

404 TABLE 1. *Burkholderia* spp. genomic sequences used to generate signatures.

405

406	Species	Strain	GenBank Reference
407	<i>B. pseudomallei</i>	K96243	BX571965, BX571966
408		1710b	CP000123, CP000125
409		S13	AAHW00000000
410		1655	AAHR00000000
411		Pasteur	AAHV00000000
412		406e	AAMM00000000
413	<i>B. mallei</i>	ATCC 23344	CP000010, CP000011
414		10399	AAHN00000000
415		2002721280	AANX00000000
416	<i>B. ambifaria</i>	LMG 19182, AMMD	CP000440, CP000441, CP000442
417	<i>B. vietnamiensis</i>	G4	CP000614, CP000615, CP000616
418	<i>B. thailandensis</i>	E264	AACX00000000

419 TABLE 2. *Burkholderia* genomic DNA used for assay evaluation.

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421	Species	Strain	Repository ID ¹	Source	Geographic Origin	Year Isolated	Genome Sequenced
422	<i>B. pseudomallei</i>	China 3	BEI NR-2536	human	Burma	unknown	No
423		S397	BEI NR-2537	monkey	Singapore	1935	No
424		286	BEI NR-2538	human	Louisiana, USA	1953	No
425		S13	BEI NR-8217	unknown	unknown	unknown	Yes
426		1710b	BEI NR-8219	unknown	unknown	unknown	Yes
427		K96243	BEI NR-9320	human	Thailand	1996	Yes
428	<i>B. mallei</i>	China 5	BEI NR-2533	horse	China	1942	No
429		NCTC 10230	BEI NR-2534	horse	Hungry	1961	No
430		ATCC 23344	BEI NR-2535	human	Burma	1944	Yes
431	<i>B. ambifaria</i>		ATCC BAA-244	soil	Wisconsin, USA	1985	Yes
432	<i>B. vietnamiensis</i>		ATCC BAA-248	soil	Vietnam	unknown	No
433	<i>B. thailandensis</i>		ATCC 700388, E264	soil	Thailand	1994	Yes

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435 ¹ BEI = Biodefense and Emerging Infections Research Resources Repository (<http://www.beiresources.org/>). ATCC = American Type
 436 Culture Collection (<http://www.atcc.org/>)

437 TABLE 3. Summary of 20-mer signature chains.

438	Signature chain	Number of Signatures Found in		
439		both <i>B. pseudomallei</i>	<i>B. pseudomallei</i> only	<i>B. mallei</i> only
440	length (bp)	and <i>B. mallei</i>		
441	20-98	196,297	44,626	11,723
442	99-149	1,052	525	17
443	150-198	131	98	3
444	≥ 199	58	30	5
445	Total	197,538	45,279	11,748

446 TABLE 4. Results of duplex assay validation. Ct values are shown for fluorescence measurements in the FAM channel (*B.*
 447 *pseudomallei*-specific probe) and the VIC channel (*B. mallei*-specific probe).

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449		<i>B. mallei</i> strains			<i>B. pseudomallei</i> strains						Near neighbor strains			Mixed DNA
450		NR-2533	NR-2534	NR-2535	NR-2536	NR-2537	NR-2538	NR-8217	NR-8219	NR-9320	BAA-244	BAA-248	700388	NR-8219+NR-2535
451	FAM	>50	>50	>50	19.7	19.9	18.4	20.4	17.8	17.1	>50	>50	>50	17.8
452	VIC	19.9	16.9	16.1	>50	>50	>50	>50	>50	38.0	>50	>50	>50	16.1

453 TABLE 5. Results of alignment between each of the ten *B. pseudomallei* signature sequences and the corresponding loci in all known
 454 *B. pseudomallei* genomes. “+” indicates that the signature sequence was identical to that in the specified genome. “(+)” indicates
 455 that there was at least one difference in the signature sequence, but the primers and probe sequences used in the assay were identical to
 456 the same sequences in the specified genome. “F”, “P” or “R” indicates that there was one difference in the forward primer, probe or
 457 reverse primer, respectively. “N” indicates that the signature sequence does not exist in the genome of the specified strain.

