TABLE S1. Genes required for *B. anthracis* growth, sporulation, or germination in the WAD205 mutant population.

Gene Name	**Description**[*]	***p* value**
BA0011	glutamine amidotransferase, SNO family	0.00241
BA0040	yabG protein	0.000498
BA0048	UDP-N-acetylglucosamine pyrophosphorylase	1.84E-08
BA0049	ribose-phosphate pyrophosphokinase	0.000947
BA0054	stage V sporulation protein B, putative	0.0015
BA0055	tetrapyrrole methylase family protein/MazG family protein	0.00086
BA0061	stage II sporulation protein E	0.000855
BA0065	transcriptional activator, putative, Baf family	0.000871
BA0075	TIM-barrel protein, putative, NifR3 family	0.0277
BA0079	phosphotransferase domain protein	0.00205
BA0091	RNA methyltransferase, TrmH family, group 3	0.00357
BA0107	translation elongation factor G	0.00197
BA0157	phosphoglucosamine mutase	0.00174
BA0177	lipoprotein, putative	0.00226
BA0180	conserved domain protein	4.01E-05
BA0189	oligopeptide ABC transporter, oligopeptide-binding protein	0.00264
BA0216	sugar-binding transcriptional regulator, LacI family	0.00132
BA0223	conserved hypothetical protein	0.000597
BA0240	4-hydroxyphenylpyruvate dioxygenase	0.000648
BA0309	delta-1-pyrroline-5-carboxylate dehydrogenase, putative	0.00115
BA0365	Rieske 2Fe-2S iron-sulfur protein, putative	0.00148
BA0369	methyl-accepting chemotaxis protein	0.00124
BA0371	glycosyl hydrolase family protein	0.000248
BA0379	methyl-accepting chemotaxis protein	0.00356
BA0383	ABC transporter, ATP-binding protein	0.00426
BA0390	major facilitator family transporter	0.000498
BA0403	conserved hypothetical protein	0.000572
BA0404	tellurite resistance protein, putative	0.000914
BA0410	heavy metal-transporting ATPase	0.000825
BA0411	transporter, EamA family	0.000912
BA0467	prophage LambdaBa04, prohead protease, putative	0.00105
BA0468	prophage LambdaBa04, major capsid protein, putative	0.000498
BA0501	PTS system, N-acetylglucosamine-specific IIBC component, putative	0.000914
BA0505	glycosyl transferase, group 2 family protein	0.000498
BA0514	chlorohydrolase family protein	0.00237
BA0554	glycine betaine transporter	0.000488
BA0555	microbial collagenase,putative	0.000597
BA0572	sensor histidine kinase	0.00384
BA0584	sensor histidine kinase	0.000805
BA0595	heavy metal-transporting ATPase	0.00176
BA0629	amino acid permease family protein	0.00154
BA0663	multidrug resistance protein, putative, authentic frameshift	0.000488
BA0675	alcohol dehydrogenase, zinc-containing	0.00264
BA0679	conserved hypothetical protein	0.000441
BA0687	conserved hypothetical protein	0.000119
BA0691	membrane protein, putative	0.000834
BA0709	spore germination protein GerLA	0.000119
BA0710	spore germination protein GerLB	0.000719
BA0715	phosphate ABC transporter, phosphate-binding protein, putative	0.0135
BA0716	phosphate ABC transporter, permease protein, putative	0.000282
BA0717	phosphate ABC transporter, permease protein, putative	2.43E-05
BA0719	transporter, AcrB/AcrD/AcrF family	0.00152

BA0789	conserved hypothetical protein	0.0041
BA0819	germination protein gerN	0.000914
BA0839	ABC transporter, substrate-binding protein, putative	0.0018
BA0872	N-acetylmuramoyl-L-alanine amidase, family 2	0.00151
BA0875	oxygen-independent coproporphyrinogen III oxidase, putative	0.00363
