

**Table S1. List of strains used in this study.**

Strain	Source	Disease association	Genotype	<i>netB</i>	Country	MLST type	Reference
MLST49	Chicken	Healthy	A, cpb2+	-	Canada	C19	Chalmers, 2008a
PFGE A	Chicken	Healthy	A	-	Canada	n/a	Chalmers, 2008b
PFGE C	Chicken	Healthy	A	-	Canada	n/a	Chalmers, 2008b
PFGE F	Chicken	Healthy	A	-	Canada	n/a	Chalmers, 2008b
PFGE B	Chicken	Healthy	A, cpb2+	-	Canada	n/a	Chalmers, 2008b
PFGE E	Chicken	Healthy	A, cpb2+	-	Canada	n/a	Chalmers, 2008b
PFGE H	Chicken	Healthy	A, cpb2+	-	Canada	n/a	Chalmers, 2008b
JGS4042	Chicken	Necrotic enteritis	A	-	United States	n/a	n/a
JGS4043	Chicken	Necrotic enteritis	A	-	United States	n/a	n/a
JGS4066	Chicken	Necrotic enteritis	A	-	United States	n/a	n/a
JP120	Chicken	Necrotic enteritis	A	-	Canada	n/a	n/a
JGS4120	Chicken	Necrotic enteritis	A, cpb2+	-	United States	n/a	n/a
JGS4141	Chicken	Necrotic enteritis	A, cpb2+	-	United States	n/a	n/a
JP121	Chicken	Necrotic enteritis	A, cpb2+	-	Canada	n/a	n/a
JP123	Chicken	Necrotic enteritis	A, cpb2+	-	Canada	n/a	n/a
JP148	Chicken	Necrotic enteritis	A, cpb2+	-	Canada	n/a	n/a
JP149	Chicken	Necrotic enteritis	A, cpb2+	-	Canada	n/a	n/a
CP5	Chicken	Healthy	A	-	Canada	n/a	Thompson, 2006
CP6	Chicken	Healthy	A, cpb2+	-	Canada	n/a	Thompson, 2006
JGS4143	Chicken	Necrotic enteritis	A, cpb2+	+	United States	H31	Barbara, 2008
MLST11	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	C4	Chalmers, 2008a
MLST19	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	C8	Chalmers, 2008a
MLST23	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	C10	Chalmers, 2008a
MLST29	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	C13	Chalmers, 2008a
MLST31	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	C10	Chalmers, 2008a
PFGE G	Chicken	Healthy	A, cpb2+	+	Canada	n/a	Chalmers, 2008b
JP125	Chicken	Necrotic enteritis	A	+	Canada	n/a	n/a
JGS4059	Chicken	Necrotic enteritis	A, cpb2+	+	United States	n/a	n/a
JGS4135	Chicken	Necrotic enteritis	A, cpb2+	+	United States	C3/4	n/a
JP150	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	n/a	n/a
CP1	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	n/a	Thompson, 2006
CP2	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	n/a	Thompson, 2006
CP3	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	n/a	Thompson, 2006
CP4	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	H39/C1	Thompson, 2006
JP122	Chicken	Necrotic enteritis	A, cpb2+	+	Canada	n/a	n/a
JP116	Retail chicken	Healthy	A	-	Canada	n/a	Nowell, 2010
JP67	Retail chicken	Healthy	A	-	Canada	n/a	Nowell, 2010
JP73	Retail chicken	Healthy	A	-	Canada	n/a	Nowell, 2010
JP79	Retail chicken	Healthy	A	-	Canada	n/a	Nowell, 2010
JP83	Retail chicken	Healthy	A	-	Canada	n/a	Nowell, 2010
JP88	Retail chicken	Healthy	A	-	Canada	n/a	Nowell, 2010
JP97	Retail chicken	Healthy	A	-	Canada	n/a	Nowell, 2010
JP69	Retail chicken	Healthy	A, cpb2+	-	Canada	n/a	Nowell, 2010
JP75	Retail chicken	Healthy	A, cpb2+	-	Canada	n/a	Nowell, 2010
JP78	Retail chicken	Healthy	A, cpb2+	-	Canada	n/a	Nowell, 2010
JP80	Retail chicken	Healthy	A, cpb2+	-	Canada	n/a	Nowell, 2010
JP84	Retail chicken	Healthy	A, cpb2+	-	Canada	n/a	Nowell, 2010
JP90	Retail chicken	Healthy	A, cpb2+	-	Canada	n/a	Nowell, 2010
JP93	Retail chicken	Healthy	A, cpb2+	-	Canada	n/a	Nowell, 2010
JP77	Retail chicken	Healthy	A, cpb2+	+	Canada	n/a	Nowell, 2010
JP82	Retail chicken	Healthy	A, cpb2+	+	Canada	n/a	Nowell, 2010
JP86	Retail chicken	Healthy	A, cpb2+	+	Canada	n/a	Nowell, 2010
JP91	Retail chicken	Healthy	A, cpb2+	+	Canada	n/a	Nowell, 2010
JP94	Retail chicken	Healthy	A, cpb2+	+	Canada	n/a	Nowell, 2010
Str13	Soil	n/a	A	-	Canada	n/a	Mahoney, 1976
ATCC13124	Human	Gas gangrene	A	-	n/a	n/a	n/a
NCTC8239	Human	Food poisoning	A	-	n/a	n/a	n/a
SM101	Human	Food poisoning	A	-	n/a	n/a	n/a
F4969	Human	Non-food-borne disease	A	-	n/a	n/a	n/a
ATCC3626	Lamb	N/A	B	-	n/a	n/a	n/a
JGS1495	Pig	Diarrhea	C	-	n/a	n/a	n/a
JGS1721	Sheep	Enteritis	D	-	n/a	n/a	n/a
JGS1987	Cow	Enteritis	E	-	n/a	n/a	n/a

n/a; not available

**Table S2. Primers used for detection of *netB* and *cpb2* and for PCR confirmation of CGH results.**

Locus tag <sup>1</sup>	Forward primer (5'-3')	Reverse primer (5'-3')	Product size (bp)
CP4_3449 ( <i>netB</i> )	GCTGGTGCTGGAATAAATGC	TCGCCATTGAGTAGTTTCCC	383
CP4_3441 ( <i>cpb2</i> )	AGATTTTAAATATGATCCTAACC	CAATACCCTTCACCAAATACTC	567
CP4_0445	TGGGATTCTTTGGTTCTTGG	CATTCCAAGCTTCCTCTGG	155
CP4_0448	GCATGGGGAAGAGAAAGACA	ATCAGGATGAATTCCCATCA	223
CP4_0463	ATGCCAAACTTGGAGGAGAG	GCAGCTTCTGCAATTGGACT	210
CP4_0468	TTGGACAACAAGGGTTTGGT	GCGCTTGAGACCAACAAATA	223
CP4_0783	GAGGAGCATTATGGACAGCTT	CCCATCATTCTTGATTTGG	136
CP4_1608	TGTGGGGCGAAAAATAAAAA	CATCTTTTTCTCCGCCTTGA	170
CP4_2645	CAAGTTCGCACTAGACGGATT	GACAACCTGGACATTCTCAAAGG	214
CP4_2821	TTACCTGGAGTGGCTCCAAC	ACACCTGGTCCTTGAGCATC	175
JGS4143-0169	GTGCAGATGCTGCTTTTGAT	TTAAACCACCAGCCTGATCC	194
JGS4143-0500	CCATCAGAGCATATTGCAAGG	TTGAAAAAGTTGGTTGGATAAAAA	175

<sup>1</sup> Representative CDS from either the CP4 or JGS4143 genome sequence

Table S3. Variable genes identified among 63 poultry and non-poultry isolates.

Variable Region	Locus_tag	Product	Start	Stop	Size (bp)	Functional Category/Subcategory	Prevalence	phage/IS	Plasmid Hit	pNet8 Hit	
VR-01	CP4_0296	galactoside O-acetyltransferase	323322	323936	614	Carbohydrates/Lactose utilization	0.67				
VR-02	CP4_0377	conserved hypothetical protein	411726	412112	386	None/None	0.82				
	CP4_0378	conserved hypothetical protein	412128	412532	404	None/None	0.74				
	CP4_0379	conserved hypothetical protein	412603	412806	203	None/None	0.76				
VR-03	CP4_0391	conserved hypothetical protein	428535	429779	1244	None/None	0.82				
	CP4_0392	RNA polymerase ECF-type sigma factor	429793	430329	536	None/None	0.79				
	CP4_0430	caudovirus prohead protease	461245	461898	653	None/None	0.45	Yes			
VR-04	CP4_0439	phage tail tape measure protein, family	465787	469560	3773	Phages, Prophages, Transposable elements, Plasmids/Phage tail proteins	0.65	Yes			
	CP4_0444	transcriptional regulator	476909	477766	857	Carbohydrates/Fructooligosaccharides(FOS) and Raffinose Utilization	0.82				
	CP4_0445	extracellular solute-binding protein	477955	479223	1268	Miscellaneous/COG3533 Carbohydrates/Chitin and N-acetylglucosamine utilization	0.76				
	CP4_0446	ABC transporter	479297	480223	926	Carbohydrates/Chitin and N-acetylglucosamine utilization	0.82				
	CP4_0447	sugar ABC transporter	480240	481067	827	Carbohydrates/Fructooligosaccharides(FOS) and Raffinose Utilization	0.76				
	CP4_0448	alpha-galactosidase 1	481095	483302	2207	Miscellaneous/COG3533 Carbohydrates/Fructooligosaccharides(FOS) and Raffinose Utilization	0.76				
						Carbohydrates/Lactose and Galactose Uptake and Utilization					
						Sulfur Metabolism/Galactosylceramide and Sulfatide metabolism					
VR-06	CP4_0458	sigma factor SglI	496054	496704	650	RNA Metabolism/Transcription initiation, bacterial sigma factors	0.61				
	CP4_0459	conserved hypothetical protein	496717	497763	1046	None/None	0.67				
	CP4_0460	putative VTC domain superfamily	497902	498600	698	None/None	0.61				
	CP4_0461	putative tubulin/FtsZ, GTPase	498633	499313	680	None/None	0.70				
	CP4_0462	resolvase	499492	500043	551	None/None	0.56	Yes			
	CP4_0464	putative VTC domain superfamily	500285	500977	692	None/None	0.58				
	CP4_0464	tubulin/FtsZ, GTPase	501023	501571	548	None/None	0.56				
	CP4_0465	Coth protein	501673	503166	1493	None/None	0.61				
	CP4_0466	conserved hypothetical protein	503180	505237	2057	None/None	0.56				
	CP4_0467	putative heat repeat	505247	506380	1133	None/None	0.56				
	CP4_0468	chitin synthase	506374	507774	1400	Cell Wall and Capsule/Exopolysaccharide Biosynthesis	0.56				
	VR-07	CP4_0526	iron uptake protein A1	569626	570678	1052	None/None	0.82			
CP4_0528		Fe(3+) ions import ATP-binding protein FbpC	572273	572953	680	None/None	0.82				
CP4_0529		nitrite reductase	573243	573932	689	None/None	0.82				
VR-08	CP4_0540	transposase	581374	582468	1094	None/None	0.38	Yes			
	CP4_0543	conserved hypothetical protein	584187	584819	632	None/None	0.89				
VR-09	CP4_0547	conserved hypothetical protein	590383	590796	413	None/None	0.89				
	CP4_0552	UDP-N-acetyl-D-mannosamine dehydrogenase	594668	595897	1229	Cell Wall and Capsule/Streptococcal Hyaluronic Acid Capsule	0.36				
VR-10B	CP4_0573	signal peptidase I	622794	623174	380	Protein Metabolism/Signal peptidase	0.60				
	CP4_0575	sortase, SrtB family	624275	625024	749	Cell Wall and Capsule/Sortase	0.47				
						Iron acquisition and metabolism/Heme, hemin uptake and utilization systems in GramPositives					
	CP4_0577	DNA-binding response regulator	626518	627234	716	None/None	0.67				
	CP4_0578	sensor histidine kinase	627239	628537	1298	None/None	0.52				
VR-10A	JGS4143-0549	signal peptidase I	592665	593213	548	Protein Metabolism/Signal peptidase	0.55				
	JGS4143-0551	conserved hypothetical protein	593950	594681	731	None/None	0.82				
	JGS4143-0552	conserved hypothetical protein	594584	595310	726	None/None	0.45				
	JGS4143-0553	von Willebrand factor type A domain protein	595327	597171	1844	None/None	0.81				
	JGS4143-0554	two-component response regulator	597449	597883	434	None/None	0.45				
	JGS4143-0555	two-component response regulator	597964	598164	200	None/None	0.55				
	JGS4143-0556	hypothetical protein	598378	598542	164	None/None	0.86				
	CP4_0615	conserved hypothetical protein	666705	667352	647	None/None	0.85				
VR-12	CP4_0621	conserved hypothetical protein	675901	676992	1091	None/None	0.88				
VR-13	CP4_0677	undecaprenyl phosphate galactose phosphotransferase	745810	746472	662	Cell Wall and Capsule/Exopolysaccharide Biosynthesis	0.83				
	CP4_0678	glycosyl transferase, group 2 family protein	746473	747387	914	None/None	0.77				
	CP4_0679	glucose-1-phosphate thymidyltransferase	747410	748291	881	Cell Wall and Capsule/dTDP-rhamnose synthesis	0.89				
	CP4_0681	dTDP-4-dehydroammonse reductase	748980	749864	884	Cell Wall and Capsule/dTDP-rhamnose synthesis	0.89				
	CP4_0682	dTDP-glucose 4,6-dehydratase	749892	750941	1049	Cell Wall and Capsule/dTDP-rhamnose synthesis	0.89				
	CP4_0683	membrane protein, putative	750966	752180	1214	None/None	0.61				
	CP4_0684	glycosyl transferase, group 2 family protein	752177	753025	848	None/None	0.65				
	CP4_0685	conserved hypothetical protein	753119	753859	740	None/None	0.79				
	CP4_0686	polysaccharide biosynthesis protein	753868	755319	1451	None/None	0.88				
	CP4_0687	cell wall binding repeat-containing protein/mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase domain-containing protein	755341	757548	2207	Stress Response/Choline and Betaine Uptake and Betaine Biosynthesis	0.86				
	VR-14	CP4_0688	cell wall binding repeat-containing protein/mannosyl-glycoprotein endo-beta-N-acetylglucosaminidase domain-containing protein	757630	757761	131	Stress Response/Choline and Betaine Uptake and Betaine Biosynthesis	0.70			
		CP4_0689	cell wall binding repeat-containing protein/zinc carboxypeptidase family protein	757890	759542	1652	Stress Response/Choline and Betaine Uptake and Betaine Biosynthesis	0.74			
		CP4_0690	cell wall binding repeat-containing protein	759744	760046	302	Stress Response/Choline and Betaine Uptake and Betaine Biosynthesis	0.64			
VR-15	CP4_0691	cell wall binding repeat-containing protein	760109	761134	1025	Stress Response/Choline and Betaine Uptake and Betaine Biosynthesis	0.88				
VR-16	CP4_0783	oxidoreductase, FAD/FMN-binding	864456	865562	1106	None/None	0.63				
VR-17	CP4_0797	RNA polymerase ECF-type sigma factor	878906	879424	518	None/None	0.89				
VR-18	CP4_0831	conserved hypothetical protein	917627	918571	944	None/None	0.73				
	CP4_0833	hypothetical protein	920211	920720	509	None/None	0.89				
VR-19	CP4_0841	conserved hypothetical protein	929745	930323	578	None/None	0.47				
VR-20	CP4_0850	conserved hypothetical protein	939101	939595	494	None/None	0.88				
VR-21	CP4_0859	rubredoxin	952749	952910	161	Stress Response/Rubredoxin	0.89				
VR-22	CP4_0874	probable iron(III) dicitrate ABC transporter	967641	968591	950	None/None	0.80				
	CP4_0875	iron compound ABC transporter, permease protein	968721	969725	1004	None/None	0.79				
	CP4_0876	ABC transport system permease protein	969725	970747	1022	None/None	0.85				
	CP4_0877	ferrichrome transport ATP-binding protein FhuC	970753	971523	770	None/None	0.82				
	CP4_0896	conserved hypothetical protein	991376	991693	317	None/None	0.86				

Table S3. Variable genes identified among 63 poultry and non-poultry isolates.

