

## Appendix A Oligonucleotide primers used in this study

Target gene	Primer name	Primer sequence (5'-3')
<i>dxs</i>	RTdxs5	GGACCTCCTCATAATTAAGGGCTG
	RTdxs3	CCCTTCCAGTTTGGAGCCGACC
<i>dxr</i>	RTdxr5	TGTAGCAGTCGGCGACATGGATACA
	RTdxr3	GGAGCTTGAGTCTGTAACGATTGCC
<i>ispD</i>	RTispD5	CCTGGTGATAAACGAGAGTGAA
	RTispD3	AGCTGCCTTCAACGATACTC
<i>ispE</i>	RTispE5	CCCTCGATGTGACGAGTAAAC
	RTispE3	GAGCGTAACCGACTCCAATAC
<i>ispF</i>	RTispF5	CCTCTCATCATCGGCGGAATTGAAA
	RTispF3	ACAGAAAAGCTCGGGTTTACCGGAA
<i>ispG</i>	RTispG5	TTAGAAAAATACGGCTATCCGACTG
	RTispG3	ATTGATCTCATCAGCATCGCAAATG
<i>ispH</i>	RTispH5	CGTCATATACATCGGTA AAAAAGGC
	RTispH3	GCCTACCGAATCGGAGACATCAGTG
<i>idi</i>	RTidi5	CCGTT CAGAAAGCCAGTGATGTGTC
	RTidi3	TCCCTGCTCATTCCGAAGCCGACTT
<i>ispA</i>	RTispA5	TTTGCCGATCCTCTCCTCATGCCCT
	RTispA3	CGACCATTCCTTCCGTTCCCGCCGC
16S rDNA	16SrDNA5	ATCTTCCGCAATGGACGAAAGTC
	16SrDNA3	TCAAGTTCCCCAGTTTCCAATGAC
NA	11205-11210-F	GTTGTTTGTGCGCACCTTTAC
	11205-11210-R	GACTGTCCCTTCTCACCGATTAC
NA	11210-DXS-F	GTATACGATGCCCGCCATAAT
	11210-DXS-R	GCATCCCAGACCGGTTTATT
NA	DXS-ispA-F	TGTGCCCTGTTTCCCATAC
	DXS-ispA-R	CGTCTGTT CAGCAGCCATATC
NA	ispA-11225-F	GTCCATGCAAGGCAAATCATC
	ispA-11225-R	GAGGAAGACGAAGGTGACAAATA
NA	11225-11230-F	CTTCTTCAAGCTTTGCCACAAT
	11225-11230-R	TCAGGTGATGGAGAGAGGATAC
NA	11230-11235-F	TCATTCCGTCTTCTGGCTTAAA
	11230-11235-R	GATAACCGGAGACAGTCACAAA
NA	11235-11240-F	CCTTGTGCTTTCAGCTCTTCTA
	11235-11240-R	TTCTGACGACATTCTGCTAAC
NA	11240-11245-F	CGTACACCAGCTGTTCAAAGA
	11240-11245-R	TGACACGAAAGCCCAAGAAG
NA	08075-08080-F	GGTGGACCATCTCGCATTAAA
	08075-08080-R	CAGCAGCAATGACGGGAATA
NA	08080-08085-F	CAATATGCGAGAGAGCATTATC

