

patB-nifH-Conclusion

April 24, 2020

```
[1]: from patB_nifH_Analysis_file import *
```

1 Results and Conclusions

1.1 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 carbon 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.

1.2 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 patB 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.

2 Appendix A

2.1 Part 1: Top 25 Negative Fold Changed Genes

```
[2]: top_fold_changed_genes(patB_info,direction='negative')
```

```
[2]:
```

	orf	fold_change \
0	cce_0553	-11.442278
346	cce_5300	-10.514506
176	cce_5304	-9.851966
448	cce_5310	-9.455302
464	cce_5301	-9.202687
548	cce_5309	-8.669706
1	cce_0558	-8.113775
2	cce_0563	-8.049914
3	cce_0561	-8.007431
4	cce_0564	-7.895628
5	cce_0555	-7.809400
6	cce_0556	-7.769557
7	cce_0560	-7.592669
8	cce_0557	-7.589244
12	cce_0562	-7.564148
11	cce_0559	-7.559985
9	cce_0554	-7.470252
10	cce_0565	-7.270134
267	cce_5303	-7.109080
885	cce_5306	-6.887250
14	cce_0549	-6.593598
1068	cce_5307	-6.247834
23	cce_0550	-6.236064
57	cce_5302	-6.182524

25 cce_0548 -6.013562

	function	CommonName	mi
0	serine O-acetyltransferase	cysE2	0.739322
346	probable integrase/recombinase	cce_5300	0.063098
176	hypothetical protein	cce_5304	0.662139
448	hypothetical protein	cce_5310	0.805988
464	hypothetical protein	cce_5301	0.000000
548	hypothetical protein	cce_5309	0.247027
1	iron-sulfur cluster assembly protein	nifU	0.736544
2	nitrogenase molybdenum-iron cofactor biosynthe...	nifE	0.692100
3	nitrogenase molybdenum-iron protein beta chain	nifK	0.832377
4	nitrogenase molybdenum-iron cofactor biosynthe...	nifN	0.732377
5	hypothetical protein	cce_0555	0.761544
6	4Fe-4S ferredoxin	cce_0556	0.822655
7	nitrogenase molybdenum-iron protein alpha chain	nifD	0.792100
8	nitrogenase cofactor synthesis protein	nifS	0.729600
12	hypothetical protein	cce_0562	0.782377
11	nitrogenase iron protein	nifH	0.874044
9	nitrogenase cofactor biosynthesis protein	nifB	0.819877
10	probable nitrogen fixation protein	nifX	0.754600
267	hypothetical protein	cce_5303	0.127351
885	hypothetical protein	cce_5306	0.000000
14	homocitrate synthase	nifV	0.735155
1068	hypothetical protein	cce_5307	0.398746
23	conserved hypothetical protein	cce_0550	0.696266
57	hypothetical protein	cce_5302	0.203905
25	iron-sulfur cofactor synthesis protein	nifZ	0.782377

2.2 Part 2: Top 25 Positive Fold Changed Genes

```
[3]: top_fold_changed_genes(patB_info,direction='positive',top=25)
```

```
[3]:      orf  fold_change  \
1545  cce_0974      4.292311
5195  cce_3132      4.198740
517   cce_2635      4.148493
5194  cce_1360      3.979413
5193  cce_1459      3.973594
1862  cce_4789      3.645460
53    cce_2619      3.598078
162   cce_0528      3.587099
1179  cce_3054      3.572080
34    cce_4140      3.563909
229   cce_2909      3.542357
80    cce_3146      3.524015
5188  cce_1985      3.504618
```

