# SUPPLEMENTAL MATERIAL

TABLE S1. Primers used in this study

| **Primer (gene)** | **5' to 3' sequence**[a] |
|---|---|
| **Primers used for constructing RpoE overexpression vectors** | |
| P1 (*rpoE* F) | ATATATCATATGATGGGTGACCAAATAACCGATCAAG |
| P2 (*rpoE* R1) | ATATATGGATCCTTAACTCTGTTGCATCAGTGGATTG |
| P3 (*rpoE-FLAG* F) | TTCGCACTAGAAATAATTTTGTTTAACTTTAAGAAGGAGATATACATATGGACTACAAAGACCATGACGGTGATT |
| P4 (*rpoE-FLAG* R) | TCACCTTGCTGTGCACGCTCAACCAATACTTGATCGGTTATTTGGTCACCCTTGTCATCGTCATCCTTGTAATCG |
| P5 (*FLAG* F) | ATGGACTACAAAGACCATGACGGTG |
| P6 (*rpoE* R2) | TAAAATATTAACTCTGTTGCATCAGTGGATTG |
| **Primers used for RT-PCR** | |
| P7 (*rpoE-rseA* F) | CATATCGAATTCGGGCGCAACTTCGAGAAAGTGATA |
| P8 (*rpoE-rseA* R) | CATATCGGATCCGCAATGCCCGCTTGTATGATAGGA |
| P9 (*rseA-rseC* F) | TAGCTAACTAGTCGATGGGTGCGAAGTTGATGATGT |
| P10 (*rseA-rseC* R) | CATATCGGATCCCCTGCGACCAACGGCATATTTACT |
| P11 (*rseC-fadD* F) | AGCTATCCATGGATGATGGTTGAAACAGCAAC |
| P12 (*rseC-fadD* R) | TAGCTAACTAGTCTTCAATAACGGCTCAGCAACCCA |
| **Primers used for qRT-PCR** | |
| P13 (*HD0518* RT F) | GGCTGAATTGACCGCTTTATC |
| P14 (*HD0518* RT R) | CAGGGTCTGGGTTGTTTACT |
| P15 (*rluA* RT F) | CGGGCAATCGACCAGAATA |
| P16 (*rluA* RT R) | CCGCTCGTTGCCATATCTAA |
| P17 (*dsbA* RT F) | TAGCGGCTGATGCTGTTGAAGGAA |
| P18 (*dsbA* RT R) | GGCAACGCTTGCTTAATTTGTGCTGG |
| P19 (*degP* RT F) | TGCGTTATCGGATGTTGCGCTAGT |
| P20 (*degP* RT R) | ATACCAGATGTCACCGTTTGCCCT |
| P21 (*HD0192* RT F) | GTAACAGACACTGCAGCAAAC |
| P22 (*HD0192* RT R) | CAGCCGATTCTTTCATGTCTTC |
| **Primers used for generating the reporter constructs** | |
| P23 (*dsbA* rep F) | ATATATAGATCTGGTTTTTTAAGGAACTAAAAGGTG |
| P24 (*dsbA* rep R) | ATATATAGATCTTAGTGTTCCTTAAAATAATTAGTG |
| P25 (*degP* rep F) | GGCCATAGATCTCACGCAAATTAAGGTTTTCATAAA |
| P26 (*degP* rep R) | GGCCATAGATCTGACTTTATTCATTCGTATCATCCT |
| P27 (*hfq* rep F) | ATATATAGATCTGAGGTCGAAAAGTTATACGCGA |
| P28 (*hfq* rep R) | AGATATAGATCTTCTCTTTTCCTTTTTATTTTGTTT |
| P29 (*rpoE* rep F) | ATATATAGATCTCCGCTTAATTTTGAAAAATTCGAG |
| P30 (*rpoE* rep R) | ATATATAGATCTTTTATTTGCGTTCTCCTACTCAAT |
| P31 (*rpoH* rep F) | ATATATAGATCTGCGCGAAGGCTAAATGCAGGTTAT |
| P32 (*rpoH* rep R) | AGATATAGATCTGCTCTTTCTCGTGTAGTTCTTTGA |
| P33 (*p15A* F) | CTACCAGCGGTGGTTTTTCAAATATGTATCCGCTCATGAG |
| P34 (*p15A* R) | GACCGGAGGCTTTTGGCGCTAGCGGAGTGTATAC |
| P35 (*pT* F) | CAAAAGCCTCCGGTCGGA |
| P36 (*pT* R) | AAACCACCGCTGGTAGCG |
| **Primers used for site directed mutagenesis** | |
| P37 (*rpoH* mut F1) | GGGATTAGCGAAGTCCAAAAAGCACGTCGAGGTGCGGTA |
| P38 (*rpoH* mut R1) | TACCGCACCTCGACGTGCTTTTTGGACTTCGCTAATCCC |
| P39 (*rpoH* mut F2) | CCACTTTGACAGCTAATAAAAAAACCAAAAACCGTGCAATTTACAAATACCGTTTACAG |
| P40 (*rpoH* mut R2) | CTGTAAACGGTATTTGTAAATTGCACGGTTTTTGGTTTTTTTATTAGCTGTCAAAGTGG |

Underlining indicates regions corresponding to restriction enzyme sites as mentioned in the text. *H. ducreyi* sequences are from GenBank accession no. AE017143. Primers used for qRT-PCR analysis of *dnaE*, *HD0430*, *HD0930*, *fimA*, *hfq*, and *ompP2B* have been described previously (11).

