

**Table S3. Sequences of spacers from 35 DMS3vir-resistant and spacer-acquisition positive isolates from the biofilm enrichment assay in WT *P. aeruginosa* PA14 and DMS3vir co-incubation condition.**

| Isolate Number | Spacer Number | CRISPR1 Sequences*                | CRISPR2 Sequences*               | Targeted Sense Orientation | PAM | Location on DMS3 Genome** | Distance from Primed Protospacer*** |
|----------------|---------------|-----------------------------------|----------------------------------|----------------------------|-----|---------------------------|-------------------------------------|
| 1              | 1             | CATGTTCCGTTCCGAACCTCCCGCCGCGCCGCA |                                  | neg                        | GG  | 30162                     | 2315                                |
|                | 2             | TACCTCGGGCCAGGCGCTGGGCTCCATTATCA  |                                  | neg                        | GG  | 30573                     | 2726                                |
|                | 3             | GGCCGATCCTAGAGCAGATGGCCCGCAGCCT   |                                  | pos                        | GG  | 26639                     | -1208                               |
| 2              | 4             |                                   | TCTGACCAGCGAGTTGCAACGTACCACGGTA  | neg                        | GG  | 28160                     | 313                                 |
|                | 5             | GCCTTGGGTTTAGCGCCATCAGCCACCTCCT   |                                  | neg                        | GG  | 32483                     | 4636                                |
| 3              | 6             | TCCGCCGACGCGCGTGGTTACCAGCAAGAA    |                                  | neg                        | GG  | 24605                     | -3242                               |
|                | 7             |                                   | CATTACATCGTCTGGGTGAACAAGAACCGCCA | pos                        | GG  | 27550                     | -297                                |
| 4              | 8             | AACCTCGCGCAGTGTGTCCAGCGGCATCAT    |                                  | pos                        | GG  | 26896                     | -951                                |
|                | 9             | TCGGCGTTGTGACAAAGCCATTCCGATGCCGA  |                                  | neg                        | GG  | 28701                     | 854                                 |
|                | 10            |                                   | GTCGTCAATGGCGGATCGTGTGGACGCTCCA  | pos                        | GG  | 29944                     | 2097                                |
| 5              | 11            |                                   | CGCAAGCCGCTGAAGAAGTGGGGCAGCCAG   | pos                        | GC  | 25088                     | -2759                               |
|                | 12            |                                   | GACGTCTGACCAGCGAGTTGCAAGTACCAC   | neg                        | GG  | 28164                     | 317                                 |
| 6              | 13            | TCGGACACGCAGTTATCGACTGCTGTCCAC    |                                  | neg                        | GG  | 31578                     | 3731                                |
|                | 14            | GTATCGTCCAGCCGGTCCAGCGTGGGCTGTT   |                                  | neg                        | GG  | 30515                     | 2668                                |
| 7              | 15            | AGACAGCTCGACGGTGGCCATCGCCGGAGT    |                                  | pos                        | GG  | 29107                     | 1260                                |
|                | 16            | AACCTCGCGCAGTGTGTCCAGCGGCATCAT    |                                  | pos                        | GG  | 26896                     | -951                                |
| 8              | 17            | TGCGCTCGCGTGTGATCAGCCACGTCGGGAT   |                                  | neg                        | GG  | 29248                     | 1401                                |
|                | 18            | CGAGGCGCGACCGCTGCCAGGCTGATGTCT    |                                  | neg                        | GG  | 29619                     | 1772                                |
| 11             | 19            | GTCAACCAGCAACCGAGGGCGCCGCTATCT    |                                  | pos                        | GG  | 28396                     | 549                                 |
|                | 20            | ACTTTCACGACGACCCAGAAGCTCGCCGCTT   |                                  | neg                        | GG  | 28037                     | 190                                 |
| 12             | 21            | GTACGGATACTGCGACGCGGACAGGTTGGCA   |                                  | neg                        | GG  | 28107                     | 260                                 |
|                | 22            |                                   | TTGCAGCGGTGGTCCGCCAAGTCCGCGTGCA  | neg                        | GG  | 31659                     | 3812                                |
| 13             | 23            |                                   | CCGTTCAGCAAGAGTCCGACTACAACAATC   | pos                        | GG  | 28257                     | 410                                 |
|                | 24            |                                   | GTGATGCGTCTGCATCTTCCCGTCCGATGGC  | neg                        | GG  | 29855                     | 2008                                |
| 14             | 25            |                                   | GAAATCGGCACCGCCAGCAACCCAGAACT    | pos                        | GG  | 27625                     | -222                                |
|                | 26            |                                   | ACAACAAACGGGCAACCTCCAGCAGTTGACC  | pos                        | GG  | 24201                     | -3646                               |
| 16             | 27            |                                   | CGTAGGCCCGCACCCTCTCGCTGGTGGAGCC  | neg                        | AG  | 26191                     | -1656                               |
|                | 28            |                                   | GCCTCCAGCGCTGAGCAGTTGGCAAGAGCCA  | pos                        | GG  | 26086                     | -1761                               |
