TABLE S1 Antimicrobial Resistance Determinant Microarray (ARDM) v.2 content

Gene	Genbank accession no.	Locus	# probes/gene
ARTHNAC1 (control)	AF198054	100-1158	20
ARTHTIM (control)	AF247559	100-1160	20
blaVEB-1	DQ393569	1955-2854	9
penA	U85041	1163-2017	9
bla1	AF367983	626-1555	10
bla2	AF367984	791-1561	10
pbp5	AF375986	1-668	9
blaZ	M60253	142-987	6
mecA	AB096217	20340-22346	10
pbp1A	AF446215	1-1766	10
blaVIM-2	AF369871	553-1353	9
blaIMP-2	AJ243491	539-1279	10
blaSIM-1	AY887066	494-1234	9
blaOXA-51-like	DQ385606.1	669-1493	10
ampC (Acinetobacter)	EF016355.1	1-1152	9
blaIMP-1	EU686386	1137-1877	10
blaOXA-23	FJ959346.1	192-1013	9
blaOXA-58-like	HQ219687.1	280-1122	10
blaOXA-24	NC_012813.1	2519-3346	10
blaCTX-M-8 family	AF189721	274-1149	10
blaSHV-1/PIT-2 family	AF148850	6-866	10
blaCTX-M-9 family	AF174129	6336-7211	10
blaOXA-1	J02967	1359-2189	9
blaACC-2	AF180952	1565-2737	9
blaSME-2	AF275256	1-885	9
blaIMI-3/nmc	AY780889.1	7813-8691	9
blaKPC family	AF297554	131-1012	10
blaTEM family	AF309824	119-979	9
blaOXY-2	AJ871866	1-873	9
blaLEN-1	AY037780	89-949	6
blaMOX	D13304	233-1381	10
blaGES family	EF219163	1-795	10
blaNDM	FN396876	2407-3219	10
blaMIR-1	M37839.2	928-2073	10
blaOXA-9	M55547	2314-3138	9
blaFOX-1	X77455	701-1849	10
blaLAT-1/LAT-4	X78117	142-1287	9
blaOXY-1	Z30177	349-1224	10
blaOXA-48	AY236073.2	2188-2985	10
blaCTX-M-1 family	EF570052	240-1115	10
blaGIM-1	AJ620678	1041-1793	9
blaSPM-1	AY341249	2291-3121	10
blaBEL	DQ089809.1	1006-1857	9
blaOXA-10/PSE-2	EU708817	2161-2961	8
blaPSE-1/CARB-2	M69058	146-1012	8
amp(C)	AJ237702	4744-5883	9

blaCTX-M-2 family	X92507	6-881	10
blaPER-2	X93314	278-1204	9
grmA	AY524043	12798-13622	8
grmO	AY524043	6802-7695	6
grm	M55521	121-945	10
nbrB	AF038408	116-961	9
kmr	AB164642	18982-19815	9
aad(K)	M26879	90-944	10
aph/aph(3')-Iva	X03364	277-1065	10
aph(2')-Id	AF016483	131-1036	9
aad(E)	AF516335	14900-15808	9
aac(6')-Ii	L12710	169-717	10
aph(2')-Ic	U51479	1-1270	9
aph(3')-iii/aph(A3) family	M36771	293-1084	10
ant(9)-Ia	X02588	331-1113	9
fmrO	D13171	1477-2358	6
ant(6)-Ia	DQ112355	2075-2533	8
aphA6	EU977572.1	1-780	9
aac(6')-ig	L09246	544-981	10
aac(6')-ik	L29510	396-806	10
armA	AF550415.2	72385-73158	10
aac(6')-Im	AF337947	1215-1751	9
aph(2')-Ib	AF337947	272-1171	8
aad(A1)	AY339625	10986-11777	8
aac(3)-Iva	X01385	244-1029	10
aph(A2)	X57709	1-795	8
aad(A4)	Z50802	1306-2094	10
rmtB	AB117036	1-756	9
npmA	AB261016	3069-3728	9
rmtE	GU201947	55-876	10
rmtC	AB194779.2	6903-7748	9
rmtA	AB120321.1	6677-7432	9
rmtD	DQ914960	8889-9632	9
ant(4')-IIa	M98270	136-903	10
aad(B)	AY204504	2058-2591	9
aac(3)-Id	AY458224	707-1183	9
aad(A7)	AY458224	1259-2056	9
aph3''/str(A)	AY055428	19405-20208	9
aph6/str(B)	AY055428	18569-19405	9
aac(6)-Ib family	AY103455	143-721	10
ant(2'')-Ia	X04555	1149-1829	8
aac(C1)	U04610	670-1203	9
aph(AI)	U13633	6554-7369	10
aac(3)-III	X13542	186-1046	10
erm(36)/erm(ML)	AF462611	186-1031	9
erm(U)/lmr(B)	AF237667	101-1546	10
erm(X)/erm(CD)	M36726	296-1150	10
erm(30)/pik(R1)	AF079138	1283-2293	10
erm(Z)/srm(D)	AM709783	2817-3665	10

