Table of Contents

[patB 1](#_Toc38640348)

[nifH 1](#_Toc38640349)

[Appendix A 2](#_Toc38640350)

[Part 1: Top 25 Negative Fold Changed Genes 2](#_Toc38640351)

[Part 2: Top 25 Positive Fold Changed Genes 3](#_Toc38640352)

[Part 3: Sigma Factors repressed and induced 4](#_Toc38640353)

[Repressed 4](#_Toc38640354)

[Induced 4](#_Toc38640355)

[Part 4: Clock genes repressed and induced 5](#_Toc38640356)

[Repressed 5](#_Toc38640357)

[Induced 5](#_Toc38640358)

[Part 5: Regulators repressed and induced 5](#_Toc38640359)

[Repressed 5](#_Toc38640360)

[Induced 6](#_Toc38640361)

[Part 6: Sensors repressed and induced 7](#_Toc38640362)

[Repressed 7](#_Toc38640363)

[Induced 8](#_Toc38640364)

[Appendix B 9](#_Toc38640365)

[Part 1: Top 25 Negative Fold Changed Genes 9](#_Toc38640366)

[Part 2: Top 25 Positive Fold Changed Genes 10](#_Toc38640367)

[Part 3: Sigma Factors repressed and induced 11](#_Toc38640368)

[Repressed 11](#_Toc38640369)

[Induced 12](#_Toc38640370)

[Part 4: Clock genes repressed and induced 12](#_Toc38640371)

[Repressed 12](#_Toc38640372)

[Induced 12](#_Toc38640373)

[Part 5: Regulators repressed and induced 12](#_Toc38640374)

[Repressed 12](#_Toc38640375)

[Induced 14](#_Toc38640376)

[Part 6: Sensors repressed and induced 15](#_Toc38640377)

[Repressed 15](#_Toc38640378)

[Induced 16](#_Toc38640379)

Results and Conclusions

# patB

1. The top 25 genes whose expression has been repressed, arranged according to the magnitude of their fold change, is given below in Appendix A. Most of them are part of the nif gene cluster which is in accordance to our proposition that patB regulates the nif genes. The list of the gene names along with their fold change with respect to wild-type and mutual information score with patB gene is given in Appendix A.
2. The top 25 genes whose expression has been induced, arranged according to the magnitude of their fold change, is given in Appendix B. The ones with mutual information score of 0 with patB are particularly interesting since they are not correlated with patB in normal environmental conditions but they are induced when patB is knocked-out. The most interesting ones are the transcriptional regulator from the TetR family, cce\_0974 and the phycocyanin unit, apcA, apcB, cpcA and cpcB. The TetR family of transcriptional regulators have been shown to respond to environmental insults; Ref: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC1197418/. The list of the gene names along with their fold change with respect to wild-type and mutual information score with patB gene is given below in Appendix A.
3. Amongst the sigma factors, cce\_2337 and sigH have shown negative fold change while sigG and sigE have shown positive fold change values. SigE has been proposed to maintain the balance of carnon and nitrogen metabolism; Ref: https://www.ncbi.nlm.nih.gov/pmc/articles/PMC2758279/.
4. Amongst the clock genes, kaiB3 is repressed while kaiB4 and kaiA have shown induced expression levels.
5. Amongst the regulators, the Fur family transcriptional regulator, cce\_3127 is repressed while the ArsR family regulator, cce\_4396 is induced.

# nifH

1. The top 25 genes whose expression has been repressed, arranged according to the magnitude of their fold change, is given below in Appendix B. Most of them are part of the nif gene cluster which makes sense because we would expect the other nif genes to be affected by nifH knockout. The list of the gene names along with their fold change with respect to wild-type and mutual information score with nifH gene is given in Appendix B.
2. The top 25 genes whose expression has been induced, arranged according to the magnitude of their fold change, is given in Appendix B. The most interesting one amongst them is aphA which has shown a very high fold change due to the knockout. The list of the gene names along with their fold change with respect to wild-type and mutual information score with nifH gene is given below in Appendix B.
3. Amongst the sigma factors, cce\_2337 and sigH have again shown a negative fold change while sigE have shown positive fold change values like in the patB case.
4. Amongst the clock genes, kaiA is repressed while kaiB4 and kaiB3 have shown induced expression levels. It is worth noticing that kaiB3 was repressed in patB's case.
5. Amongst the regulators, the most interesting fold change was observed in patB which was repressed due to the nifH knockout. Another interesting gene which was induced is glnB.

