Supporting Information

Sequence analysis and specificity of distinct types of menaquinone methyltransferases indicate the widespread potential of methylmenaquinone production in Bacteria and Archaea

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References

Supplemental Excel file with accession numbers of MqnK/MenK/MenK2 cluster sequences.

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Additional experimental procedures

MqnK/MenK/MenK2 primary structures were aligned using ClustalOmega 1.2.2 command-line version.

One-dimensional SDS-PAGE was carried out with 50 µg of total cell protein applied to each lane. Proteins were transferred from polyacrylamide gel onto PVDF (polyvinylidene difluoride) membranes using the horizontal semi-dry electrophoretic system. Strep-tagged proteins were detected by ELISA using a Strep-Tactin-HRP conjugate (IBA Lifesciences).

Nuclear magnetic resonance spectroscopy (NMR). All NMR spectra were measured on a Bruker DRX 500 MHz spectrometer equipped with a room temperature 5 mm PABBO probe (Bruker Biospin, Karlsruhe, Germany) at 303 K using CDCl₃ (99.9% D from Sigma) as solvent. The concentrations of the samples were ~ 10^{-2} mol I⁻¹. The solvent signals were used for referencing the ¹H- and ¹³C-NMR spectra at 7.20 ppm and 77.20 ppm respectively. Chemical shift assignment was achieved with ¹H-, ¹³C- and ¹³C-DEPT-135 1D spectra, 2D ¹H-¹H COSY (correlated spectroscopy), 2D ¹H-¹H NOESY (nuclear overhauser enhancement correlated spectroscopy), 2D ¹H-¹³C HSQC (heteronuclear single guantum correlation) and 2D ¹H-¹³C HMBC (heteronuclear multiple-bond correlation) spectra, using the Bruker pulse sequences za30, zapa30, dept135, cosvapmfaf, noesvaptp, invietapsi and inv4gplrl2ndqf respectively. 1D spectra were recorded using an excitation pulse of 30° and a repetition time of 3.7 s (¹H) and 1.5 s (¹³C). 128 scans (¹H, 8.000 scans ¹³C) were added and Fourier transformed with a final digital resolution of 0.08 Hz (¹H, 0.26 Hz ¹³C). The hetero-nuclear long-range correlation spectrum (HMBC) was recorded by a matrix of 1 k data points (f2, ¹H dimension) and 256 increments (data points in f1 ¹³C dimension). 64 scans for every increment were added resulting in an experimental time of nearly 6 h. The spectrum has been optimized for a heteronuclear coupling constant of 9 Hz. Raw data were processed with Topspin (Bruker Biospin, Karlsruhe, Germany) and 2D data were analyzed using MestReNova 11.0.3 (Metrelab Research S.L.). Fig. S3 shows the ¹H-NMR spectra of MK₈, 7-MMK₈, 8-MMK₈, 5,8-DMMK₈ and 7,8-DMMK₈. Differences in the shift ranges of aromatic protons and of methyl groups are shown clearly. All ¹H- and ¹³C NMR signals could be assigned completely (Figs S6 and S7).

Mass spectra were acquired by Alexander Schießer and Christiane Rudolph (Clemens Schöpf Institute, Department of Chemistry, Technical University of Darmstadt) on an Impact II quadrupole time-of-flight (QTOF) mass spectrometer (Bruker Daltonik) using atmospheric pressure chemical ionization (APCI) (5 kV corona discharge) as ion source. The samples were diluted in methanol. **Table S1.** Taxonomic classification of 237 microbial species predicted to contain at least one protein of the MqnK/MenK/MenK2 family (see Fig. 3).Experimentally characterized MMK-producing species are shown in red.

