

Table S1. Metadata and ID of the 100 Elizabethkingia NCBI and SRA reference genomes used in this study.

Reference accession	Elizabethkingia species	Strain	Year	Country	Host	Disease	Publication
GCA_000447375.1	<i>anophelis</i>	502	2012	UK: Birmingham	<i>H. sapiens</i> wound swab		Quick J et al., "Draft Genome Sequence of Elizabethkingia meningoseptica Isolated from a Traumatic Wound.", <i>Genome Announc</i> , 2014 May 8;2(3)
GCA_002022065.1	<i>anophelis</i>	3375	1957	USA: South Carolina	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_003293835.1	<i>anophelis</i>	6499925	2017	USA	<i>H. sapiens</i> blood		walter reed army institute of research
GCA_003293825.1	<i>anophelis</i>	40313151	2016	USA	<i>H. sapiens</i> blood		walter reed army institute of research
GCA_002023235.2	<i>anophelis</i>	E6809	1979	USA: California	<i>H. sapiens</i> blood		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_001482795.1	<i>anophelis</i>	12012-2 PRCM	2009	China: Quanzhou	<i>H. sapiens</i> sputum 82yo M	Respiratory infection	
SAMEA4026799	<i>anophelis</i>	AmMS250	1994	USA	<i>H. sapiens</i>		INSTITUT PASTEUR
GCA_000240095.3	<i>anophelis</i>	Ag1	2010	USA: New Mexico	<i>A. gambiae</i> gut		Kukutla P et al., "Draft Genome Sequences of Elizabethkingia anophelis Strains R26T and Ag1 from the Midgut of the Malaria Mosquito Anopheles gambiae.", <i>Genome Announc</i> , 2013 Dec 5;1(6)
GCA_001051975.1	<i>anophelis</i>	As1	2013	USA	whole mosquito body		Raygoza Garay JA et al., "Genome Sequence of Elizabethkingia anophelis Strain EaAs1, Isolated from the Asian Malaria Mosquito Anopheles stephensi.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_000735205.1	<i>anophelis</i>	B2D	2013	Malaysia	Dental Plaque		
GCA_900157025.1	<i>anophelis</i>	CIP111046	2018				
GCA_900156995.1	<i>anophelis</i>	CIP111067	2016				
GCA_900156985.1	<i>anophelis</i>	CIP60.58	2017				
SAMEA4026797	<i>anophelis</i>	8707	1962	USA			
GCA_002023325.1	<i>anophelis</i>	CSID_3000516074	2016	USA: Illinois	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_002023425.1	<i>anophelis</i>	CSID_3000516810	2016	USA: Arizona	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_002023565.1	<i>anophelis</i>	CSID_3000516978	2016	USA: California	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)

