

Supplementary figure and table legends

Supplementary methods

A detailed description of all the methods used in this manuscript.

Supplementary discussion

Here we discuss the “transcriptomic ruler” and the validation experiments in more detail. Furthermore the findings in the SPELL database are more elaborately discussed.

Supplementary fig. S1. Expression of all genes.

The expression of all genes during the 44-58 h time-course sorted alphabetically. The lines represent the log₂ ratios with the mean over all time-points. If the expression activity of a gene was measured with multiple probes on the microarrays, multiple lines are shown.

Supplementary fig. S2. Pearson correlation between time-points.

Heat-plot of the Pearson correlations of the expression (log₂ ratios with the mean) between the time points. Remarkably, there is a clear distinction between early- and late-L4. The same analysis carried out per chromosome revealed the same correlations.

Supplementary fig. S3. The k-means clusters.

Twelve individual k-means clusters are shown; in the small boxes the number of the cluster (large numbers) and the number of individual genes in each cluster (small numbers) are shown. The thin white lines represent individual genes; the blue lines indicate the average pattern of all genes in the cluster. The twelve clusters can be divided over six groups: up-regulation (clusters 1, 2, 3 and 4), down-regulation (clusters 5, 6 and 10), down-regulation in early L4 (cluster 7), down regulation in late L4 (cluster 8), no change (cluster 11 and 12) and up-regulation mid-L4 (cluster 9).

Supplementary fig. S4. Overlap and enrichment between the expression pattern clusters found in this paper and in (Kim *et al.* 2013; fig. 2a).

In our paper gene expression during the complete L4 stage was measured, in the Kim *et al.* 2013 paper gene expression from L1 to L4 stage was measured. Cluster numbers 1 to 12 shown at the thick marks. Left or under the cluster number the number of genes in the cluster and a letter indicating the general pattern type; U: up-regulated, D: down regulated, O: oscillating, S: stable (not changing), Capital letters were used when the pattern was stronger compare to the rest of the patterns. The clusters showing up-regulation in this paper (1, 2 and 3) are showing significant overlap with the specifically during L4 up-regulated clusters 8 and 9 from Kim *et al.* 2013. The oscillating clusters (1, 2, 3, 4, 5 and 6) from Kim *et al.* 2013 show significant overlap with clusters showing down-regulation during L4 (5, 6, 7 and 8).

Supplementary fig. S5. Relative expression of *lin-4* (red) and *lin-14*(black) during L4 (44 to 58 hours at 20oC). *Lin-4* shows a steady decrease, which in Kim *et al.* 2013 marks the time just after moulting. *Lin-14* shows some variation in expression possibly a slight increase at the later time points.

Supplementary fig. S6. Physical distance between genes within the same expression cluster.

The distance between the nearest neighbouring gene within the same expression cluster is shown. The grey lines indicate the outcomes of 1,000 permutations, whereas the black line is the actual set of genes. Significant overrepresentation of a distance is shown by a red line at the bottom of the graphs (FDR<0.01).

Supplementary fig. S7. Enrichment analysis on physical location.

Pattern-enrichment analysis on physical location per 100 kb bins and per chromosomal region. (A) Per 100 kb bin we find that all of the clusters are characterized by local enrichment. For example, genes belonging to cluster 1 are overrepresented on chromosome IV at 13.7 Mb, chromosome V at 14.1 Mb and at chromosome X at 3.5 and 11.9 Mb. (B) Enrichment analysis based on the region of the chromosomes (left-tip, left-arm, center, right-arm and right-tip) (Rockman & Kruglyak, 2009). This shows that the two unresponsive clusters both are enriched on the arms of the autosomal chromosomes 7 out of 10 times (FDR<0.05).

Supplementary fig. S8. Dynamic gene expression patterns of all the GO-annotation terms.

Dynamic patterns per gene in log₂ ratio of the mean per GO-annotation term.

Supplementary fig. S9. Dynamic gene expression patterns of all Gene Classes.

Dynamic patterns per gene in log₂ ratio of the mean per Gene class.

Supplementary fig. S10. Dynamic gene expression patterns of all Anatomy terms.

Dynamic patterns per gene in log₂ ratio of the mean per Anatomy term.

Supplementary fig. S11. Dynamic gene expression patterns of all KEGG pathways.

Dynamic patterns per gene in log₂ ratio of the mean per KEGG pathway.

Supplementary fig. S12. Dynamic gene expression patterns of all Protein Domains.

Dynamic patterns per gene in log₂ ratio of the mean per protein domain.

Supplementary fig. S13. Dynamic gene expression patterns of all Wormbook Chapters.

Dynamic patterns per gene in log₂ ratio of the mean per Wormbook chapter (www.wormbook.org).

Supplementary fig. S14. The transcriptomic ruler.

Validation and application of the transcriptomic ruler. (A) The real age of a data point versus the transcriptome age-estimate. The blue dots represent biological replicates on which the ruler was designed and red dots represent an application on a validation experiment. (B) The estimated age of different genotypes on two food sources, *E. coli* and *E. rhapsodica*. The vertical lines represent SE. There is a significant increase in estimated age when *C. elegans* is fed on *E. rhapsodica* (P<0.001). (C) The age after synchronization when the first eggs were laid for different genotypes feeding on different food sources (*E. coli* in yellow and *E.*

rhapontici in green). *C. elegans* lays its eggs significantly later when fed on *E. coli* ($P \ll 0.001$). **(D)** The relative age of recombinant inbred lines in a genetical genomics experiment (Viñuela *et al.* 2010). All lines were profiled at the same absolute age. See also comments for **Supplementary fig. S14E** **(E)** The relative age of recombinant inbred lines in a genetical genomics experiment (Rockman *et al.* 2010). All lines were profiled at the same absolute age. Developmental differences between recombinant inbred lines of a N2 x CB4856 cross were described in (Gutteling *et al.* 2007). This difference in development is reflected in the transcript profiles of these lines. It shows that the transcriptomic ruler can be used to determine the developmental age of each individual line. This can subsequently be used for a better understanding of the results, for example eQTL analysis in contrast with developmental age.

Supplementary fig. S15. Development as a source of variation in SPELL transcript profiles.

All the sample comparisons of the micro-array experiments in the SPELL data base (Hibbs *et al.* 2007) were tested for enrichment of developmental marker genes (cluster 1) in the top 10% up or down regulated genes.

Supplementary table S1. The genes per cluster as found by k-means clustering.
The names of the genes in the 12 k-means clusters.

Supplementary table S2. Enrichment analyses on the k-means clusters.

Outcome of enrichment analyses on the genes in the k-means clusters. Enrichment was tested for gene ontology (GO) terms, gene classes, anatomy terms, KEGG pathway, protein domains and WormBook chapters. Only significantly enriched groups with more than 3 genes overlap are shown.

Supplementary table S3. Number of mutations in gene structures from the million mutation project.

The number of mutations that were used in the analysis on the expression clusters, as extracted from the million mutation project database (Thompson *et al.* 2013).

Supplementary table S4. Number of photographed *C. elegans* individuals per time point.

Time points in hours after synchronisation.

Supplementary table S5. Information about the photographs of individual worms.

Per photograph is given: time point at which it was taken, name of photograph, and category of development that the worm is in.

Supplementary table S6. Method of RNA isolation per sample.

The RNA isolation methods used.

Supplementary Materials and Methods

Nematode strains and population maintenance

Wild type *C. elegans* Bristol N2 was used and maintained at 12°C on Nematode Growth Medium (NGM) with *E. coli* OP50 as a food source (Lewis, J. A. & Fleming 1995). In two experiments (timing of egg laying and transcriptomics of strains grown on different food sources), other strains were used next to N2, namely: CB4856, JU1581, JU1921, JU1930, JU1932, JU1944, and JU1949 (Volkers *et al.* 2013).

Analysis of morphological changes

After synchronisation by bleaching, pictures of individual worms were taken between 48 and 67 hours of growth at 20°C with an AxioCam MRc5 (Carl Zeiss Microscopy GmbH, Jena, Germany) mounted on a light microscope (100x magnification), with Axiovision software, version 4.8 (Carl Zeiss Microscopy). The pictures were taken in black and white, 1292x968 pixels; post-imaging sharpening with a strength of 0.5 was used. Ten nematodes per patch were placed onto 3% agarose patches on microscope glass slides. The glass slides were put on ice for 5 minutes to slow down movement of the nematodes. Per time point, 15 – 59 larvae were photographed see Supplementary table S4. The pictures are available upon request.

The pictures were scored for morphological changes in *C. elegans* between 48 and 67 hours after synchronisation. Development was divided into five stages: no vulva, developing vulva (vulval groove absent), fully developed vulva (vulval groove present), eggs in uterus, and eggs in uterus with developing oocytes visible. Each individual worm was categorized into one of these developmental categories (see Supplementary table S5 for information about the category that each individual worm was placed into. Because the distinction between the categories 'eggs in uterus' and 'developing oocytes visible' could not always be made reliably, these categories were joined in later analyses.)

Timing of egg laying

After synchronisation by bleaching, the eggs were left to hatch in 1 ml M9 at 20°C overnight. Larvae were then deposited on NGM with either *E. coli* OP50 or *Erwinia rhapontici* (Volkers *et al.* 2013) and cultured at 20°C. Starting from 46 hours after they were placed on NGM they were checked every hour for the first eggs to appear on the plates. After the first eggs were observed the plates were followed several hours to ensure egg laying fully started. Per bacterial food source 17 biological replicate populations were used (2 to 3 per genotype).

Worm culturing for transcriptome analysis

For the mRNA microarrays of N2, populations of hermaphrodites grown on *E. coli* OP50 were used. Up to three independent replicates per time point were used to generate the transcription patterns during development. The populations were stage synchronized by bleaching and the eggs were placed on NGM-plates and incubated at 20°C for 41.5, 42, 43, 44, 45, 46, 47, 48, 49, 50, 51, 52, 53, 54, 55, 56, 58, 60.5, 62 or 64 hours. After harvesting the larvae, they were flash frozen in liquid nitrogen and stored at -80°C. For the mRNA microarrays of different genotypes on either *E. coli* OP50 or *E. rhapontici*, synchronized hermaphrodites were grown for 48 hours (L4 stage) before harvesting and flash freezing in liquid nitrogen.

RNA isolation

For mRNA isolation of the samples, two different methods were used, see Supplementary table S6 for all method-, sample- and replicate information. The first method used an RNEasy Micro Kit from Qiagen (Hilden, Germany), following the 'Purification of Total RNA from Animal and Human Tissues' -protocol provided with the kit, with modified lysing procedure. The frozen pellets were lysed in 150 μ l RLT buffer, 295 μ l RNase-free water, 800 μ g/ml proteinase K and 1% β -mercaptoethanol. This suspension was incubated in a Thermomixer (Eppendorf, Hamburg, Germany) at 55°C and 1200 rpm for one hour or until the sample was clear. To the lysate 0.5 volume of 96% ethanol was added. The second method used a Maxwell® 16 AS2000 instrument with a Maxwell® 16 LEV simplyRNA Tissue Kit (both Promega Corporation, Madison, WI, USA). The mRNA isolation was preceded by a modified lysis step. In short, 200 μ l homogenization buffer, 200 μ l lysis buffer and 10 μ l of a 20 mg/ml stock solution of proteinase K were added to each sample. The samples were then incubated for 10 minutes at 65°C, 1000 rpm in a Thermomixer (Eppendorf, Hamburg, Germany). After cooling on ice for 1 minute, the samples were pipetted into the cartridges and the standard protocol for this Maxwell® kit was followed.

Microarray sample preparation, scanning and normalization

After mRNA isolation, the 'Two-Color Microarray-Based Gene Expression Analysis; Low Input Quick Amp Labeling' -protocol, version 6.0 from Agilent (Agilent Technologies, Santa Clara, CA, USA) was followed, starting from step 5. The microarrays used were *C. elegans* (V2) Gene Expression Microarray 4X44K slides, manufactured by Agilent. The microarrays were scanned using an Agilent High Resolution C Scanner, using the settings as recommended in the above mentioned manual. Data was extracted with the Agilent Feature Extraction Software version 10.5, following manufacturers' guidelines.

For normalization the Limma package for the "R" environment (version 2.13.1 x64) was used. No background correction of the RNA-array data was performed as recommended by (Zahurak *et al.* 2007). For within-array normalization of the RNA-array data the Loess method was used and for between-array normalization the Quantile method was used. The obtained log₂ normalized intensities (single channel data) were used for further analysis.

Statistical analysis of developmental effects

All statistical analyses were carried out in "R" (version 2.13.1 x64). The intensities were batch corrected by calculating the batch effect per gene and subtracting the effect from the above mentioned log₂ normalized intensities. The batch effect was calculated by a linear model taking the factor 'time' into account

$$I_{x,y} \sim B_y + T_x$$

where I is the intensity of gene x in batch y, B is the batch and T is time.

Further analysis were done on the log₂ ratios of the batch corrected intensities of individual time points with the mean intensity of all time points per spot. These were calculated by

$$R_x = \log_2(I_x/\bar{I})$$

where R is the log₂ ratio of time point x and I is the normalized intensity measured on the microarray. From now on called “the log₂ ratios with the mean”.

To find major sources of variation a principal component analysis (PCA) was performed on the log₂ ratios with the mean.

The overall activity of genomic regions was studied by dividing the chromosomes into 100 kb bins and take the average the log₂ ratios with the mean for the genes per bin per time point.

Gene expression clusters were determined by the K-means clustering method, 20 iterations on 10 different starting situations were performed, at a setting of 12 different clusters. As input the log₂ ratios with the mean was used.

Enrichments

Enrichment studies were done using a hyper-geometric test. Release WS220 of the GO-, Anatomy-, Protein Domains- and Gene Class- annotations, release 65.0 of the KEGG database, and the Wormbook (www.wormbook.org) version of 2012 were used. For determining the false discovery rate of the enrichment studies on the bins (genetic loci) of the K-means clusters a 1000 permutations were done per cluster. Using equally sized randomly picked sets of genes. P-values were scaled according to the false discovery rate found by the permutations. Only loci containing >2 genes of the same Kmeans clusters were considered.

Physical distance of K-means cluster genes

The physical distance from one gene to the closest neighbour-gene within the same K-means cluster was measured as the distance from start-site to start-site. The obtained distances were counted in bins of 1kb and the results presented as the percentage of genes per cluster per bin. To assess the significance of findings, a permutation analysis was done; testing 1000 equally sized random sets of genes in the same way.

Mutation frequency of k-means cluster genes

The mutation frequency of the genes per k-means cluster was tested on the datasets of the million mutation project (Thompson *et al.* 2013), for the induced and the wild-type mutations (<http://genome.sfu.ca/mmp/>). The frequency of mutations per gene was counted per 1 kb, the intron and coding sequence sizes were obtained from WS220 (www.wormbase.org). To determine the relative abundance of mutations, a permutation analysis was done testing the number of mutations found in a random set of equal size. To determine the significance of the mutation frequency found per k-means cluster 1000 permutations were executed.

Heat-maps and clustering

Heat-maps of the log₂ ratios with the mean of all GO-terms, anatomy-terms, gene classes, KEGG, protein domains and Wormbook chapters were made and clustering was performed by the default settings of the “heatmap” function in the “R” environment.

Age estimation by transcription profiles

Linear regression in which the ratio with the mean was regressed over time was used to determine which genes had a significant in- or decrease during L4 development. The samples from time point 44 unto 58 hours (Supplementary table S6) were used to determine the slope of the linear in- or decrease per spot by linear regression. The

effects of the spots/genes above the significance threshold ($-\log_{10}(p) > 6$ for conservative settings (782 spots or 596 genes) or 4 (4268 spots or 2836 genes) to have more spots/genes as input for the age estimation) could then be used to determine the age of samples which' transcript profile was measured. We used spots when the same microarray design was used or genes in case of a different design. This was done for each spot/gene above the threshold and the average was taken as the estimated age. [Age \sim effect* gene expression level]. This was used on the samples used to determine the effect originally, on the samples used to test the age estimation, and used on the samples grown on the two different bacterial food-sources.

Determining the effect of development in the SPELL dataset experiments

The effect of development in the SPELL (<http://spell.caltech.edu:3000>; Hibbs *et al.* 2007) experiments was determined by transforming each experiment into a set of ratios. When not in ratios downloaded from the SPELL website, the log₂ ratio per spot was calculated with the mean. With these ratios it was determined whether the top 10% of genes with the lowest or highest ratios were enriched for the 115 genes in cluster 1 (Supplementary table S1). To calculate enrichment a hypergeometric test was used.

Development was considered to play a role in the variation in gene expression between the samples from an experiment stored in SPELL when $> 25\%$ of the samples showed a significant enrichment above the threshold ($-\log_{10}(p) > 6$). The data from Coolon *et al.* (2009) was averaged per bacterial food comparison per spot and tested for developmental differences with the method described above.

Supplementary Discussion | The transcriptome as genetic ruler

Age estimation by transcription profiles

The transcription profiles allow for age estimation of worms (**Supplementary fig. S14a**). The genetic ruler consisting of 782 spots (596 genes) with a significant ($\log_{10}(p) > 6$) linear up or down regulation during the time period from 44 to 58 hours were used. The blue dots in **Supplementary fig. S14a** represent these samples and they lie on an almost perfect straight line ($R^2 = 0.97$), as expected. Using genes with a less significant linear effect ($-\log_{10}(p) > 4$, 4268 spots, 2836 genes) works equally well (not shown). A second batch of samples, not included in constructing the ruler, was used to identify the accuracy of the age estimators (red dots in **Supplementary fig. S14a**). These samples lie on the same line, meaning that their age can be estimated accurately, especially when the samples fall within the time range that was used to calculate the straight line. Outside the original time range the estimation was less accurate, however the early samples (around 43h) were still estimated much younger than the older samples (around 62 hours). This shows that within a certain time frame transcription profiles can be used to precisely estimate the age of a worm sample. More important, this experiment shows that age estimation by transcription profile is a necessity as expression levels of hundreds (if not thousands) of genes change significantly within two hours or less (**Fig. 2 & Supplementary fig. S3**).

Age estimation in different genotypes and environments

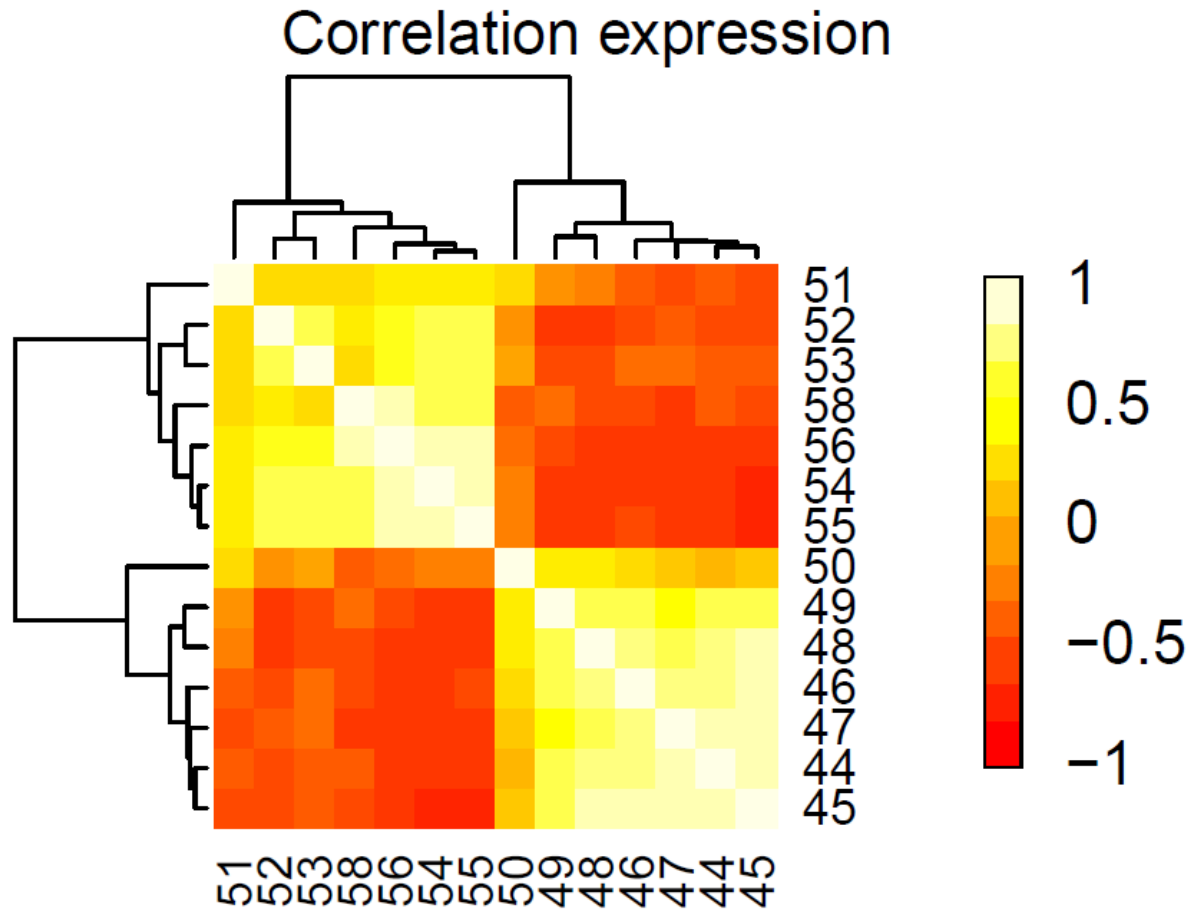
To validate the transcriptomic ruler further, we show the performance on multiple genotypes raised on different food-sources (environments). We find that environmental parameters can have an effect on development that is visible in microarray results. We used the canonical strain N2, the frequently used lab strain CB4856 and freshly isolated strains from Orsay (JU1581, JU1944 and JU1949) and Santeuil (JU1921, JU1930 and JU1932) (Volkers et al. 2013). As food source we used the standard lab food *E.coli* OP50 and the Gram-negative plant pathogen *Erwinia rhapontici* (Volkers et al. 2013).

First, we investigated if a difference in development could be detected by eye, by measuring the time between synchronization and the start of egg laying. Worms fed with *E. coli* and grown at 20°C on average started laying eggs 51.3 hours after synchronization, while worms grown on *E. rhapontici* were faster (49.3 hours) (**Supplementary fig. S14c**). This difference was highly significant ($p < 0.001$). Next, the transcription profiles of the same strains grown on the same two bacteria were determined at exactly 48 hours after synchronization. The age of the worms was estimated as described before and most strains grown on *E. coli* were estimated to be 48 hours of age (47-49.5 hours; **Supplementary fig. S12b**). After feeding on *E. rhapontici* all lines had a transcriptional profile that estimated them a few hours older than the 48 hours of development on *E. coli* (49 -52 hours, 51 hours on average **Supplementary fig. S12b**). This difference also was significant ($p < 0.001$). The differences in developmental timing of worms grown on *E. coli* compared to *E. rhapontici* are remarkably similar in both experiments. This is not only the case on average: for example, the strain with the youngest estimated age (transcript profile), JU1930, was the strains with the longest time between synchronization and start of egg laying (**Supplementary fig. S12b & c**). A linear relationship between the estimated age by transcript profile and the start of egg laying was found. The start of egg laying can be significantly explained by the estimated age (**Fig. 4b**; $R^2=0.63$, $p < 0.001$) which shows that under these conditions *C. elegans* develops faster on *E.*

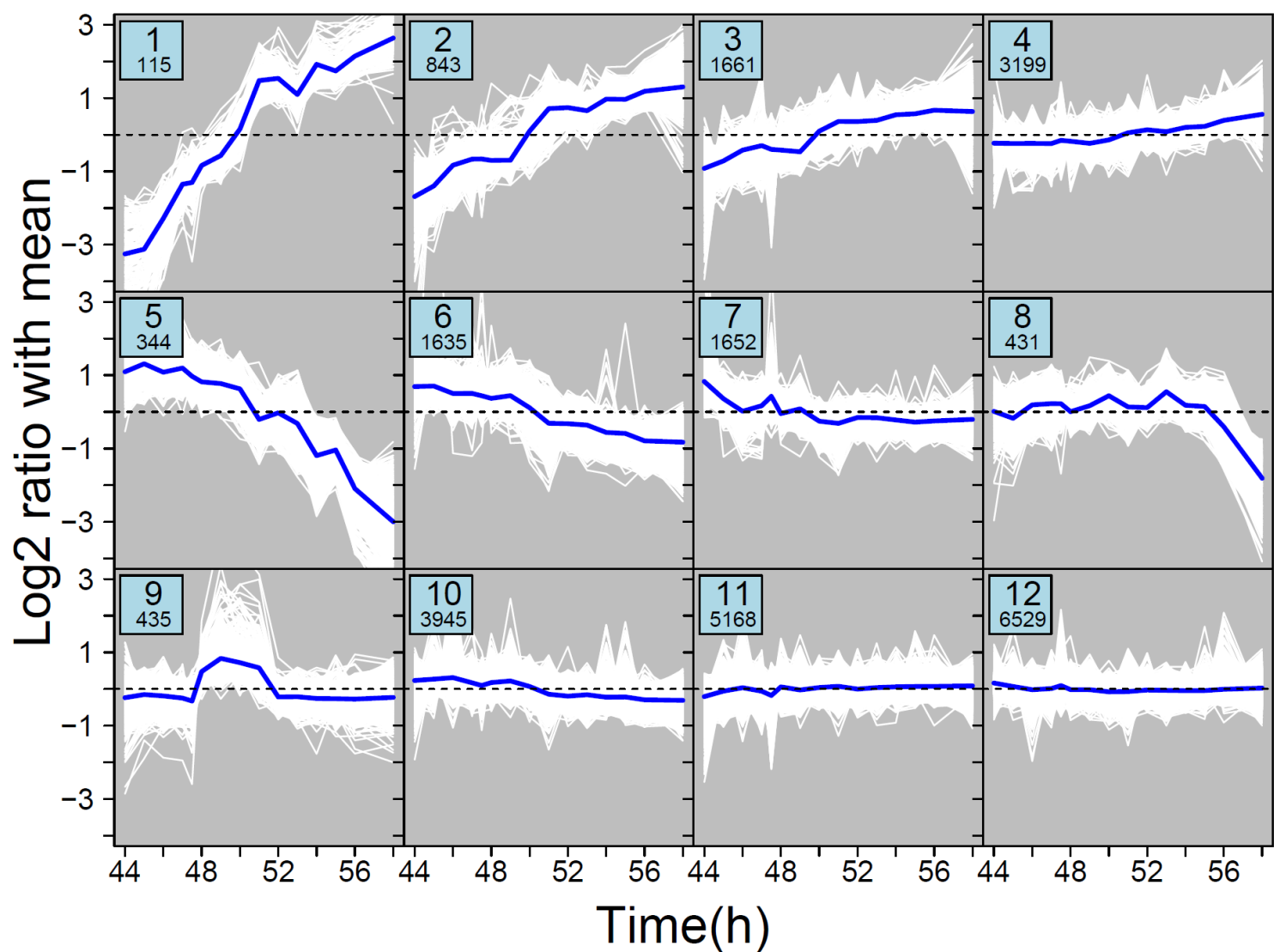
rhapontici than on *E. coli* OP50. More important, it is now shown that developmental differences as small as only 2 hours can be visible in transcriptomics results, while remaining invisible by most optical assessments.

Application of the data to genetical genomics experiments

The effect of the genetic background on development and subsequent gene expression differences could be found in experiments using recombinant inbred lines or different genotypes (Li et al., 2006; Li et al., 2010; Rockman et al., 2010; Viñuela et al., 2010; Viñuela et al., 2012). To illustrate this, the age estimations of an experiment with age as a variable is shown (**Supplementary fig. S12d & e**). This provides interesting opportunities for re-mapping the expression quantitative trait loci (eQTLs) found in these studies, taking in account the dynamics of expression. Or, alternatively, correct samples for their transcriptomic age-bias and find more specific eQTLs influenced by the actual experimental variation.

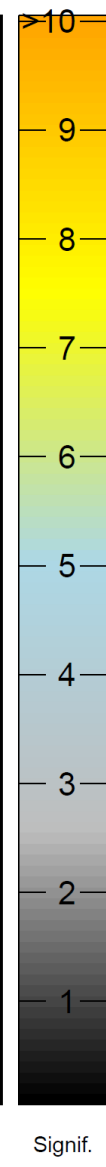
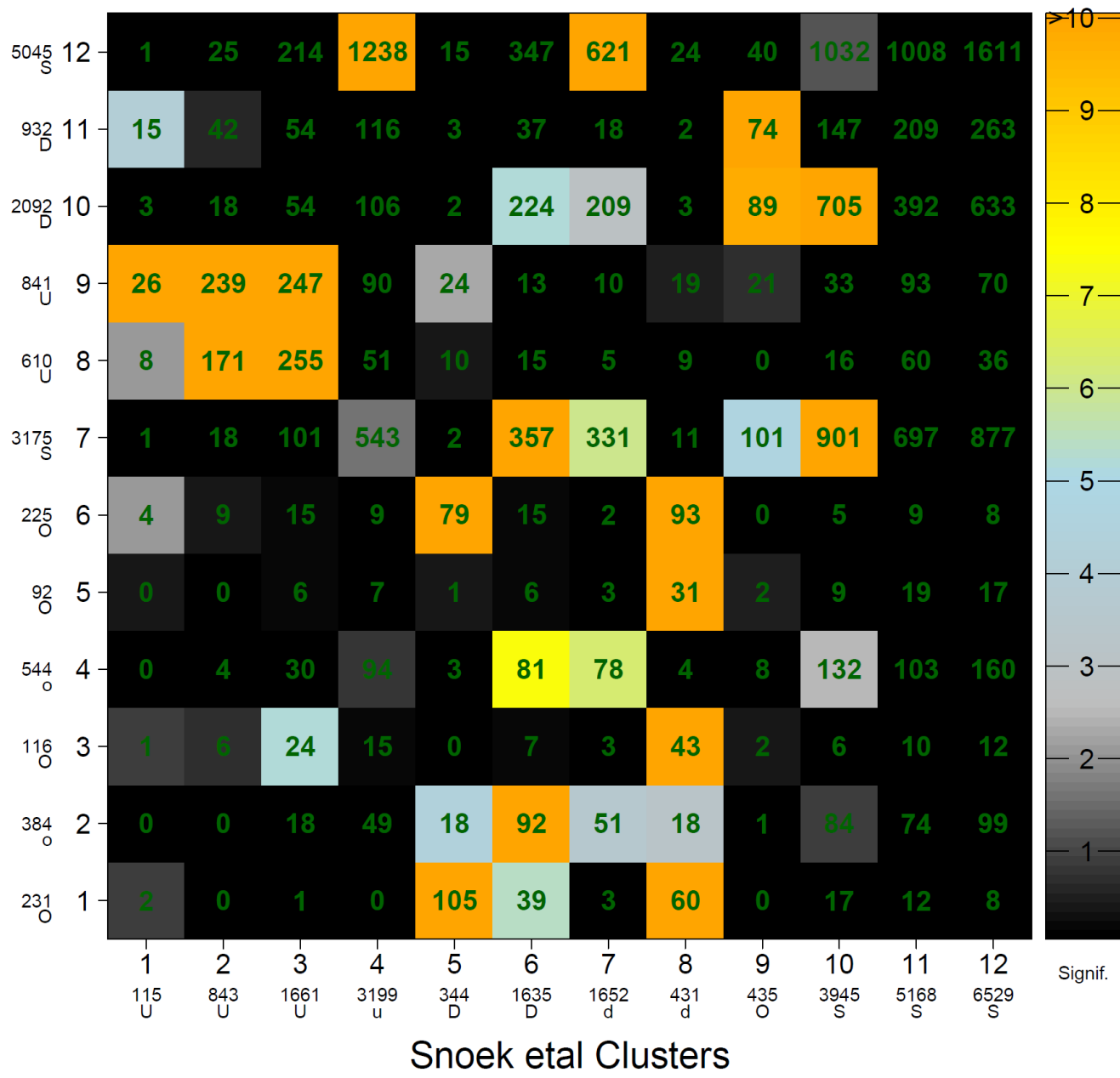


Supplementary fig. S2. Pearson correlation between time-points. Heat-plot of the Pearson correlation of the expression (log₂ ratios with the mean) between the time points. Remarkably, there is a clear distinction between early- and late-L4. The same analysis carried out per chromosome revealed the same correlations.

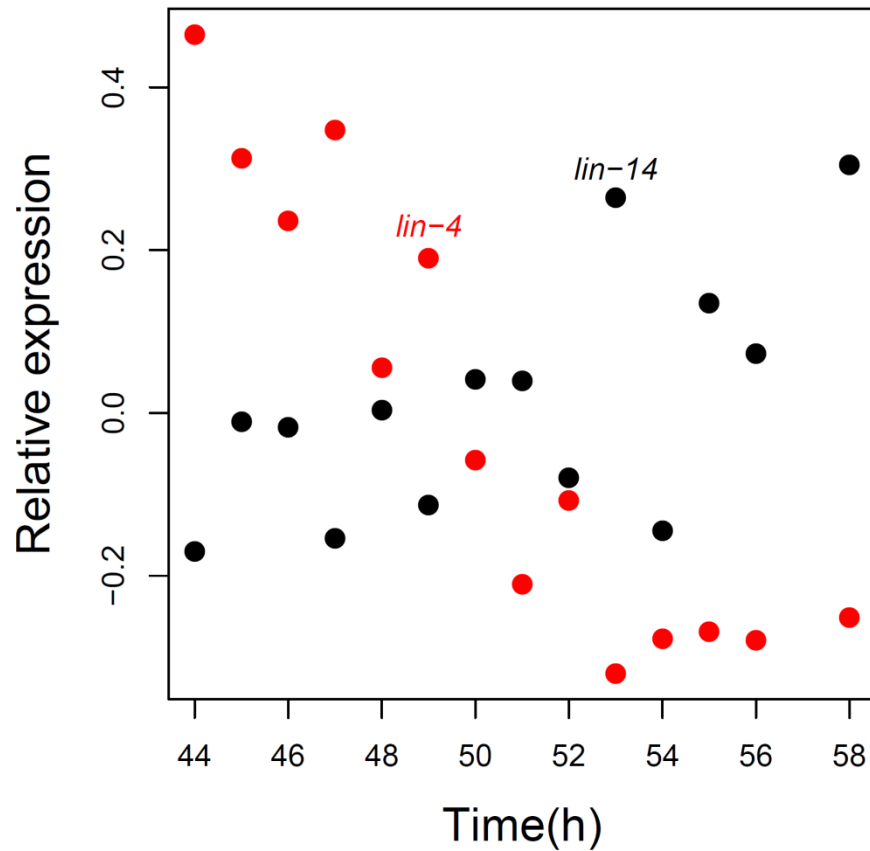


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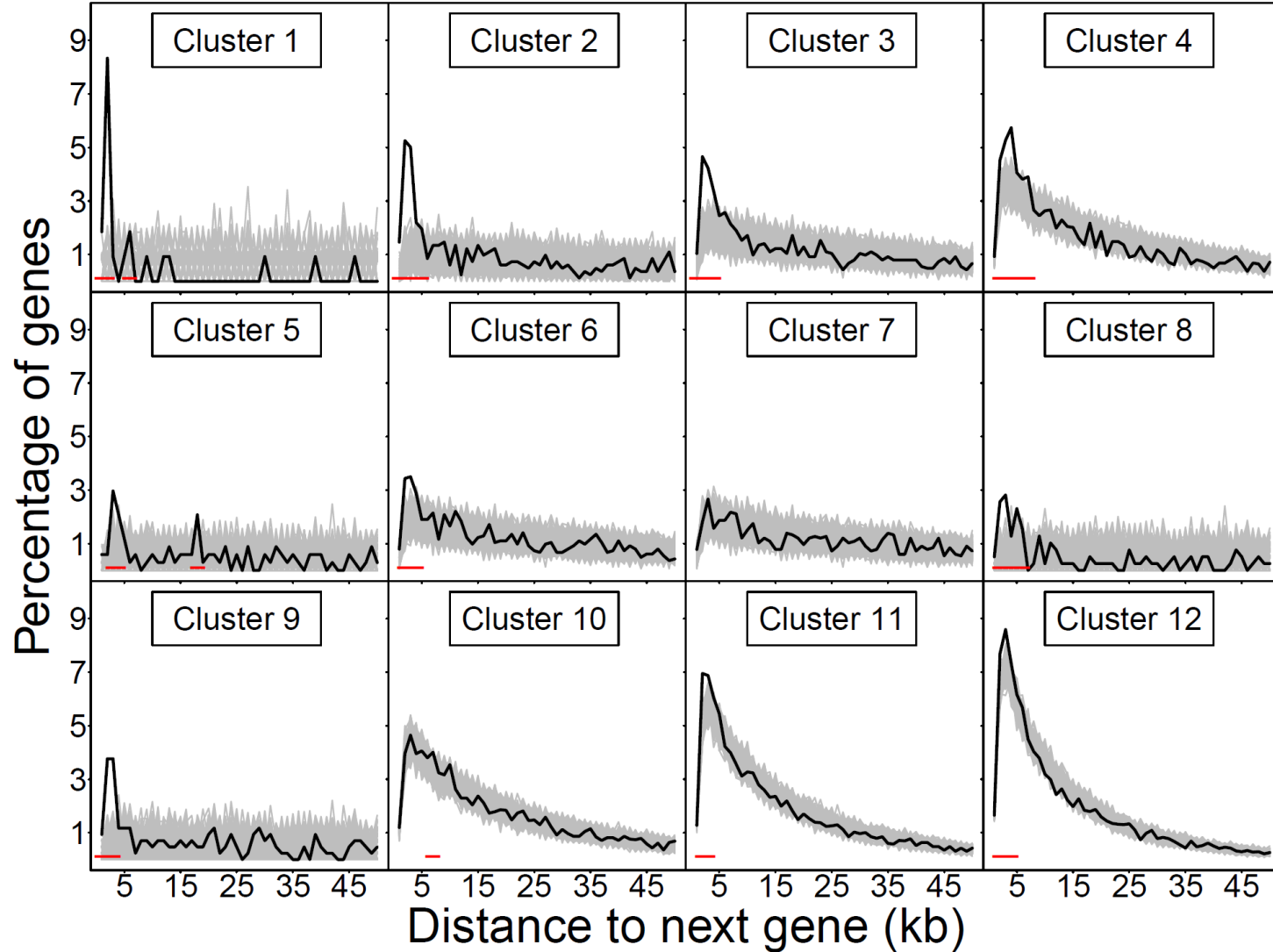
Kim, Grun, Oudenaarden Clusters



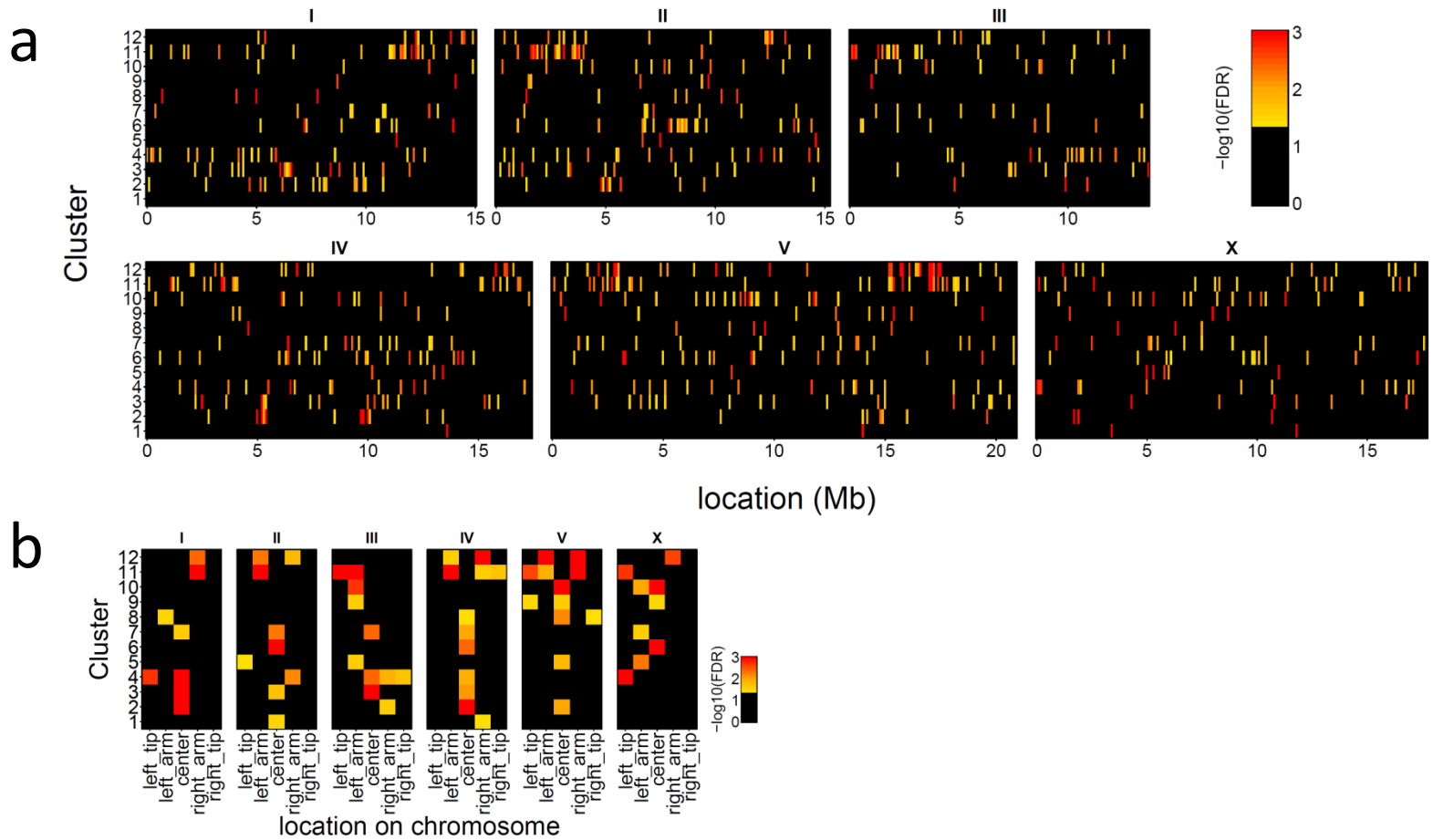
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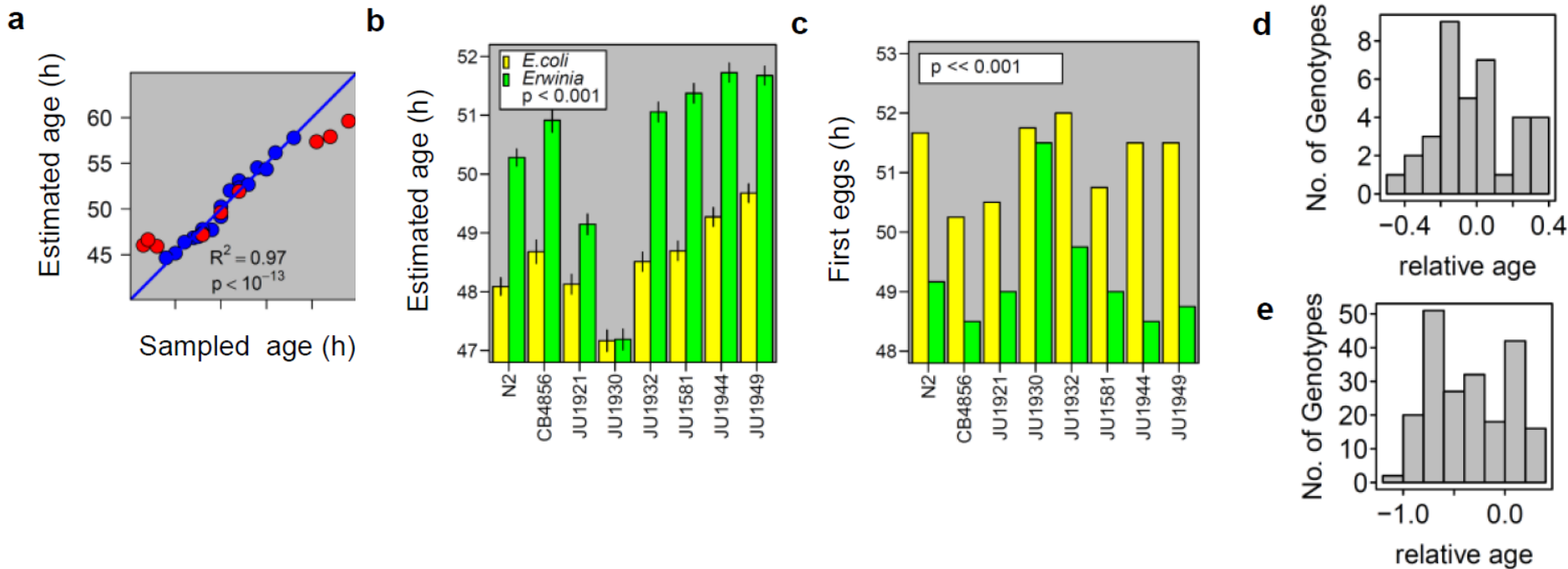
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Supplementary fig. S14. The transcriptomic ruler. Validation and application of the transcriptomic ruler. (A)

The real age of a data point versus the transcriptome age-estimate. The blue dots represent biological replicates on which the ruler was designed and red dots represent an application on a validation experiment. (B) The estimated age of different genotypes on two food sources, *E. coli* and *E. rhapontici*. The vertical lines represent SE. There is a significant increase in estimated age when *C. elegans* is fed on *E. rhapontici* ($P < 0.001$). (C) The age after synchronization when the first eggs were laid for different genotypes feeding on different food sources (*E. coli* in yellow and *E. rhapontici* in green). *C. elegans* lays its eggs significantly later when fed on *E. coli* ($P < 0.001$). (D) The relative age of recombinant inbred lines in a genetical genomics experiment (Viñuela *et al.* 2010). All lines were profiled at the same absolute age. See also comments for **fig. S14E** (E) The relative age of recombinant inbred lines in a genetical genomics experiment (Rockman *et al.* 2010). All lines were profiled at the same absolute age. Developmental differences between recombinant inbred lines of a N2 x CB4856 cross were described in (Gutteling *et al.* 2007), this difference in development is reflected in the transcript profiles of these lines. It shows that the transcriptomic ruler can be used to determine the developmental age of each individual line. This can subsequently be used for a better understanding of the results, for example eQTL analysis in contrast with developmental age.

Supplementary table S3 | Number of mutations in gene structures from the million mutation project.

| Gene structure | Mutants | Wild isolates |
|-----------------------|----------------|----------------------|
| intron | 242,341 | 298,191 |
| exon | 250,599 | 144,721 |
| missense | 172,112 | 64,763 |
| synonymous | 68,237 | 68,024 |
| 5'UTR | 7,172 | 5,519 |
| 3'UTR | 17,874 | 16,559 |
| Total SNPs | 758,335 | 597,777 |

Supplementary table S3. Number of mutations in gene structures from the million mutation project. The number of mutations that were used in the analysis on the expression clusters, as extracted from the million mutation project database (Thompson *et al.* 2013).

Supplementary table S4 Number of photographed *C. elegans* individuals per time point. Time points in hours after synchronisation.

| Time point | No. of worms | Time point | No. of worms |
|-------------------|---------------------|-------------------|---------------------|
| 48 | 19 | 58 | 36 |
| 49 | 41 | 59 | NA |
| 50 | 54 | 60 | 16 |
| 51 | 58 | 61 | 15 |
| 52 | 59 | 62 | 18 |
| 53 | 38 | 63 | 19 |
| 54 | 39 | 64 | 15 |
| 55 | 40 | 65 | 20 |
| 56 | 40 | 66 | 20 |
| 57 | 41 | 67 | 20 |

Supplementary table S4. Number of photographed *C. elegans* individuals per time point. Time points in hours after synchronisation.

Supplementary table S6 Method of RNA isolation per sample. Q = RNEasy Micro Kit from Qiagen, M = Maxwell® 16 LEV simplyRNA Tissue Kit from Promega.

| Samples used to calculate the slope of linear in- or decrease ^a | | | | Test samples ^b | |
|--|--------|--------|--------|---------------------------|--------|
| Sample ^c | Method | Sample | Method | Sample | Method |
| 44 | Q | 51 | Q | 41.5 | M |
| 45 | Q | 52A | Q | 42 | M |
| 46 | Q | 52B | M | 43 | M |
| 47 | Q | 53 | M | 48C | M |
| 48A | Q | 54 | M | 50C | M |
| 48B | M | 55 | M | 52C | M |
| 49 | Q | 56 | M | 60.5 | M |
| 50A | Q | 58 | M | 62 | M |
| 50B | M | | | 64 | M |

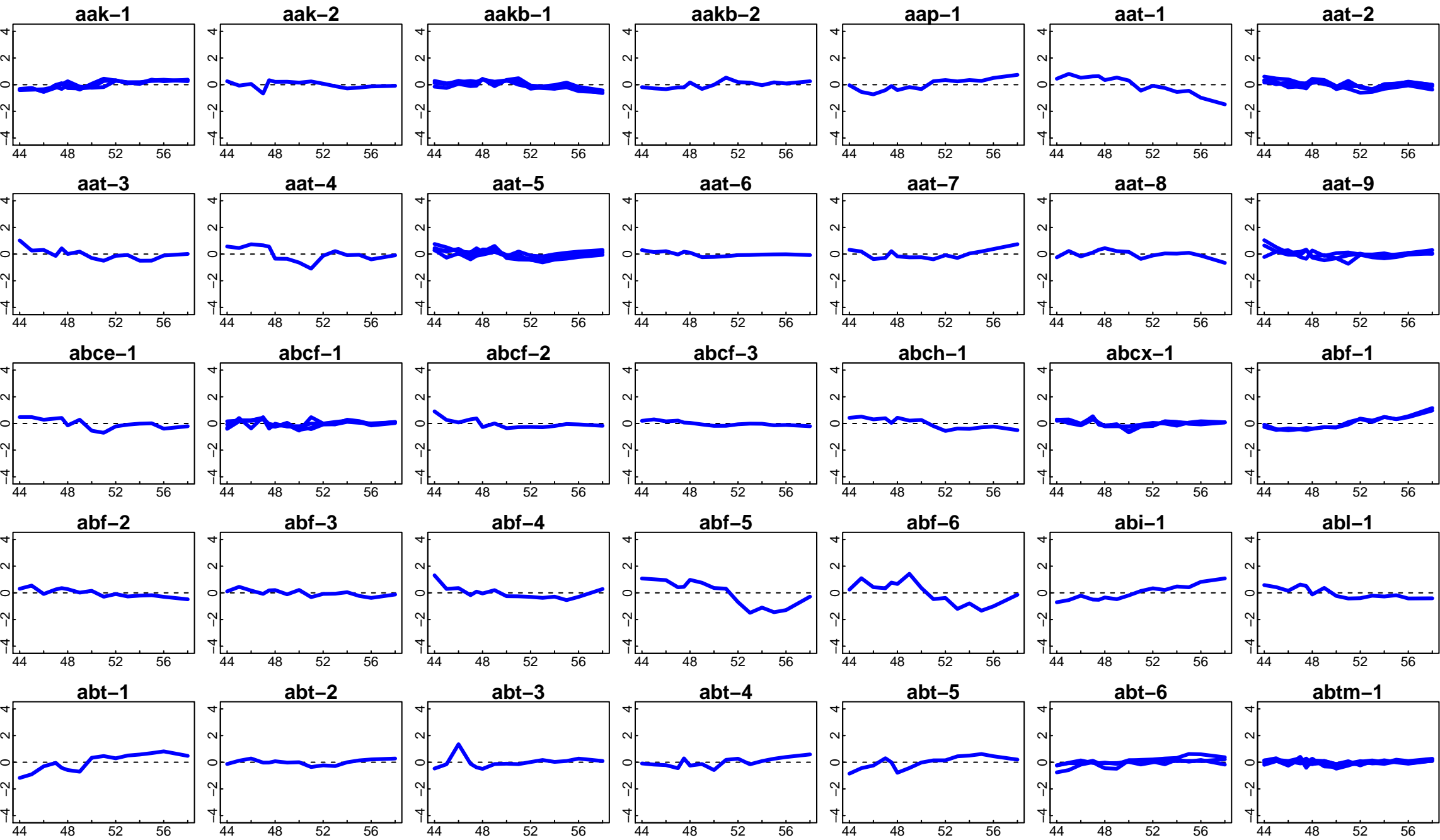
a) Samples used to calculate the slope of linear in- or decrease per spot, in order to be able to estimate the age of other samples

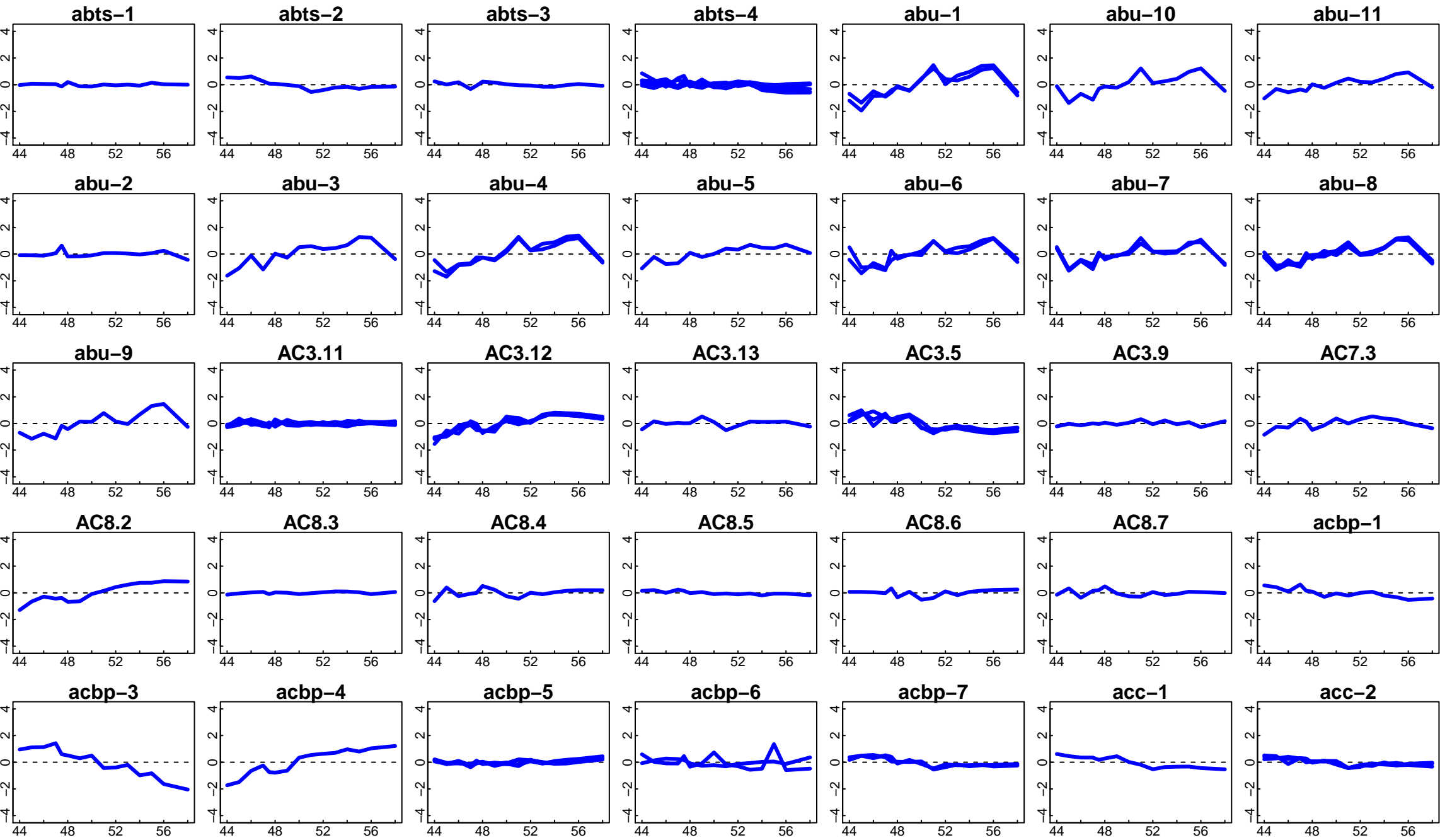
b) Samples used to test whether it is possible to estimate age by transcript profile

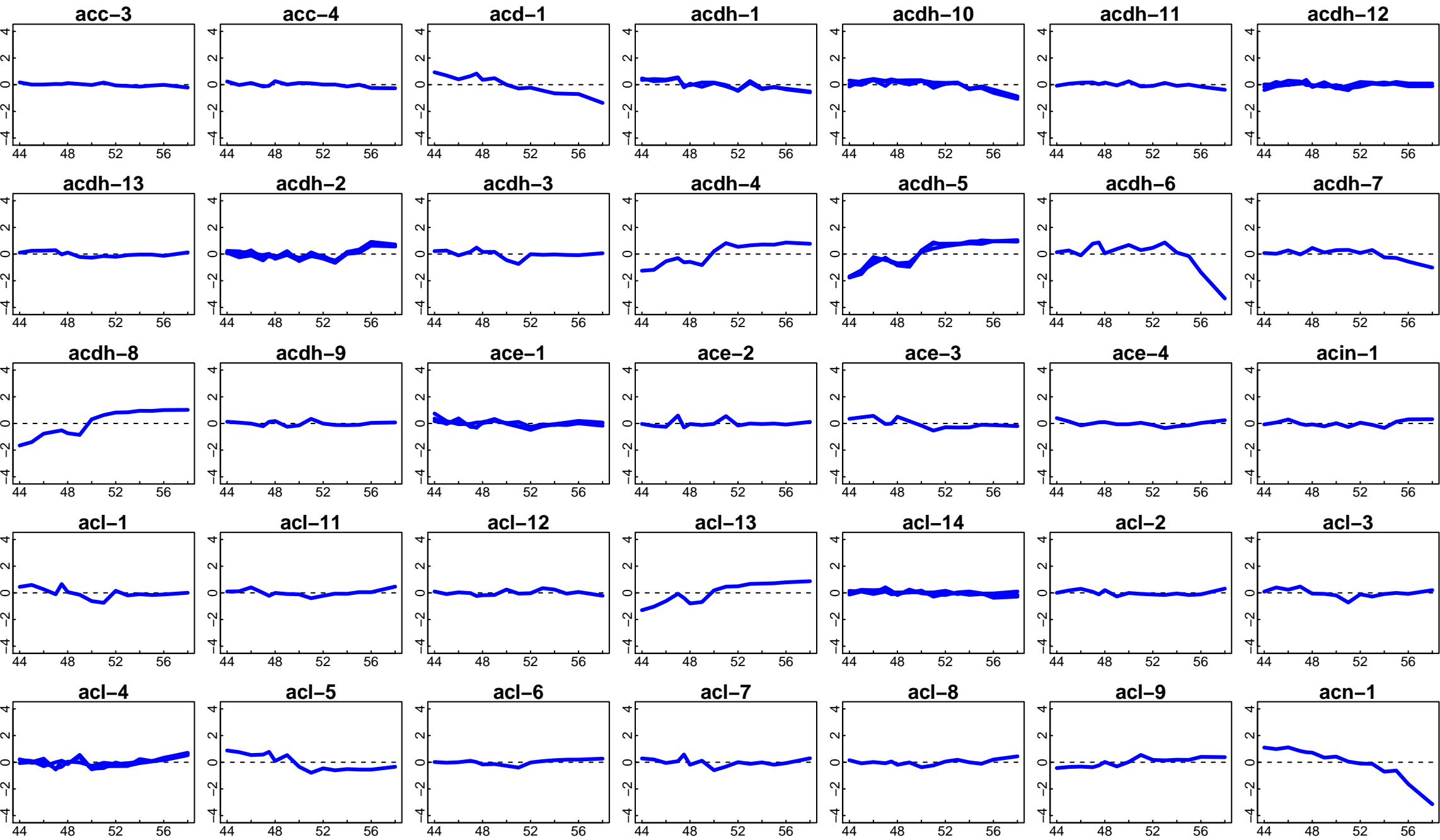
c) Samples are named according to time point

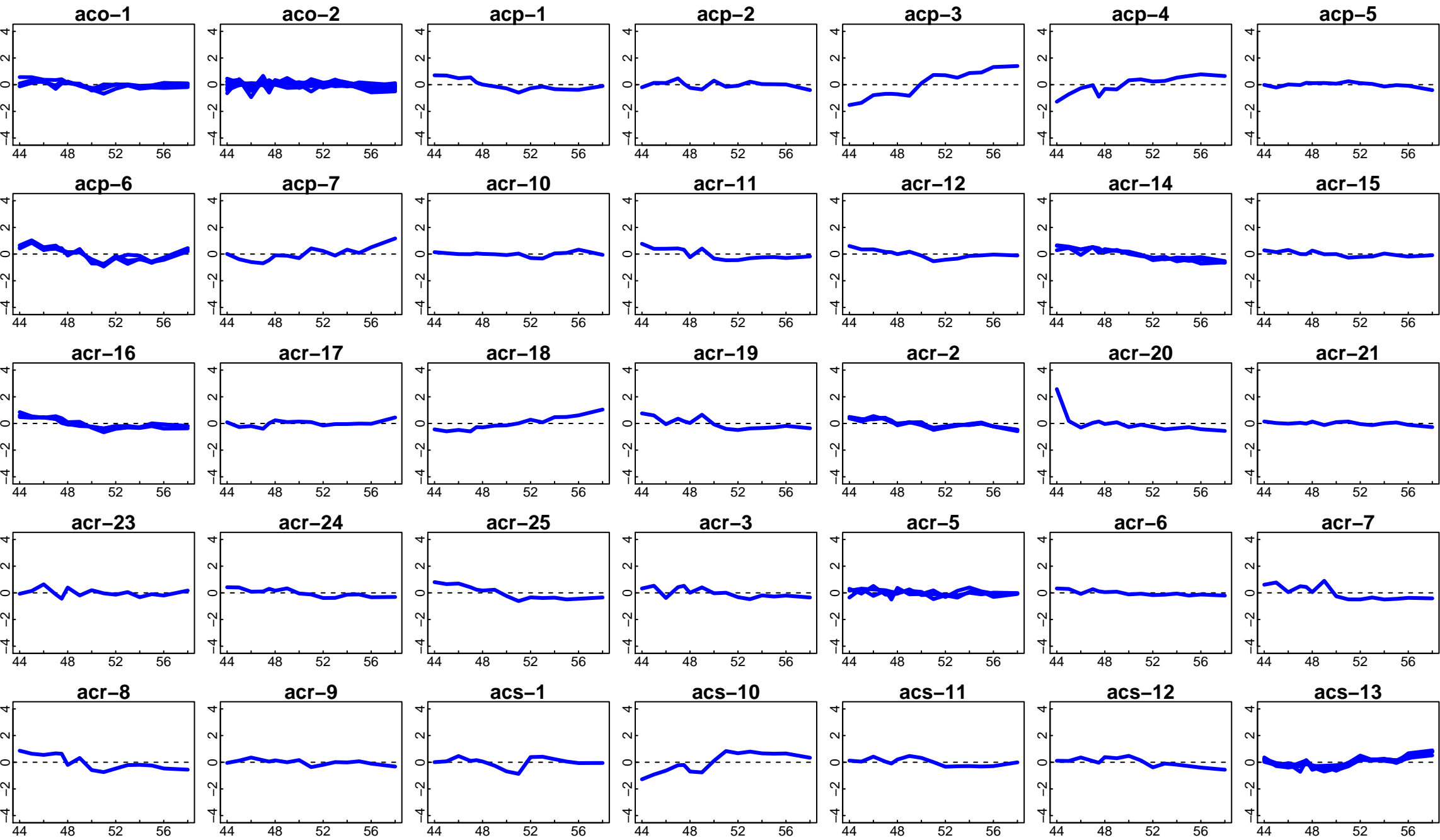
Supplementary table S6. Method of RNA isolation per sample.

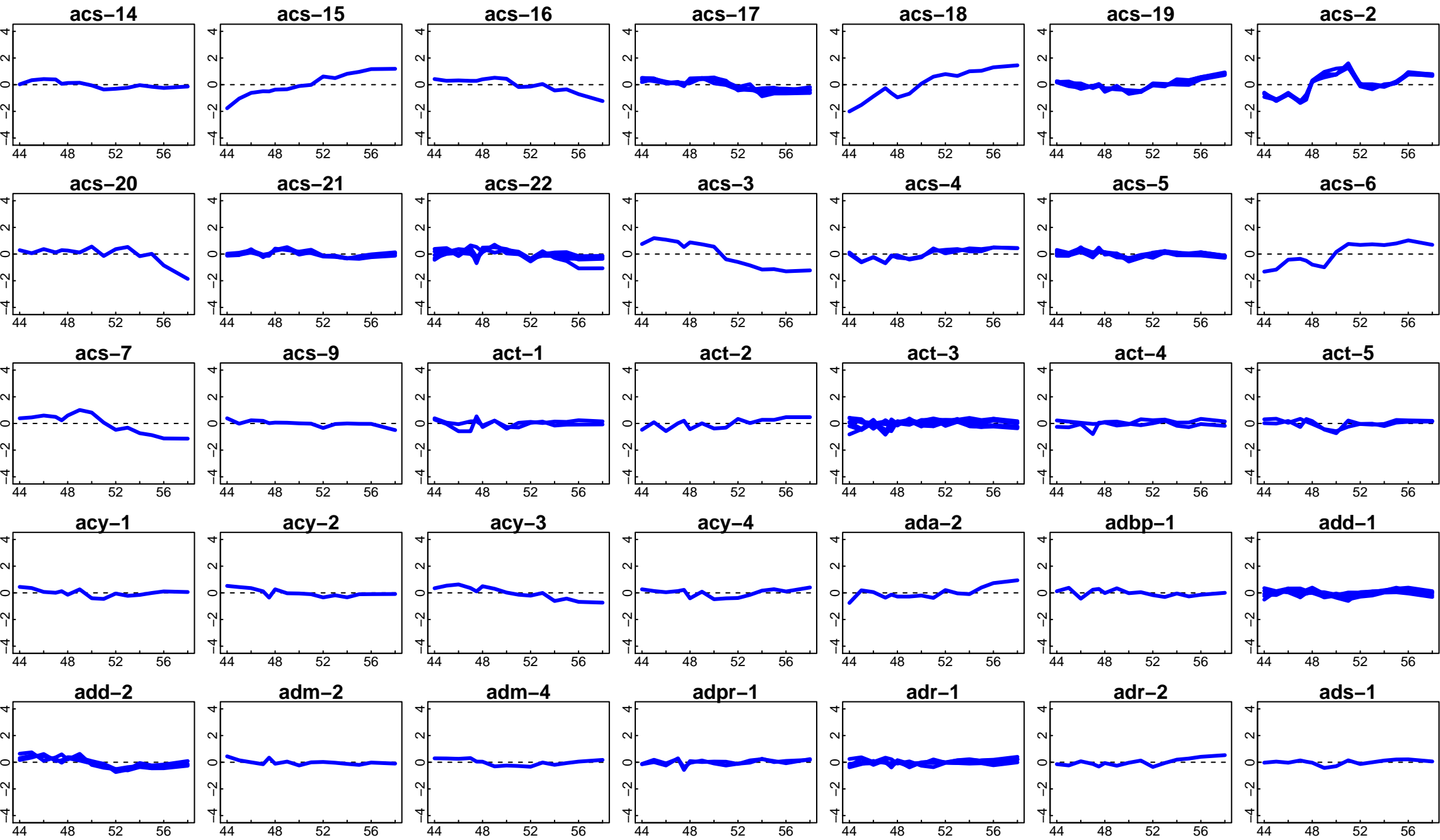
The RNA isolation methods used.

