Table S2. Oligoprimer sequence for 80-tagSNPs typing for *B. anthracis*

	SNPs		Forward primer		Reverse primer						
Well	Target	Position [a]	primer name	primer sequence	primer name	primer sequence	Position of amplicon [a]	Amplicon size (bp)	ORF ID	Gene	Product
A1	Chromosome	4429	01_BA_grs4429_F1	GCACTGTCCCTAAAATTAGC	01_BA_grs4429_R1	GGGATTACGCCCTATCTATTT	4291 - 4549	259	GBAA0004	*recF*	recombination protein F
B1	Chromosome	23173	02_BA_grs23173_F1	TAGCTAATGCAGTTGTCATAGT	02_BA_grs23173_R1	ACTACAGCTCACAAAAGATTAT	23025 - 23298	274	GBAA0015	–	deoxynucleoside kinase family protein
C1	Chromosome	39396	03_BA_grs39396_F1	GAAAGATATGCCGGAGAAAC	03_BA_grs39396_R1	TCTTTCCCTGCCTTAGGATA	39249 - 39548	300	GBAA0031	–	hypothetical protein
D1	Chromosome	40930	04_BA_grs40930_F1	GTCGCTAAAGATCGAGATTTGT	04_BA_grs40930_R1	TCCAATCGAATTACGCCGTAC	40737 - 41054	318	GBAA0034	*abrB*	transition state transcriptional regulatory protein AbrB
E1	Chromosome	69952	05_BA_grs69952_F1	TAACTCTAGCCAGGGAGAAC	05_BA_grs69952_R1	ATAACTTCGCCTTACTTTTCC	69806 - 70056	251	GBAA0064	*ftsH*	cell division protein FtsH
F1	Chromosome	97542	06_BA_grs97542_F1	TGCTCGTCATCAAGATGGTAA	06_BA_grs97542_R1	TGCCTCTAGCTCTTCTTCTGT	97415 - 97673	259	GBAA0086	*gltX*	glutamyl–tRNA synthetase
G1	Chromosome	176587	07_BA_grs176587_F1	GGCTTAATTTTGCACCTAATG	07_BA_grs176587_R1	ACCGAAGTATTTTCAACAGTAA	176441 - 176762	322	GBAA0175	–	ABC transporter substrate–binding protein
H1	Chromosome	182106	08_BA_grs182106_F1	AAAGCGGAGACAATTCCAGG	08_BA_grs182106_R1	CTACTACTACAACGCCCTCTA	181932 - 182205	274	GBAA0180	–	hypothetical protein
A2	Chromosome	199433	09_BA_grs199433_F1	GCATCGGTCATGGGAATTATT	09_BA_grs199433_R1	CCCAACCAATCCATGCAACTA	199256 - 199538	283	GBAA0199	–	nucleoside transporter
B2	Chromosome	240050	10_BA_grs240050_F1	GCGCCAATTTTGGTGTTAGGT	10_BA_grs240050_R1	TGCGTATAAACTCCTTCCAACT	239952 - 240211	260	GBAA0252	*dal1*	alanine racemase
C2	Chromosome	333553	11_BA_grs333553_F1	ACGCGGCCTACTTCTACTAT	11_BA_grs333553_R1	AGCCACCCCTAACTTCCAAT	333442 - 333707	266	GBAA0325	*gabT*	4–aminobutyrate aminotransferase
D2	Chromosome	350432	12_BA_grs350432_F1	TTGCGAGTATAGAAGGAATGAT	12_BA_grs350432_R1	TCTGCTGCTGTAAACTTCAATG	350277 - 350583	307	GBAA0340	–	transcriptional regulator domain–containing protein
E2	Chromosome	364527	13_BA_grs364527_F1	TGGAATGGTTTCTTCGCATAA	13_BA_grs364527_R1	CTAAAGGAACAGCGTAATGTAA	364393 - 364678	286	GBAA0352 – 0353	noncoding region	noncoding region