Bacteria	Campylobacter sp. P159	Betaproteobacteria	Shewanella sp. cp20	Eggerthellales	Desulfurobacterium indicum
Proteobacteria	Campylobacter sp. P160	Burkholderiales	Shewanella sp. GutCb	Eggerthellaceae	Desulfurobacterium sp. TC5-1
Epsilonproteobacteria	Campylobacter sp. P255	Sutterellaceae	Shewanella sp. HN-41	Adlercreutzia equolifaciens	Bacteroidetes
Campylobacterales	Campylobacter sp. RM12175	Dakarella massiliensis	Shewanella sp. MR-4	Arabia massiliensis	Bacteroidia
Campylobacteraceae	Campylobacter sp. RM16704	Duodenibacillus massiliensis	Shewanella sp. P1-14-1	Asaccharobacter celatus	Bacteroidales
Arcobacter canalis	Campylobacter sp. RM6137	Mesosutterella multiformis	Shewanella sp. Pdp11	Cryptobacterium curtum	Bacteroidaceae
Arcobacter halophilus	Campylobacter sp. RM8835	Parasutterella excrementihominis	Shewanella sp. R106	Denitrobacterium detoxificans	Bacteroides caecimuris
Arcobacter marinus	Campylobacter sp. RM8964	Sutterella megalosphaeroides	Shewanella sp. SACH	Eggerthella lenta	Deferribacteres
Campylobacter avium	Campylobacter sp. RM8965	Sutterella parvirubra	Shewanella sp. Shew256	Eggerthella sinensis	Deferribacteres
Campylobacter blaseri	Campylobacter sp. RM8966	Sutterella sp. AM11-39	Shewanella sp. UCD-FRSSP16_17	Eggerthella sp. AM16-19	Deferribacterales
Campylobacter coli	Campylobacter sp. RM8970	Sutterella sp. CAG:521	Shewanella sp. UCD-KL12	Eggerthella sp. YY7918	Deferribacteraceae
Campylobacter concisus	Campylobacter sp. RM9262	Sutterella wadsworthensis	Shewanella sp. UCD-KL21	Eggerthella timonensis	Denitrovibrio acetiphilus
Campylobacter corcagiensis	Campylobacter sp. S0112	Turicimonas muris	Shewanella sp. W3-18-1	Enterorhabdus caecimuris	Denitrovibrio sp.
Campylobacter curvus	Campylobacter sputorum	Gammaproteobacteria	Shewanella sp. WE21	Enterorhabdus mucosicola	Flexistipes sinusarabici
Campylobacter fetus	Campylobacter subantarcticus	Alteromonadales	Shewanella vesiculosa	Enteroscipio rubneri	Firmicutes
Campylobacter geochelonis	Campylobacter upsaliensis	Shewanellaceae	Shewanella waksmanii	Gordonibacter massiliensis	Clostridia
Campylobacter gracilis	Campylobacter ureolyticus	Shewanella algae	Shewanella woodyi	Gordonibacter pamelaeae	Thermoanaerobacterales
Campylobacter helveticus	Campylobacter volucris	Shewanella algidipiscicola	Shewanella xiamenensis	Gordonibacter sp. 28C	Thermoanaerobacteraceae
Campylobacter hepaticus	Sulfurospirillum arcachonense	Shewanella amazonensis	Ferrimonadaceae	Gordonibacter sp. An230	Brockia lithotrophica
Campylobacter hominis	Sulfurospirillum arsenophilum	Shewanella baltica	Ferrimonas balearica	Gordonibacter sp. An232A	Clostridiales
Campylobacter hyointestinalis	Sulfurospirillum barnesii	Shewanella benthica	Ferrimonas futtsuensis	Gordonibacter urolithinfaciens	Peptococcaceae
Campylobacter iguaniorum	Sulfurospirillum cavolei	Shewanella carassii	Ferrimonas kyonanensis	Paraeggerthella hongkongensis	Desulfosporosinus infrequens
Campylobacter insulaenigrae	Sulfurospirillum deleyianum	Shewanella chilikensis	Ferrimonas marina	Raoultibacter massiliensis	Desulfosporosinus sp. Tol-M
Campylobacter jejuni	Sulfurospirillum halorespirans	Shewanella colwelliana	Ferrimonas sediminum	Raoultibacter timonensis	Peptostreptococcaceae