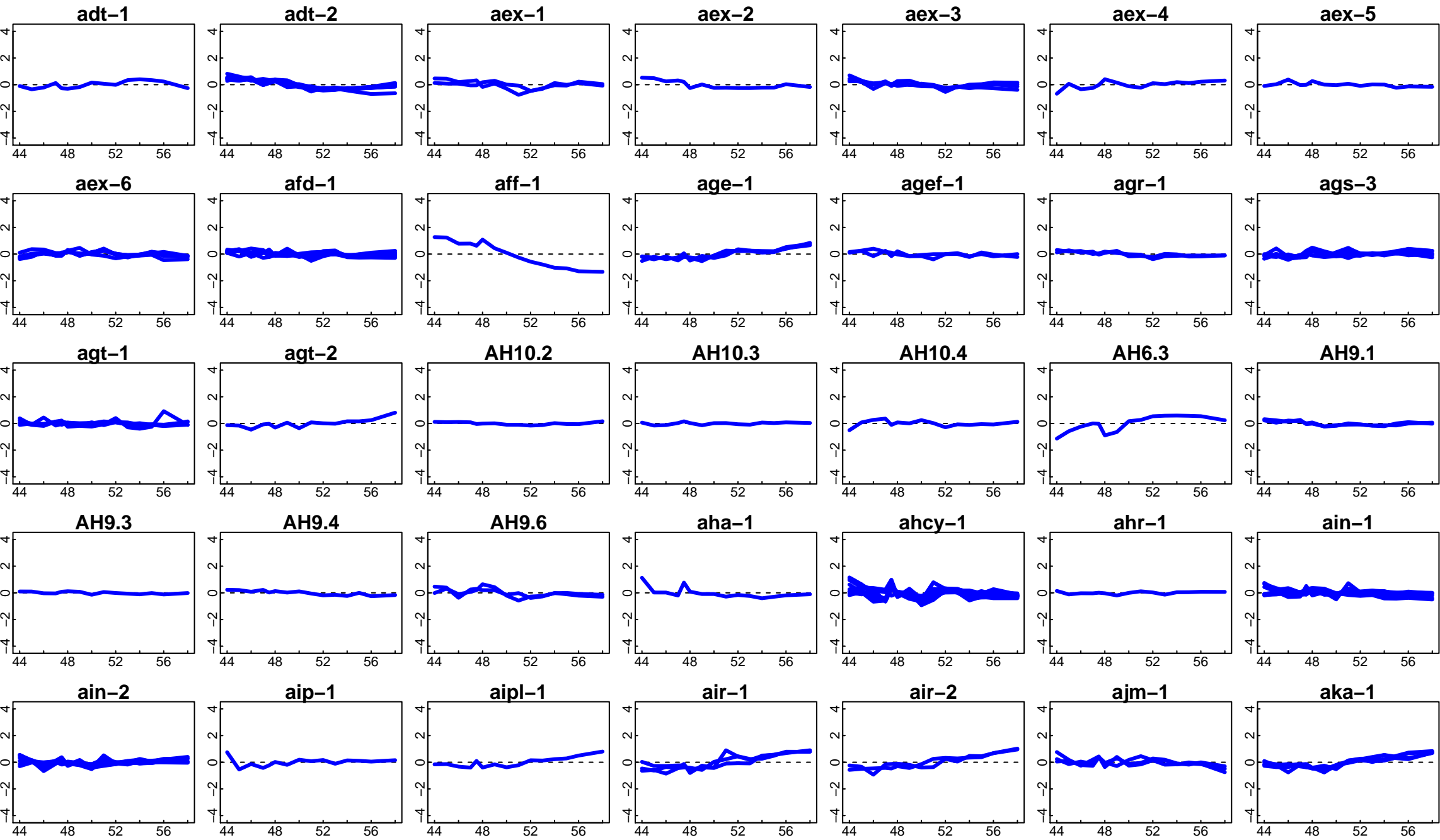


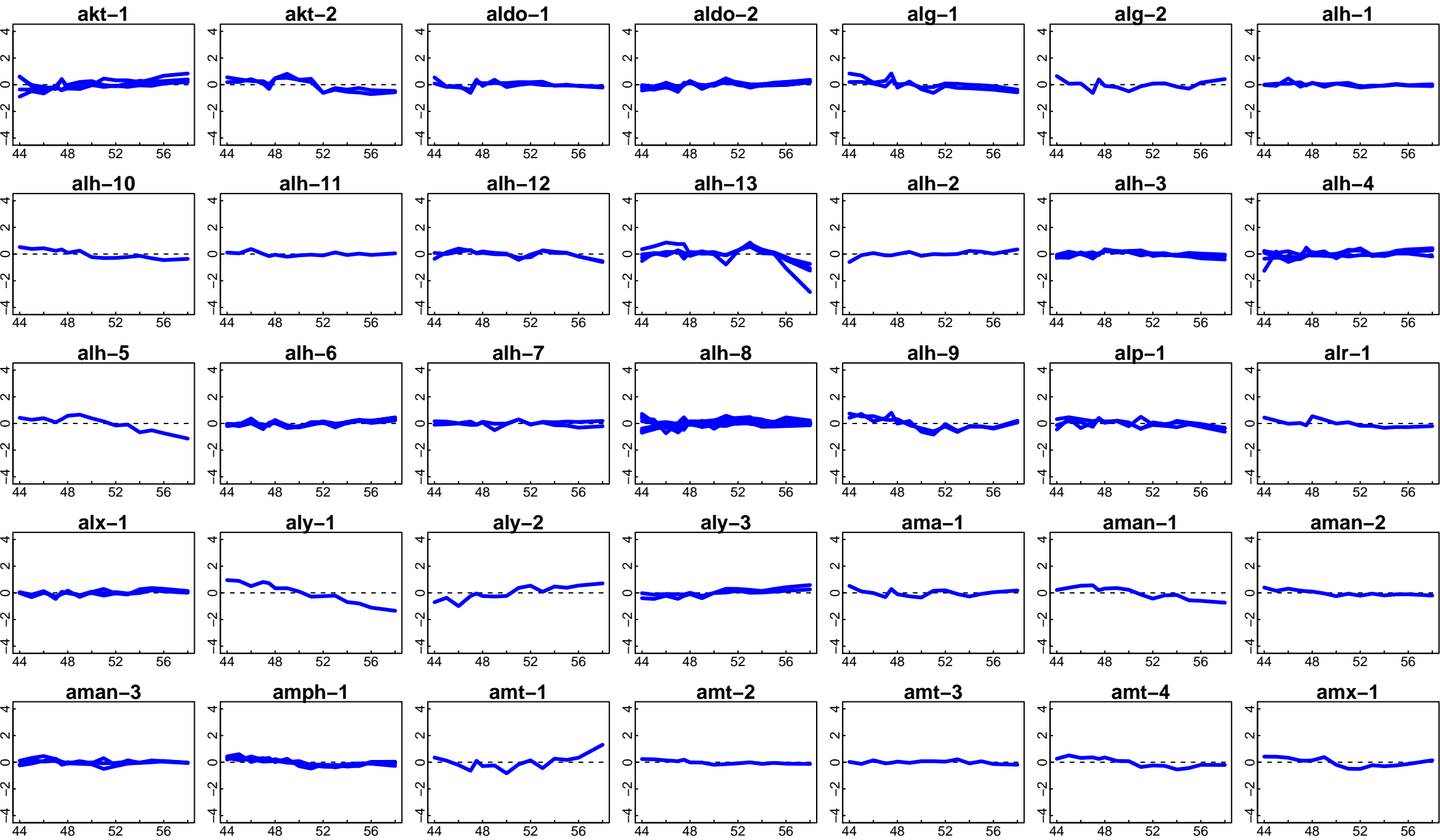


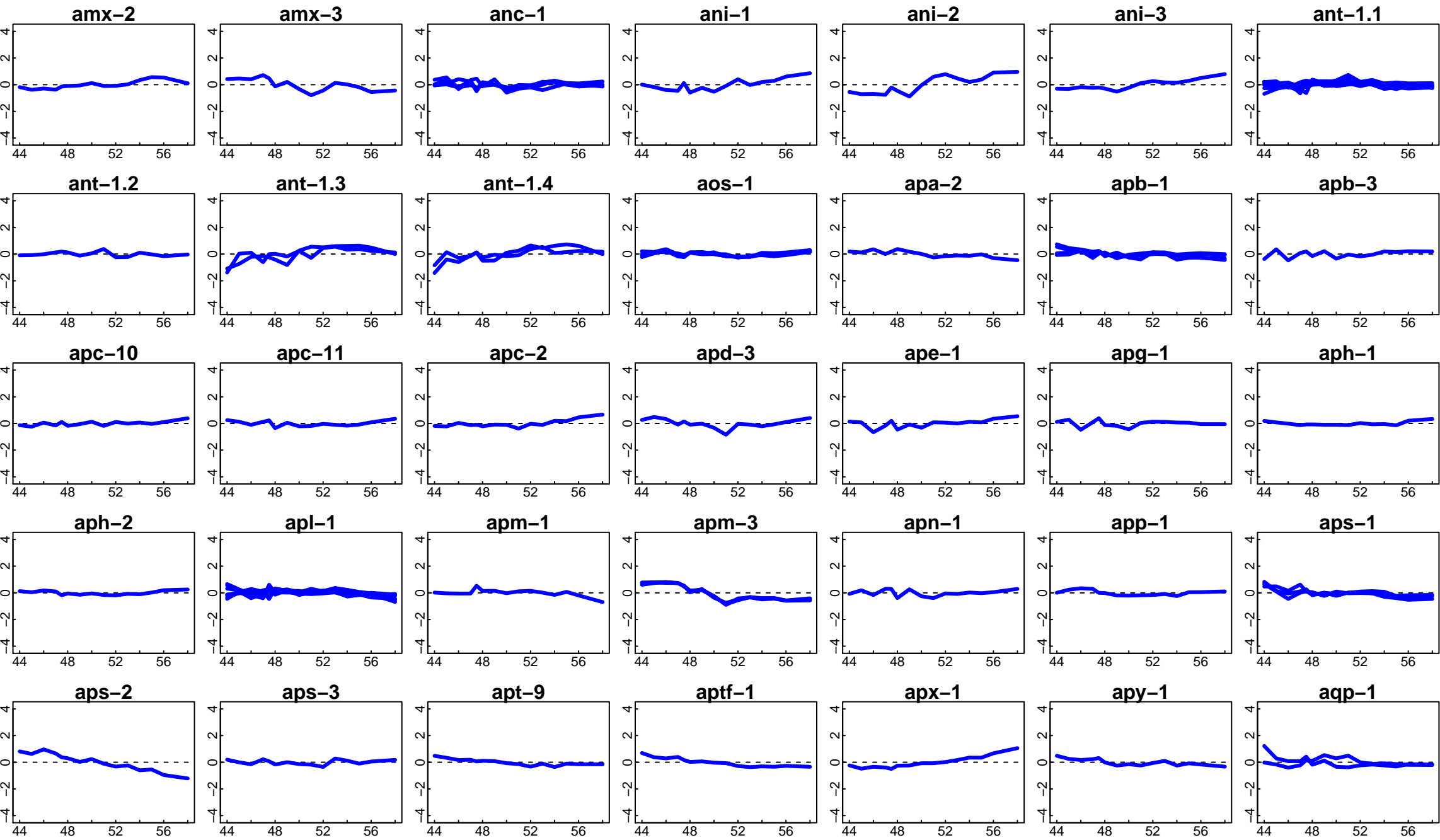


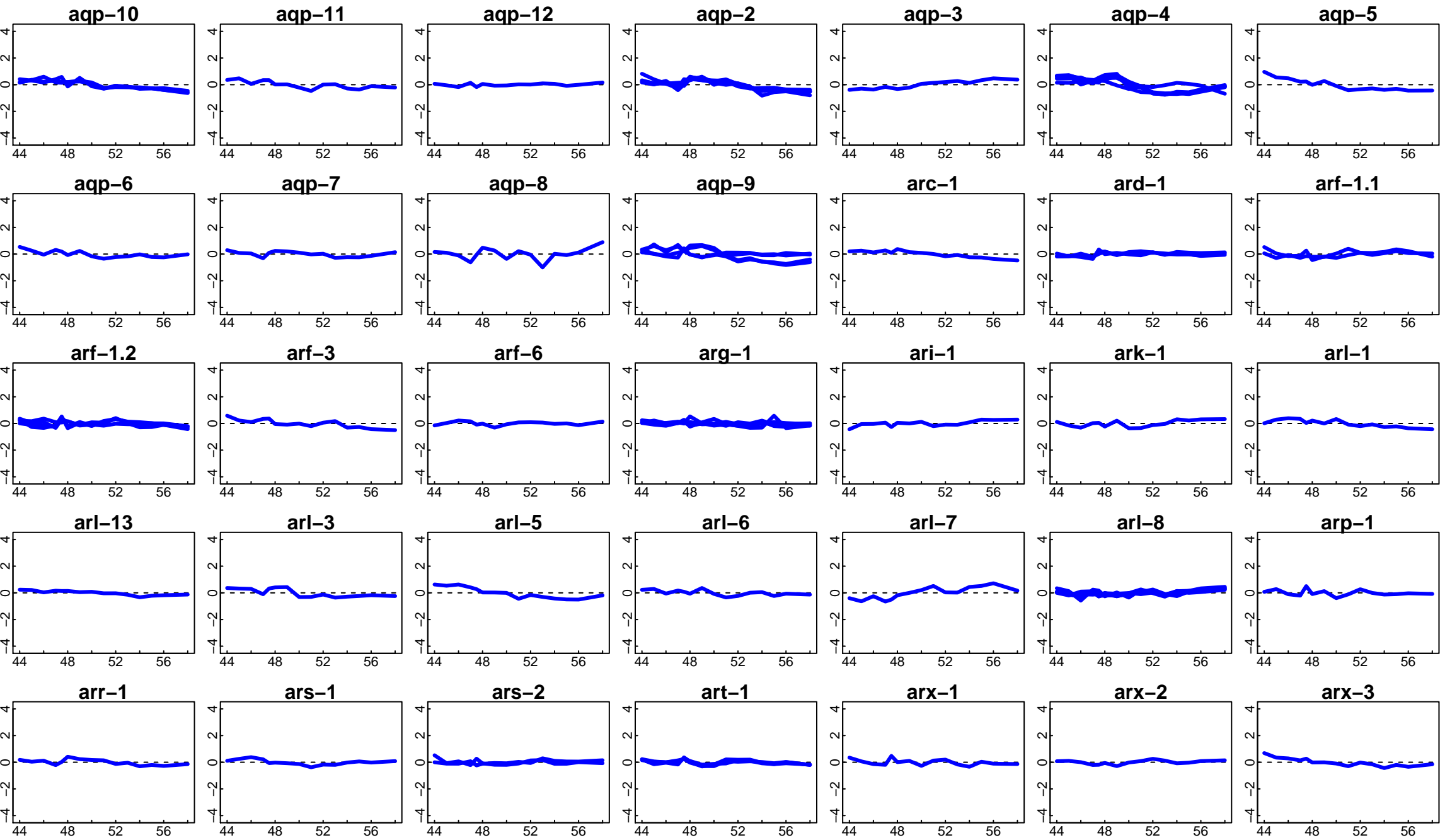


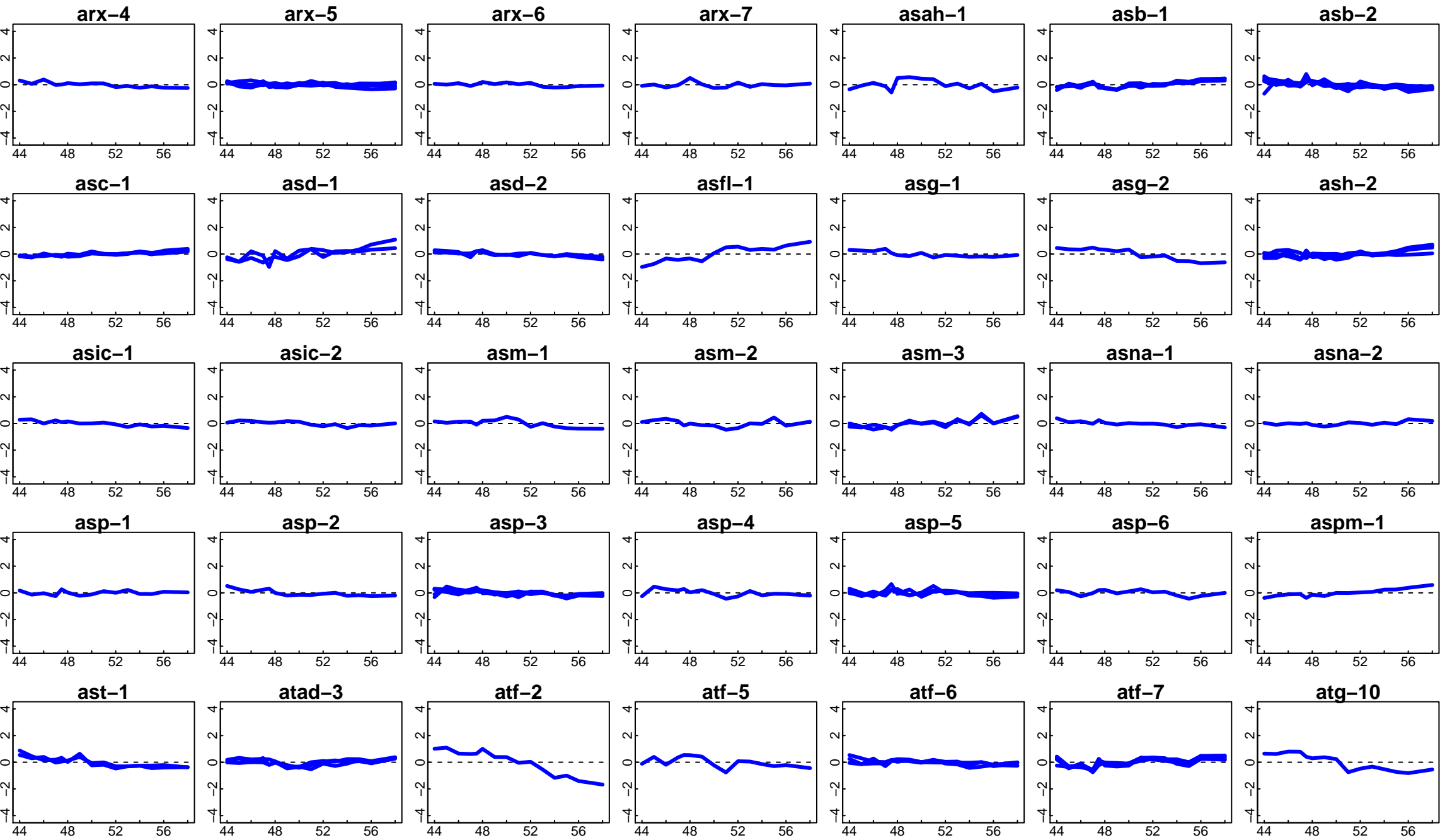


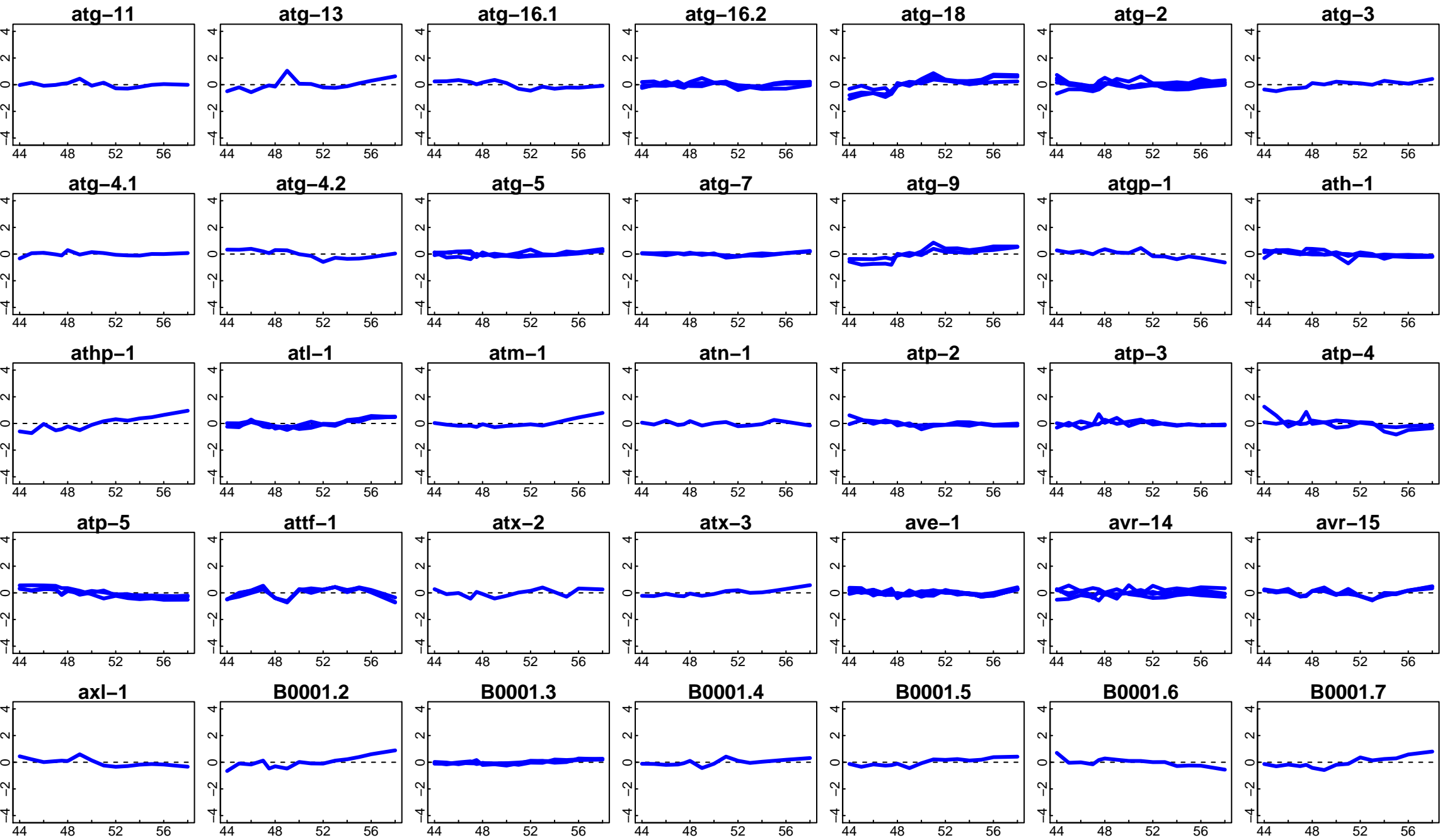


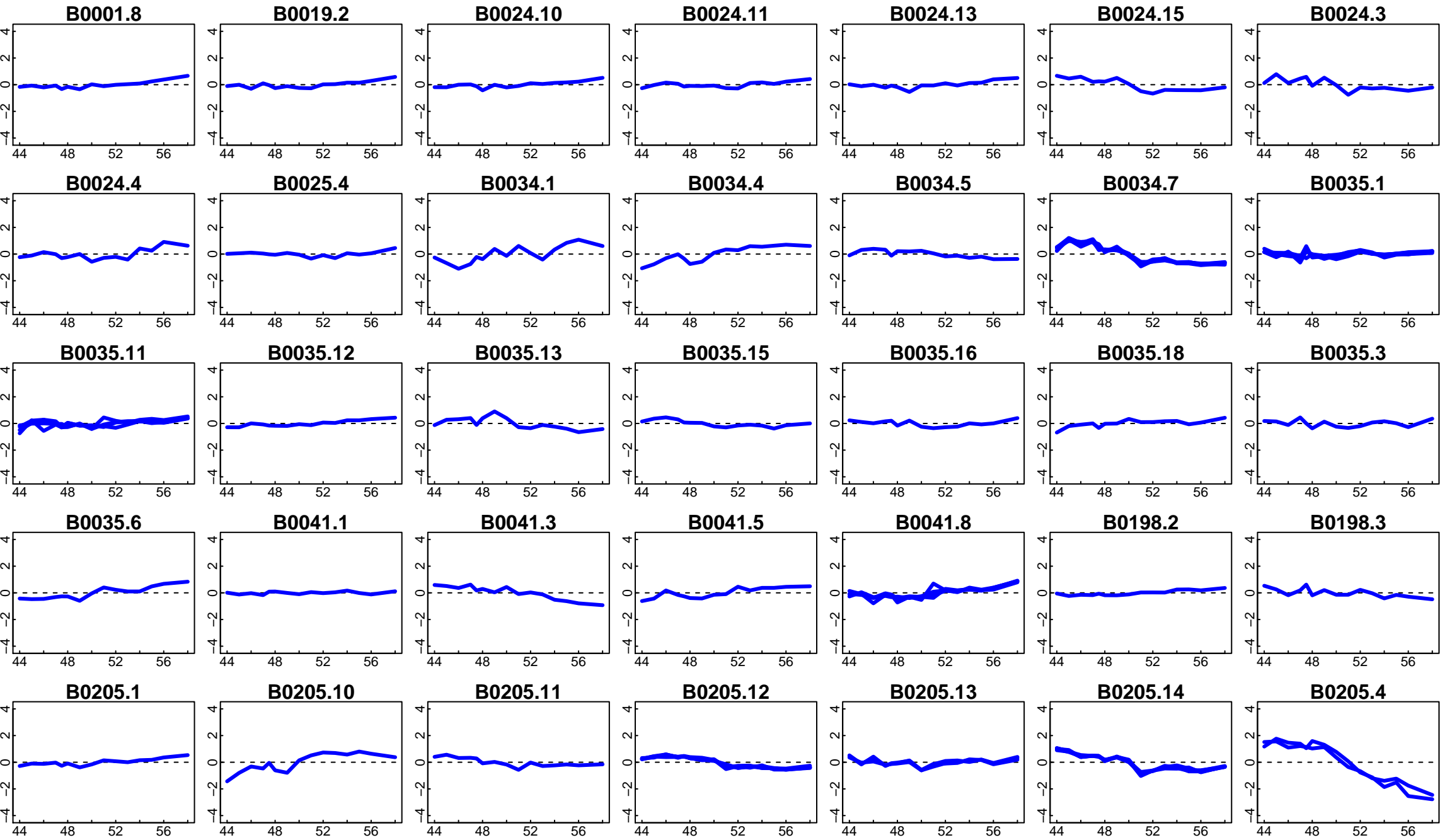


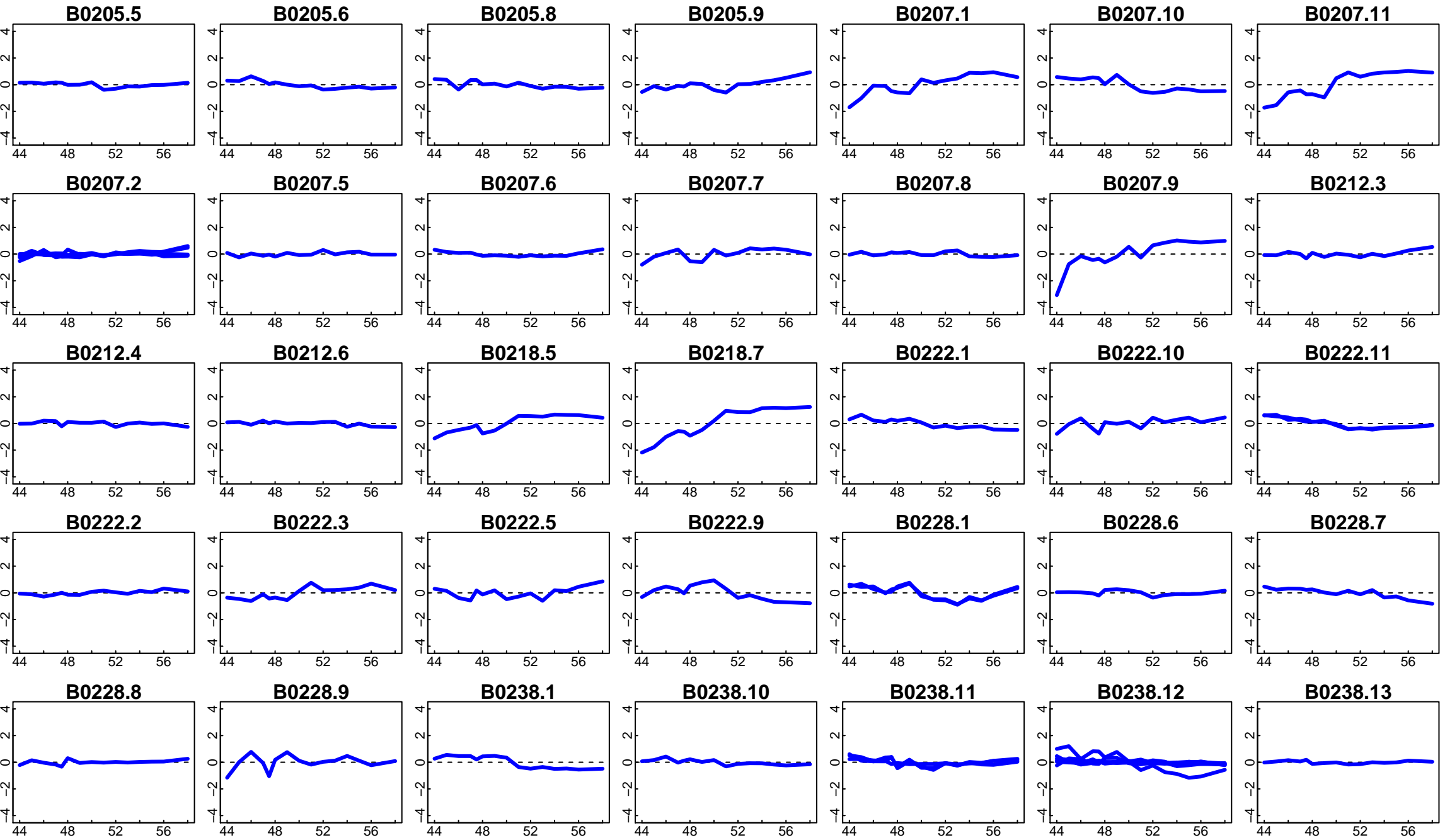


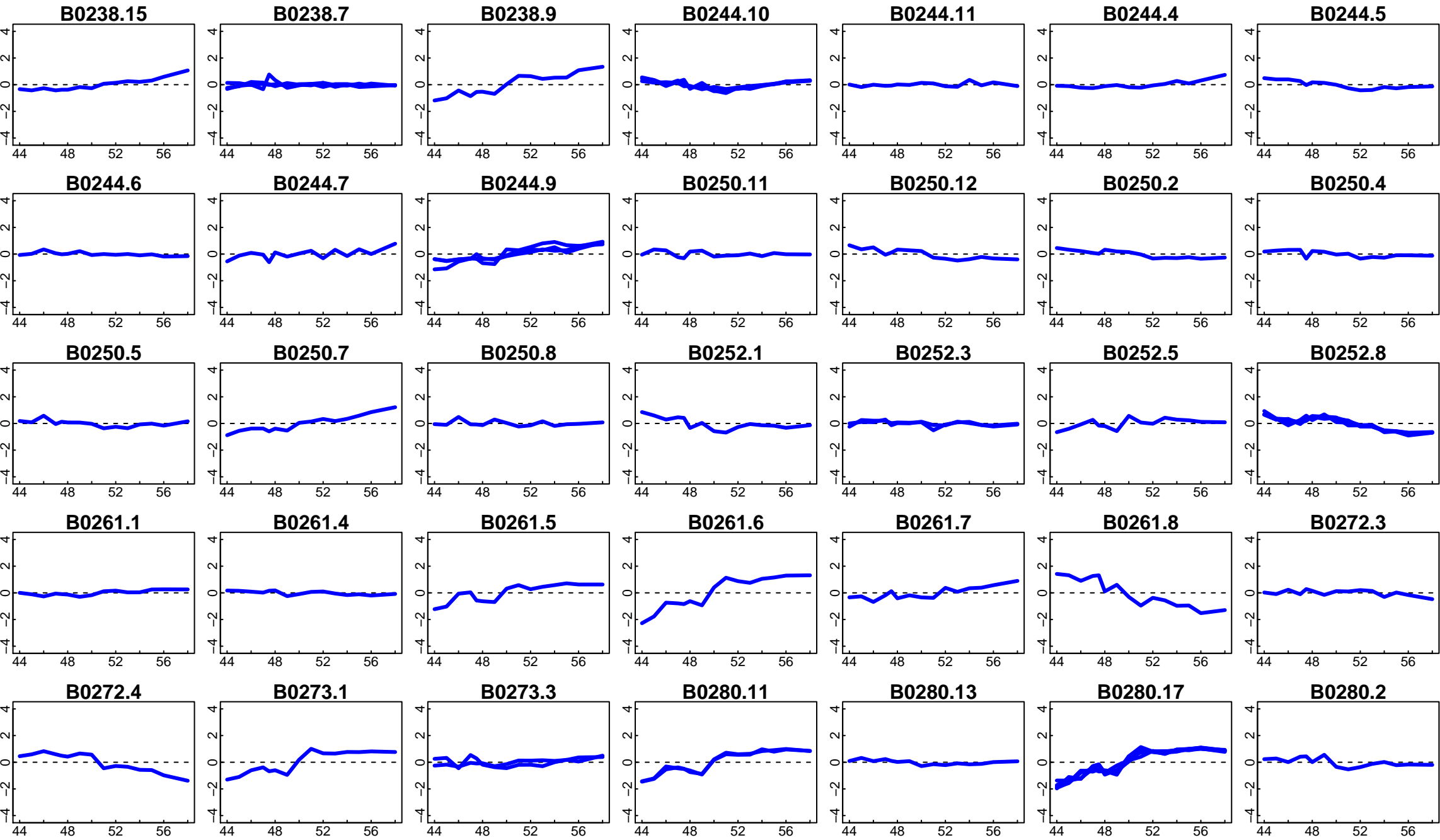


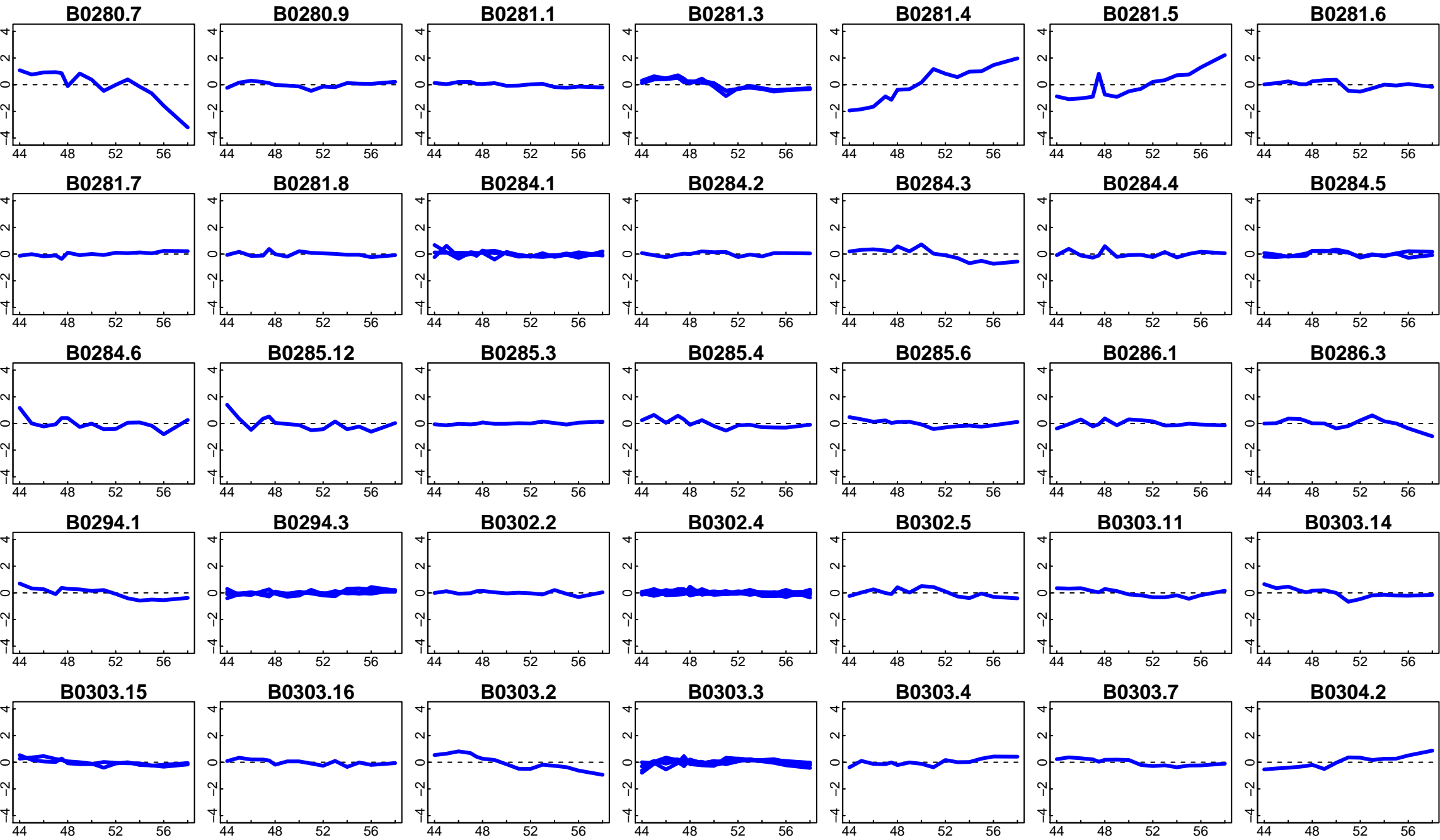


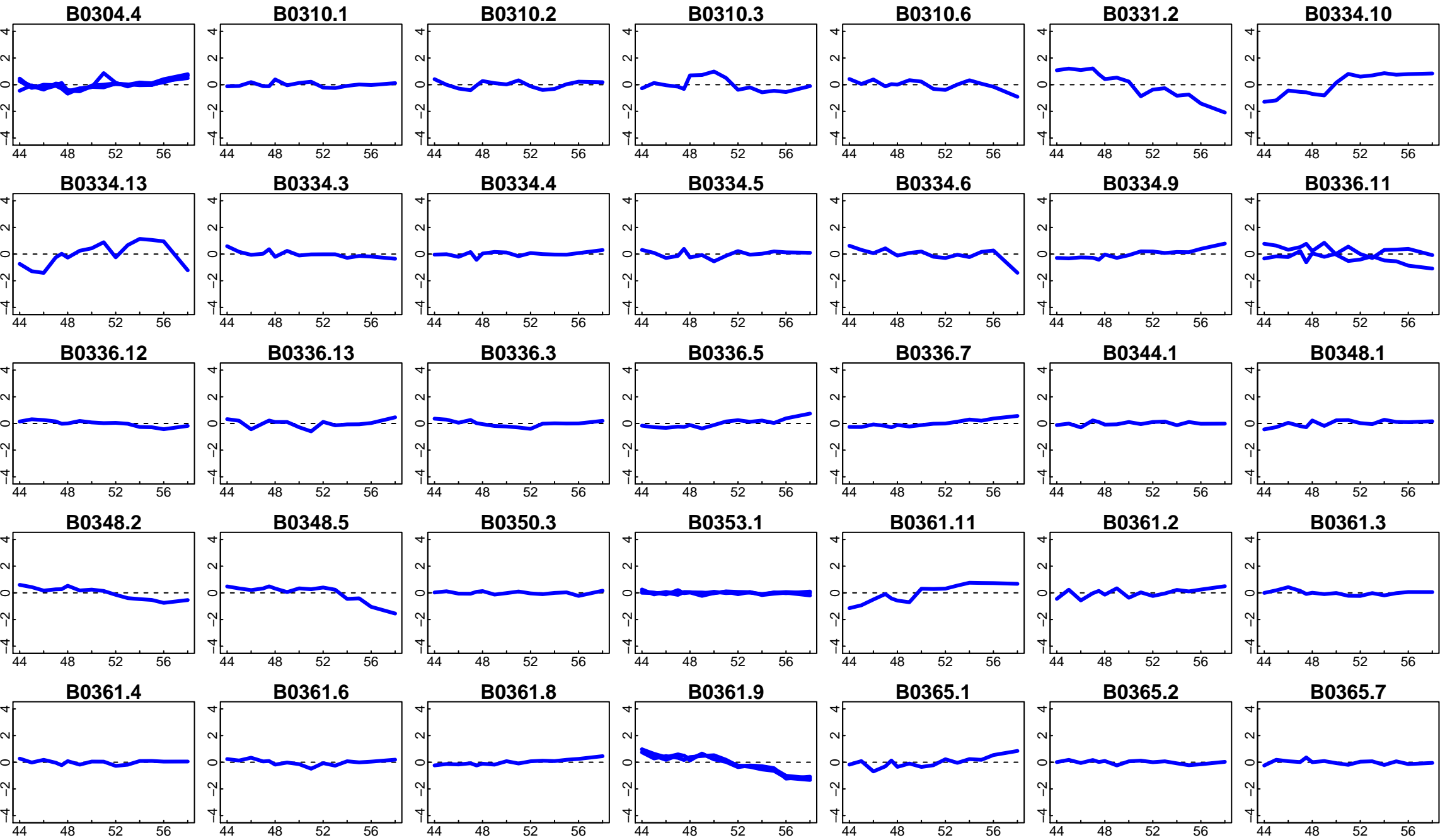


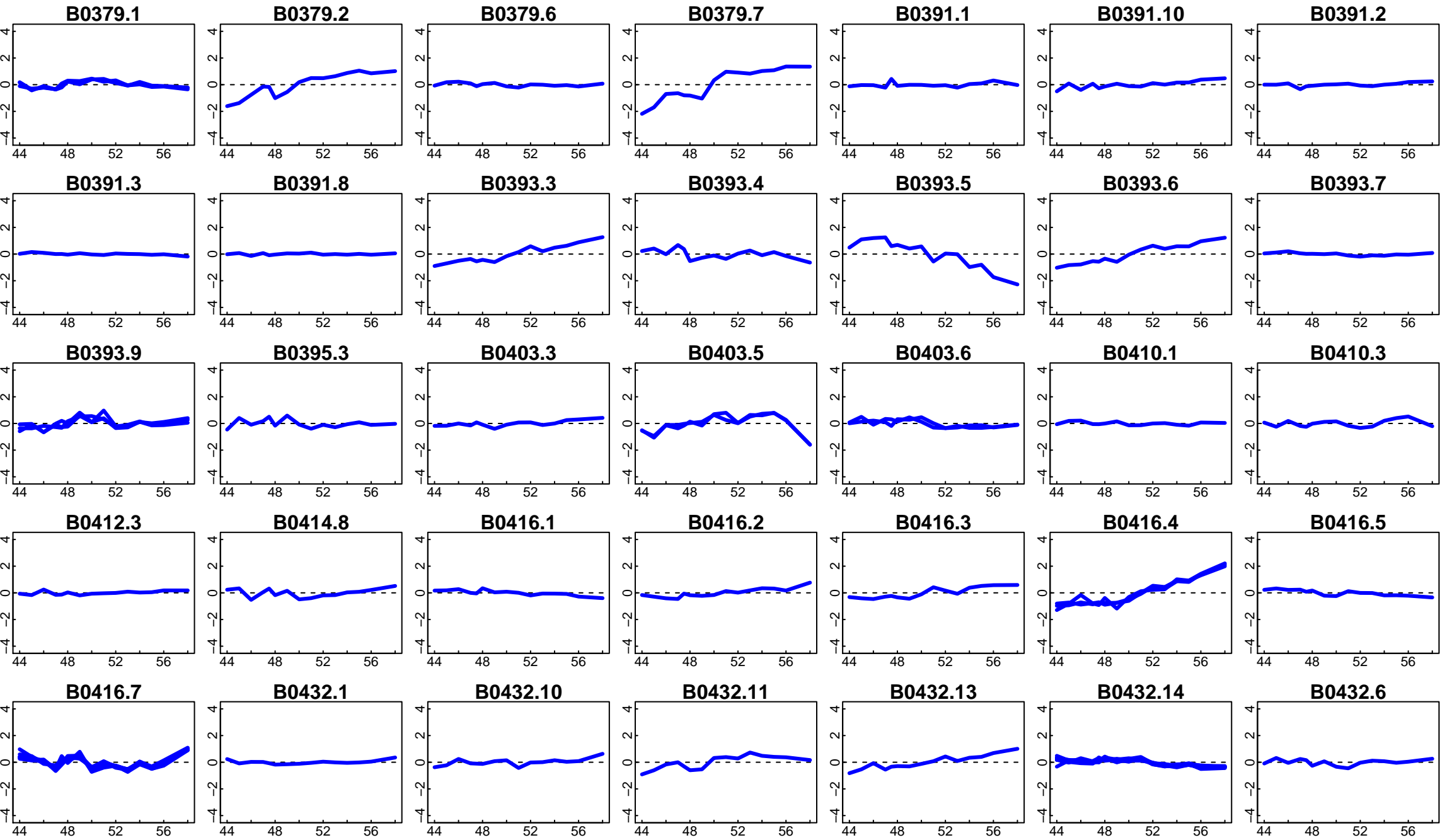


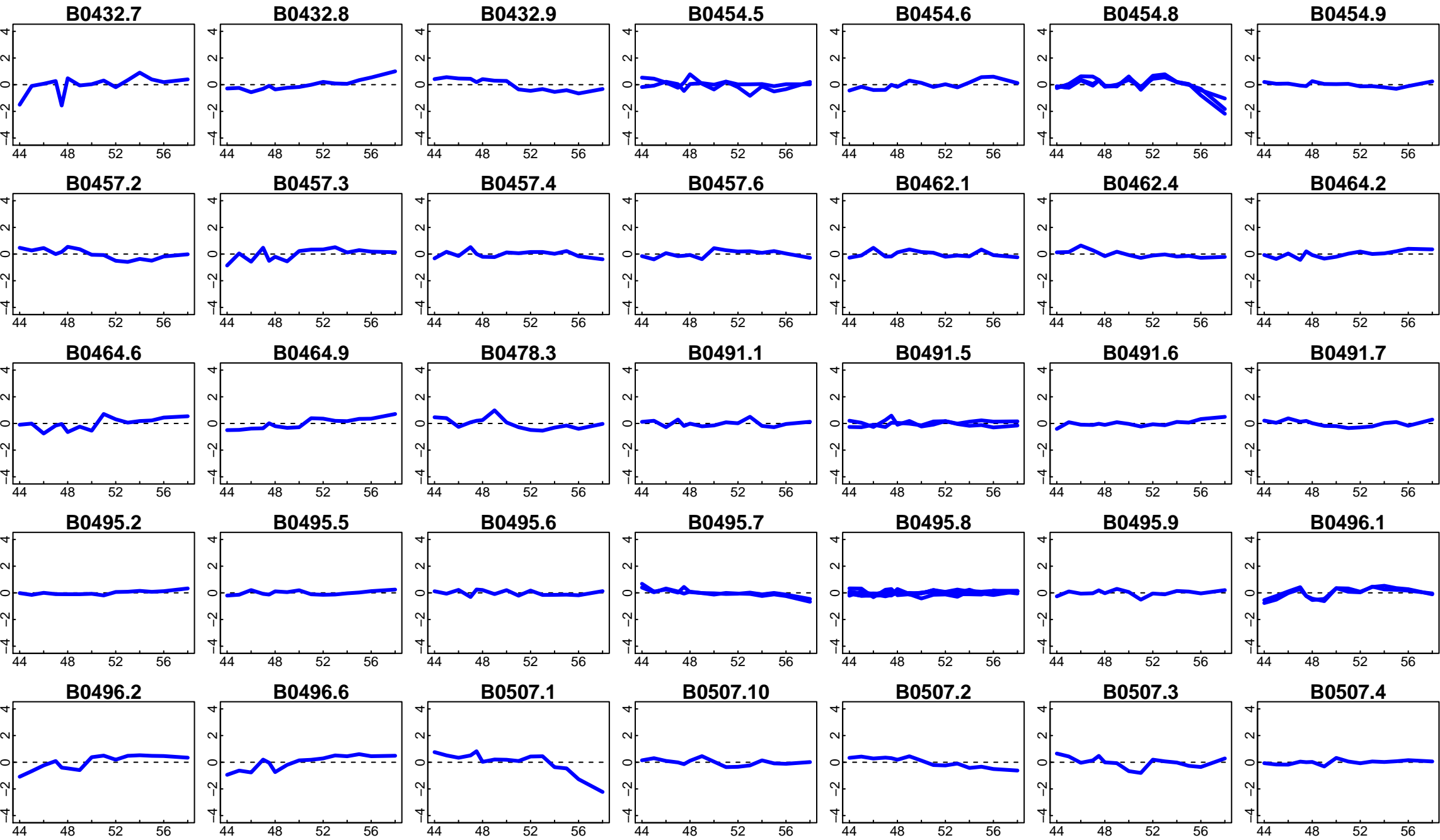


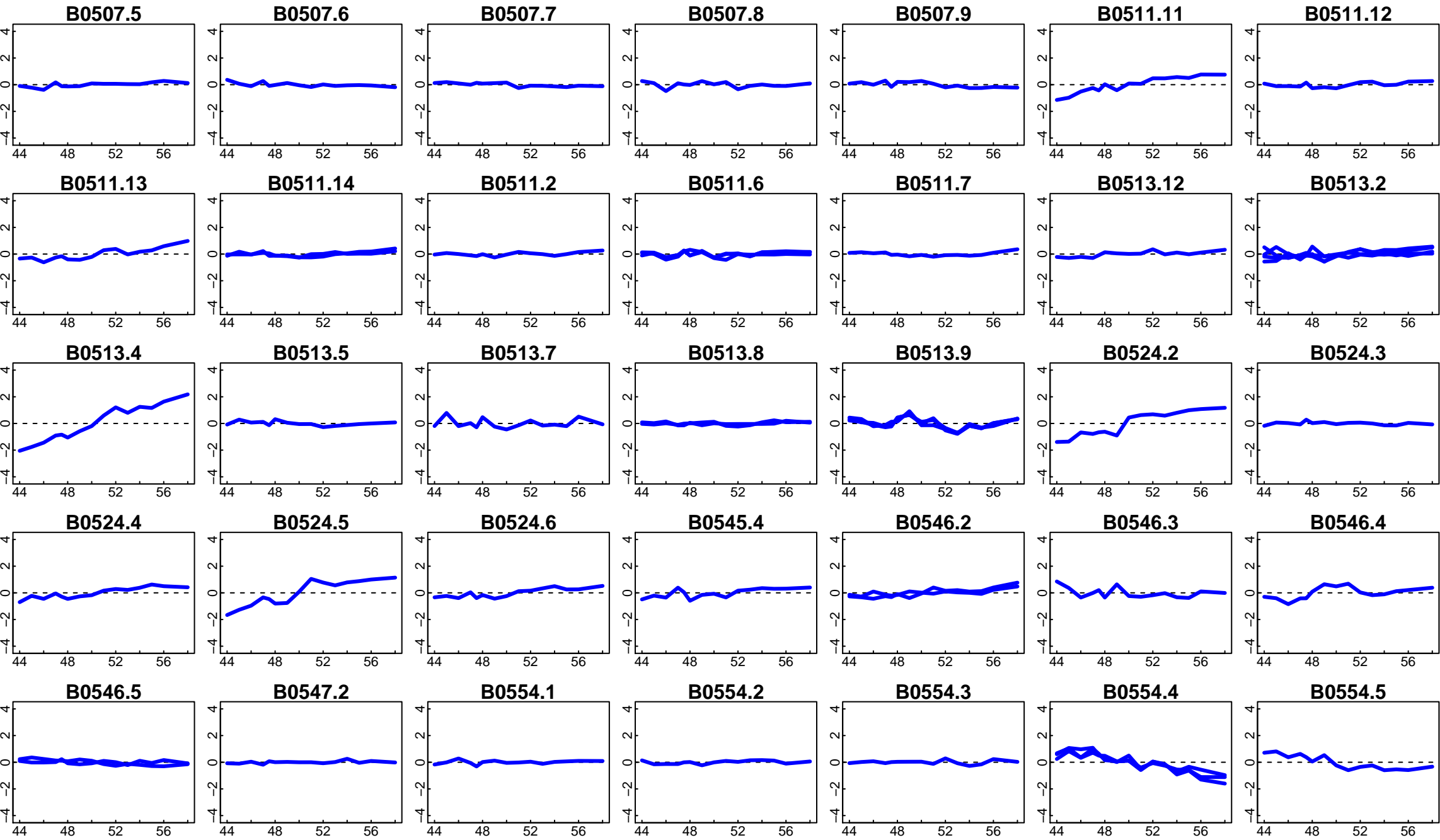


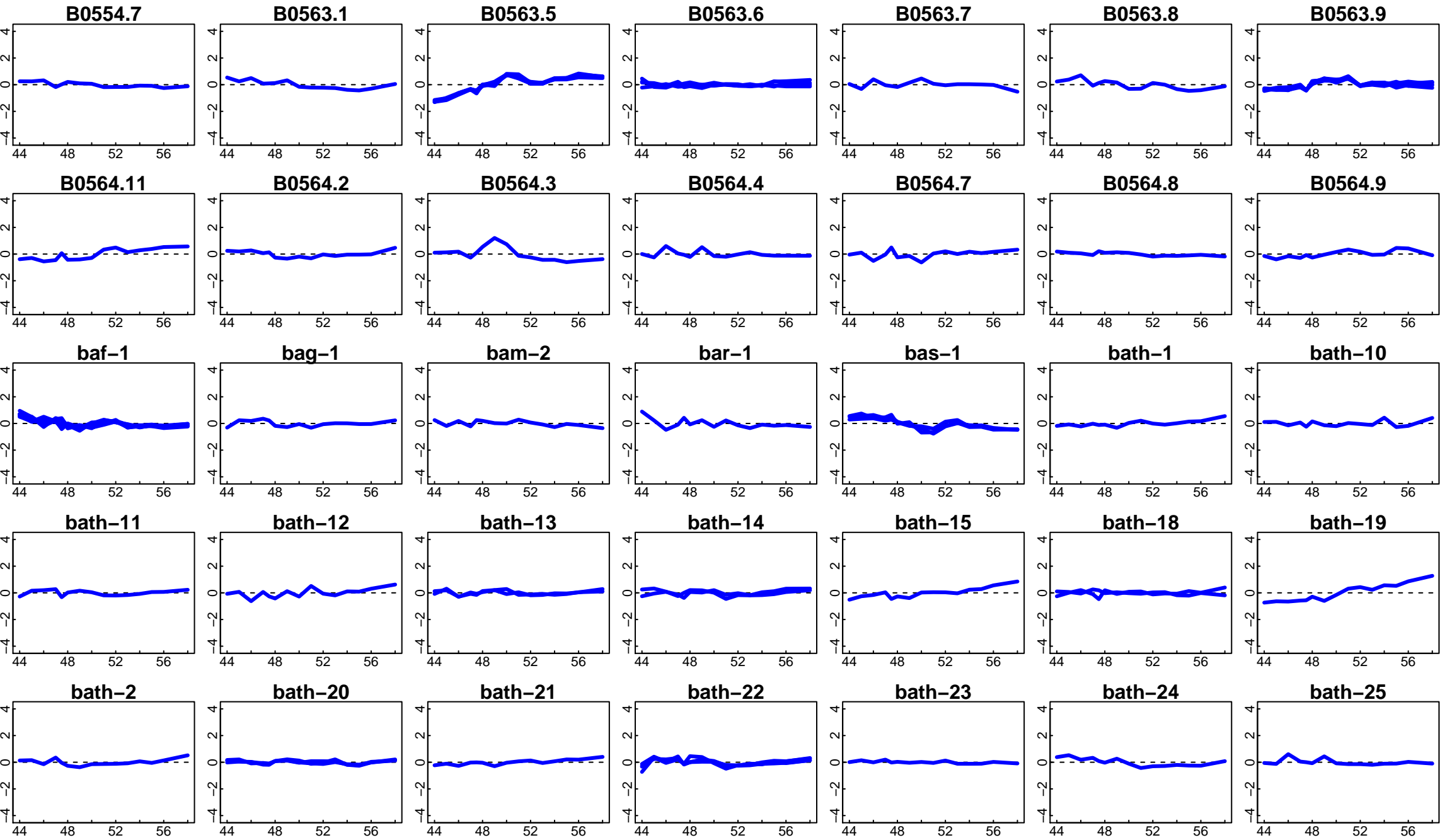


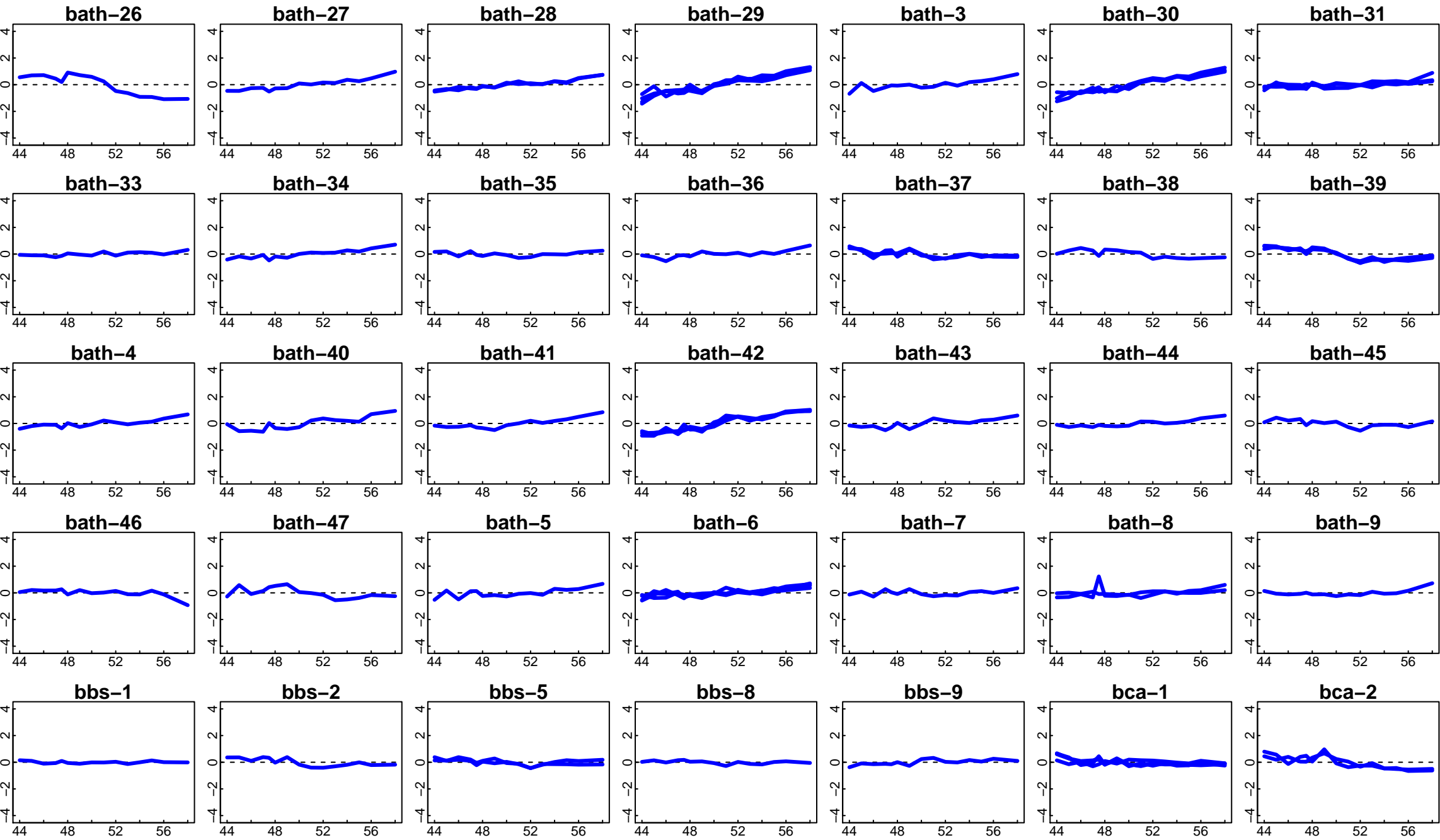


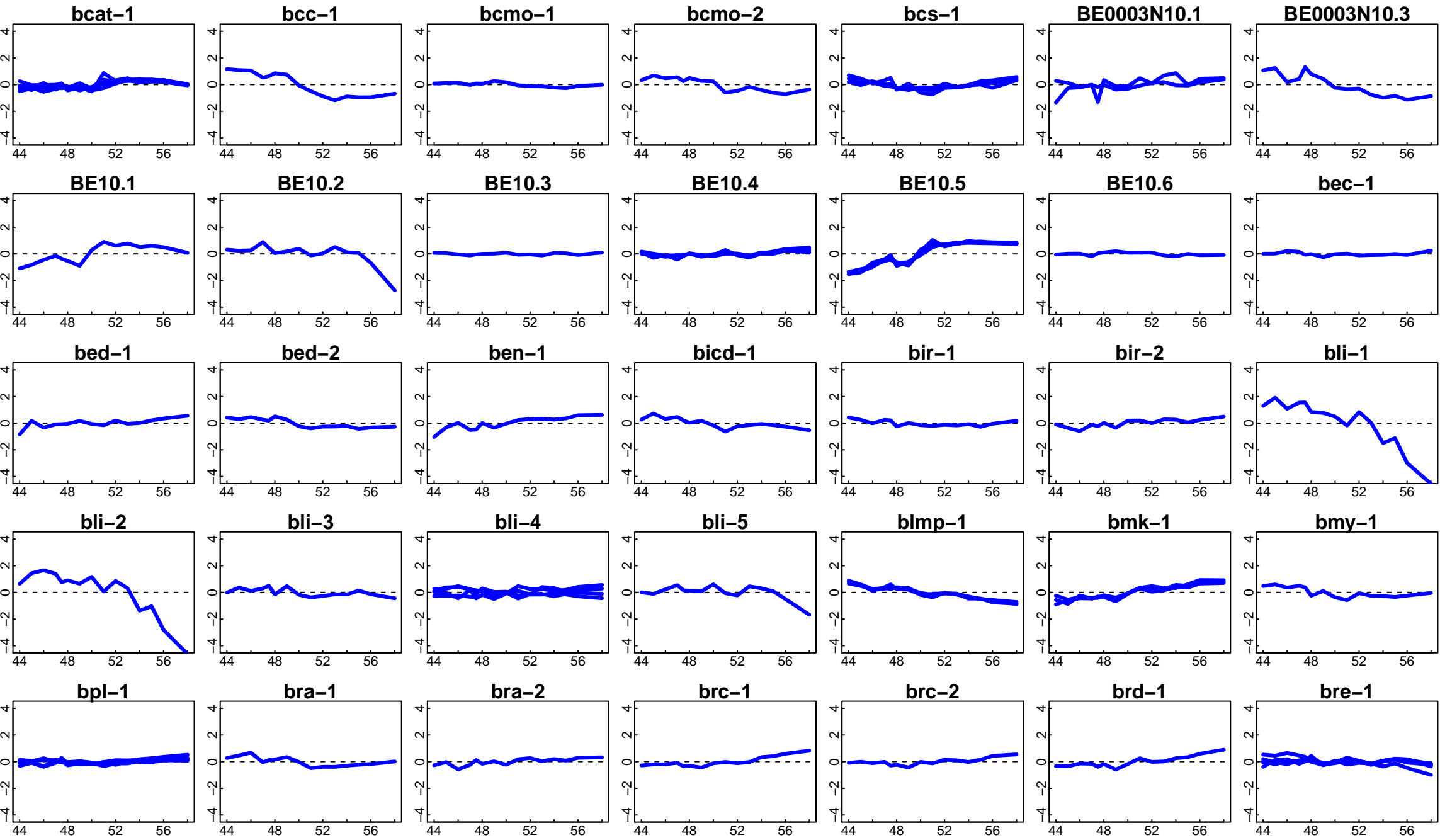


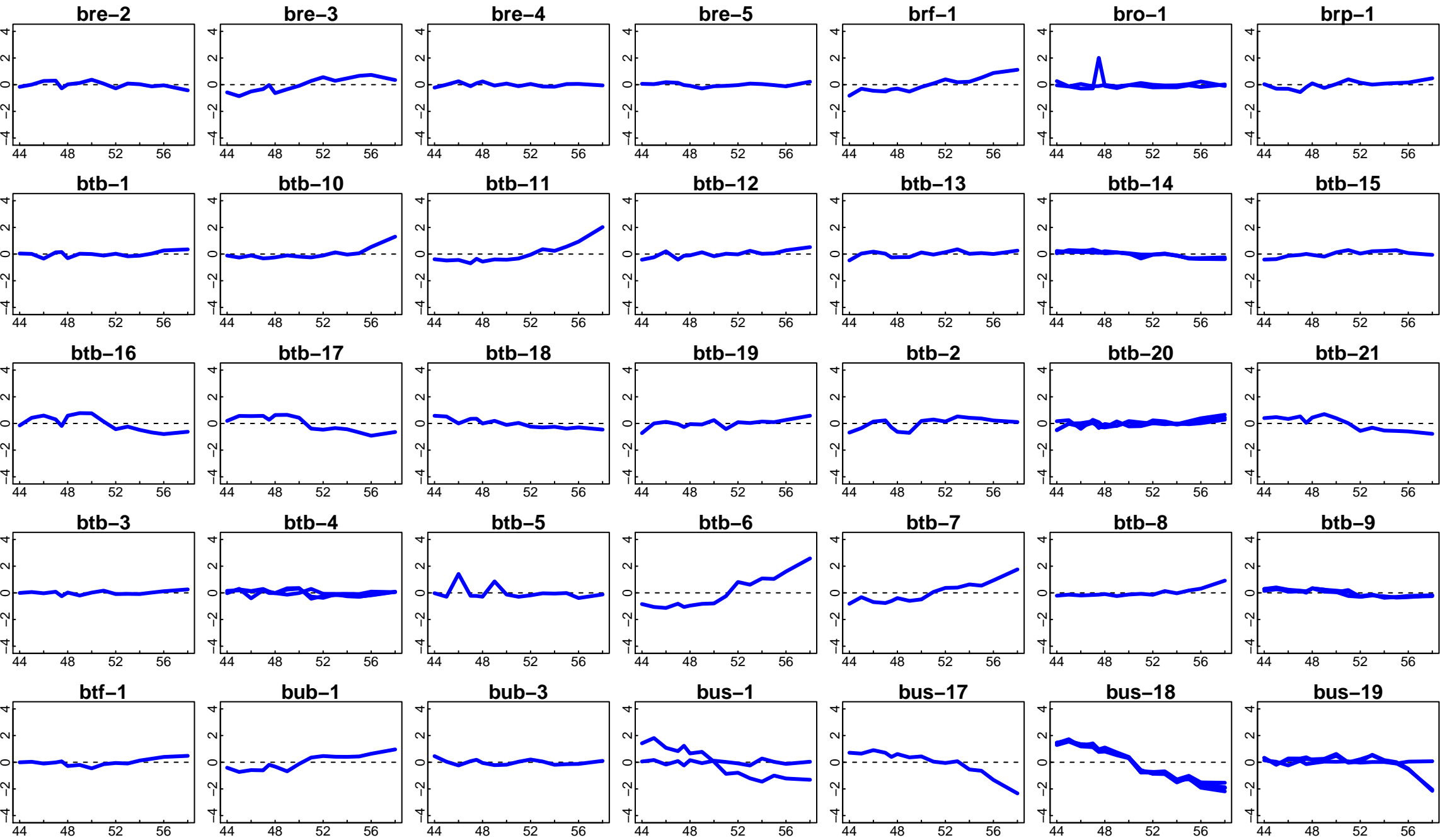


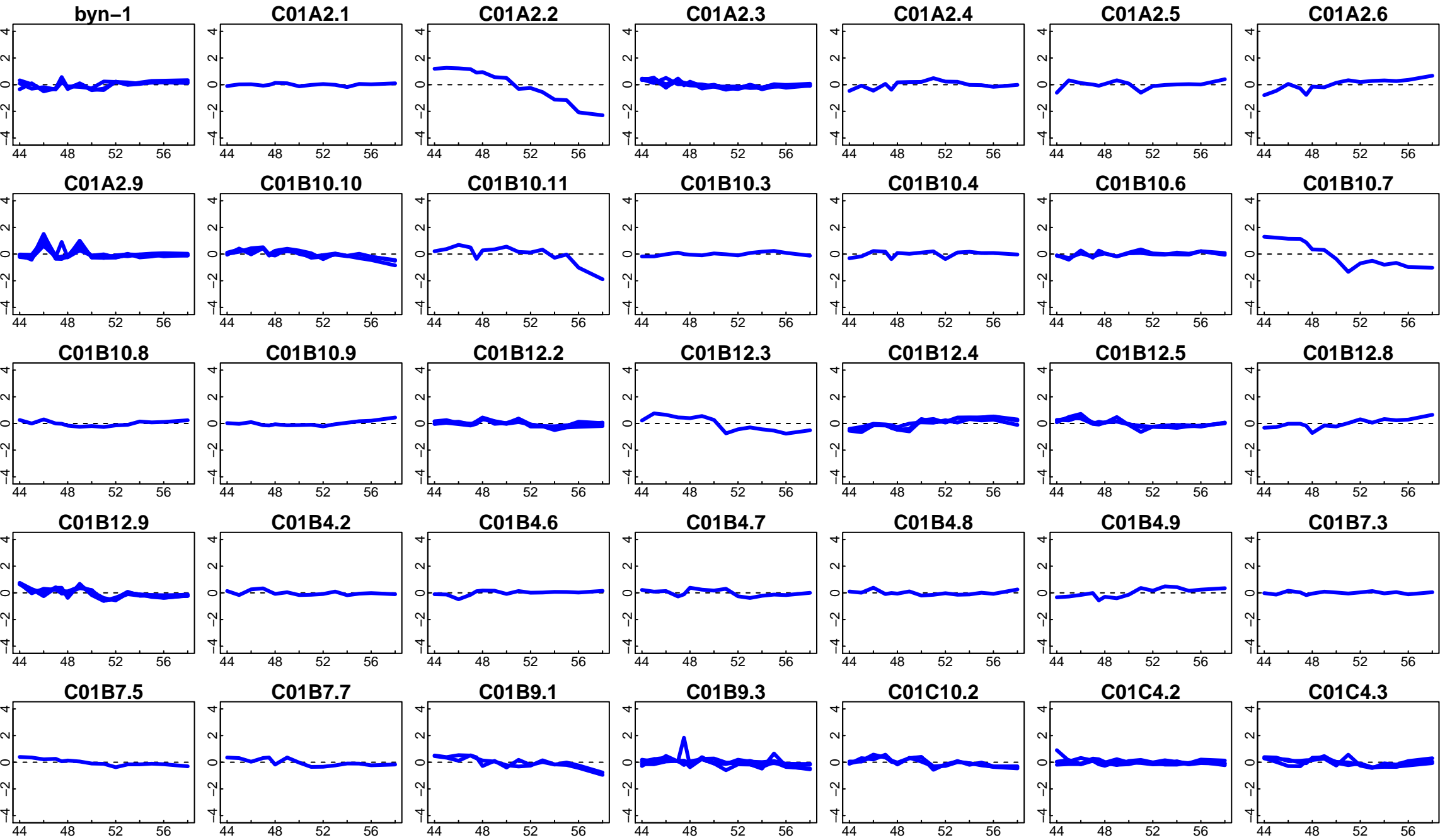


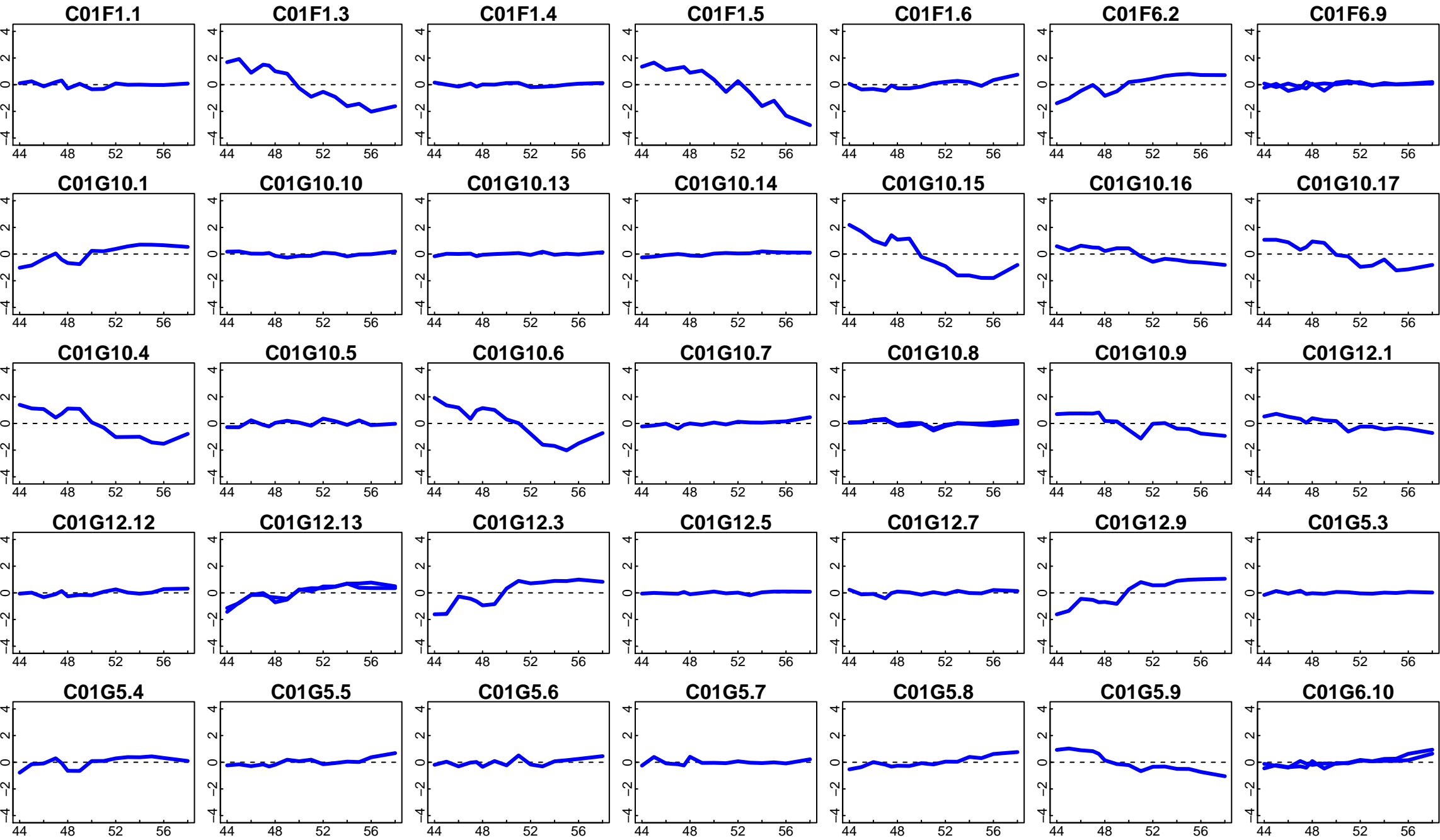


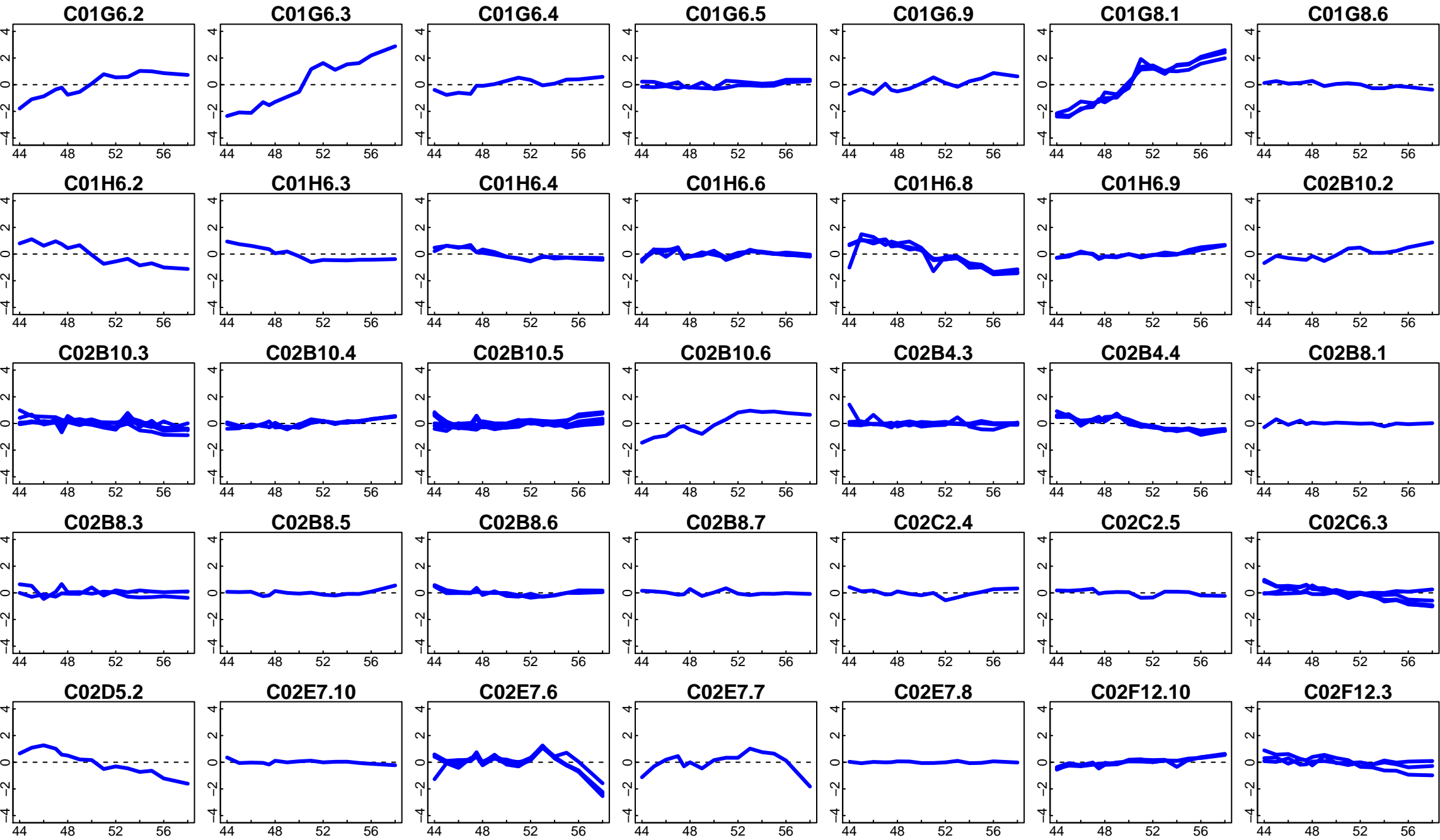


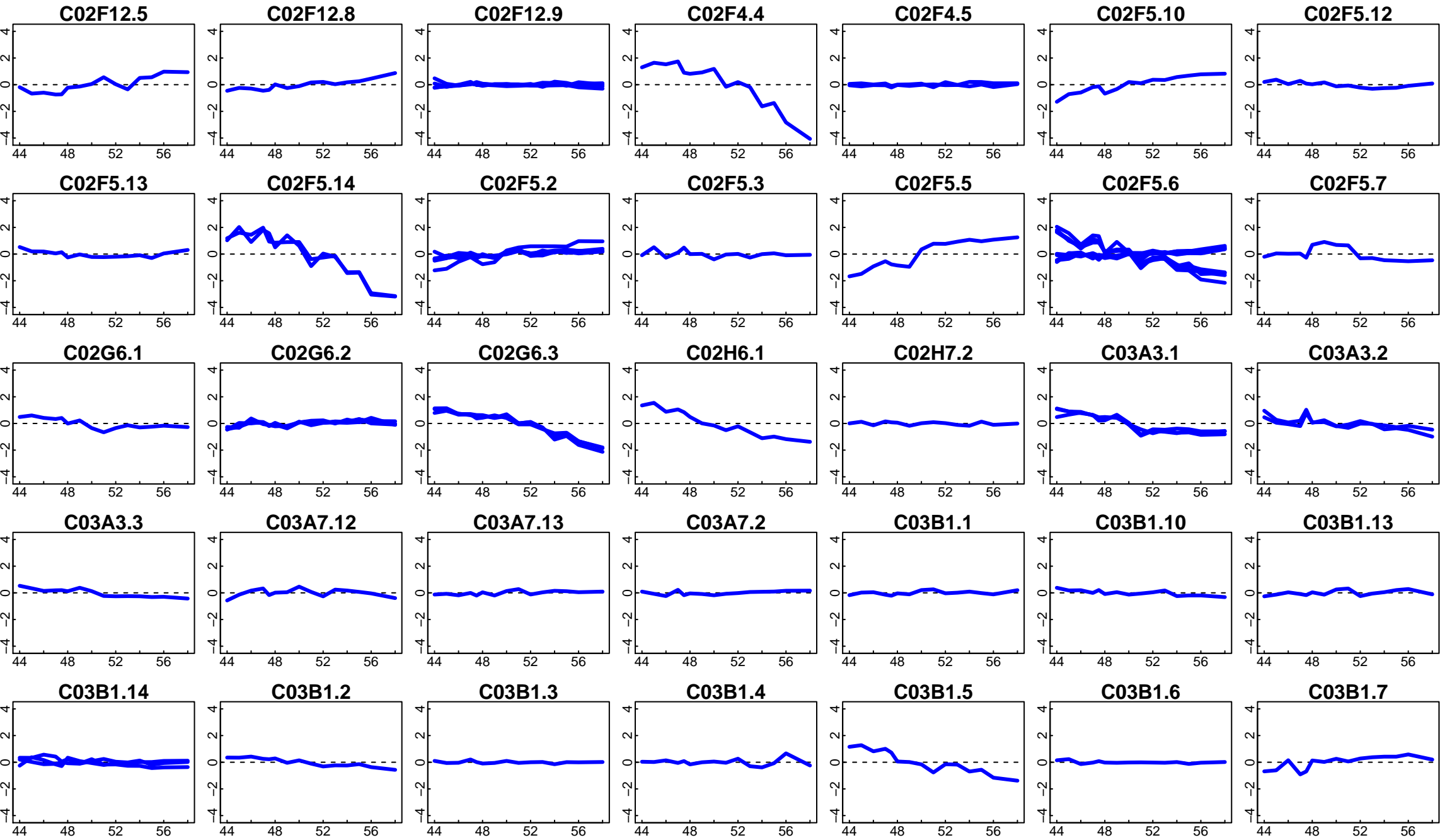


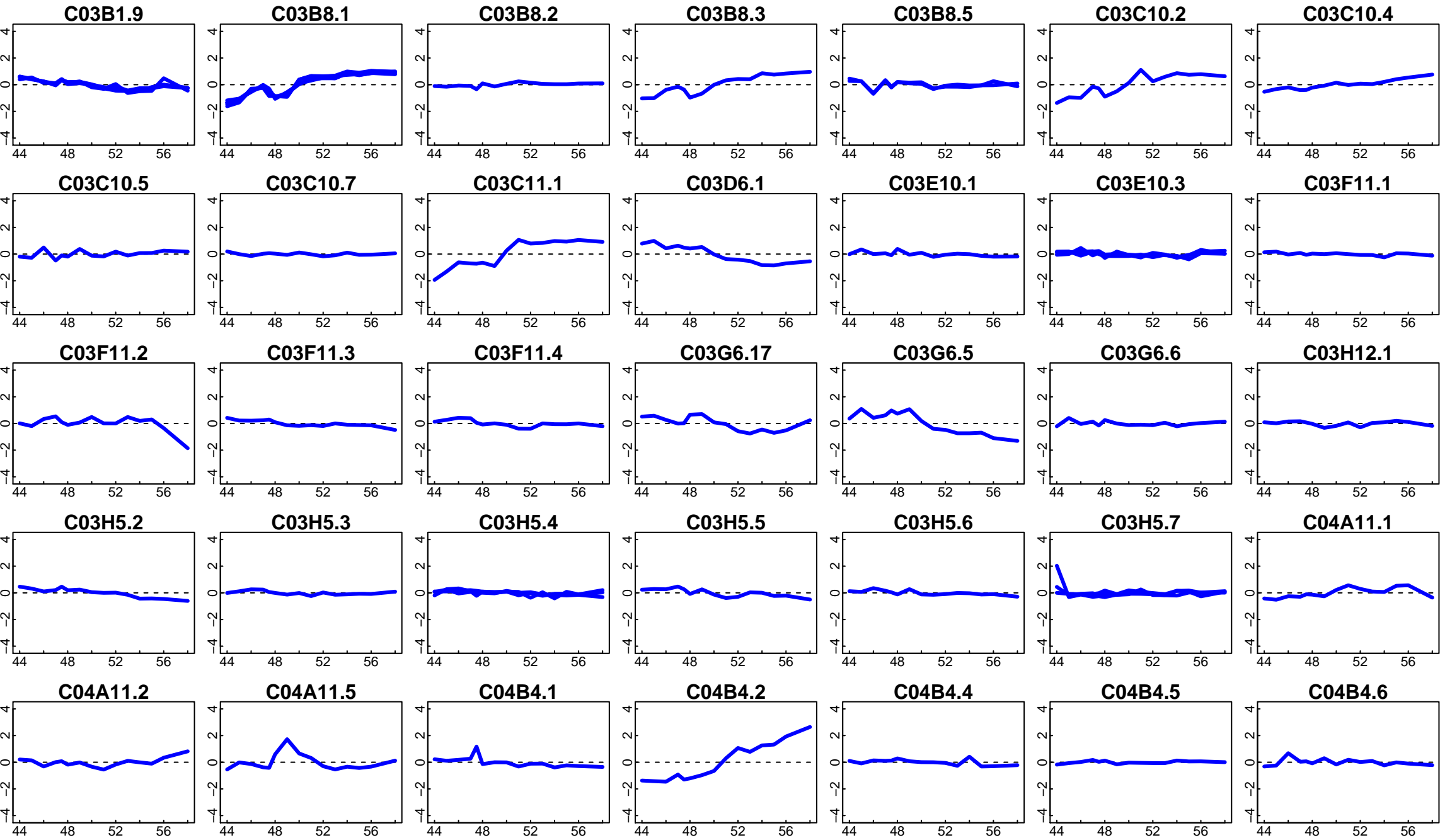


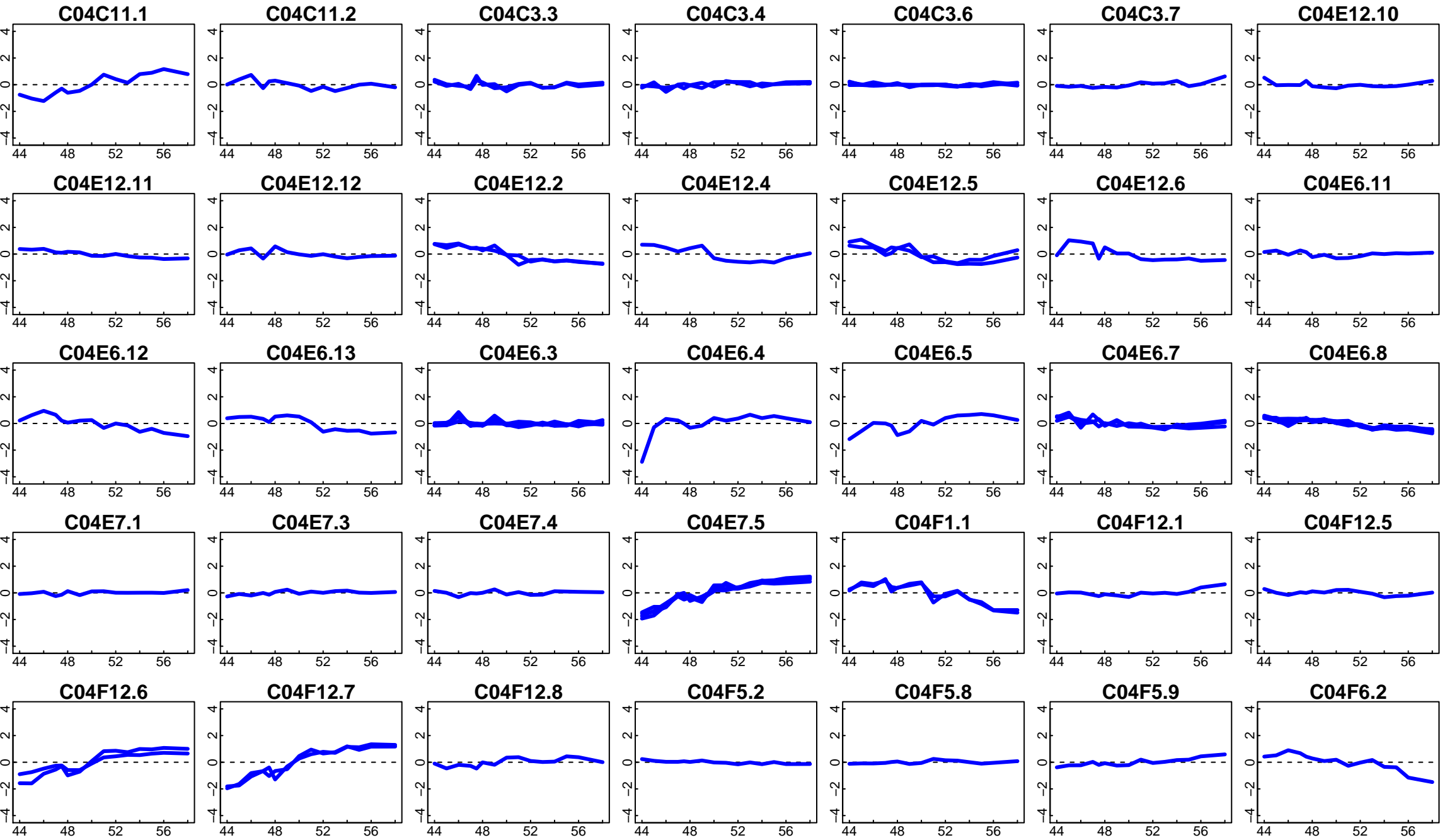


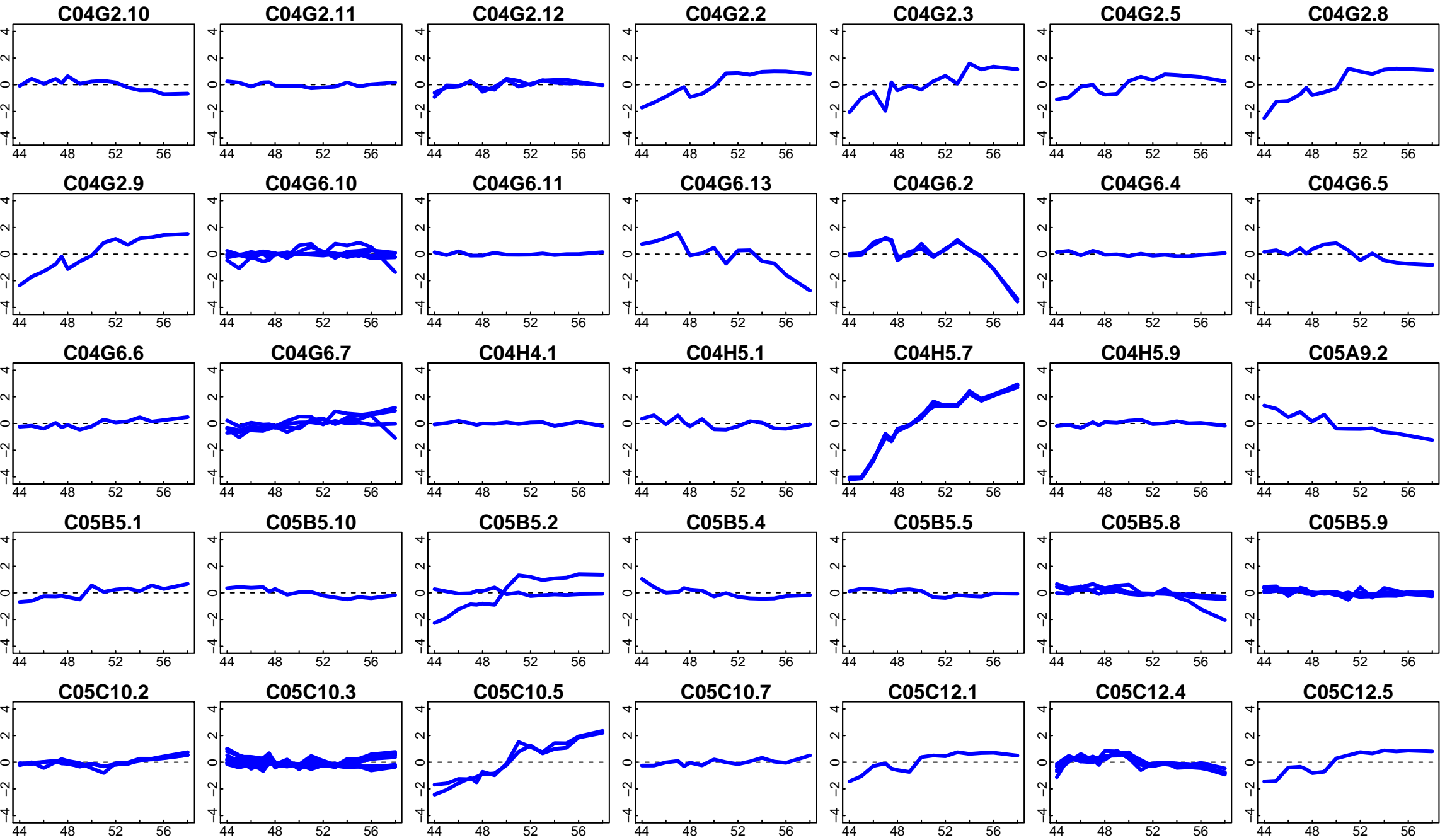


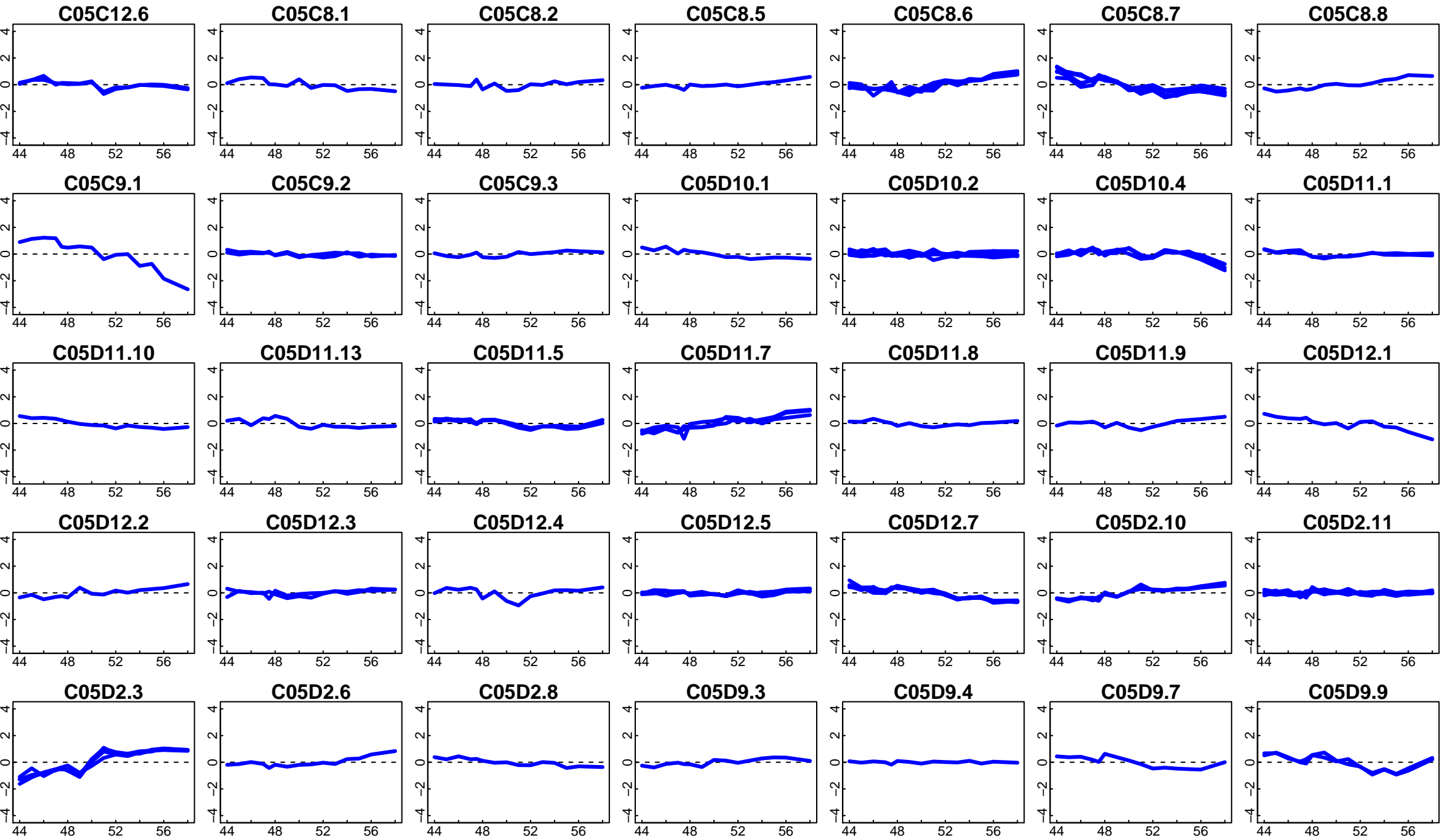


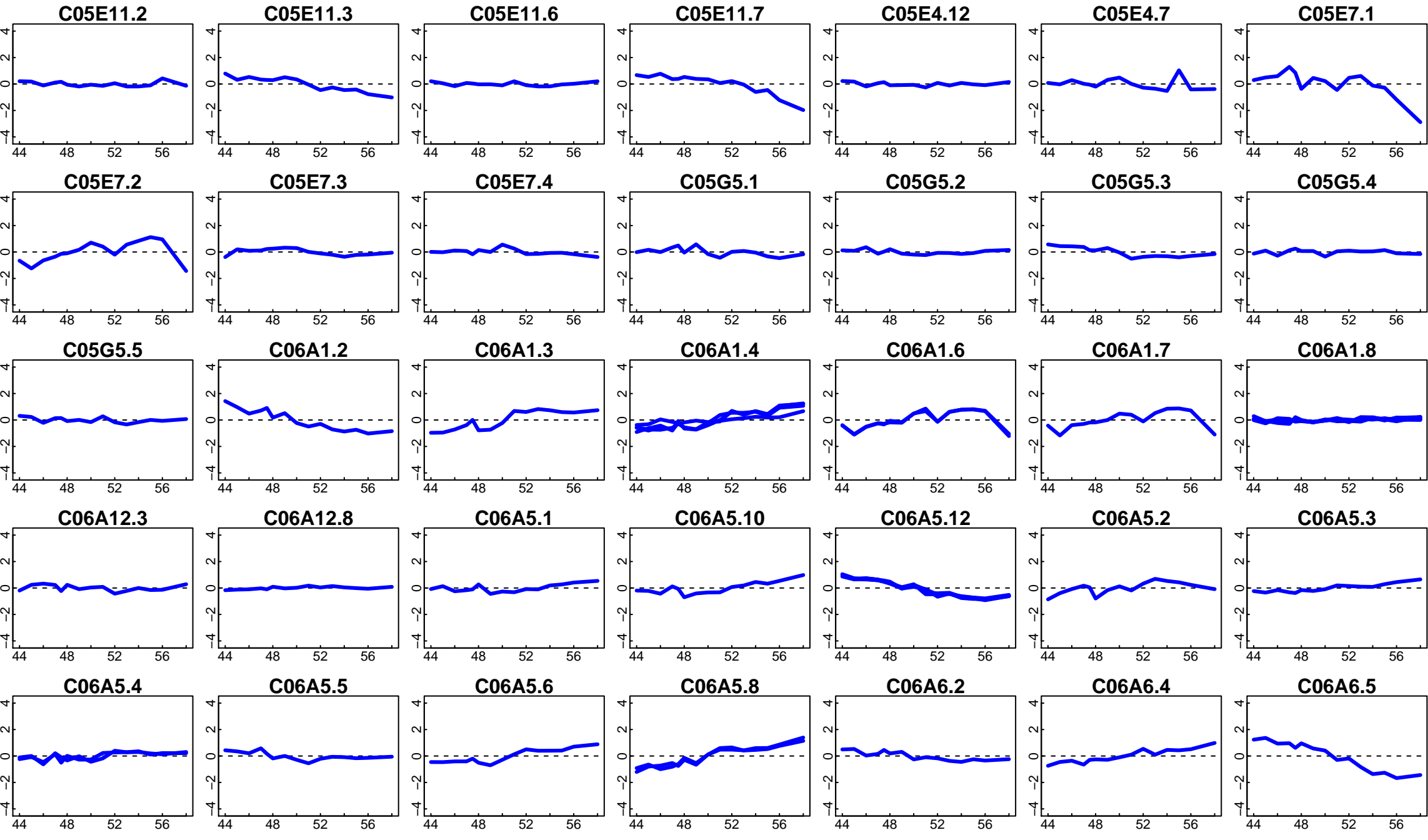


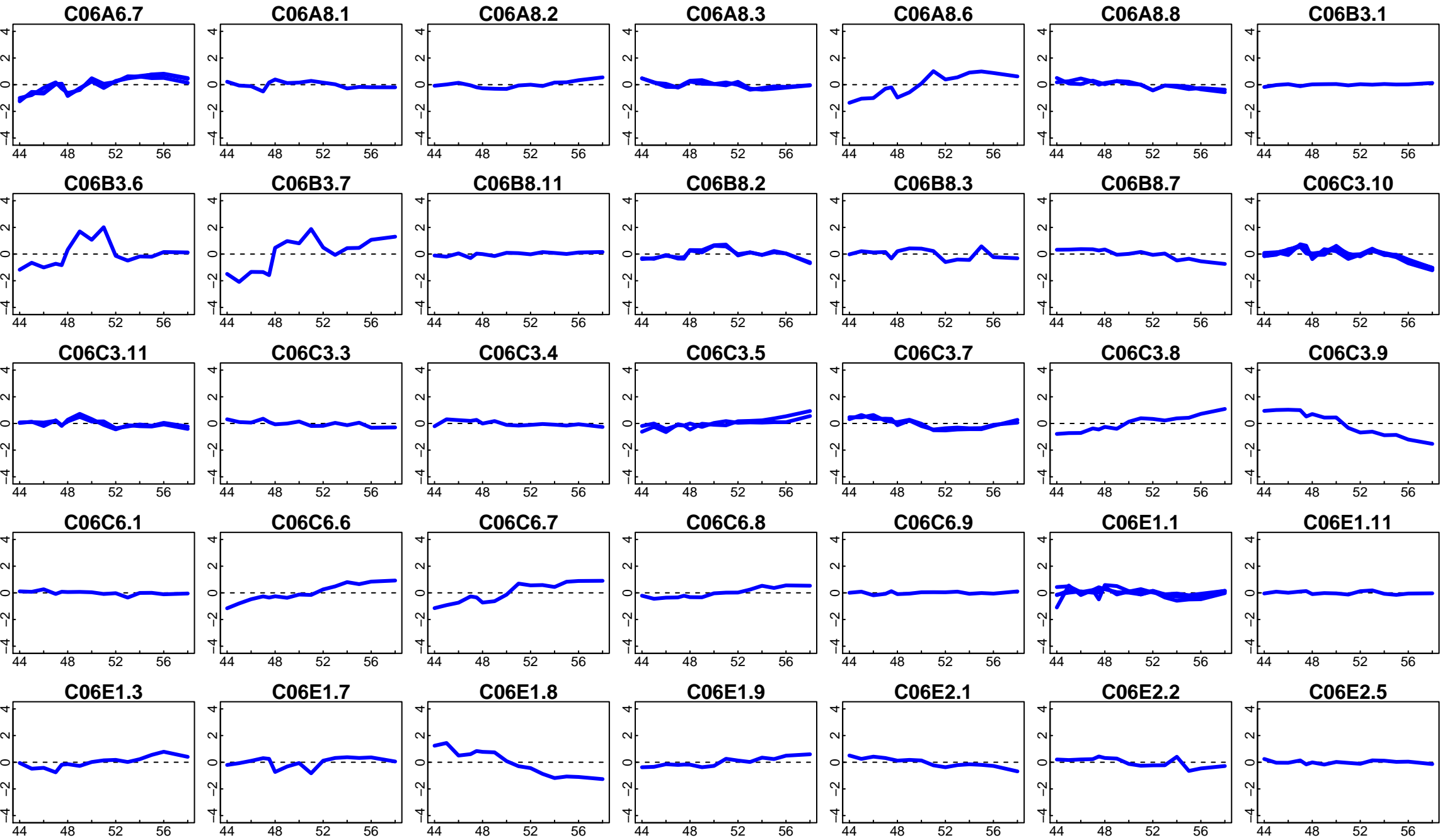


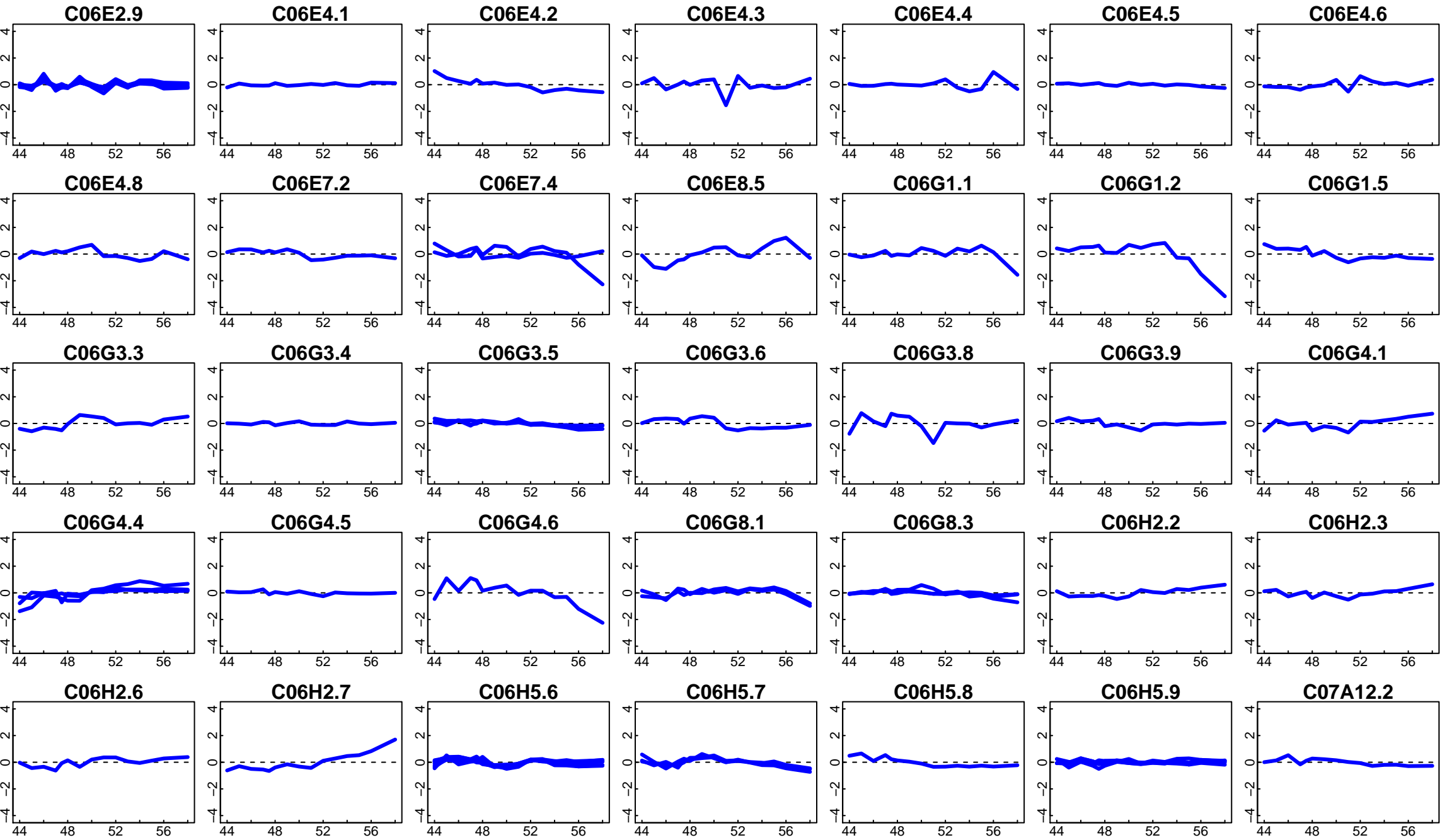


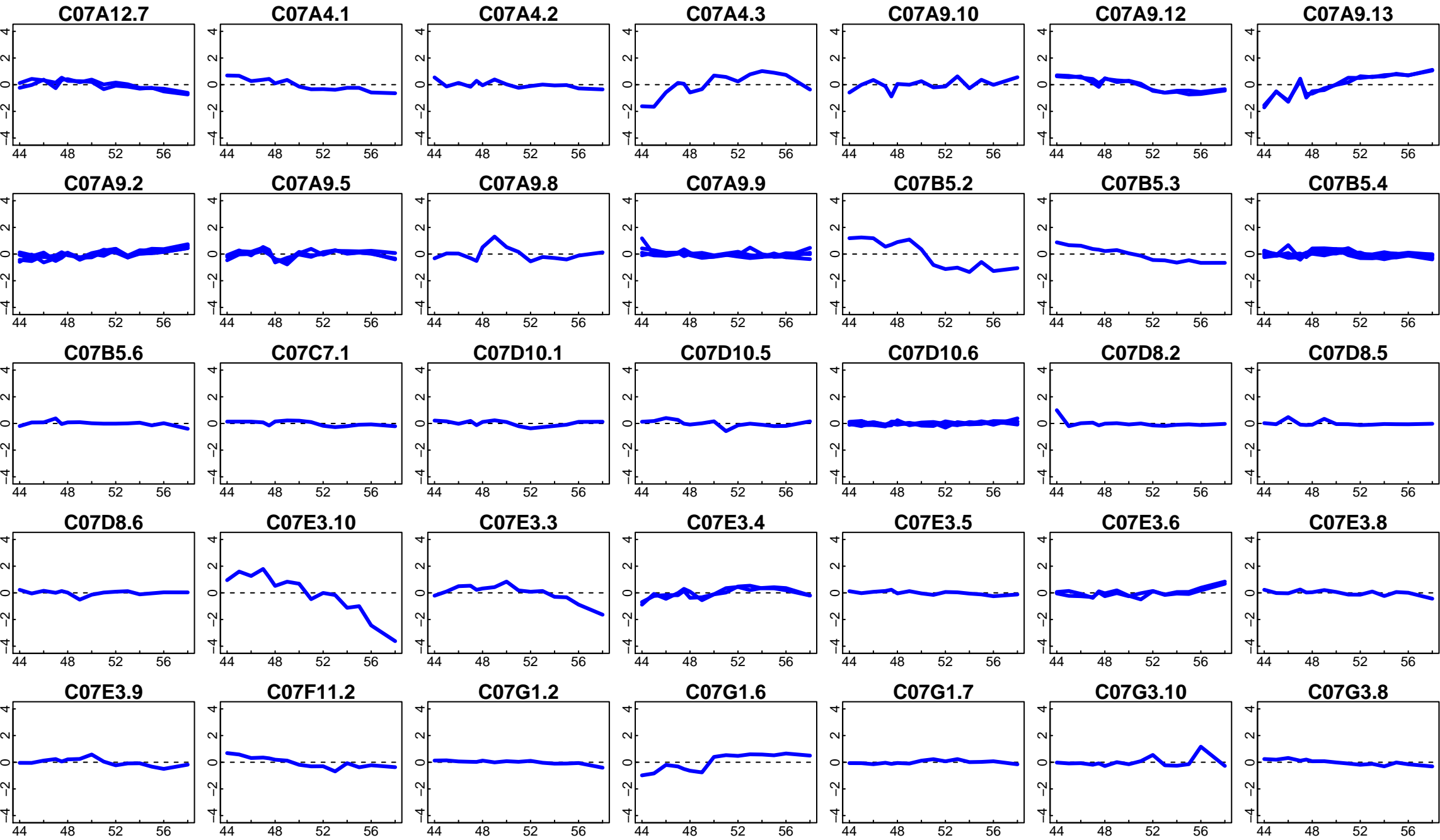


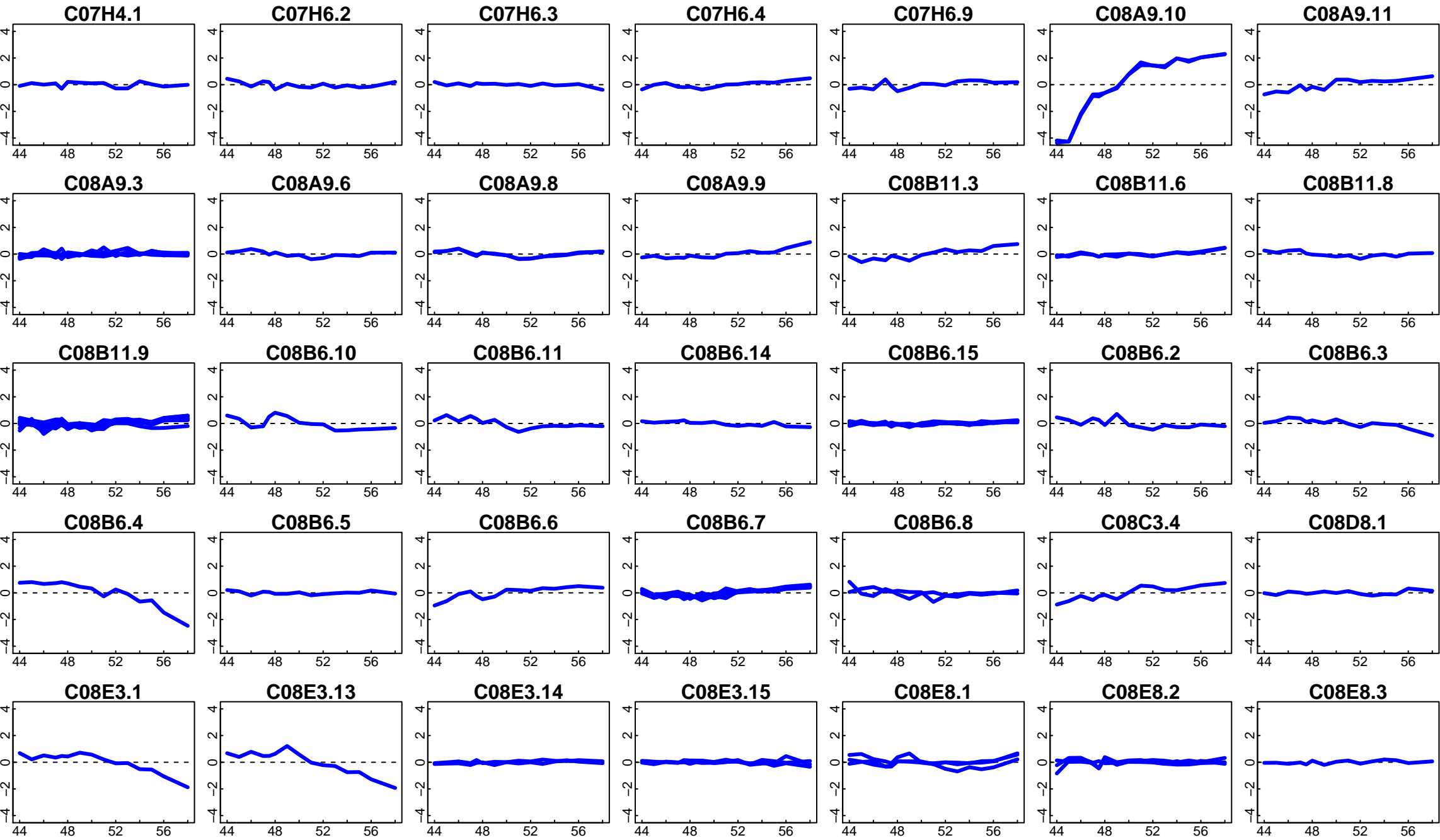


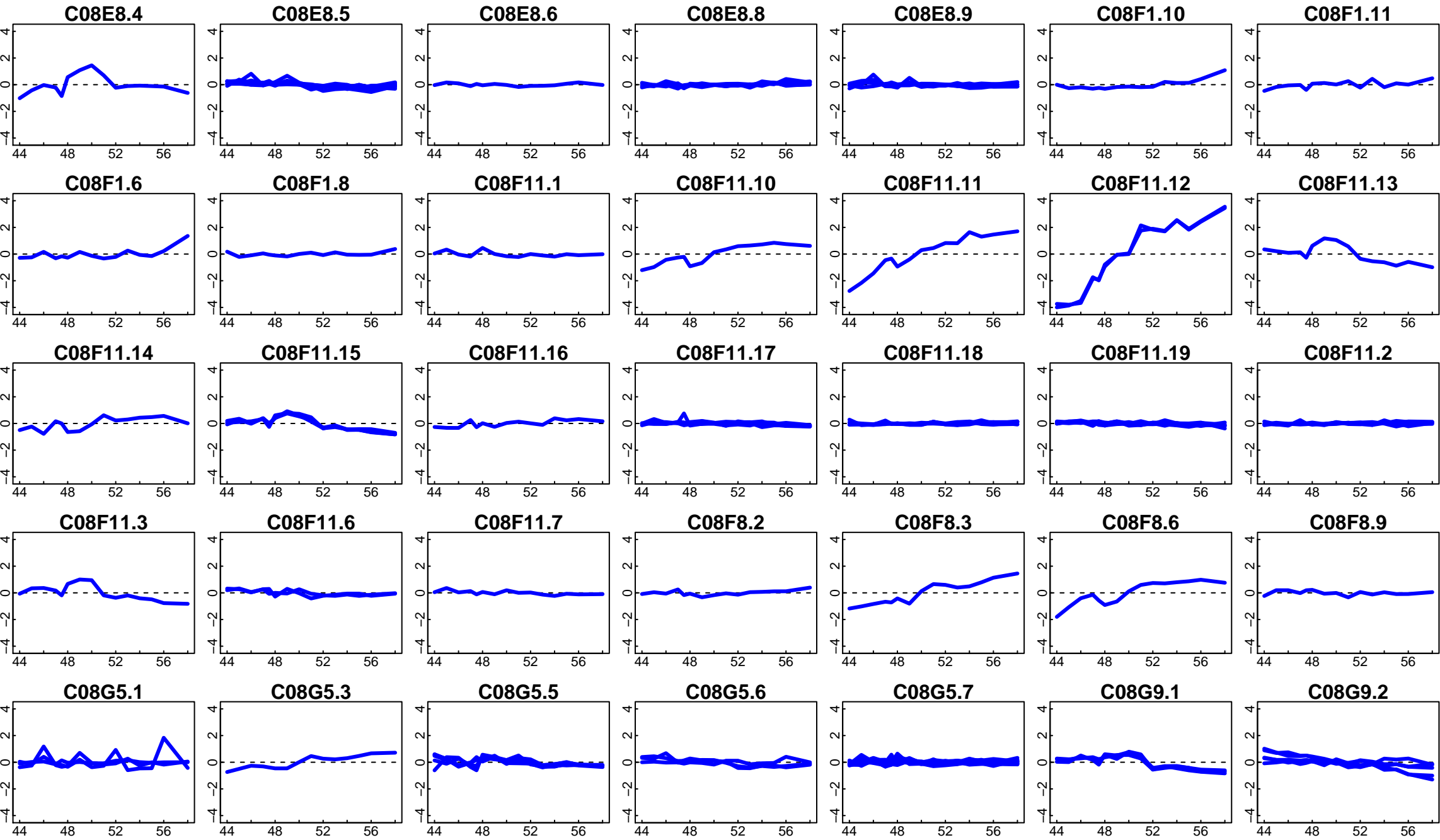


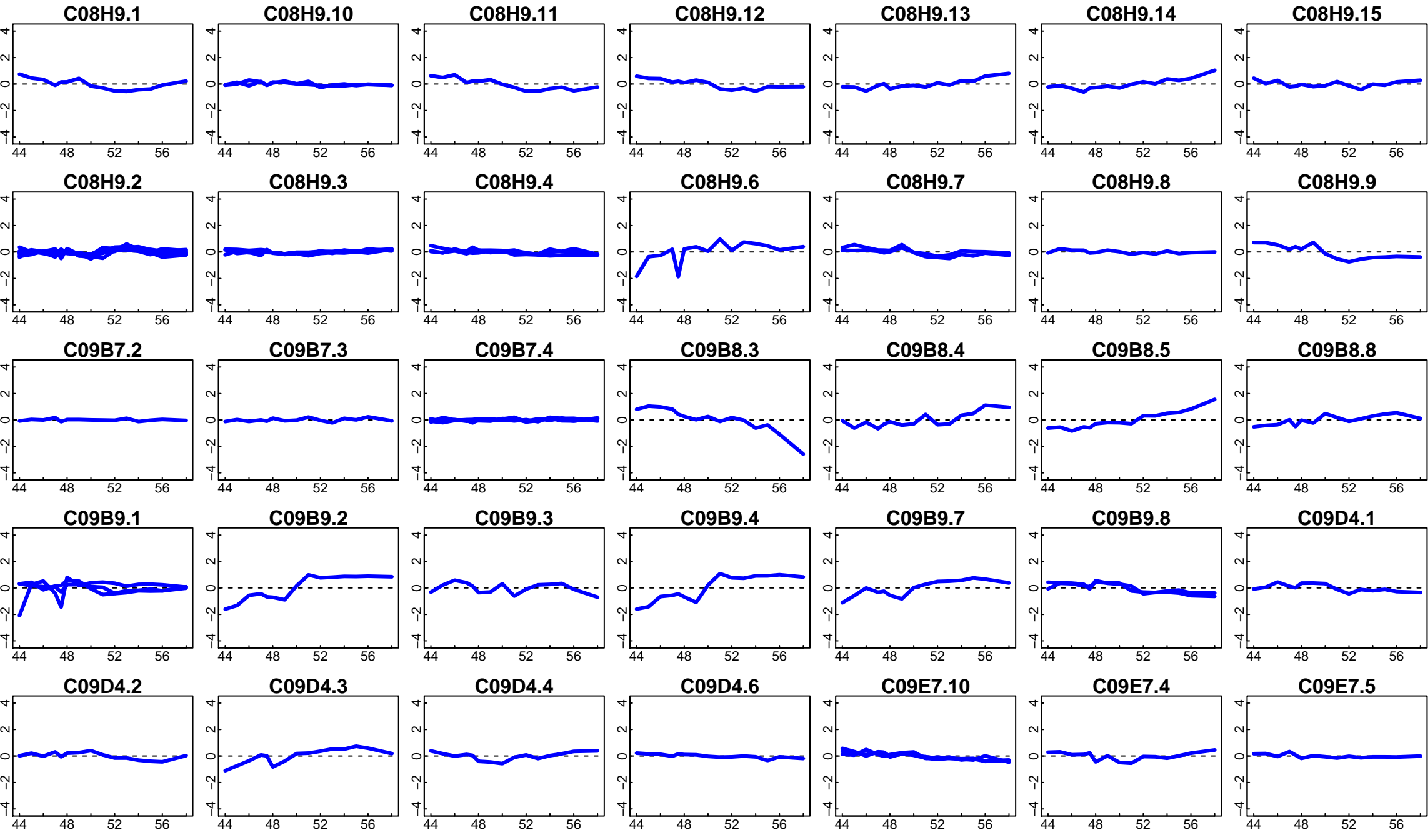


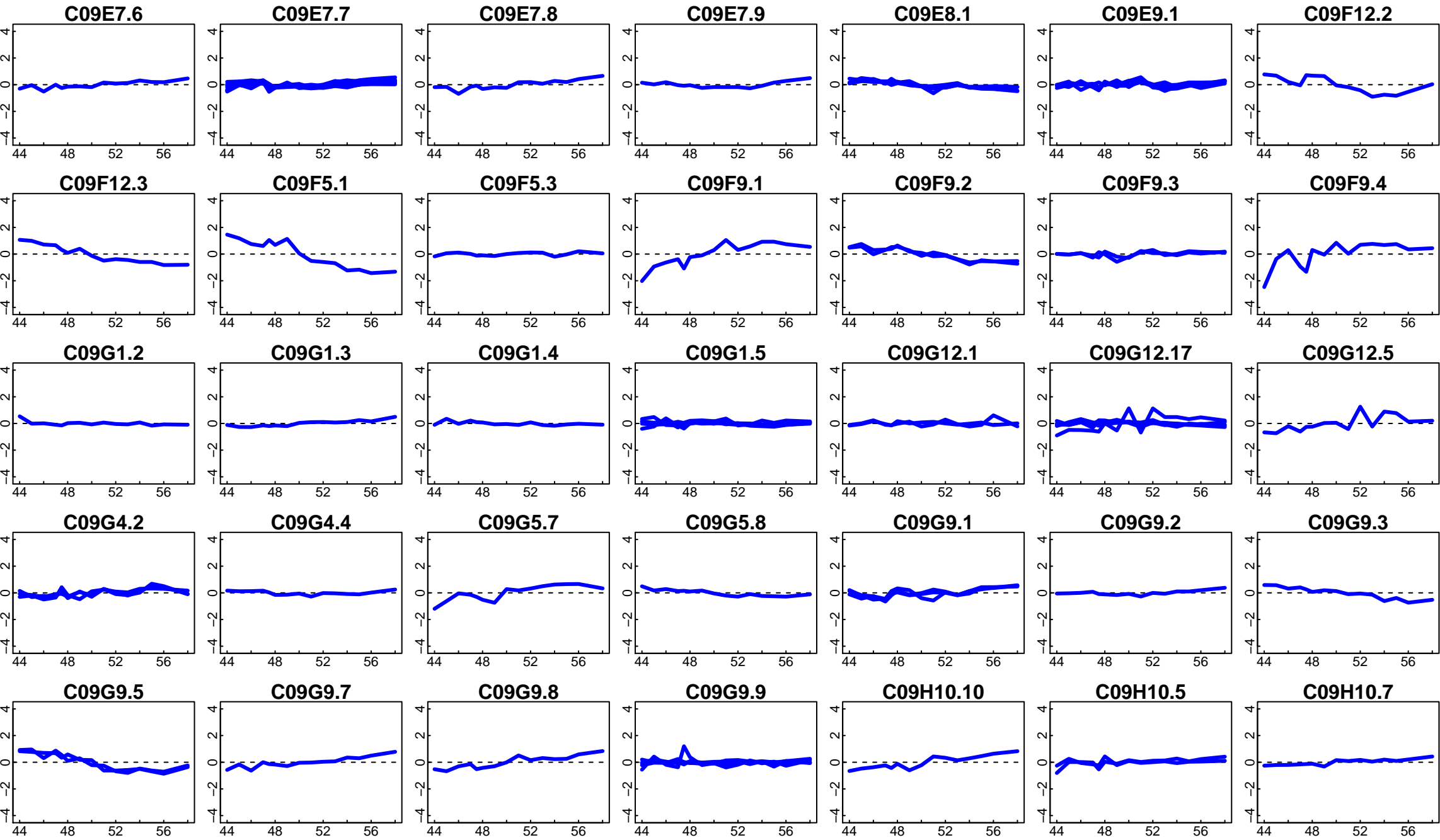


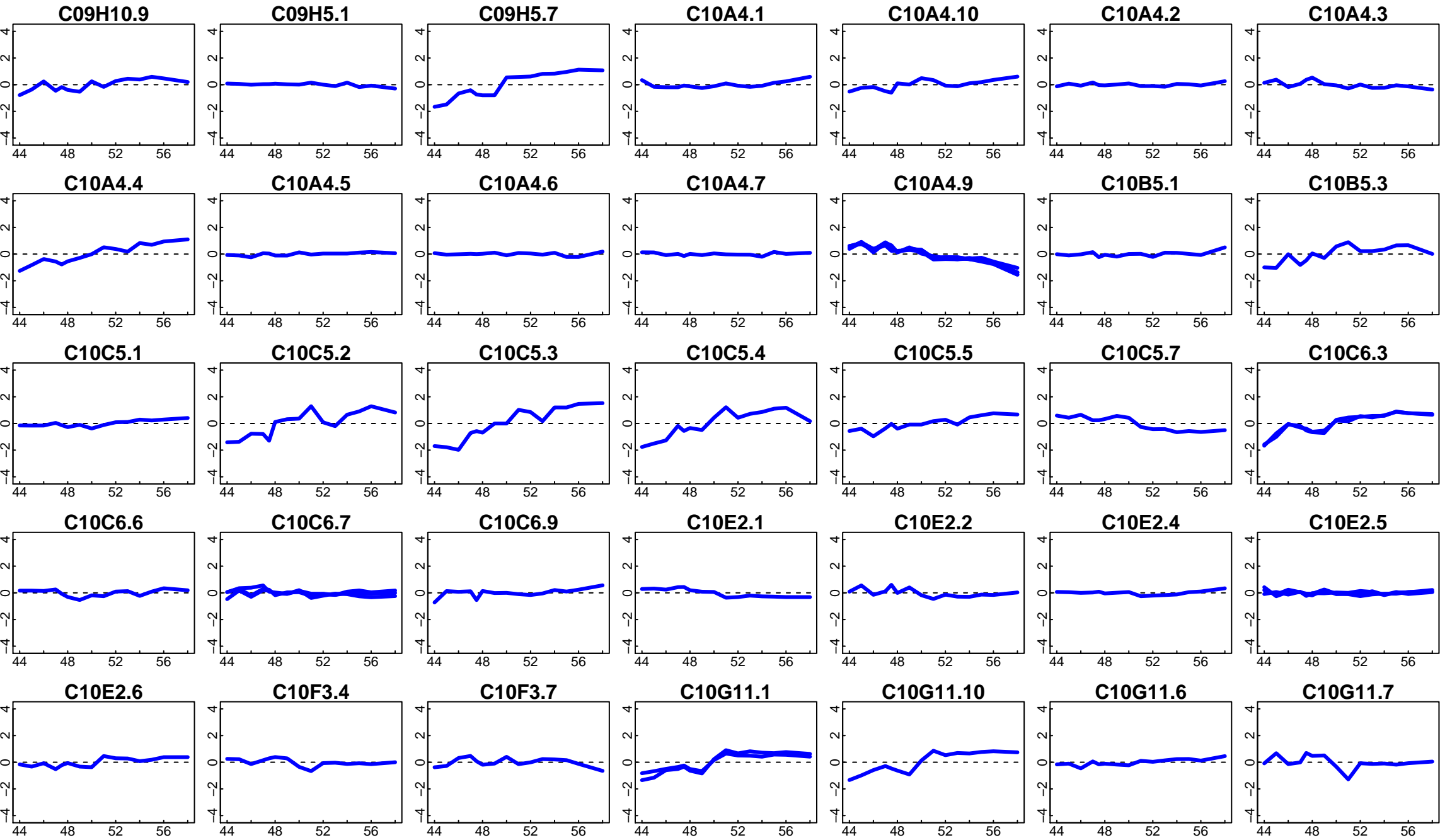


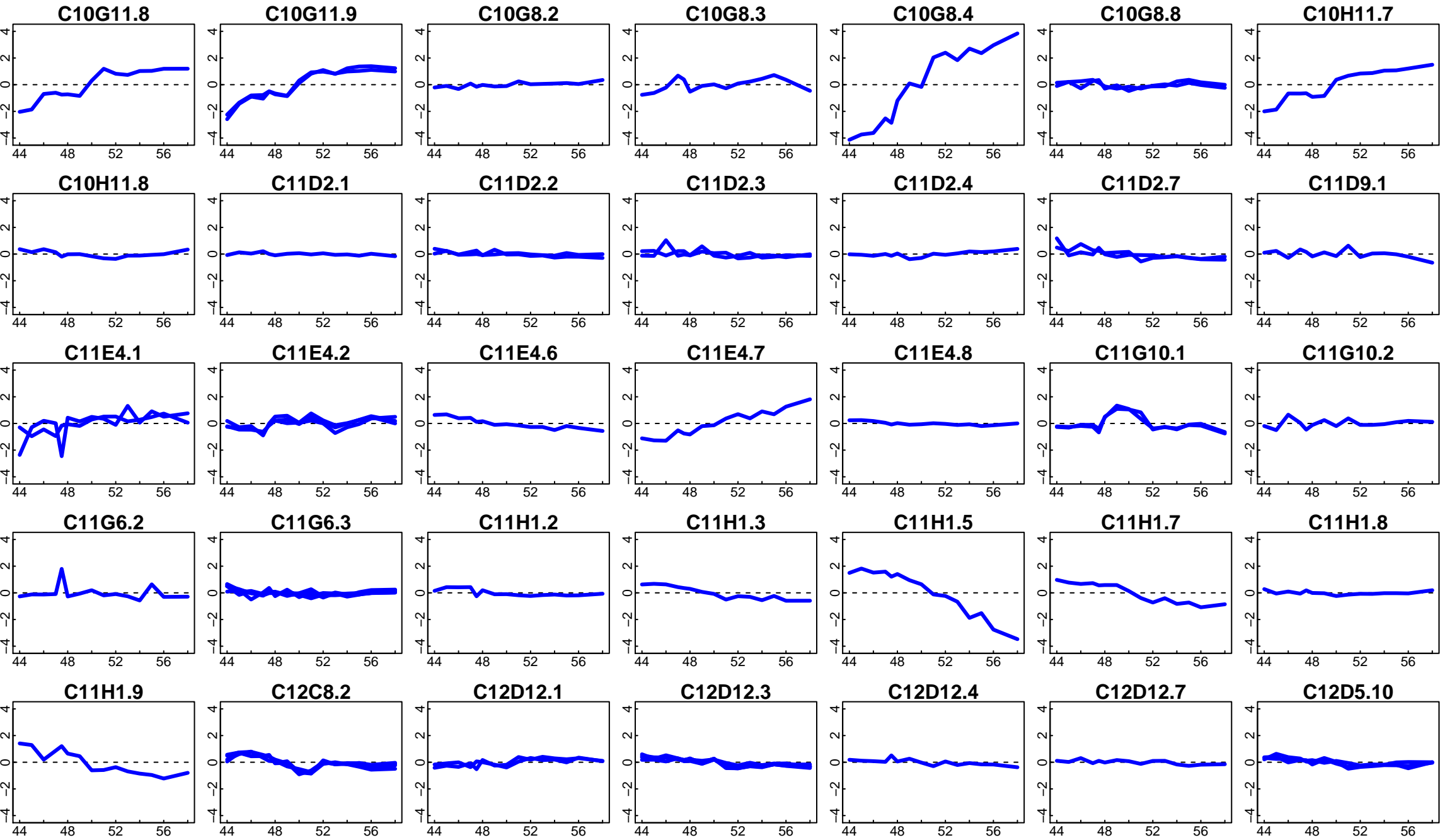


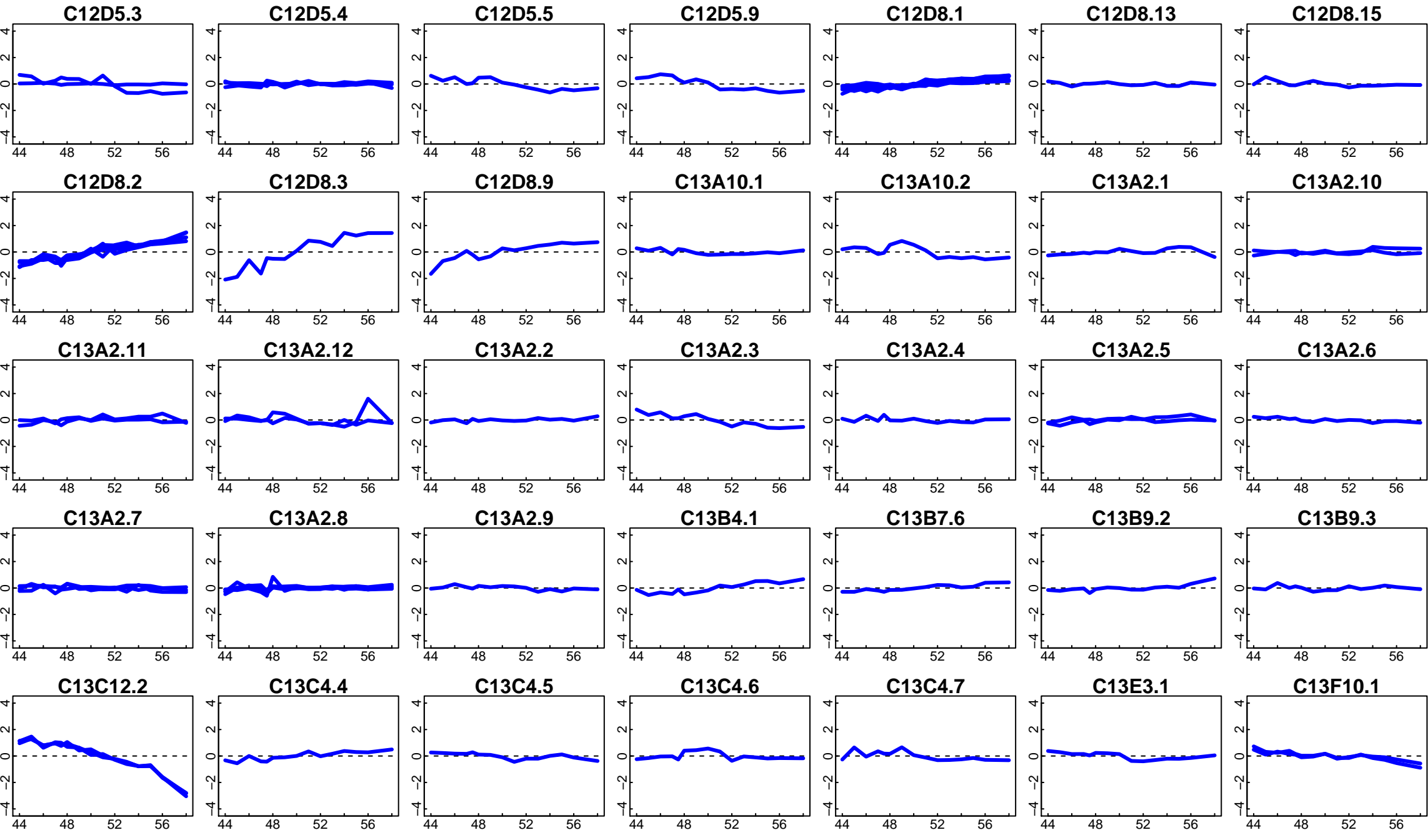


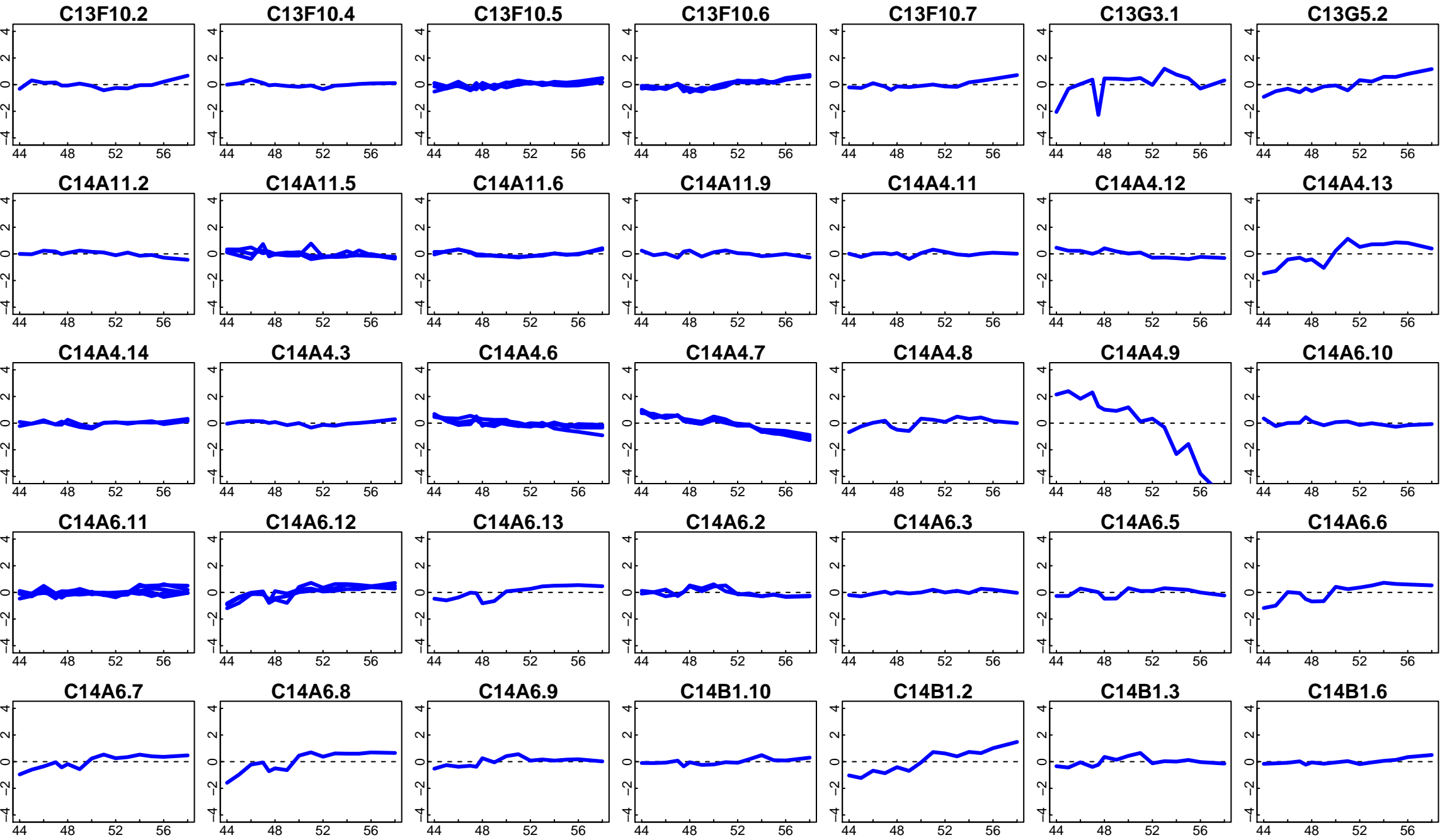


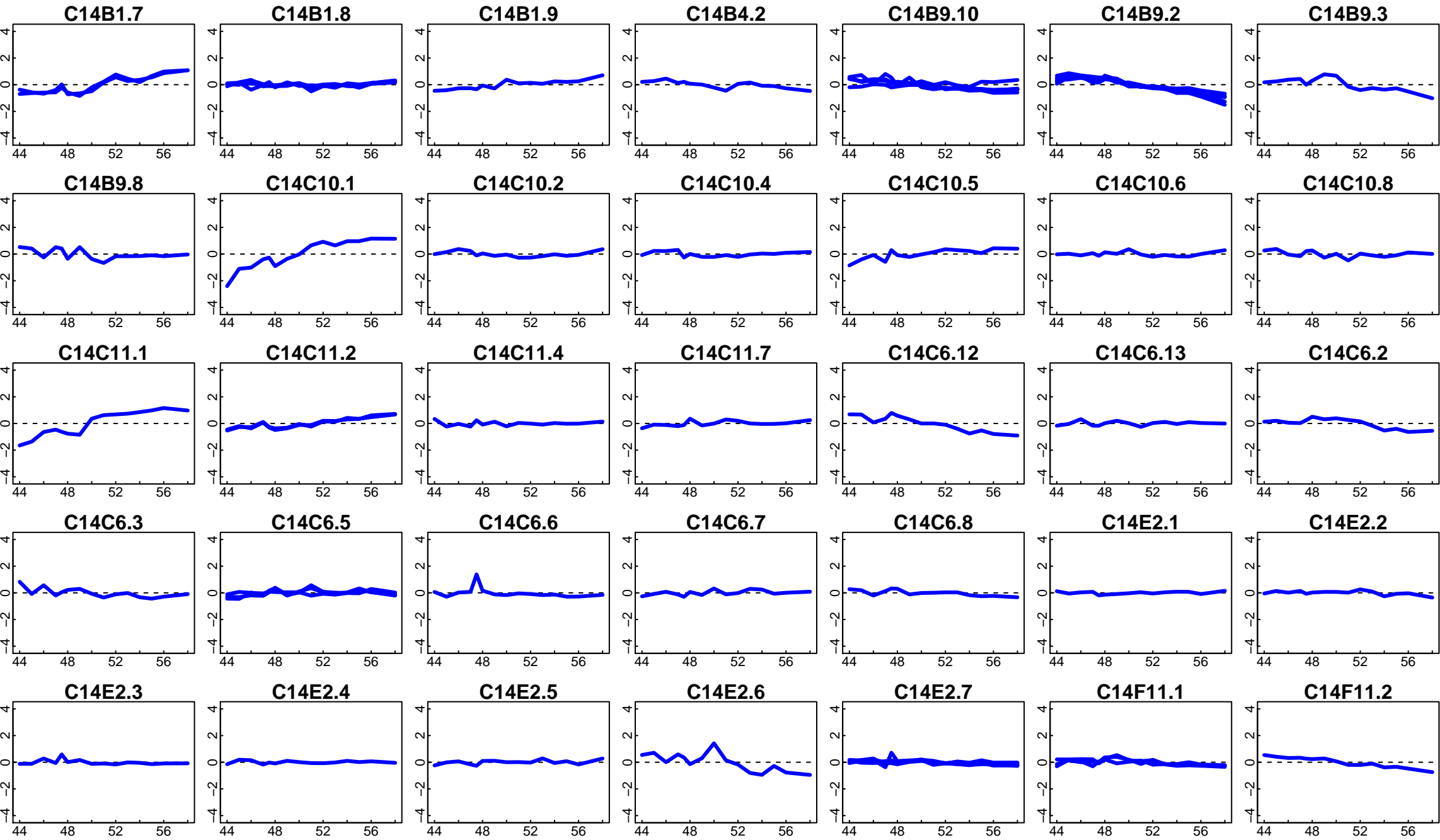


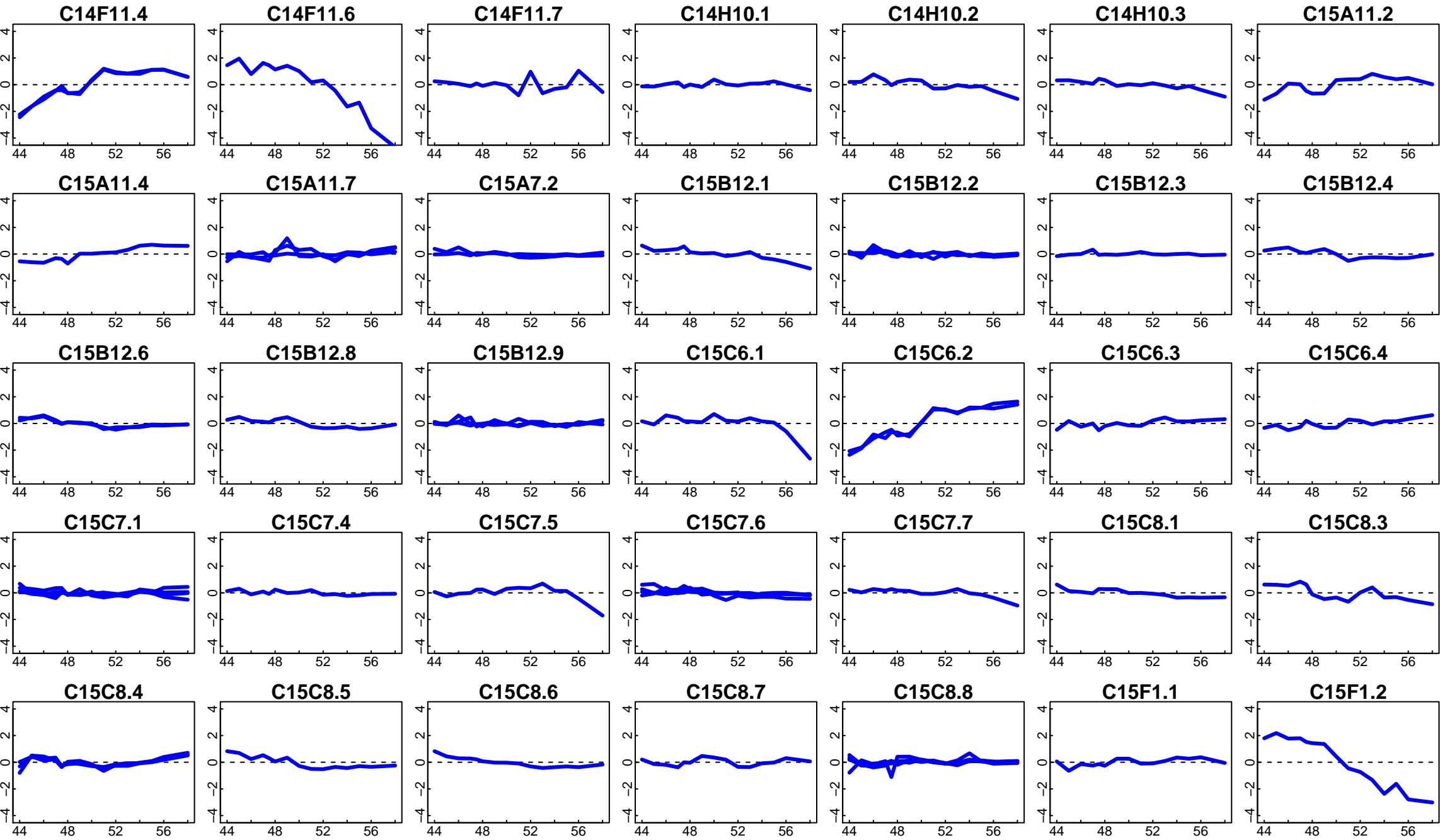


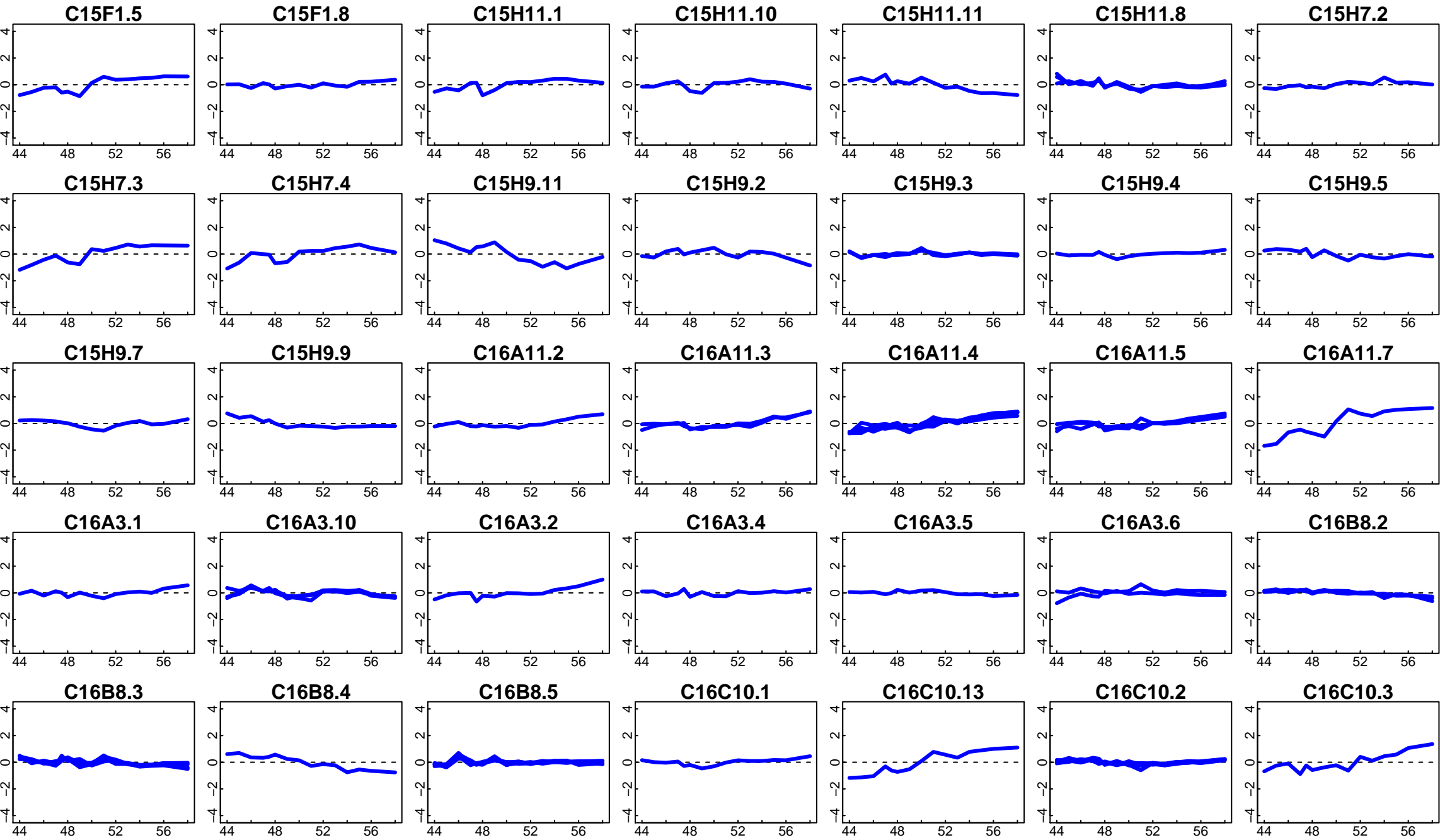


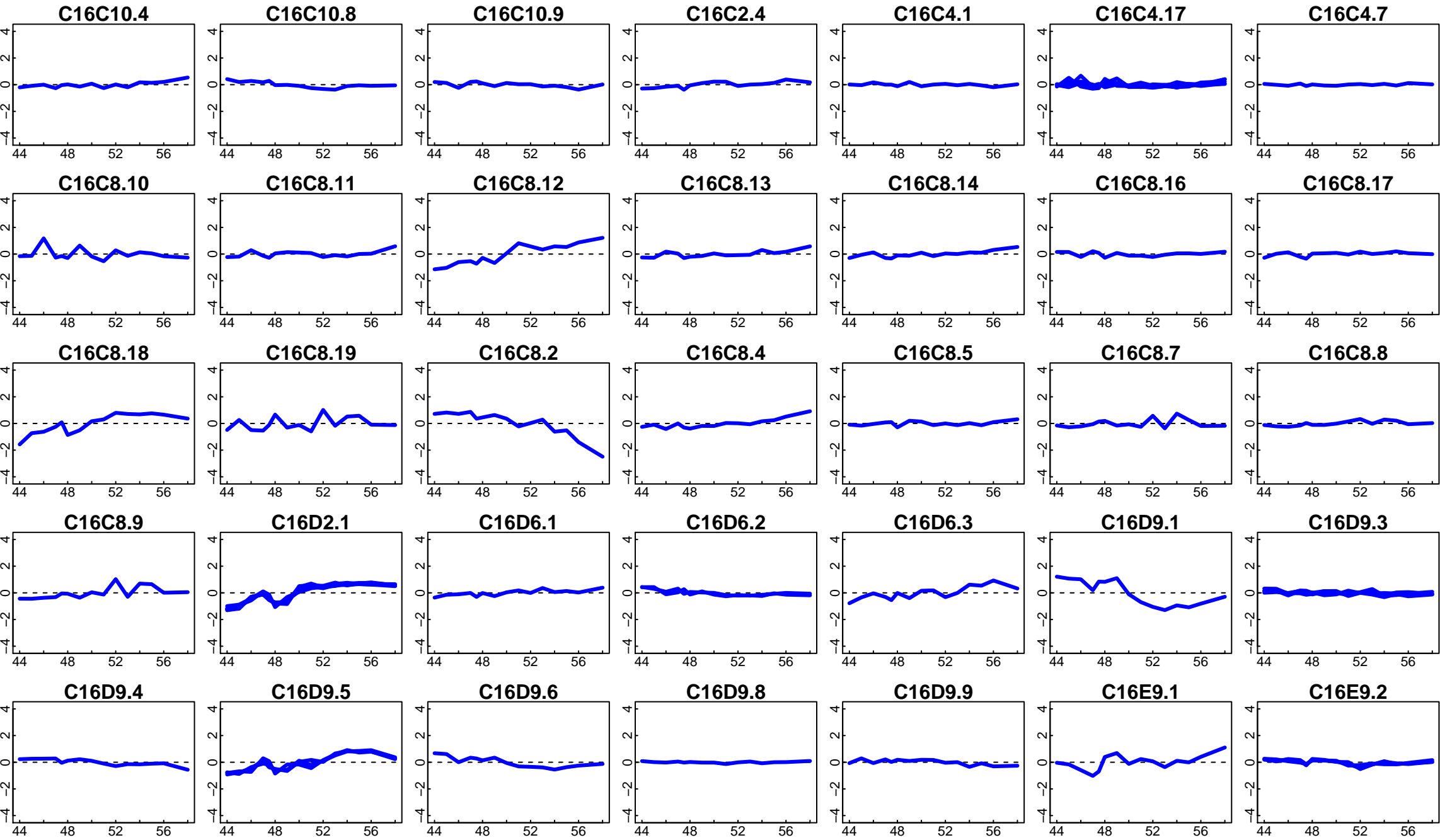


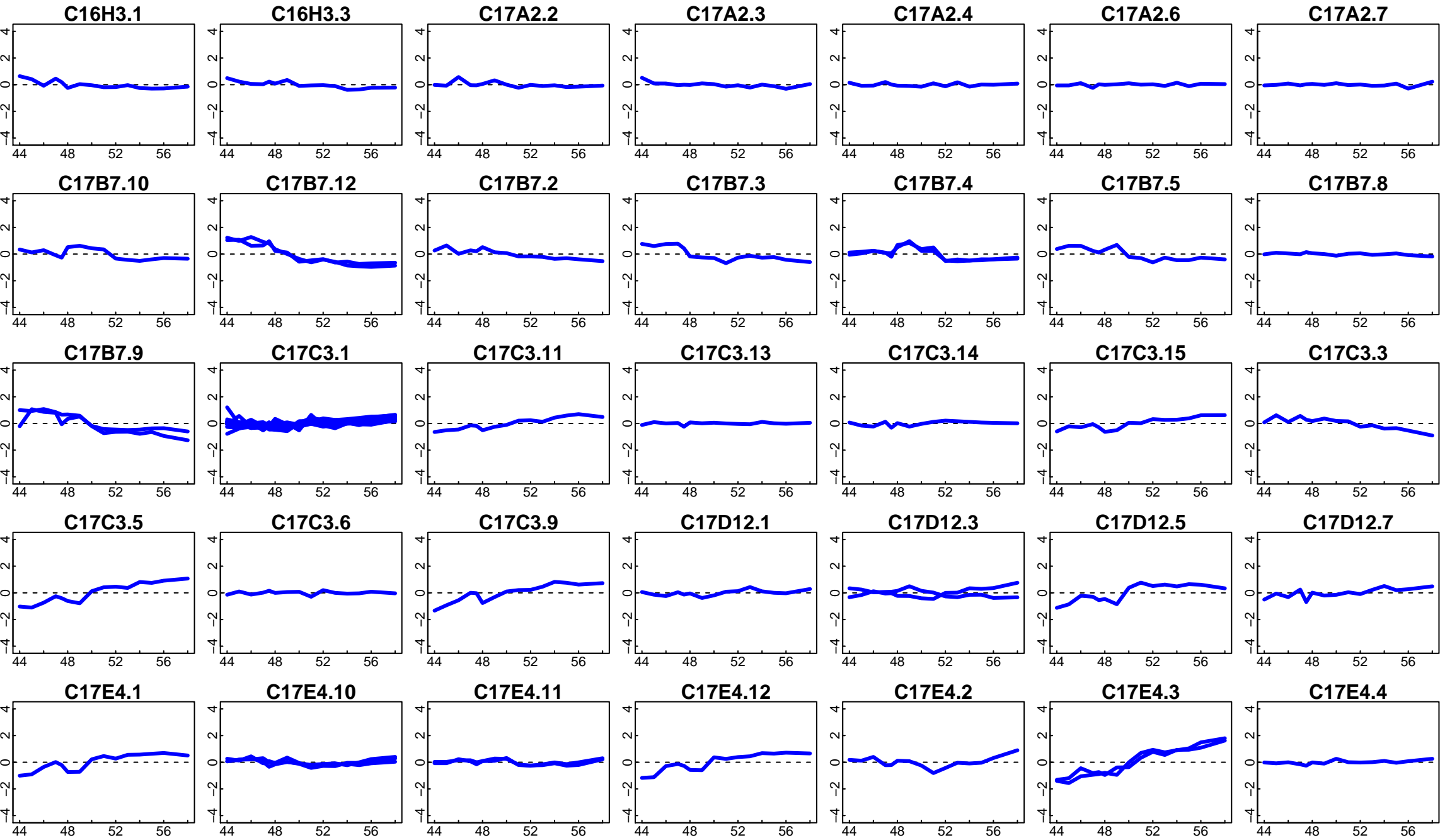


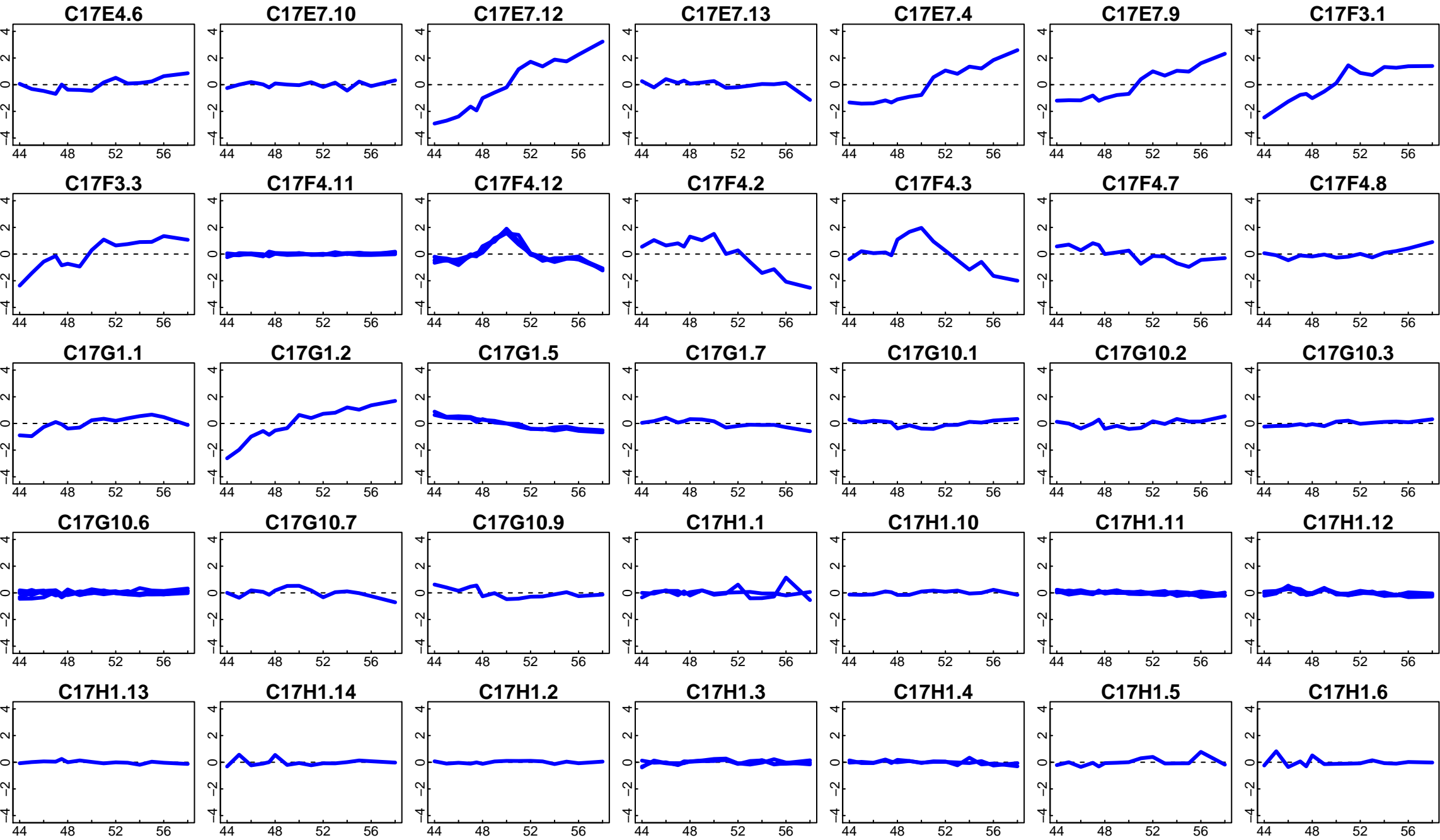


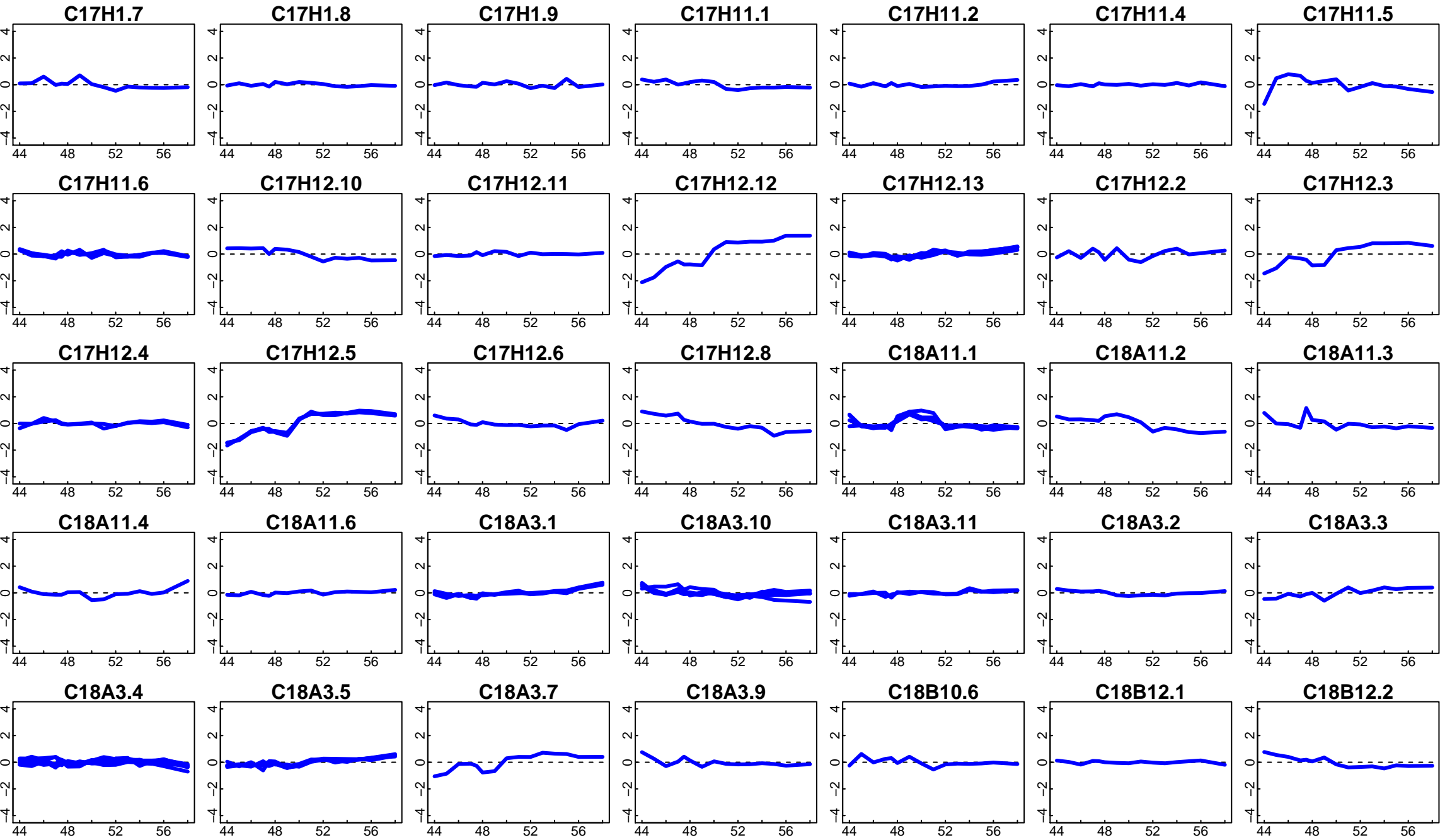


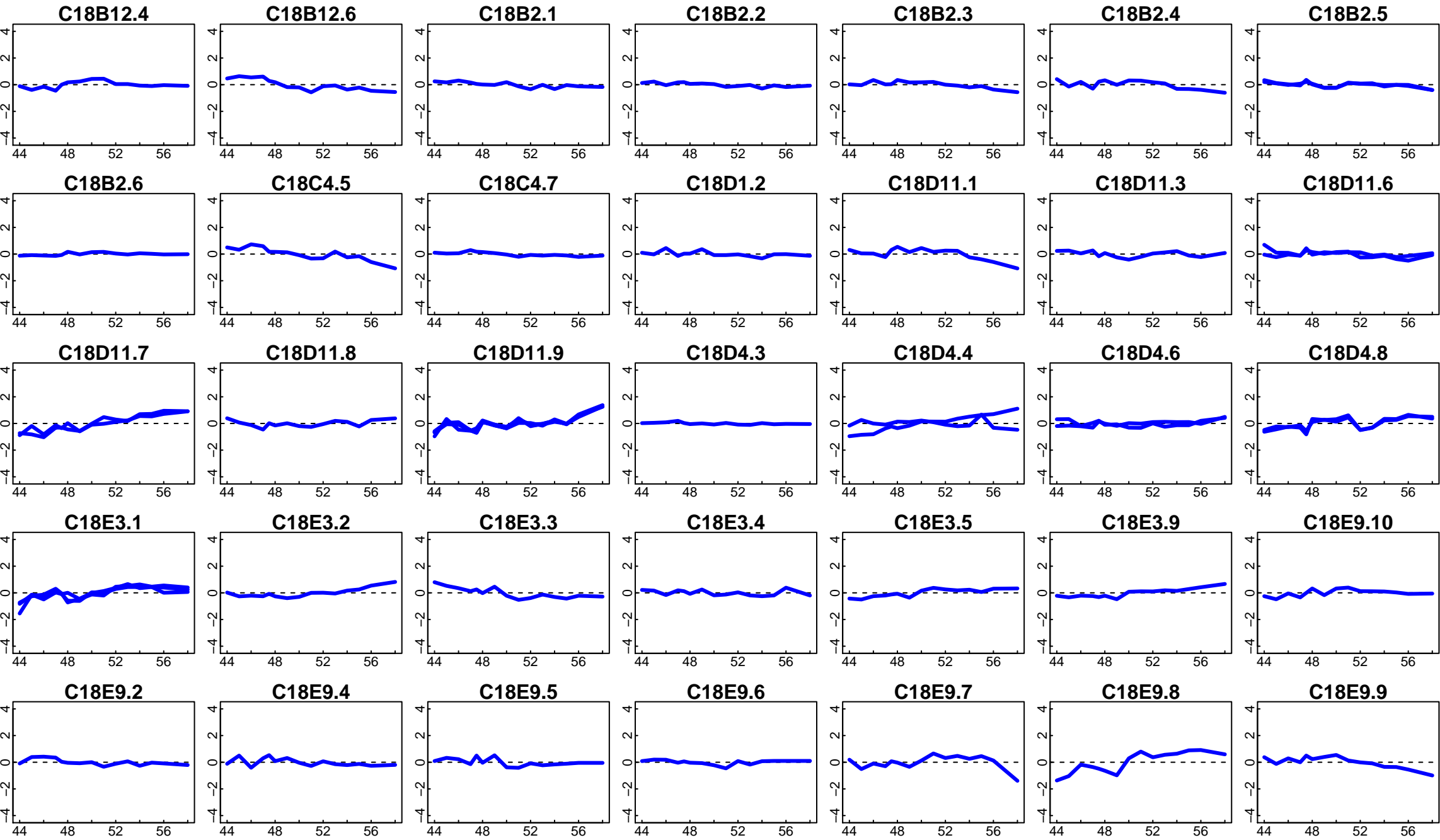


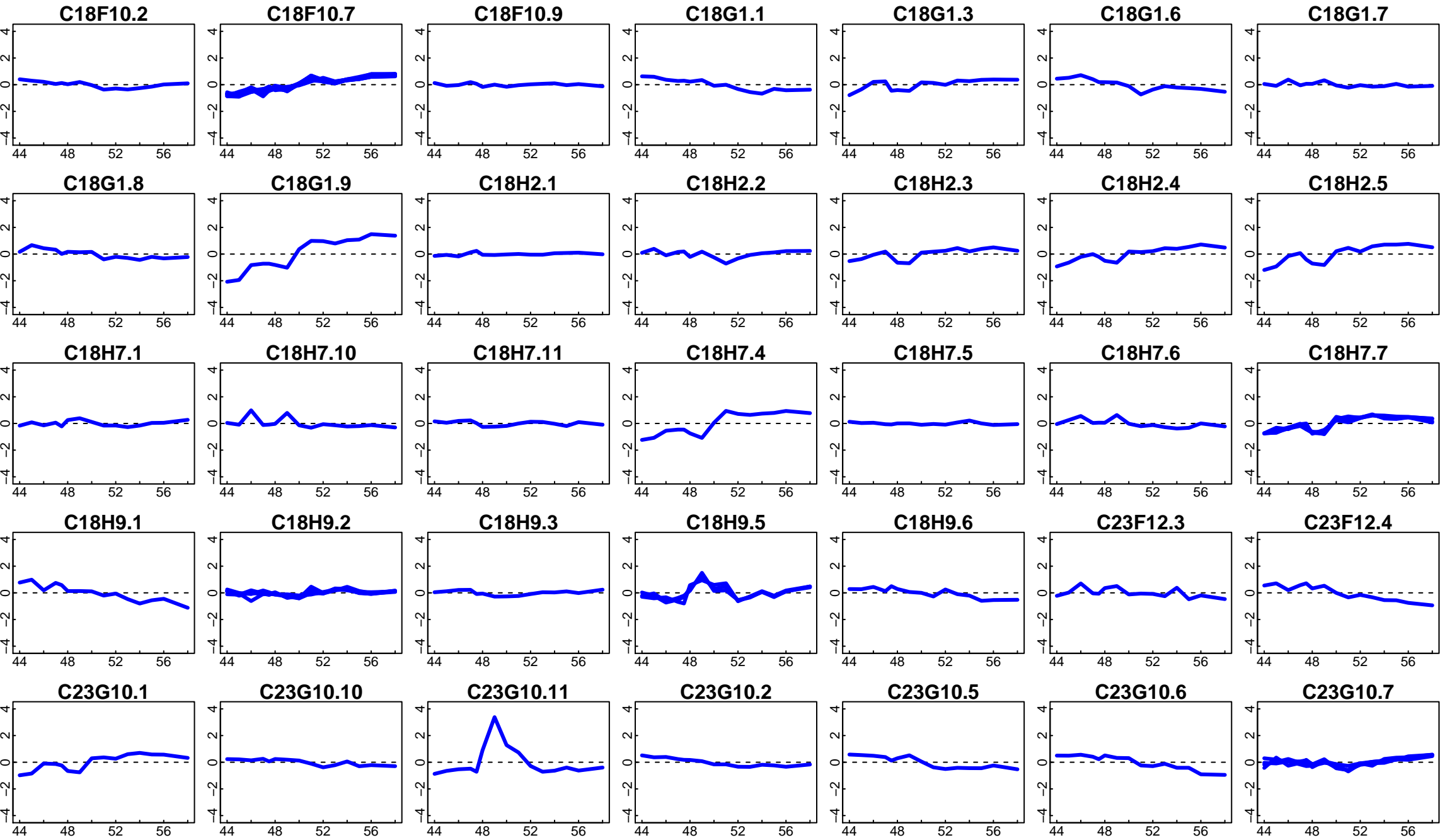


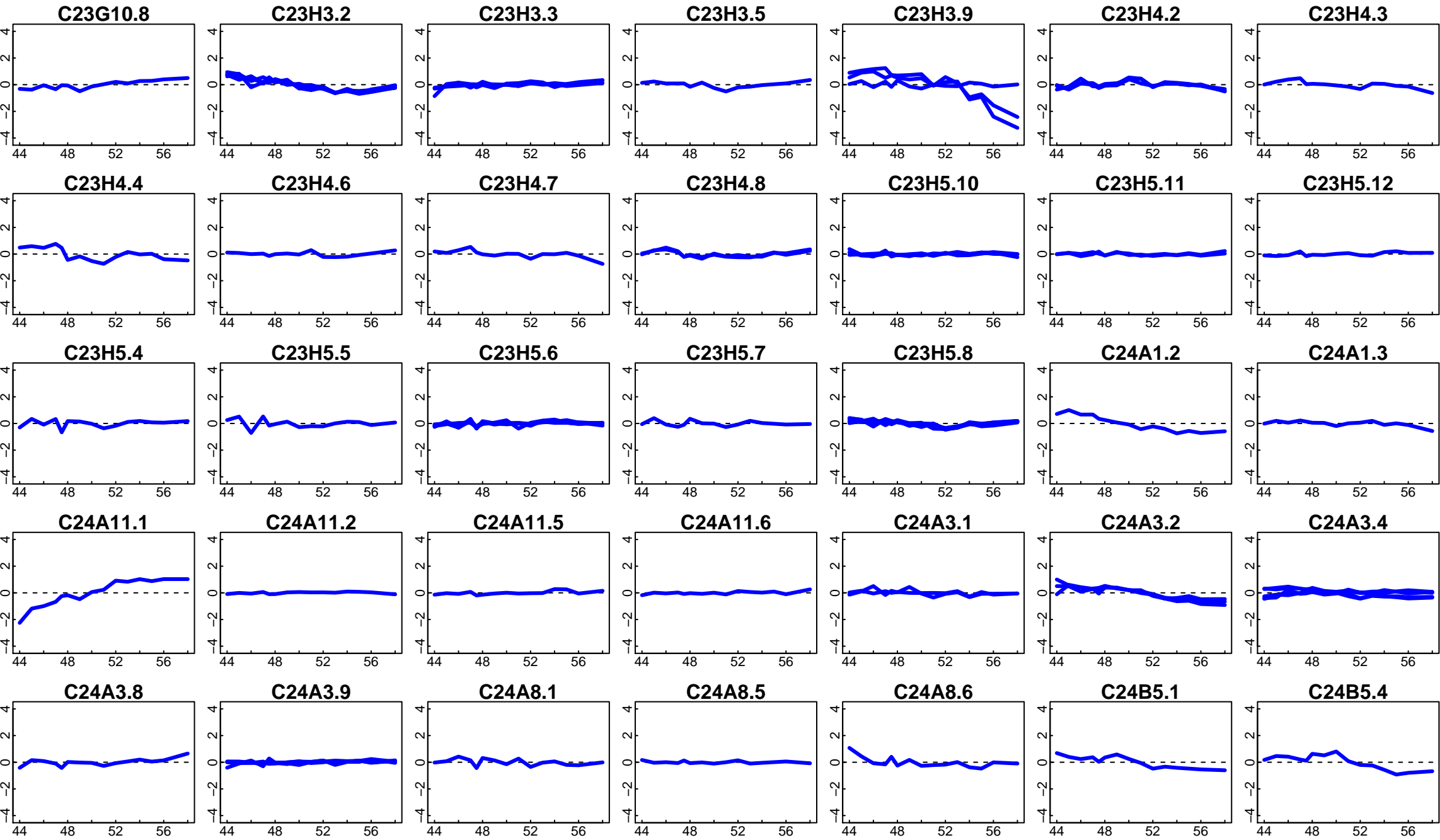


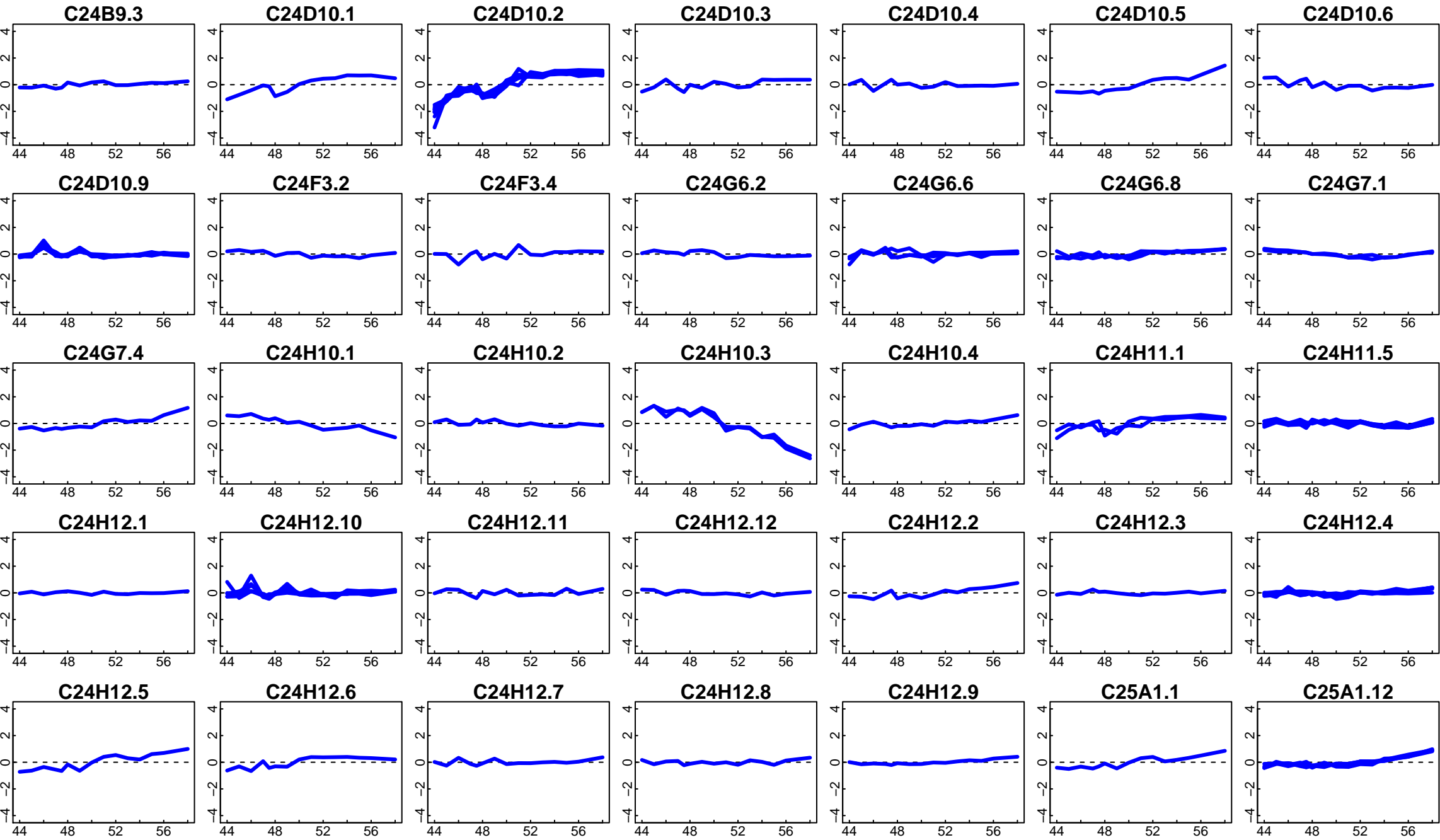


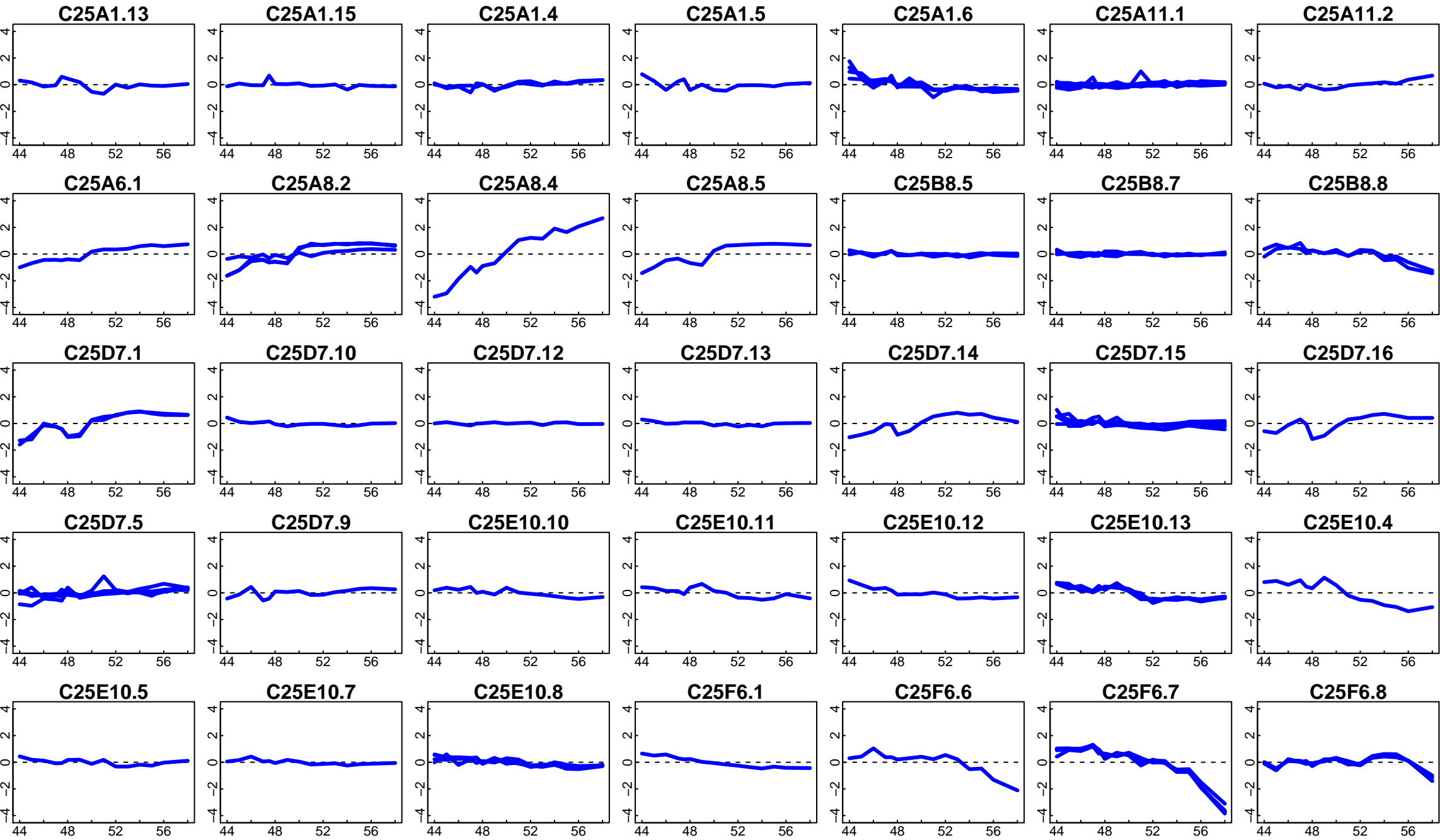


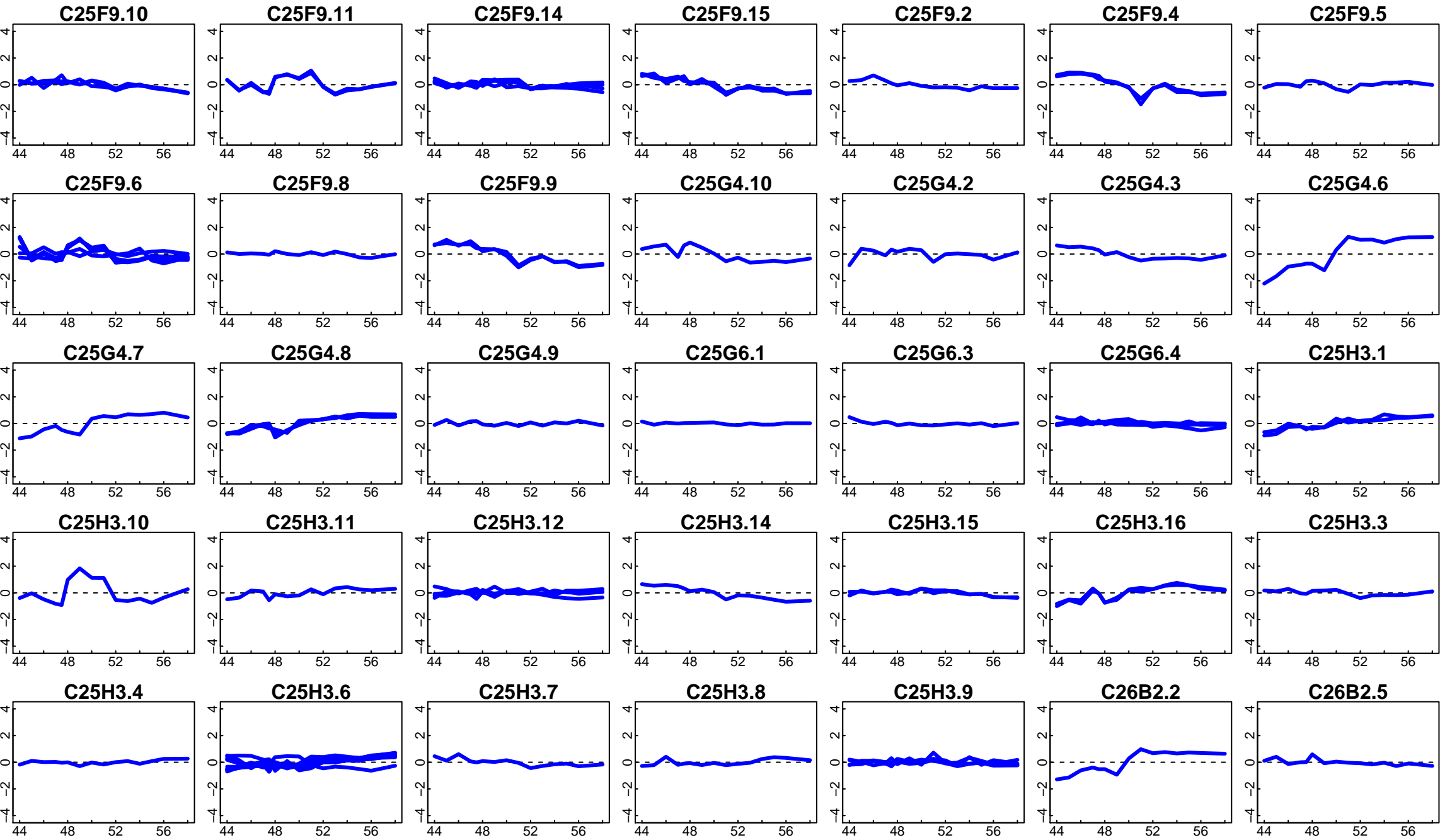


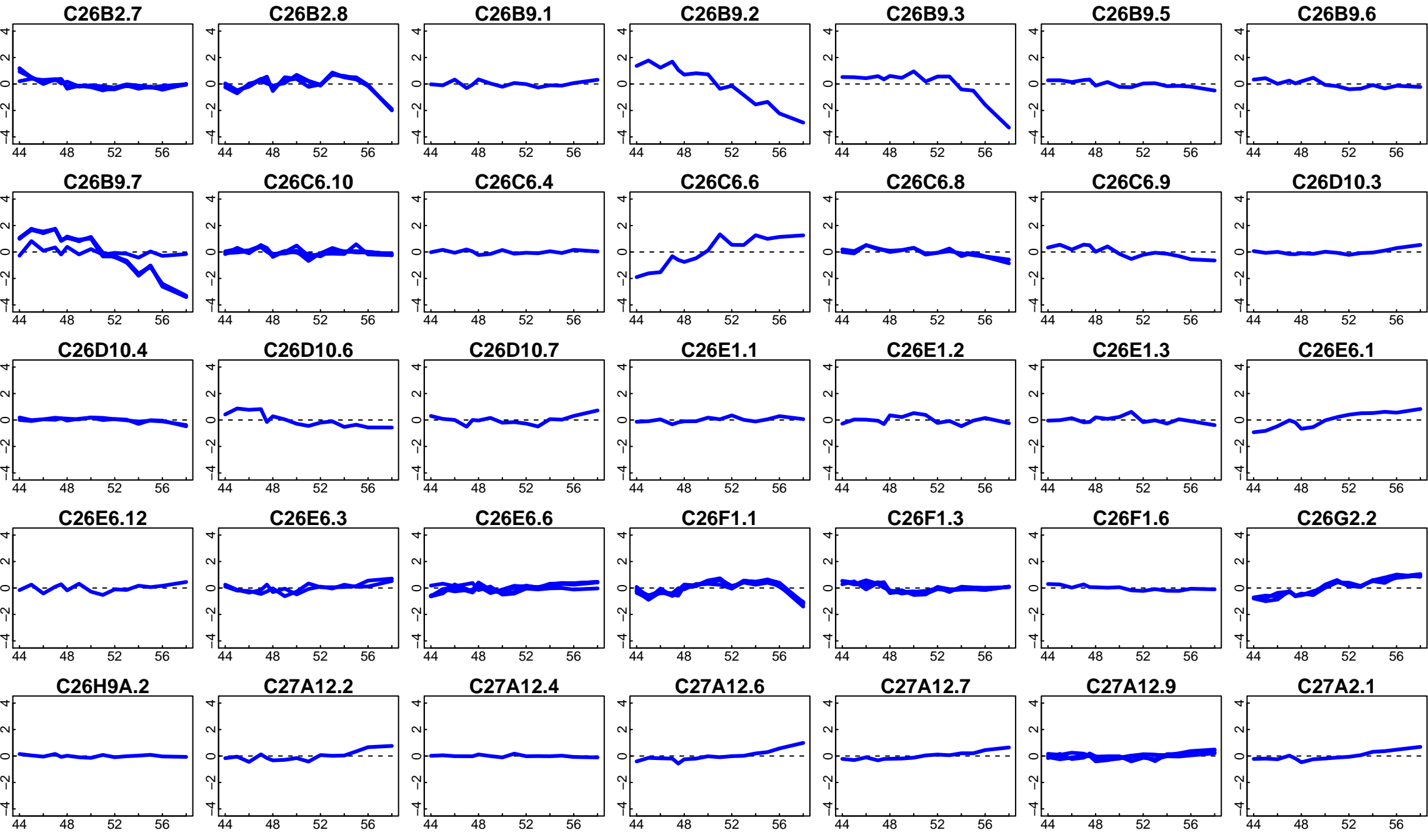


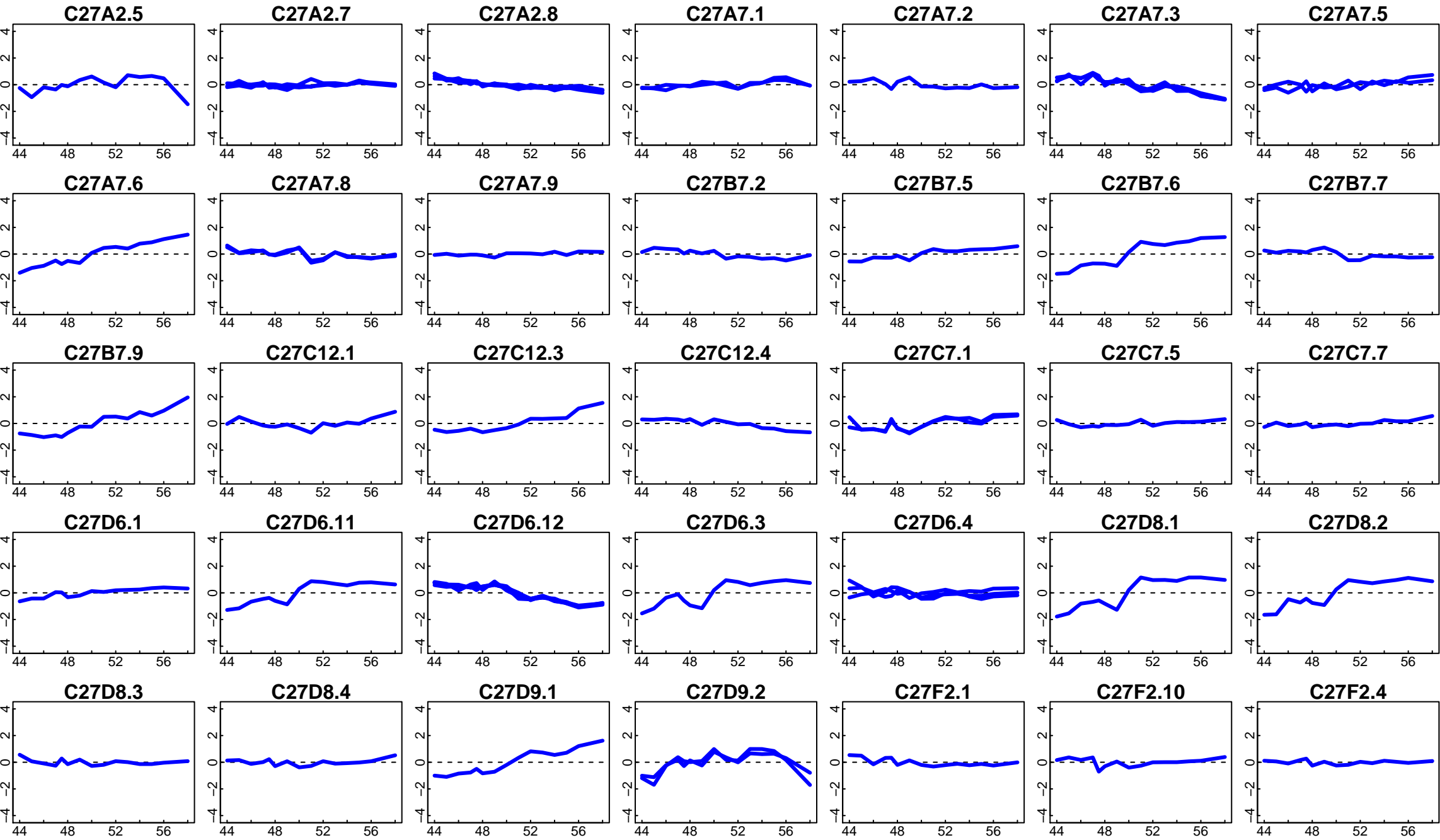


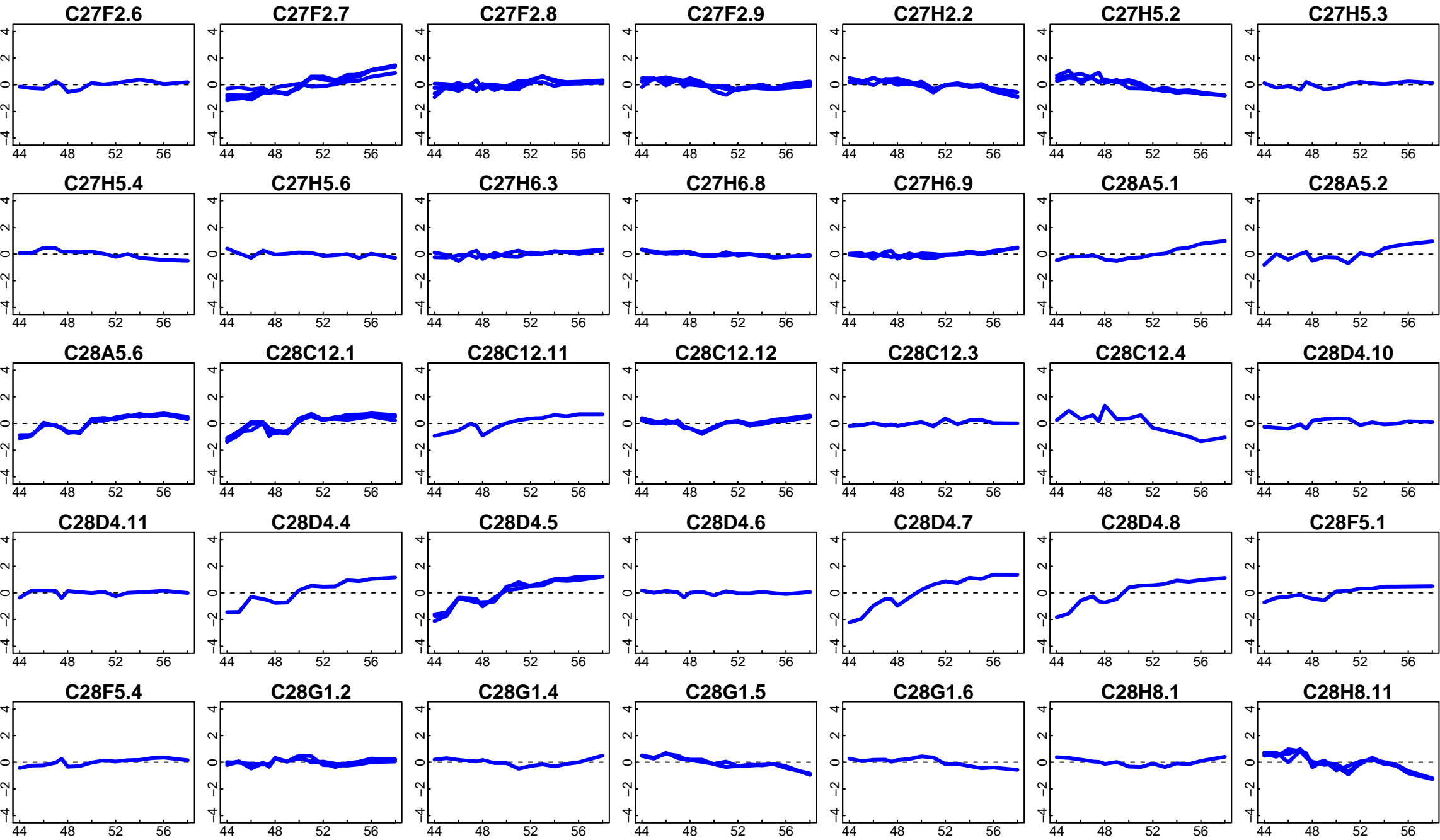


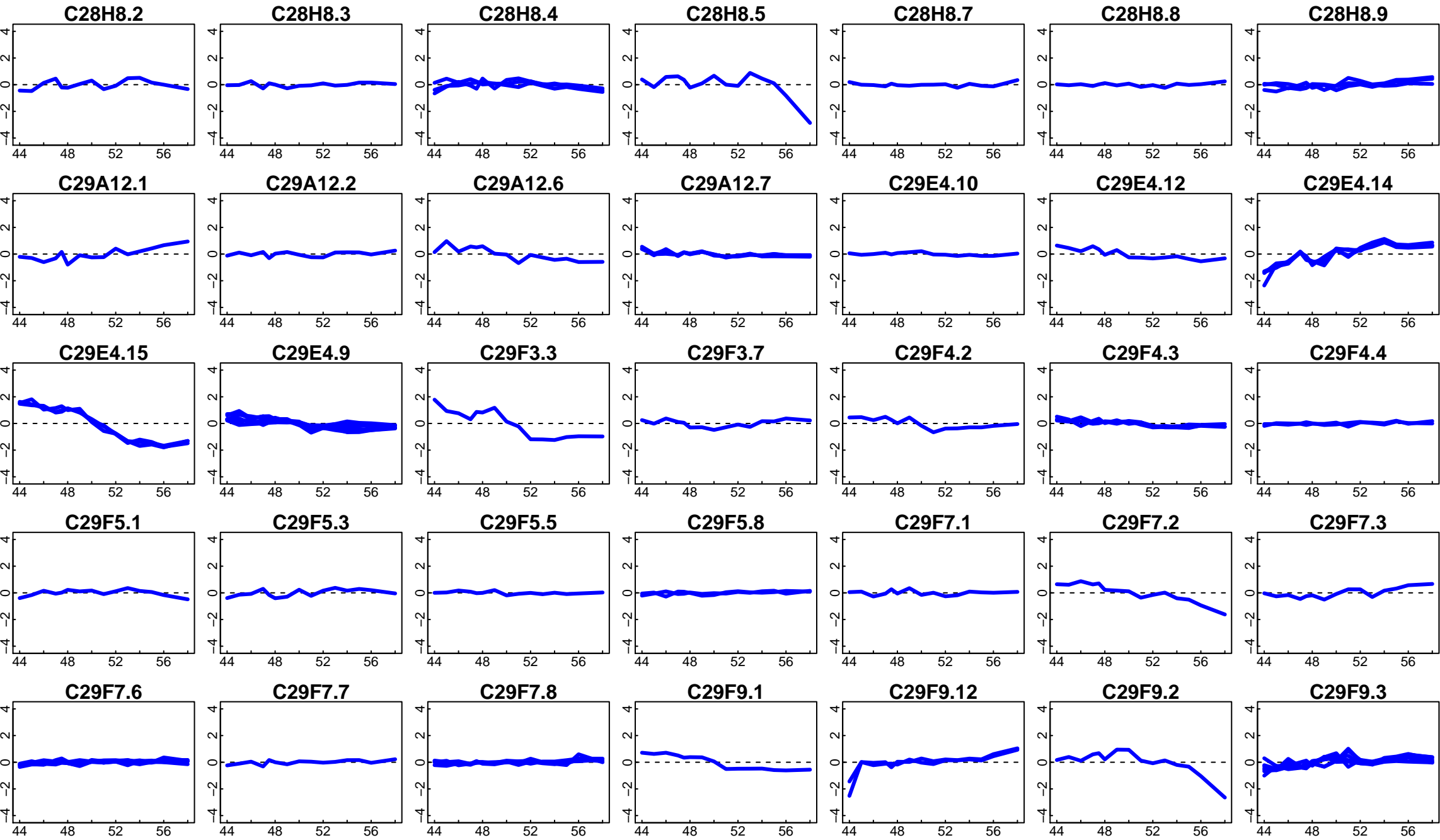


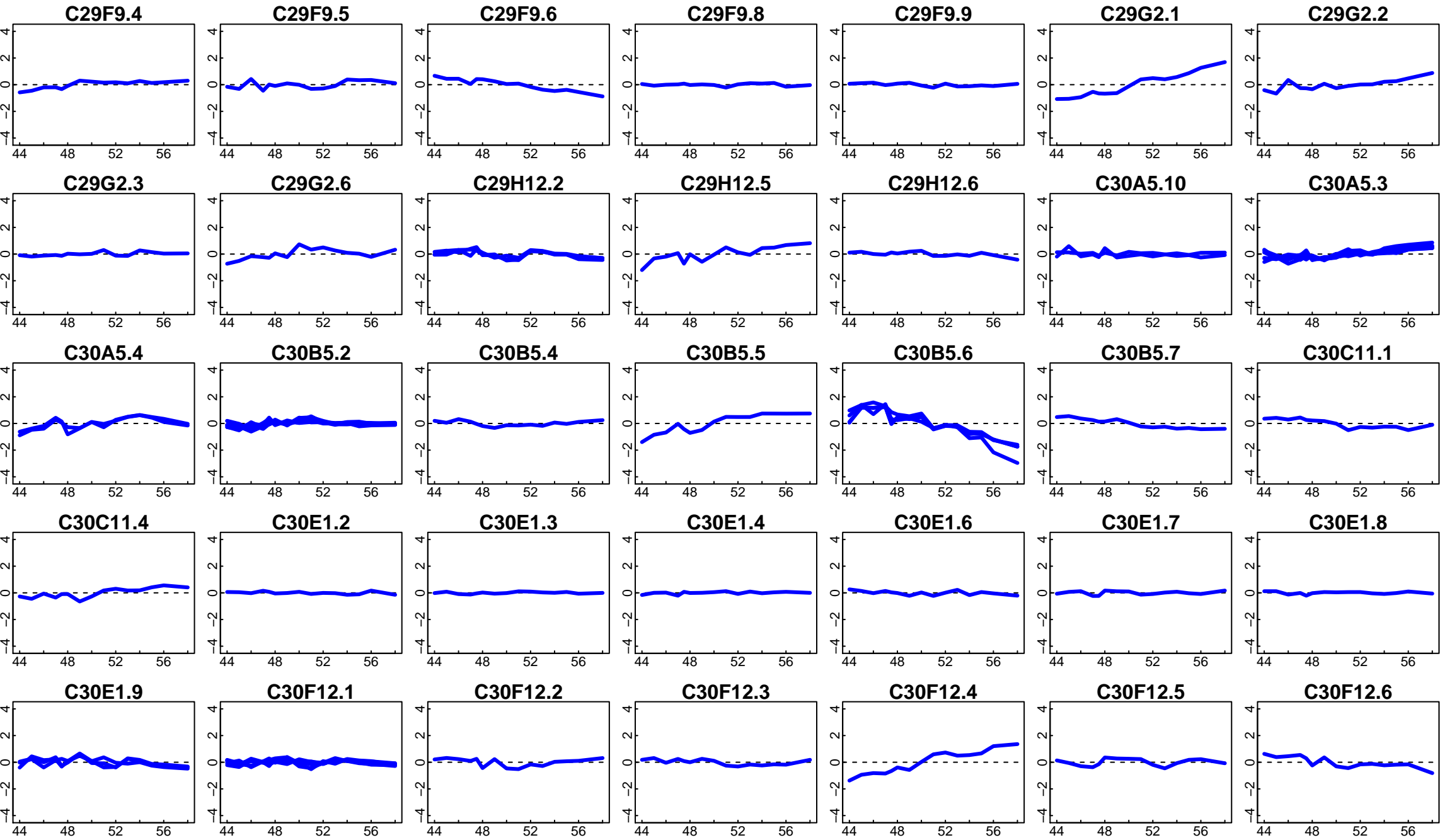


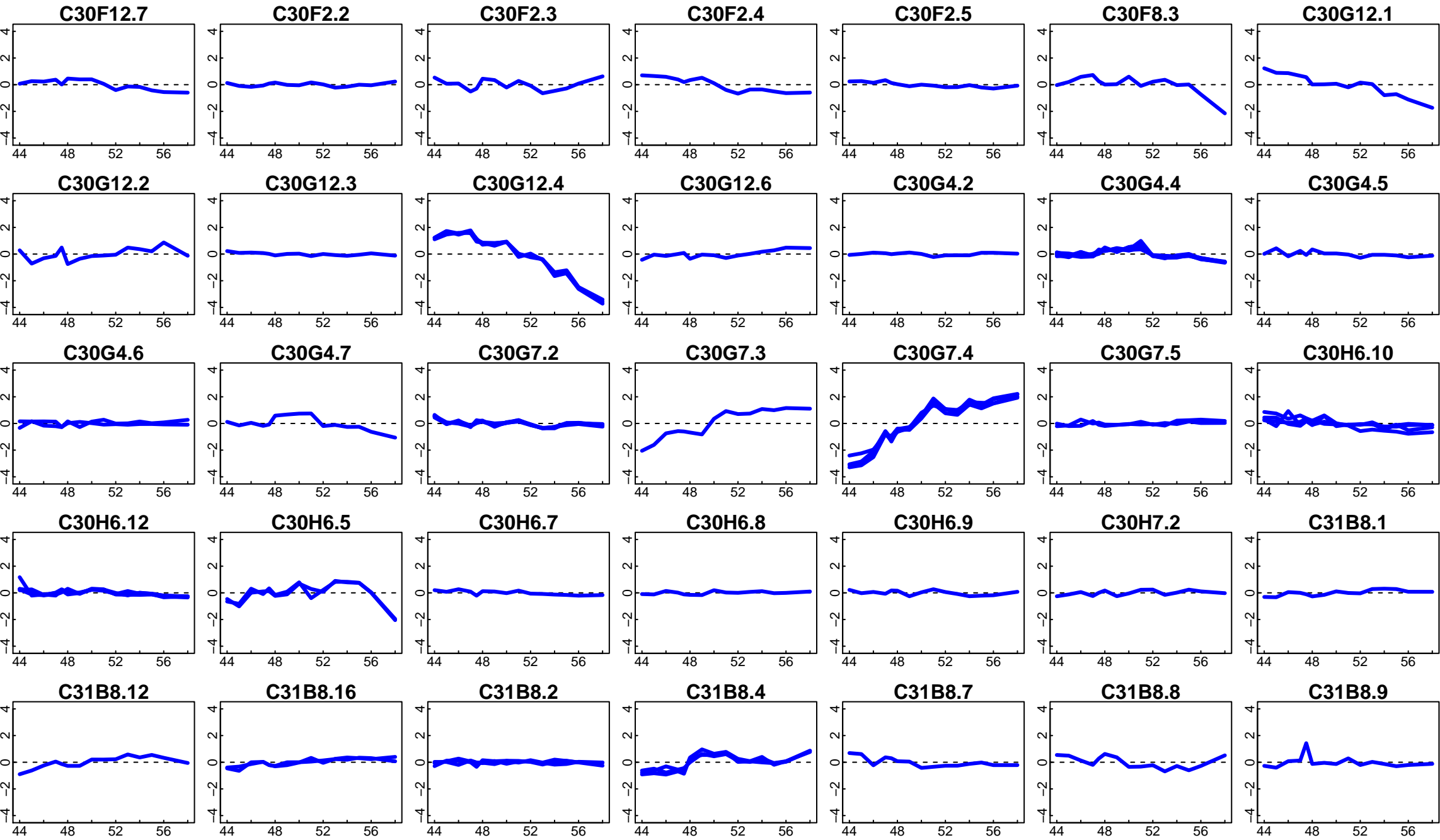


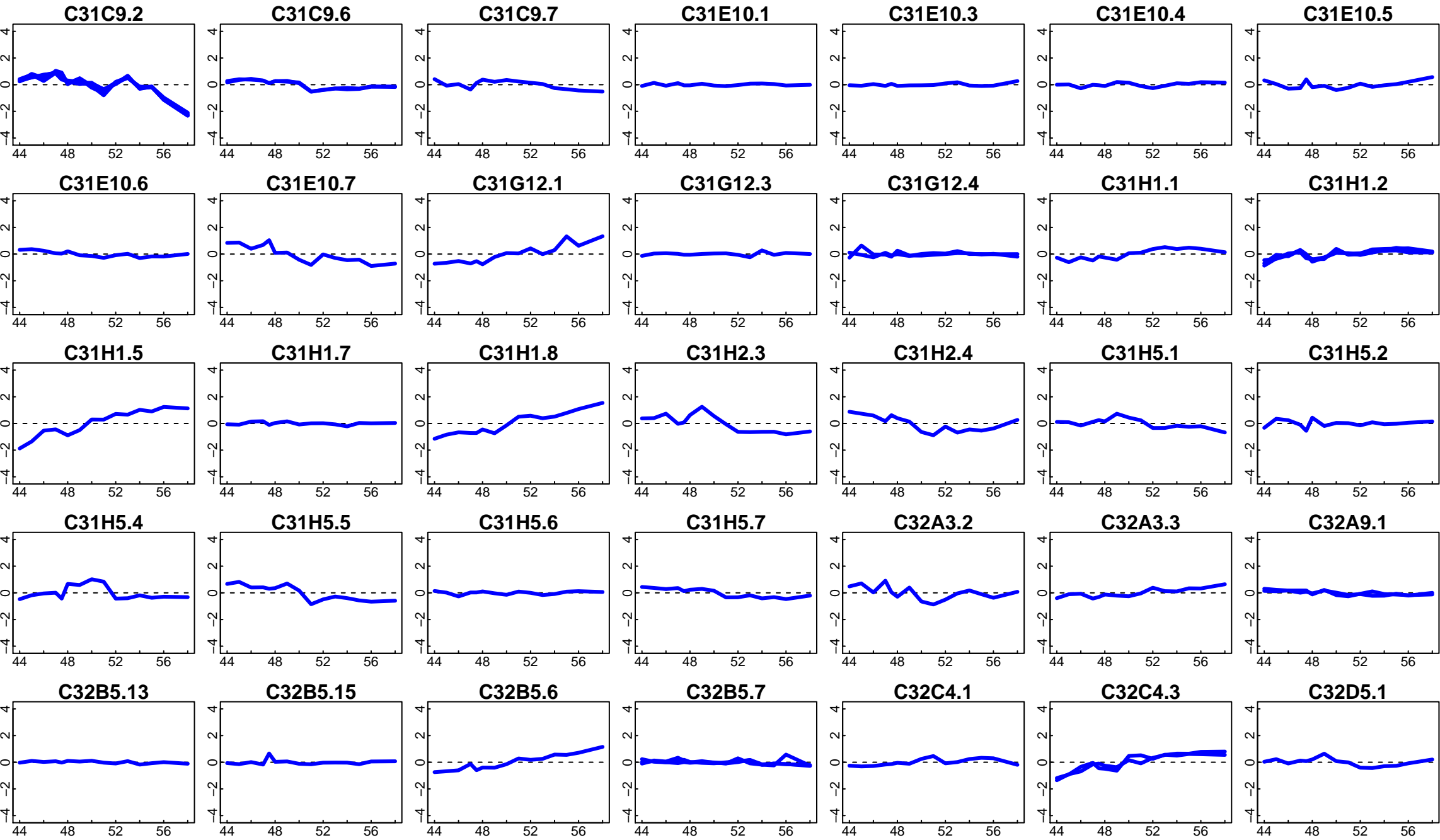


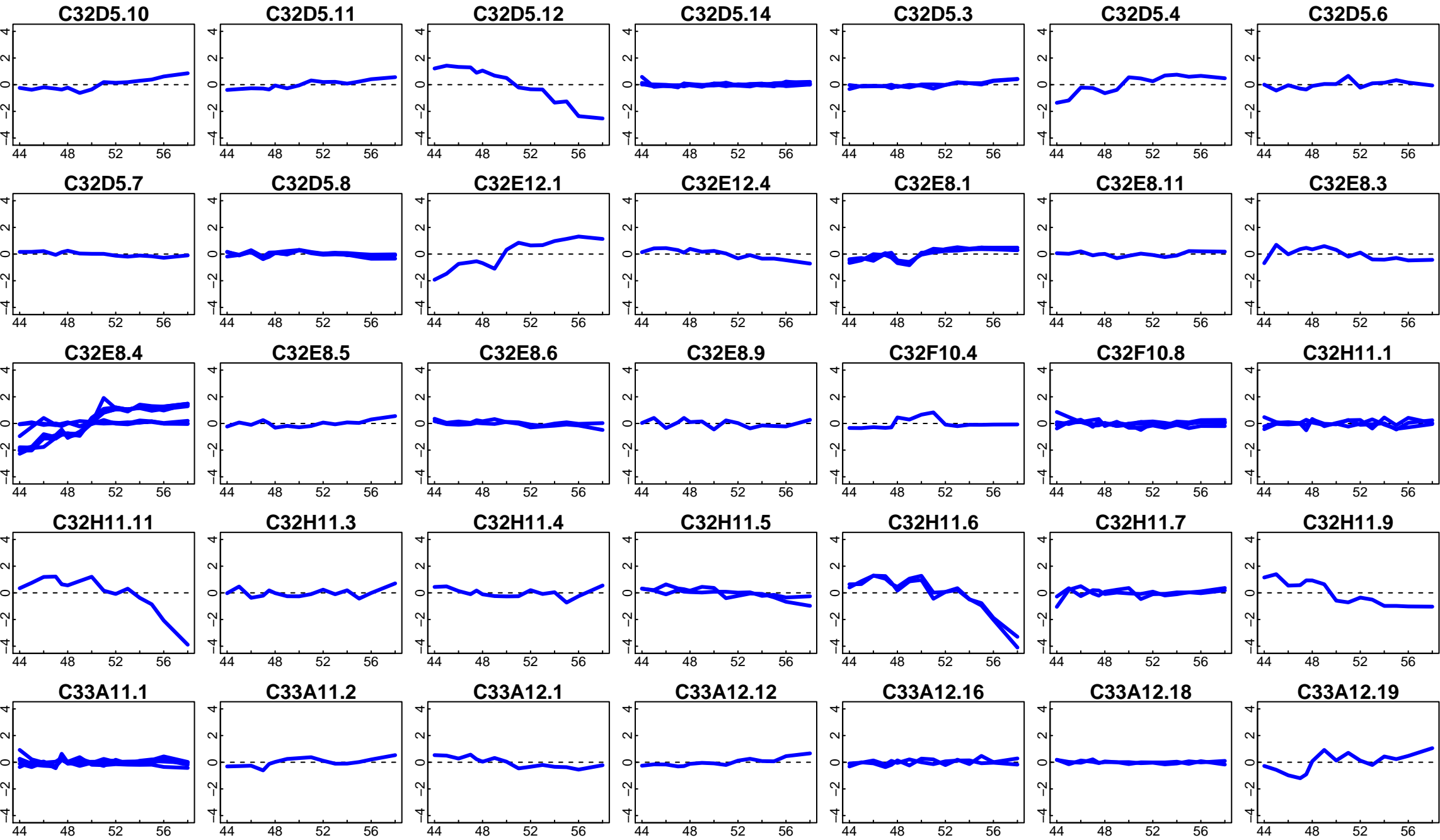


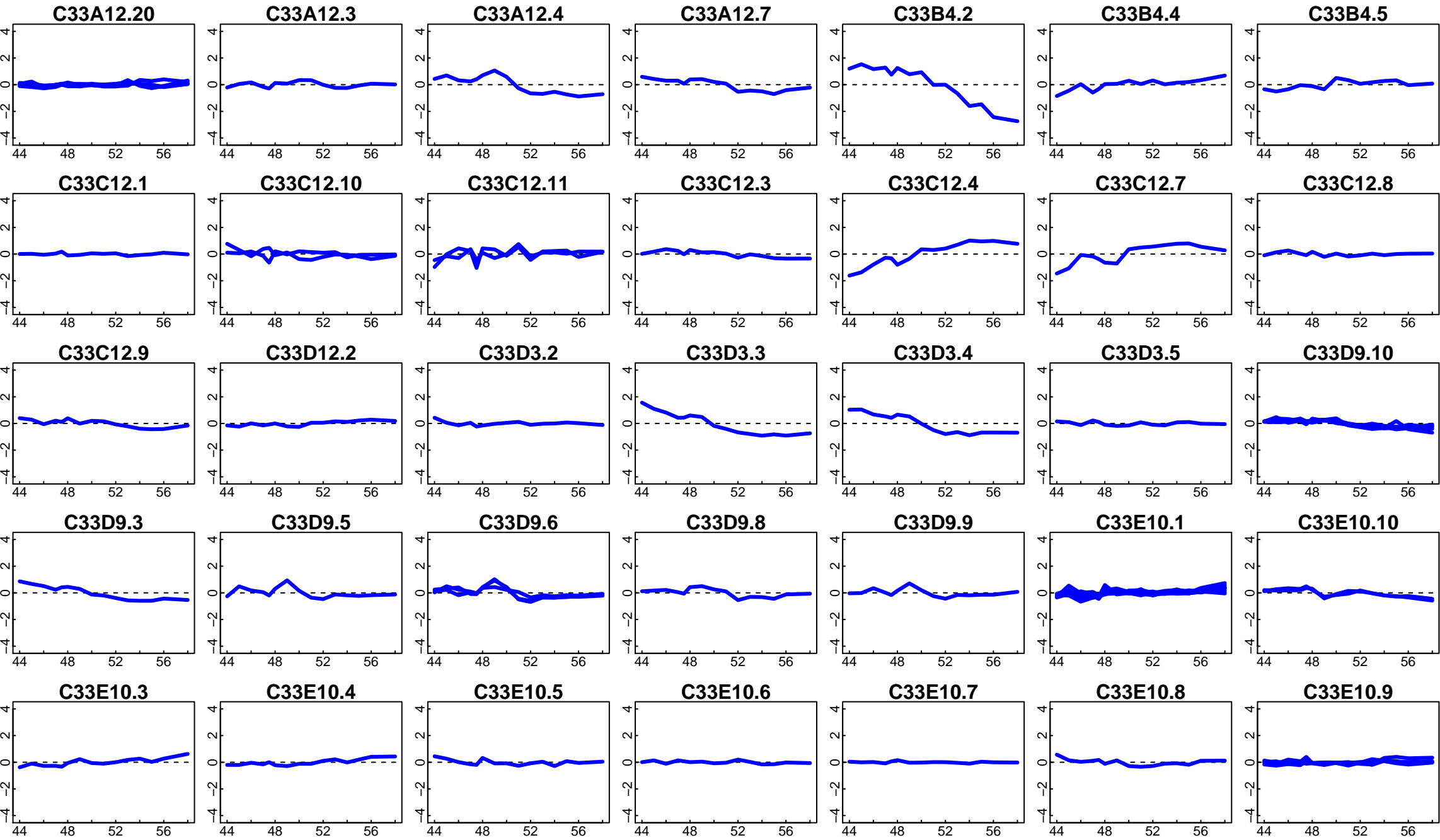


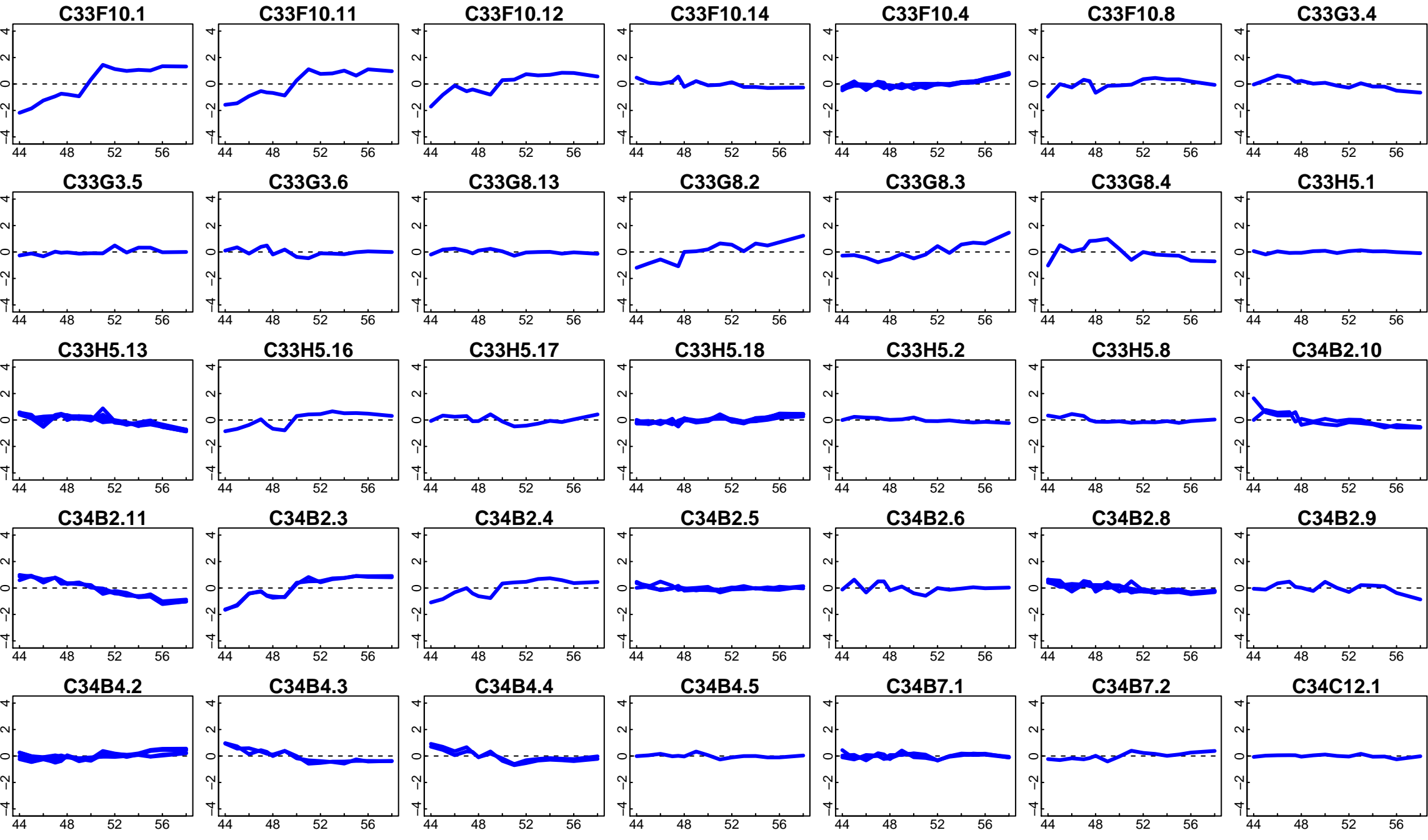


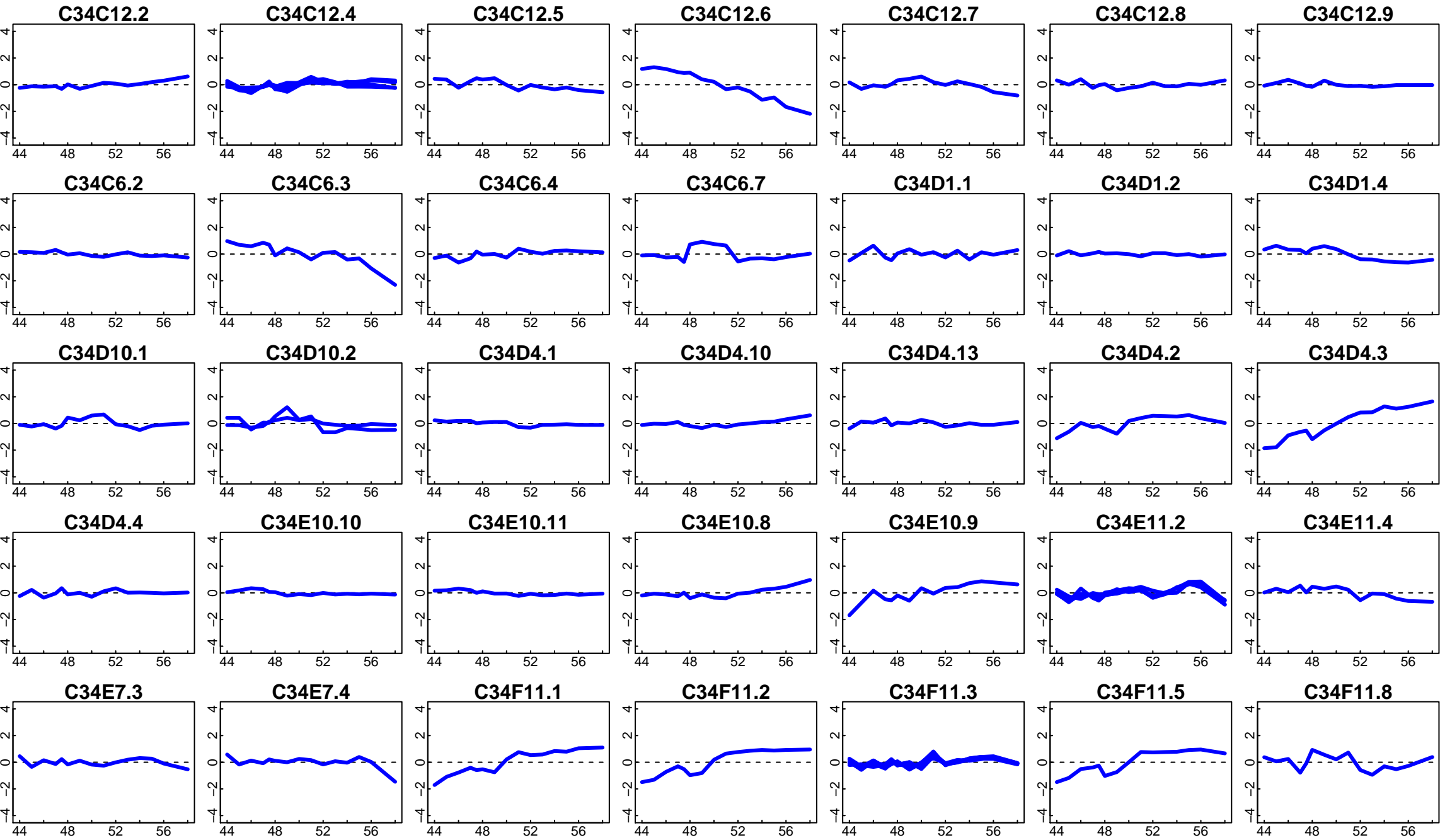


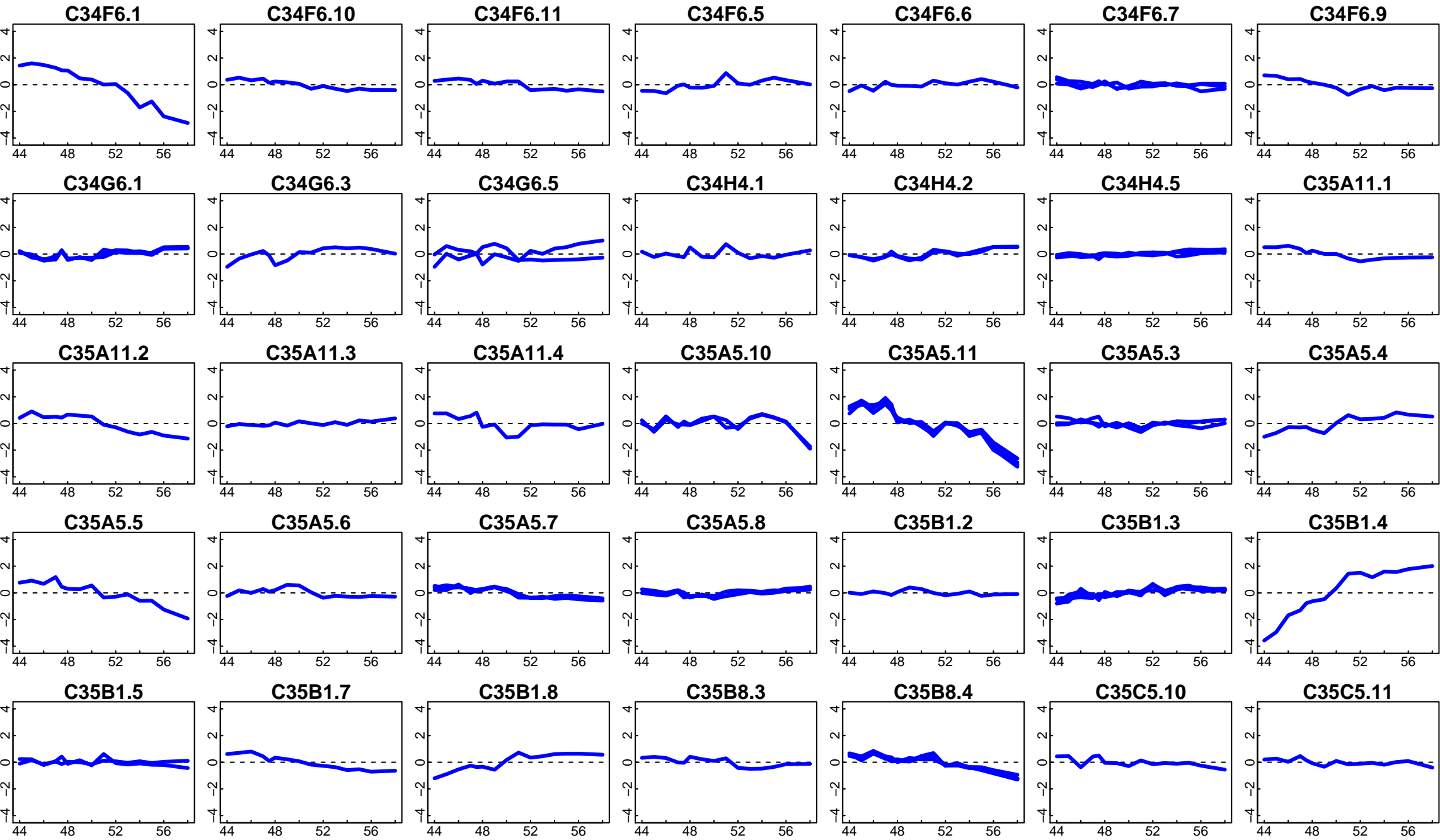


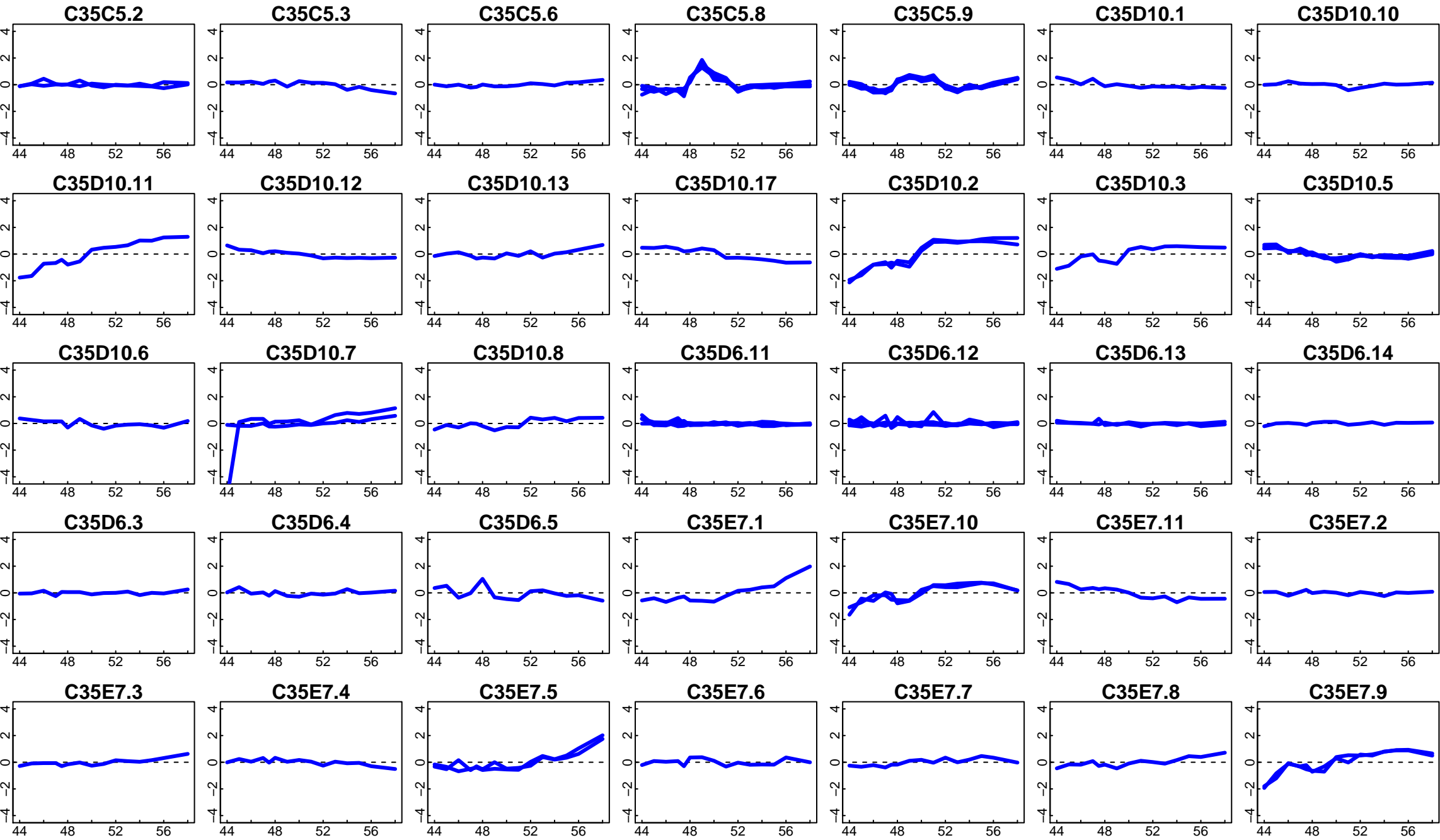


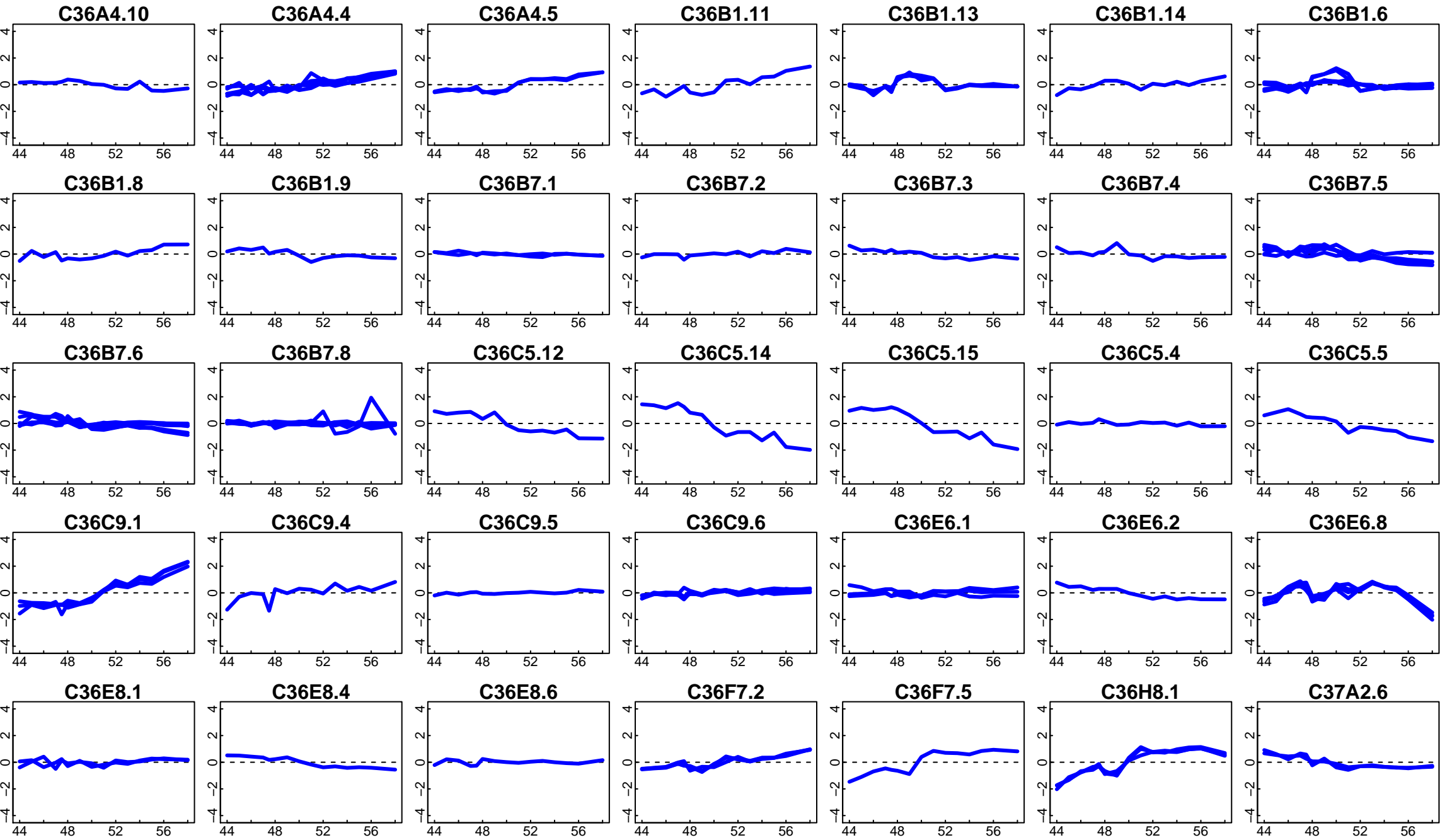


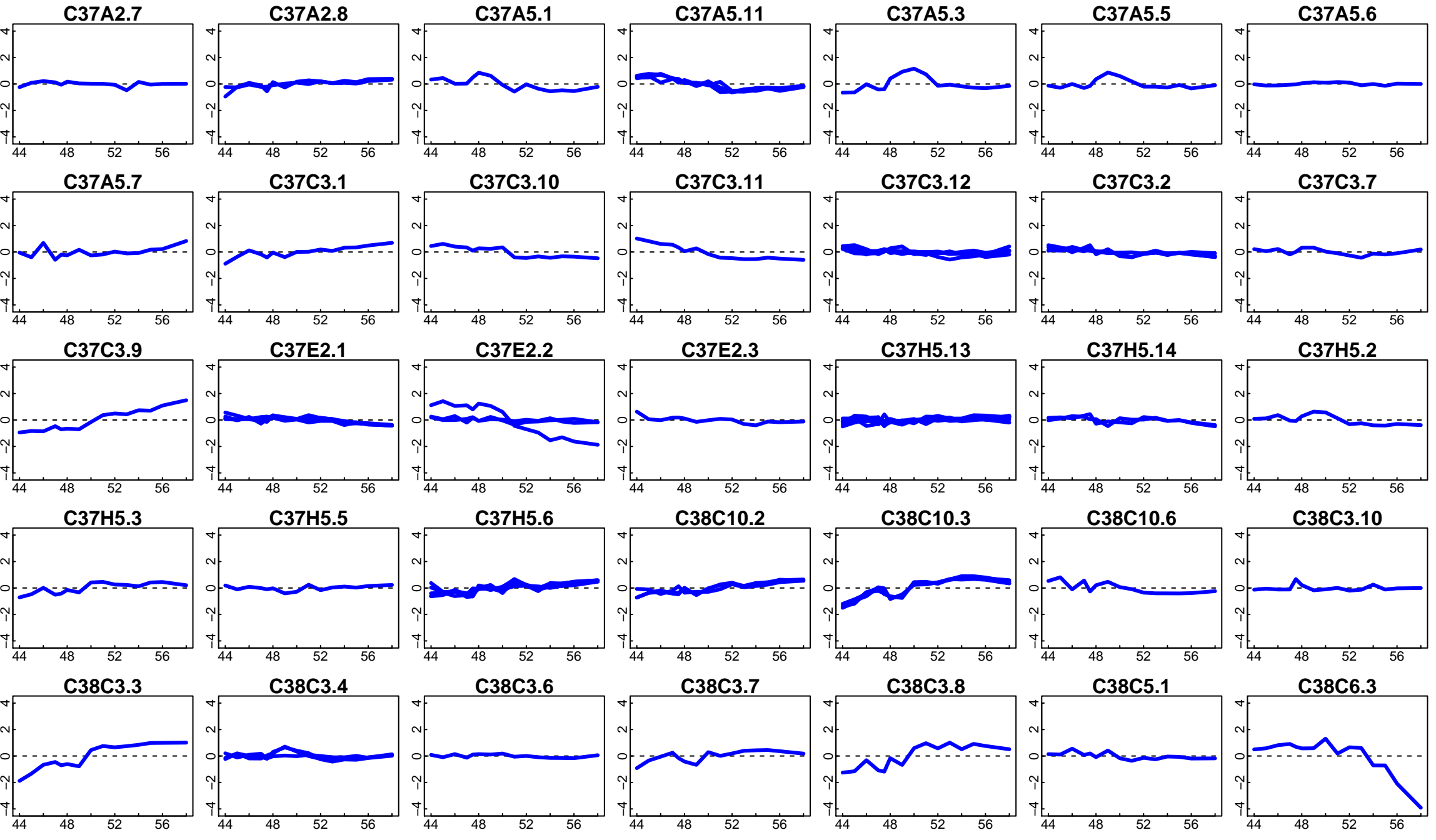


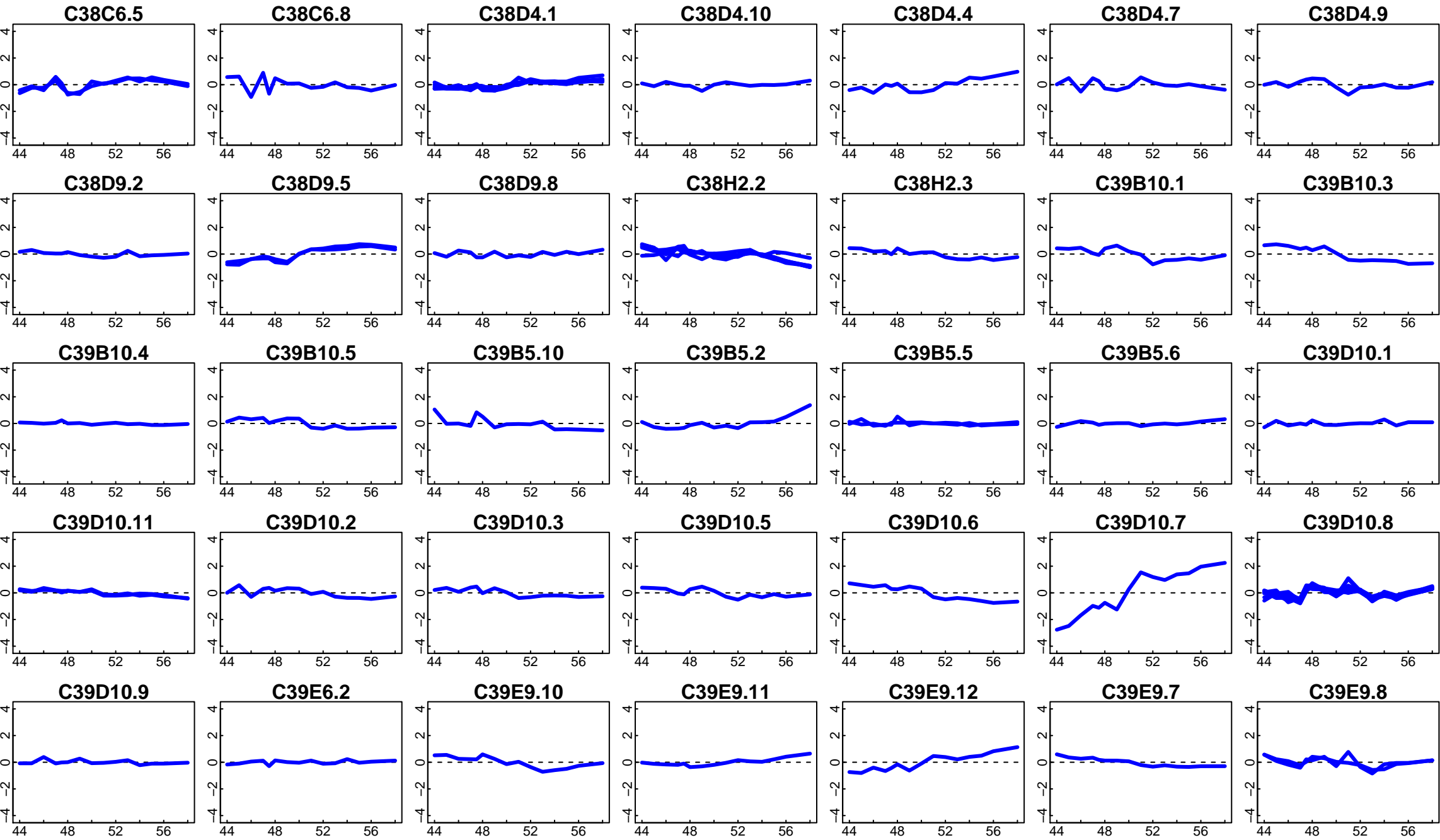


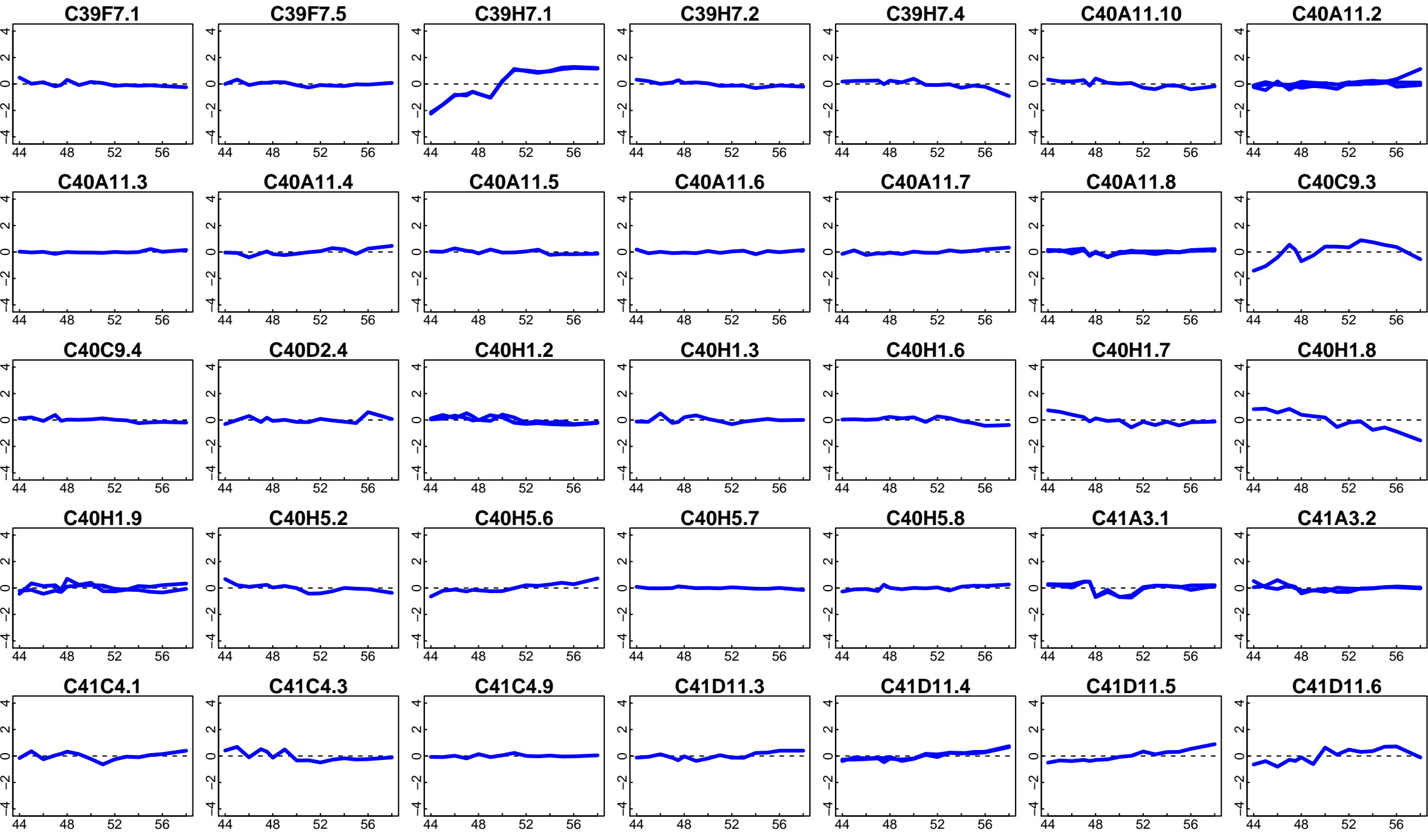


