

**Table S4. Sequence variations detected in strain 3725**

gene <sup>1</sup>	position <sup>2</sup>	variation type	Ref.	Obs.	change <sup>3</sup> aminoacid	function	functional category	essential	
<b>Common variations to wild type and mutant strains (relative to the published 168 sequence)</b>									
<b>INTRAGENIC</b>									
<i>uvrX</i>	2271523	Non Synonymous Coding	A	C	D45E	UV DNA damage repair	DNA repair	information processing	no
<i>rrnI-16S</i>	161239	untranslated region	T	TC	NA	ribosomal RNA 16S	translation	information processing	no
<i>trnI-asn</i>	165825	untranslated region	G	GC	NA	transfer RNA-asn	translation	information processing	no
<i>rrnG-16S</i>	171679	untranslated region	TA	T	NA	ribosomal RNA 16S	translation	information processing	no
<i>rrnB-16S</i>	3178443	untranslated region	T	C	NA	ribosomal RNA 16S	translation	information processing	no
<i>pstS</i> (5'UTR)	2581726	untranslated region	G	GT	NA	phosphate ABC transporter	Phosphate metabolism	Metabolism	no
<i>ydcN</i> (5'UTR)	557865	untranslated region	G	GT	NA	unknown	unknown	unknown	no
<i>yjpA</i> (3'UTR)	1317152	untranslated region	G	GGT	NA	unknown	unknown	unknown	no
<i>yjpA</i> (3'UTR)	1317153	untranslated region	C	CT	NA	unknown	unknown	unknown	no
<i>zwf</i> (ter)	2480646	untranslated region	T	A	NA	glucose 6P deshydrogenase	carbon metabolism	Metabolism	no
<i>zwf</i> (ter)	2480647	untranslated region	A	T	NA	glucose 6P deshydrogenase	carbon metabolism	Metabolism	no
<i>zwf</i> (ter)	2480653	untranslated region	CT	C	NA	glucose 6P deshydrogenase	carbon metabolism	Metabolism	no
<i>zwf</i> (ter)	2480666	untranslated region	GT	G	NA	glucose 6P deshydrogenase	carbon metabolism	Metabolism	no
<i>ywbD</i> (ter)	3935822	untranslated region	AT	A	NA	unknown	unknown	unknown	no
<b>synonymous codon (silent)</b>									
<i>uvrX</i>	2271424	Synonymous coding	T	C	R78	UV DNA damage repair	DNA repair	information processing	no
<i>uvrX</i>	2271505	Synonymous coding	C	T	V51	UV DNA damage repair	DNA repair	information processing	no
<b>INTERGENIC</b>									
<i>int</i> (up <i>trnI-asn</i> )	165748	untranslated region	TC	T	NA	transfer RNA-asn	translation	information processing	no
<i>int</i> (up <i>trnI-asn</i> )	165750	untranslated region	TC	T	NA	transfer RNA-asn	translation	information processing	no
<i>int</i> (dn <i>trnI-gly</i> )	166037	untranslated region	A	AT	NA	transfer RNA-gly	translation	information processing	no
<i>int</i> (dn <i>trnI-ala</i> )	166343	untranslated region	AG	A	NA	transfer RNA-ala	translation	information processing	no
<i>int</i> ( <i>s1555/purA</i> )	4155390	untranslated region	C	CA	NA	tRNA-lys/adenylosuccinate synthetase	translation/purine acquisition	information processing/Metabolism	no
<i>int</i> ( <i>s1555/azoR1</i> )	2097080	untranslated region	C	CA	NA	ethanol response/azoreductase	stress response/stress response	Lifestyle/Lifestyle	no
<i>s1417</i>	3770058	untranslated region	G	GAAA	NA	unknown	unknown	unknown	no
<i>int</i> ( <i>ydgF/dinB</i> )	608214	untranslated region	G	GA	NA	unknown/nuclease inhibitor	unknown/DNA repair	unknown/inhibitor processing	no
<b>Variations in <i>ΔmreB</i> 3725 relative to its parental wild type 168 strain</b>									