## TABLE S2. Summary of RNA-Seq read statistics.

| Bacterial strain | Time (minutes) | Biological replicate | Total reads | Aligned reads | % aligned reads | Average coverage/nt | Intergenic reads | % intergenic reads |
|---|---|---|---|---|---|---|---|---|
| 35000HP-(pDG10) | 0 | R1 | 13,589,450 | 12,736,961 | 93.7 | 7.5 | 2,357,729 | 18.5 |
| | | R2 | 14,596,082 | 13,545,067 | 92.8 | 8.0 | 2,424,639 | 17.9 |
| | | R3 | 14,420,320 | 13,340,948 | 92.5 | 7.9 | 1,962,803 | 14.7 |
| | | R4 | 19,580,696 | 17,757,964 | 90.7 | 10.5 | 2,551,870 | 14.4 |
| | 5 | R1 | 14,131,185 | 13,214,407 | 93.5 | 7.8 | 2,180,469 | 16.5 |
| | | R2 | 13,415,750 | 12,437,051 | 92.7 | 7.3 | 1,993,433 | 16.0 |
| | | R3 | 14,505,393 | 13,425,485 | 92.6 | 7.9 | 1,577,955 | 11.8 |
| | | R4 | 14,191,670 | 12,976,132 | 91.4 | 7.6 | 1,995,425 | 15.4 |
| | 10 | R1 | 13,984,110 | 13,157,018 | 94.1 | 7.7 | 2,001,501 | 15.2 |
| | | R2 | 12,397,169 | 11,561,606 | 93.3 | 6.8 | 2,062,093 | 17.8 |
| | | R3 | 14,663,147 | 13,621,679 | 92.9 | 8.0 | 1,428,346 | 10.5 |
| | | R4 | 14,095,207 | 12,906,685 | 91.6 | 7.6 | 1,896,426 | 14.7 |
| 35000HP-(pDG9) | 0 | R1 | 16,414,348 | 15,657,482 | 95.4 | 9.2 | 2,905,343 | 18.6 |
| | | R2 | 13,254,910 | 12,618,611 | 95.2 | 7.4 | 2,363,239 | 18.7 |
| | | R3 | 13,654,380 | 13,074,424 | 95.8 | 7.7 | 1,440,740 | 11.0 |
| | | R4 | 11,194,376 | 10,733,401 | 95.9 | 6.3 | 1,709,079 | 15.9 |
| | 5 | R1 | 12,025,896 | 11,562,282 | 96.1 | 6.8 | 1,518,910 | 13.1 |
| | | R2 | 12,994,803 | 12,470,595 | 96.0 | 7.3 | 1,991,359 | 16.0 |
| | | R3 | 13,319,602 | 12,812,443 | 96.2 | 7.5 | 1,683,514 | 13.1 |
| | | R4 | 11,262,696 | 10,815,640 | 96.0 | 6.4 | 1,086,657 | 10.0 |
| | 10 | R1 | 12,226,178 | 11,793,624 | 96.5 | 6.9 | 1,501,448 | 12.7 |
| | | R2 | 14,346,417 | 13,817,520 | 96.3 | 8.1 | 2,092,132 | 15.1 |
| | | R3 | 13,923,212 | 13,459,211 | 96.7 | 7.9 | 1,157,958 | 8.6 |
| | | R4 | 10,305,741 | 9,956,442 | 96.6 | 5.9 | 913,060 | 9.2 |

TABLE S3. ORFs annotated as encoding hypothetical proteins differentially expressed by overexpression of RpoE in *H. ducreyi*.