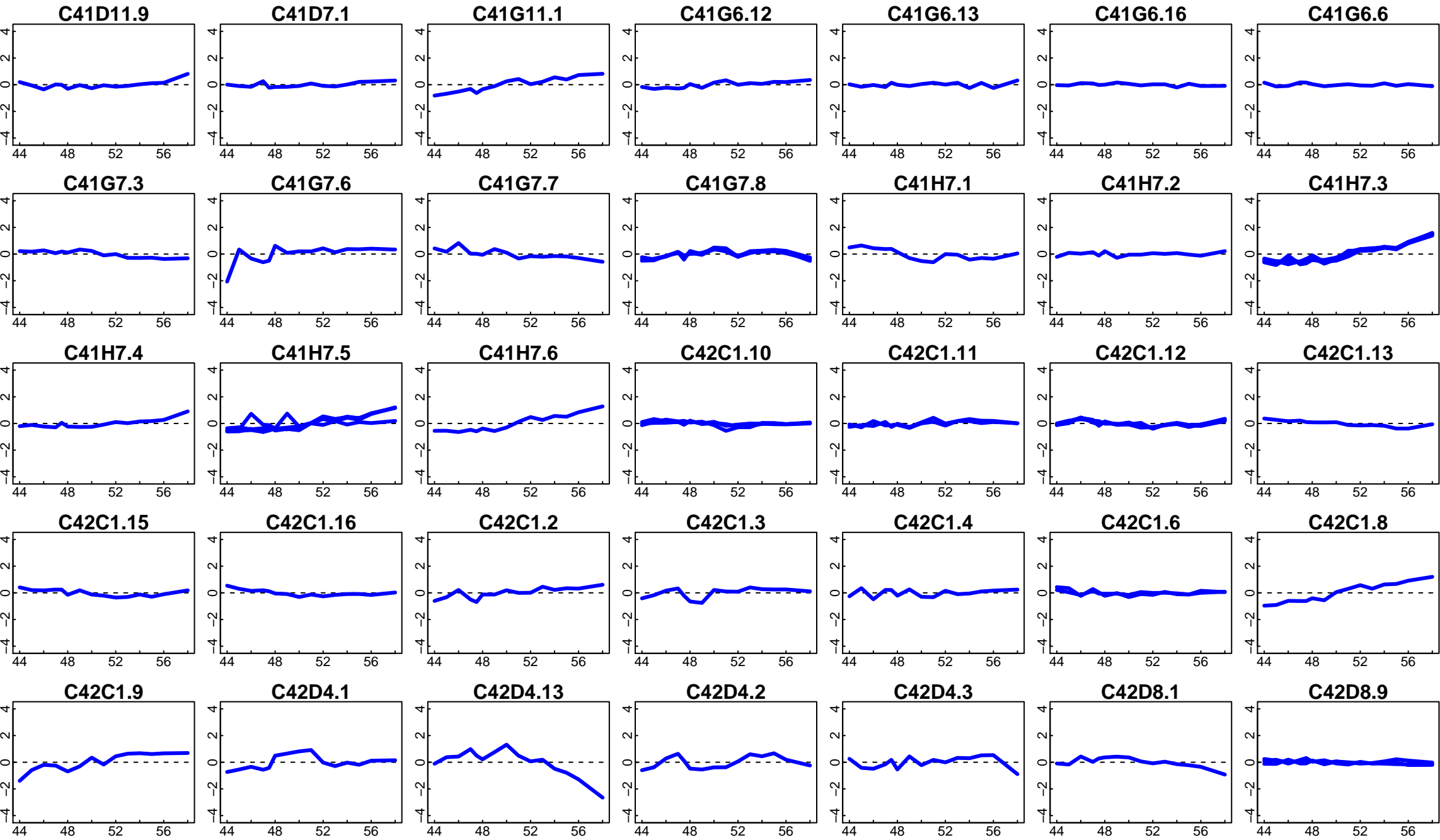


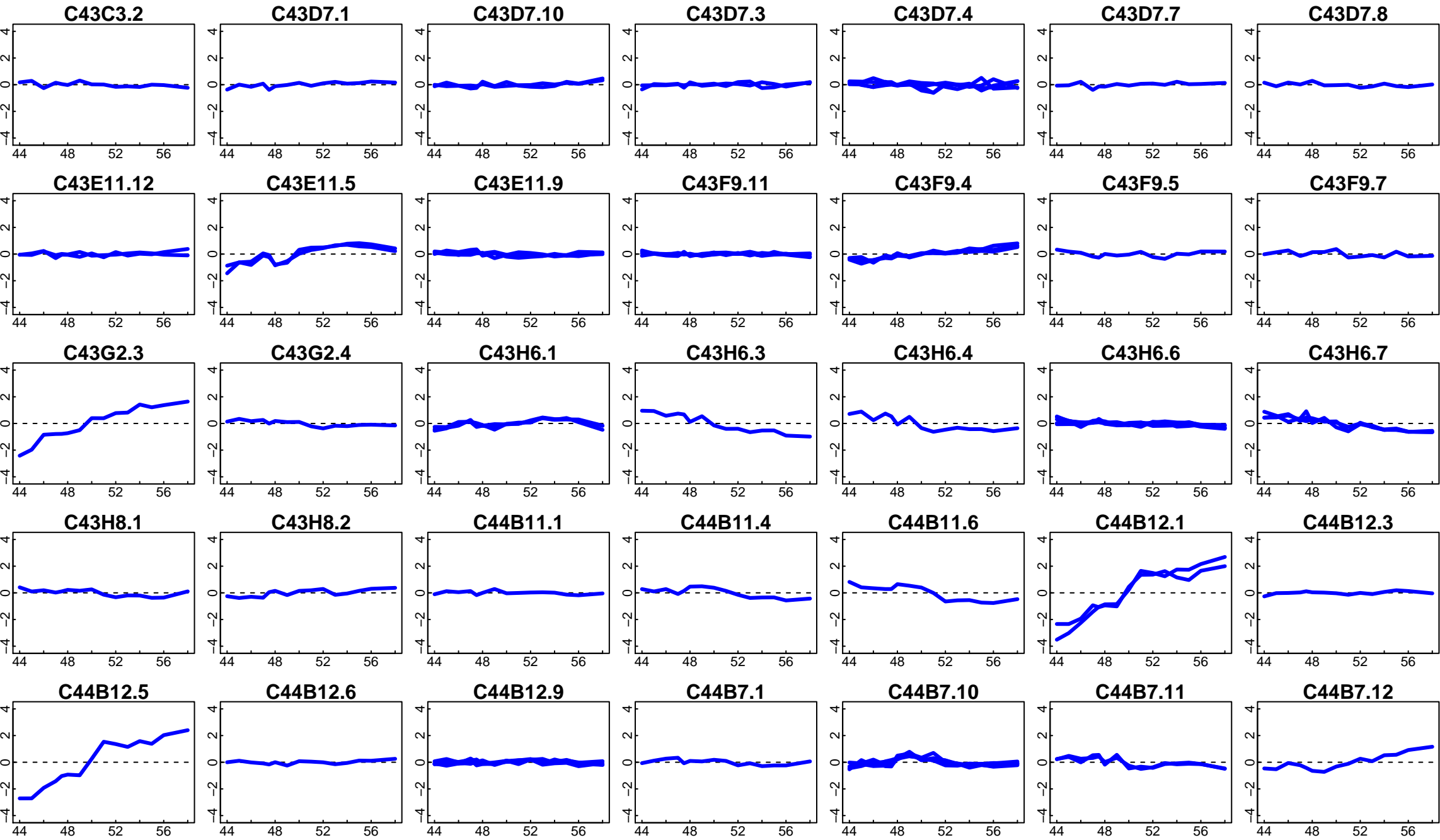


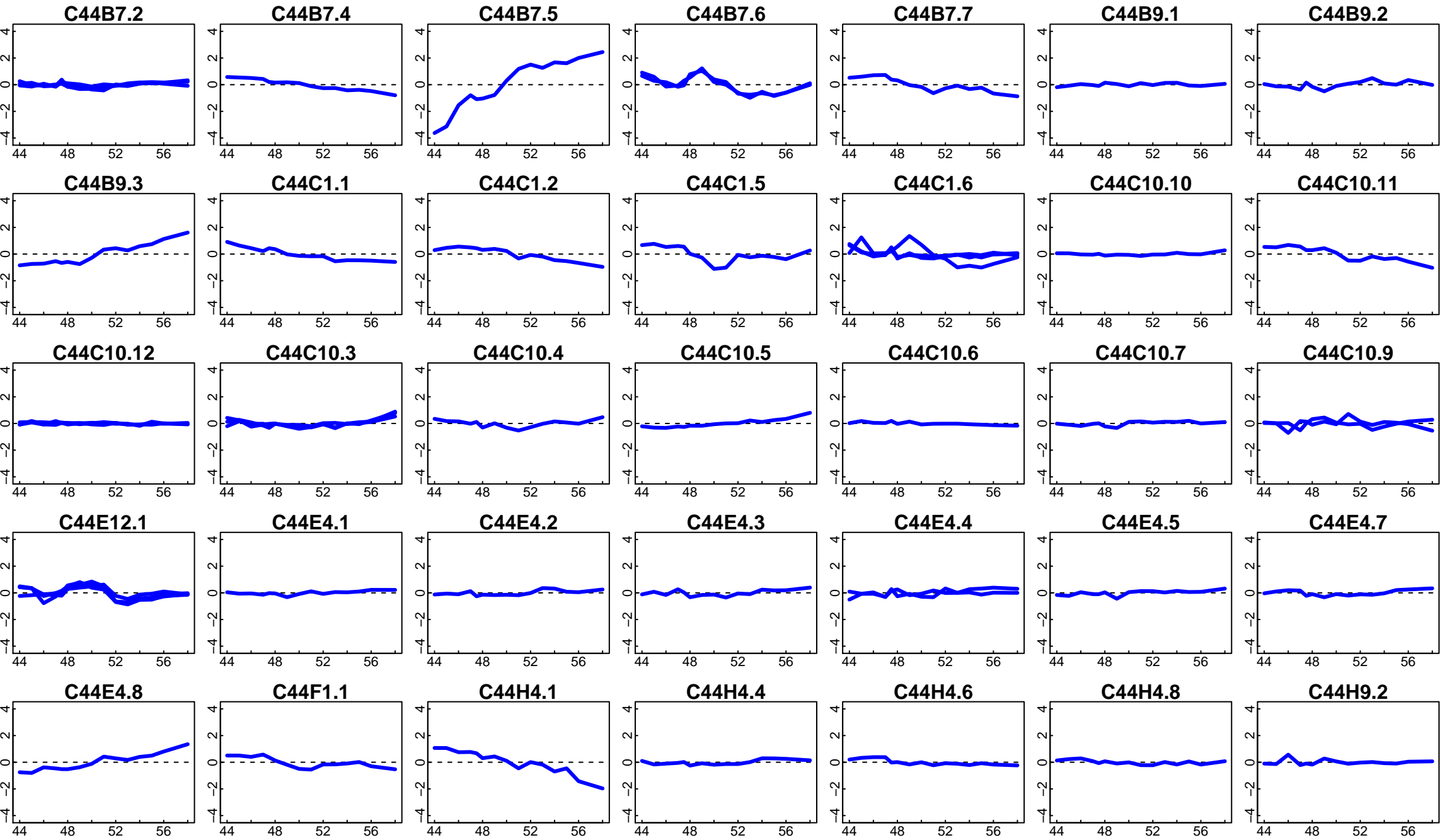


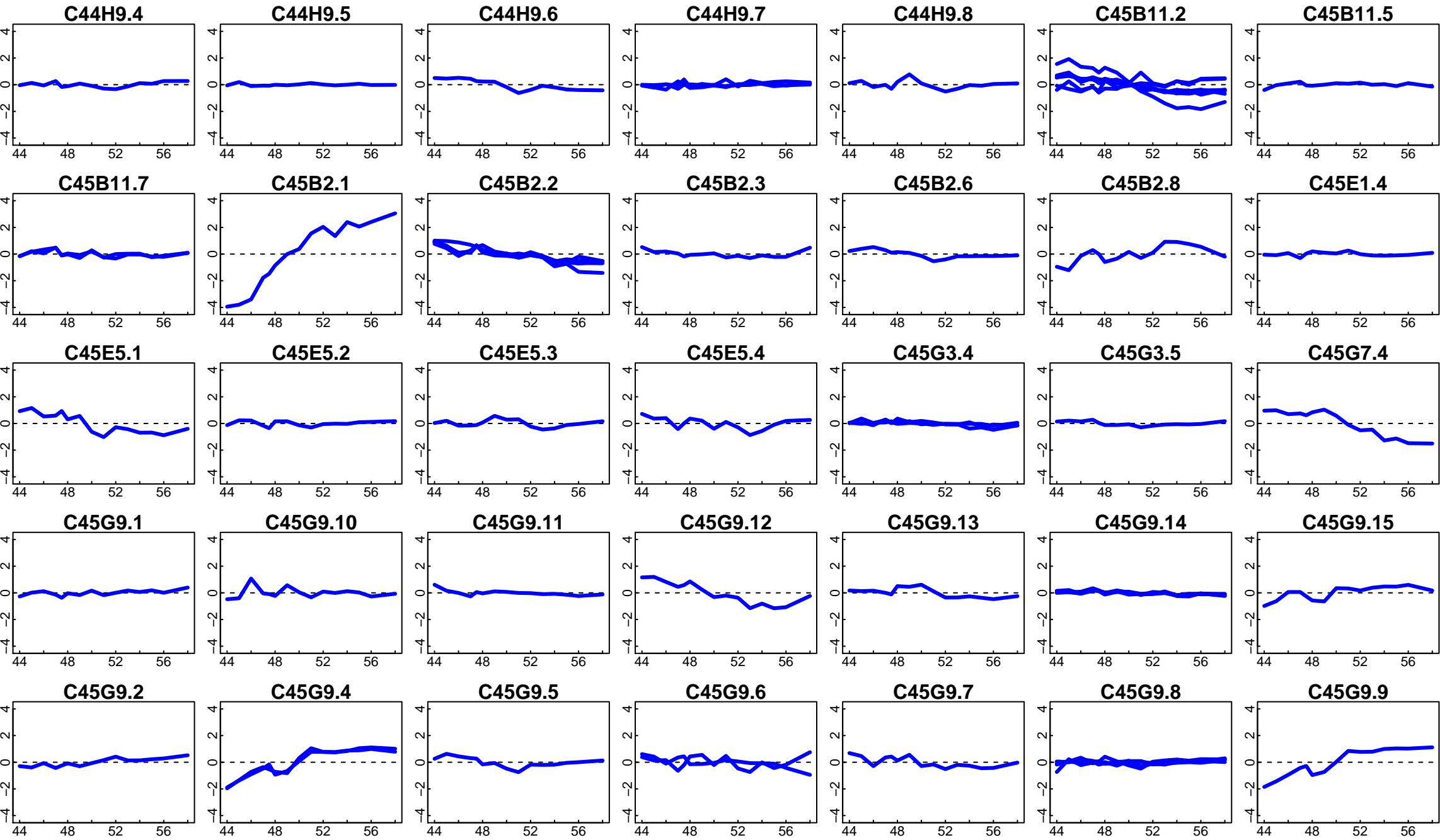


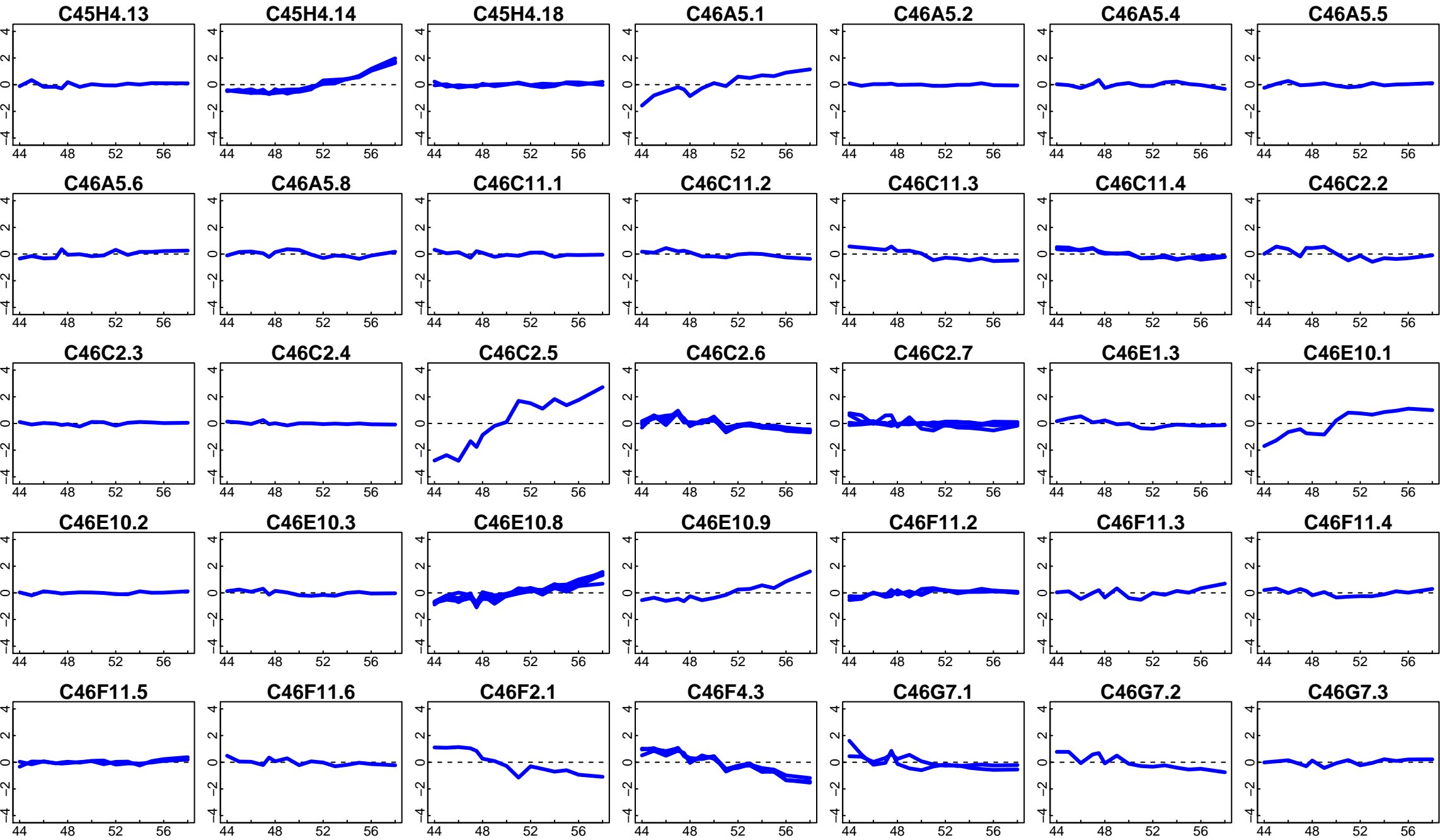


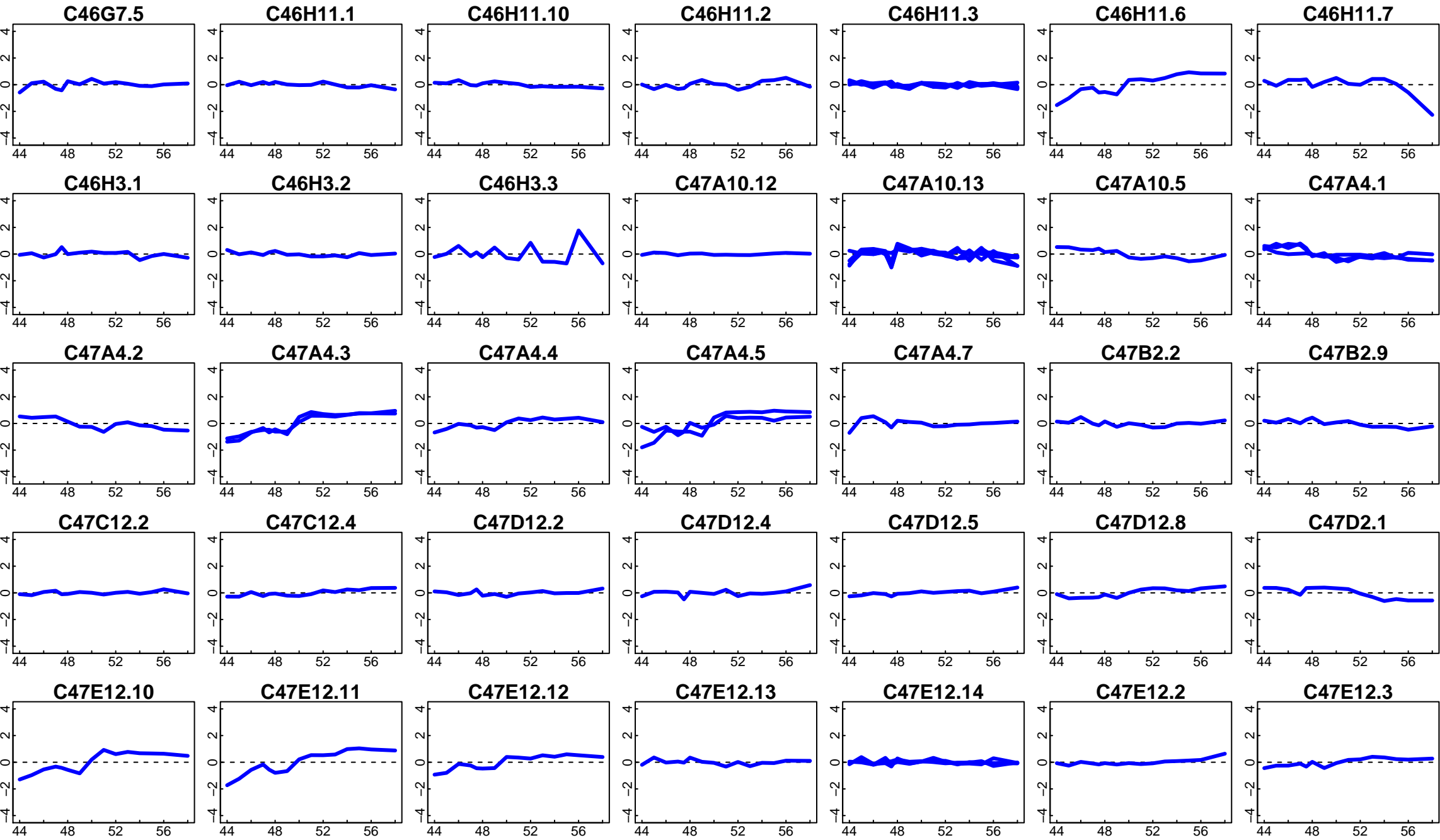


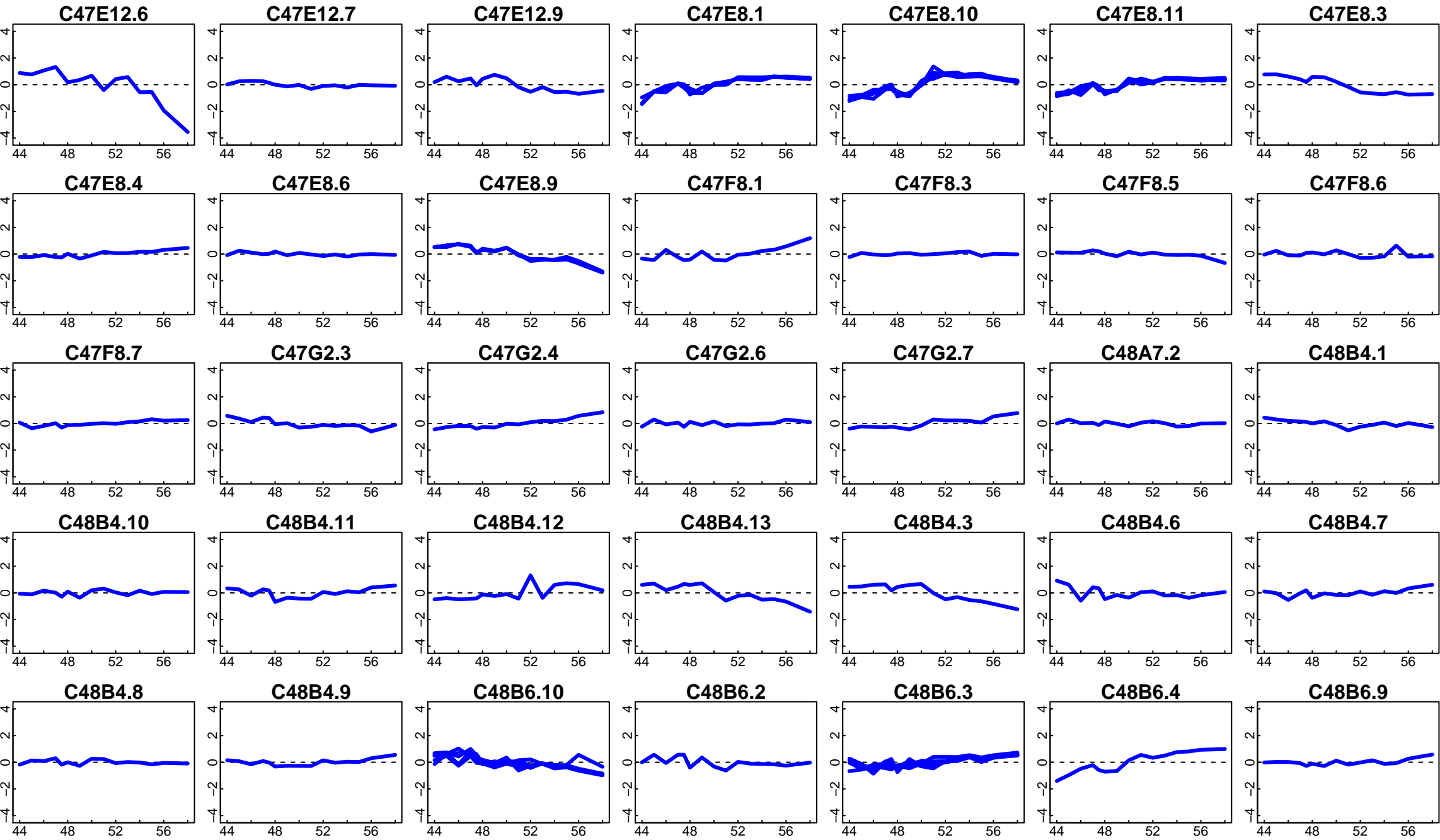


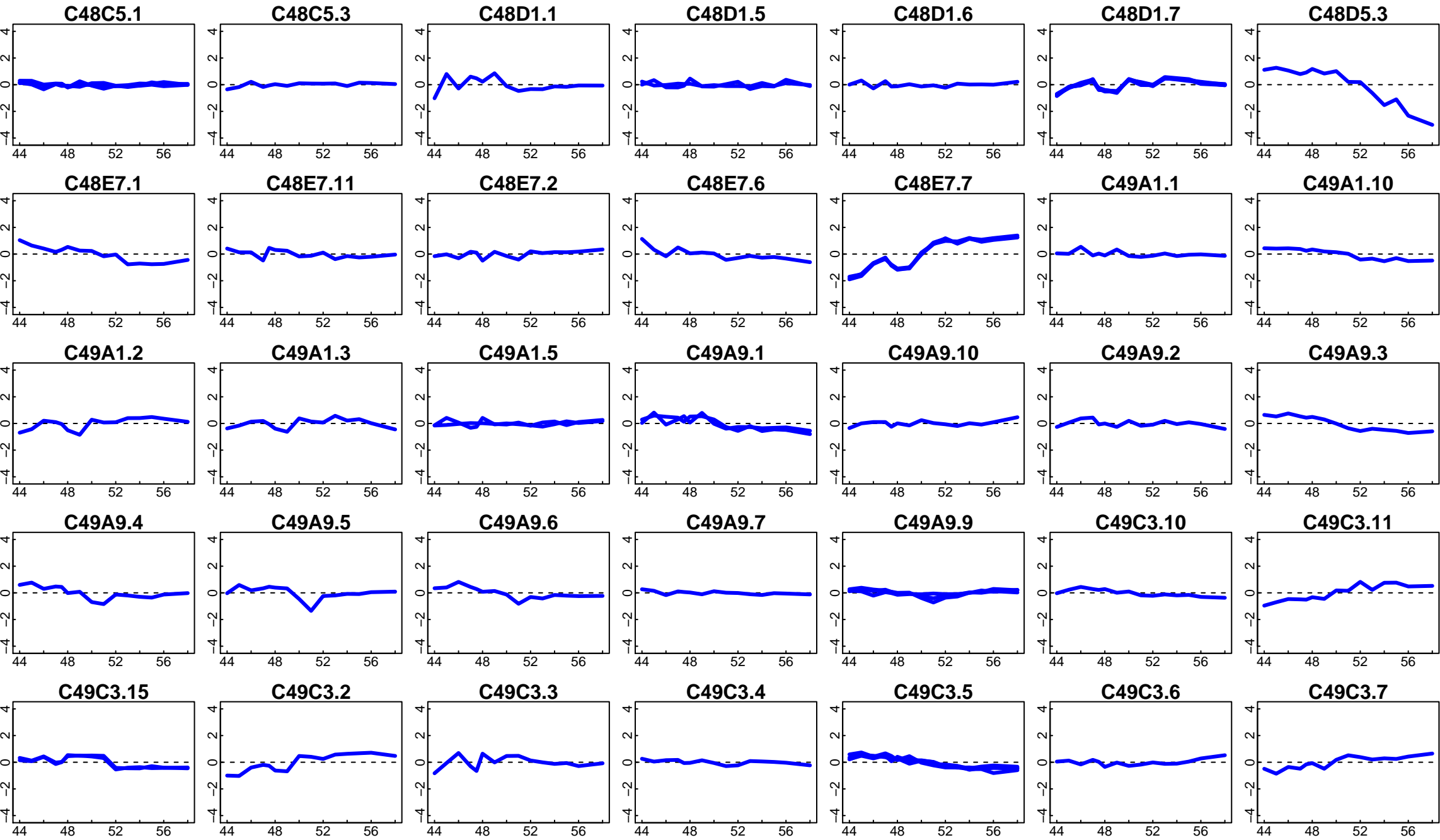


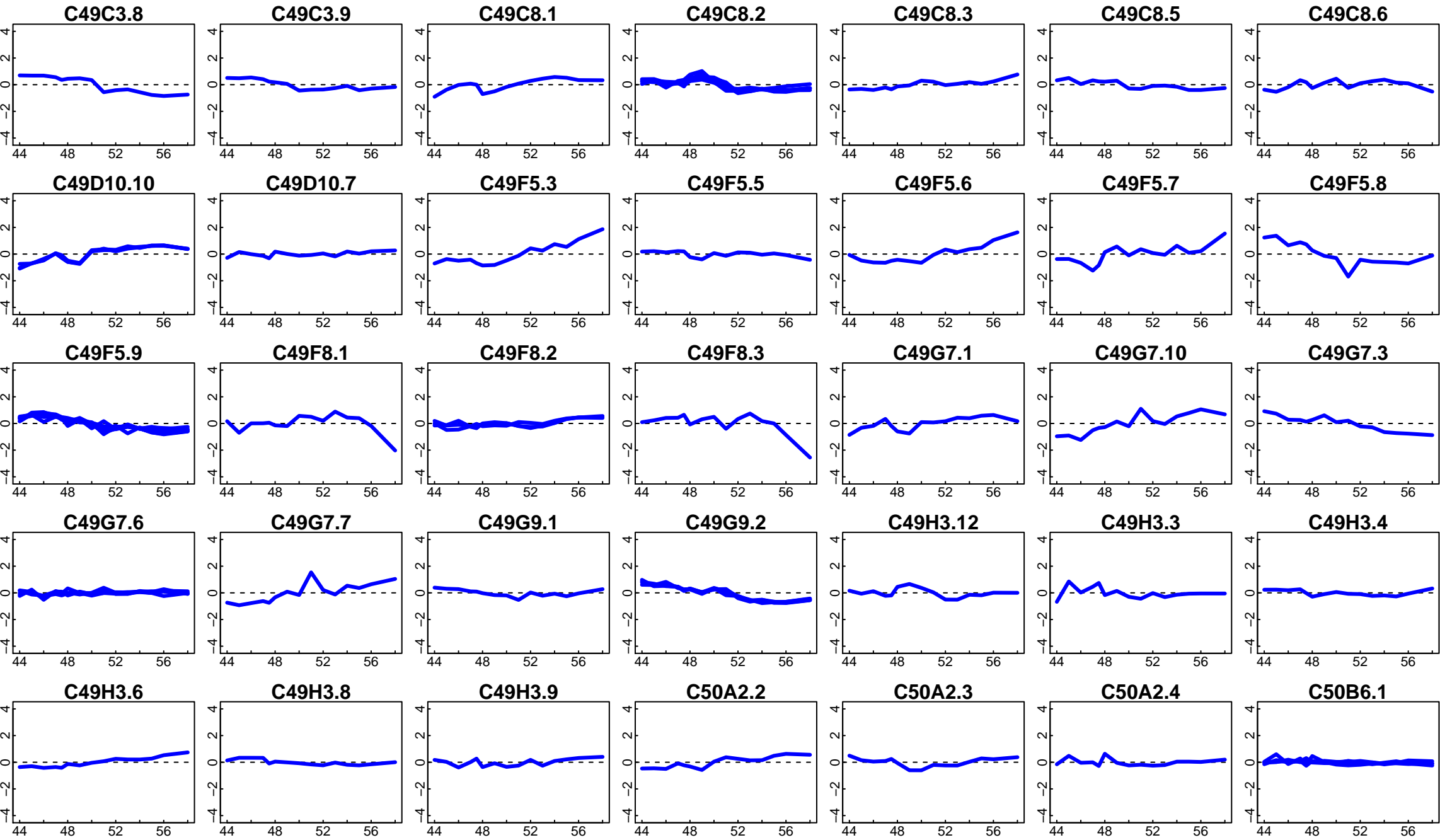


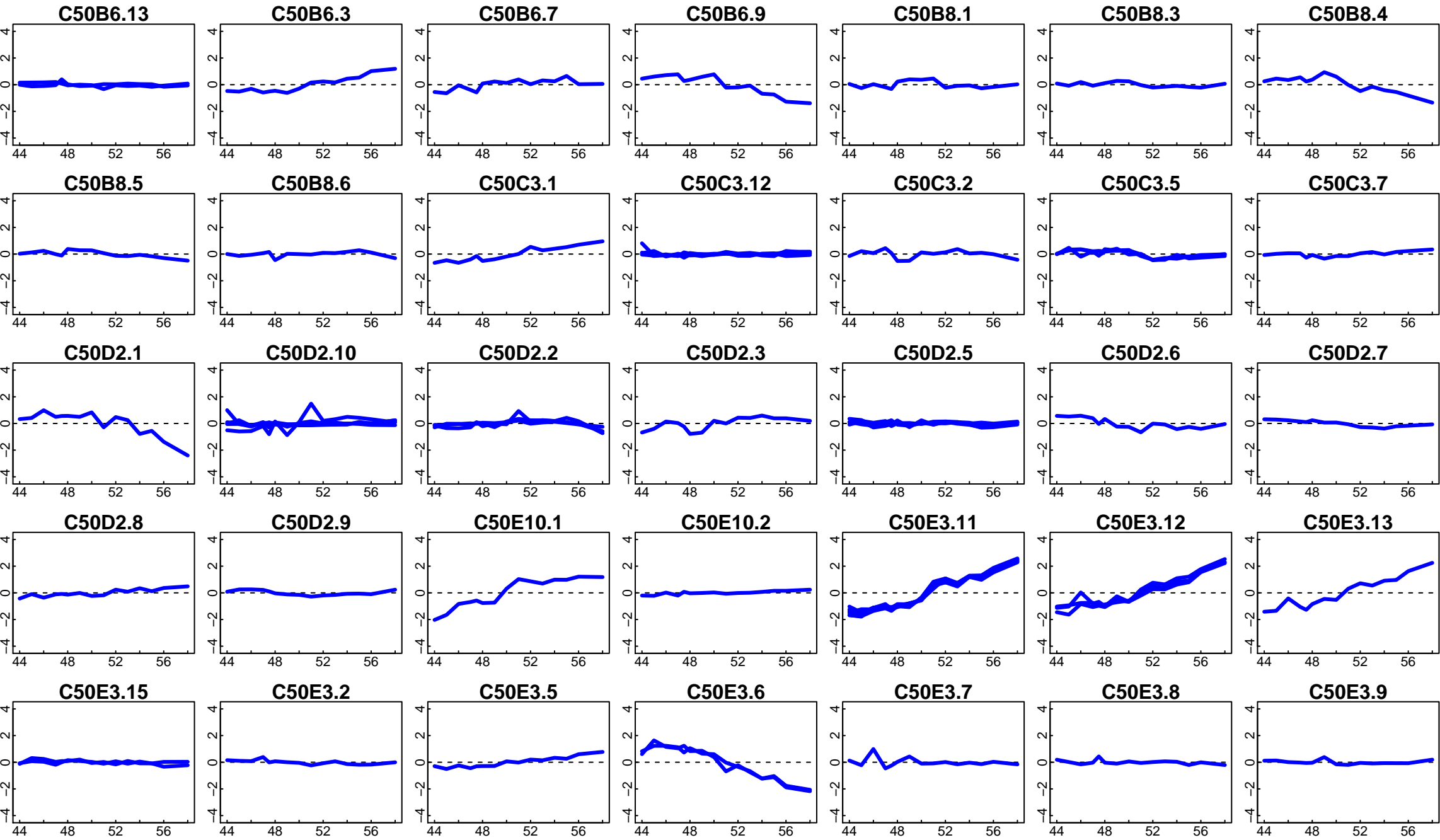


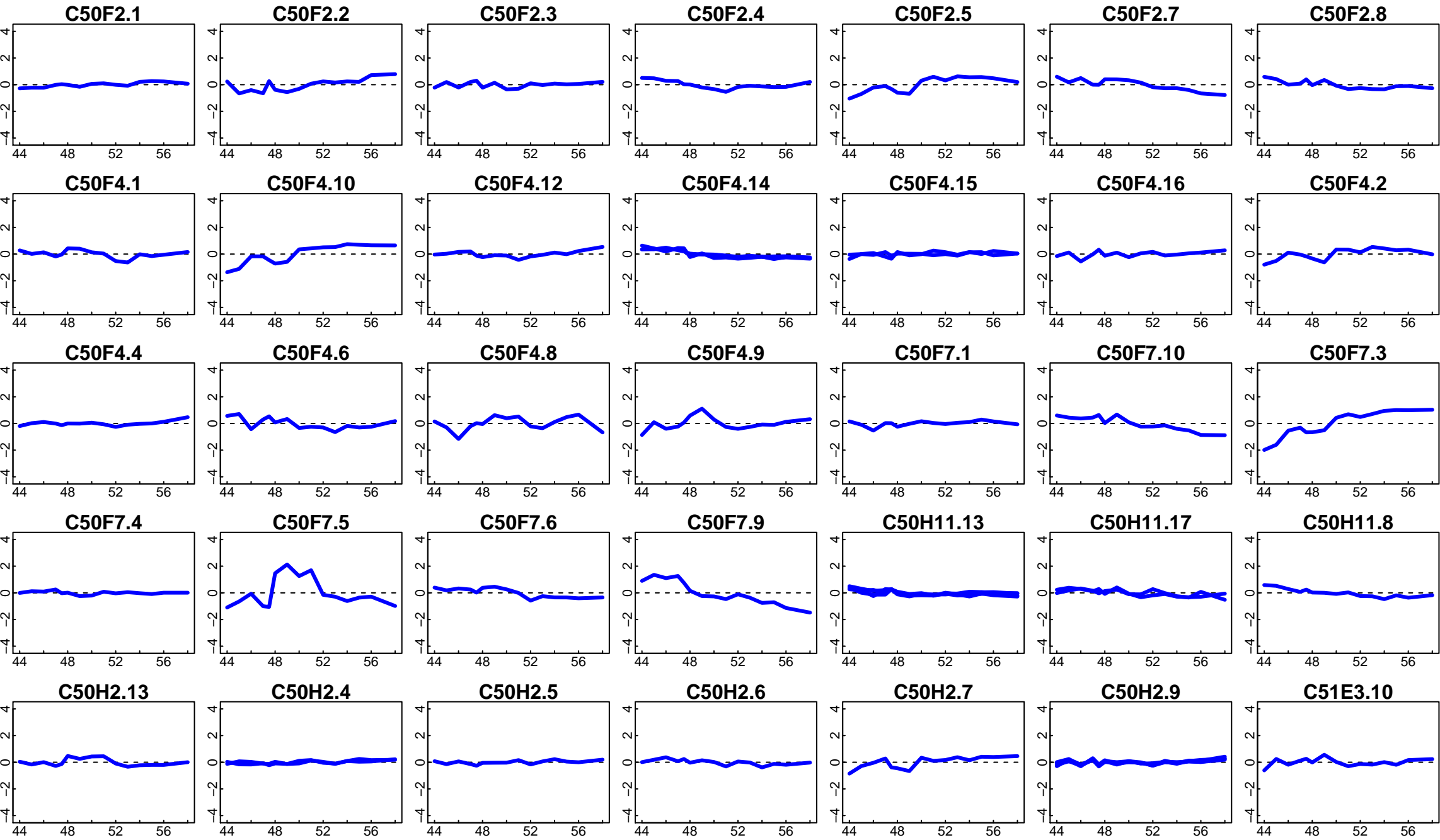


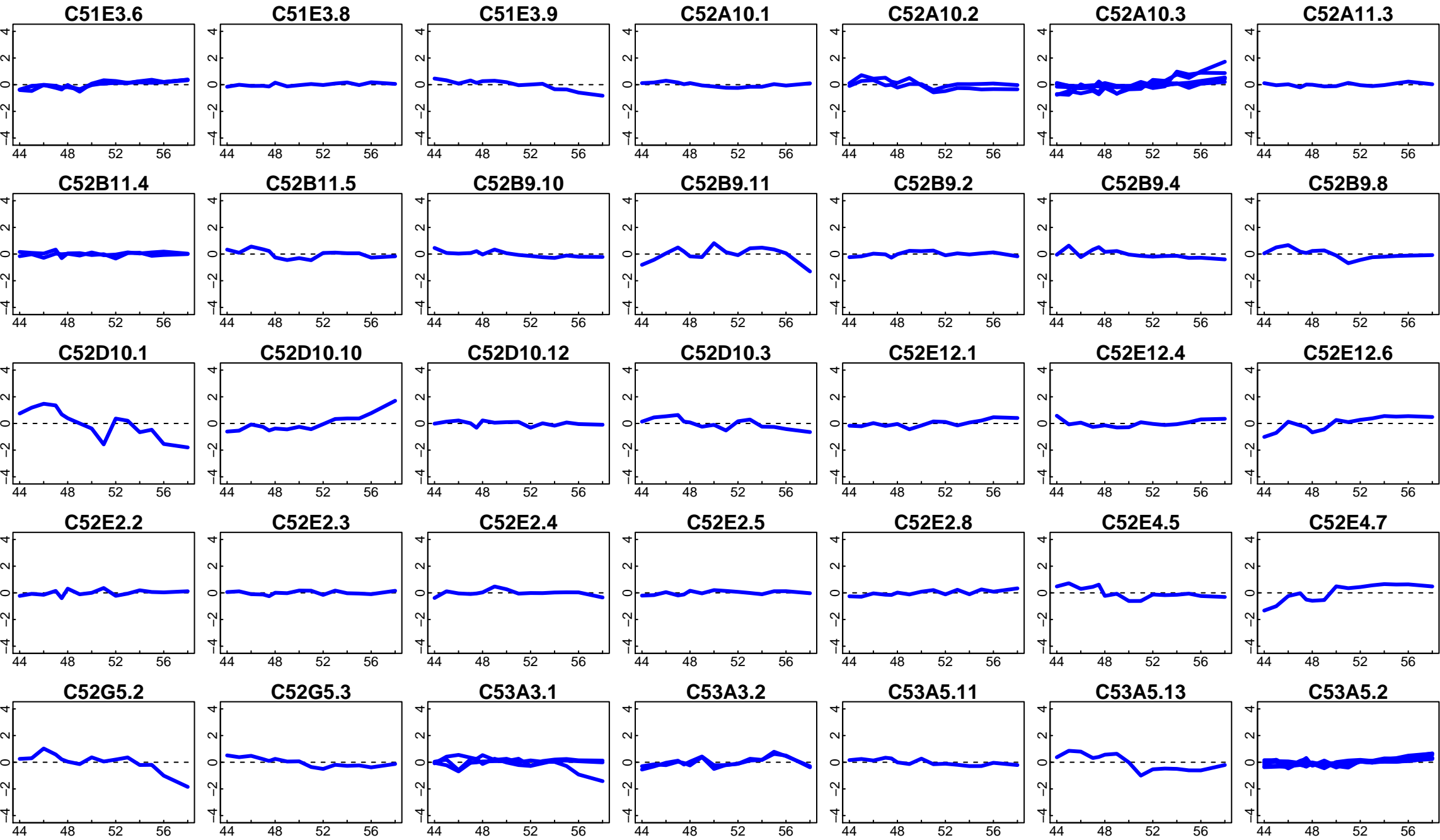


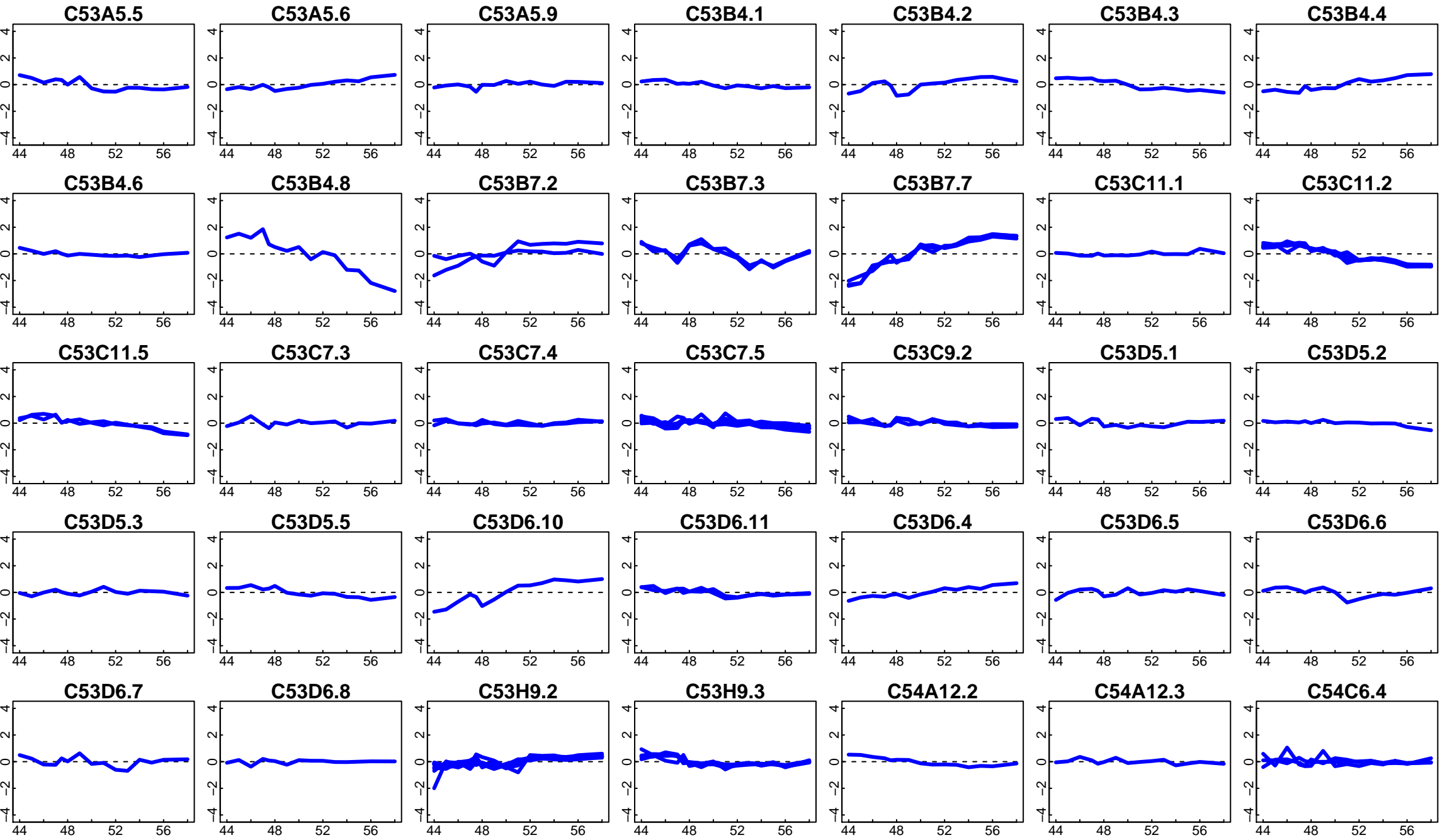


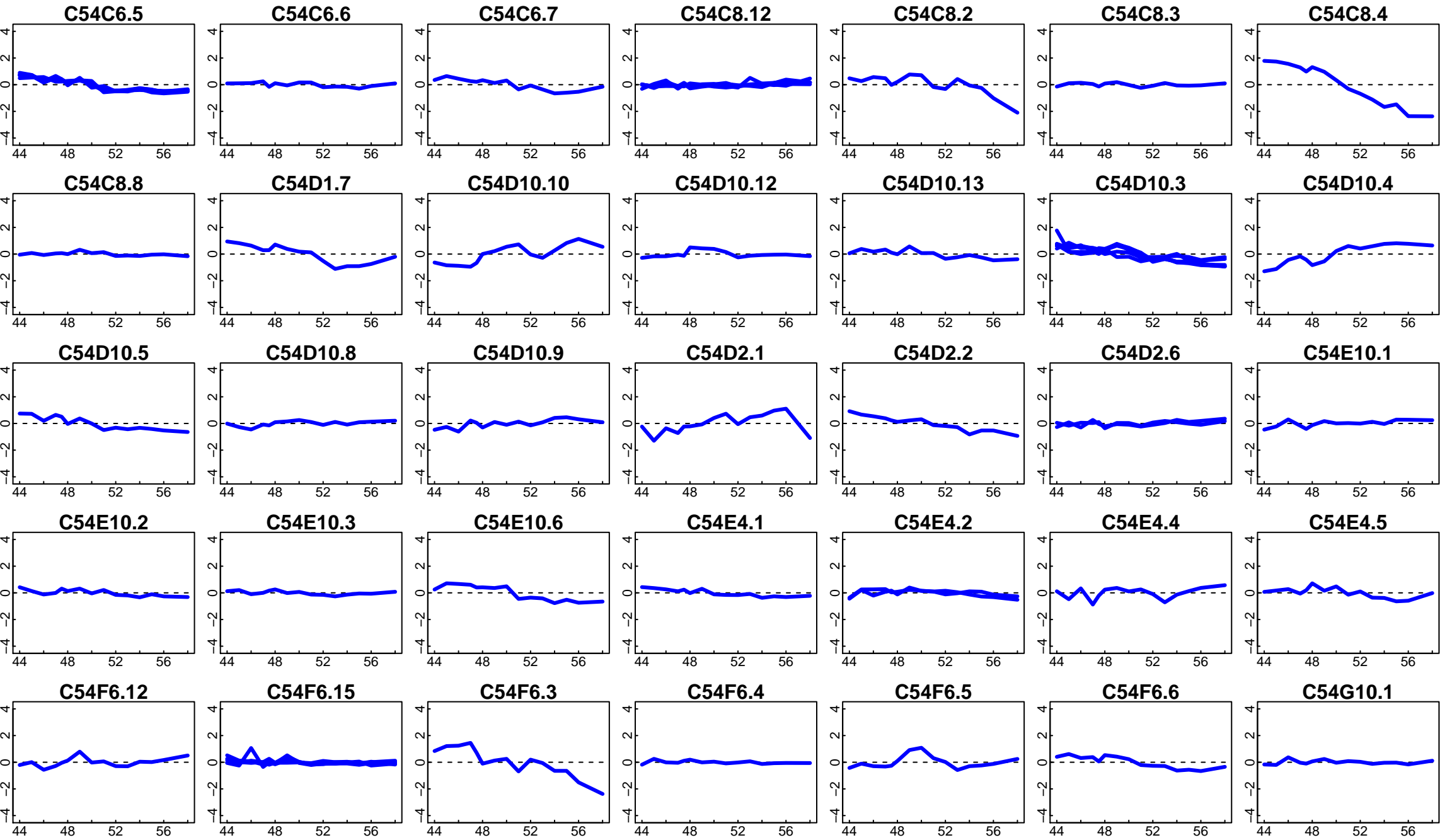


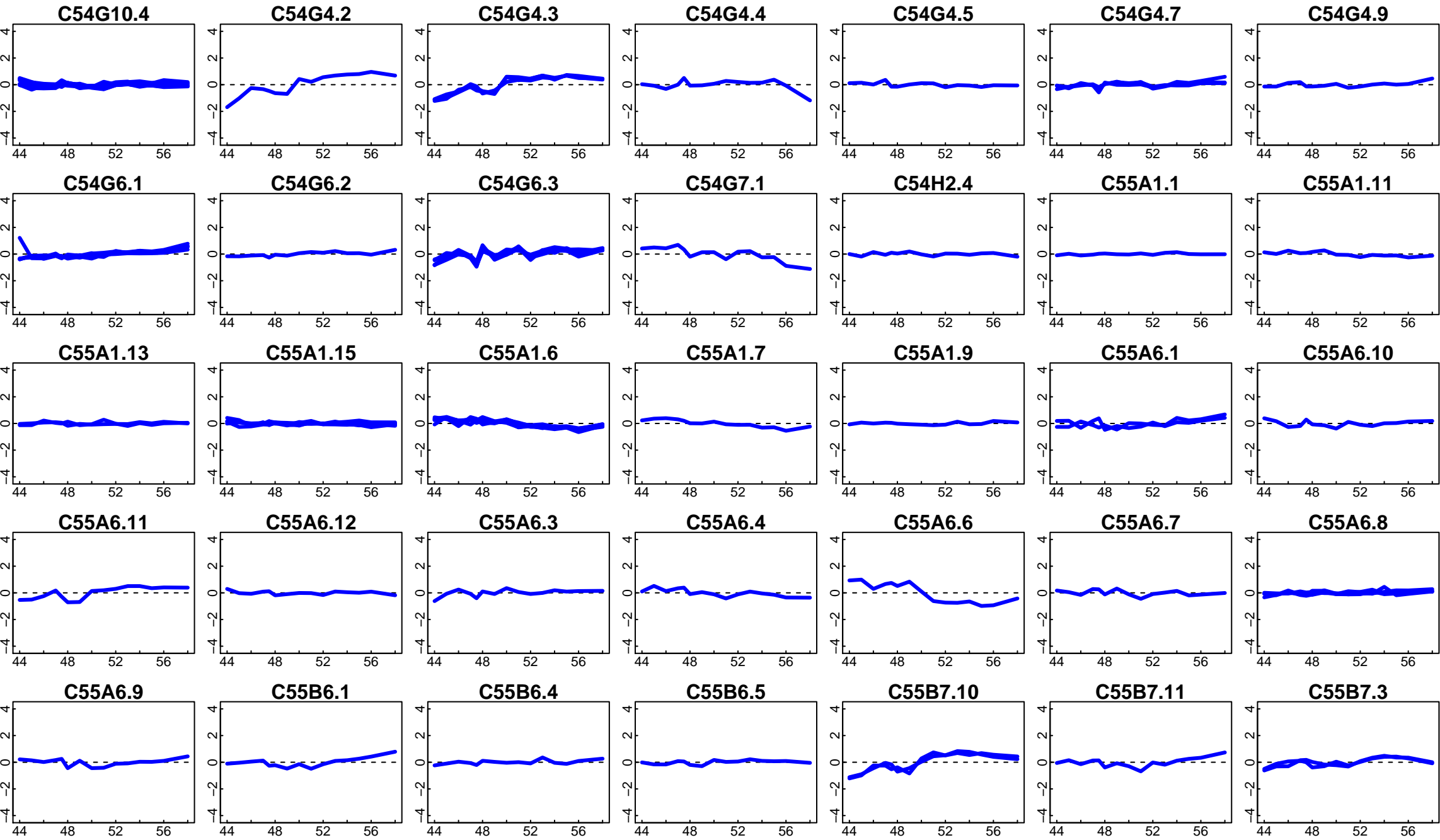


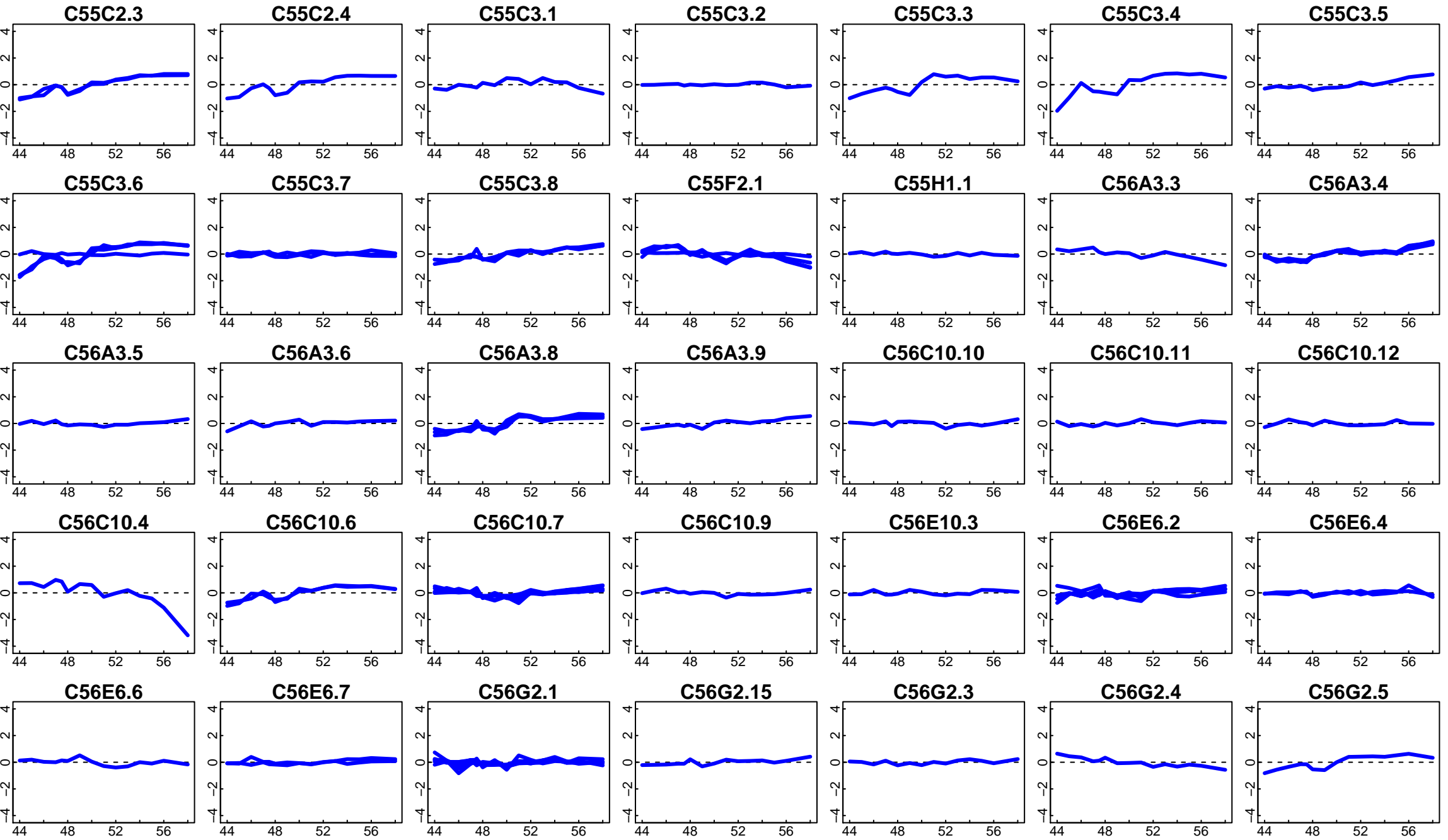


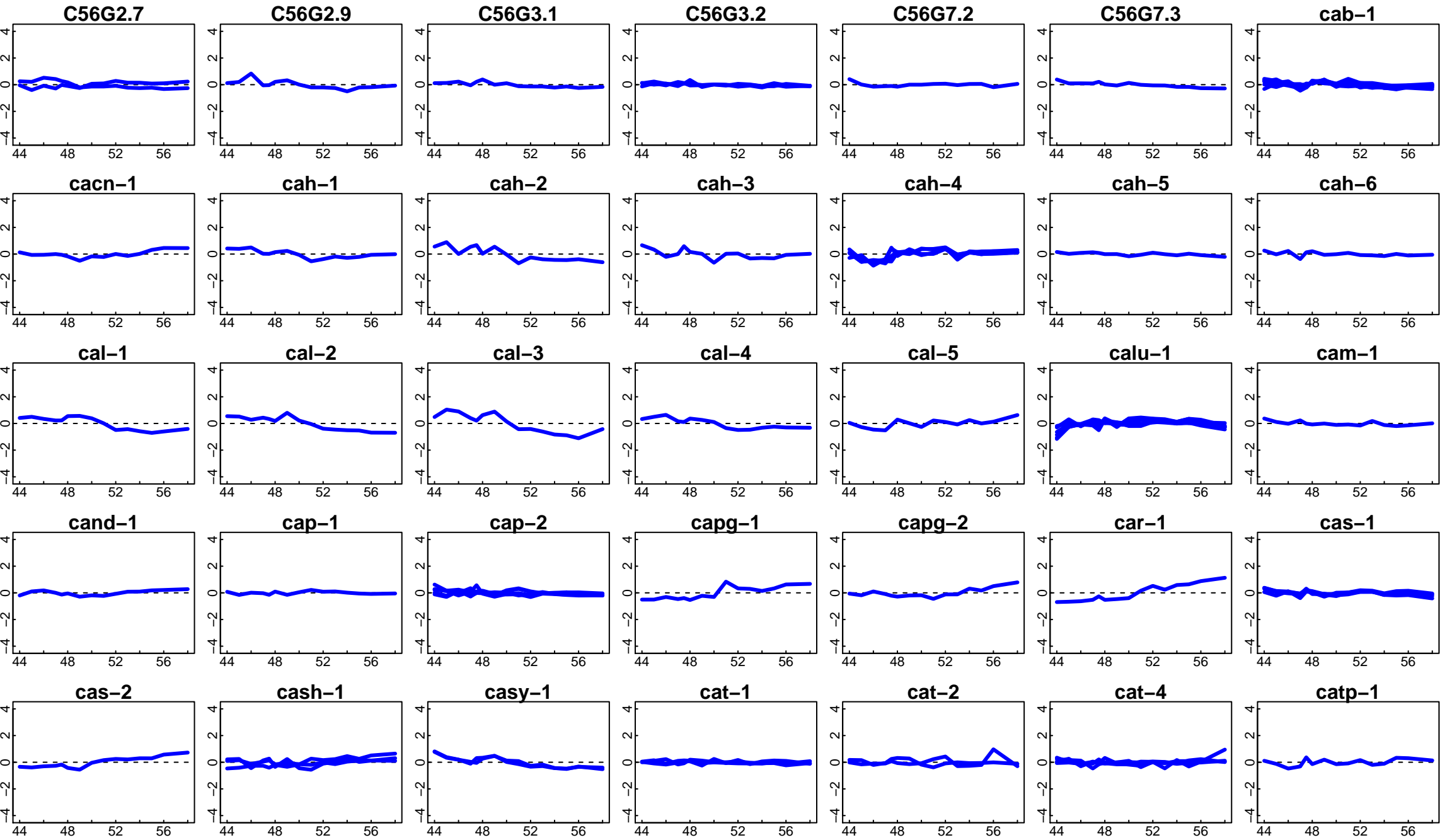


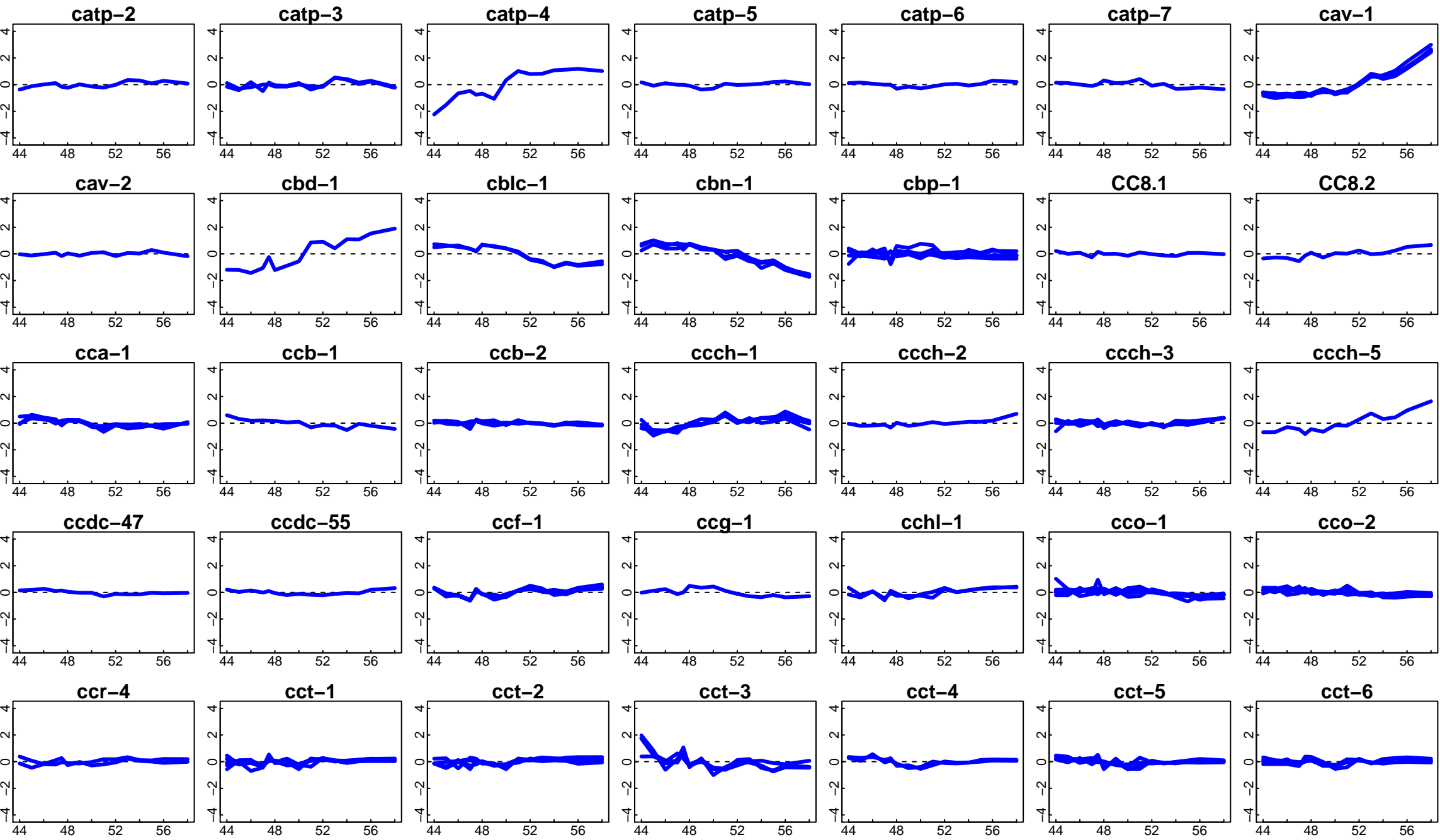


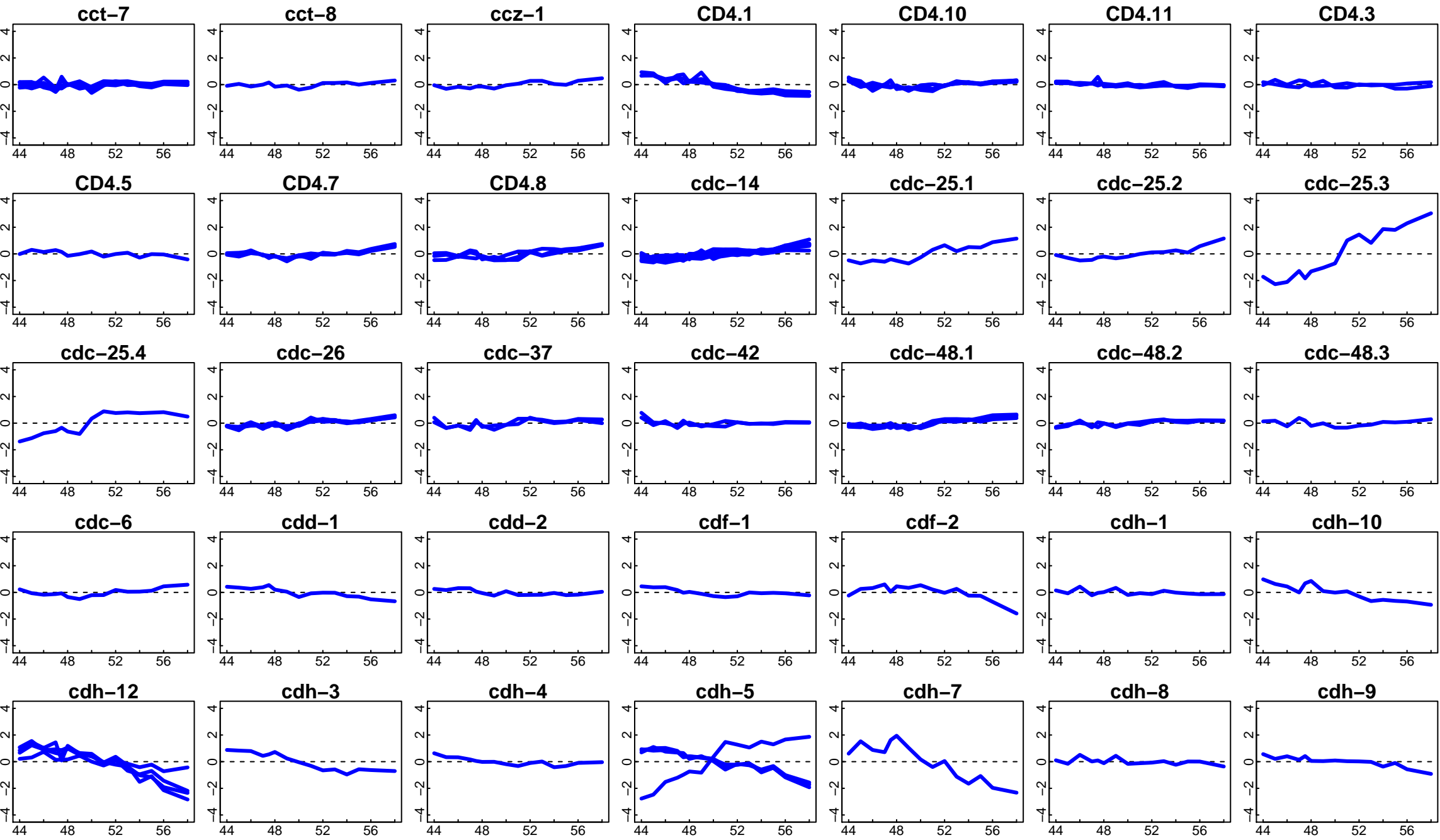


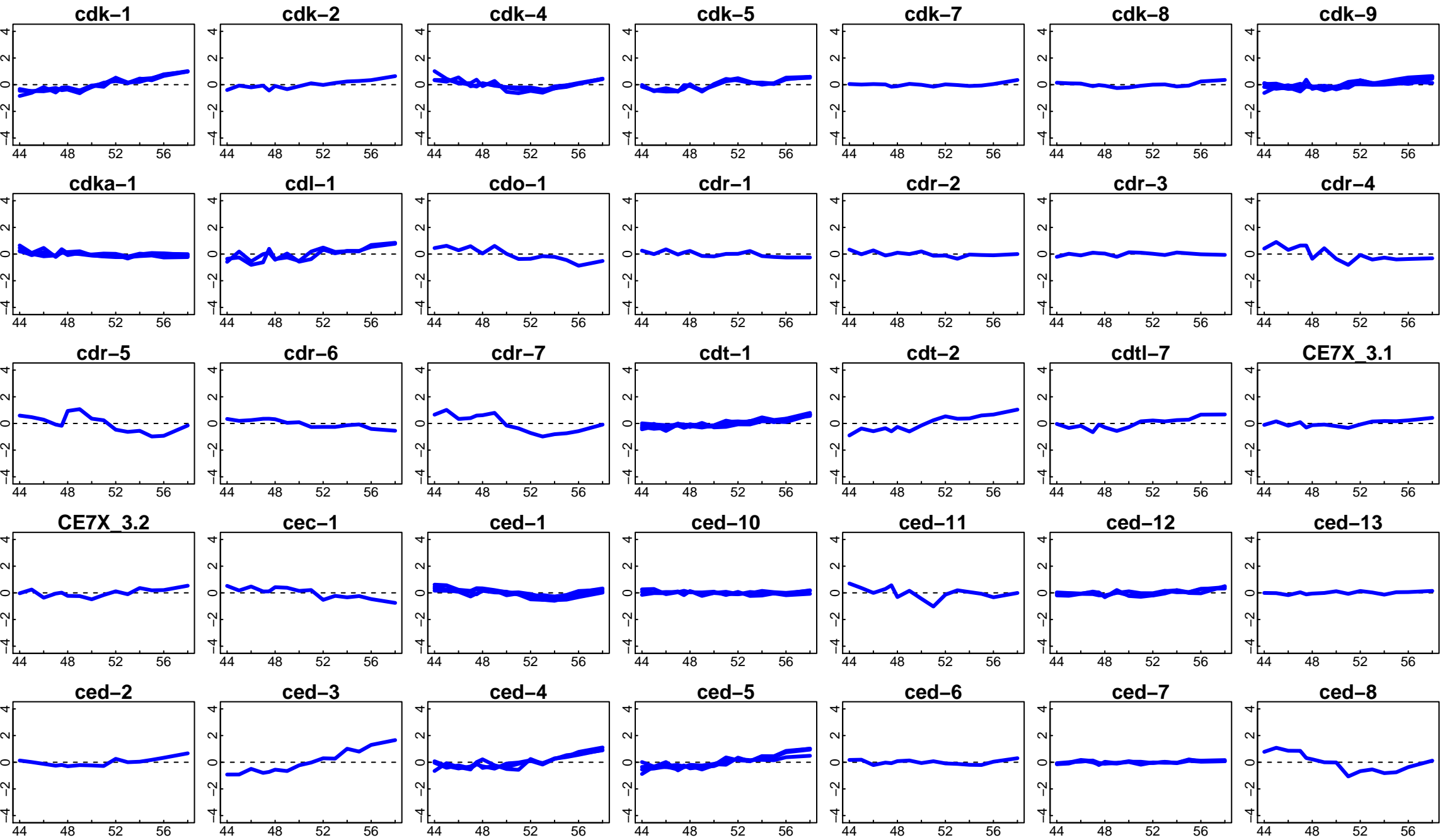


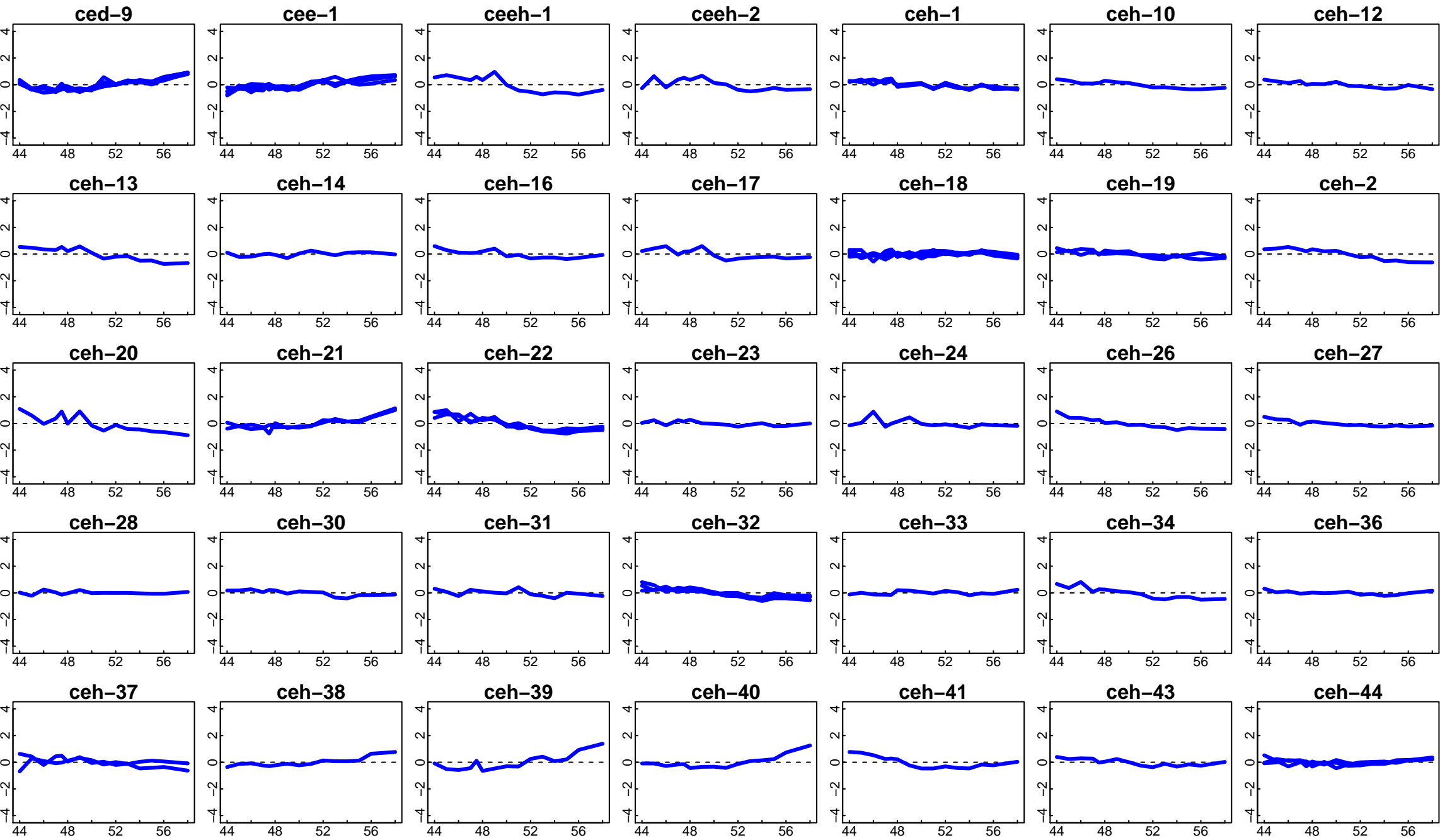


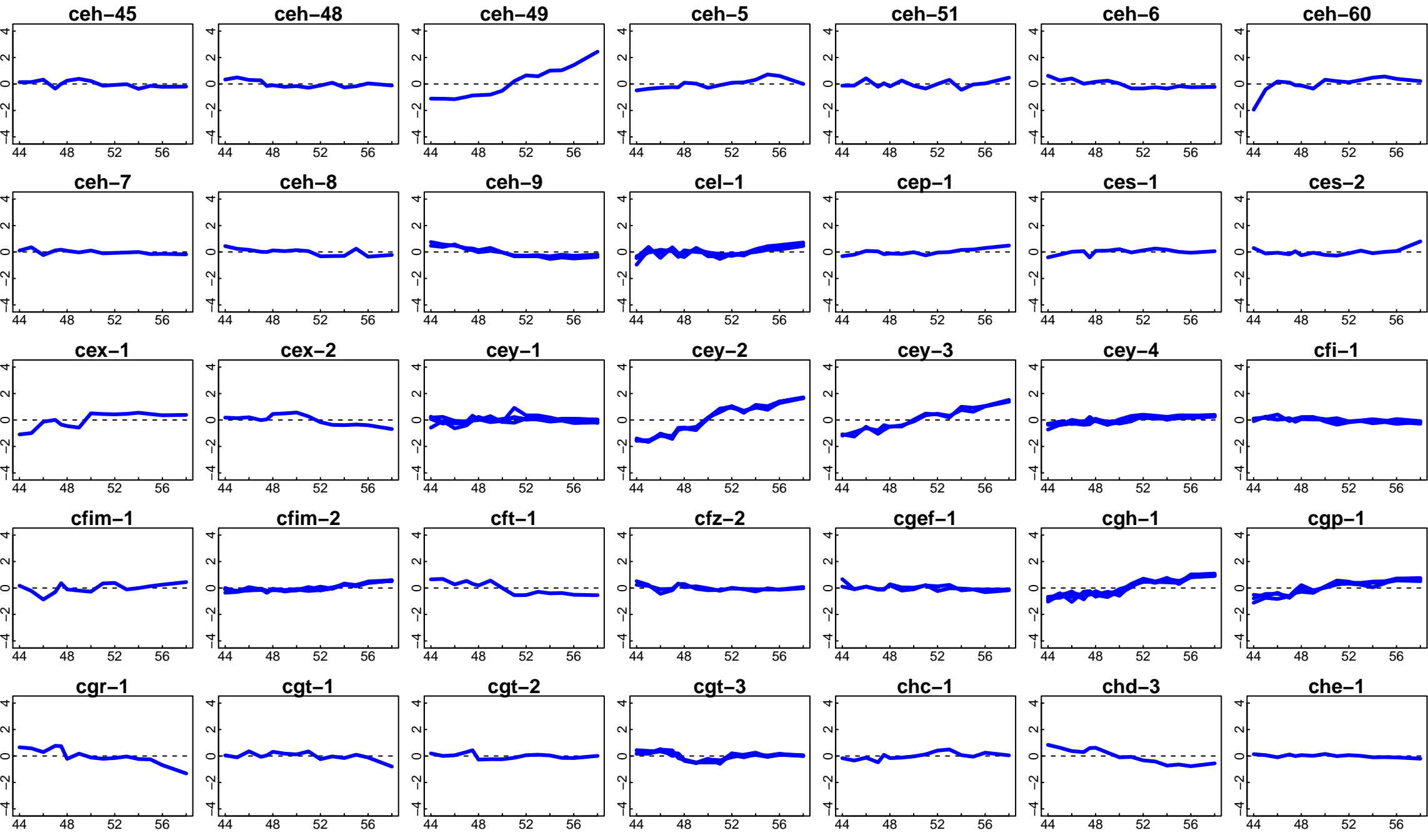


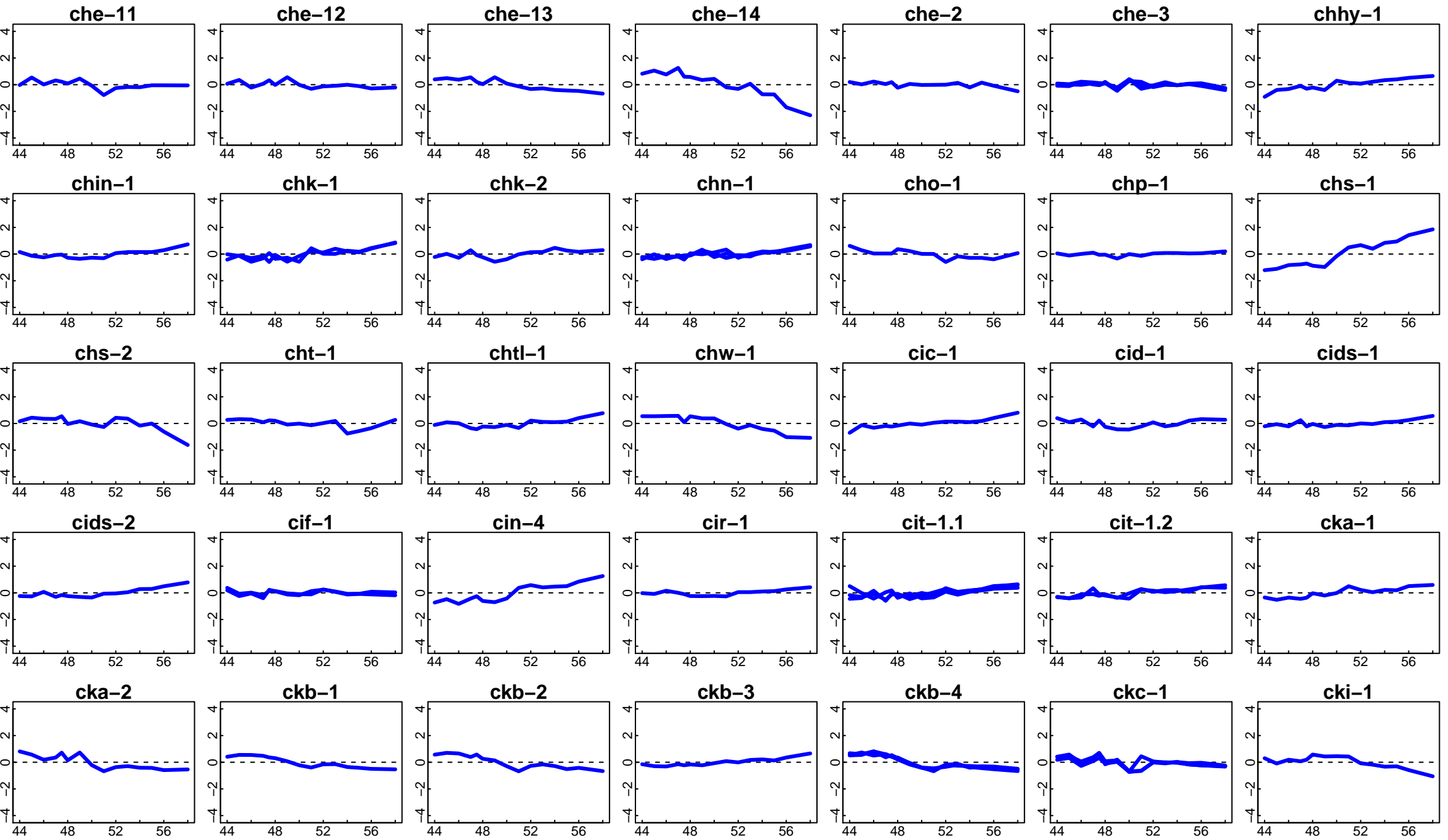


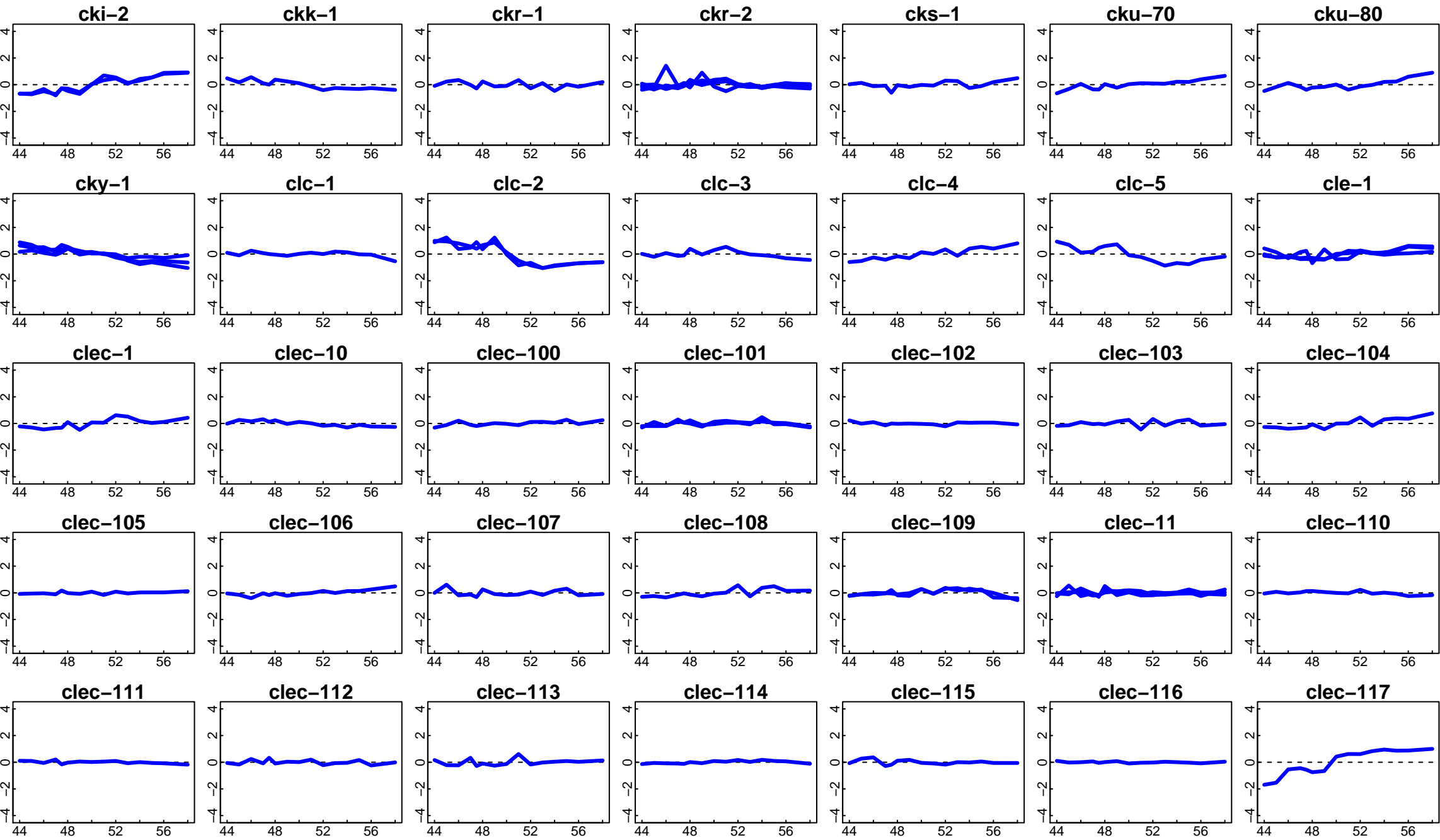


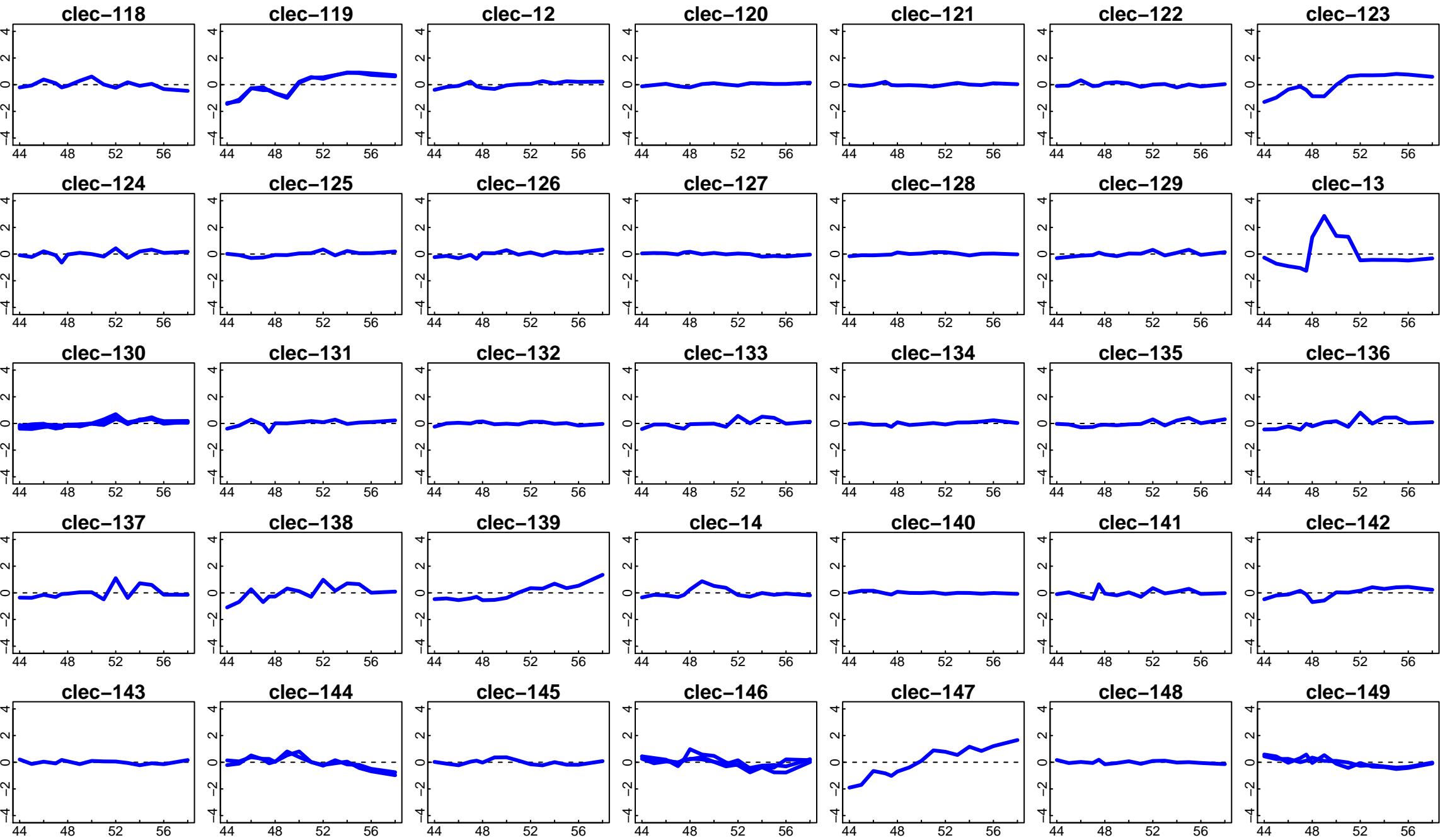


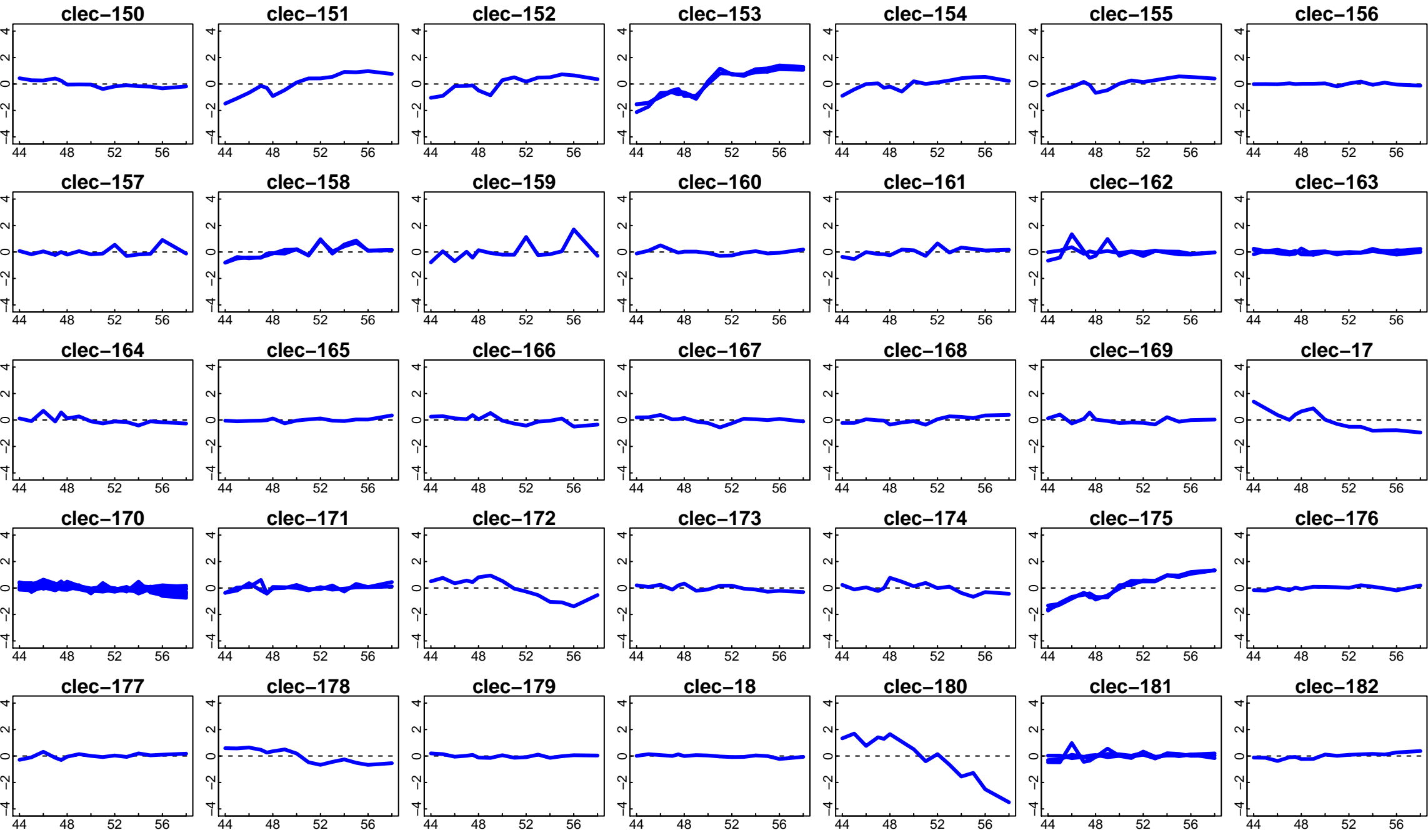


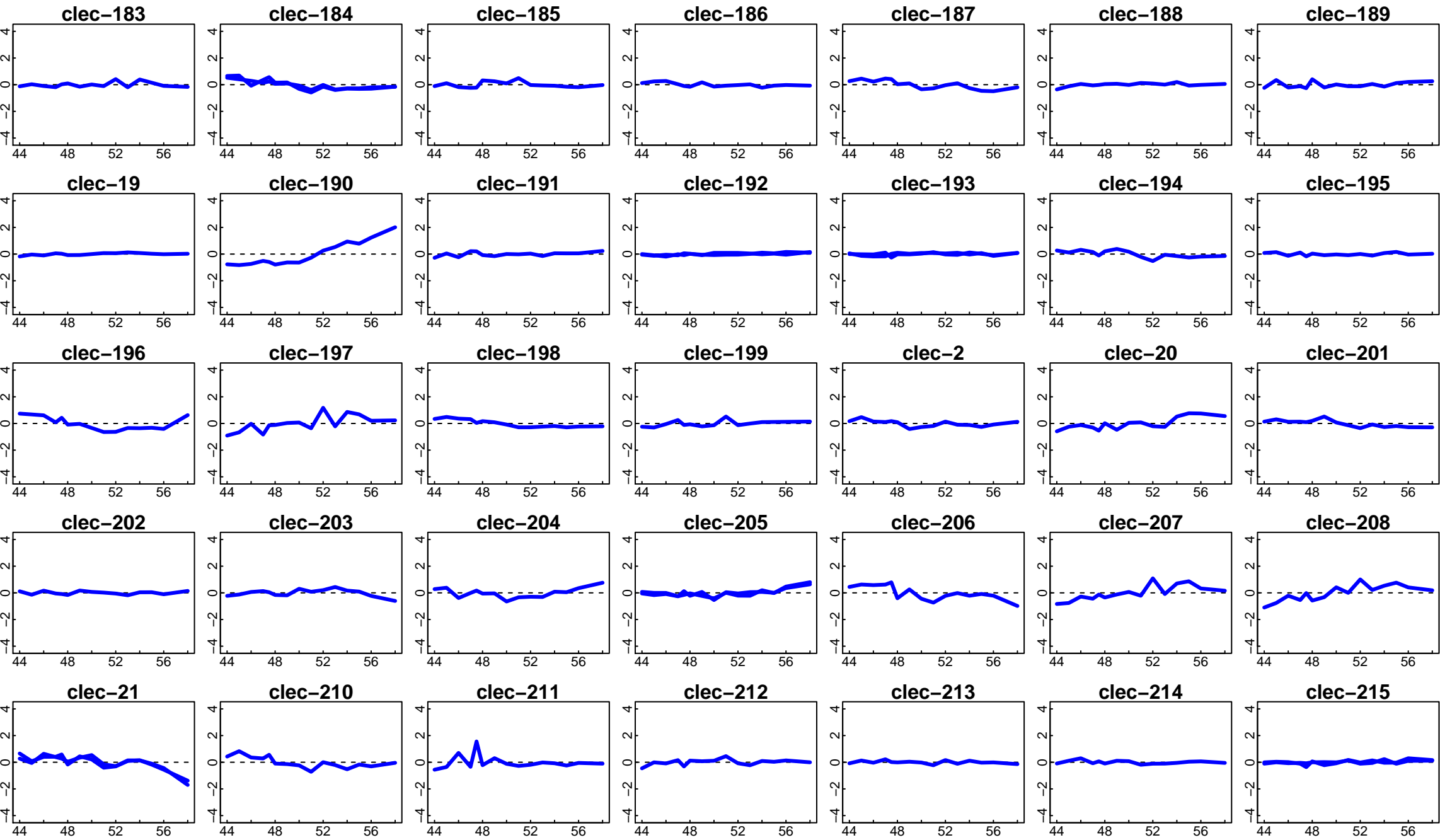


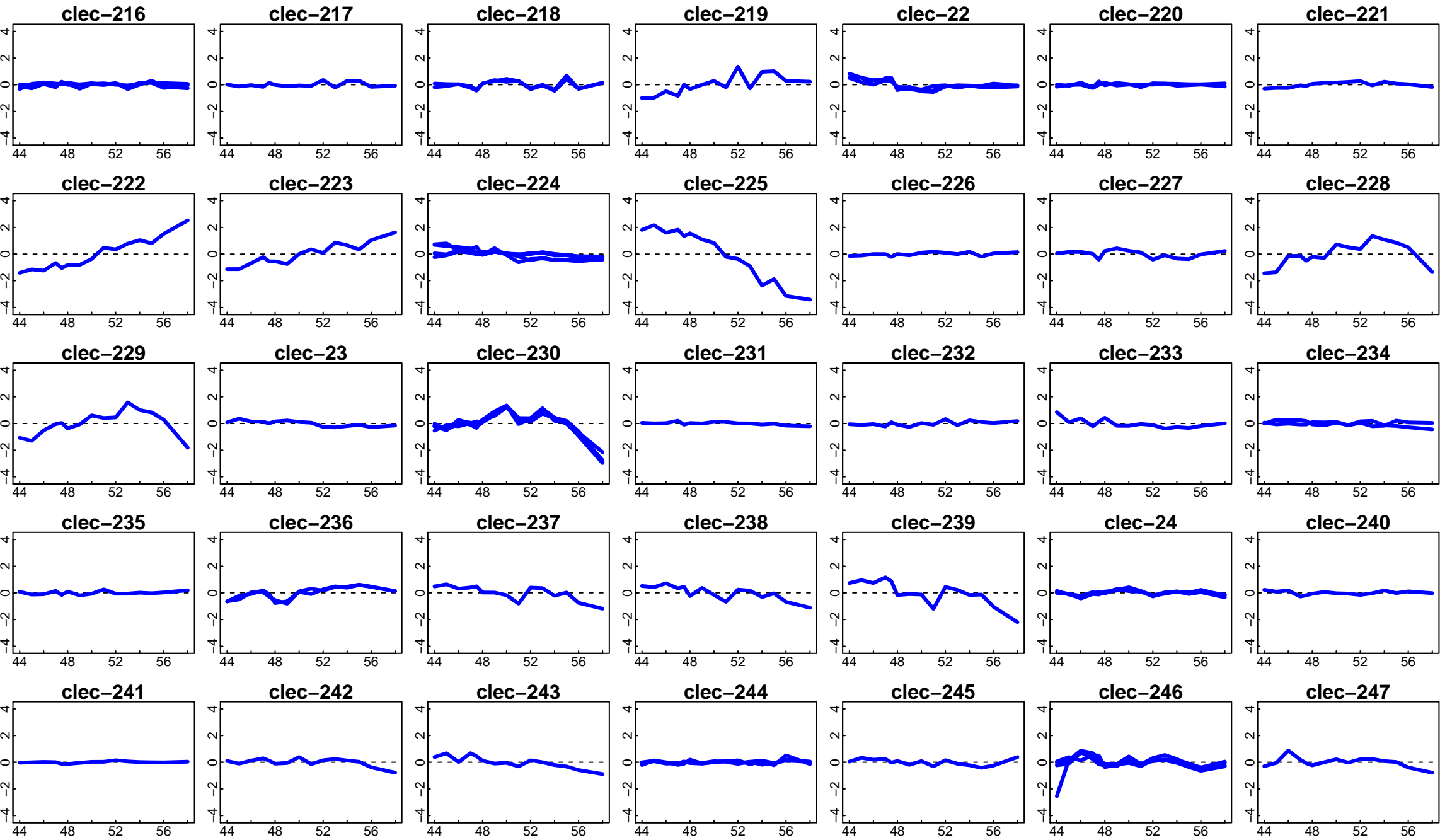


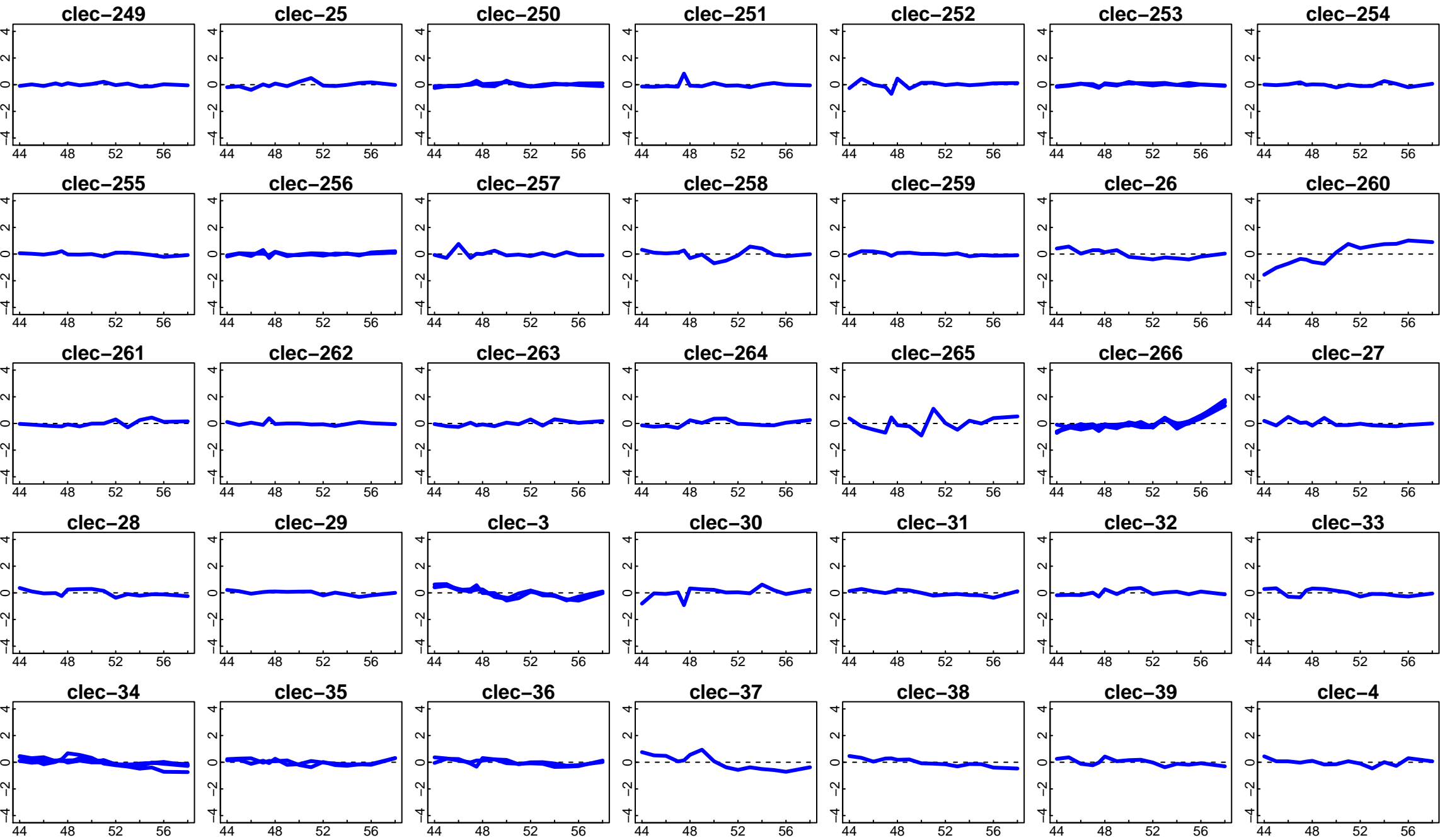


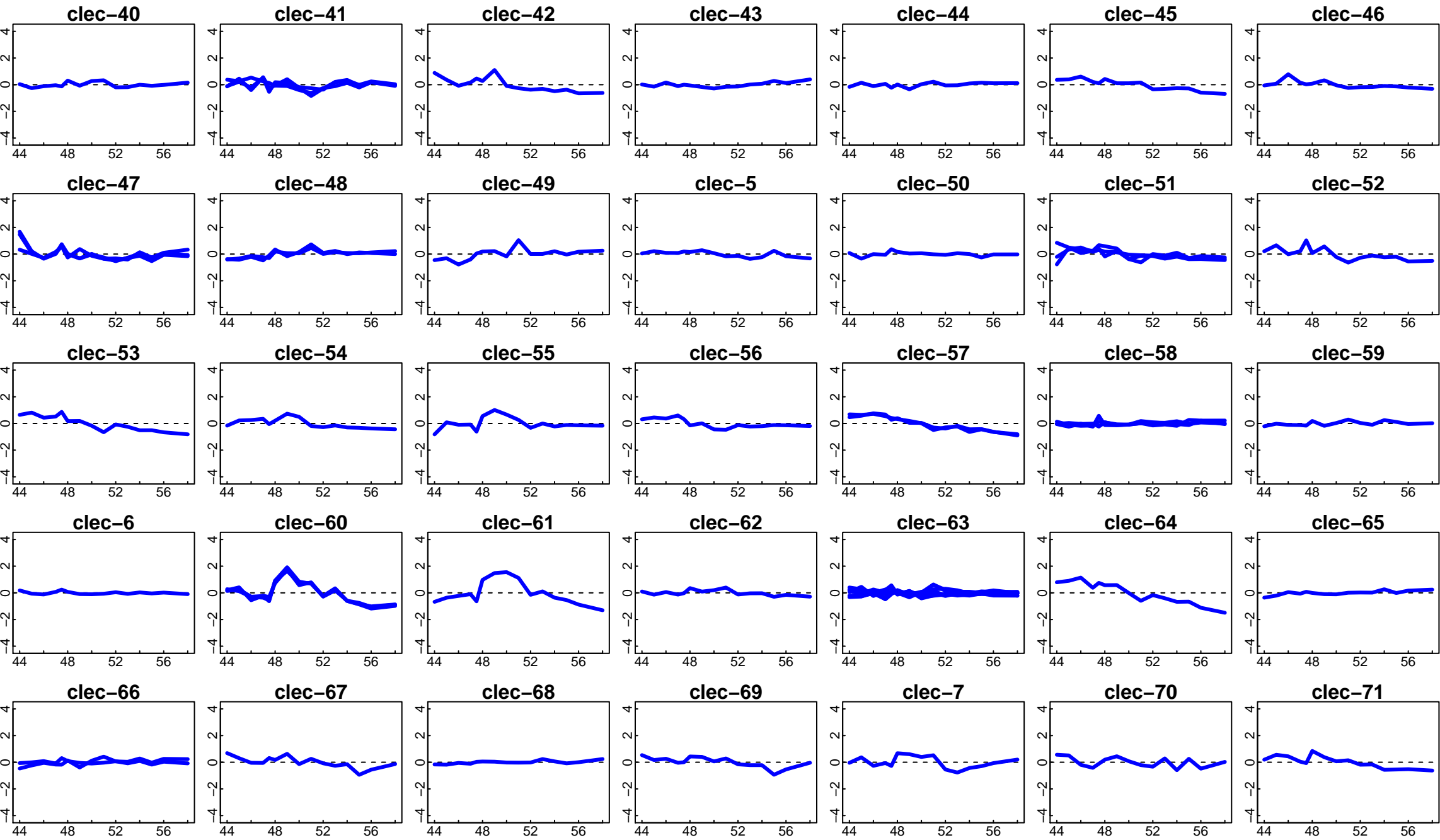


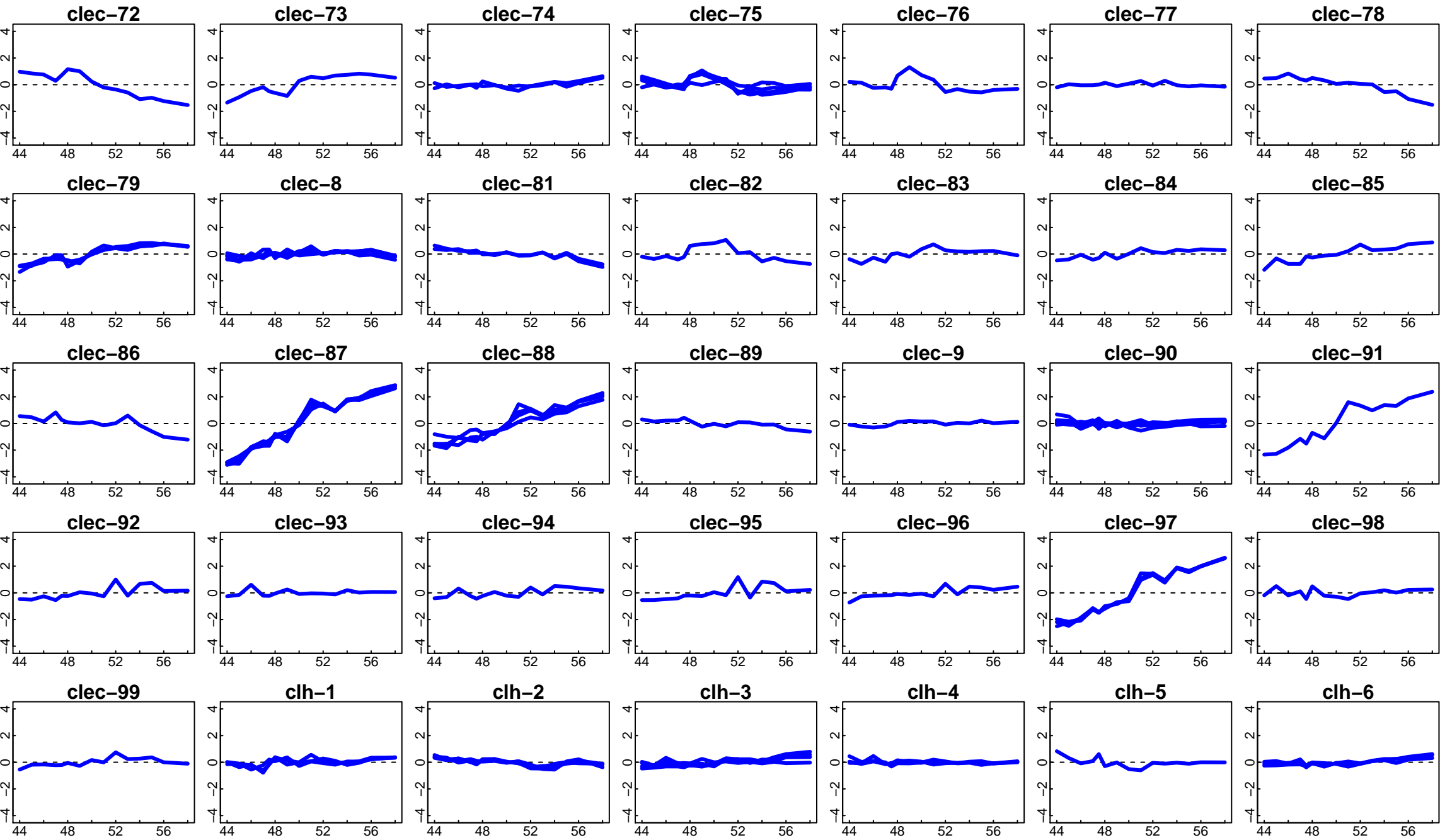


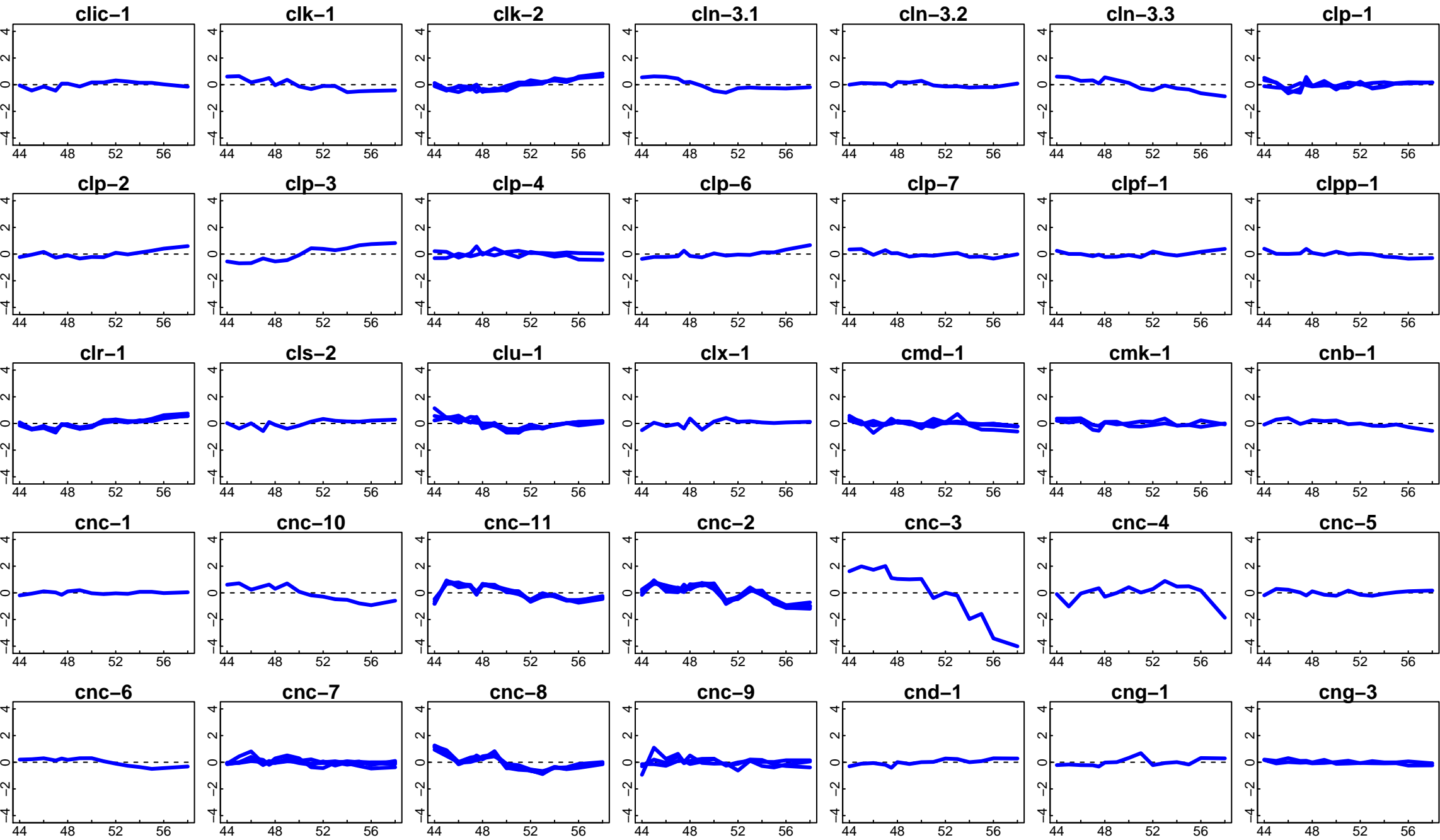


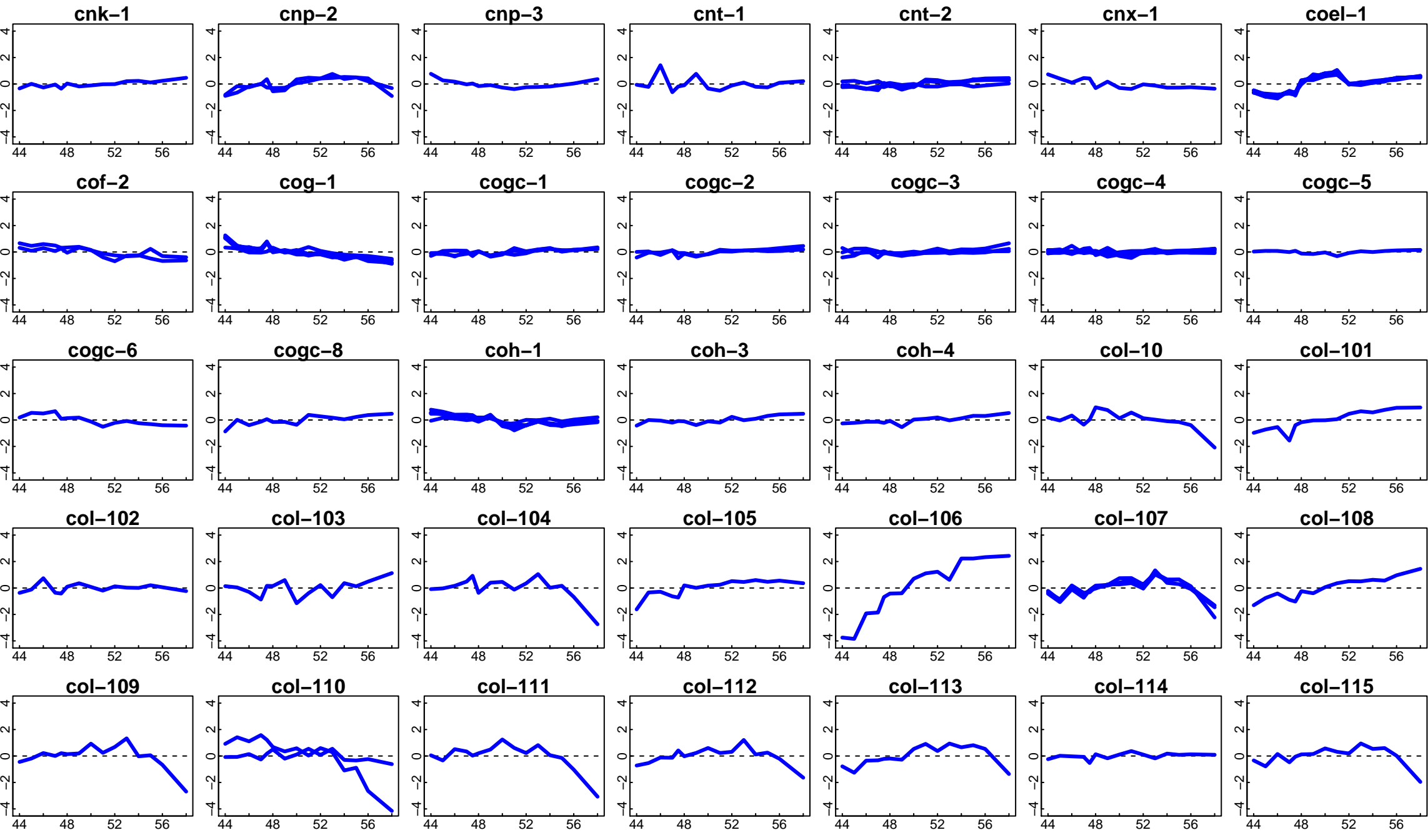


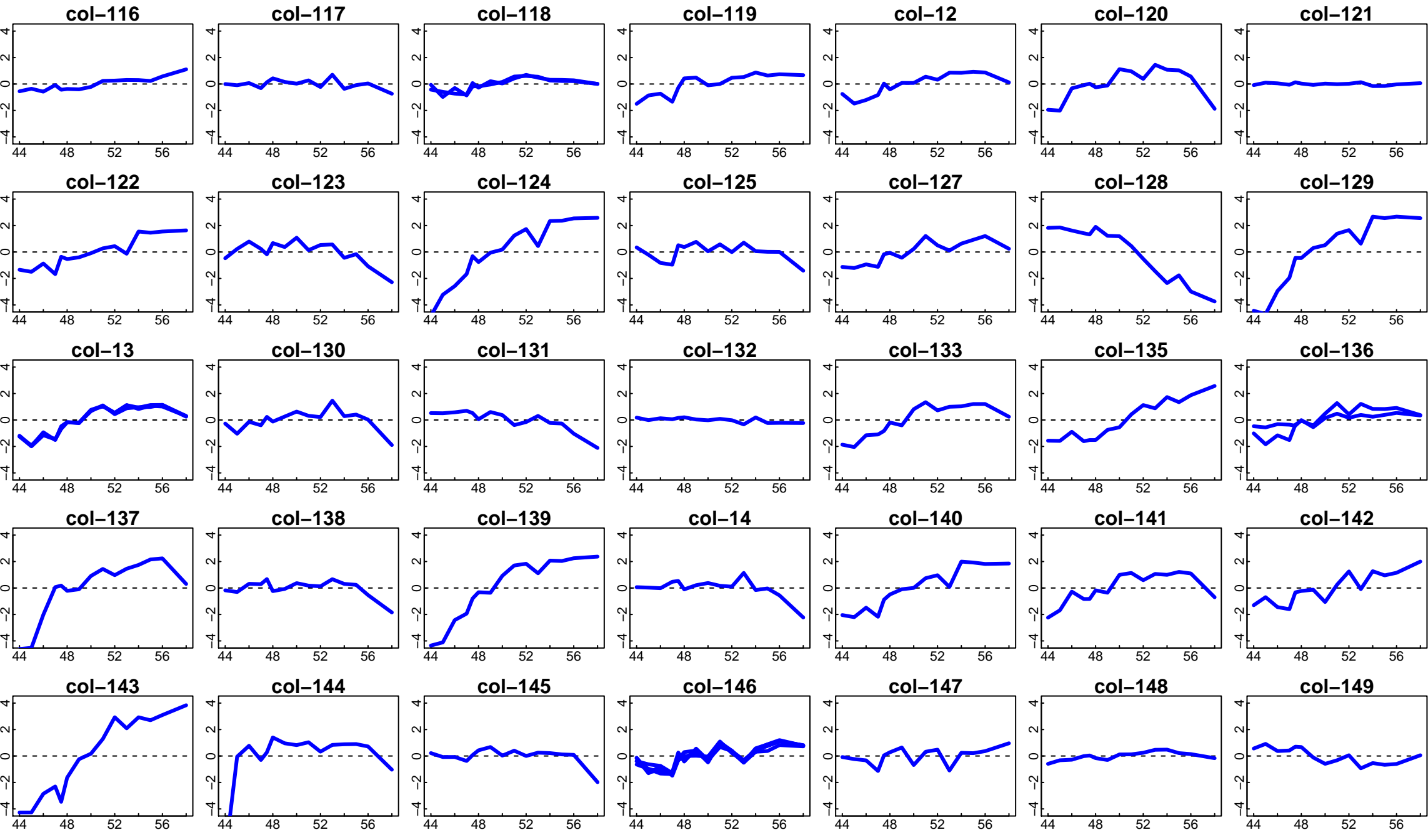


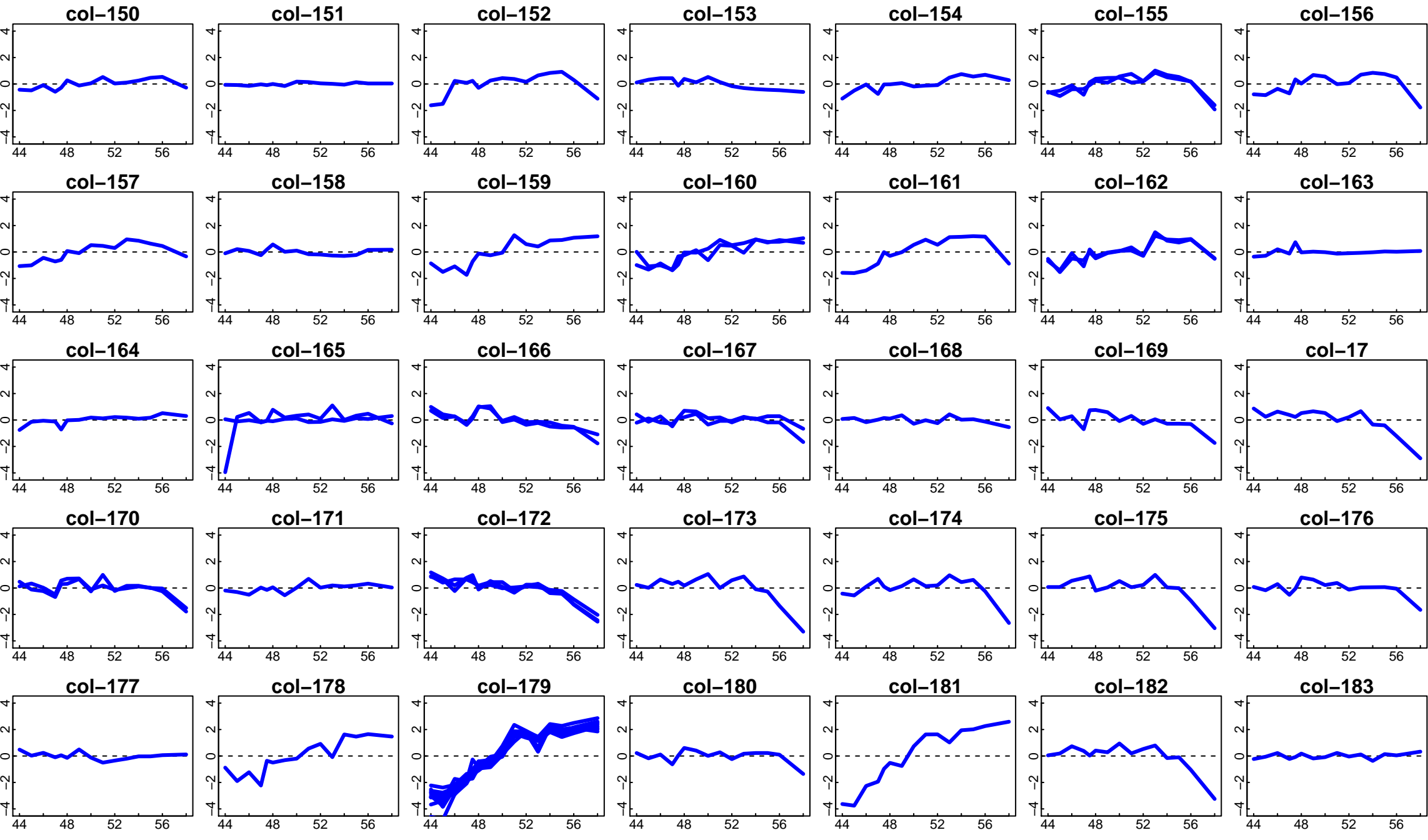


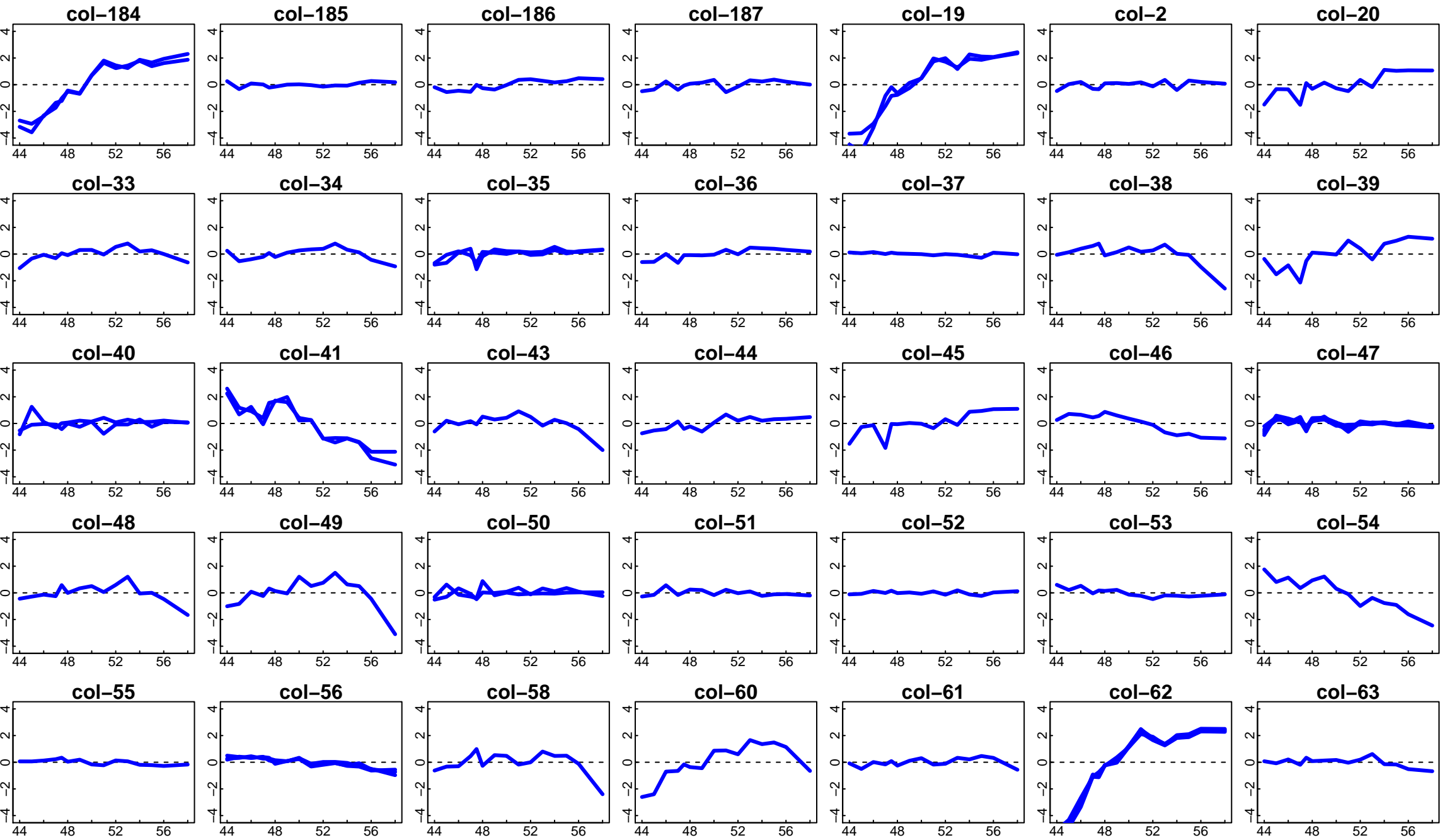


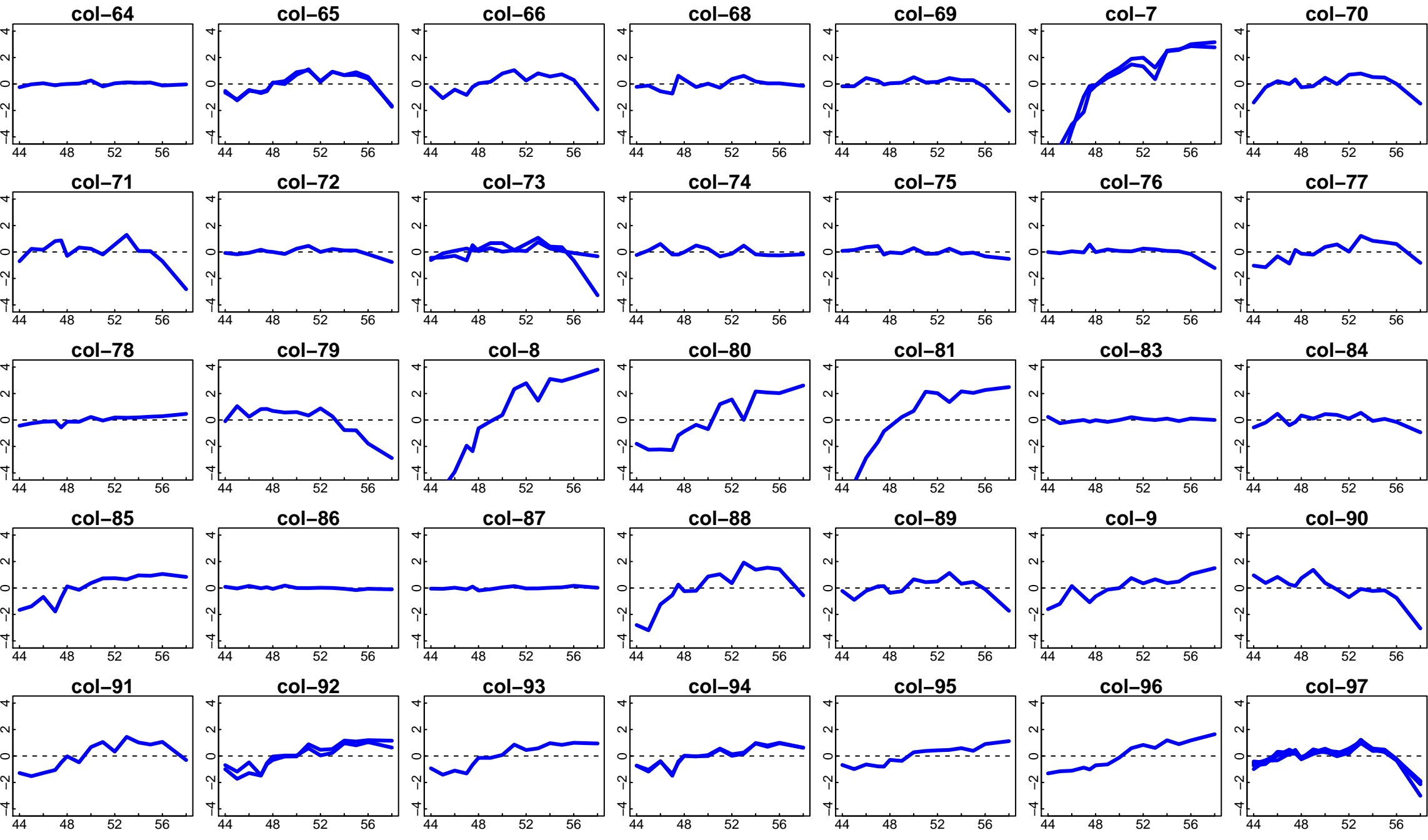


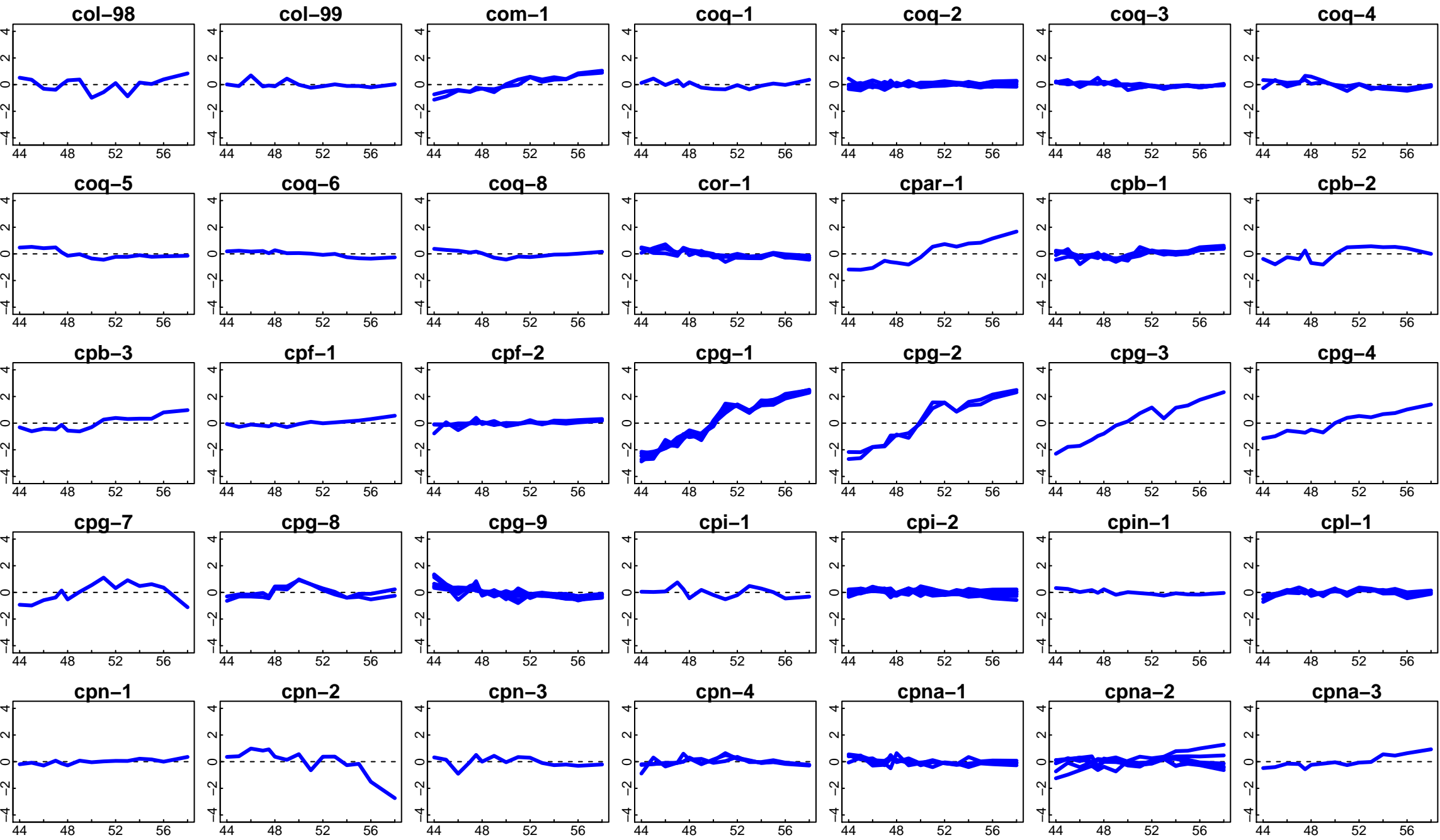


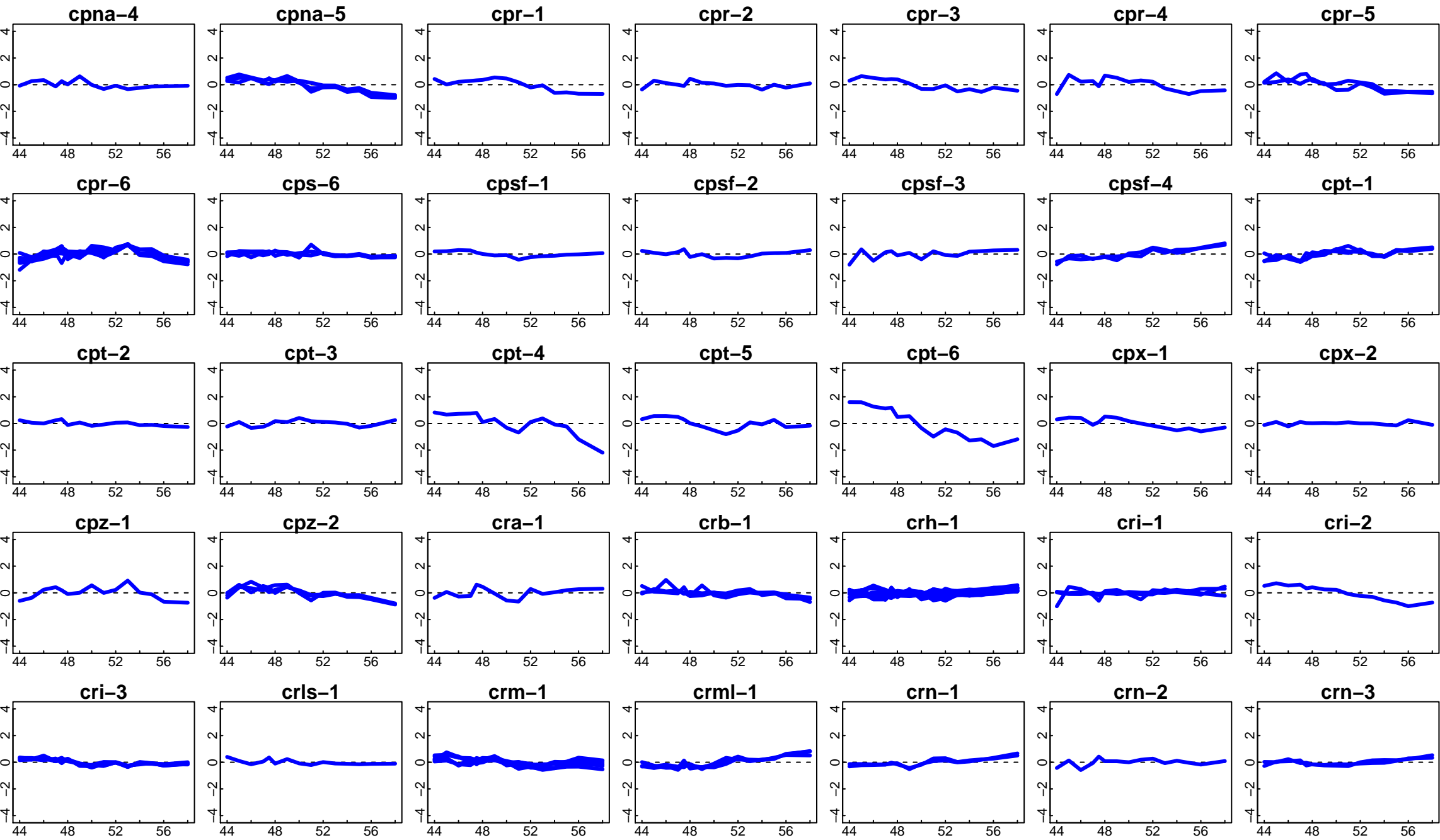


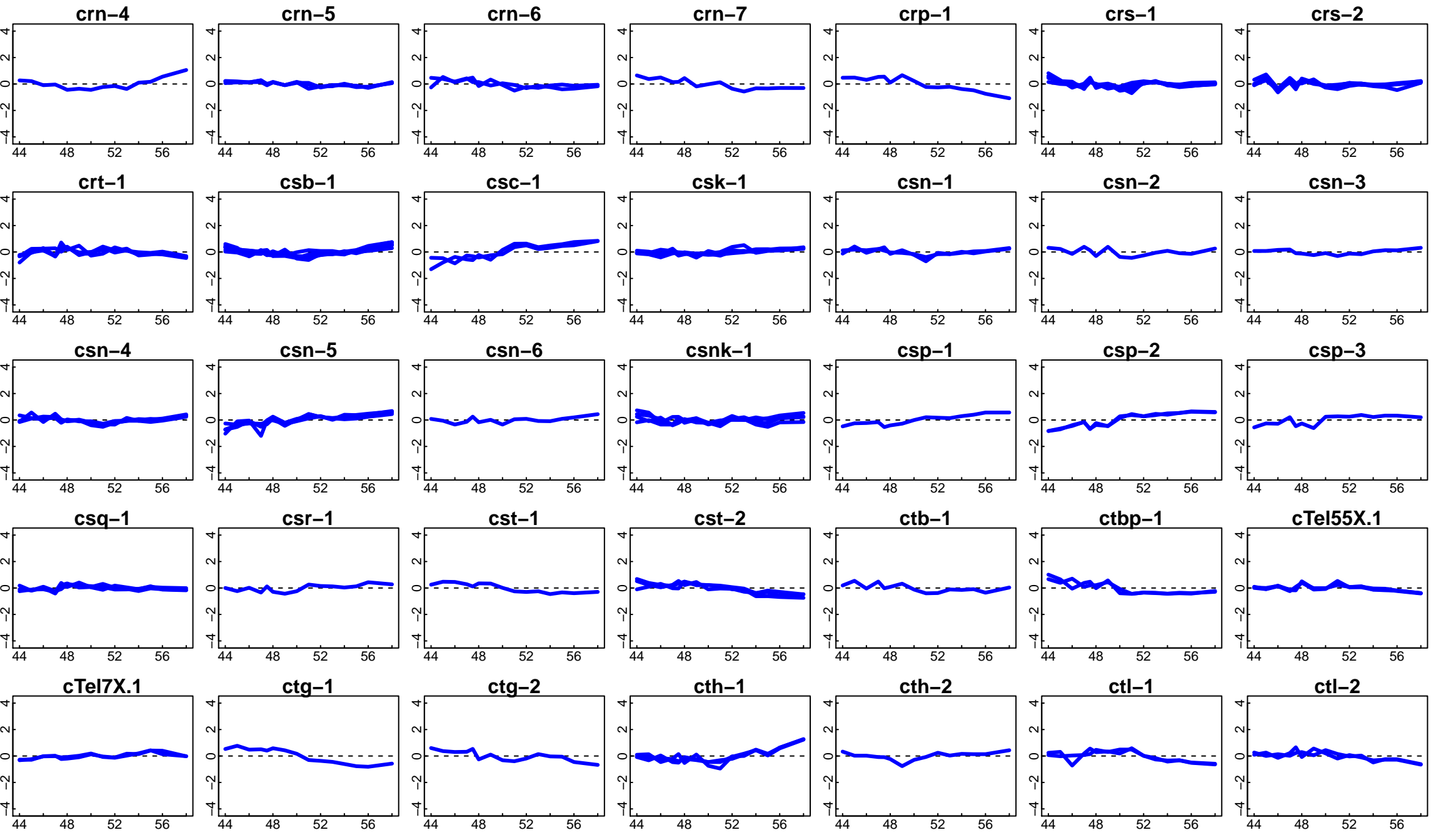


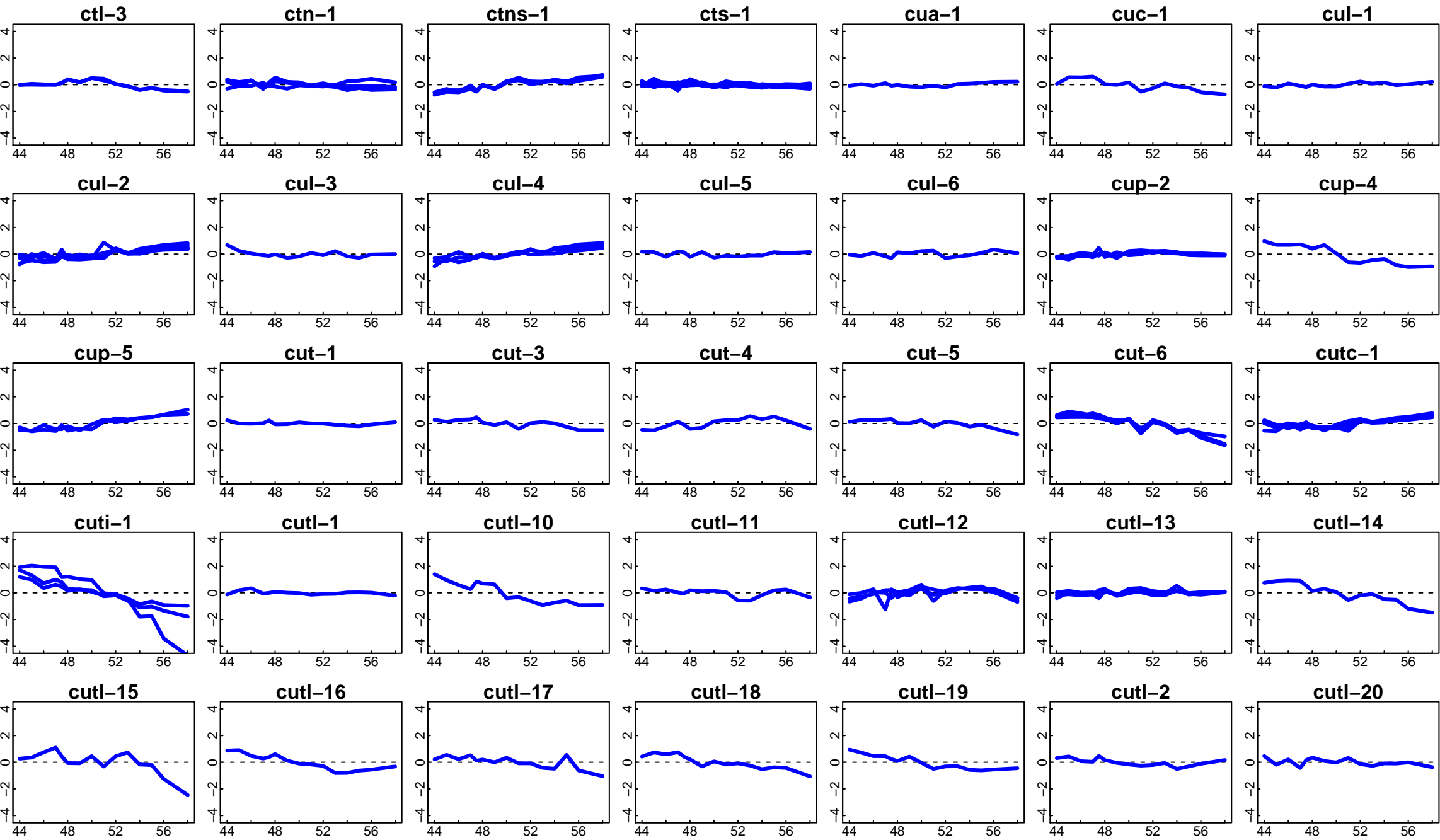


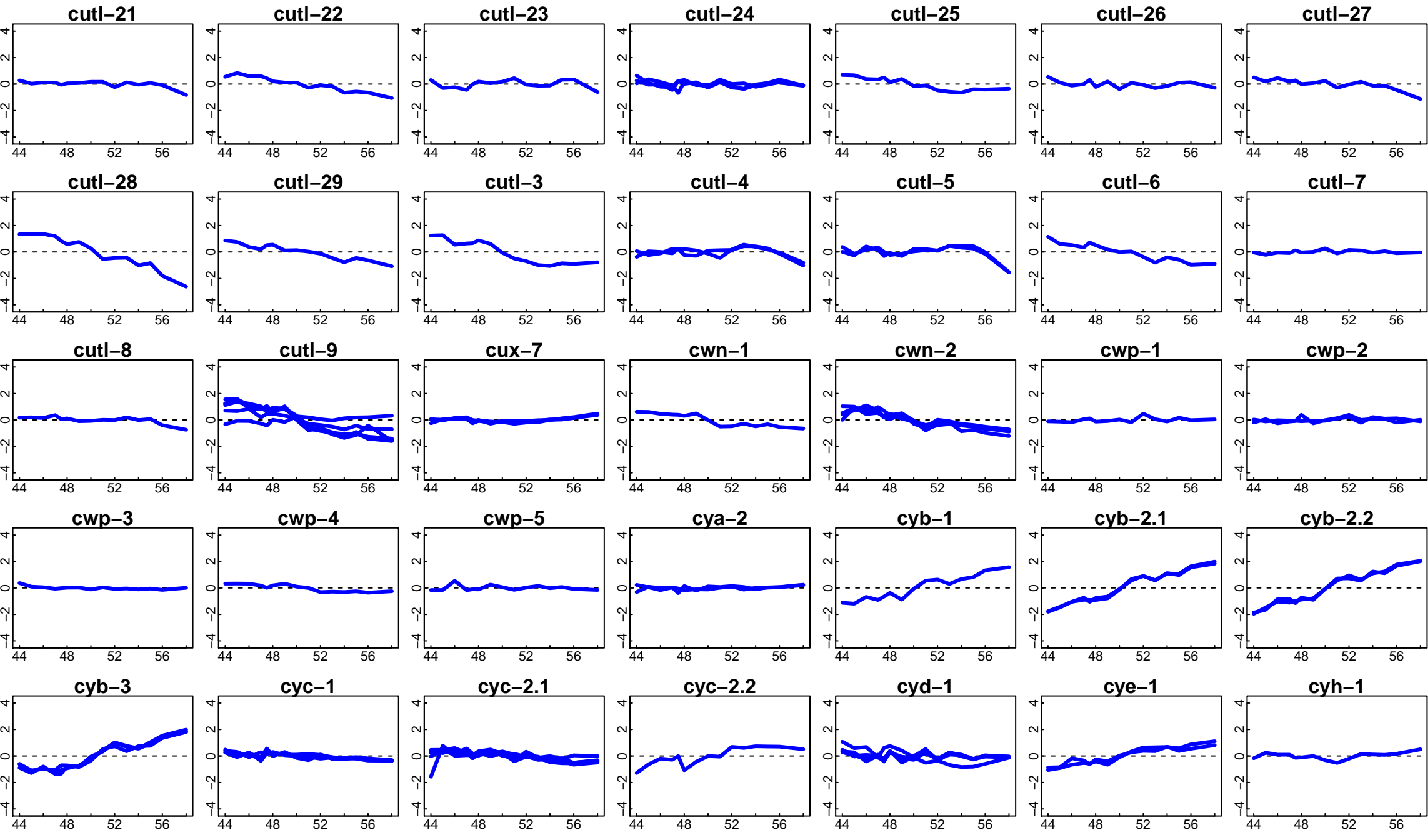


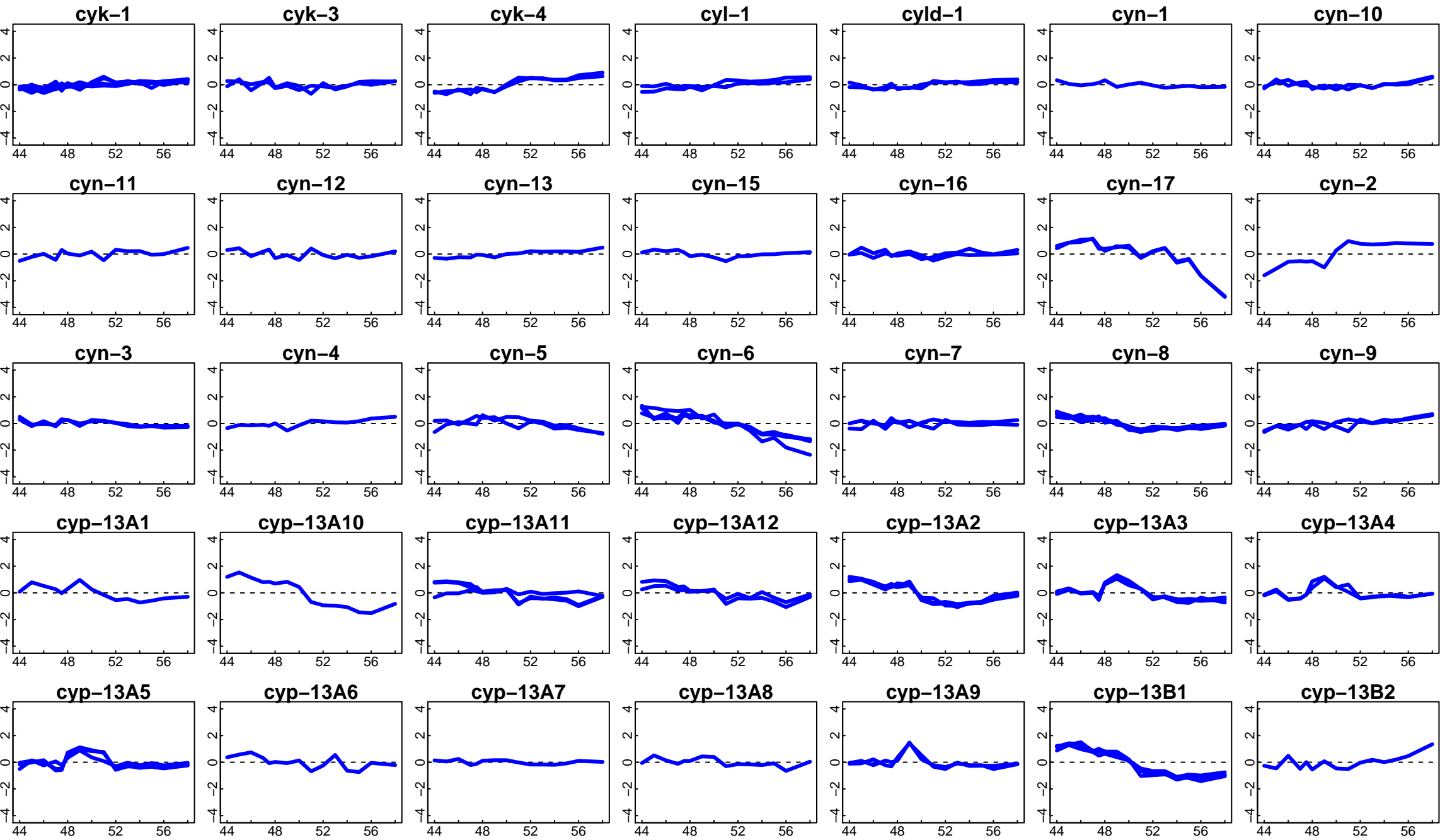


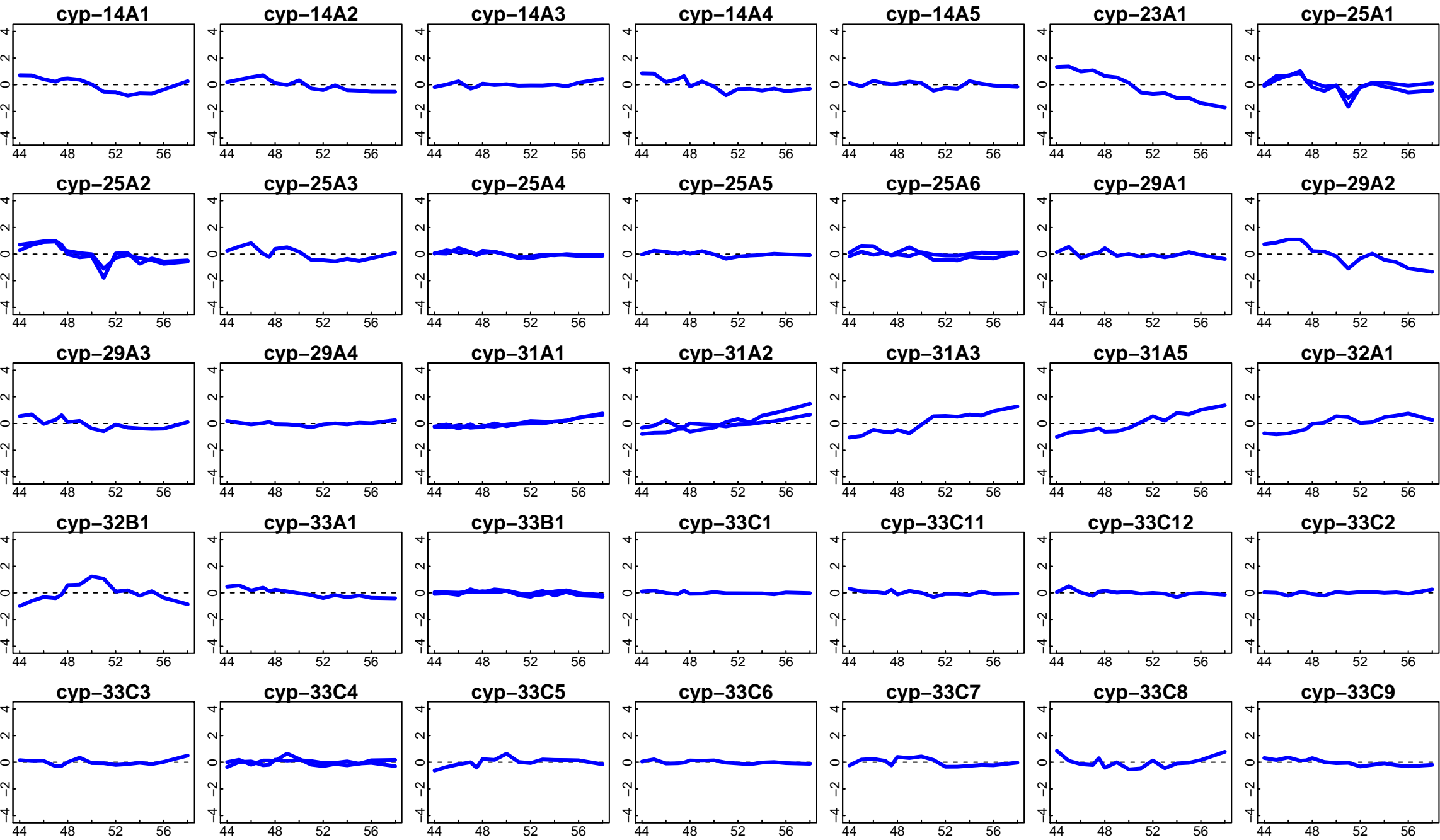


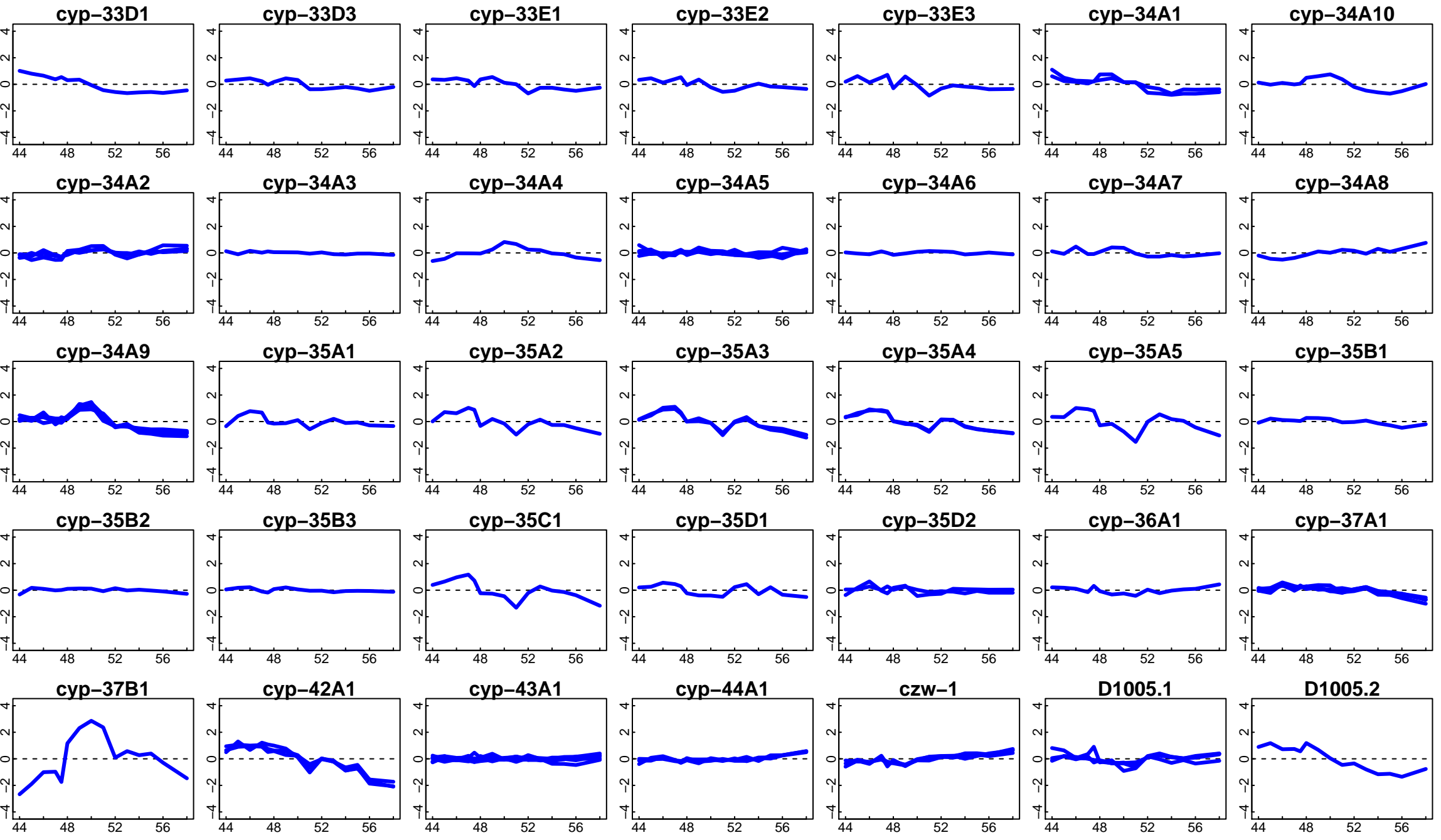


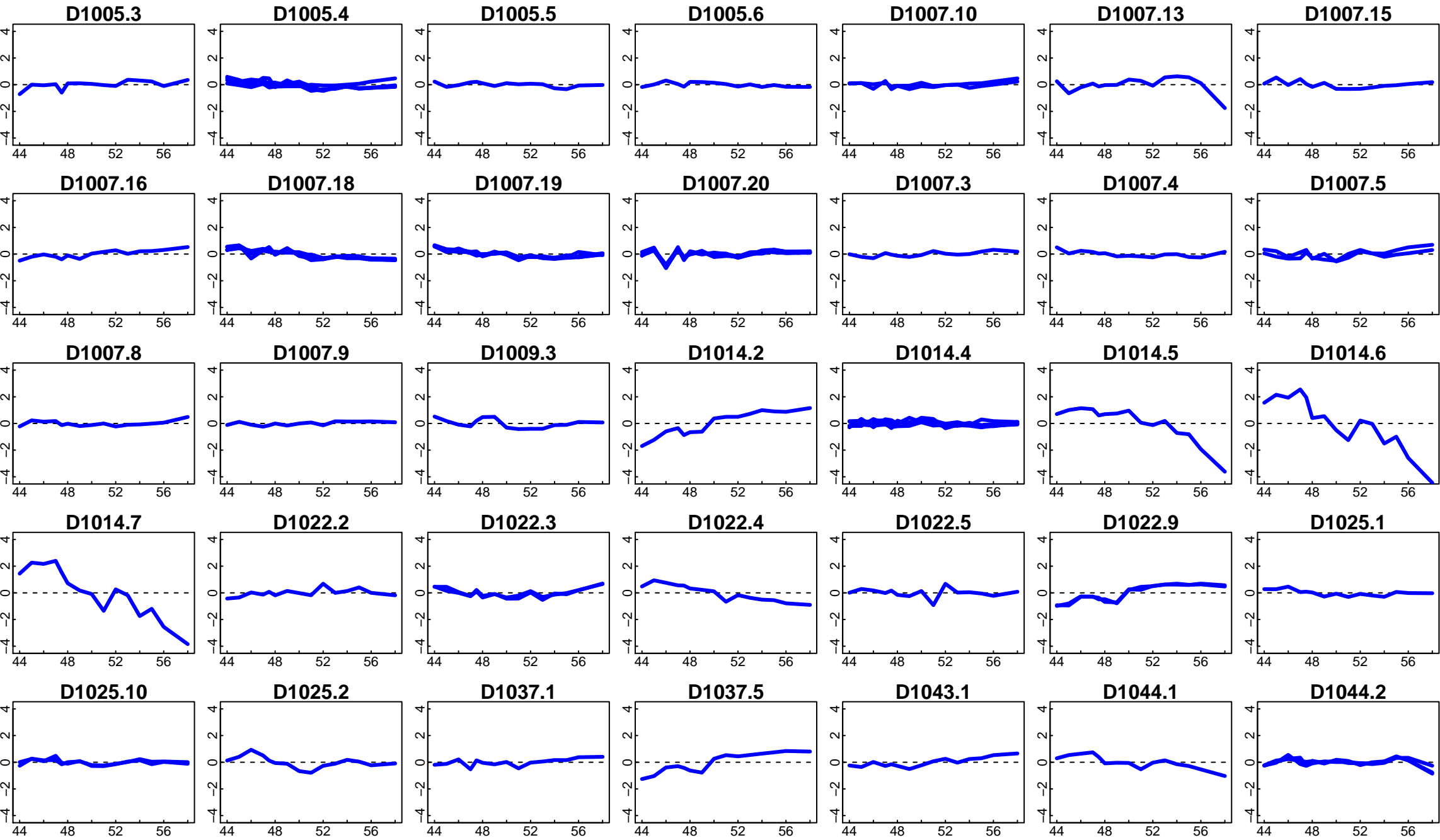


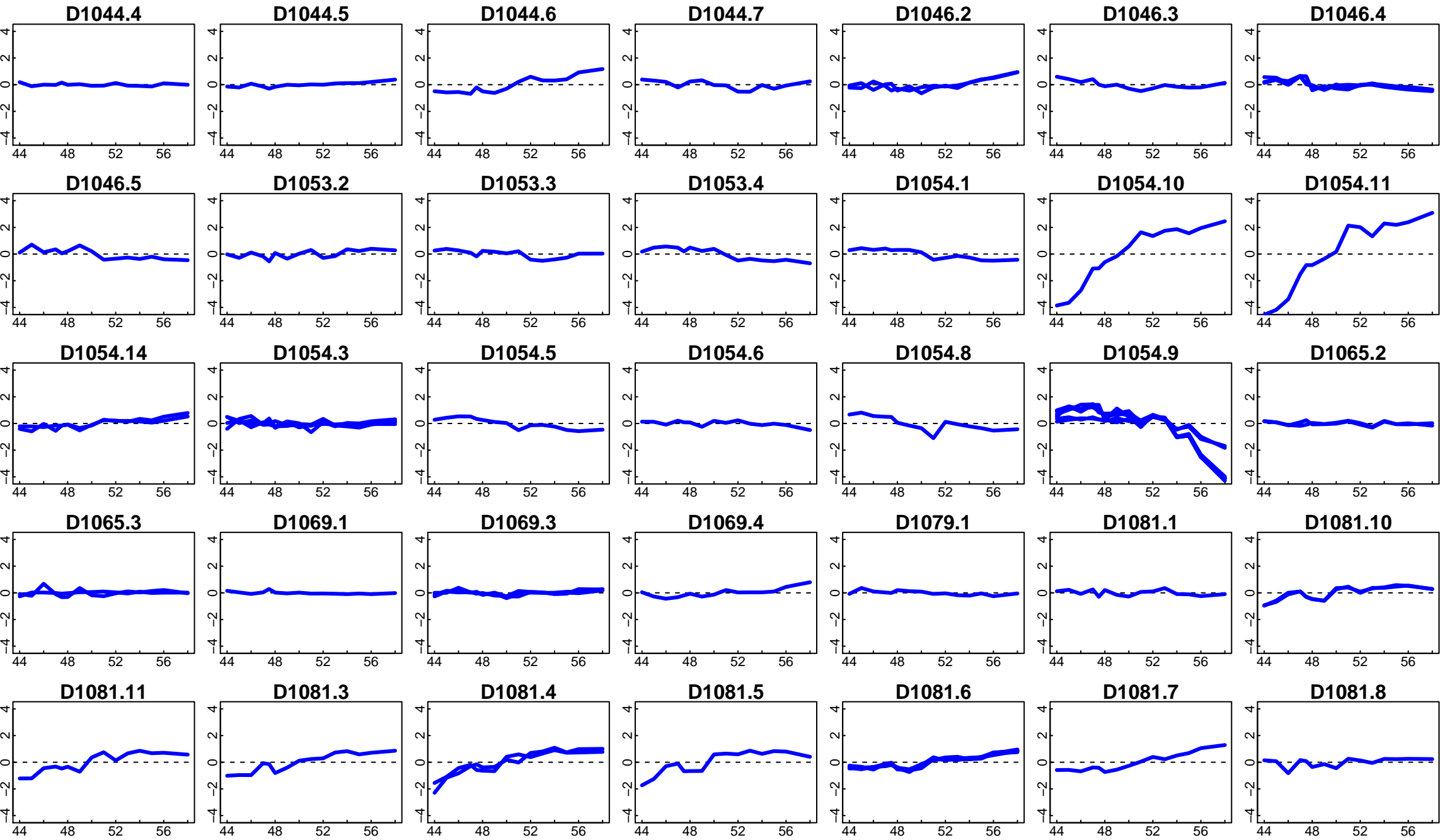


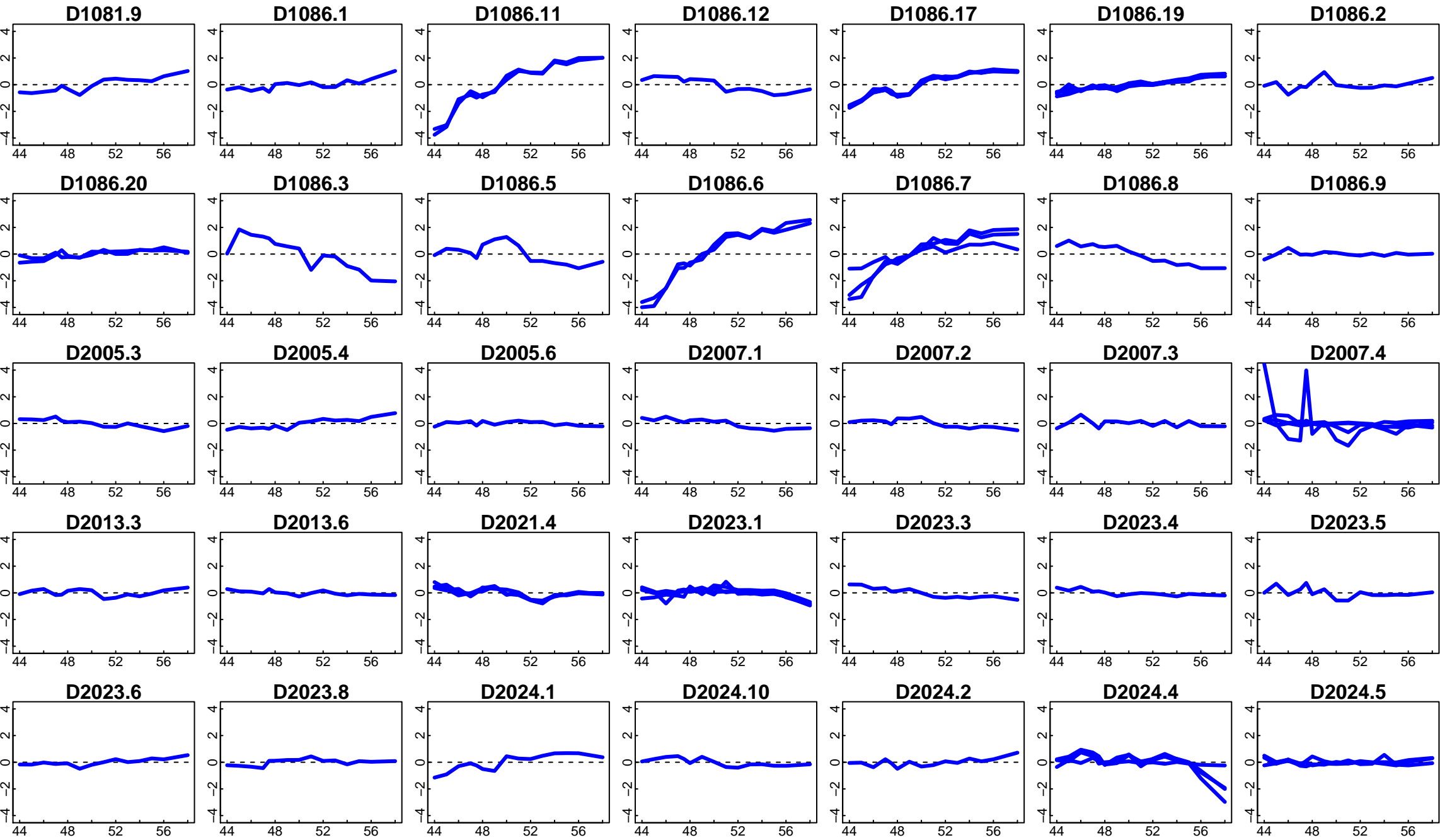


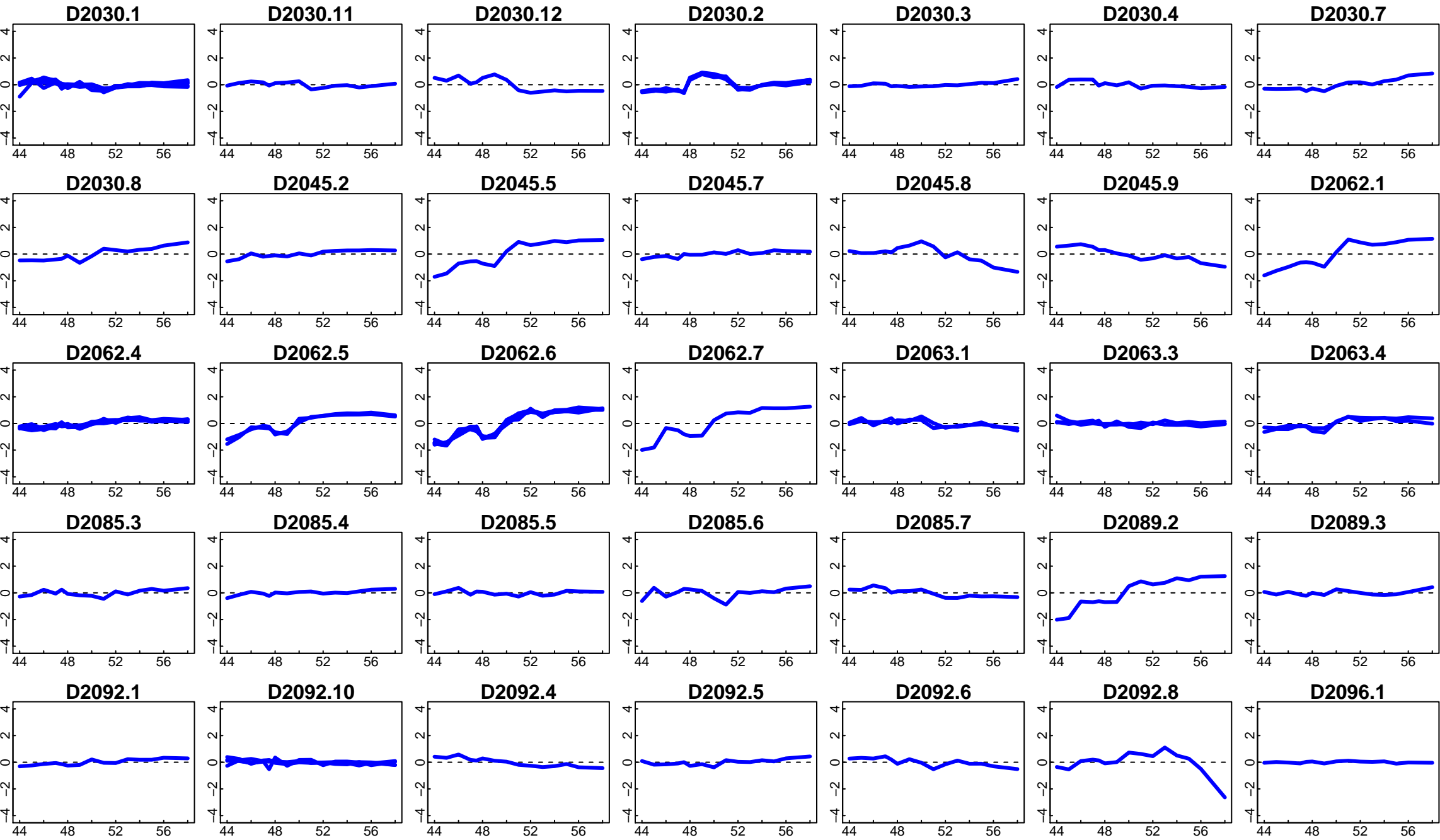


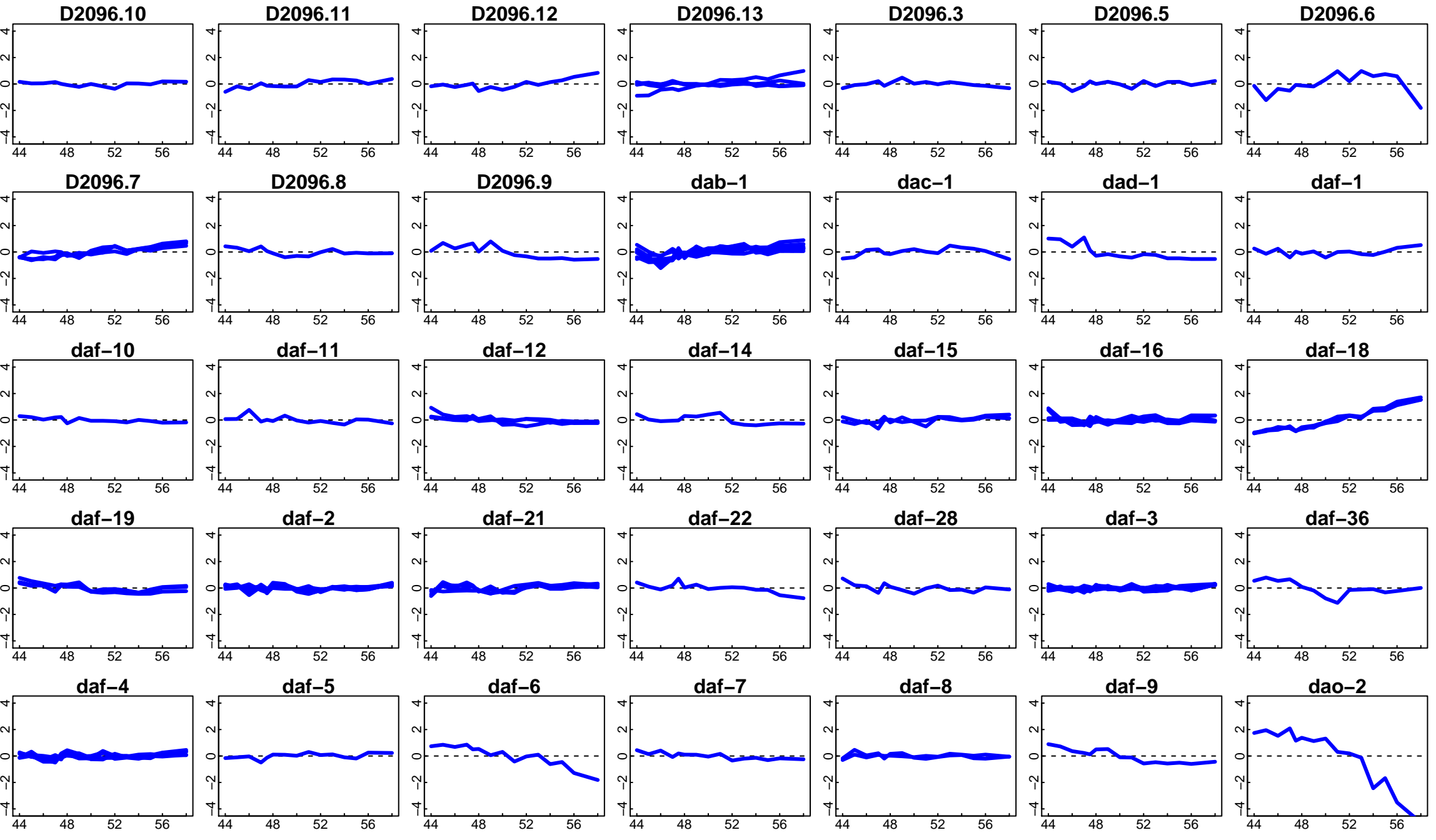


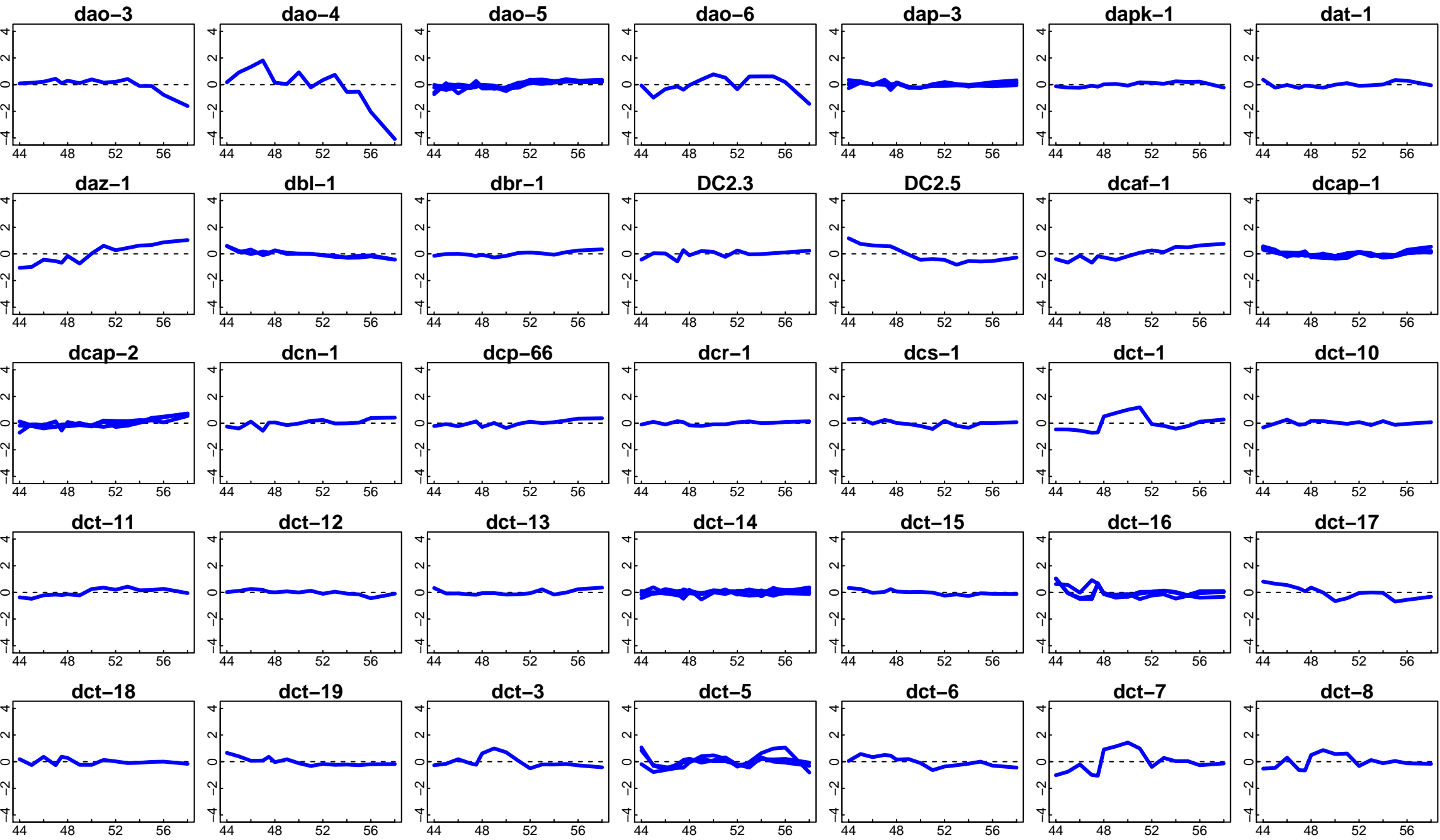


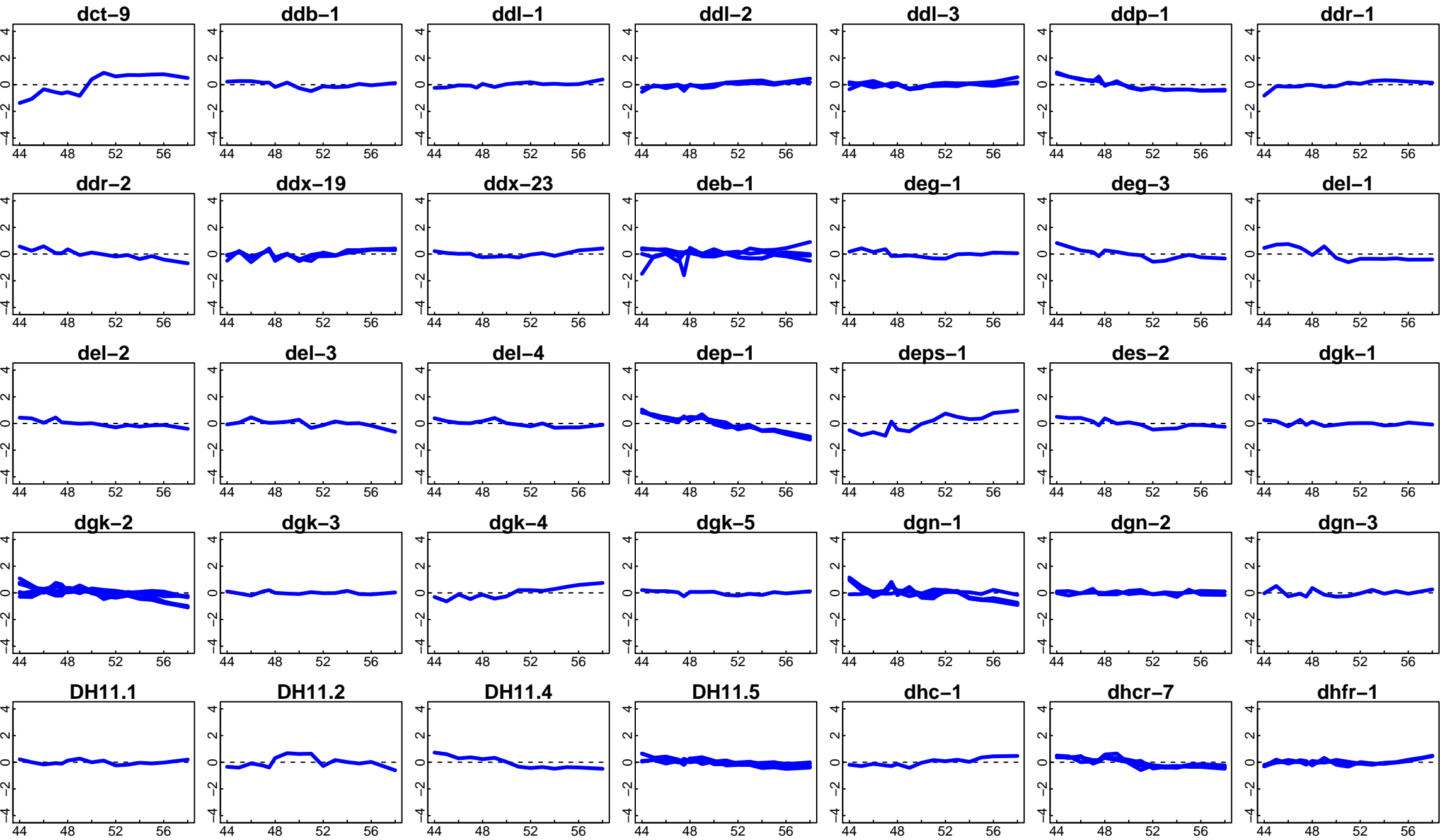


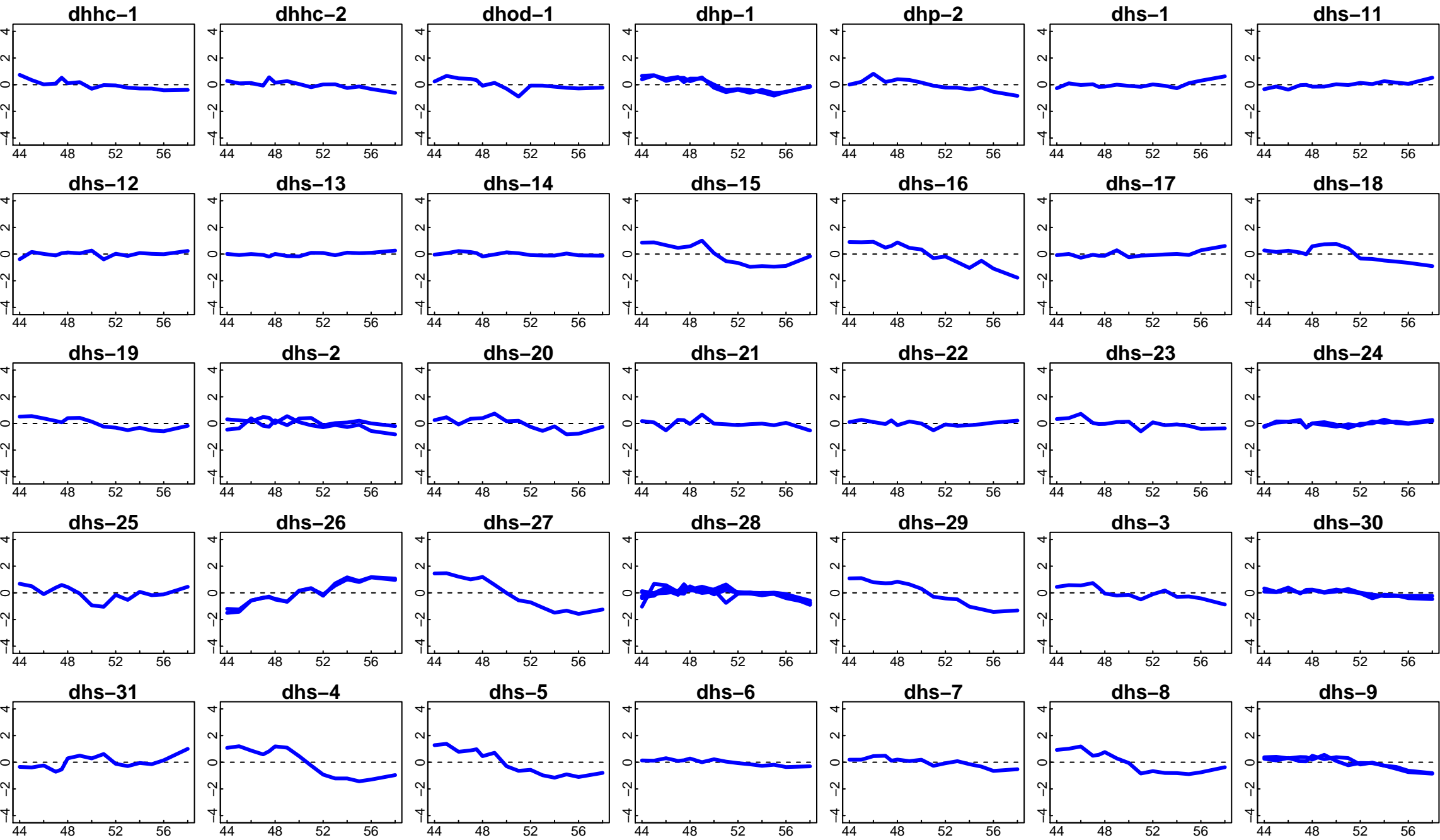


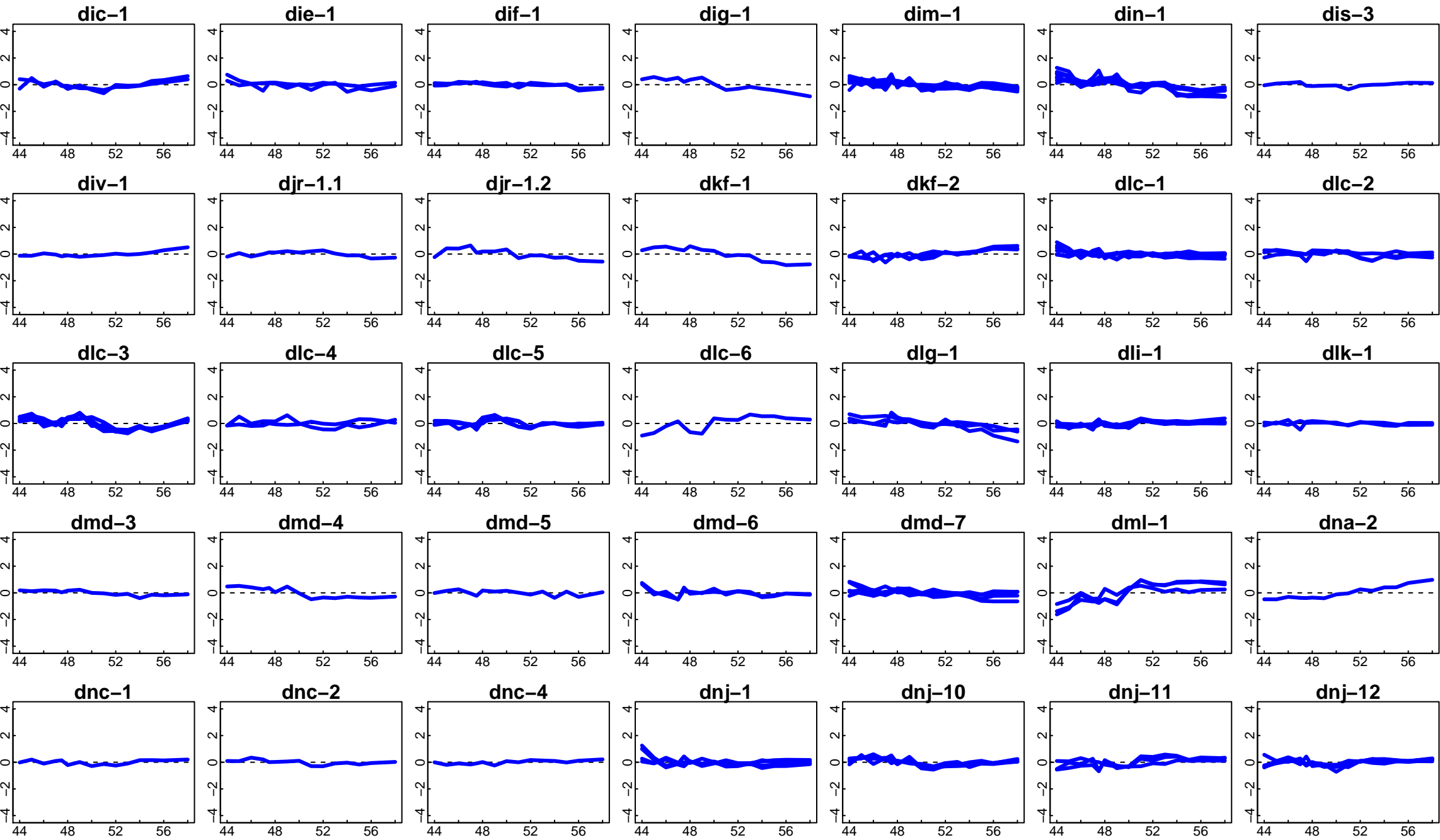


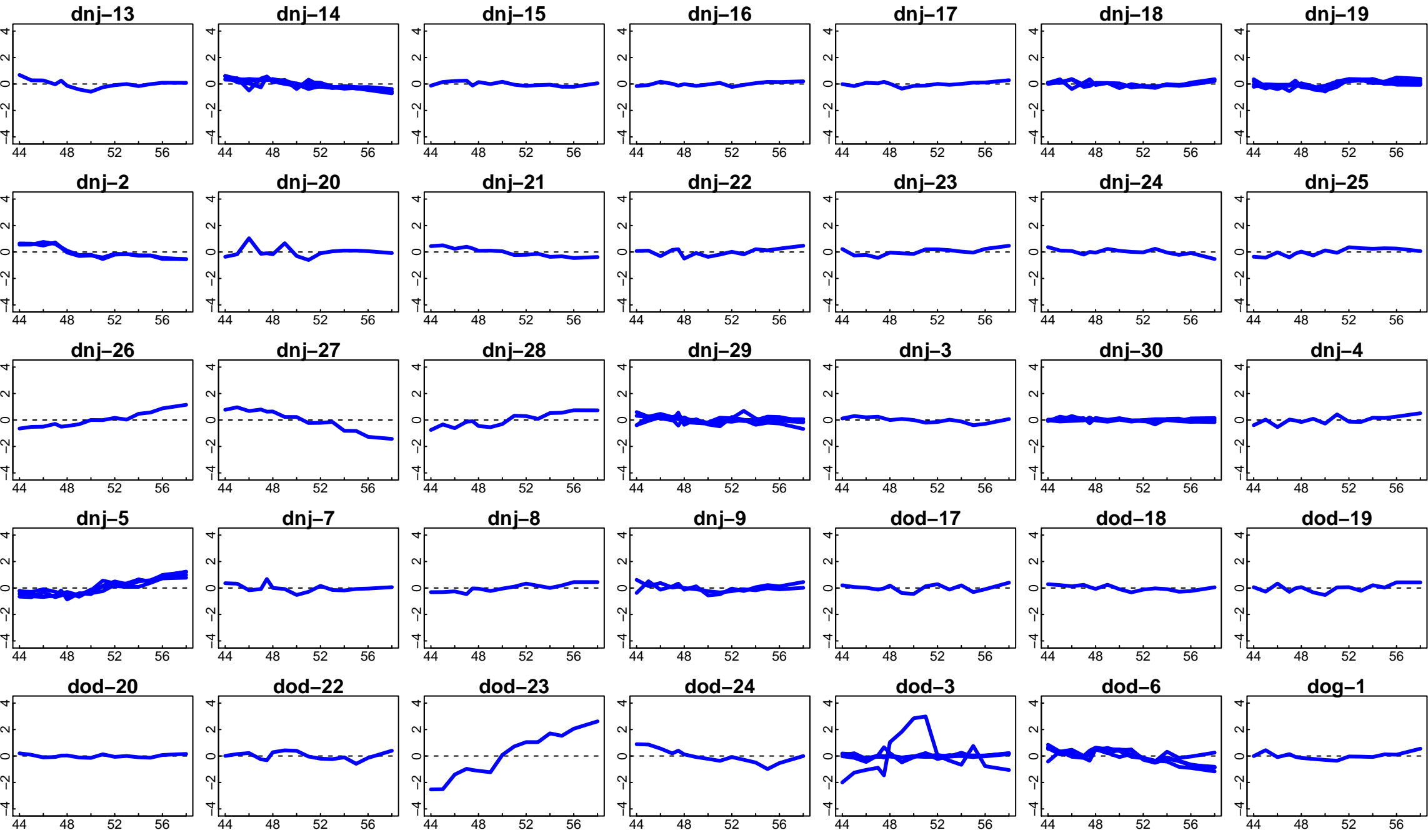


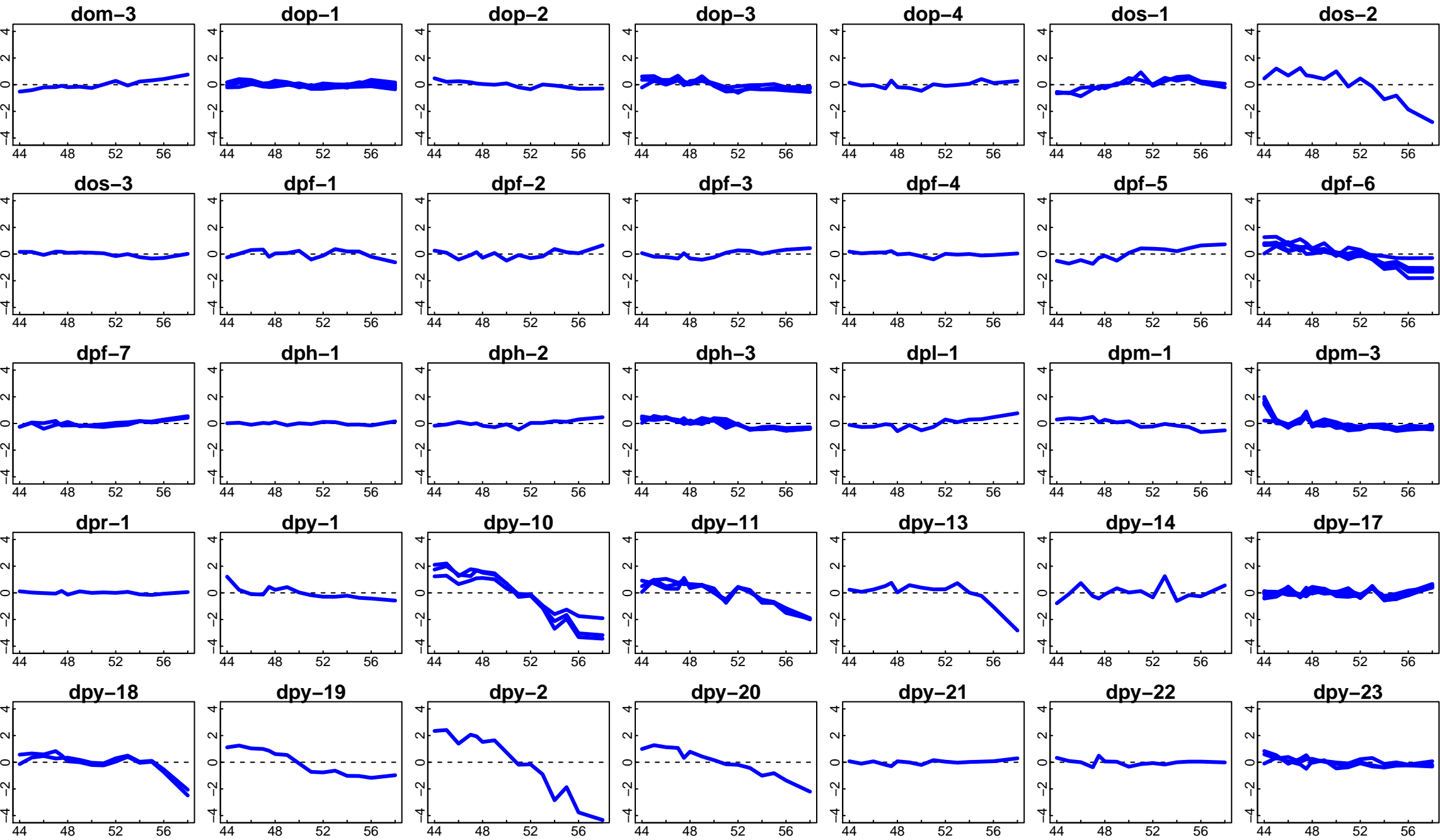


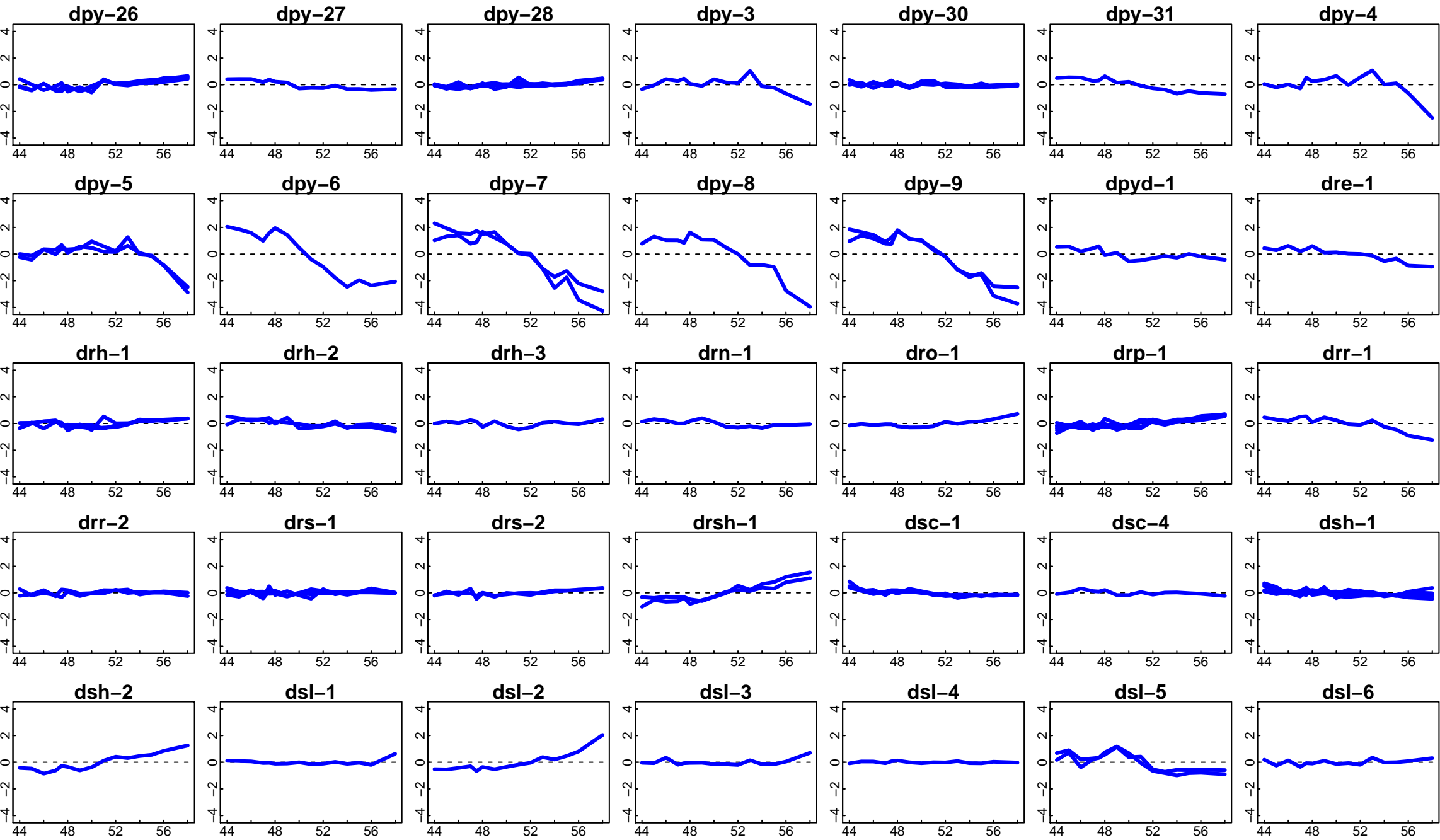


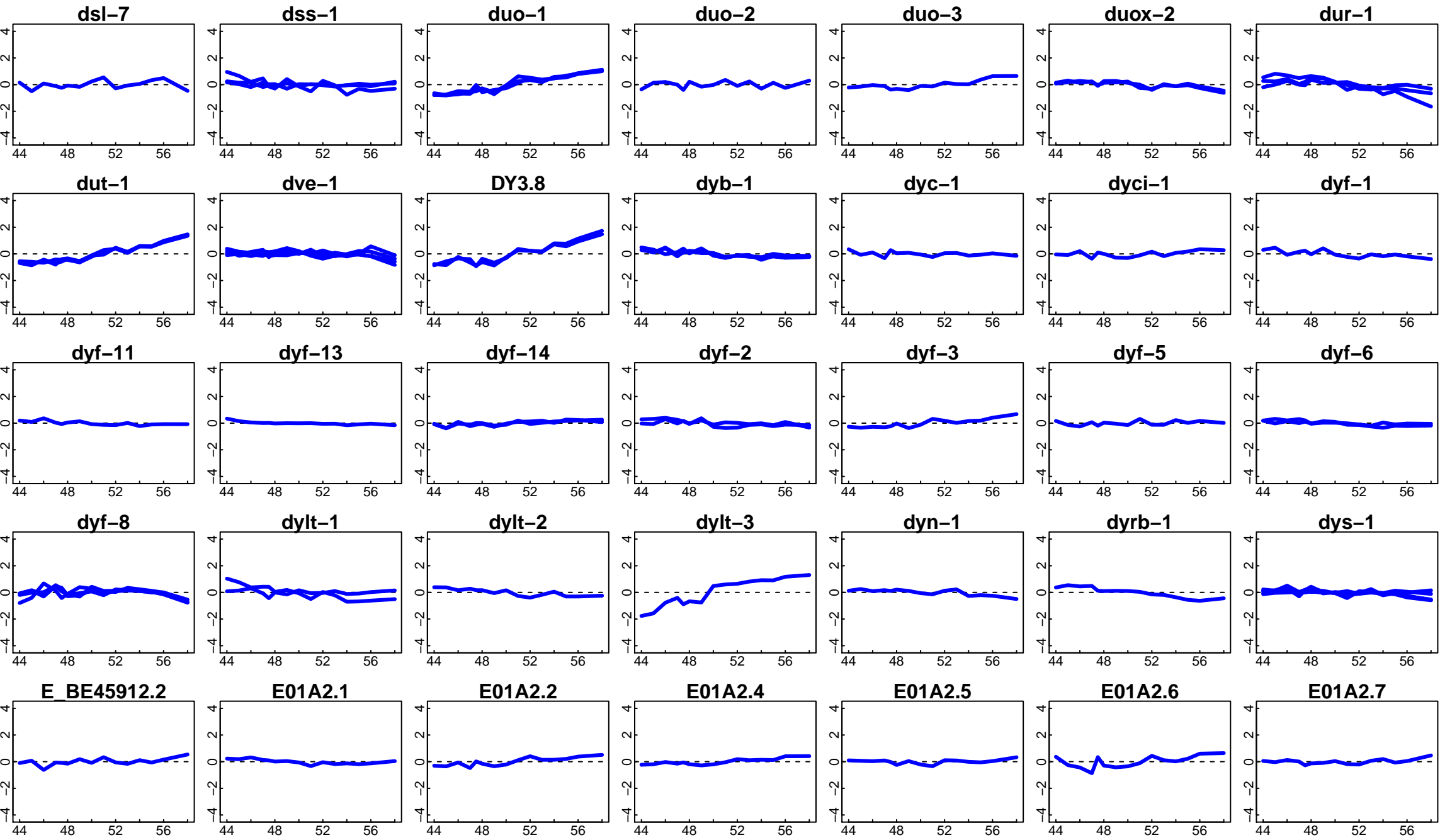


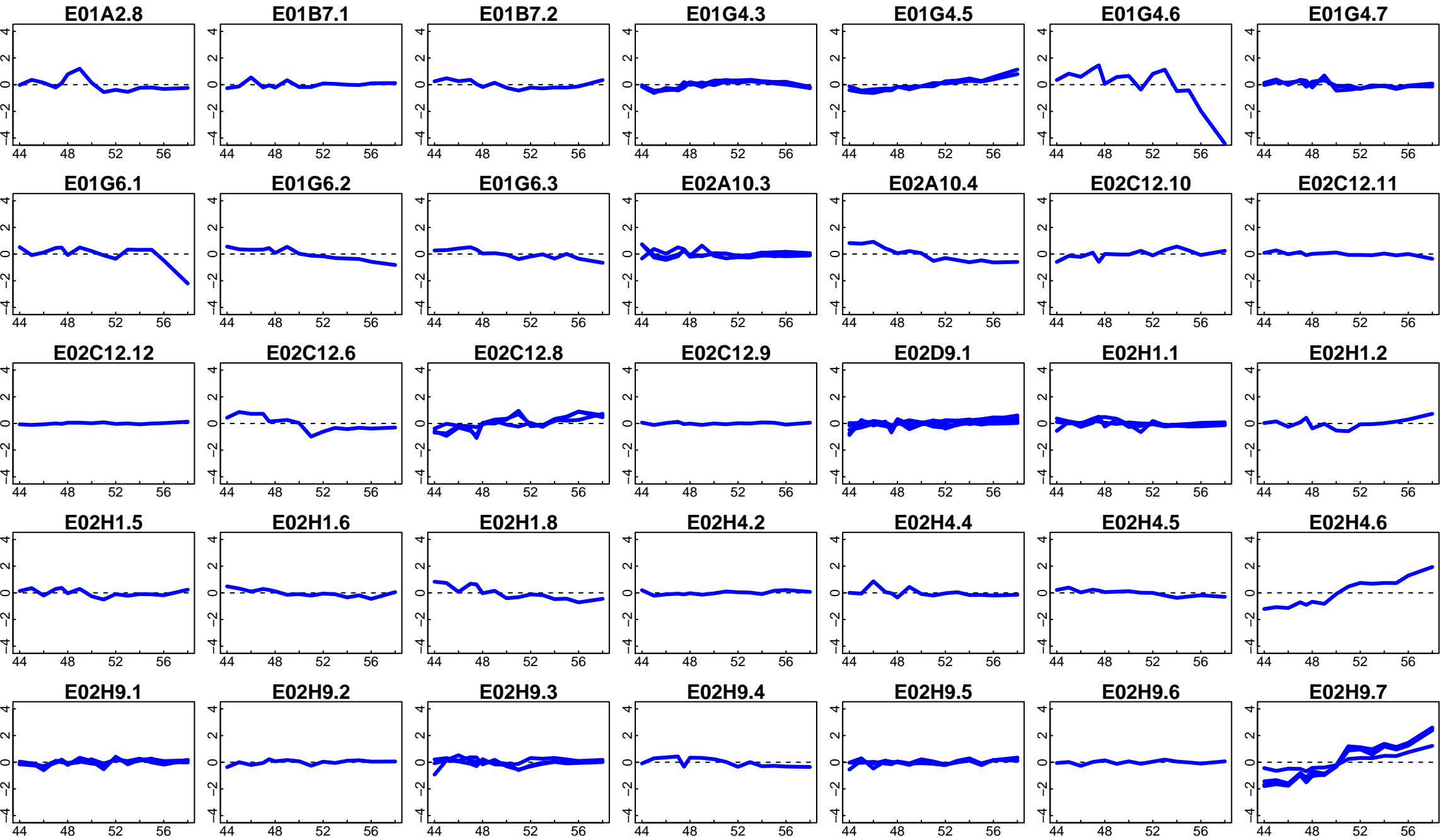


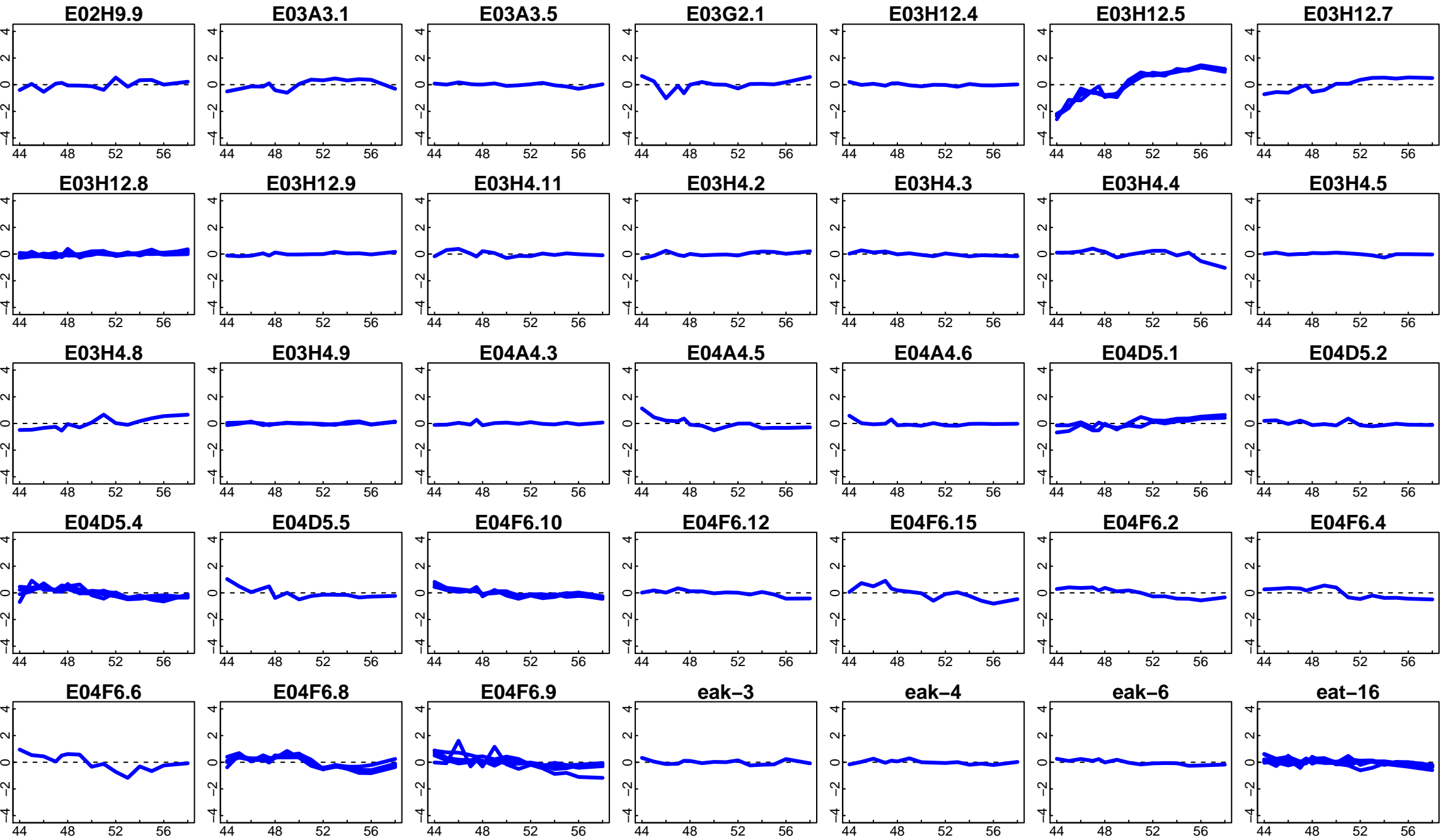


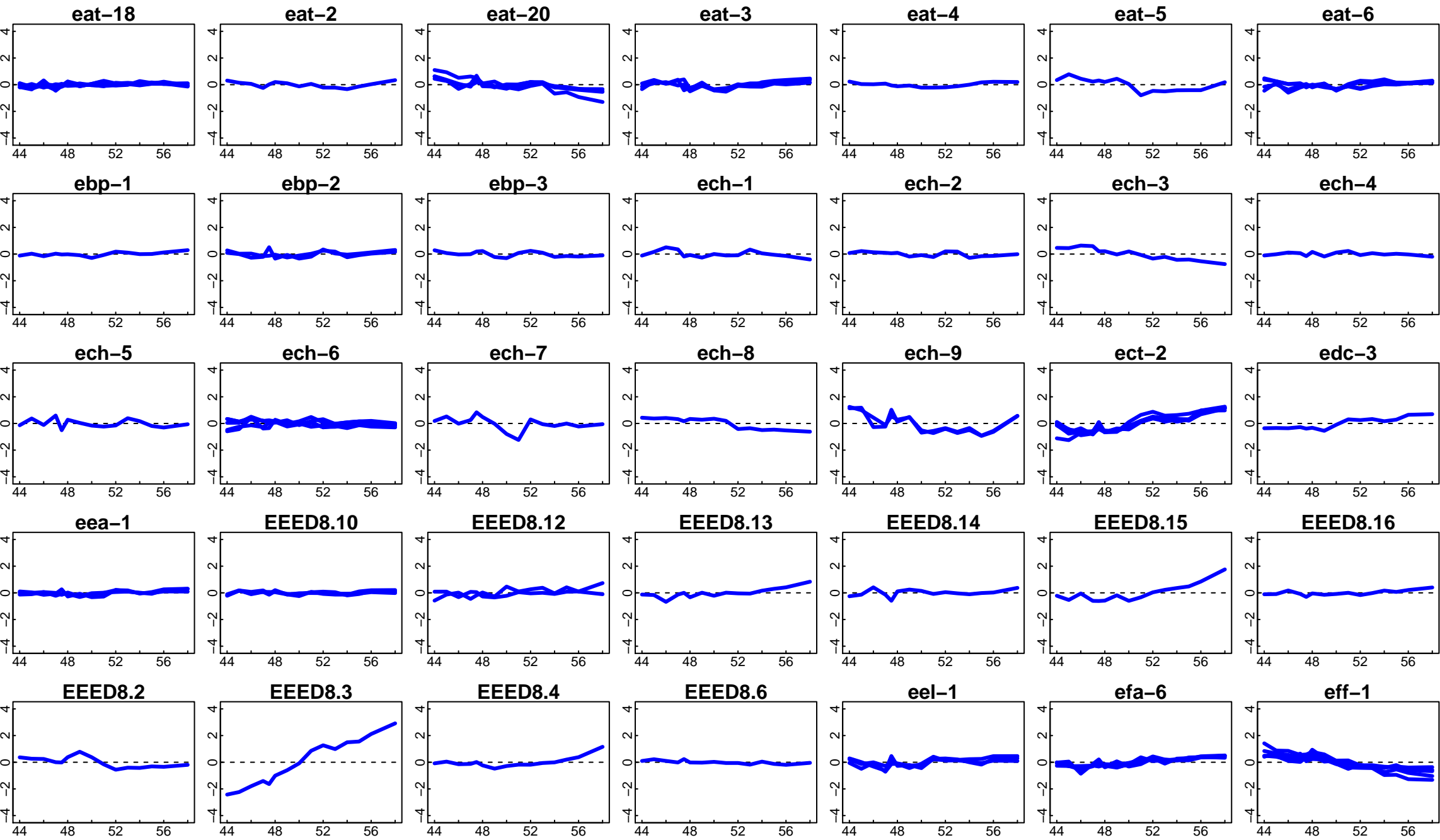


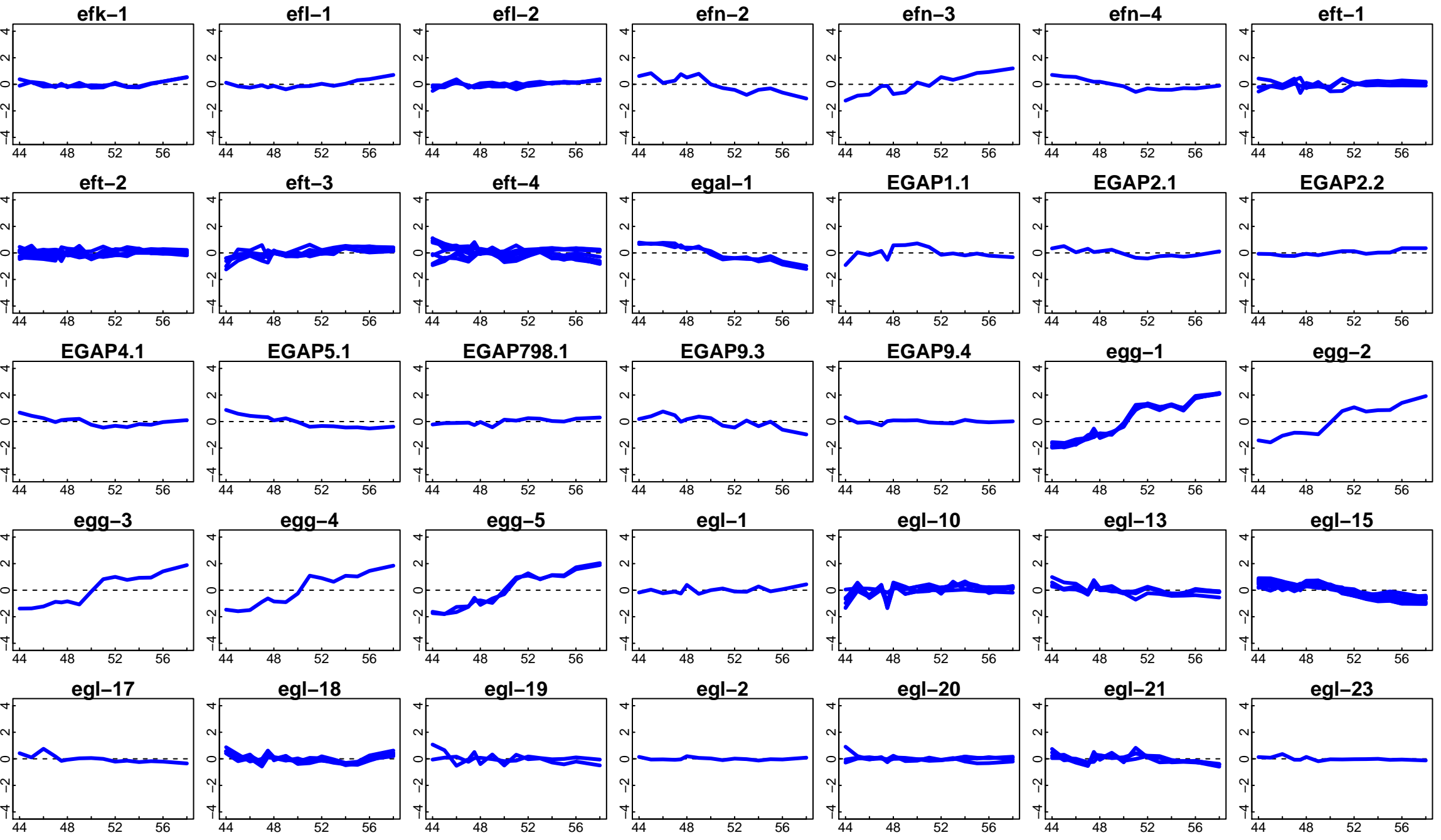


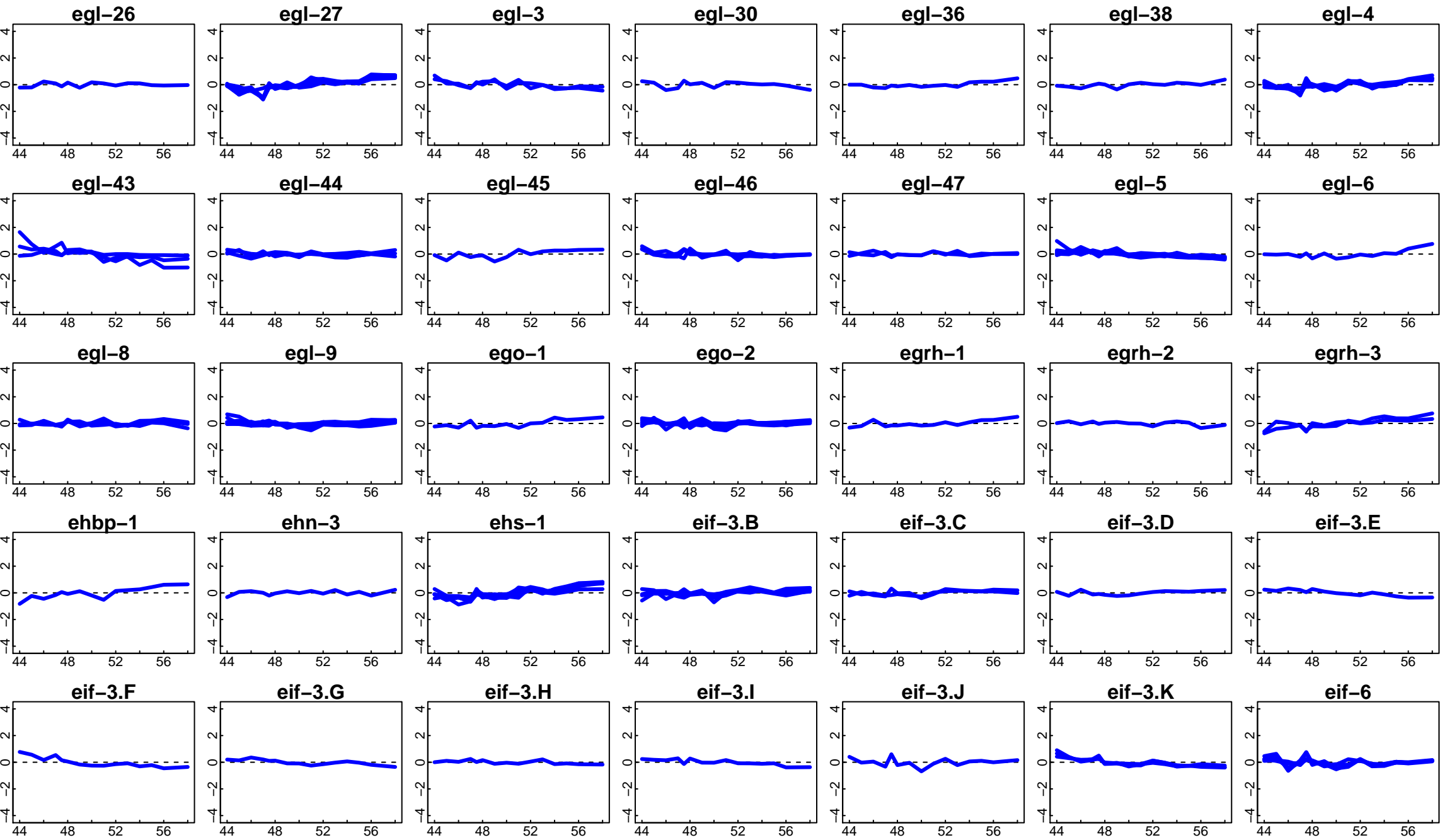


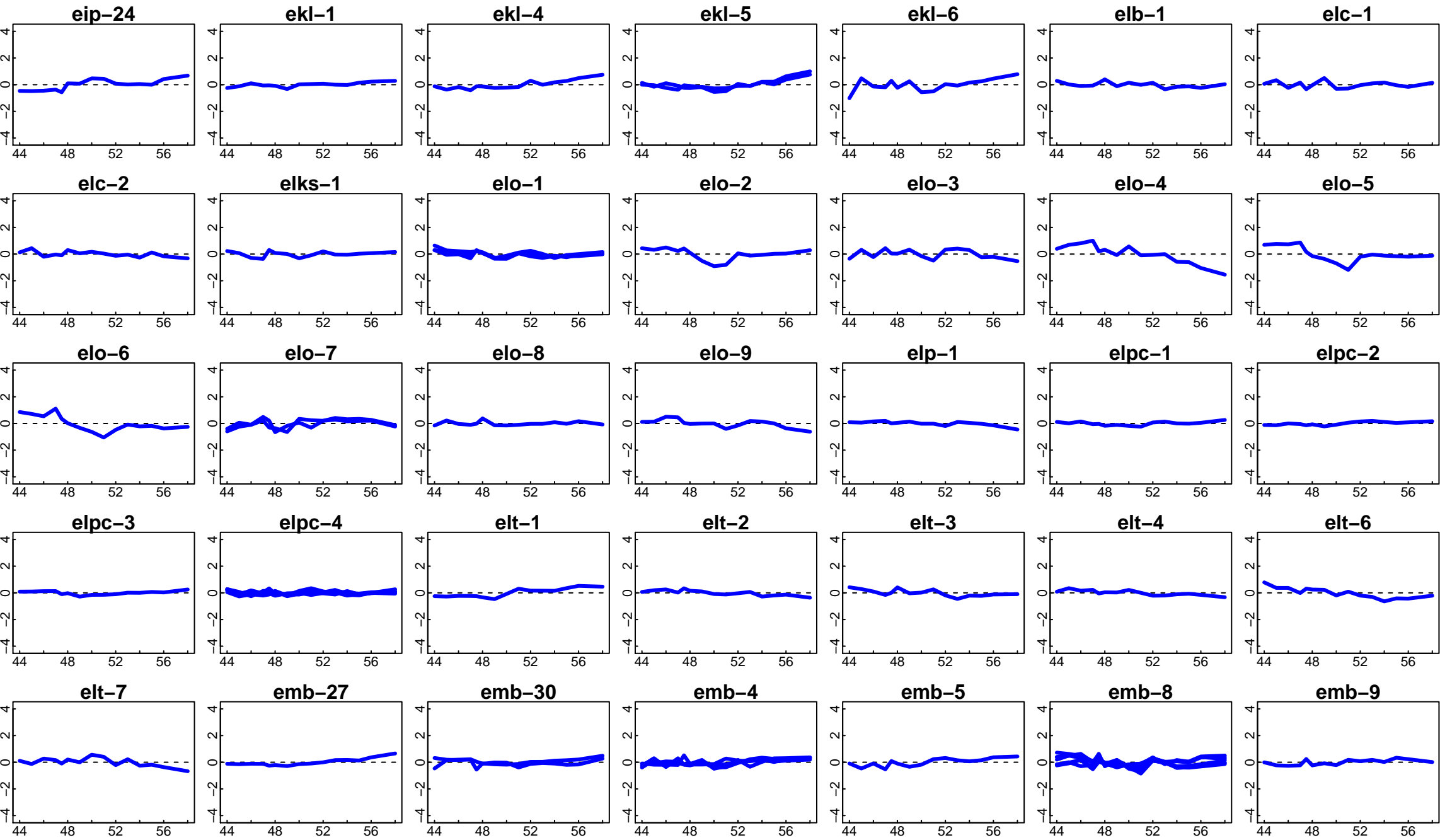


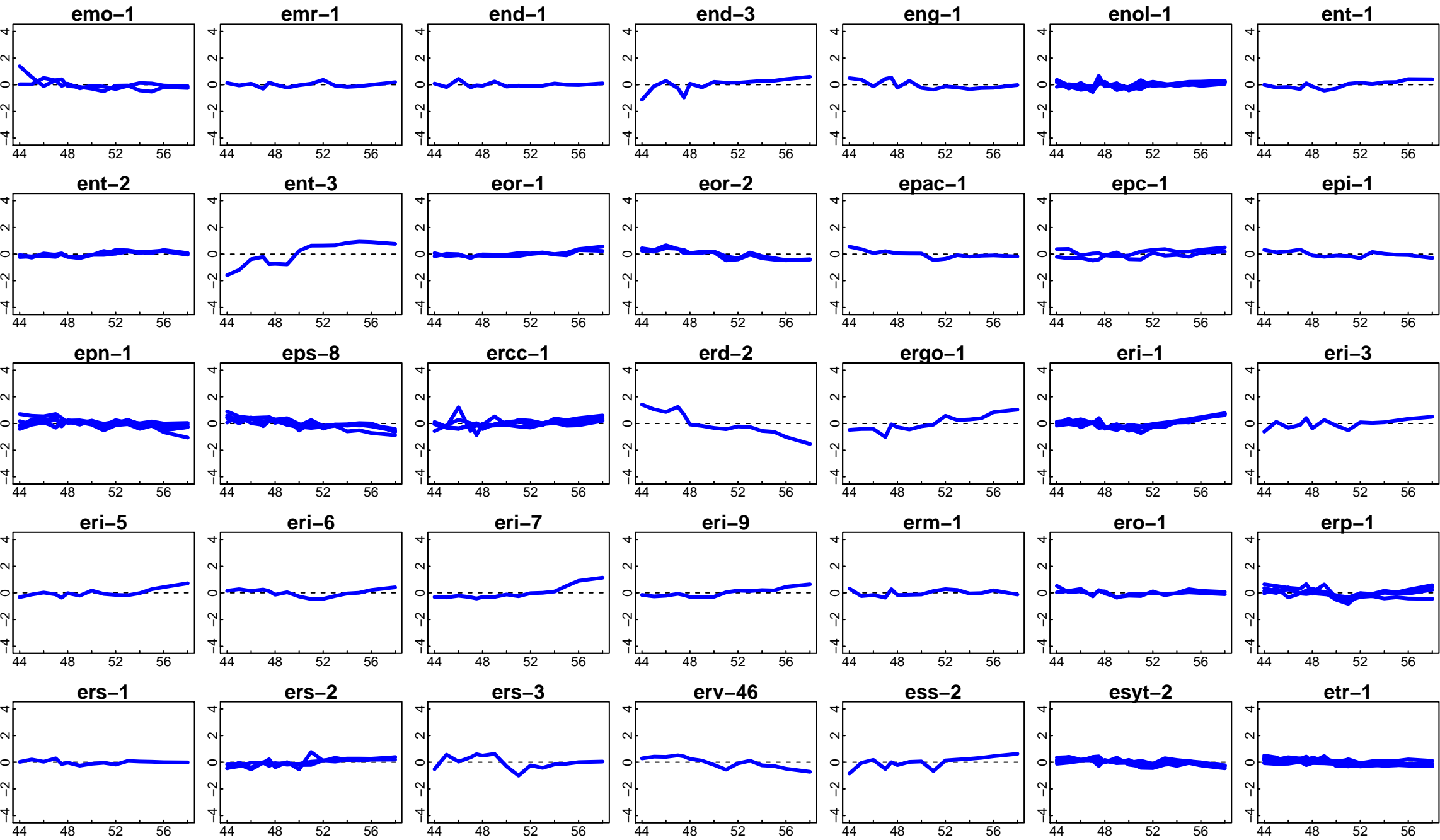


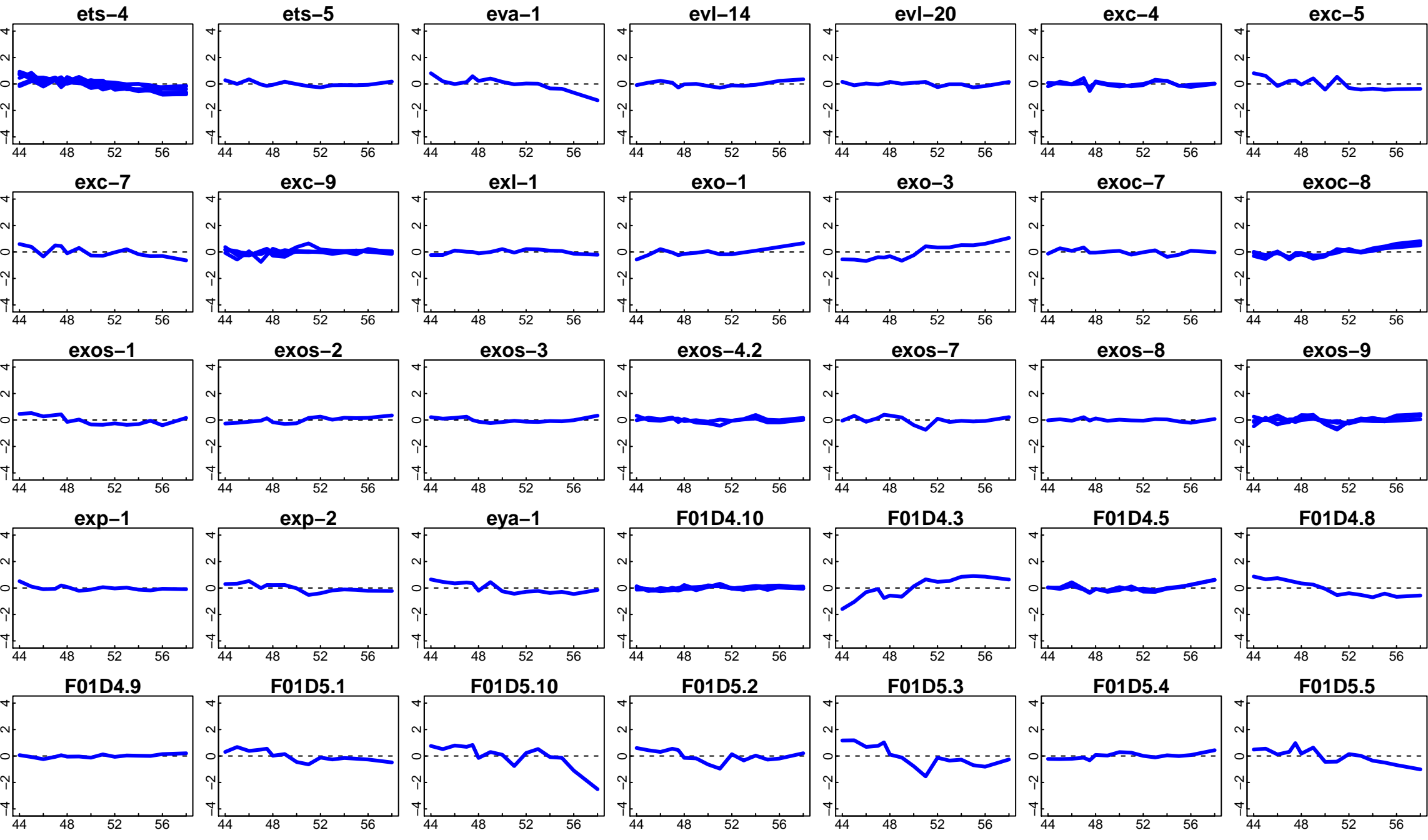


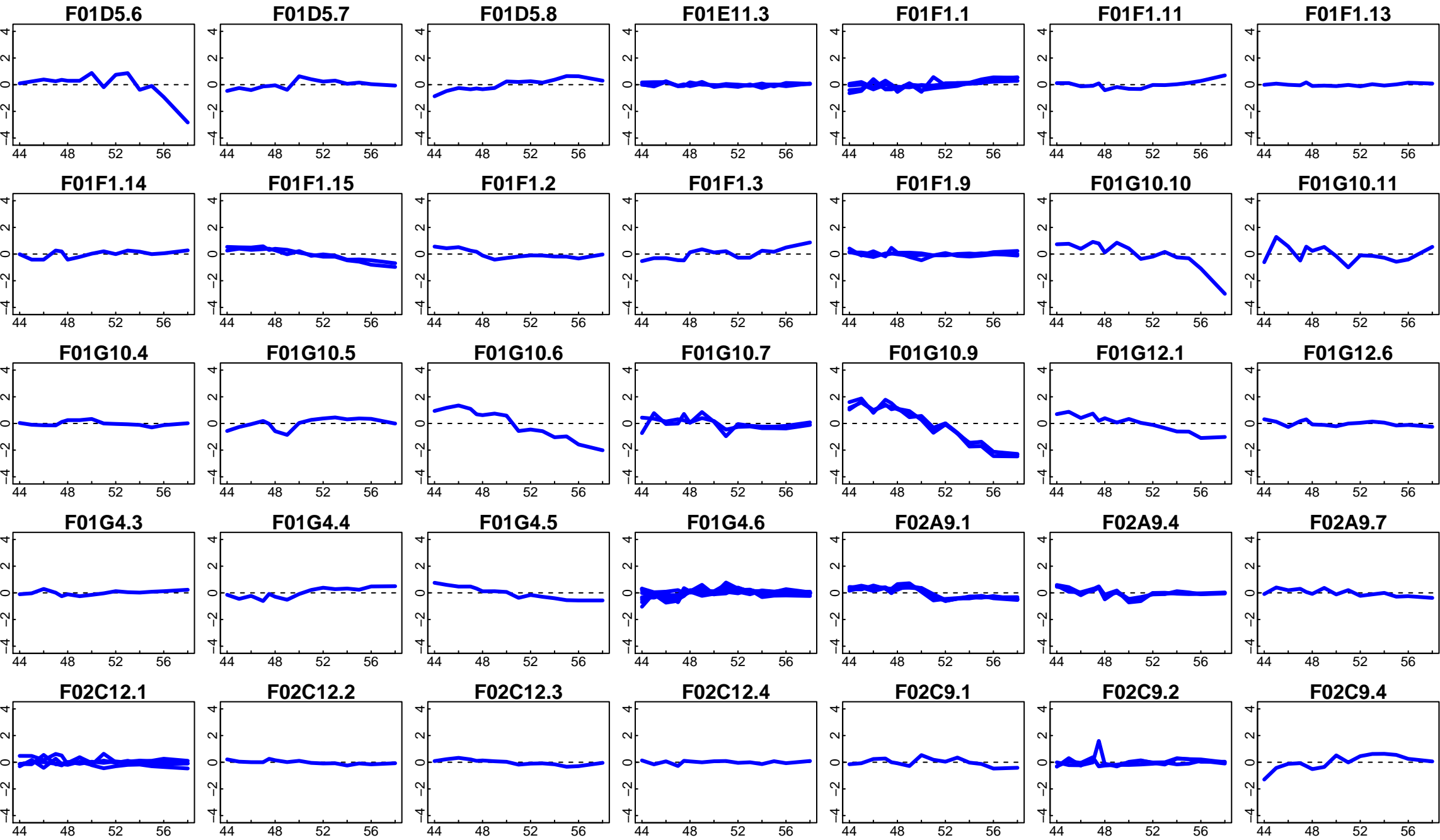


