Supplementary Material for SREP-15-29607A. This file contains four supplementary figures (Figure S1-S4) and six supplementary tables (Table S1-S6).

Clonal Complex 17 Group B *Streptococcus* strains causing invasive disease in neonates and adults originate from the same genetic pool

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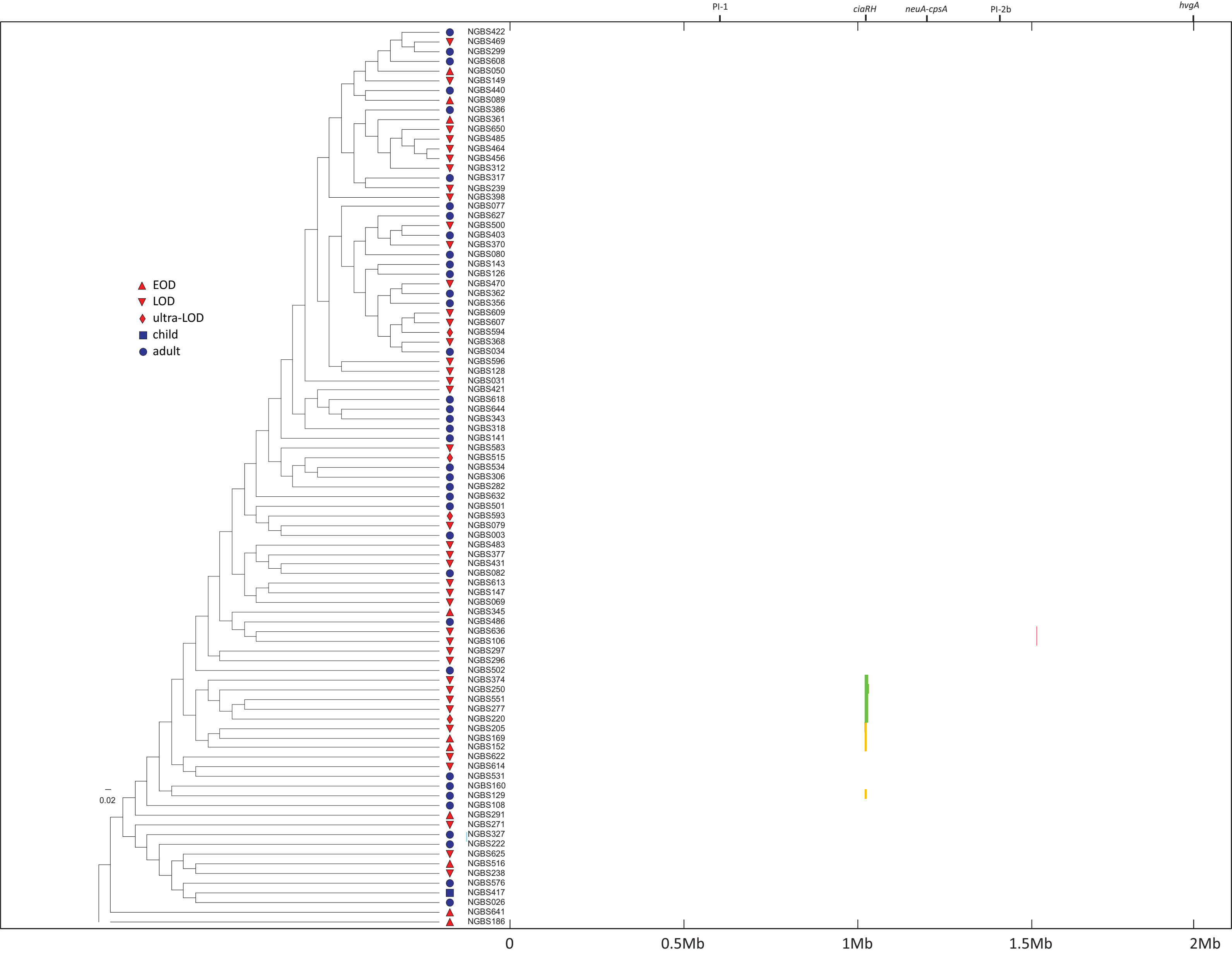

Figure S1. Recombination in CC17 GBS isolates. The cladogram depicted in Fig. 3 is shown on left-hand side. Genome size of the reference strain (NGBS128) is marked in 0.5Mbp increments along the bottom. Recombination is shown in the right-hand panel as vertical coloured bars. The colouring of the bars at a specific genomic location reflects the clustering of the recombination events into groups, and is unrelated to other bars at distant genomic locations.