Variable Region	Locus_tag	Product	Start	Stop	Size (bp)	Functional Category/Subcategory	Prevalence	phage/IS	Plasmid Hit	pNet8 Hit
VR-24	CP4_0919	sensory transduction protein BceR	1019475	1020143	668	None/None	0.89			
	CP4_0924	bactiracin export ATP-binding protein BceA	1024417	1025184	767	None/None	0.89			
	CP4_0927	stress responsive alpha-beta barrel domain-containing protein	1029259	1029561	302	None/None	0.82			
CP4_0929	conserved hypothetical protein	1031131	1032048	917	None/None	0.86				
	CP4_0947	conserved hypothetical protein	1057864	1057986	122	None/None	0.86			
VR-25	CP4_0950	conserved hypothetical protein	1060835	1061071	236	None/None	0.87			
	CP4_0963	resolvase domain-containing protein	1066623	1066748	125	None/None	0.86	Yes		
VR-27	CP4_1008	conserved hypothetical protein	1107491	1108213	722	None/None	0.82			
	CP4_1010	putative toxin-antitoxin system, toxin component	1109470	1109934	464	None/None	0.60	Yes		
VR-28	CP4_1036	putative phage terminase, large subunit	1121539	1122906	1367	Phages, Prophages, Transposable elements, Plasmids/Phage packaging machinery	0.65	Yes		
VR-29	CP4_1061	DNA adenine-specific methyltransferase	1141541	1142320	779	None/None	0.33	Yes		
VR-30	CP4_1069	probable autolytic lysozyme	1148003	1149031	1028	None/None	0.76	Yes		
	CP4_1071	conserved hypothetical protein	1150159	1150590	431	None/None	0.73			
	CP4_1076	phosphorylase family protein	1155215	1155400	185	None/None	0.86			
VR-31	CP4_1098	caax amino protease family protein	1175507	1176310	803	None/None	0.89			
	CP4_1099	ProFAR isomerase associated superfamily	1176593	1179449	356	None/None	0.87			
	CP4_1100	conserved hypothetical protein	1177033	1177227	194	Protein Metabolism/Aminopeptidases [EC 3.4.11.-]	0.88			
VR-32	CP4_1106	conserved hypothetical protein	1182472	1182585	113	None/None	0.82			
	CP4_1107	methionyl-tRNA formyltransferase	1182759	1183712	953	Protein Metabolism/Translation initiation factors bacterial	0.88			
	CP4_1110	transcriptional regulator	1185544	1185858	314	None/None	0.90			
VR-33	CP4_1114	conserved hypothetical protein	1187176	1187508	332	None/None	0.88			
	CP4_1130	putative toxin-antitoxin system, toxin component	1205424	1205867	443	None/None	0.82			
	CP4_1131	toxin-antitoxin system, antitoxin component, Xre family	1205976	1206518	542	None/None	0.82			
CP4_1134	conserved hypothetical protein	1208275	1208493	218	None/None	0.86				
	CP4_1135	conserved hypothetical protein	1208934	1209164	230	None/None	0.88			
	CP4_1136	acetyltransferase	1209487	1210803	1316	None/None	0.82			
VR-34	CP4_1150	lipoprotein, putative	1225050	1225979	929	None/None	0.80			
	CP4_1153	conserved hypothetical protein	1226401	1227090	689	None/None	0.88			
	CP4_1154	conserved hypothetical protein	1227249	1227566	317	None/None	0.81			
CP4_1158	conserved hypothetical protein	1229563	1230120	557	None/None	0.77				
CP4_1159	conserved hypothetical protein	1230670	1231020	350	None/None	0.89				
CP4_1165	UBA/TIS-N domain-containing protein	1235711	1236259	548	None/None	0.86				
CP4_1167	sensor histidine kinase	1236962	1238218	1256	None/None	0.89				
VR-35	CP4_1169	acetyltransferase	1239436	1239996	560	None/None	0.83			
	CP4_1181	discodin domain-containing protein	1249401	1255829	6428	None/None	0.47			
	CP4_1184	[Fe] hydrogenase	1258112	1259617	1505	Stress Response/Oxidative stress Stress Response/Rubrythrin	0.88			
VR-36	CP4_1238	collagen adhesion protein	1316719	1320288	3569	None/None	0.88			
VR-37	CP4_1251	hydroxylamine reductase	1333284	1334939	1655	Nitrogen Metabolism/Nitrosative stress	0.68			
VR-38	CP4_1323	lipoprotein-releasing system ATP-binding protein LoD	1407692	1408357	665	None/None	0.87			
CP4_1324	conserved hypothetical protein	1408413	1409330	917	None/None	0.86				
	CP4_1325	putative permease	1409341	1410636	1295	None/None	0.71			
	CP4_1329	nudix family hydrolase	1413140	1413754	614	None/None	0.86			
VR-39	CP4_1336	histidine kinase KlpD	1420205	1422907	2702	Potassium metabolism/Potassium homeostasis	0.89			
	CP4_1342	conserved hypothetical protein	1427580	1427702	122	None/None	0.87			
VR-40	CP4_1388	ggd/feal domain-containing protein	1482643	1484166	1523	Stress Response/Bacterial hemoglobins	0.89			
VR-41	CP4_1461	AP endonuclease	1553838	1554656	818	DNA Metabolism/DNA repair, bacterial	0.88			
VR-42	CP4_1477	lipoprotein, putative	1568892	1569686	794	None/None	0.82			
VR-43	CP4_1594	chromosome segregation ATPase	1689390	1690826	1436	None/None	0.51			
VR-44	CP4_1608	conserved hypothetical protein	1706749	1707519	770	None/None	0.73			
VR-45	CP4_1619	lysine-N-methylase	1723665	1724813	1148	None/None	0.79			
VR-46	CP4_1641	xanthine phosphoribosyltransferase	1756609	1757187	578	Nucleosides and Nucleotides/Purine conversions Nucleosides and Nucleotides/Xanthine Metabolism in Bacteria	0.89			
VR-47	CP4_1710	conserved hypothetical protein	1832279	1832653	374	None/None	0.89			
VR-48	CP4_1730	transposon, resolvase	1852098	1852250	152	None/None	0.70	Yes		
VR-49	CP4_1860	BNR/Asp-box repeat-containing protein	1984235	1985950	1715	None/None	0.74			
VR-50	CP4_1876	O-GlcNAcase NagJ [CPE_1523]	2004673	2008056	3383	None/None	0.82			
VR-51	CP4_1926	lipoprotein, putative	2064007	2064708	701	None/None	0.86			
VR-52	CP4_1976	hypothetical protein	2115311	2115814	503	None/None	0.73			
VR-53	CP4_2009	conserved hypothetical protein	2151691	2152023	332	None/None	0.89			
VR-54	CP4_2074	chromosome segregation protein SMC	2218087	2221644	3557	DNA Metabolism/DNA structural proteins, bacterial	0.88			
VR-55	CP4_2126	penicillin binding protein transpeptidase domain-containing protein	2272364	2274031	1667	None/None	0.89			
VR-56	CP4_2168	conserved hypothetical protein	2315919	2316224	305	None/None	0.89			
VR-57	CP4_2195	sensor histidine kinase	2336562	2336912	350	None/None	0.87			
	CP4_2196	conserved hypothetical protein	2336959	2337255	296	None/None	0.74			
VR-58	CP4_2309	flavochemoprotein	2465252	2465686	434	Stress Response/Bacterial hemoglobins	0.90			
VR-59	CP4_2359	hypothetical protein	2516454	2516582	128	None/None	0.33			
VR-60	CP4_2372	Gp10 protein	2530832	2531182	350	None/None	0.34	Yes		
	CP4_2376	phage major capsid protein, HK97 family	2532246	2533430	1184	Phages, Prophages, Transposable elements, Plasmids/Phage capsid proteins	0.29	Yes		
	CP4_2377	phage prohead protease, HK97 family	2533471	2534076	605	None/None	0.24	Yes		
CP4_2379	phage portal protein, HK97 family	2534232	2535479	1247	Phages, Prophages, Transposable elements, Plasmids/Phage packaging machinery	0.33	Yes			
VR-61	CP4_2382	Gp50 protein	2537815	2538237	422	None/None	0.23	Yes		
VR-62	CP4_2398	integrase family protein	2545360	2546520	1160	None/None	0.28	Yes		
VR-62	CP4_2429	VanZ family membrane protein	2573948	2574463	515	None/None	0.68			
	CP4_2431	conserved hypothetical protein	2574989	2576170	1181	None/None	0.45			
	CP4_2432	membrane protein, putative	2576184	2577008	824	None/None	0.70			
CP4_2433	ABC transporter, ATP-binding protein	2576995	2577690	695	None/None	0.50				
VR-63	CP4_2512	conserved hypothetical protein	2672144	2673389	3245	None/None	0.85			
VR-64	CP4_2645	sporulation initiation inhibitor protein Soj	2816355	2817110	755	Cell Division and Cell Cycle/Bacterial Cytoskeleton	0.58		NP_149993.1_Soj_protein_[Clostridium_perfringens_str_13] (99.6% coverage, 86.4% ID)	
VR-65	CP4_2697	conserved hypothetical protein	2874962	2877589	2627	None/None	0.69			
	CP4_2699	conserved hypothetical protein	2878199	2880307	2108	None/None	0.76			
	CP4_2700	conserved hypothetical protein	2880312	2881313	1001	None/None	0.83			
VR-66	CP4_2736	type I restriction-modification system, M subunit	2920302	2921819	1517	DNA Metabolism/Restriction-Modification System	0.47			
VR-67	CP4_2932	DNA-binding protein HU	3106077	3106352	275	DNA Metabolism/DNA structural proteins, bacterial	0.88			
VR-68	CP4_3079	AraC family transcriptional regulator	3263120	3263989	869	None/None	0.68		YP_001967745.1_probable_AraC-related_transcriptional_regulator_[Clostridium_perfringens ns] (100% coverage, 100% ID)	

Table S3. Variable genes identified among 63 poultry and non-poultry isolates.

Variable Region	Locus_tag	Product	Start	Stop	Size (bp)	Functional Category/Subcategory	Prevalence	phage/IS	Plasmid Hit	pNet8 Hit
	CP4_3080	tetracycline resistance protein TetP	3264910	3268688	1958	Virulence, Disease and Defense/Tetracycline resistance, ribosome protection type	0.77		YP_001967743.1_ribosomal_protection-like_tetracycline_resistance_protein_[Clostridium_perfringens] (100% coverage, 99.54% ID)	
	CP4_3081	tetracycline resistance protein	3266852	3268114	1262	None/None	0.89		YP_001967742.1_tetracycline_efflux_protein_[Clostridium_perfringens] (100% coverage, 97.86% ID)	
VR-69	CP4_3109	conserved hypothetical protein (pCP13_CPC36)	3284906	3286732	1826	None/None	0.45			
VR-70	CP4_3124	conserved hypothetical protein (pCW3_0007)	3291941	3292597	656	None/None	0.68		YP_001967748.1_hypothetical_protein_pCW3_0007_[Clostridium_perfringens] (100% coverage, 99.68% ID)	
	CP4_3125	hypothetical protein	3292630	3292746	116	None/None	0.73			
	CP4_3127	conserved hypothetical protein (pCW3_0008)	3293069	3293230	161	None/None	0.76		YP_001967749.1_hypothetical_protein_pCW3_0008_[Clostridium_perfringens] (100% coverage, 100% ID)	AEP94979.1_hypothetical_protein_pNet8_00001_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 92.59% ID)
VR-71	CP4_3126	LexA repressor (pCW3_0015)	3293270	3293829	559	None/None	0.69	Yes	YP_001967756.1_probable_transcriptional_regulator_[Clostridium_perfringens] (100% coverage, 100% ID)	
VR-72	CP4_3128	putative plasmid partitioning protein (pCW3_0013)	3294331	3295257	926	None/None	0.71		YP_001967754.1_possible_plasmid_partitioning_protein_[Clostridium_perfringens] (100% coverage, 99.68% ID)	
	CP4_3129	conserved hypothetical protein (pCW3_0012)	3295236	3295466	230	None/None	0.62		YP_001967753.1_hypothetical_protein_pCW3_0012_[Clostridium_perfringens] (100% coverage, 100% ID)	
VR-73	CP4_3132	toxin A	3297965	3301840	3875	None/None	0.84			
	CP4_3133	bacteriocin-related protein	3302060	3302257	197	None/None	0.56		YP_699914.1_bacteriocin-related_protein_[Clostridium_perfringens_SM101] (100% coverage, 86.15% ID)	
	CP4_3134	UviA protein	3302301	3302867	566	None/None	0.33	Yes		
	CP4_3136	transposase for insertion sequence element isrm3	3304270	3304389	119	None/None	0.19			
VR-74	CP4_3138	putative ATPase of HSP70 class (pNet8_00004)	3305250	3306095	845	None/None	0.86		AEP94982.1_putative_ATPase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 99.64% ID)	AEP94982.1_putative_ATPase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 99.64% ID)
	CP4_3139	conserved hypothetical protein (pNet8_00003)	3306098	3306349	251	None/None	0.52		AEP94981.1_hypothetical_protein_pNet8_00003_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)	AEP94981.1_hypothetical_protein_pNet8_00003_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
VR-75	CP4_3153	thymidine kinase	3312878	3313459	581	Nucleosides and Nucleotides/pyrimidine conversions	0.51	Yes		
VR-76	CP4_3216	conserved hypothetical protein	3372021	3372323	302	None/None	0.80			
VR-77	CP4_3229	conserved hypothetical protein	3378524	3379292	768	None/None	0.52			
VR-78	CP4_3246	ISCpe2, transposase OrfB	3385854	3387008	1154	None/None	0.32	Yes		
VR-79	CP4_3270	conserved hypothetical protein	3398974	3399285	311	None/None	0.86			
	CP4_3271	putative transcriptional regulator	3399534	3399743	209	None/None	0.31	Yes		
VR-80	CP4_3286	conserved hypothetical protein	3410751	3411494	743	None/None	0.29			
VR-81	CP4_3340	plectrovirus Spv1-c74 orf 1 and c-terminal truncated protein	3456498	3456671	173	None/None	0.39			
VR-82	CP4_3348	collagen adhesion protein	3460957	3462036	1079	None/None	0.24			
VR-83	CP4_3359	conserved hypothetical protein	3469944	3471065	1121	None/None	0.51			
	CP4_3360	collagen adhesin (partial)	3471309	3474698	3389	None/None	0.76		NP_150050.1_collagen_adhesin_[Clostridium_perfringens_str_13] (99.65% coverage, 92.63% ID)	
VR-84	CP4_3361	collagen adhesin (partial)	3474737	3475402	665	None/None	0.42		NP_150050.1_collagen_adhesin_[Clostridium_perfringens_str_13] (99.1% coverage, 88.58% ID)	
VR-85	CP4_3398	HNH endonuclease domain protein	3503059	3503517	458	None/None	0.49	Yes		
	CP4_3403	phage prohead protease, HK97 family	3507336	3507926	590	None/None	0.73	Yes		
	CP4_3404	phage major capsid protein, HK97 family	3507984	3509102	1118	Phages, Prophages, Transposable elements, Plasmids/Phage	0.23	Yes		
	CP4_3406	phage protein, HK97 gp10 family	3509754	3510107	353	None/None	0.71			
	CP4_3407	conserved hypothetical protein	3510107	3510457	350	None/None	0.66			
	CP4_3408	prophage LambdaSa04, Phi13 family major tail protein	3510503	3511090	587	None/None	0.58			
	CP4_3411	family phage tail tape measure protein	3511831	3515166	3335	Phages, Prophages, Transposable elements, Plasmids/Phage tail proteins	0.48	Yes		
VR-86	CP4_3421	FtsK/Spol	3519170	3520486	1316	None/None	0.49	Yes	YP_473424.1_FtsK/Spol_[Clostridium_perfringens] (100% coverage, 99.32% ID)	
VR-87	CP4_3422	integrase/recombinase	3520758	3521774	1016	None/None	0.84			
	CP4_3426	hypothetical protein	3523520	3524119	599	None/None	0.25			
VR-88	CP4_3431	LexA repressor	3525594	3525998	404	None/None	0.51	Yes	AEP94898.1_putative_transcription_regulator_[Clostridium_perfringens] (100% coverage, 99.25% ID)	
VR-89	CP4_3432	transporter, major facilitator family	3526521	3527768	1247	None/None	0.34			
	CP4_3433	putative heme biosynthesis protein	3527773	3528915	1142	None/None	0.25			
	CP4_3434	putative radical SAM domain-containing protein	3528930	3530042	1112	None/None	0.53			
	CP4_3435	conserved hypothetical protein	3530064	3530258	194	None/None	0.33			
VR-90	CP4_3436	conserved hypothetical protein	3531541	3531810	269	None/None	0.40		AEP94894.1_hypothetical_protein_pBeta2_00004_[Clostridium_perfringens] (100% coverage, 97.75% ID)	
	CP4_3437	conserved hypothetical protein	3531847	3532185	338	None/None	0.62		AEP94895.1_hypothetical_protein_pBeta2_00005_[Clostridium_perfringens] (100% coverage, 100% ID)	
	CP4_3438	putative ATPase	3532185	3533102	917	None/None	0.71		AEP94896.1_putative_ATPase_[Clostridium_perfringens] (100% coverage, 100% ID)	
VR-91	CP4_3439	transcriptional regulator	3534507	3534830	323	None/None	0.82		AEP94973.1_transcriptional_regulator_[Clostridium_perfringens] (100% coverage, 99.07% ID)	
	CP4_3441	beta2 toxin	3535486	3536283	797	None/None	0.61		AEP94971.1_beta2-toxin_[Clostridium_perfringens] (100% coverage, 100% ID)	
VR-92	CP4_3442	transcriptional regulator, MarR family	3537230	3537676	446	Stress Response/Oxidative stress	0.39		AEP95056.1_transcriptional_regulator_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)	AEP95056.1_transcriptional_regulator_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3443	beta-lactamase domain-containing protein	3537812	3538561	749	None/None	0.48		AEP95055.1_beta-lactamase_domain-containing_protein_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)	AEP95055.1_beta-lactamase_domain-containing_protein_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3444	M protein trans-acting positive regulator (MGA)	3539337	3540827	1490	None/None	0.34		AEP95054.1_hypothetical_protein_pNet8_00081_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)	AEP95054.1_hypothetical_protein_pNet8_00081_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3445	putative radical SAM domain-containing protein	3540991	3542247	1256	None/None	0.34		AEP95053.1_SAM_domain-containing_protein_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)	AEP95053.1_SAM_domain-containing_protein_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3446	putative internalin	3542876	3544051	1175	None/None	0.29		AEP95052.1_putative_surface_protein_Net1_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)	AEP95052.1_putative_surface_protein_Net1_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3447	hypothetical protein	3544300	3544443	143	None/None	0.36		AEP95051.1_hypothetical_protein_pNet8_00078_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)	AEP95051.1_hypothetical_protein_pNet8_00078_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3448	hypothetical protein	3544427	3544555	128	None/None	0.47		AEP95050.1_hypothetical_protein_pNet8_00077_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)	AEP95050.1_hypothetical_protein_pNet8_00077_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3449	necrotic enteritis toxin B	3544776	3545744	968	None/None	0.42			
	CP4_3450	ricin-type beta-trefoil domain protein	3546298	3547473	1175	None/None	0.70	Yes	AEP95047.1_putative_carbohydrate_binding_protein_NetH_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 99.74% ID)	AEP95047.1_putative_carbohydrate_binding_protein_NetH_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 99.74% ID)
	CP4_3451	transposase for transposon	3548149	3548430	281	None/None	0.52			