F2	Chromosome	382874	14_BA_grs382874_F1	CGCTTCGAAAGTTAGAGGAG	14_BA_grs382874_R1	TCAGCGCCAGAAGAAATCTC	382756 - 383026	271	GBAA0370	–	methyl–accepting chemotaxis protein
G2	Chromosome	515111	15_BA_grs515111_F1	GGGGGATCAAGTTTGACAC	15_BA_grs515111_R1	CCTTCCCATGCTTTTAACAC	514971 - 515239	269	GBAA0522	*mutY*	A/G–specific adenine glycosylase
H2	Chromosome	569295	16_BA_grs569295_F1	CCTGGTATAAGTGGTGTAAAG	16_BA_grs569295_R1	TGATTGATAGCGGTTTATTCG	569148 - 569469	322	GBAA0561	–	citrate transporter
A3	Chromosome	610254	17_BA_grs610254_F1	ATGCAATGCGTGTACTACGA	17_BA_grs610254_R1	GAATACCCTGTCGATTTAAGC	610118 - 610451	334	GBAA0595 – 0596	noncoding region	noncoding region
B3	Chromosome	701044	18_BA_grs701044_F1	AGAGAGGGTACAAGATATGC	18_BA_grs701044_R1	AGCGAGTCATTCTATTACACTA	700968 - 701224	257	GBAA0682	–	hypothetical protein
C3	Chromosome	835614	19_BA_grs835614_F1	TAGGCATTTTAGTCGGCTGGA	19_BA_grs835614_R1	TGCTACCGGCTGAATTGCTAA	835445 - 835740	296	GBAA0823	–	PTS system, sucrose–specific IIBC component
D3	Chromosome	965285	20_BA_grs965285_F1	ACCATCGAAATTGGATGATCAG	20_BA_grs965285_R1	CCTCAATATGACAGCAGATTC	965143 - 965393	251	GBAA0961	–	hypothetical protein
E3	Chromosome	973706	21_BA_grs973706_F1	GGAAATTAAACGGTAAACTTGG	21_BA_grs973706_R1	CAAGCAACATAATCCCCTAAT	973613 - 973863	251	GBAA0972	–	hypothetical protein
F3	Chromosome	1052069	22_BA_grs1052069_F1	GGAGCTGCACACTTAGTGA	22_BA_grs1052069_R1	GGATTTACTTCTGGGAATACA	1051906 - 1052156	251	GBAA1070	*hemE*	uroporphyrinogen decarboxylase
G3	Chromosome	1136244	23_BA_grs1136244_F1	GCGTTTGTTACTTCAGGTAATT	23_BA_grs1136244_R1	TGTTCAATCGATCCTATTTGTA	1136046 - 1136375	330	GBAA1166 – 1167	noncoding region	noncoding region
H3	Chromosome	1296700	24_BA_grs1296700_F1	GAAATTGAAGCATGGCTACAC	24_BA_grs1296700_R1	CGTGGTTTTACATTCACTTCTG	1296531 - 1296835	305	GBAA1353 – 1354	noncoding region	noncoding region
A4	Chromosome	2423657	25_BA_grs2423657_F1	GTTAAGCATATTAAAGAGTAGC	25_BA_grs2423657_R1	CTAACACTCAACCGTTAATTTT	2423550 - 2423815	266	GBAA2601 – 2602	noncoding region	noncoding region
B4	Chromosome	2548040	26_BA_grs2548040_F1	ACCGTCTGTTCTTTAATGATC	26_BA_grs2548040_R1	TGGGTTTTATGTTGTTATTGAG	2547877 - 2548167	291	GBAA2732 – 2733	noncoding region	noncoding region
C4	Chromosome	2619247	27_BA_grs2619247_F1	TAGCTCTTTGCTCTCTTAATTC	27_BA_grs2619247_R1	AGATTATCCAACTGCCATCGTA	2619137 - 2619414	278	GBAA2823	–	hypothetical protein
D4	Chromosome	2637448	28_BA_grs2637448_F1	CTGATCGAAGTGATGACTTAAT	28_BA_grs2637448_R1	GGCTTCACATCTAAATTCTGTA	2637327 - 2637636	310	GBAA2841	–	hypothetical protein