Campylobacter lanienae	Sulfurospirillum multivorans	Shewanella corallii	Ferrimonas senticii	Rubneribacter badeniensis	Clostridioides difficile
Campylobacter lari	Sulfurospirillum sp. JPD-1	Shewanella fidelis	Paraferrimonas haliotis	Slackia equolifaciens	Clostridiaceae
Campylobacter mucosalis	Sulfurospirillum sp. MES	Shewanella frigidimarina	Paraferrimonas sedimenticola	Slackia exigua	Clostridium cochlearium
Campylobacter ornithocola	Sulfurospirillum sp. SCADC	Shewanella halifaxensis	Oceanospirillales	Slackia faecicanis	Clostridium formicaceticum
Campylobacter peloridis	Sulfurospirillum sp. SL2-1	Shewanella japonica	Saccharospirillaceae	Slackia heliotrinireducens	Clostridium tetani
Campylobacter pinnipediorum	Sulfurospirillum sp. UBA11407	Shewanella loihica	Reinekea blandensis	Slackia isoflavoniconvertens	Clostridium tetanomorphum
Campylobacter rectus	Sulfurospirillum sp. UBA12182	Shewanella mangrovi	Deltaproteobacteria	Slackia piriformis	Archaea
Campylobacter showae	Sulfurospirillum sp. UCH001	Shewanella marina	Syntrophobacterales	Slackia sp. CM382	Crenarchaeota
Campylobacter sp. 10_1_50	Helicobacteraceae	Shewanella marisflavi	Syntrophorhabdaceae	Chloroflexi	Thermoprotei
Campylobacter sp. 114	Helicobacter burdigaliensis	Shewanella morhuae	Syntrophorhabdus aromaticivorans	Anaerolineae	Thermoproteales
Campylobacter sp. 251/13	Helicobacter canadensis	Shewanella oneidensis	Syntrophaceae	Anaerolineales	Thermoproteaceae
Campylobacter sp. 73/13	Helicobacter ganmani	Shewanella pealeana	Desulfomonile tiedjei	Anaerolineaceae	Thermoproteus sp. AZ2
Campylobacter sp. BCW_6462	Helicobacter macacae	Shewanella piezotolerans	Smithella sp. SDB	Anaerolinea thermolimosa	Thermoproteus tenax
Campylobacter sp. P0087	Helicobacter pullorum	Shewanella psychrophila	Syntrophus aciditrophicus	Anaerolinea thermophila	Acidilobales
Campylobacter sp. P0094	Helicobacter rodentium	Shewanella putrefaciens	Syntrophus gentianae	Bellilinea caldifistulae	Acidilobaceae
Campylobacter sp. P0103	Helicobacter sp. 11-8110	Shewanella sediminis	Syntrophus sp. GWC2_56_31	Levilinea saccharolytica	Acidilobus saccharovorans
Campylobacter sp. P0106	Helicobacter sp. MIT 01-3238	Shewanella sp. 10N.286.48.A6	Syntrophus sp. RIFOXYC2_FULL_54_9	Longilinea arvoryzae	Acidilobus sp. 7A
Campylobacter sp. P0107	Helicobacter sp. MIT 05-5294	Shewanella sp. 10N.286.51.B7	Actinobacteria	Deinococcus-Thermus	Acidilobus sp. CIS
Campylobacter sp. P0136	Helicobacter sp. MIT 11-5569	Shewanella sp. 10N.286.52.B9	Coriobacteriia	Deinococci	Acidilobus sp. JCHS
Campylobacter sp. P0138	Helicobacter valdiviensis	Shewanella sp. 10N.286.52.C2	Coriobacteriales	Thermales	Caldisphaeraceae
Campylobacter sp. P0139	Helicobacter winghamensis	Shewanella sp. 11B5	Coriobacteriaceae	Thermaceae	Caldisphaera lagunensis
Campylobacter sp. P0209	Sulfuricurvum sp. PD_MW2	Shewanella sp. 38A_GOM-205m	Collinsella tanakaei	Oceanithermus profundus	Caldisphaera sp.
Campylobacter sp. P0227	Wolinella succinogenes	Shewanella sp. Actino-trap-3	Collinsella vaginalis	Aquificae	Desulfurococcales
Campylobacter sp. P031		Shewanella sp. ALD9	Parvibacter caecicola	Aquificae	Pyrodictiaceae
Campylobacter sp. P148		Shewanella sp. Alg231_23	Senegalimassilia anaerobia	Desulfurobacteriales	Hyperthermus butylicus
Campylobacter sp. P155		Shewanella sp. Bg11-22		Desulfurobacteriaceae	Pyrodictium delaneyi