GCA_002023625.1	<i>anophelis</i>	CSID_3000517066	2016	USA: Texas	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_001618505.2	<i>anophelis</i>	CSID_3000521207	2016	USA: Wisconsin	<i>H. sapiens</i>		Nicholson AC et al., "Complete Genome Sequences of Four Strains from the 2015-2016 Elizabethkingia anophelis Outbreak.", <i>Genome Announc</i> , 2016 Jun 16;4(3)
GCA_002995695.1	<i>anophelis</i>	CSID_3000653323	2016	USA: Tennessee	<i>H. sapiens</i> blood		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_002995725.1	<i>anophelis</i>	CSID_3000726811	2017	USA: Minnesota	<i>H. sapiens</i> Urine		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_001596175.2	<i>anophelis</i>	CSID_3015183678	2016	USA: Wisconsin	<i>H. sapiens</i>		Nicholson AC et al., "Complete Genome Sequences of Four Strains from the 2015-2016 Elizabethkingia anophelis Outbreak.", <i>Genome Announc</i> , 2016 Jun 16;4(3)
GCA_002023645.1	<i>anophelis</i>	CSID_3015183679	2016	USA: Wisconsin	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_002023695.1	<i>anophelis</i>	CSID_3015183680	2016	USA: Wisconsin	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_001618545.2	<i>anophelis</i>	CSID_3015183681	2016	USA: Wisconsin	<i>H. sapiens</i>		Nicholson AC et al., "Complete Genome Sequences of Four Strains from the 2015-2016 Elizabethkingia anophelis Outbreak.", <i>Genome Announc</i> , 2016 Jun 16;4(3)
GCA_001618465.2	<i>anophelis</i>	CSID_3015183684	2016	USA: Wisconsin	<i>H. sapiens</i> blood		Nicholson AC et al., "Complete Genome Sequences of Four Strains from the 2015-2016 Elizabethkingia anophelis Outbreak.", <i>Genome Announc</i> , 2016 Jun 16;4(3)
GCA_002023705.1	<i>anophelis</i>	CSID_3015183686	2016	USA: Wisconsin	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_001703835.1	<i>anophelis</i>	EM361-97	2010	Taiwan: Kaohsiung	<i>H. sapiens</i> blood	Lung cancer (47yo male)	Lin JN et al., "Draft Genome Sequence of Elizabethkingia anophelis Strain EM361-97 Isolated from the Blood of a Cancer Patient.", <i>Genome Announc</i> , 2016 Oct 27;4(5)
GCA_002022085.1	<i>anophelis</i>	F3201	1982	Kuwait	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_002024825.1	<i>anophelis</i>	F3543	1982	USA: Florida	<i>H. sapiens</i> CFS		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", <i>Genome Announc</i> , 2016 Mar 10;4(2)
GCA_002951455.1	<i>anophelis</i>	FDAARGOS_134	2014	USA: Washington DC	Imo M tracheal aspirate	Trachitis	FDA Grant
GCA_002277995.2	<i>anophelis</i>	FDAARGOS_198		Sweden	<i>H. sapiens</i> blood	Infection?	FDA Grant
GCA_001011675.1	<i>anophelis</i>	FMS-007	2015	China	<i>H. sapiens</i> sputum		Sun G et al., "Complete Genome Sequence of Elizabethkingia meningoseptica, Isolated from a T-Cell

							Non-Hodgkin's Lymphoma Patient.", Genome Announc, 2015 Jun 25;3(3)
GCA_002022045.1	<i>anophelis</i>	JM-87	2011	USA: Atlanta	Zea mays (maise)	nil	Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_900156945.1	<i>anophelis</i>	LDVH-AR107	2004	France	Cyprinus carpio (Internal organs)		
GCA_000496055.1	<i>anophelis</i>	NUH11	2012	Singapore	Hospital sink	nil	Teo J et al., "First case of E anophelis outbreak in an intensive-care unit.", Lancet, 2013 Sep 7;382(9895):855-7
GCA_000496015.1	<i>anophelis</i>	NUH4	2012	Singapore	Hospital sink	nil	Teo J et al., "First case of E anophelis outbreak in an intensive-care unit.", Lancet, 2013 Sep 7;382(9895):855-6
GCA_000496035.1	<i>anophelis</i>	NUH6	2012	Singapore	Hospital sink	nil	Teo J et al., "First case of E anophelis outbreak in an intensive-care unit.", Lancet, 2013 Sep 7;382(9895):855-6
GCA_000495935.2	<i>anophelis</i>	NUHP1	2012	Singapore	<i>H. sapiens</i>	Cardio-thoracic ICU patient	Li Y et al., "Complete Genome Sequence and TranSouth Carolinariptomic Analysis of the Novel Pathogen Elizabethkingia anophelis in Response to Oxidative Stress.", Genome Biol Evol, 2015 May 26;7(6):1676-85
GCA_002843925.1	<i>anophelis</i>	OSUVM1	2016	USA: Oklahoma	Equine Stall	nil	
GCA_000689515.1	<i>anophelis</i>	Po0527107	2014				
GCA_000982575.1	<i>anophelis</i>	PW2806	2015				
GCA_002888615.1	<i>anophelis</i>	PW2810	2015				
GCA_002023665.2	<i>anophelis</i>	R26	2006	Sweden	Anopheles gambiae lab colony		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
SAMD00012202	<i>meningoseptica</i>	GTC_09686					Gifu University South Carolinahool of Medicine Pathogenic Bacterial Genetic Resorce Stock Center (GMGC); 2014-04-21
SAMD00009502	<i>meningoseptica</i>	GTC_10754					Gifu University South Carolinahool of Medicine Pathogenic Bacterial Genetic Resorce Stock Center (GMGC); 2014-04-21
SAMEA104652859	<i>meningoseptica</i>	ERR2719365					Wellcome Sanger Institute
GCA_900156975.1	<i>meningoseptica</i>	58-80	1980	Israel	<i>H. sapiens</i> (tracheal exudate)		
GCA_002002525.1	<i>meningoseptica</i>	61421 PRCM	2006	China, Quanzhou	<i>H. sapiens</i>	Intracranial infection	
GCA_000401415.1	<i>meningoseptica</i>	ATCC 13253					Matyi SA et al., "Draft Genome Sequences of Elizabethkingia meningoseptica.", Genome Announc, 2013 Jul 11;1(4)
GCA_900092105.1	<i>meningoseptica</i>	CCUG 214					
GCA_900156965.1	<i>meningoseptica</i>	CIP111048					
GCA_002023305.1	<i>meningoseptica</i>	CSID_3000515919	2016	USA: Minnesota	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023465.1	<i>meningoseptica</i>	CSID_3000516359	2016	USA: Wisconsin	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies

GCA_002023435.1	<i>meningoseptica</i>	CSID_3000516465	2016	USA: Michigan	<i>H. sapiens</i>		Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023505.1	<i>meningoseptica</i>	CSID_3000516535	2016	USA: Florida	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023585.1	<i>meningoseptica</i>	CSID_3000516977	2016	USA: Texas	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_001718075.1	<i>meningoseptica</i>	EM1	2016		<i>H. sapiens</i> (blood)	Bloodstream infection	
GCA_001853405.1	<i>meningoseptica</i>	EM2	2016	USA: Michigan	<i>H. sapiens</i> (tracheal)	Infection	
GCA_001853425.1	<i>meningoseptica</i>	EM3	2016		<i>H. sapiens</i> (tracheal)	Infection	
GCA_002023055.1	<i>meningoseptica</i>	G4076		England	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002022145.1	<i>meningoseptica</i>	G4120	1983	France	<i>H. sapiens</i> (urine)		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_001521755.1	<i>meningoseptica</i>	KC1913	1949	USA: Massachusetts	<i>H. sapiens</i> (CSF)		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_000367325.1	<i>meningoseptica</i>	NBRC 12535					Matyi SA et al., "Draft Genome Sequences of Elizabethkingia meningoseptica.", Genome Announc, 2013 Jul 11;1(4)
GCA_900475375.1	<i>meningoseptica</i>	NCTC10016	1958		<i>H. sapiens</i> (infant CSF)		
GCA_900447345.1	<i>meningoseptica</i>	NCTC10586	1956	USA: South Carolina	<i>H. sapiens</i> (newborn, spinal fluid)		
GCA_900447425.1	<i>meningoseptica</i>	NCTC10588	2017				
GCA_900447195.1	<i>meningoseptica</i>	NCTC11305	1978		<i>H. sapiens</i> (tracheal exudate)		
GCA_900143665.1	<i>meningoseptica</i>	NV2016			<i>H. sapiens</i> (rectal swab)	Aortic valve replacement surgery	
GCA_002294465.1	<i>meningoseptica</i>	UBA907		USA: New York	Wood		Parks DH et al., "Recovery of nearly 8,000 metagenome-assembled genomes substantially expands the tree of life.", Nat Microbiol, 2017 Sep 11;2(11):1533-1542
GCA_000955665.1	<i>miricola</i>	BM10	2009	South Korea: Seoul	Reticulitermes (hindgut)	speratus nil	Lee D et al., "Complete Genome Sequence of Elizabethkingia sp. BM10, a Symbiotic Bacterium of the Wood-Feeding Termite Reticulitermes speratus KMT1.", Genome Announc, 2015 Oct 8;3(5)

