Table 1: Numerical counts of genes for the strain dHAP4 at the differing significance levels

ANOVA	dHAP4
$p<0.05$	2479 (40%)
$p<0.01$	1583 (26%)
$p<0.001$	739 (12%)
$p<0.0001$	280 (4.5%)
B & H $p<0.05$	1735 (28%)
Bonferroni $p<0.05$	75 (1.2%)

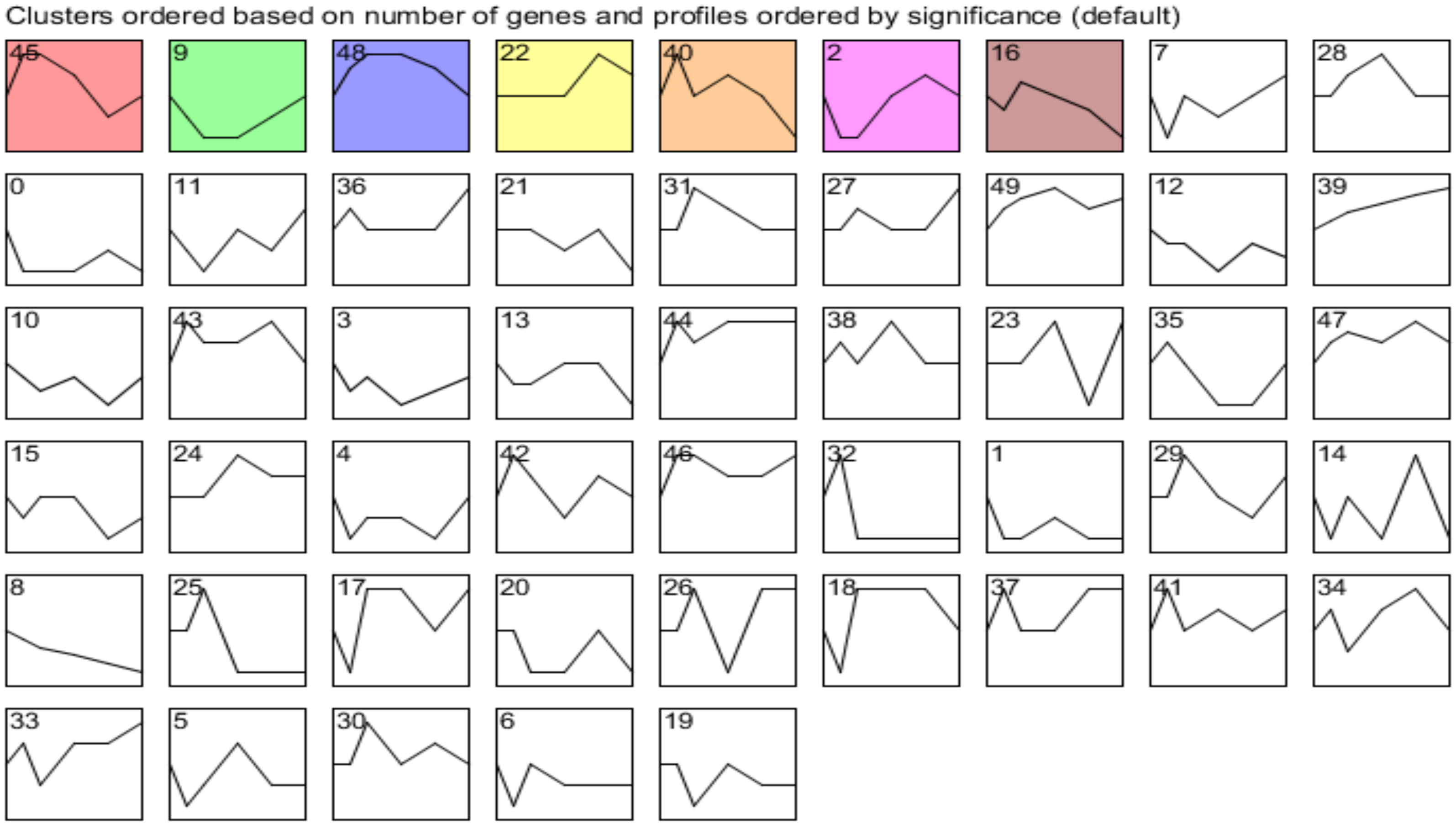
