# Outline

RNAseq samples

Control VS treatment

Control Samples along time

Treatment Samples along time

Controls

Treatment

Control genes

ATACseq - mapping stats

# Outline

RNAseq samples

Control VS treatment

Control Samples along time

Treatment Samples along time

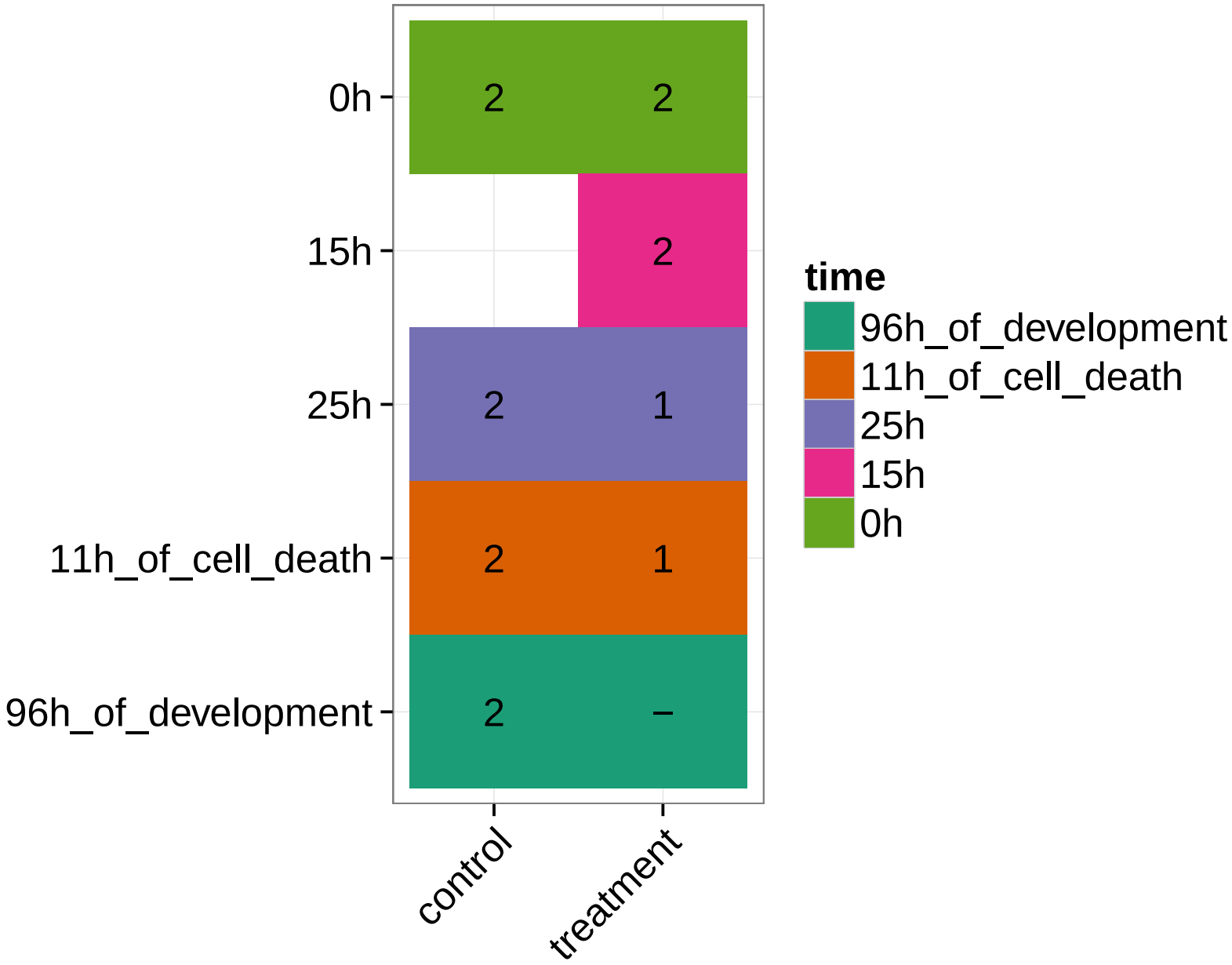
Controls

Treatment

Control genes

ATACseq - mapping stats

# RNAseq samples



# Outline

RNAseq samples

Control VS treatment

Control Samples along time

Treatment Samples along time

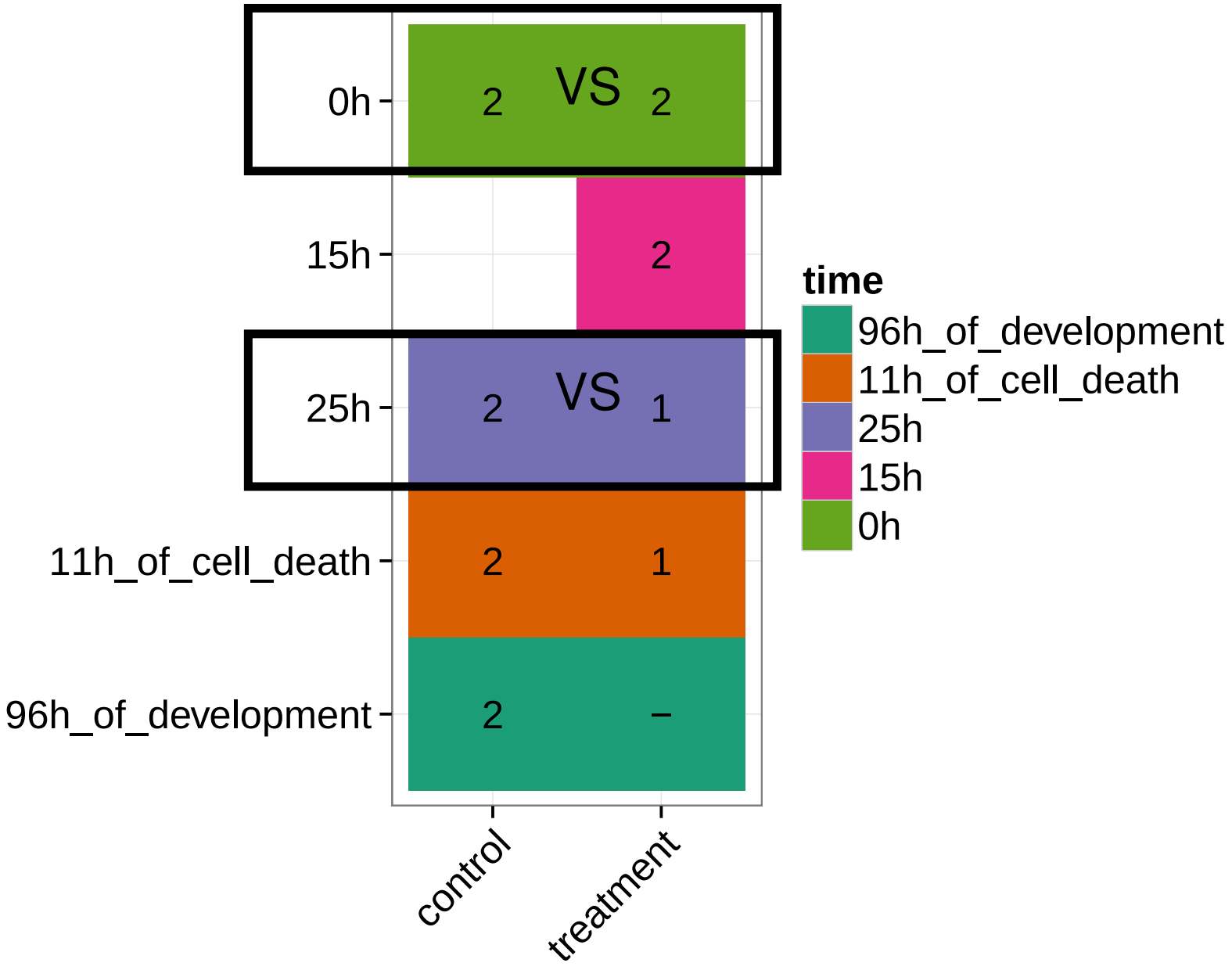
Controls

Treatment

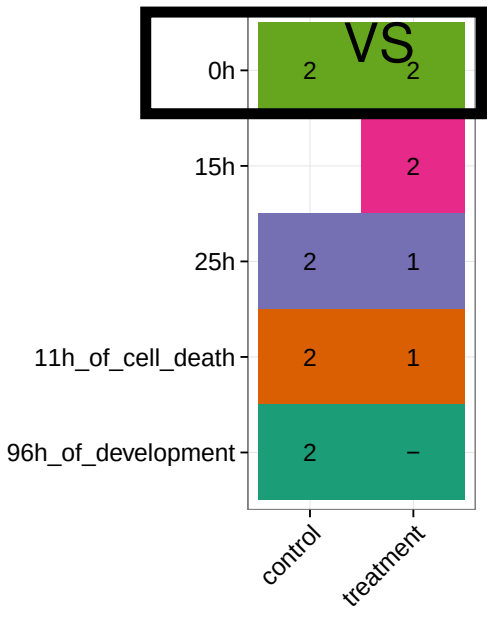
Control genes

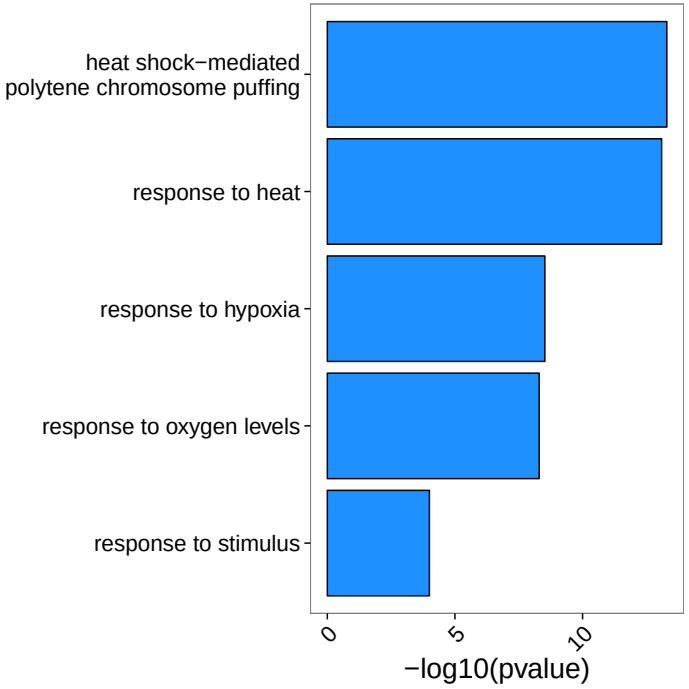
ATACseq - mapping stats

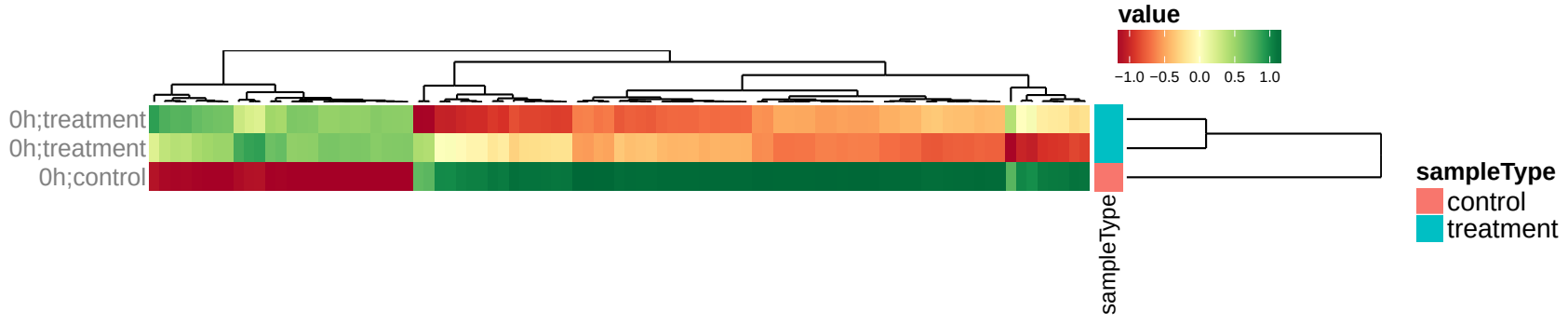
# DEG - control VS treatment (EdgeR, FDR¡0.01)



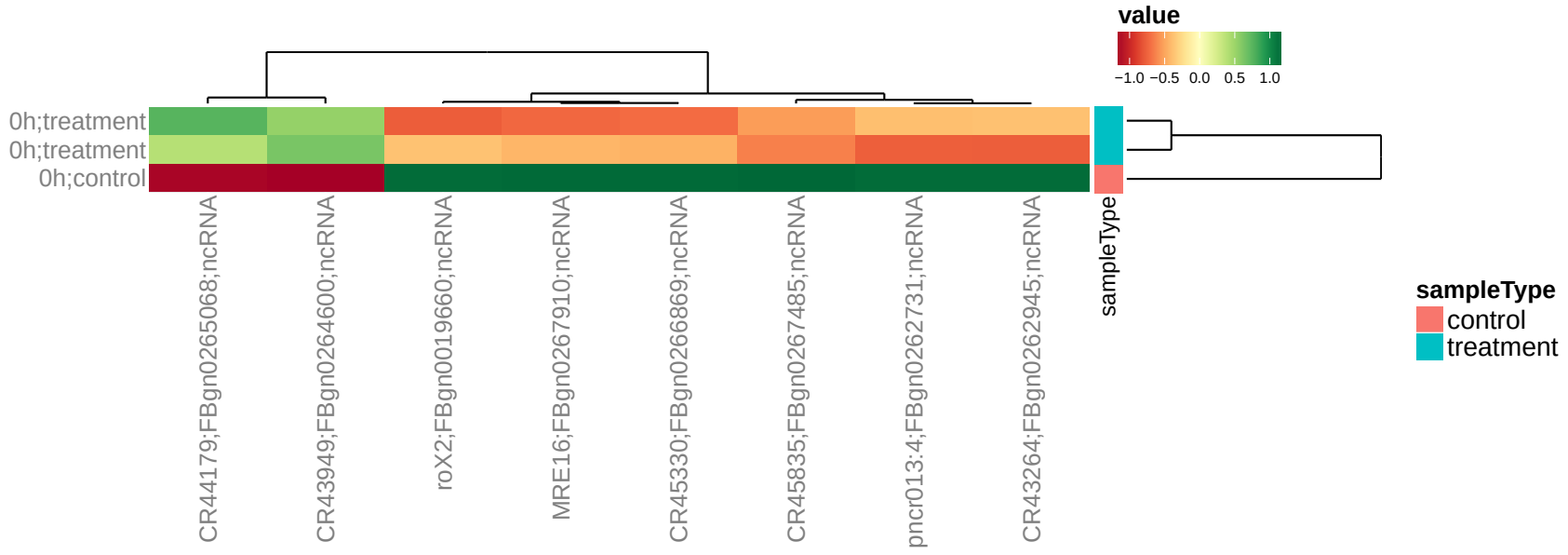
# DEG - control VS treatment **0h** - 89 genes



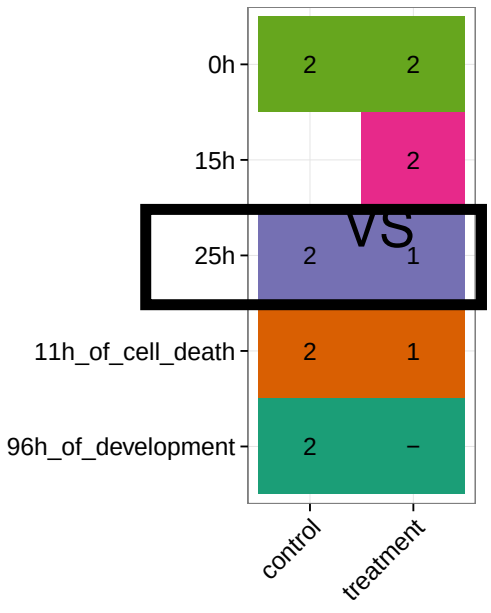



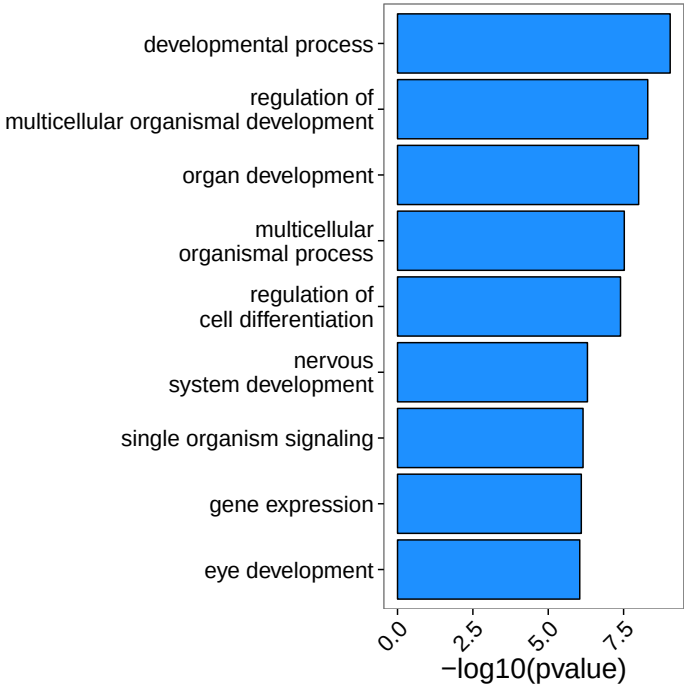



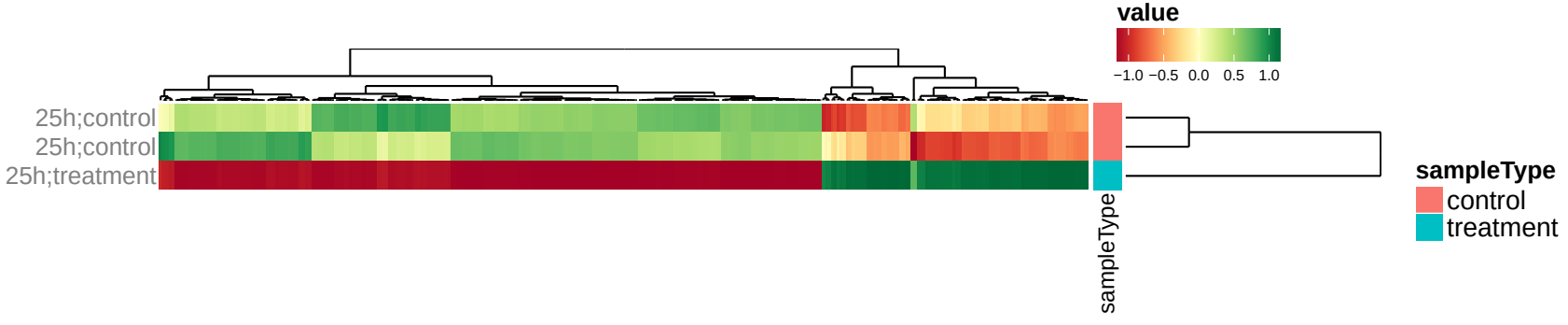
# DEG - control VS treatment **0h** - ncRNA