Table S3. Variable genes identified among 63 poultry and non-poultry isolates.

Variable Region	Locus_tag	Product	Start	Stop	Size (bp)	Functional Category/Subcategory	Prevalence	phage/S	Plasmid Hit	pNet8 Hit
	CP4_3452	hypothetical protein	3548798	3549127	329	None/None	0.65		YP_001967791.1_hypothetical_protein_pCW3_0050_[Clostridium_perfringens] (100% coverage, 93.64% ID)	AEP95046.1_putative_transposase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3453	hypothetical protein	3549134	3549613	479	None/None	0.59		BAE79145.1_hypothetical_protein_[Clostridium_perfringens] (100% coverage, 97.5% ID)	AEP95019.1_nuclease_family_transposase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 96.88% ID)
	CP4_3454	chitinase B	3550620	3552419	1799	Carbohydrates/Chitin and N-acetylglucosamine utilization	0.38		AEP95045.1_glycosyl_hydrolase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 99.83% ID)	AEP95045.1_glycosyl_hydrolase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 99.83% ID)
	CP4_3455	chitin deacetylase	3552505	3554340	1835	Carbohydrates/Chitin and N-acetylglucosamine utilization	0.39		AEP95044.1_glycosyl_hydrolase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 99.84% ID)	AEP95044.1_glycosyl_hydrolase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 99.84% ID)
	CP4_3456	protein Tlet_1264	3554782	3555102	320	None/None	0.76		AEP95043.1_hypothetical_protein_pNet8_00067_[Conjugative_transfer_v	AEP95043.1_hypothetical_protein_pNet8_00067_[Conjugative_transfer_v
	CP4_3457	CAAX amino terminal protease family	3555378	3556232	854	None/None	0.41		ector_pNet8::catP] (100% coverage, 100% ID)	ector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3458	putative beta-toxin	3556453	3556743	290	None/None	0.32		AEP95042.1_CAAX_amino_terminal_protease_family_protein_[Conjugative	AEP95042.1_CAAX_amino_terminal_protease_family_protein_[Conjugative
	CP4_3459	putative beta-toxin	3556870	3557214	344	None/None	0.34		_transfer_vector_pNet8::catP] (100% coverage, 99.65% ID)	_transfer_vector_pNet8::catP] (100% coverage, 99.65% ID)
	CP4_3460	conserved hypothetical protein	3557874	3558050	176	None/None	0.54		AEP95041.1_pore-forming_toxin_Net8_[part]_[Conjugative_transfer_vector_p	AEP95041.1_pore-forming_toxin_Net8_[part]_[Conjugative_transfer_vector_p
	CP4_3461	conserved hypothetical protein	3558419	3558619	200	None/None	0.37		Net8::catP] (96.49% coverage, 99.09% ID)	Net8::catP] (96.49% coverage, 99.09% ID)
	CP4_3462	conserved hypothetical protein	3559076	3559678	602	None/None	0.66		AEP95039.1_hypothetical_protein_pNet8_00063_[Conjugative_transfer	AEP95039.1_hypothetical_protein_pNet8_00063_[Conjugative_transfer
	CP4_3464	resolvase/recombinase	3560522	3560635	113	None/None	0.59		_vector_pNet8::catP] (100% coverage, 98.28% ID)	_vector_pNet8::catP] (100% coverage, 98.28% ID)
	CP4_3465	resolvase/recombinase	3560669	3560887	218	None/None	0.48		AEP95038.1_hypothetical_protein_pNet8_00062_[Conjugative_transfer	AEP95038.1_hypothetical_protein_pNet8_00062_[Conjugative_transfer
	CP4_3466	membrane protein, putative	3561094	3563193	2099	None/None	0.58		_vector_pNet8::catP] (100% coverage, 98.48% ID)	_vector_pNet8::catP] (100% coverage, 98.48% ID)
	CP4_3468	F5/8 type C domain-containing protein	3563893	3568830	4937	None/None	0.62		AEP95037.1_hypothetical_protein_pNet8_00061_[Conjugative_transfer_v	AEP95037.1_hypothetical_protein_pNet8_00061_[Conjugative_transfer_v
	CP4_3469	diguanylate cyclase/phosphodiesterase domain 2	3569337	3570689	1352	Stress Response/Bacterial hemoglobins	0.45		ector_pNet8::catP] (100% coverage, 99% ID)	ector_pNet8::catP] (100% coverage, 99% ID)
	CP4_3470	sortase family protein	3570743	3571537	794	None/None Cell Wall and Capsule/Sortase Iron acquisition and metabolism/Heme, hemin uptake and utilization systems in Gram-positives	0.41		AEP94940.1_resolvase_[Clostridium_perfringens] (100% coverage, 100% ID)	AEP94940.1_resolvase_[Clostridium_perfringens] (100% coverage, 100% ID)
	CP4_3471	putative surface protein	3571648	3573678	2030	None/None Cell Wall and Capsule/Sortase	0.62		AEP95034.1_resolvase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 98.63% ID)	AEP95034.1_resolvase_[Conjugative_transfer_vector_pNet8::catP] (100% coverage, 98.63% ID)
	CP4_3472	peptidoglycan bound protein	3573723	3574820	1097	None/None	0.47		AEP95033.1_lysoyl-tRNA_synthetase_[Conjugative_transfer_vector_pNet8::catP ]	AEP95033.1_lysoyl-tRNA_synthetase_[Conjugative_transfer_vector_pNet8::catP ]
	CP4_3473	cell wall surface anchor family protein	3574931	3575449	518	None/None	0.53		(100% coverage, 99.86% ID)	(100% coverage, 99.86% ID)
	CP4_3474	signal peptidase I	3576462	3576596	134	Protein Metabolism/Signal peptidase	0.74		AEP95031.1_F5/8_type_C_domain-containing_protein_[Conjugative_transfer_vector_pNet8::ca tP] (98.24% coverage, 91.65% ID)	AEP95031.1_F5/8_type_C_domain-containing_protein_[Conjugative_transfer_vector_pNet8::ca tP] (98.24% coverage, 91.65% ID)
	CP4_3476	hypothetical protein	3577283	3577429	146	None/None	0.35		AEP95030.1_putative_diguanylate_cyclase_[Conjugative_transfer_vecto	AEP95030.1_putative_diguanylate_cyclase_[Conjugative_transfer vecto
	CP4_3477	swim zinc finger domain protein	3577548	3577712	164	None/None	0.73		r_pNet8::catP] (100% coverage, 100% ID)	r_pNet8::catP] (100% coverage, 100% ID)
	CP4_3478	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor	3578197	3579249	1052	None/None	0.38		AEP94952.1_hypothetical_protein_pBeta2_00062_[Clostridium_perfringens ns] (100% coverage, 99.42% ID)	AEP94952.1_hypothetical_protein_pBeta2_00062_[Clostridium_perfringens ns] (100% coverage, 99.42% ID)
VR-93	CP4_3522	putative phage terminase, large subunit	3604089	3605774	1685	Phages, Prophages, Transposable elements, Plasmids/Phage packaging machinery	0.15	Yes	AEP95024.1_hypothetical_protein_pNet8_00048_[Conjugative_transfer	AEP95024.1_hypothetical_protein_pNet8_00048_[Conjugative_transfer
VR-94	CP4_3559	conserved hypothetical protein	3629823	3630542	719	None/None	0.53		_vector_pNet8::catP] (100% coverage, 100% ID)	_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3560	conserved hypothetical protein	3630617	3630937	320	None/None	0.30		AEP95026.1_cell_wall_surface_protein_[Conjugative_transfer_vector_p	AEP95026.1_cell_wall_surface_protein_[Conjugative_transfer_vector_p
VR-95	CP4_3561	putative ATPase	3631535	3632413	878	None/None	0.89		Net8::catP] (100% coverage, 96.71% ID)	Net8::catP] (100% coverage, 96.71% ID)
	CP4_3562	immunoglobulin heavy chain variable region	3632416	3632709	293	None/None	0.57		AEP95025.1_hypothetical_protein_pNet8_00049_[Conjugative_transfer_v	AEP95025.1_hypothetical_protein_pNet8_00049_[Conjugative_transfer_v
	CP4_3563	conserved hypothetical protein	3632769	3633038	269	None/None	0.58		ector_pNet8::catP] (100% coverage, 98.26% ID)	ector_pNet8::catP] (100% coverage, 98.26% ID)
VR-96	CP4_3564	hypothetical protein	3633402	3633713	311	None/None	0.88		YP_002291138.1_putative_ATPase_[Clostridium_perfringens] (100% coverage, 100% ID)	YP_002291138.1_putative_ATPase_[Clostridium_perfringens] (100% coverage, 100% ID)
	CP4_3565	hypothetical protein	3635359	3635868	509	None/None	0.44		AEP95022.1_hypothetical_protein_pNet8_00046_[Conjugative_transfer	AEP95022.1_hypothetical_protein_pNet8_00046_[Conjugative_transfer
VR-97	CP4_3567	conserved hypothetical protein	3637457	3637909	452	None/None	0.61		_vector_pNet8::catP] (100% coverage, 100% ID)	_vector_pNet8::catP] (100% coverage, 100% ID)
	CP4_3568	hypothetical protein	3638371	3639297	926	None/None	0.47		AEP95014.1_putative_amidoligase_enzyme_[Conjugative_transfer_vector	AEP95014.1_putative_amidoligase_enzyme_[Conjugative_transfer_vector
	CP4_3569	resolvase/recombinase	3639501	3640142	641	None/None	0.57		pNet8::catP] (96.3% coverage, 92.31% ID)	pNet8::catP] (96.3% coverage, 92.31% ID)
	CP4_3570	conserved hypothetical protein	3640922	3641233	311	None/None	0.74		AEP95020.1_GDDEF_domain-containing_protein_[Conjugative_transfer_vector_pNet8::a tP] (100% coverage, 99.71% ID)	AEP95020.1_GDDEF_domain-containing_protein_[Conjugative_transfer_vector_pNet8::a tP] (100% coverage, 99.71% ID)
	CP4_3572	NADP-dependent 7-alpha-hydroxysteroid dehydrogenase	3643156	3643944	788	Fatty Acids, Lipids, and Isoprenoids/Fatty Acid Biosynthesis	0.39		AEP94941.1_hypothetical_protein_pBeta2_00059_[Clostridium_perfringens ns] (100% coverage, 100% ID)	AEP94941.1_hypothetical_protein_pBeta2_00059_[Clostridium_perfringens ns] (100% coverage, 100% ID)
VR-98	JGS4143-0023	phage integrase	24844	26043	1199	None/None	0.65	Yes	AEP94940.1_resolvase_[Clostridium_perfringens] (100% coverage, 98.12% ID)	AEP94940.1_resolvase_[Clostridium_perfringens] (100% coverage, 98.12% ID)
	JGS4143-0024	conserved hypothetical protein	28488	28661	173	None/None	0.48		AEP94942.1_hypothetical_protein_pBeta2_00052_[Clostridium_perfringens ns] (100% coverage, 98.06% ID)	AEP94942.1_hypothetical_protein_pBeta2_00052_[Clostridium_perfringens ns] (100% coverage, 98.06% ID)
	JGS4143-0025	phage protein	28799	29254	455	None/None	0.32	Yes	AEP94944.1_short_chain_dehydrogenase_[Clostridium_perfringens] (100% coverage, 99.62% ID)	AEP94944.1_short_chain_dehydrogenase_[Clostridium_perfringens] (100% coverage, 99.62% ID)
	JGS4143-0026	DNA-binding protein, putative	29268	30465	872	None/None	0.39		AEP94943.1_hypothetical_protein_pBeta2_00049_[Clostridium_perfringens ns] (100% coverage, 100% ID)	AEP94943.1_hypothetical_protein_pBeta2_00049_[Clostridium_perfringens ns] (100% coverage, 100% ID)
	JGS4143-0027	conserved domain protein	30307	30516	209	None/None	0.51		AEP94949.1_hypothetical_protein_pBeta2_00059_[Clostridium_perfringens ns] (100% coverage, 100% ID)	AEP94949.1_hypothetical_protein_pBeta2_00059_[Clostridium_perfringens ns] (100% coverage, 100% ID)
	JGS4143-0028	DNA binding protein, excisionase family,	30712	30936	224	None/None	0.53			
	JGS4143-0029	hypothetical protein	31090	32088	998	None/None	0.56			
	JGS4143-0030	replicative DNA helicase	32104	33405	1301	DNA Metabolism/DNA-replication	0.56	Yes		
	JGS4143-0031	hypothetical protein	33418	33537	119	None/None	0.63			
	JGS4143-0032	kinetochore protein Nuf2 (Cell division)	34063	34329	266	None/None	0.30			
	JGS4143-0033	hypothetical protein	34322	34465	143	None/None	0.69			
	JGS4143-0035	hypothetical protein	36525	36659	134	None/None	0.66			
	JGS4143-0036	hypothetical protein	36748	37260	512	None/None	0.42			
	JGS4143-0037	hypothetical protein	37605	38315	710	None/None	0.42			

Table S3. Variable genes identified among 63 poultry and non-poultry isolates.

