTGCCCC
442.	embC_C_20_2	4242353	4242492	GCGCGGGAGCCGTTGATTCC-(BRIDGE)-CGCTGCTCGTTGGTGGGCAG
443.	embC_C_21_2	4242493	4242632	CCAGCAGCGGCGCCCTGTCC-(BRIDGE)-GCGCGGCACCGACGTCGGCG
444.	embC_C_22_2	4242633	4242772	GCGCAGGTTGCGCCAGGCCG-(BRIDGE)-CGTGCGCACCCGCGGAATCC
445.	embC_C_22_2a	4242633	4242772	GCGCAGGTTACGCCAGGCCG-(BRIDGE)-CGTGCGCACCCGCGGAATCC
446.	embC_C_23_2	4242773	4242912	GCGCCCACCACGTTCTGCAG-(BRIDGE)-CCGAACCGGTCCGGCAGGAT
447.	embC_C_24_2	4242913	4243052	CCGGTGAGTTGGCTTCGGCG-(BRIDGE)-TCAACCGCTGTAACGCGCCC
448.	iniB-iniA-iniC_W_1_1	409162	409301	CGGGGTGAGGCGGAATCCATAGC-(BRIDGE)-ATCCACGGATAAGTTCCGGACCGG
449.	iniB-iniA-iniC_W_2_1	409302	409441	TTCGTTGCCGCTCCGGGACG-(BRIDGE)-GTCGATGGCACAGCGCCGGT
450.	iniB-iniA-iniC_W_3_1	409442	409581	CGTCGCCGCTCGGCATGGCT-(BRIDGE)-GGCCATGACCAGTGCCGGGC
451.	iniB-iniA-iniC_W_4_1	409582	409721	AGGGTGGCCTGGCTCTCGCC-(BRIDGE)-TTGCGCAGGACGTCGCCAATG
452.	iniB-iniA-iniC_W_5_1	409722	409861	GGTCTGGGTGCTCAGGCCGG-(BRIDGE)-GCGTCAAGCGGTGGTTTCGGC
453.	iniB-iniA-iniC_W_6_1	409862	410001	AGATCGGAGTTGCCGGCCAGG-(BRIDGE)-TATGGGCTTTGGCGGCGGGG
454.	iniB-iniA-iniC_W_7_1	410002	410141	GGGTCAGCAGCAACGCAGTGTTG-(BRIDGE)-GTGCCGTTGGCGCTGGTGTC
455.	iniB-iniA-iniC_W_8_1	410142	410281	GCCGCTGGCGGCGCCGGGTT-(BRIDGE)-GCTTCCAACGCAAGCGGCCA

#	Probe name	Start	End	Sequence
456.	iniB-iniA-iniC_W_9_1	410282	410421	CGGGGTCGGCGGGGCACACG-(BRIDGE)-GGGCTTCGGAGCGGTCGGGC
457.	iniB-iniA-iniC_W_10_1	410422	410561	GGCGGCTATGGCGGCATGAAC-(BRIDGE)-GCGACATCCTGGGCCACGAGG
458.	iniB-iniA-iniC_W_11_1	410562	410701	CCACGATAAGCCGCCGAGCCA-(BRIDGE)-CCGCCAGTGACCGATGCGCC
459.	iniB-iniA-iniC_W_12_1	410702	410841	CGAACCGGTGGGGACGTTCATGG-(BRIDGE)-TTCGGTGTTTGACGTCGGTCACGA
460.	iniB-iniA-iniC_W_13_1	410842	410981	TCGATCACACTATCGCCATCGCCAAA-(BRIDGE)-TCCCCGCCGGTTTGTGCGCA
461.	iniB-iniA-iniC_W_14_1	410982	411121	TCGTTGCTCAACCTGCCCGC-(BRIDGE)-CTGAACGAGCGTGGTGATCTAGTACAGC
462.	iniB-iniA-iniC_W_15_1	411122	411261	TGACATTCCCGTCGATGACATCAGCA-(BRIDGE)-GGCGCGAGTAGGCGATGACG
463.	iniB-iniA-iniC_W_16_1	411262	411401	TCGGACAGCCCCACCTGTCG-(BRIDGE)-CCGATGTGCGTCGGGCTCCG
464.	iniB-iniA-iniC_W_17_1	411402	411541	GCGGTCGTGGCCACCAAGAC-(BRIDGE)-GCGACGCTGGGGCTGCTACC
465.	iniB-iniA-iniC_W_18_1	411542	411681	TCACGCTTAACGACAAAGAGCTCAACG-(BRIDGE)-CGACCTGTATCCGCGCTGGC
466.	iniB-iniA-iniC_W_19_1	411682	411821	TGGCGGTGTCTCTAGGTTCCGAACTA-(BRIDGE)-AAGAGTCCAACTTTCCGGCGATCGT
467.	iniB-iniA-iniC_W_20_1	411822	411961	CGGGTTCAACGACCTGACTGCTGA-(BRIDGE)-TCGGTGGTCAACGACCCGAACC
468.	iniB-iniA-iniC_W_21_1	411962	412101	CGCCACAGCGGTCGGCGACA-(BRIDGE)-CGTGGACCACGACCTACGAACCC
469.	iniB-iniA-iniC_W_22_1	412102	412241	ACTTCGGCCGGCTCAAAGCG-(BRIDGE)-ACTTCGTGTGGGCATACCAGCGT
470.	iniB-iniA-iniC_W_23_1	412242	412381	GTTGTTCAACCCGCTATCGGTGGG-(BRIDGE)-CTGGGCCGGATGGAATCGAAACCG
471.	iniB-iniA-iniC_W_24_1	412382	412521	CGTCGTCAGCAAACAATCACGGGATC-(BRIDGE)-GGCCGGGTTGATCCTCGGCC
472.	iniB-iniA-iniC_W_25_1	412522	412661	CCGAGCGGGACAATCGAATTCGG-(BRIDGE)-GGCTCAAGATGATCCAGCGTCTGCT
473.	iniB-iniA-iniC_W_26_1	412662	412801	GCGCGATTCTGCACGCAACCATC-(BRIDGE)-GAACTTCAGCGGCAATTGGGTATCCTG
474.	iniB-iniA-iniC_W_27_1	412802	412941	AGGCCGGAAAATCCACTCTCGTCAA-(BRIDGE)-CAGGCCTACCGGGGTGCGCC
475.	iniB-iniA-iniC_W_28_1	412942	413081	CCAACGTGCCGATCACCCGTC-(BRIDGE)-CGCCCTTGTCGGCGACGACA
476.	iniB-iniA-iniC_W_29_1	413082	413221	TCGTTGGCATGCGATGCCTCC-(BRIDGE)-GGGGCGGGCTGAGTTTCGAC
477.	iniB-iniA-iniC_W_30_1	413222	413361	GTCGGCGGGTCGGTGGGAGC-(BRIDGE)-GAGCGCACGTTGCGGCTGCT
478.	iniB-iniA-iniC_W_31_1	413362	413501	TTGCCAGGCGGTGGTGCCGG-(BRIDGE)-CCTGGGCATCATCGGGGTGGC
479.	iniB-iniA-iniC_W_32_1	413502	413641	TTGTGCGCCGGGACAGTCCG-(BRIDGE)-TATCCGGACTTCTTGCGCTGACCG
480.	iniB-iniA-iniC_W_33_1	413642	413781	CTGCTGGAGCGCAGCGGGCT-(BRIDGE)-CTACCGGTGGACGCGGGCAT
481.	iniB-iniA-iniC_W_34_1	413782	413921	CCCGTACGTCATTGCCGACATCG-(BRIDGE)-GGTGGCGCTGCGCAATGTGA
482.	iniB-iniA-iniC_W_34_1a	413782	413921	CCCGCACGTCATTGCCGACATCG-(BRIDGE)-GGTGGCGCTGCGCAATGTGA
483.	iniB-iniA-iniC_W_35_1	413922	414061	CGGGCACCAGTGCCGCCGCT-(BRIDGE)-ACCCGTTGCTAGCCGACACCC
484.	iniB-iniA-iniC_W_36_1	414062	414201	CGCGCGGCGGTGCGCAGCGC-(BRIDGE)-CGGCTGGGCCTGGATCCCGC
485.	iniB-iniA-iniC_W_37_1	414202	414341	GTTTTCGAGCCCAAGGGGCAGC-(BRIDGE)-CGAGGCGATGGTGGCGGAGT
486.	iniB-iniA-iniC_C_1_2	409212	409351	CCTGGCCGCCGCGTTAGGGG-(BRIDGE)-CTTCAATCGAAGAAGCTGTTCGCCGG
487.	iniB-iniA-iniC_C_2_2	409352	409491	GGATGTAATCGATAAGCGAGGTCATCTTCATTTCC-(BRIDGE)-ATGAGATTTGGTGCGGCGCGATATC
488.	iniB-iniA-iniC_C_3_2	409492	409631	CACCACATTGGCCGCCACCG-(BRIDGE)-CCCCGCGCCCGCGTCACCGG
489.	iniB-iniA-iniC_C_4_2	409632	409771	CGGTCGTGATGACGCTTGCCAC-(BRIDGE)-CCGACCTGGGCAGCCAAGCC
490.	iniB-iniA-iniC_C_5_2	409772	409911	GCCTCAATCACGGCAGTAAAACCCAGA-(BRIDGE)-CGCCGGCCTGACCACCCAGA
491.	iniB-iniA-iniC_C_6_2	409912	410051	CGCGCTCCCACCGATCACAC-(BRIDGE)-GATGCCCGCCTGGCCGCCGA
492.	iniB-iniA-iniC_C_7_2	410052	410191	GGCTGAGACACCGATCTGGCTAGC-(BRIDGE)-GCAGCGCCTTCACTGGCGAT
493.	iniB-iniA-iniC_C_8_2	410192	410331	AGGCATAGCAGCGCCGTTCAAG-(BRIDGE)-CGCCCAGGGCCGCCGGCTGA
494.	iniB-iniA-iniC_C_9_2	410332	410471	CTTGGCCACCACGCCAGCCG-(BRIDGE)-GACCGTGTCGACACTGCCCAGT
495.	iniB-iniA-iniC_C_10_2	410472	410611	ACGGGCGTGACACCGGCGTT-(BRIDGE)-GGCTGGGCCCGCGCCGGAAC
496.	iniB-iniA-iniC_C_11_2	410612	410751	GCTCGGCCGCCGTGGTCATC-(BRIDGE)-CCGGCGGCGTGTGCGTCACC
497.	iniB-iniA-iniC_C_12_2	410752	410891	CGACGGCAGTTCGATGGGCG-(BRIDGE)-TCTCGCTCGTTTACGCCTCAGATCAC
498.	iniB-iniA-iniC_C_13_2	410892	411031	GGTCACCGTGTCGCCCCACTT-(BRIDGE)-CGCTGGCGAGCCCGCGTCAA
499.	iniB-iniA-iniC_C_14_2	411032	411171	CGGACCTGCGGGTCGGTGATC-(BRIDGE)-AGCTTACGACGGTGATCACCACGG
500.	iniB-iniA-iniC_C_15_2	411172	411311	GGCCGACGGTTGGGCGCTGT-(BRIDGE)-GACCCGCAACACCTCGCGGC
501.	iniB-iniA-iniC_C_16_2	411312	411451	GGGCTGGGCGCGCCGACCTC-(BRIDGE)-TCGCTGACCACCAAGACGGCA
502.	iniB-iniA-iniC_C_17_2	411452	411591	GGTTCGGTGAATTCCTGGCTGGTG-(BRIDGE)-GATGTGCTGCATTGGCATTGACGATCT
503.	iniB-iniA-iniC_C_18_2	411592	411731	CGGAACCCGGGCCCGCTGCA-(BRIDGE)-AAGCACCTGCTCGCTGAGAAACTTGA
504.	iniB-iniA-iniC_C_19_2	411732	411871	ACTCGCTCCGTCGCGCGGGA-(BRIDGE)-TCCAAATCCGAAGCAAGTCGGTCACG
505.	iniB-iniA-iniC_C_20_2	411872	412011	GGGCTTCCCGTTTGCGCCGC-(BRIDGE)-CGGCGTCTTCGGTGACGGTG
506.	iniB-iniA-iniC_C_21_2	412012	412151	GTCACAGGAGTCGATCTGGCGCT-(BRIDGE)-AGCGACGTCGTCGGCCAACG
507.	iniB-iniA-iniC_C_22_2	412152	412291	CCCGCGTCGGCAAAGGAGCG-(BRIDGE)-ATAATCATTTTATGGCCCCGGCGCAG
508.	iniB-iniA-iniC_C_23_2	412292	412431	GCCATAGGAACCCCGCATGCCG-(BRIDGE)-GGTTTTGTTTGTCCTCTTTATATGCCATCCGG
509.	iniB-iniA-iniC_C_24_2	412432	412571	GCTGCGCACCCGCAGCAACC-(BRIDGE)-GGCGATCTCGCGGTAGTGGTCG
510.	iniB-iniA-iniC_C_25_2	412572	412711	GGTGAGCGACCGGGTGATCTCTTC-(BRIDGE)-GCAAGGTTGTCGTTGACCTGGCTC
511.	iniB-iniA-iniC_C_26_2	412712	412851	CGTCAAGGTTGGCTCCAAGCCG-(BRIDGE)-CAAAAAACGTCGCCACGCTGACG
512.	iniB-iniA-iniC_C_27_2	412852	412991	CACCGATGCGGTCCAGCTGG-(BRIDGE)-GGGTGGCCTCGGTGGCATCG
513.	iniB-iniA-iniC_C_28_2	412992	413131	CGTGCCGGAACCAGGTCACAATCC-(BRIDGE)-GATCAGCTCGGCCGGGTTGATCC
514.	iniB-iniA-iniC_C_29_2	413132	413271	GCTGGCCACTCGACTTCCAGGTC-(BRIDGE)-TCCACCCGAGGCACCCCGTC
515.	iniB-iniA-iniC_C_30_2	413272	413411	CGCAACAGGAACACCACCGCA-(BRIDGE)-GGCCCGCGCCGATCTCATCC
516.	iniB-iniA-iniC_C_31_2	413412	413551	CCGAGAGCATCGCGTCGATGC-(BRIDGE)-GAACTCGGTCTGGCGCAGTGTG
517.	iniB-iniA-iniC_C_32_2	413552	413691	GCCAGCTTGCGCAGCGCGAT-(BRIDGE)-ATGCCGAACCGCTCGAGCAATTG
518.	iniB-iniA-iniC_C_33_2	413692	413831	GCAATCGACATCCGGATGCCGAAC-(BRIDGE)-TGTCGGAGCGCTGCGCGAAC
519.	iniB-iniA-iniC_C_34_2	413832	413971	CAAGGCGGTATGCGCCTTAAGCA-(BRIDGE)-GCTTAGCATTCGGAGTTCTTCGAAGGC
520.	iniB-iniA-iniC_C_35_2	413972	414111	CGTTGCCCGCGAAGGCAAAAG-(BRIDGE)-AGCGCGGCGCGCGGGGCCTC
521.	iniB-iniA-iniC_C_36_2	414112	414251	GCCAGTGTTGCGCTGCGGCC-(BRIDGE)-AGGGCCTGACGCGTCAGCGG