| **ORF** | **Description** | **5 minutes**[a] | | **10 minutes**[b] | |
|---|---|---|---|---|---|
| | | **Fold change** | ***P* value** | **Fold change** | ***P* value** |
| **UPREGULATED ORFs** | | | | | |
| *HD0035* | | 2.5 | 5.0E-29 | 4.1 | 1.7E-73 |
| *HD0055* | | 3.7 | 1.9E-45 | 5.4 | 1.3E-83 |
| *HD0065* | | | | 3.0 | 1.5E-49 |
| *HD0087* | | 6.3 | 6.6E-35 | 8.6 | 9.0E-58 |
| *HD0095* | | | | 2.1 | 8.3E-03 |
| *HD0096* | | | | 2.7 | 2.0E-05 |
| *HD0097* | | | | 2.5 | 7.1E-09 |
| *HD0098* | | 2.2 | 1.3E-03 | 2.6 | 9.9E-08 |
| *HD0099* | | | | 3.1 | 1.4E-02 |
| *HD0102* | | | | 2.1 | 4.5E-07 |
| *HD0107* | | | | 2.4 | 3.9E-05 |
| *HD0108* | | | | 2.3 | 2.4E-09 |
| *HD0109* | | | | 2.5 | 3.3E-07 |
| *HD0110* | | | | 2.8 | 1.4E-11 |
| *HD0111* | | 2.0 | 3.9E-05 | 3.5 | 2.0E-22 |
| *HD0112* | | 2.4 | 1.1E-04 | 2.7 | 1.2E-06 |
| *HD0118* | | 3.6 | 1.3E-04 | 5.6 | 2.1E-12 |
| *HD0119* | | 2.3 | 2.9E-06 | 4.1 | 1.0E-18 |
| *HD0120* | | | | 2.0 | 3.6E-07 |
| *HD0121* | | | | 2.7 | 5.3E-14 |
| *HD0123* | | | | 3.1 | 9.0E-34 |
| *HD0124* | | | | 2.4 | 2.2E-22 |
| *HD0132* | | | | 3.3 | 1.3E-27 |
| *HD0133* | | 2.5 | 4.0E-09 | 4.7 | 7.2E-32 |
| *HD0134* | | 2.2 | 1.8E-11 | 4.7 | 2.0E-47 |
| *HD0135* | | 2.3 | 8.7E-12 | 5.7 | 8.7E-52 |
| *HD0136* | | 2.7 | 8.1E-18 | 6.6 | 1.0E-68 |
| *HD0137* | | 3.3 | 3.3E-15 | 6.9 | 3.7E-48 |
| *HD0138* | | 2.1 | 5.6E-08 | 5.2 | 7.9E-27 |
| *HD0140* | | | | 3.3 | 3.0E-37 |
| *HD0141* | | | | 2.1 | 1.2E-14 |
| *HD0142* | | | | 3.6 | 3.4E-15 |
| *HD0143* | | 2.2 | 1.2E-02 | 3.6 | 2.6E-09 |
| *HD0145* | | | | 2.4 | 5.0E-17 |
| *HD0146* | | 2.1 | 1.3E-15 | 3.7 | 1.2E-51 |
| *HD0147* | | 2.7 | 6.2E-17 | 4.8 | 2.6E-48 |
| *HD0148* | | 3.4 | 9.9E-51 | 6.9 | 1.2E-132 |
| *HD0149* | | | | 4.0 | 3.5E-14 |
| *HD0150* | | | | 2.3 | 1.4E-17 |
| *HD0153* | | | | 3.7 | 4.6E-16 |
| *HD0192* | | 10.6 | 1.1E-157 | 18.7 | 4.8E-290 |
| *HD0222* | | | | 2.3 | 1.6E-24 |
| *HD0236* | | | | 2.6 | 1.5E-09 |
| *HD0254* | | 3.0 | 9.6E-42 | 4.6 | 1.2E-95 |
| *HD0255* | | 3.9 | 1.5E-64 | 6.7 | 6.6E-146 |
| *HD0256* | | 5.4 | 1.1E-101 | 10.3 | 9.7E-219 |
| *HD0257* | | 5.5 | 1.4E-103 | 9.8 | 6.2E-211 |
| *HD0261* | | 3.7 | 4.6E-53 | 5.6 | 4.5E-115 |
| *HD0267* | | 2.0 | 2.6E-15 | 2.5 | 4.3E-31 |
| *HD0280* | | 2.4 | 1.4E-09 | 3.3 | 2.8E-26 |
| *HD0285* | | 2.1 | 6.1E-19 | 3.3 | 2.3E-59 |
| *HD0286* | | 2.0 | 1.2E-15 | 3.3 | 3.5E-53 |
| *HD0425* | | | | 2.3 | 3.2E-30 |
| *HD0429* | | | | 2.7 | 5.1E-04 |
| *HD0430* | | 2.6 | 5.8E-04 | 3.1 | 1.2E-07 |
| *HD0431* | | 3.8 | 2.9E-08 | 5.2 | 7.2E-17 |