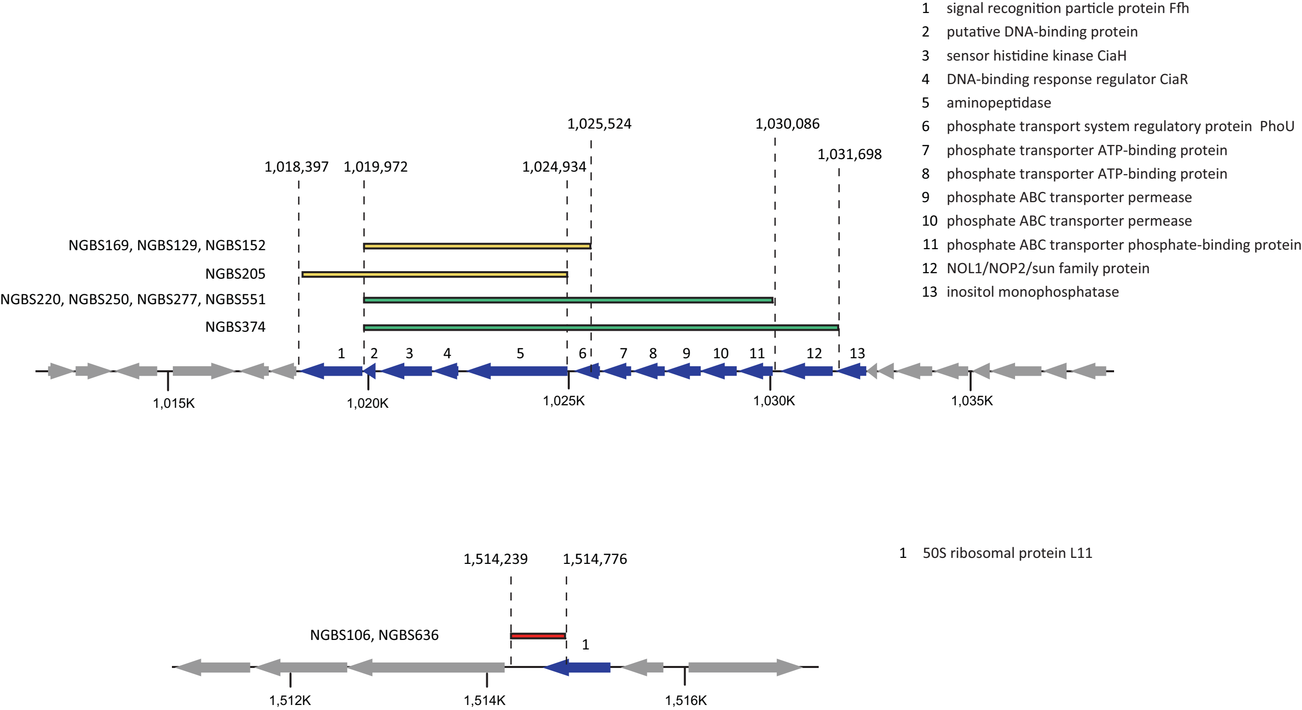

Figure S2. Genes found within recombined areas of CC17 GBS isolates. Genes found in the two areas of recombination described in Fig. S1 are shown as numbered blue arrows. Numbers correspond to gene names shown on the right. Surrounding genes not affected by recombination are coloured grey. Areas of recombination are shown by horizontal coloured bars and the start and end positions (relative to the genome of strain NGBS128) are marked by dashed lines.

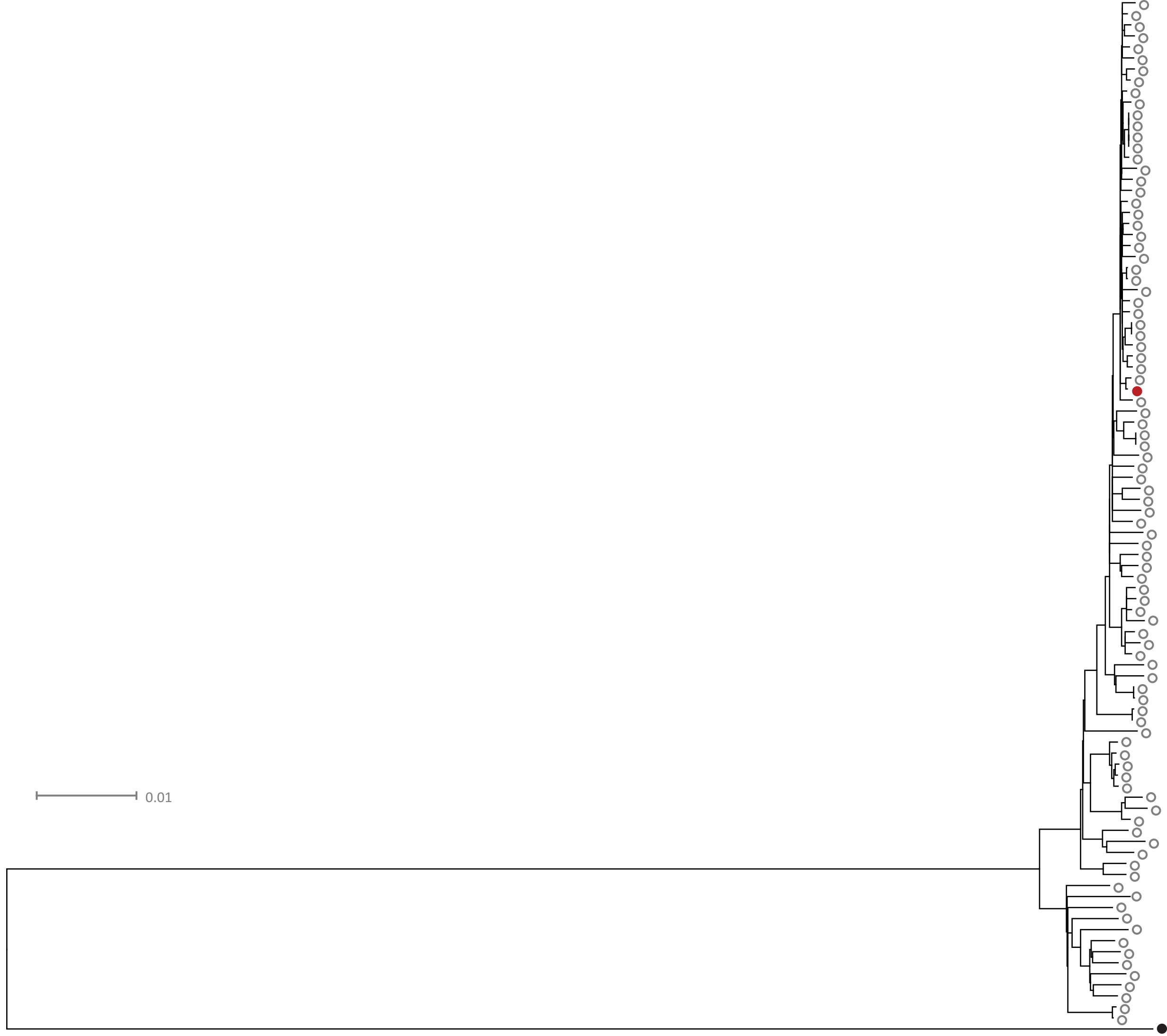

Figure S3. Rooted phylogenetic tree of CC17 strains. Phylogeny based on 13,876 non-redundant single-nucleotide polymorphic loci identified among the genomes of 93 serotype III CC17 isolates plus serotype V ST1 strain SS1 relative to the ST17 reference strain NGBS128. CC17 isolates represented by open grey circles. Reference NGBS128 is marked in red. Strain SS1 is shown as black filled circle.