100	cce_2988	3.475597
110	cce_0527	3.470725
231	cce_2908	3.467748
67	cce_3445	3.415150
414	cce_2718	3.388609
5185	cce_3856	3.387714
44	cce_1780	3.387532
895	cce_2802	3.354930
46	cce_2467	3.332179
197	cce_3732	3.329837
84	cce_1821	3.320255
5182	cce_0833	3.263234

	function	CommonName	mi
1545	transcriptional Regulator, TetR family	cce_0974	0.000000
5195	unknown	cce_3132	0.000000
517	hypothetical protein	cce_2635	0.556584
5194	hypothetical protein	cce_1360	0.000000
5193	unknown	cce_1459	0.197754
1862	hypothetical protein	cce_4789	0.725433
53	ABC transporter, substrate binding protein, po...	cce_2619	0.294977
162	hypothetical protein	cce_0528	0.255063
1179	putative biopolymer transport protein	exbB2	0.000000
34	phosphoribosylformimino-5-aminoimidazole carbo...	hisA	0.138330
229	allophycocyanin beta subunit	apcB	0.054996
80	geranylgeranyl hydrogenase	chlP	0.351822
5188	carbohydrate kinase, thermoresistant glucokinase	cce_1985	0.000000
100	hypothetical protein	cce_2988	0.359758
110	unknown	cce_0527	0.298250
231	allophycocyanin alpha subunit	apcA	0.021663
67	conserved hypothetical protein	cce_3445	0.732377
414	putative DoxX	cce_2718	0.593488
5185	hypothetical protein	cce_3856	0.033568
44	unknown	cce_1780	0.367893
895	hypothetical protein	cce_2802	0.052119
46	N-acetylmuramoyl-L-alanine amidase	amiA2	0.637933
197	unknown	cce_3732	0.420373
84	putative HAD-superfamily hydrolase, subfamily IA	cce_1821	0.619877
5182	hypothetical protein	cce_0833	0.091008

2.3 Part 3: Sigma Factors repressed and induced

2.3.1 Repressed

```
[4]: get_sigma_factors(patB_info,direction='negative')
```

```
[4]:      orf  fold_change      function \
77  cce_2337  -1.750043  group 2 sigma-70 RNA polymerase sigma factor
373  cce_2424  -1.612567  group 4 sigma-70 RNA polymerase sigma factor H

      CommonName      mi
77  cce_2337  0.088528
373  sigH  0.033270
```

2.3.2 Induced

```
[5]: get_sigma_factors(patB_info,direction='positive')
```

```
[5]:      orf  fold_change      function \
43  cce_4142  3.090441  group 4 sigma-70 RNA polymerase sigma factor G
208  cce_0601  2.226739  group 2 sigma-70 RNA polymerase sigma factor E

      CommonName      mi
43  sigG  0.359361
208  sigE  0.000000
```

2.4 Part 4: Clock genes repressed and induced

2.4.1 Repressed

```
[6]: get_circadian(patB_info,direction='negative')
```

```
[6]:      orf  fold_change      function CommonName  mi
166  cce_0435  -1.720292  circadian clock protein      kaiB3  0.0
```

2.4.2 Induced

```
[7]: get_circadian(patB_info,direction='positive')
```

```
[7]:      orf  fold_change      function CommonName \
361  cce_0145  2.147813  putative circadian clock protein      kaiB4
445  cce_0424  1.689841      circadian clock protein      kaiA

      mi
361  0.000000
445  0.556584
```

2.5 Part 5: Regulators repressed and induced

2.5.1 Repressed

```
[8]: get_regulators(patB_info,direction='negative')
```

```
[8]:          orf  fold_change  \
55      cce_3127    -3.465545
170     cce_3559    -2.531986
63      cce_1135    -2.252211
56      cce_1001    -2.185784
137     cce_1186    -2.061627
4807    cce_1412    -1.639944
265     cce_1185    -1.571860
315     cce_0448    -1.473907
303     cce_3731    -1.454199
1152    cce_4542    -1.375491
502     cce_2508    -1.216945
710     cce_4183    -1.211873
434     cce_2509    -1.206459
590     cce_0683    -1.205853
821     cce_4405    -1.194678
1404    cce_4714    -1.177715
```

	function	CommonName	mi
55	transcription regulator, Fur family	cce_3127	0.491901
170	two-component response regulator	cce_3559	0.615711
63	two-component response regulator	cce_1135	0.457873
56	ATP-dependent Clp protease, regulatory subunit	clpC2	0.248250
137	two-component hybrid sensor and regulator	cce_1186	0.714719
4807	two-component response regulator	cce_1412	0.641306
265	two-component hybrid sensor and regulator	cce_1185	0.787139
315	response regulator	cce_0448	0.147490
303	putative Rubisco transcriptional regulator, Ly...	rbcR	0.815711
1152	two-component response regulator	cce_4542	0.302715
502	two-component hybrid sensor and regulator	cce_2508	0.103707
710	two-component response regulator	cce_4183	0.181385
434	two-component hybrid sensor and regulator	cce_2509	0.271068
590	putative transcriptional regulator	cce_0683	0.243485
821	two-component hybrid sensor and regulator	cce_4405	0.000000
1404	two-component response regulator, NarL subfamily	cce_4714	0.083369