<b>Variations in strain 3725 also reported in strain PDC134</b>									
<b>INTRAGENIC</b>									
<i>sepF</i>	1610896	Non Synonymous Coding	T	C	M11T	recruits cell division FtsZ protein to membrane	Cell division	cellular process	no
<i>walR</i>	4153797	Non Synonymous Coding	G	A	R203C	two component response regulator	CW homeostasis	cellular process	YES
<i>ytpS</i> (=sftA)	3051461	Non Synonymous Coding	G	A	P375S	DNA translocase (paralog of SpoIIIE)	DNA segregation	information processing	no
<i>epsC</i>	3527377	Non Synonymous Coding	G	A	A276V	udp-sugar epimerase (inactive in 168)	biofilm	Lifestyle	no
<i>comP</i>	3253956	Non Synonymous Coding	T	C	E628G	two component sensor kinase, snsing ComX	competence and sporulation	Lifestyle	no
<i>sigI</i>	1412484	Non Synonymous Coding	T	G	L198R	alternative sigma factor	stress response	Lifestyle	no
<i>bscR</i> (=FatR)	2777176	Non Synonymous Coding	A	C	I160R	Transcriptional repressor of <i>fatR-yrhJ</i> operon	Fatty acid metabolism	Metabolism	no
<i>ymfD</i>	1756603	Non Synonymous Coding	G	A	A319T	baicillibactin exporter	iron acquisition	Metabolism	no
<i>mmgA</i>	2513699	Non Synonymous Coding	A	C	M115R	degradative acetoacetyl-CoA thiolase	Leucine metabolism	Metabolism	no
<i>yuxG</i> (=rahEW)	3202213	Non Synonymous Coding	C	T	G573R	bifunctional rhamnulose-P aldolase/lactate deshydrogenase	Rhamnose catabolism	Metabolism	no
<i>ydcH</i>	525386	indel: Frame Shift	CA	C	frame shift	unknown	unknown	unknown	no
<i>yhgE</i>	1091083	Non Synonymous Coding	G	A	G228E	unknown	unknown	unknown	no
<i>yisQ</i> & <i>S389</i>	1161993	Non Synonymous Coding	C	T	D51N	unknown	unknown	unknown	no
<i>yjcM</i> & <i>S430</i>	1264284	Non Synonymous Coding	T	A	K216N	unknown	unknown	unknown	no
<i>BSU_misc_RNA_20</i>	1424639	untranslated region	T	G	NA	unknown; coexpressed with MtnK (methionine salvage)	unknown	unknown	no
<i>panE</i>	1514277	Non Synonymous Coding	G	A	A76T	unknown; putative ketopentolate reductase	unknown	unknown	no
<i>BSU_misc_RNA_28</i>	1620435	untranslated region	GT	G	NA	unknown	unknown	unknown	no
<i>yxbD</i>	4095811	Non Synonymous Coding	C	T	V9I	unknown	unknown	unknown	no
<b>INTERGENIC</b>									
<i>s1123</i> (5'utr <i>NifZ</i> ) / <i>s1124</i> (5'utr <i>braB</i> )	3028250	untranslated region	A	T	NA	cystein desulfurase/branched-chain aa transporter	tRNA modification/metabolism	information processing/metabolism	no
<i>s1145</i> (5' utr <i>ytnP</i> )	3059481	untranslated region	AC	A	NA	lactonase homologue	antibacterial compound	lifestyle	no
<i>s125</i> (5' utr <i>hxlR</i> )	376017	untranslated region	AG	A	NA	Transcriptional regulator (formaldehyde detoxification)	stress resistance	lifestyle	no
<i>s486</i> (5' UTR <i>mtnE</i> )	1425560	untranslated region	C	A	NA	glutamine transaminase	methionine salvage	Metabolism	no
<i>int</i> <i>yorN</i> / <i>yorM</i>	2174751	untranslated region	ACT	A	NA	Sbeta prophage	prophage	prophage & Mobile genetic elements	no
<i>s352</i> (3' Utr <i>yhaH</i> )	1073872	untranslated region	AT	A	NA	unknown	unknown	unknown	no
<i>s736</i> (dnstream <i>yocI</i> )	2096245	untranslated region	TA	T	NA	unknown	unknown	unknown	no
<i>s596</i> (5'utr <i>ylxY</i> )	1741603	untranslated region	AG	A	NA	unknown; similar to deacetylase	unknown	unknown	no

