TYPE (STRAIN) GENOME SERVER

JOB SUMMARY

PRINT DATE:	2026-10-16 10:04:37 +0200
JOB ID:	6d4dfe5e-decf-41d5-b14f-82efc2c9cdc9
RESULT PAGE:	https://tygs.dsmz.de/user_results/show?guid=6d4dfe5e-decf-41d5-b14f-82efc2c9cdc9

Table 1: Phylogenies

Publication-ready versions of both the genome-scale GBDP tree and the 16S rRNA gene sequence tree can be customized and exported either in SVG (vector graphic) or PNG format from within the phylogeny viewers in your TYGS result page. For publications the **SVG format is recommended** because it is lossless, always keeps its high resolution and can also be easily converted to other popular formats such as PDF or EPS. Please follow the link provided above!

Table 2: Identification

The below list contains the result of the TYGS species identification routine.

Explanation of remarks that might occur in the below table:

remark [R1]: The TYGS type strain database is automatically updated on an almost daily basis. However, if a particular type strain genome is not available in the TYGS database, this can have several reasons which are detailed in the FAQ. You can request an extended 16S rRNA gene analysis via the 16S tree viewer found in your result page to detect **not yet genome-sequenced** type strains relevant for your study.

remark [R2]: > 70% dDDH value (formula d_4) and (almost) minimal dDDH values for gene-content formulae d_0 and d_6 indicate a potentially unreliable identification result and should thus be checked via the 16S rRNA gene sequence similarity. Such strong deviations can, in principle, be caused by sequence contamination.

remark [R3]: G+C content difference of > 1 % indicates a potentially unreliable identification result because within species G+C content varies no more than 1 %, if computed from genome sequences (PMID: 24505073).

Strain	Conclusion	Identification result	Remark
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	belongs to known species	*Escherichia hermannii*	
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	belongs to known species	*Escherichia albertii*	
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	belongs to known species	*Escherichia coli*	
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	belongs to known species	*Escherichia coli*	
'Escherichia coli str. K-12 substr. W3110' (AP009048)	belongs to known species	*Escherichia coli*	
'Escherichia coli O157:H7 str. Sakai' (BA000007)	belongs to known species	*Escherichia coli*	
'Shigella dysenteriae Sd197' (CP000034)	belongs to known species	*Escherichia coli*	
'Escherichia coli SMS-3-5' (CP000970)	belongs to known species	*Escherichia coli*	
'Escherichia coli str. 'clone D i2'' (CP002211)	belongs to known species	*Escherichia coli*	
'Escherichia coli str. 'clone D i14'' (CP002212)	belongs to known species	*Escherichia coli*	
'Escherichia coli S88' (CU928161)	belongs to known species	*Escherichia coli*	

Strain	Conclusion	Identification result	Remark
'Escherichia coli UMN026' (CU928163)	belongs to known species	*Escherichia coli*	
'Escherichia coli IAI39' (CU928164)	belongs to known species	*Escherichia coli*	
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	belongs to known species	*Escherichia coli*	
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	belongs to known species	*Escherichia coli*	
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	belongs to known species	*Escherichia coli*	
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	belongs to known species	*Escherichia coli*	
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	belongs to known species	*Escherichia coli*	
'Escherichia sp. TW09308' (AEME00000000)	belongs to known species	*Escherichia marmotae*	
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	belongs to known species	*Shimwellia blattae*	
'Escherichia fergusonii ECD227' (CM001142)	belongs to known species	*Escherichia fergusonii*	
'Escherichia fergusonii ATCC 35469' (CU928158)	belongs to known species	*Escherichia fergusonii*	

Table 3: Pairwise comparisons of user genomes vs. type-strain genomes

The following table contains the pairwise dDDH values between your user genomes and the selected type-strain genomes. The dDDH values are provided along with their confidence intervals (C.I.) for the three different GBDP formulas:

- formula d_0 (a.k.a. GGDC formula 1): length of all HSPs divided by total genome length
- formula d_4 (a.k.a. GGDC formula 2): sum of all identities found in HSPs divided by overall HSP length
- formula d_6 (a.k.a. GGDC formula 3): sum of all identities found in HSPs divided by total genome length

Note: Formula d_4 is independent of genome length and is thus robust against the use of incomplete draft genomes. For other reasons for preferring formula d_4, see the FAQ.

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Shimwellia blattae* DSM 4481	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	0.0
'Escherichia coli str. 'clone D i2" (CP002211)	**'Escherichia coli str. 'clone D i14" (CP002212)**	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	0.0
'Escherichia fergusonii ATCC 35469' (CU928158)	*Escherichia fergusonii* ATCC 35469	99.9	[99.7 - 99.9]	99.7	[99.5 - 99.8]	99.9	[99.9 - 100.0]	0.02
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	98.6	[97.5 - 99.2]	99.6	[99.3 - 99.7]	99.3	[98.8 - 99.6]	0.04
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli UMN026' (CU928163)**	95.4	[93.2 - 96.9]	99.3	[98.9 - 99.5]	97.5	[96.2 - 98.3]	0.05
'Escherichia coli S88' (CU928161)	*Escherichia coli* DSM 30083	98.6	[97.5 - 99.2]	99.2	[98.7 - 99.5]	99.3	[98.8 - 99.6]	0.04
'Shigella dysenteriae Sd197' (CP000034)	*Shigella dysenteriae* ATCC 13313	98.8	[97.8 - 99.3]	98.9	[98.4 - 99.3]	99.4	[98.9 - 99.6]	0.27
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Escherichia hermannii* NCTC 12129	100.0	[100.0 - 100.0]	95.7	[94.3 - 96.8]	99.9	[99.9 - 100.0]	0.0
'Escherichia sp. TW09308' (AEME00000000)	*Escherichia marmotae* HT073016	81.2	[77.3 - 84.6]	94.2	[92.5 - 95.6]	86.3	[83.2 - 88.9]	0.04
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia coli str. 'clone D i2" (CP002211)**	91.4	[88.4 - 93.7]	91.3	[89.2 - 93.1]	93.8	[91.6 - 95.4]	0.07
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia coli str. 'clone D i14" (CP002212)**	91.4	[88.4 - 93.7]	91.3	[89.2 - 93.1]	93.8	[91.6 - 95.4]	0.07
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Escherichia coli* DSM 30083	85.6	[81.9 - 88.7]	90.3	[88.0 - 92.2]	89.2	[86.4 - 91.5]	0.16
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia coli S88' (CU928161)**	85.8	[82.2 - 88.8]	90.3	[88.0 - 92.1]	89.4	[86.6 - 91.7]	0.19
'Escherichia fergusonii ECD227' (CM001142)	*Escherichia fergusonii* ATCC 35469	92.8	[90.0 - 94.8]	90.1	[87.8 - 92.0]	94.6	[92.6 - 96.1]	0.09
'Escherichia fergusonii ECD227' (CM001142)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	93.7	[91.1 - 95.6]	90.1	[87.8 - 92.0]	95.3	[93.4 - 96.6]	0.07
'Escherichia coli str. 'clone D i14" (CP002212)	*Escherichia coli* DSM 30083	87.0	[83.4 - 89.9]	90.0	[87.7 - 91.9]	90.2	[87.5 - 92.4]	0.08
'Escherichia coli str. 'clone D i2" (CP002211)	*Escherichia coli* DSM 30083	87.0	[83.4 - 89.9]	90.0	[87.7 - 91.9]	90.2	[87.5 - 92.4]	0.08

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli str. 'clone D i14" (CP002212)	**'Escherichia coli S88' (CU928161)**	86.5	[82.9 - 89.4]	89.8	[87.4 - 91.7]	89.8	[87.0 - 92.0]	0.12
'Escherichia coli str. 'clone D i2" (CP002211)	**'Escherichia coli S88' (CU928161)**	86.5	[82.9 - 89.4]	89.8	[87.4 - 91.7]	89.8	[87.0 - 92.0]	0.12
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli UMN026' (CU928163)**	88.2	[84.8 - 91.0]	89.1	[86.7 - 91.1]	91.1	[88.5 - 93.1]	0.14
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)**	83.5	[79.7 - 86.7]	88.6	[86.2 - 90.7]	87.3	[84.2 - 89.8]	0.09
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli IAI39' (CU928164)**	79.3	[75.3 - 82.7]	87.0	[84.4 - 89.2]	83.5	[80.2 - 86.3]	0.24
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Shigella sonnei* ATCC 29930	78.4	[74.4 - 81.9]	86.5	[83.9 - 88.8]	82.7	[79.4 - 85.6]	0.21
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Shigella boydii* ATCC 8700	74.8	[70.8 - 78.4]	86.5	[83.9 - 88.8]	79.5	[76.1 - 82.6]	0.32
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli SMS-3-5' (CP000970)**	78.9	[74.9 - 82.4]	86.4	[83.8 - 88.7]	83.1	[79.8 - 85.9]	0.1
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)**	84.5	[80.7 - 87.6]	85.4	[82.7 - 87.7]	87.6	[84.6 - 90.0]	0.2
'Escherichia coli SMS-3-5' (CP000970)	**'Escherichia coli IAI39' (CU928164)**	83.1	[79.2 - 86.3]	85.1	[82.4 - 87.5]	86.3	[83.2 - 88.9]	0.13
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)**	82.2	[78.3 - 85.5]	85.0	[82.3 - 87.4]	85.6	[82.5 - 88.3]	0.29
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli UMN026' (CU928163)**	84.1	[80.3 - 87.2]	85.0	[82.3 - 87.4]	87.2	[84.1 - 89.7]	0.34
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Shigella flexneri* ATCC 29903	73.4	[69.5 - 77.1]	84.9	[82.2 - 87.3]	78.1	[74.6 - 81.2]	0.13
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Shigella dysenteriae Sd197' (CP000034)**	62.5	[58.7 - 66.0]	84.0	[81.2 - 86.4]	67.7	[64.3 - 70.9]	0.71
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Shigella dysenteriae* ATCC 13313	61.2	[57.5 - 64.8]	83.9	[81.1 - 86.3]	66.5	[63.1 - 69.7]	0.44
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Shigella dysenteriae Sd197' (CP000034)**	57.4	[53.8 - 60.9]	83.4	[80.6 - 85.8]	62.6	[59.3 - 65.8]	0.67
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Shigella dysenteriae* ATCC 13313	56.9	[53.3 - 60.4]	83.1	[80.3 - 85.6]	62.1	[58.8 - 65.3]	0.41
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	72.7	[68.7 - 76.3]	83.0	[80.2 - 85.5]	77.1	[73.6 - 80.2]	0.26
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	65.9	[62.1 - 69.6]	82.7	[79.8 - 85.2]	70.8	[67.4 - 74.1]	0.22
'Shigella dysenteriae Sd197' (CP000034)	*Shigella sonnei* ATCC 29930	69.4	[65.5 - 73.1]	82.6	[79.8 - 85.1]	74.1	[70.6 - 77.3]	0.24
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Shigella dysenteriae Sd197' (CP000034)**	68.7	[64.9 - 72.4]	82.5	[79.7 - 85.1]	73.4	[70.0 - 76.6]	0.45

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Shigella dysenteriae* ATCC 13313	66.2	[62.4 - 69.9]	82.5	[79.7 - 85.0]	71.1	[67.6 - 74.3]	0.18
'Shigella dysenteriae Sd197' (CP000034)	*Shigella boydii* ATCC 8700	70.7	[66.8 - 74.4]	81.0	[78.1 - 83.6]	75.0	[71.5 - 78.2]	0.13
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Shigella boydii* ATCC 8700	64.4	[60.6 - 68.0]	80.8	[77.9 - 83.4]	69.1	[65.6 - 72.3]	0.58
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Shigella flexneri* ATCC 29903	63.7	[59.9 - 67.3]	80.1	[77.2 - 82.8]	68.3	[64.9 - 71.5]	0.13
'Shigella dysenteriae Sd197' (CP000034)	*Shigella flexneri* ATCC 29903	72.4	[68.4 - 76.0]	80.0	[77.1 - 82.7]	76.3	[72.9 - 79.5]	0.58
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Escherichia albertii* NBRC 107761	99.8	[99.6 - 99.9]	79.9	[77.0 - 82.6]	99.0	[98.3 - 99.4]	0.1
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli H299' (ADBC01000001-ADBC01000229)**	71.7	[67.8 - 75.4]	79.7	[76.8 - 82.4]	75.7	[72.2 - 78.8]	0.18
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli IAI39' (CU928164)**	78.3	[74.4 - 81.8]	79.7	[76.7 - 82.3]	81.4	[78.1 - 84.4]	0.04
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Shigella boydii* ATCC 8700	60.3	[56.6 - 63.9]	79.6	[76.7 - 82.3]	65.0	[61.6 - 68.2]	0.54
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli SMS-3-5' (CP000970)**	81.9	[78.0 - 85.2]	79.6	[76.7 - 82.3]	84.5	[81.2 - 87.2]	0.08
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli str. 'clone D i14" (CP002212)**	79.1	[75.2 - 82.6]	79.5	[76.6 - 82.2]	82.1	[78.8 - 85.0]	0.19
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)**	71.9	[67.9 - 75.6]	79.5	[76.5 - 82.2]	75.8	[72.3 - 79.0]	0.38
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli str. 'clone D i2" (CP002211)**	79.1	[75.2 - 82.6]	79.5	[76.6 - 82.2]	82.1	[78.8 - 85.0]	0.19
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli SMS-3-5' (CP000970)**	81.6	[77.7 - 84.9]	79.5	[76.5 - 82.1]	84.2	[80.9 - 86.9]	0.12
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli IAI39' (CU928164)**	80.3	[76.4 - 83.7]	79.4	[76.5 - 82.1]	83.1	[79.8 - 85.9]	0.26
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Shigella sonnei* ATCC 29930	70.3	[66.4 - 74.0]	79.4	[76.4 - 82.1]	74.4	[70.9 - 77.6]	0.48
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)**	76.4	[72.4 - 79.9]	79.4	[76.4 - 82.0]	79.7	[76.3 - 82.7]	0.02
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)**	75.0	[71.0 - 78.6]	79.4	[76.5 - 82.1]	78.5	[75.1 - 81.6]	0.18
'Escherichia coli UMN026' (CU928163)	**'Escherichia coli IAI39' (CU928164)**	79.5	[75.5 - 82.9]	79.3	[76.4 - 82.0]	82.4	[79.0 - 85.3]	0.09
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	76.6	[72.7 - 80.2]	79.3	[76.4 - 82.0]	79.9	[76.5 - 83.0]	0.13
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Escherichia coli* DSM 30083	82.0	[78.1 - 85.3]	79.1	[76.2 - 81.8]	84.5	[81.2 - 87.2]	0.11

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia coli UMN026' (CU928163)**	79.6	[75.6 - 83.1]	79.1	[76.2 - 81.8]	82.4	[79.1 - 85.3]	0.08
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)**	75.5	[71.5 - 79.1]	79.1	[76.1 - 81.8]	78.9	[75.5 - 82.0]	0.27
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli UMN026' (CU928163)**	73.2	[69.3 - 76.9]	79.0	[76.0 - 81.7]	76.9	[73.4 - 80.0]	0.04
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)**	73.6	[69.6 - 77.2]	78.9	[76.0 - 81.6]	77.2	[73.7 - 80.3]	0.09
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli S88' (CU928161)**	79.3	[75.4 - 82.8]	78.9	[76.0 - 81.6]	82.2	[78.8 - 85.1]	0.07
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Shigella flexneri* ATCC 29903	59.3	[55.6 - 62.8]	78.9	[76.0 - 81.6]	63.9	[60.5 - 67.1]	0.09
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli UMN026' (CU928163)**	76.6	[72.6 - 80.1]	78.9	[75.9 - 81.6]	79.8	[76.4 - 82.8]	0.32
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)**	79.8	[75.8 - 83.2]	78.8	[75.9 - 81.5]	82.5	[79.2 - 85.4]	0.27
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli IAI39' (CU928164)**	78.2	[74.2 - 81.7]	78.8	[75.8 - 81.4]	81.1	[77.8 - 84.1]	0.06
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	77.5	[73.5 - 81.1]	78.6	[75.7 - 81.3]	80.6	[77.2 - 83.6]	0.42
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Shigella sonnei* ATCC 29930	65.5	[61.7 - 69.1]	78.5	[75.6 - 81.2]	69.8	[66.3 - 73.0]	0.44
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Escherichia coli* DSM 30083	72.9	[68.9 - 76.5]	78.5	[75.5 - 81.1]	76.5	[73.0 - 79.7]	0.25
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli IAI39' (CU928164)**	72.5	[68.6 - 76.2]	78.4	[75.4 - 81.1]	76.2	[72.7 - 79.3]	0.12
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)**	71.1	[67.1 - 74.7]	78.4	[75.4 - 81.1]	74.8	[71.4 - 78.0]	0.09
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli SMS-3-5' (CP000970)**	77.7	[73.7 - 81.2]	78.3	[75.3 - 81.0]	80.6	[77.2 - 83.6]	0.17
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Shigella boydii* ATCC 8700	65.5	[61.7 - 69.1]	78.2	[75.2 - 80.9]	69.7	[66.3 - 72.9]	0.45
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli SMS-3-5' (CP000970)**	74.3	[70.3 - 77.9]	78.2	[75.3 - 80.9]	77.7	[74.2 - 80.8]	0.26
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	81.5	[77.6 - 84.9]	78.2	[75.3 - 80.9]	83.9	[80.6 - 86.7]	0.22
'Escherichia coli SMS-3-5' (CP000970)	**'Escherichia coli UMN026' (CU928163)**	78.9	[74.9 - 82.4]	78.2	[75.3 - 80.9]	81.7	[78.3 - 84.6]	0.22
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli S88' (CU928161)**	73.3	[69.4 - 77.0]	78.0	[75.0 - 80.7]	76.8	[73.3 - 79.9]	0.29
'Escherichia coli UMN026' (CU928163)	*Shigella boydii* ATCC 8700	66.7	[62.8 - 70.3]	78.0	[75.0 - 80.7]	70.8	[67.3 - 74.0]	0.4

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)**	71.8	[67.8 - 75.4]	77.9	[74.9 - 80.6]	75.4	[71.9 - 78.6]	0.36
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia coli IAI39' (CU928164)**	75.9	[71.9 - 79.4]	77.7	[74.7 - 80.4]	79.0	[75.5 - 82.0]	0.17
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli str. 'clone D i2" (CP002211)**	70.9	[67.0 - 74.6]	77.6	[74.7 - 80.4]	74.6	[71.1 - 77.8]	0.17
'Escherichia coli str. 'clone D i14" (CP002212)	**'Escherichia coli IAI39' (CU928164)**	75.4	[71.5 - 79.0]	77.6	[74.6 - 80.3]	78.6	[75.1 - 81.7]	0.07
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia coli IAI39' (CU928164)**	73.9	[69.9 - 77.5]	77.6	[74.6 - 80.3]	77.2	[73.8 - 80.4]	0.14
'Escherichia coli str. 'clone D i2" (CP002211)	**'Escherichia coli IAI39' (CU928164)**	75.4	[71.5 - 79.0]	77.6	[74.6 - 80.3]	78.6	[75.1 - 81.7]	0.07
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli str. 'clone D i14" (CP002212)**	70.9	[67.0 - 74.6]	77.6	[74.7 - 80.4]	74.6	[71.1 - 77.8]	0.17
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Shigella boydii* ATCC 8700	65.0	[61.2 - 68.7]	77.6	[74.6 - 80.3]	69.2	[65.7 - 72.4]	0.54
'Escherichia coli UMN026' (CU928163)	*Shigella sonnei* ATCC 29930	72.1	[68.2 - 75.8]	77.4	[74.4 - 80.1]	75.6	[72.2 - 78.8]	0.3
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Shigella flexneri* ATCC 29903	64.8	[61.0 - 68.4]	77.3	[74.3 - 80.0]	68.9	[65.5 - 72.2]	0.09
'Escherichia coli IAI39' (CU928164)	*Shigella sonnei* ATCC 29930	70.0	[66.1 - 73.7]	77.3	[74.3 - 80.0]	73.7	[70.3 - 76.9]	0.38
'Shigella dysenteriae Sd197' (CP000034)	**'Escherichia coli UMN026' (CU928163)**	64.7	[60.9 - 68.3]	77.2	[74.2 - 79.9]	68.8	[65.4 - 72.0]	0.53
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	73.0	[69.1 - 76.7]	77.2	[74.2 - 80.0]	76.4	[72.9 - 79.6]	0.05
'Escherichia coli SMS-3-5' (CP000970)	*Escherichia coli* DSM 30083	75.6	[71.6 - 79.2]	77.2	[74.2 - 79.9]	78.6	[75.2 - 81.7]	0.15
'Escherichia coli UMN026' (CU928163)	*Shigella dysenteriae* ATCC 13313	62.9	[59.1 - 66.5]	77.2	[74.2 - 79.9]	67.1	[63.7 - 70.3]	0.26
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Shigella sonnei* ATCC 29930	68.7	[64.8 - 72.3]	77.1	[74.1 - 79.9]	72.5	[69.0 - 75.7]	0.64
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Shigella flexneri* ATCC 29903	65.7	[61.9 - 69.3]	77.1	[74.1 - 79.8]	69.7	[66.3 - 73.0]	0.0
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Shigella boydii* ATCC 8700	62.5	[58.8 - 66.1]	77.1	[74.1 - 79.9]	66.8	[63.4 - 70.0]	0.74
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Shigella sonnei* ATCC 29930	68.7	[64.8 - 72.4]	77.0	[74.0 - 79.7]	72.5	[69.0 - 75.7]	0.44
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	71.4	[67.4 - 75.0]	77.0	[74.0 - 79.7]	74.9	[71.4 - 78.1]	0.41
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Shigella dysenteriae* ATCC 13313	59.9	[56.2 - 63.4]	77.0	[74.0 - 79.8]	64.2	[60.8 - 67.4]	0.41
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Shigella dysenteriae Sd197' (CP000034)**	62.4	[58.7 - 66.0]	77.0	[74.0 - 79.7]	66.6	[63.2 - 69.8]	0.67

