SUPPLEMENTAL MATERIAL

LacI-family transcriptional regulator DagR acts as a repressor of the agarolytic pathway genes in *Streptomyces coelicolor* A3(2)

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**TABLE S1.** List of primers used in this work

| Primers | Sequence (5’-3’) | Comment |
|---------|------------------|---------|
| SCO3485-F | GTCGATAAGCTTACGACCACGCGCTCGAGGTCG | cloning of pET-3485 |
| SCO3485-R | GGGCACCATATGACATCGGAGGCAGGG | cloning of pET-3485 |
| SCO3485com-F | GTTGCGGAATTCATCATCACCAGGGAG | cloning of pWHM3-3485 |
| SCO3485com-R | AACCTCGAAGCTTACACGTCGA | cloning of pWHM3-3485 |
| sgRNA-3485F | AAACGCTTTCCGAGGCGCGGTGA | cloning of dCRI3485 (sgRNA) |
| sgRNA-3485R | ACGCTACGCGCTGCGGAGGC | cloning of dCRI3485 (sgRNA) |
| 3586-XbaI | TCTAGAAGCGCAACTTCGAGCCACCGG | cloning of dCRI3485 (1 kb *dagR* editing template – left) |
| 3586-HindIII | AAGCTTCGGAGCAGGCACACGGGAG | cloning of dCRI3485 (1 kb *dagR* editing template – left) |
| 3485-HindIII | AAGCTTCGAGATCAGGGGATGAGCGCG | cloning of dCRI3485 (1 kb *dagR* editing template – right) |
| 3485-XbaI | TCTAGAGCCCCGTGTCCGAGCG | cloning of dCRI3485 (1 kb *dagR* editing template – right) |
| C3485-F | ATGCCCATCGCATGAAGGTGG | PCR check for *dagR* deletion in Δsco3485 mutant |
| C3485-R | GACGACACCACGCCTCGGATCA | PCR check for *dagR* deletion in Δsco3485 mutant |
| pdagA-F | (Biotin)-GAATTCTGAGATCCTGAGCCCG | EMSA (upstream region of *dagA*) |
| pdagA-R | GGATCTCGATCGTCTCCTCCTTT | EMSA (upstream region of *dagA*) |
| pdagB-F | (Biotin)-GAATTCCGGCGAGGCCCGCGCG | EMSA (upstream region of *dagB*) |
### DagR represses agarase genes in *S. coelicolor*

| pdagB-R | CTGCAGGCTTCCCTCCATCT | EMSA (upstream region of dagB) |
|---------|------------------------|--------------------------------|
| pdagC-F | (Biotin)-GAATTCCACCCCCCATGAGGAGT | EMSA (upstream region of dagC) |
| pdagC-R | CTGCAGAGACGTGTTACCGCCCCTGT | EMSA (upstream region of dagC) |
| pdagA-F | (FAM)-GAATTCTGAATCGTGACC| Footprinting(upstream region of dagA) |
| pdagA-R | GGATCCGATCGTTCTCTTCTT | Footprinting(upstream region of dagA) |
| pdagB-F | (FAM)-GAATTCCCGGCGAGGCCCCGCCG | Footprinting(upstream region of dagB) |
| pdagB-R | CTGCAGGCTTCCCTCCATCT | Footprinting(upstream region of dagB) |
| pdagC-F | (FAM) GAATTCCACCCCCCATGAGGAGT | Footprinting(upstream region of dagC) |
| pdagC-R | CTGCAGAGACGTGTTACCGCCCCTGT | Footprinting(upstream region of dagC) |
DagR represses agarase genes in *S. coelicolor*

**TABLE S2.** List of up-regulated genes in the Δsco3485 mutant as compared to that in the wild type strain.

| Up regulated genes | Δsco3485 (4-day) vs WT (4-day) | Gene name | fold change | description |
|--------------------|--------------------------------|-----------|-------------|-------------|
| SCO0019            | 2.80                           | hypothetical protein SCO0019 |
| SCO0025            | 2.33                           | IS element ATP-binding protein, partial |
| SCO0037            | 2.26                           | sigma factor |
| SCO0140            | 6.04                           | MerR family transcriptional regulator |
| SCO0141            | 4.81                           | calcium-binding protein |
| SCO0166            | 2.79                           | regulator |
| SCO0167            | 4.31                           | hypothetical protein SCO0167 |
| SCO0168            | 2.43                           | regulator protein |
| SCO0169            | 2.79                           | hypothetical protein SCO0169 |
| SCO0171            | 4.74                           | nicotinate phosphoribosyltransferase |
| SCO0172            | 2.25                           | hypothetical protein SCO0172 |
| SCO0173            | 4.26                           | hypothetical protein SCO0173 |
| SCO0174            | 4.30                           | DNA-binding protein |
| SCO0178            | 3.10                           | hypothetical protein SCO0178 |
| SCO0196            | 3.49                           | hypothetical protein SCO0196 |
| SCO0201            | 4.23                           | hypothetical protein SCO0201 |
| SCO0207            | 2.39                           | hypothetical protein SCO0207 |
| SCO0208            | 5.71                           | pyruvate phosphate dikinase |
| SCO0209            | 6.12                           | hypothetical protein SCO0209 |
| SCO0210            | 6.22                           | hypothetical protein SCO0210 |
| SCO0211            | 2.22                           | hypothetical protein SCO0211 |
| SCO0215            | 2.02                           | hypothetical protein SCO0215 |
| SCO0284            | 4.15                           | alpha-galactosidase |
| SCO0323            | 3.01                           | hypothetical protein SCO0323 |
| SCO0342            | 3.99                           | hypothetical protein SCO0342, partial |
| SCO0421            | 2.88                           | two-component response regulator |
| SCO0430            | 2.33                           | tetR family transcriptional regulator |
| SCO0431            | 2.61                           | hypothetical protein SCO0431 |
| SCO0501            | 2.03                           | hypothetical protein SCO0501 |
| SCO0518            | 3.48                           | hypothetical protein SCO0518, partial |
| SCO0536            | 2.75                           | hypothetical protein SCO0536 |
| SCO0615            | 2.00                           | hypothetical protein SCO0615 |
| SCO0616            | 12.38                          | hypothetical protein SCO0616 |
DagR represses agarase genes in *S. coelicolor*