Variable Region	Locus_tag	Product	Start	Stop	Size (bp)	Functional Category/Subcategory	Prevalence	phage/IS	Plasmid Hit	pNet8 Hit
	JGS4143-0038	RNA polymerase, sigma 32 subunit, RpoH	38315	38998	683	RNA Metabolism/Transcription initiation, bacterial sigma factors Cell Division and Cell Cycle/Macromolecular synthesis operon	0.39			
	JGS4143-0039	hypothetical protein	39034	39396	362	None/None	0.35			
	JGS4143-0040	conserved hypothetical protein	39443	39703	260	None/None	0.32			
	JGS4143-0041	conserved hypothetical protein	40069	40320	251	None/None	0.11			
	JGS4143-0042	protein of unknown function	40363	40851	488	None/None	0.29			
VR-99	JGS4143-0139	sensor histidine kinase	141936	142139	203	None/None	0.85			
	JGS4143-0141	hypothetical protein	143036	143221	185	None/None	0.86			
VR-100	JGS4143-0157	conserved hypothetical protein	159764	161580	1816	None/None	0.29			
	JGS4143-0158	hypothetical protein	161971	162726	755	None/None	0.61			
	JGS4143-0159	conserved hypothetical protein	162760	162921	161	None/None	0.76			
	JGS4143-0160	BR0 family, N- domain protein	163032	163607	575	None/None	0.58			
	JGS4143-0163	2-keto-3-deoxygluconate kinase	165851	166876	1025	Carbohydrates/D-Galacturonate and D-Glucuronate Utilization	0.56			
	JGS4143-0164	beta-glucuronidase (GUS)	166939	168738	1799	Carbohydrates/D-Galacturonate and D-Glucuronate Utilization	0.89			
	JGS4143-0165	probable transcriptional regulator	168881	169570	689	None/None	0.74			
	JGS4143-0167	khg/kdpg aldolase	170626	171234	608	Carbohydrates/D-Galacturonate and D-Glucuronate Utilization	0.64			
	JGS4143-0168	mannonate dehydratase	171325	172377	1052	Carbohydrates/D-Galacturonate and D-Glucuronate Utilization	0.59			
	JGS4143-0169	glucuronate isomerase	172406	173806	1400	Carbohydrates/D-Galacturonate and D-Glucuronate Utilization	0.55			
	JGS4143-0170	glucuronide permease	173927	175318	1391	Miscellaneous/COG3533	0.61			
	JGS4143-0171	beta-N-acetylglucosaminidase/beta-glucosidase	175382	177151	1769	Carbohydrates/N-Acetyl-Galactosamine and Galactosamine Utilization Carbohydrates/Chitin and N-acetylglucosamine utilization	0.58			
VR-101	JGS4143-0278	conserved hypothetical protein	302596	304461	1865	None/None	0.45			
	JGS4143-0280	conserved hypothetical protein	306563	307366	803	None/None	0.56			
	JGS4143-0281	conserved hypothetical protein	307356	308023	667	None/None	0.86			
VR-102	JGS4143-0283	conserved hypothetical protein	309213	309353	140	None/None	0.27			
	JGS4143-0284	conserved domain protein	309387	309596	209	None/None	0.32			
VR-103	JGS4143-0370	conserved hypothetical protein	401266	401637	371	None/None	0.71			
VR-104	JGS4143-0394	hypothetical protein	434926	435051	125	None/None	0.86			
	JGS4143-0395	prophage dna primase	435239	435460	221	None/None	0.12			
	JGS4143-0396	hypothetical protein	435910	436029	119	None/None	0.11			
	JGS4143-0397	hypothetical protein	436711	436899	188	None/None	0.36			
	JGS4143-0398	modification methylase EcoRI	437422	438450	1028	None/None	0.25			
	JGS4143-0400	hypothetical protein	439565	440437	872	None/None	0.29			
	JGS4143-0401	hypothetical protein	440430	440930	500	None/None	0.11			
	JGS4143-0403	hypothetical protein	441700	441855	155	None/None	0.20			
VR-105	JGS4143-0472	conserved hypothetical protein	517607	520567	2960	None/None	0.74	Yes		
	JGS4143-0473	conserved hypothetical protein	520882	521835	953	None/None	0.62			
	JGS4143-0474	hypothetical protein	521875	522023	148	None/None	0.78			
	JGS4143-0475	hypothetical protein	522170	523216	1046	None/None	0.50			
	JGS4143-0476	helix-turn-helix domain protein	523289	523978	689	None/None	0.26			
	JGS4143-0477	conserved hypothetical protein	524123	524425	302	None/None	0.30			
	JGS4143-0478	hypothetical protein	524443	525132	689	None/None	0.67			
	JGS4143-0480	conserved domain protein	525467	525676	209	None/None	0.58	Yes		
VR-106	JGS4143-0483	conserved hypothetical protein	527109	527327	218	None/None	0.65			
VR-107	JGS4143-0498	transposon, resolvase	540967	541467	500	None/None	0.72	Yes		
	JGS4143-0499	transposase	541568	541759	191	None/None	0.82	Yes		
	JGS4143-0500	hypothetical protein	541898	542266	368	None/None	0.39			
	JGS4143-0501	transposase, <i>OrfB</i> family	542319	542684	365	None/None	0.76	Yes		
VR-108	JGS4143-0507	4Fe-4S ferredoxin iron-sulfur binding domain	547750	548571	821	Nitrogen Metabolism/Nitrate and nitrite ammonification	0.29			
VR-109	JGS4143-0520	conserved hypothetical protein	561553	561708	155	None/None	0.84			
	JGS4143-0524	capsular polysaccharide biosynthesis protein	564062	565378	1316	Protein Metabolism/N-linked Glycosylation in Bacteria	0.58			
	JGS4143-0525	sugar transferases involved in	566164	566595	431	None/None	0.36			
	JGS4143-0526	dtidp-4 dehydroharnose 3,5-epimerase, putative	566621	567523	902	None/None	0.61			
	JGS4143-0527	capsular polysaccharide biosynthesis protein	567524	568714	1190	None/None	0.40			
	JGS4143-0528	polysaccharide biosynthesis protein CapD	568734	569780	1046	Protein Metabolism/N-linked Glycosylation in Bacteria	0.15			
	JGS4143-0529	NAD-dependent epimerase/dehydratase	569795	570919	1124	None/None	0.32			
	JGS4143-0530	UDP-N-acetylglucosamine 2-epimerase	570906	572030	1124	Cell Wall and Capsule/Sialic Acid Metabolism	0.18			
	JGS4143-0531	putative glycosyl transferase	572032	573219	1187	Cofactors, Vitamins, Prosthetic Groups, Pigments/Biotin biosynthesis	0.20			
	JGS4143-0532	putative transferase	573219	574334	1115	None/None	0.15			
	JGS4143-0534	glycosyl transferase, group 2 family protein	575461	576276	815	None/None	0.61			
	JGS4143-0535	flippase Wzx	576293	577738	1445	None/None	0.20			
VR-110	JGS4143-0536	udp-glucose 6-dehydrogenase (udp-glc)	577919	579085	1166	Cell Wall and Capsule/Streptococcal Hyaluronic Acid Capsule	0.42			
	JGS4143-0537	transcriptional regulator, <i>LytR</i> family	579160	579780	620	Regulation and Cell signaling/Cell envelope-associated <i>LytR</i> - <i>CpsA</i> - <i>Psr</i> transcriptional attenuators	0.64			
VR-111	JGS4143-0546	transcriptional regulator, <i>AraC</i> family	588172	589026	854	Carbohydrates/Fructooligosaccharides(FOS) and Raffinose Utilization	0.45			
VR-113	JGS4143-0593	conserved hypothetical protein	636367	637008	641	None/None	0.63			
VR-114	JGS4143-0613	cell wall binding repeat domain protein	659365	660237	872	Stress Response/Choline and Betaine Uptake and Betaine Biosynthesis	0.58			
VR-115	JGS4143-0727	conserved hypothetical protein	789160	789339	179	None/None	0.55			
	JGS4143-0728	voltage-gated chloride channel family protein	789381	790154	773	None/None	0.50			
	JGS4143-0729	voltage-gated chloride channel family protein	790196	790636	440	None/None	0.71			
VR-116	JGS4143-0804	conserved hypothetical protein	874496	874915	419	None/None	0.64			
VR-117	JGS4143-0810	hypothetical protein	881055	881792	737	None/None	0.61			
VR-118	JGS4143-0827	conserved hypothetical protein	897179	898132	953	None/None	0.89			
VR-119	JGS4143-0843	hypothetical protein	912475	912798	323	None/None	0.64			
VR-120	JGS4143-0907	<i>YhbE</i>	970000	970716	716	None/None	0.71			
	JGS4143-0908	<i>YhbF</i>	970768	971511	743	None/None	0.66			
	JGS4143-0909	<i>YhbD</i>	971496	972125	629	None/None	0.76			
VR-121	JGS4143-0922	phage protein	982919	984214	1295	None/None	0.58			
	JGS4143-0925	hypothetical protein	986785	986964	179	None/None	0.81			
	JGS4143-0926	VanZ like family	986992	987558	566	None/None	0.83			

Table S3. Variable genes identified among 63 poultry and non-poultry isolates.

Variable Region	Locus_tag	Product	Start	Stop	Size (bp)	Functional Category/Subcategory	Prevalence	phage/IS	Plasmid Hit	pNet8 Hit
	JGS4143-0927	hypothetical protein	987562	987987	425	None/None	0.59			
	JGS4143-0928	hypothetical protein	988221	988466	245	None/None	0.72			
	JGS4143-0929	hypothetical protein	988721	988858	137	None/None	0.54			
	JGS4143-0930	Fun2 family protein	989070	989593	623	None/None	0.81			
	JGS4143-0931	FunZ family protein	989699	990628	929	None/None	0.73			
VR-122	JGS4143-0934	two-component sensor kinase YesM, putative	993040	995730	1790	None/None	0.32			
	JGS4143-0936	ABC-type sugar transport system, periplasmic	997410	998678	1268	Carbohydrates/Chitin and N-acetylglucosamine utilization Miscellaneous/COG3533	0.73			
	JGS4143-0937	ABC transporter, permease protein	998768	999673	905	Carbohydrates/Chitin and N-acetylglucosamine utilization	0.35			
	JGS4143-0938	ABC transporter, permease protein	999689	1000564	875	Carbohydrates/Chitin and N-acetylglucosamine utilization	0.44			
	JGS4143-0939	glycosyl hydrolase, family 31	1000592	1002133	1541	Carbohydrates/Maltose and Maltodextrin Utilization	0.82			
	JGS4143-0940	alpha-N-acetylglucosaminidase family protein	1002157	1004256	2099	None/None	0.53			
VR-123	JGS4143-0949	glycosyl hydrolase, family 20, putative	1009130	1010149	1019	None/None	0.24			
	JGS4143-0950	glycosyl hydrolase, family 20	1010227	1013115	2888	None/None	0.52			
VR-124	JGS4143-0969	two-component sensor histidine kinase	1040291	1040991	680	None/None	0.89			
VR-125	JGS4143-1023	phosphorylase family protein	1089237	1090022	785	None/None	0.88			
VR-126	JGS4143-1062	RNA polymerase sigma-70 factor	1120388	1120930	542	RNA Metabolism/Transcription initiation, bacterial sigma factors	0.77			
	JGS4143-1063	hypothetical protein	1120932	1122263	1331	None/None	0.89			
VR-127	JGS4143-1246	HNH endonuclease domain protein	1276572	1276892	320	None/None	0.65	Yes		
	JGS4143-1247	phage Terminase Small Subunit	1277161	1277382	221	None/None	0.71			
	JGS4143-1248	putative phage terminase, large subunit	1277375	1279042	1667	None/None	0.81	Yes		
	JGS4143-1249	hypothetical protein	1279119	1279247	128	None/None	0.62			
	JGS4143-1250	conserved hypothetical protein	1279247	1279675	428	None/None	0.70	Yes		
	JGS4143-1251	portal protein	1279659	1280477	818	None/None	0.48	Yes		
	JGS4143-1252	phage prohead protease, HK97 family	1280578	1281054	476	None/None	0.69	Yes		
	JGS4143-1253	phage major capsid protein, HK97 family	1281104	1282207	1103	Phages, Prophages, Transposable elements, Plasmids/Phage capsid proteins	0.52	Yes		
	JGS4143-1254	conserved hypothetical protein	1282260	1282550	290	None/None	0.65			
	JGS4143-1255	phage head tail adaptor, putative	1282543	1283878	1335	None/None	0.44	Yes		
	JGS4143-1256	phage protein, HK97 gp10 family	1282879	1283238	359	None/None	0.82			
	JGS4143-1257	conserved hypothetical protein	1283241	1283600	359	None/None	0.75			
	JGS4143-1258	phage major tail protein, Phi13 family	1283621	1284238	617	None/None	0.12			
	JGS4143-1259	conserved hypothetical protein	1284260	1284601	341	None/None	0.80			
	JGS4143-1260	phage tail tape measure protein, family, core	1285225	1285473	248	None/None	0.71			
VR-128	JGS4143-1337	nucleotidyltransferase family protein	1343563	1343844	281	None/None	0.72			
VR-129	JGS4143-1380	hypothetical protein	1374445	1375617	1172	None/None	0.77			
VR-130	JGS4143-1385	endo-alpha-N-acetylgalactosaminidase	1381009	1381161	152	None/None	0.87			
VR-131	JGS4143-1408	hypothetical protein	1401591	1401797	206	None/None	0.59			
VR-132	JGS4143-1441	putative alpha-N-acetylgalactosaminidase	1436799	1438238	1439	None/None	0.59			
VR-133	JGS4143-1447	hypothetical protein	1441281	1441811	530	None/None	0.17			
	JGS4143-1448	type III restriction enzyme, res subunit	1441804	1444026	2222	None/None	0.58			
	JGS4143-1449	conserved hypothetical protein	1444185	1444406	221	None/None	0.25			
	JGS4143-1450	RNA polymerase sigma factor, sigma-70 family	1444809	1445402	593	None/None	0.40			
	JGS4143-1451	nucleoside triphosphatase, D5 family, putative	1445807	1448710	2903	None/None	0.30			
	JGS4143-1452	DNA-directed DNA polymerase	1448836	1450764	1928	DNA Metabolism/DNA Repair Base Excision DNA Metabolism/DNA-replication	0.26	Yes		
	JGS4143-1453	DNA-binding protein	1451590	1452129	539	None/None	0.14			
	JGS4143-1454	conserved hypothetical protein	1452369	1452725	356	None/None	0.15			
	JGS4143-1455	conserved hypothetical protein	1452930	1453418	488	None/None	0.76			
VR-134	JGS4143-1456	F5/8 type C domain containing protein	1453508	1456894	3386	None/None	0.60			
VR-135	JGS4143-1460	Flh family protein	1463424	1464611	1187	None/None	0.43			
VR-136	JGS4143-1482	NADH oxidase	1489168	1491090	1922	None/None	0.86			
	JGS4143-1483	hydrolases of the alpha/beta superfamily	1491106	1491867	761	None/None	0.38			
VR-137	JGS4143-1484	C4-dicarboxylate transport system	1492061	1493368	1307	Membrane Transport/TRAP Transporter collection	0.53			
	JGS4143-1486	C4-dicarboxylate transport system	1493929	1494936	1007	Membrane Transport/TRAP Transporter collection	0.81			
VR-138	JGS4143-1847	hypothetical protein	1832445	1833809	1364	None/None	0.64			
VR-139	JGS4143-2057	hypothetical protein	2025433	2025549	116	None/None	0.85			
VR-140	JGS4143-2323	ABC transporter, ATP-binding protein	2283841	2284533	692	None/None	0.89			
VR-141	JGS4143-2973	transporter, monovalent cation:proton	2955883	2957316	1433	None/None	0.59			
VR-142	pBCNF5603_uvIA	UvIA protein			0	None/None	0.85			
	pBCNF5603_uvIB	UvIB protein			0	None/None	0.88			
	pCPF4969_51	putative SpaC protein			0	None/None	0.78			
	pCPF5603_10	collagen adhesion protein			0	None/None	0.76			
	pCPF5603_68	putative TrnI16 ORF15 protein			0	None/None	0.63			
	pCPF5603_70	putative TrnI16 ORF16 protein			0	None/None	0.79			



