Table S1. The *Elizabethkingia anophelis* isolates with available genome data included in the core-genome multi-locus sequence typing

| Strain | source | Region                  | Level                | Size (Mb) | GC (%) | Accession number                           | Scaffolds | Genes | Proteins (CDS) |
|--------|--------|-------------------------|----------------------|-----------|--------|---------------------------------------------|-----------|-------|----------------|
| R26    | Mosquito | Stockholm, Sweden       | Complete Genome      | 4.06      | 35.5   | chromosome: NZ_CP023401.1/CP023401.1       | 1         | 3741  | 3635           |
| DSM-23781 |        | Justus Liebig University, Germany | Contig | 4.07      | 35.4   | FLST01                                     | 58        | 3779  | 3675           |
| As1    | Mosquito | US                      | Contig               | 3.59      | 35.5   | LFKT01                                     | 12        | 3315  | 3237           |
| AR4-6  | Mosquito | Sichuan, China          | Complete Genome      | 4.09      | 35.5   | chromosome: NZ_CP023404.1/CP023404.1       | 1         | 3785  | 3678           |
| AR6-8  | Mosquito | Sichuan, China          | Complete Genome      | 4.09      | 35.5   | chromosome: NZ_CP023403.1/CP023403.1       | 1         | 3785  | 3678           |
| 277-17 | Human patient | Taiwan                | Complete Genome      | 4.00      | 35.6   | CP071549                                   | 2         |       | 3842           |
| ID     | Type       | Region | Genome Type          | Year | Ratio | Accession | Length |
|--------|------------|--------|----------------------|------|-------|-----------|--------|
| 346-72 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071543  | 1      |
| 347-96 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071540  | 1      |
| 354-72 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071536  | 1      |
| 354-87 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.9  | CP071535  | 1      |
| 355-58 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071534  | 1      |
| 356-17 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071533  | 1      |
| 346-66 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071544  | 1      |
| 347-10 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071542  | 1      |
| 343-63 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071546  | 1      |
| 347-50 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.9  | CP071541  | 1      |
| 348-50 | Human patient | Taiwan | Complete Genome      | 4.10 | 35.8  | CP071539  | 1      |
| Case | Type                  | Location                   | Genome Type            | Coverage | Quality     | Accession | Length |
|------|-----------------------|----------------------------|------------------------|----------|-------------|-----------|--------|
| 349-83 | Human patient | Taiwan | Complete Genome | 4.10 | 35.8 | CP071538 | 1 | 3967 |
| 351-72 | Human patient | Taiwan | Complete Genome | 4.10 | 35.8 | CP071537 | 1 | 3964 |
| 362-2 | Human patient | Taiwan | Complete Genome | 4.10 | 35.8 | CP071532 | 1 | 3962 |
| 367-19 | Human patient | Taiwan | Complete Genome | 4.10 | 35.8 | CP071531 | 1 | 3967 |
| 296-96 | Human patient | Taiwan | Complete Genome | 4.20 | 35.8 | chromosome:NZ_CP046080.1/CP046080.1 | 1 | 3898 | 3779 |
| 344-1 | Human patient | Taiwan | Complete Genome | 4.10 | 35.9 | CP071545 | 2 | 4017 |
| 2-62 | Suction Rotary knob | Taiwan | Complete Genome | 4.10 | 35.8 | CP071551 | 1 | 3982 |
| GX130 | Human patient | Guangxi Zhuang Autonomous Region, China | Contig | 3.87 | 35.6 | SYWB01 | 38 | 3543 | 3452 |
| 313-22 | Human patient | Taiwan | Complete Genome | 4.00 | 35.8 | CP071547 | 1 | 3799 |
| CSID     | Patient ID | Country          | Genome Type     | Coverage | GC%  | Accession Numbers            | Contig Length | Assembler |
|----------|------------|------------------|-----------------|----------|------|-------------------------------|---------------|-----------|
| CSID_301 | 5183678    | Wisconsin, US    | Complete Genome  | 3.93     | 35.8 | chromosome:NZ_CP014805.2/CP0 | 1             | 3587      | 3483      |
| CSID_301 | 5183684    | Wisconsin, US    | Complete Genome  | 3.93     | 35.8 | chromosome:NZ_CP015066.2/CP0 | 1             | 3587      | 3481      |