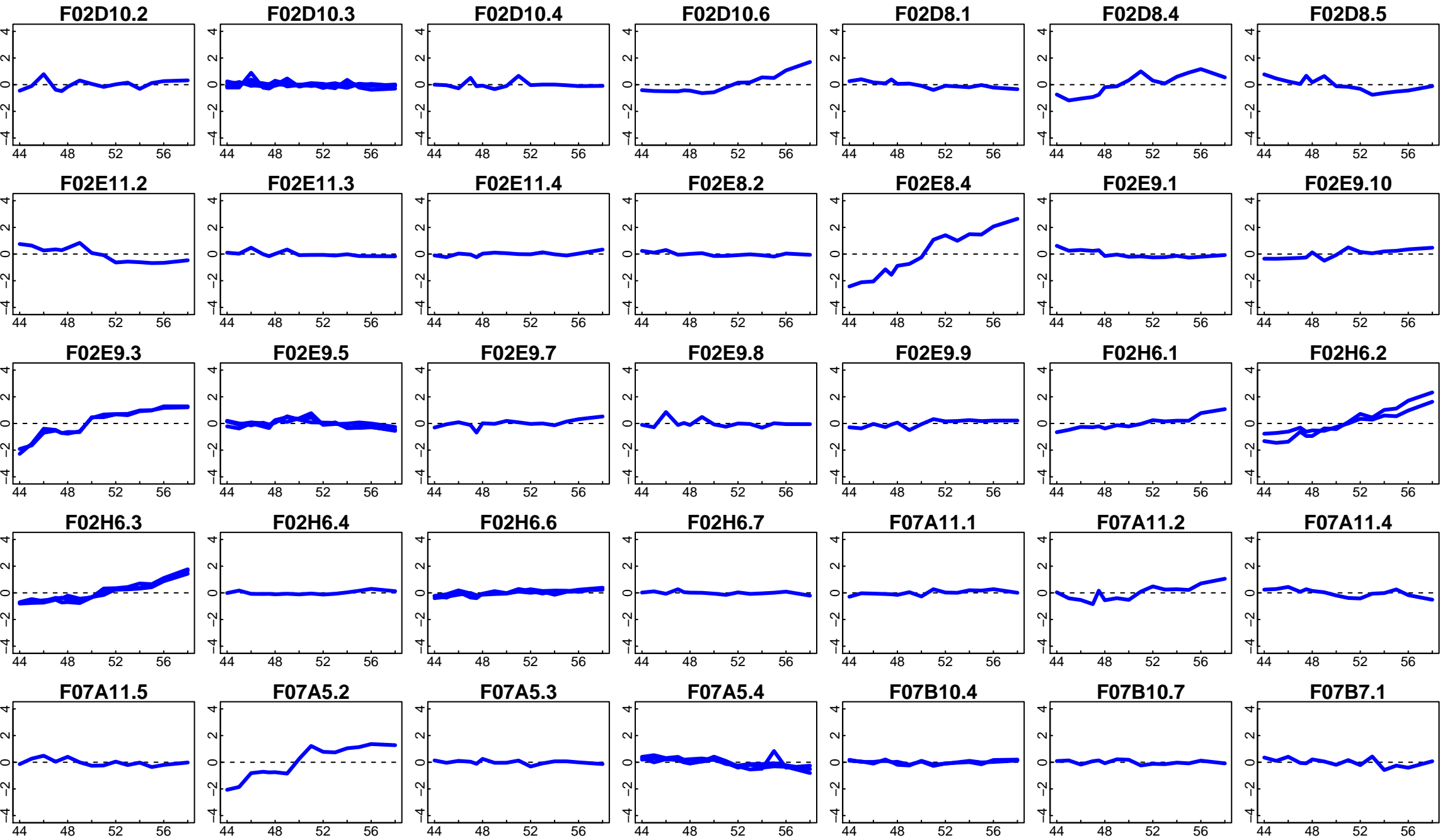


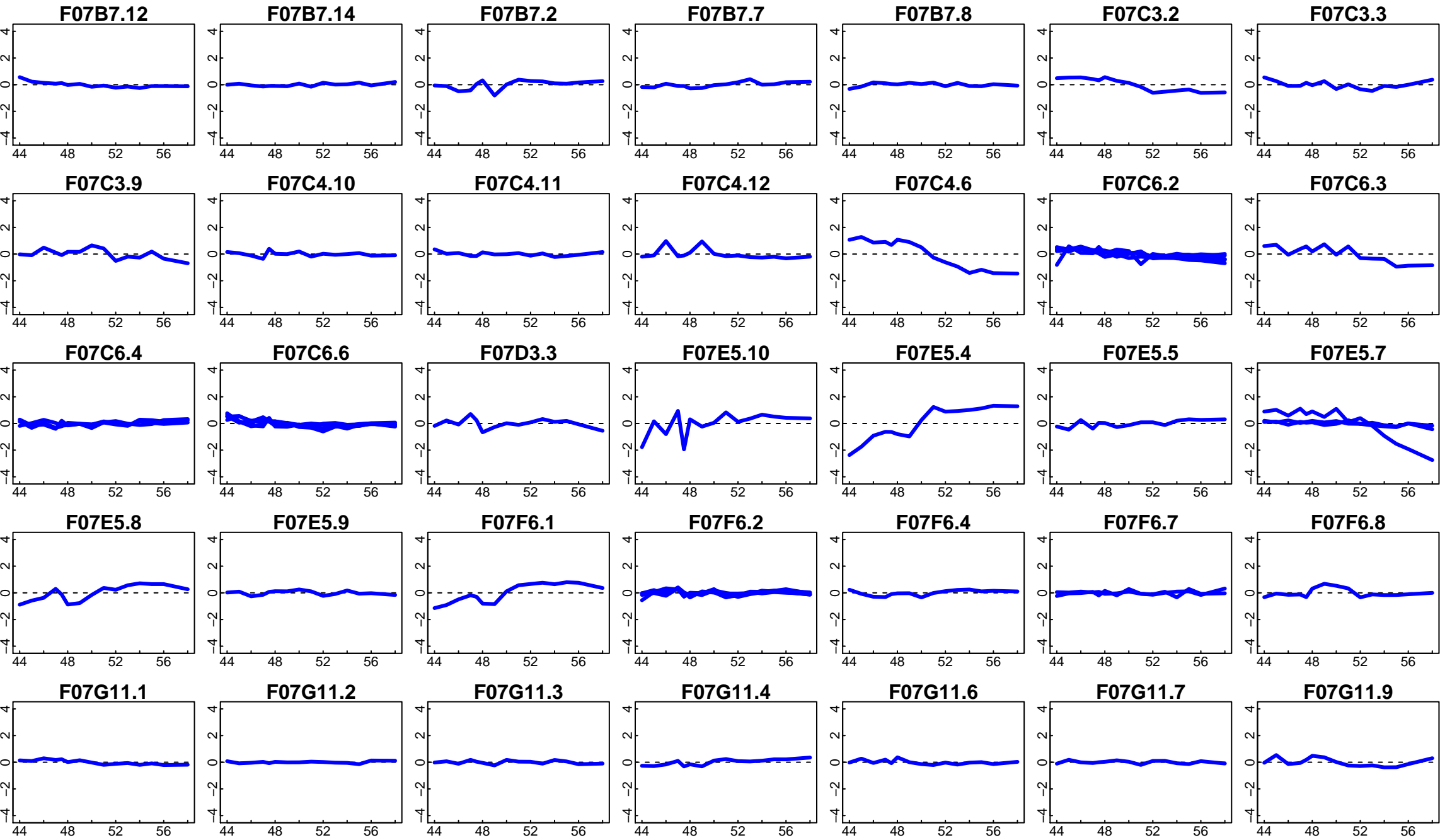


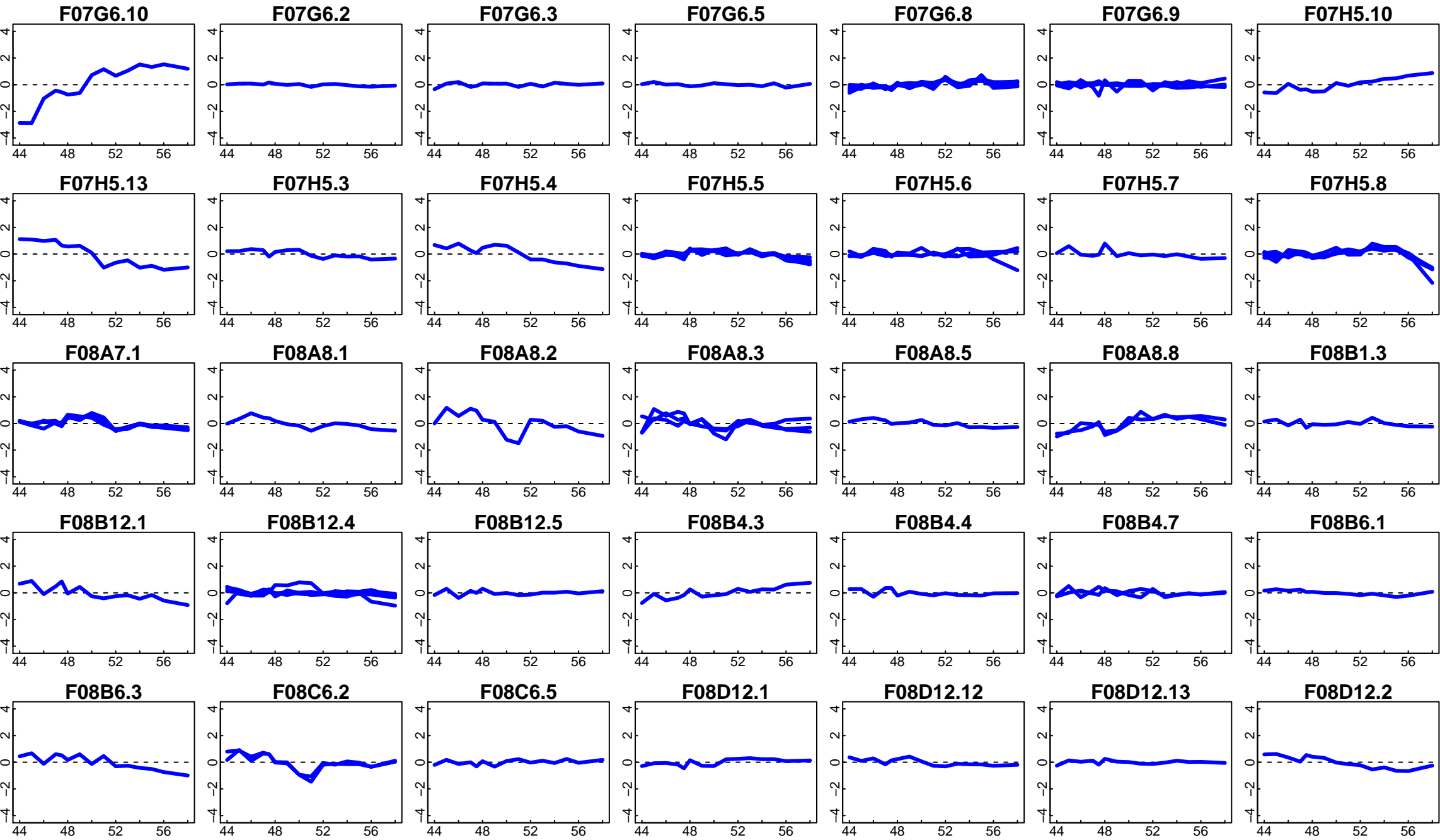


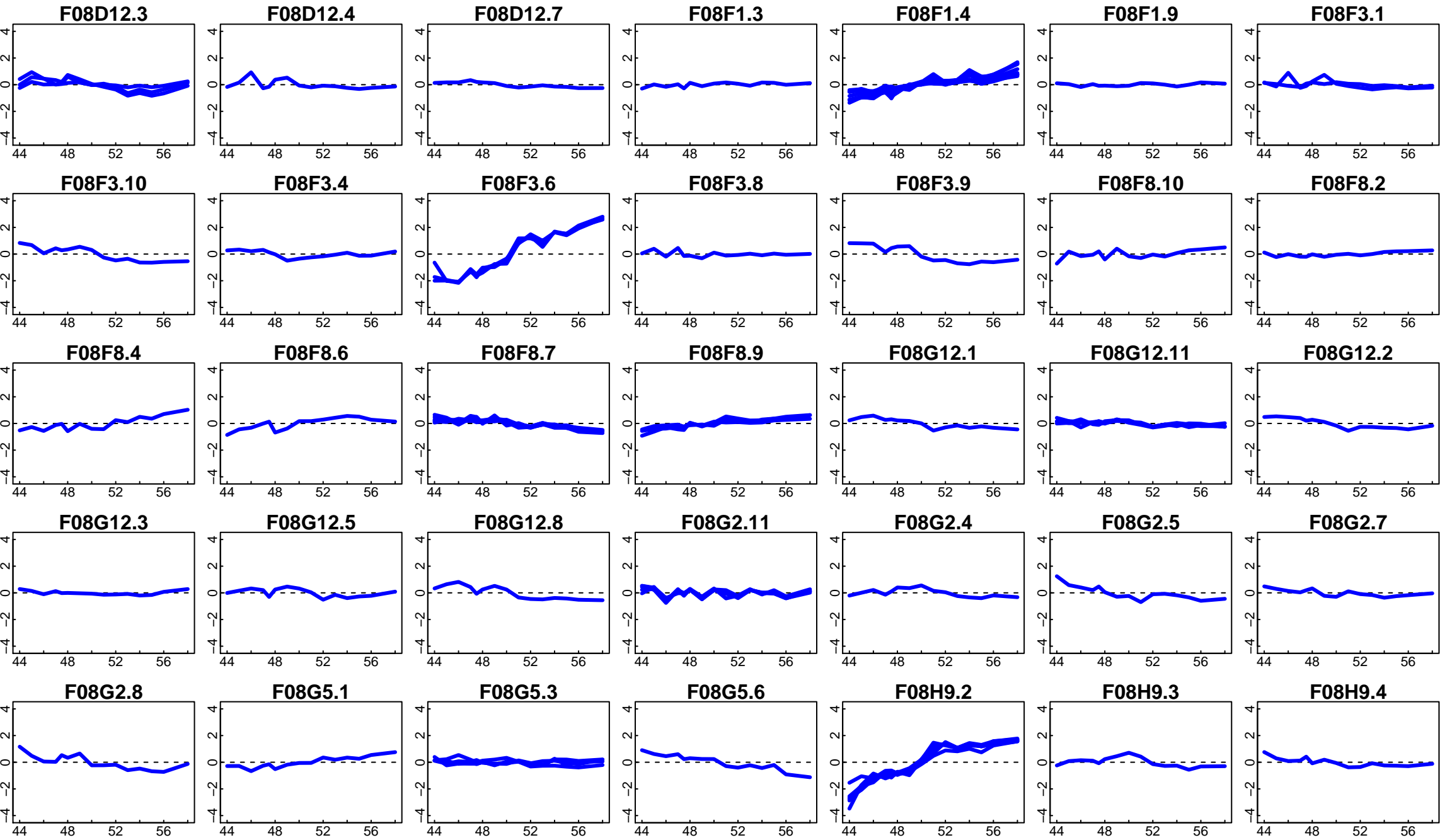


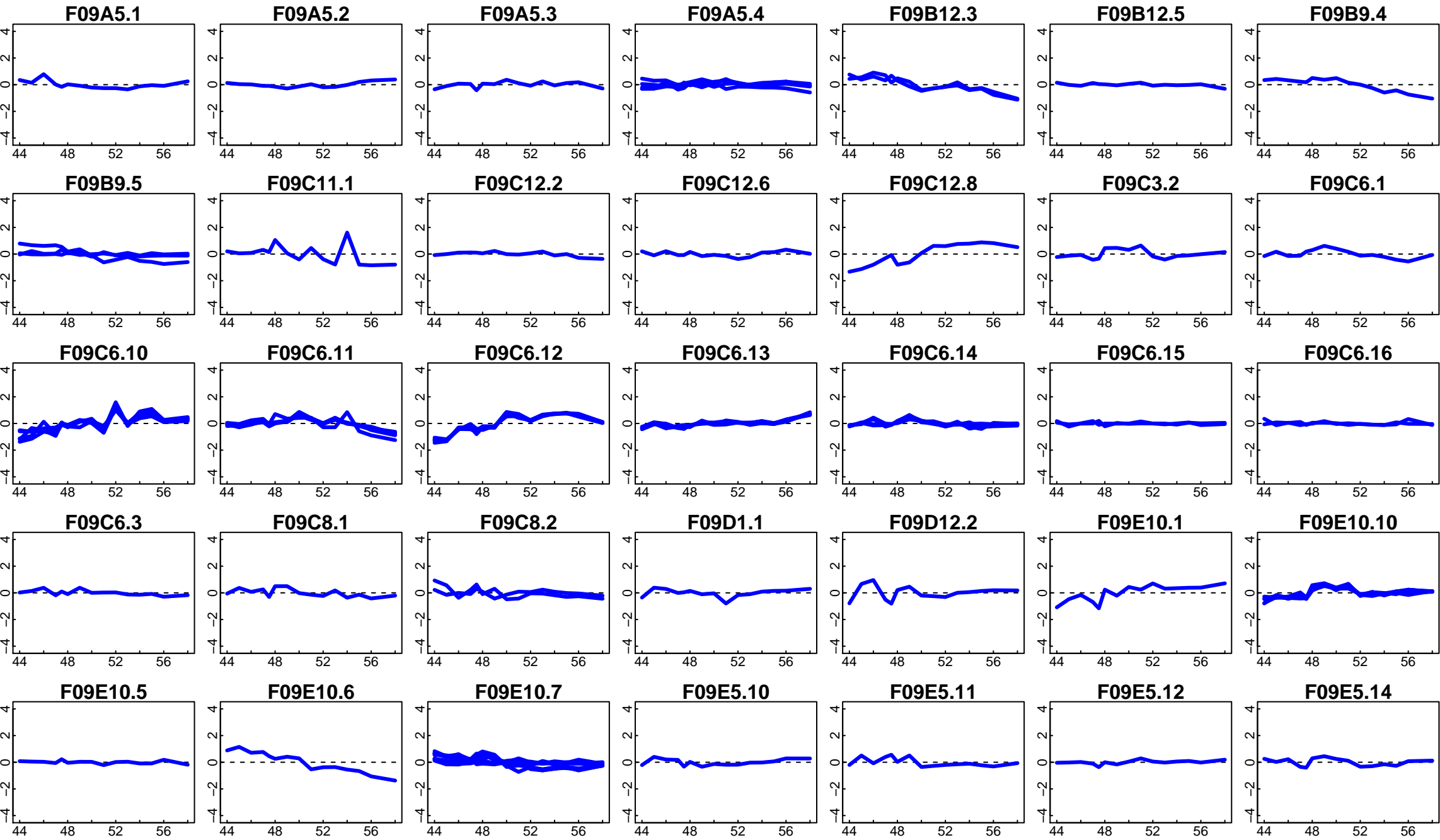


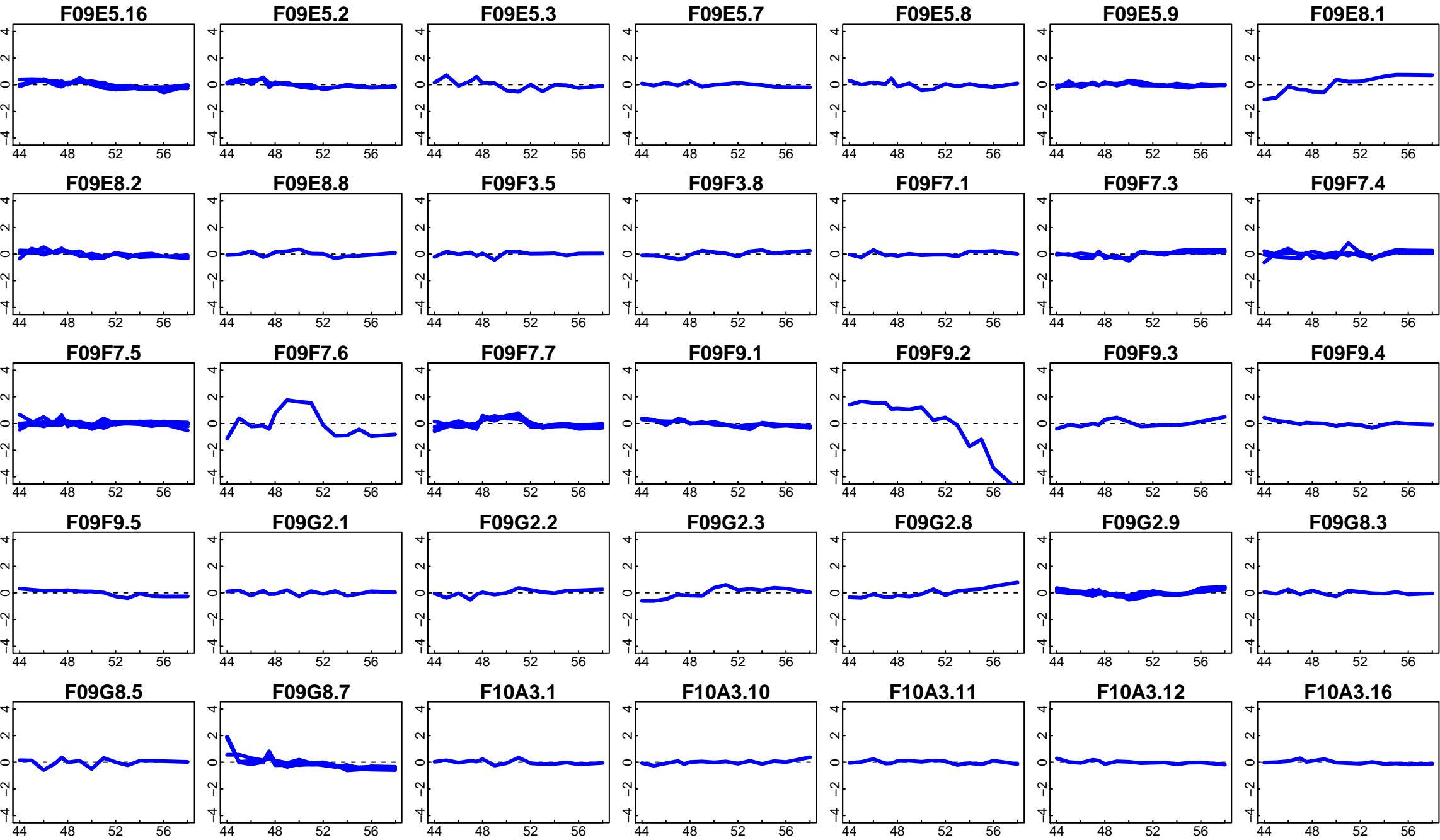


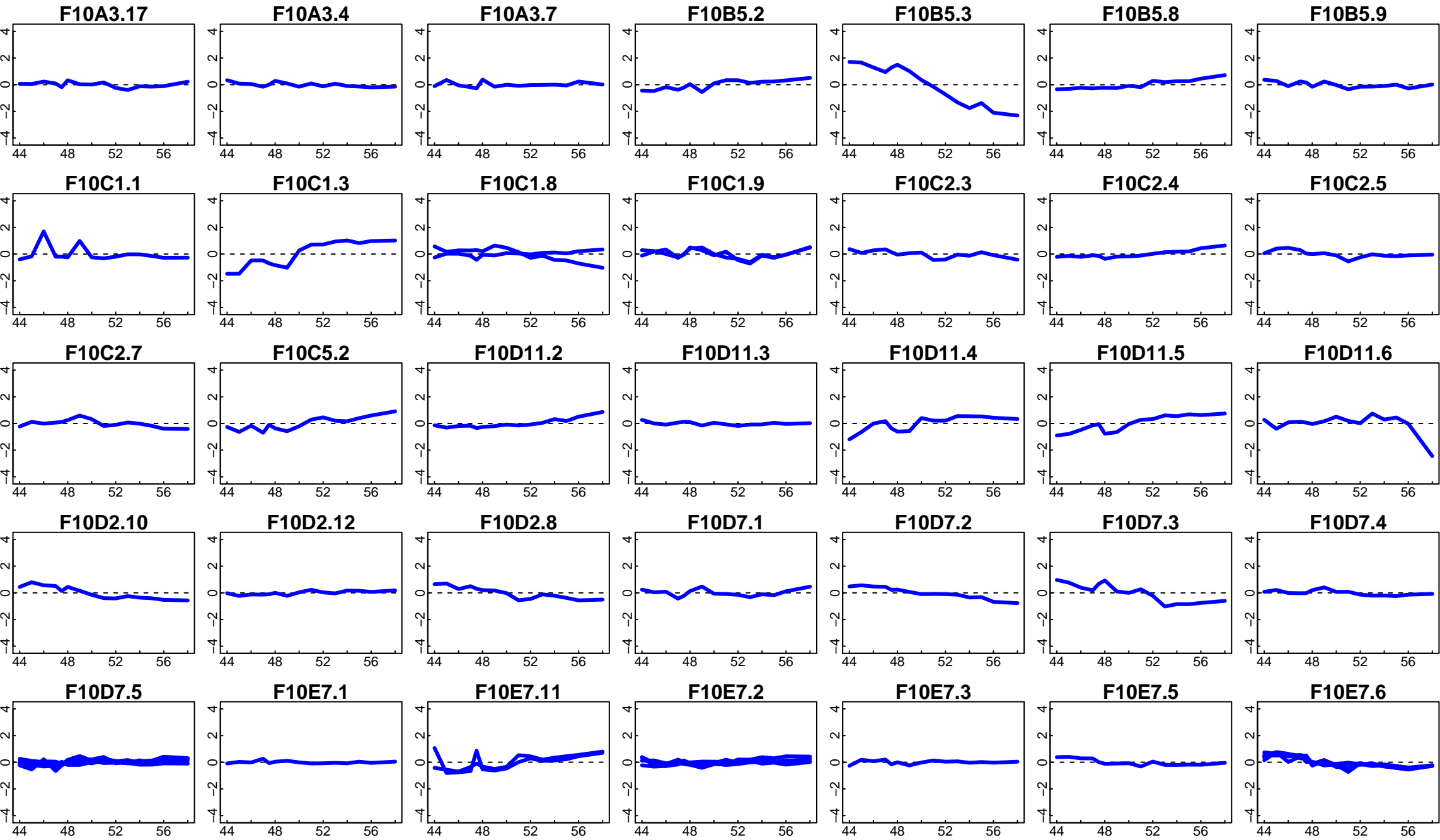


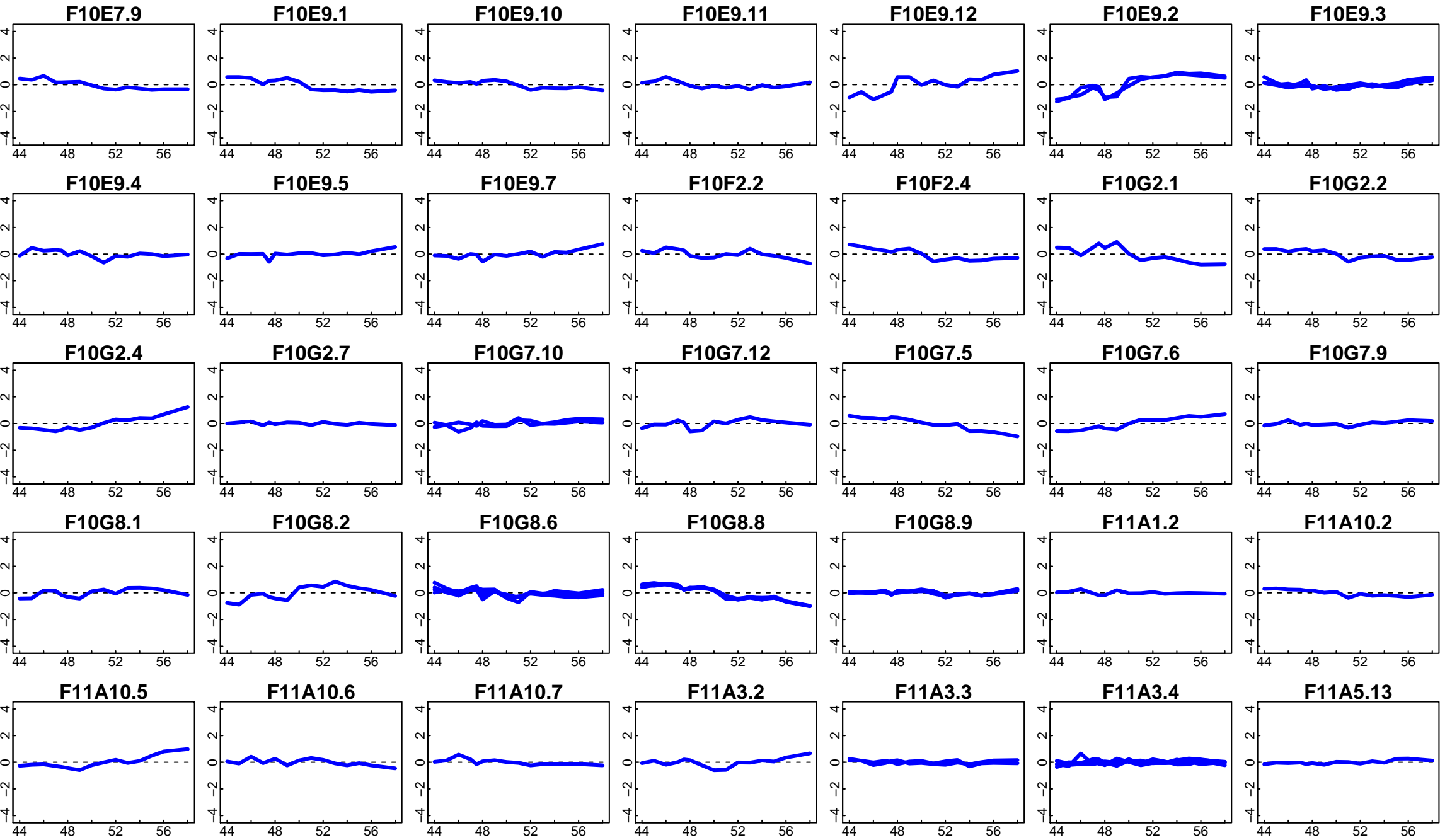


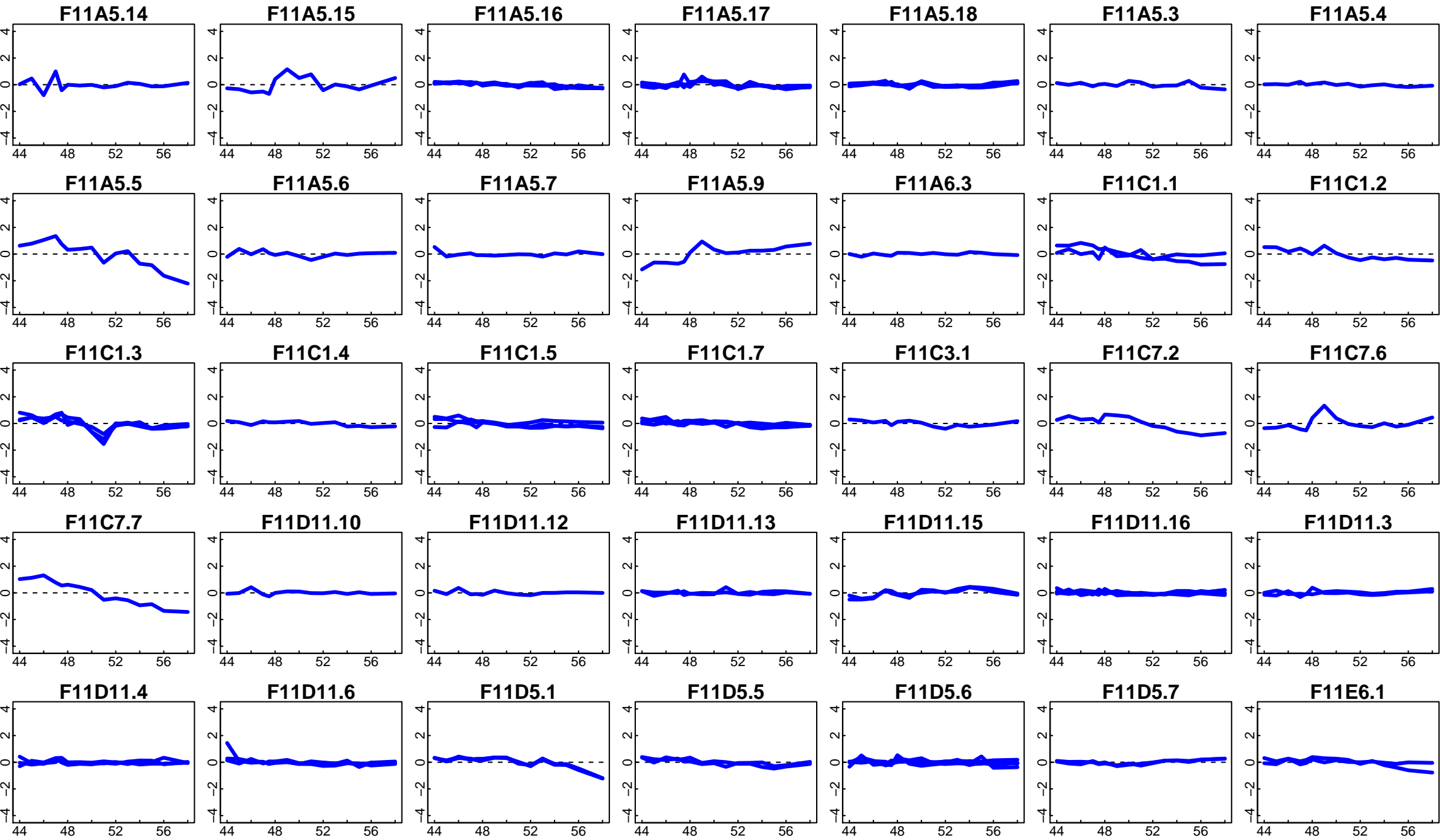


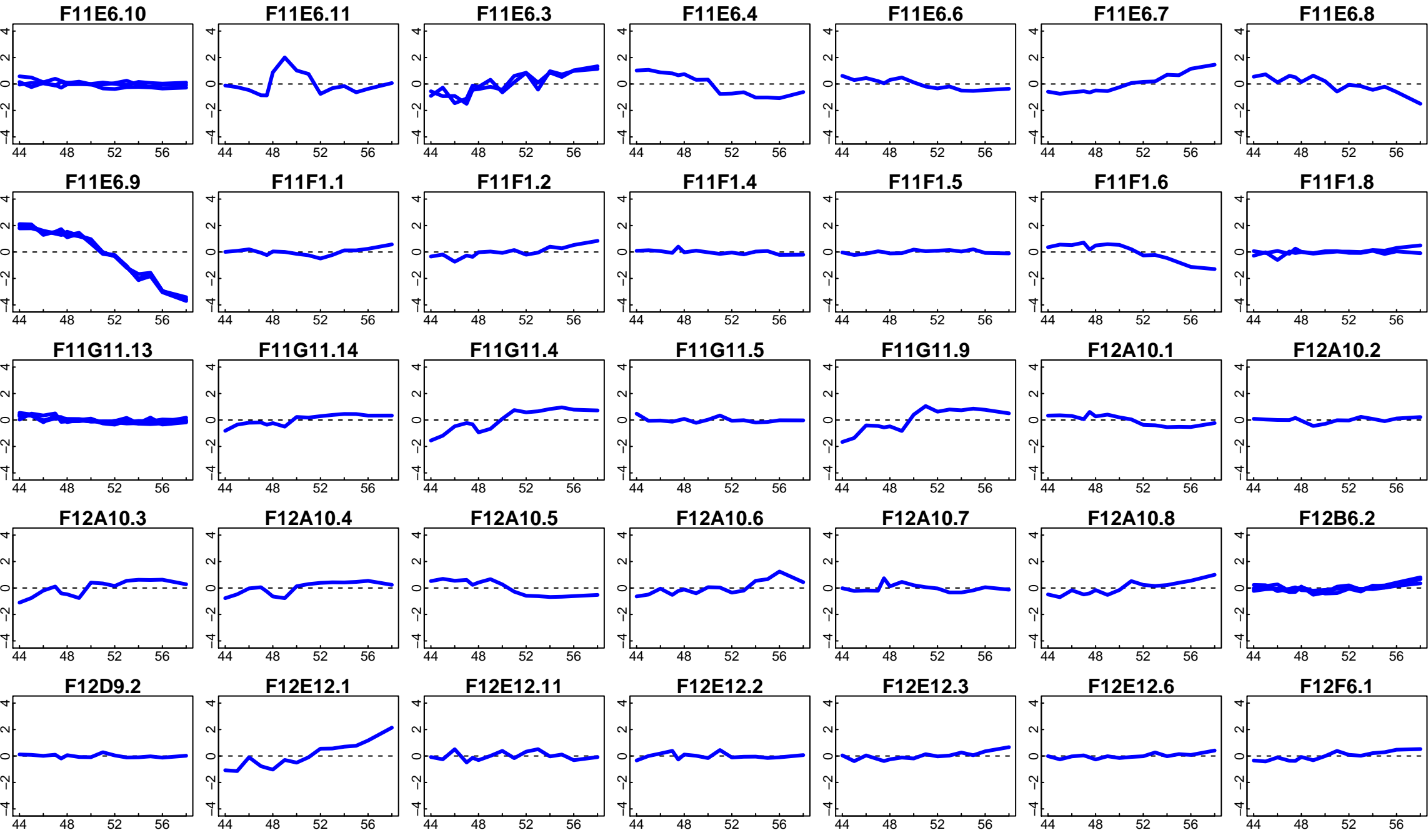


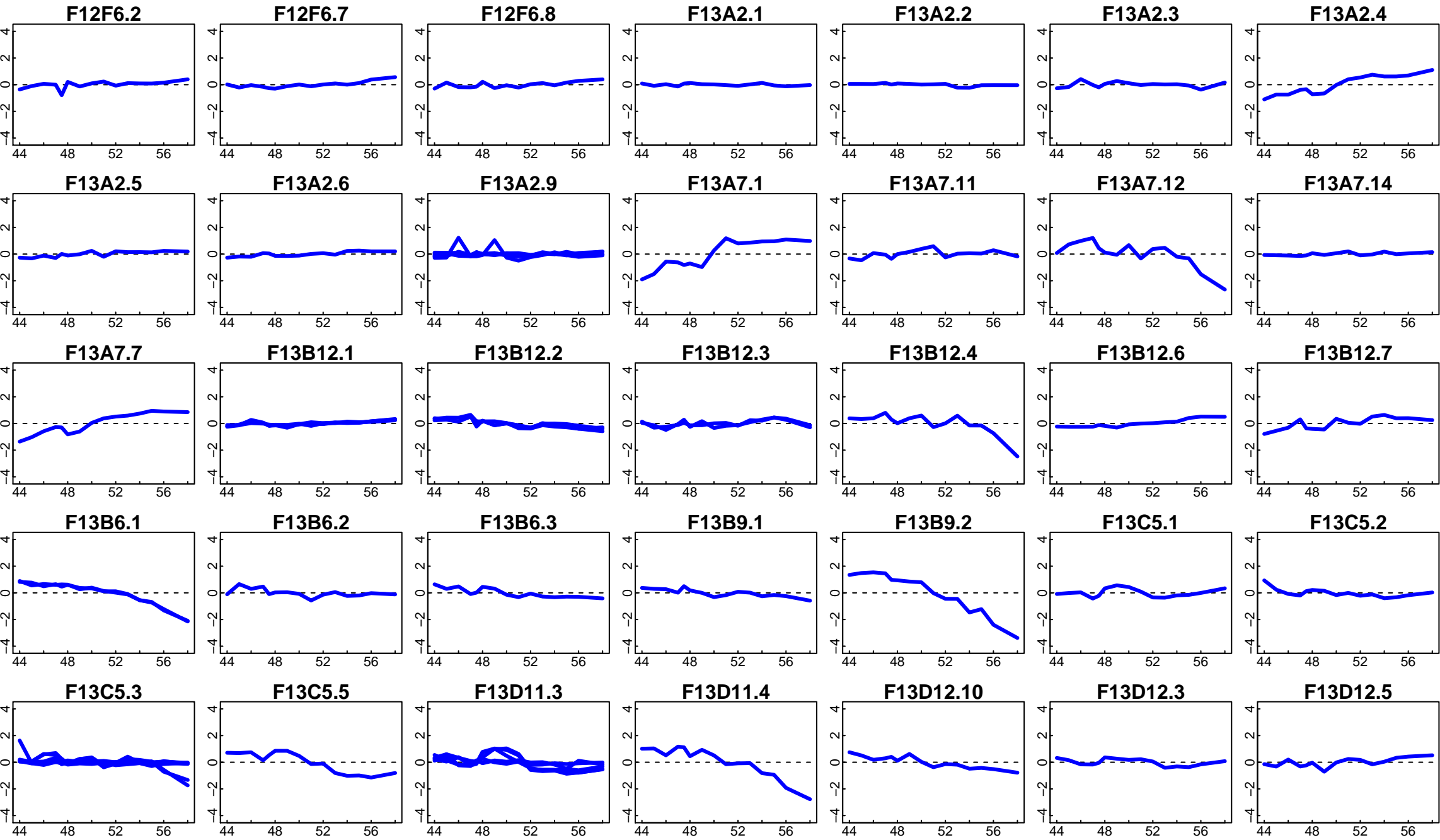


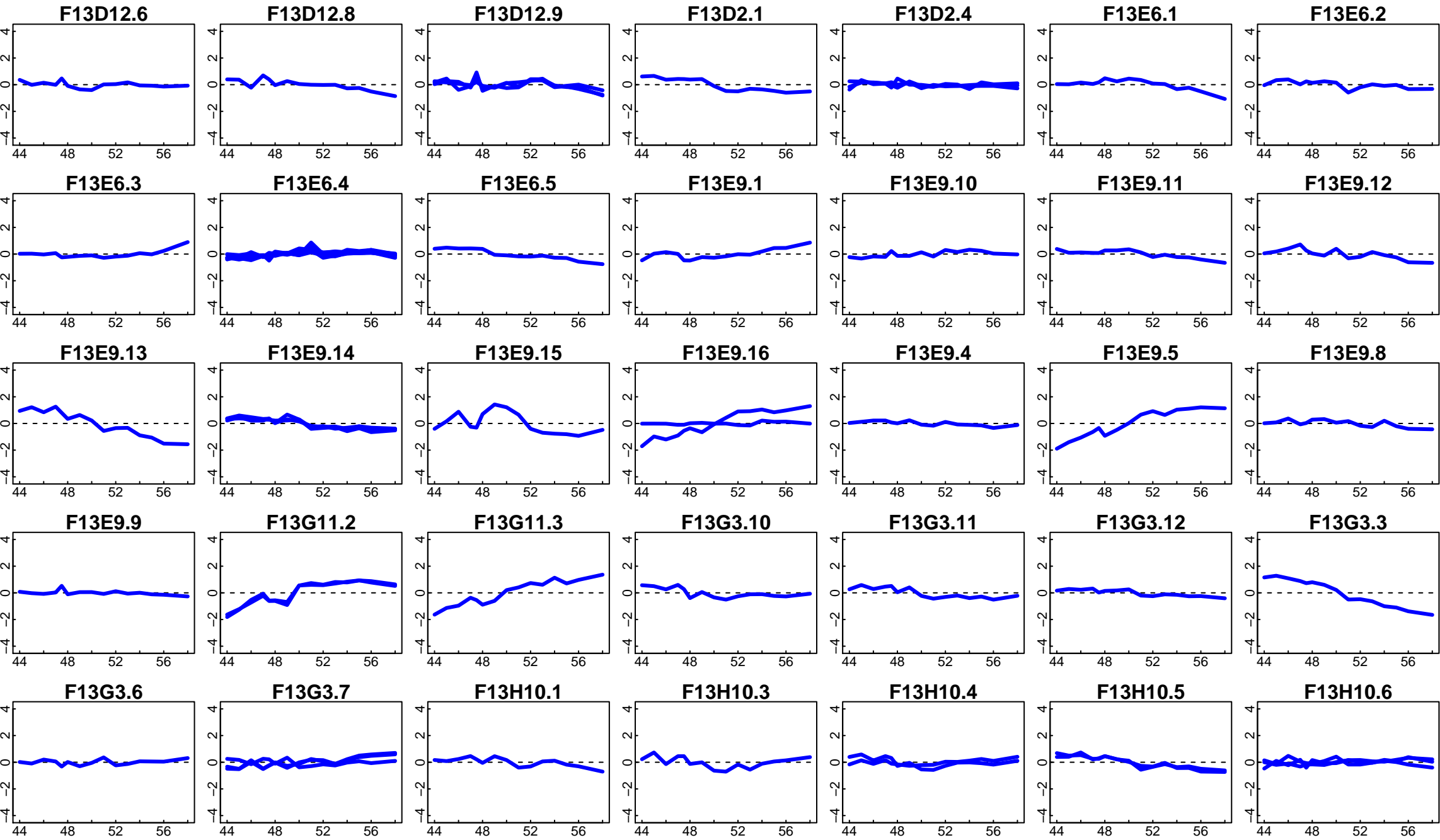


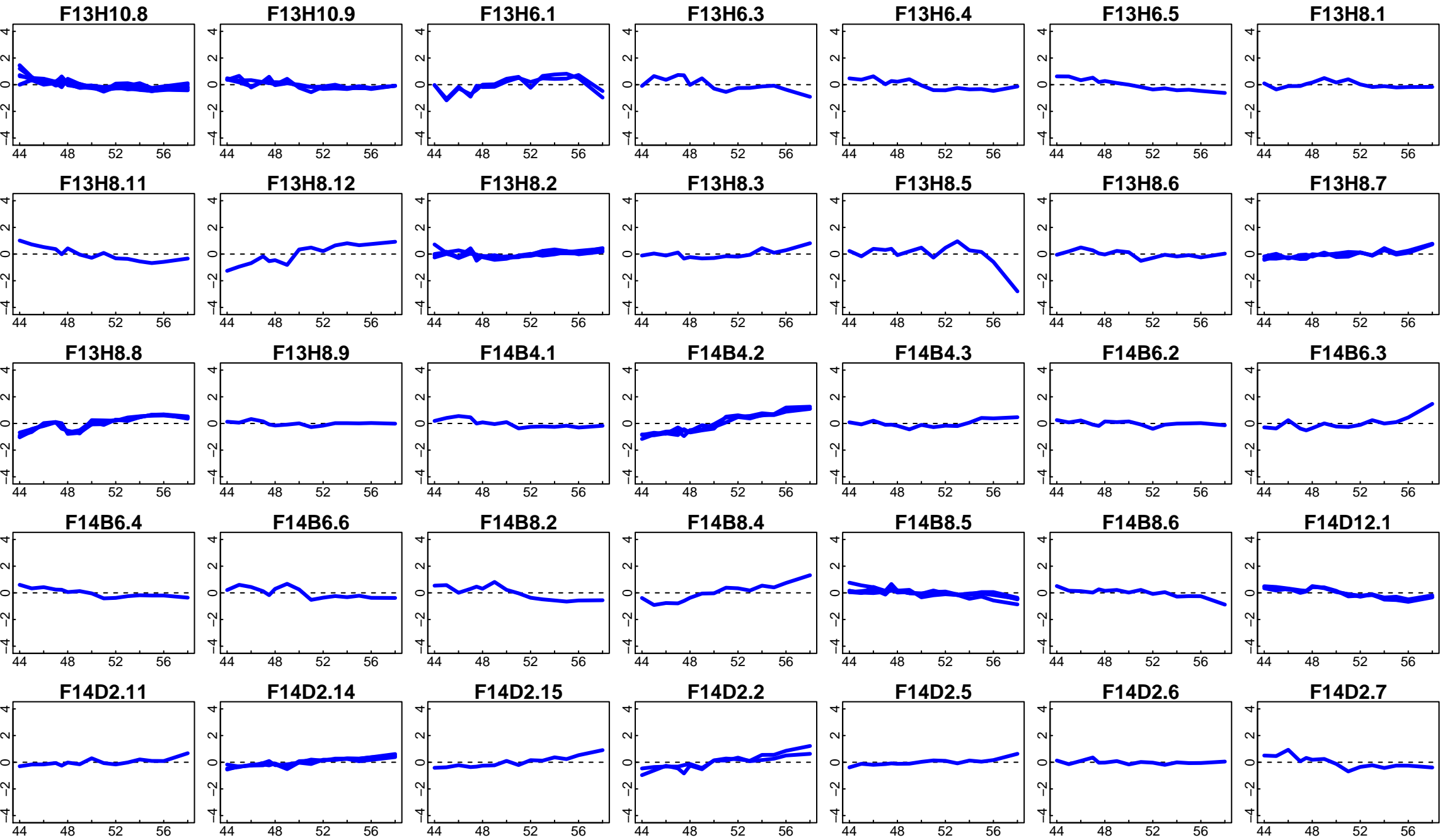


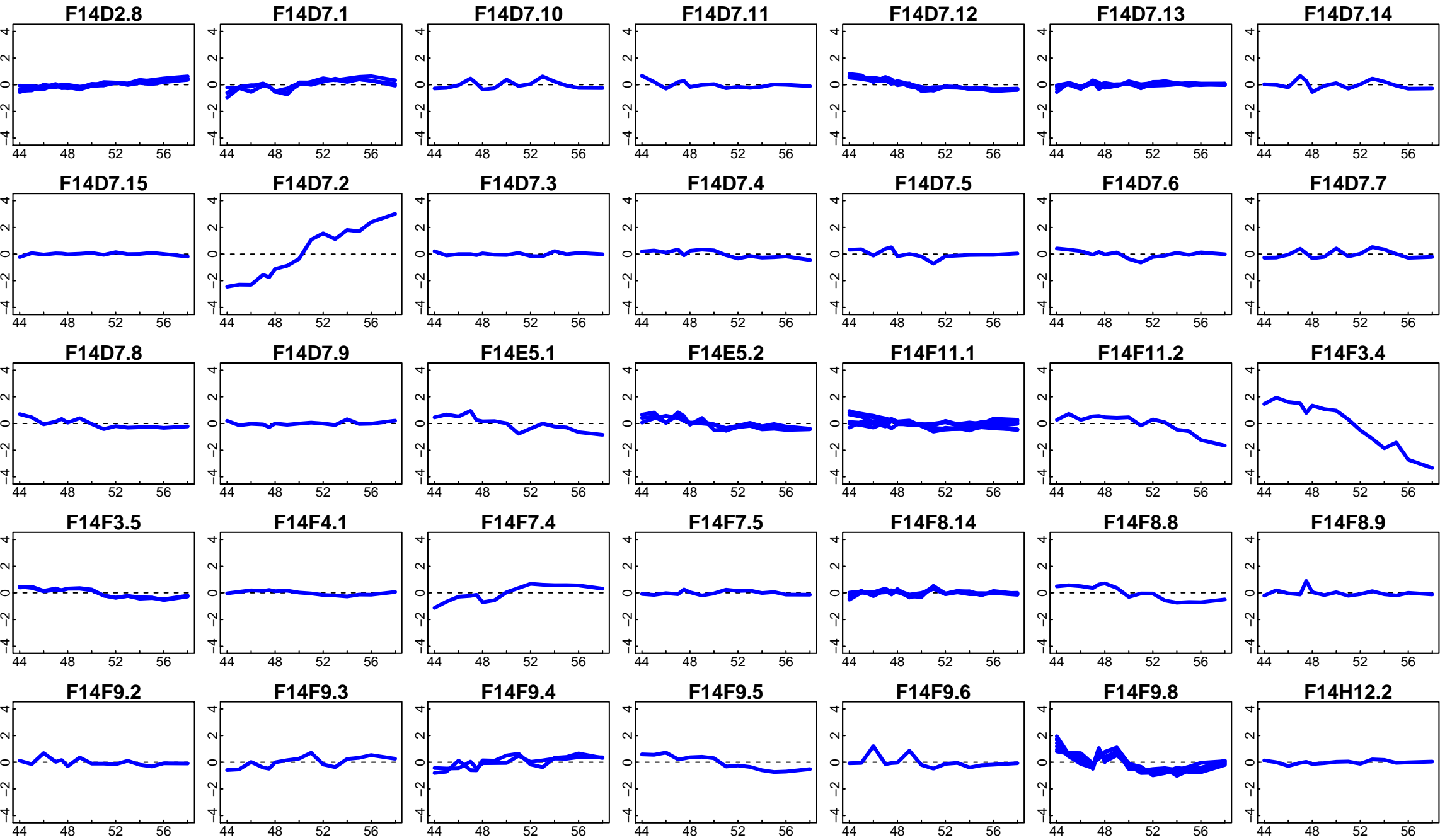


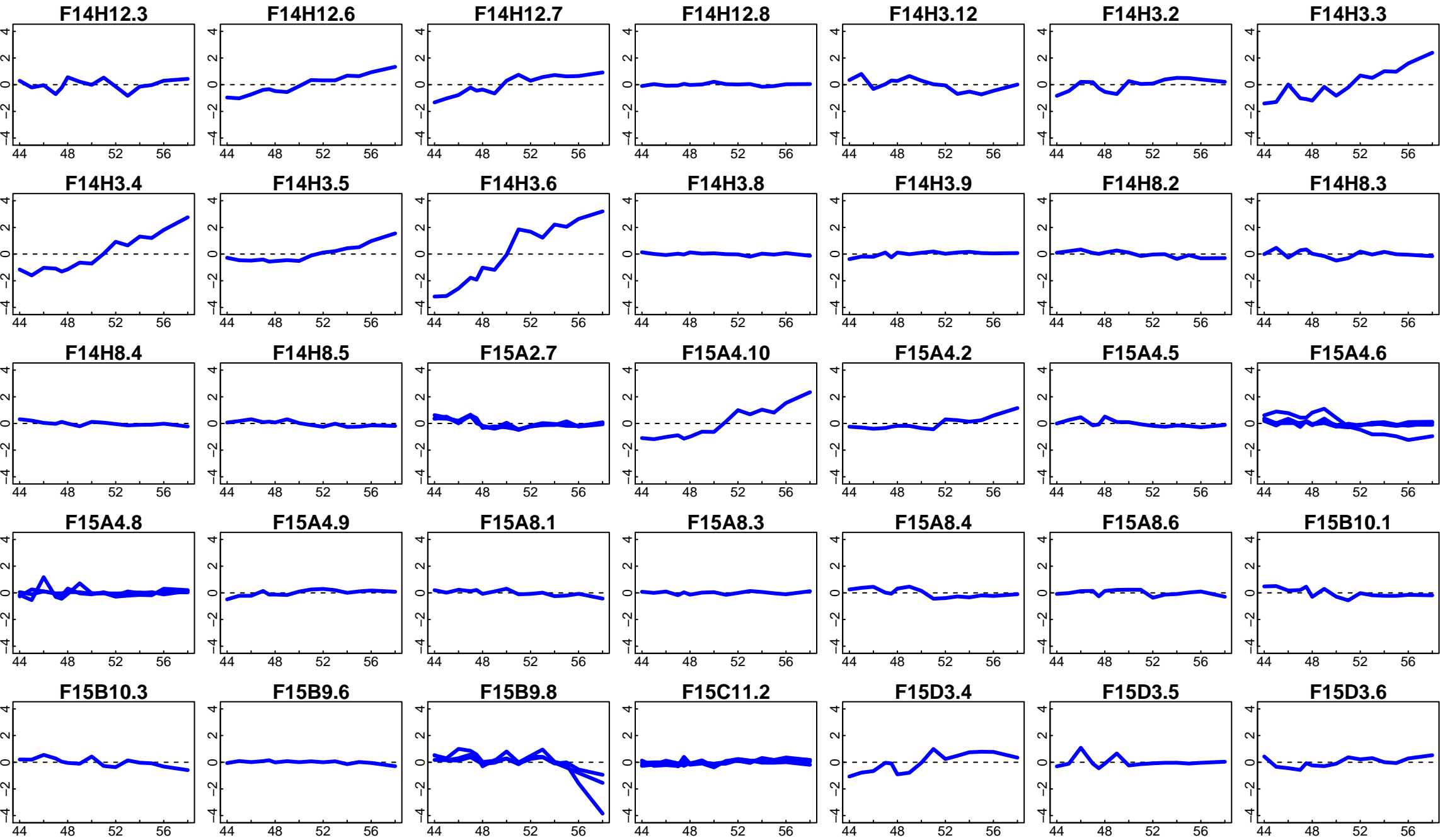


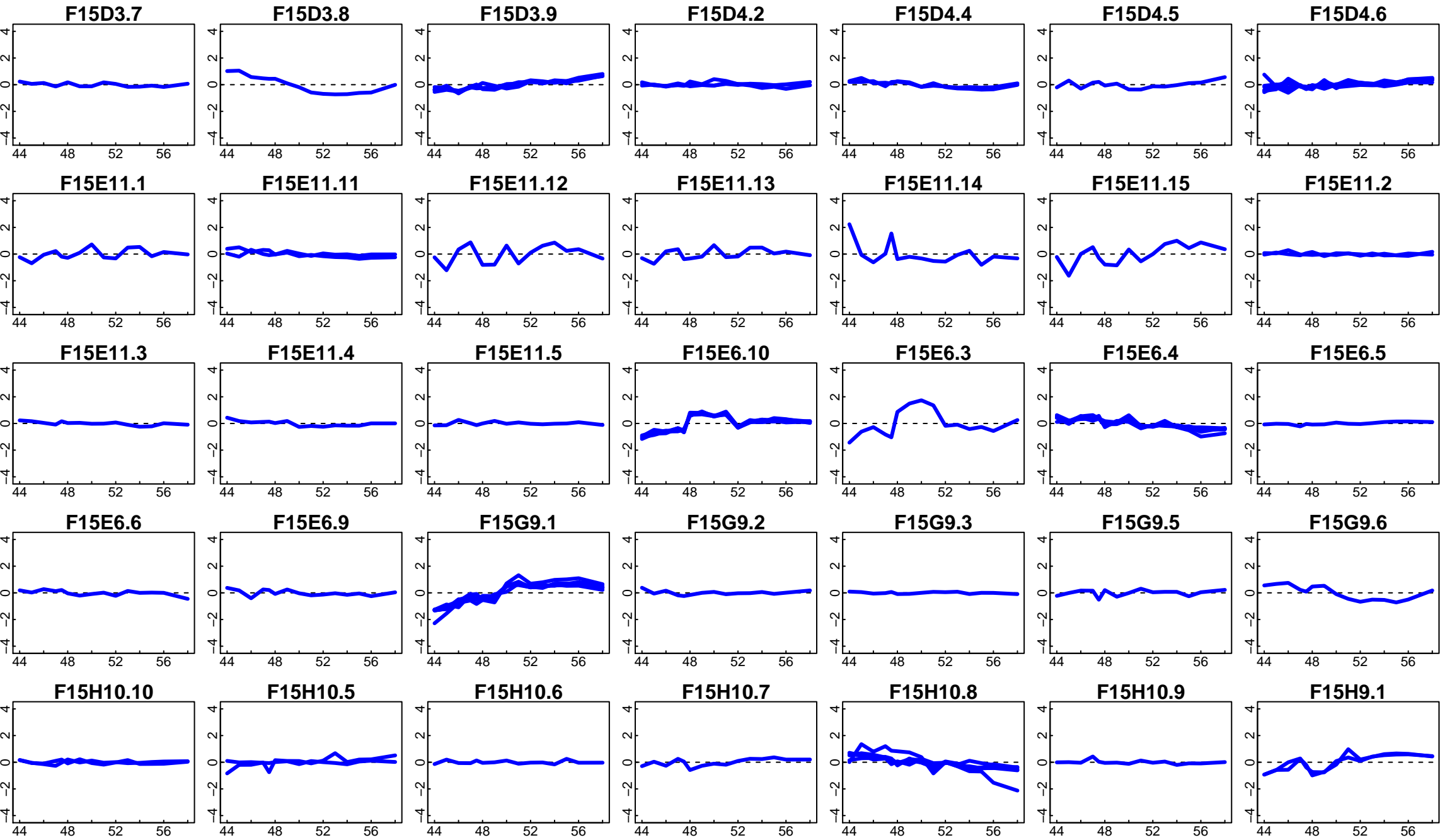


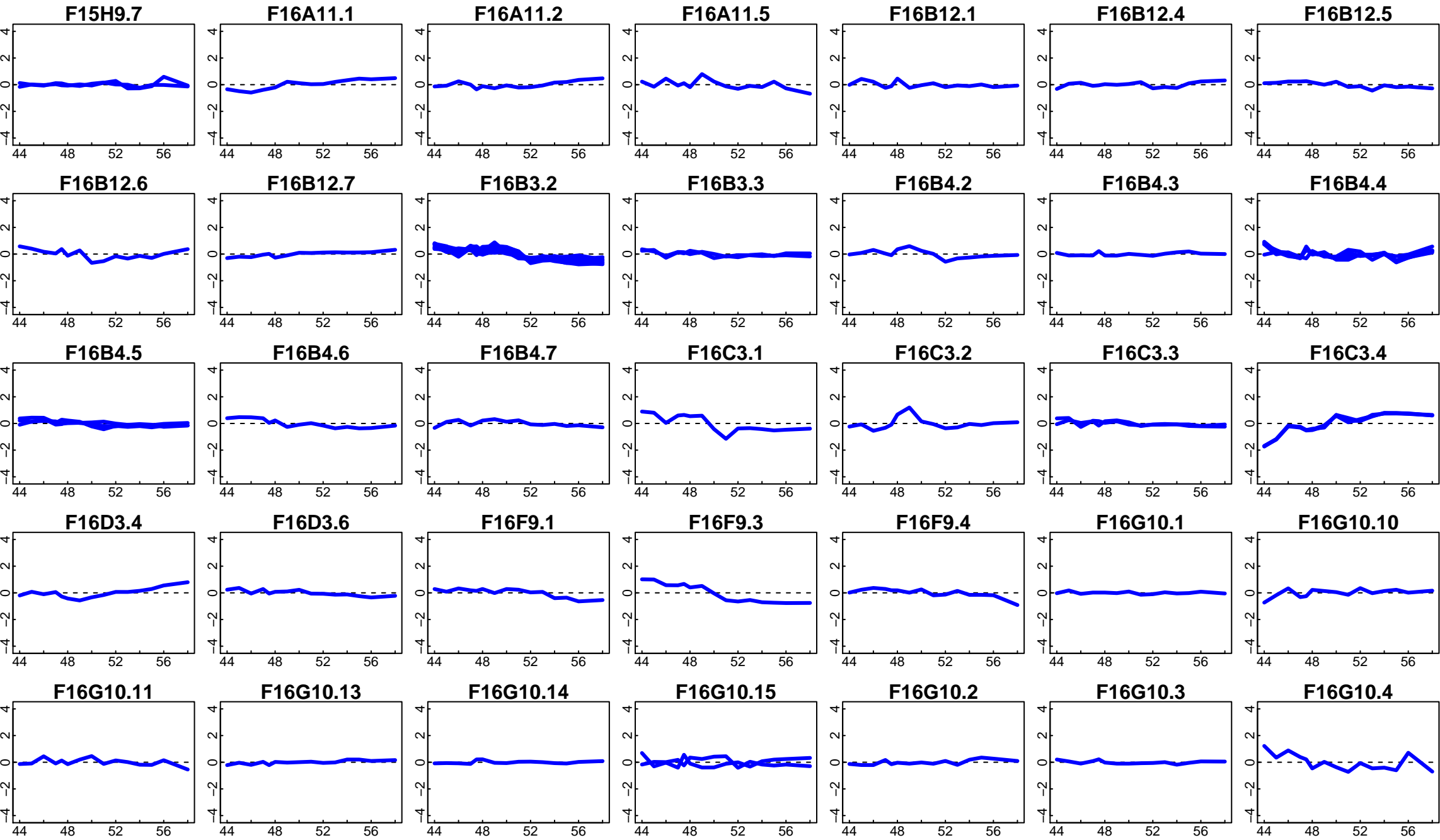


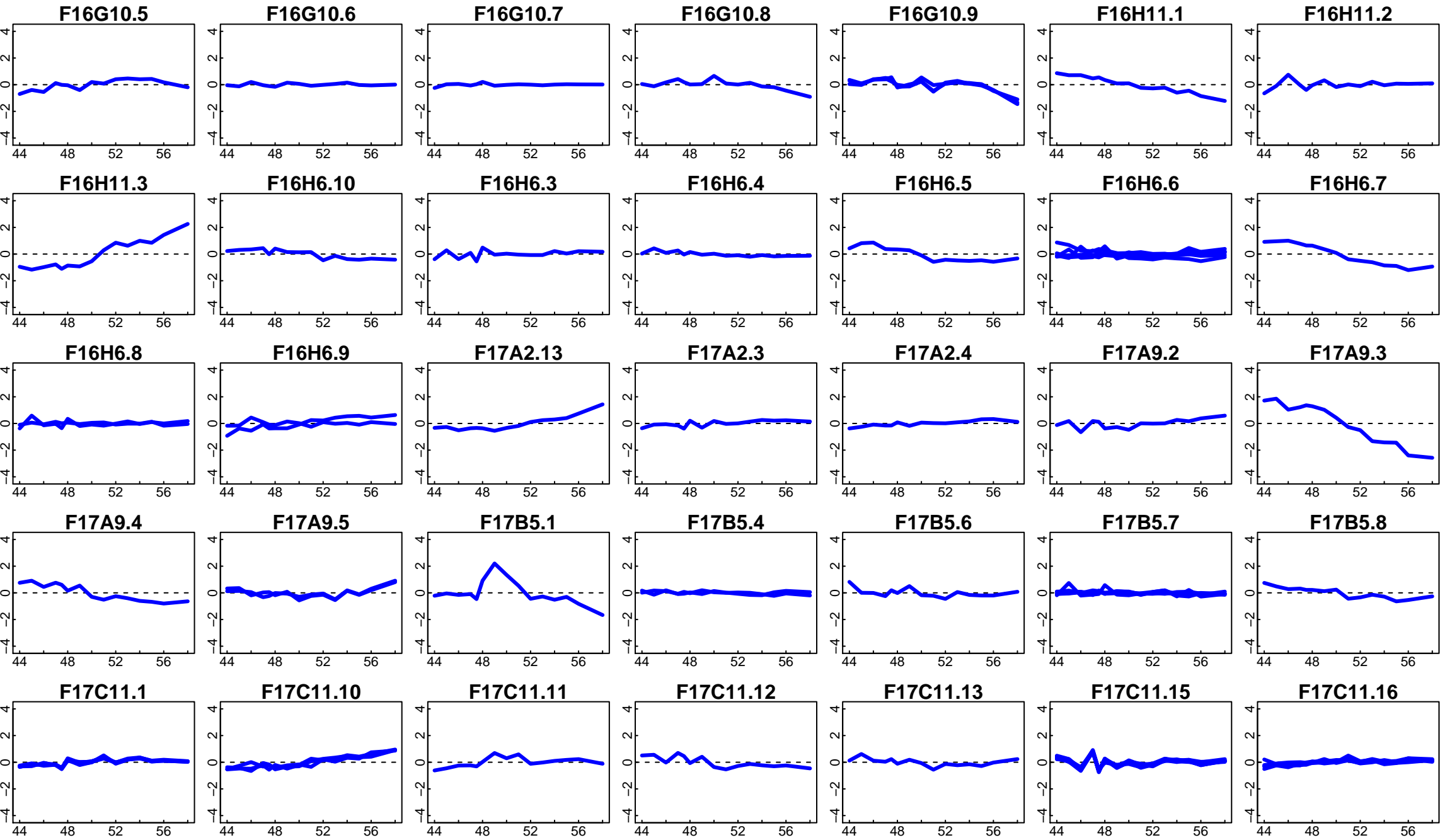


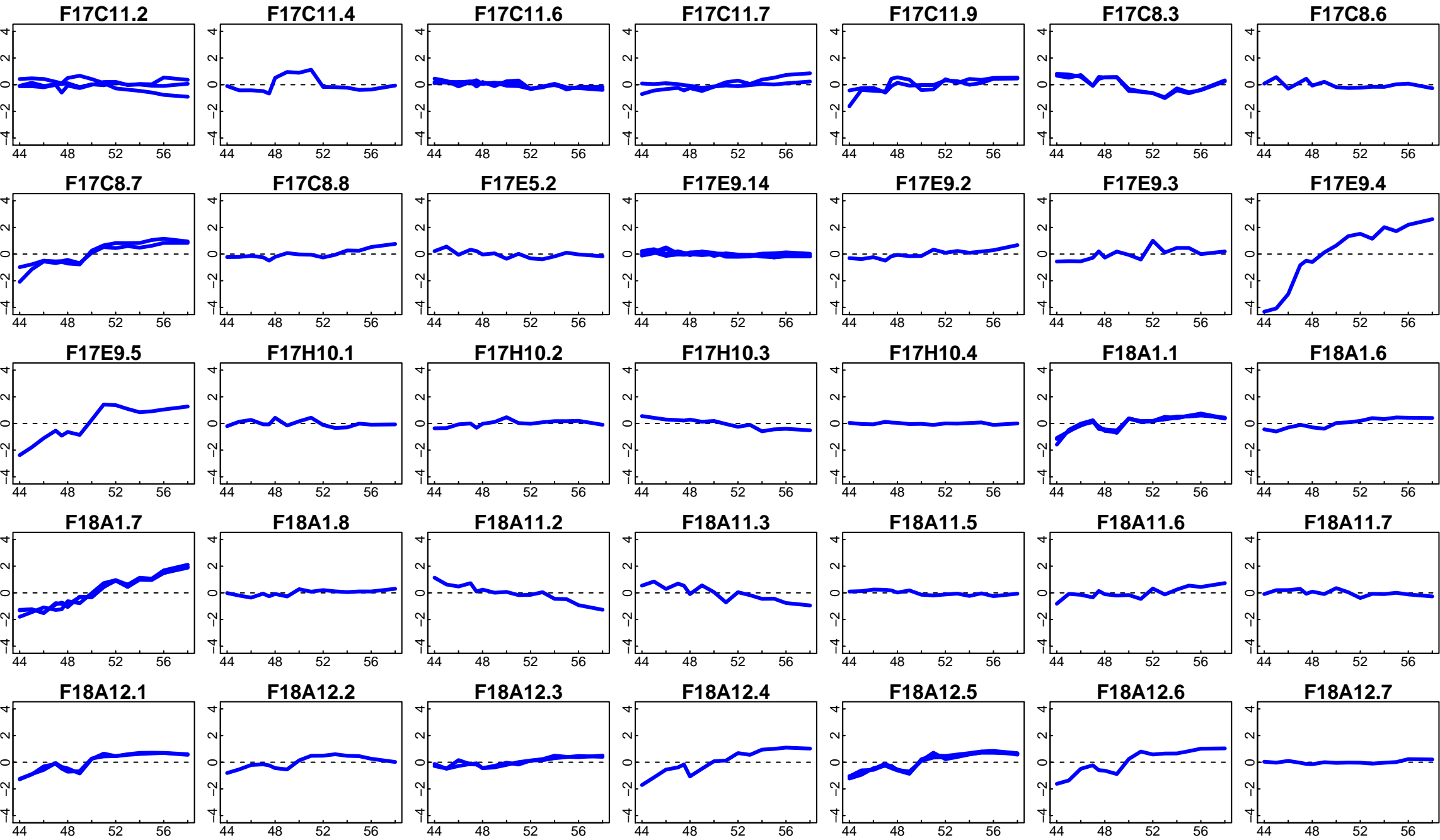


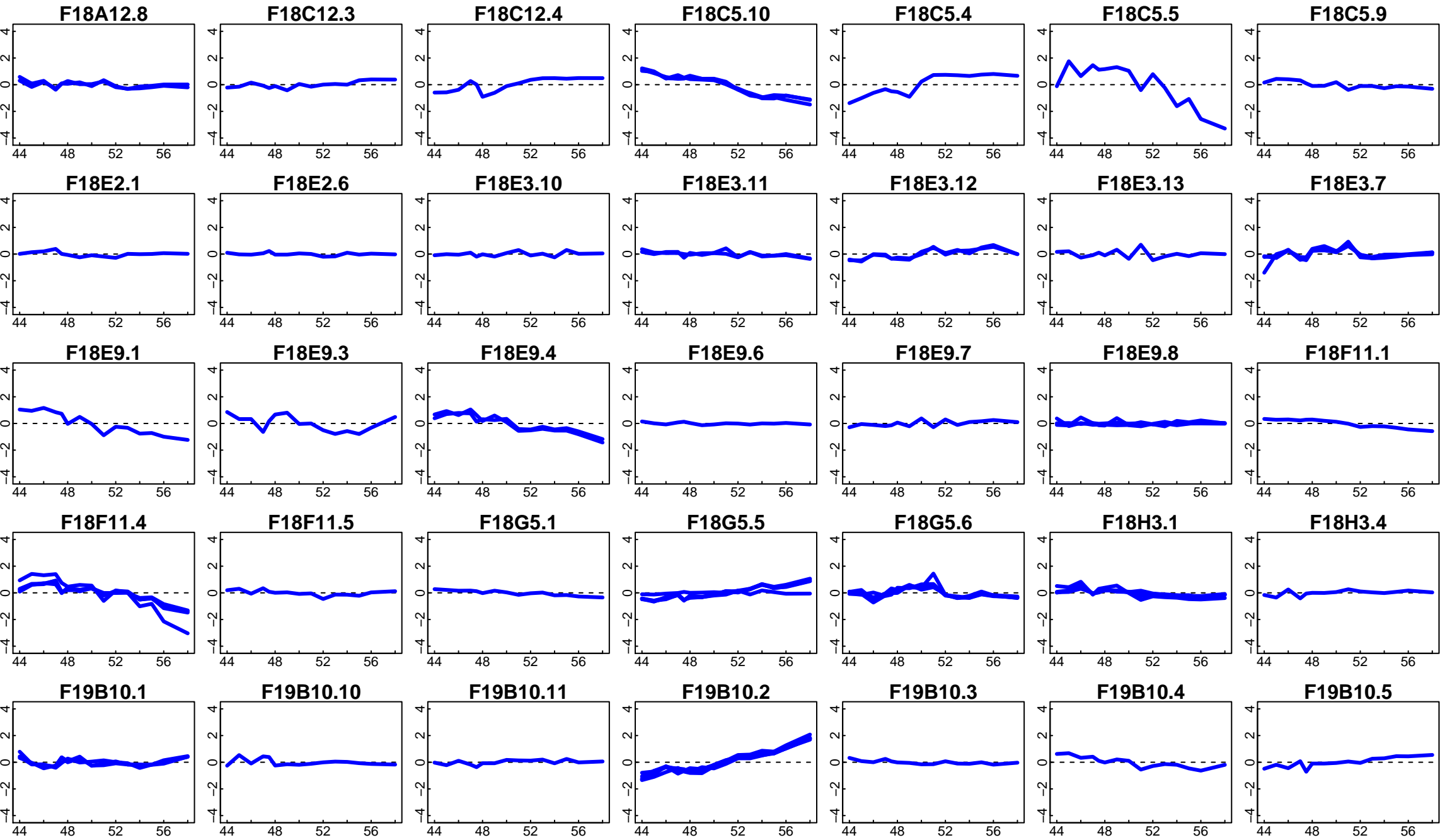


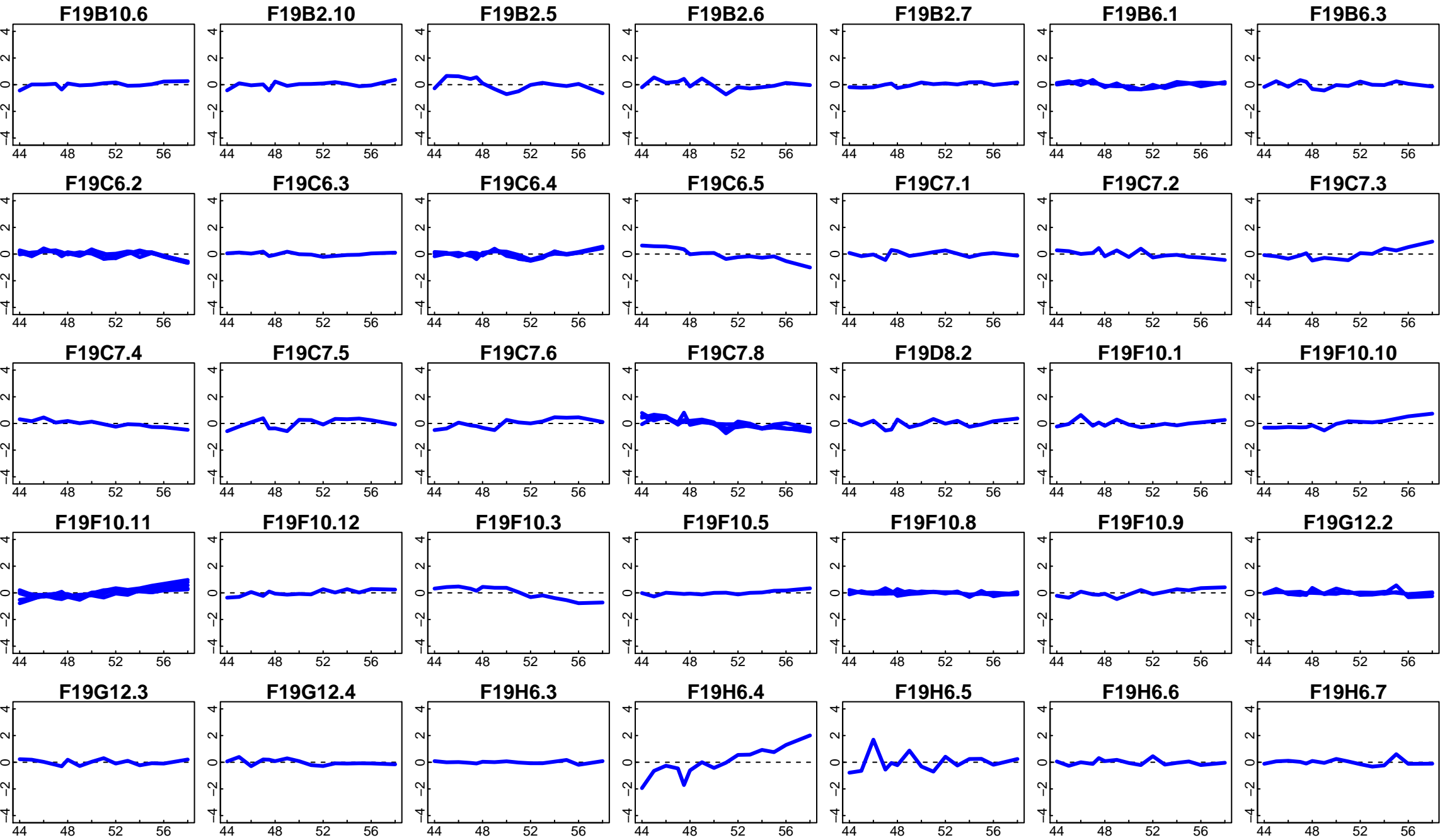


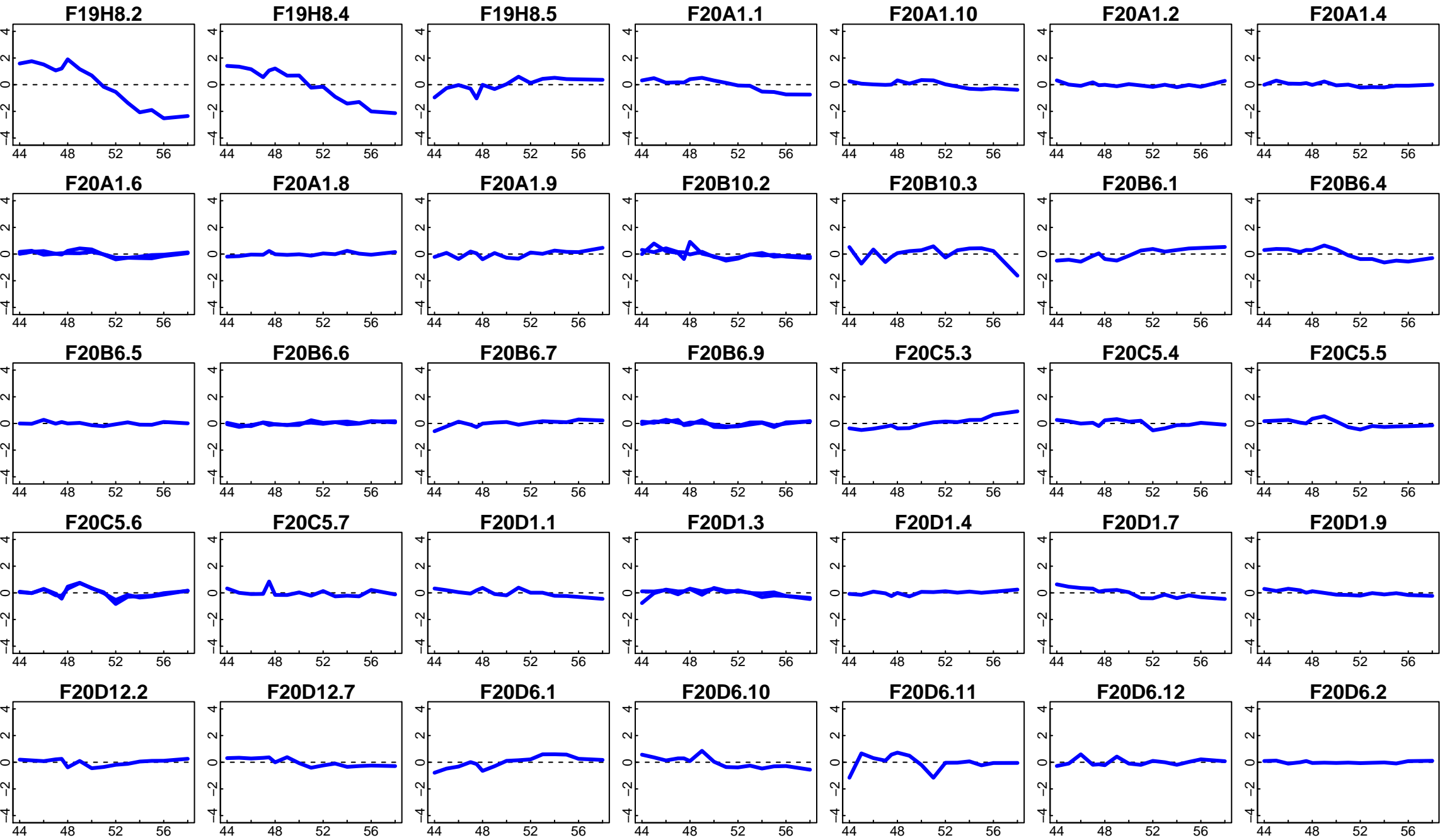


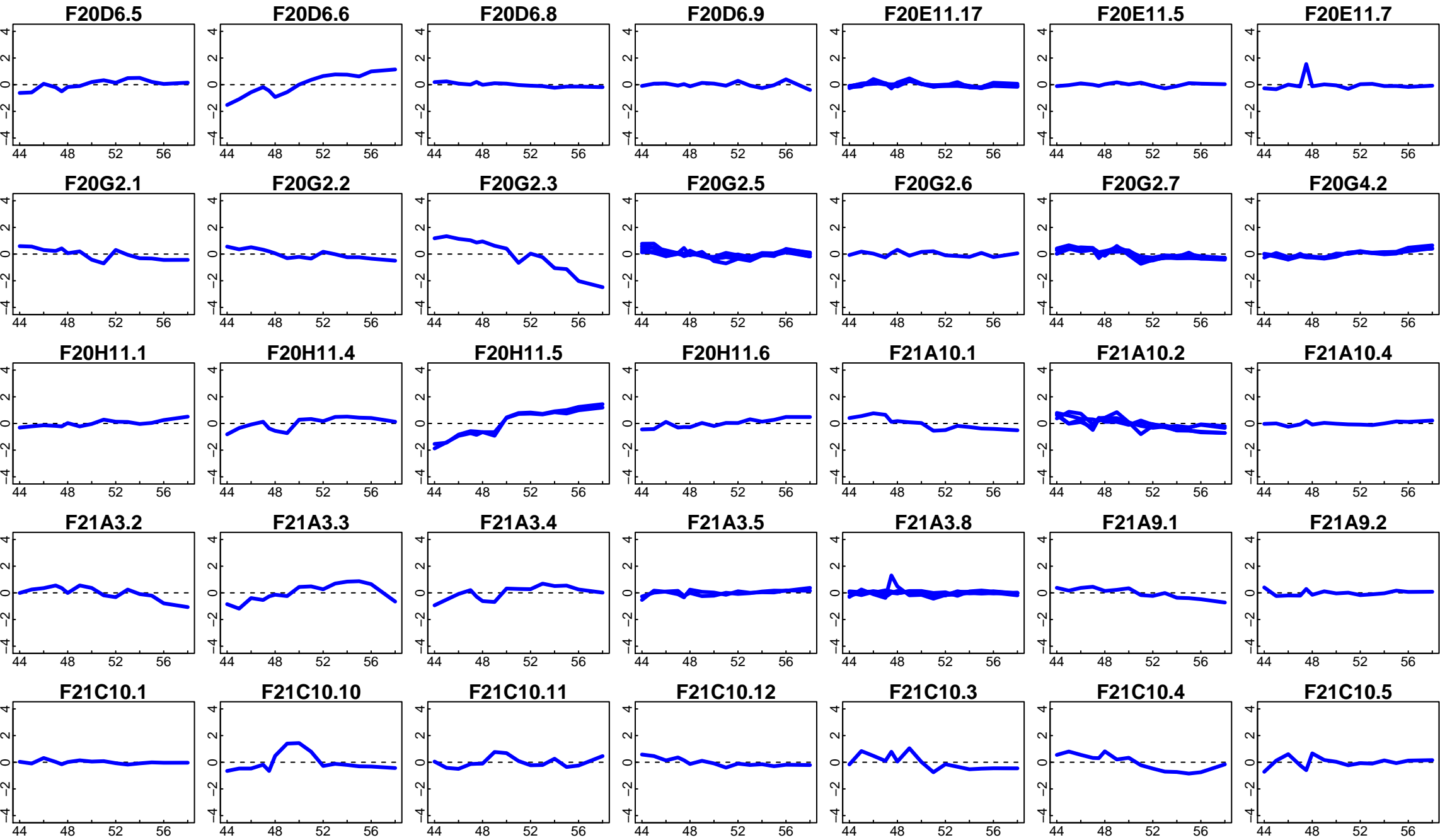


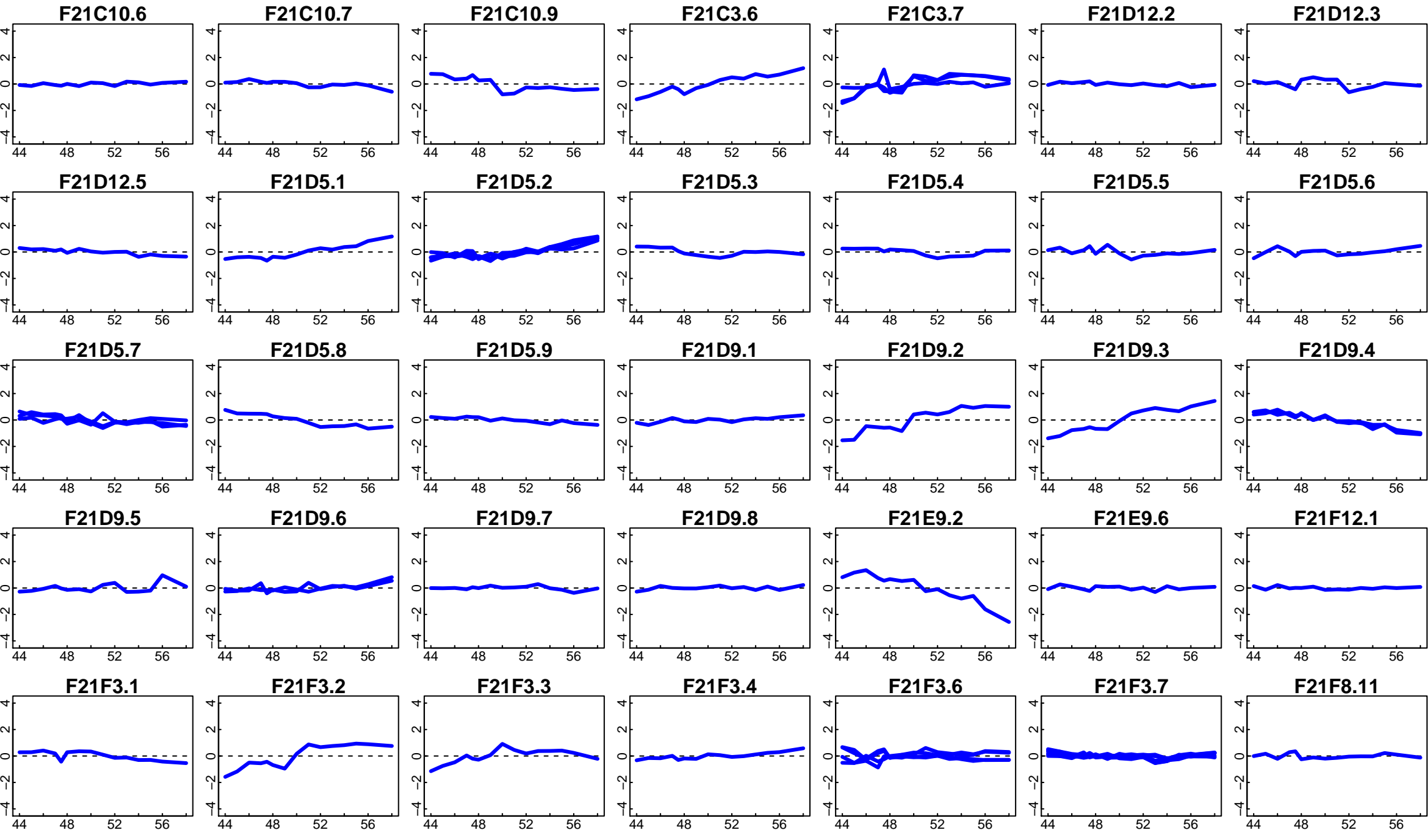


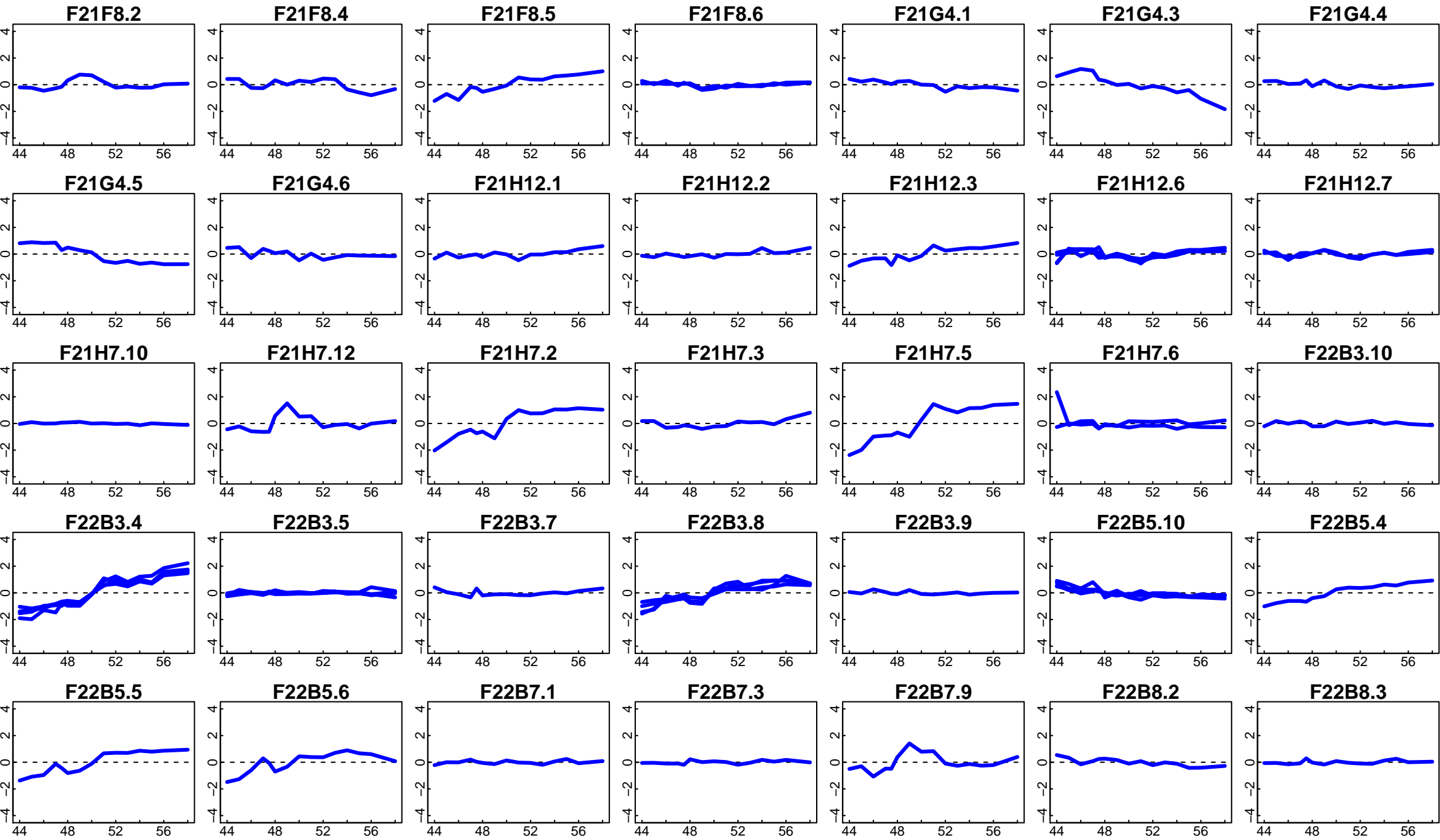


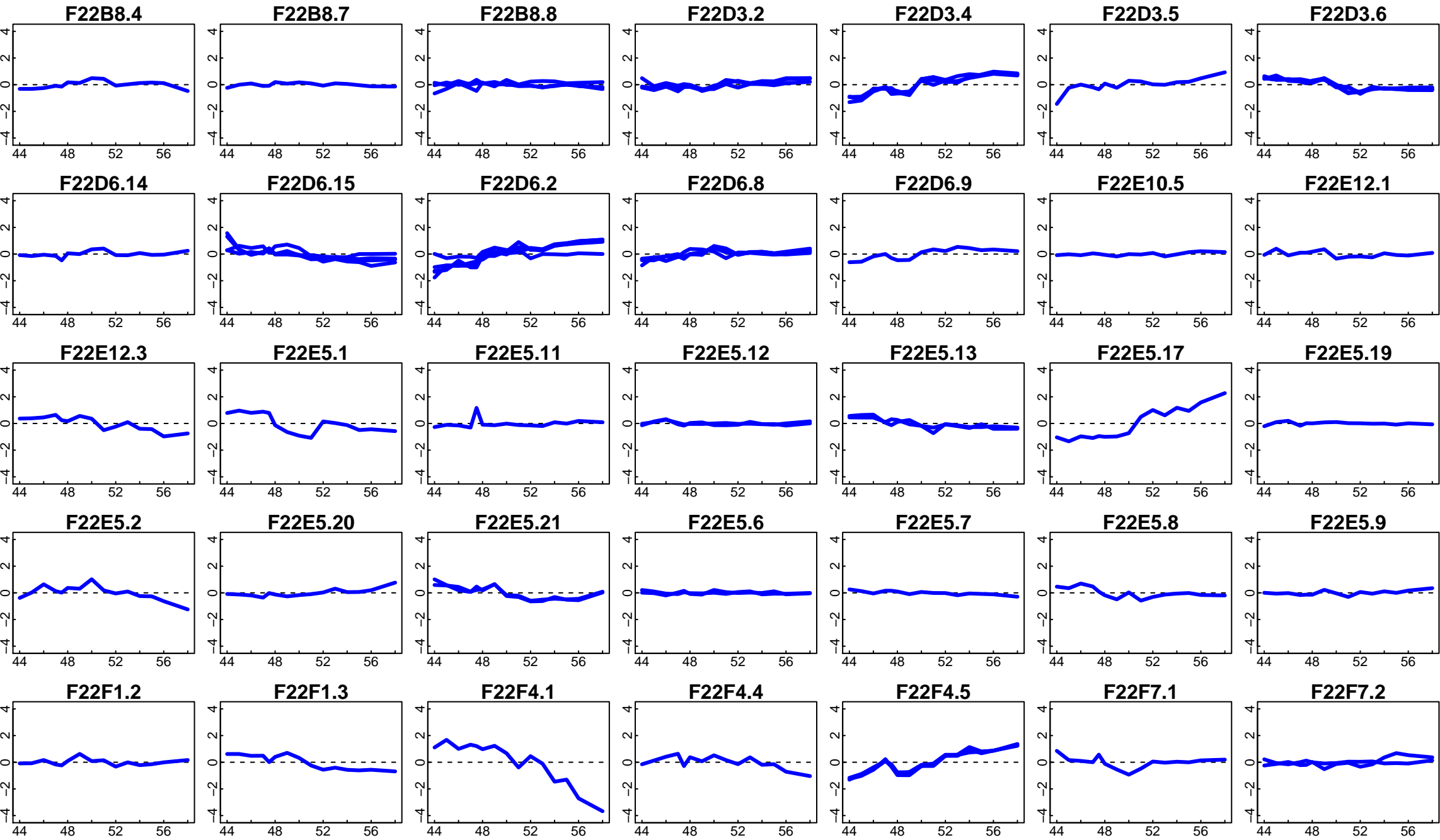


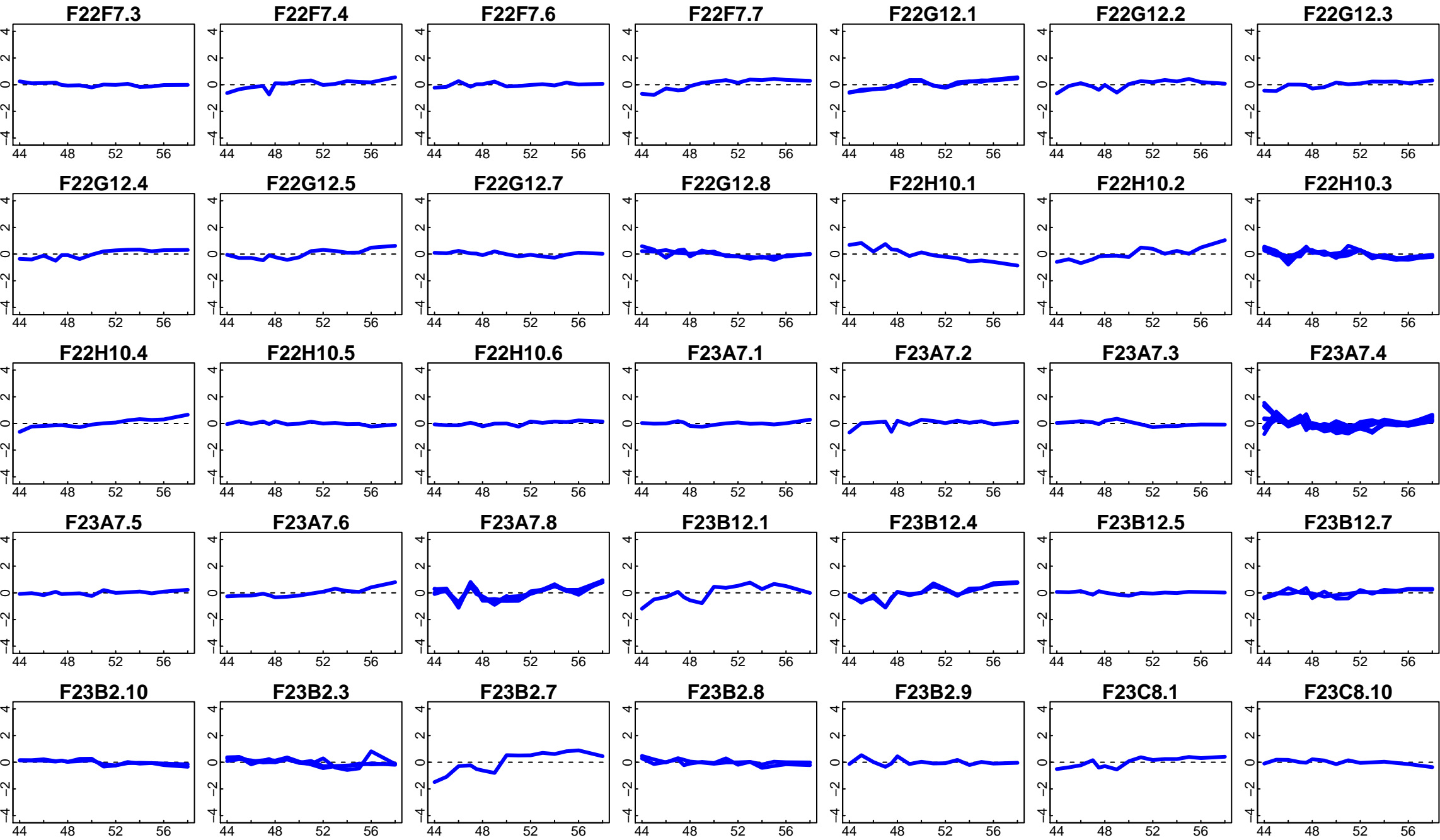


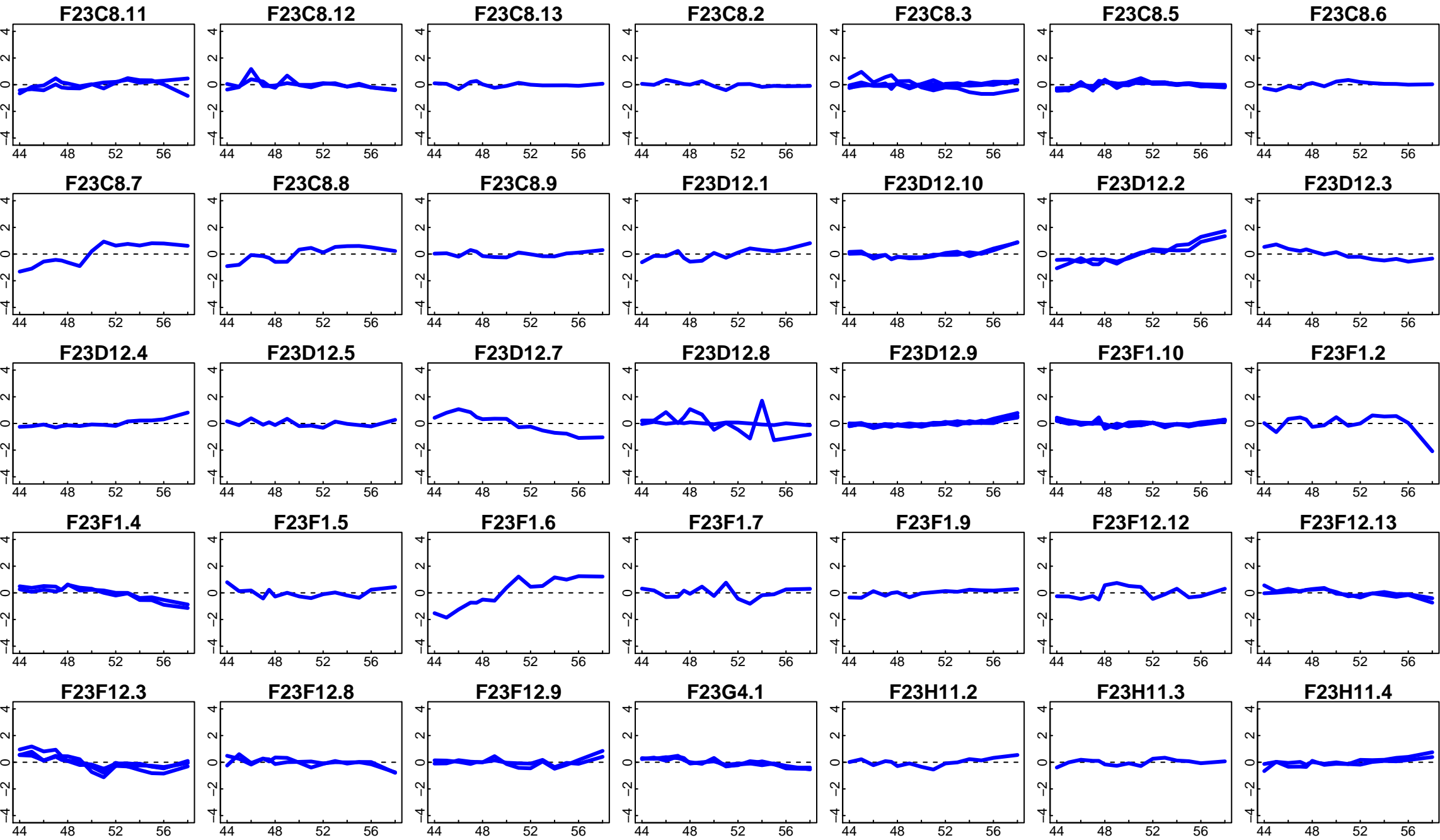


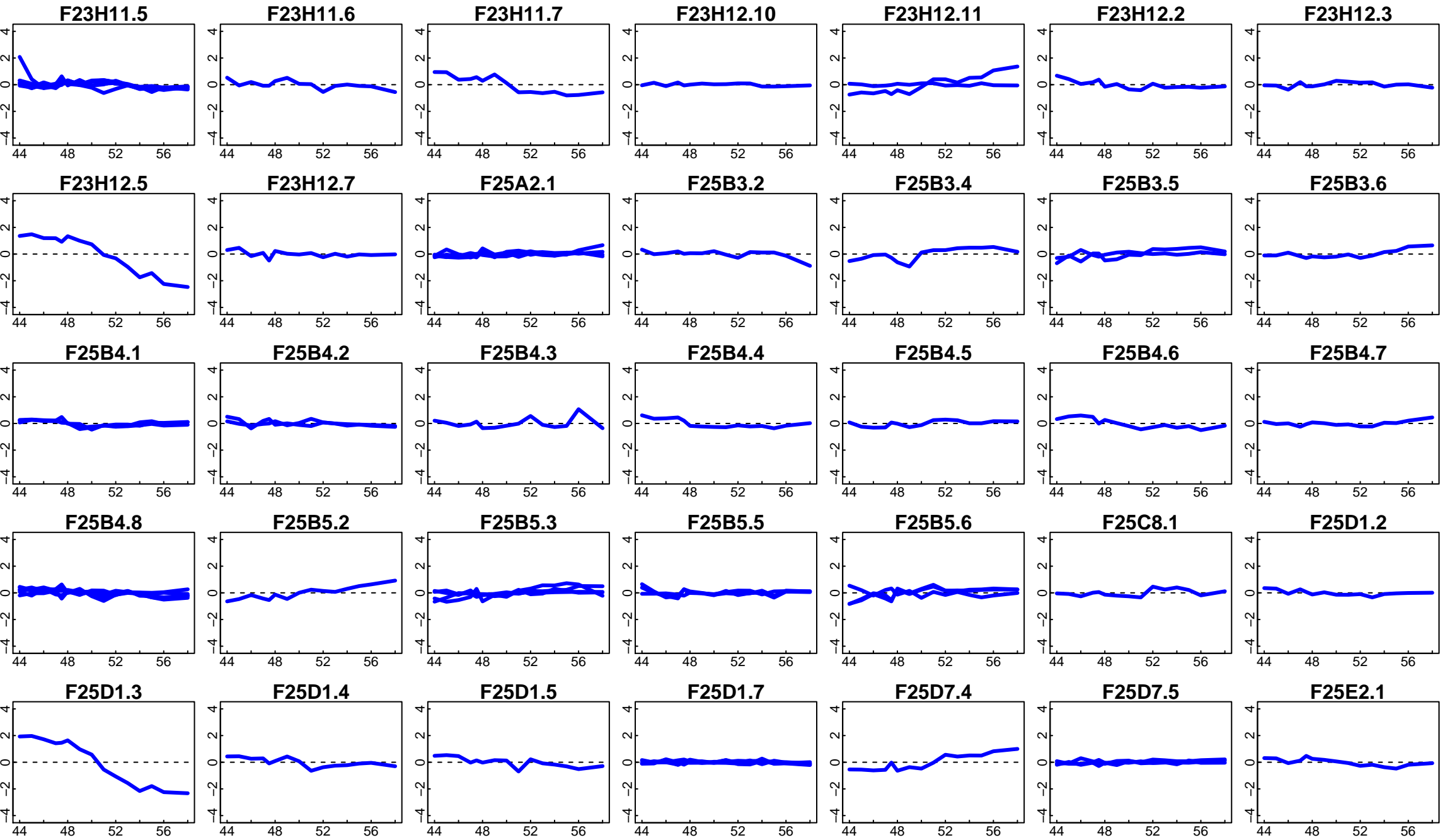


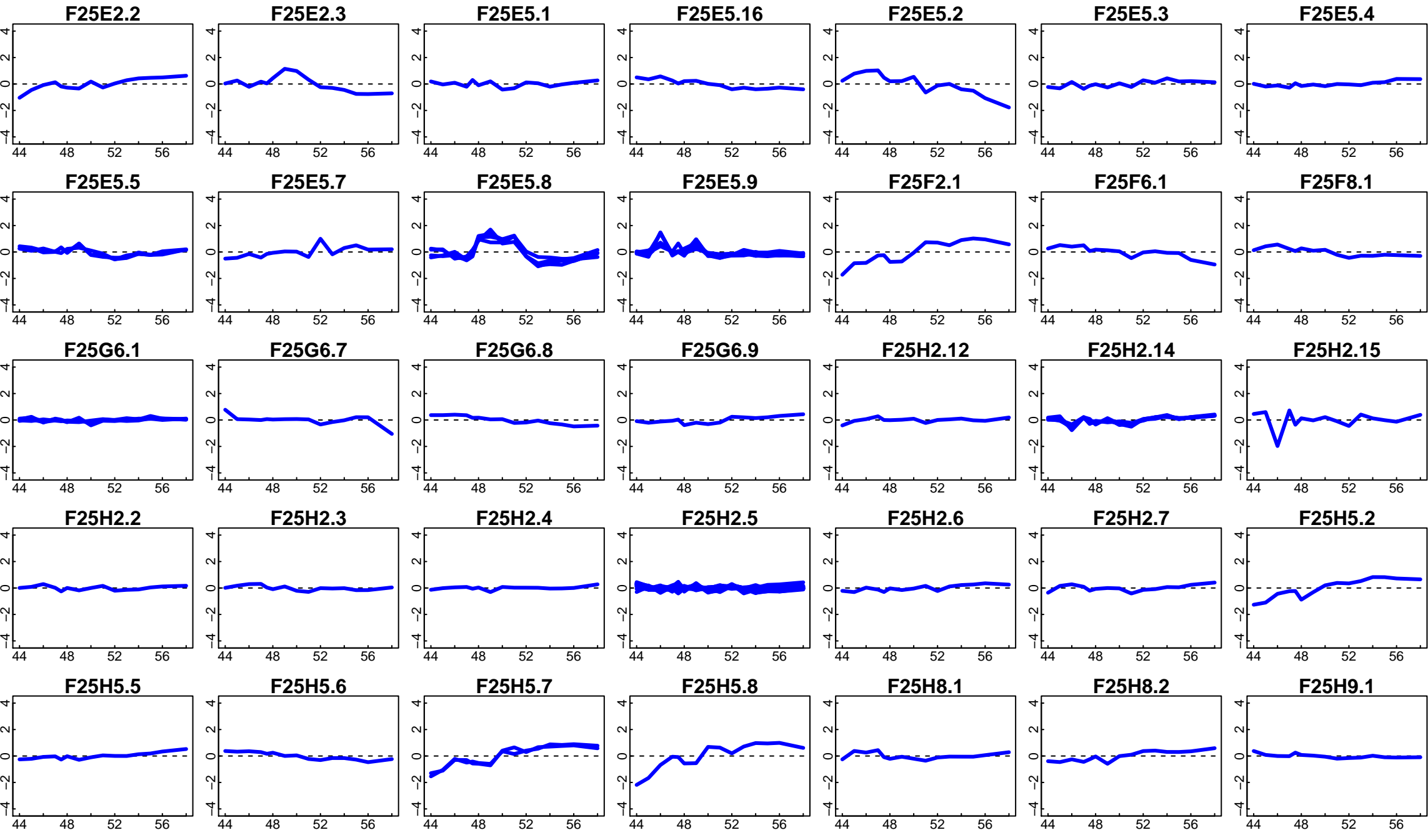


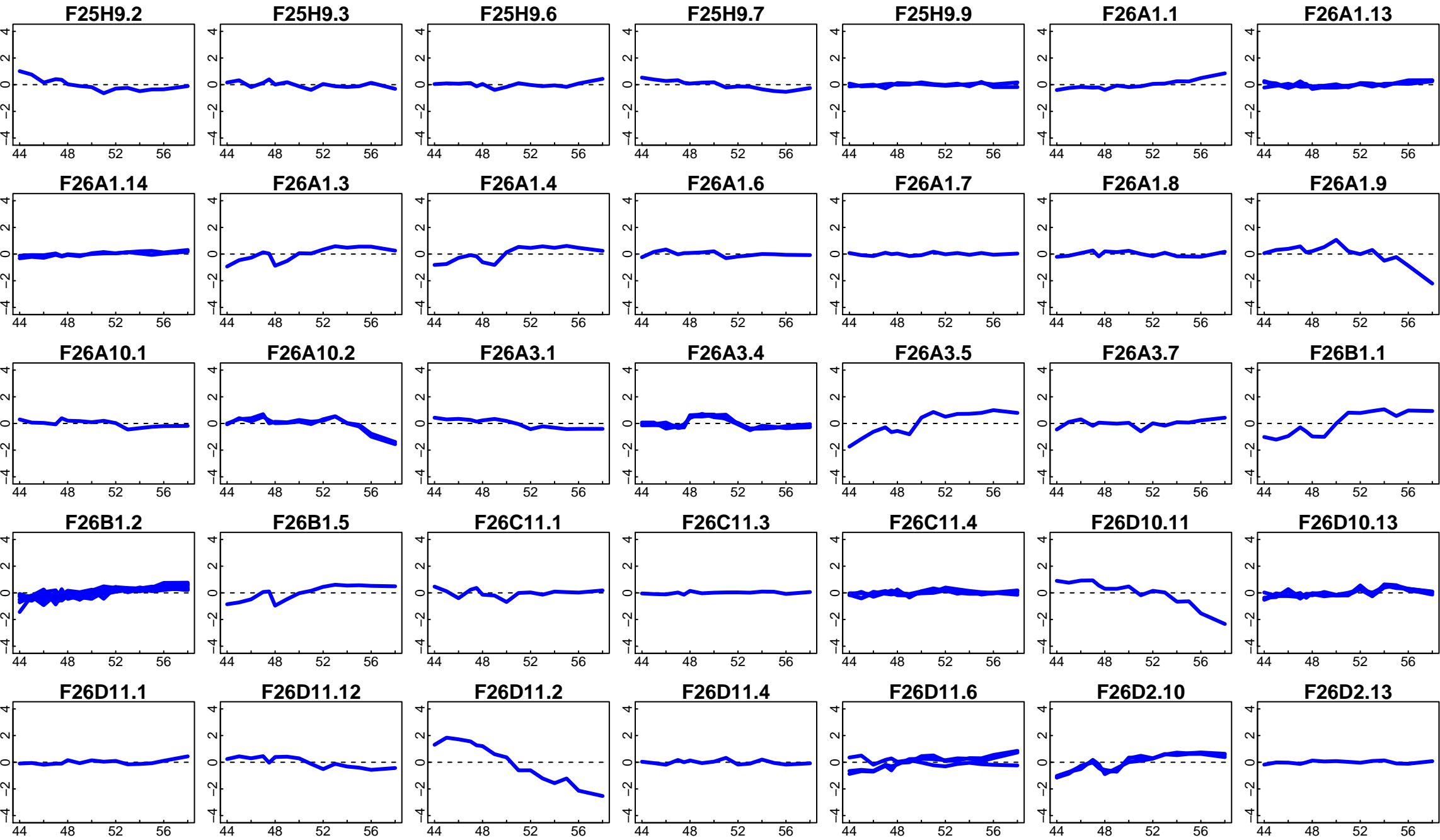


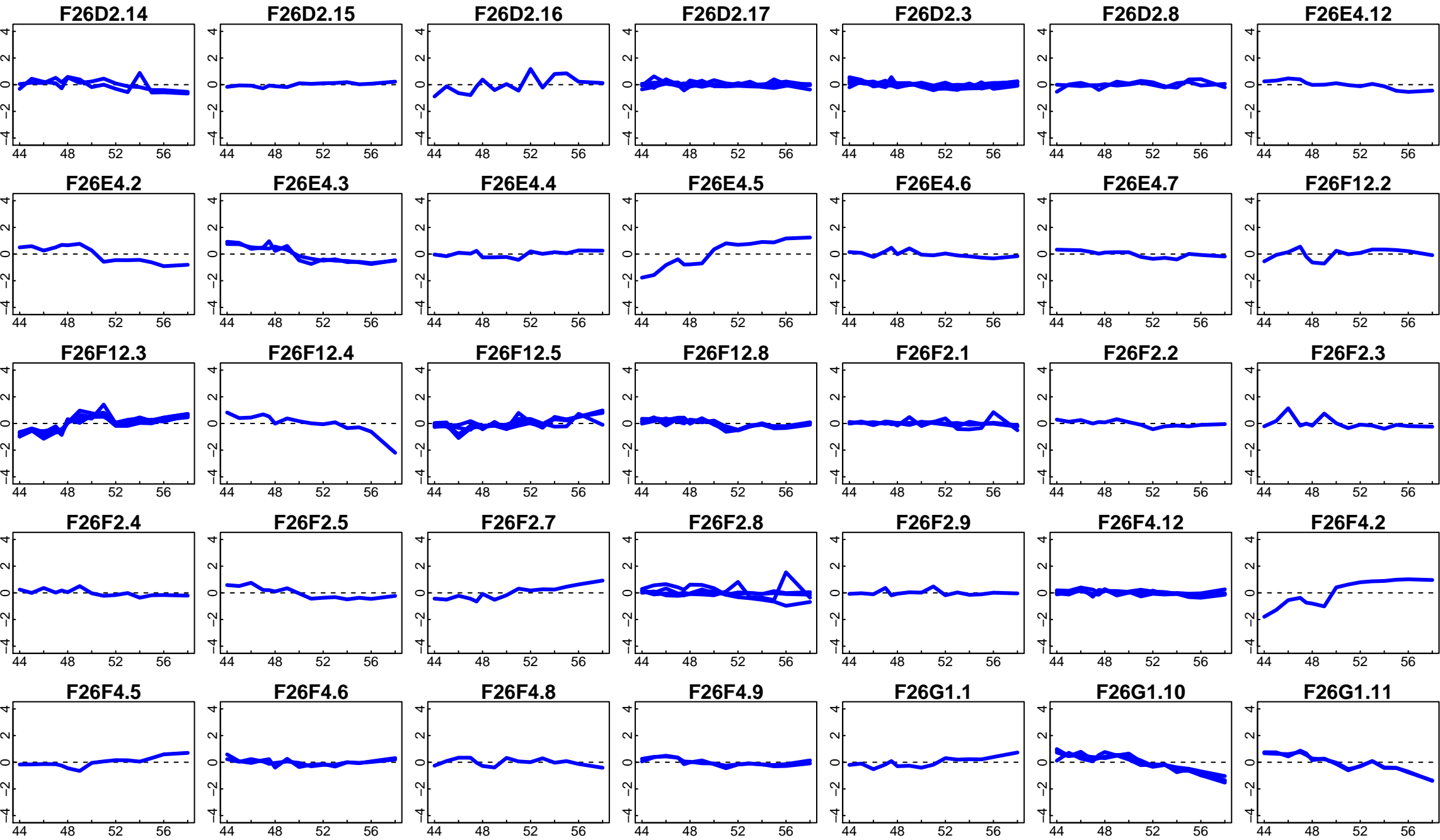


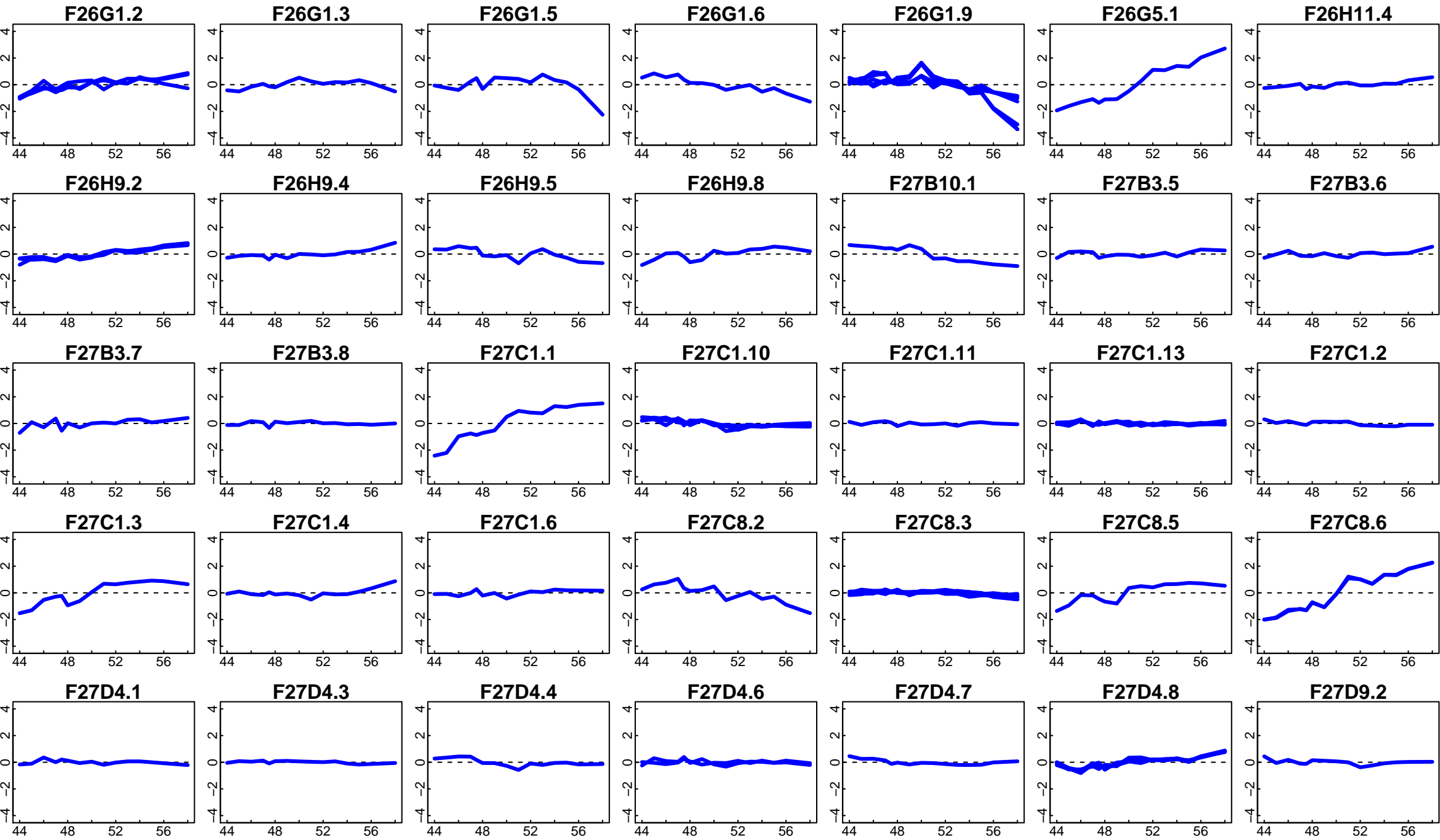


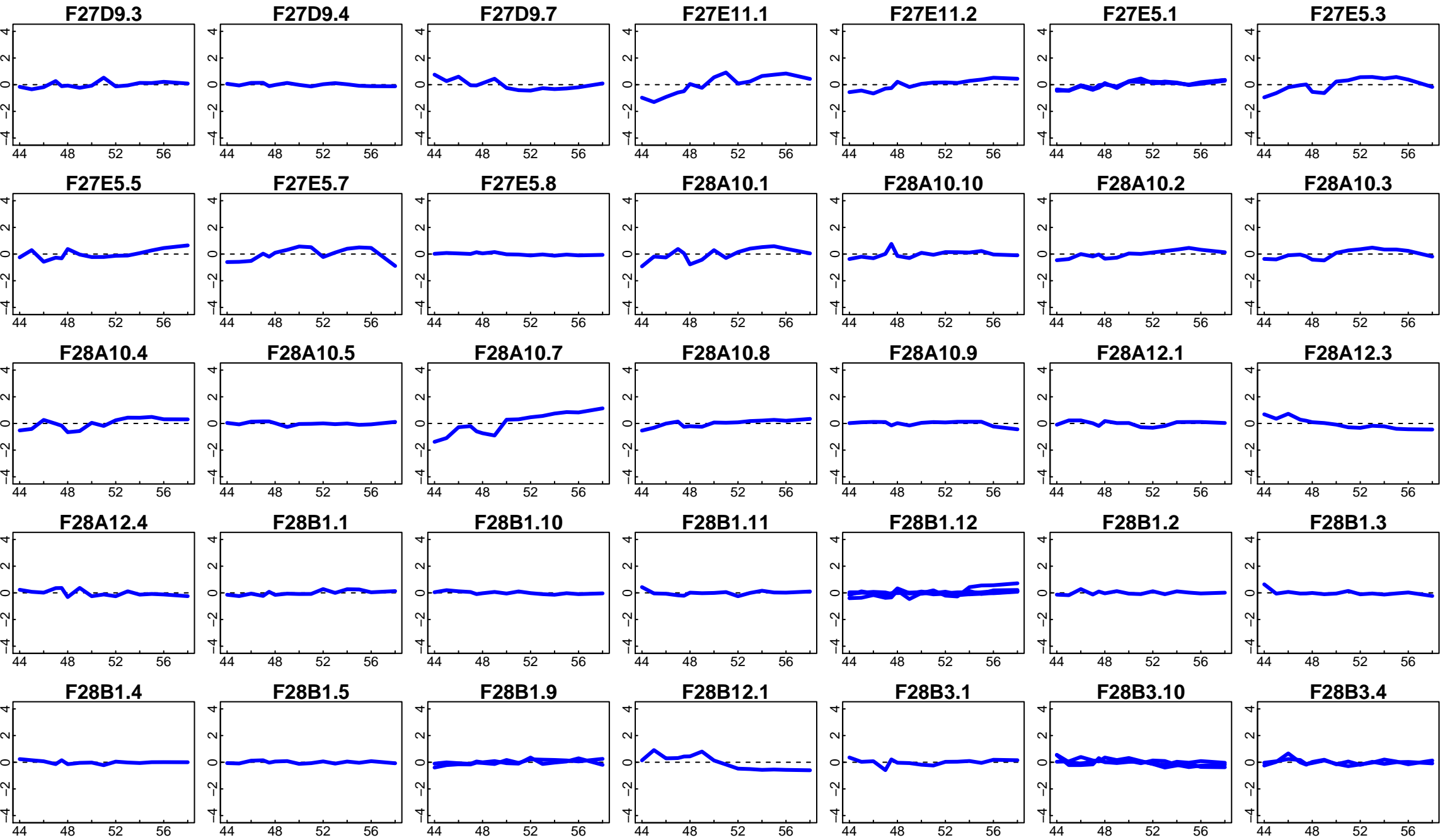


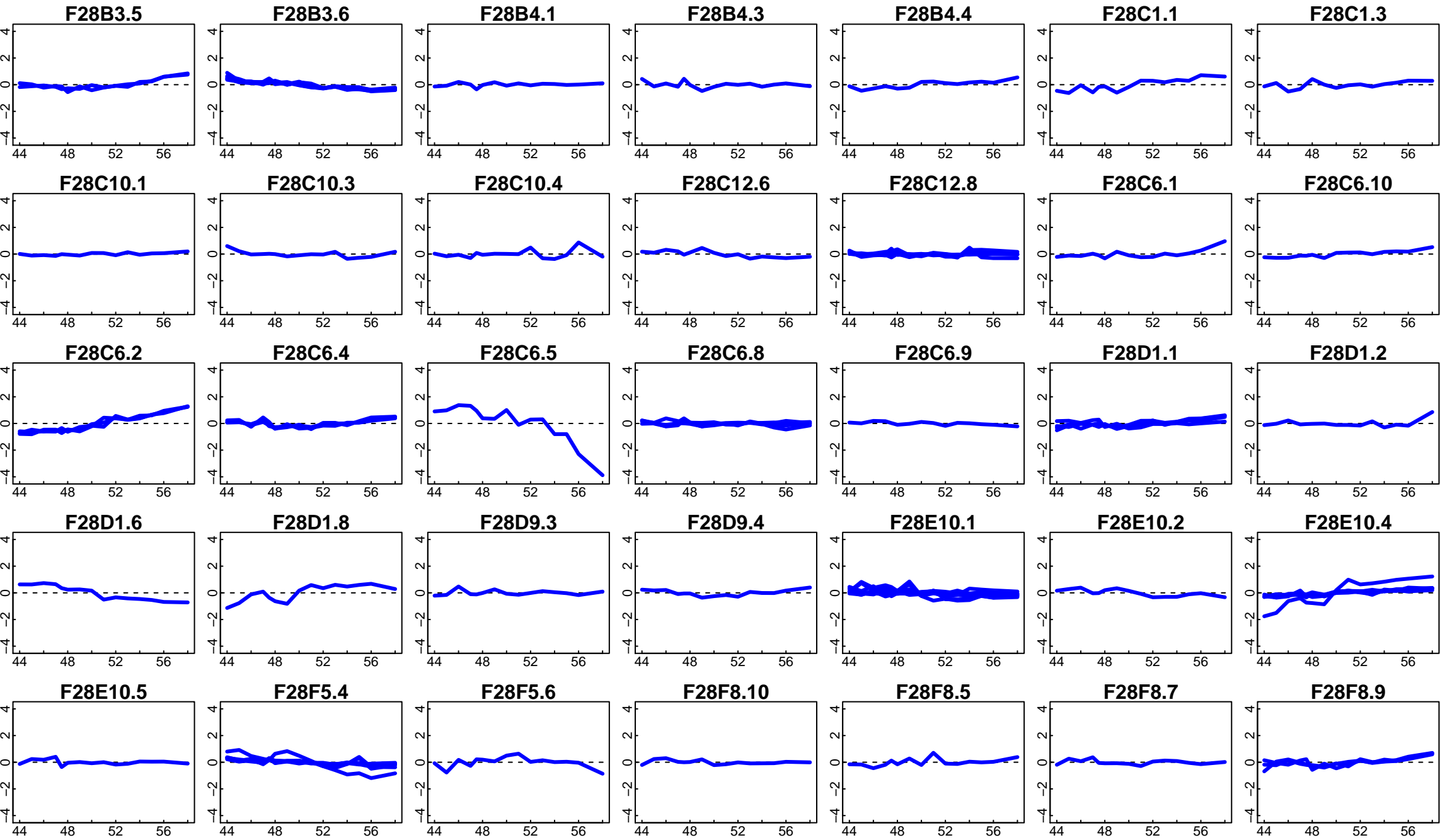


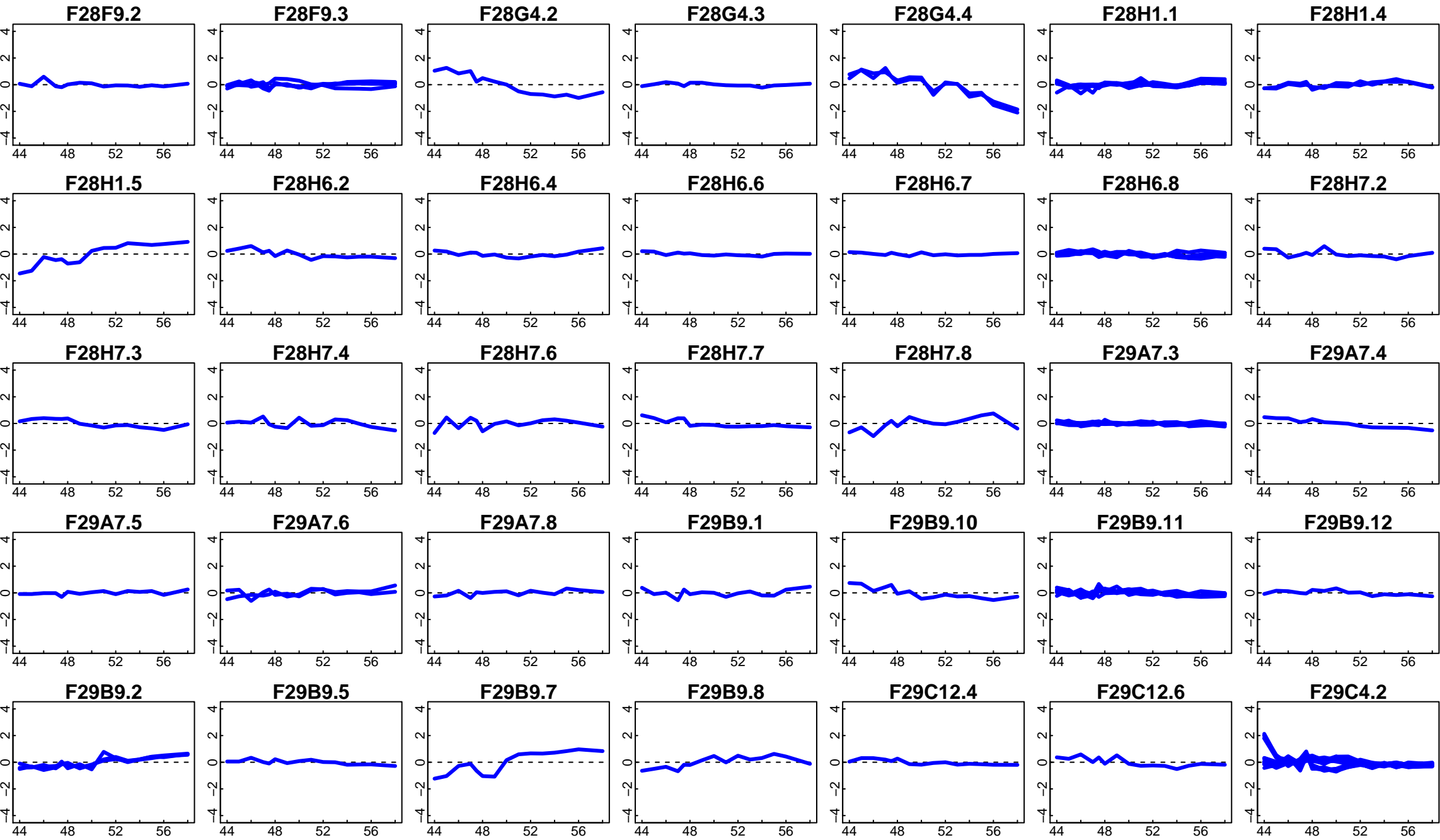


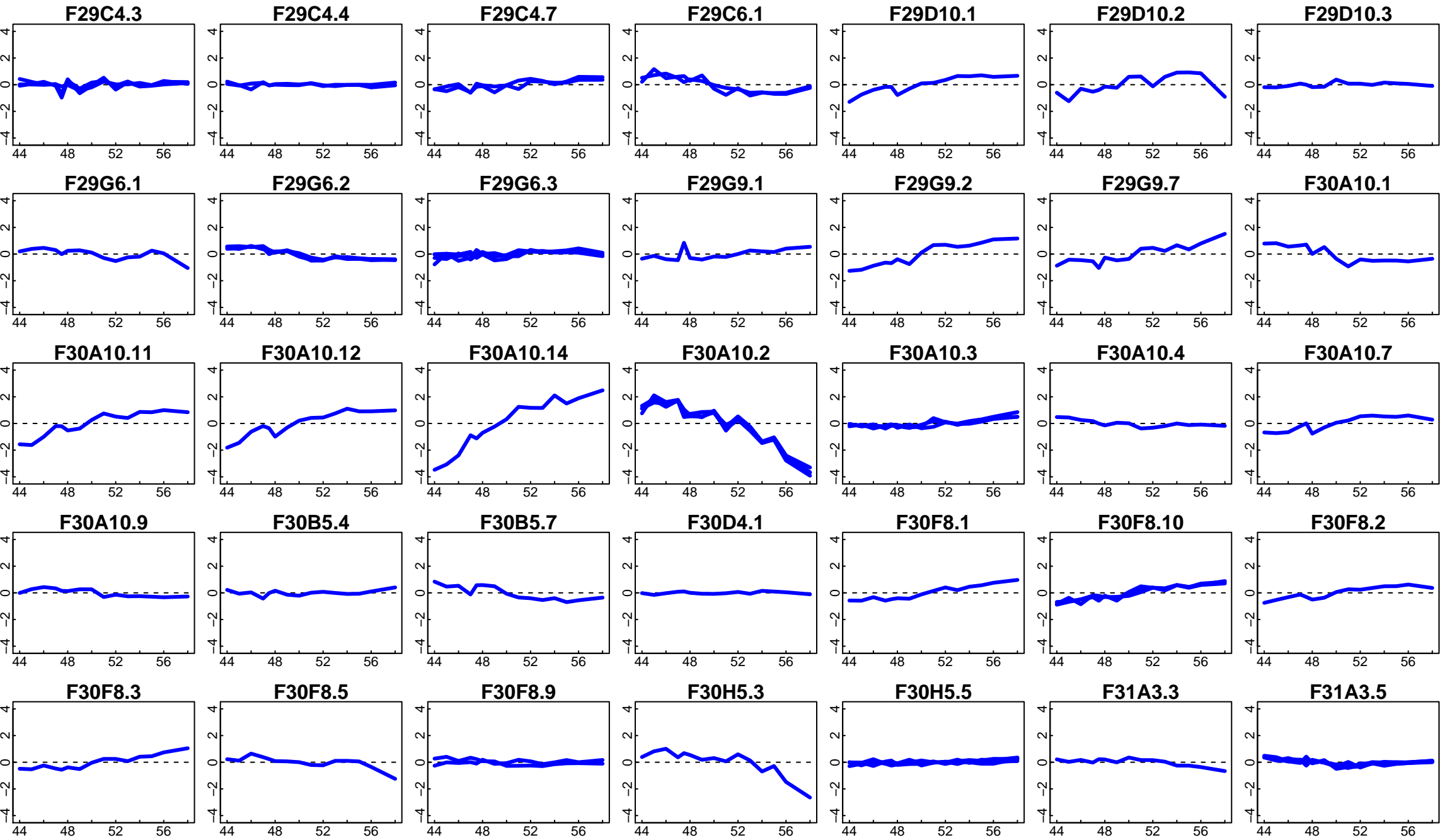


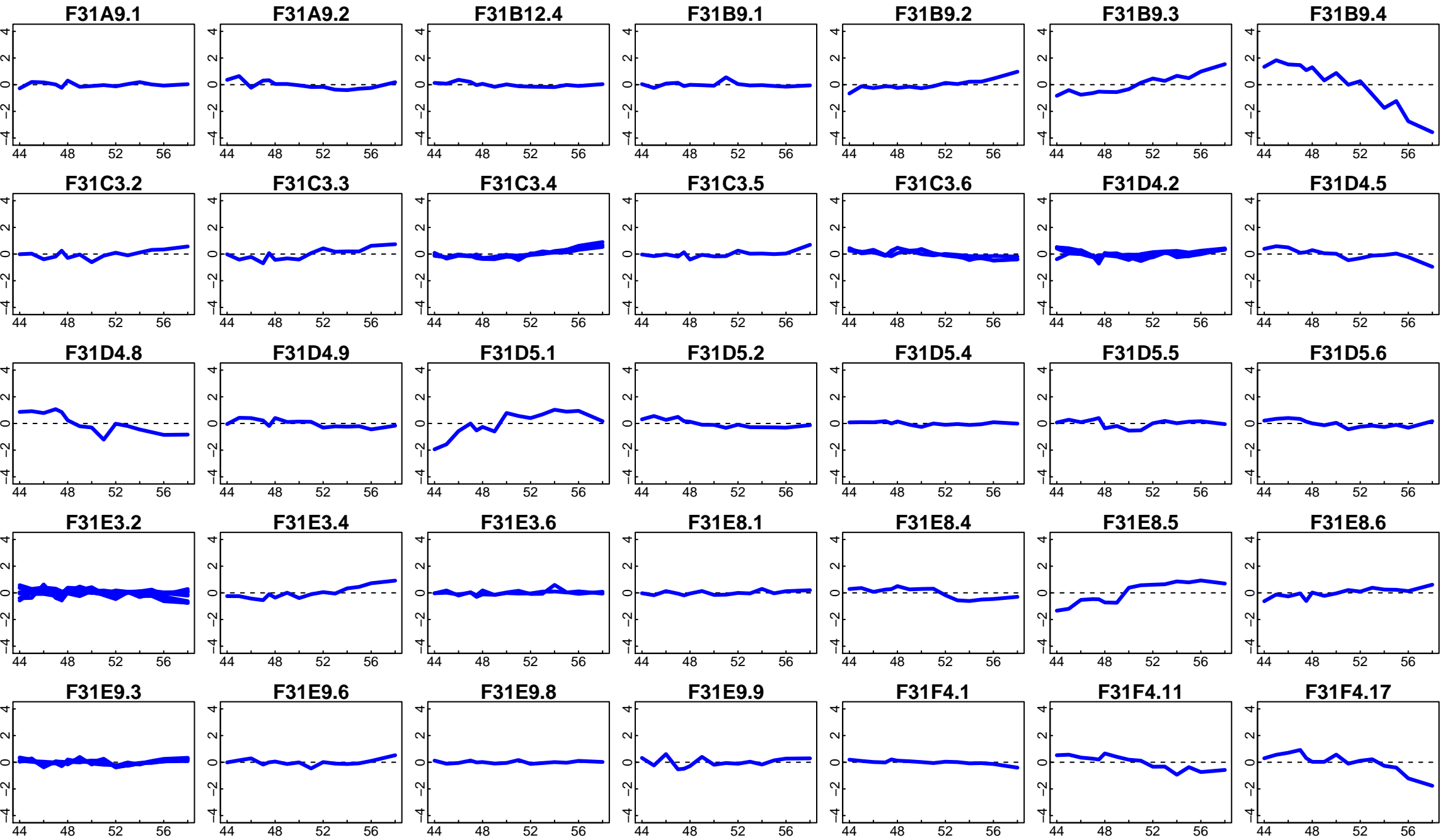


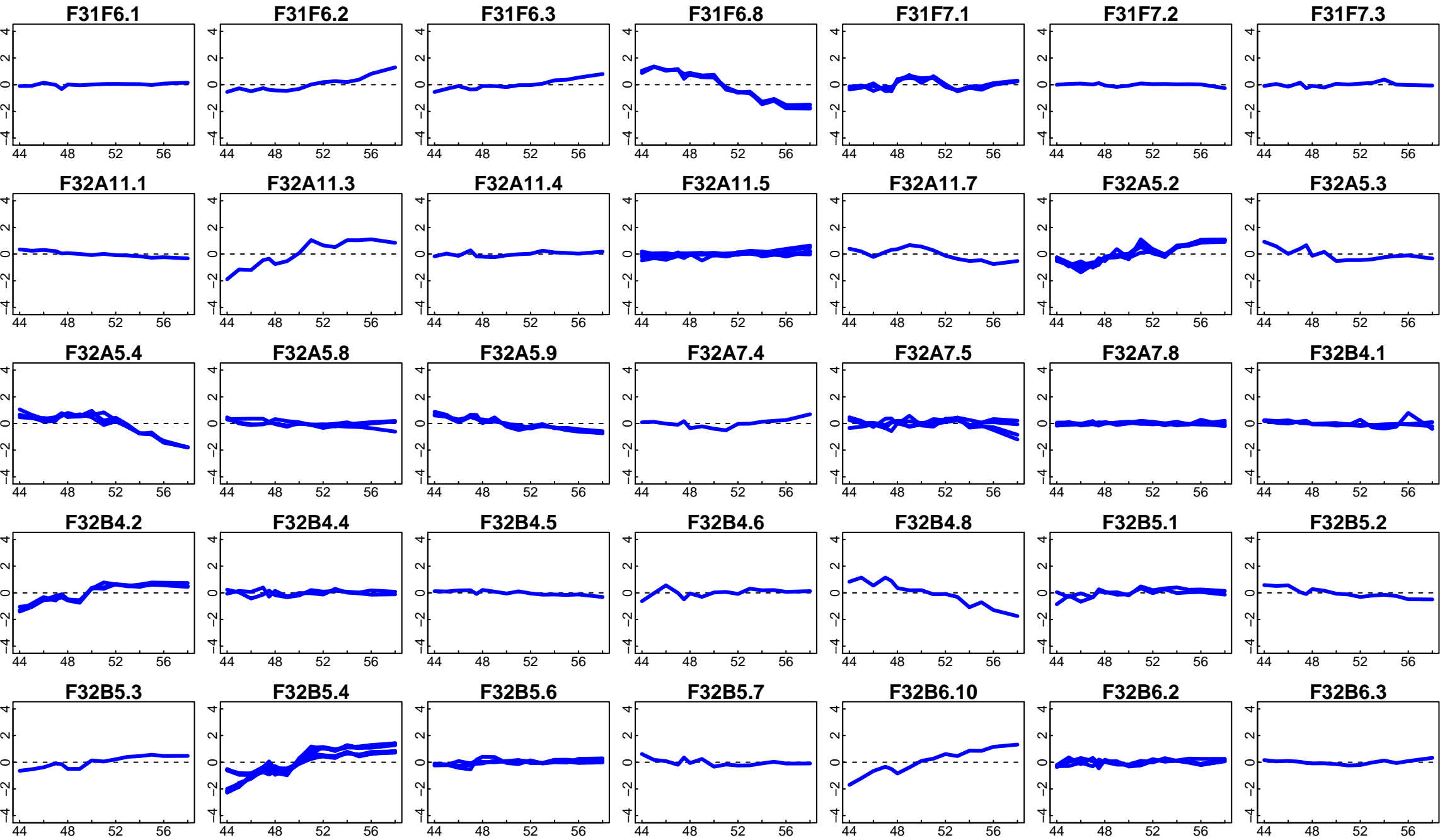


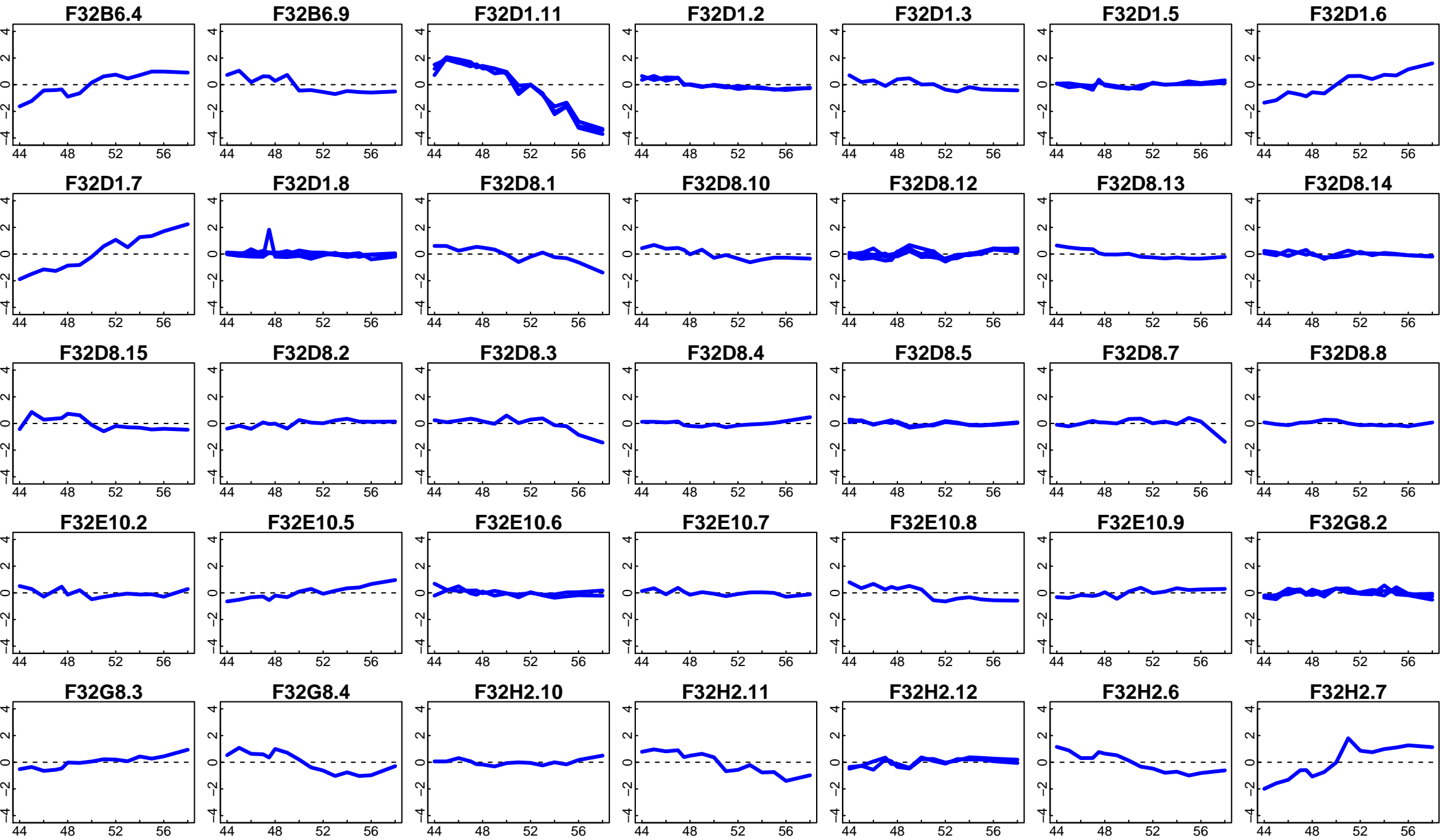


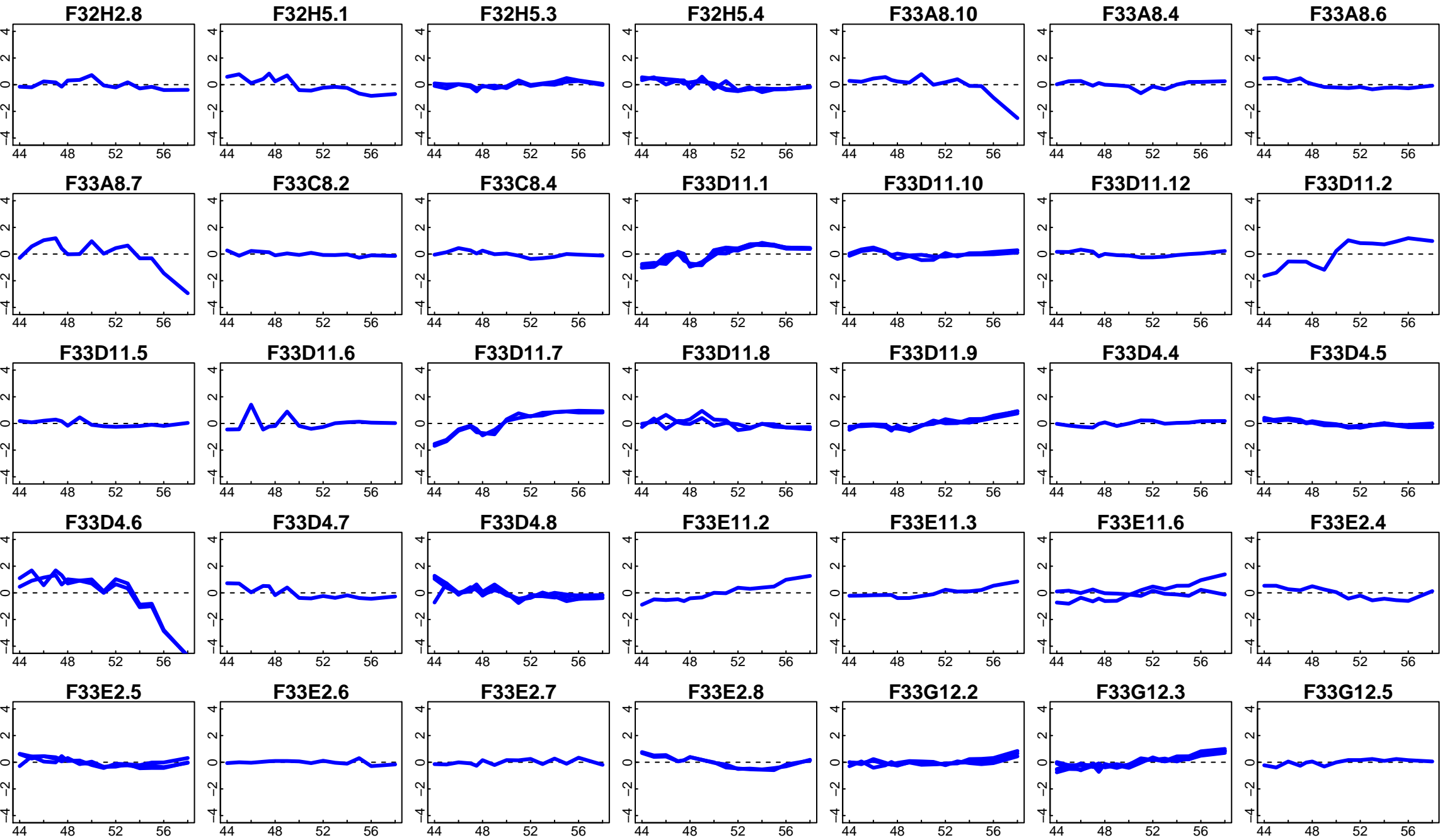


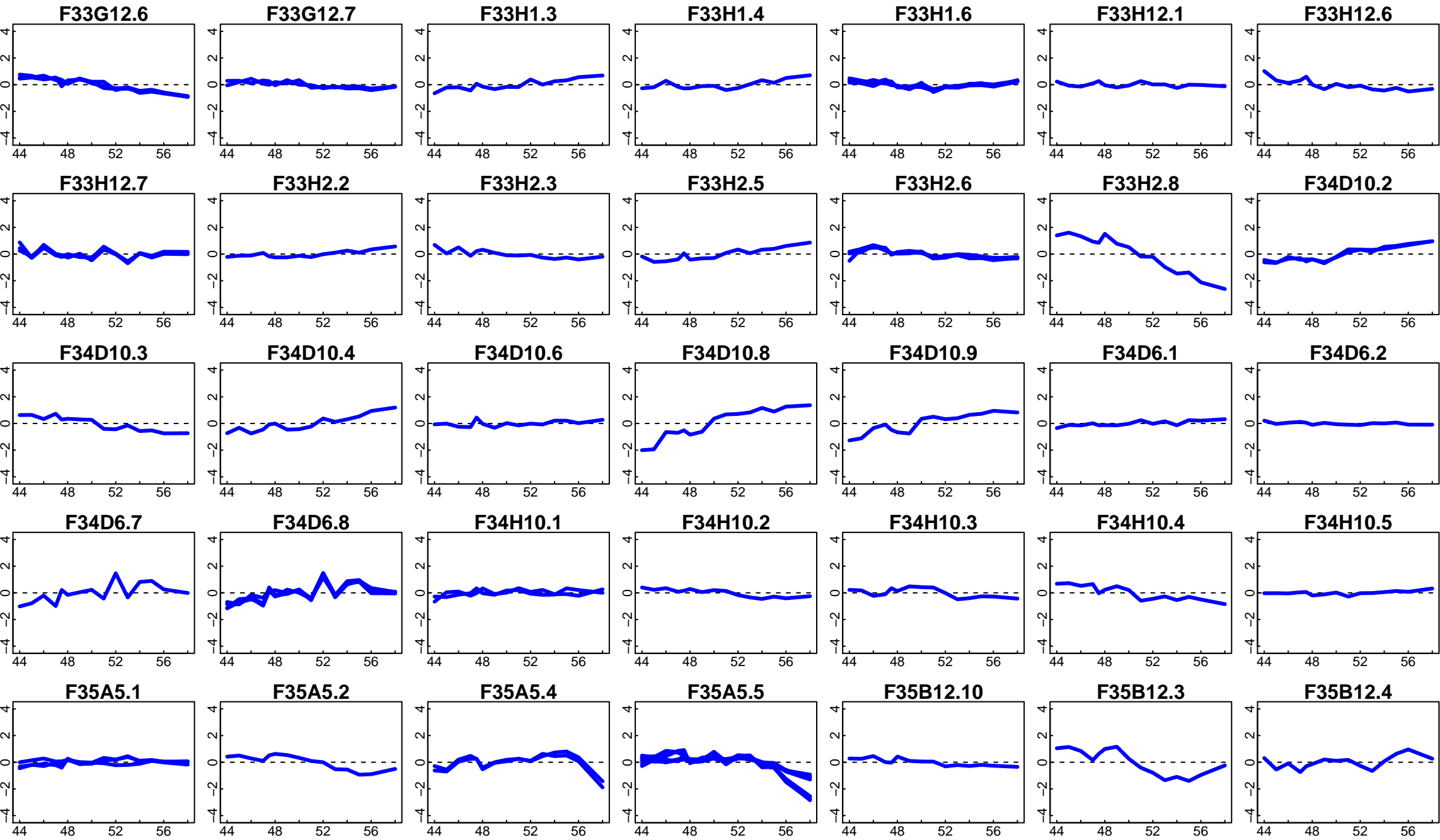


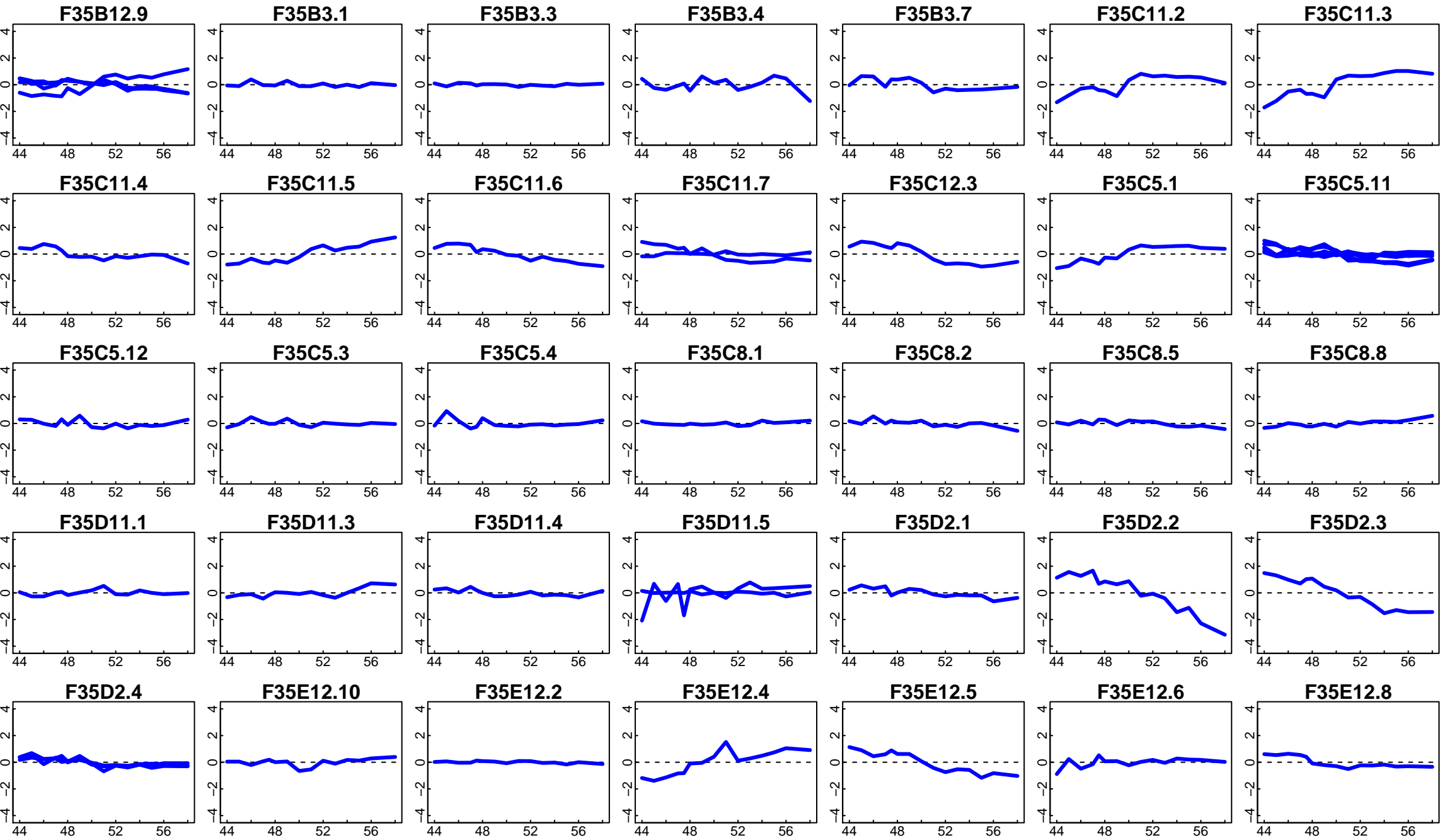


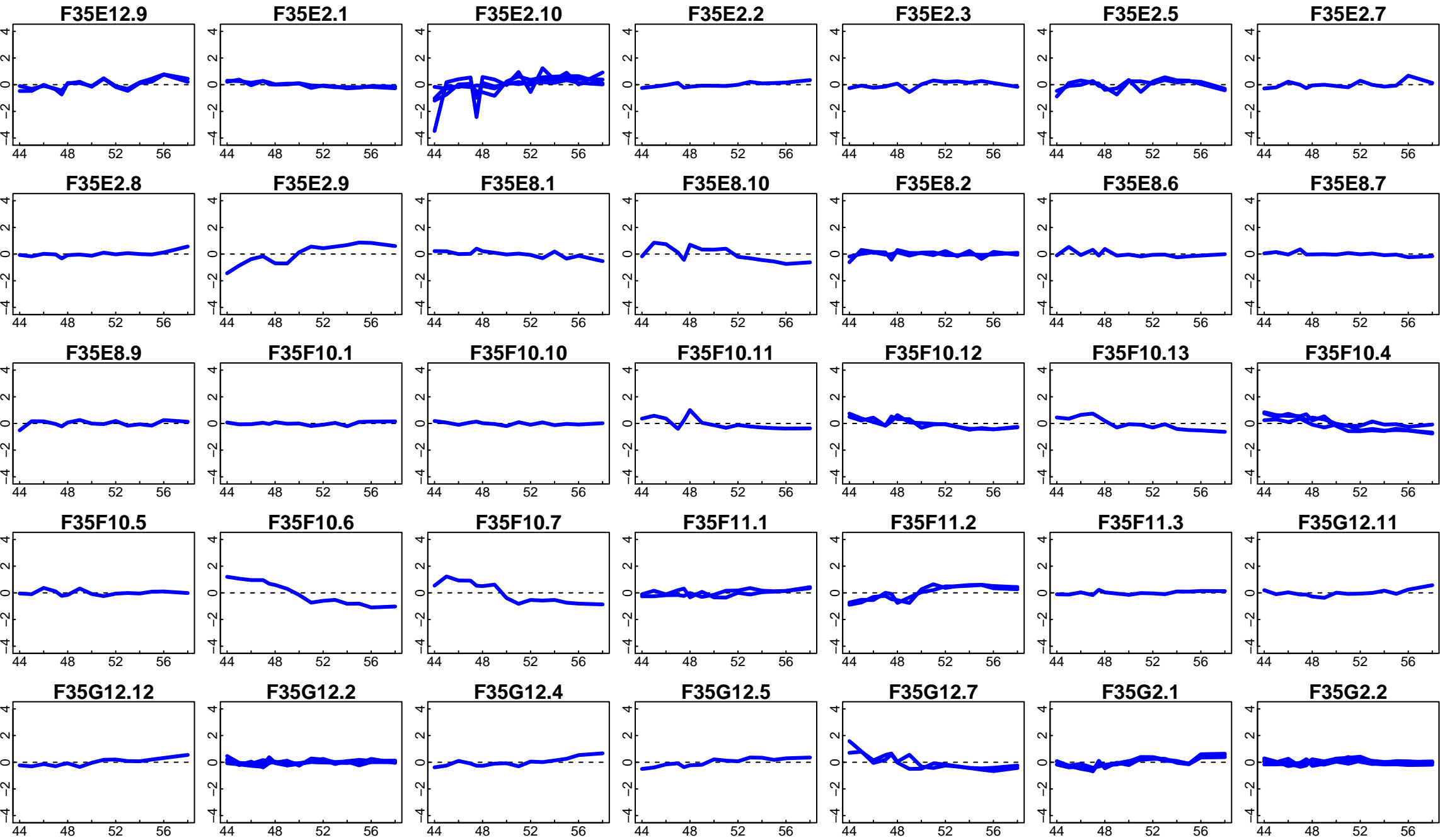


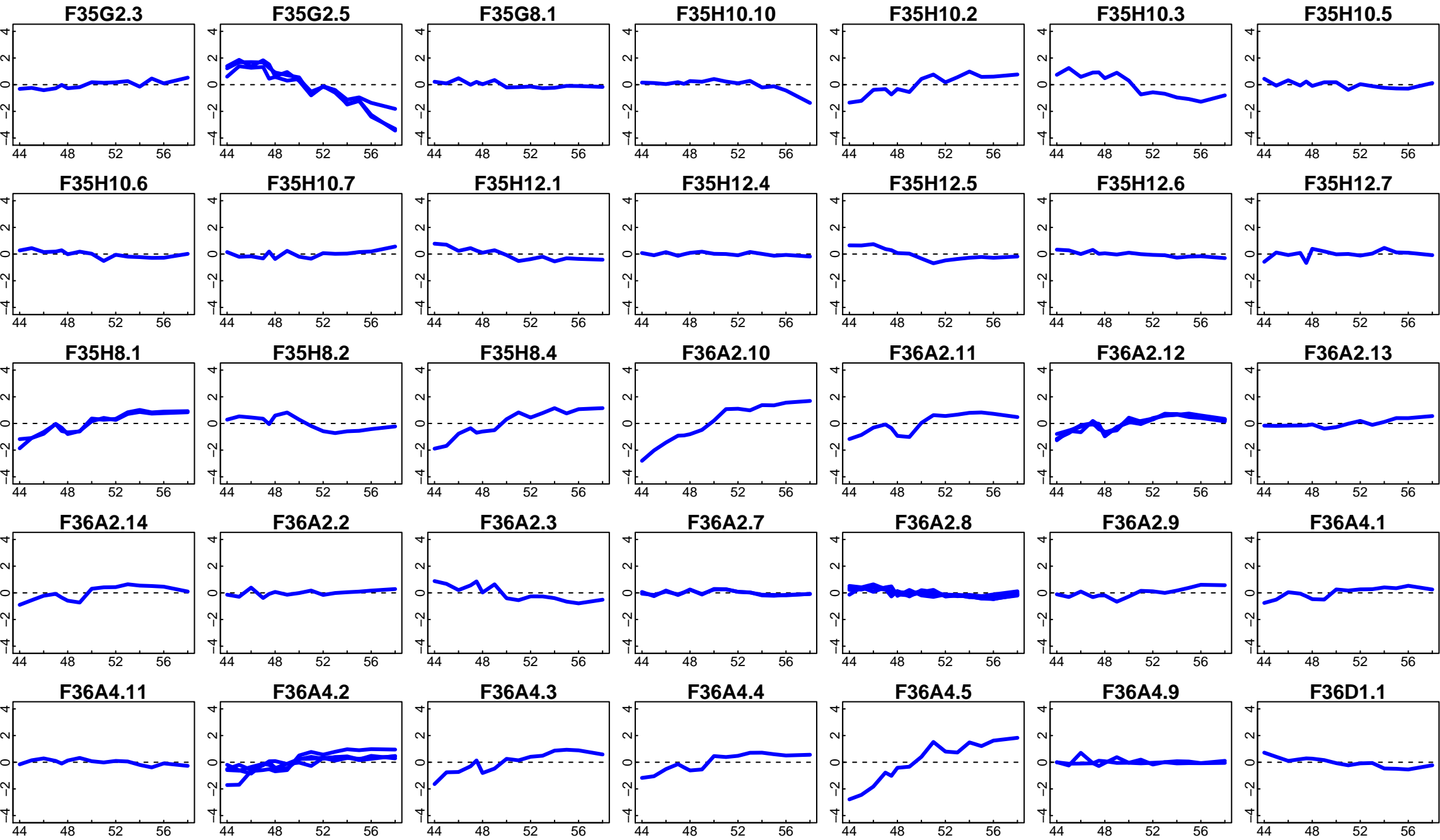


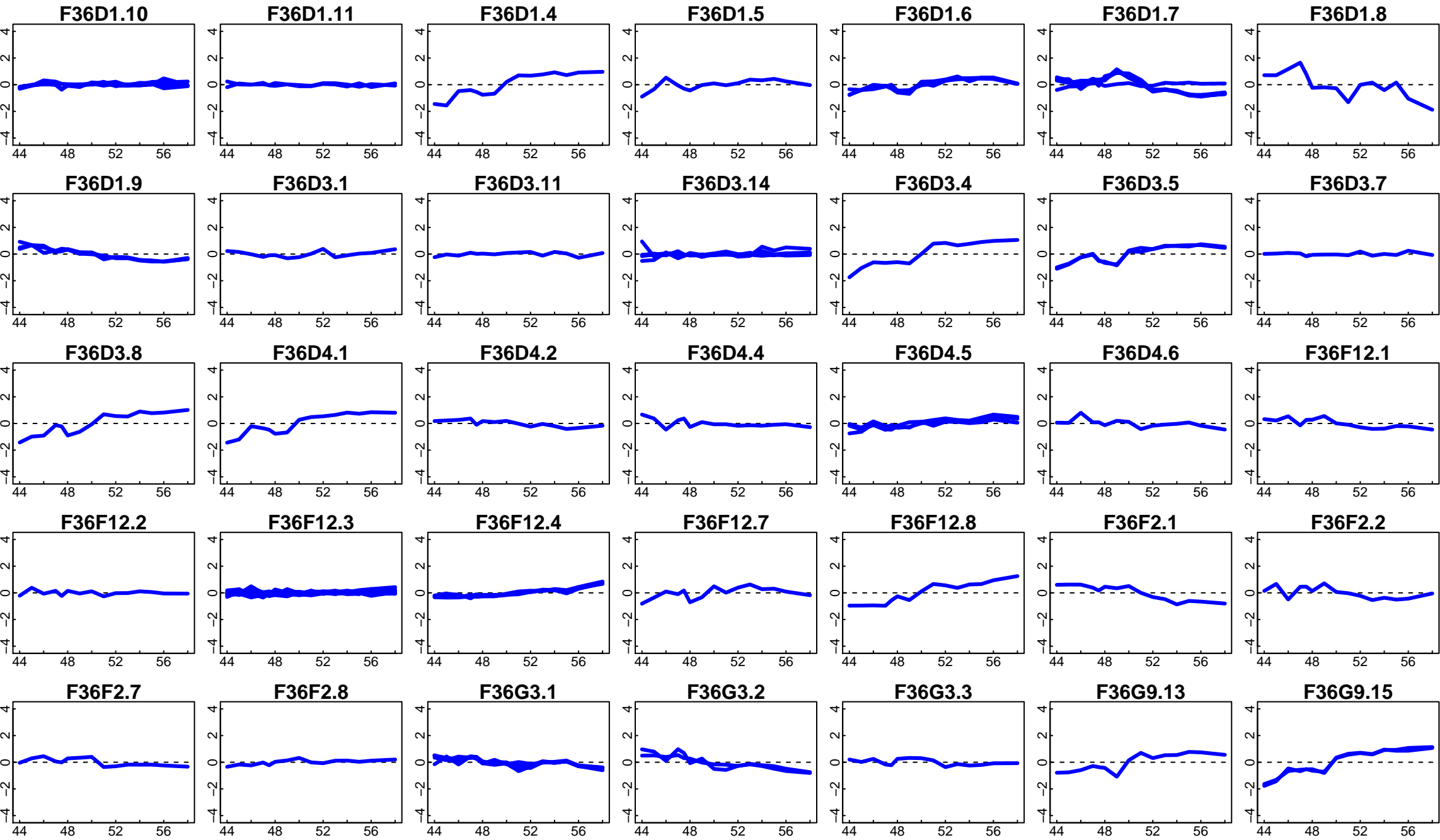


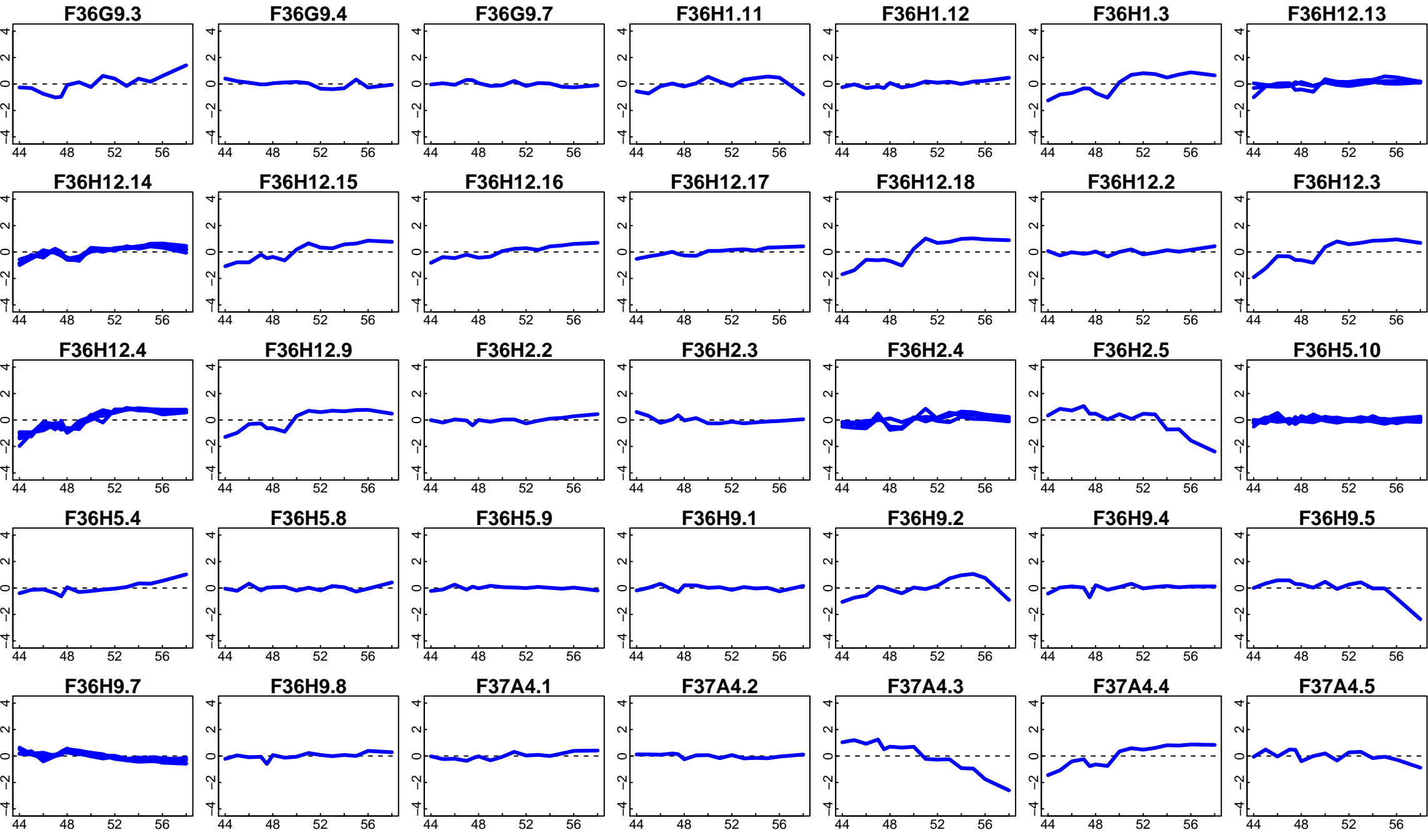


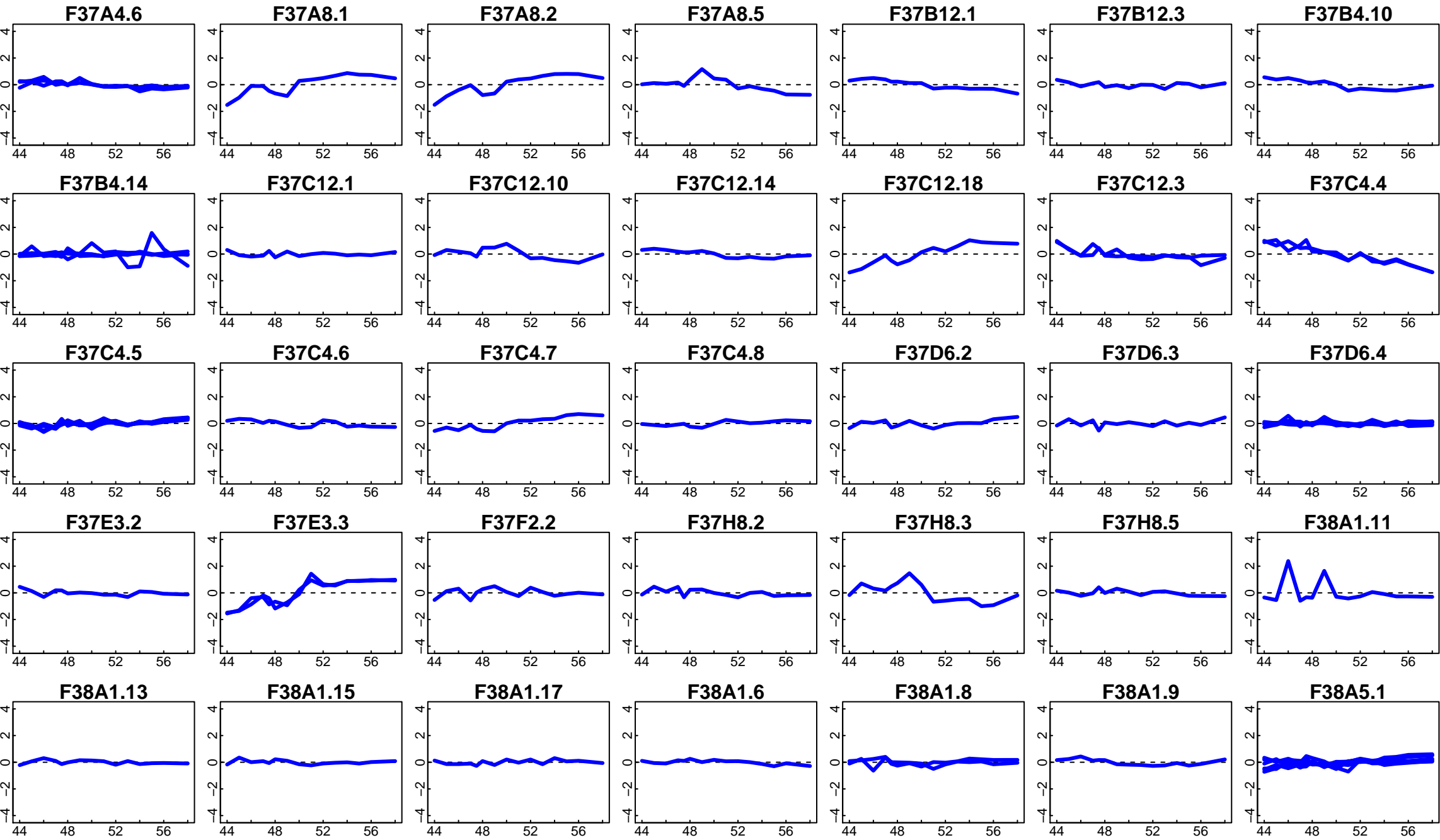


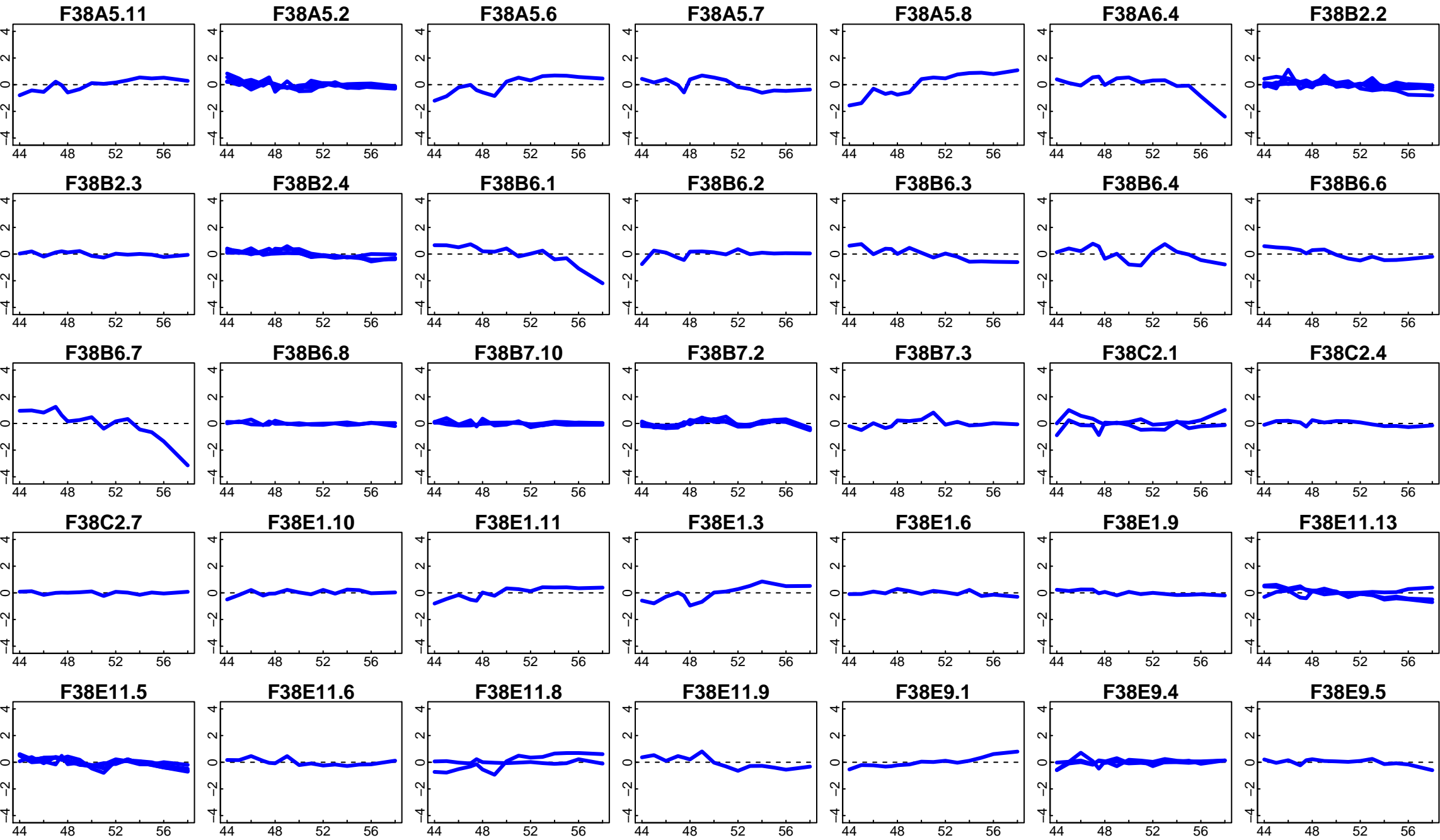


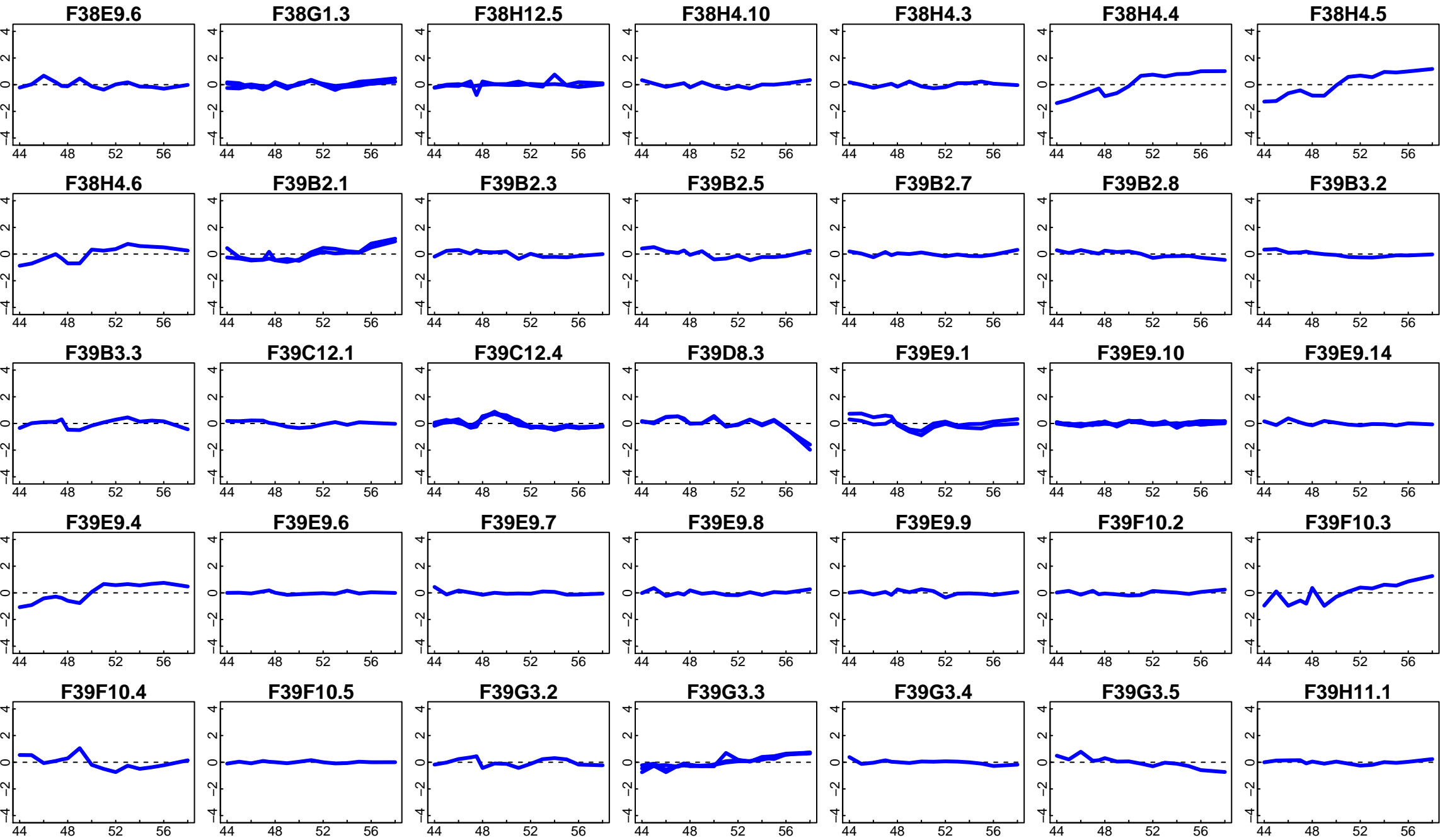


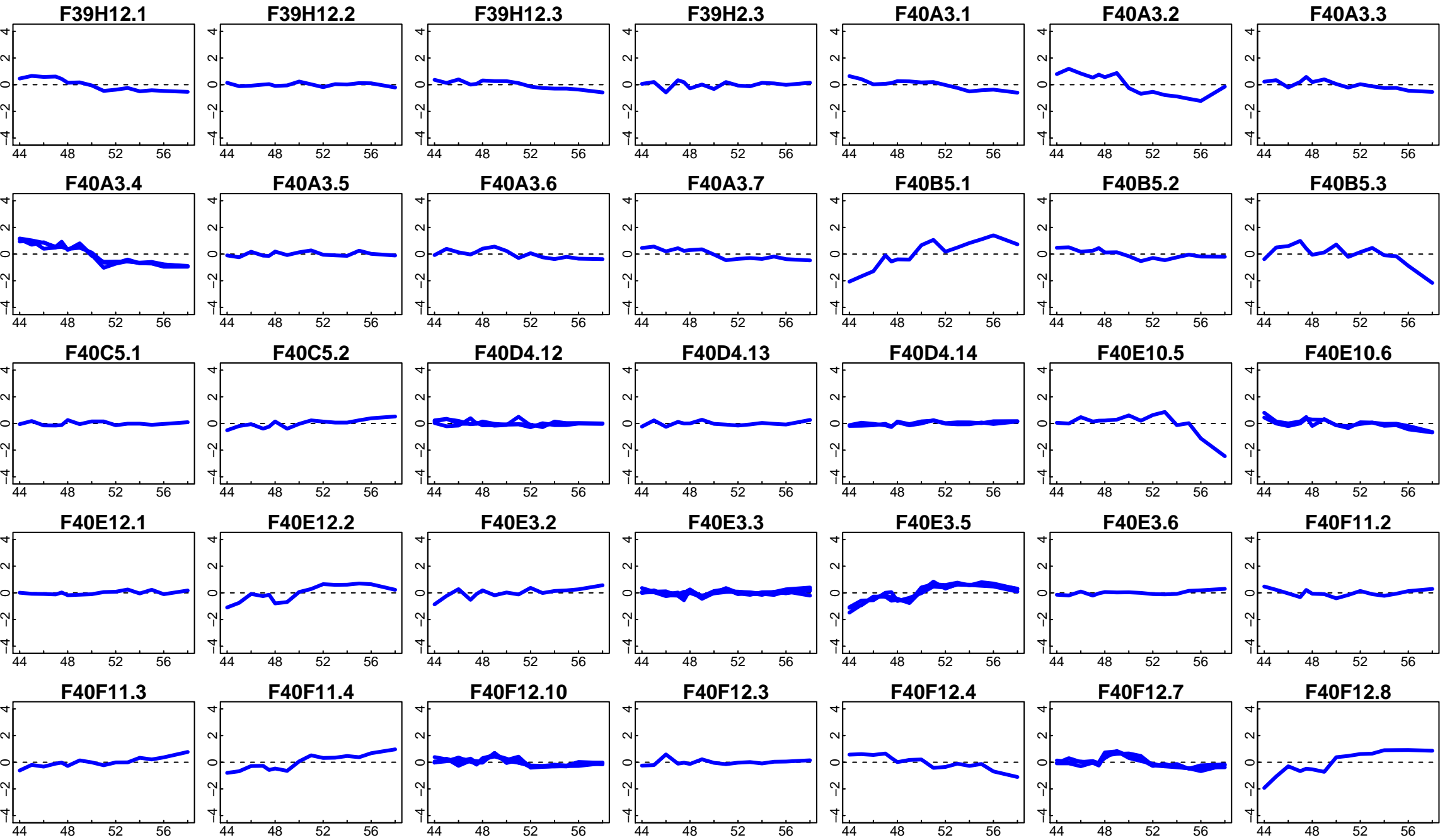


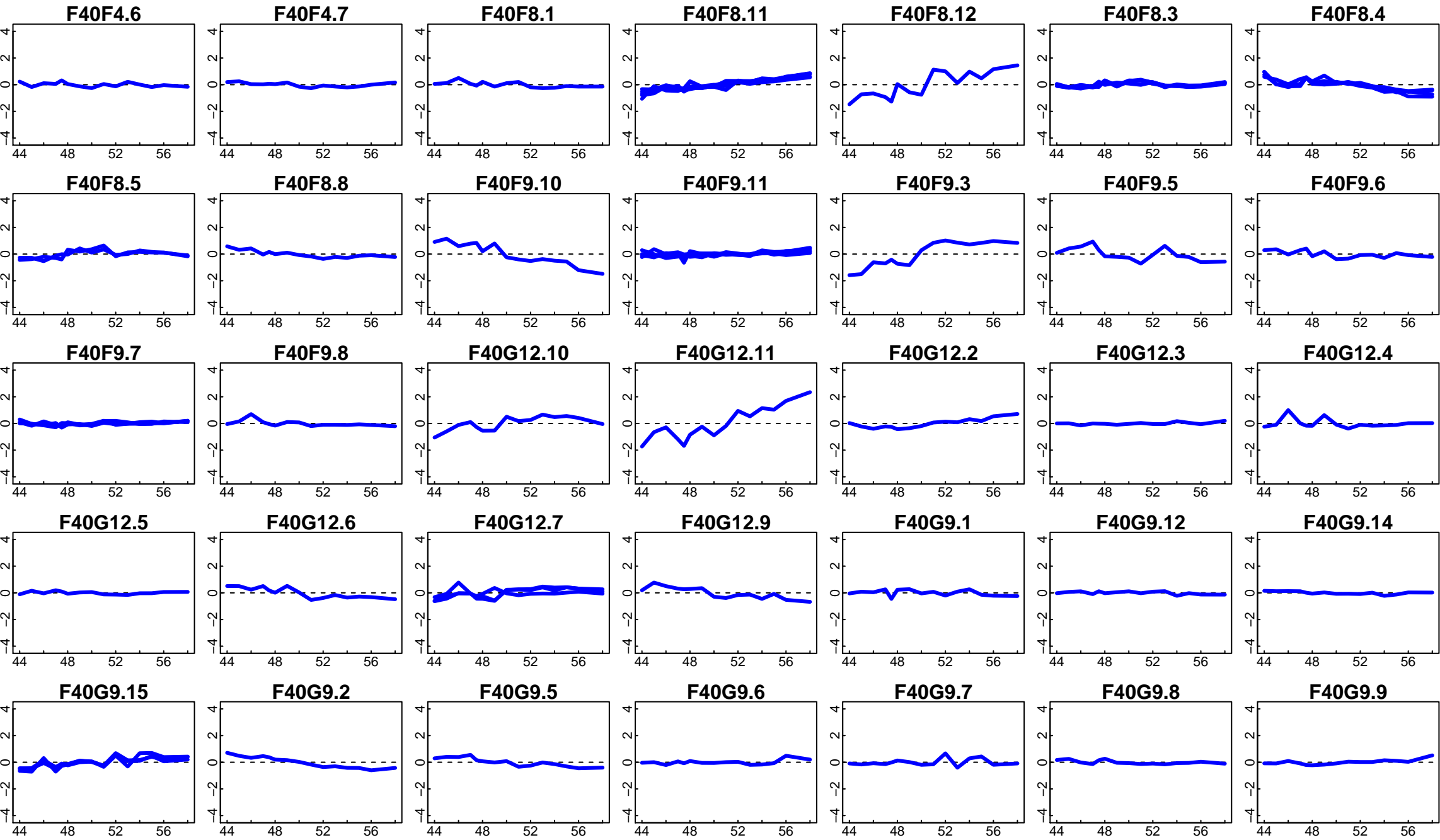


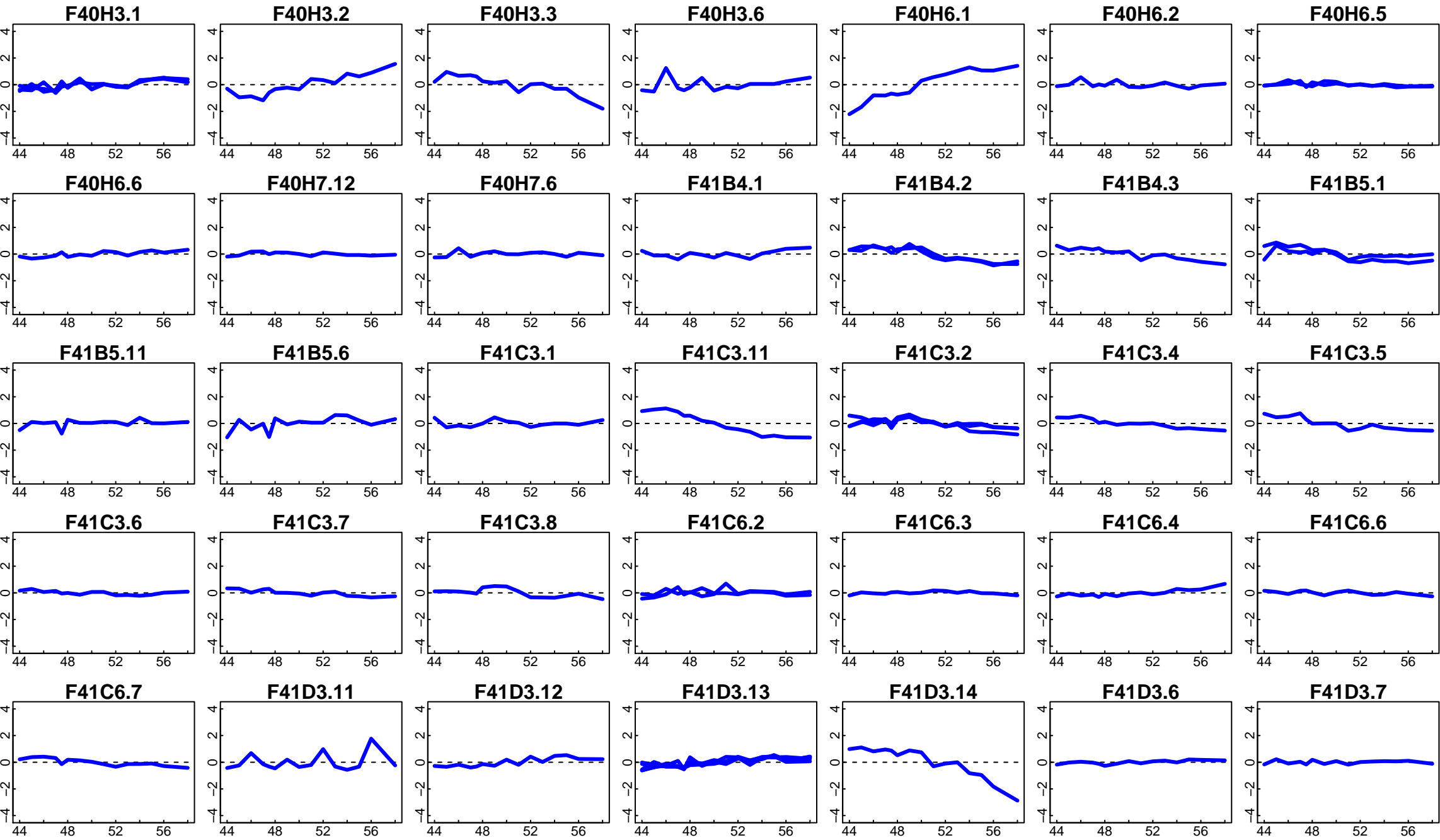


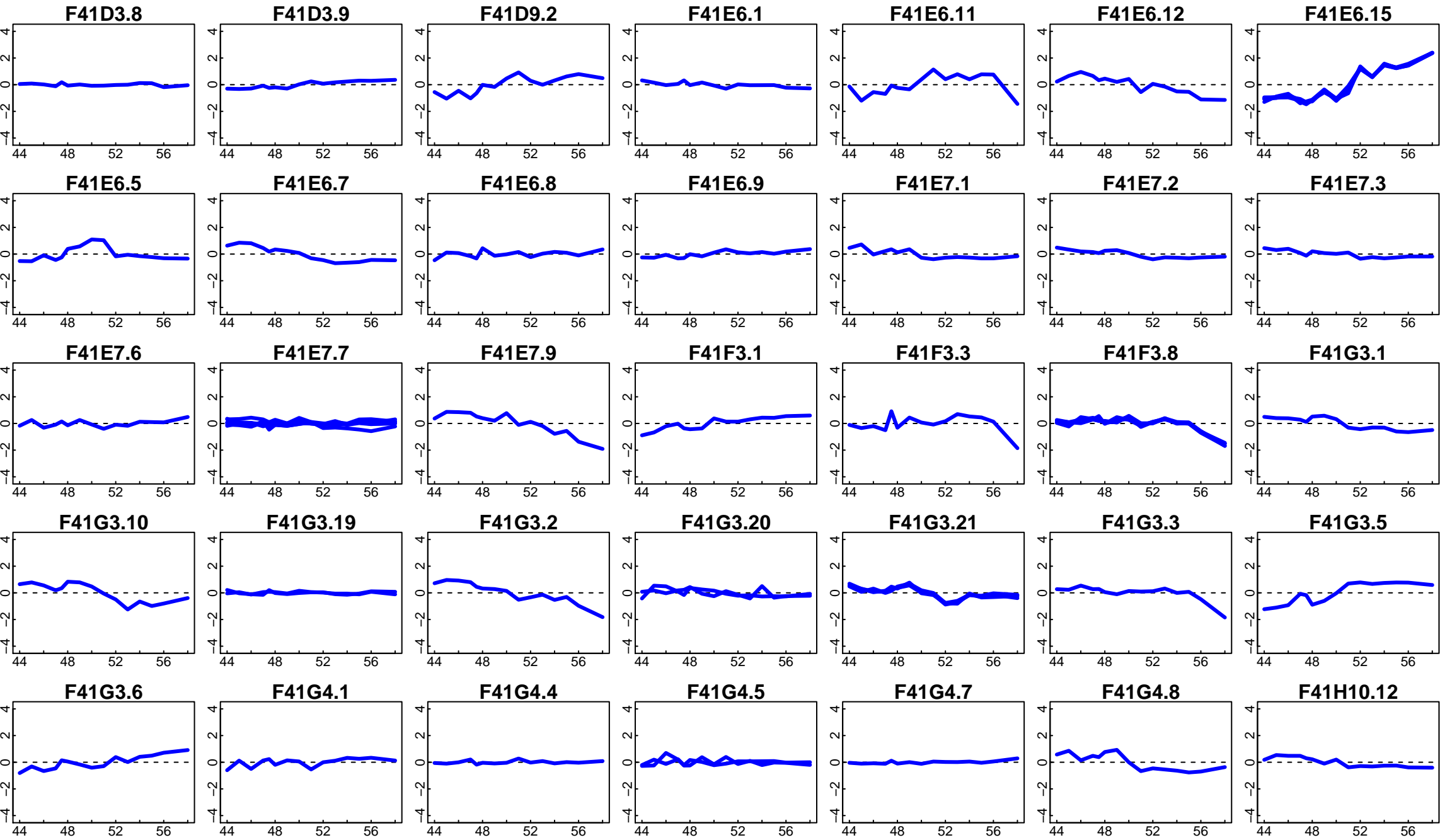


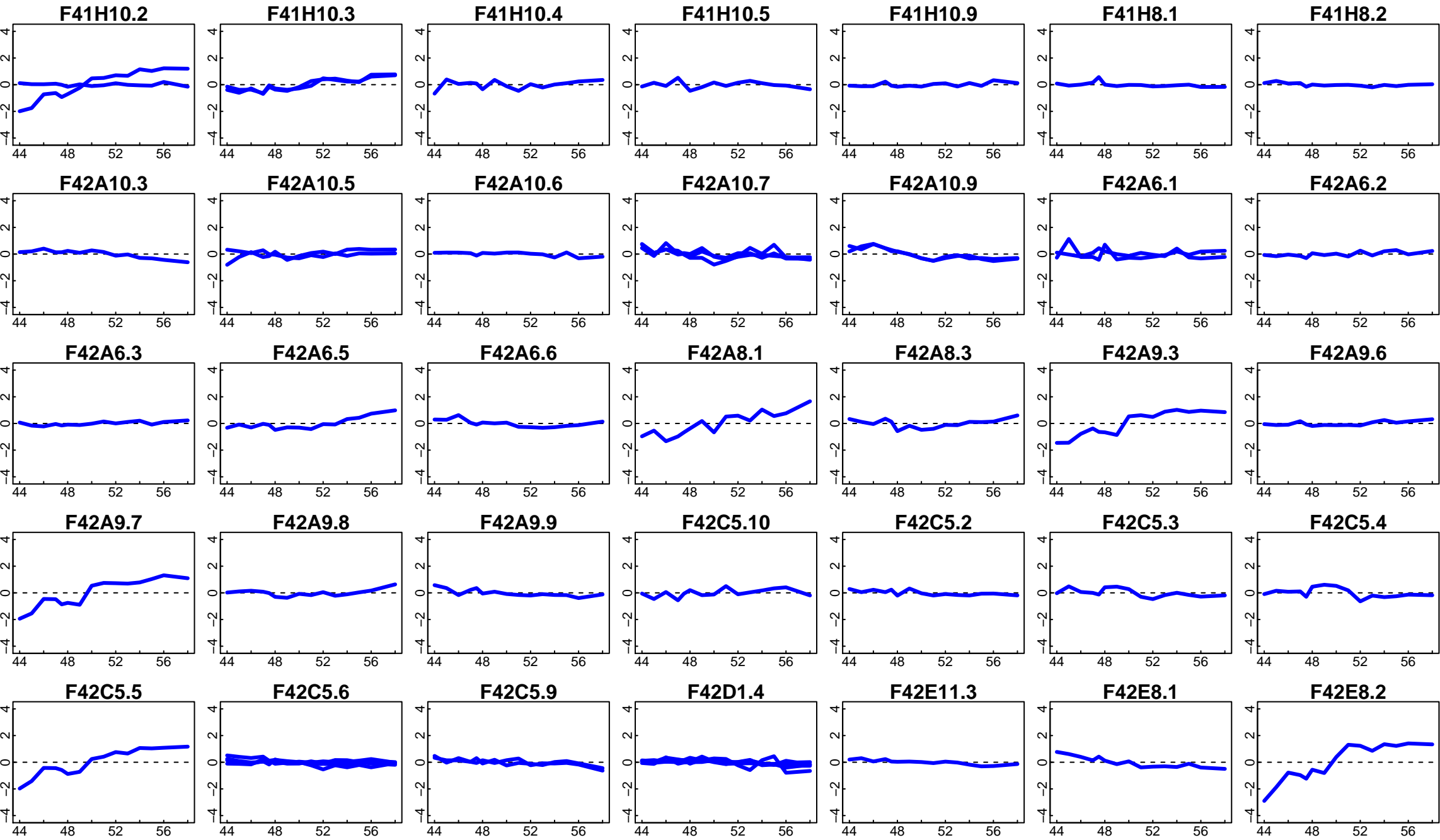


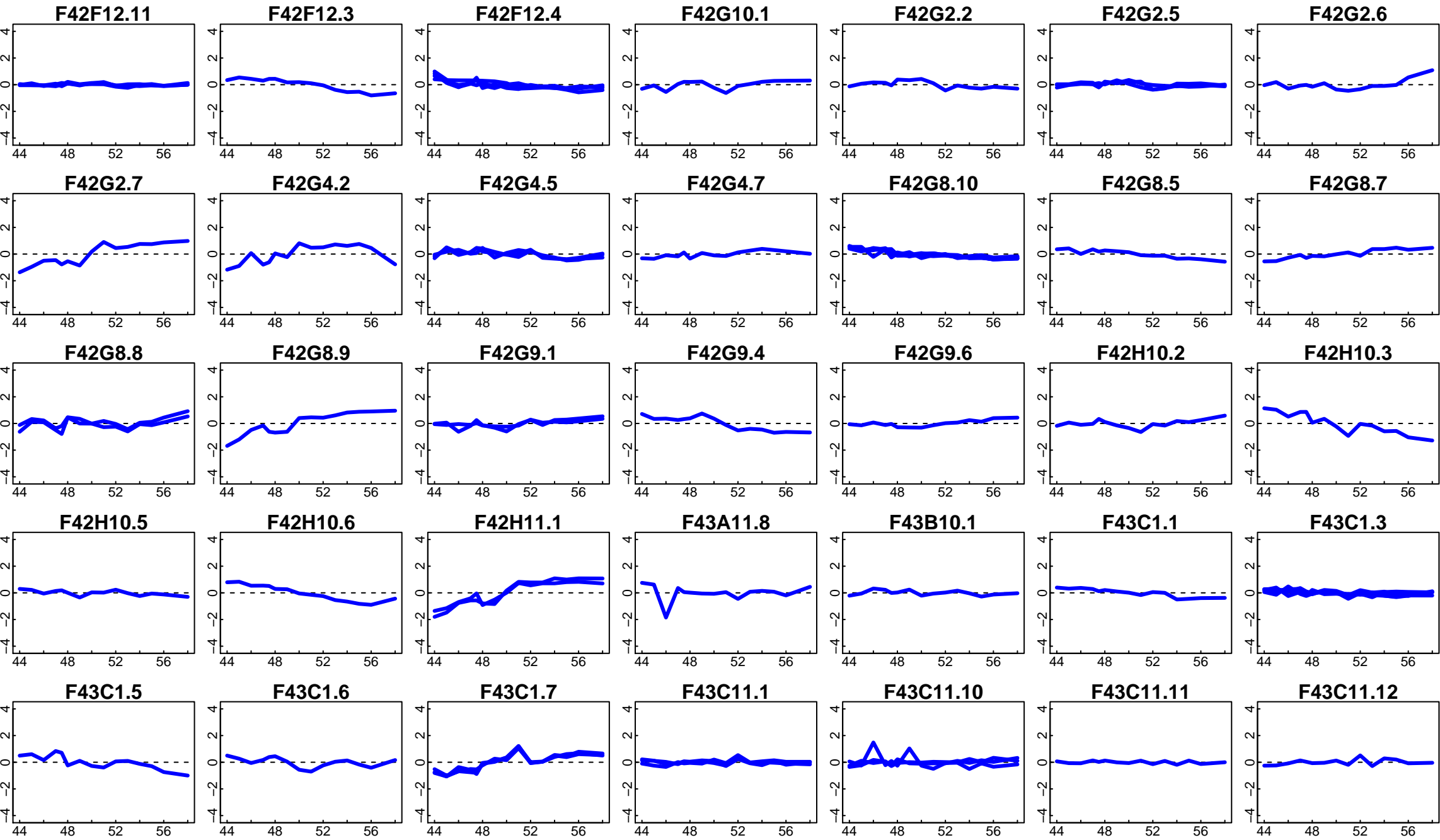


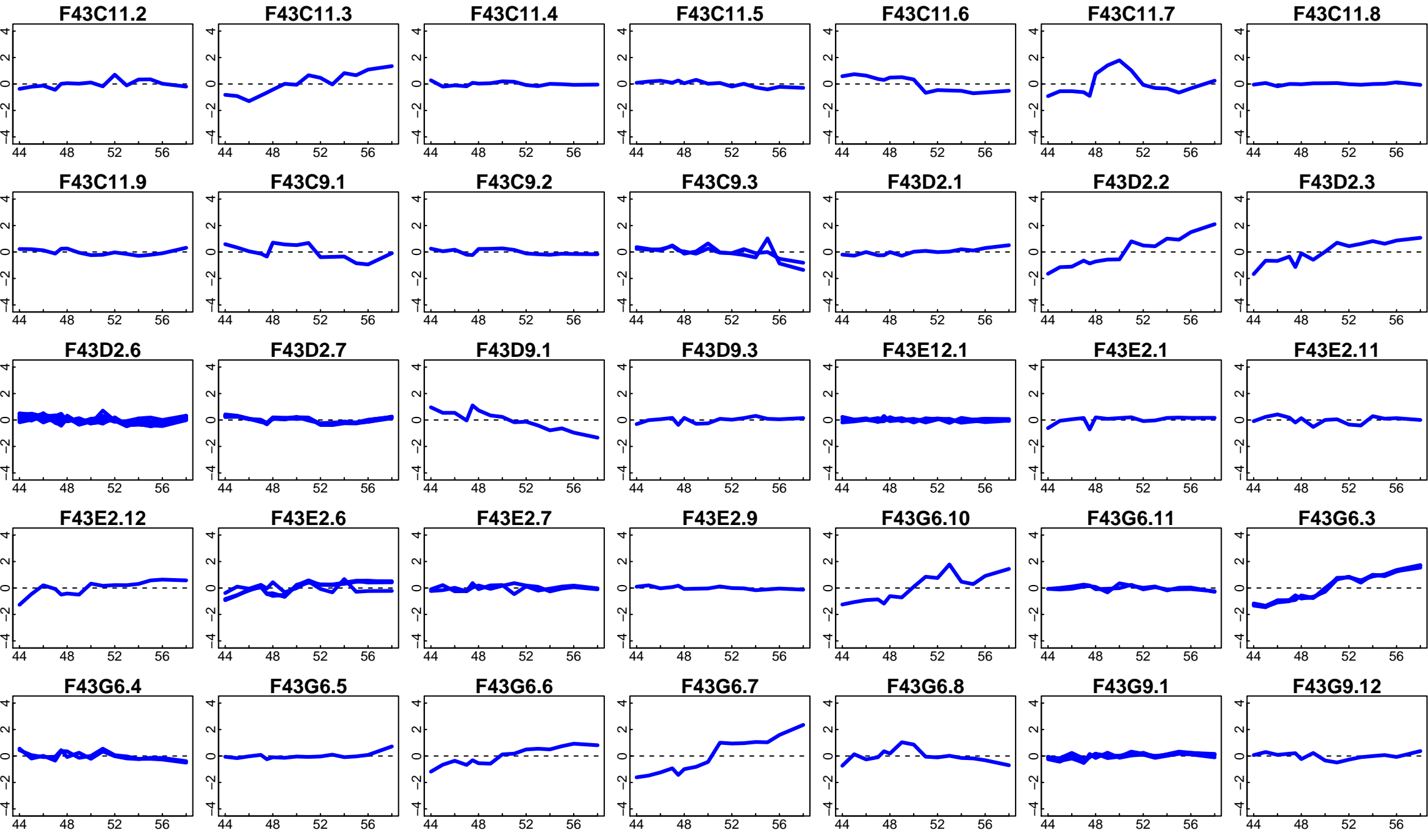


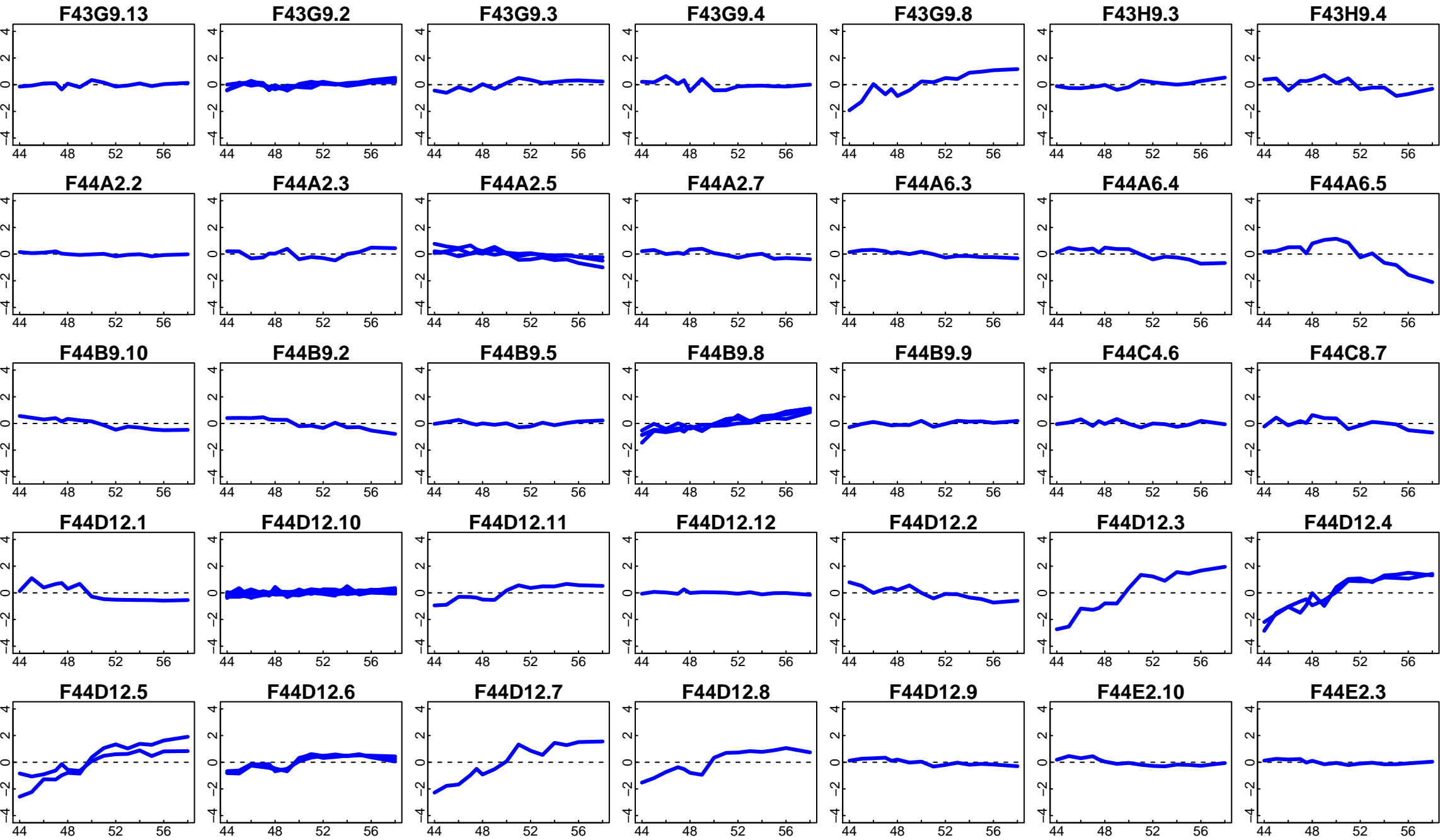


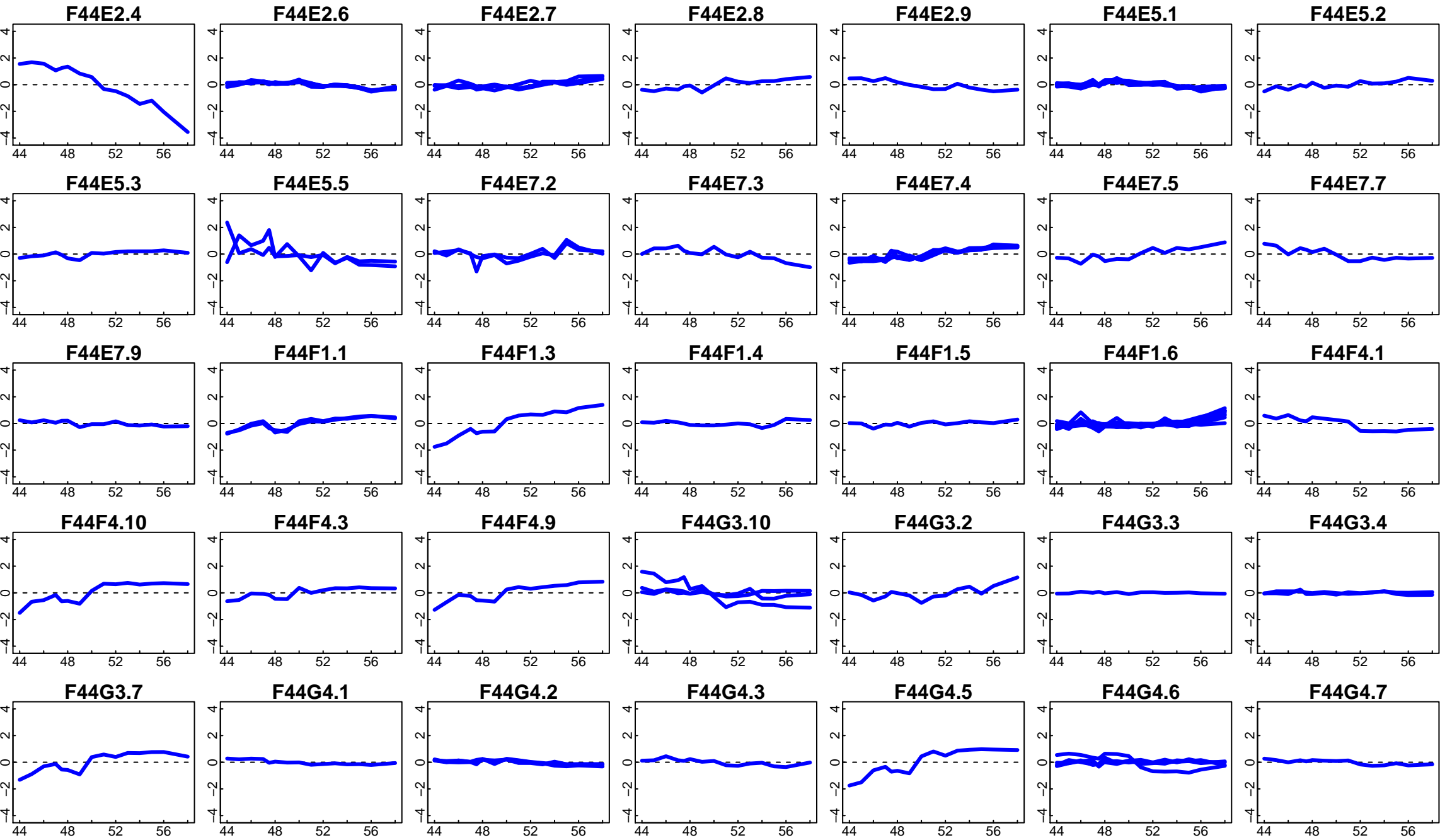


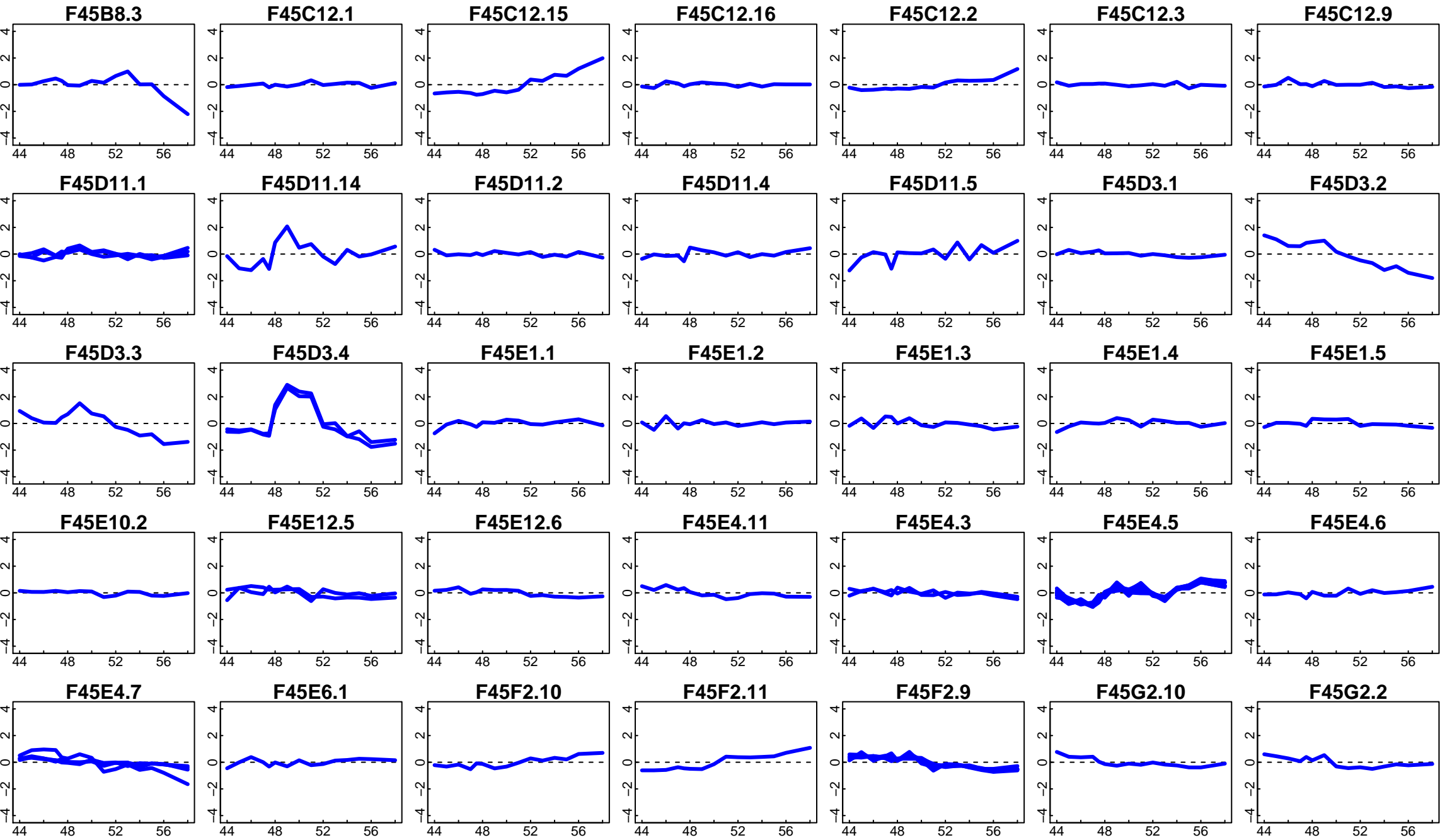


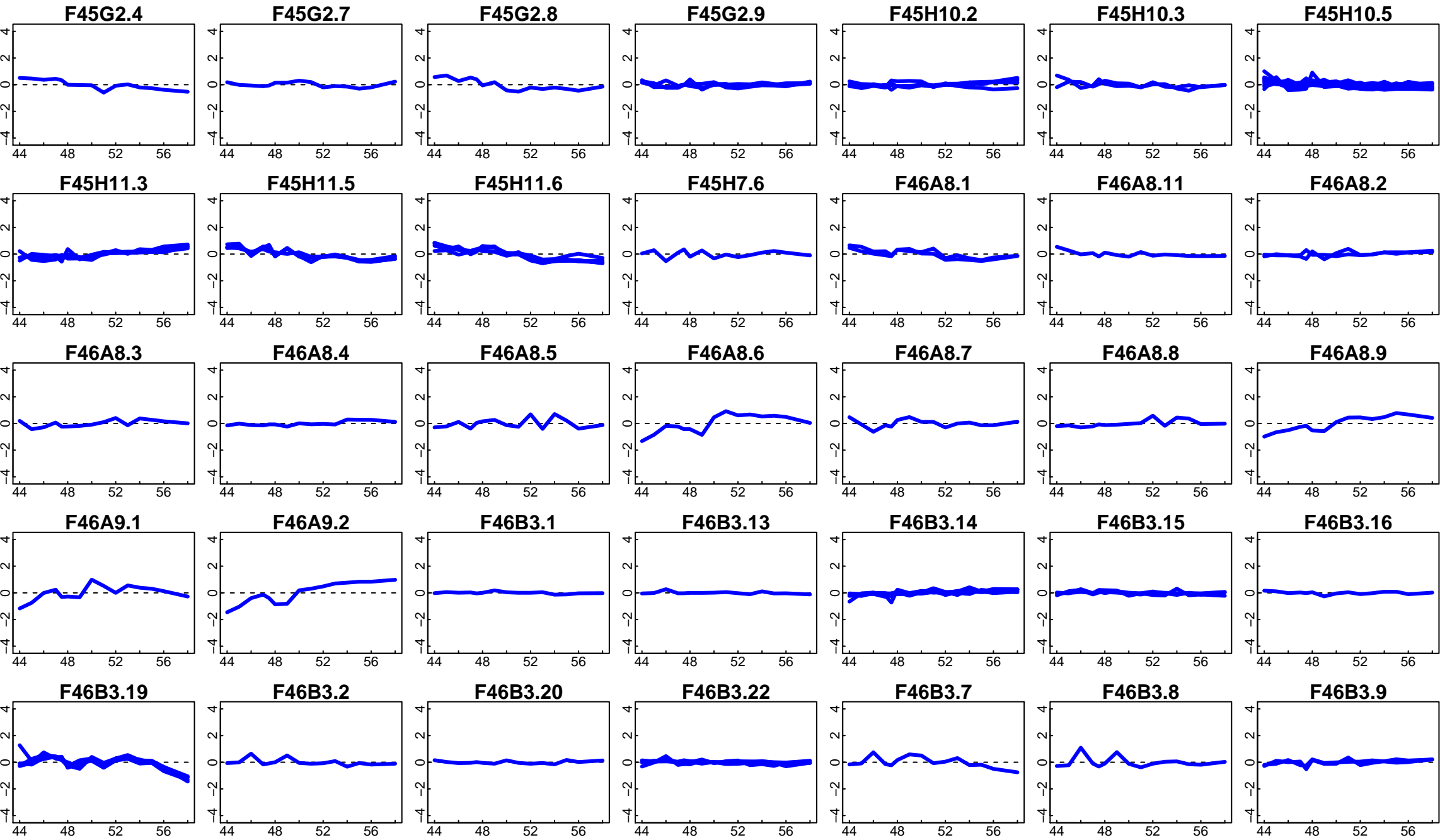


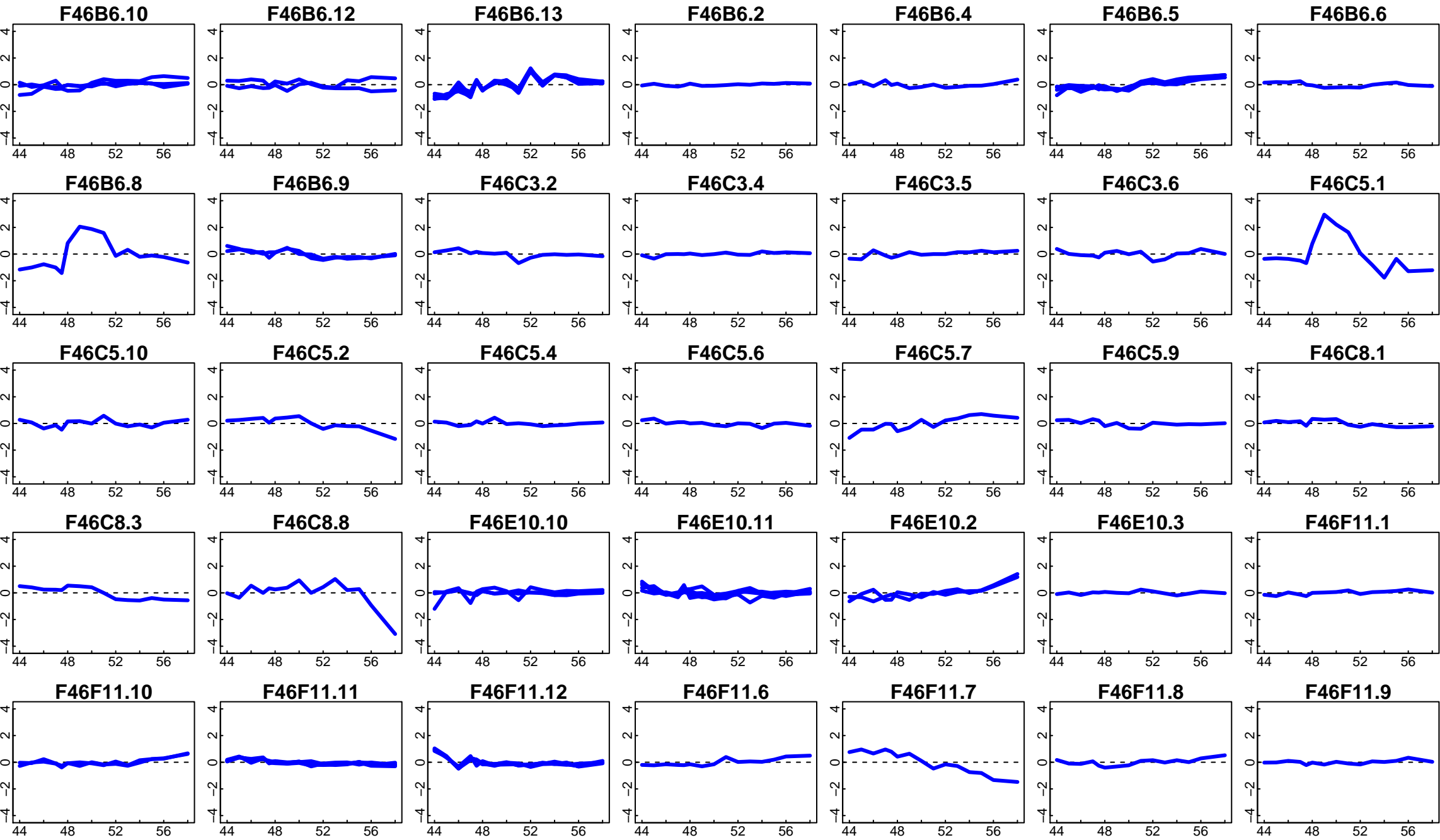


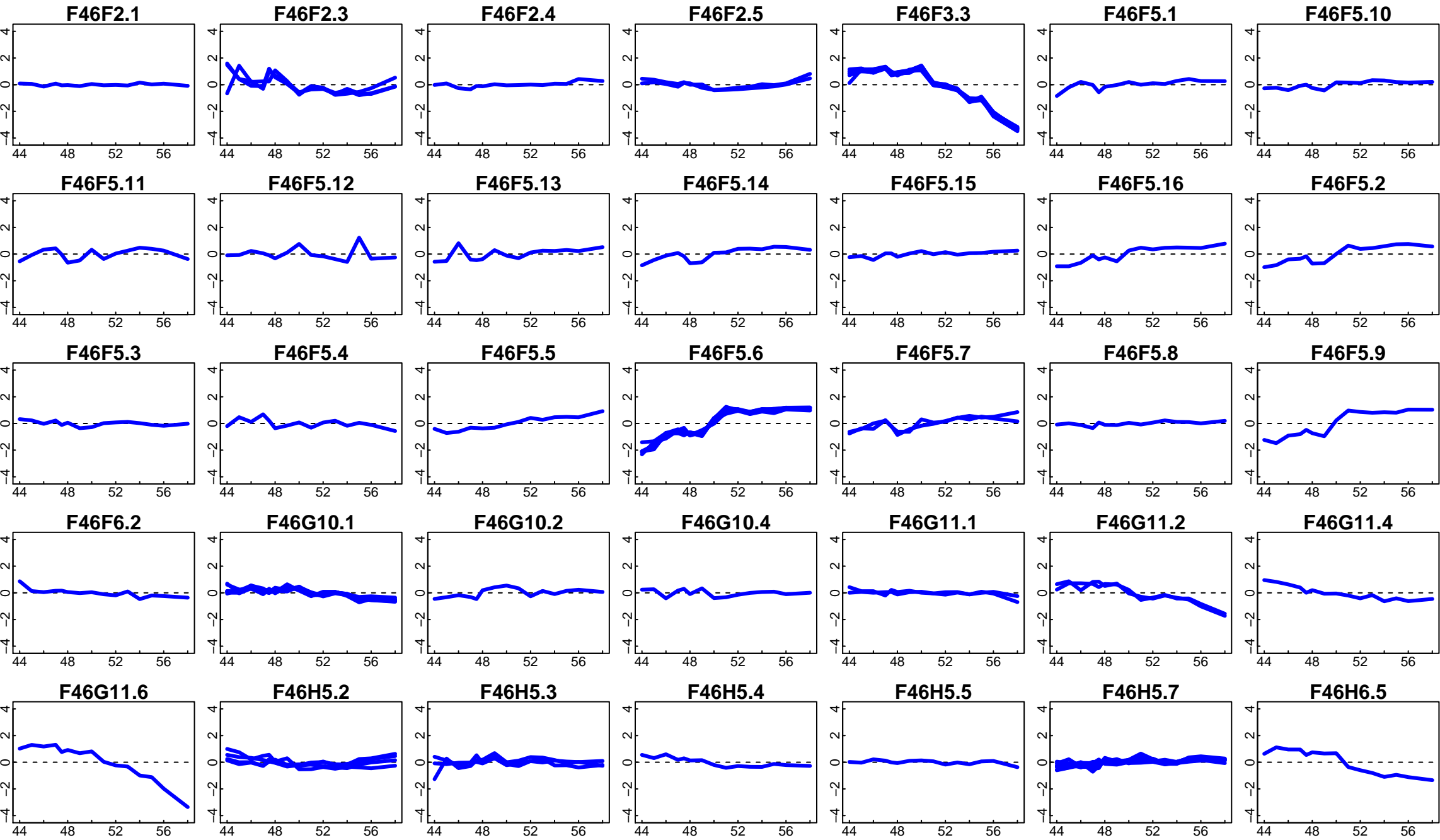


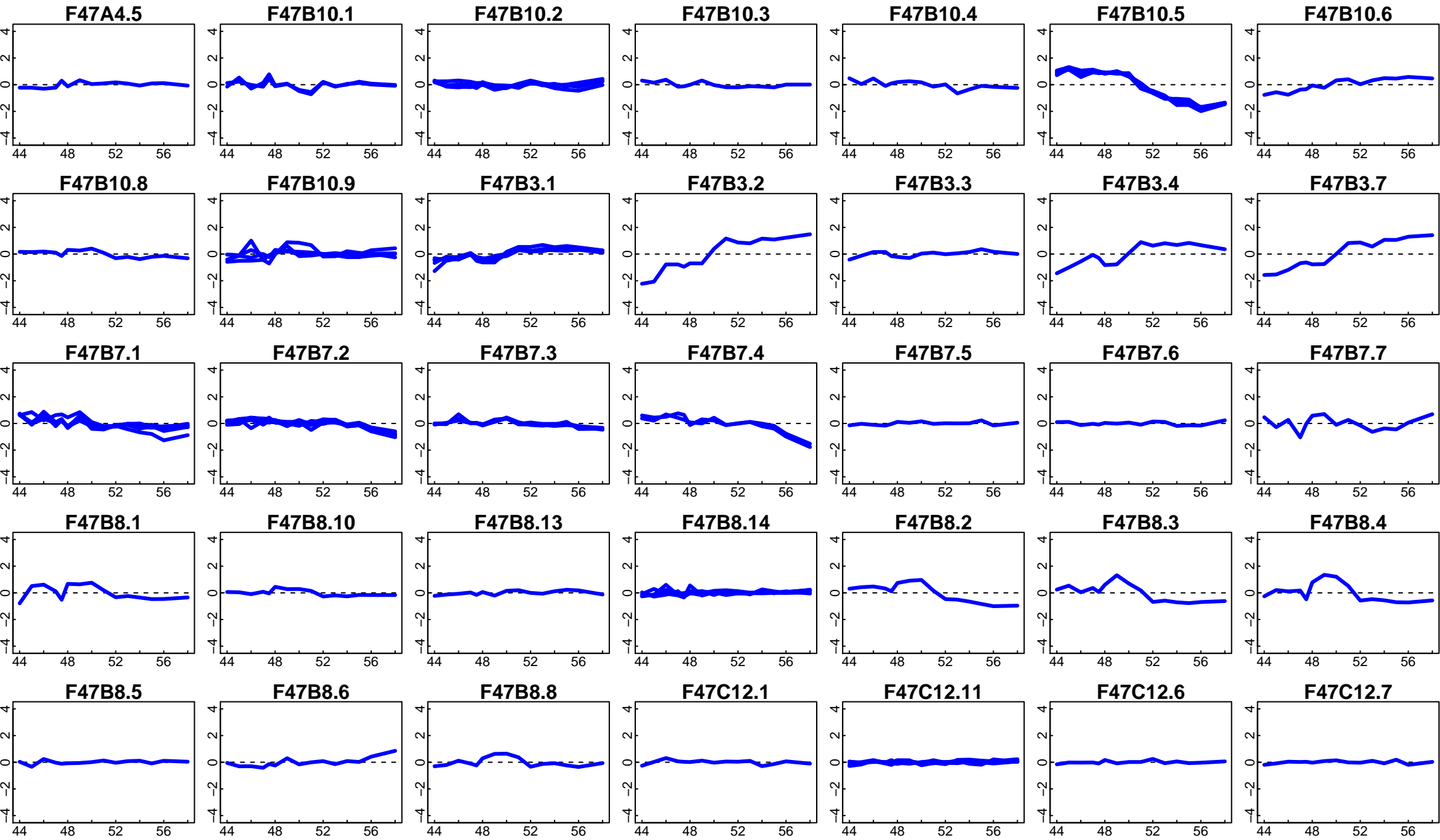


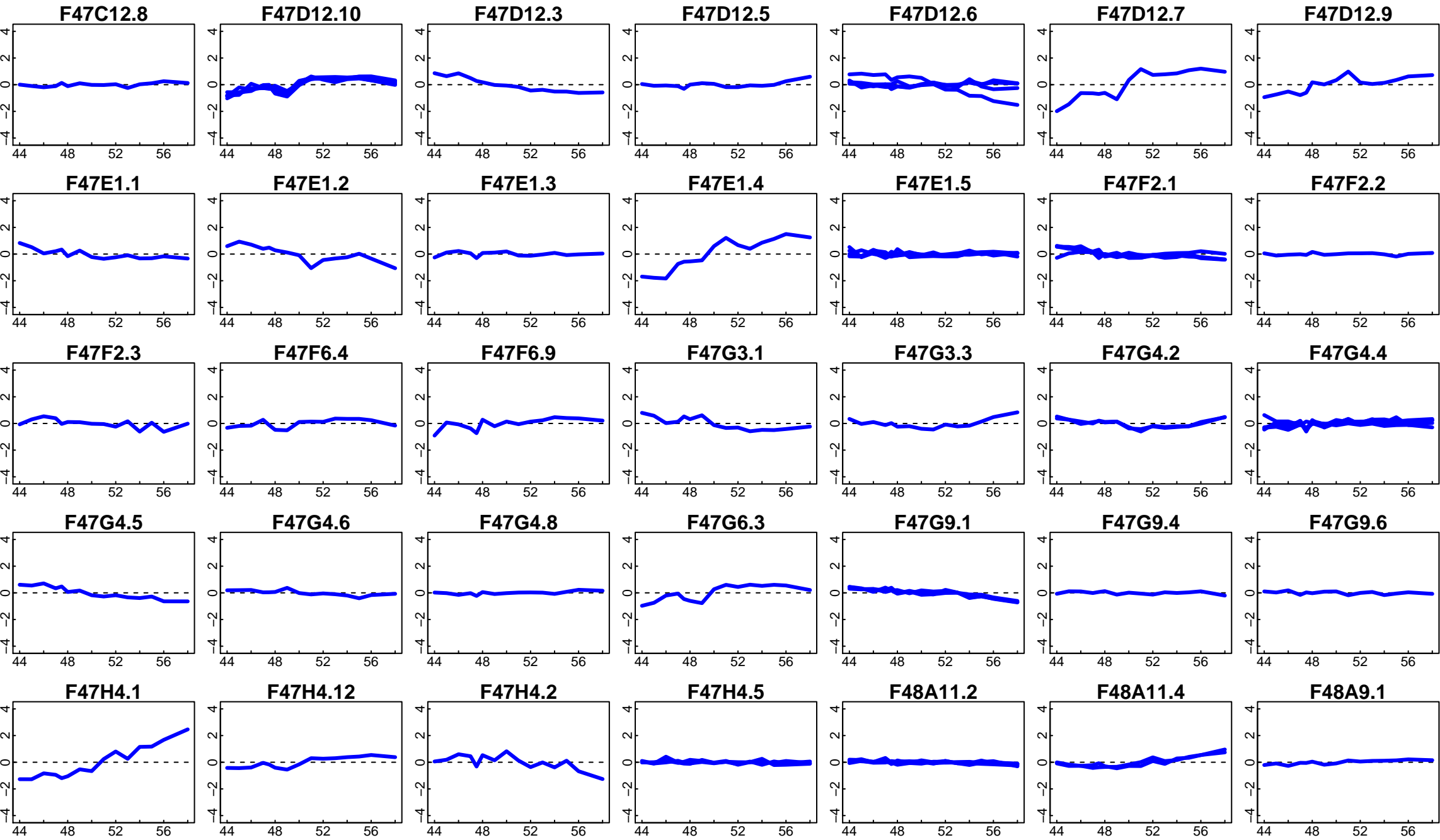


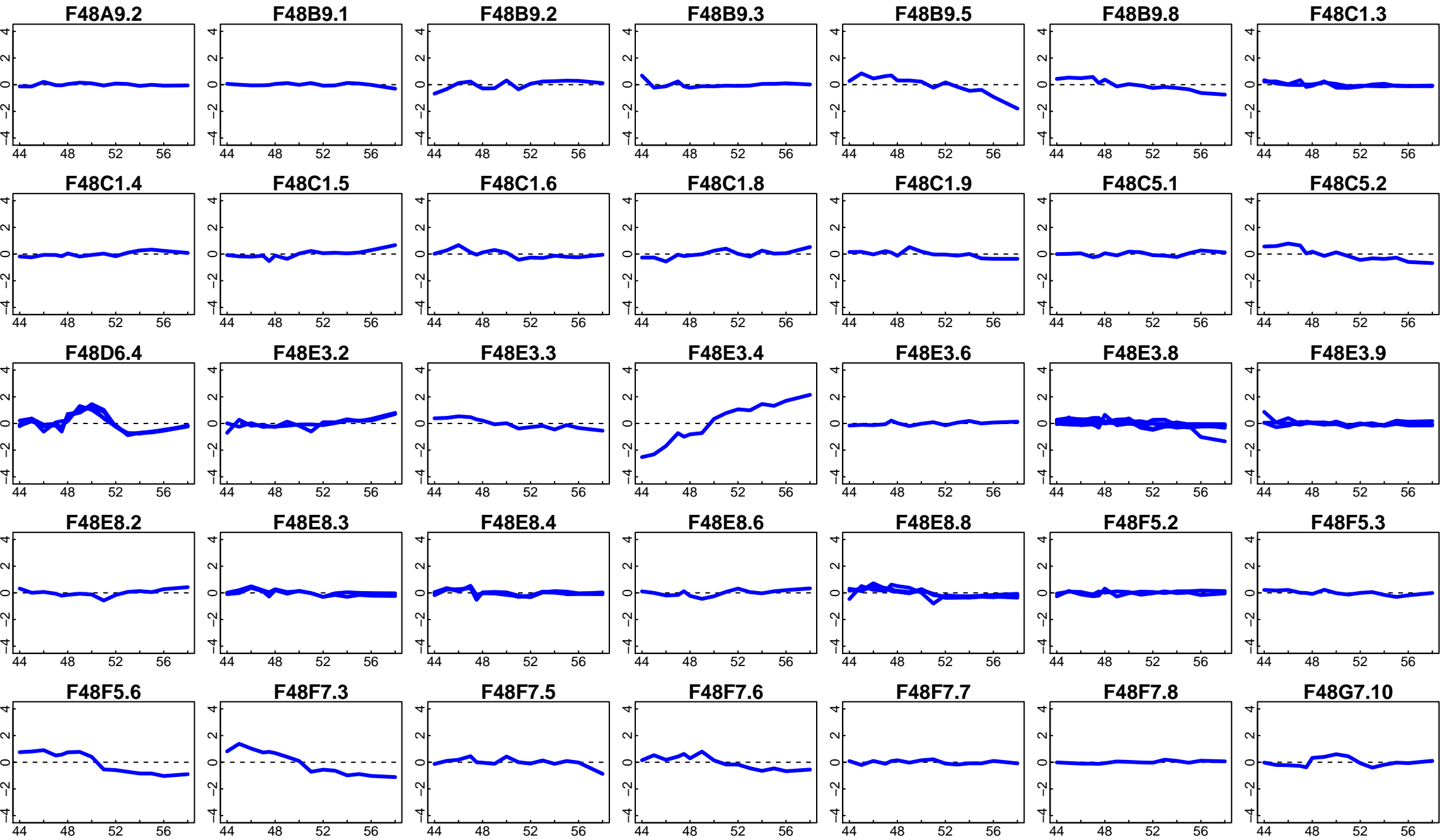


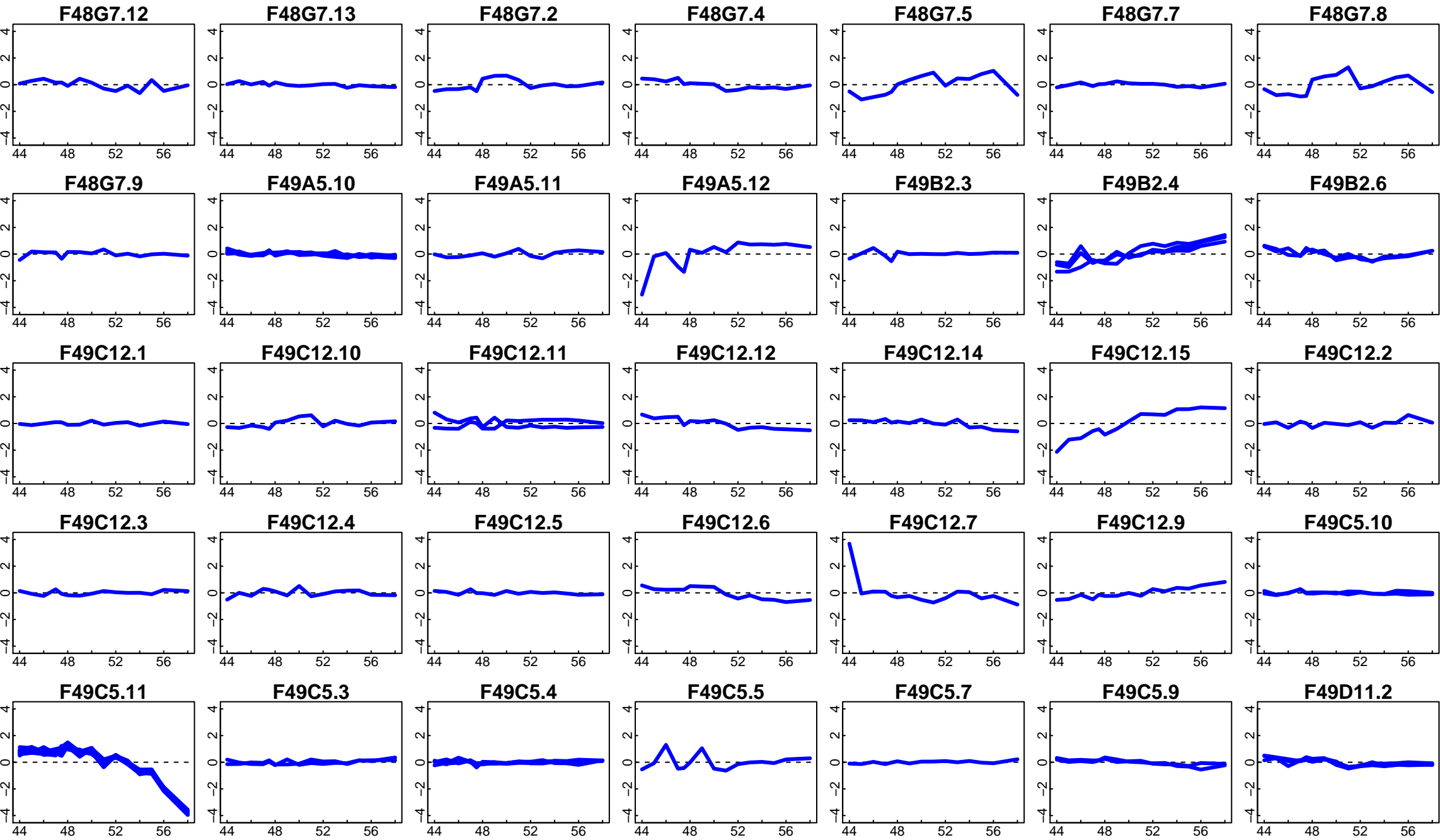


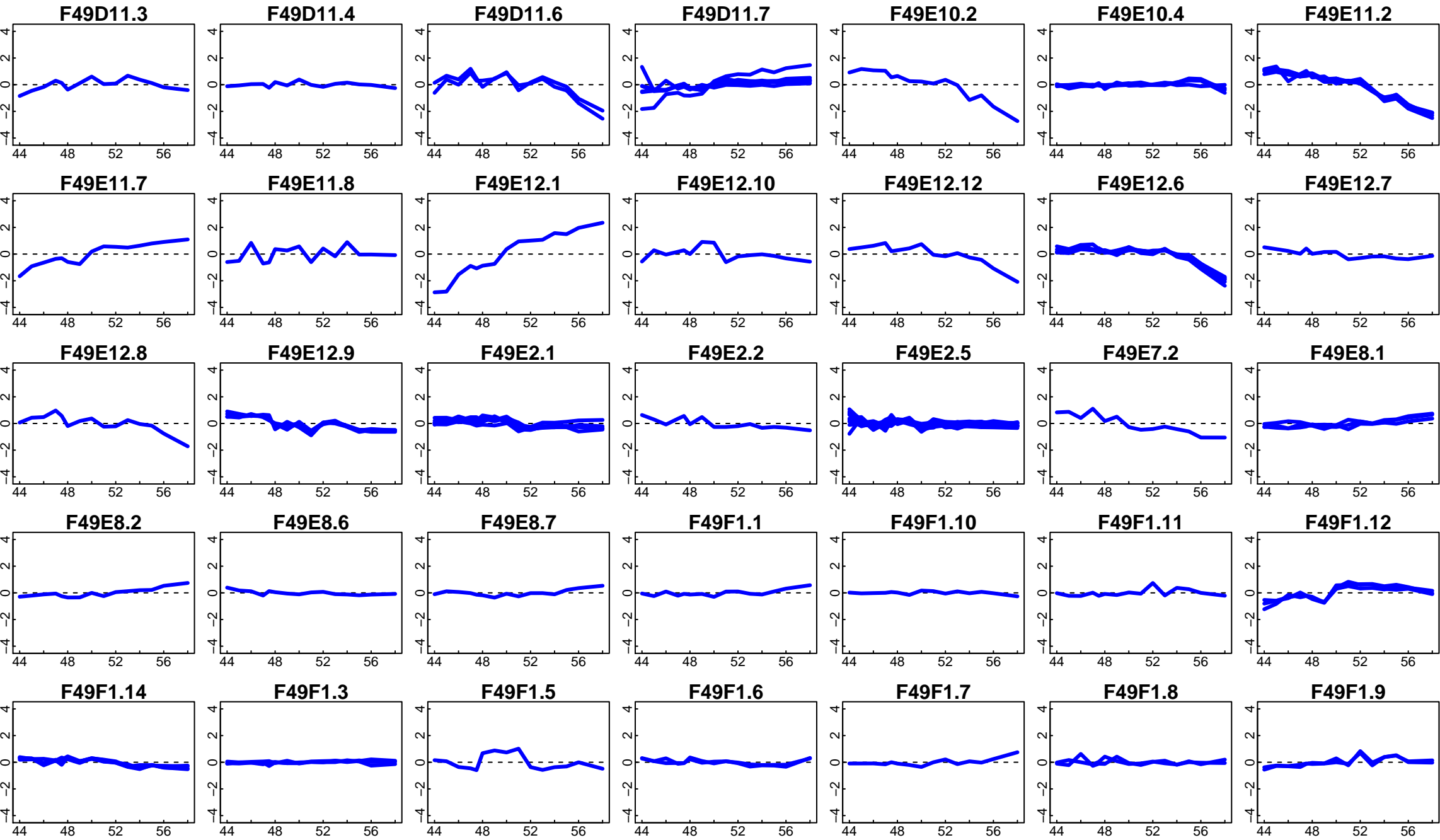