458

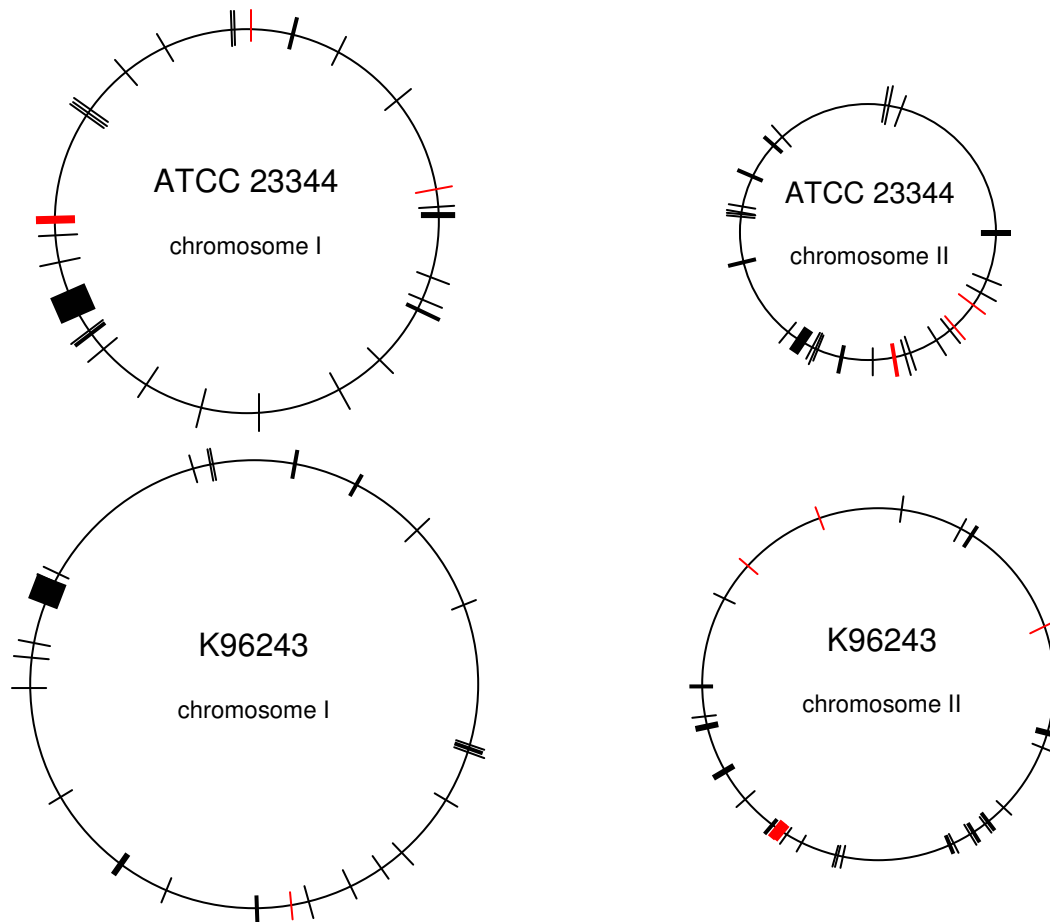
		Alignment result with signature sequence									
459	<i>B. pseudomallei</i> genome	81	82	83	84	85	86	87	88	89	90
460											
461	1106a	(+)	+	+	+	+	(+)	+	+	+	+
462	1106b	(+)	+	+	+	+	(+)	+	+	+	+
463	112	(+)	+	R	+	+	+	+	+	+	+
464	14	+	+	R	+	+	+	+	+	+	+
465	1710a	+	+	+	+	+	+	+	+	+	+
466	305	F	(+)	+	+	+	(+)	FPR	+	+	+

467	668	N	(+)	(+)	R	N	(+)	+	(+)	(+)	+
468	7894	+	+	+	+	(+)	+	(+)	+	+	+
469	9	+	+	+	+	N	+	+	+	+	+
470	91	+	+	+	+	+	+	+	+	+	+
471	E7210	+	+	+	+	+	(+)	+	+	+	(+)
472	BCC215	+	+	+	+	+	+	+	+	+	+
473	DM98	+	+	+	+	(+)	(+)	+	+	+	+
474	13177	+	+	+	+	+	(+)	+	+	(+)	(+)

475 TABLE 6. Results of alignment between each of the ten *B. mallei* signature sequences and the corresponding loci in all known *B.*
 476 *mallei* genomes. “+” indicates that the signature sequence was identical to that in the specified genome. “(+)” indicates that there
 477 was at least one difference in the signature, but the primers and probe sequences used in the assay were identical to the same
 478 sequences in the specified genome. “N” indicates that the signature sequence does not exist in the genome of the specified strain.

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480	Alignment result with signature sequence										
481	<i>B. mallei</i> genome	91	92	93	94	95	96	97	98	99	100
482	FMH	+	+	+	+	+	+	+	+	+	+
483	GB8	+	+	+	+	+	+	+	+	+	+
484	JHU	+	+	+	+	+	+	+	+	+	+
485	10229	+	+	+	+	+	+	+	+	+	+
486	10247	+	+	+	+	+	+	+	+	+	+
487	PRL-20	+	(+)	N	+	+	+	+	+	+	+
488	SAVP1	+	(+)	N	+	+	+	+	+	+	+



489

490 FIGURE 1. Distribution of signatures used for assay development on chromosome I and/or II of
 491 *B. mallei* (ATCC 23344) and *B. pseudomallei* (K96243). Positions in black are signatures
 492 common to both, while positions in red are species-specific signatures.

497 Supplemental TABLE 1. The genome locations of the 100 20-mer signature sequences chains used to
 498 develop TaqMan assays.

Signature#	Signature chain	Position in genome of			
		length (nt)	chromosome	<i>B. pseudomallei</i> K96243 ⁽¹⁾	<i>B. mallei</i> ATCC 23344 ⁽²⁾
501	1	150	I	1240053-1240202	2295699-2295848
502	2	150	I	2034357-2034506	1165140-1165289
503	3	150	II	C ⁽³⁾ 1319711-1319860	1314353-1314502
504	4	150	I	119810-119959	136172-136321
505	5	151	I	3200854-3201004	2075958-2076108
506	6	151	II	2071787-2071937	1646194-1646344
507	7	151	II	C1925220-1925370	590010-590160
508	8	151	I	C1417373-1417523	1899465-1899615
509	9	151	II	C1323076-1323226	1309674-1309824
510	10	152	II	C253924-254075	2070911-2071062
511	11	152	I	3337108-3337259	2380576-2380727
512	12	152	I	3355574-3355725	2399042-2399193
513	13	153	II	C287612-287460	2036773-2036925
514	14	153	II	C1269250-1269402	1366007-1366159
515	15	154	I	C2476936-2477089	871207-871360
516	16	154	II (2) ⁽⁴⁾	C1838269-1838422	945574-945727
517	17	154	II	C1380512-1380665	1253157-1253310
518	18	154	I	C1797577-1797730	1359809-1359962

