

Ncol\_Nvec\_vc1.1\_XM\_032380374.2

fraction genes in fg and bg

|                 |           |      |
|-----------------|-----------|------|
| BTB_2           | p=1.9E-03 | n=9  |
| lon_trans_2     | p=2.0E-03 | n=9  |
| lon_trans       | p=1.4E-02 | n=10 |
| COX6C           | p=1.1E-01 | n=2  |
| 7tm_2           | p=1.3E-01 | n=3  |
| ADAM_CR_2       | p=1.3E-01 | n=1  |
| AIRS            | p=1.3E-01 | n=1  |
| APP_amyloid     | p=1.3E-01 | n=1  |
| APP_Cu_bd       | p=1.3E-01 | n=1  |
| APP_E2          | p=1.3E-01 | n=1  |
| APP_N           | p=1.3E-01 | n=1  |
| ATP_synt_H      | p=1.3E-01 | n=1  |
| BACK            | p=1.3E-01 | n=4  |
| BTB             | p=1.3E-01 | n=6  |
| CaM_bdg_C0      | p=1.3E-01 | n=1  |
| CDK5_activator  | p=1.3E-01 | n=1  |
| CEBP_ZZ         | p=1.3E-01 | n=1  |
| cNMP_binding    | p=1.3E-01 | n=3  |
| Coatomer_WDAD   | p=1.3E-01 | n=1  |
| Cu_amine_oxid   | p=1.3E-01 | n=1  |
| Cu_amine_oxidN2 | p=1.3E-01 | n=1  |
| DUF1180         | p=1.3E-01 | n=1  |
| DUF3399         | p=1.3E-01 | n=1  |
| DUF3583         | p=1.3E-01 | n=1  |
| DUF719          | p=1.3E-01 | n=1  |
| EAF             | p=1.3E-01 | n=1  |
| ECH_2           | p=1.3E-01 | n=1  |
| EF-hand_7       | p=1.3E-01 | n=6  |
| EF-hand_like    | p=1.3E-01 | n=2  |
| ELL             | p=1.3E-01 | n=1  |

|         |         |
|---------|---------|
| fg=0.02 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.03 | bg=0.01 |
| fg=0.01 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.01 | bg=0.00 |
| fg=0.02 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.00 | bg=0.00 |
| fg=0.02 | bg=0.01 |
| fg=0.01 | bg=0.00 |
| fg=0.00 | bg=0.00 |

-log<sub>10</sub>(p)

n=254/278 input genes with annotations



fraction