**Table S4. Prevalence of chromosomally-encoded toxins and extracellular enzymes among 54 poultry isolates.**

<b>Toxin</b>	<b>Gene</b>	<b>Reference locus_tag</b>	<b>CP4 locus_tag</b>	<b>Prevalence</b>
Perfringolysin	<i>pfoA</i>	CPF_0156	CP4_0202	0.98
Sialidase/neuramindase	<i>nanJ</i>	CPF_0523	CP4_0614	0.98
Sialidase/neuramindase	<i>nanI</i>	CPF_0721	CP4_0806	0.98
Sialidase/neuramindase	<i>nanH</i>	CPF_0985	CP4_1082	0.98
Enterotoxin	<i>EntC</i>	CPF_0454	absent	n/a <sup>1</sup>
Enterotoxin	<i>EntD</i>	CPF_0587	CP4_0668-9	0.98
Enterotoxin	<i>EntD</i>	CPF_1439	CP4_1569-70	1.00
Enterotoxin	<i>EntA</i>	CPF_1467	CP4_1606	1.00
Collagenases (kappa-toxin)	<i>colA</i>	CPF_0166	CP4_0211-2	1.00
Hyaluronidase (mu-toxin)	<i>nagH</i>	CPF_0184	CP4_0231	1.00
Hyaluronidase (mu-toxin)	<i>nagE</i>	CPF_0071	CP4_0122	1.00
Hyaluronidase (mu-toxin)	<i>nagJ</i>	CPF_1442	CP4_1581	1.00
Hyaluronidase (mu-toxin)	<i>nagA</i>	CPF_2434	CP4_2582	1.00
Hyaluronidase (mu-toxin)	<i>nagL</i>	CPE_1523	CP4_1876	0.82
a-clostripain		CPF_0840	CP4_0923	1.00
hemolysin III		CPF_1725	CP4_1826	0.98
Hemolysin A		CPF_2072	CP4_2174	1.00
hemolysin III	<i>hlyIII</i>	CPF_2171	CP4_2271	1.00

n/a, not applicable.

**Table S5. PCR confirmation of CGH results.** The specificity and sensitivity of the array probes for 10 genes are shown based on PCR confirmation in 30 poultry isolates.

Locus_tag	True positives	True negatives	False positives	False negatives	Specificity	Sensitivity
CP4_0445	24	5	0	0	1.00	1.00
CP4_0448	24	5	0	0	1.00	1.00
CP4_0463	22	8	0	0	1.00	1.00
CP4_0468	22	8	0	0	1.00	1.00
CP4_0783	20	7	1	0	0.88	1.00
CP4_1608	20	9	0	0	1.00	1.00
CP4_2645	19	9	0	0	1.00	1.00
JGS4143-0169	12	16	1	0	0.94	1.00
JGS4143-0500	8	18	3	0	0.86	1.00
CP4_2821	30	0	0	0	1.00	1.00



**Table S6. Fisher's exact tests performed on variable genes.** Q-values represent p-values corrected for multiple-testing. Only q-values < 0.05 are shown.

Variable Region	Locus_tag	Product	<i>netB</i> +	<i>netB</i> +	<i>netB</i> +	<i>netB</i> -	<i>netB</i> -	<i>netB</i> -	<i>netB</i> + vs <i>netB</i> - q-value	Non-poultry	Non-poultry	Non-poultry	Poultry	Poultry	Poultry	Poultry vs Non-poultry	
			Absent	Present	Prevalence	Absent	Present	Prevalence		Absent	Present	prevalence	Absent	Present	prevalence	q-value	
VR-14	CP4_0688	cell wall binding repeat-containing protein/mannosyl glycoprotein endo-beta-N-acetylglucosamidase domain-containing protein	4	17	0.81	11	22	0.67			5	4	0.44	14	40	0.74	4.43E-02
	CP4_0689	cell wall binding repeat-containing protein/zinc carboxypeptidase family protein	6	15	0.71	9	24	0.73									
	CP4_0690	cell wall binding repeat-containing protein	5	16	0.76	14	19	0.58									
VR-15	CP4_0691	cell wall binding repeat-containing protein	1	20	0.95	5	27	0.84									
VR-16	CP4_0783	oxidoreductase, FAD/FMN-binding	3	18	0.86	15	17	0.53	2.12E-02	6	3	0.33	18	35	0.66	3.47E-02	
VR-17	CP4_0797	RNA polymerase ECF-type sigma factor	1	20	0.95	5	24	0.83									
VR-18	CP4_0831	conserved hypothetical protein	4	17	0.81	6	27	0.82		8	1	0.11	10	44	0.81	5.42E-05	
	CP4_0833	hypothetical protein	1	20	0.95	1	31	0.97		5	4	0.44	2	51	0.96	3.06E-04	
VR-19	CP4_0841	conserved hypothetical protein	7	14	0.67	20	13	0.39		8	1	0.11	27	27	0.50	1.55E-02	
VR-20	CP4_0850	conserved hypothetical protein	0	20	1.00	1	28	0.97		6	3	0.33	1	48	0.98	8.30E-06	
VR-21	CP4_0859	rubredoxin	0	21	1.00	6	27	0.82									
VR-22	CP4_0874	probable iron(III) dicitrate ABC transporter	0	21	1.00	11	22	0.67	4.30E-03								
	CP4_0875	iron compound ABC transporter, permease protein	0	21	1.00	12	21	0.64	2.17E-03								
	CP4_0876	ABC transport system permease protein	0	21	1.00	8	25	0.76	2.00E-02								
	CP4_0877	ferrichrome transport ATP-binding protein FhuC	0	21	1.00	10	23	0.70	5.25E-03								
VR-23	CP4_0896	conserved hypothetical protein	4	17	0.81	3	30	0.91									
VR-24	CP4_0919	sensory transduction protein BceR	2	17	0.89	4	22	0.85									
	CP4_0924	bacitracin export ATP-binding protein BceA	2	14	0.88	2	21	0.91									
	CP4_0927	stress responsive alpha-beta barrel domain-containing protein	3	18	0.86	6	27	0.82									
	CP4_0929	conserved hypothetical protein	1	14	0.93	3	21	0.88		3	6	0.67	4	36	0.90	4.25E-02	
VR-25	CP4_0947	conserved hypothetical protein	3	17	0.85	4	24	0.86									
	CP4_0950	conserved hypothetical protein	0	18	1.00	5	20	0.80									
VR-26	CP4_0963	resolvase domain-containing protein	0	21	1.00	6	26	0.81									
VR-27	CP4_1008	conserved hypothetical protein	0	20	1.00	7	23	0.77	3.64E-02	4	5	0.56	7	43	0.86	2.07E-02	
	CP4_1010	putative toxin-antitoxin system, toxin component	2	19	0.90	16	16	0.50	3.71E-03	8	1	0.11	18	35	0.66	1.59E-03	
VR-28	CP4_1036	putative phage terminase, large subunit	6	15	0.71	9	24	0.73		8	1	0.11	15	39	0.72	7.21E-04	
VR-29	CP4_1061	DNA adenine-specific methyltransferase	7	7	0.50	14	6	0.30									
VR-30	CP4_1069	probable autolytic lysozyme	1	20	0.95	9	24	0.73		6	3	0.33	10	44	0.81	3.58E-03	
	CP4_1071	conserved hypothetical protein	4	17	0.81	5	28	0.85		9	0	0.00	9	45	0.83	3.55E-06	
	CP4_1076	phosphorylase family protein	0	21	1.00	4	29	0.88		5	4	0.44	4	50	0.93	1.00E-03	
VR-31	CP4_1098	caax amino protease family protein	1	20	0.95	3	30	0.91		3	6	0.67	4	50	0.93	2.23E-02	
	CP4_1099	ProFAR isomerase associated superfamily	1	20	0.95	3	26	0.90		4	5	0.56	4	46	0.92	6.76E-03	
	CP4_1100	conserved hypothetical protein	1	20	0.95	1	32	0.97		6	3	0.33	2	52	0.96	2.17E-05	
VR-32	CP4_1106	conserved hypothetical protein	2	19	0.90	6	27	0.82		4	5	0.56	8	46	0.85	2.43E-02	
	CP4_1107	methionyl-tRNA formyltransferase	0	21	1.00	4	29	0.88		4	5	0.56	4	50	0.93	5.96E-03	
	CP4_1110	transcriptional regulator	0	21	1.00	1	28	0.97		5	4	0.44	1	49	0.98	1.34E-04	
	CP4_1114	conserved hypothetical protein	0	21	1.00	1	32	0.97		7	2	0.22	1	53	0.98	3.55E-06	
VR-33	CP4_1130	putative toxin-antitoxin system, toxin component	3	14	0.82	2	21	0.91		4	5	0.56	5	36	0.88	1.77E-02	
	CP4_1131	toxin-antitoxin system, antitoxin component, Xre family	0	21	1.00	7	23	0.77	3.64E-02	4	5	0.56	7	44	0.86	1.99E-02	
	CP4_1134	conserved hypothetical protein	2	19	0.90	4	28	0.88									
	CP4_1135	conserved hypothetical protein	4	17	0.81	1	32	0.97		3	6	0.67	5	49	0.91	3.50E-02	
	CP4_1136	acetyltransferase	6	15	0.71	3	30	0.91									
	CP4_1137	conserved hypothetical protein	1	20	0.95	7	25	0.78									
VR-34	CP4_1150	lipoprotein, putative	1	20	0.95	7	25	0.78		5	4	0.44	8	45	0.85	7.01E-03	
	CP4_1153	conserved hypothetical protein	4	17	0.81	0	33	1.00	2.19E-02	4	5	0.56	4	50	0.93	5.96E-03	
	CP4_1154	conserved hypothetical protein	0	20	1.00	6	22	0.79	3.65E-02	5	4	0.44	6	42	0.88	5.00E-03	
	CP4_1158	conserved hypothetical protein	1	20	0.95	10	18	0.64	1.92E-02								
	CP4_1159	conserved hypothetical protein	4	17	0.81	1	32	0.97									
	CP4_1165	UBA/TS-N domain-containing protein	0	21	1.00	6	27	0.82		3	6	0.67	6	48	0.89	4.43E-02	
	CP4_1167	sensor histidine kinase	0	21	1.00	4	29	0.88		3	6	0.67	4	50	0.93	2.23E-02	
CP4_1169	acetyltransferase	1	20	0.95	6	25	0.81		4	5	0.56	7	45	0.87	1.77E-02		

**Table S6. Fisher's exact tests performed on variable genes.** Q-values represent p-values corrected for multiple-testing. Only q-values < 0.05 are shown.

Variable Region	Locus_tag	Product	netB +	netB +	netB +	netB -	netB -	netB -	netB + vs netB -	Non-poultry	Non-poultry	Non-poultry	Poultry	Poultry	Poultry	Poultry vs Non-poultry
			Absent	Present	Prevalence	Absent	Present	Prevalence	q-value	Absent	Present	prevalence	Absent	Present	prevalence	q-value
VR-35	CP4_1181	discoidin domain-containing protein	8	12	0.60	18	12	0.40								
	CP4_1184	[Fe] hydrogenase	0	21	1.00	6	27	0.82								
VR-36	CP4_1238	collagen adhesion protein	0	21	1.00	1	32	0.97		7	2	0.22	1	53	0.98	3.55E-06
VR-37	CP4_1251	hydroxylamine reductase	0	21	1.00	15	17	0.53	1.28E-04	6	3	0.33	15	38	0.72	1.99E-02
VR-38	CP4_1323	lipoprotein-releasing system ATP-binding protein LoID	0	21	1.00	4	25	0.86		4	5	0.56	4	46	0.92	6.76E-03
	CP4_1324	conserved hypothetical protein	0	20	1.00	5	26	0.84		4	5	0.56	5	46	0.90	9.61E-03
	CP4_1325	putative permease	2	19	0.90	13	20	0.61	3.45E-02							
	CP4_1329	nudix family hydrolase	1	19	0.95	7	25	0.78								
VR-39	CP4_1336	histidine kinase KdpD	0	17	1.00	3	19	0.86								
	CP4_1342	conserved hypothetical protein	2	13	0.87	3	18	0.86								
VR-40	CP4_1388	ggdef/eal domain-containing protein	1	19	0.95	4	23	0.85								
VR-41	CP4_1461	AP endonuclease	1	18	0.95	1	27	0.96		5	4	0.44	2	46	0.96	4.08E-04
VR-42	CP4_1477	lipoprotein, putative	3	18	0.86	5	25	0.83								
VR-43	CP4_1594	chromosome segregation ATPase	4	9	0.69	5	8	0.62		8	1	0.11	9	17	0.65	3.66E-03
VR-44	CP4_1608	conserved hypothetical protein	1	20	0.95	15	18	0.55	2.23E-03	3	6	0.67	6	48	0.89	4.43E-02
VR-45	CP4_1619	lysine-N-methylase	3	17	0.85	4	23	0.85		5	4	0.44	7	39	0.85	7.16E-03
VR-46	CP4_1641	xanthine phosphoribosyltransferase	1	12	0.92	4	17	0.81								
VR-47	CP4_1710	conserved hypothetical protein	0	21	1.00	5	28	0.85								
VR-48	CP4_1730	transposon, resolvase	2	19	0.90	14	19	0.58	1.68E-02							
VR-49	CP4_1860	BNR/Asp-box repeat-containing protein	5	16	0.76	8	25	0.76								
VR-50	CP4_1876	O-GlcNAcase NagJ (CPE_1523)	2	19	0.90	4	29	0.88		6	3	0.33	6	48	0.89	5.86E-04
VR-51	CP4_1926	lipoprotein, putative	3	15	0.83	4	20	0.83								
VR-52	CP4_1976	hypothetical protein	1	20	0.95	11	22	0.67	2.11E-02	6	3	0.33	12	42	0.78	6.31E-03
VR-53	CP4_2009	conserved hypothetical protein	4	17	0.81	3	28	0.90								
VR-54	CP4_2074	chromosome segregation protein SMC	3	17	0.85	4	25	0.86								
VR-55	CP4_2126	penicillin binding protein transpeptidase domain-containing protein	3	17	0.85	4	28	0.88								
VR-56	CP4_2168	conserved hypothetical protein	2	12	0.86	3	20	0.87								
VR-57	CP4_2195	sensor histidine kinase	0	12	1.00	0	20	1.00		5	2	0.29	0	32	1.00	2.17E-05
	CP4_2196	conserved hypothetical protein	2	19	0.90	11	22	0.67								
VR-58	CP4_2309	flavohepotoxin	0	21	1.00	5	23	0.82								
VR-59	CP4_2359	hypothetical protein	8	12	0.60	19	6	0.24	3.45E-02	9	0	0.00	27	18	0.40	9.27E-03
VR-60	CP4_2372	Gp10 protein	12	9	0.43	21	11	0.34		9	0	0.00	33	20	0.38	1.86E-02
	CP4_2376	phage major capsid protein, HK97 family	13	8	0.38	23	9	0.28								
	CP4_2377	phage prohead protease, HK97 family	14	7	0.33	27	6	0.18								
	CP4_2379	phage portal protein, HK97 family	10	8	0.44	16	9	0.36								
	CP4_2382	Gp50 protein	13	8	0.38	27	6	0.18								
VR-61	CP4_2398	integrase family protein	12	9	0.43	25	7	0.22								
VR-62	CP4_2429	VanZ family membrane protein	3	18	0.86	9	24	0.73		9	0	0.00	12	42	0.78	8.30E-06
	CP4_2431	conserved hypothetical protein	9	12	0.57	18	15	0.45		9	0	0.00	27	27	0.50	3.90E-03
	CP4_2432	membrane protein, putative	6	15	0.71	5	28	0.85		9	0	0.00	11	43	0.80	3.55E-06
	CP4_2433	ABC transporter, ATP-binding protein	7	11	0.61	12	15	0.56		9	0	0.00	19	26	0.58	1.10E-03
VR-63	CP4_2512	conserved hypothetical protein	2	19	0.90	3	30	0.91		5	4	0.44	5	49	0.91	1.89E-03
VR-64	CP4_2645	sporulation initiation inhibitor protein Soj	4	17	0.81	18	15	0.45	1.43E-02							
VR-65	CP4_2697	conserved hypothetical protein	0	21	1.00	13	19	0.59	1.05E-03	7	2	0.22	13	40	0.75	1.89E-03
	CP4_2699	conserved hypothetical protein	0	21	1.00	13	20	0.61	1.26E-03							
	CP4_2700	conserved hypothetical protein	0	20	1.00	7	22	0.76	3.59E-02							
VR-66	CP4_2736	type I restriction-modification system, M subunit	9	12	0.57	18	15	0.45		8	1	0.11	26	28	0.52	1.35E-02
VR-67	CP4_2932	DNA-binding protein HU	1	17	0.94	3	26	0.90		3	6	0.67	4	44	0.92	3.06E-02
VR-68	CP4_3079	AraC family transcriptional regulator	1	20	0.95	11	17	0.61	8.25E-03	7	2	0.22	12	37	0.76	2.17E-03
	CP4_3080	tetracycline resistance protein TetP	1	20	0.95	7	26	0.79		7	2	0.22	8	46	0.85	1.99E-04
	CP4_3081	tetracycline resistance protein	0	21	1.00	1	32	0.97		6	3	0.33	1	53	0.98	3.55E-06
VR-69	CP4_3109	conserved hypothetical protein (pCP13_CPC36)	7	14	0.67	17	12	0.41		8	1	0.11	25	25	0.50	2.61E-02
VR-70	CP4_3124	conserved hypothetical protein (pCW3_0007)	1	20	0.95	11	22	0.67	2.11E-02	9	0	0.00	12	42	0.78	8.30E-06
	CP4_3125	hypothetical protein	0	21	1.00	12	21	0.64	2.17E-03	6	3	0.33	12	42	0.78	6.31E-03
	CP4_3127	conserved hypothetical protein (pCW3_0008)	0	21	1.00	13	20	0.61	1.26E-03							
VR-71	CP4_3126	LexA repressor (pCW3_0015)	0	21	1.00	14	18	0.56	3.71E-04							