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Shigella sonnei* ATCC 29930	69.1	[65.2 - 72.8]	76.9	[73.9 - 79.6]	72.8	[69.4 - 76.1]	0.26
'Escherichia coli S88' (CU928161)	**'Escherichia coli IAI39' (CU928164)**	77.6	[73.6 - 81.1]	76.9	[73.9 - 79.7]	80.3	[76.9 - 83.3]	0.05
'Escherichia coli SMS-3-5' (CP000970)	**'Escherichia coli S88' (CU928161)**	75.1	[71.1 - 78.7]	76.9	[73.9 - 79.7]	78.2	[74.7 - 81.3]	0.18
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia coli SMS-3-5' (CP000970)**	79.1	[75.2 - 82.6]	76.9	[73.9 - 79.7]	81.6	[78.3 - 84.6]	0.3
'Escherichia coli SMS-3-5' (CP000970)	*Shigella sonnei* ATCC 29930	70.6	[66.7 - 74.3]	76.9	[74.0 - 79.7]	74.2	[70.7 - 77.4]	0.52
'Escherichia coli IAI39' (CU928164)	*Escherichia coli* DSM 30083	75.7	[71.7 - 79.3]	76.8	[73.8 - 79.6]	78.7	[75.2 - 81.8]	0.01
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Shigella dysenteriae Sd197' (CP000034)**	60.4	[56.8 - 64.0]	76.8	[73.8 - 79.5]	64.7	[61.3 - 67.9]	0.5
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Shigella dysenteriae Sd197' (CP000034)**	59.7	[56.1 - 63.3]	76.7	[73.7 - 79.4]	64.0	[60.6 - 67.2]	0.87
'Escherichia coli IAI39' (CU928164)	*Shigella boydii* ATCC 8700	68.3	[64.4 - 71.9]	76.7	[73.7 - 79.5]	72.0	[68.6 - 75.3]	0.49
'Escherichia coli UMN026' (CU928163)	*Shigella flexneri* ATCC 29903	67.7	[63.8 - 71.4]	76.7	[73.7 - 79.4]	71.5	[68.0 - 74.7]	0.05
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Shigella dysenteriae* ATCC 13313	58.0	[54.4 - 61.5]	76.6	[73.6 - 79.3]	62.3	[59.0 - 65.5]	0.61
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Shigella flexneri* ATCC 29903	64.3	[60.5 - 67.9]	76.6	[73.6 - 79.3]	68.3	[64.8 - 71.5]	0.29
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Shigella dysenteriae* ATCC 13313	59.2	[55.6 - 62.8]	76.6	[73.6 - 79.3]	63.5	[60.1 - 66.7]	0.23
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia coli SMS-3-5' (CP000970)**	72.9	[68.9 - 76.5]	76.6	[73.6 - 79.3]	76.1	[72.7 - 79.3]	0.01
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Shigella sonnei* ATCC 29930	71.3	[67.4 - 75.0]	76.6	[73.6 - 79.3]	74.8	[71.3 - 77.9]	0.35
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Shigella dysenteriae Sd197' (CP000034)**	62.1	[58.4 - 65.7]	76.4	[73.4 - 79.1]	66.2	[62.8 - 69.5]	0.58
'Escherichia coli SMS-3-5' (CP000970)	**'Escherichia coli str. 'clone D i2" (CP002211)**	75.3	[71.3 - 78.9]	76.3	[73.3 - 79.0]	78.2	[74.8 - 81.3]	0.06
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Shigella dysenteriae* ATCC 13313	61.0	[57.3 - 64.6]	76.3	[73.3 - 79.1]	65.2	[61.8 - 68.4]	0.31
'Escherichia coli SMS-3-5' (CP000970)	**'Escherichia coli str. 'clone D i14" (CP002212)**	75.3	[71.3 - 78.9]	76.3	[73.3 - 79.0]	78.2	[74.8 - 81.3]	0.06
'Escherichia coli IAI39' (CU928164)	*Shigella flexneri* ATCC 29903	68.1	[64.2 - 71.7]	76.3	[73.3 - 79.1]	71.8	[68.3 - 75.0]	0.04
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Shigella sonnei* ATCC 29930	63.4	[59.6 - 67.0]	76.3	[73.3 - 79.1]	67.4	[64.0 - 70.7]	0.62
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Shigella boydii* ATCC 8700	65.6	[61.7 - 69.2]	76.1	[73.1 - 78.9]	69.4	[66.0 - 72.7]	0.36
'Escherichia coli IAI39' (CU928164)	*Shigella dysenteriae* ATCC 13313	61.6	[57.9 - 65.2]	76.1	[73.1 - 78.8]	65.7	[62.3 - 68.9]	0.35

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Shigella dysenteriae Sd197' (CP000034)	**'Escherichia coli IAI39' (CU928164)**	62.6	[58.8 - 66.1]	76.0	[73.0 - 78.8]	66.6	[63.2 - 69.8]	0.62
'Escherichia coli SMS-3-5' (CP000970)	*Shigella flexneri* ATCC 29903	66.9	[63.0 - 70.5]	76.0	[73.0 - 78.8]	70.6	[67.1 - 73.8]	0.17
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Shigella boydii* ATCC 8700	61.3	[57.6 - 64.8]	75.9	[72.9 - 78.7]	65.3	[62.0 - 68.6]	0.72
'Escherichia coli SMS-3-5' (CP000970)	*Shigella boydii* ATCC 8700	68.2	[64.3 - 71.8]	75.9	[72.9 - 78.7]	71.8	[68.3 - 75.0]	0.62
'Shigella dysenteriae Sd197' (CP000034)	**'Escherichia coli SMS-3-5' (CP000970)**	63.7	[59.9 - 67.3]	75.9	[72.9 - 78.6]	67.6	[64.2 - 70.9]	0.75
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	74.2	[70.2 - 77.8]	75.9	[72.9 - 78.6]	77.1	[73.7 - 80.3]	0.04
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Shigella flexneri* ATCC 29903	60.7	[57.1 - 64.3]	75.9	[72.9 - 78.6]	64.8	[61.5 - 68.1]	0.28
'Escherichia coli SMS-3-5' (CP000970)	*Shigella dysenteriae* ATCC 13313	62.1	[58.4 - 65.7]	75.8	[72.8 - 78.6]	66.2	[62.8 - 69.4]	0.48
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Shigella flexneri* ATCC 29903	65.1	[61.2 - 68.7]	75.5	[72.5 - 78.3]	68.8	[65.4 - 72.1]	0.08
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	74.1	[70.1 - 77.7]	75.3	[72.3 - 78.1]	77.0	[73.5 - 80.1]	0.16
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Escherichia coli IAI39' (CU928164)**	68.6	[64.7 - 72.2]	75.3	[72.3 - 78.1]	72.0	[68.6 - 75.3]	0.09
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)**	70.4	[66.5 - 74.0]	75.3	[72.3 - 78.1]	73.7	[70.2 - 76.9]	0.09
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)**	68.0	[64.1 - 71.6]	75.3	[72.3 - 78.1]	71.5	[68.0 - 74.7]	0.18
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli str. 'clone D i14" (CP002212)**	72.5	[68.6 - 76.2]	75.2	[72.2 - 78.0]	75.6	[72.1 - 78.8]	0.18
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Escherichia coli* DSM 30083	74.2	[70.3 - 77.9]	75.2	[72.2 - 78.0]	77.1	[73.6 - 80.2]	0.16
'Escherichia coli str. 'clone D i14" (CP002212)	*Shigella sonnei* ATCC 29930	65.5	[61.7 - 69.2]	75.2	[72.2 - 78.0]	69.2	[65.8 - 72.5]	0.45
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Escherichia coli UMN026' (CU928163)**	74.9	[70.9 - 78.5]	75.2	[72.1 - 77.9]	77.6	[74.2 - 80.7]	0.18
'Escherichia coli str. 'clone D i2" (CP002211)	*Shigella sonnei* ATCC 29930	65.5	[61.7 - 69.2]	75.2	[72.2 - 78.0]	69.2	[65.8 - 72.5]	0.45
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli TA143' (ADAY01000001-ADAY01000168)**	67.6	[63.7 - 71.2]	75.2	[72.1 - 77.9]	71.1	[67.6 - 74.3]	0.0
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli str. 'clone D i2" (CP002211)**	72.5	[68.6 - 76.2]	75.2	[72.2 - 78.0]	75.6	[72.1 - 78.8]	0.18
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Escherichia coli* DSM 30083	73.9	[69.9 - 77.5]	75.2	[72.2 - 78.0]	76.8	[73.3 - 79.9]	0.07
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Escherichia coli* DSM 30083	73.4	[69.4 - 77.0]	75.1	[72.0 - 77.8]	76.3	[72.8 - 79.5]	0.27

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	65.2	[61.4 - 68.8]	75.1	[72.1 - 77.9]	68.9	[65.5 - 72.2]	0.21
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia coli UMN026' (CU928163)**	69.6	[65.7 - 73.2]	75.1	[72.0 - 77.8]	72.9	[69.4 - 76.1]	0.23
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia coli S88' (CU928161)**	74.4	[70.4 - 78.0]	75.0	[72.0 - 77.8]	77.2	[73.7 - 80.3]	0.12
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli S88' (CU928161)**	76.0	[72.0 - 79.6]	75.0	[72.0 - 77.8]	78.6	[75.2 - 81.7]	0.11
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	72.5	[68.5 - 76.1]	75.0	[72.0 - 77.8]	75.5	[72.0 - 78.7]	0.13
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli S88' (CU928161)**	74.6	[70.6 - 78.2]	75.0	[72.0 - 77.8]	77.4	[73.9 - 80.5]	0.31
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli S88' (CU928161)**	72.8	[68.8 - 76.4]	75.0	[72.0 - 77.8]	75.8	[72.3 - 78.9]	0.01
'Escherichia coli UMN026' (CU928163)	*Escherichia coli* DSM 30083	73.9	[69.9 - 77.5]	74.9	[71.9 - 77.7]	76.7	[73.3 - 79.9]	0.07
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	70.6	[66.6 - 74.2]	74.8	[71.8 - 77.6]	73.7	[70.3 - 77.0]	0.31
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli str. 'clone D i14" (CP002212)**	70.1	[66.2 - 73.8]	74.8	[71.8 - 77.6]	73.4	[69.9 - 76.6]	0.11
'Escherichia coli S88' (CU928161)	**'Escherichia coli UMN026' (CU928163)**	75.1	[71.2 - 78.7]	74.8	[71.8 - 77.6]	77.8	[74.4 - 80.9]	0.04
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia coli str. 'clone D i2" (CP002211)**	70.1	[66.2 - 73.8]	74.8	[71.8 - 77.6]	73.4	[69.9 - 76.6]	0.11
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)**	71.1	[67.1 - 74.7]	74.8	[71.8 - 77.6]	74.2	[70.7 - 77.4]	0.11
'Escherichia coli str. 'clone D i14" (CP002212)	**'Escherichia coli UMN026' (CU928163)**	72.4	[68.5 - 76.1]	74.7	[71.7 - 77.5]	75.4	[71.9 - 78.6]	0.16
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Shigella flexneri* ATCC 29903	61.4	[57.7 - 65.0]	74.7	[71.7 - 77.5]	65.3	[61.9 - 68.5]	0.18
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli IAI39' (CU928164)**	63.5	[59.8 - 67.1]	74.7	[71.7 - 77.5]	67.3	[63.9 - 70.5]	0.06
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)**	68.5	[64.6 - 72.1]	74.7	[71.7 - 77.5]	71.8	[68.4 - 75.1]	0.2
'Escherichia coli str. 'clone D i2" (CP002211)	**'Escherichia coli UMN026' (CU928163)**	72.4	[68.5 - 76.1]	74.7	[71.7 - 77.5]	75.4	[71.9 - 78.6]	0.16
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli str. 'clone D i2" (CP002211)**	71.2	[67.2 - 74.8]	74.6	[71.6 - 77.4]	74.3	[70.8 - 77.5]	0.02
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia coli str. 'clone D i14" (CP002212)**	72.1	[68.1 - 75.7]	74.6	[71.6 - 77.4]	75.1	[71.6 - 78.3]	0.24
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia coli str. 'clone D i2" (CP002211)**	72.1	[68.1 - 75.7]	74.6	[71.6 - 77.4]	75.1	[71.6 - 78.3]	0.24

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia coli str. 'clone D i14" (CP002212)**	71.2	[67.2 - 74.8]	74.6	[71.6 - 77.4]	74.3	[70.8 - 77.5]	0.02
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Escherichia coli* DSM 30083	73.8	[69.8 - 77.4]	74.6	[71.6 - 77.4]	76.6	[73.1 - 79.7]	0.02
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli UMN026' (CU928163)**	69.2	[65.2 - 72.8]	74.5	[71.5 - 77.3]	72.4	[69.0 - 75.7]	0.14
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Shigella boydii* ATCC 8700	61.9	[58.2 - 65.5]	74.5	[71.5 - 77.3]	65.7	[62.3 - 68.9]	0.63
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Escherichia coli SMS-3-5' (CP000970)**	71.5	[67.5 - 75.1]	74.5	[71.5 - 77.3]	74.5	[71.0 - 77.7]	0.04
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	68.1	[64.3 - 71.8]	74.4	[71.4 - 77.2]	71.5	[68.0 - 74.7]	0.15
'Shigella dysenteriae Sd197' (CP000034)	**'Escherichia coli str. 'clone D i14" (CP002212)**	60.9	[57.2 - 64.5]	74.4	[71.3 - 77.2]	64.7	[61.4 - 67.9]	0.69
'Shigella dysenteriae Sd197' (CP000034)	**'Escherichia coli str. 'clone D i2" (CP002211)**	60.9	[57.2 - 64.5]	74.4	[71.3 - 77.2]	64.7	[61.4 - 67.9]	0.69
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Shigella dysenteriae Sd197' (CP000034)**	61.3	[57.6 - 64.9]	74.3	[71.3 - 77.1]	65.1	[61.8 - 68.4]	0.86
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)**	67.8	[63.9 - 71.5]	74.3	[71.3 - 77.1]	71.2	[67.7 - 74.4]	0.09
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Shigella dysenteriae* ATCC 13313	59.3	[55.7 - 62.9]	74.3	[71.3 - 77.1]	63.2	[59.9 - 66.4]	0.59
'Escherichia coli str. 'clone D i14" (CP002212)	*Shigella dysenteriae* ATCC 13313	59.5	[55.9 - 63.1]	74.2	[71.2 - 77.0]	63.4	[60.0 - 66.6]	0.42
'Escherichia coli str. 'clone D i2" (CP002211)	*Shigella dysenteriae* ATCC 13313	59.5	[55.9 - 63.1]	74.2	[71.2 - 77.0]	63.4	[60.0 - 66.6]	0.42
'Escherichia coli S88' (CU928161)	*Shigella sonnei* ATCC 29930	65.8	[61.9 - 69.4]	74.1	[71.1 - 76.9]	69.3	[65.8 - 72.5]	0.33
'Escherichia coli S88' (CU928161)	*Shigella boydii* ATCC 8700	64.1	[60.3 - 67.7]	74.1	[71.1 - 76.9]	67.7	[64.3 - 70.9]	0.44
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli H299' (ADBC01000001-ADBC01000229)**	61.6	[57.8 - 65.1]	74.1	[71.1 - 76.9]	65.3	[62.0 - 68.5]	0.18
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli SMS-3-5' (CP000970)**	65.3	[61.5 - 68.9]	74.0	[71.0 - 76.8]	68.8	[65.4 - 72.0]	0.08
'Escherichia coli S88' (CU928161)	*Shigella flexneri* ATCC 29903	62.0	[58.3 - 65.6]	73.9	[70.9 - 76.7]	65.7	[62.3 - 68.9]	0.01
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Shigella sonnei* ATCC 29930	63.9	[60.2 - 67.5]	73.9	[70.9 - 76.7]	67.5	[64.1 - 70.8]	0.53
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Shigella dysenteriae* ATCC 13313	57.1	[53.6 - 60.7]	73.7	[70.6 - 76.5]	61.0	[57.7 - 64.2]	0.49
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)**	63.3	[59.5 - 66.9]	73.7	[70.6 - 76.5]	66.9	[63.5 - 70.1]	0.18

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Shigella dysenteriae Sd197' (CP000034)**	58.9	[55.2 - 62.4]	73.7	[70.7 - 76.5]	62.7	[59.4 - 65.9]	0.76
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	60.9	[57.2 - 64.5]	73.6	[70.6 - 76.4]	64.6	[61.3 - 67.9]	0.05
'Shigella dysenteriae Sd197' (CP000034)	*Escherichia coli* DSM 30083	64.0	[60.2 - 67.6]	73.5	[70.4 - 76.3]	67.5	[64.1 - 70.7]	0.61
'Escherichia coli str. 'clone D i14" (CP002212)	*Shigella flexneri* ATCC 29903	64.3	[60.5 - 67.9]	73.3	[70.2 - 76.1]	67.7	[64.3 - 71.0]	0.11
'Escherichia coli str. 'clone D i2" (CP002211)	*Shigella flexneri* ATCC 29903	64.3	[60.5 - 67.9]	73.3	[70.2 - 76.1]	67.7	[64.3 - 71.0]	0.11
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Escherichia coli* DSM 30083	64.3	[60.5 - 67.9]	73.2	[70.2 - 76.0]	67.8	[64.4 - 71.0]	0.11
'Shigella dysenteriae Sd197' (CP000034)	**'Escherichia coli S88' (CU928161)**	62.7	[59.0 - 66.3]	73.1	[70.1 - 75.9]	66.2	[62.9 - 69.5]	0.57
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Escherichia coli str. 'clone D i2" (CP002211)**	64.2	[60.4 - 67.8]	73.1	[70.1 - 76.0]	67.6	[64.2 - 70.9]	0.02
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Escherichia coli str. 'clone D i14" (CP002212)**	64.2	[60.4 - 67.8]	73.1	[70.1 - 75.9]	67.6	[64.2 - 70.9]	0.02
'Escherichia coli S88' (CU928161)	*Shigella dysenteriae* ATCC 13313	60.5	[56.9 - 64.1]	73.1	[70.1 - 75.9]	64.2	[60.8 - 67.4]	0.3
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Escherichia coli S88' (CU928161)**	65.7	[61.9 - 69.3]	73.1	[70.1 - 75.9]	69.0	[65.6 - 72.3]	0.14
'Escherichia coli str. 'clone D i2" (CP002211)	*Shigella boydii* ATCC 8700	64.3	[60.5 - 67.9]	72.9	[69.9 - 75.8]	67.7	[64.3 - 70.9]	0.56
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)**	56.3	[52.8 - 59.8]	72.9	[69.9 - 75.7]	60.1	[56.8 - 63.3]	0.09
'Escherichia coli str. 'clone D i14" (CP002212)	*Shigella boydii* ATCC 8700	64.3	[60.5 - 67.9]	72.9	[69.9 - 75.8]	67.7	[64.3 - 70.9]	0.56
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli str. 'clone D i14" (CP002212)**	59.3	[55.6 - 62.8]	72.5	[69.4 - 75.3]	62.9	[59.5 - 66.1]	0.02
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli str. 'clone D i2" (CP002211)**	59.3	[55.6 - 62.8]	72.5	[69.4 - 75.3]	62.9	[59.5 - 66.1]	0.02
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia coli S88' (CU928161)**	60.8	[57.2 - 64.4]	72.4	[69.3 - 75.2]	64.4	[61.0 - 67.6]	0.11
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Escherichia coli* DSM 30083	60.1	[56.4 - 63.6]	72.3	[69.3 - 75.1]	63.6	[60.3 - 66.8]	0.07
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	49.2	[46.6 - 51.9]	12.9	[10.6 - 15.7]	15.29
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Skermanella stibiiresistens* SB22	12.5	[9.8 - 15.8]	48.3	[45.7 - 50.9]	12.9	[10.6 - 15.6]	15.49

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	47.7	[45.1 - 50.3]	12.9	[10.6 - 15.7]	15.98
'Escherichia coli S88' (CU928161)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	46.8	[44.2 - 49.3]	13.0	[10.6 - 15.7]	15.18
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Skermanella stibiiresistens* SB22	12.5	[9.8 - 15.8]	46.8	[44.2 - 49.4]	12.9	[10.6 - 15.7]	15.47
'Shigella dysenteriae Sd197' (CP000034)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	46.8	[44.3 - 49.4]	13.0	[10.6 - 15.7]	14.61
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Skermanella stibiiresistens* SB22	12.5	[9.8 - 15.8]	46.7	[44.2 - 49.3]	12.9	[10.6 - 15.7]	11.79
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	45.4	[42.8 - 47.9]	13.0	[10.6 - 15.7]	15.06
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	45.1	[42.5 - 47.6]	13.0	[10.6 - 15.7]	15.33
'Escherichia fergusonii ATCC 35469' (CU928158)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	44.9	[42.4 - 47.5]	13.0	[10.6 - 15.7]	15.93
'Escherichia coli IAI39' (CU928164)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	44.8	[42.3 - 47.4]	13.0	[10.6 - 15.7]	15.23
'Escherichia fergusonii ECD227' (CM001142)	*Skermanella stibiiresistens* SB22	12.5	[9.8 - 15.8]	44.4	[41.8 - 46.9]	12.9	[10.6 - 15.7]	15.85
'Escherichia coli SMS-3-5' (CP000970)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	44.3	[41.7 - 46.8]	13.0	[10.6 - 15.7]	15.37
'Escherichia coli UMN026' (CU928163)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	44.3	[41.8 - 46.9]	13.0	[10.6 - 15.7]	15.15
'Escherichia coli str. 'clone D i14" (CP002212)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	44.2	[41.7 - 46.8]	13.0	[10.6 - 15.7]	15.3
'Escherichia coli str. 'clone D i2" (CP002211)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	44.2	[41.7 - 46.8]	13.0	[10.6 - 15.7]	15.3
'Escherichia sp. TW09308' (AEME00000000)	*Shigella sonnei* ATCC 29930	60.0	[56.3 - 63.5]	44.1	[41.6 - 46.7]	57.2	[54.0 - 60.3]	0.74
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia sp. TW09308' (AEME00000000)**	63.1	[59.3 - 66.7]	44.0	[41.5 - 46.6]	59.7	[56.4 - 62.8]	0.1
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Skermanella stibiiresistens* SB22	12.5	[9.8 - 15.8]	44.0	[41.4 - 46.5]	12.9	[10.6 - 15.7]	15.2
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	66.9	[63.1 - 70.6]	43.9	[41.4 - 46.4]	62.7	[59.4 - 65.9]	0.52
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia sp. TW09308' (AEME00000000)**	69.9	[66.0 - 73.6]	43.9	[41.3 - 46.4]	65.1	[61.8 - 68.4]	0.3
'Escherichia sp. TW09308' (AEME00000000)	*Shigella boydii* ATCC 8700	55.9	[52.3 - 59.4]	43.8	[41.2 - 46.3]	53.7	[50.5 - 56.7]	0.84
'Escherichia sp. TW09308' (AEME00000000)	*Escherichia coli* DSM 30083	69.7	[65.8 - 73.3]	43.7	[41.2 - 46.3]	64.9	[61.5 - 68.1]	0.37
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia coli UMN026' (CU928163)**	64.3	[60.5 - 67.9]	43.7	[41.2 - 46.3]	60.6	[57.3 - 63.7]	0.44

