Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
ECRC	*Escherichia*	*coli*	O26	0_0761	Chicken	N/A[c]	I	JN871617	4
ECRC	*Escherichia*	*coli*	O26	0_0824	Chicken	N/A	I	JN871618	4
ECRC	*Escherichia*	*coli*	O26:H11	0.1015	Bovine	N/A	III		
Acheson - MA	*Escherichia*	*coli*	O26:H11	10	Human	USA	III		
Acheson - MA	*Escherichia*	*coli*	O26:NM	22	Human	USA	III		
ECRC	*Escherichia*	*coli*	O26:H11	81.0193	Conure, (Psittacine)	N/A	III		
ECRC	*Escherichia*	*coli*	O26:H11	81.0211	Antelope	N/A	III		
SDSU	*Escherichia*	*coli*	O26:H11	88-1577	N/A	USA	III		
SDSU	*Escherichia*	*coli*	O26:H11	89.4911	N/A	USA	III		
ECRC	*Escherichia*	*coli*	O26:H11	90.0105	Human	N/A	III		
ECRC	*Escherichia*	*coli*	O26	90.0157	Turkey	N/A	I	JN871663	4
ECRC	*Escherichia*	*coli*	O26:H11	93.0495	Human	N/A	I	JN871646	4
ECRC	*Escherichia*	*coli*	O26:H11	93.0506	Human	N/A	III		
ECRC	*Escherichia*	*coli*	O26	94.0003	N/A	N/A	I	JN871613	
ECRC	*Escherichia*	*coli*	O26:H11	95.0256	Bovine	N/A	I	JN871647	4
ECRC	*Escherichia*	*coli*	O26:H11	95.0274	Bovine	N/A	III		
ECRC	*Escherichia*	*coli*	O26:H11	99.0285	Bovine	N/A	III		
ECRC	*Escherichia*	*coli*	O26:H11	99.0703	Bovine	N/A	I	JN871633	4
ECRC	*Escherichia*	*coli*	O26:H11	99.0849	Human	N/A	III		
ECRC	*Escherichia*	*coli*	O26:H11	99.0862	Bovine	N/A	III		
ECRC	*Escherichia*	*coli*	O26:H11	99.0869	Human	N/A	III		
IDPHD	*Escherichia*	*coli*	O26:H11	7922	Human	USA	I	JN871644	
IDPHD	*Escherichia*	*coli*	O26:H11	10140	Human	USA	I	JN871639	
IDPHD	*Escherichia*	*coli*	O26:H11	10469	Human	USA	I	JN871629	
ATCC	*Escherichia*	*coli*	O26:H11	11840	N/A	N/A	III		
IDPHD	*Escherichia*	*coli*	O26:H11	12690	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O26:H11	12795	Human	USA	I	JN871666	
IDPHD	*Escherichia*	*coli*	O26:H11	13081	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	00-3230	Human	USA	I	JN871635	
CDC	*Escherichia*	*coli*	O26:H11	01-3327	Human	USA	I	JN871636	
CDC	*Escherichia*	*coli*	O26:H11	05-3471	Human	USA	I	JN871637	
CDC	*Escherichia*	*coli*	O26:H11	06-3044	Human	USA	I	JN871621	
CDC	*Escherichia*	*coli*	O26:H11	06-3288	Human	USA	I	JN871626	
CDC	*Escherichia*	*coli*	O26:H11	07-3337	Human	USA	I	JN871622	
CDC	*Escherichia*	*coli*	O26:H11	07-3722	Human	USA	I	JN871628	
CDC	*Escherichia*	*coli*	O26:H11	08-3323	Human	USA	I	JN871638	
CDC	*Escherichia*	*coli*	O26:H11	08-3449	Human	USA	I	JN871623	
CDC	*Escherichia*	*coli*	O26:H11	08-4358	Human	USA	I	JN871627	
Acheson - MA	*Escherichia*	*coli*	O26:H11	10-253	Human	USA	III		
ECRC - DECA	*Escherichia*	*coli*	O26:H11	10B	Human	Australia	I	JN871630	11
ECRC - DECA	*Escherichia*	*coli*	O26:H11	10C	Human	USA	I	JN871640	11
ECRC - DECA	*Escherichia*	*coli*	O26:H11	10E	Calf	USA	I	JN871641	11
Fair 2002	*Escherichia*	*coli*	O26:H11	18B24-2	Bovine	USA	III		

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CDC	*Escherichia*	*coli*	O26:H11	2009C-3612	Human	USA	I	JN871624	
CDC	*Escherichia*	*coli*	O26:H11	2009C-3689	Human	USA	I	JN871620	
CDC	*Escherichia*	*coli*	O26:H11	2010C-3902	Human	USA	I	JN871642	
MARC	*Escherichia*	*coli*	O26:H11	40-1	Bovine	USA	III		
Acheson - MA	*Escherichia*	*coli*	O26:H11	5-447	Human	USA	III		
ECRC	*Escherichia*	*coli*	O26:H46	5306.56	Bovine	USA	I	JN871656	4
Pop. ZX	*Escherichia*	*coli*	O26:H11	6648-1	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O26:H11	7_11_88A	Fly	USA	I	JN871645	
Fly Prevalence 2007	*Escherichia*	*coli*	O26:H11	7-12 15B	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O26:H11	7-15 5C	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O26:H11	7_29_23A	Bovine	USA	I	JN871625	
Fly Prevalence 2007	*Escherichia*	*coli*	O26:H11	7-33 80A	Fly	USA	III		
U of Georgia	*Escherichia*	*coli*	O26:H11	88-353	N/A	USA	III		
Acheson - MA	*Escherichia*	*coli*	O26:H11	9-23	Human	USA	III		
Summer showlist	*Escherichia*	*coli*	O26:H11	948-4	Bovine	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	97_3250	Human	USA	I	JN871648	
ECRC - DECA	*Escherichia*	*coli*	O26:H11	9A	Human	USA	I	JN871655	11
ECRC - DECA	*Escherichia*	*coli*	O26:H11	9B	Human	USA	I	JN871668	11
ECRC - DECA	*Escherichia*	*coli*	O26:H11	9C	Human	Switzerland	I	JN871669	11
Ben Green	*Escherichia*	*coli*	O26	B1_2	Bovine	USA	I	JN871665	
C. Park	*Escherichia*	*coli*	O26:H11	BERMUDEZ	Human	USA	III		
C. Park	*Escherichia*	*coli*	O26:H11	CHWIS	Human	USA	III		
EHEC 2	*Escherichia*	*coli*	O26:H11	CL5	N/A	N/A	III		
Fly Prevalence	*Escherichia*	*coli*	O26	D01016_1d_1	Bovine	USA	I	JN871657	
Fly Prevalence	*Escherichia*	*coli*	O26	D03004_3	Bovine	USA	I	JN871658	
Fly Prevalence	*Escherichia*	*coli*	O26	D04007_4	Dairy	USA	I	JN871659	
ECRC - DECA	*Escherichia*	*coli*	O26:H11	DEC 10A	Human	Canada	III		11
ECRC - DECA	*Escherichia*	*coli*	O26:H11	DEC 10D	Bovine	France	III		11
ECRC - DECA	*Escherichia*	*coli*	O26:H11	DEC 9D	Human	Denmark	III		11
ECRC - DECA	*Escherichia*	*coli*	O26:H11	DEC 9E	Human	Mexico	III		11
Feedlot Survey	*Escherichia*	*coli*	O26	F1_A4_1	Dairy	USA	I	JN871660	
Feedlot Survey	*Escherichia*	*coli*	O26	F1_B3_1	Bovine	USA	I	JN871673	
Feedlot Survey	*Escherichia*	*coli*	O26	F11_205_1_2	Bovine	USA	I	JN871670	
Feedlot Survey	*Escherichia*	*coli*	O26	F12_432_4_1	Bovine	USA	I	JN871671	
Feedlot Survey	*Escherichia*	*coli*	O26	F13_25_1_5	Bovine	USA	I	JN871672	
Feedlot Survey	*Escherichia*	*coli*	O26:H11	F2 407-2-2	Bovine	USA	III		
Feedlot Survey	*Escherichia*	*coli*	O26:H46	F3_13_1_3	Bovine	USA	I	JN871661	
Feedlot Survey	*Escherichia*	*coli*	O26:H11	F3_24_4_2	Bovine	USA	I	JN871674	
Feedlot Survey	*Escherichia*	*coli*	O26	F5_16_1_3	Dairy	USA	I	JN871662	
Feedlot Survey	*Escherichia*	*coli*	O26	F5_4_3_2	Bovine	USA	I	JN871675	
ECRC	*Escherichia*	*coli*	O26:H11	H311b	N/A	N/A	III		
Fair 2002	*Escherichia*	*coli*	O26:H11	L1G18-1	Goat	USA	III		
Fair 2002	*Escherichia*	*coli*	O26:H11	L3S14_1	Sheep	USA	I	JN871649	4

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MARC	*Escherichia*	*coli*	O26:H11	6629	Bovine	USA	II	JN871643	
Fair 2002	*Escherichia*	*coli*	O26:H11	MB21-1	Bovine	USA	III		
Fair 2002	*Escherichia*	*coli*	O26:H11	N5D43-1	Bovine	USA	III		
Fair 2002	*Escherichia*	*coli*	O26:H11	N9S2-1	Sheep	USA	III		
North Platte Exp. Station	*Escherichia*	*coli*	O26:H11	NP2_2	Environment	USA	I	JN871676	
U of Georgia	*Escherichia*	*coli*	O26:H11	P1331	N/A	USA	III		
Fair 2003	*Escherichia*	*coli*	O26:H11	P5_1	Bovine	USA	I	JN871650	
ZOO 2004	*Escherichia*	*coli*	O26	R28_5_1B	Chicken	USA	I	JN871619	
ZOO 2004	*Escherichia*	*coli*	O26	R32_14_1F	Goat	USA	I	JN871614	
ZOO 2004	*Escherichia*	*coli*	O26	R43_4_1	Bovine	USA	I	JN871664	
EHEC 2	*Escherichia*	*coli*	O26:H11	TW01200	Human	USA	III		
Durso Blind Panel	*Escherichia*	*coli*	O26:H32	TW01209	Human	N/A	I	JN871615	
Durso Blind Panel	*Escherichia*	*coli*	O26:H36	TW01221	Human	N/A	I	JN871634	
EHEC 2	*Escherichia*	*coli*	O26:H11	TW02295	Human	N/A	III		
EHEC 2	*Escherichia*	*coli*	O26:H11	TW04272	Human	USA	III		
EHEC 2	*Escherichia*	*coli*	O26:H11	TW05070	Human	Chile	III		
Durso Blind Panel	*Escherichia*	*coli*	O26:H11	TW07154	N/A	N/A	I	JN871667	
Durso Blind Panel	*Escherichia*	*coli*	O26:H32	TW07187	N/A	N/A	I	JN871616	
Durso Blind Panel	*Escherichia*	*coli*	O26:H11	TW07622	N/A	N/A	I	JN871651	
Durso Blind Panel	*Escherichia*	*coli*	O26:H11	TW07705	N/A	N/A	I	JN871652	
Durso Blind Panel	*Escherichia*	*coli*	O26:H11	TW07872	N/A	N/A	I	JN871653	
Durso Blind Panel	*Escherichia*	*coli*	O26:H11	TW08637	Human	N/A	I	JN871631	
Durso Blind Panel	*Escherichia*	*coli*	O26:H11	TW08998	Human	Germany	I	JN871654	
Durso Blind Panel	*Escherichia*	*coli*	O26:H11	TW09156	N/A	Uruguay	I	JN871632	
C. Park	*Escherichia*	*coli*	O26:H11	WAR	Human	USA	III		
CDC	*Escherichia*	*coli*	O45	06-224	Human	USA	I	JN859205	
MARC NOR	*Escherichia*	*coli*	O45	WDG-3	Bovine	USA	I	JN859207	
CDC - O STD's	*Escherichia*	*coli*	O45:H10	H61	N/A	USA	I	JN859208	
C. Park	*Escherichia*	*coli*	O45:H2	ALLG	Human	USA	I	JN859202	
C. Park	*Escherichia*	*coli*	O45:H2	COU	Human	USA	I	JN859203	
CDC	*Escherichia*	*coli*	O45:H2	A9619-C2	Human	USA	I	JN859204	
ECRC - DECA	*Escherichia*	*coli*	O45:H2	11C	Human	USA	I	JN859201	11
MARC MSQRU	*Escherichia*	*coli*	O45:H2	G4	N/A	USA	I	JN859200	
MARC MSQRU	*Escherichia*	*coli*	O45:H2	H3	N/A	USA	I	JN859206	
MARC NOR	*Escherichia*	*coli*	O45:H2	015-1269	Human	USA	I	JN859199	
ECRC	*Escherichia*	*coli*	O45:H4	87.1085	N/A	N/A	I	JN859197	
ECRC	*Escherichia*	*coli*	O45:H4	89.0609	N/A	N/A	I	JN859198	
ECRC	*Escherichia*	*coli*	O103	0_1623	Whitetail deer	N/A	I	JN862617	
ECRC	*Escherichia*	*coli*	O103:H11	83_1306	N/A	N/A	I	JN862600	
ECRC	*Escherichia*	*coli*	O103:H11	86_0765	Mouse	N/A	I	JN862598	
ECRC	*Escherichia*	*coli*	O103:H21	86_1202	N/A	N/A	I	JN862597	
ECRC	*Escherichia*	*coli*	O103	87_1368	Goat	N/A	I	JN862616	
ECRC	*Escherichia*	*coli*	O103	90.0393	Bovine	N/A	III		

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Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
ECRC	*Escherichia*	*coli*	O103:H4	92_0898	N/A	N/A	I	JN862599	
ECRC	*Escherichia*	*coli*	O103:H2	93_0624	Human	N/A	I	JN862606	
ECRC	*Escherichia*	*coli*	O103	95.3771	Human	N/A	III		
ECRC	*Escherichia*	*coli*	O103	95_3772	Human	N/A	I	JN862601	
ECRC	*Escherichia*	*coli*	O103	97_1377	Cattle	N/A	I	JN862607	
ECRC	*Escherichia*	*coli*	O103	98_1717	Dog	N/A	I	JN862604	
ECRC	*Escherichia*	*coli*	O103	98_2051	Water	N/A	I	JN862595	
ECRC	*Escherichia*	*coli*	O103	99_1792	Human	N/A	I	JN862614	
ECRC	*Escherichia*	*coli*	O103	99_1806	Human	N/A	I	JN862615	
ECRC	*Escherichia*	*coli*	O103	99_1807	Human	N/A	I	JN862613	
ECRC	*Escherichia*	*coli*	O103	99.1822	Human	N/A	III		
IDPHD	*Escherichia*	*coli*	O103:H25	6582	Human	USA	I	JN862603	
IDPHD	*Escherichia*	*coli*	O103:H11	11868	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O103:H2	12390	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O103:H2	12442	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O103:H2	12442	Human	USA	I	JN862602	
IDPHD	*Escherichia*	*coli*	O103:H11	13075	Human	USA	I	JN862611	
IDPHD	*Escherichia*	*coli*	O103:H2	14141	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O103:H11	15123	Human	USA	III		
SDSU	*Escherichia*	*coli*	O103:NM	89_118	N/A	USA	I	JN862610	
CDC - O STD's	*Escherichia*	*coli*	O103:H8	H_515b	N/A	USA	I	JN862596	
C. Park	*Escherichia*	*coli*	O103	MAH	Human	USA	I	JN862609	
C. Park	*Escherichia*	*coli*	O103	PARA	Human	USA	I	JN862605	
Durso Blind Panel	*Escherichia*	*coli*	O103:H2	TW08640	Human	N/A	I	JN862612	
Durso Blind Panel	*Escherichia*	*coli*	O103:H11	TW08872	N/A	N/A	I	JN862608	
ECRC	*Escherichia*	*coli*	O111:H8	0.1932	Bovine	N/A	III		
ECRC	*Escherichia*	*coli*	O111:H8	0.2056	Bovine	N/A	III		
Acheson - MA	*Escherichia*	*coli*	O111:H8	18	Human	USA	I	JN887664	4, 5
MARC	*Escherichia*	*coli*	O111:H8	1074	Bovine	USA	II	JN887665	4
ECRC	*Escherichia*	*coli*	O111:H8	94.0718	Bovine	N/A	III		
ECRC	*Escherichia*	*coli*	O111:H8	99.09	Human	N/A	III		
ECRC	*Escherichia*	*coli*	O111:H8	99.1169	Bovine	N/A	III		
IDPHD	*Escherichia*	*coli*	O111:H8	8234	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O111:H8	8361	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O111:H8	9662	Human	USA	II	JN887666	
IDPHD	*Escherichia*	*coli*	O111:H8	11474	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O111:H8	11936	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O111:H8	12893	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O111:H8	14614	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O111:H8	14892	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O111:H8	14895	Human	USA	III		
ATCC	*Escherichia*	*coli*	O111:NM	43887	Human	N/A	I	JN887676	4, 5
NYDH	*Escherichia*	*coli*	O111	04-11953	Human	Canada	I	JN887644	

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Pop. GF	*Escherichia*	*coli*	O111:H8	0474-5	Bovine	USA	III		
Winter Showlist	*Escherichia*	*coli*	O111:H8	1056-1	Bovine	USA	III		
ECRC - DECA	*Escherichia*	*coli*	O111:H2	12A	Human	England	I	JN887673	11
ECRC - DECA	*Escherichia*	*coli*	O111:H2	12B	Human	USA	I	JN887682	11
ECRC - DECA	*Escherichia*	*coli*	O111:HN	12C	Human	Panama	III		
ECRC - DECA	*Escherichia*	*coli*	O111:H2	12D	Human	Peru	I	JN887683	11
ECRC - DECA	*Escherichia*	*coli*	O111:HN	12E	Human	Kenya	I	JN887685	11
ECRC - DECA	*Escherichia*	*coli*	O111:H21	15A	Human	USA	III		
ECRC - DECA	*Escherichia*	*coli*	O111:H21	15B	Human	USA	I	JN887678	11
ECRC - DECA	*Escherichia*	*coli*	O111:H21	15C	Human	USA	I	JN887680	11
ECRC - DECA	*Escherichia*	*coli*	O111:H21	15D	Human	USA	I	JN887681	11
ECRC - DECA	*Escherichia*	*coli*	O111:H21	15E	Human	USA	I	JN887679	11
ECRC	*Escherichia*	*coli*	O111:H8	3007-85	Human	USA	I	JN887660	4, 5
MARC	*Escherichia*	*coli*	O111:H8	4-1	Bovine	USA	III		
IDPHD	*Escherichia*	*coli*	O111:H8	6617	Human	USA	III		
ECRC - DECA	*Escherichia*	*coli*	O111:H21	6A	Human	USA	I	JN887686	11
ECRC - DECA	*Escherichia*	*coli*	O111:H12	6B	Human	Germany	I	JN887687	5, 11
ECRC - DECA	*Escherichia*	*coli*	O111:H12	6C	Human	Guatemala	I	JN887674	11
ECRC - DECA	*Escherichia*	*coli*	O111:H12	6D	Human	Italy	I	JN887688	11
ECRC - DECA	*Escherichia*	*coli*	O111:HN	6E	Human	Brazil	I	JN887689	11
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-11 88A	Fly	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-14 10A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-15 17A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-16 37A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-16 64A	Fly	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-16 69A	Fly	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-20 65A	Fly	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-22 6A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-26 8A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-27 20A	Bovine	USA	I	JN887655	
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-32 9A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-33 12A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-45 80A	Fly	USA	I	JN887662	
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-51 19A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-54 11A	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-54 68A	Fly	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-55 62A	Fly	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-56 3B	Bovine	USA	III		
Fly Prevalence 2007	*Escherichia*	*coli*	O111:H8	7-58 72A	Fly	USA	I	JN887656	
IDPHD	*Escherichia*	*coli*	O111:H8	7364	Human	USA	III		
ECRC	*Escherichia*	*coli*	O111:H7	82_0549	N/A	N/A	I	JN887684	5
ECRC	*Escherichia*	*coli*	O111:H4	87-0518	N/A	N/A	I	JN887670	4, 5
ECRC	*Escherichia*	*coli*	O111:H11	87-1377	Bovine	USA	I	JN887648	