erm(H)/car(B)	M16503	244-1143	9
erm(35)	AF319779	33-833	8
erm(F)	M14730	241-1041	9
erm(34)	AY234334	355-1200	9
erm(D)	M29832	430-1293	9
msrC	AY004350	496-1974	9
erm(B)	M11180	714-1451	9
msr(A)/msrB/msrSA family	AB013298	487-1953	12
erm(33)	AJ313523	163-894	9
mphC	AM397632	1-900	9
erm(C)	M19652	988-1722	6
erm(A)	X03216	4551-5282	10
mef(A)/mefE family	AF227520	3254-4471	19
msr(D)/mel	AF227521	4607-6070	10
mre(A)	U92073	119-1054	9
erm(Q)	L22689	262-1035	8
mac(A)	AB071145	1-1143	9
mph(A)/mphK family	D16251	1626-2531	10
ere(B)	A15097	383-1642	9
mph(B)	AB020531	4167-5075	9
mac(B)	AB071146	1-1947	8
mph(D)	AB048591	1-840	9
ere(A2)	AF512546	716-1942	6
tet(Z)	AF121000	11880-13034	9
tet(33)	NC_003227	22940-24163	9
tet(30)	AF090987	1130-2314	10
tet(36)	AJ514254	2534-4456	9
tet(X)	M37699	586-1752	9
tet(L)p	M11036	189-1565	10
tet(L)c	X08034	188-1564	10
tet(Q)	X58717	586-2511	9
tet(U)	U01917	413-730	10
tet(S)	L09756	447-2372	9
tet(38)	AY825285	1-1353	10
tet(K)	M16217	305-1684	9
tet(T)	L42544	478-2433	9
tet(M)	X04388	131-2050	9
tet(W)	AJ222769	3687-5606	9
tetO/tet32 family	AJ295238	164-2083	8
tetA(P)	L20800	1063-2325	10
tetB(P)	L20800	2309-4267	9
tet(39)	AY743590	749-1936	9
tet(31)	AJ250203	1651-2883	9
tet(Y)	AF070999	1680-2855	10
tet(E)	L06940	21-1238	9
tet(B)	V00611	61-1266	9
tet(C)	Y19114	1-1138	10
tet(V)	AF030344	462-1721	10
tet(H)	U00792	716-1918	9

tet(J)	AF038993	1084-2280	9
tet(G)	AF133140	757-1932	9
tet(A)	X75761	1059-2258	9
tet(D)	X65876	1521-2705	9
tet(34)	AB061440	306-770	10
tet(35)/eff(J)	AF353562	2213-3322	9
tet(37)	AF540889	1-327	10
van(F)	AF098802	1-476	8
van(C1)	AF162694	1411-2442	9
van(G)	AF253562	3715-4764	8
vanD4/D5 family	AF277571	1262-2293	8
van(E)	AF430807	2976-4034	9
van(X)	AF516335	2787-3755	9
van(Y)	AF516335	4785-5393	9
van(H)	AF516335	15805-16347	9
van(C3)	AY033764	26-1078	8
van(S)	M97297	4649-5803	9
van(A)	M97297	6979-8010	9
van(B)/(B2) family	U00456	62-1090	8
arr-3	AY038837	555-1007	9
vcmA	AB063193	176-1549	9
vcrM	AB073219	282-1619	9
vcaM	AB073220	250-2109	9
vceA	AF012101	562-1749	9
vceB	AF012101	1759-3294	10
catTC family	U75299	657-1373	8
cfr	AJ249217	570-1619	10
cat(S)	X74948	1-492	9
cat(Q)	M55620	459-1118	9
cmr(Ecoli)	U44900.1	1-1572	10
cmlA	AY816215	1535-2921	10
floR	AF332662	1657-2871	9
catA1/cat4 family	AP000342	20342-21001	9
floR	AB114188	11605-12819	9
cat(P)	L02937	4207-4830	9
lnu(B)/lin(B)	AJ238249	127-930	9
lnu(A)/lin(A)	J03947	645-1130	9
lnuC	AY928180	1150-1644	9
lnu(D)	EF452177	19-513	9
lnu(F)/lin(F)	AJ561197	1321-2142	9
lnu(G)/lin(G)	DQ836009	1310-2131	8
lsa(A)	AY225127	41-1537	10
lsa(B)	AJ579365	4150-5628	9
norA	D90119	478-1644	10
qnr	AY259086	8075-8731	9
qepA	AB263754.2	7052-8587	6
qnrS	GQ214053.1	9109-9765	10
qacE(ABC)	CP000521.1	3291438-3291779	10
qacED1	AY259086	4692-5039	8