| CSID_300 | 0521207    | Wisconsin, US    | Complete Genome  | 3.85     | 35.7 | chromosome:NZ_CP015067.2/CP0 | 1             | 3513      | 3412      |
| CSID_301 | 5183681    | Wisconsin, US    | Complete Genome  | 3.93     | 35.8 | chromosome:NZ_CP015068.2/CP0 | 1             | 3586      | 3482      |
| FDAARGO  | S_132      | Washington, US    | Complete Genome  | 4.00     | 35.7 | chromosome:NZ_CP014020.1/CP0 | 1             | 3675      | 3565      |
| FDAARGO  | S_134      | Washington, US    | Complete Genome  | 4.00     | 35.7 | chromosome:NZ_CP014021.1/CP0 | 1             | 3676      | 3567      |
| PHOL-090 |            | Greater Toronto Area, Canada | Contig | 4.00     | 35.5 | RSAZ01                         | 27            | 3679      | 3556      |
| Sample ID   | Patient Type | Location          | Genome Type       | Complete Genome Length [kb] | Complete Genome Size [MB] | Chromosome 1 Size [bp] | Chromosome 2 Size [bp] |
|------------|--------------|-------------------|-------------------|----------------------------|--------------------------|------------------------|------------------------|
| F3543      | Human        | Florida, US       | Complete Genome   | 3.97                       | 35.6                     | chromosome: NZ_CP014340.1/CP014340.1 | 1                      | 3638                   | 3522                   |
| 3375       | Human        | South California, US | Complete Genome   | 4.01                       | 35.7                     | chromosome: NZ_CP016373.1/CP016373.1 | 1                      | 3704                   | 3583                   |
| FDAARGOS_198| Human        | Sweden            | Complete Genome   | 4.07                       | 35.8                     | chromosome: NZ_CP023010.2/CP023010.2 | 1                      | 3737                   | 3614                   |
| BP8467     | Human        | Vellore, India    | Contig            | 3.86                       | 35.6                     | VTFI01                 | 30                     | 3527                   | 3394                   |
| SP4182     | Human        | Vellore, India    | Contig            | 3.83                       | 35.5                     | PXJH01                 | 47                     | 3619                   | 873                    |
| 40313151   | Human        | US                | Contig            | 4.10                       | 35.6                     | QNTY01                 | 18                     | 3833                   | 3735                   |
| E6809      | Human        | California, US    | Complete Genome   | 4.12                       | 35.6                     | chromosome: NZ_CP014339.1/CP014339.1 | 1                      | 3821                   | 3703                   |
| 6499925    | Human        | US                | Contig            | 3.96                       | 35.8                     | QNTZ01                 | 16                     | 3641                   | 3538                   |
| CSID_3000516074 | Human Patient | Illinois, US | Contig            | 4.05                       | 35.7                     | MAHA01                 | 17                     | 3744                   | 3639                   |
| Accession   | Institution                           | Location                           | Assembly       | Contig/ Scaff    | Accession | Size | Coverage | Contig/Scaff | Size | Coverage |
|------------|---------------------------------------|------------------------------------|----------------|----------------|------------|------|----------|--------------|------|----------|
| CIP111067  | Institut Pasteur, Paris               |                                    | Scaffold       | 3.85           | FTQZ01     | 65   | 35.7     |              | 3508 | 3414     |
| PHOL-104   | Human patient                         | Greater Toronto Area, Canada       | Contig         | 3.84           | RSAW01     | 43   | 35.6     |              | 3497 | 3400     |
| CSID_300   | Human patient                         | Arkansas, US                       | Contig         | 3.87           | MAHH01     | 25   | 35.6     |              | 3530 | 3440     |
| 0516810    |                                       |                                    | Complete Genome| 4.00           | CP071530   | 1    | 35.6     |              | 3751 |          |