Figure S4. Inferred phylogenetic relationships between 93 CC17 GBS strains causing invasive disease in Canada (this study) and a previously described (DaCunha *et al*. Nature Communications 5, Article number: 4544 doi:10.1038/ncomms5544) strain collection comprising 71 ST17 carriage and neonatal disease isolates recovered in different countries. A cladogram was constructed using the concatenated sequences of 5,324 non-redundant single-nucleotide polymorphic loci relative to the genome of reference strain NGBS128. Country of origin is indicated by the differently coloured circles.

Table S1. CC17 GBS isolates used in this study.

Strain Name	Isolation Year	Age Group	Sequence Type	Pilus Content	Source [1]	SRA Accession Number
NGBS003	2009	Adult	17	PI-1+2b	Blood	SAMN04093966
NGBS026	2009	Adult	17	PI-1+2b	Blood	SAMN04093967
NGBS031	2009	LOD	17	PI-1+2b	Blood	SAMN04093968
NGBS034	2010	Adult	17	PI-1+2b	Blood	SAMN04093969
NGBS050	2010	EOD	17	PI-1+2b	Blood	SAMN04093970
NGBS069	2010	LOD	17	PI-1+2b	CSF	SAMN04093971
NGBS077	2010	Adult	17	PI-1+2b	Blood	SAMN04093972
NGBS079	2010	LOD	17	PI-1+2b	Blood	SAMN04093973
NGBS080	2010	Adult	17	PI-1+2b	Blood	SAMN04093974
NGBS082	2010	Adult	17	PI-2b	Blood	SAMN04093975
NGBS089	2010	EOD	17	PI-1+2b	Blood	SAMN04093976
NGBS106 [2]	2010	LOD	17	PI-1+2b	CSF	SAMN04093977
NGBS108	2010	Adult	17	PI-1+2b	Blood	SAMN04093978
NGBS126	2010	Adult	17	PI-1+2b	Other	SAMN04093979
NGBS128	2010	LOD	17	PI-1+2b	Blood	SAMN04007140
NGBS129	2010	Adult	31	PI-1+2b	Blood	SAMN04093980
NGBS141	2010	Adult	17	PI-1+2b	Blood	SAMN04093981
NGBS143	2010	Adult	17	PI-1+2b	Other	SAMN04093982
NGBS147	2010	LOD	17	PI-1+2b	Blood	SAMN04093983
NGBS149	2010	LOD	17	PI-1+2b	Blood	SAMN04093984
NGBS152	2010	EOD	17	PI-2b	Blood	SAMN04093985
NGBS160	2010	Adult	31	PI-1+2b	Tissue	SAMN04093986
NGBS169	2010	EOD	17	PI-2b	Blood	SAMN04093987
NGBS186 [3]	2010	EOD	17	PI-1+2b	Blood	SAMN04093988
NGBS205	2011	LOD	17	PI-2b	Blood	SAMN04093989
NGBS220	2011	Ultra LOD	17	PI-2b	Blood	SAMN04093990
NGBS222	2010	Adult	17	PI-1+2b	Blood	SAMN04093991
NGBS238	2011	LOD	17	PI-1+2b	Blood	SAMN04093992
NGBS239	2011	LOD	17	PI-1+2b	Blood	SAMN04093993
NGBS250	2011	LOD	17	PI-2b	CSF	SAMN04093994
NGBS271	2011	LOD	17	PI-1+2b	CSF	SAMN04093995
NGBS277	2010	LOD	17	PI-2b	Blood	SAMN04093996
NGBS282	2010	Adult	17	PI-1+2b	Blood	SAMN04093997
NGBS291	2010	EOD	17	PI-1+2b	Blood	SAMN04093998
NGBS296 [4]	2010	LOD	17	PI-1+2b	Blood	SAMN04093999
NGBS297 [4]	2010	LOD	17	PI-1+2b	Blood	SAMN04094000
NGBS299	2011	Adult	17	PI-1+2b	Blood	SAMN04094001
NGBS306	2011	Adult	17	PI-1+2b	Blood	SAMN04094002

NGBS312	2011	LOD	17	PI-1+2b	Blood	SAMN04094003
NGBS317	2011	Adult	17	PI-1+2b	Blood	SAMN04094004
NGBS318	2011	Adult	290	PI-1+2b	Blood	SAMN04094005
NGBS327	2011	Adult	484	PI-1+2b	Blood	SAMN04094006
NGBS343[5]	2011	Adult	17	PI-1+2b	Blood	SAMN04094007
NGBS345	2011	EOD	17	PI-1+2b	Blood	SAMN04094008
NGBS356	2011	Adult	17	PI-1+2b	Blood	SAMN04094009
NGBS361	2011	EOD	17	PI-1+2b	Blood	SAMN04094010
NGBS362	2011	Adult	17	PI-1+2b	Blood	SAMN04094011
NGBS368	2011	LOD	17	PI-1+2b	Blood	SAMN04094012
NGBS370	2011	LOD	17	PI-1+2b	Blood	SAMN04094013
NGBS374	2011	LOD	17	PI-2b	Blood	SAMN04094014
NGBS377	2011	LOD	17	PI-2b	Blood	SAMN04094015
NGBS386	2011	Adult	17	PI-1+2b	Synovial Fluid	SAMN04094016
NGBS398	2011	LOD	17	PI-1+2b	Blood	SAMN04094017
NGBS403	2011	Adult	17	PI-1+2b	Blood	SAMN04094018
NGBS417	2011	Child	17	PI-1+2b	Synovial Fluid	SAMN04094019
NGBS421	2011	LOD	17	PI-1+2b	Blood	SAMN04094020
NGBS422	2011	Adult	17	PI-1+2b	Blood	SAMN04094021
NGBS431	2011	LOD	17	PI-2b	Blood	SAMN04094022
NGBS440	2011	Adult	17	PI-1+2b	Blood	SAMN04094023
NGBS456[6]	2011	LOD	17	PI-1+2b	Blood	SAMN04094024
NGBS464[6]	2011	LOD	17	PI-1+2b	Blood	SAMN04094025
NGBS469	2011	LOD	17	PI-1+2b	Blood	SAMN04094026
NGBS470	2011	LOD	17	PI-1+2b	Blood	SAMN04094027
NGBS483	2011	LOD	17	PI-2b	Blood	SAMN04094028
NGBS485[6]	2011	LOD	17	PI-1+2b	Blood	SAMN04094029
NGBS486	2011	Adult	17	PI-1+2b	Blood	SAMN04094030
NGBS500	2012	LOD	17	PI-1+2b	Blood	SAMN04094031
NGBS501	2012	Adult	17	PI-1+2b	Blood	SAMN04094032
NGBS502	2012	Adult	95	PI-1+2b	Blood	SAMN04094033
NGBS515	2012	Ultra LOD	17	PI-1+2b	Blood	SAMN04094034
NGBS516	2012	EOD	17	PI-1+2b	Blood	SAMN04094035
NGBS531	2012	Adult	148	PI-1+2b	Blood	SAMN04094036
NGBS534	2012	Adult	17	PI-1+2b	Blood	SAMN04094037
NGBS551	2012	LOD	17	PI-2b	Blood	SAMN04094038
NGBS576	2012	Adult	17	PI-1+2b	Blood	SAMN04094039
NGBS583	2012	LOD	17	PI-1+2b	Blood	SAMN04094040
NGBS593	2012	Ultra LOD	17	PI-1+2b	Blood	SAMN04094041