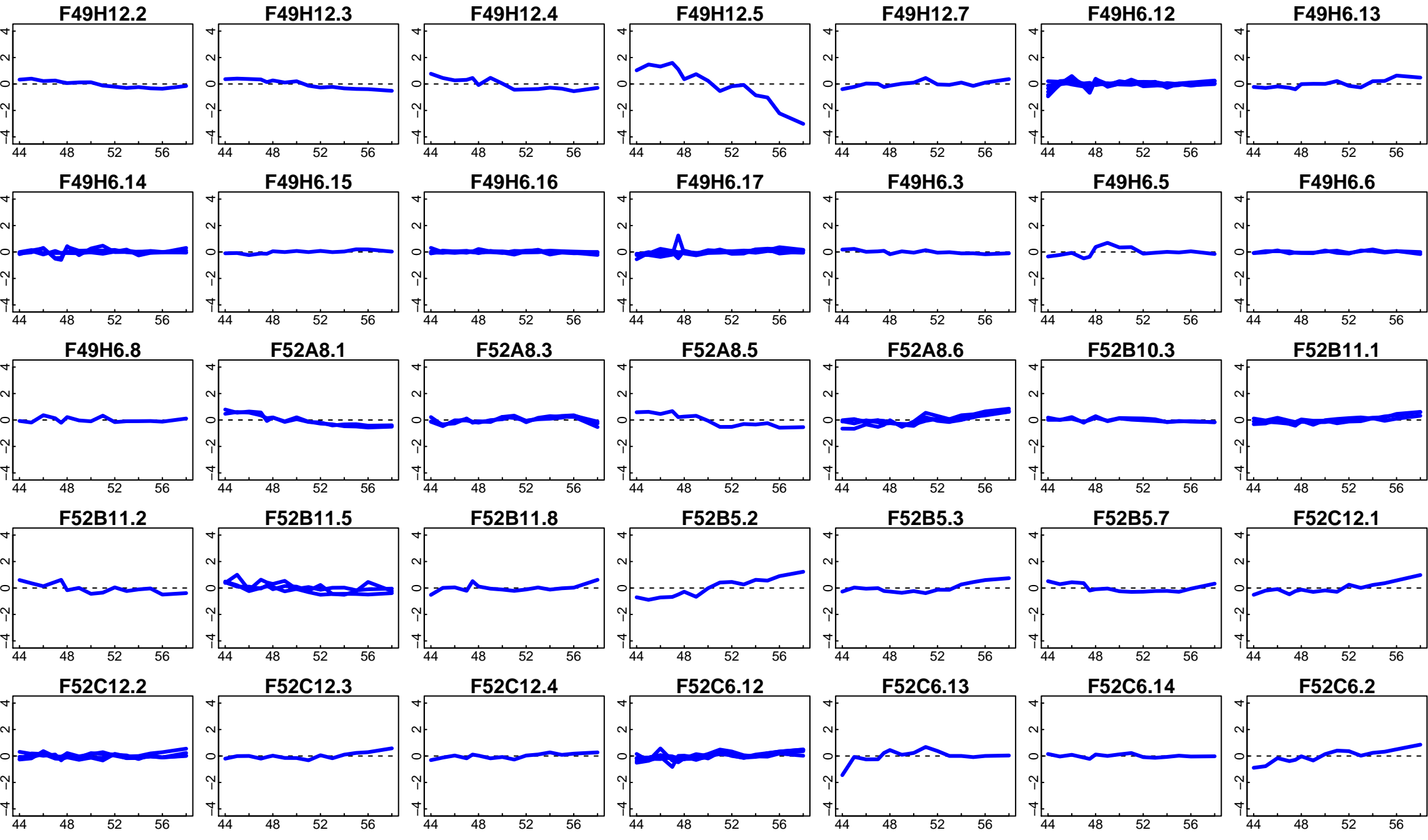


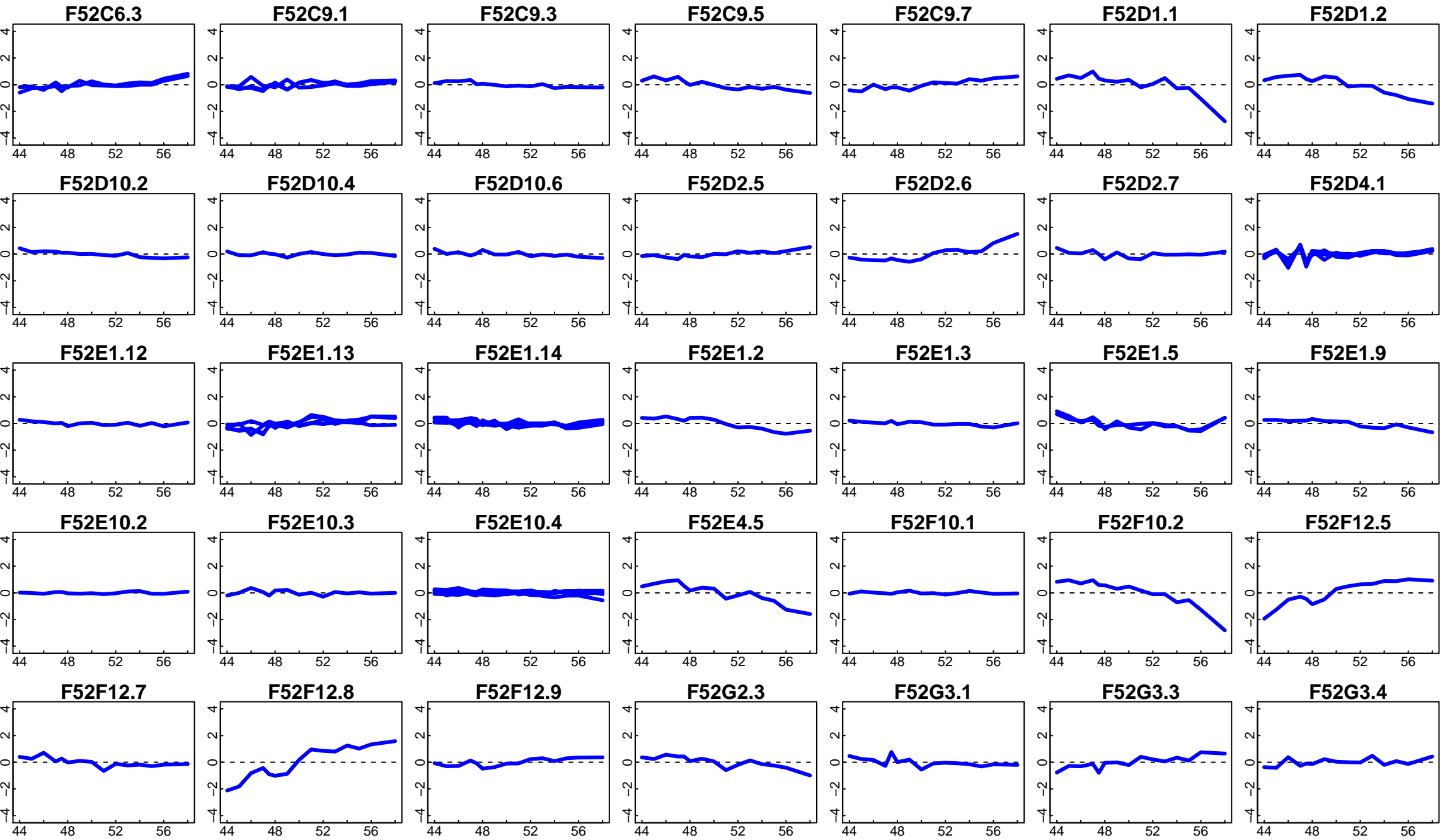


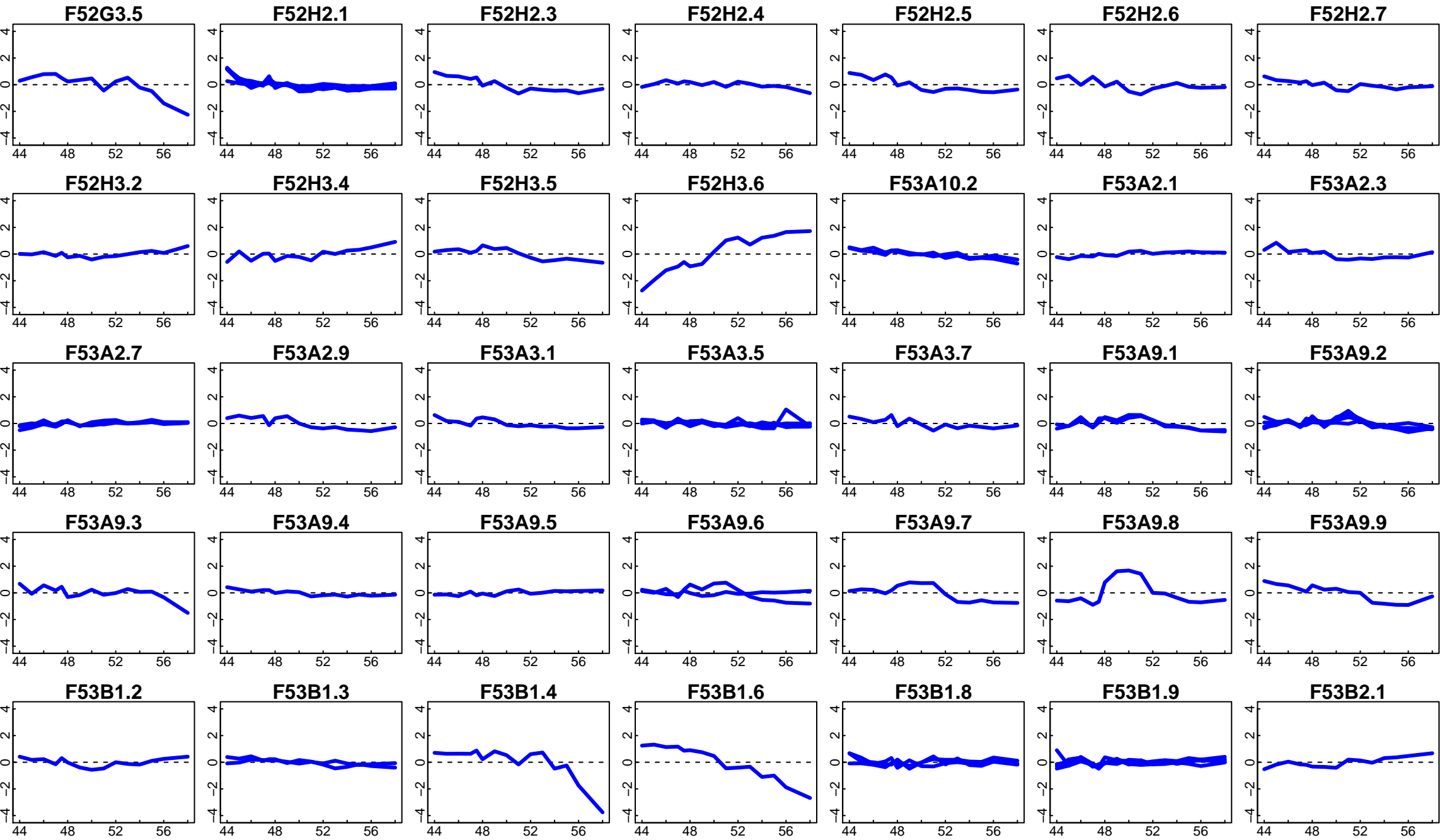


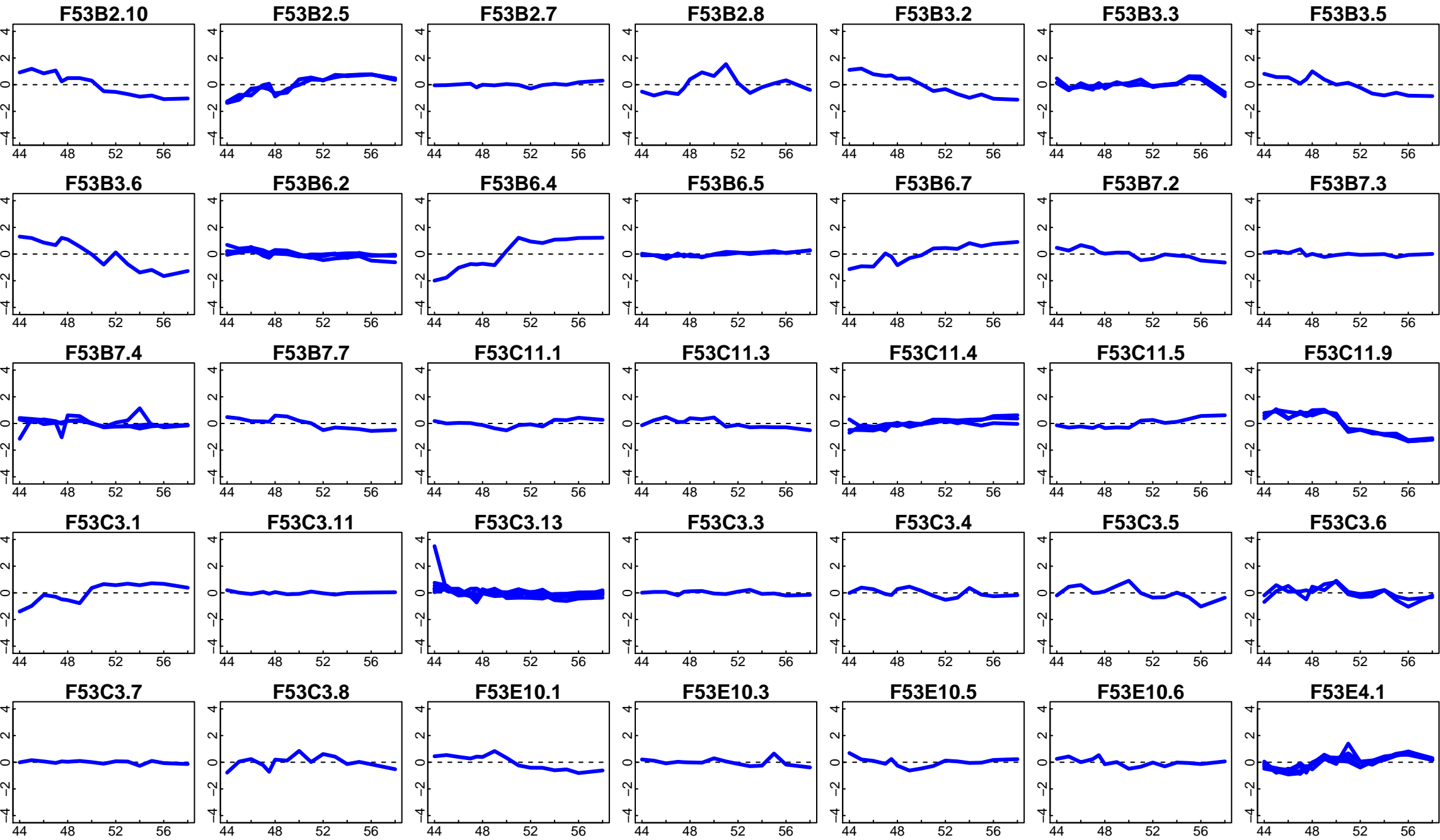


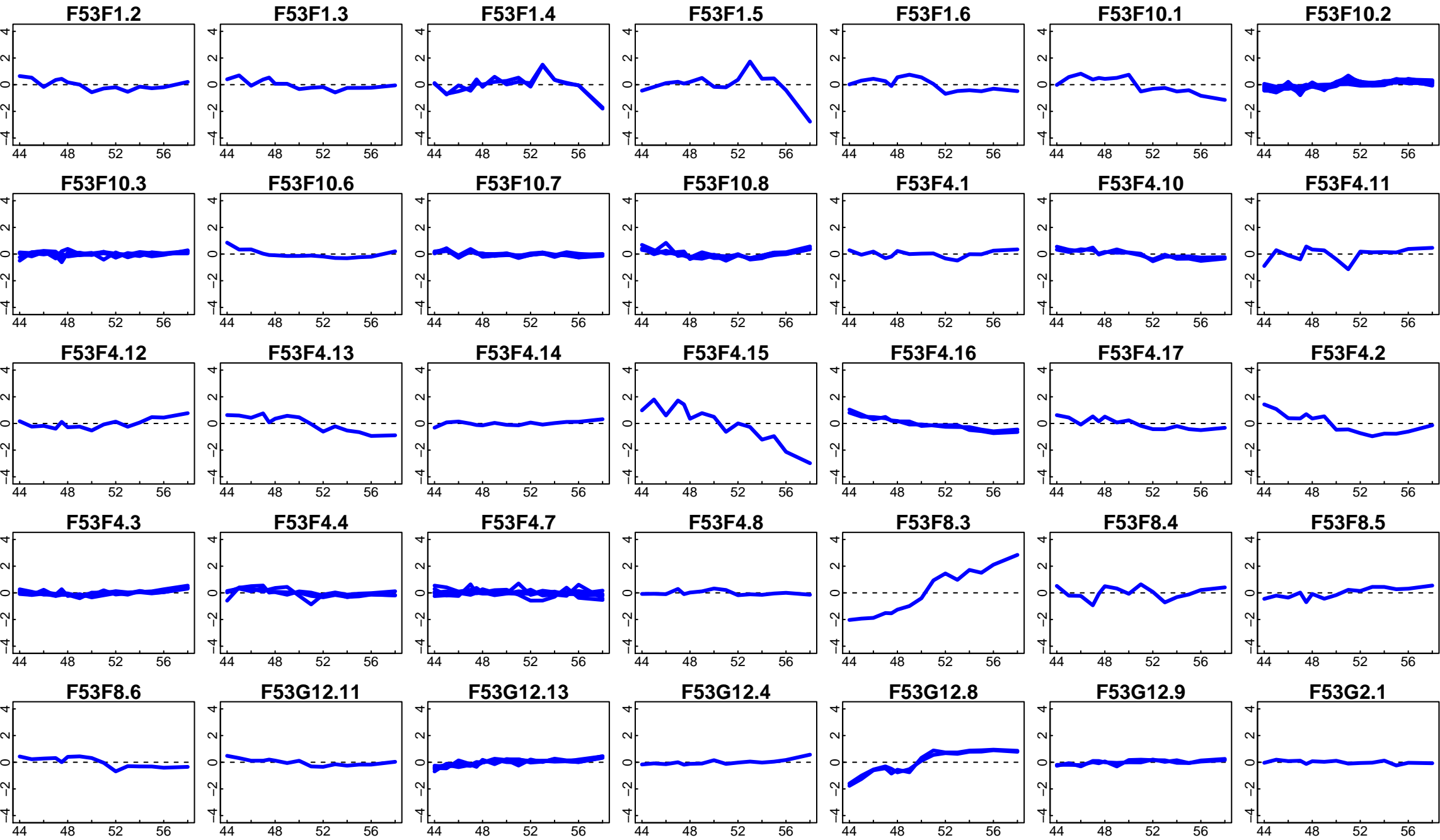


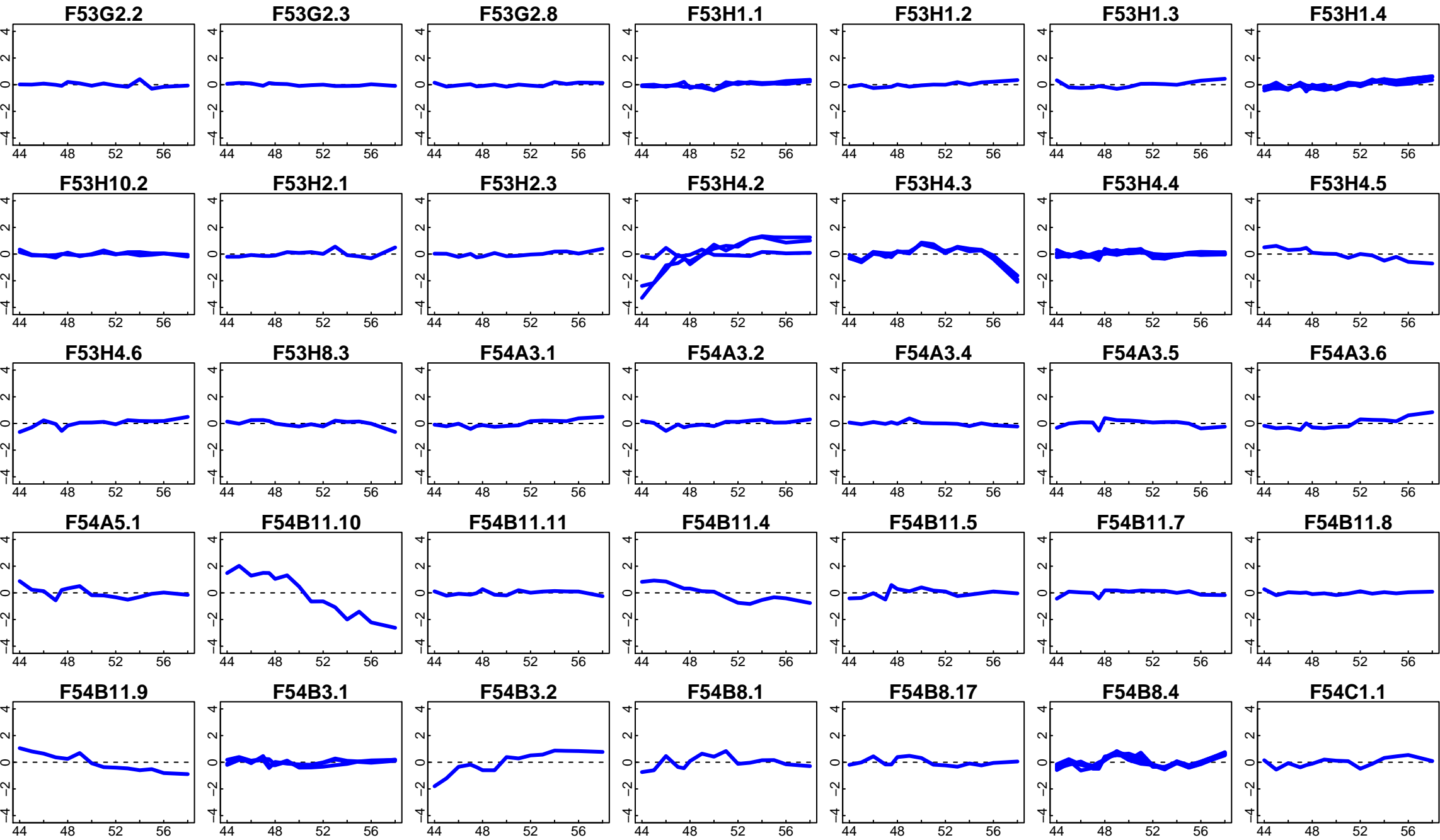


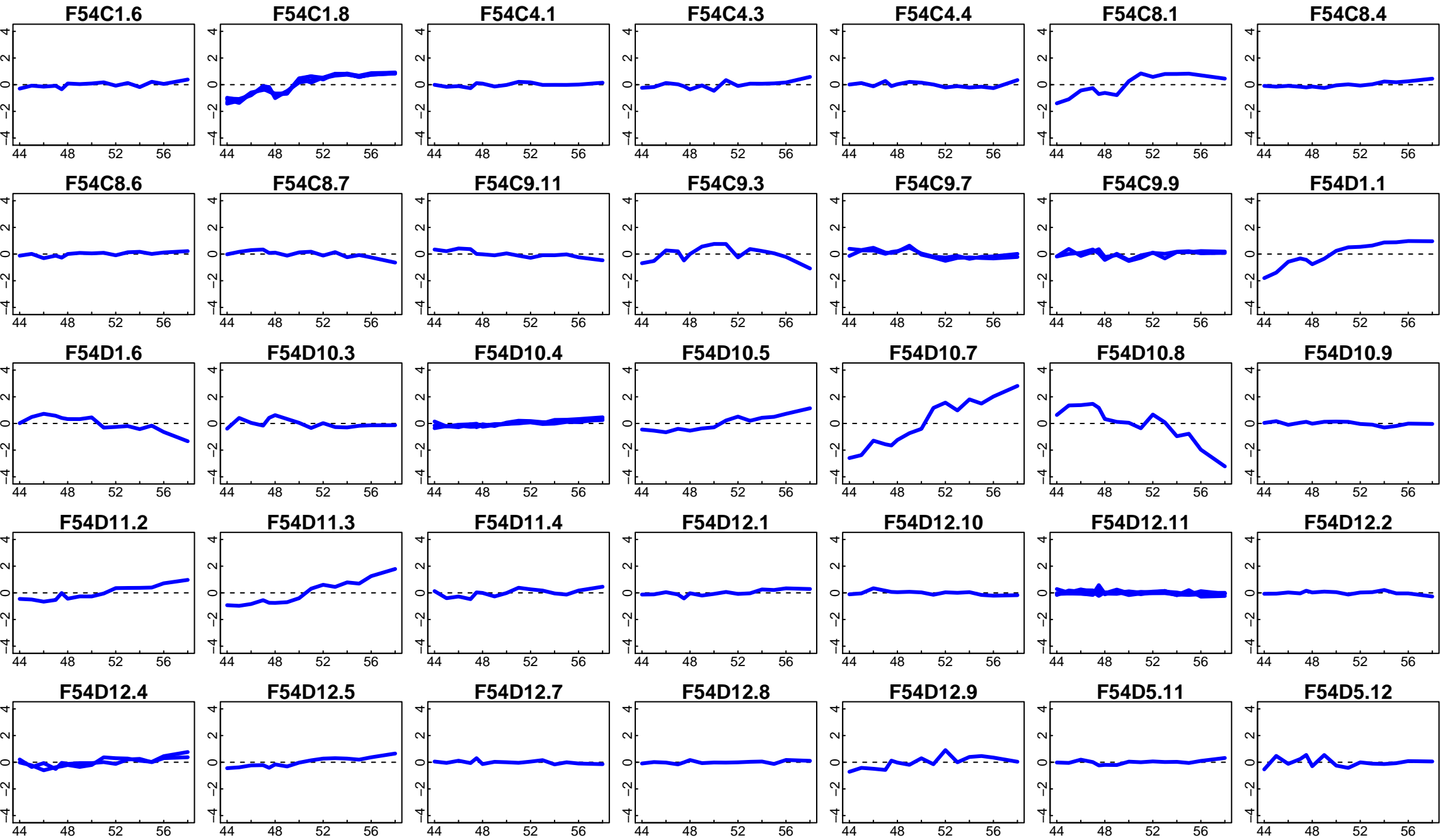


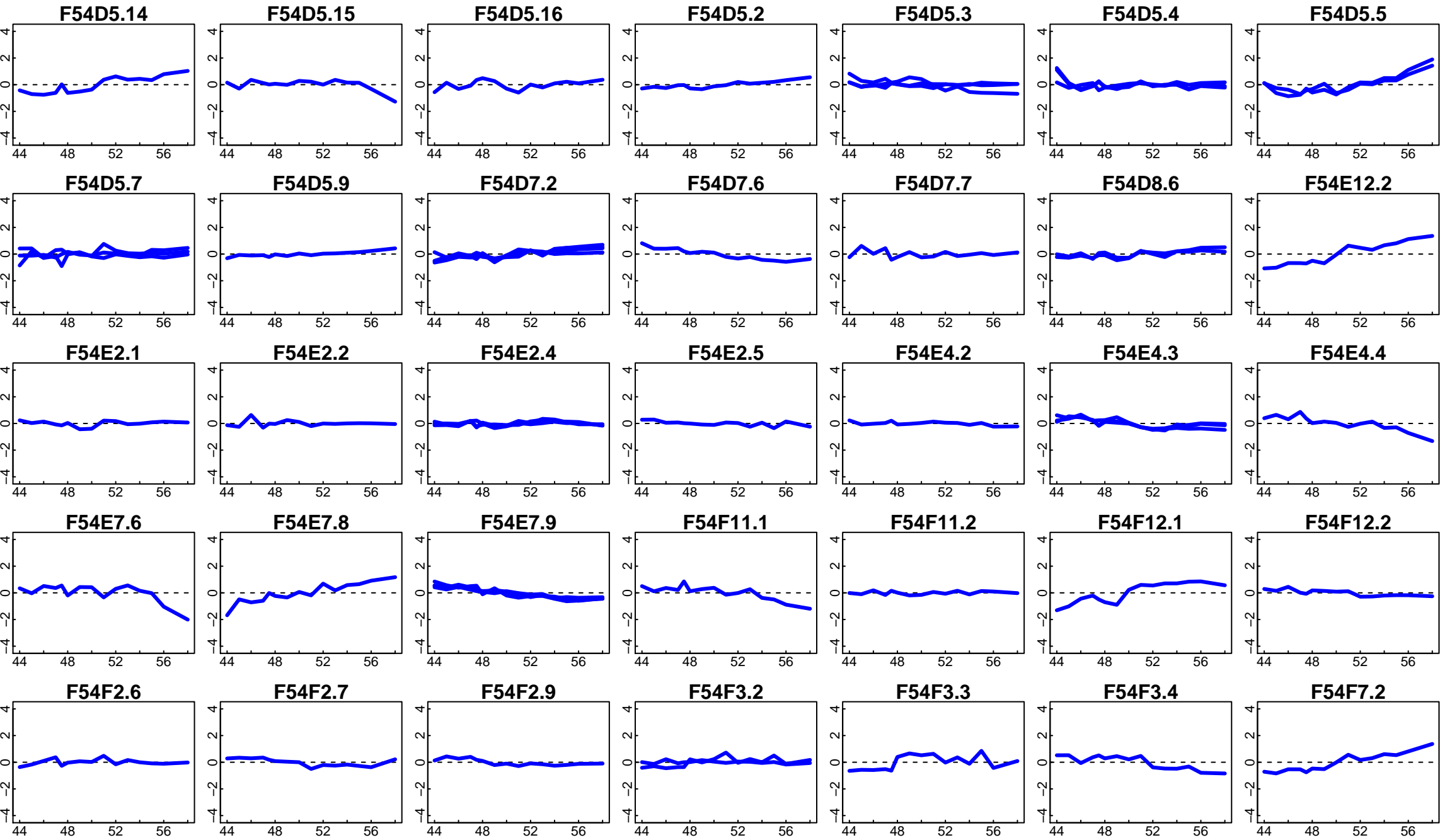


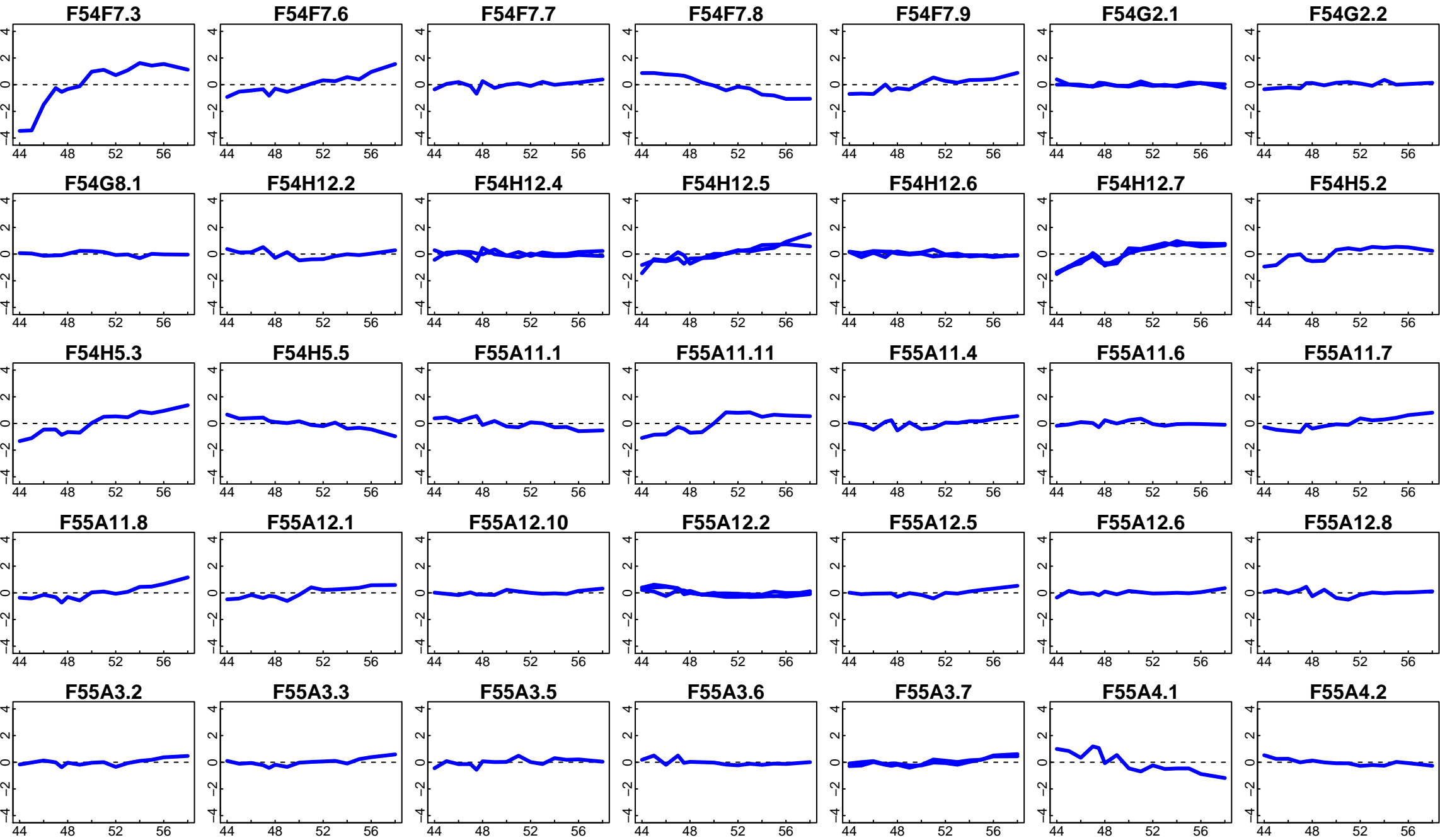


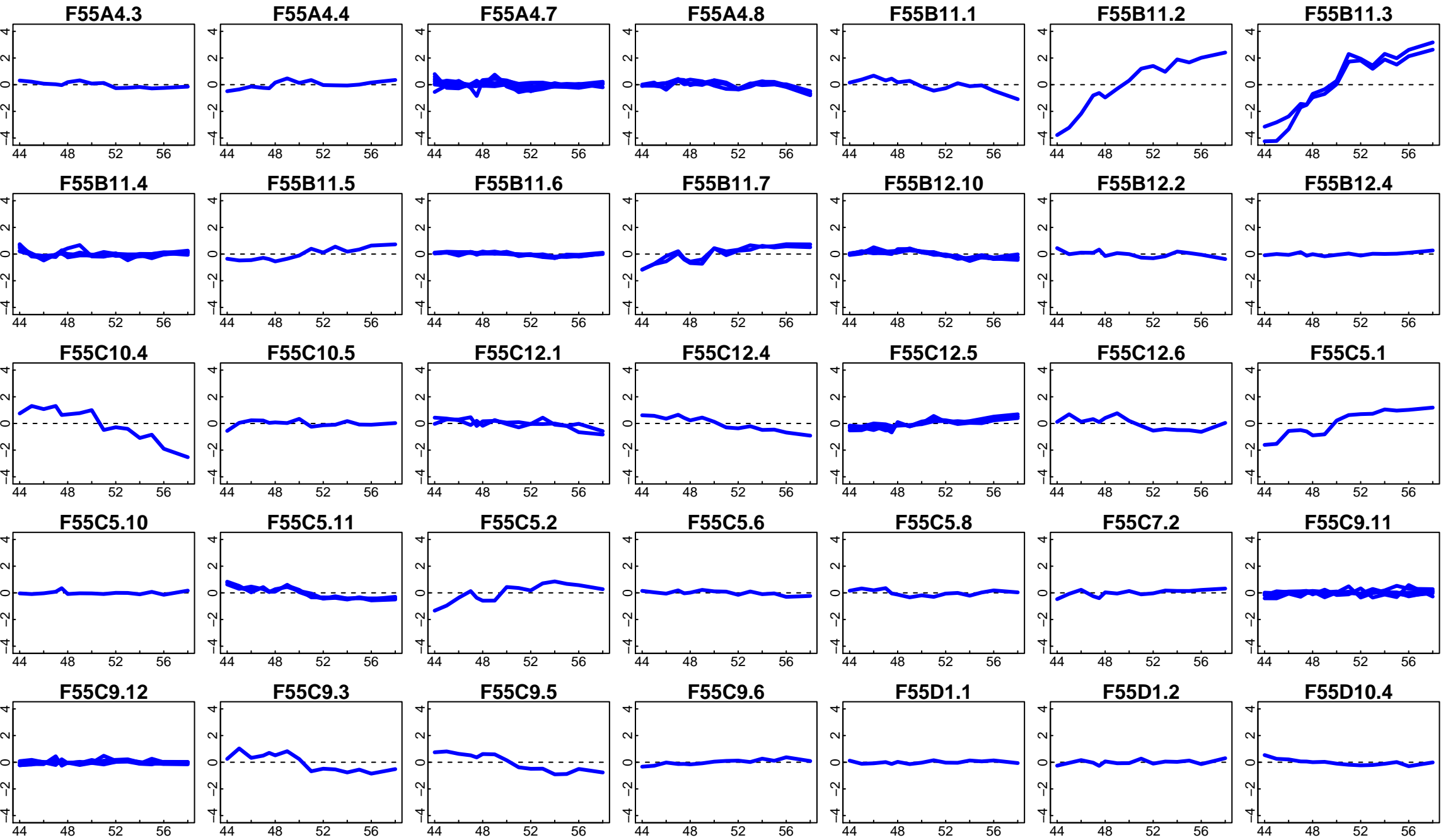


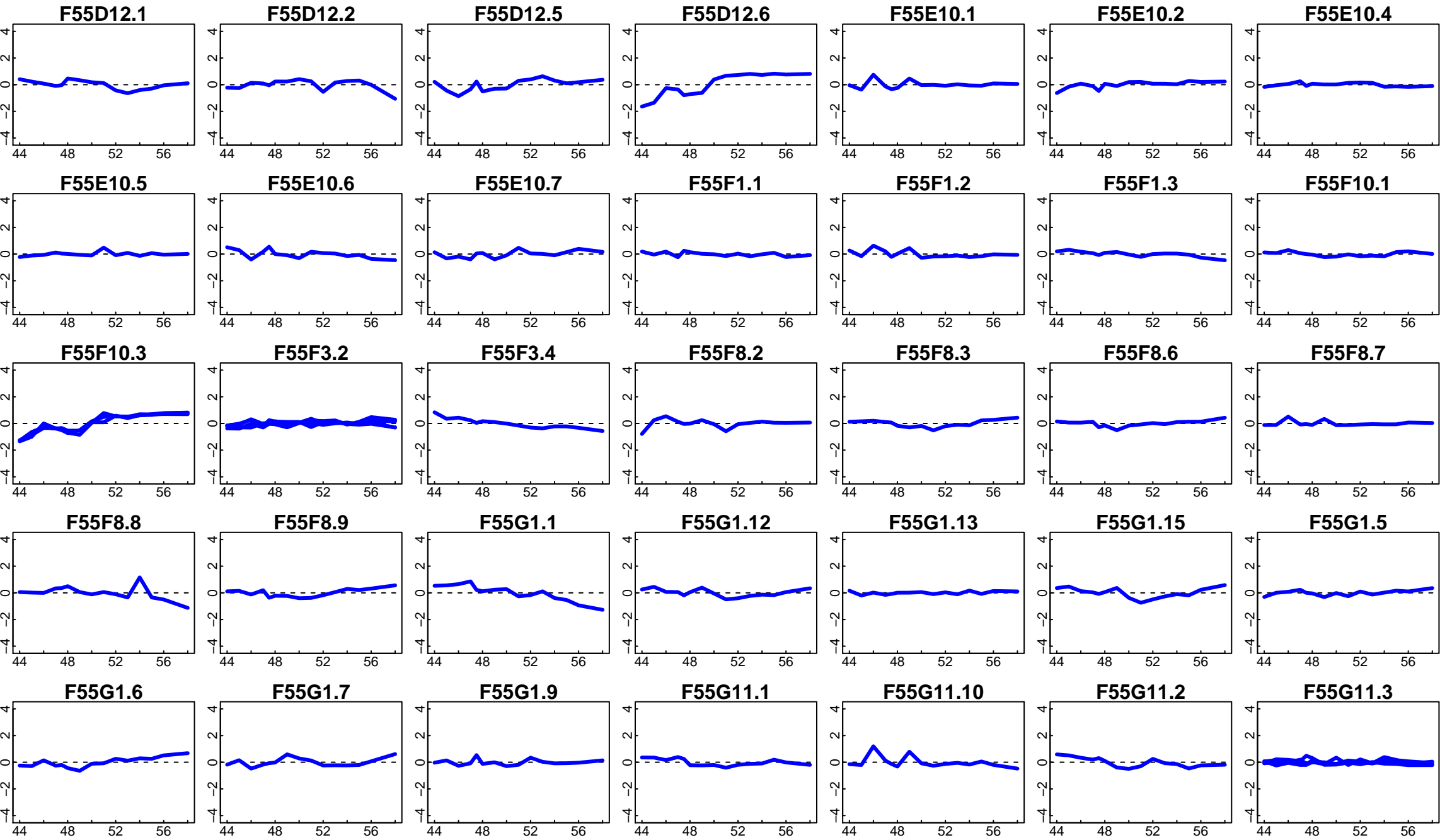


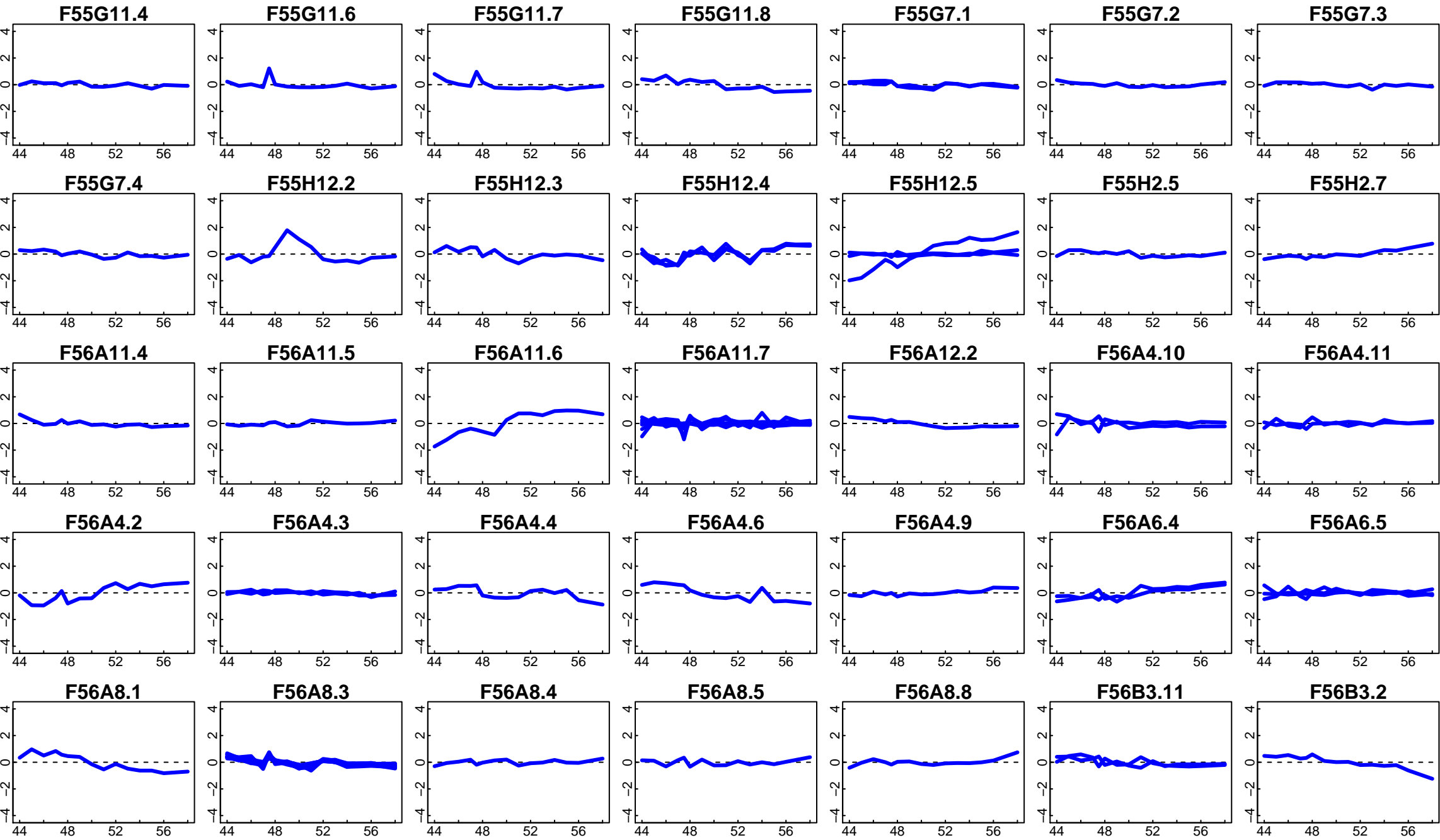


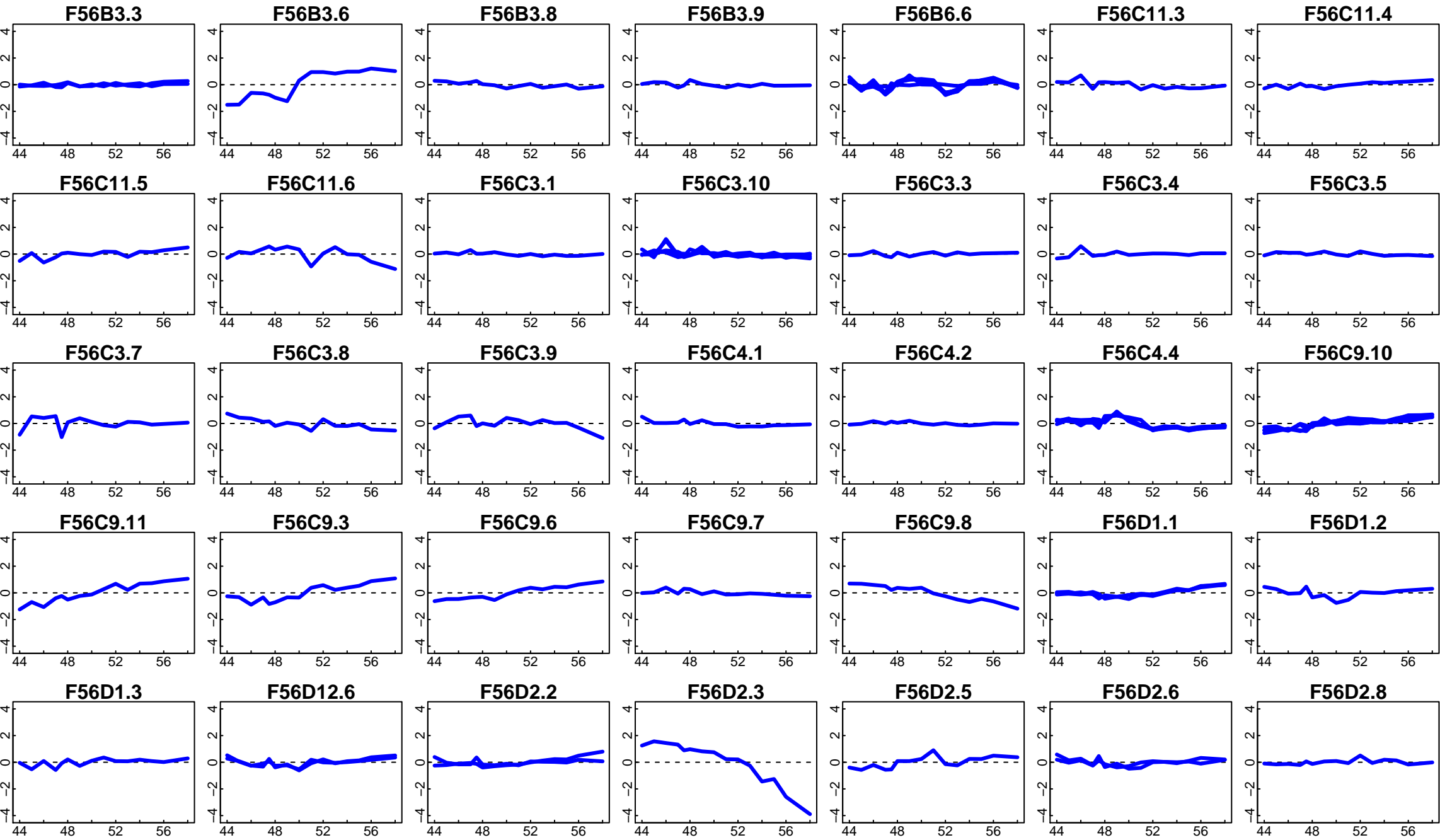


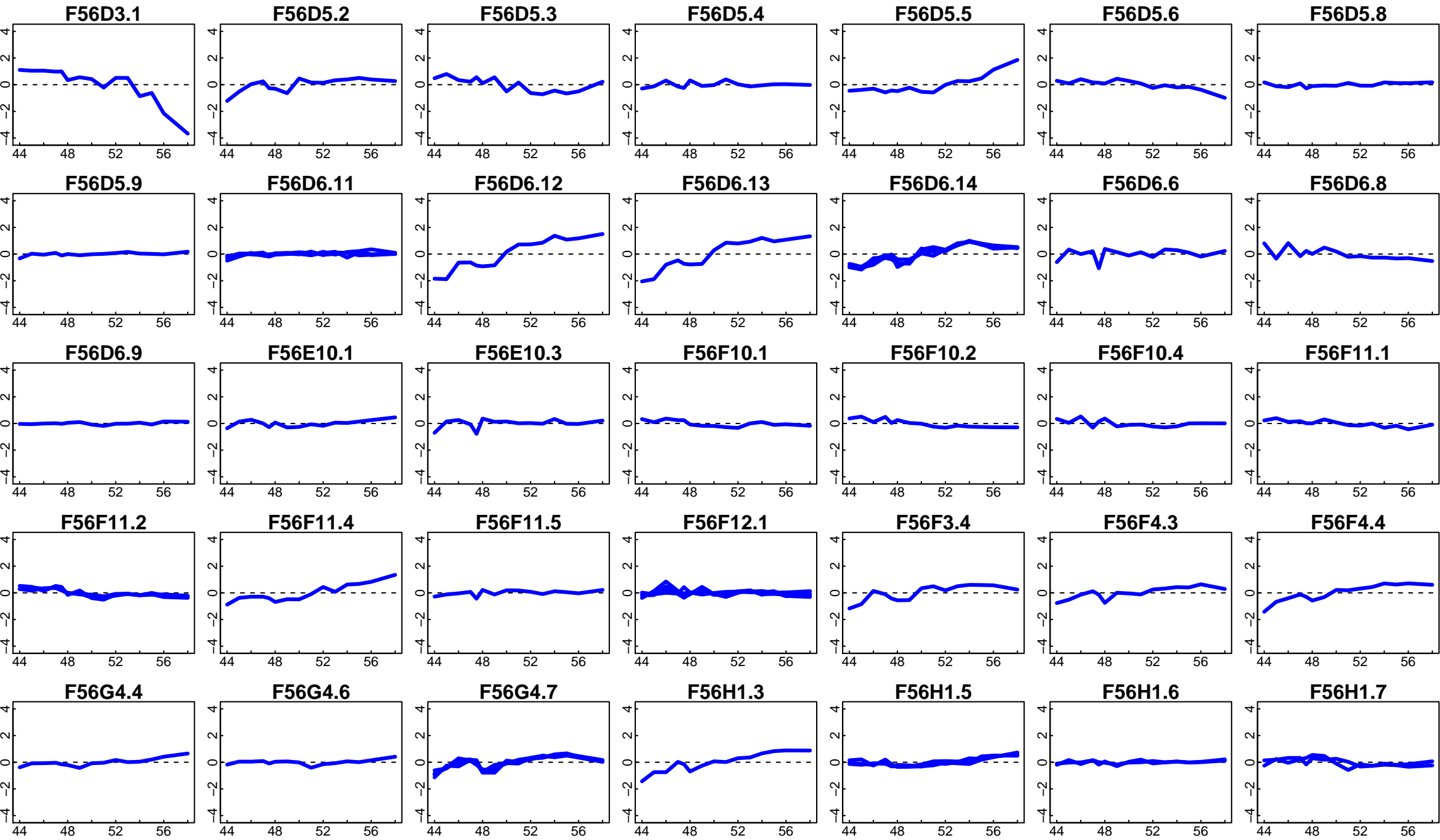


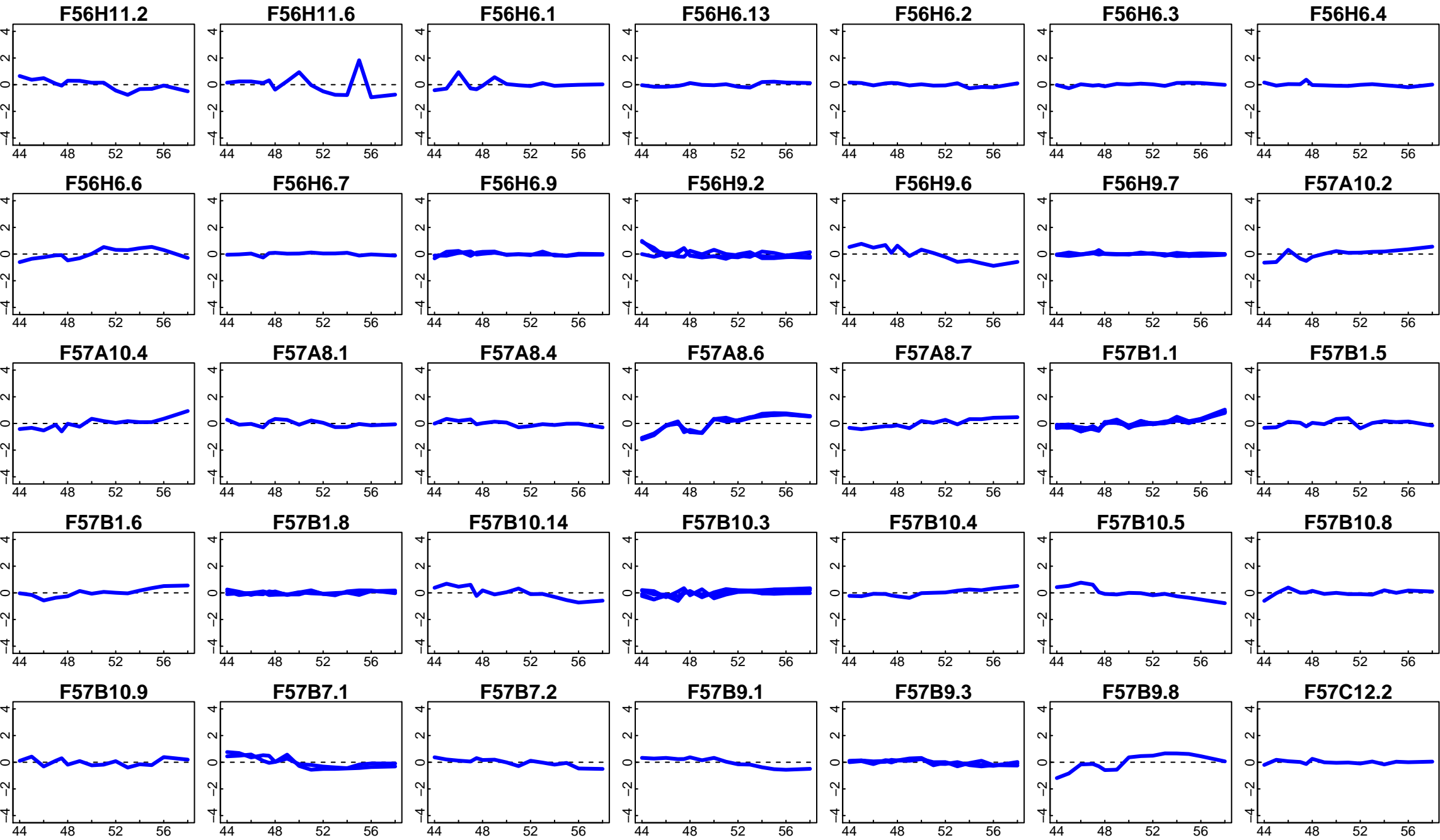


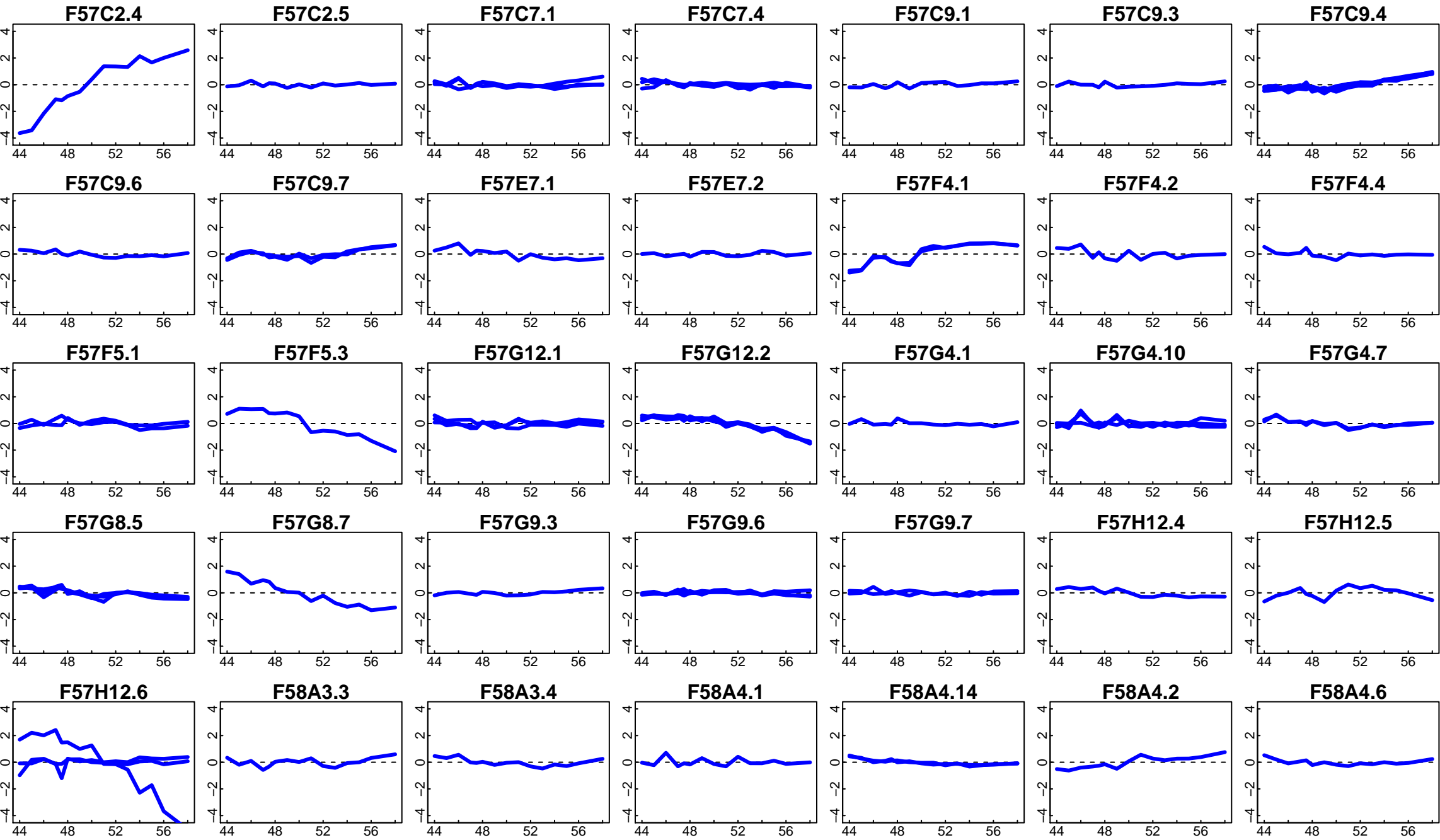


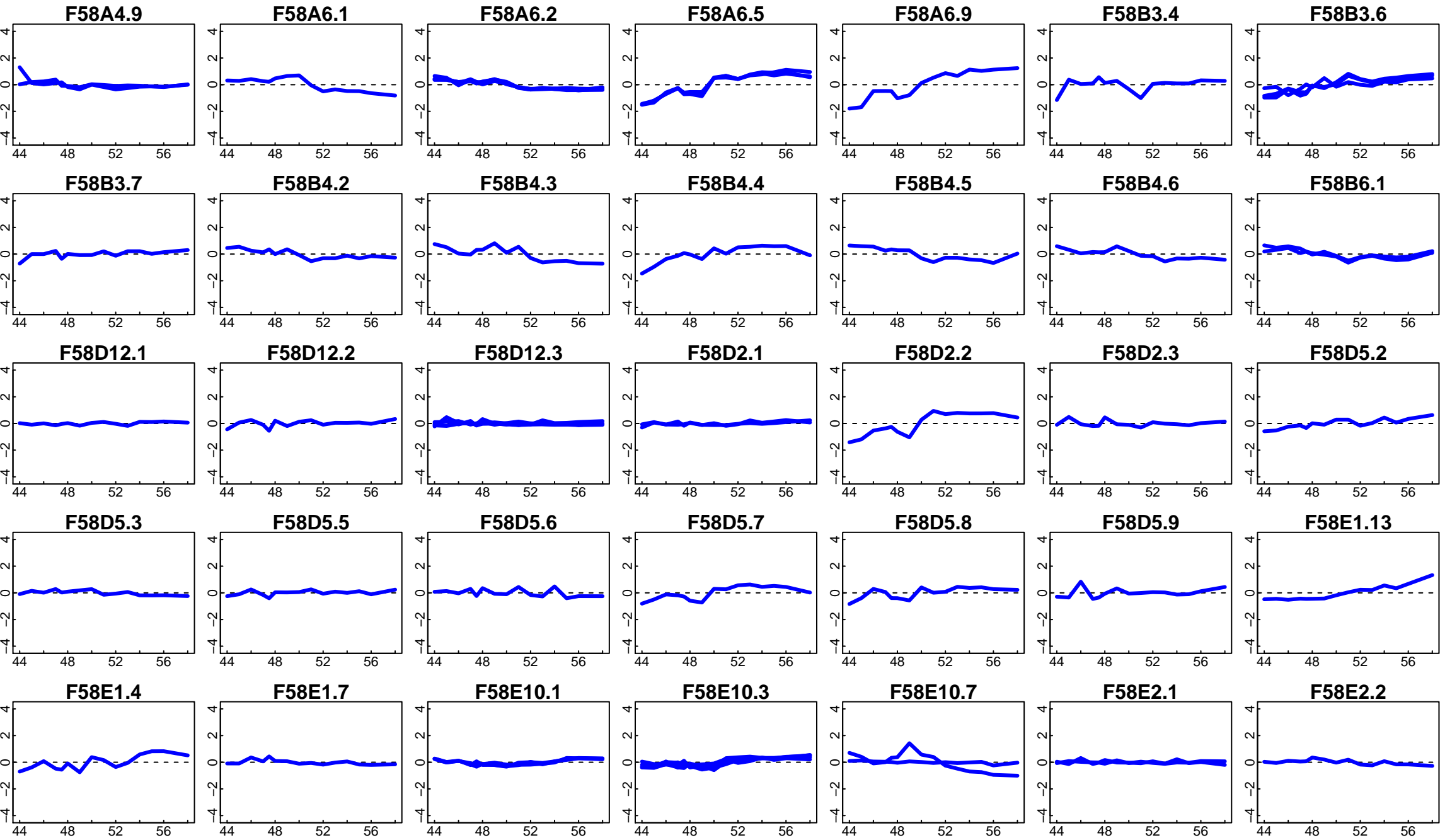


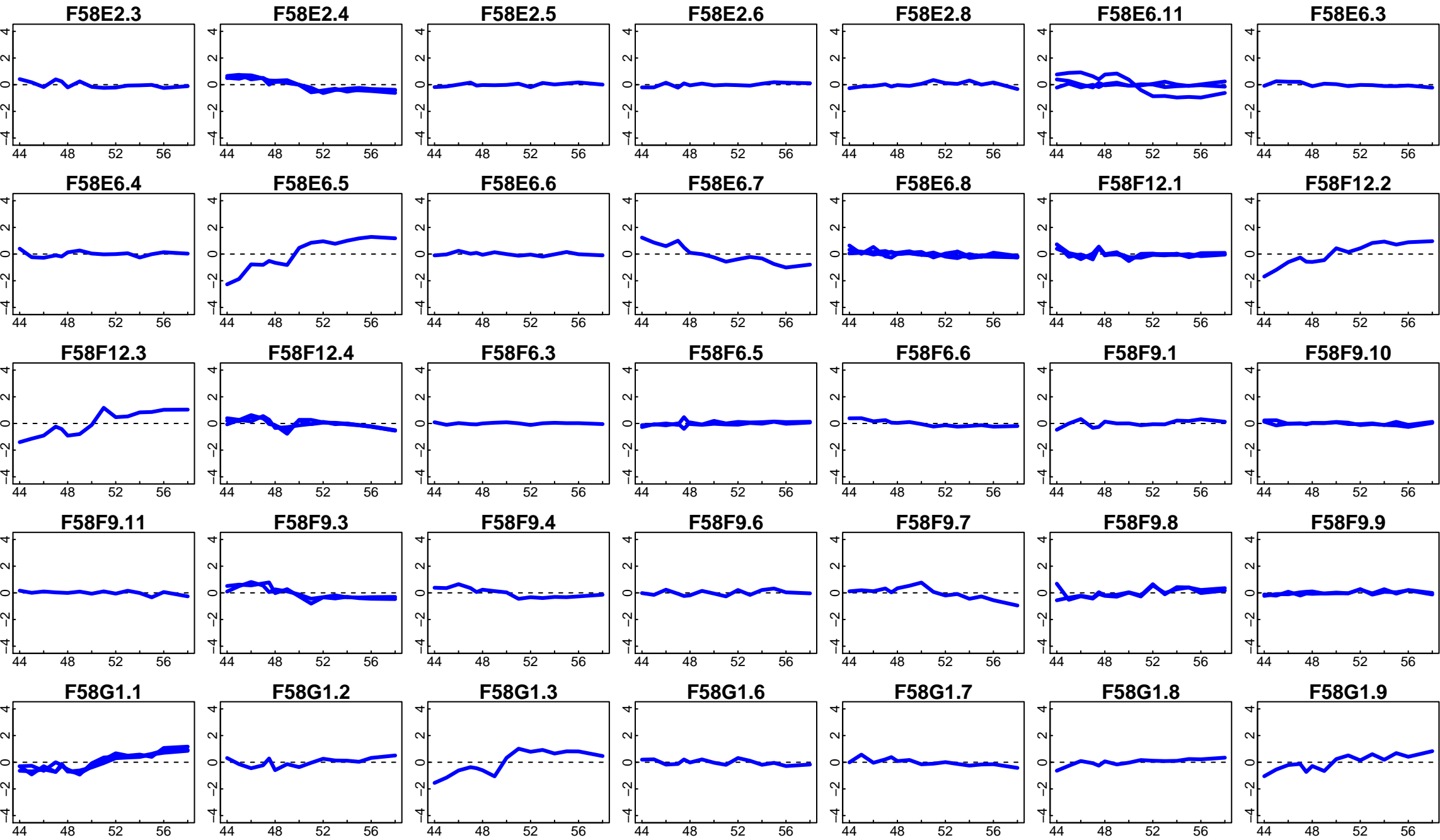


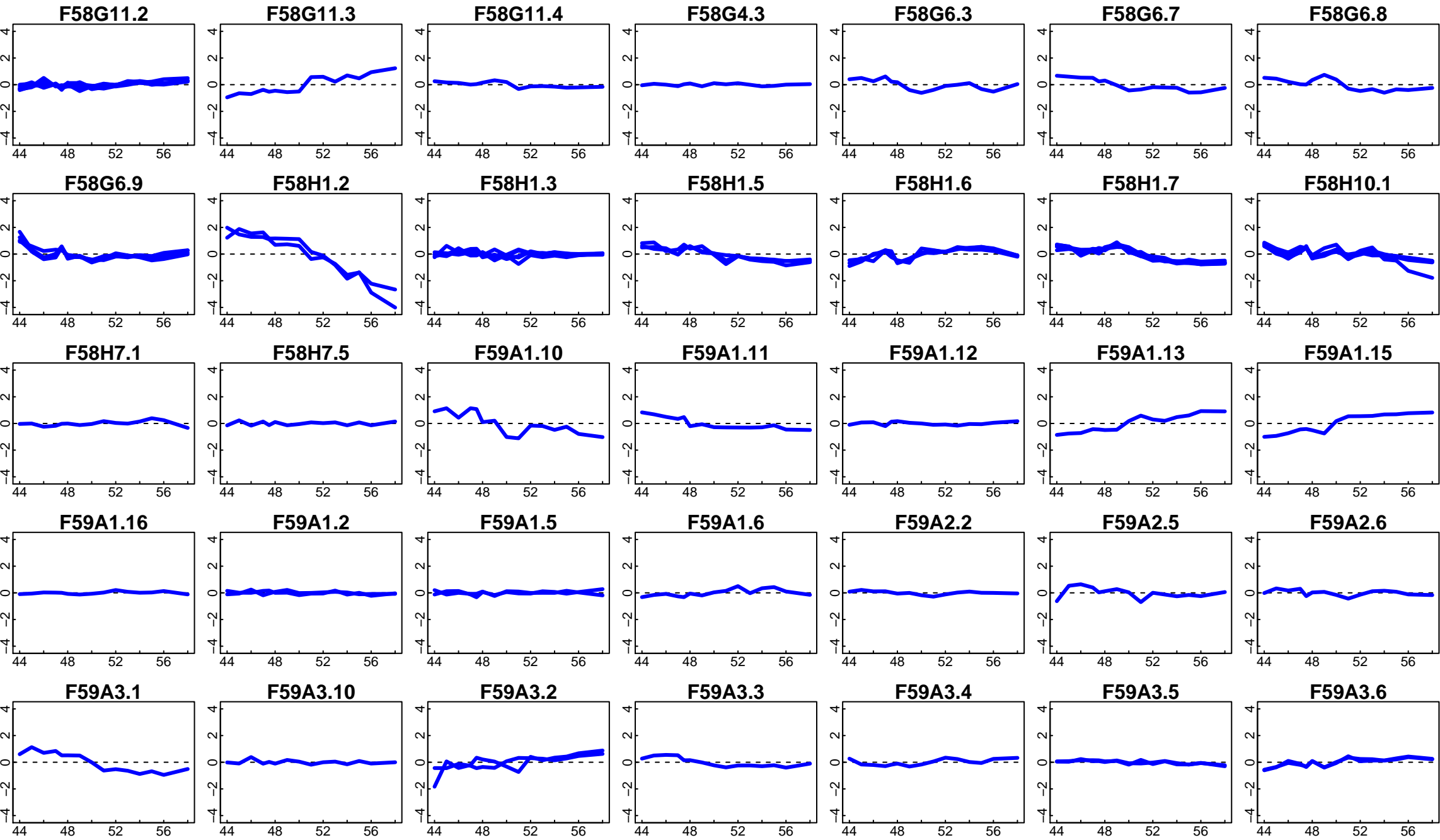


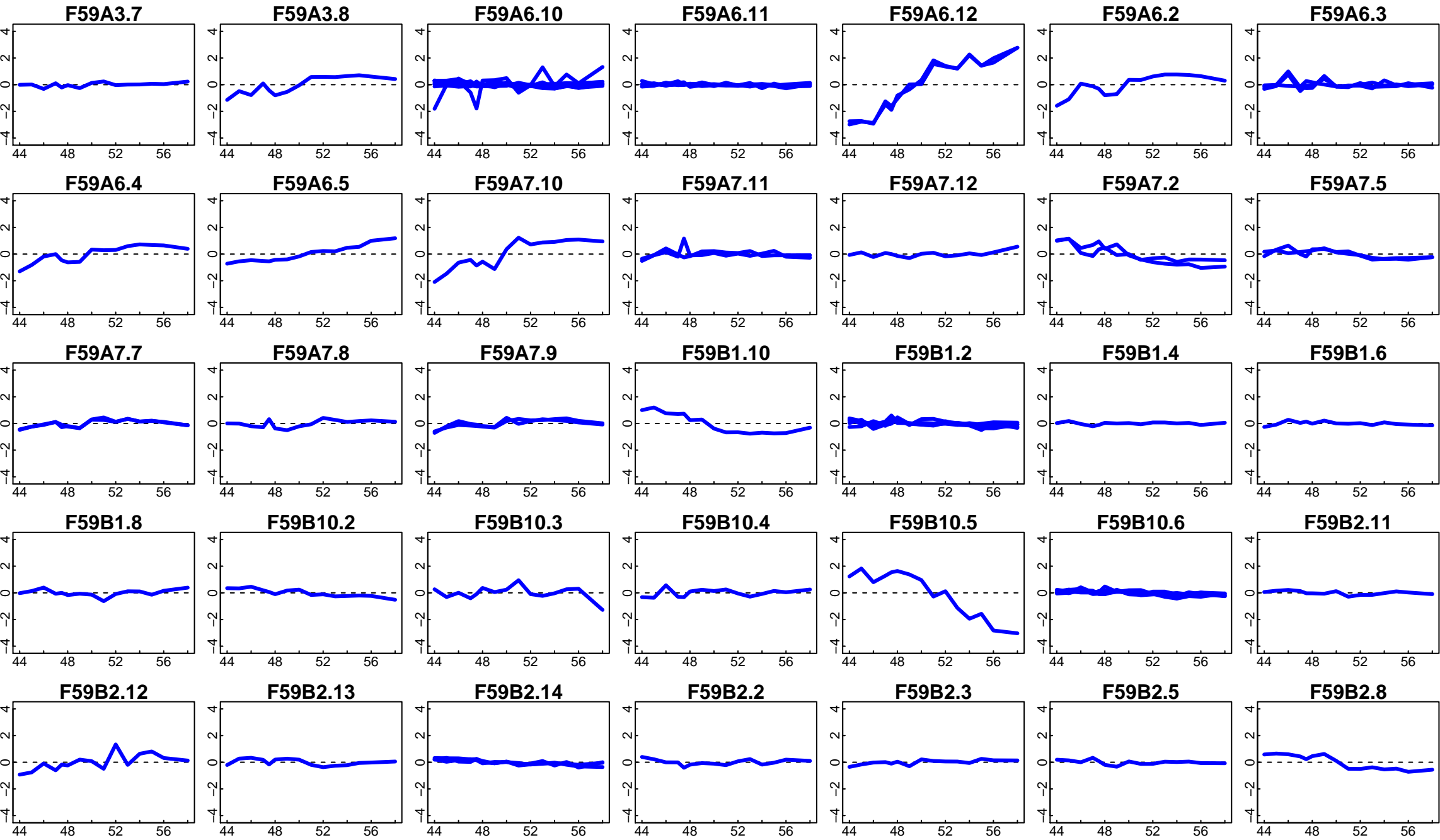


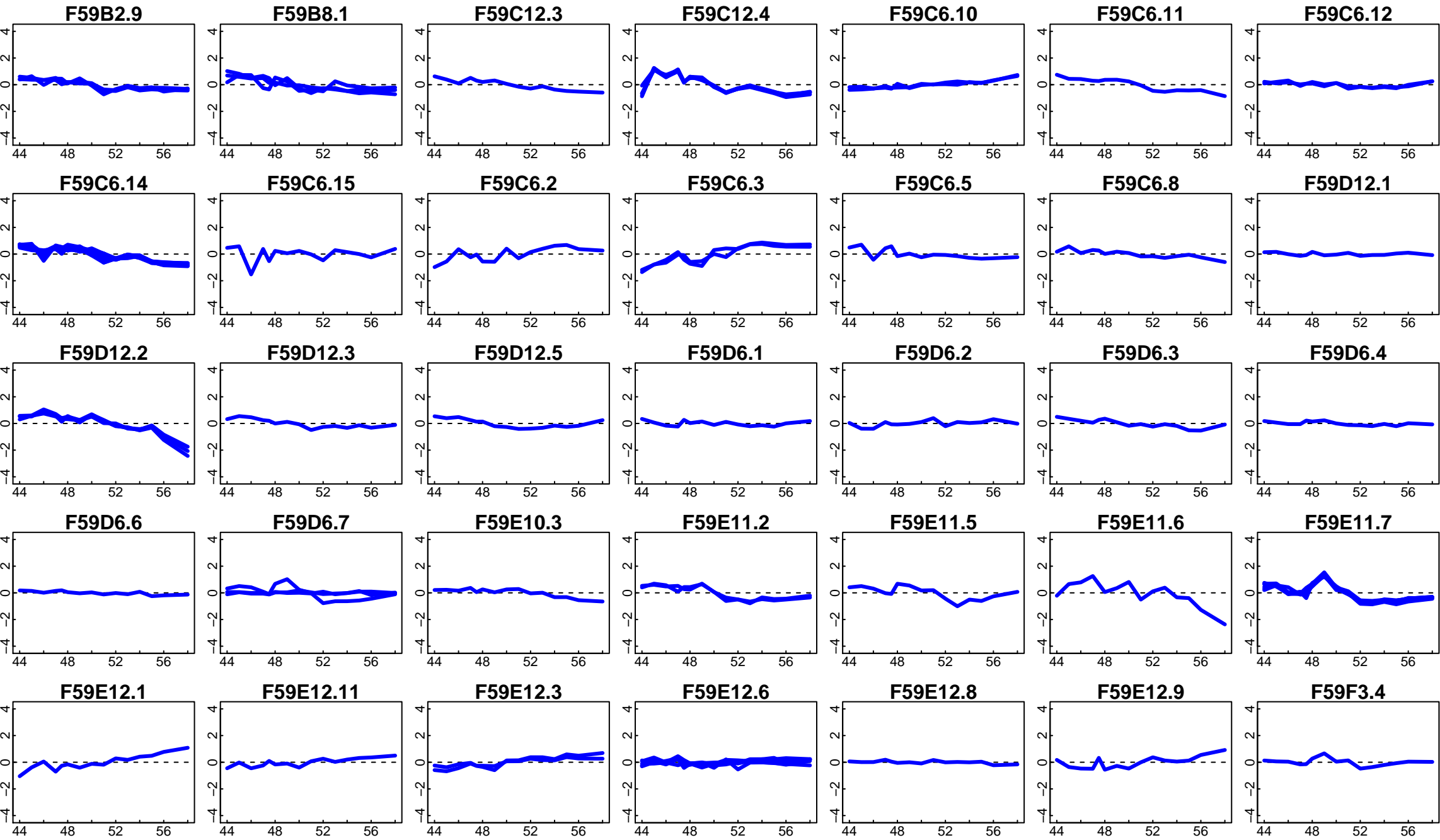


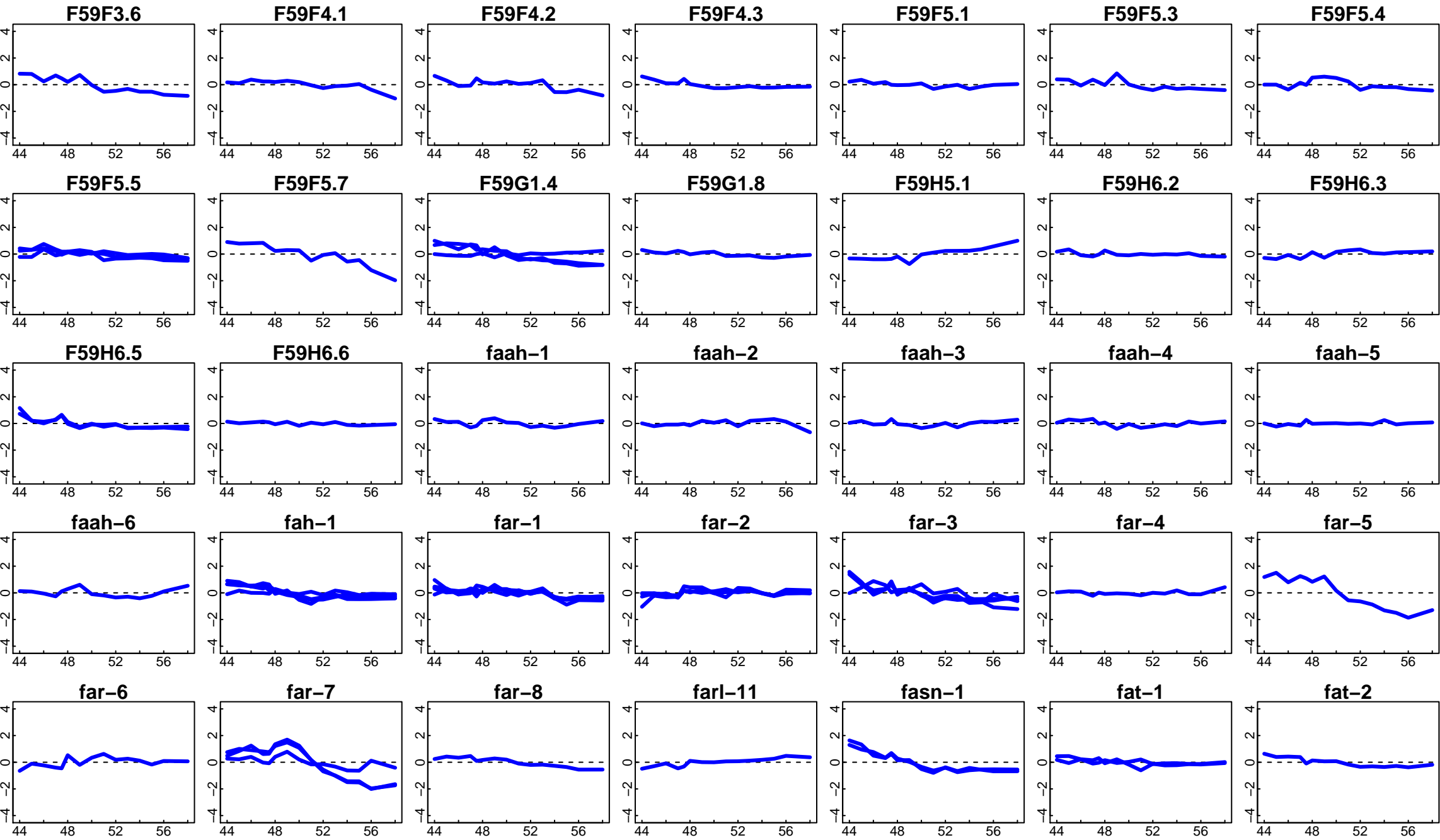


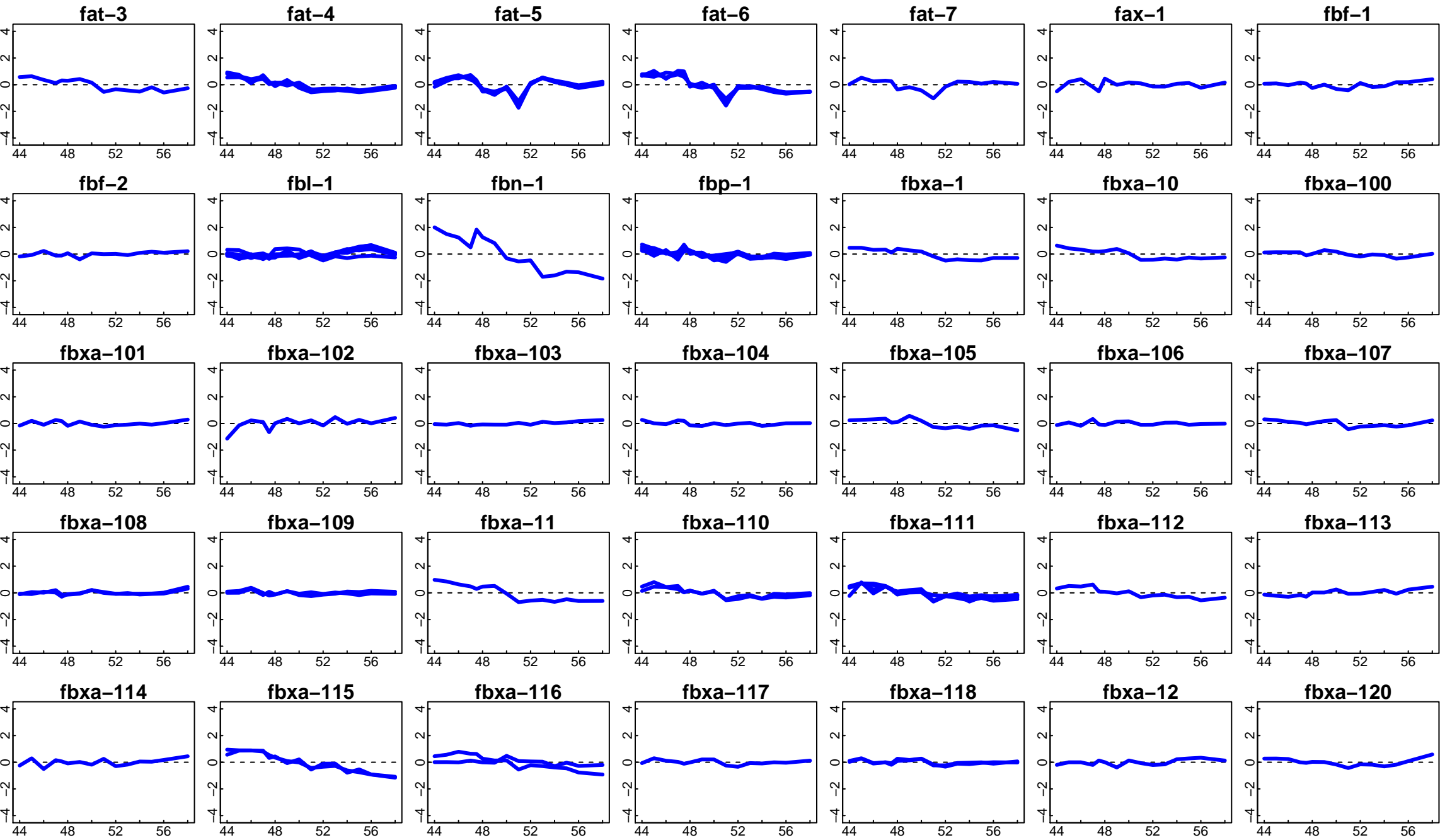


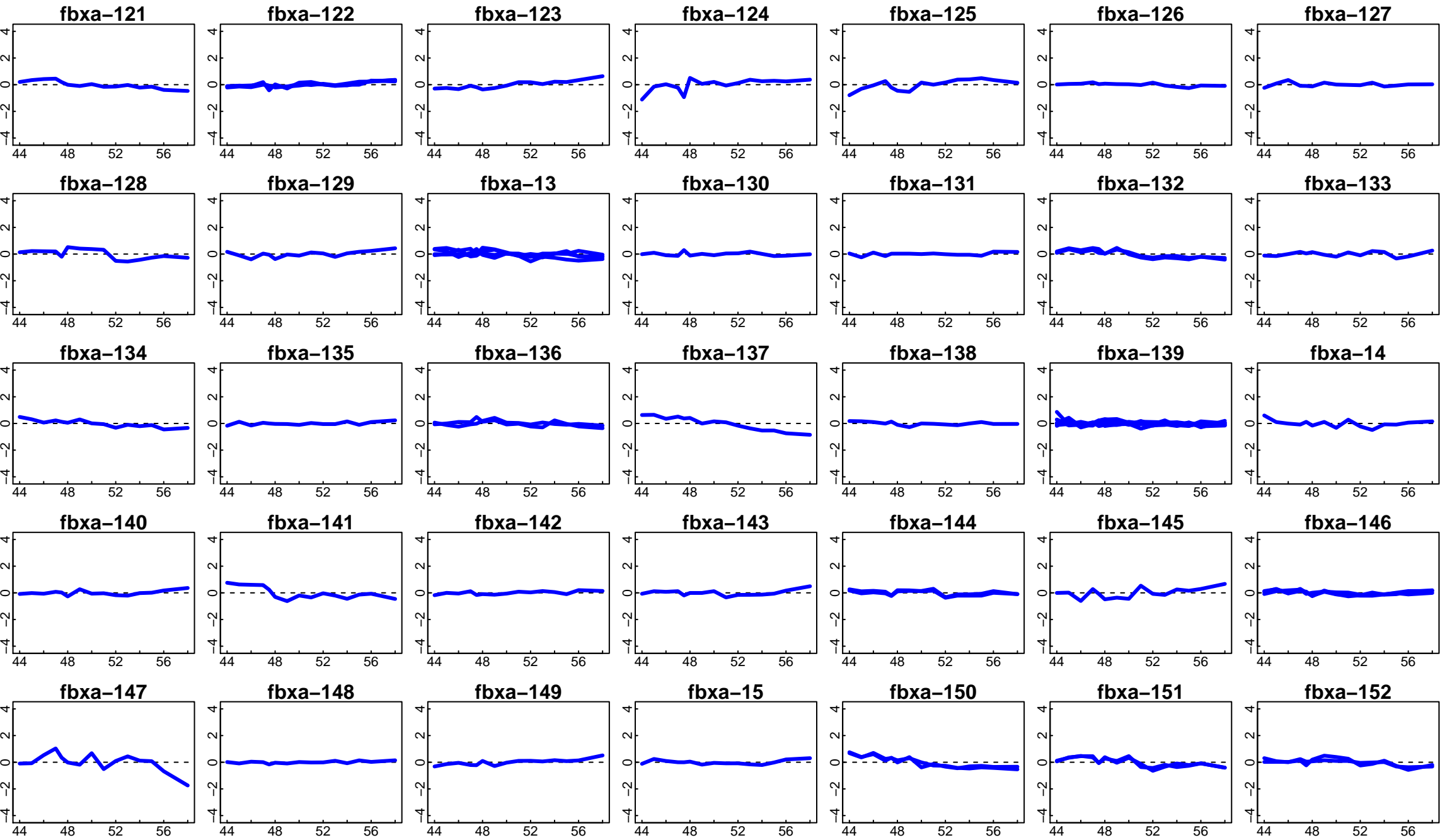


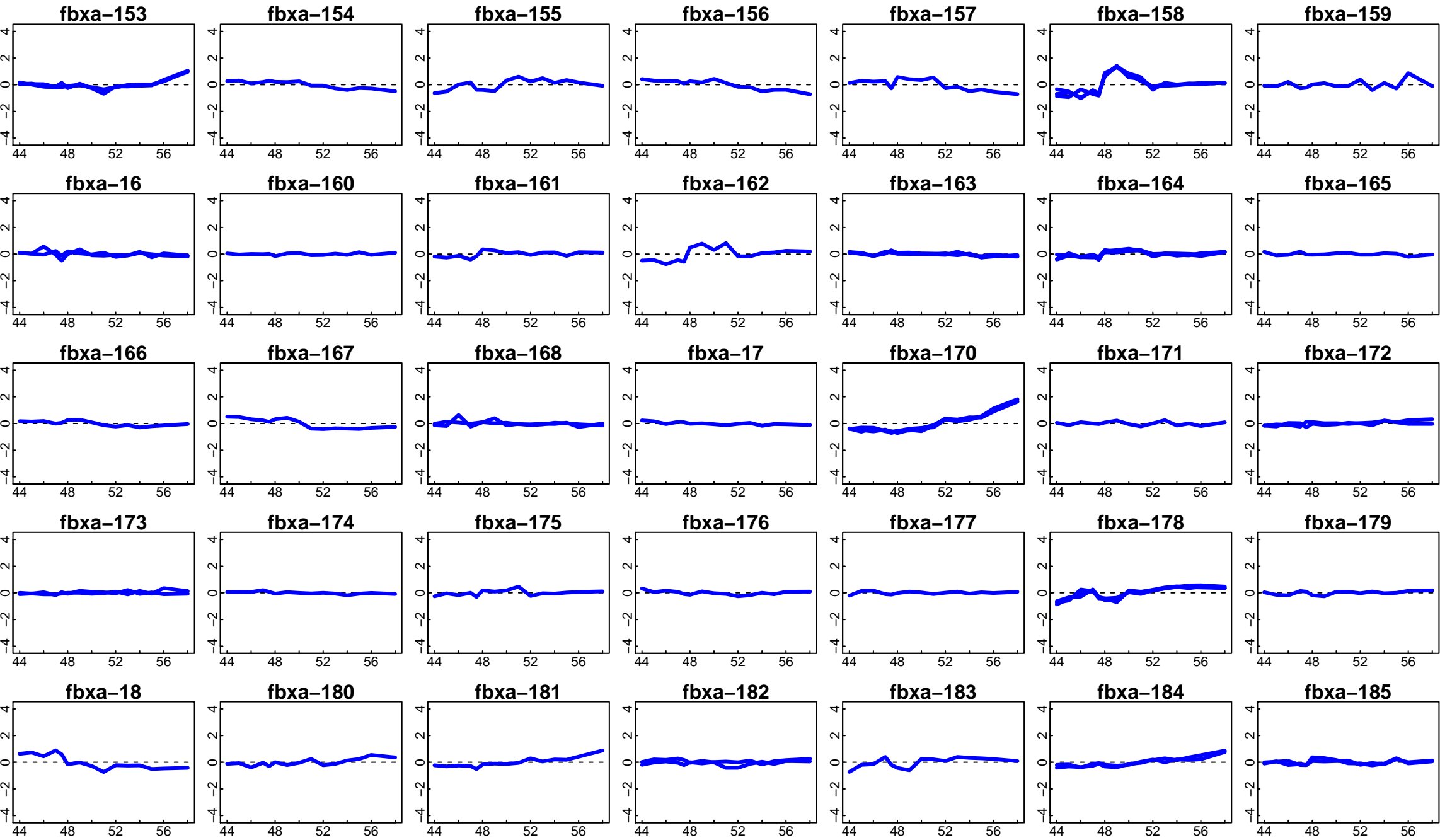


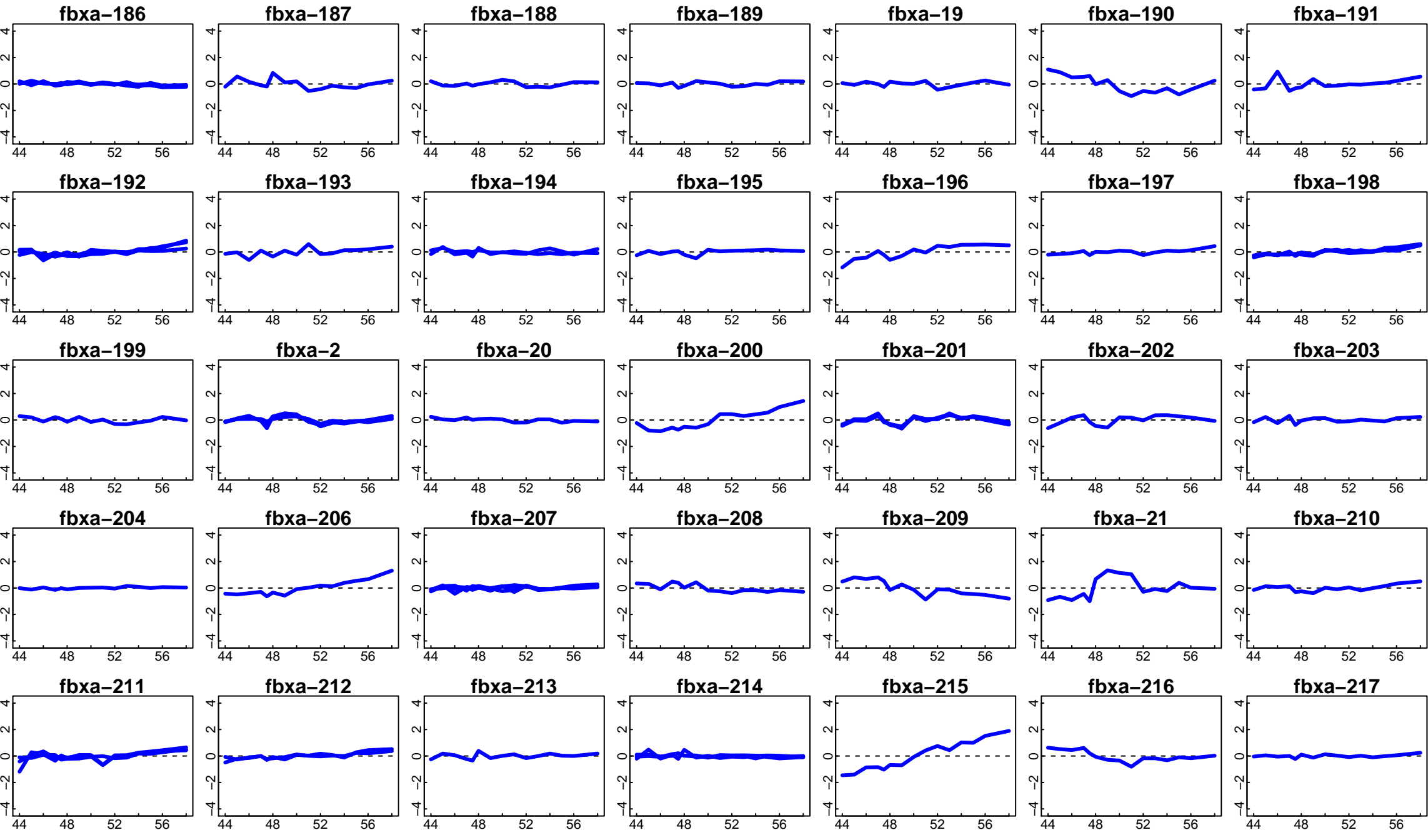


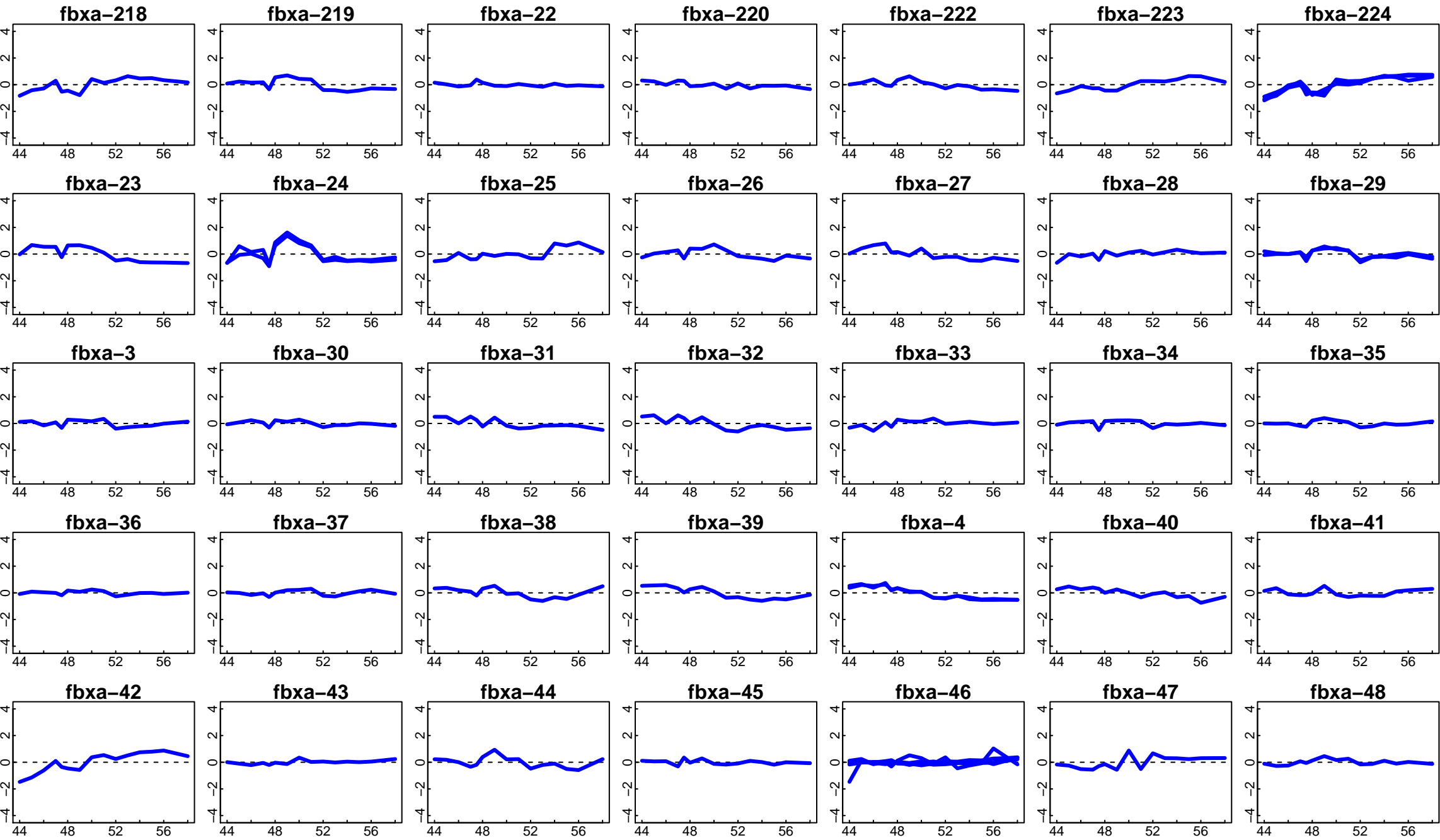


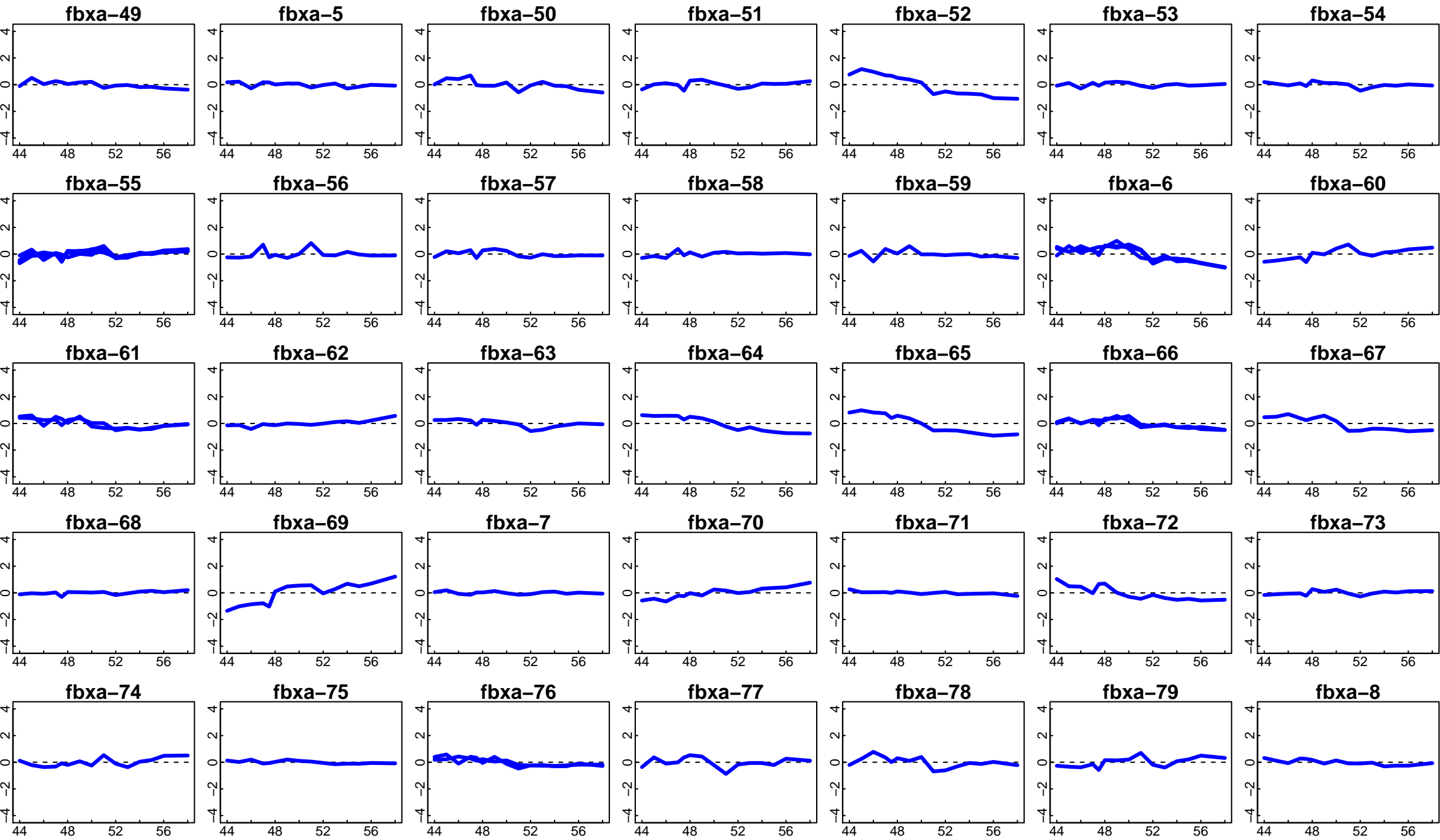


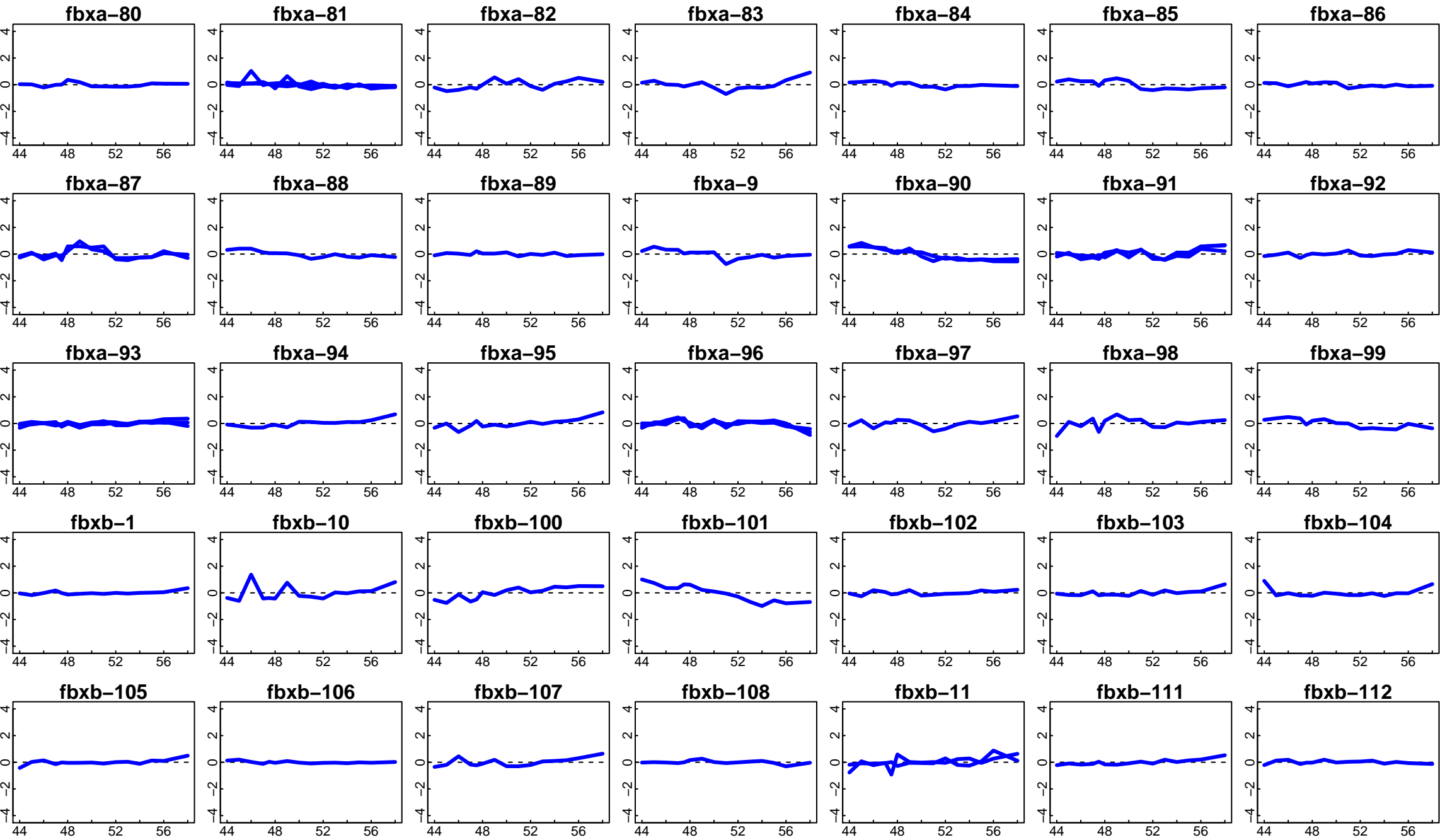


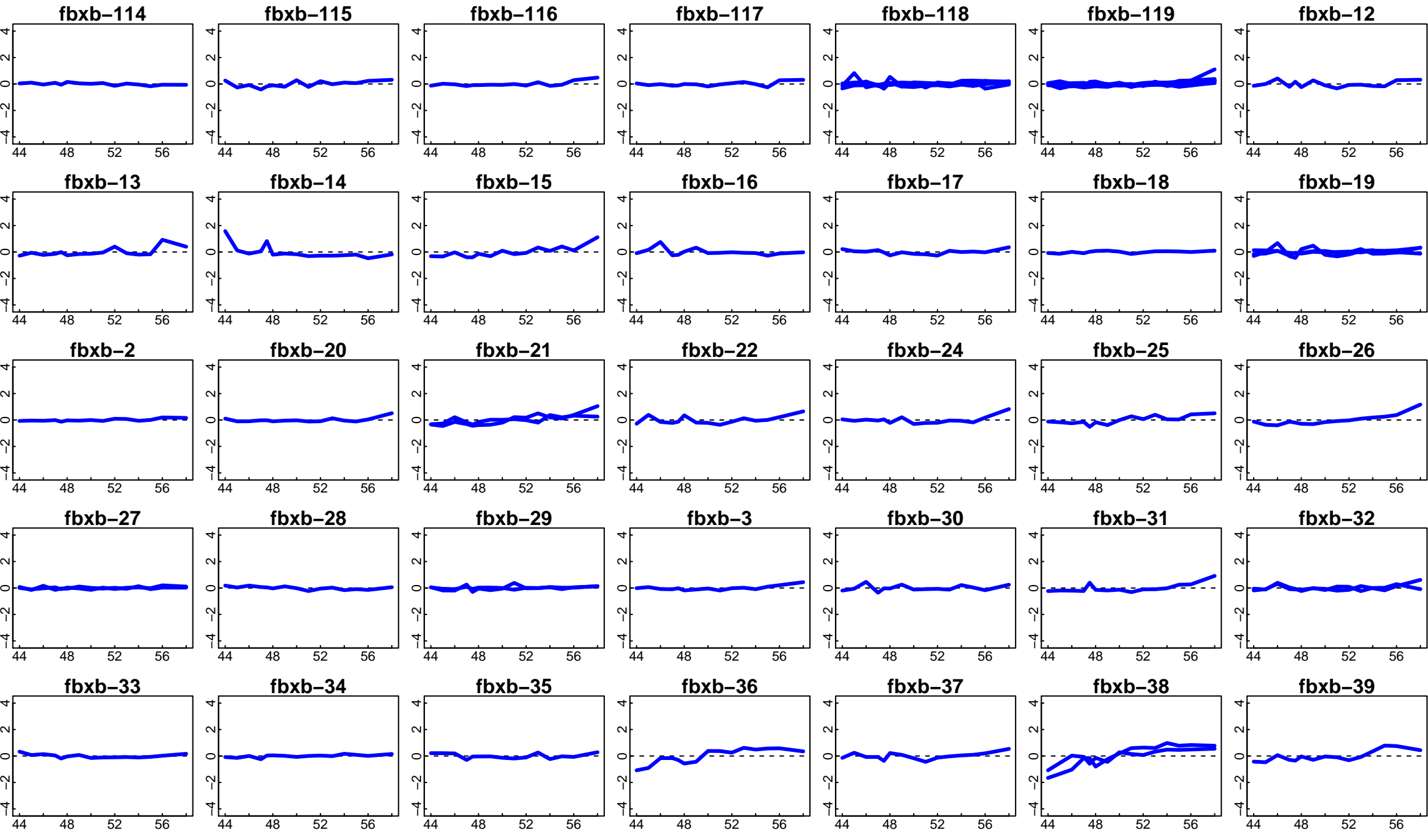


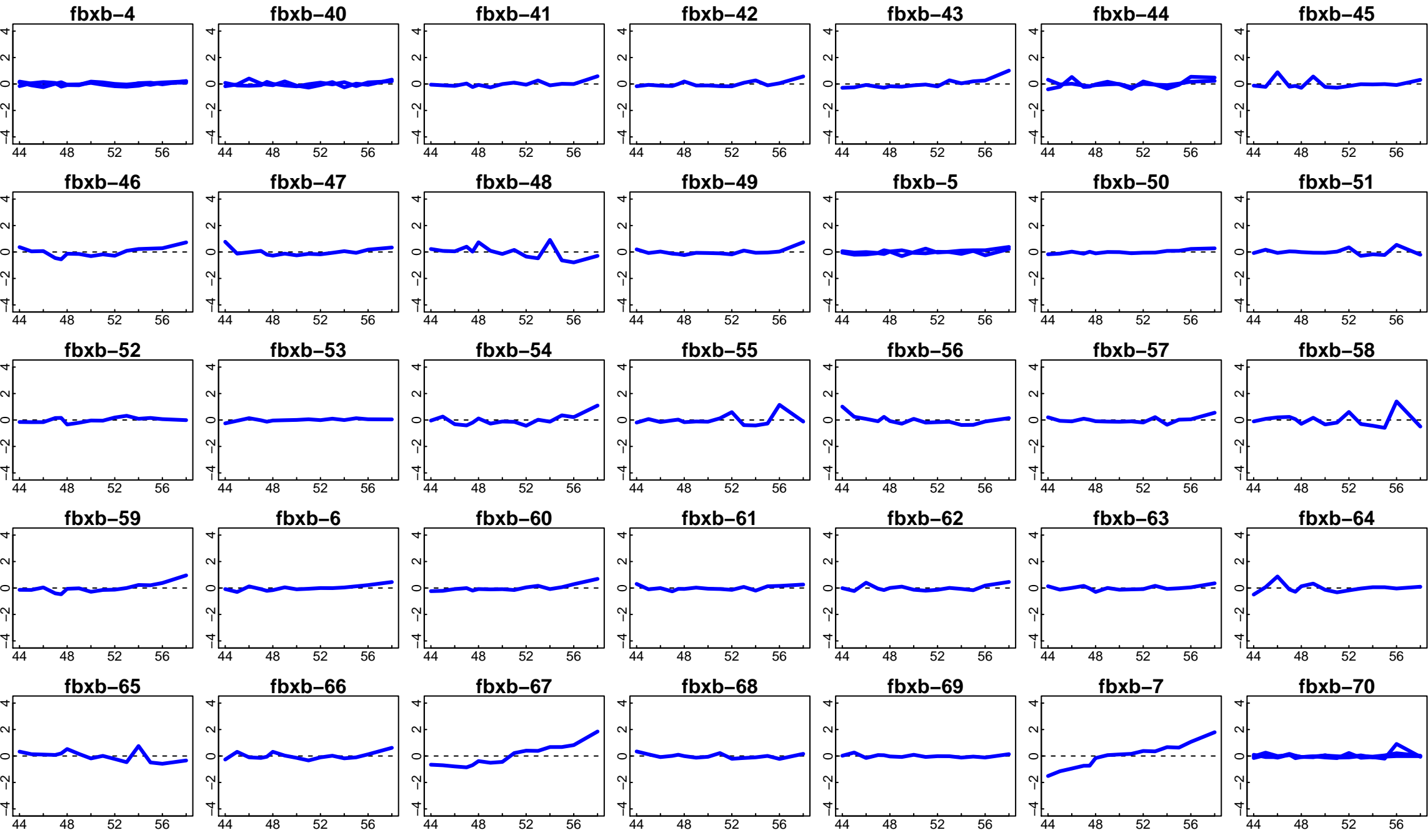


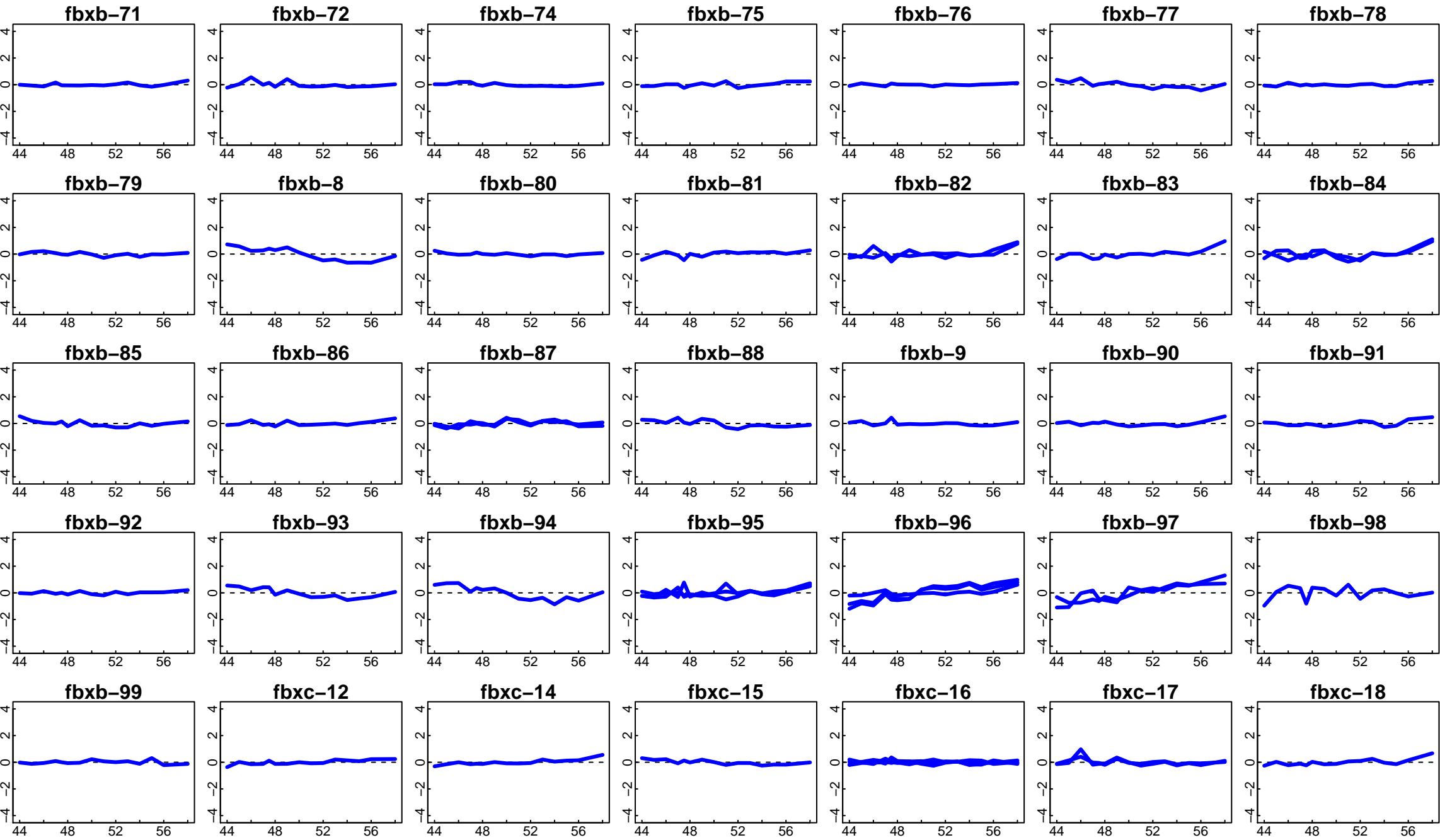


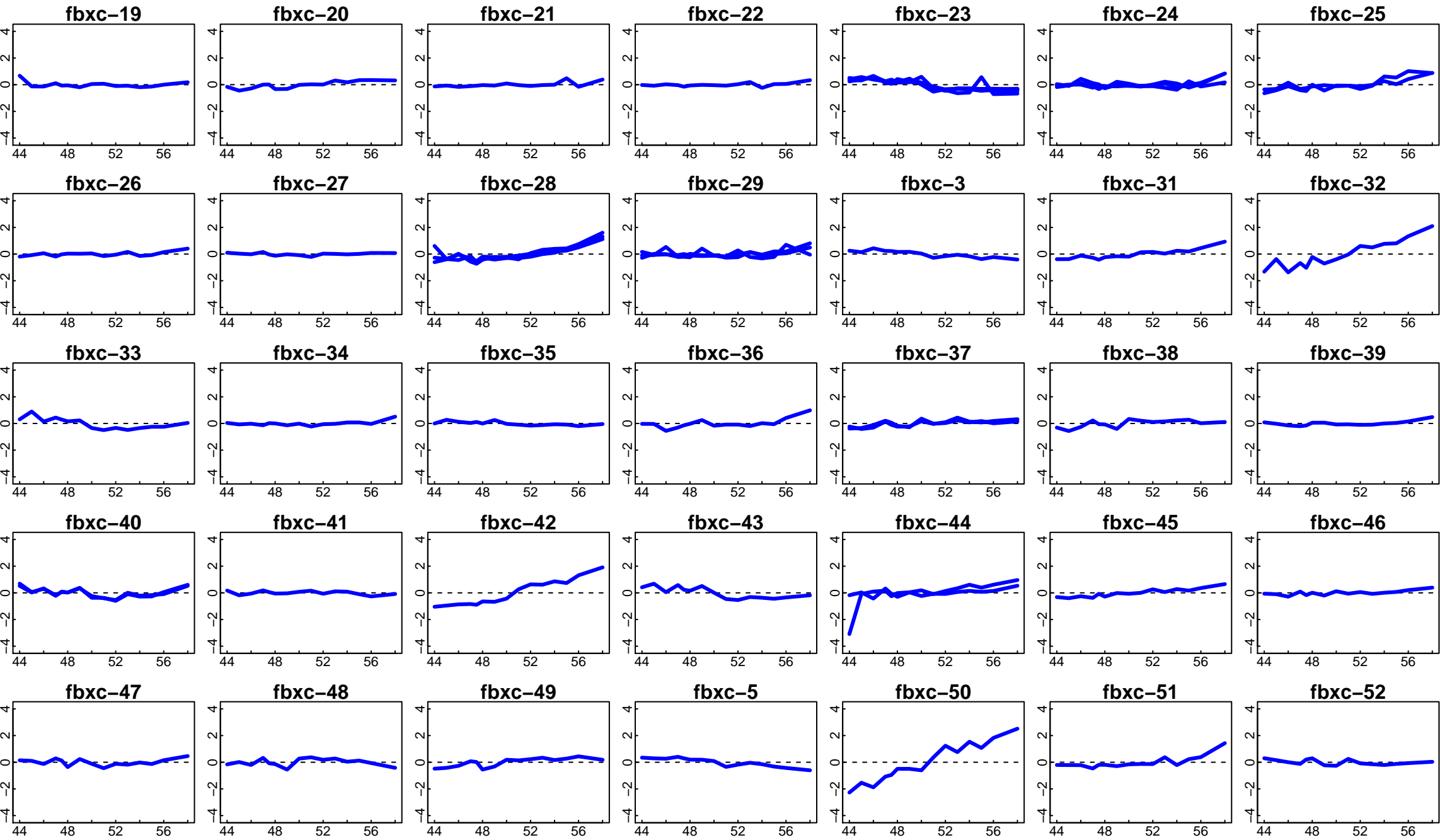


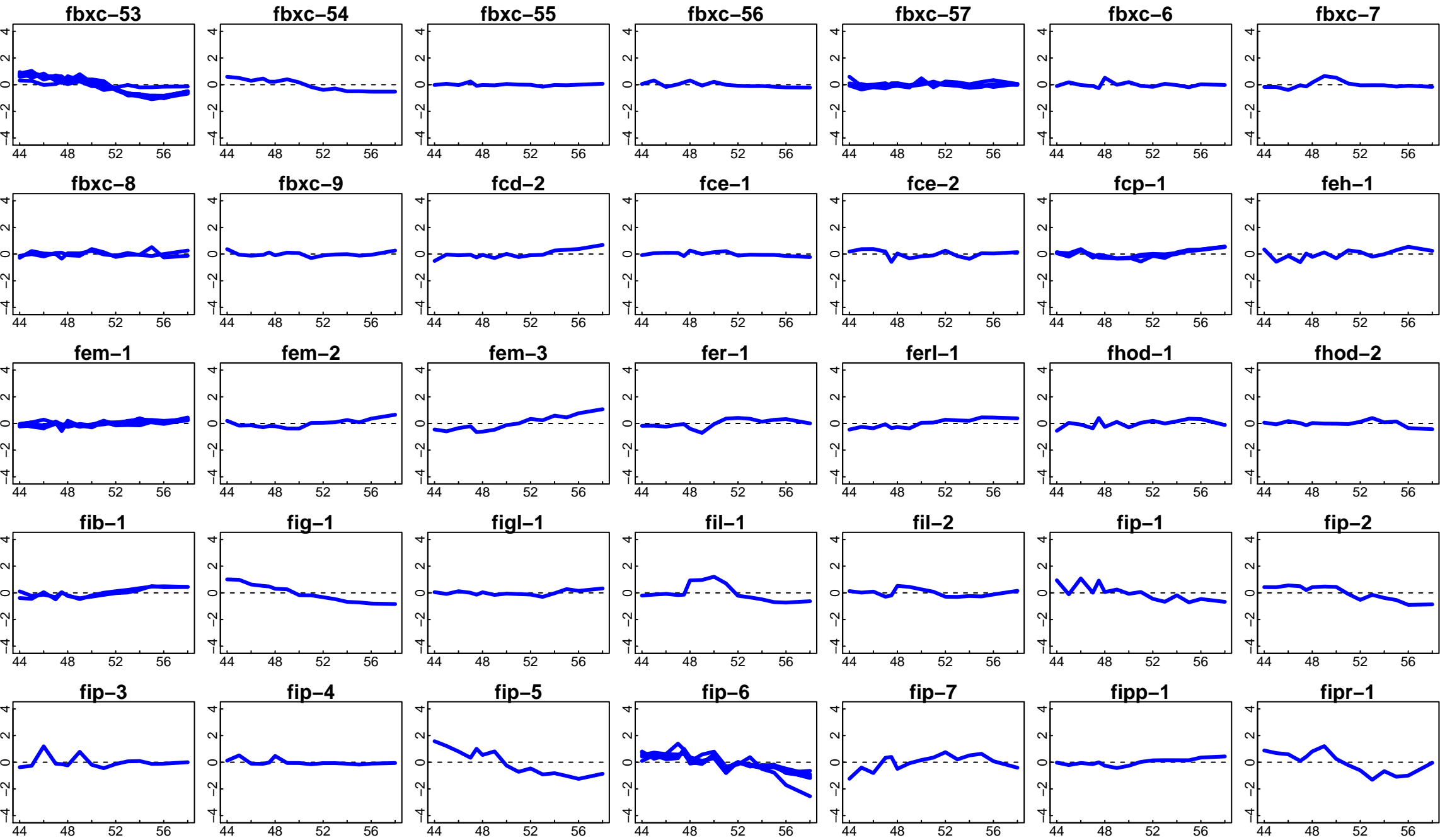


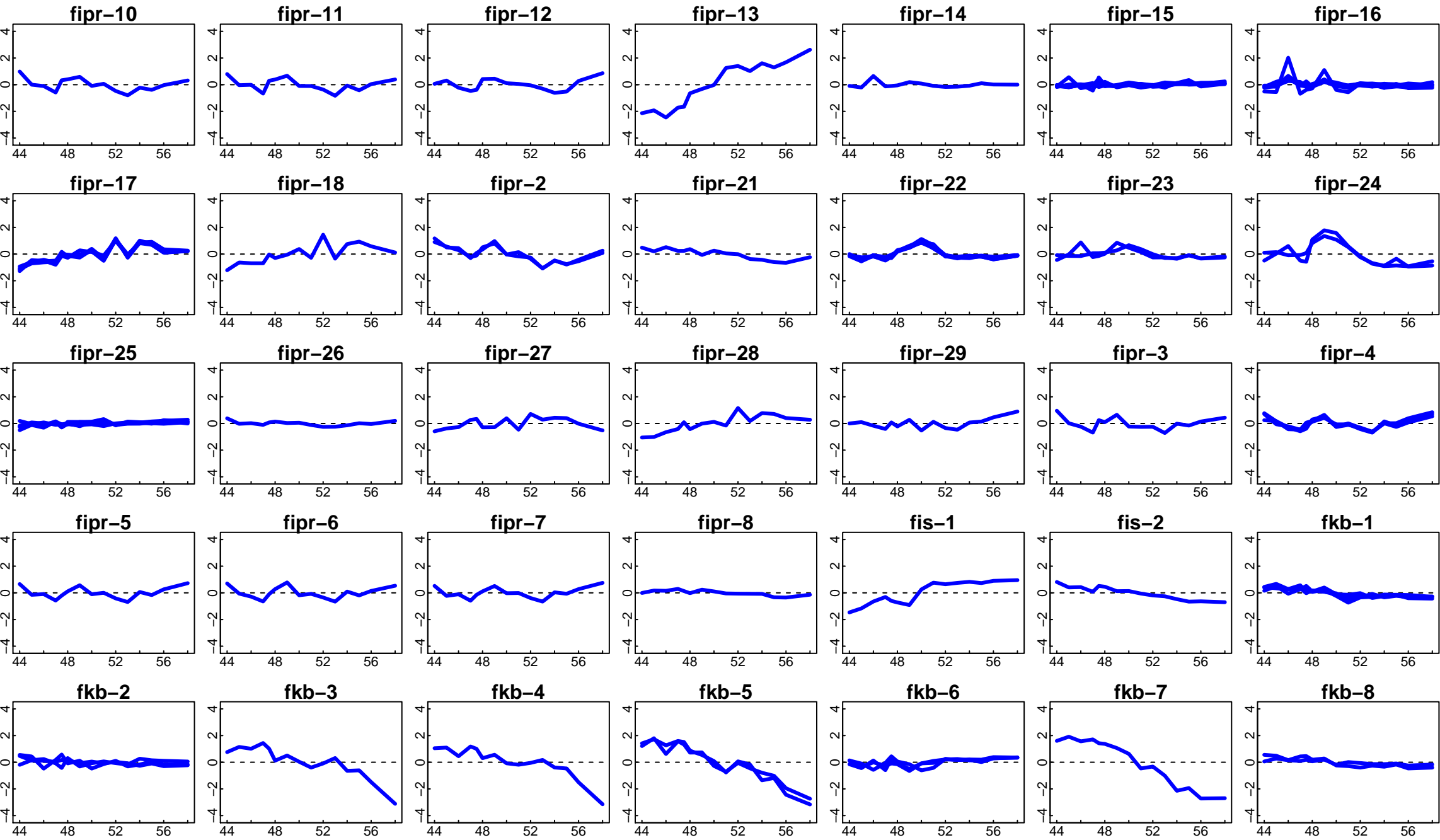


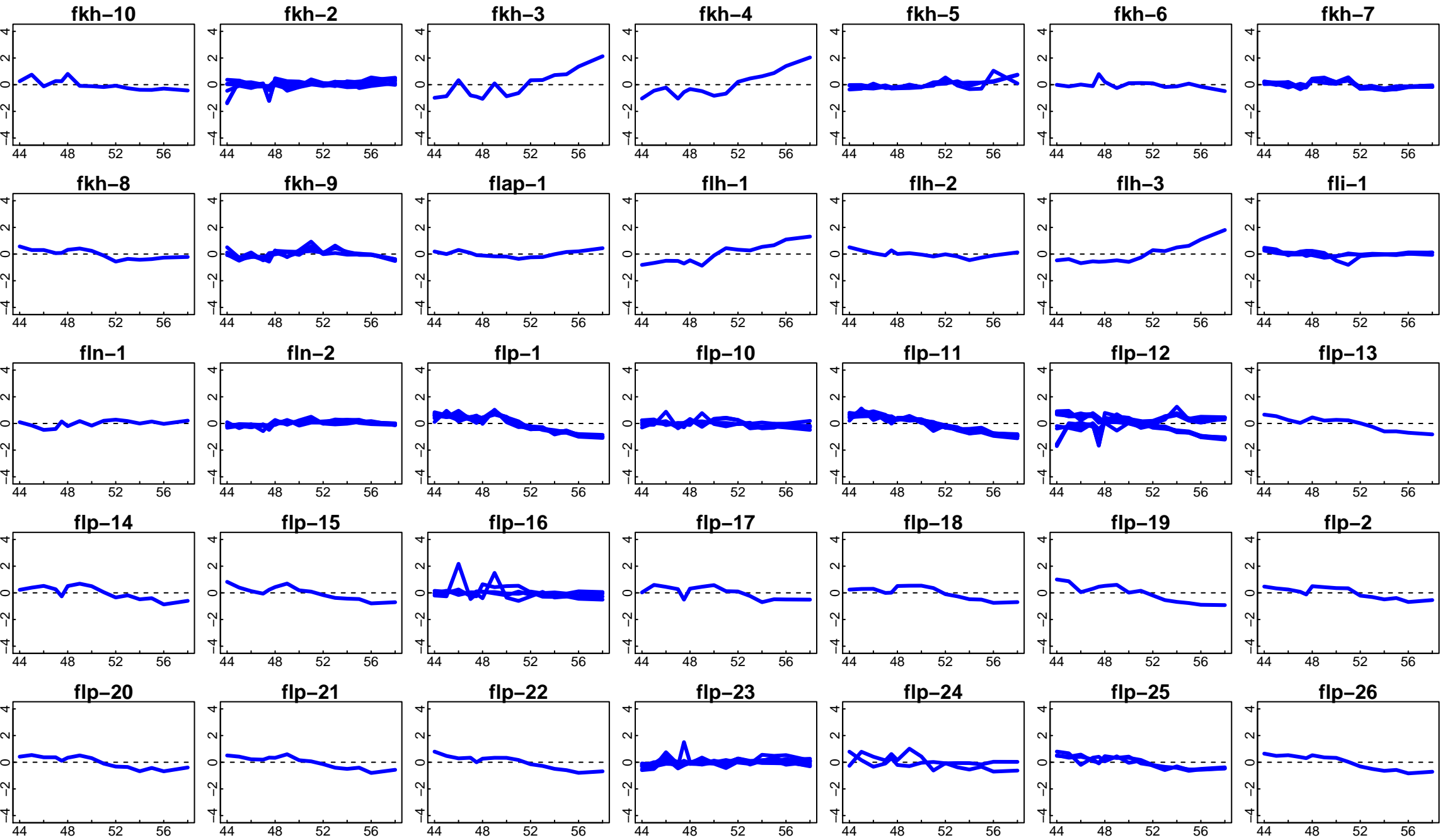


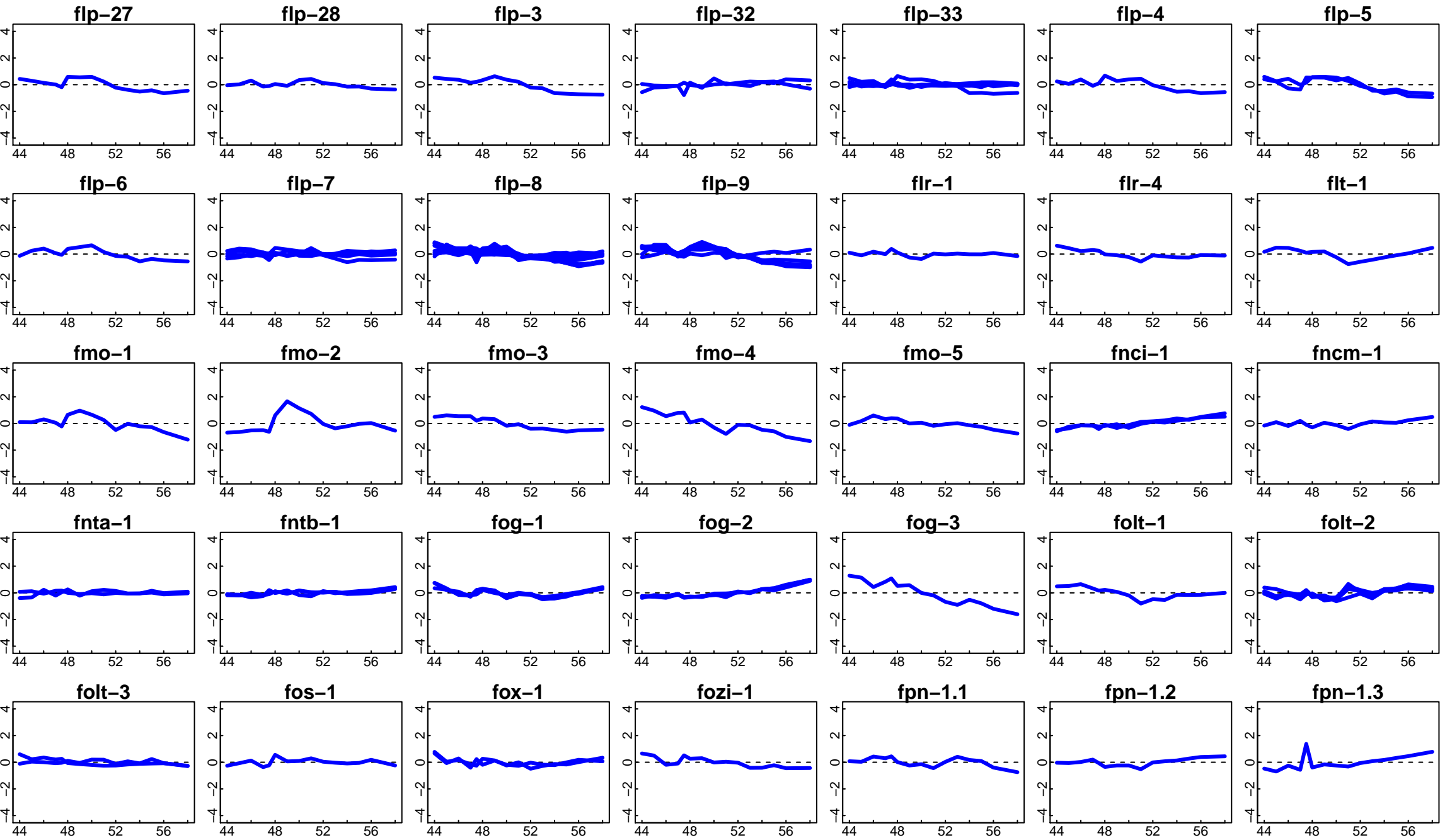


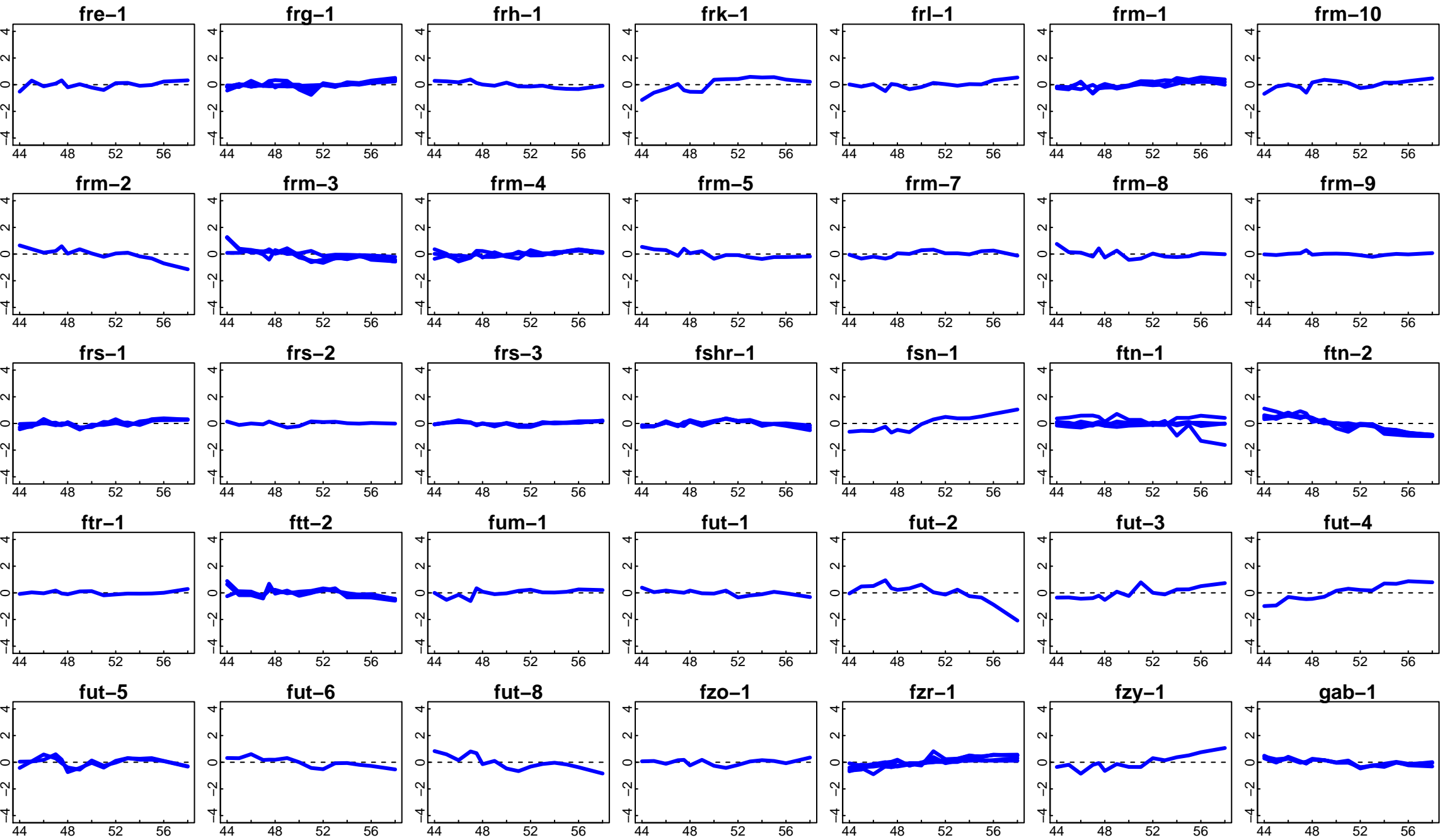


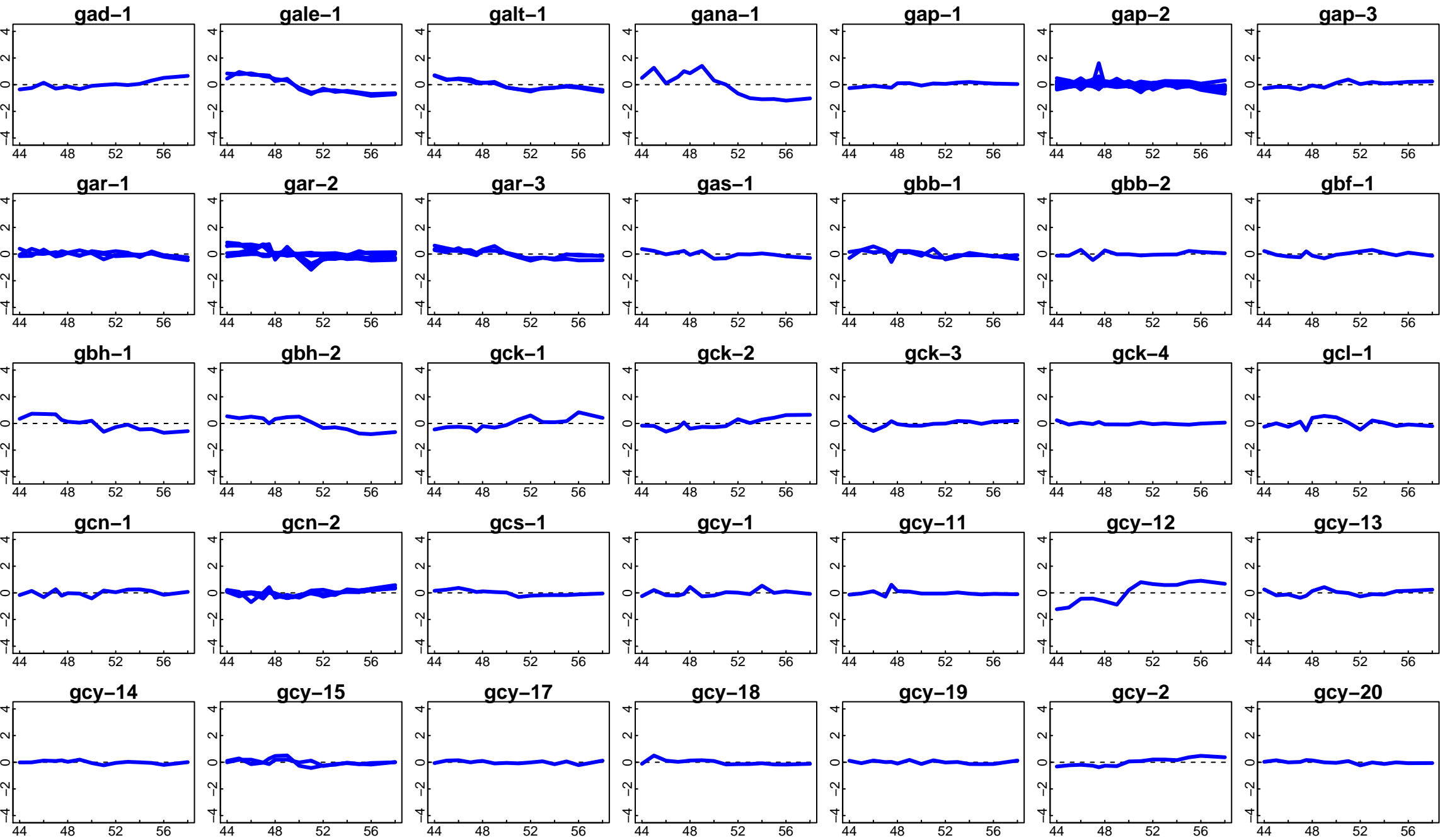


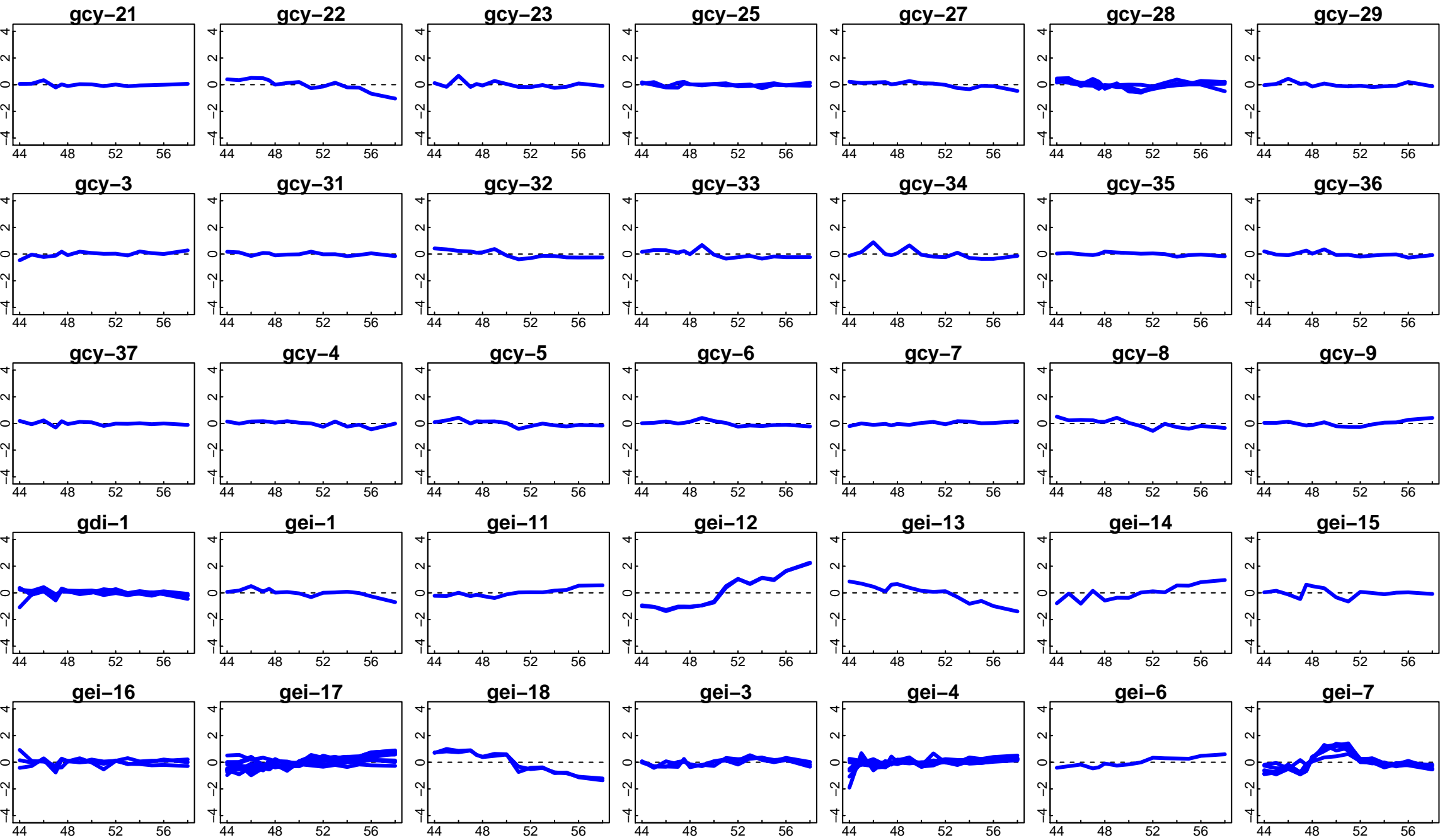


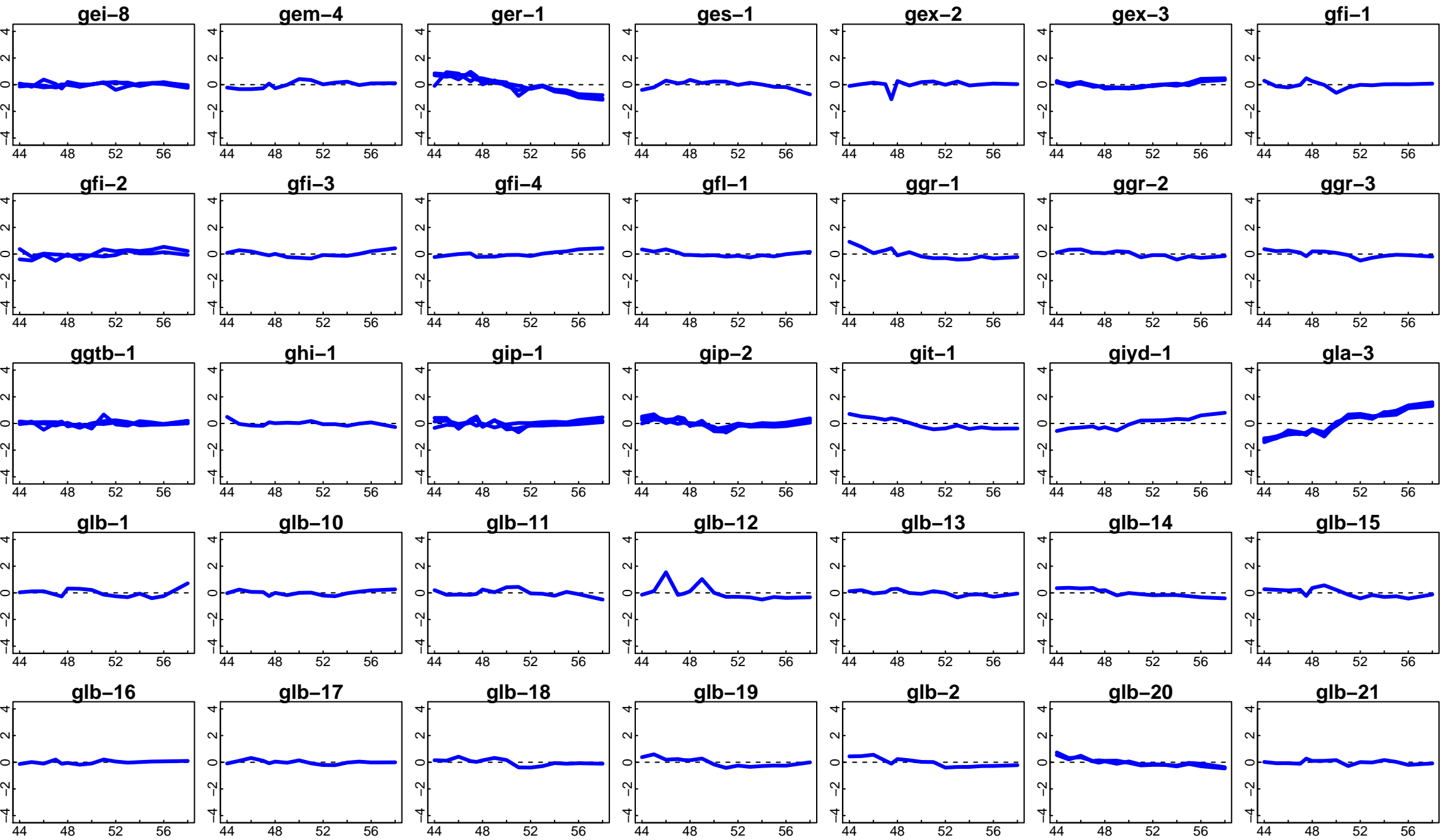


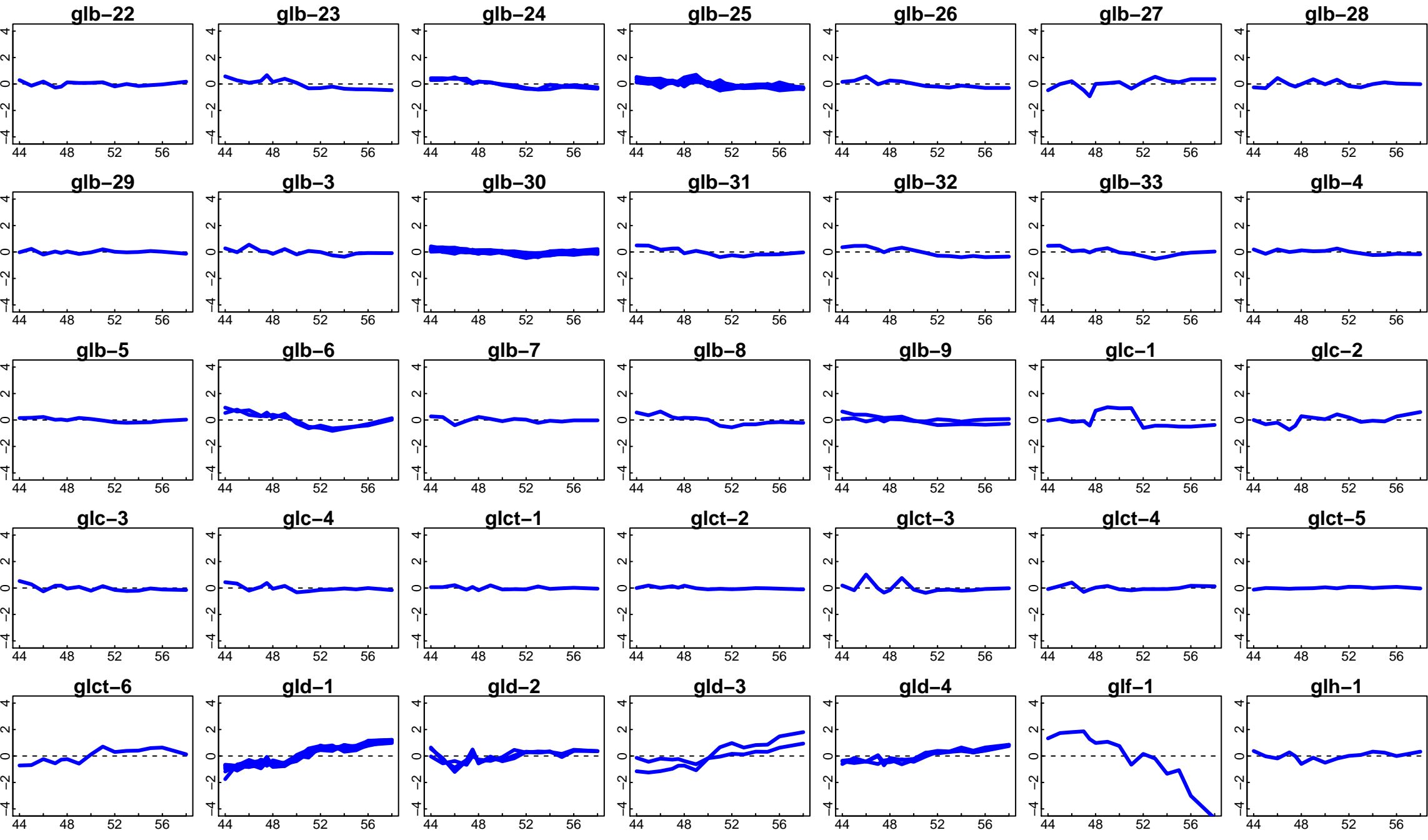


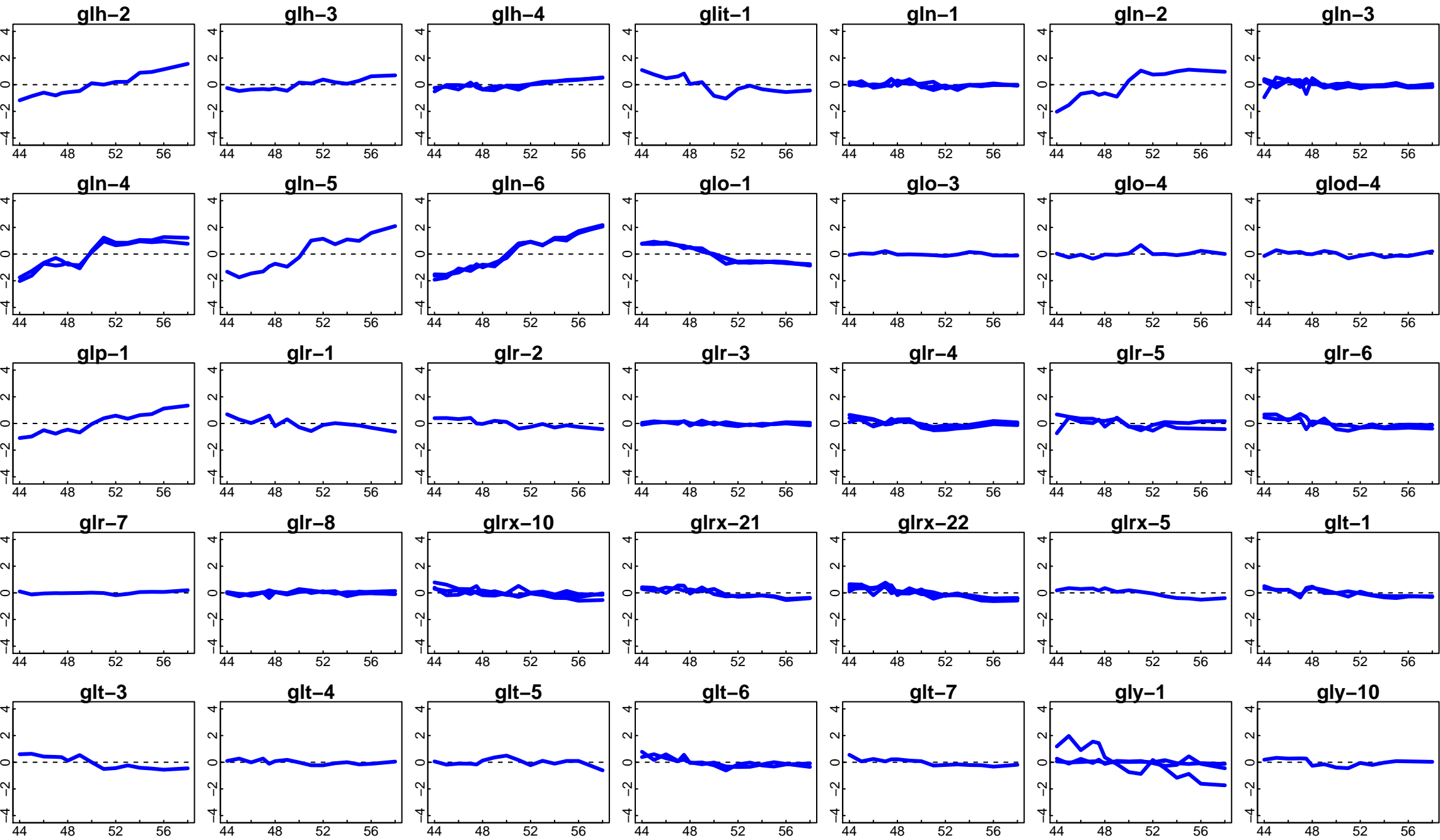


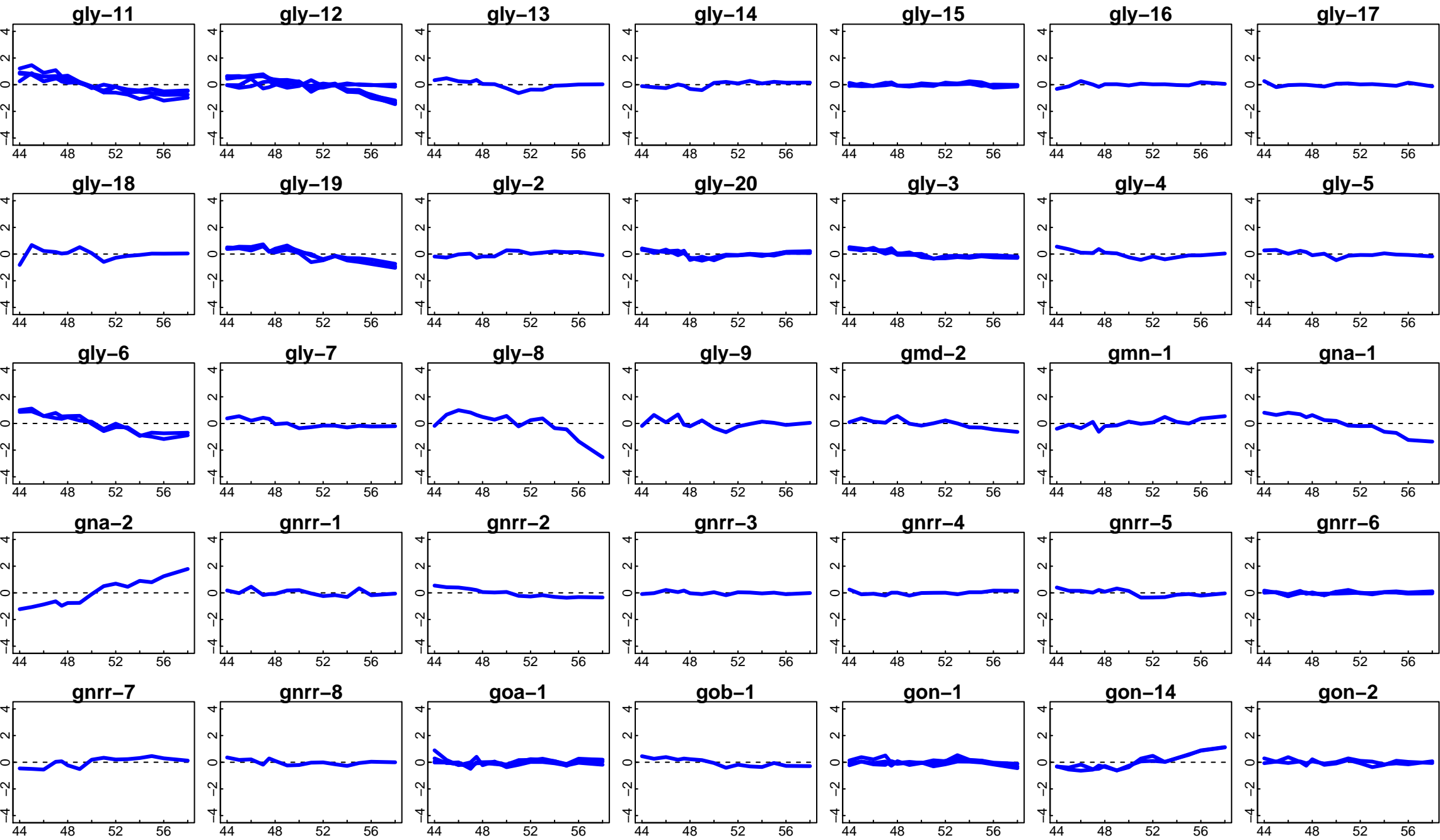


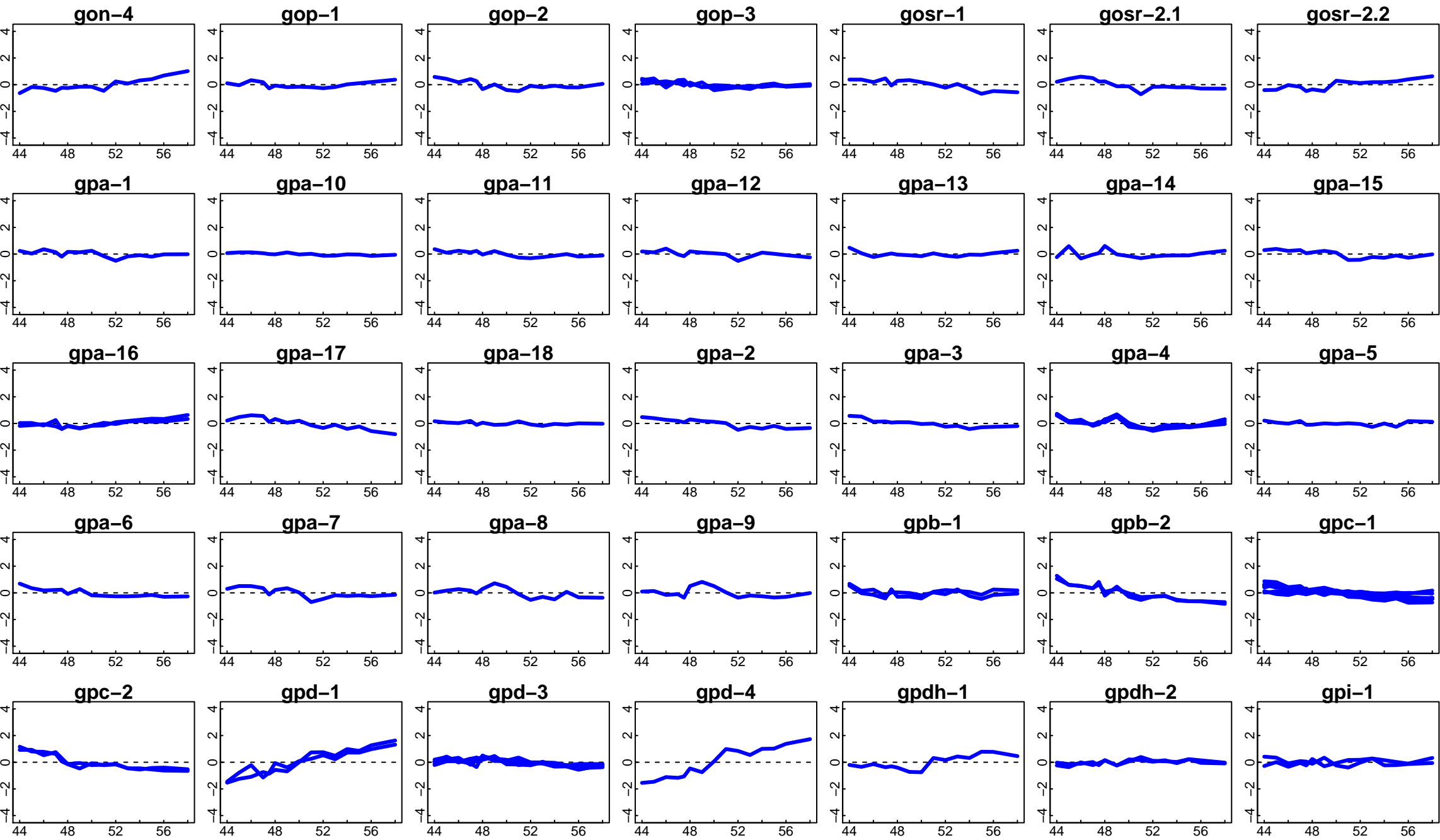


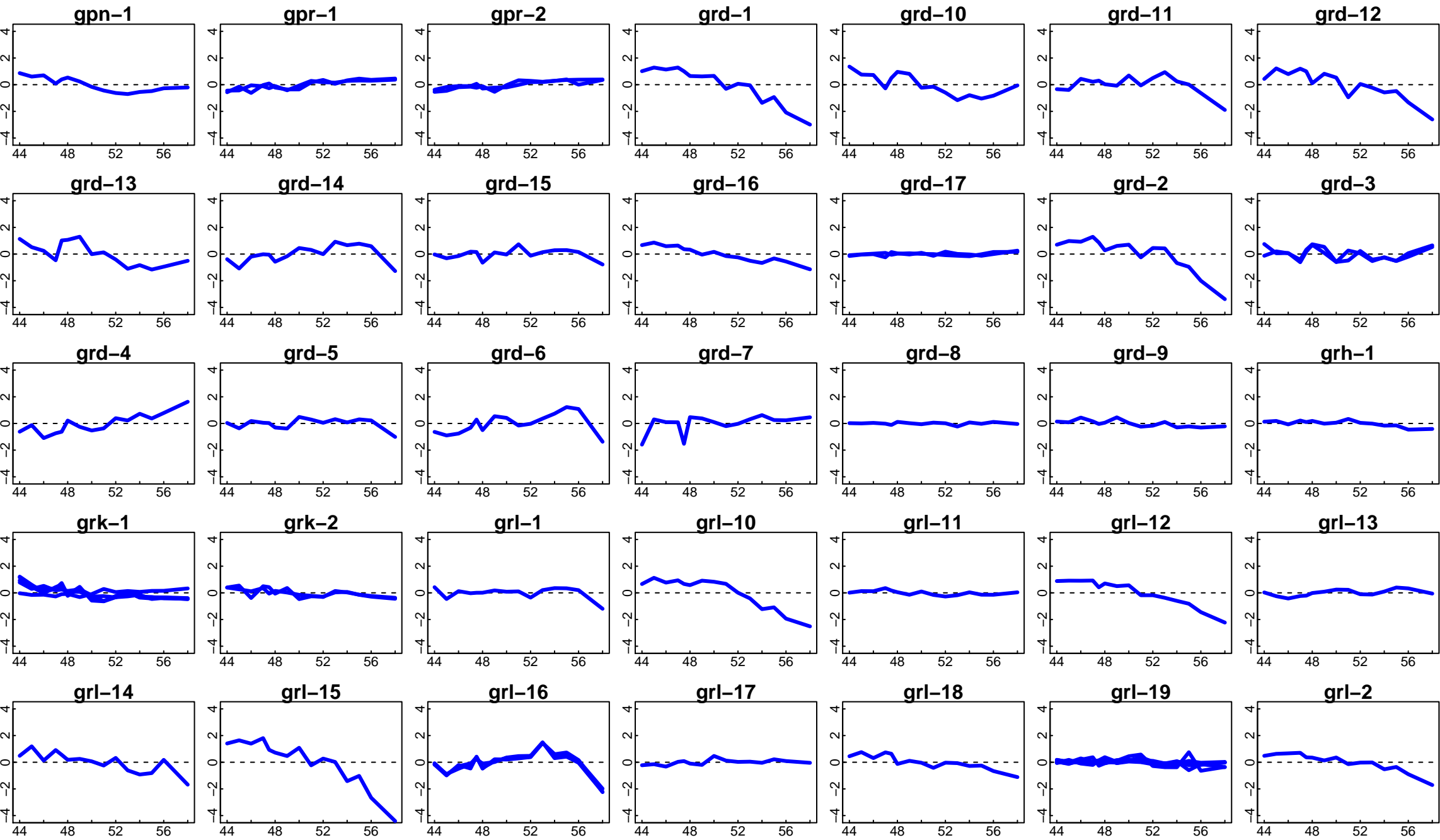


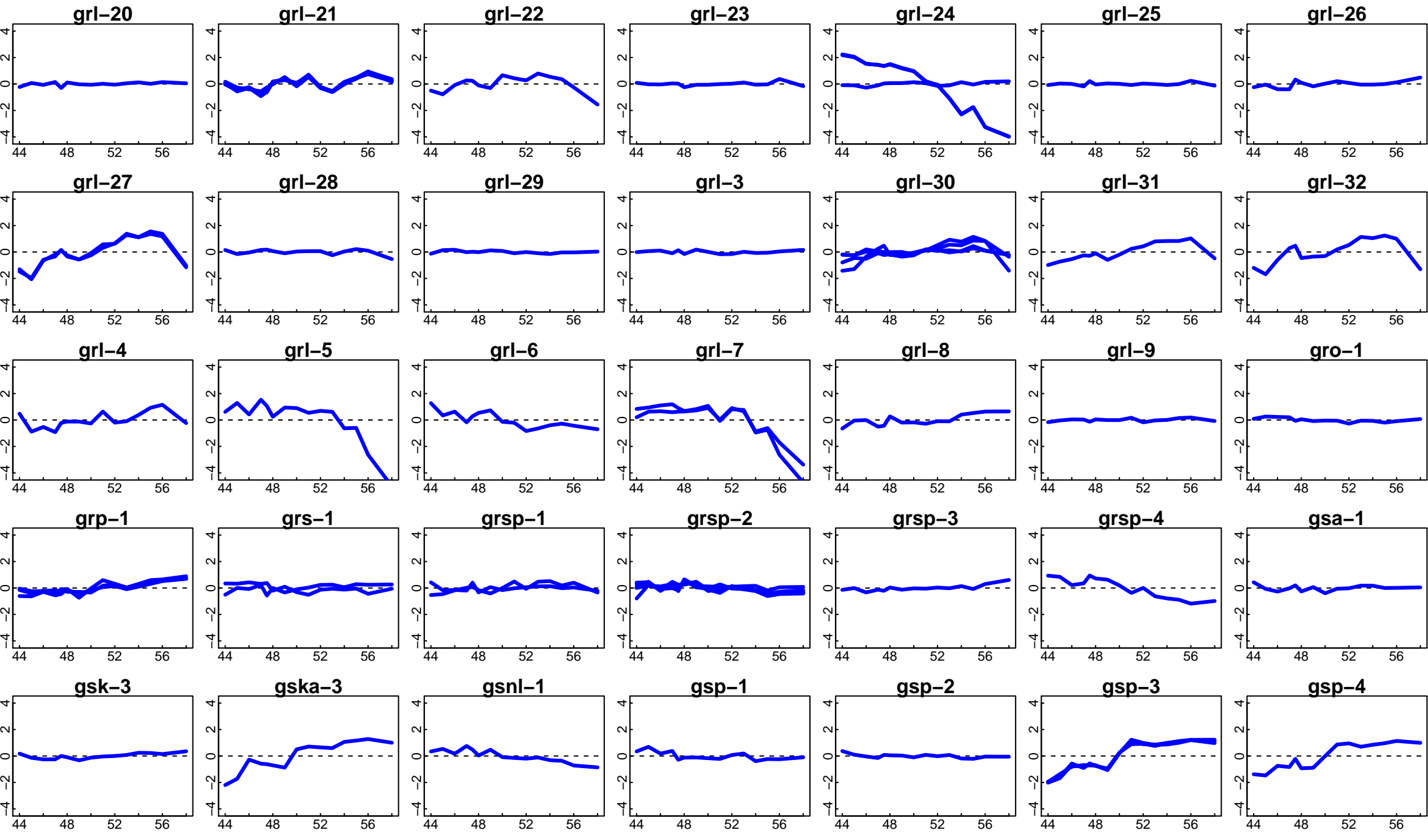


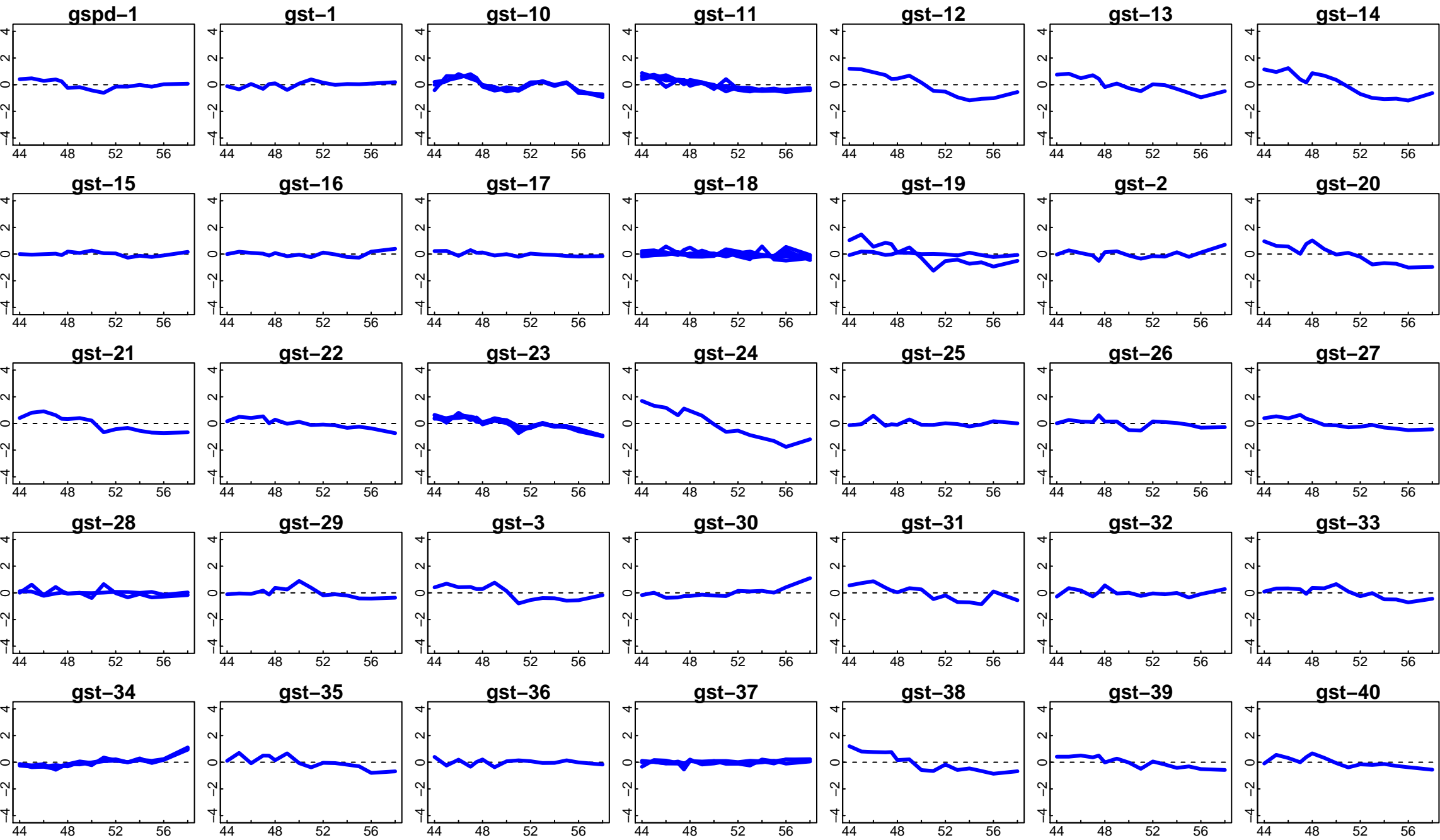


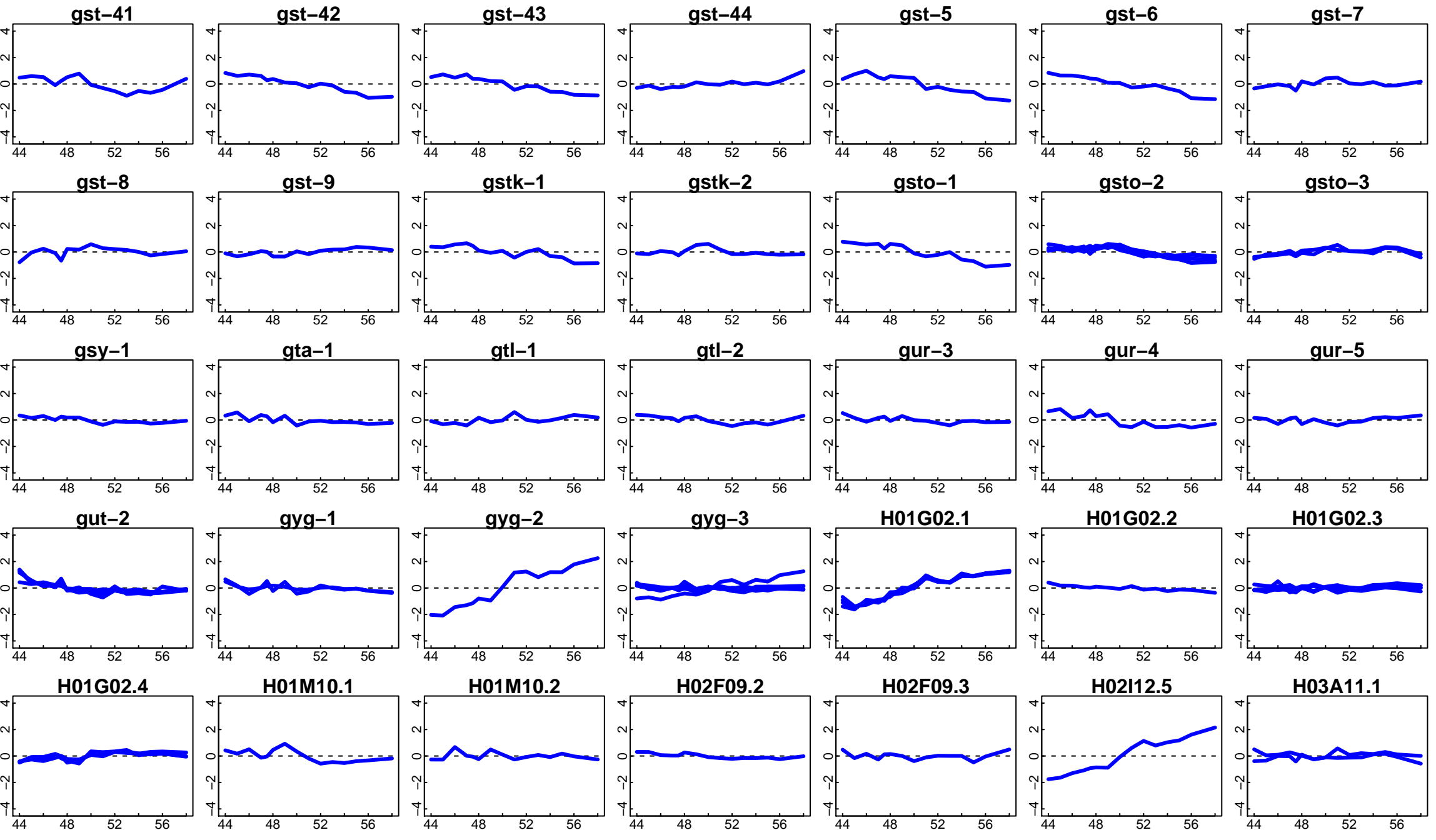


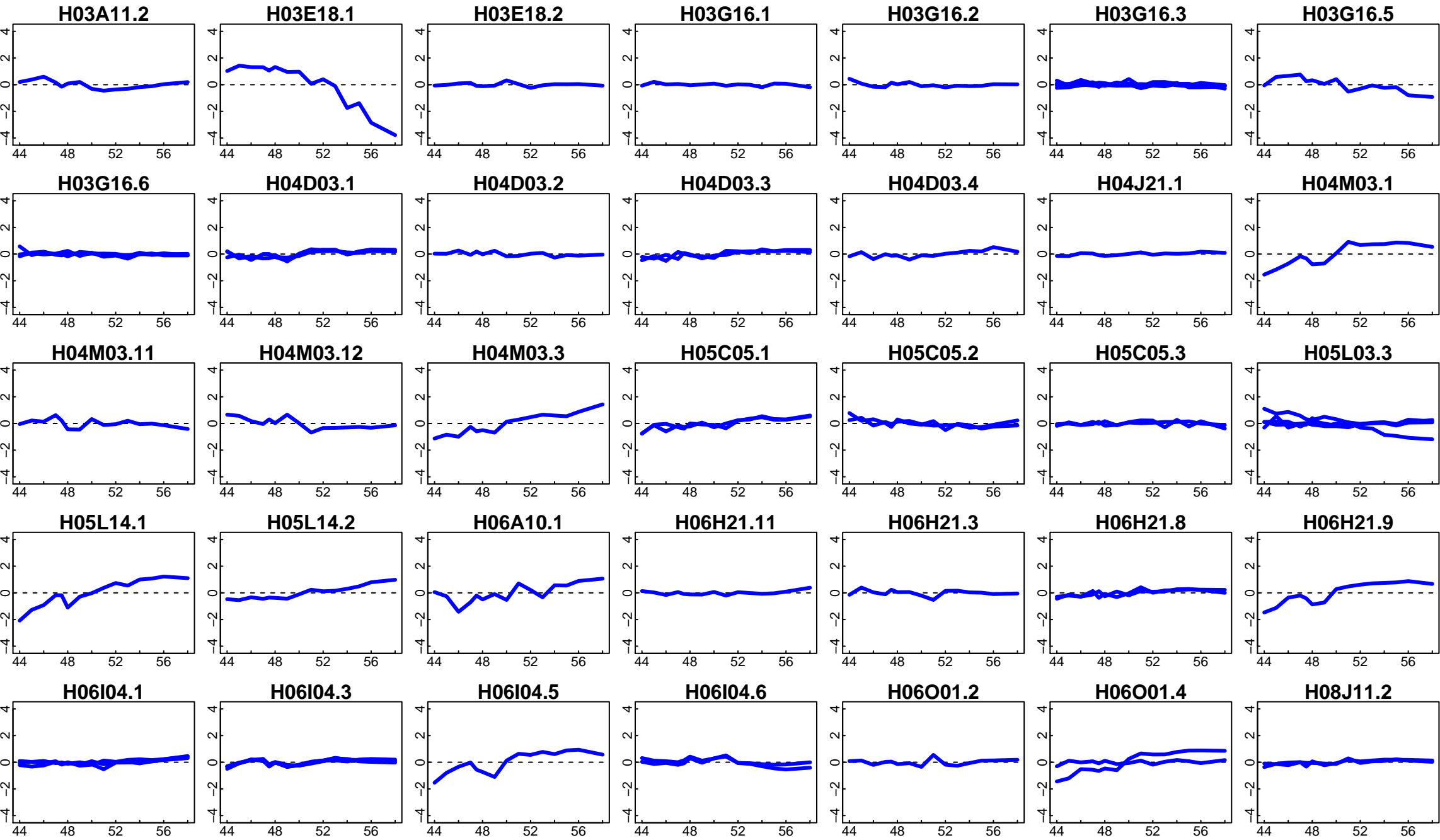


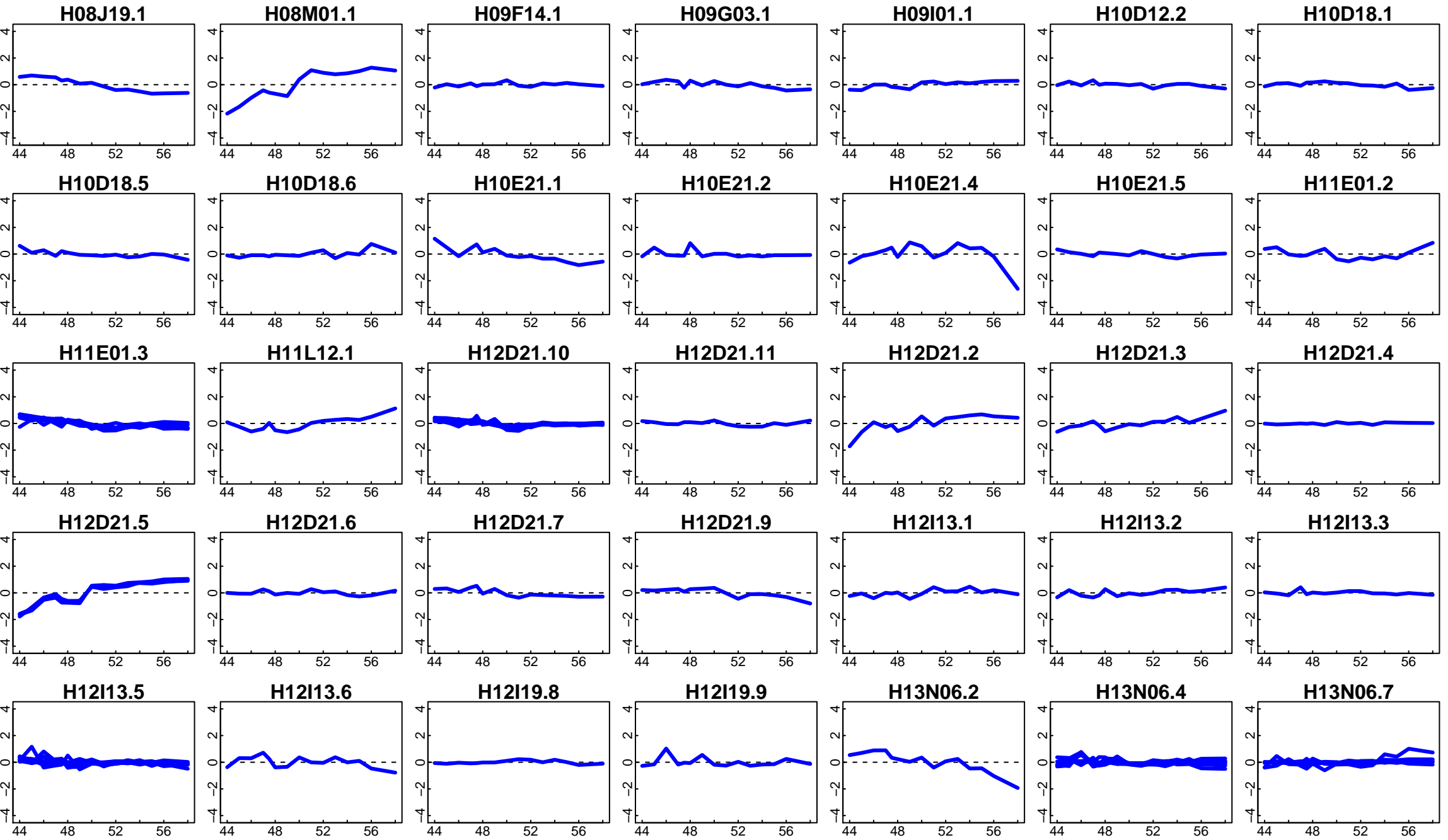


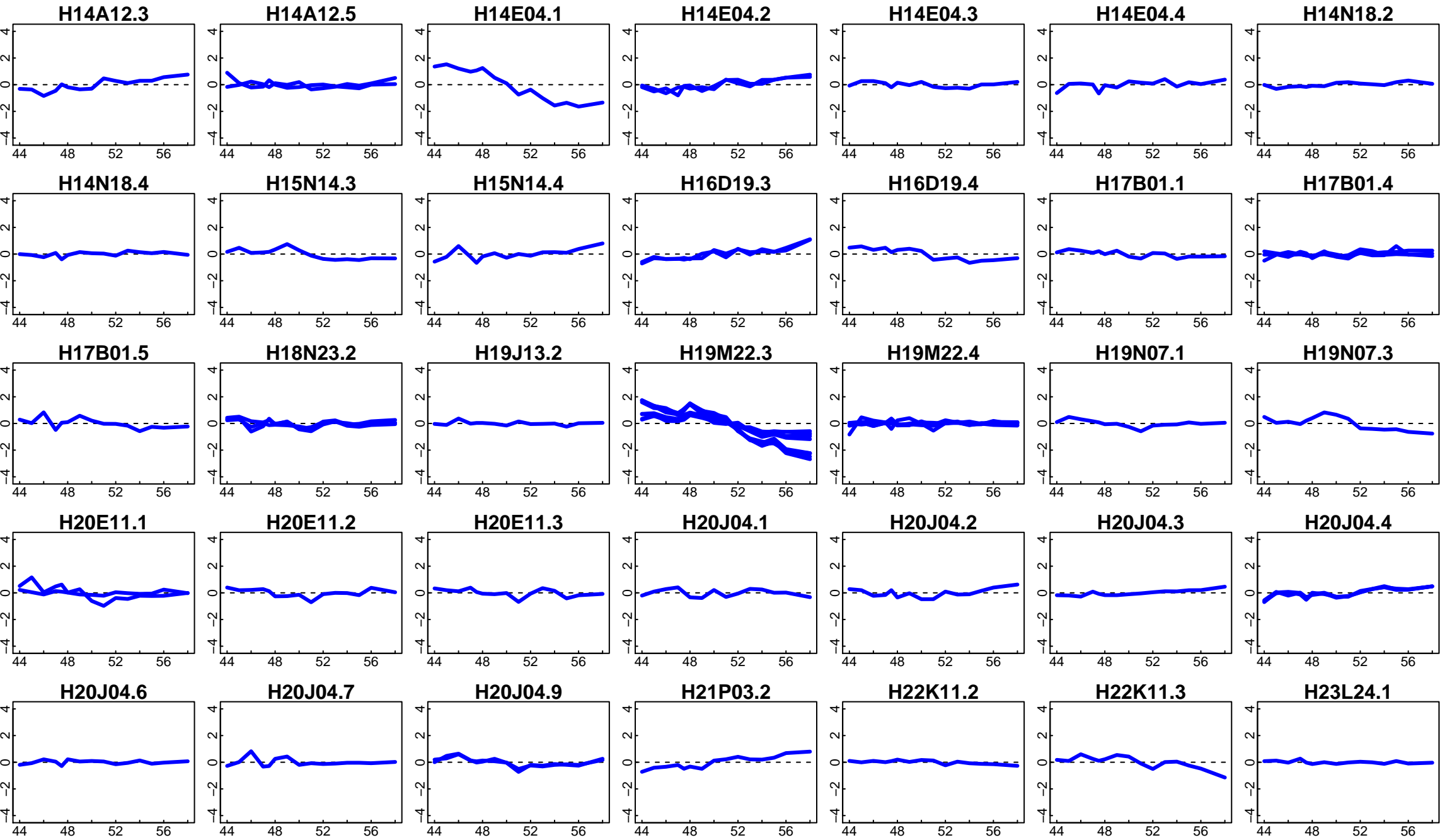


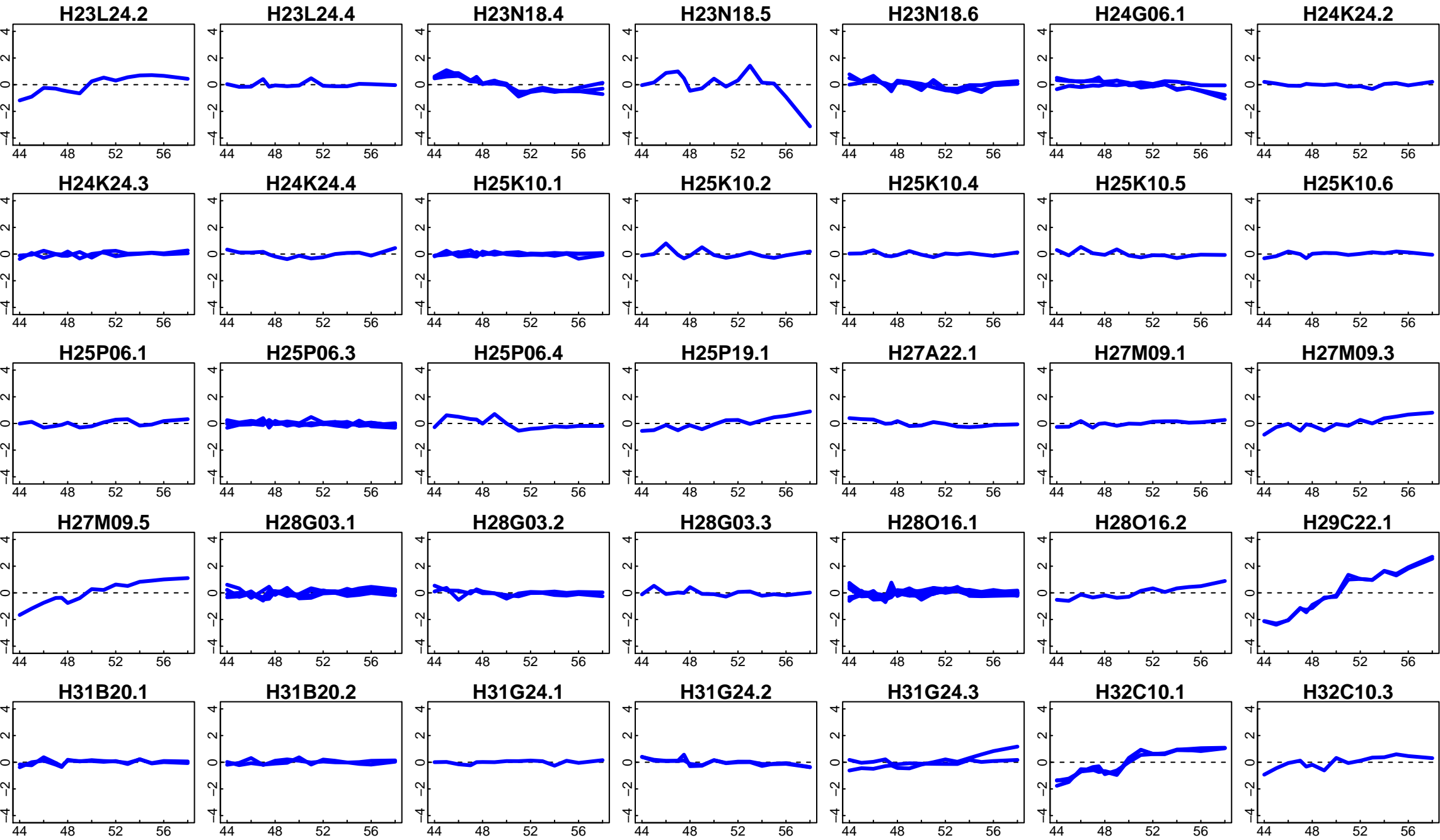


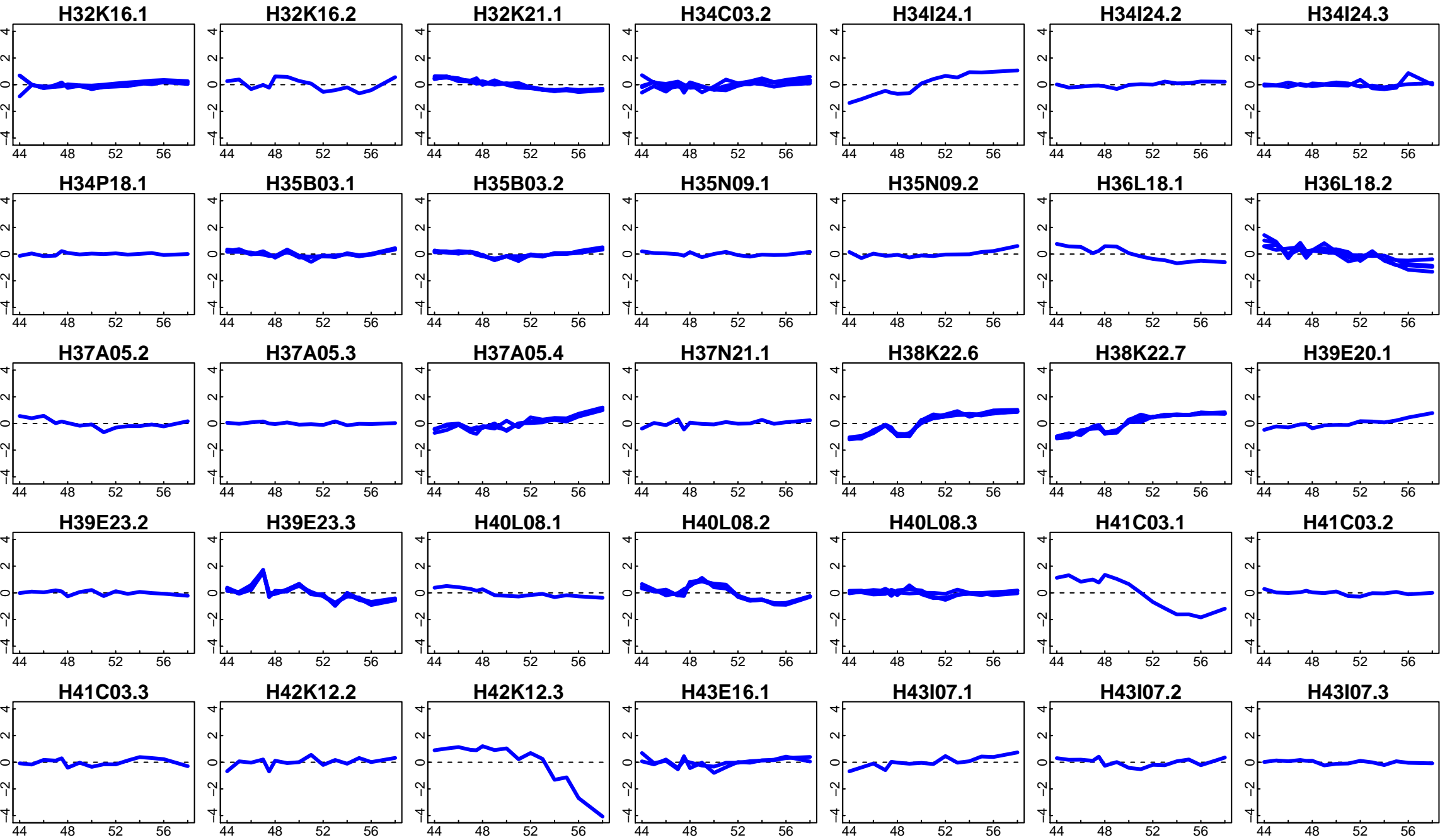


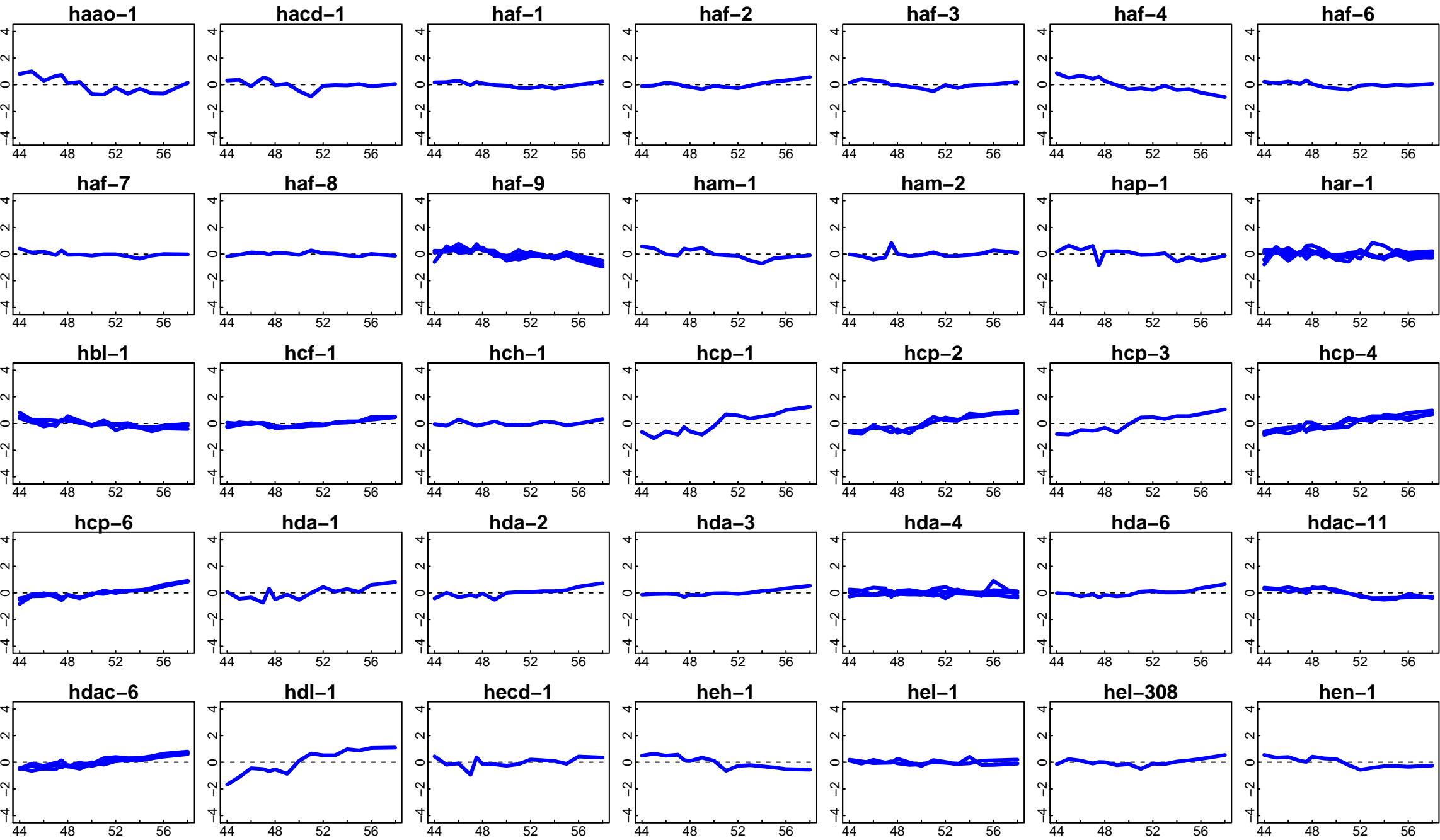


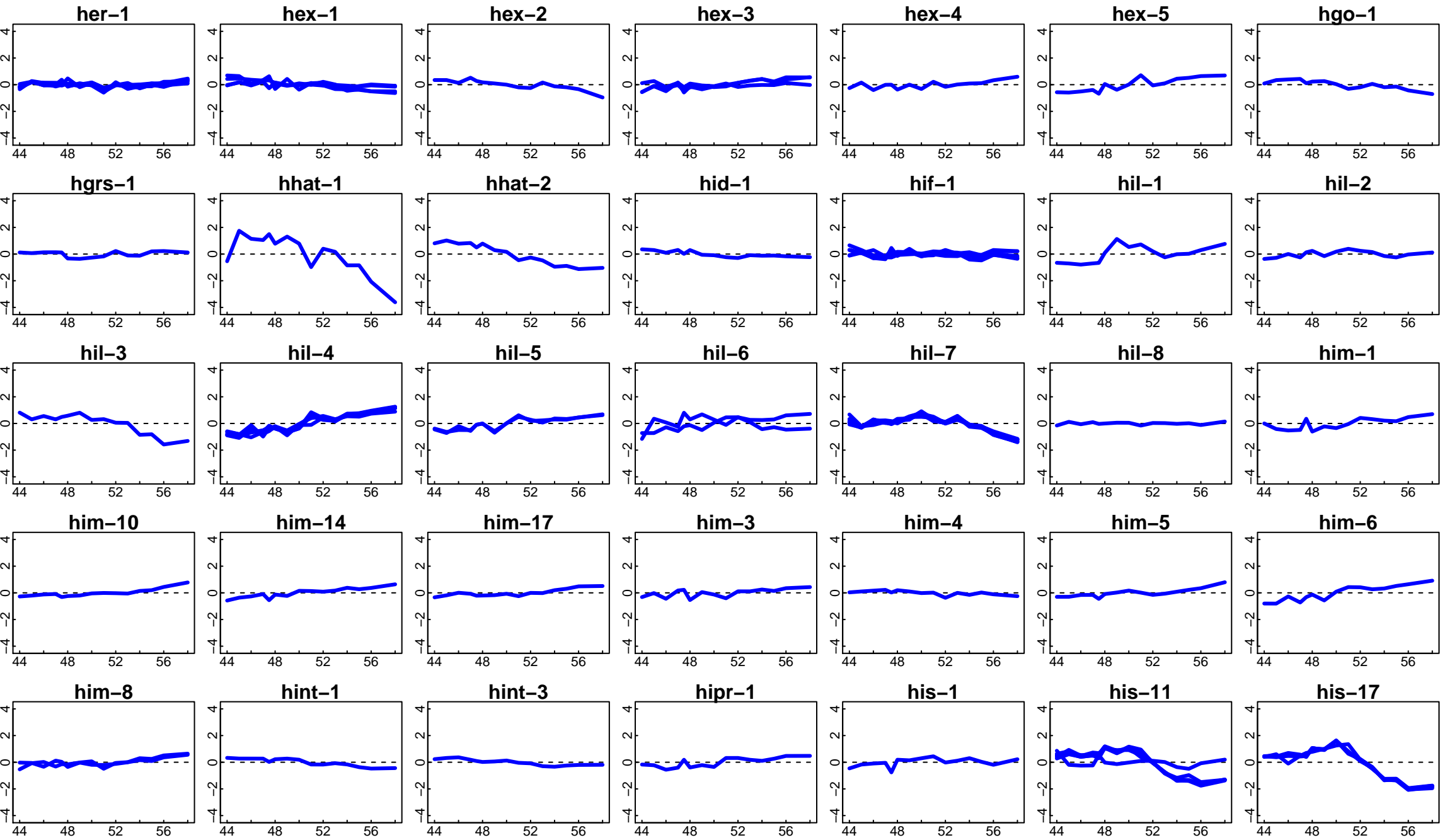


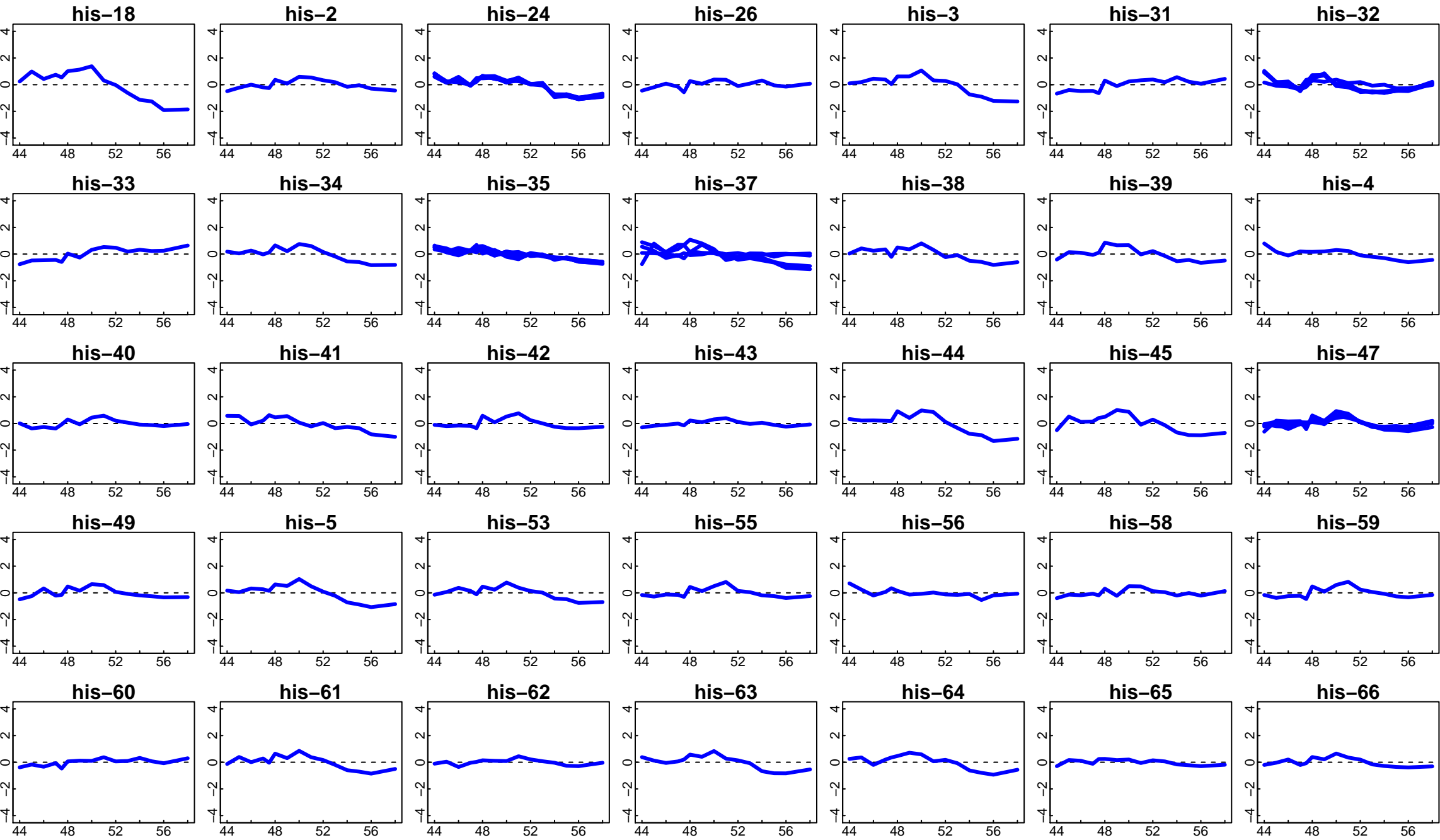


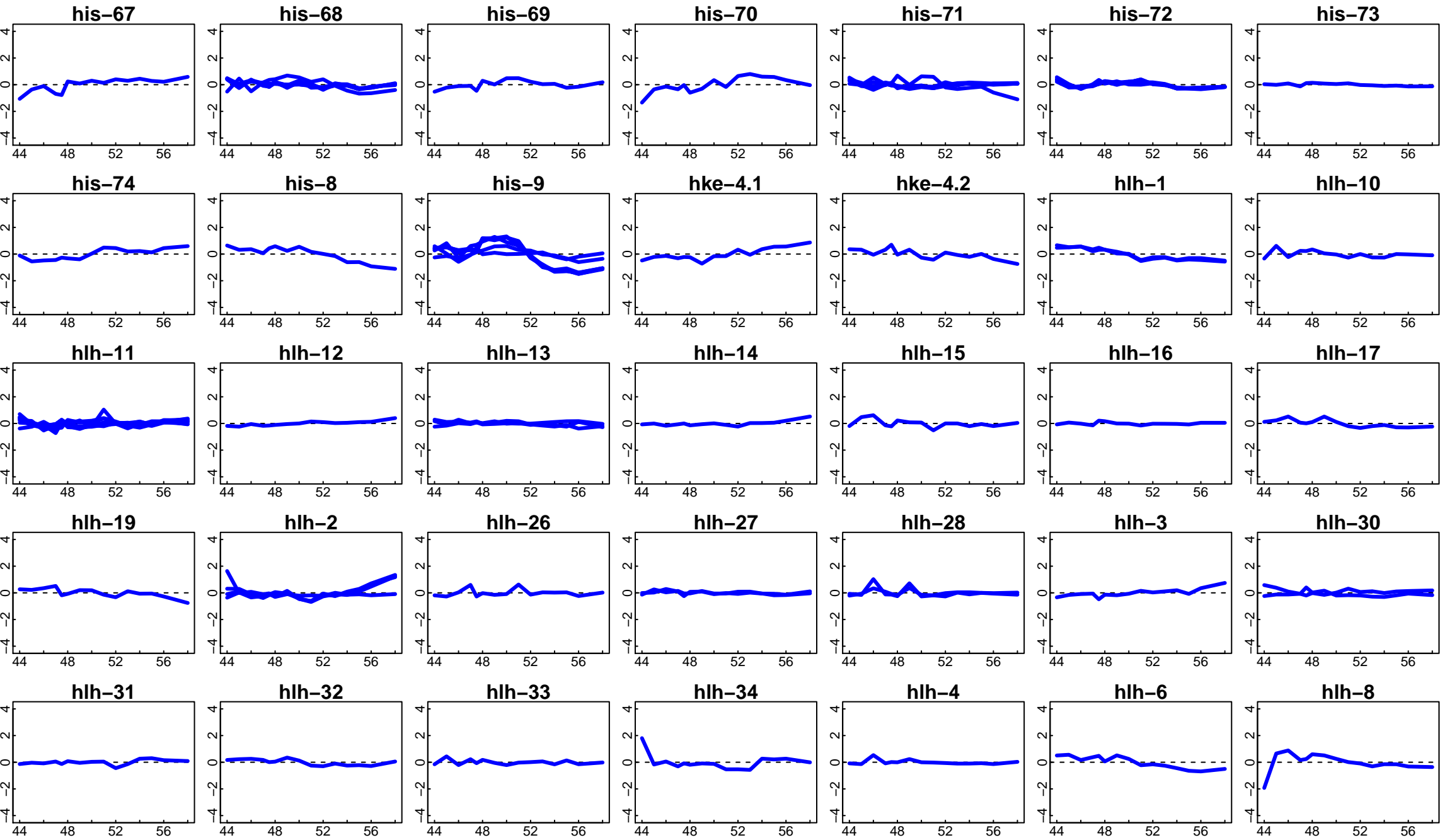


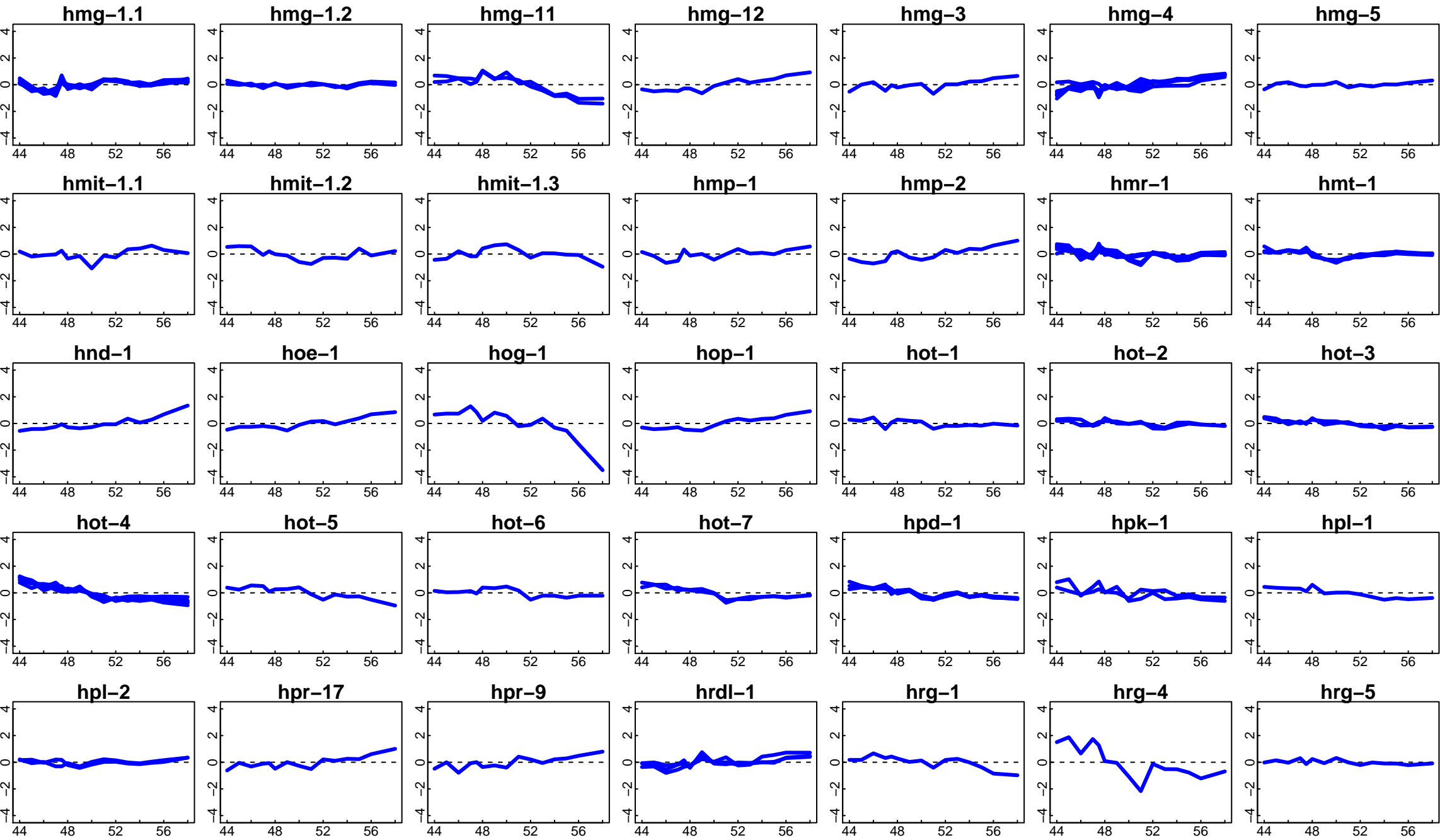


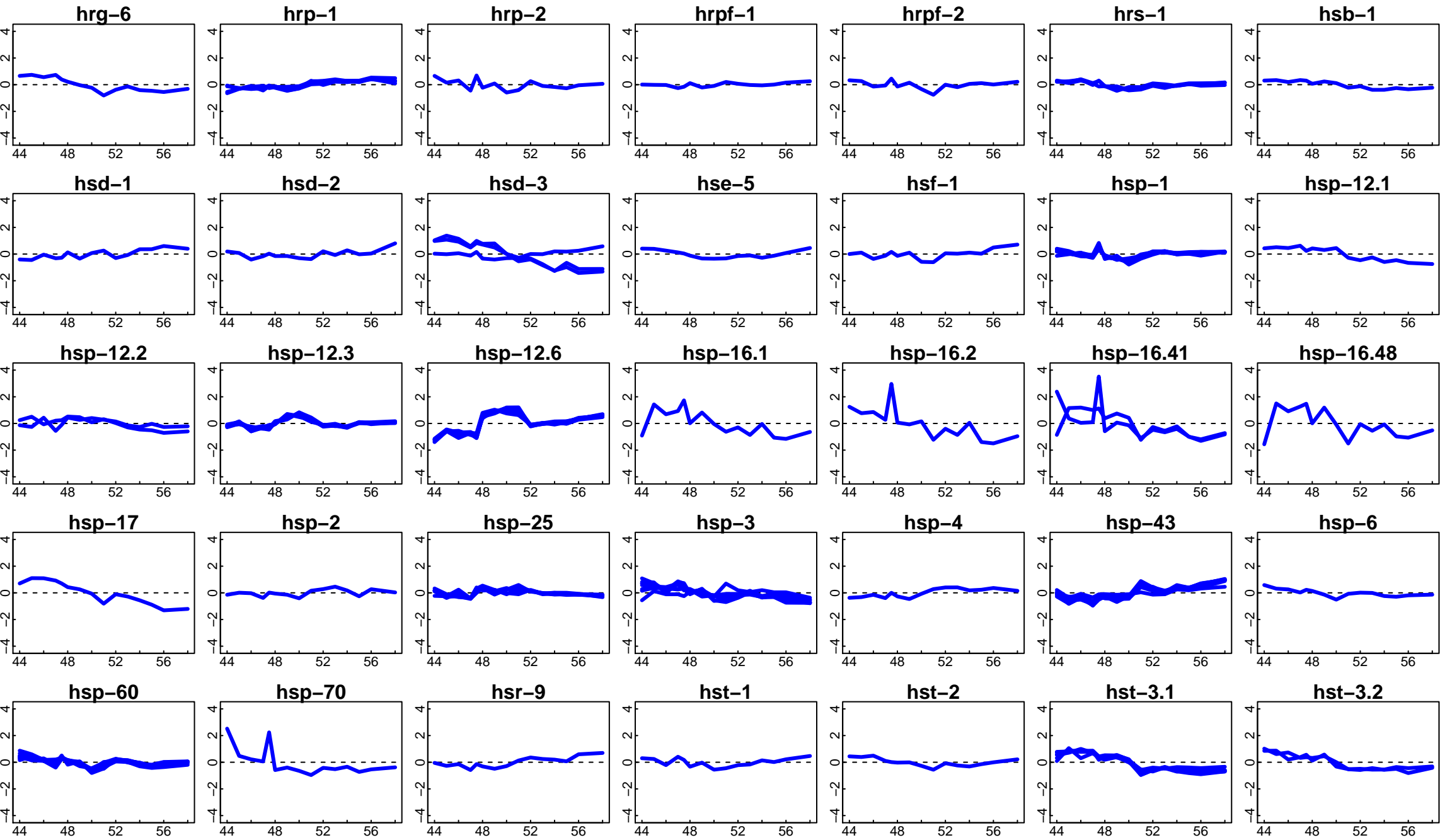


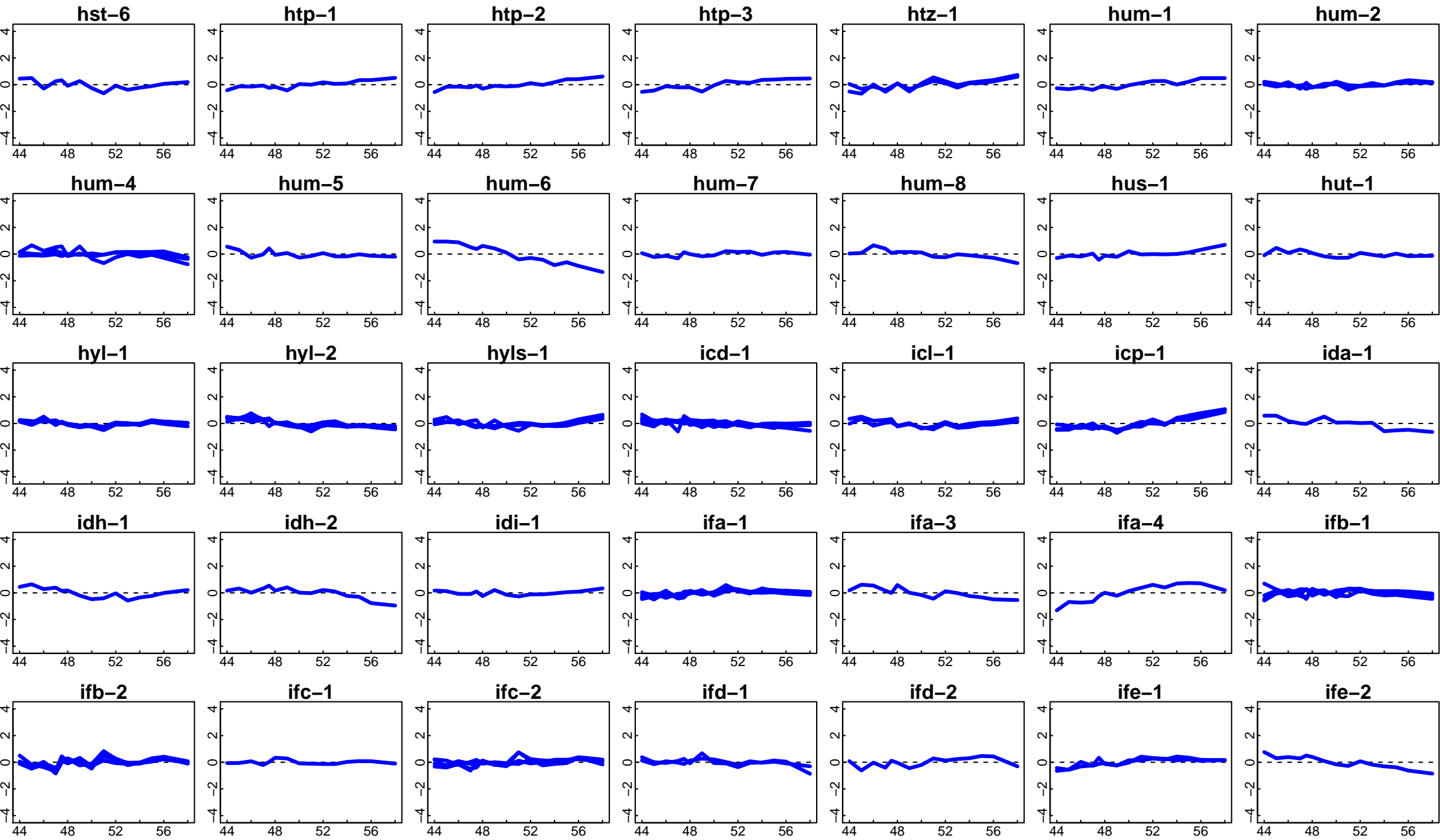


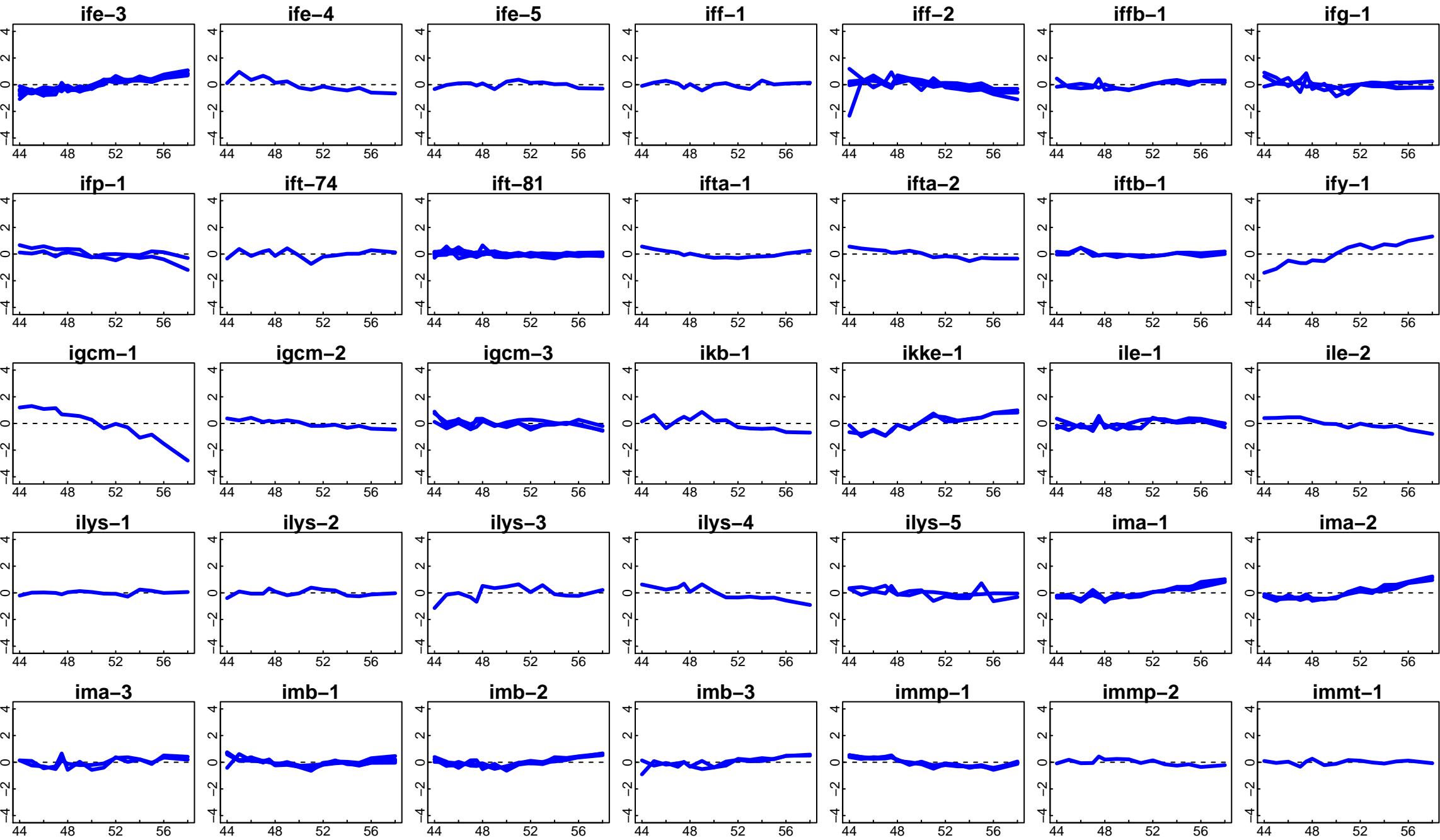


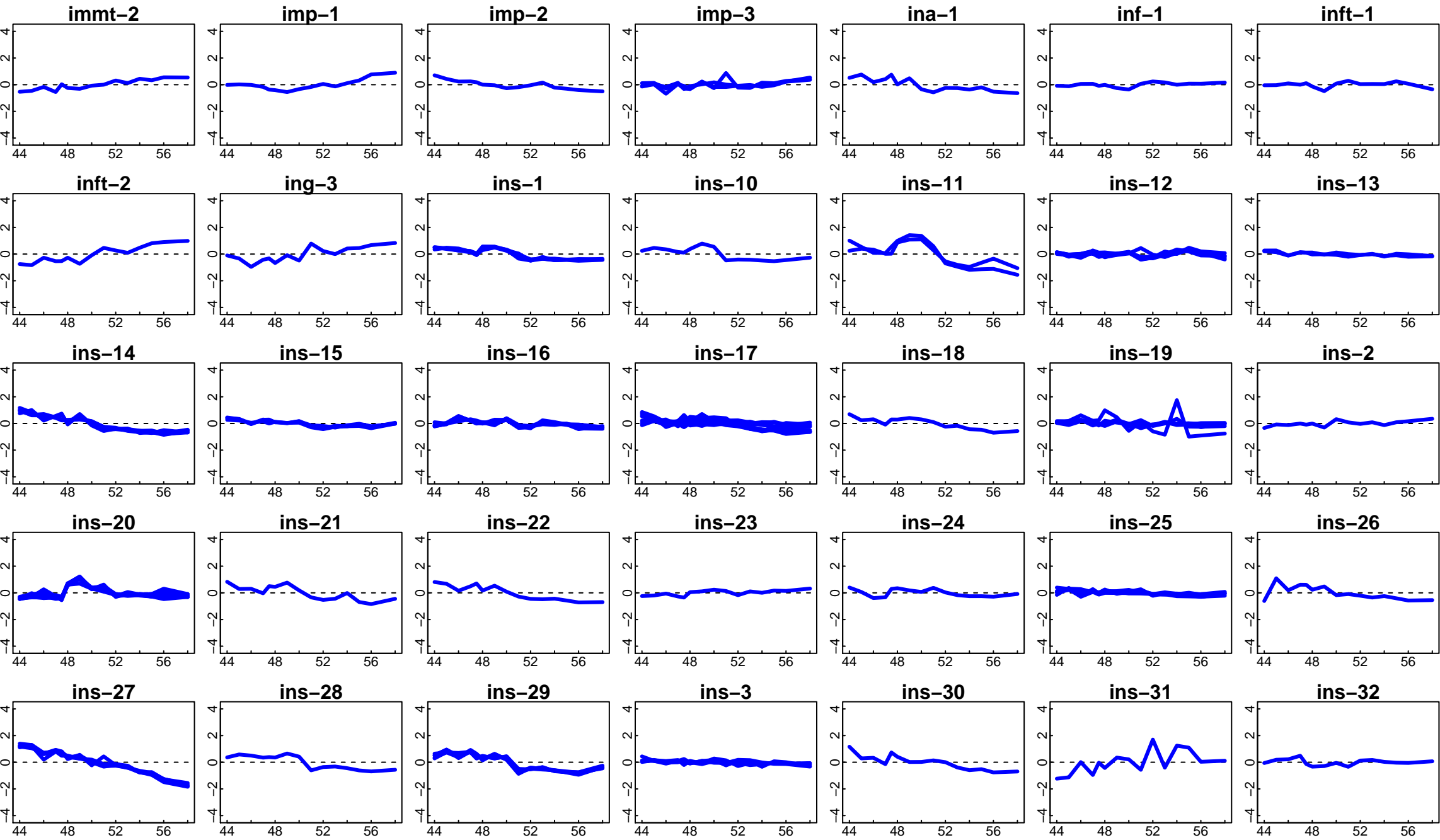


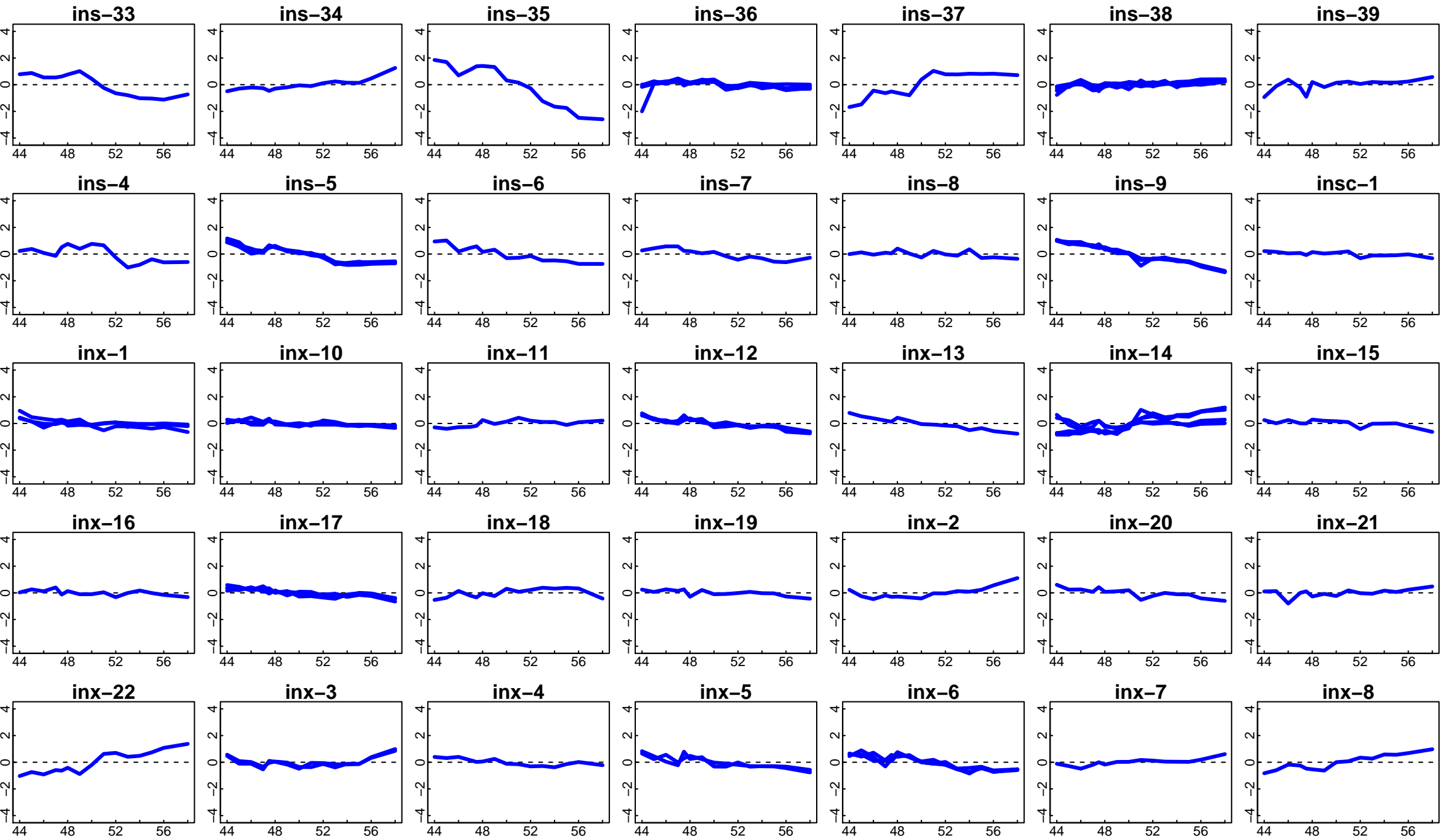


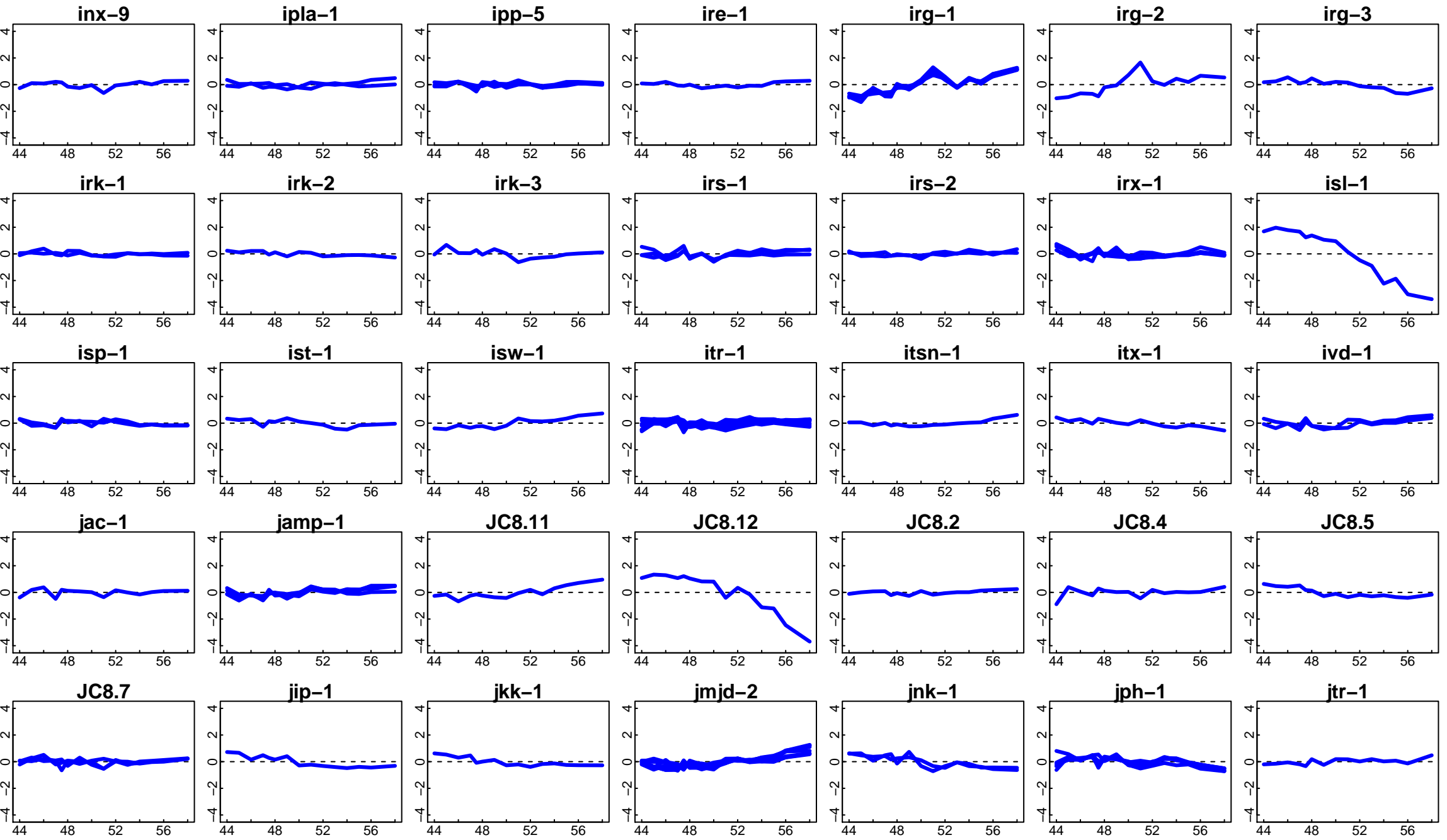


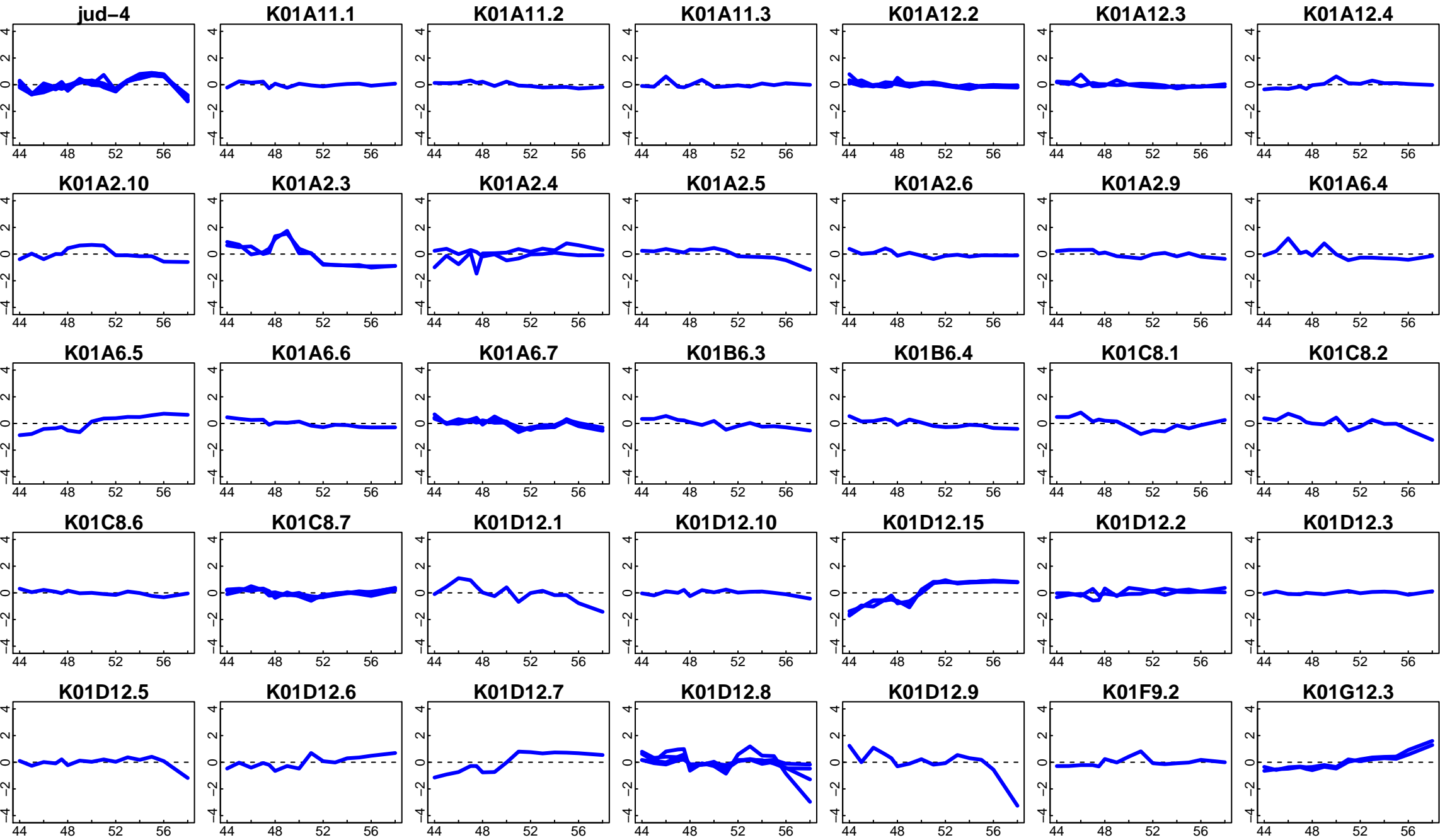


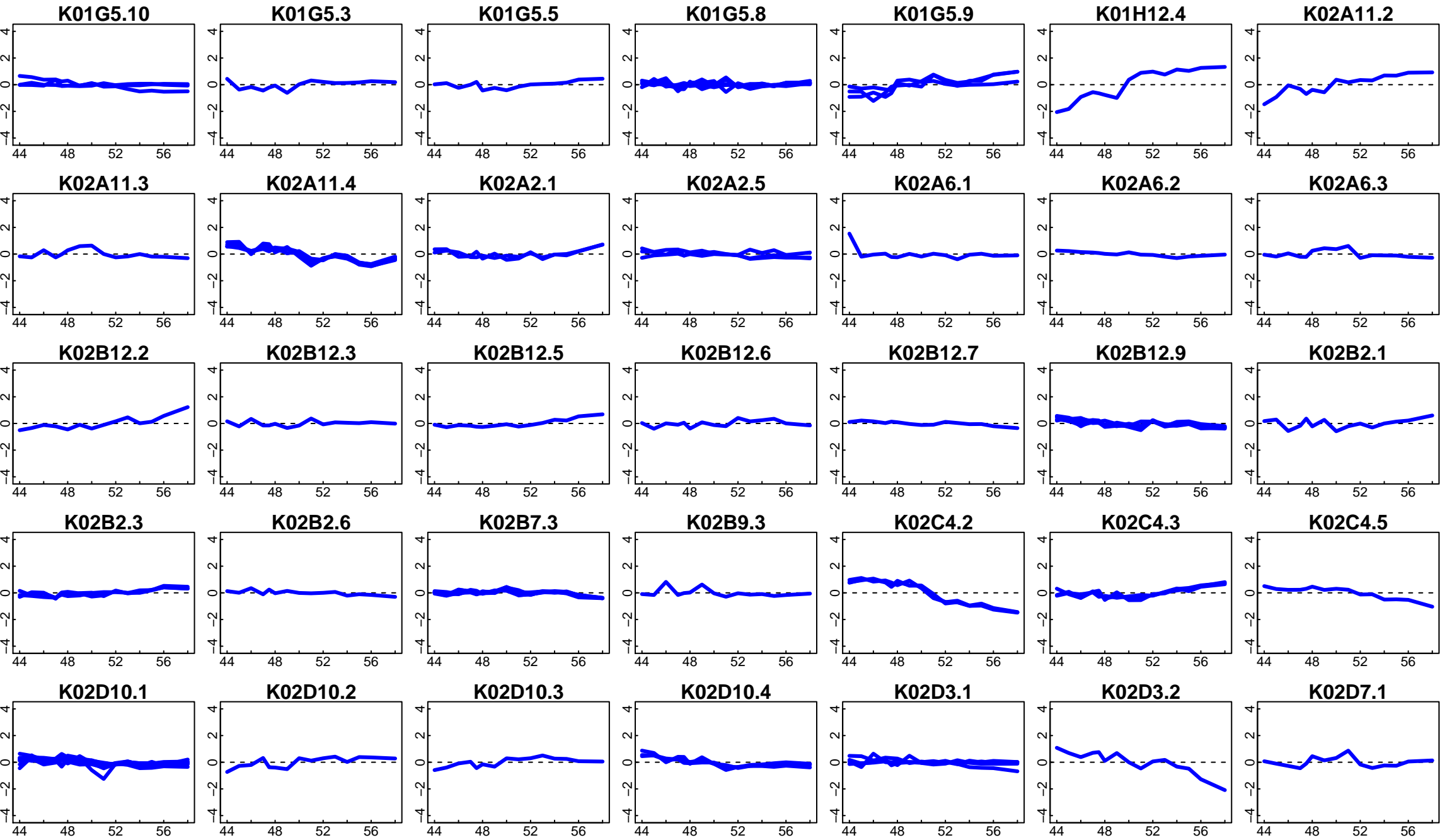


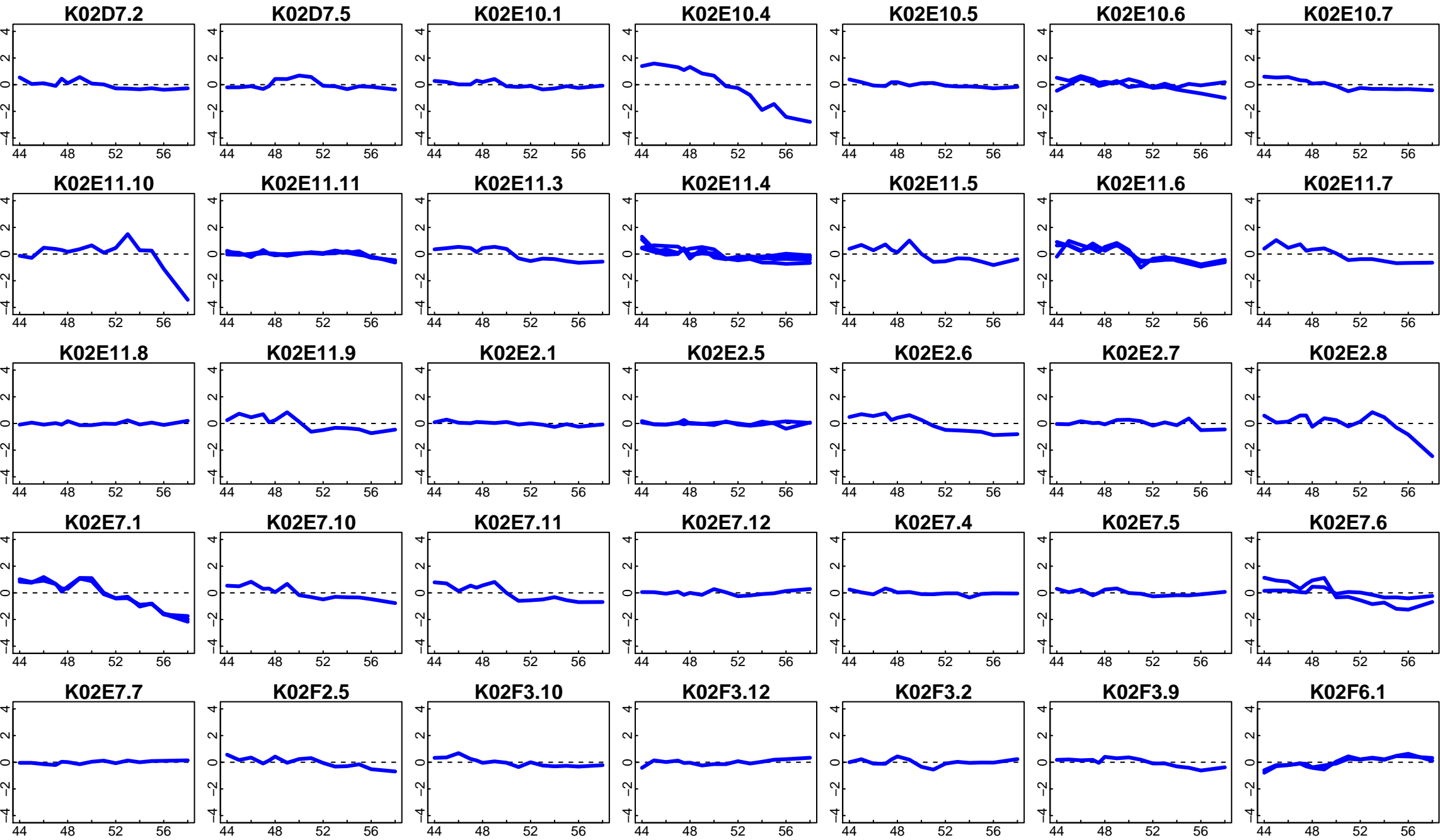