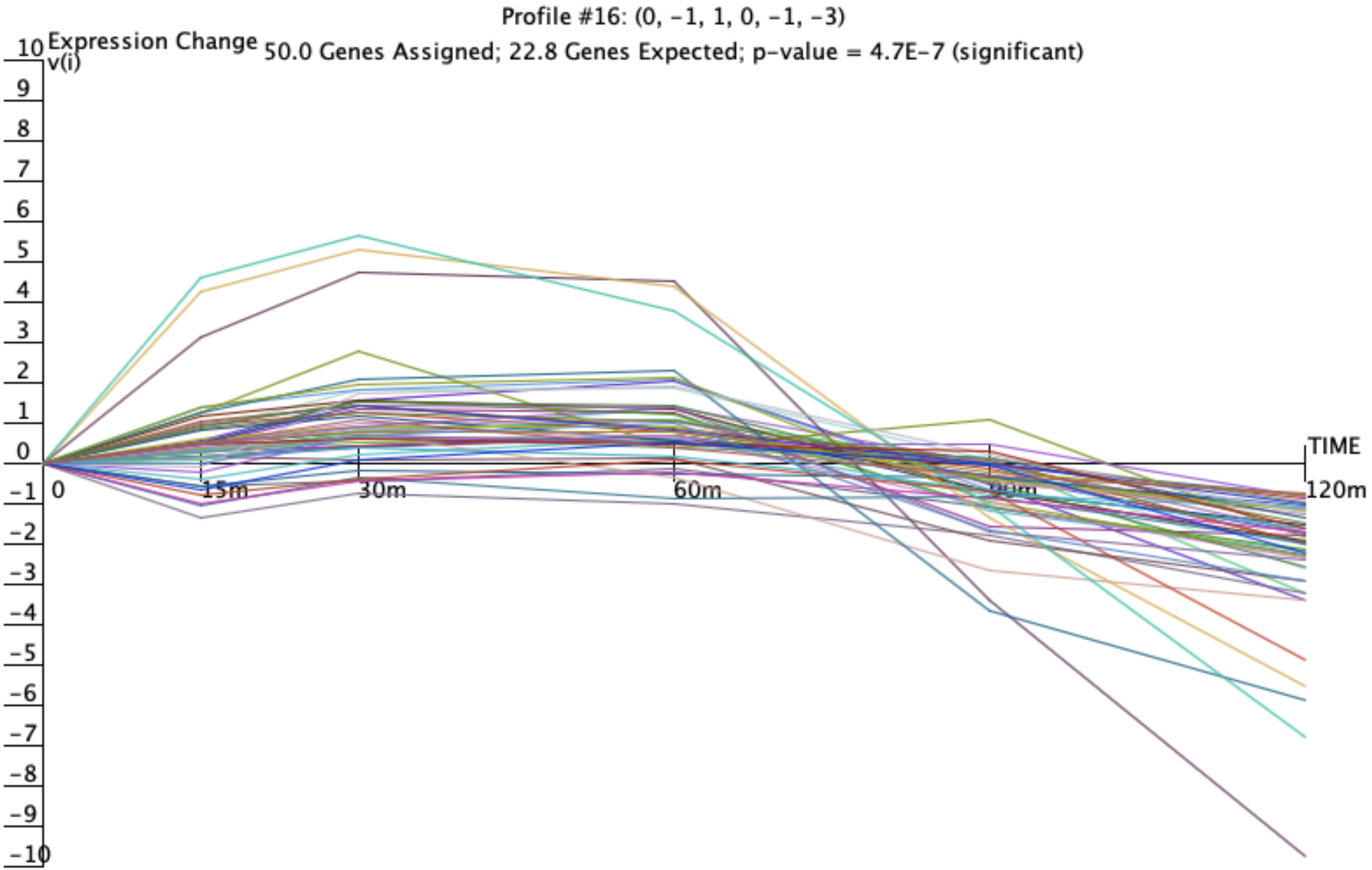
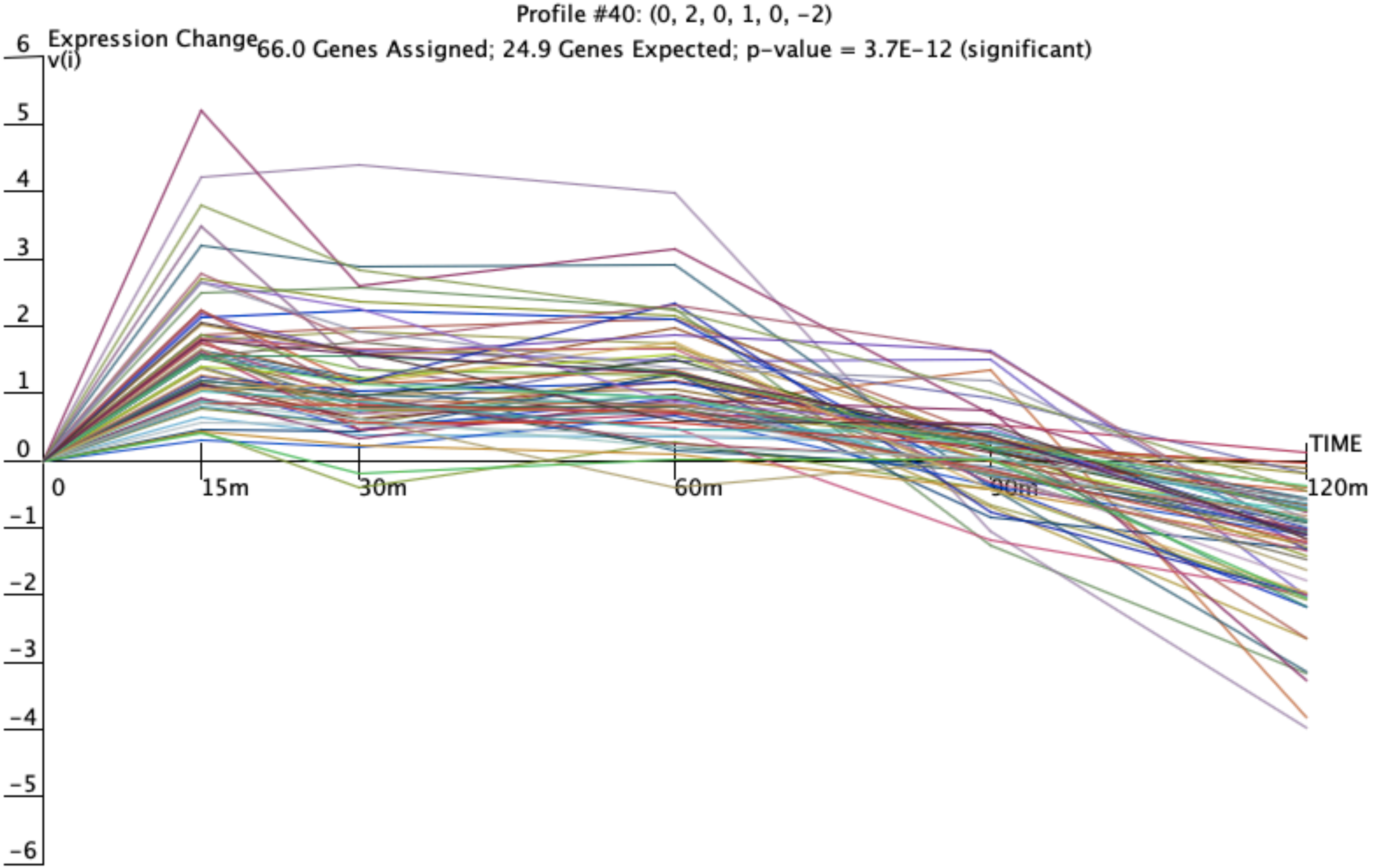
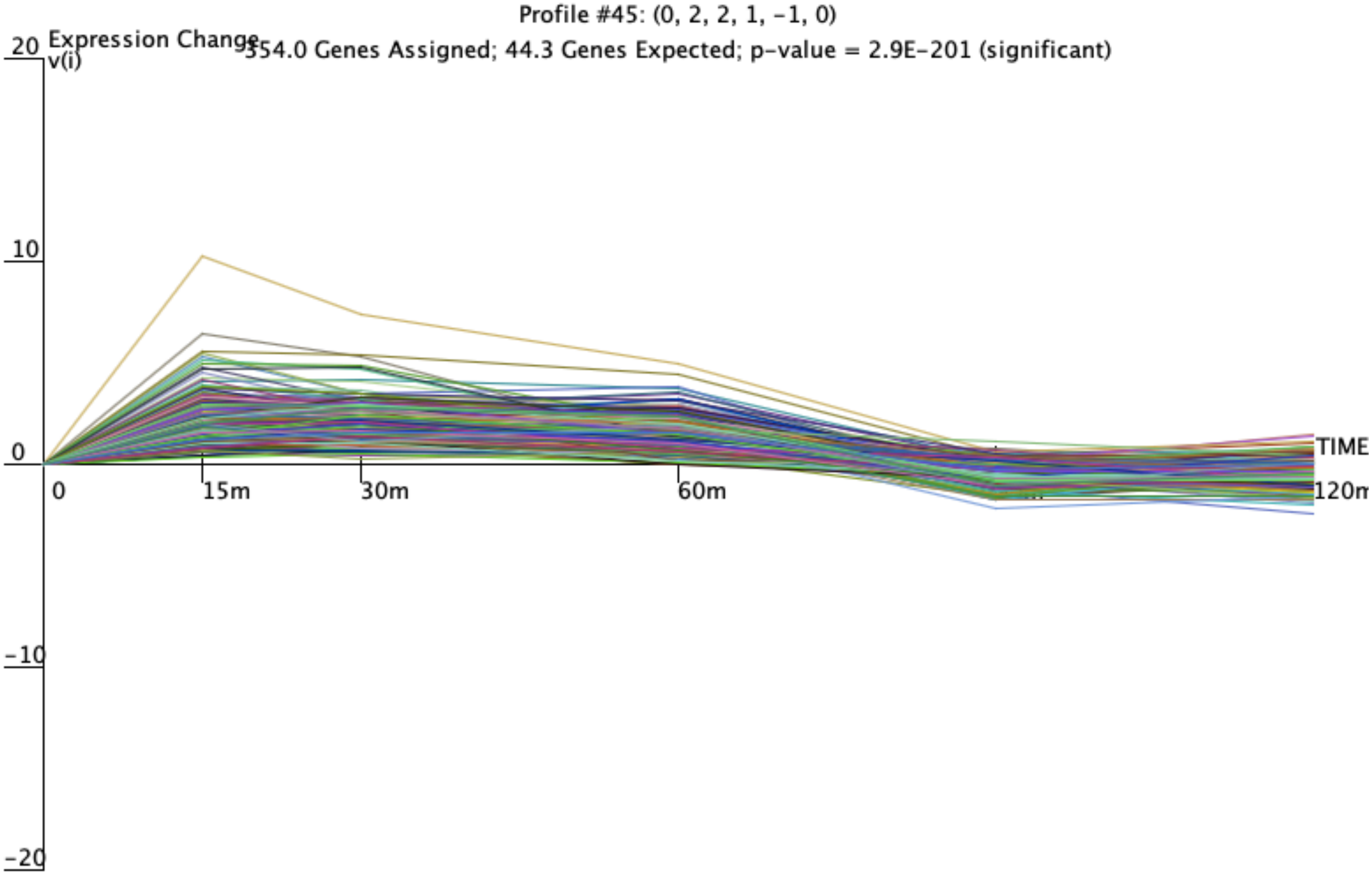


