**Table S1. Sample size computation using RNASeqPower.** We first estimated the depth sequencing of the libraries used for analysis. The coefficient of variation used in our calculations was 0.5, the cv cutoff used to filter genes in NOISeqBio analysis. In yellow we indicate the Fold change selected given a sample size of 4 individuals per group.

| Fold change | Power=0.8 | | |
| --- | --- | --- | --- |
| | FDR= 0.1 | **FDR = 0.05** | FDR = 0.01 |
| 1.5 | 20.494705 | 26.018437 | 38.714888 |
| 2 | 7.012901 | 8.903018 | 13.247504 |
| **2.75** | 3.292534 | 4.179937 | 6.219659 |
| **3.25** | 2.425355 | 3.079036 | 4.581541 |
| 3.5 | 2.146895 | 2.725526 | 4.055526 |
| | | | |
| | Power=0.9 | | |
| | FDR= 0.1 | **FDR = 0.05** | FDR = 0.01 |
| 1.5 | 28.3885 | 34.831305 | 49.324033 |
| 2 | 9.714009 | 11.918615 | 16.877753 |
| 2.75 | 4.560695 | 5.59575 | 7.924049 |
| 3.25 | 3.359511 | 4.121956 | 5.837033 |
| 3.5 | 2.973799 | 3.648706 | 5.166872 |