519	19	155	II	C1812007-1812161	971896-972050
520	20	155	II	C1741822-1741976	1041923-1042077
521	21	155	I	3340415-3340569	2383883-2384037
522	22	155	I	3356286-3356440	2399754-2399908
523	23	155	II	C1377880-1378034	1255788-1255942
524	24	155	II	C2067080-2067234	736110-736264
525	25	155	I	3948767-3948921	2975790-2975944
526	26	156	I	2031244-2031399	1162007-1162162
527	27	157	I	C2476171-2476327	871969-872125
528	28	157	II	C288990-289146	2035239-2035395
529	29	157	I	2714344-2714500	1738881-1739037
530	30	158	I	3339602-3339759	2383070-2383227
531	31	158	I	2308485-2308642	1132414-1132571
532	32	158	II	C1923499-1923656	591724-591881
533	33	158	II	68090-68247	69106-69263
534	34	158	II	C1267092-1267249	1368160-1368317
535	35	158	I	C3892602-3892759	3001057-3001214
536	36	159	I	317846-318004	3472997-3473155
537	37	159	II	54827-54985	55865-56023
538	38	159	II	2372071-2372229	1920554-1920712
539	39	159	I	1603366-1603524	829937-830095
540	40	160	II	C1210557-1210716	1417207-1417366

541	41	160	I	3140623-3140782	2226041-2226200
542	42	160	II	2247307-2247466	1794959-1795118
543	43	161	II	C1729654-1729814	1054066-1054226
544	44	162	I	3359712-3359873	2403180-2403341
545	45	164	I	120012-120175	136374-136537
546	46	165	I	1229289-1229453	2285019-2285183
547	47	165	II	C1268252-1268416	1366993-1367157
548	48	167	I	C3412038-3412204	2513565-2513731
549	49	167	I	3948205-3948371	2975228-2975394
550	50	169	I	1886090-1886258	1070517-1070685
551	51	169	I	3358991-3359159	2402459-2402627
552	52	170	II	C1314827-1314996	1319151-1319320
553	53	171	I	C2471587-2471757	876547-876717
554	54	172	II	2252215-2252386	1799872-1800043
555	55	172	II	2255360-2255531	1803017-1803188
556	56	173	I	1231218-1231390	2286948-2287120
557	57	174	I	3350793-3350966	2394261-2394434
558	58	175	II	C2650191-2650365	109983-110157
559	59	175	I	780729-780903	256057-256231
560	60	176	I	308703-308878	3462263-3462438
561	61	176	I	3341891-3342066	2385359-2385534
562	62	178	I	3344570-3344747	2388038-2388215

563	63	178	II	2280518-2280695	1828187-1828364
564	64	178	II	C1266394-1266571	1368838-1369015
565	65	179	I	534021-534199	3267049-3267227
566	66	181	II	C1864613-1864793	918484-918664
567	67	181	I	3043112-3043292	468324-468504
568	68	182	II	2070917-2071098	1645762-1645943
569	69	183	I	3344267-3344449	2387735-2387917
570	70	183	II	1709507-1709689	1159685-1159867
571	71	184	I	3344979-3345162	2388447-2388630
572	72	185	II	2371055-2371239	1919538-1919722
573	73	188	I	C1669095-1669282	1483664-1483851
574	74	191	II	1003590-1003780	593786-593976
575	75	192	I & II(M) ⁽⁵⁾	2276002-2276193	1650475-1650666
576	76	194	I	1216978-1217171	3115984-3116177
577	77	194	II	C2016073-2016266	786946-787139
578	78	196	I	3960116-3960311	2987122-2987317
579	79	199	I	3337686-3337884	2381154-2381352
580	80	199	I	3352880-3353078	2396348-2396546
581	81	205	I	1943452-1943656	NP ⁽⁶⁾
582	82	210	II	1890445-1890654	NP
583	83	211	II	667379-667589	NP
584	84	215	II	1905197-1905411	NP

585	85	216	II	2775587-2775802	NP
586	86	216	II	2999705-2999920	NP
587	87	218	II	1891344-1891561	NP
588	88	219	II	1912160-1912378	NP
589	89	225	II	1903202-1903426	NP
590	90	232	II	1903890-1904121	NP
591	91	103	II	NP	1093949-1094051
592	92	105	II	NP	834580-834684
593	93	107	I	NP	787807-787913
594	94	115	I	NP	2633324-2633438
595	95	131	I	NP	5722-5852
596	96	132	I	NP	2632735-2632866
597	97	134	II	NP	1094639-1094772
598	98	152	I	NP	2632337-2632488
599	99	186	II	NP	909144-909329
600	100	208	I	NP	2633134-2633341

601 ⁽¹⁾*B. pseudomallei* K96243 GenBank sequence: chromosome I: BX571965; chromosome II: BX571966.

602 ⁽²⁾*B. mallei* ATCC 23344 GenBank sequence: chromosome I: CP000010; chromosome II: CP000011.

603 ⁽³⁾C: complement sequence.

604 ⁽⁴⁾II(2): there are 2 copies of this signature on chromosome II;

605 ⁽⁵⁾I & II(M): there are multiple copies on both chromosome I and chromosome II: for *B. pseudomallei* K96243: there are 4 copies on I,
606 and 1 copy on II; for *B. mallei* ATCC 23344, there are 36 copies on I, 10 copies on II.

607 ⁽⁶⁾NP: Not Present.