#	Probe name	Start	End	Sequence
522.	iniB-iniA-iniC_C_37_2	414252	414391	CGCCCACCACTGTGACACCCG-(BRIDGE)-ACACATTCTGAGCGCATGCCCTTATGA
523.	rrs-rrl_W_1_1	1471687	1471826	TTTTGTCAGGATATTTCTAAATACCTTTGGCTCCCTTT-(BRIDGE)-CGTGTTGTTTGAGAACTCAATAGTGTGTTTGGT
524.	rrs-rrl_W_2_1	1471827	1471966	GGCGAACGGGTGAGTAACACGTG-(BRIDGE)-TCCAAAGGGAGTGTTTGGGTTTTGTTTGG
525.	rrs-rrl_W_3_1	1471967	1472106	GGCCTATCAGCTTGTTGGTGGGGTG-(BRIDGE)-GGTGATCTGCCCTGCACTTCGGG
526.	rrs-rrl_W_4_1	1472107	1472246	AGCCTGATGCAGCGACGCCG-(BRIDGE)-ACGGCCTACCAAGGCGACGA
527.	rrs-rrl_W_5_1	1472247	1472386	GCGGTAATACGTAGGGTGCGAGCG-(BRIDGE)-CGTGGGGGATGACGGCCTTCG
528.	rrs-rrl_W_6_1	1472387	1472526	GGGAGACTGGAATTCCTGGTGTAGCG-(BRIDGE)-TTGTCCGGAATTACTGGGCGTAAAGAGC
529.	rrs-rrl_W_7_1	1472527	1472666	ACGCCGTAAACGGTGGGTACTAGG-(BRIDGE)-GTGGAATGCGCAGATATCAGGAGGAACA
530.	rrs-rrl_W_8_1	1472667	1472806	GCGGAGCATGTGGATTAATTCGATGCA-(BRIDGE)-TGTGGGTTTCCTTCCTTGGGATCCG
531.	rrs-rrl_W_9_1	1472807	1472946	GTTAAGTCCCGCAACGAGCGCA-(BRIDGE)-ACGCGAAGAACCTTACCTGGGTTTGA
532.	rrs-rrl_W_10_1	1472947	1473086	CTTCACACATGCTACAATGGCCGGTAC-(BRIDGE)-ACCCTTGTCTCATGTTGCCAGCACG
533.	rrs-rrl_W_11_1	1473087	1473226	GCGGTGAATACGTTCCCGGGC-(BRIDGE)-AAAGGGCTGCGATGCCGCGA
534.	rrs-rrl_W_12_1	1473227	1473366	CCGTACCGGAAGGTGCGGCT-(BRIDGE)-CTTGTACACACCGCCCGTCACG
535.	rrs-rrl_W_12_1a	1473227	1473366	CCGTACCGGAAGGTGCGGCT-(BRIDGE)-CTTGTACACACCGCCCGTCGCG
536.	rrs-rrl_W_13_1	1473367	1473506	ACCAACACACTGTTGGGTCCTGAGG-(BRIDGE)-GGATCACCTCCTTTCTAAGGAGCACCAC
537.	rrs-rrl_W_14_1	1473507	1473646	TGGCGTGTTCTTTGTGCAATATTCTTTGGT-(BRIDGE)-CAACACTCGGACTTGTTCCAGGTGTTG
538.	rrs-rrl_W_15_1	1473647	1473786	TCCGAGGATTTCCGAATGGGGAAACC-(BRIDGE)-TTTTGTTGTGTTTGTAAGTGTCTAAGGGCGC
539.	rrs-rrl_W_16_1	1473787	1473926	GCGAGCGAACGCGGAACAGG-(BRIDGE)-CAGCACGAGTGATGTCGTGCTACCC
540.	rrs-rrl_W_17_1	1473927	1474066	CCTGGGATGGTCTGCCGTAGACG-(BRIDGE)-CTAAACCGCACGCATGGGTAACCG
541.	rrs-rrl_W_18_1	1474067	1474206	ACTCCTCGATGACCGATAGCGGATTAGTA-(BRIDGE)-GTGAGAGCCCGGTACGCGAAAAC
542.	rrs-rrl_W_19_1	1474207	1474346	TGCCTTTTGAAGAATGAGCCTGCGAG-(BRIDGE)-CCGTGAGGGAATGGTGAAAAGTACCCC
543.	rrs-rrl_W_20_1	1474347	1474486	GCGGAGTGATCTACCCATGGCCAG-(BRIDGE)-TCAGGGACATGTCGCAAGGTTAACCC
544.	rrs-rrl_W_21_1	1474487	1474626	CCCGAAATGCATTTAGGTGCAGCGTT-(BRIDGE)-GGTGAAGCGCGGGTAAGACCG
545.	rrs-rrl_W_22_1	1474627	1474766	GGATAAGCTCCGTACGTCGAAAGGGAA-(BRIDGE)-GCGTGGTTCACCGCGGAGGT
546.	rrs-rrl_W_23_1	1474767	1474906	TGCGTAATAGCTCACTGGTCAAGTGATTGTG-(BRIDGE)-ACAGCCCAGATCGCCGGCTA
547.	rrs-rrl_W_24_1	1474907	1475046	GGAGGGTGGGGGAGTGAGAATGCA-(BRIDGE)-CGCCGATAATGTAGCGGGGCTCA
548.	rrs-rrl_W_25_1	1475047	1475186	GCGTAGTCGATGGACAACGGGTTGATATTC-(BRIDGE)-GGCATGAGTAGCGACAAGGCAAGTG
549.	rrs-rrl_W_26_1	1475187	1475326	AGTCAAGCGAAGGGGTGACGCA-(BRIDGE)-CCGTACCCGTGTGTGGGCGC
550.	rrs-rrl_W_27_1	1475327	1475466	TCGGTGATCCTCTGCTGCCAAGAAAA-(BRIDGE)-GGAAGGTAGCCGTACCAGTCAGTGG
551.	rrs-rrl_W_28_1	1475467	1475606	TCGGGAGAAGGGGGACCGGAAT-(BRIDGE)-GCCTCTAGCGAGCACACACACG
552.	rrs-rrl_W_29_1	1475607	1475746	CCTGCCCGGTGCTGGAAGGTTAAG-(BRIDGE)-ATCGTGAACACCCTTGCGGTGGG
553.	rrs-rrl_W_30_1	1475747	1475886	GCACGAATGGCGTAACGACTTCTCAACT-(BRIDGE)-AGGACCCGTTAACCCGCAAGGG
554.	rrs-rrl_W_31_1	1475887	1476026	CGGTTTGTGTAGGATAGGTGGGAGACTGT-(BRIDGE)-GTCTCAACCATAGACTCGGCGAAATTGC
555.	rrs-rrl_W_32_1	1476027	1476166	CTGGGGCGGTTGCCTCCTAAAATG-(BRIDGE)-GAAACCTCGACGCCAGTTGGGGC
556.	rrs-rrl_W_33_1	1476167	1476306	ATCCGGCACCCCCGAGTGGA-(BRIDGE)-TAACGGAGGCGCCCAAAGGTTCC
557.	rrs-rrl_W_34_1	1476307	1476446	AGCAGGTCCCAAGGGTTGGGC-(BRIDGE)-AGGGGTGTCGCTCAACGGATAAAAGG
558.	rrs-rrl_W_35_1	1476447	1476586	GGACGGACGAACCTCTGGTGCAC-(BRIDGE)-TGTTCGCCCATTAAAGCGGCACG
559.	rrs-rrl_W_36_1	1476587	1476726	CCCCCGCAGAACACGGGTTCA-(BRIDGE)-CAGTTGTCCCGCCAGGGGCA
560.	rrs-rrl_W_37_1	1476727	1476866	CACGGCGCTAGCCGTGCGTC-(BRIDGE)-ATAGGTCAGACCTGGAAGCTCAGTAATGGG
561.	rrs-rrl_C_1_2	1471737	1471876	GGGGCATCAAGAGCATGGCCAAAAATAAC-(BRIDGE)-CCTGAGCCAGGATCAAACTCTCCAAACA
562.	rrs-rrl_C_2_2	1471877	1472016	AGCACGCCGCCAGCGTTCGT-(BRIDGE)-GTATTAGACCCAGTTTCCCAGGCTTATCCCG
563.	rrs-rrl_C_3_2	1472017	1472156	ACATGCATCCCGTGGTCCTATCCG-(BRIDGE)-GGCCGGACACCCTCTCAGGC
564.	rrs-rrl_C_4_2	1472157	1472296	TGGGCCGTATCTCAGTCCCAGTGT-(BRIDGE)-TTCGTCGATGGTGAAAGAGGTTTACAACCC
565.	rrs-rrl_C_5_2	1472297	1472436	CGTCAATCCGAGAGAACCCGGACC-(BRIDGE)-CAACGCGACAAACCACCTACGAGC
566.	rrs-rrl_C_6_2	1472437	1472576	GCTCACAGTTAAGCCGTGAGATTTCACGAA-(BRIDGE)-AGAGACCCGCCTTCGCCACC
567.	rrs-rrl_C_7_2	1472577	1472716	GCTCCTCAGCGTCAGTTACTGCCC-(BRIDGE)-GGTACTTAATGCGTTAGCTACGGCACG
568.	rrs-rrl_C_8_2	1472717	1472856	CGGCCGTACTCCCCAGGCGG-(BRIDGE)-ATCTCTAGACGCGTCCTGTGCATGTC
569.	rrs-rrl_C_9_2	1472857	1472996	ACAGGCCACAAGGGAACGCCT-(BRIDGE)-AGTCTCTCACGAGTCCCCACCATTACG
570.	rrs-rrl_C_10_2	1472997	1473136	TCCTCCGAGTTGACCCCGGC-(BRIDGE)-TGAGACCGGCTTTTAAGGATTCGCTTAACC
571.	rrs-rrl_C_11_2	1473137	1473276	CGAGTTGCAGACCCCGATCCGAAC-(BRIDGE)-TGGCTTCGGGTGTTACCGACTTTCA
572.	rrs-rrl_C_12_2	1473277	1473416	CCCTCCCGAGGGTTAGGCCAC-(BRIDGE)-CCCCACCAGTTGGGGCGTTTTC
573.	rrs-rrl_C_13_2	1473417	1473556	ACAAGAACCCCTCACGGCCTACG-(BRIDGE)-ACCCCACCACCAAGGCGGTG
574.	rrs-rrl_C_14_2	1473557	1473696	CGCAACCACTATCCAGTTCTCAAACACCAC-(BRIDGE)-ATGCCAAGGCATCCACCATGCG
575.	rrs-rrl_C_15_2	1473697	1473836	CCCACGTCCTTCATCGGCTCTCG-(BRIDGE)-TCCCGCACCCTATATATTCAGATGCGGG
576.	rrs-rrl_C_16_2	1473837	1473976	GATGTTTCACTTCCCCGCGTTCCC-(BRIDGE)-ACAACCCCGCACACACAACCC
577.	rrs-rrl_C_17_2	1473977	1474116	GGGTAGCGCTGAGACATATCCTCCC-(BRIDGE)-CGGGAATTGATACTAGGCAGGTGCCG
578.	rrs-rrl_C_17_2a	1473977	1474116	AGGTAGCGCTGAGACATATCCTCCC-(BRIDGE)-CGGGAATTGATACTAGGCAGGTGCCG
579.	rrs-rrl_C_18_2	1474117	1474256	TCCACGGGCCCGCTGCTACT-(BRIDGE)-AGGTACTCTTTCACTCCCCTCCCGG
580.	rrs-rrl_C_19_2	1474257	1474396	CTGACGGATTGTAGGCACACGGTTTC-(BRIDGE)-GCTTTCGCTGCGGCTACCCC
581.	rrs-rrl_C_19_2a	1474257	1474396	CTGACGGATTGTAGGCACACGGTTTC-(BRIDGE)-GCTTTCGCTGCGGCTATCCC
582.	rrs-rrl_C_20_2	1474397	1474536	CGTGTGGGTCGCCCTATTCAGACTC-(BRIDGE)-TTCAACCTAAGTGGGTTCGGGCCTC
583.	rrs-rrl_C_21_2	1474537	1474676	CCTACCCACAGCTCATCCCCTCAGTC-(BRIDGE)-AGTAGGGCCCATCGGCCATCC
584.	rrs-rrl_C_22_2	1474677	1474816	CGGAGTTTGGCTGACGTCAGTAACCT-(BRIDGE)-CTTTCCCACTTAGCACACGCTTGGG
585.	rrs-rrl_C_23_2	1474817	1474956	CCTGGTTGTCTTTGCGACTGCACATC-(BRIDGE)-GATGTGCCGCGGCTTCGGCG
586.	rrs-rrl_C_24_2	1474957	1475096	CCTACCCACACCCACCACAAGGTG-(BRIDGE)-TTGGTCTTTCGGCGGGCAAGGT
587.	rrs-rrl_C_25_2	1475097	1475236	CTGGCCTGGCCCAGGAACCC-(BRIDGE)-TGGGTGGTTAGTACCGCTGATTCGTC

#	Probe name	Start	End	Sequence
588.	rrs-rrl_C_26_2	1475237	1475376	CGAAGGGGAGTGATCGATCCGGTTT-(BRIDGE)-TCCCTACCGGCTTGCCCCAG
589.	rrs-rrl_C_27_2	1475377	1475516	GAGCGACGGATTTGCCTATCGCTC-(BRIDGE)-ACCACCTGTGTCGGTTTGGGGT
590.	rrs-rrl_C_28_2	1475517	1475656	CTCGTACGCCTTGGTATGCTCTACCTG-(BRIDGE)-CACTGGTTTCTGCGACCGGATCCC
591.	rrs-rrl_C_29_2	1475657	1475796	GGACCTGTGTTTTTAGTAAACAGTCGCTCCT-(BRIDGE)-TTTACTGGGGCTTAAATTCTCCGCTTCACC
592.	rrs-rrl_C_30_2	1475797	1475936	CCTTAGGATGGTTATAGTTACCACCGCCG-(BRIDGE)-AACGAGCATCTTTACTCGTAGTGCAATTTCGC
593.	rrs-rrl_C_31_2	1475937	1476076	CTTTTCGTCCTGCCGCGCGT-(BRIDGE)-TCAGAGTGGTATTTCAACAACGACTCCGC
594.	rrs-rrl_C_31_2a	1475937	1476076	CTTTTCGTCCTGCCGCGCGT-(BRIDGE)-TCAGAGTGGTATTTCAACAATGACTCCGC
595.	rrs-rrl_C_32_2	1476077	1476216	GGGTTCGAGGTTAGATGCCCAATACGA-(BRIDGE)-CGCCACCTGATTGCCGTCCAG
596.	rrs-rrl_C_33_2	1476217	1476356	GCAGTCAAGCTCCCTTGTGCATTTACACT-(BRIDGE)-GATCAGCCTGTTATCCCCGGGGTAC
597.	rrs-rrl_C_34_2	1476357	1476496	TCCCGTCGATATGGACTCTTGGGGAA-(BRIDGE)-GTCTCACGACGTTCTAAACCCAGCTCG
598.	rrs-rrl_C_35_2	1476497	1476636	CGCGGCGGATAGAGACCGAACT-(BRIDGE)-TTATCCTGACCGAACGTGGCTATCCAGC
599.	rrs-rrl_C_36_2	1476637	1476776	GTTTCCCGCTTAGATGCTTTCAGCGG-(BRIDGE)-GTTAGCACCAGTTCCCTACACCCATTACTG
600.	rrs-rrl_C_37_2	1476777	1476916	GGAGGGTGTTGTAAGTTTTCGGCCG-(BRIDGE)-CCGCTGTGGCCGCCGTAACT
601.	alr_W_1_1	3841573	3841433	GGGGCAATCGGGCACAGGCC-(BRIDGE)-CTATTGACGCCAACCATCATGCGGC
602.	alr_W_2_1	3841433	3841293	GCCGAGGCCATGGTGGATCTGG-(BRIDGE)-GGAATACTGCTCAGTGAAACGGTTCTGGG
603.	alr_W_3_1	3841293	3841153	GAGCCGGTGCGGCCGAACTC-(BRIDGE)-GCGCTATTGAACACAACGTGCGGG
604.	alr_W_4_1	3841153	3841013	GTCGCGGTGTCCTCGCTGCG-(BRIDGE)-GGCGTCGCCACCGTCGACGA
605.	alr_W_5_1	3841013	3840873	GACCGCGTTACGCCAAGCCA-(BRIDGE)-CCAACTCGACGAACTGTTGCACGC
606.	alr_W_6_1	3840873	3840733	CGCGAACAAGGGGTGCGGTTC-(BRIDGE)-TGGCCGAGGACGCCGTCCGG
607.	alr_W_7_1	3840733	3840593	GGGCTGGTGCCGGCGATGAC-(BRIDGE)-GAGGTGGCGCATCTATCGAACTCATCA
608.	alr_W_8_1	3840593	3840453	CGGCGTGTTCCGGTCGCTGG-(BRIDGE)-CGTGAAATGTGCTGTTGCGCTGG
609.	alr_W_9_1	3840453	3840313	GCGATTTTGTTCGGGCCGGGC-(BRIDGE)-GCGGGCGGCTGGAGGTGCTG
610.	alr_W_10_1	3840313	3840173	GAGCCGTGAGGGTATCCGCAGA-(BRIDGE)-ATCCGGGGTGAGCCCACGGC
611.	alr_W_11_1	3840173	3840033	CTCTCCGGTCCGCTCGGTGC-(BRIDGE)-CGACCGAAAGCCAGGGCTGG
612.	alr_C_1_2	3841523	3841383	CTCGGTGGTTGGTTGCCGATCAC-(BRIDGE)-CGTTTGGCTTTCCGACATTCTCCCAG
613.	alr_C_2_2	3841383	3841243	GCCCCGCCCATCTGTCGTGT-(BRIDGE)-CGCGTGGCCGGCGTGCTCAC
614.	alr_C_3_2	3841243	3841103	CCTTGACCACCGCCATCAGCTG-(BRIDGE)-GTAATGCCATCAGCGCGCAGCG
615.	alr_C_4_2	3841103	3840963	GCCAGGCCAGCACCGGTGCG-(BRIDGE)-TCGCCGTCCGGCCGGTCCGG
616.	alr_C_5_2	3840963	3840823	CGGTATCCACCTTGACGGTCACCG-(BRIDGE)-GTAAACCATATGCGACATCAGCCCCCG
617.	alr_C_6_2	3840823	3840683	GATGGAATCGTCAGGCTTGTCGGC-(BRIDGE)-AGGTCGGGGCGCGCCATAGT
618.	alr_C_7_2	3840683	3840543	GCCGCACCAGGTCGAACGTC-(BRIDGE)-CGCCCTCCCCCGCACGAATC
619.	alr_C_8_2	3840543	3840403	GCGATCCATGTGTGCCCATACGACA-(BRIDGE)-CCCCACACCGGGGCATCGTC
620.	alr_C_9_2	3840403	3840263	ACCATGAACTGGTCCATGCAGATCCG-(BRIDGE)-ATGGTGCCGACAAGATCGGCCC
621.	alr_C_10_2	3840263	3840123	GGGCTGGTGACCACTTCGTAGTGG-(BRIDGE)-GGCAGCGTCGCCGTGCCGCC
622.	ethA_W_1_1	4327673	4327533	AGGTGGTCACCCTGGCAGCTTACTA-(BRIDGE)-AGCGGACGGTCCTCGAGAAGG
623.	ethA_W_2_1	4327533	4327393	CTGGCACCTGCAGGACCGTTG-(BRIDGE)-CGTGTCGATAGTGTCGACATCTCGTTGA
624.	ethA_W_3_1	4327393	4327253	TCCCTGGACCGGACGGCAGG-(BRIDGE)-CCCGACCAAGAGCTACGCCATCC
625.	ethA_W_4_1	4327253	4327113	GGAAAACCGCTGGACCGTTCACATC-(BRIDGE)-CGATCGCCGACGGCAAGCCC
626.	ethA_W_5_1	4327113	4326973	GCCGATCATCCATCCGCAGCACTG-(BRIDGE)-CAAAGCCACGGCACGCTCAGC
627.	ethA_W_6_1	4326973	4326833	GCGCTCACCCACCTACATCGTGT-(BRIDGE)-GCCCGAGGACCTCGACTACGAC
628.	ethA_W_7_1	4326833	4326693	AGAAGTGGCCACGGCGCATG-(BRIDGE)-CGCAGCCAGACCGGGACGGC
629.	ethA_W_8_1	4326693	4326553	ACCTGTTCCGGGCCATTCGTCA-(BRIDGE)-CGGAAGATGTTCCTGAGCCTGATCCA
630.	ethA_W_8_1a	4326693	4326553	ACCTGGTCCGGGCCATTCGTCA-(BRIDGE)-CGGAAGATGTTCCTGAGCCTGATCCA
631.	ethA_W_9_1	4326553	4326413	AGCTTTTTGGTGGGGCGACGG-(BRIDGE)-CGGGAAGGTCGAGGTGGTGACC
632.	ethA_W_10_1	4326413	4326273	AGGCCGACCTGGTGTCGGAG-(BRIDGE)-CGACTATCGACGGACAACAAGTGGACA
633.	ethA_W_11_1	4326273	4326133	CGCTCGCTGGACGAGCTGCC-(BRIDGE)-TTTGTCTGTCGCTTGTTGAATTACATGGACG
634.	ethA_W_12_1	4326133	4325993	CCGGTGGGGGTTTAGCTTTAGCGAC-(BRIDGE)-CAAGCAGGGTTCGCGTACACCG
635.	ethA_W_13_1	4325993	4325853	GGCACCGGTCTTGGTGCTCTTG-(BRIDGE)-GGTTTAGCGCCGGTTTAGGCCATAGT
636.	ethA_C_1_2	4327623	4327483	GGCCGTCCGGCGACGATCGT-(BRIDGE)-TATCAACGTAATGTCGAGGCCGTCAACG
637.	ethA_C_2_2	4327483	4327343	GTGCTCGGTCATGGATCCACGC-(BRIDGE)-TGCCGCCCATGGATTCCCGC
638.	ethA_C_2_2a	4327483	4327343	GTGCTCGGTCATGGATCCACGC-(BRIDGE)-TGCTGCCCATGGATTCCCGC
639.	ethA_C_3_2	4327343	4327203	TCCGGGATAACGGAACAAATCCCAGG-(BRIDGE)-GGCCGCGGTGCTCTTGACGT
640.	ethA_C_3_2a	4327343	4327203	TCCGGGACAACGGAACAAATCCCAGG-(BRIDGE)-GGCCGCGGTGCTCTTGACGT
641.	ethA_C_4_2	4327203	4327063	GAACCGGATATGCCTGTCGATTCCATACAT-(BRIDGE)-CACAGAAAGAGGAATTCGCAGGTGAGGG
642.	ethA_C_4_2a	4327203	4327063	GAACCGGATATGCCTGTCGATTCCATACAT-(BRIDGE)-CGCAGAAAGAGGAATTCGCAGGTGAGGG
643.	ethA_C_5_2	4327063	4326923	CCTCGTCGTAGTTGTAGTAGCCGCTG-(BRIDGE)-CACTGCCGATCACGACGATGTTCTTAGC
644.	ethA_C_6_2	4326923	4326783	GAGCGTGACCGCCGTTGCGC-(BRIDGE)-CGGCAGCCAGCGGTTGAGCT
645.	ethA_C_7_2	4326783	4326643	CCGCGGTGTAGGCCATGGTCTC-(BRIDGE)-TCGTACCCCTCGGGTAGCTGGC
646.	ethA_C_8_2	4326643	4326503	GGGCCGAAGTGCTTTCGCACG-(BRIDGE)-CGGTCGCGGTGAACCGTTCAA
647.	ethA_C_8_2a	4326643	4326503	GGGCCGACGTGCTTTCGCACG-(BRIDGE)-CGGTCGCGGTGAACCGTTCAA
648.	ethA_C_9_2	4326503	4326363	CGCGACCTGAGTTCAGCCGGATTC-(BRIDGE)-CTTGTAGGCCATCGTCGTGGTGATGT
649.	ethA_C_10_2	4326363	4326223	GGGATGCCGGAAAGCATCATGCC-(BRIDGE)-ACGGTGTCAAAACCGTTGTCGTCC
650.	ethA_C_11_2	4326223	4326083	AGCCCGGTCGCTCGACGACC-(BRIDGE)-CACGTAGGTAGTTCTGATTCAGGCGCC
651.	ethA_C_12_2	4326083	4325943	GCGCCGGATGAGCCGGATGT-(BRIDGE)-CGACGACGGCATCATCGTCGTC
652.	ethA_C_13_2	4325943	4325803	CGGGCGATATCGCCTACAGCGA-(BRIDGE)-GCGCTGCGCGGCATCGACAT
653.	gidB_W_1_1	4408437	4408297	TCCGACCGACGCCGCAGTAA-(BRIDGE)-TCGAACGGAAGATCGTCCACGATGC