2.5.2 Induced

```
[9]: get_regulators(patB_info,direction='positive')
```

```
[9]:          orf  fold_change          function  \
1226  cce_1768    2.046999  probable transcriptional regulator
2497  cce_0712    1.519371    two-component response regulator
603   cce_4396    1.494147  transcriptional regulator, ArsR family
2816  cce_0165    1.413458    two-component response regulator
2302  cce_1816    1.392781    transcriptional regulatory protein
690   cce_0461    1.302513  nitrogen-responsive regulatory protein
```

2995	cce_0310	1.222808	putative arylsulfatase regulatory protein
5075	cce_1695	1.054570	two-component response regulator

	CommonName	mi
1226	cce_1768	0.231286
2497	cce_0712	0.382377
603	cce_4396	0.000000
2816	cce_0165	0.006319
2302	cce_1816	0.624044
690	ntcA	0.716306
2995	aslB	0.426028
5075	cce_1695	0.408667

2.6 Part 6: Sensors repressed and induced

2.6.1 Repressed

```
[10]: get_sensors(patB_info,direction='negative')
```

```
[10]:      orf  fold_change      function \
89   cce_1413   -2.150160  probable sensory transduction histidine kinase
137  cce_1186   -2.061627      two-component hybrid sensor and regulator
106  cce_2366   -1.885599      two-component sensor histidine kinase
265  cce_1185   -1.571860      two-component hybrid sensor and regulator
227  cce_0257   -1.473346      two-component sensor histidine kinase
502  cce_2508   -1.216945      two-component hybrid sensor and regulator
434  cce_2509   -1.206459      two-component hybrid sensor and regulator
821  cce_4405   -1.194678      two-component hybrid sensor and regulator
601  cce_4426   -1.155178      two-component sensor histidine kinase
857  cce_1737   -1.043445      two-component sensor histidine kinase
```

	CommonName	mi
89	cce_1413	0.679600
137	cce_1186	0.714719
106	cce_2366	0.000000
265	cce_1185	0.787139
227	cce_0257	0.283601
502	cce_2508	0.103707
434	cce_2509	0.271068
821	cce_4405	0.000000
601	cce_4426	0.520241
857	cce_1737	0.209957

2.6.2 Induced

```
[11]: get_sensors(patB_info,direction='positive')
```

```
[11]:          orf  fold_change          function \
1772  cce_4006    1.225434          two-component sensor histidine kinase
378   cce_4097    1.185860  two-component sensor serine/threonine kinase
1978  cce_1694    1.144460          two component sensor histidine kinase

          CommonName          mi
1772  cce_4006  0.015082
378   cce_4097  0.678211
1978  cce_1694  0.000000
```

3 Appendix B

3.1 Part 1: Top 25 Negative Fold Changed Genes

```
[12]: top_fold_changed_genes(nifH_info,direction='negative')
```

```
[12]:          orf  fold_change \
0      cce_0553   -7.505597
74     cce_0579   -7.346330
22     cce_0577   -7.302174
29     cce_0576   -7.267055
38     cce_0575   -7.200949
39     cce_0574   -7.081767
7      cce_0560   -6.940473
2      cce_0563   -6.882549
3      cce_0561   -6.798208
4      cce_0564   -6.692806
1      cce_0558   -6.664385
18     cce_0571   -6.658731
1731   cce_1663   -6.604403
42     cce_0578   -6.529344
14     cce_0549   -6.490041
8      cce_0557   -6.436896
16     cce_0572   -6.430689
25     cce_0548   -6.419047
10     cce_0565   -6.415021
15     cce_0547   -6.356028
5      cce_0555   -6.314751
19     cce_0546   -6.312210
2395   cce_2746   -6.309769
20     cce_0570   -6.261746
12     cce_0562   -6.261197

          function CommonName          mi
0          serine O-acetyltransferase      cysE2  0.864322
74         4Fe-4S ferredoxin              fdxB  0.651822
```