608 Supplemental TABLE 2. Assay primer and probe sequences.

609	Assay number	Forward primer (5'-3')	Reverse primer (5'-3')	Probe (5'-3')	PCR product size (bp)
610	1	GGAGCGATCCGTGATGTG	GGCCTCGGTTGACAATGG	ATTTGCGATGCGCGATTTCGATC	76
611	2	TTCACTGGACTGTGGAAACG	ATCGCAAGCGCGTGATAC	GTTGAATCGTGCGGAGGCGAAC	107
612	3	GCTCGTTCACGACACCTACC	TCGCTATCCATGAACGACAG	GTTCTGCGCCCGAGCTACG	75
613	4	TGCGCTTCATCGATTACATT	TTCGGATTCCGGTACATCAC	GTCGTGCGGAAGATCAGCAACAAG	76
614	5	ATCTCGTAGCGTGCCAGG	ACGCAATATTTGTGCAGACG	GAGAGAATGCGTTCGGAATGCCAG	110
615	6	TCAATGGATCGTTGAGCGTA	TGAGAAATGCCTCGTGAATG	TGAGAAATGCCTCGTGAATG	99
616	7	TGTCATCGGCATCTTTACGA	CGAACCCCGAGAAAATCCC	AGTGCGTGTACATCCTGTCCGGGT	112
617	8	TGTTGACACGATGACGTTT	GTACGGAACGTGCAGAAGG	ATCGTAGGTGTTGCGGGGTCTTC	91
618	9	ACATGGCGAGATTCCAGAAC	CGTTGACGCCATAGGTGAT	GAAAAATCGGTTGCGCTGCCCTAT	84
619	10	CCTTGGATCTCGTCTTCGG	AAAGGCTCGGCGAATAGC	GTCGAGCCATGCGATGGTCG	76
620	11	GCCTACCCGTCGTCTTCAT	AATTCGGGGAACACGCT	GAAGCAACGCGGTGCCAAGTTC	91
621	12	ATGAATACGCCCTTTGCATC	GGGCAAGAATGACGAAATCA	GCGTGATGCCCTTCGCTTCAAAT	111
622	13	CTTCATCCGGCTCAGATCG	AAGGACAACCTCGCGGATTC	GTACATCGGCATCACGTGCTCGCT	108
623	14	TGATGGTGAATTGAGCGTGT	GTCGTGCCTTCGGGTTATG	GTTTTCAACCGATGCGAAACGAGG	120
624	15	GCTCTGGGTGATCAACTTCC	GCGGTCTTGTTGCTCTTGAT	CTTCGGGCGTGAACCTGCATACC	111
625	16	GCGAGGAAGTGGGAAGAAG	GTTTCATCGAAGCAATCGCAC	GAGCACTGCGATGGTTCGAGCAT	104
626	17	AGGTGAAGCTGGCCGTAGT	ACTGCTCGTACCTCTCGTGG	ACCACGCGTTCAGAGCGGATAGT	91

627	18	ACAGCCTGTGGAATCTGTCC	GTCGCGTACTGGTACAGGCT	AGCACGTATGGACGCGACAATCTG	133
628	19	CGATACCGAGACGACGAAGA	CACTCCACGGCCTTGTCT	GTTCCGGCGAAAACCGCCTGAAC	81
629	20	ATGACGTCGTCGTTCCAGTC	CATCAATTGCAGCGGGATAC	ACGATCGCCATCATCCAATTGAGC	128
630	21	ACATCCGTCACTCCATTGGT	GAAAGCGCTTGAACTATCG	GATACCACGCAACCAGGCCTTCG	86
631	22	TGTTTCGATCAGCAAACAGC	CCGGTTGCTCAAGTATCCCT	CGACGATCTGAATTCCGGATGGAC	132
632	23	CAGATCGAAGAAGTGCGACA	CCTGTATGCGTTCGAGTATG	GACGTATGCGGCTGGGTGCC	85
633	24	GGTATGTGCGGCGTCTATCT	GATGTCCACCACCATTCTCC	ACAGGCCATGAGCAAGCTACCGAC	123
634	25	GTTTCATCCGAGACACTCG	GAGATTGAAGAAGCGCTTGAG	AGAACGTGTTTCGACGGCGTCAATT	141
635	26	ATTTCGAAGTGTCTCAGCCC	CCGAATTTTCGTCGATGC	CGGCCATGCGGTAACGAAGC	94
636	27	GTTTGGCGGTGCAATGAG	CACGAACGCACGTAAATGAC	GGTTTCGCGCAAATTCGATGAAAG	122
637	28	CACGTAGCCGTCGCAGTT	GAGCTCGCGTGGAAGAAC	ACATCTTCAGCTTCGGCGGCAC	93
638	29	ACTCGAAACGGTCGACTTCA	CATGCGACTTCAATCGAGAA	AAAGAAATATCCGGCAACGCCGC	76
639	30	CATCGAATAGATCGCGGTG	CGTGGTCGTGATAAACAGCA	ATGGTGGACGGCGGACAAACC	88
640	31	GAACATGCGCATTCTCGTC	CGAGACCACGTCACGGTAAT	ACGGGTGCGCTTCGATCTCTACG	79
641	32	CTTTGAGCGCGGTCAAGTC	GAGAGCAAACCGTAATAATGGC	CTTTCGACGCGTCATCGGGG	143
642	33	ATACGAAGCCGCGTTGAC	ATACGAAGCCGCGTTGAC	AAGAGCGGGGATGTCGTGTTGCT	76
643	34	GTAATGCGCATCCACGACTT	GTACGCGCCATTACGAGTG	ATCGTAGCGCCAGCGGTCCTG	128
644	35	TGTTCCGAGGACGTCTTTTC	CGACGAATCGGTAATGGATG	CCTTCCGTGACGCCGTCAATG	90
645	36	CGCTTGACCTTCCCACAGT	ACTTCGAGCTTCATGTTGCC	GGGAAGATCGATCCTTCAATCGATTCA	79
646	37	GTGACGGCCAATCAGGTC	TGACCATCAAGTTCGCAAAG	AGGCAGGACCCATACGAAGCAGGT	94
647	38	AATGGACCACCACGATCAG	TTCTACTATGGCCGCGGTT	CTTCCCCTCGACAGGTTTTGCTC	88