# Appendix A

## Part 1: Top 25 Negative Fold Changed Genes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_0553 | -11.4423 | serine O-acetyltransferase | cysE2 | 0.7393 |
| cce\_5300 | -10.5145 | probable integrase/recombinase | cce\_5300 | 0.0631 |
| cce\_5304 | -9.852 | hypothetical protein | cce\_5304 | 0.6621 |
| cce\_5310 | -9.4553 | hypothetical protein | cce\_5310 | 0.806 |
| cce\_5301 | -9.2027 | hypothetical protein | cce\_5301 | 0.0 |
| cce\_5309 | -8.6697 | hypothetical protein | cce\_5309 | 0.247 |
| cce\_0558 | -8.1138 | iron-sulfur cluster assembly protein | nifU | 0.7365 |
| cce\_0563 | -8.0499 | nitrogenase molybdenum-iron cofactor biosynthesis protein | nifE | 0.6921 |
| cce\_0561 | -8.0074 | nitrogenase molybdenum-iron protein beta chain | nifK | 0.8324 |
| cce\_0564 | -7.8956 | nitrogenase molybdenum-iron cofactor biosynthesis protein | nifN | 0.7324 |
| cce\_0555 | -7.8094 | hypothetical protein | cce\_0555 | 0.7615 |
| cce\_0556 | -7.7696 | 4Fe-4S ferredoxin | cce\_0556 | 0.8227 |
| cce\_0560 | -7.5927 | nitrogenase molybdenum-iron protein alpha chain | nifD | 0.7921 |
| cce\_0557 | -7.5892 | nitrogenase cofactor synthesis protein | nifS | 0.7296 |
| cce\_0562 | -7.5641 | hypothetical protein | cce\_0562 | 0.7824 |
| cce\_0559 | -7.56 | nitrogenase iron protein | nifH | 0.874 |
| cce\_0554 | -7.4703 | nitrogenase cofactor biosynthesis protein | nifB | 0.8199 |
| cce\_0565 | -7.2701 | probable nitrogen fixation protein | nifX | 0.7546 |
| cce\_5303 | -7.1091 | hypothetical protein | cce\_5303 | 0.1274 |
| cce\_5306 | -6.8873 | hypothetical protein | cce\_5306 | 0.0 |
| cce\_0549 | -6.5936 | homocitrate synthase | nifV | 0.7352 |
| cce\_5307 | -6.2478 | hypothetical protein | cce\_5307 | 0.3987 |
| cce\_0550 | -6.2361 | conserved hypothetical protein | cce\_0550 | 0.6963 |
| cce\_5302 | -6.1825 | hypothetical protein | cce\_5302 | 0.2039 |
| cce\_0548 | -6.0136 | iron-sulfur cofactor synthesis protein | nifZ | 0.7824 |