**Table S6. Fisher's exact tests performed on variable genes.** Q-values represent p-values corrected for multiple-testing. Only q-values < 0.05 are shown.

Variable Region	Locus_tag	Product	netB +	netB +	netB +	netB -	netB -	netB -	netB + vs netB -	Non-poultry	Non-poultry	Non-poultry	Poultry	Poultry	Poultry	Poultry vs Non-poultry
			Absent	Present	Prevalence	Absent	Present	Prevalence	q-value	Absent	Present	prevalence	Absent	Present	prevalence	q-value
VR-72	CP4_3128	putative plasmid partitioning protein (pCW3_0013)	1	19	0.95	11	20	0.65	1.97E-02	6	3	0.33	12	39	0.76	7.16E-03
	CP4_3129	conserved hypothetical protein (pCW3_0012)	3	10	0.77	6	11	0.65		6	3	0.33	9	21	0.70	2.61E-02
VR-73	CP4_3132	toxin A	1	19	0.95	2	28	0.93		7	2	0.22	3	47	0.94	8.30E-06
	CP4_3133	bacteriocin-related protein	9	12	0.57	12	19	0.61		7	2	0.22	21	31	0.60	2.95E-02
	CP4_3134	UviA protein	7	5	0.42	8	4	0.33								
	CP4_3136	transposase for insertion sequence element isrm3	9	3	0.25	14	1	0.07								
VR-74	CP4_3138	putative ATPase of HSP70 class (pNetB_00004)	0	21	1.00	4	29	0.88		5	4	0.44	4	50	0.93	1.00E-03
	CP4_3139	conserved hypothetical protein (pNetB_00003)	1	20	0.95	22	9	0.29	8.70E-06							
VR-75	CP4_3153	thymidine kinase	4	10	0.71	11	14	0.56		9	0	0.00	15	24	0.62	8.91E-04
VR-76	CP4_3216	conserved hypothetical protein	3	18	0.86	1	32	0.97		9	0	0.00	4	50	0.93	3.55E-06
VR-77	CP4_3229	conserved hypothetical protein	8	13	0.62	15	18	0.55		9	0	0.00	23	31	0.57	1.17E-03
VR-78	CP4_3246	ISCpe2, transposase OrfB	8	1	0.11	10	6	0.38								
VR-79	CP4_3270	conserved hypothetical protein	0	21	1.00	0	33	1.00		9	0	0.00	0	54	1.00	3.55E-06
	CP4_3271	putative transcriptional regulator	14	7	0.33	20	13	0.39		9	0	0.00	34	19	0.36	1.77E-02
VR-80	CP4_3286	conserved hypothetical protein	8	5	0.38	13	7	0.35		9	0	0.00	21	12	0.36	1.66E-02
	CP4_3340	plectovirus Spv1-c74 orf 1 and c-terminal truncated protein	7	8	0.53	9	8	0.47		9	0	0.00	16	16	0.50	3.63E-03
VR-82	CP4_3348	collagen adhesion protein	8	4	0.33	10	7	0.41								
VR-83	CP4_3359	conserved hypothetical protein	4	17	0.81	22	9	0.29	9.46E-04							
	CP4_3360	collagen adhesin (partial)	2	19	0.90	9	24	0.73		5	4	0.44	11	43	0.80	1.66E-02
VR-84	CP4_3361	collagen adhesin (partial)	8	13	0.62	23	10	0.30	3.17E-02							
VR-85	CP4_3398	HNH endonuclease domain protein	5	10	0.67	6	9	0.60		9	0	0.00	11	19	0.63	7.42E-04
	CP4_3403	phage prohead protease, HK97 family	3	17	0.85	5	24	0.83		8	1	0.11	8	42	0.84	4.04E-05
	CP4_3404	phage major capsid protein, HK97 family	8	4	0.33	10	4	0.29		9	0	0.00	18	8	0.31	3.50E-02
	CP4_3406	phage protein, HK97 gp10 family	3	18	0.86	7	26	0.79		9	0	0.00	10	44	0.81	3.55E-06
	CP4_3407	conserved hypothetical protein	7	14	0.67	5	25	0.83		9	0	0.00	12	39	0.76	8.30E-06
	CP4_3408	prophage LambdaSa04, Phi13 family major tail protein	6	15	0.71	12	20	0.63		9	0	0.00	18	35	0.66	1.60E-04
	CP4_3411	family phage tail tape measure protein	8	12	0.60	14	15	0.52		9	0	0.00	22	27	0.55	1.30E-03
VR-86	CP4_3421	FtsK/Spol	3	18	0.86	22	10	0.31	2.56E-04	8	1	0.11	25	28	0.53	1.28E-02
VR-87	CP4_3422	integrase/recombinase	1	20	0.95	2	28	0.93		7	2	0.22	3	48	0.94	8.30E-06
	CP4_3426	hypothetical protein	13	7	0.35	18	5	0.22		9	0	0.00	31	12	0.28	3.96E-02
VR-88	CP4_3431	LexA repressor	0	21	1.00	22	7	0.24	8.70E-06	8	1	0.11	22	28	0.56	1.17E-02
VR-89	CP4_3432	transporter, major facilitator family	7	14	0.67	27	5	0.16	6.43E-04							
	CP4_3433	putative heme biosynthesis protein	9	10	0.53	27	3	0.10	2.80E-03							
	CP4_3434	putative radical SAM domain-containing protein	3	18	0.86	20	13	0.39	2.04E-03	8	1	0.11	23	31	0.57	6.40E-03
	CP4_3435	conserved hypothetical protein	6	14	0.70	23	3	0.12	9.78E-05							
VR-90	CP4_3436	conserved hypothetical protein	3	11	0.79	15	4	0.21	2.04E-03							
	CP4_3437	conserved hypothetical protein	0	21	1.00	19	13	0.41	8.70E-06							
	CP4_3438	putative ATPase	0	21	1.00	13	20	0.61	1.26E-03	6	3	0.33	13	41	0.76	8.06E-03
VR-91	CP4_3439	transcriptional regulator	0	21	1.00	7	26	0.79	4.04E-02	5	4	0.44	7	47	0.87	5.26E-03
	CP4_3441	beta2 toxin	1	10	0.91	6	7	0.54		6	3	0.33	7	17	0.71	4.25E-02
VR-92	CP4_3442	transcriptional regulator, MarR family	1	12	0.92	12	2	0.14	9.78E-05	9	0	0.00	13	14	0.52	3.00E-03
	CP4_3443	beta-lactamase domain-containing protein	0	21	1.00	24	9	0.27	8.70E-06	9	0	0.00	25	29	0.54	1.54E-03
	CP4_3444	M protein trans-acting positive regulator (MGA)	1	19	0.95	29	2	0.06	8.70E-06	9	0	0.00	31	20	0.39	9.63E-03
	CP4_3445	putative radical SAM domain-containing protein	1	15	0.94	19	0	0.00	8.70E-06	9	0	0.00	20	14	0.41	8.23E-03
	CP4_3446	putative internalin	5	15	0.75	25	1	0.04	8.70E-06	9	0	0.00	30	15	0.33	1.90E-02
	CP4_3447	hypothetical protein	2	19	0.90	28	3	0.10	8.70E-06	9	0	0.00	31	21	0.40	9.27E-03
	CP4_3448	hypothetical protein	0	18	1.00	18	5	0.22	8.70E-06	9	0	0.00	18	23	0.56	1.25E-03
	CP4_3449	necrotic enteritis toxin B	0	21	1.00	28	5	0.15	8.70E-06	9	0	0.00	29	25	0.46	4.71E-03
	CP4_3450	ricin-type beta-trefoil domain protein	0	21	1.00	11	22	0.67	4.30E-03	9	0	0.00	11	43	0.80	3.55E-06
	CP4_3451	transposase for transposon	0	21	1.00	24	9	0.27	8.70E-06							
	CP4_3452	hypothetical protein	0	21	1.00	19	14	0.42	8.70E-06							
	CP4_3453	hypothetical protein	0	21	1.00	23	10	0.30	8.70E-06							
	CP4_3454	chitinase B	1	20	0.95	30	3	0.09	8.70E-06	9	0	0.00	32	22	0.41	9.15E-03

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Variable Region	Locus_tag	Product	<i>netB</i> +		<i>netB</i> -		<i>netB</i> + vs <i>netB</i> - q-value	Non-poultry		Poultry		Poultry vs Non-poultry				
			Absent	Present	Prevalence	Absent		Present	Prevalence	Absent	Present	prevalence	q-value			
	CP4_3455	chitodextrinase	0	21	1.00	29	4	0.12	8.70E-06	9	0	0.00	30	24	0.44	5.96E-03
	CP4_3456	protein Tlet_1264	0	21	1.00	7	26	0.79	4.04E-02	9	0	0.00	7	47	0.87	3.55E-06
	CP4_3457	CAAX amino terminal protease family	1	20	0.95	28	5	0.15	8.70E-06	9	0	0.00	30	24	0.44	5.96E-03
	CP4_3458	putative beta-toxin	2	19	0.90	32	1	0.03	8.70E-06	9	0	0.00	35	19	0.35	1.83E-02
	CP4_3459	putative beta-toxin	2	19	0.90	31	2	0.06	8.70E-06	9	0	0.00	34	20	0.37	1.79E-02
	CP4_3460	conserved hypothetical protein	0	21	1.00	21	12	0.36	8.70E-06	9	0	0.00	21	33	0.61	5.23E-04
	CP4_3461	conserved hypothetical protein	0	21	1.00	28	2	0.07	8.70E-06	9	0	0.00	29	22	0.43	8.23E-03
	CP4_3462	conserved hypothetical protein	0	21	1.00	12	21	0.64	2.17E-03	9	0	0.00	13	41	0.76	1.52E-05
	CP4_3464	resolvase/recombinase	0	21	1.00	20	13	0.39	8.70E-06	7	2	0.22	20	34	0.63	1.48E-02
	CP4_3465	resolvase/recombinase	2	19	0.90	24	9	0.27	8.70E-06	8	1	0.11	26	28	0.52	1.35E-02
	CP4_3466	membrane protein, putative	0	21	1.00	18	15	0.45	2.74E-05	9	0	0.00	19	35	0.65	1.99E-04
	CP4_3468	F5/8 type C domain-containing protein	1	20	0.95	13	18	0.58	4.30E-03	9	0	0.00	15	37	0.71	4.14E-05
	CP4_3469	diguanylate cyclase/phosphodiesterase domain 2	0	21	1.00	24	8	0.25	8.70E-06	9	0	0.00	25	28	0.53	1.59E-03
	CP4_3470	sortase family protein	3	18	0.86	26	6	0.19	8.70E-06							
	CP4_3471	putative surface protein	0	21	1.00	16	17	0.52	2.56E-04	9	0	0.00	16	38	0.70	5.42E-05
	CP4_3472	peptidoglycan bound protein	3	18	0.86	24	9	0.27	8.11E-05	8	1	0.11	27	27	0.50	1.55E-02
	CP4_3473	cell wall surface anchor family protein	0	21	1.00	22	11	0.33	8.70E-06	9	0	0.00	22	32	0.59	5.86E-04
	CP4_3474	signal peptidase I	0	21	1.00	14	19	0.58	6.43E-04							
	CP4_3476	hypothetical protein	1	20	0.95	28	2	0.07	8.70E-06	9	0	0.00	30	21	0.41	8.70E-03
	CP4_3477	swim zinc finger domain protein	0	21	1.00	14	19	0.58	6.43E-04							
	CP4_3478	diguanylate cyclase/phosphodiesterase with PAS/PAC sensor	0	21	1.00	29	4	0.12	8.70E-06	9	0	0.00	30	24	0.44	5.96E-03
VR-93	CP4_3522	putative phage terminase, large subunit	13	1	0.07	12	4	0.25								
VR-94	CP4_3559	conserved hypothetical protein	6	15	0.71	19	14	0.42								
	CP4_3560	conserved hypothetical protein	9	10	0.53	22	1	0.04	1.26E-03							
VR-95	CP4_3561	putative ATPase	0	21	1.00	0	33	1.00		7	2	0.22	0	54	1.00	3.55E-06
	CP4_3562	immunoglobulin heavy chain variable region	1	15	0.94	13	11	0.46	3.00E-03	7	2	0.22	14	26	0.65	1.27E-02
	CP4_3563	conserved hypothetical protein	2	19	0.90	21	11	0.34	8.11E-05							
VR-96	CP4_3564	hypothetical protein	0	21	1.00	0	33	1.00		8	1	0.11	0	54	1.00	3.55E-06
	CP4_3565	hypothetical protein	5	16	0.76	20	8	0.29	1.94E-03	8	1	0.11	25	24	0.49	2.61E-02
VR-97	CP4_3567	conserved hypothetical protein	4	17	0.81	18	15	0.45	1.43E-02							
	CP4_3568	hypothetical protein	2	19	0.90	24	9	0.27	8.70E-06	9	0	0.00	26	28	0.52	1.80E-03
	CP4_3569	resolvase/recombinase	2	14	0.88	13	10	0.43	8.98E-03							
	CP4_3570	conserved hypothetical protein	0	21	1.00	11	22	0.67	4.30E-03	6	3	0.33	11	43	0.80	4.86E-03
	CP4_3572	NADP-dependent 7-alpha-hydroxysteroid dehydrogenase	4	17	0.81	26	7	0.21	7.44E-05	9	0	0.00	25	28	0.53	1.59E-03
VR-98	JGS4143-0023	phage integrase	6	15	0.71	9	24	0.73		7	2	0.22	14	40	0.74	3.00E-03
	JGS4143-0024	conserved hypothetical protein	9	12	0.57	15	18	0.55		9	0	0.00	25	29	0.54	1.54E-03
	JGS4143-0025	phage protein	12	9	0.43	23	10	0.30								
	JGS4143-0026	DNA-binding protein, putative	9	11	0.55	15	11	0.42		9	0	0.00	24	22	0.48	4.06E-03
	JGS4143-0027	conserved domain protein	7	14	0.67	16	15	0.48								
	JGS4143-0028	DNA binding protein, excisionase family,	7	14	0.67	15	18	0.55		7	2	0.22	23	31	0.57	3.34E-02
	JGS4143-0029	hypothetical protein	8	13	0.62	13	18	0.58								
	JGS4143-0030	replicative DNA helicase	9	12	0.57	11	22	0.67		7	2	0.22	20	34	0.63	1.48E-02
	JGS4143-0031	hypothetical protein	6	15	0.71	11	20	0.65								
	JGS4143-0032	kinetochore protein Nuf2 (Cell division	12	9	0.43	22	11	0.33		9	0	0.00	34	20	0.37	1.79E-02
	JGS4143-0033	hypothetical protein	7	14	0.67	8	22	0.73								
	JGS4143-0035	hypothetical protein	6	15	0.71	8	24	0.75		8	1	0.11	13	40	0.75	3.06E-04
	JGS4143-0036	hypothetical protein	11	10	0.48	17	16	0.48								
	JGS4143-0037	hypothetical protein	11	10	0.48	18	15	0.45								
	JGS4143-0038	RNA polymerase, sigma 32 subunit, RpoH	11	10	0.48	19	11	0.37								
	JGS4143-0039	hypothetical protein	14	7	0.33	19	14	0.42								
	JGS4143-0040	conserved hypothetical protein	12	9	0.43	25	8	0.24								
	JGS4143-0041	conserved hypothetical protein	16	5	0.24	31	2	0.06								
	JGS4143-0042	protein of unknown function	13	8	0.38	23	10	0.30		9	0	0.00	36	18	0.33	1.99E-02
VR-99	JGS4143-0139	sensor histidine kinase	0	21	1.00	1	32	0.97		9	0	0.00	1	53	0.98	3.55E-06
	JGS4143-0141	hypothetical protein	0	21	1.00	1	32	0.97		8	1	0.11	1	53	0.98	3.55E-06
VR-100	JGS4143-0157	conserved hypothetical protein	12	9	0.43	24	9	0.27		9	0	0.00	36	18	0.33	1.99E-02
	JGS4143-0158	hypothetical protein	8	13	0.62	9	22	0.71		8	1	0.11	17	35	0.67	1.35E-03