| Gene   | Log2 Ratio | Description                                    |
|--------|------------|-----------------------------------------------|
| SCO0617| 18.03      | phosphoketolase, partial                      |
| SCO0658| 2.04       | gas vesicle synthesis protein                 |
| SCO0713| 2.04       | lipase                                        |
| SCO0746| 2.30       | Ser/Thr protein kinase                        |
| SCO0753| 4.42       | hypothetical protein SCO0753                 |
| SCO0766| 3.56       | beta-galactosidase                            |
| SCO0864| 3.22       | ECF family RNA polymerase sigma factor        |
| SCO0987| 2.15       | hypothetical protein SCO0987                 |
| SCO1105| 3.78       | hypothetical protein SCO1105                 |
| SCO1201| 3.64       | reductase                                     |
| SCO1267| 5.97       | acyl carrier protein                          |
| SCO1304| 3.26       | hypothetical protein SCO1304                 |
| SCO1486| 2.33       | dihydroorotase                                |
| SCO1490| 2.01       | transcription antitermination protein NusB   |
| SCO1611| 2.50       | short chain dehydrogenase                     |
| SCO1612| 2.93       | aldehyde dehydrogenase                        |
| SCO1613| 3.54       | glutamine synthetase                          |
| SCO1614| 5.38       | transcriptional regulator                     |
| SCO1615| 3.02       | hypothetical protein SCO1615                 |
| SCO1673| 3.07       | hypothetical protein SCO1673                 |
| SCO1674| 2.62       | hypothetical protein SCO1674                 |
| SCO1675| 3.48       | small membrane protein                        |
| SCO1736| 2.18       | MarR family transcriptional regulator        |
| SCO1749| 3.92       | hypothetical protein SCO1749                 |
| SCO1795| 2.62       | hypothetical protein SCO1795                 |
| SCO1824| 2.17       | subtilisin-like protease                      |
| SCO1904| 2.29       | transcriptional regulator                     |
| SCO1948| 3.14       | zinc-binding carboxypeptidase                 |
| SCO1972| 2.34       | sugar kinase                                  |
| SCO1987| 2.41       | hypothetical protein SCO1987, partial         |
| SCO1997| 2.09       | hypothetical protein SCO1997                 |
| SCO2016| 2.49       | monoxygenase                                  |
| SCO2105| 2.35       | transcriptional regulator, partial            |
| SCO2138| 2.58       | hypothetical protein SCO2138                 |
| SCO2164| 2.91       | integral membrane efflux protein             |
| SCO2202| 2.38       | heat shock protein HtpX                       |
| SCO2205| 3.47       | hypothetical protein SCO2205                 |
| SCO2263| 2.06       | hypothetical protein SCO2263                 |
| SCO2264| 2.48       | hypothetical protein SCO2264                 |
DagR represses agarase genes in *S. coelicolor*

| Gene   | Expression Ratio | Function/Description                                      |
|--------|-----------------|----------------------------------------------------------|
| SCO2321| 2.22            | hypothetical protein SCO2321                             |
| SCO2326| 2.03            | hypothetical protein SCO2326                             |
| SCO2407| 2.06            | aldose 1-epimerase                                        |
| SCO2443| 3.15            | hypothetical protein SCO2443                             |
| SCO2460| 2.29            | hypothetical protein SCO2460                             |
| SCO2517| 3.62            | two-component system response regulator                   |
| SCO2518| 5.04            | two-component sensor kinase                               |
| SCO2519| 6.80            | hypothetical protein SCO2519                             |
| SCO2637| 2.02            | serine protease                                           |
| SCO2638| 2.11            | hypothetical protein SCO2638                             |
| SCO2670| 2.21            | O-methyltransferase                                       |
| SCO2786| 2.90            | beta-N-acetylhexosaminidase                               |
| SCO2791| 3.70            | hypothetical protein SCO2791                             |
| SCO3082| 2.29            | hypothetical protein SCO3082                             |
| SCO3097| 2.08            | hypothetical protein SCO3097                             |
| SCO3119| 2.26            | hypothetical protein SCO3119                             |
| SCO3124| 2.22            | 50S ribosomal protein L25/general stress protein Ctc     |
| SCO3125| 2.28            | peptidyl-tRNA hydrolase                                   |
| SCO3146| 2.00            | hypothetical protein SCO3146                             |
| SCO3163| 2.85            | hypothetical protein SCO3163                             |
| SCO3190| 2.35            | mechanosensitive channel                                  |
| SCO3265| 12.25           | hypothetical protein SCO3265                             |
| SCO3330| 2.15            | acetoin utilization protein                               |
| SCO3434| 2.38            | DNA polymerase I, partial                                 |
| SCO3469| 7.68            | transposase                                               |
| SCO3470| 9.91            | transposase                                               |
| SCO3471| 29.48           | extracellular agarase                                      |
| SCO3473| 62.51           | aldolase                                                  |
| SCO3485| 3.46            | LacI family transcriptional regulator                    |
| SCO3490| 7.68            | transposase                                               |
| SCO3512| 2.06            | hypothetical protein SCO3512                             |
| SCO3562| 2.63            | integral membrane transport protein                       |
| SCO3628| 2.17            | hypothetical protein SCO3628                             |
| SCO3661| 2.20            | ATP-dependent protease ATP-binding subunit, partial       |
| SCO3707| 2.16            | lipoprotein                                               |
| SCO3749| 2.03            | hypothetical protein SCO3749                             |
| SCO3808| 2.04            | hypothetical protein SCO3808                             |
| SCO3814| 2.99            | DNA-binding protein                                       |
| SCO3829| 2.10            | branched-chain alpha-keto acid dehydrogenase E2          |
### DagR represses agarase genes in *S. coelicolor*