## Part 2: Top 25 Positive Fold Changed Genes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_0974 | 4.2923 | transcriptional Regulator, TetR family | cce\_0974 | 0.0 |
| cce\_3132 | 4.1987 | unknown | cce\_3132 | 0.0 |
| cce\_2635 | 4.1485 | hypothetical protein | cce\_2635 | 0.5566 |
| cce\_1360 | 3.9794 | hypothetical protein | cce\_1360 | 0.0 |
| cce\_1459 | 3.9736 | unknown | cce\_1459 | 0.1978 |
| cce\_4789 | 3.6455 | hypothetical protein | cce\_4789 | 0.7254 |
| cce\_2619 | 3.5981 | ABC transporter, substrate binding protein, possibly oligopeptides | cce\_2619 | 0.295 |
| cce\_0528 | 3.5871 | hypothetical protein | cce\_0528 | 0.2551 |
| cce\_3054 | 3.5721 | putative biopolymer transport protein | exbB2 | 0.0 |
| cce\_4140 | 3.5639 | phosphoribosylformimino-5-aminoimidazole carboxamide ribotide isomerase | hisA | 0.1383 |
| cce\_2909 | 3.5424 | allophycocyanin beta subunit | apcB | 0.055 |
| cce\_3146 | 3.524 | geranylgeranyl hydrogenase | chlP | 0.3518 |
| cce\_1985 | 3.5046 | carbohydrate kinase, thermoresistant glucokinase | cce\_1985 | 0.0 |
| cce\_2988 | 3.4756 | hypothetical protein | cce\_2988 | 0.3598 |
| cce\_0527 | 3.4707 | unknown | cce\_0527 | 0.2983 |
| cce\_2908 | 3.4677 | allophycocyanin alpha subunit | apcA | 0.0217 |
| cce\_3445 | 3.4151 | conserved hypothetical protein | cce\_3445 | 0.7324 |
| cce\_2718 | 3.3886 | putative DoxX | cce\_2718 | 0.5935 |
| cce\_3856 | 3.3877 | hypothetical protein | cce\_3856 | 0.0336 |
| cce\_1780 | 3.3875 | unknown | cce\_1780 | 0.3679 |
| cce\_2802 | 3.3549 | hypothetical protein | cce\_2802 | 0.0521 |
| cce\_2467 | 3.3322 | N-acetylmuramoyl-L-alanine amidase | amiA2 | 0.6379 |
| cce\_3732 | 3.3298 | unknown | cce\_3732 | 0.4204 |
| cce\_1821 | 3.3203 | putative HAD-superfamily hydrolase, subfamily IA | cce\_1821 | 0.6199 |
| cce\_0833 | 3.2632 | hypothetical protein | cce\_0833 | 0.091 |

## Part 3: Sigma Factors repressed and induced

### Repressed

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_2337 | -1.75 | group 2 sigma-70 RNA polymerase sigma factor | cce\_2337 | 0.0885 |
| cce\_2424 | -1.6126 | group 4 sigma-70 RNA polymerase sigma factor H | sigH | 0.0333 |

### Induced

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_4142 | 3.0904 | group 4 sigma-70 RNA polymerase sigma factor G | sigG | 0.3594 |
| cce\_0601 | 2.2267 | group 2 sigma-70 RNA polymerase sigma factor E | sigE | 0.0 |

## Part 4: Clock genes repressed and induced

### Repressed

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_0435 | -1.7203 | circadian clock protein | kaiB3 | 0.0 |

### Induced

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_0145 | 2.1478 | putative circadian clock protein | kaiB4 | 0.0 |
| cce\_0424 | 1.6898 | circadian clock protein | kaiA | 0.5566 |

## Part 5: Regulators repressed and induced

### Repressed

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_3127 | -3.4655 | transcription regulator, Fur family | cce\_3127 | 0.4919 |
| cce\_3559 | -2.532 | two-component response regulator | cce\_3559 | 0.6157 |
| cce\_1135 | -2.2522 | two-component response regulator | cce\_1135 | 0.4579 |
| cce\_1001 | -2.1858 | ATP-dependent Clp protease, regulatory subunit | clpC2 | 0.2483 |
| cce\_1186 | -2.0616 | two-component hybrid sensor and regulator | cce\_1186 | 0.7147 |
| cce\_1412 | -1.6399 | two-component response regulator | cce\_1412 | 0.6413 |
| cce\_1185 | -1.5719 | two-component hybrid sensor and regulator | cce\_1185 | 0.7871 |
| cce\_0448 | -1.4739 | response regulator | cce\_0448 | 0.1475 |
| cce\_3731 | -1.4542 | putative Rubisco transcriptional regulator, LysR family | rbcR | 0.8157 |
| cce\_4542 | -1.3755 | two-component response regulator | cce\_4542 | 0.3027 |
| cce\_2508 | -1.2169 | two-component hybrid sensor and regulator | cce\_2508 | 0.1037 |
| cce\_4183 | -1.2119 | two-component response regulator | cce\_4183 | 0.1814 |
| cce\_2509 | -1.2065 | two-component hybrid sensor and regulator | cce\_2509 | 0.2711 |
| cce\_0683 | -1.2059 | putative transcriptional regulator | cce\_0683 | 0.2435 |
| cce\_4405 | -1.1947 | two-component hybrid sensor and regulator | cce\_4405 | 0.0 |
| cce\_4714 | -1.1777 | two-component response regulator, NarL subfamily | cce\_4714 | 0.0834 |

