Expression pattern analysis by gene

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1. Normalize Read Counts
2. Calculate Averages and Standard Error
3. Include Annotation, Differential Expression and Log2 Fold Change Data
4. Remove High Standard Error Genes
5. Pattern Analysis - ARF2 (HORVU5Hr1G111500)

## Using mostly log2 fold change (restricted)

## Adjusted p-value: <= 0.001 for timepoint 20; No limits set for other timepoints

## Log2 fold change: < .5 and > -.5 for timepoints 0, 16, 24, 32, 48; > 1 for timepoint 20

## Number of genes: 85

## Gene names: HORVU0Hr1G002960 HORVU0Hr1G038680 HORVU1Hr1G016490 HORVU1Hr1G037250 HORVU1Hr1G040050 HORVU1Hr1G047180 HORVU1Hr1G063720 HORVU1Hr1G071260 HORVU1Hr1G071840 HORVU1Hr1G075620 HORVU1Hr1G077430 HORVU1Hr1G077520 HORVU1Hr1G078340 HORVU2Hr1G019190 HORVU2Hr1G020810 HORVU2Hr1G023140 HORVU2Hr1G023850 HORVU2Hr1G027810 HORVU2Hr1G054760 HORVU2Hr1G061910 HORVU2Hr1G061930 HORVU2Hr1G062330 HORVU2Hr1G067150 HORVU2Hr1G082080 HORVU2Hr1G082090 HORVU2Hr1G101670 HORVU3Hr1G010780 HORVU3Hr1G021320 HORVU3Hr1G028060 HORVU3Hr1G031030 HORVU3Hr1G059060 HORVU3Hr1G080630 HORVU3Hr1G080640 HORVU3Hr1G081590 HORVU3Hr1G092590 HORVU3Hr1G096550 HORVU3Hr1G110590 HORVU3Hr1G113850 HORVU3Hr1G113860 HORVU3Hr1G114920 HORVU3Hr1G117890 HORVU4Hr1G006740 HORVU4Hr1G006780 HORVU4Hr1G011940 HORVU4Hr1G013520 HORVU4Hr1G033020 HORVU4Hr1G035380 HORVU4Hr1G062930 HORVU4Hr1G080140 HORVU4Hr1G080420 HORVU5Hr1G006730 HORVU5Hr1G012710 HORVU5Hr1G014350 HORVU5Hr1G019640 HORVU5Hr1G028810 HORVU5Hr1G033420 HORVU5Hr1G048030 HORVU5Hr1G083360 HORVU5Hr1G093590 HORVU5Hr1G094250 HORVU5Hr1G111500 HORVU5Hr1G123590 HORVU6Hr1G002580 HORVU6Hr1G030260 HORVU6Hr1G033070 HORVU6Hr1G035180 HORVU6Hr1G054000 HORVU6Hr1G059420 HORVU6Hr1G060010 HORVU6Hr1G067060 HORVU6Hr1G067180 HORVU6Hr1G075400 HORVU6Hr1G088570 HORVU7Hr1G001070 HORVU7Hr1G007940 HORVU7Hr1G022270 HORVU7Hr1G032750 HORVU7Hr1G039900 HORVU7Hr1G045060 HORVU7Hr1G058250 HORVU7Hr1G073550 HORVU7Hr1G082980 HORVU7Hr1G088250 HORVU7Hr1G088450 HORVU7Hr1G097010

* Checking to see if any of the genes using mostly log2 fold change (restricted) align with Barley1 probesets in 1HS or 2HL eQTL

## Number of overlapping genes: 15

## Overlapping gene - probeset pairs:

## probeset hv\_gene qvalue\_16h most\_associated\_marker\_16h  
## 1 Contig14332\_at HORVU2Hr1G023140 0.154097333 2H.68  
## 2 Contig14465\_at HORVU7Hr1G088250 0.000002700 2H.66  
## 3 Contig3108\_at HORVU4Hr1G080140 0.000689093 2H.66  
## 4 Contig4245\_s\_at HORVU4Hr1G035380 0.000003630 2H.63  
## 5 Contig4415\_at HORVU2Hr1G027810 0.000001990 2H.65  
## 6 Contig5165\_at HORVU2Hr1G019190 0.000002700 2H.68  
## 7 Contig5367\_at HORVU2Hr1G023850 0.000001990 2H.67  
## 8 Contig5449\_at HORVU1Hr1G016490 0.000002700 2H.66  
## 9 Contig6942\_at HORVU3Hr1G031030 0.000001990 2H.67  
## 10 Contig6945\_at HORVU5Hr1G014350 0.000002700 2H.66  
## 11 Contig7253\_at HORVU3Hr1G028060 0.000017200 2H.65  
## 12 Contig7332\_at HORVU1Hr1G047180 0.000001990 2H.66  
## 13 Contig7484\_at HORVU6Hr1G054000 0.000002700 2H.66  
## 14 Contig8214\_at HORVU5Hr1G048030 0.000062300 2H.63  
## 15 Contig9269\_s\_at HORVU6Hr1G002580 0.002865958 2H.66  
## qvalue\_32h most\_associated\_marker\_32h bb4\_expression\_pattern  
## 1 0.000000735 1H.03 n/a  
## 2 0.007279341 1H.03 n/a  
## 3 0.019131713 1H.06 PacMan  
## 4 0.126320214 5H.10 n/a  
## 5 0.000385581 1H.09 n/a  
## 6 0.000008060 1H.05 iPacMan  
## 7 0.017393917 1H.05 n/a  
## 8 0.013538480 2H.65 n/a  
## 9 0.000000735 1H.05 n/a  
## 10 0.000000735 1H.09 n/a  
## 11 0.256781048 5H.23 n/a  
## 12 0.000000735 1H.05 n/a  
## 13 0.161501541 1H.05 n/a  
## 14 0.000002420 1H.05 n/a  
## 15 0.000000735 1H.04 PacMan