**Table S6. Fisher's exact tests performed on variable genes.** Q-values represent p-values corrected for multiple-testing. Only q-values < 0.05 are shown.

Variable Region	Locus_tag	Product	netB +			netB -			netB + vs netB - q-value	Non-poultry		Poultry		Poultry vs Non-poultry		
			Absent	Present	Prevalence	Absent	Present	Prevalence		Absent	Present	prevalence	Absent	Present	prevalence	q-value
	JGS4143-0159	conserved hypothetical protein	4	12	0.75	4	20	0.83		4	4	0.50	7	33	0.83	2.95E-02
	JGS4143-0160	BRO family, N- domain protein	9	12	0.57	13	19	0.59								
	JGS4143-0163	2-keto-3-deoxygluconate kinase	11	10	0.48	13	20	0.61								
	JGS4143-0164	beta-glucuronidase (GUS)	1	20	0.95	3	30	0.91		3	6	0.67	4	50	0.93	2.23E-02
	JGS4143-0165	probable transcriptional regulator	4	16	0.80	8	23	0.74								
	JGS4143-0167	khg/kdpg aldolase	8	13	0.62	9	19	0.68								
	JGS4143-0168	mannonate dehydratase	9	12	0.57	13	20	0.61								
	JGS4143-0169	glucuronate isomerase	11	10	0.48	14	19	0.58								
	JGS4143-0170	glucuronide permease	9	12	0.57	12	21	0.64								
	JGS4143-0171	beta-N-acetylglucosaminidase/beta-glucosidase	9	12	0.57	14	19	0.58								
VR-101	JGS4143-0278	conserved hypothetical protein	10	11	0.52	14	15	0.52		9	0	0.00	23	27	0.54	1.45E-03
	JGS4143-0280	conserved hypothetical protein	7	14	0.67	12	21	0.64		9	0	0.00	19	35	0.65	1.99E-04
	JGS4143-0281	conserved hypothetical protein	0	21	1.00	0	33	1.00		9	0	0.00	0	54	1.00	3.55E-06
VR-102	JGS4143-0283	conserved hypothetical protein	17	4	0.19	22	11	0.33								
	JGS4143-0284	conserved domain protein	13	8	0.38	21	9	0.30								
VR-103	JGS4143-0370	conserved hypothetical protein	0	21	1.00	14	19	0.58	6.43E-04	5	4	0.44	14	40	0.74	4.43E-02
VR-104	JGS4143-0394	hypothetical protein	0	21	1.00	0	33	1.00		9	0	0.00	0	54	1.00	3.55E-06
	JGS4143-0395	prophage dna primase	17	4	0.19	30	3	0.09								
	JGS4143-0396	hypothetical protein	17	4	0.19	30	3	0.09								
	JGS4143-0397	hypothetical protein	14	7	0.33	23	10	0.30		9	0	0.00	37	17	0.31	3.99E-02
	JGS4143-0398	modification methylase EcoRI	16	5	0.24	22	11	0.33		9	0	0.00	38	16	0.30	3.94E-02
	JGS4143-0400	hypothetical protein	12	9	0.43	25	8	0.24		9	0	0.00	38	16	0.30	3.94E-02
	JGS4143-0401	hypothetical protein	17	4	0.19	30	3	0.09								
	JGS4143-0403	hypothetical protein	14	7	0.33	27	6	0.18								
VR-105	JGS4143-0472	conserved hypothetical protein	1	13	0.93	3	20	0.77		8	1	0.11	4	33	0.89	8.30E-06
	JGS4143-0473	conserved hypothetical protein	2	19	0.90	13	18	0.58	1.63E-02	9	0	0.00	15	37	0.71	4.14E-05
	JGS4143-0474	hypothetical protein	0	20	1.00	5	27	0.84		9	0	0.00	5	47	0.90	3.55E-06
	JGS4143-0475	hypothetical protein	4	17	0.81	20	13	0.39	5.40E-03	9	0	0.00	24	30	0.56	1.29E-03
	JGS4143-0476	helix-turn-helix domain protein	12	8	0.40	23	7	0.23								
	JGS4143-0477	conserved hypothetical protein	11	8	0.42	20	6	0.23								
	JGS4143-0478	hypothetical protein	0	20	1.00	12	19	0.61	2.04E-03	9	0	0.00	12	39	0.76	8.30E-06
	JGS4143-0480	conserved domain protein	7	14	0.67	13	20	0.61		8	1	0.11	19	35	0.65	2.09E-03
VR-106	JGS4143-0483	conserved hypothetical protein	7	14	0.67	10	23	0.70								
VR-107	JGS4143-0498	transposon, resolvase	2	15	0.88	6	20	0.77		7	2	0.22	8	36	0.82	7.21E-04
	JGS4143-0499	transposase	0	13	1.00	2	20	0.91		6	3	0.33	2	34	0.94	1.71E-04
	JGS4143-0500	hypothetical protein	11	10	0.48	20	13	0.39								
	JGS4143-0501	transposase, OrfB family	4	16	0.80	4	24	0.86		6	3	0.33	8	40	0.83	2.28E-03
VR-108	JGS4143-0507	4Fe-4S ferredoxin iron-sulfur binding domain	18	3	0.14	20	13	0.39								
VR-109	JGS4143-0520	conserved hypothetical protein	4	17	0.81	2	29	0.94		4	5	0.56	5	47	0.90	9.15E-03
	JGS4143-0524	capsular polysaccharide biosynthesis protein	6	13	0.68	9	20	0.69		9	0	0.00	14	34	0.71	7.83E-05
	JGS4143-0525	sugar transferases involved in	13	8	0.38	19	14	0.42		9	0	0.00	32	22	0.41	9.15E-03
	JGS4143-0526	dtdp-4-dehydrorhamnose 3,5-epimerase, putative	7	14	0.67	9	24	0.73		9	0	0.00	15	39	0.72	4.04E-05
	JGS4143-0527	capsular polysaccharide biosynthesis protein	11	10	0.48	16	15	0.48		9	0	0.00	27	25	0.48	3.91E-03
	JGS4143-0528	polysaccharide biosynthesis protein CapD	17	4	0.19	27	6	0.18								
	JGS4143-0529	NAD-dependent epimerase/dehydratase	17	4	0.19	17	16	0.48	4.58E-02	9	0	0.00	34	20	0.37	1.79E-02
	JGS4143-0530	UDP-N-acetylglucosamine 2-epimerase	18	3	0.14	24	9	0.27								
	JGS4143-0531	putative glycosyl transferase	16	5	0.24	27	6	0.18								
	JGS4143-0532	putative transferase	17	4	0.19	27	6	0.18								
	JGS4143-0534	glycosyl transferase, group 2 family protein	5	16	0.76	11	22	0.67		9	0	0.00	16	38	0.70	5.42E-05
	JGS4143-0535	flippase Wzx	15	6	0.29	27	6	0.18								
VR-110	JGS4143-0536	udp-glucose 6-dehydrogenase (udp-glc)	8	13	0.62	21	12	0.36		9	0	0.00	29	25	0.46	4.71E-03
	JGS4143-0537	transcriptional regulator, LytR family	7	14	0.67	8	25	0.76		8	1	0.11	16	38	0.70	7.80E-04
VR-111	JGS4143-0546	transcriptional regulator, AraC family	10	11	0.52	17	15	0.47								
VR-113	JGS4143-0593	conserved hypothetical protein	8	13	0.62	8	23	0.74								
VR-114	JGS4143-0613	cell wall binding repeat domain protein	7	14	0.67	14	19	0.58								
VR-115	JGS4143-0727	conserved hypothetical protein	9	12	0.57	13	20	0.61								
	JGS4143-0728	voltage-gated chloride channel family protein	9	12	0.57	15	18	0.55								
	JGS4143-0729	voltage-gated chloride channel family protein	4	17	0.81	8	25	0.76		6	3	0.33	13	41	0.76	8.06E-03

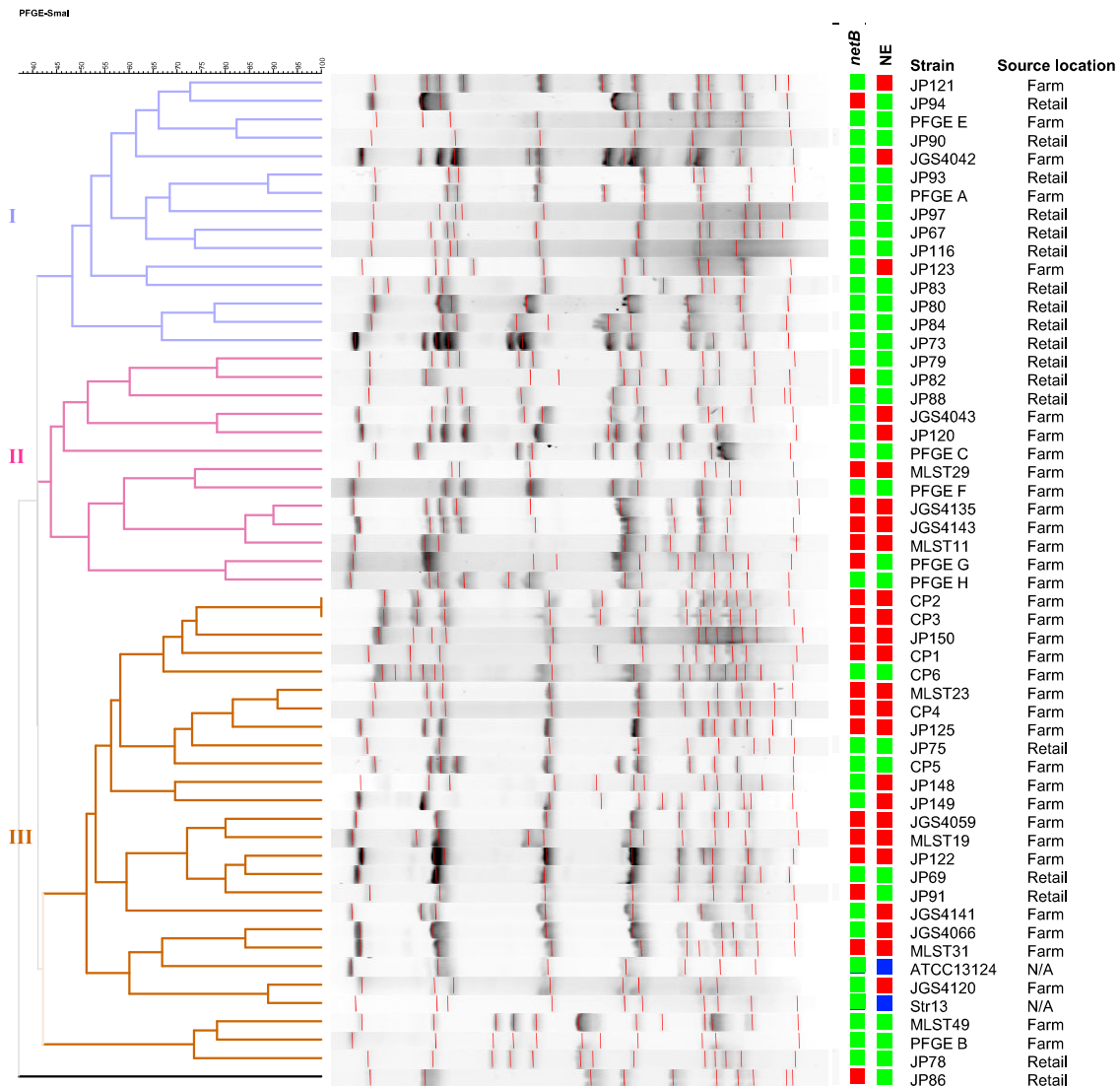


**Table S6. Fisher's exact tests performed on variable genes.** Q-values represent p-values corrected for multiple-testing. Only q-values < 0.05 are shown.