| PW2806     | European Bioinformatics Institute, UK |                                    | Scaffold       | 3.91           | CBYD01     | 42   | 35.9     |              | 3616 | 3494     |
| PW2809     | European Bioinformatics Institute, UK |                                    | Scaffold       | 3.92           | CBYE01     | 32   | 35.8     |              | 3623 | 3499     |
| Sample Code | Sample Type          | Location          | Type            | Size | Reference Genome | Chromosome | Size | GenBank Accession | Future Grease | Country    |
|-------------|----------------------|-------------------|-----------------|------|------------------|------------|------|------------------|---------------|------------|
| Ea_0422     | Human patient        | Florida, US       | Complete Genome | 3.99 | 35.6             | chromosome: NZ_CP016370.1/CP016370.1 | 1    | 3698             | 3585          | US         |
| CIP60.58    | Human patient        | Institut Pasteur, Paris | Contig          | 3.96 | 35.6             | FTQY01     | 24   | 3679             | 3581          |           |
| CSID_301    | Human patient        | Wisconsin, US     | Contig          | 3.84 | 35.6             | MAHO01     | 23   | 3567             | 3472          |           |
| CSID_301    | Human patient        | Wisconsin, US     | Contig          | 4.00 | 35.5             | MAHP01     | 38   | 3711             | 3605          |           |
| JUNP 353    | Human patient        | Kathmandu, Nepal  | Complete Genome | 4.32 | 35.8             | chromosome: NZ_AP022313.1/AP022313.1 | 1    | 4049             | 3897          | Nepal      |
| NUH4        | hand hygiene sink aerator of the neonatal ICU ward of National University Hospital | Singapore | Contig          | 4.24 | 35.6             | ASYI01     | 50   | 3943             | 3831          | Singapore  |
| Ref     | Description                  | Location       | Type  | L  | R  | Cnt | Length  |
|---------|------------------------------|----------------|-------|----|----|-----|---------|
| NUHP1   | Human patient                | Singapore      | Complete Genome | 4.37 | 35.6 | chromosome:NZ_CP007547.1/CP007547.1 | 1       | 4040  | 3915  |
| NUHP3   | Human patient                | Singapore      | Contig | 4.33 | 35.5 | ASYG01 | 71     | 4026  | 3909  |
| NUH1    | hand hygiene sink aerator    | Singapore      | Contig | 4.33 | 35.6 | ASYH01 | 59     | 4026  | 3908  |
| NUHP2   | Human patient                | Singapore      | Contig | 4.33 | 35.5 | ASYF01 | 59     | 4026  | 3915  |
| 12012-2 PRCM | Human patient            | Fujian Quanzhou Hospital, China | Contig | 4.02 | 35.6 | LPXG01 | 83     | 3711  | 3595  |
| LDVH-AR107 | Cyprinus carpio            | France         | Scaffold | 3.99 | 35.7 | FTPG01 | 105    | 3667  | 3555  |
| Po0527107 | European Bioinformatics Institute, UK | Contig | 4.03 | 35.5 | CCAC01 | 89     | 3708  | 3601  |
| V0378064 | European Bioinformatics Institute, UK | Scaffold | 4.04 | 35.7 | CCAB01 | 213    | 3735  | 3627  |
| CSID_301 5183686 | Human patient | Wisconsin, US | Contig | 4.20 | 35.6 | MAHR01 | 49 | 3908 | 3809 |
|------------------|---------------|---------------|--------|------|------|--------|----|------|------|
| NUH11            | hand hygiene sink aerator | Singapore | Contig | 4.09 | 35.6 | ASYK01 | 59 | 3791 | 3676 |
| NUH6             | hand hygiene sink aerator | Singapore | Contig | 4.12 | 35.6 | ASYJ01 | 74 | 3847 | 3733 |
| EM361-97         | Human patient | Kaohsiung, Taiwan | Scaffold | 4.08 | 35.7 | LWDS00000000.1 | 18 | 3763 | 3634 |
| FMS-007          | Human patient | China | Complete Genome | 3.94 | 35.6 | chromosome:NZ_CP006576.1/CP006576.1 | 1 | 3611 | 3501 |
| Ea_2-14          | Tap water | Taiwan | Complete Genome | 4.00 | 35.5 | CP071550 | 1 | 3725 |
| 502              | Human patient | Birmingham, UK | Contig | 3.96 | 35.5 | AVCQ01 | 21 | 3642 | 3537 |
| PHOL-515         | Human patient | Greater Toronto Area, Canada | Contig | 4.11 | 35.4 | RSAY01 | 55 | 3765 | 3634 |
| Accession | Sample Description | Location | Platform | Library | Read 1 Start | Read 1 End | Read 2 Start | Read 2 End |
|-----------|--------------------|----------|----------|---------|--------------|------------|--------------|------------|