| ORF | Description | 5 minutes[a] | | 10 minutes[b] | |
|---|---|---|---|---|---|
| | | **Fold change** | ***P* value** | **Fold change** | ***P* value** |
| *HD0432* | | 2.1 | 3.4E-07 | 2.5 | 8.1E-15 |
| *HD0470* | | 4.2 | 1.2E-64 | 5.7 | 1.2E-119 |
| *HD0478* | | 3.7 | 2.0E-42 | 4.6 | 8.5E-73 |
| *HD0489* | | | | 2.6 | 6.2E-13 |
| *HD0495* | | 3.9 | 8.9E-13 | 5.9 | 4.6E-30 |
| *HD0496* | | 3.4 | 1.2E-23 | 5.4 | 3.1E-53 |
| *HD0497* | | 2.0 | 3.8E-08 | 3.6 | 6.0E-30 |
| *HD0501* | | | | 2.6 | 2.9E-32 |
| *HD0502* | | | | 2.0 | 1.2E-03 |
| *HD0503* | | | | 3.4 | 4.7E-05 |
| *HD0504* | | | | 2.7 | 3.6E-16 |
| *HD0506* | | | | 4.3 | 6.6E-10 |
| *HD0507* | | | | 2.7 | 9.6E-12 |
| *HD0509* | | 2.0 | 3.3E-07 | 3.3 | 8.1E-24 |
| *HD0514* | | | | 2.9 | 1.3E-32 |
| *HD0518* | | 6.1 | 6.3E-83 | 10.5 | 8.8E-162 |
| *HD0519* | | 2.8 | 1.6E-18 | 4.3 | 3.6E-45 |
| *HD0520* | | | | 3.3 | 1.3E-21 |
| *HD0521* | | | | 3.3 | 2.2E-21 |
| *HD0522* | | | | 2.7 | 9.1E-24 |
| *HD0523* | | | | 2.9 | 2.1E-34 |
| *HD0527* | | | | 3.0 | 2.6E-36 |
| *HD0529* | | | | 2.9 | 1.6E-27 |
| *HD0530* | | | | 3.0 | 1.5E-29 |
| *HD0531* | | 2.1 | 4.1E-11 | 3.9 | 6.0E-45 |
| *HD0532* | | | | 2.7 | 3.2E-28 |
| *HD0538* | | | | 2.1 | 7.3E-18 |
| *HD0552* | | 3.1 | 2.1E-43 | 4.8 | 5.2E-99 |
| *HD0553* | | 2.6 | 1.9E-34 | 3.7 | 3.5E-77 |
| *HD0584* | | 2.3 | 1.3E-20 | 3.4 | 1.7E-55 |
| *HD0586* | | 2.7 | 3.1E-30 | 3.8 | 1.5E-69 |
| *HD0587* | | 2.7 | 1.5E-33 | 3.7 | 2.4E-71 |
| *HD0627* | | | | 2.1 | 4.2E-12 |
| *HD0664* | | 6.5 | 4.2E-74 | 11.3 | 6.0E-148 |
| *HD0665* | | 8.4 | 6.3E-131 | 17.5 | 1.1E-274 |
| *HD0680* | | 7.4 | 3.9E-116 | 12.3 | 6.7E-221 |
| *HD0681* | | 5.0 | 1.1E-84 | 8.2 | 5.4E-171 |
| *HD0694* | | | | 2.9 | 3.1E-36 |
| *HD0697* | | 3.7 | 1.5E-59 | 5.8 | 1.1E-126 |
| *HD0698* | | 4.2 | 2.0E-74 | 6.6 | 8.3E-151 |
| *HD0713* | | | | 2.3 | 3.8E-27 |
| *HD0720* | | 7.6 | 2.7E-36 | 10.0 | 5.2E-61 |
| *HD0746* | | | | 2.2 | 2.9E-34 |
| *HD0754* | | 2.4 | 1.4E-13 | 4.1 | 2.4E-54 |
| *HD0756* | | 2.6 | 5.3E-35 | 4.8 | 7.2E-103 |
| *HD0757* | | 4.3 | 2.9E-71 | 7.7 | 3.1E-162 |
| *HD0799* | | 4.5 | 2.2E-76 | 6.4 | 4.3E-140 |
| *HD0800* | | | | 2.0 | 4.8E-19 |
| *HD0884* | | 3.2 | 1.3E-41 | 5.8 | 2.7E-115 |
| *HD0899* | | | | 2.5 | 6.1E-20 |
| *HD0918* | | 5.1 | 1.0E-78 | 7.7 | 1.1E-144 |
| *HD0919* | | 3.5 | 9.1E-44 | 6.5 | 1.5E-105 |
| *HD0920* | | 2.6 | 8.5E-19 | 4.5 | 1.0E-50 |
| *HD0921* | | 2.5 | 2.9E-23 | 5.5 | 6.9E-81 |
| *HD0922* | | 2.6 | 9.3E-35 | 5.4 | 1.7E-108 |
| *HD0927* | | 3.1 | 1.4E-17 | 6.3 | 1.8E-55 |
| *HD0928* | | 3.4 | 1.6E-42 | 6.9 | 1.1E-114 |
| *HD0930* | | 6.0 | 6.6E-72 | 9.1 | 1.9E-129 |
| *HD0931* | | 6.4 | 2.3E-97 | 11.5 | 2.8E-186 |
| *HD0932* | | 6.0 | 4.8E-75 | 12.2 | 3.1E-162 |