648	39	TAGCTGGTCGAACTGCACCT	TCGATGACGAGACCTACGTG	ACCATTTGGGTGCAGACGAAATGC	122
649	40	CGCGACGTATACCAGTTCG	GCATCCGCTGTATCGTTTTT	GTAATCGACCCACTCGACGGGCTT	75
650	41	CGCTCTCGACGAAACTGAAC	GCTTCACGTGGATGTGCGC	CTGCAGTACTTGCCGCGCCTGT	114
651	42	GTCGTGATGCTCGATCAATG	GACGTCAATGCGTTCTCTCA	GCGTGCCAATGTTGTCGACCTC	87
652	43	GACGTGCCGTTTCGAGTATCT	GAATTCGCACGAGAAGATCG	GGCGCAATCCGGTGTTCAG	93
653	44	GCGACCGCTGACGAGTAT	GTGTGGCTACTTTCCGCATT	AAGCTGTCTGCGCCATCTCCTCTG	112
654	45	GGCTTCATTCTGACGAGGAG	ATACACGAGATCACCTGCC	GAATTGATTCCCACCGACTGCTG	92
655	46	GATAAATGCCGAGGTAGCGT	AATCATCGCGCACTACGAG	CCGTCGTTTTTCCGGAACGTGAT	86
656	47	AGAACTCGTGCTCGGGATTA	GTAGGCGATCACAACGTCAA	GCACTGTTCTTGCCGGTCCATTC	121
657	48	AACTTCGGCATCATCTCCAC	GTCTTGCGGTTTCATGTCGT	GATTGTCGGCGGTGCTCAAG	83
658	49	AACGCCGTGCTCTATACGAT	GACAGCCGAGATGCCAGT	CCCGGAAGAAGCTCTGACATGAA	89
659	50	GAAGTGACGATTACCGAGGC	GACGTTATACCGCCACGAAC	GACATTCACGCAACCGTACTCCGC	102
660	51	GATCGAAGCGGCCTCTATTT	GTCGAAGTCGGTTTCGTTCA	GCCGAGCGATCTCACGACCATT	75
661	52	GCACCATCACGGTCATCTC	TGTACAGCTGTTGCGAATGG	ATCCTGTAAGTGCCTCGGAAGGTG	89
662	53	TGGACGATTTTAGCCATGTG	TCATCCAATTAGAAACGGCA	GATTGCTTATTCGAGATAGCGGCGC	78
663	54	ACGTTTGCTTCGAATGAGGA	ACCGGCTTTTTTCGATGAAC	CTTGCTTGCGCCGTTATTAGCAOG	92
664	55	TATTCGGTCACGACGAGATG	CAAGTCGATCCTCGCGTT	TCAATTGCGGAACGATCTTCGACA	120
665	56	ATGCCTTGCTCCATCAGTCT	GGTCAGCGAGGAAATATGGA	GAATGGCTGAAACGCGTGAAGTAC	81
666	57	GACGATACTCGGCGAATGTT	CCCTTACTCCGTCGAATCAA	GAGATCGCCTCGCGTATTCCACC	86
667	58	GAAACGGAAAAGCGATGGAC	ATCGTATCGATCCTCGAAACAC	GAATGGAACGCGCGCTTTTCC	75
668	59	GGTGATCTCGACGTAATGCC	TTCGAGCACTTCGACGACTA	ACTTCACCGCGACCGTCGTGTT	120

669	60	AATCTGACGGCGAGAAATTG	CACGCTTCCTCTGATTGTT	AAACAGCATGACTGCGCTCCCGT	127
670	61	CTGAATACGCGAGGTCGATT	AAGTTTTCTCGGGTGGTCCT	AAGCGATCACCGAAATGGCTCATG	97
671	62	GAGAGGTAATCGCGCAAATC	CTGGAGAATACGGATTGGGA	TCTCGTTGATACGCGGAAGCAGGT	137
672	63	AACTGCCGATCATCTTCCAC	GTCACGGAGATTTGCTTTT	AAACGGGATATGCGGCGTACAGCT	112
673	64	CTTTTCGGTTACCTGTCCCA	GGCAGCACTGGAAGTTCG	TCGGATTGAGGACATACCGCGTG	113
674	65	GATACGCCTGAACCTTCGC	CATTTCAAGCCGTTTCATGC	GTCCTGTTCCGGCGTCAGGAAGAG	88
675	66	CTCGATTGCTCGTGCTGAT	GGCGTAGAGGATGTCGAAGA	GACCACGCGCATGCACACATT	77
676	67	GGACTTTTCGGGTTCCCC	TGACCTCATGCAACTGTCGT	ACCGCCTTCGACGGCTGCAT	92
677	68	ACGACCTCGATTCCCCTC	GACGAAATTGCCGACCATAC	AACGCCCCATACGGGACAGGTC	125
678	69	TGTTGTACGCTTCGGCATAG	AAAGTTGCCGATCGATGAAG	TCAGGTCCGTACCCACCTTGGAGA	107
679	70	AAAGGCGCCTATCCCTATG	CATTTGCGGTAGCTCGATG	GTCTGGGGCTACGACCCGAATCAC	119
680	71	CCAACGAAATTGATCACTCG	GCCGACATATTCAAGCCTTT	CCCTCCACGACGTGCTCAAGTAC	119
681	72	ATACAGACACGCCGCTATCC	CGACAGCAAGTTCGTCATTG	TAGGCAGACCGGATCTTGAAGCCG	86
682	73	AATCCTCATAAGCGGGTTCC	CAGACGATATGACGTCGAGC	GTCGTCATTTCGCGTCTTTCGCG	140
683	74	TAGGACTTTGCGTAGACGGC	TCGCGTATAGCGTACTCGAC	GATTCGTTTCGGCGACAATTGAA	136
684	75	TACAAATCCAATGCGCAGAT	CGCGTTACCACCTTCACC	GGTACGATCGCAGTGCACGAACAG	86
685	76	CTTCGTGGTTCCGTTCCC	CCGCATACGCCTTCACTATC	AGGATGGCTGAACGGCCGAGTC	97
686	77	GCTTCTTTCATCCGACCATT	CGACGAGCGTCTCGGTATAG	GAGGTGTCCCGTCCGCGCTAC	149
687	78	GATCGAGGAGAGCATGAAGG	CCCTAGAGCGAAAACACCAG	TATTGGTTTACGGCTGCGCAAACG	116
688	79	GAATGGCCGTCGTACGATAA	TACGCGCGATTCTATCCCTA	GGAACCAGCCGGCCAGTGAAG	94
689	80	GAATCATTCTGGCGTGACCT	GCGGCACATTATGATATCGG	GAGACCGACCAGAGACATCGCCAG	108