22	hypothetical protein	cce_0577	0.724044
29	ferrous iron transport protein A	feoA2	0.701822
38	ferrous iron transport protein B	feoB2	0.833766
39	GTP-binding protein, HSR1-related	cce_0574	0.754600
7	nitrogenase molybdenum-iron protein alpha chain	nifD	0.871266
2	nitrogenase molybdenum-iron cofactor biosynthe...	nifE	0.796266
3	nitrogenase molybdenum-iron protein beta chain	nifK	0.846266
4	nitrogenase molybdenum-iron cofactor biosynthe...	nifN	0.708667
1	iron-sulfur cluster assembly protein	nifU	0.719877
18	2Fe-2S ferredoxin, putative nitrogen fixation ...	cce_0571	0.875433
1731	hypothetical protein	cce_1663	0.000000
42	putative molybdate ABC transporter, permease p...	cce_0578	0.707377
14	homocitrate synthase	nifV	0.696266
8	nitrogenase cofactor synthesis protein	nifS	0.718488
16	hypothetical protein	cce_0572	0.664322
25	iron-sulfur cofactor synthesis protein	nifZ	0.701822
10	probable nitrogen fixation protein	nifX	0.782377
15	nifT/fixU	cce_0547	0.722655
5	hypothetical protein	cce_0555	0.705988
19	hypothetical protein	cce_0546	0.675433
2395	putative DoxX family protein	cce_2746	0.000000
20	Fe-S cluster biosynthesis, putative nitrogen f...	hesB	0.812933
12	hypothetical protein	cce_0562	0.735155

3.2 Part 2: Top 25 Positive Fold Changed Genes

```
[13]: top_fold_changed_genes(nifH_info,direction='positive')
```

```
[13]:      orf  fold_change  \
2555  cce_2071      7.532596
519   cce_2604      6.319160
2578  cce_2603      5.928810
581   cce_1723      5.807798
1459  cce_2602      5.685601
1723  cce_2072      5.678918
460   cce_2070      5.678425
269   cce_4139      5.372815
261   cce_2195      5.340014
2666  cce_2193      5.205408
4749  cce_0593      5.162948
4057  cce_2192      5.058925
1878  cce_2194      5.010950
5172  cce_2181      4.873490
3992  cce_2175      4.816412
3999  cce_1983      4.742154
5173  cce_2286      4.633129
394   cce_2708      4.457325
```

2365	cce_1465	4.444855
2987	cce_2073	4.336926
858	cce_4821	4.333295
2504	cce_2303	4.192712
254	cce_0433	4.117491
3632	cce_0032	4.011391
5193	cce_1459	3.996246

		function	CommonName	mi
2555		hypothetical protein	cce_2071	0.724044
519		hypothetical protein	cce_2604	0.228012
2578		hypothetical protein	cce_2603	0.000000
581		unknown	cce_1723	0.047556
1459		hypothetical protein	cce_2602	0.000000
1723		unknown	cce_2072	0.711544
460		unknown	cce_2070	0.686544
269		hypothetical protein	cce_4139	0.093389
261		hypothetical protein	cce_2195	0.053012
2666	toxin secretion ABC transporter ATP-binding pr...		hlyB1	0.000000
4749		protease	cce_0593	0.290611
4057	putative HlyD-family secretion protein		cce_2192	0.000000
1878	conserved hypothetical protein		cce_2194	0.000000
5172	hypothetical protein		cce_2181	0.506584
3992	hypothetical protein		cce_2175	0.000000
3999	probable phytochrome A, two-component sensor p...		aphA	0.144580
5173	hypothetical protein		cce_2286	0.029765
394	rfrA family pentapeptide repeat		cce_2708	0.073578
2365	hypothetical protein		cce_1465	0.420274
2987	unknown		cce_2073	0.314123
858	5-methyltetrahydropteroyltriglutamate--homocys...		metE	0.248746
2504	hypothetical protein		cce_2303	0.590711
254	conserved hypothetical protein		cce_0433	0.000000
3632	ferrous iron transport protein B		feoB1	0.355453
5193	unknown		cce_1459	0.287040