vat(E6)	AY043210	1-645	8
vat(D)/sat(A)	L12033	162-791	10
vat(C)	AF015628	1307-1945	10
vgb(B)	AF015628	399-1286	9
vga(A)lc	DQ823382	1-1569	9
vat(A)	L07778	258-917	9
vgb(A)/vgh	M20129	641-1540	10
vat(B)	U19459	67-705	9
vga(B)	U82085	629-2287	9
vat(F)/sat	AF170730	70-735	9
sat4	AF516335	5821-6366	9
sat2	AB161463.1	1073-1597	9
sulII	AJ313522	449-1264	9
sulIII	AJ459418	2979-3770	9
sulI	X12870	2595-3434	9
dfrA3	NC_006526	317899-318396	9
dfr(A)	AF051916	2823-3308	9
dfr(D)	Z50141	82-582	8
folA	CP000521.1	494601-495110	9
dfrA25	AB280920	132-590	8
dfrA3b	AY162283	5616-6095	9
dfrA16	EU158182	117-590	9
dfrA17	AF169041	162-635	8
dfrA14	AJ313522	1873-2346	8
dfrA5	AJ419169	117-590	9
dfrA7	AJ419170	118-687	9
dfrA2d	AJ429132	69-305	6
dfrA24	AJ972619	83-640	9
dfrA26	AM403715	303-854	9
dfrA10	L06418	5494-6057	10
dfrA8	NC_010064	711-1220	9
dfrA2a	U36276	717-953	9
dfrA9	X57730	726-1259	9
dfrA12	Z21672	310-807	9
dfrA13/21/22/23 family	Z50802	718-1215	8
dfrA15	DQ989302	248-721	9
dfrA19	AJ310778	7004-7573	9
dfrA20	AJ605332	1304-1813	9
dfrA6	Z86002	336-809	10
dfrA1	AJ628353	2654-3112	9
dfrA18	AY034138	7413-7967	10
dfrA27	EU678897	1039-1512	10
ileS	HQ625437.1	850-3929	10
ptmP3	FJ655920.1	42293-43507	6
uppP	CP000521.1	3207904-3208722	9