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Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
ECRC	*Escherichia*	*coli*	O111:H11	87-1883	Bovine	USA	I	JN887653	
ECRC	*Escherichia*	*coli*	O111:H11	87-1917	Swine	USA	I	JN887651	4
ECRC	*Escherichia*	*coli*	O111:H11	88-0502	Bovine	USA	I	JN887652	
SDSU	*Escherichia*	*coli*	O111:NM	88-19539	N/A	USA	I	JN887649	4, 5
SDSU	*Escherichia*	*coli*	O111:H11	88-4110	N/A	USA	I	JN887646	4, 5
ECRC - DECA	*Escherichia*	*coli*	O111:H8	8A	Human	USA	III		
ECRC - DECA	*Escherichia*	*coli*	O111:H8	8B	Human	USA	III		
ECRC - DECA	*Escherichia*	*coli*	O111:HN	8C	Calf	USA	I	JN887647	11
ECRC - DECA	*Escherichia*	*coli*	O111:H11	8D	Human	Cuba	I	JN887668	11
ECRC - DECA	*Escherichia*	*coli*	O111:H8	8E	Human	Denmark	I	JN887659	11
Acheson - MA	*Escherichia*	*coli*	O111:H8	9-54	Human	USA	III		
ECRC	*Escherichia*	*coli*	O111:H8	90.0101	Bovine	N/A	III		
ECRC	*Escherichia*	*coli*	O111:H8	90.0102	Bovine	N/A	III		
ECRC	*Escherichia*	*coli*	O111:H8	95-0122	N/A	N/A	III		
ECRC	*Escherichia*	*coli*	O111	96-0533	Turkey	N/A	I	JN887672	4
ECRC	*Escherichia*	*coli*	O111	96-1487	Human	N/A	I	JN887667	4
ECRC	*Escherichia*	*coli*	O111	98-0136	Swine	N/A	I	JN887671	4
ECRC	*Escherichia*	*coli*	O111:H8	99.1145	Bovine	N/A	III		
ZOO	*Escherichia*	*coli*	O111:H8	A010005-1	Sheep	N/A	III		
U. of CA, Riley	*Escherichia*	*coli*	O111	B171	N/A	USA	I	JN887677	4, 5
TX-DH	*Escherichia*	*coli*	O111:H8	BE 00749	N/A	USA	III		
TX-DH	*Escherichia*	*coli*	O111:H8	BE-99-1202	N/A	USA	III		
State Flies	*Escherichia*	*coli*	O111:H8	FL43-1	Bovine	USA	III		
State Flies	*Escherichia*	*coli*	O111:H8	GF6-1	Fly	USA	III		
Fly - Cohort	*Escherichia*	*coli*	O111	GY3-1	Fly	USA	I	JN887690	
TN Face Fly 2003	*Escherichia*	*coli*	O111:H8	H36-1	Bovine	USA	III		
Ohio Hamburger	*Escherichia*	*coli*	O111:H8	HB133-1BG	Bovine	USA	III		
Fair 2002	*Escherichia*	*coli*	O111:H8	L1G30-1A	Goat	USA	III		
Fair 2002	*Escherichia*	*coli*	O111:H8	L3S15-2	Sheep	USA	III		
MARC	*Escherichia*	*coli*	O111:H8	MARC 1074-2	Bovine	USA	III		
State Flies	*Escherichia*	*coli*	O111:H8	NCF4-3	Fly	USA	III		
Fair 2002	*Escherichia*	*coli*	O111:H8	PG12-1	Goat	USA	III		
C. Park	*Escherichia*	*coli*	O111:H8	PLAV	Human	USA	I	JN887657	
C. Park	*Escherichia*	*coli*	O111:H8	SCHAF	Human	USA	III		
Fair 2003	*Escherichia*	*coli*	O111:H8	SF26 102-1	Bovine	USA	III		
TN Face Fly 2003	*Escherichia*	*coli*	O111:H8	SF4-1	Fly	USA	III		
ECRC	*Escherichia*	*coli*	O111:NM	Stoke W	N/A	N/A	I	JN887675	4, 5
EHEC 2	*Escherichia*	*coli*	O111:H8	TW00970	Human	USA	II		10
EHEC 2	*Escherichia*	*coli*	O111:H8	TW01387	Human	Canada	I	JN887661	4, 10
EHEC 2	*Escherichia*	*coli*	O111:H8	TW04257	Human	USA	I	JN887658	4, 5, 10
EHEC 2	*Escherichia*	*coli*	O111:H8	TW04519	Calf	Scotland	III		
EHEC 2	*Escherichia*	*coli*	O111:H8	TW05614	Human	Germany	III		
EHEC 2	*Escherichia*	*coli*	O111:H8	TW05651	Human	Italy	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
EHEC 2	*Escherichia*	*coli*	O111:H8	TW07502	Human	Germany	I	JN887654	4, 5, 10
Durso Blind Panel	*Escherichia*	*coli*	O111:H8	TW07926	Human	USA	III	JN887645	
Durso Blind Panel	*Escherichia*	*coli*	O111:H11	TW03810	N/A	N/A	III	JN887669	
Durso Blind Panel	*Escherichia*	*coli*	O111:H11	TW05355	Human	Canada	III	JN887650	
CDC - O STD's	*Escherichia*	*coli*	O121:H10	W39	N/A	USA	I	JN859209	
CDC	*Escherichia*	*coli*	O121:H19	3056_85	Human	USA	I	JN859216	
Durso Blind Panel	*Escherichia*	*coli*	O121:H19	TW08868	Human	USA	I	JN859213	
IDPHD	*Escherichia*	*coli*	O121:H19	5518	Human	USA	I	JN859215	
IDPHD	*Escherichia*	*coli*	O121:H19	13247	Human	USA	I	JN859217	
IDPHD	*Escherichia*	*coli*	O121:H19	11287	Human	USA	I	JN859218	
IDPHD	*Escherichia*	*coli*	O121:H19	6507	Human	USA	I	JN859220	
IDPHD	*Escherichia*	*coli*	O121:H19	11215	Human	USA	I	JN859219	
ECRC	*Escherichia*	*coli*	O121:H7	86_0698	N/A	N/A	I	JN859210	
ECRC	*Escherichia*	*coli*	O121:H7	90_0373	N/A	N/A	I	JN859211	
ECRC - ECOR	*Escherichia*	*coli*	O121:HN	EC21	Bovine	N/A	I	JN859212	9
IDPHD	*Escherichia*	*coli*	O121:NM	9918	Human	USA	I	JN859214	
MARC	*Escherichia*	*coli*	O145:Hneg	307A2	Packing Plant	USA	I	JN850043	
CDC - O STD's	*Escherichia*	*coli*	O145:NM	E1385	N/A	USA	I	JN850039	
IDPHD	*Escherichia*	*coli*	O145:NM	6896	Human	USA	I	JN850044	
IDPHD	*Escherichia*	*coli*	O145:NM	6940	Human	USA	I	JN850040	
IDPHD	*Escherichia*	*coli*	O145:NM	8235	Human	USA	I	JN850041	
IDPHD	*Escherichia*	*coli*	O145:NM	14728	Human	USA	I	JN850042	
USMARC	*Escherichia*	*coli*	O157:H7	CO 1185-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	CO 147-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	CO 50-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	CO 713-5	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	KS 1534-4A	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	KS 368-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	KS 411-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	KS 448-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	KS 546	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	LSU 56	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	LSU 58	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	MARC 6635-2	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 1060-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 1092-2	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 1127-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 1169-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 122-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 1270-2	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 1370-3	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 5-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 81-1	Bovine	USA	III		1, 2

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
USMARC	*Escherichia*	*coli*	O157:H7	NE 92-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	NE 972-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	Show KS 470-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	Show NE 175-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	Show NE 184-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	Show NE 235-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS CO 81-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS NE 1040-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS NE 1183-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS NE 1339-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS NE 1400-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS TX 313-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS TX 426-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS TX 754-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	SS TX 781-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	TX 265-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	TX 291-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	TX 349-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	TX 376-2	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	TX 723-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	TX 864-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	TX 909-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	TX 931-2	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	WS NE 21-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	WS NE 274-2	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	WS NE 340-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	WS NE 48-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	WS TX 886-1	Bovine	USA	III		1, 2
USMARC	*Escherichia*	*coli*	O157:H7	YB14-1	Bovine	USA	III		1, 2
Mandrell	*Escherichia*	*coli*	O157:H7	RM1239	Human	USA	III		3
Acheson - MA	*Escherichia*	*coli*	O157:H7	2	Human	USA	III		2
USMARC	*Escherichia*	*coli*	O157:H7	3-5-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	105-4-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	106-2-2	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	107-1-1	Bovine	USA	III		6
USMARC	*Escherichia*	*coli*	O157:H7	107-2-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	112-5-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	120-4-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	2-2-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	2-3	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	2-6-2	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	207-8-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	209-1-1	Bovine	USA	III		2, 6

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
USMARC	*Escherichia*	*coli*	O157:H7	211-2-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	214-1-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	23-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	30-3	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	38-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	4-3	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	5-11-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	Ex1-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	Gim1-1	Bovine	USA	III		2, 6
USMARC	*Escherichia*	*coli*	O157:H7	L47-1	Bovine	USA	III		2, 6
CDC	*Escherichia*	*coli*	O157:H7	F4552	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F4586	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F5606	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F5707	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F5733	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6141	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6142	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6569	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6667	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6748	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6749	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6750	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6751	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6851	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6854	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6856	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6857	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6858	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6859	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6861	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6862	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6862	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6883	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6884	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6891	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6892	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6893	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6913	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6942	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F6953	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7345	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7349	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7350	Human	USA	III		

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Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O157:H7	F7351	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7353	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7382	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7383	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7384	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7386	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7388	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7508	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F7639	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8092	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8092B	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8289-D	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8774	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8778	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8783	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8784	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8797	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8798	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8799	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8801	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8802	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8803	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F8952	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	F9019	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5285	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5295	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5297	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5303	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5307	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5307	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5321	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5425	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G6063	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G7560	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G7602	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H0672	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H0706	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H1949	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H2014	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H2495	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H2498	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H6039	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H6436	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O157:H7	H6437	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	H6437	Human	USA	III		
CDC	*Escherichia*	*coli*	O157:H7	G5244	Human	USA	III		
RMID	*Escherichia*	*coli*	O157:H7	Sakai	Human	USA	III		2, 7
IDPHD	*Escherichia*	*coli*	O157:H7	31277	Human	USA	III		2
USMARC	*Escherichia*	*coli*	O157:H7	05-115	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	05-955	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	12B5-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	13B3-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	17B6-2	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	19B18-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	1B8-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	B11-3	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	BB24-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	BB27-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	FB12-2	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	HB20-3	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	MB32-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	MB40-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	MB41-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	MB9-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	N2B24-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	N2B53-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	N5D2-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	N8B7-2	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	SF18 28-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	SF26 94-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	TB19-1	Bovine	USA	III		2, 8
USMARC	*Escherichia*	*coli*	O157:H7	TB21-1	Bovine	USA	III		2, 8
DECA	*Escherichia*	*coli*	O157:H7	3A	Human	USA	III		2
DECA	*Escherichia*	*coli*	O157:H7	3C	Human	USA	III		2
DECA	*Escherichia*	*coli*	O157:H7	3D	Human	USA	III		2
DECA	*Escherichia*	*coli*	O157:H7	3E	Human	USA	III		2
DECA	*Escherichia*	*coli*	O157:H7	4B	Human	USA	III		2
DECA	*Escherichia*	*coli*	O157:H7	4E	Human	USA	III		2
EHEC 1-4	*Escherichia*	*coli*	O157:H7	TW00116	Human	USA	III		2, 10
EHEC 1-5	*Escherichia*	*coli*	O157:H7	TW00975	Human	USA	III		2, 10
EHEC 1-7	*Escherichia*	*coli*	O157:H7	TW02883	Human	USA	III		2, 10
EHEC 1-2	*Escherichia*	*coli*	O157:H7	TW04863	Human	USA	III		2, 10
EHEC 1-8	*Escherichia*	*coli*	O157:H7	TW05356	Human	USA	III		2, 10
EHEC 1-6	*Escherichia*	*coli*	O157:H7	TW06555	Human	USA	III		2, 10
EHEC 1-3	*Escherichia*	*coli*	O157:H7	TW07587	Human	USA	III		2, 10
IDPHD	*Escherichia*	*coli*	O128:NM	12698	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
IDPHD	*Escherichia*	*coli*	O165:NM	12820	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O135:H15	14339	Human	USA	III		
CDC - Test Panel	*Escherichia*	*coli*	O157:H16	CDC 20	Human	USA	III		
CDC - Test Panel	*Escherichia*	*coli*	O157:H45	CDC-2	Human	USA	III		
CDC - Test Panel	*Escherichia*	*coli*	O157:H12	CDC17A	Human	USA	III		
CDC - Test Panel	*Escherichia*	*coli*	O27:H7	CDC-15	Human	USA	III		
DECA	*Escherichia*	*coli*	O55:H6	DECA 1A	Human	USA	III		
DECA	*Escherichia*	*coli*	O55:H6	DECA 1B	Human	D. Guiana	III		
EHEC 1	*Escherichia*	*coli*	O55:H7	TW05353	Meat	N/A	III		
EHEC 1	*Escherichia*	*coli*	O55:H7	TW07512	Human	USA	III		
EHEC 1	*Escherichia*	*coli*	O55:H7	TW00947	Human	Sri Lanka	III		
EHEC 1	*Escherichia*	*coli*	O55:H7	TW04062	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O76:H19	12974	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O8:H14	13627	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O-undet:H34	6853	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O'undet:NM	9655	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O'undet:NM	9823	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O'undet:NM	9972	Human	USA	III		
STEC	*Escherichia*	*coli*	O118:H16	TW14	N/A	N/A	III		
EIEC	*Escherichia*	*coli*	O124:H30	TW1	N/A	N/A	III		
IDPHD	*Escherichia*	*coli*	O146:H21	7606	Human	USA	III		
STEC	*Escherichia*	*coli*	O15:H11	TW11	N/A	N/A	III		
IDPHD	*Escherichia*	*coli*	O165:NM	9773	Human	USA	III		
IDPHD	*Escherichia*	*coli*	O28:H25	10596	Human	USA	III		
STEC	*Escherichia*	*coli*	O70:H11	TW4	N/A	N/A	III		
CDC - O STD's	*Escherichia*	*coli*	O1:K1:H7	U 5-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O2:K1:H4	U 9-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O3:K2a,2b:H2	U 14-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O4:K3:H5	U 4-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O5:K4:H4	U 1-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O6:K2a,2c:H1	Bi 7458-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O7:K1:HNM	Bi 7509-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O8:K8:H4	G 3404-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O9:K9:H12	Bi 316-42	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O10:K5:H4	Bi 8337-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O11:K10:H10	Bi 623-42	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O12:K5:HNM	Bi 626-42	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O13:K11:H11	Su 4321-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O14:K7:HNM	Su 4411-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O15:K14:H4	F 7902-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O16:K1:HNM	F 11119-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O17:K16:H18	K 12a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O18:K(b):H14	F 10018-41	N/A	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC - O STD's	*Escherichia*	*coli*	O19a	F 8858-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O19ab:H7	F 8188-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O20:K17:HNM	P 7a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O21:K20:HNM	E 19a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O22:K13:H1	E 14a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O23:K18:H15	E 39a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O24:KAP(+):HNM	E 41a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O25:K19:H12	E 47a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O26:K(b):H11	H 311b	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O27:K-:HNM	F 9884-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O28:K-:HNM	K 1a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O29:K-:H10	Su 4338-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O30:K-:HNM	P 2a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O32:K-:H19	P 6a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O33:K-:HNM	E 40	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O34:K-:H10	H 304	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O35:K-:H10	E 77a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O36:K-:H9	H 502a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O37:K-:H10	H 510c	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O38:H26	F 11621-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O39:HNM	H 7	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O40:K-:H4	H 316	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O41:K-:H40	H 710c	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O42:K-:H37	P 11a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O43:K-:H2	Bi 7455-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O44:K74:H18	H 702c	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O45:K1:H10	H 61	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O46:K-:H16	P 1c	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O48:K-:HNM	U 8-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O49:KAP(+):H12	U 12-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O50:K-:HNM(4)	U 18-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O51:K-:H24	U 19-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O52:K-:H10	U 20-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O53:K-:H3	Bi 7327-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O54:K-:H2	Bi 3972-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O55:K(b):HNM	Su 3912-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O56:KAP(+):HNM	Su 3684-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O57:K-:HNM	F 8198-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O58:K-:HNM(27)	F 8962-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O59:K-:H19	F 9095-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O60:K-:HNM(33)	F 10167a-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O61:K-:H19	F 10167b-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O62:K-:H30	F 10524-41	N/A	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC - O STD's	*Escherichia*	*coli*	O63:K-:HNM	F 10598-41	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O64:K-:HNM	K 6b	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O65:K-:HNM	K 11a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O66:K-:H25	P 6a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O68:K-:H4	P 7d	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O69:K-:H38	P 9b	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O70:K-:H38	P 9c	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O71:K-:H12	P 10a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O73:K-:H31	P 12a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O74:K-:H39	E 3a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O75:K95:H5	E 3b	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O76:K-:H8	E 5d	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O77:K96:HNM	E 10	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O78:K(b):HNM	E 38	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O79:K-:H40	E 49	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O80:K-:H26	E 71	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O81:K97:HNM	H 5	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O82:K-:HNM	H 14	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O83:K24:H31	H 17a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O84:K-:H21	H 19	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O85:K-:H1	H 23	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O86:K-:H25	H 35	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O87:K-:H12	H 40	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O88:K-:H25	H 53	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O89:K-:H16	H 68	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O90:K-:HNM	H 77	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O91:K-:HNM	H 307b	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O92:K-:H33	1930-58	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O95:KAP(+):HNM(33)	H 311a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O96:K-:H19	H 319	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O97:K-:HNM	H 320a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O98:K-:H8	H 510d	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O99:K-:H33	H 504c	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O100:K-:H2	H 509a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O101:K-:H33	H 501a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O102:K-:H8	H 511	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O103:KAP(+):H8	H 515b	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O104:K-:H12	H 519	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O105:K-:H8	H 520b	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O106:K-:H33	H 521a	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O107:K98:H27	H 705	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O108:K-:H10	H 708b	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O109:K-:H19	H 709c	N/A	USA	III		

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Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC - O STD's	*Escherichia*	*coli*	O110:K-:H39	H 711c	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O111:K(b):HNM	Stoke W	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O112:K(b):H18	1411-50	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O113:K-:H21	6182-50	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O114:K-:H32	W 26	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O115:K-:H18	W 27	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O116:KAP(+):H10	W 28	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O117:K98:H4	W 30	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O118:K-:HNM	W 31	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O119:K(b):H27	W 34	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O120:KAP(+):H6	W 35	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O121:K-:H10	W 39	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O123:K-:H16	W 43	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O124:K(b):H32	227	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O125:K(b):H19	Canioni (2745-53)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O126:K(b):H2	E 611 (6021-50)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O127:K(b):HNM	Holcomb (4932-53)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O128:K(b):H2	Cigleris (56-54)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O129:K-:H11	178-54 (1986-54)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O130:K-:H9	4866-53	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O131:K-:H26	HW 27	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O132:KAP(+):H28	HW 30	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O133:K-:H29	HW 31	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O134:K-:H35	4370-53	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O135:K-:HNM	3278-55	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O136:K(b):HNM	1111-55	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O137:K(b):H41	RVC 1787	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O138:K(b):H14	62-57	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O139:K(b):H1	63-57	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O140:K-:H43	149-51	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O141:K88ab(L):H4	RVC 2907	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O142:K(b):H6	C 771	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O143:K-:HNM	4608-58	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O144:K-:HNM	1624-56	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O145:K-:HNM	E 1385 (3)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O146:K-:H21	2950-54	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O147:K88ac(L):H19	G 1253	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O148:K-:H28	E 519-66	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O149:K(b):H10	D616 (CS 1483)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O150:K93:H6	Ch S	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O151:K-:H10	880-67	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O152:K-:HNM	1184-68	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O153:K-:H7	14097	N/A	USA	III		