3.3 Part 3: Sigma Factors repressed and induced

3.3.1 Repressed

```
[14]: get_sigma_factors(nifH_info,direction='negative')
```

```
[14]:      orf  fold_change      function \
4543 cce_2566  -3.535429  group 3 sigma-70 RNA polymerase sigma factor F
4605 cce_3586  -2.687199  group 3 sigma-70 RNA polymerase sigma factor J
1287 cce_0644  -2.053902  group 2 sigma-70 RNA polymerase sigma factor B
77   cce_2337  -1.803669  group 2 sigma-70 RNA polymerase sigma factor
373  cce_2424  -1.555899  group 4 sigma-70 RNA polymerase sigma factor H
```

```
1022 cce_0875 -1.012185 group 1 sigma-70 RNA polymerase sigma factor A
```

	CommonName	mi
4543	sigF	0.195701
4605	sigJ	0.092923
1287	sigB	0.562933
77	cce_2337	0.000000
373	sigH	0.182873
1022	sigA	0.027417

3.3.2 Induced

```
[15]: get_sigma_factors(nifH_info,direction='positive')
```

```
[15]:          orf  fold_change  \
208  cce_0601      1.445092
5016 cce_5029      1.217904

                                function CommonName  mi
208  group 2 sigma-70 RNA polymerase sigma factor E      sigE  0.0
5016 putative group 3/4 sigma-70 RNA polymerase sig... cce_5029  0.0
```

3.4 Part 4: Clock genes repressed and induced

3.4.1 Repressed

```
[16]: get_circadian(nifH_info,direction='negative')
```

```
[16]:          orf  fold_change          function CommonName  mi
445  cce_0424  -1.118655  circadian clock protein      kaiA  0.7921
```

3.4.2 Induced

```
[17]: get_circadian(nifH_info,direction='positive')
```

```
[17]:          orf  fold_change          function CommonName  mi
361  cce_0145  2.826462  putative circadian clock protein      kaiB4  0.0
166  cce_0435  1.741937          circadian clock protein      kaiB3  0.0
```

3.5 Part 5: Regulators repressed and induced

3.5.1 Repressed

```
[18]: get_regulators(nifH_info,direction='negative')
```

```
[18]:          orf  fold_change  \
3487 cce_4195  -3.629378
```

56	cce_1001	-3.573785
55	cce_3127	-3.551802
652	cce_0198	-3.257695
17	cce_1898	-2.986488
4009	cce_0970	-2.708480
3940	cce_0713	-2.273586
170	cce_3559	-2.218372
4007	cce_4543	-2.150760
3994	cce_0446	-1.939965
4807	cce_1412	-1.887990
3629	cce_2624	-1.644243
3298	cce_4196	-1.642839
2187	cce_3937	-1.525176
3519	cce_0754	-1.519930
137	cce_1186	-1.380433
1152	cce_4542	-1.287402
63	cce_1135	-1.234215
2497	cce_0712	-1.185699
2515	cce_1196	-1.164772
303	cce_3731	-1.157707
434	cce_2509	-1.084254
315	cce_0448	-1.045645
2304	cce_2365	-1.015668