| ORF | Description | 5 minutes[a] | | 10 minutes[b] | |
|---|---|---|---|---|---|
| | | **Fold change** | ***P* value** | **Fold change** | ***P* value** |
| *HD0933* | | 4.4 | 8.8E-77 | 8.5 | 1.3E-182 |
| *HD0937* | | 3.5 | 4.5E-19 | 4.5 | 3.4E-37 |
| *HD0938* | | 3.2 | 1.3E-30 | 7.1 | 1.5E-93 |
| *HD0939* | | 5.4 | 2.9E-58 | 9.5 | 1.1E-121 |
| *HD0940* | | 2.4 | 1.0E-15 | 4.7 | 4.1E-50 |
| *HD0941* | | | | 2.9 | 1.8E-34 |
| *HD0947* | | | | 2.6 | 1.4E-32 |
| *HD0959* | | | | 2.1 | 2.7E-05 |
| *HD0960* | | 2.0 | 2.6E-08 | 3.0 | 2.6E-23 |
| *HD0961* | | | | 2.4 | 1.0E-23 |
| *HD0965* | | | | 2.3 | 2.6E-07 |
| *HD1011* | | | | 2.4 | 3.6E-32 |
| *HD1031* | | 7.0 | 9.1E-121 | 12.7 | 9.3E-239 |
| *HD1060* | | 9.5 | 2.2E-170 | | |
| *HD1090* | | 3.0 | 4.1E-05 | 3.1 | 6.8E-07 |
| *HD1126* | | | | 2.1 | 3.3E-10 |
| *HD1136* | | | | 3.0 | 3.0E-50 |
| *HD1137* | | 2.3 | 1.6E-26 | 3.5 | 2.7E-66 |
| *HD1138* | | 2.4 | 3.6E-28 | 3.7 | 3.4E-74 |
| *HD1190* | | | | 2.6 | 4.4E-40 |
| *HD1216* | | 2.3 | 1.0E-24 | 3.0 | 3.1E-52 |
| *HD1218* | | 13.5 | 2.4E-195 | | |
| *HD1239* | | 3.0 | 1.1E-45 | 5.3 | 7.5E-120 |
| *HD1339* | | 3.5 | 6.6E-63 | 5.1 | 3.0E-124 |
| *HD1343* | | 2.6 | 1.8E-39 | 4.7 | 2.0E-106 |
| *HD1400* | | 6.9 | 2.0E-128 | 11.9 | 9.3E-244 |
| *HD1408* | | 3.1 | 3.3E-48 | 4.1 | 3.6E-90 |
| *HD1409* | | 3.7 | 3.7E-54 | 5.4 | 1.6E-111 |
| *HD1410* | | 2.9 | 1.1E-35 | 4.0 | 1.1E-74 |
| *HD1413* | | | | 2.4 | 6.9E-32 |
| *HD1437* | | | | 2.3 | 6.4E-14 |
| *HD1444* | | 2.2 | 2.0E-10 | 2.6 | 1.6E-20 |
| *HD1452* | | 2.1 | 2.4E-09 | 2.5 | 6.4E-21 |
| *HD1471* | | 2.1 | 2.5E-20 | 2.6 | 3.3E-41 |
| *HD1517* | | | | 2.5 | 2.8E-04 |
| *HD1528* | | | | 2.2 | 6.7E-18 |
| *HD1530* | | | | 2.2 | 2.2E-13 |
| *HD1532* | | | | 2.0 | 8.9E-14 |
| *HD1533* | | | | 2.4 | 5.6E-12 |
| *HD1534* | | 2.4 | 8.3E-06 | 2.7 | 1.5E-08 |
| *HD1548* | | 2.9 | 2.7E-14 | 3.7 | 9.7E-27 |
| *HD1549* | | 2.3 | 4.5E-14 | 3.5 | 2.0E-36 |
| *HD1550* | | | | 2.4 | 3.2E-16 |
| *HD1552* | | 2.0 | 2.5E-07 | 2.5 | 7.8E-14 |
| *HD1553* | | | | 2.4 | 3.1E-14 |
| *HD1554* | | | | 2.8 | 5.4E-25 |
| *HD1555* | | 2.3 | 5.4E-18 | 3.7 | 1.1E-51 |
| *HD1556* | | | | 3.4 | 1.7E-41 |
| *HD1557* | | 2.6 | 1.3E-29 | 4.7 | 3.4E-85 |
| *HD1558* | | 2.4 | 1.3E-14 | 3.8 | 1.0E-39 |
| *HD1559* | | | | 2.4 | 6.0E-22 |
| *HD1560* | | | | 2.5 | 1.0E-16 |
| *HD1561* | | | | 2.6 | 2.1E-29 |
| *HD1562* | | | | 2.5 | 1.4E-21 |
| *HD1563* | | | | 2.6 | 4.0E-19 |
| *HD1564* | | | | 2.8 | 1.2E-19 |
| *HD1565* | | | | 2.8 | 2.7E-37 |
| *HD1567* | | | | 2.1 | 2.7E-08 |
| *HD1569* | | | | 3.0 | 8.0E-36 |
| *HD1571* | | | | 2.5 | 6.5E-25 |

| ORF | Description | 5 minutes[a] | | 10 minutes[b] | |
|---|---|---|---|---|---|
| | | Fold change | *P* value | Fold change | *P* value |
| *HD1572* | | | | 2.5 | 2.6E-27 |
| *HD1573* | | | | 3.3 | 2.0E-37 |
| *HD1574* | | | | 2.5 | 2.9E-24 |
| *HD1694* | | | | 2.0 | 2.8E-06 |
| *HD1714* | | | | 2.5 | 7.3E-24 |
| *HD1730* | | | | 3.2 | 4.7E-04 |
| *HD1749* | | | | 2.2 | 1.1E-28 |
| *HD1769* | | 3.0 | 1.6E-46 | 4.4 | 6.2E-97 |
| *HD1770* | | 2.0 | 1.2E-20 | 2.5 | 4.9E-41 |
| *HD1820* | | 2.5 | 2.8E-23 | 3.8 | 3.6E-62 |
| *HD1821* | | 2.4 | 2.0E-19 | 3.6 | 1.8E-52 |
| *HD1825* | | | | 2.7 | 4.7E-32 |
| *HD1827* | | 2.2 | 4.2E-21 | 3.1 | 5.4E-54 |
| *HD1828* | | 3.3 | 4.2E-46 | 4.8 | 1.4E-97 |
| *HD1829* | | 4.6 | 1.2E-76 | 7.2 | 1.4E-152 |
| *HD1904* | | | | 2.1 | 2.9E-06 |
| *HD1916* | | | | 2.3 | 3.2E-30 |
| *HD1936* | | 2.8 | 7.1E-27 | 4.5 | 2.4E-75 |
| *HD1937* | | 2.2 | 5.2E-17 | 3.5 | 7.5E-56 |
| *HD1989* | | | | 2.2 | 6.5E-04 |
| *HD2011* | | | | 2.2 | 1.2E-19 |
| *HD2014* | | 3.0 | 1.7E-29 | 4.4 | 1.1E-70 |
| *HD2015* | | 2.2 | 8.3E-30 | 3.1 | 5.4E-67 |
| *HD2017* | | | | 2.1 | 2.8E-34 |
| **DOWNREGULATED ORFs** | | | | | |
| *HD1434* | | -2.4 | 3.1E-23 | -3.1 | 2.9E-46 |

[a] Mean fold change in expression in 35000HP(pDG9) compared to 35000HP(pDG10) at 5 minutes after induction of RpoE; the fold change was normalized by dividing the fold change at 5 minutes with that of 0 minutes.