Desulfurobacterium atlanticum

Pyrodictium occultum

Shewanella sp. CG12

Campylobacter sp. P157

Table S2. Taxonomic classification of 63 species for which the presence of MMK and/or DMMK has been demonstrated biochemically. Organisms for which MqnK/MenK/MenK/2-encoding genes have been assigned are shown in red. Modified from Hein *et al.* (2017).

Organism	Major naphthoquinones	Reference (MMK identification)	Organism	Major naphthoquinones	Reference (MMK identification)
Bacteria			Actinobacteria		
Proteobacteria			Coriobacteriia		
Epsilonproteobacteria			Coriobacteriales		
Campylobacterales			Coriobacteriaceae		
Campylobacteraceae			Parvibacter caecicola NR06	MMK ₆ , DMMK ₆	Clavel et al. 2013
Campylobacter coli LMG 23344	MK ₅ , MMK ₅	Moss et al. 1990	Eggerthellales		
Campylobacter concisus UNSWCD	MK6, MMK6	Moss et al. 1990	Eggerthellaceae		
Campylobacter curvus DSM 6644	MMK ₆ , MK ₆	Fernandez and Collins 1987	Adlercreutzia equolifaciens DSM 19450	DMMK ₆ , MMK ₆	Maruo et al. 2008, Hein et al. 2018
Campylobacter faecalis	MK ₆ , MMK ₆	Moss et al. 1990	Eggerthella lenta DSM 2243	MMKe, MKe	Collins et al. 1985, Fernandez and
Campylobacter fetus subsp. fetus 82-40	MK ₆ , MMK ₆	Carlone and Anet 1983			Collins 1987, Maruo et al. 2008
Campylobacter fetus subsp. Venerealis UM	MK ₆ , MMK ₆ , MK ₅	Moss et al. 1984	Eggerthella sinensis DSM 16107	MMK6, DMMK6, MK6	Maruo et al. 2008
Campylobacter gracilis RM 3268	MMK6, MK6	Fernandez and Collins 1987	Enterorhabdus caecimuris B7	MMK6, DMMK6	Clavel et al. 2009
Campylobacter hyointestinalis DSM 19053	MK6, MMK6	Moss et al. 1990	Enterorhabdus mucosicola DSM 19490	MMK6	Clavel et al. 2009
Campylobacter jejuni subsp. jejuni NCTC 11168	MK ₆ , MMK ₆	Carlone and Anet 1983	Gordonibacter faecihominis CAT-2	MK6, MMK6, DMMK6	Jin et al. 2014
Campylobacter Ian NCTC 11845	MK6, MMK6	Moss et al. 1990	Gordonibacter pamelaeae DSM 19378	MK6, MMK6, DMMK6	Jin et al. 2014
Campylobacter mucosalis DSM 21682	MK6, MMK6	Moss et al. 1990	Paraeggertnella nongkongensis DSM 16106	MMK6, DMMK6, MK6	Maruo et al. 2008
Campylobacter rectus RM 3267	MK6, MMK6	Mana at al 1000	Actinobacteria		
Campylobacter sputorum INTX 06/209	MIK6, MINIK6, MIK5	Moss et al. 1990	Micrococcales		
Campylobacter upsaliensis RM 3165		Moss et al. 1990	Micrococcaceae	MK (H.) MMK (H.)	Pukall at al. 2006
Sulfuseepisillum esseehenese DSM 0755	MIK6, MIMIK6	Finator of al. 1997	Acancomes priytoseiun DSM 14247	MIK10*(H2), MIMIK10*(H2)	Pukali et al. 2000
Sulfurospinium arcacronese DSM 5755	MK- MMK- MK-	Filister et al. 2010. Collins and Widdel 1996	Greenershaaata		
Sullarospinium deleyianum DSM 6946	WIN6, WIWIN6, WIN5	Sikorski et al. 2010, Collins and Widder 1966	Thermoprotei		
Wolinella succinogenes DSM 1740	MK- 8-MMK-	Colline and Eemandez 1984, Hein et al. 2017	Thermoprotecles		
Nautilialos	WINE, O-WININE	Collins and remandez 1304, Hein et al. 2017	Thermoproteaceae		
Nautiliaceae			Thermonroteus teney Kra 1	MMKe MMKe MKe MKe MMKe	Thurl et al. 1985
Cetia pacifica DSM 27783	MK ^a MMK ^a	Grosche et al. 2015	Desulfurococcales	Winte, Wintes, Wines, Wines, Winter,	man et al. 1900
Betanroteobacteria	(iii)(), iiiiii)()	Croscile of al. 2010	Pyrodictiaceae		
Burkholderiales			1 froutotaceae	DMKe, MKe, DMKs, MTKe, MKs,	
Sutterellaceae			Pyrolobus fumarii 1A	MMKs	Elling et al. 2016
Mesosutterella multiformis DSM 106860	MMKs. MKs	Sakamoto et al. 2018	Desulfurococcaceae		
Parasutterella excrementihominis YIT 11859	MMKs. MKs	Nagai et al. 2009		DMKs, MKs, DMKs, MTKs, MKs,	
Parasutterella secunda YIT 12071	MMKs, MKs	Morotomi et al. 2011	Aeropyrum pernix K1	MMKs	Elling et al. 2016
Sutterella faecalis KGMB03119	MMKs	Oh et al. 2020	Ignicoccus hospitalis KIN4/1	MMK6, MK6, MMK5, MK5, MK7	Elling et al. 2016
Sutterella megalosphaeroides DSM 106861	MMKs, MKs	Sakamoto et al. 2018	Eurvarchaeota		
Sutterella parvirubra YIT 11816	MMKs	Morotomi et al. 2011	Thermoplasmata		
Sutterella stercoricanis DSM 17807	MMK ₅ , MK ₅	Morotomi et al. 2011	Thermoplasmatales		
Sutterella wadsworthensis DSM 14016	MMK5, MK5	Morotomi et al. 2011	Thermoplasmataceae		
Gammaproteobacteria			Thermoplasma acidophilum 122-1B2	MK ₇ , MMK ₇ , various MTKs	Elling et al. 2016
Alteromonadales			Thermoplasma acidophilum HO-62	8-MMK7, MK7	Collins 1985 and Shimada et al. 2001
Shewanellaceae			Halobacteria		
Shewanella aestuarii JCM 17801	MMK ₇ , MK ₇	HY et al. 2013	Natrialbales		
Shewanella algae JCM 21037	MK ₇ , MMK ₇	Bozal et al. 2002	Natrialbaceae		
Shewanella arctica KCTC 23109	MK ₇ , MMK ₇	Hwang et al. 2019	Natropobacterium gregonyi SP 2	MK ₈ , MK ₈ (VIII-H ₂), MMK ₈ , MMK ₈	Collins and Tindall 1987
Shewanella baltica OS 185	MMK7, MK7	Bozal et al. 2002	Han on obdition and grogory or 2	(VIII-H ₂), DMMK ₈ ,DMMK ₈ (VIII-H ₂)	Sound and Findan 1997
Shewanella colwelliana ATCC 39565	MK ₇ , MMK ₇	Frolova et al. 2005	Eukaryota		
Shewanella fidelis ATCC BAA-318	MK7, MMK7	Frolova et al. 2005	Evosea		
Shewanella frigidimarina NCIMB 400	MK7, MMK7	Frolova et al. 2005	Archamoebae		
Shewanella gelidii RZB5-4	MK7, MMK7	Wang et al. 2016	Mastigamoebida		
Shewanella litoralis JCM 32306	MK7, MK8, MMK7	Yun et al. 2018	Entamoebidae		
Shewanella maritima JCM 33294	MK7, MMK7	Bae et al. 2019	Entamoeba histolytica HM-1:IMSS	MMK ₇	Thurl et al. 1985
Shewanella oneidensis MR-1	MK7, MMK7	Venkateswaran et al. 1999			
Shewanella pacifica KMM 3597	MK7, MMK7	Frolova et al. 2005			
Shewanella profunda DSM 157900	MMK7, MK7, MMK8, MK8	Toffin et al. 2004			
Shewanella psychromarinicola JCM 32090	MK7, MMK7	Hwang et al. 2019			
Shewanella putrefaciens IAM 12079	MK7, 8-MMK7	Itoh et al. 1985, Akagawa-Matsushita et al. 1992			
Shewanella saliphila JCM 32304	MK7, MMK7, MK8, MMK8	Yun et al. 2018			
Shewanella ulleungensis JCM 32305	MK7, MMK7, MMK8, MK9	Yun et al. 2018			
Shewanella vesiculosa M7	MK7, MMK7	Bozal et al. 2009			