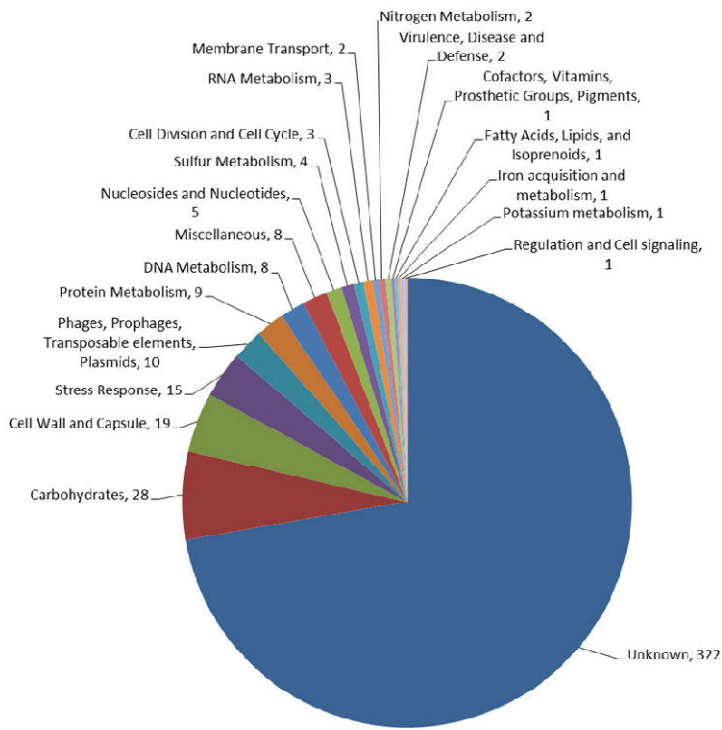
Variable Region	Locus_tag	Product	netB+	netB+	netB+	netB-	netB-	netB-	netB+ vs netB-	Non-poultry		Poultry		Poultry vs Non-poultry		
			Absent	Present	Prevalence	Absent	Present	Prevalence	q-value	Absent	Present	prevalence	Absent	Present	prevalence	q-value
VR-116	JGS4143-0804	conserved hypothetical protein	6	15	0.71	12	21	0.64								
VR-117	JGS4143-0810	hypothetical protein	6	15	0.71	10	23	0.70		9	0	0.00	17	37	0.69	8.58E-05
VR-118	JGS4143-0827	conserved hypothetical protein	1	20	0.95	1	32	0.97		5	4	0.44	2	52	0.96	2.47E-04
VR-119	JGS4143-0843	hypothetical protein	12	9	0.43	7	26	0.79	1.43E-02							
VR-120	JGS4143-0907	YhbE	3	15	0.83	4	19	0.83		8	1	0.11	7	35	0.83	4.14E-05
	JGS4143-0908	YhbF	6	13	0.68	7	21	0.75		6	2	0.25	12	35	0.74	5.96E-03
	JGS4143-0909	YhbD	3	16	0.84	4	21	0.84		6	3	0.33	7	37	0.84	2.19E-03
VR-121	JGS4143-0922	phage protein	9	12	0.57	13	20	0.61								
	JGS4143-0925	hypothetical protein	0	12	1.00	0	18	1.00		7	0	0.00	0	30	1.00	3.55E-06
	JGS4143-0926	VanZ like family	0	21	1.00	2	29	0.94		9	0	0.00	2	50	0.96	3.55E-06
	JGS4143-0927	hypothetical protein	7	13	0.65	8	21	0.72		9	0	0.00	14	35	0.71	4.14E-05
	JGS4143-0928	hypothetical protein	1	20	0.95	8	24	0.75		9	0	0.00	9	44	0.83	3.55E-06
	JGS4143-0929	hypothetical protein	8	13	0.62	9	17	0.65		9	0	0.00	16	31	0.66	1.71E-04
	JGS4143-0930	FunZ family protein	0	10	1.00	0	18	1.00		7	0	0.00	0	29	1.00	3.55E-06
	JGS4143-0931	FunZ family protein	1	12	0.92	3	19	0.86		8	0	0.00	4	32	0.89	3.55E-06
VR-122	JGS4143-0934	two-component sensor kinase YesM, putative	13	8	0.38	22	9	0.29								
	JGS4143-0936	ABC-type sugar transport system, periplasmic	3	13	0.81	5	19	0.79		5	3	0.38	8	33	0.80	9.63E-03
	JGS4143-0937	ABC transporter, permease protein	14	7	0.33	20	13	0.39								
	JGS4143-0938	ABC transporter, permease protein	10	11	0.52	19	14	0.42								
	JGS4143-0939	glycosyl hydrolase, family 31	0	14	1.00	4	19	0.83		4	3	0.43	4	34	0.89	6.76E-03
	JGS4143-0940	alpha-N-acetylglucosaminidase family protein	6	13	0.68	14	14	0.50								
VR-123	JGS4143-0949	glycosyl hydrolase, family 20, putative	16	5	0.24	26	7	0.21								
	JGS4143-0950	glycosyl hydrolase, family 20	9	11	0.55	15	15	0.50								
VR-124	JGS4143-0969	two-component sensor histidine kinase	2	19	0.90	3	30	0.91								
VR-125	JGS4143-1023	phosphorylase family protein	0	21	1.00	3	30	0.91		5	4	0.44	3	51	0.94	5.23E-04
VR-126	JGS4143-1062	RNA polymerase sigma-70 factor	7	12	0.63	2	27	0.93	2.82E-02	4	3	0.43	8	40	0.83	1.48E-02
	JGS4143-1063	hypothetical protein	0	12	1.00	0	18	1.00		4	3	0.43	0	31	1.00	3.24E-04
VR-127	JGS4143-1246	HNH endonuclease domain protein	2	13	0.87	5	17	0.77		9	0	0.00	7	30	0.81	8.30E-06
	JGS4143-1247	phage Terminase Small Subunit	2	14	0.88	3	20	0.87		9	0	0.00	5	35	0.88	3.55E-06
	JGS4143-1248	putative phage terminase, large subunit	2	19	0.90	2	30	0.94		8	1	0.11	4	49	0.92	3.55E-06
	JGS4143-1249	hypothetical protein	5	15	0.75	9	20	0.69		9	0	0.00	14	35	0.71	4.14E-05
	JGS4143-1250	conserved hypothetical protein	1	20	0.95	9	22	0.71	4.11E-02	9	0	0.00	9	43	0.83	3.55E-06
	JGS4143-1251	portal protein	9	11	0.55	11	16	0.59		9	0	0.00	19	28	0.60	1.10E-03
	JGS4143-1252	phage prohead protease, HK97 family	3	18	0.86	10	22	0.69		7	2	0.22	13	40	0.75	1.89E-03
	JGS4143-1253	phage major capsid protein, HK97 family	6	14	0.70	13	14	0.52		9	0	0.00	19	28	0.60	1.10E-03
	JGS4143-1254	conserved hypothetical protein	5	16	0.76	8	23	0.74		9	0	0.00	12	40	0.77	8.30E-06
	JGS4143-1255	phage head-tail adaptor, putative	6	12	0.67	12	10	0.45		9	0	0.00	18	22	0.55	1.35E-03
	JGS4143-1256	phage protein, HK97 gp10 family	0	21	1.00	5	28	0.85		7	2	0.22	5	49	0.91	4.04E-05
	JGS4143-1257	conserved hypothetical protein	0	17	1.00	5	22	0.81		9	0	0.00	5	40	0.89	3.55E-06
	JGS4143-1258	phage major tail protein, Phi13 family	15	5	0.25	25	2	0.07								
	JGS4143-1259	conserved hypothetical protein	0	21	1.00	4	27	0.87		9	0	0.00	4	48	0.92	3.55E-06
	JGS4143-1260	phage tail tape measure protein, family, core	1	15	0.94	5	21	0.81		9	0	0.00	6	36	0.86	3.55E-06
VR-128	JGS4143-1337	nucleotidyltransferase family protein	0	14	1.00	4	19	0.83		9	0	0.00	4	33	0.89	3.55E-06
VR-129	JGS4143-1380	hypothetical protein	1	20	0.95	5	27	0.84		9	0	0.00	5	48	0.91	3.55E-06
VR-130	JGS4143-1385	endo-alpha-N-acetylglucosaminidase	4	17	0.81	0	30	1.00	2.82E-02	4	5	0.56	3	48	0.94	3.66E-03
VR-131	JGS4143-1408	hypothetical protein	0	21	1.00	18	15	0.45	2.74E-05	9	0	0.00	18	36	0.67	1.34E-04
VR-132	JGS4143-1441	putative alpha-N-acetylglucosaminidase	10	11	0.52	13	20	0.61								
VR-133	JGS4143-1447	hypothetical protein	16	5	0.24	26	5	0.16								
	JGS4143-1448	type III restriction enzyme, res subunit	3	18	0.86	16	17	0.52	2.11E-02	8	1	0.11	19	35	0.65	2.09E-03
	JGS4143-1449	conserved hypothetical protein	15	6	0.29	24	8	0.25								
	JGS4143-1450	RNA polymerase sigma factor, sigma-70 family	8	9	0.53	14	10	0.42								
	JGS4143-1451	nucleoside triphosphatase, D5 family, putative	12	9	0.43	24	9	0.27								
	JGS4143-1452	DNA-directed DNA polymerase	12	9	0.43	27	6	0.18								
	JGS4143-1453	DNA-binding protein	16	5	0.24	29	3	0.09								
	JGS4143-1454	conserved hypothetical protein	13	4	0.24	21	3	0.13								
	JGS4143-1455	conserved hypothetical protein	2	14	0.88	3	23	0.88		8	1	0.11	5	38	0.88	8.30E-06
VR-134	JGS4143-1456	F5/8 type C domain containing protein	11	10	0.48	10	20	0.67								
VR-135	JGS4143-1460	FLIB family protein	10	9	0.47	17	10	0.37								
VR-136	JGS4143-1482	NADH oxidase	3	18	0.86	2	30	0.94		4	5	0.56	5	48	0.91	8.13E-03
	JGS4143-1483	hydrolases of the alpha/beta superfamily	17	4	0.19	17	16	0.48	4.58E-02							

**Table S6. Fisher's exact tests performed on variable genes.** Q-values represent p-values corrected for multiple-testing. Only q-values < 0.05 are shown.

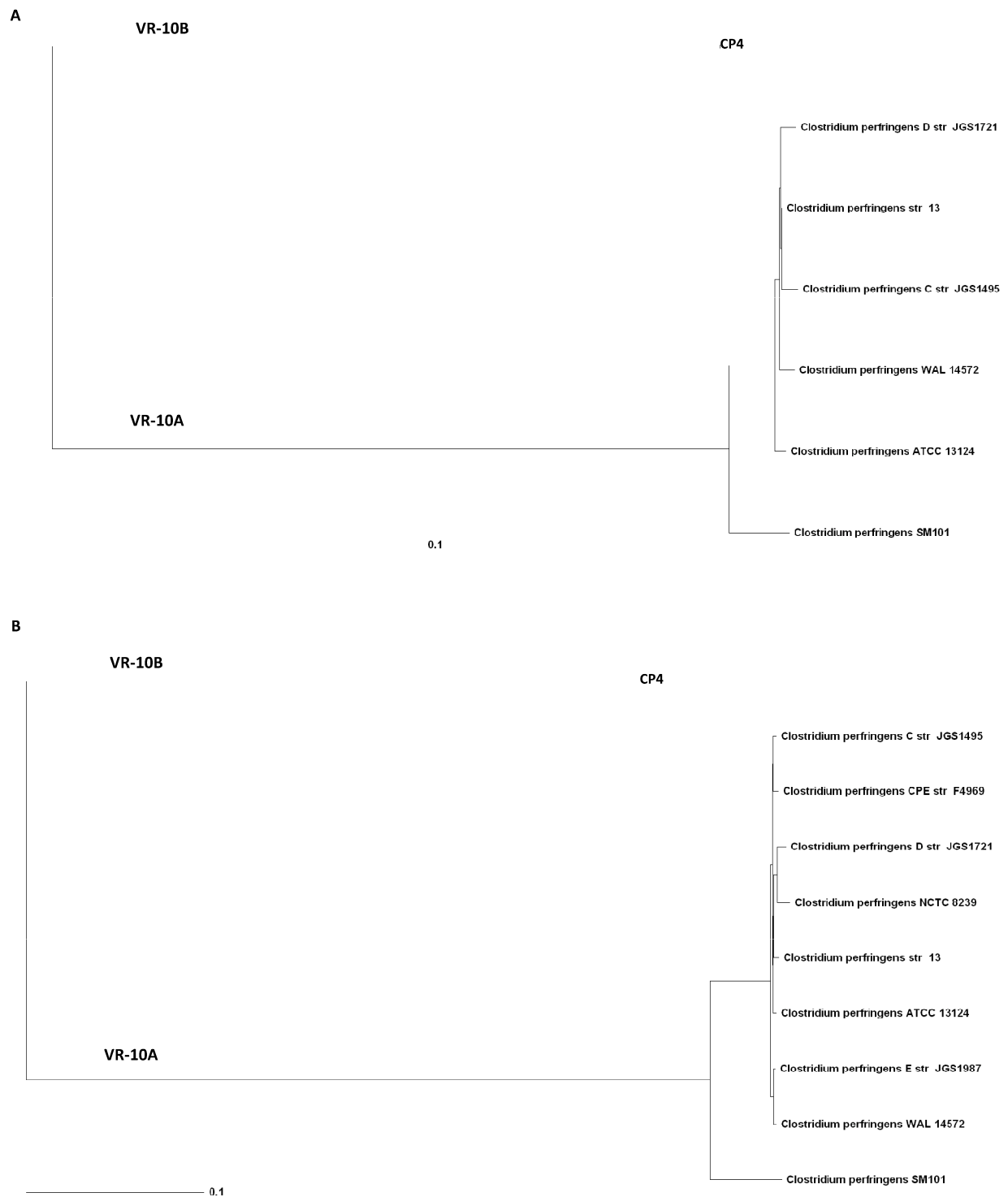
Variable Region	Locus_tag	Product	<i>netB</i> +		<i>netB</i> -		<i>netB</i> - vs <i>netB</i> -	Non-poultry	Non-poultry	Non-poultry	Poultry	Poultry	Poultry	Poultry vs Non-poultry		
			Absent	Present	Prevalence	Absent									Present	Prevalence
VR-137	JGS4143-1484	C4-dicarboxylate transport system	12	6	0.33	9	18	0.67	4.58E-02	5	4	0.44	4	34	0.89	3.68E-03
	JGS4143-1486	C4-dicarboxylate transport system	3	13	0.81	1	20	0.95								
VR-138	JGS4143-1847	hypothetical protein	6	14	0.70	8	20	0.71	7	2	0.22	14	34	0.71	5.00E-03	
VR-139	JGS4143-2057	hypothetical protein	4	15	0.79	4	24	0.86								
VR-140	JGS4143-2323	ABC transporter, ATP-binding protein	3	18	0.86	4	29	0.88								
VR-141	JGS4143-2973	transporter, monovalent cation:proton	8	13	0.62	12	21	0.64								
VR-142	pBCNF5603_uviA	UviA protein	0	11	1.00	1	18	0.95	5	4	0.44	1	29	0.97	7.42E-04	
	pBCNF5603_uviB	UviB protein	0	19	1.00	4	27	0.87	3	5	0.63	4	46	0.92	1.86E-02	
	pCPF4969_51	putative SpaC protein	1	15	0.94	1	18	0.95	8	1	0.11	2	33	0.94	3.55E-06	
	pCPF5603_10	collagen adhesion protein	1	20	0.95	9	24	0.73	4	5	0.56	10	44	0.81	4.07E-02	
	pCPF5603_68	putative Tn916 ORF15 protein	3	18	0.86	16	16	0.50	1.13E-02							
	pCPF5603_70	putative Tn916 ORF16 protein	0	21	1.00	10	23	0.70	5.25E-03	4	5	0.56	10	44	0.81	4.07E-02



**Figure S1. PFGE of *C. perfringens* poultry isolates from diseased and healthy birds.** PFGE patterns obtained from *SmaI*-digested DNA from *C. perfringens* poultry isolates. The dendrogram was obtained by unweighted pair group method using arithmetic averages clustering with a Dice coefficient and 1% position tolerance. The presence of *netB* (red, present; green, absent) is indicated in the first column and disease association (red, NE; green, healthy; blue, non-poultry) in the second. The three major clusters are indicated by roman numerals.



**Figure S2. Functional categories of genes exhibiting variability among *C. perfringens* strains.** Functional categories were identified by the RAST server (<http://rast.nmpdr.org/>).



**Figure S3. Sequence alignment of VR-10 two-component system genes from two different alleles. A) response regulator, B) sensor histidine kinase. The distance trees represent Blast alignments of protein sequences from the two-component systems found in VR-10A and VR-10B .**