

Supplementary Table S2. Summary information of *Pseudomonas* strains containing the CRISPR type IV-A(1–4) systems, including designated system name, the genome that the system is located in, genome accession number, genes of the system, repeat consensus sequence, and spacer sequence

System name	Genome name	Genome accession	Gene 1	Gene 2	Gene 3	Gene 4	Gene 5	Repeat consensus	Spacer sequences
A1_1	<i>Pseudomonas</i> sp. 34-62-33 04302015_34_scaffold_57	NCJV01000006.1	<i>csf4</i> -reverse, OZB34657.1	<i>csf5</i> , OZB34658.1	<i>csf1</i> , OZB34659.1	<i>csf2</i> , OZB34660.1	<i>csf3</i> , OZB34661.1	GTATTCCCCGCGTGCGCGG GGTGAGCG	>GCCCAAACCTGTGCCACCAAGCACCACAAC>CAGATGCCT GAGATTGGCGCAAAACCACTTAC>TTCTCTTGGGTAAACCAG CCCTCGATCAGTCC>GTTTGTGGCGATCTTCTCAGCTCCCAT CATT>GCGAAGTAGGCGATCAGCAGTGCAGCATGCC>CAT GTTTGCGAACTGAACAGCATGGCGTCCA>GCATACGATGA GAGCGGTGGCGTGTTCGG>TCCTGTAGCGCACGTTGCGA AACCGCAGCAAC>TATTTTGGGGATTTGAAGGGGTATTGACG GTT>GGCTGTGGGGGTGAGAAATGAGCAAGCGCGAA>CATC ATGCTGAGGGCCGATTTGGCGGATAAGG>TCTGGCAGGTCTGT CCCAGTCTCTGCGTTG>GATTCTGACGAACGTCATATGA GTCAGCCGAT
A1_2	<i>Pseudomonas aeruginosa</i> genome assembly P40_Scotland_4_VIM_2_09_12	CVUM01000112.1	<i>csf4</i> -reverse, CRN66652.1	<i>csf5</i> , CRN66678.1	<i>csf1</i> , CRN66706.1	<i>csf2</i> , CRN66744.1	<i>csf3</i> , CRN66771.1	GTATTCCCCGCGTGCGCG GGGGTGAGCG	>GAAACAACCTGTTTTCAGAGCATCGGAACC>GACGGTGGC CAAGAAGGTCACCCGGCAATTACG>ATCACGACCTGCCTGA AGGCTGGGTCACTAAT>GATCGCCCGCTCGGAAGCTGCC AGCTTT>GGTACTCATCGGACAACGTAATGGCTCCCGGCC AA>GGTCGCCAGCTCGGAACGTGCCTGCTCGATCT>GAGAA AGCCGAGGAATCACCGAACCGGATTC>GTCAGCCAGGCTAG CCCGCTGGCAGCTGCTCAC>GGAGGCATACGACGACGACGCC CAGGCCCGCAGC>GATGGTCCAAGAGCATGGTCAGGAGAGCC AGC>GGGTGCTGAACGGCAGCTACCTACGTCAACT>GAA TGTGTACGACGATGCTGACGAGAAATGGC>GTCTAGGTACA GCAGCACTGCCAGCACTGCA
A1_3	<i>P. aeruginosa</i> strain PA83 Plasmid	CP017294	<i>csf3</i> -reverse, ASJ88789.1	<i>csf2</i> -reverse, ASJ88790.1	<i>csf1</i> -reverse, ASJ88791.1	<i>csf5</i> -reverse, ASJ88792.1	<i>csf4</i> , ASJ88793.1	GTGTCCCCGCTTACG CGGGGTGAACG	>GAATGAAATCACCCCTTCCCAGCTTCGAAACCT>GTGGATGG ATTAACGCATGGCTGGAAAGGTGCC>AATCGCAGCGGGAATA TTCCCTGCGCCCTTACC>GGTGGCAAGCGGCTGCGATCCCT TCCGGCGTGA>GATTCAAGATGGCTGTAATGTTGGTCTGCTT GCA>TATGTAACCCGTTACTTTTCGCTGTTCCGGTA>TATC GCTGAACCTAAAGCACTAGCTGCCGACG>GAACCCCTGCTGG CTAGCCGGCTGCAAGTACTTTT>GCGGCATACCTGCTTACTC CGCAGACTGT>GGAATGCCATCTGGCTGCGTTACGTCGT ATGT