 Table S3.
 Nucleotide primers used in this study.

Primer	Sequence 5'→3'
PS_ubiE_F	GTATGTTCAGGCGAACGCTGGTTTTAGAGCTAGAAATAGCAAG
PS_ubiE_R	CAGCGTTCGCCTGAACATACGTGCTCAGTATCTCTATCACTGA
CPEC2F	CGGCGTCACACTTTGCTAT
gamR	TTTATAACCTCCTTAGAGCTCGA
ubiE_FFA_F	AGCCGAATGATGAAGCTTATCAAC
ubiE_FFA_R	GGTTTAAAAGGCATTTCCGGTCTCCTGCTCAATGCCTGCTCATCAAAAAATTGTTCC
ubiE_RFA_F	GGAACAATTTTTTGATGAGCAGGCATTGAGCAGGAGACCGGAAATGCCTTTTAAACC
ubiE_RFA_R	TGGCGTTCGCTGAACACCAGAATC
Ferri_975_I_F	GGAGATATACATATGGCTCAGGTTCGCTTTC
Ferri_975_I_R	GCTCCATGCACTGGCGGCCTGCACCTCGATG
Ferri_975_O_F	GTGCAGGCCGCCAGTGCATGGAGCCATCCG
Ferri_975_O_R	AACCTGAGCCATATGTATATCTCCTTCTTATAC
Ferri_647_I_F	AAGGAGATATACATATGTCATTAGCCGAACGC
Ferri_647_I_R	GGATGGCTCCATGCACTCATGTCGGACGCTTTG
Ferri_647_O_F	TCCGACATGAGTGCATGGAGCCATCCGCAGTTC
Ferri_647_O_R	TTCGGCTAATGACATATGTATATCTCCTTC
Colli_032_I_F	GAAGGAGATATACATATGCTATCCGAACGCCTACTTTC
Colli_032_I_R	GCTCCATGCACTGAACATCTTGCGCTCGCACTC
Colli_032_O_F	CGCAAGATGTTCAGTGCATGGAGCCATCCGCAGTTC
Colli_032_O_R	GCGTTCGGATAGCATATGTATATCTCCTTC
Colli_643_I_F	ATAAGAAGGAGATATACATATGCTTTCAGAAAGAATG
Colli_643_I_R	GCTCCATGCACTCTTCTGGGTGCCGTCGCCAAAGAGC
Colli_643_O_F	ACGGCACCCAGAAGAGTGCATGGAGCCATC
Colli_643_O_R	AGCATTCTTTCTGAAAGCATATGTATATCTCCTTCTTATAC

The primer pairs labelled Ferri (or Colli)_ xxx_I_F (or R) were used to amplify the (methyl)menaquinone methyltransferase genes, while the primer pairs Ferri (or Colli)_ xxx_O_F (or R) were used to amplify a suitable fragment of vector pACYCDuet-1.

Protein	Accession no.	Organism
Blm-Orf8	AAG02372.1	Streptomyces verticillus
C10P	ARK19493.1	Streptomyces zelensis
ChuW	WP_000993317.1	Escherichia coli
ChuW	ASJ24187.1	Laribacter hongkongensis
HemN	AAN83245.1	Escherichia coli
HutW	WP_080284587.1	Vibrio cholerae
HutW	AIC83437.1	Vibrio alginolyticus
Jaw5	WP_120753176.1	Streptomyces klenkii
MenK	WP_022738066.1	Adlercreutzia equolifaciens
MenK	WP_011074137.1	Shewanella oneidensis
MenK2	WP_022739874.1	Adlercreutzia equolifaciens
MqnK	CAE09279.1	Wolinella succinogenes
NocN	ADR01089.1	Nocardia sp. ATCC 202099
NosN	AQM75227.1	Streptomyces sp.
NosN	ACR48343.1	Streptomyces actuosus
PbtM2	AGY49586.1	Planobispora rosea
PbtM3	AGY49595.1	Planobispora rosea
Tbtl	ADG87272.1	Thermobispora bispora
Tlm-Orf11	ABL74954.1	Streptoalloteichus hindustanus
Tpdl	ACS83777.1	Nonomuraea sp. Bp3714-39
TpdL	ACS83774.1	Nonomuraea sp. WU8817
TpdU	ACS83765.1	Nonomuraea sp. WU8817
YtkT	WP_055490826.1	Streptomyces sp. TP-A0356
Zbm-Orf26	ACG60749.1	Streptomyces flavoviridis

 Table S4. Accession numbers of sequences used in Fig. 2.