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Escherichia marmotae* HT073016	65.9	[62.1 - 69.6]	43.7	[41.2 - 46.2]	61.9	[58.6 - 65.1]	0.49
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia sp. TW09308' (AEME00000000)**	65.3	[61.5 - 68.9]	43.6	[41.1 - 46.2]	61.3	[58.1 - 64.5]	0.48
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia coli S88' (CU928161)**	69.5	[65.6 - 73.1]	43.6	[41.1 - 46.2]	64.7	[61.3 - 67.9]	0.4
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia sp. TW09308' (AEME00000000)**	63.7	[59.9 - 67.3]	43.6	[41.1 - 46.2]	60.0	[56.8 - 63.2]	0.39
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia coli IAI39' (CU928164)**	62.0	[58.3 - 65.6]	43.6	[41.1 - 46.2]	58.6	[55.4 - 61.8]	0.35
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Escherichia marmotae* HT073016	59.1	[55.5 - 62.7]	43.5	[41.0 - 46.1]	56.3	[53.1 - 59.4]	0.06
'Escherichia sp. TW09308' (AEME00000000)	*Shigella dysenteriae* ATCC 13313	51.8	[48.4 - 55.3]	43.5	[41.0 - 46.0]	50.2	[47.1 - 53.2]	0.7
'Escherichia coli UMN026' (CU928163)	*Escherichia marmotae* HT073016	63.0	[59.3 - 66.6]	43.5	[41.0 - 46.1]	59.4	[56.2 - 62.6]	0.4
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Escherichia marmotae* HT073016	61.4	[57.7 - 65.0]	43.5	[41.0 - 46.1]	58.1	[54.9 - 61.3]	0.35
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Escherichia marmotae* HT073016	63.3	[59.5 - 66.9]	43.4	[40.9 - 46.0]	59.6	[56.4 - 62.8]	0.44
'Escherichia sp. TW09308' (AEME00000000)	**'Shigella dysenteriae Sd197' (CP000034)**	53.1	[49.6 - 56.5]	43.4	[40.9 - 46.0]	51.2	[48.1 - 54.3]	0.97
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Skermanella stibiiresistens* SB22	12.5	[9.8 - 15.8]	43.4	[40.9 - 46.0]	12.9	[10.6 - 15.7]	15.38
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia sp. TW09308' (AEME00000000)**	61.0	[57.3 - 64.5]	43.4	[40.9 - 46.0]	57.7	[54.5 - 60.9]	0.12
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia coli SMS-3-5' (CP000970)**	65.8	[62.0 - 69.4]	43.4	[40.9 - 45.9]	61.7	[58.4 - 64.8]	0.22
'Escherichia sp. TW09308' (AEME00000000)	*Shigella flexneri* ATCC 29903	55.3	[51.7 - 58.8]	43.4	[40.9 - 46.0]	53.1	[49.9 - 56.1]	0.39
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Escherichia marmotae* HT073016	60.5	[56.8 - 64.0]	43.3	[40.8 - 45.8]	57.3	[54.1 - 60.4]	0.08
'Escherichia coli SMS-3-5' (CP000970)	*Escherichia marmotae* HT073016	65.0	[61.2 - 68.6]	43.3	[40.8 - 45.9]	60.9	[57.7 - 64.1]	0.18
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia sp. TW09308' (AEME00000000)**	63.6	[59.9 - 67.3]	43.3	[40.7 - 45.8]	59.9	[56.6 - 63.0]	0.21
'Escherichia coli IAI39' (CU928164)	*Escherichia marmotae* HT073016	59.9	[56.3 - 63.5]	43.3	[40.7 - 45.8]	56.8	[53.7 - 60.0]	0.32
'Shigella dysenteriae Sd197' (CP000034)	*Escherichia marmotae* HT073016	53.6	[50.1 - 57.0]	43.3	[40.8 - 45.9]	51.6	[48.5 - 54.6]	0.94
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Escherichia marmotae* HT073016	65.6	[61.7 - 69.2]	43.3	[40.8 - 45.9]	61.4	[58.1 - 64.6]	0.26
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Escherichia marmotae* HT073016	61.8	[58.1 - 65.4]	43.2	[40.7 - 45.7]	58.4	[55.1 - 61.5]	0.17

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli S88' (CU928161)	*Escherichia marmotae* HT073016	64.8	[61.0 - 68.5]	43.2	[40.7 - 45.8]	60.8	[57.5 - 64.0]	0.37
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Escherichia marmotae* HT073016	56.6	[53.0 - 60.1]	43.2	[40.7 - 45.7]	54.1	[50.9 - 57.2]	0.22
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	57.8	[54.2 - 61.3]	43.1	[40.6 - 45.7]	55.1	[51.9 - 58.2]	0.26
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia coli str. 'clone D i14" (CP002212)**	64.6	[60.8 - 68.2]	43.1	[40.6 - 45.7]	60.6	[57.3 - 63.7]	0.28
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia coli str. 'clone D i2" (CP002211)**	64.6	[60.8 - 68.2]	43.1	[40.6 - 45.7]	60.6	[57.3 - 63.7]	0.28
'Escherichia coli str. 'clone D i2" (CP002211)	*Escherichia marmotae* HT073016	63.0	[59.3 - 66.6]	43.0	[40.5 - 45.6]	59.3	[56.0 - 62.4]	0.25
'Escherichia coli str. 'clone D i14" (CP002212)	*Escherichia marmotae* HT073016	63.0	[59.3 - 66.6]	43.0	[40.5 - 45.6]	59.3	[56.0 - 62.4]	0.25
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia sp. TW09308' (AEME00000000)**	53.8	[50.3 - 57.2]	43.0	[40.4 - 45.5]	51.6	[48.6 - 54.7]	0.3
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Escherichia marmotae* HT073016	52.0	[48.5 - 55.4]	42.9	[40.4 - 45.5]	50.2	[47.1 - 53.2]	0.26
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Skermanella stibiiresistens* SB22	12.6	[9.9 - 15.8]	41.9	[39.4 - 44.4]	13.0	[10.6 - 15.7]	9.35
'Escherichia sp. TW09308' (AEME00000000)	*Skermanella stibiiresistens* SB22	12.5	[9.8 - 15.8]	41.8	[39.3 - 44.4]	12.9	[10.6 - 15.7]	15.59
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Shigella sonnei* ATCC 29930	58.2	[54.6 - 61.7]	41.8	[39.3 - 44.4]	55.0	[51.8 - 58.1]	1.13
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Shigella dysenteriae* ATCC 13313	54.6	[51.1 - 58.1]	41.7	[39.2 - 44.2]	52.0	[48.9 - 55.0]	1.1
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Shigella dysenteriae Sd197' (CP000034)**	55.5	[52.0 - 59.0]	41.5	[39.0 - 44.0]	52.6	[49.5 - 55.7]	1.37
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli IAI39' (CU928164)**	57.6	[54.0 - 61.2]	41.3	[38.8 - 43.9]	54.3	[51.2 - 57.4]	0.75
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Escherichia coli* DSM 30083	60.5	[56.9 - 64.1]	41.3	[38.8 - 43.8]	56.7	[53.5 - 59.8]	0.76
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli str. 'clone D i2" (CP002211)**	59.2	[55.6 - 62.8]	41.2	[38.7 - 43.7]	55.6	[52.4 - 58.7]	0.68
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia fergusonii ECD227' (CM001142)**	49.6	[46.2 - 53.1]	41.2	[38.7 - 43.7]	47.7	[44.7 - 50.8]	0.36
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli str. 'clone D i14" (CP002212)**	59.2	[55.6 - 62.8]	41.2	[38.7 - 43.7]	55.6	[52.4 - 58.7]	0.68

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	48.0	[44.5 - 51.4]	41.2	[38.7 - 43.7]	46.3	[43.3 - 49.3]	0.44
'Escherichia fergusonii ECD227' (CM001142)	**'Escherichia coli IAI39' (CU928164)**	50.0	[46.5 - 53.4]	41.2	[38.7 - 43.8]	48.0	[45.0 - 51.0]	0.62
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia fergusonii ECD227' (CM001142)**	49.8	[46.3 - 53.2]	41.2	[38.7 - 43.7]	47.8	[44.8 - 50.8]	0.66
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Escherichia fergusonii* ATCC 35469	47.5	[44.1 - 51.0]	41.2	[38.7 - 43.7]	45.9	[42.9 - 49.0]	0.46
'Escherichia fergusonii ATCC 35469' (CU928158)	*Shigella boydii* ATCC 8700	45.8	[42.4 - 49.2]	41.2	[38.7 - 43.8]	44.4	[41.5 - 47.5]	1.18
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Shigella boydii* ATCC 8700	57.2	[53.6 - 60.7]	41.2	[38.7 - 43.8]	53.9	[50.8 - 57.0]	1.23
'Escherichia fergusonii ECD227' (CM001142)	*Shigella dysenteriae* ATCC 13313	43.2	[39.8 - 46.6]	41.2	[38.7 - 43.7]	42.2	[39.2 - 45.2]	0.97
'Escherichia fergusonii ATCC 35469' (CU928158)	*Shigella flexneri* ATCC 29903	44.8	[41.4 - 48.2]	41.2	[38.7 - 43.8]	43.6	[40.6 - 46.6]	0.73
'Escherichia fergusonii ECD227' (CM001142)	*Shigella boydii* ATCC 8700	45.8	[42.5 - 49.3]	41.2	[38.7 - 43.7]	44.5	[41.5 - 47.5]	1.11
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli S88' (CU928161)**	60.8	[57.1 - 64.4]	41.1	[38.7 - 43.7]	56.8	[53.7 - 60.0]	0.8
'Escherichia coli IAI39' (CU928164)	*Escherichia fergusonii* ATCC 35469	48.7	[45.2 - 52.1]	41.1	[38.6 - 43.6]	46.9	[43.8 - 49.9]	0.71
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia fergusonii ECD227' (CM001142)**	47.1	[43.7 - 50.5]	41.1	[38.6 - 43.6]	45.5	[42.5 - 48.6]	0.38
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	47.9	[44.5 - 51.3]	41.1	[38.6 - 43.6]	46.2	[43.2 - 49.3]	0.73
'Escherichia fergusonii ECD227' (CM001142)	*Shigella flexneri* ATCC 29903	44.9	[41.5 - 48.3]	41.1	[38.6 - 43.6]	43.7	[40.7 - 46.7]	0.66
'Escherichia fergusonii ECD227' (CM001142)	**'Shigella dysenteriae Sd197' (CP000034)**	44.2	[40.8 - 47.6]	41.1	[38.6 - 43.7]	43.0	[40.1 - 46.1]	1.24
'Escherichia fergusonii ATCC 35469' (CU928158)	**'Escherichia coli IAI39' (CU928164)**	49.0	[45.6 - 52.5]	41.1	[38.6 - 43.6]	47.2	[44.2 - 50.2]	0.69
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Escherichia fergusonii* ATCC 35469	47.6	[44.2 - 51.0]	41.1	[38.6 - 43.7]	46.0	[43.0 - 49.0]	0.75
'Escherichia coli UMN026' (CU928163)	*Escherichia fergusonii* ATCC 35469	50.6	[47.2 - 54.1]	41.1	[38.6 - 43.6]	48.5	[45.5 - 51.5]	0.8
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli H299' (ADBC01000001-ADBC01000229)**	57.4	[53.8 - 60.9]	41.0	[38.5 - 43.6]	54.0	[50.9 - 57.1]	0.87
'Shigella dysenteriae Sd197' (CP000034)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	44.0	[40.6 - 47.4]	41.0	[38.5 - 43.5]	42.9	[39.9 - 45.9]	1.31
'Escherichia fergusonii ATCC 35469' (CU928158)	**'Escherichia coli UMN026' (CU928163)**	51.1	[47.6 - 54.5]	41.0	[38.6 - 43.6]	48.9	[45.8 - 51.9]	0.78

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Escherichia fergusonii* ATCC 35469	40.4	[37.0 - 43.8]	41.0	[38.6 - 43.6]	39.7	[36.7 - 42.8]	0.66
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Escherichia fergusonii* ATCC 35469	47.4	[44.0 - 50.8]	41.0	[38.5 - 43.5]	45.8	[42.8 - 48.8]	0.83
'Escherichia fergusonii ATCC 35469' (CU928158)	*Shigella sonnei* ATCC 29930	46.1	[42.7 - 49.5]	41.0	[38.5 - 43.5]	44.7	[41.7 - 47.7]	1.08
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	47.7	[44.3 - 51.1]	41.0	[38.5 - 43.5]	46.0	[43.0 - 49.1]	0.82
'Shigella dysenteriae Sd197' (CP000034)	*Escherichia fergusonii* ATCC 35469	45.1	[41.7 - 48.5]	41.0	[38.5 - 43.6]	43.8	[40.8 - 46.9]	1.33
'Escherichia fergusonii ATCC 35469' (CU928158)	*Shigella dysenteriae* ATCC 13313	43.0	[39.6 - 46.5]	41.0	[38.5 - 43.6]	42.0	[39.1 - 45.1]	1.04
'Escherichia coli SMS-3-5' (CP000970)	*Escherichia fergusonii* ATCC 35469	48.9	[45.5 - 52.4]	41.0	[38.5 - 43.5]	47.1	[44.1 - 50.1]	0.58
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli SMS-3-5' (CP000970)**	59.7	[56.1 - 63.3]	41.0	[38.5 - 43.5]	55.9	[52.7 - 59.0]	0.61
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	40.7	[37.3 - 44.1]	41.0	[38.6 - 43.6]	40.0	[37.0 - 43.0]	0.64
'Escherichia fergusonii ECD227' (CM001142)	**'Escherichia coli SMS-3-5' (CP000970)**	50.2	[46.8 - 53.7]	41.0	[38.5 - 43.5]	48.2	[45.1 - 51.2]	0.49
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Escherichia fergusonii* ATCC 35469	46.0	[42.6 - 49.4]	41.0	[38.6 - 43.6]	44.6	[41.6 - 47.6]	0.47
'Escherichia coli SMS-3-5' (CP000970)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	49.3	[45.9 - 52.7]	41.0	[38.5 - 43.5]	47.4	[44.3 - 50.4]	0.56
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	46.3	[42.9 - 49.8]	41.0	[38.5 - 43.6]	44.9	[41.9 - 47.9]	0.46
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)**	56.1	[52.5 - 59.6]	40.9	[38.5 - 43.5]	52.9	[49.8 - 56.0]	0.78
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia fergusonii ECD227' (CM001142)**	42.0	[38.6 - 45.4]	40.9	[38.4 - 43.4]	41.1	[38.1 - 44.1]	0.56
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli UMN026' (CU928163)**	57.4	[53.8 - 61.0]	40.9	[38.4 - 43.4]	54.0	[50.9 - 57.1]	0.83
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Shigella flexneri* ATCC 29903	54.7	[51.1 - 58.1]	40.9	[38.4 - 43.4]	51.8	[48.7 - 54.8]	0.78
'Escherichia fergusonii ECD227' (CM001142)	*Shigella sonnei* ATCC 29930	47.4	[44.0 - 50.8]	40.9	[38.4 - 43.4]	45.7	[42.7 - 48.8]	1.0
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	53.1	[49.6 - 56.6]	40.9	[38.4 - 43.5]	50.5	[47.4 - 53.6]	0.86
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Escherichia fergusonii* ATCC 35469	52.6	[49.1 - 56.0]	40.9	[38.4 - 43.5]	50.1	[47.0 - 53.1]	0.88

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	51.6	[48.1 - 55.0]	40.8	[38.3 - 43.4]	49.2	[46.2 - 52.3]	0.64
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Escherichia fergusonii ECD227' (CM001142)**	52.5	[49.0 - 56.0]	40.8	[38.3 - 43.3]	50.0	[46.9 - 53.1]	0.56
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia fergusonii ECD227' (CM001142)**	49.0	[45.6 - 52.5]	40.8	[38.3 - 43.3]	47.1	[44.1 - 50.1]	0.48
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Escherichia fergusonii* ATCC 35469	47.9	[44.5 - 51.4]	40.8	[38.3 - 43.3]	46.2	[43.2 - 49.2]	0.57
'Escherichia fergusonii ECD227' (CM001142)	**'Escherichia coli UMN026' (CU928163)**	51.9	[48.5 - 55.4]	40.8	[38.3 - 43.3]	49.5	[46.5 - 52.6]	0.71
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Escherichia fergusonii* ATCC 35469	51.0	[47.5 - 54.4]	40.8	[38.3 - 43.4]	48.7	[45.7 - 51.8]	0.66
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Escherichia fergusonii ECD227' (CM001142)**	49.1	[45.7 - 52.6]	40.8	[38.3 - 43.3]	47.2	[44.2 - 50.2]	0.74
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli str. K-12 substr. W3110' (AP009048)**	60.1	[56.5 - 63.7]	40.8	[38.3 - 43.3]	56.1	[53.0 - 59.3]	0.92
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)**	56.0	[52.4 - 59.5]	40.7	[38.2 - 43.2]	52.8	[49.7 - 55.9]	0.6
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	48.3	[44.9 - 51.7]	40.7	[38.3 - 43.3]	46.5	[43.5 - 49.5]	0.55
'Shigella dysenteriae Sd197' (CP000034)	*Escherichia albertii* NBRC 107761	55.3	[51.7 - 58.8]	40.7	[38.2 - 43.3]	52.2	[49.1 - 55.3]	1.46
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Escherichia fergusonii ECD227' (CM001142)**	52.9	[49.4 - 56.4]	40.7	[38.2 - 43.2]	50.3	[47.2 - 53.3]	0.79
'Escherichia coli S88' (CU928161)	*Escherichia albertii* NBRC 107761	60.8	[57.1 - 64.4]	40.6	[38.1 - 43.2]	56.6	[53.5 - 59.8]	0.89
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Escherichia albertii* NBRC 107761	55.8	[52.2 - 59.3]	40.6	[38.1 - 43.2]	52.6	[49.5 - 55.7]	0.88
'Escherichia fergusonii ECD227' (CM001142)	**'Escherichia coli S88' (CU928161)**	53.1	[49.6 - 56.6]	40.6	[38.1 - 43.1]	50.4	[47.3 - 53.5]	0.67
'Escherichia coli IAI39' (CU928164)	*Escherichia albertii* NBRC 107761	57.3	[53.7 - 60.8]	40.6	[38.1 - 43.1]	53.8	[50.7 - 56.9]	0.84
'Escherichia coli S88' (CU928161)	*Escherichia fergusonii* ATCC 35469	50.8	[47.4 - 54.3]	40.5	[38.0 - 43.0]	48.5	[45.5 - 51.6]	0.76
'Escherichia fergusonii ATCC 35469' (CU928158)	**'Escherichia coli S88' (CU928161)**	51.4	[47.9 - 54.8]	40.5	[38.0 - 43.0]	48.9	[45.9 - 52.0]	0.74
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Escherichia albertii* NBRC 107761	55.8	[52.3 - 59.3]	40.5	[38.0 - 43.0]	52.6	[49.5 - 55.6]	0.7
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)**	54.0	[50.5 - 57.5]	40.5	[38.0 - 43.1]	51.2	[48.1 - 54.2]	0.49
'Escherichia coli str. 'clone D i14'' (CP002212)	*Escherichia albertii* NBRC 107761	59.0	[55.4 - 62.5]	40.5	[38.0 - 43.1]	55.2	[52.0 - 58.3]	0.77

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Escherichia fergusonii* ATCC 35469	44.4	[41.1 - 47.9]	40.5	[38.0 - 43.1]	43.1	[40.1 - 46.2]	0.62
'Escherichia coli str. 'clone D i2" (CP002211)	*Escherichia albertii* NBRC 107761	59.0	[55.4 - 62.5]	40.5	[38.0 - 43.1]	55.2	[52.0 - 58.3]	0.77
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	44.8	[41.4 - 48.2]	40.5	[38.0 - 43.1]	43.5	[40.5 - 46.5]	0.6
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Escherichia albertii* NBRC 107761	57.2	[53.6 - 60.7]	40.4	[37.9 - 42.9]	53.6	[50.5 - 56.7]	0.96
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)**	52.6	[49.1 - 56.0]	40.4	[37.9 - 42.9]	49.9	[46.9 - 53.0]	0.51
'Escherichia coli UMN026' (CU928163)	*Escherichia albertii* NBRC 107761	57.5	[53.9 - 61.0]	40.4	[37.9 - 42.9]	53.9	[50.8 - 57.0]	0.93
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)**	53.8	[50.3 - 57.3]	40.4	[37.9 - 42.9]	50.9	[47.8 - 54.0]	0.69
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Escherichia fergusonii ECD227' (CM001142)**	46.2	[42.8 - 49.6]	40.4	[37.9 - 42.9]	44.6	[41.6 - 47.6]	0.53
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Escherichia albertii* NBRC 107761	61.3	[57.6 - 64.8]	40.3	[37.8 - 42.8]	56.9	[53.7 - 60.0]	1.01
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli O157:H7 str. Sakai' (BA000007)**	57.7	[54.1 - 61.2]	40.3	[37.8 - 42.9]	54.1	[50.9 - 57.1]	0.65
'Escherichia fergusonii ECD227' (CM001142)	*Escherichia coli* DSM 30083	51.9	[48.4 - 55.3]	40.3	[37.8 - 42.8]	49.3	[46.3 - 52.4]	0.63
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Escherichia albertii* NBRC 107761	54.3	[50.8 - 57.8]	40.3	[37.8 - 42.8]	51.3	[48.2 - 54.4]	0.6
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Escherichia albertii* NBRC 107761	55.7	[52.2 - 59.2]	40.3	[37.9 - 42.9]	52.5	[49.4 - 55.5]	0.59
'Escherichia coli SMS-3-5' (CP000970)	*Escherichia albertii* NBRC 107761	59.6	[55.9 - 63.1]	40.3	[37.8 - 42.8]	55.5	[52.4 - 58.6]	0.71
'Escherichia fergusonii ATCC 35469' (CU928158)	*Escherichia coli* DSM 30083	50.3	[46.9 - 53.7]	40.2	[37.7 - 42.8]	48.0	[45.0 - 51.0]	0.71
'Escherichia fergusonii ECD227' (CM001142)	**'Escherichia coli str. 'clone D i2" (CP002211)**	50.1	[46.7 - 53.6]	40.2	[37.7 - 42.7]	47.8	[44.8 - 50.9]	0.55
'Escherichia fergusonii ECD227' (CM001142)	**'Escherichia coli str. 'clone D i14" (CP002212)**	50.1	[46.7 - 53.6]	40.2	[37.7 - 42.7]	47.8	[44.8 - 50.9]	0.55
'Escherichia coli str. 'clone D i14" (CP002212)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	49.3	[45.9 - 52.7]	40.1	[37.7 - 42.7]	47.1	[44.1 - 50.2]	0.62
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia coli TA143' (ADAY01000001-ADAY01000168)**	56.4	[52.8 - 59.9]	40.1	[37.6 - 42.6]	52.9	[49.8 - 56.0]	0.69
'Escherichia coli str. 'clone D i2" (CP002211)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	49.3	[45.9 - 52.7]	40.1	[37.7 - 42.7]	47.1	[44.1 - 50.2]	0.62
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Escherichia albertii* NBRC 107761	53.7	[50.2 - 57.2]	40.1	[37.7 - 42.7]	50.8	[47.7 - 53.9]	0.79

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Escherichia albertii* NBRC 107761	58.9	[55.2 - 62.4]	40.1	[37.6 - 42.6]	54.9	[51.7 - 58.0]	0.79
'Escherichia coli str. 'clone D i14" (CP002212)	*Escherichia fergusonii* ATCC 35469	48.9	[45.5 - 52.3]	40.1	[37.6 - 42.6]	46.8	[43.8 - 49.8]	0.64
'Escherichia coli str. 'clone D i2" (CP002211)	*Escherichia fergusonii* ATCC 35469	48.9	[45.5 - 52.3]	40.1	[37.6 - 42.6]	46.8	[43.8 - 49.8]	0.64
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Escherichia albertii* NBRC 107761	57.9	[54.3 - 61.4]	40.1	[37.6 - 42.7]	54.1	[51.0 - 57.2]	0.75
'Escherichia sp. TW09308' (AEME00000000)	*Escherichia albertii* NBRC 107761	59.9	[56.3 - 63.5]	38.5	[36.1 - 41.1]	55.1	[52.0 - 58.3]	0.49
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia sp. TW09308' (AEME00000000)**	57.2	[53.6 - 60.7]	38.5	[36.1 - 41.1]	53.0	[49.9 - 56.1]	0.39
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Escherichia marmotae* HT073016	56.3	[52.7 - 59.7]	38.2	[35.8 - 40.7]	52.1	[49.1 - 55.2]	0.43
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia fergusonii ECD227' (CM001142)**	51.5	[48.0 - 54.9]	34.6	[32.2 - 37.2]	47.1	[44.1 - 50.2]	0.27
'Escherichia sp. TW09308' (AEME00000000)	*Escherichia fergusonii* ATCC 35469	49.5	[46.1 - 53.0]	34.6	[32.1 - 37.1]	45.6	[42.6 - 48.6]	0.36
'Escherichia sp. TW09308' (AEME00000000)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	50.1	[46.6 - 53.5]	34.6	[32.1 - 37.1]	46.0	[43.0 - 49.0]	0.34
'Escherichia fergusonii ATCC 35469' (CU928158)	*Escherichia marmotae* HT073016	49.5	[46.1 - 52.9]	34.5	[32.1 - 37.0]	45.6	[42.6 - 48.6]	0.38
'Escherichia fergusonii ECD227' (CM001142)	*Escherichia marmotae* HT073016	50.1	[46.7 - 53.6]	34.4	[32.0 - 36.9]	46.0	[43.0 - 49.0]	0.3
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Escherichia fergusonii* ATCC 35469	44.3	[40.9 - 47.7]	34.4	[32.0 - 36.9]	41.4	[38.4 - 44.4]	0.04
'Escherichia fergusonii ECD227' (CM001142)	*Escherichia albertii* NBRC 107761	46.7	[43.3 - 50.1]	34.3	[31.9 - 36.8]	43.3	[40.3 - 46.3]	0.22
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia fergusonii ECD227' (CM001142)**	44.9	[41.6 - 48.4]	34.3	[31.9 - 36.8]	41.9	[38.9 - 44.9]	0.13
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	43.2	[39.9 - 46.7]	34.2	[31.8 - 36.7]	40.5	[37.5 - 43.5]	0.05
'Escherichia fergusonii ATCC 35469' (CU928158)	*Escherichia albertii* NBRC 107761	44.9	[41.5 - 48.3]	34.1	[31.7 - 36.6]	41.8	[38.8 - 44.8]	0.15
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Skermanella stibiiresistens* SB22	12.5	[9.8 - 15.8]	33.5	[31.1 - 36.0]	12.9	[10.6 - 15.7]	15.11
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Skermanella stibiiresistens* SB22	12.5	[9.9 - 15.8]	30.5	[28.1 - 33.0]	12.9	[10.6 - 15.7]	15.29
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Citrobacter diversus* NCTC 10849	34.3	[30.9 - 37.9]	26.6	[24.2 - 29.0]	31.4	[28.5 - 34.5]	2.92