BA0927	conserved hypothetical protein	0.000397
BA0928	conserved domain protein	0.000726
BA0963	dihydroxyacetone kinase family protein	0.000678
BA1012	HD domain protein	1.84E-08
BA1027	glycerol-3-phosphate dehydrogenase, aerobic	0.000794
BA1075	endonuclease/exonuclease/phosphatase family	0.000783
BA1112	conserved hypothetical protein	0.000572
BA1126	transporter, EamA family	0.00343
BA1193	oligopeptide ABC transporter, permease protein	0.0148
BA1231	dTDP-4-dehydrorhamnose reductase	0.000834
BA1239	ATP-dependent DNA helicase, UvrD/REP family	0.00328
BA1299	spermidine/putrescine ABC transporter, permease protein	0.00556
BA1300	spermidine/putrescine ABC transporter, spermidine/putrescine-binding protein	0.002
BA1302	transporter, putative	0.00101
BA1304	ribosomal large subunit pseudouridine synthase, RluD subfamily	0.0211
BA1321	formate/nitrite transporter family protein	4.88E-06
BA1341	aminotransferase, class V	0.00141
BA1371	ribonucleoside-diphosphate reductase, alpha subunit, group I intron-containing	0.00189
BA1389	D-alanine-activating enzyme/D-alanine-D-alanyl carrier protein ligase	0.0012
BA1432	histidinol phosphatase, putative	0.00116
BA1456	sensor histidine kinase	0.0395
BA1490	D-alanyl-D-alanine carboxypeptidase family protein	0.000467
BA1492	spore maturation protein	0.000908
BA1495	ResB protein	0.0012
BA1496	ResC protein	0.00525
BA1510	negative regulator of competence MecA, putative	0.00192
BA1511	glutamate dehydrogenase	0.00153
BA1530	stage IV sporulation protein A	4.95E-06
BA1558	glycosyl transferase, group 1 family protein	0.000834
BA1559	polyA polymerase	3.57E-05
BA1563	pantoate--beta-alanine ligase	0.00155
BA1568	aspartate aminotransferase	5.34E-05
BA1583	conserved hypothetical protein	0.000634
BA1662	flagellar motor switch protein, putative	1.36E-05
BA1669	flagellar hook-associated protein, putative	0.00199
BA1715	flagellar biosynthetic protein FlhB, putative	2.44E-06
BA1747	hydrolase, alpha/beta fold family	5.91E-05
BA1799	proton/sodium-glutamate symporter	0.000536
BA1856	membrane protein, putative	0.000441
BA1868	oligopeptide ABC transporter, oligopeptide-binding protein, putative	0.0207
BA1887	enterotoxin	0.00476
BA1900	BNR repeat domain protein	0.0015
BA1917	rrf2 family protein	0.00202
BA2062	hypothetical protein	0.000691
BA2129	transcriptional regulator, GntR family	0.00138
BA2144	uroporphyrin-III C-methyltransferase, putative	0.0011
BA2175	arginyl-tRNA synthetase	0.000691
BA2238	penicillin-binding protein 3	0.00134
BA2258	lipoprotein, putative	0.000421
BA2370	2,3-dihydroxybenzoate-AMP ligase	0.000947
BA2372	nonribosomal peptide synthetase DhbF	0.000969

BA2393	ABC transporter, permease protein, putative	0.0274
BA2577	permease, putative	0.00137
BA2644	sporulation kinase B	0.000255
BA2688	conserved hypothetical protein	0.000834
BA2725	bacitracin synthetase, putative, authentic frameshift	0.000691
BA2975	sugar ABC transporter, sugar-binding protein, putative	0.00226
BA2999	conserved hypothetical protein	0.000129
BA3051	conserved domain protein	4.58E-05
BA3134	catalase, Mn-containing	0.000834
BA3199	arsenical resistance operon repressor	0.000488
BA3382	pyruvate kinase	0.0026
BA3394	protein-tyrosine phosphatase-like protein	0.00328