A1_4	<i>Pseudomonas putida</i> plasmid pKF715A DNA	AP015030.1	<i>csf3</i> -reverse, BAW26656.1	<i>csf2</i> -reverse, BAW26657.1	<i>csf1</i> -reverse, BAW26658.1	<i>csf5</i> -reverse, BAW26659.1	<i>csf4</i> , BAW26660.1	GTATTCCCCGCGTGCG CGGGGTGAACG	>GTGACTATCGAGCAAAACAGGGGGATTAATCC>AGTGCCCT TGAATAACCCATGATTACCAGAT>CTCCGGCGTGAGCAATTCT GTTATGCGCAAGAGC>TAAGTACCGCCAAGCGGGTGAGCA GTGCCCG>ACTGGACTGGCTGCACGCGAGGCTGCCTAGGGC >TTGAGAACTAAGGGAGATCGGTATGAAACA>CGGGGCA GGTTCATTCTGTCACCCACTGGCTG>GGTTCCTGGATTCCCA CCGGCACCGGAATCC>TCCTGTAGCGCACGTCGCGAAACCGC AGCAAC>TATTTTGGGGATTTGAAGGGGTATTGACGGTT>AA CCGTCAATACCCCTTCAAATCCCAAAAATA>TGGCGCCTCT GCTGAAAGCGAGCTGACGTGTA
A1_5	<i>Pseudomonas stutzeri</i> B1SMN1	AMVM01000016.1	<i>csf4</i> -reverse, EPL60777.1	<i>csf5</i> , EPL60778.1	<i>csf1</i> , EPL60779.1	<i>csf2</i> , EPL60779.1	<i>csf3</i> , EPL60781.1	GTATTCCCCGCGTGCG CGGGGTGAACG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>GTGACTAT CGAGCAAAACAGGGGGATTAATCC>AGTGCCTTGAAT ACCCATGATTACCAGAT>CTCCGGCGTGAGCATTTCTGTTA TGCGCAAGAGC>TAAGTACCGCCAAGCGGGTGAGCAGTGC CCG>GGTTCCTGGATTCCCACCGGCACCGGAATCC>TCCT GTAGCGCACGTCGCGAAACCGCAGCAAC>TATTTTGGGGA TTTGAAGGGGTATTGACGGTT>TGCGGCCTCTGCTGAAAGCG AGCTGACGTGTA>GGCTGTGGGGATGAGAAATGAGCAAGC GCGAA

(continued)

Supplementary Table ST2. (Continued)

System name	Genome name	Genome accession	Gene 1	Gene 2	Gene 3	Gene 4	Gene 5	Repeat consensus	Spacer sequences
A1_6	<i>Pseudomonas oleovorans</i> subsp. <i>oleovorans</i> strain DSM 1045	NIUB01000035.1	<i>csf3</i> -reverse, OWK40672.1	<i>csf2</i> -reverse, OWK40673.1	<i>csf1</i> -reverse, OWK40674.1	<i>csf5</i> -reverse, OWK40675.1	<i>csf4</i> , OWK40676.1	GTATTCCCCGCGTGCG CGGGGGTTAGCG	>TAAGGTTTCGAGGTGCATAGGCCGACGGGAGGG>GTGACTATC GAGCAAAAACAGGGGGATTAATCC>AGTGCCCTTGAAATA CCCATGATTACAGAT>CTCCGGCGTGAGCATTTCTGTATGC GCAAGAGC>GTTTGTGGCGATCTCTCAGTCCCATCATT >TAAGTACCGCCCAAGCGGGTGAAGCAGTCCCG>GGTTCCC TGGATTCCCACCGGCACCGAATCC>TCCTGTAGCGCACGT CGCGAAACCGCAGCAAC>GTTTGTGGCGATCTCTCAGTCC ATCATT>TATTTTGGGGATTGAAGGGGATTGACGGTT>CA TGTTTGCGAACTGAACAGCATGCGGTGCCA>GCATACGATGA GAGCGGTGGCGTGTTCGG>TACACGTCAGCTCGCTTCAG CAGAGGCCGA>TCCTGTAGCGCACGTTCGAAACCGCAGC AAC>TATTTTGGGGATTGAAGGGGATTGACGGTT>GGCTGT GGGGGTGAGAAATGAGCAAGCGCGAA
A2_1	<i>P. aeruginosa</i> BL14	AXPM01000021.1	<i>csf4</i> -reverse, ERV23968.1	<i>csf5</i> , ERV23969.1	<i>csf1</i> , ERV23970.1	<i>csf2</i> , ERV23971.1	<i>csf3</i> , ERV23972.1	GTATTCCCCGCGCAGGCGG GGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC GATTCCTTCTTCCA
A2_2	<i>P. aeruginosa</i> BWHPA028	AXQA01000038.1	<i>csf3</i> -reverse, ERV69443.1	<i>csf2</i> -reverse, ERV69444.1	<i>csf1</i> -reverse, ERV69445.1	<i>csf5</i> -reverse, ERV69446.1	<i>csf4</i> , ERV69447.1	GTATTCCCCGCGCAG GCGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC GATTCCTTCTTCCA
A2_3	<i>P. aeruginosa</i> PS42	AZZD01000055.1	<i>csf4</i> -reverse, ETU71866.1	<i>csf5</i> , ETU71867.1	<i>csf1</i> , ETU71868.1	<i>csf2</i> , ETU71869.1	<i>csf3</i> , ETU71870.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC GCGATTTCCTTCTTCCA