E4	Chromosome	2832579	29_BA_grs2832579_F1	TGGCTTATTCGCTGGATTCG	29_BA_grs2832579_R1	TACGCCAAGTAAATGAGATGGT	2832482 - 2832764	283	GBAA3074	–	hypothetical protein
F4	Chromosome	2979236	30_BA_grs2979236_F1	CACTCCTACATAAGCGAAATA	30_BA_grs2979236_R1	GTATATGGGGCTTACAGTTTT	2979043 - 2979346	304	GBAA3232 – 3234	noncoding region	noncoding region
G4	Chromosome	3237313	31_BA_grs3237313_F1	CTTACTCACCGTAAAACGTTA	31_BA_grs3237313_R1	GCTTTTGATTCATGCATATGG	3237173 - 3237453	281	GBAA3527 – 3529	noncoding region	noncoding region
H4	Chromosome	3491802	32_BA_grs3491802_F1	CTCTGATTTTGCGCTAGTTAA	32_BA_grs3491802_R1	GAGTATAAAGAGTTGGGAAGAT	3491676 - 3491928	253	GBAA3805	–	prophage LambdaBa01, acyltransferase, putative
A5	Chromosome	3494352	33_BA_grs3494352_F1	CATTAATTCGGGATGCTTCTTC	33_BA_grs3494352_R1	AACGGTACTTTAGTGGGTTTTA	3494204 - 3494548	345	GBAA3807	–	hypothetical protein
B5	Chromosome	3495050	34_BA_grs3495050_F1	CACCATATACTTTAGCGATATT	34_BA_grs3495050_R1	GGTTTCGTGTTATAAGAGAACT	3494932 - 3495199	268	GBAA3809 – 3810	noncoding region	noncoding region
C5	Chromosome	3755462	35_BA_grs3755462_F1	TCAATCTCATACGACTGTACT	35_BA_grs3755462_R1	ACACTATGGTTAGACATAAGTA	3755296 - 3755588	293	GBAA4078	–	phage minor structural protein
D5	Chromosome	4285510	36_BA_grs4285510_F1	GTCCGCCTCTTTTTCTAGATTT	36_BA_grs4285510_R1	AGCGAAGTAAACCAATCTTCTA	4285357 - 4285658	302	GBAA4706 – 4707	noncoding region	noncoding region
E5	Chromosome	4347810	37_BA_grs4347810_F1	GCTCTTCCATCGGACTTTTTT	37_BA_grs4347810_R1	CGAGATTGTTACGAAAGGTAAG	4347661 - 4348002	342	GBAA4783	–	hypothetical protein
F5	Chromosome	4703906	38_BA_grs4703906_F1	ATTTCTATATAGTGCCATAGTC	38_BA_grs4703906_R1	TTTGAATGGCAAGAAGTATATG	4703792 - 4704045	254	phnA – GBAA5178	noncoding region	noncoding region
G5	Chromosome	4847882	39_BA_grs4847882_F1	ATGGAGCTGAACTGTTAGAAG	39_BA_grs4847882_R1	TCTTGTTTCGAAAACGTTGTAA	4847744 - 4847995	252	GBAA5352	–	hypothetical protein
H5	Chromosome	4853350	40_BA_grs4853350_F1	AATGCAGCTAAAACTGTTGTAC	40_BA_grs4853350_R1	CGGATAAGCTCTGAAGTATCA	4853223 - 4853542	320	GBAA5358	–	hypothetical protein
A6	Chromosome	5205097	41_BA_grs5205097_F1	TGCCATTTCAATCGCTTGTCT	41_BA_grs5205097_R1	GAAGGATGGTCGTACAGGT	5205006 - 5205261	256	GBAA5714	*yycG*	sensory box histidine kinase YycG
B6	pXO1	6815	42_BA_p1rs6815_F1	AGCCTCTCTTTATCCTTAACAA	42_BA_p1rs6815_R1	GGAACCACTTGAAAGTAATCAC	6655 - 6915	261	GBAA_pXO1_0011	-	reverse transcriptase/endonuclease protein, (pxo1–07)