1. Remove Low Read Count Genes

## Genes in original dataset: 31064

## Genes after removing for high standard error: 24442

## Genes after also removing for low read counts: 13042

1. Repeat Pattern Analysis - ARF2 (HORVU5Hr1G111500).

## Using mostly log2 fold change (restricted)

## Adjusted p-value: <= 0.001 for timepoint 20; No limits set for other timepoints

## Log2 fold change: < .5 and > -.5 for timepoints 0, 16, 24, 32, 48; > 1 for timepoint 20

## Number of genes: 71

## Gene names: HORVU0Hr1G002960 HORVU0Hr1G038680 HORVU1Hr1G016490 HORVU1Hr1G037250 HORVU1Hr1G040050 HORVU1Hr1G047180 HORVU1Hr1G063720 HORVU1Hr1G071260 HORVU1Hr1G075620 HORVU1Hr1G077430 HORVU1Hr1G077520 HORVU1Hr1G078340 HORVU2Hr1G019190 HORVU2Hr1G023140 HORVU2Hr1G023850 HORVU2Hr1G061930 HORVU2Hr1G082080 HORVU2Hr1G082090 HORVU2Hr1G101670 HORVU3Hr1G010780 HORVU3Hr1G028060 HORVU3Hr1G031030 HORVU3Hr1G059060 HORVU3Hr1G080630 HORVU3Hr1G080640 HORVU3Hr1G081590 HORVU3Hr1G092590 HORVU3Hr1G096550 HORVU3Hr1G110590 HORVU3Hr1G113850 HORVU3Hr1G114920 HORVU3Hr1G117890 HORVU4Hr1G006740 HORVU4Hr1G006780 HORVU4Hr1G011940 HORVU4Hr1G033020 HORVU4Hr1G035380 HORVU4Hr1G062930 HORVU4Hr1G080140 HORVU4Hr1G080420 HORVU5Hr1G006730 HORVU5Hr1G012710 HORVU5Hr1G014350 HORVU5Hr1G019640 HORVU5Hr1G033420 HORVU5Hr1G048030 HORVU5Hr1G083360 HORVU5Hr1G093590 HORVU5Hr1G094250 HORVU5Hr1G111500 HORVU5Hr1G123590 HORVU6Hr1G002580 HORVU6Hr1G030260 HORVU6Hr1G033070 HORVU6Hr1G035180 HORVU6Hr1G054000 HORVU6Hr1G059420 HORVU6Hr1G060010 HORVU6Hr1G067060 HORVU6Hr1G067180 HORVU6Hr1G075400 HORVU6Hr1G088570 HORVU7Hr1G001070 HORVU7Hr1G007940 HORVU7Hr1G022270 HORVU7Hr1G032750 HORVU7Hr1G058250 HORVU7Hr1G073550 HORVU7Hr1G088250 HORVU7Hr1G088450 HORVU7Hr1G097010

* Checking to see if any of the genes from method #4 (Using mostly log2 fold change - restricted) align with Barley1 probesets in 1HS or 2HL eQTL

## Number of overlapping genes: 14

## Overlapping gene - probeset pairs:

## probeset hv\_gene qvalue\_16h most\_associated\_marker\_16h  
## 1 Contig14332\_at HORVU2Hr1G023140 0.154097333 2H.68  
## 2 Contig14465\_at HORVU7Hr1G088250 0.000002700 2H.66  
## 3 Contig3108\_at HORVU4Hr1G080140 0.000689093 2H.66  
## 4 Contig4245\_s\_at HORVU4Hr1G035380 0.000003630 2H.63  
## 5 Contig5165\_at HORVU2Hr1G019190 0.000002700 2H.68  
## 6 Contig5367\_at HORVU2Hr1G023850 0.000001990 2H.67  
## 7 Contig5449\_at HORVU1Hr1G016490 0.000002700 2H.66  
## 8 Contig6942\_at HORVU3Hr1G031030 0.000001990 2H.67  
## 9 Contig6945\_at HORVU5Hr1G014350 0.000002700 2H.66  
## 10 Contig7253\_at HORVU3Hr1G028060 0.000017200 2H.65  
## 11 Contig7332\_at HORVU1Hr1G047180 0.000001990 2H.66  
## 12 Contig7484\_at HORVU6Hr1G054000 0.000002700 2H.66  
## 13 Contig8214\_at HORVU5Hr1G048030 0.000062300 2H.63  
## 14 Contig9269\_s\_at HORVU6Hr1G002580 0.002865958 2H.66  
## qvalue\_32h most\_associated\_marker\_32h bb4\_expression\_pattern  
## 1 0.000000735 1H.03 n/a  
## 2 0.007279341 1H.03 n/a  
## 3 0.019131713 1H.06 PacMan  
## 4 0.126320214 5H.10 n/a  
## 5 0.000008060 1H.05 iPacMan  
## 6 0.017393917 1H.05 n/a  
## 7 0.013538480 2H.65 n/a  
## 8 0.000000735 1H.05 n/a  
## 9 0.000000735 1H.09 n/a  
## 10 0.256781048 5H.23 n/a  
## 11 0.000000735 1H.05 n/a  
## 12 0.161501541 1H.05 n/a  
## 13 0.000002420 1H.05 n/a  
## 14 0.000000735 1H.04 PacMan