| Gene    | Fold Change | Description                                           |
|---------|-------------|-------------------------------------------------------|
| SCO3830 | 3.64        | branched-chain alpha-keto acid dehydrogenase E1 subunit beta |
| SCO3831 | 4.07        | E1-alpha branched-chain alpha keto acid dehydrogenase, partial |
| SCO3910 | 5.48        | hypothetical protein SCO3910                           |
| SCO3948 | 2.23        | two component sensor                                    |
| SCO4000 | 2.65        | hypothetical protein SCO4000                            |
| SCO4002 | 15.07       | hypothetical protein SCO4002                            |
| SCO4015 | 2.34        | hypothetical protein SCO4015                            |
| SCO4021 | 2.95        | two component system histidine kinase                   |
| SCO4097 | 2.63        | amino acid/metabolite permease, partial                 |
| SCO4107 | 2.01        | hypothetical protein SCO4107                            |
| SCO4112 | 2.78        | hypothetical protein SCO4112                            |
| SCO4140 | 2.26        | phosphate ABC transporter permease                       |
| SCO4157 | 5.15        | protease                                               |
| SCO4166 | 2.40        | hypothetical protein SCO4166                            |
| SCO4214 | 2.43        | AbaA-like regulatory protein                           |
| SCO4222 | 2.12        | hypothetical protein SCO4222                            |
| SCO4240 | 7.09        | ABC transporter ATP-binding protein                     |
| SCO4382 | 2.15        | acyl CoA dehydrogenase                                  |
| SCO4399 | 2.07        | hypothetical protein SCO4399                            |
| SCO4428 | 2.20        | hypothetical protein SCO4428                            |
| SCO4442 | 3.42        | hypothetical protein SCO4442                            |
| SCO4443 | 4.75        | MerR family transcriptional regulator                   |
| SCO4476 | 3.82        | hypothetical protein SCO4476                            |
| SCO4481 | 2.15        | Ser/Thr protein kinase                                  |
| SCO4527 | 2.27        | hypothetical protein SCO4527                            |
| SCO4529 | 2.38        | hypothetical protein SCO4529                            |
| SCO4544 | 2.42        | hypothetical protein SCO4544                            |
| SCO4594 | 2.13        | 2-oxoglutarate ferredoxin oxidoreductase subunit beta    |
| SCO4608 | 2.15        | NADH dehydrogenase subunit NuoN2                         |
| SCO4609 | 2.16        | heat shock protein HtpX                                  |
| SCO4653 | 2.21        | 50S ribosomal protein L7/L12                            |
| SCO4734 | 2.33        | 50S ribosomal protein L13                               |
| SCO4756 | 2.59        | hypothetical protein SCO4756                            |
| SCO4807 | 2.08        | hypothetical protein SCO4807                            |
| SCO4831 | 2.76        | glycine/betaine ABC transporter integral membrane protein |
| SCO4832 | 2.01        | glycine/betaine-binding lipoprotein                     |
| SCO4945 | 2.59        | dehydrogenase                                           |
| SCO4962 | 2.11        | threonine dehydratase                                   |
| SCO4971 | 4.11        | dehydrogenase                                           |
DagR represses agarase genes in *S. coelicolor*

| Gene  | Log2 Fold Change | Description                                      |
|-------|-----------------|--------------------------------------------------|
| SCO4972 | 4.15            | dehydrogenase                                    |
| SCO4973 | 3.54            | hypothetical protein SCO4973                    |
| SCO5054 | 2.56            | hypothetical protein SCO5054                    |
| SCO5137 | 2.34            | ATP-binding protein                              |
| SCO5190 | 5.83            | DNA-binding protein                              |
| SCO5191 | 5.65            | hypothetical protein SCO5191                    |
| SCO5207 | 2.40            | hypothetical protein SCO5207                    |
| SCO5249 | 3.81            | nucleotide-binding protein                       |
| SCO5250 | 3.36            | polyprenyl synthetase                            |
| SCO5304 | 30.27           | hypothetical protein SCO5304                    |
| SCO5345 | 3.74            | hypothetical protein SCO5345                    |
| SCO5441 | 2.40            | hypothetical protein SCO5441                    |
| SCO5442 | 2.40            | trehalose synthase                               |
| SCO5443 | 2.81            | alpha-amylose                                    |
| SCO5505 | 53.51           | hypothetical protein SCO5505                    |
| SCO5551 | 2.63            | hypothetical protein SCO5551                    |
| SCO5625 | 2.24            | elongation factor Ts                             |
| SCO5693 | 2.44            | acyl CoA dehydrogenase                           |
| SCO5762 | 2.55            | AraC family transcription regulator, partial     |
| SCO5839 | 2.23            | hypothetical protein SCO5839                    |
| SCO5882 | 2.90            | RedV protein                                     |
| SCO5883 | 2.73            | hypothetical protein SCO5883                    |
| SCO5991 | 2.59            | peptide synthase                                 |
| SCO5892 | 2.70            | polyketide synthase                              |
| SCO5893 | 2.60            | oxidoreductase                                   |
| SCO5894 | 2.57            | thioesterase                                     |
| SCO5895 | 2.92            | methyltransferase                                |
| SCO5896 | 3.29            | phosphoenolpyruvate-utilizing enzyme, partial     |
| SCO5897 | 3.67            | oxidase                                          |
| SCO5898 | 2.16            | hypothetical protein SCO5898                    |
| SCO5899 | 2.89            | hypothetical protein SCO5899                    |
| SCO5972 | 2.37            | hypothetical protein SCO5972                    |
| SCO5978 | 3.31            | hypothetical protein SCO5978                    |
| SCO5979 | 3.74            | enoyl-CoA hydratase                              |
| SCO5980 | 4.75            | salicyl-CoA 5-hydroxylase                        |
| SCO5983 | 14.63           | fatty acid-CoA ligase                            |
| SCO5984 | 5.13            | acyl-CoA dehydrogenase                           |
| SCO5991 | 2.17            | hypothetical protein SCO5991                    |
| SCO5994 | 2.07            | integral membrane cytochrome biogenesis protein  |
DagR represses agarase genes in *S. coelicolor*