Variations unique to strain 3725

**INTRAGENIC**

<i>parC</i>	1936310	Non Synonymous Coding	C	T	S288L	subunit of DNA topoisomerase IV	DNA segregation	information processing	YES
<i>rRNA23S</i>	34740	untranslated region	A	G	NA	ribosomal RNA 23S	translation	information processing	no
<i>ylyB</i>	1618068	Non Synonymous Coding	C	T	P287S	unknown, similar to pseudouridylylase synthase	translation	information processing	no
<i>trmD</i>	1675849	Non Synonymous Coding	C	T	H227Y	tRNA methyltransferase	translation	information processing	YES
<i>pksN</i>	1841168	indel: Frame Shift	C	CA	frame shift	polyketide synthase, type I	antibacterial compound synthesis	Lifestyle	no
<i>oppD</i>	1224524	Non Synonymous Coding	T	G	V357G	oligopeptide ABC transporter	competence and sporulation	Lifestyle	no
<i>gerAA</i>	3391676	Non Synonymous Coding	A	G	T299A	nutrient receptor (L-Ala) promoting spore germination	germination	Lifestyle	no
<i>s1255 /sspG</i>	3354116	indel: codon deletions	G(8)*	G	8 codons deleted	sspG: small acidic soluble protein/S1255: unknown	sporulation	Lifestyle	no
<i>accC</i>	2530964	Non Synonymous Coding	T	C	D248G	acetyl-coA carboxylase	fatty acid biosynthesis	Metabolism	YES
<i>glcK</i>	2571163	indel: Frame Shift	G	GT	frame shift	glucose kinase	glucose metabolism	Metabolism	no
<i>gltA</i>	2011091	Non Synonymous Coding	G	A	A1181V	glutamate synthase	metabolism	Metabolism	no
<i>sacA</i>	3902306	Non Synonymous Coding	C	A	L448F	phosphosucrase	sucrose catabolism	Metabolism	no
<i>ilvC &amp; s1070</i>	2893906	Non Synonymous Coding	G	A	A268	ketol-ac reductoisomerase/unknown	aminoacids synthesis/unknown	Metabolism/unknown	no
<i>yaqA</i>	2201408	Non Synonymous Coding	A	G	L23P	unknown; SPβ prophage	prophage	Prophage & Mobile genetic elements	no
<i>yaqB</i>	2670611	Non Synonymous Coding	A	G	Y60H	unknown; skin element	prophage	Prophage & Mobile genetic elements	no
<i>yesY</i>	774697	indel: Frame Shift	CA	C	frame shift	unknown, similar to rhamnogalacturonan acetyltransferase	unknown	unknown	no
<i>yutE</i>	3319154	Non Synonymous Coding	C	T	A37T	unknown	unknown	unknown	no
<b>synonymous codon (silent)</b>									
<i>pgdS</i>	3696869	Synonymous coding	T	C	L210	gamma-DL-glutamyl hydrolase	capsule biosynthesis	cellular process	no
<i>rluB</i>	2421606	Synonymous coding	T	C	Q189	pseudouridine synthase	translation	information processing	no
<i>yqeZ</i>	2619105	Synonymous coding	C	T	A225	Ser protease, resistance to subclancin	stress response	Lifestyle	no
<i>ygaN</i>	965353	Synonymous coding	A	T	S31	unknown	unknown	unknown	no
<i>yazT</i>	2041099	Synonymous coding	A	G	D43	unknown	unknown	unknown	no

**INTERGENIC**

<i>int bsrB /yrvM</i>	2814468	untranslated region	C	T	NA	bsrB: sigA antagonist / yrvM: cyclase	gene regulation/ modification	information processing	no
<i>s1101 (5' utr CitZ)</i>	2982417	untranslated region	T	A	NA	citrate synthase (TCA cycle)	metabo	Metabolism	no
<i>s1101 (5' utr CitZ)</i>	2982437	untranslated region	T	C	NA	citrate synthase (TCA cycle)	metabo	Metabolism	no

<sup>1</sup> "int" stands for intergenic region, "utr" for untranslated region

<sup>2</sup> nucleotide position relative to the *B. subtilis* 168 sequence from GenBank (AL009126.3)

<sup>3</sup> "Ref." and "Obs." stand for nucleotide(s) present in the reference and the 3725 sequences, respectively

\*G(GCAAAAAGTCCAAAACAGCGTAAT)