[b] Mean fold change in expression in 35000HP(pDG9) compared to 35000HP(pDG10) at 10 minutes after induction of RpoE; the fold change was normalized by dividing the fold change at 10 minutes with that of 0 minutes.

TABLE S4. TSSs predicted based on the RNA-Seq data.

| Gene[a] | TSS[b] |
|---|---|
| *ampD* | 1471939 |
| *apt* | 1523764 |
| *asnC* | 1608803 |
| *cysZ* | 662685 |
| *dacA* | * |
| *degP* | 196542 |
| *glmM* | * |
| *HD0035* | 31995 |
| *HD0055* | 49635 |
| *HD0112* | * |
| *HD0119* | * |
| *HD0133* | * |
| *HD0192* | 137210 |
| *HD0267* | * |
| *HD0285* | * |
| *HD0286* | 220667 |
| *HD0470* | 370043 |
| *HD0478* | * |
| *HD0518* | * |
| *HD0531* | * |
| *HD0553* | 425006 |
| *HD0665* | 527663 |
| *HD0681* | * |
| *HD0720* | * |
| *HD0799* | 634226 |
| *HD0918* | * |
| *HD0919* | 734893 |
| *HD0920* | 735284 |
| *HD0921* | * |
| *HD0939* | * |
| *HD0940* | * |
| *HD0947* | * |
| *HD0961* | * |
| *HD1060* | 843443 |
| *HD1218* | 988319 |
| *HD1239* | 1007377 |
| *HD1339* | * |
| *HD1400* | 1146714 |
| *HD1408* | * |
| *HD1409* | 1153213 |
| *HD1410* | 1153873 |
| *HD1471* | * |
| *HD1534* | * |
| *HD1548* | * |
| *HD1552* | * |
| *HD1558* | * |
| *HD1770* | * |
| *HD1829* | 1533088 |
| *HD2015* | 1678014 |
| *lsgA* | 704913 |
| *lysA* | * |

| Gene[a] | TSS[b] |
|---|---:|
| *mazG* | 1203420 |
| *mdh* | * |
| *mogA* | 52322 |
| *murA* | * |
| *mutT* | 1496726 |
| *nlpD* | * |
| *oapA* | 514734 |
| *oapB* | 516147 |
| *prc* | 802045 |
| *proQ* | 801373 |
| *rpoE* | 952467 |
| *rpoH* | 71151 |
| *rseC* | 953992 |
| *rsuA* | * |
| *sbcB* | 1156700 |
| *smpA* | 985518 |
| *surA* | 958955 |
| *surE* | 597140 |
| *upp* | 956224 |
| *uppS* | 975038 |
| *uvrD* | * |
| *waaF* | * |
| *hfq* | 583087 |
| *dsbA* | 501598 |
| *lspB* | 921940 |

[a] Gene or the first gene in the operon; operon structures predicted by the DOOR database were used.

[b] Coordinates of the TSS predicted using the RNA-Seq data.

*Genes for which TSSs were unclear.

TABLE S5. Putative RpoE promoters in the upstream regions of RpoE-dependent TUs.