TABLE S2 Polymerase chain reaction and sequencing primers used in this study

Primer name	Primer sequence	Target	Reference
Int1F	CAG TGG ACA TAA GCC TGT TC	*intI1* - detection	1
Int1R	CCC GAG GCA TAG ACT GTA		
Int2F	TTG CGA GTA TCC ATA ACC TG	*intI2* - detection	
Int2R	TTA CCT GCA CTG GAT TAA GC		
intI3L	GCC TCC GGC AGC GAC TTT CAG	*intI3* - detection	4
intI3R	ACGGATCTGCCAAACCTGACT		4
5'-CS	GGC ATC CAA GCA GCA AG	Class 1 integron cassette array	2
3'-CS	AAG CAG ACT TGA CCT GA		
5'-CSa	TCT CGG GTA ACA TCA AGG		3
int2S	ACC TTT TTG TCG CATATCCGTG	Class 2 integron cassette array	4
intCS2	TAC CTG TTC TGC CCG TAT CT		
GES-5-int-2-F	TCG AAT GGT CTC CTG CCA CG	bla_{GES11}-containing integron sequencing	This study
GES-3-int-2-R	TAC CTT GCC TCT CAA ACC CC		
aac(3)-III/IV-F	GAC GAC GAG CCG TTC GAY CC	*aac(3)*-III/IV - detection	5
aac(3)-III/IV-R	CCA TCA ACT CGG CAA GAT GSA G		
dfrA19-F	TCG CTG TGG ATT CTA AGT TGG	*dfrA19* - detection	6
dfrA19-R	CGC CAT CCT TTT CTA ACT GC		
CMLAF2	ACT AAT GAT GGC AGG CAA G	*cmlA* - detection	7
CMLAR2	AAG ACA GAC CGA GCA CGA CT		
armA-F	AGG TTG TTT CCA TTT CTG AG	*armA* - detection	8
armA-R	TCT CTT CCA TTC CCT TCT CC		
aac(6')-F	TTG CGA TGC TCT ATG AGT GGC TA	*aac(6')-Ib* - detection	9
aac(6')-R	CTC GAA TGC CTG GCG TGT TT		
tetA-F	GCG CGA TCT GGT TCA CTC G	*tet*(A) - detection	10
tetA-R	AGT CGA CAG YRG CGC CGG C		
tetB-F	CGT TTG CTT TCA GGG ATC A	*tet*(B) - detection	11
tetB-R	ACC ATC ATG CTA TTC CAT CC		
tet39-F	CTC CTT CTC TAT TGT GGC TA	*tet*(39) - detection	12
tet39-R	CAC TAA TAC CTC TGG ACA TCA		
OXA51-like-F	TAA TGC TTT GAT CGG CCT TG	$bla_{OXA51\text{-}like}$ - detection	13
OXA51-like-R	TGG ATT GCA CTT CAT CTT GG		
5'OXA-51-like-all-F	ATG AAC ATT AAA GCA CTC	bla_{OXA51} – full gene amplification	14
3'OXA-51-like-all-R	CTA TAA AAT ACC TAA TTG TTC		
OXA51-5ext-F	AAT TGG CCG ATG CTT TTA TC		This study
OXA51-5ext-R	TGT TGA GTT TGG CCT TGT TG		
OXA51-3ext-F	TGC AAT CCA TGT TAT TCA TAG AAG		
OXA51-3ext-R	GGC CCA GAT CAA AAT GGT AA		
IS*Aba1*-F	CAC GAA TGC AGA AGT TG	IS*Aba1* - detection	15
IS*Aba1*-R	CGA CGA ATA CTA TGA CAC		
OXA23-like-F	GAT CGG ATT GGA GAA CCA GA	bla_{OXA23}-like - detection	13
OXA23-like-R	ATT TCT GAC CGC ATT TCC AT		
OXA58-like-F	AAG TAT TGG GGC TTG TGC TG	bla_{OXA58}-like - detection	
OXA58-like-R	CCC CTC TGC GCT CTA CAT AC		

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Table S3. Sensitivity, Selectivity Determination using Genome-Sequenced Strains