SoMenK FmMenK WsMenK AeMenK2 CtMenK2 AeMenK CtMenK Fm0975	MSSVIQTLNGAIATPYQANITVPNWMLSSMERVMQYYVDKNLRLDTLSADIMPAPVE MSLAERALNNAAIHNAAEITTPKWMLSSMESLMQHYTKRHLKMDTRACD-AIPAPIE MAEMKKMELMEGEGFSSPSCLLPSLEGLEEIKPGMLATRIVNRAMRQASGKYLSLRPIDRDRLPAPRE MLSERMLTTVVRAMTDKTLTHPVPEG-ALPDPVP MLSERMLTGVIKTMTKHELAMEPTTET-HLPGFKP MLSERMLSKVVEACTANYLQLKPCDEAFMPSPNP MLSERLLSKTVGIGARQLFRSKGECARTLPAPEA MAQVRFPQLSQQALDYVMGGKIKSLLDLQQLSPGGYDLAELSG : : :	57 56 68 34 34 34 34 34 43
SoMenK FmMenK WsMenK AeMenK2 CtMenK2 AeMenK CtMenK Fm0975	GKKYMLYAHVPFCHTLCSYCTFHRFMFKEDKARAYFISLRKEMEMVKALGYDFESMYIGGGTTTVLEDEL GRKYTLYMHIPFCHTLCSFCTFHRFIFKEEKARAYFASLRQEMHMAKALGYDFEELYIGGGTTTVLVDEL GKHYLLYAHVPFCSTLCTYCTFNRFIFEEKARRYFRSLRQEMHMAKALGYDFEELYIGGGTTVLVDEL GRPYTLYVHVPFCERLCPYCSFNRFFYREQAARDYFQALCQEMAMLAAGYDFDESVYUGGGTPTVDIDEL NMKYMLYMHIPFCQRLCPYCSFNRFFYREDFARPYFANLRREMLMLKDLGYDFESVYUGGGTPTIMIDEL GQPYMLYMVPFCERLCPYCSFNRFFPREEIARPYFANLRREMLMLKDLGYDFDSVYIGGGTPTIMIDEL GHEYLLYVHIPFCDRLCPYCSFNRFFPREDAARPYFEALRRELKMIHDLGYDFDSVYIGGGTPTIMIDEL KRVPTLYIHIPFCHTLCRFCSFFRLKYDEAKAREYFKLLRQEVEILAQVGVQFDRLYIGGGTTTIIESEL LY H PFC *C C F * * YF R F G F Y GGGT **	127 126 138 104 104 104 104 113
SoMenK FmMenK WsMenK AeMenK2 CtMenK CtMenK Fm0975	ARTIEHAKTLFPSIKEVSCESDPQHLDSPGFKQLKGLVDRMSIGVQSFNDDILKMTDRLEKFGTGQQTFD AKTIELAKTLFPAIKQVSCESDPLHLTSTEFMQLHGLVDRLSVGVQSFDDDILARTDRLEKFGEPEVVFE CATIDLARELFP-LKEVSCESDPNNIDKETMAHLKGRVDRISVGVQSFDDDILKRVGRYEKFGGEETLS CETIDLARDLFH-VKEVNSETNPNHLIPEYLDKLHGRIQRLSVGVQSFDDDLLRQMDRYEKYGSGEIFE CETLDLARDLFS-IKEVSSETNPNHLTHPYLEKLKGRVQRLSVGVQSFDDDLLRQMDRYEKYGSQEIFE CETIDMARDLFS-IKEVSSETNPNHLTHEYLEKLKGRVQRLSVGVQSFDDDLLRQMDRYEKYGSQEILE ERTIDYMRELFPTIKEVSSETNPNHLTHEYLEKLKGRVQRSVQSFDDDLLRQMDRYEKYGSQEILE IETIELIKSRFD-IQEVSCESDPIYFENSNPLALKGLVDRFSIGIQSFDDEILKHSGRYEKFGSGDAIAD * * * * * * R & R S G Q*F L * * *	197 196 207 173 173 173 174 182
SoMenK FmMenK WsMenK AeMenK2 CtMenK2 AeMenK CtMenK Fm0975	FDKIMAAKELFPIINVDLIFGFRGQTDEVIQHDLDMASRLDPRQITTYPLMITHQTRKSVKGKL FEKLARAKENFPILNVDMIFGFDGQTTEVLAQDMATLRKLNPRQITTYPLMVSDLTKRHAATKIGTKANL LSKLQALMGALPVVNIDLIFNFPTQDEQUEKMLRRDLEIIKRLSPTQVTAYPLMSSPSVKSLIKRSIG FERIGEAAPYFESLNVDMIFNFFTQTEDILLSDCEKIALGCGOTFFSPLYQSHATTRKMLQVLG- FERIGEAPYFESLNVDMIFNFFSQTEEVLRRDIELIKECGCOTFFSPLYQSHATTRKMLDTLG- LERIQEASPYFISMNADMIFNFFSQTEDTLIRDIEMVASGASQTFFYPLMASPSVQRSLAATVG- VBRIQSVHDMPDTPNVDMIFNFFGQTEMVSRDIDVFRTTGANQITYYPLMASPGSEKKMAGKL * * * * * Q T YPL	259 264 270 236 236 236 238 244