| 17             | 29            |                                   | CTGCACATCACCAGTTCCTTCTTCTGCT     | pos                        | GG  | 24550                     | -3297                               |
|                | 30            |                                   | TTTATGACCCGCGCCGAGTTGACGACAGCCT  | pos                        | GG  | 27259                     | -588                                |
| 18             | 31            |                                   | GTGCGCGCCAGCAGGACACAGCATGACTACC  | pos                        | GG  | 26939                     | -908                                |
|                | 32            |                                   | TGCATTACGCCCACTCGTCAACTCCGGCGAA  | pos                        | GG  | 22281                     | -5566                               |
|                | 33            |                                   | TCTCACCAGCGCAGAGTGGCGGCTACGAGC   | pos                        | TG  | 26163                     | -1684                               |
| 19             | 34            |                                   | CGAGCGTGGAGTGGACTGGAAGTCCGTGAT   | pos                        | GG  | 25639                     | -2208                               |
|                | 35            |                                   | TTGCCGCCCAATTCGGCCGCATCTGGCT     | neg                        | GG  | 27539                     | -308                                |
| 20             | 36            |                                   | GCGGTGGTACCAGCCGAGCGACTCGGCT     | pos                        | GG  | 28666                     | 819                                 |
|                | 37            |                                   | CAGGAGCCGCTGCTCTGTCGAACAGCGGcA   | neg                        | GG  | 33219                     | 5372                                |
| 21             | 38            |                                   | ACGTCCAGCGCAGTGGACAGCTGCGAGACGGT | neg                        | GG  | 30890                     | 3043                                |
|                | 39            | GTATCGTCCAGCCGGTCCAGCGTGGGCTGTT   |                                  | Pos                        | GG  | 30484                     | 2637                                |
| 22             | 40            | ATGCGGATATCGGACGACCCGGTCCGCCATT   |                                  | Neg                        | GG  | 30950                     | 3103                                |
|                | 41            | ACTTCCGCGACGCGGCTCGGGATGCTGCGC    |                                  | Pos                        | GG  | 30317                     | 2470                                |
|                | 42            | ACCATGGAGCTGGGCAACGCTCAGCACCCA    |                                  | Pos                        | GG  | 29740                     | 1893                                |
|                | 43            | GACGCCCTCACCTATGAAGTCTCGAGGTCAA   |                                  | Pos                        | GG  | 30355                     | 2508                                |
|                | 44            | GGTCCAGCGGGGAATCGCGTGGCGTTGTCCA   |                                  | Neg                        | GG  | 30702                     | 2855                                |
| 23             | 45            | CCTGATATCCAACCTGCTCCAAGAACCGCTGCC |                                  | pos                        | GG  | 30244                     | 2397                                |
|                | 46            | GACCAGATGGCGCCGAAATGTGGCCGGCA     |                                  | pos                        | GG  | 27508                     | -339                                |
| 24             | 47            | GCGCTCAGCAAACTAACGGGCAACTCCAGCA   |                                  | pos                        | GG  | 24193                     | -3654                               |
|                | 48            | TCGACCCGGATAACCTGGCGCTCACCCTAT    |                                  | pos                        | GG  | 22933                     | -4914                               |
|                | 49            | TATCGCCGCTGGCGAAGCCCAAGATTGTGA    |                                  | neg                        | GG  | 24497                     | -3350                               |
|                | 50            |                                   | GGGCTGGCGCTGCTGGGTTGGTGGCGGTC    | pos                        | GG  | 27091                     | -756                                |
|                | 51            | ACTTTCACGACGACCCAGAAGCTCGCCGCTT   |                                  | neg                        | GG  | 28037                     | 190                                 |
| 25             | 52            | GAGCTGTTCAAGTTCGCGACCCGACCCGCTCCA |                                  | pos                        | GG  | 23319                     | -4528                               |
|                | 53            | TCCTGGAGCAATCCCGCTGGCGGCGACTACT   |                                  | pos                        | GG  | 27928                     | 81                                  |
|                | 54            |                                   | TCCTGGAGCAATCCCGCTGGCGGCGACTACT  | pos                        | GG  | 27897                     | 50                                  |
|                | 55            |                                   | ACCTGGGTGCTGACGACGTTGCCAGCTCCAT  | neg                        | GG  | 29774                     | 1927                                |
|                | 56            |                                   | ACTTTCACGACGCCAGAGCGTCCGCGGTT    | neg                        | GG  | 28037                     | 190                                 |
| 26             | 57            |                                   | GAGCGCGGTCGTTGACCCAGCCGAGCGACTC  | neg                        | GG  | 28671                     | 824                                 |
|                | 58            |                                   | GTACGGTAICTGCGACGCGGACAGGTTGGCAC | neg                        | GG  | 28107                     | 260                                 |
|                | 59            |                                   | TGATCGCGCAACGATCCCCAGCAGCGGCTTT  | neg                        | GG  | 29557                     | 1710                                |