| Gene | Putative RpoE promoter[a] | Spacer[b] | Position[c] | Score[d] | Position of additional putative promoters[e] |
|---|---|---|---|---|---|
| *HD0035*[f] | **TAAACTA**TAATGTAATAAA**TCAAA** | 12 | -135, -116 | 3.3, 3.8 | |
| *HD0055* | **GCATCAT**TAGCTTGGAAG**GCTAA** | 11 | -348, -330 | 3.4, 2.9 | |
| *HD0112*[f] | **TGCACTT**ATTTTTACCCATCA**CCAAA** | 14 | -30, -9 | 2.7, 3.3 | |
| *HD0119*[f] | **GCATTTT**TTATTCCTTTTTAT**TCAAA** | 14 | 35, 56 | 3.3, 3.8 | |
| *HD0133*[f] | **TAATCGT**TGCCGATTATCTGTAAATT**TCAAA** | 19 | -97, -71 | 2.5, 3.8 | |
| *HD0192*[f] | **TGAACCC**GCTACCGAACAGCAA**CCAAA** | 15 | -448, -426 | 2.7, 3.3 | |
| *HD0267*[f] | **TCAACCA**TATCACTTACATCAAGGTTA**TCTAA** | 20 | -317, -290 | 3.2, 3.7 | |
| *HD0280*[f] | **GGATGTT**TACATTAGTTTTTGAACCA**TCTAA** | 19 | -432, -406 | 2.8, 3.7 | |
| *HD0285* | **TGATCCT**GTTGATATTTGGAGT**GCTAA** | 15 | 35, 57 | 3.7, 2.9 | |
| *HD0286*[f] | **TAAATTT**TGGTGAAATGAGC**CCAAA** | 13 | -415, -395 | 2.9, 3.3 | |
| *HD0470*[f] | **TGAACTT**AGCAAAGTGCCATTGG**TCAAA** | 16 | -85, -62 | 4.8, 3.8 | 40, 61; 40, 66 |
| *HD0478*[f] | **TAAACTT**TGACGCATTTCCCG**CCAAA** | 14 | -281, -260 | 4.1, 3.3 | -419, -400; -35,-12 |
| *HD0518*[f] | **TCAACTG**CATTTTACAAAAATCCC**TCAAA** | 17 | -102, -78 | 4.0, 3.8 | -96, -78; -38, -17 |
| *HD0531* | **CCACCCT**GATGCCTTACTCG**TCTAT** | 13 | -297, -277 | 2.1, 3.0 | |
| *HD0553* | **TGATCTT**GATAAACCCCCACAA**TCAAG** | 15 | -403, -381 | 4.3, 2.6 | |
| *HD0665*[f] | **TGAACTT**ATCTACATTGCAAGAT**TCTAA** | 16 | -132, -109 | 4.8, 3.7 | |
| *HD0681*[f] | **TGAACTA**ATAAACAAATTATATC**TCTAA** | 16 | -36, -13 | 4.0, 3.7 | |
| *HD0720*[f] | **TCATCTT**CAAAAAAGCGCGCAGAAGCT**TCTAA** | 20 | -382, -355 | 4.1, 3.7 | -277, -260 |
| *HD0754* | **CGATCCG**TTATTTGCCGATCCGA**CCATA** | 16 | -183, -160 | 2.9, 2.6 | |
| *HD0799*[f] | **TCAATTA**CCTGACACGATTG**CCAAA** | 13 | -394, -374 | 2.6, 3.3 | -322, -296 |
| *HD0918* | **GCATCTT**CAAATATGGAACAAC**TCATT** | 15 | -404, -382 | 4.5, 2.4 | |
| *HD0919*[f] | **CGAATTG**GCTGATTAGACCGAGTG**TCAAA** | 17 | -419, -395 | 2.8, 3.8 | |
| *HD0920* | **TCATCCT**GAACTTGCCCATCA**GCTAT** | 14 | -154, -133 | 3.5, 2.1 | |
| *HD0921*[f] | **GAAACGG**ATGTGGTCAAGG**CCAAA** | 12 | -331, -312 | 2.9, 3.3 | |
| *HD0939*[f] | **GAAACTA**AGGGAGCAGTAATGT**CCAAA** | 15 | -278, -256 | 3.7, 3.3 | 13,35 |
| *HD0940*[f] | **CTATCTT**TCACGATAGCCTTTTCTT**TCAAA** | 18 | -123, -98 | 2.7, 3.8 | |
| *HD0960*[f] | **CCAACAG**GCGACGATCTATGCAA**TCAAA** | 16 | -410, -387 | 2.7, 3.8 | |
| *HD1060*[f] | **TGAACAA**CAAACCAAAAAAA**TCAAA** | 13 | 75, 95 | 2.9, 3.8 | |
| *HD1218*[f] | **TCAACTC**GCAGAAATACTTCA**TCAAA** | 14 | -370, -349 | 3.1, 3.8 | |
| *HD1239*[f] | **GCATTCT**ACCCCAAAAAAATCACCACT**TCTAA** | 20 | -156, -129 | 2.7, 3.7 | -95, -78 |
| *HD1339*[f] | **TGAATTT**TTTTAGAGAATGCTTG**TCAAA** | 16 | -51, -28 | 3.6, 3.8 | -50, -28 |
| *HD1400* | **GAAACTT**CAGGCGGTTTTTTCTG**CCTAA** | 16 | -63, -40 | 4.5, 3.1 | |
| *HD1408*[f] | **TGAACTA**CCCACTATTGTGGCTTG**TCAAA** | 17 | 39, 63 | 4.0, 3.8 | -270, -245 |
| *HD1409*[f] | **TGAACTA**CCCACTATTGTGGCTTG**TCAAA** | 17 | -114, -90 | 4.0, 3.8 | -441, -423; -422, -397 |
| *HD1410*[f] | **TGAATTT**AAAAGCATTGGCGG**TCAAA** | 14 | -245, -224 | 3.6, 3.8 | -3, 18; -124, -106 |
| *HD1444* | **GAAACTA**AGATTATTTTTTAT**TCTTT** | 14 | -38, -17 | 3.7, 2.2 | |
| *HD1452* | **GAAACTA**AGATTATTTTTTAT**TCTTT** | 14 | -26, -5 | 3.7, 2.2 | |
| *HD1471*[f] | **AGAACTA**GAACAGATTATTAA**TCAAA** | 14 | 18, 39 | 3.4, 3.8 | |
| *HD1534*[f] | **GAAACAA**AGTCAAATTA**TCAAA** | 10 | -344, -327 | 2.6, 3.8 | -357, -335 |
| *HD1548* | **TGTACTG**CTAAATACCCC**TCTAA** | 11 | -446, -428 | 2.1, 3.7 | |
| *HD1552* | **CAAACTG**CCAAACTGGAATGTGAGATT**GCTAA** | 20 | -423, -396 | 3.3, 2.9 | |
| *HD1558* | **CAAACTT**TAGCTAATCCAAAA**GCTAT** | 14 | 64, 85 | 3.9, 2.1 | |
| *HD1770*[f] | **TCAATTA**GCTATTCAAATTTACCCAT**TCAAA** | 19 | -37, -11 | 2.6, 3.8 | |
| *HD1829* | **GGAACGT**TTAAAACAATCAGCACAA**GCTAT** | 18 | -182, -157 | 4.1, 2.1 | |
| *HD2015*[f] | **TGATTTT**GTGCAACTTTTG**TCAAA** | 12 | -58, -39 | 3.1, 3.8 | |
| *ampD*[f] | **TCAAATT**TAATTGACTAAT**TCTAA** | 12 | -61, -42 | 2.7, 3.7 | -60, -42 |
| *apt*[f] | **GCAACAA**CATTTAATCA**TCAAA** | 10 | -277, -260 | 3.1, 3.8 | -28, -6; -283, -260 |
| *asnC* | **TGATCTG**ATAAAGTTCAGTTAATTT**GCAAA** | 18 | -252, -227 | 3.7, 3.0 | |
| *comA* | **GGATCTA**CGCCTTTGTGT**TCATA** | 11 | -428, -410 | 3.9, 3.1 | |
| *cysZ*[f] | **GGATTTT**GTCCATATTGGAGTGGA**TCTAA** | 17 | -309, -285 | 3.5, 3.7 | |
| *dacA* | **TCAATTT**AATGGTCGTTTAACC**GCTAA** | 15 | -396, -374 | 3.4, 2.9 | |
| *degP* | **TCAATTT**TATCTTCATTAG**TCTTA** | 12 | 10, 29 | 3.4, 3.0 | |
| *glmM* | **TAAACTT**AATATAATTT**GCAAT** | 10 | -53, -36 | 4.1, 2.3 | |
| *lsgA*[f] | **GCAATAT**TAAAAGGCGGTAAAA**CCAAA** | 15 | -190, -168 | 2.7, 3.3 | |
| *mazG* | **TGAATTT**ATTAACACAGTA**GCAAA** | 12 | 15, 34 | 3.6, 3.0 | |
| *mdh*[f] | **GCATTTT**AAAAGCTTCTGACAAGCGG**TCTAA** | 19 | -229, -203 | 3.3, 3.7 | -139, -121; -144, -121; -143, -121 |
| *mogA* | **GCAACGT**AACCCAAACAAT**GCAAA** | 12 | -432, -413 | 3.9, 3.0 | |
| *murA*[f] | **GAAATTT**TACGTAATGCCCTA**CCAAA** | 14 | -342, -321 | 3.3, 3.3 | |
| *mutT* | **GAAACTT**TTTGTGTATTTACTGG**CCTTA** | 16 | -86, -63 | 4.5, 2.4 | |
| *nlpD*[f] | **AGAATTT**TTAAGGATAATACT**TCAAA** | 14 | -27, -6 | 3.0, 3.8 | -26, -6 |
| *oapA* | **CAATCTT**ACTCTTGCTTCA**TCAAA** | 12 | 39, 58 | 3.4, 3.8 | 38, 58 |
| *oapB*[f] | **ACATCTG**TAAAAACGGATAATATATCT**TCTAA** | 20 | -387, -360 | 3.0, 3.7 | |
| *prc* | **GCAACGT**AAAGAACAGCGAAAAGACT**TCTTT** | 19 | -239, -213 | 3.9, 2.2 | |
| *proQ* | **GAAACTA**TGCCAGATAGTAGCA**ACAAA** | 15 | 16, 38 | 3.7, 2.4 | |
| *rpoE*[f] | **TTAACTT**ACTCGTCGTGCGTTA**TCAAA** | 15 | 65, 87 | 3.5, 3.8 | |
| *rpoH*[f] | **GGAACTT**GGTTTTTTTATTAGCTG**TCAAA** | 17 | -106, -82 | 5.2, 3.8 | -214, -189 |
| *rseC*[f] | **GCAACAG**TTGTGCAATA**TCAAA** | 10 | 16, 33 | 3.3, 3.8 | 10, 33 |