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli IAI39' (CU928164)	*Citrobacter diversus* NCTC 10849	34.4	[31.1 - 38.0]	26.1	[23.7 - 28.5]	31.4	[28.5 - 34.5]	2.96
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Levinea malonatica* NCTC 10810	33.4	[30.0 - 37.0]	25.8	[23.4 - 28.2]	30.5	[27.6 - 33.6]	3.12
'Shigella dysenteriae Sd197' (CP000034)	*Levinea malonatica* NCTC 10810	32.0	[28.7 - 35.6]	25.8	[23.5 - 28.3]	29.5	[26.6 - 32.6]	2.53
'Shigella dysenteriae Sd197' (CP000034)	*Citrobacter diversus* NCTC 10849	31.1	[27.7 - 34.7]	25.8	[23.4 - 28.2]	28.8	[25.9 - 31.9]	2.34
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Citrobacter diversus* NCTC 10849	34.5	[31.2 - 38.1]	25.8	[23.5 - 28.3]	31.4	[28.5 - 34.5]	2.84
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Citrobacter diversus* NCTC 10849	32.6	[29.2 - 36.1]	25.7	[23.3 - 28.1]	29.9	[27.0 - 33.0]	3.2
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Citrobacter diversus* NCTC 10849	32.0	[28.6 - 35.5]	25.6	[23.3 - 28.1]	29.4	[26.5 - 32.5]	3.21
'Shigella dysenteriae Sd197' (CP000034)	*Citrobacter koseri* NCTC 10786	31.8	[28.4 - 35.4]	25.6	[23.3 - 28.1]	29.3	[26.4 - 32.4]	2.56
'Escherichia coli str. 'clone D i14" (CP002212)	*Citrobacter diversus* NCTC 10849	34.3	[30.9 - 37.8]	25.6	[23.3 - 28.1]	31.1	[28.2 - 34.2]	3.03
'Escherichia coli str. 'clone D i2" (CP002211)	*Citrobacter diversus* NCTC 10849	34.3	[30.9 - 37.8]	25.6	[23.3 - 28.1]	31.1	[28.2 - 34.2]	3.03
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Citrobacter koseri* NCTC 10786	33.0	[29.6 - 36.5]	25.6	[23.2 - 28.0]	30.2	[27.2 - 33.3]	3.14
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Citrobacter diversus* NCTC 10849	33.3	[29.9 - 36.9]	25.5	[23.2 - 28.0]	30.4	[27.5 - 33.5]	3.1
'Escherichia coli IAI39' (CU928164)	*Citrobacter koseri* NCTC 10786	35.3	[32.0 - 38.9]	25.5	[23.1 - 27.9]	31.9	[29.0 - 35.0]	3.17
'Escherichia coli str. 'clone D i2" (CP002211)	*Levinea malonatica* NCTC 10810	36.0	[32.6 - 39.5]	25.5	[23.1 - 28.0]	32.4	[29.4 - 35.4]	3.22
'Escherichia coli S88' (CU928161)	*Citrobacter diversus* NCTC 10849	34.2	[30.8 - 37.8]	25.5	[23.2 - 28.0]	31.1	[28.1 - 34.2]	2.91
'Escherichia coli IAI39' (CU928164)	*Levinea malonatica* NCTC 10810	35.2	[31.8 - 38.7]	25.5	[23.2 - 28.0]	31.8	[28.8 - 34.9]	3.15
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Citrobacter koseri* NCTC 10786	32.9	[29.5 - 36.5]	25.5	[23.1 - 28.0]	30.1	[27.2 - 33.2]	3.43
'Escherichia coli UMN026' (CU928163)	*Citrobacter diversus* NCTC 10849	35.0	[31.6 - 38.5]	25.5	[23.2 - 28.0]	31.6	[28.7 - 34.7]	2.87
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Levinea malonatica* NCTC 10810	34.8	[31.4 - 38.3]	25.5	[23.2 - 28.0]	31.5	[28.6 - 34.6]	3.03
'Escherichia coli str. 'clone D i14" (CP002212)	*Levinea malonatica* NCTC 10810	36.0	[32.6 - 39.5]	25.5	[23.1 - 28.0]	32.4	[29.4 - 35.4]	3.22
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Levinea malonatica* NCTC 10810	33.6	[30.2 - 37.1]	25.5	[23.2 - 28.0]	30.6	[27.7 - 33.7]	3.39
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Levinea malonatica* NCTC 10810	32.9	[29.5 - 36.4]	25.5	[23.2 - 28.0]	30.1	[27.2 - 33.2]	3.41
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Levinea malonatica* NCTC 10810	36.8	[33.4 - 40.3]	25.4	[23.1 - 27.9]	32.9	[30.0 - 36.0]	2.98

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli str. 'clone D i14" (CP002212)	*Citrobacter koseri* NCTC 10786	35.6	[32.2 - 39.1]	25.4	[23.1 - 27.9]	32.0	[29.1 - 35.1]	3.25
'Escherichia coli S88' (CU928161)	*Levinea malonatica* NCTC 10810	35.3	[31.9 - 38.8]	25.4	[23.1 - 27.9]	31.9	[28.9 - 35.0]	3.1
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Citrobacter diversus* NCTC 10849	35.4	[32.1 - 39.0]	25.4	[23.1 - 27.9]	32.0	[29.0 - 35.0]	2.79
'Escherichia coli S88' (CU928161)	*Citrobacter koseri* NCTC 10786	35.3	[32.0 - 38.9]	25.4	[23.1 - 27.9]	31.9	[28.9 - 35.0]	3.12
'Escherichia coli str. 'clone D i2" (CP002211)	*Citrobacter koseri* NCTC 10786	35.6	[32.2 - 39.1]	25.4	[23.1 - 27.9]	32.0	[29.1 - 35.1]	3.25
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Levinea malonatica* NCTC 10810	35.2	[31.9 - 38.8]	25.4	[23.1 - 27.9]	31.8	[28.9 - 34.9]	3.3
'Escherichia coli SMS-3-5' (CP000970)	*Citrobacter diversus* NCTC 10849	34.0	[30.6 - 37.5]	25.4	[23.1 - 27.9]	30.9	[28.0 - 34.0]	3.09
'Escherichia coli UMN026' (CU928163)	*Levinea malonatica* NCTC 10810	35.1	[31.8 - 38.7]	25.4	[23.1 - 27.9]	31.7	[28.8 - 34.8]	3.07
'Escherichia coli UMN026' (CU928163)	*Citrobacter koseri* NCTC 10786	35.0	[31.6 - 38.5]	25.4	[23.1 - 27.9]	31.6	[28.7 - 34.7]	3.09
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Citrobacter diversus* NCTC 10849	30.0	[26.6 - 33.6]	25.4	[23.1 - 27.9]	27.9	[25.0 - 31.0]	3.01
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Citrobacter diversus* NCTC 10849	32.3	[28.9 - 35.9]	25.3	[23.0 - 27.8]	29.6	[26.7 - 32.7]	3.05
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Citrobacter koseri* NCTC 10786	36.6	[33.2 - 40.1]	25.3	[23.0 - 27.8]	32.7	[29.8 - 35.8]	3.01
'Escherichia coli SMS-3-5' (CP000970)	*Levinea malonatica* NCTC 10810	35.4	[32.0 - 38.9]	25.3	[23.0 - 27.8]	31.9	[28.9 - 35.0]	3.29
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Citrobacter koseri* NCTC 10786	33.2	[29.8 - 36.8]	25.3	[23.0 - 27.8]	30.3	[27.4 - 33.4]	3.41
'Escherichia sp. TW09308' (AEME00000000)	*Citrobacter diversus* NCTC 10849	33.1	[29.7 - 36.6]	25.3	[22.9 - 27.7]	30.2	[27.2 - 33.3]	3.31
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Citrobacter koseri* NCTC 10786	34.5	[31.1 - 38.1]	25.3	[23.0 - 27.8]	31.2	[28.3 - 34.3]	3.32
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Levinea malonatica* NCTC 10810	33.0	[29.6 - 36.5]	25.2	[22.9 - 27.7]	30.1	[27.1 - 33.2]	3.25
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Citrobacter koseri* NCTC 10786	34.7	[31.3 - 38.2]	25.2	[22.9 - 27.7]	31.3	[28.4 - 34.4]	3.05
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Levinea malonatica* NCTC 10810	34.8	[31.5 - 38.4]	25.2	[22.9 - 27.7]	31.5	[28.5 - 34.5]	3.21
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Citrobacter diversus* NCTC 10849	32.2	[28.8 - 35.7]	25.2	[22.9 - 27.7]	29.5	[26.5 - 32.6]	3.7
'Escherichia coli SMS-3-5' (CP000970)	*Citrobacter koseri* NCTC 10786	35.2	[31.8 - 38.7]	25.2	[22.9 - 27.7]	31.7	[28.8 - 34.8]	3.31
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Citrobacter diversus* NCTC 10849	34.0	[30.6 - 37.5]	25.2	[22.9 - 27.7]	30.8	[27.9 - 33.9]	3.01

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Citrobacter koseri* NCTC 10786	34.8	[31.4 - 38.3]	25.2	[22.8 - 27.7]	31.4	[28.5 - 34.5]	3.23
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Levinea malonatica* NCTC 10810	30.2	[26.9 - 33.8]	25.1	[22.8 - 27.6]	28.0	[25.1 - 31.1]	3.21
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Citrobacter koseri* NCTC 10786	33.1	[29.7 - 36.6]	25.1	[22.8 - 27.6]	30.1	[27.2 - 33.2]	3.27
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Citrobacter koseri* NCTC 10786	30.2	[26.8 - 33.8]	25.0	[22.7 - 27.5]	27.9	[25.0 - 31.0]	3.23
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Levinea malonatica* NCTC 10810	32.9	[29.5 - 36.5]	25.0	[22.6 - 27.4]	30.0	[27.0 - 33.1]	3.9
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Citrobacter koseri* NCTC 10786	32.6	[29.2 - 36.1]	24.9	[22.6 - 27.4]	29.7	[26.8 - 32.8]	3.92
'Shigella dysenteriae Sd197' (CP000034)	*Citrobacter amalonaticus* NCTC 10805	31.8	[28.4 - 35.3]	24.9	[22.6 - 27.4]	29.1	[26.2 - 32.2]	2.18
'Escherichia sp. TW09308' (AEME00000000)	*Citrobacter koseri* NCTC 10786	33.3	[29.9 - 36.8]	24.8	[22.5 - 27.3]	30.2	[27.2 - 33.3]	3.53
'Escherichia fergusonii ATCC 35469' (CU928158)	*Citrobacter diversus* NCTC 10849	32.4	[29.0 - 36.0]	24.8	[22.5 - 27.3]	29.5	[26.6 - 32.6]	3.65
'Escherichia fergusonii ATCC 35469' (CU928158)	*Citrobacter koseri* NCTC 10786	33.6	[30.2 - 37.1]	24.8	[22.5 - 27.2]	30.4	[27.5 - 33.5]	3.87
'Escherichia sp. TW09308' (AEME00000000)	*Levinea malonatica* NCTC 10810	34.1	[30.8 - 37.7]	24.8	[22.5 - 27.3]	30.8	[27.9 - 33.9]	3.51
'Escherichia fergusonii ATCC 35469' (CU928158)	*Levinea malonatica* NCTC 10810	33.6	[30.2 - 37.1]	24.7	[22.4 - 27.2]	30.4	[27.5 - 33.5]	3.85
'Escherichia coli IAI39' (CU928164)	*Salmonella typhi* NCTC 8385	30.5	[27.1 - 34.1]	24.6	[22.3 - 27.1]	28.1	[25.2 - 31.2]	1.46
'Escherichia fergusonii ECD227' (CM001142)	*Citrobacter diversus* NCTC 10849	32.6	[29.2 - 36.1]	24.6	[22.3 - 27.1]	29.6	[26.7 - 32.7]	3.58
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Citrobacter amalonaticus* NCTC 10805	32.7	[29.3 - 36.3]	24.6	[22.3 - 27.0]	29.7	[26.8 - 32.8]	2.76
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Citrobacter amalonaticus* NCTC 10805	36.2	[32.9 - 39.8]	24.6	[22.3 - 27.0]	32.3	[29.3 - 35.3]	2.63
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Citrobacter amalonaticus* NCTC 10805	33.6	[30.2 - 37.1]	24.5	[22.2 - 27.0]	30.3	[27.4 - 33.4]	2.89
'Escherichia fergusonii ECD227' (CM001142)	*Citrobacter koseri* NCTC 10786	33.4	[30.0 - 37.0]	24.5	[22.2 - 27.0]	30.2	[27.3 - 33.3]	3.79
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Citrobacter amalonaticus* NCTC 10805	32.1	[28.7 - 35.7]	24.5	[22.2 - 26.9]	29.2	[26.3 - 32.3]	2.94
'Shigella dysenteriae Sd197' (CP000034)	*Salmonella enterica* LT2	28.1	[24.7 - 31.7]	24.5	[22.2 - 27.0]	26.2	[23.3 - 29.3]	0.99
'Escherichia coli S88' (CU928161)	*Citrobacter amalonaticus* NCTC 10805	35.1	[31.7 - 38.6]	24.5	[22.1 - 26.9]	31.4	[28.5 - 34.5]	2.75

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Shigella dysenteriae Sd197' (CP000034)	*Salmonella typhi* NCTC 8385	28.7	[25.3 - 32.3]	24.5	[22.2 - 27.0]	26.7	[23.8 - 29.8]	0.84
'Escherichia fergusonii ECD227' (CM001142)	*Levinea malonatica* NCTC 10810	33.8	[30.4 - 37.3]	24.5	[22.2 - 27.0]	30.5	[27.5 - 33.6]	3.77
'Shigella dysenteriae Sd197' (CP000034)	*Salmonella typhimurium* ATCC 13311	28.4	[25.1 - 32.1]	24.5	[22.2 - 27.0]	26.5	[23.6 - 29.6]	0.86
'Escherichia coli UMN026' (CU928163)	*Citrobacter amalonaticus* NCTC 10805	35.2	[31.8 - 38.7]	24.5	[22.1 - 26.9]	31.5	[28.5 - 34.6]	2.71
'Escherichia coli SMS-3-5' (CP000970)	*Citrobacter amalonaticus* NCTC 10805	35.8	[32.4 - 39.3]	24.4	[22.1 - 26.9]	31.9	[28.9 - 35.0]	2.93
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Citrobacter amalonaticus* NCTC 10805	32.3	[28.9 - 35.9]	24.4	[22.1 - 26.8]	29.3	[26.4 - 32.4]	3.04
'Escherichia coli IAI39' (CU928164)	*Citrobacter amalonaticus* NCTC 10805	34.2	[30.8 - 37.8]	24.4	[22.1 - 26.9]	30.8	[27.8 - 33.9]	2.8
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Citrobacter amalonaticus* NCTC 10805	35.7	[32.3 - 39.2]	24.4	[22.1 - 26.9]	31.8	[28.9 - 34.9]	2.86
'Escherichia coli str. 'clone D i2" (CP002211)	*Citrobacter amalonaticus* NCTC 10805	34.8	[31.4 - 38.4]	24.4	[22.1 - 26.9]	31.2	[28.3 - 34.3]	2.87
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Citrobacter amalonaticus* NCTC 10805	31.4	[28.0 - 35.0]	24.4	[22.1 - 26.9]	28.7	[25.8 - 31.8]	3.55
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Citrobacter amalonaticus* NCTC 10805	33.1	[29.7 - 36.7]	24.4	[22.1 - 26.9]	30.0	[27.0 - 33.1]	3.06
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Citrobacter amalonaticus* NCTC 10805	30.5	[27.2 - 34.1]	24.4	[22.1 - 26.8]	28.0	[25.1 - 31.2]	2.85
'Escherichia coli str. 'clone D i14" (CP002212)	*Citrobacter amalonaticus* NCTC 10805	34.8	[31.4 - 38.4]	24.4	[22.1 - 26.9]	31.2	[28.3 - 34.3]	2.87
'Shigella dysenteriae Sd197' (CP000034)	*Salmonella choleraesuis* DSM 14846	28.4	[25.0 - 32.0]	24.3	[22.0 - 26.8]	26.4	[23.5 - 29.5]	0.89
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Citrobacter amalonaticus* NCTC 10805	33.5	[30.1 - 37.0]	24.3	[22.0 - 26.8]	30.2	[27.3 - 33.3]	2.68
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Salmonella typhi* NCTC 8385	29.0	[25.7 - 32.7]	24.3	[22.0 - 26.8]	26.9	[24.0 - 30.0]	1.7
'Escherichia coli S88' (CU928161)	*Salmonella typhi* NCTC 8385	31.3	[27.9 - 34.8]	24.3	[22.0 - 26.8]	28.6	[25.6 - 31.7]	1.41
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Salmonella typhi* NCTC 8385	31.2	[27.8 - 34.7]	24.3	[22.0 - 26.8]	28.5	[25.6 - 31.6]	1.51
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Salmonella typhi* NCTC 8385	28.4	[25.1 - 32.1]	24.2	[21.9 - 26.7]	26.4	[23.5 - 29.5]	1.42
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Salmonella enterica* LT2	29.7	[26.3 - 33.3]	24.2	[21.9 - 26.7]	27.3	[24.4 - 30.4]	1.57
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Salmonella typhimurium* ATCC 13311	32.5	[29.1 - 36.0]	24.2	[21.9 - 26.6]	29.4	[26.5 - 32.5]	1.31
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Salmonella typhi* NCTC 8385	31.5	[28.1 - 35.1]	24.2	[21.9 - 26.6]	28.7	[25.8 - 31.8]	1.29

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Salmonella typhimurium* ATCC 13311	29.7	[26.3 - 33.3]	24.2	[21.9 - 26.7]	27.3	[24.4 - 30.4]	1.45
'Escherichia coli UMN026' (CU928163)	*Salmonella typhi* NCTC 8385	30.4	[27.0 - 34.0]	24.2	[21.9 - 26.6]	27.9	[25.0 - 31.0]	1.37
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Salmonella typhimurium* ATCC 13311	30.3	[26.9 - 33.9]	24.2	[21.9 - 26.6]	27.8	[24.9 - 30.9]	1.74
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Salmonella enterica* LT2	32.0	[28.6 - 35.5]	24.2	[21.8 - 26.6]	29.0	[26.1 - 32.1]	1.44
'Shigella dysenteriae Sd197' (CP000034)	*Salmonella typhimurium* JCM 1652	28.2	[24.9 - 31.8]	24.2	[21.9 - 26.7]	26.3	[23.4 - 29.4]	0.81
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Salmonella typhi* NCTC 8385	29.0	[25.6 - 32.6]	24.1	[21.8 - 26.6]	26.8	[23.9 - 29.9]	1.55
'Escherichia coli SMS-3-5' (CP000970)	*Salmonella typhimurium* ATCC 13311	30.9	[27.6 - 34.5]	24.1	[21.8 - 26.6]	28.3	[25.4 - 31.4]	1.62
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Salmonella typhimurium* JCM 1652	30.0	[26.7 - 33.6]	24.1	[21.8 - 26.6]	27.6	[24.7 - 30.7]	1.69
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Salmonella typhimurium* JCM 1652	29.4	[26.0 - 33.0]	24.1	[21.8 - 26.6]	27.1	[24.2 - 30.2]	1.4
'Escherichia sp. TW09308' (AEME00000000)	*Citrobacter amalonaticus* NCTC 10805	33.8	[30.4 - 37.4]	24.1	[21.8 - 26.5]	30.4	[27.4 - 33.5]	3.15
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Salmonella typhi* NCTC 8385	28.6	[25.2 - 32.2]	24.1	[21.8 - 26.6]	26.5	[23.6 - 29.6]	1.71
'Shigella dysenteriae Sd197' (CP000034)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	28.6	[25.3 - 32.2]	24.1	[21.8 - 26.6]	26.5	[23.6 - 29.6]	0.27
'Escherichia coli UMN026' (CU928163)	*Salmonella typhimurium* ATCC 13311	32.0	[28.6 - 35.6]	24.1	[21.8 - 26.5]	29.0	[26.1 - 32.1]	1.4
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Salmonella typhi* NCTC 8385	29.1	[25.7 - 32.7]	24.1	[21.8 - 26.5]	26.9	[24.0 - 30.0]	1.6
'Escherichia fergusonii ATCC 35469' (CU928158)	*Citrobacter amalonaticus* NCTC 10805	33.8	[30.4 - 37.4]	24.1	[21.8 - 26.6]	30.4	[27.5 - 33.5]	3.49
'Escherichia coli SMS-3-5' (CP000970)	*Salmonella enterica* LT2	30.5	[27.1 - 34.1]	24.1	[21.8 - 26.6]	27.9	[25.0 - 31.0]	1.74
'Escherichia coli UMN026' (CU928163)	*Salmonella enterica* LT2	31.5	[28.1 - 35.1]	24.1	[21.8 - 26.5]	28.7	[25.8 - 31.8]	1.52
'Escherichia coli SMS-3-5' (CP000970)	*Salmonella typhi* NCTC 8385	30.4	[27.1 - 34.0]	24.1	[21.8 - 26.6]	27.9	[25.0 - 31.0]	1.59
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Salmonella enterica* LT2	29.2	[25.8 - 32.8]	24.0	[21.7 - 26.5]	26.9	[24.0 - 30.0]	1.7
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Salmonella typhimurium* ATCC 13311	29.1	[25.7 - 32.7]	24.0	[21.7 - 26.5]	26.9	[24.0 - 30.0]	1.72
'Escherichia sp. TW09308' (AEME00000000)	*Salmonella typhi* NCTC 8385	30.0	[26.6 - 33.6]	24.0	[21.7 - 26.5]	27.5	[24.6 - 30.6]	1.81
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Salmonella choleraesuis* DSM 14846	29.1	[25.7 - 32.7]	24.0	[21.7 - 26.4]	26.9	[24.0 - 30.0]	1.47
'Escherichia coli S88' (CU928161)	*Salmonella enterica* LT2	30.9	[27.5 - 34.5]	24.0	[21.7 - 26.4]	28.2	[25.3 - 31.3]	1.56