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Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC - O STD's	*Escherichia*	*coli*	O154:K94:H4	E 1551-68	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O155:K-:H9	E 1529-68	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O156:K-:H47	E 1585-68	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O157:K88ac(L):H19	A 2	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O158:K-:H23	E 1020-72	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O159:K-:H20	E 2476-72	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O160:K-:H34	E 110-69	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O161:K-:H54	E 223-69	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O162:K-:H10	10B1/1	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O163:K-:H19	SN3B/1	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O164:K-:HNM	145/46	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O165:K-:HNM	E78634	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O166:K-:H4	3866-54 (OX8)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O167:K-:H-	E10702	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O168:K-:H-	179-54 (OX5)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O169:K-:H8	2112-76	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O170:K-:H1	3872-69 (OX1)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O171	244-55 (OX6)	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O172	85-3288	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O173	L119B-10	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O174	2531-54	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O175	2533-54	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O176	E29518/83	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O177	E40874/85	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O178	E54071/88	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O179	E434478	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O180	86-381	N/A	USA	III		
CDC - O STD's	*Escherichia*	*coli*	O181	92-1250	N/A	USA	III		
JN ATCC	*Acinetobacter*	*calcoacetions*		19606	N/A	N/A	III		
NOBL ATCC	*Actinobacillus*	*suis*		15557	N/A	N/A	III		
JN ATCC	*Aeromones*	*hydrophila*		7965	N/A	N/A	III		
ATCC	*Alcaligenes*	*faecalis*		8750	N/A	N/A	III		
NOBL ATCC	*Arcanobacterium*	*pyogenes*		19411	Swine	N/A	III		
NOBL ATCC	*Bordetella*	*bronchiseptica*		10580	Canine	USA	III		
ATCC	*Cedecea*	*lapagei*		33432	Human	Canada	III		
JN ATCC	*Citrobacter*	*freandii*		8090	N/A	N/A	III		
CDC	*Citrobacter*	*freandii*		CDC-11	Human	USA	III		
Dayna Harhay	*Enterococcus*	*faecalis*		06-582	N/A	USA	III		
ATCC	*Edwardsiella*	*tarda*		15947	Human	USA	III		
ATCC	*Enterobacter*	*aerogenes*		13048	Human	USA	III		
JN ATCC	*Enterobacter*	*cloacae*		23395	N/A	N/A	III		
ATCC	*Enterococcus*	*faecalis*		19433	N/A	N/A	III		
ATCC	*Escherichia*	*fergusonii*		35469	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
ATCC	*Escherichia*	*hermanii*		33650	Human	USA	III		
CDC	*Escherichia*	*hermannii*		CDC-12	Human	USA	III		
ATCC	*Escherichia*	*vulgaris*		33821	Human	USA	III		
ATCC	*Hafnia*	*alvei*		13337	N/A	N/A	III		
ATCC	*Klebsiella*	*oxytaca*		8724	N/A	N/A	III		
JN ATCC	*Klebsiella*	*pneumoniae*		13883	N/A	N/A	III		
ATCC	*Leminorella*	*grimontii*		33999	Human	N/A	III		
ATCC	*Morganella*	*morganii*		25830	Human	N/A	III		
NOBL ATCC	*Pasturella*	*haemolytica*		33396	Sheep	England	III		
ATCC	*Pasturella*	*multocida*		12948	Swine	N/A	III		
ATCC	*Proteus*	*mirabilis*		7002	Human	N/A	III		
JN ATCC	*Proteus*	*vulgaris*		13315	N/A	N/A	III		
ATCC	*Providencia*	*rettgeri*		29944	N/A	N/A	III		
ATCC	*Providencia*	*stuartii*		29914	Human	USA	III		
NOBL ATCC	*Pseudomonas*	*aeruginosa*		27853	N/A	N/A	III		
CDC	*Salmonella*		O30	CDC-9	Human	USA	III		
ATCC	*Salmonella*	*adelaide*		10718	N/A	N/A	III		
CDC	*Salmonella*	*agona*		B94-007406	Human	USA	III		
ATCC	*Salmonella*	*anatum*		9270	Swine	USA	III		
ATCC	*Salmonella*	*arizonae*		13314	N/A	N/A	III		
BURWELL	*Salmonella*	*berta*		788	N/A	N/A	III		
CDC	*Salmonella*	*berta*		B94-007417	Human	USA	III		
APHIS/NVSL	*Salmonella*	*blegdam*		95-6319	Chicken	USA	III		
CDC	*Salmonella*	*braenburg*		H9812	Human	USA	III		
CDC	*Salmonella*	*braenderup*		B94-007413	Human	USA	III		
CDC	*Salmonella*	*brandenburg*		B94-007420	Human	USA	III		
ATCC	*Salmonella*	*california*		23201	Turkey	N/A	III		
APHIS/NVSL	*Salmonella*	*cerro*		94-6513	N/A	USA	III		
ATCC	*Salmonella*	*cholerasuis*		13312	N/A	N/A	III		
APHIS/NVSL	*Salmonella*	*cholersuis*		94-6531	N/A	USA	III		
CDC	*Salmonella*	*derby*		B94-007419	Human	USA	III		
APHIS/NVSL	*Salmonella*	*dublin*		95-10963	Bovine	USA	III		
APHIS/NVSL	*Salmonella*	*dublin*		95-16283	Bovine	USA	III		
ATCC	*Salmonella*	*dublin*		15480	N/A	N/A	III		
APHIS/NVSL	*Salmonella*	*duesseldorf*		94-16453	N/A	USA	III		
APHIS/NVSL	*Salmonella*	*enteritidis*		94-6510	N/A	USA	III		
APHIS/NVSL	*Salmonella*	*enteritidis*		94-15238	Bovine	USA	III		
ATCC	*Salmonella*	*gallinarum*		9184	N/A	N/A	III		
APHIS/NVSL	*Salmonella*	*give*		94-6283	N/A	USA	III		
CDC	*Salmonella*	*hadar*		B94-007404	Human	USA	III		
CDC	*Salmonella*	*heidelberg*		B94-007403	Human	USA	III		
CDC	*Salmonella*	*infantis*		B94-007412	Human	USA	III		
APHIS/NVSL	*Salmonella*	*istanbul*		94-5693	N/A	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Salmonella*	*javiana*		B94-007408	Human	USA	III		
APHIS/NVSL	*Salmonella*	*johannesburg*		94-5154	N/A	USA	III		
APHIS/NVSL	*Salmonella*	*kentucky*		94-6327	N/A	USA	III		
APHIS/NVSL	*Salmonella*	*landau*		92-8402	N/A	USA	III		
APHIS/NVSL	*Salmonella*	*mbandka*		10013	Bovine	USA	III		
SGSC	*Salmonella*	*miami*		SARB 28	Human	N/A	III		
CDC	*Salmonella*	*montevideo*		B94-007410	Human	USA	III		
CDC	*Salmonella*	*muenchen*		B94-007414	Human	USA	III		
SGSC	*Salmonella*	*newport*		SARB 36	Human	N/A	III		
UNL - E. Erickson	*Salmonella*	*newport*		22851-95	Bovine	USA	III		
ATCC	*Salmonella*	*newport*		27869	Human	N/A	III		
APHIS/NVSL	*Salmonella*	*ohio*		94-5310	N/A	USA	III		
CDC	*Salmonella*	*oranienburg*		B94-007409	Human	USA	III		
SGSC	*Salmonella*	*panama*		SARB 40	Human	N/A	III		
ATCC	*Salmonella*	*paratyphi*	A	9150	N/A	N/A	III		
SGSC	*Salmonella*	*paratyphi*	B	SARA 45	Bovine	France	III		
SGSC	*Salmonella*	*paratyphi*	C	SARB 49	Human	N/A	III		
CDC	*Salmonella*	*poona*		B94-007418	Human	USA	III		
ATCC	*Salmonella*	*pullorum*		19945	N/A	N/A	III		
ATCC	*Salmonella*	*reading*		6967	Guinea pig	N/A	III		
CDC	*Salmonella*	*saintpaul*		B94-007411	Human	USA	III		
SGSC	*Salmonella*	*senftenberg*		SARB 59	Chicken	N/A	III		
APHIS/NVSL	*Salmonella*	*soerenga*		90-13724	N/A	USA	III		
CDC	*Salmonella*	*thompson*		B94-007407	Human	USA	III		
CDC	*Salmonella*	*typhi*		B94-007415	Human	USA	III		
NADC	*Salmonella*	*typhimurium*		18898	Bovine	USA	III		
NADC	*Salmonella*	*typhimurium*		19617	Bovine	USA	III		
SGSC	*Salmonella*	*typhimurium*		SARB 65	Human	N/A	III		
ATCC	*Salmonella*	*typhimurium*		14028	Chicken	USA	III		
ATCC	*Salmonella*	*typhimurium*	copenhagen	6994	N/A	N/A	III		
CDC	*Salmonella*	*typhimurium*	DT104	G7601	Human	USA	III		
ATCC	*Salmonella*	*typhimurium*	LT2 wild type	19585	N/A	N/A	III		
SGSC	*Salmonella*	*wien*		SARB 71	Human	N/A	III		
JN ATCC	*Serratia*	*marcescens*		8100	N/A	N/A	III		
ATCC	*Shigella*	*flexneri*		12022	Human	USA	III		
JN ATCC	*Shigella*	*sonnei*		25931	Human	USA	III		
ATCC	*Stenotrophomonas*	*maltophilia*		13637	Human	N/A	III		
ATCC	*Yersina*	*pseudotuberculosis*		29910	Human	USA	III		
ATCC	*Yersinia*	*enterocolitica*		55075	N/A	Canada	III		
CDC	*Escherichia*	*coli*	O103:H2	03-3058	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	03-3112	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:NM	03-3243	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	03-3297	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O103:H25	03-3313	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	03-3356	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	03-3399	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	03-3444	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	04-3021	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	04-3027	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	04-3056	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	04-3092	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	04-3508	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	05-3048	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	05-3112	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	05-3286	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	05-3319	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	05-3546	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	05-3554	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	06-3008	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	06-3066	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	06-3088	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	06-3539	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	06-3562	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	06-3584	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	06-3908	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	06-3938	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	07-3006 A	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	07-3008	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	07-3009	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	07-3070	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	07-3081	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	07-3137	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	07-3138	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	07-3202	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	07-3261	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	07-3482	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	07-3691	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:NM	07-3787	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:NM	07-3841	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	07-3855	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	07-4192	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	07-4284	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	08-3073	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	08-3268	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	08-3321	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	08-3366	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O103:H2	08-3367	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	08-3368	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	08-3466	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	08-3567	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	08-3644	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	08-4010	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	08-4032	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	08-4040	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	08-4050	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	08-4066	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	08-4082	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	08-4273	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	08-4363	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	08-4373	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	08-4631	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2009C-3015	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2009C-3025	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2009C-3274	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2009C-3279	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2009C-3333	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2009C-3690	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2009C-3786	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2009C-4002	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2009c-4089	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2009C-4822	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2010C-3032	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2010C-3047	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2010C-3213	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2010C-3214	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2010C-3403	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2010C-3450	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2010C-3652	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2010C-3669	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2010C-3788 A	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:NM	2010C-3845	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2010C-3848	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2010C-3943 C1	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2010C-4097	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2010C-4216	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2010C-4302 C2	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2010C-4433	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2010C-4529	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2010C-4766	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O103:H11	2011C-3009 C1	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2011C-3085	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2011C-3201	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2011C-3307	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2011C-3370	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2011C-3528	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H25	2011C-3553	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2011C-3593	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2011C-3618	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H2	2011C-3750	Human	USA	III		
CDC	*Escherichia*	*coli*	O103:H11	2011C-4249 C2	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	00-3305	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	01-3276	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	02-3274	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	03-3318	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	03-3469	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	03-3502	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	03-3503	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	03-3505	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	03-3507	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	04-3120	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	04-3162	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	04-3195	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	04-3197	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	04-3313	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	04-3517	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	05-3646	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:NM	06-3235	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	06-3603	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	06-3653	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	06-3695	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	07-3721	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	07-3769	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	07-3862	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	07-3986	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:NM	08-3084	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:NM	08-3200	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	08-3502	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	08-3832	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	08-4361	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	08-4392	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	08-4484	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:NM	2009C-3523	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O26:H11	2009C-3568	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2009C-3589	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2009C-3753	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2009C-3904	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H32	00-3258 (ETEC)	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	03-3500	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	06-3464	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2009C-3996	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2009C-4747	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2009C-4760	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2009C-4826	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2010C-3051	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2010C-3472	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2010C-3871	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2010C-4244	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:NM	2010C-4347	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2010C-4430	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:NM	2010C-4788	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2010C-4834	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2010C-5028	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2010EL-1699	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2011C-3270	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2011C-3274	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2011C-3282	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2011C-3387	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2011C-3506	Human	USA	III		
CDC	*Escherichia*	*coli*	O26:H11	2011C-3655	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H31	00-3140	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	01-3080	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	01-3147	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	01-3510	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	02-3169	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	02-3351	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	03-3322	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	03-3395	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	04-3206	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	04-3409	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	05-3269	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	05-3508	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	06-3559	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	06-3990	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H19	07-3668 C1	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	07-4310	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O45:H2	07-4361	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	08-3079	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	08-4498	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2009C-3023	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2009C-3619	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2009C-3686	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:NM	2009C-3772	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2009C-4040	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:NM	2009C-4401	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2009C-4603	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2009C-4780	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2009C-4781	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2009C-4801	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2010C-3166	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2010C-3419	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2010C-3657	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2010C-3876	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2010C-4211	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2010C-4340 C1	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2010C-4397	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2010C-4884	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:NM	2011C-3025	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2011C-3398	Human	USA	III		
CDC	*Escherichia*	*coli*	O45:H2	2011C-3536	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	97-3215	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	99-3215	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	00-3158	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	01-3076	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	01-3464	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	02-3194	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	02-3334	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	02-3342	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	03-3296	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	03-3390	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	03-3428	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	03-3484	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	05-3004	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	06-3682	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	06-3805	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	07-3376	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H2	08-3342	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-3753	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	08-4347	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O111:NM	08-4374	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4376	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4377	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4378	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	08-4386	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4387	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4391	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4414	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	08-4455	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4487	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4616	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2009C-3342	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	2009C-3586	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2009C-3675	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2009C-3728	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2009C-3920	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2009C-3984	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2009C-4006	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	2009EL-1666	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	01-3076	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	03-3484	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	04-3211	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	08-4487	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2009C-4006	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2009C-4052	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	2009C-4126	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:H8	2009EL-2169	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-3053	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-3977	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4086	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4221	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4592	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4622	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4715	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4735	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4746	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4799	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2010C-4818	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2011C-3170	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2011C-3362	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2011C-3453	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2011C-3573	Human	USA	III		
CDC	*Escherichia*	*coli*	O111:NM	2011C-3632	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O111:NM	2011C-3679	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	03-3227	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	06-3003	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	06-3822	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H7	2009C-3299	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2009C-4050	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2009C-4659	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2009C-4750	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2009EL-1302	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2009EL-1412	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2010C-3609	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2010C-3794	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2010C-3840	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2010C-4254	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2010C-4732 C1	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2010C-4966	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2010C-4989	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2011C-3108	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2011C-3216	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2011C-3500	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2011C-3537	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	2011C-3609	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	K5269	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	97-3093	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	98-3221	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	99-3323 C1	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	00-3024	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	00-3071	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	00-3100	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H19	00-3266	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:H7	00-3395	Human	USA	III		
CDC	*Shigella*	*dysenteriae 7*		53-4788	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:NM	98-3306	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:NM	2010C-4003	Human	USA	III		
CDC	*Escherichia*	*coli*	O121:NM	2010C-4005	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	01-3013	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	01-3131	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	01-3472	Human	USA	III		
CDC	*Escherichia*	*coli*	O118:NM	02-3132	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	02-3136	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	02-3333	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	03-3016	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	03-3226	Human	USA	III		

Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]
CDC	*Escherichia*	*coli*	O145:NM	03-3466	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	04-3312	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	04-3377	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	04-3447	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	05-3158	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	05-3287	Human	USA	III		
CDC	*Escherichia*	*coli*	O118:H25	05-3579	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	05-3589	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	06-3397	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	06-3484	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	06-3672	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:H34	07-3471	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	07-3854	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:H25	07-3858	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	07-3942	Human	USA	III		
CDC	*Escherichia*	*coli*	145	07-4001	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:H25	08-3202	Human	USA	III		
CDC	*Escherichia*	*coli*	O118:H16	08-3267	Human	USA	III		
CDC	*Escherichia*	*coli*	O118:NM	08-3717	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	08-4270	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	08-4695	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:H28	2009C-3292	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	2009C-3620	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	2009C-3691	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	2009C-3770	Human	USA	III		
CDC	*Escherichia*	*coli*	O118:H16	2009C-4467	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	2010C-3232	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	2010C-4243 C1	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	2010C-4557 C2	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:H34	2010C-4848	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	2011C-3160	Human	USA	III		
CDC	*Escherichia*	*coli*	O145:NM	2011C-3330	Human	USA	III		

[a]Application: I=sequenced; II=sequenced and PFGE ; III= MALDI-TOF

[b]References :

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Supplemental Table 1. Bacterial strains used for sequencing and MALDI-TOF validation

Collection	Genus	Species	Serotype	Strain Designation	Source	Country	Application[a]	Genbank accession number	Reference[b]