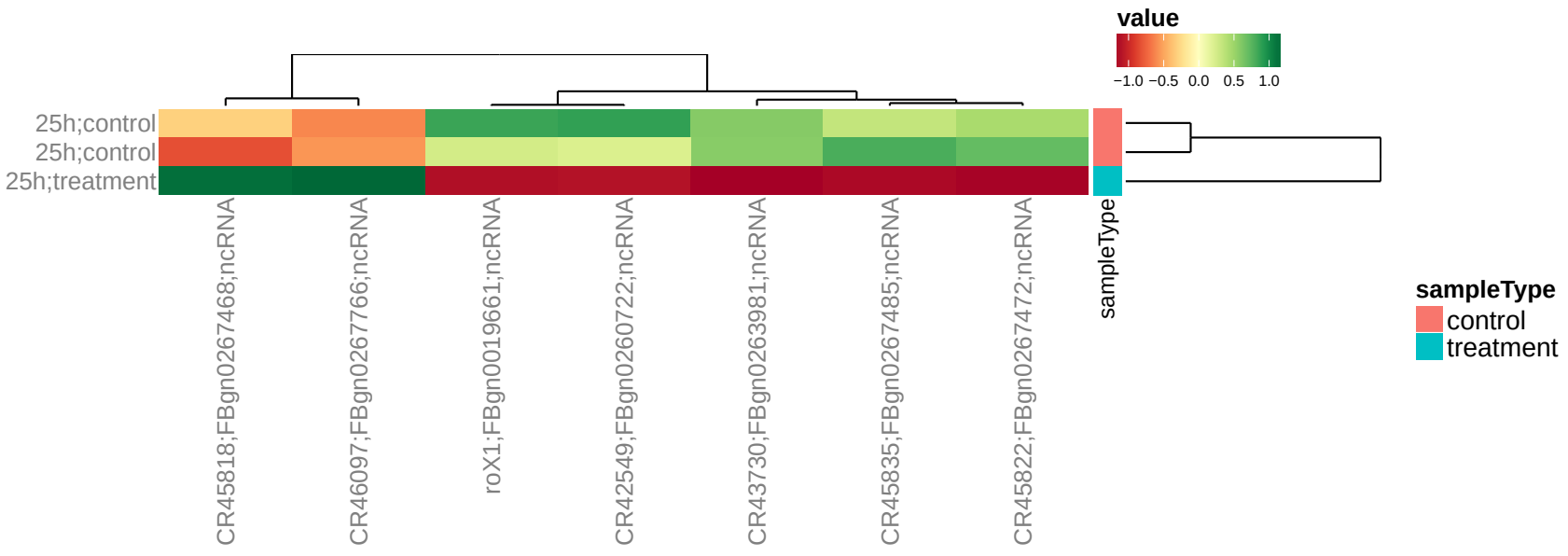
# DEG - control VS treatment **25h** - 313 genes