#	Probe name	Start	End	Sequence
654.	gidB_W_2_1	4408297	4408157	CTGCGATCTTCGGACCGCGG-(BRIDGE)-GCGATGCGTGGCCGAGCGGC
655.	gidB_W_2_1a	4408297	4408157	CTGCGATCTTCGGACCGCCG-(BRIDGE)-GCGATGCGTGGCCGAGCGGC
656.	gidB_W_3_1	4408157	4408017	CGGTGAGCTCCTCGAACGCGG-(BRIDGE)-CTTGGCCTTGCTCGGCGGTAC
657.	gidB_W_3_1a	4408157	4408017	CGGTGAGCTCCTCGAACGCGG-(BRIDGE)-CGTGGCCTTGCTCGGCGGTAC
658.	gidB_W_4_1	4408017	4407877	AGTCTCTTCGAGAGATGGTGACAGATCTGG-(BRIDGE)-TGACCGGGTCGTGGATATCGGTAGC
659.	gidB_W_4_1a	4408017	4407877	AGTTTCTTCGAGAGATGGTGACAGATCTGG-(BRIDGE)-TGACCGGGTCGTGGATATCGGTAGC
660.	gidB_W_5_1	4407877	4407737	AGCATGCCGTTGATACGGCCG-(BRIDGE)-GCGTGGCCGTTGAGATCGTGC
661.	gidB_W_6_1	4407737	4407597	TTGCGTCCGCCCGCGACCGT-(BRIDGE)-AACGGGCGAATGCTCGCCATC
662.	gidB_W_7_1	4407597	4407457	GTCGGGCCAGGCTTCAACTATCGA-(BRIDGE)-GGTGTTCGCACGACGTGGAAAGC
663.	gidB_W_7_1a	4407597	4407457	GTCGGGCCAGGCTTCAACTATCGA-(BRIDGE)-GGTGTTCGCGCGACGTGGAAAGC
664.	gidB_C_1_2	4408387	4408247	CTCCACGCCTTCGCTTTCGCT-(BRIDGE)-AACATTCTCCGCTCTCGAGACGCT
665.	gidB_C_2_2	4408247	4408107	CGTGAGGTCTGTGTCATGTTTCACGTGA-(BRIDGE)-TCCACACCGGGTCCCGCCAA
666.	gidB_C_3_2	4408107	4407967	GGGGTCCCACCAGCCCCCGC-(BRIDGE)-ATGGCACGCCCGGCAACCCG
667.	gidB_C_4_2	4407967	4407827	GTCCGGCCGCGCTATCGCCA-(BRIDGE)-CTGCACCCAGGACTCCTCGGC
668.	gidB_C_5_2	4407827	4407687	TCGCTGCCGCCCAATTGGTC-(BRIDGE)-CGTACTTCGTCGTGAGCCCGC
669.	gidB_C_6_2	4407687	4407547	GATCATCACACGCCGGTGCTCC-(BRIDGE)-CCATCCGTGCCGACCCTCGG
670.	gidB_C_7_2	4407547	4407407	TCACGCCGTCCCTCCACTCG-(BRIDGE)-GCGCGGCCTCAGGCGTCGGT
671.	kasA_W_1_1	2517865	2518004	CGGTGACGTTGTCGCCTACATCCAG-(BRIDGE)-CGTTCGTCGACGACCTGGACATCG
672.	kasA_W_2_1	2518005	2518144	GCCTTCCACCGCTAATGGCGGT-(BRIDGE)-AAGCTCGAGGAAGAAAACCCGGAGG
673.	kasA_W_3_1	2518145	2518284	CGAGTTCGTCACCAAGTGGGATCTAGC-(BRIDGE)-TTCCCCAGCGTTGTGGTGACCG
674.	kasA_W_4_1	2518285	2518424	CGCCGGCAGCCCGGAGGTCG-(BRIDGE)-GGTCAAGATCGGCGGTCACCTCA
675.	kasA_W_5_1	2518425	2518564	CAGATGATCATGCCCAACGGTGCC-(BRIDGE)-ATCCAGACCGGTTCGCCGTTGT
676.	kasA_W_6_1	2518565	2518704	GACGTCGCCGTCTGCGGCGG-(BRIDGE)-GCGGCGGTGATCGGTCTGCA
677.	kasA_W_7_1	2518705	2518844	TGTGTTCGGCGAGGCCGGTG-(BRIDGE)-TGTCGAAGGACCCATCGAGGCG
678.	kasA_W_8_1	2518845	2518984	GTGTTCGTGCCGGTAGGGCG-(BRIDGE)-CGCTGATGCTCATCGAGACGGAGG
679.	kasA_W_9_1	2518985	2519124	GGTTGTGATCAGGCCGCGGTGTA-(BRIDGE)-ATGACTCGCTCGCTGGAGCTGG
680.	kasA_W_10_1	2519125	2519264	CCGATCCCGAGATCGACCTTGACG-(BRIDGE)-CGCGCCGAAGTCTGCGCTGG
681.	kasA_W_11_1	2519265	2519404	CGAGGCCCGAGGTGGGGGTC-(BRIDGE)-TCGTCGCCGGCGAACCGCGC
682.	kasA_W_12_1	2519405	2519544	GCGCTCGCGACCGACGCGGA-(BRIDGE)-CCCCCGCTTGCGGGGGCGAG
683.	kasA_C_1_2	2517915	2518054	GCCGTACTTGTCCTCGGTCTGCAC-(BRIDGE)-ATCTTCGCGCGCAACGCCTG
684.	kasA_C_2_2	2518055	2518194	GGCATCGGGGTTCTCCGACTCA-(BRIDGE)-GGCGAGATCGACGTCGTCGC
685.	kasA_C_3_2	2518195	2518334	CCCTTCCACGTGCTCTCGATGTCC-(BRIDGE)-GGCCCATGTGGCTGTCGACC
686.	kasA_C_4_2	2518335	2518474	CGACATGCGTCGCATGTCGAGTC-(BRIDGE)-CTCGGCTCCACCTAGACCGGTG
687.	kasA_C_5_2	2518475	2518614	TCATCAGGTCGTAGCTCTCGACAATCCT-(BRIDGE)-GGGGTCATCACCCCGGCGCG
688.	kasA_C_6_2	2518615	2518754	CCGACGAACAGGCCGACACC-(BRIDGE)-GCATCATGGAGAACGCCGCGA
689.	kasA_C_7_2	2518755	2518894	GTTGCGGGTCGACATGGCCC-(BRIDGE)-CTTGGCGCCACGGGCTTTGG
690.	kasA_C_8_2	2518895	2519034	CCCAGCAATCGGGCCAACGG-(BRIDGE)-TGGTCGATGTCCGCCGGCGA
691.	kasA_C_9_2	2519035	2519174	CCGTGCCGTGCGCGTTGACG-(BRIDGE)-CGAGCGCACCGACCGCGCCG
692.	kasA_C_10_2	2519175	2519314	TCAGCACCGTGAGCACCGACT-(BRIDGE)-GTTGTTGACTGCGTAGCGGTAATCGC
693.	kasA_C_11_2	2519315	2519454	TGGCCGCCGAACCCGAACGA-(BRIDGE)-CTTGCGAACGTTCCTTCCATATCGGTCC
694.	ndh_W_1_1	2103242	2103102	GGCCTGCAGCGGTCGGGTTG-(BRIDGE)-ATCTGCCCGGGGTCATCACCAC
695.	ndh_W_2_1	2103102	2102962	GGATCTGGGTTCGGCGGGCT-(BRIDGE)-ACTACCGTAGTAGCTAACTGAACTCGCTCA
696.	ndh_W_3_1	2102962	2102822	AATCGCTCCGCCGACCCGGG-(BRIDGE)-AAACGCGGCAAAGAAGCTCAAGCG
697.	ndh_W_4_1	2102822	2102682	GCCTGATCGTCGCCGCGGGT-(BRIDGE)-TCGTGCTGCGTAAGCAGCGC
698.	ndh_W_5_1	2102682	2102542	TCCAGCGATCCGGAACGGCG-(BRIDGE)-GCTGGCCAGTCTTATTTCGGCAACG
699.	ndh_W_6_1	2102542	2102402	CCAAGGCGCGGGTGATTCTGC-(BRIDGE)-GGCCAAGCTACTGACATTCACCGTTG
700.	ndh_W_7_1	2102402	2102262	CCGCAACGGCATCACCGTCAAG-(BRIDGE)-TTGACGCCGCCCCGGCGGTG
701.	ndh_W_8_1	2102262	2102122	GGCCGGGTCCAAGTGCTGCC-(BRIDGE)-GACTCCGACGGCACCGTCCG
702.	ndh_W_9_1	2102122	2101982	CAAGGCCGAACTGGCCGGCG-(BRIDGE)-CGACCTGTCCATTCCCGGGTACC
703.	ndh_W_10_1	2101982	2101842	GGCTGATTTGGCTGGTGCTGCAC-(BRIDGE)-CCAACCCGGCGGAGCGTGAG
704.	ndh_W_11_1	2101842	2101702	CGGCTCGAACAGCTGGCCGA-(BRIDGE)-CTGGCGTACCTGATCGGGTTCAAGA
705.	ndh_W_12_1	2101702	2101562	CGACCGTGCGTCGATGGCGT-(BRIDGE)-GCTGGCCGCCGAGGCGCAGG
706.	ndh_C_1_2	2103192	2103052	GCCCCCGGTGGCTACACACC-(BRIDGE)-TCCTGACGGGGTCACCTCGATGA
707.	ndh_C_2_2	2103052	2102912	GCTGGGGACTCATGTTCCGCTGC-(BRIDGE)-CGATCAGCTTGATGTCAACGTCGGC
708.	ndh_C_3_2	2102912	2102772	CAGGTGATGGGTGGTGCGCG-(BRIDGE)-GGTGACGTTGCCCAACAGTACCTGG
709.	ndh_C_4_2	2102772	2102632	TGCCCGGCCAGGTCGATGTG-(BRIDGE)-CCGGGTGCGAATTCGGCGAA
710.	ndh_C_5_2	2102632	2102492	CAACGCGTCGTCGATGGACTTCATG-(BRIDGE)-CAACACCGGTGGGGCCAGCC
711.	ndh_C_6_2	2102492	2102352	TCGGCGATCTGTCCGGCCATTT-(BRIDGE)-CTGACCGAGCTTTGCGCCCAT
712.	ndh_C_7_2	2102352	2102212	TGCAACCGGGCAGCCGCCCG-(BRIDGE)-GACCAGACCTTGCAGGCCGACT
713.	ndh_C_8_2	2102212	2102072	GACTGGCCGAAACCCCGGCC-(BRIDGE)-CCATATCGCCCACCACGAACACG
714.	ndh_C_9_2	2102072	2101932	CGGCACACCCTCCACAGCGG-(BRIDGE)-CATCGATCCCTTGTCGAAGTACTGGAATGG
715.	ndh_C_10_2	2101932	2101792	GCCGAAAACCTCGAAACCGTGGC-(BRIDGE)-CACGACAGCAGAGTGGTGATCTTGGT
716.	ndh_C_11_2	2101792	2101652	GGCGAGTACTGAGGAAAGTCACCGTC-(BRIDGE)-AGCTGGCCACCTTAGCGCTTGC
717.	ndh_C_12_2	2101652	2101512	ACCGGTTGCCTGGCTAACGCT-(BRIDGE)-GCCGCGCGCCACTATCAGCG
718.	pncA_W_1_1	2289441	2289301	TCGCGGCGTCATGGACCCTATATC-(BRIDGE)-CACCAAGGCCGCGATGACACC
719.	pncA_W_2_1	2289301	2289161	GTAACCGGTGGCGCCGCGCT-(BRIDGE)-TGTGGCTGCCGCGTCGGTAG