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli str. 'clone D i14" (CP002212)	*Salmonella typhi* NCTC 8385	30.1	[26.8 - 33.7]	24.0	[21.7 - 26.5]	27.6	[24.7 - 30.8]	1.53
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Salmonella enterica* LT2	29.5	[26.2 - 33.2]	24.0	[21.7 - 26.4]	27.2	[24.3 - 30.3]	1.86
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Salmonella typhimurium* ATCC 13311	26.7	[23.4 - 30.4]	24.0	[21.7 - 26.4]	25.1	[22.2 - 28.2]	1.54
'Escherichia coli str. 'clone D i2" (CP002211)	*Salmonella typhi* NCTC 8385	30.1	[26.8 - 33.7]	24.0	[21.7 - 26.5]	27.6	[24.7 - 30.8]	1.53
'Escherichia fergusonii ATCC 35469' (CU928158)	*Salmonella typhi* NCTC 8385	29.7	[26.3 - 33.3]	24.0	[21.7 - 26.4]	27.3	[24.4 - 30.4]	2.15
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Salmonella typhimurium* ATCC 13311	30.1	[26.7 - 33.7]	24.0	[21.7 - 26.4]	27.6	[24.7 - 30.7]	1.63
'Escherichia coli IAI39' (CU928164)	*Salmonella enterica* LT2	30.4	[27.0 - 34.0]	24.0	[21.7 - 26.5]	27.8	[24.9 - 30.9]	1.61
'Shigella dysenteriae Sd197' (CP000034)	*Salmonella bongori* NCTC 12419	28.2	[24.8 - 31.8]	24.0	[21.6 - 26.4]	26.1	[23.3 - 29.3]	0.08
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Salmonella enterica* LT2	29.6	[26.3 - 33.2]	24.0	[21.7 - 26.4]	27.3	[24.4 - 30.4]	1.75
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Salmonella enterica* LT2	28.7	[25.3 - 32.3]	24.0	[21.7 - 26.4]	26.6	[23.7 - 29.7]	1.85
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Salmonella typhi* NCTC 8385	29.6	[26.2 - 33.2]	24.0	[21.7 - 26.4]	27.2	[24.3 - 30.3]	1.34
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Salmonella typhimurium* ATCC 13311	29.5	[26.1 - 33.1]	24.0	[21.7 - 26.5]	27.2	[24.3 - 30.3]	1.58
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Salmonella typhi* NCTC 8385	26.5	[23.2 - 30.2]	24.0	[21.7 - 26.4]	24.9	[22.0 - 28.0]	1.51
'Escherichia coli IAI39' (CU928164)	*Salmonella typhimurium* ATCC 13311	30.6	[27.2 - 34.2]	24.0	[21.7 - 26.5]	28.0	[25.1 - 31.1]	1.48
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Salmonella enterica* LT2	28.6	[25.3 - 32.2]	23.9	[21.6 - 26.3]	26.5	[23.6 - 29.6]	2.36
'Escherichia coli str. 'clone D i2" (CP002211)	*Salmonella typhimurium* ATCC 13311	31.4	[28.0 - 35.0]	23.9	[21.6 - 26.4]	28.6	[25.6 - 31.7]	1.55
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	27.8	[24.4 - 31.4]	23.9	[21.6 - 26.4]	25.8	[23.0 - 29.0]	0.85
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Salmonella choleraesuis* DSM 14846	28.8	[25.4 - 32.4]	23.9	[21.6 - 26.4]	26.6	[23.7 - 29.7]	1.65
'Escherichia coli SMS-3-5' (CP000970)	*Salmonella choleraesuis* DSM 14846	30.3	[26.9 - 33.9]	23.9	[21.6 - 26.3]	27.7	[24.8 - 30.8]	1.64
'Escherichia coli str. 'clone D i2" (CP002211)	*Salmonella enterica* LT2	31.0	[27.7 - 34.6]	23.9	[21.6 - 26.4]	28.3	[25.4 - 31.4]	1.68
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Salmonella typhimurium* JCM 1652	29.0	[25.6 - 32.6]	23.9	[21.6 - 26.3]	26.8	[23.9 - 29.9]	1.67
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Salmonella choleraesuis* DSM 14846	28.7	[25.4 - 32.4]	23.9	[21.6 - 26.4]	26.6	[23.7 - 29.7]	1.75

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Salmonella typhimurium* JCM 1652	29.7	[26.4 - 33.4]	23.9	[21.6 - 26.3]	27.3	[24.4 - 30.4]	1.58
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Salmonella choleraesuis* DSM 14846	31.9	[28.5 - 35.5]	23.9	[21.6 - 26.4]	28.9	[26.0 - 32.0]	1.34
'Escherichia coli str. 'clone D i14" (CP002212)	*Salmonella typhimurium* ATCC 13311	31.4	[28.0 - 35.0]	23.9	[21.6 - 26.4]	28.6	[25.6 - 31.7]	1.55
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Salmonella typhimurium* ATCC 13311	30.0	[26.6 - 33.6]	23.9	[21.6 - 26.4]	27.5	[24.6 - 30.6]	1.36
'Escherichia fergusonii ECD227' (CM001142)	*Citrobacter amalonaticus* NCTC 10805	33.7	[30.3 - 37.3]	23.9	[21.6 - 26.4]	30.2	[27.3 - 33.3]	3.42
'Escherichia coli SMS-3-5' (CP000970)	*Salmonella typhimurium* JCM 1652	30.6	[27.2 - 34.2]	23.9	[21.6 - 26.3]	27.9	[25.0 - 31.0]	1.57
'Escherichia coli IAI39' (CU928164)	*Salmonella choleraesuis* DSM 14846	29.7	[26.3 - 33.3]	23.9	[21.6 - 26.4]	27.3	[24.4 - 30.4]	1.51
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	31.3	[27.9 - 34.9]	23.9	[21.6 - 26.4]	28.5	[25.6 - 31.6]	0.72
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Salmonella typhimurium* ATCC 13311	29.0	[25.6 - 32.6]	23.9	[21.6 - 26.4]	26.8	[23.9 - 29.9]	2.23
'Escherichia coli S88' (CU928161)	*Salmonella typhimurium* ATCC 13311	31.2	[27.8 - 34.8]	23.9	[21.6 - 26.4]	28.4	[25.5 - 31.5]	1.43
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Salmonella enterica* LT2	26.6	[23.2 - 30.2]	23.9	[21.6 - 26.4]	24.9	[22.1 - 28.0]	1.66
'Escherichia coli str. 'clone D i14" (CP002212)	*Salmonella enterica* LT2	31.0	[27.7 - 34.6]	23.9	[21.6 - 26.4]	28.3	[25.4 - 31.4]	1.68
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Salmonella enterica* LT2	30.0	[26.6 - 33.6]	23.9	[21.6 - 26.4]	27.5	[24.6 - 30.6]	1.49
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Salmonella choleraesuis* DSM 14846	29.1	[25.7 - 32.7]	23.9	[21.6 - 26.4]	26.9	[24.0 - 30.0]	1.76
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Salmonella enterica* LT2	32.0	[28.6 - 35.6]	23.9	[21.6 - 26.3]	29.0	[26.1 - 32.1]	1.66
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Salmonella typhimurium* JCM 1652	32.2	[28.8 - 35.7]	23.9	[21.6 - 26.4]	29.1	[26.2 - 32.2]	1.26
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Salmonella typhi* NCTC 8385	28.7	[25.3 - 32.3]	23.9	[21.6 - 26.4]	26.5	[23.6 - 29.6]	2.2
'Escherichia fergusonii ATCC 35469' (CU928158)	*Salmonella enterica* LT2	30.4	[27.0 - 34.0]	23.8	[21.5 - 26.2]	27.8	[24.9 - 30.9]	2.3
'Escherichia coli IAI39' (CU928164)	*Salmonella typhimurium* JCM 1652	30.3	[26.9 - 33.9]	23.8	[21.5 - 26.3]	27.7	[24.8 - 30.8]	1.43
'Escherichia fergusonii ATCC 35469' (CU928158)	*Salmonella typhimurium* ATCC 13311	30.8	[27.5 - 34.4]	23.8	[21.5 - 26.2]	28.1	[25.2 - 31.2]	2.18
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Salmonella typhimurium* JCM 1652	29.1	[25.8 - 32.8]	23.8	[21.5 - 26.3]	26.9	[24.0 - 30.0]	1.53

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli UMN026' (CU928163)	*Salmonella choleraesuis* DSM 14846	30.8	[27.4 - 34.4]	23.8	[21.5 - 26.2]	28.1	[25.1 - 31.2]	1.42
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Salmonella choleraesuis* DSM 14846	29.0	[25.6 - 32.6]	23.8	[21.5 - 26.3]	26.7	[23.8 - 29.8]	1.6
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Salmonella typhimurium* JCM 1652	26.5	[23.1 - 30.1]	23.8	[21.5 - 26.3]	24.8	[21.9 - 27.9]	1.49
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Salmonella choleraesuis* DSM 14846	26.4	[23.0 - 30.0]	23.8	[21.5 - 26.3]	24.7	[21.9 - 27.8]	1.56
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Salmonella choleraesuis* DSM 14846	31.4	[28.0 - 34.9]	23.8	[21.5 - 26.2]	28.5	[25.6 - 31.6]	1.56
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Salmonella choleraesuis* DSM 14846	29.3	[25.9 - 32.9]	23.8	[21.5 - 26.3]	27.0	[24.1 - 30.1]	1.39
'Escherichia coli UMN026' (CU928163)	*Salmonella typhimurium* JCM 1652	31.6	[28.3 - 35.2]	23.8	[21.5 - 26.3]	28.7	[25.8 - 31.8]	1.35
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Salmonella typhimurium* JCM 1652	29.6	[26.2 - 33.2]	23.8	[21.5 - 26.2]	27.2	[24.3 - 30.3]	1.31
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Salmonella typhimurium* ATCC 13311	32.2	[28.9 - 35.8]	23.8	[21.5 - 26.3]	29.2	[26.2 - 32.3]	1.54
'Escherichia coli UMN026' (CU928163)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	29.8	[26.4 - 33.4]	23.8	[21.5 - 26.3]	27.3	[24.4 - 30.4]	0.8
'Escherichia coli S88' (CU928161)	*Salmonella typhimurium* JCM 1652	30.8	[27.4 - 34.4]	23.7	[21.4 - 26.2]	28.1	[25.1 - 31.2]	1.38
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	28.6	[25.2 - 32.2]	23.7	[21.4 - 26.2]	26.4	[23.5 - 29.5]	0.98
'Escherichia coli str. 'clone D i2" (CP002211)	*Salmonella typhimurium* JCM 1652	31.0	[27.6 - 34.6]	23.7	[21.4 - 26.1]	28.2	[25.3 - 31.3]	1.5
'Escherichia coli str. 'clone D i14" (CP002212)	*Salmonella typhimurium* JCM 1652	31.0	[27.6 - 34.6]	23.7	[21.4 - 26.1]	28.2	[25.3 - 31.3]	1.5
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Salmonella typhimurium* JCM 1652	28.8	[25.4 - 32.4]	23.7	[21.4 - 26.2]	26.6	[23.7 - 29.7]	2.18
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	27.9	[24.5 - 31.5]	23.7	[21.4 - 26.1]	25.9	[23.0 - 29.0]	1.13
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	28.3	[25.0 - 32.0]	23.7	[21.4 - 26.2]	26.2	[23.3 - 29.3]	1.15
'Escherichia coli S88' (CU928161)	*Salmonella choleraesuis* DSM 14846	30.4	[27.0 - 34.0]	23.7	[21.4 - 26.2]	27.8	[24.8 - 30.9]	1.46
'Escherichia coli SMS-3-5' (CP000970)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	30.1	[26.7 - 33.7]	23.7	[21.4 - 26.2]	27.6	[24.7 - 30.7]	1.02
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	28.0	[24.7 - 31.7]	23.7	[21.4 - 26.1]	26.0	[23.1 - 29.1]	1.64
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Salmonella typhimurium* JCM 1652	31.9	[28.5 - 35.5]	23.7	[21.4 - 26.2]	28.9	[25.9 - 32.0]	1.49

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli str. 'clone D i2" (CP002211)	*Salmonella choleraesuis* DSM 14846	30.4	[27.0 - 34.0]	23.7	[21.4 - 26.1]	27.7	[24.8 - 30.9]	1.58
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	30.2	[26.8 - 33.8]	23.7	[21.4 - 26.1]	27.6	[24.7 - 30.7]	0.95
'Escherichia coli S88' (CU928161)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	29.5	[26.1 - 33.1]	23.7	[21.4 - 26.2]	27.1	[24.2 - 30.2]	0.84
'Escherichia coli IAI39' (CU928164)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	30.3	[26.9 - 33.9]	23.7	[21.4 - 26.2]	27.7	[24.8 - 30.8]	0.89
'Escherichia coli str. 'clone D i14" (CP002212)	*Salmonella choleraesuis* DSM 14846	30.4	[27.0 - 34.0]	23.7	[21.4 - 26.1]	27.7	[24.8 - 30.9]	1.58
'Escherichia fergusonii ATCC 35469' (CU928158)	*Salmonella choleraesuis* DSM 14846	30.1	[26.8 - 33.7]	23.7	[21.4 - 26.2]	27.6	[24.7 - 30.7]	2.2
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	28.8	[25.5 - 32.4]	23.6	[21.3 - 26.1]	26.6	[23.7 - 29.7]	0.77
'Escherichia coli str. 'clone D i14" (CP002212)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	29.9	[26.5 - 33.5]	23.6	[21.3 - 26.1]	27.4	[24.4 - 30.5]	0.96
'Escherichia fergusonii ATCC 35469' (CU928158)	*Salmonella typhimurium* JCM 1652	30.4	[27.1 - 34.0]	23.6	[21.3 - 26.0]	27.8	[24.8 - 30.9]	2.13
'Escherichia sp. TW09308' (AEME00000000)	*Salmonella enterica* LT2	30.1	[26.7 - 33.7]	23.6	[21.3 - 26.1]	27.5	[24.6 - 30.6]	1.96
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	28.3	[25.0 - 31.9]	23.6	[21.3 - 26.1]	26.2	[23.3 - 29.3]	1.03
'Escherichia coli UMN026' (CU928163)	*Salmonella bongori* NCTC 12419	30.1	[26.8 - 33.7]	23.6	[21.3 - 26.0]	27.5	[24.6 - 30.6]	0.61
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Salmonella bongori* NCTC 12419	28.2	[24.9 - 31.9]	23.6	[21.3 - 26.0]	26.1	[23.2 - 29.2]	0.66
'Escherichia coli IAI39' (CU928164)	*Salmonella bongori* NCTC 12419	29.8	[26.4 - 33.4]	23.6	[21.3 - 26.0]	27.3	[24.4 - 30.4]	0.7
'Escherichia sp. TW09308' (AEME00000000)	*Salmonella typhimurium* ATCC 13311	29.8	[26.5 - 33.4]	23.6	[21.3 - 26.1]	27.3	[24.4 - 30.4]	1.84
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Salmonella bongori* NCTC 12419	32.0	[28.6 - 35.5]	23.6	[21.3 - 26.0]	28.9	[26.0 - 32.0]	0.53
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Salmonella choleraesuis* DSM 14846	28.6	[25.2 - 32.2]	23.6	[21.3 - 26.1]	26.4	[23.5 - 29.5]	2.25
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	26.4	[23.0 - 30.0]	23.6	[21.3 - 26.1]	24.7	[21.8 - 27.8]	0.95
'Escherichia coli str. 'clone D i2" (CP002211)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	29.9	[26.5 - 33.5]	23.6	[21.3 - 26.1]	27.4	[24.4 - 30.5]	0.96
'Escherichia fergusonii ECD227' (CM001142)	*Salmonella typhimurium* ATCC 13311	31.2	[27.8 - 34.8]	23.5	[21.2 - 26.0]	28.3	[25.4 - 31.4]	2.1
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Salmonella bongori* NCTC 12419	28.7	[25.4 - 32.4]	23.5	[21.2 - 25.9]	26.5	[23.6 - 29.6]	0.95

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia sp. TW09308' (AEME00000000)	*Salmonella choleraesuis* DSM 14846	29.4	[26.0 - 33.0]	23.5	[21.2 - 26.0]	27.0	[24.1 - 30.1]	1.86
'Escherichia sp. TW09308' (AEME00000000)	*Salmonella typhimurium* JCM 1652	29.6	[26.2 - 33.2]	23.5	[21.2 - 25.9]	27.1	[24.2 - 30.2]	1.79
'Escherichia fergusonii ECD227' (CM001142)	*Salmonella typhi* NCTC 8385	29.8	[26.5 - 33.4]	23.5	[21.2 - 26.0]	27.3	[24.4 - 30.4]	2.08
'Escherichia coli S88' (CU928161)	*Salmonella bongori* NCTC 12419	30.3	[26.9 - 33.9]	23.5	[21.2 - 25.9]	27.6	[24.7 - 30.7]	0.65
'Escherichia fergusonii ECD227' (CM001142)	*Salmonella enterica* LT2	30.7	[27.4 - 34.3]	23.5	[21.2 - 26.0]	28.0	[25.1 - 31.1]	2.23
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Salmonella bongori* NCTC 12419	29.1	[25.8 - 32.7]	23.5	[21.2 - 25.9]	26.8	[23.9 - 29.9]	0.79
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Pseudocitrobacter faecalis* DSM 27453	24.7	[21.4 - 28.3]	23.5	[21.2 - 26.0]	23.4	[20.5 - 26.5]	2.35
'Escherichia fergusonii ATCC 35469' (CU928158)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	29.2	[25.9 - 32.9]	23.5	[21.2 - 26.0]	26.9	[24.0 - 30.0]	1.58
'Escherichia coli SMS-3-5' (CP000970)	*Salmonella bongori* NCTC 12419	30.2	[26.8 - 33.8]	23.5	[21.2 - 26.0]	27.6	[24.7 - 30.7]	0.83
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Salmonella bongori* NCTC 12419	28.5	[25.2 - 32.2]	23.5	[21.2 - 25.9]	26.3	[23.4 - 29.4]	0.84
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Salmonella bongori* NCTC 12419	30.2	[26.8 - 33.8]	23.5	[21.2 - 25.9]	27.5	[24.6 - 30.6]	0.75
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Salmonella bongori* NCTC 12419	28.8	[25.4 - 32.4]	23.5	[21.2 - 25.9]	26.5	[23.6 - 29.6]	1.45
'Escherichia fergusonii ECD227' (CM001142)	*Salmonella choleraesuis* DSM 14846	30.8	[27.4 - 34.4]	23.4	[21.1 - 25.9]	28.0	[25.1 - 31.1]	2.13
'Escherichia sp. TW09308' (AEME00000000)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	28.9	[25.5 - 32.5]	23.4	[21.1 - 25.9]	26.6	[23.7 - 29.7]	1.24
'Escherichia fergusonii ECD227' (CM001142)	*Salmonella typhimurium* JCM 1652	30.8	[27.4 - 34.4]	23.4	[21.1 - 25.8]	28.0	[25.1 - 31.1]	2.05
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Enterobacter cloacae* ATCC 13047	23.4	[20.1 - 27.1]	23.4	[21.1 - 25.9]	22.4	[19.6 - 25.5]	4.7
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Salmonella bongori* NCTC 12419	28.5	[25.1 - 32.1]	23.4	[21.1 - 25.9]	26.3	[23.4 - 29.4]	0.94
'Escherichia coli UMN026' (CU928163)	*Pseudocitrobacter faecalis* DSM 27453	26.1	[22.7 - 29.7]	23.4	[21.1 - 25.8]	24.4	[21.6 - 27.5]	2.3
'Shigella dysenteriae Sd197' (CP000034)	*Enterobacter cloacae* ATCC 13047	24.6	[21.3 - 28.3]	23.4	[21.2 - 25.9]	23.3	[20.5 - 26.4]	3.33
'Escherichia coli str. 'clone D i14" (CP002212)	*Salmonella bongori* NCTC 12419	30.2	[26.8 - 33.8]	23.4	[21.1 - 25.9]	27.5	[24.6 - 30.6]	0.77
'Escherichia coli str. 'clone D i2" (CP002211)	*Salmonella bongori* NCTC 12419	30.2	[26.8 - 33.8]	23.4	[21.1 - 25.9]	27.5	[24.6 - 30.6]	0.77
'Escherichia fergusonii ATCC 35469' (CU928158)	*Salmonella bongori* NCTC 12419	29.2	[25.9 - 32.8]	23.4	[21.1 - 25.8]	26.8	[23.9 - 29.9]	1.39

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Pseudocitrobacter faecalis* DSM 27453	24.8	[21.5 - 28.4]	23.3	[21.0 - 25.7]	23.4	[20.6 - 26.5]	2.62
'Escherichia fergusonii ECD227' (CM001142)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	29.0	[25.7 - 32.7]	23.3	[21.0 - 25.8]	26.7	[23.8 - 29.8]	1.51
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Salmonella bongori* NCTC 12419	26.6	[23.3 - 30.3]	23.3	[21.1 - 25.8]	24.9	[22.0 - 28.0]	0.75
'Shigella dysenteriae Sd197' (CP000034)	*Pseudocitrobacter faecalis* DSM 27453	25.0	[21.7 - 28.7]	23.3	[21.0 - 25.8]	23.6	[20.8 - 26.7]	1.77
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Salmonella bongori* NCTC 12419	29.2	[25.8 - 32.8]	23.3	[21.0 - 25.8]	26.8	[23.9 - 29.9]	0.58
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Pseudocitrobacter faecalis* DSM 27453	23.3	[20.0 - 26.9]	23.2	[21.0 - 25.7]	22.2	[19.4 - 25.3]	2.44
'Escherichia sp. TW09308' (AEME00000000)	*Salmonella bongori* NCTC 12419	29.3	[25.9 - 32.9]	23.2	[20.9 - 25.7]	26.8	[23.9 - 29.9]	1.05
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Pseudocitrobacter faecalis* DSM 27453	25.0	[21.7 - 28.7]	23.2	[20.9 - 25.6]	23.6	[20.8 - 26.7]	2.48
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Pseudocitrobacter faecalis* DSM 27453	24.8	[21.5 - 28.5]	23.1	[20.8 - 25.6]	23.4	[20.6 - 26.5]	2.64
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Pseudocitrobacter faecalis* DSM 27453	24.9	[21.6 - 28.6]	23.1	[20.9 - 25.6]	23.5	[20.7 - 26.6]	2.26
'Escherichia coli SMS-3-5' (CP000970)	*Pseudocitrobacter faecalis* DSM 27453	26.0	[22.7 - 29.6]	23.1	[20.8 - 25.6]	24.3	[21.5 - 27.4]	2.52
'Escherichia coli IAI39' (CU928164)	*Pseudocitrobacter faecalis* DSM 27453	25.0	[21.7 - 28.7]	23.1	[20.8 - 25.5]	23.6	[20.7 - 26.7]	2.39
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Pseudocitrobacter faecalis* DSM 27453	24.1	[20.8 - 27.7]	23.1	[20.8 - 25.6]	22.8	[20.0 - 25.9]	2.53
'Escherichia fergusonii ECD227' (CM001142)	*Salmonella bongori* NCTC 12419	29.8	[26.4 - 33.4]	23.1	[20.8 - 25.5]	27.2	[24.3 - 30.3]	1.32
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Pseudocitrobacter faecalis* DSM 27453	27.2	[23.8 - 30.8]	23.0	[20.7 - 25.5]	25.2	[22.3 - 28.3]	2.22
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Pseudocitrobacter faecalis* DSM 27453	26.2	[22.9 - 29.8]	23.0	[20.7 - 25.4]	24.5	[21.6 - 27.6]	2.44
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Enterobacter cloacae* ATCC 13047	25.6	[22.2 - 29.2]	23.0	[20.7 - 25.5]	24.0	[21.1 - 27.1]	3.78
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Pseudocitrobacter faecalis* DSM 27453	23.8	[20.5 - 27.4]	23.0	[20.7 - 25.5]	22.6	[19.8 - 25.7]	3.13
'Escherichia fergusonii ATCC 35469' (CU928158)	*Pseudocitrobacter faecalis* DSM 27453	24.5	[21.2 - 28.1]	23.0	[20.7 - 25.5]	23.1	[20.3 - 26.2]	3.08
'Escherichia coli IAI39' (CU928164)	*Enterobacter cloacae* ATCC 13047	24.5	[21.2 - 28.2]	23.0	[20.7 - 25.4]	23.2	[20.3 - 26.2]	3.95
'Escherichia coli str. 'clone D i14'' (CP002212)	*Pseudocitrobacter faecalis* DSM 27453	25.1	[21.7 - 28.7]	22.9	[20.7 - 25.4]	23.6	[20.7 - 26.7]	2.46