C6	pXO1	7452	43_BA_p1rs7452_F1	GGTGACCAGTAATTTGCTATA	43_BA_p1rs7452_R1	GAAGAAGCTGAAAGTATGTATG	7303 - 7604	302	GBAA_pXO1_0011	-	reverse transcriptase/endonuclease protein, (pxo1–07)
D6	pXO1	8226	44_BA_p1rs8226_F1	CGACATTCCCATTGAGGTTCT	44_BA_p1rs8226_R1	ATCTATCGTGCCGAACAATTC	8032 - 8381	350	GBAA_pXO1_0011	-	reverse transcriptase/endonuclease protein, (pxo1–07)
E6	pXO1	16266	45_BA_p1rs16266_F1	CCTCTAACACATTTCCTTTAAC	45_BA_p1rs16266_R1	GCTTGTGTGATGTTTGGAAAGA	16121 - 16459	339	GBAA_pXO1_0019	-	hypothetical protein
F6	pXO1	16661	46_BA_p1rs16661_F1	TAAGCCCTCTACCATTTTAGC	46_BA_p1rs16661_R1	CTGAAAGCGTTAAGGCATATT	16509 - 16802	294	GBAA_pXO1_0019	-	hypothetical protein
G6	pXO1	21211	47_BA_p1rs21211_F1	GCGTACTCTTTCTGTAAAACA	47_BA_p1rs21211_R1	CCGCTATTCTCATCCATTACT	21072 - 21397	326	GBAA_pXO1_0021 – 0022	noncoding region	noncoding region
H6	pXO1	22801	48_BA_p1rs22801_F1	GGCGTCATTCCAAATGTAAC	48_BA_p1rs22801_R1	ATAGCTTAAAGAAAGCCTTTGT	22661 - 22919	259	GBAA_pXO1_0023	-	hypothetical protein
A7	pXO1	30910	49_BA_p1rs30910_F1	GCAGCATTAAAAGGTTATGAGT	49_BA_p1rs30910_R1	CGTTGTTCGCTTAGAACTTAT	30748 - 31087	340	GBAA_pXO1_0034	-	hypothetical protein
B7	pXO1	33638	50_BA_p1rs33638_F1	CCTTTTCGAGGCGTACATTC	50_BA_p1rs33638_R1	CAGGATAACTGTTCAGATAAG	33478 - 33746	269	GBAA_pXO1_0036 – 0037	noncoding region	noncoding region
C7	pXO1	41424	51_BA_p1rs41424_F1	ACCTGCTACTATAGAGCATCAT	51_BA_p1rs41424_R1	AGAAGCAGTGTTCATCACTTAT	41290 - 41567	278	GBAA_pXO1_0048	-	TetR family transcriptional regulator
D7	pXO1	45155	52_BA_p1rs45155_F1	AAGTTTCCTTTATCCGCAATCT	52_BA_p1rs45155_R1	TGAATCTGATGCGAAGAACTAT	45038 - 45340	303	GBAA_pXO1_0052	-	hypothetical protein
E7	pXO1	45588	53_BA_p1rs45588_F1	TCAATTCATATTCAGGTTGATC	53_BA_p1rs45588_R1	TAATCGTGAGGGAGGTTATTAT	45429 - 45698	270	GBAA_pXO1_0053	-	hypothetical protein
F7	pXO1	61814	54_BA_p1rs61814_F1	GCGATGAATGTGATTGGTTTCT	54_BA_p1rs61814_R1	CAATGAAGTAGTTGGCGCTAT	61685 - 61979	295	GBAA_pXO1_0071 – 0072	noncoding region	noncoding region
G7	pXO1	106657	55_BA_p1rs106657_F1	TGATGATTGTTCGTGCTACTTA	55_BA_p1rs106657_R1	GACGTAATAGCTTTTATCTTTC	106486 - 106854	369	GBAA_pXO1_0123 – 0124	noncoding region	noncoding region
H7	pXO1	123207	56_BA_p1rs123207_F1	TGAAATTGGAAAGGGGATTTCT	56_BA_p1rs123207_R1	ACTCTAATACCGTTCTATGGTC	123120 - 123382	263	GBAA_pXO1_0142	*cyaA*	calmodulin–sensitive adenylate cyclase
A8	pXO1	126170	57_BA_p1rs126170_F1	TTTCTCCCATATATGATGAGTG	57_BA_p1rs126170_R1	GCGGGTTATTTTACAGGCTA	126039 - 126340	302	GBAA_pXO1_0142 – 0145	noncoding region	noncoding region