#	Probe name	Start	End	Sequence
720.	pncA_W_2_1a	2289301	2289161	GGAACCGGTGGCGCCGCGCT-(BRIDGE)-TGTGGCTGCCGCGTCGGTAG
721.	pncA_W_3_1	2289161	2289021	GTGGCCACCGCATTGCGTCA-(BRIDGE)-GGCCCGCGCCATCAGCGACT
722.	pncA_W_3_1b	2289161	2289021	GGGGCCACCGCATTGCGTCA-(BRIDGE)-GGCCCGCGCCATCAGCGACT
723.	pncA_W_3_1d	2289161	2289021	GTTGCCACCGCATTGCGTCA-(BRIDGE)-GGCCCGCGCCATCAGCGACT
724.	pncA_W_4_1	2289021	2288881	GCACGCCACTGCTGAATTGGCTG-(BRIDGE)-GCGGTACTCCCGGCGCGGAC
725.	pncA_W_4_1a	2289021	2288881	GCACGCCACGGCTGAATTGGCTG-(BRIDGE)-GCGGTACTCCCGGCGCGGAC
726.	pncA_W_4_1b	2289021	2288881	GCACGCCACTGCTGAATTGGCTG-(BRIDGE)-GCGGTCCTCCCGGCGCGGAC
727.	pncA_W_4_1c	2289021	2288881	GCCCGCCACTGCTGAATTGGCTG-(BRIDGE)-GCGGTACTCCCGGCGCGGAC
728.	pncA_W_5_1	2288881	2288741	GCGGGTGTGTCGGCCGATAC-(BRIDGE)-CGGCAACGCGGCGTCGATGA
729.	pncA_W_5_1a	2288881	2288741	CCGGGTGTGTCGGCCGATAC-(BRIDGE)-CGGCAACGCGGCGTCGATGA
730.	pncA_W_5_1c	2288881	2288741	GCGGATGTGTCGGCCGATAC-(BRIDGE)-CGGCAACGCGGCGTCGATGA
731.	pncA_W_6_1	2288741	2288601	GCCGCGCACGACCGCGCCGG-(BRIDGE)-CACCGTCGCCGCGCTGGAGG
732.	pncA_W_6_1b	2288741	2288601	GCCGCGCACGACCGCGCCGG-(BRIDGE)-CACCGTCGCCGAGCTGGAGG
733.	pncA_C_1_2	2289391	2289251	CGGGATAGATCACGCCGGTGATGT-(BRIDGE)-TACGTTCGGGCGACTGCCCG
734.	pncA_C_1_2a	2289391	2289251	CGGGATAGATCACGCCGGTGATGT-(BRIDGE)-CACGTTCGGGCGACTGCCCG
735.	pncA_C_2_2	2289251	2289111	ACGCCCGCATACGTCCACCA-(BRIDGE)-CGTGATGGTAGTCCGCCGCTTCG
736.	pncA_C_2_2a	2289251	2289111	ACGCCCGCATACGTCCACCA-(BRIDGE)-CGTGATGCTAGTCCGCCGCTTCG
737.	pncA_C_3_2	2289111	2288971	TGTGGAAGTCCTTGGTTGCCACGA-(BRIDGE)-GATTGCCGACGTGTCCAGACTGGG
738.	pncA_C_3_2a	2289111	2288971	TGGGGAAGTCCTTGGTTGCCACGA-(BRIDGE)-GATTGCCGACGTGTCCAGACTGGG
739.	pncA_C_3_2d	2289111	2288971	TGTGGAAGTCCTTGGTTGCCACGA-(BRIDGE)-GATTGCCGACGTGTCCGGACTGGG
740.	pncA_C_4_2	2288971	2288831	GGCACCCTTGTAGAACACCGCCTC-(BRIDGE)-TGATCGGTGGCAATACCGACCACA
741.	pncA_C_4_2b	2288971	2288831	GGCACCCTTGTAGAACACCGCCTC-(BRIDGE)-TGATCGGTGGCAATACCGACCCCA
742.	pncA_C_4_2c	2288971	2288831	GGCACCCTTGTAGAACACCGCCTC-(BRIDGE)-TGATCGGTGGCAATACTGACCACA
743.	pncA_C_4_2h	2288971	2288831	GGCACCCTTGTAGAACACCGCCTC-(BRIDGE)-TGATCGGTGGCAATAGCGACCACA
744.	pncA_C_5_2	2288831	2288691	CGGCCGTCTGGCGCACACAA-(BRIDGE)-AAACCAACTCGACGCTGGCGG
745.	pncA_C_5_2d	2288831	2288691	CGGCCGTCTGGCGCACATAA-(BRIDGE)-AAACCAACTCGACGCTGGCGG
746.	pncA_C_5_2e	2288831	2288691	CGGCCGTCGGGCGCACACAA-(BRIDGE)-AAACCAACTCGACGCTGGCGG
747.	pncA_C_6_2	2288691	2288551	GCGGTGCCATCAGGAGCTGC-(BRIDGE)-AACCCACCGGGTCTTCGACCC
748.	rpsL_W_1_1	781323	781462	GATGCCTCGGATGAGACGAATCGAGT-(BRIDGE)-GGCCGCAACGCCCGCTTTGA
749.	rpsL_W_2_1	781463	781602	CCGCAAGGGTCGTCGGGACA-(BRIDGE)-TTGAGGCAAGCTATGCGACACACCC
750.	rpsL_W_3_1	781603	781742	CGCGTGAAGTTGACGAGTCAGGTC-(BRIDGE)-AGATCAGTAAGGTCAAGACCGCGGC
751.	rpsL_W_4_1	781743	781882	TCGCTGGATACGCAGGGTGTCAA-(BRIDGE)-GAGGTCACGGCGTACATTCCCGG
752.	rpsL_W_5_1	781883	782022	TGGTCACCCAGTTGGTGAACAAGGT-(BRIDGE)-GAACCGCAAACAGGCACGCAGC
753.	rpsL_C_1_2	781373	781512	GTAAGCCGCCAGGCACGAGC-(BRIDGE)-TGCCCCGCCACGGTTACCCG
754.	rpsL_C_2_2	781513	781652	GCTTTCACGTTCTGTTTGTCGGCCA-(BRIDGE)-ACGACGCTGCGGGCTGCCCT
755.	rpsL_C_3_2	781653	781792	GTGTACACGCGGGTGCATACACC-(BRIDGE)-GAGTGCTCCTGCAGGTTGTGGC
756.	rpsL_C_4_2	781793	781932	CGCCGCGCACCAGCACCATC-(BRIDGE)-AGCCCTTCTCTTTCTTAGCGCCGT
757.	rpsL_C_4_2a	781793	781932	CGCCGCGCACCAGCACCATC-(BRIDGE)-AGCCCTTCTCCTTCTTAGCGCCGT
758.	rpsL_C_5_2	781933	782072	CGGGCCCCTTGCGTGGCATC-(BRIDGE)-GCGCACCATAAACAATGCGCTCG
759.	thyA_W_1_1	3074661	3074521	GTTTGGCGGCGAGTCGCTGC-(BRIDGE)-GCGGCGGTGTCGGTGGTTTT
760.	thyA_W_2_1	3074521	3074381	CCGGAACCCGCAGCCTGTTC-(BRIDGE)-GGCGGCTTCGCCGCGCTTGC
761.	thyA_W_3_1	3074381	3074241	TGGCTGCACGAGCACGGAGT-(BRIDGE)-GGCCAGCAGATGCGCTATGATTTGT
762.	thyA_W_4_1	3074241	3074101	TTTGCTGCGCACCGATCCCG-(BRIDGE)-CACCATCTGGGACGAATGGGCAAGT
763.	thyA_W_5_1	3074101	3073961	ACCAACGCAGCGCCGACCTG-(BRIDGE)-ATTCCCGGCGCATCATCGTGTCG
764.	thyA_W_6_1	3073961	3073821	TCTACGACAATCACGTCGAGCAAGTACG-(BRIDGE)-TTTCTGGGTGTGCCGTTCAACATCG
765.	thyA_W_7_1	3073821	3073681	GCGATCAAAGCTCCAGTCGCGGTAT-(BRIDGE)-GCTGCAGCTCAGCCGCGAGC
766.	thyA_W_8_1	3073681	3073541	GGCGGCGACATCCCCTGGCG-(BRIDGE)-GAGGCGCGCCGACGACAATG
767.	thyA_C_1_2	3074611	3074471	GTCGACGGGAATACACCCAGATCCG-(BRIDGE)-GATTGACACGCGGTCAGCCTAGC
768.	thyA_C_2_2	3074471	3074331	AGCAGGTCCTCGTATGGCGTCAC-(BRIDGE)-GTAGTGAGCAGCGGGAAACCGGC
769.	thyA_C_3_2	3074331	3074191	TCGTAGGCTACCGATTTGAAATGGACTTTCTTG-(BRIDGE)-AGATCGGCCCGAGTTCGCCT
770.	thyA_C_4_2	3074191	3074051	GCCACGATCGCCATTGTACACCGT-(BRIDGE)-CCGCTCGATTTCGCCGACGT
771.	thyA_C_5_2	3074051	3073911	TGACAGGGCGGCAGCGCCAT-(BRIDGE)-ATGTGGGTGAGCAACGCATAGCTGG
772.	thyA_C_6_2	3073911	3073771	AGCCGGCCTGGGCGGCCATC-(BRIDGE)-CGGCTAGAAGTAGTTTCGGATATGGCCG
773.	thyA_C_7_2	3073771	3073631	TCATAGGTGTACTCGAAGATTGAATCCCGGT-(BRIDGE)-TTCCGGCTTGAAGGCTGTCCGA
774.	thyA_C_8_2	3073631	3073491	TCGTCACACGCGTCACTCCTTGA-(BRIDGE)-TCGTGTGCCCCATGGTGATCTCC
775.	tlyA_W_1_1	1917740	1917879	CGAAGGCATCGCACGTCGTCTTT-(BRIDGE)-CTAGCGTAGGAACGCAATGACCATCGA
776.	tlyA_W_2_1	1917880	1918019	CGTCAACAGGCCGCGGAGTTGAT-(BRIDGE)-CCGAGGCGCACGAGGTGTTG
777.	tlyA_W_3_1	1918020	1918159	GCGCACAAACTAGTCGGTGCGC-(BRIDGE)-CGGCGCCGGCAAGGTGCGCA
778.	tlyA_W_4_1	1918160	1918299	GATACGGCCAGCTGGCGTGG-(BRIDGE)-TGGAGGCGTTCGCGATCGCG
779.	tlyA_W_5_1	1918300	1918439	GCTACCGTGTTGCCCGCGCT-(BRIDGE)-TCGCTGCGCAACGATCCTCG
780.	tlyA_W_6_1	1918440	1918579	GGTGCTCGCGGTCGCGCGGC-(BRIDGE)-GGTTGGATGCGCTTCGCGCG
781.	tlyA_W_7_1	1918580	1918719	GCCAAGGGATTGGAGGATGCGGTG-(BRIDGE)-GGGCACAGGAGCTGGGCTGG
782.	tlyA_W_8_1	1918720	1918859	GCGACAATAAAATTGCGCTTCGCGTG-(BRIDGE)-CACCGTGCGATTAGCGAGGGC
783.	tlyA_C_1_2	1917790	1917929	AGCGAAGCAAGTAGGGCGTCGA-(BRIDGE)-ACCCTTCTCCGCCGACTCCAGG
784.	tlyA_C_2_2	1917930	1918069	GTCGTGCCACGCCGCACTCA-(BRIDGE)-TGGCCGGCTTGACCGCCGGC
785.	tlyA_C_3_2	1918070	1918209	GGTGGTGTCGGACACGGCGG-(BRIDGE)-GCCCGCGTCCAGACAGCGCC

#	Probe name	Start	End	Sequence
786.	tlyA_C_4_2	1918210	1918349	GGTGAACCCACCGGTCGATGC-(BRIDGE)-CGTGCGTTGGTCCGCTCGAG
787.	tlyA_C_5_2	1918350	1918489	TCGCCTCCGGTGTGAGGCCA-(BRIDGE)-GCGGCTTCACCAGTGGAACGATATCG
788.	tlyA_C_6_2	1918490	1918629	GACCTGACCTTTCCCCACCTCAAACT-(BRIDGE)-CAGCGGGCTGGCCTTGACGC
789.	tlyA_C_7_2	1918630	1918769	ACATTGCCCGATGGGCCCGG-(BRIDGE)-CAGAACACTGCGATGAGCGGTCAC
790.	tlyA_C_8_2	1918770	1918909	CGCCCGGTGTGGACGACCAG-(BRIDGE)-TCGTCGGGAGCCAGATGCAACG
791.	embA-embB_C_12_R	4244618	4244757	CCACCACGGTGATCAGCGACAAC-(BRIDGE)-TCTCCACGGTAAGGAAGTAGTAGCGCA
792.	embA-embB_C_14_R	4244898	4245037	AGCAGCAGGCCGACCGCCGT-(BRIDGE)-TTGCGTCGACTATGTAGACCGATGCG
793.	embA-embB_C_24_R	4246298	4246437	GACCGCCGGTCGAGCTGGAC-(BRIDGE)-CCTGATCGGCCGGCACCAGC
794.	embA-embB_C_30_R	4247138	4247277	GTCGGCCGGGTGGAGAACCG-(BRIDGE)-GGCCTGAGGAGGAGCTGGGC
795.	embA-embB_C_41_R	4248678	4248817	TCGCACGATCCCGGCCACCA-(BRIDGE)-GTCCAGCGGCTTCATGAAACCCG
796.	embA-embB_C_4_R	4243498	4243637	GGCCGGCAGTGTGGACAGCA-(BRIDGE)-GCCTCCCGCTGCGATCGTGG
797.	embA-embB_C_9_R	4244198	4244337	TGGCGGGCAGGCGCATCCAG-(BRIDGE)-GGAACACCGCACCAGCGGTG
798.	embA-embB_W_19_R	4245548	4245687	CGCCGGAGGGAAGGGCCCGG-(BRIDGE)-CAAACCCGAGGGCGTGGGCG
799.	embA-embB_W_3_R	4243308	4243447	GCGCCACGCGCGCTGGACAT-(BRIDGE)-CTGCTGTGCGGCATCGTTCCG
800.	embA-embB_W_42_R	4248768	4248907	GGCGTACCGGAACACACGGTG-(BRIDGE)-ACGTACTCGTCGAGCCTGATACCAATG
801.	embA-embB_W_7_R	4243868	4244007	CGCTGACGCAGCGGTGATCG-(BRIDGE)-GGCGGTCCTGGTAGCCATGGT
802.	embC_C_19_R	4242238	4242377	CCGGGTCGGCGGTGACGTCG-(BRIDGE)-GCCGGGCGCGGGAGCCGTTG
803.	embC_C_20_R	4242378	4242517	CCGGGTCCAGGTTGTAGGGCA-(BRIDGE)-CACCACCAGCAGCGGCGCCC
804.	embC_C_21_Ra	4242518	4242657	TCGAATCGCCCGGCCGCCGT-(BRIDGE)-GGTGCGCGCAGGTTACGCCA
805.	embC_C_21_R	4242518	4242657	TCGAATCGCCCGGCCGCCGT-(BRIDGE)-GGTGCGCGCAGGTTGCGCCA
806.	embC_C_5_R	4240278	4240417	ACTCAGCGGGGCGGTGACCA-(BRIDGE)-GCGCAGCGGTGCACCGGGGT
807.	embC_C_6_R	4240418	4240557	TCGTAGCCGCTGCGCTCACC-(BRIDGE)-GCCATCTTCAGCGGCGTGGG
808.	embC_C_7_R	4240558	4240697	CGCTACCCCGAGGATCATGGCG-(BRIDGE)-CGATAACCAGGGTGTCCAGACCGC
809.	embC_W_20_R	4242328	4242467	CATGCTGCGGTCGGGCTGGT-(BRIDGE)-CGAAGGGGGCACCACGGCCG
810.	embC_W_21_R	4242468	4242607	CGGACACCACGGTGGGTCGATG-(BRIDGE)-ACCGGCTGCCCACCAACGAG
811.	embC_W_6_R	4240368	4240507	GCCACCGGGTCTGAGCTTCTCG-(BRIDGE)-TCGGACTGGTGCAGGGACCC
812.	embC_W_8_R	4240648	4240787	GGTGTCCGAGCATGCGGGCT-(BRIDGE)-CCTGCCCGCGCGCTGGTGGT
813.	gyrB-gyrA_C_14_R	6868	7007	GCATGAACCGGAACAACAACGTCAACAAC-(BRIDGE)-GACCGTCGCGCTCGCGGTCG
814.	gyrB-gyrA_C_20_R	7708	7847	CCCTCAGCATCTCCATCGCCAACG-(BRIDGE)-CGCGATGCCGCCTGACCCGT
815.	gyrB-gyrA_C_21_R	7848	7987	CGGGATATTGGTTGCCATGCCGAC-(BRIDGE)-GGGAAGTCCGGGCCTTTAACCCG
816.	gyrB-gyrA_C_31_R	9248	9387	TGTCGCGCAGGTTGACCGCC-(BRIDGE)-CACGACCCATTGGCCGCAGC
817.	gyrB-gyrA_C_33_R	9528	9667	CCTTTACCGCCGCGGCCCTG-(BRIDGE)-CGTGCCGCGGTGCGGATCAC
818.	gyrB-gyrA_C_4_R	5468	5607	CCGCGGCCGTCGTCGGCGAC-(BRIDGE)-ACGCCGTGCAGACCACCAGA
819.	gyrB-gyrA_W_33_R	9478	9617	GCGTTGATTGTCGACGACGACAGC-(BRIDGE)-CGACGTCAGGGGGCTATGCGA
820.	gyrB-gyrA_W_34_R	9618	9757	TTGGCCATCGCGCGCAACGC-(BRIDGE)-GAGCTGTATGCCGTCACTTCCGGC
821.	gyrB-gyrA_W_4_R	5418	5557	GGTGATGACACAACTACATGCCGGC-(BRIDGE)-GTTATGCAACCACAGTGAACGTAGTGCTG
822.	iniB-iniA-iniC_C_11_R	410637	410776	TGCGGTTGGGTAACCGCCGG-(BRIDGE)-CCGTACGACGGCAGTTCGATGGG
823.	iniB-iniA-iniC_C_15_R	411197	411336	CGGGCCCGGCGGCCAGCACA-(BRIDGE)-GCAGCGGGCTGGGCGCGCCG
824.	iniB-iniA-iniC_C_19_R	411757	411896	CGAACGTATTTCGCCGAGTACCCCAG-(BRIDGE)-CTGCTGGGCTTCCCGTTTGCG
825.	iniB-iniA-iniC_C_29_R	413157	413296	ACAATGGTGGCGTCGATGAGTTCCT-(BRIDGE)-GGTGCGCAACAGGAACACCACC
826.	iniB-iniA-iniC_C_4_R	409657	409796	GCTAGCCAGGCCCGCACCGA-(BRIDGE)-CTCAATCACGGCAGTAAAACCCAGACCG
827.	iniB-iniA-iniC_C_5_R	409797	409936	ACCTGAGCGCCGACCTCGGC-(BRIDGE)-CCGGCCGCGCTCCCACCGAT
828.	iniB-iniA-iniC_C_6_R	409937	410076	CGACGCCGGCACCGATAGCC-(BRIDGE)-CGGCTGAGACACCGATCTGGCT
829.	iniB-iniA-iniC_W_11_R	410587	410726	CGGTGTTTGACGTCGGTCACGAG-(BRIDGE)-CGCAAGTTCCGGCGCGGGCC
830.	iniB-iniA-iniC_W_16_R	411287	411426	GCTGGGGCTGCTACCCGAGG-(BRIDGE)-CGGTGGCCGCGAGGTGTTGC
831.	iniB-iniA-iniC_W_20_R	411847	411986	GGACCACGACCTACGAACCCGC-(BRIDGE)-GTGACCGACTTGCTTCGGATTTGGAG
832.	iniB-iniA-iniC_W_5_R	409747	409886	GCTTTGGCGGCGGGGTTGGC-(BRIDGE)-AGGTCGGCTTGGCTGCCCAG
833.	iniB-iniA-iniC_W_6_R	409887	410026	GTTGGCGCTGGTGTCGGCGC-(BRIDGE)-CTGGGTCTGGGTGGTCAGGCC
834.	kasA_C_2_R	2518080	2518219	AAGCCTCGCCTGAACGTTGGC-(BRIDGE)-ACCCTTCCACGTGCTCTCGATGTC
835.	kasA_C_3_R	2518220	2518359	CCGCTCTCGCCGGCCAACAG-(BRIDGE)-TACGACATGCGTCGCATGTCGAGT
836.	kasA_C_5_R	2518500	2518639	CCGGGGGCCGCCCGCATTCA-(BRIDGE)-CGAGCCCGACGAACAGGCCG
837.	kasA_W_4_R	2518310	2518449	CAGACCGGTTCGCCGTTGTTGT-(BRIDGE)-GATCCGGTCGACAGCCACATGGG
838.	kasA_W_6_R	2518590	2518729	CGAAGGACCCATCGAGGCGCTG-(BRIDGE)-GGGCCCGCGCCGGGGTGATG
839.	katG_C_7_Ra	2155257	2155396	CGCCGCGGCCATGGGGTCCG-(BRIDGE)-GCCGACCAGATCGGCCGGGT
840.	katG_C_7_R	2155257	2155396	CGCCGCGGCCATGGGGTCCG-(BRIDGE)-GCCGACCAGATCGGCCGGGC
841.	katG_W_4_R	2155727	2155866	CGGGGGCGGCATGCAGCGGT-(BRIDGE)-AGTGATGACCACCTCGCAGCCG
842.	katG_W_8_R	2155167	2155306	CCGGTAAGGACGCGATCACCAGC-(BRIDGE)-GTCACACTTTCGGTAAGACCCATGGCG
843.	mabA_inhA_C_12_R	1674715	1674854	TCGCGCGCCACGAACCTGTT-(BRIDGE)-AGCAGCTGGATCTGGGCGCC
844.	mabA_inhA_C_13_R	1674855	1674994	CGCTGATCCCAGCCCTCCTCG-(BRIDGE)-GCGCGCCGCCGTCGGCGTAG
845.	mabA_inhA_C_3_R	1673455	1673594	ATGGGGGTTTGGCCCCTTCAGT-(BRIDGE)-GGCGCTCCGGATCCACGGTG
846.	mabA_inhA_W_13_R	1674805	1674944	GTGTGCGCGCTGCTGTCTGA-(BRIDGE)-ATCGTCGGCGGTGCGCTCGG
847.	mabA_inhA_W_14_R	1674945	1675084	CCCGAGCAGGTGCGGCCGTT-(BRIDGE)-CTGGCTGCCGGCGACCACGG
848.	mabA_inhA_W_4_R	1673545	1673684	GGTAGAAGAGCACCAGGGTCCGGT-(BRIDGE)-GCTGCCGACGGCCACAAGGT
849.	oxyR-ahpC_C_10_R	2725466	2725605	CGCCCCTGATCAGCTTGCCG-(BRIDGE)-TGGCACGGTCATTGCCCCAGG
850.	oxyR-ahpC_C_2_R	2726586	2726725	ACGAGCTGTGCGCATGCAACTG-(BRIDGE)-GACCGCGTGACCTTTATCGTCGACC
851.	oxyR-ahpC_C_8_Ra	2725746	2725885	CTCATGCAGTCACAACAAAGTCAGCTCTG-(BRIDGE)-TGCGGAATCAGTGTCCCCCCCA