| Gene ID   | Log2 Fold Change | Function                                      |
|-----------|------------------|-----------------------------------------------|
| SCO6073   | 5.46             | cyclase                                       |
| SCO6074   | 3.84             | hypothetical protein SCO6074                 |
| SCO6087   | 2.24             | transport system integral membrane protein    |
| SCO6088   | 2.19             | solute-binding transport protein              |
| SCO6121   | 2.13             | transcriptional regulator                     |
| SCO6174   | 2.96             | hypothetical protein SCO6174                 |
| SCO6220   | 2.06             | hypothetical protein SCO6220                 |
| SCO6234   | 3.49             | beta-mannosidase                              |
| SCO6277   | 2.60             | epoxide hydrolase                             |
| SCO6312   | 2.23             | transcriptional regulator                     |
| SCO6372   | 5.36             | hypothetical protein SCO6372                 |
| SCO6414   | 4.87             | hypothetical protein SCO6414                 |
| SCO6415   | 4.45             | phenylhydantoinsase                           |
| SCO6417   | 4.47             | integral membrane transporter                 |
| SCO6418   | 2.61             | hypothetical protein SCO6418                 |
| SCO6430   | 3.30             | hypothetical protein SCO6430                 |
| SCO6431   | 4.46             | peptide synthase                              |
| SCO6432   | 3.76             | peptide synthase                              |
| SCO6434   | 4.29             | oxidoreductase, partial                       |
| SCO6436   | 4.18             | tRNA synthetase                               |
| SCO6437   | 3.40             | hypothetical protein SCO6437                 |
| SCO6438   | 2.42             | diaminopimelate decarboxylase                 |
| SCO6440   | 8.44             | hypothetical protein SCO6440                 |
| SCO6441   | 9.55             | aldehyde dehydrogenase                        |
| SCO6442   | 8.83             | alcohol dehydrogenase                         |
| SCO6443   | 6.80             | hypothetical protein SCO6443                 |
| SCO6457   | 6.50             | beta-galactosidase                            |
| SCO6458   | 6.54             | hypothetical protein SCO6458                 |
| SCO6492   | 2.04             | hypothetical protein SCO6492, partial         |
| SCO6526   | 2.15             | hypothetical protein SCO6526                 |
| SCO6543   | 4.04             | hypothetical protein SCO6543                 |
| SCO6547   | 136.66           | hypothetical protein SCO6547                 |
| SCO6558   | 2.60             | formate dehydrogenase accessory protein       |
| SCO6559   | 23.97            | respiratory chain oxidoreductase              |
| SCO6560   | 23.33            | respiratory chain oxidoreductase              |
| SCO6561   | 43.93            | respiratory chain oxidoreductase              |
| SCO6562   | 26.46            | 2-dehydropantoate 2-reductase                 |
| SCO6581   | 18.09            | transmembrane transport protein               |
DagR represses agarase genes in *S. coelicolor*

| Gene   | Similarity | Description                                      |
|--------|------------|--------------------------------------------------|
| SCO6582| 103.82     | hypothetical protein SCO6582                    |
| SCO6583| 18.41      | formyl-coenzyme A transferase                    |
| SCO6584| 90.47      | TPP-requiring enzyme                             |
| SCO6586| 29.18      | succinyl-CoA synthetase subunit alpha             |
| SCO6587| 40.30      | dehydrogenase                                    |
| SCO6588| 2.32       | hypothetical protein SCO6588                     |
| SCO6666| 2.41       | hypothetical protein SCO6666                     |
| SCO6727| 74.96      | hypothetical protein SCO6727                     |
| SCO6773| 2.37       | peptidase                                        |
| SCO6854| 2.18       | hypothetical protein SCO6854                     |
| SCO6902| 2.05       | hypothetical protein SCO6902                     |
| SCO6931| 3.98       | hypothetical protein SCO6931                     |
| SCO6934| 2.59       | hypothetical protein SCO6934                     |
| SCO6935| 2.04       | hypothetical protein SCO6935                     |
| SCO6936| 2.56       | hypothetical protein SCO6936                     |
| SCO6944| 2.23       | hypothetical protein SCO6944                     |
| SCO6946| 8.50       | hypothetical protein SCO6946                     |
| SCO6992| 3.13       | regulatory protein                               |
| SCO6995| 2.08       | protease                                         |
| SCO7033| 2.41       | regulatory protein                               |
| SCO7034| 27.94      | aminotransferase, partial                        |
| SCO7035| 29.35      | succinate-semialdehyde dehydrogenase             |
| SCO7127| 2.20       | hypothetical protein SCO7127                     |
| SCO7166| 2.07       | sugar-transporter integral membrane protein       |
| SCO7174| 2.08       | hypothetical protein SCO7174                     |
| SCO7189| 5.56       | hypothetical protein SCO7189                     |
| SCO7227| 3.11       | hypothetical protein SCO7227                     |
| SCO7303| 2.12       | TetR family transcriptional regulator            |
| SCO7368| 2.03       | hypothetical protein SCO7368                     |
| SCO7405| 8.96       | acetyltransferase, partial                        |
| SCO7406| 12.58      | hypothetical protein SCO7406                     |
| SCO7407| 9.84       | beta-galactosidase                               |
| SCO7409| 5.88       | binding-protein dependent transport protein       |
| SCO7410| 5.48       | binding-protein dependent transport protein       |
| SCO7411| 2.25       | LacI family transcriptional regulator            |
| SCO7536| 2.43       | hypothetical protein SCO7536                     |
| SCO7551| 23.86      | hypothetical protein SCO7551                     |
| SCO7623| 2.04       | NAD(P) transhydrogenase subunit alpha             |
| SCO7626| 4.08       | monooxygenase                                     |
DagR represses agarase genes in *S. coelicolor*

| SCO7658 | 1616.05 | hypothetical protein SCO7658 |
|---------|---------|-------------------------------|
| SCO7699 | 5.58    | nucleotide-binding protein    |
| SCO7700 | 5.97    | cyclase                       |
| SCO7701 | 3.89    | methyltransferase             |
| SCO7790 | 5.05    | oxidoreductase                |
| SCO7791 | 2.37    | oxidoreductase                |
| SCO7791a| 2.38    | oxidoreductase                |
| SCO7792 | 2.92    | hypothetical protein SCO7792 |
| SCO7804 | 2.27    | hypothetical protein SCO7804, partial |
| SCO7828 | 2.80    | DNA-binding protein           |
| SCP1.276| 7.66    | insertion element is466s transposase (plasmid) |
**TABLE S3.** List of down-regulated genes in the Δsco3485 mutant as compared to that in the wild type strain.