BA3428	gluconate kinase	0.000634
BA3438	alcohol dehydrogenase, zinc-containing	0.000834
BA3534	iron compound ABC transporter, permease protein	0.00152
BA3556	major facilitator family transporter	0.00285
BA3584	microbial collagenase, putative	0.00115
BA3604	argininosuccinate lyase	0.000834
BA3624	molybdopterin biosynthesis protein MoeB, putative	0.000597
BA3660	serine protease	0.00188
BA3705	sodium/proline symporter family protein	3.57E-05
BA3737	N-acetylmuramoyl-L-alanine amidase, family 2	0.0395
BA3744	transketolase	2.46E-05
BA3763	hypothetical protein	0.000397
BA3772	conserved hypothetical protein, authentic frameshift	0.00141
BA3778	prophage LambdaBa01, major tail protein, putative	0.0018
BA3820	hypothetical protein	0.000775
BA3872	peptidase T	0.00131
BA3879	sensory box/GGDEF family protein	0.00141
BA3923	conserved hypothetical protein	4.38E-07
BA3927	lipoprotein, Bmp family	0.00061
BA3933	metallo-beta-lactamase family protein	0.000805
BA3942	zinc protease, insulinase family	0.000507
BA3946	riboflavin biosynthesis protein RibC	0.00397
BA3982	ribosomal protein S16	0.000914
BA3983	signal recognition particle protein	2.15E-06
BA4007	phosphopantothenoylcysteine decarboxylase/phosphopantothenate--cysteine ligase	0.00115
BA4048	UDP-N-acetylenolpyruvoylglucosamine reductase	0.000908
BA4050	stage V sporulation protein E	0.000691
BA4053	UDP-N-acetylmuramoylalanyl-D-glutamyl-2,6-diaminopimelate ligase	0.000648
BA4077	hypothetical protein	0.000441
BA4078	phage minor structural protein	3.57E-05
BA4079	conserved hypothetical protein	0.000247
BA4157	pyruvate carboxylase	0.0135
BA4166	GTP-binding protein TypA	0.000571
BA4168	inositol monophosphatase family protein	0.00422
BA4228	maltosaccharide ABC transporter, permease protein	0.0011
BA4251	translation initiation factor, putative, aIF-2BI family	0.00241
BA4313	transcriptional regulator, Fur family	0.0108
BA4336	biotin synthetase	0.000507
BA4339	8-amino-7-oxononanoate synthase	6.18E-05
BA4341	adenosylmethionine--8-amino-7-oxononanoate aminotransferase	0.000888
BA4385	dihydrolipoamide dehydrogenase	0.000914
BA4386	butyrate kinase	0.00155
BA4396	stage IV sporulation protein B	0.000536
BA4449	glycine cleavage system T protein	0.00148

BA4451	conserved hypothetical protein	1.01E-05
BA4466	comG operon protein 1	0.000507
BA4515	RNA polymerase sigma-43 factor	0.00188
BA4528	HDIG domain protein	0.002
BA4530	sporulation protein	0.00117
BA4535	conserved hypothetical protein	0.01
BA4539	chaperone protein DnaK	0.000248
BA4546	spore protease	0.000488
BA4574	alkaline phosphatase	0.000969
BA4601	O-acetylserine lyase	0.000507
BA4609	peptidase, U32 family	0.000578
BA4610	peptidase, U32 family	0.000691
BA4643	stage V sporulation protein B	0.000492
BA4654	membrane protein, putative, authentic frameshift	3.32E-05
BA4668	ABC transporter, permease protein	0.000597
BA4688	stage II sporulation protein B, putative	0.000467
BA4691	conserved hypothetical protein	0.0035
BA4698	glutamyl-tRNA reductase	0.0018
BA4718	major facilitator family transporter	0.000536
BA4728	N-acyl-D-amino-acid deacylase family protein	0.000248
BA4744	membrane protein, putative	1.01E-05
BA4763	long-chain-fatty-acid--CoA ligase	0.000587
BA4794	MutS2 family protein	0.00101