GCA_002557775.1	<i>miricola</i>	EM798-26	2015	Taiwan: Kaohsiung	<i>H. sapiens</i> (blood)	Lymphoma (81 yo M)	
GCA_000769445.1	<i>miricola</i>	ATCC 33958	1982	USA	contaminated commercial preparation of carboxipeptidase A		Matyi SA et al., "Draft Genome Sequence of Strain ATCC 33958, Reported To Be Elizabethkingia miricola.", Genome Announc, 2015 Jul 23;3(4)
GCA_001483145.1	<i>miricola</i>	EM_CHUV	2014	Switzerland	<i>H. sapiens</i> (endotracheal sections)	Pneumonia	
GCA_001675285.1	<i>miricola</i>	GTC_862					Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomespecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023335.1	<i>miricola</i>	CSID_3000517120	2016	USA: Michigan	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomespecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023475.1	<i>miricola</i>	G4121	1982	Sweden	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomespecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
NZ_MCJF00000000	<i>miricola</i>	HvH-WGS333	2015	Denmark: Frederiksberg			Eriksen, Helle Brander et al. "Determination of Elizabethkingia Diversity by MALDI-TOF Mass Spectrometry and Whole-Genome Sequencing." Emerging infectious diseases vol. 23,2 (2017): 320-323.
GCA_002023515.1	<i>miricola</i>	CSID_3000516464	2016	USA: Michigan	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomespecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023575.1	<i>miricola</i>	CSID_3000516998	2016	USA: South Carolina	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomespecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023685.1	<i>miricola</i>	G4074		England	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomespecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002738605.1	<i>miricola</i>	FL160902	2016	China: Hunan	Frog from farming pond	Meningitis	
GCA_003014895.1	<i>miricola</i>	QZY.EM	2016	China: Sichuan	Pelophylax nigromaculatus (brain)		
GCA_003298875.1	<i>miricola</i>	6012926	2015	USA	<i>H. sapiens</i> (blood)		
GCA_900092045.1	<i>miricola</i>	KCTC 12492					
GCA_900157035.1	<i>miricola</i>	LDVH-337.01	2002	France	<i>Xenopus laevi</i> (spleen)		
GCA_001521745.1	<i>miricola</i>	G4071	1978	France: Strasbourg	<i>H. sapiens</i> (tracheal exudate)		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomespecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_900157015.1	<i>miricola</i>	CIP111047					INSTITUT PASTEUR
SAMEA50780668	<i>miricola</i>	ERS1505822					INSTITUT PASTEUR
GCA_002023775.1	<i>bruuniana</i>	G0146		England	<i>H. sapiens</i>		Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomespecies

GCA_002023765.1	<i>bruuniana</i>	CSID_3000516589	2016	USA: Michigan	<i>H. sapiens</i>	Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023545.1	<i>bruuniana</i>	CSID_3015183685	2016	USA: Wisconsin	<i>H. sapiens</i>	Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023205.1	<i>bruuniana</i>	G0153		Ireland	<i>H. sapiens</i> blood	Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023385.1	<i>occulta</i>	F8124			<i>H. sapiens</i>	Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023715.1	<i>occulta</i>	G4070	1977	Australia: Melbourne	<i>H. sapiens</i> sputum	Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023365.1	<i>ursingii</i>	C1558			<i>H. sapiens</i>	Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002023405.1	<i>ursingii</i>	CSID_3000516135	2016	USA: Wisconsin	<i>H. sapiens</i>	Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_002022125.1	<i>ursingii</i>	G4123	1982	Denmark	<i>H. sapiens</i>	Nicholson AC et al., "Draft Genome Sequences of Strains Representing Each of the Elizabethkingia Genomospecies Previously Determined by DNA-DNA Hybridization.", Genome Announc, 2016 Mar 10;4(2)
GCA_003053575.1	Species	YR191	2017			DOE Joint Genome Institute
GCA_003058195.1	Species	YR214				DOE Joint Genome Institute

Table S2: SPAdes and prokka genome assembly and annotation statistics of Australian clinical isolates analysed in this study.