### Induced

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_1768 | 2.047 | probable transcriptional regulator | cce\_1768 | 0.2313 |
| cce\_0712 | 1.5194 | two-component response regulator | cce\_0712 | 0.3824 |
| cce\_4396 | 1.4941 | transcriptional regulator, ArsR family | cce\_4396 | 0.0 |
| cce\_0165 | 1.4135 | two-component response regulator | cce\_0165 | 0.0063 |
| cce\_1816 | 1.3928 | transcriptional regulatory protein | cce\_1816 | 0.624 |
| cce\_0461 | 1.3025 | nitrogen-responsive regulatory protein | ntcA | 0.7163 |
| cce\_0310 | 1.2228 | putative arylsulfatase regulatory protein | aslB | 0.426 |
| cce\_1695 | 1.0546 | two-component response regulator | cce\_1695 | 0.4087 |

## Part 6: Sensors repressed and induced

### Repressed

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_1413 | -2.1502 | probable sensory transduction histidine kinase | cce\_1413 | 0.6796 |
| cce\_1186 | -2.0616 | two-component hybrid sensor and regulator | cce\_1186 | 0.7147 |
| cce\_2366 | -1.8856 | two-component sensor histidine kinase | cce\_2366 | 0.0 |
| cce\_1185 | -1.5719 | two-component hybrid sensor and regulator | cce\_1185 | 0.7871 |
| cce\_0257 | -1.4733 | two-component sensor histidine kinase | cce\_0257 | 0.2836 |
| cce\_2508 | -1.2169 | two-component hybrid sensor and regulator | cce\_2508 | 0.1037 |
| cce\_2509 | -1.2065 | two-component hybrid sensor and regulator | cce\_2509 | 0.2711 |
| cce\_4405 | -1.1947 | two-component hybrid sensor and regulator | cce\_4405 | 0.0 |
| cce\_4426 | -1.1552 | two-component sensor histidine kinase | cce\_4426 | 0.5202 |
| cce\_1737 | -1.0434 | two-component sensor histidine kinase | cce\_1737 | 0.21 |

### Induced

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_4006 | 1.2254 | two-component sensor histidine kinase | cce\_4006 | 0.0151 |
| cce\_4097 | 1.1859 | two-component sensor serine/threonine kinase | cce\_4097 | 0.6782 |
| cce\_1694 | 1.1445 | two component sensor histidine kinase | cce\_1694 | 0.0 |