| Gene name | fold change | description |
|-----------|-------------|-------------|
| SCO0016   | 0.19        | hypothetical protein SCO0016 |
| SCO0064   | 0.42        | hypothetical protein SCO0064 |
| SCO0117   | 0.18        | short chain dehydrogenase |
| SCO0128   | 0.04        | hypothetical protein SCO0128 |
| SCO0133   | 0.33        | hypothetical protein SCO0133 |
| SCO0154   | 0.41        | hypothetical protein SCO0154 |
| SCO0216   | 0.24        | nitrate reductase subunit alpha NarG2 |
| SCO0217   | 0.29        | nitrate reductase subunit beta NarH2 |
| SCO0218   | 0.27        | nitrate reductase subunit delta NarJ2 |
| SCO0220   | 0.34        | hypothetical protein SCO0220 |
| SCO0257   | 0.44        | hypothetical protein SCO0257 |
| SCO0258   | 0.37        | hypothetical protein SCO0258 |
| SCO0259   | 0.29        | alcohol dehydrogenase, partial |
| SCO0260   | 0.42        | hypothetical protein SCO0260 |
| SCO0282   | 0.49        | deoR family transcriptional regulator |
| SCO0283   | 0.32        | hypothetical protein SCO0283 |
| SCO0303   | 0.11        | hypothetical protein SCO0303 |
| SCO0322   | 0.15        | ABC transport ATP-binding subunit, partial |
| SCO0335   | 0.42        | hypothetical protein SCO0335 |
| SCO0336   | 0.47        | hypothetical protein SCO0336 |
| SCO0338   | 0.48        | dehydrogenase |
| SCO0365   | 0.37        | oxidoreductase |
| SCO0411   | 0.45        | hypothetical protein SCO0411 |
| SCO0412   | 0.37        | hypothetical protein SCO0412 |
| SCO0425   | 0.48        | hypothetical protein SCO0425 |
| SCO0426   | 0.08        | hypothetical protein SCO0426 |
| SCO0435   | 0.30        | aminotransferase |
| SCO0436   | 0.00        | 50S ribosomal protein L32 |
| SCO0439   | 0.31        | hypothetical protein SCO0439 |
| SCO0440   | 0.29        | hypothetical protein SCO0440 |
| SCO0441   | 0.23        | LamB/YcsF family protein |
| SCO0442   | 0.25        | hypothetical protein SCO0442 |
| SCO0443   | 0.35        | hypothetical protein SCO0443 |
DagR represses agarase genes in *S. coelicolor*

| Gene   | Expression Level | Function                                                                 |
|--------|------------------|--------------------------------------------------------------------------|
| SCO0476| 0.33             | ABC transporter ATP-binding protein                                         |
| SCO0505| 0.11             | large, multifunctional hypothetical protein, partial                       |
| SCO0517| 0.09             | hypothetical protein SCO0517, partial                                      |
| SCO0524| 0.45             | gluconolactonase                                                          |
| SCO0531| 0.40             | sugar transporter sugar binding protein                                     |
| SCO0545| 0.32             | hypothetical protein SCO0545                                             |
| SCO0618| 0.33             | hypothetical protein SCO0618                                             |
| SCO0620| 0.46             | hypothetical protein SCO0620                                             |
| SCO0644| 0.30             | hypothetical protein SCO0644                                             |
| SCO0694| 0.03             | hypothetical protein SCO0694                                             |
| SCO0716| 0.29             | glycosyl hydrolase                                                        |
| SCO0732| 0.45             | protease                                                                  |
| SCO0752| 0.21             | protease                                                                  |
| SCO0758| 0.03             | hypothetical protein SCO0758                                             |
| SCO0761| 0.01             | hypothetical protein SCO0761                                             |
| SCO0811| 0.48             | ABC transporter ATP-binding protein, partial                              |
| SCO0843| 0.39             | hypothetical protein SCO0843                                             |
| SCO0887| 0.47             | TetR family transcriptional regulator                                     |
| SCO0903| 0.39             | hypothetical protein SCO0903                                             |
| SCO0930| 0.26             | lipoprotein                                                               |
| SCO0942| 0.50             | RNA polymerase sigma factor SigL                                          |
| SCO0944| 0.42             | hypothetical protein SCO0944                                             |
| SCO0950| 0.14             | transport system permease                                                 |
| SCO0951| 0.25             | transport system permease                                                 |
| SCO0952| 0.26             | solute-binding protein                                                    |
| SCO0953| 0.28             | LacI family transcriptional regulator                                     |
| SCO0963| 0.50             | hypothetical protein SCO0963                                             |
| SCO1001| 0.34             | hypothetical protein SCO1001                                             |
| SCO1002| 0.43             | hypothetical protein SCO1002                                             |
| SCO1010| 0.03             | integral membrane transport protein                                        |
| SCO1012| 0.03             | oxidoreductase                                                            |
| SCO1034| 0.27             | TetR family transcriptional regulator                                     |
| SCO1035| 0.19             | hypothetical protein SCO1035                                             |
| SCO1044| 0.35             | hypothetical protein SCO1044                                             |
| SCO1045| 0.16             | metal associated protein                                                  |
| SCO1046| 0.28             | metal transporter ATPase                                                  |
| SCO1087| 0.28             | aldolase                                                                  |
| SCO1088| 0.26             | oxidoreductase                                                            |
| SCO1089| 0.31             | hypothetical protein SCO1089                                             |
DagR represses agarase genes in *S. coelicolor*