690	81	ATGAAGAGCGAGTTGAAGCC	GGACATAGTCGCCCTGTACC	ACCTTCGGTCCGGACTGGAACAAC	148
691	82	AAGGAGGTGATACCCATTGC	CGAAATGAAATTGACGCGAT	AATCGGCATGCTGAATCCGCTTTT	75
692	83	CGTCCCTCAAAAATCGAGTG	GCACTTTTTGCCCTATGTG	TAGTTATCGGCGTGACGGGCTGAT	75
693	84	ACGGTACCTTGAACATTGCC	AGGAGTACGGTCGTGCATGT	GCGGCAAAAATCCCTCAGTACGTCC	116
694	85	CTGGAATGTCTTGACCGTCG	GCGGGTATCAATACAGACC	CTCAGCTTCGTACGGTGTGGC	122
695	86	GGATTGTGTCATCCTCGTC	CGGTTCTCAACTGCAACTCA	AGCACGTCTGGATGCATAGCGGAT	126
696	87	CGAAGGAATAGCGTAGGCAC	CTTCAAATAAGCGTCGGGTG	CCATATAGGCGTTGGCGAAGAGGG	135
697	88	CTCCTTCTTACAACCGGCAA	TGATGAAGAACCAGTGACGC	GTGAAGCGGCACACGTCCGAATAT	147
698	89	CAGTTCGACAACAACGCAAT	CGCCGCATCCTGACTAGTAT	CATTTCCGCCTCCGTCAAAGTCAA	140
699	90	TATTGATTCGCTGCTCGTG	GAGACCCGGATCAAGATGAA	GGTTATCGACCTGGTCGCCTGTCA	97
700	91	GCCTCTTCCGATAGGCAC	CGAACGACTATGAGGCCATT	ACTCGTGCAACGACAGCCAGGACT	79
701	92	GTCGTGCAATCGACGTTT	GGTCGGACATCATGCTGAG	TACAGCCATTTCGACAGGTCCGTC	79
702	93	AAAGCAGCAGACGATCCATT	ACTCGAAGACGTAAGCCCG	CTTATGTGTGACTGCGGCTGGCAC	89
703	94	TAGGGTAGGTTCCGAGGGTT	GAGCGGGTCTTACGTTTTCA	GTTTGATGCATGTCGGGCCTCCTA	78
704	95	CATTGATGGCGCTACGCT	TGACTCAAGAATAACAGCGTCC	ACAGTGGGGCGTGAGTCTGCTTTC	77
705	96	GGGGAGATGTTTAAATTGCG	TTTTTGCAGATAGGGATATTTG	CCCCGTGACACCGACAGTTCAAC	77
706	97	GTCGATGGAATGGGTCTCAC	AAGGTGATGATGGAGATGG	GATGCATTTTCGATGACGGGCAGAT	103
707	98	ACCCATTACAACCGTTGCTG	GCTGAAGAGTGGCTGCAAT	GCCCCAGTCCTCCCGATGCC	84
708	99	CTCTATCGAATTTTCGGCTCG	TTACGATTTTCGCTTAACCG	AGAATCTCGCCACACTCTCGCCAC	134
709	100	CGTCTAAATCCAAACCGGAA	CTCGTCGGTGTGATAACCT	TCCTTGGCTGACAGCAACCTCGAT	88

710 Supplemental TABLE 3. Taqman PCR results for 100 assays run using *B. mallei*, *B. pseudomallei*, and near neighbor strain DNA
 711 samples. CT values shown are average of two assays, except in cases where both results are shown. Detailed strain information is
 712 shown in TABLE 2.