| PW2810    | European Bioinformatics Institute, UK | Scaffold | 3.98 | 35.5 | CBYF01 | 38 | 3614 | 3481 |
| CIP111046 | Institut Pasteur, Paris | Scaffold | 3.96 | 35.6 | FTRB01 | 41 | 3619 | 3522 |
| PHOL-785  | Human patient | Greater Toronto Area, Canada | Contig | 4.06 | 35.6 | RAV01 | 15 | 3707 | 3603 |
| CSID_3000516978 | Human patient | California, US | Contig | 3.99 | 35.5 | MAHJ01 | 16 | 3647 | 3551 |
| CSID_3000517066 | Human patient | Texas, US | Contig | 3.96 | 35.6 | MAHL01 | 18 | 3631 | 3540 |
| Endophthalamitis | Human patient | Puttaparthi, India | Contig | 4.02 | 35.5 | JSAA01 | 167 | 3729 | 2302 |
| Ngouso | Anopheles coluzzii | Cameroon | Chromosome | 4.24 | 35.3 | chromosome: CP034594.1 |
| Sample ID | Genus/Species | Location | Type | Genome | Length | Chromosome Start | Chromosome End | Chromosome Reference | Contig Start | Contig End | Contig Reference |
|-----------|---------------|----------|------|--------|--------|-----------------|----------------|----------------------|--------------|------------|-----------------|
| JM-87     | Corn zea mays | Alabama, US | Complete Genome | 4.18 | 35.5 | chromosome: NZ_CP016372.1/CP016372.1 | 1 | 3837 | 3695 |
| F3201     | Human patient | Kuwait | Complete Genome | 4.28 | 35.5 | chromosome: NZ_CP016374.1/CP016374.1 | 2 | 3927 | 3797 |
| PHOL-537  | Human patient | Greater Toronto Area, Canada | Contig | 4.15 | 35.4 | RSAX01 | 38 | 3788 | 3676 |
| B2D       |                | Malaysia | Contig | 3.94 | 35.5 | JNCG01 | 50 | 3589 | 3501 |
| OSVUM1    | Equine Stall | Oklahoma, US | Contig | 4.14 | 35.5 | PJMA01 | 5 | 3778 | 3653 |
| OSVUM2    | Equus ferus caballus | Oklahoma, US | Contig | 4.10 | 35.4 | PJLZ01 | 9 | 3754 | 3644 |
| CSID_300 0653323 | Human patient | Tennessee , US | Contig | 4.18 | 35.4 | NWMM01 | 35 | 3833 | 3721 |
| CSID_300 0726633 | Human patient | Illinois, US | Contig | 4.18 | 35.4 | NWMI01 | 43 | 3832 | 3710 |
| CSID_300 0726811 | Human patient | Minnesota, US | Contig | 4.18 | 35.4 | NWMH01 | 28 | 3829 | 3710 |
Table S2. The genomic island prediction results regarding to the seven genomic regions (GRs) of the *Elizabethkingia anophelis* 296-96 genome

| Genomic region | SIGI-HMM (start-end) | IslandPath-DIMOB (start-end) |
|----------------|----------------------|-----------------------------|
| GR1            | 562,287-566,801      |                             |
| GR2            |                      |                             |
| GR3            |                      | 1,419,188-1,447,202         |
| GR4            | 1,681,211-1,711,208  | 1,677,749-1,712,346         |
|                | 1,713,464-1,719,154  |                             |
|                | 1,729,117-1,736,020  |                             |
| GR5            |                      |                             |
| GR6            | 3,690,665-3,695,482  | 3,689,204-3,780,934         |
|                | 3,699,314-3,705,182  |                             |
|                | 3,718,986-3,730,938  |                             |
|                | 3,750,559-3,757,860  |                             |
|                | 3,773,194-3,777,216  |                             |
| GR7            | 4,126,500-4,131,283  | 4,105,728-4,113,454         |
Figure S1. Illustration of seven genomic regions (GRs, triangle) among *Elizabethkingia anophelis* strains including Changhua Christian Hospital (CCH) strains, outbreak strains from Wisconsin and Singapore, R26 and *E. anophelis* SUE. All 18 outbreak
strains had GR1 to GR6 but GR7 only presented in *E. anophelis* 2-62, 344-1 and 296-96. GR1 included integrative and conjugative elements (ICEs) ICEEaIII and GR6 included ICEEaI. Three types of ICEs were marked in all *E. anophelis* genomes at the locus of insertion (arrow). *ICEs with different cargo gene from the ICEs in the CCH outbreak strains.*
Figure S2. The comparison of the gene structure of integrative and conjugative elements (ICEEal) between the *Elizabethkingia anophelis* 296-96 in our study and the Wisconsin strain (CSID_3015183678).
Figure S3. The annual number of *Elizabethkingia anophelis* strains in the Taiwan Surveillance of Antimicrobial Resistance (TSAR) program from 2002 to 2018 and the percentage of *E. anophelis* strains belonging to the dominant lineage.