| Gene    | Expression Level | Function                                    |
|---------|------------------|---------------------------------------------|
| SCO1095 | 0.42             | hypothetical protein SCO1095                |
| SCO1107 | 0.26             | hypothetical protein SCO1107                |
| SCO1114 | 0.48             | hypothetical protein SCO1114                |
| SCO1150 | 0.47             | 50S ribosomal protein L31                   |
| SCO1157 | 0.39             | ATP/GTP binding protein                     |
| SCO1190 | 0.44             | export protein                              |
| SCO1193 | 0.47             | TetR family transcriptional regulator       |
| SCO1236 | 0.44             | urease subunit gamma                        |
| SCO1258 | 0.41             | ABC transporter ATP-binding protein         |
| SCO1276 | 0.22             | RNA polymerase ECF sigma factor             |
| SCO1278 | 0.47             | ATP/GTP-binding protein                     |
| SCO1293 | 0.25             | hypothetical protein SCO1293                |
| SCO1294 | 0.14             | cystathionine gamma-synthase                |
| SCO1317 | 0.29             | hypothetical protein SCO1317                |
| SCO1356 | 0.29             | iron sulfur protein                         |
| SCO1358 | 0.50             | LysR family transcriptional regulator       |
| SCO1359 | 0.39             | hypothetical protein SCO1359, partial       |
| SCO1367 | 0.18             | ABC transporter ATP-binding protein         |
| SCO1368 | 0.21             | ABC transporter                             |
| SCO1369 | 0.30             | two component system histidine kinase       |
| SCO1379 | 0.37             | hypothetical protein SCO1379                |
| SCO1411 | 0.20             | transmembrane transport protein             |
| SCO1412 | 0.23             | hypothetical protein SCO1412                |
| SCO1439 | 0.16             | phosphoribosyl-ATP pyrophosphatase          |
| SCO1442 | 0.49             | hypothetical protein SCO1442                |
| SCO1522 | 0.35             | glutamine amidotransferase subunit PdxT     |
| SCO1523 | 0.46             | pyridoxal biosynthesis lyase PdxS           |
| SCO1573 | 0.21             | oxidoreductase membrane protein             |
| SCO1656 | 0.41             | hydrolase                                   |
| SCO1687 | 0.49             | hypothetical protein SCO1687                |
| SCO1705 | 0.37             | alcohol dehydrogenase                       |
| SCO1706 | 0.41             | aldehyde dehydrogenase                      |
| SCO1708 | 0.05             | hypothetical protein SCO1708                |
| SCO1722 | 0.44             | hypothetical protein SCO1722                |
| SCO1734 | 0.21             | cellulose-binding protein                   |
| SCO1784 | 0.24             | hypothetical protein SCO1784                |
| SCO1792 | 0.47             | 3-methyladenine DNA glycosylase             |
| SCO1895 | 0.45             | 5-dehydro-4-deoxyglucarate dehydratase      |
| SCO1995 | 0.48             | hypothetical protein SCO1995                |
DagR represses agarase genes in *S. coelicolor*

| Gene ID   | Expression | Description                                   |
|-----------|------------|-----------------------------------------------|
| SCO2068   | 0.48       | alkaline phosphatase, partial                  |
| SCO2108   | 0.05       | hypothetical protein SCO2108                  |
| SCO2146   | 0.31       | aminotransferase                              |
| SCO2207   | 0.15       | hypothetical protein SCO2207                  |
| SCO2217   | 0.26       | hypothetical protein SCO2217                  |
| SCO2218   | 0.27       | lipoprotein                                   |
| SCO2261   | 0.08       | hypothetical protein SCO2261                  |
| SCO2289   | 0.26       | hypothetical protein SCO2289                  |
| SCO2347   | 0.31       | hypothetical protein SCO2347                  |
| SCO2350   | 0.33       | hypothetical protein SCO2350                  |
| SCO2360   | 0.43       | hypothetical protein SCO2360                  |
| SCO2361   | 0.49       | hypothetical protein SCO2361                  |
| SCO2382   | 0.47       | hypothetical protein SCO2382                  |
| SCO2401   | 0.41       | dehydratase                                   |
| SCO2402   | 0.37       | dehydrogenase                                 |
| SCO2403   | 0.26       | hypothetical protein SCO2403                  |
| SCO2488   | 0.47       | nitrite reductase small subunit NirC          |
| SCO2495   | 0.34       | hypothetical protein SCO2495                  |
| SCO2516   | 0.30       | hypothetical protein SCO2516                  |
| SCO2543   | 0.34       | 5-dehydro-4-deoxyglucarate dehydratase        |
| SCO2628   | 0.49       | amino acid permease                           |
| SCO2646   | 0.47       | hypothetical protein SCO2646                  |
| SCO2658   | 0.30       | sugar-binding protein                         |
| SCO2659   | 0.28       | sugar transport system permease               |
| SCO2660   | 0.28       | sugar transport membrane protein              |
| SCO2661   | 0.36       | sugar hydrolase                               |
| SCO2662   | 0.46       | kinase                                        |
| SCO2795   | 0.33       | sugar binding hypothetical protein            |
| SCO2798   | 0.11       | cellobiose hydrolase                          |
| SCO2799   | 0.41       | sugar hydrolase                               |
| SCO2814   | 0.28       | methyltransferase                             |
| SCO2851   | 0.36       | hypothetical protein SCO2851                  |
| SCO2857   | 0.47       | hypothetical protein SCO2857                  |
| SCO2922   | 0.48       | hypothetical protein SCO2922                  |
| SCO2953   | 0.40       | hypothetical protein SCO2953                  |
| SCO3111   | 0.41       | ABC transporter ATP-binding protein           |
| SCO3120   | 0.05       | hypothetical protein SCO3120                  |
| SCO3203   | 0.20       | phosphinothricin acetyltransferase           |
| SCO3205   | 0.42       | MarR family transcriptional regulator        |
DagR represses agarase genes in *S. coelicolor*

| Gene   | Score | Description                           |
|--------|-------|---------------------------------------|
| SCO3263 | 0.34  | hypothetical protein SCO3263          |
| SCO3280 | 0.33  | hypothetical protein SCO3280          |
| SCO3343 | 0.19  | hypothetical protein SCO3343          |
| SCO3425 | 0.27  | 30S ribosomal protein S18             |
| SCO3426 | 0.36  | hypothetical protein SCO3426          |
| SCO3429 | 0.14  | 50S ribosomal protein L28             |
| SCO3442 | 0.07  | hypothetical protein SCO3442          |
| SCO3445 | 0.00  | small membrane protein                |
| SCO3451 | 0.06  | hypothetical protein SCO3451          |
| SCO3454 | 0.28  | ABC-transporter membrane protein      |
| SCO3509 | 0.38  | hypothetical protein SCO3509          |
| SCO3527 | 0.11  | hypothetical protein SCO3527          |
| SCO3635 | 0.34  | hypothetical protein SCO3635          |
| SCO3662 | 0.46  | hypothetical protein SCO3662          |
| SCO3682 | 0.21  | delta fatty acid desaturase           |
| SCO3685 | 0.28  | hypothetical protein SCO3685          |
| SCO3692 | 0.33  | anti-sigma factor antagonist          |
| SCO3695 | 0.42  | hypothetical protein SCO3695          |
| SCO3762 | 0.37  | hypothetical protein SCO3762          |
| SCO3817 | 0.46  | branched-chain alpha-keto acid dehydrogenase E1 subunit alpha |
| SCO3924 | 0.23  | hypothetical protein SCO3924          |
| SCO3925 | 0.42  | transcriptional regulator             |
| SCO3955 | 0.45  | hypothetical protein SCO3955          |
| SCO3956 | 0.48  | ABC transporter ATP-binding protein   |
| SCO3978 | 0.33  | oxidoreductase                        |
| SCO3987 | 0.29  | hypothetical protein SCO3987          |
| SCO3996 | 0.12  | excisionase                           |
| SCO4027 | 0.45  | anti sigma factor antagonist          |
| SCO4050 | 0.33  | acetyltransferase                     |
| SCO4063 | 0.30  | hypothetical protein SCO4063          |
| SCO4190 | 0.35  | GntR family transcriptional regulator |
| SCO4294 | 0.39  | hypothetical protein SCO4294          |
| SCO4299 | 0.44  | hypothetical protein SCO4299          |
| SCO4302 | 0.18  | hypothetical protein SCO4302          |
| SCO4308 | 0.44  | transcriptional regulator             |
| SCO4324 | 0.44  | hypothetical protein SCO4324          |
| SCO4437 | 0.38  | sodium-coupled permease               |
| SCO4466 | 0.36  | hypothetical protein SCO4466          |
| SCO4537 | 0.37  | hypothetical protein SCO4537          |
DagR represses agarase genes in *S. coelicolor*