NGBS594	2012	Ultra LOD	17	PI-1+2b	Blood	SAMN04094042
NGBS596	2012	LOD	17	PI-1+2b	Blood	SAMN04094043
NGBS607	2012	LOD	17	PI-1+2b	Blood	SAMN04094044
NGBS608	2012	Adult	17	PI-1+2b	Other	SAMN04094045
NGBS609	2012	LOD	17	PI-1+2b	Blood	SAMN04094046
NGBS613	2012	LOD	17	PI-1+2b	Blood	SAMN04094047
NGBS614	2012	LOD	148	PI-1+2b	CSF	SAMN04094048
NGBS618	2012	Adult	17	PI-1+2b	Blood	SAMN04094049
NGBS622	2012	LOD	148	PI-1+2b	Blood	SAMN04094050
NGBS625	2012	LOD	17	PI-1+2b	Blood	SAMN04094051
NGBS627	2012	Adult	17	PI-1+2b	Blood	SAMN04094052
NGBS632	2012	Adult	17	PI-1+2b	Tissue	SAMN04094053
NGBS636 [2]	2010	LOD	17	PI-1+2b	Blood	SAMN04094054
NGBS641 [3]	2010	EOD	17	PI-1+2b	Blood	SAMN04094055
NGBS644 [5]	2011	Adult	17	PI-1+2b	Synovial Fluid	SAMN04094056
NGBS650 [6]	2011	LOD	17	PI-1+2b	CSF	SAMN04094057

[1] CSF, cerebrospinal fluid.

[2, 3, 4, 5, 6] Isolates indicated by the same superscript number were isolated from a single patient.

Table S2. Pairwise SNP comparison of adult CC17 strains.

	NGBS128	NGBS003	NGBS026	NGBS034	NGBS077	NGBS080	NGBS082	NGBS108	NGBS126	NGBS129	NGBS141	NGBS143	NGBS160	NGBS222	NGBS282	NGBS299	NGBS306	NGBS317	NGBS318	NGBS327	NGBS343	NGBS356	NGBS362	NGBS386	NGBS403	NGBS422	NGBS440	NGBS486	NGBS501	NGBS502	NGBS531	NGBS534	NGBS576	NGBS608	NGBS618	NGBS627	NGBS632
NGBS128																																					
NGBS003	63																																				
NGBS026	228	243																																			
NGBS034	27	70	235																																		
NGBS077	18	63	228	23																																	
NGBS080	29	74	239	34	29																																
NGBS082	60	75	240	67	60	71																															
NGBS108	218	233	124	225	218	229	230																														
NGBS126	18	63	228	21	16	25	60	218																													
NGBS129	126	141	222	133	126	137	138	214	126																												
NGBS141	49	72	237	56	49	60	69	227	49	135																											
NGBS143	18	63	228	21	16	27	60	218	2	126	49																										
NGBS160	126	141	228	133	126	137	138	218	126	62	135	126																									
NGBS222	240	255	112	247	240	251	252	136	240	234	249	240	240																								
NGBS282	47	70	235	54	47	58	67	225	47	133	56	47	133	247																							
NGBS299	30	73	238	37	30	41	70	228	30	136	59	30	136	250	57																						
NGBS306	57	80	245	64	57	68	77	235	57	143	66	57	143	257	64	67																					
NGBS317	27	70	235	34	27	38	67	225	27	133	56	27	133	247	54	33	64																				
NGBS318	54	77	242	61	54	65	74	232	54	140	63	54	140	254	61	64	71	61																			
NGBS327	230	245	124	237	230	241	242	128	230	224	239	230	230	136	237	240	247	237	244																		
NGBS343	51	76	241	58	51	62	73	231	51	139	62	51	139	253	60	61	70	58	63	243																	
NGBS356	24	67	232	25	20	31	64	222	18	130	53	18	130	244	51	34	61	31	58	234	55																
NGBS362	23	66	231	24	19	30	63	221	17	129	52	17	129	243	50	33	60	30	57	233	54	21															