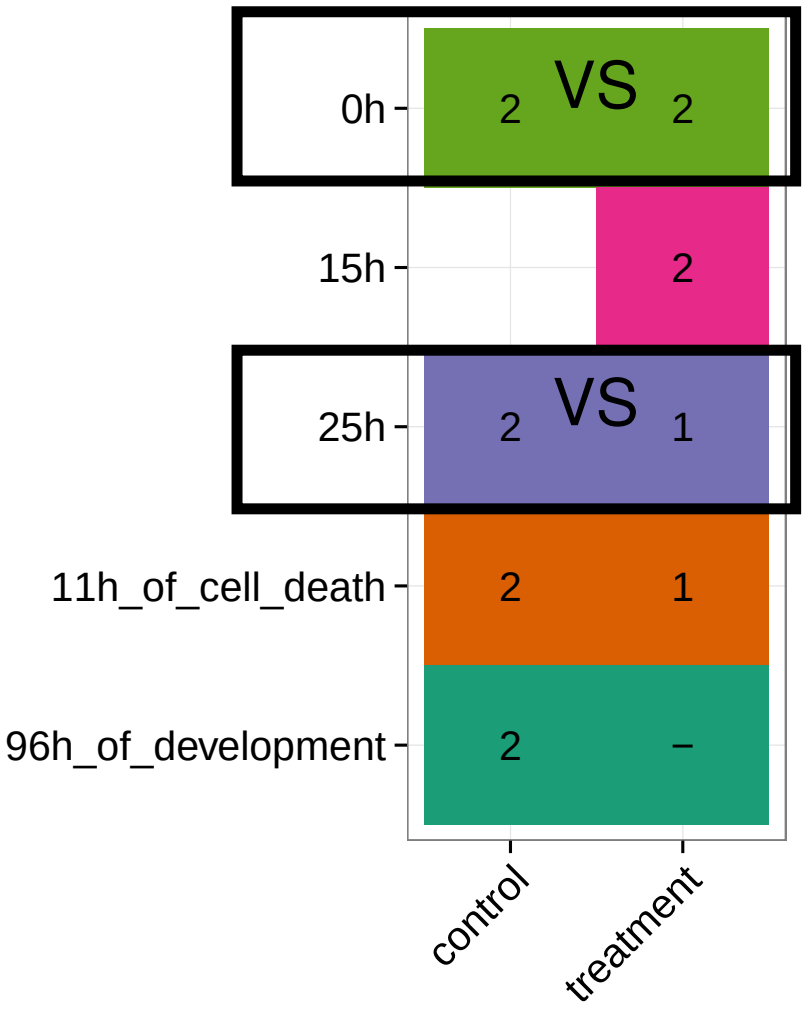



# DEG - control VS treatment **25h** - ncRNA



# DEG - control VS treatment



# Outline

RNAseq samples

Control VS treatment

Control Samples along time

Treatment Samples along time

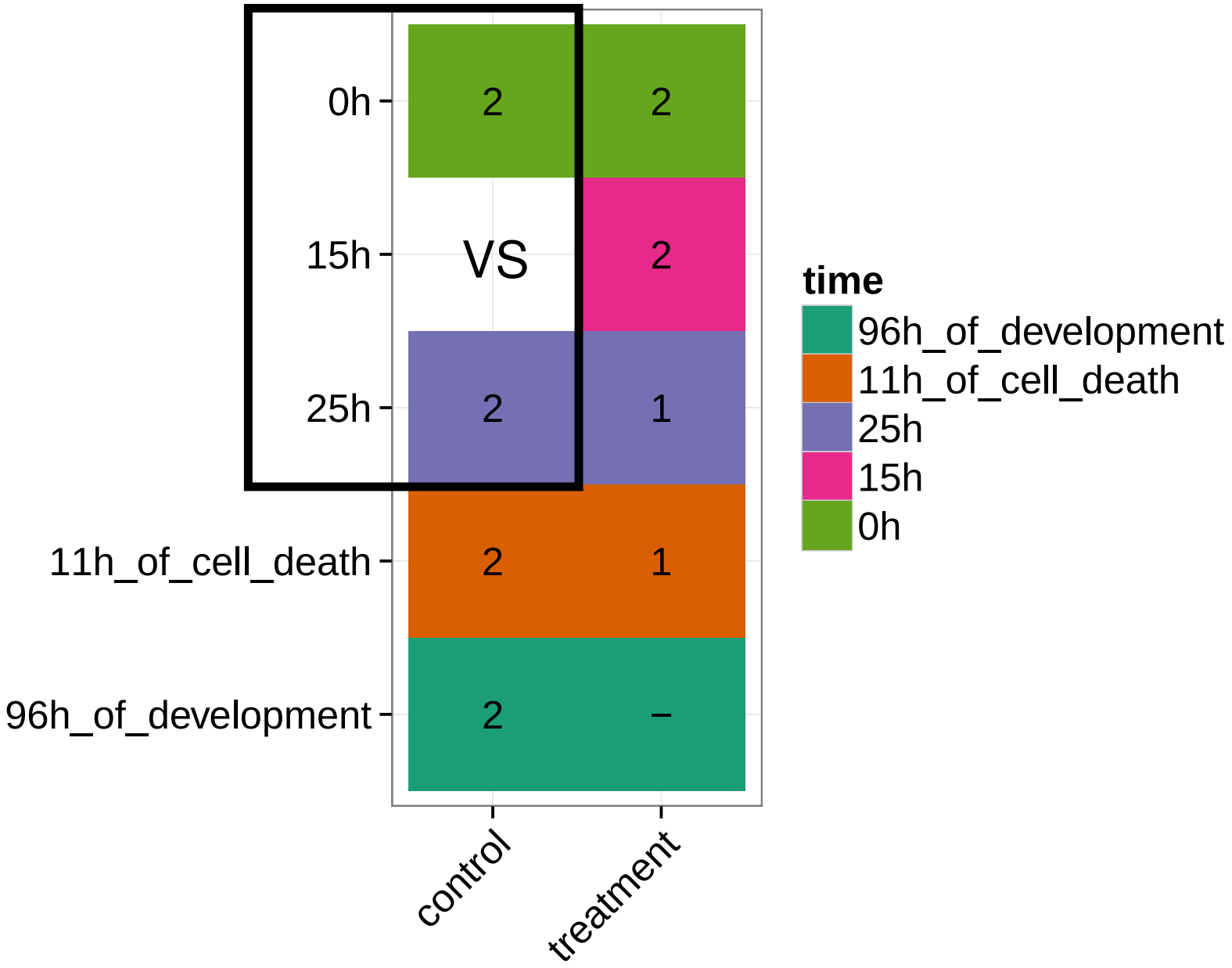
Controls

Treatment

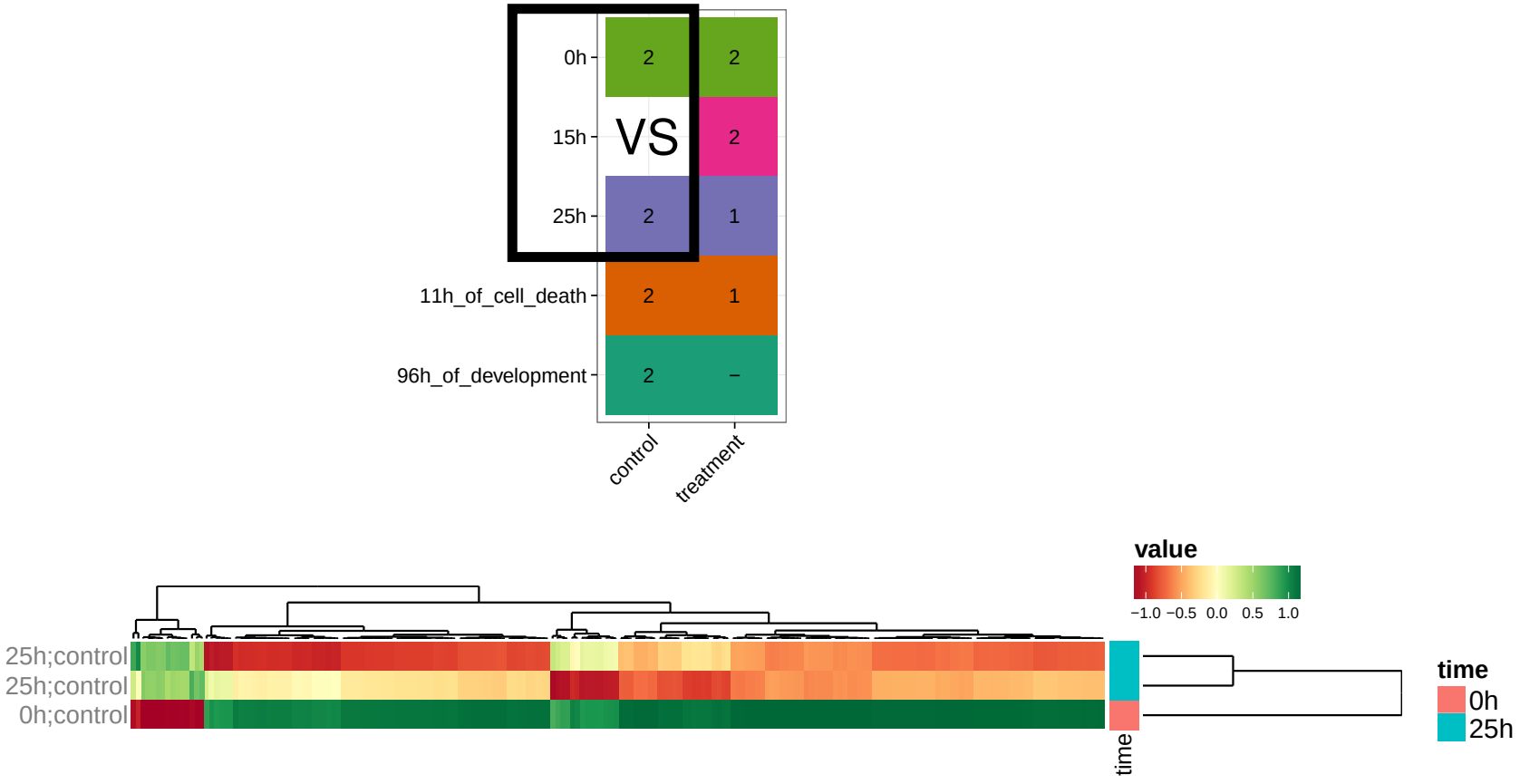
Control genes

ATACseq - mapping stats

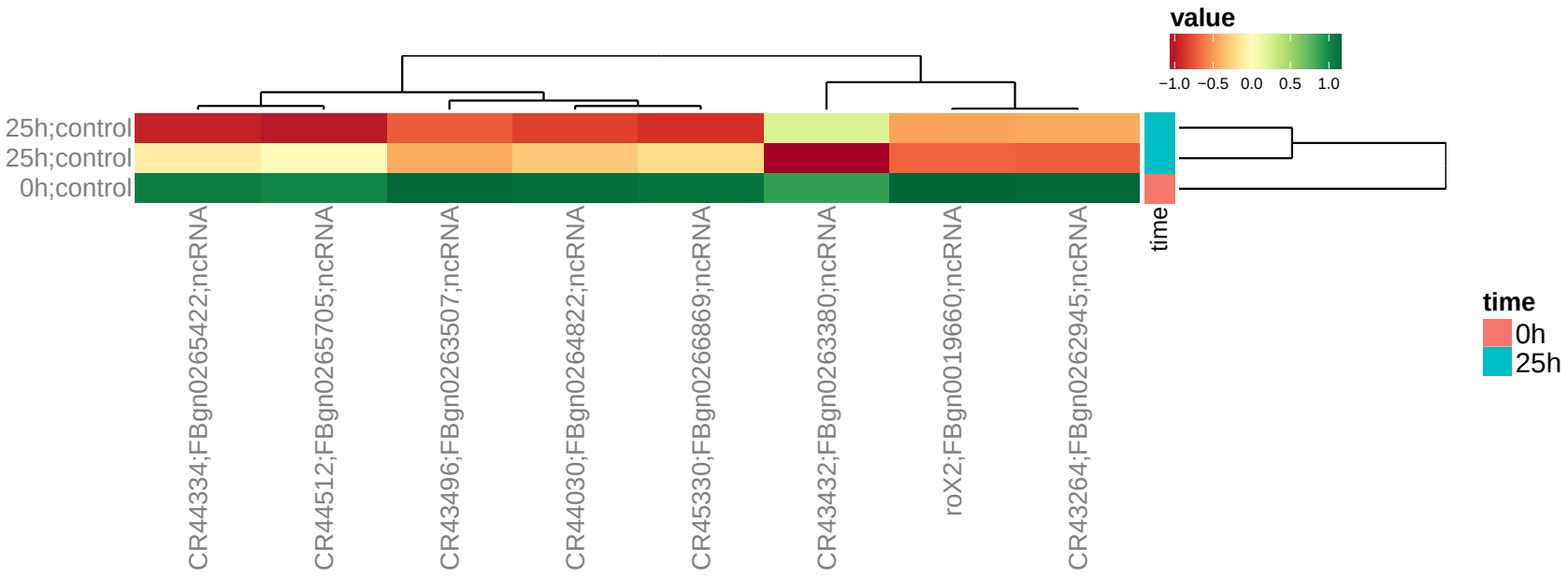
# DEG - control samples along time



# DEG - **control 0h** VS **control 25h** - 200 genes



# DEG - **control 0h** VS **control 25h** - ncRNA



# Outline

RNAseq samples

Control VS treatment

Control Samples along time

Treatment Samples along time

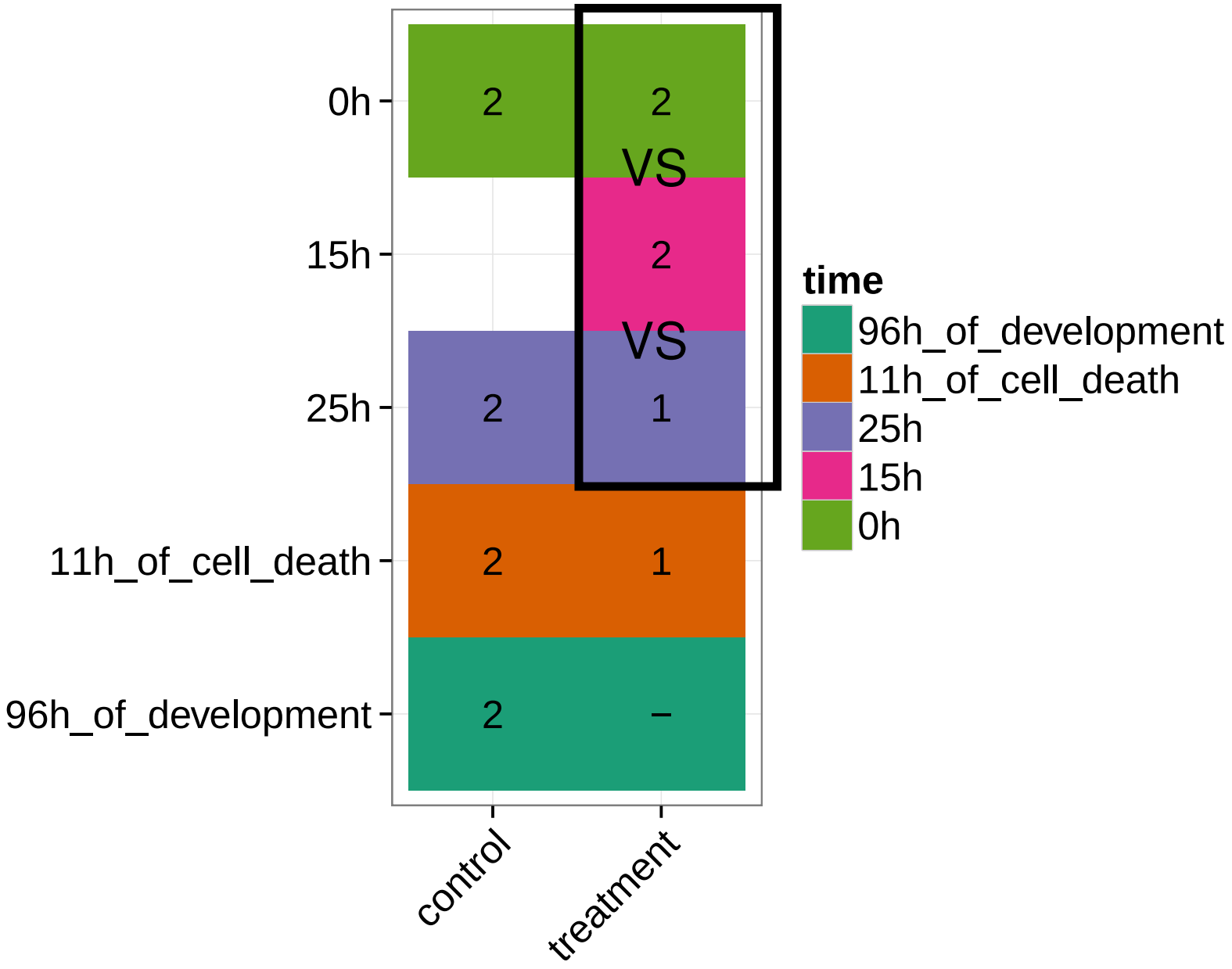
Controls

Treatment

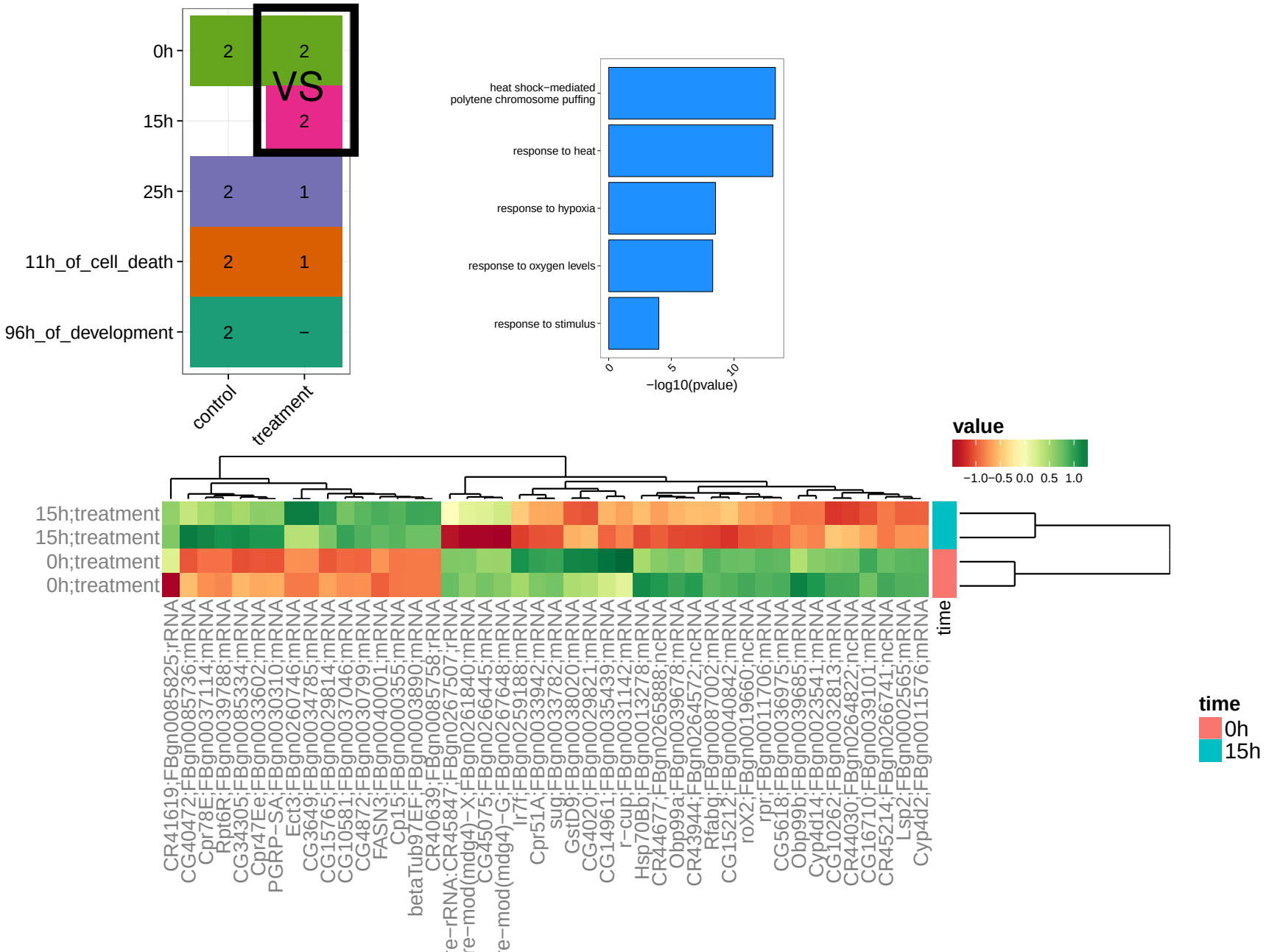
Control genes

ATACseq - mapping stats

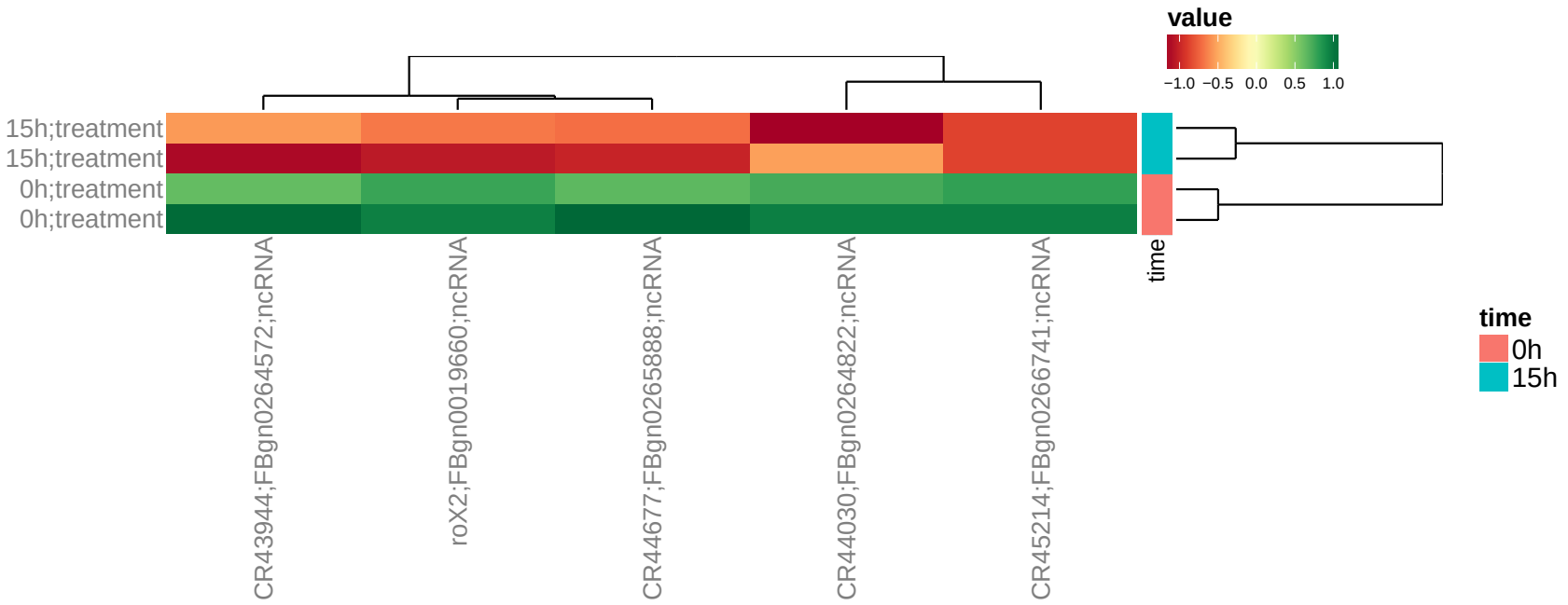
# DEG - treatment samples along time



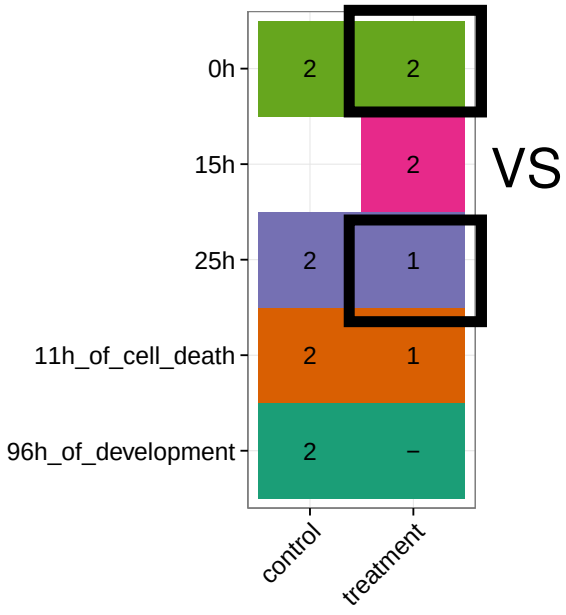
# DEG - treatment **0h** VS **15h** - 44 genes

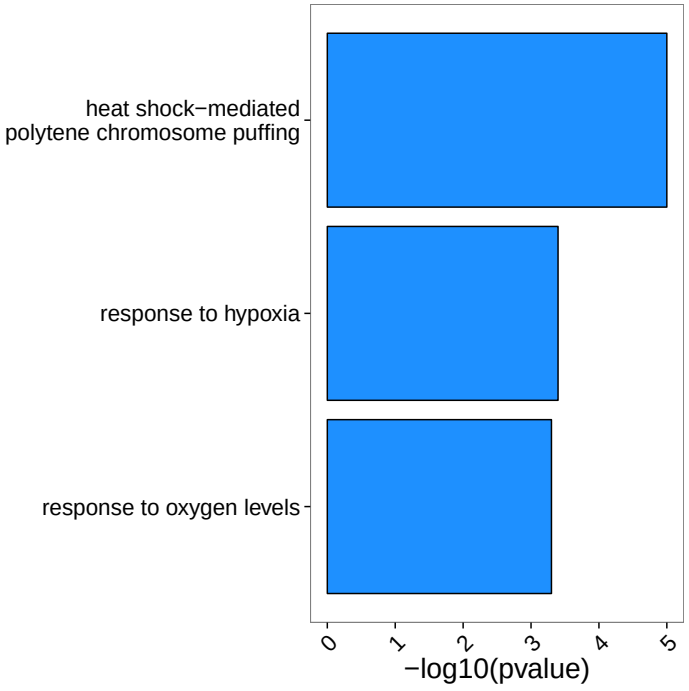


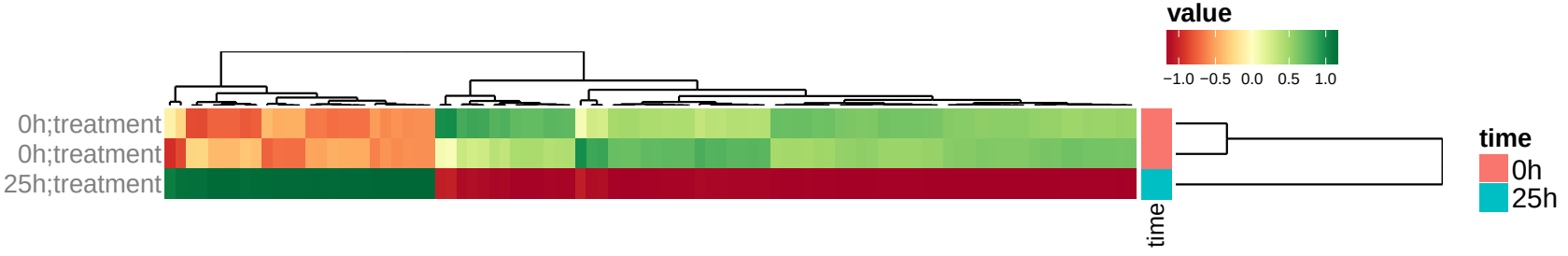
# DEG - treatment **0h** VS **15h** - ncRNA



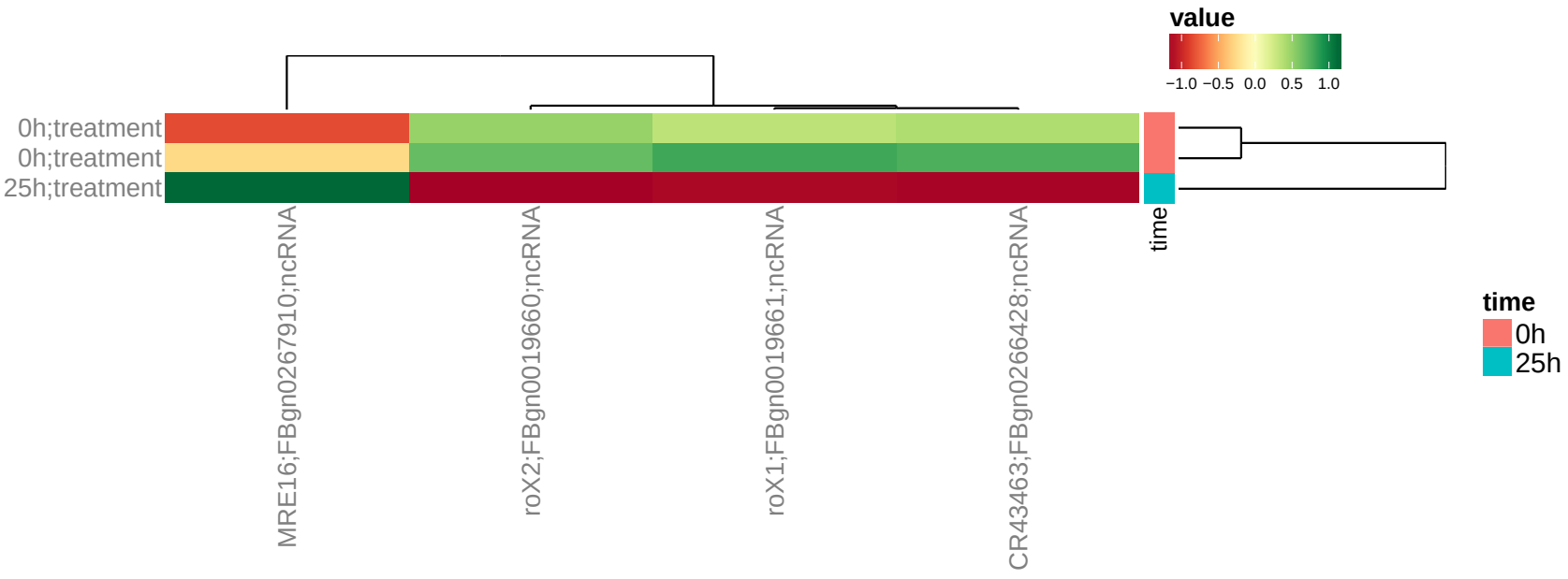
# DEG - treatment **0h** VS **25h** - 90 genes