Figure 1: Cluster profiles made via STEM software

Profiles that were up-regulated during cold-shock and down-regulated during recovery

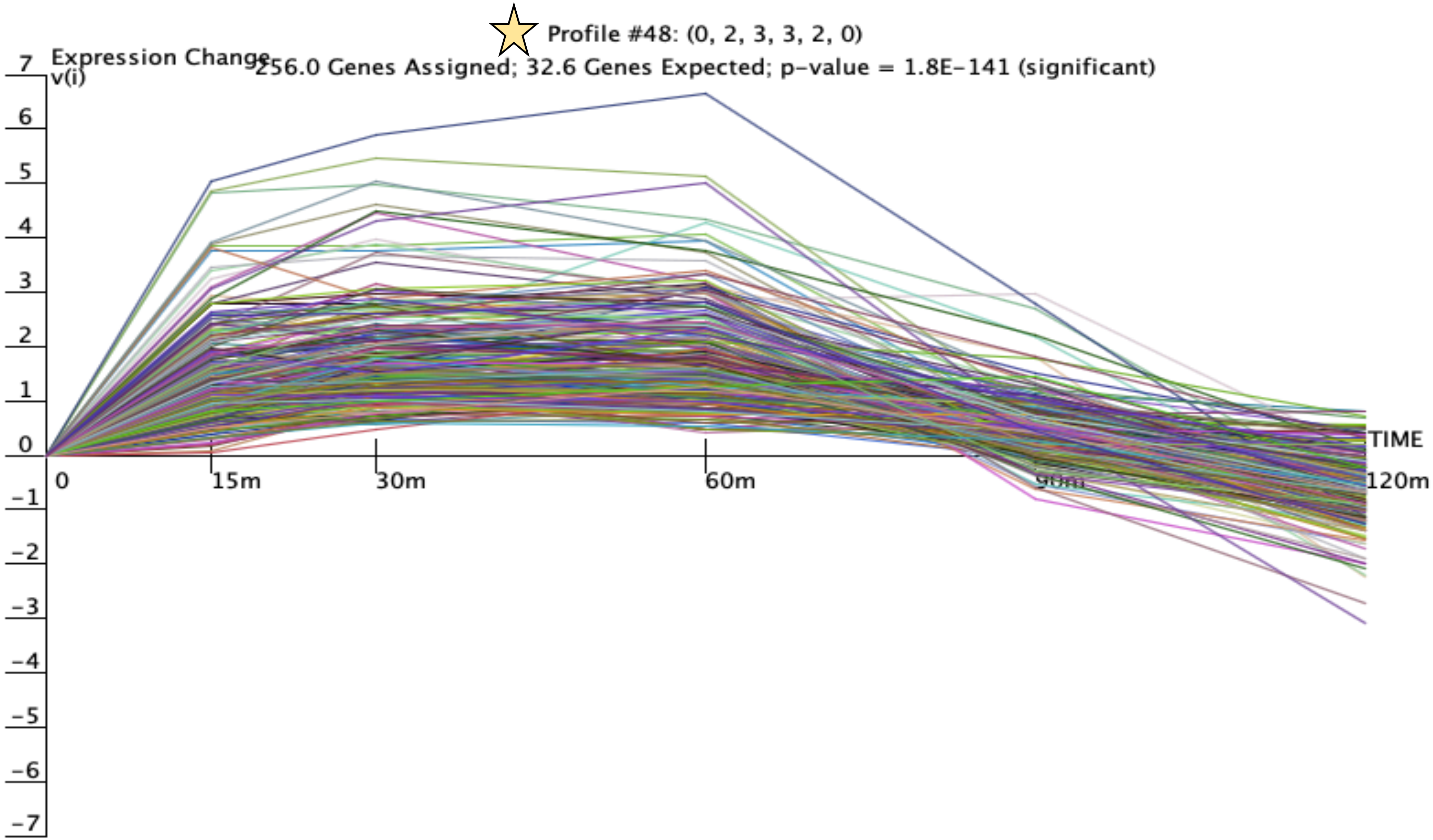

Profile #16: (0, −1, 1, 0, −1, −3)
50.0 Genes Assigned; 22.8 Genes Expected; p−value = 4.7E−7 (significant)
Expression Change
v(i)
10
9
8
7
6
5
4
3
2
1
0
−1
−2
−3
−4
−5
−6
−7
−8
−9
−10
TIME
0
15m
30m
60m
120m


Profile #40: (0, 2, 0, 1, 0, -2)
66.0 Genes Assigned; 24.9 Genes Expected; p-value = 3.7E-12 (significant)
Expression Change
v(i)
6
5
4
3
2
1
0
-1
-2
-3
-4
-5
-6
0
15m
30m
60m
90m
120m
TIME