#	Probe name	Start	End	Sequence
852.	oxyR-ahpC_C_8_R	2725746	2725885	CTCATGCAGTCACAACAAAGTCAGCTCTG-(BRIDGE)-TGCGGAATCAGTGTCACCCCCA
853.	oxyR-ahpC_W_3_R	2726496	2726635	GCATCGGGAAGGGTAACGTTTTGAGGTC-(BRIDGE)-GAGACGAACTGGATCTCGTTGTTGGGG
854.	oxyR-ahpC_W_9_R	2725656	2725795	GCGCGACGAATCGGTTTGGTGTTT-(BRIDGE)-ACCGTCGTGCAGTGCGTGAC
855.	pncA_C_1_R	2289227	2289366	GAGCGGCGGCCACCCAACCG-(BRIDGE)-GATCAACGCCCGCATACGTCCAC
856.	pncA_C_5_R	2288667	2288806	GGCCAAGCCATTGCGTACCGC-(BRIDGE)-GTTCGGCGGTGCCATCAGGAG
857.	pncA_W_2_R	2289137	2289276	CGCGCCATCAGCGACTACCTG-(BRIDGE)-CTGCCCGGGCAGTCGCCCGA
858.	pncA_W_6_R	2288577	2288716	GGGTCGGGTTGTTCACCGGTGAC-(BRIDGE)-CGCACCGCCAGCGTCGAGTT
859.	rpoB_C_14_R	761532	761671	GACACCATCTGGCGGGGCGA-(BRIDGE)-GTGCCCACCAGCGGGGCCTC
860.	rpoB_C_26_R	763212	763351	CGCAGTTCGATCGCCGCACC-(BRIDGE)-ACGGGTTTAGTAATTTTGCGACAGCTTTACG
861.	rpoB_C_9_R	760832	760971	TCATCGTGGTCTGACCCTCGTGC-(BRIDGE)-GCGACATGCCGACCCGGATC
862.	rpoB_W_10_R	760922	761061	CAACATCCGGCCGGTGGTCG-(BRIDGE)-GCGTACGGTCGGCGAGCTGA
863.	rpoB_W_15_R	761622	761761	CGAGGAGGTGTCGGCCGACTACAT-(BRIDGE)-CAGCGCCAGGCGGTGCCGCT
864.	rpoB_W_17_R	761902	762041	AGGACGTGCTCACCTCGATCCAC-(BRIDGE)-GTCCCTGTACTGACGACGGCGA
865.	rrs-rrl_C_13_R	1473442	1473581	ACCCGGCTCTCGCCCACTAC-(BRIDGE)-CCACTATCCAGTTCTCAAACACCACACCC
866.	rrs-rrl_C_23_R	1474842	1474981	GGGTGGCTGCTTCTAAGCCAACCTC-(BRIDGE)-CCCTACCCACACCCACCACAAGG
867.	rrs-rrl_C_30_R	1475822	1475961	AACTTACCCGACAAGGAATTTCGCTACCTT-(BRIDGE)-GGGGTCTTTTCGTCCTGCCGC
868.	rrs-rrl_W_10_R	1472947	1473086	CGTGCTGGCAACATGAGACAAGGGT-(BRIDGE)-GTACCGGCCATTGTAGCATGTGTGAAG
869.	rrs-rrl_W_11_R	1473087	1473226	TCGCGGCATCGCAGCCCTTT-(BRIDGE)-GCCCGGGAACGTATTCACCGC
870.	rrs-rrl_W_12_R	1473227	1473366	CGTGACGGGCGGTGTGTACAAG-(BRIDGE)-AGCCGCACCTTCCGGTACGG
871.	rrs-rrl_W_15_R	1473647	1473786	GCGCCCTTAGACACTTACAAACACAACAAAA-(BRIDGE)-GGTTTCCCCATTCGGAAATCCTCGGA
872.	rrs-rrl_W_16_R	1473787	1473926	GGGTAGCACGACATCACTCGTGCTG-(BRIDGE)-CCTGTTCCGCGTTCGCTCGC
873.	rrs-rrl_W_17_R	1473927	1474066	CGGTTACCCATGCGTGCGGTTTAG-(BRIDGE)-CGTCTACGGCAGACCATCCCAGG
874.	rrs-rrl_W_18_R	1474067	1474206	GTTTTCGCGTACCGGGCTCTCAC-(BRIDGE)-TACTAATCCGCTATCGGTCATCGAGGAGT
875.	rrs-rrl_W_19_R	1474207	1474346	GGGGTACTTTTCACCATTCCCTCACGG-(BRIDGE)-CTCGCAGGCTCATTCTTCAAAAGGCA
876.	rrs-rrl_W_20_R	1474347	1474486	GGGTTAACCTTGCGACATGTCCCTGA-(BRIDGE)-CTGGCCATGGGTAGATCACTCCGC
877.	rrs-rrl_W_21_R	1474487	1474626	CGGTCTTACCCGCGCTTCACC-(BRIDGE)-AACGCTGCACCTAAATGCATTTCGGG
878.	rrs-rrl_W_22_R	1474627	1474766	ACCTCCGCGGTGAACCACGC-(BRIDGE)-TTCCCTTTCGACGTACGGAGCTTATCC
879.	rrs-rrl_W_24_R	1474907	1475046	TGAGCCCCGCTACATTATCGGCG-(BRIDGE)-TGCATTCTCACTCCCCCACCCTCC
880.	rrs-rrl_W_25_R	1475047	1475186	CACTTGCCTTGTCGCTACTCATGCC-(BRIDGE)-GAATATCAACCCGTTGTCCATCGACTACGC
881.	rrs-rrl_W_26_R	1475187	1475326	GCGCCCACACACGGGTACGG-(BRIDGE)-TGCGTCACCCCTTCGCTTGACT
882.	rrs-rrl_W_27_R	1475327	1475466	CCACTGACTGGTACGGCTACCTTCC-(BRIDGE)-TTTTCTTGGCAGCAGAGGATCACCGA
883.	rrs-rrl_W_28_R	1475467	1475606	CGTGTGTGTGCTCGCTAGAGGC-(BRIDGE)-ATTCCGGTCCCCCTTCTCCCGA
884.	rrs-rrl_W_29_R	1475607	1475746	CCCACCGCAAGGGTGTTCACGAT-(BRIDGE)-CTTAACCTTCCAGCACCGGGCAGG
885.	rrs-rrl_W_2_R	1471827	1471966	CCAAACAAAACCCAAACACTCCCTTTGGA-(BRIDGE)-CACGTGTTACTCACCCGTTCGCC
886.	rrs-rrl_W_30_R	1475747	1475886	CCCTTGCGGGTTAACGGGTCCT-(BRIDGE)-AGTTGAGAAGTCGTTACGCCATTCGTGC
887.	rrs-rrl_W_32_R	1476027	1476166	GCCCCAACTGGCGTCGAGGTTTC-(BRIDGE)-CATTTTAGGAGGCAACCGCCCCAG
888.	rrs-rrl_W_33_R	1476167	1476306	GGAACCTTTGGGCGCCTCCGTTA-(BRIDGE)-TCCACTCGGGGGTGCCGGAT
889.	rrs-rrl_W_34_R	1476307	1476446	CCTTTTATCCGTTGAGCGACACCCCT-(BRIDGE)-GCCCAACCCTTGGGACCTGCT
890.	rrs-rrl_W_35_R	1476447	1476586	CGTGCCGCTTTAATGGGCGAACA-(BRIDGE)-GTGCACCAGAGGTTCGTCCGTCC
891.	rrs-rrl_W_36_R	1476587	1476726	TGCCCCTGGCGGGACAACTG-(BRIDGE)-TGAACCCGTGTTCTGCGGGGG
892.	rrs-rrl_W_3_R	1471967	1472106	CCCGAAGTGCAGGGCAGATCACC-(BRIDGE)-CACCCCACCAACAAGCTGATAGGCC
893.	rrs-rrl_W_4_R	1472107	1472246	TCGTCGCCTTGGTAGGCCGT-(BRIDGE)-CGGCGTCGCTGCATCAGGCT
894.	rrs-rrl_W_5_R	1472247	1472386	CGAAGGCCGTCATCCCCCACG-(BRIDGE)-CGCTCGCACCCTACGTATTACCGC
895.	rrs-rrl_W_6_R	1472387	1472526	GCTCTTTACGCCCAGTAATTCCGGACAA-(BRIDGE)-CGCTACACCAGGAATTCCAGTCTCCC
896.	rrs-rrl_W_7_R	1472527	1472666	TGTTCCTCCTGATATCTGCGCATTCCAC-(BRIDGE)-CCTAGTACCCACCGTTTACGGCGT
897.	rrs-rrl_W_8_R	1472667	1472806	CGGATCCCAAGGAAGGAAACCCACA-(BRIDGE)-TGCATCGAATTAATCCACATGCTCCGC
898.	rrs-rrl_W_9_R	1472807	1472946	TCAAACCCAGGTAAGGTTCTTCGCGT-(BRIDGE)-TGCGCTCGTTGCGGGACTTAAC
899.	thyA_C_1_R	3074447	3074586	GGCGAAGCCGGGCACAGCGA-(BRIDGE)-GCAGCAGGTCCTCGTATGGCGT
900.	thyA_C_6_Ra	3073747	3073886	CCGGCCCAGATGAACTCGCCGAC-(BRIDGE)-GTGTACTCGAAGATTGAATCCCGGTCGG
901.	thyA_C_6_R	3073747	3073886	CCGGTCCAGATGAACTCGCCGAC-(BRIDGE)-GTGTACTCGAAGATTGAATCCCGGTCGG
902.	thyA_W_1_R	3074497	3074636	CTTCGCCGCGCTTGCGATCG-(BRIDGE)-TGGCCTCCGTTGTACTCCTGTGG
903.	thyA_W_2_R	3074357	3074496	GGCCAGCAGATGCGCTATGATTTGT-(BRIDGE)-CCGCTAGGCTGACCGCGTGT
904.	thyA_W_6_R	3073797	3073936	AGCTCAGCCGCGAGCCGCGG-(BRIDGE)-CCAGCTATGCGTTGCTCACCCAC
905.	tlyA_C_5_R	1918375	1918514	CCACTACCAGGTCGACGCGACC-(BRIDGE)-ACCTGACCTTTCCCCACCTCAAACTG

Supplementary Table 4: Parameters used in the different software used to call variants from MIP read data.

Program	*Version*	*Parameters*
megablast (used by MIPCleaner)	2.2.14	-p 90 -W 10 -e 1e-1 -X16 –JF –m8 –FF -v9000000 -b9000000
Bowtie	0.12.7	-q -k 2 -l 20 -m 5 --best –strata (with the additional filtering out of alignments with NM:i:x tags having x>5)
samtools	0.1.18	mpileup -u -R -B -q0 -Q0 -C0 -d1000000
bcftools	0.1.18	view -vg -p0.05
vcfutils.pl	0.1.18	varFilter -d 10 -a 5 -D1000000 -W10 -10 -20 -30 -40 -e0
Stampy	1.0.23	Default
Platypus	0.5.2	Default. Filtered variants with platypusfilter='badreads' or quality≤30 or purity <40%.

Supplementary Table 8: Isolate count and major drug resistance profiles.

The count of isolates resistant to one or more of the first line drugs but not to both INH and RIF is the sum of the number in rows 4, 5 and 6. There were no strains resistant to PZA but sensitive to both INH and RIF. Note: INH DST results were missing for 20 strains, RIF DST results were missing for 6 strains, and 20 strains were missing DST data for both INH and RIF. * INH: isoniazid, RIF: rifampicin, EMB: ethambutol, STR: Streptomycin, PZA: pyrazinamide. ** FLQ: Fluoroquinolones (Resistance defined as resistance to one or more of CIP, LEVO, OFLX, MOXI, and GATI). ***INJ: Second line Injectables (Resistance defined as resistance to more or more of KAN, CAP, AMK). R: resistant, S: sensitive, S^T: sensitive or not tested. Blank cells imply any resistance status to the drug.

Description	*INH*	*RIF*	*EMB*	*STR*	*PZA*	*FLQ***	*INJ****	*Number of isolates*
	S							136
		S						206
Drug sensitive	S	S	S	S	S^T			78
INH-resistant not MDR	R	S						83
RIF-resistant not MDR	S	R						21
EMB or STR resistant, INH & RIF sensitive	S	S	R or	R				37
MDR +	R	R						1130
MDR (+PZA R)	R	R	S		R			80
MDR (+EMB R)	R	R	R		S			203
MDR (+EMB & PZA R)	R	R	R		R			499
MDR (+FLQ R)	R	R				R	S	44
MDR (+INJ R)	R	R				S	R	384
XDR	R	R				R	R	219

Supplementary Table 9: Representative coverage statistics per strain.