A2_4	<i>P. aeruginosa</i> genome assembly P26_Wales_1_VIM_2_11_10	CVVN01000207.1	<i>csf4</i> -reverse, CRP74518.1	<i>csf5</i> , CRP74545.1	<i>csf1</i> , CRP74569.1	<i>csf2</i> , CRP74593.1	<i>csf3</i> , CRP74621.1	GTATTCCCCGCGCAGGCG GGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC GATTCCTTCTTCCA
A2_5	<i>P. aeruginosa</i> genome assembly P31_Wales_1_VIM_2_11_11	CVVS01000266.1	<i>csf4</i> -reverse, CRQ25908.1	<i>csf5</i> , CRQ25928.1	<i>csf1</i> , CRQ25947.1	<i>csf2</i> , CRQ25962.1	<i>csf3</i> , CRQ25982.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC ATTCCTTCTTCCA
A2_6	<i>P. aeruginosa</i> genome assembly P44_Wales_1_VIM_2_11_12	CVWL01000377.1	<i>csf4</i> -reverse, CRR52784.1	<i>csf5</i> , CRR52812.1	<i>csf1</i> , CRR52838.1	<i>csf2</i> , CRR52863.1	<i>csf3</i> , CRR52884.1	GTATTCCCCGCGCAG GCGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC ATTCCTTCTTCCA
A2_7	<i>P. aeruginosa</i> genome assembly P59_Wales_1_VIM_2_09_13	CVXN01000299.1	<i>csf4</i> -reverse, CRS25516.1	<i>csf5</i> , CRS25518.1	<i>csf1</i> , CRS25519.1	<i>csf2</i> , CRS25521.1	<i>csf3</i> , CRS25523.1	GTATTCCCCGCGCAGG GGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC GATTCCTTCTTCCA
A2_8	<i>P. aeruginosa</i> genome assembly P27_Wales_1_VIM_2_02_11	CVVX01000279.1	<i>csf4</i> -reverse, CRQ02815.1	<i>csf5</i> , CRQ02834.1	<i>csf1</i> , CRQ02856.1	<i>csf2</i> , CRQ02885.1	<i>csf3</i> , CRQ02903.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC CGATTTCCTTCTTCCA
A2_9	<i>P. aeruginosa</i> genome assembly P19_London_7_VIM_2_05_10	CVVU01000234.1	<i>csf4</i> -reverse, CRP63394.1	<i>csf5</i> , CRP63426.1	<i>csf1</i> , CRP63451.1	<i>csf2</i> , CRP63481.1	<i>csf3</i> , CRP63510.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC CGATTTCCTTCTTCCA
A2_10	<i>P. aeruginosa</i> strain 105819	LOHH01000035.1	<i>csf3</i> -reverse, KYO74799.1	<i>csf2</i> -reverse, KYO74800.1	<i>csf1</i> -reverse, KYO74801.1	<i>csf5</i> -reverse, KYO74802.1	<i>csf4</i> , KYO74803.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC CGATTTCCTTCTTCCA
A2_11	<i>P. aeruginosa</i> isolate RW109	LT969521.1	<i>csf4</i> -reverse, SOV33091.1	<i>csf5</i> , SOV33092.1	<i>csf1</i> , SOV33093.1	<i>csf2</i> , SOV33094.1	<i>csf3</i> , SOV33095.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC CGATTTCCTTCTTCCA
A2_12	<i>P. aeruginosa</i> strain WH-SGI-V-07240	LLNL01000085.1	<i>csf4</i> -reverse, KSG28518.1	<i>csf5</i> , KSG28519.1	<i>csf1</i> , KSG28520.1	<i>csf2</i> , KSG28521.1	<i>csf3</i> , KSG28522.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC GATTCCTTCTTCCA