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[c]Not Applicable

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AY763106:80U20	AGATACTTGTTACTGGTGGC	O26 O operon sequencing
AY763106:353U20	CTGCGGCATTTATTGAAACC	O26 O operon sequencing
AY763106:667U20	TACGGCCCTTATCACTTTCC	O26 O operon sequencing
AY763106:981U20	CCGTTATGCGATTGATGCTG	O26 O operon sequencing
AY763106:1283U20	TAATCCTGAAGGTGTAGCTG	O26 O operon sequencing
AY763106:1580U20	GGAATATTGCGCAAAGCATC	O26 O operon sequencing
AY763106:1884U20	GCACTCAACAAGCTCAACGC	O26 O operon sequencing
AY763106:2156U24	GGGTACTCGTCTTTATCCTGTAAC	O26 O operon sequencing
AY763106:2476U21	CGAAGTTAATGGATGTCGCTG	O26 O operon sequencing
AY763106:2781U20	TATGCATGGCTGGACACGGG	O26 O operon sequencing
AY763106:3063U20	TGAGCGTGGTTTCTTTATGG	O26 O operon sequencing
AY763106:3366U22	GGTGTTAAGCGAGATAGCAGAG	O26 O operon sequencing
AY763106:3689U20	TGTTGGTGAAGTACTAGCAC	O26 O operon sequencing
AY763106:3969U20	AACAATAGGCCATTGGCTGT	O26 O operon sequencing
AY763106:4293U20	TCTGTACGCGACGGCAGAGA	O26 O operon sequencing
AY763106:4586U24	GGGGATATACAATTTTATGTTTGG	O26 O operon sequencing
AY763106:4888U23	TGTGATGGTTTTAGGTTTATGGA	O26 O operon sequencing
AY763106:5195U20	CTGCTTTACATGTTGTGTCC	O26 O operon sequencing
AY763106:5487U20	ACACTAGGACGTTACATGCA	O26 O operon sequencing
AY763106:5798U20	TCATATTTACTGTTATTCAC	O26 O operon sequencing
AY763106:6100U20	GAATTTGGGATATTTTGGCG	O26 O operon sequencing
AY763106:6371U20	TTAACGTGGGGAAGCAGGTT	O26 O operon sequencing
AY763106:6700U20	GTAAAAGGTGAAAATATGTT	O26 O operon sequencing
AY763106:6996U20	GGAGGCGGTTAAGACAAATG	O26 O operon sequencing
AY763106:7302U20	TCGTTTCATGATGACGCTTG	O26 O operon sequencing
AY763106:7604U20	ATGGTGACCGTCGTATCTCG	O26 O operon sequencing
AY763106:7877U21	GGACTTAAGCAGGCAGATTTC	O26 O operon sequencing
AY763106:8204U20	CGCATTGCAAATGATGAAGC	O26 O operon sequencing
AY763106:8485U21	GTTTGCGTATACGGTTCCTTC	O26 O operon sequencing
AY763106:8782U21	GCTAGTTGTTATGCTTTGGGC	O26 O operon sequencing
AY763106:9110U20	AGGAAAAACCAGAAGCCATG	O26 O operon sequencing
AY763106:9410U20	CCGATGTACTTTCTCGCCTG	O26 O operon sequencing
AY763106:9698U22	GCGGGACTATTACAGAGGAGTC	O26 O operon sequencing
AY763106:10011U20	TATTTGCCCCATAGCACACG	O26 O operon sequencing
AY763106:10311U20	TTTTGGGGAGGCTTGGTTAA	O26 O operon sequencing
AY763106:10589U24	CGGCGATGATTATCATTCACTTCG	O26 O operon sequencing
AY763106:10896U20	TCTTCACATAATTTCCCCGG	O26 O operon sequencing
AY763106:11214U20	AACTTTTTCGCACTGCAGCA	O26 O operon sequencing
AY763106:11508U20	TGTCACCAAAAGCCCTTATG	O26 O operon sequencing
AY763106:11630L22	GCTAAGATGGTAACCCAGCATG	O26 O operon sequencing
AY763106:11266L20	TCTCCTGATGAGATGCGTGC	O26 O operon sequencing
AY763106:10934L20	GGATCGGGATTGATTGAACC	O26 O operon sequencing
AY763106:10557L20	GTCATTGAGGCCCAATTACG	O26 O operon sequencing
AY763106:10224L22	GCCATGCACGAAAAGATAAAAG	O26 O operon sequencing
AY763106:9855L20	AGCGTACTTCTCCACGAGGC	O26 O operon sequencing
AY763106:9511L24	AGCCACGGTATTAAGTATATTTGC	O26 O operon sequencing
AY763106:9163L20	CGACGCTTTGCTGGTATTGC	O26 O operon sequencing
AY763106:8819L24	CGCTATAGTATCTGGTTCAGAACG	O26 O operon sequencing
AY763106:8477L22	CCGTATACGCAAACTGTTTAGG	O26 O operon sequencing
AY763106:8102L20	TTAGCGTTTGTCGTTTCCCC	O26 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AY763106:7770L20	ACCGATAAACCCTGCAGCGC	O26 O operon sequencing
AY763106:7396L20	AATGTTTGAATTGTTGCCGC	O26 O operon sequencing
AY763106:7052L20	CACGCGTTTAATCCCATTCG	O26 O operon sequencing
AY763106:6698L20	CATATTTTCACCTTTTACAG	O26 O operon sequencing
AY763106:6368L20	CTGCTTCCCCACGTTAAAAC	O26 O operon sequencing
AY763106:6016L20	GCTCTTGCTCATTAGAACAG	O26 O operon sequencing
AY763106:5649L22	ACGGAAAGAAATAACATTAGCG	O26 O operon sequencing
AY763106:5312L23	GGTGCCATAAAGACAAAACAAAG	O26 O operon sequencing
AY763106:4942L20	CAATTACCAAATTACTTAGC	O26 O operon sequencing
AY763106:4608L20	ATGGACAATCCAACCGAACC	O26 O operon sequencing
AY763106:4264L20	AACAGGCGAAGCAAGAGTGC	O26 O operon sequencing
AY763106:3886L20	TCCCAAGTATACACTTAATG	O26 O operon sequencing
AY763106:3535L30	TTTTTTCAACATCAATAGTC	O26 O operon sequencing
AY763106:3183L20	AGGGTTCCAGCTGATAGTGC	O26 O operon sequencing
AY763106:2847L20	TTCAGCCCCTGACGTTCTTC	O26 O operon sequencing
AY763106:2486L20	CTTTGTTAACAGCGACATCC	O26 O operon sequencing
AY763106:2148L20	AGACGAGTACCCGAACCACC	O26 O operon sequencing
AY763106:1779L20	TACAAGCCTGCGACTTCTGG	O26 O operon sequencing
AY763106:1445L20	AATGAATAAGCCAGGCGCCG	O26 O operon sequencing
AY763106:1094L22	CCACTTTTCACATTTTCGACCC	O26 O operon sequencing
AY763106:749L20	GCGAATTTGATCCCCTTTGC	O26 O operon sequencing
AY763106:393L20	TGCGAGCGGCTTCCAAAAGG	O26 O operon sequencing
AY763106:31L20	CATGCTGTGAAATAAGCGGC	O26 O operon sequencing
AY771223:69U20	TTCAGAACGCCAGTATCCAG	O45 O operon sequencing
AY771223:427U20	TTATGTGCTTCTGGAAGCCG	O45 O operon sequencing
AY771223:761U20	CTGGACGGTAAAGTTTTGCC	O45 O operon sequencing
AY771223:1126U20	TACAGAATGGGTGGAAAACG	O45 O operon sequencing
AY771223:1477U20	AAAGCCGAAGATACGCTGAC	O45 O operon sequencing
AY771223:1811U20	TGCCACTGCCTTTTAAATCG	O45 O operon sequencing
AY771223:2179U20	ATTGAAGGTAACAAATAATG	O45 O operon sequencing
AY771223:2512U20	TCATCGCTGCAGCTATAGGG	O45 O operon sequencing
AY771223:2863U20	TCACCATTGGGCTGATGATC	O45 O operon sequencing
AY771223:3239U20	TCTGATCATTGTTGGAGCTG	O45 O operon sequencing
AY771223:3577U22	CAAACTCAGCTCTTGGTGTAGG	O45 O operon sequencing
AY771223:3935U20	CGTATTGATTCAATGACGCC	O45 O operon sequencing
AY771223:4291U20	GTTACTTCCTGCGCTAAGCC	O45 O operon sequencing
AY771223:4613U20	GATCCTGTTACCCCGATCCC	O45 O operon sequencing
AY771223:4991U20	TTATGTTGTGCCCAAGCTGC	O45 O operon sequencing
AY771223:5326U24	TGGGGATGTTTTCGTATTGG	O45 O operon sequencing
AY771223:5686U24	TGACTTACTTTGGAAAGAACACAA	O45 O operon sequencing
AY771223:6037U20	GATGTTGCAGTGGATTTGCG	O45 O operon sequencing
AY771223:6398U20	TTTGGCTAAGGGTGAGGATG	O45 O operon sequencing
AY771223:6723U23	CGAGATACGATTATTGTCAGACC	O45 O operon sequencing
AY771223:7100U20	AGATATAGAAATAATGATTG	O45 O operon sequencing
AY771223:7448U20	GTCTGGCTGCAGGGACTTTC	O45 O operon sequencing
AY771223:7771U22	GGGTTTCGATTTGTGAAGGTTG	O45 O operon sequencing
AY771223:8131U21	GGTGAAAAGCTTGTTAATGCC	O45 O operon sequencing
AY771223:8504U20	TTAATTCTTATTGACGATTG	O45 O operon sequencing
AY771223:8836U20	AGCGCGTAATATCCCTGAAG	O45 O operon sequencing
AY771223:9180U20	GACTCCGCAGTAAATTACTC	O45 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AY771223:9548U20	GACTCCGCAGTAAATTACTC	O45 O operon sequencing
AY771223:9904U20	AAAAATTCACTAAAAAGATG	O45 O operon sequencing
AY771223:10259U20	AAAGCTAATGCCCGATCTTG	O45 O operon sequencing
AY771223:10605U20	CGGAATGAAAATGACTCCAG	O45 O operon sequencing
AY771223:10956U20	TGTCGCTGCTAATGCTGTTG	O45 O operon sequencing
AY771223:11281U25	CAAAGGTGAATCTCTTGATAGAAAA	O45 O operon sequencing
AY771223:11642U23	CCTTCAATTGTTGTCTTGGTAGG	O45 O operon sequencing
AY771223:11988U23	CGCGTTATAGTATAGACTCGTGG	O45 O operon sequencing
AY771223:12352U20	ATGGCCTCGTGCAAGCATTC	O45 O operon sequencing
AY771223:12713U20	TCTCGAGCAGGGGAATCTTC	O45 O operon sequencing
AY771223:13067U20	TTCTGTTACCTTCTGCGTTC	O45 O operon sequencing
AY771223:13402U20	ACTCAGGAACCTCTTGCAGC	O45 O operon sequencing
AY771223:13769U20	CATTACCTAGGGAAAACCTG	O45 O operon sequencing
AY771223:14111U22	GGCTATCTATTTTGGAGCTTGC	O45 O operon sequencing
AY771223:14388L20	TCCCGGTGGATATATTATCG	O45 O operon sequencing
AY771223:14039L20	TGAGATAGTCTACTCGCAAC	O45 O operon sequencing
AY771223:13690L20	TACTGAATGAGGGTATTCCC	O45 O operon sequencing
AY771223:13339L20	CTTCTGCTACCAAAATTTTC	O45 O operon sequencing
AY771223:12983L20	ATATGATATTGTTAGATAAC	O45 O operon sequencing
AY771223:12658L20	GCGTGCTGATGGCTTGACAC	O45 O operon sequencing
AY771223:12288L20	CTGCCATCACCCAGTAAACG	O45 O operon sequencing
AY771223:11957L20	AGGTGCGCATCGTTATATGG	O45 O operon sequencing
AY771223:11579L20	TCATAAACCTCTCCCAATAC	O45 O operon sequencing
AY771223:11229L20	TGTTTGAAGCAAAATCTTCTCAA	O45 O operon sequencing
AY771223:10899L20	TAGCCCCAGATGCAATAACC	O45 O operon sequencing
AY771223:10545L20	TATTTCGCCCAGTCAGTTTG	O45 O operon sequencing
AY771223:10192L24	TGGTATCATGGAATCCTAAATCAC	O45 O operon sequencing
AY771223:9829L20	TCTGAAGACCAGCATTTCCC	O45 O operon sequencing
AY771223:9473L23	TTGATAAAAACACCACCATCTCA	O45 O operon sequencing
AY771223:9123L20	ACTATCCTTCACGCACTCCG	O45 O operon sequencing
AY771223:8772L20	AAGTCTGGCAGGGTCGATTC	O45 O operon sequencing
AY771223:8419L20	GTTCACAATAGGCAGGGACC	O45 O operon sequencing
AY771223:8073L20	TAAATAATGCGCCCGTGCAG	O45 O operon sequencing
AY771223:7724L24	AGATAAAGCCACAAGGTAAAAGTG	O45 O operon sequencing
AY771223:7367L20	AATTACCATCTCGGCTCCAC	O45 O operon sequencing
AY771223:7029L20	TCTGTTGGCGGGAAATATTC	O45 O operon sequencing
AY771223:6665L20	TAAGATTGAAAAGCCTTCGG	O45 O operon sequencing
AY771223:6329L20	TATAATATGCTTTCATAAAG	O45 O operon sequencing
AY771223:5985L20	TACCCTGGGGTTTCGTTTTC	O45 O operon sequencing
AY771223:5609L20	CCCTCATAATCAAAGTTGCG	O45 O operon sequencing
AY771223:5269L20	CTGCCTCAGGAATGGTCATG	O45 O operon sequencing
AY771223:4909L20	TATAAGCAGCCGCATGGTAG	O45 O operon sequencing
AY771223:4556L20	GCATCGATTCTTGCTTTTCC	O45 O operon sequencing
AY771223:4205L20	AACATTCTCATTGCAAGGCG	O45 O operon sequencing
AY771223:3860L22	GCGTTATAATCCGTTTTATTGG	O45 O operon sequencing
AY771223:3504L20	GGGCTCACAAATGCAAAAGG	O45 O operon sequencing
AY771223:3157L20	CAATGGTAACCAAGCGATGG	O45 O operon sequencing
AY771223:2802L20	GCCACAGGGAAGTTCCACAC	O45 O operon sequencing
AY771223:2450L20	CGTCGAGGAAACCAATAACC	O45 O operon sequencing
AY771223:2111L20	CGTCCATTGAAGGTGCTCTC	O45 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AY771223:1757L20	GTTACCCGGTGCATTTGGAC	O45 O operon sequencing
AY771223:1416L21	GTATCACAACCCTGGAGAAGG	O45 O operon sequencing
AY771223:1050L20	CGTCCATCCCAACTCAGCAC	O45 O operon sequencing
AY771223:706L20	GGAAATGATACGGGCCATAG	O45 O operon sequencing
AY771223:349L20	GACTTTCAGCCGCCAAATGC	O45 O operon sequencing
AY532664:63U20	CCGCTTATTTCACAGCATGC	O103 O operon sequencing
AY532664:431U20	GAAGCGGCTCGCAATTACTG	O103 O operon sequencing
AY532664:781U20	TAAAGGGGATCAAATTCGCG	O103 O operon sequencing
AY532664:1130U20	CGACGAGTTCAAGATGGCTC	O103 O operon sequencing
AY532664:1471U25	GGAAATGACACAGTATGTCTTATGC	O103 O operon sequencing
AY532664:1834U20	TTTGCATGGCTGGATACAGG	O103 O operon sequencing
AY532664:2180U20	GTAAGACGGGGATATCACGC	O103 O operon sequencing
AY532664:2524U20	TGCGGGTAGATTCTCGTCTC	O103 O operon sequencing
AY532664:2880U22	GGAGCCACCATAATAAAAGAGG	O103 O operon sequencing
AY532664:3223U23	CGGAGATGAAATTATTGTACCTG	O103 O operon sequencing
AY532664:3580U20	AGGTGCGATAACAACGAGTG	O103 O operon sequencing
AY532664:3938U20	GCGCCTCATAATCAAGAAGC	O103 O operon sequencing
AY532664:4292U20	CAGAAAATCAAGGTGATTAC	O103 O operon sequencing
AY532664:4637U20	ATAATGCGGTTGCAGGTGTC	O103 O operon sequencing
AY532664:4985U20	GTATTGTTGTACCGCTCGCG	O103 O operon sequencing
AY532664:5325U20	GCATCTGACAAAAAAGGCCC	O103 O operon sequencing
AY532664:5674U22	GCTCCGATGCTGGATAATAAAG	O103 O operon sequencing
AY532664:6046U20	TATAAAGTTATAAATAATGC	O103 O operon sequencing
AY532664:6396U20	ATACTAGAGACATTAGAGTC	O103 O operon sequencing
AY532664:6717U24	GCAGTGTTTACTTATTTCCAAACC	O103 O operon sequencing
AY532664:7097U20	TGGTTATTATTTGGCTTACC	O103 O operon sequencing
AY532664:7421U21	TTTACCTCGTTTGAATTTGGG	O103 O operon sequencing
AY532664:7799U20	ATCATAATTACGGTATCCTC	O103 O operon sequencing
AY532664:8146U20	ATTAAATGACAAGACCCCGC	O103 O operon sequencing
AY532664:8492U21	TTGTCGTGTTGAATGGAAATG	O103 O operon sequencing
AY532664:8850U20	CAAATCGAAGTCAATTCCCG	O103 O operon sequencing
AY532664:9205U20	GGCTTTGGTTTGGTTGTAGC	O103 O operon sequencing
AY532664:9554U20	GTTAAAAATAAAATTCGGTG	O103 O operon sequencing
AY532664:9907U20	ATCCTGATTCTGTTCTTTGC	O103 O operon sequencing
AY532664:10254U20	CATTTTGGTATGGTGGCAAG	O103 O operon sequencing
AY532664:10581U23	TGTCGAGAAACAGTAATTGATGG	O103 O operon sequencing
AY532664:10959U20	CATAATTCTTCAGTTGAATC	O103 O operon sequencing
AY532664:112881U22	TGGCACTACTAATCCCTATGGG	O103 O operon sequencing
AY532664:11661U20	TCGGTTCTTGAACTTTTGGC	O103 O operon sequencing
AY532664:11964L20	TGTCAGGGGTTACTGCGAAC	O103 O operon sequencing
AY532664:11593L20	ATCTCGGTGCTTCAAGGCAG	O103 O operon sequencing
AY532664:11244L22	CGGGTATCTTCTCTGGAGTACC	O103 O operon sequencing
AY532664:10881L20	GAGCCAATATATCCAGCACC	O103 O operon sequencing
AY532664:10532L20	GACCTATTGCCATTGCTTCC	O103 O operon sequencing
AY532664:10188L20	ACACCTATGCCACCAATAAC	O103 O operon sequencing
AY532664:9835L20	AGGATTAATACCAGATCGTG	O103 O operon sequencing
AY532664:9477L20	TATTTTTCCATTAAGCTATG	O103 O operon sequencing
AY532664:9132L24	GCGACATTAGCAATACTACCTAGC	O103 O operon sequencing
AY532664:8786L20	TACATTAGTCGTAGCATCAC	O103 O operon sequencing
AY532664:8425L20	ATTTGTTTTTCAGCCCCACC	O103 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AY532664:8079L20	GCGAGCCAGAAAAGTAATCG	O103 O operon sequencing
AY532664:7736L24	CGGTAAAATTATTACTGCAGACAC	O103 O operon sequencing
AY532664:7398L20	CCCCTCATCCTCGATGAATC	O103 O operon sequencing
AY532664:7021L20	TTTAATGTTATTAAGCGAGG	O103 O operon sequencing
AY532664:6694L25	GCACCTATATTATCCAAATTTGAGC	O103 O operon sequencing
AY532664:6328L20	TTTCATATTTAGCTAACAAG	O103 O operon sequencing
AY532664:5981L20	AAAGAAATATCTTCCAGATG	O103 O operon sequencing
AY532664:5633L25	GCATCTGAACTTAAAGAGTCATCAC	O103 O operon sequencing
AY532664:5269L20	GCATAAGTGATGCTGTAGGC	O103 O operon sequencing
AY532664:4931L20	ATATCTTCTTGCGGCTGCAG	O103 O operon sequencing
AY532664:4568L20	GCCCACCATAGATAACAACG	O103 O operon sequencing
AY532664:4212L20	CAAAATTTTGCAATTGTCCC	O103 O operon sequencing
AY532664:3870L20	TTGCAAAGAATCACGCTCTG	O103 O operon sequencing
AY532664:3514L20	CAGCTGCATGACCCCAACTG	O103 O operon sequencing
AY532664:3173L21	CCGAAGAACAAGGATTAGTGC	O103 O operon sequencing
AY532664:2819L20	CAACTTGAAAATATGAATAC	O103 O operon sequencing
AY532664:2458L20	TGTATTTTTTGTAAAGAGCG	O103 O operon sequencing
AY532664:2114L24	AATTGGGATATCTTTATTTTGCTC	O103 O operon sequencing
AY532664:1765L24	AACTTCATTAACTGCCGTAATTTC	O103 O operon sequencing
AY532664:1412L22	CCATCTGGACTAGGTTGAATTG	O103 O operon sequencing
AY532664:1053L20	CGTTTCCTGTGGTTTCCATC	O103 O operon sequencing
AY532664:702L20	TTCCGGGAAATGATACGGAC	O103 O operon sequencing
AY532664:351L20	ACGATCCACATGGCTTTCAG	O103 O operon sequencing
AF078736:74U20	CCTGGGGACGTATTCAACTG	O111 O operon sequencing
AF078736:431U20	TTTTTTCTTGTTTCTGGTCG	O111 O operon sequencing
AF078736:776U20	TACTTTTAGAATGTGATATG	O111 O operon sequencing
AF078736:1129U20	GGAATGATTGAAGGTCTAGG	O111 O operon sequencing
AF078736:1462U25	ACAACTTATCCAAGTTCTGAATTTG	O111 O operon sequencing
AF078736:1832U20	AAATGGGGCTTGCTGGAAGG	O111 O operon sequencing
AF078736:2181U20	GATACTTCCAATCTGACCCG	O111 O operon sequencing
AF078736:2537U20	TAACCACGAATCACCTCGCC	O111 O operon sequencing
AF078736:2867U20	TAAAGCTGTAAACCCGGGCG	O111 O operon sequencing
AF078736:3239U20	GCTAATTGAAAACGAGAATG	O111 O operon sequencing
AF078736:3556U25	GGCTAACTAAACACCAAATAAATGC	O111 O operon sequencing
AF078736:3930U20	CCTGCCATAGCTTTAGCTGC	O111 O operon sequencing
AF078736:4277U20	TCGCGCCAGTAAATATCTTG	O111 O operon sequencing
AF078736:4641U20	ATTGTCCAAACCAAGGATGC	O111 O operon sequencing
AF078736:4991U20	TCCAGGCGTAATACCTTTGC	O111 O operon sequencing
AF078736:5331U20	GAATGTGTGGTACTGAAGAG	O111 O operon sequencing
AF078736:5667U23	TTATTGATGCTATTGAGGAATGC	O111 O operon sequencing
AF078736:6040U20	CGGTCATGCTTACATTAAGC	O111 O operon sequencing
AF078736:6390U20	CAGAACCTGTAGTACGATTG	O111 O operon sequencing
AF078736:6730U20	CAGGCCGTTTGATTTTCTGG	O111 O operon sequencing
AF078736:7099U20	CCCAGAGATCGAAATTTGGG	O111 O operon sequencing
AF078736:7450U20	TACCCACTTGCTAGTAATAC	O111 O operon sequencing
AF078736:7801U20	AATGCTATTTCAGATAAAAC	O111 O operon sequencing
AF078736:8135U23	GTGATGATATTTTCGAAGAGTCG	O111 O operon sequencing
AF078736:8499U20	TGATACGGTAGCAAATGCCG	O111 O operon sequencing
AF078736:8838U20	GGATGTTCCGCATGGATTGC	O111 O operon sequencing
AF078736:9200U20	TTTAGCCTTTACCATTAAAG	O111 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AF078736:9555U20	CTAATTTCTGTTTTGCCTTG	O111 O operon sequencing
AF078736:9904U20	TCTATTGATTTACTTTTTTC	O111 O operon sequencing
AF078736:10259U20	TGTTTTACTTGTTTAGATTG	O111 O operon sequencing
AF078736:10584U20	TTTGGTTTCACAGCTTGGTG	O111 O operon sequencing
AF078736:10961U20	TGTAATGGAAATTTAGACGC	O111 O operon sequencing
AF078736:11299U20	ATCTAATGGCGCCCCTGTGG	O111 O operon sequencing
AF078736:11646U23	CGCTAGAAAGTTTCATTGTACGC	O111 O operon sequencing
AF078736:11990U20	TGGATAAAAATTTTAGAAGC	O111 O operon sequencing
AF078736:12343U20	AGAAAGAAAACGCGAGATGC	O111 O operon sequencing
AF078736:12702U20	TGCTACCGATTCTGGTGGAG	O111 O operon sequencing
AF078736:13066U20	AGACTACATTCAAGCCGCGC	O111 O operon sequencing
AF078736:13413U20	TTATTGATGGTGGCAACACC	O111 O operon sequencing
AF078736:13767U20	TGGCAACCACTTTTACCGAG	O111 O operon sequencing
AF078736:14119U20	TTATGCCCAAGGCTTCTCTC	O111 O operon sequencing
AF078736:14468U20	GGTGCGCACACGTATAAACG	O111 O operon sequencing
AF078736:14425L20	TCAGATTAGCCGGCAGTACC	O111 O operon sequencing
AF078736:14074L20	CGCGACGGACTTTCTCAACG	O111 O operon sequencing
AF078736:13730L20	TTAAGGCCGCCTTTAAGCAG	O111 O operon sequencing
AF078736:13367L20	TTCAGGGAATCGATAGCAGC	O111 O operon sequencing
AF078736:13020L20	GATATATAACAAAATCCAGC	O111 O operon sequencing
AF078736:12663L20	CCATAGCTTCTGCAACAACG	O111 O operon sequencing
AF078736:12340L20	TCTCGCGTTTTCTTTCTGAC	O111 O operon sequencing
AF078736:11960L20	ATGAATATTAATATTTTGTG	O111 O operon sequencing
AF078736:11609L20	GAAATATCAGTCGAAACCCC	O111 O operon sequencing
AF078736:11277L21	CCATAACCCCCTTCATCAATG	O111 O operon sequencing
AF078736:10907L20	AACTCCAACTGTAAGCCCGC	O111 O operon sequencing
AF078736:10558L20	ATCATCCCCGTACGTTCAAT	O111 O operon sequencing
AF078736:10218L24	AAAGGAAATGAGCTAAACTTATCG	O111 O operon sequencing
AF078736:9863L20	AGACAAAAGCTACATAAAGG	O111 O operon sequencing
AF078736:9504L20	GAGGGAAATGTGTTAGATGC	O111 O operon sequencing
AF078736:9165L20	AGTGCATTTCCGTAAATGCC	O111 O operon sequencing
AF078736:8825L23	CGGAACATCCTCCACATATTAAC	O111 O operon sequencing
AF078736:8464L25	AATCAAAATAACTCAAAACACGTTC	O111 O operon sequencing
AF078736:8110L20	GTGCCTGTAACCATATTCTC	O111 O operon sequencing
AF078736:7749L20	CTTTATTGATATCGACAAAC	O111 O operon sequencing
AF078736:7397L20	TTATAGGTCTTTCTGATGCC	O111 O operon sequencing
AF078736:7055L22	GGATTTTTTTTATAACTGCCGG	O111 O operon sequencing
AF078736:6697L20	GAATGCCTCCAACTAATCCC	O111 O operon sequencing
AF078736:6349L20	AACGCCAATCAGAGAACTCC	O111 O operon sequencing
AF078736:6001L20	TACCACCATGACTTTCTACG	O111 O operon sequencing
AF078736:5647L20	CAGGACCAGCTGCACCATTC	O111 O operon sequencing
AF078736:5296L20	TTACGCCTGCATCACATAGC	O111 O operon sequencing
AF078736:4961L21	CTATATTTTGCTCCCTGAGGG	O111 O operon sequencing
AF078736:4597L20	CGCAACCAGACTTGACTCAG	O111 O operon sequencing
AF078736:4253L21	AAAAACATTCCGCTATTCCAG	O111 O operon sequencing
AF078736:3908L20	CAGTATTACGGCCTTTCGGC	O111 O operon sequencing
AF078736:3543L20	GTTAGCCAAAGGTATTCACG	O111 O operon sequencing
AF078736:3201L20	GGAACTAACTTGATAATTTC	O111 O operon sequencing
AF078736:2835L20	TTGACCGAAACAACAACACC	O111 O operon sequencing
AF078736:2508L20	CCATTGCAGGCAAACATACC	O111 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AF078736:2160L20	GTCAAATCGCCATAGTGTAG	O111 O operon sequencing
AF078736:1783L20	TATTTCATTTTTTCTGCCAG	O111 O operon sequencing
AF078736:1445L20	TGTCTTAACGAACTTTGCGG	O111 O operon sequencing
AF078736:1104L20	TCCTTGGCACTTTTGACAAC	O111 O operon sequencing
AF078736:731L20	GCATAGTAACATCAACTGCC	O111 O operon sequencing
AF078736:401L24	AAAAAGCAGATTAAACTTGGTAGG	O111 O operon sequencing
AF078736:34L21	CAACTCAGCCCAGATATCAGC	O111 O operon sequencing
AY208937:77U20	GGCTATTTAAGCGCTACATG	O121 O operon sequencing
AY208937:402U22	ACGGTACCTACTCCAATTGATG	O121 O operon sequencing
AY208937:782U20	GATTGAGAACACCCAGCGTG	O121 O operon sequencing
AY208937:1131U20	GAAAACTGTCCGGATCTTCG	O121 O operon sequencing
AY208937:1482U20	AAAATAGAAGACGCTTTGTC	O121 O operon sequencing
AY208937:1831U20	TTAATATGTTGGTTGCCGCC	O121 O operon sequencing
AY208937:2178U21	ATTGAGAATGTCGTGCAAATG	O121 O operon sequencing
AY208937:2527U20	TGGTTTTATTGGGTCAGCTG	O121 O operon sequencing
AY208937:2877U24	TTATTTTTCATCATGTTTCGACAG	O121 O operon sequencing
AY208937:3223U22	GGCACTTCATCTTGTCATCAGC	O121 O operon sequencing
AY208937:3587U20	TGAAAGGAATAATCCTCGCC	O121 O operon sequencing
AY208937:3937U20	CCAAAACTCAAAGAGGCTGC	O121 O operon sequencing
AY208937:4267U20	CAAAGCATGTTGGAAGCATC	O121 O operon sequencing
AY208937:4643U20	GCTTATAACCGCAGTACAGG	O121 O operon sequencing
AY208937:4964U20	TCGCCATGGAGATCTAAGTG	O121 O operon sequencing
AY208937:5327U20	TCCGTTATCTCGTGATGAAC	O121 O operon sequencing
AY208937:5696U20	GGATCTGCATATAGGTTTAC	O121 O operon sequencing
AY208937:6043U20	TGCAAGTGGTGGACAAAATC	O121 O operon sequencing
AY208937:6385U25	CAATAATTTCAATCAGAGAGAATGG	O121 O operon sequencing
AY208937:6749U20	TCAGTGCTGTCGGGATTTTA	O121 O operon sequencing
AY208937:7100U20	CATTACGATGGATAGGTGGG	O121 O operon sequencing
AY208937:7449U20	CATCTTGTCGGGTATATTGG	O121 O operon sequencing
AY208937:7799U20	TACAATATGCTCAAGGGCGG	O121 O operon sequencing
AY208937:8135U23	TGGTTTCAATAGTATCATGCTGG	O121 O operon sequencing
AY208937:8504U20	TAAATTAAGTTTACAAGCAC	O121 O operon sequencing
AY208937:8853U20	AAAACTCGCATTGCTCTTCG	O121 O operon sequencing
AY208937:9189U20	TCATGATACGCTTAGGGCAG	O121 O operon sequencing
AY208937:9557U20	CCAGATTCTGTTGCTGTTGG	O121 O operon sequencing
AY208937:9880U20	GGGGAAGGGCGTTACTTATC	O121 O operon sequencing
AY208937:10247U20	GAAATGGGCAATGAGGACCG	O121 O operon sequencing
AY208937:1060920	TTTTTGCGTTTTATATAATG	O121 O operon sequencing
AY208937:10931U23	GACCAGATGGTACAGGAATATGG	O121 O operon sequencing
AY208937:11301U20	GTACTGGGGATGGCAAGATG	O121 O operon sequencing
AY208937:11662U20	CTTGGCGCTTTTCTTAGTGG	O121 O operon sequencing
AY208937:12007U20	ACGCCATATAGCTTTACGCC	O121 O operon sequencing
AY208937:12365U20	AAACCCGAGTGCCATTATTG	O121 O operon sequencing
AY208937:12698U24	TGTTTCAATCATGGTTAGAAAACC	O121 O operon sequencing
AY208937:13054U20	GGTGTGTTAGAAGTACTGAC	O121 O operon sequencing
AY208937:13417U20	TATTAGTCGGTCGTGGCTTG	O121 O operon sequencing
AY208937:13769U20	AAGGCTGCGAATTGAGAATG	O121 O operon sequencing
AY208937:14091U21	GACCTTGTCCATCTTGTCACG	O121 O operon sequencing
AY208937:14468U20	TGAGTTTATCGAAGCCGCTC	O121 O operon sequencing
AY208937:14815U20	CGTTAGCAGATGCGATTGAG	O121 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AY208937:15056L20	GCGGCTTGAATGTATTGAAG	O121 O operon sequencing
AY208937:14713L20	AACTGCCCTACCACACGCTG	O121 O operon sequencing
AY208937:14356L20	CCCCGAACCTCTGATCAGAC	O121 O operon sequencing
AY208937:14004L20	CCTCCTCTGGAAAGAAAGAG	O121 O operon sequencing
AY208937:13674L20	GAGTTTCCGGCTGGAACAAC	O121 O operon sequencing
AY208937:13317L21	GCGACCAACTGAACATACCAC	O121 O operon sequencing
AY208937:12969L22	TCCAGGTATGAACAACATCAGG	O121 O operon sequencing
AY208937:12622L20	CAGCAACTTCTCACAGCAGC	O121 O operon sequencing
AY208937:12255L20	CATATCCGCCATTTACAGGG	O121 O operon sequencing
AY208937:11901L20	GCAACTGAGAACTATCAGCG	O121 O operon sequencing
AY208937:11568L21	GGTGATCCCATGAAAGGATTC	O121 O operon sequencing
AY208937:11202L20	CAACACATGCCTGCAATGTC	O121 O operon sequencing
AY208937:10850L23	TAAATTTGATTCAAGGAAACCAG	O121 O operon sequencing
AY208937:10496L20	GATAAAAGCTGAGCTTATAC	O121 O operon sequencing
AY208937:10168L24	CCAAAAAAGTTTTTAGTGAGATCC	O121 O operon sequencing
AY208937:9792L20	AAAATAAGACAGATAGCTTG	O121 O operon sequencing
AY208937:9440L20	TTATCACCCACTACTGGTTG	O121 O operon sequencing
AY208937:9097L20	CATGTAAGTCCTCGTTAACG	O121 O operon sequencing
AY208937:8738L20	TAACGAGGTAGTCAACGAGC	O121 O operon sequencing
AY208937:8400L21	AACCCCAAGATTCTTTTCATG	O121 O operon sequencing
AY208937:8060L21	CGCTAAATCGGACAATAAAGG	O121 O operon sequencing
AY208937:7698L20	CTTCTGCATCACCAGTCCAG	O121 O operon sequencing
AY208937:7364L21	GCATCAGTGACATAATAGGCG	O121 O operon sequencing
AY208937:7005L20	CCGAAATGATGGGTGCTAAG	O121 O operon sequencing
AY208937:6634L20	CTCAGATTCTGATAATATTG	O121 O operon sequencing
AY208937:6299L24	CATTTCAGGTTTAGATCATCTTGG	O121 O operon sequencing
AY208937:5948L20	TCAMTATTACTTGAGAAGAC	O121 O operon sequencing
AY208937:5602L20	CTGATGCCGTGATCAATTGG	O121 O operon sequencing
AY208937:5257L20	GCCGCTGGGAATTACTATGC	O121 O operon sequencing
AY208937:4907L20	GCGCAGCATCATAAATGACC	O121 O operon sequencing
AY208937:4549L22	TGATGCATTGGACCATTATTTG	O121 O operon sequencing
AY208937:4192L20	TTCCCATTGCGAAGATAGAC	O121 O operon sequencing
AY208937:3833L20	AGCCTGTGCTAACCCTTCAG	O121 O operon sequencing
AY208937:3475L20	CTGTTTTTCTAATACCAGAC	O121 O operon sequencing
AY208937:3133L20	CTTGCAGCGCATTAAGGATC	O121 O operon sequencing
AY208937:2774L20	TGTATAAACTCAAACGGGCC	O121 O operon sequencing
AY208937:2427L21	GCCCTCCGATATACTGAACTG	O121 O operon sequencing
AY208937:2071L20	AGCAGCATATGCCCCATTAG	O121 O operon sequencing
AY208937:1737L23	GCCTGATGTAGGACATGATCAAC	O121 O operon sequencing
AY208937:1374L20	TTCAAATCATAAATAACACC	O121 O operon sequencing
AY208937:1018L20	ACTCATTCCATCATTAATTC	O121 O operon sequencing
AY208937:682L20	AATCTCAGCAATTTCAGGCG	O121 O operon sequencing
AY208937:319L20	TTGAGCCAGTTCATCAGAAC	O121 O operon sequencing
AY763106:80U20	AGATACTTGTTACTGGTGGC	O145 O operon sequencing
AY763106:353U20	CTGCGGCATTTATTGAAACC	O145 O operon sequencing
AY763106:667U20	TACGGCCCTTATCACTTTCC	O145 O operon sequencing
AY763106:981U20	CCGTTATGCGATTGATGCTG	O145 O operon sequencing
AY763106:1283U20	TAATCCTGAAGGTGTAGCTG	O145 O operon sequencing
AY763106:1580U20	GGAATATTGCGCAAAGCATC	O145 O operon sequencing
AY763106:1884U20	GCACTCAACAAGCTCAACGC	O145 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AY763106:2156U24	GGGTACTCGTCTTTATCCTGTAAC	O145 O operon sequencing
AY763106:2476U21	CGAAGTTAATGGATGTCGCTG	O145 O operon sequencing
AY763106:2781U20	TATGCATGGCTGGACACGGG	O145 O operon sequencing
AY763106:3063U20	TGAGCGTGGTTTCTTTATGG	O145 O operon sequencing
AY763106:3366U22	GGTGTTAAGCGAGATAGCAGAG	O145 O operon sequencing
AY763106:3689U20	TGTTGGTGAAGTACTAGCAC	O145 O operon sequencing
AY763106:3969U20	AACAATAGGCCATTGGCTGT	O145 O operon sequencing
AY763106:4293U20	TCTGTACGCGACGGCAGAGA	O145 O operon sequencing
AY763106:4586U24	GGGGATATACAATTTTATGTTTGG	O145 O operon sequencing
AY763106:4888U23	TGTGATGGTTTTAGGTTTATGGA	O145 O operon sequencing
AY763106:5195U20	CTGCTTTACATGTTGTGTCC	O145 O operon sequencing
AY763106:5487U20	ACACTAGGACGTTACATGCA	O145 O operon sequencing
AY763106:5798U20	TCATATTTACTGTTATTCAC	O145 O operon sequencing
AY763106:6100U20	GAATTTGGGATATTTTGGCG	O145 O operon sequencing
AY763106:6371U20	TTAACGTGGGGAAGCAGGTT	O145 O operon sequencing
AY763106:6700U20	GTAAAAGGTGAAAATATGTT	O145 O operon sequencing
AY763106:6996U20	GGAGGCGGTTAAGACAAATG	O145 O operon sequencing
AY763106:7302U20	TCGTTTCATGATGACGCTTG	O145 O operon sequencing
AY763106:7604U20	ATGGTGACCGTCGTATCTCG	O145 O operon sequencing
AY763106:7877U21	GGACTTAAGCAGGCAGATTTC	O145 O operon sequencing
AY763106:8204U20	CGCATTGCAAATGATGAAGC	O145 O operon sequencing
AY763106:8485U21	GTTTGCGTATACGGTTCCTTC	O145 O operon sequencing
AY763106:8782U21	GCTAGTTGTTATGCTTTGGGC	O145 O operon sequencing
AY763106:9110U20	AGGAAAAACCAGAAGCCATG	O145 O operon sequencing
AY763106:9410U20	CCGATGTACTTTCTCGCCTG	O145 O operon sequencing
AY763106:9698U22	GCGGGACTATTACAGAGGAGTC	O145 O operon sequencing
AY763106:10011U20	TATTTGCCCCATAGCACACG	O145 O operon sequencing
AY763106:10311U20	TTTTGGGGAGGCTTGGTTAA	O145 O operon sequencing
AY763106:10589U24	CGGCGATGATTATCATTCACTTCG	O145 O operon sequencing
AY763106:10896U20	TCTTCACATAATTTCCCCGG	O145 O operon sequencing
AY763106:11214U20	AACTTTTTCGCACTGCAGCA	O145 O operon sequencing
AY763106:11508U20	TGTCACCAAAAGCCCTTATG	O145 O operon sequencing
AY763106:11630L22	GCTAAGATGGTAACCCAGCATG	O145 O operon sequencing
AY763106:11266L20	TCTCCTGATGAGATGCGTGC	O145 O operon sequencing
AY763106:10934L20	GGATCGGGATTGATTGAACC	O145 O operon sequencing
AY763106:10557L20	GTCATTGAGGCCCAATTACG	O145 O operon sequencing
AY763106:10224L22	GCCATGCACGAAAAGATAAAAG	O145 O operon sequencing
AY763106:9855L20	AGCGTACTTCTCCACGAGGC	O145 O operon sequencing
AY763106:9511L24	AGCCACGGTATTAAGTATATTTGC	O145 O operon sequencing
AY763106:9163L20	CGACGCTTTGCTGGTATTGC	O145 O operon sequencing
AY763106:8819L24	CGCTATAGTATCTGGTTCAGAACG	O145 O operon sequencing
AY763106:8477L22	CCGTATACGCAAACTGTTTAGG	O145 O operon sequencing
AY763106:8102L20	TTAGCGTTTGTCGTTTCCCC	O145 O operon sequencing
AY763106:7770L20	ACCGATAAACCCTGCAGCGC	O145 O operon sequencing
AY763106:7396L20	AATGTTTGAATTGTTGCCGC	O145 O operon sequencing
AY763106:7052L20	CACGCGTTTAATCCCATTCG	O145 O operon sequencing
AY763106:6698L20	CATATTTTCACCTTTTACAG	O145 O operon sequencing
AY763106:6368L20	CTGCTTCCCCACGTTAAAAC	O145 O operon sequencing
AY763106:6016L20	GCTCTTGCTCATTAGAACAG	O145 O operon sequencing
AY763106:5649L22	ACGGAAAGAAATAACATTAGCG	O145 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AY763106:5312L23	GGTGCCATAAAGACAAAACAAAG	O145 O operon sequencing
AY763106:4942L20	CAATTACCAAATTACTTAGC	O145 O operon sequencing
AY763106:4608L20	ATGGACAATCCAACCGAACC	O145 O operon sequencing
AY763106:4264L20	AACAGGCGAAGCAAGAGTGC	O145 O operon sequencing
AY763106:3886L20	TCCCAAGTATACACTTAATG	O145 O operon sequencing
AY763106:3535L30	TTTTTTCAACATCAATAGTC	O145 O operon sequencing
AY763106:3183L20	AGGGTTCCAGCTGATAGTGC	O145 O operon sequencing
AY763106:2847L20	TTCAGCCCCTGACGTTCTTC	O145 O operon sequencing
AY763106:2486L20	CTTTGTTAACAGCGACATCC	O145 O operon sequencing
AY763106:2148L20	AGACGAGTACCCGAACCACC	O145 O operon sequencing
AY763106:1779L20	TACAAGCCTGCGACTTCTGG	O145 O operon sequencing
AY763106:1445L20	AATGAATAAGCCAGGCGCCG	O145 O operon sequencing
AY763106:1094L22	CCACTTTTCACATTTTCGACCC	O145 O operon sequencing
AY763106:749L20	GCGAATTTGATCCCCTTTGC	O145 O operon sequencing
AY763106:393L20	TGCGAGCGGCTTCCAAAAGG	O145 O operon sequencing
AY763106:31L20	CATGCTGTGAAATAAGCGGC	O145 O operon sequencing
AF078736:74U20	CCTGGGGACGTATTCAACTG	O145 O operon sequencing
AF078736:431U20	TTTTTTCTTGTTTCTGGTCG	O145 O operon sequencing
AF078736:776U20	TACTTTTAGAATGTGATATG	O145 O operon sequencing
AF078736:1129U20	GGAATGATTGAAGGTCTAGG	O145 O operon sequencing
AF078736:1462U25	ACAACTTATCCAAGTTCTGAATTTG	O145 O operon sequencing
AF078736:1832U20	AAATGGGGCTTGCTGGAAGG	O145 O operon sequencing
AF078736:2181U20	GATACTTCCAATCTGACCCG	O145 O operon sequencing
AF078736:2537U20	TAACCACGAATCACCTCGCC	O145 O operon sequencing
AF078736:2867U20	TAAAGCTGTAAACCCGGGCG	O145 O operon sequencing
AF078736:3239U20	GCTAATTGAAAACGAGAATG	O145 O operon sequencing
AF078736:3556U25	GGCTAACTAAACACCAAATAAATGC	O145 O operon sequencing
AF078736:3930U20	CCTGCCATAGCTTTAGCTGC	O145 O operon sequencing
AF078736:4277U20	TCGCGCCAGTAAATATCTTG	O145 O operon sequencing
AF078736:4641U20	ATTGTCCAAACCAAGGATGC	O145 O operon sequencing
AF078736:4991U20	TCCAGGCGTAATACCTTTGC	O145 O operon sequencing
AF078736:5331U20	GAATGTGTGGTACTGAAGAG	O145 O operon sequencing
AF078736:5667U23	TTATTGATGCTATTGAGGAATGC	O145 O operon sequencing
AF078736:6040U20	CGGTCATGCTTACATTAAGC	O145 O operon sequencing
AF078736:6390U20	CAGAACCTGTAGTACGATTG	O145 O operon sequencing
AF078736:6730U20	CAGGCCGTTTGATTTTCTGG	O145 O operon sequencing
AF078736:7099U20	CCCAGAGATCGAAATTTGGG	O145 O operon sequencing
AF078736:7450U20	TACCCACTTGCTAGTAATAC	O145 O operon sequencing
AF078736:7801U20	AATGCTATTTCAGATAAAAC	O145 O operon sequencing
AF078736:8135U23	GTGATGATATTTTCGAAGAGTCG	O145 O operon sequencing
AF078736:8499U20	TGATACGGTAGCAAATGCCG	O145 O operon sequencing
AF078736:8838U20	GGATGTTCCGCATGGATTGC	O145 O operon sequencing
AF078736:9200U20	TTTAGCCTTTACCATTAAAG	O145 O operon sequencing
AF078736:9555U20	CTAATTTCTGTTTTGCCTTG	O145 O operon sequencing
AF078736:9904U20	TCTATTGATTTACTTTTTTC	O145 O operon sequencing
AF078736:10259U20	TGTTTTACTTGTTTAGATTG	O145 O operon sequencing
AF078736:10584U20	TTTGGTTTCACAGCTTGGTG	O145 O operon sequencing
AF078736:10961U20	TGTAATGGAAATTTAGACGC	O145 O operon sequencing
AF078736:11299U20	ATCTAATGGCGCCCCTGTGG	O145 O operon sequencing
AF078736:11646U23	CGCTAGAAAGTTTCATTGTACGC	O145 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
AF078736:11990U20	TGGATAAAAATTTTAGAAGC	O145 O operon sequencing
AF078736:12343U20	AGAAAGAAAACGCGAGATGC	O145 O operon sequencing
AF078736:12702U20	TGCTACCGATTCTGGTGGAG	O145 O operon sequencing
AF078736:13066U20	AGACTACATTCAAGCCGCGC	O145 O operon sequencing
AF078736:13413U20	TTATTGATGGTGGCAACACC	O145 O operon sequencing
AF078736:13767U20	TGGCAACCACTTTTACCGAG	O145 O operon sequencing
AF078736:14119U20	TTATGCCCAAGGCTTCTCTC	O145 O operon sequencing
AF078736:14468U20	GGTGCGCACACGTATAAACG	O145 O operon sequencing
AF078736:14425L20	TCAGATTAGCCGGCAGTACC	O145 O operon sequencing
AF078736:14074L20	CGCGACGGACTTTCTCAACG	O145 O operon sequencing
AF078736:13730L20	TTAAGGCCGCCTTTAAGCAG	O145 O operon sequencing
AF078736:13367L20	TTCAGGGAATCGATAGCAGC	O145 O operon sequencing
AF078736:13020L20	GATATATAACAAAATCCAGC	O145 O operon sequencing
AF078736:12663L20	CCATAGCTTCTGCAACAACG	O145 O operon sequencing
AF078736:12340L20	TCTCGCGTTTTCTTTCTGAC	O145 O operon sequencing
AF078736:11960L20	ATGAATATTAATATTTTGTG	O145 O operon sequencing
AF078736:11609L20	GAAATATCAGTCGAAACCCC	O145 O operon sequencing
AF078736:11277L21	CCATAACCCCCTTCATCAATG	O145 O operon sequencing
AF078736:10907L20	AACTCCAACTGTAAGCCCGC	O145 O operon sequencing
AF078736:10558L20	ATCATCCCCGTACGTTCAAT	O145 O operon sequencing
AF078736:10218L24	AAAGGAAATGAGCTAAACTTATCG	O145 O operon sequencing
AF078736:9863L20	AGACAAAAGCTACATAAAGG	O145 O operon sequencing
AF078736:9504L20	GAGGGAAATGTGTTAGATGC	O145 O operon sequencing
AF078736:9165L20	AGTGCATTTCCGTAAATGCC	O145 O operon sequencing
AF078736:8825L23	CGGAACATCCTCCACATATTAAC	O145 O operon sequencing
AF078736:8464L25	AATCAAAATAACTCAAAACACGTTC	O145 O operon sequencing
AF078736:8110L20	GTGCCTGTAACCATATTCTC	O145 O operon sequencing
AF078736:7749L20	CTTTATTGATATCGACAAAC	O145 O operon sequencing
AF078736:7397L20	TTATAGGTCTTTCTGATGCC	O145 O operon sequencing
AF078736:7055L22	GGATTTTTTTTATAACTGCCGG	O145 O operon sequencing
AF078736:6697L20	GAATGCCTCCAACTAATCCC	O145 O operon sequencing
AF078736:6349L20	AACGCCAATCAGAGAACTCC	O145 O operon sequencing
AF078736:6001L20	TACCACCATGACTTTCTACG	O145 O operon sequencing
AF078736:5647L20	CAGGACCAGCTGCACCATTC	O145 O operon sequencing
AF078736:5296L20	TTACGCCTGCATCACATAGC	O145 O operon sequencing
AF078736:4961L21	CTATATTTTGCTCCCTGAGGG	O145 O operon sequencing
AF078736:4597L20	CGCAACCAGACTTGACTCAG	O145 O operon sequencing
AF078736:4253L21	AAAAACATTCCGCTATTCCAG	O145 O operon sequencing
AF078736:3908L20	CAGTATTACGGCCTTTCGGC	O145 O operon sequencing
AF078736:3543L20	GTTAGCCAAAGGTATTCACG	O145 O operon sequencing
AF078736:3201L20	GGAACTAACTTGATAATTTC	O145 O operon sequencing
AF078736:2835L20	TTGACCGAAACAACAACACC	O145 O operon sequencing
AF078736:2508L20	CCATTGCAGGCAAACATACC	O145 O operon sequencing
AF078736:2160L20	GTCAAATCGCCATAGTGTAG	O145 O operon sequencing
AF078736:1783L20	TATTTCATTTTTTCTGCCAG	O145 O operon sequencing
AF078736:1445L20	TGTCTTAACGAACTTTGCGG	O145 O operon sequencing
AF078736:1104L20	TCCTTGGCACTTTTGACAAC	O145 O operon sequencing
AF078736:731L20	GCATAGTAACATCAACTGCC	O145 O operon sequencing
AF078736:401L24	AAAAAGCAGATTAAACTTGGTAGG	O145 O operon sequencing
AF078736:34L21	CAACTCAGCCCAGATATCAGC	O145 O operon sequencing