SoMenK FmMenK WsMenK AeMenK2 CtMenK CtMenK Fm0975	AAPQADMANQYRQILNSLNGQYNQLSAWAFGKANDEGFDEYVIDYDEYLGVGSGS ANINQDIRKDYALILNSLRGDYEQLTAWSFGKSNDEGFDEYVVNADDYLGLGSGS DISLDKEATLYRVILEELLGGYNQISSWAFSKKGDDIDEYVVNHDEYVGIGSGS RMDYDKERRFYHILDEILAGGDAPFFERRTLWTFNRLGMDLHACGEVPVDEFGVSYEEVAIGSGS DPNYTREYEYYKLDHELAGGSDPAFERRTVWTFNRKGMDLHACGEVPVDEFGVSYEEYPAIGSGS KVDYNRERRFYEIICDLLLGDLPGGQPGLFELGSAWTFNRRGTGAAG-EDAMIDEYVVDYEEYPAIGSGG QVDYNLEKDLYNLFDKMTAPVEKGGVGFYATDVYTFAKDRDAMIDEYVVDYEEYPAIGSGG AGNPADLLGLYQTGRNVLEPGYEREYAWTYRRATGLPVEHDYVLDGEOVGIGCGA * * *	314 319 325 302 302 305 300 300
SoMenK FmMenK WsMenK AeMenK2 CtMenK CtMenK Fm0975	FSFLNDTLYVNTFSLRKYQERIAAGKMGVEQQKNYNKKDVMQYRFLLGMFSGRLSRKYFRETFGVNLDTA FSFLHDNLYVNSFSLRRYNEKIANGKMGVESSKAYDRKAVLQYRFLLSMFGGRLSKRYFKEGYDANLYTA FSFLDGVLYINTFSLKEYATRIESGKMGLSRARKYGRLSQMQYRLMYGLFGGGVHKESFSRQFKMPIEVG ITHLGDNLFVNTFNLEEYGELVRAGVTPLLGKTDLPRRDLMRYKFLLQLYSLRFDKHEFERDFGVSVERG VTHLDGTIYVNTFSIREYNEAIESGRMSLMGKTKMGKRDLMRYKFLQLYSLRFDKHEFERDFGVSVERG ITYLGENLYVNTFSIREYNEAIESGRMSLMGKTKNGKRDLMRYKFMQELYALRLDKNRFKRDFGVSVERG YSFLGDDIYTNDSSLDGYCRRIEEGTMSVASHISMGHANGKRYRMGRELFGLRLDNRAWRRDFGKYIQYD FGRIGNKFYLSSFNLDDYARRVKAGELSCTSHKDLSTPLMRRYHLLMMMVKGHLPNSVFEKLYGRSLYTA NF Y * *	384 389 395 372 372 375 370 370
SoMenK FmMenK WsMenK AeMenK2 CtMenK CtMenK Fm0975	LFKEMTSMKLIGAIKNDPTDPDNLIITDNGKMMGLLMMKEFYAGMDNVRAQLRKPLKPCDM LTKEMAFMHAIGGLETDPNDADKLQATPNGLMMGLLMMKNFYTGMDNVRAELRRPLKASDM LFKELLFLRCAGAIREKEGVLYPTLKGKYLFLSMMKEFYIGMDTVREESRARLSSEDM LPVEMAFMRANGAFATDDADELTLTPAGRYLTVVLYRQYLAGLNNLREQARALPGDERDLLFGDGTE LPVEMAFMRANGAFATDDADELTLTTKGRYYTLVMQRQFLSGLNELRDQARAALTGPEHDLLFGDGTQ LPVEMGFMRACGAFATDNADELTLTPKGRYLVVVMMRQFFIGVNNLRDQARAALTGEEHDLLFGDGKD MPVEYGYLAANGAFATDNADELTLTRKGRYLVLVMMRQFFIGWNLRDQARAALTGEERELIFGDGKD MPVEYGYLAANGAFDKNNADELTLTRKGRYLVLVMMRQFFIGMNTERDRLRTLLPECERKMFADSAAK LPAEMAFHRLHGAIVPSAC-GDGYRTPTGEFVALKMFSGFLAGMDWLREQAGSAAEEAQIARGQAIEVQ * * * * * * * * *	445 450 453 440 440 443 438 439
SoMenK FmMenK WsMenK AeMenK2 CtMenK2 AeMenK CtMenK Fm0975	445 450 453 K	