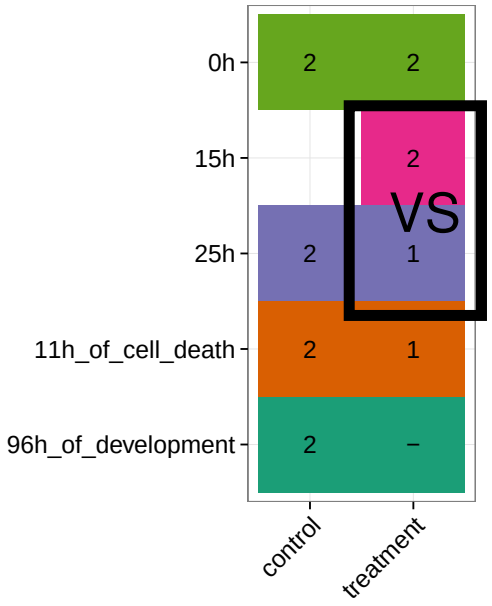



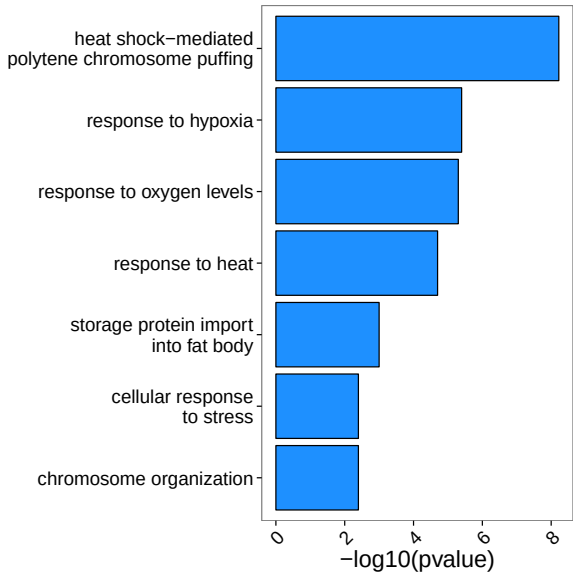



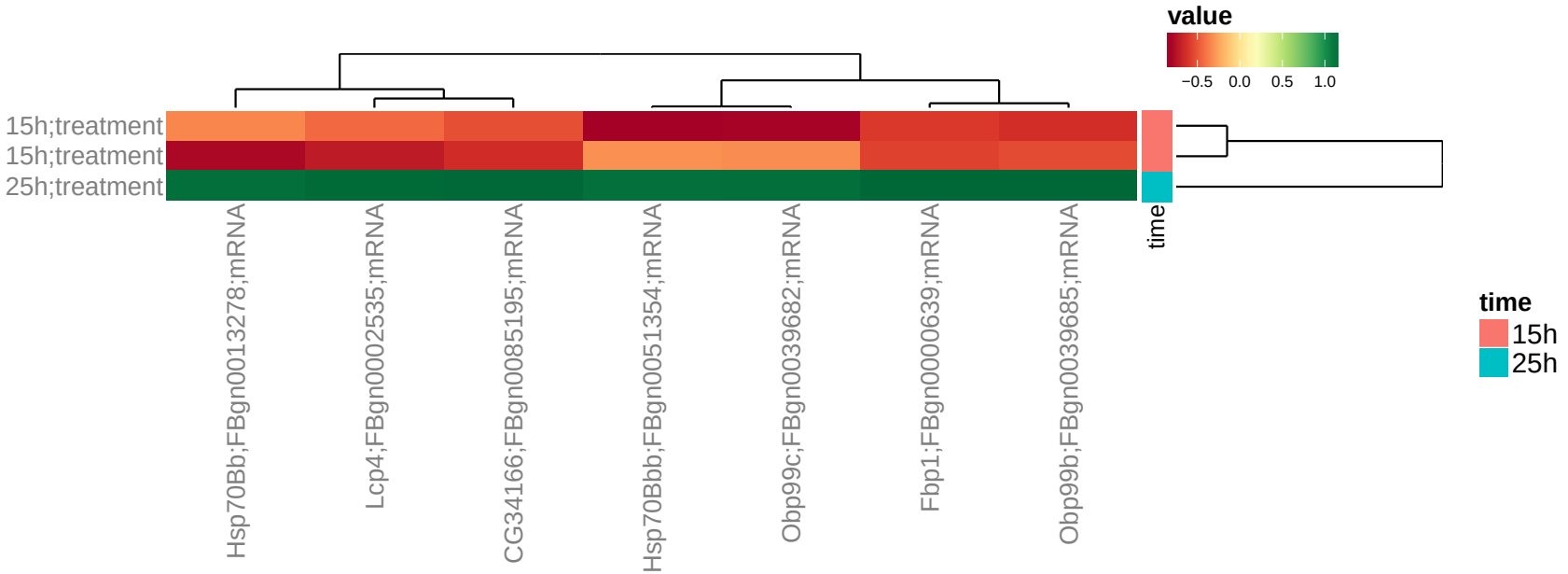
# DEG - treatment **0h** VS **25h** - ncRNA



# DEG - treatment **15h** VS **25h** - 7 genes



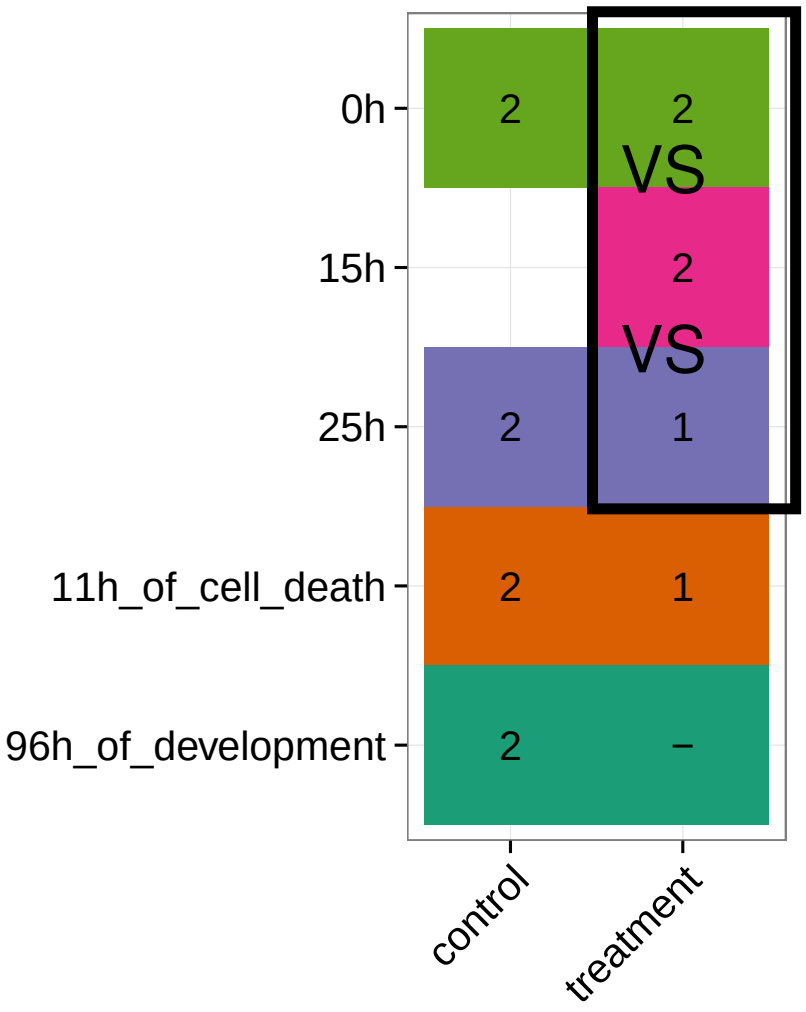



# DEG - treatment **15h** VS **25h** - ncRNA

Not found

# DEG - treatment samples along time



# Outline

RNAseq samples

Control VS treatment

Control Samples along time

Treatment Samples along time

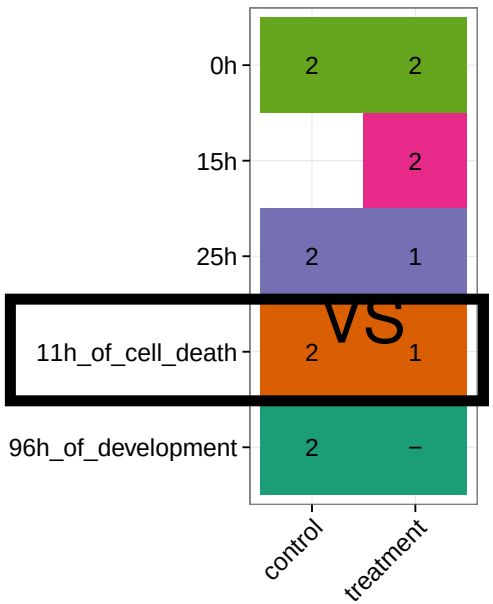
Controls

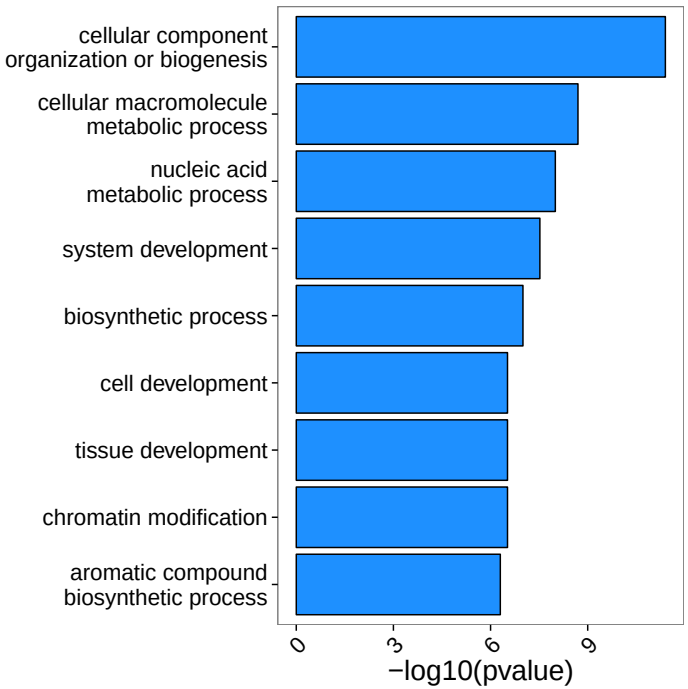
Treatment

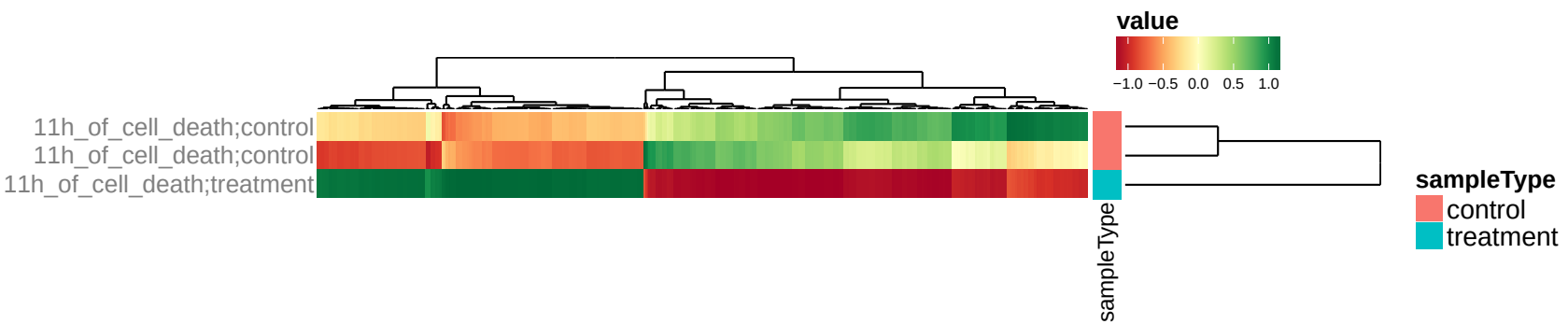
Control genes

ATACseq - mapping stats

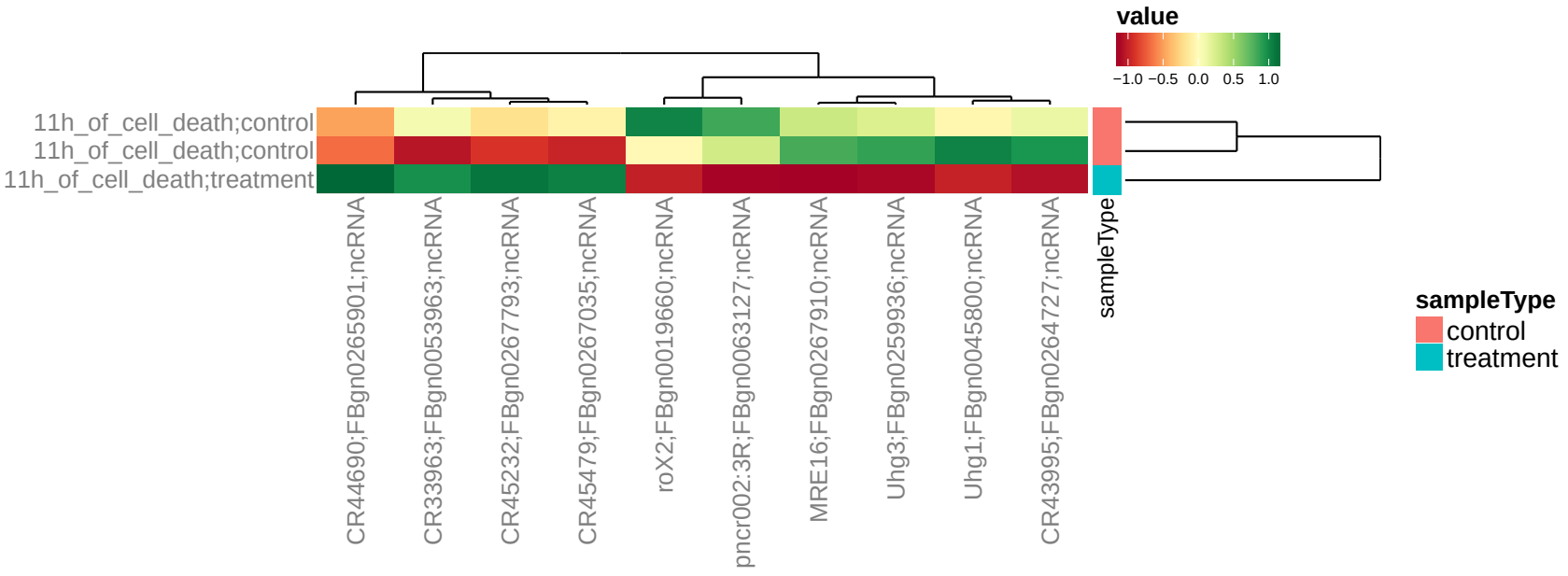
# DEG - **control** VS **treatment** 11h of cell death - 463 genes