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
O26_rmlA_30_2F	ACGTTGGATGCAGGATAAAGACGAGTACCC	O26 O operon MALDI
O26_rmlA_30_2P	CGAGTACCCGAACCACC	O26 O operon MALDI
O26_rmlA_30_2R	ACGTTGGATGGTGATGGTGGAGCAAGATG	O26 O operon MALDI
O26_wzx_953_2F	ACGTTGGATGTAAAGGGATGAACGCGCTTC	O26 O operon MALDI
O26_wzx_953_2P	GAGCCTTATATCCCAATATAGTACCC	O26 O operon MALDI
O26_wzx_953_2R	ACGTTGGATGCATGGTTTTCATTGTCCTGAG	O26 O operon MALDI
O26_fnl1_88_2F	ACGTTGGATGTCATCCCTGCTAAATATTCG	O26 O operon MALDI
O26_fnl1_88_2P	CCTGCTAAATATTCGTATTTCAG	O26 O operon MALDI
O26_fnl1_88_2R	ACGTTGGATGTGGTGGCACTGGTTCTTTTG	O26 O operon MALDI
O45_rmlB_966F	ACGTTGGATGCGTATGTTACTGATCGTCCG	O45 O operon MALDI
O45_rmlB_966P	CTCGTCCGGGCCATGACCGTCG	O45 O operon MALDI
O45_rmlB_966R	ACGTTGGATGGGTAAATCTAAGCTTGTTGC	O45 O operon MALDI
O45_wbhQ_721F	ACGTTGGATGAAAACACCCAGCAGACAGAG	O45 O operon MALDI
O45_wbhQ_721P	GCAGCAGACAGAGTTCTGCGA	O45 O operon MALDI
O45_wbhQ_721R	ACGTTGGATGCTTTTGATCGCTAATGCGATG	O45 O operon MALDI
O45_wbhU_241_2F	ACGTTGGATGCAACGAGTTTGTCGCTAAAG	O45 O operon MALDI
O45_wbhU_241_2P	ACCAACATTGCGGGAAA	O45 O operon MALDI
O45_wbhU_241_2R	ACGTTGGATGGGAATCAGATAAATTCTGGC	O45 O operon MALDI
O45_wbhU_543_2F	ACGTTGGATGTCTTGTTCGTGATGGTGGAG	O45 O operon MALDI
O45_wbhU_543_2P	TGATAGAACGTCTCATCAAA	O45 O operon MALDI
O45_wbhU_543_2R	ACGTTGGATGCGGTATTATCCTGACACGAG	O45 O operon MALDI
O45_wzy_752F	ACGTTGGATGCCTGGAAGCTTGTGAAATCG	O45 O operon MALDI
O45_wzy_752P	ACCGGAACTATGTGC	O45 O operon MALDI
O45_wzy_752R	ACGTTGGATGTTCTGGTCGCATTTGGTAAG	O45 O operon MALDI
O45_wzy_906F	ACGTTGGATGTACCATGGAGCTAGTAGACG	O45 O operon MALDI
O45_wzy_906P	GCGACAATGTTTGAAAAGCTAATGCC	O45 O operon MALDI
O45_wzy_906R	ACGTTGGATGAAACGTGAATATAAAGAAAG	O45 O operon MALDI
O45_wbhW_21F	ACGTTGGATGGGCCGTTGTGAAGAAGAGTA	O45 O operon MALDI
O45_wbhW_21P	GAAATGAAAGTGTTGTTTTTATG	O45 O operon MALDI
O45_wbhW_21R	ACGTTGGATGCAAATGGAGGTATCAAAAAGC	O45 O operon MALDI
O45_wbhW_997F	ACGTTGGATGGCCTTTCATTTTACCACCTC	O45 O operon MALDI
O45_wbhW_997P	TTAGATATCTTTATTTAAACAACATCTT	O45 O operon MALDI
O45_wbhW_997R	ACGTTGGATGCAAGCTCCTCATCTTCACAG	O45 O operon MALDI
O45_inter_325F	ACGTTGGATGATTTACCACTGGAACACGCC	O45 O operon MALDI
O45_inter_325P	GAAGTTGGTCTAATCCTGA	O45 O operon MALDI
O45_inter_325R	ACGTTGGATGTTCTGGGTATCACCATTGGG	O45 O operon MALDI
O45_inter_366_2F	ACGTTGGATGGGAATCAGATAAATTCTGGC	O45 O operon MALDI
O45_inter_366_2P	AGAAATATGCACAAGTGATTTTT	O45 O operon MALDI
O45_inter_366_2R	ACGTTGGATGAAAACGTATCCTTCAGGCTC	O45 O operon MALDI
O45_inter_560F	ACGTTGGATGTAGTGCAATCCCAATACGCC	O45 O operon MALDI
O45_inter_560P	CATATTTTGCTTTGTGATAATTAC	O45 O operon MALDI
O45_inter_560R	ACGTTGGATGTTCATATTTAGCTAACAAG	O45 O operon MALDI
O103_wbtD_937F	ACGTTGGATGAAAAAATCAATAACAATAAG	O103 O operon MALDI
O103_wbtD_937P	TCAATAACAATAAGAATATTAACCTG	O103 O operon MALDI
O103_wbtD_937R	ACGTTGGATGTCATCCCTGCTAAATATTCG	O103 O operon MALDI
O111_inter_219_2F	ACGTTGGATGCCAAAGATGTGAGCAGTTCC	O111 O operon MALDI
O111_inter_219_2P	TAGCAGTTCCGCGAGATCC	O111 O operon MALDI
O111_inter_219_2R	ACGTTGGATGTTCTGGTCGCATTTGGTAAG	O111 O operon MALDI
O111_wbdH_1006_2F	ACGTTGGATGTAATGTACCTGGGTGTAGGG	O111 O operon MALDI
O111_wbdH_1006_2P	TGTAGGGATATAATAAATGATGGG	O111 O operon MALDI