A2_13	<i>P. aeruginosa</i> strain WH-SGI-V-07368	LLNS01000021.1	<i>csf4</i> -reverse, KSG54638.1	<i>csf5</i> , KSG54639.1	<i>csf1</i> , KSG54640.1	<i>csf2</i> , KSG54641.1	<i>csf3</i> , KSG54642.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC ATTCCTTCTTCCA
A2_14	<i>P. aeruginosa</i> strain 560747	MPVA01000073.1	<i>csf4</i> -reverse, OKR80896.1	<i>csf5</i> , OKR80897.1	<i>csf1</i> , OKR80898.1	<i>csf2</i> , OKR80899.1	<i>csf3</i> , OKR80900.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC ATTCCTTCTTCCA

(continued)

Supplementary Table ST2. (Continued)

System name	Genome name	Genome accession	Gene 1	Gene 2	Gene 3	Gene 4	Gene 5	Repeat consensus	Spacer sequences
A2_15	<i>P. aeruginosa</i> strain WH-SGI-V-07263	LLTV01000009.1	<i>csf4</i> -reverse, KSQ21174.1	<i>csf5</i> , KSQ21175.1	<i>csf1</i> , KSQ21176.1	<i>csf2</i> , KSQ21177.1	<i>csf3</i> , KSQ21178.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCA AGTTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTG GTGCGATTTCCTTCTTCCA
A2_16	<i>P. aeruginosa</i> strain ICBDVIM-2	MZND01000202.1	<i>csf4</i> -reverse, OPL23682.1	<i>csf5</i> , OPL23683.1	<i>csf1</i> , OPL23684.1	<i>csf2</i> , OPL23685.1	<i>csf3</i> , OPL23686.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGTGC ATTTCCTTCTTCCA
A2_17	<i>P. aeruginosa</i> strain S122_C02_RS_S122_C02_RS_NODE_21_length_133376	NFGS01000021.1	<i>csf3</i> -reverse, OTJ82652.1	<i>csf2</i> -reverse, OTJ82653.1	<i>csf1</i> -reverse, OTJ82654.1	<i>csf5</i> -reverse, OTJ82655.1	<i>csf4</i> , OTJ82656.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_18	<i>P. aeruginosa</i> strain HSV3483	NINV01000001.1	<i>csf4</i> -reverse, OVZ72674.1	<i>csf5</i> , OVZ72675.1	<i>csf1</i> , OVZ72676.1	<i>csf2</i> , OVZ72677.1	<i>csf3</i> , OVZ72678.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_19	<i>P. aeruginosa</i> strain 833	NIPF01000020.1	<i>csf4</i> -reverse, OWJ33422.1	<i>csf5</i> , OWJ33423.1	<i>csf1</i> , OWJ33424.1	<i>csf2</i> , OWJ33425.1	<i>csf3</i> , OWJ33426.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAA GTTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTG GTGCGATTTCCTTCTTCCA
A2_20	<i>P. aeruginosa</i> strain env172	NRAF01000016.1	<i>csf4</i> -reverse, PBX11570.1	<i>csf5</i> , PBX11571.1	<i>csf1</i> , PBX11572.1	<i>csf2</i> , PBX11573.1	<i>csf3</i> , PBX11574.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GATTTCCTTCTTCCA