The table lists the number of raw and filtered reads and the numbers and percentages of nucleotides covered by at least one, 20 or 100 reads for each strain. The average across the 1397 strains for coverage of >=20 reads was 97.1%. Strain CDC-26 and all strains with less than 95% 20 fold coverage were excluded from the analysis.

Strain	*Raw*	*Filtered*	*%*	*Mapped*	*%*	*total bases*	*bases with >1 reads*	*%*	*bases with >20 reads*	*%*	*bases with >100 reads*	*%*
CDC-1	1332475	661480	49.64	593186	89.67	42367	42181	99.56	40538	95.68	36928	87.16
CDC-2	1140934	888377	77.86	834275	93.91	42367	42076	99.31	39969	94.33	37714	89.01
CDC-3	1127476	864265	76.65	813794	94.16	42367	42160	99.51	40103	94.65	37044	87.43
CDC-4	1271267	977264	76.87	916578	93.79	42367	42307	99.85	40597	95.82	38274	90.33
CDC-5	1280316	1019478	79.62	956616	93.83	42367	42058	99.27	40189	94.85	38270	90.32
CDC-6	1425663	788775	55.32	718103	91.04	42367	42254	99.73	40625	95.88	37577	88.69
CDC-7	1182549	884482	74.79	826942	93.49	42367	42123	99.42	39872	94.11	37231	87.87
CDC-8	802869	507251	63.17	465113	91.69	42367	42187	99.57	40077	94.59	35555	83.92
CDC-9	1131109	926413	81.90	873982	94.34	42367	42288	99.81	40479	95.54	37849	89.33
CDC-10	1183926	1025972	86.65	969370	94.48	42367	41816	98.69	39888	94.14	38117	89.96
CDC-11	1241962	857267	69.02	796556	92.91	42367	42182	99.56	39990	94.38	37696	88.97
CDC-12	1258136	803934	63.89	743964	92.54	42367	42300	99.84	40776	96.24	37703	88.99
CDC-13	1483784	872030	58.77	805457	92.36	42367	42221	99.65	40469	95.52	37783	89.18
CDC-14	1408847	619702	43.98	549706	88.70	42367	42301	99.84	40902	96.54	36777	86.80
CDC-15	1197985	879377	73.40	823343	93.62	42367	42019	99.17	39787	93.91	37869	89.38
CDC-16	1439593	548695	38.11	476889	86.91	42367	42231	99.67	40406	95.37	36037	85.05
CDC-17	1392928	863975	62.02	796024	92.13	42367	42277	99.78	40720	96.11	37851	89.34
CDC-18	1390106	1035578	74.49	970765	93.74	42367	42241	99.70	40445	95.46	38065	89.84
CDC-19	1350358	937661	69.43	872850	93.08	42367	42017	99.17	39767	93.86	37584	88.71
CDC-20	1100454	790026	71.79	736114	93.17	42367	42134	99.45	40307	95.13	37441	88.37
CDC-21	1196697	915027	76.46	860158	94.00	42367	41938	98.98	39796	93.93	37465	88.42
CDC-22	1143123	1011827	88.51	960456	94.92	42367	42236	99.69	40458	95.49	38003	89.69
CDC-23	971048	444426	45.76	396557	89.22	42367	42121	99.41	39808	93.95	34544	81.53
CDC-24	1191376	647398	54.34	592547	91.52	42367	42080	99.32	40134	94.72	36684	86.58
CDC-25	1592348	1050713	65.98	978170	93.09	42367	42294	99.82	40650	95.94	38425	90.69
CDC-26	2125259	153823	7.23	27156	17.65	42367	42019	99.17	29487	69.59	4648	10.97
CDC-27	1468007	685090	46.66	617514	90.13	42367	42194	99.59	40164	94.80	37057	87.46
CDC-28	1435655	933140	64.99	870938	93.33	42367	42121	99.41	40045	94.51	38186	90.13
CDC-29	1547957	985023	63.63	913906	92.78	42367	42326	99.90	40965	96.69	38449	90.75
CDC-30	1501204	1070529	71.31	1004002	93.78	42367	42299	99.83	40523	95.64	38377	90.58
Average	1310514	821633	64.41	758701	90.00	42367	42167	99.52	39931	94.25	36373	85.85

Supplementary Table 10: Bases detected with WGS for the SNPs called using MIPs.

For each strain in which MIPs detected additional SNPs, the SNPs are listed with genomic coordinates, reference and variant base, reference base, depth of coverage, and bases detected with WGS. (uppercase/lowercase letter=base in +/- direction and ./, = reference base in +/- direction). These data show that the SNP detected by MIPs was frequently a WGS low coverage site (<20 reads). In 80/84 cases WGS detected the MIP allele as a minor allele with a read count of <20.

Strain/SNP	***Reference base***	***Depth***	***Bases detected (./, = reference base in +/- direction)***
01-R0450			
1673818AG	A	38	,....,,.,,...,...,.,.,,.,,,,..,,,..,,,
4247884CA	C	19	AA,aaAaAaAa,aAaAAaa
01-R0572			
761161TC	T	19	CcCccCCcCCcCcCCCccc
4242182GT	G	18	tTtTtTtTtTtttttctt
02-R1848			
9304GA	G	19	CAaAaaAAaaaAaaAaAaa
1917972AG	A	13	GGggGGgGgGGgG
3073852TC	T	17	cCCCcccccccCcccc
4242803GC	G	18	CCCCCCCccCCCccCCCC
4247729GA	G	14	AAAAaaaaaAaAaa
03-R0268			
9304GA	G	19	AaaAAAAAAaa,AAaAaAA
761155CT	C	20	.t...,,t...,,.T,.,,,
4242643CT	C	18	tTTttTTtttTttTTttT
03-R0303			
4408091GT	G	6	TT,.,.
4408092TC	T	9	CC,.,.c..
03-R0483			
763031TC	T	15	CccccCcCccCcCc
4326996GC	G	37	C,,T,.,,,.,.,,........,,,,,,,.c.,.,,.
03-R0888			
4408156AC	A	15	cccCCCCccccccCC
4408159CG	C	14	gGGGGggggggGGg
03-R1082			
2155783GA	G	18	a,aaCA,a,AaAaA.AAa
3073868TC	T	17	cCccccCCcCAccCCcc
04-R0292			
761155CT	C	17	TtttTTtTttTttgttg
761156GC	G	17	CcccCCcCccCcccccc
1917972AG	A	15	GGggGgggGgGGggg
4408091GT	G	15	tTTTtCT,.,.....
4408092TC	T	14	CCCcCC,.,g...c
CDC-604			
781687AG	A	19	GgGgGgggggggGgGgGgg
4407927TG	T	17	GggGGggGgGgGggggG
CDC-605			
781395TC	T	17	cccCcCccccCCCccCc

Strain/SNP	***Reference base***	***Depth***	***Bases detected (./, = reference base in +/- direction)***
1673425CT	C	12	ttTtTtTgTTgt
CDC-606			
2289103TC	T	16	cGcCcCCCCCCccCCC
4242643CT	C	10	TTTTtGTttT
4243460CT	C	19	tttttTTtTTtttTtTtTt
4326996GA	G	21	,,...,.,..,.,,...,,,.
4407927TG	T	19	GGGGggGGGGGg.ggGggG
CDC-607			
4242643CT	C	14	ttTtTTTttTttTt
CDC-608			
7362GC	G	18	CCccccccccCcccCcccc
7582AC	A	14	CCCCCccCCcCccc
7585GC	G	13	CCCccCCcCcccC
9304GA	G	19	aaa.AaAAa,AAaAaaaaa
763031TC	T	14	ccCcCccccccCcCc
781395TC	T	16	CcCcCcCCcCCcCcCC
1917972AG	A	15	GggggGgGGGggGGG
2154724CA	C	16	,aAAaaAAAAaaaAAa
2288775AG	A	18	GGGCGgGGGGGGggggGg
4242643CT	C	19	tt,tttttTtttTtTgTTT
4243460CT	C	15	TttttttTtTtttgT
4407588TC	T	18	CcCcccCCCCcCccCcCc
4407620AG	A	19	gGgGGGGGgGGgGGGCggg
CDC-610			
1476468CT	C	63	,.....,..,..,.......,,.,.,,..,,,,..,.,.,,,.,,,.,,..,..,a,..,..,
M200HiQ			
3841083AC	A	13	cCcCccCCccccCc
M230HiQ			
7582AC	A	8	Cccccccc
7585GC	G	11	CccccccccCCc
9304GA	G	11	aAA.AcA.aA.
761155CT	C	13	ttTttttTTttgg
1917972AG	A	14	GGggGGgggggggG
4242643CT	C	19	tttttTTTtttttTTTTtt
M27HiQ			
7362GC	G	10	ccCCCcCCca
7582AG	A	12	CGGggGGgGgGg
7585GC	G	11	CCccCCcCcCc
9304GA	G	10	AaAAaaAaAa
761155CT	C	12	tTttTgTTTggt
781395TC	T	10	CcCcccCCCC
781435GC	G	14	cCcCCCcCcCCcCC
781687AG	A	11	ggggGggGGgg
781922AG	A	14	GGggggggggggggG
1917972AG	A	7	GggggGG
2155168CG	C	14	gG,gGgGgGGGGgg

Strain/SNP	***Reference base***	***Depth***	***Bases detected (./, = reference base in +/- direction)***
2288848CT	C	15	TtTtTTtTTtTtTt
4242643CT	C	17	TTtTtTtTTTTtTtTt
4242803GC	G	6	CCCccC
4243190GC	G	12	cCCcccCCcCcC
4247502TC	T	11	cCCCccCCCCC
4249408GA	G	15	aaaAaaAAaACAaaa
4326630AC	A	12	cCCcCcccCcCc
4407904GA	G	10	aAAAAaaaaa
M41HiQ			
1476288TC	T	84	,,.,CC..,,....,...,.,,.,,,..,,.,,,,CA..,,,,.,,.,,,..,..,...,,....,,...,..,.,,.a.....
M6HiQ			
4242643CT	C	17	TTTTTtTtTTTTTTTTT
M95HiQ			
4242643CT	C	17	GAtTTTttTTTTTTtTTt
P2-ITL			
1673818AG	A	173	C,...,g,,.T..,,.,,,,,.,,,.,,,..,,.,,.,,,,.,...,......,,..,,.,...,...,,..,,,..,..,,,,,,,,.....,...,,,...,.....,,..,,,......,,,.........,.......,,,,,..,,,,,,,,...,,,...,,,....
R257HiQ			
1917972AG	A	8	GggggcGg
2288777CT	C	6	GTT,..
4242643CT	C	10	ttTtTttTTT
4243460CT	C	17	,TtTttTtTTtTtTttt
4327409TG	T	25	GGgGggGGgGG,GGGgggggGGGGG

Supplementary Table 11: Mutations missed by MIPs and detected by Sanger.

Sanger sequencing was performed in 133 strains with MIP results that did not explain the resistance phenotype.

Isolate ID	gene	Genomic coordinate (gene coord)	Sanger detected variant	Note
2419	*embB*	4249195 (codon 894)	A	High coverage but no variant
2304	*rrl*	1476698	G	High coverage but no variant
825	*katG*	2153739	delcgagacggggat	long deletion
737	*pncA*	2288862	delAGGTCGATG	long deletion
711	*pncA*	2288862	delAGGTCGATG	long deletion
2227	*pncA*	2289016	delACTCCCGGCGC	long deletion
2252	*pncA*	2288862	delAGGTCGATG	long deletion
781	*rrl*	1475790 (3945)	insC	Low coverage <5 reads at the site
2498	*rrs*	1472723 (878)	G	Low coverage <5 reads at the site
2315	*pncA*	2289099	T	low mapping quality
2321	*pncA*	2288752	A	low mapping quality
2523	*pncA*	2288740	T	low mapping quality
2320	*pncA*	2289099	T	low mapping quality
2222	*pncA*	2289099	T	low mapping quality
2266	*rrs*	1473246 (1401)	A	Minor allele in 28% of reads
763	*rrs*	1473246 (1401)	A	Minor allele in 24% of reads
2445	*rrs*	1473246 (1401)	A	Minor allele in 33% of reads
2316	*pncA*	2289066	G	Minor allele in 31% of reads

Supplementary Table 12: Number of variants found in each locus targeted.

*only non-synonymous or non-coding/promoter mutations were included in the count. See Supplementary Table 2 for H37Rv gene coordinates targeted, in addition 100bp of 5’ and 3’ flanking sequence was targeted to capture neighboring promoter regions. Region labeled promoter if it precedes one or more genes designated to be an operon on the +/sense strand, or it follows such genes on the –/anti-sense strand.

Sequenced Region	number of different variants*	Length	Diversity
promoter_*ahpC*	15	105	14%
ahpC	20	588	3%
alr	26	1227	2%
ddl	19	1122	2%
embA	63	3285	2%
embB	107	3297	3%
embC	50	3285	2%
ethA	262	1470	18%
gid	173	675	26%
gyrA	77	2517	3%
gyrB	52	2145	2%
inhA	13	810	2%
iniA	37	1923	2%
iniB	21	1440	1%
iniC	22	1482	1%
kasA	30	1251	2%
katG	192	2223	9%
intergenic_*murA-rrs*	6	126	5%
fabG1	13	744	2%
ndh	31	1392	2%
oxyR'	4	517	1%
pncA	254	561	45%
rpoB	169	3519	5%
rpsL	8	375	2%
rrl	219	3138	7%
rrs	142	1537	9%
thyA	45	792	6%
tlyA	30	807	4%
promoter_*gyrB-gyrA*	5	125	4%
intergenic_*gyrB-gyrA*	3	34	9%
intergenic_*gyrA*-Rv0007	3	95	3%
promoter_*iniB-iniA-iniC*	5	176	3%
intergenic_*iniB-iniA*	2	36	6%
promoter_*rpoB*	2	143	1%
intergenic_*iniC-lpqJ*	4	126	3%
intergenic_*rpoB-rpoC*	0	45	0%
promoter_*rpsL*	7	217	3%
promoter_*fabG1-inhA*	8	140	6%
intergenic_*rrs-rrl*	11	275	4%

intergenic_*rrl-rrf*	3	101	3%
intergenic_*fabG1-inhA*	1	18	6%
intergenic_*inhA-hemZ*	0	5	0%
intergenic_Rv1693-*tlyA*	0	7	0%
promoter_*ndh*	3	141	2%
intergenic_*katG-furA*	7	34	21%
promoter_*pncA*	8	40	20%
intergenic_*kasA-kasB*	1	30	3%
intergenic_*ahpC-ahpD*	0	24	0%
intergenic_*dfrA-thyA*	3	70	4%
promoter_*thyA*	12	164	7%
promoter_*ddl*	3	77	4%
intergenic_*alr*-Rv3792	2	128	2%
promoter_*embA-embB*	18	85	21%
intergenic_*embB*-Rv3796	18	67	27%
intergenic_*menG-ethA*	0	35	0%
promoter_*ethA*	5	75	7%
promoter_*gid*	7	131	5%
total	2241		

*** only non-synonmous variants, or non-coding/promoter variants are included in the count**

Supplementary Table 13: Results of univariate analysis associating mutations with drug resistance across the 1397 strain set.

The results are for the purpose of data description and were not used in the subsequent predictive modeling. The Fisher Exact test was used. Only significant mutations are shown in order of their odds ratio (OR). Bonferroni corrected P-value=raw P-value*total number of mutations tested, for each drug. The number of variables/drug is listed in Supplementary Table 6 under 'Including Singleton Variables'. Of the 54 mutations listed 47 were positively associated (*i.e.* OR>1). Resist: Resistant isolate, Sens: Sensitive isolate.