Supplemental Table 2. Primers and probes used for sequencing and genotyping

Primer name	Primer Sequence (5' - 3')	Application
O111_wbdH_1006_2F	ACGTTGGATGCAAATGGAGGTATCAAAAAGC	O111 O operon MALDI
O111_wbdK_687_2F	ACGTTGGATGGTATTGTTGTGCCTTCGAGC	O111 O operon MALDI
O111_wbdK_687_2P	AAAAGAGAATATGGTTACAGG	O111 O operon MALDI
O111_wbdK_687_2R	ACGTTGGATGCGACTCTTCGAAAATATCATC	O111 O operon MALDI
O111_wzx_1128_2F	ACGTTGGATGAAAGGCCATAATGAGCTGCG	O111 O operon MALDI
O111_wzx_1128_2P	TTAACGTTGAAGCAGCAAG	O111 O operon MALDI
O111_wzx_1128_2R	ACGTTGGATGGGTAAATCTAAGCTTGTTGC	O111 O operon MALDI
O121_vioA_313_2F	ACGTTGGATGCTCCTTGGTCTTAAATGGGC	O121 O operon MALDI
O121_vioA_313_2P	CCTGTTTTTGTCGATATTGAT	O121 O operon MALDI
O121_vioA_313_2R	ACGTTGGATGGCCTCTTCAATTCTTCTCGG	O121 O operon MALDI
O121_wbqE_437F	ACGTTGGATGAATGGGTATCAGCAGAGTGG	O121 O operon MALDI
O121_wbqE_437P	GCAGAGTGGAACTAATTTTG	O121 O operon MALDI
O121_wbqE_437R	ACGTTGGATGTTTCAAAGGTCTCCTGTGGC	O121 O operon MALDI
O121_wbqI_582F	ACGTTGGATGAGTAGCCTGGAGGCCATTAC	O121 O operon MALDI
O121_wbqI_582P	GAGGCCATTACTACAGT	O121 O operon MALDI
O121_wbqI_582R	ACGTTGGATGGAGCTGTTTTTACCGACAGA	O121 O operon MALDI
O145_wzy_37F	ACGTTGGATGGTCAACACCAGAAAAAATAGC	O145 O operon MALDI
O145_wzy_37P	AACGAAGAAATAATTAACCAAAAAAAAA	O145 O operon MALDI
O145_wzy_37R	ACGTTGGATGCACCAGTTTGGTTTGAGAAA	O145 O operon MALDI

Supplemental Table 3. Nucleotide polymorphism allele frequecies of O-antigen operon from serogroups.

Serotype	Sequence Name	Reference sequence position	Gene sequence position	Change	Codon Change	A.A. Change	gene	Polymorphism Type	product	Reference Frequency	Reference Nucleotide(s)	Variant Frequency	Variant Nucleotide(s)
O26													
	AY763106	237	162	T -> C	TTT -> TTC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	273	198	G -> A	GCG -> GCA		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	A
	AY763106	279	204	T -> C	ATT -> ATC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	318	243	T -> A	GCT -> GCA		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	A
	AY763106	333	258	T -> G	GTT -> GTG		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	G
	AY763106	336	261	C -> T	GAC -> GAT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	342	267	A -> C	TCA -> TCC		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	C
	AY763106	348	273	C -> A	ACC -> ACA		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	A
	AY763106	387	312	T -> A	ACT -> ACA		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	A
	AY763106	393	318	C -> T	GTC -> GTT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	399	324	G -> A	TTG -> TTA		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	A
	AY763106	440	365	AG -> GA	AAG -> AGA	K -> R	*rmlB*	Substitution	dTDP-glucose 4,6-dehydratase		AG	3.10%	GA
	AY763106	521	446	C -> A	ACA -> AAA	T -> K	*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	A
	AY763106	526	451	G -> A	GAA -> AAA	E -> K	*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	A
	AY763106	570	495	T -> C	AGT -> AGC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	594	519	T -> C	TCT -> TCC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	633	558	T -> A	GGT -> GGA		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	A
	AY763106	654	579	C -> T	AAC -> AAT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	657	582	T -> C	TGT -> TGC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	660	585	G -> T	TCG -> TCT		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	T
	AY763106	666	591	C -> T	AAC -> AAT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	669	594	C -> T	TAC -> TAT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	672	597	C -> T	GGC -> GGT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	681	606	C -> T	CAC -> CAT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	684	609	T -> C	TTT -> TTC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	702	627	GC -> AT	CCG,CTG -> CCA,TTG		*rmlB*	Substitution	dTDP-glucose 4,6-dehydratase		GC	3.10%	AT
	AY763106	708	633	A -> T	GTA -> GTT		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	T
	AY763106	714	639	T -> C	CTT -> CTC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	732	657	G -> A	AAG -> AAA		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	A
	AY763106	734	659	C -> G	GCA -> GGA	A -> G	*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	G
	AY763106	750	675	C -> T	GGC -> GGT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	771	696	T -> C	GAT -> GAC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	777	702	A -> G	CTA -> CTG		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	G
	AY763106	813	738	T -> C	GTT -> GTC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	816	741	C -> A	GTC -> GTA		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	A
	AY763106	852	777	C -> T	GGC -> GGT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	882	807	T -> A	GTT -> GTA		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	A
	AY763106	888	813	G -> C	CTG -> CTC		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	C
	AY763106	918	843	A -> C	GTA -> GTC		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	C
	AY763106	928	853	C -> A	CAA -> AAA	Q -> K	*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	A
	AY763106	936	861	T -> C	TAT -> TAC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	939	864	T -> C	CGT -> CGC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	948	873	T -> C	ATT -> ATC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	972	897	A -> T	GGA -> GGT		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	T
	AY763106	1009	934	A -> G	AGC -> GGC	S -> G	*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	G
	AY763106	1011	936	C -> T	AGC -> AGT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	1012	937	C -> T	CGC -> TGC	R -> C	*rmlB*	transition	dTDP-glucose 4,6-dehydratase	98.40%	C	1.60%	T
	AY763106	1023	948	C -> A	GGC -> GGA		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	A
	AY763106	1032	957	G -> A	CCG -> CCA		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	A
	AY763106	1050	975	C -> T	AGC -> AGT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	1059	984	G -> T	CGG -> CGT		*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	T
	AY763106	1062	987	G -> A	AAG -> AAA		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	A
	AY763106	1065	990	A -> G	ACA -> ACG		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	G
	AY763106	1098	1023	C -> T	GTC -> GTT		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	T
	AY763106	1101	1026	A -> T	GAA -> GAT	E -> D	*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	T
	AY763106	1125	1050	G -> A	CAG -> CAA		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	G	3.10%	A
	AY763106	1128	1053	A -> G	TCA -> TCG		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	A	3.10%	G
	AY763106	1136	1061	C -> A	GCA -> GAA	A -> E	*rmlB*	transversion	dTDP-glucose 4,6-dehydratase	96.90%	C	3.10%	A
	AY763106	1155	1080	T -> C	CGT -> CGC		*rmlB*	transition	dTDP-glucose 4,6-dehydratase	96.90%	T	3.10%	C
	AY763106	1178		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	1259		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1268		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1271		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	1406		A -> G			intergenic	transition		96.90%	A	3.10%	G

Supplemental Table 3. Nucleotide polymorphism allele frequecies of O-antigen operon from serogroups.

Serotype	Sequence Name	Reference sequence position	Gene sequence position	Change	Codon Change	A.A. Change	gene	Polymorphism Type	product	Reference Frequency	Reference Nucleotide(s)	Variant Frequency	Variant Nucleotide(s)
	AY763106	1409		AA -> GG			intergenic	Substitution			AA	3.10%	GG
	AY763106	1424		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1455		C -> G			intergenic	transversion		96.90%	C	3.10%	G
	AY763106	1460		T -> A			intergenic	transversion		96.90%	T	3.10%	A
	AY763106	1463		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1469		G -> T			intergenic	transversion		96.90%	G	3.10%	T
	AY763106	1475		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1481		C -> A			intergenic	transversion		96.90%	C	3.10%	A
	AY763106	1484		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	1487		T -> G			intergenic	transversion		96.90%	T	3.10%	G
	AY763106	1490		A -> G			intergenic	transition		96.90%	A	3.10%	G
	AY763106	1492		A -> C			intergenic	transversion		96.90%	A	3.10%	C
	AY763106	1496		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	1499		T -> A			intergenic	transversion		96.90%	T	3.10%	A
	AY763106	1502		G -> A			intergenic	transition		96.90%	G	3.10%	A
	AY763106	1510		G -> A			intergenic	transition		96.90%	G	3.10%	A
	AY763106	1515		A -> G			intergenic	transition		96.90%	A	3.10%	G
	AY763106	1532		A -> G			intergenic	transition		96.90%	A	3.10%	G
	AY763106	1562		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	1574		G -> A			intergenic	transition		96.90%	G	3.10%	A
	AY763106	1580		G -> A			intergenic	transition		96.90%	G	3.10%	A
	AY763106	1583		AT -> GC			intergenic	Substitution			AT	3.10%	GC
	AY763106	1589		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	1592		A -> G			intergenic	transition		96.90%	A	3.10%	G
	AY763106	1596		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	1598		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1616		C -> T			intergenic	transition		98.40%	C	1.60%	T
	AY763106	1631		A -> T			intergenic	transversion		96.90%	A	3.10%	T
	AY763106	1655		G -> A			intergenic	transition		96.90%	G	3.10%	A
	AY763106	1661		A -> G			intergenic	transition		96.90%	A	3.10%	G
	AY763106	1691		G -> C/A			intergenic	SNP		95.30%	G	3.1%/1.6%	C/A
	AY763106	1721		A -> T			intergenic	transversion		96.90%	A	3.10%	T
	AY763106	1724		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1727		T -> A			intergenic	transversion		96.90%	T	3.10%	A
	AY763106	1730		AC -> GT			intergenic	Substitution			AC	3.10%	GT
	AY763106	1733		G -> A			intergenic	transition		96.90%	G	3.10%	A
	AY763106	1748		A -> G			intergenic	transition		96.90%	A	3.10%	G
	AY763106	1766		C -> G			intergenic	transversion		96.90%	C	3.10%	G
	AY763106	1781		A -> G			intergenic	transition		96.90%	A	3.10%	G
	AY763106	1807		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1811		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	1826		C -> G			intergenic	transversion		96.90%	C	3.10%	G
	AY763106	1862		A -> G			intergenic	transition		96.90%	A	3.10%	G
	AY763106	1874		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	1943		G -> A			intergenic	transition		96.90%	G	3.10%	A
	AY763106	1982		A -> C			intergenic	transversion		96.90%	A	3.10%	C
	AY763106	1994		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	2003		T -> C			intergenic	transition		96.90%	T	3.10%	C
	AY763106	2030		C -> T			intergenic	transition		96.90%	C	3.10%	T
	AY763106	2099		A -> T			intergenic	transversion		96.90%	A	3.10%	T
	AY763106	2144	27	A -> G	TTA -> TTG		*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	96.90%	A	3.10%	G
	AY763106	2147	30	T -> G	GCT -> GCG		*rmlA*	transversion	glucose-1-phosphate thymidylyltransferase	43.80%	T	56.30%	G
	AY763106	2156	39	G -> T	TCG -> TCT		*rmlA*	transversion	glucose-1-phosphate thymidylyltransferase	96.90%	G	3.10%	T
	AY763106	2177	60	A -> G	GTA -> GTG		*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	96.90%	A	3.10%	G
	AY763106	2180	63	T -> G	ACT -> ACG		*rmlA*	transversion	glucose-1-phosphate thymidylyltransferase	96.90%	T	3.10%	G
	AY763106	2186	69	T -> C	GCT -> GCC		*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	96.90%	T	3.10%	C
	AY763106	2199	82	T -> C	TTG -> CTG		*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	96.90%	T	3.10%	C
	AY763106	2238	121	T -> C	TTG -> CTG		*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	96.90%	T	3.10%	C
	AY763106	2240	123	G -> T	TTG -> TTT	L -> F	*rmlA*	transversion	glucose-1-phosphate thymidylyltransferase	96.90%	G	3.10%	T
	AY763106	2262	145	C -> A	CTT -> ATT	L -> I	*rmlA*	transversion	glucose-1-phosphate thymidylyltransferase	96.90%	C	3.10%	A
	AY763106	2276	159	G -> A	CTG -> CTA		*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	96.90%	G	3.10%	A
	AY763106	2282	165	T -> A	ATT -> ATA		*rmlA*	transversion	glucose-1-phosphate thymidylyltransferase	96.90%	T	3.10%	A
	AY763106	2333	216	C -> T	AGC -> AGT		*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	96.90%	C	3.10%	T
	AY763106	2536	419	T -> C	GTT -> GCT	V -> A	*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	98.40%	T	1.60%	C
	AY763106	2651	534	T -> C	TTT -> TTC		*rmlA*	transition	glucose-1-phosphate thymidylyltransferase	96.90%	T	3.10%	C

Supplemental Table 3. Nucleotide polymorphism allele frequecies of O-antigen operon from serogroups.

