

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 HORVU1Hr1G040050 HORVU1Hr1G040050 HORVU1Hr1G040050 HORVU1Hr1G040050 HORVU1Hr1G040050

- 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

6. 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

7. 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 HORVU1Hr1G040050 HORVU1Hr1G040050

- 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	