| Gene   | Expression Level | Description                          |
|--------|-----------------|--------------------------------------|
| SCO4561| 0.35            | hypothetical protein SCO4561        |
| SCO4587| 0.37            | hypothetical protein SCO4587        |
| SCO4590| 0.48            | hypothetical protein SCO4590        |
| SCO4694| 0.15            | hypothetical protein SCO4694        |
| SCO4767| 0.15            | regulatory protein                  |
| SCO4792| 0.47            | two-component system DNA-binding response regulator |
| SCO4843| 0.44            | hypothetical protein SCO4843        |
| SCO4872| 0.45            | hypothetical protein SCO4872        |
| SCO4932| 0.26            | histidine ammonia-lyase             |
| SCO4999| 0.19            | hypothetical protein SCO4999        |
| SCO5029| 0.49            | hypothetical protein SCO5029        |
| SCO5034| 0.19            | hypothetical protein SCO5034        |
| SCO5035| 0.22            | ABC transporter ATP-binding protein |
| SCO5036| 0.24            | hypothetical protein SCO5036        |
| SCO5235| 0.50            | sugar hydrolase                     |
| SCO5265| 0.38            | hypothetical protein SCO5265        |
| SCO5299| 0.33            | hypothetical protein SCO5299        |
| SCO5300| 0.11            | hypothetical protein SCO5300        |
| SCO5310| 0.46            | hypothetical protein SCO5310        |
| SCO5311| 0.29            | hypothetical protein SCO5311        |
| SCO5401| 0.28            | hypothetical protein SCO5401        |
| SCO5402| 0.11            | hypothetical protein SCO5402        |
| SCO5404| 0.48            | two-component sensor kinase         |
| SCO5464| 0.50            | hypothetical protein SCO5464        |
| SCO5479| 0.48            | oligopeptide ABC transporter ATP-binding protein |
| SCO5561| 0.06            | transcriptional regulator           |
| SCO5700| 0.45            | kinase                              |
| SCO5763| 0.31            | hypothetical protein SCO5763        |
| SCO5765| 0.44            | hypothetical protein SCO5765        |
| SCO5774| 0.47            | glutamate permease                  |
| SCO5775| 0.46            | glutamate permease                  |
| SCO5777| 0.31            | glutamate uptake system ATP-binding protein |
| SCO5977| 0.46            | amino acid permease                 |
| SCO5990| 0.46            | hypothetical protein SCO5990        |
| SCO6027| 0.46            | acetyl-CoA acetyltransferase        |
| SCO6038| 0.30            | hypothetical protein SCO6038        |
| SCO6097| 0.47            | sulfate adenylytransferase subunit 1 |
| SCO6099| 0.47            | adenylylsulfate kinase              |
| SCO6101| 0.23            | hypothetical protein SCO6101        |
| Gene     | Expression Ratio | Description                                      |
|----------|------------------|--------------------------------------------------|
| SCO6117  | 0.50             | hypothetical protein SCO6117                     |
| SCO6158  | 0.36             | hypothetical protein SCO6158                     |
| SCO6160  | 0.39             | bifunctional preprotein translocase subunit SecD/SecF |
| SCO6165  | 0.40             | hypothetical protein SCO6165, partial            |
| SCO6178  | 0.38             | deacetylase                                      |
| SCO6186  | 0.44             | phosphoheptose isomerase                         |
| SCO6195  | 0.24             | acetyl-coenzyme A synthetase                     |
| SCO6196  | 0.29             | AMP-binding domain-containing protein            |
| SCO6204  | 0.30             | catalase                                         |
| SCO6208  | 0.31             | DNA-binding protein                              |
| SCO6209  | 0.30             | OHCU decarboxylase                               |
| SCO6210  | 0.21             | hypothetical protein SCO6210                    |
| SCO6211  | 0.34             | uricase, partial                                 |
| SCO6213  | 0.38             | hydroxydechloroatrazine ethylaminohydrolase      |
| SCO6214  | 0.30             | permease                                         |
| SCO6241  | 0.27             | hypothetical protein SCO6241                    |
| SCO6243  | 0.38             | malate synthase                                  |
| SCO6246  | 0.44             | transcriptional regulator for glyoxylate bypass  |
| SCO6248  | 0.24             | allantoicase                                     |
| SCO6356  | 0.50             | hypothetical protein SCO6356                    |
| SCO6404  | 0.02             | hypothetical protein SCO6404                    |
| SCO6507  | 0.35             | gas vesicle synthesis protein                    |
| SCO6548  | 0.21             | cellulase                                        |
| SCO6566  | 0.05             | ROK family protein, partial                      |
| SCO6567  | 0.02             | ABC transporter ATP-binding protein              |
| SCO6568  | 0.03             | ABC transporter                                  |
| SCO6569  | 0.03             | solute binding protein                           |
| SCO6570  | 0.04             | oxidoreductase                                   |
| SCO6571  | 0.04             | DNA-binding protein                              |
| SCO6572  | 0.05             | glycosyl hydrolase                               |
| SCO6574  | 0.06             | hypothetical protein SCO6574                    |
| SCO6575  | 0.08             | hypothetical protein SCO6575                    |
| SCO6576  | 0.06             | hypothetical protein SCO6576                    |
| SCO6577  | 0.10             | hypothetical protein SCO6577                    |
| SCO6578  | 0.13             | hypothetical protein SCO6578                    |
| SCO6579  | 0.12             | hypothetical protein SCO6579                    |
| SCO6580  | 0.12             | hypothetical protein SCO6580, partial            |
| SCO6593  | 0.34             | hypothetical protein SCO6593                    |
| SCO6594  | 0.20             | hypothetical protein SCO6594                    |
DagR represses agarase genes in *S. coelicolor*