Fig. S1. Alignment of selected MqnK/MenK/MenK2 primary structures. The N-terminal trip-wire (grey), the catalytic domain (green), the linker (orange) and the C-terminal HemN domain (blue) are highlighted. Cluster-specific motifs denoted in Table 1 are highlighted in red. *, strictly conserved residue.



Fig. S2. (**A**,**B**) Immunodetection of Strep-tagged MenK and MenK2 homologues from *C. tanakaei* and *F. marina* using a Strep-Tactin-HRP conjugate (IBA Lifesciences). The proteins were produced in *Escherichia coli* BL21(DE3) (**A**) or *E. coli* BL21(DE3) $\Delta ubiE$ (**B**). 50 µg of total cell protein was applied to each lane. M, Color Prestained Protein Standard (NEB). *E. coli* BL21(DE3) or *E. coli* BL21(DE3) $\Delta ubiE$ served as controls. Predicted protein masses are 52.1 kDa (*Ct*MenK2), 52.3 kDa (*Fm*975), 51.2 kDa (*Ct*MenK) and 50.3 (*Fm*MenK). (**C**) HPLC chromatogram of purified quinones from *E. coli Fm*975.



Fig. S3. Parts of 500 MHz ¹H-NMR spectra of MK₈, 7-MMK₈, 8-MMK₈, 5,8-DMMK₈ and 7,8-DMMK₈ (from top to bottom). All spectra were calibrated at the signal of residual protons in CDCl₃ at 7.20 ppm. Asterisks mark small amounts of impurities. The signal assignments are given in the top line.





Fig. S4. Mass spectra of DMK $_8$, 7-MDMK $_8$, 8-MDMK $_8$, 5,8-DMDMK $_8$ and 5,8-DMMK $_8$. Insets show simulated isotopic distribution patterns.



Fig. S5. Mass spectra of DMK₇, 7-MDMK₇, 8-MDMK₇ and 5,8-DMDMK₇. Insets show simulated isotopic distribution patterns.



	MK ₈	7-MMK ₈	8-MMK ₈	5,8-DMMK ₈	7,8-DMMK ₈
1	-	-	-	-	-
2	-	-	-	-	-
3	-	-	-	-	-
4	-	-	-	-	-
5	7.61	7.89	7.93	-	7.84
6	8.02	7.39	7.45	7.26	7.37
7	8.02	-	7.39	7.26	-
8	7.61	7.80	-	-	-
9	-	-	-	-	-
10	-	-	-	-	-
11	-	2.40	2.67	2.62	2.35
11'	-	-	-	2.62	2.59
12	2.13	2.10	2.08	2.06	2.09
13	3.31	3.28	3.26	3.25	3.26
14	4.96	4.97	4.94	4.97	4.97
15	-	-	-	-	-
16	1.73	1.71	1.70	1.71	1.72
17	1.92	1.88	1.89	1.91	1.91
18	2.00	2.00	1.97	2.00	1.98
19	5.05	5.03	5.03	5.06	5.03
20	-	-	-	-	-
21	1.53	1.52	1.51	1.53	1.53
22	1.92	1.9	1.89	1.88	1.88
23	1.99	2.0	1.97	1.99	1.99
24	5.00	4.94	4.98	5.00	5.00
25	-	-	-	-	-
26	1.53	1.52	1.52	1.54	1.52
27	1.62	1.60	1.60	1.62	1.61

Fig S6. ¹H chemical shifts of spectra of MK₈, 7-MMK₈, 8-MMK₈, 5,8-DMMK₈ and 7,8-DMMK₈ calibrated at the ¹H signal of residual protons in CDCl₃ at 7.20 ppm.



	MK ₈	7-MMK ₈	8-MMK ₈	5,8-DMMK ₈	7,8-DMMK ₈
1	185.4	185.7	186.4	188.3	188.3
2	143.3	143.0	143.5	142.8	143.9
3	146.1	146.0	143.6	145.8	145.1
4	184.4	184,4	183.9	187.4	184,7
5	133.6	126,3	124.2	139.1	124,6
6	126.6	133.9	131.4	136.6	134.2
7	126.6	144.0	136.2	136.6	144.2
8	133.6	126.2	139.7	139.1	139.1
9	133.1	132.0	128.9	131.5	130.5
10	133.1	130.2	132.7	136.6	132.0
11	-	21.6	21.8	23.3	21.4
11'	-	-	-	23.3	17.2
12	13.0	12.7	11.9	12.9	13.1
13	26.5	26.8	24.7	25.8	25.6
14	119.6	118.9	118.3	119.9	119.3
15	137.5	137.3	136.3	137.4	137.3
16	17.2	15.8	15.4	16.2	16.4
17	40.1	39.6	38.6	39.7	39.7
18	27.0	26.5	24.5	26.7	26.6
19	124.7	124.2	123.5	124.5	124.2
20	134.7	134.9	133.7	135.1	134.3
21	16.6	15.8	15.1	16.2	16.0
22	39.7	39.6	38.5	39.8	39.7
23	25.8	27.1	24.7	26.9	26.4
24	124.5	124.3	123.3	124.5	124.4
25	131.1	131.1	130.1	131.3	131.2
26	17.6	17.6	16.5	17.9	17.7
27	26.0	24.3	24.7	25.9	25.5

Fig S7. ¹³C chemical shifts of spectra of MK₈, 7-MMK₈, 8-MMK₈, 5,8-DMMK₈ and 7,8-DMMK₈ calibrated at the ¹³C signal of CDCl₃ at 77.20 ppm.



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