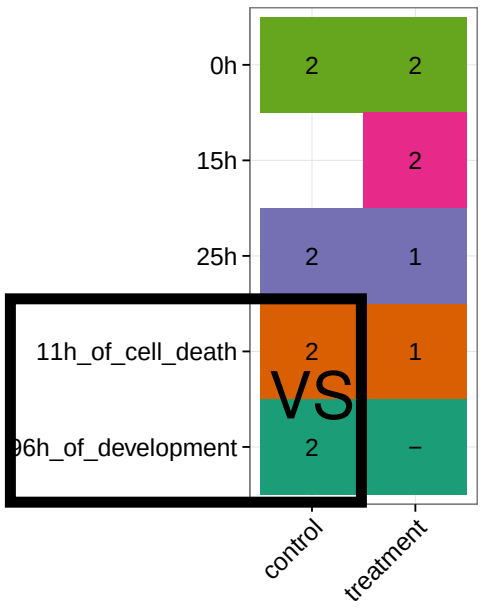



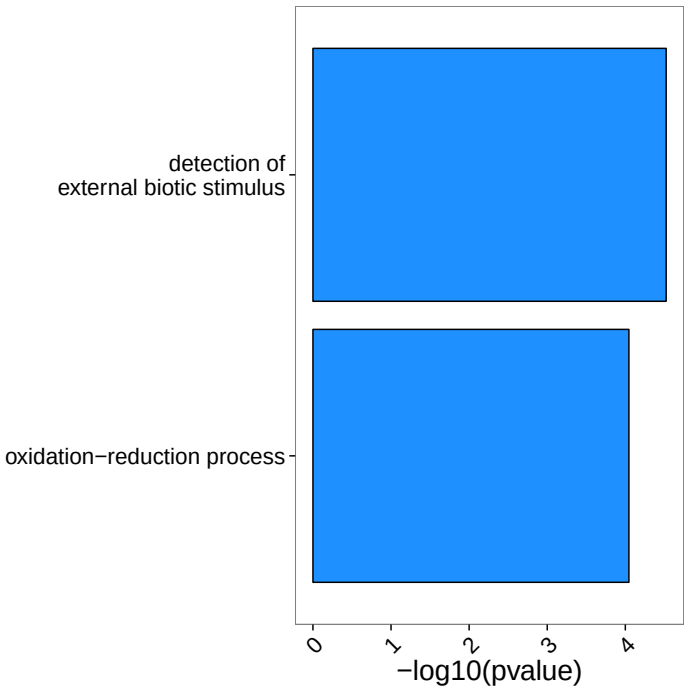



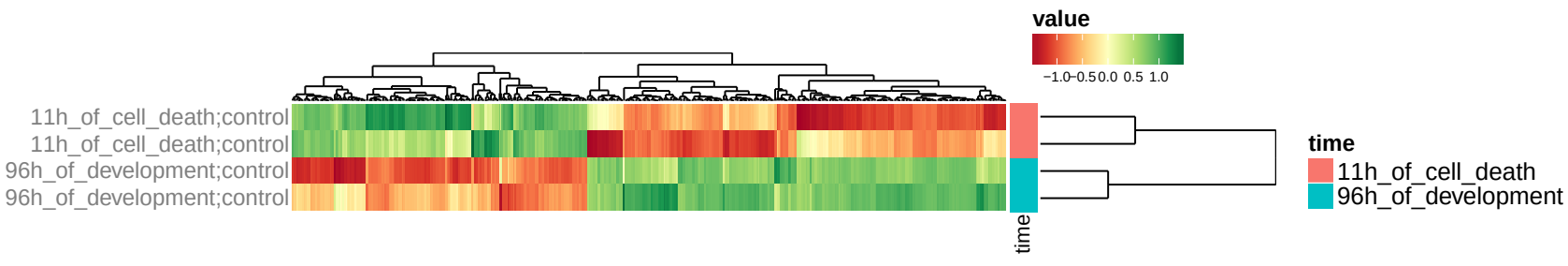
# DEG - **control** VS **treatment** 11h of cell death - ncRNA



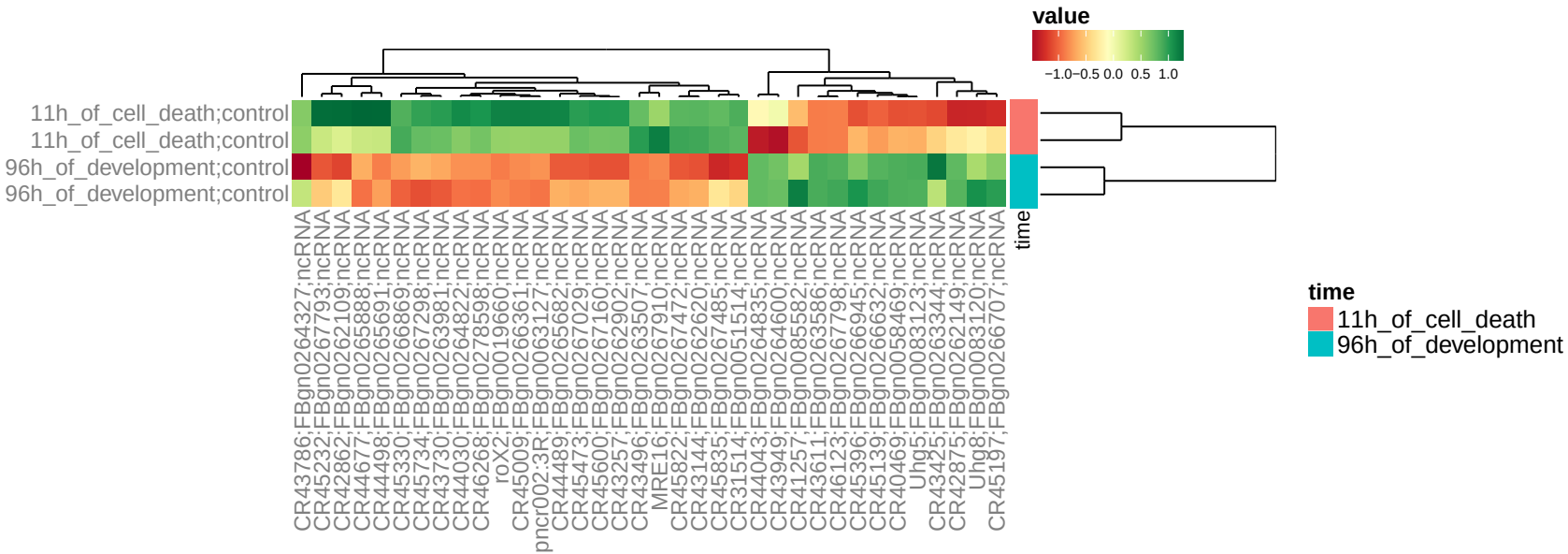
# DEG - control 11h of cell death VS 96h of development - 494 genes



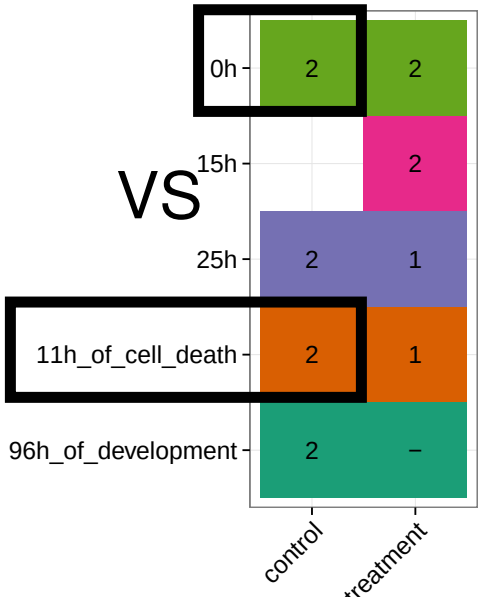



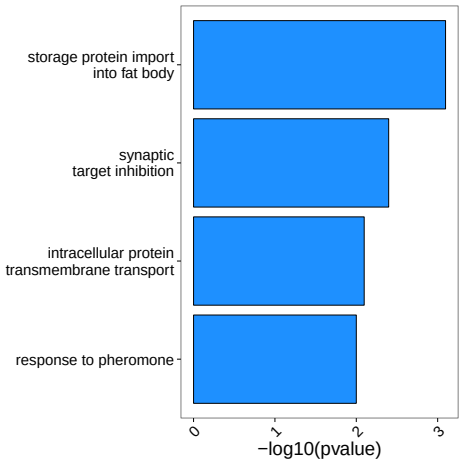



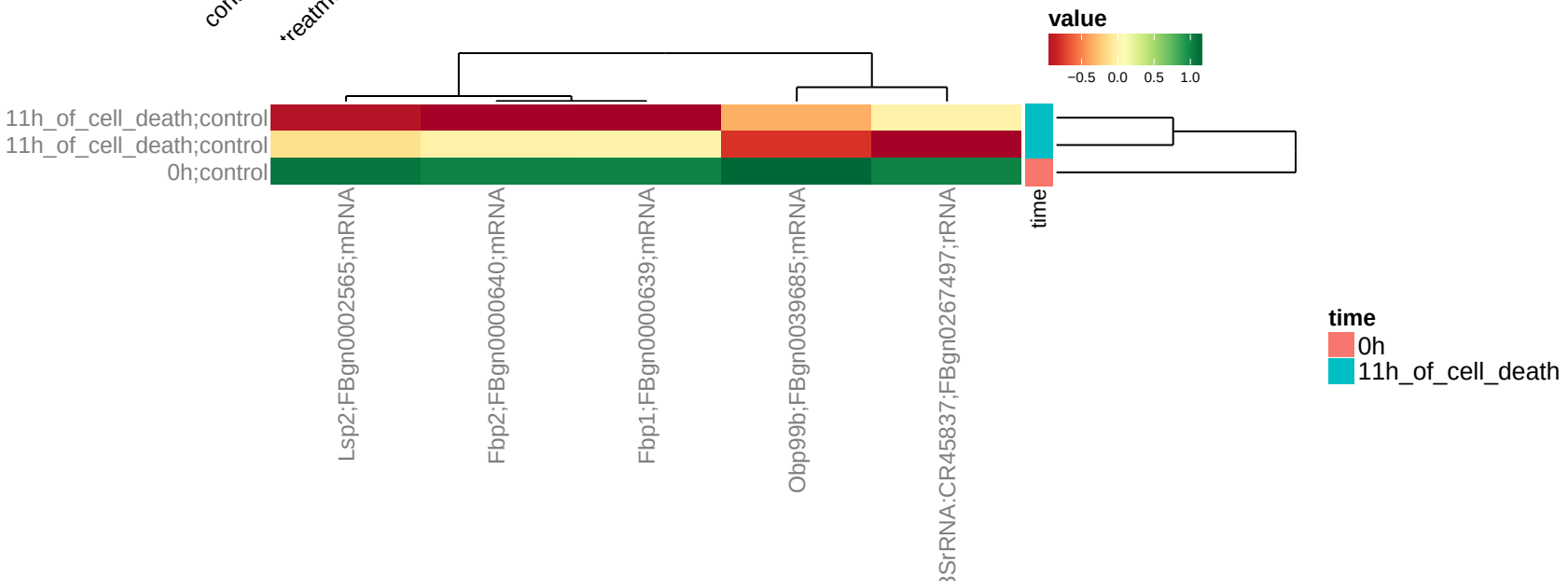
# DEG - control 11h of cell death VS 96h of development - ncRNA



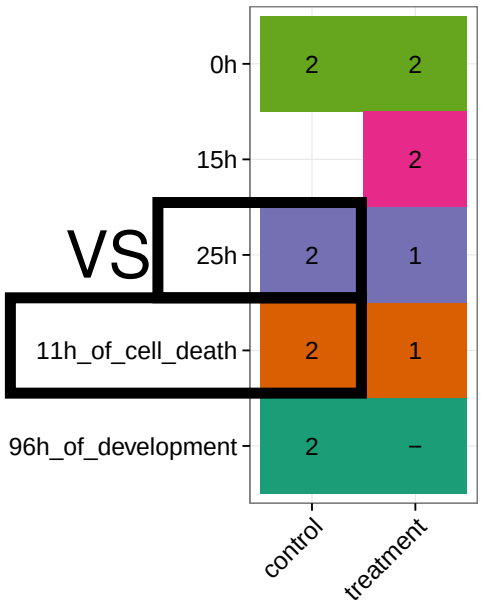
# DEG - control **11h of cell death** VS control **0h** - 5 genes

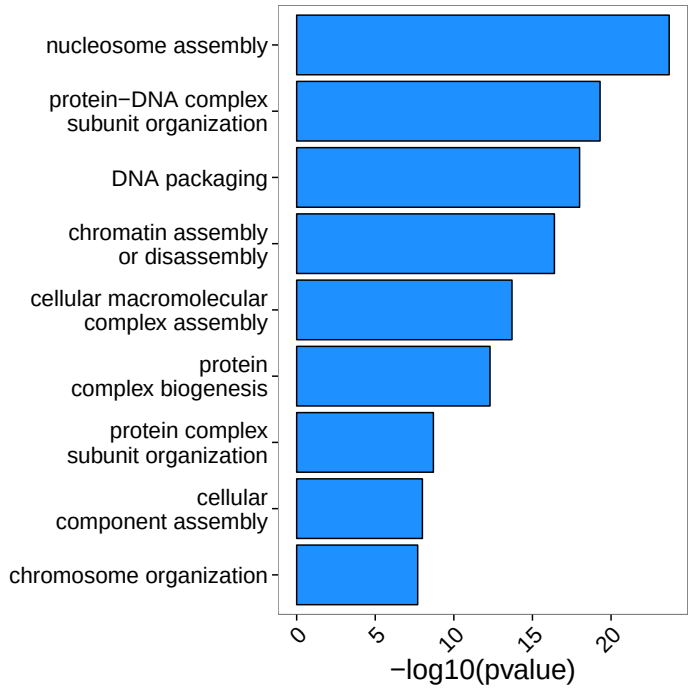


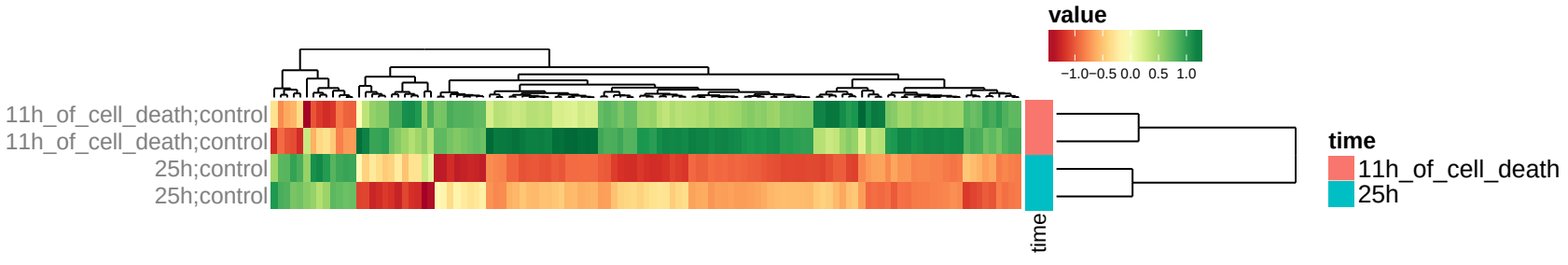



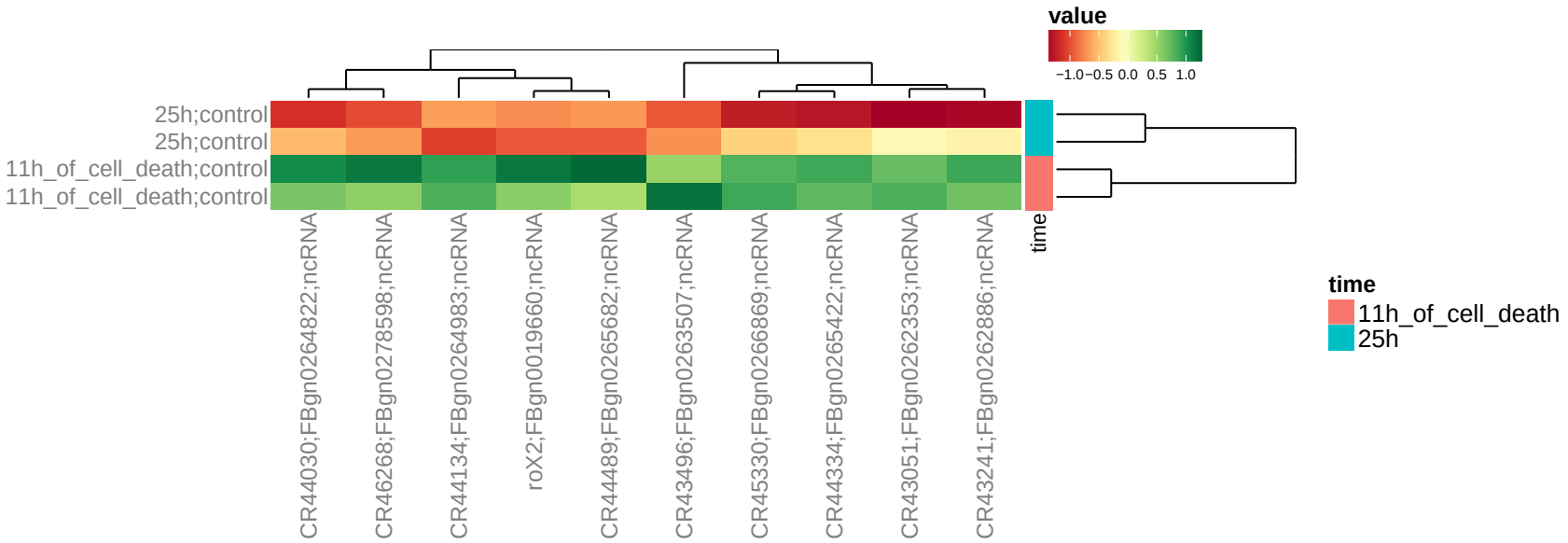
# DEG - control **11h of cell death** VS control **25h** - 116 genes