A2_21	<i>P. aeruginosa</i> strain ICBBVIM-2	NWBV01000032.1	<i>csf4</i> -reverse, PCC88976.1	<i>csf5</i> , PCC88977.1	<i>csf1</i> , PCC88978.1	<i>csf2</i> , PCC88979.1	<i>csf3</i> , PCC88980.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_22	<i>P. aeruginosa</i> strain ICBSVIM-2	NWBW01000020.1	<i>csf4</i> -reverse, PCC94571.1	<i>csf5</i> , PCC94572.1	<i>csf1</i> , PCC94573.1	<i>csf2</i> , PCC94574.1	<i>csf3</i> , PCC94575.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTCGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_23	<i>P. aeruginosa</i> strain S04_90 plasmid	CP011370.1	<i>csf3</i> -reverse, AKG03092.1	<i>csf2</i> -reverse, AKG03093.1	<i>csf1</i> -reverse, AKG03094.1	<i>csf5</i> -reverse, AKG03095.1	<i>csf4</i> , AKG03096.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_24	<i>P. aeruginosa</i> strain WH-SGI-V-07259	LLTS01000090.1	<i>csf3</i> -reverse, KSQ08350.1	<i>csf2</i> -reverse, KSQ08351.1	<i>csf1</i> -reverse, KSQ08352.1	<i>csf5</i> -reverse, KSQ08353.1	<i>csf4</i> , KSQ08354.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_25	<i>P. aeruginosa</i> strain WH-SGI-V-07273	LLUB01000009.1	<i>csf3</i> -reverse, KSQ35844.1	<i>csf2</i> -reverse, KSQ35845.1	<i>csf1</i> -reverse, KSQ35846.1	<i>csf2</i> -reverse, KSQ35847.1	<i>csf4</i> , KSQ35848.1	GTATTCCCCGCGCAGG CGGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_26	<i>P. aeruginosa</i> strain WH-SGI-V-07327	LLVN01000097.1	<i>csf3</i> -reverse, KSS90966.1	<i>csf2</i> -reverse, KSS90967.1	<i>csf1</i> -reverse, KSS90968.1	<i>csf5</i> -reverse, KSS90969.1	<i>csf4</i> , KSS90970.1	GTATTCCCCGCGCAGG GGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_27	<i>P. aeruginosa</i> strain Br993	LZQI01000014.1	<i>csf3</i> -reverse, OFC00169.1	<i>csf2</i> -reverse, OFC00170.1	<i>csf1</i> -reverse, OFC00171.1	<i>csf5</i> -reverse, OFC00172.1	<i>csf4</i> , OFC00173.1	GTATTCCCCGCGCAGG GGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_28	<i>P. aeruginosa</i> strain WH-SGI-V-07172	LLMB01000016.1	<i>csf4</i> -reverse, KSD76398.1	<i>csf5</i> , KSD76399.1	<i>csf1</i> , KSD76400.1	<i>csf2</i> , KSD76401.1	<i>csf3</i> , KSD76402.1	GTATTCCCCGCGCAGG GGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GATTTCCTTCTTCCA
A2_29	<i>P. aeruginosa</i> strain S700_C14_RS_S700_C14_RS_NODE_20_length_141227	NFFQ01000020.1	<i>csf3</i> -reverse, OTI20239.1	<i>csf2</i> -reverse, OTI20240.1	<i>csf1</i> -reverse, OTI20241.1	<i>csf5</i> -reverse, OTI20242.1	<i>csf4</i> , OTI20243.1	GTATTCCCCGCGCAGG GGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_30	<i>P. aeruginosa</i> strain env408	NRFQ01000019.1	<i>csf3</i> -reverse, PCA65643.1	<i>csf2</i> -reverse, PCA65644.1	<i>csf1</i> -reverse, PCA65645.1	<i>csf5</i> -reverse, PCA65646.1	<i>csf4</i> , PCA65647.1	GTATTCCCCGCGCAGG GGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_31	<i>P. aeruginosa</i> strain S742_C15_BS_S742_C15_BS_NODE_39_length_75586	NFFQ01000039.1	<i>csf3</i> -reverse, OTH77721.1	<i>csf2</i> -reverse, OTH77722.1	<i>csf1</i> -reverse, OTH77723.1	<i>csf5</i> -reverse, OTH77724.1	<i>csf4</i> , OTH77725.1	GTATTCCCCGCGCAGG GGGGGTTAGCG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAGT TACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA
A2_32	<i>P. aeruginosa</i> strain SPA01	LQBU01000137.1	<i>csf3</i> -reverse, KWR92602.1	<i>csf2</i> -reverse, KWR92603.1	<i>csf1</i> -reverse, KWR92604.1	<i>csf5</i> -reverse, KWR92605.1	<i>csf4</i> , KWR92606.1	TGTTTCCCGCGTATAGG CGGCTGAAGG	>GGCTGTGGGGATGAGAAATGAGCAAGCGCGAA>CATCCAAG TTACGCATCAGATTCGAGACGCGA>CTATGCAGGGCTGGT GCGATTTCCTTCTTCCA

(continued)

Supplementary Table ST2. (Continued)

System name	Genome name	Genome accession	Gene 1	Gene 2	Gene 3	Gene 4	Gene 5	Repeat consensus	Spacer sequences
A3_1	<i>P. aeruginosa</i> BL23	AXPD01000036.1	<i>csf2</i> , ERX94041.1	<i>csf3</i> , ERX94042.1	<i>csf4</i> , ERX94043.1	<i>csf3</i> , ERX94044.1		TGTTTGCCGCCGTATAGG CGGCTTGAAGG	>GTCGCCCTTCCTTGAGTGGCTTTTTTGGAGCCGA>CGAACGGGGC TCTCAGCGAGATGGTCGTTGGC>GTTTGTGGCGATCTTCTC AGCTCCCATCATT>CCCAGTCCACCTTACGAAAAGCCTCTGG ATGA>TCAGCTTCTCAAAATTAAGGGATATAGGGACC>ACGT TGCCATGAAATCCTTCTCGGTACGTGTG>GCGAAGTAGGCGA TCAGCAGTGCAGCATGCC>TACATGGCCAGGGCAAGTGC CCGGCCTGCGGC>CATGTTTGGCAACTGAACAGCATGCGGT GCCA>GCATACGATGAGAGCGGTGGCGCTGTTTTCGG>ATGC TGTTCAACGACTACGGCAGCGTGTTC
A3_2	<i>Pseudomonas chengduensis</i> strain DSM 26382	FMZQ01000007.1	<i>csf2</i> , SDC86395.1	<i>csf3</i> , SDC86423.1	<i>csf4</i> , SDC86447.1	<i>csf3</i> , SDC86471.1		TGTTTGCCGCCGTATAGG GGCTTGAAGG	>TCCTGTAGCGCAGTTCGCAAACCGCAGCAAC>TATTTGGGG ATTTGAAAGGGATTGACGGTT>GGCTGTGGGGGTGAGAAA TGAGCAAAGCGCAA>GATCGTAGTGTATGCGATAAAGAGCA TGCCCGC>AGCCTTACACTTATAGTCCGTTACTGTGTATGA >TTGGTTGTACCAATAGCCGGCGAAGAGCCAGTC>TAACCCG TGGTGGACGTTCCGGCGGTCAAGGAA>TAAGTCGGTCGATCA GGTGACTAATCTGCCAG>TGTGCTGAGCCAGCAACCCGATC TGCTGTGTC>TAGGAAGATGCCACTGCGCTGGCTGCCTGG GTG>GAGGCTGGCTGCCAAGGGCAAAGCTATCATTC
A3_3	<i>P. aeruginosa</i> strain WH-SGI-V-07067	LLL01000002.1	<i>csf2</i> , KSC76904.1	<i>csf3</i> , KSC76905.1	<i>csf4</i> , KSC76906.1	<i>csf3</i> , KSC76907.1		TGTTTGCCGCCGTATAGG GGCTTGAAGG	>GTCCGATAGTCAGGCCACTGACGATTGCAAGCA>CTGCGGAA TCGTTGAAGACGGCTGCGAAACT>GTACGATCTCGGAAIT TGCGTATCTGGGATAC>AACAGTGGGGCATCGTATCGGAC GGCTTT>GCATAAGCAGGAAATGGGAGGTGAGCCCTGTT >TAATCGACCGATCTAGGGGACAGCGGGTAG>CGCGCGA GAACATACAGGTCAGA>GGCGATAGGTTTCAATTGGGCT TAACGCATC>TTCGCTGCTCTCGATCCGGGGACGCTTACAC >CAGTACCCGACGTGACGATCGTATTAGCAG>GCGGAA TGTCCGGCAGTCTCCGGCGGCGACTC>AGGTCCGACGCTG GCACTCGGCCACTCATAC>AGGTTGCTCCAGTACCCCTGCT CTCGCGGCTC>AAACGAGGCGGGCACCCCAACGAAACCT GGT>GGAGCGGGAGCGCGCAAGACAAGCCACAGCA>TG GCGCATGGATTCCATTACATCCCGTCAAC>GGAGCGGGAGC GCGACCAAGACAAGCCACAGCA>TTCGCTGCTCTCGATCCG GGGACGCTTACAC>AGCAGTGTATTGCGTCTGATCATTC CCCCACC>GCGGAATGTCGGCGAGTCTCCGGCGGCGACTC