Assay	CT Values for											
	<i>B. mallei</i> Strains			<i>B. pseudomallei</i> Strains						Near Neighbor Strains		
	NR-2533	NR-2534	NR-2535	NR-2536	NR-2537	NR-2538	NR-8217	NR-8219	NR-9320	BAA-244	BAA-248	700388
1	17.0	15.8	15.0	15.7	17.4	15.0	17.9	19.3	17.6	>50	>50	>50
2	19.8	18.1	16.6	18.4	20.6	18.1	20.3	22.3	20.9	>50	>50	>50
3	18.6	17.3	16.4	18.0	18.9	16.5	19.2	20.6	19.7	>50	>50	>50
4	19.0	17.5	16.5	17.5	19.4	16.3	20.0	21.5	20.8	>50	>50	>50
5	18.7	17.6	16.4	17.1	19.6	16.4	20.9	28.8	20.3	>50	>50	>50
6	17.1	16.2	15.4	>50	17.4	15.1	18.1	19.5	17.3	>50	>50	>50
7	20.4	19.3	17.4	19.2	20.1	18.2	23.7	26.4	24.0	>50	>50	>50
8	18.4	16.5	15.1	17.5	18.2	15.2	19.2	20.3	17.3	>50	>50	>50
9	18.2	19.0	18.7	18.3	18.4	18.7	16.5	16.5	17.7	>50	>50	>50
10	20.4	21.0	20.4	19.5	20.1	20.0	18.3	19.3	19.2	>50	>50	>50
11	18.0	17.7	17.8	17.7	18.1	18.2	16.4	16.8	17.2	>50	>50	>50
12	21.2	20.1	19.7	19.1	19.8	19.8	17.2	18.0	20.6	>50	>50	>50
13	20.2	20.1	22.0	20.6	18.9	21.3	18.8	22.6	19.6	>50	>50	>50
14	18.8	19.7	19.4	18.8	19.1	19.3	17.1	18.0	17.8	>50	>50	>50
15	18.9	18.5	17.8	17.7	17.2	17.4	15.7	16.1	17.0	>50	>50	>50
16	19.7	20.7	20.6	19.7	20.1	20.3	18.2	19.1	19.2	>50	>50	>50
17	17.1	17.5	17.5	17.3	17.3	17.5	15.5	16.7	16.3	>50	>50	>50

18	17.6	18.2	17.6	16.8	17.5	17.5	15.6	16.2	17.3	>50	>50	>50
19	20.2	20.3	20.2	19.7	20.1	20.2	17.9	18.6	19.0	>50	>50	>50
20	17.8	18.2	18.1	18.1	18.1	18.3	16.5	16.8	16.9	>50	>50	>50
21	17.4	17.9	17.4	17.2	17.8	18.0	16.0	16.2	17.4	>50	>50	>50
22	16.6	17.3	16.9	16.8	17.1	17.0	15.2	15.2	16.8	>50	>50	>50
23	19.9	20.3	19.9	20.2	20.1	20.1	18.4	19.9	18.2	>50	>50	>50
24	17.1	17.1	17.0	>50	15.6	18.1	16.0	18.9	16.2	>50	>50	>50
25	18.2	18.6	18.1	18.1	18.7	18.4	16.6	17.4	17.7	>50	>50	>50
26	17.0	18.0	16.6	17.1	17.3	17.6	15.2	16.0	16.7	>50	>50	>50
27	19.2	20.2	19.7	19.7	20.1	20.1	17.9	18.7	19.5	>50	>50	>50
28	17.1	17.4	16.9	17.4	17.4	17.4	16.0	17.2	16.5	>50	>50	>50
29	19.1	20.2	19.2	19.2	19.4	19.2	17.6	17.9	18.9	>50	>50	>50
30	15.9	16.5	16.1	16.0	16.2	16.4	14.5	15.1	16.0	>50	>50	>50
31	16.2	16.9	15.8	16.1	16.2	16.5	14.2	14.8	16.1	>50	>50	29.8
32	16.0	16.8	16.5	16.1	16.2	16.5	14.3	14.6	16.1	>50	>50	>50
33	16.2	16.9	16.8	16.3	16.4	17.3	14.8	15.0	16.3	>50	>50	>50
34	18.2	18.8	18.8	18.0	18.4	18.5	16.2	17.0	17.5	>50	>50	>50
35	16.5	16.5	16.5	16.0	16.8	16.7	14.9	14.4	16.6	>50	>50	26.0
36	19.8	20.5	19.9	19.6	20.3	20.2	18.3	19.6	19.5	>50	>50	>50
37	16.8	17.4	17.1	16.5	16.9	17.2	15.1	15.5	16.8	>50	>50	>50
38	16.1	17.0	16.7	16.1	16.7	16.8	14.6	15.1	16.1	>50	>50	>50
39	16.5	17.0	17.1	16.8	17.0	17.3	15.0	15.8	16.7	>50	>50	>50
40	18.5	18.6	18.6	18.2	18.3	19.0	16.3	16.8	17.7	>50	>50	>50
41	17.0	17.5	16.8	16.9	17.5	17.4	15.7	16.4	16.5	>50	>50	>50
42	20.3	21.5	20.5	>50	20.5	20.9	18.4	18.4	20.5	>50	>50	>50
43	18.9	19.9	19.3	19.0	19.1	19.3	17.0	18.8	18.4	>50	>50	>50
44	17.3	17.4	17.1	16.7	17.1	17.2	15.3	15.7	17.1	>50	>50	>50
45	17.8	18.1	18.1	17.3	17.9	17.9	16.1	16.0	17.3	>50	>50	>50
46	16.1	17.0	16.3	16.0	16.3	16.6	14.5	14.7	16.1	>50	>50	>50
47	18.6	19.4	19.1	18.4	18.9	18.8	16.7	17.2	18.3	>50	>50	>50
48	17.4	18.4	17.8	17.8	18.2	18.2	16.1	16.7	17.5	>50	>50	>50
49	18.7	19.2	18.8	18.2	19.2	19.1	17.3	17.5	18.7	>50	>50	>50
50	19.9	>50	20.1	19.7	20.0	20.1	18.0	18.3	19.6	>50	>50	>50
51	20.1	21.0	20.3	19.7	20.4	20.5	18.7	19.1	20.3	>50	>50	>50