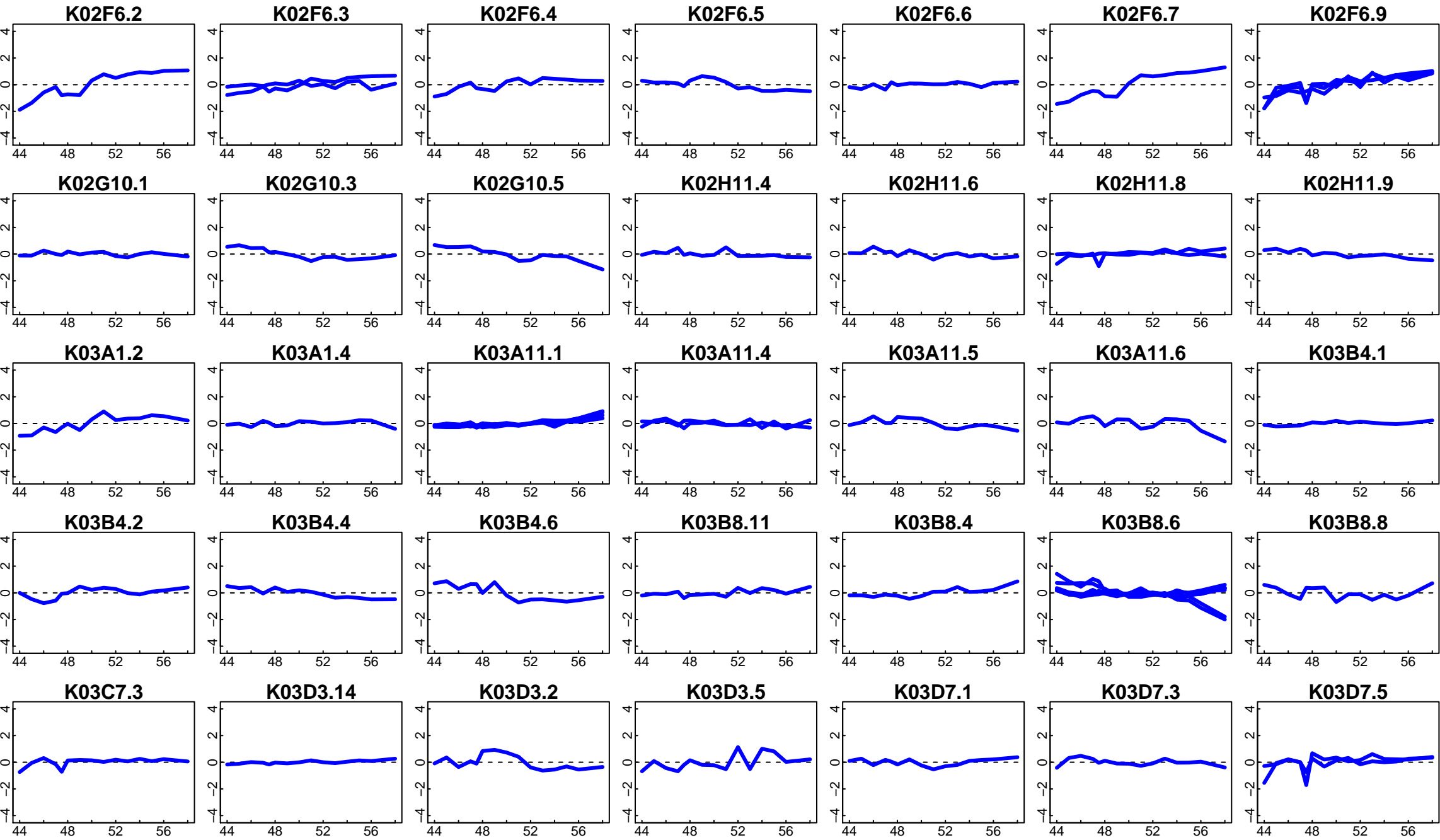


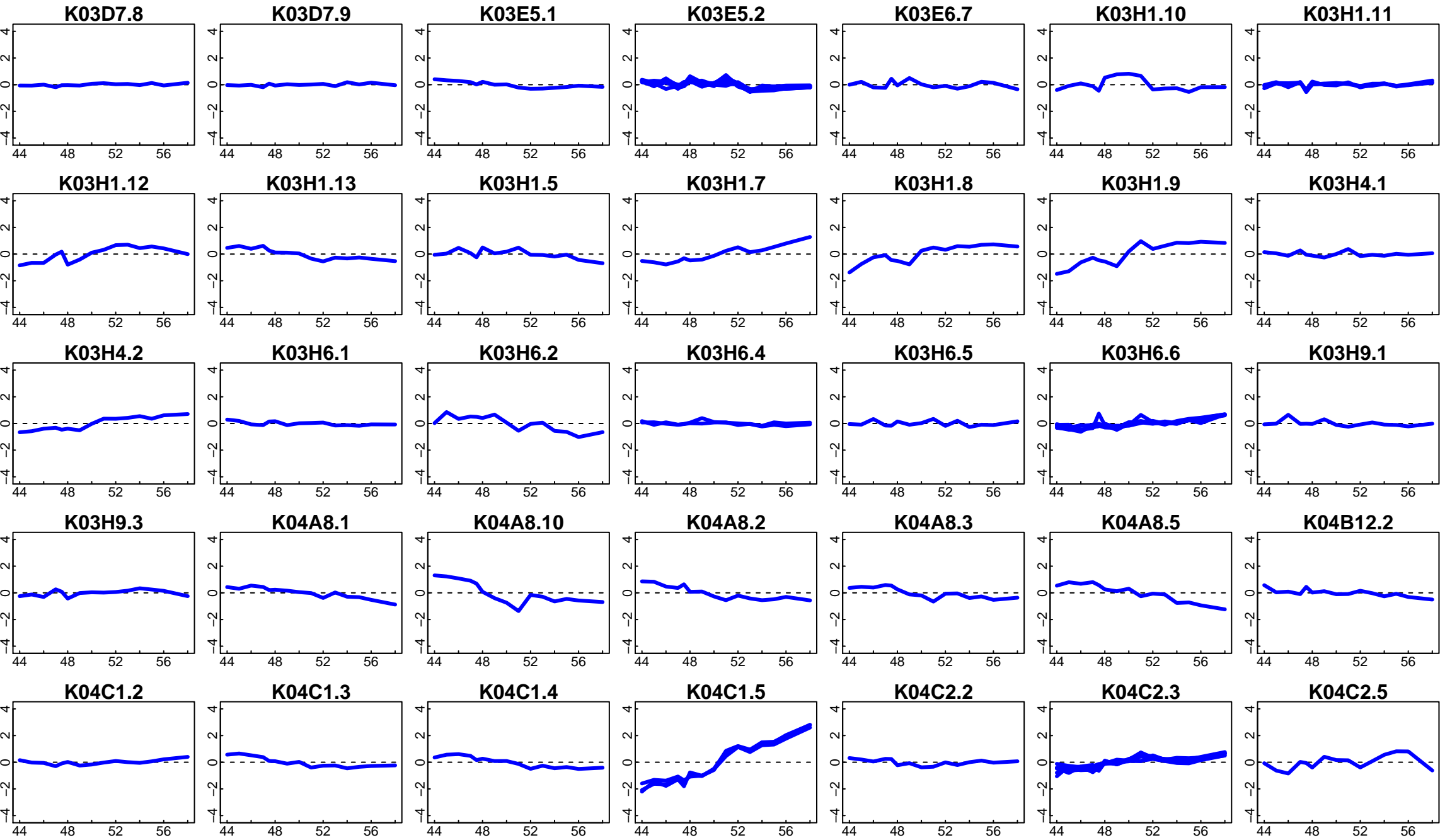


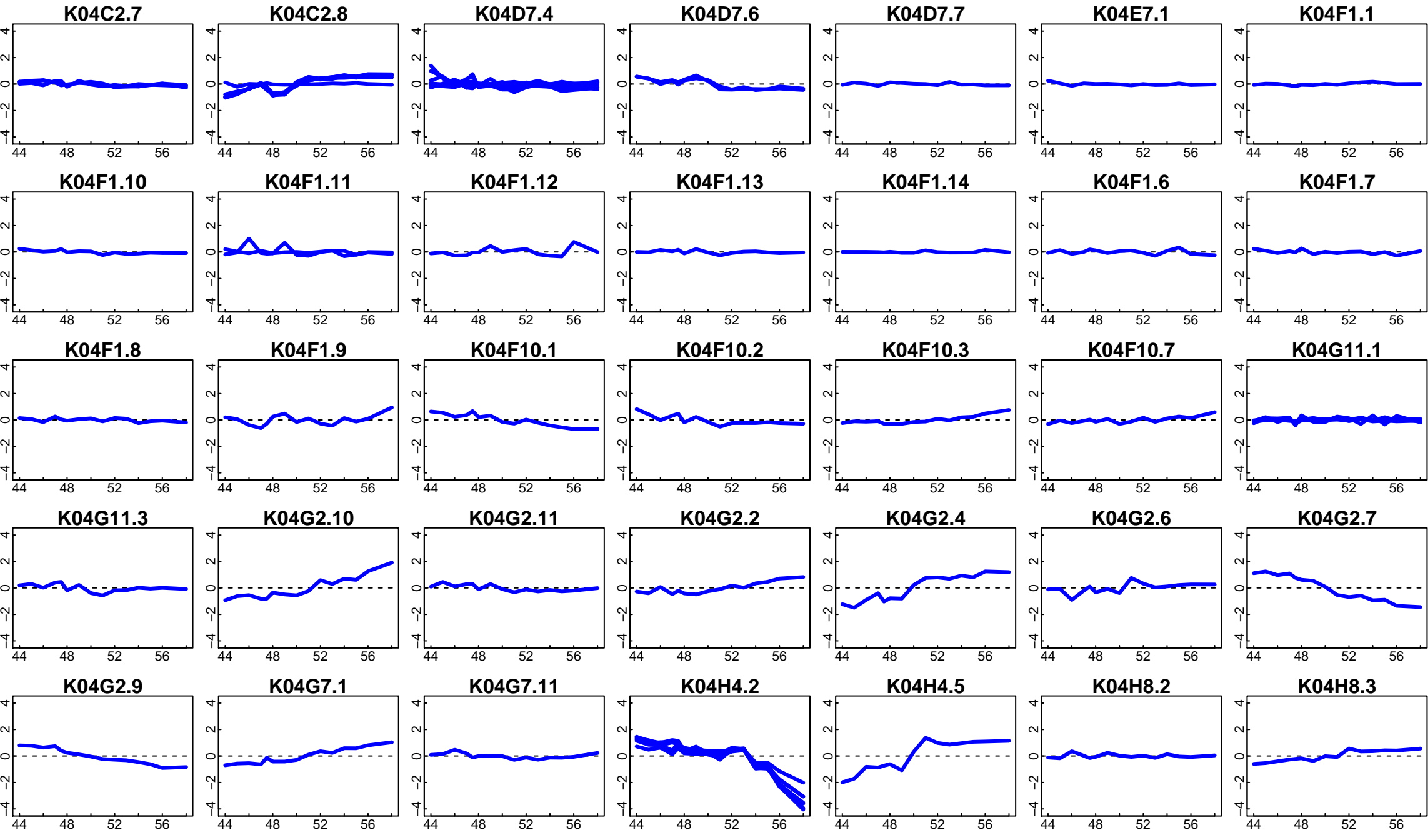


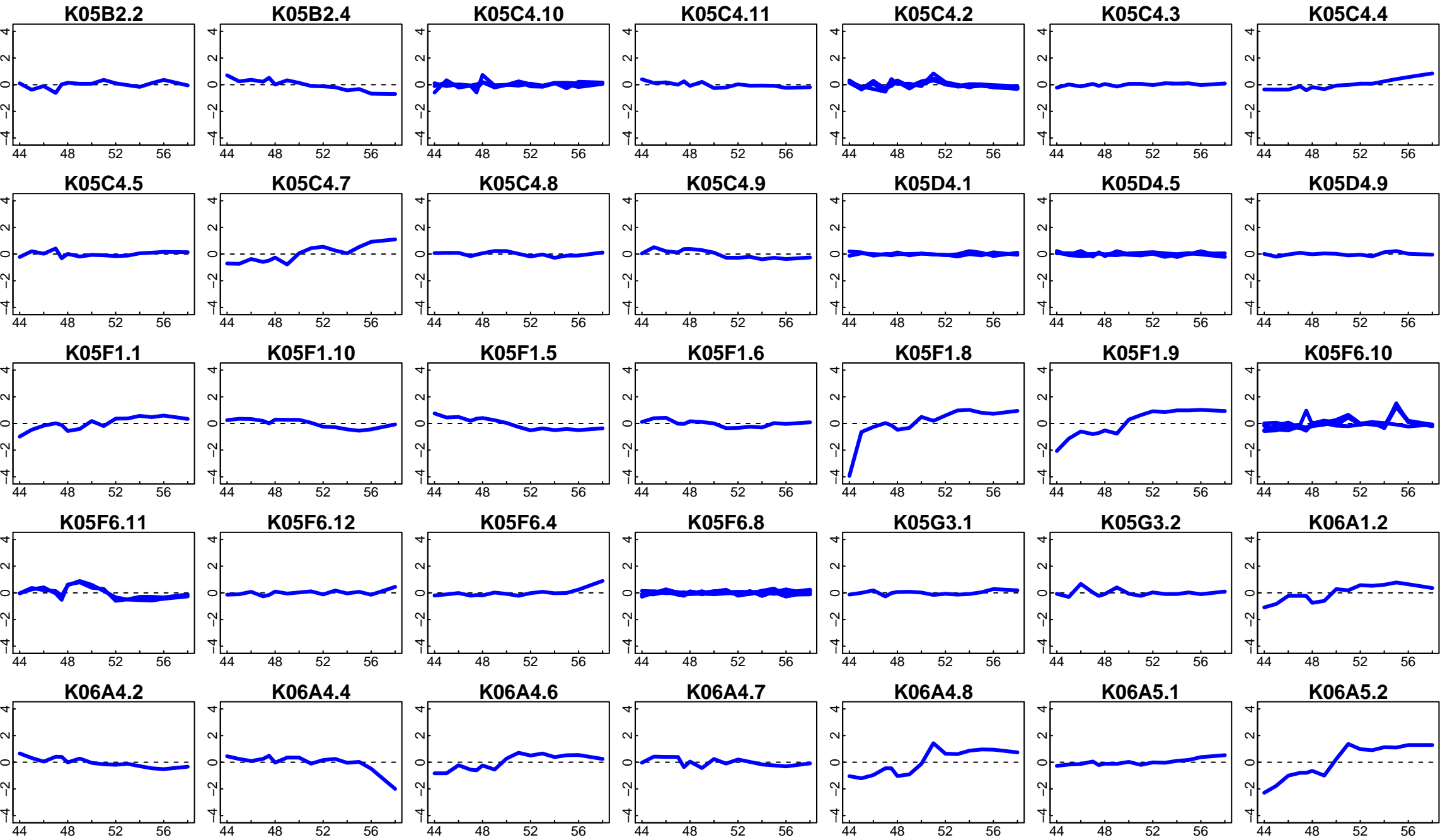


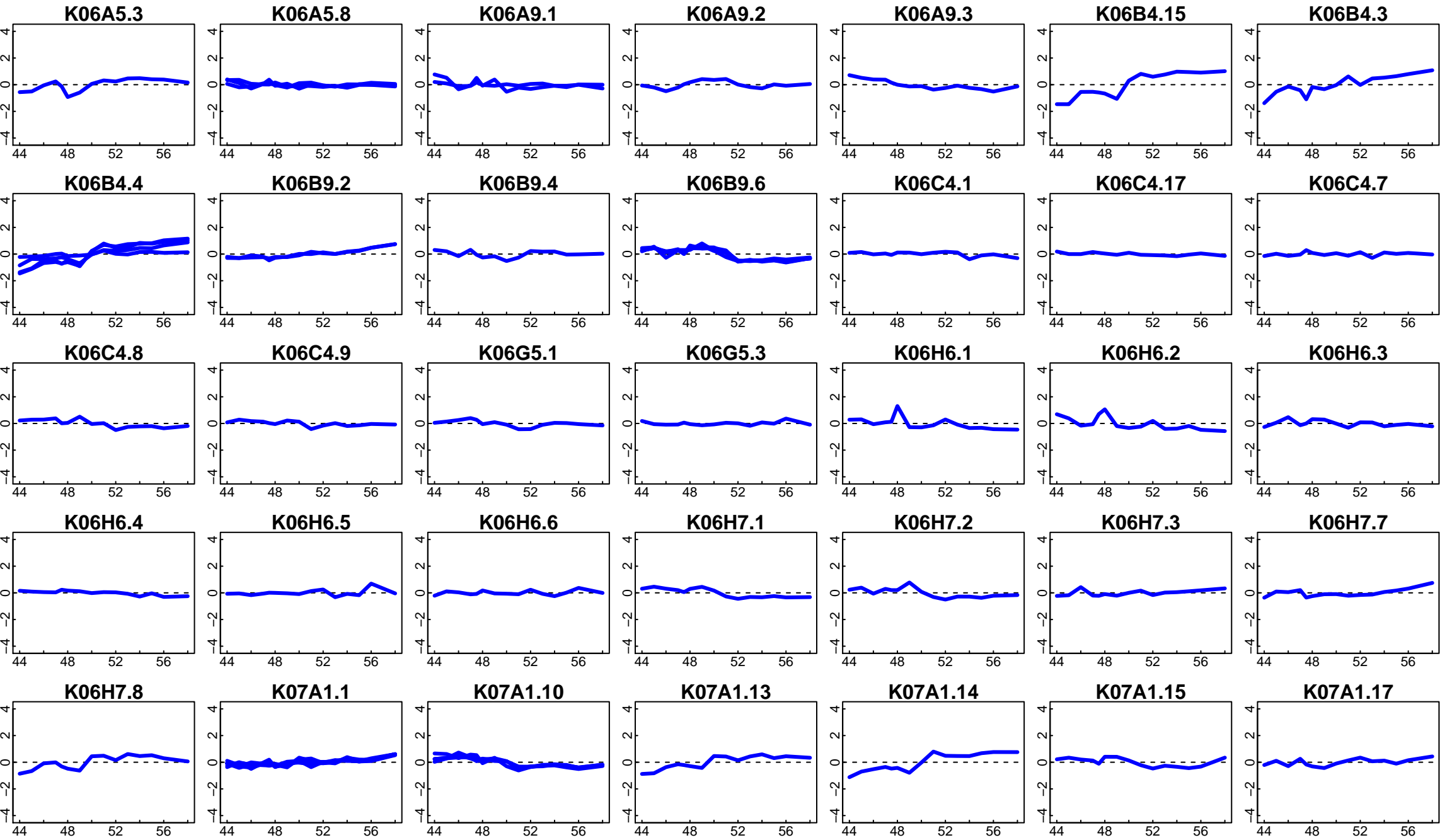


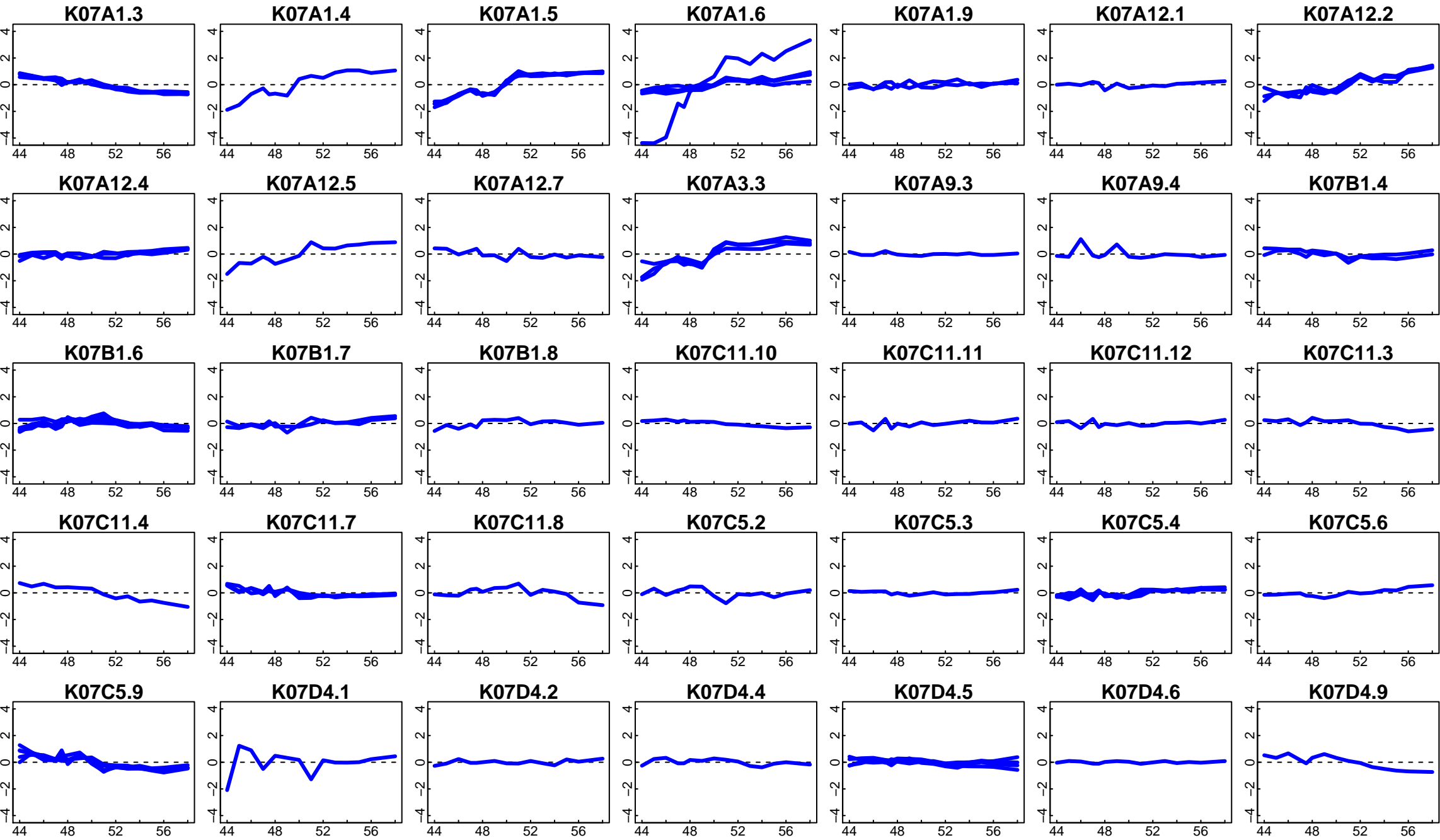


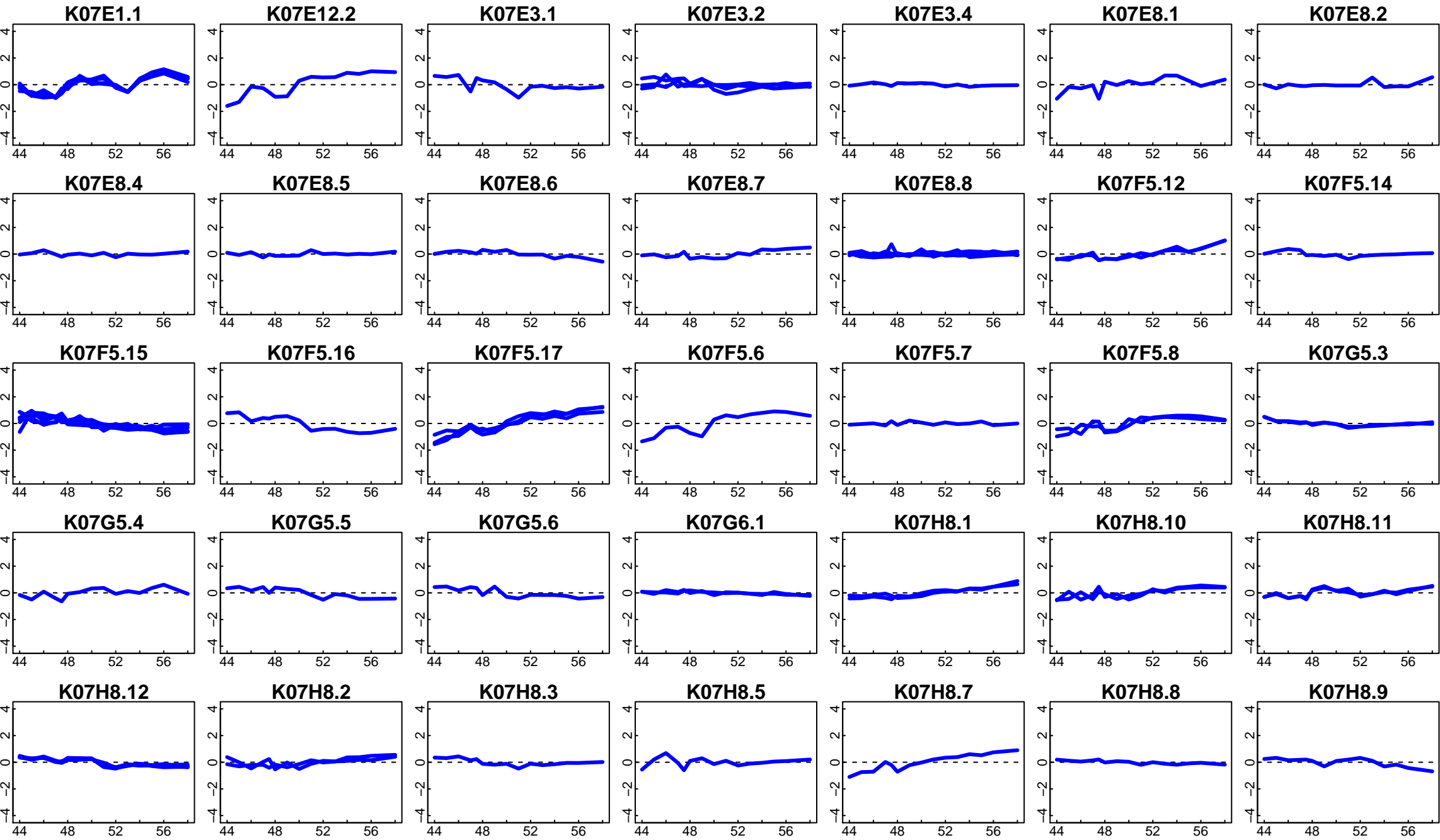


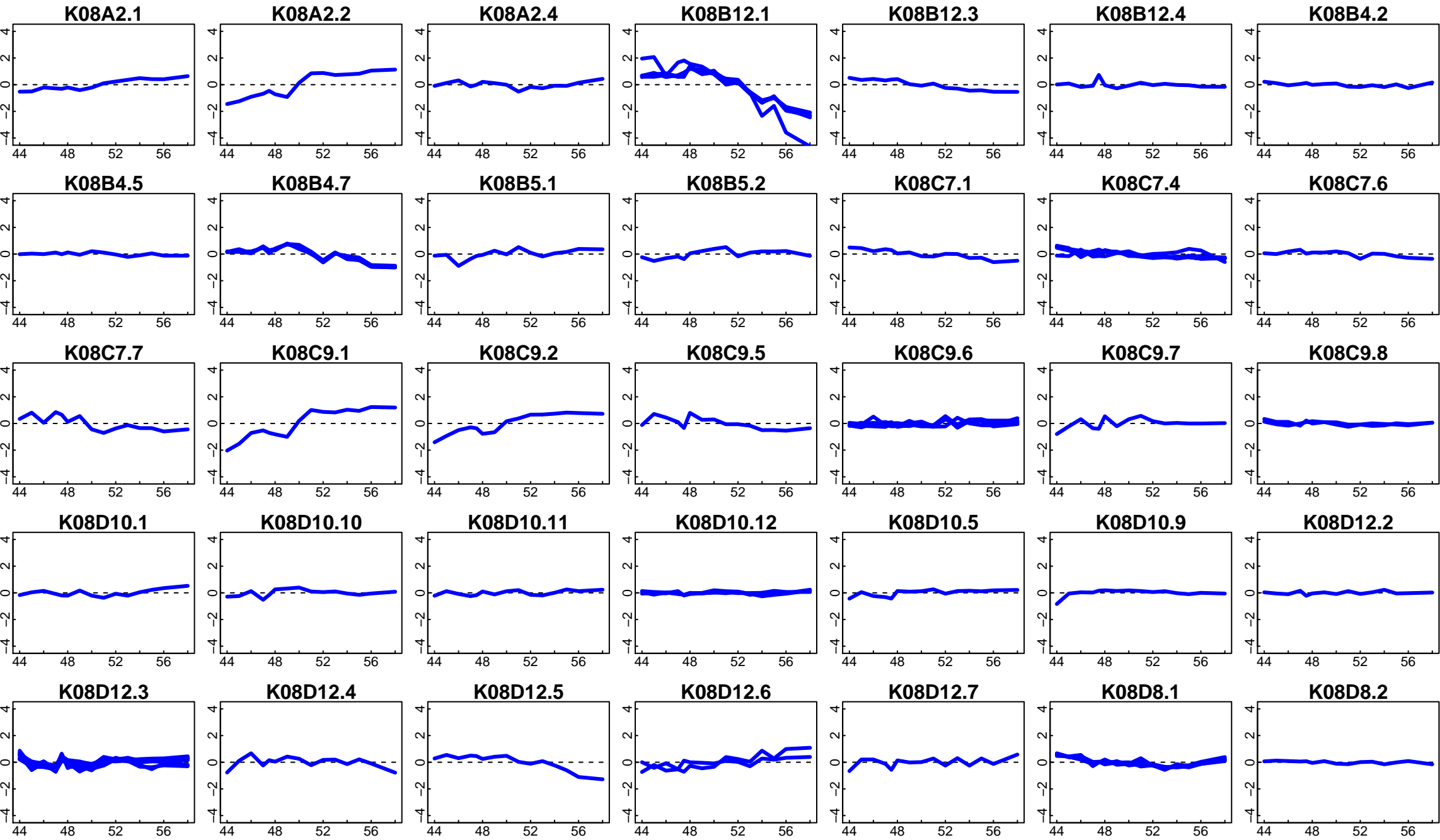


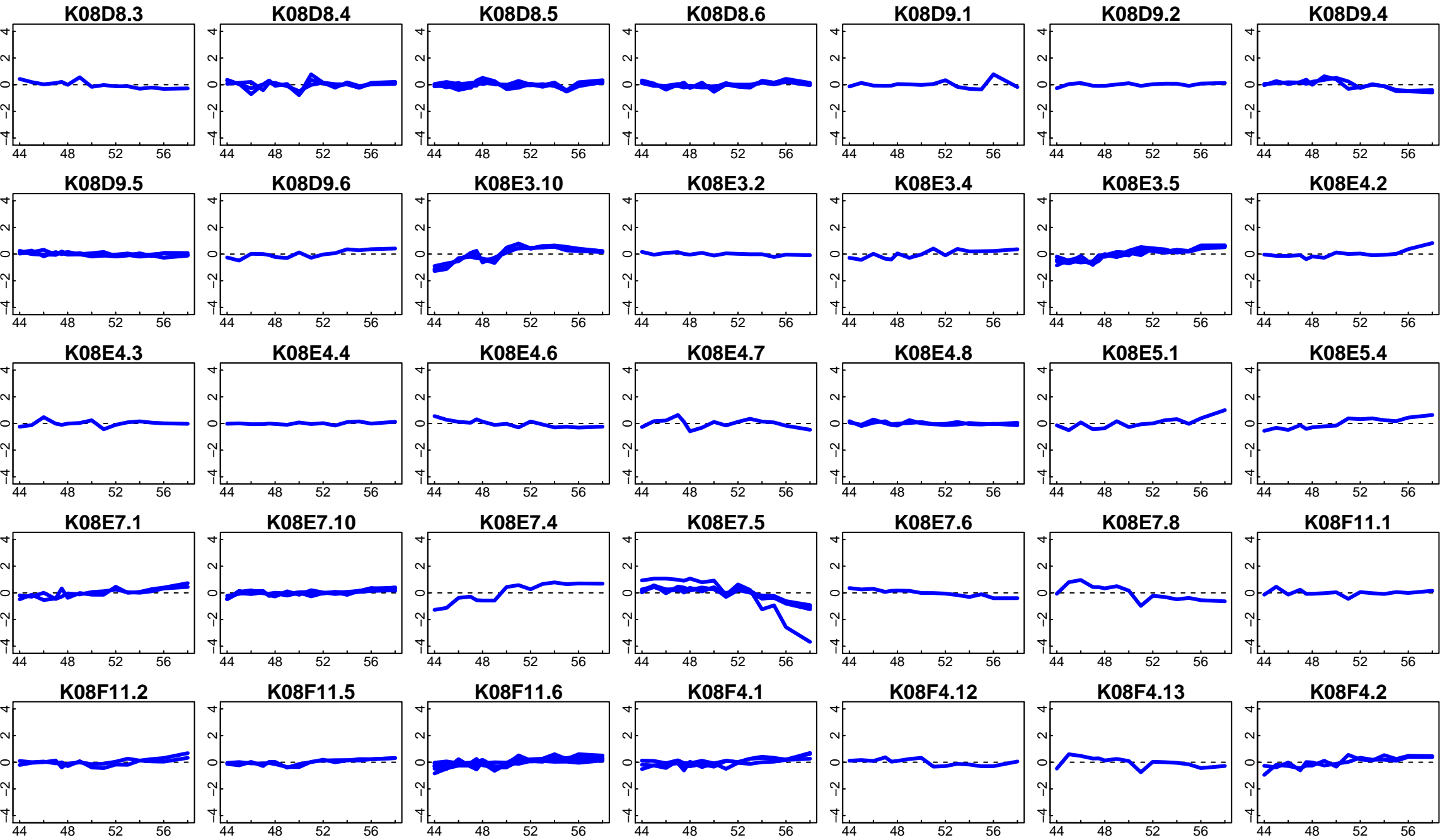


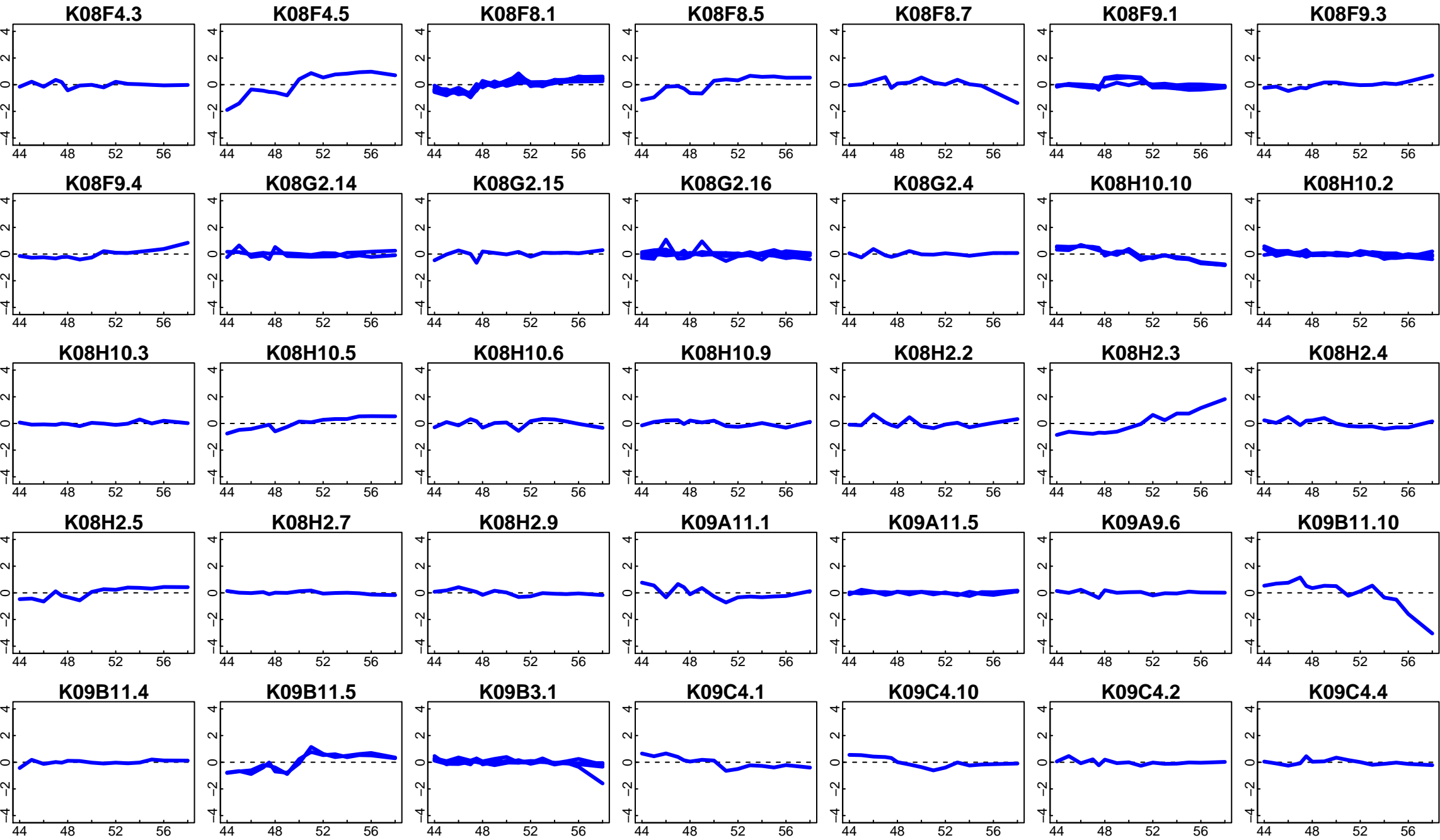


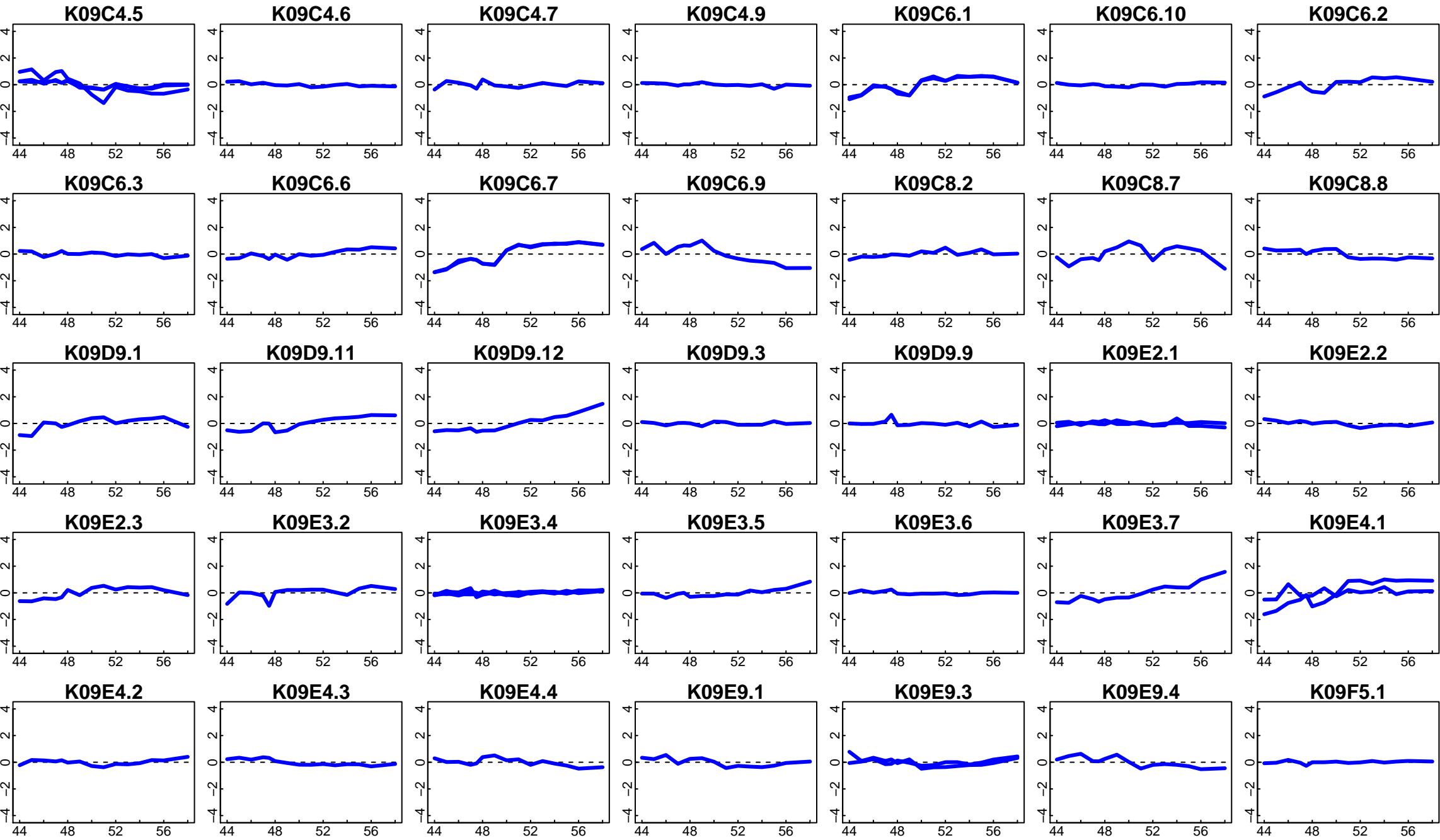


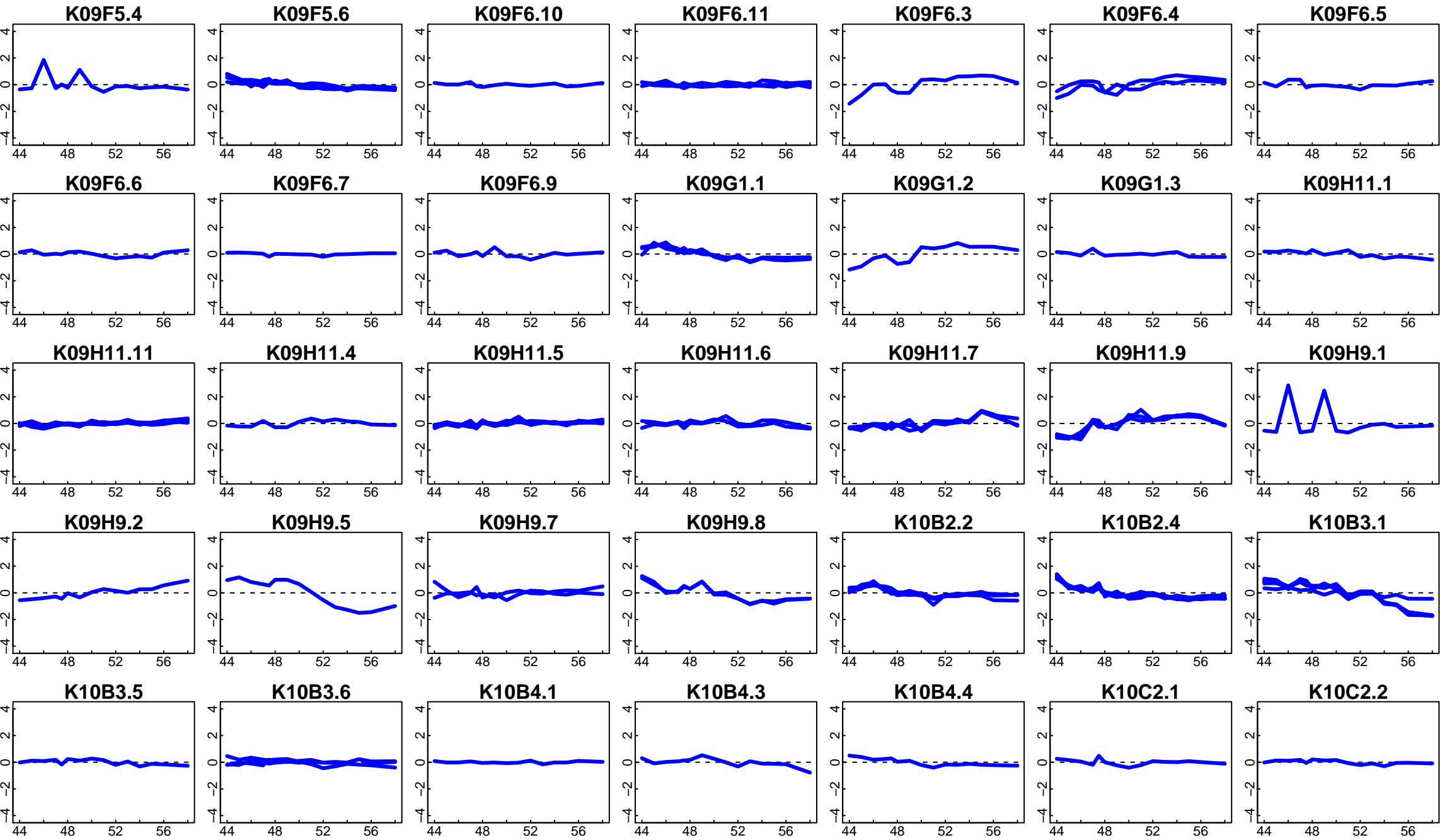


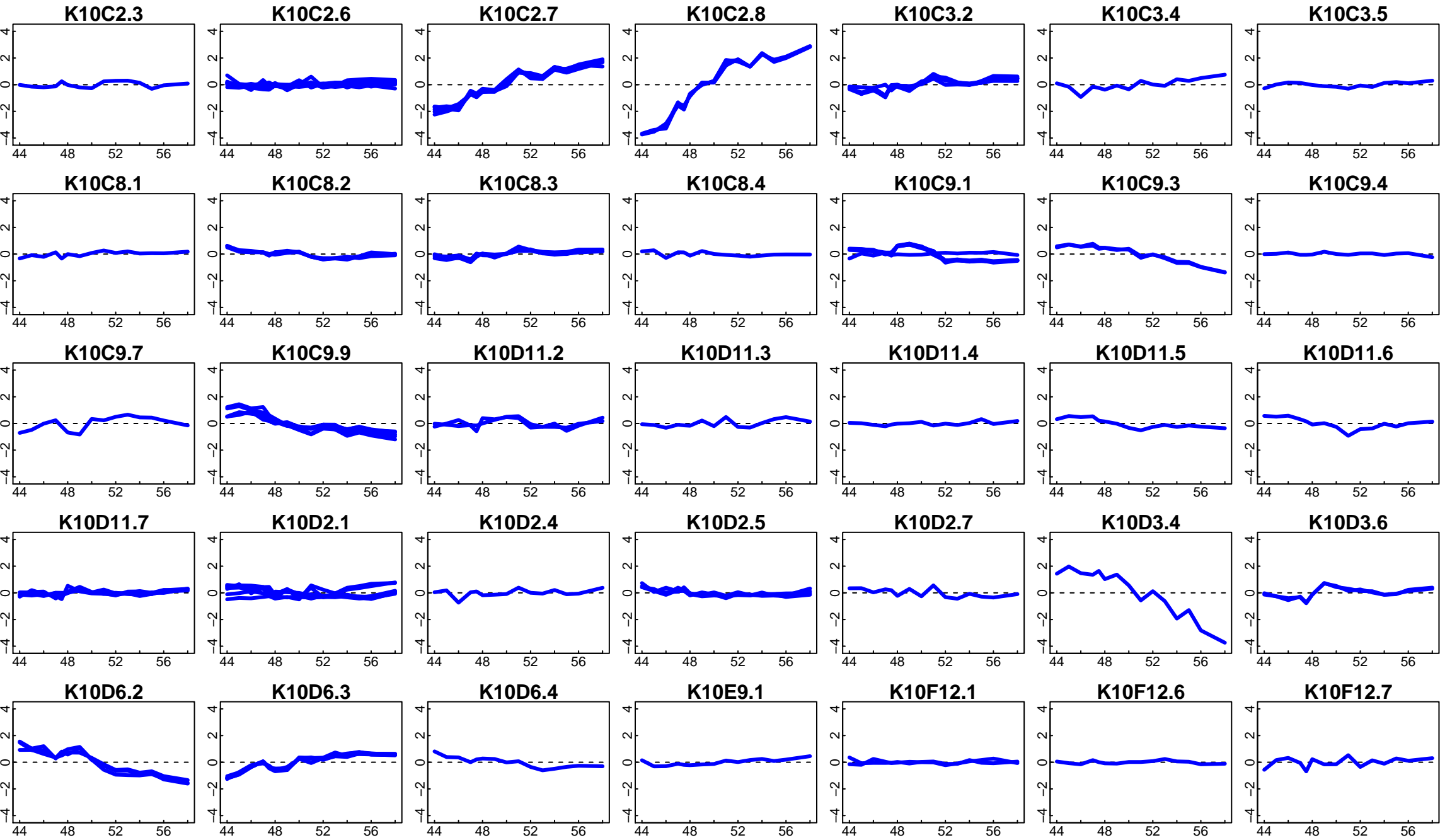


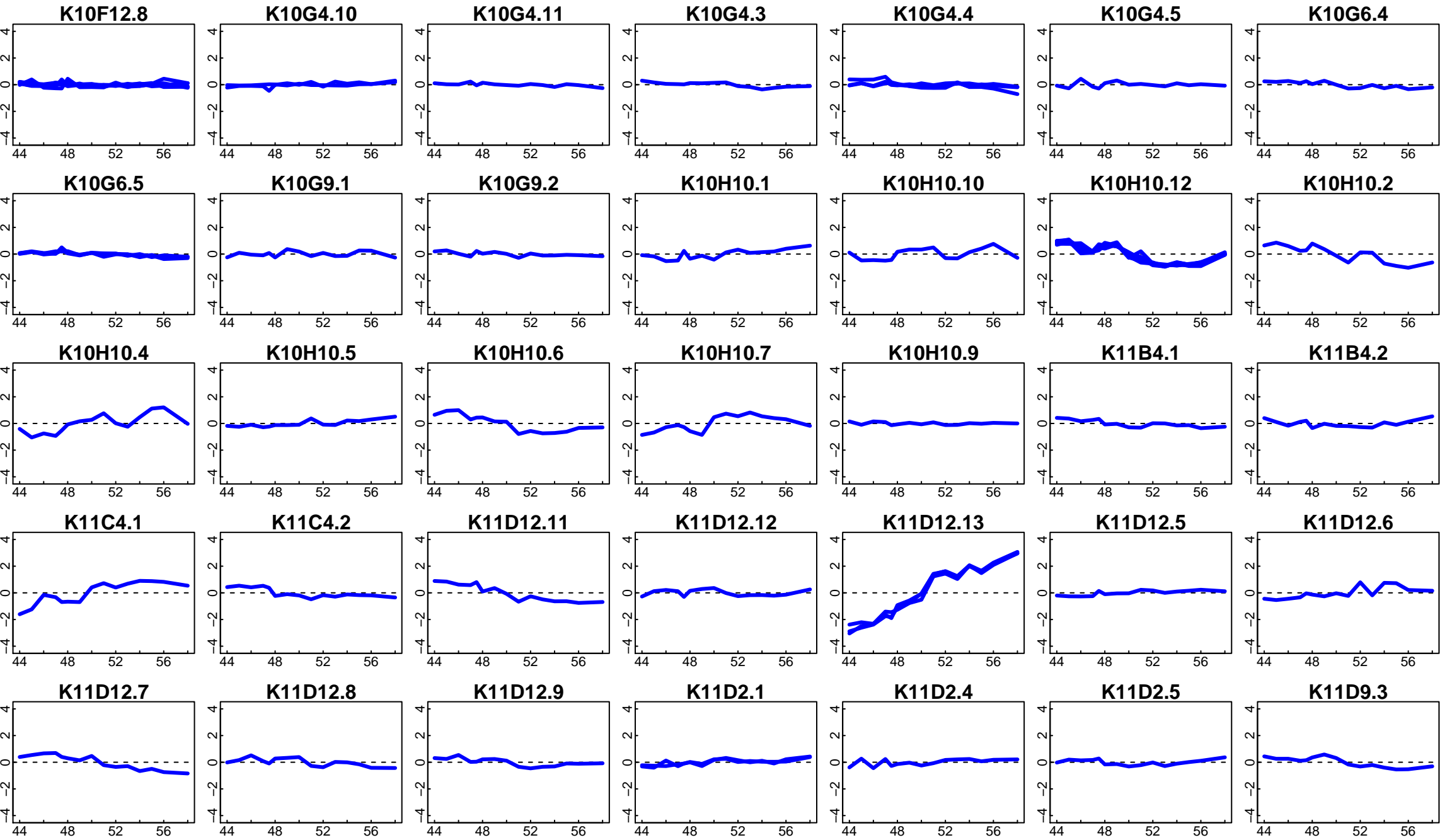


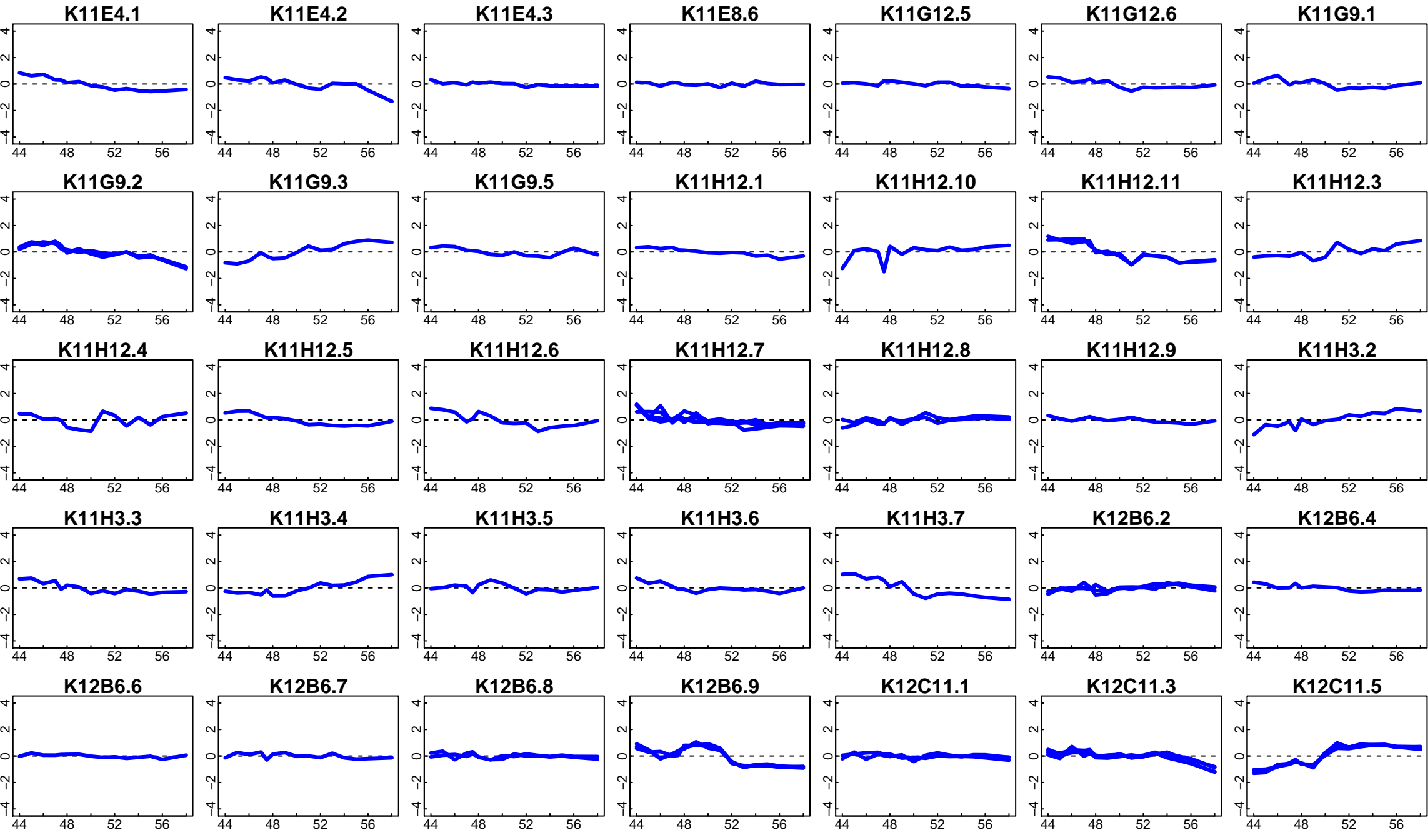


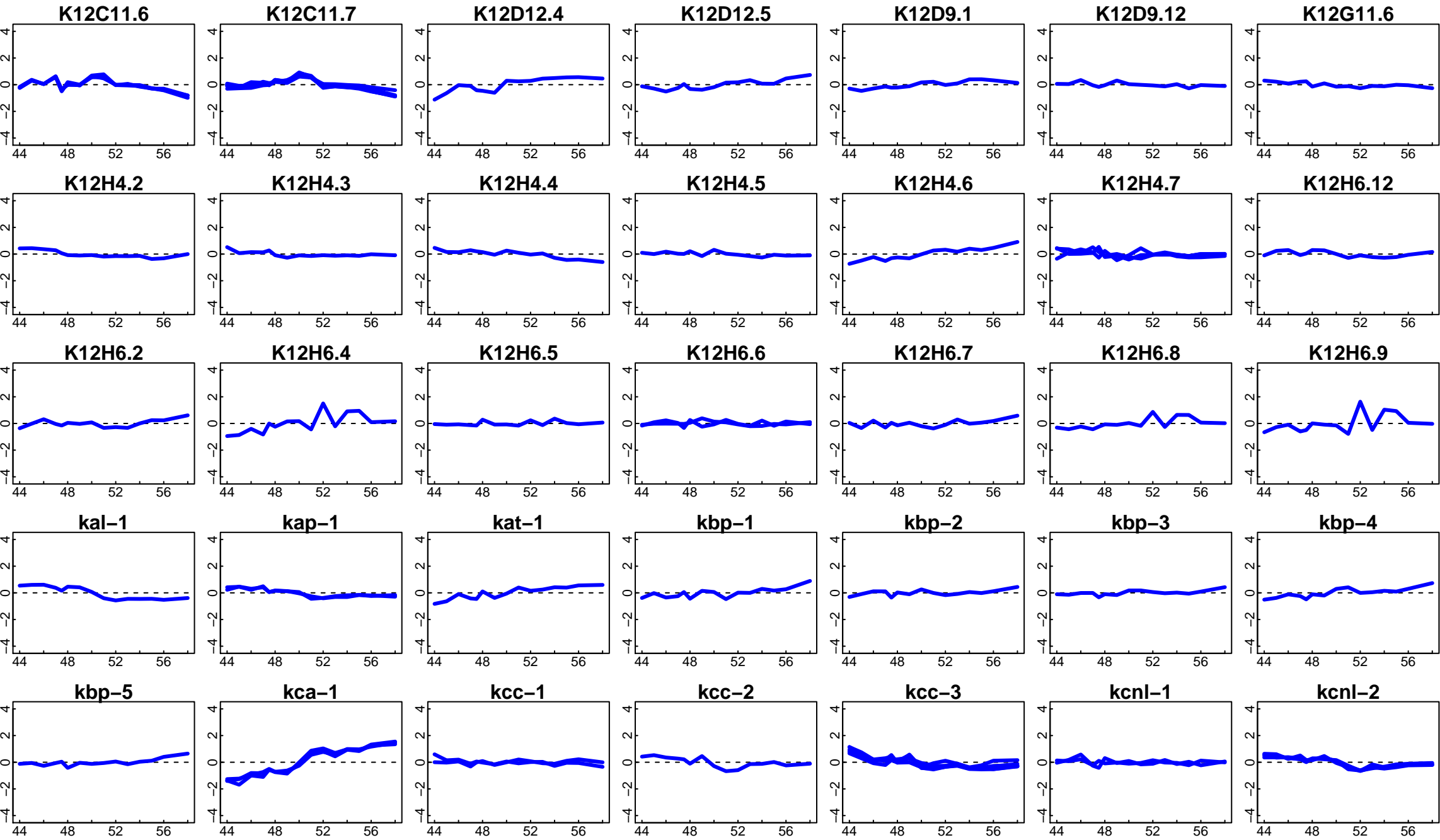


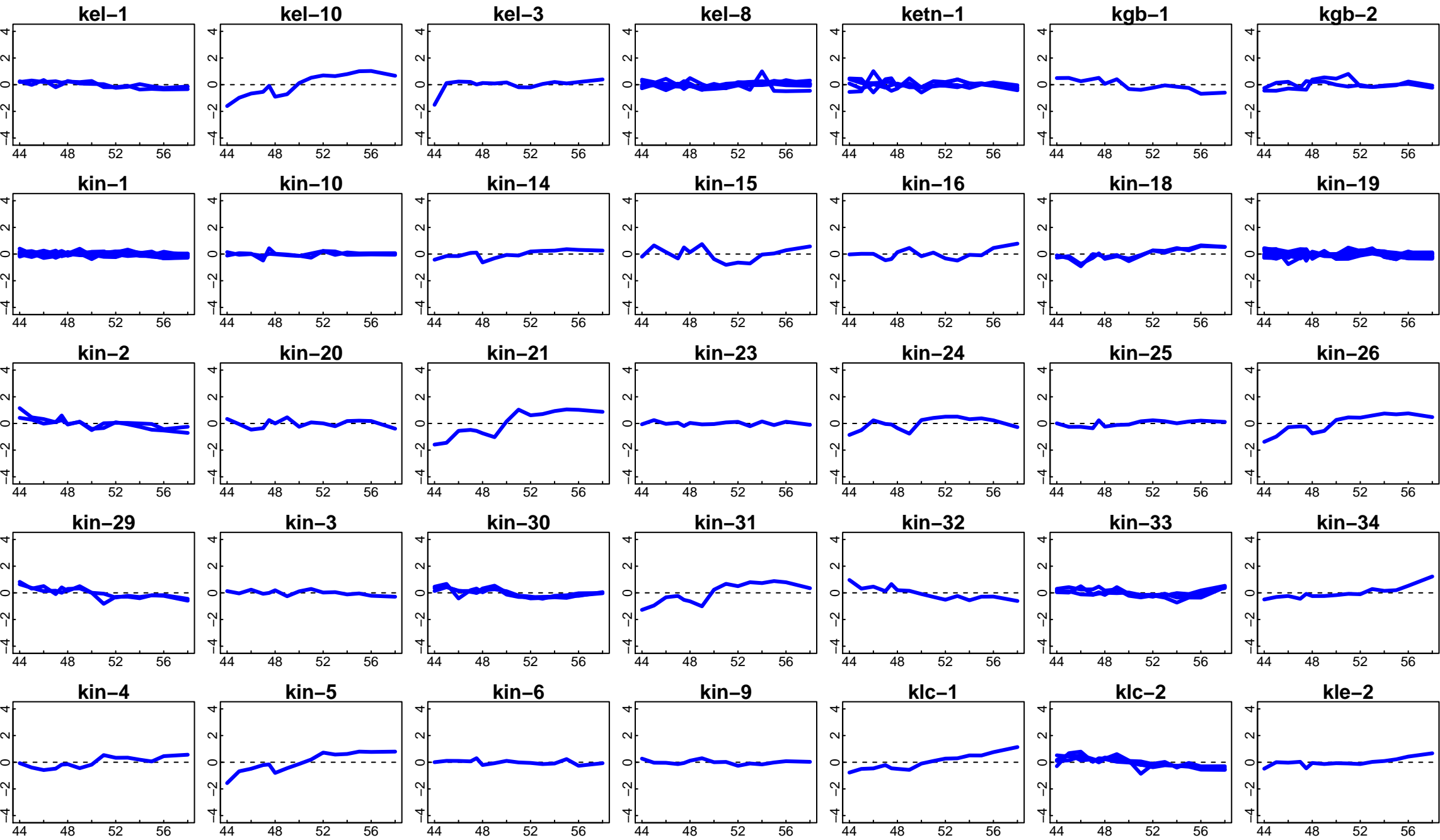


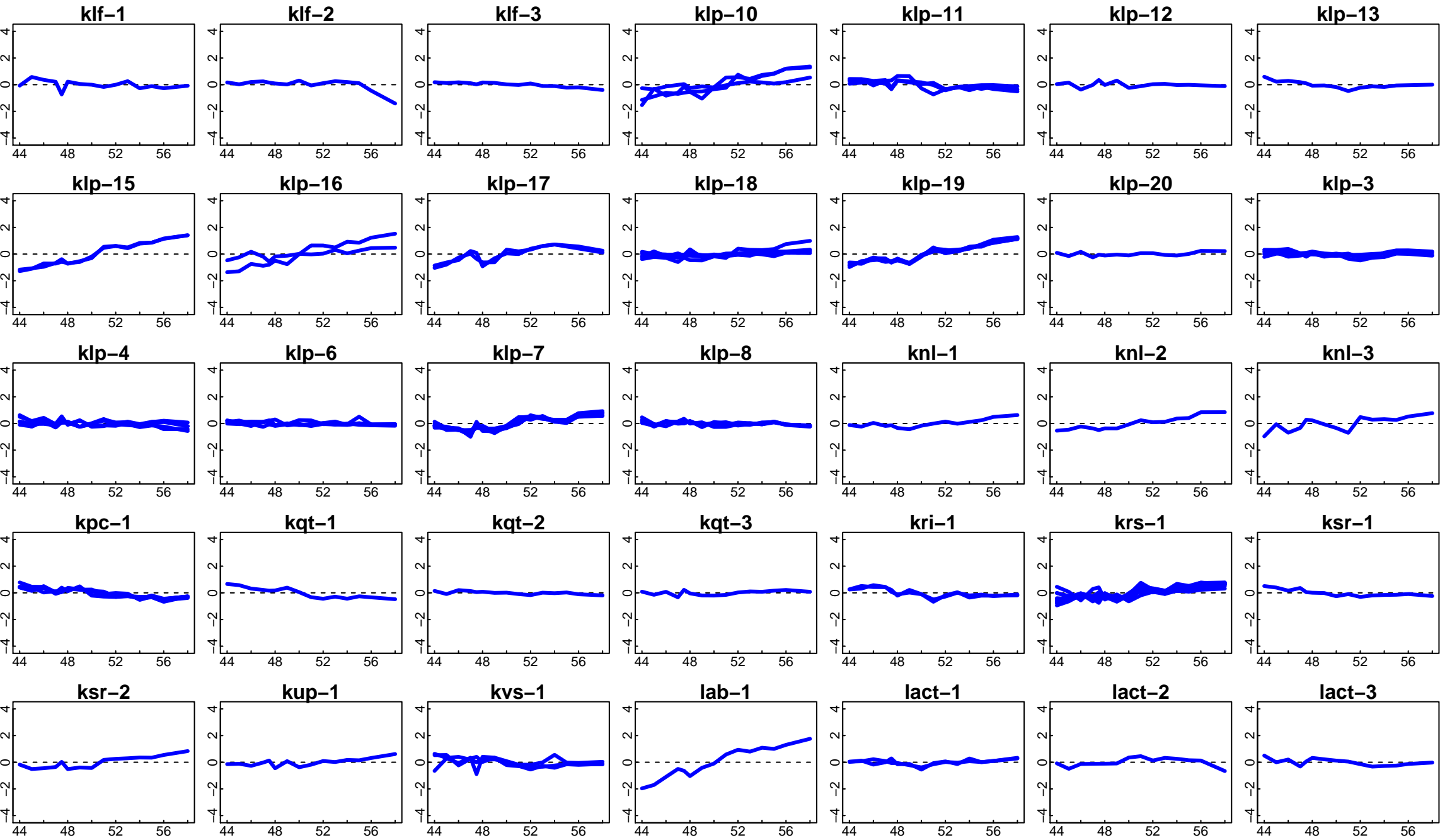


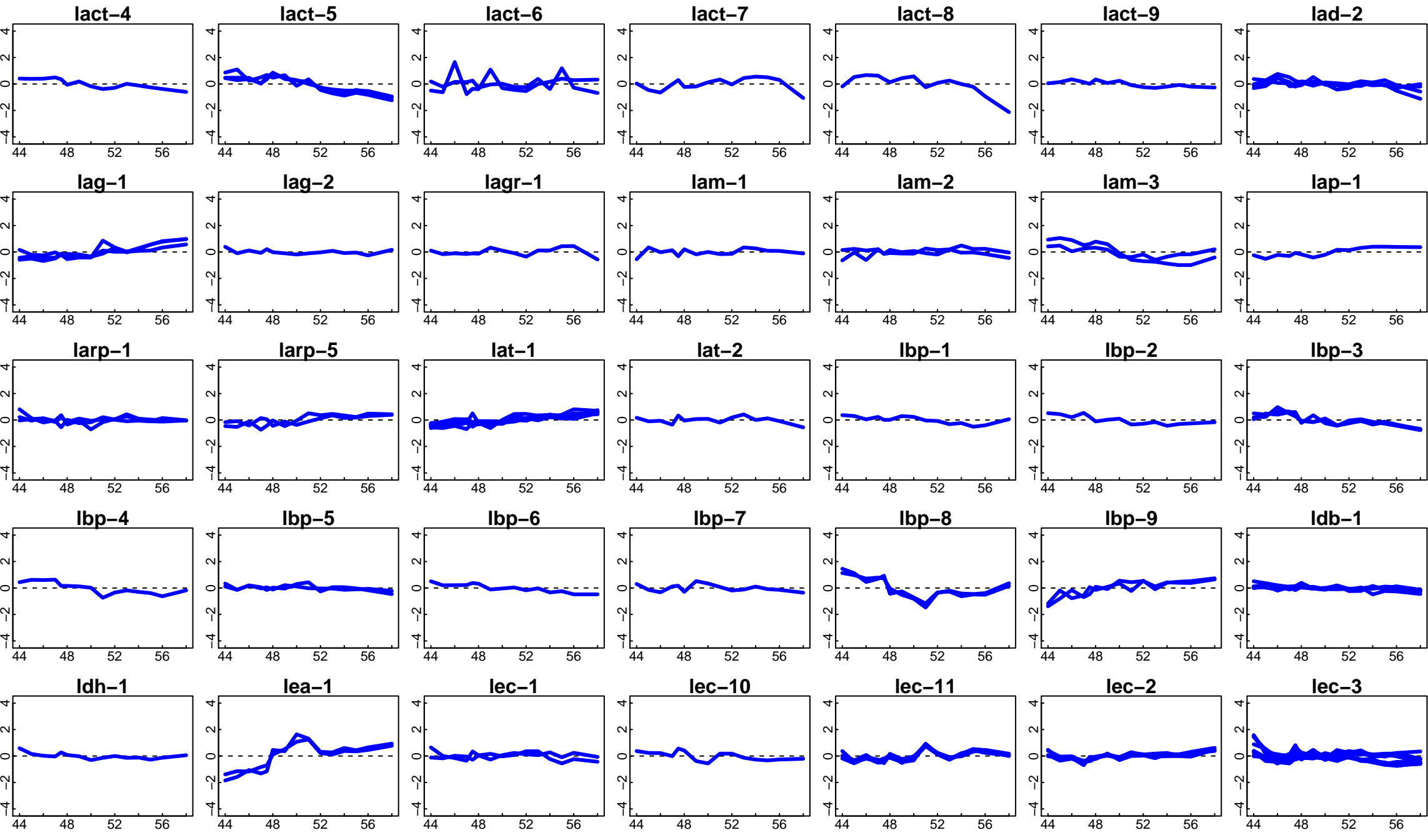


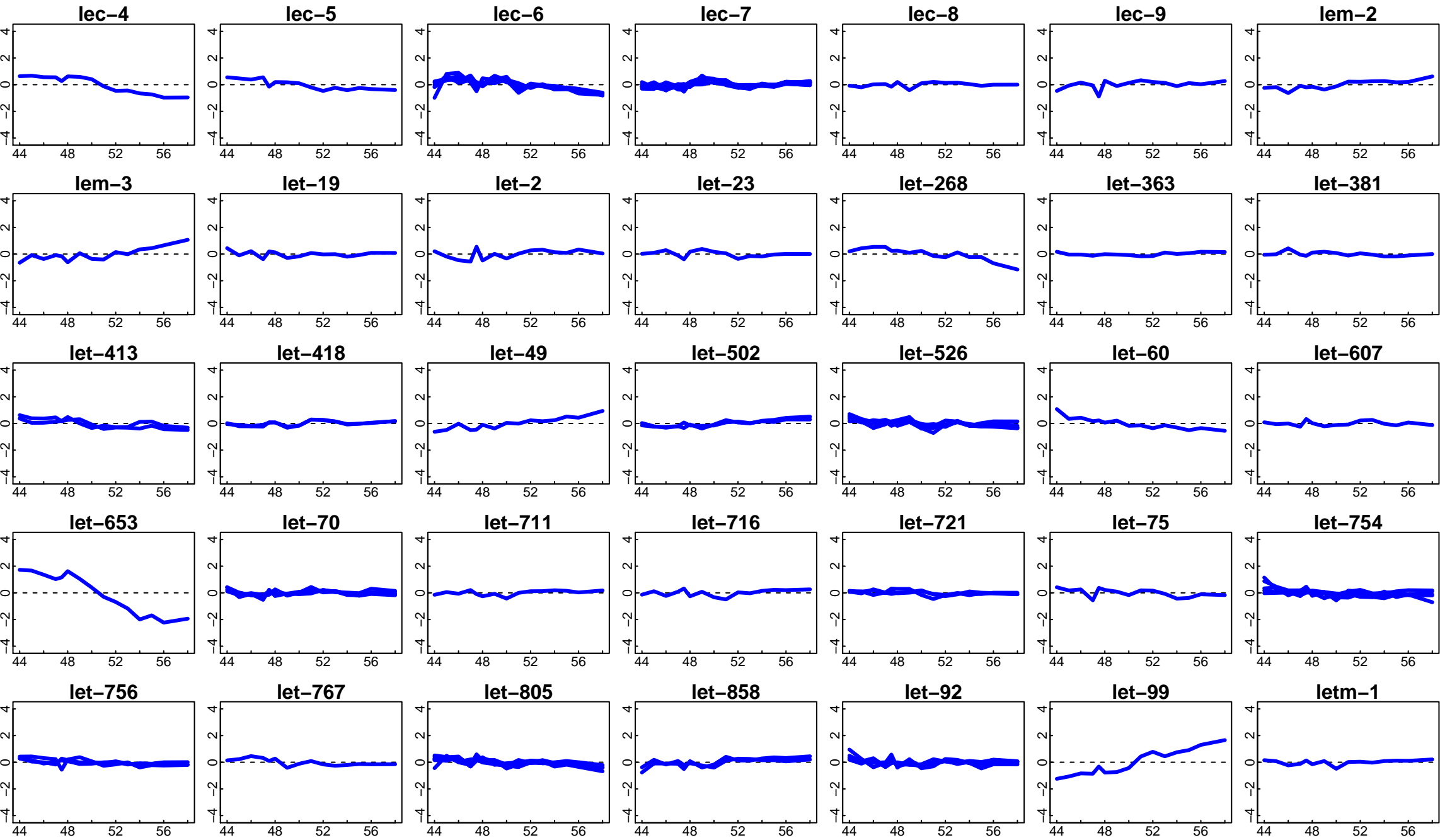


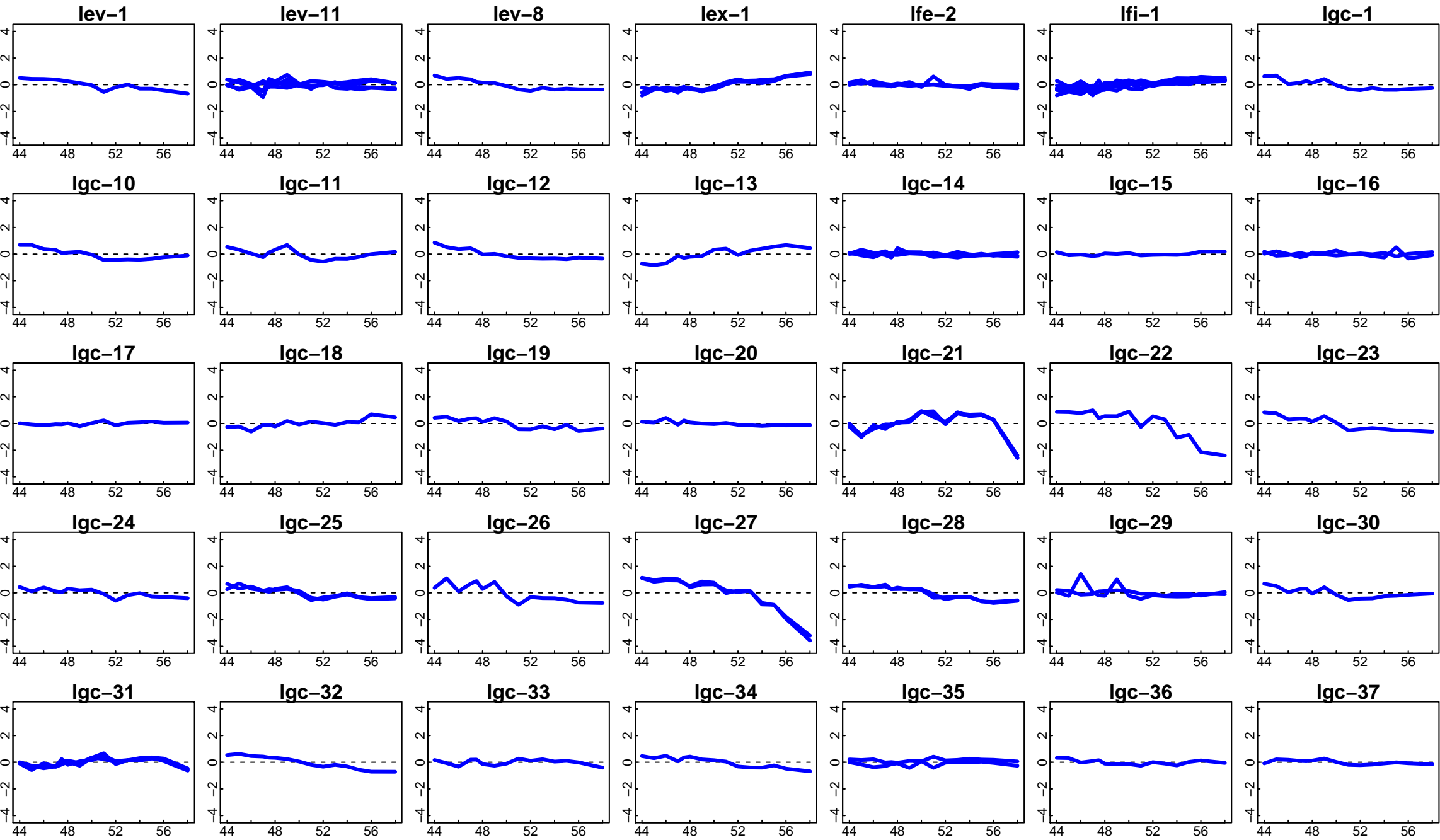


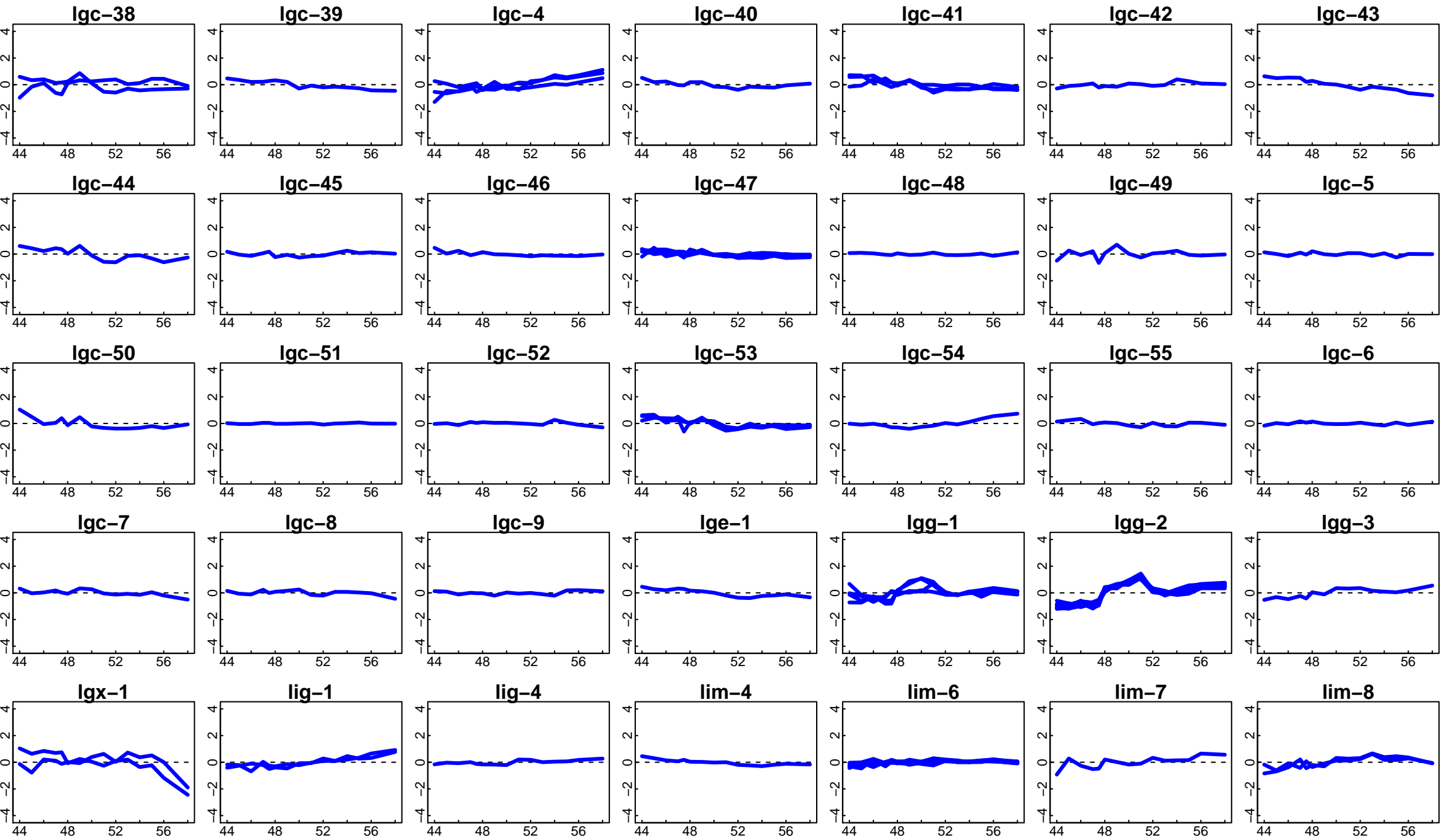


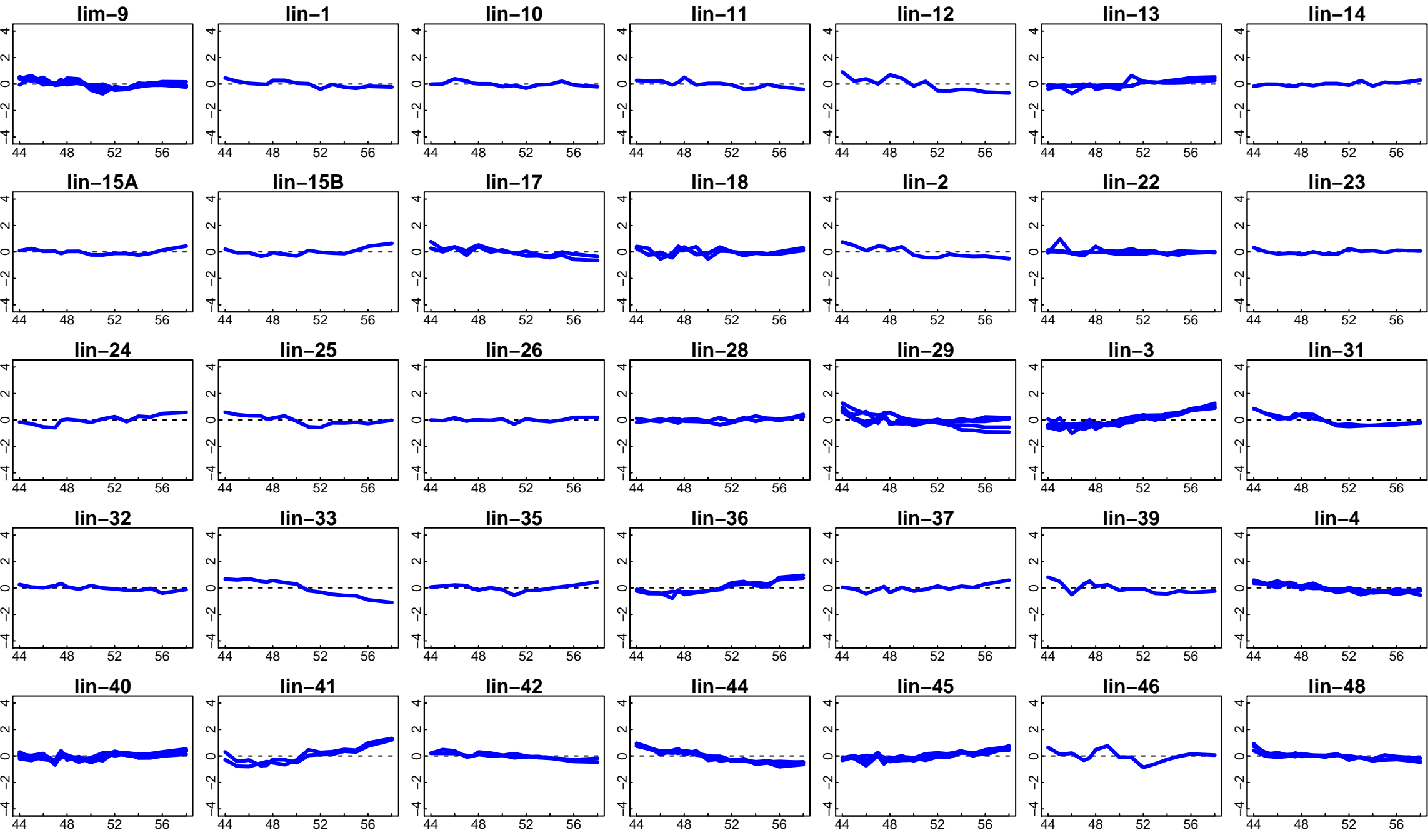


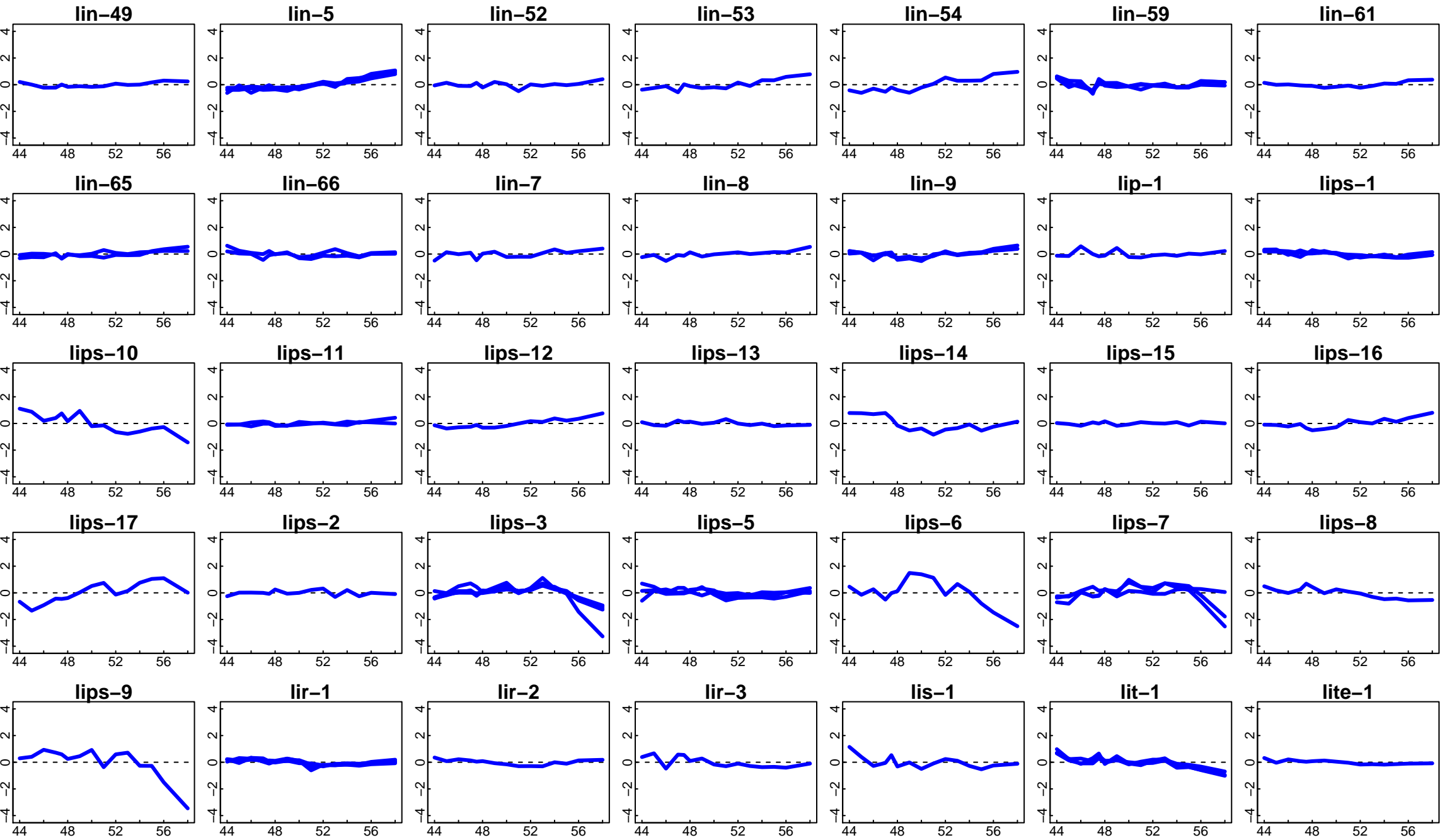


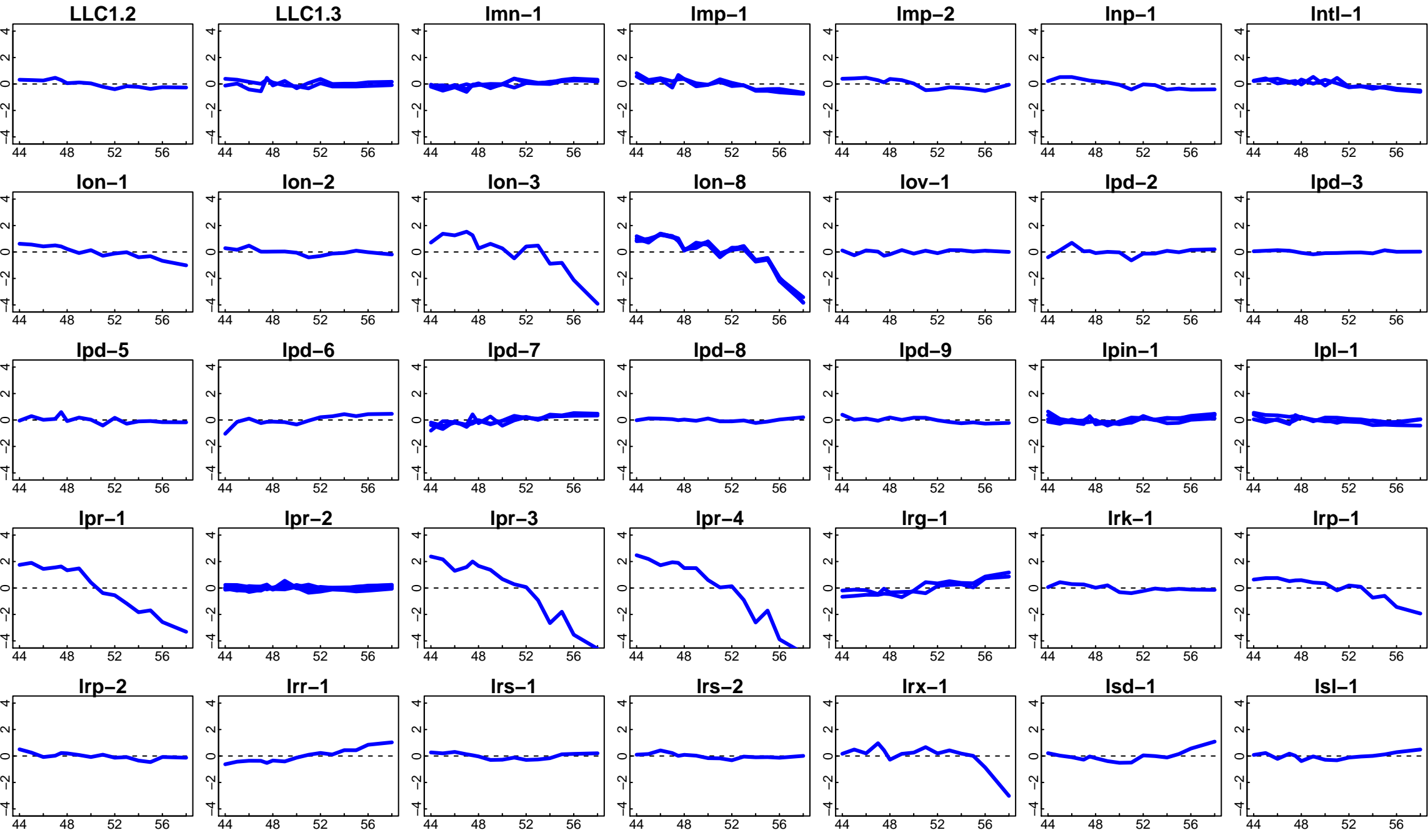


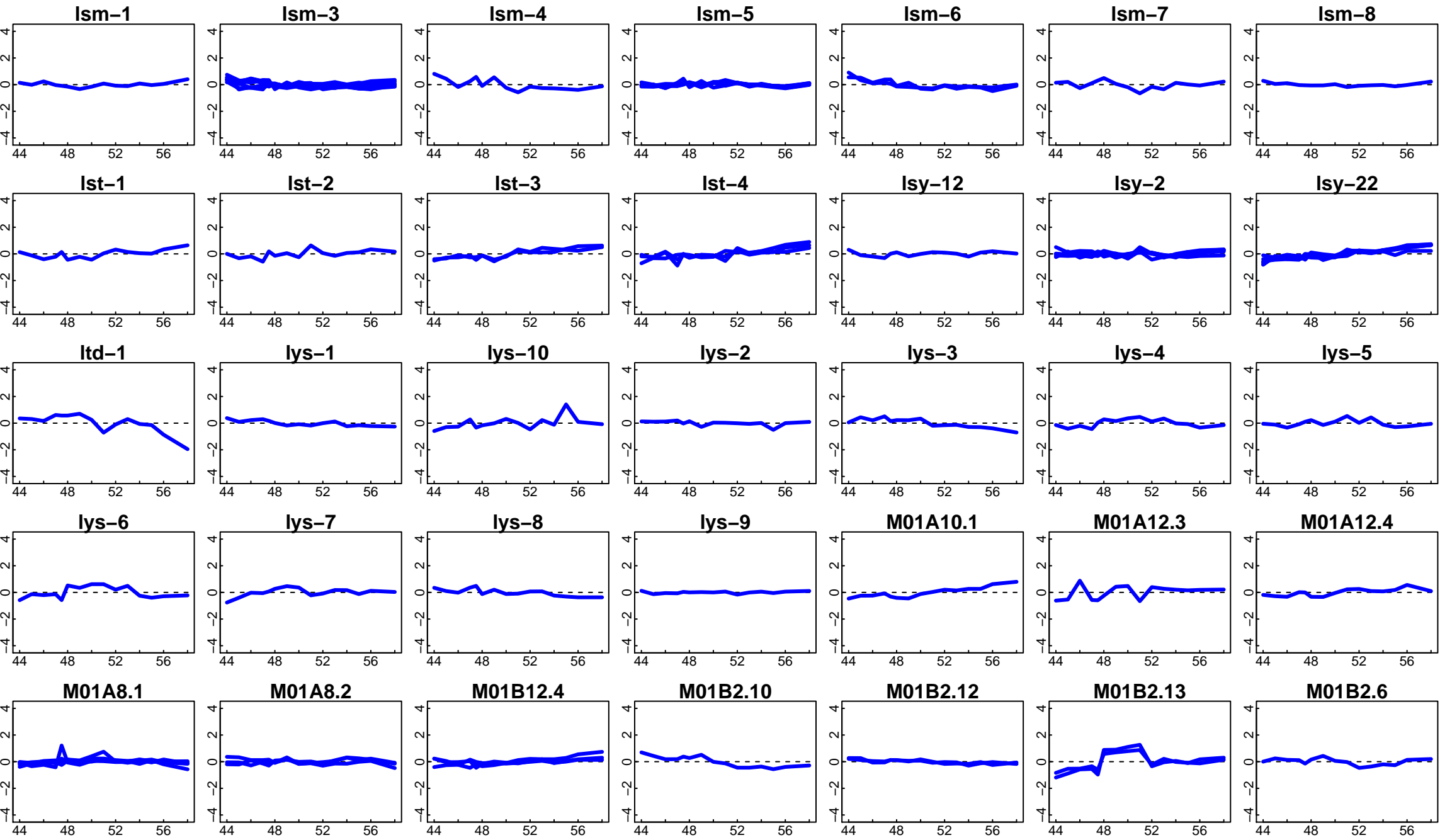


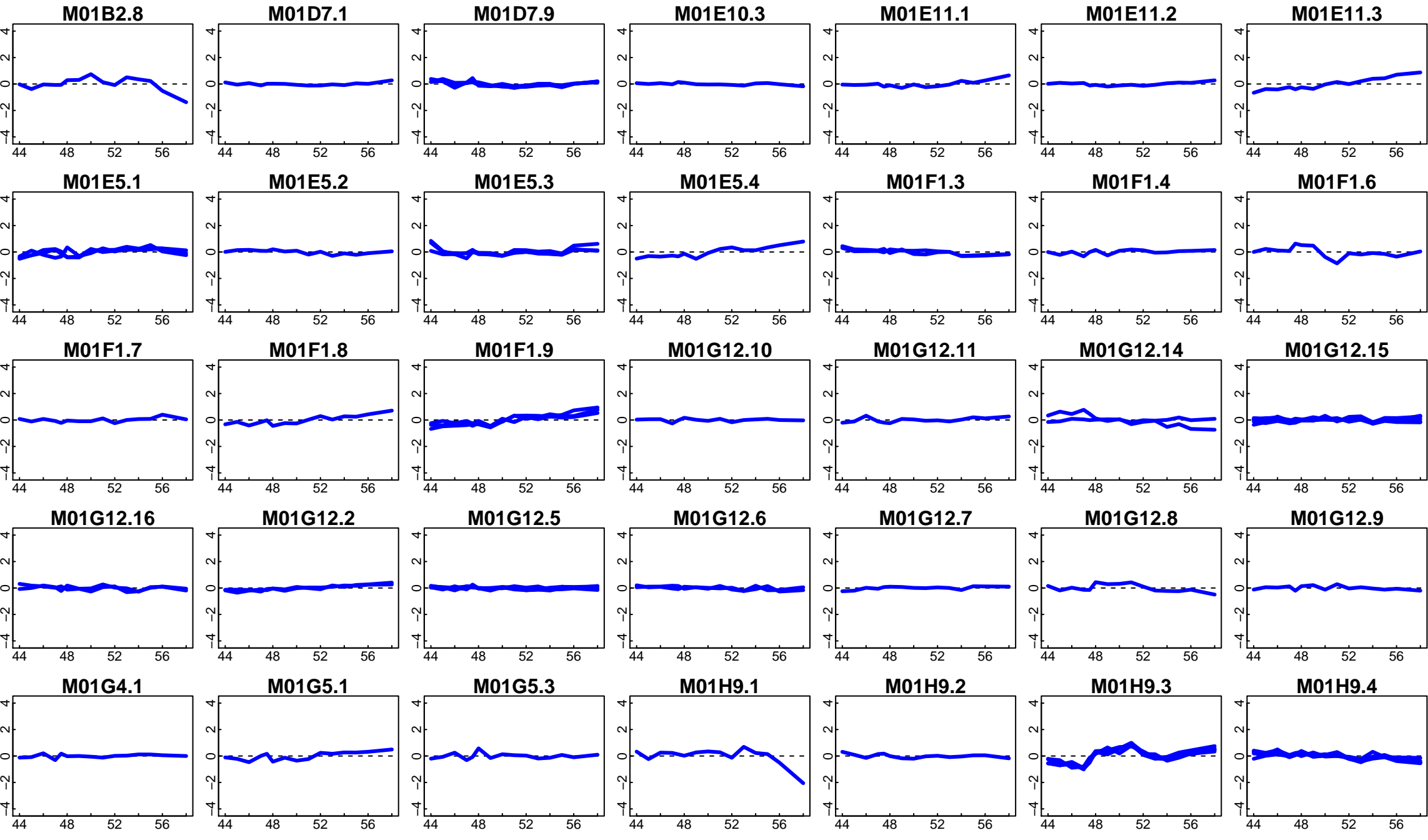


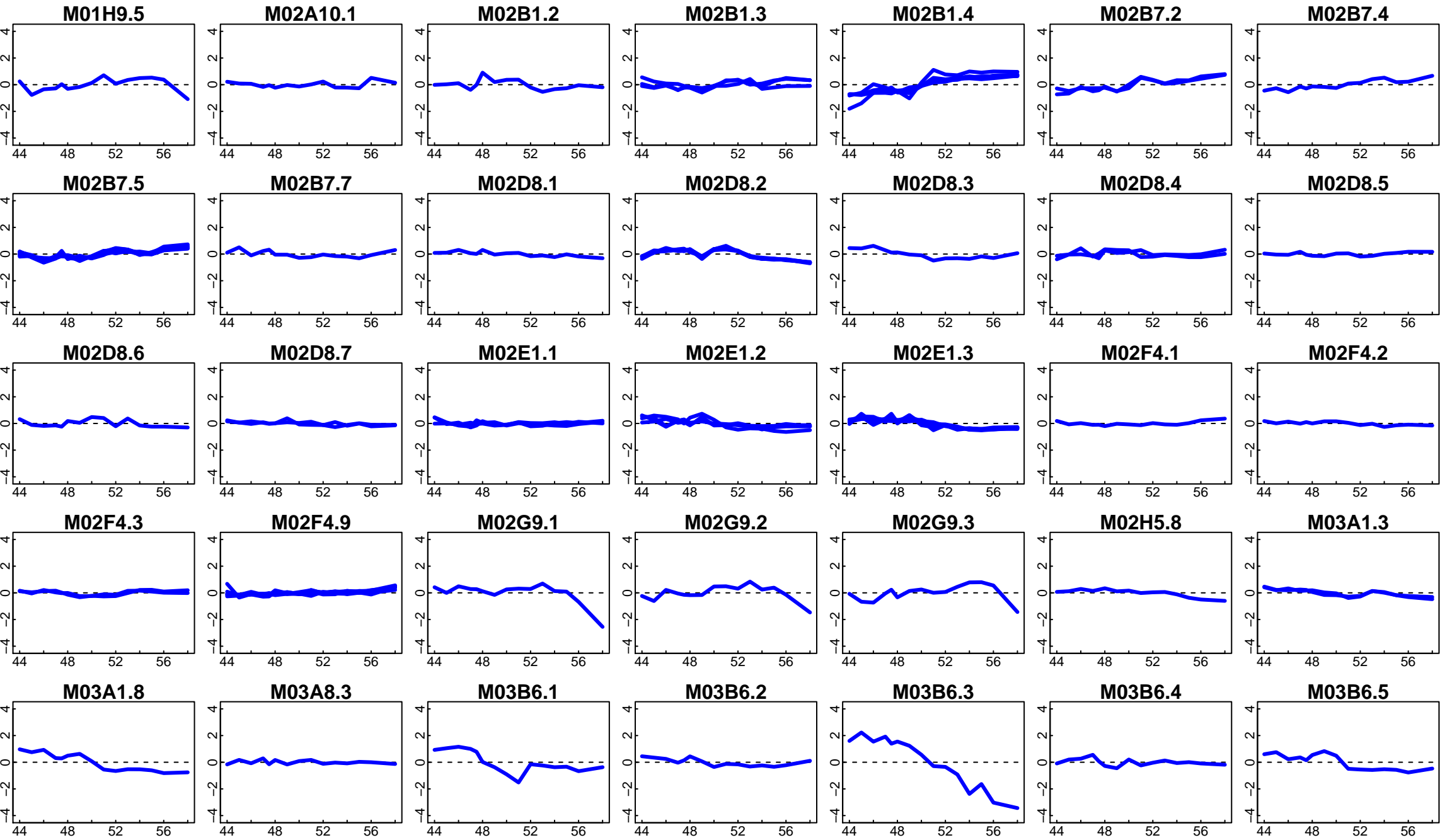


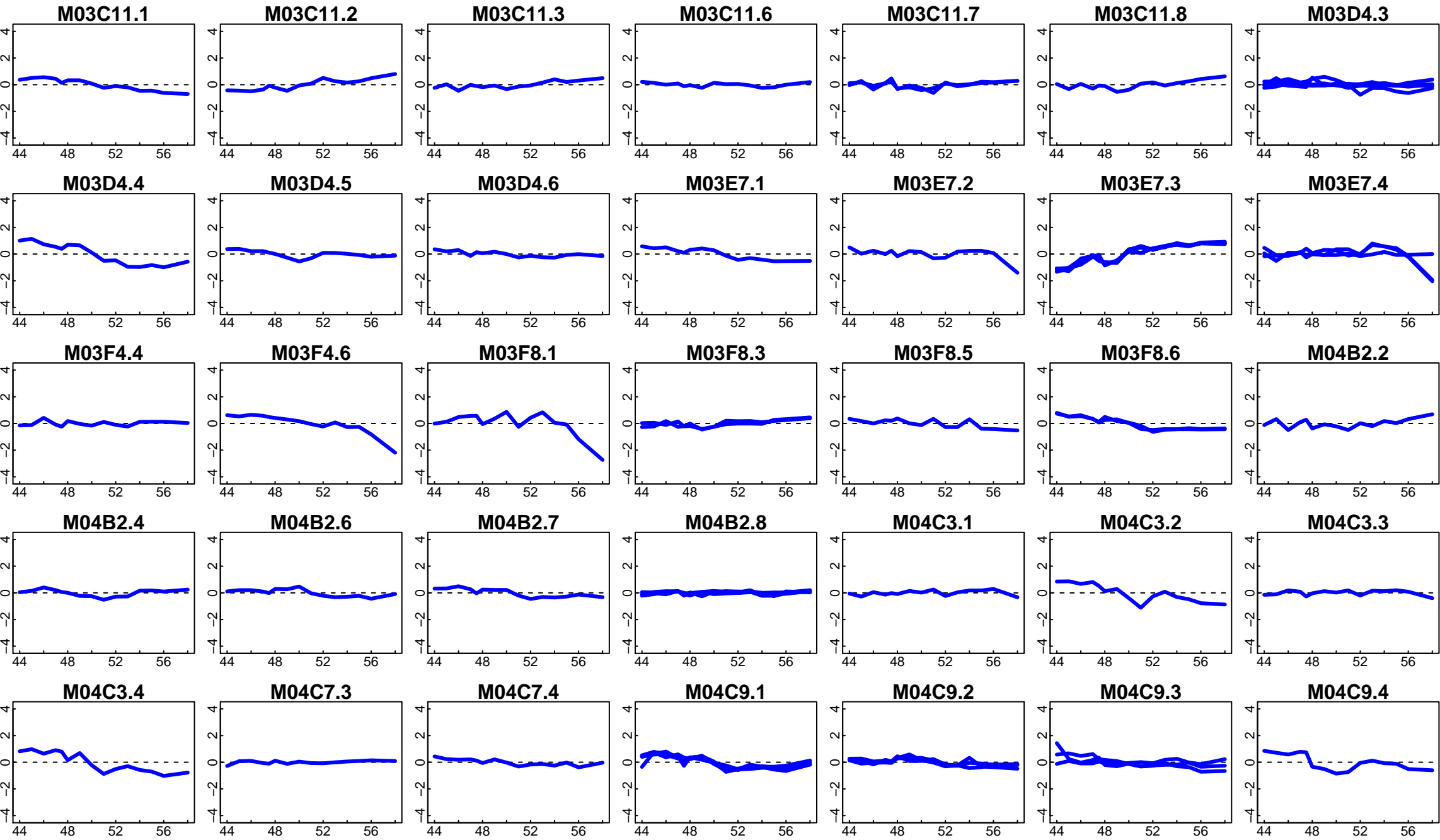


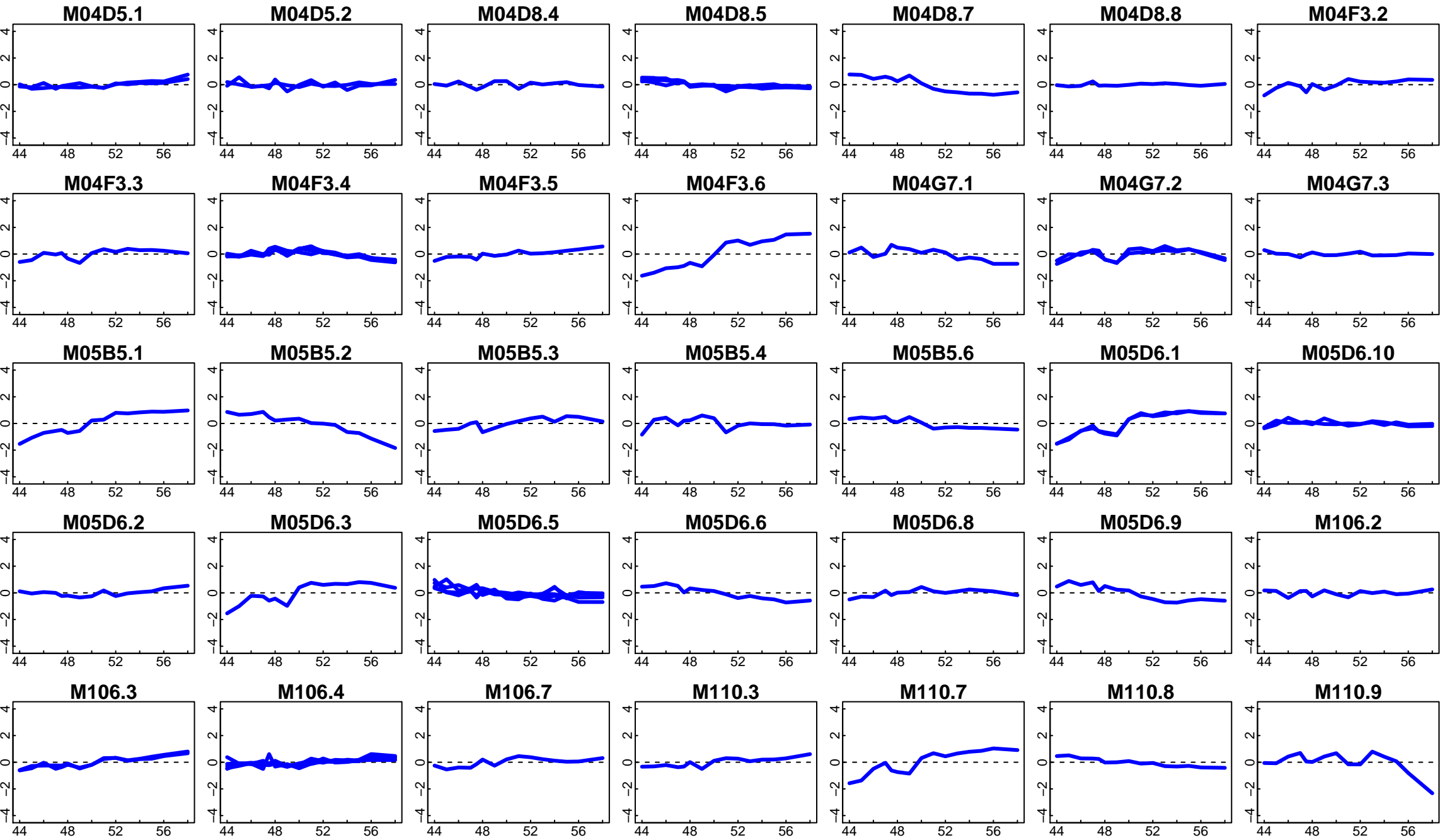


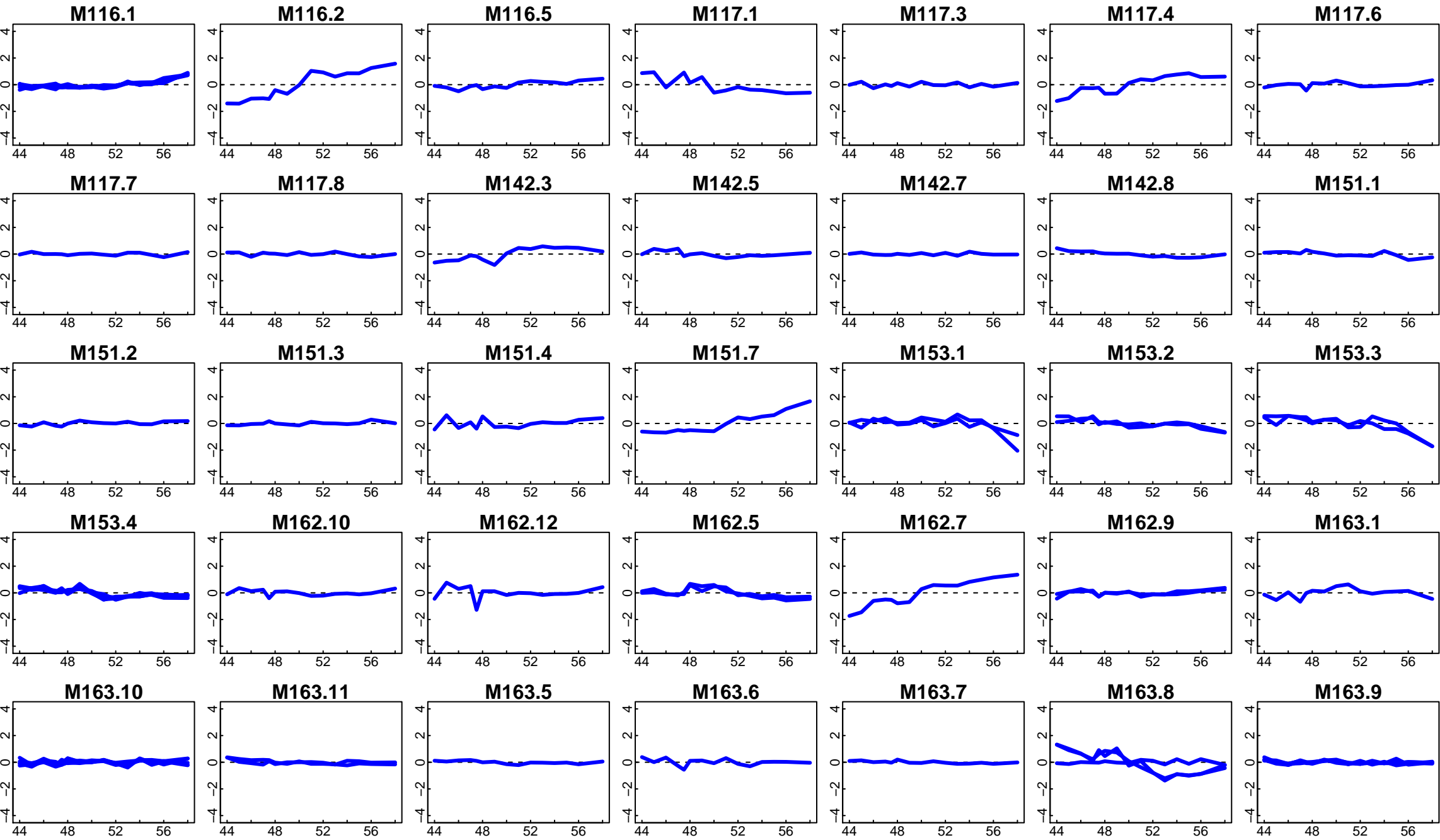


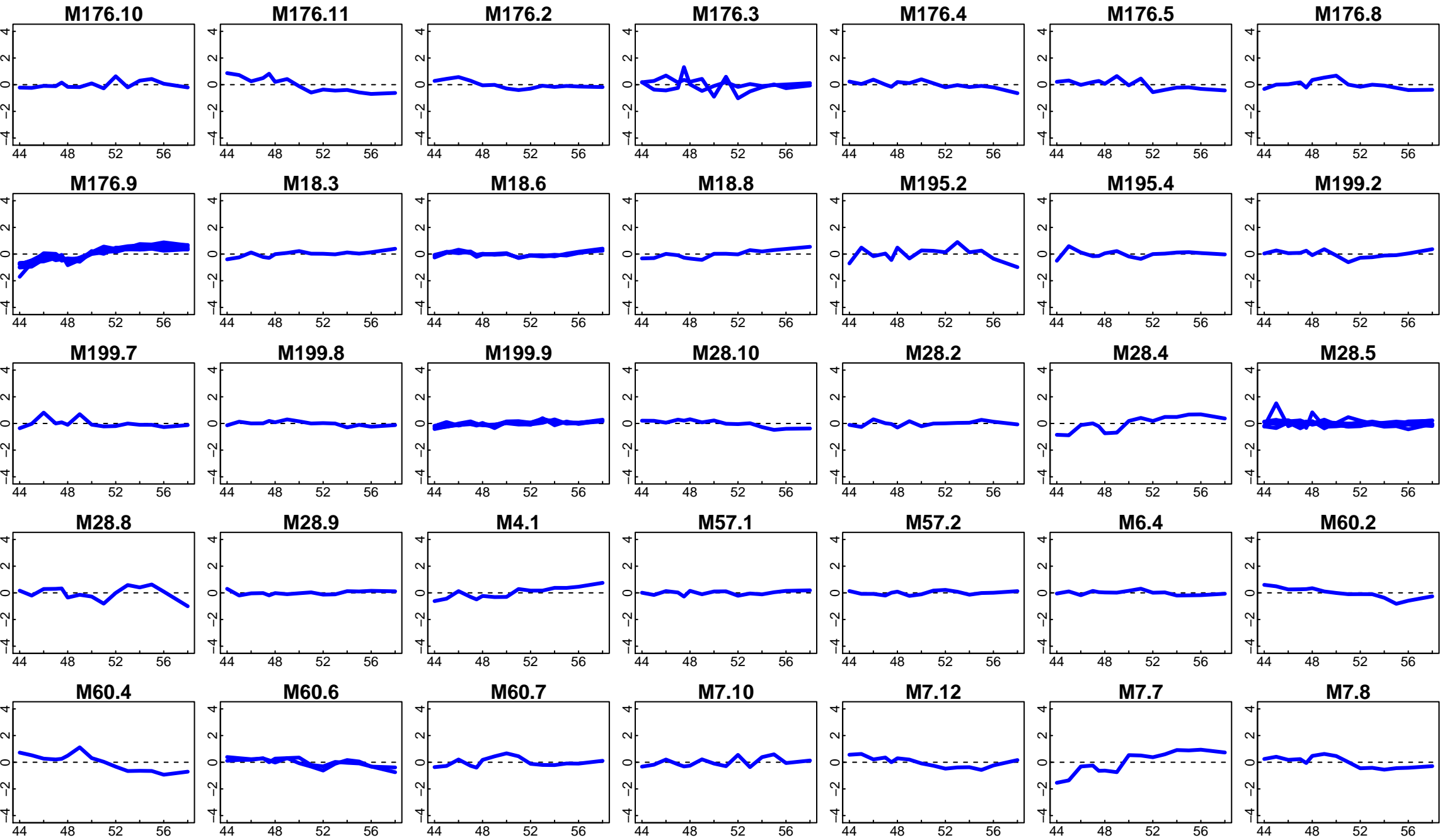


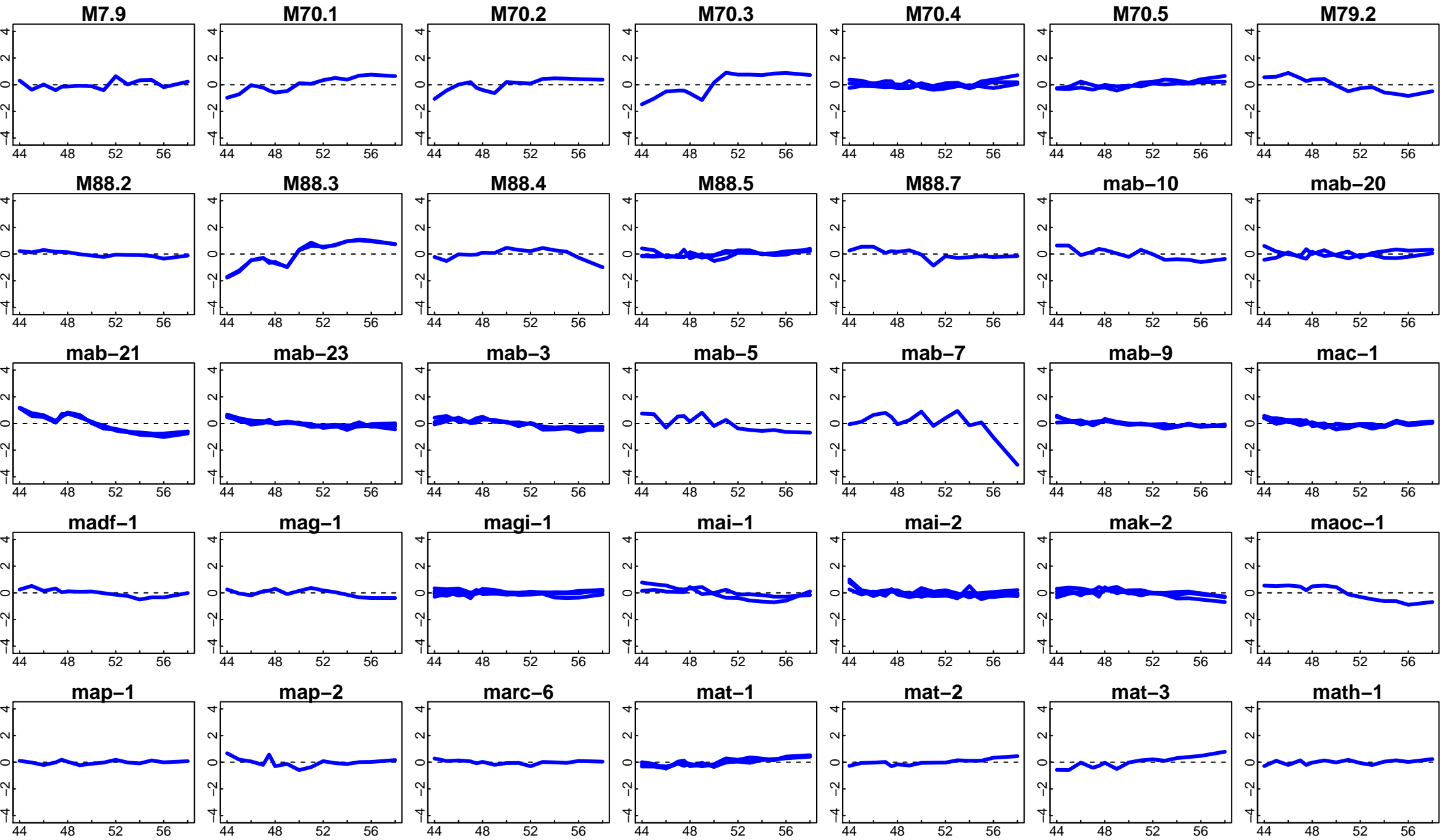


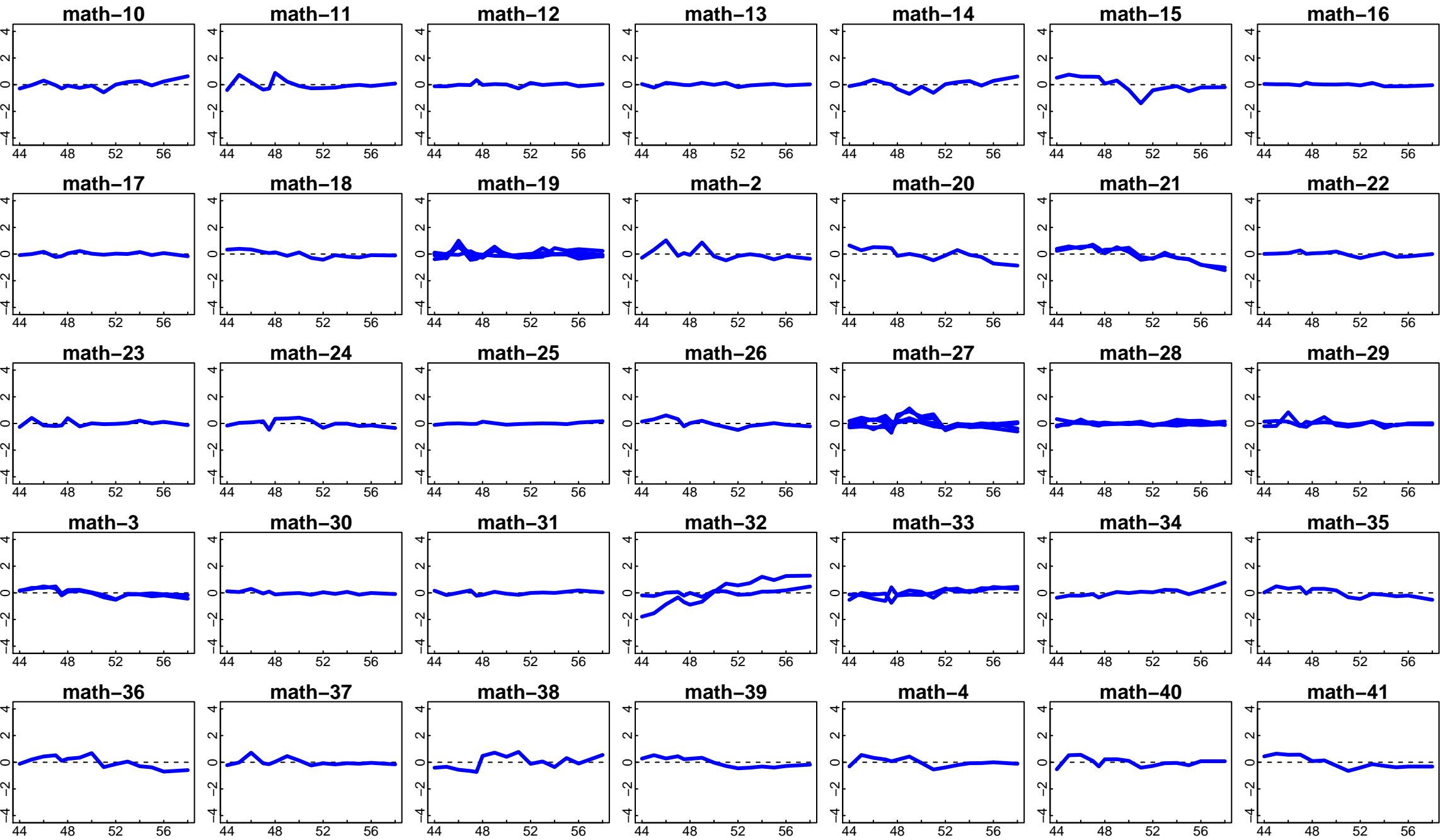


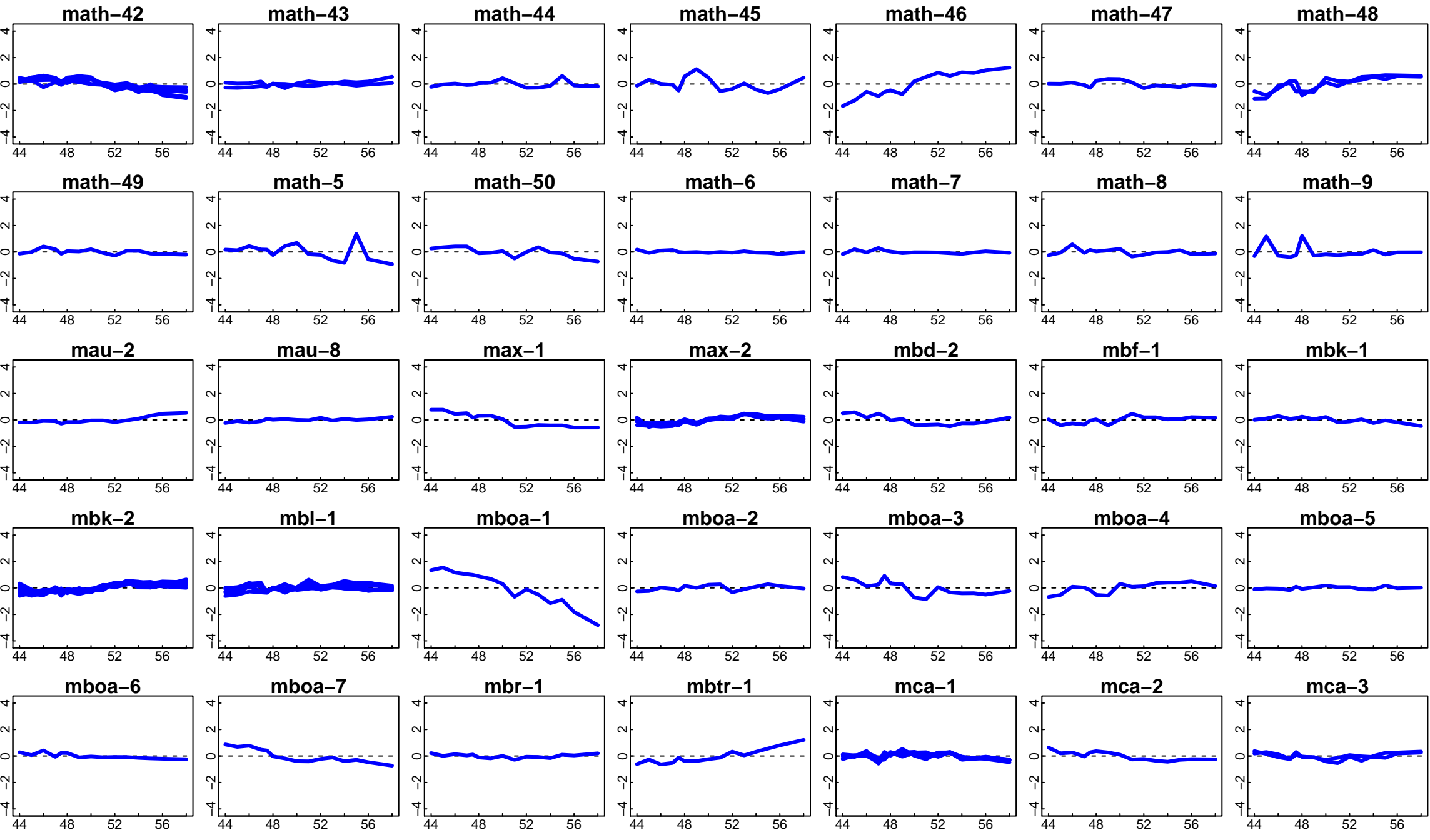


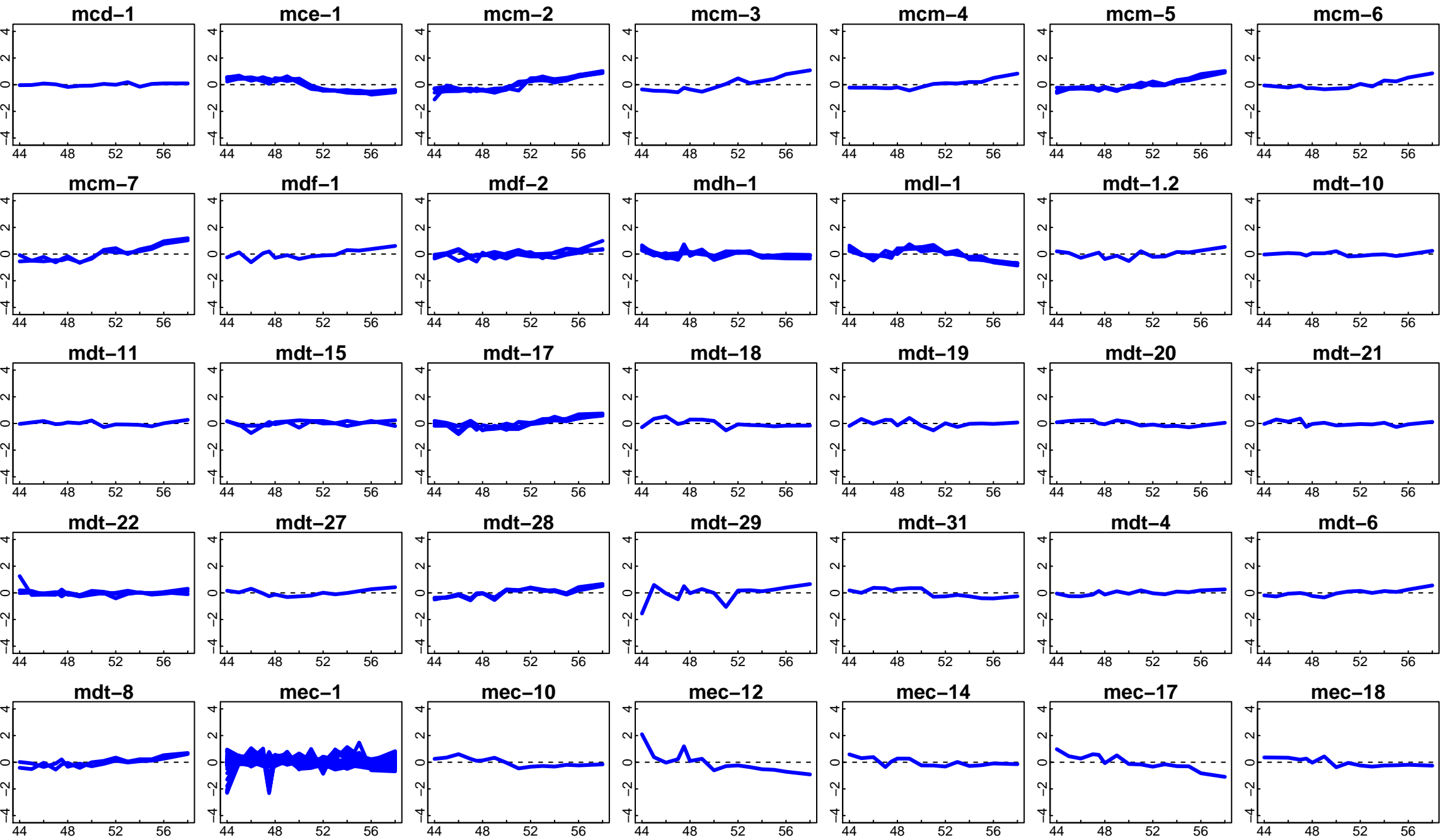


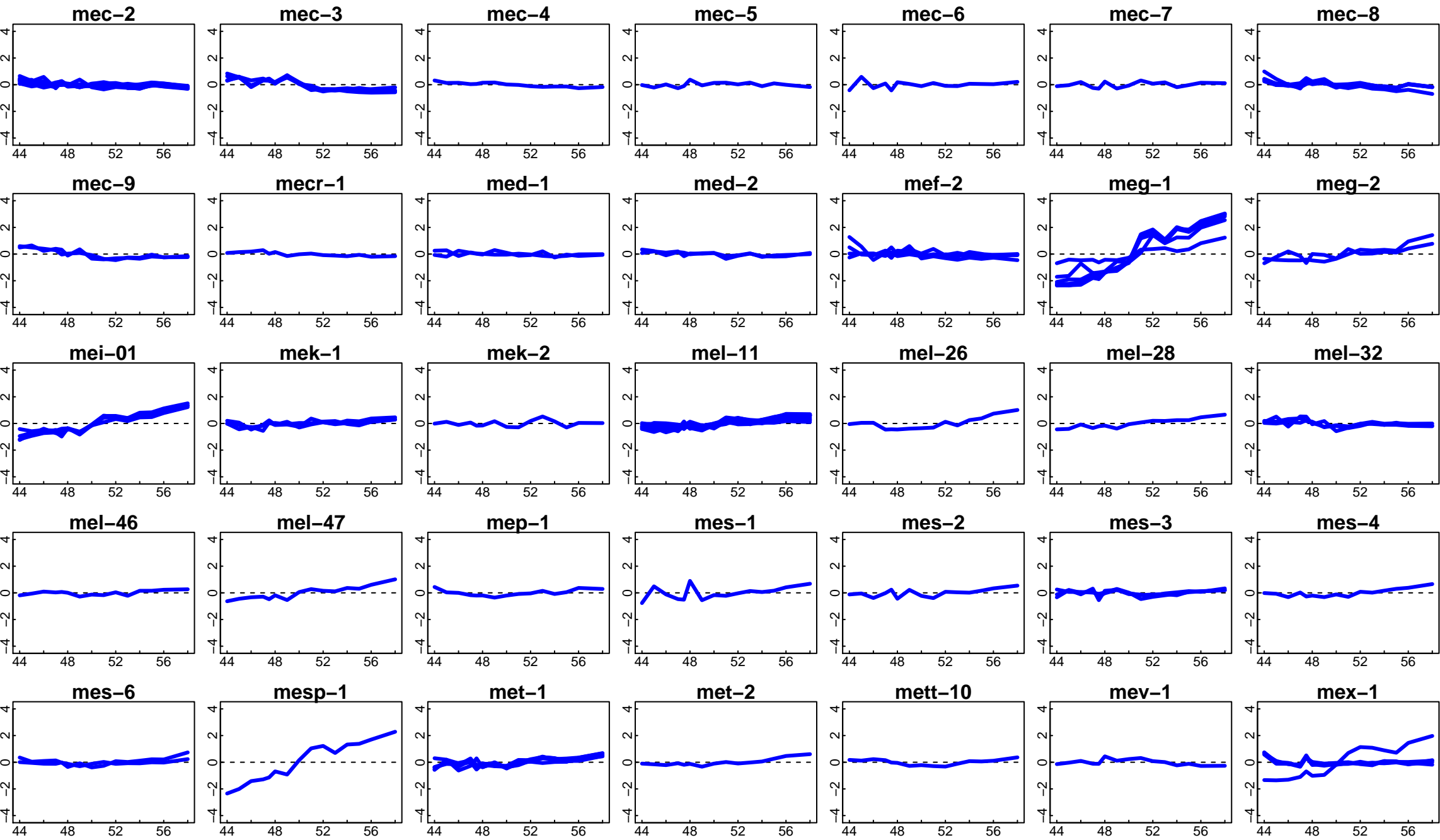


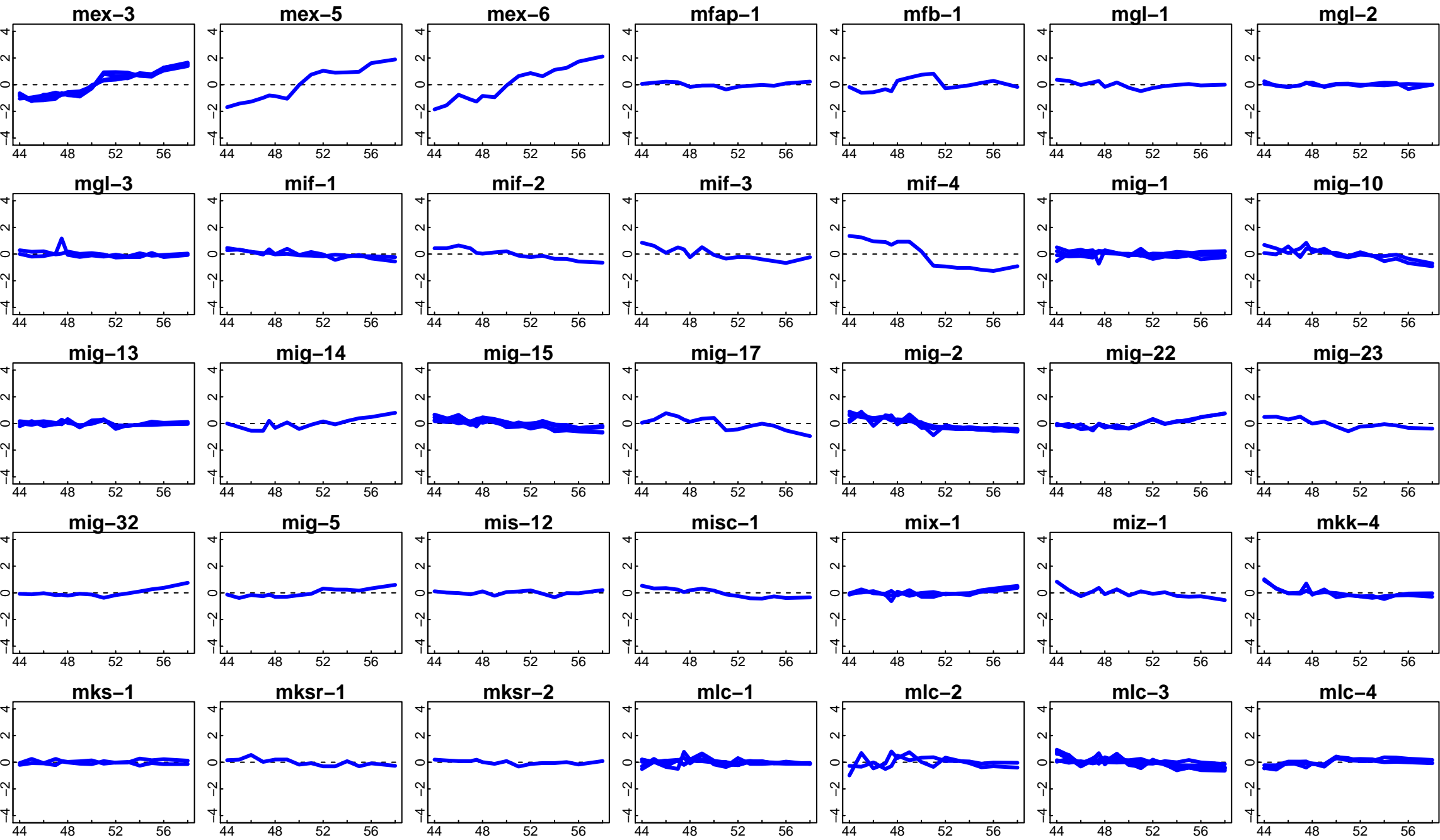


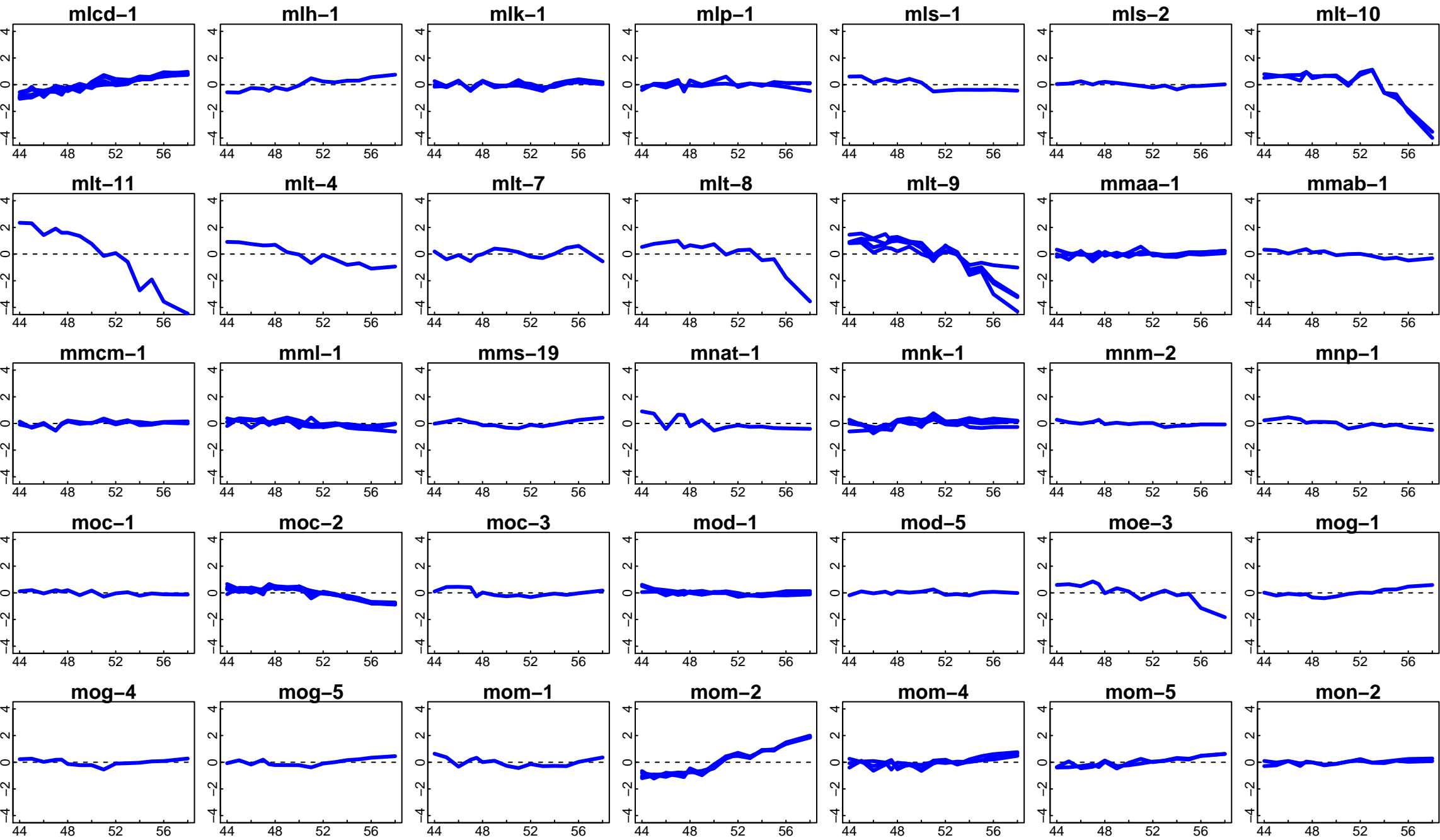


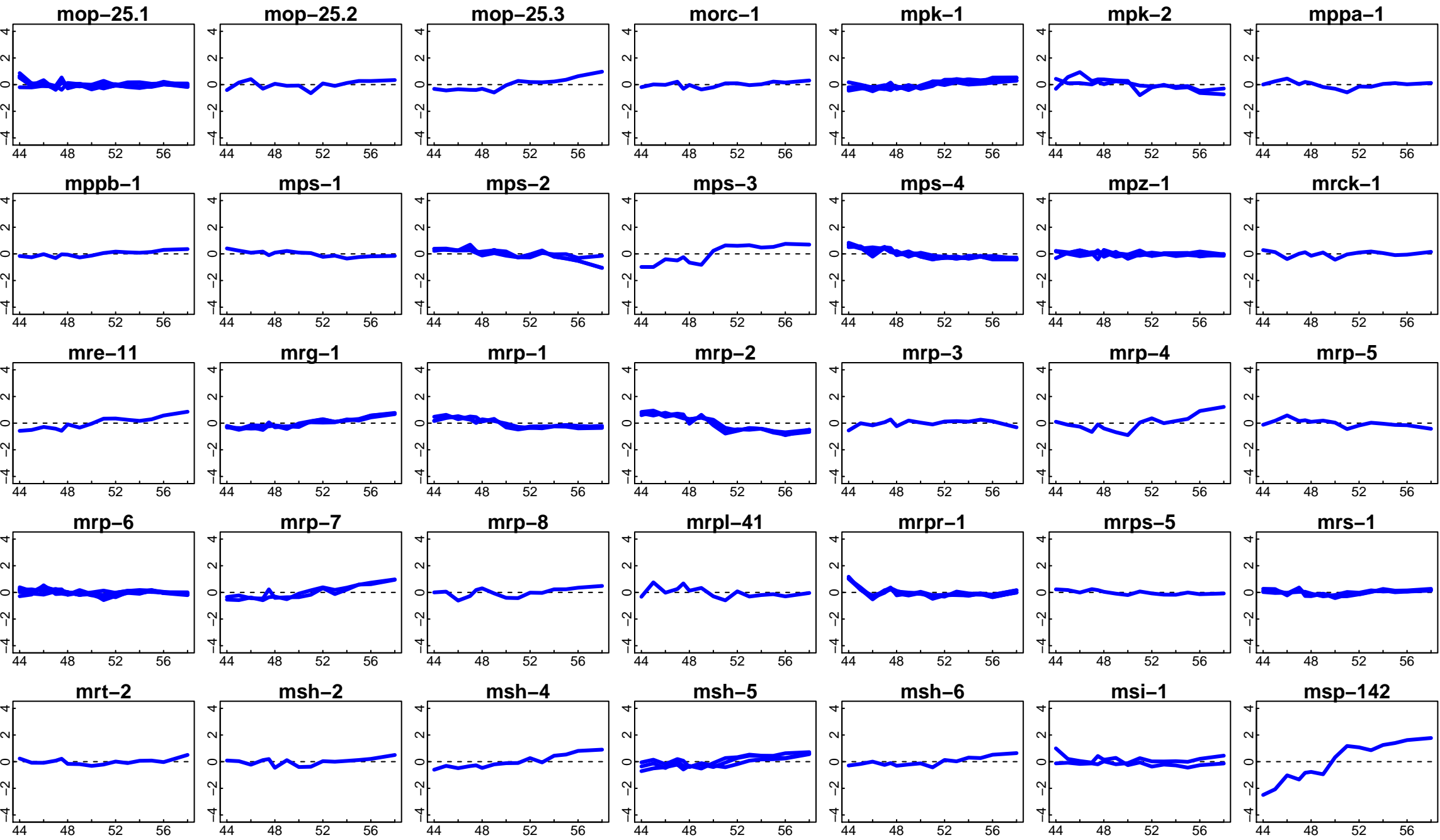


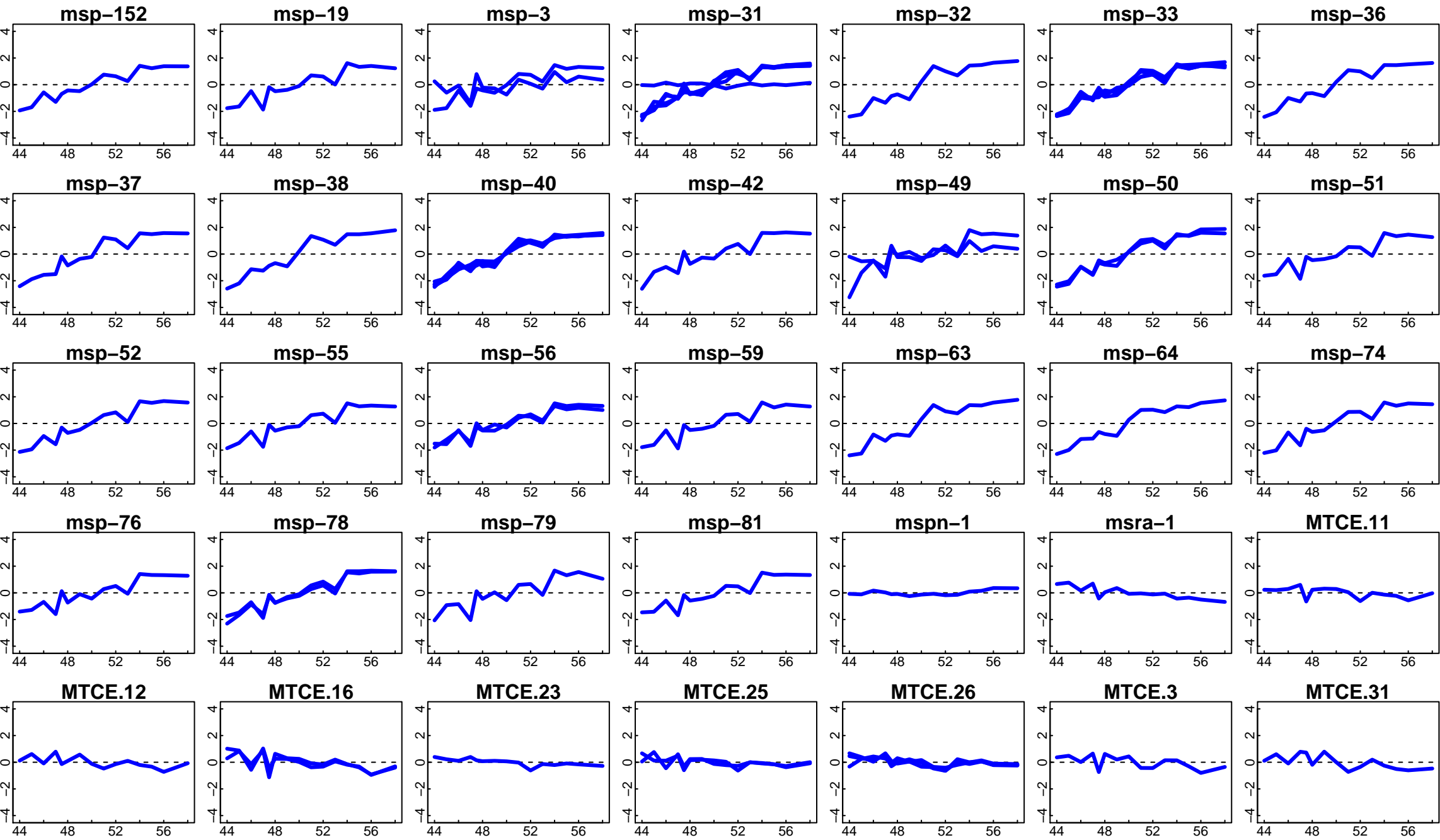


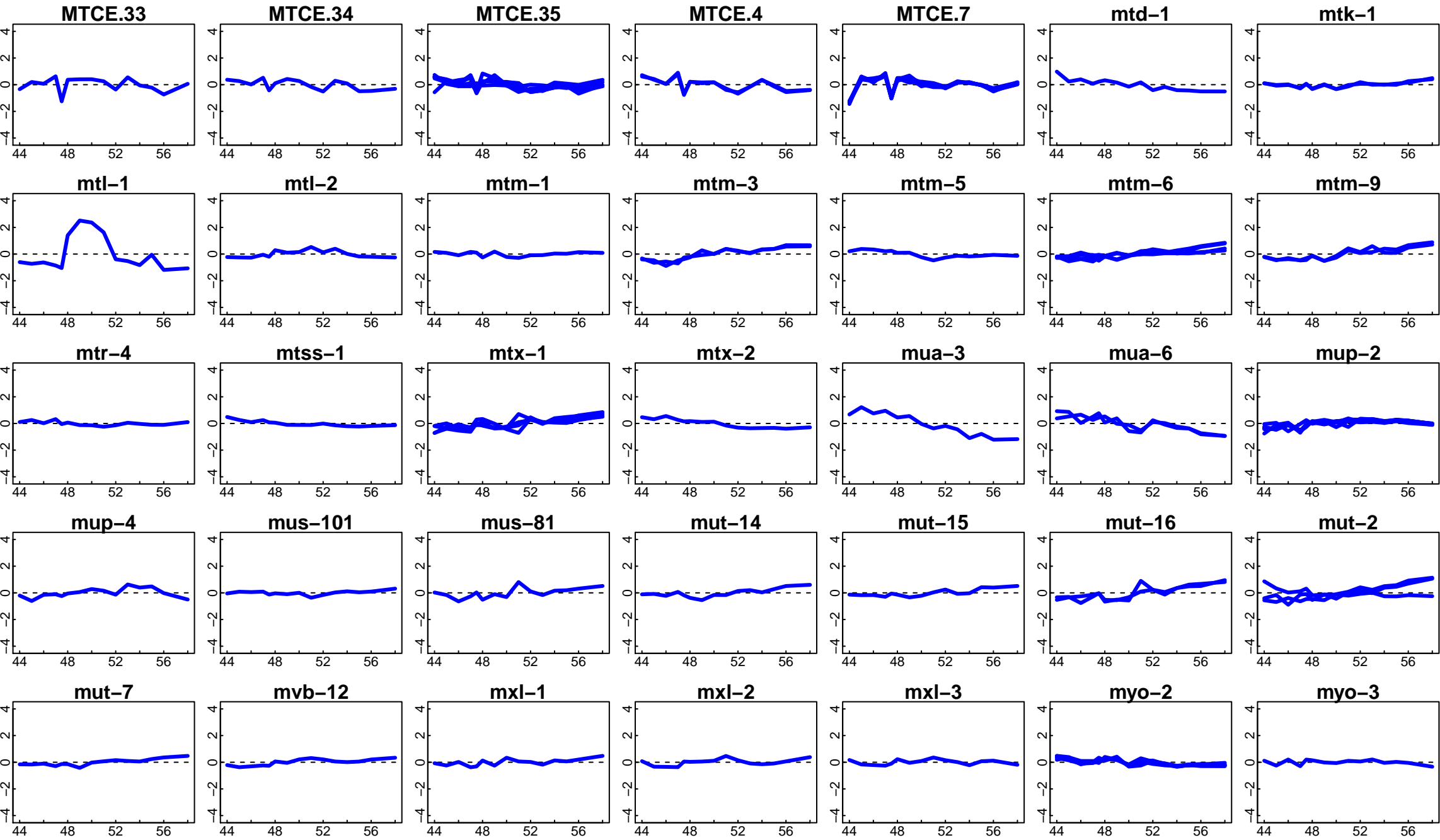


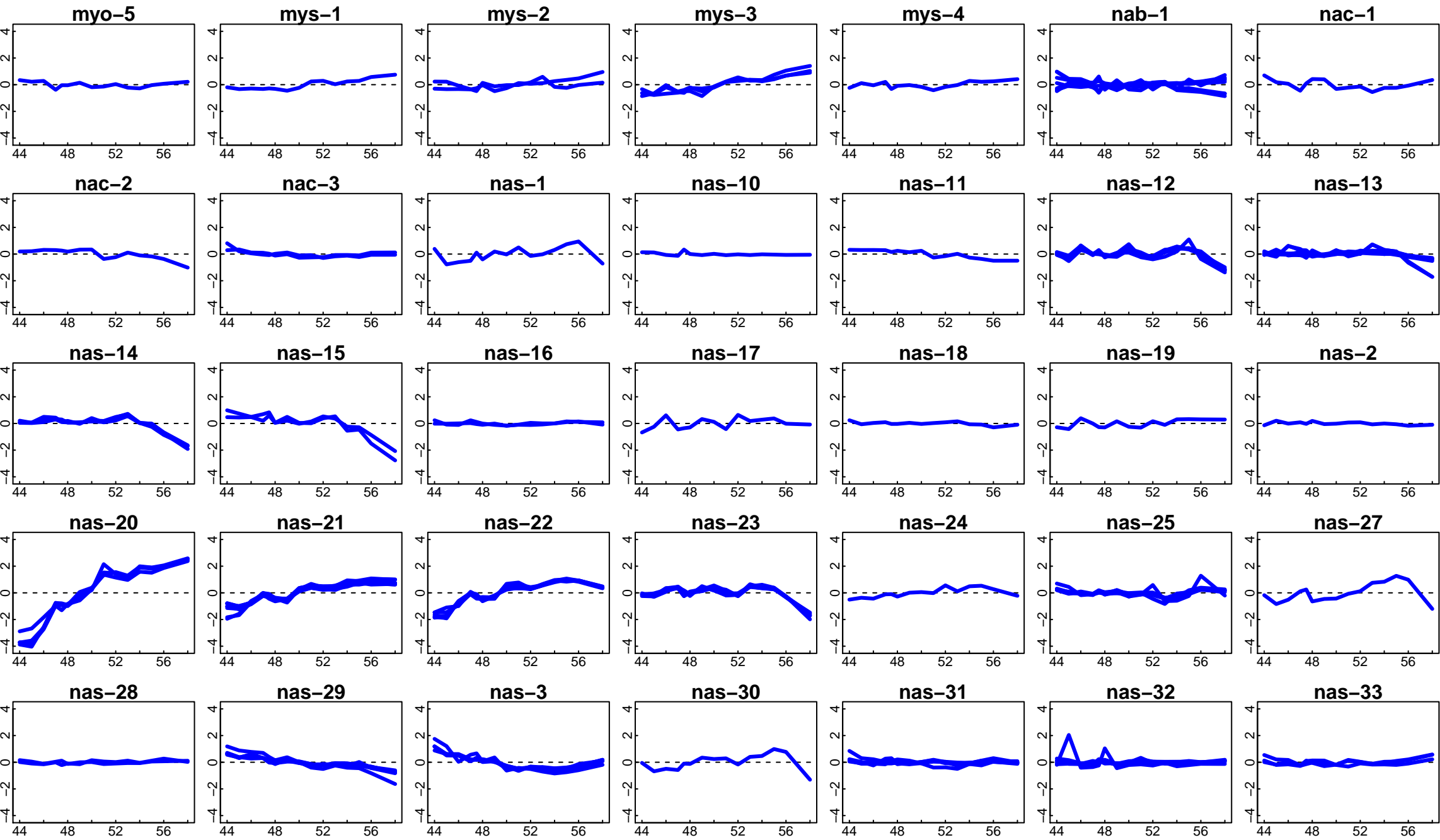


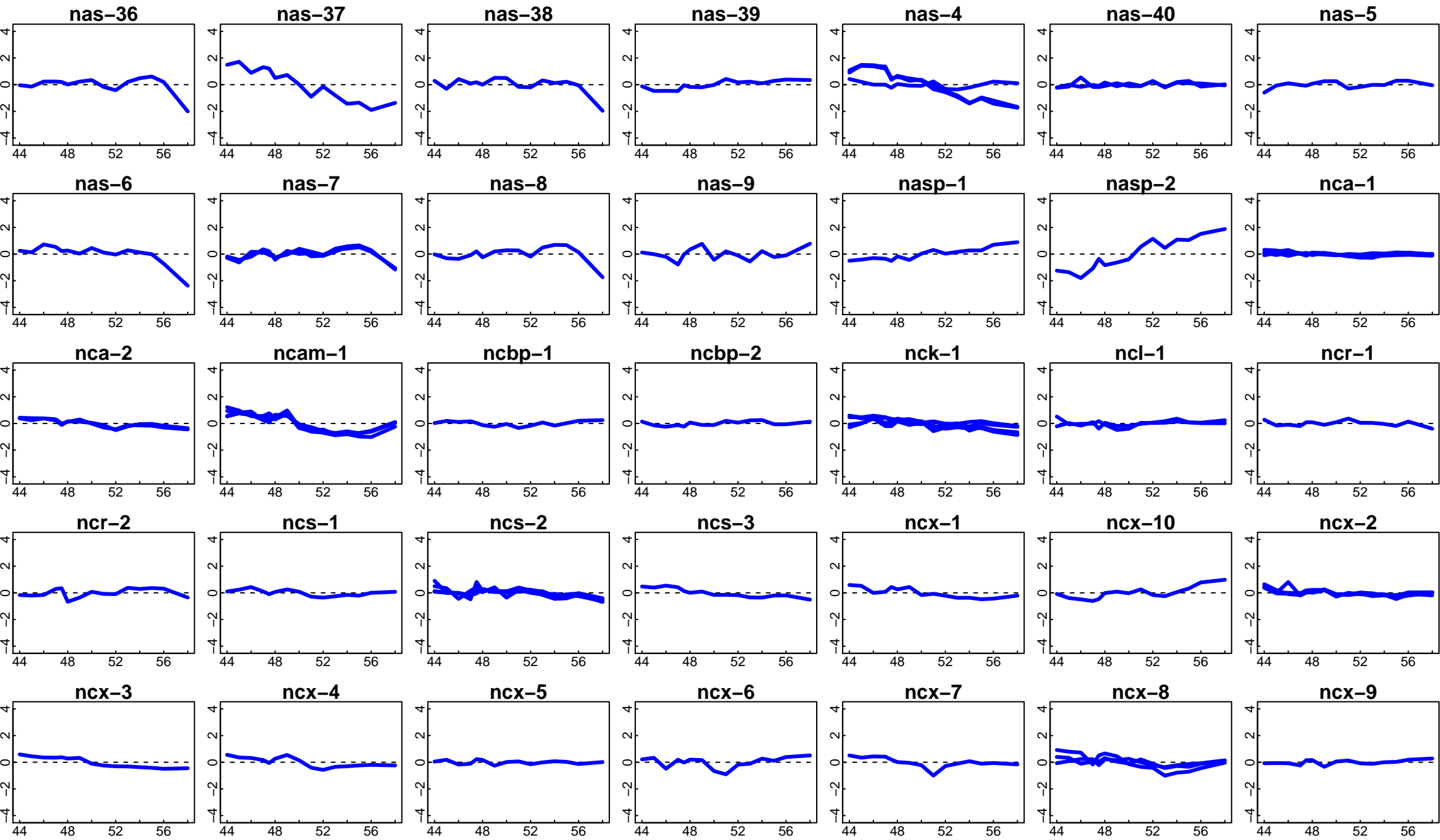


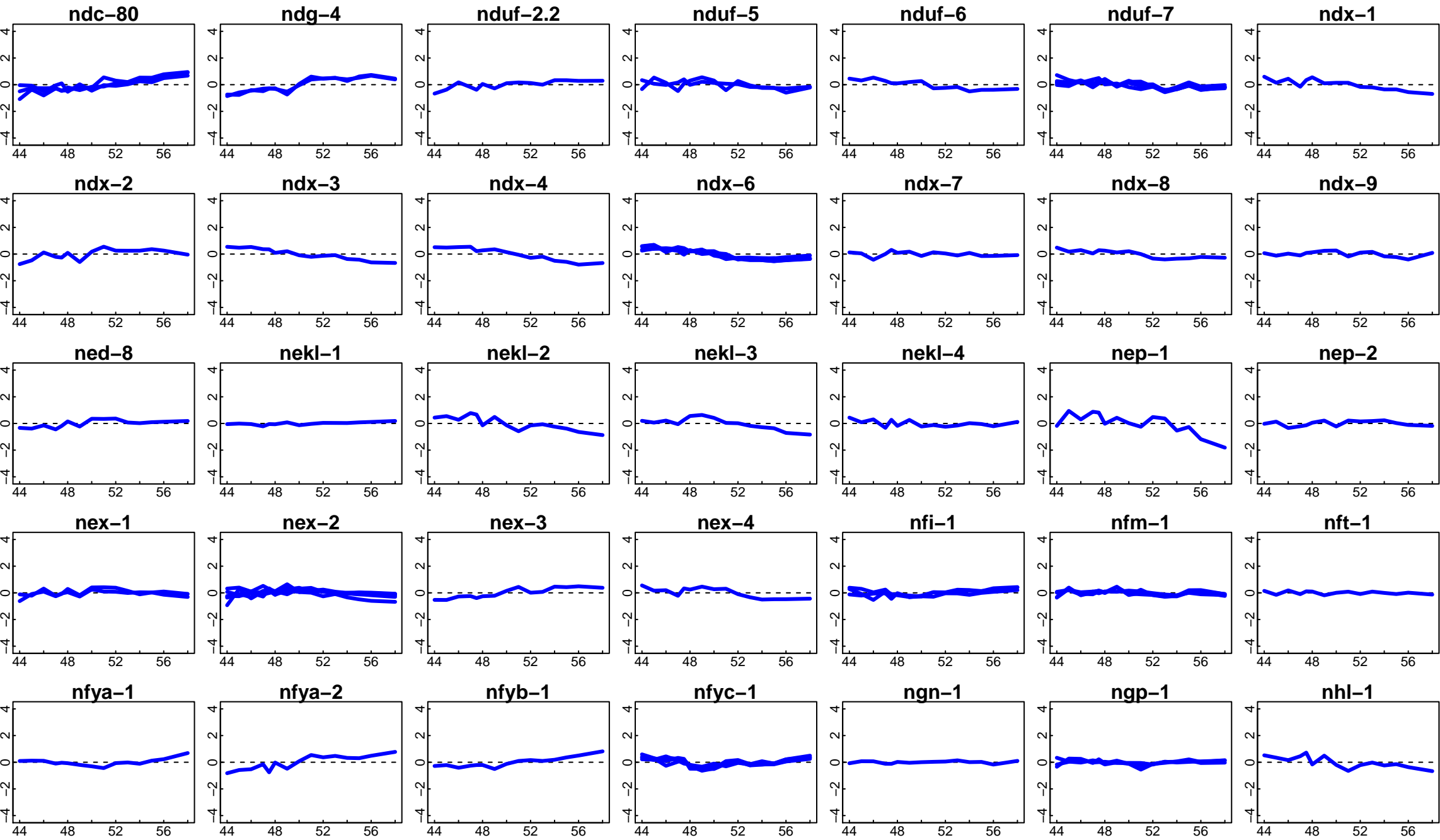


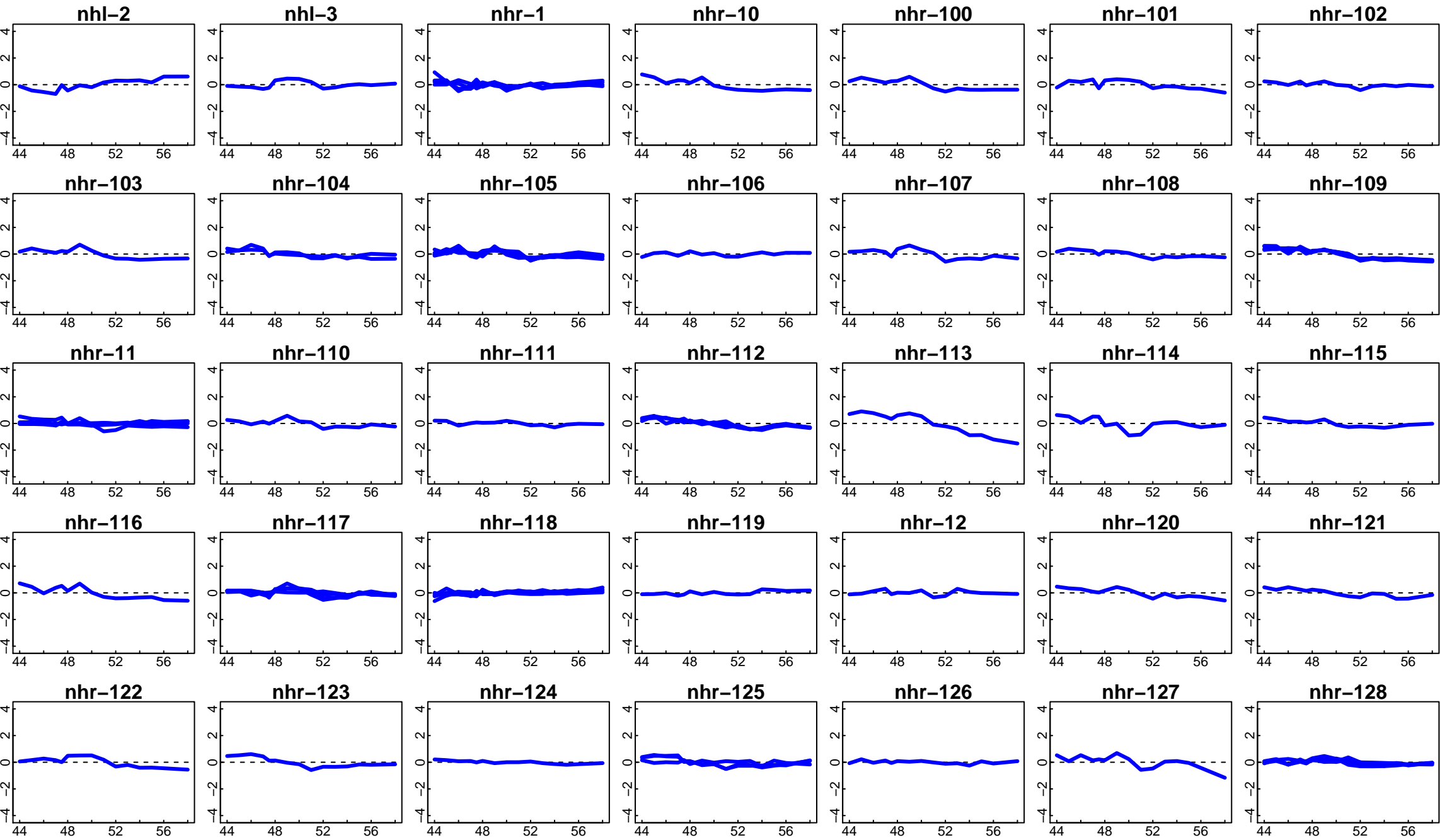


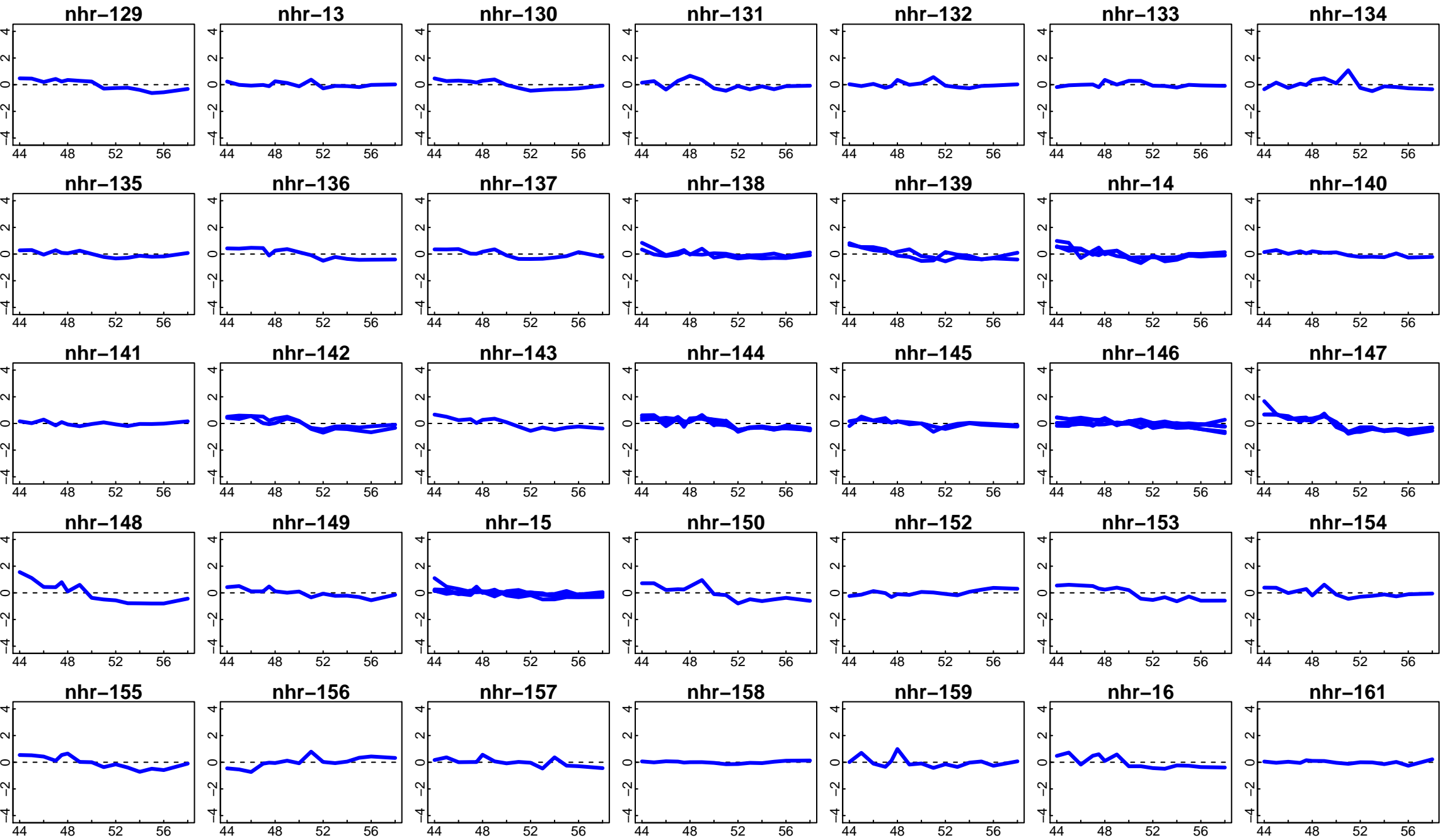


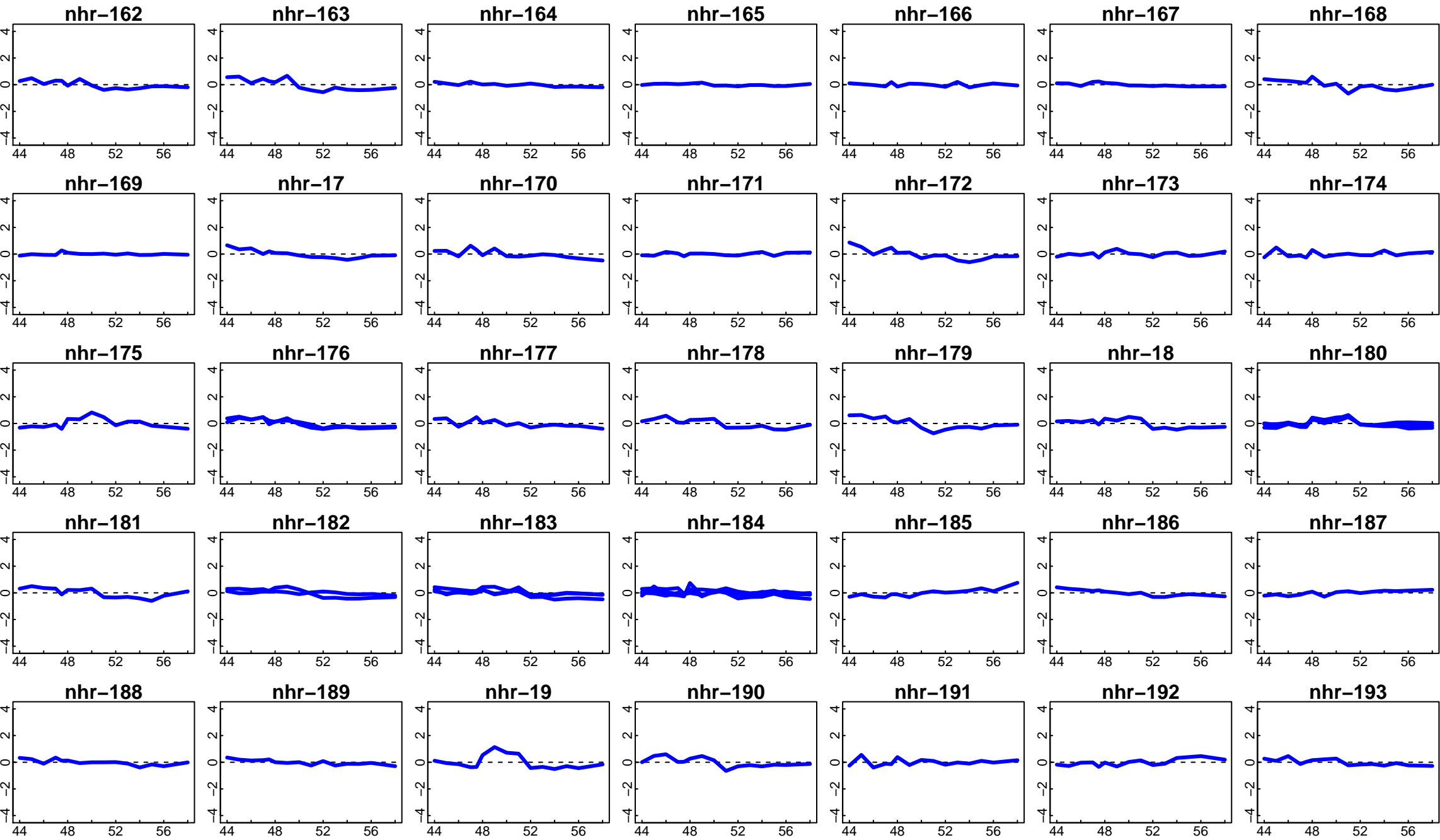


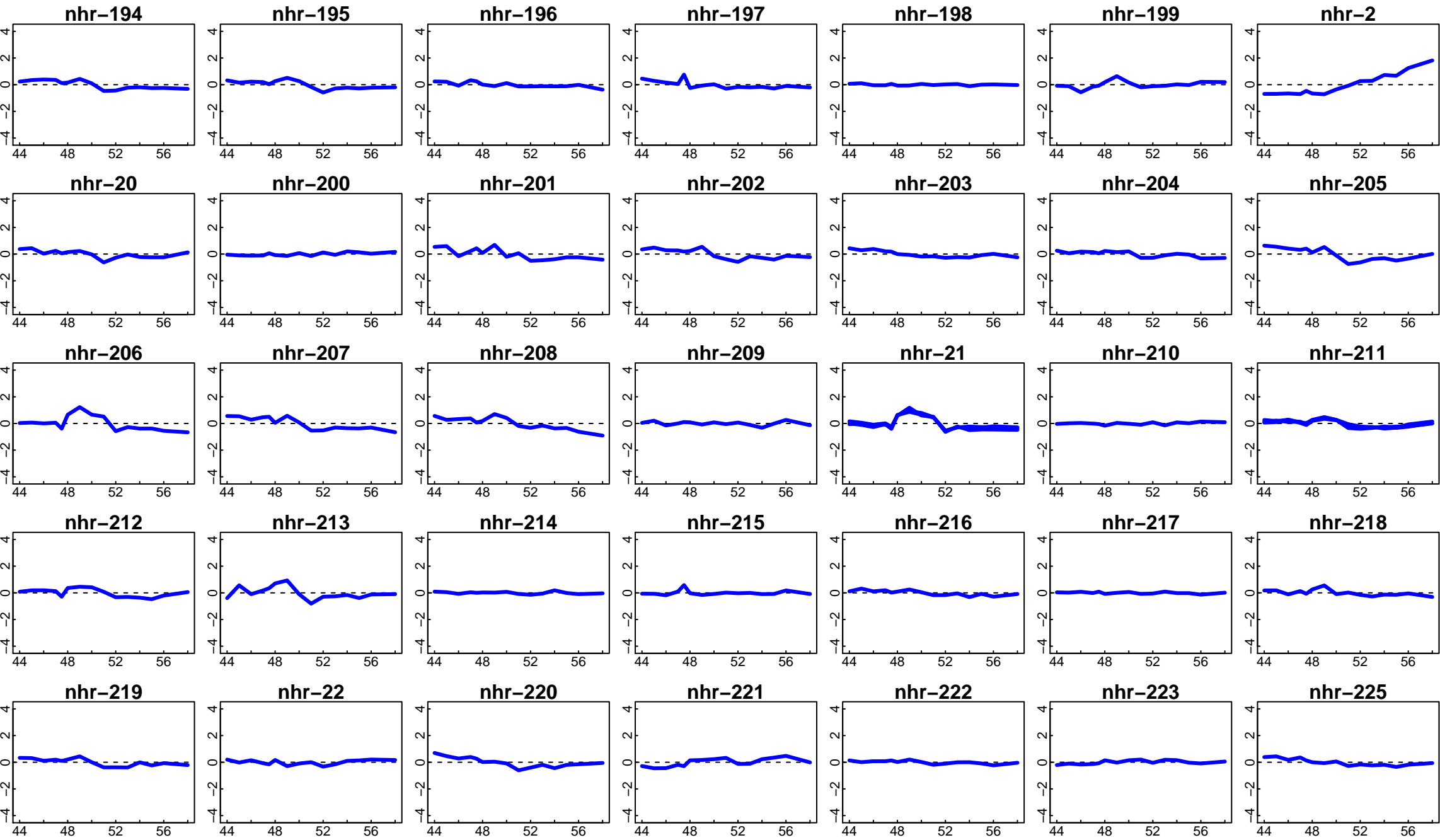


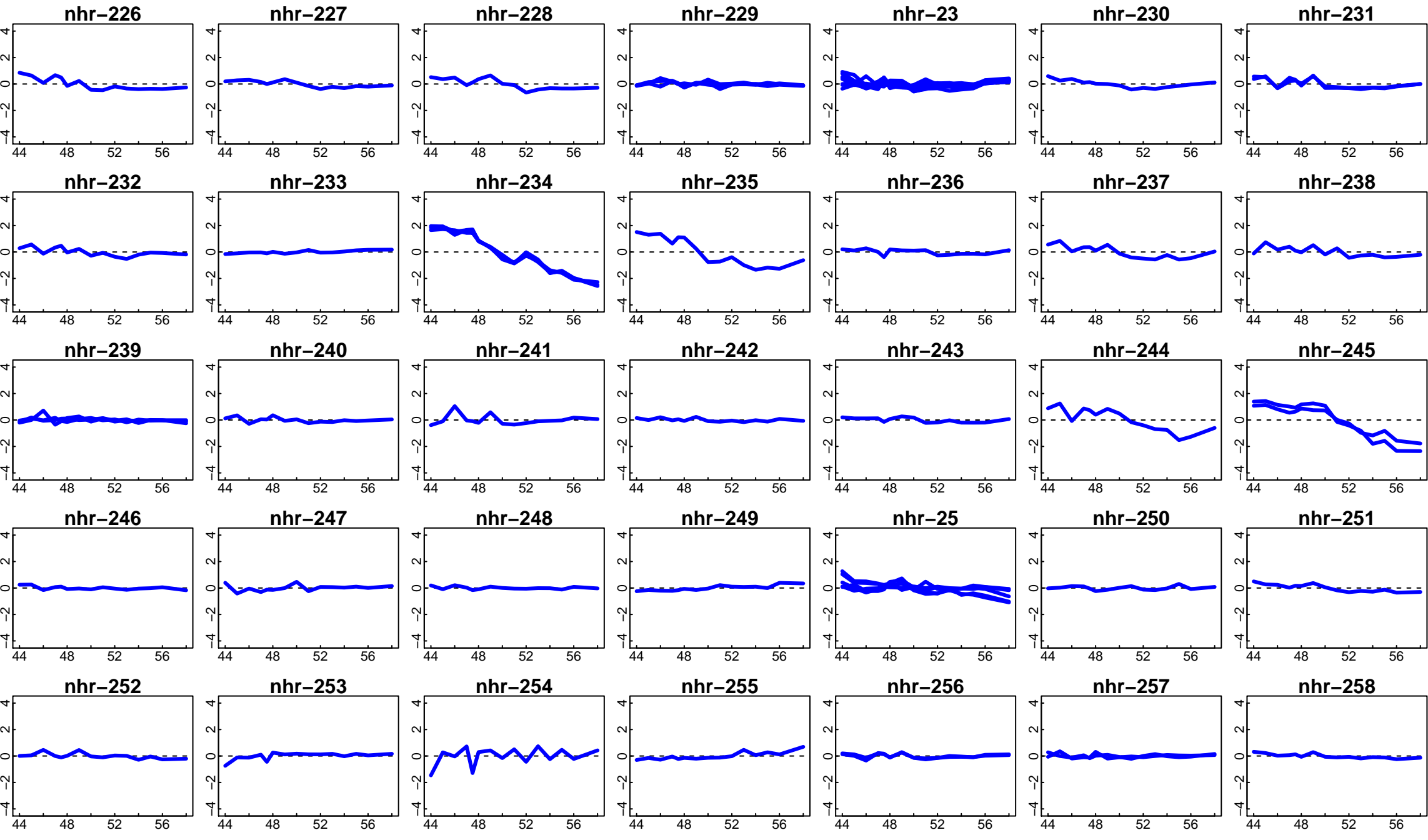


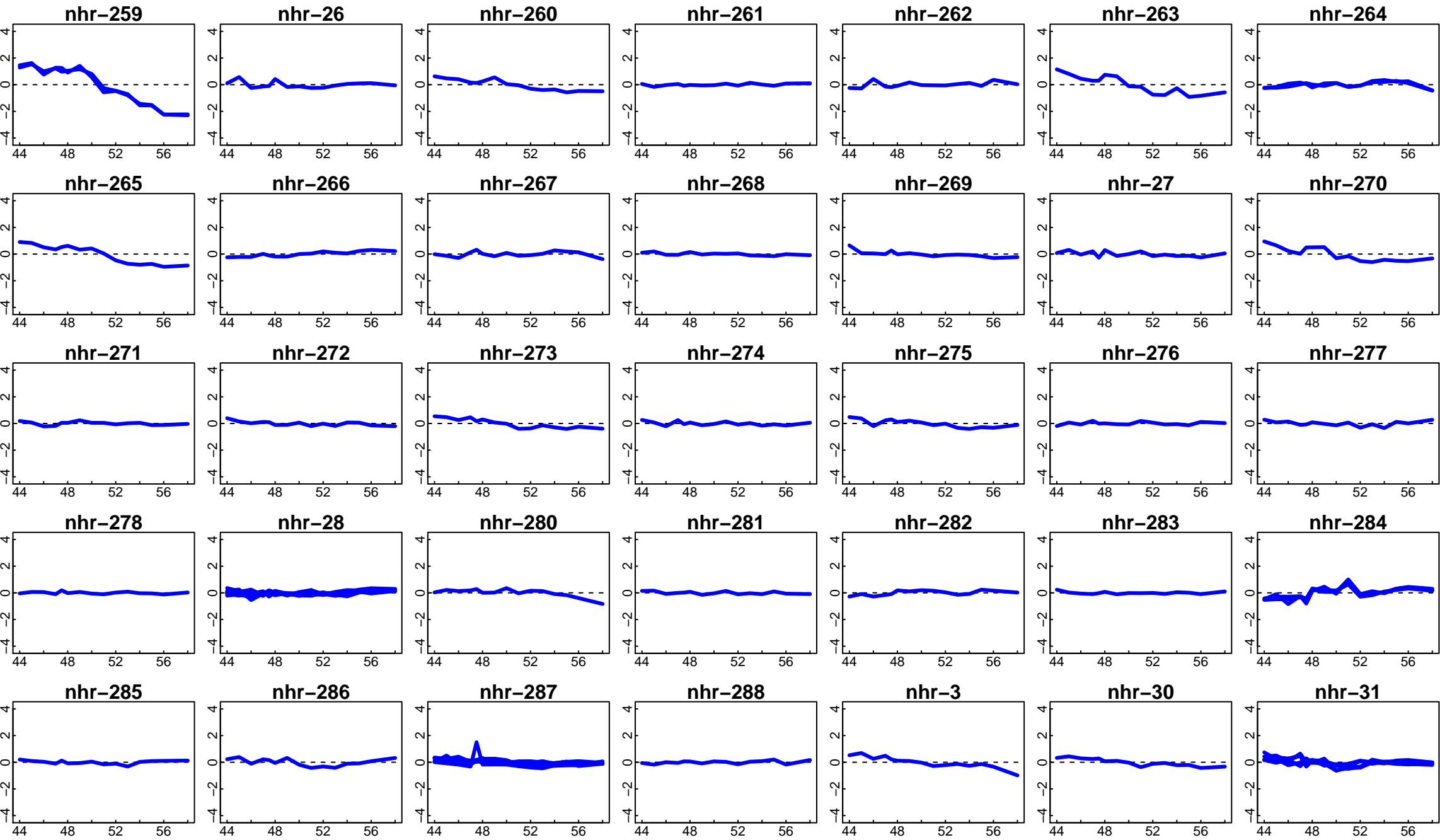


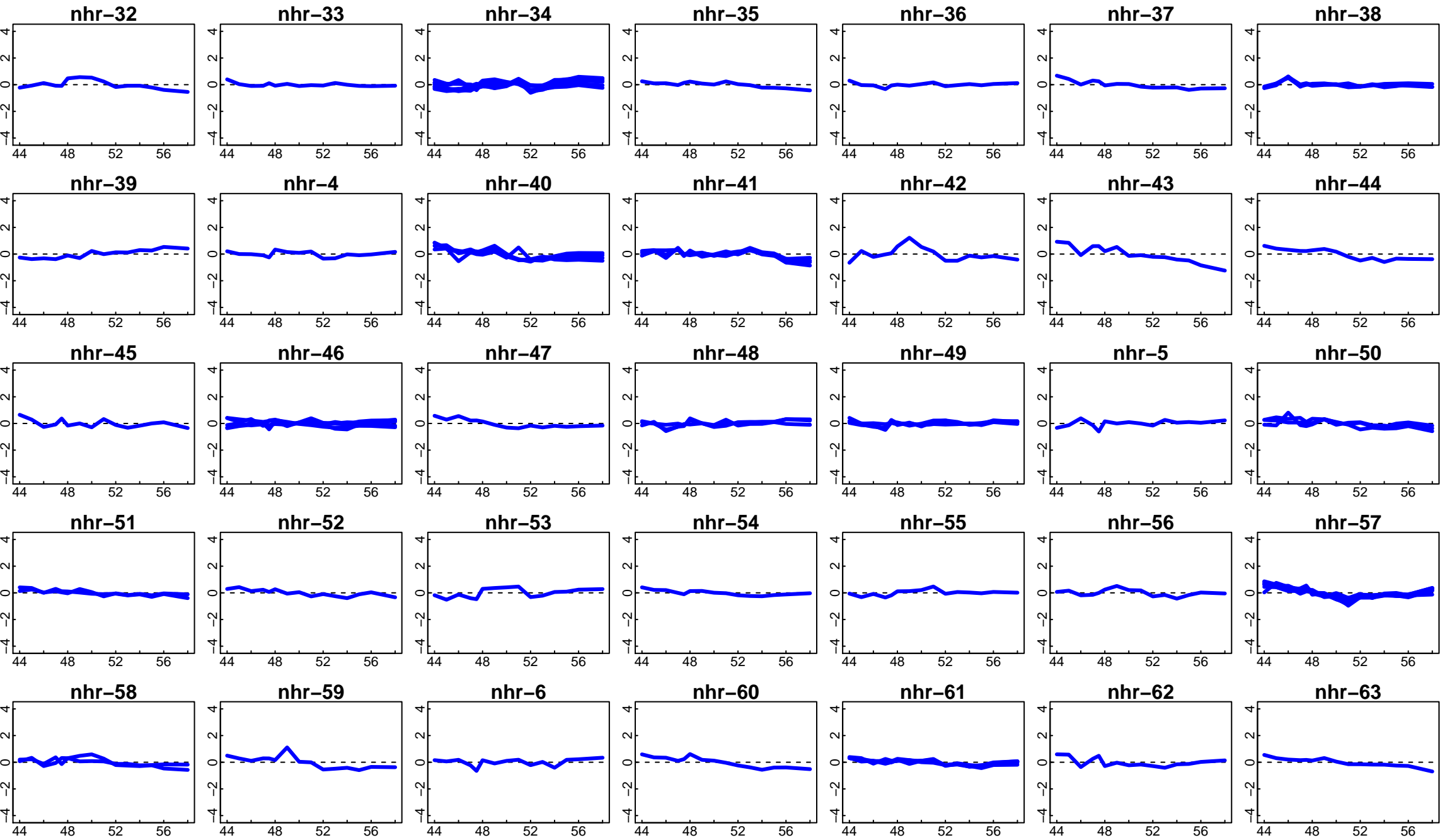


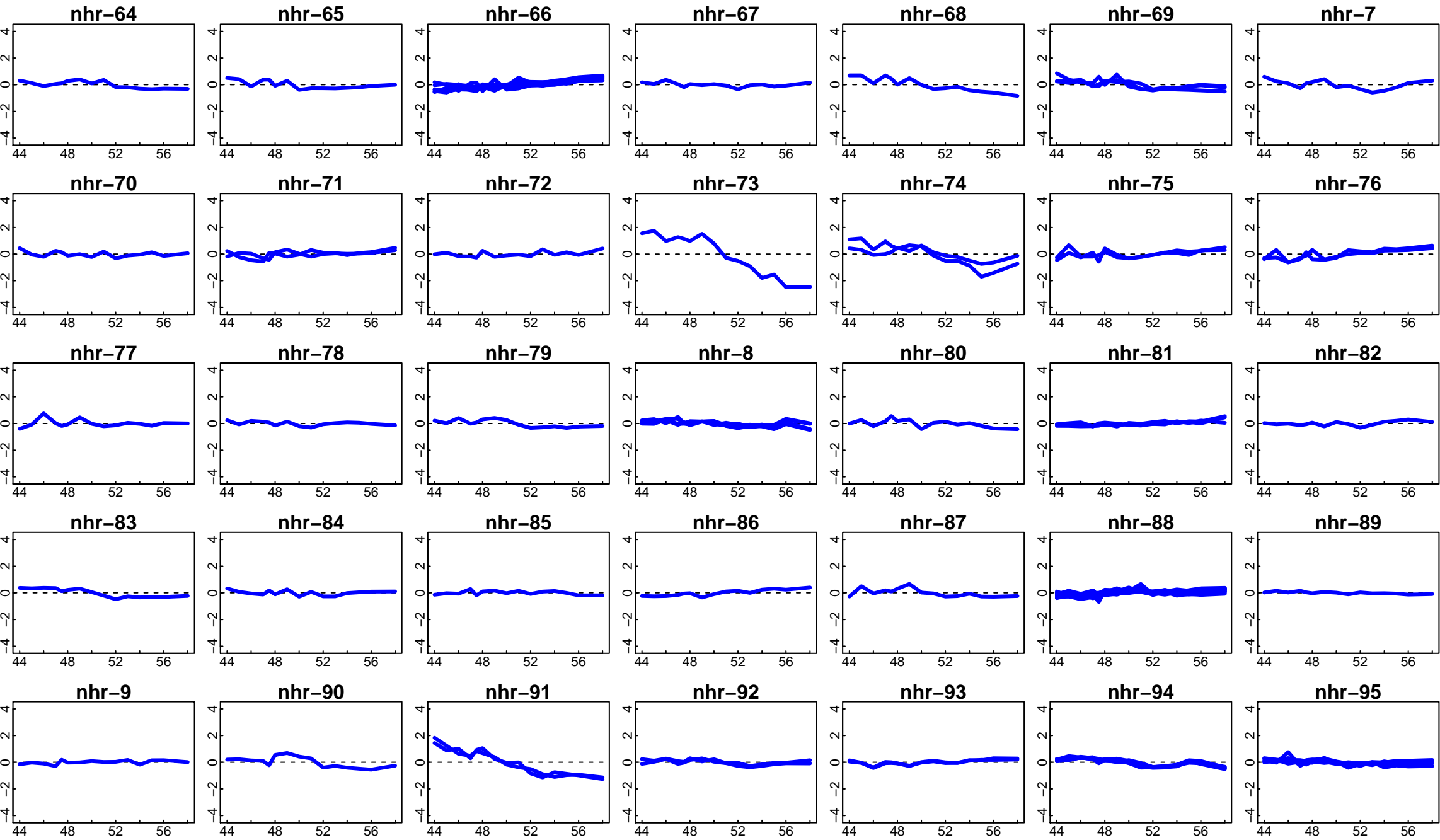


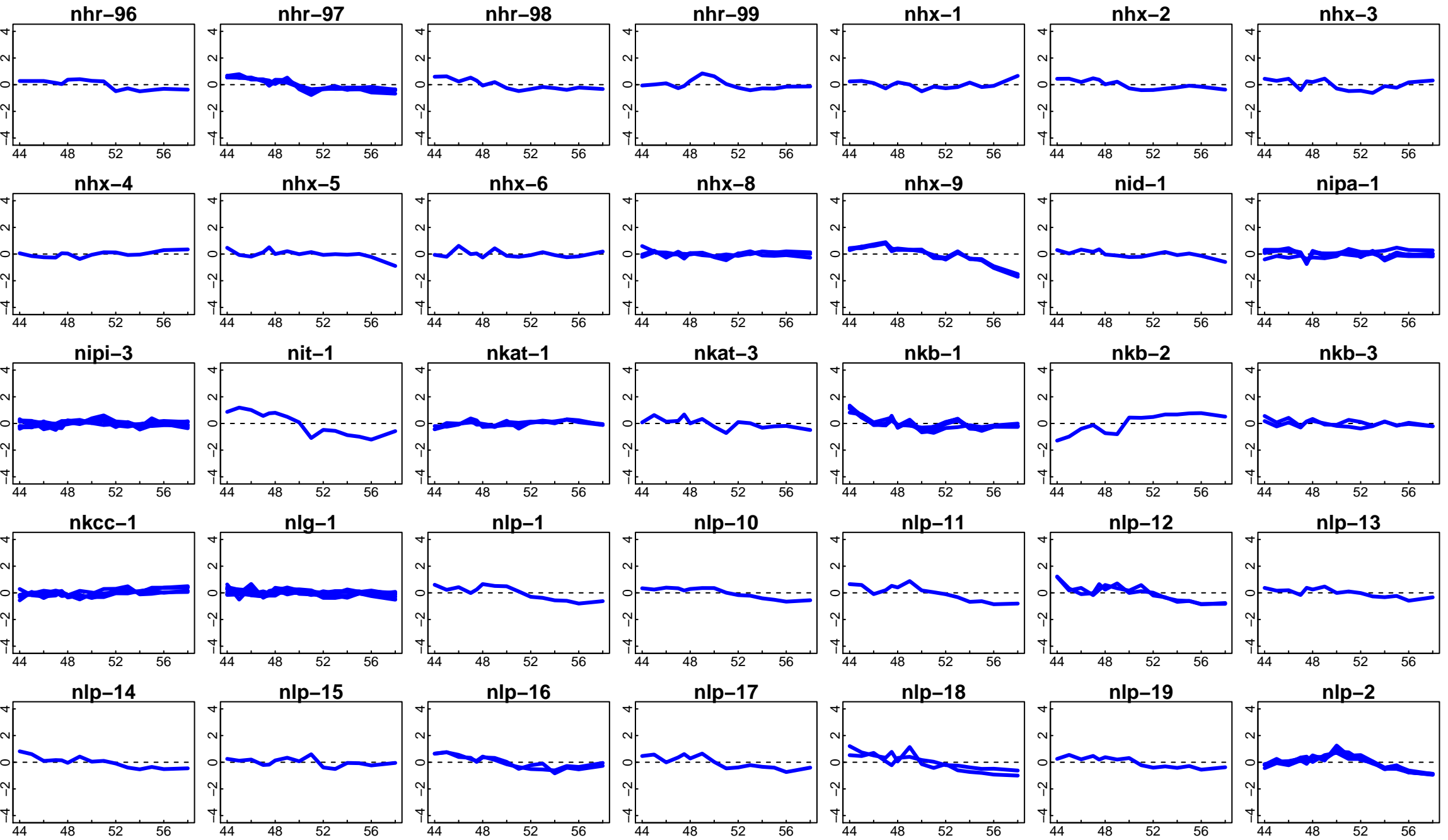


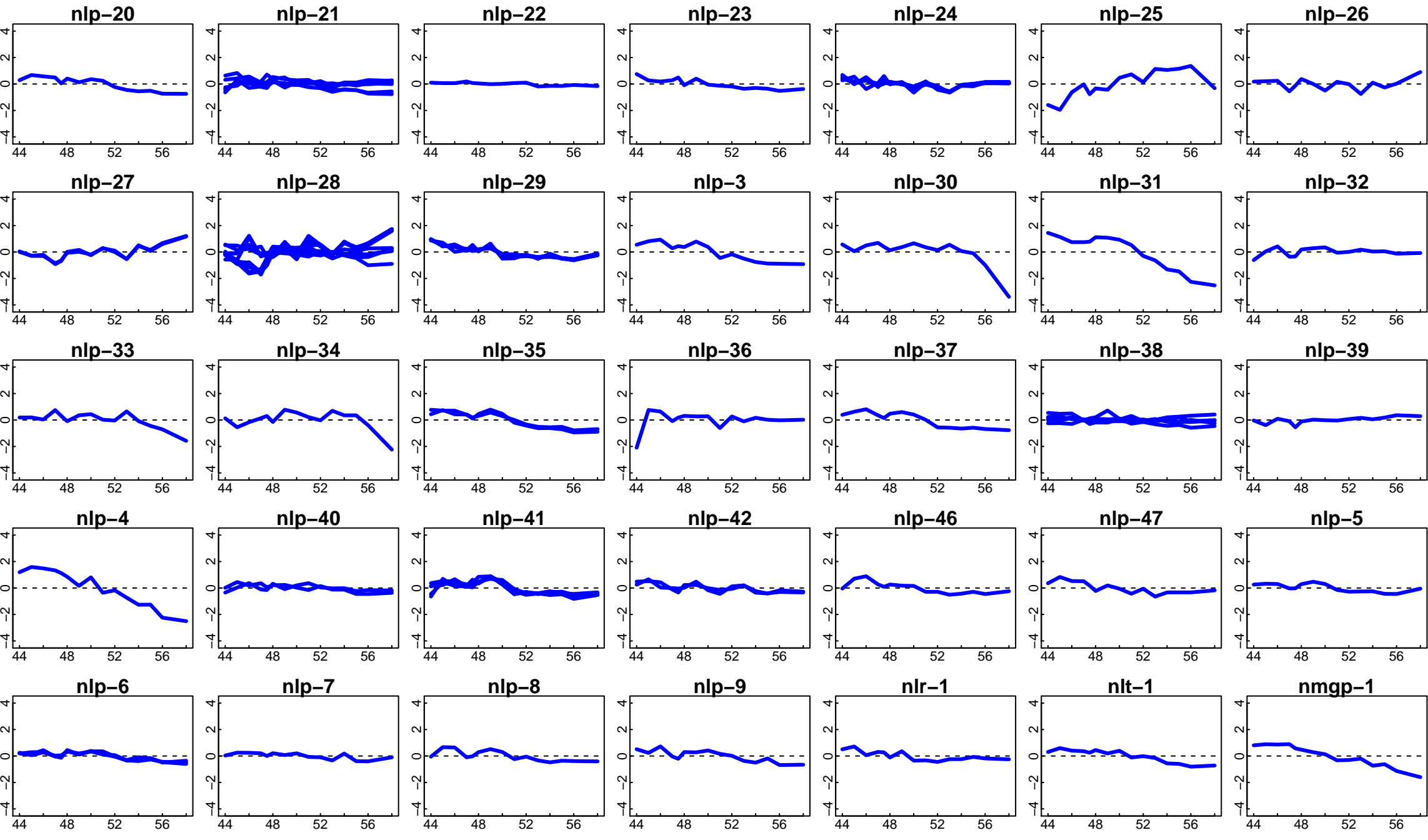


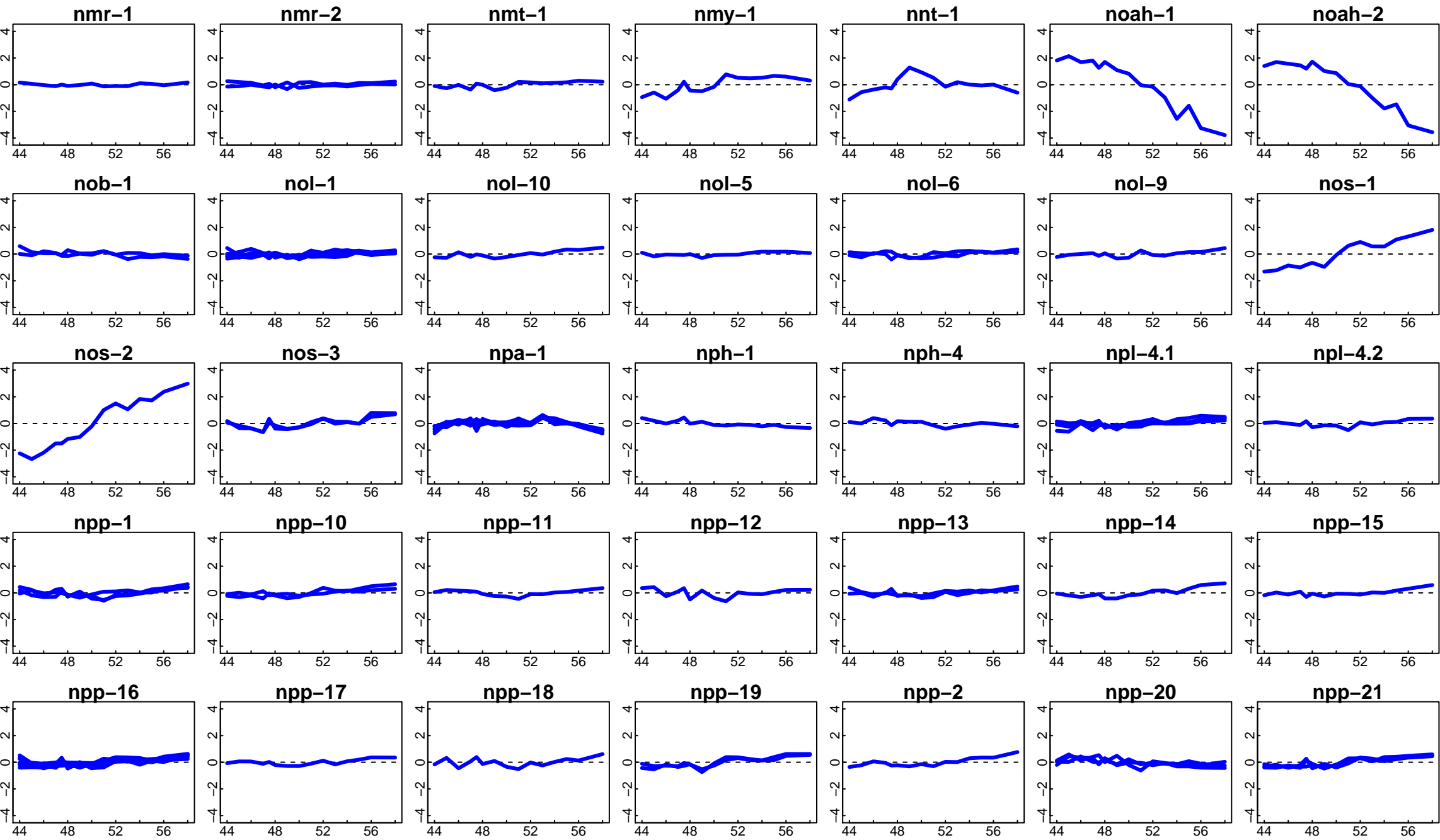


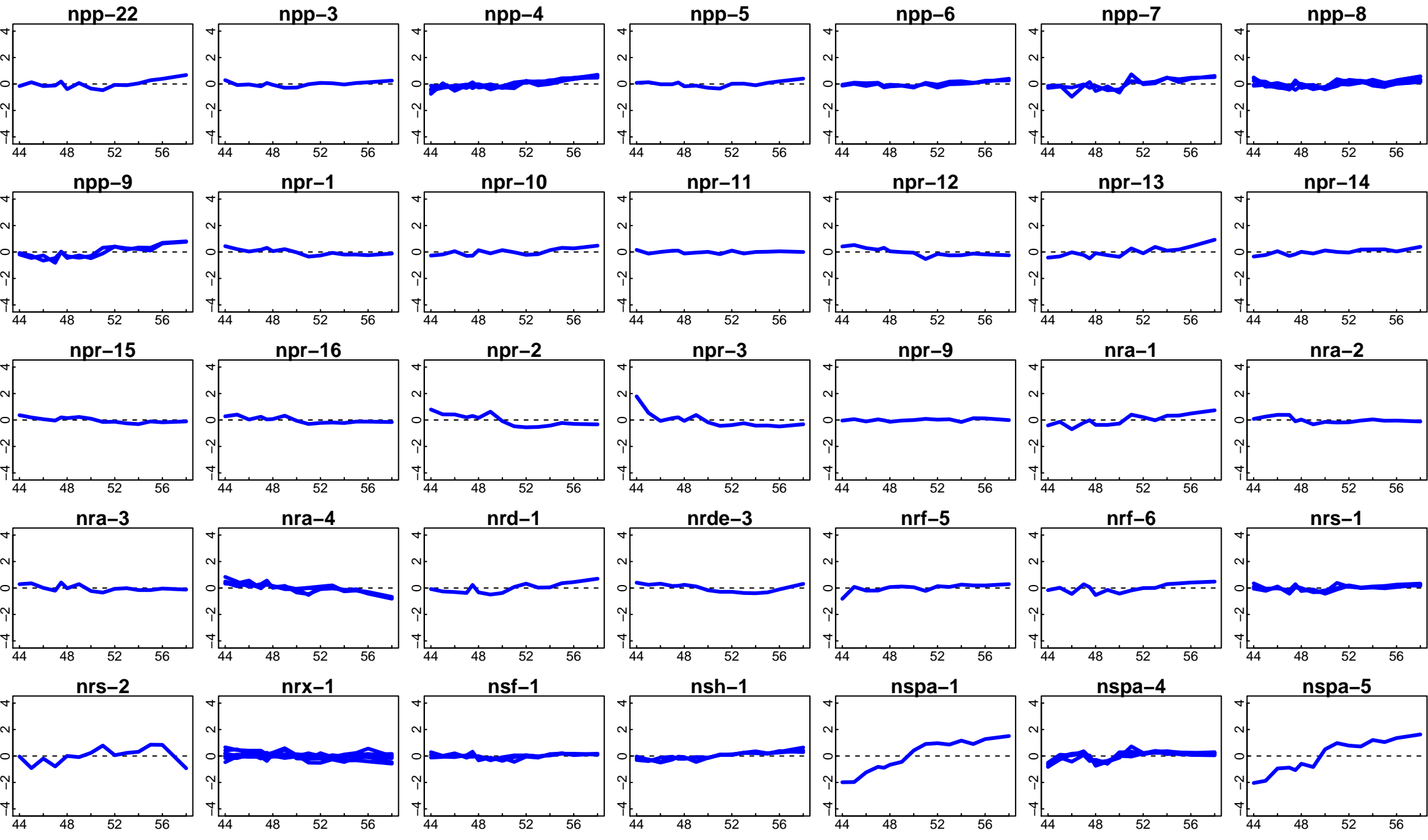


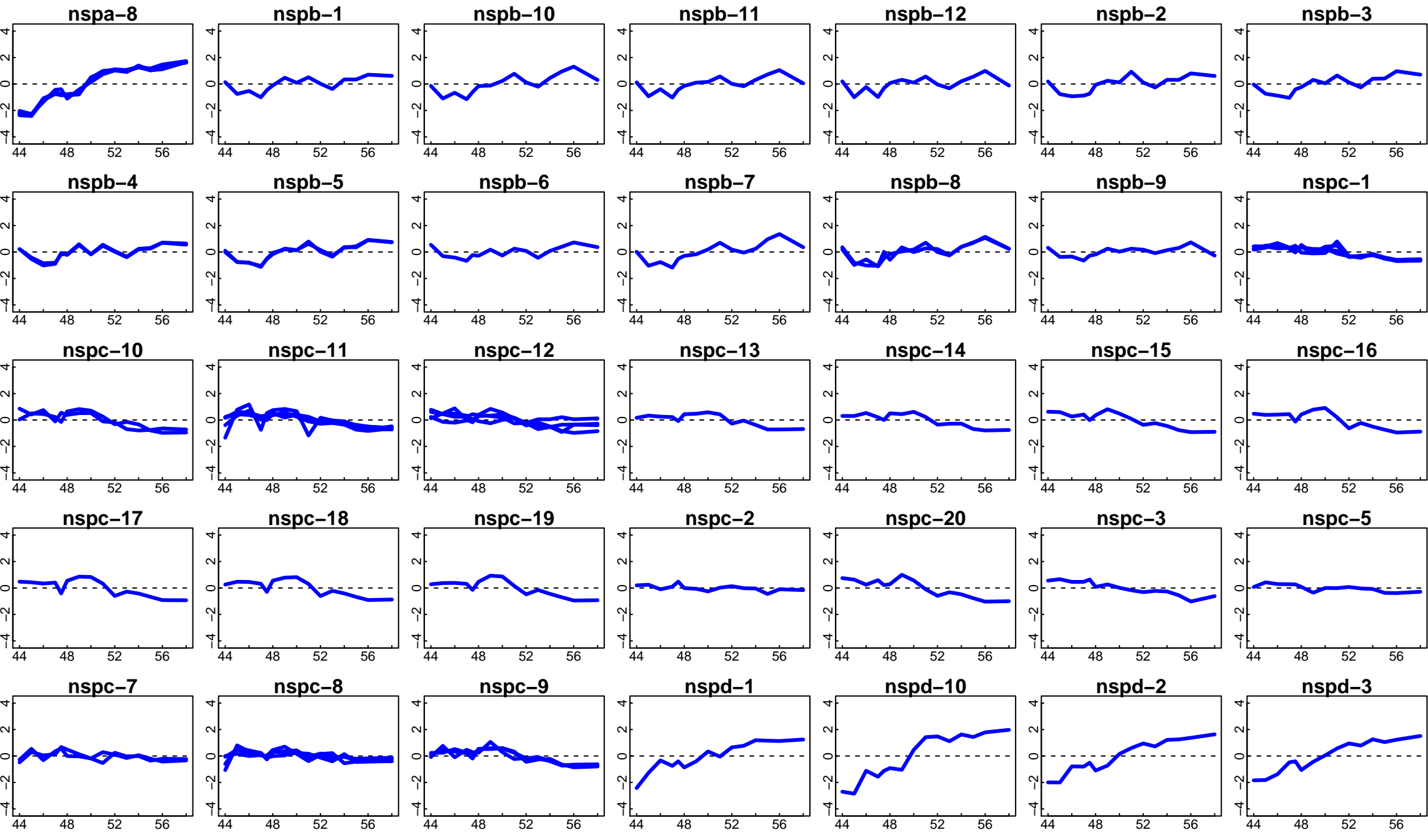


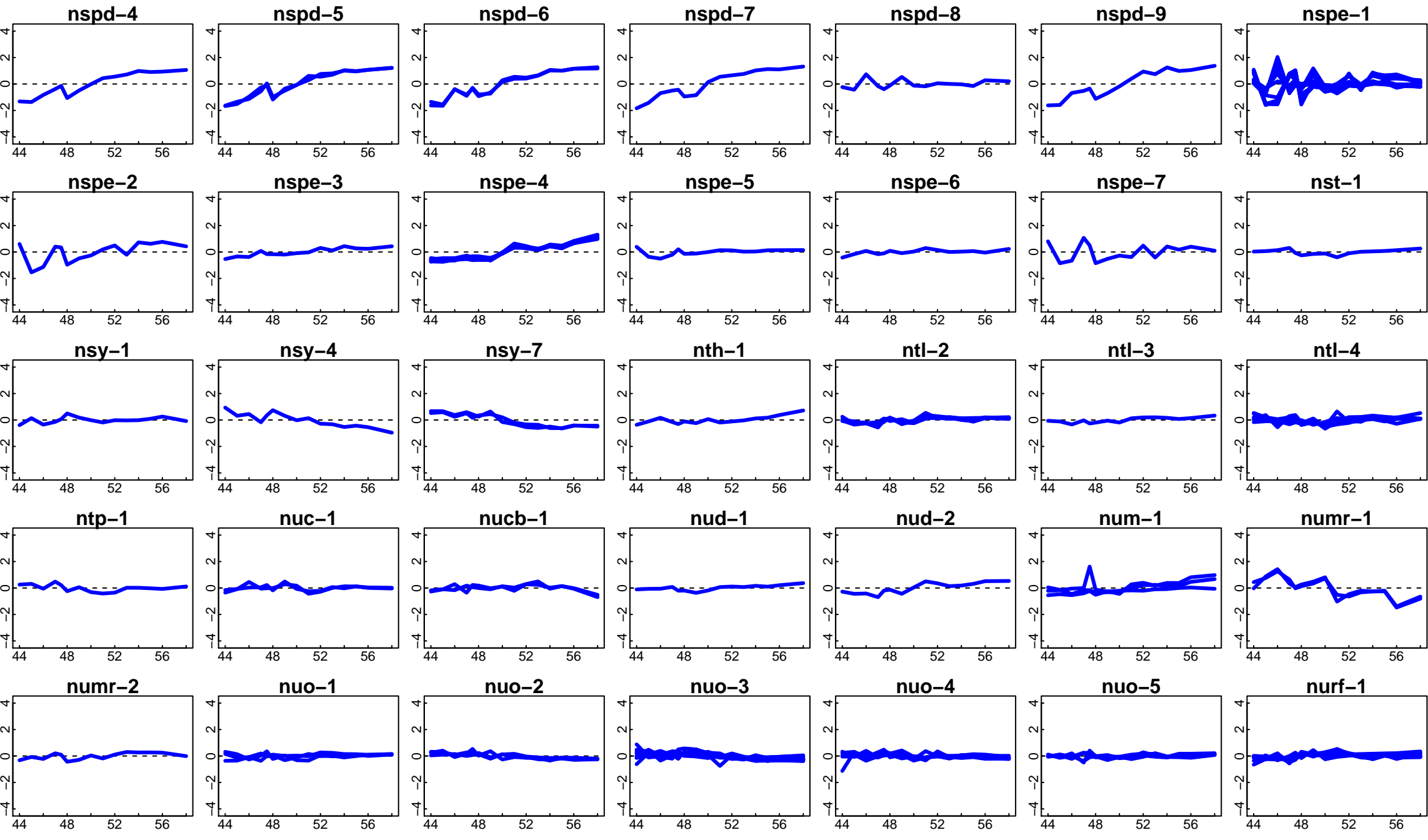


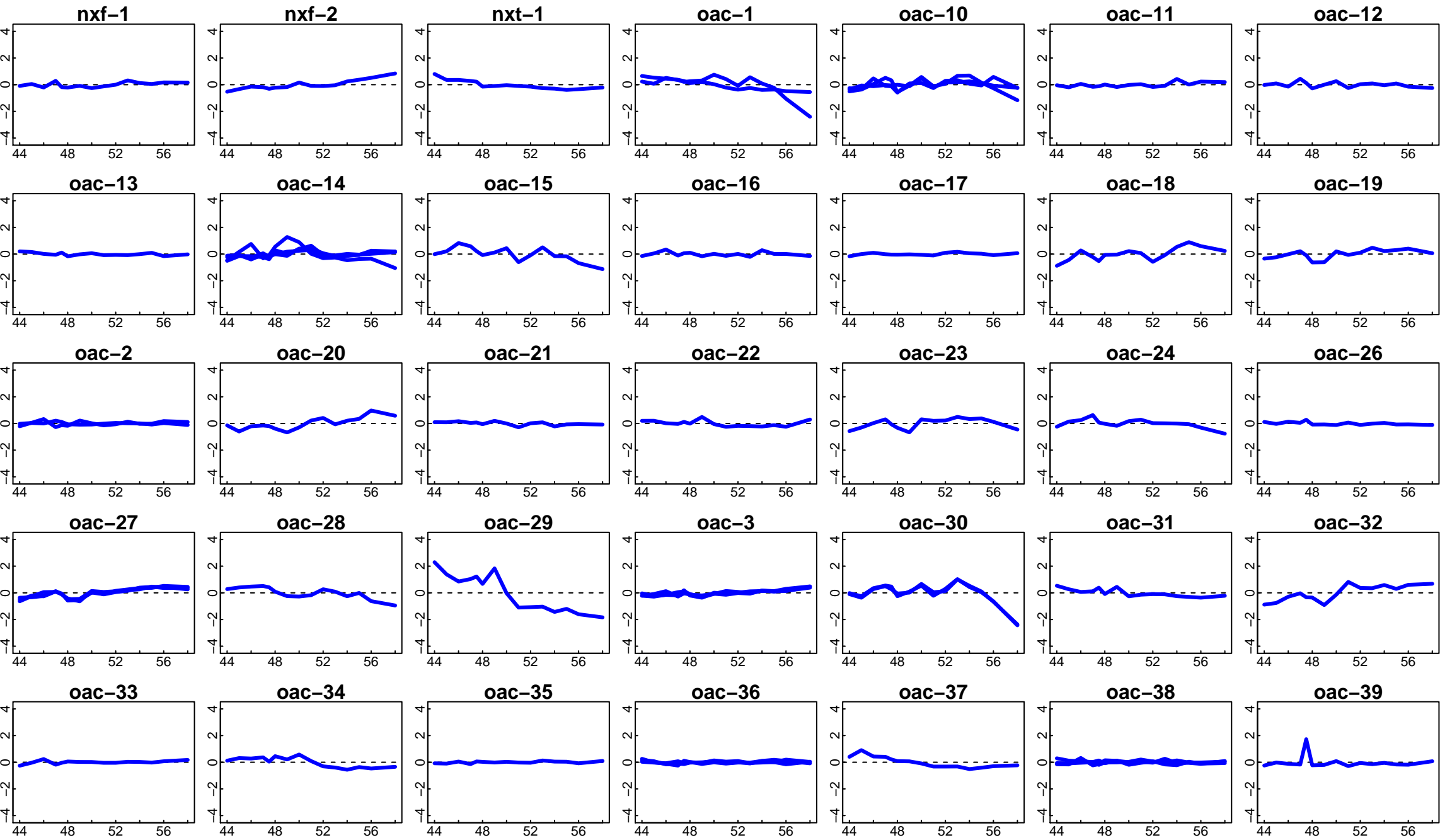


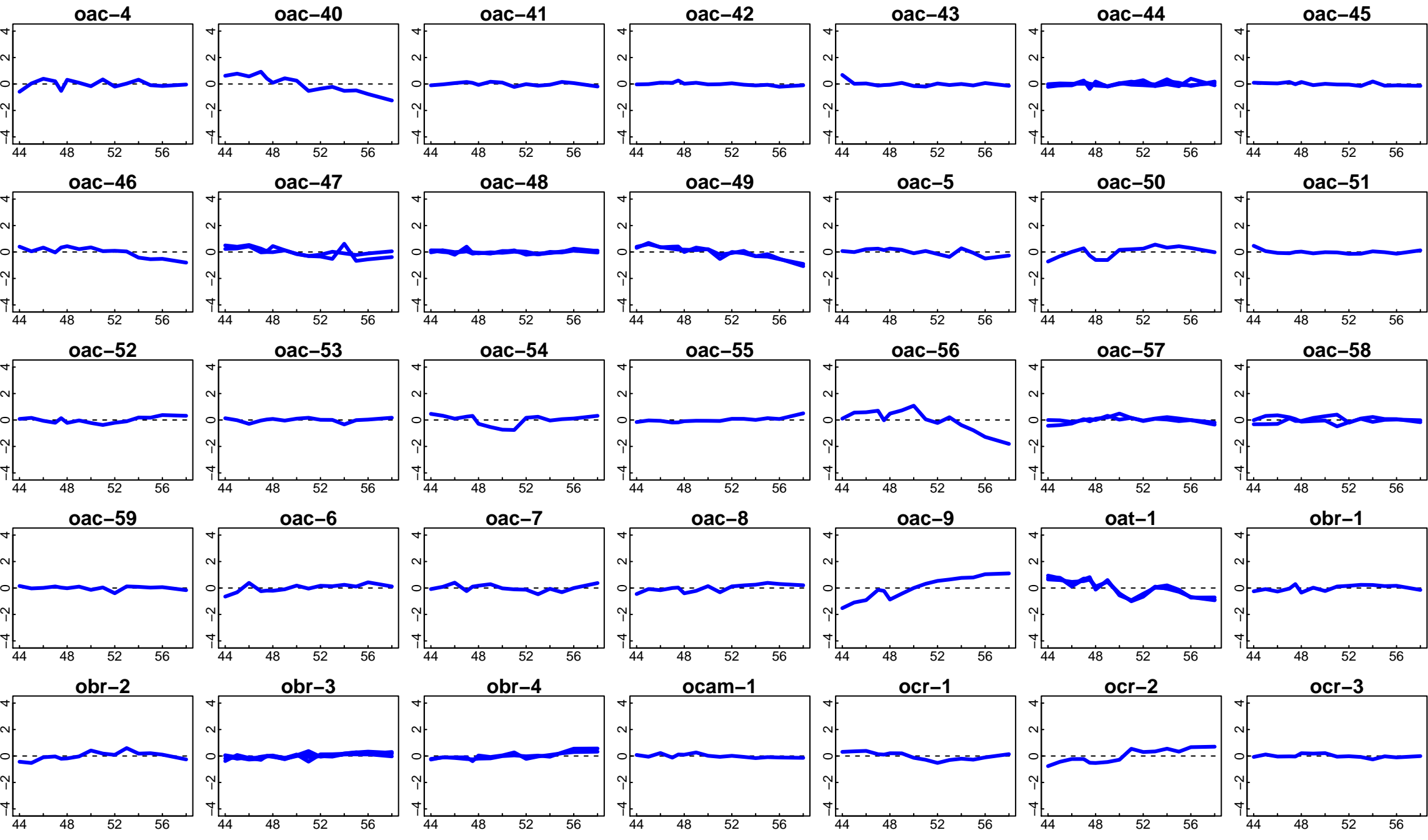


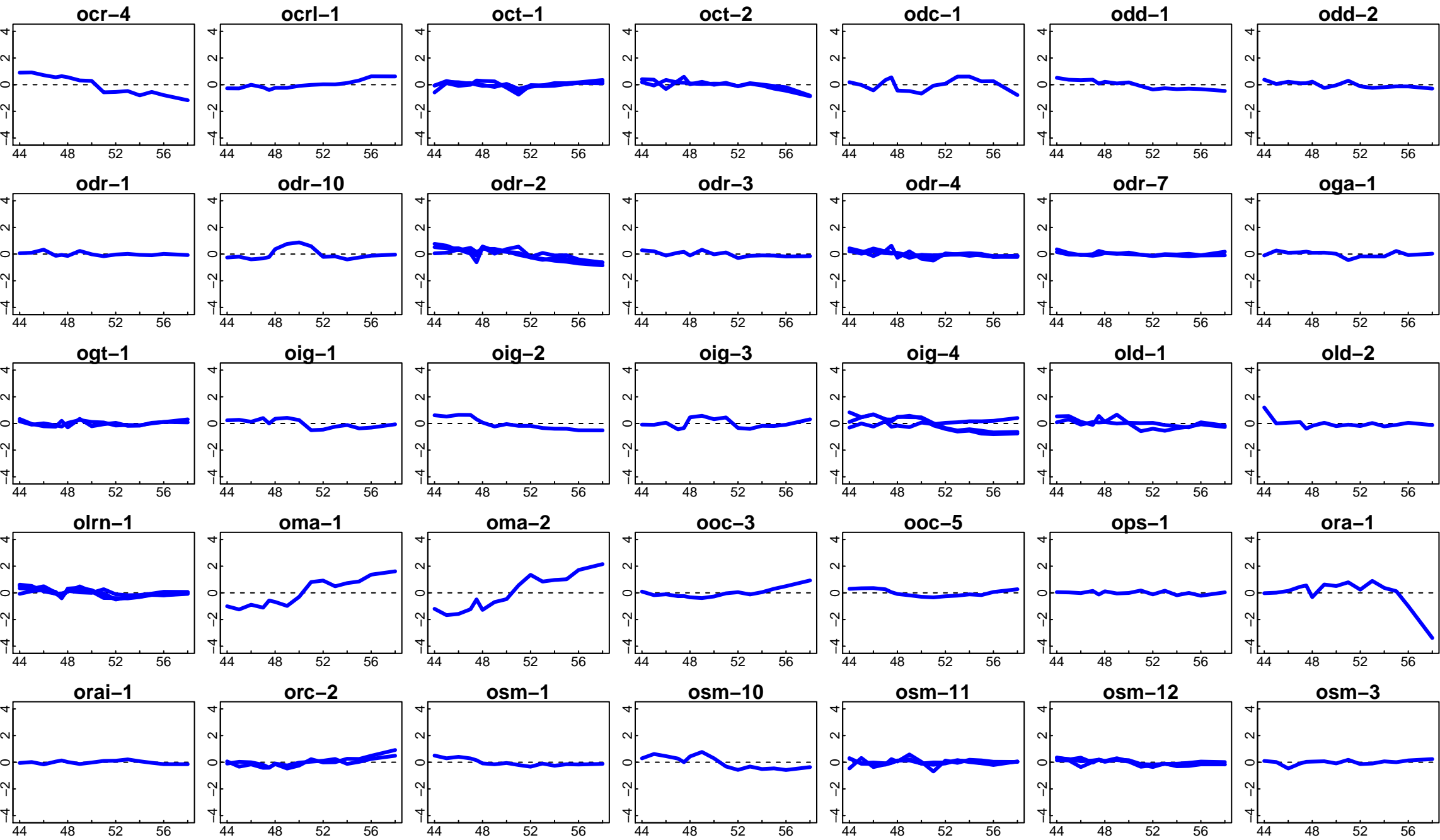


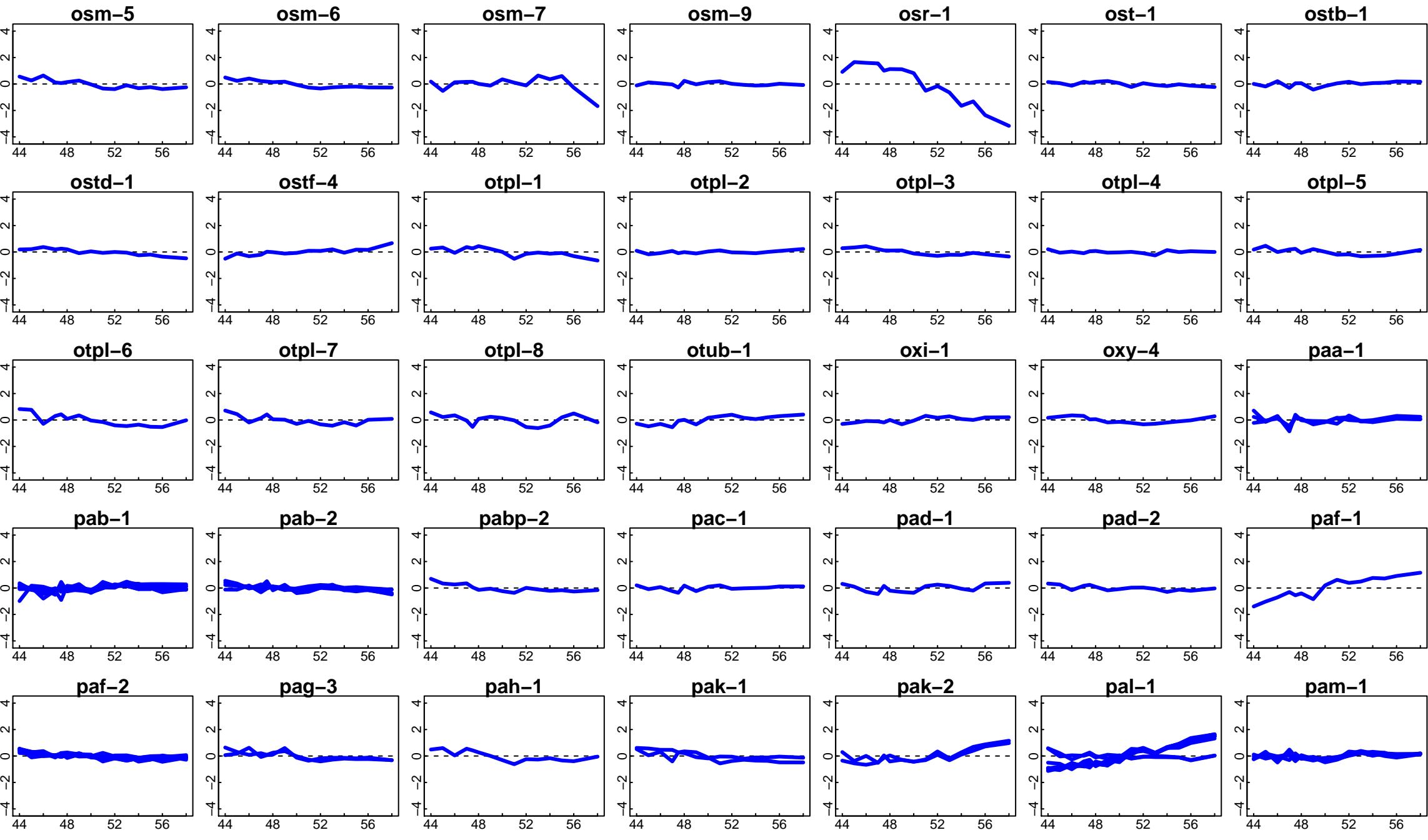


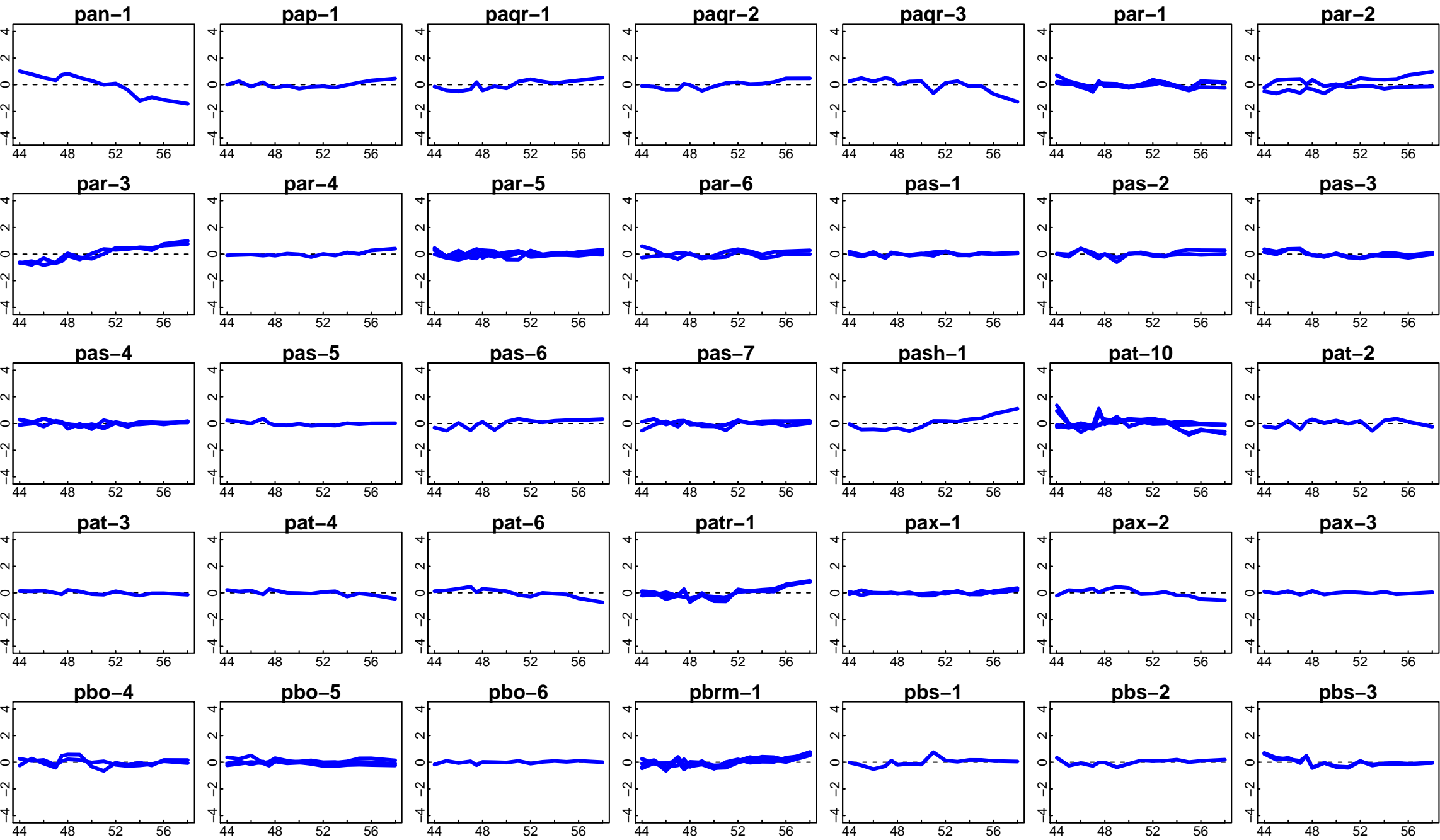


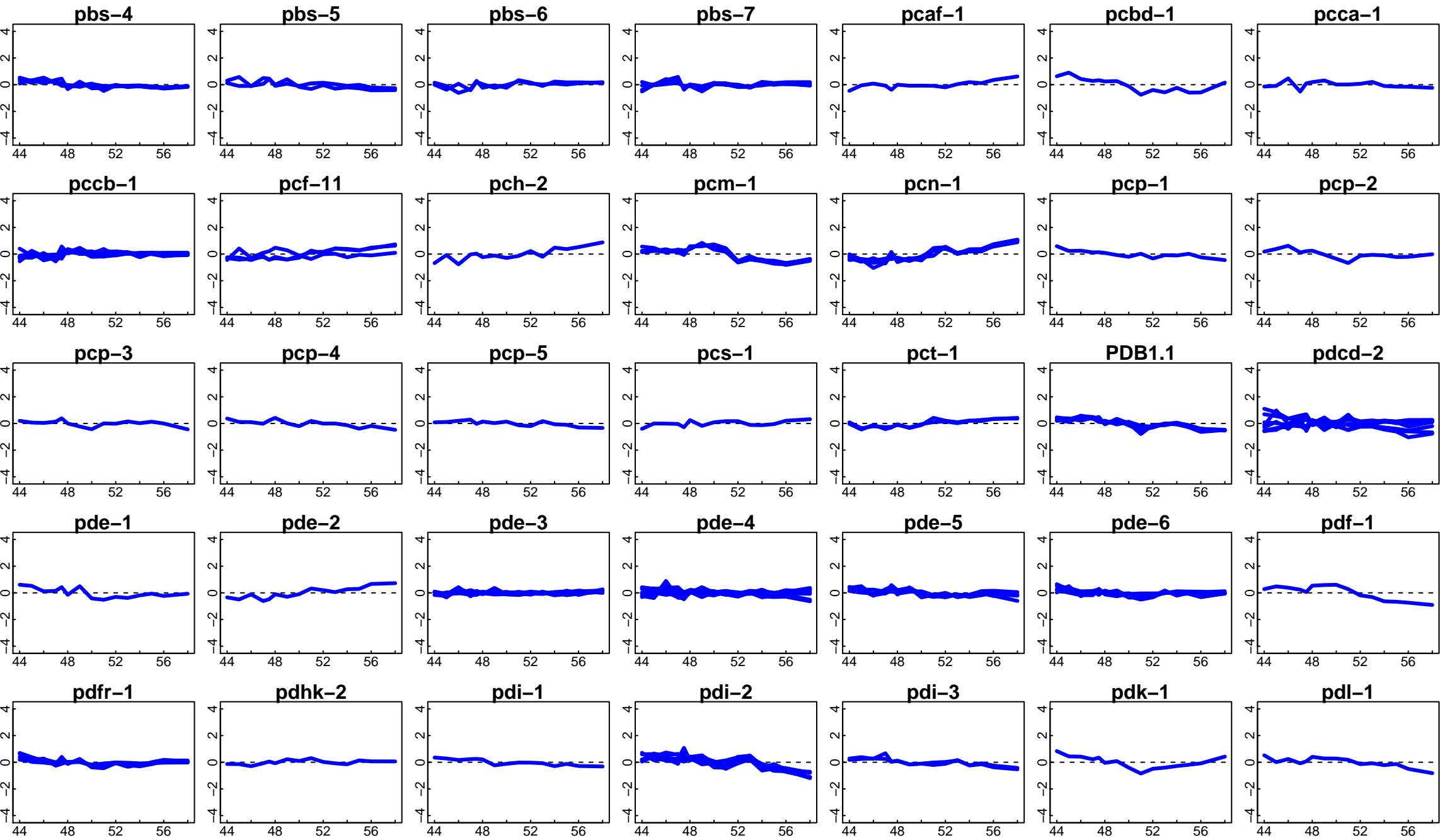


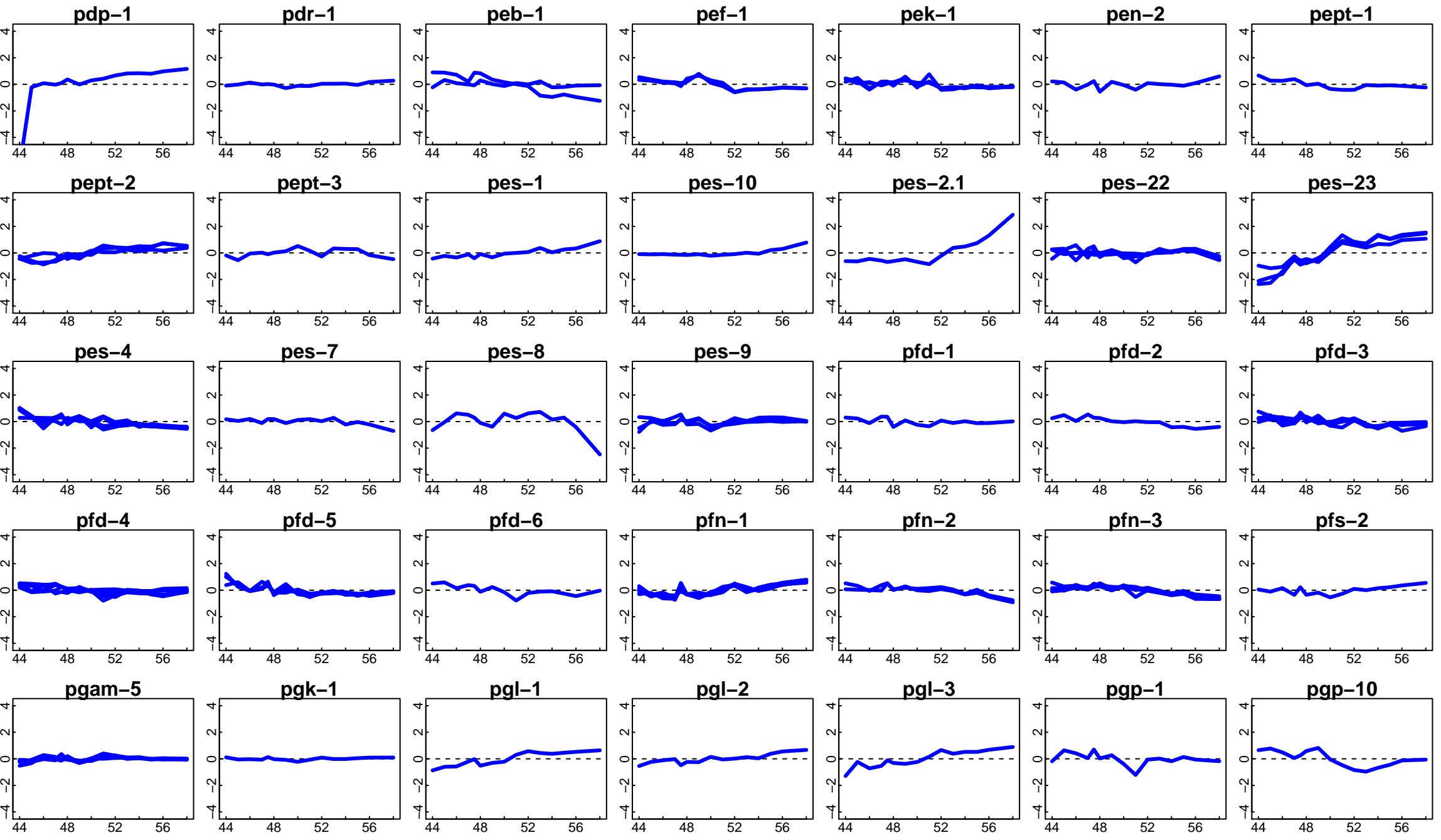


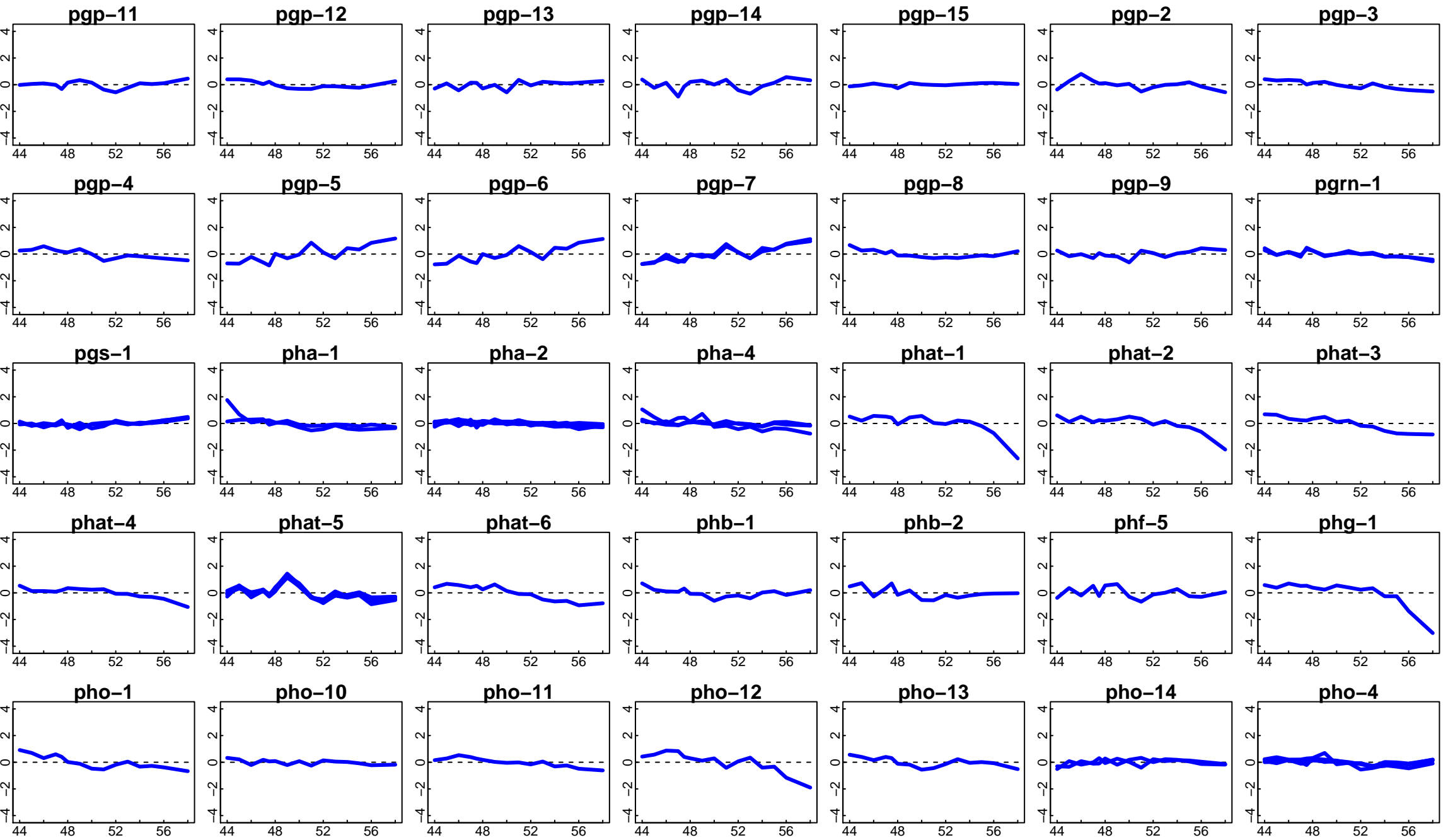


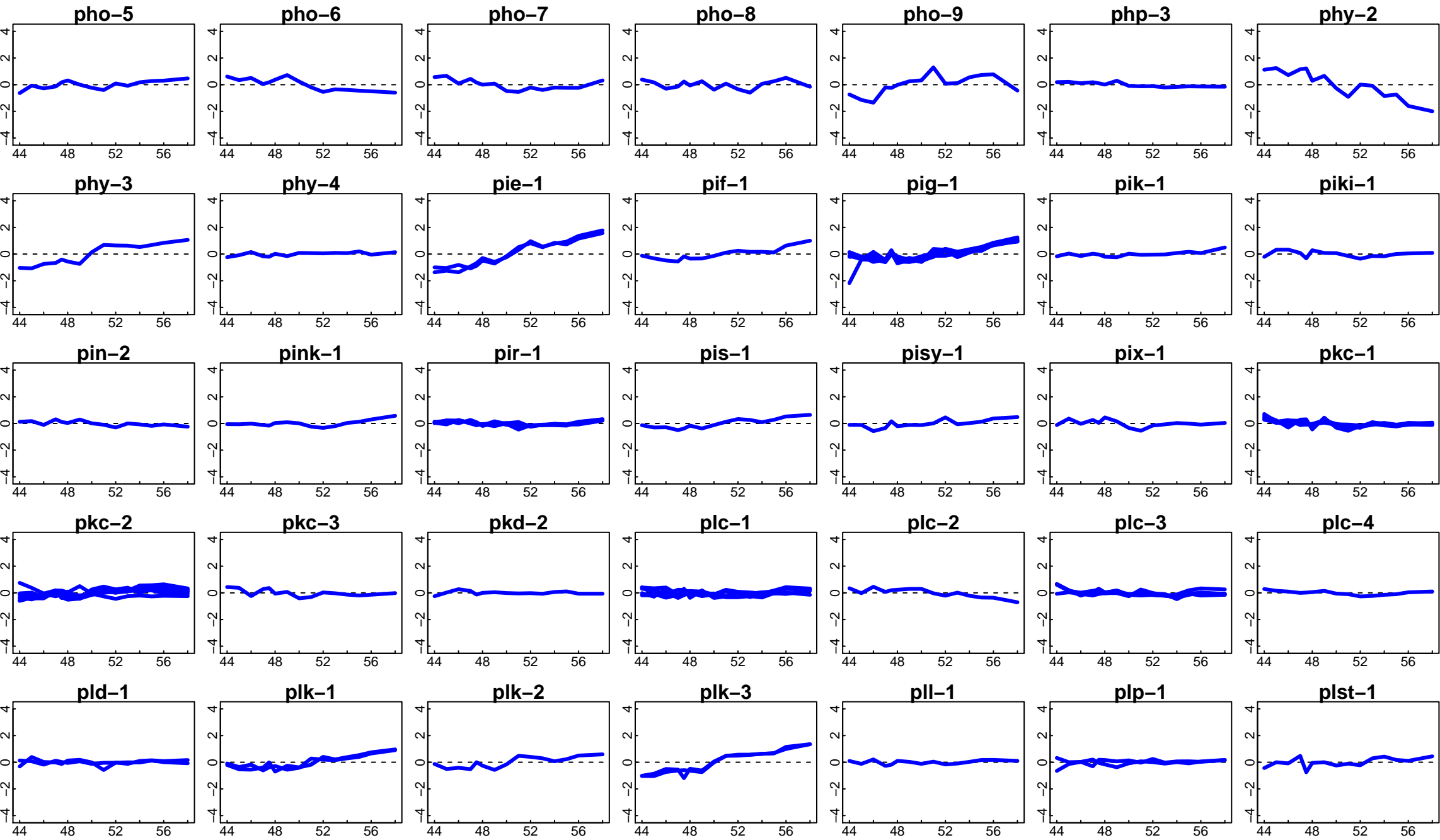