A3_4	<i>Pseudomonas saponiphila</i> strain DSM 9751	FNTJ01000003.1	<i>csf3</i> -reverse, SED27694.1	<i>csf4</i> -reverse, SED27713.1	<i>csf5</i> -reverse, SED27736.1	<i>csf2</i> -reverse, SED27762.1		TGTTTGCCGCCGTATAGG GGCTTGAAGG	>AAAAAGATCAGTAGGCGGTAGCCACAGCTG>CTCGTGTCA GCCCTCCTTTACCGTGAACCGTT>ATCGATACAGCGTCTG CTGGCCGATACTGA>AATGGAGCGGATGTTGCTCTGCA TATCAGC>CGAGGGTCATACCGAGGCGCTGTTTGGC TA>ATGGACGTAGCGCCAGTGTCTAGCCTGGGTGC>ACAG TCACGCATACACTTCACTTGTAAAGC>ACTGCATGACGGGAGC CTGGGGCGCATCCA>CACACCTGCGAAGGCTTCAATGTCG CGCTATA>TGTACCGCATTACCCTCAGAATGCCAATTC>GTC ATGCAGGGGCTCGTTAATGCGCTTGAT>CGCGAGGACGCTG TCCACGCATTATCTCGGGCA>ATAAACCAGGCAAAACCCGC CCAATCCTCTG>TGATTACAACATCACTCAACTGGTCTATCTG A>AACTGCATCGGGTTCGGTGGATGACACAGGAA>CAGCT GTGGGCTACCGCCTACTGATCTTTT>ACTGCATGCTGGGAA CCCTGGGGCGCATCCA>TATAGCGCGACATGAAGCCTTCGC AGGTGTG>TGTACCGCATTACCCTCAGAATGCCAATTC>TC GAGTATGCAAGGGCTCGTTAATACGCTTGAT
A3_5	<i>Pseudomonas</i> sp. J237	MKEP01000030.1	<i>csf3</i> -reverse, OEO24419.1	<i>csf4</i> -reverse, OEO24420.1	<i>csf5</i> -reverse, OEO24421.1	<i>csf2</i> -reverse, OEO24422.1		TGTTTGCCGCCGTATAGG GGCTTGAAGG	>TCCTGTAGCGCAGTTCGCAAACCGCAGCAAC>TATTTGGGG ATTTGAAAGGGATTGACGGTT>GGCTGTGGGGGTGAGAAA TGAGCAAAGCGCAA>GATCGTAGTGTATGCGATAAAGAGCAT GCCCGC>AGCCTTACACTTATAGTCCGTTACTGTGTATGA>TT GGTTGTACCAATAGCCGGCGAAGAGCCAGTC>TAACCCGT GGTGACGTTCCGGCGGTCAAGGAA>TAAGTCGGTCGATCAG GTGACTAATCTGCCAG>TGTGCTGAGCCAGCAACCGATC TGCTGTGTC>TAGGAAGATGCCACTGCGCTGGCTGCCTTG GGT>CGCGAGGACGTGTCCACGCATTATCTCGGGCA

(continued)

Supplementary Table ST2. (Continued)

System name	Genome name	Genome accession	Gene 1	Gene 2	Gene 3	Gene 4	Gene 5	Repeat consensus	Spacer sequences
A4_1	<i>P. aeruginosa</i> strain S650_C13_BS S650_C13_BS_NODE_13_length_207944	NFFU01000013.1	Cas1-reverse, OTI18532.1	<i>csf3</i> -reverse, OTI18533.1	<i>csf4</i> -reverse, OTI18534.1	<i>csf5</i> -reverse, OTI18535.1	<i>csf2</i> -reverse, OTI18536.1	TGTGTGCCGCGGTGATAGG TGGCTTGAAGT	>CAGTTGATCATGTCTACCCGAATATCCTTGATG>TTGATCATA GGGTCCCAACTGCATCGATTGAGGT>ATTGAAGGTGCGCTG CCGCGTACGCTGCCAGGA>CGAACGGGCGTCTCAGCGAGAT GGTTCGCTTGGC>GTTTGTGGCGATCTTCTCAGTCCCATCA TTT>CCCGATCCACCTTACGAAAAGCCTCTGGATGA>TCAG CTTCTCAAATAAAGGGATATAGGGACC>ACGTTGCCATGAA ATCCTTCTCGGTACGTGTG>GCGAAGTAGGGCATCAGCAG TCGCAGCATGCC>TACATGCGCAAGGGCAAGTCCCGGCC TGGCGC>CATGTTTGCCTGAACTGAACAGCATGCGGTGCCA>G CATACGATGAGAGCGGTGGCGCTGTTTTCGG>ATGCTGTC CAACGACTACGGCAGCGTGTAC>AGTCGTACCCCGCC ACGTCCGCGTAAACATCCA