B8	pXO1	138295	58_BA_p1rs138295_F1	GGGTTATTCTTGTTTTCTATGC	58_BA_p1rs138295_R1	TTACACATTTCAGGAGCTATCG	138164 - 138460	297	GBAA_pXO1_0157	*gerXA*	spore germination protein xa
C8	pXO1	139826	59_BA_p1rs139826_F1	GGCAAAGGACAAATAATGATG	59_BA_p1rs139826_R1	TCCCTCACCTTTTCCAATATA	139723 - 139974	252	GBAA_pXO1_0158	*gerXC*	spore germination protein xc, (pxo1–112)
D8	pXO1	144759	60_BA_p1rs144759_F1	AGGACGGATTGATAAGAATGTA	60_BA_p1rs144759_R1	TTTCAGCCCAAGTTCTTTCC	144585 - 144910	326	GBAA_pXO1_0164	*pagA*	protective antigen
E8	pXO1	149661	61_BA_p1rs149661_F1	GTTCTCCCATACGAAGTTAAAT	61_BA_p1rs149661_R1	GTTTTTACCGATATTACTCTCC	149496 - 149800	305	GBAA_pXO1_0172	*lef*	lethal factor
F8	pXO1	159234	62_BA_p1rs159234_F1	AGCTCGTACAAGGATATAAAGA	62_BA_p1rs159234_R1	CCTTATCTACTTCCAGTGTATC	159112 - 159400	289	GBAA_pXO1_0186 – 0191	noncoding region	noncoding region
G8	pXO1	180878	63_BA_p1rs180878_F1	GCCTTTGGCATATGTACTATCA	63_BA_p1rs180878_R1	GCCAATATGTCCACTACTCTA	180753 - 181061	309	GBAA_pXO1_0217	–	hypothetical protein
H8	pXO2	1546	64_BA_p2rs1546_F1	ATTTCCATATACCCACCTACT	64_BA_p2rs1546_R1	CAAAACGCATACGAAGTGCT	1431 - 1702	272	GBAA_pXO2_0002 – 0003	noncoding region	noncoding region
A9	pXO2	2846	65_BA_p2rs2846_F1	CGTTAACACTTGGCTGATATT	65_BA_p2rs2846_R1	ATCCAGTGAAACGATGAATAGA	2677 - 2971	295	GBAA_pXO2_0005	-	hypothetical protein
B9	pXO2	4060	66_BA_p2rs4060_F1	AGGATTACCGTTGTACTTCAAA	66_BA_p2rs4060_R1	GTTAGCAGCAAATAATAAAACC	3916 - 4210	295	GBAA_pXO2_0007	-	nlp/p60 family protein, (pxo2-08)
C9	pXO2	9741	67_BA_p2rs9741_F1	CCGCCTTTGGCAGTATTCTTT	67_BA_p2rs9741_R1	GGGTTTAAATTTACGAGTCTAC	9567 - 9938	372	GBAA_pXO2_0013	-	membrane protein, putative, (pxo2-14)
D9	pXO2	14993	68_BA_p2rs14993_F1	GTCTCTGCTTCGCTAAGGT	68_BA_p2rs14993_R1	TGAAGAAATGCCAATGCATGAA	14817 - 15170	354	GBAA_pXO2_0016	-	hypothetical protein
E9	pXO2	18963	69_BA_p2rs18963_F1	CGAGCCTTTTCGGTGATGTT	69_BA_p2rs18963_R1	TGATTGAGGATGTCCCTGAAA	18833 - 19084	252	GBAA_pXO2_0023	-	type II/IV secretion system protein, (pxo2-25)
F9	pXO2	22433	70_BA_p2rs22433_F1	TACACCATGAAAGGCAGAAC	70_BA_p2rs22433_R1	CGCAAGGAAATCAAGTAGGA	22290 - 22566	277	GBAA_pXO2_0028	-	hypothetical protein
G9	pXO2	23320	71_BA_p2rs23320_F1	CTGCGATTTCTCCATATTTTC	71_BA_p2rs23320_R1	TTAAATGTTCATGCTGTTACTG	23182 - 23470	289	GBAA_pXO2_0028	-	hypothetical protein
H9	pXO2	25290	72_BA_p2rs25290_F1	AAGGATTGGTGGACTTCTAGT	72_BA_p2rs25290_R1	AAGGAATGAAAGTTAGTACTGA	25163 - 25445	283	GBAA_pXO2_0029	-	hypothetical protein