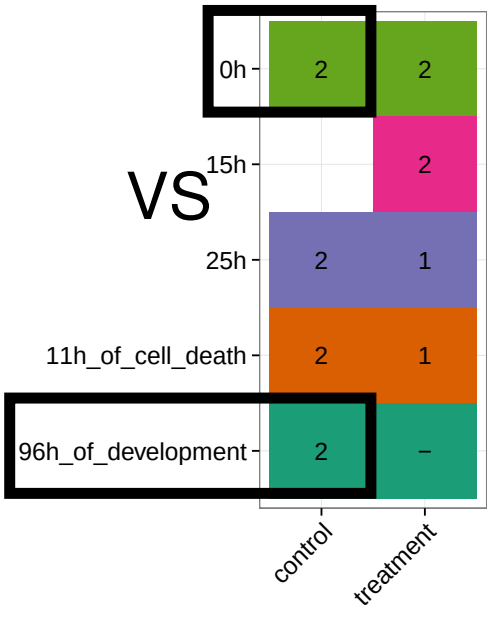



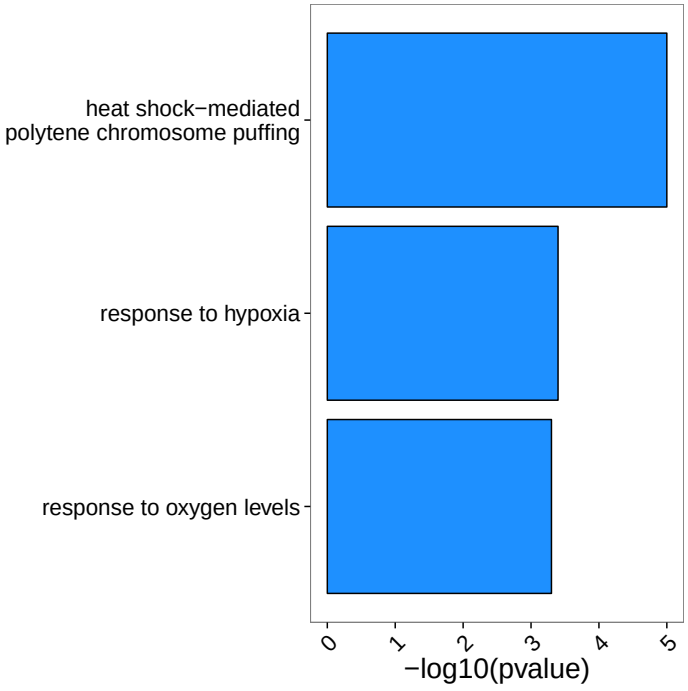



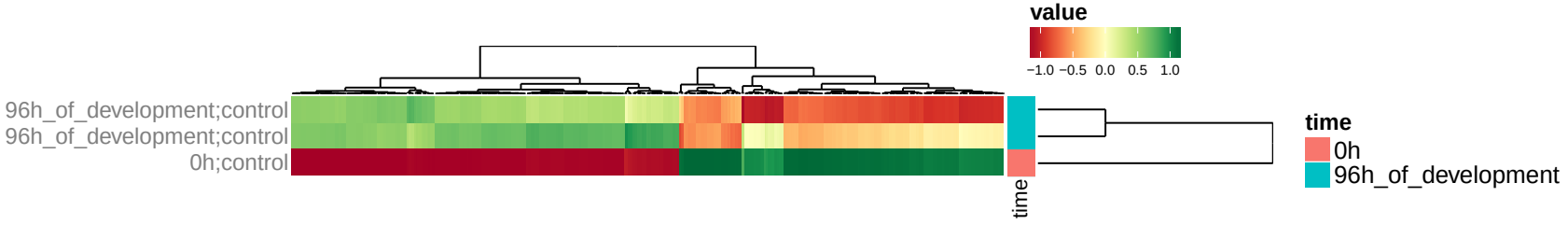
# DEG - control **11h of cell death** VS control **25h** - ncRNA



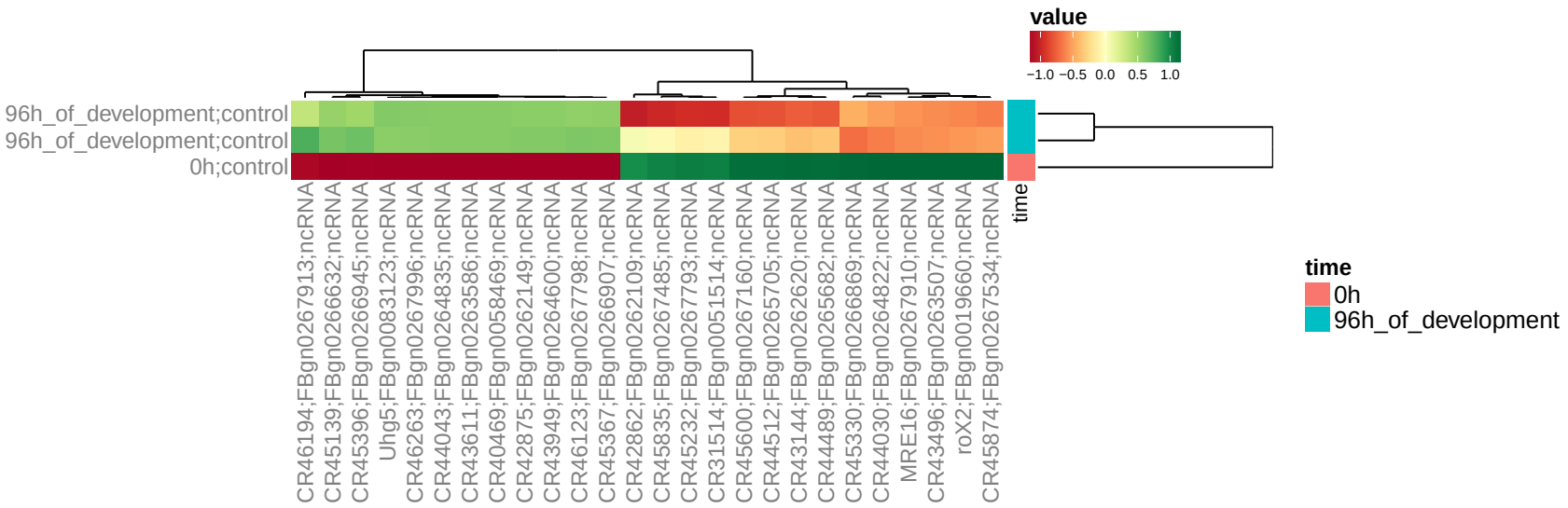
# DEG - control **96h of development** VS control **0h** - 46 genes



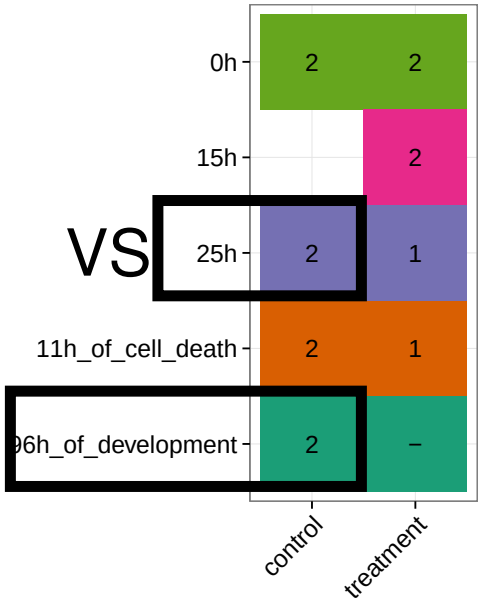



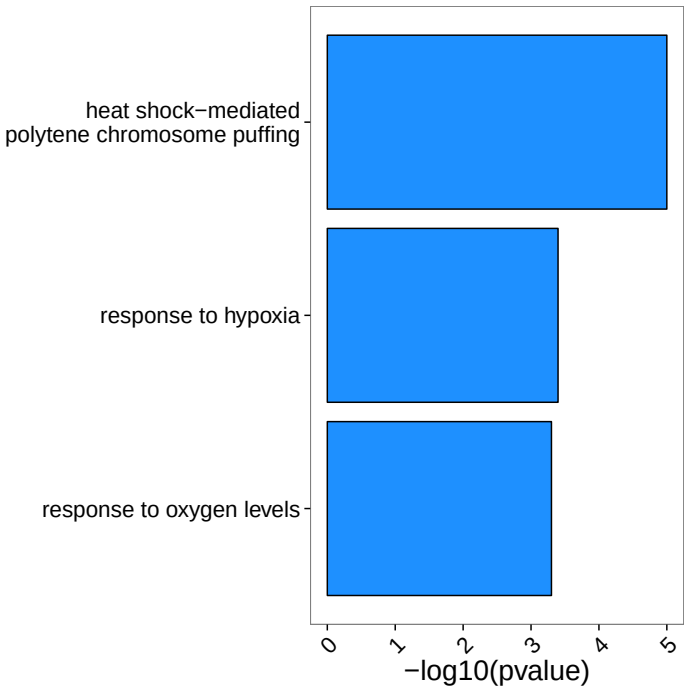



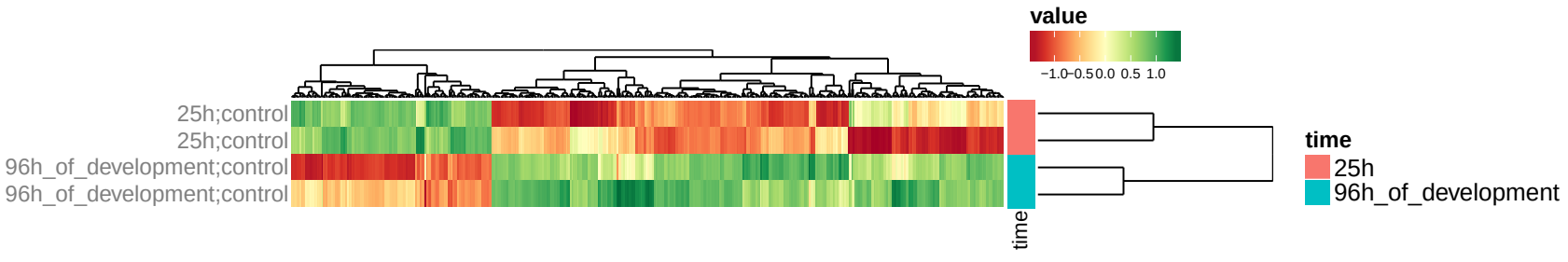
# DEG - control **96h of development** VS control **0h** - 46 genes



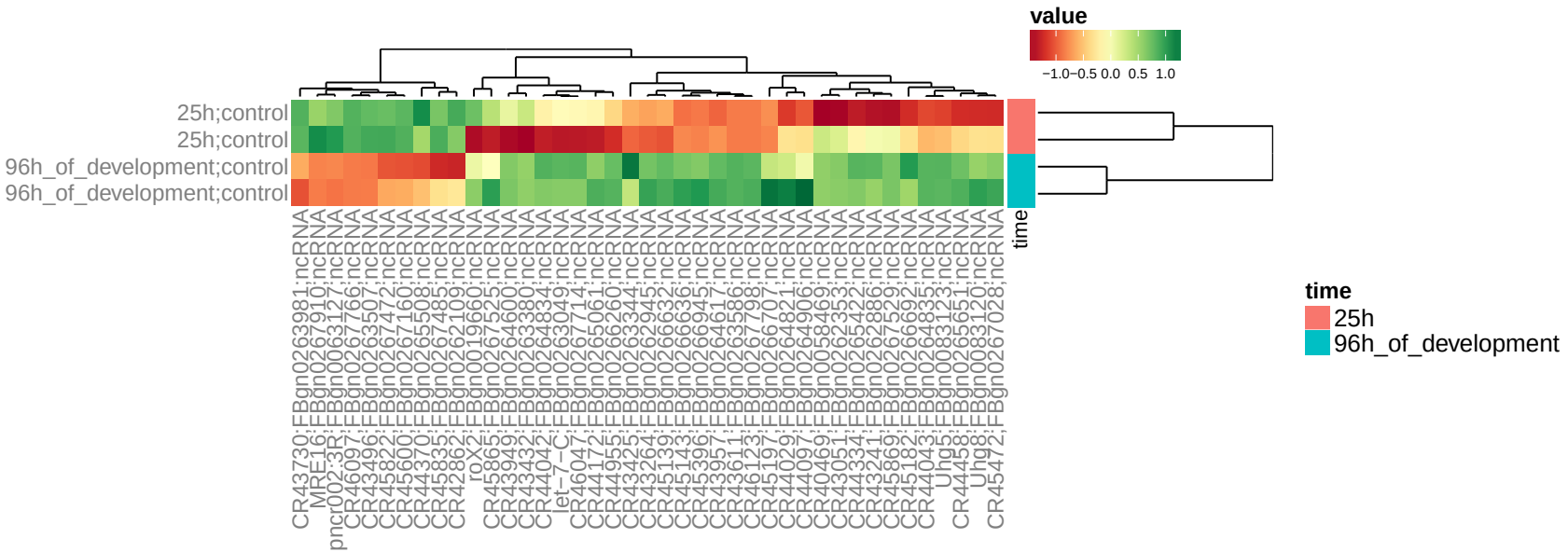
# DEG - control **96h of development** VS control **25h** - 501 genes