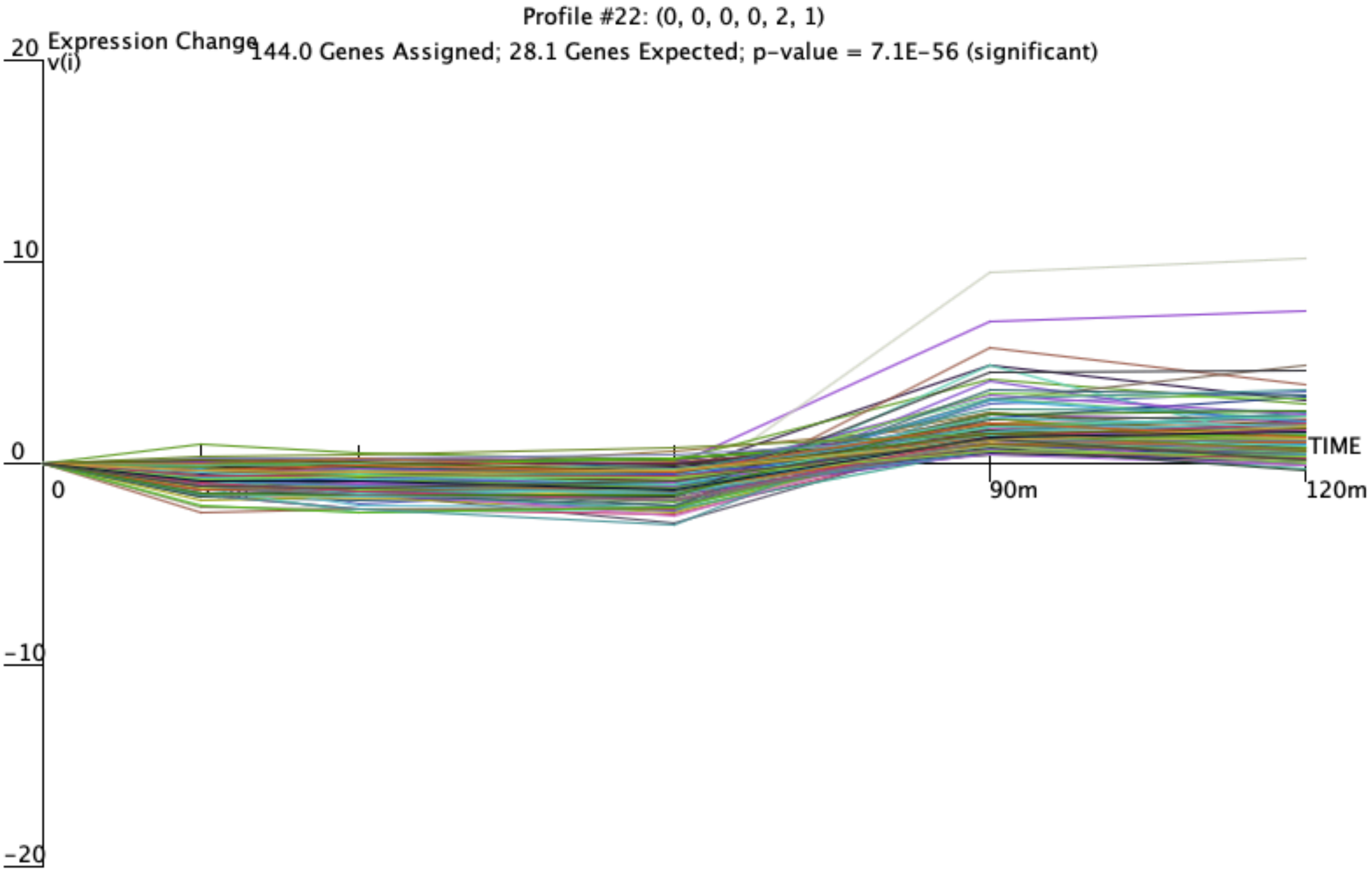