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	08080-08085-R	GCAGTTTGGAGCTGACATTATC
NA	08085-08090-F	AAGTGCTGTCGGAATCAAGAA
	08085-08090-R	TCAATAATGGTGCGGGAAGAA
NA	08090-08095-F	TACCCGATGACCCGTTAGTA
	08090-08095-R	TCCGGTTTGAGAAGCTCTATTT
NA	08095-08100-F	TGCCGAAGTCAGCGATAAAG
	08095-08100-R	GTATGGGCAGCTCTGAAGATG
NA	08100-08105-F	GGAGAAGTGGCGCTGATTAT
	08100-08105-R	TGATAACGCCGCGGATATAAG
NA	08105-08110-F	GCAAGATAACAGGCTCCTCAA
	08105-08110-R	AACGGCACTTCCATGTCTATC
NA	08110-08115-F	GCCATTGTCGTGGATACTTCTA
	08110-08115-R	CCTGCCGTTTGTCTTCTTAT
NA	08115-08120-F	GGGAGCGGAGATGTTTAAAGT
	08115-08120-R	GATAGTCTTTATGCACCGATTTC
NA	08120-08125-F	ACCAGGATGACGGTGAGAATA
	08120-08125-R	GGGTGAGCCCTTGTTTCATATAAT
NA	08125-08130-F	GCCTGATATTCCTGACCACAT
	08125-08130-R	CAGAGCGTACAGCTTCTTCTT
NA	08130-08135-F	TTCTTCGGCGGAATTAAGACA
	08130-08135-R	GTCCATATCTCCGTCAGTTTCAG
NA	08135-pyrH-F	GCTACGAAGTTGGAGAAGGTATT
	08135-pyrH-R	TACCTGTTTAGCGATGGATTGG
NA	pyrH-08145-F	GTCATGGATTCTACGGCTTCTT
	pyrH-08145-R	CAGCTGGTTTAAAGGTGTTTGG
NA	08145-08150-F	CGGAGACATTACAGAAGACGAG
	08145-08150-R	CGTCCGTTTCCGTCCATAATA
NA	08150-08155-F	CATCAGAACGAGCGGAGAAA
	08150-08155-R	CCGGCATCATATACAGCCATAA
NA	08155-DXR-F	GCGACACTATGATGTGAAGGA
	08155-DXR-R	GCATGCGCAATACGTCTAAC
NA	DXR-08165-F	GCCGGACGGATTCATTCTTA
	DXR-08165-R	AAAGGATTCCCGCTCTTTGG
NA	08165-08170-F	CCGTGACAAGGAAGCATTTG
	08165-08170-R	CATTCCACCGCGTTGATTT
NA	08170-polC-F	GATTGAGGTCGGACAAGTCTTTA
	08170-polC-R	CCTCTGTCACTGTAGGATCAATG
NA	polC-08180-F	GTTAGAGCTTGCGCTTGAAATG
	polC-08180-R	CAGCCGTTCTCTGCATAAA
NA	00575-00580-F	CTGCATGTAAGACGGCAAATG
	00575-00580-R	CGAATTGCTGAATGATGGATGAG
NA	00580-00585-F	CAAATGTAGGGACGGGACTAAG
	00580-00585-R	CCTTCACGAACCAGACCTAATAA
NA	00585-00590-F	GAGGACCGGTTATCAGAAGAAC

	00585-00590-R	ATGGTTTCTGGACGGTTTGA
NA	00590-00595-F	GAATCCCGCAGATTGCTTTATC
	00590-00595-R	GCCCGAAGTACATTCTCTATCC
NA	00595-00600-F	GCCACTGTAGAAGAGCTTGA
	00595-00600-R	CCGCCACAATAATGAAGAAC
NA	00600-ISPD-F	AGGTGTGGCTTACTTGGATG
	00600-ISPD-R	CTTCCCGTTCACTCTCGTTTAT
NA	ISPD-ISPF-F	TCTCATCATCGGCGGAATTG
	ISPD-ISPF-R	CTTCGGCTCTTCCGGTAAAC
NA	ISPF-00615-F	AGGAGATATCGGCAAGCATT
	ISPF-00615-R	GGCTGCGGGCAAATAAATAG
NA	00615-00620-F	TACGCCTGAGCTGATCAAAG
	00615-00620-R	CCCATATAGCATGTAAACCAGAATAAG
NA	00620-00625-F	TACGCCTGAGCTGATCAAAG
	00620-00625-R	CGTCACGTTATTGCCGATTTC
NA	00625-00630-F	AGCTTGTCGACGAAGAGATTG
	00625-00630-R	GGTGATGCCGGACGTATATTT
NA	00630-00635-F	GTGCTGAGAAGAGGCAGAAA
	00630-00635-R	CAGCTCGTCCAGTATGAGAAAAG
NA	00635-00640-F	CCGGCTTGTGAAAGAGAAATG
	00635-00640-R	AATGACTCTGATTCCCGTGTAG
NA	00640-00645-F	TGAGGGAAGTGGATACGATAGA
	00640-00645-R	CGGTAATAATCTGGCGGGTAAT
NA	00645-00655-F	CTGAGCGATCTGGAAGAAAAG
	00645-00655-R	TTTGCATGCCAGCGTAATC
NA	00655-00660-F	CACGGTGATTTCAACGGTTATC
	00655-00660-R	ACCCGGGAACACTTTCTTT
NA	00660-00665-F	TCAAAGTCATAGACGGACCTTTC
	00660-00665-R	TCACCAGAACCAGACTCAATTC
NA	00665-00670-F	CCGCAGTATGGGTATCGTTAT
	00665-00670-R	CGTCGAATTTAGCTGTGTTTGT
NA	00670-00675-F	ACGTTGCCGTTACTTCTACTATG
	00670-00675-R	ACGGCGAGTCATTGTGTT
NA	00675-00680-F	GAAATCAAAGCGGGCGTTATC
	00675-00680-R	CAGCAGTTACGCCAAATTCTTC
NA	00680-00685-F	CACTGGTCTTGGCTTGAAAGA
	00680-00685-R	CCGCTGTCACTTGTGAATGTA
NA	00685-00690-F	CAGGTGAATTGTGGATCGTTATAC
	00685-00690-R	AGAGAGAGGTTACCAGTGAAATC
NA	10425-FNI-F	ACGGTTCCATAATCGCTCCTCCTCT
	10425-FNI-R	AAGGCGCCTTTGGTCATAAA
NA	IDI-10435-F	CGGTAGACAGCGCATGATTTAT
	IDI-10435-R	ACGTGAACGAAAGCGAAGAG
NA	10435-10440-F	ACCTCTGGCACTTGAACATC