52	19.4	19.6	19.4	19.9	19.2	19.2	18.2	19.4	18.7	>50	>50	>50
53	21.3	20.9	19.8	21.5	21.5	20.5	20.0	21.4	21.2	>50	>50	>50
54	18.5	18.2	17.9	36.93/>50	18.2	17.9	16.4	20.1	18.1	>50	>50	>50
55	25.1	24.6	24.9	>50	23.8	24.3	22.0	23.0	24.7	>50	>50	>50
56	20.4	20.3	19.6	20.1	20.3	19.6	19.0	19.4	21.1	>50	>50	>50
57	19.9	20.0	19.2	19.8	19.7	19.5	18.7	19.3	20.4	>50	>50	>50
58	21.2	>50	21.6	21.9	22.1	20.9	21.4	22.0	21.4	>50	>50	>50
59	16.7	16.4	16.3	16.3	16.2	16.2	15.0	15.7	17.4	>50	>50	>50
60	17.8	19.0	17.8	18.5	18.5	18.4	16.8	18.4	17.8	>50	>50	>50
61	17.0	16.2	16.4	16.8	16.4	16.4	15.3	16.1	17.0	>50	>50	>50
62	18.3	18.2	17.5	17.8	17.6	17.5	16.4	17.1	18.3	>50	>50	>50
63	18.3	18.4	18.4	18.5	16.9	18.0	17.0	17.9	18.2	>50	>50	>50
64	16.5	17.0	16.8	16.9	16.6	16.4	15.3	16.2	16.3	>50	>50	>50
65	23.5	24.4	23.8	24.6	24.1	24.2	24.1	26.2	24.6	>50	>50	>50
66	17.9	18.5	17.4	18.9	18.4	18.4	17.4	19.0	18.1	>50	>50	>50
67	18.6	18.3	18.5	18.2	18.3	18.2	16.5	17.2	18.4	>50	>50	>50
68	17.7	17.1	17.9	>50	17.2	17.3	16.2	17.1	17.2	>50	>50	>50
69	16.5	16.4	16.3	16.4	16.4	16.2	15.1	15.6	16.7	>50	>50	>50
70	20.1	20.8	20.6	20.3	20.1	20.2	19.1	20.8	20.7	>50	>50	>50
71	16.3	16.4	16.4	16.2	16.2	16.0	15.0	15.3	17.5	>50	>50	>50
72	16.2	16.4	16.3	16.5	16.7	16.5	15.1	15.9	16.3	>50	>50	>50
73	20.2	20.5	20.2	20.3	20.3	19.5	19.1	19.5	20.1	>50	>50	>50
74	18.9	18.8	19.9	19.8	18.1	20.4	17.7	20.3	18.0	>50	>50	>50
75	12.7	11.8	13.0	15.5	>50	38.8	15.4	18.1	15.2	>50	>50	>50
76	16.9	16.9	16.9	17.2	15.7	17.9	15.9	18.6	16.3	>50	>50	>50
77	19.8	19.3	19.7	>50	18.1	20.7	18.6	21.4	18.0	>50	>50	>50
78	16.3	15.7	16.0	16.7	14.9	17.1	15.3	17.6	15.8	>50	>50	>50
79	18.8	18.2	19.1	18.1	17.5	18.4	15.5	16.9	17.3	>50	>50	>50
80	18.2	18.1	19.1	17.5	17.1	17.7	15.1	16.0	16.5	>50	>50	>50
81	>50	>50	>50	16.3	17.4	15.4	18.1	18.8	18.5	>50	>50	>50
82	>50	>50	>50	17.8	18.5	15.6	19.1	19.8	17.8	>50	>50	>50
83	>50	>50	>50	16.3	16.1	16.0	14.9	15.3	16.3	>50	>50	>50
84	>50	>50	>50	18.8	18.5	18.2	17.1	17.7	18.6	>50	>50	>50
85	>50	>50	>50	16.7	16.4	16.5	15.0	15.4	16.7	>50	>50	>50

86	>50	>50	>50	18.9	18.4	18.1	17.7	18.3	17.6	>50	>50	>50
87	>50	>50	>50	17.3	17.0	17.2	15.5	16.2	16.8	>50	>50	>50
88	>50	>50	>50	18.6	18.2	18.3	16.9	17.3	18.6	>50	>50	>50
89	>50	>50	>50	17.3	16.9	17.2	15.5	15.8	16.9	>50	>50	>50
90	>50	>50	>50	18.3	17.9	18.1	16.6	17.2	18.4	>50	>50	>50
91	18.0	16.4	16.0	38.01/>50	>50	>50	>50	>50	33.0	>50	>50	>50
92	19.2	17.2	15.4	>50	>50	>50	>50	>50	32.5	>50	>50	>50
93	16.2	16.2	16.0	>50	>50	>50	>50	>50	30.8	>50	>50	>50
94	18.0	18.0	19.0	>50	>50	>50	>50	>50	33.1	>50	>50	>50
95	16.5	16.4	16.3	36.18/>50	>50	>50	>50	>50	31.6	>50	>50	>50
96	15.7	15.7	15.7	>50	>50	>50	>50	>50	31.2	>50	>50	>50
97	18.4	18.4	18.3	>50	>50	>50	>50	>50	33.1	>50	>50	>50
98	16.0	15.8	15.9	>50	>50	>50	>50	>50	32.4	>50	>50	>50
99	18.3	18.2	18.1	>50	>50	>50	>50	>50	33.6	>50	>50	>50
100	16.1	15.9	16.0	>50	>50	>50	>50	>50	31.2	>50	>50	>50