Isolate ID	<i>Elizabethkingia</i> Species	Genome Size (Mbp)	No. of Contigs	No. of CDs	Sample accession number
EkQ1	<i>miricola</i>	4.08	72	3738	SRS5502595
EkQ3	<i>anophelis</i>	4.12	47	3789	SRS5502596
EkQ4	<i>meningoseptica</i>	3.97	97	3573	SRS5502607
EkQ5	<i>anophelis</i>	3.86	86	3553	SRS5502610
EkQ6	<i>anophelis</i>	4.27	158	3893	SRS5502611
EkQ7	<i>anophelis</i>	4.05	94	3742	SRS5502612
EkQ8	<i>anophelis</i>	3.96	68	3612	SRS5502613
EkQ10	<i>miricola</i>	4.20	106	3868	SRS5502614
EkQ11	<i>bruuniana</i>	4.39	83	4118	SRS5502615
EkQ12	<i>meningoseptica</i>	3.97	97	3571	SRS5502616
EkQ13	<i>miricola</i>	4.18	124	3883	SRS5502597
EkQ15	<i>anophelis</i>	4.18	144	3808	SRS5502598
EkQ16	<i>anophelis</i>	3.95	50	3645	SRS5502599
EkQ17	<i>anophelis</i>	3.88	85	3556	SRS5502600
EkM1	<i>anophelis</i>	3.92	99	3577	SRS5502601
EkM2	<i>anophelis</i>	3.92	86	3577	SRS5502602
EkM3	<i>anophelis</i>	4.01	91	3681	SRS5502603
EkS1	<i>anophelis</i>	4.04	103	3690	SRS5502604
EkS2	<i>anophelis</i>	3.36	101	3660	SRS5502605
EkS3	<i>anophelis</i>	3.97	101	3667	SRS5502606
EkS4	<i>anophelis</i>	3.94	79	3675	SRS5502608
EkS5	<i>anophelis</i>	4.28	87	3981	SRS5502609

Table S3. dN/dS ratios of clonal *Elizabethkingia anophelis* identified from Australian clinical and environmental isolates

Positive selection				
	EkQ5	EK2	EK6	EkQ17
EkQ5				
EK2	n/c			
EK6	1.000	n/c		
EkQ17	1.000	1.000	0.154	
Purifying selection				
	EkQ5	EK2	EK6	EkQ17
EkQ5				
EK2	n/c			
EK6	0.121	n/c		
EkQ17	0.198	0.07	1	
Neutral selection				
	EkQ5	EK2	EK6	EkQ17
EkQ5				
EK2	n/c			
EK6	0.243	n/c		
EkQ17	0.396	0.137	0.307	

The probability of rejecting the null hypothesis of strict-neutrality ($dN = dS$) in favor of the alternative hypothesis ($dN > dS$) (below diagonal) is shown. Values of P less than 0.05 are considered significant at the 5% level and are highlighted. dS and dN are the numbers of synonymous and nonsynonymous substitutions per site, respectively. The variance of the difference was computed using the analytical method. Analyses were conducted using the Nei-Gojobori method [1]. Evolutionary analyses were conducted in MEGA X [2]. The presence of n/c in the results denotes cases in which it was not possible to estimate evolutionary distances.

1. Nei M. and Gojobori T. (1986). Simple methods for estimating the numbers of synonymous and nonsynonymous nucleotide substitutions. *Molecular Biology and Evolution* 3:418-426.
2. Kumar S., Stecher G., Li M., Knyaz C., and Tamura K. (2018). MEGA X: Molecular Evolutionary Genetics Analysis across computing platforms. *Molecular Biology and Evolution* 35:1547-1549.

Table S4. Minimum inhibitory concentration data derived from broth microdilution testing of the 16 Australian *Elizabethkingia anophelis* clinical isolates against 39 clinically relevant antimicrobials. White cells represent the range of concentration tested for each antimicrobial. EUCAST and CLSI breakpoints are shown on the right where available. Blue and yellow cells indicate no breakpoint is currently available for this antimicrobial.

Table S5. Minimum inhibitory concentration data derived from broth microdilution testing of the 2 *Elizabethkingia meningoseptica* (blue) and 3 *Elizabethkingia miricola* (orange) Australian clinical isolates against 39 clinically relevant antimicrobials. White cells represent the range of concentration tested for each antimicrobial. EUCAST and CLSI breakpoints are shown on the right where available. Blue and yellow cells indicate no breakpoint is currently available for this antimicrobial.