Variant	Drug	Resist with	Sens with	Resist without	Sens without	OR	corr P-value
SNP_N_1473246_A1401G_rrs	AMK	186	14	42	715	222.9	8.01E-134
SNP_N_1472359_A514C_rrs	AMK	45	27	183	702	6.4	2.56E-10
SNP_N_1473246_A1401G_rrs	CAP	193	16	384	347	10.9	4.48E-27
SNP_N_1473343_G1498T_rrs	CAP	15	31	562	332	0.3	1.13E-02
SNP_CN_7582_AG_gyrA_D94G	CIP	48	0	167	695	Inf	6.17E-30
SNP_CN_6735_AC_gyrB_N538T	CIP	7	0	208	695	Inf	3.89E-03
SNP_CN_7581_GT_gyrA_D94Y	CIP	6	0	209	695	Inf	1.26E-02
SNP_CN_7570_CT_gyrA_A90V	CIP	31	2	184	693	58.1	6.67E-16
SNP_CN_7582_AC_gyrA_D94A	CIP	15	1	200	694	51.8	7.02E-07
SNP_CN_7572_TC_gyrA_S91P	CIP	7	1	208	694	23.3	1.66E-02
SNP_CS_6208_GA_gyrB_A362A	CIP	10	2	205	693	16.8	2.34E-03
SNP_CN_6140_GT_gyrB_V340L	CIP	14	9	201	686	5.3	1.05E-02
SNP_CN_4243392_AG_embA_N54D	EMB	40	0	874	416	Inf	1.42E-04
SNP_CN_4247429_AG_embB_M306V	EMB	272	12	642	404	14.2	2.71E-32
SNP_CN_4248003_AG_embB_Q497R	EMB	40	2	874	414	9.5	1.11E-02
SNP_CN_4247431_GC_embB_M306I	EMB	85	7	829	409	6.0	1.99E-05
SNP_CN_4247431_GA_embB_M306I	EMB	160	19	754	397	4.4	8.23E-09
SNP_CN_409569_GA_iniB_A70T	EMB	66	8	848	408	4.0	1.46E-02
SNP_CS_412316_CG_iniA_G493G	EMB	138	118	776	298	0.4	1.99E-05
SNP_CS_4247887_CG_embB_G458G	EMB	102	97	812	319	0.4	1.99E-05
SNP_CN_4242075_GA_embC_R738Q	EMB	8	20	906	396	0.2	4.97E-03
SNP_CN_1674263_TC_inhA_I21T	ETH	30	1	582	373	19.2	6.50E-03
SNP_CN_4326116_GA_ethA_T453I	ETH	26	1	586	373	16.5	2.38E-02
SNP_CN_4326333_CG_ethA_A381P	ETH	51	4	561	370	8.4	1.52E-04
SNP_P_1673425_CT.15_fabG1-inhA	ETH	194	30	418	344	5.3	2.38E-16
SNP_CS_4326259_CT_ethA_L405L	ETH	4	17	608	357	0.1	3.15E-02
SNP_CN_7582_AG_gyrA_D94G	GATI	13	1	13	27	25.4	6.61E-03
SNP_CN_4247431_GA_embB_M306I	INH	188	0	1031	136	Inf	1.04E-06
SNP_CN_2155168_CG_katG_S315T	INH	874	2	345	134	169.0	6.38E-60
SNP_P_1673425_CT.15_fabG1-inhA	INH	264	2	955	134	18.5	6.83E-08
SNP_CN_4247429_AG_embB_M306V	INH	280	7	939	129	5.5	1.14E-04
SNP_N_1473246_A1401G_rrs	KAN	160	8	97	623	127.4	8.26E-93
SNP_CN_7582_AC_gyrA_D94A	LEVO	6	0	104	437	Inf	3.48E-03
SNP_CN_7581_GT_gyrA_D94Y	LEVO	5	0	105	437	Inf	1.34E-02
SNP_CN_7582_AG_gyrA_D94G	LEVO	38	1	72	436	228.1	9.10E-26
SNP_CN_7570_CT_gyrA_A90V	LEVO	25	1	85	436	126.8	1.18E-15
SNP_CN_6735_AC_gyrB_N538T	LEVO	6	1	104	436	24.9	1.34E-02
SNP_CS_6208_GA_gyrB_A362A	LEVO	8	2	102	435	16.9	3.48E-03
SNP_CN_6140_GT_gyrB_V340L	LEVO	11	5	99	432	9.5	1.92E-03
SNP_CN_7581_GA_gyrA_D94N	OFLX	7	1	62	200	22.3	2.97E-02
SNP_CN_7582_AC_gyrA_D94A	OFLX	10	2	59	199	16.6	3.27E-03
SNP_CN_7570_CT_gyrA_A90V	OFLX	14	6	55	195	8.2	2.89E-03

SNP_CN_7582_AG_gyrA_D94G	OFLX	22	11	47	190	8.0	3.53E-05
SNP_CN_3073852_TC_thyA_H207R	PAS	5	1	73	848	57.5	2.72E-03
SNP_CN_3074449_AT_thyA_L8Q	PAS	5	2	73	847	28.8	4.45E-03
SNP_CN_2289090_TC_pncA_H51R	PZA	49	0	562	374	Inf	6.65E-08
SNP_CN_2289202_AC_pncA_C14G	PZA	0	10	611	364	0.0	3.63E-02
SNP_CN_761155_CT_rpoB_S450L	RIF	739	5	424	201	70.0	1.40E-66
SNP_CN_761110_AT_rpoB_D435V	RIF	140	1	1023	205	28.0	8.42E-07
SNP_CS_762836_CG_rpoB_G1010G	RIF	178	58	985	148	0.5	1.00E-02
SNP_CN_781822_AG_rpsL_K88R	STR	30	0	911	414	Inf	5.03E-03
SNP_CN_781687_AG_rpsL_K43R	STR	224	5	717	409	25.5	1.49E-29
SNP_N_1472359_A514C_rrs	STR	84	2	857	412	20.2	2.27E-09
SNP_N_1473246_A1401G_rrs	STR	225	25	716	389	4.9	2.20E-14

Supplementary Table 14: Association between *embB* M306I and *embB* M306V mutations and isoniazid resistance stratified by ethambutol resistance.

The p-value was calculated using the Fisher Exact test. Resist: resistant isolate. Sens: Sensitive isolate.

EMB	INH Resistant with *embB* 306 mutation	INH Resistant without *embB* 306 mutation	INH Sensitive with *embB* 306 mutation	INH Sensitive without *embB* 306 mutation	OR	P-value
Sens	19	278	0	115	[1.9, Inf)	0.002
Resist	160	732	0	20	[1.1, Inf)	0.03

Supplementary Table 15: Promoter Regions and their association with drug resistance across the 1397 strain set.

The results are for the purpose of data description and were not used in the subsequent predictive modeling. Variants were counted regardless of their position within the presumptive promoter region (see online-only text). Strains with one or more promoter variants were tallied across the resistant and sensitive pools for each relevant drug.

Promoter Region	Drug	Resistant with Variant	Sensitive with Variant	Resistant without Variant	Sensitive without Variant	Raw P-value	Corrected P-value
fabG1-inhA	ETH	236	46	376	328	2.2E-16	3.08E-15
fabG1-inhA	INH	324	3	895	133	2.0E-13	2.80E-12
pncA	PZA	31	3	580	371	0.000	0.003
embA-embB	EMB	94	20	820	396	0.001	0.010
embA-embB	INH	112	2	1107	134	0.001	0.012
iniB-iniA-iniC	EMB	7	11	907	405	0.009	0.130
iniB-iniA-iniC	INH	13	5	1206	131	0.028	0.392
rpoB	RIF	20	8	1143	198	0.057	0.798
ahpC	INH	126	9	1093	127	0.230	1.000
gyrB-gyrA	LEVO	1	2	109	435	0.490	1.000
ndh	INH	4	0	1216	136	1	1
ethA	ETH	6	3	606	371	1	1
gid	STR	8	3	933	411	1	1

Supplementary Table 17: The minimum list of predictive variables by drug ordered by decreasing measure of predictive importance.

INH

1. SNP_CN_2155168_CG_katG_S315T
2. SNP_P_1673425_CT.15_fabG1.inhA
3. SNP_CN_4247429_AG_embB_M306V
4. SNP_CN_4247431_GA_embB_M306I
5. SNP_CN_1674481_TG_inhA_S94A
6. SNP_CN_4247431_GC_embB_M306I
7. SNP_CN_2155168_CT_katG_S315N
8. SNP_CN_409569_GA_iniB_A70T
9. SNP_CN_4247730_GC_embB_G406A
10. SNP_P_1673423_GT.17_fabG1.inhA
11. SNP_CN_4247729_GA_embB_G406S
12. SNP_CN_4247402_TG_embB_S297A
13. SNP_CN_2518919_GA_kasA_G269S
14. SNP_CN_2726338_TG_ahpC_V49G
15. SNP_P_4243221_CT.12_embA.embB
16. SNP_P_1673432_TC.8_fabG1.inhA
17. SNP_P_1673432_TG.8_fabG1.inhA
18. SNP_CN_2155167_GT_katG_S315R

RIF

1. SNP_CN_761155_CT_rpoB_S450L
2. SNP_CN_761110_AT_rpoB_D435V
3. SNP_CN_761139_CT_rpoB_H445Y
4. SNP_CN_761140_AG_rpoB_H445R
5. SNP_CN_761140_AT_rpoB_H445L
6. SNP_CN_761155_CG_rpoB_S450W
7. SNP_CN_761139_CG_rpoB_H445D
8. SNP_CN_761277_AT_rpoB_I491F
9. SNP_CN_760314_GT_rpoB_V170F
10. SNP_CN_761109_GT_rpoB_D435Y
11. SNP_CN_761161_TC_rpoB_L452P
12. SNP_CN_761102_AC_rpoB_Q432H
13. SNP_CN_761095_TC_rpoB_L430P
14. SNP_CN_761155_CA_rpoB_S450.

PZA

1. SNP_CN_2289090_TC_pncA_H51R
2. SNP_P_2289252_TC.30_pncA
3. SNP_CN_2289070_AG_pncA_F58L
4. SNP_CN_2288883_AG_pncA_L120P
5. SNP_CN_2289213_TG_pncA_Q10P
6. SNP_CN_2288839_TG_pncA_T135P
7. SNP_CN_2289081_GA_pncA_P54L

8 SNP_CN_2288883_AC_pncA_L120R
9 INS_F_2288725_i516C_pncA
10 SNP_CN_2289016_TG_pncA_T76P
11 SNP_CN_2288953_CT_pncA_G97S
12 SNP_CN_2288933_GC_pncA_Y103.
13 SNP_CN_2288818_TC_pncA_T142A
14 SNP_CN_2288847_CT_pncA_G132D
15 SNP_CN_2289212_CG_pncA_Q10H
16 SNP_CN_2288841_GA_pncA_A134V
17 INS_F_2288851_i390C_pncA
18 INS_F_2288887_i354A_pncA
19 SNP_CN_2288848_CT_pncA_G132S
20 SNP_P_2289245_TA.37_pncA
21 SNP_CN_2289207_TC_pncA_D12G
22 SNP_CN_2288820_TG_pncA_Q141P
23 SNP_CN_2288704_CA_pncA_V180F
24 SNP_CN_2288805_GT_pncA_A146E
25 SNP_CN_2289180_AC_pncA_V21G
26 SNP_CN_2288973_AG_pncA_I90T
27 INS_F_2288851_i390CC_pncA
28 SNP_CN_2289216_AC_pncA_V9G
29 SNP_CN_2289072_TA_pncA_H57L
30 SNP_CN_2288887_AC_pncA_W119G
31 SNP_CN_2289097_CT_pncA_D49N
32 SNP_CN_2288805_GA_pncA_A146V
33 DEL_F_2288939_d302TCCGGTGTAG_pncA
34 SNP_CN_2288988_AG_pncA_L85P
35 SNP_CN_2289207_TG_pncA_D12A
36 SNP_CN_2289228_AG_pncA_I5T
37 SNP_CN_2289220_CT_pncA_D8N
38 DEL_F_2289069_d172A_pncA_F58L
39 DEL_N_2288942_d299GGTGTA_pncA
40 SNP_CN_2289015_GA_pncA_T76I
41 DEL_F_2288776_d465GCACCCTG_pncA
42 SNP_CN_2288925_AG_pncA_F106S
43 SNP_CN_2288835_TC_pncA_D136G
44 SNP_CN_2289040_AG_pncA_W68R
45 SNP_CN_2289099_TG_pncA_K48T
46 SNP_CN_2289214_GA_pncA_Q10.
47 SNP_CN_2288944_TG_pncA_T100P
48 INS_F_2288825_i416C_pncA
49 SNP_CN_2289042_GT_pncA_S67.
50 SNP_CN_2288826_AG_pncA_V139A
51 SNP_CN_2288878_GA_pncA_Q122.
52 SNP_CN_2288697_AC_pncA_L182W

53 SNP_CN_2289073_GA_pncA_H57Y
54 SNP_CN_2289150_AC_pncA_I31S
55 SNP_CN_2288727_AG_pncA_L172P
56 SNP_CN_2288919_CT_pncA_G108E
57 SNP_CN_2288935_AG_pncA_Y103H
58 INS_F_2288835_i406T_pncA
59 SNP_CN_2288952_CT_pncA_G97D
60 SNP_CN_2288697_AG_pncA_L182S
61 SNP_CN_2288853_AT_pncA_V130E
62 SNP_CN_2288730_GA_pncA_A171V
63 SNP_CN_2288775_AG_pncA_L156P
64 SNP_CN_2288850_AC_pncA_V131G
65 INS_F_2289009_i232C_pncA_G78G
66 INS_F_2289050_i191T_pncA_Y64.
67 SNP_CN_2288964_AC_pncA_V93G
68 SNP_CN_2288853_AC_pncA_V130G
69 DEL_F_2288697_d544AACT_pncA
70 SNP_CN_2289009_CA_pncA_G78V
71 SNP_CN_2289043_AG_pncA_S67P
72 SNP_CN_2288938_CG_pncA_A102P
73 SNP_P_2289252_TG.30_pncA
74 SNP_CN_2289073_GC_pncA_H57D
75 SNP_CN_2289206_GC_pncA_D12E
76 DEL_F_2289060_d181GTGCCGGA_pncA
77 SNP_CN_2289202_AG_pncA_C14R
78 SNP_CN_2289050_AT_pncA_Y64.
79 SNP_CN_2289046_AG_pncA_S66P
80 SNP_CN_2288784_GT_pncA_T153N
81 SNP_CN_2289037_GA_pncA_P69S
82 SNP_CN_2288718_AC_pncA_M175R
83 SNP_CN_2289042_GC_pncA_S67W
84 SNP_CN_2288956_TG_pncA_K96Q
85 SNP_CN_2289142_AC_pncA_Y34D
86 SNP_CN_2288844_AG_pncA_I133T
87 SNP_CN_2289040_AC_pncA_W68G
88 SNP_CN_2289054_TG_pncA_D63A
89 SNP_CN_2289090_TG_pncA_H51P
90 SNP_CN_2289186_AG_pncA_L19P
91 SNP_CN_2288826_AC_pncA_V139G
92 SNP_CN_2288818_TG_pncA_T142P
93 SNP_CN_2288817_GA_pncA_T142M
94 SNP_CN_2289219_TC_pncA_D8G
95 SNP_CN_2289072_TC_pncA_H57R
96 SNP_CN_2289028_AG_pncA_C72R
97 INS_F_2288942_i299T_pncA

98 DEL_F_2288923_d318C_pncA
99 SNP_CN_2288742_GA_pncA_T167I
100 SNP_CN_2289095_GC_pncA_D49E
101 SNP_CN_2288956_TC_pncA_K96E
102 SNP_CN_2288703_AC_pncA_V180G
103 SNP_CN_2289069_AC_pncA_F58C
104 SNP_CN_2288955_TG_pncA_K96T
105 SNP_CN_2288764_TC_pncA_T160A
106 SNP_P_2289251_AC.31_pncA
107 SNP_CN_2288696_CA_pncA_L182F
108 SNP_CN_2288778_AC_pncA_V155G
109 SNP_CN_2289103_TC_pncA_T47A
110 SNP_CN_2288943_GA_pncA_T100I
111 SNP_CN_2288718_AG_pncA_M175T
112 SNP_CN_2289030_TC_pncA_H71R
113 SNP_CN_2289162_AG_pncA_L27P
114 SNP_CN_2289030_TG_pncA_H71P
115 SNP_CN_2288827_CT_pncA_V139M
116 SNP_CN_2289231_AG_pncA_L4S
117 SNP_CN_2289213_TC_pncA_Q10R
118 SNP_CN_2288965_CA_pncA_V93L
119 SNP_CN_2289001_AC_pncA_F81V
120 SNP_CN_2289054_TC_pncA_D63G
121 SNP_CN_2288766_AC_pncA_L159R
122 SNP_CN_2288869_CA_pncA_V125F
123 SNP_CN_2289091_GA_pncA_H51Y
124 SNP_CN_2288859_AC_pncA_V128G

EMB

1 SNP_CN_4247429_AG_embB_M306V
2 SNP_CN_4247431_GA_embB_M306I
3 SNP_CN_4247431_GC_embB_M306I
4 SNP_CN_4247730_GC_embB_G406A
5 SNP_CN_4248003_AG_embB_Q497R
6 SNP_CN_4249518_AG_embB_H1002R
7 SNP_CN_409569_GA_iniB_A70T
8 SNP_CN_4247729_GA_embB_G406S
9 SNP_CN_4247431_GT_embB_M306I
10 SNP_CN_4247429_AC_embB_M306L
11 SNP_P_4243222_CA.11_embA.embB
12 SNP_CN_4247574_AC_embB_D354A
13 SNP_CN_4247495_GT_embB_D328Y
14 SNP_CN_4249583_GA_embB_D1024N
15 SNP_CN_4243392_AG_embA_N54D
16 SNP_P_4243225_CT.8_embA.embB
17 SNP_CN_4242182_GT_embC_A774S

18 SNP_CN_4247729_GT_embB_G406C

STR

1 SNP_CN_781687_AG_rpsL_K43R
2 SNP_N_1472359_A514C_rrs
3 SNP_CN_781822_AC_rpsL_K88T
4 SNP_N_1473246_A1401G_rrs
5 SNP_CN_781822_AG_rpsL_K88R
6 SNP_CN_4407809_CA_gid_D132Y
7 SNP_N_1472358_C513T_rrs
8 SNP_CN_4407927_TG_gid_E92D
9 SNP_N_1472751_A906G_rrs
10 SNP_CN_4407934_AC_gid_L90R
11 SNP_N_1472362_C517T_rrs
12 SNP_N_1472753_A908C_rrs
13 SNP_CN_781822_AT_rpsL_K88M
14 SNP_CN_4407832_AG_gid_V124A
15 SNP_CN_4408091_GT_gid_P38T
16 SNP_I_1473637_A.21_rrs.rrl
17 SNP_CN_4408094_CT_gid_G37R
18 DEL_F_4407640_d562A_gid
19 SNP_N_1473109_T1264G_rrs
20 SNP_CN_4407967_AC_gid_L79W
21 SNP_CN_4407967_AG_gid_L79S
22 SNP_CN_4407768_CA_gid_L145F
23 SNP_CN_4407995_TG_gid_S70R
24 DEL_F_4407852_d350C_gid
25 SNP_N_1473167_T1322G_rrs
26 DEL_F_4408023_d179T_gid
27 DEL_F_4408116_d86G_gid
28 SNP_CN_4408060_TG_gid_H48P
29 SNP_CN_4408138_TC_gid_Y22C
30 SNP_CN_4408064_GA_gid_R47W
31 SNP_CN_4408148_CG_gid_A19P
32 SNP_CN_4407947_GA_gid_L86F
33 SNP_CN_4407916_CA_gid_R96L
34 SNP_CN_4407748_AG_gid_L152S
35 SNP_N_1473343_G1498T_rrs
36 SNP_CN_4407985_CG_gid_G73A
37 SNP_CN_4408102_CT_gid_G34E

ETH

1 SNP_P_1673425_CT.15_fabG1.inhA
2 SNP_CN_4326333_CG_ethA_A381P
3 SNP_CN_4326116_GA_ethA_T453I
4 SNP_CN_1674481_TG_inhA_S94A
5 SNP_CN_4326714_GA_ethA_Q254.