	function	CommonName	mi
3487	CheY-like two-component hybrid sensor and regu...	cce_4195	0.162169
56	ATP-dependent Clp protease, regulatory subunit	clpC2	0.174044
55	transcription regulator, Fur family	cce_3127	0.390413
652	LysR family transcriptional regulatory protein...	ntcB	0.569778
17	probable transcriptional regulator	patB	0.874044
4009	two-component transcription regulator	cce_0970	0.584361
3940	two-component response regulator	cce_0713	0.022854
170	two-component response regulator	cce_3559	0.567695
4007	two-component response regulator	cce_4543	0.047159
3994	two-component response regulator	cce_0446	0.038228
4807	two-component response regulator	cce_1412	0.562139
3629	CheA-like two-component hybrid sensor and regu...	cce_2624	0.169114
3298	two-component response regulator	cce_4196	0.087368
2187	two-component hybrid sensor and regulator	cce_3937	0.097685
3519	two-component response regulator	cce_0754	0.000000
137	two-component hybrid sensor and regulator	cce_1186	0.525433
1152	two-component response regulator	cce_4542	0.341901
63	two-component response regulator	cce_1135	0.389123
2497	two-component response regulator	cce_0712	0.580988
2515	putative CRISPR-associated negative autoregulator	cce_1196	0.618488
303	putative Rubisco transcriptional regulator, Ly...	rbcR	0.865711
434	two-component hybrid sensor and regulator	cce_2509	0.255988

315		response regulator	cce_0448	0.225929
2304		two-component response regulator	cce_2365	0.505790

3.5.2 Induced

```
[19]: get_regulators(nifH_info,direction='positive')
```

```
[19]:      orf  fold_change  \
1338  cce_1982      3.894370
2302  cce_1816      2.018677
1529  cce_1775      1.806693
4898  cce_5156      1.638463
3575  cce_3174      1.551538
1226  cce_1768      1.370489
4181  cce_1520      1.270428
5075  cce_1695      1.029246
```

	function	CommonName	mi
1338	CheY-like two-component hybrid sensor and regu...	cce_1982	0.329401
2302	transcriptional regulatory protein	cce_1816	0.655988
1529	nitrogen regulatory protein P-II	glnB	0.114256
4898	putative transcriptional regulator	cce_5156	0.580988
3575	transcriptional regulator	cce_3174	0.000000
1226	probable transcriptional regulator	cce_1768	0.282873
4181	two-component response regulator	cce_1520	0.482278
5075	two-component response regulator	cce_1695	0.448250

3.6 Part 6: Sensors repressed and induced

3.6.1 Repressed

```
[20]: get_sensors(nifH_info,direction='negative')
```

```
[20]:      orf  fold_change  \
3487  cce_4195     -3.629378
106   cce_2366     -2.502369
3552  cce_0969     -2.490431
227   cce_0257     -2.109204
857   cce_1737     -1.732493
3629  cce_2624     -1.644243
2187  cce_3937     -1.525176
137   cce_1186     -1.380433
4058  cce_1535     -1.377125
601   cce_4426     -1.184739
434   cce_2509     -1.084254
```

function	CommonName	mi
----------	------------	----

3487	CheY-like two-component hybrid sensor and regu...	cce_4195	0.162169
106	two-component sensor histidine kinase	cce_2366	0.000000
3552	two-component sensor histidine kinase	cce_0969	0.527781
227	two-component sensor histidine kinase	cce_0257	0.461246
857	two-component sensor histidine kinase	cce_1737	0.203707
3629	CheA-like two-component hybrid sensor and regu...	cce_2624	0.169114
2187	two-component hybrid sensor and regulator	cce_3937	0.097685
137	two-component hybrid sensor and regulator	cce_1186	0.525433
4058	two-component sensor histidine kinase	cce_1535	0.153935
601	two-component sensor histidine kinase	cce_4426	0.610750
434	two-component hybrid sensor and regulator	cce_2509	0.255988

3.6.2 Induced

```
[21]: get_sensors(nifH_info,direction='positive')
```

```
[21]:      orf  fold_change  \
3999  cce_1983      4.742154
1338  cce_1982      3.894370
4657  cce_0220      3.128532
1978  cce_1694      2.188686
2126  cce_1878      2.076519
3648  cce_1848      1.389880
```

	function	CommonName	mi
3999	probable phytochrome A, two-component sensor p...	aphA	0.144580
1338	CheY-like two-component hybrid sensor and regu...	cce_1982	0.329401
4657	two-component sensor histidine kinase	cce_0220	0.171861
1978	two component sensor histidine kinase	cce_1694	0.127913
2126	two-component sensor histidine kinase	cce_1878	0.000000
3648	probable two-component sensor histidine kinase	cce_1848	0.282774