	sequence with >90% identity present?				Detected on ARDM			
probe name	Isolate 20	Isolate 26	Isolate 28	Isolate 30	Isolate 20	Isolate 26	Isolate 28	Isolate 30
aac(3)-Id	n	n	n	n	n	n	n	n
aac(3)-III	n	n	Y	n	n	n	N	n
aac(3)-Iva	n	n	n	n	n	n	n	n
aac(6)-Ib family	n	Y	n	n	n	Y	n	n
aac(6')-ig	n	n	n	n	n	n	n	n
aac(6')-Ii	n	n	n	n	n	n	n	n
aac(6')-ik	n	n	n	n	n	n	n	n
aac(6')-Im	n	n	n	n	n	n	n	n
aac(C1)	n	n	n	Y	n	n	n	Y
aad(A1)	n	Y	n	n	n	Y	n	n
aad(A4)	n	n	n	n	n	n	n	n
aad(A7)	n	Y	n	n	n	N	n	n
aad(B)	Y	Y	n	n	Y	Y	n	n
aad(E)	n	n	n	n	n	n	n	n
aad(K)	n	n	n	n	n	n	n	n
amp(C)	n	n	n	n	n	n	n	n
ampC (Acinetobacter)	Y	Y	Y	Y	Y	N	N	Y
ant(2'')-Ia	Y	Y	n	n	Y	Y	n	n
ant(4')-IIa	n	n	n	n	n	n	n	n
ant(6)-Ia	n	n	n	n	n	n	n	n
ant(9)-Ia	n	n	n	n	n	n	n	n
aph(2')-Ib	n	n	n	n	n	n	n	n
aph(2')-Ic	n	n	n	n	n	n	n	n
aph(2')-Id	n	n	n	n	n	n	n	n
aph(3')-iii/aph(A3) family	n	n	n	n	n	n	n	n
aph(A2)	n	n	n	n	n	n	n	n
aph(AI)	n	n	n	n	n	n	n	n
aph/aph(3')-Iva	n	n	n	n	n	n	n	n
aph3''/str(A)	n	Y	Y	Y	n	Y	Y	Y
aph6/str(B)	n	Y	Y	Y	n	Y	Y	Y
aphA6	Y	Y	n	Y	Y	Y	n	Y
armA	n	n	n	n	n	n	n	n
arr-3	n	n	n	n	n	n	n	n
ARTHNAC1 (control)	n	n	n	n	n	n	n	n
ARTHTIM (control)	n	n	n	n	n	n	n	n
bla1	n	n	n	n	n	n	n	n
bla2	n	n	n	n	n	n	n	n
blaACC-2	n	n	n	n	n	n	n	n
blaBEL	n	n	n	n	n	n	n	n
blaCTX-M-1 family	n	n	n	n	n	n	n	n
blaCTX-M-2 family	n	n	n	n	n	n	n	n
blaCTX-M-8 family	n	n	n	n	n	n	n	n
blaCTX-M-9 family	n	n	n	n	n	n	n	n
blaFOX-1	n	n	n	n	n	n	n	n
blaGES family	n	Y	n	n	n	Y	n	n
blaGIM-1	n	n	n	n	n	n	n	n
blaIMI-3/nmc	n	n	n	n	n	n	n	n
blaIMP-1	n	n	n	n	n	n	n	n
blaIMP-2	n	n	n	n	n	n	n	n
blaKPC family	n	n	n	n	n	n	n	n
blaLAT-1/LAT-4	n	n	n	n	n	n	n	n
blaLEN-1	n	n	n	n	n	n	n	n
blaMIR-1	n	n	n	n	n	n	n	n
blaMOX	n	n	n	n	n	n	n	n
blaNDM	n	n	n	n	n	n	n	n
blaOXA-1	n	n	n	n	n	n	n	n
blaOXA-10/PSE-2	n	n	n	n	n	n	n	n
blaOXA-23	n	Y	n	Y	n	Y	n	Y
blaOXA-24	n	n	n	n	n	n	n	n
blaOXA-48	n	n	n	n	n	n	n	n
blaOXA-51-like	Y	Y	Y	Y	Y	Y	Y	Y
blaOXA-58-like	n	n	n	n	n	n	n	n
blaOXA-9	n	n	n	n	n	n	n	n
blaOXY-1	n	n	n	n	n	n	n	n
blaOXY-2	n	n	n	n	n	n	n	n