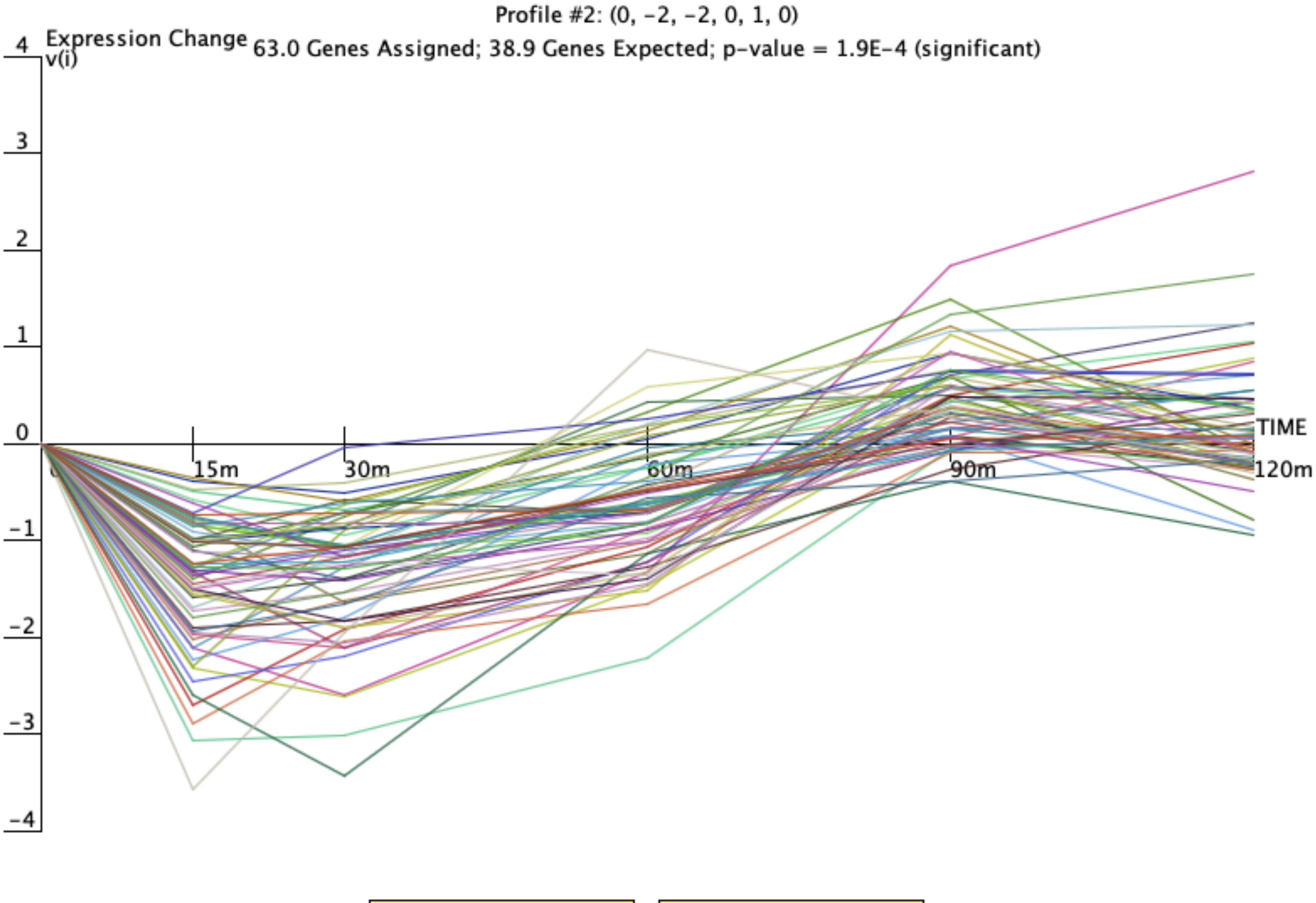
Profile #45: (0, 2, 2, 1, -1, 0)