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli S88' (CU928161)	*Enterobacter cloacae* ATCC 13047	24.3	[21.0 - 28.0]	22.9	[20.6 - 25.4]	23.0	[20.2 - 26.1]	3.9
'Escherichia coli SMS-3-5' (CP000970)	*Enterobacter cloacae* ATCC 13047	24.9	[21.6 - 28.6]	22.9	[20.6 - 25.4]	23.4	[20.6 - 26.5]	4.09
'Escherichia coli S88' (CU928161)	*Pseudocitrobacter faecalis* DSM 27453	25.4	[22.1 - 29.1]	22.9	[20.6 - 25.3]	23.8	[21.0 - 26.9]	2.34
'Shigella dysenteriae Sd197' (CP000034)	*Cronobacter sakazakii* NBRC 102416	20.1	[16.9 - 23.7]	22.9	[20.7 - 25.4]	19.6	[16.9 - 22.6]	5.47
'Escherichia coli str. 'clone D i2" (CP002211)	*Pseudocitrobacter faecalis* DSM 27453	25.1	[21.7 - 28.7]	22.9	[20.7 - 25.4]	23.6	[20.7 - 26.7]	2.46
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Enterobacter cloacae* ATCC 13047	23.3	[20.0 - 26.9]	22.9	[20.6 - 25.3]	22.2	[19.4 - 25.2]	3.92
'Escherichia coli UMN026' (CU928163)	*Enterobacter cloacae* ATCC 13047	25.0	[21.6 - 28.6]	22.9	[20.6 - 25.4]	23.5	[20.6 - 26.6]	3.87
'Escherichia coli str. 'clone D i2" (CP002211)	*Enterobacter cloacae* ATCC 13047	23.9	[20.6 - 27.6]	22.8	[20.5 - 25.3]	22.7	[19.9 - 25.8]	4.02
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Enterobacter cloacae* ATCC 13047	24.0	[20.7 - 27.6]	22.8	[20.5 - 25.2]	22.7	[19.9 - 25.8]	4.05
'Escherichia coli str. 'clone D i14" (CP002212)	*Enterobacter cloacae* ATCC 13047	23.9	[20.6 - 27.6]	22.8	[20.5 - 25.3]	22.7	[19.9 - 25.8]	4.02
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Enterobacter cloacae* ATCC 13047	23.3	[20.1 - 27.0]	22.8	[20.5 - 25.3]	22.2	[19.4 - 25.3]	4.19
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Cronobacter sakazakii* NBRC 102416	19.5	[16.4 - 23.1]	22.8	[20.5 - 25.2]	19.1	[16.4 - 22.1]	6.83
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Enterobacter cloacae* ATCC 13047	24.8	[21.5 - 28.5]	22.7	[20.4 - 25.1]	23.3	[20.5 - 26.4]	4.01
'Escherichia sp. TW09308' (AEME00000000)	*Pseudocitrobacter faecalis* DSM 27453	24.5	[21.2 - 28.2]	22.7	[20.4 - 25.1]	23.1	[20.3 - 26.2]	2.74
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Enterobacter cloacae* ATCC 13047	24.1	[20.8 - 27.8]	22.7	[20.4 - 25.1]	22.8	[20.0 - 25.9]	3.83
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Enterobacter cloacae* ATCC 13047	23.6	[20.3 - 27.2]	22.7	[20.4 - 25.1]	22.4	[19.6 - 25.4]	4.21
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Enterobacter cloacae* ATCC 13047	23.0	[19.7 - 26.6]	22.7	[20.4 - 25.1]	21.9	[19.1 - 25.0]	4.1
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Enterobacter cloacae* ATCC 13047	22.5	[19.2 - 26.2]	22.7	[20.4 - 25.1]	21.5	[18.7 - 24.6]	4.01
'Escherichia fergusonii ECD227' (CM001142)	*Pseudocitrobacter faecalis* DSM 27453	25.0	[21.6 - 28.6]	22.7	[20.4 - 25.1]	23.5	[20.6 - 26.6]	3.01
'Escherichia fergusonii ATCC 35469' (CU928158)	*Enterobacter cloacae* ATCC 13047	24.8	[21.5 - 28.5]	22.5	[20.2 - 25.0]	23.3	[20.5 - 26.4]	4.65
'Escherichia sp. TW09308' (AEME00000000)	*Enterobacter cloacae* ATCC 13047	23.3	[20.0 - 26.9]	22.3	[20.1 - 24.8]	22.1	[19.3 - 25.2]	4.31
'Escherichia fergusonii ECD227' (CM001142)	*Enterobacter cloacae* ATCC 13047	24.8	[21.4 - 28.4]	22.1	[19.8 - 24.5]	23.2	[20.4 - 26.3]	4.57

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Kosakonia sacchari* SP1	20.8	[17.6 - 24.4]	22.1	[19.9 - 24.6]	20.1	[17.4 - 23.1]	3.88
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Kosakonia sacchari* SP1	21.5	[18.2 - 25.1]	22.1	[19.8 - 24.5]	20.6	[17.8 - 23.7]	3.89
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Kosakonia sacchari* SP1	21.3	[18.1 - 25.0]	22.1	[19.8 - 24.5]	20.5	[17.8 - 23.6]	3.52
'Shigella dysenteriae Sd197' (CP000034)	*Kosakonia sacchari* SP1	21.6	[18.4 - 25.2]	22.1	[19.9 - 24.6]	20.7	[18.0 - 23.8]	3.02
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Kosakonia sacchari* SP1	21.2	[18.0 - 24.9]	22.1	[19.8 - 24.5]	20.4	[17.7 - 23.5]	3.6
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Kosakonia sacchari* SP1	20.0	[16.9 - 23.6]	22.1	[19.8 - 24.5]	19.5	[16.7 - 22.5]	3.69
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Kosakonia sacchari* SP1	22.5	[19.2 - 26.1]	22.1	[19.8 - 24.5]	21.4	[18.7 - 24.5]	3.47
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Kosakonia sacchari* SP1	21.5	[18.3 - 25.1]	22.0	[19.8 - 24.5]	20.6	[17.9 - 23.7]	3.78
'Escherichia coli S88' (CU928161)	*Kosakonia sacchari* SP1	22.1	[18.8 - 25.7]	22.0	[19.7 - 24.4]	21.1	[18.3 - 24.2]	3.59
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Kosakonia sacchari* SP1	21.5	[18.3 - 25.1]	22.0	[19.8 - 24.5]	20.6	[17.9 - 23.7]	4.38
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Kosakonia sacchari* SP1	21.3	[18.0 - 24.9]	22.0	[19.7 - 24.4]	20.4	[17.7 - 23.5]	3.73
'Escherichia coli IAI39' (CU928164)	*Kosakonia sacchari* SP1	21.8	[18.6 - 25.5]	22.0	[19.7 - 24.4]	20.9	[18.1 - 24.0]	3.64
'Escherichia coli str. 'clone D i2" (CP002211)	*Kosakonia sacchari* SP1	22.1	[18.8 - 25.7]	21.9	[19.7 - 24.4]	21.1	[18.3 - 24.2]	3.71
'Escherichia coli UMN026' (CU928163)	*Kosakonia sacchari* SP1	22.3	[19.0 - 25.9]	21.9	[19.7 - 24.4]	21.2	[18.4 - 24.3]	3.55
'Escherichia coli SMS-3-5' (CP000970)	*Kosakonia sacchari* SP1	22.1	[18.8 - 25.7]	21.9	[19.7 - 24.4]	21.1	[18.3 - 24.2]	3.77
'Escherichia coli str. 'clone D i14" (CP002212)	*Kosakonia sacchari* SP1	22.1	[18.8 - 25.7]	21.9	[19.7 - 24.4]	21.1	[18.3 - 24.2]	3.71
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Cronobacter sakazakii* NBRC 102416	20.8	[17.6 - 24.4]	21.9	[19.6 - 24.3]	20.1	[17.3 - 23.1]	5.92
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Salmonella typhi* NCTC 8385	17.1	[14.1 - 20.7]	21.9	[19.7 - 24.4]	17.0	[14.4 - 20.0]	4.42
'Escherichia sp. TW09308' (AEME00000000)	*Kosakonia sacchari* SP1	21.2	[17.9 - 24.8]	21.9	[19.7 - 24.4]	20.3	[17.6 - 23.4]	3.99
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Kosakonia sacchari* SP1	22.4	[19.2 - 26.1]	21.9	[19.6 - 24.3]	21.3	[18.6 - 24.4]	3.69
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Kosakonia oryzendophytica* REICA_082	21.2	[18.0 - 24.8]	21.8	[19.5 - 24.2]	20.4	[17.6 - 23.4]	3.24
'Escherichia coli IAI39' (CU928164)	*Kosakonia oryzendophytica* REICA_082	22.0	[18.7 - 25.6]	21.8	[19.5 - 24.2]	21.0	[18.2 - 24.0]	3.1

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Cronobacter sakazakii* NBRC 102416	25.9	[22.6 - 29.6]	21.8	[19.6 - 24.3]	24.0	[21.2 - 27.1]	2.64
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Cronobacter sakazakii* NBRC 102416	18.9	[15.7 - 22.4]	21.8	[19.5 - 24.2]	18.5	[15.8 - 21.5]	6.05
'Shigella dysenteriae Sd197' (CP000034)	*Cronobacter malonaticus* LMG 23826	19.5	[16.3 - 23.1]	21.8	[19.5 - 24.2]	19.0	[16.3 - 22.0]	5.59
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Kosakonia oryzendophytica* REICA_082	21.1	[17.9 - 24.7]	21.8	[19.5 - 24.2]	20.3	[17.5 - 23.3]	3.34
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Shigella boydii* ATCC 8700	17.4	[14.3 - 20.9]	21.8	[19.5 - 24.2]	17.2	[14.6 - 20.2]	5.39
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Kosakonia oryzendophytica* REICA_082	20.8	[17.6 - 24.5]	21.8	[19.5 - 24.2]	20.1	[17.3 - 23.1]	3.84
'Escherichia coli SMS-3-5' (CP000970)	*Cronobacter sakazakii* NBRC 102416	19.8	[16.7 - 23.4]	21.8	[19.6 - 24.3]	19.3	[16.6 - 22.3]	6.22
'Shigella dysenteriae Sd197' (CP000034)	*Kosakonia oryzendophytica* REICA_082	21.9	[18.6 - 25.5]	21.8	[19.5 - 24.2]	20.9	[18.1 - 24.0]	2.48
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Kosakonia oryzendophytica* REICA_082	21.3	[18.1 - 25.0]	21.8	[19.5 - 24.2]	20.5	[17.7 - 23.5]	3.06
'Escherichia coli IAI39' (CU928164)	*Cronobacter sakazakii* NBRC 102416	20.1	[16.9 - 23.7]	21.7	[19.5 - 24.2]	19.5	[16.8 - 22.5]	6.09
'Escherichia coli UMN026' (CU928163)	*Cronobacter sakazakii* NBRC 102416	19.7	[16.5 - 23.3]	21.7	[19.5 - 24.2]	19.1	[16.4 - 22.2]	6.0
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Salmonella typhimurium* ATCC 13311	16.9	[13.9 - 20.4]	21.7	[19.5 - 24.2]	16.8	[14.2 - 19.8]	4.39
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Kosakonia oryzendophytica* REICA_082	22.9	[19.6 - 26.6]	21.7	[19.4 - 24.1]	21.7	[18.9 - 24.8]	2.93
'Escherichia fergusonii ATCC 35469' (CU928158)	*Kosakonia sacchari* SP1	22.4	[19.2 - 26.1]	21.7	[19.4 - 24.1]	21.3	[18.5 - 24.4]	4.33
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Cronobacter malonaticus* LMG 23826	19.2	[16.1 - 22.8]	21.7	[19.4 - 24.1]	18.7	[16.1 - 21.8]	6.47
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Cronobacter malonaticus* LMG 23826	19.4	[16.2 - 23.0]	21.7	[19.4 - 24.1]	18.9	[16.2 - 21.9]	6.96
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Salmonella enterica* LT2	16.8	[13.8 - 20.4]	21.7	[19.4 - 24.1]	16.8	[14.2 - 19.7]	4.27
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Cronobacter sakazakii* NBRC 102416	18.1	[15.1 - 21.7]	21.7	[19.4 - 24.1]	17.9	[15.2 - 20.8]	6.14
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Cronobacter sakazakii* NBRC 102416	19.2	[16.1 - 22.8]	21.7	[19.4 - 24.1]	18.8	[16.1 - 21.8]	6.34
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Cronobacter malonaticus* LMG 23826	26.3	[23.0 - 30.0]	21.7	[19.5 - 24.2]	24.3	[21.5 - 27.4]	2.77

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Salmonella bongori* NCTC 12419	16.9	[13.8 - 20.4]	21.7	[19.4 - 24.1]	16.8	[14.2 - 19.7]	5.18
'Escherichia coli SMS-3-5' (CP000970)	*Cronobacter malonaticus* LMG 23826	19.5	[16.3 - 23.1]	21.7	[19.4 - 24.1]	19.0	[16.3 - 22.0]	6.35
'Escherichia fergusonii ECD227' (CM001142)	*Kosakonia sacchari* SP1	22.1	[18.9 - 25.8]	21.6	[19.4 - 24.1]	21.1	[18.3 - 24.2]	4.26
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Kosakonia oryzendophytica* REICA_082	22.0	[18.8 - 25.7]	21.6	[19.3 - 24.0]	21.0	[18.2 - 24.1]	2.98
'Escherichia coli S88' (CU928161)	*Kosakonia oryzendophytica* REICA_082	22.5	[19.3 - 26.2]	21.6	[19.4 - 24.1]	21.4	[18.6 - 24.5]	3.05
'Escherichia coli IAI39' (CU928164)	*Cronobacter malonaticus* LMG 23826	19.7	[16.6 - 23.3]	21.6	[19.3 - 24.0]	19.2	[16.5 - 22.2]	6.21
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Cronobacter muytjensii* ATCC 51329	24.6	[21.3 - 28.3]	21.6	[19.3 - 24.0]	23.0	[20.2 - 26.1]	3.64
'Escherichia coli str. 'clone D i14" (CP002212)	*Kosakonia oryzendophytica* REICA_082	22.7	[19.4 - 26.3]	21.6	[19.3 - 24.0]	21.5	[18.7 - 24.6]	3.17
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Cronobacter sakazakii* NBRC 102416	19.2	[16.1 - 22.8]	21.6	[19.4 - 24.1]	18.8	[16.1 - 21.8]	6.33
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Escherichia hermannii* NCTC 12129	19.6	[16.4 - 23.2]	21.6	[19.4 - 24.1]	19.0	[16.3 - 22.1]	4.19
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Kosakonia oryzendophytica* REICA_082	21.6	[18.3 - 25.2]	21.6	[19.4 - 24.1]	20.6	[17.9 - 23.7]	3.35
'Escherichia coli str. 'clone D i2" (CP002211)	*Kosakonia oryzendophytica* REICA_082	22.7	[19.4 - 26.3]	21.6	[19.3 - 24.0]	21.5	[18.7 - 24.6]	3.17
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Cronobacter sakazakii* NBRC 102416	19.3	[16.1 - 22.9]	21.6	[19.4 - 24.1]	18.8	[16.1 - 21.8]	6.18
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Kosakonia oryzendophytica* REICA_082	22.6	[19.3 - 26.2]	21.6	[19.3 - 24.0]	21.4	[18.7 - 24.5]	3.15
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Cronobacter sakazakii* NBRC 102416	19.4	[16.3 - 23.0]	21.6	[19.4 - 24.0]	18.9	[16.2 - 21.9]	6.23
'Escherichia coli SMS-3-5' (CP000970)	*Kosakonia oryzendophytica* REICA_082	22.8	[19.6 - 26.5]	21.6	[19.4 - 24.1]	21.6	[18.8 - 24.7]	3.23
'Escherichia coli UMN026' (CU928163)	*Kosakonia oryzendophytica* REICA_082	22.4	[19.1 - 26.0]	21.6	[19.4 - 24.1]	21.3	[18.5 - 24.4]	3.01
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Enterobacter cloacae* ATCC 13047	22.5	[19.2 - 26.2]	21.6	[19.4 - 24.1]	21.4	[18.6 - 24.5]	0.51
'Escherichia fergusonii ATCC 35469' (CU928158)	*Cronobacter sakazakii* NBRC 102416	19.2	[16.1 - 22.8]	21.6	[19.3 - 24.0]	18.8	[16.1 - 21.8]	6.78
'Escherichia coli S88' (CU928161)	*Cronobacter sakazakii* NBRC 102416	20.3	[17.1 - 23.9]	21.6	[19.4 - 24.1]	19.6	[16.9 - 22.6]	6.04
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Kosakonia oryzendophytica* REICA_082	20.1	[16.9 - 23.7]	21.6	[19.3 - 24.0]	19.4	[16.7 - 22.5]	3.15

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Kosakonia oryzendophytica* REICA_082	21.7	[18.4 - 25.3]	21.6	[19.3 - 24.0]	20.7	[18.0 - 23.8]	3.19
'Escherichia coli S88' (CU928161)	*Cronobacter malonaticus* LMG 23826	19.9	[16.7 - 23.5]	21.5	[19.2 - 23.9]	19.3	[16.5 - 22.3]	6.16
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Cronobacter malonaticus* LMG 23826	20.5	[17.3 - 24.1]	21.5	[19.3 - 23.9]	19.8	[17.0 - 22.8]	6.04
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Cronobacter malonaticus* LMG 23826	19.7	[16.6 - 23.3]	21.5	[19.2 - 23.9]	19.2	[16.5 - 22.2]	6.27
'Escherichia coli str. 'clone D i2" (CP002211)	*Cronobacter sakazakii* NBRC 102416	20.0	[16.9 - 23.6]	21.5	[19.3 - 23.9]	19.4	[16.7 - 22.4]	6.16
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Citrobacter koseri* NCTC 10786	18.5	[15.4 - 22.1]	21.5	[19.2 - 23.9]	18.2	[15.5 - 21.2]	2.7
'Escherichia coli str. 'clone D i14" (CP002212)	*Cronobacter sakazakii* NBRC 102416	20.0	[16.9 - 23.6]	21.5	[19.3 - 23.9]	19.4	[16.7 - 22.4]	6.16
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Cronobacter malonaticus* LMG 23826	19.1	[15.9 - 22.7]	21.5	[19.3 - 24.0]	18.6	[15.9 - 21.6]	6.45
'Escherichia coli UMN026' (CU928163)	*Cronobacter malonaticus* LMG 23826	19.7	[16.5 - 23.3]	21.5	[19.3 - 23.9]	19.1	[16.4 - 22.1]	6.13
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Levinea malonatica* NCTC 10810	22.7	[19.4 - 26.3]	21.5	[19.2 - 23.9]	21.5	[18.7 - 24.5]	0.29
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Cronobacter malonaticus* LMG 23826	19.4	[16.2 - 23.0]	21.5	[19.2 - 23.9]	18.9	[16.2 - 21.9]	6.31
'Escherichia coli str. 'clone D i2" (CP002211)	*Cronobacter malonaticus* LMG 23826	19.7	[16.6 - 23.4]	21.5	[19.2 - 23.9]	19.2	[16.5 - 22.2]	6.28
'Shigella dysenteriae Sd197' (CP000034)	*Shimwellia blattae* DSM 4481	17.2	[14.2 - 20.7]	21.5	[19.2 - 23.9]	17.1	[14.5 - 20.0]	5.26
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Cronobacter malonaticus* LMG 23826	18.3	[15.2 - 21.8]	21.5	[19.3 - 23.9]	18.0	[15.3 - 20.9]	6.27
'Escherichia coli str. 'clone D i14" (CP002212)	*Cronobacter malonaticus* LMG 23826	19.7	[16.6 - 23.4]	21.5	[19.2 - 23.9]	19.2	[16.5 - 22.2]	6.28
'Shigella dysenteriae Sd197' (CP000034)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	17.2	[14.2 - 20.7]	21.5	[19.2 - 23.9]	17.1	[14.5 - 20.0]	5.26
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Cronobacter sakazakii* NBRC 102416	19.8	[16.7 - 23.4]	21.5	[19.3 - 23.9]	19.2	[16.5 - 22.3]	6.14
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Cronobacter malonaticus* LMG 23826	19.2	[16.1 - 22.8]	21.5	[19.2 - 23.9]	18.7	[16.1 - 21.7]	6.36
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Shigella dysenteriae* ATCC 13313	17.1	[14.1 - 20.7]	21.5	[19.2 - 23.9]	17.0	[14.4 - 20.0]	5.53
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Salmonella typhi* NCTC 8385	19.4	[16.2 - 23.0]	21.5	[19.2 - 23.9]	18.9	[16.2 - 21.9]	1.99
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Citrobacter diversus* NCTC 10849	22.8	[19.5 - 26.5]	21.5	[19.2 - 23.9]	21.6	[18.8 - 24.7]	0.49