# DEG - control **96h of development** VS control **25h** - 501 genes



# Outline

RNAseq samples

Control VS treatment

Control Samples along time

Treatment Samples along time

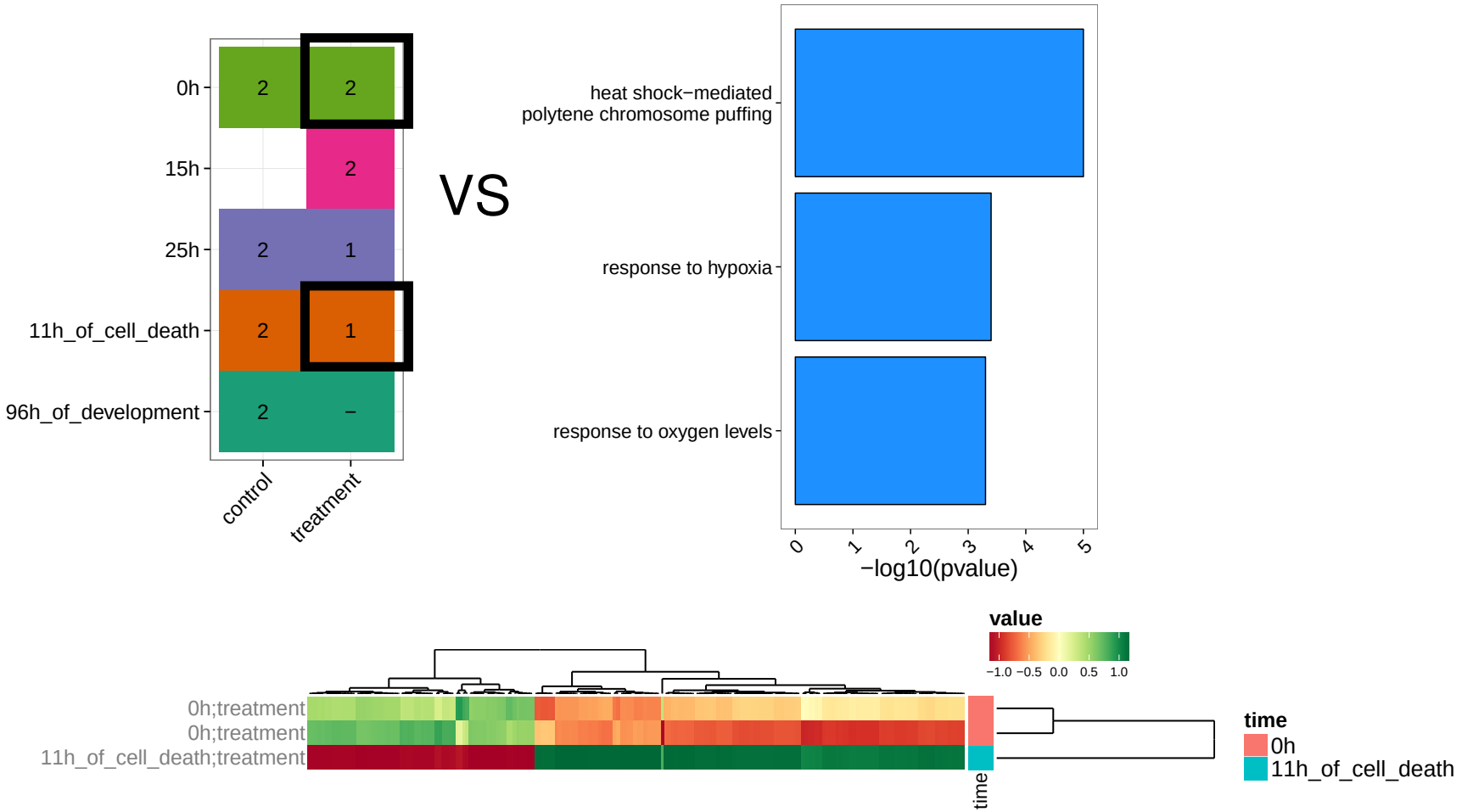
Controls

Treatment

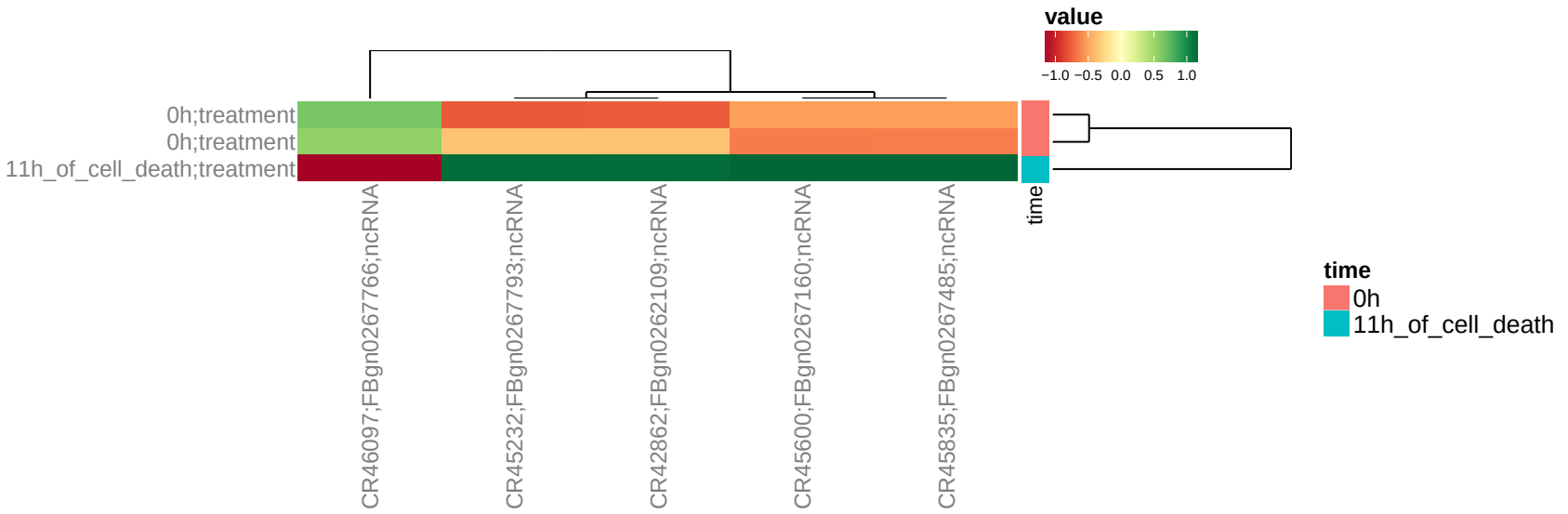
Control genes

ATACseq - mapping stats

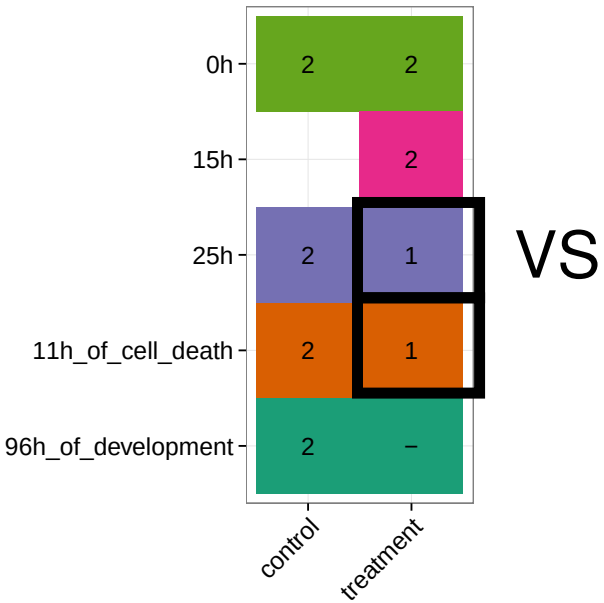
# DEG - treatment **11h of cell death** VS treatment **0h** - 192 genes



# DEG - treatment **11h of cell death** VS treatment **0h** - 192 genes

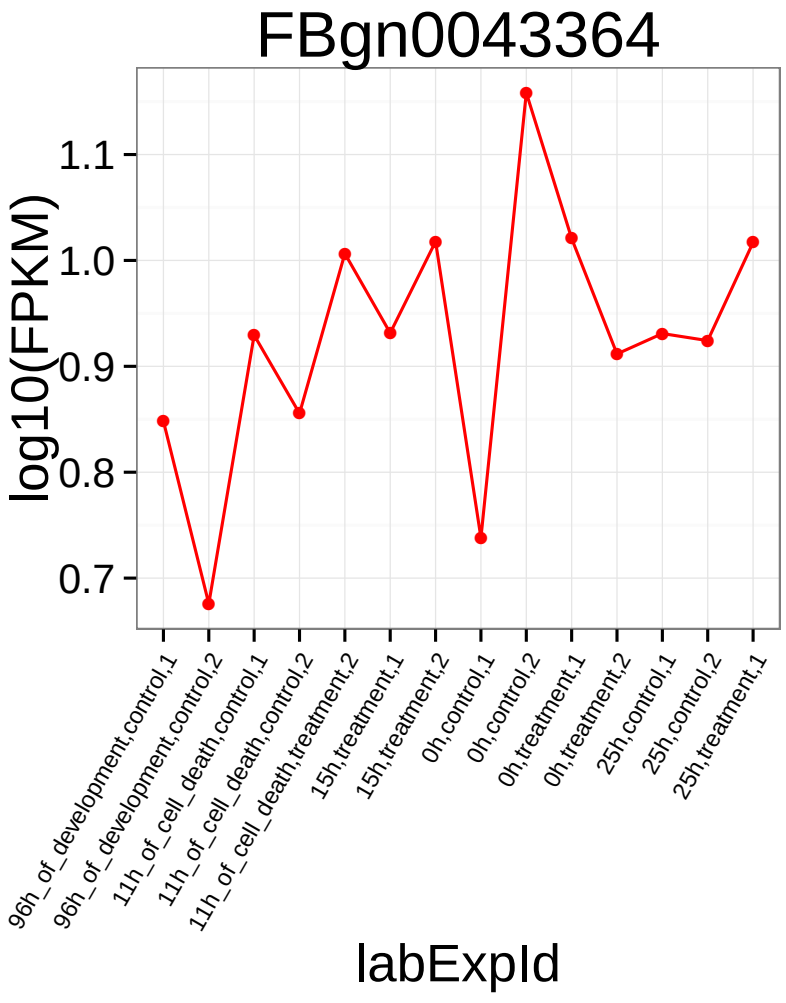


# DEG - treatment **11h of cell death** VS treatment **25h**




Not enough samples

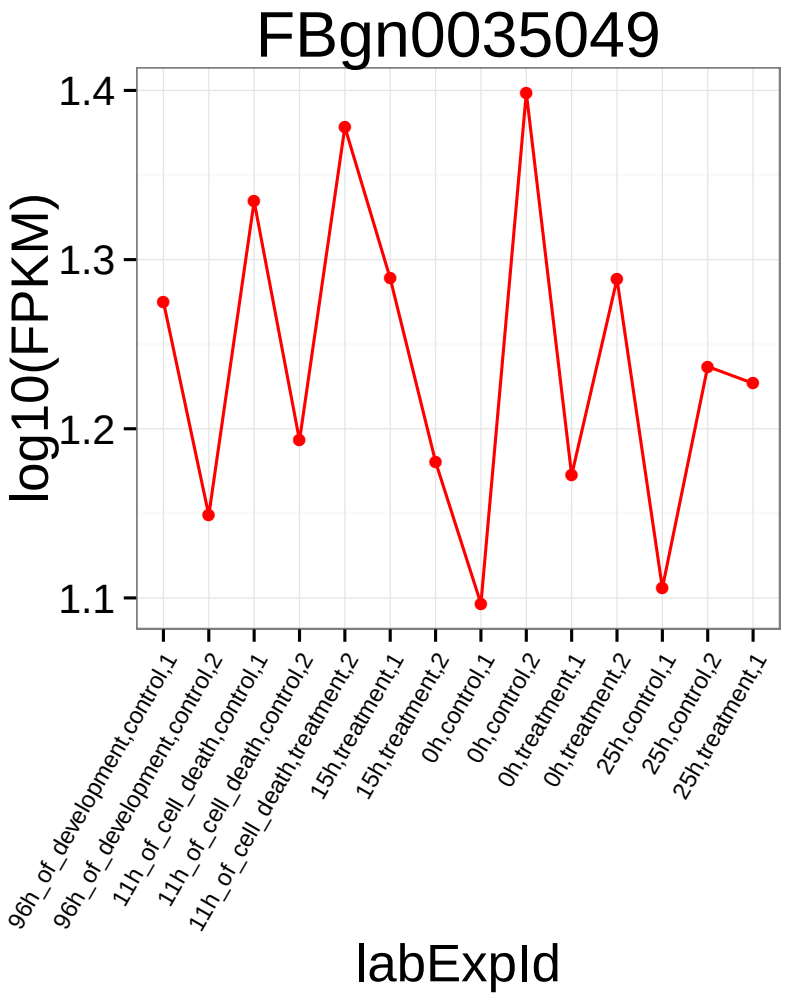
# Control genes - differential expression analysis



# Control genes - differential expression analysis

| gene id | gene name | gene type | DEG | logFC | PValue | FDR |
|---|---|---|---|---|---|---|
| FBgn0043364 | cbt | mRNA | control.fer.cdv | -0.33 | 1.8e-01 | 5.0e-01 |
| FBgn0043364 | cbt | mRNA | control.fer.ser | 0.36 | 3.5e-01 | 1.0e+00 |
| FBgn0043364 | cbt | mRNA | control.fer.slr | -0.25 | 3.8e-01 | 9.3e-01 |
| FBgn0043364 | cbt | mRNA | control.ser.cdv | 0.02 | 9.8e-01 | 1.0e+00 |
| FBgn0043364 | cbt | mRNA | control.ser.slr | 0.11 | 8.0e-01 | 9.7e-01 |
| FBgn0043364 | cbt | mRNA | control.slr.cdv | -0.1 | 6.9e-01 | 8.5e-01 |
| FBgn0043364 | cbt | mRNA | fer | -0.08 | 8.3e-01 | 9.6e-01 |
| FBgn0043364 | cbt | mRNA | ser | 0.28 | 5.8e-01 | 1.0e+00 |
| FBgn0043364 | cbt | mRNA | slr | 0.19 | 5.8e-01 | 8.4e-01 |
| FBgn0043364 | cbt | mRNA | treatment.fer.flr | -0.24 | 6.6e-01 | 1.0e+00 |
| FBgn0043364 | cbt | mRNA | treatment.fer.ser | 0.08 | 8.5e-01 | 9.9e-01 |
| FBgn0043364 | cbt | mRNA | treatment.flr.slr | 0.21 | 7.0e-01 | 1.0e+00 |
| FBgn0043364 | cbt | mRNA | treatment.ser.flr | -0.16 | 7.2e-01 | 1.0e+00 |
| FBgn0043364 | cbt | mRNA | treatment.ser.slr | 0.06 | 8.9e-01 | 1.0e+00 |

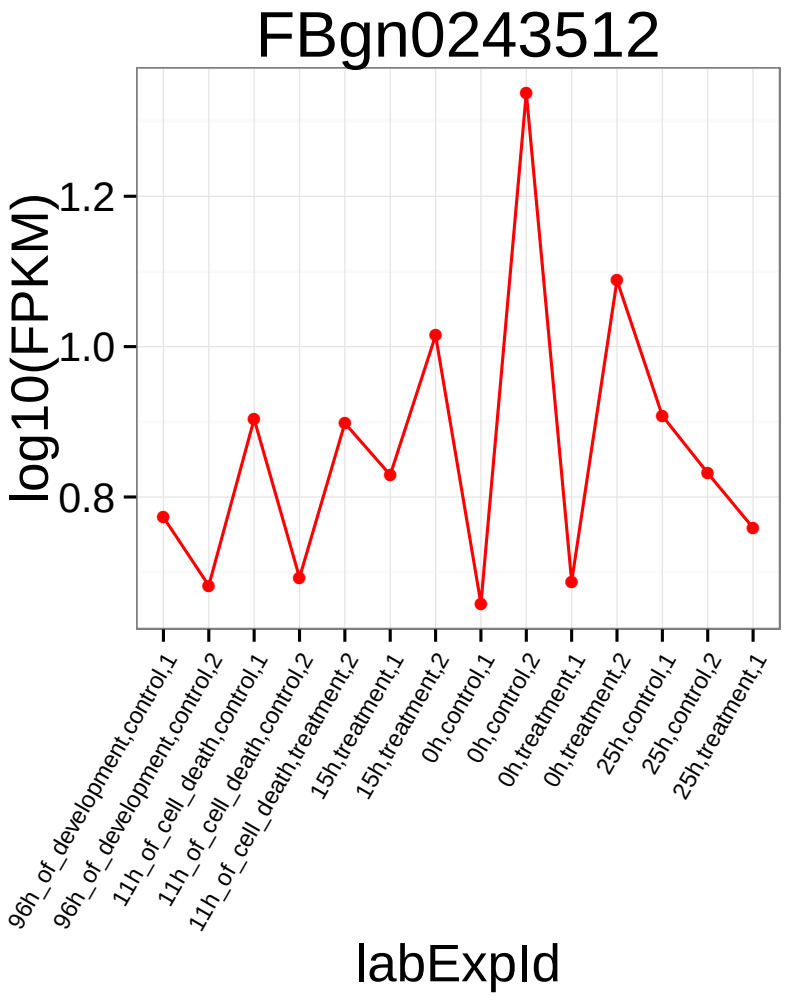
# Control genes - differential expression analysis



# Control genes - differential expression analysis

| gene id | gene name | gene type | DEG | logFC | PValue | FDR |
|---|---|---|---|---|---|---|
| FBgn0035049 | Mmp1 | mRNA | control.fer.cdv | -0.1 | 6.2e-01 | 8.6e-01 |
| FBgn0035049 | Mmp1 | mRNA | control.fer.ser | 0.45 | 1.7e-01 | 1.0e+00 |
| FBgn0035049 | Mmp1 | mRNA | control.fer.slr | -0.62 | 1.2e-02 | 1.9e-01 |
| FBgn0035049 | Mmp1 | mRNA | control.ser.cdv | 0.34 | 1.1e-01 | 3.8e-01 |
| FBgn0035049 | Mmp1 | mRNA | control.ser.slr | -0.18 | 5.1e-01 | 8.8e-01 |
| FBgn0035049 | Mmp1 | mRNA | control.slr.cdv | 0.5 | 8.5e-03 | 5.6e-02 |
| FBgn0035049 | Mmp1 | mRNA | fer | -0.1 | 7.4e-01 | 9.2e-01 |
| FBgn0035049 | Mmp1 | mRNA | ser | 0.03 | 9.5e-01 | 1.0e+00 |
| FBgn0035049 | Mmp1 | mRNA | slr | 0.1 | 6.8e-01 | 8.9e-01 |
| FBgn0035049 | Mmp1 | mRNA | treatment.fer.flr | -0.49 | 4.0e-01 | 1.0e+00 |
| FBgn0035049 | Mmp1 | mRNA | treatment.fer.ser | 0.39 | 2.3e-01 | 6.5e-01 |
| FBgn0035049 | Mmp1 | mRNA | treatment.flr.slr | 0.02 | 9.4e-01 | 1.0e+00 |
| FBgn0035049 | Mmp1 | mRNA | treatment.ser.flr | -0.09 | 8.2e-01 | 1.0e+00 |
| FBgn0035049 | Mmp1 | mRNA | treatment.ser.slr | -0.07 | 8.7e-01 | 9.9e-01 |

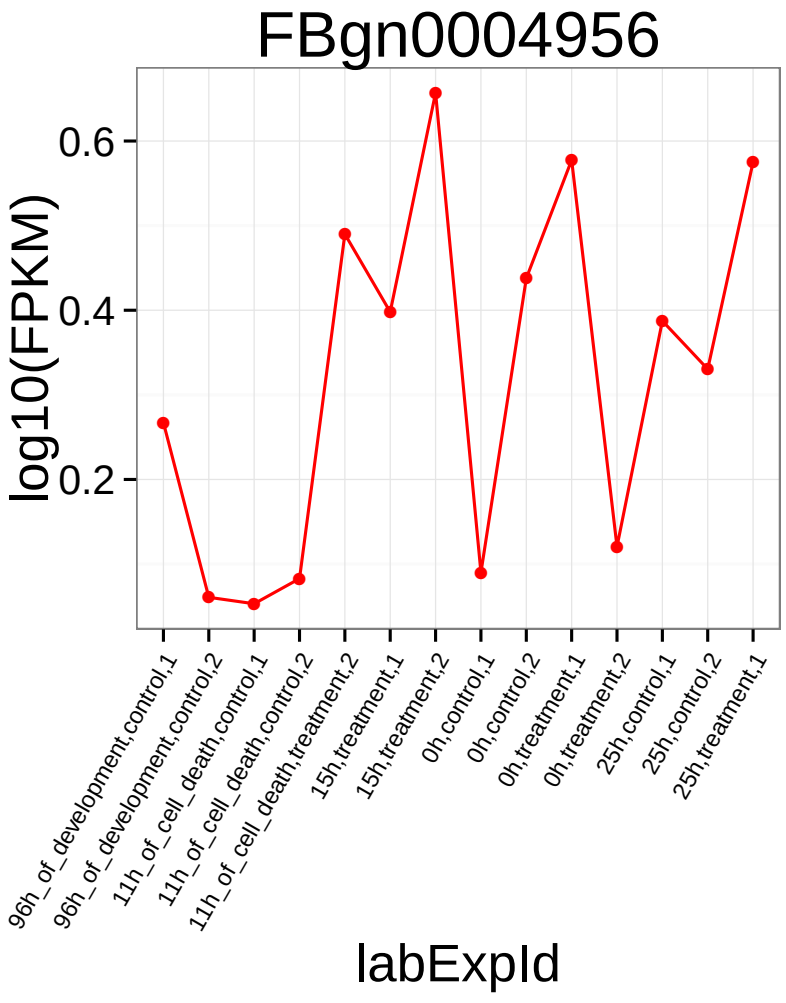
# Control genes - differential expression analysis