NGBS386	19	62	227	26	19	30	59	217	19	125	48	19	125	239	46	25	56	22	53	229	50	23	22														
NGBS403	22	65	230	23	18	27	62	220	16	128	51	16	128	242	49	32	59	29	56	232	53	20	19	21													
NGBS422	31	74	239	38	31	42	71	229	31	137	60	31	137	251	58	35	68	34	65	241	62	35	34	26	33												
NGBS440	30	73	238	37	30	41	70	228	30	136	59	30	136	250	57	34	67	33	64	240	61	34	33	25	32	35											
NGBS486	83	98	251	90	83	94	95	241	83	149	92	83	149	263	90	93	100	90	97	253	96	87	86	82	85	94	93										
NGBS501	61	76	241	68	61	72	73	231	61	139	70	61	139	253	68	71	78	68	75	243	74	65	64	60	63	72	71	96									
NGBS502	130	145	242	137	130	141	142	232	130	138	139	130	140	254	137	140	147	137	144	244	143	134	133	129	132	141	140	153	143								
NGBS531	148	163	252	155	148	159	160	242	148	150	157	148	152	264	155	158	165	155	162	252	161	152	151	147	150	159	158	171	161	162							
NGBS534	57	80	245	64	57	68	77	235	57	143	66	57	143	257	64	67	48	64	71	247	70	61	60	56	59	68	67	100	78	147	165						
NGBS576	239	254	85	246	239	250	251	135	239	233	248	239	239	123	246	249	256	246	253	135	252	243	242	238	241	250	249	262	252	253	263	256					
NGBS608	20	63	228	27	20	31	60	218	20	126	49	20	126	240	47	24	57	23	54	230	51	24	23	15	22	25	24	83	61	130	148	57	239				
NGBS618	48	71	236	55	48	59	68	226	48	134	57	48	134	248	55	58	65	55	58	238	29	52	51	47	50	59	58	91	69	138	156	65	247	48			
NGBS627	21	66	231	24	17	28	63	221	17	129	52	17	129	243	50	33	60	30	57	233	54	21	20	22	17	34	33	86	64	133	151	60	242	23	51		
NGBS632	70	85	250	75	70	81	82	240	70	148	79	70	148	262	77	80	87	77	84	252	83	74	73	69	72	81	80	105	83	152	170	87	261	70	78	73	
NGBS644	51	76	241	58	51	62	73	231	51	139	62	51	139	253	60	61	70	58	63	243	0	55	54	50	53	62	61	96	74	143	161	70	252	51	29	54	83

Table S3. Pairwise SNP comparison in Neonatal CC17 Strains

	NGBS128	NGBS031	NGBS050	NGBS069	NGBS079	NGBS089	NGBS106	NGBS128	NGBS147	NGBS149	NGBS152	NGBS169	NGBS186	NGBS205	NGBS220	NGBS238	NGBS239	NGBS250	NGBS271	NGBS277	NGBS291	NGBS296	NGBS297	NGBS312	NGBS345	NGBS361	NGBS368	NGBS370	NGBS374	NGBS377	NGBS398	NGBS421	NGBS431	NGBS456	NGBS464	NGBS469	NGBS470	NGBS483	NGBS485	NGBS500	NGBS515	NGBS516	NGBS551	NGBS583	NGBS593	NGBS594	NGBS596	NGBS607	NGBS609	NGBS613	NGBS614	NGBS622	NGBS625	NGBS636	NGBS641	NGBS650
NGBS128																																																								
NGBS031	27																																																							
NGBS050	23	30																																																					
NGBS069	51	60	56																																																			
NGBS079	56	63	59	61																																																	
NGBS089	22	31	21	55	60																																																
NGBS106	68	75	71	73	76	72																																														
NGBS128	0	27	23	51	56	22	68																																												
NGBS147	57	64	60	20	65	61	77	57																																										
NGBS149	29	36	26	62	65	27	77	29	66																																									
NGBS152	122	131	127	127	132	126	132	122	133	133																																								
NGBS169	148	155	151	153	156	152	156	148	157	157	46																																							
NGBS186	219	228	223	226	229	225	229	219	230	230	229	249																																						
NGBS205	141	148	144	146	149	145	149	141	150	150	39	53	242																																					
NGBS220	105	114	110	114	117	111	117	105	118	116	97	117	210	110																																				
NGBS238	228	235	231	233	236	232	236	228	237	236	234	254	133	247	217																																			
NGBS239	33	40	32	66	69	33	81	33	70	38	137	161	234	154	120	241																																		
NGBS250	101	110	106	108	113	105	113	101	114	112	91	117	212	110	16	217	116																																	
NGBS271	218	227	223	223	228	222	228	218	229	229	224	250	127	243	213	128	233	207																																
NGBS277	109	116	112	114	117	113	117	109	118	118	95	115	210	108	12	215	122	14	211																															
NGBS291	246	253	249	249	254	250	254	246	255	255	252	272	153	265	235	154	259	235	150	233																														
NGBS296	92	99	95	97	100	94	100	92	101	101	136	156	231	149	119	236	105	117	232	117	254																													
NGBS297	90	97	93	95	98	92	98	90	99	99	134	154	229	147	117	234	103	115	230	115	252	2																														
NGBS312	21	28	20	54	57	21	69	21	58	26	125	149	222	142	108	229	30	104	221	110	247	93	91																																	