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Shigella dysenteriae Sd197' (CP000034)	*Cronobacter muytjensii* ATCC 51329	19.2	[16.1 - 22.8]	21.5	[19.2 - 23.9]	18.7	[16.1 - 21.8]	6.47
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Cronobacter malonaticus* LMG 23826	19.0	[15.9 - 22.6]	21.5	[19.2 - 23.9]	18.6	[15.9 - 21.6]	6.18
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Cronobacter sakazakii* NBRC 102416	20.0	[16.9 - 23.7]	21.5	[19.3 - 24.0]	19.4	[16.7 - 22.4]	5.97
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	17.3	[14.3 - 20.9]	21.4	[19.1 - 23.8]	17.2	[14.6 - 20.1]	5.71
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Shigella sonnei* ATCC 29930	17.2	[14.2 - 20.7]	21.4	[19.1 - 23.8]	17.0	[14.4 - 20.0]	5.49
'Escherichia coli S88' (CU928161)	*Escherichia hermannii* NCTC 12129	20.2	[17.0 - 23.8]	21.4	[19.2 - 23.9]	19.5	[16.8 - 22.6]	3.4
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Salmonella typhimurium* ATCC 13311	19.7	[16.6 - 23.4]	21.4	[19.1 - 23.8]	19.2	[16.5 - 22.2]	1.96
'Escherichia coli SMS-3-5' (CP000970)	*Cronobacter muytjensii* ATCC 51329	19.2	[16.1 - 22.8]	21.4	[19.2 - 23.9]	18.7	[16.0 - 21.7]	7.22
'Escherichia fergusonii ATCC 35469' (CU928158)	*Kosakonia oryzendophytica* REICA_082	22.9	[19.6 - 26.5]	21.4	[19.1 - 23.8]	21.6	[18.8 - 24.7]	3.79
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Shimwellia blattae* DSM 4481	17.3	[14.3 - 20.9]	21.4	[19.1 - 23.8]	17.2	[14.6 - 20.1]	5.71
'Escherichia fergusonii ATCC 35469' (CU928158)	*Cronobacter malonaticus* LMG 23826	19.5	[16.4 - 23.1]	21.4	[19.2 - 23.9]	19.0	[16.3 - 22.0]	6.91
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Citrobacter diversus* NCTC 10849	18.6	[15.5 - 22.2]	21.4	[19.2 - 23.8]	18.2	[15.6 - 21.2]	2.92
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	19.5	[16.3 - 23.1]	21.4	[19.2 - 23.9]	18.9	[16.2 - 21.9]	4.19
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Cronobacter malonaticus* LMG 23826	19.6	[16.4 - 23.2]	21.4	[19.1 - 23.8]	19.0	[16.3 - 22.1]	6.09
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	17.6	[14.5 - 21.1]	21.4	[19.2 - 23.8]	17.4	[14.8 - 20.4]	6.57
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Citrobacter koseri* NCTC 10786	22.6	[19.3 - 26.2]	21.4	[19.1 - 23.8]	21.4	[18.6 - 24.5]	0.27
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Escherichia fergusonii* ATCC 35469	17.6	[14.5 - 21.1]	21.4	[19.2 - 23.8]	17.3	[14.7 - 20.3]	6.59
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Shigella flexneri* ATCC 29903	17.2	[14.2 - 20.8]	21.4	[19.2 - 23.9]	17.1	[14.5 - 20.0]	5.84
'Escherichia fergusonii ATCC 35469' (CU928158)	*Shimwellia blattae* DSM 4481	17.6	[14.5 - 21.1]	21.4	[19.2 - 23.8]	17.4	[14.8 - 20.4]	6.57
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Cronobacter muytjensii* ATCC 51329	18.6	[15.5 - 22.2]	21.3	[19.1 - 23.8]	18.2	[15.6 - 21.2]	7.34
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	**'Escherichia coli IAI39' (CU928164)**	17.3	[14.2 - 20.8]	21.3	[19.0 - 23.7]	17.1	[14.5 - 20.1]	5.88

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Cronobacter muytjensii* ATCC 51329	19.1	[15.9 - 22.7]	21.3	[19.0 - 23.7]	18.6	[15.9 - 21.6]	7.32
'Escherichia sp. TW09308' (AEME00000000)	*Kosakonia oryzendophytica* REICA_082	22.4	[19.1 - 26.0]	21.3	[19.0 - 23.7]	21.2	[18.5 - 24.3]	3.45
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Escherichia coli* DSM 30083	17.2	[14.1 - 20.7]	21.3	[19.1 - 23.8]	17.0	[14.4 - 20.0]	5.87
'Escherichia coli IAI39' (CU928164)	*Cronobacter muytjensii* ATCC 51329	19.5	[16.3 - 23.1]	21.3	[19.0 - 23.7]	18.9	[16.2 - 21.9]	7.08
'Shigella dysenteriae Sd197' (CP000034)	*Cronobacter condimenti* 1330	18.8	[15.7 - 22.4]	21.3	[19.0 - 23.7]	18.4	[15.7 - 21.4]	4.52
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Salmonella typhimurium* JCM 1652	16.7	[13.6 - 20.2]	21.3	[19.0 - 23.7]	16.6	[14.0 - 19.5]	4.45
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	16.5	[13.5 - 20.0]	21.3	[19.0 - 23.7]	16.5	[13.9 - 19.4]	6.02
'Escherichia coli S88' (CU928161)	*Shimwellia blattae* DSM 4481	17.2	[14.1 - 20.7]	21.3	[19.1 - 23.8]	17.0	[14.4 - 20.0]	5.83
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	**'Escherichia coli UMN026' (CU928163)**	17.3	[14.2 - 20.8]	21.3	[19.1 - 23.8]	17.1	[14.5 - 20.1]	5.79
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Salmonella enterica* LT2	19.7	[16.6 - 23.3]	21.3	[19.1 - 23.7]	19.1	[16.4 - 22.2]	1.84
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	**'Escherichia coli S88' (CU928161)**	17.2	[14.1 - 20.7]	21.3	[19.1 - 23.8]	17.0	[14.4 - 20.0]	5.83
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Cronobacter muytjensii* ATCC 51329	18.0	[14.9 - 21.6]	21.3	[19.0 - 23.7]	17.7	[15.1 - 20.7]	7.14
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Levinea malonatica* NCTC 10810	18.7	[15.6 - 22.3]	21.3	[19.1 - 23.8]	18.3	[15.7 - 21.3]	2.73
'Escherichia coli UMN026' (CU928163)	*Shimwellia blattae* DSM 4481	17.3	[14.2 - 20.8]	21.3	[19.1 - 23.8]	17.1	[14.5 - 20.1]	5.79
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Escherichia albertii* NBRC 107761	19.6	[16.5 - 23.3]	21.3	[19.1 - 23.7]	19.1	[16.4 - 22.1]	4.29
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	16.5	[13.5 - 20.0]	21.3	[19.0 - 23.7]	16.4	[13.9 - 19.4]	5.84
'Escherichia fergusonii ECD227' (CM001142)	*Kosakonia oryzendophytica* REICA_082	22.6	[19.3 - 26.2]	21.3	[19.1 - 23.8]	21.4	[18.6 - 24.5]	3.72
'Escherichia coli IAI39' (CU928164)	*Shimwellia blattae* DSM 4481	17.3	[14.2 - 20.8]	21.3	[19.0 - 23.7]	17.1	[14.5 - 20.1]	5.88
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Shimwellia blattae* DSM 4481	16.5	[13.5 - 20.0]	21.3	[19.0 - 23.7]	16.5	[13.9 - 19.4]	6.02
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Shimwellia blattae* DSM 4481	16.5	[13.5 - 20.0]	21.3	[19.0 - 23.7]	16.4	[13.9 - 19.4]	5.84
'Escherichia fergusonii ECD227' (CM001142)	*Cronobacter sakazakii* NBRC 102416	19.3	[16.2 - 22.9]	21.3	[19.1 - 23.7]	18.8	[16.1 - 21.8]	6.71

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia sp. TW09308' (AEME00000000)	*Cronobacter sakazakii* NBRC 102416	19.2	[16.0 - 22.8]	21.3	[19.1 - 23.7]	18.7	[16.0 - 21.7]	6.44
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Cronobacter condimenti* 1330	17.8	[14.7 - 21.3]	21.2	[19.0 - 23.6]	17.5	[14.9 - 20.5]	5.2
'Escherichia coli UMN026' (CU928163)	*Cronobacter muytjensii* ATCC 51329	19.5	[16.3 - 23.0]	21.2	[19.0 - 23.6]	18.9	[16.2 - 21.9]	7.0
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Escherichia hermannii* NCTC 12129	21.5	[18.3 - 25.1]	21.2	[18.9 - 23.6]	20.5	[17.8 - 23.6]	3.28
'Shigella dysenteriae Sd197' (CP000034)	*Escherichia hermannii* NCTC 12129	20.4	[17.3 - 24.1]	21.2	[18.9 - 23.6]	19.7	[17.0 - 22.7]	2.83
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Escherichia hermannii* NCTC 12129	19.3	[16.2 - 22.9]	21.2	[19.0 - 23.6]	18.8	[16.1 - 21.8]	3.7
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	17.1	[14.1 - 20.6]	21.2	[19.0 - 23.6]	17.0	[14.4 - 19.9]	4.99
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Cronobacter muytjensii* ATCC 51329	20.3	[17.1 - 23.9]	21.2	[18.9 - 23.6]	19.5	[16.8 - 22.6]	6.92
'Escherichia coli str. 'clone D i2" (CP002211)	*Shimwellia blattae* DSM 4481	17.4	[14.4 - 20.9]	21.2	[19.0 - 23.7]	17.2	[14.6 - 20.2]	5.95
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Shimwellia blattae* DSM 4481	16.4	[13.4 - 19.9]	21.2	[19.0 - 23.6]	16.3	[13.8 - 19.3]	6.13
'Escherichia fergusonii ECD227' (CM001142)	*Cronobacter malonaticus* LMG 23826	19.5	[16.4 - 23.1]	21.2	[18.9 - 23.6]	18.9	[16.3 - 22.0]	6.83
'Escherichia coli str. 'clone D i2" (CP002211)	*Escherichia hermannii* NCTC 12129	20.2	[17.0 - 23.8]	21.2	[19.0 - 23.6]	19.5	[16.8 - 22.6]	3.52
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Salmonella typhimurium* JCM 1652	19.6	[16.4 - 23.2]	21.2	[19.0 - 23.6]	19.0	[16.3 - 22.0]	2.01
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Escherichia hermannii* NCTC 12129	18.5	[15.4 - 22.0]	21.2	[19.0 - 23.7]	18.1	[15.4 - 21.1]	2.43
'Escherichia coli SMS-3-5' (CP000970)	*Shimwellia blattae* DSM 4481	17.3	[14.2 - 20.8]	21.2	[19.0 - 23.7]	17.1	[14.5 - 20.1]	6.01
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	**'Escherichia coli str. 'clone D i14" (CP002212)**	17.4	[14.4 - 20.9]	21.2	[19.0 - 23.7]	17.2	[14.6 - 20.2]	5.95
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	**'Escherichia coli str. 'clone D i2" (CP002211)**	17.4	[14.4 - 20.9]	21.2	[19.0 - 23.7]	17.2	[14.6 - 20.2]	5.95
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Cronobacter muytjensii* ATCC 51329	18.8	[15.7 - 22.4]	21.2	[19.0 - 23.6]	18.4	[15.7 - 21.4]	7.05
'Escherichia coli SMS-3-5' (CP000970)	*Escherichia hermannii* NCTC 12129	20.8	[17.6 - 24.4]	21.2	[18.9 - 23.6]	19.9	[17.2 - 23.0]	3.58
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Cronobacter muytjensii* ATCC 51329	19.2	[16.0 - 22.7]	21.2	[19.0 - 23.6]	18.7	[16.0 - 21.7]	7.18
'Escherichia coli IAI39' (CU928164)	*Escherichia hermannii* NCTC 12129	20.2	[17.0 - 23.8]	21.2	[18.9 - 23.6]	19.5	[16.8 - 22.5]	3.45
'Escherichia coli str. 'clone D i14" (CP002212)	*Shimwellia blattae* DSM 4481	17.4	[14.4 - 20.9]	21.2	[19.0 - 23.7]	17.2	[14.6 - 20.2]	5.95

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Cronobacter muytjensii* ATCC 51329	18.9	[15.8 - 22.5]	21.2	[19.0 - 23.7]	18.4	[15.8 - 21.4]	7.23
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Shimwellia blattae* DSM 4481	17.2	[14.2 - 20.7]	21.2	[19.0 - 23.7]	17.0	[14.4 - 20.0]	6.63
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Shimwellia blattae* DSM 4481	16.0	[13.1 - 19.5]	21.2	[19.0 - 23.6]	16.0	[13.5 - 18.9]	5.93
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Escherichia hermannii* NCTC 12129	19.2	[16.1 - 22.8]	21.2	[19.0 - 23.7]	18.7	[16.1 - 21.7]	3.59
'Escherichia coli SMS-3-5' (CP000970)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	17.3	[14.2 - 20.8]	21.2	[19.0 - 23.7]	17.1	[14.5 - 20.1]	6.01
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Escherichia hermannii* NCTC 12129	19.6	[16.5 - 23.2]	21.2	[18.9 - 23.6]	19.0	[16.3 - 22.1]	3.68
'Escherichia coli str. 'clone D i14" (CP002212)	*Escherichia hermannii* NCTC 12129	20.2	[17.0 - 23.8]	21.2	[19.0 - 23.6]	19.5	[16.8 - 22.6]	3.52
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Shigella boydii* ATCC 8700	20.2	[17.0 - 23.8]	21.2	[18.9 - 23.6]	19.5	[16.8 - 22.5]	2.96
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	16.0	[13.1 - 19.5]	21.2	[19.0 - 23.6]	16.0	[13.5 - 18.9]	5.93
'Escherichia coli S88' (CU928161)	*Cronobacter muytjensii* ATCC 51329	19.5	[16.3 - 23.1]	21.2	[18.9 - 23.6]	18.9	[16.2 - 21.9]	7.03
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	16.8	[13.8 - 20.3]	21.2	[19.0 - 23.6]	16.7	[14.1 - 19.6]	5.97
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	17.2	[14.2 - 20.7]	21.2	[19.0 - 23.7]	17.0	[14.4 - 20.0]	6.63
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	16.4	[13.4 - 19.9]	21.2	[19.0 - 23.6]	16.3	[13.8 - 19.3]	6.13
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Salmonella choleraesuis* DSM 14846	16.8	[13.8 - 20.3]	21.2	[19.0 - 23.6]	16.7	[14.1 - 19.6]	4.37
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Shimwellia blattae* DSM 4481	16.8	[13.8 - 20.3]	21.2	[19.0 - 23.6]	16.7	[14.1 - 19.6]	5.97
'Escherichia sp. TW09308' (AEME00000000)	*Cronobacter malonaticus* LMG 23826	19.4	[16.3 - 23.0]	21.2	[18.9 - 23.6]	18.9	[16.2 - 21.9]	6.57
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	19.2	[16.1 - 22.8]	21.1	[18.8 - 23.5]	18.7	[16.0 - 21.7]	3.59
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	16.8	[13.8 - 20.3]	21.1	[18.9 - 23.6]	16.7	[14.1 - 19.6]	5.76
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Cronobacter condimenti* 1330	24.0	[20.7 - 27.7]	21.1	[18.9 - 23.6]	22.5	[19.7 - 25.6]	1.69

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Escherichia fergusonii ATCC 35469' (CU928158)	*Escherichia hermannii* NCTC 12129	21.0	[17.8 - 24.6]	21.1	[18.8 - 23.5]	20.1	[17.4 - 23.1]	4.14
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Shigella sonnei* ATCC 29930	19.8	[16.6 - 23.4]	21.1	[18.9 - 23.6]	19.2	[16.5 - 22.2]	3.06
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Cronobacter muytjensii* ATCC 51329	19.4	[16.3 - 23.0]	21.1	[18.9 - 23.6]	18.9	[16.2 - 21.9]	7.14
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Cronobacter muytjensii* ATCC 51329	19.0	[15.9 - 22.6]	21.1	[18.8 - 23.5]	18.5	[15.9 - 21.5]	7.83
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Cronobacter condimenti* 1330	18.9	[15.7 - 22.5]	21.1	[18.9 - 23.6]	18.4	[15.7 - 21.4]	5.23
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Shimwellia blattae* DSM 4481	16.8	[13.8 - 20.3]	21.1	[18.9 - 23.6]	16.7	[14.1 - 19.6]	5.76
'Escherichia coli str. 'clone D i2" (CP002211)	*Cronobacter muytjensii* ATCC 51329	19.5	[16.4 - 23.1]	21.1	[18.9 - 23.5]	18.9	[16.2 - 22.0]	7.16
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Salmonella choleraesuis* DSM 14846	19.6	[16.5 - 23.2]	21.1	[18.9 - 23.5]	19.0	[16.3 - 22.0]	1.94
'Escherichia coli str. K-12 substr. W3110' (AP009048)	*Cronobacter condimenti* 1330	19.4	[16.3 - 23.0]	21.1	[18.9 - 23.5]	18.9	[16.2 - 21.9]	4.97
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Shimwellia blattae* DSM 4481	16.5	[13.5 - 20.0]	21.1	[18.9 - 23.5]	16.4	[13.9 - 19.4]	6.12
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Citrobacter amalonaticus* NCTC 10805	18.0	[14.9 - 21.5]	21.1	[18.9 - 23.5]	17.7	[15.0 - 20.7]	3.08
'Escherichia coli O157:H7 str. Sakai' (BA000007)	*Escherichia hermannii* NCTC 12129	20.2	[17.0 - 23.8]	21.1	[18.9 - 23.5]	19.5	[16.8 - 22.5]	3.54
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	*Cronobacter condimenti* 1330	18.7	[15.6 - 22.3]	21.1	[18.9 - 23.5]	18.3	[15.6 - 21.3]	5.38
'Escherichia fergusonii ECD227' (CM001142)	*Cronobacter muytjensii* ATCC 51329	19.0	[15.9 - 22.6]	21.1	[18.9 - 23.5]	18.5	[15.8 - 21.5]	7.7
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Cronobacter sakazakii* NBRC 102416	20.0	[16.8 - 23.6]	21.1	[18.9 - 23.6]	19.3	[16.6 - 22.3]	0.21
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	16.5	[13.5 - 20.0]	21.1	[18.9 - 23.5]	16.4	[13.9 - 19.4]	6.12
'Escherichia coli str. 'clone D i2" (CP002211)	*Cronobacter condimenti* 1330	19.4	[16.2 - 23.0]	21.1	[18.8 - 23.5]	18.8	[16.1 - 21.8]	5.21
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Cronobacter muytjensii* ATCC 51329	19.3	[16.2 - 22.9]	21.1	[18.9 - 23.5]	18.8	[16.1 - 21.8]	6.96
'Escherichia coli str. 'clone D i14" (CP002212)	*Cronobacter condimenti* 1330	19.4	[16.2 - 23.0]	21.1	[18.8 - 23.5]	18.8	[16.1 - 21.8]	5.21
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Escherichia hermannii* NCTC 12129	19.5	[16.4 - 23.1]	21.1	[18.8 - 23.5]	18.9	[16.3 - 22.0]	3.41

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Salmonella enterica* subsp. *arizonae* NCTC 8297	19.7	[16.6 - 23.3]	21.1	[18.8 - 23.5]	19.1	[16.4 - 22.1]	2.56
'Escherichia fergusonii ATCC 35469' (CU928158)	*Cronobacter muytjensii* ATCC 51329	19.2	[16.0 - 22.8]	21.1	[18.9 - 23.6]	18.7	[16.0 - 21.7]	7.78
'Escherichia coli UMN026' (CU928163)	*Escherichia hermannii* NCTC 12129	20.6	[17.4 - 24.2]	21.1	[18.9 - 23.6]	19.8	[17.1 - 22.8]	3.36
'Escherichia coli str. 'clone D i14" (CP002212)	*Cronobacter muytjensii* ATCC 51329	19.5	[16.4 - 23.1]	21.1	[18.9 - 23.5]	18.9	[16.2 - 22.0]	7.16
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Escherichia albertii* NBRC 107761	17.1	[14.1 - 20.6]	21.0	[18.7 - 23.4]	16.9	[14.3 - 19.9]	6.72
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)	*Cronobacter condimenti* 1330	18.7	[15.6 - 22.3]	21.0	[18.8 - 23.5]	18.3	[15.6 - 21.3]	5.28
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Pseudocitrobacter faecalis* DSM 27453	20.6	[17.4 - 24.2]	21.0	[18.7 - 23.4]	19.8	[17.1 - 22.8]	1.06
'Escherichia sp. TW09308' (AEME00000000)	*Cronobacter muytjensii* ATCC 51329	18.9	[15.8 - 22.5]	21.0	[18.7 - 23.4]	18.4	[15.8 - 21.4]	7.44
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	19.6	[16.5 - 23.2]	21.0	[18.8 - 23.4]	19.0	[16.3 - 22.0]	3.68
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	*Escherichia hermannii* NCTC 12129	18.8	[15.7 - 22.4]	21.0	[18.8 - 23.4]	18.3	[15.7 - 21.3]	3.5
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	*Cronobacter condimenti* 1330	18.5	[15.4 - 22.0]	21.0	[18.7 - 23.4]	18.1	[15.4 - 21.1]	5.1
'Escherichia coli SMS-3-5' (CP000970)	*Cronobacter condimenti* 1330	19.5	[16.4 - 23.1]	21.0	[18.8 - 23.5]	18.9	[16.2 - 21.9]	5.27
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)	*Cronobacter condimenti* 1330	18.9	[15.7 - 22.5]	21.0	[18.7 - 23.4]	18.4	[15.7 - 21.4]	5.89
'Escherichia sp. TW09308' (AEME00000000)	*Escherichia hermannii* NCTC 12129	19.7	[16.5 - 23.3]	21.0	[18.7 - 23.4]	19.1	[16.4 - 22.1]	3.8
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Enterobacter cloacae* ATCC 13047	18.7	[15.5 - 22.2]	21.0	[18.8 - 23.5]	18.2	[15.6 - 21.2]	1.92
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	19.4	[16.3 - 23.0]	21.0	[18.7 - 23.4]	18.8	[16.2 - 21.9]	3.41
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Escherichia coli* DSM 30083	20.1	[16.9 - 23.7]	21.0	[18.8 - 23.5]	19.4	[16.7 - 22.4]	3.43
'Escherichia coli S88' (CU928161)	*Cronobacter condimenti* 1330	19.4	[16.3 - 23.0]	21.0	[18.7 - 23.4]	18.9	[16.2 - 21.9]	5.09
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Cronobacter malonaticus* LMG 23826	19.8	[16.7 - 23.4]	21.0	[18.8 - 23.4]	19.2	[16.5 - 22.2]	0.34

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Escherichia coli S88' (CU928161)**	20.1	[16.9 - 23.7]	21.0	[18.8 - 23.5]	19.4	[16.7 - 22.4]	3.4
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Escherichia marmotae* HT073016	19.4	[16.2 - 23.0]	21.0	[18.8 - 23.4]	18.8	[16.1 - 21.9]	3.76
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	19.2	[16.1 - 22.8]	21.0	[18.8 - 23.5]	18.7	[16.0 - 21.7]	3.7
'Escherichia coli IAI39' (CU928164)	*Cronobacter condimenti* 1330	19.3	[16.1 - 22.9]	21.0	[18.8 - 23.4]	18.7	[16.1 - 21.8]	5.14
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)	*Cronobacter condimenti* 1330	18.5	[15.4 - 22.1]	21.0	[18.8 - 23.5]	18.1	[15.5 - 21.1]	5.4
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Shigella flexneri* ATCC 29903	20.3	[17.1 - 23.9]	20.9	[18.7 - 23.4]	19.5	[16.8 - 22.6]	3.41
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Salmonella bongori* NCTC 12419	19.9	[16.7 - 23.5]	20.9	[18.7 - 23.4]	19.2	[16.5 - 22.3]	2.75
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Shimwellia blattae* DSM 4481	17.1	[14.1 - 20.6]	20.9	[18.7 - 23.3]	16.9	[14.3 - 19.9]	5.93
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Kosakonia oryzendophytica* REICA_082	21.3	[18.1 - 24.9]	20.9	[18.7 - 23.3]	20.3	[17.6 - 23.4]	0.35
'Escherichia coli UMN026' (CU928163)	*Cronobacter condimenti* 1330	19.3	[16.2 - 22.9]	20.9	[18.7 - 23.4]	18.7	[16.1 - 21.8]	5.05
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Cronobacter condimenti* 1330	19.5	[16.3 - 23.1]	20.9	[18.7 - 23.3]	18.9	[16.2 - 21.9]	5.2
'Escherichia fergusonii ATCC 35469' (CU928158)	*Cronobacter condimenti* 1330	19.3	[16.2 - 22.9]	20.9	[18.7 - 23.3]	18.8	[16.1 - 21.8]	5.83
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Cronobacter muytjensii* ATCC 51329	19.3	[16.2 - 22.9]	20.9	[18.7 - 23.3]	18.8	[16.1 - 21.8]	1.21
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Cronobacter condimenti* 1330	19.0	[15.8 - 22.5]	20.9	[18.7 - 23.4]	18.5	[15.8 - 21.5]	5.02
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	*Escherichia hermannii* NCTC 12129	20.8	[17.6 - 24.4]	20.9	[18.7 - 23.4]	19.9	[17.2 - 23.0]	3.5
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Citrobacter amalonaticus* NCTC 10805	22.5	[19.2 - 26.1]	20.9	[18.7 - 23.4]	21.3	[18.5 - 24.3]	0.65
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	*Escherichia hermannii* NCTC 12129	20.2	[17.0 - 23.8]	20.9	[18.7 - 23.4]	19.4	[16.7 - 22.5]	3.32
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	17.1	[14.1 - 20.6]	20.9	[18.7 - 23.3]	16.9	[14.3 - 19.9]	5.93
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Kosakonia sacchari* SP1	22.5	[19.2 - 26.1]	20.8	[18.6 - 23.2]	21.3	[18.5 - 24.3]	0.19