6 SNP_CN_1674263_TC_inhA_I21T
7 SNP_CN_4327416_CA_ethA_A20S
8 DEL_F_4326184_d1289G_ethA
9 SNP_CN_4327380_AC_ethA_Y32D
10 SNP_CN_1674434_TG_inhA_V78G
11 INS_F_4326141_i1332C_ethA
12 SNP_CN_4326600_GA_ethA_R292.
13 SNP_CN_4326713_TG_ethA_Q254P
14 SNP_CN_4326305_GA_ethA_S390F
15 SNP_P_1673423_GT.17_fabG1.inhA
16 INS_F_4326722_i751C_ethA
17 SNP_CN_1673449_AC_fabG1_T4P
18 SNP_CN_4327311_AG_ethA_S55P
19 SNP_CN_4326278_GT_ethA_S399.
20 SNP_CN_4327148_CT_ethA_W109.

KAN

1 SNP_N_1473246_A1401G_rrs
2 SNP_CN_1918745_AG_tlyA_.269W

CAP

1 SNP_N_1473246_A1401G_rrs
2 SNP_N_1473109_T1264G_rrs
3 SNP_N_1472753_A908C_rrs
4 SNP_N_1473160_G1315A_rrs
5 SNP_N_1473343_G1498T_rrs

AMK

1 SNP_N_1473246_A1401G_rrs
2 SNP_N_1472359_A514C_rrs

CIP

1 SNP_CN_7582_AG_gyrA_D94G
2 SNP_CN_7570_CT_gyrA_A90V
3 SNP_CN_7582_AC_gyrA_D94A
4 SNP_CN_7581_GT_gyrA_D94Y
5 SNP_CN_6735_AC_gyrB_N538T
6 SNP_CN_7572_TC_gyrA_S91P
7 SNP_CN_7566_GA_gyrA_D89N

LEVO

1 SNP_CN_7582_AG_gyrA_D94G
2 SNP_CN_7570_CT_gyrA_A90V
3 SNP_CN_7581_GT_gyrA_D94Y
4 SNP_CN_7581_GA_gyrA_D94N
5 SNP_CN_7582_AC_gyrA_D94A
6 SNP_CN_7572_TC_gyrA_S91P
7 SNP_CN_7563_GT_gyrA_G88C
8 SNP_CN_7566_GA_gyrA_D89N

OFLX

1 SNP_CN_7582_AG_gyrA_D94G
2 SNP_CN_7570_CT_gyrA_A90V
3 SNP_CN_7582_AC_gyrA_D94A
4 SNP_CN_7581_GA_gyrA_D94N
5 SNP_CN_6735_AC_gyrB_N538T
6 SNP_CN_7581_GC_gyrA_D94H

PAS

1 SNP_CN_3073852_TC_thyA_H207R
2 SNP_CN_3074449_AT_thyA_L8Q
3 SNP_CN_3074182_TC_thyA_Q97R
4 SNP_P_3074479_AG.157_thyA

Supplementary Table 18: *rpoB* MTB H37RV – E.coli codon number conversion table

Genetic Variant	H37Rv codon number	E.coli codon number
SNP_CN_759814_AG_rpoB_D3G	3	3
SNP_CN_759831_AC_rpoB_T9P	9	NA
SNP_CN_759861_CT_rpoB_Q19*	19	NA
SNP_CN_759873_AG_rpoB_N23D	23	NA
SNP_CN_759886_CA_rpoB_P27H	27	NA
SNP_CN_759903_GT_rpoB_V33F	33	13
SNP_CN_759930_CT_rpoB_L42F	42	22
SNP_CN_759940_CT_rpoB_P45L	45	25
SNP_CN_759939_CA_rpoB_P45T	45	25
SNP_CN_759939_CG_rpoB_P45A	45	25
SNP_CN_759939_CT_rpoB_P45S	45	25
SNP_CN_760033_CT_rpoB_P76L	76	45
DEL_N_760050_d243GAG_rpoB	82	51
SNP_CN_760081_AG_rpoB_D92G	92	61
SNP_CN_760130_TG_rpoB_D108E	108	77
SNP_CN_760164_GA_rpoB_D120N	120	89
SNP_CN_760216_AC_rpoB_N137T	137	106
SNP_CN_760224_GA_rpoB_E140K	140	116
SNP_CN_760234_GA_rpoB_S143N	143	119
SNP_CN_760256_CG_rpoB_D150E	150	126
INS_F_760254_i447GGTCCTAGTCC_rpoB	150	126
SNP_CN_760270_CT_rpoB_T155I	155	131
SNP_CN_760295_CA_rpoB_N163K	163	139
SNP_CN_760305_CT_rpoB_R167C	167	143
SNP_CN_760309_TG_rpoB_V168G	168	144
SNP_CN_760315_TC_rpoB_V170A	170	146
INS_F_760316_i509TTCC_rpoB	170	146
SNP_CN_760314_GT_rpoB_V170F	170	146
SNP_CN_760321_AG_rpoB_Q172R	172	148
SNP_CN_760429_TC_rpoB_F208S	208	186
SNP_CN_760461_CT_rpoB_R219C	219	197
SNP_CN_760479_CG_rpoB_R225G	225	203
SNP_CN_760500_CA_rpoB_L232I	232	210
SNP_CN_760522_GA_rpoB_S239N	239	217
SNP_CN_760525_AG_rpoB_E240G	240	218
SNP_CN_760527_CA_rpoB_Q241K	241	219
SNP_CN_760534_TC_rpoB_V243A	243	221
SNP_CN_760555_AG_rpoB_E250G	250	228
INS_F_760570_i763CTGCTCAAGG_rpoB	255	350
SNP_CN_760616_CA_rpoB_D270E	270	365
SNP_CN_760645_CT_rpoB_P280L	280	375
SNP_CN_760663_CT_rpoB_A286V	286	381
SNP_CN_760666_AT_rpoB_Q287L	287	382
SNP_CN_760701_CT_rpoB_R299C	299	394
INS_N_760731_i924TCAACGAAGGATTCCACA_rpoB	309	404
SNP_CN_760799_CG_rpoB_D331E	331	424
INS_F_760867_i1060A_rpoB_G354D	354	NA
SNP_CN_760882_TG_rpoB_V359G	359	NA

SNP_CN_760914_CT_rpoB_R370C	370	451
SNP_CN_760927_CT_rpoB_T374M	374	455
SNP_CN_760969_CT_rpoB_S388L	388	469
SNP_CN_761002_CT_rpoB_T399I	399	480
SNP_CN_761001_AG_rpoB_T399A	399	480
SNP_CN_761005_CA_rpoB_T400N	400	481
SNP_CN_761004_AG_rpoB_T400A	400	481
SNP_CN_761004_AC_rpoB_T400P	400	481
SNP_CN_761008_AG_rpoB_Q401R	401	482
SNP_CN_761032_AG_rpoB_Q409R	409	490
SNP_CN_761043_AG_rpoB_N413D	413	494
SNP_CN_761064_GT_rpoB_A420S	420	501
SNP_CN_761074_AC_rpoB_E423A	423	504
SNP_CN_761089_GA_rpoB_S428N	428	509
SNP_CN_761090_CG_rpoB_S428R	428	509
SNP_CN_761090_CA_rpoB_S428R	428	509
SNP_CN_761092_AC_rpoB_Q429P	429	510
SNP_CN_761093_GT_rpoB_Q429H	429	510
SNP_CN_761095_TC_rpoB_L430P	430	511
SNP_CN_761095_TG_rpoB_L430R	430	511
SNP_CN_761097_AC_rpoB_S431R	431	512
INS_N_761098_i1291GCC_rpoB	431	512
SNP_CN_761097_AG_rpoB_S431G	431	512
SNP_CN_761100_CA_rpoB_Q432K	432	513
SNP_CN_761100_CG_rpoB_Q432E	432	513
SNP_CN_761102_AC_rpoB_Q432H	432	513
SNP_CN_761101_AC_rpoB_Q432P	432	513
SNP_CN_761101_AT_rpoB_Q432L	432	513
INS_N_761103_i1296TTC_rpoB	433	514
DEL_N_761105_d1298CATGGACCAGAA_rpoB	433	514
SNP_CN_761108_GT_rpoB_M434I	434	515
SNP_CN_761108_GA_rpoB_M434I	434	515
INS_N_761107_i1300TGG_rpoB	434	515
SNP_CN_761110_AC_rpoB_D435A	435	516
SNP_CN_761109_GC_rpoB_D435H	435	516
SNP_CN_761110_AG_rpoB_D435G	435	516
SNP_CN_761109_GT_rpoB_D435Y	435	516
SNP_CN_761110_AT_rpoB_D435V	435	516
SNP_CN_761109_GA_rpoB_D435N	435	516
SNP_CN_761117_CA_rpoB_N437K	437	518
SNP_CN_761115_AC_rpoB_N437H	437	518
SNP_CN_761118_AC_rpoB_N438H	438	519
SNP_CN_761121_CT_rpoB_P439S	439	520
SNP_CN_761127_TC_rpoB_S441P	441	522
SNP_CN_761128_CA_rpoB_S441*	441	522
SNP_CN_761128_CT_rpoB_S441L	441	522
SNP_CN_761134_TG_rpoB_L443W	443	524
SNP_CN_761136_AC_rpoB_T444P	444	525
SNP_CN_761140_AG_rpoB_H445R	445	526
DEL_N_761140_d1333ACA_rpoB	445	526
SNP_CN_761139_CG_rpoB_H445D	445	526
SNP_CN_761139_CA_rpoB_H445N	445	526
SNP_CN_761139_CT_rpoB_H445Y	445	526

SNP_CN_761140_AT_rpoB_H445L	445	526
SNP_CN_761141_CA_rpoB_H445Q	445	526
SNP_CN_761140_AC_rpoB_H445P	445	526
SNP_CN_761142_AC_rpoB_K446Q	446	527
SNP_CN_761149_GA_rpoB_R448Q	448	529
SNP_CN_761155_CG_rpoB_S450W	450	531
SNP_CN_761154_TC_rpoB_S450P	450	531
SNP_CN_761155_CA_rpoB_S450*	450	531
SNP_CN_761155_CT_rpoB_S450L	450	531
SNP_CN_761161_TC_rpoB_L452P	452	533
SNP_CN_761160_CG_rpoB_L452V	452	533
SNP_CN_761167_CG_rpoB_P454R	454	535
SNP_CN_761167_CT_rpoB_P454L	454	535
SNP_CN_761208_GA_rpoB_D468N	468	549
SNP_CN_761241_CA_rpoB_P479T	479	560
SNP_CN_761244_AG_rpoB_I480V	480	561
SNP_CN_761248_AC_rpoB_E481A	481	562
SNP_CN_761251_CA_rpoB_T482N	482	563
SNP_CN_761253_CT_rpoB_P483S	483	564
SNP_CN_761268_AG_rpoB_I488V	488	569
SNP_CN_761268_AC_rpoB_I488L	488	569
SNP_CN_761277_AT_rpoB_I491F	491	572
SNP_CN_761277_AG_rpoB_I491V	491	572
SNP_CN_761277_AC_rpoB_I491L	491	572
SNP_CN_761278_TG_rpoB_I491S	491	572
SNP_CN_761287_TC_rpoB_L494P	494	575
SNP_CN_761292_GA_rpoB_V496M	496	577
SNP_CN_761293_TG_rpoB_V496G	496	577
SNP_CN_761314_TC_rpoB_F503S	503	584
INS_N_761316_i1509GGG_rpoB	504	585
SNP_CN_761338_GC_rpoB_R511P	511	592
INS_F_761362_i1555C_rpoB_S519T	519	600
SNP_CN_761364_GA_rpoB_D520N	520	601
SNP_CN_761407_TG_rpoB_V534G	534	615
SNP_CN_761407_TC_rpoB_V534A	534	615
SNP_CN_761427_CT_rpoB_P541S	541	622
SNP_CN_761441_CG_rpoB_D545E	545	626
SNP_CN_761476_GA_rpoB_R557H	557	638
SNP_CN_761482_CT_rpoB_A559V	559	NA
SNP_CN_761490_GA_rpoB_V562M	562	642
SNP_CN_761494_AC_rpoB_E563A	563	643
SNP_CN_761502_CA_rpoB_P566T	566	646
SNP_CN_761518_AC_rpoB_D571A	571	651
SNP_CN_761535_CG_rpoB_P577A	577	657
SNP_CN_761539_GA_rpoB_R578H	578	658
SNP_CN_761547_GT_rpoB_V581L	581	661
SNP_CN_761550_TC_rpoB_S582P	582	662
SNP_CN_761557_CA_rpoB_A584D	584	664
SNP_CN_761559_AG_rpoB_T585A	585	665
SNP_CN_761664_GA_rpoB_V620M	620	700
SNP_CN_761698_AG_rpoB_D631G	631	711
SNP_CN_761701_CT_rpoB_A632V	632	712
SNP_CN_761723_AC_rpoB_E639D	639	719

SNP_CN_761739_GA_rpoB_E645K	645	725
SNP_CN_761770_TC_rpoB_M655T	655	735
SNP_CN_761832_AG_rpoB_T676A	676	763
SNP_CN_761851_CT_rpoB_P682L	682	769
SNP_CN_761880_GA_rpoB_A692T	692	779
SNP_CN_761884_GA_rpoB_G693D	693	780
SNP_CN_761889_GC_rpoB_V695L	695	782
SNP_CN_761905_CT_rpoB_P700L	700	787
SNP_CN_761911_CT_rpoB_T702I	702	789
SNP_CN_761923_AG_rpoB_E706G	706	793
SNP_CN_761974_AG_rpoB_H723R	723	810
INS_F_761980_i2173GCTC_rpoB	725	812
SNP_CN_761998_TC_rpoB_L731P	731	818
SNP_CN_762027_CT_rpoB_L741F	741	828
SNP_CN_762042_AG_rpoB_I746V	746	833
INS_F_762068_i2261ACCT_rpoB	754	841
SNP_CN_762089_GC_rpoB_E761D	761	848
SNP_CN_762201_AC_rpoB_K799Q	799	886
SNP_CN_762256_CT_rpoB_A817V	817	904
SNP_CN_762277_GT_rpoB_R824L	824	911
SNP_CN_762279_GT_rpoB_E825*	825	912
SNP_CN_762285_CT_rpoB_R827C	827	914
SNP_CN_762300_AG_rpoB_K832E	832	919
SNP_CN_762310_AC_rpoB_H835P	835	922
SNP_CN_762310_AG_rpoB_H835R	835	922
SNP_CN_762312_GA_rpoB_G836S	836	923
SNP_CN_762362_GC_rpoB_E852D	852	1005
SNP_CN_762391_TG_rpoB_L862R	862	1049
SNP_CN_762418_GA_rpoB_R871H	871	1058
SNP_CN_762427_CA_rpoB_S874Y	874	1061
SNP_CN_762477_AG_rpoB_K891E	891	1078
SNP_CN_762492_GA_rpoB_E896K	896	1083
SNP_CN_762564_AG_rpoB_M920V	920	1107
SNP_CN_762612_AC_rpoB_S936R	936	1123
SNP_CN_762636_AG_rpoB_K944E	944	1163
SNP_CN_762640_GA_rpoB_G945E	945	1164
SNP_CN_762676_TC_rpoB_L957P	957	1176
SNP_CN_762675_CG_rpoB_L957V	957	1176
SNP_CN_762715_TC_rpoB_V970A	970	1186
SNP_CN_762717_TC_rpoB_F971L	971	1187
SNP_CN_762745_AG_rpoB_Q980R	980	1196
SNP_CN_762783_GA_rpoB_D993N	993	NA
SNP_CN_762790_TC_rpoB_L995P	995	NA
SNP_CN_762815_GC_rpoB_M1003I	1003	1211
SNP_CN_762833_CG_rpoB_S1009R	1009	1217
SNP_CN_762841_CT_rpoB_P1012L	1012	1220
SNP_CN_762840_CA_rpoB_P1012T	1012	1220
SNP_CN_762910_TC_rpoB_I1035T	1035	1243
SNP_CN_762911_CG_rpoB_I1035M	1035	1243
SNP_CN_762928_GT_rpoB_G1041V	1041	1249
SNP_CN_762941_GA_rpoB_M1045I	1045	1253
SNP_CN_762951_CT_rpoB_Q1049*	1049	1257
SNP_CN_763005_TG_rpoB_C1067G	1067	1275

INS_F_763041_i3234GGGT_rpoB	1079	1287
DEL_F_763043_d3236GCAG_rpoB	1079	1287
SNP_CN_763059_AG_rpoB_I1085V	1085	1293
SNP_CN_763075_CT_rpoB_T1090I	1090	1298
SNP_CN_763090_AG_rpoB_K1095R	1095	1303
SNP_CN_763102_CA_rpoB_A1099E	1099	1307
SNP_CN_763216_CT_rpoB_A1137V	1137	NA
SNP_CN_763258_GA_rpoB_R1151Q	1151	NA
SNP_CN_763300_CT_rpoB_S1165F	1165	NA
SNP_CN_763302_GA_rpoB_A1166T	1166	NA
SNP_CN_763303_CT_rpoB_A1166V	1166	NA