| Gene | Putative RpoE promoter[a] | Spacer[b] | Position[c] | Score[d] | Position of additional putative promoters[e] |
|---|---|---|---|---|---|
| *rsuA*[f] | **AGATTTT**GTGGTAAAGAAAGAG**CCAAA** | 15 | -421, -399 | 2.5, 3.3 | |
| *sbcB* | **TGAACTT**TATCAGATCACGTCAG**TCATA** | 16 | -260, -237 | 4.8, 3.1 | |
| *smpA*[f] | **TGAACTA**AATGACACATTGACAA**TCAAA** | 16 | -141, -118 | 4.0, 3.8 | 46, 65 |
| *surA*[f] | **TGAACCT**TTTTATAAAATTTTAC**TCTAA** | 16 | -71, -48 | 4.2, 3.7 | -70, -48 |
| *surE*[f] | **TGATTTT**GTACAACTTGCCGGA**TCAAA** | 15 | -359, -337 | 3.1, 3.8 | |
| *uppS*[f] | **GAAACTT**CTGTGAATTTTGATCCT**TCAAA** | 17 | 4, 28 | 4.5, 3.8 | 3, 28 |
| *uvrD*[f] | **TGAATGT**TAATTTGAAAAAGGA**TCAAA** | 15 | -363, -341 | 2.5, 3.8 | |
| *waaF*[f] | **ACAACTT**AAACAGCAATAT**CCAAA** | 12 | -76, -57 | 4.0, 3.3 | -79, -57 |

[a] Corresponds to putative RpoE promoter with the highest match score; putative -35 and -10 regions are highlighted in bold.

[b] Corresponds to putative RpoE promoter with the highest match score; spacer is the distance between putative -35 and -10 regions in the promoter.

[c] Corresponds to putative RpoE promoter with the highest match score; position of putative -35 and -10 regions in the promoter relative to TSS.

[d] Corresponds to putative RpoE promoter with the highest match score; match score is the sum of individual position scores from each letter in the sequence; and the indicated match scores correspond to putative -35 and -10 regions in the promoter, respectively.

[e] Position of putative -35 and -10 regions of additional promoters identified in the upstream region relative to TSS.

[f] TUs that were enriched in whole genome enrichment analysis.