# Appendix B

## Part 1: Top 25 Negative Fold Changed Genes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_0553 | -7.5056 | serine O-acetyltransferase | cysE2 | 0.8643 |
| cce\_0579 | -7.3463 | 4Fe-4S ferredoxin | fdxB | 0.6518 |
| cce\_0577 | -7.3022 | hypothetical protein | cce\_0577 | 0.724 |
| cce\_0576 | -7.2671 | ferrous iron transport protein A | feoA2 | 0.7018 |
| cce\_0575 | -7.2009 | ferrous iron transport protein B | feoB2 | 0.8338 |
| cce\_0574 | -7.0818 | GTP-binding protein, HSR1-related | cce\_0574 | 0.7546 |
| cce\_0560 | -6.9405 | nitrogenase molybdenum-iron protein alpha chain | nifD | 0.8713 |
| cce\_0563 | -6.8825 | nitrogenase molybdenum-iron cofactor biosynthesis protein | nifE | 0.7963 |
| cce\_0561 | -6.7982 | nitrogenase molybdenum-iron protein beta chain | nifK | 0.8463 |
| cce\_0564 | -6.6928 | nitrogenase molybdenum-iron cofactor biosynthesis protein | nifN | 0.7087 |
| cce\_0558 | -6.6644 | iron-sulfur cluster assembly protein | nifU | 0.7199 |
| cce\_0571 | -6.6587 | 2Fe-2S ferredoxin, putative nitrogen fixation related protein | cce\_0571 | 0.8754 |
| cce\_1663 | -6.6044 | hypothetical protein | cce\_1663 | 0.0 |
| cce\_0578 | -6.5293 | putative molybdate ABC transporter, permease protein | cce\_0578 | 0.7074 |
| cce\_0549 | -6.49 | homocitrate synthase | nifV | 0.6963 |
| cce\_0557 | -6.4369 | nitrogenase cofactor synthesis protein | nifS | 0.7185 |
| cce\_0572 | -6.4307 | hypothetical protein | cce\_0572 | 0.6643 |
| cce\_0548 | -6.419 | iron-sulfur cofactor synthesis protein | nifZ | 0.7018 |
| cce\_0565 | -6.415 | probable nitrogen fixation protein | nifX | 0.7824 |
| cce\_0547 | -6.356 | nifT/fixU | cce\_0547 | 0.7227 |
| cce\_0555 | -6.3148 | hypothetical protein | cce\_0555 | 0.706 |
| cce\_0546 | -6.3122 | hypothetical protein | cce\_0546 | 0.6754 |
| cce\_2746 | -6.3098 | putative DoxX family protein | cce\_2746 | 0.0 |
| cce\_0570 | -6.2617 | Fe-S cluster biosynthesis, putative nitrogen fixation related protein | hesB | 0.8129 |
| cce\_0562 | -6.2612 | hypothetical protein | cce\_0562 | 0.7352 |

## Part 2: Top 25 Positive Fold Changed Genes

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_2071 | 7.5326 | hypothetical protein | cce\_2071 | 0.724 |
| cce\_2604 | 6.3192 | hypothetical protein | cce\_2604 | 0.228 |
| cce\_2603 | 5.9288 | hypothetical protein | cce\_2603 | 0.0 |
| cce\_1723 | 5.8078 | unknown | cce\_1723 | 0.0476 |
| cce\_2602 | 5.6856 | hypothetical protein | cce\_2602 | 0.0 |
| cce\_2072 | 5.6789 | unknown | cce\_2072 | 0.7115 |
| cce\_2070 | 5.6784 | unknown | cce\_2070 | 0.6865 |
| cce\_4139 | 5.3728 | hypothetical protein | cce\_4139 | 0.0934 |
| cce\_2195 | 5.34 | hypothetical protein | cce\_2195 | 0.053 |
| cce\_2193 | 5.2054 | toxin secretion ABC transporter ATP-binding protein | hlyB1 | 0.0 |
| cce\_0593 | 5.1629 | protease | cce\_0593 | 0.2906 |
| cce\_2192 | 5.0589 | putative HlyD-family secretion protein | cce\_2192 | 0.0 |
| cce\_2194 | 5.0109 | conserved hypothetical protein | cce\_2194 | 0.0 |
| cce\_2181 | 4.8735 | hypothetical protein | cce\_2181 | 0.5066 |
| cce\_2175 | 4.8164 | hypothetical protein | cce\_2175 | 0.0 |
| cce\_1983 | 4.7422 | probable phytochrome A, two-component sensor protein | aphA | 0.1446 |
| cce\_2286 | 4.6331 | hypothetical protein | cce\_2286 | 0.0298 |
| cce\_2708 | 4.4573 | rfrA family pentapeptide repeat | cce\_2708 | 0.0736 |
| cce\_1465 | 4.4449 | hypothetical protein | cce\_1465 | 0.4203 |
| cce\_2073 | 4.3369 | unknown | cce\_2073 | 0.3141 |
| cce\_4821 | 4.3333 | 5-methyltetrahydropteroyltriglutamate--homocysteine S-methyltransferase | metE | 0.2487 |
| cce\_2303 | 4.1927 | hypothetical protein | cce\_2303 | 0.5907 |
| cce\_0433 | 4.1175 | conserved hypothetical protein | cce\_0433 | 0.0 |
| cce\_0032 | 4.0114 | ferrous iron transport protein B | feoB1 | 0.3555 |
| cce\_1459 | 3.9962 | unknown | cce\_1459 | 0.287 |