A4_2	<i>P. aeruginosa</i> strain S625_C13_RS S625_C13_RS_NODE_13_length_206276	NFFW01000013.1	Cas1-reverse, OTI37122.1	<i>csf3</i> -reverse, OTI37123.1	<i>csf4</i> -reverse, OTI37124.1	<i>csf5</i> -reverse, OTI37125.1	<i>csf2</i> -reverse, OTI37126.1	TGTGTGCCGCGGTGATAG GTGGCTTGAAGT	>CAGTTGATCATGTCTACCCGAATATCCTTGATG>TTGATCATA GGGTCCCAACTGCATCGATTGAGGT>ATTGAAGGTGCGCTG CCGCGTACGCTGCCAGGA>CGAACGGGCGTCTCAGCGAGAT GGTTCGCTTGGC>GTTTGTGGCGATCTTCTCAGTCCCATCA TTT>CCCGATCCACCTTACGAAAAGCCTCTGGATGA>TCAGC TTTCAAATAAAGGGATATAGGGACC>ACGTTGCCATGAAA TCCTTCTCGGTACGTGTG>GCGAAGTAGGGCATCAGCAGTG CGACGATGCC>TACATGCGCAAGGGCAAGTCCCGGCC TGGC>CATGTTTGCCTGAACTGAACAGCATGCGGTGCCA>GCATAC GATGAGAGCGGTGGCGCTGTTTTCGG>ATGCTGTCCAACGAC TACGGCAGCGTGTAC>AGTCGTACCCCGCCACGTCCGGC TAAACATCCA
A4_3	<i>P. aeruginosa</i> strain S619_C13_RS S619_C13_RS_NODE_15_length_187807	NFFX01000015.1	Cas1-reverse, OTI43277.1	<i>csf3</i> -reverse, OTI43278.1	<i>csf4</i> -reverse, OTI43279.1	<i>csf5</i> -reverse, OTI43280.1	<i>csf2</i> -reverse, OTI43281.1	TGTGTGCCGCGGTGATAGG TGGCTTGAAGT	>CAGTTGATCATGTCTACCCGAATATCCTTGATG>TTGATCATA GGGTCCCAACTGCATCGATTGAGGT>ATTGAAGGTGCGCTG CCGCGTACGCTGCCAGGA>CGAACGGGCGTCTCAGCGAG ATGGTCGCTTGGC>GTTTGTGGCGATCTTCTCAGTCCCA TCATTT>CCCGATCCACCTTACGAAAAGCCTCTGGATGA >TCAGCTTCTCAAATAAAGGGATATAGGGACC>ACGTTGCC ATGAAATCCTTCTCGGTACGTGTG>GCGAAGTAGGGCA TCAGCAGTGCAGCATGCC>TACATGCGCAAGGGCAAGTG CCCGGCCTGCGGC>CATGTTTGCCTGAACTGAACAGCATGCGGT GCCA>GCATACGATGAGAGCGGTGGCGCTGTTTTCGG>ATGC TGTCACGACTACGGCAGCGTGTAC>AGTCGTACCCCG CCACGTCCGCGTAAACATCCA
A4_4	<i>P. putida</i> strain MC4-5222	JOJW01000110.1	<i>csf2</i> , KEX94883.1	<i>csf5</i> , KEX94884.1	<i>csf4</i> , KEX94885.1	<i>csf3</i> , KEX94886.1	Cas1, KEX94887.1	TGTGTGCCGCGGTGATAG GTGGCTTGAAGT	>TTCAATCTCACGCATCACTTACGCTATATGCAA>AGAGTTCTG CATCCGCACTCGATCGTTCGAG>CCACCAGGAGCGCTC ACCCGCGCCCGCTCGCG>CCATTTATGCGGGTTTTGGGGCGT ATGCTTTGA>CTCAGAGCAAGCTGCGCGGAGCGTGAGGC ACA>GCCGCATCGACTCACGCAAGCTGCGCAGC>CTGG AAGTGCATTTGCTTGTGACAACCTGCGG>GACATACGCG GGCAACAGCGTGTGAGGTGCGAG>TATATGGGTTACTGCAC GAGTGTGACTCGGG>AGTTGTTGCGCTGTGCGGGGGAC ATGCACCG>TATAACCAGTTCACGCTAATGGAGCTGAGGAAG >GXXXFXAFTTXXAFTXATGXXTTATXGAAA>XXXGATXX AXXTTAXGAAAFTXXTTTATG>TXAFTTXXAAAAT AAFTTATATATGTTAXX>TTAATXFTXATGAXXXTTXXGAX GXAXATXA>AXFTTXXAFTGAAATXXTTXFTTAXFTTFT >FXGAAFTATXGATXATXATFTXGAXGATXX>TAXATFXA AAFTXAAFTTXXXITXXTTXFTX>XATTTTTXGAAFTTAA XAFTXATFTTXXA>FXATAXATGATGATXFTTXXFTT TTXT>ATFTTXXAAXGAXTAXFTXATFTTXXA>XAT AXXTTXGAAFTTXXAAXTXGXXGXXGATG
A4_5	<i>Pseudomonas rhodesiae</i> strain BS2777	LT629801.1	<i>csf2</i> , SDV17078.1	<i>csf5</i> , SDV17080.1	<i>csf4</i> , SDV17082.1	<i>csf3</i> , SDV17084.1	Cas1, SDV17086.1	TGTGTGCCGCGGTGATAGG TGGCTTGAAGT	>CAGTGTCTAAATGACTGGCTGAGCGCTGTCGG>ATCAAGGG TGGCTTCTGCTCGATCCTCACCTA>ACGTTGCCATGAAAT CCTTCTCGGTACGTGTG>GCGAAGTAGGGCATCAGCAGTGC GACGATGCC>TACATGCGCAAGGGCAAGTCCCGGCCCTGC GGC>CATGTTTGCCTGAACTGAACAGCATGCGGTGCCA>GAG CGCGGAGAACATACAGGTGAGA>ATGCTGTCCAACGACTAC GGCAGCGTGTAC>GGCGGATAGGTTTTCAATTGGGCTTA ACGCATC