Serotype	Sequence Name	Reference sequence position	Gene sequence position	Change	Codon Change	A.A. Change	gene	Polymorphism Type	product	Reference Frequency	Reference Nucleotide(s)	Variant Frequency	Variant Nucleotide(s)
	AY763106	2661	544	T -> G	TAC -> GAC	Y -> D	*rmlA*	transversion	glucose-1-phosphate thymidylyltransferase	96.90%	T	3.10%	G
	AY763106	2903	786	G -> T	GGG -> GGT		*rmlA*	transversion	glucose-1-phosphate thymidylyltransferase	96.90%	G	3.10%	T
	AY763106	3075	75	C -> T	TTC -> TTT		*rmlC*	transition	dTDP-6-deoxy-D-glucose-3,5 epimerase	96.90%	C	3.10%	T
	AY763106	3201	201	C -> T	CCC -> CCT		*rmlC*	transition	dTDP-6-deoxy-D-glucose-3,5 epimerase	96.90%	C	3.10%	T
	AY763106	3776	234	G -> A	GTG -> GTA		*wzx*	transition	putative O-antigen flippase	96.90%	G	3.10%	A
	AY763106	3829	287	G -> C	TGT -> TCT	C -> S	*wzx*	transversion	putative O-antigen flippase	81.30%	G	18.80%	C
	AY763106	4083	541	G -> A	GTG -> ATG	V -> M	*wzx*	transition	putative O-antigen flippase	98.40%	G	1.60%	A
	AY763106	4121	579	T -> A	CTT -> CTA		*wzx*	transversion	putative O-antigen flippase	96.90%	T	3.10%	A
	AY763106	4326	784	A -> G	ATT -> GTT	I -> V	*wzx*	transition	putative O-antigen flippase	98.40%	A	1.60%	G
	AY763106	4454	912	G -> A	CAG -> CAA		*wzx*	transition	putative O-antigen flippase	96.90%	G	3.10%	A
	AY763106	4495	953	T -> G	GTG -> GGG	V -> G	*wzx*	transversion	putative O-antigen flippase	84.40%	T	15.60%	G
	AY763106	4795	1253	A -> G	AAA -> AGA	K -> R	*wzx*	transition	putative O-antigen flippase	96.90%	A	3.10%	G
	AY763106	5242	372	G -> A	AGG -> AGA		*wzy*	transition	putative O-antigen polymerase	98.40%	G	1.60%	A
	AY763106	5276	406	C -> T	CTT -> TTT	L -> F	*wzy*	transition	putative O-antigen polymerase	95.30%	C	4.70%	T
	AY763106	5425	555	T -> G	TTT -> TTG	F -> L	*wzy*	transversion	putative O-antigen polymerase	90.60%	T	9.40%	G
	AY763106	6034	126	G -> A	GAG -> GAA		*wbuA*	transition	putative rhamnosyl transferase	96.90%	G	3.10%	A
	AY763106	6622	714	T -> C	AGT -> AGC		*wbuA*	transition	putative rhamnosyl transferase	96.90%	T	3.10%	C
	AY763106	6673	765	C -> T	AGC -> AGT		*wbuA*	transition	putative rhamnosyl transferase	96.90%	C	3.10%	T
	AY763106	6802	88	A -> G	ACT -> GCT	T -> A	*fnl1*	transition	Fnl1	43.80%	A	56.30%	G
	AY763106	7050	336	T -> A	ATT -> ATA		*fnl1*	transversion	Fnl1	96.90%	T	3.10%	A
	AY763106	7233	519	G -> A	TCG -> TCA		*fnl1*	transition	Fnl1	95.30%	G	4.70%	A
	AY763106	7356	642	A -> G	GAA -> GAG		*fnl1*	transition	Fnl1	96.90%	A	3.10%	G
	AY763106	8029	297	A -> T	TCA -> TCT		*fnl2*	transversion	Fnl2	96.90%	A	3.10%	T
	AY763106	8076	344	T -> C	GTT -> GCT	V -> A	*fnl2*	transition	Fnl2	85.90%	T	14.10%	C
	AY763106	8131	399	T -> C	ATT -> ATC		*fnl2*	transition	Fnl2	96.90%	T	3.10%	C
	AY763106	8194	462	T -> A	ACT -> ACA		*fnl2*	transversion	Fnl2	96.90%	T	3.10%	A
	AY763106	8371	639	A -> G	GCA -> GCG		*fnl2*	transition	Fnl2	98.40%	A	1.60%	G
	AY763106	8480	748	A -> G	AAA -> GAA	K -> E	*fnl2*	transition	Fnl2	96.90%	A	3.10%	G
	AY763106	9003	132	C -> T	TTC -> TTT		*fnl3*	transition	Fnl3	96.90%	C	3.10%	T
	AY763106	9612	741	T -> C	TTT -> TTC		*fnl3*	transition	Fnl3	96.90%	T	3.10%	C
	AY763106	9975	1104	G -> A	AAG -> AAA		*fnl3*	transition	Fnl3	96.90%	G	3.10%	A
	AY763106	10265	282	C -> T	ATC -> ATT		*wbuB*	transition	putative L-fucosamine transferase	98.40%	C	1.60%	T
	AY763106	10349	366	C -> T	TGC -> TGT		*wbuB*	transition	putative L-fucosamine transferase	98.40%	C	1.60%	T
	AY763106	10424	441	C -> T	GGC -> GGT		*wbuB*	transition	putative L-fucosamine transferase	96.90%	C	3.10%	T
	AY763106	10782	799	T -> G	TCT -> GCT	S -> A	*wbuB*	transversion	putative L-fucosamine transferase	96.90%	T	3.10%	G
	AY763106	10871	888	C -> T	GGC -> GGT		*wbuB*	transition	putative L-fucosamine transferase	96.90%	C	3.10%	T
	AY763106	10910	927	C -> T	TTC -> TTT		*wbuB*	transition	putative L-fucosamine transferase	96.90%	C	3.10%	T
	AY763106	10928	945	G -> A	GGG -> GGA		*wbuB*	transition	putative L-fucosamine transferase	96.90%	G	3.10%	A
	AY763106	11015	1032	C -> T	TTC -> TTT		*wbuB*	transition	putative L-fucosamine transferase	95.30%	C	4.70%	T
	AY763106	11122	1139	A -> C	AAG -> ACG	K -> T	*wbuB*	transversion	putative L-fucosamine transferase	96.90%	A	3.10%	C
	AY763106	11207		A -> C			intergenic	transversion		96.90%	A	3.10%	C
	AY763106	11423		C -> A			intergenic	transversion		78.10%	C	21.90%	A
	AY763106	11449		C -> T			intergenic	transition		98.40%	C	1.60%	T
	AY763106	11482		A -> T			intergenic	transversion		98.40%	A	1.60%	T
	AY763106	11645		T -> C			intergenic	transition		98.40%	T	1.60%	C
O45													
	AY771223	1024	966	C -> T	CGC -> CGT		*rmlB*	transition	dTDP-D-glucose-4,6-dehydratase	91.70%	C	8.30%	T
	AY771223	2916	721	A -> C	ATC -> CTC	I -> L	*wbhQ*	transversion	glycosyl transferase	91.70%	A	8.30%	C
	AY771223	6780	448	G -> T	GTA -> TTA	V -> L	*wbhT*	transversion	dTDP-glucose-4,6-dehydratase		G	100.00%	T
	AY771223	7777	634	C -> A	CGA -> AGA		*wzx*	transversion	O antigen flippase	91.70%	C	8.30%	A
	AY771223	7792	649	G -> A	GAT -> AAT	D -> N	*wzx*	transition	O antigen flippase	91.70%	G	8.30%	A
	AY771223	8627	241	A -> G	GTT -> ATT	L -> I	wbhU	transition	glycosyl transferase	91.70%	A	8.30%	G
	AY771223	8929	543	T -> C	GGT -> GGC		wbhU	transition	glycosyl transferase	91.70%	T	8.30%	C
	AY771223	9444	79	G -> T	GTG -> TTG	V -> L	*wzy*	transversion	O antigen polymerase		G	100.00%	T
	AY771223	10117	752	C -> T	GCG -> GTG	A -> V	*wzy*	transition	O antigen polymerase	91.70%	C	8.30%	T
	AY771223	10271	906	C -> T	CCC -> CCT		*wzy*	transition	O antigen polymerase	91.70%	C	8.30%	T
	AY771223	11065	21	T -> C	TGT -> TGC		*wbhW*	transition	unknown	91.70%	T	8.30%	C
	AY771223	11527	483	T -> C	AAT -> AAC		*wbhW*	transition	unknown	91.70%	T	8.30%	C
	AY771223	11545	501	A -> T	GCA -> GCT		*wbhW*	transversion	unknown	91.70%	A	8.30%	T
	AY771223	12041	997	G -> T			*wbhW*	transversion	unknown	91.70%	G	8.30%	T
	AY771223	13165		Deletion			intergenic	Deletion			A	8.30%	
	AY771223	13299		A -> C			intergenic	transversion		91.70%	A	8.30%	C

Supplemental Table 3. Nucleotide polymorphism allele frequecies of O-antigen operon from serogroups.

Serotype	Sequence Name	Reference sequence position	Gene sequence position	Change	Codon Change	A.A. Change	gene	Polymorphism Type	product	Reference Frequency	Reference Nucleotide(s)	Variant Frequency	Variant Nucleotide(s)
	AY771223	13343		Deletion			intergenic	Deletion			A	16.70%	
	AY771223	13534		C -> A			intergenic	transversion		91.70%	C	8.30%	A
	AY771223	13646		A -> T			intergenic	transversion			A	100.00%	T
	AY771223	13673		G -> A			intergenic	transition		91.70%	G	8.30%	A
O103													
	AY532664	145	39	T -> C	GGT -> GGC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	C
	AY532664	208	102	G -> A	TTG -> TTA		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	A
	AY532664	229	123	G -> A	GAG -> GAA		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	A
	AY532664	238	132	T -> A	GCT -> GCA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	29.20%	T	70.80%	A
	AY532664	250	144	T -> C	GAT -> GAC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	T	75.00%	C
	AY532664	254	148	G -> A	GAA -> AAA	E -> K	*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	G	70.80%	A
	AY532664	290	184	T -> G	TCT -> GCT	S -> A	*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	T	75.00%	G
	AY532664	294	188	T -> C	GTT -> GCT	V -> A	*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	T	75.00%	C
	AY532664	304	198	G -> A	GCG -> GCA		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	G	4.20%	A
	AY532664	331	225	T -> G	GAT -> GAG	D -> E	*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	G
	AY532664	364	258	G -> T	GTG -> GTT		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	G	4.20%	T
	AY532664	367	261	T -> C	GAT -> GAC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	C
	AY532664	382	276	C -> T	GGC -> GGT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	418	312	T -> A	ACT -> ACA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	A
	AY532664	436	330	G -> C	GCG -> GCC		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	C
	AY532664	464	358	G -> A	GGC -> AGC	G -> S	*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	A
	AY532664	465	359	G -> A	GGC -> GAC	G -> D	*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	G	4.20%	A
	AY532664	514	408	C -> A	GTC -> GTA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	29.20%	C	70.80%	A
	AY532664	520	414	C -> T	GGC -> GGT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	C	75.00%	T
	AY532664	524	418	C -> T	CTG -> TTG		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	C	75.00%	T
	AY532664	535	429	T -> A	CCT -> CCA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	A
	AY532664	538	432	C -> T	GAC -> GAT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	541	435	A -> G	GAA -> GAG		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	A	70.80%	G
	AY532664	552	446	CA -> AC	ACA -> AAC	T -> N	*rmlB*	Substitution	putative dTDP-glucose 4,6-dehydratase		CA	4.20%	AC
	AY532664	566	460	C -> T	CTC -> TTC	L -> F	*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	C	75.00%	T
	AY532664	568	462	C -> A	CTC -> CTA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	C	75.00%	A
	AY532664	580	474	G -> A	ACG -> ACA		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	G	70.80%	A
	AY532664	601	495	T -> C	AGT -> AGC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	T	75.00%	C
	AY532664	604	498	T -> A	CCT -> CCA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	A
	AY532664	610	504	C -> T	TCC -> TCT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	625	519	C -> T	TCC -> TCT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	C	70.80%	T
	AY532664	646	540	T -> G	GCT -> GCG		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	T	75.00%	G
	AY532664	655	549	T -> A	CGT -> CGA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	A
	AY532664	673	567	T -> C	ACT -> ACC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	T	75.00%	C
	AY532664	685	579	C -> T	AAC -> AAT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	688	582	T -> C	TGT -> TGC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	C
	AY532664	691	585	G -> T	TCG -> TCT		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	G	4.20%	T
	AY532664	694	588	T -> C	AAT -> AAC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	C
	AY532664	697	591	C -> T	AAC -> AAT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	700	594	C -> T	TAC -> TAT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	706	600	G -> T	CCG -> CCT		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	T
	AY532664	712	606	T -> C	CAT -> CAC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	T	70.80%	C
	AY532664	715	609	C -> T	TTC -> TTT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	C	70.80%	T
	AY532664	733	627	CT -> AC	CCC,TTG -> CCA,CTG		*rmlB*	Substitution	putative dTDP-glucose 4,6-dehydratase		CT	70.8% -> 75.0%	AC
	AY532664	736	630	G -> A	TTG -> TTA		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	G	70.80%	A
	AY532664	739	633	T -> A	GTT -> GTA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	29.20%	T	70.80%	A
	AY532664	745	639	C -> T	CTC -> CTT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	C	75.00%	T
	AY532664	751	645	T -> A	GCT -> GCA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	A
	AY532664	763	657	A -> G	AAA -> AAG		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	A	70.80%	G
	AY532664	765	659	G -> C	GGA -> GCA	G -> A	*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	C
	AY532664	806	700	C -> T	CTG -> TTG		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	826	720	G -> A	GCG -> GCA		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	G	70.80%	A
	AY532664	886	780	A -> G	GGA -> GGG		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	A	4.20%	G
	AY532664	907	801	C -> A	ATC -> ATA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	A
	AY532664	935	829	T -> C	TTG -> CTG		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	C
	AY532664	949	843	C -> A	GTC -> GTA		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	C	75.00%	A
	AY532664	967	861	C -> T	TAC -> TAT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	970	864	T -> C	CGT -> CGC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	T	70.80%	C
	AY532664	979	873	T -> C	ATT -> ATC		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	T	4.20%	C

Supplemental Table 3. Nucleotide polymorphism allele frequecies of O-antigen operon from serogroups.

Serotype	Sequence Name	Reference sequence position	Gene sequence position	Change	Codon Change	A.A. Change	gene	Polymorphism Type	product	Reference Frequency	Reference Nucleotide(s)	Variant Frequency	Variant Nucleotide(s)
	AY532664	997	891	C -> T	CGC -> CGT		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	C	75.00%	T
	AY532664	1021	915	G -> C	GCG -> GCC		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	C
	AY532664	1043	937	C -> T	CGC -> TGC	R -> C	*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	95.80%	C	4.20%	T
	AY532664	1090	984	G -> T	CGG -> CGT		*rmlB*	transversion	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	T
	AY532664	1093	987	G -> A	AAG -> AAA		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	25.00%	G	75.00%	A
	AY532664	1132	1026	A -> G	CGA -> CGG		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	A	70.80%	G
	AY532664	1174	1068	G -> A	GTG -> GTA		*rmlB*	transition	putative dTDP-glucose 4,6-dehydratase	29.20%	G	70.80%	A
	AY532664	1200		C -> T			intergenic	transition		29.20%	C	70.80%	T
	AY532664	1212		G -> A			intergenic	transition		29.20%	G	70.80%	A
	AY532664	1215		T -> A			intergenic	transversion		29.20%	T	70.80%	A
	AY532664	1296		G -> A			intergenic	transition		95.80%	G	4.20%	A
	AY532664	1356		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	1488		T -> C			intergenic	transition		25.00%	T	75.00%	C
	AY532664	1515		T -> C			intergenic	transition		95.80%	T	4.20%	C
	AY532664	1617		G -> A			intergenic	transition		95.80%	G	4.20%	A
	AY532664	1629		A -> G			intergenic	transition		29.20%	A	70.80%	G
	AY532664	1899		T -> C			intergenic	transition		95.80%	T	4.20%	C
	AY532664	2037		T -> C			intergenic	transition		95.80%	T	4.20%	C
	AY532664	2071	27	C -> G	CAC -> CAG	H -> Q	*wbtA*	transversion	putative dTDP-6-deoxy-3,4-keto-hexulose isomerase	95.80%	C	4.20%	G
	AY532664	2110	66	T -> G	GTT -> GTG		*wbtA*	transversion	putative dTDP-6-deoxy-3,4-keto-hexulose isomerase	95.80%	T	4.20%	G
	AY532664	2375	331	T -> C	TTG -> CTG		*wbtA*	transition	putative dTDP-6-deoxy-3,4-keto-hexulose isomerase	29.20%	T	70.80%	C
	AY532664	2432	388	C -> A	CGG -> AGG		*wbtA*	transversion	putative dTDP-6-deoxy-3,4-keto-hexulose isomerase	29.20%	C	70.80%	A
	AY532664	2440	396	G -> A	ATG -> ATA	M -> I	*wbtA*	transition	putative dTDP-6-deoxy-3,4-keto-hexulose isomerase	25.00%	G	75.00%	A
	AY532664	2500		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	2510		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	2529		G -> A			intergenic	transition		25.00%	G	75.00%	A
	AY532664	2678		C -> T			intergenic	transition		95.80%	C	4.20%	T
	AY532664	2738		A -> T			intergenic	transversion		95.80%	A	4.20%	T
	AY532664	2858		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	2957		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	2977	3	G -> A	TTG -> TTA		*wbtC*	transition	putative aminotransferase	95.80%	G	4.20%	A
	AY532664	2990	16	A -> G	ATG -> GTG	M -> V	*wbtC*	transition	putative aminotransferase	91.70%	A	8.30%	G
	AY532664	3035	61	A -> G	ATG -> GTG	M -> V	*wbtC*	transition	putative aminotransferase	29.20%	A	70.80%	G
	AY532664	3085	111	T -> A	ATT -> ATA		*wbtC*	transversion	putative aminotransferase	95.80%	T	4.20%	A
	AY532664	3092	118	A -> G	ACG -> GCG	T -> A	*wbtC*	transition	putative aminotransferase	95.80%	A	4.20%	G
	AY532664	3266	292	G -> A	GTT -> ATT	V -> I	*wbtC*	transition	putative aminotransferase	95.80%	G	4.20%	A
	AY532664	3409	435	A -> C	ATA -> ATC		*wbtC*	transversion	putative aminotransferase	95.80%	A	4.20%	C
	AY532664	3475	501	T -> A	GCT -> GCA		*wbtC*	transversion	putative aminotransferase	95.80%	T	4.20%	A
	AY532664	3496	522	T -> C	ATT -> ATC		*wbtC*	transition	putative aminotransferase	25.00%	T	75.00%	C
	AY532664	3532	558	T -> A	GCT -> GCA		*wbtC*	transversion	putative aminotransferase	95.80%	T	4.20%	A
	AY532664	3552	578	G -> T	GGA -> GTA	G -> V	*wbtC*	transversion	putative aminotransferase	95.80%	G	4.20%	T
	AY532664	3580	606	A -> T	GCA -> GCT		*wbtC*	transversion	putative aminotransferase	95.80%	A	4.20%	T
	AY532664	3643	669	T -> A	GGT -> GGA		*wbtC*	transversion	putative aminotransferase	95.80%	T	4.20%	A
	AY532664	3694	720	T -> C	GAT -> GAC		*wbtC*	transition	putative aminotransferase	95.80%	T	4.20%	C
	AY532664	3934	960	A -> G	CCA -> CCG		*wbtC*	transition	putative aminotransferase	95.80%	A	4.20%	G
	AY532664	3971	997	A -> G	AGT -> GGT	S -> G	*wbtC*	transition	putative aminotransferase	95.80%	A	4.20%	G
	AY532664	4269		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	4313		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	4464		C -> T			intergenic	transition		95.80%	C	4.20%	T
	AY532664	4557		C -> T			intergenic	transition		25.00%	C	75.00%	T
	AY532664	4734		C -> T			intergenic	transition		29.20%	C	70.80%	T
	AY532664	4820		C -> T			intergenic	transition		95.80%	C	4.20%	T
	AY532664	4840		G -> T			intergenic	transversion		95.80%	G	4.20%	T
	AY532664	4975		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	5030		G -> C			intergenic	transversion		95.80%	G	4.20%	C
	AY532664	5193		G -> A			intergenic	transition		95.80%	G	4.20%	A
	AY532664	5196		T -> G			intergenic	transversion		29.20%	T	70.80%	G
	AY532664	5420	68	A -> G	AAT -> AGT	N -> S	*wbtD*	transition	putative glycosyltransferase	95.80%	A	4.20%	G
	AY532664	5598	246	T -> A	AAT -> AAA	N -> K	*wbtD*	transversion	putative glycosyltransferase	95.80%	T	4.20%	A
	AY532664	5880	528	T -> C	TAT -> TAC		*wbtD*	transition	putative glycosyltransferase	95.80%	T	4.20%	C
	AY532664	5884	532	A -> G	ATT -> GTT	I -> V	*wbtD*	transition	putative glycosyltransferase	95.80%	A	4.20%	G
	AY532664	5937	585	T -> C	GTT -> GTC		*wbtD*	transition	putative glycosyltransferase	95.80%	T	4.20%	C
	AY532664	5974	622	T -> C	TAT -> CAT	Y -> H	*wbtD*	transition	putative glycosyltransferase	95.80%	T	4.20%	C
	AY532664	6147	795	A -> T	GTA -> GTT		*wbtD*	transversion	putative glycosyltransferase	95.80%	A	4.20%	T
	AY532664	6175	823	T -> C	TAT -> CAT	Y -> H	*wbtD*	transition	putative glycosyltransferase	95.80%	T	4.20%	C

Supplemental Table 3. Nucleotide polymorphism allele frequecies of O-antigen operon from serogroups.