## Part 3: Sigma Factors repressed and induced

### Repressed

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_2566 | -3.5354 | group 3 sigma-70 RNA polymerase sigma factor F | sigF | 0.1957 |
| cce\_3586 | -2.6872 | group 3 sigma-70 RNA polymerase sigma factor J | sigJ | 0.0929 |
| cce\_0644 | -2.0539 | group 2 sigma-70 RNA polymerase sigma factor B | sigB | 0.5629 |
| cce\_2337 | -1.8037 | group 2 sigma-70 RNA polymerase sigma factor | cce\_2337 | 0.0 |
| cce\_2424 | -1.5559 | group 4 sigma-70 RNA polymerase sigma factor H | sigH | 0.1829 |
| cce\_0875 | -1.0122 | group 1 sigma-70 RNA polymerase sigma factor A | sigA | 0.0274 |

### Induced

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_0601 | 1.4451 | group 2 sigma-70 RNA polymerase sigma factor E | sigE | 0.0 |
| cce\_5029 | 1.2179 | putative group 3/4 sigma-70 RNA polymerase sigma factor | cce\_5029 | 0.0 |

## Part 4: Clock genes repressed and induced

### Repressed

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_0424 | -1.1187 | circadian clock protein | kaiA | 0.7921 |

### Induced

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_0145 | 2.8265 | putative circadian clock protein | kaiB4 | 0.0 |
| cce\_0435 | 1.7419 | circadian clock protein | kaiB3 | 0.0 |

## Part 5: Regulators repressed and induced

### Repressed

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_4195 | -3.6294 | CheY-like two-component hybrid sensor and regulator | cce\_4195 | 0.1622 |
| cce\_1001 | -3.5738 | ATP-dependent Clp protease, regulatory subunit | clpC2 | 0.174 |
| cce\_3127 | -3.5518 | transcription regulator, Fur family | cce\_3127 | 0.3904 |
| cce\_0198 | -3.2577 | LysR family transcriptional regulatory protein, nitrogen assimilation transcriptional activator | ntcB | 0.5698 |
| cce\_1898 | -2.9865 | probable transcriptional regulator | patB | 0.874 |
| cce\_0970 | -2.7085 | two-component transcription regulator | cce\_0970 | 0.5844 |
| cce\_0713 | -2.2736 | two-component response regulator | cce\_0713 | 0.0229 |
| cce\_3559 | -2.2184 | two-component response regulator | cce\_3559 | 0.5677 |
| cce\_4543 | -2.1508 | two-component response regulator | cce\_4543 | 0.0472 |
| cce\_0446 | -1.94 | two-component response regulator | cce\_0446 | 0.0382 |
| cce\_1412 | -1.888 | two-component response regulator | cce\_1412 | 0.5621 |
| cce\_2624 | -1.6442 | CheA-like two-component hybrid sensor and regulator | cce\_2624 | 0.1691 |
| cce\_4196 | -1.6428 | two-component response regulator | cce\_4196 | 0.0874 |
| cce\_3937 | -1.5252 | two-component hybrid sensor and regulator | cce\_3937 | 0.0977 |
| cce\_0754 | -1.5199 | two-component response regulator | cce\_0754 | 0.0 |
| cce\_1186 | -1.3804 | two-component hybrid sensor and regulator | cce\_1186 | 0.5254 |
| cce\_4542 | -1.2874 | two-component response regulator | cce\_4542 | 0.3419 |
| cce\_1135 | -1.2342 | two-component response regulator | cce\_1135 | 0.3891 |
| cce\_0712 | -1.1857 | two-component response regulator | cce\_0712 | 0.581 |
| cce\_1196 | -1.1648 | putative CRISPR-associated negative autoregulator | cce\_1196 | 0.6185 |
| cce\_3731 | -1.1577 | putative Rubisco transcriptional regulator, LysR family | rbcR | 0.8657 |
| cce\_2509 | -1.0843 | two-component hybrid sensor and regulator | cce\_2509 | 0.256 |
| cce\_0448 | -1.0456 | response regulator | cce\_0448 | 0.2259 |
| cce\_2365 | -1.0157 | two-component response regulator | cce\_2365 | 0.5058 |