| Gene     | Expression | Function                      |
|----------|------------|-------------------------------|
| SCO6600  | 0.29       | transcriptional regulator     |
| SCO6602  | 0.24       | transmembrane sugar transport protein |
| SCO6603  | 0.19       | transmembrane sugar transport protein |
| SCO6604  | 0.13       | beta-glucosidase, partial     |
| SCO6617  | 0.33       | hypothetical protein SCO6617 |
| SCO6646  | 0.25       | transport system permease     |
| SCO6647  | 0.20       | hypothetical protein SCO6647 |
| SCO6652  | 0.27       | hypothetical protein SCO6652 |
| SCO6653  | 0.25       | hypothetical protein SCO6653 |
| SCO6654  | 0.46       | hypothetical protein SCO6654 |
| SCO6665  | 0.26       | glucosidase                   |
| SCO6710  | 0.03       | glycosyl hydrolase            |
| SCO6711  | 0.03       | hypothetical protein SCO6711 |
| SCO6716  | 0.45       | hypothetical protein SCO6716 |
| SCO6717  | 0.24       | acyl-ACP desaturase           |
| SCO6830  | 0.40       | transcription regulator ArsR  |
| SCO6831  | 0.08       | hypothetical protein SCO6831 |
| SCO6839  | 0.43       | hypothetical protein SCO6839 |
| SCO6913  | 0.29       | hypothetical protein SCO6913 |
| SCO6914  | 0.27       | hypothetical protein SCO6914 |
| SCO6923  | 0.37       | hypothetical protein SCO6923 |
| SCO6925  | 0.07       | hypothetical protein SCO6925 |
| SCO6968  | 0.29       | long-chain-fatty-acid-CoA ligase |
| SCO7010  | 0.47       | alpha glucosidase             |
| SCO7027  | 0.39       | LacI family transcriptional regulator |
| SCO7086  | 0.13       | MerR family transcriptional regulator |
| SCO7106  | 0.40       | hypothetical protein SCO7106 |
| SCO7172  | 0.25       | hypothetical protein SCO7172 |
| SCO7208  | 0.25       | hypothetical protein SCO7208 |
| SCO7291  | 0.42       | Ser/Thr protein kinase, partial |
| SCO7350  | 0.33       | membrane efflux protein       |
| SCO7352  | 0.49       | hypothetical protein SCO7352 |
| SCO7386  | 0.40       | serine protease               |
| SCO7442  | 0.31       | hypothetical protein SCO7442 |
| SCO7455  | 0.39       | isochorismatase               |
| SCO7484  | 0.05       | hypothetical protein SCO7484 |
| SCO7492  | 0.46       | hypothetical protein SCO7492 |
| SCO7575  | 0.47       | hydrolase                     |
| SCO7576  | 0.38       | hydrolase                     |
DagR represses agarase genes in *S. coelicolor*

| Gene   | Log2 Fold Change | Description                                      |
|--------|-----------------|--------------------------------------------------|
| SCO7593| 0.39            | hypothetical protein SCO7593                    |
| SCO7595| 0.48            | anhydro-N-acetylmuramic acid kinase              |
| SCO7628| 0.49            | hypothetical protein SCO7628                    |
| SCO7668| 0.47            | hypothetical protein SCO7668                    |
| SCO7680| 0.46            | ABC transporter ATP-binding protein              |
| SCO7750| 0.45            | hypothetical protein SCO7750                    |
| SCO7756| 0.24            | hypothetical protein SCO7756                    |
| SCO7784| 0.46            | oxidoreductase                                   |
| SCO7788| 0.08            | hypothetical protein SCO7788                    |
| SCO7801| 0.43            | hypothetical protein SCO7801                    |
| SCO7808| 0.34            | hypothetical protein SCO7808                    |
| SCO7820| 0.23            | hypothetical protein SCO7820                    |
| SCO7831| 0.19            | hypothetical protein SCO7831                    |
DagR represses agarase genes in *S. coelicolor*

**FIGURE S1.**  (A) Verified PCR results from *dagR* (*sco3485*) gene deletion in Δsco3485 mutant using primers C3485-F and C3485-R, as described in Table S1, (B) Representative sequencing traces from *S. coelicolor* A3(2)(bottom) and Δsco3485 mutant (up) at the *dagR* gene region. Arrow line indicates the sequences of the defined deletion. The sgRNA sequences used is indicated by a black background.

**FIGURE S2.** Scatter plot of gene expression detected between Δsco3485 mutant (4 day culture) vs wild type strain (4 day culture) by RNA-seq analysis. Most agar hydrolytic genes (*sco3471-sco3487*) show a more pronounced increase in expression than other genes.

**FIGURE S3.** Sodium dodecyl sulfate polyacrylamide electrophoresis (SDS-PAGE) of the purified His-tagged DagR. Lanes: M, protein size marker; 1, cell free extract before IPTG induction; 2, cell free extract after IPTG induction; 3, cell free extract after sonication; 4, cell pellet debris after sonication; 5, purified His-tagged DagR; 6, dialyzed His-tagged DagR protein.
FIGURE S1. A) Verified PCR results from *dagR (sco3485)* gene deletion in Δsco3485 mutant using primers C3485-F and C3485-R, as described in Table S1. B) Representative sequencing traces from *S. coelicolor* (bottom) and Δsco3485 mutant (up) at the *dagR* gene region.
FIGURE S2. Scatter plot of gene expression detected between Δsco3485 (4 day culture) vs WT (4 day culture) by RNA-seq analysis.
FIGURE S3. Sodium dodecyl sulfate polyacrylamide electrophoresis (SDS-PAGE) of the purified His-tagged DagR.