Serotype	Sequence Name	Reference sequence position	Gene sequence position	Change	Codon Change	A.A. Change	gene	Polymorphism Type	product	Reference Frequency	Reference Nucleotide(s)	Variant Frequency	Variant Nucleotide(s)
	AY532664	6215	863	G -> A	GGT -> GAT	G -> D	*wbtD*	transition	putative glycosyltransferase	95.80%	G	4.20%	A
	AY532664	6253	901	AT -> GC	ATA -> GCA	I -> A	*wbtD*	Substitution	putative glycosyltransferase		AT	4.20%	GC
	AY532664	6289	937	C -> T	CAT -> TAT	H -> Y	*wbtD*	transition	putative glycosyltransferase	33.30%	C	66.70%	T
	AY532664	6292	940	A -> G	ATT -> GTT	I -> V	*wbtD*	transition	putative glycosyltransferase	95.80%	A	4.20%	G
	AY532664	6327	975	A -> G	AAA -> AAG		*wbtD*	transition	putative glycosyltransferase	95.80%	A	4.20%	G
	AY532664	6347	6	A -> G	AAA -> AAG		*wbtE*	transition	putative glycosyltransferase	95.80%	A	4.20%	G
	AY532664	6458	117	A -> G	GTA -> GTG		*wbtE*	transition	putative glycosyltransferase	95.80%	A	4.20%	G
	AY532664	6556	215	G -> A	AGC -> AAC	S -> N	*wbtE*	transition	putative glycosyltransferase	95.80%	G	4.20%	A
	AY532664	6606	265	A -> G	ATT -> GTT	I -> V	*wbtE*	transition	putative glycosyltransferase	95.80%	A	4.20%	G
	AY532664	6665	324	C -> A	ATC -> ATA		*wbtE*	transversion	putative glycosyltransferase	95.80%	C	4.20%	A
	AY532664	6957	616	A -> G	AAT -> GAT	N -> D	*wbtE*	transition	putative glycosyltransferase	95.80%	A	4.20%	G
	AY532664	6968	627	G -> A	ACG -> ACA		*wbtE*	transition	putative glycosyltransferase	95.80%	G	4.20%	A
	AY532664	7082	741	T -> C	TAT -> TAC		*wbtE*	transition	putative glycosyltransferase	29.20%	T	70.80%	C
	AY532664	7109	768	G -> A	TTG -> TTA		*wbtE*	transition	putative glycosyltransferase	95.80%	G	4.20%	A
	AY532664	7160	819	A -> T	CGA -> CGT		*wbtE*	transversion	putative glycosyltransferase	95.80%	A	4.20%	T
	AY532664	7166	825	C -> T	TAC -> TAT		*wbtE*	transition	putative glycosyltransferase	25.00%	C	75.00%	T
	AY532664	7294		T -> C			intergenic	transition		95.80%	T	4.20%	C
	AY532664	7300		A -> G			intergenic	transition		25.00%	A	75.00%	G
	AY532664	7374		T -> A			intergenic	transversion		29.20%	T	70.80%	A
	AY532664	7418		T -> G			intergenic	transversion		91.70%	T	8.30%	G
	AY532664	7428		C -> T			intergenic	transition		95.80%	C	4.20%	T
	AY532664	7435		A -> G			intergenic	transition		25.00%	A	75.00%	G
	AY532664	7481		G -> A			intergenic	transition		95.80%	G	4.20%	A
	AY532664	7492		C -> T			intergenic	transition		95.80%	C	4.20%	T
	AY532664	7578		T -> G			intergenic	transversion		95.80%	T	4.20%	G
	AY532664	7591		A -> T			intergenic	transversion		95.80%	A	4.20%	T
	AY532664	7701		T -> C			intergenic	transition		29.20%	T	70.80%	C
	AY532664	7719		C -> T			intergenic	transition		95.80%	C	4.20%	T
	AY532664	7795		T -> C			intergenic	transition		95.80%	T	4.20%	C
	AY532664	7882		G -> A			intergenic	transition		95.80%	G	4.20%	A
	AY532664	7922		T -> A			intergenic	transversion		25.00%	T	75.00%	A
	AY532664	7944		G -> T			intergenic	transversion		95.80%	G	4.20%	T
	AY532664	8065		T -> C			intergenic	transition		95.80%	T	4.20%	C
	AY532664	8078		T -> A			intergenic	transversion		29.20%	T	70.80%	A
	AY532664	8116		C -> T			intergenic	transition		29.20%	C	70.80%	T
	AY532664	8224		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	8256		A -> G			intergenic	transition		79.20%	A	20.80%	G
	AY532664	8312		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	8358		G -> T			intergenic	transversion		95.80%	G	4.20%	T
	AY532664	8370		G -> A			intergenic	transition		29.20%	G	70.80%	A
	AY532664	8607	225	G -> A	GTG -> GTA		*wbtF*	transition	putative glycosyltransferase	95.80%	G	4.20%	A
	AY532664	8621	239	A -> C	TAT -> TCT	Y -> S	*wbtF*	transversion	putative glycosyltransferase	95.80%	A	4.20%	C
	AY532664	8792	410	CT -> TG	GCT -> GTG	A -> V	*wbtF*	Substitution	putative glycosyltransferase		CT	4.20%	TG
	AY532664	8871	489	T -> C	GTT -> GTC		*wbtF*	transition	putative glycosyltransferase	95.80%	T	4.20%	C
	AY532664	8892	510	T -> A	GAT -> GAA	D -> E	*wbtF*	transversion	putative glycosyltransferase	95.80%	T	4.20%	A
	AY532664	8937	555	T -> C	AGT -> AGC		*wbtF*	transition	putative glycosyltransferase	95.80%	T	4.20%	C
	AY532664	9222	840	A -> T	GTA -> GTT		*wbtF*	transversion	putative glycosyltransferase	95.80%	A	4.20%	T
	AY532664	9368	986	A -> T	CAC -> CTC	H -> L	*wbtF*	transversion	putative glycosyltransferase	95.80%	A	4.20%	T
	AY532664	9494		Deletion			intergenic	Deletion			A	4.20%	
	AY532664	9528		G -> A			intergenic	transition		25.00%	G	75.00%	A
	AY532664	9540		T -> G			intergenic	transversion		95.80%	T	4.20%	G
	AY532664	9545		T -> C			intergenic	transition		29.20%	T	70.80%	C
	AY532664	9580		G -> A			intergenic	transition		95.80%	G	4.20%	A
	AY532664	9613		T -> C			intergenic	transition		8.30%	T	91.70%	C
	AY532664	9634		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AY532664	9645		G -> A			intergenic	transition		95.80%	G	4.20%	A
	AY532664	9882	223	T -> C	TTG -> CTG		*wbtG*	transition	putative galactosyltransferase	25.00%	T	75.00%	C
	AY532664	9944	285	C -> T	GTC -> GTT		*wbtG*	transition	putative galactosyltransferase	29.20%	C	70.80%	T
	AY532664	9951	292	G -> A	GGT -> AGT	G -> S	*wbtG*	transition	putative galactosyltransferase	95.80%	G	4.20%	A
	AY532664	10094	435	G -> A	ATG -> ATA	M -> I	*wbtG*	transition	putative galactosyltransferase	95.80%	G	4.20%	A
	AY532664	10127	468	C -> T	CTC -> CTT		*wbtG*	transition	putative galactosyltransferase	95.80%	C	4.20%	T
	AY532664	10180	521	A -> G	GAT -> GGT	D -> G	*wbtG*	transition	putative galactosyltransferase	95.80%	A	4.20%	G
	AY532664	10292	633	C -> A	GGC -> GGA		*wbtG*	transversion	putative galactosyltransferase	95.80%	C	4.20%	A
	AY532664	10355	696	T -> C	AGT -> AGC		*wbtG*	transition	putative galactosyltransferase	95.80%	T	4.20%	C
	AY532664	10638	979	C -> A	CAA -> AAA	Q -> K	*wbtG*	transversion	putative galactosyltransferase	95.80%	C	4.20%	A

Supplemental Table 3. Nucleotide polymorphism allele frequecies of O-antigen operon from serogroups.

Serotype	Sequence Name	Reference sequence position	Gene sequence position	Change	Codon Change	A.A. Change	gene	Polymorphism Type	product	Reference Frequency	Reference Nucleotide(s)	Variant Frequency	Variant Nucleotide(s)
	AY532664	10715	1056	G -> A	AGG -> AGA		*wbtG*	transition	putative galactosyltransferase	25.00%	G	75.00%	A
	AY532664	10818		C -> T			intergenic	transition		25.00%	C	75.00%	T
	AY532664	10935	76	G -> A	GAA -> AAA	E -> K	*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	G	4.20%	A
	AY532664	10952	93	T -> C	GAT -> GAC		*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	T	4.20%	C
	AY532664	11099	240	T -> C	TTT -> TTC		*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	T	4.20%	C
	AY532664	11106	247	C -> T	CTG -> TTG		*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	C	4.20%	T
	AY532664	11255	396	G -> A	GAG -> GAA		*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	G	4.20%	A
	AY532664	11333	474	A -> C	AAA -> AAC	K -> N	*galE*	transversion	putative UDP-galactose-4-epimerase	25.00%	A	75.00%	C
	AY532664	11366	507	T -> C	TTT -> TTC		*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	T	4.20%	C
	AY532664	11405	546	C -> T	GGC -> GGT		*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	C	4.20%	T
	AY532664	11636	777	C -> T	TAC -> TAT		*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	C	4.20%	T
	AY532664	11762	903	C -> T	TCC -> TCT		*galE*	transition	putative UDP-galactose-4-epimerase	95.80%	C	4.20%	T
	AY532664	11899		C -> G			intergenic	transversion		25.00%	C	75.00%	G
O111													
	AF078736	425		G -> A			intergenic	transition		97.90%	G	2.10%	A
	AF078736	478		T -> G			intergenic	transversion		93.80%	T	6.30%	G
	AF078736	492		G -> T			intergenic	transversion		43.80%	G	56.30%	T
	AF078736	948	210	Deletion	GTT -> GTA		*wbdH*	Deletion	putative glycosyl transferase		T	2.10%	
	AF078736	1022	284	A -> C	AAA -> ACA	K -> T	*wbdH*	transversion	putative glycosyl transferase	37.50%	A	62.50%	C
	AF078736	1453	715	T -> C	TTC -> CTC	F -> L	*wbdH*	transition	putative glycosyl transferase	97.90%	T	2.10%	C
	AF078736	1744	1006	G -> A	GTC -> ATC	V -> I	*wbdH*	transition	putative glycosyl transferase	43.80%	G	56.30%	A
	AF078736	1957		C -> A				transversion	intergenic	97.90%	C	2.10%	A
	AF078736	1963		G -> A				transition	intergenic	95.80%	G	4.20%	A
	AF078736	1994	12	G -> A	GTG -> GTA		*gmd*	transition	GDP-D-mannose dehydratase	91.70%	G	8.30%	A
	AF078736	2594	612	G -> A	GGG -> GGA		*gmd*	transition	GDP-D-mannose dehydratase	97.90%	G	2.10%	A
	AF078736	2621	639	T -> G	GAT -> GAG	D -> E	*gmd*	transversion	GDP-D-mannose dehydratase	27.10%	T	72.90%	G
	AF078736	3121		A -> G			intergenic	transition		97.90%	A	2.10%	G
	AF078736	3133		T -> C			intergenic	transition		97.90%	T	2.10%	C
	AF078736	3149		A -> G			intergenic	transition		93.80%	A	6.30%	G
	AF078736	3155		Deletion			intergenic	Deletion			A	4.20%	
	AF078736	3157		T -> A			intergenic	transversion		97.90%	T	2.10%	A
	AF078736	3163		Deletion			intergenic	Deletion			TT	95.8% -> 100.0%	
	AF078736	3167		G -> T			intergenic	transversion		95.80%	G	4.20%	T
	AF078736	3170		A -> G			intergenic	transition		97.90%	A	2.10%	G
	AF078736	3728	72	A -> C	GTA -> GTC		*manC*	transversion	mannose-1-phosphate guanylyltransferase	37.50%	A	62.50%	C
	AF078736	4682	1026	T -> A	GAT -> GAA	D -> E	*manC*	transversion	mannose-1-phosphate guanylyltransferase	83.30%	T	16.70%	A
	AF078736	5688	575	G -> A	TGC -> TAC	C -> Y	*manB*	transition	phosphomannomutase	93.80%	G	6.30%	A
	AF078736	5805	692	G -> A	AGT -> AAT	S -> N	*manB*	transition	phosphomannomutase	97.90%	G	2.10%	A
	AF078736	6273	1160	A -> G	CAA -> CGA	Q -> R	*manB*	transition	phosphomannomutase	97.90%	A	2.10%	G
	AF078736	6453	1340	C -> A	ACA -> AAA	T -> K	*manB*	transversion	phosphomannomutase	95.80%	C	4.20%	A
	AF078736	7045	525	A -> G	TCA -> TCG		*wbdJ*	transition	WbdJ	97.90%	A	2.10%	G
	AF078736	7216	696	A -> G	GTA -> GTG		*wbdJ*	transition	WbdJ	97.90%	A	2.10%	G
	AF078736	7882	442	A -> G	ATA -> GTA	I -> V	*wbdK*	transition	WbdK	31.30%	A	68.80%	G
	AF078736	8041	601	G -> A	GAT -> AAT	D -> N	*wbdK*	transition	WbdK	97.90%	G	2.10%	A
	AF078736	8127	687	C -> T	GGC -> GGT		*wbdK*	transition	WbdK	43.80%	C	56.30%	T
	AF078736	8366	926	A -> C	AAG -> ACG	K -> T	*wbdK*	transversion	WbdK	97.90%	A	2.10%	C
	AF078736	8892	247	T -> G	TTA -> GTA	L -> V	*wzx*	transversion	putative O unit flippase	97.90%	T	2.10%	G
	AF078736	8906	261	T -> C	AAT -> AAC		*wzx*	transition	putative O unit flippase	97.90%	T	2.10%	C
	AF078736	8973	328	C -> T	CTT -> TTT	L -> F	*wzx*	transition	putative O unit flippase	31.30%	C	68.80%	T
	AF078736	8985	340	A -> G	ATT -> GTT	I -> V	*wzx*	transition	putative O unit flippase	97.90%	A	2.10%	G
	AF078736	9009	364	A -> G	AAT -> GAT	N -> D	*wzx*	transition	putative O unit flippase	97.90%	A	2.10%	G
	AF078736	9078	433	G -> A	GGT -> AGT	G -> S	*wzx*	transition	putative O unit flippase	37.50%	G	62.50%	A
	AF078736	9660	1015	A -> G	ATT -> GTT	I -> V	*wzx*	transition	putative O unit flippase	95.80%	A	4.20%	G
	AF078736	9666	1021	G -> A	GCT -> ACT	A -> T	*wzx*	transition	putative O unit flippase	95.80%	G	4.20%	A
	AF078736	9773	1128	A -> T	GCA -> GCT		*wzx*	transversion	putative O unit flippase	43.80%	A	56.30%	T
	AF078736	10212		G -> A			intergenic	transition		2.10%	G	97.90%	A
	AF078736	10440		A -> G			intergenic	transition		93.80%	A	6.30%	G
	AF078736	10851		A -> G			intergenic	transition		95.80%	A	4.20%	G
	AF078736	11870	50	A -> T	CAC -> CTC	H -> L	*wbdM*	transversion	putative glycosyl transferase	31.30%	A	68.80%	T
	AF078736	12153	333	C -> T	CAC -> CAT		*wbdM*	transition	putative glycosyl transferase	97.90%	C	2.10%	T
	AF078736	12155	335	A -> G	AAC -> AGC	N -> S	*wbdM*	transition	putative glycosyl transferase	33.30%	A	66.70%	G
	AF078736	12201	381	T -> C	AGT -> AGC		*wbdM*	transition	putative glycosyl transferase	97.90%	T	2.10%	C
	AF078736	12295	475	A -> G	ATT -> GTT	I -> V	*wbdM*	transition	putative glycosyl transferase	97.90%	A	2.10%	G
	AF078736	12381	561	T -> C	AGT -> AGC		*wbdM*	transition	putative glycosyl transferase	83.30%	T	16.70%	C

Supplemental Table 3. Nucleotide polymorphism allele frequecies of O-antigen operon from serogroups.

Serotype	Sequence Name	Reference sequence position	Gene sequence position	Change	Codon Change	A.A. Change	gene	Polymorphism Type	product	Reference Frequency	Reference Nucleotide(s)	Variant Frequency	Variant Nucleotide(s)
	AF078736	12564	744	G -> T	GTG -> GTT		*wbdM*	transversion	putative glycosyl transferase	97.90%	G	2.10%	T
	AF078736	12585	765	G -> A	GGG -> GGA		*wbdM*	transition	putative glycosyl transferase	97.90%	G	2.10%	A
	AF078736	13093		G -> A			intergenic	transition		97.90%	G	2.10%	A
	AF078736	13883	760	C -> T	CTG -> TTG		*gnd*	transition	6-phosphogluconate dehydrogenase	97.90%	C	2.10%	T
O121													
	AY208937	1609	161	T -> A	TTT -> TAT	F -> Y	wbqB	transversion	putative UDP-glucose-4-epimerase	92.30%	T	7.70%	A
	AY208937	1730	282	T -> C	GTT -> GTC		wbqB	transition	putative UDP-glucose-4-epimerase	76.90%	T	23.10%	C
	AY208937	2015	567	C -> T	TAC -> TAT		wbqB	transition	putative UDP-glucose-4-epimerase	92.30%	C	7.70%	T
	AY208937	3412	912	C -> G	CGC -> CGG		rmlB	transversion	putative dTDP-glucose-4,6-dehydratase	92.30%	C	7.70%	G
	AY208937	3868		A -> G				transition		92.30%	A	7.70%	G
	AY208937	4658	204	A -> G	GTA -> GTG		vioA	transition	putative dTDP-4-amino-4,6-dideoxyglucose aminotransferase	76.90%	A	23.10%	G
	AY208937	4671	217	G -> A	GTT -> ATT	V -> I	vioA	transition	putative dTDP-4-amino-4,6-dideoxyglucose aminotransferase	76.90%	G	23.10%	A
	AY208937	4767	313	T -> C	TCC -> CCC	S -> P	vioA	transition	putative dTDP-4-amino-4,6-dideoxyglucose aminotransferase	61.50%	T	38.50%	C
	AY208937	5255	801	A -> T	ATA -> ATT		vioA	transversion	putative dTDP-4-amino-4,6-dideoxyglucose aminotransferase	92.30%	A	7.70%	T
	AY208937	5303	849	C -> T	TTC -> TTT		vioA	transition	putative dTDP-4-amino-4,6-dideoxyglucose aminotransferase	92.30%	C	7.70%	T
	AY208937	5964		K -> T				SNP			K	100.00%	T
	AY208937	6104		G -> A				transition		76.90%	G	23.10%	A
	AY208937	6247		A -> G				transition		92.30%	A	7.70%	G
	AY208937	6350	90	A -> G	ATA -> ATG	I -> M	wbqD	transition	putative acetyltransferase	92.30%	A	7.70%	G
	AY208937	6689		C -> T				transition		92.30%	C	7.70%	T
	AY208937	7212	420	T -> C	TTT -> TTC		wzx	transition	O antigen flippase	92.30%	T	7.70%	C
	AY208937	8603	411	G -> A	GGG -> GGA		wbqE	transition	putative glycosyl transferase	76.90%	G	23.10%	A
	AY208937	8615	423	T -> C	AGT -> AGC		wbqE	transition	putative glycosyl transferase	92.30%	T	7.70%	C
	AY208937	8623	431	A -> G	AAT -> AGT	N -> S	wbqE	transition	putative glycosyl transferase	92.30%	A	7.70%	G
	AY208937	8629	437	T -> C	GTC -> GCC	V -> A	wbqE	transition	putative glycosyl transferase	61.50%	T	38.50%	C
	AY208937	8792	600	T -> C	TAT -> TAC		wbqE	transition	putative glycosyl transferase	92.30%	T	7.70%	C
	AY208937	8939	747	G -> A	TTG -> TTA		wbqE	transition	putative glycosyl transferase	92.30%	G	7.70%	A
	AY208937	9167	82	A -> G	AGC -> GGC	S -> G	wbqF	transition	putative acetyltransferase	92.30%	A	7.70%	G
	AY208937	9172	87	T -> C	CAT -> CAC		wbqF	transition	putative acetyltransferase	92.30%	T	7.70%	C
	AY208937	9821	183	C -> T	TAC -> TAT		wzy	transition	O antigen polymerase	92.30%	C	7.70%	T
	AY208937	9980	342	G -> A	TCG -> TCA		wzy	transition	O antigen polymerase		G	100.00%	A
	AY208937	10404	766	T -> A	TTA -> ATA	L -> I	wzy	transversion	O antigen polymerase	92.30%	T	7.70%	A
	AY208937	10457	819	T -> G	ATT -> ATG	I -> M	wzy	transversion	O antigen polymerase	76.90%	T	23.10%	G
	AY208937	10467	829	C -> T	CTT -> TTT	L -> F	wzy	transition	O antigen polymerase	76.90%	C	23.10%	T
	AY208937	11901	1065	C -> T	TTC -> TTT		wbqG	transition	putative asparagine synthase	92.30%	C	7.70%	T
	AY208937	12045	1209	G -> A	GCG -> GCA		wbqG	transition	putative asparagine synthase	92.30%	G	7.70%	A
	AY208937	12246	1410	T -> C	TCT -> TCC		wbqG	transition	putative asparagine synthase	92.30%	T	7.70%	C
	AY208937	12526	1690	G -> A	GTA -> ATA	V -> I	wbqG	transition	putative asparagine synthase	76.90%	G	23.10%	A
	AY208937	12546	1710	A -> G	TTA -> TTG		wbqG	transition	putative asparagine synthase	76.90%	A	23.10%	G
	AY208937	12860		T -> C				transition		76.90%	T	23.10%	C
	AY208937	12872		A -> G				transition		92.30%	A	7.70%	G
	AY208937	13199		T -> G				transversion		92.30%	T	7.70%	G
	AY208937	13880	39	T -> C	TTT -> TTC		wbqI	transition	putative glycosyl transferase	92.30%	T	7.70%	C
	AY208937	14050	209	C -> T	ACT -> ATT	T -> I	wbqI	transition	putative glycosyl transferase	92.30%	C	7.70%	T
	AY208937	14423	582	A -> G	AAA -> AAG		wbqI	transition	putative glycosyl transferase	61.50%	A	38.50%	G
	AY208937	14605	764	T -> C	GTT -> GCT	V -> A	wbqI	transition	putative glycosyl transferase	92.30%	T	7.70%	C
	AY208937	14615	774	C -> T	TGC -> TGT		wbqI	transition	putative glycosyl transferase	92.30%	C	7.70%	T
	AY208937	14930	1089	G -> A	CAG -> CAA		wbqI	transition	putative glycosyl transferase	92.30%	G	7.70%	A
O145													
	AY863412	2026	230	C -> T	TCG -> TTG	S -> L	*nnaC*	transition	CMP-NeuNAc synthetase	85.70%	C	14.30%	T
	AY863412	2481	684	Deletion			*nnaC*	Insertion	CMP-NeuNAc synthetase			28.60%	A
	AY863412	2483	687	Deletion			*nnaC*	Deletion	CMP-NeuNAc synthetase		T	14.30%	
	AY863412	5308	939	A -> T	ATA -> ATT		*wzx*	transversion	O antigen flippase	85.70%	A	14.30%	T
	AY863412	5652	37	C -> A	CTT -> ATT	L -> I	*wzy*	transversion	O antigen polymerase	71.40%	C	28.60%	A
	AY863412	9277	150	T -> C	GCT -> GCC		*wbeD*	transition	glutamine amidotransferase	85.70%	T	14.30%	C
	AY863412	9318	191	T -> C	CTG -> CCG	L -> P	*wbeD*	transition	glutamine amidotransferase	85.70%	T	14.30%	C
	AY863412	14364		A -> G			intergenic	transition		85.70%	A	14.30%	G