NGBS345	79	88	84	84	89	83	63	79	90	90	143	169	242	162	130	249	94	124	239	130	267	113	111	82																												
NGBS361	25	32	24	58	61	25	73	25	62	30	129	153	226	146	112	233	34	108	225	114	251	97	95	18	86																											
NGBS368	27	34	30	60	63	31	75	27	64	36	131	155	228	148	114	235	40	110	227	116	253	99	97	28	88	32																										
NGBS370	24	31	27	57	60	28	72	24	61	33	128	152	225	145	111	232	37	107	224	113	250	96	94	25	85	29	25																									
NGBS374	106	113	109	111	114	110	114	106	115	115	92	112	207	105	19	212	119	21	208	17	230	114	112	107	127	111	113	110																								
NGBS377	72	79	75	45	80	76	92	72	49	81	148	172	245	165	133	252	85	129	244	133	270	116	114	73	105	77	79	76	130																							
NGBS398	25	32	26	58	61	27	73	25	62	32	129	153	226	146	112	233	36	108	225	114	251	97	95	24	86	28	32	29	111	77																						
NGBS421	51	58	54	64	67	55	79	51	68	60	135	159	232	152	118	239	64	116	231	120	257	103	101	52	92	56	58	55	117	83	56																					
NGBS431	54	61	57	27	62	58	74	54	31	63	130	154	227	147	115	234	67	111	226	115	252	98	96	55	87	59	61	58	112	32	59	65																				
NGBS456	21	28	20	54	57	21	69	21	58	26	125	149	222	142	108	229	30	104	221	110	247	93	91	12	82	18	28	25	107	73	24	52	55																			
NGBS464	21	28	20	54	57	21	69	21	58	26	125	149	222	142	108	229	30	104	221	110	247	93	91	12	82	18	28	25	107	73	24	52	55	0																		
NGBS469	25	32	22	58	61	23	73	25	62	28	129	153	226	146	112	233	34	108	225	114	251	97	95	22	86	26	32	29	111	77	28	56	59	22	22																	
NGBS470	34	41	37	67	70	38	82	34	71	43	138	162	235	155	121	242	47	117	234	123	260	106	104	35	95	39	35	32	120	86	39	65	68	35	35	39																
NGBS483	60	67	63	33	68	64	80	60	37	69	136	160	233	153	121	240	73	117	232	121	258	104	102	61	93	65	67	64	118	38	65	71	20	61	61	65	74															
NGBS485	21	28	20	54	57	21	69	21	58	26	125	149	222	142	108	229	30	104	221	110	247	93	91	12	82	18	28	25	107	73	24	52	55	0	0	22	35	61														
NGBS500	27	34	28	60	63	31	75	27	64	36	131	155	226	148	114	235	40	110	227	116	253	99	97	28	88	32	28	23	113	79	32	58	61	28	28	32	35	67	28													
NGBS515	59	66	62	72	75	63	87	59	76	68	143	167	240	160	126	247	72	124	239	128	265	111	109	60	100	64	66	63	125	91	64	70	73	60	60	64	73	79	60	66												
NGBS516	229	236	232	234	237	233	237	229	238	237	235	259	138	252	222	73	242	218	129	220	159	241	239	230	248	234	236	233	217	253	234	240	235	230	230	234	243	241	230	236	248											
NGBS551	107	114	110	112	115	111	115	107	116	116	93	113	208	106	10	213	120	12	209	8	231	115	113	108	128	112	114	111	15	131	112	118	113	108	108	112	121	119	108	114	126	218										
NGBS583	46	53	49	59	62	50	74	46	63	55	130	154	227	147	113	234	59	111	226	115	252	98	96	47	87	51	53	50	112	78	51	57	60	47	47	51	60	66	47	53	65	235	113									
NGBS593	63	70	66	68	43	67	83	63	72	72	139	163	236	156	124	243	76	120	235	124	261	107	105	64	96	68	70	67	121	87	68	74	69	64	64	68	77	75	64	70	82	244	122	69								
NGBS594	27	34	30	60	63	31	75	27	64	36	131	155	228	148	114	235	40	110	227	116	253	99	97	28	88	32	26	25	113	79	32	58	61	28	28	32	35	67	28	28	66	236	114	53	70							
NGBS596	9	32	28	56	61	27	73	9	62	34	127	153	224	146	110	233	38	106	223	114	251	97	95	26	84	30	32	29	111	77	30	56	59	26	26	30	39	65	26	32	64	234	112	51	68	32						
NGBS607	26	33	29	59	62	30	74	26	63	35	130	154	227	147	113	234	39	109	226	115	252	98	96	27	87	31	25	24	112	78	31	57	60	27	27	31	34	66	27	27	65	235	113	52	69	19	31					
NGBS609	26	33	29	59	62	30	74	26	63	35	130	154	227	147	113	234	39	109	226	115	252	98	96	27	87	31	25	24	112	78	31	57	60	27	27	31	34	66	27	27	65	235	113	52	69	19	31	0				
NGBS613	66	73	69	29	74	70	86	66	33	75	142	166	239	159	127	246	79	123	238	127	264	110	108	67	99	71	73	70	124	58	71	77	40	67	67	71	80	46	67	73	85	247	125	72	81	73	71	72	72			
NGBS614	130	139	135	135	140	134	140	130	141	141	136	162	235	155	125	240	145	119	230	123	258	144	142	133	151	137	139	136	120	156	137	143	138	133	133	137	146	144	133	139	151	241	121	138	147	139	135	138	138	150		
NGBS622	125	132	128	132	135	129	135	125	136	134	133	153	226	146	116	231	138	116	227	114	249	135	133	126	148	130	132	129	111	151	130	138	133	126	126	130	139	139	126	132	146	236	112	133	142	132	130	131	131	145	79	
NGBS625	222	229	225	227	230	226	230	222	231	230	228	250	129	243	213	70	235	211	122	211	150	232	230	223	243	227	229	226	208	246	227	233	228	223	223	227	236	234	223	229	241	73	209	228	237	229	227	228	228	240	234	227

NGBS636	69	76	72	74	77	73	1	69	78	78	133	157	230	150	118	237	82	114	229	118	255	101	99	70	64	74	76	73	115	93	74	80	75	70	70	74	83	81	70	76	88	238	116	75	84	76	74	75	75	87	141	136	231		
NGBS641	226	233	228	231	234	230	234	226	235	235	232	252	7	245	215	130	239	215	124	213	152	234	232	227	247	231	233	230	210	250	231	237	232	227	227	231	240	238	227	231	245	135	211	232	241	233	231	232	232	244	238	229	126	235	
NGBS650	21	28	20	54	57	21	69	21	58	26	125	149	222	142	108	229	30	104	221	110	247	93	91	12	82	18	28	25	107	73	24	52	55	0	0	22	35	61	0	28	60	230	108	47	64	28	26	27	27	67	133	126	223	70	227

Table S4. Predicted function of genes found in MGEs depicted in Figure 4.