	10435-10440-R	GATACGACGTCACTCAGCATT
NA	00280-00285-F	ATACGCTGACGAGAGAGAAAAG
	00280-00285-R	GAAGGGTACGTCTCAGCTAAA
NA	00285-00290-F	ATGCGGCAAGCTCAGTAGCA
	00285-00290-R	GTCCTTCGCCAGCTCATATT
NA	00290-IPK-F	ACGCCGGGAATATGGTAAAG
	00290-IPK-R	CACATCGAGGGACAGATTGATT
NA	IPK-00300-F	CCGAGGTGGCGATGATTAAG
	IPK-00300-R	AGCTCCTGTATAAACGCTTCTG
NA	00300-00305-F	GCAAACGTTGCGGGAATAG
	00300-00305-R	GAATCTGGCCTGAGCTGTAA
NA	00305-00310-F	GTCATTGCGCTGGTGAAATC
	00305-00310-R	CTCATGCGACCATCGGTATT
NA	11570-11575-F	CCGGATATAACAAGCCCGATAAA
	11570-11575-R	GGTGCCTGAGGAAAGGTAATAA
NA	11575-11580-F	TGTTATTACGGTGCCGAGTG
	11575-11580-R	GTATGCTGGAAGGTCTTGAGAA
NA	11580-ISPG-F	CGATAGTCGGCGCACATAAA
	11580-ISPG-R	GGTCGTCGTCATACTCTGAATG
NA	ISPG-11590-F	CCATGGTCGAAGAGCTGAAA
	ISPG-11590-R	GATGATAATCGGGACGGAGTAAG
NA	11620-11625-F	GGCGGTGAACTGCATCTATAA
	11620-11625-R	GGTCTTCCTCCCATCATCATAAC
NA	11625-ISPH-F	AGAACATCGGGCAGATCAAAG
	11625-ISPH-R	TCAACAACGCCGTAACAGTAG
NA	ISPH-11635-F	CAACACCGACACCGATTACA
	ISPH-11635-R	CGTGACGGGCGATCTTTATT
NA	dxsRACE	GCCAGCTCGATTGCTTCGTTTAATGACA
	NESTRACE	ATTTTGCAGCTTTATCGTCGCCGAACCG

**Appendix B** Identification of *B. subtilis* 916 genes with similarity to genes known to be involved in the MEP pathway in *B. subtilis* 168

<i>B. subtilis</i> 168 gene		<i>B. subtilis</i> 916 homolog
Gene Name (Locus Accession Number)	<i>B. subtilis</i> 916 Genome Annotation	% Amino Acid Identity Shared with <i>B. subtilis</i> 168 Homolog
<i>dxs</i> (BSU24270)	KO64_RS11215	93
<i>dxr</i> (BSU16550)	KO64_RS08160	88
<i>ispD</i>	KO64_RS00605	73

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(BSU00900)		
<i>ispE</i>	KO64_RS00295 ( <i>ipK</i> )	90
(BSU00460)		
<i>ispF</i>	KO64_RS00610	95
(BSU00910)		
<i>ispG</i>	KO64_RS11585	97
(BSU25070)		
<i>ispH</i>	KO64_RS11630	91
(BSU25160)		
<i>idi</i>	KO64_RS10430	77
(BSU22870)		
<i>ispA</i>	KO64_RS11220	84
(BSU24280)		

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