A10	pXO2	29080	73_BA_p2rs29080_F1	ACTGCTATATCTAACCAAACTA	73_BA_p2rs29080_R1	GGCATGGGTTAATCTATAAATA	28908 - 29251	344	GBAA_pXO2_0033 – 0034	noncoding region	noncoding region
B10	pXO2	47449	74_BA_p2rs47449_F1	CACACGTCTAATAATGGACATC	74_BA_p2rs47449_R1	GGGAAAACCCATTGGAAGATA	47305 - 47617	313	GBAA_pXO2_0058 – 0059	noncoding region	noncoding region
C10	pXO2	54091	75_BA_p2rs54091_F1	TGTTGTCTCCACTGATACTTG	75_BA_p2rs54091_R1	TAAGCAAGGGATTATCTTCTAT	53894 - 54254	361	GBAA_pXO2_0064	*capA*	capsule biosynthesis protein capa, (pxo2-56)
D10	pXO2	55346	76_BA_p2rs55346_F1	ACCCTTGTCTTTGAATTGTATT	76_BA_p2rs55346_R1	GGTTTAGTTGTACCTGGTTATT	55212 - 55497	286	GBAA_pXO2_0065	*capC*	capsule biosynthesis protein capc, (pxo2-57)
E10	pXO2	57326	77_BA_p2rs57326_F1	TGAGAGAGTTTCATTCGGATTT	77_BA_p2rs57326_R1	GGAAAGGCATTTCTTCATTAC	57157 - 57464	308	GBAA_pXO2_0067	-	hypothetical protein
F10	pXO2	64320	78_BA_p2rs64320_F1	TGTCCCAAAATACCAAAGTAAA	78_BA_p2rs64320_R1	TAGTTCTTTATCCGTTGGCATA	64170 - 64420	251	GBAA_pXO2_0075 – 0077	noncoding region	noncoding region
G10	pXO2	79909	79_BA_p2rs79909_F1	CCTTAGGGGTTTTTGTTTTCAC	79_BA_p2rs79909_R1	GTGAGATTTCTACCAAGAATGA	79752 - 80048	297	GBAA_pXO2_0097	-	funz family protein, (pxo2-71)
H10	pXO2	83376	80_BA_p2rs83376_F1	CCGATATTAAAGTAGCAATTGA	80_BA_p2rs83376_R1	AGTGAAATGTATTCGGAAAGTT	83254 - 83547	294	GBAA_pXO2_0100	-	hypothetical protein
A11	anthrax toxin	*cyaA*	81_BA_cyaA_123560_F1	CCGACATGTTTGAGTATATGA	81_BA_cyaA_123560_R	TCCGAACTCTTTCCATGAACA	123392 - 123674	283	GBAA_pXO1_0142	*cyaA*	calmodulin–sensitive adenylate cyclase
B11	anthrax toxin	*pagA*	82_BA_pagA_143973_F1	AATGGCATTGTCTACGATATTA	82_BA_pagA_143973_R	CCCACATTGTTACATGATTATC	143808 - 144136	329	GBAA_pXO1_0164	*pagA*	protective antigen
C11	anthrax toxin	*capA*	83_capA_54568_F1	TCCTTTGCCTTACTAATTTGC	83_capA_54568_R1	AAGAAGCCGGATTTACAGTAT	54423 - 54717	295	GBAA_pXO2_0064	*capA*	capsule biosynthesis protein capa, (pxo2-56)
D11	anthrax toxin	*capB*	84_BA_capB_F1	GATTAAGCGCCGTAAAGAAG	84_BA_capB_R1	TTCTGCAACCTCTTTAAAGTAA	56241 - 56550	310	GBAA_pXO2_0066	*capB*	capsule biosynthesis protein capb, (pxo2–58)
E11	cereulide toxin	*cesA*	85_BC_cesA_F1	CGGGAAATGCAATTTACTGAA	85_BC_cesA_R1	TCCGTATTGTACTCTAATTTGA					
F11	cereulide toxin	*cesB*	86_BC_cesB_F1	CTGGCTAAAATTTGGCGTGAT	86_BC_cesB_R1	TATCTTTGGAATGCGCTCCG					

[a] Reference genome sequence of the *B. anthracis* Ames 0581 (chromosome, NC_007530; pXO1, NC_007322; pXO2, NC_007323)