# Control genes - differential expression analysis

| gene id | gene name | gene type | DEG | logFC | PValue | FDR |
|---|---|---|---|---|---|---|
| FBgn0243512 | puc | mRNA | control.fer.cdv | -0.2 | 4.2e-01 | 7.4e-01 |
| FBgn0243512 | puc | mRNA | control.fer.ser | 0.34 | 4.0e-01 | 1.0e+00 |
| FBgn0243512 | puc | mRNA | control.fer.slr | -0.13 | 6.6e-01 | 9.8e-01 |
| FBgn0243512 | puc | mRNA | control.ser.cdv | 0.13 | 6.5e-01 | 8.7e-01 |
| FBgn0243512 | puc | mRNA | control.ser.slr | 0.2 | 6.0e-01 | 9.1e-01 |
| FBgn0243512 | puc | mRNA | control.slr.cdv | -0.08 | 7.1e-01 | 8.6e-01 |
| FBgn0243512 | puc | mRNA | fer | -0.12 | 7.6e-01 | 9.3e-01 |
| FBgn0243512 | puc | mRNA | ser | 0.45 | 4.2e-01 | 1.0e+00 |
| FBgn0243512 | puc | mRNA | slr | -0.55 | 1.4e-01 | 4.5e-01 |
| FBgn0243512 | puc | mRNA | treatment.fer.flr | -0.07 | 8.9e-01 | 1.0e+00 |
| FBgn0243512 | puc | mRNA | treatment.fer.ser | -0.15 | 8.0e-01 | 9.8e-01 |
| FBgn0243512 | puc | mRNA | treatment.flr.slr | -0.55 | 4.1e-01 | 1.0e+00 |
| FBgn0243512 | puc | mRNA | treatment.ser.flr | -0.22 | 6.5e-01 | 1.0e+00 |
| FBgn0243512 | puc | mRNA | treatment.ser.slr | -0.75 | 1.7e-01 | 6.8e-01 |

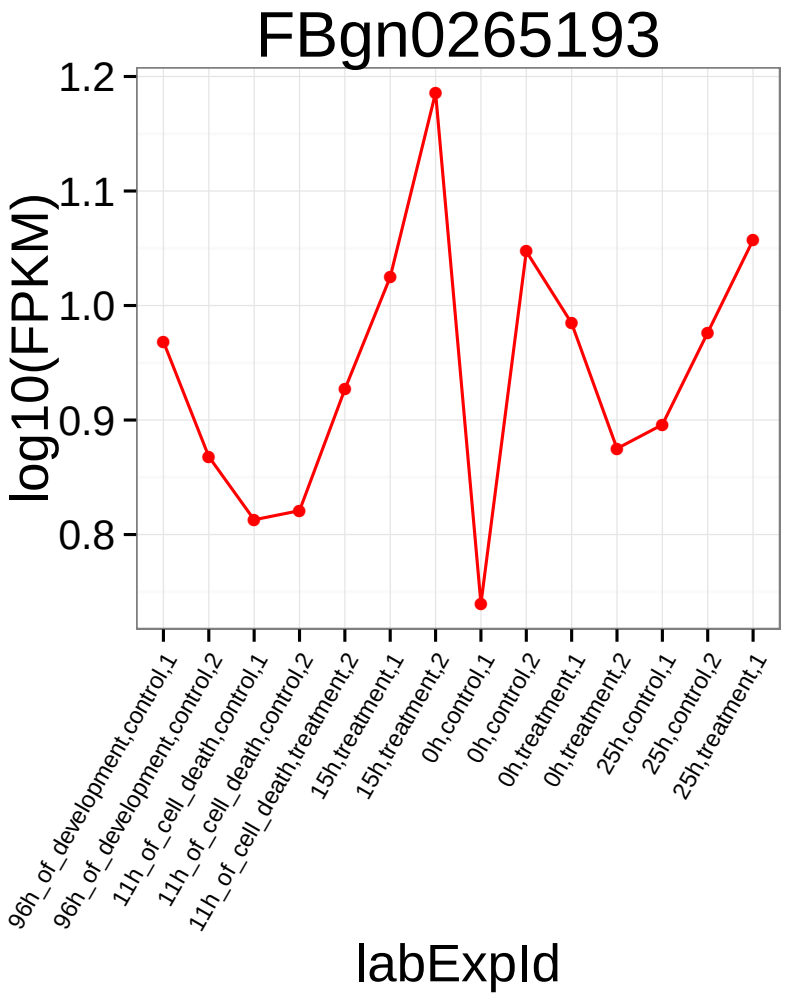
# Control genes - differential expression analysis



# Control genes - differential expression analysis

| gene id | gene name | gene type | DEG | logFC | PValue | FDR |
|---|---|---|---|---|---|---|
| FBgn0004956 | upd1 | mRNA | control.fer.cdv | 0.37 | 3.5e-01 | 6.7e-01 |
| FBgn0004956 | upd1 | mRNA | control.fer.ser | -0.22 | 6.9e-01 | 1.0e+00 |
| FBgn0004956 | upd1 | mRNA | control.fer.slr | 0.6 | 2.0e-01 | 8.1e-01 |
| FBgn0004956 | upd1 | mRNA | control.ser.cdv | 0.14 | 8.1e-01 | 9.5e-01 |
| FBgn0004956 | upd1 | mRNA | control.ser.slr | 0.36 | 5.8e-01 | 9.0e-01 |
| FBgn0004956 | upd1 | mRNA | control.slr.cdv | -0.23 | 5.4e-01 | 7.5e-01 |
| FBgn0004956 | upd1 | mRNA | fer | 0.85 | 1.0e-01 | 3.3e-01 |
| FBgn0004956 | upd1 | mRNA | ser | 0.57 | 5.3e-01 | 1.0e+00 |
| FBgn0004956 | upd1 | mRNA | slr | 0.64 | 2.3e-01 | 5.7e-01 |
| FBgn0004956 | upd1 | mRNA | treatment.fer.flr | 0.13 | 9.2e-01 | 1.0e+00 |
| FBgn0004956 | upd1 | mRNA | treatment.fer.ser | 0.13 | 8.4e-01 | 9.9e-01 |
| FBgn0004956 | upd1 | mRNA | treatment.flr.slr | 0.2 | 7.5e-01 | 1.0e+00 |
| FBgn0004956 | upd1 | mRNA | treatment.ser.flr | 0.25 | 7.0e-01 | 1.0e+00 |
| FBgn0004956 | upd1 | mRNA | treatment.ser.slr | 0.46 | 5.2e-01 | 9.0e-01 |

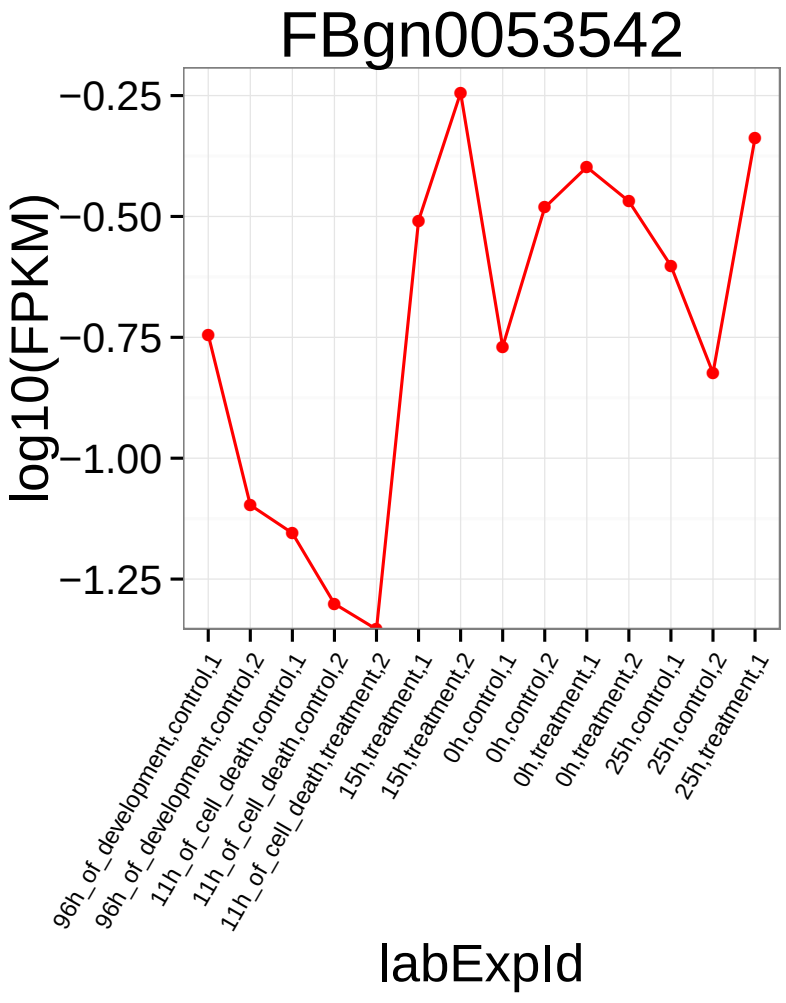
# Control genes - differential expression analysis



# Control genes - differential expression analysis

| gene id | gene name | gene type | DEG | logFC | PValue | FDR |
|---|---|---|---|---|---|---|
| FBgn0265193 | Atf-2 | mRNA | control.fer.cdv | 0.45 | 1.0e-01 | 3.7e-01 |
| FBgn0265193 | Atf-2 | mRNA | control.fer.ser | 0.07 | 9.3e-01 | 1.0e+00 |
| FBgn0265193 | Atf-2 | mRNA | control.fer.slr | 0.06 | 8.9e-01 | 1.0e+00 |
| FBgn0265193 | Atf-2 | mRNA | control.ser.cdv | 0.51 | 1.2e-01 | 3.9e-01 |
| FBgn0265193 | Atf-2 | mRNA | control.ser.slr | 0.12 | 8.7e-01 | 9.9e-01 |
| FBgn0265193 | Atf-2 | mRNA | control.slr.cdv | 0.38 | 1.6e-01 | 3.8e-01 |
| FBgn0265193 | Atf-2 | mRNA | fer | -0.12 | 8.4e-01 | 9.6e-01 |
| FBgn0265193 | Atf-2 | mRNA | ser | 0.16 | 8.2e-01 | 1.0e+00 |
| FBgn0265193 | Atf-2 | mRNA | slr | 0.34 | 4.3e-01 | 7.5e-01 |
| FBgn0265193 | Atf-2 | mRNA | treatment.fer.flr | 0.53 | 4.6e-01 | 1.0e+00 |
| FBgn0265193 | Atf-2 | mRNA | treatment.fer.ser | -0.14 | 8.5e-01 | 9.9e-01 |
| FBgn0265193 | Atf-2 | mRNA | treatment.flr.slr | -0.06 | 9.8e-01 | 1.0e+00 |
| FBgn0265193 | Atf-2 | mRNA | treatment.ser.flr | 0.39 | 4.2e-01 | 1.0e+00 |
| FBgn0265193 | Atf-2 | mRNA | treatment.ser.slr | 0.33 | 5.3e-01 | 9.1e-01 |

# Control genes - differential expression analysis



# Outline

RNAseq samples

Control VS treatment

Control Samples along time

Treatment Samples along time

Controls

Treatment

Control genes

ATACseq - mapping stats

| id | reads | Uniquely mapped reads | % Uniquely mapped reads | mapped multiple loci | % mapped multiple loci | unmapped too short |
|---|---|---|---|---|---|---|
| eye1 | 38,164,421 | 25,859,480 | 67.76% | 1,086,242 | 2.85% | 26.11% |
| eye2 | 39,553,256 | 33,523,739 | 84.76% | 1,422,159 | 3.60% | 7.81% |
| ctrl-96h-1 | 31,165,523 | 23,912,148 | 76.73% | 790,514 | 2.54% | 18.22% |
| ctrl-96h-2 | 42,554,815 | 33,301,213 | 78.25% | 1,940,209 | 4.56% | 13.04% |
| 11h-0h-ctrl-1 | 42,755,866 | 33,232,371 | 77.73% | 996,926 | 2.33% | 17.32% |
| 11h-0h-ctrl-2 | 40,629,916 | 30,849,827 | 75.93% | 1,318,698 | 3.25% | 17.48% |
| 11h-0h-1 | 37,206,314 | 23,521,988 | 63.22% | 2,055,780 | 5.53% | 26.39% |
| 11h-0h-2 | 39,172,203 | 28,179,076 | 71.94% | 1,530,227 | 3.91% | 20.77% |
| 16h-0h-ctrl-1 | 27,229,630 | 23,345,989 | 85.74% | 924,314 | 3.39% | 7.59% |
| 16h-0h-ctrl-2 | 31,163,300 | 24,285,870 | 77.93% | 887,087 | 2.85% | 16.46% |
| 16h-0h-1 | 33,530,934 | 25,385,401 | 75.71% | 985,095 | 2.94% | 18.69% |
| 16h-0h-2 | 39,498,659 | 26,695,941 | 67.59% | 959,131 | 2.43% | 27.88% |
| 16h-15h-ctrl-1 | 33,805,236 | 19,462,562 | 57.57% | 1,109,199 | 3.28% | 35.99% |
| 16h-15h-ctrl-2 | 35,428,731 | 25,439,143 | 71.80% | 1,383,546 | 3.91% | 20.37% |
| 16h-15h-1 | 34,716,712 | 28,706,599 | 82.69% | 1,433,437 | 4.13% | 9.57% |
| 16h-15h-2 | 30,936,937 | 22,732,653 | 73.48% | 952,562 | 3.08% | 20.47% |
| 16h-25h-ctrl-1 | 36,511,208 | 29,609,781 | 81.10% | 1,102,594 | 3.02% | 12.67% |
| 16h-25h-ctrl-2 | 39,248,886 | 30,389,394 | 77.43% | 929,551 | 2.37% | 17.50% |
| 16h-25h-1 | 32,414,365 | 23,552,045 | 72.66% | 1,348,374 | 4.16% | 19.53% |
| 16h-25h-2 | 36,262,439 | 26,846,043 | 74.03% | 1,172,847 | 3.23% | 19.68% |
| wing Marina | 97,722,180 | 83,644,595 | 85.59% | 2,877,021 | 2.94% | 8.20% |
| Aerts et al 2015 | 16,077,656 | 14,138,498 | 87.94% | 537,516 | 3.34% | 4.21% |

# Number of peaks called

| id | extsize | number of peaks |
|---|---|---|
| eye1 | 50 | C8D2LACXX-6-N701-N502-NX-peak-26165 |
| 11h-0h-ctrl-2 | 50 | C8D2LACXX-6-N701-N517-NX-peak-28151 |
| eye2 | 50 | C8D2LACXX-8-N701-N503-NX-peak-27501 |
| ctrl-96h-1 | 50 | C8D2LACXX-8-N706-N504-NX-peak-30739 |
| ctrl-96h-2 | 50 | C8D7CACXX-4-N705-N503-NX-peak-30947 |
| 11h-0h-ctrl-1 | 50 | C8D7CACXX-4-N706-N503-NX-peak-29791 |
| wing Marina | 25 | FCC6YA8ACXX-L6-CHKPEI15020080-peak-39309 |
| Aerts et al 2015 | 25 | SRR1506107-peak-34541 |
| | 100 | SRR1506107-peak-25086 |

# Number of peaks called

| chr | id | number of peaks |
|---|---|---|
| chr2L | eye1 | 4595 |
| chr2L | 11h-0h-ctrl-2 | 4912 |
| chr2L | eye2 | 4883 |
| chr2L | ctrl-96h-1 | 5392 |
| chr2L | ctrl-96h-2 | 5176 |
| chr2L | 11h-0h-ctrl-1 | 5269 |
| chr2R | eye1 | 4888 |
| chr2R | 11h-0h-ctrl-2 | 5305 |
| chr2R | eye2 | 5152 |
| chr2R | ctrl-96h-1 | 5728 |
| chr2R | ctrl-96h-2 | 5653 |
| chr2R | 11h-0h-ctrl-1 | 5696 |
| chr3L | eye1 | 5276 |
| chr3L | 11h-0h-ctrl-2 | 5746 |
| chr3L | eye2 | 5586 |
| chr3L | ctrl-96h-1 | 6252 |
| chr3L | ctrl-96h-2 | 6111 |
| chr3L | 11h-0h-ctrl-1 | 6145 |
| chr3R | eye1 | 5717 |
| chr3R | 11h-0h-ctrl-2 | 6389 |
| chr3R | eye2 | 6173 |
| chr3R | ctrl-96h-1 | 6939 |
| chr3R | ctrl-96h-2 | 6823 |
| chr3R | 11h-0h-ctrl-1 | 6861 |

| chr | id | number of peaks |
|---|---|---|
| chr4 | eye1 | 446 |
| chr4 | 11h-0h-ctrl-2 | 299 |
| chr4 | eye2 | 349 |
| chr4 | ctrl-96h-1 | 279 |
| chr4 | ctrl-96h-2 | 293 |
| chr4 | 11h-0h-ctrl-1 | 338 |
| chrM | eye1 | 13 |
| chrM | 11h-0h-ctrl-2 | 10 |
| chrM | eye2 | 13 |
| chrM | ctrl-96h-1 | 13 |
| chrM | ctrl-96h-2 | 9 |
| chrM | 11h-0h-ctrl-1 | 9 |