blaPER-2	n	n	n	n	n	n	n	n
blaPSE-1/CARB-2	n	n	n	n	n	n	n	n
blaSHV-1/PIT-2 family	n	n	n	n	n	n	n	n
blaSIM-1	n	n	n	n	n		n	n
blaSME-2	n	n	n	n	n	n	n	n
blaSPM-1	n	n	n	n	n	n	n	n
blaTEM family	n	n	n	n	n	n	n	n
blaVEB-1	n	n	n	n	n	n	n	n
blaVIM-2	n	n	n	n	n	n	n	n
blaZ	n	n	n	n	n	n	n	n
cat(P)	n	n	n	n	n	n	n	n
cat(Q)	n	n	n	n	n	n	n	n
cat(S)	n	n	n	n	n	n	n	n
catA1/cat4 family	n	n	n	n	n	n	n	n
catTC family	n	n	n	n	n	n	n	n
cfr	n	n	n	n	n	n	n	n
cmlA	n	Y	n	n	n	Y	n	n
cmr(Ecoli)	n	n	n	n	n	n	n	n
dfr(A)	n	n	n	n	n	n	n	n
dfr(D)	n	n	n	n	n	n	n	n
dfrA1	n	n	n	n	n	n	n	n
dfrA10	n	n	n	n	n	n	n	n
dfrA12	n	n	n	n	n	n	n	n
dfrA13/21/22/23 family	n	n	n	n	n	n	n	n
dfrA14	n	n	n	n	n	n	n	n
dfrA15	n	n	n	n	n	n	n	n
dfrA16	n	n	n	n	n	n	n	n
dfrA17	n	Y	n	n	n	N	n	n
dfrA18	n	n	n	n	n	n	n	n
dfrA19	n	n	n	n	n	n	n	n
dfrA20	n	n	n	n	n	n	n	n
dfrA24	n	n	n	n	n	n	n	n
dfrA25	n	n	n	n	n	n	n	n
dfrA26	n	n	n	n	n	n	n	n
dfrA27	n	n	n	n	n	n	n	n
dfrA2a	n	n	n	n	n	n	n	n
dfrA2d	n	n	n	n	n	n	n	n
dfrA3	n	n	n	n	n	n	n	n
dfrA3b	n	n	n	n	n	n	n	n
dfrA5	n	n	n	n	n	n	n	n
dfrA6	n	n	n	n	n	n	n	n
dfrA7	n	Y	n	n	n	Y	n	n
dfrA8	n	n	n	n	n	n	n	n
dfrA9	n	n	n	n	n	n	n	n
ere(A2)	n	n	n	n	n	n	n	n
ere(B)	n	n	n	n	n	n	n	n
erm(30)/pik(R1)	n	n	n	n	n	n	n	n
erm(33)	n	n	n	n	n	n	n	n
erm(34)	n	n	n	n	n	n	n	n
erm(35)	n	n	n	n	n	n	n	n
erm(36)/erm(ML)	n	n	n	n	n	n	n	n
erm(A)	n	n	n	n	n	n	n	n
erm(B)	n	n	n	n	n	n	n	n
erm(C)	n	n	n	n	n	n	n	n
erm(D)	n	n	n	n	n	n	n	n
erm(F)	n	n	n	n	n	n	n	n
erm(H)/car(B)	n	n	n	n	n	n	n	n
erm(Q)	n	n	n	n	n	n	n	n
erm(U)/lmr(B)	n	n	n	n	n	n	n	n
erm(X)/erm(CD)	n	n	n	n	n	n	n	n
erm(Z)/srm(D)	n	n	n	n	n	n	n	n
floR	n	n	n	n	n	n	n	n
floR	n	n	n	n	n	n	n	n
fmrO	n	n	n	n	n	n	n	n
folA	Y	Y	Y	Y	Y	Y	Y	Y
grm	n	n	n	n	n	n	n	n
grmA	n	n	n	n	n	n	n	n
grmO	n	n	n	n	n	n	n	n
ileS	n	n	n	n	n	n	n	n
kmr	n	n	n	n	n	n	n	n