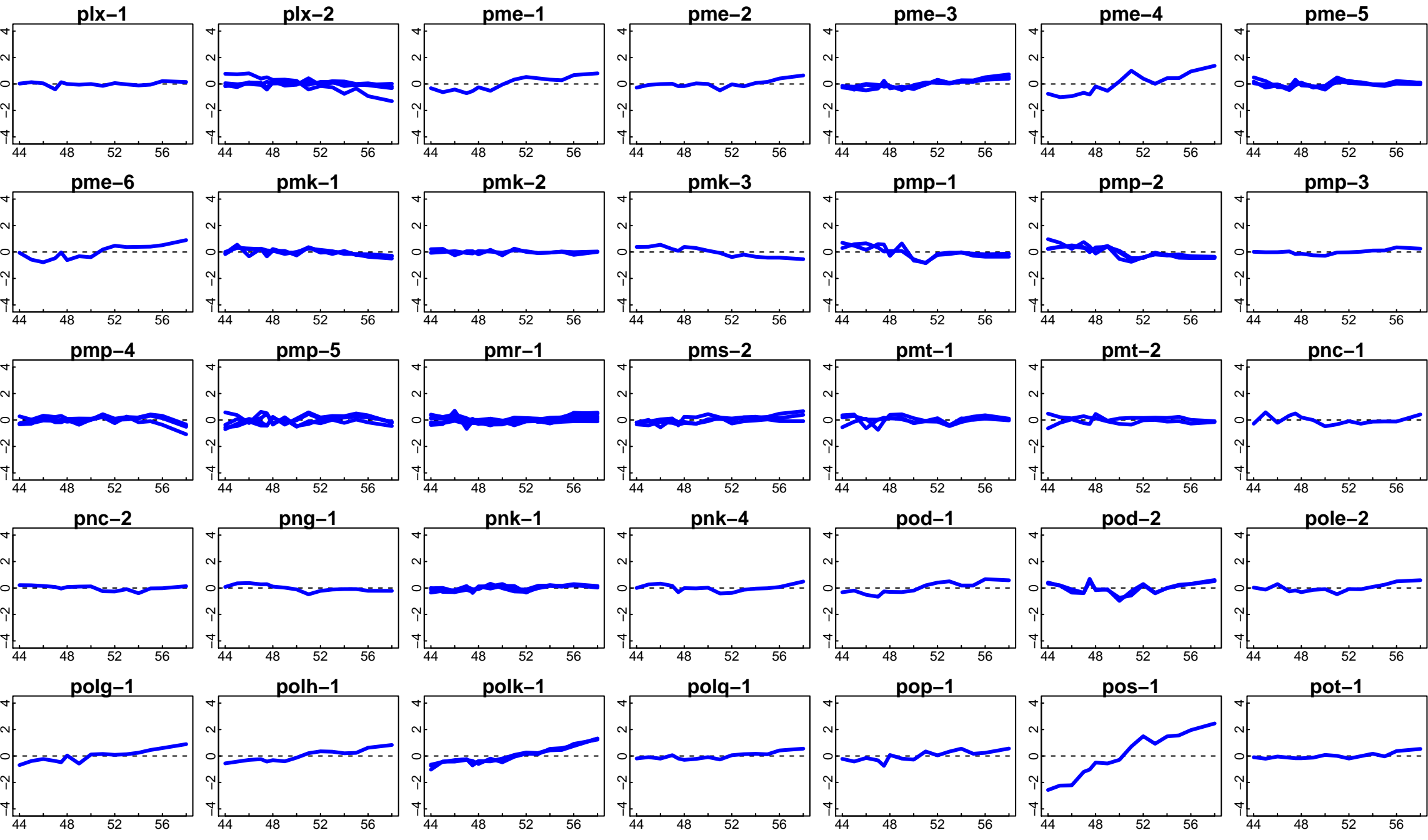


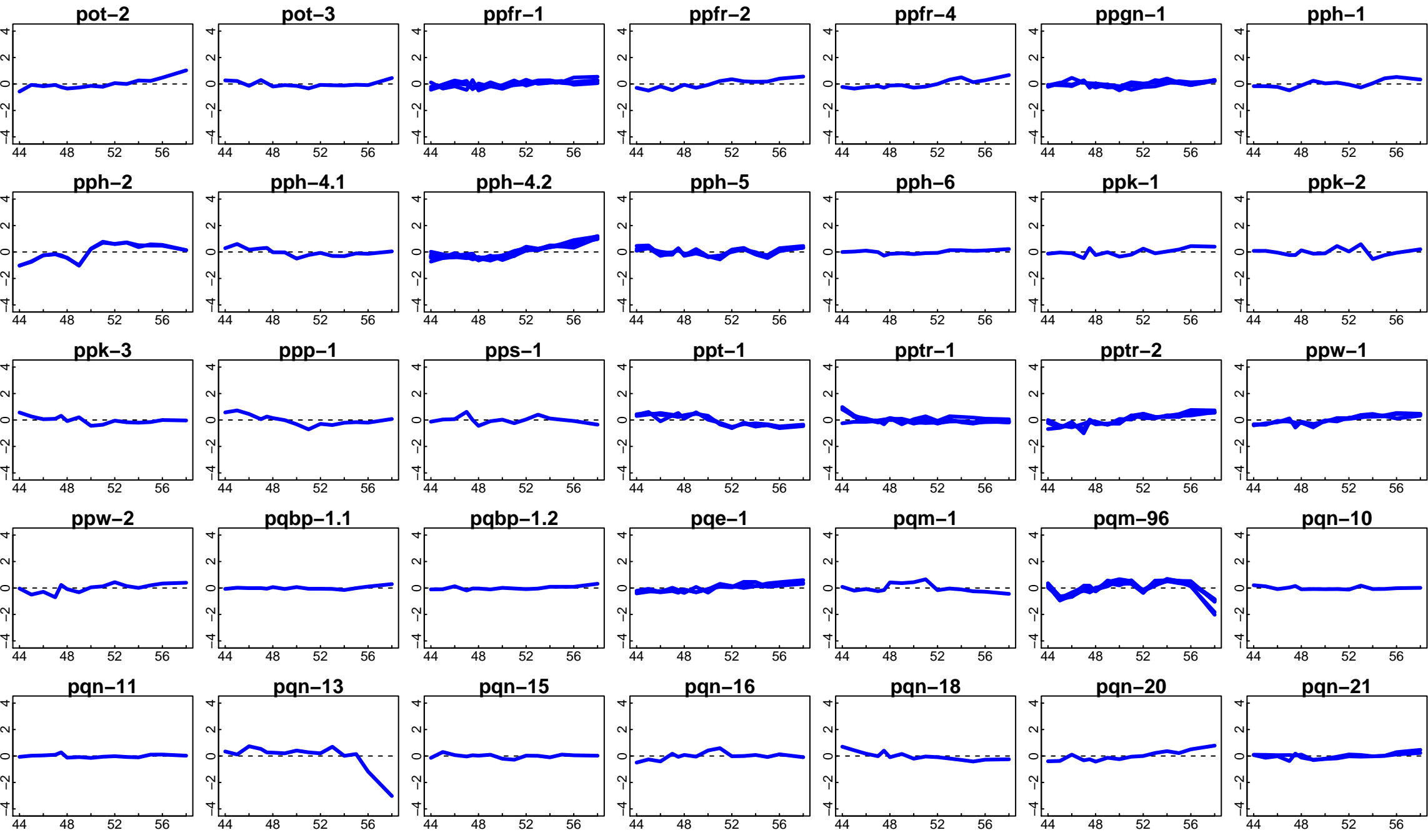


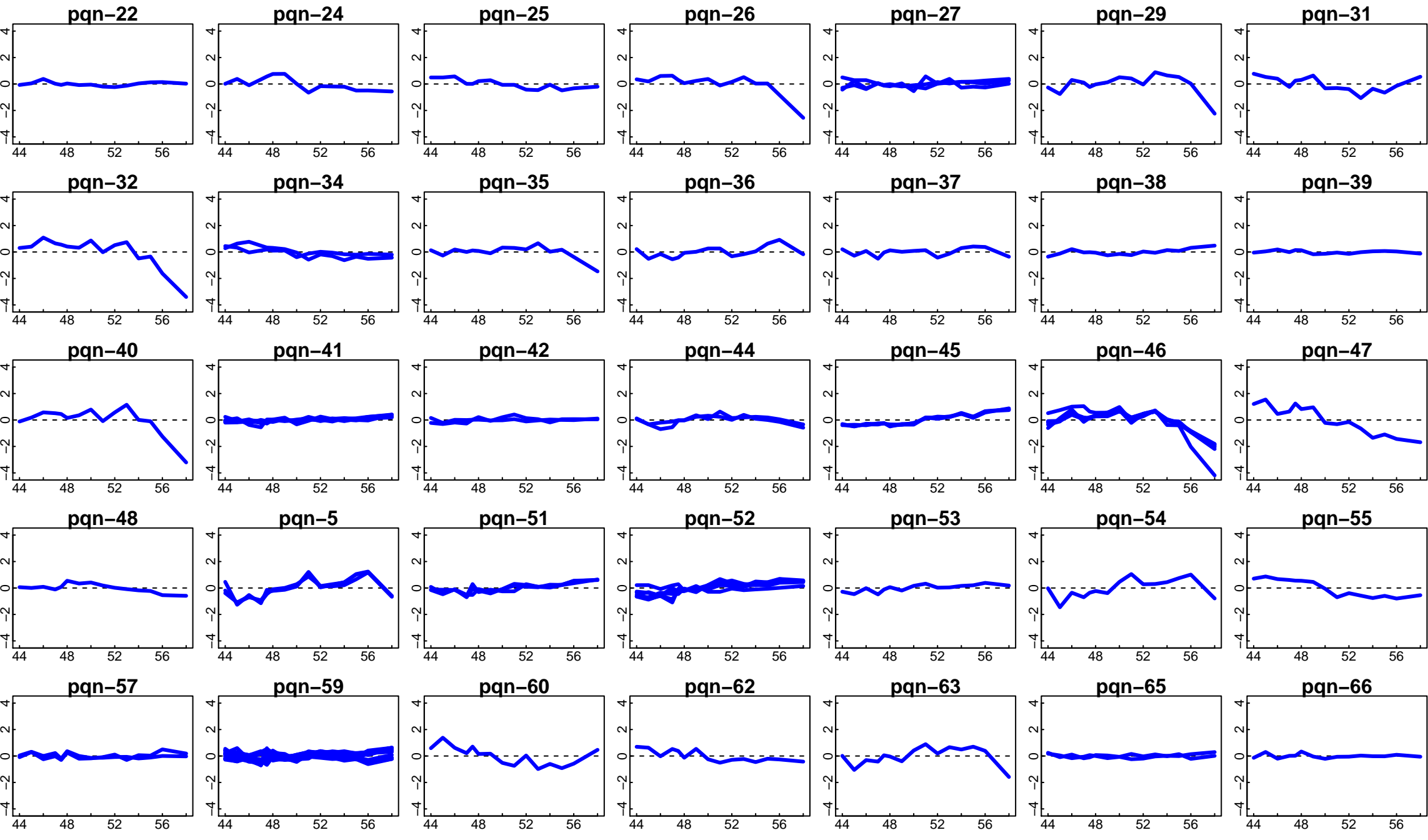


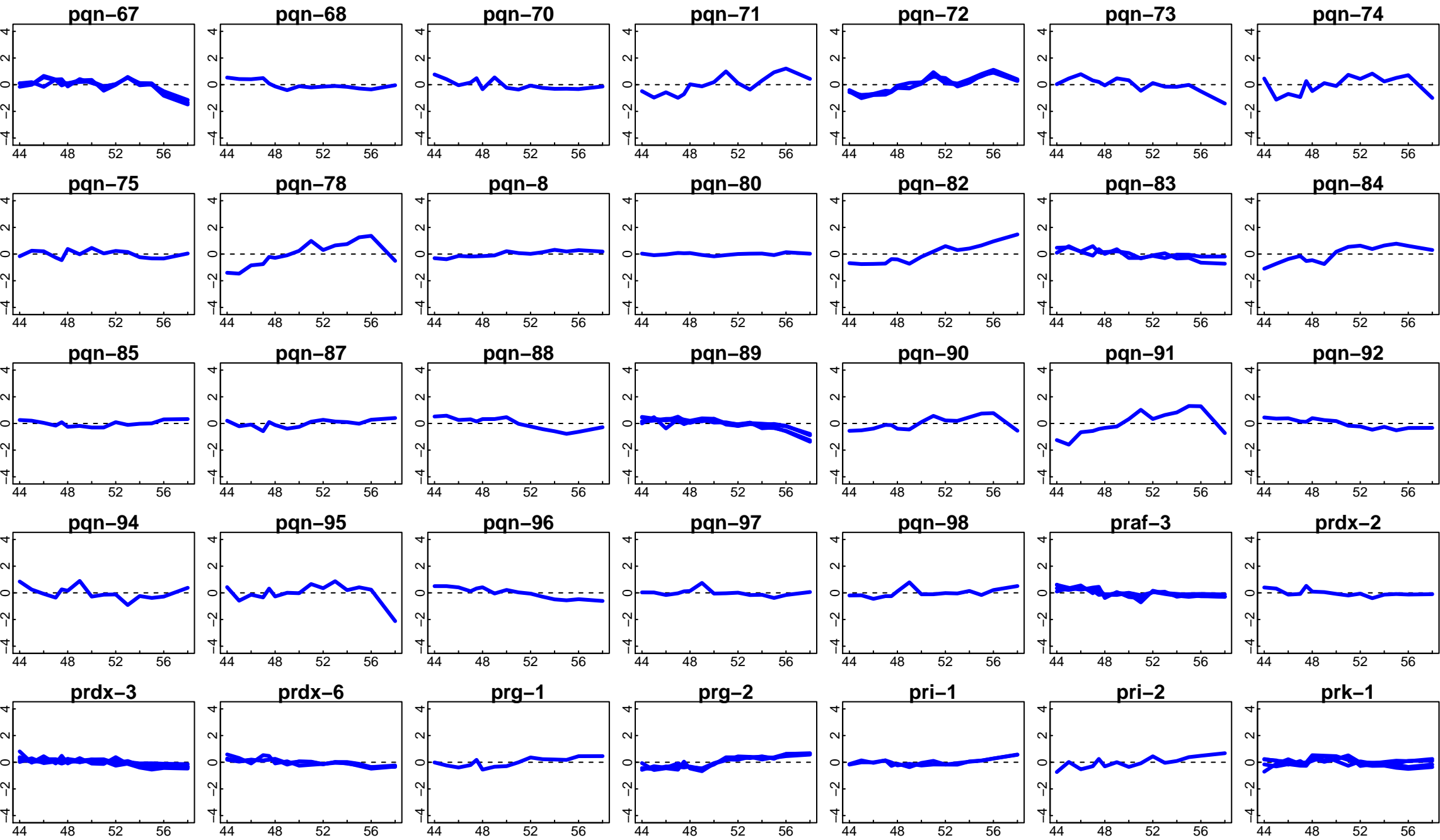


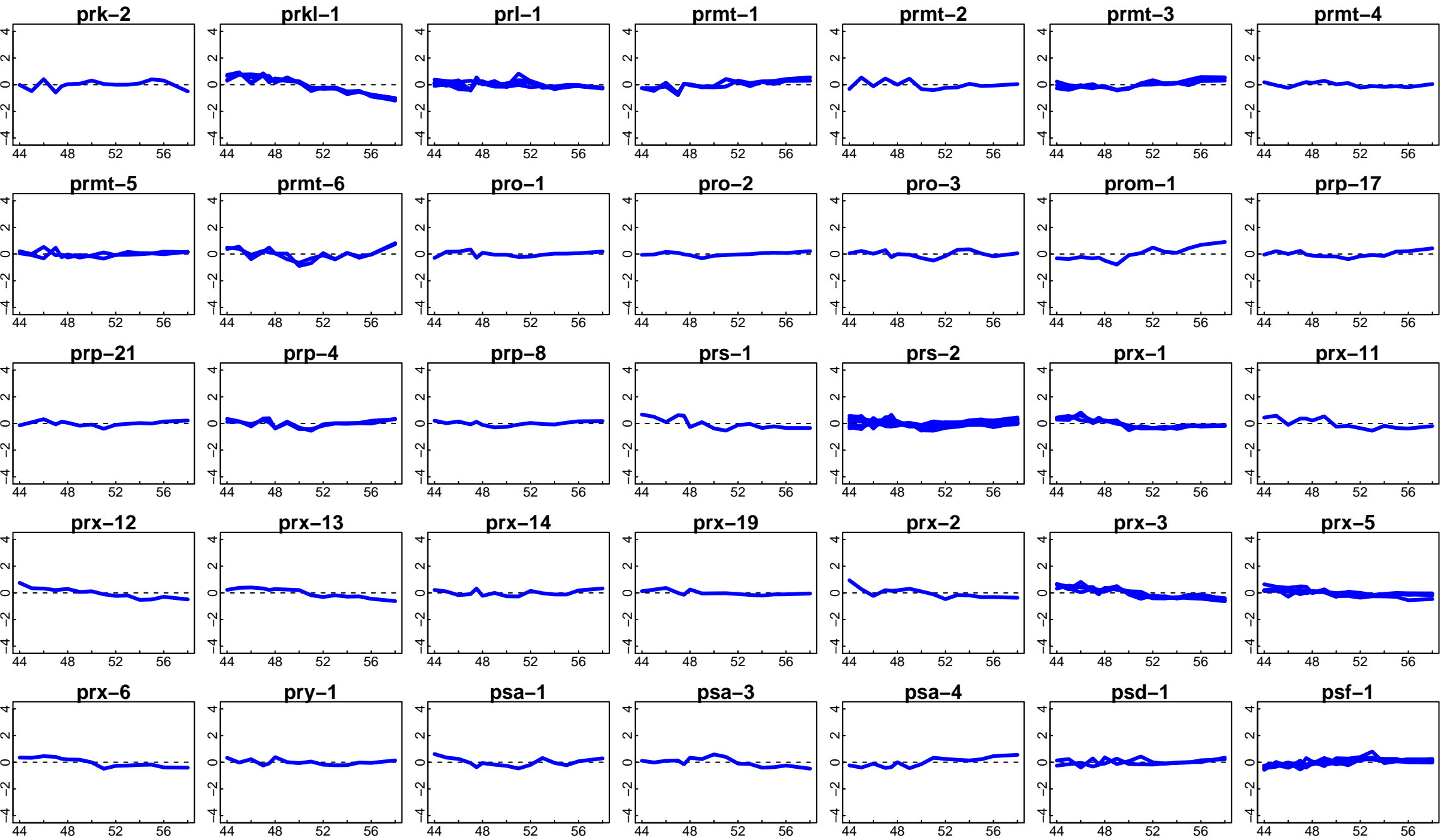


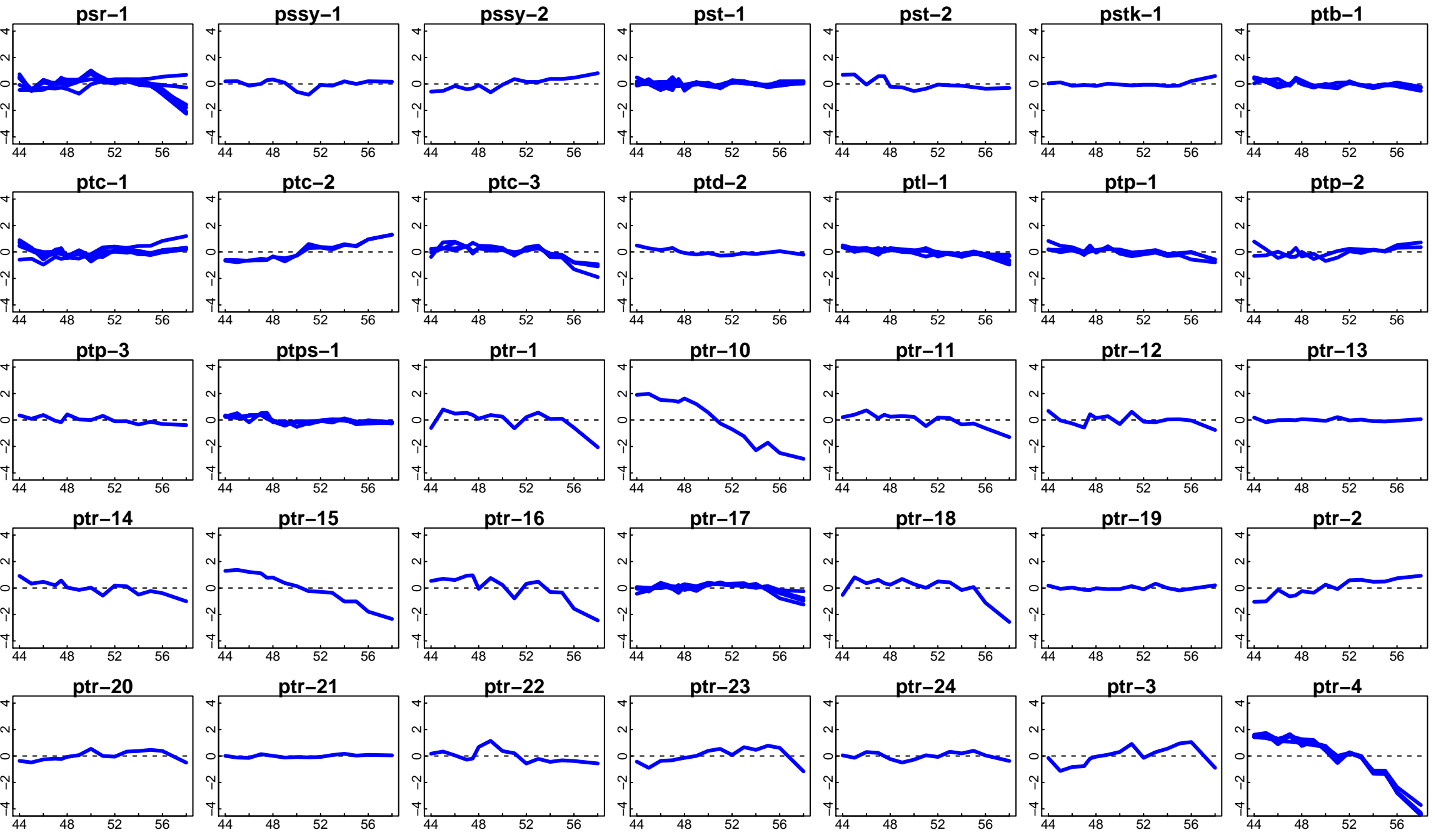


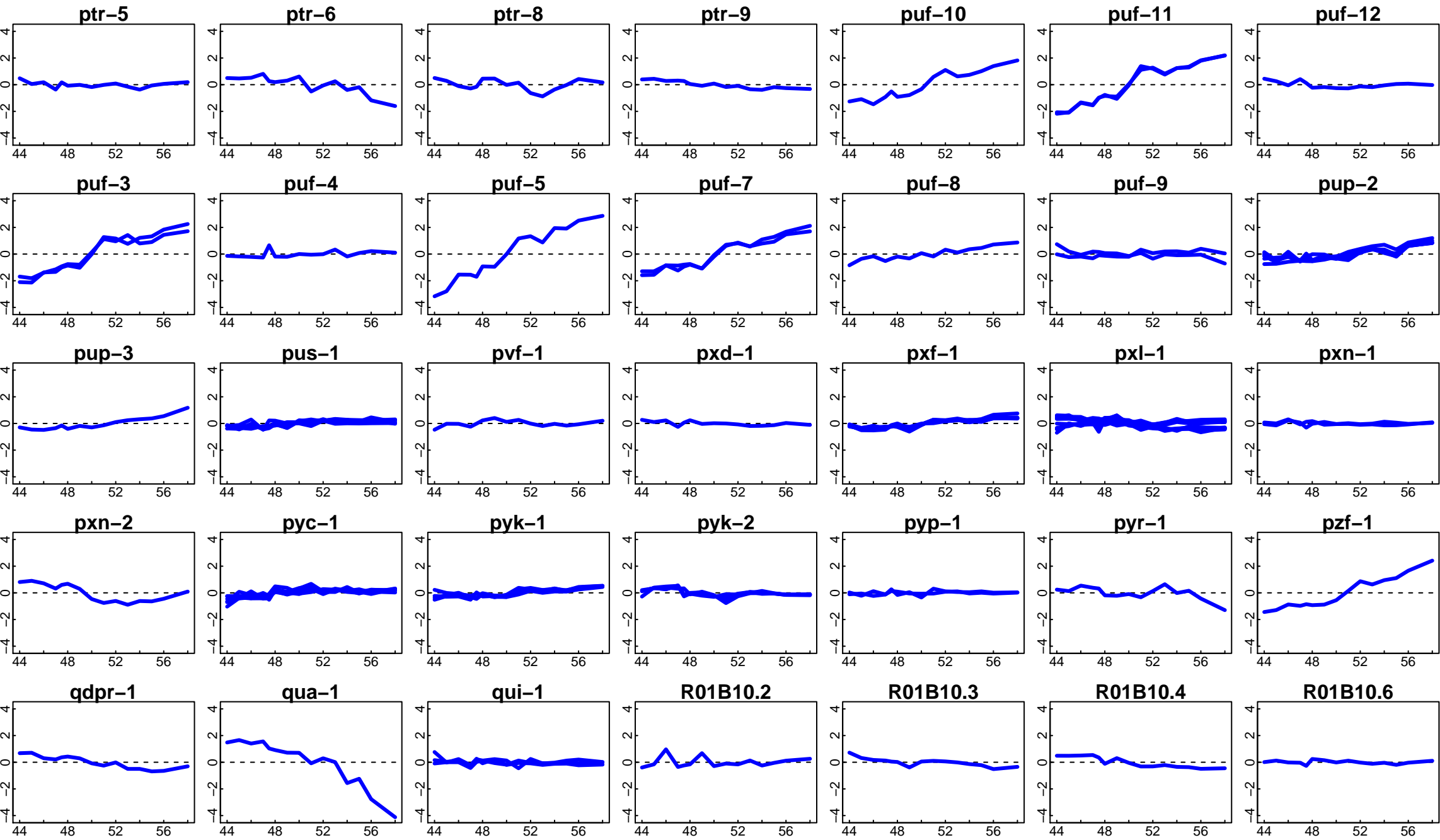


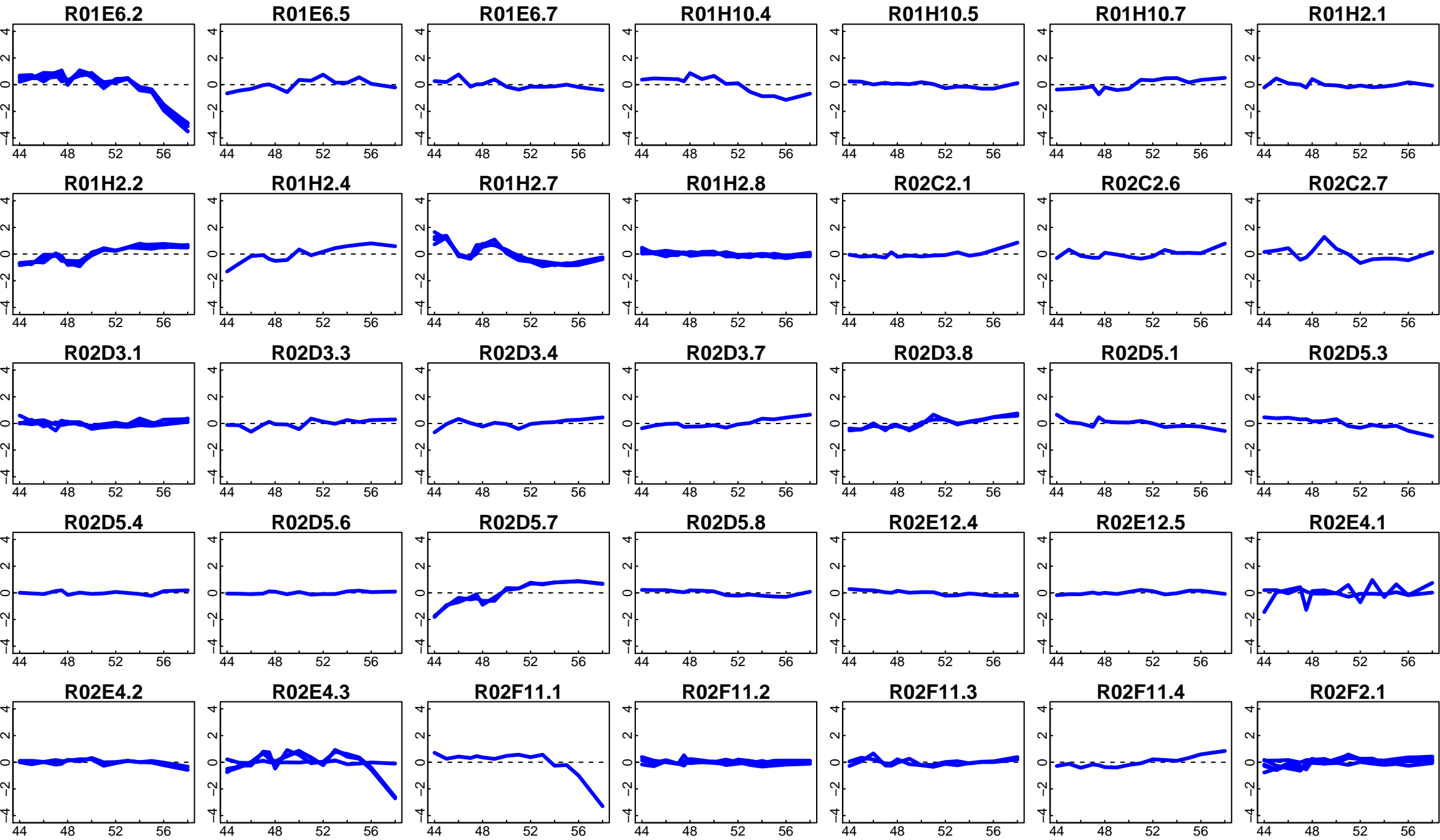


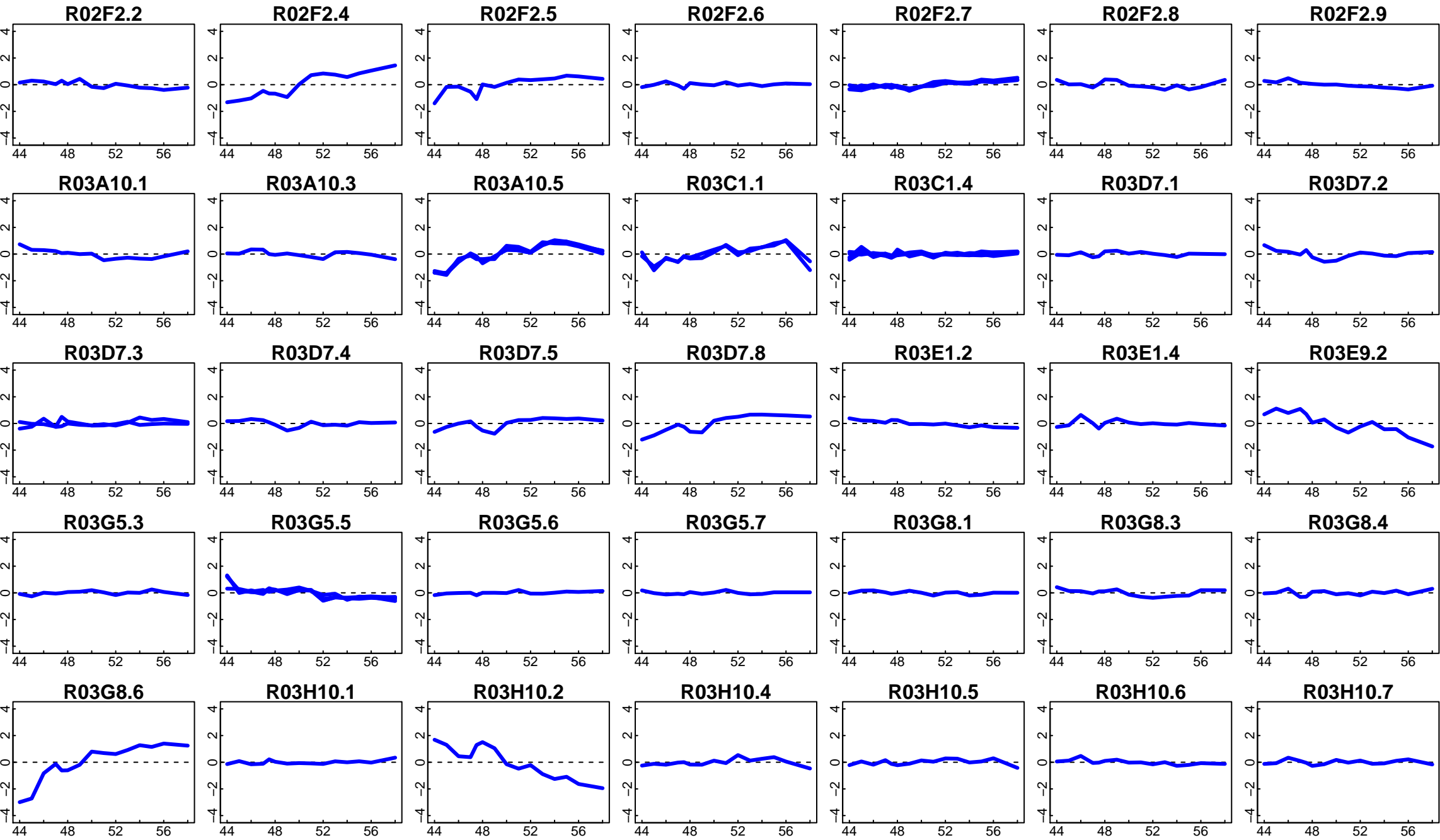


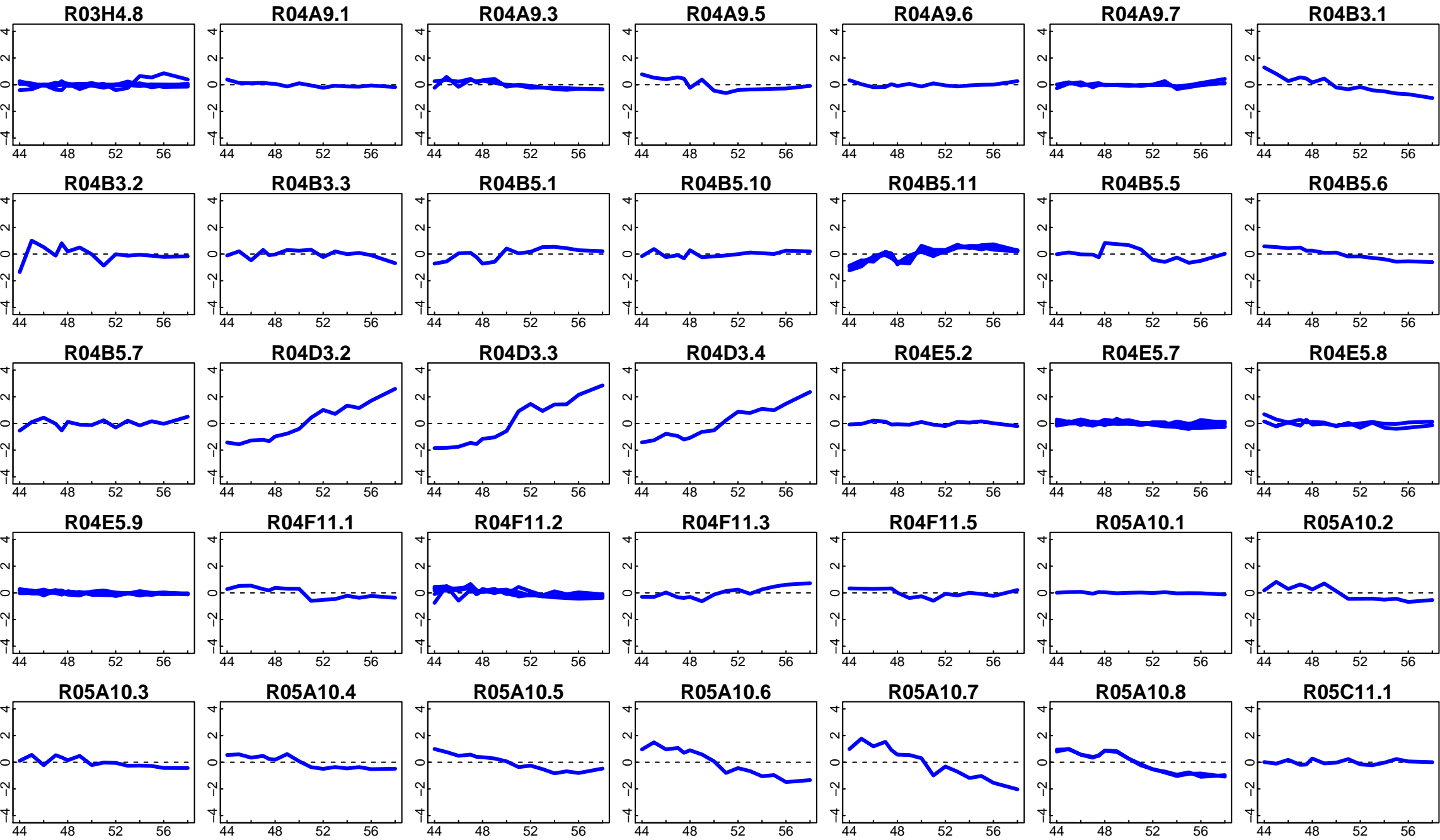


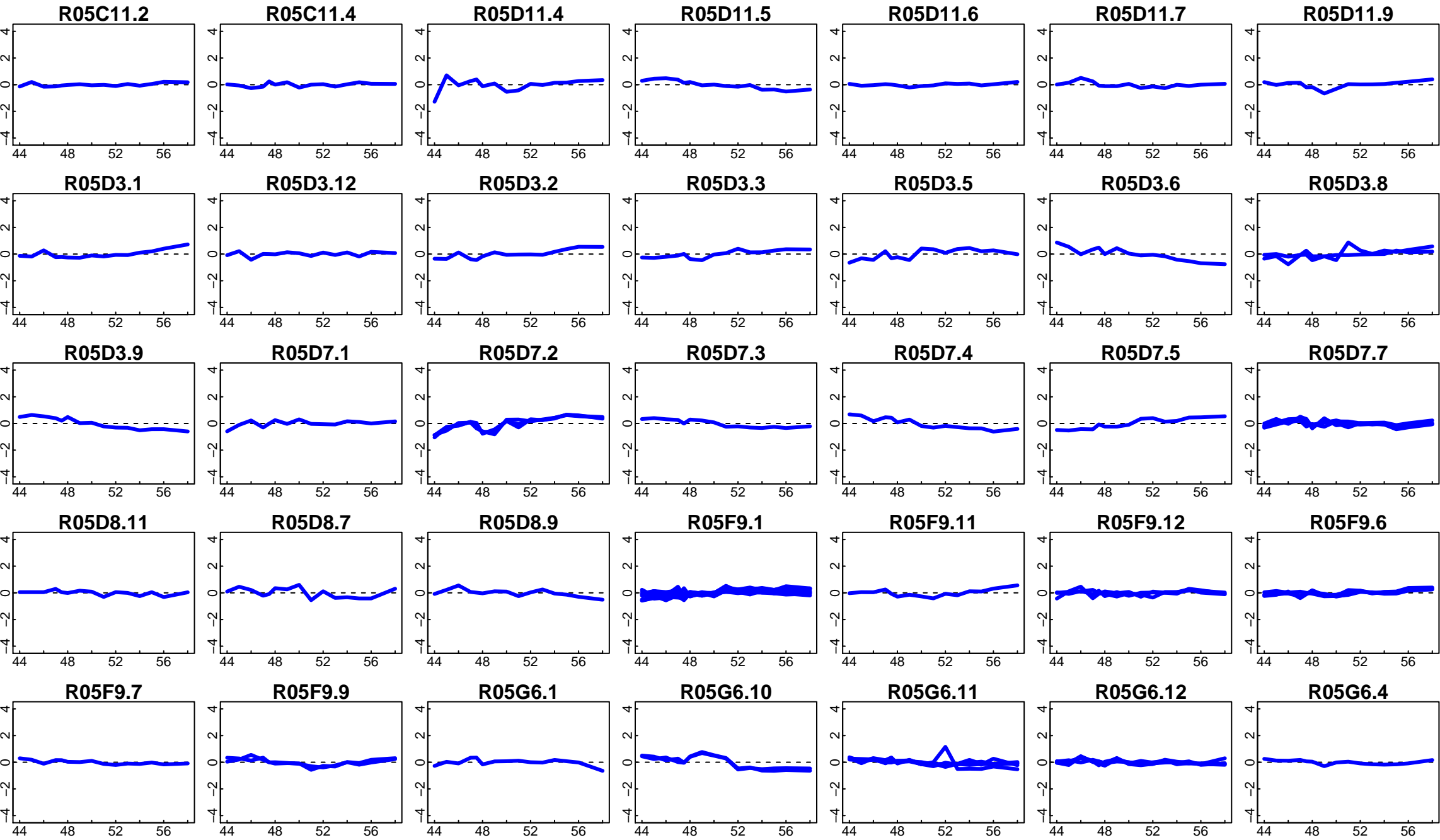


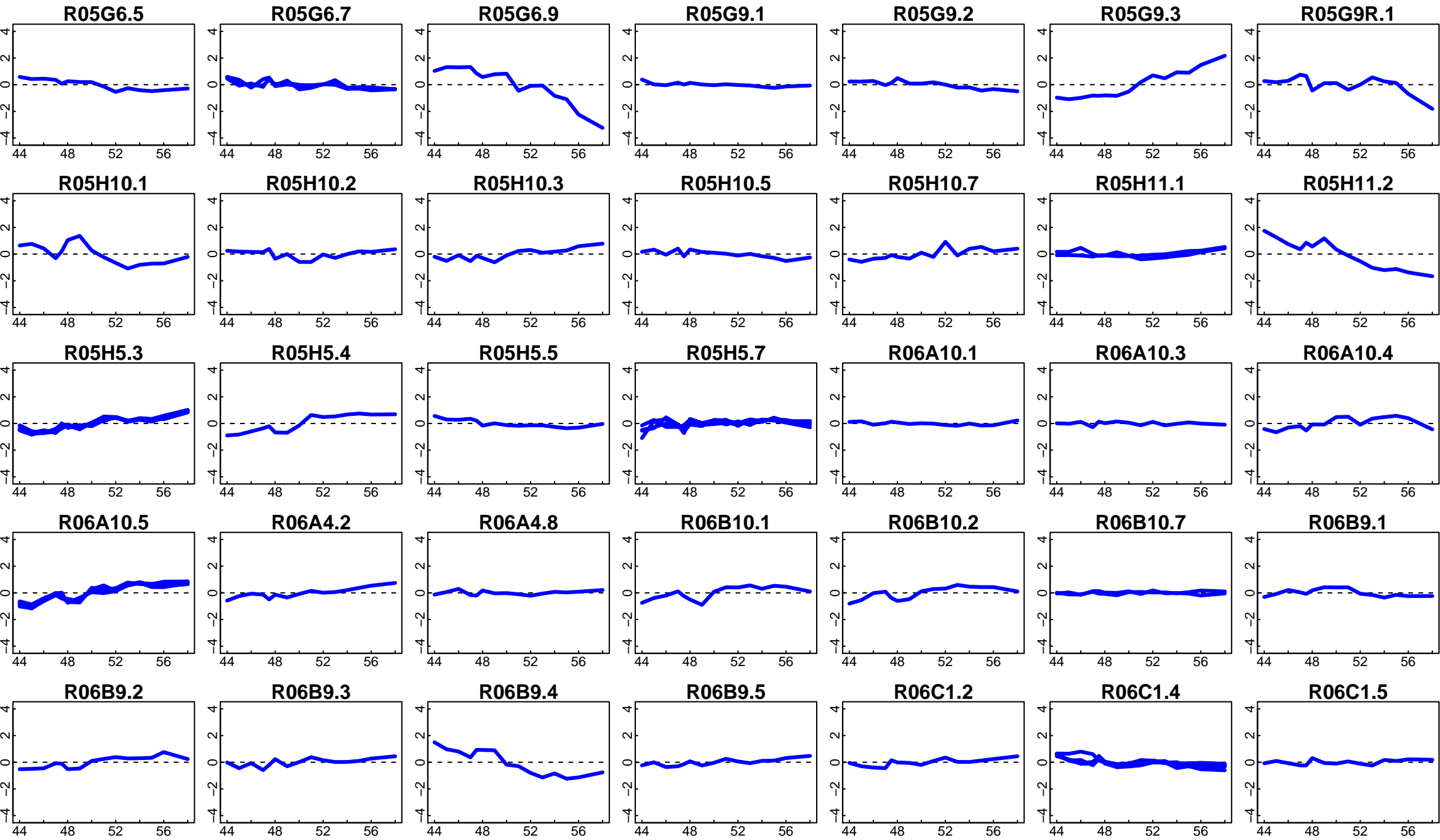


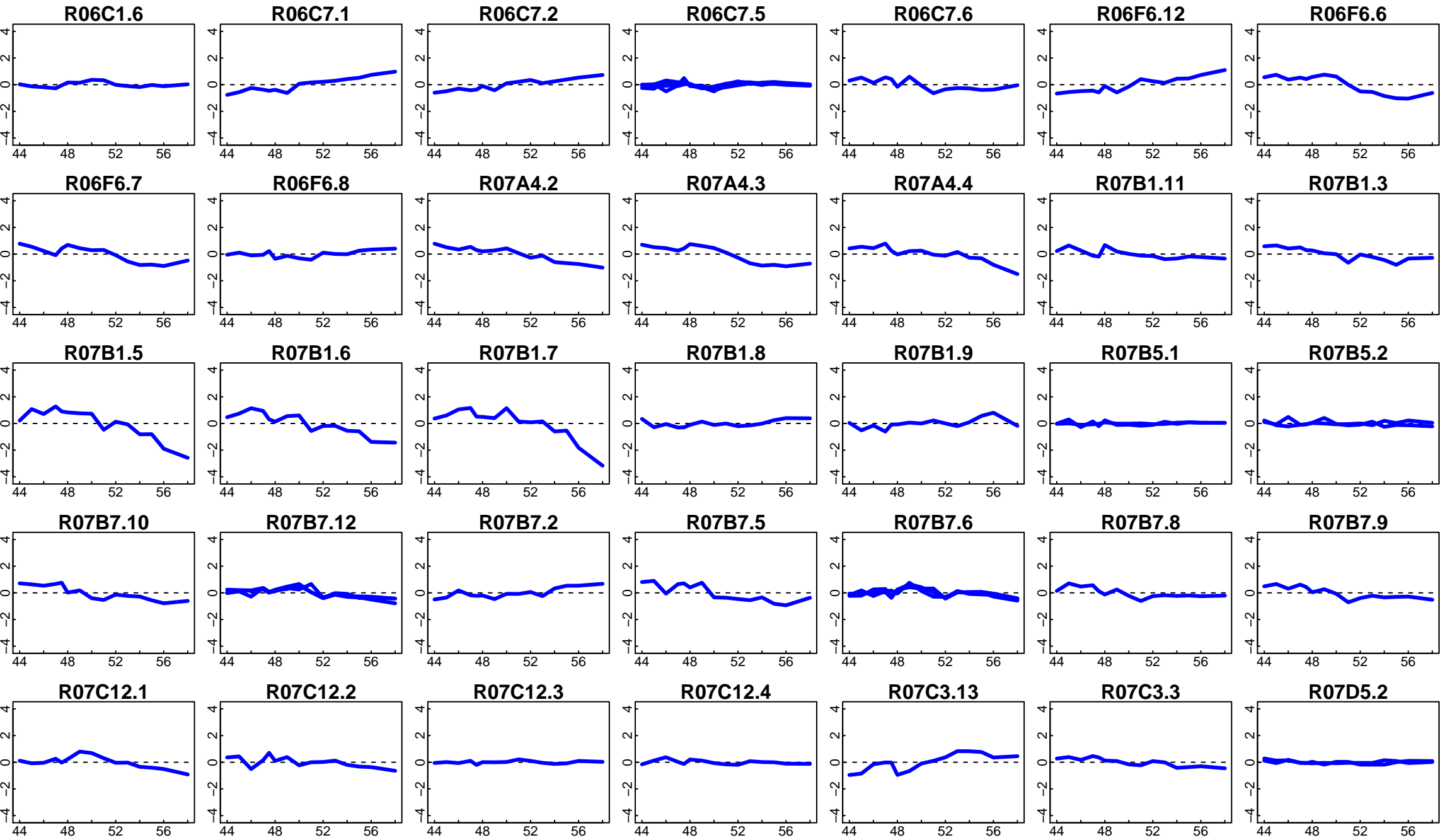


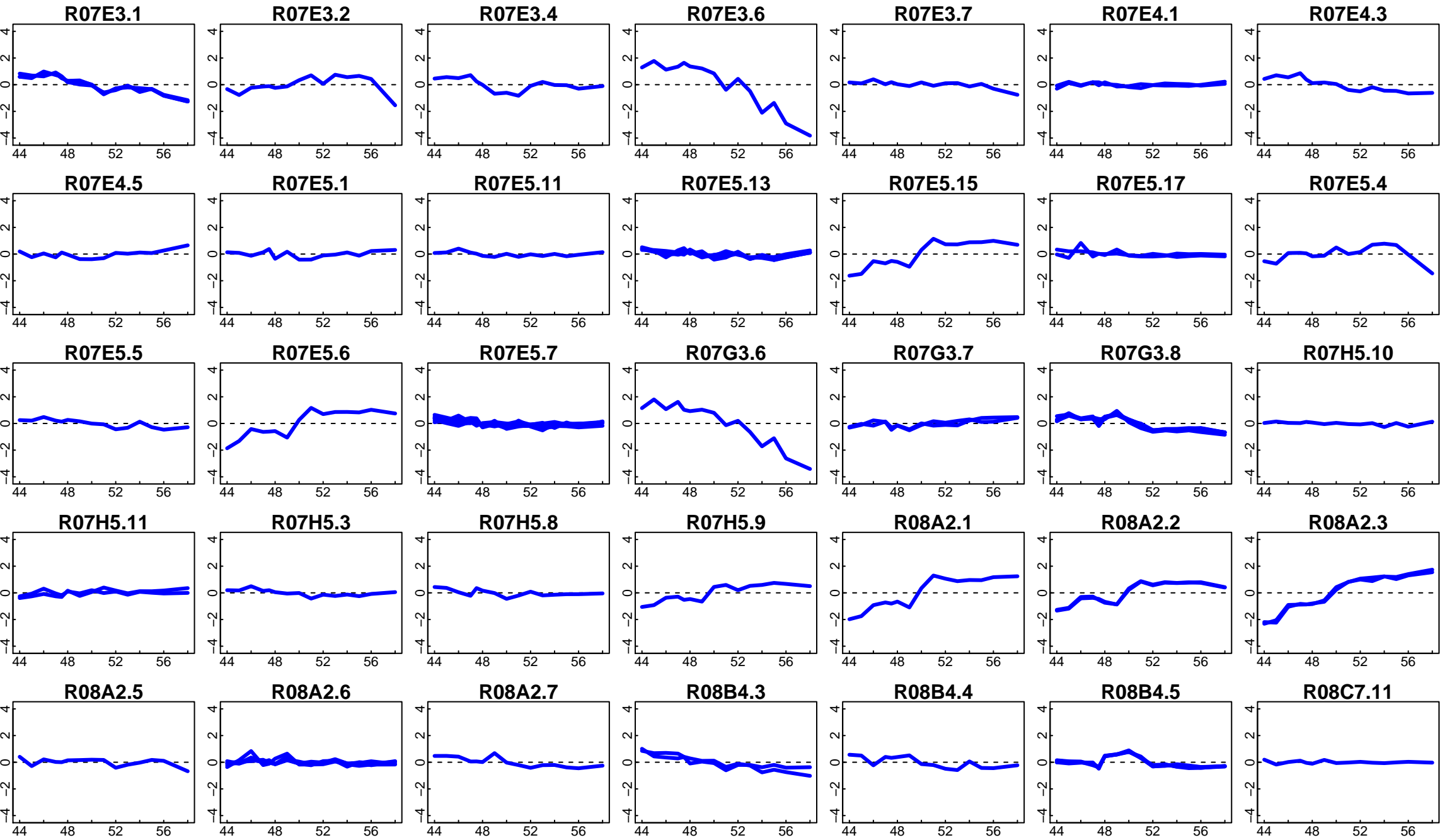


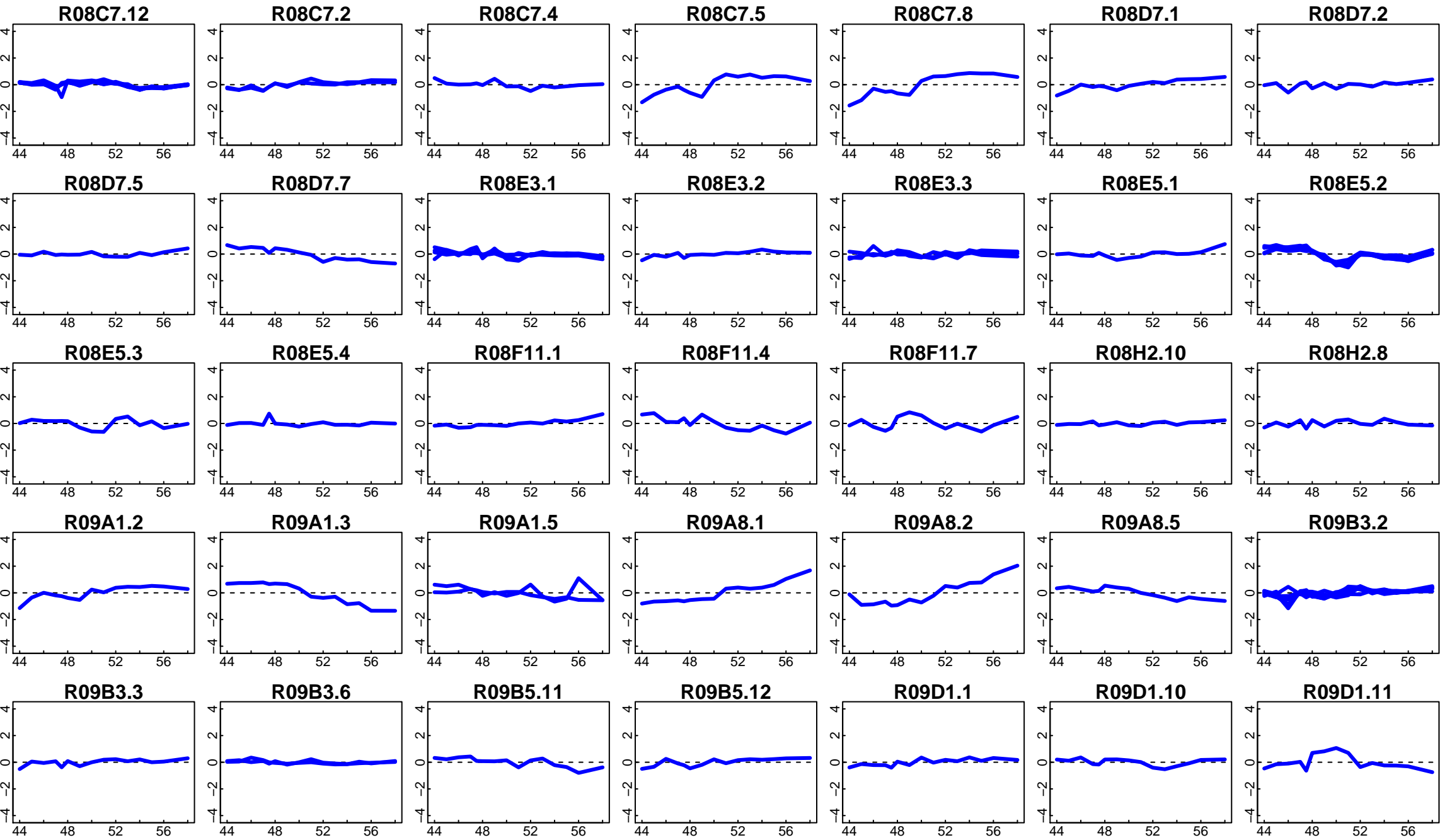


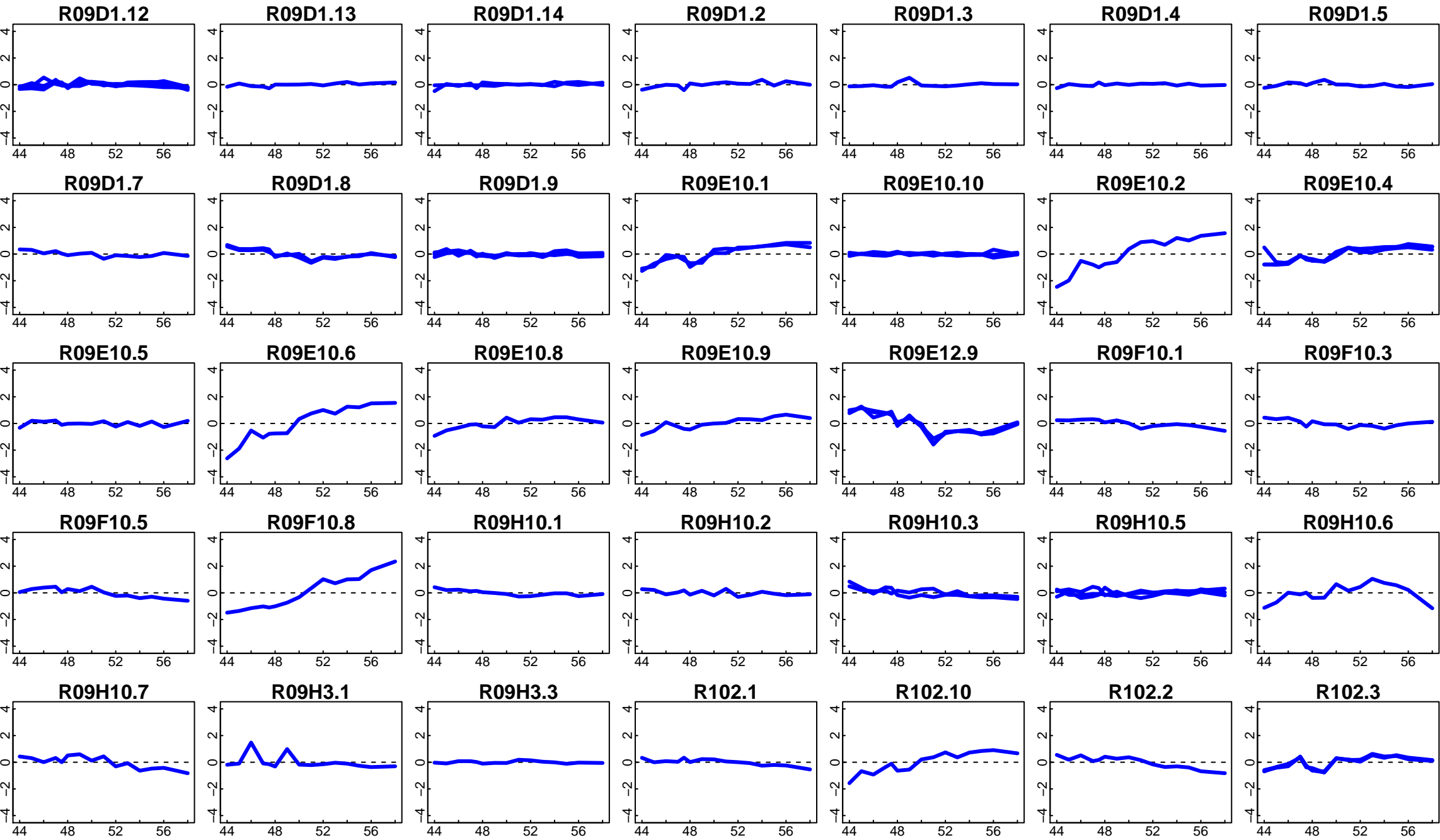


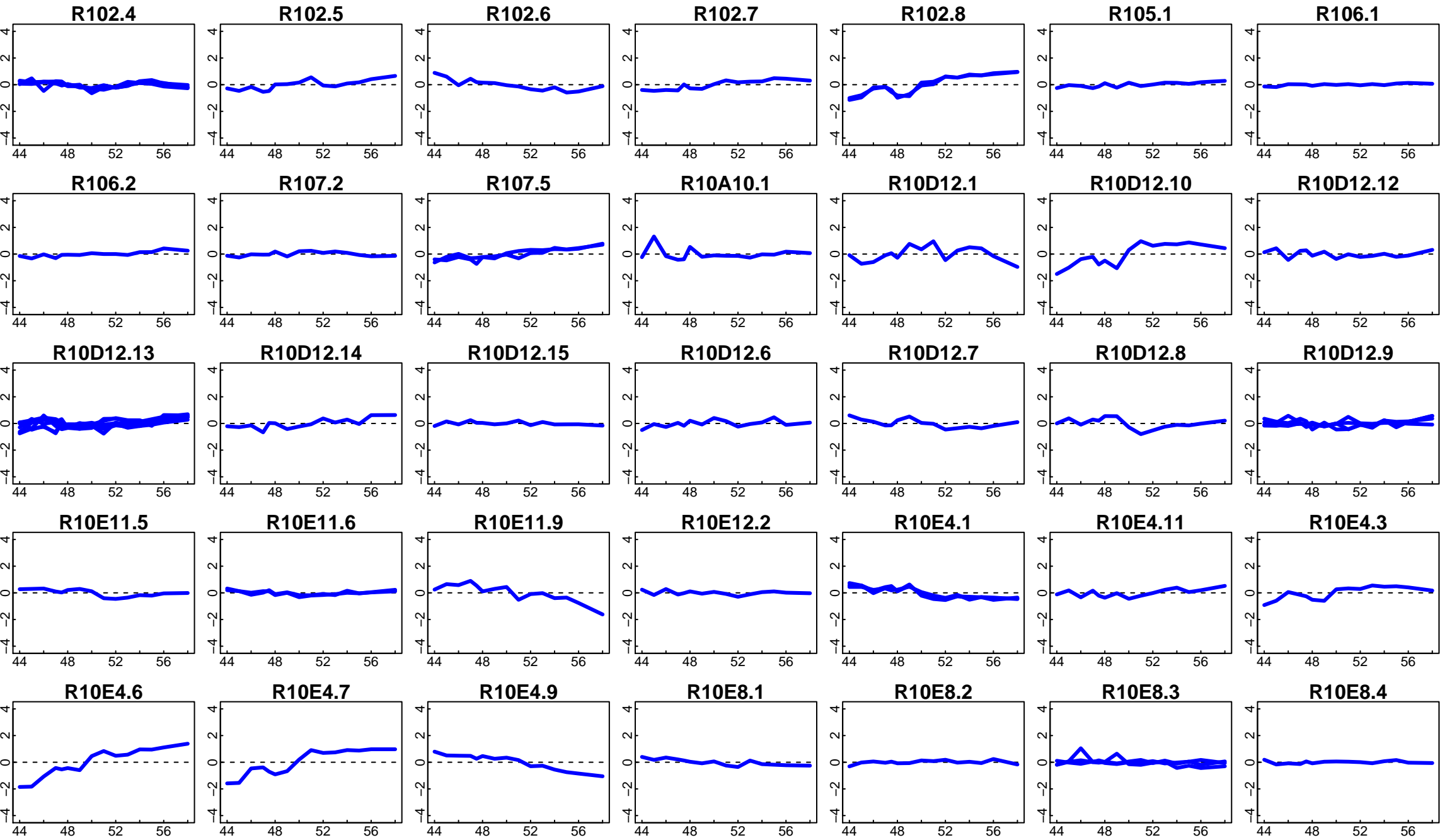


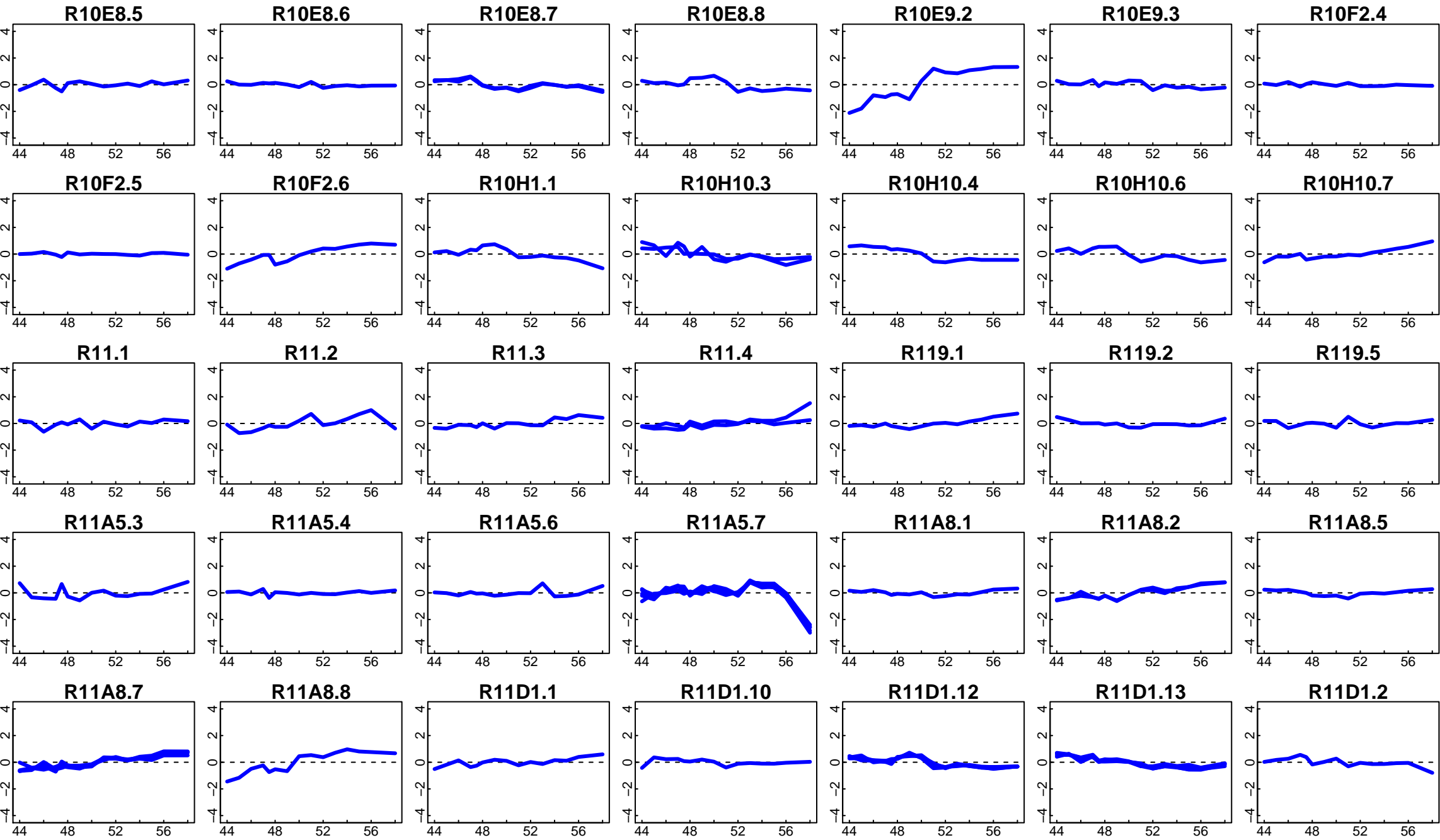


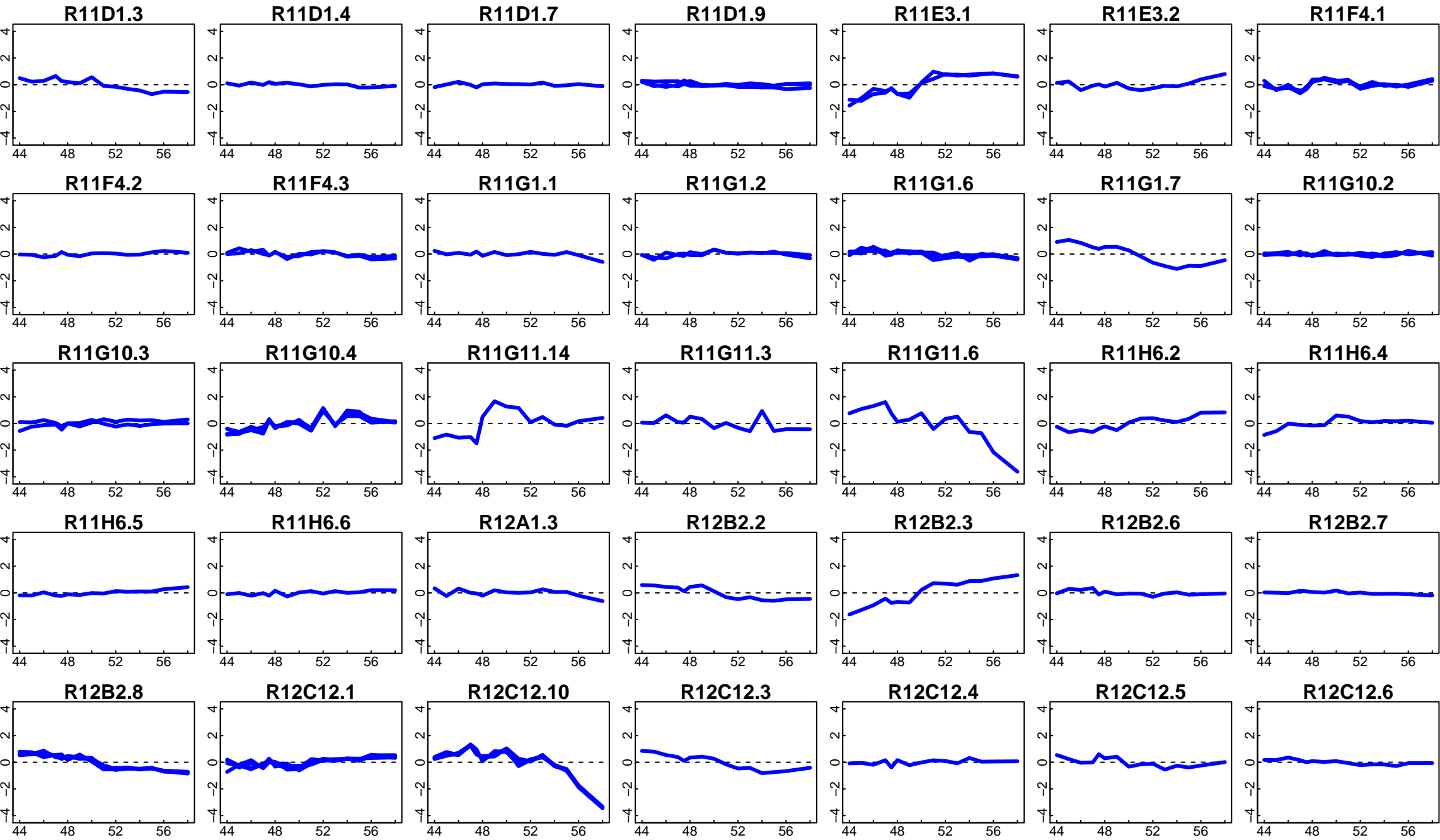


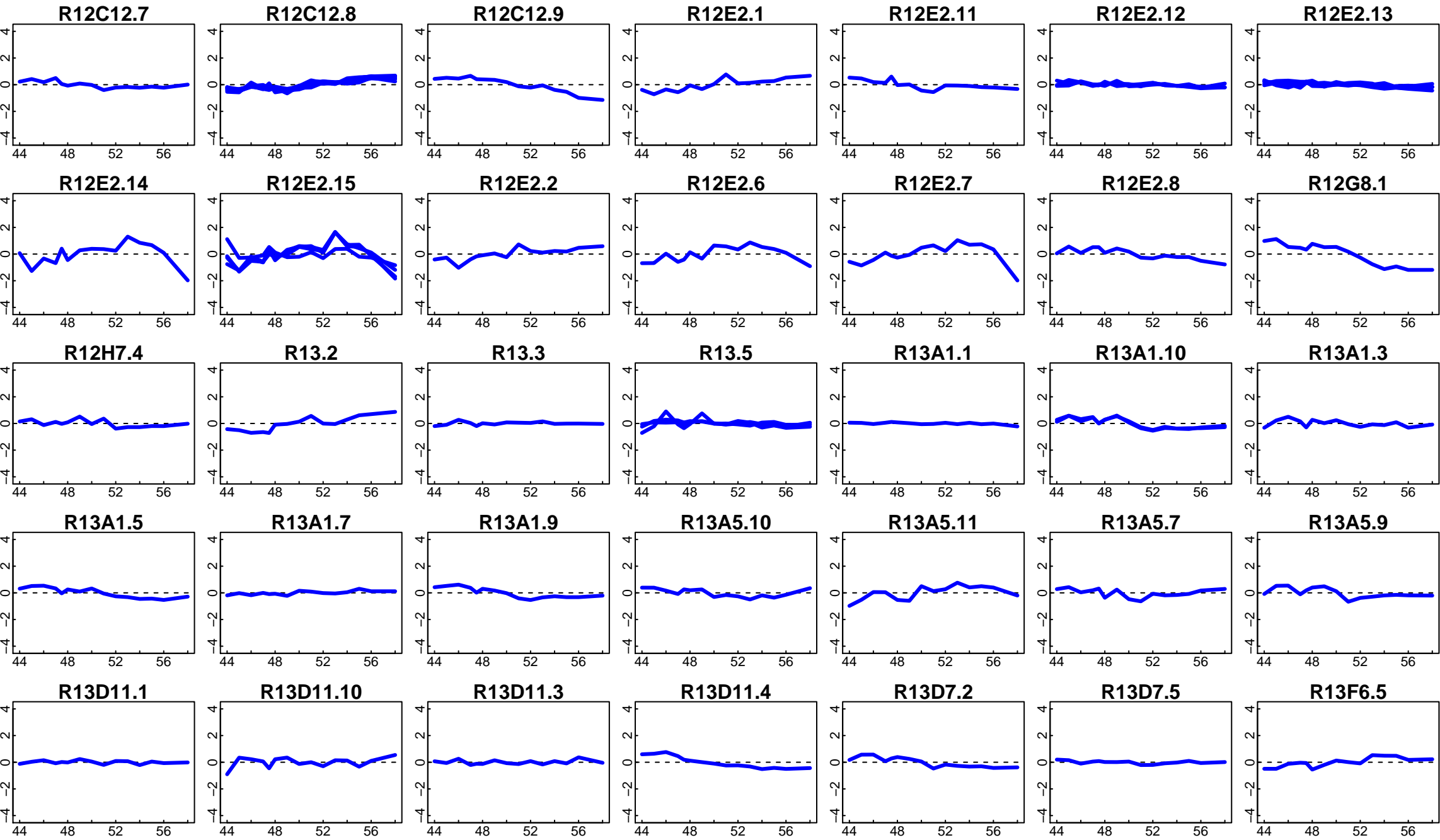


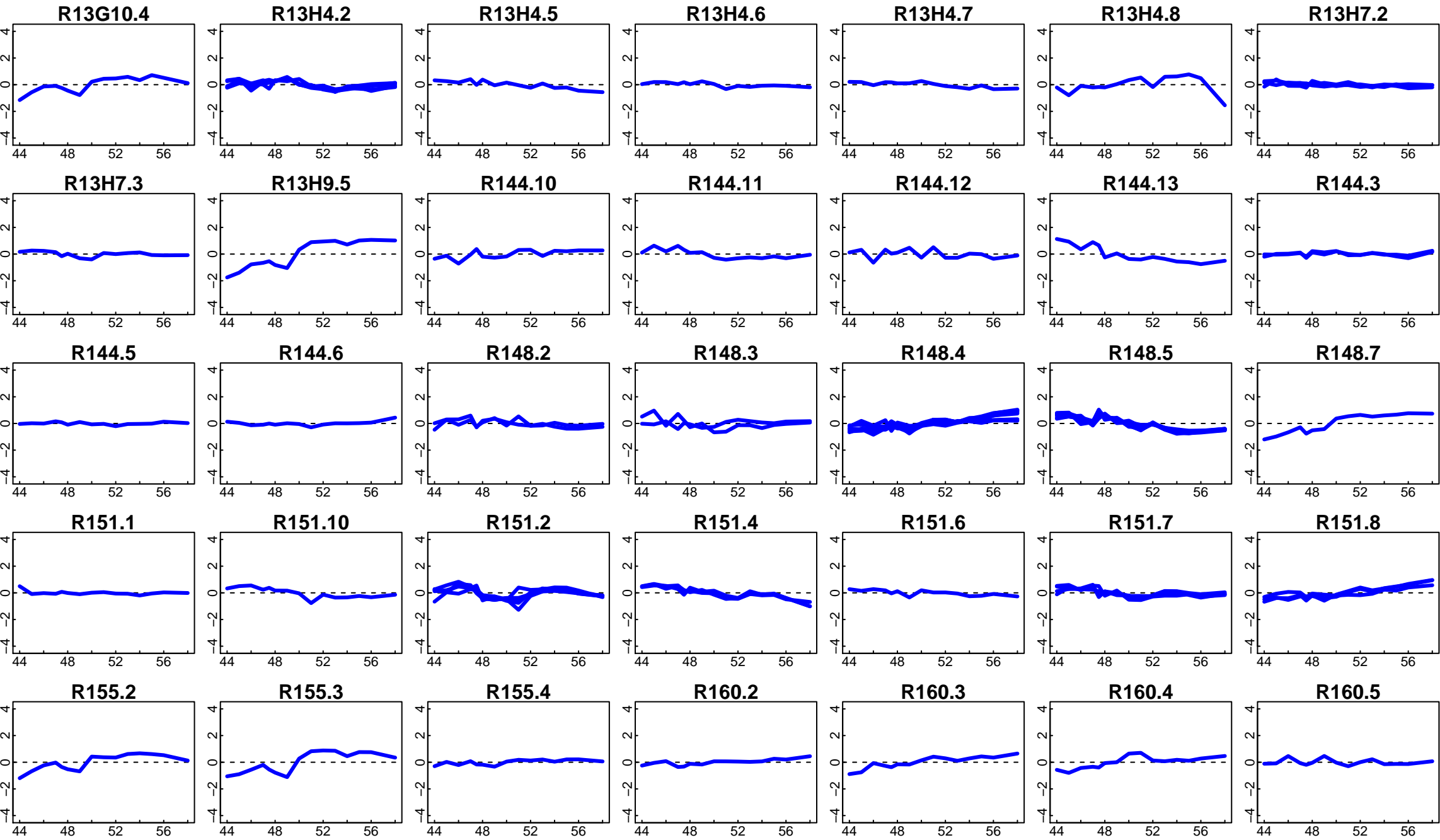


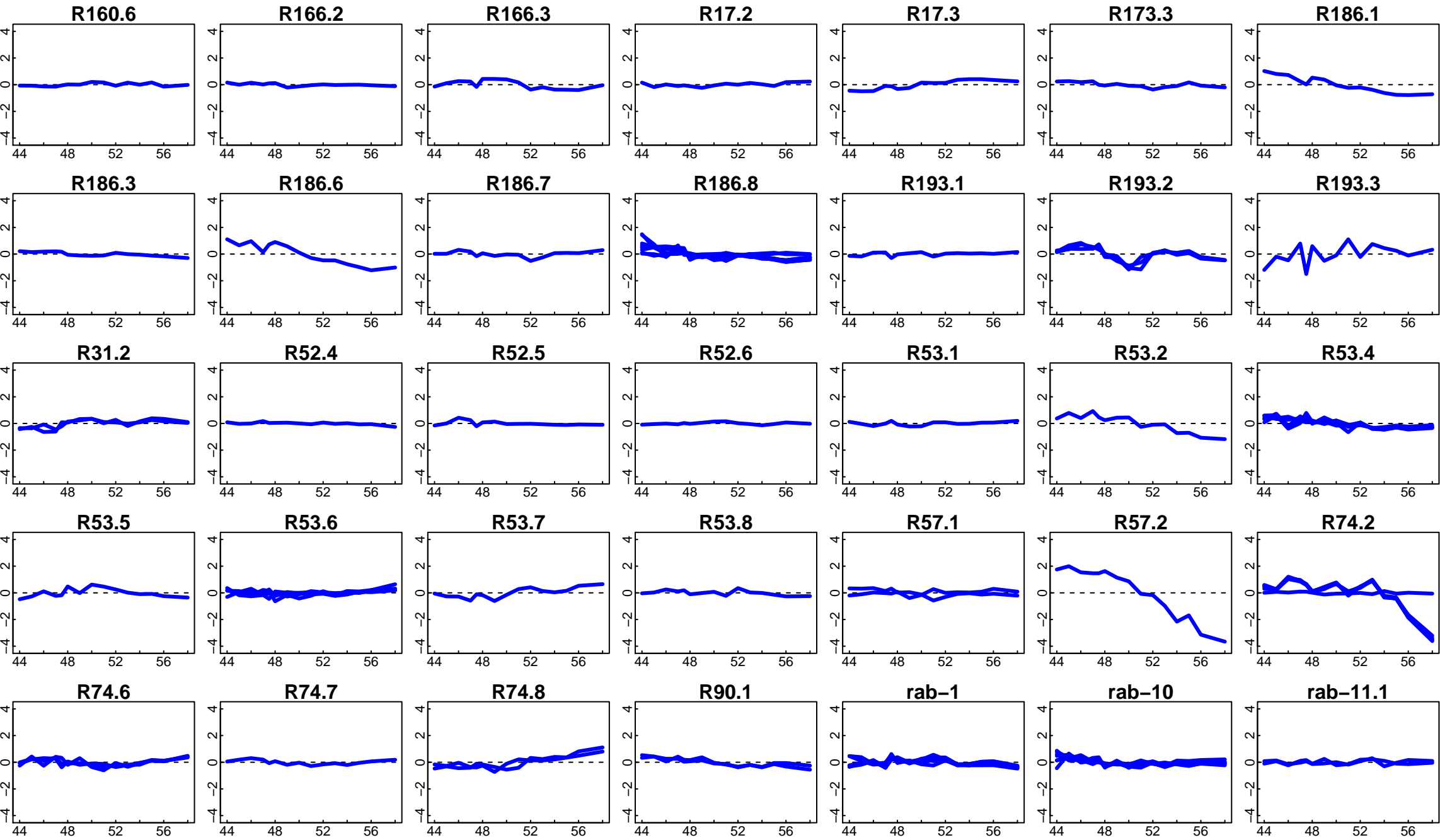


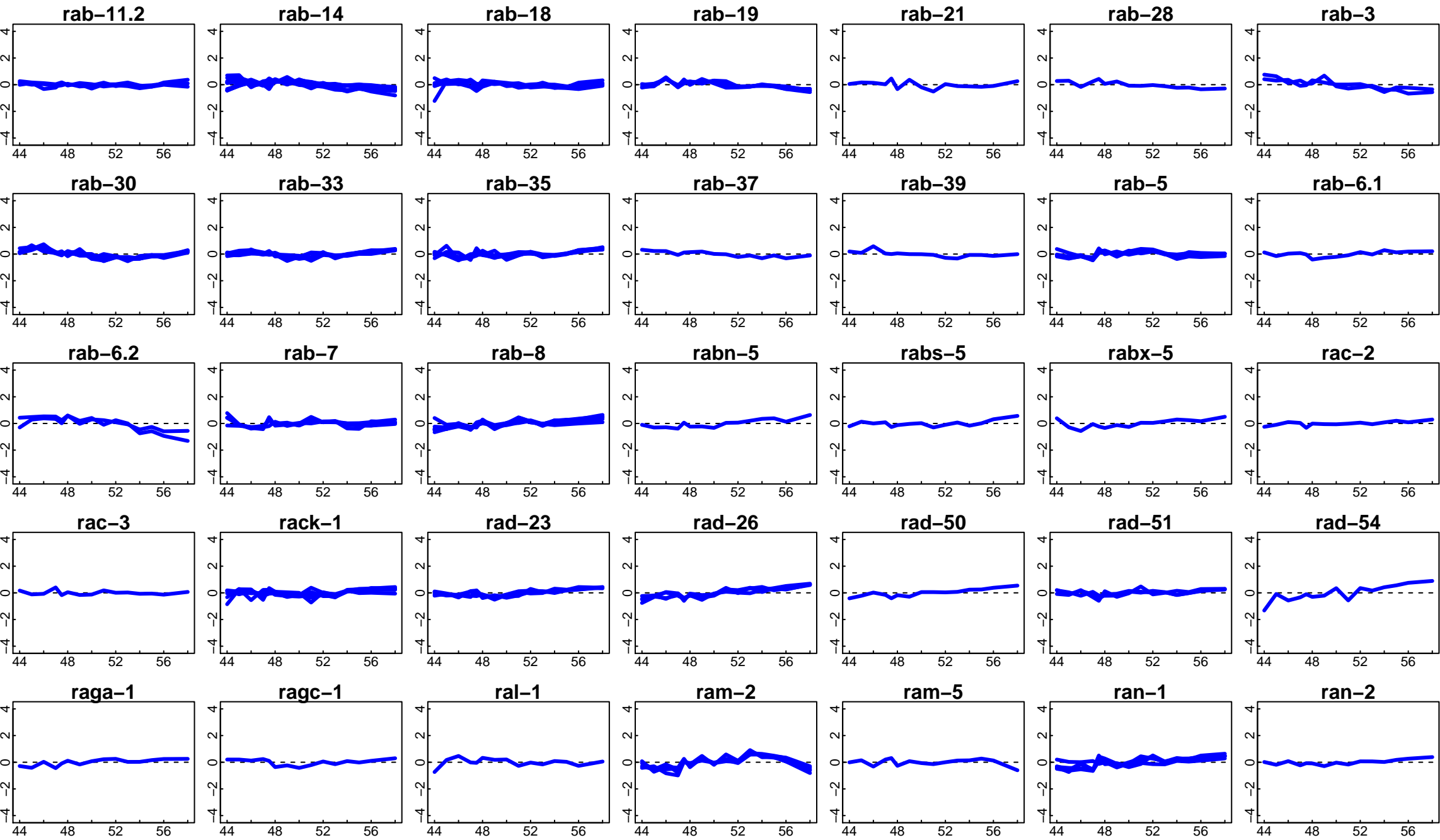


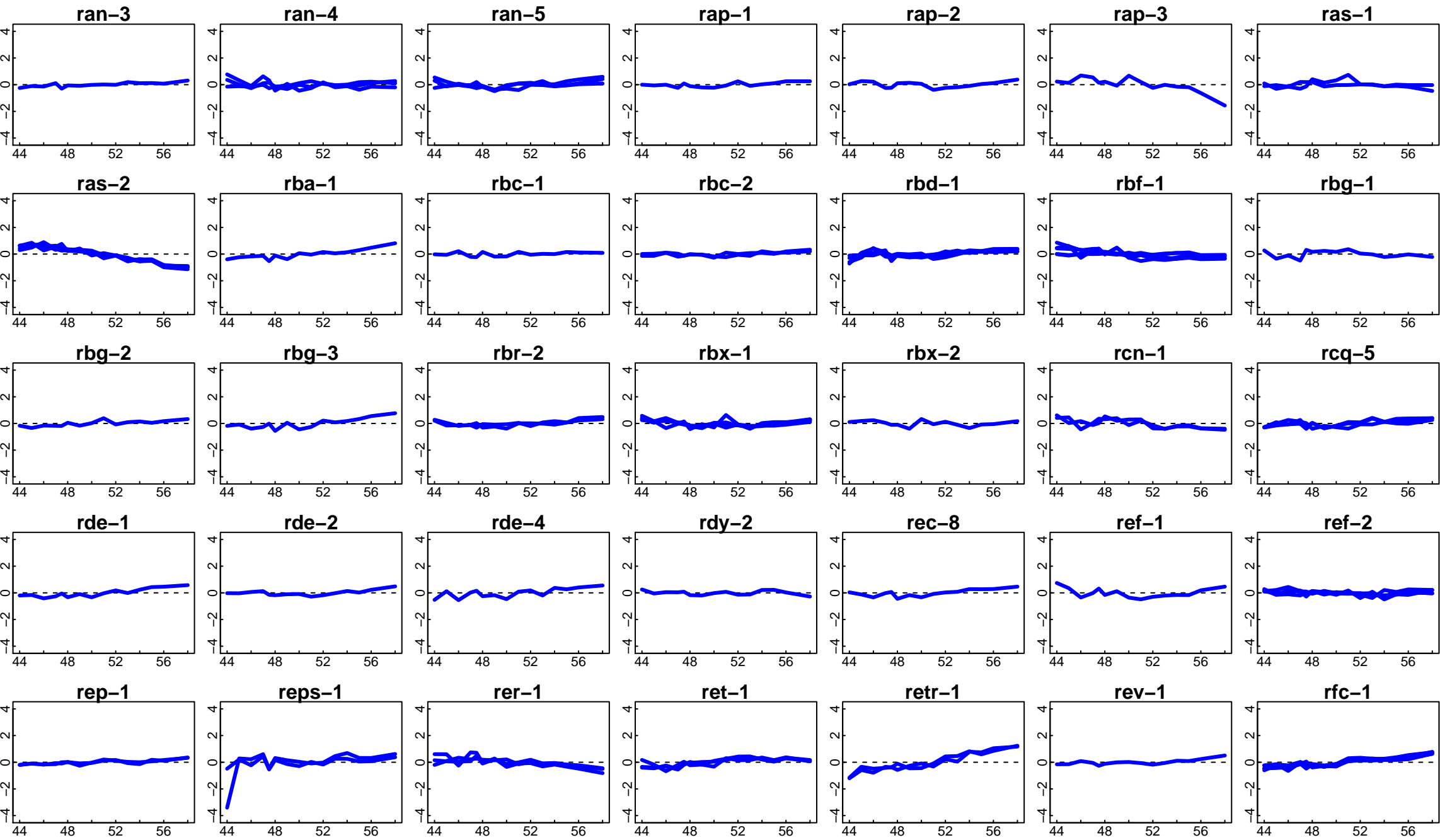


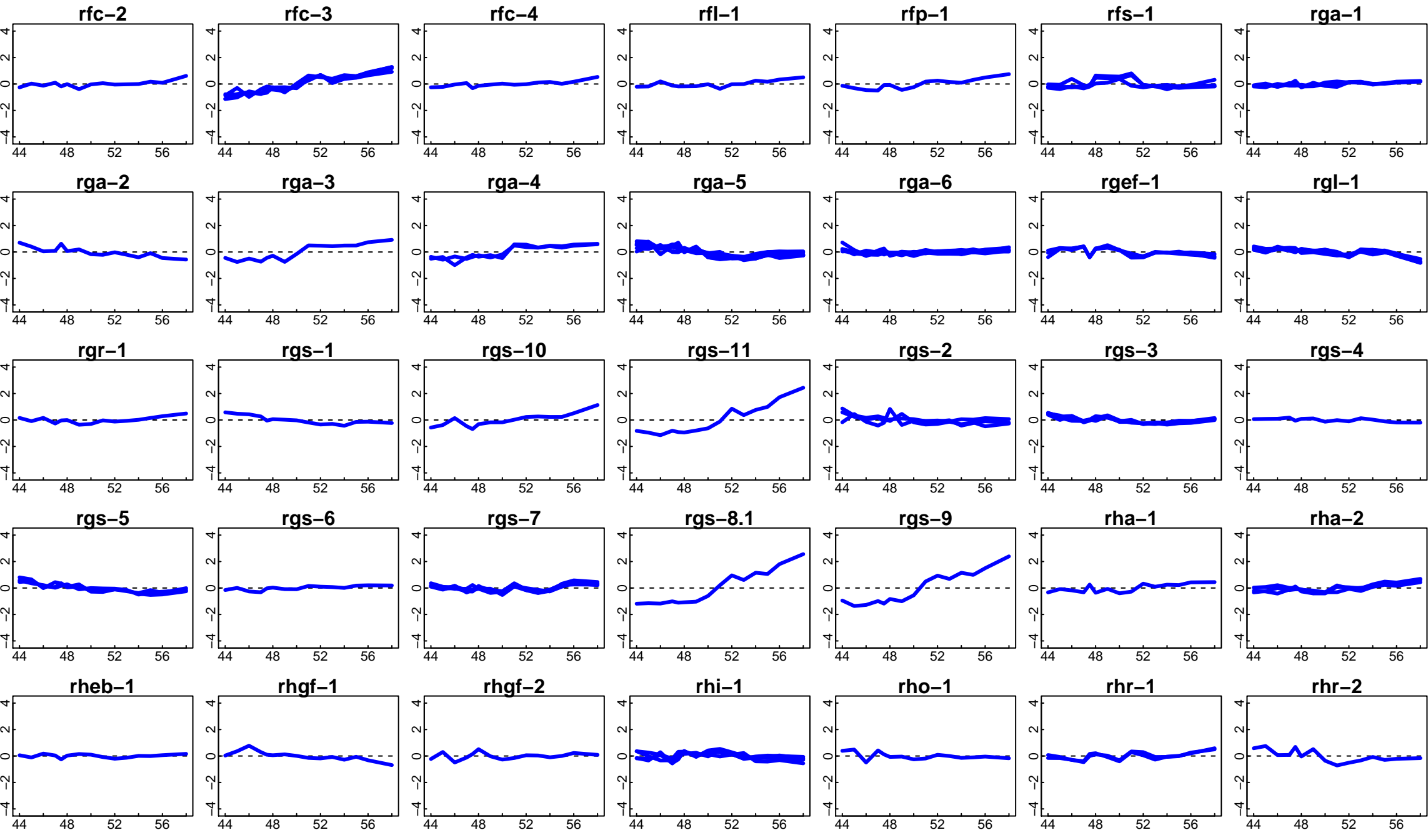


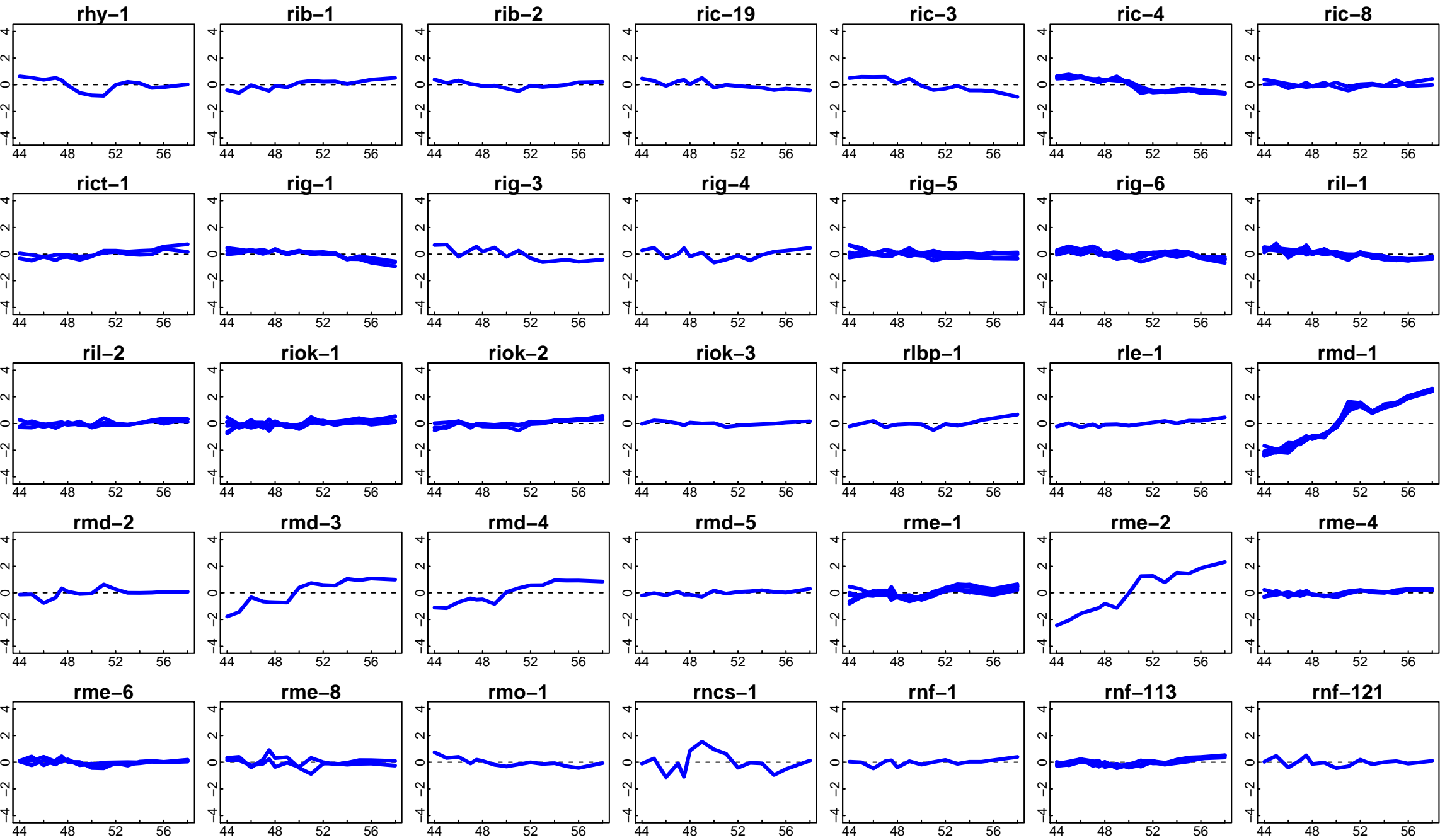


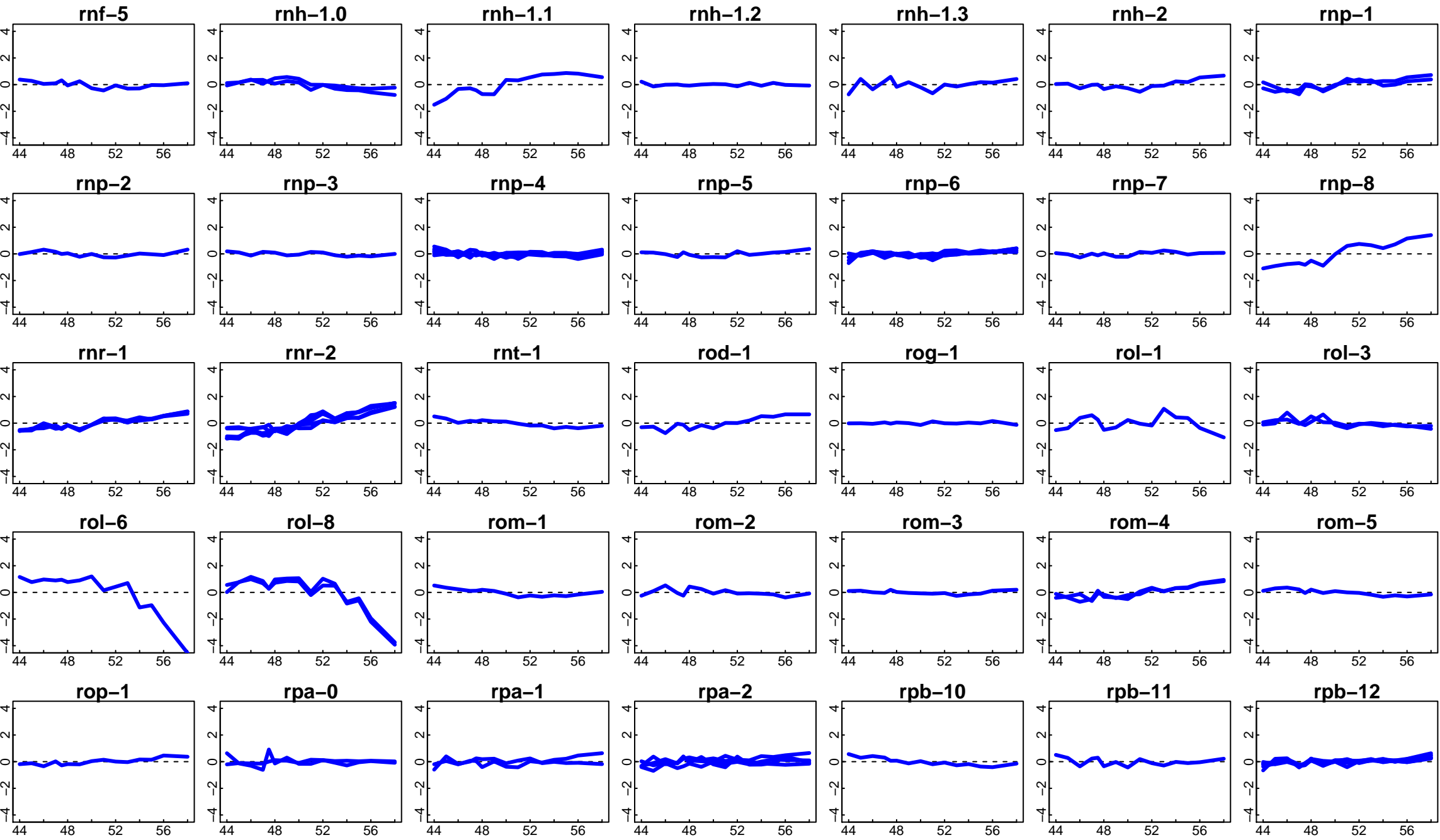


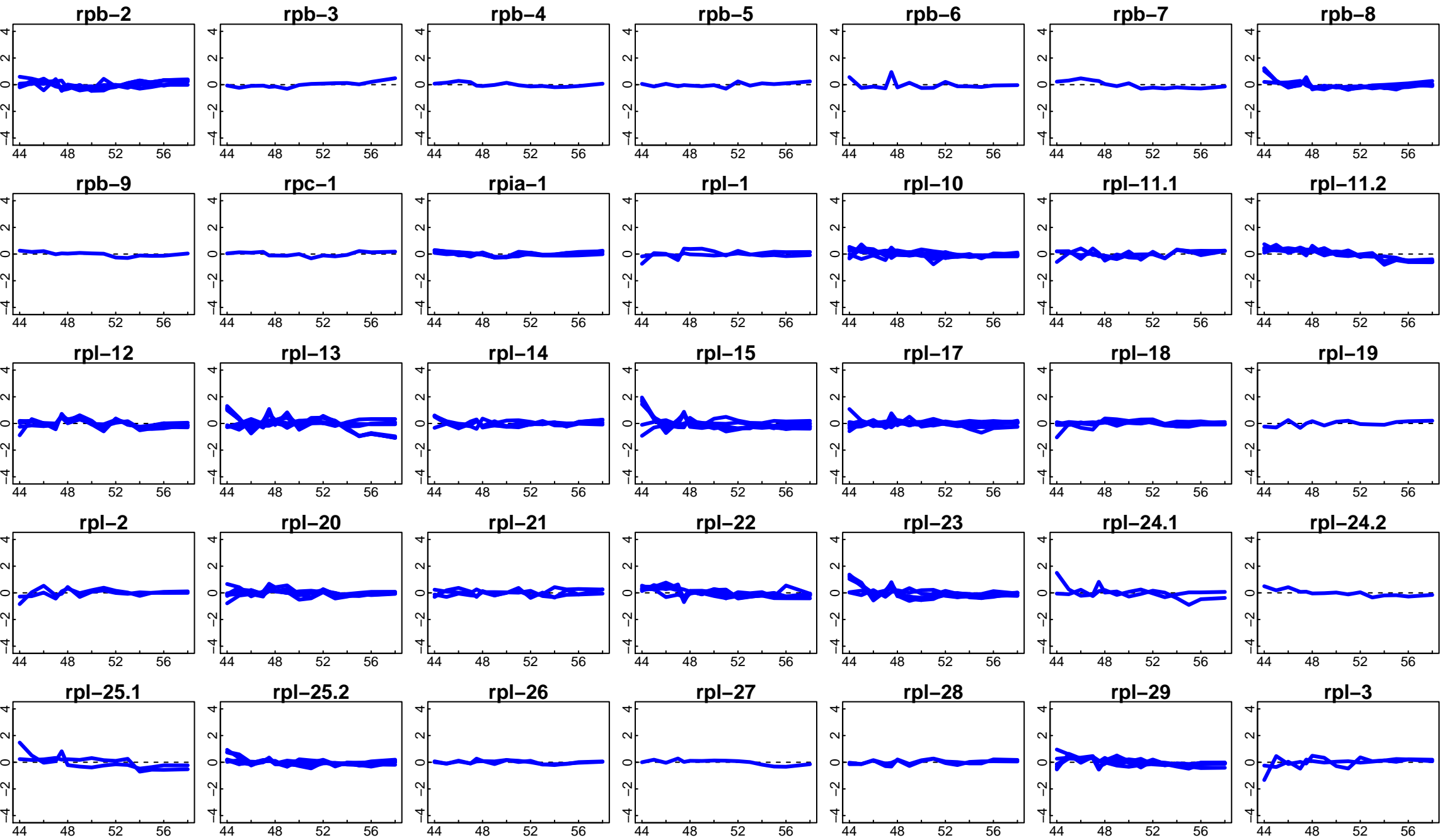


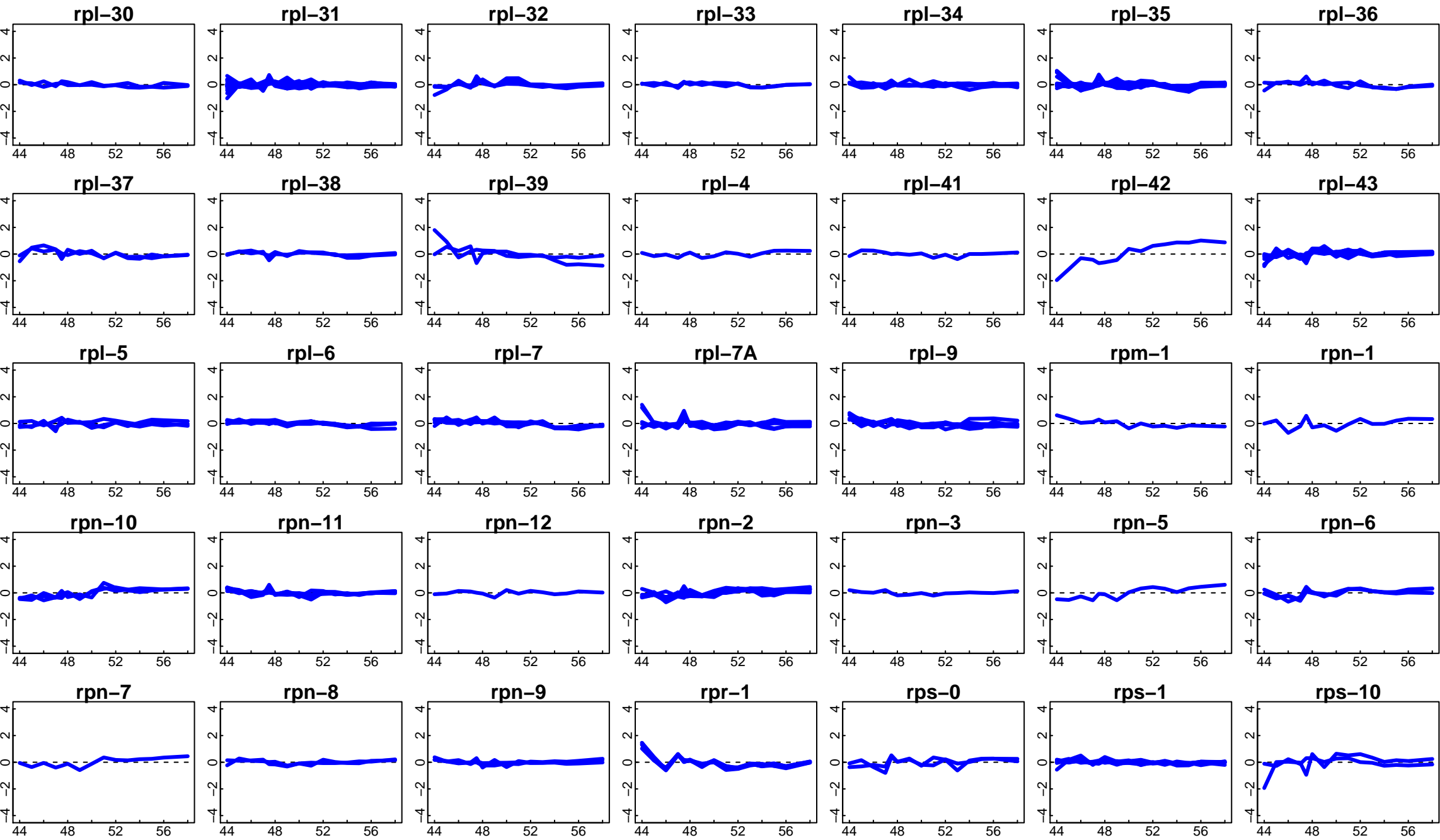


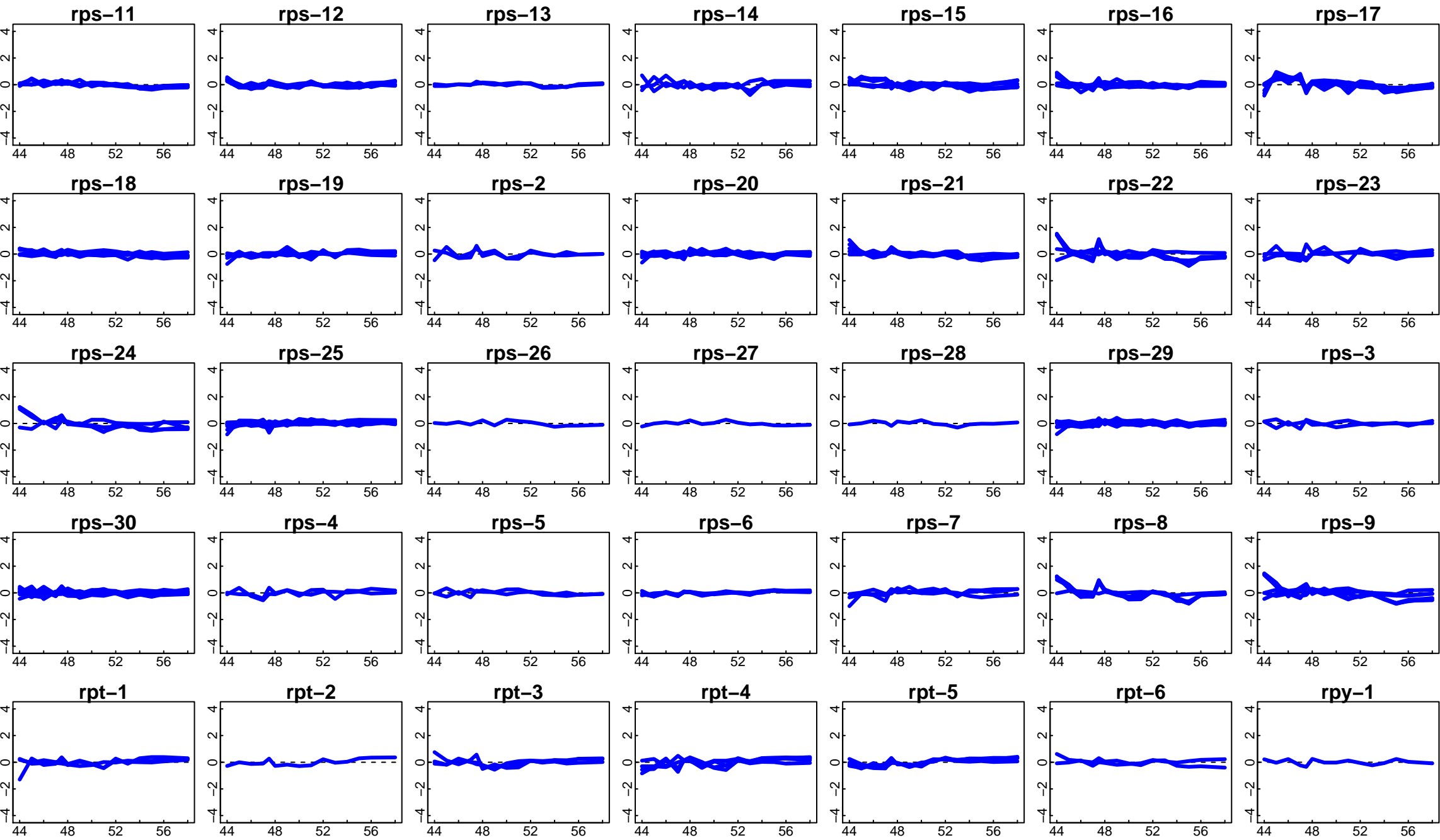


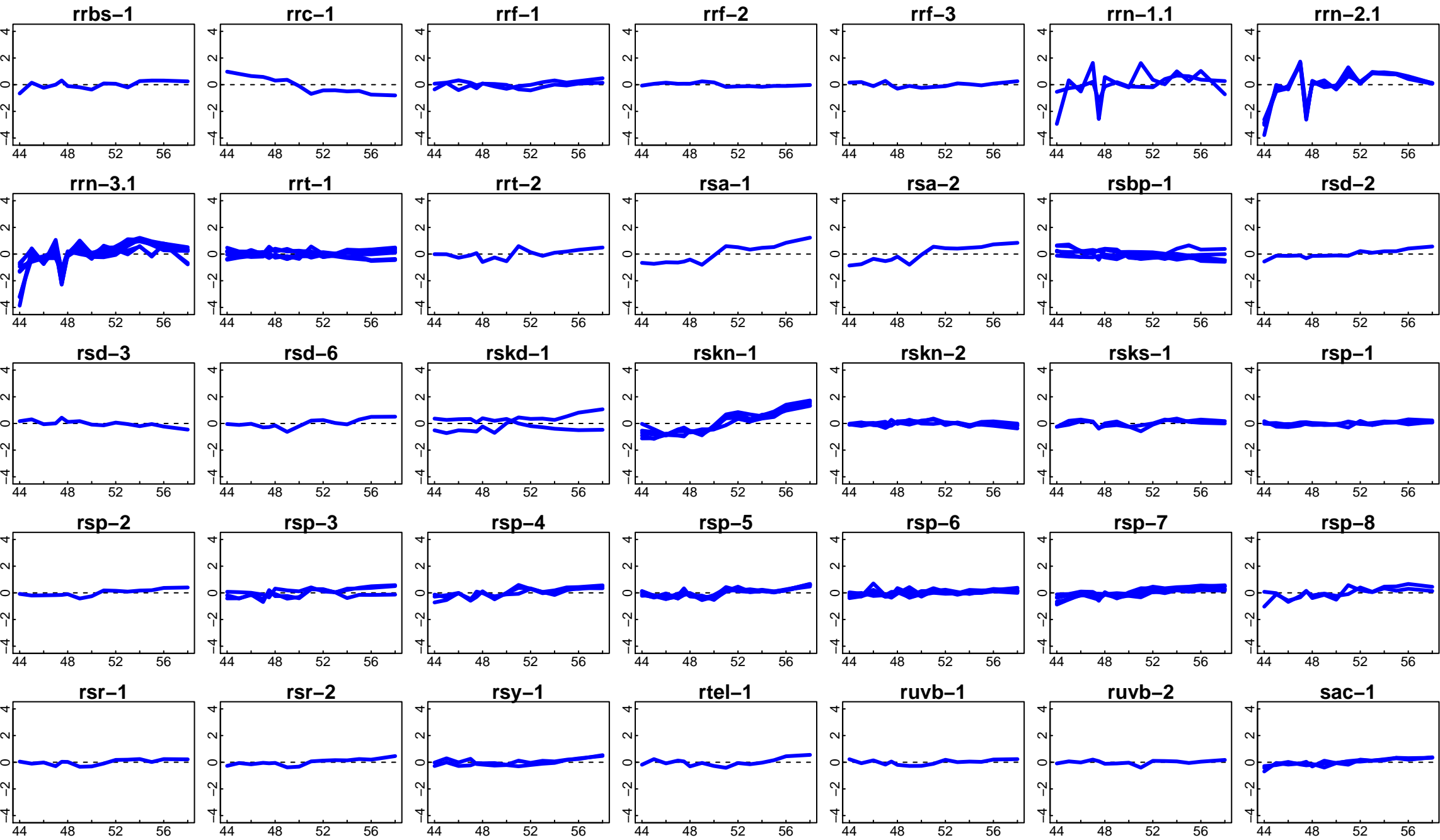


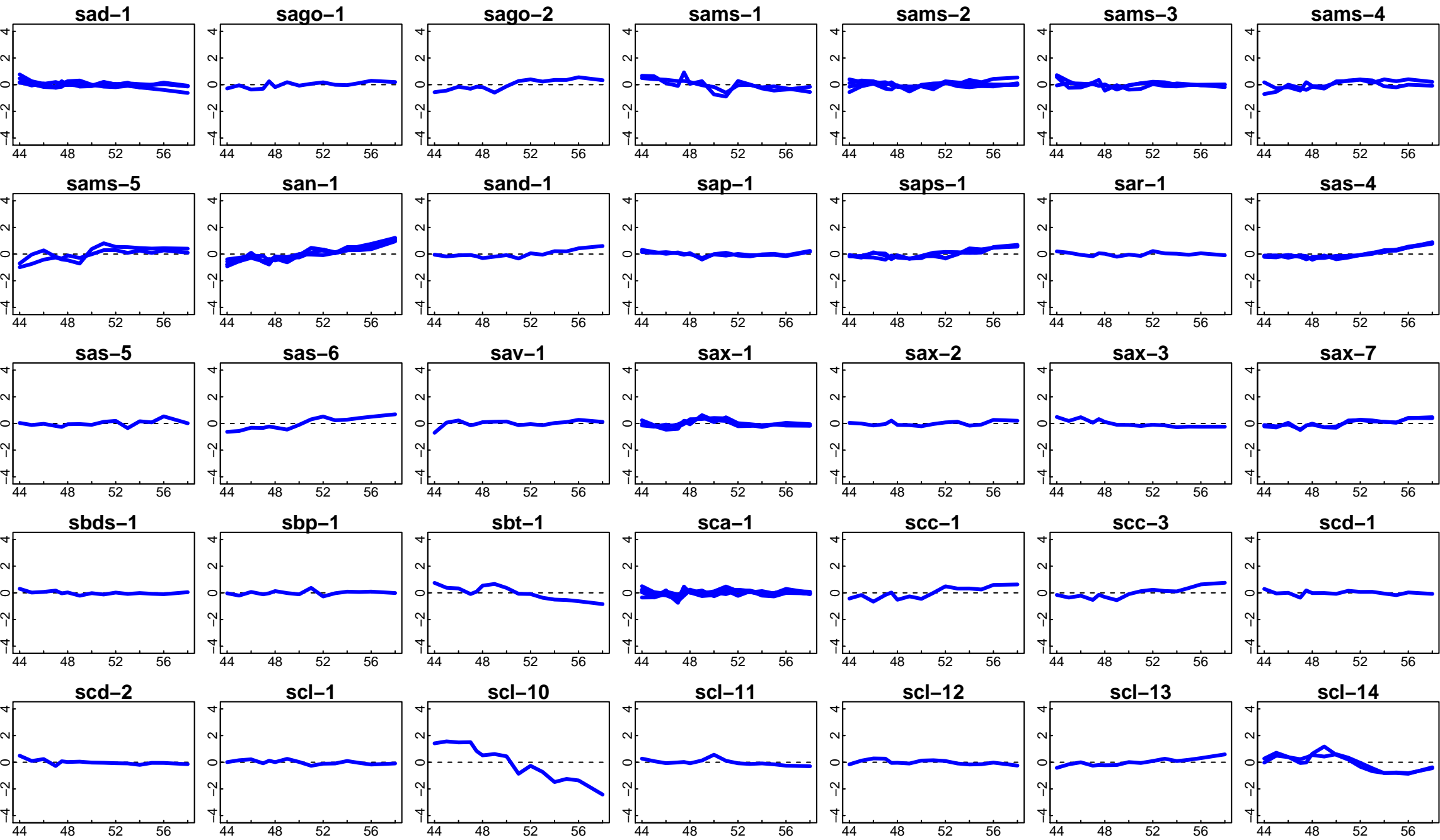


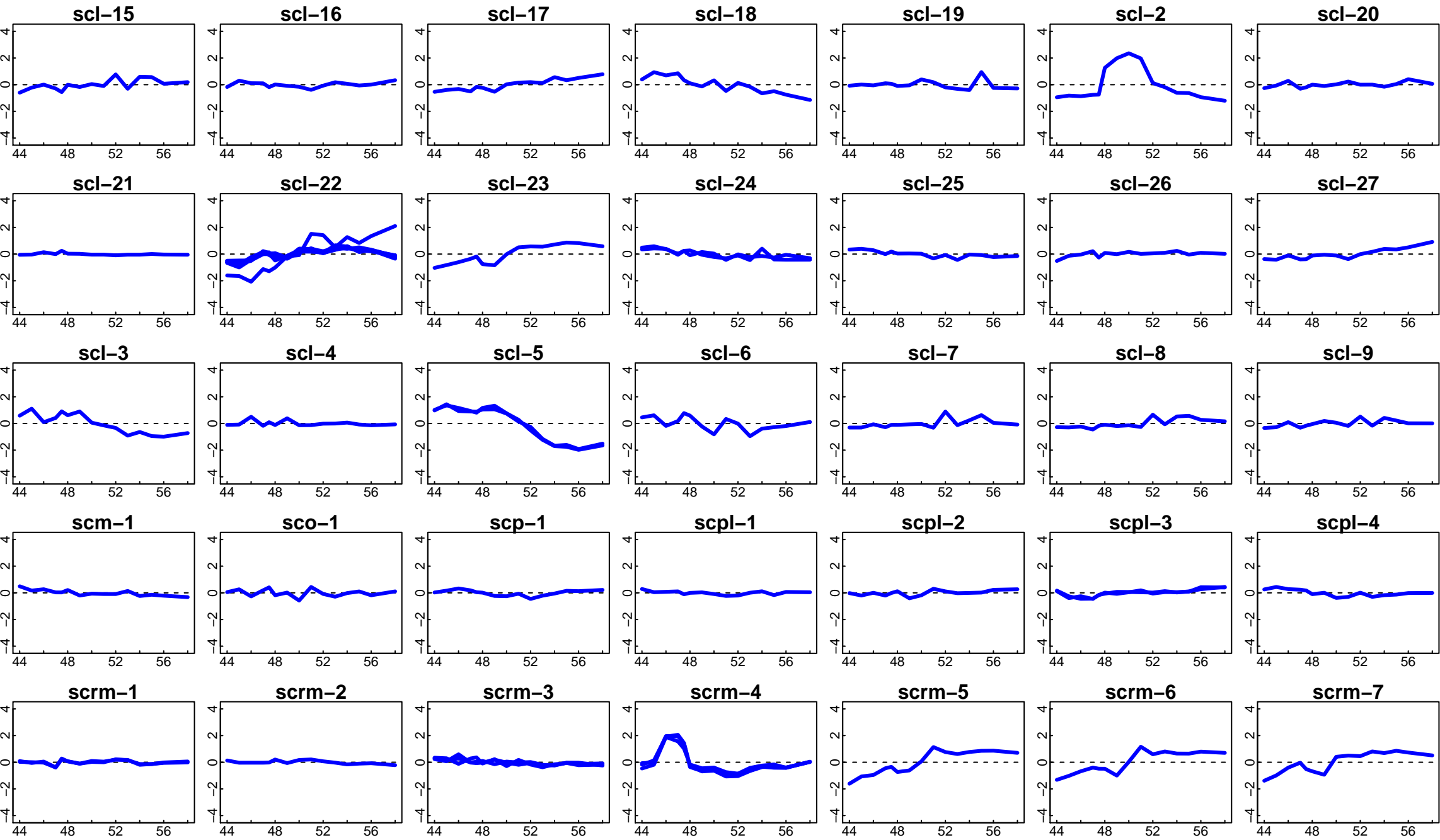


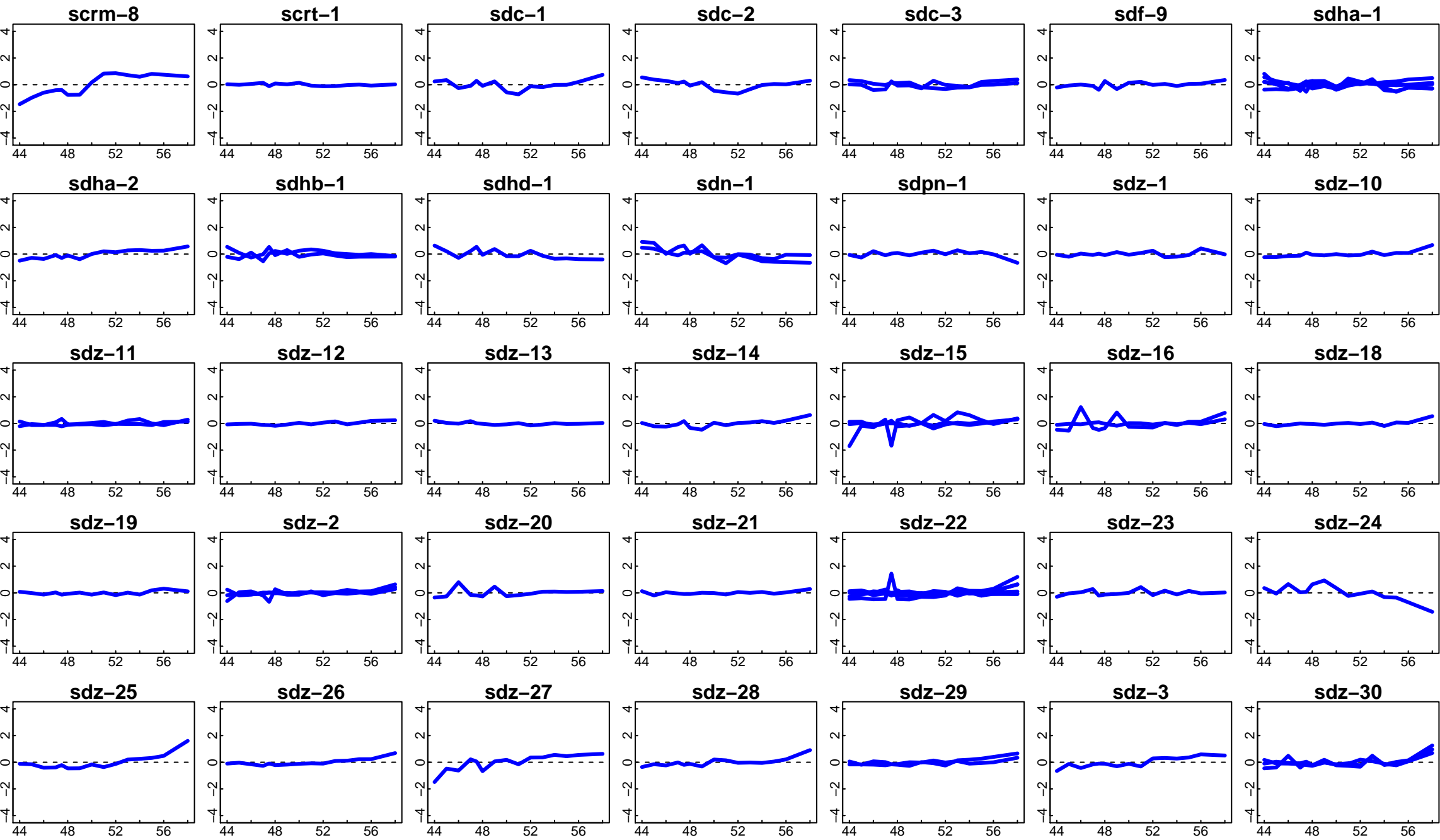


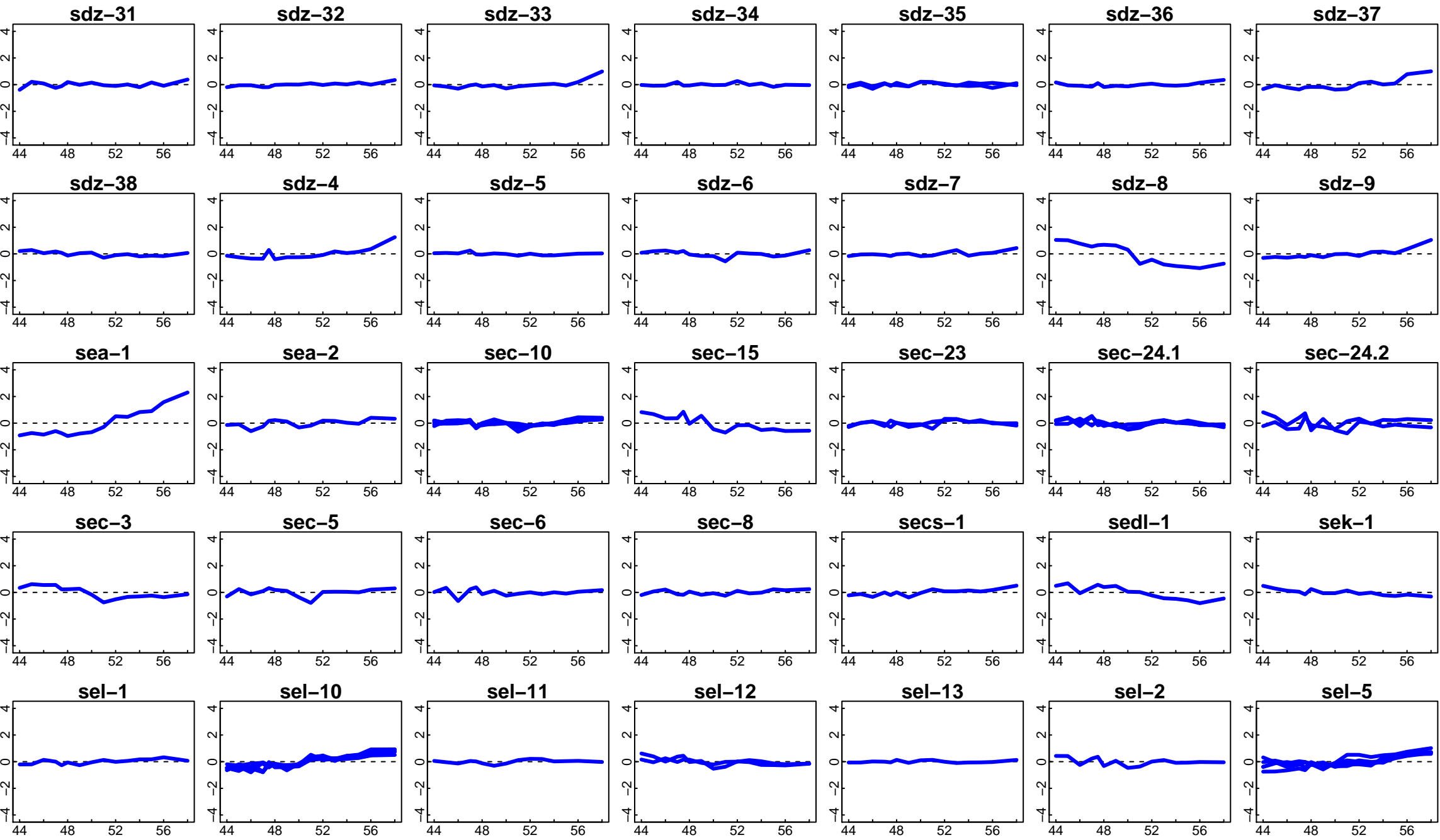


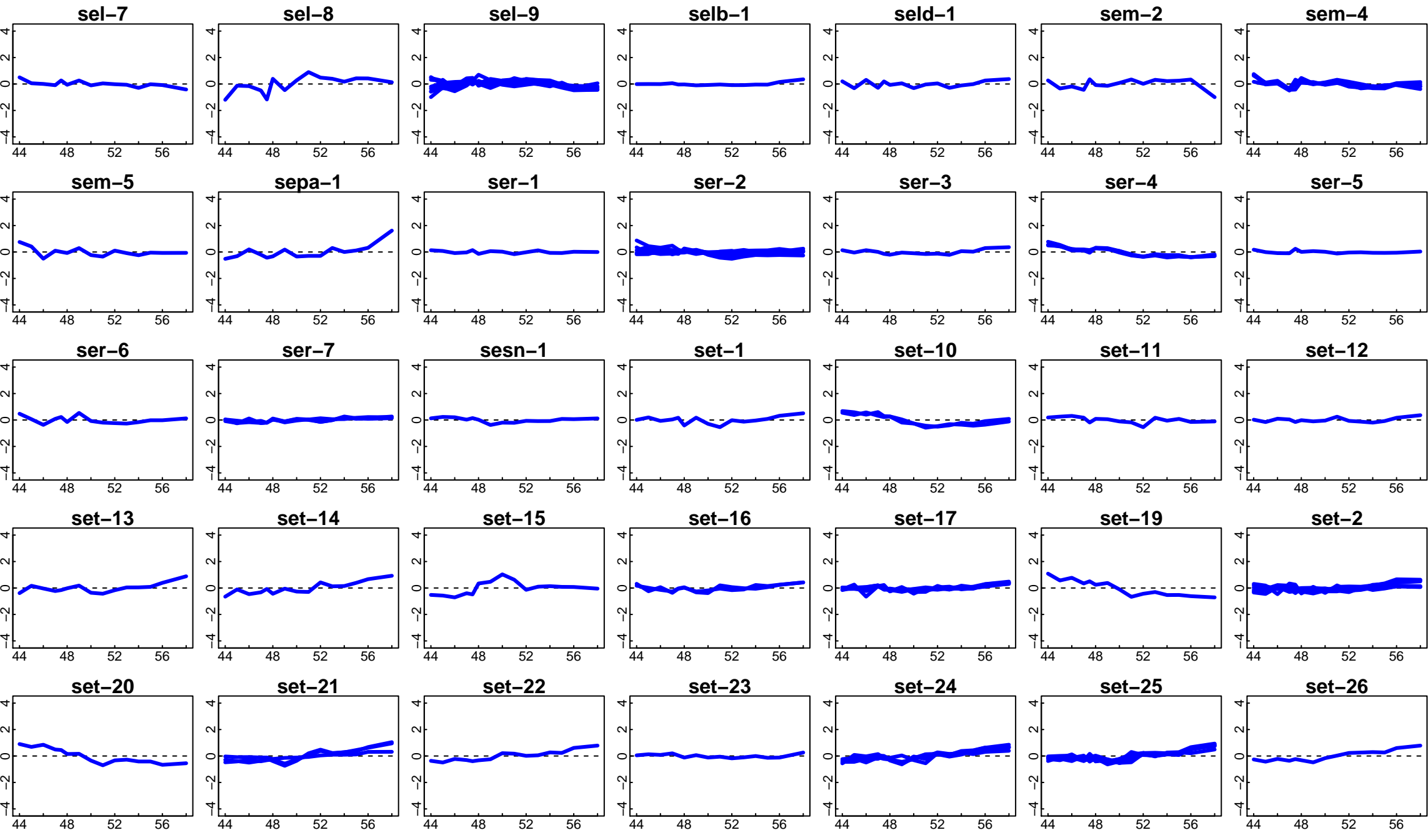


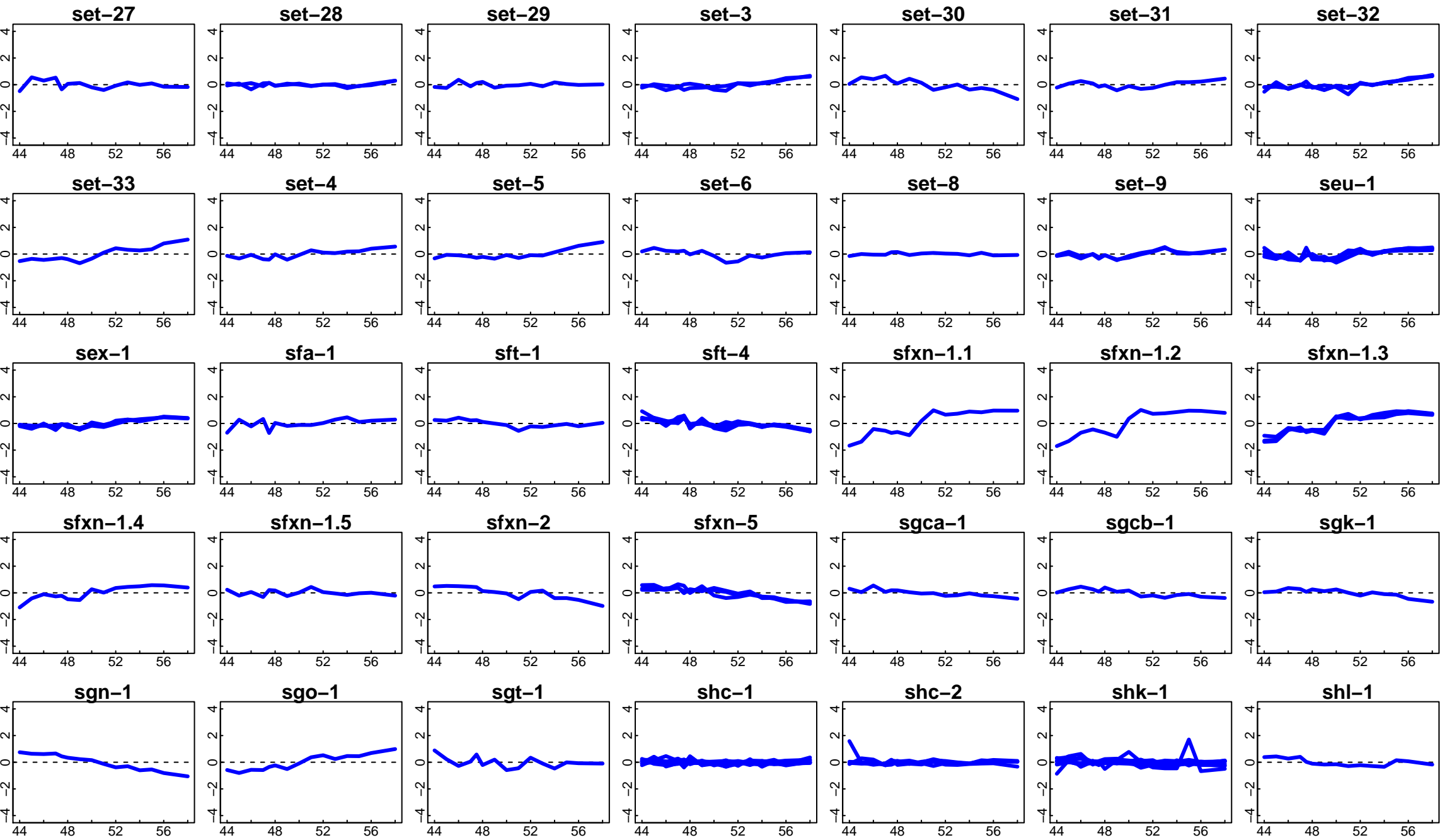


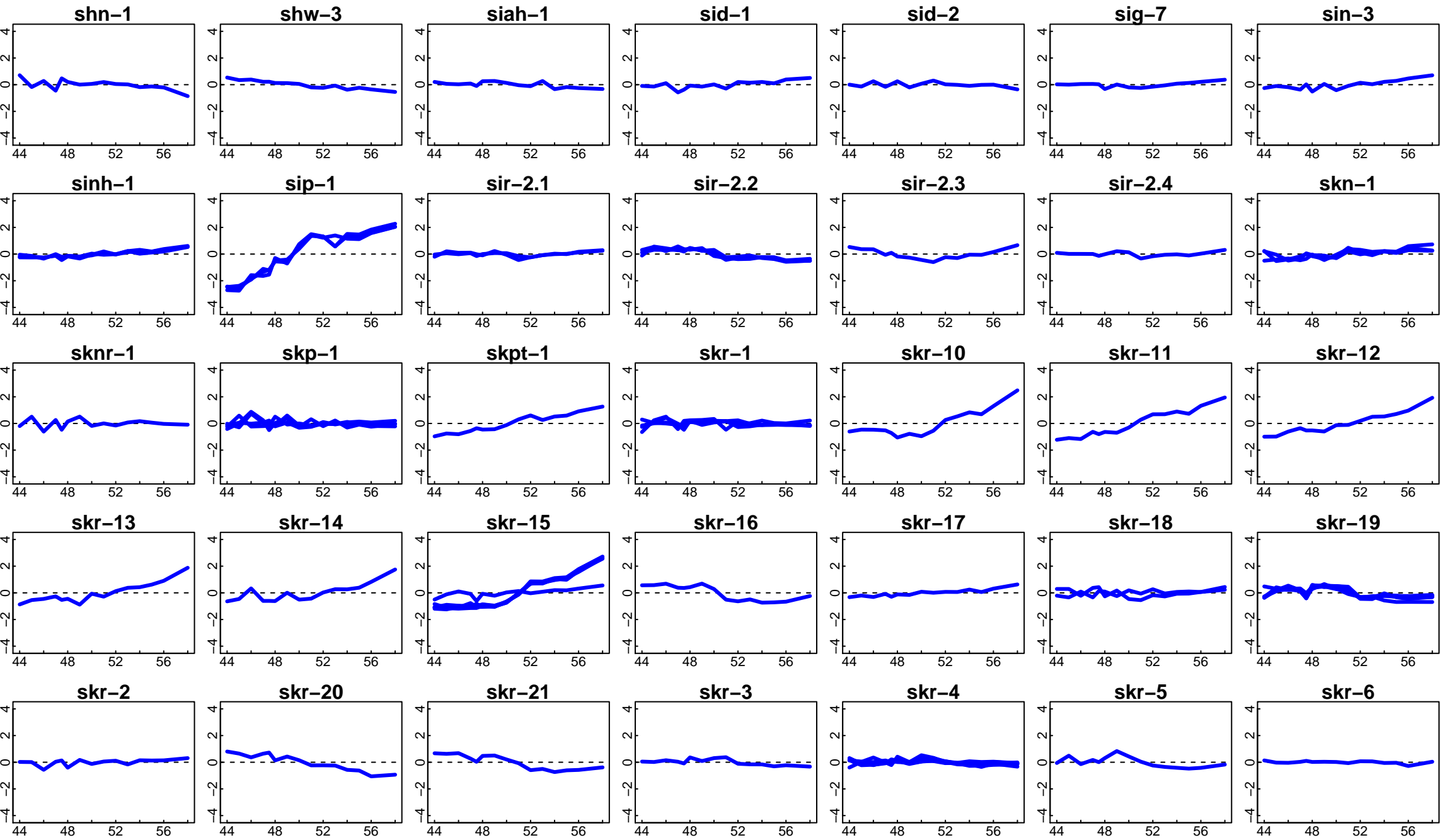


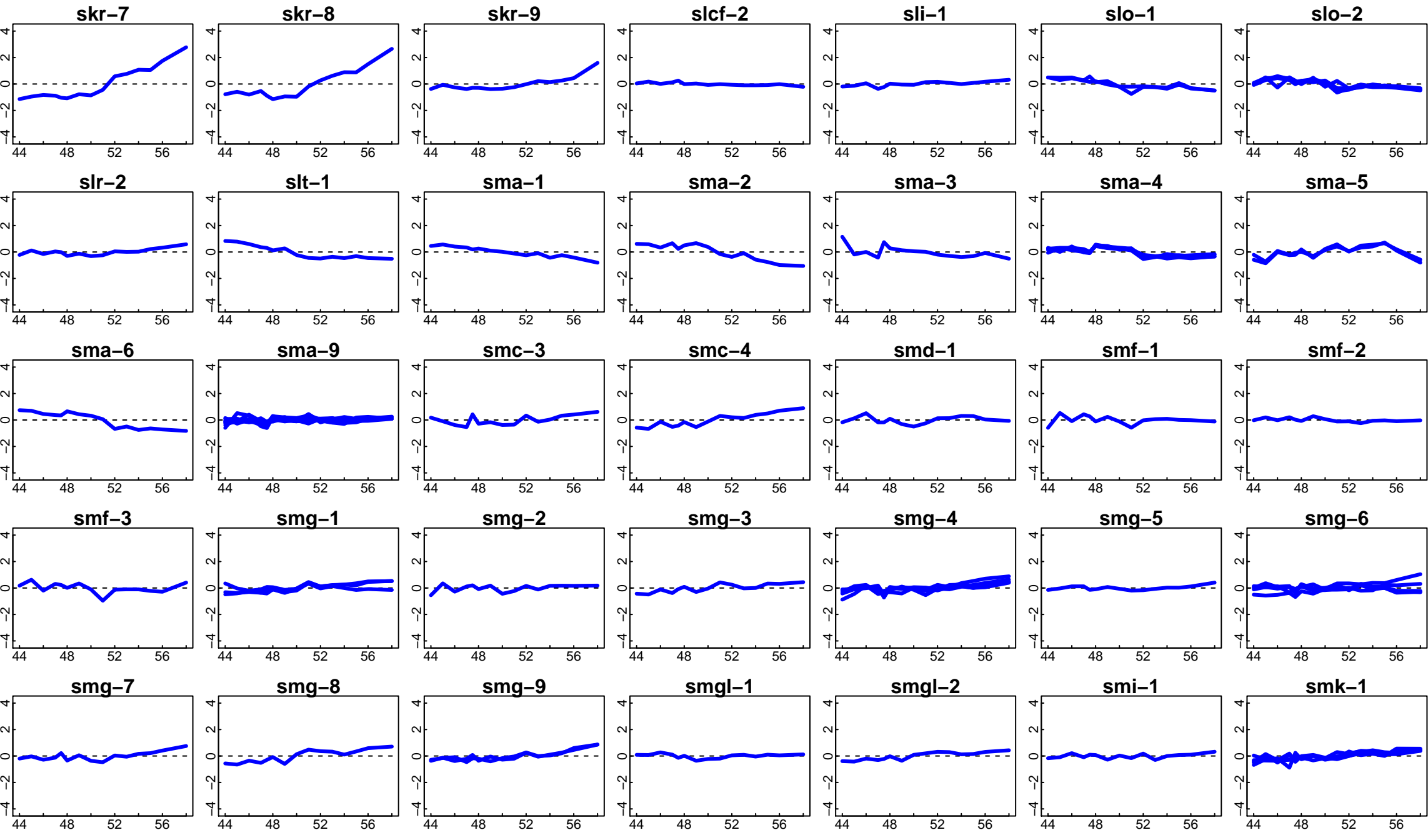


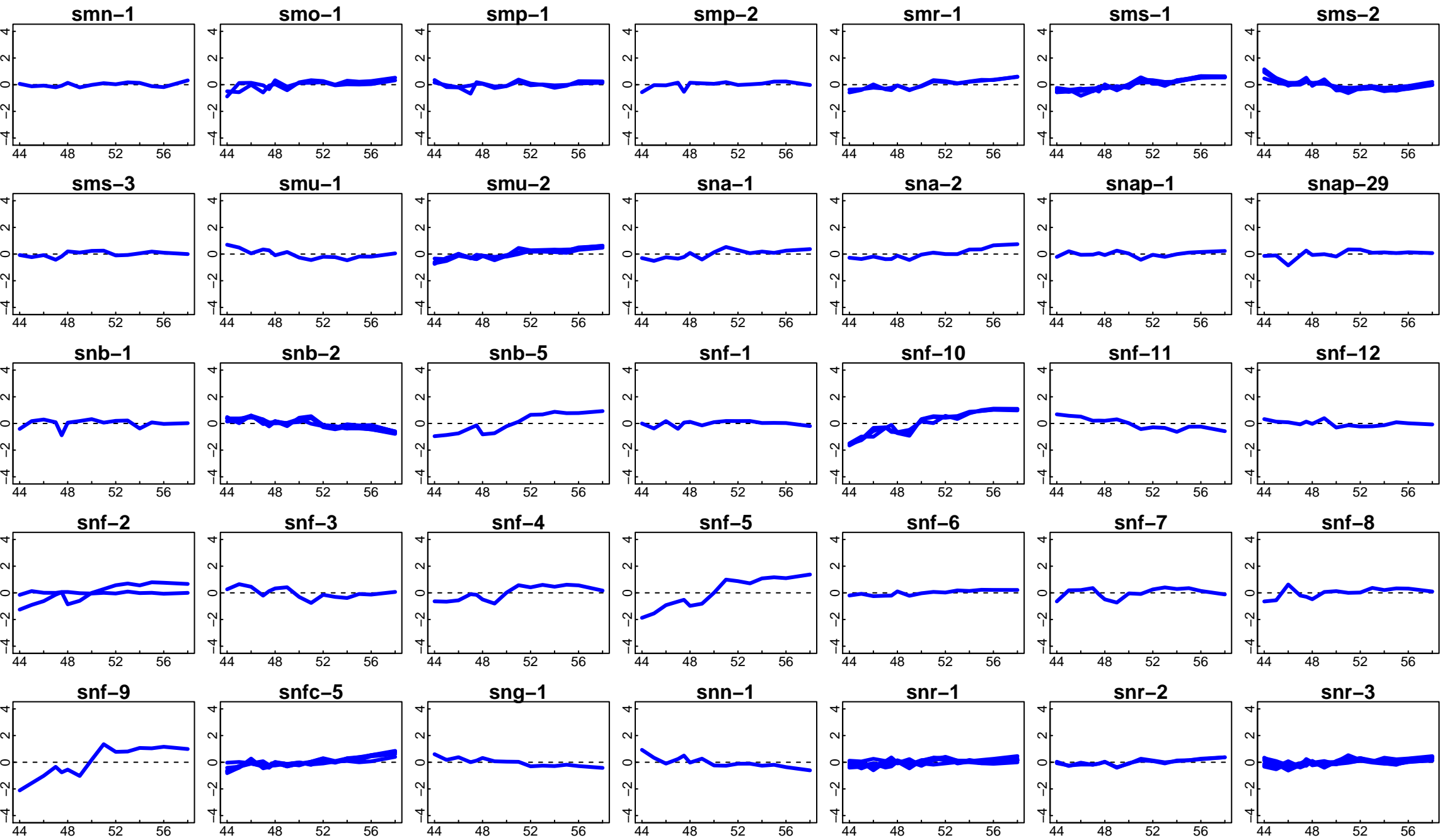


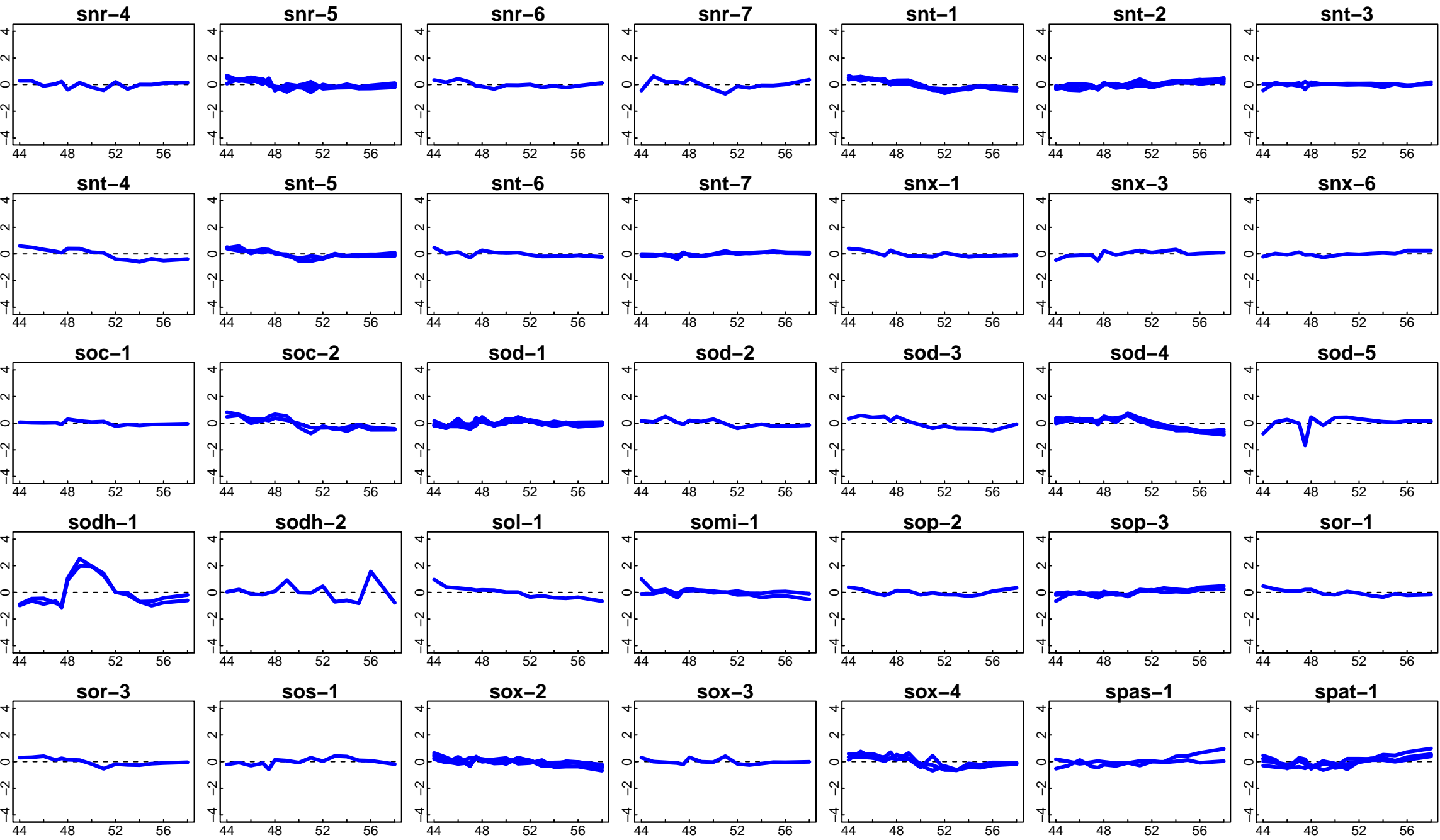


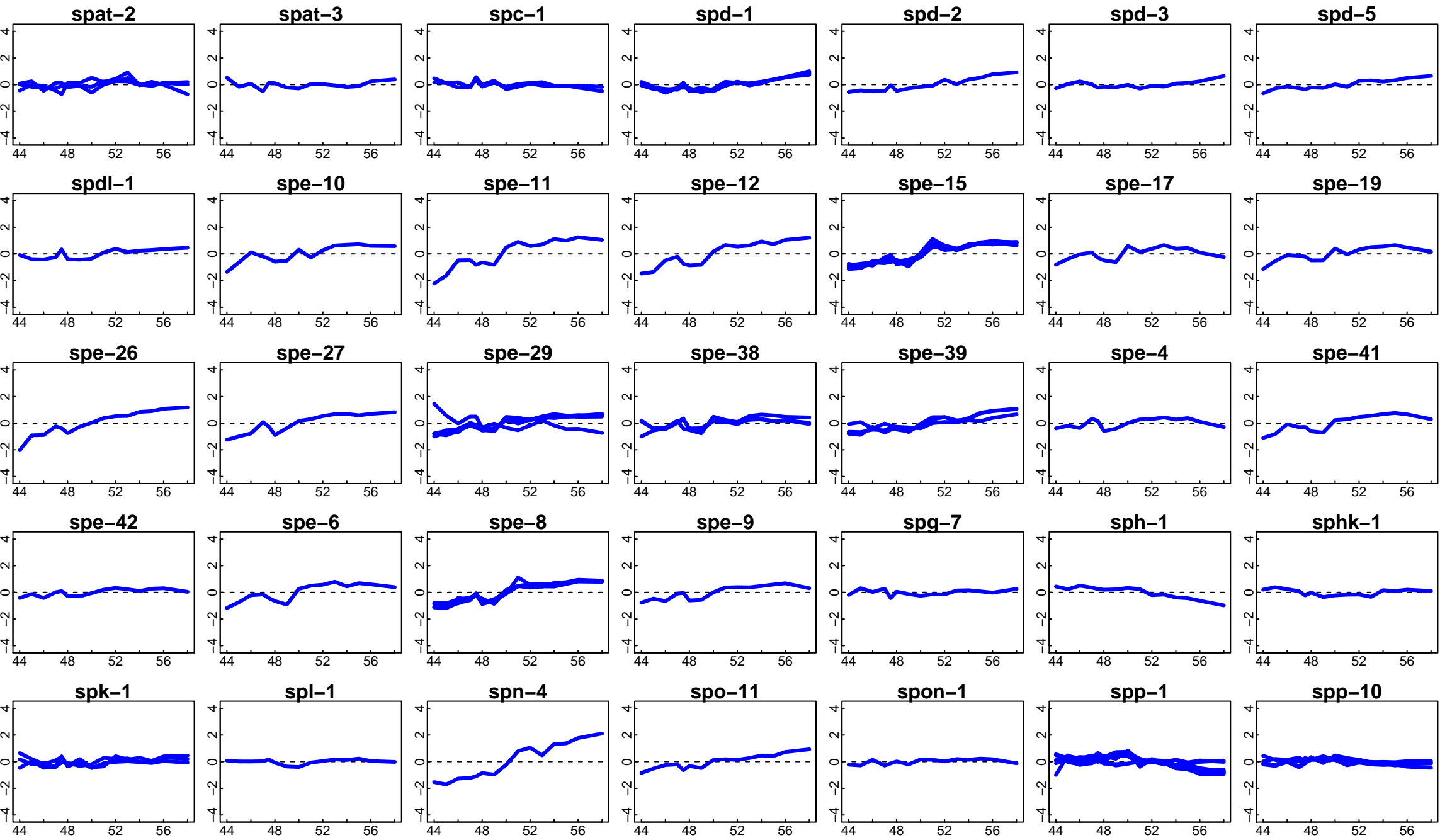


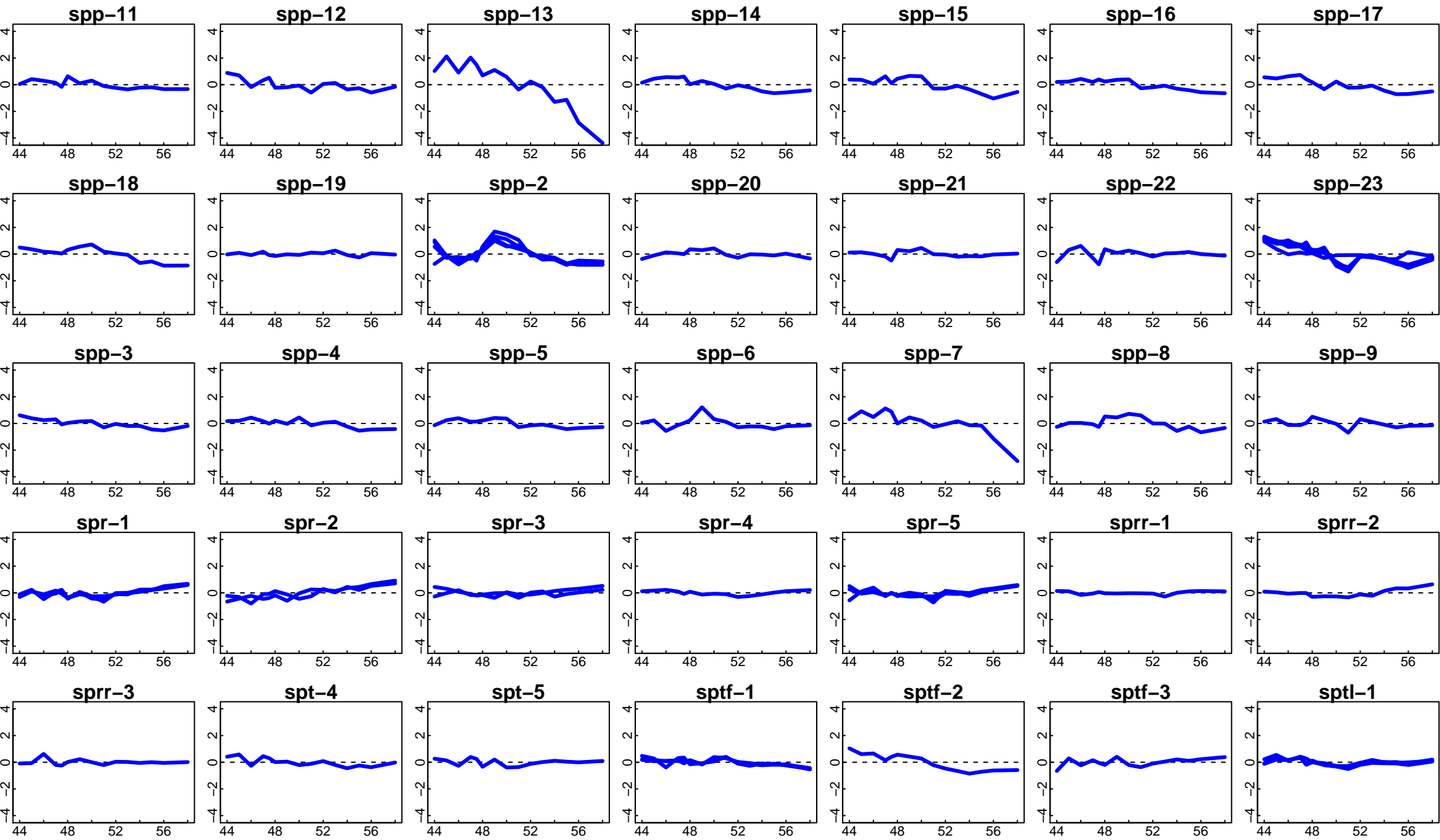


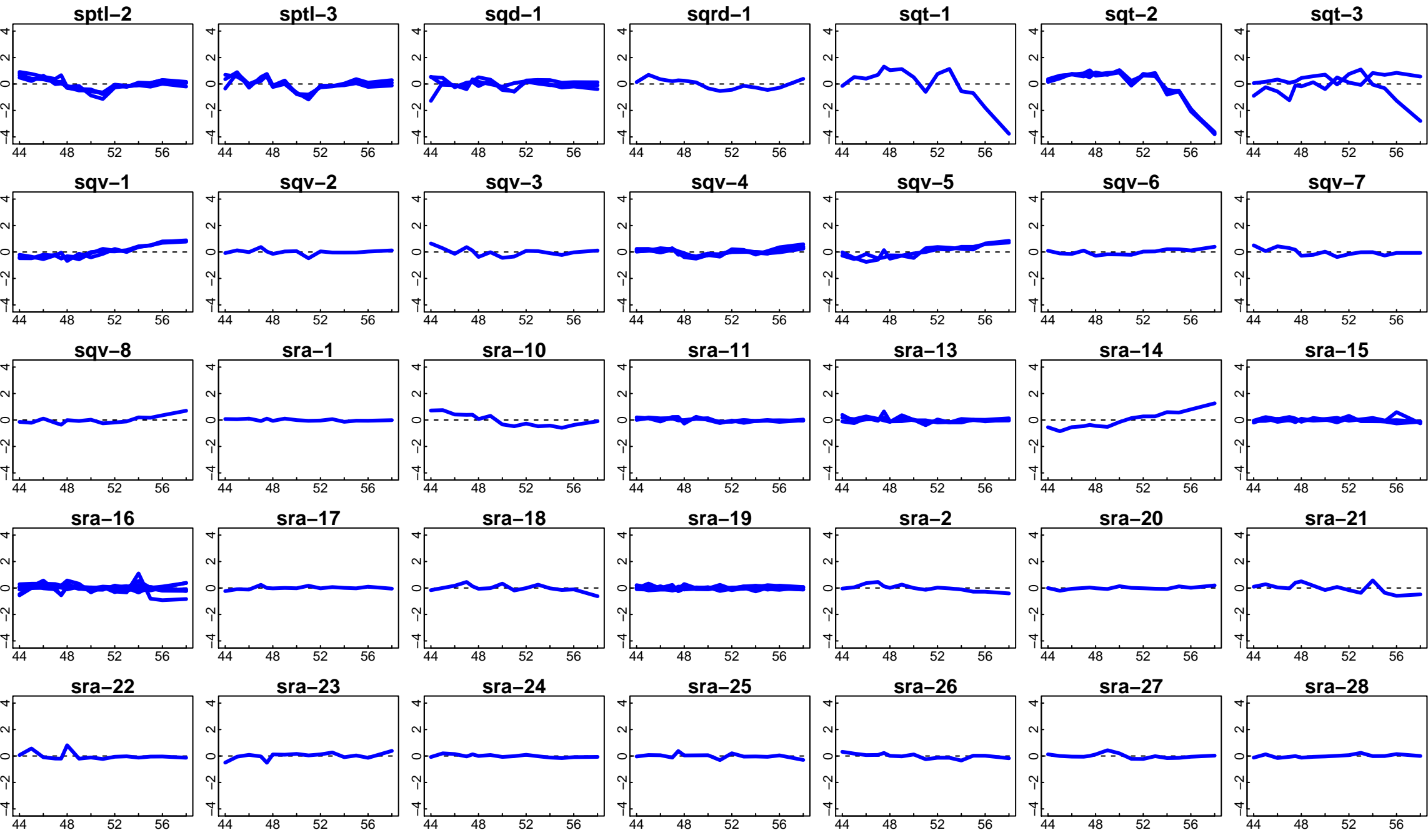


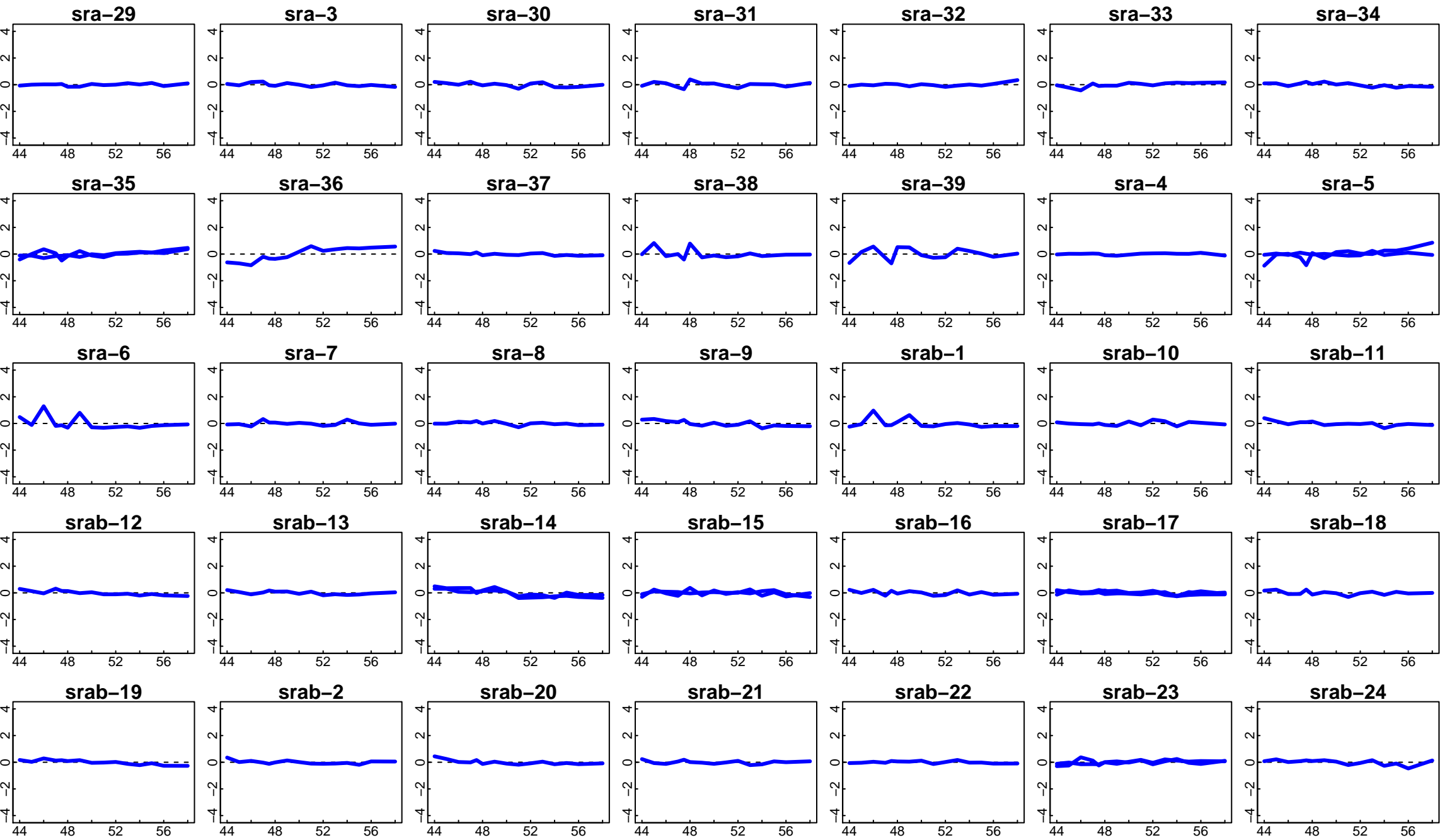


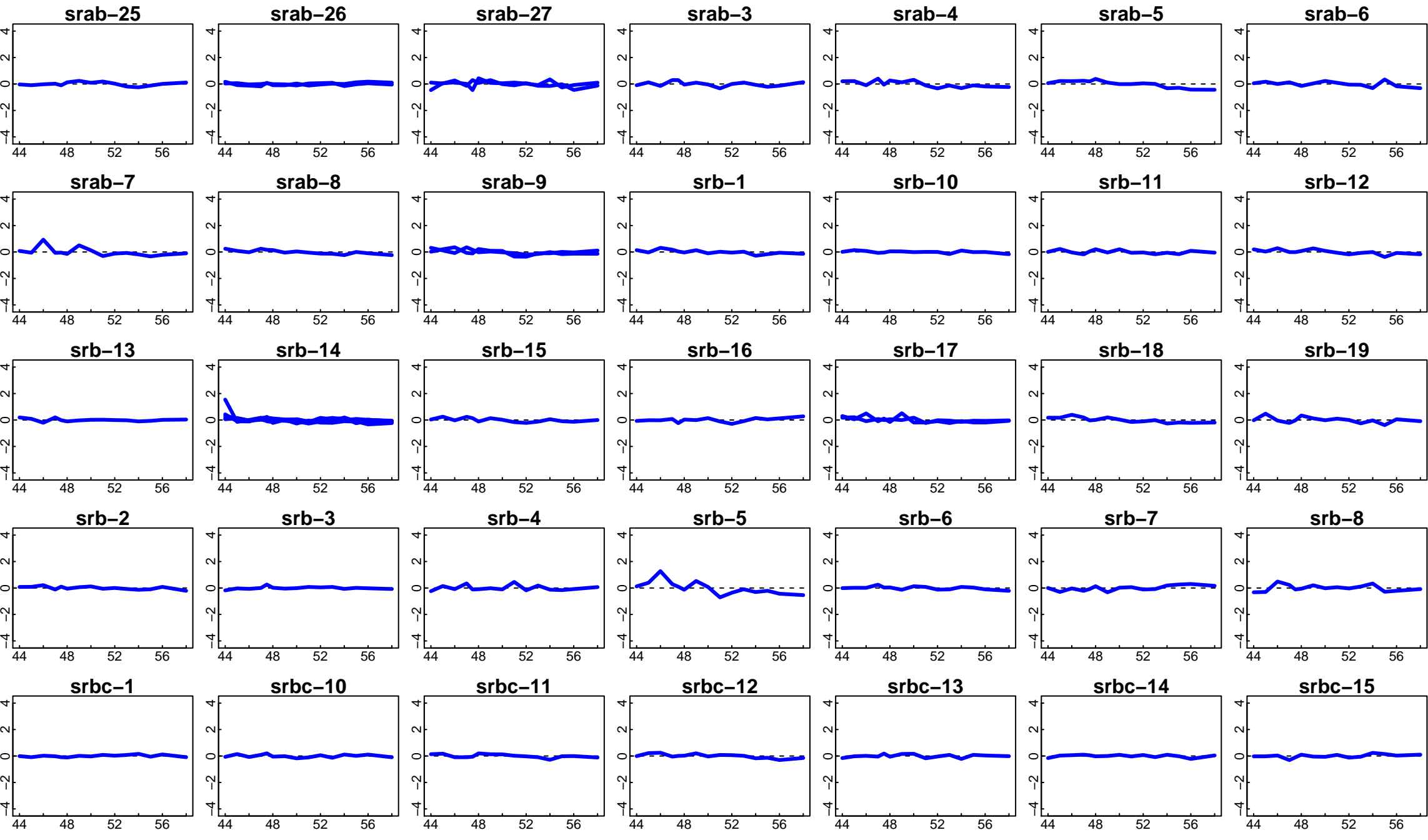


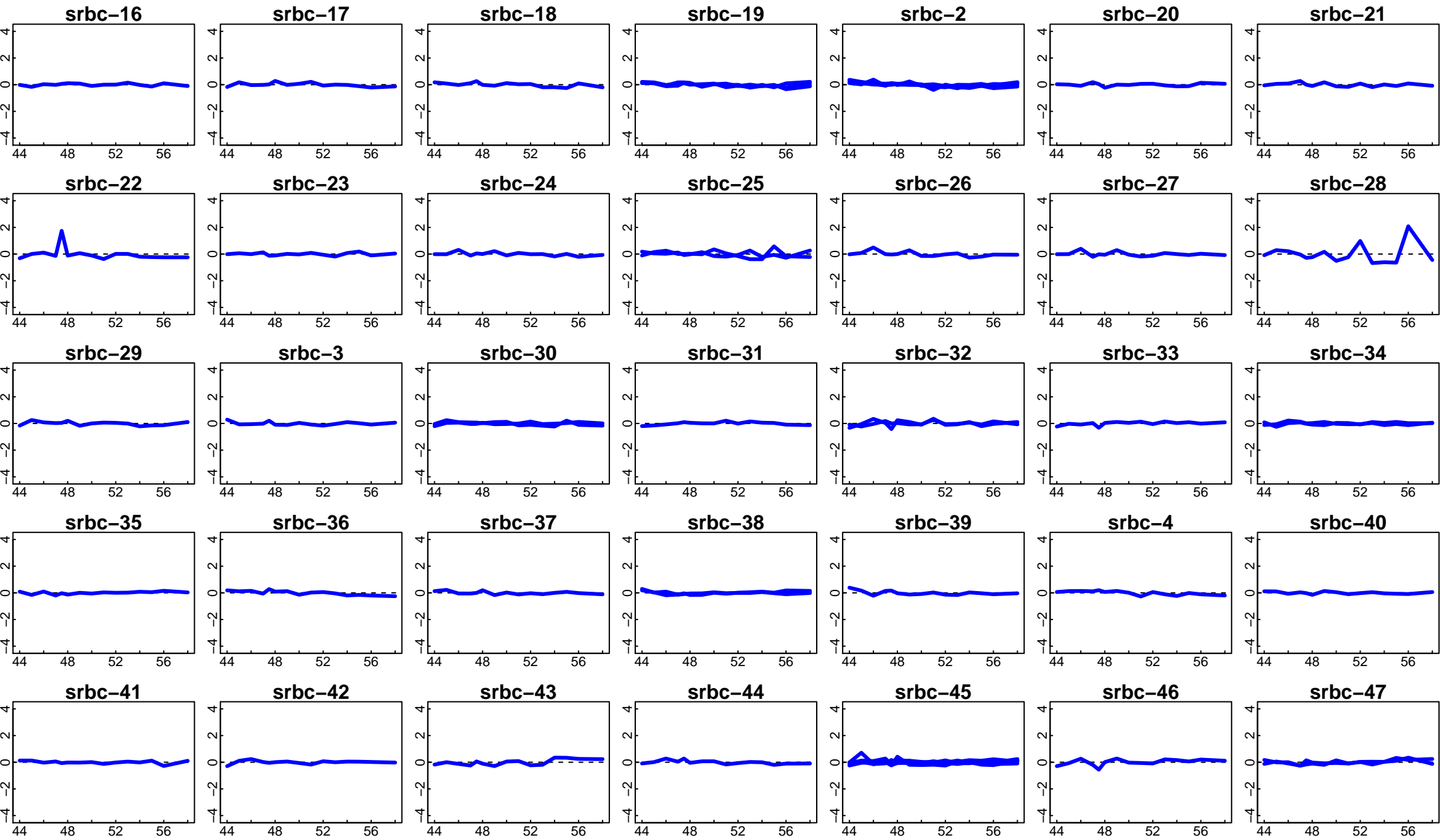


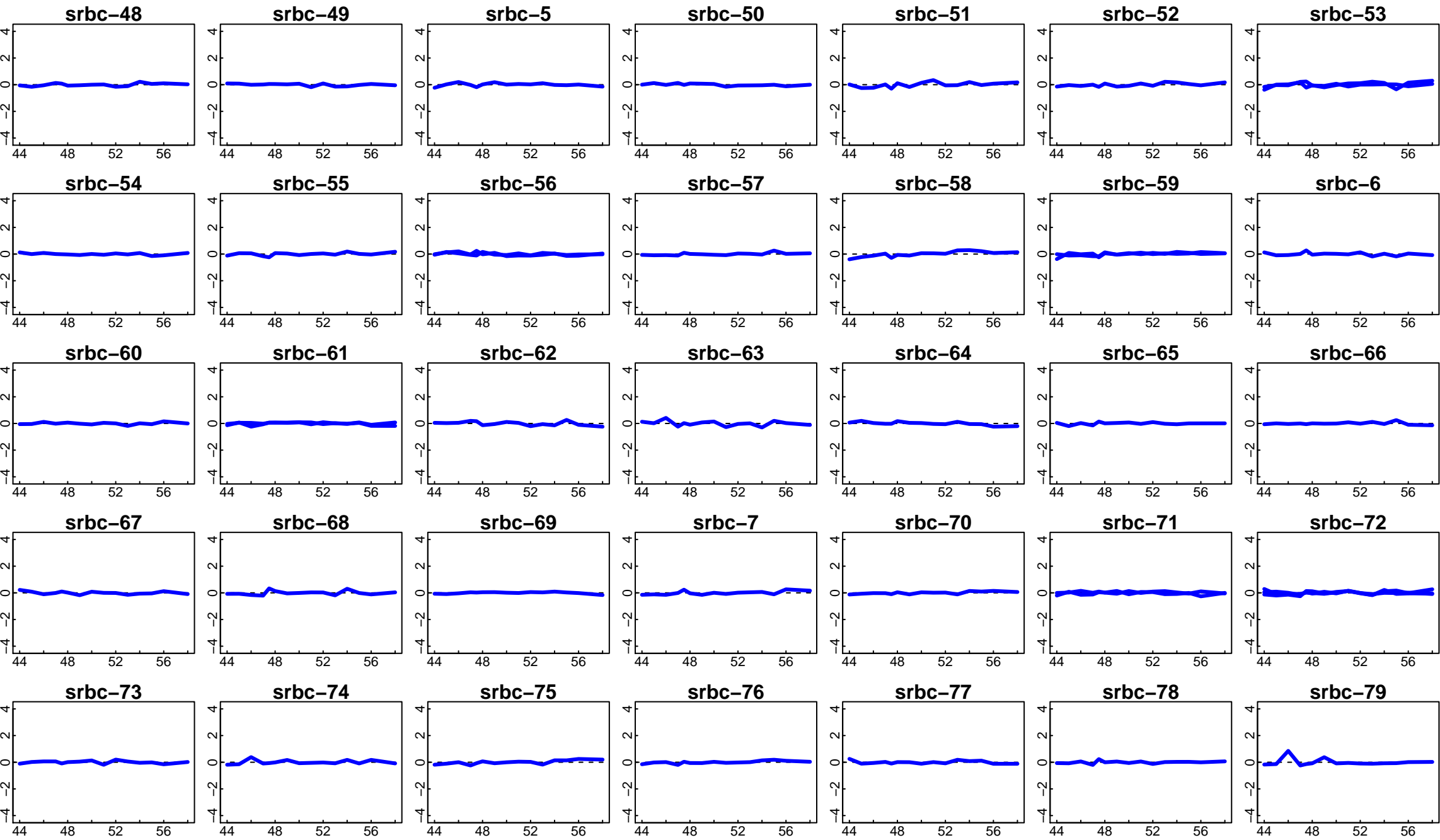


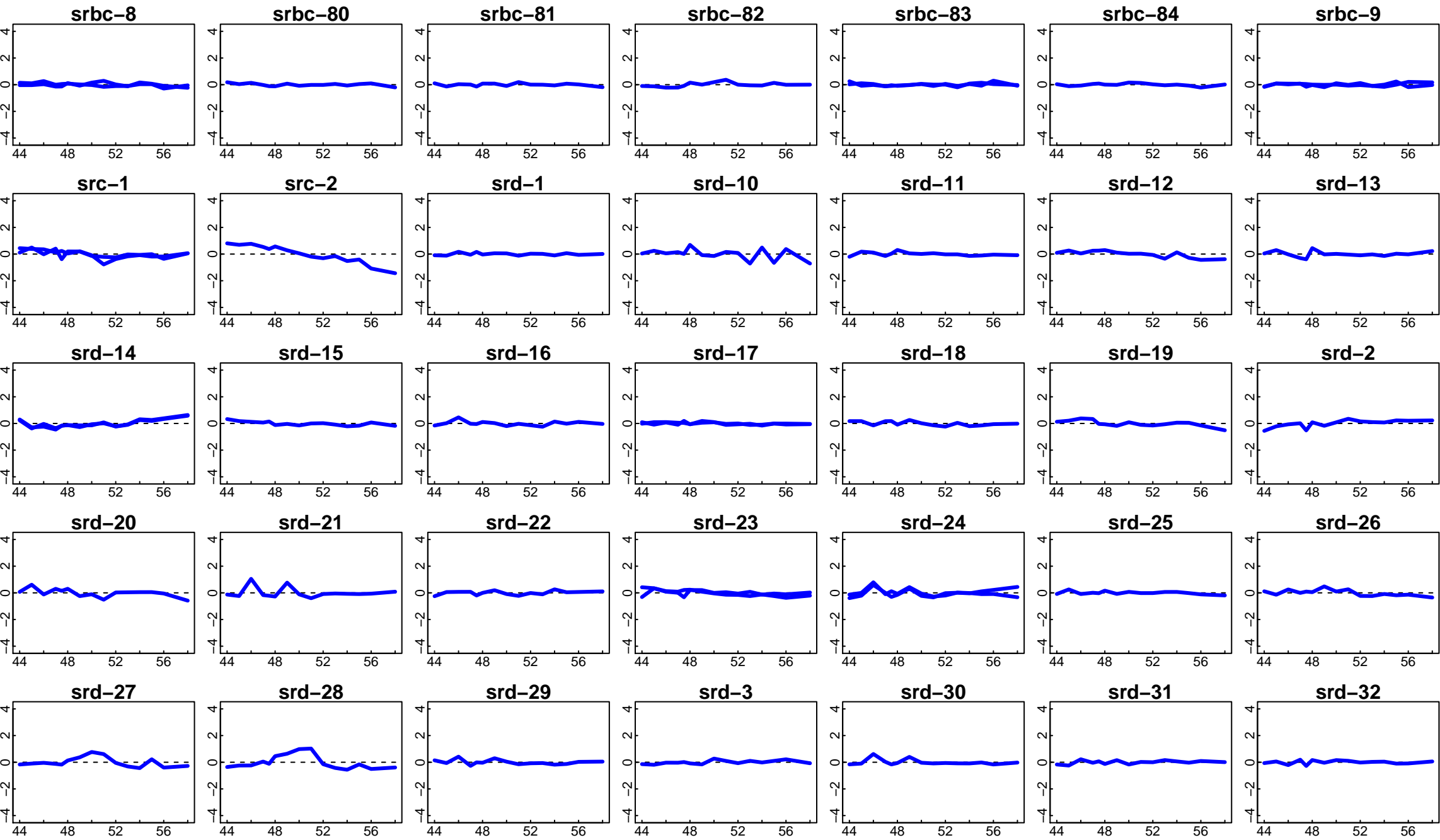


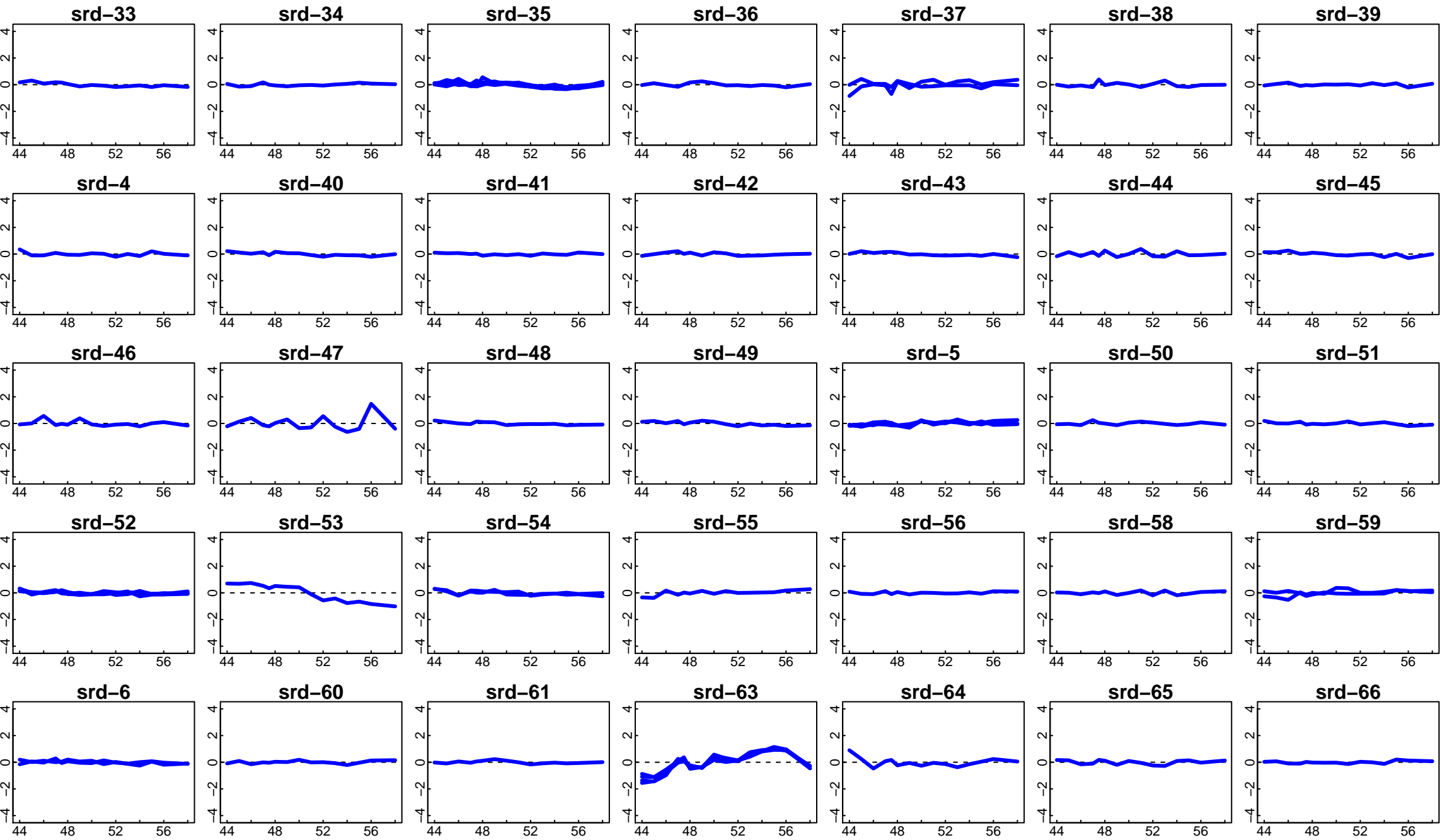


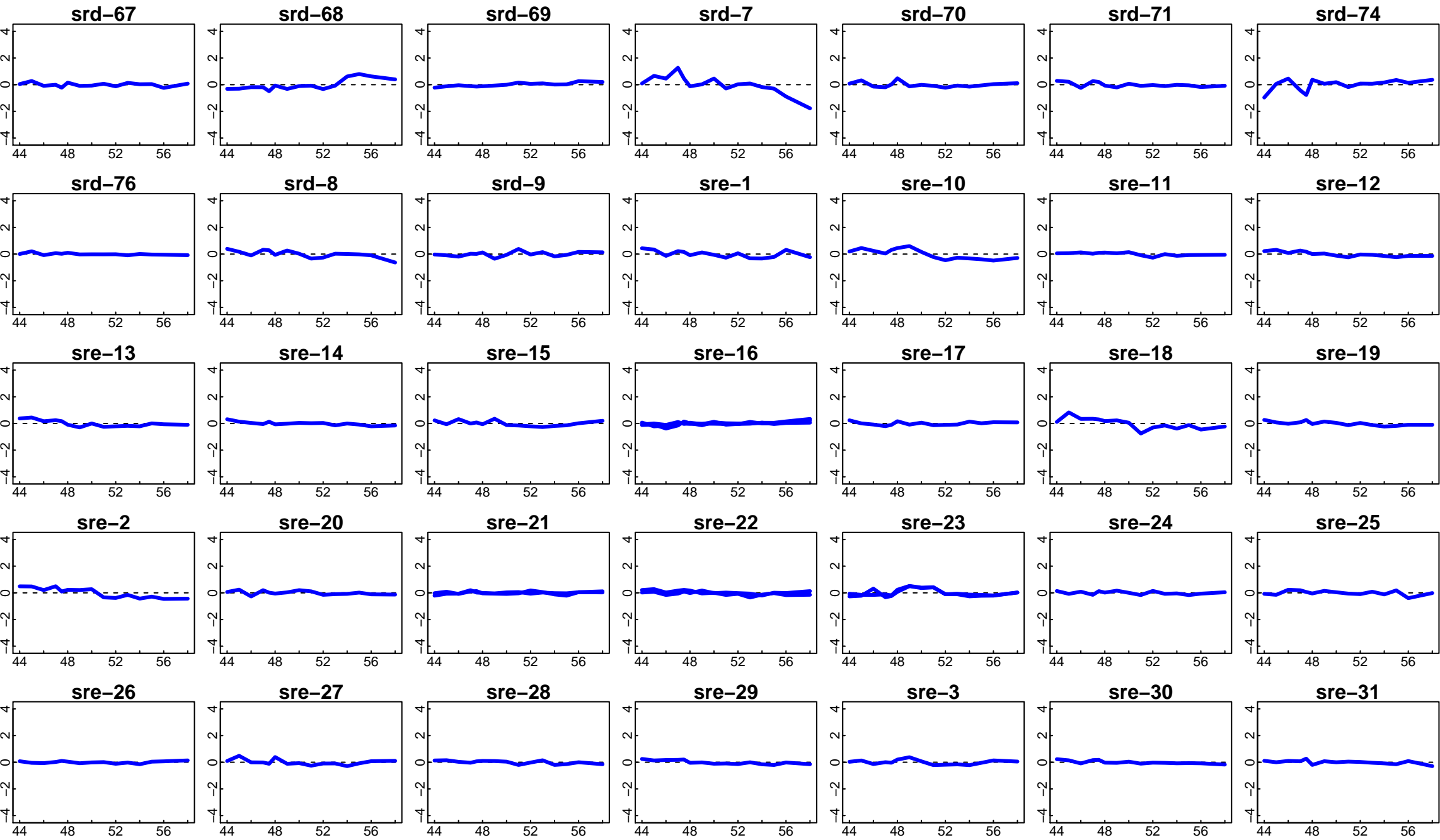


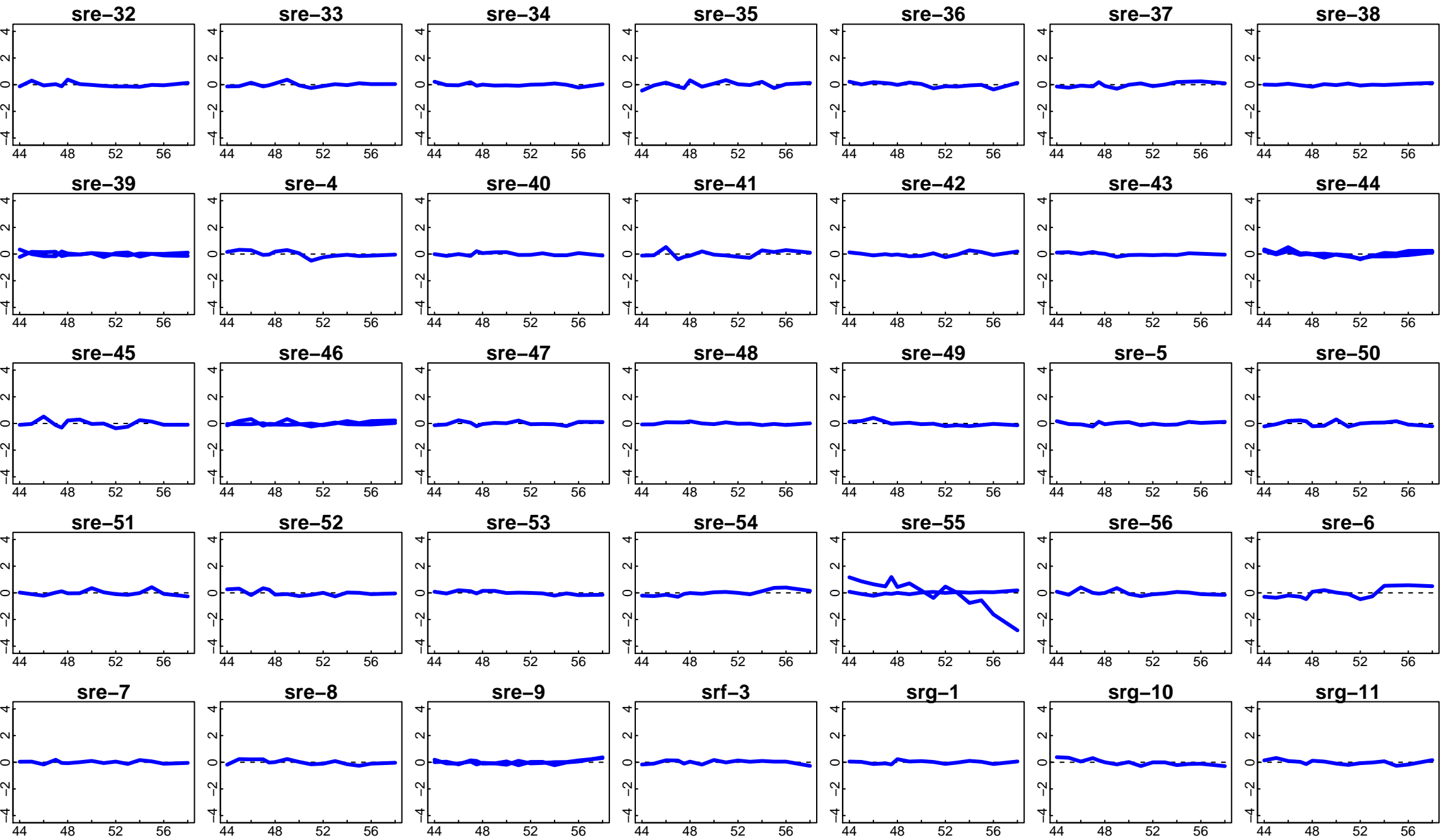


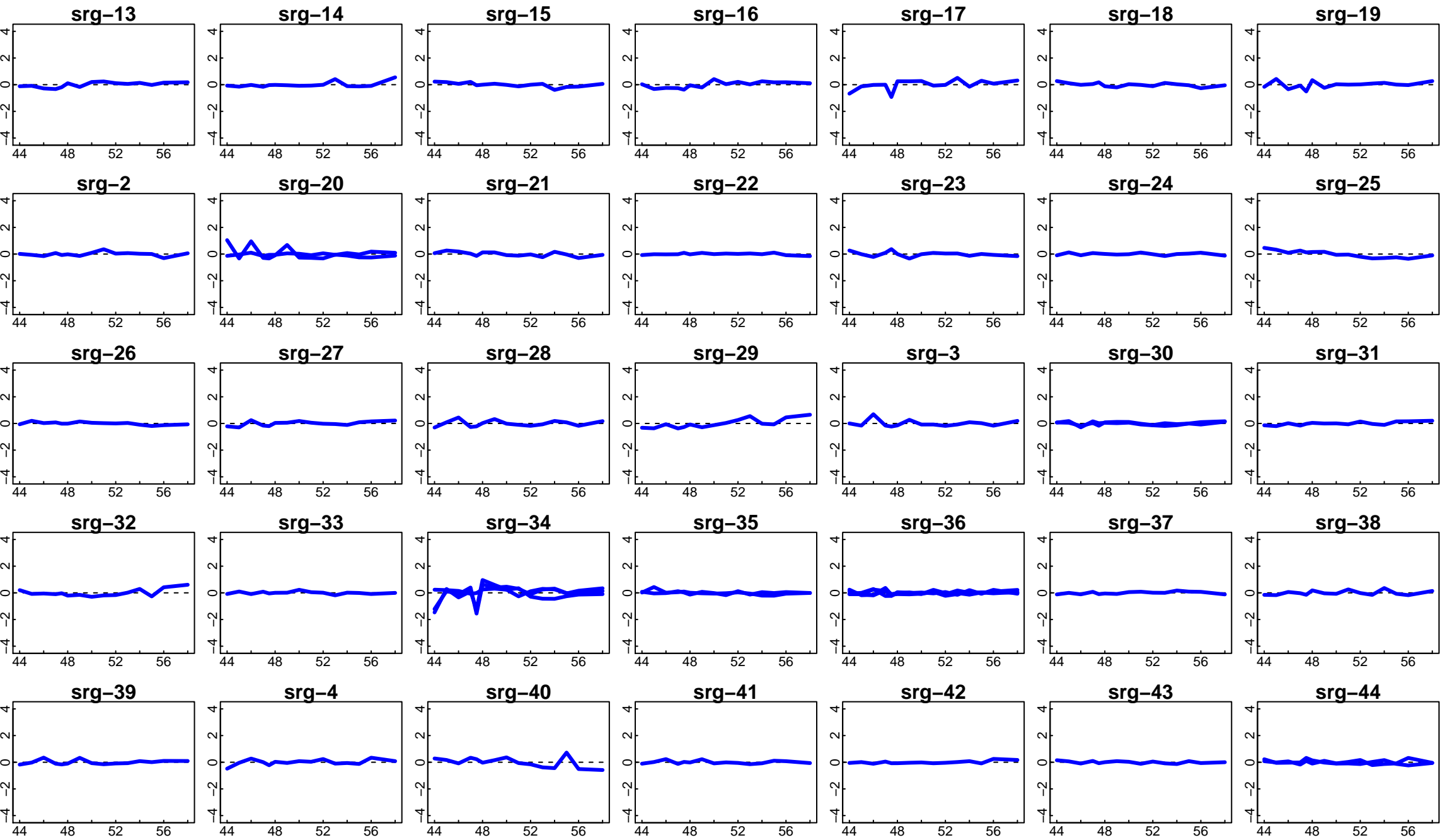


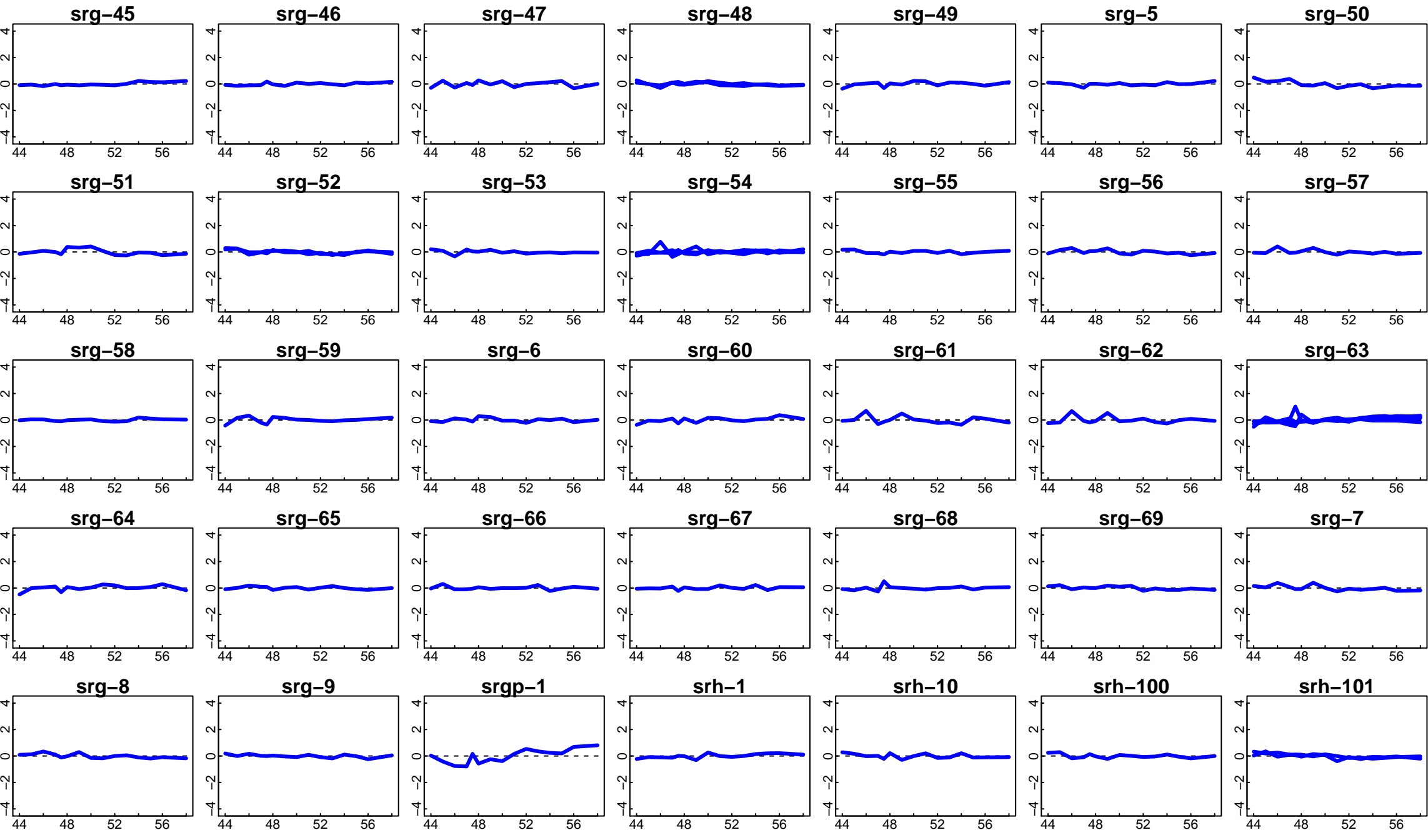


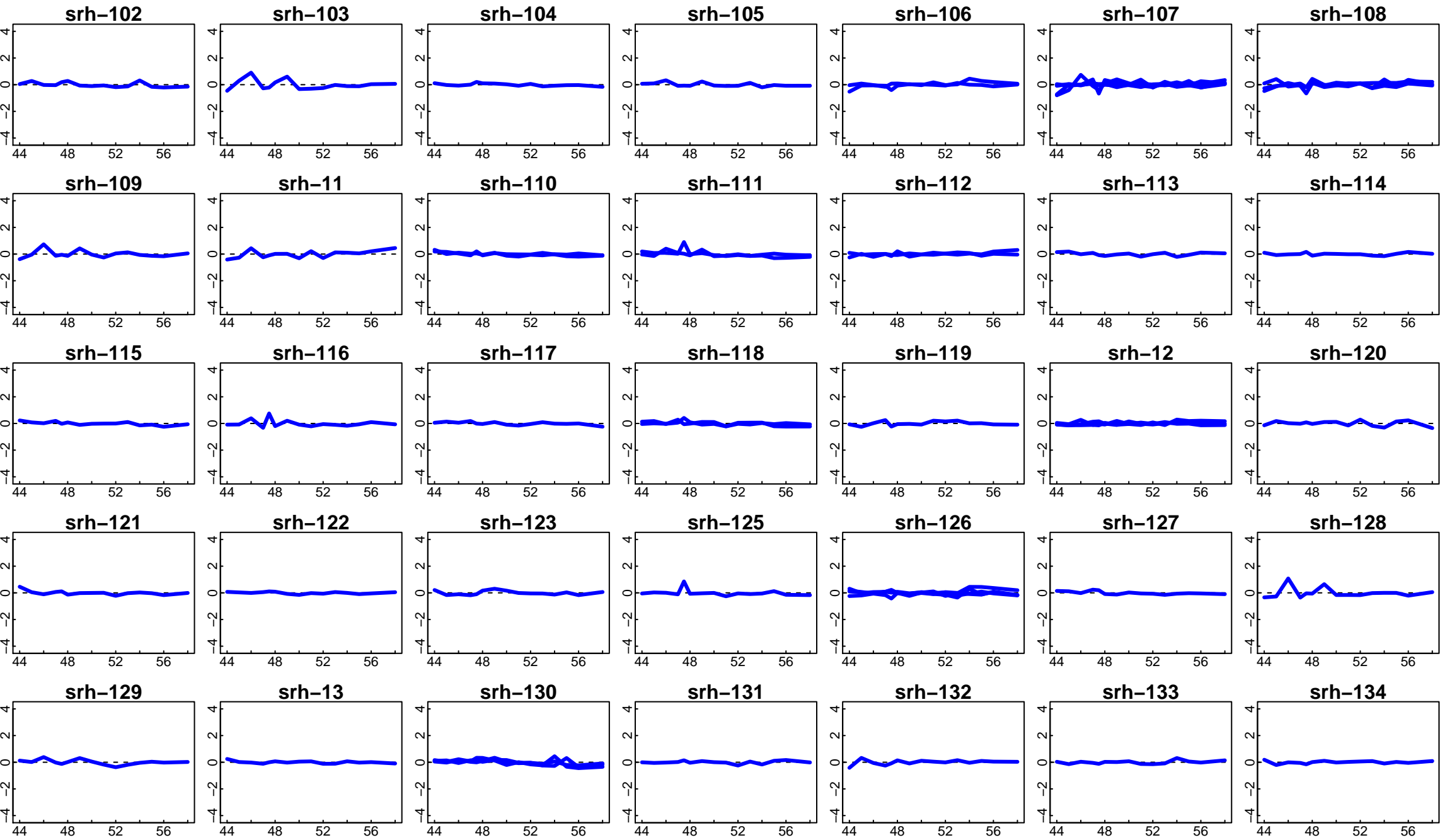


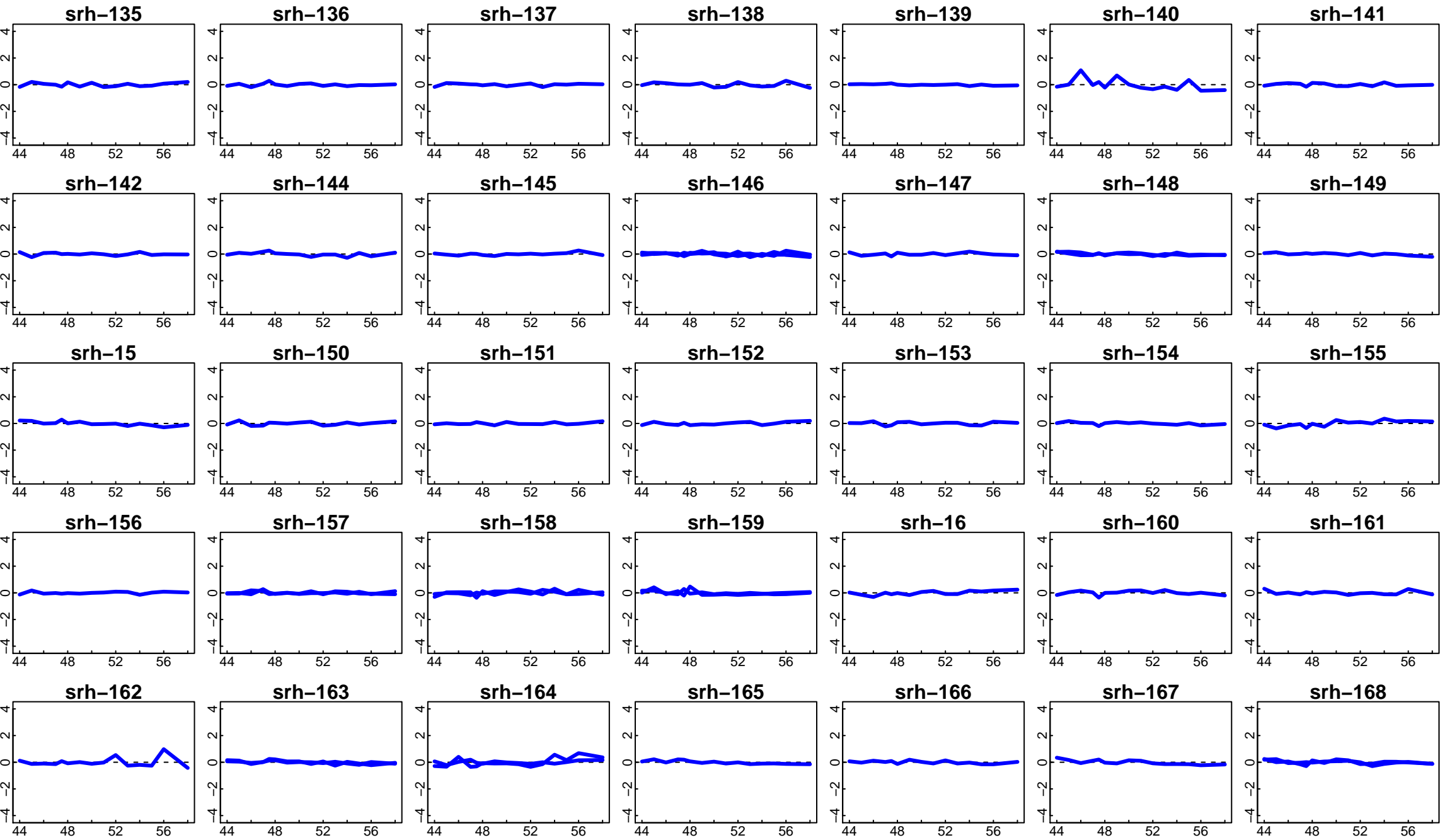


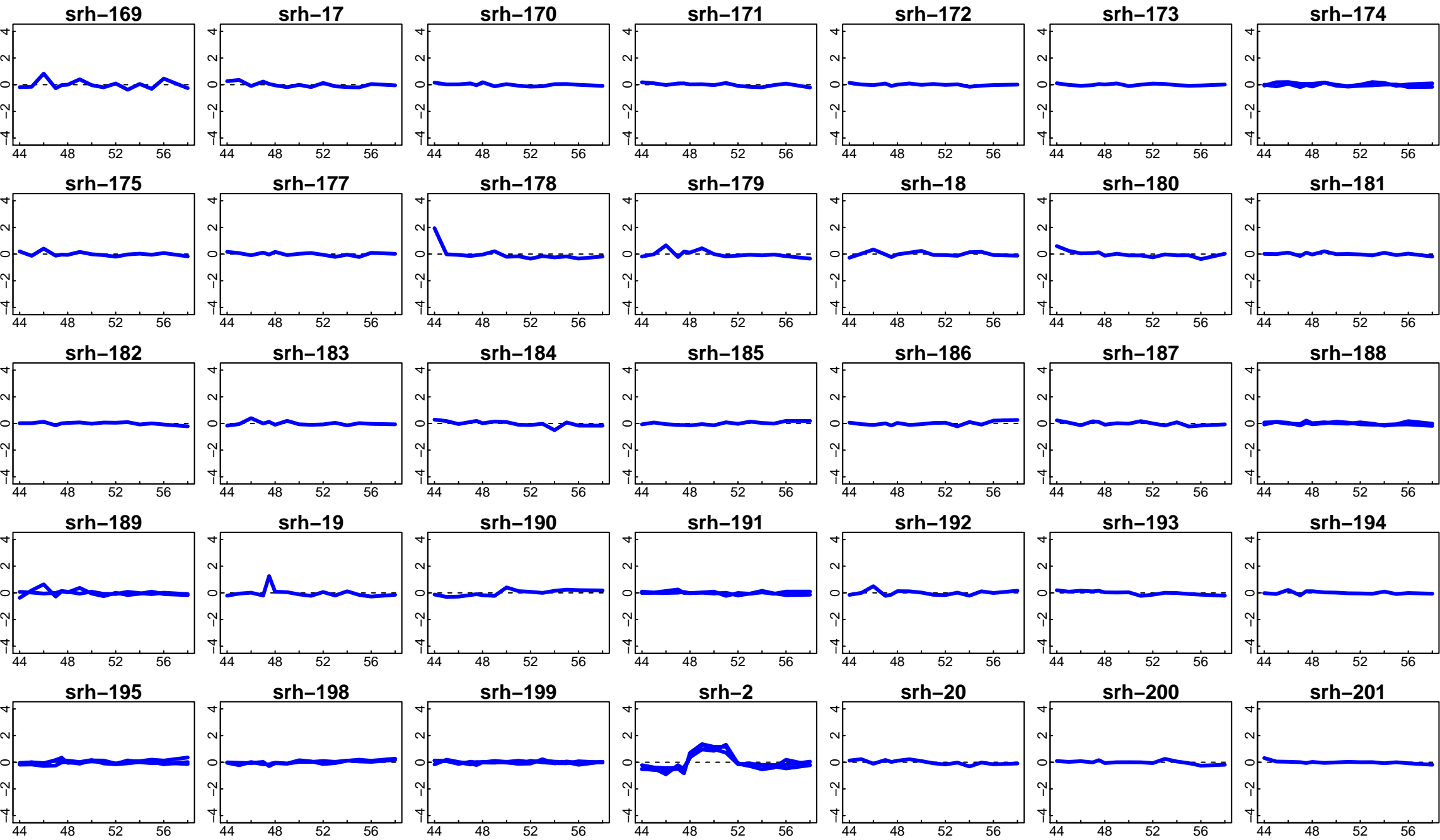


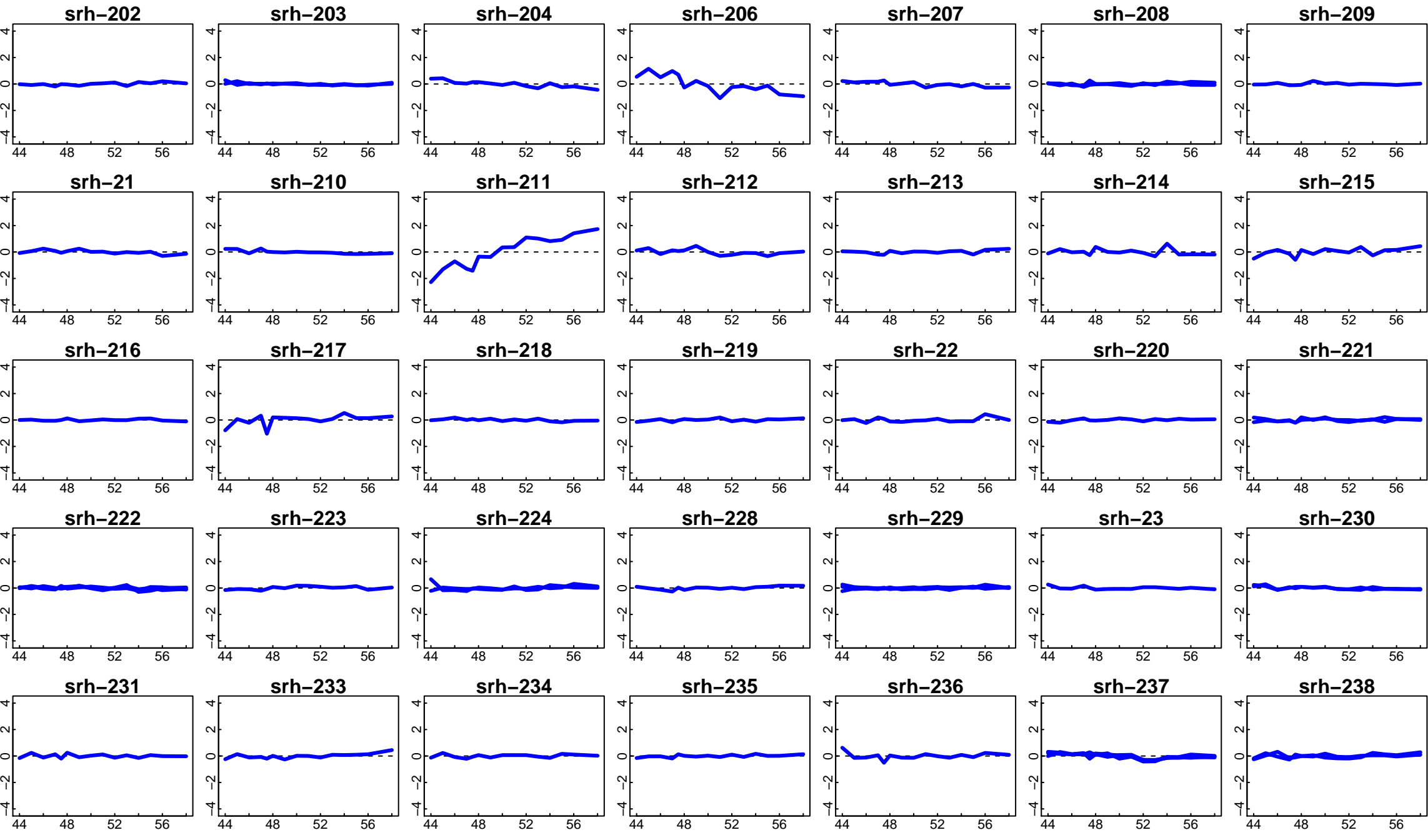


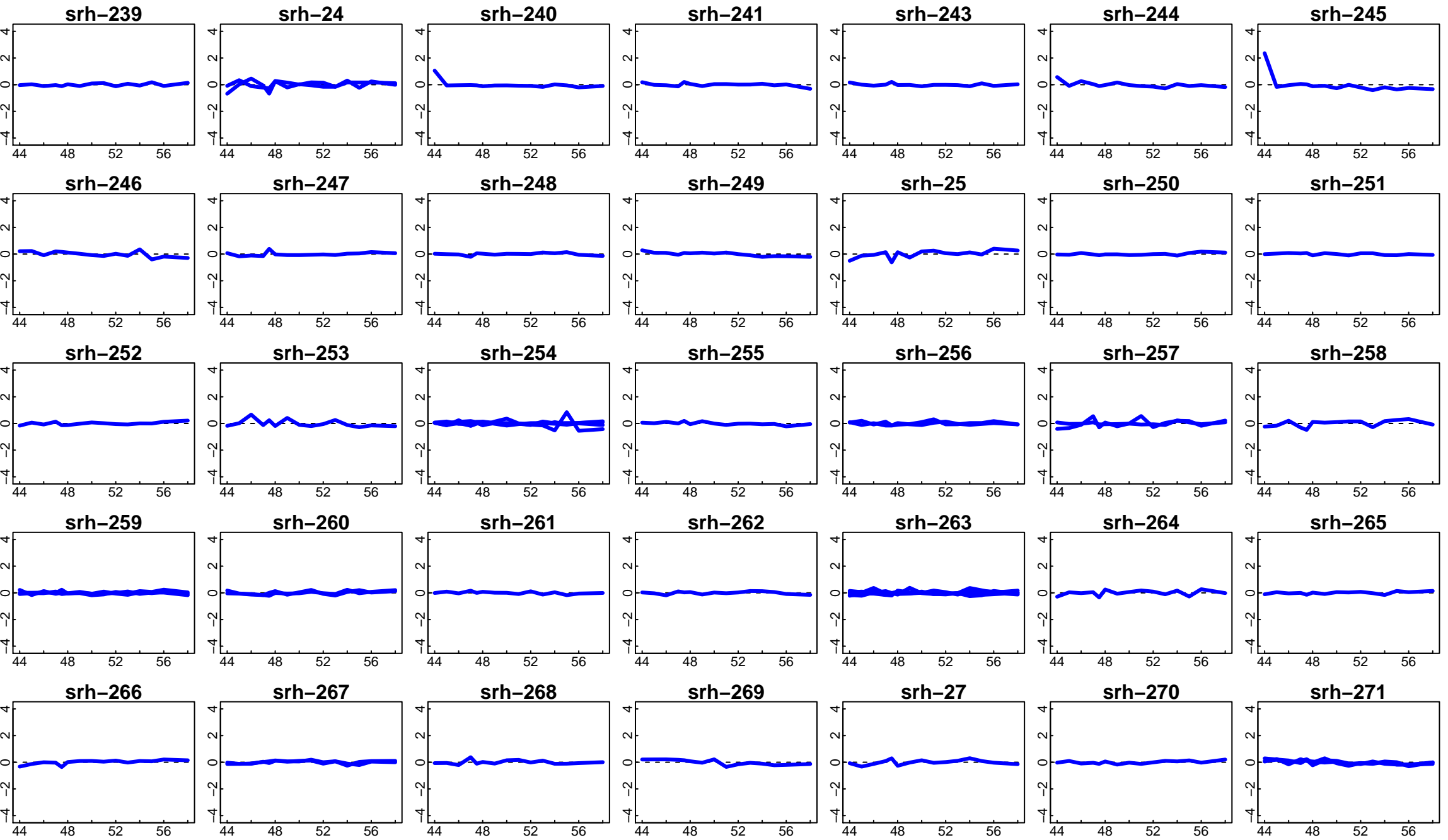


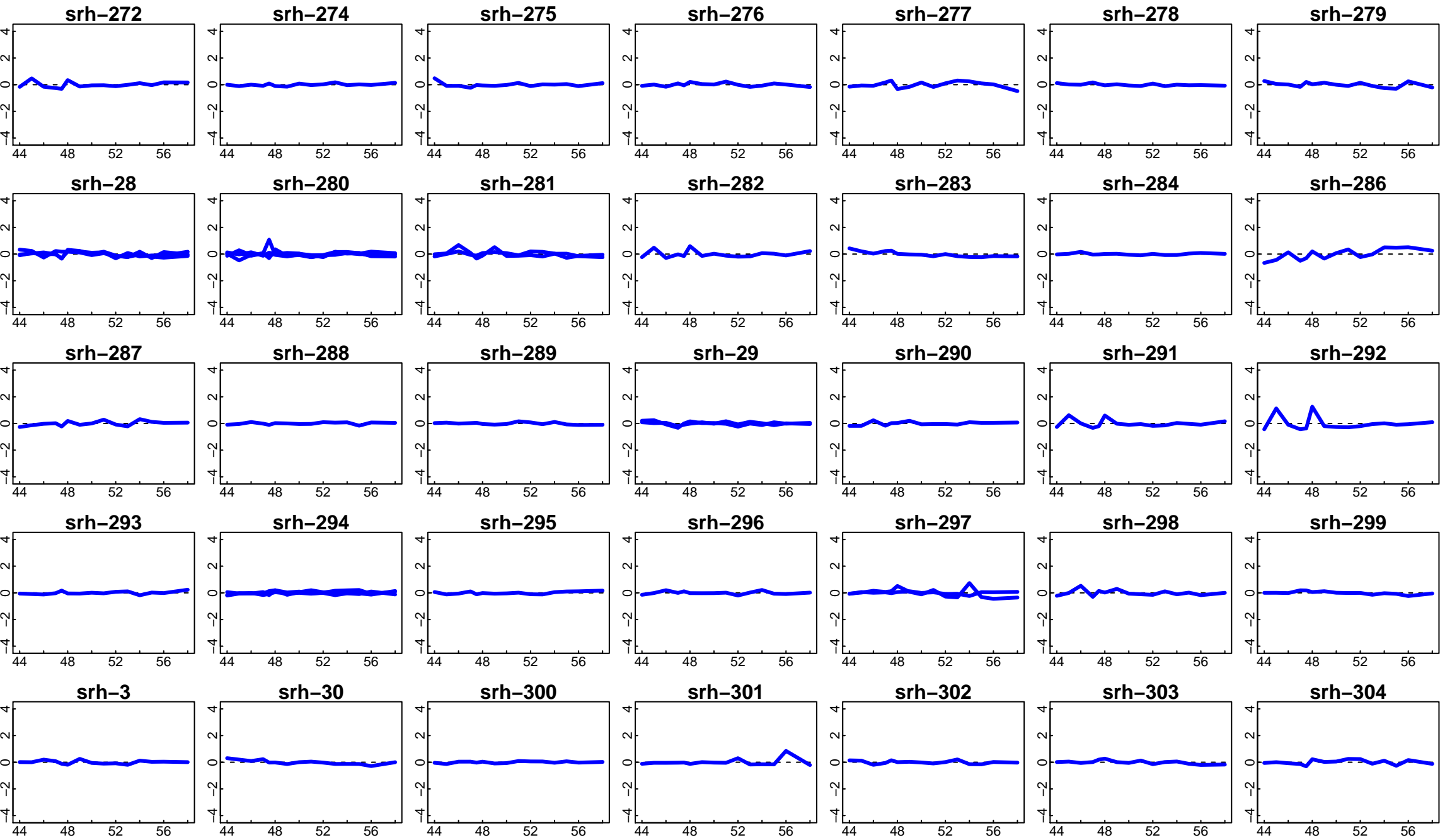


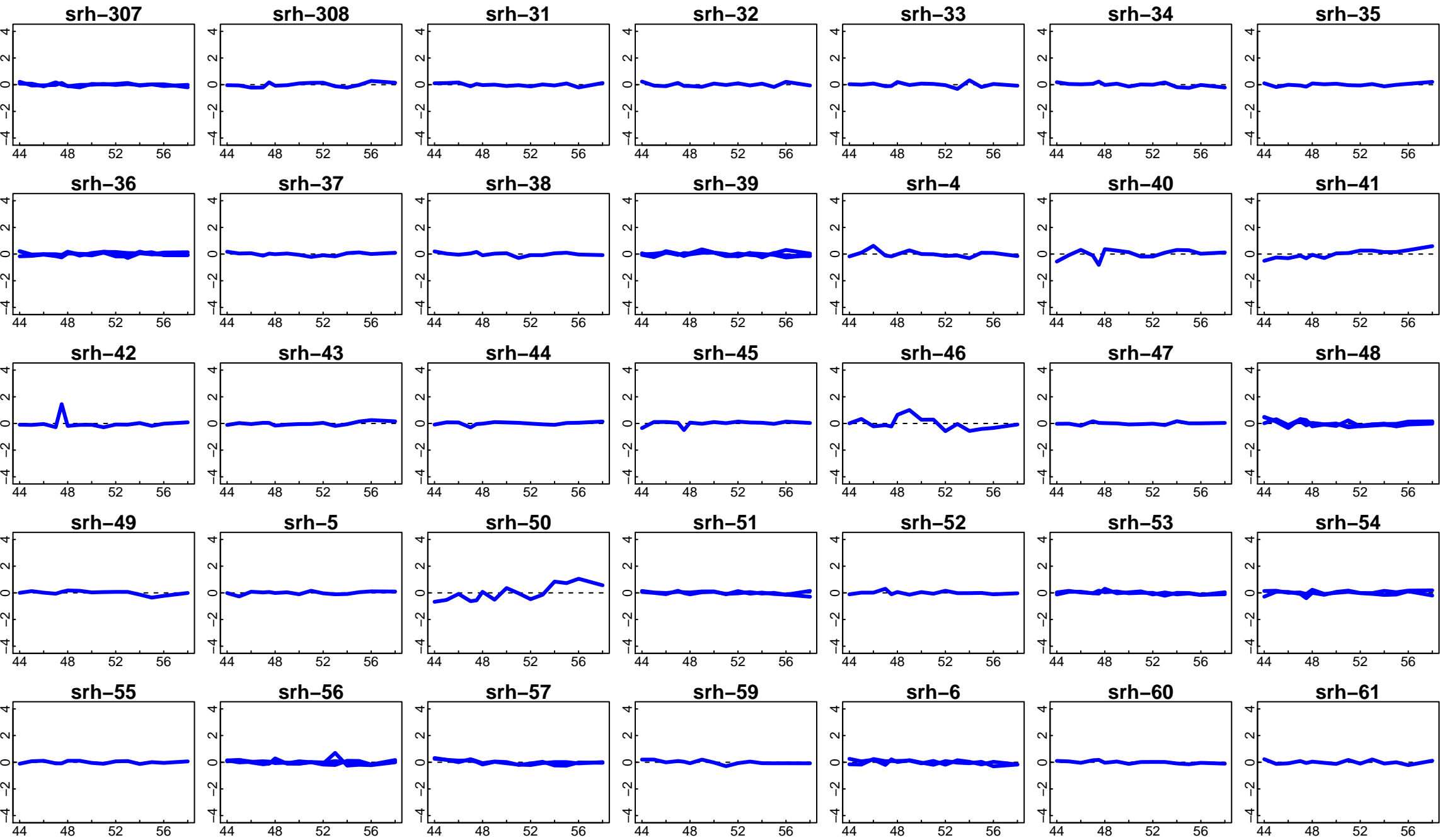


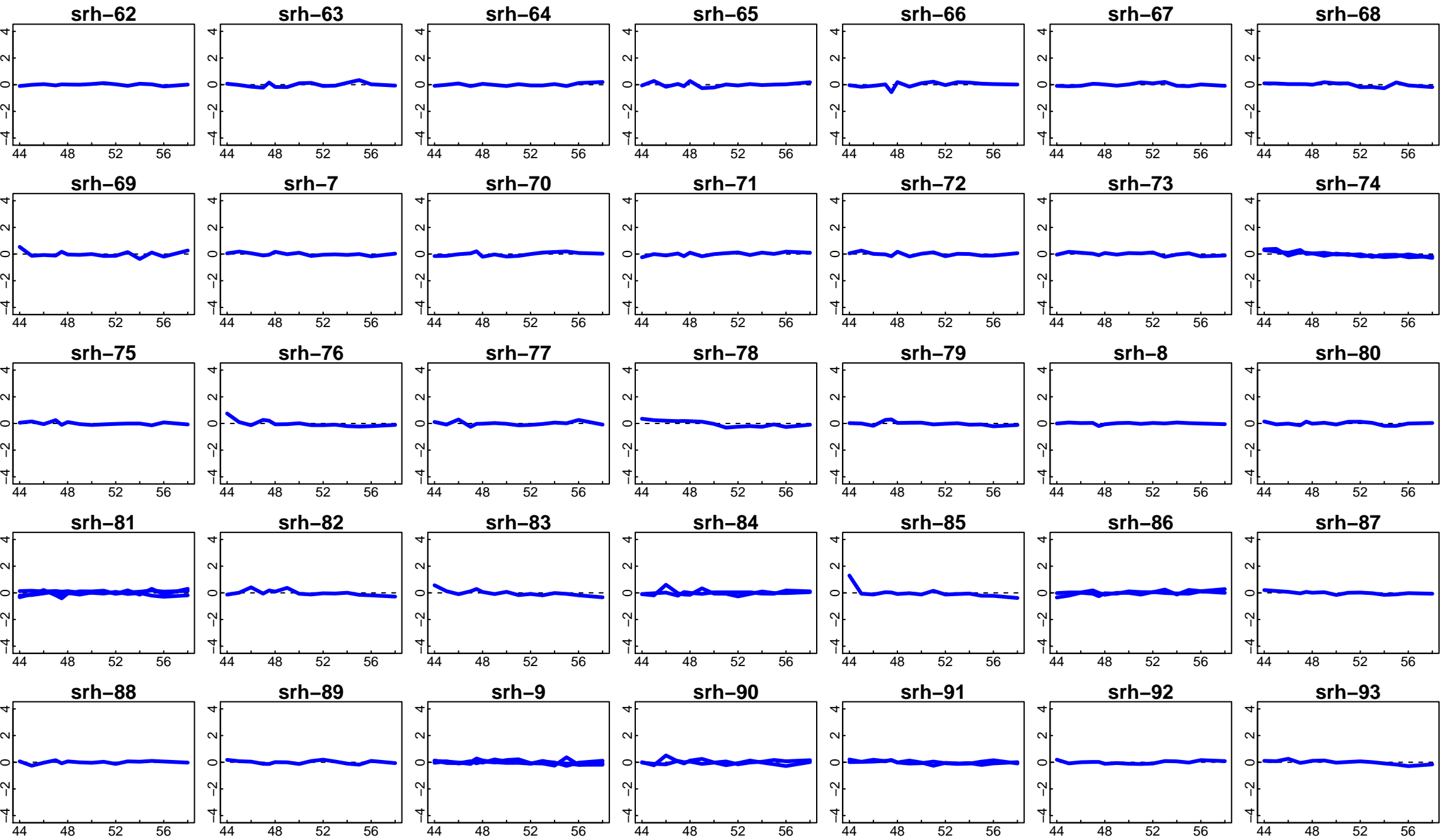


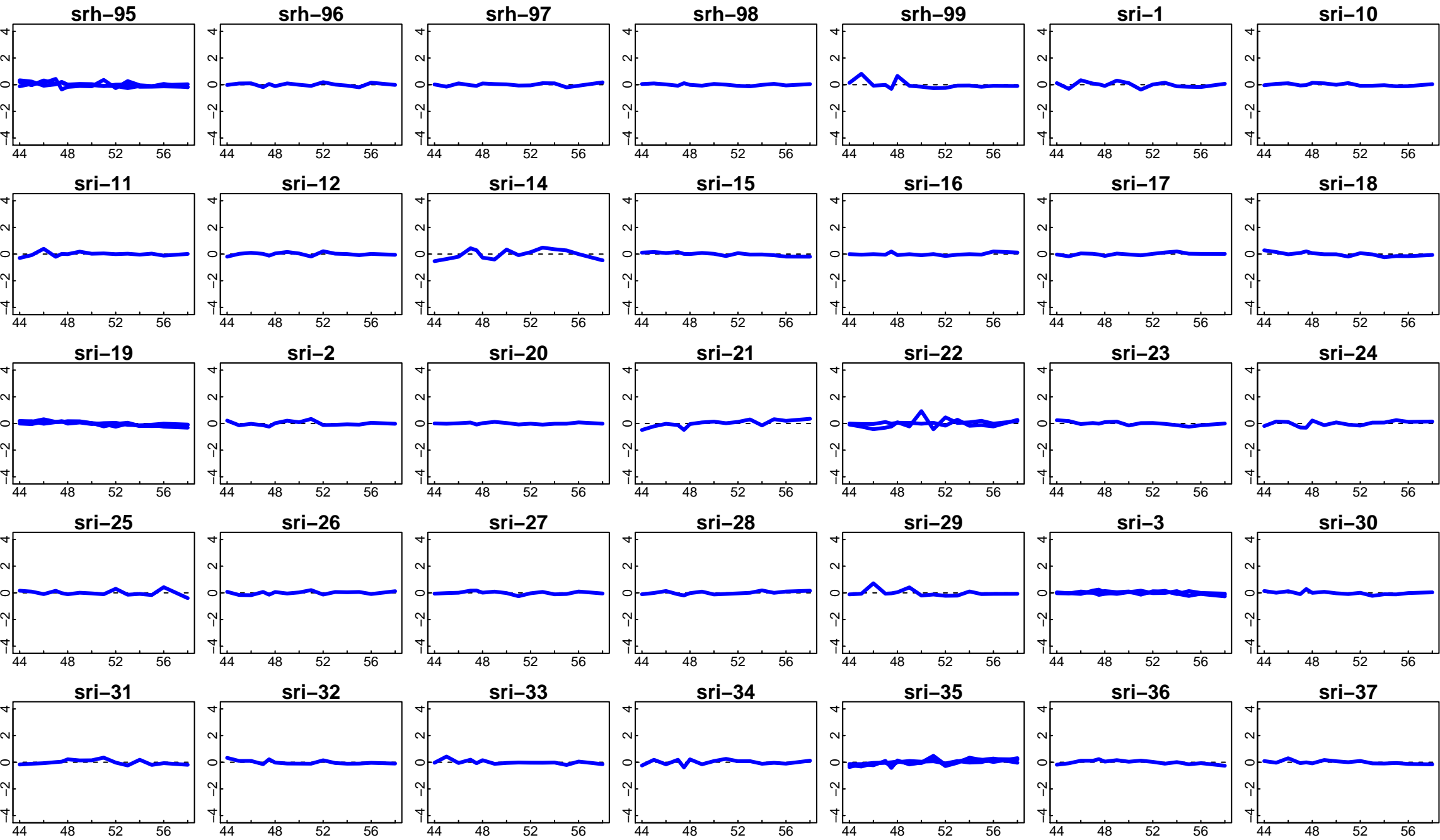


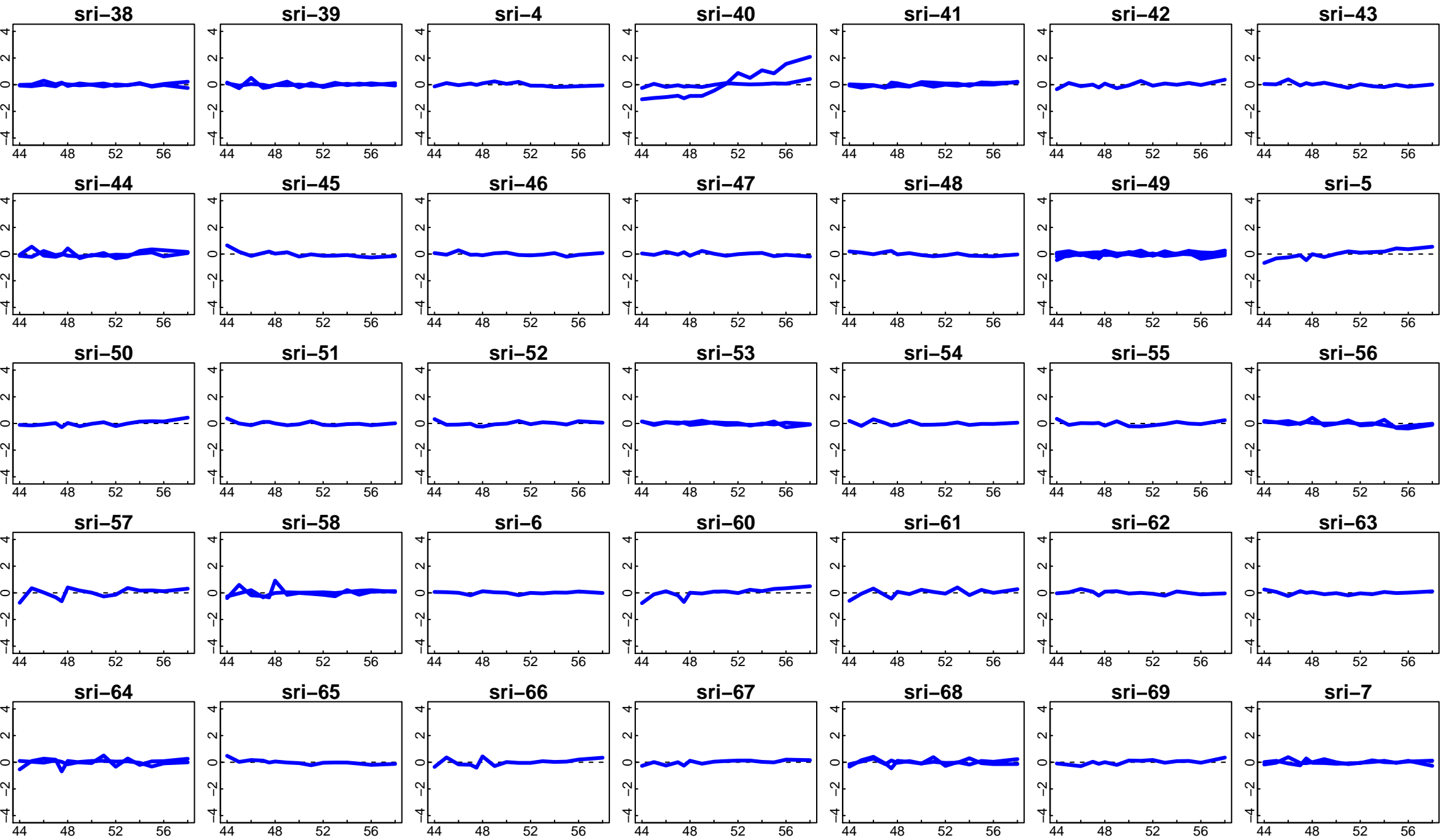


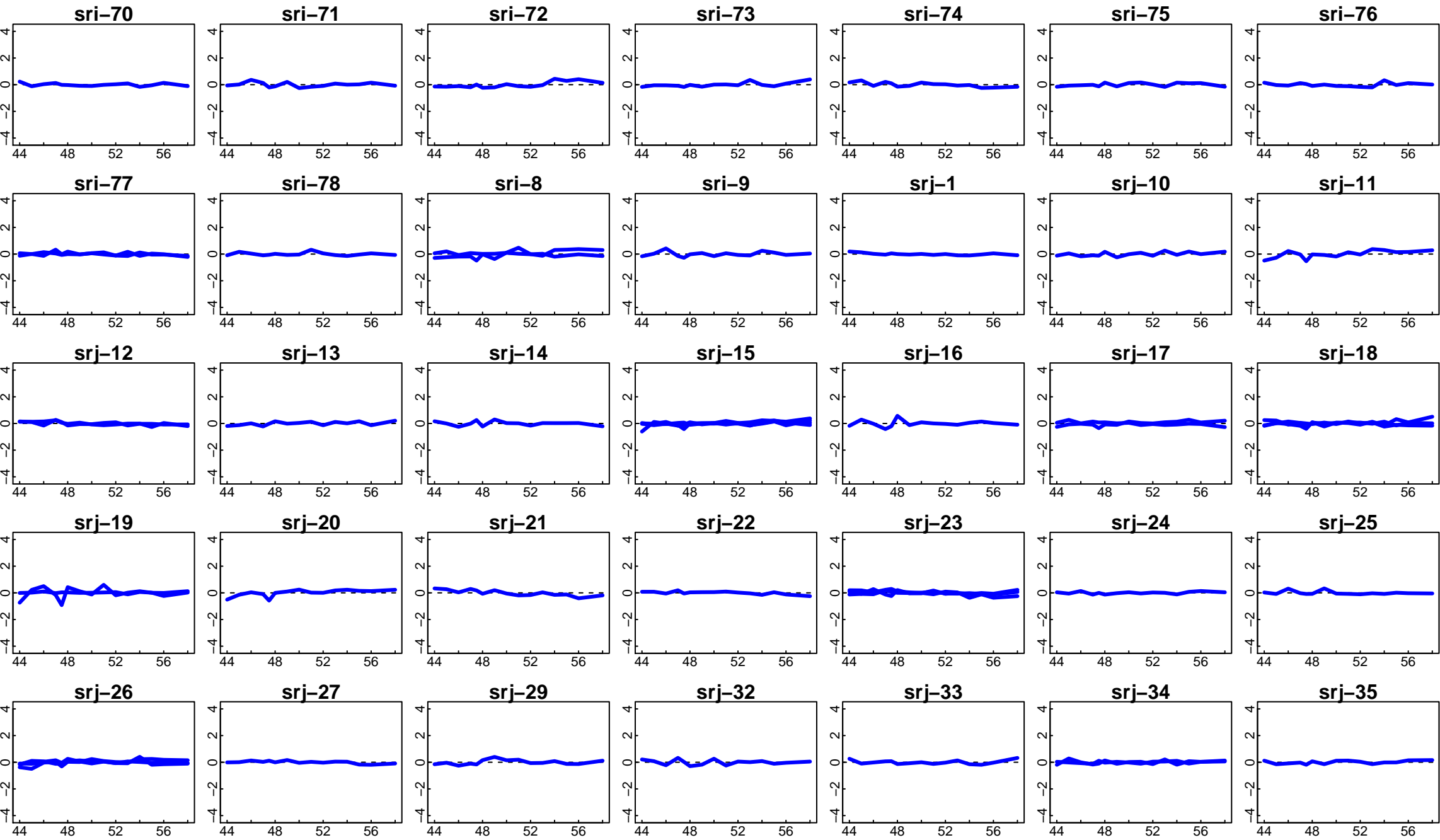


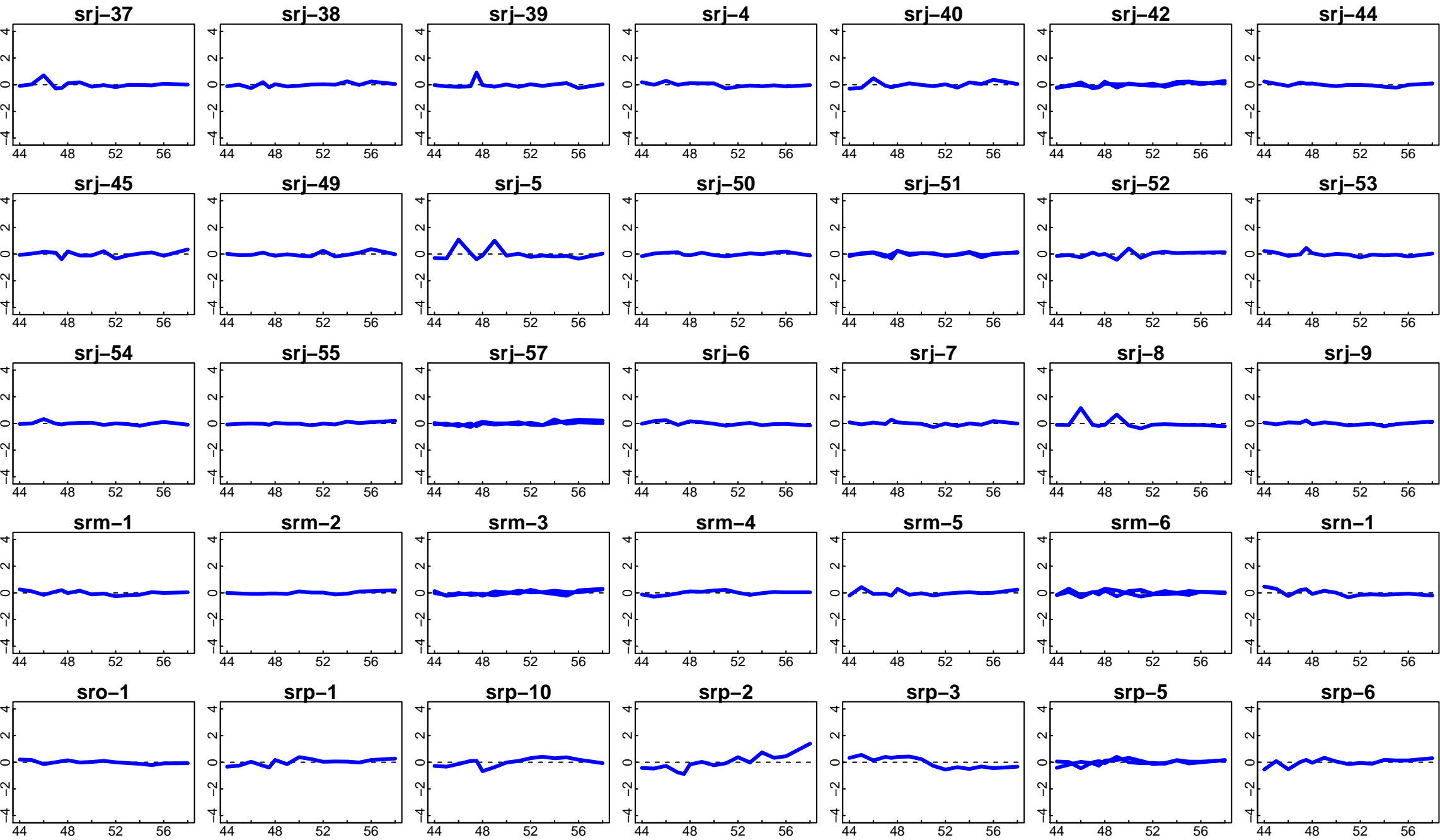


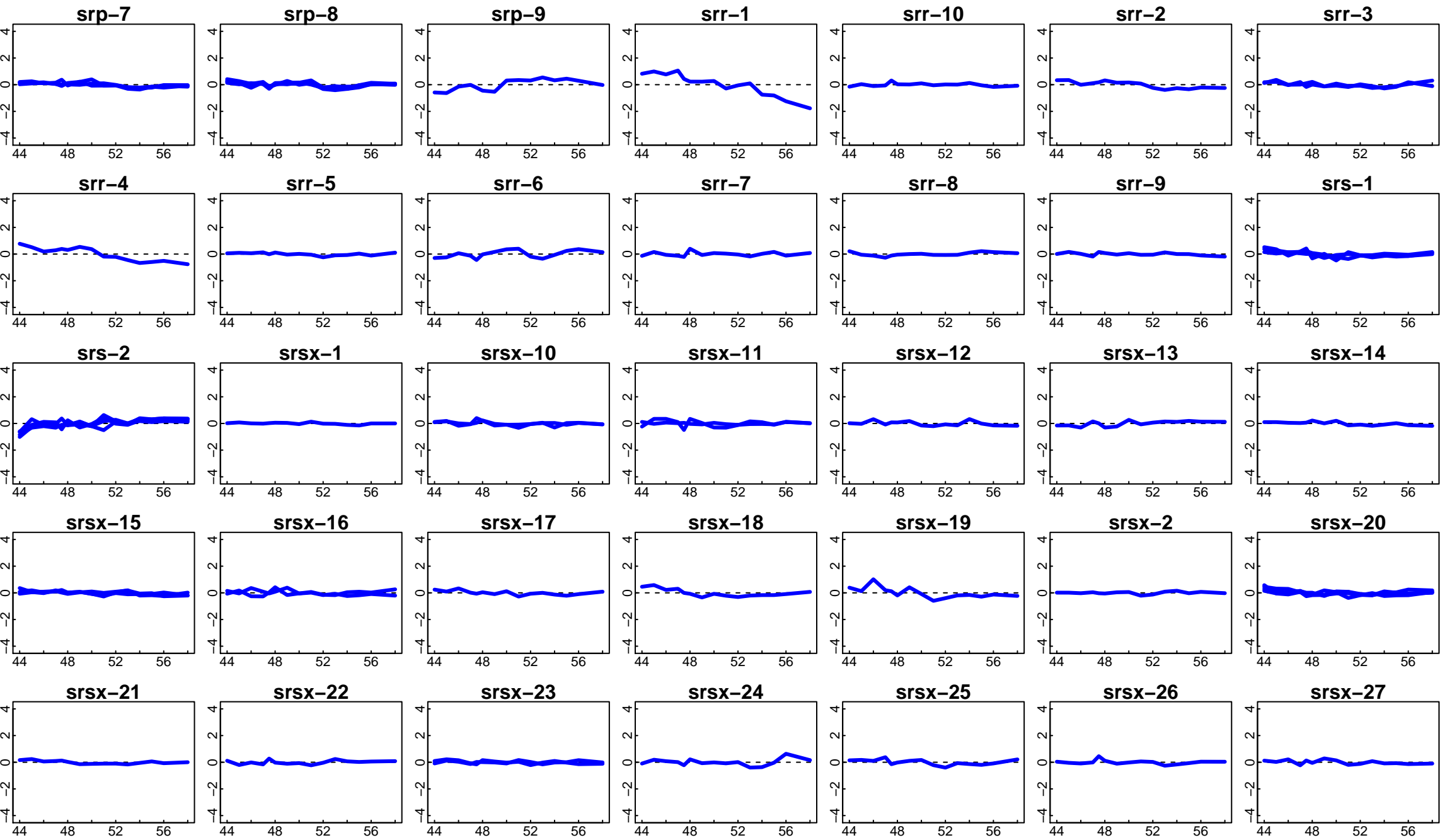