Genetic Element	Gene Number (Fig. 4)	Putative function	Encoded Protein size (aa)	Top BLASTp hit description	GenBank Accession Number	% Identity (/aa)
Tn*5801*	1	Tn916 hypothetical protein	104	MULTISPECIES: hypothetical protein [Bacilli]	WP_000421280.1	100% (/104)
	2	Tn916 hypothetical protein	125	MULTISPECIES: hypothetical protein [Bacilli]	WP_001234189.1	100% (/125)
	3	Hypothetical protein	257	MULTISPECIES: hypothetical protein [Bacilli]	WP_000185760.1	100% (/257)
	4	DNA translocase FtsK	467	MULTISPECIES: cell division protein FtsK [Bacilli]	WP_002320760.1	100% (/467)
	5	Transcriptional regulator, Tn916	394	MULTISPECIES: Cro/Cl family transcriptional regulator [Bacilli]	WP_000426691.1	100% (/394)
	6	Tn916 hypothetical protein	90	MULTISPECIES: hypothetical protein [Bacilli]	WP_000055367.1	100% (/90)
	7	Tn916 hypothetical protein	253	Hypothetical protein [*Streptococcus agalactiae*]	WP_047199803.1	100% (/253)
	8	Tn916 ORF16 ATP/GTP-binding protein	166	MULTISPECIES: antirestriction protein ArdA [Bacilli]	WP_000421245.1	99% (/166)
	9	Hypothetical protein	341	Hypothetical protein HMPREF9524_00211 [*Enterococcus faecium* TX0133a01]	EFR69551.1	100% (/341)
	10	Hypothetical protein	131	Tn*916* ORF17-like protein lmo1107 [*Streptococcus agalactiae* COH1]	EAO75913.1	100% (/131)
	11	ATP/GTP-binding protein	817	MULTISPECIES: ATP/GTP-binding protein [Bacilli]	WP_000941001.1	100% (/817)
	12	Transmembrane amino acid transporter protein	675	MULTISPECIES: membrane protein [Bacilli]	WP_000192390.1	100% (/675)
	13	Cell wall hydrolase, lytic transglycolase	309	Peptidase P60 [*Streptococcus agalactiae*]	WP_000768375.1	100% (/309)
	14	Tn*916* ORF13 protein	198	Tn*916* ORF13 protein [*Streptococcus agalactiae*]	CFR23594.1	100% (/198)

	15	Tn*916* ORF13 protein	91	Tn*916* ORF13 protein [*Streptococcus agalactiae*]	CFQ21202.1	100% (/91)
	16	Tetracycline resistance protein TetM	639	MULTISPECIES: tetracycline resistance protein TetM [Firmicutes]	WP_000691737.1	100% (/639)
	17	Transcriptional regulator, Tn916	117	MULTISPECIES: DNA-binding protein [Bacilli]	WP_001227349.1	100% (/117)
	18	Tn916 hypothetical protein	140	conserved hypothetical protein [*Enterococcus faecalis* T8]	EEU24686.1	100% (/140)
	19	Polyribonucleotide nucleotidyltransferase	76	MULTISPECIES: hypothetical protein [Bacilli]	WP_000845144.1	100% (/76)
	20	Hypothetical protein	66	Conserved hypothetical protein *[Streptococcus agalactiae* COH1]	EAO75937.1	100% (/66)
	21	Site-specific recombinase, phage integrase family	397	MULTISPECIES: integrase [Bacilli]	WP_000237798.1	100% (/397)
Tn*916*	1	Tn*916* hypothetical protein	104	MULTISPECIES: hypothetical protein [Bacteria]	WP_000420682.1	100% (/104)
	2	Tn*916* hypothetical protein	127	MULTISPECIES: hypothetical protein [Bacteria]	WP_000985015.1	100% (/127)
	3	DNA translocase FtsK	461	MULTISPECIES: cell division protein FtsK [Bacteria]	WP_000813488.1	100% (/461)
	4	Cro/CI family transcriptional regulator	401	Cro/Cl family transcriptional regulator [*Streptococcus pseudopneumoniae*]	WP_049519213.1	100% (/401)
	5	Tn*916* hypothetical protein	73	MULTISPECIES: conjugal transfer protein [Bacteria]	WP_001009056.1	100% (/73)
	6	Tn*916* hypothetical protein	165	MULTISPECIES: antirestriction protein ArdA [Bacteria]	WP_000342539.1	100% (/165)
	7	Tn*916* hypothetical protein	168	MULTISPECIES: membrane protein [Bacteria]	WP_000506270.1	100% (/168)
	8	Tn*916* ORF16 ATP/GTP-binding protein	815	MULTISPECIES: ATP/GTP-binding protein [Bacteria]	WP_000331160.1	100% (/815)
	9	Tn*916* ORF15 signal peptide containing protein	725	MULTISPECIES: membrane protein [Bacteria]	WP_000804748.1	100% (/725)
	10	Tn*916*, NLP/P60 family protein	333	Peptidase P60 [*Streptococcus agalactiae*]	WP_029141002.1	99% (/333)

11	Tn*916* ORF13 protein	311	hypothetical protein SII_0646 [*Streptococcus intermedius* C270]	AGU77833.1	100% (/311)
12	Tetracycline resistance protein TetM	639	tetracycline resistance ribosomal protection protein [*Streptococcus agalactiae*]	WP_000691753.1	100% (/639)
13	Tn*916*, transcriptional regulator	117	MULTISPECIES: DNA-binding protein [Bacteria]	WP_001227347.1	100% (/117)
14	Tn*916* hypothetical protein	140	MULTISPECIES: DNA-binding protein [Bacteria]	WP_000804885.1	100% (/140)
15	Tn*916* hypothetical protein	76	MULTISPECIES: hypothetical protein [Bacteria]	WP_000857133.1	100% (/76)
16	Tn*916*, excisionase	67	MULTISPECIES: excisionase [Bacteria]	WP_000814511.1	100% (/67)
17	Tn*916*, transposase	405	MULTISPECIES: transposase [Bacteria]	WP_001291561.1	100% (/405)

Table S5. Predicted function of genes found in the strains depicted in Figure 5.