### Induced

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_1982 | 3.8944 | CheY-like two-component hybrid sensor and regulator | cce\_1982 | 0.3294 |
| cce\_1816 | 2.0187 | transcriptional regulatory protein | cce\_1816 | 0.656 |
| cce\_1775 | 1.8067 | nitrogen regulatory protein P-II | glnB | 0.1143 |
| cce\_5156 | 1.6385 | putative transcriptional regulator | cce\_5156 | 0.581 |
| cce\_3174 | 1.5515 | transcriptional regulator | cce\_3174 | 0.0 |
| cce\_1768 | 1.3705 | probable transcriptional regulator | cce\_1768 | 0.2829 |
| cce\_1520 | 1.2704 | two-component response regulator | cce\_1520 | 0.4823 |
| cce\_1695 | 1.0292 | two-component response regulator | cce\_1695 | 0.4483 |

## Part 6: Sensors repressed and induced

### Repressed

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_4195 | -3.6294 | CheY-like two-component hybrid sensor and regulator | cce\_4195 | 0.1622 |
| cce\_2366 | -2.5024 | two-component sensor histidine kinase | cce\_2366 | 0.0 |
| cce\_0969 | -2.4904 | two-component sensor histidine kinase | cce\_0969 | 0.5278 |
| cce\_0257 | -2.1092 | two-component sensor histidine kinase | cce\_0257 | 0.4612 |
| cce\_1737 | -1.7325 | two-component sensor histidine kinase | cce\_1737 | 0.2037 |
| cce\_2624 | -1.6442 | CheA-like two-component hybrid sensor and regulator | cce\_2624 | 0.1691 |
| cce\_3937 | -1.5252 | two-component hybrid sensor and regulator | cce\_3937 | 0.0977 |
| cce\_1186 | -1.3804 | two-component hybrid sensor and regulator | cce\_1186 | 0.5254 |
| cce\_1535 | -1.3771 | two-component sensor histidine kinase | cce\_1535 | 0.1539 |
| cce\_4426 | -1.1847 | two-component sensor histidine kinase | cce\_4426 | 0.6108 |
| cce\_2509 | -1.0843 | two-component hybrid sensor and regulator | cce\_2509 | 0.256 |

### Induced

|  |  |  |  |  |
| --- | --- | --- | --- | --- |
| **orf** | **fold\_change** | **function** | **CommonName** | **mi** |
| cce\_1983 | 4.7422 | probable phytochrome A, two-component sensor protein | aphA | 0.1446 |
| cce\_1982 | 3.8944 | CheY-like two-component hybrid sensor and regulator | cce\_1982 | 0.3294 |
| cce\_0220 | 3.1285 | two-component sensor histidine kinase | cce\_0220 | 0.1719 |
| cce\_1694 | 2.1887 | two component sensor histidine kinase | cce\_1694 | 0.1279 |
| cce\_1878 | 2.0765 | two-component sensor histidine kinase | cce\_1878 | 0.0 |
| cce\_1848 | 1.3899 | probable two-component sensor histidine kinase | cce\_1848 | 0.2828 |