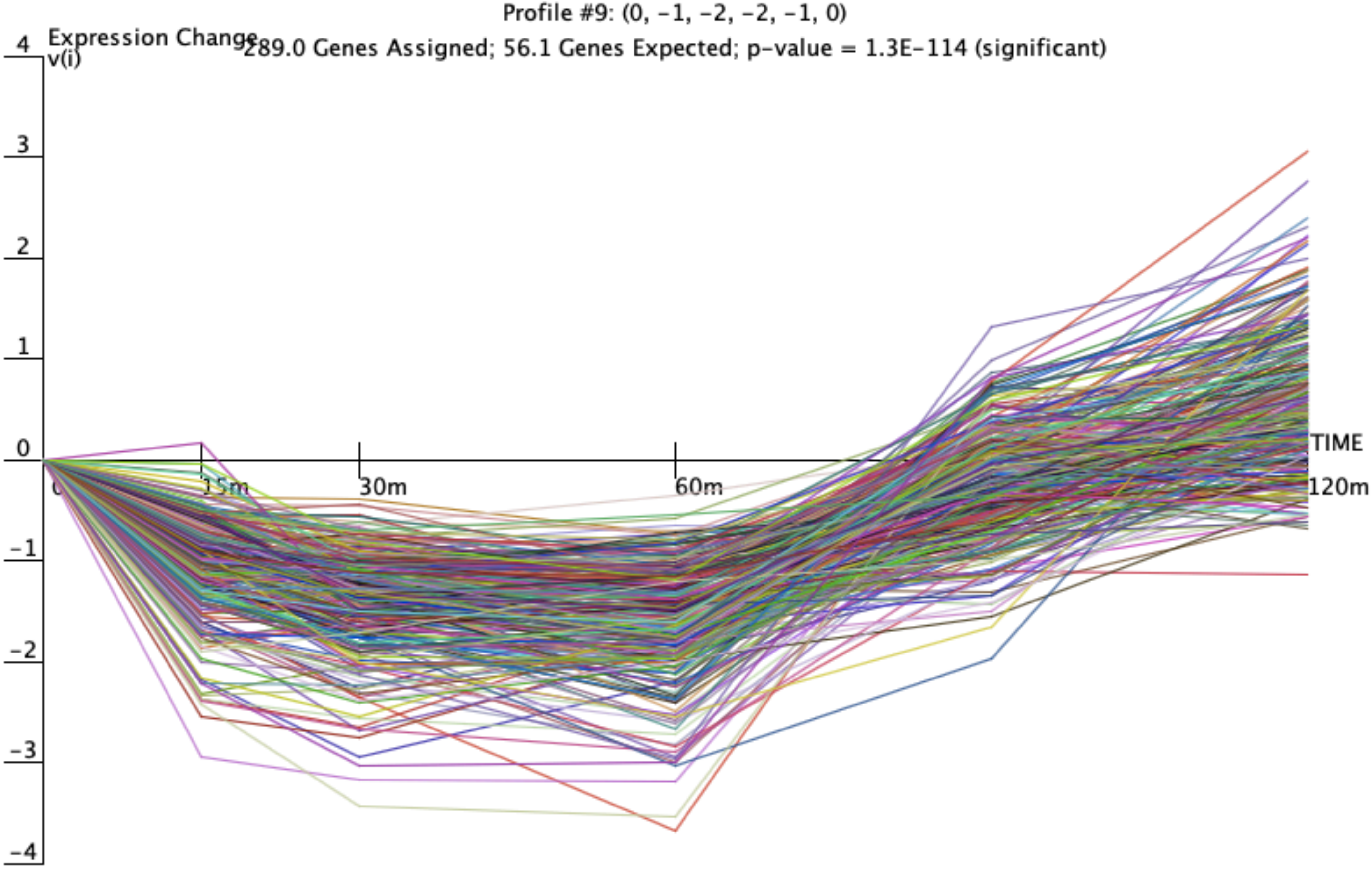
354.0 Genes Assigned; 44.3 Genes Expected; p-value = 2.9E-201 (significant)