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Escherichia coli SMS-3-5' (CP000970)**	20.7	[17.5 - 24.3]	20.8	[18.6 - 23.2]	19.8	[17.1 - 22.9]	3.58
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Escherichia coli str. 'clone D i14" (CP002212)**	20.2	[17.0 - 23.8]	20.8	[18.6 - 23.3]	19.4	[16.7 - 22.4]	3.52
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Shigella dysenteriae Sd197' (CP000034)**	20.3	[17.1 - 23.9]	20.8	[18.6 - 23.2]	19.5	[16.8 - 22.6]	2.83
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	18.8	[15.7 - 22.4]	20.8	[18.5 - 23.2]	18.3	[15.6 - 21.3]	3.5
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Escherichia coli UMN026' (CU928163)**	20.4	[17.2 - 24.0]	20.8	[18.6 - 23.3]	19.6	[16.9 - 22.7]	3.36
'Escherichia fergusonii ECD227' (CM001142)	*Cronobacter condimenti* 1330	19.3	[16.1 - 22.9]	20.8	[18.6 - 23.2]	18.7	[16.0 - 21.7]	5.76
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	20.7	[17.5 - 24.3]	20.8	[18.5 - 23.2]	19.9	[17.1 - 22.9]	3.5
'Escherichia sp. TW09308' (AEME00000000)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	19.6	[16.4 - 23.2]	20.8	[18.6 - 23.2]	19.0	[16.3 - 22.0]	3.8
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Escherichia coli IAI39' (CU928164)**	20.1	[16.9 - 23.7]	20.8	[18.6 - 23.3]	19.4	[16.7 - 22.4]	3.45
'Escherichia sp. TW09308' (AEME00000000)	*Cronobacter condimenti* 1330	18.6	[15.5 - 22.2]	20.8	[18.6 - 23.2]	18.1	[15.5 - 21.1]	5.49
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Escherichia coli str. 'clone D i2" (CP002211)**	20.2	[17.0 - 23.8]	20.8	[18.6 - 23.3]	19.4	[16.7 - 22.4]	3.52
'Escherichia coli str. K-12 substr. W3110' (AP009048)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	21.5	[18.2 - 25.1]	20.8	[18.6 - 23.3]	20.5	[17.7 - 23.5]	3.28
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Shigella dysenteriae* ATCC 13313	20.0	[16.9 - 23.7]	20.8	[18.6 - 23.2]	19.3	[16.6 - 22.4]	3.1
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Escherichia fergusonii ATCC 35469' (CU928158)**	20.9	[17.6 - 24.5]	20.7	[18.5 - 23.2]	20.0	[17.2 - 23.0]	4.14
'Escherichia coli O157:H7 str. Sakai' (BA000007)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	20.2	[17.0 - 23.8]	20.7	[18.5 - 23.2]	19.4	[16.7 - 22.4]	3.54
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	18.4	[15.3 - 21.9]	20.7	[18.4 - 23.1]	18.0	[15.3 - 21.0]	2.43
'Escherichia sp. TW09308' (AEME00000000)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	17.0	[14.0 - 20.5]	20.7	[18.5 - 23.2]	16.8	[14.3 - 19.8]	6.23

Query	Subject	d_0	C.I. d_0	d_4	C.I. d_4	d_6	C.I. d_6	Diff. G+C Percent
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Shimwellia blattae* DSM 4481	18.4	[15.3 - 21.9]	20.7	[18.4 - 23.1]	18.0	[15.3 - 21.0]	2.43
'Escherichia coli H299' (ADBC01000001-ADBC01000229)	**'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)**	20.1	[16.9 - 23.7]	20.7	[18.5 - 23.2]	19.4	[16.7 - 22.4]	3.33
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	*Escherichia fergusonii* ATCC 35469	20.8	[17.6 - 24.4]	20.7	[18.5 - 23.2]	19.9	[17.2 - 23.0]	4.16
'Escherichia fergusonii ECD227' (CM001142)	**'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)**	17.5	[14.4 - 21.0]	20.7	[18.4 - 23.1]	17.2	[14.6 - 20.2]	6.5
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Escherichia marmotae* HT073016	17.2	[14.2 - 20.7]	20.7	[18.4 - 23.1]	17.0	[14.4 - 20.0]	6.2
'Escherichia sp. TW09308' (AEME00000000)	*Shimwellia blattae* DSM 4481	17.0	[14.0 - 20.5]	20.7	[18.5 - 23.2]	16.8	[14.3 - 19.8]	6.23
'Escherichia fergusonii ECD227' (CM001142)	*Escherichia hermannii* NCTC 12129	21.0	[17.8 - 24.6]	20.7	[18.5 - 23.2]	20.1	[17.3 - 23.1]	4.07
'Escherichia fergusonii ECD227' (CM001142)	*Shimwellia blattae* DSM 4481	17.5	[14.4 - 21.0]	20.7	[18.4 - 23.1]	17.2	[14.6 - 20.2]	6.5
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)	**'Escherichia fergusonii ECD227' (CM001142)**	20.9	[17.7 - 24.5]	20.6	[18.4 - 23.0]	20.0	[17.2 - 23.0]	4.07
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Pseudocitrobacter faecalis* DSM 27453	17.9	[14.8 - 21.4]	20.6	[18.4 - 23.0]	17.5	[14.9 - 20.5]	3.49
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Kosakonia sacchari* SP1	18.4	[15.3 - 22.0]	20.5	[18.2 - 22.9]	18.0	[15.3 - 21.0]	2.24
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Cronobacter condimenti* 1330	18.7	[15.6 - 22.3]	20.5	[18.3 - 22.9]	18.2	[15.6 - 21.2]	0.74
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)	*Kosakonia oryzendophytica* REICA_082	18.7	[15.6 - 22.3]	20.2	[18.0 - 22.6]	18.2	[15.5 - 21.2]	2.78

Table 4: Strains in your dataset

Joint dataset of automatically determined closest type strains (if this mode was chosen), manually selected type strains (if selected accordingly) and the provided user strains, if provided (marked in yellow).

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Citrobacter koseri NCTC 10786	Frederiksen 1970	CIP 105014; CIP 82.87; ATCC 27028; CCUG 4859; DSM 4570; DSM 4595; JCM 1658; LMG 5519	*Citrobacter koseri*	4661 458	53.8	6398		PRJEB6403	SAMEA2665132	GCA_900446925	
Citrobacter amalonaticus NCTC 10805	(Young et al. 1971) Brenner and Farmer 1982	9823; CIP 82.89; ATCC 25405; CCUG 4860 A; CCUG 4860; CECT 863; DSM 4593; JCM 1661; NCTC 10805; LMG 7873	*Citrobacter amalonaticus*; *Levinea amalonatica*	5093 340	53.4	5330		PRJEB6403	SAMEA2612491	GCA_900460855	
Levinea malonatica NCTC 10810	Young et al. 1971	ATCC 25408; DSM 4596; JCM 1660	*Levinea malonatica*	4732 730	53.8	5321		PRJEB6403	SAMEA2665133	GCA_900461075	
Escherichia hermannii NCTC 12129	Brenner et al. 1983	LMG 7867; CCUG 15714; DSM 4560; ATCC 33650; JCM 1473; CDC 980-72; CIP 103176; CIP 104946; HAMBI 1693	*Escherichia hermannii*	4553 773	54.1	4875		PRJNA224116	SAMEA2612498	GCF_900635495	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Escherichia albertii NBRC 107761	Huys et al. 2003	Albert 19982; CCUG 46494; DSM 17582; LMG 20976	*Escherichia albertii*	4416 104	49.8	4285	Gp0016729	PRJDB13	SAMD00019863	GCA_000759775	
Kosakonia sacchari SP1	(Zhu et al. 2013) Gu et al. 2014	CGMCC 1.12102; DSM 100203; LMG 26783; SP 1	*Enterobacter sacchari*; *Kosakonia sacchari*	5530 608	54.3	5194	Gp0106921	PRJEB16854	SAMN04487787	GCA_900109485	
Escherichia coli DSM 30083	(Migula 1895) Castellani and Chalmers 1919	CIP 54.8; NCCB 54008; ATCC 11775; CCUG 24; CCUG 29300; JCM 1649; NBIMCC 3398; NBRC 102203; NCTC 9001; LMG 2092	*Bacillus coli*; *Escherichia coli*	5037 933	50.6	4762	Gp0007996	PRJNA50621	SAMN00718807	GCA_000690815	2528311135
Citrobacter diversus NCTC 10849	(Burkey 1928) Werkman and Gillen 1932	ATCC 27156; JCM 1659; CDC 3613-63; LMG 5741	*Aerobacter diversum*; *Citrobacter diversus*	4915 694	53.6	4814		PRJEB6403	SAMEA2580312	GCA_900706735	
Salmonella enterica subsp. *arizonae* NCTC 8297	(Borman 1957) Le Minor and Popoff 1987	CIP 82.30; ATCC 13314; CCUG 6322; DSM 9386	*Paracolobactrum arizonae*; *Salmonella arizonae*; *Salmonella choleraesuis* subsp. *arizonae*; *Salmonella enterica* subsp. *arizonae*	4545 679	51.5	5747		PRJEB6403	SAMEA2665124	GCA_900456225	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Salmonella typhi NCTC 8385	(Schroeter 1886) Warren and Scott 1930	ATCC 19430; CUETM 79-394; HAMBI 1306	*Bacillus typhi*; *Salmonella typhi*	4832830	52.1	4632	Gp0342001	PRJEB6403	SAMEA104281633	GCA_900456745	
Shigella flexneri ATCC 29903	Castellani and Chalmers 1919	CIP 82.48; DSM 4782	*Shigella flexneri*	4938295	50.7	5112	Gp0307840	PRJNA218110	SAMN08330274	GCA_002950215	
Shigella boydii ATCC 8700	Ewing 1949	CIP 82.50; CCUG 49022; DSM 7532; NCTC 12985; P288	*Shigella boydii*	4525323	51.1	4913	Gp0307838	PRJNA218110	SAMN08330244	GCA_002946735	
Pseudocitrobacter faecalis DSM 27453	Kämpfer et al. 2014 emend. Kämpfer et al. 2020	25 CIT; CCM 8479; LMG 27751	*Pseudocitrobacter faecalis*	5155180	53.0	4895	Gp0290553	PRJNA463351	SAMN09074683	GCA_003315335	2770939623
Salmonella choleraesuis DSM 14846	(Smith 1894) Weldin 1927	CIP 55.133; ATCC 13312; JCM 1651; NCTC 5735; F. Kauffmann 1348	*Bacillus choleraesuis*; *Salmonella choleraesuis*; *Salmonella choleraesuis* subsp. *choleraesuis*	4679634	52.1	4514	Gp0251884	PRJNA439983	SAMN08769612	GCA_003201315	2756170275
Cronobacter condimenti 1330	Joseph et al. 2012	CECT 7863; LMG 26250	*Cronobacter condimenti*	4480460	55.8	4272	Gp0023163	PRJEB164	SAMEA2272515	GCA_000319285	2534681767
Skermanella stibiiresistens SB22	Luo et al. 2012 emend. Hördt et al. 2020	CGMCC 1.10751; KCTC 23364	*Skermanella stibiiresistens*	7868338	65.9	7269	Gp0048174	PRJNA214805	SAMN02951888	GCA_000576635	
Kosakonia oryzendophytica REICA_082	(Hardoim et al. 2015) Li et al. 2016	NCCB 100390; LMG 26432	*Enterobacter oryzendophyticus*; *Kosakonia oryzendophytica*	4837282	53.7	4486	Gp0108252	PRJEB15027	SAMN04487791	GCA_900094925	
Cronobacter malonaticus LMG 23826	Iversen et al. 2008	DSM 18702; CDC 1058-77; E825	*Cronobacter malonaticus*; *Cronobacter sakazakii* subsp. *malonaticus*	4434037	56.8	4130	Gp0020487	PRJNA89099	SAMN02952929	GCA_000409305	2548876974
Cronobacter muytjensii ATCC 51329	Iversen et al. 2008	CIP 103581; DSM 21870	*Cronobacter muytjensii*	4322611	57.7	3916	Gp0020623	PRJNA89111	SAMN02952928	GCA_000409285	2548876993

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Escherichia marmotae HT073016	Liu et al. 2015	CGMCC 1.12862; DSM 28771	*Escherichia marmotae*	4493998	50.3	4255	Gp0117761	PRJNA247449	SAMN02777259	GCA_000807695	
Cronobacter sakazakii NBRC 102416	(Farmer et al. 1980) Iversen et al. 2008	CIP 103183; ATCC 29544; CCUG 14558; DSM 4485; JCM 1233; NBIMCC 8667; NCTC 11467; CDC 4562-70; CDC 4562-70 (78-067947); LMG 5740	*Cronobacter sakazakii*; *Cronobacter sakazakii* subsp. *sakazakii*; *Enterobacter sakazakii*	4548307	56.7	4241	Gp0024044	PRJDB277	SAMD00000350	GCA_000684935	2576861057
Enterobacter cloacae ATCC 13047	(Jordan 1890) Hormaeche and Edwards 1960	CIP 60.85; CCUG 28448; CCUG 29301; CCUG 6323; DSM 30054; JCM 1232; NBIMCC 8570; IFO 13535; NBRC 13535; NCTC 10005; HAMBI 1295; HAMBI 96; LMG 2783	*Bacillus cloacae*; *Bacterium cloacae*; *Cloaca cloacae*; *Enterobacter cloacae*; *Enterobacter cloacae* subsp. *cloacae*	5598795	54.6	5518	Gp0006802	PRJNA45793	SAMN02603901	GCA_000025565	646564529

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Shimwellia blattae DSM 4481	(Burgess et al. 1973) Priest and Barker 2010	CIP 103175; CIP 104942; ATCC 29907; JCM 1650; NCTC 12127; CDC 9005-74; HAMBI 1692; LMG 3030	*Escherichia blattae*; *Shimwellia blattae*	4158 725	56.5	3904	Gp0001398	PRJNA36307	SAMN02603253	GCA_000262305	2513020017
Escherichia fergusonii ATCC 35469	Farmer et al. 1985	CIP 103357; CIP 104947; DSM 13698; JCM 21226; NBRC 102419; NCTC 12128; CDC 568-73; LMG 7866	*Escherichia fergusonii*	4643 861	49.9	4324	Gp0001407	PRJNA33369	SAMEA3138228	GCA_000026225	643692022
Salmonella enterica LT2	(ex Kauffmann and Edwards 1952) Le Minor and Popoff 1987	CIP 60.62; NCIMB 11450; ATCC 43971; CCUG 42060; DSM 17058; DSM 27656; IFO 13245; NBRC 13245; NCTC 12416; NCIB 11450	*Salmonella enterica*; *Salmonella enterica* subsp. *enterica*	4951 371	52.2	4554	Gp0000715	PRJNA241	SAMN02604315	GCA_000006945	637000255
Salmonella typhimurium ATCC 13311	(Loeffler 1892) Castellani and Chalmers 1919	CIP 58.58; ATCC 13311; JCM 1652; NCTC 74	*Bacillus typhimurium*; *Salmonella typhimurium*	4831 756	52.1	4361	Gp0103826	PRJNA256479	SAMN02943517	GCA_000743055	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Salmonella typhimurium JCM 1652	(Loeffler 1892) Castellani and Chalmers 1919	CIP 58.58; ATCC 13311; JCM 1652; NCTC 74	*Bacillus typhimurium*; *Salmonella typhimurium*	4747 271	52.1	5270	Gp0092156	PRJDB611	SAMD00009942	GCA_000614485	
Shigella sonnei ATCC 29930	(Levine 1920) Weldin 1927	CIP 82.49; CECT 4887; DSM 5570; NCTC 12984	*Bacterium sonnei*; *Shigella sonnei*	4994 001	51.0	5043	Gp0307839	PRJNA218110	SAMN08330284	GCA_002950395	
Shigella dysenteriae ATCC 13313	(Shiga 1897) Castellani and Chalmers 1919	CIP 57.28; DSM 4781; NCTC 4837	*Bacillus dysentericus*; *Escherichia coli* subsp. *shigellae*; *Shigella dysenteriae*	4578 459	51.0	5232	Gp0309783	PRJNA218110	SAMN08330256	GCA_002949675	
Salmonella bongori NCTC 12419	(Le Minor et al. 1985) Reeves et al. 1989	CIP 82.33; ATCC 43975; CCUG 30042; DSM 13772	*Salmonella bongori*; *Salmonella choleraesuis* subsp. *bongori*; *Salmonella enterica* subsp. *bongori*	4460 105	51.3	3864	Gp0001845	PRJNA351	SAMEA3138409	GCA_000252995	650716084
'Escherichia coli MS 21-1' (ADTR01000001-ADTR01000540)				5282 923	50.4	5267					
'Escherichia coli MS 200-1' (ADUC01000001-ADUC01000445)				5042 708	50.5	4768					
'Escherichia sp. TW09308' (AEME00000000)				4809 826	50.3	4639					
'Escherichia coli str. K-12 substr. W3110' (AP009048)				4646 332	50.8	4327					
'Escherichia coli O157:H7 str. Sakai' (BA000007)				5498 578	50.5	5299					

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
'Atlantibacter hermannii NBRC 105704' (BAFF01000001-BAFF01000044)				4495280	54.1	4168					
'Escherichia fergusonii ECD227' (CM001142)				4509864	50.0	4237					
'Shigella dysenteriae Sd197' (CP000034)				4369232	51.2	4977					
'Escherichia coli SMS-3-5' (CP000970)				5068389	50.5	4651					
'Shimwellia blattae DSM 4481 = NBRC 105725' (CP001560)				4158725	56.5	3825					
'Escherichia coli str. 'clone D i2'' (CP002211)				5038386	50.6	4609					
'Escherichia coli str. 'clone D i14'' (CP002212)				5038386	50.6	4609					
'Escherichia fergusonii ATCC 35469' (CU928158)				4588711	49.9	4262					
'Escherichia coli S88' (CU928161)				5032268	50.7	4747					
'Escherichia coli UMN026' (CU928163)				5202090	50.7	4825					
'Escherichia coli IAI39' (CU928164)				5132068	50.6	4863					

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
'Escherichia coli O157:H7 str. EC4501' (ABHT01000001-ABHT01000250)				5677181	50.6	5721					
'Escherichia albertii TW07627' (ABKX01000001-ABKX01000064)				4698533	49.9	4870					
'Escherichia coli TA143' (ADAY01000001-ADAY01000168)				4829725	50.6	4603					
'Escherichia coli H299' (ADBC01000001-ADBC01000229)				5248906	50.8	5102					
'Escherichia coli MS 198-1' (ADTJ01000001-ADTJ01000564)				5236490	50.7	5113					
'Escherichia coli MS 69-1' (ADTP01000001-ADTP01000425)				5207549	50.4	4952					

Methods, Results and References

The genome sequence data were uploaded to the Type (Strain) Genome Server (TYGS), a free bioinformatics platform available under https://tygs.dsmz.de, for a whole genome-based taxonomic analysis [1]. The analysis also made use of recently introduced methodological updates and features [2,3]. Information on nomenclature, synonymy and associated taxonomic literature was provided by TYGS's sister database, the List of Prokaryotic names with Standing in Nomenclature (LPSN, available at https://lpsn.dsmz.de) [2,3]. The results were provided by the TYGS on 2019-10-02. The TYGS analysis was subdivided into the following steps:

Determination of closely related type strains

Determination of closest type strain genomes was done in two complementary ways: First, all user genomes were compared against all type strain genomes available in the TYGS database via the MASH algorithm, a fast approximation of intergenomic relatedness [4], and, the ten type strains with the smallest MASH distances chosen per user genome. Second, an additional set of ten closely related type strains was determined via the 16S rDNA gene sequences. These were extracted from the user genomes using RNAmmer [5] and each sequence was subsequently BLASTed [6] against the 16S rDNA gene sequence of each of the currently 25466 type strains available in the TYGS database. This was used as a proxy to find the best 50 matching type strains (according to the bitscore) for each user genome and to subsequently calculate precise distances using the Genome BLAST Distance Phylogeny approach (GBDP) under the algorithm 'coverage' and distance formula d_5 [7]. These distances were finally used to determine the 10 closest type strain genomes for each of the user genomes.

Pairwise comparison of genome sequences

For the phylogenomic inference, all pairwise comparisons among the set of genomes were conducted using GBDP and accurate intergenomic distances inferred under the algorithm 'trimming' and distance formula d_5 [7]. 100 distance replicates were calculated each. Digital DDH values and confidence intervals were calculated using the recommended settings of the GGDC 4.0 [2,7].

Phylogenetic inference

The resulting intergenomic distances were used to infer a balanced minimum evolution tree with branch support via FASTME 2.1.6.1 including SPR postprocessing [8]. Branch support was inferred from 100 pseudo-bootstrap replicates each. The trees were rooted at the midpoint [9] and visualized with PhyD3 [10].

Type-based species and subspecies clustering

The type-based species clustering using a 70% dDDH radius around each of the 30 type strains was done as previously described [1]. The resulting groups are shown in Table 1 and 4. Subspecies clustering was done using a 79% dDDH threshold as previously introduced [11].

Results

Type-based species and subspecies clustering

The resulting species and subspecies clusters are listed in Table 4, whereas the taxonomic identification of the query strains is found in Table 1. Briefly, the clustering yielded 20 species clusters and the provided query strains were assigned to 6 of these. Moreover, user strains were located in 8 of 22 subspecies clusters.

Figure caption SSU tree

Figure 1. Tree inferred with FastME 2.1.6.1 [8] from GBDP distances calculated from 16S rDNA gene sequences. The branch lengths are scaled in terms of GBDP distance formula d_5. The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 62.6 %. The tree was rooted at the midpoint [9].

Figure caption genome tree

Figure 2. Tree inferred with FastME 2.1.6.1 [8] from GBDP distances calculated from genome sequences. The branch lengths are scaled in terms of GBDP distance formula d_5. The numbers above branches are GBDP pseudo-bootstrap support values > 60 % from 100 replications, with an average branch support of 66.4 %. The tree was rooted at the midpoint [9].

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