| 27             | 60            |                                   | GCGTAGAGCCAAAGGTTACCCTACGCCAAGC  | neg                        | GG  | 28556                     | 709                                 |
|                | 61            |                                   | TGCTCGCGCTGCTGCGGTCGCTATCGCGGT   | pos                        | GG  | 28295                     | 448                                 |
|                | 62            |                                   | TGGATGcAIGAcCAGTTGTTGTGAGCGCT    | neg                        | GG  | 29056                     | 1209                                |
| 28             | 63            |                                   | TGGATCACTTACCGGCTGATGCGCCCGTA    | neg                        | GG  | 29666                     | 1819                                |
|                | 64            |                                   | CGCACCGGTTACAGTCCGAGCCAGTTACCCA  | neg                        | GG  | 30467                     | 2620                                |
|                | 65            |                                   | CGCGCCGAGTTGACGACGCTGGCGCCCT     | pos                        | GG  | 27268                     | -679                                |
|                | 66            |                                   | CGGCTTCTGCTGGCTCGACGCGATAGACCA   | neg                        | GG  | 30816                     | 2969                                |
| 29             | 67            |                                   | CTGGTACCATGTTGACCAATAGGGCAAAT    | pos                        | GG  | 24349                     | -3498                               |
|                | 68            |                                   | CAGGCGCTCGCCCTCGATCAGCATTGGTTCA  | neg                        | GG  | 35798                     | 7951                                |
|                | 69            |                                   | CTCCAGCAGTTGCGGGCCGACCTCAATGCCGA | pos                        | GC  | 25945                     | -1902                               |
| 30             | 70            |                                   | ATGCGGATATCGCGACGACCCGCTCGCCATT  | neg                        | GG  | 30950                     | 3103                                |
|                | 71            |                                   | CCACGCTGAGCAGTTGGCGAAGAGCCAGGAA  | pos                        | GG  | 26090                     | -1757                               |
|                | 72            |                                   | TGGACCTCCAGGGCGAGCCGACCTGGTCTCT  | pos                        | GG  | 29965                     | 2118                                |
| 31             | 73            |                                   | TTCCGCGTGTGCTGCTGATGATGCTGATGC   | neg                        | GG  | 24420                     | -3427                               |
|                | 74            |                                   | ATGATCCCCTGTGCGGTGATGCCGCCGCGCAC | neg                        | GG  | 31359                     | 3512                                |
| 32             | 75            |                                   | GCGATTCGCGCTGACCGAGTCCGCGGGAT    | pos                        | GG  | 30685                     | 2838                                |
|                | 76            |                                   | ATGGCGCTTGAAGAACTCCCGCGCTGGCGAT  | neg                        | GG  | 32351                     | 4504                                |
|                | 77            | ACaagGgcAATCGCGCGAGTTGCTGGCGGT    |                                  | pos                        | GG  | 12414                     | 107                                 |
| 33             | 78            | TCCAACCGCTCCAGCACCTCGGCGAATGCCT   |                                  | neg                        | GG  | 12736                     | -215                                |
|                | 79            | GGTGGTANTCGAGCAGCTCGCGCGACGTCCT   |                                  | pos                        | GG  | 9804                      | 2717                                |
|                | 80            | ATcAgATTAGCAGCCAGGTTACTGAAGTTTTT  |                                  | neg                        | GG  | 27482                     | -365                                |
| 34             | 81            | AAGCGCGCTTAGAGTACGcggcGACTCGCCA   |                                  | pos                        | GG  | 23199                     | -4648                               |
|                | 82            | GAGCTGTTCAAGTTCGCGACCCGCTCGCTCCA  |                                  | pos                        | GG  | 23319                     | -4528                               |
|                | 83            | atcGACAAcTAATCCCGCTCGCCAGcGccaa   |                                  | pos                        | GG  | 26437                     | -1410                               |
| 35             | 84            | CTCAACTCCGcGCCAAGACGTATTGTCTGA    |                                  | pos                        | GG  | 28462                     | 615                                 |
|                | 85            | TCCGGCAGGAGCGGACGCGCGCGCGCGAGTT   |                                  | pos                        | GG  | 27120                     | -727                                |
|                | 86            | GCGGTCGTTGACCCAGCGGACGCTGGCGT     |                                  | neg                        | GG  | 28666                     | 819                                 |
|                | 87            | GTGTTCGGTTcGcCACCgCGCGCCacatcaa   |                                  | pos                        | GG  | 27172                     | -675                                |

\*For each isolate, spacers in columns 3 and 4 are listed in order of predicted integration based on the spacer position relative to the leader sequence in their respective CRISPR array with the leader-proximal spacer listed last.

\*\*The location of the DMS3 target is displayed as the base pair position of the 3' end of the target in the DMS3 genome

\*\*\*The distance from the primed protospacer was calculated by subtracting the position of DMS3 target (column 7) from the 3' position of the nearest primed protospacer with positive values indicating the DMS3 target is downstream of the primed protospacer with negative values indicating the DMS3 target is upstream of the primed protospacer.