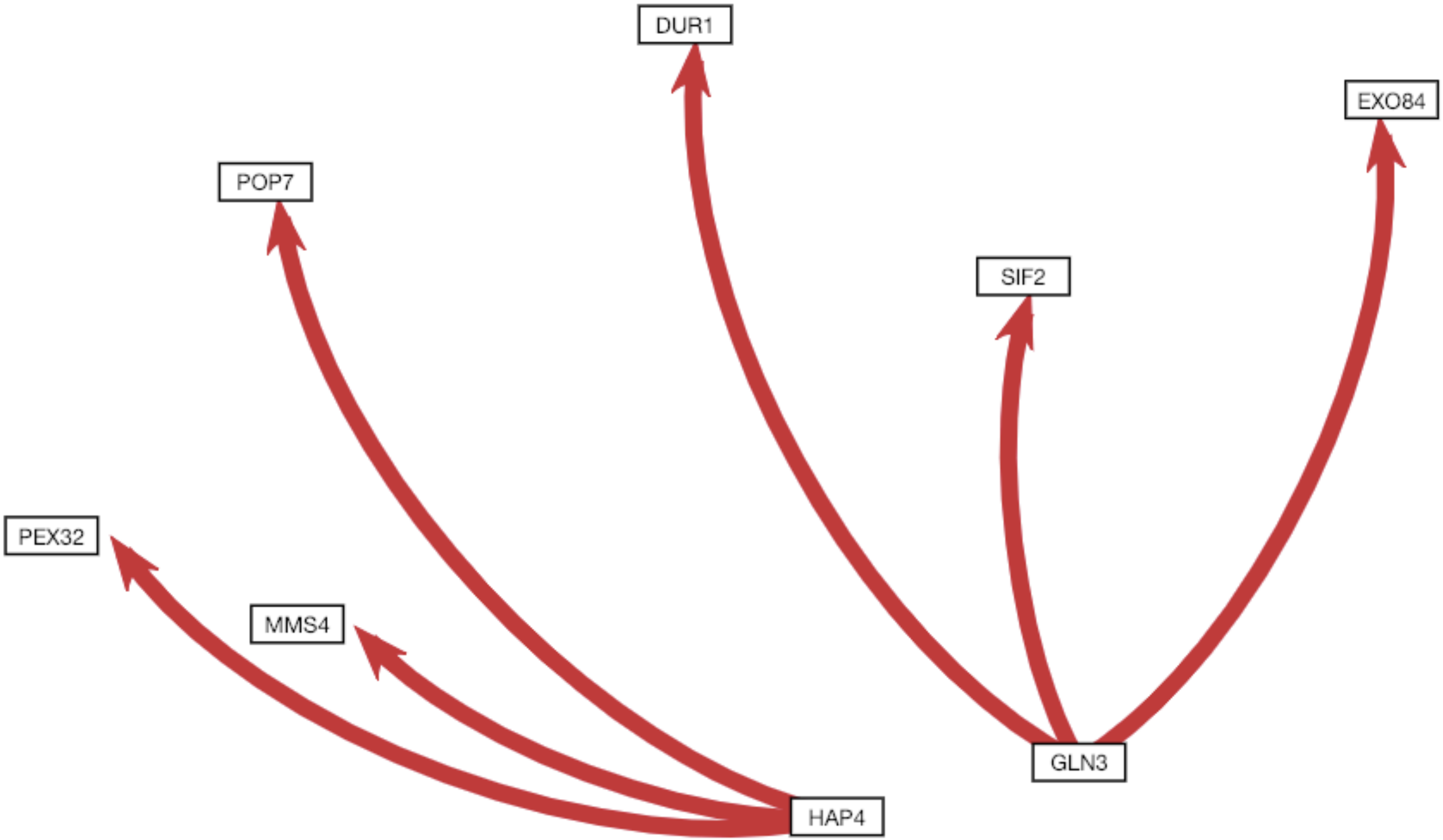

Profile #48: (0, 2, 3, 3, 2, 0)
256.0 Genes Assigned; 32.6 Genes Expected; p-value = 1.8E-141 (significant)
Expression Change
v(i)
7
6
5
4
3
2
1
0
-1
-2
-3
-4
-5
-6
-7
0
15m
30m
60m
90m
120m
TIME

Profiles that were down-regulated during cold-shock and up-regulated during recovery


Profile #22: (0, 0, 0, 0, 2, 1)
144.0 Genes Assigned; 28.1 Genes Expected; p-value = 7.1E-56 (significant)
Expression Change
v(i)
20
10
0
-10
-20
0
90m
120m
TIME


Profile #2: (0, −2, −2, 0, 1, 0)
63.0 Genes Assigned; 38.9 Genes Expected; p−value = 1.9E−4 (significant)
Expression Change
v(i)
4
3
2
1
0
−1
−2
−3
−4
15m
30m
60m
90m
120m
TIME


Profile #9: (0, −1, −2, −2, −1, 0)
289.0 Genes Assigned; 56.1 Genes Expected; p−value = 1.3E−114 (significant)
Expression Change
v(i)
4
3
2
1
0
−1
−2
−3
−4
TIME
0
15m
30m
60m
120m


DUR1
EXO84
POP7
SIF2
PEX32
MMS4
GLN3
HAP4