BA4827	glyceraldehyde 3-phosphate dehydrogenase	0.00117
BA4831	DNA polymerase I	0.000783
BA4837	malate dehydrogenase	0.000634
BA4838	isocitrate dehydrogenase, NADP-dependent	0.000255
BA4839	citrate synthase CitZ	0.00133
BA4889	conserved hypothetical protein	0.000597
BA4901	septation ring formation regulator	0.00455
BA4940	FtsK/SpoIIIE family protein	0.00368
BA4953	pullulanase, putative	0.00155
BA4996	ABC transporter, permease protein, putative	0.00042
BA5041	conserved hypothetical protein, authentic point mutation	0.000914
BA5042	conserved hypothetical protein	4.38E-07
BA5099	pyridoxal phosphate-dependent enzyme, putative	0.000726
BA5120	glycogen synthase	0.000507
BA5152	UTP-glucose-1-phosphate uridylyltransferase	8.72E-06
BA5156	conserved hypothetical protein	0.00377
BA5161	cell wall surface anchor domain protein, authentic frameshift	0.000571
BA5256	methyl-accepting chemotaxis protein	0.00101
BA5261	amino acid permease family protein	0.00123
BA5268	cytolysin immunity CylI domain protein	0.000805
BA5269	hypothetical protein	0.00101
BA5278	methionyl-tRNA synthetase, putative	0.00127
BA5305	conserved domain protein	0.000129
BA5326	lipoprotein, putative	0.00193
BA5328	iron compound ABC transporter, permease protein	0.000507
BA5335	carboxylesterase	0.00142
BA5360	phage major capsid protein, HK97 family	0.000969
BA5361	hypothetical protein	0.0178
BA5388	TPR domain protein	0.0026
BA5399	conserved hypothetical protein	0.000295
BA5414	carboxyl-terminal protease	0.00137
BA5436	polysaccharide deacetylase, putative	0.00454
BA5455	conserved hypothetical protein	0.000993

BA5470	sulfatase	0.00061
BA5483	conserved hypothetical protein	0.00343
BA5492	competence transcription factor, degenerate	0.014
BA5512	UDP-N-acetyl-D-mannosamine dehydrogenase	0.00142
BA5516	conserved domain protein	0.000691
BA5517	hypothetical protein	0.000538
BA5518	glycosyl transferase, group 1 family protein	0.00199
BA5581	stage 0 sporulation protein F	8.55E-06
BA5591	cardiolipin synthetase domain protein	0.0018
BA5597	DNA-binding response regulator	0.000923
BA5599	ABC transporter, permease protein, putative	0.000536
BA5600	ABC transporter, ATP-binding protein	0.00107
BA5607	hypothetical protein	0.0149
BA5645	xanthine/uracil permease family protein	0.000446
BA5655	homoserine O-succinyltransferase	0.00115
BA5673	methyl-accepting chemotaxis protein	0.00357
BA5676	polysaccharide biosynthesis protein, putative	0.000648
BA5689	membrane protein, putative	0.000923
BA5694	osmoprotectant transporter, BCCT family	0.000726
BA5695	nitric-oxide synthase, oxygenase subunit	0.000587
BA5700	UDP-glucose 4-epimerase	0.000975
BA5705	guanosine monophosphate reductase	0.000787
BA5713	YycH protein	0.000283
BA5714	sensory box histidine kinase YycG	0.00285
BA5717	replicative DNA helicase	0.000648
BA5726	mechanosensitive ion channel family protein	0.00187
BA5728	conserved hypothetical protein	0.000316
BA5730	sporulation initiation inhibitor protein Soj	0.0131
pXO2-29	hypothetical protein	0.00127
pXO2-38	plasmid replication protein	0.000805
pXO2-56	capsule biosynthesis protein CapA	0.00154
pXO2-81	hypothetical protein	5.42E-05
pXO2-84	hypothetical protein	0.000787

[*] Gene descriptions derived from The Institute for Genomic Research (TIGR) genome annotation (19).