

Table S11. REP HMM hits across genome sequences of *Pseudomonas* spp.

| | Number of HMM hits using E value limit of 10 ⁻³ ^a | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
|------------------------------------|-------------------------------------------------------------------------|-------|-----|-------|---------|-------|-------|-------|------|-------|--------------------|-----|-------|-----------|-------|-----------------------|--------|-----|------|------------------|------|-----|------|----------------------|-------|-----|-------|----|----------------------------|--|--|--|
| | <i>P. fluorescens</i> group | | | | | | | | | | <i>P. syringae</i> | | | | | <i>P. entomophila</i> | | | | <i>P. putida</i> | | | | <i>P. aeruginosa</i> | | | | | Other species ^c | | | |
| | Pf-5 | 30-84 | O6 | Pf0-1 | Q8r1-96 | Q2-87 | BG33R | SBW25 | A506 | SS101 | DC3000 | T1 | 1448A | NCPBP3681 | B728a | L48 | KT2440 | F1 | GB-1 | W619 | PAO1 | PA7 | PA14 | LESB58 | PACS2 | ymp | A1501 | DJ | MG1655 | | | |
| REPa (primary REP sequence) | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Pf-5 REPa | 999 | 106 | 149 | 56 | 153 | 272 | 128 | 38 | 348 | 403 | 6 | 7 | 27 | 28 | 81 | 1019 | 457 | 544 | 109 | 309 | 2 | 2 | 3 | 2 | 2 | 32 | 6 | 4 | 0 | | | |
| 30-84 REPa | 623 | 620 | 876 | 169 | 1931 | 1409 | 911 | 781 | 1329 | 1509 | 37 | 39 | 108 | 88 | 352 | 868 | 483 | 658 | 357 | 333 | 4 | 3 | 2 | 3 | 3 | 43 | 9 | 11 | 0 | | | |
| O6 REPa | 545 | 601 | 888 | 66 | 1794 | 905 | 202 | 62 | 428 | 733 | 15 | 16 | 42 | 39 | 175 | 1042 | 318 | 407 | 65 | 159 | 2 | 3 | 2 | 2 | 2 | 34 | 11 | 6 | 1 | | | |
| Q8r1-96 REPa | 49 | 487 | 785 | 110 | 1987 | 1127 | 251 | 71 | 578 | 810 | 13 | 12 | 48 | 42 | 128 | 242 | 135 | 154 | 54 | 152 | 1 | 3 | 1 | 1 | 1 | 7 | 1 | 2 | 0 | | | |
| Q2-87 REPa | 470 | 456 | 611 | 172 | 1776 | 1276 | 965 | 729 | 1394 | 1586 | 54 | 51 | 100 | 77 | 257 | 685 | 685 | 980 | 302 | 244 | 1 | 0 | 0 | 1 | 1 | 13 | 3 | 7 | 0 | | | |
| BG33r REPa | 252 | 397 | 516 | 134 | 1574 | 1807 | 1119 | 1140 | 1419 | 1613 | 18 | 18 | 40 | 46 | 118 | 421 | 474 | 642 | 182 | 253 | 0 | 1 | 0 | 0 | 0 | 23 | 6 | 4 | 0 | | | |
| SBW25 REPa ^b | 45 | 260 | 348 | 123 | 1581 | 1468 | 1017 | 1024 | 1308 | 1113 | 25 | 23 | 48 | 46 | 110 | 52 | 295 | 360 | 125 | 195 | 0 | 0 | 0 | 0 | 0 | 3 | 1 | 2 | 0 | | | |
| A506 REPa | 763 | 303 | 423 | 140 | 1582 | 1175 | 879 | 718 | 1397 | 1350 | 27 | 22 | 51 | 44 | 94 | 558 | 412 | 523 | 171 | 315 | 0 | 1 | 1 | 0 | 0 | 13 | 2 | 3 | 0 | | | |
| SS101 REPa | 823 | 367 | 547 | 136 | 1666 | 1190 | 932 | 738 | 1434 | 1559 | 40 | 34 | 83 | 64 | 154 | 571 | 518 | 719 | 183 | 309 | 0 | 0 | 0 | 0 | 0 | 17 | 4 | 4 | 1 | | | |
| REPb | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| 30-84 REPb | 186 | 801 | 683 | 0 | 13 | 1 | 3 | 14 | 16 | 6 | 0 | 0 | 0 | 1 | 2 | 2 | 1 | 3 | 0 | 1 | 3 | 1 | 3 | 3 | 3 | 1 | 1 | 3 | 0 | | | |
| O6 REPb | 185 | 804 | 676 | 1 | 27 | 1 | 4 | 21 | 18 | 7 | 0 | 0 | 0 | 0 | 1 | 1 | 0 | 1 | 0 | 2 | 1 | 1 | 1 | 1 | 1 | 0 | 1 | 2 | 0 | | | |
| REPe | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| A506 REPe | 0 | 1 | 1 | 140 | 213 | 0 | 3 | 5 | 255 | 291 | 183 | 167 | 341 | 92 | 356 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 1 | 0 | 0 | 5 | 0 | 4 | 0 | | | |
| SS101 REPe | 0 | 0 | 0 | 114 | 203 | 0 | 4 | 3 | 243 | 270 | 170 | 159 | 331 | 68 | 342 | 0 | 1 | 0 | 1 | 1 | 0 | 0 | 0 | 0 | 4 | 0 | 2 | 0 | | | | |
| REPd | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| Q2-87 REPd | 22 | 8 | 7 | 2 | 101 | 774 | 32 | 514 | 35 | 25 | 0 | 1 | 0 | 0 | 0 | 3 | 0 | 5 | 0 | 1 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | 0 | | | |
| SBW25 REPd ^b | 40 | 10 | 5 | 28 | 883 | 1005 | 476 | 981 | 88 | 77 | 8 | 7 | 27 | 25 | 94 | 3 | 3 | 4 | 2 | 2 | 0 | 0 | 0 | 1 | 0 | 0 | 3 | 2 | 0 | | | |
| REPe | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
| SBW25 REPe ^b | 5 | 6 | 6 | 11 | 14 | 11 | 9 | 325 | 36 | 28 | 1 | 2 | 5 | 6 | 6 | 54 | 11 | 21 | 6 | 9 | 9 | 17 | 12 | 11 | 10 | 6 | 4 | 6 | 0 | | | |

Color codes: Grey, genomes having ≥ 100 REPa sequences; pink, genomes having ≥ 100 REPb sequences; green, genomes having ≥ 100 REPe sequences; dark orange, genomes having ≥ 100 REPd sequences; gold, genomes having ≥ 30 but <100 REPd sequences; blue, genomes having ≥ 100 REPe sequences.

a. Using an E value cut off of 10⁻³ we observed very little overlap between HMM hits of secondary REP HMMs with those of the primary REPa HMM from each strain. Refer to Figure 1 for species designations of strains.

b. Using an E value cut off of 10⁻³ we observed a degree of overlap between SBW25 REPa, REPd and REPe HMM hits. However, using a stringency of 10⁻⁷ this overlap is negligible.

c. *Pseudomonas mendocina* strain ymp, *Pseudomonas stutzeri* A1501, *Azotobacteria vinelandii* DJ, and *Escherichia coli* MG1655