lnu(A)/lin(A)	n	n	n	n	n	n	n	n
lnu(B)/lin(B)	n	n	n	n	n	n	n	n
lnu(D)	n	n	n	n	n	n	n	n
lnu(F)/lin(F)	n	n	n	n	n	n	n	n
lnu(G)/lin(G)	n	n	n	n	n	n	n	n
lnuC	n	n	n	n	n		n	n
lsa(A)	n	n	n	n	n	n	n	n
lsa(B)	n	n	n	n	n	n	n	n
mac(A)	n	n	n	n	n	n	n	n
mac(B)	n	n	n	n	n	n	n	n
mecA	n	n	n	n	n	n	n	n
mef(A)/mefE family	n	n	n	n	n	n	n	n
mph(A)/mphK family	n	n	n	n	n	n	n	n
mph(B)	n	n	n	n	n	n	n	n
mph(D)	n	n	n	n	n	n	n	n
mphC	n	n	n	n	n	n	n	n
mre(A)	n	n	n	n	n	n	n	n
msr(A)/msrB/msrSA family	n	n	n	n	n	n	n	n
msr(D)/mel	n	n	n	n	n	n	n	n
msrC	n	n	n	n	n	n	n	n
nbrB	n	n	n	n	n	n	n	n
norA	n	n	n	n	n	n	n	n
npmA	n	n	n	n	n	n	n	n
pbp1A	n	n	n	n	n	n	n	n
pbp5	n	n	n	n	n	n	n	n
penA	n	n	n	n	n	n	n	n
ptmP3	n	n	n	n	n	n	n	n
qacE(ABC)	Y	Y	Y	Y	Y	Y	Y	Y
qacED1	Y	Y	n	n	Y	Y	n	n
qepA	n	n	n	n	n	n	n	n
qnr	n	n	n	n	n	n	n	n
qnrS	n	n	n	n	n	n	n	n
rmtA	n	n	n	n	n	n	n	n
rmtB	n	n	n	n	n	n	n	n
rmtC	n	n	n	n	n	n	n	n
rmtD	n	n	n	n	n	n	n	n
rmtE	n	n	n	n	n	n	n	n
sat2	n	n	n	n	n	n	n	n
sat4	n	n	n	n	n	n	n	n
sulI	Y	Y	n	n	Y	Y	n	n
sulII	n	n	Y	Y	n	n	Y	Y
sulIII	n	n	n	n	n	n	n	n
tet(30)	n	n	n	n	n	n	n	n
tet(31)	n	n	n	n	n	n	n	n
tet(33)	n	n	n	n	n	n	n	n
tet(34)	n	n	n	n	n	n	n	n
tet(35)/eff(J)	n	n	n	n	n	n	n	n
tet(36)	n	n	n	n	n	n	n	n
tet(37)	n	n	n	n	n	n	n	n
tet(38)	n	n	n	n	n		n	n
tet(39)	n	n	n	n	n	n	n	n
tet(A)	Y	n	n	n	Y	n	n	n
tet(B)	n	n	Y	n	n	n	Y	n
tet(C)	n	n	n	n	n	n	n	n
tet(D)	n	n	n	n	n	n	n	n
tet(E)	n	n	n	n	n	n	n	n
tet(G)	n	n	n	n	n	n	n	n
tet(H)	n	n	n	n	n	n	n	n
tet(J)	n	n	n	n	n	n	n	n
tet(K)	n	n	n	n	n	n	n	n
tet(L)c	n	n	n	n	n	n	n	n
tet(L)p	n	n	n	n	n	n	n	n
tet(M)	n	n	n	n	n	n	n	n
tet(Q)	n	n	n	n	n	n	n	n
tet(S)	n	n	n	n	n	n	n	n
tet(T)	n	n	n	n	n	n	n	n
tet(U)	n	n	n	n	n	n	n	n
tet(V)	n	n	n	n	n	n	n	n
tet(W)	n	n	n	n	n	n	n	n
tet(X)	n	n	n	n	n	n	n	n

tet(Y)	n	n	n	n	n	n	n	n
tet(Z)	n	n	n	n	n	n	n	n
tetA(P)	n	n	n	n	n	n	n	n
tetB(P)	n	n	n	n	n	n	n	n
tetO/tet32 family	n	n	n	n	n	n	n	n
uppP	Y	Y	Y	Y	Y	Y	Y	Y
van(A)	n	n	n	n	n	n	n	n
van(B)/(B2) family	n	n	n	n	n	n	n	n
van(C1)	n	n	n	n	n	n	n	n
van(C3)	n	n	n	n	n	n	n	n
van(E)	n	n	n	n	n	n	n	n
van(F)	n	n	n	n	n	n	n	n
van(G)	n	n	n	n	n	n	n	n
van(H)	n	n	n	n	n	n	n	n
van(S)	n	n	n	n	n	n	n	n
van(X)	n	n	n	n	n	n	n	n
van(Y)	n	n	n	n	n	n	n	n
vanD4/D5 family	n	n	n	n	n	n	n	n
vat(A)	n	n	n	n	n	n	n	n
vat(B)	n	n	n	n	n	n	n	n
vat(C)	n	n	n	n	n	n	n	n
vat(D)/sat(A)	n	n	n	n	n	n	n	n
vat(E6)	n	n	n	n	n	n	n	n
vat(F)/sat	n	n	n	n	n	n	n	n
vcaM	n	n	n	n	n	n	n	n
vceA	n	n	n	n	n	n	n	n
vceB	n	n	n	n	n	n	n	n
vcmA	n	n	n	n	n	n	n	n
vcrM	n	n	n	n	n	n	n	n
vga(A)lc	n	n	n	n	n	n	n	n
vga(B)	n	n	n	n	n	n	n	n
vgb(A)/vgh	n	n	n	n	n	n	n	n
vgb(B)	n	n	n	n	n	n	n	n

					TOTAL
true positive	11	17	8	11	**47**
true negative	227	218	228	227	**900**
false positive	0	0	0	0	**0**
false negative	0	3	2	0	**5**

		PCR	
		Pos	Neg
ARDM	pos	47	0
	neg	5	900

Sensitivity	Specificity	Pos predict value	Neg predictive value
90%	100%	100%	99%