	NGBS128	**NGBS417**	**NGBS205**
1	AroA	AroA	AroA
2	AroK	AroK	AroK
3	Psr protein	Psr protein	Psr protein
4	RNA methyltransferase	RNA methyltransferase	RNA methyltransferase
5	group II intron-interrupted relaxase ltrB	Double zinc ribbon	Hypothetical protein
6	AphA	PlcR family transcriptional regulator	Replication initiator protein A
7	Cytoplasmic protein	Hypothetical protein	Hypothetical protein
8	TetR family transcriptional regulator	Positive control sigma-like factor	C-5 cytosine-specific DNA methylase
9	TetR family transcriptional regulator	Hypothetical protein	Hypothetical protein
10	Cell wall surface anchor family protein, truncation	Phage protein	Arsenate reductase
11	IS5 family transposase orfB	Phage protein	Hypothetical protein
12	Transposase	Phage protein	protease
13	Chaperone protein HslO	Hypothetical protein	Hypothetical protein
14	AraC family transcriptional regulator	Prophage LambdaSa04, DAN polymerase	Type IV secretory pathway, VirD4 component
15	Cell wall surface anchor family protein	Phage regulatory protein, Rha family	membrane protein
16	Cell wall surface anchor family protein	Hypothetical protein	Orf23
17	Sortase family protein	Hypothetical protein	Orf25
18	Sortase	Prophage LambdaSa04, DNA primase	Orf26
19	Cell wall surface anchor family protein	Phage protein	Orf28
20	Sortase family protein	Prophage LambdaSa04, SNF2 family helicase	AbiGII
21	Cna B domain-containing protein	Hypothetical protein	AbiGI
22	Orf28	Phage endonuclease	Agglutinin receptor
23	Hypothetical protein	Phage terminase, small subunit	Calcium-binding protein
24	Hypothetical protein	S-adenosylmethionine synthetase	Hypothetical protein
25	Lipoprotein	adenine-specific methyltrasferase	SNF2 family protein
26	ABC transporter ATP-binding protein	DNA methylase	group II intron reverse transcriptase/maturase
27	ABC transporter ATP-binding protein	Hypothetical protein	SNF2 family protein
28	Membrane protein	Hypothetical protein	Hypothetical protein
29	ABC transporter permeae	Hypothetical protein	Membrane protein

30	cylX protein	Prophage LambdaSa04, terminase, large subunit	Parvulin-like peptidyl-prolyl isomerase
31	cylD	Hypothetical protein	TnpV
32		Portal protein	Tetracycline resistance protein TetO
33		Prophage LambdaSa04, ClpP endopeptidase	Hypothetical protein
34		Prophage LambdaSa04, HK97 family major capsid protein	ResP
35		Phage protein	DNA topoisomerase
36		Phage protein	DNA recombinase
37		Prophage pi2 protein 37	Recombinase
38		Prophage pi2 protein 38	DNA recombinase
39		Hypothetical protein	Helix-turn-helix domain-containing protein
40		Prophage pi2 protein 39	Nucleotidyltransferase
41		Hypothetical protein	Aethyltransferase
42		Hypothetical protein	AadE_1
43		RelE	Sat
44		Phd_YefM	ISSdy1, transposase OrfA
45		Tail protein, phage associated	Transposase
46		Hypothetical protein	AphA
47		Hypothetical protein	Erythromycin ribosome methylase ErmB
48		Hypothetical protein	Hypothetical protein
49		Hypothetical protein	Delta protein
50		Prophage LambdaSa04, holin	Omega protein
51		Cpl-7 lysozyme C-terminal domain	Epsilon-antitoxin
52		Putative choloylglycine hydrolase	Toxin of epsilon-zeta postsegregational killing system
53		Hypothetical protein	Polynucleotide kinase
54		DNA recombinase	AadE_2
55		Resolvase family site-specific recombinase	Toxin of epsilon-zeta postsegregational killing system
56		Recombinase	Hypothetical protein
57		Site-specific recombinase	Hypothetical protein
58		Site-specific recombinase	TraG/TraD family protein
59		Erm Leader peptide	Site-specific recombinase
60		ErmTR	DNA primase
61		Spectinomycin phosphotransferase	Hypothetical protein
62		Cytidine deaminase	Glutamate-cysteine ligase
63		Cytidine deaminase	ATPases with chaperone activity, ATP-binding subunit
64		Zn-dependent hydrolase	Transcriptional regulator

65	Group II intron-interrupted relaxase ltrB	Signal recognition particle GTPase
66	AphA	phosphoesterase
67	Cytoplasmic protein	ORF10
68	TetR family transcriptional regulator	ORF9
69	TetR family transcriptional regulator	ORF4 relaxase
70	Cell wall surface anchor family protein, truncation	NsuP
71	IS5 family transposase orfB	NsuR
72	Transposase	NsuK
73	Transposase	NsuF
74	HslO	NsuE
75	Chaperone protein HslO	NsuG
76	AraC family transcriptional regulator	NsuC
77	Cell wall surface anchor family protein	NsuI
78	Cell wall surface anchor family protein	DNA-binding protein
79	Sortase family protein	Resolvase family site-specific recombinase
80	Sortase	Orf28
81	Cell wall surface anchor family protein	Hypothetical protein
82	Sortase family protein	Hypothetical protein
83	Cna B domain-containing protein	lipoprotein
84	Orf28	ABC transporter ATP-binding protein
85	Hypothetical protein	ABC transporter ATP-binding protein
86	Hypothetical protein	Membrane protein
87	Lipoprotein	ABC transporter permeae
88	ABC transporter ATP-binding protein	CylX protein
89	ABC transporter ATP-binding protein	CylD
90	Membrane protein	
91	ABC transporter permeae	
92	CylX protein	
93	CylD	

Table S6. Primers used for circularization of plasmid pNGBS128.

Primer	Sequence	Amplicon Size (bp)
pNGBS128_F1	GGGTAAAATTAGGGTTCAGGC	345
pNGBS128_R1	TCAGCGGTTACTGGATTATTTG	
pNGBS128_F2	AGCATCCTTACTTTCATGCG	273
pNGBS128_R2	ACGGTTAGAAAAAATCGGCG	