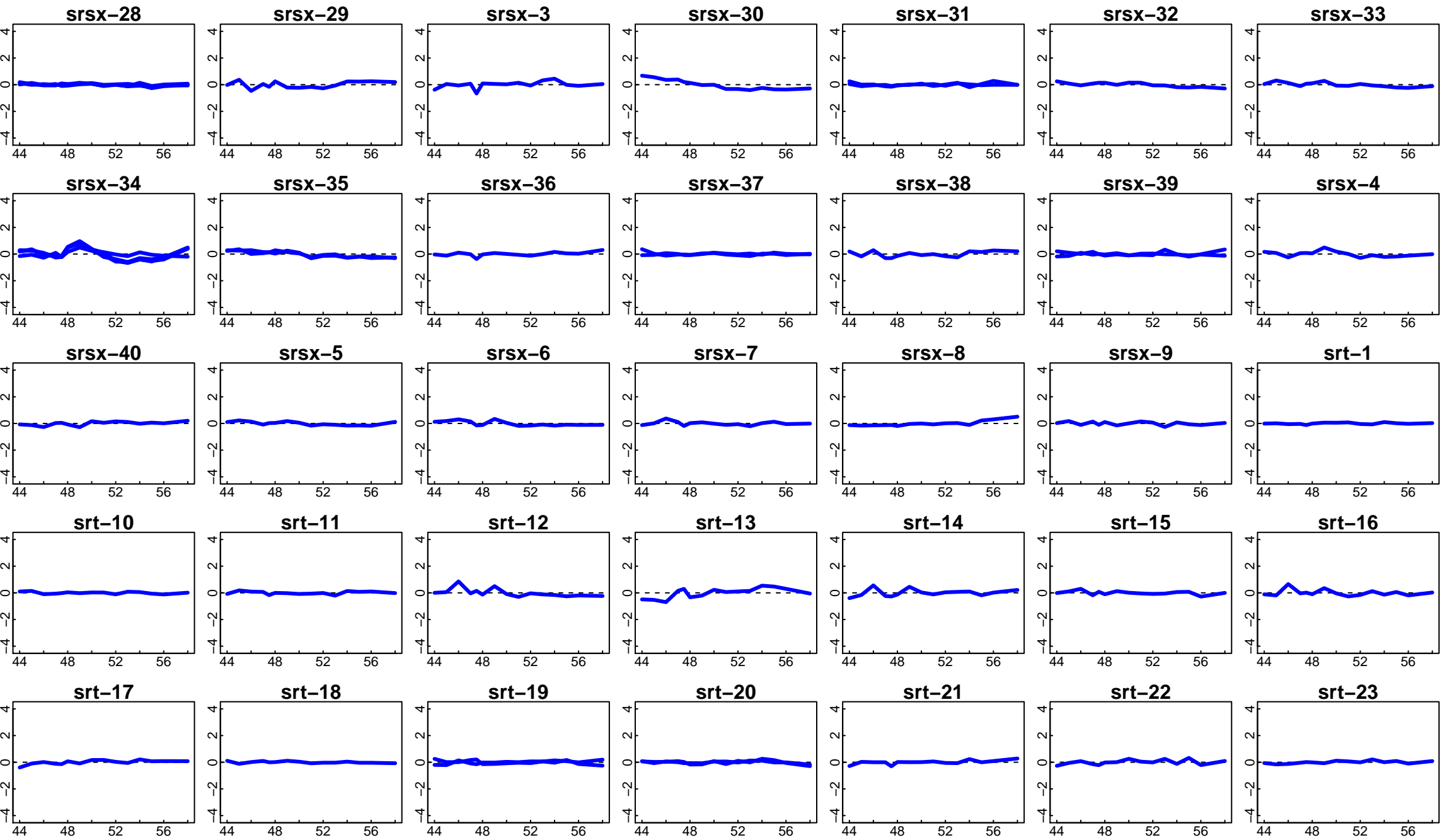


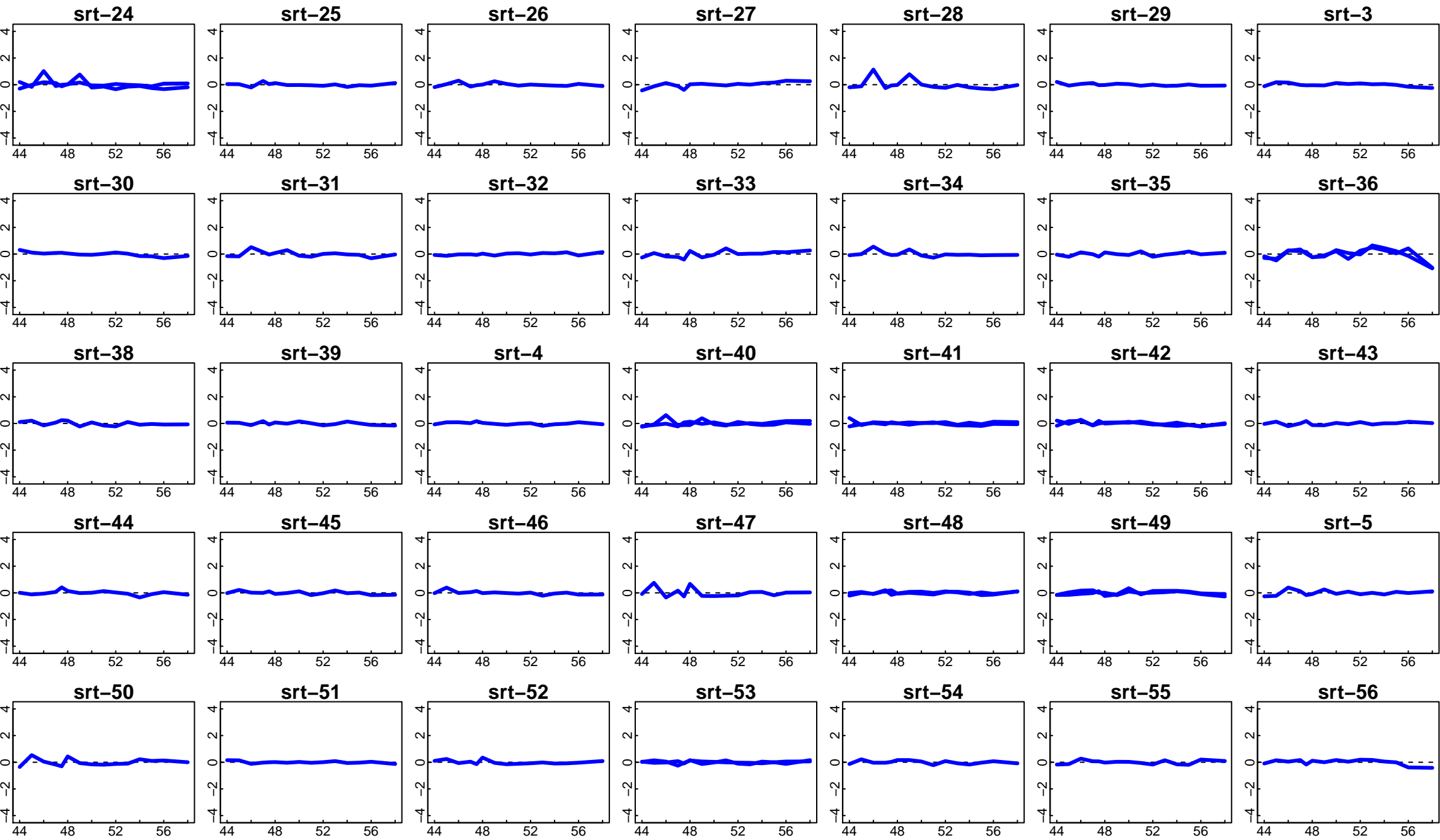


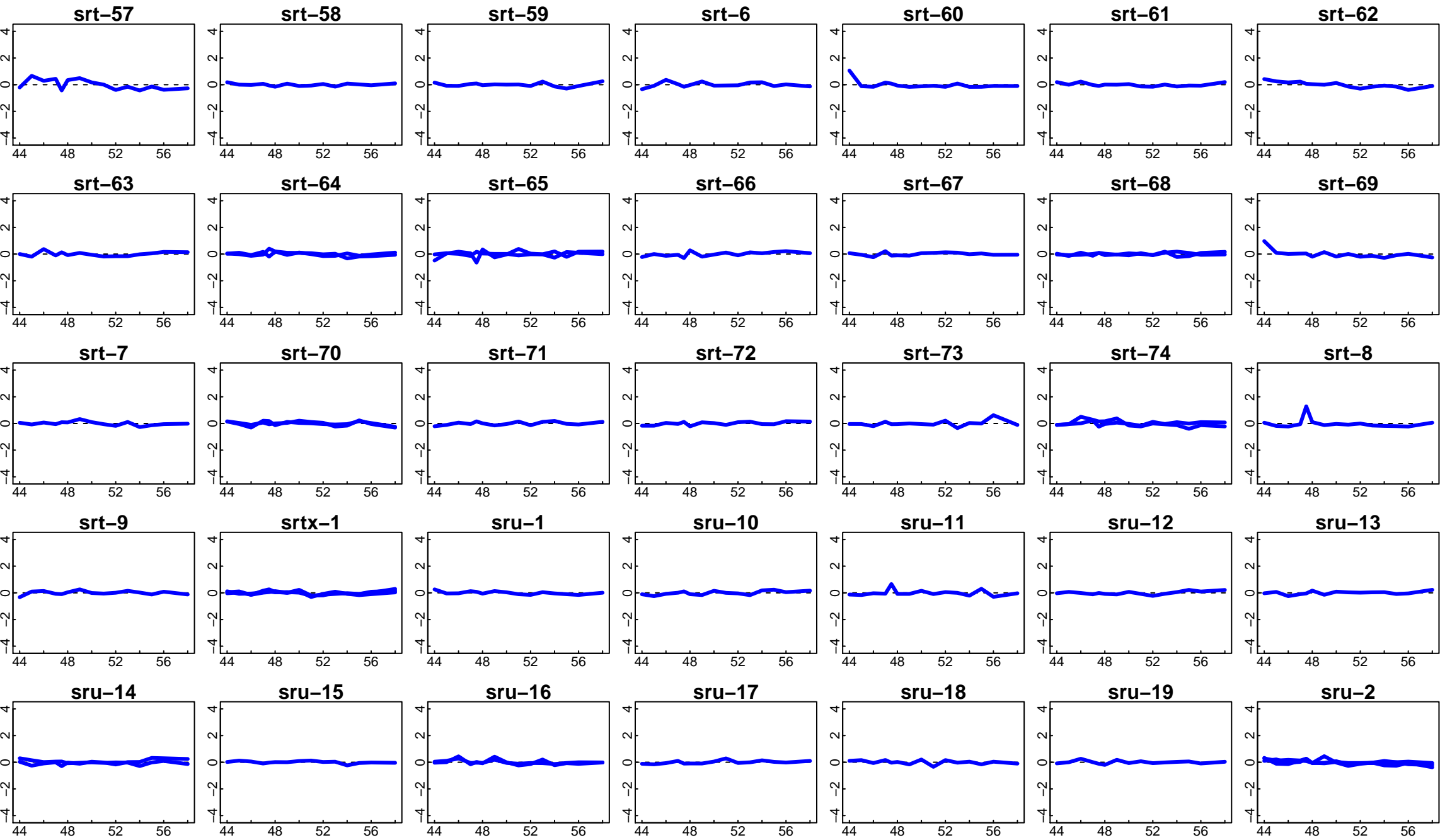


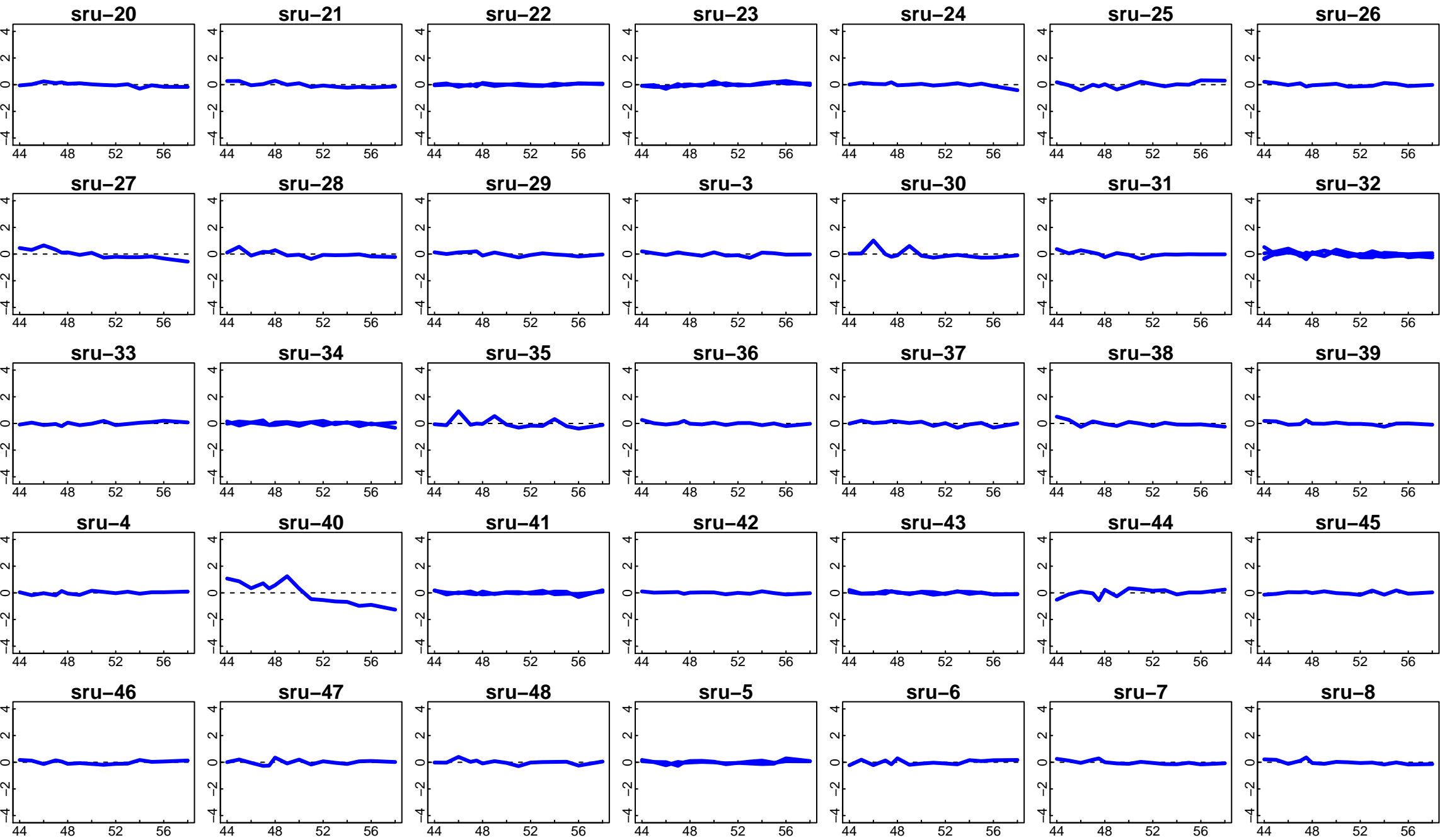


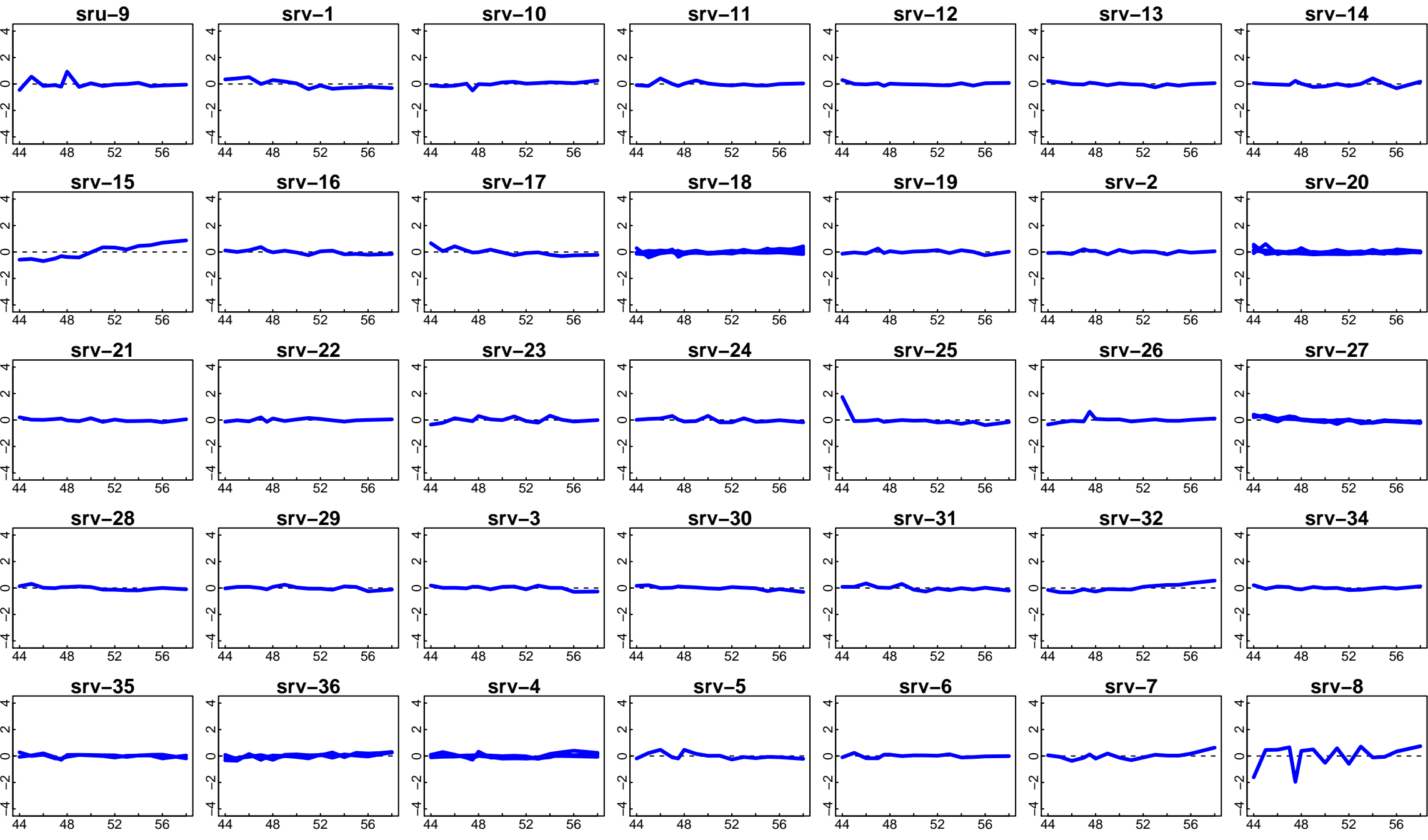


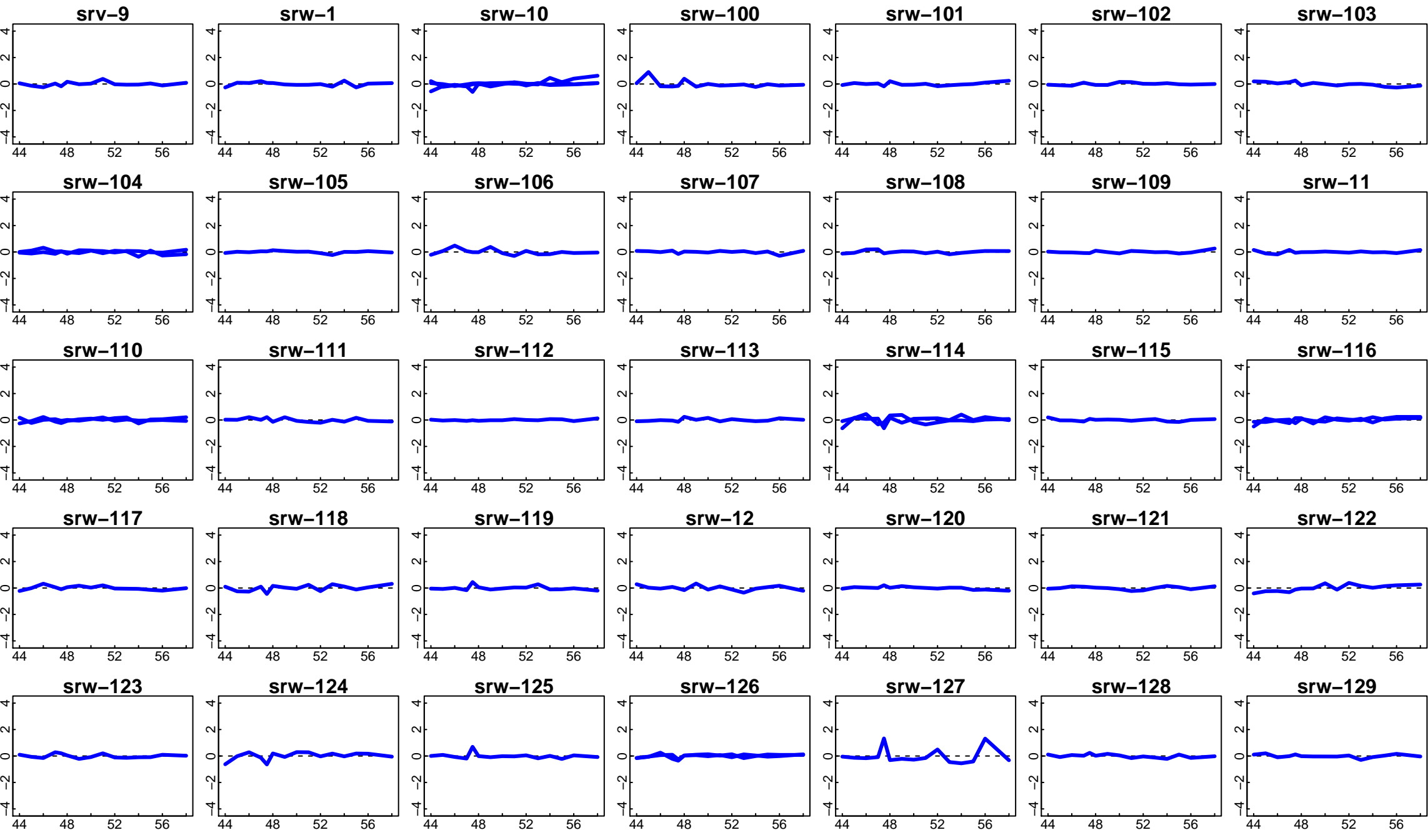


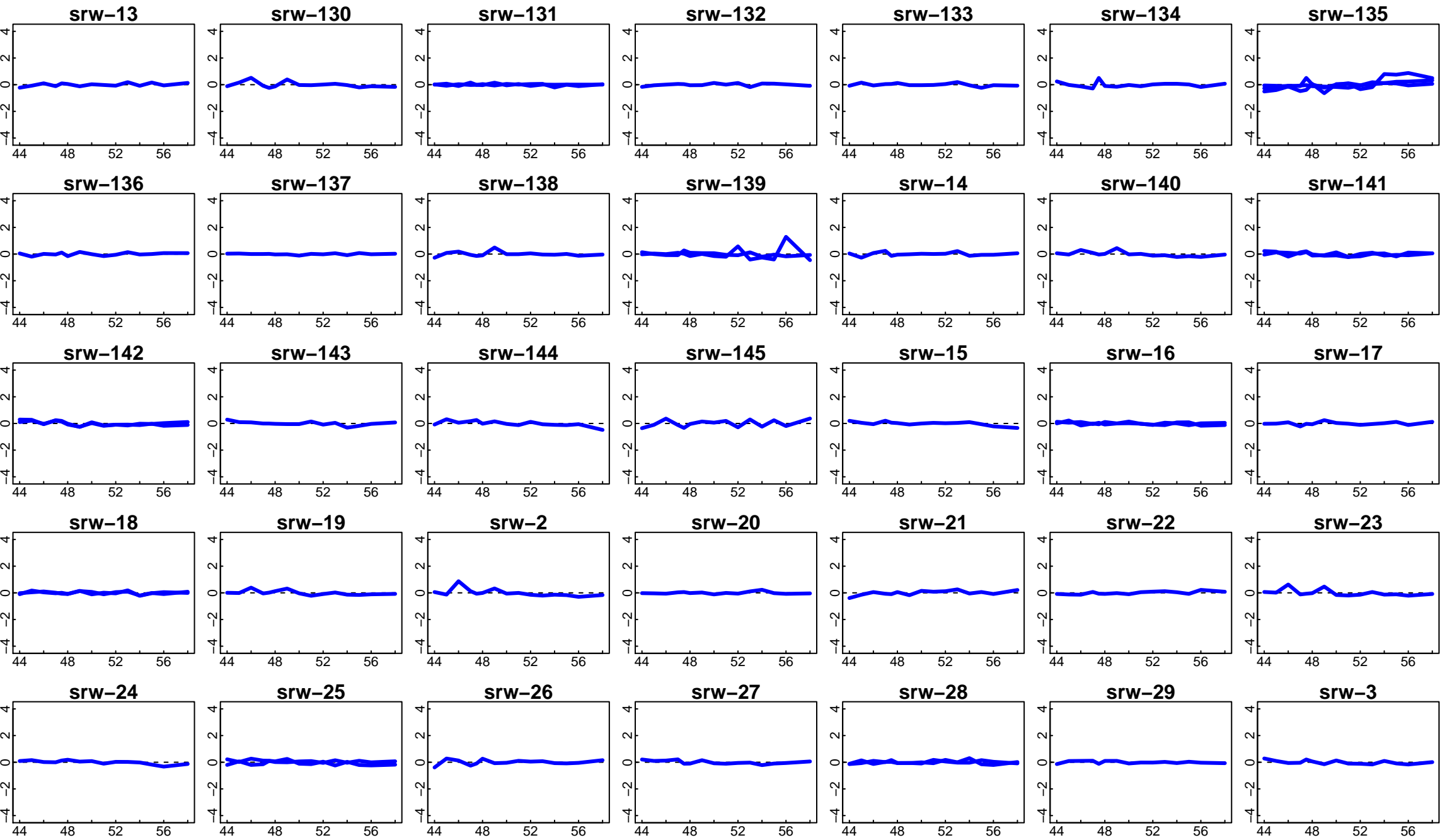


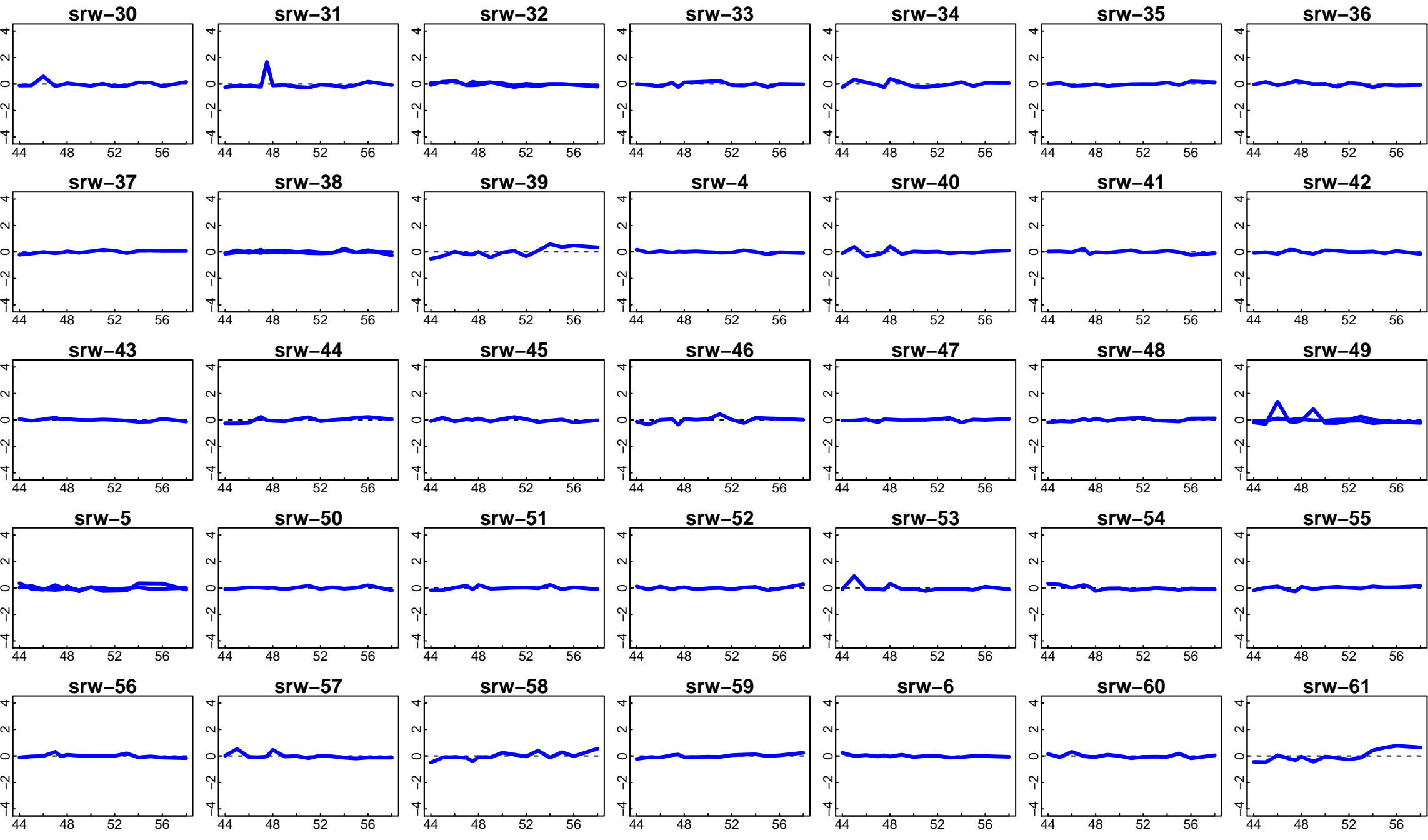


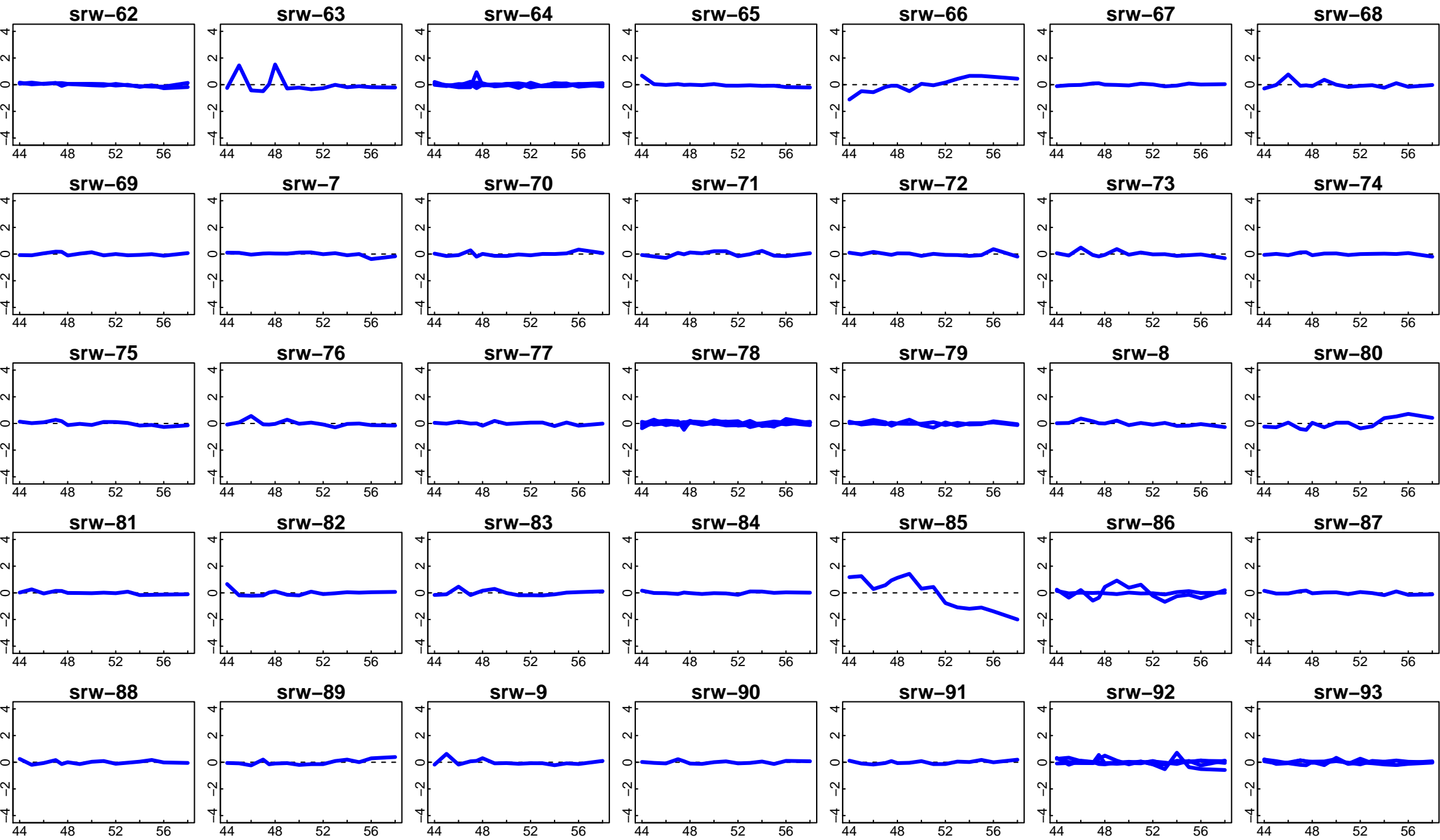


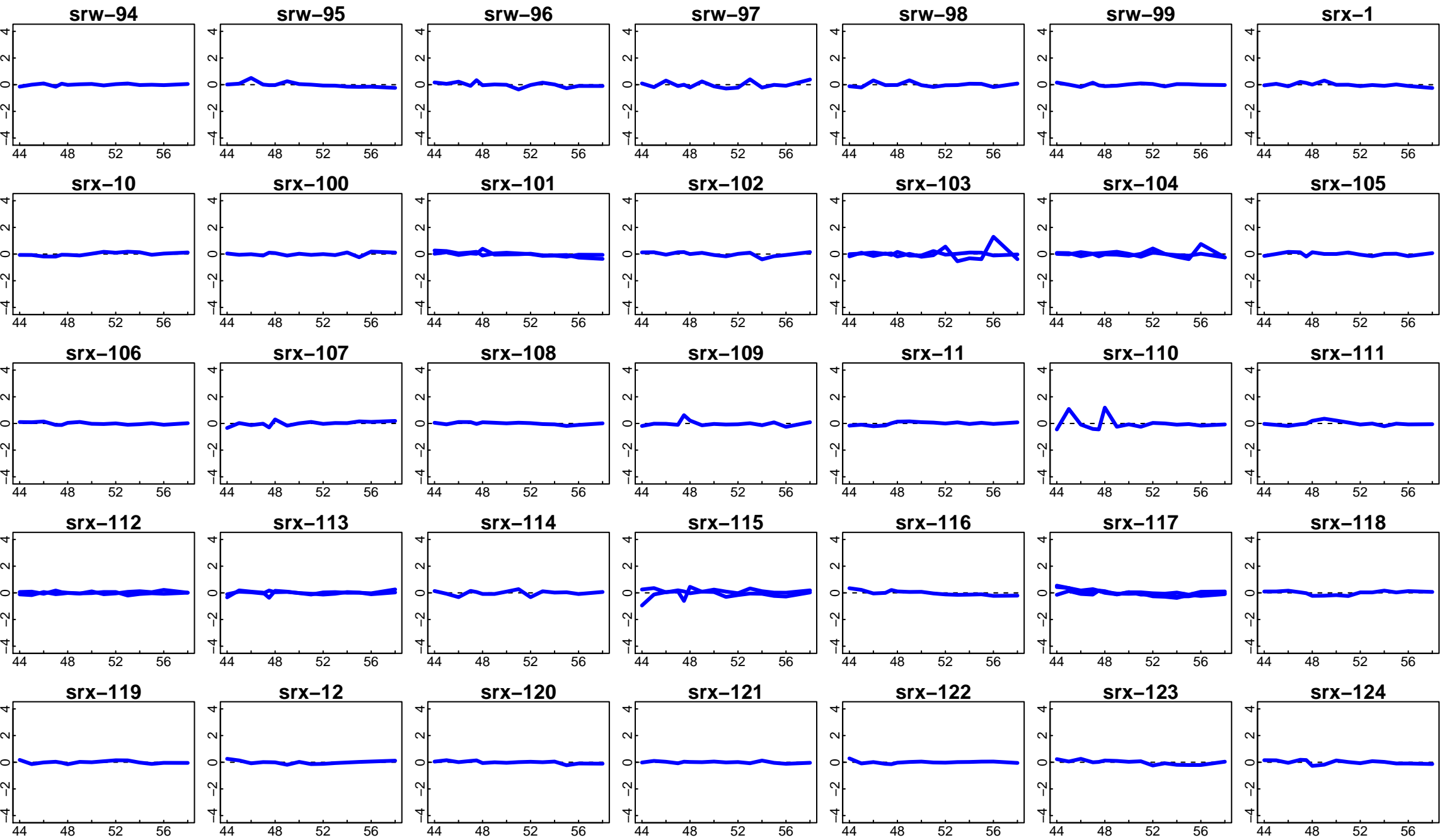


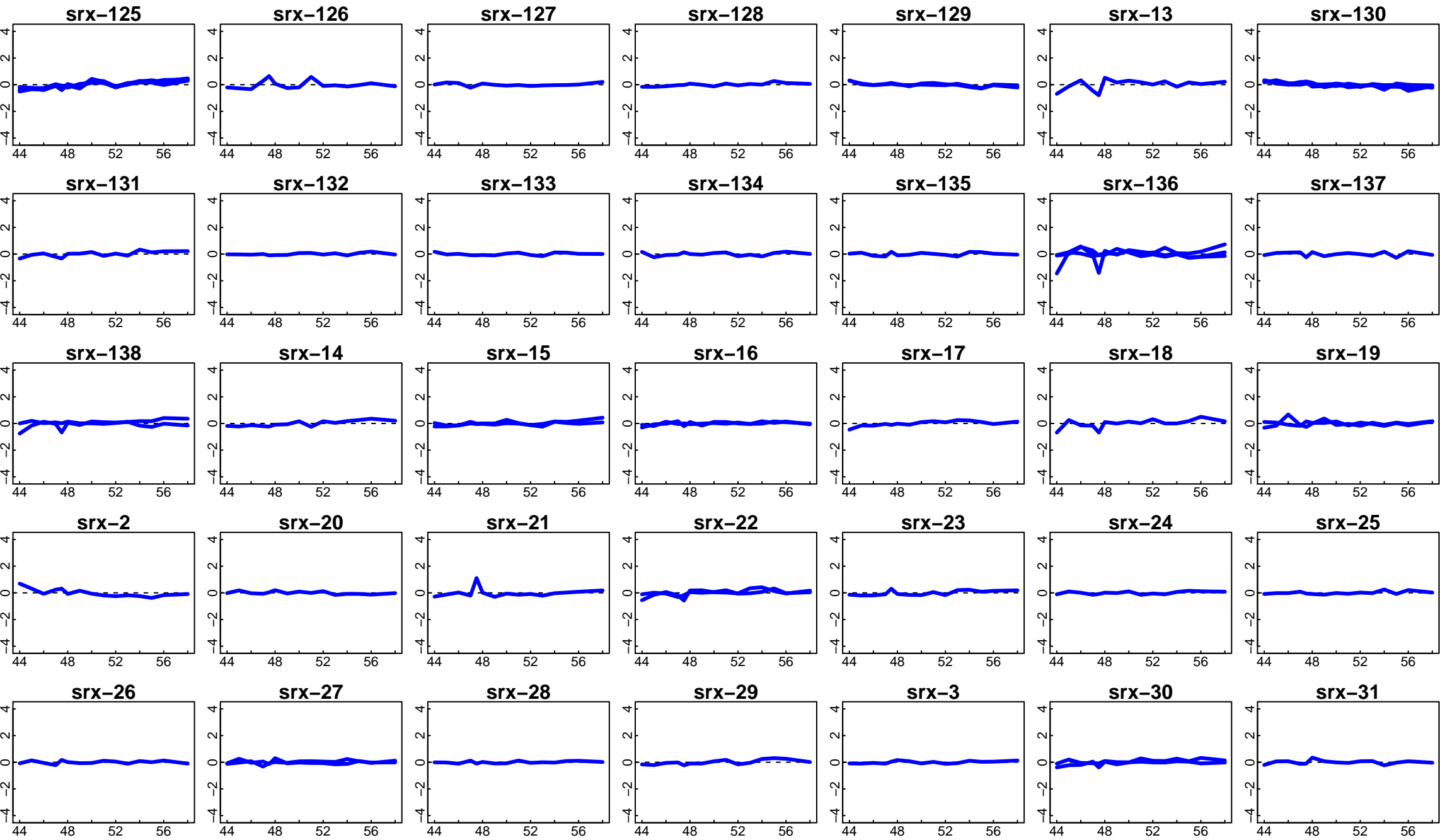


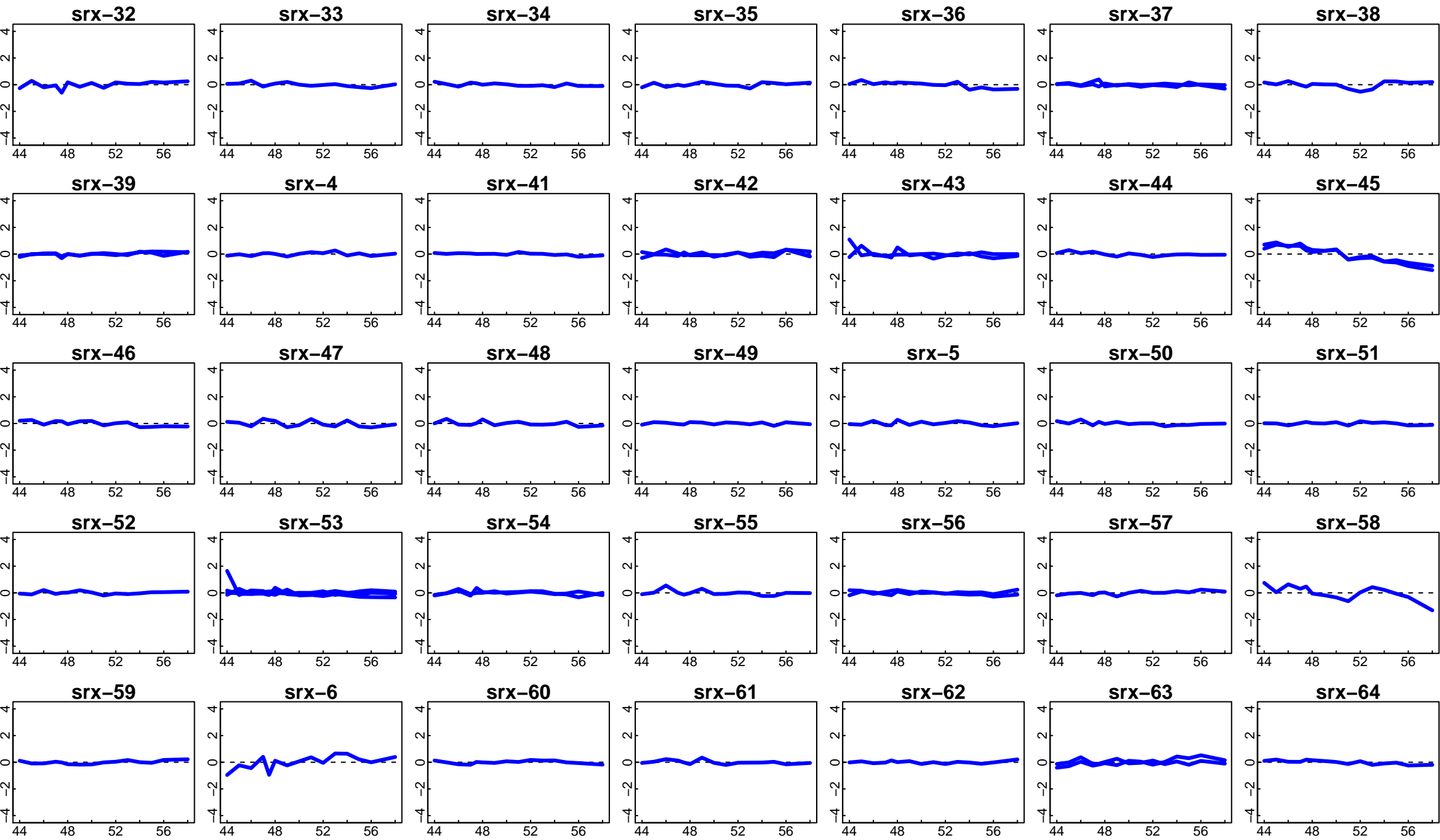


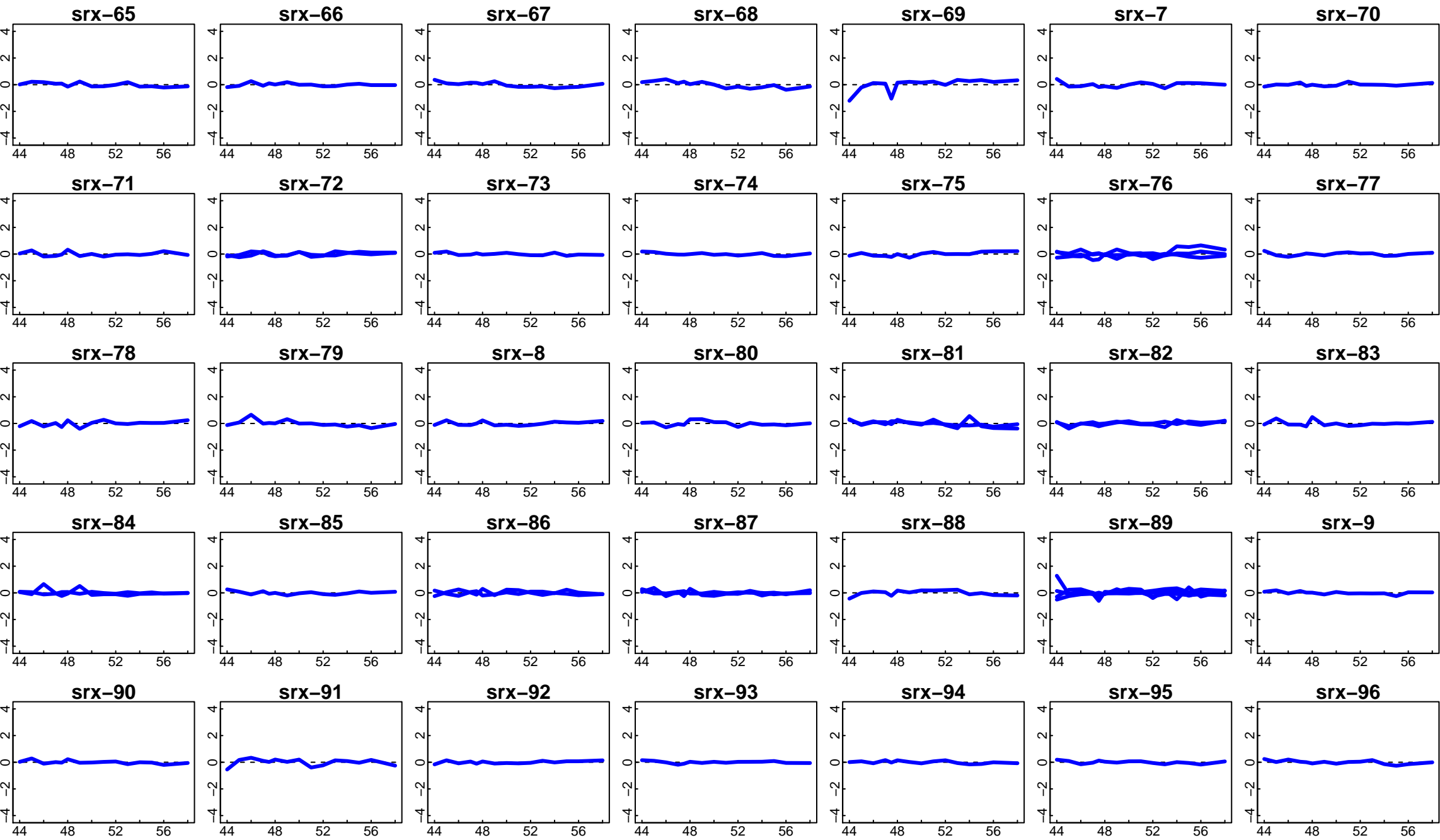


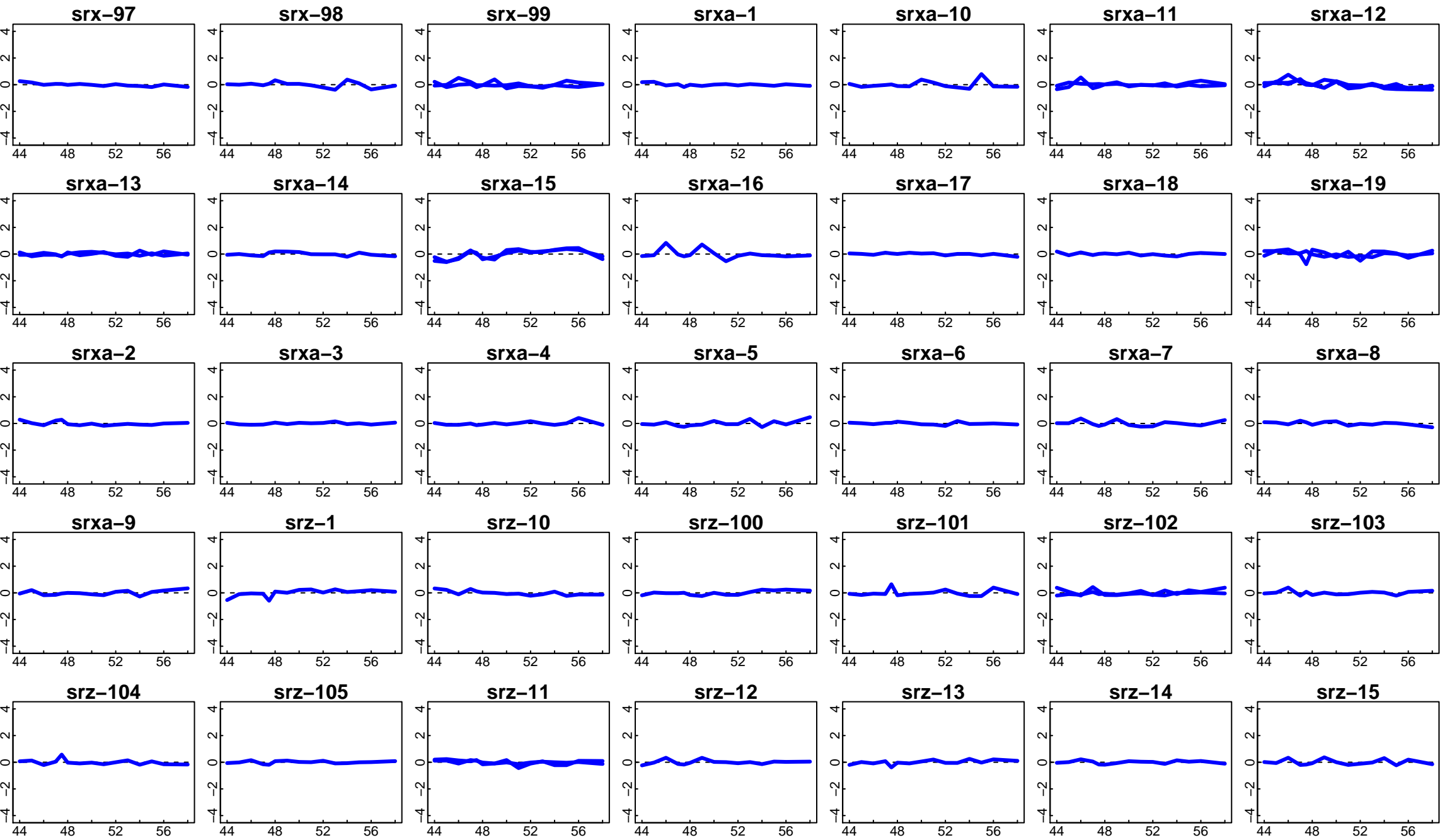


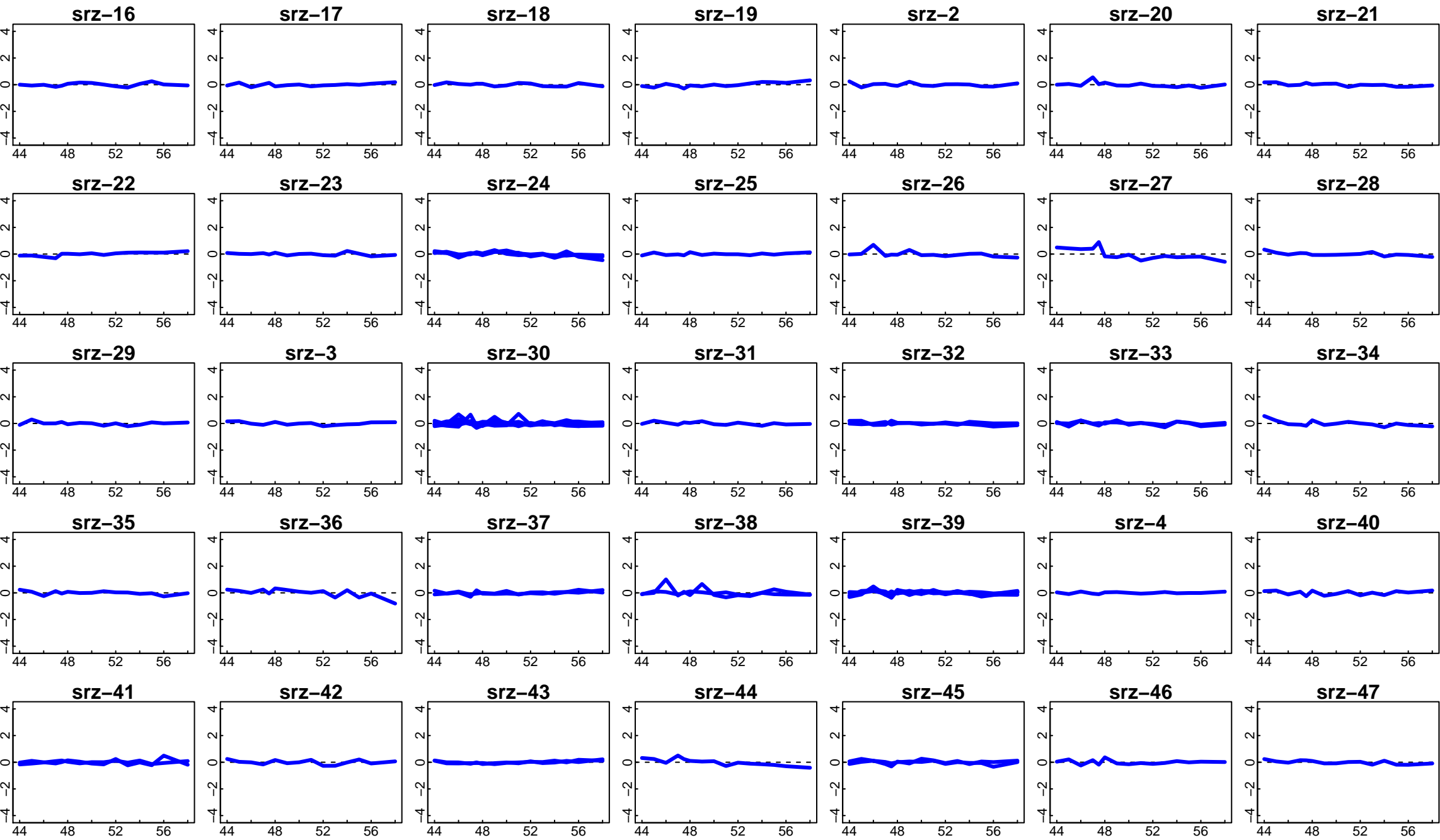


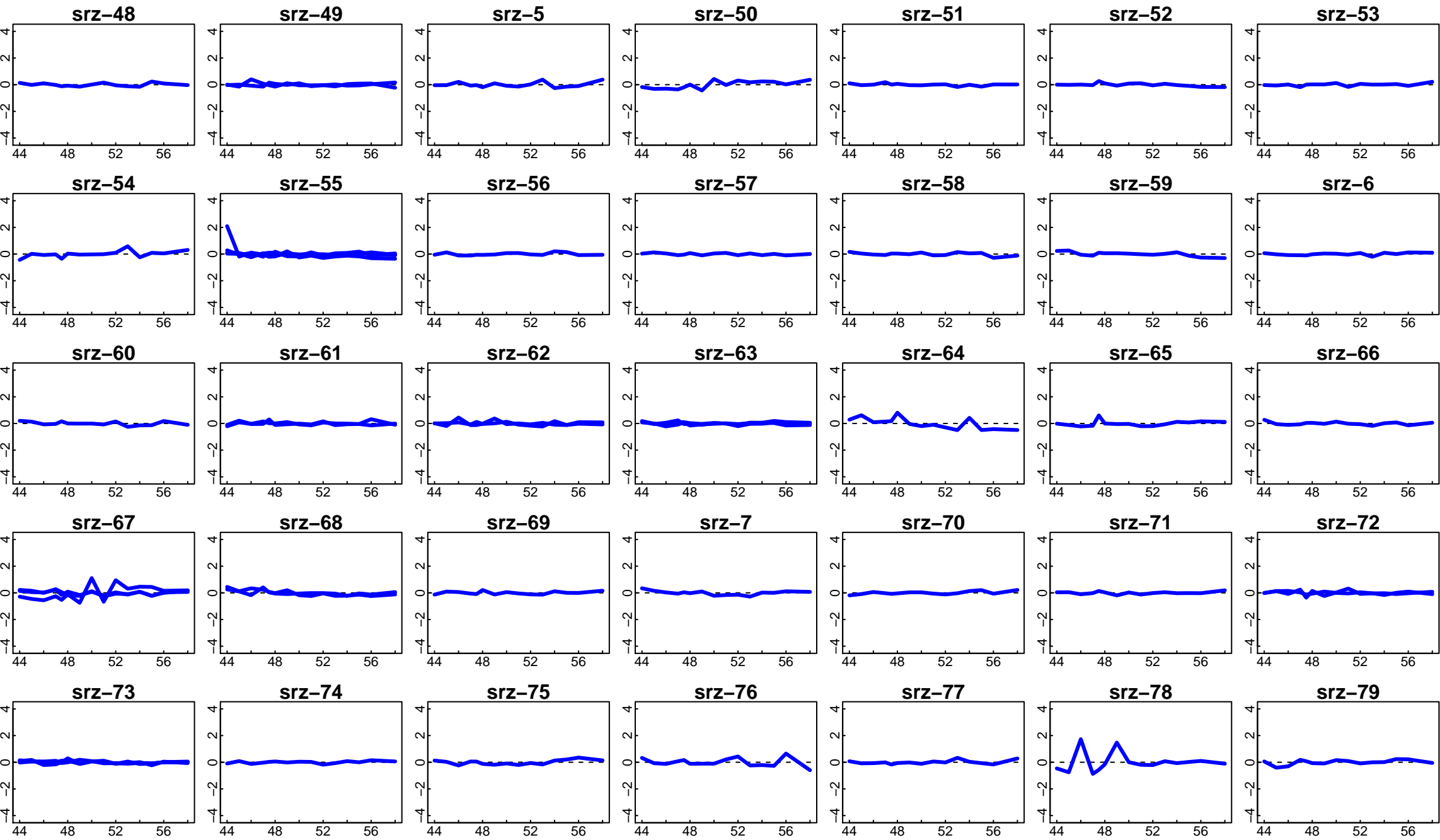


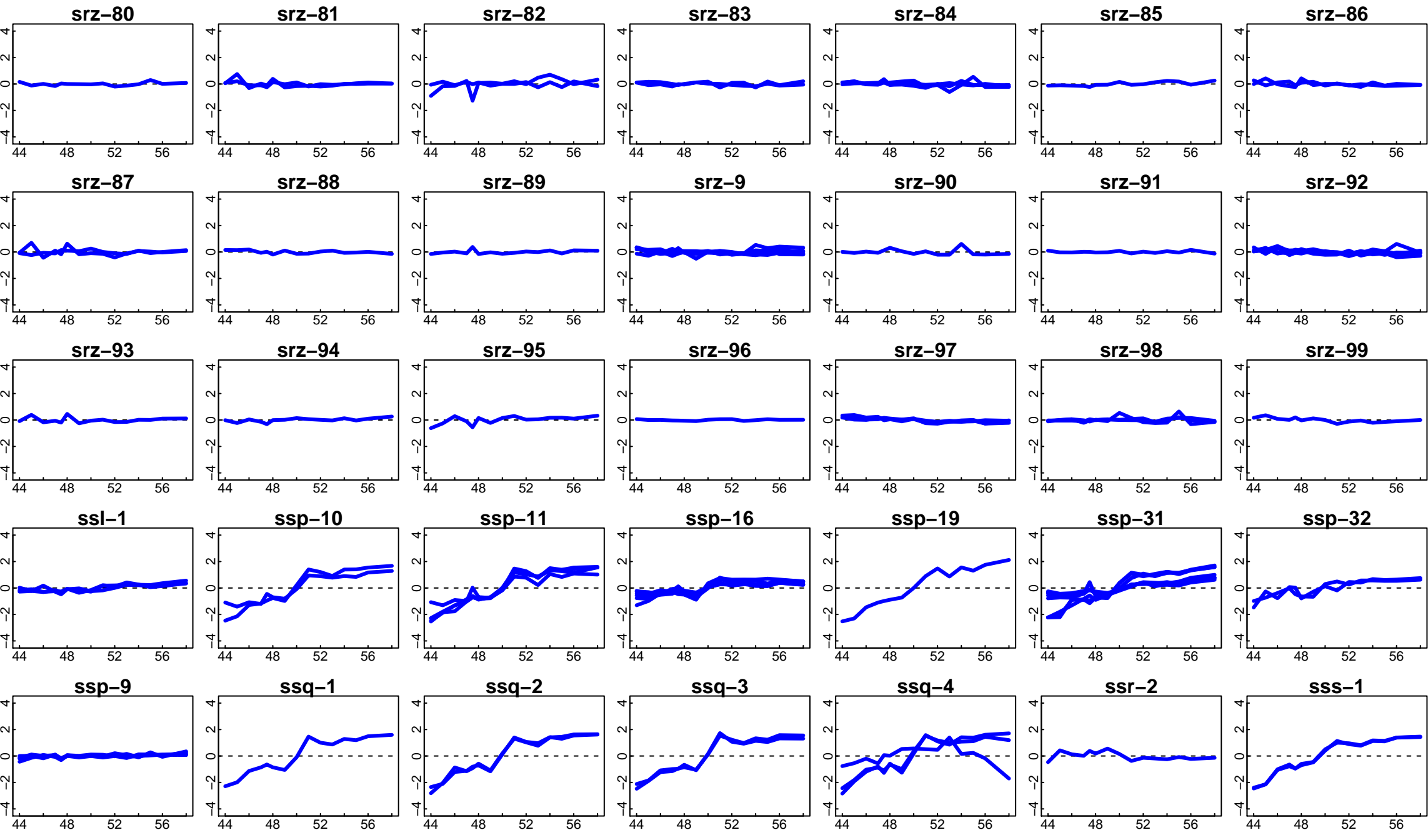


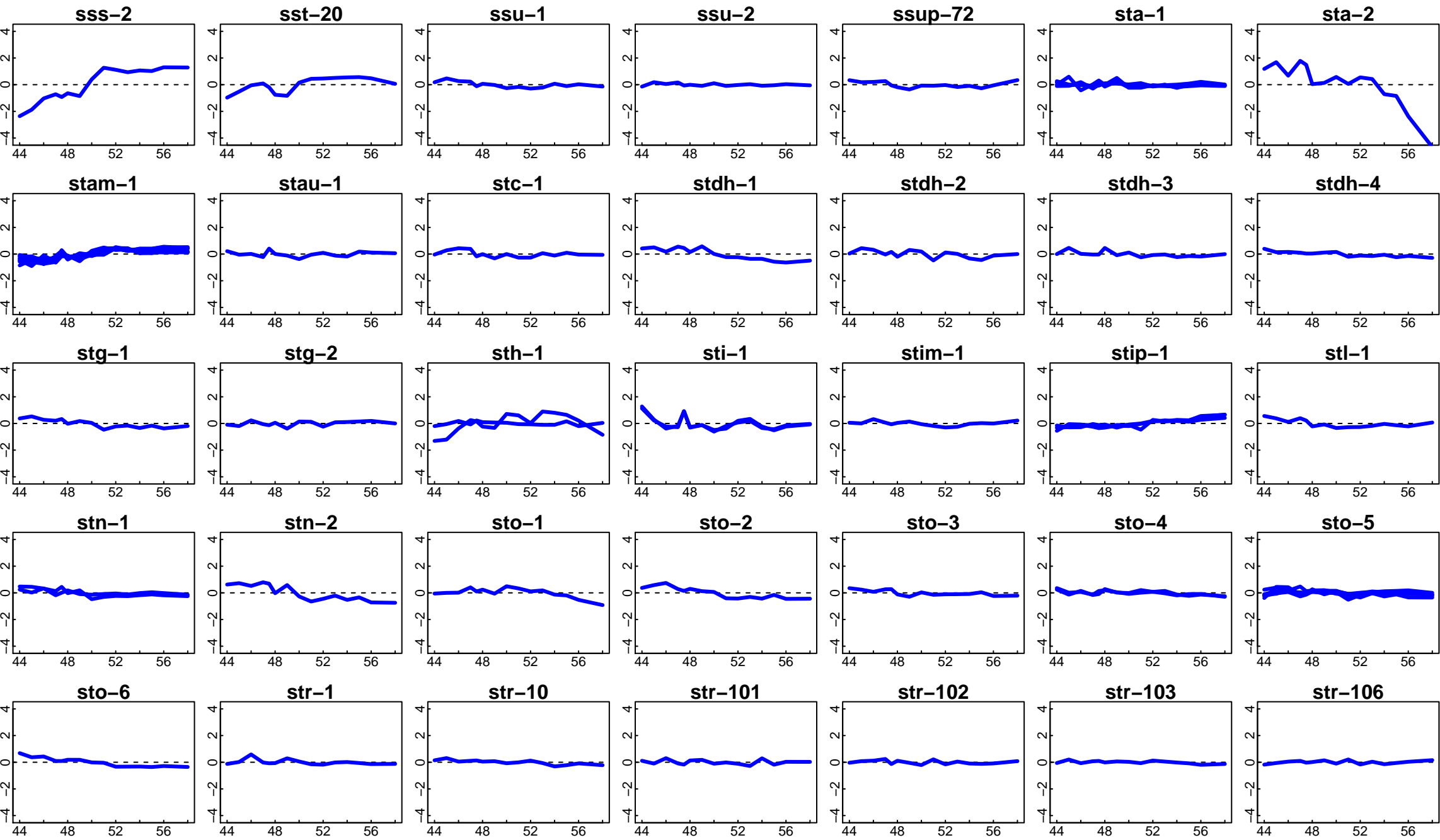


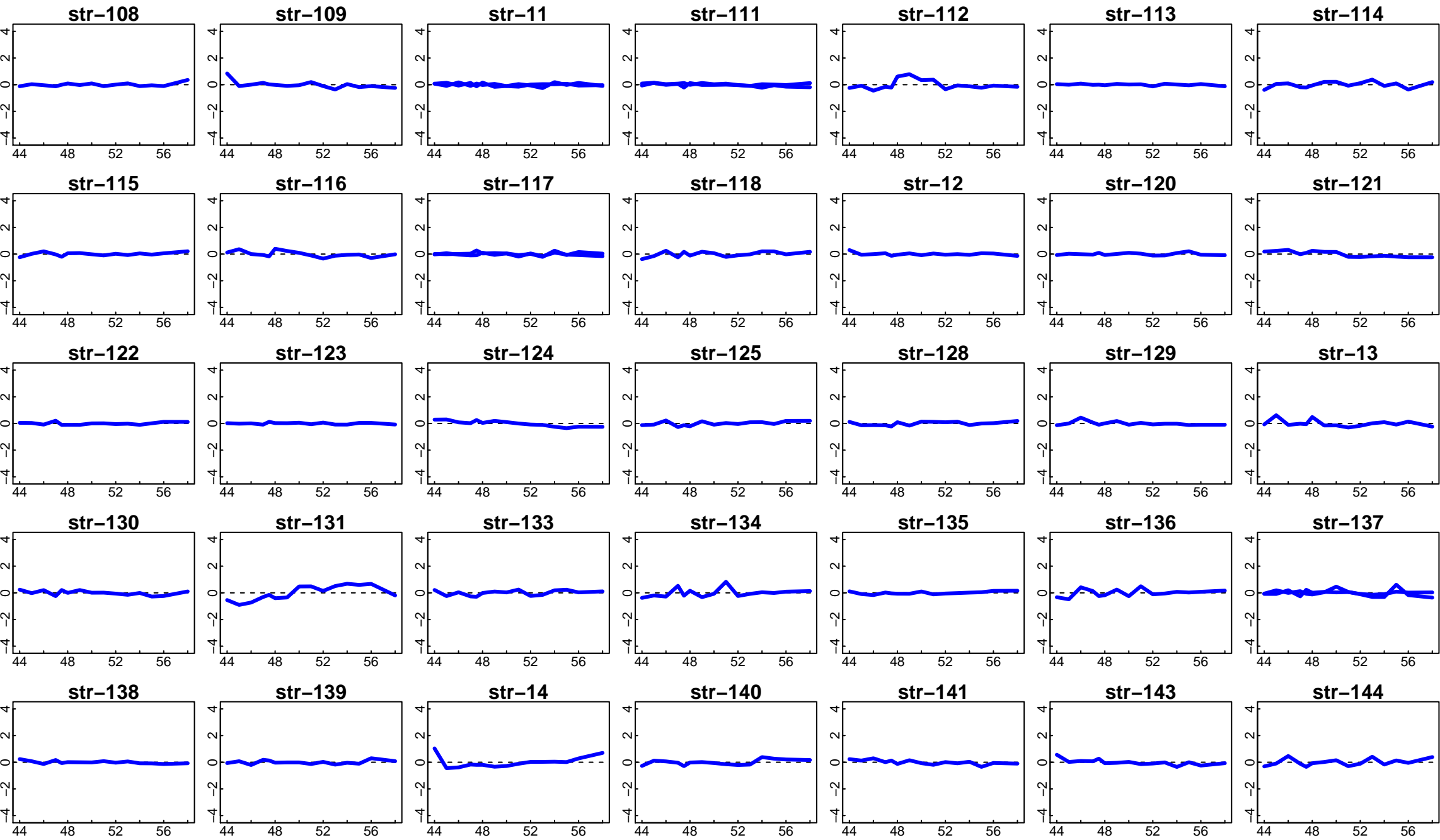


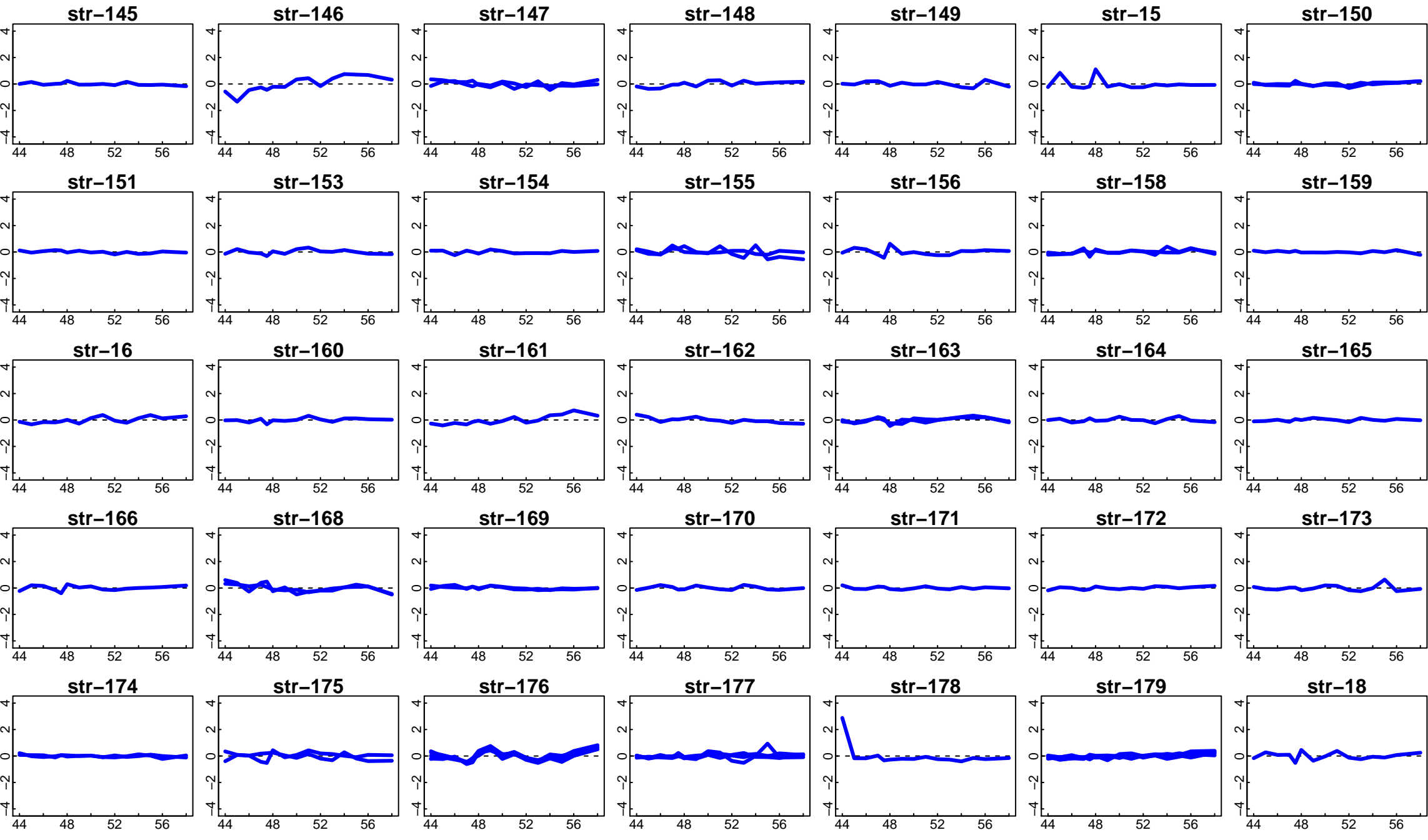


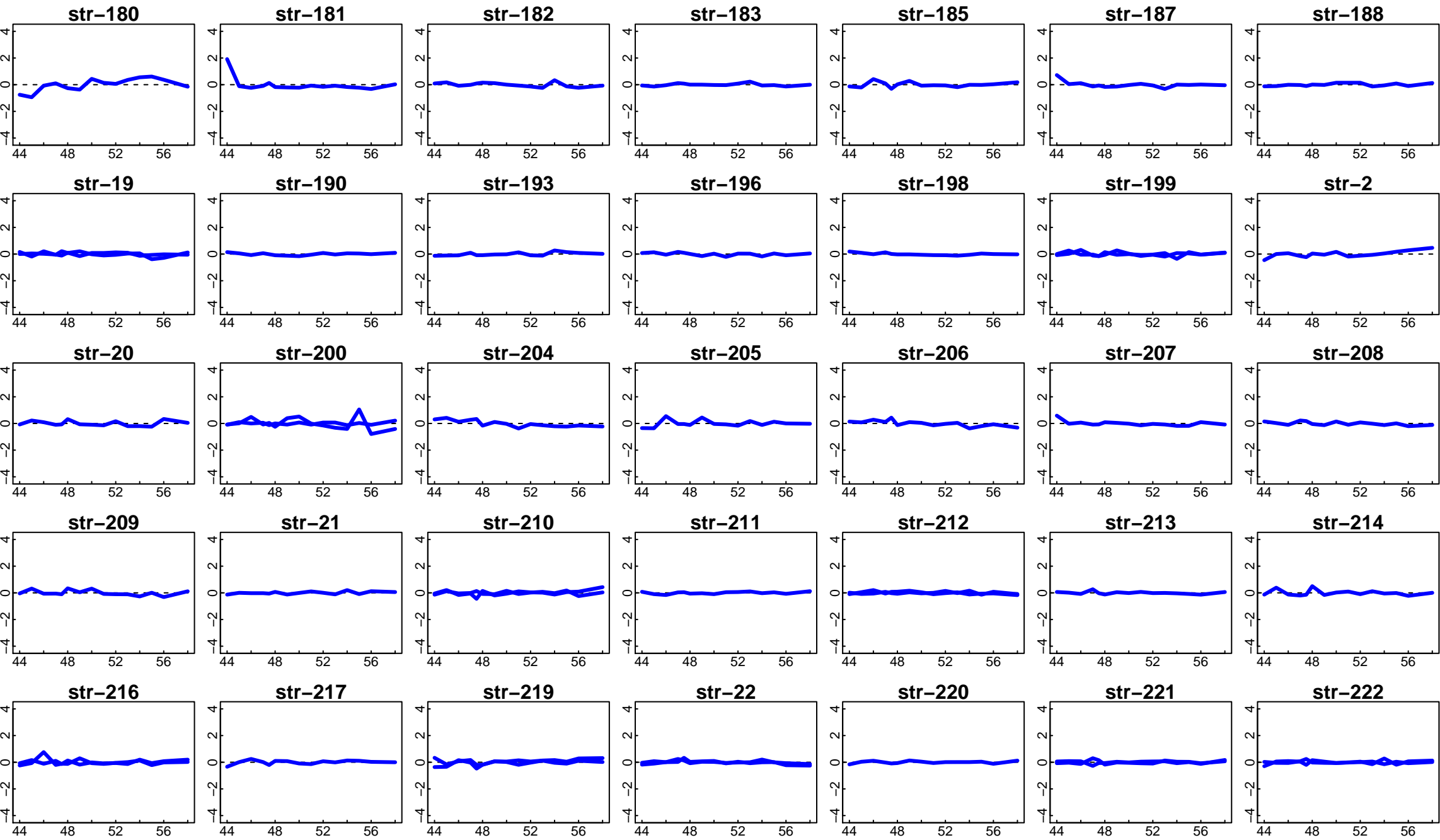


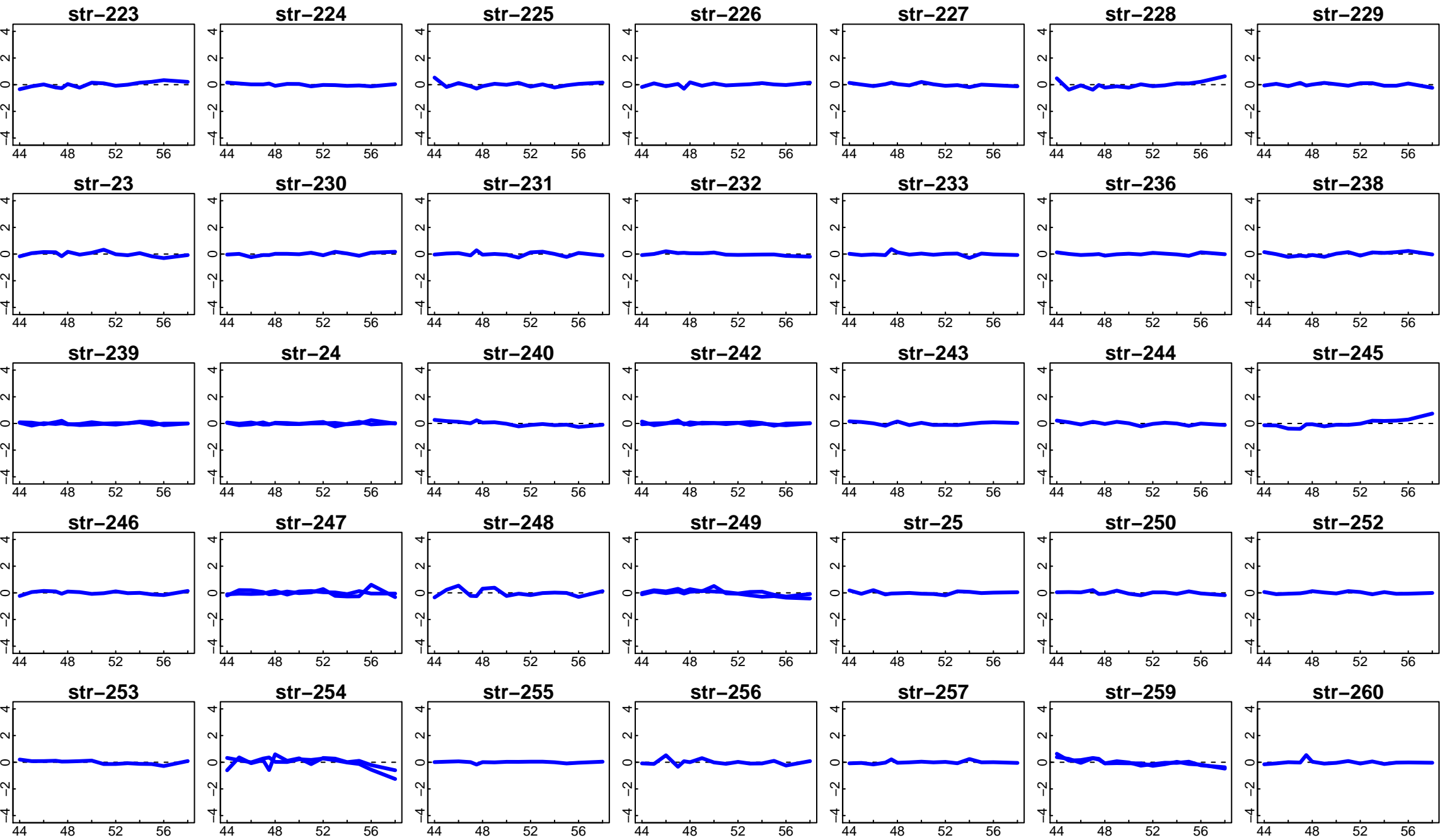


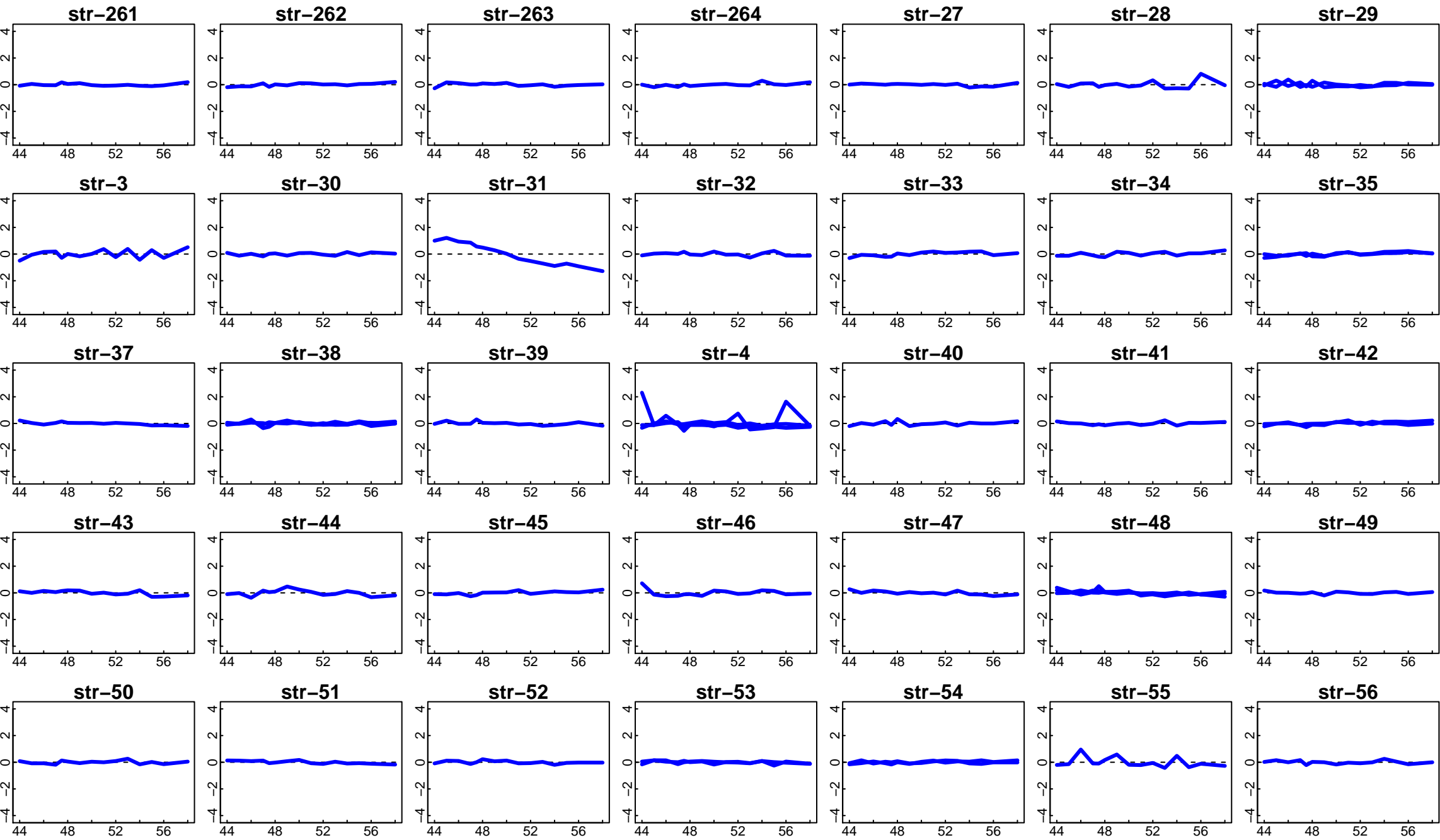


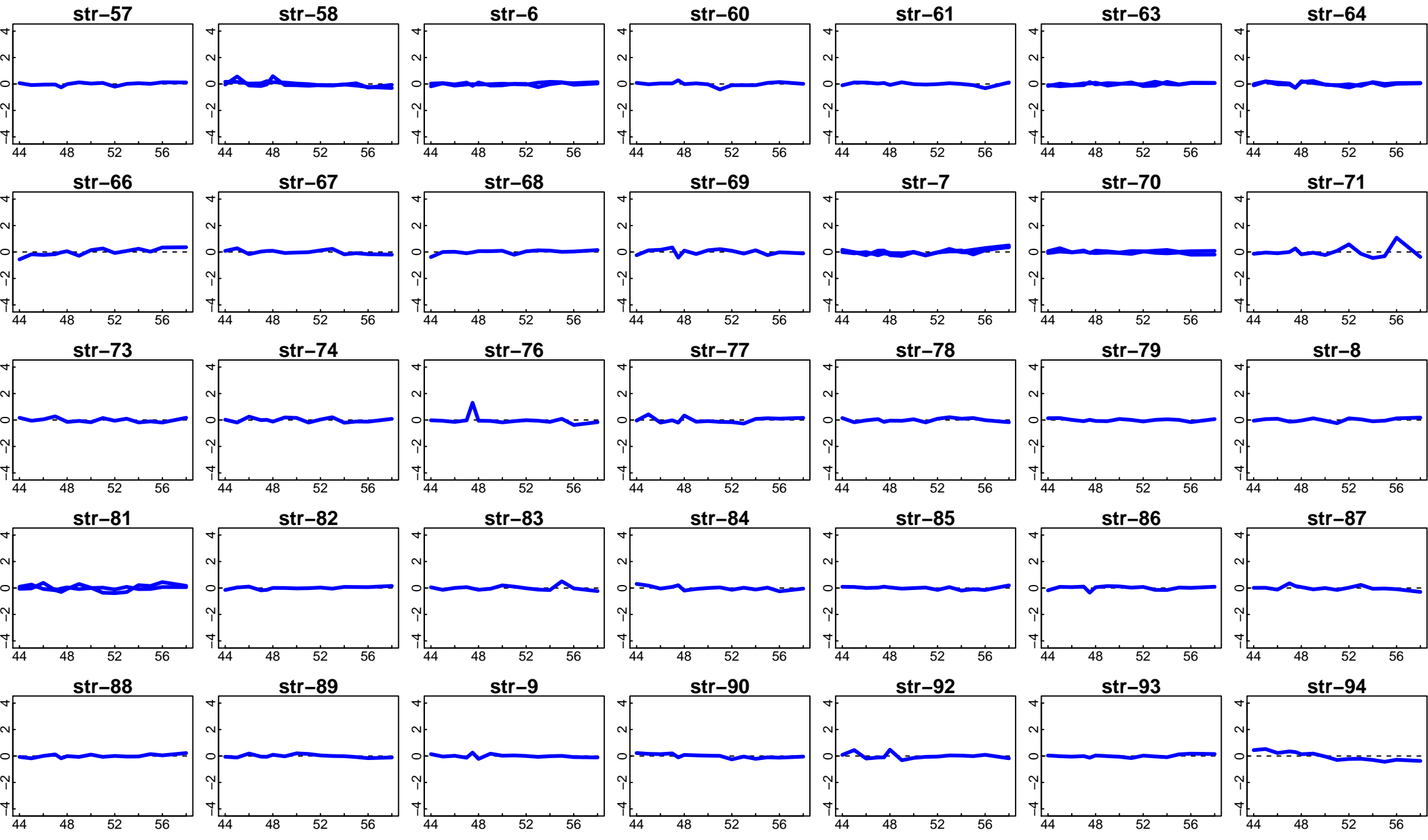


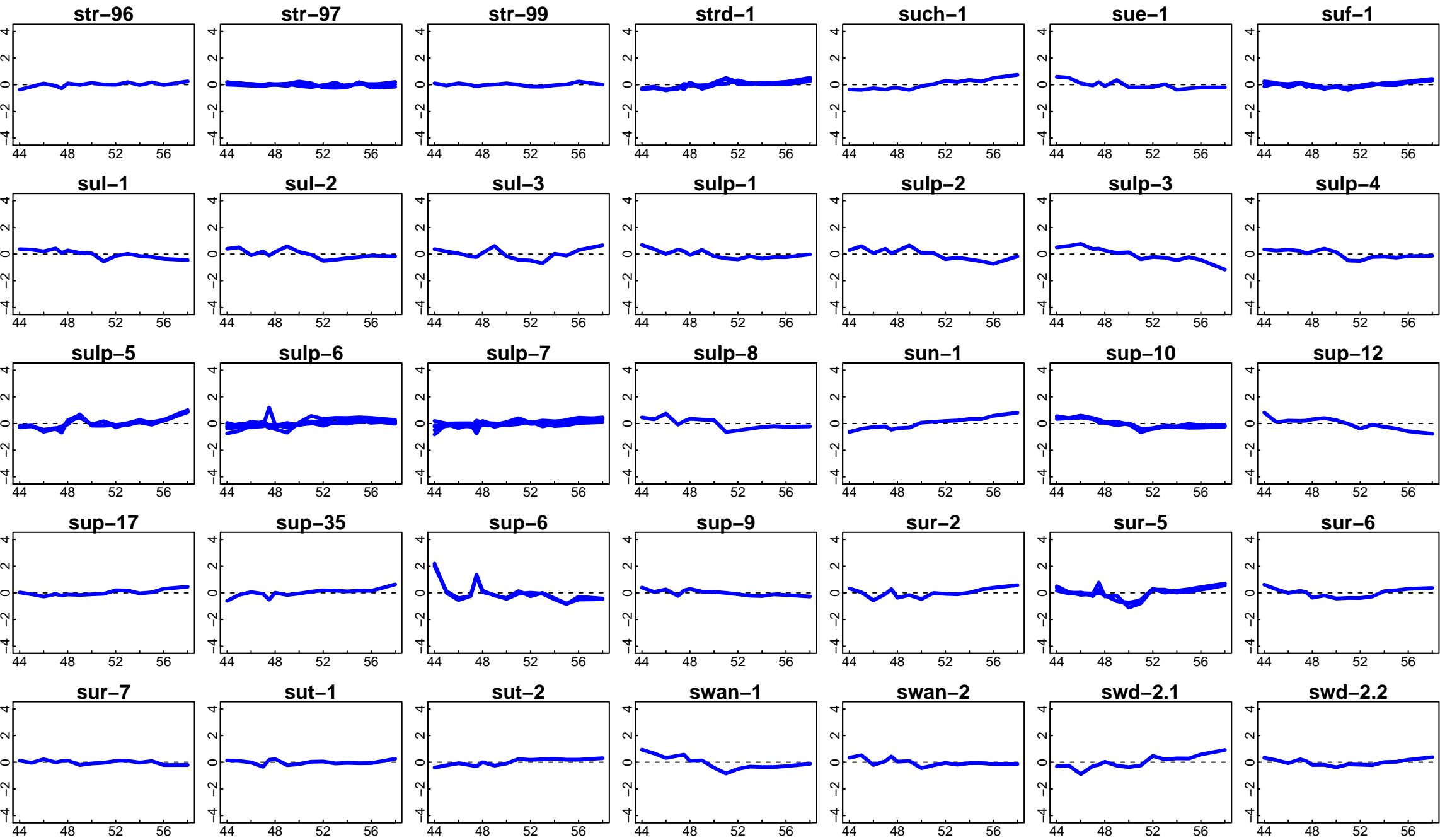


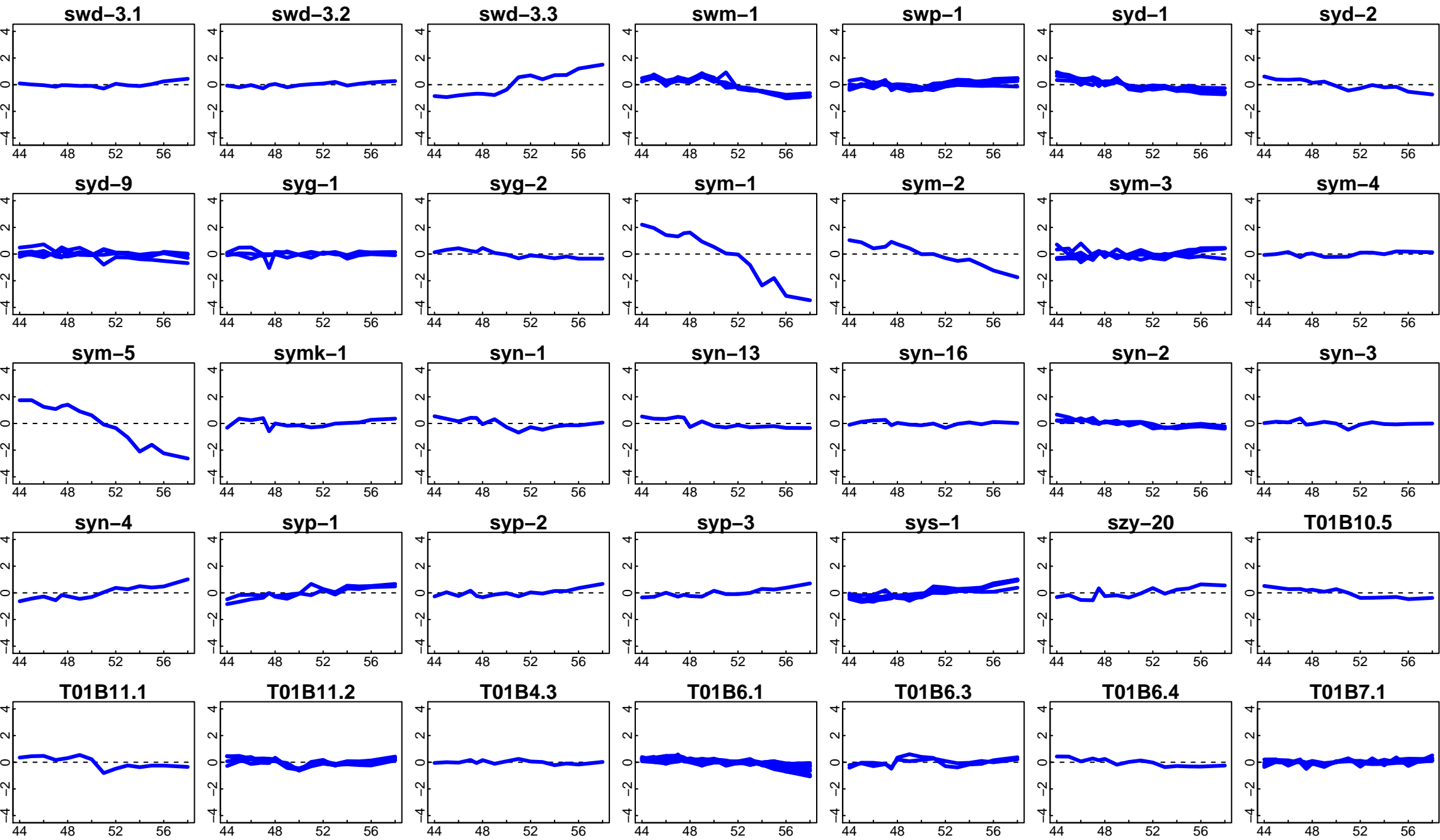


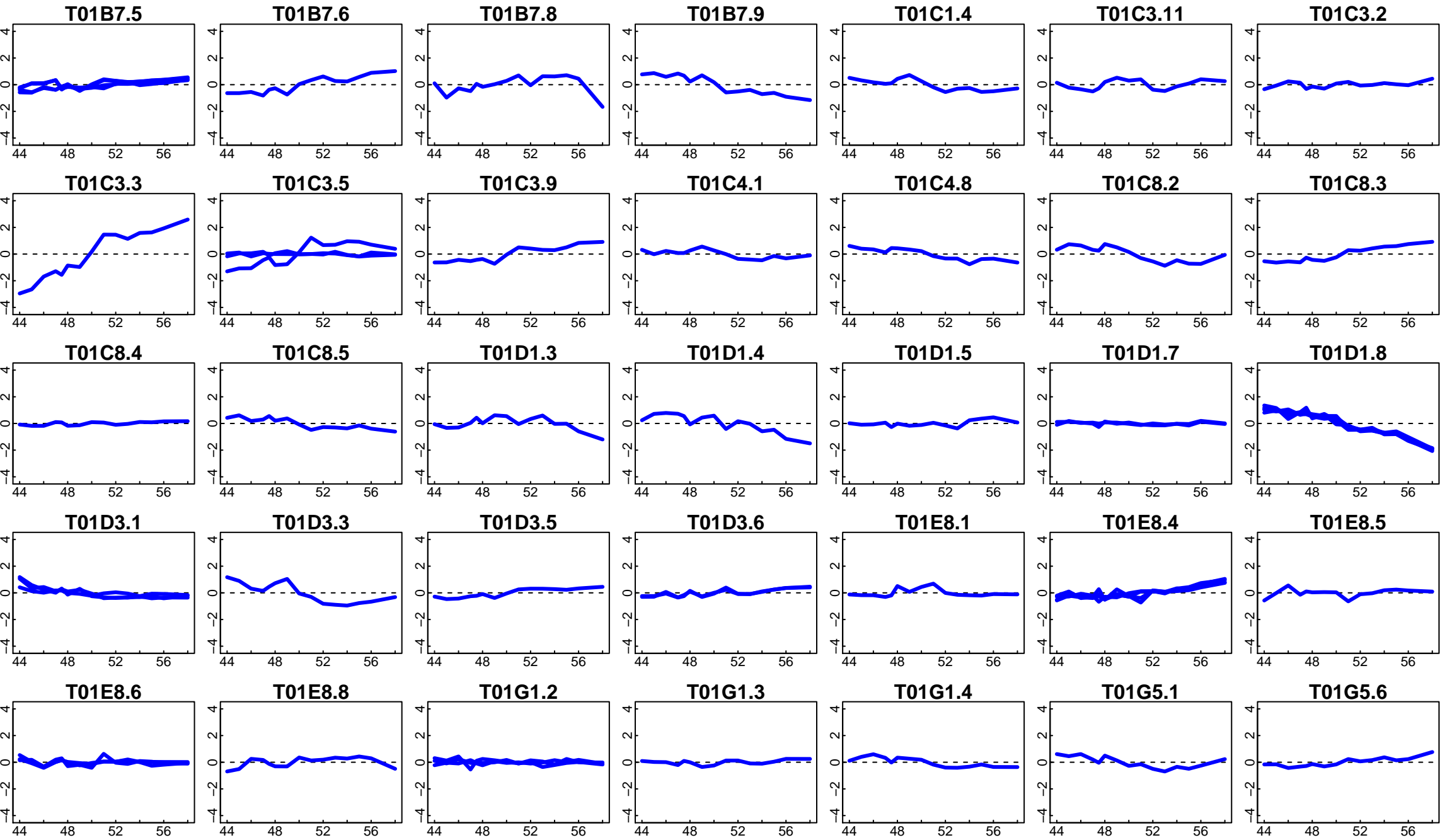


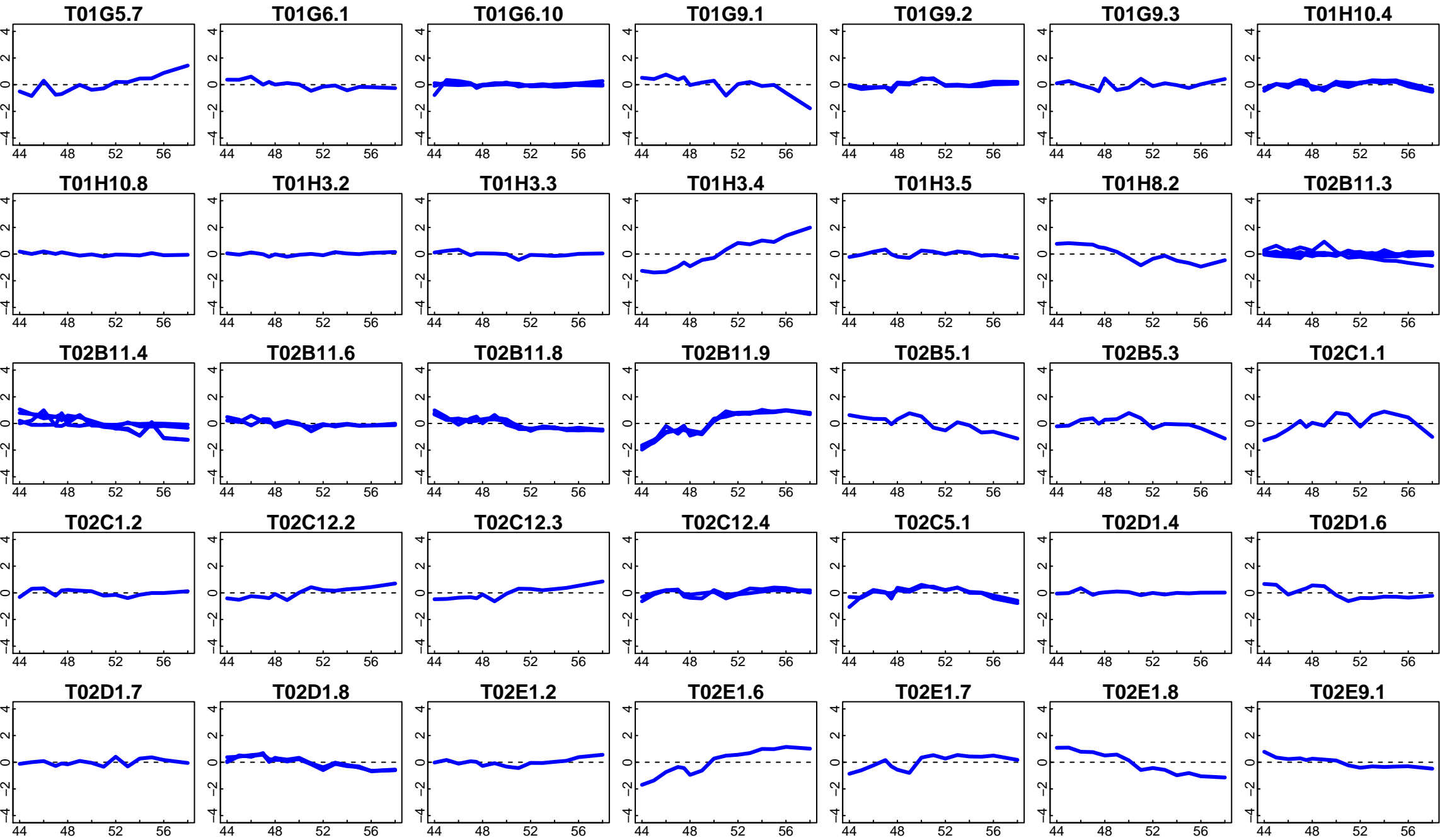


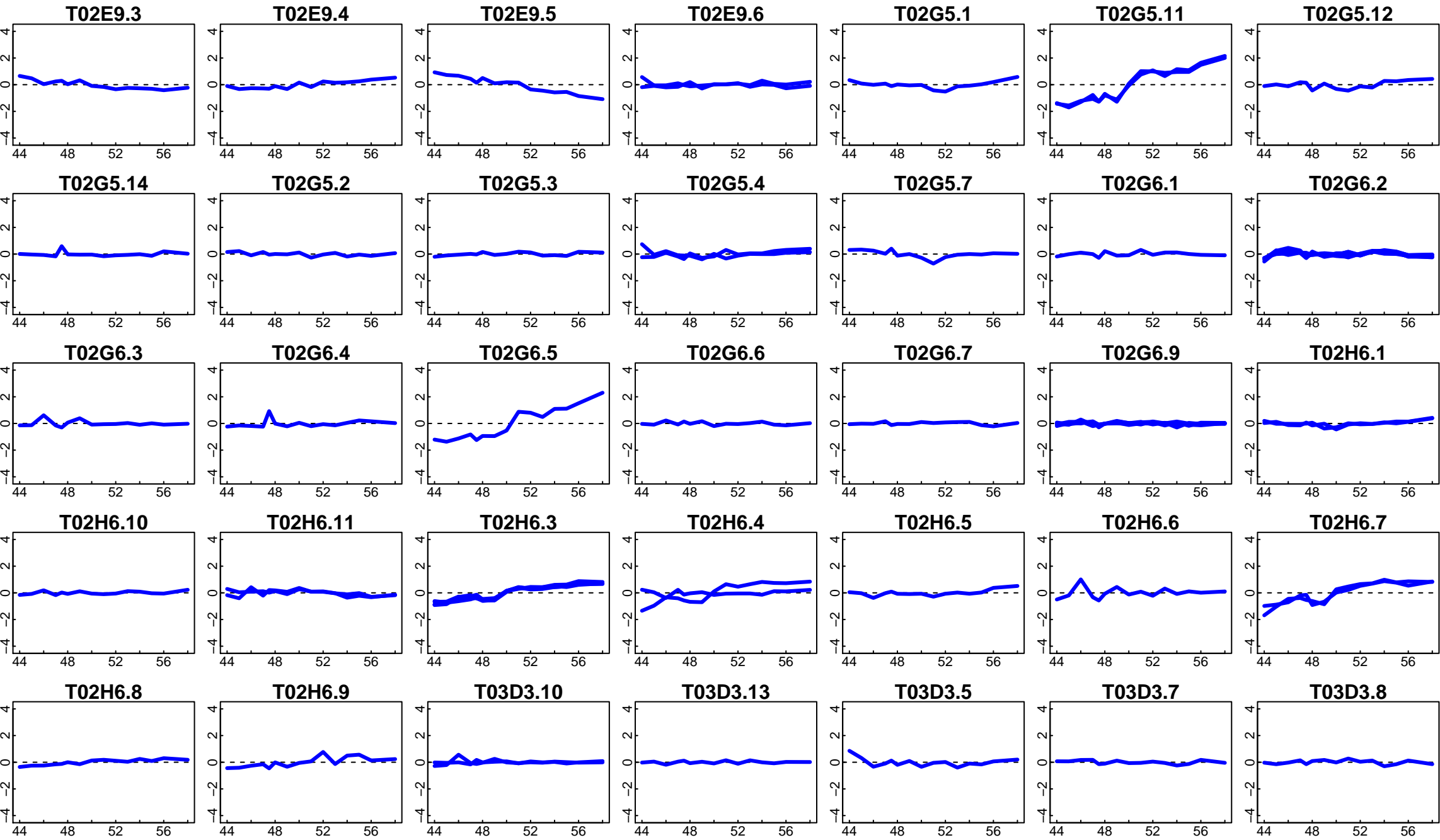


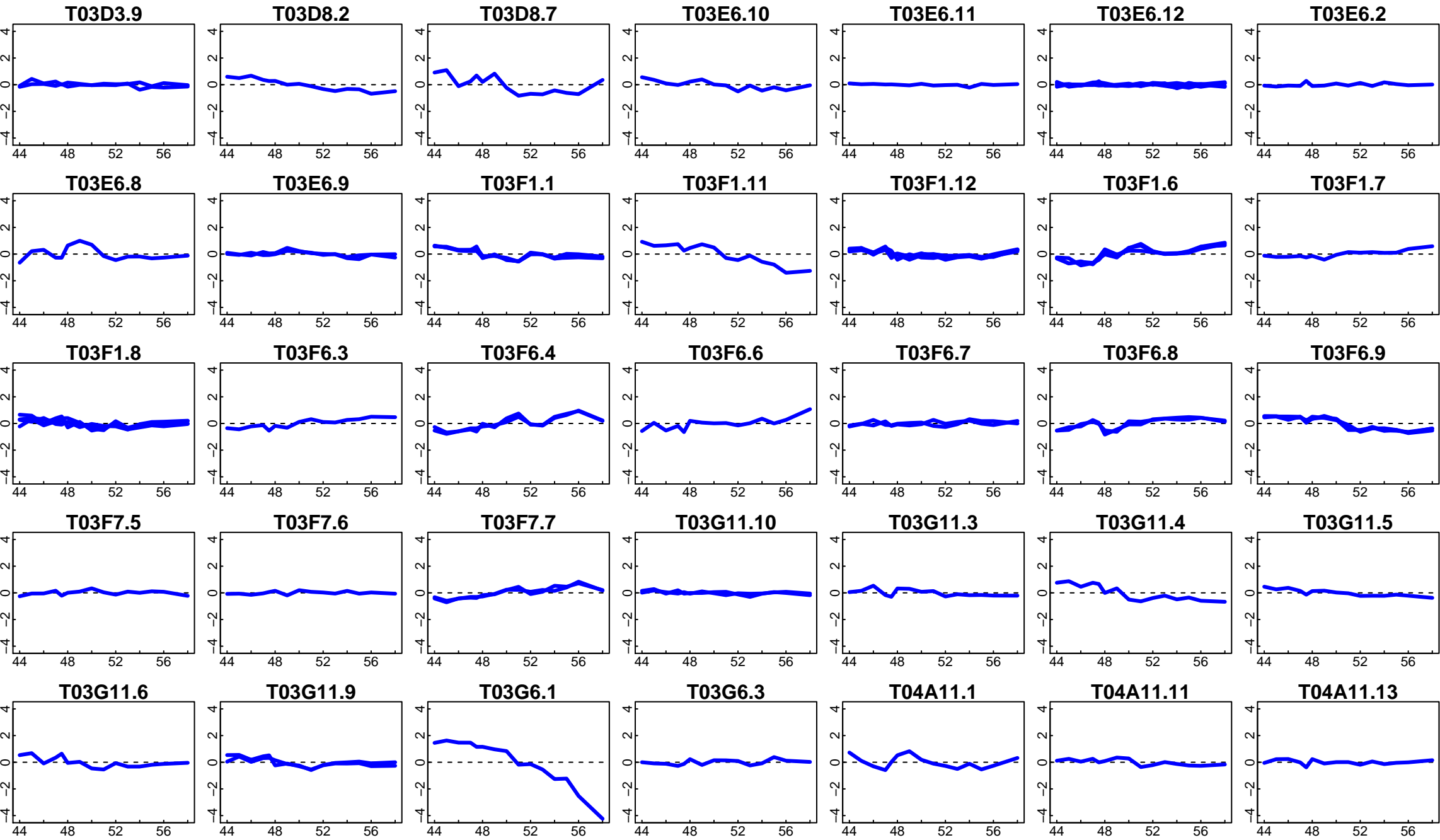


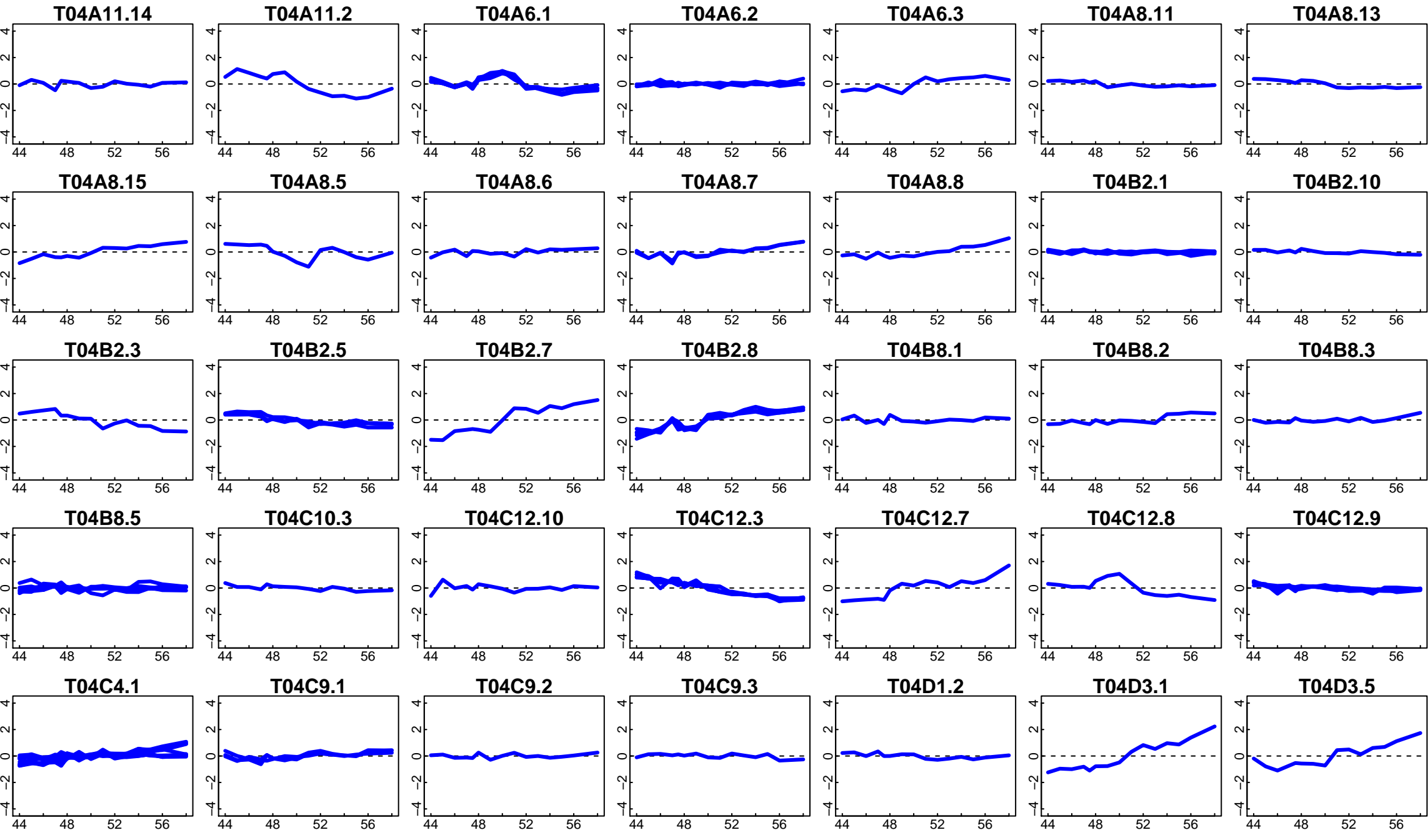


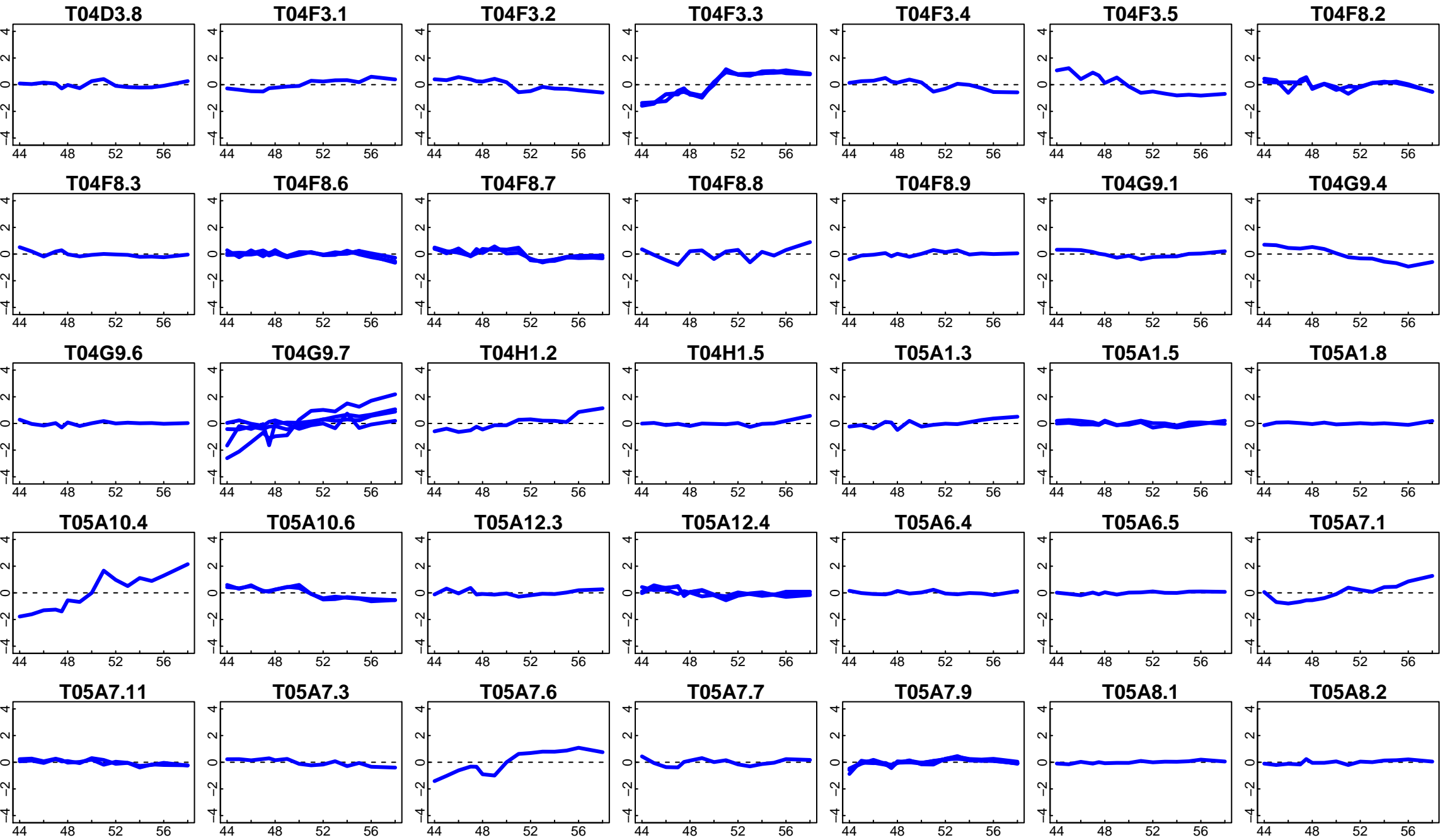


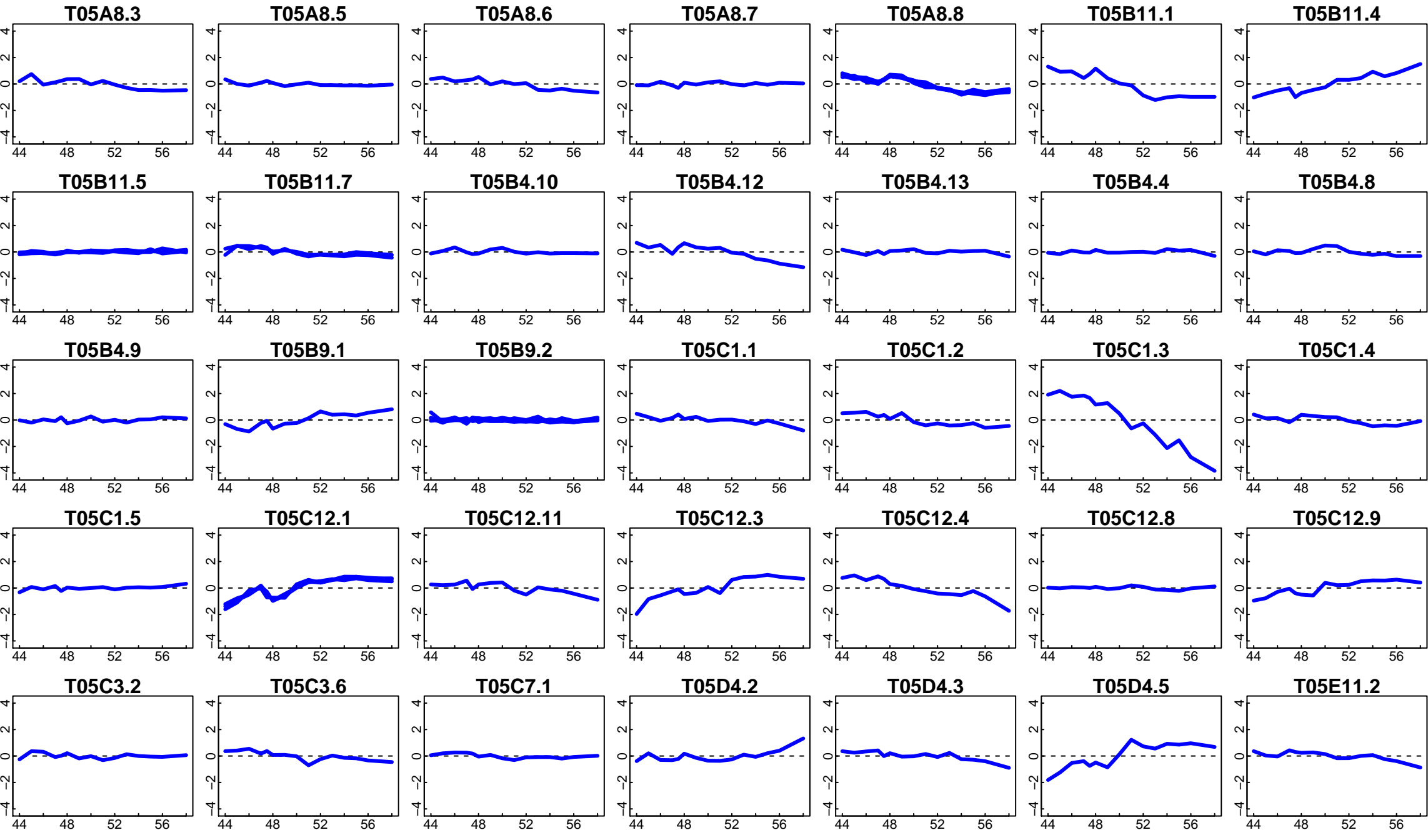


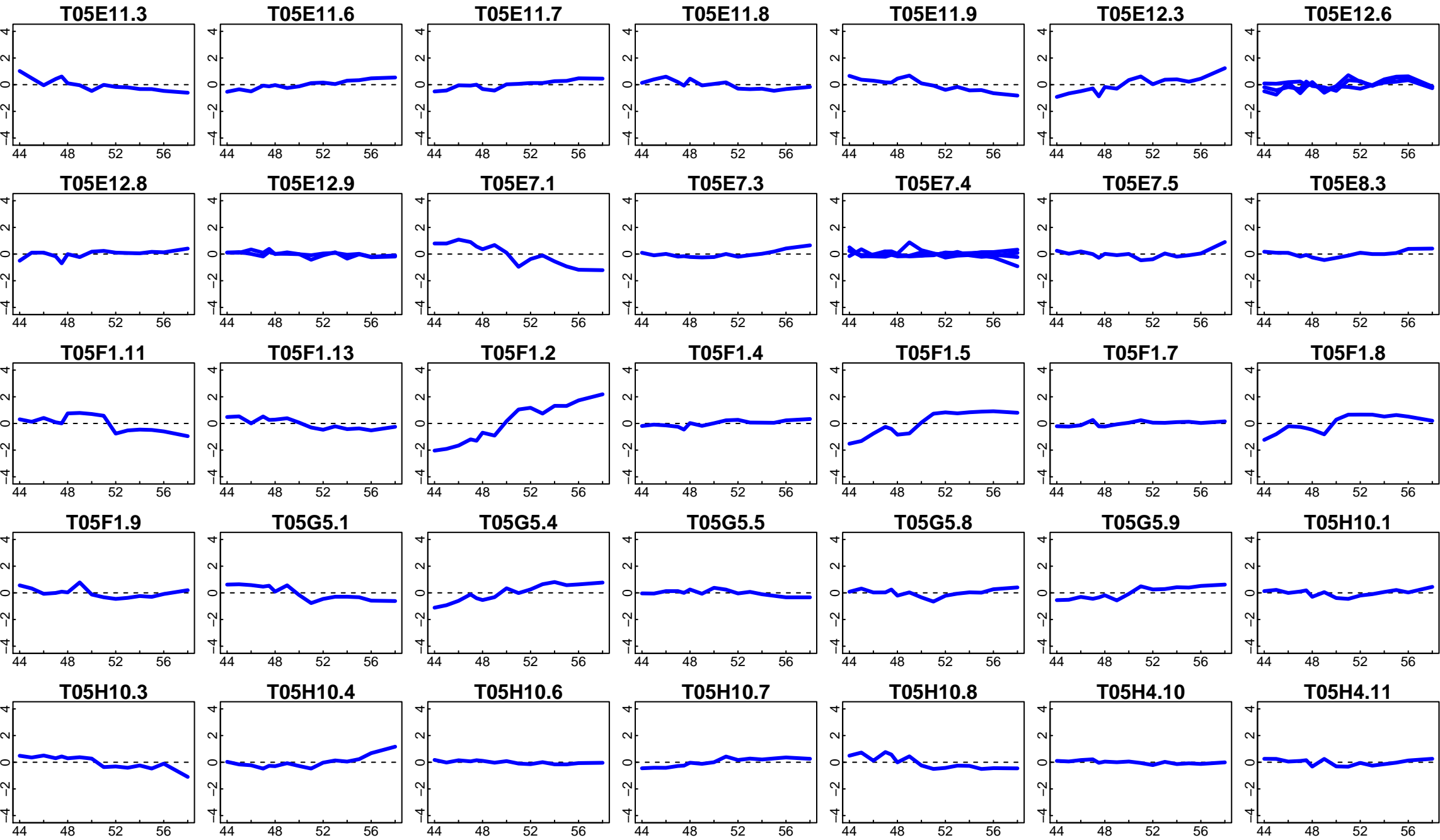


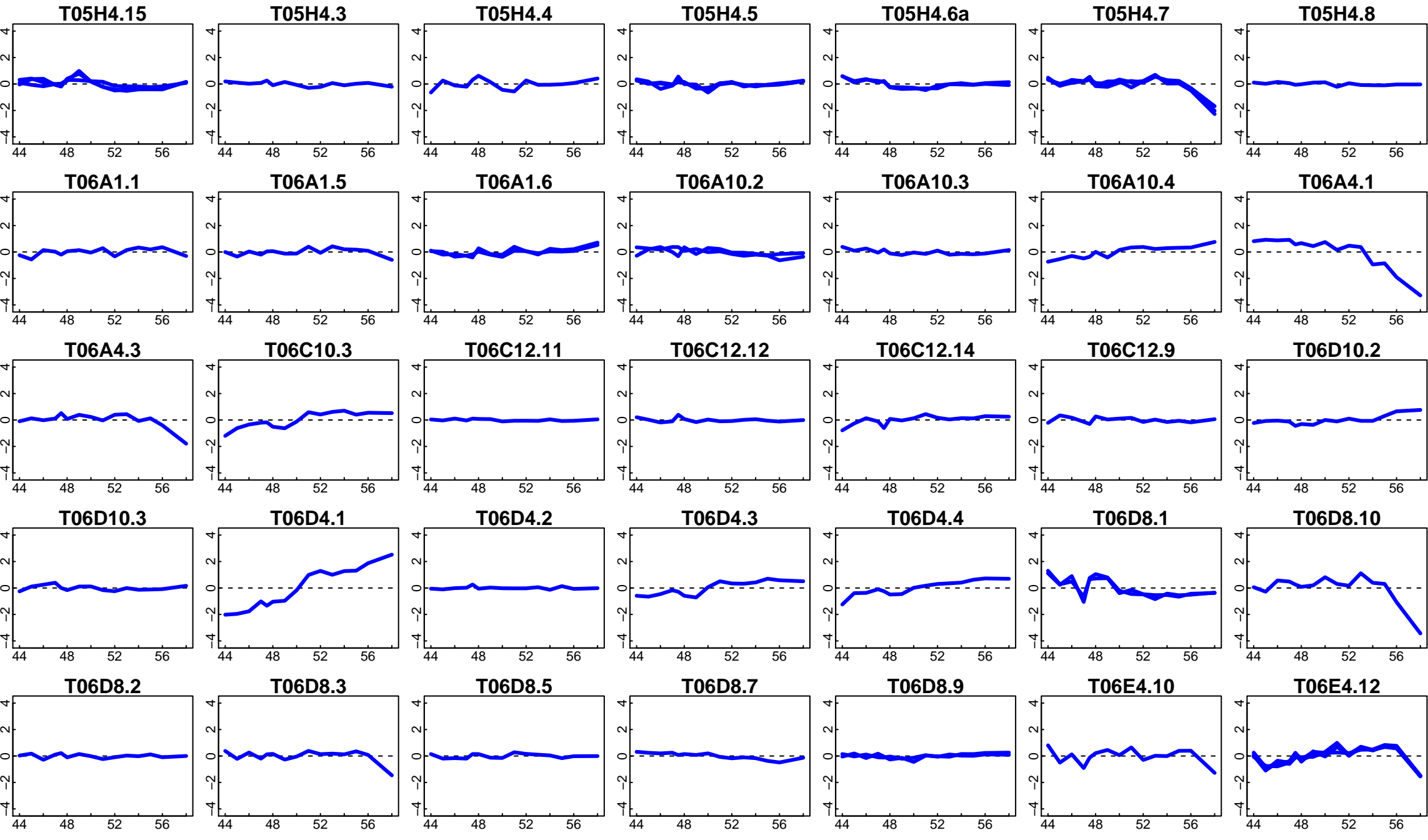


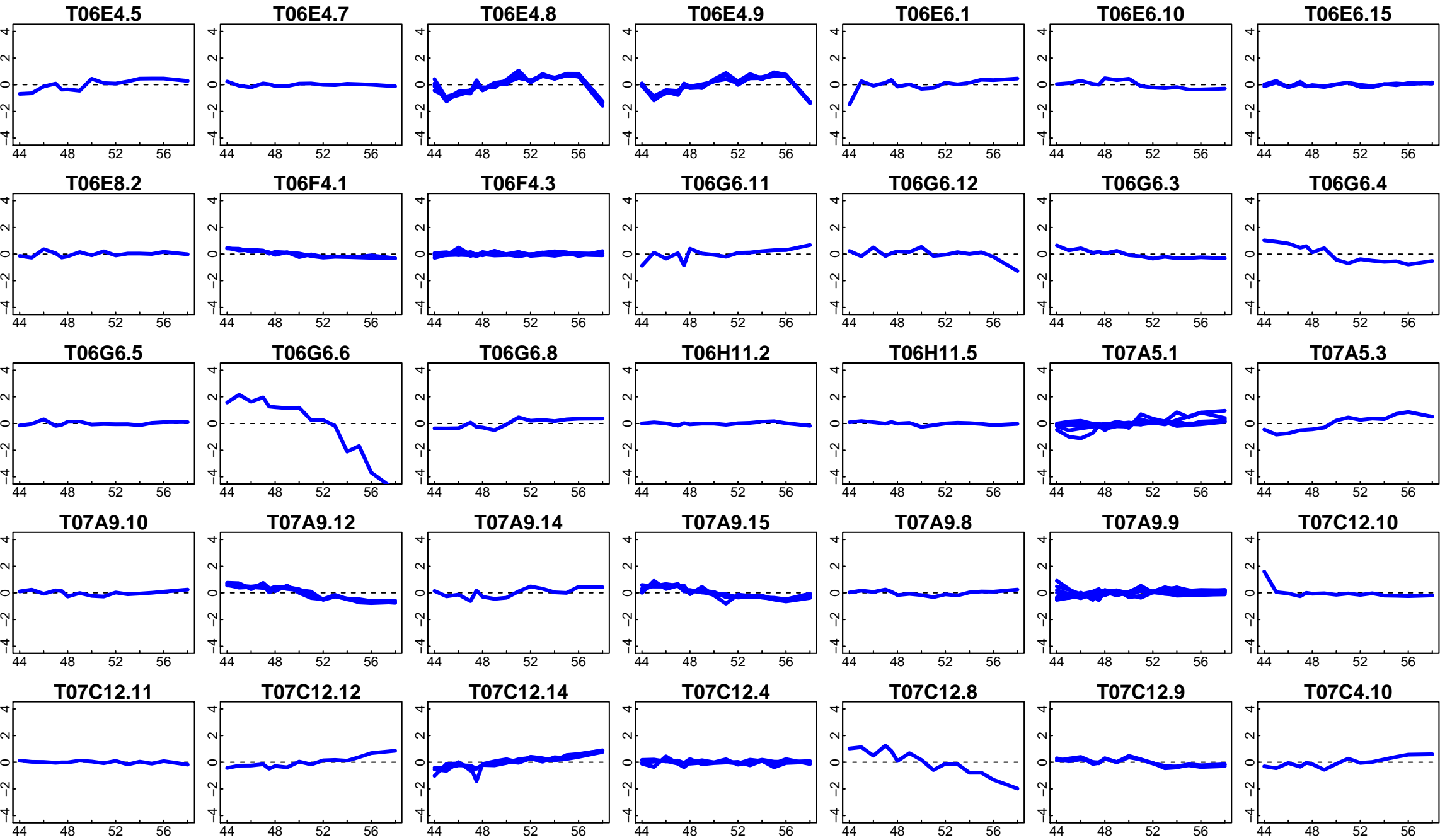


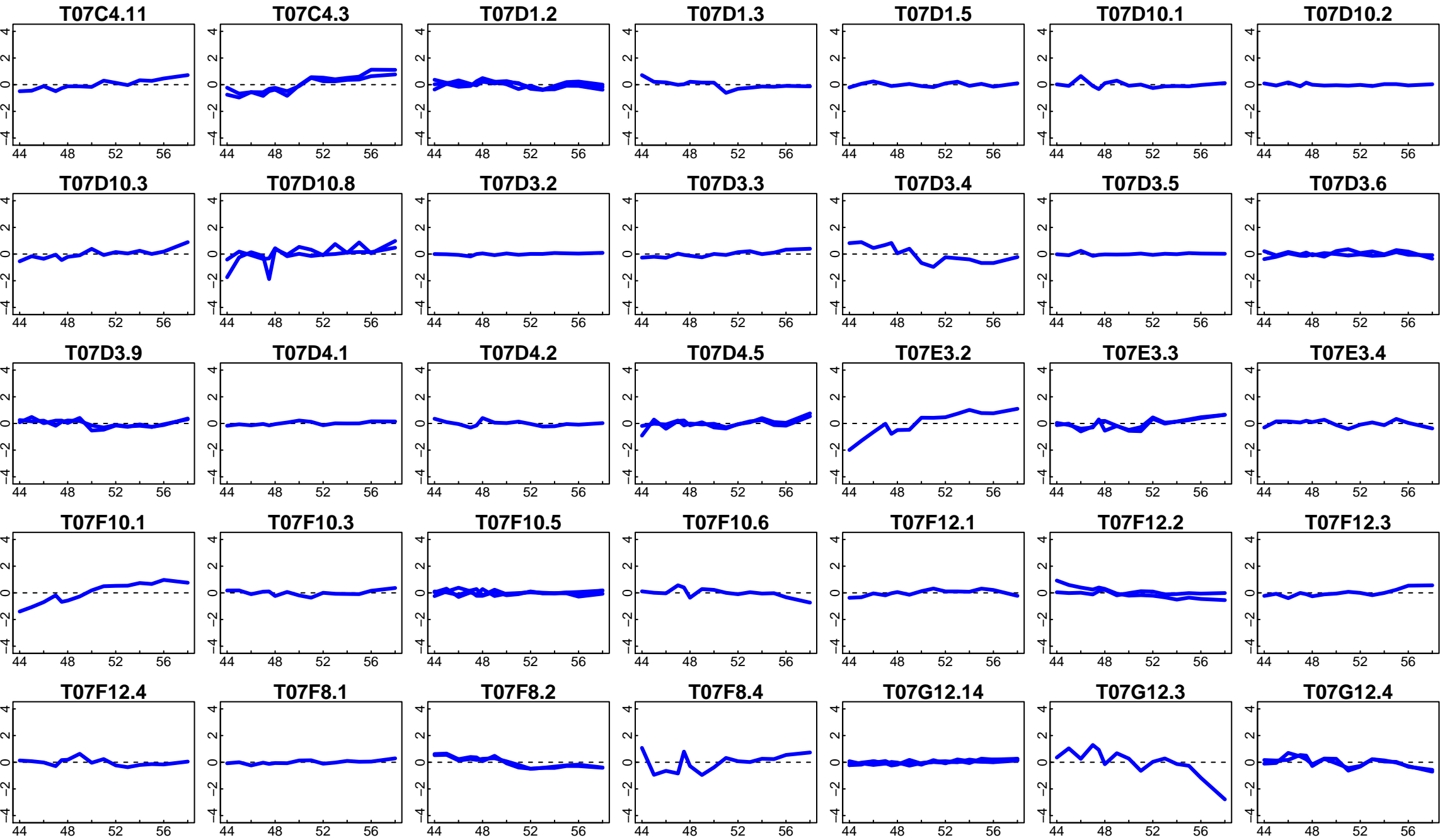


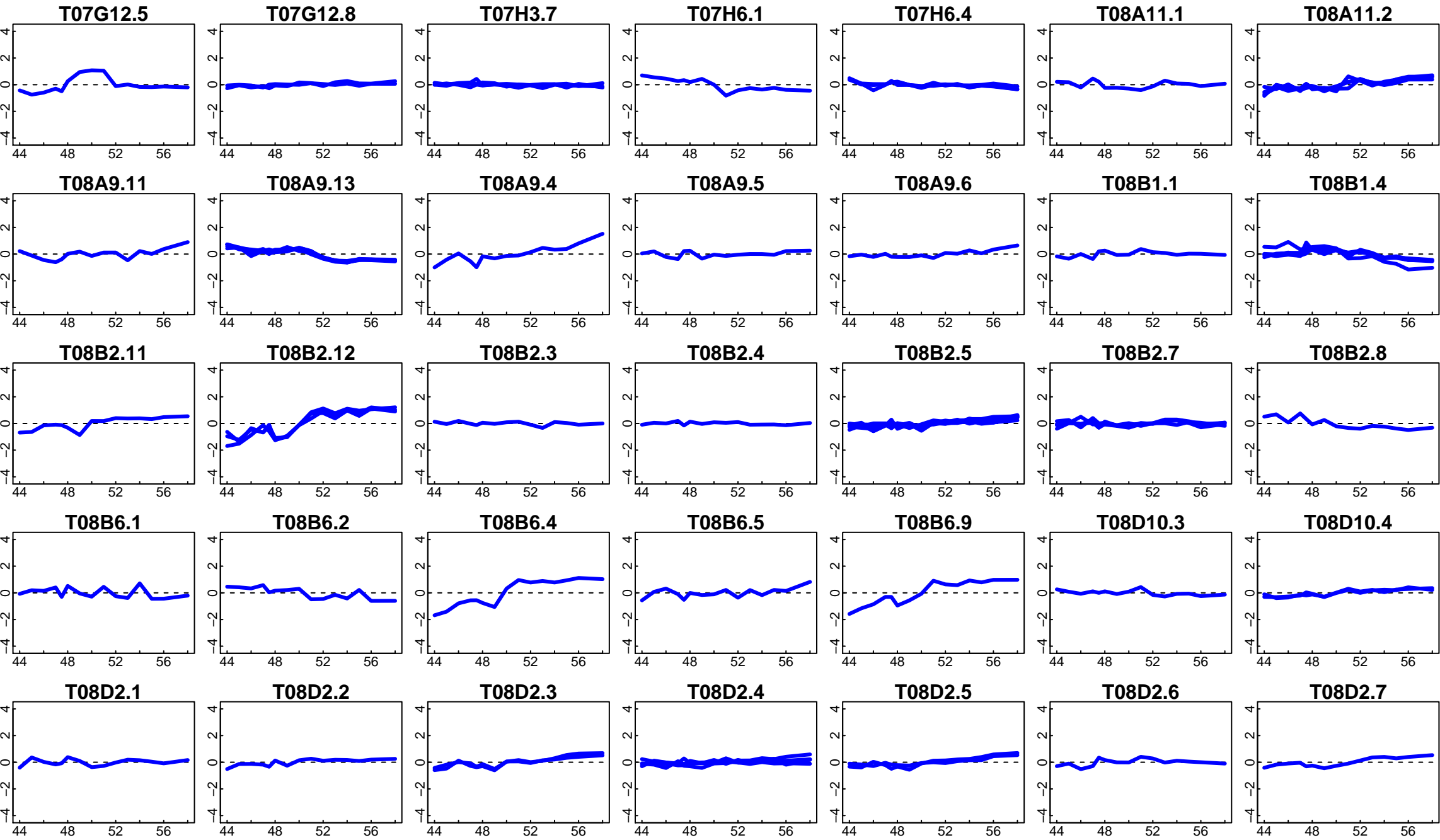


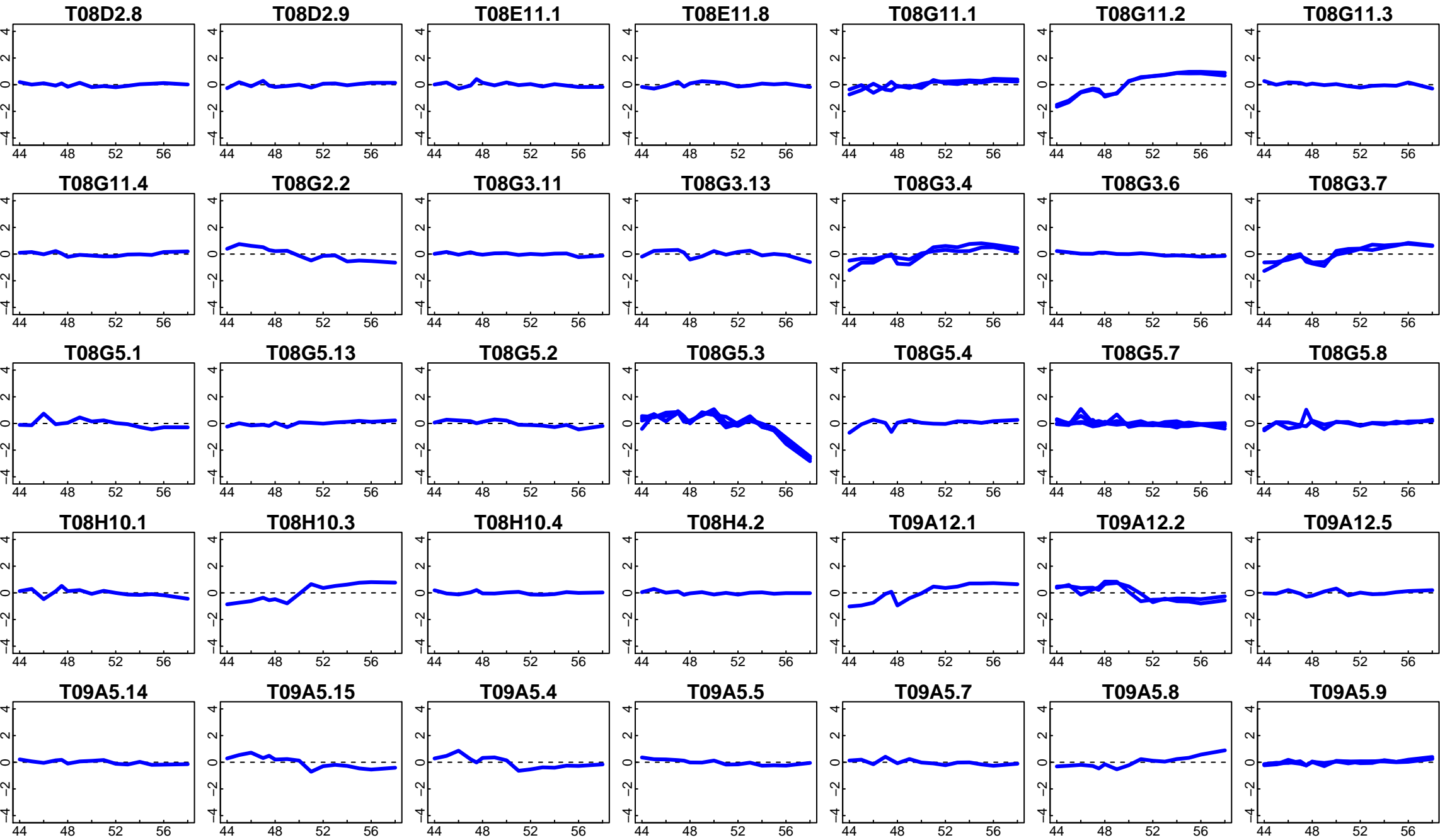


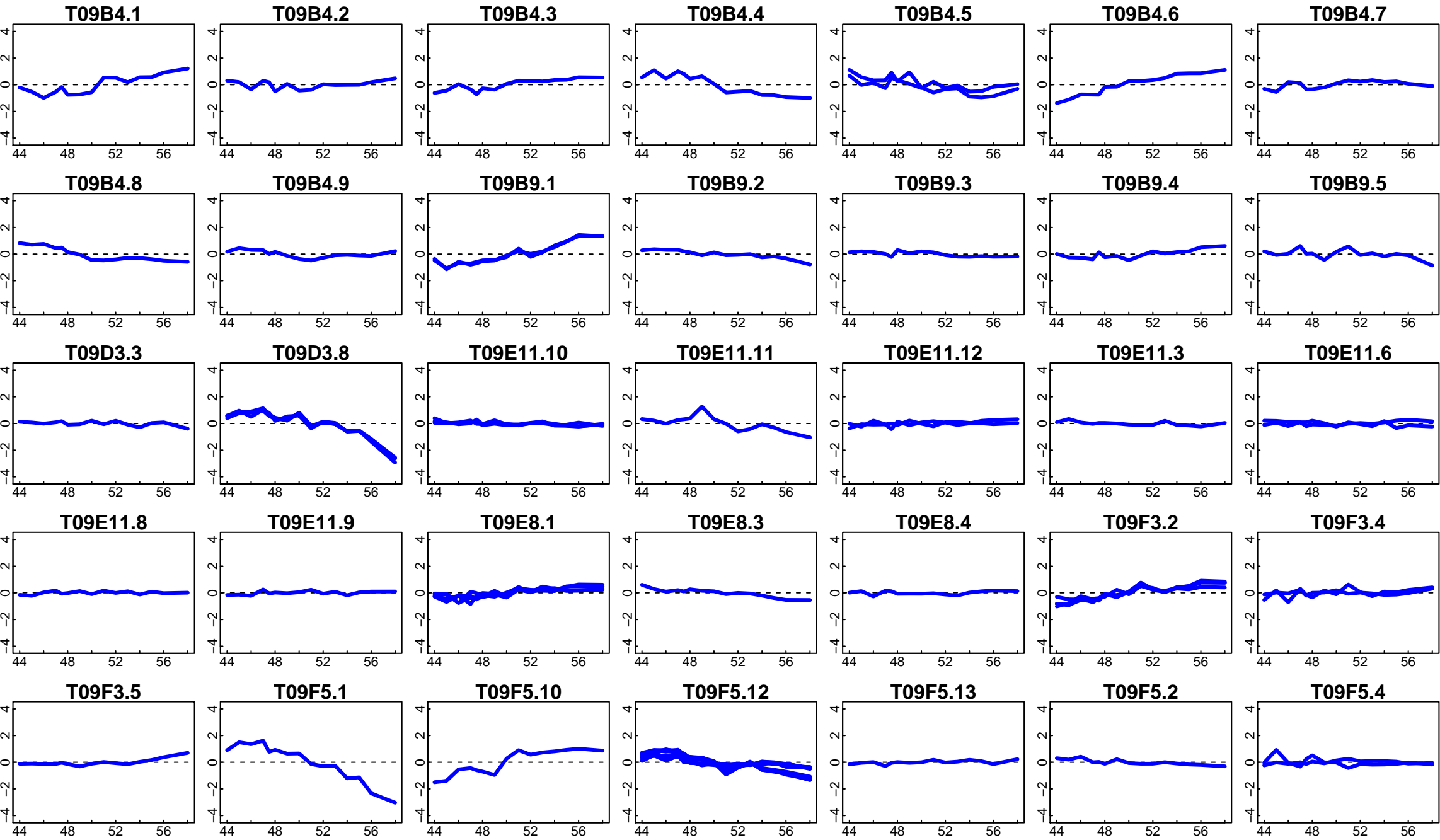


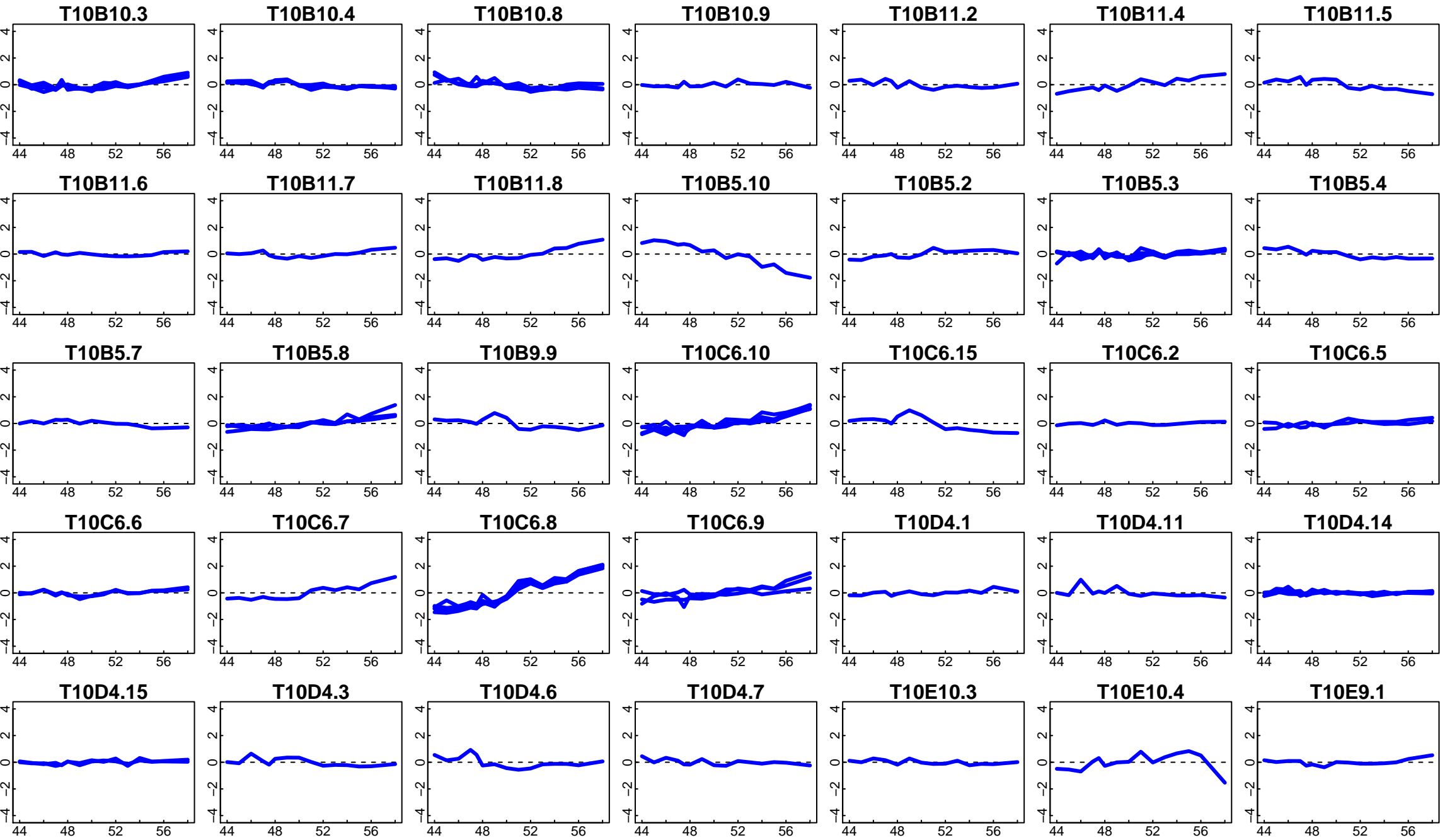


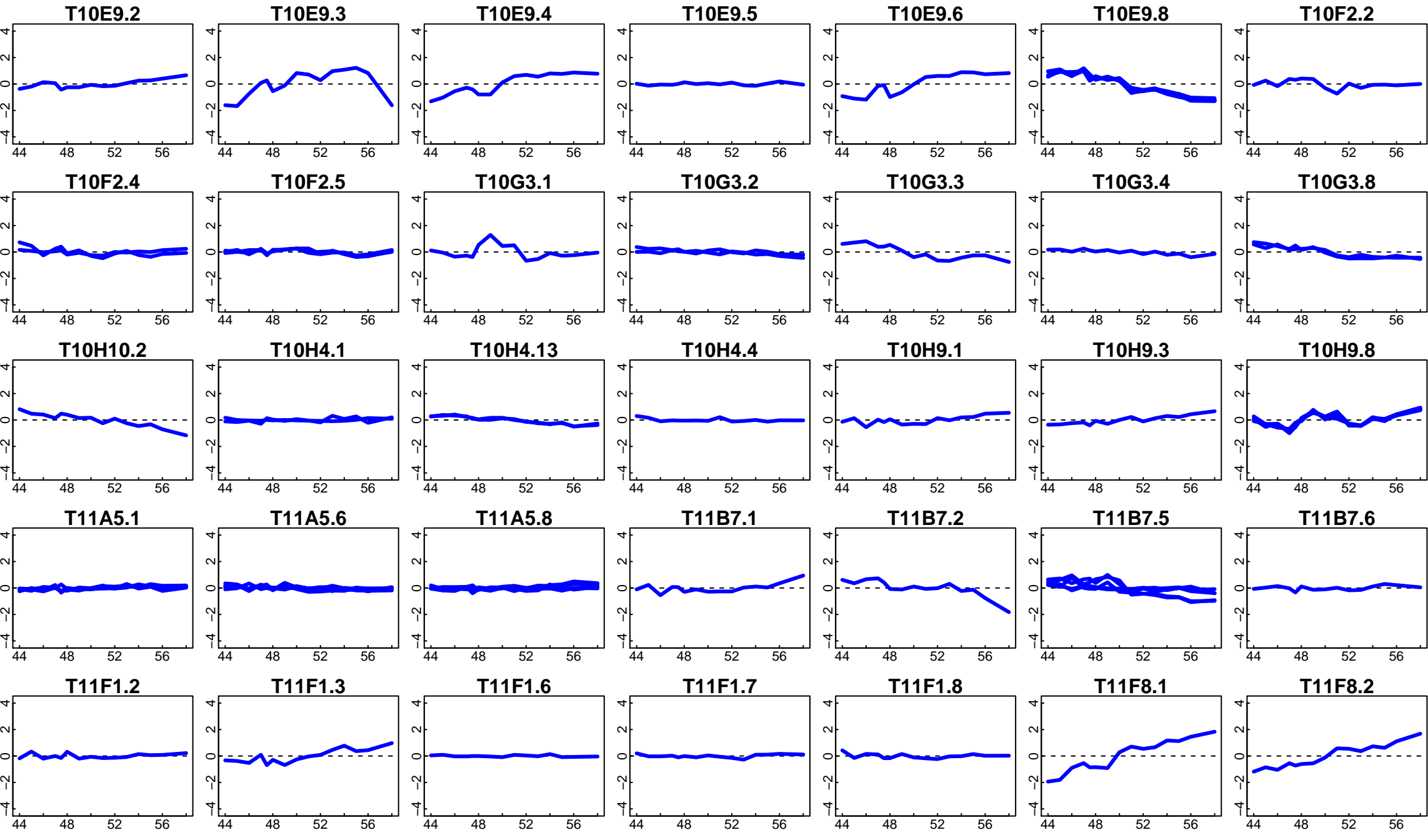


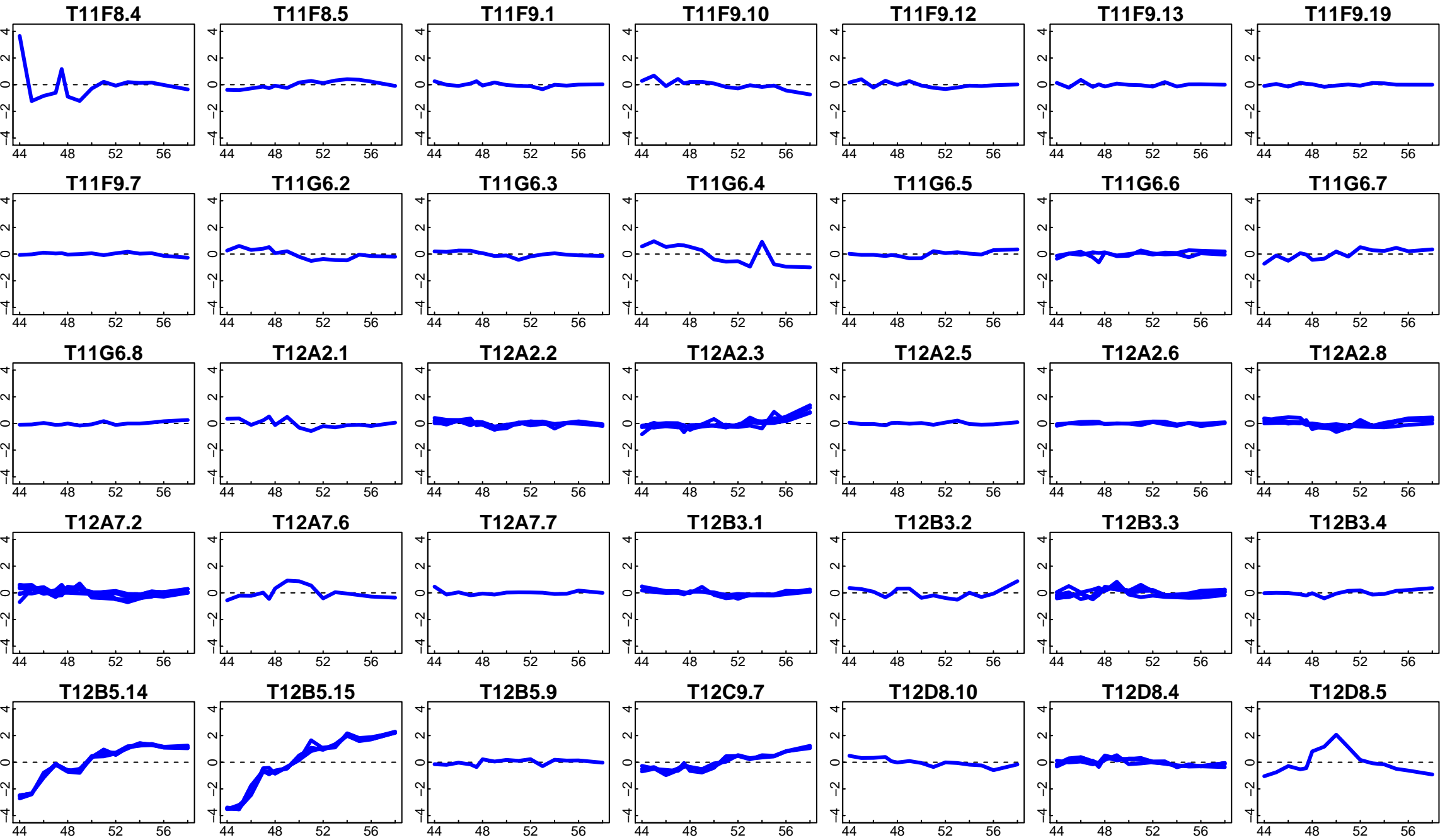


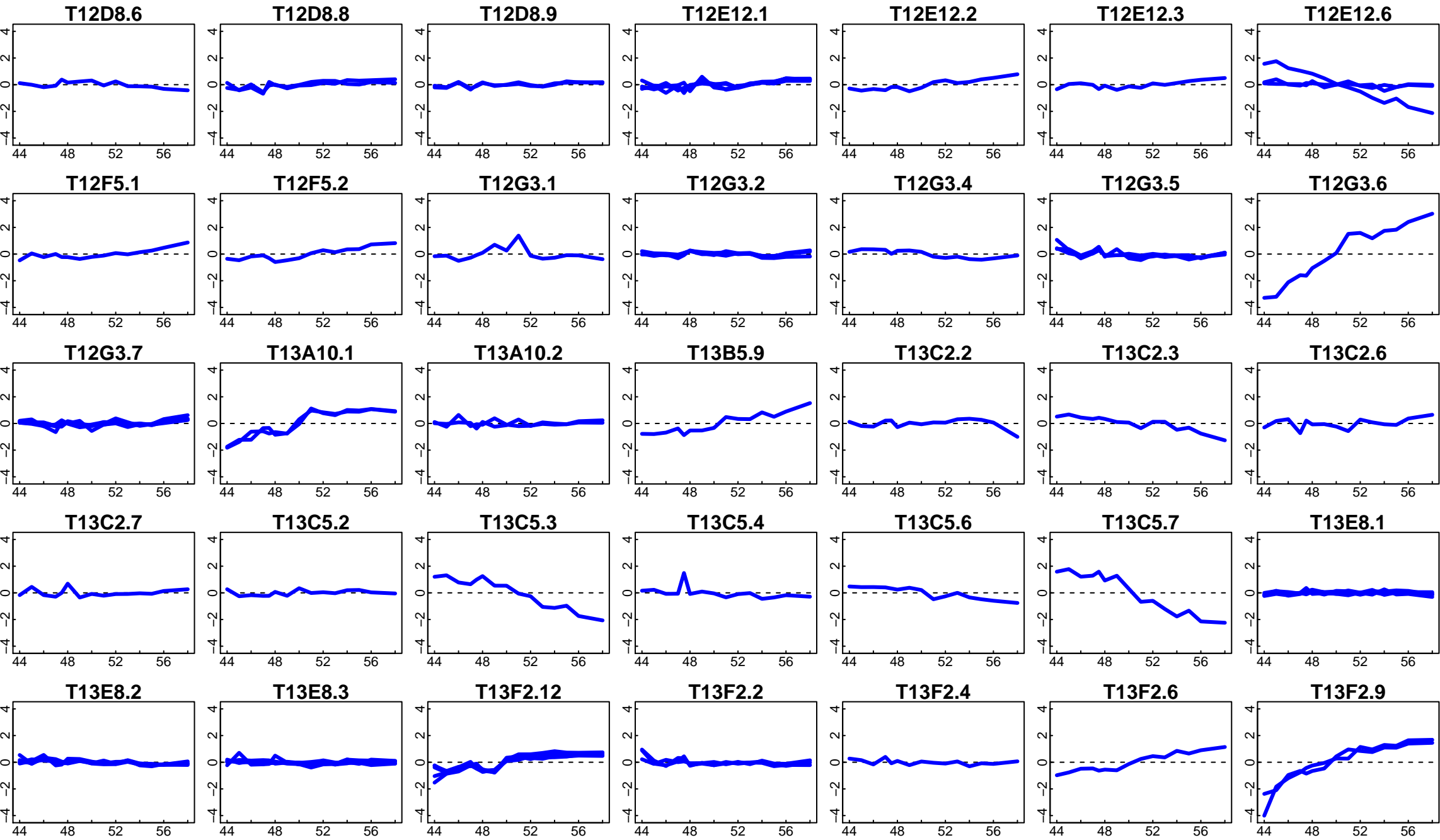


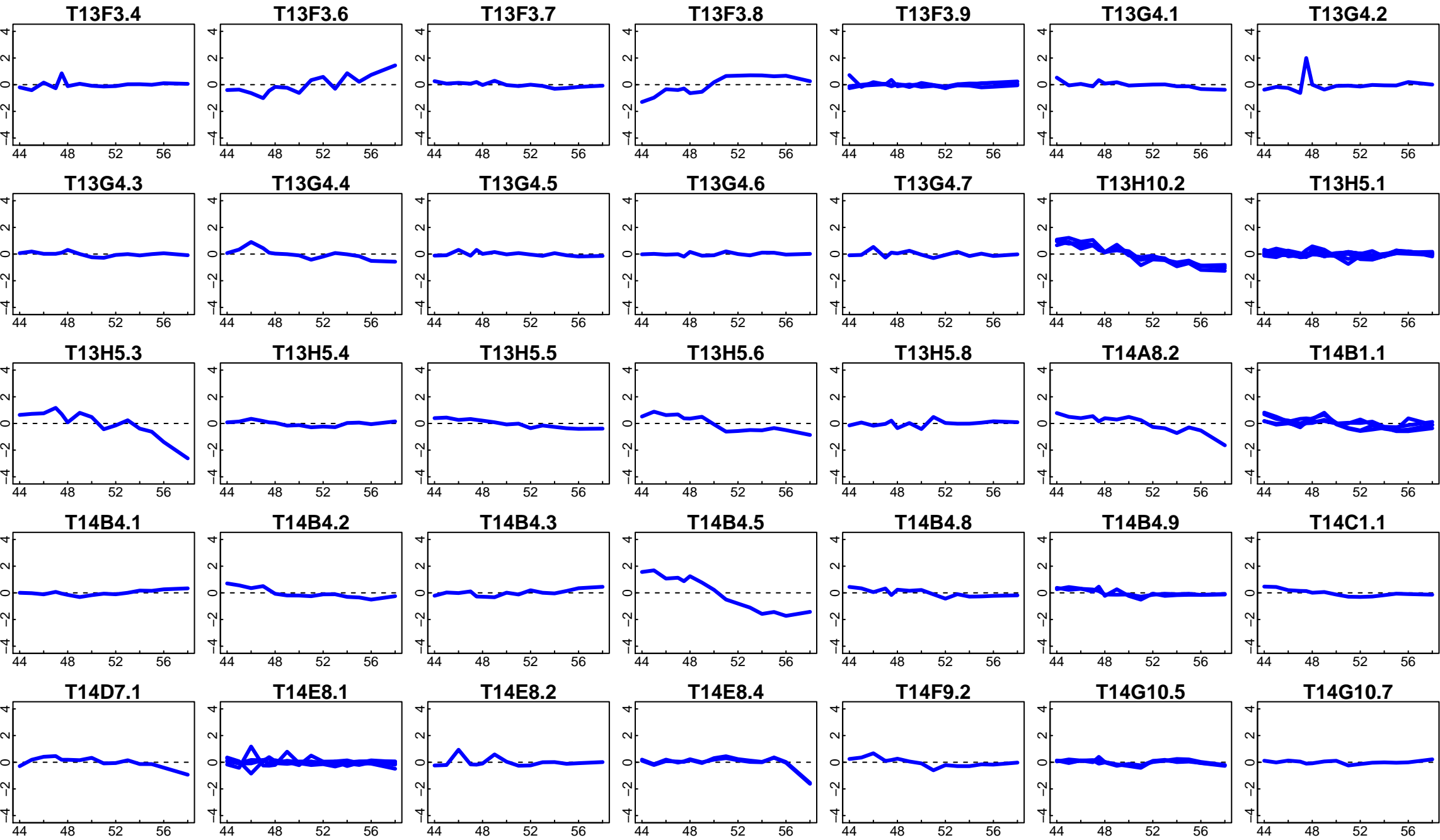


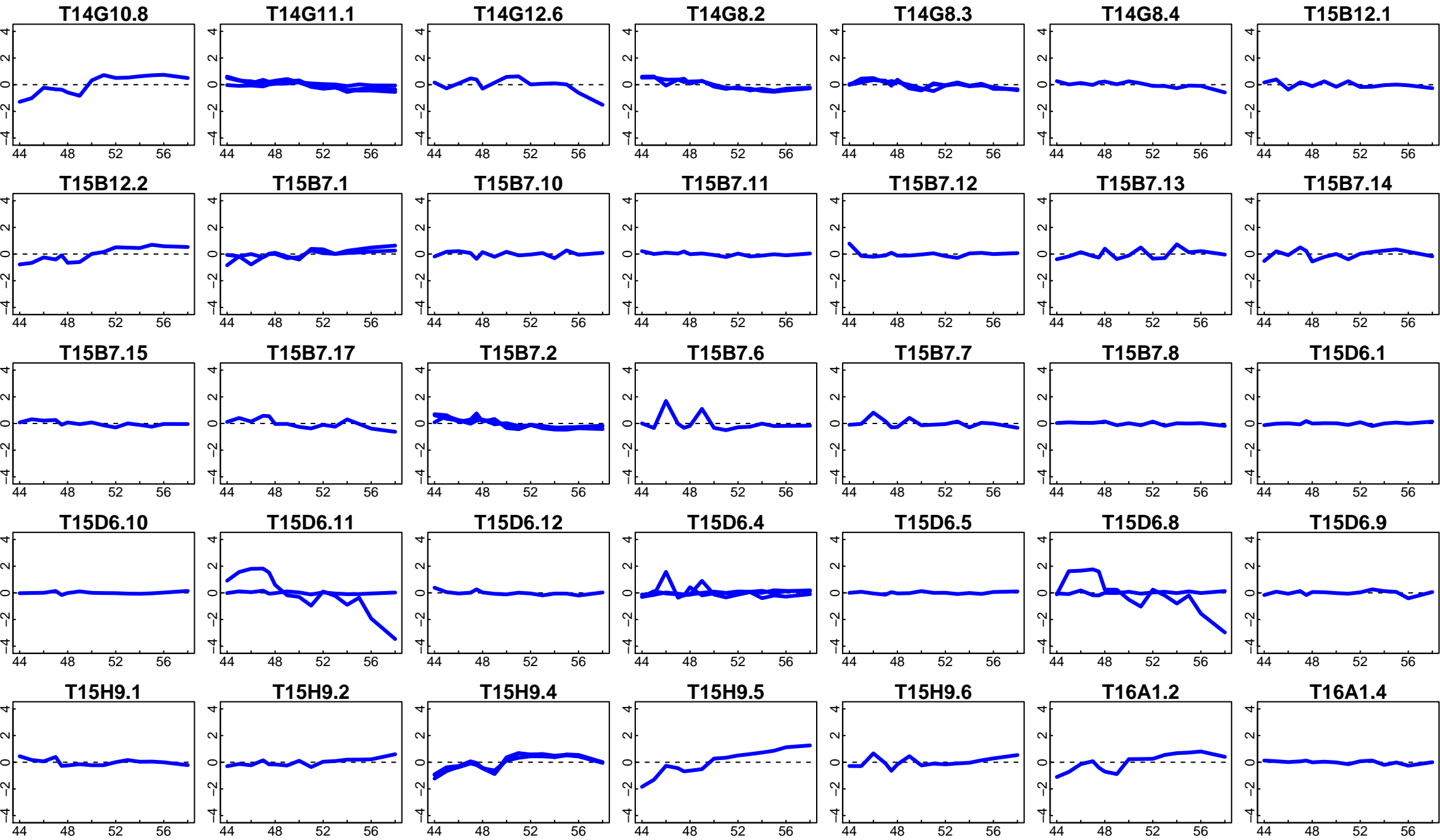


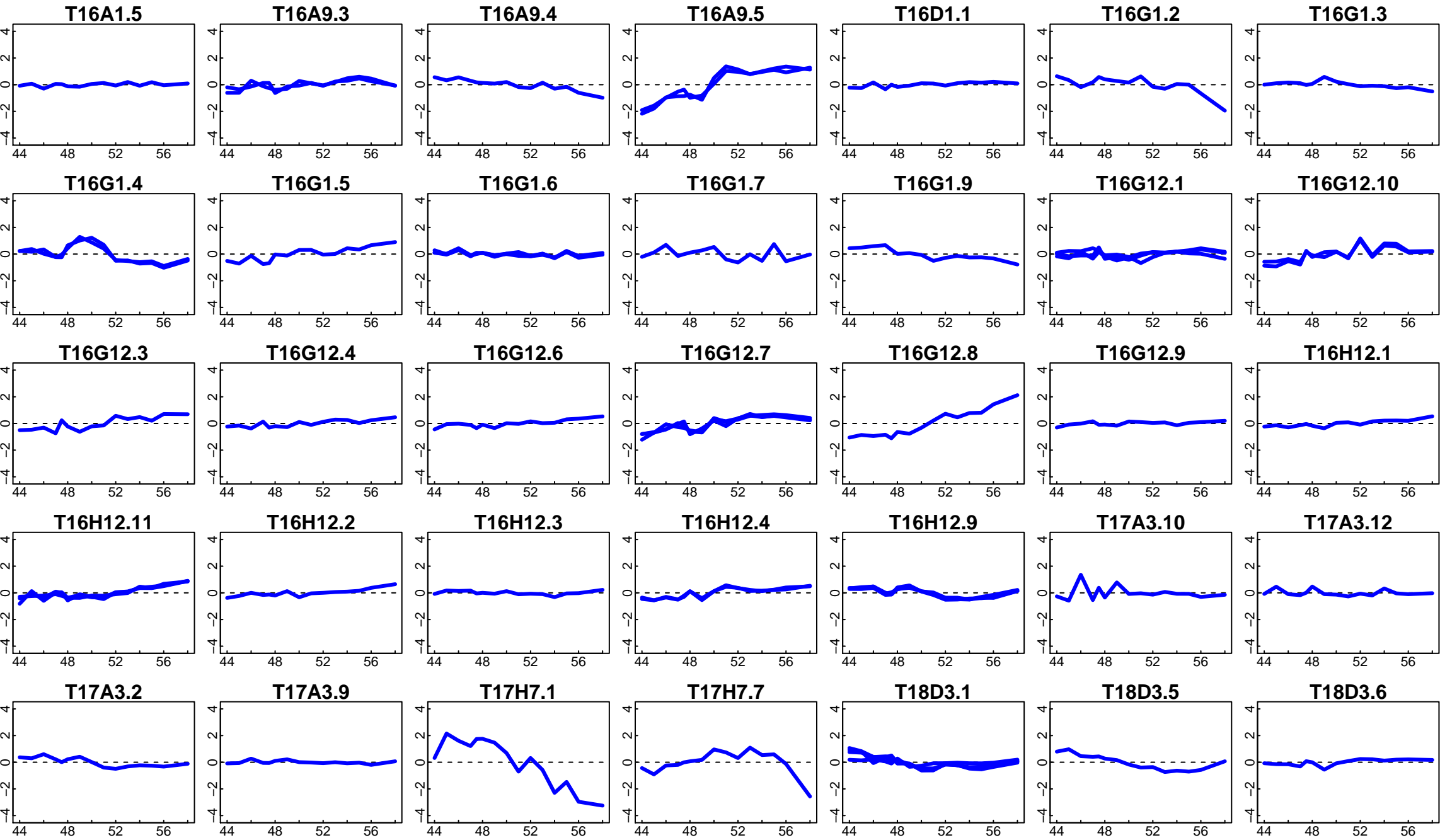


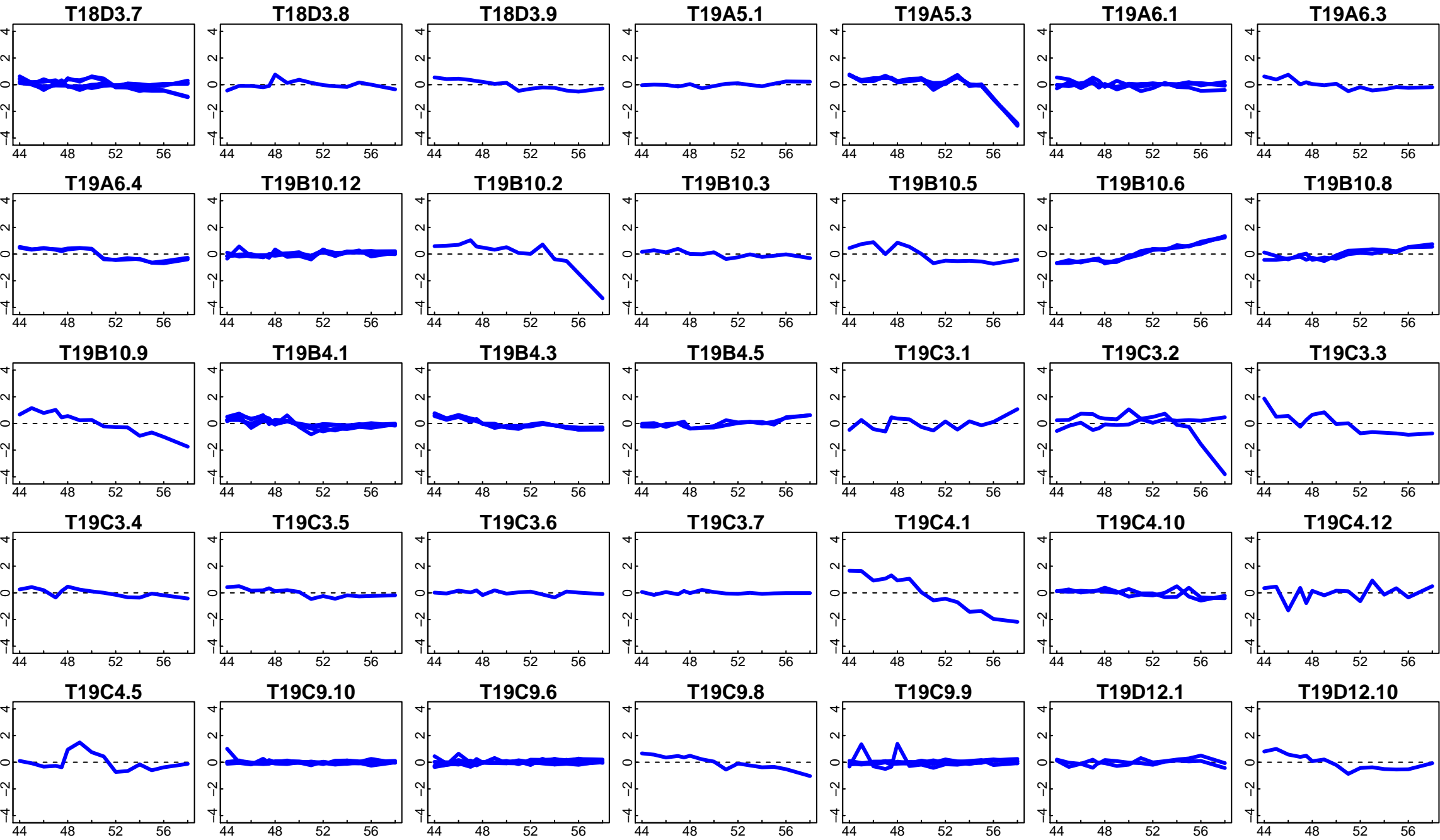


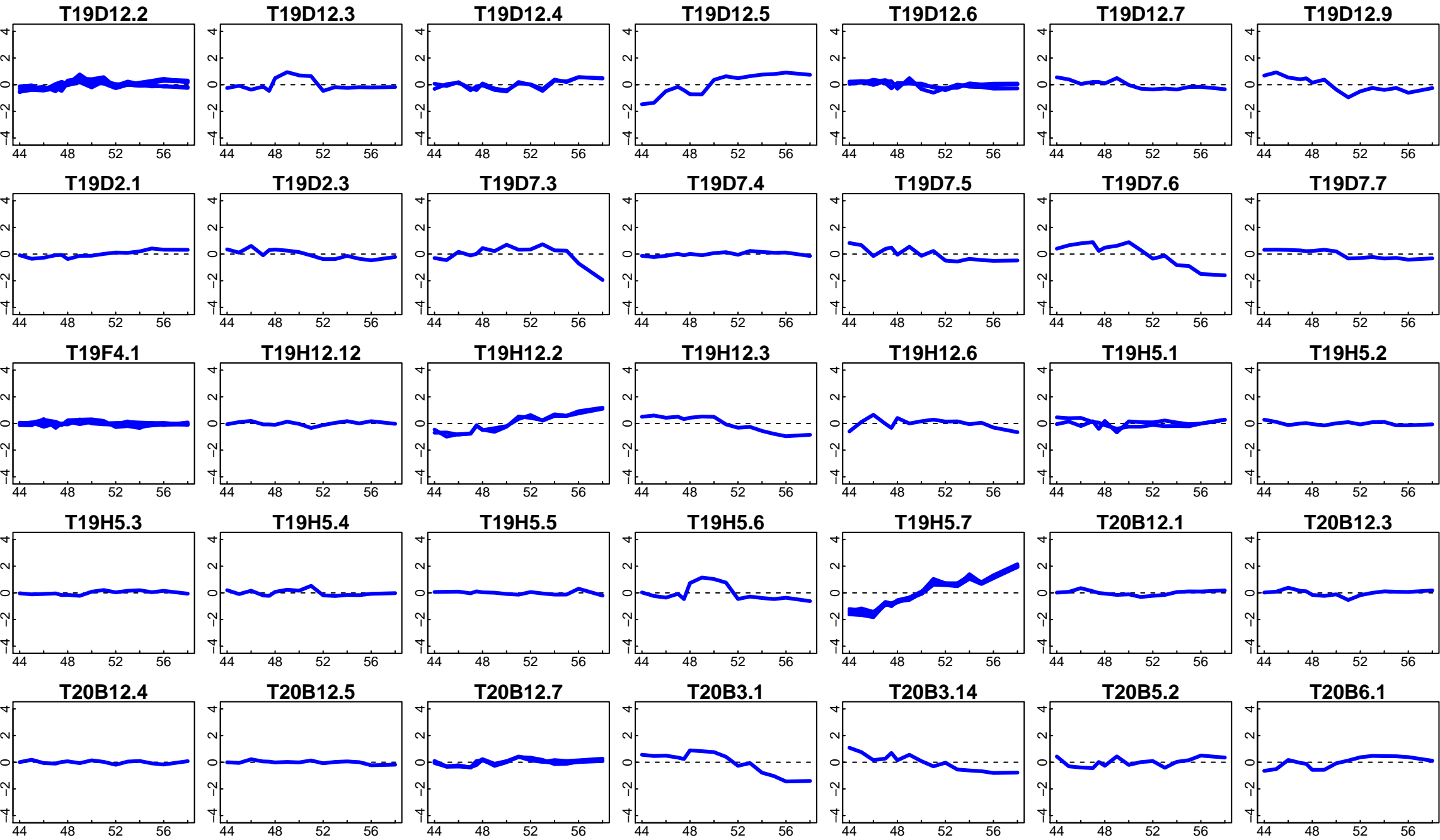


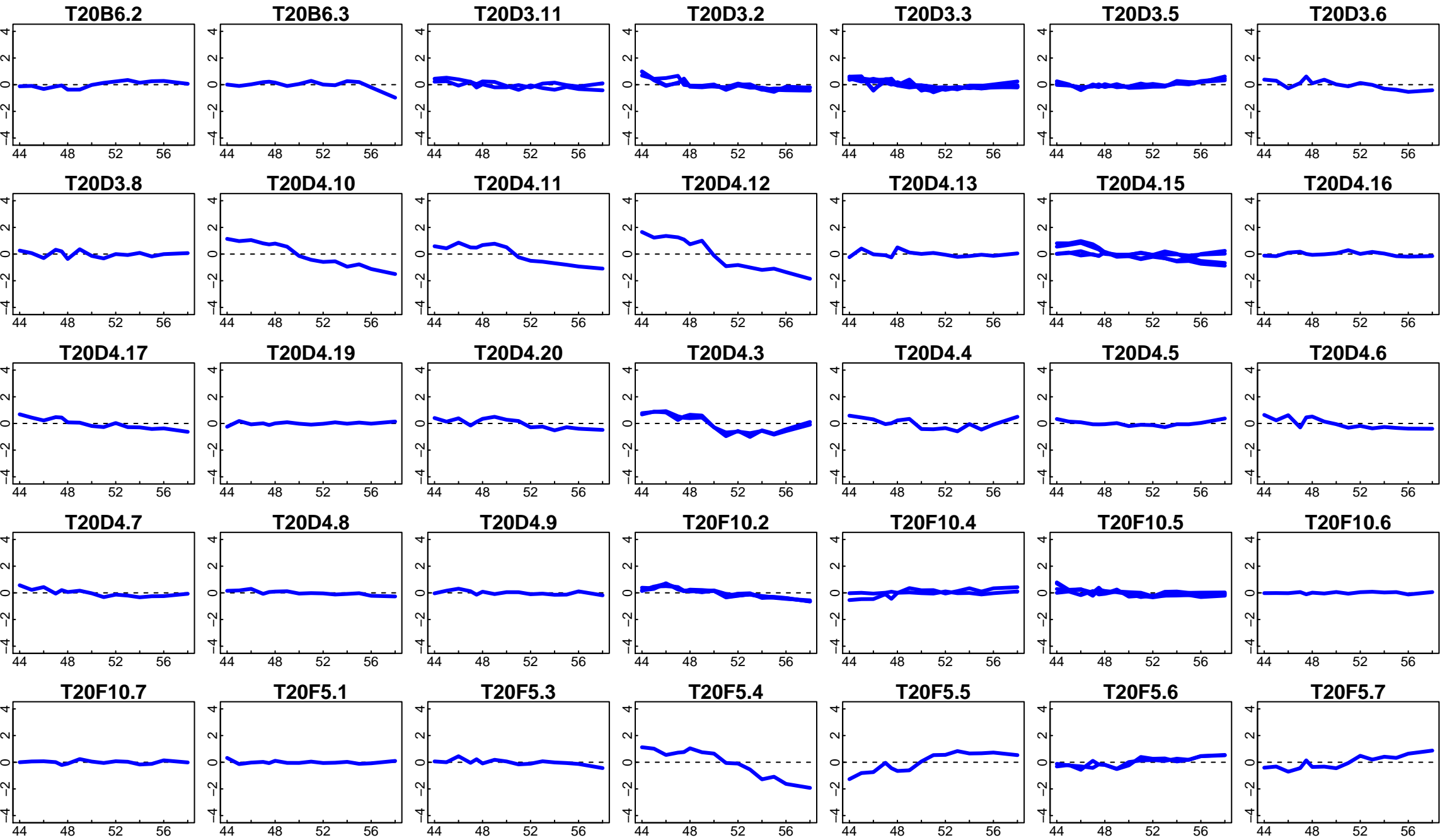


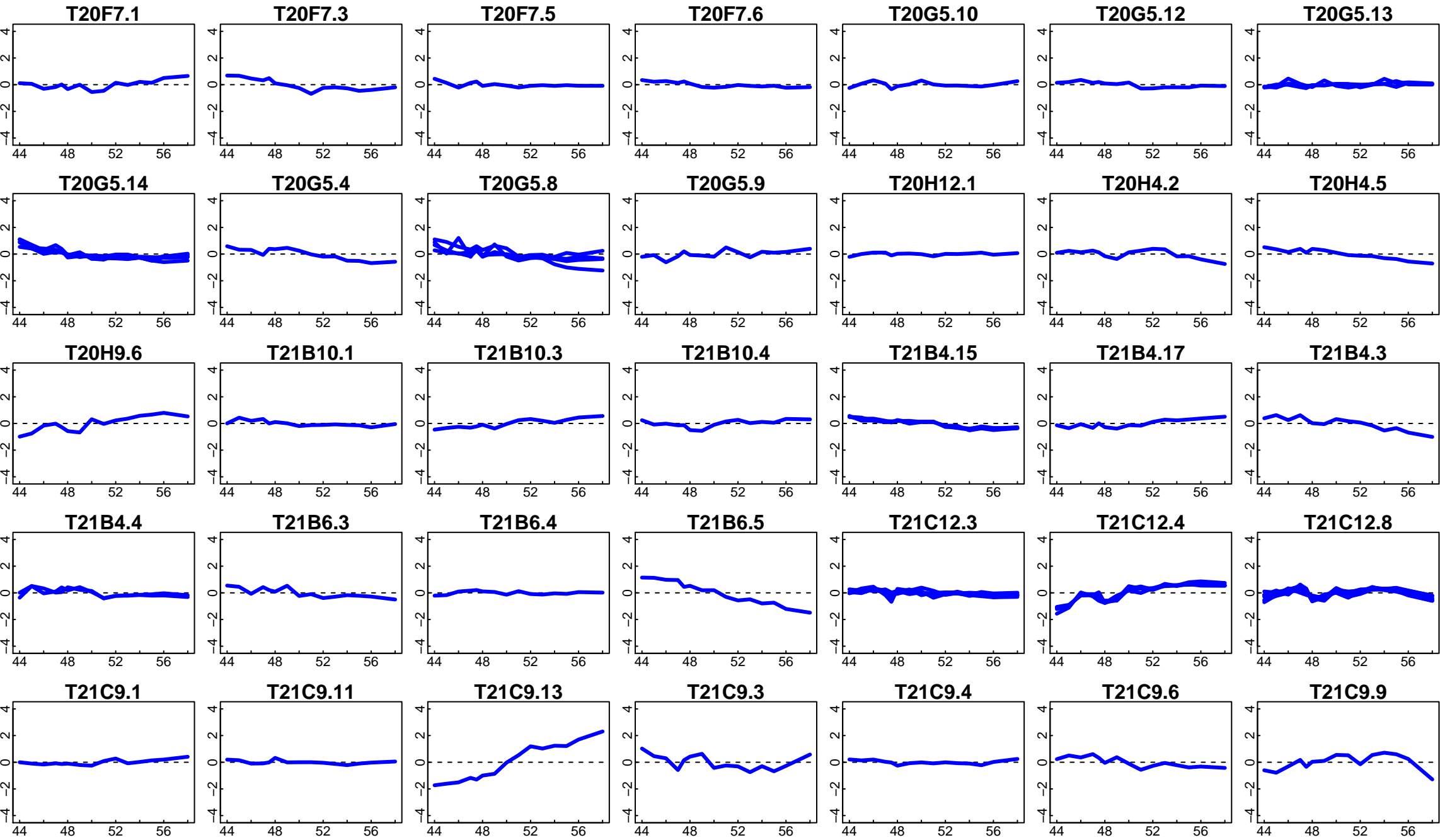


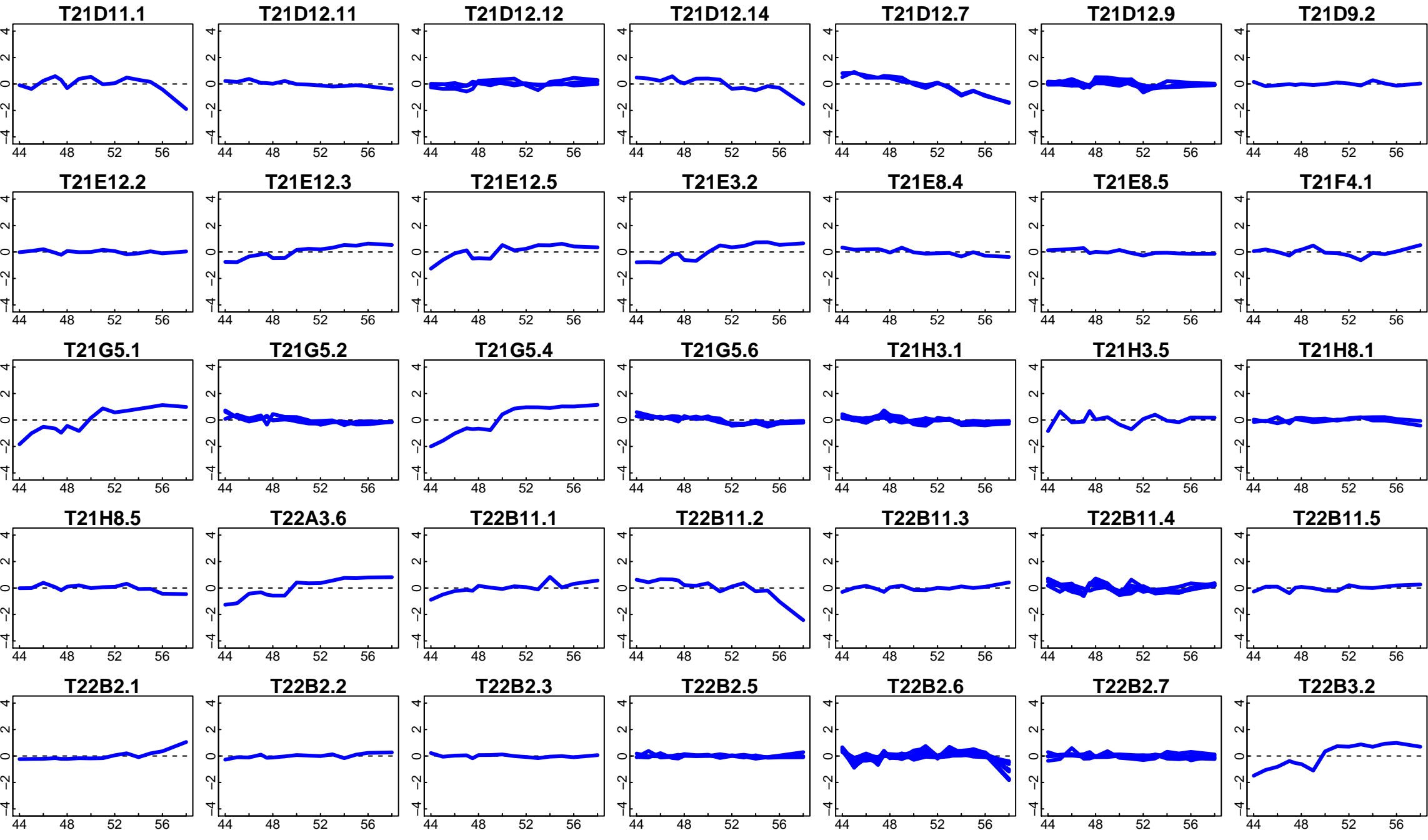


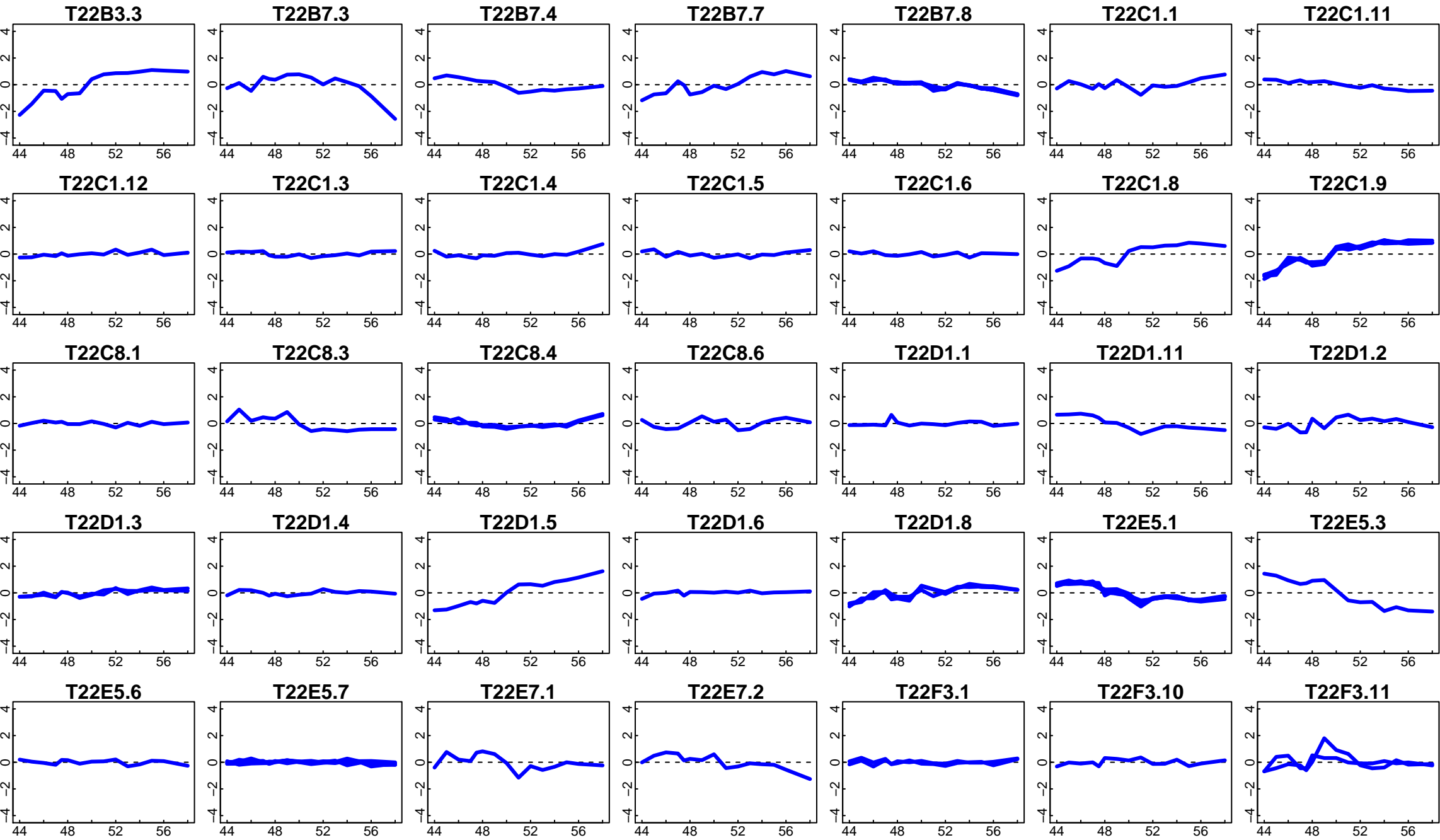


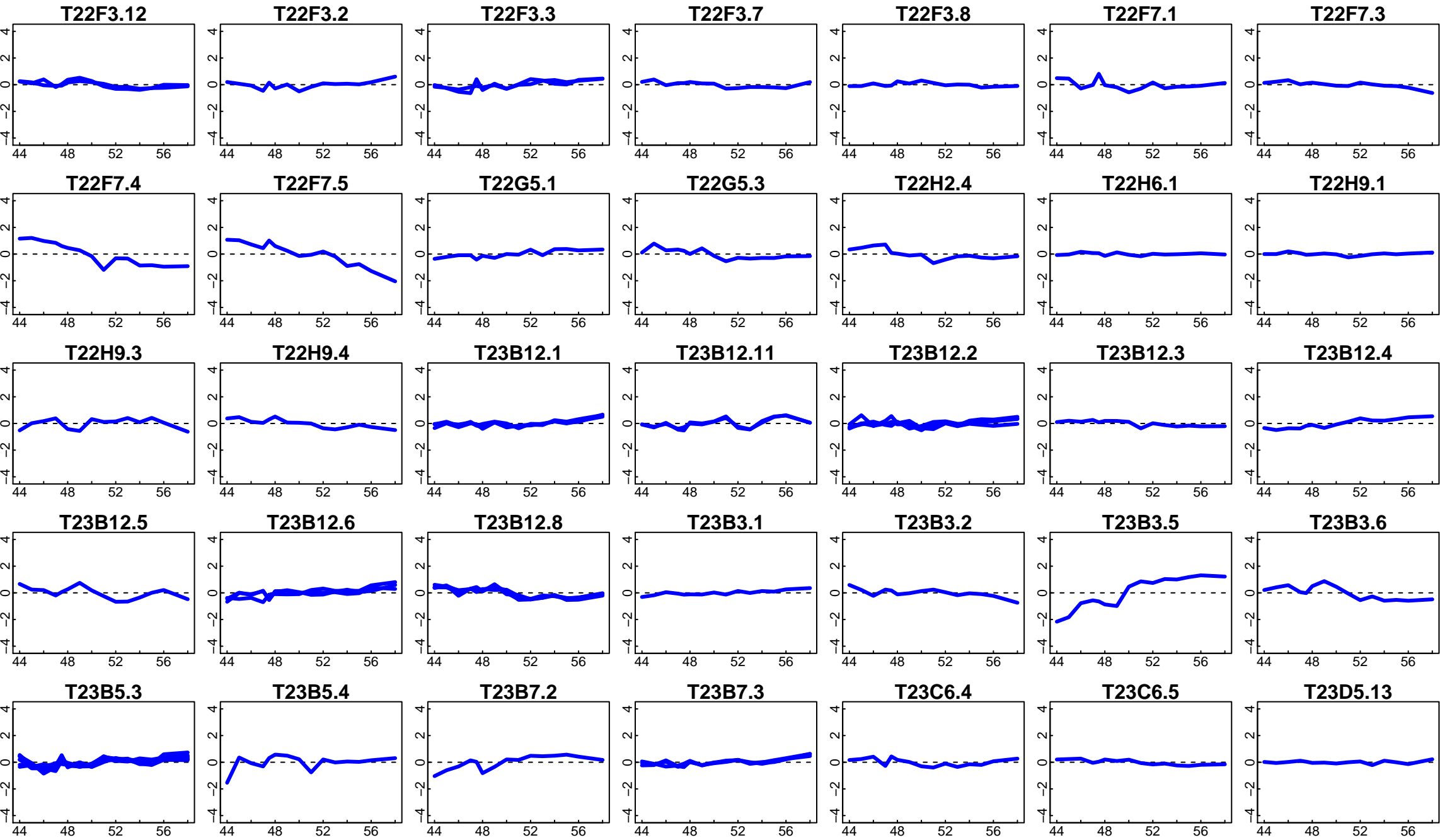


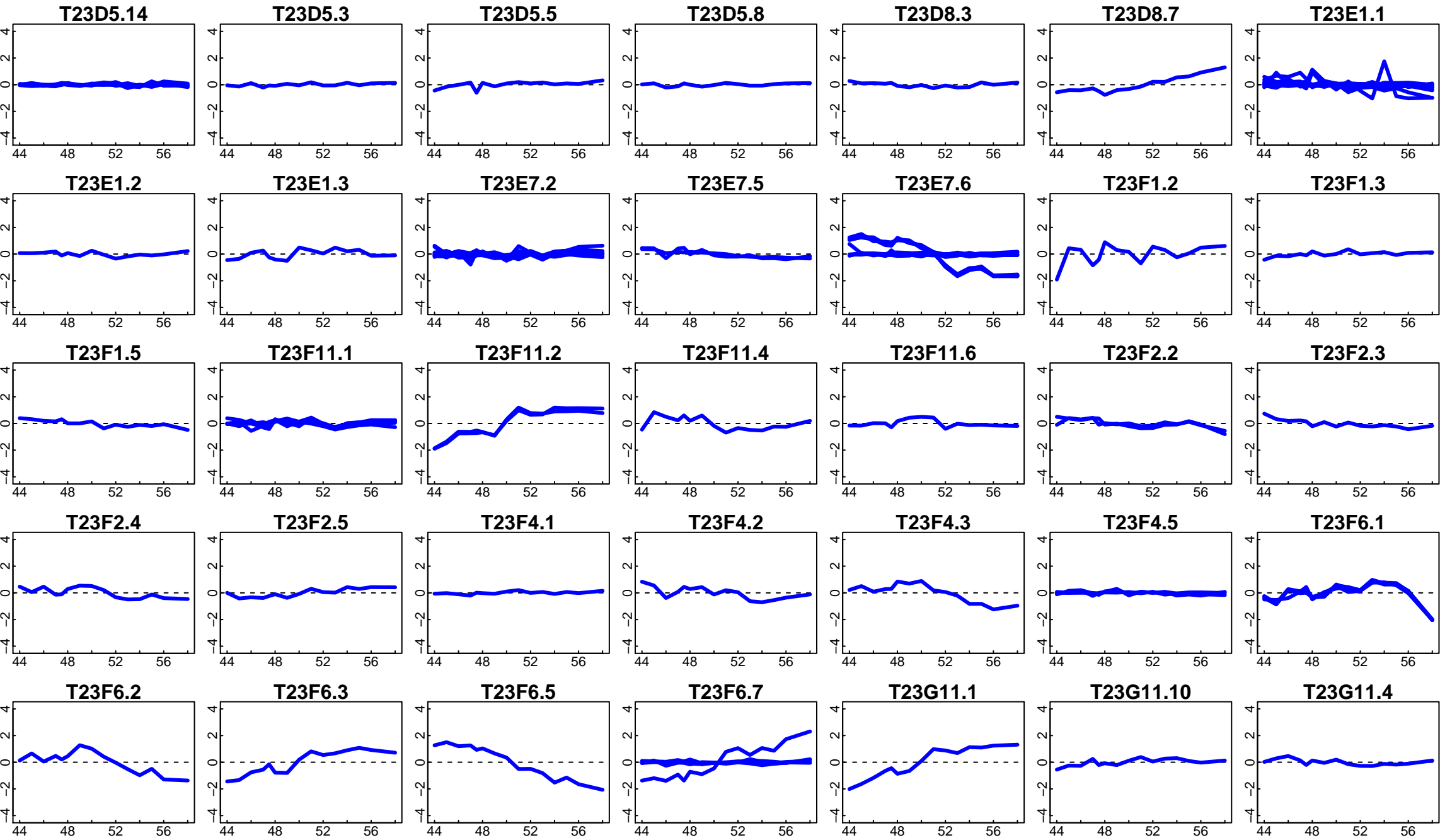


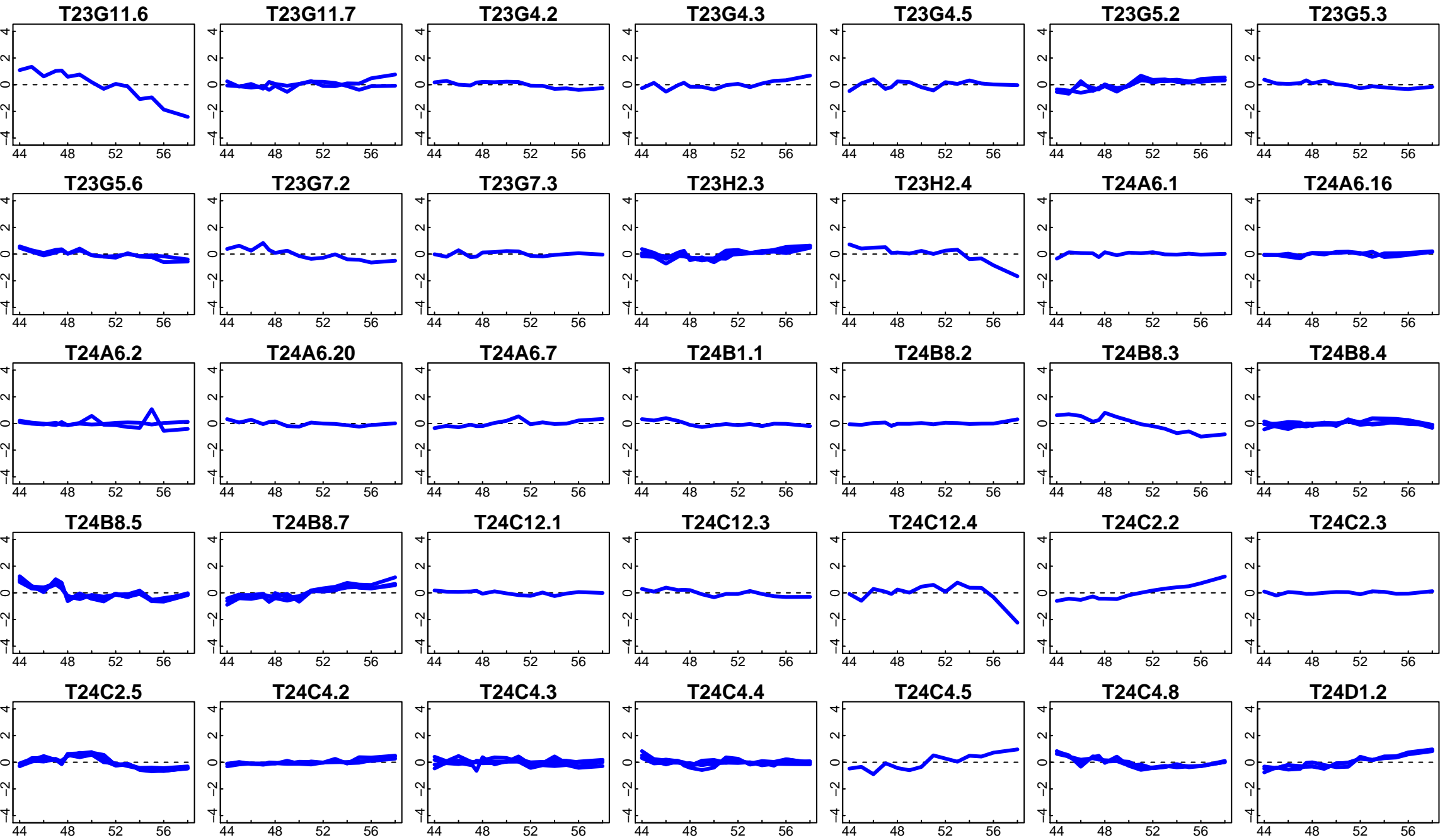


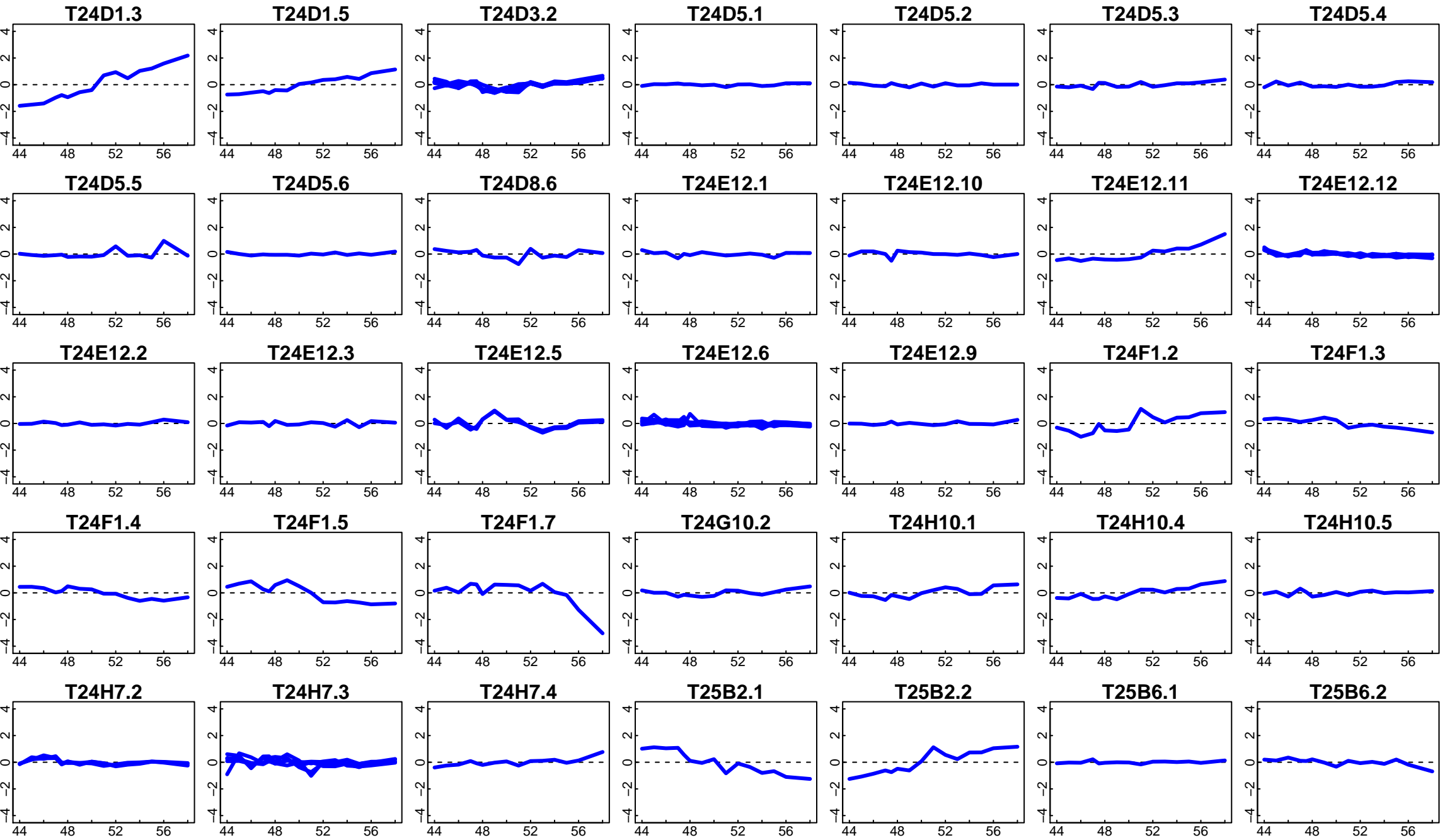


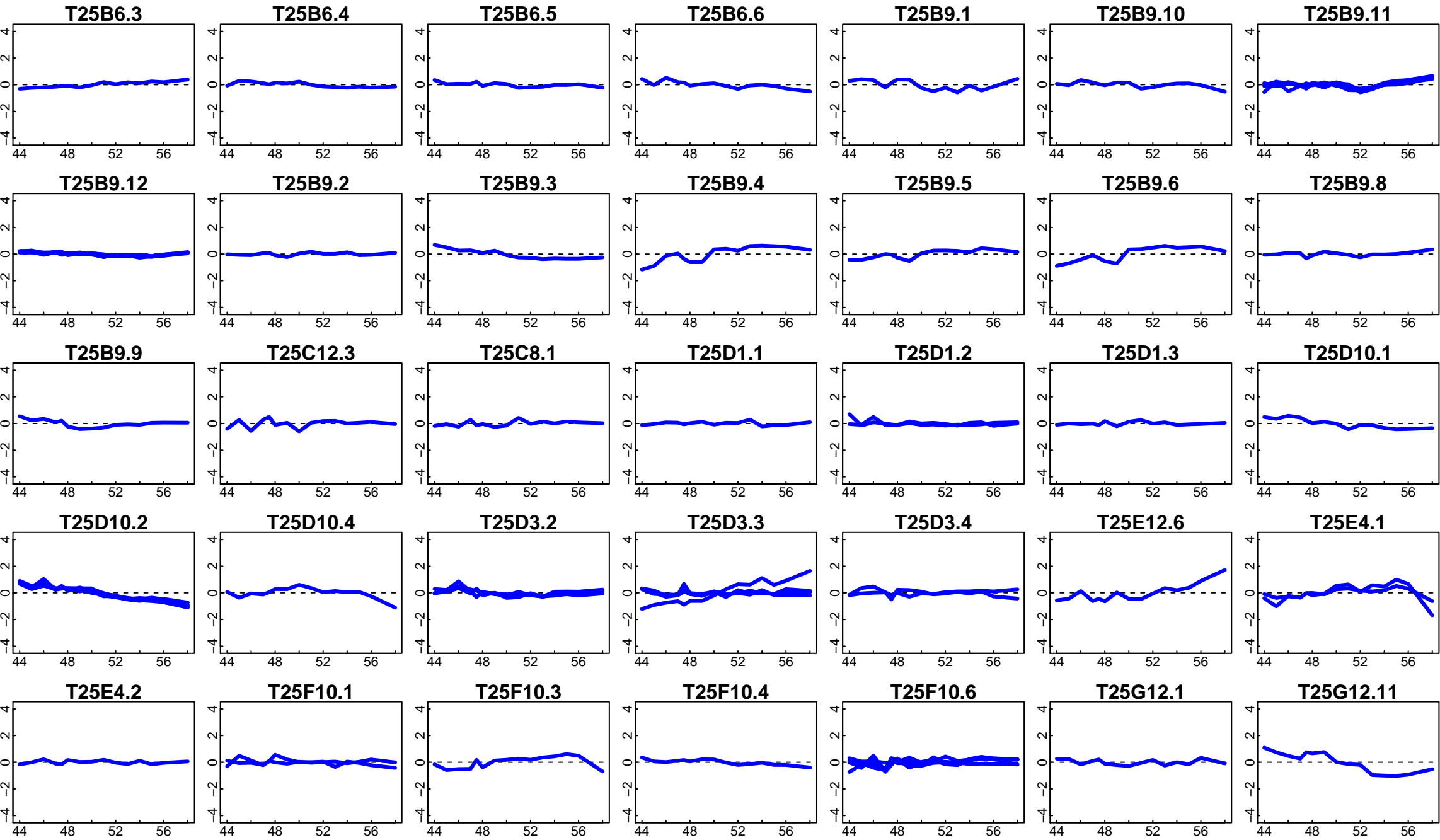


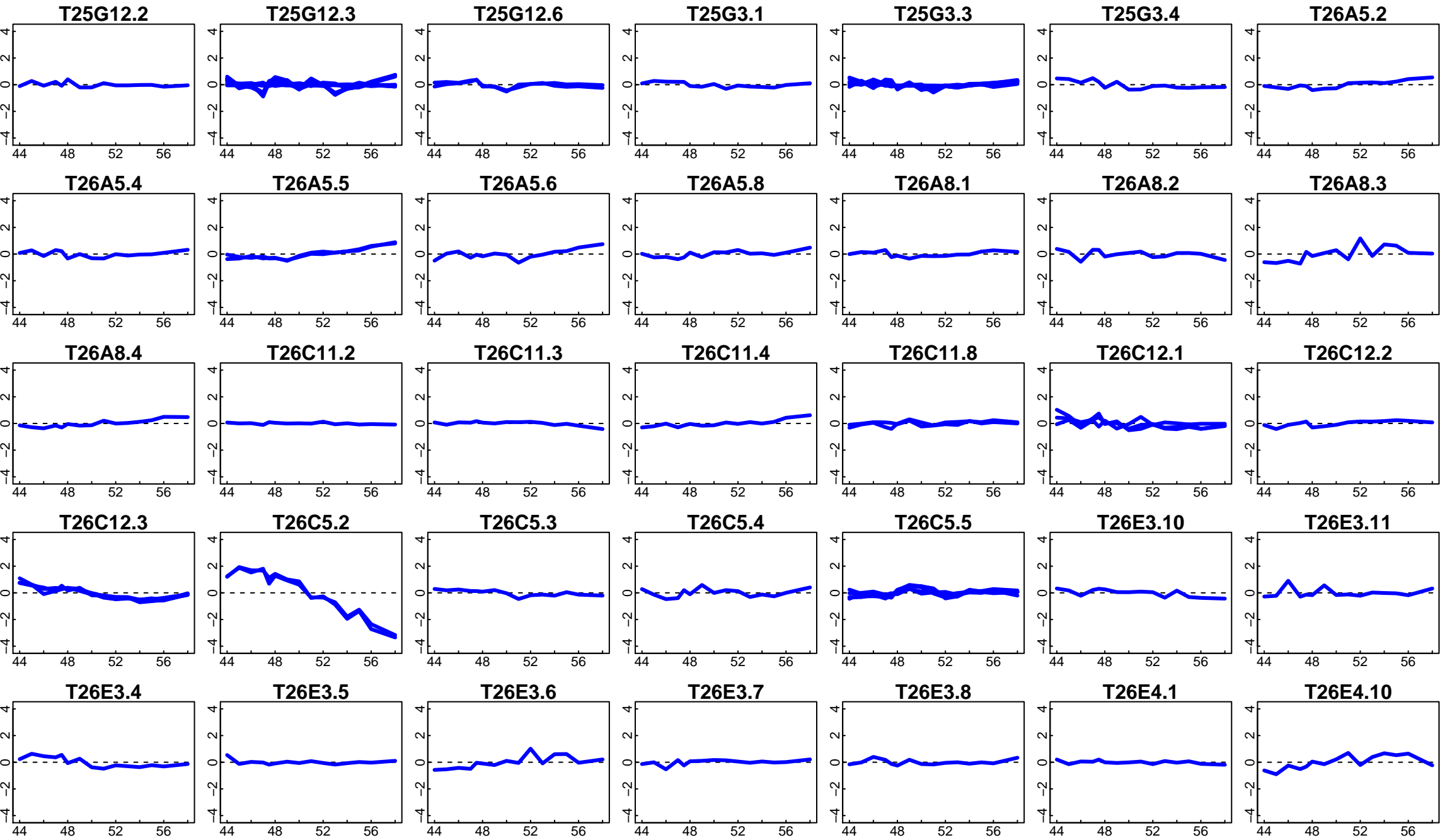


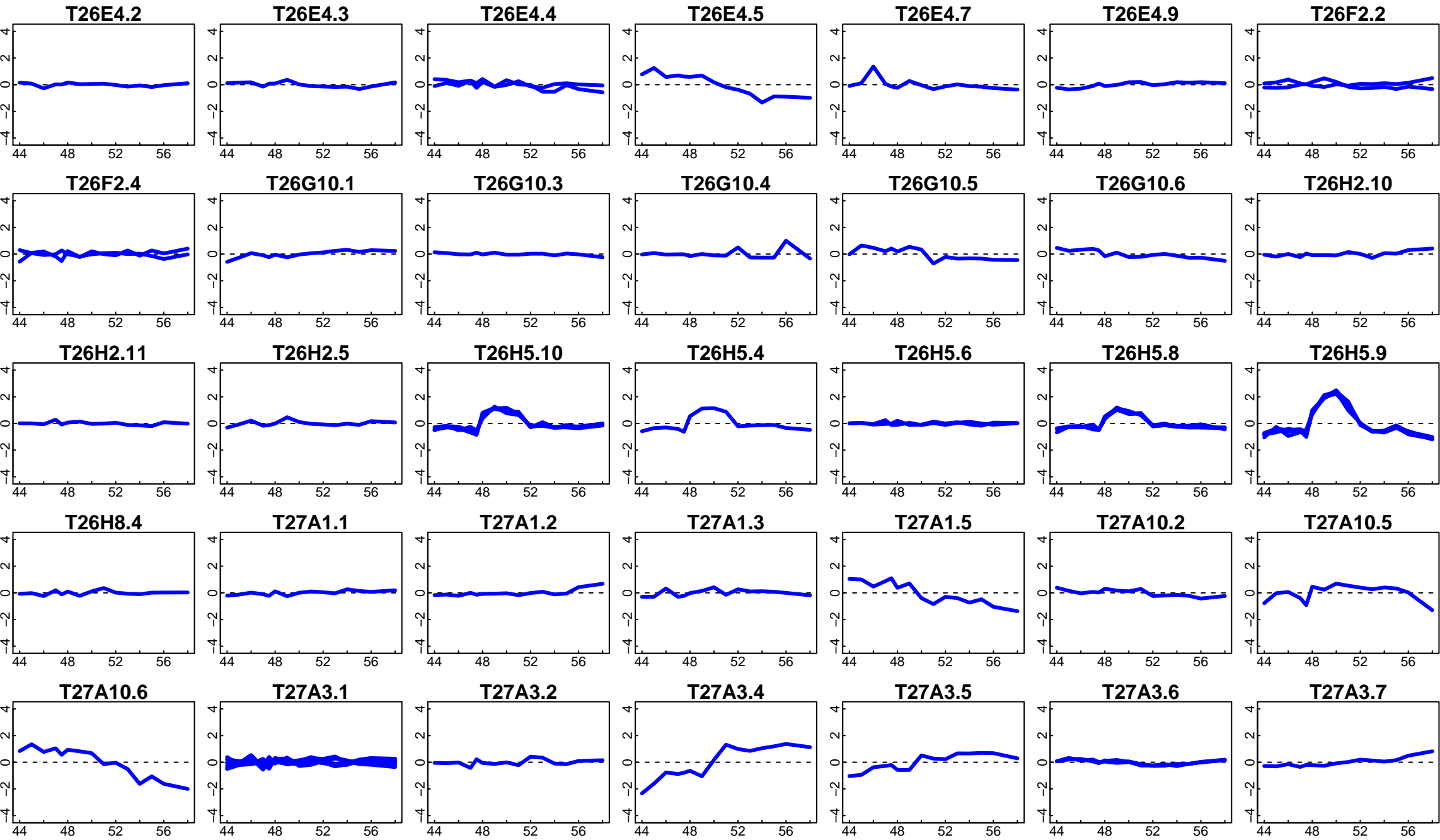


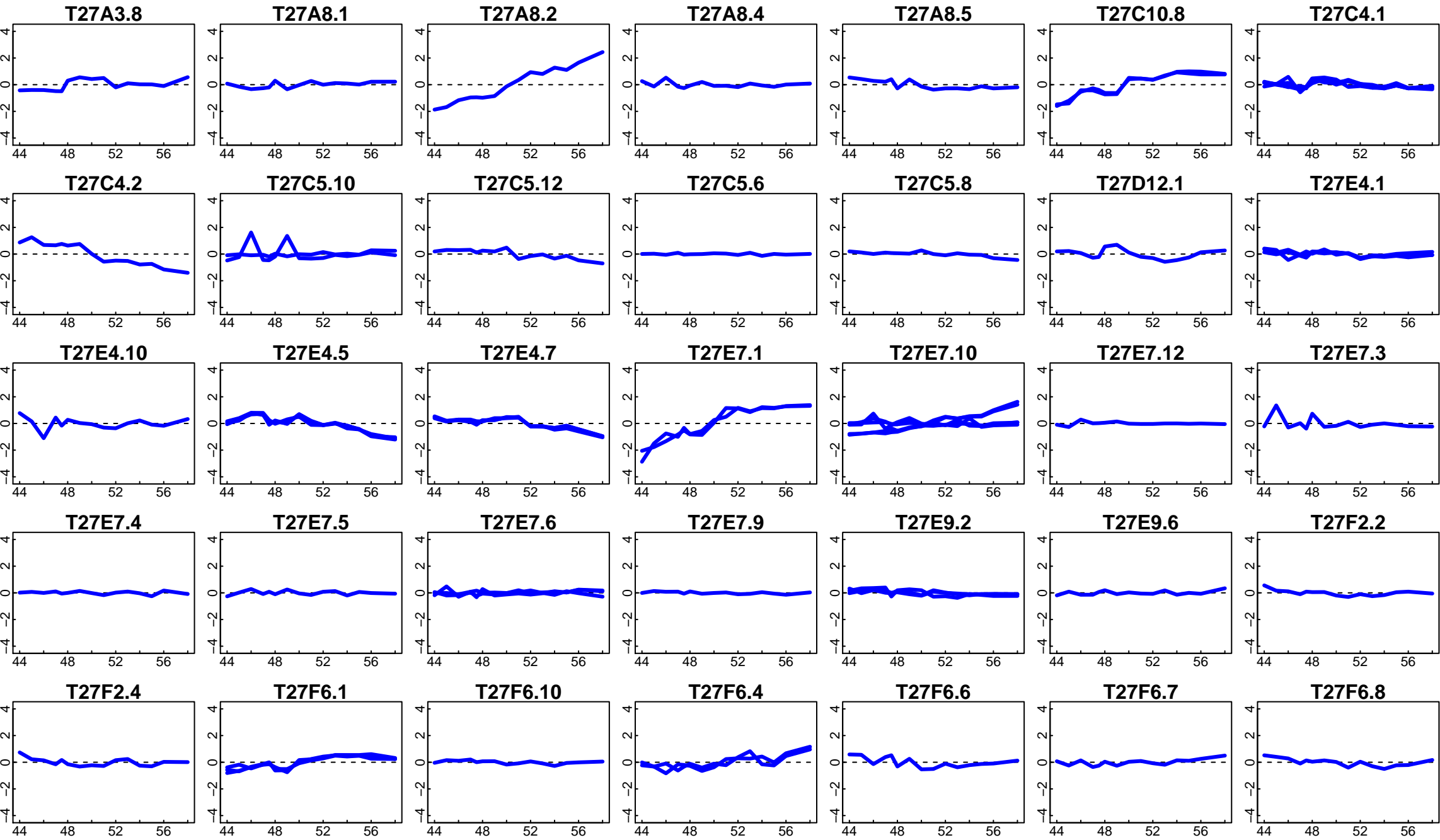


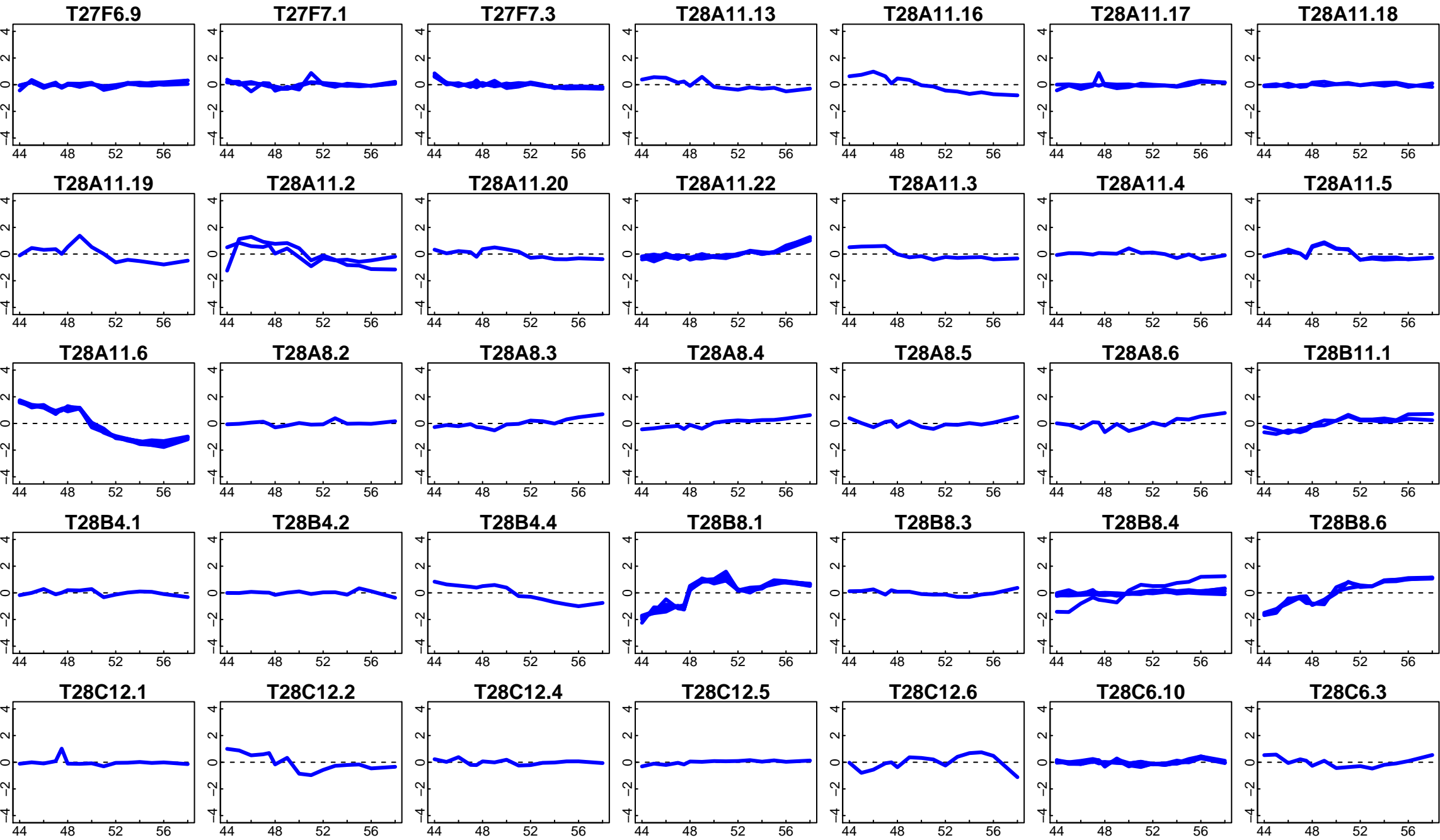


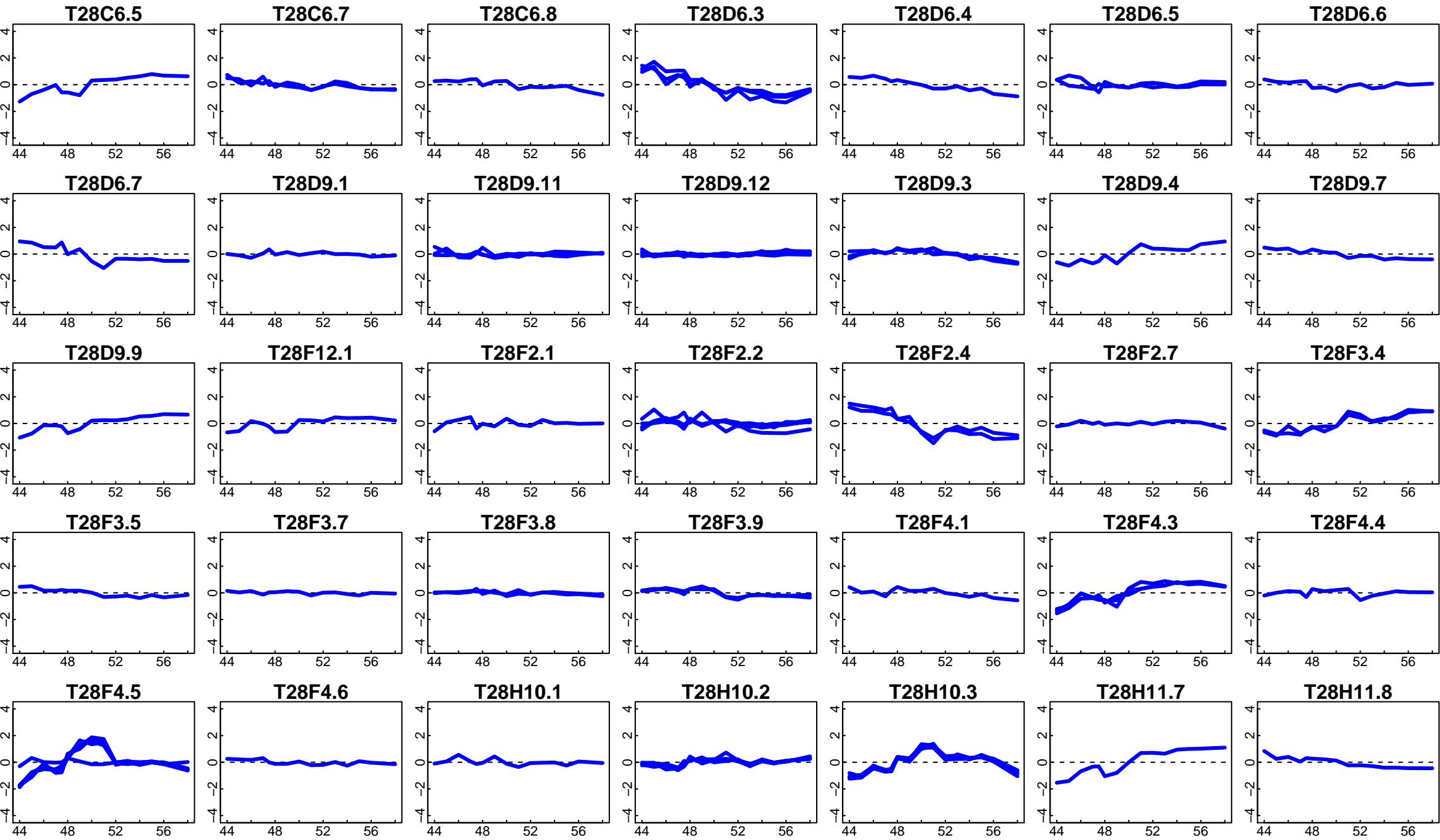


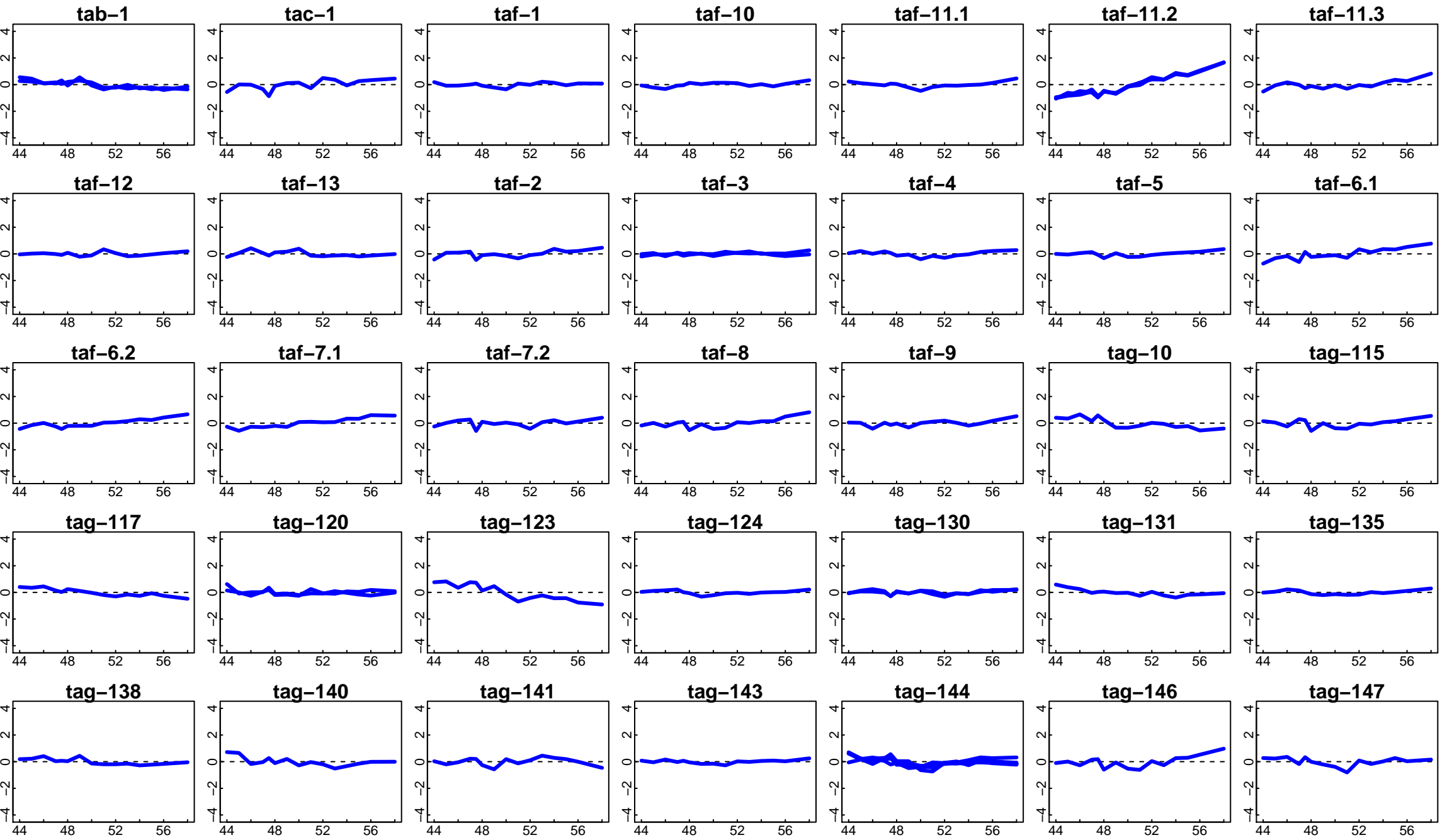


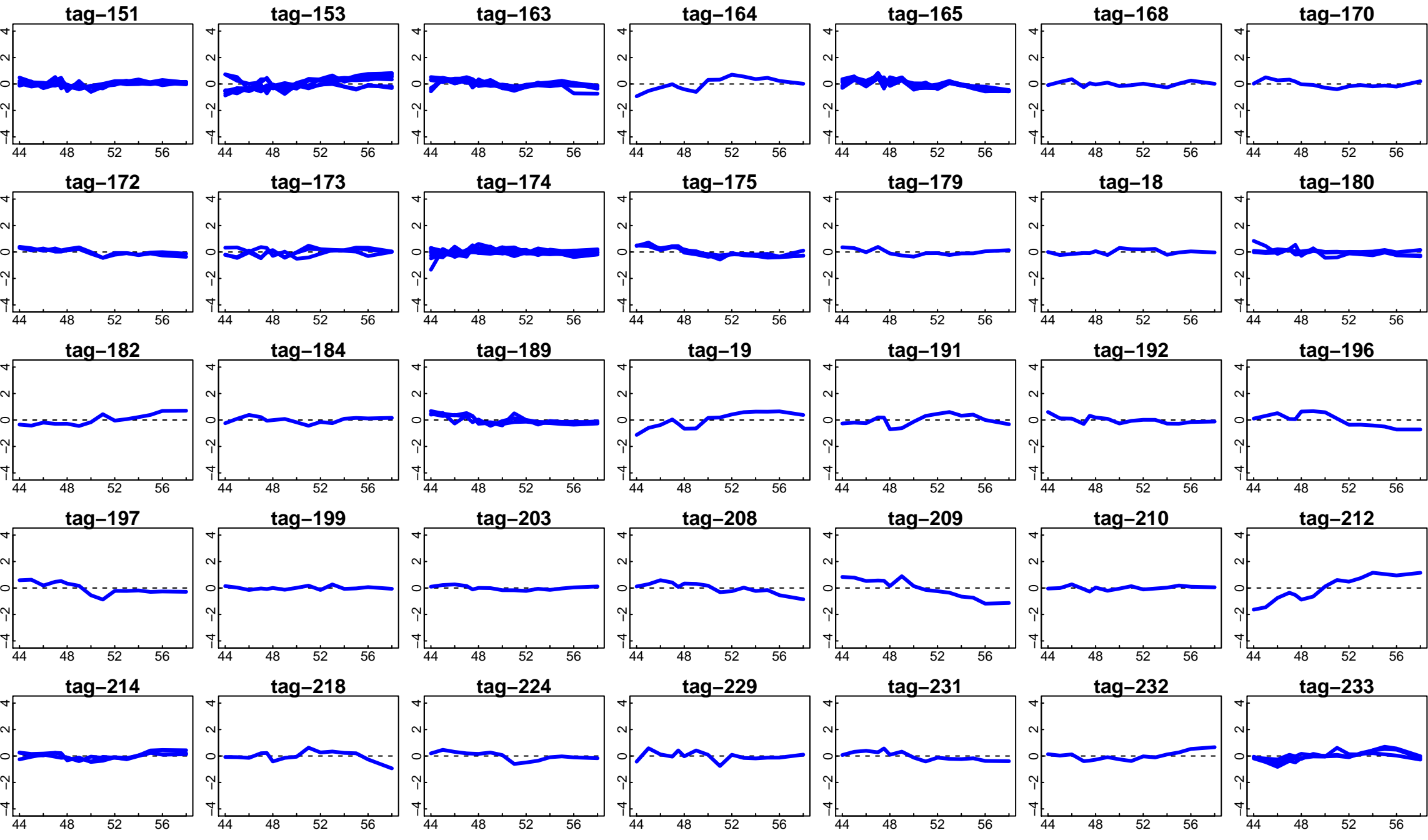


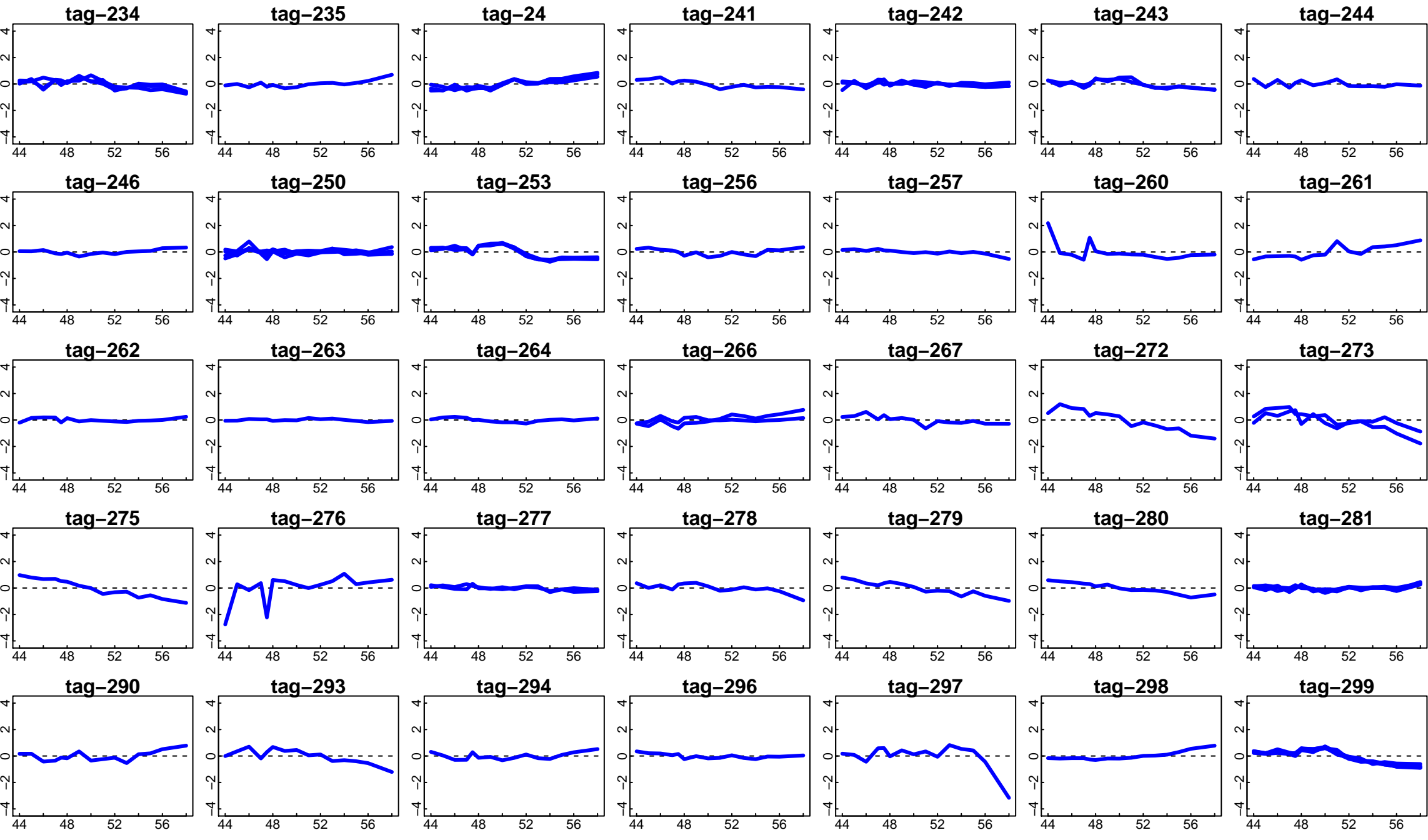


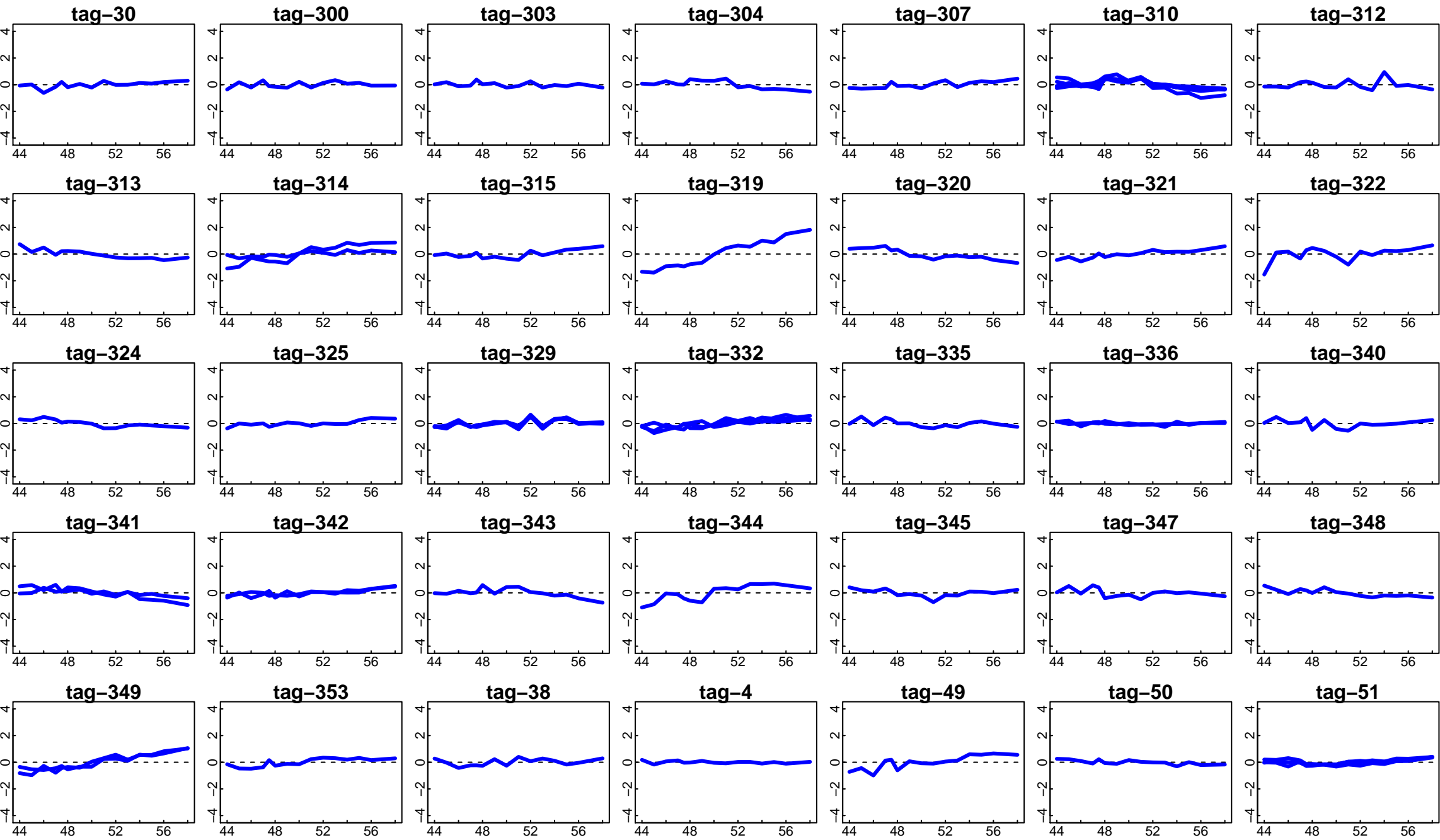


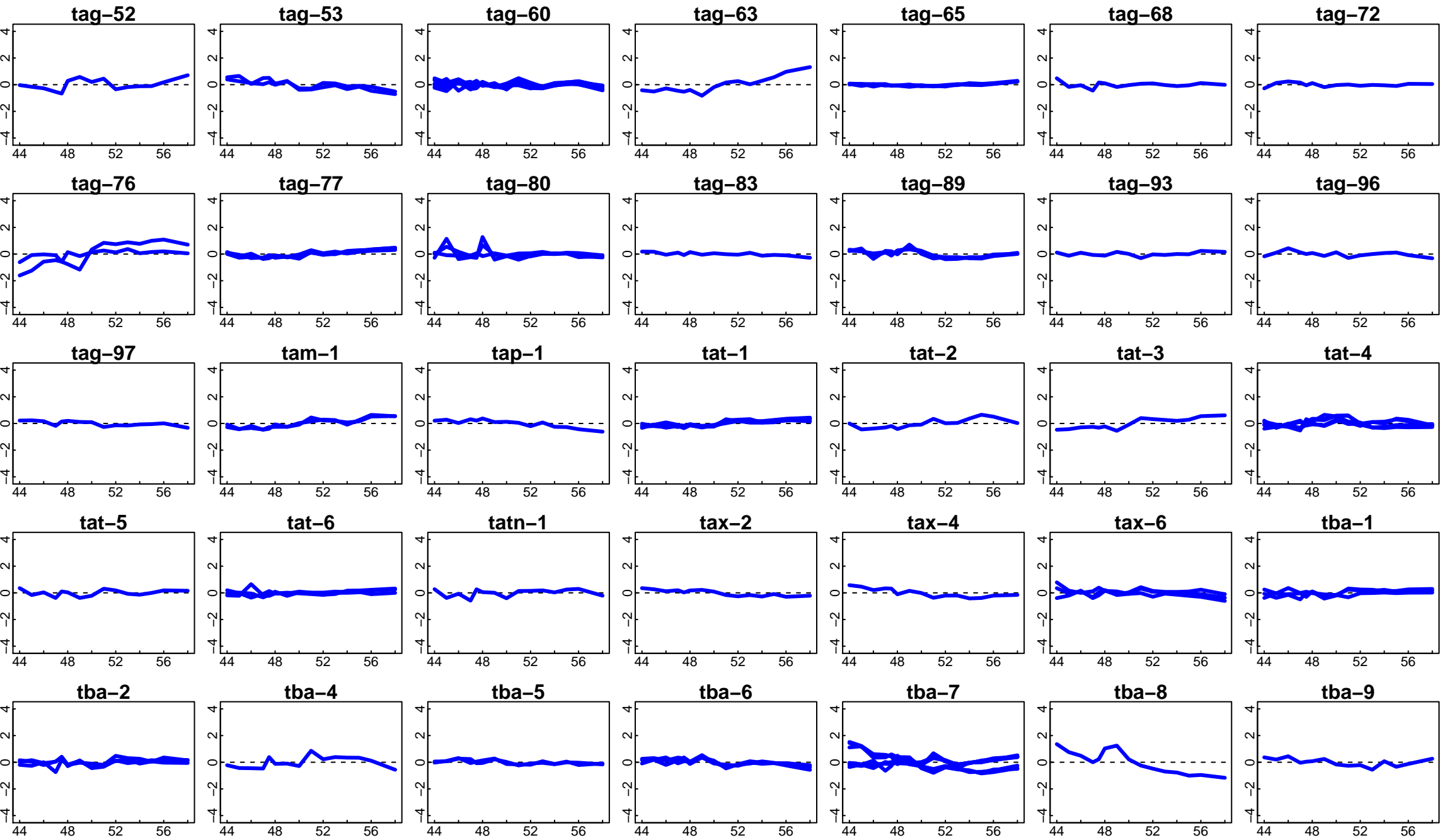


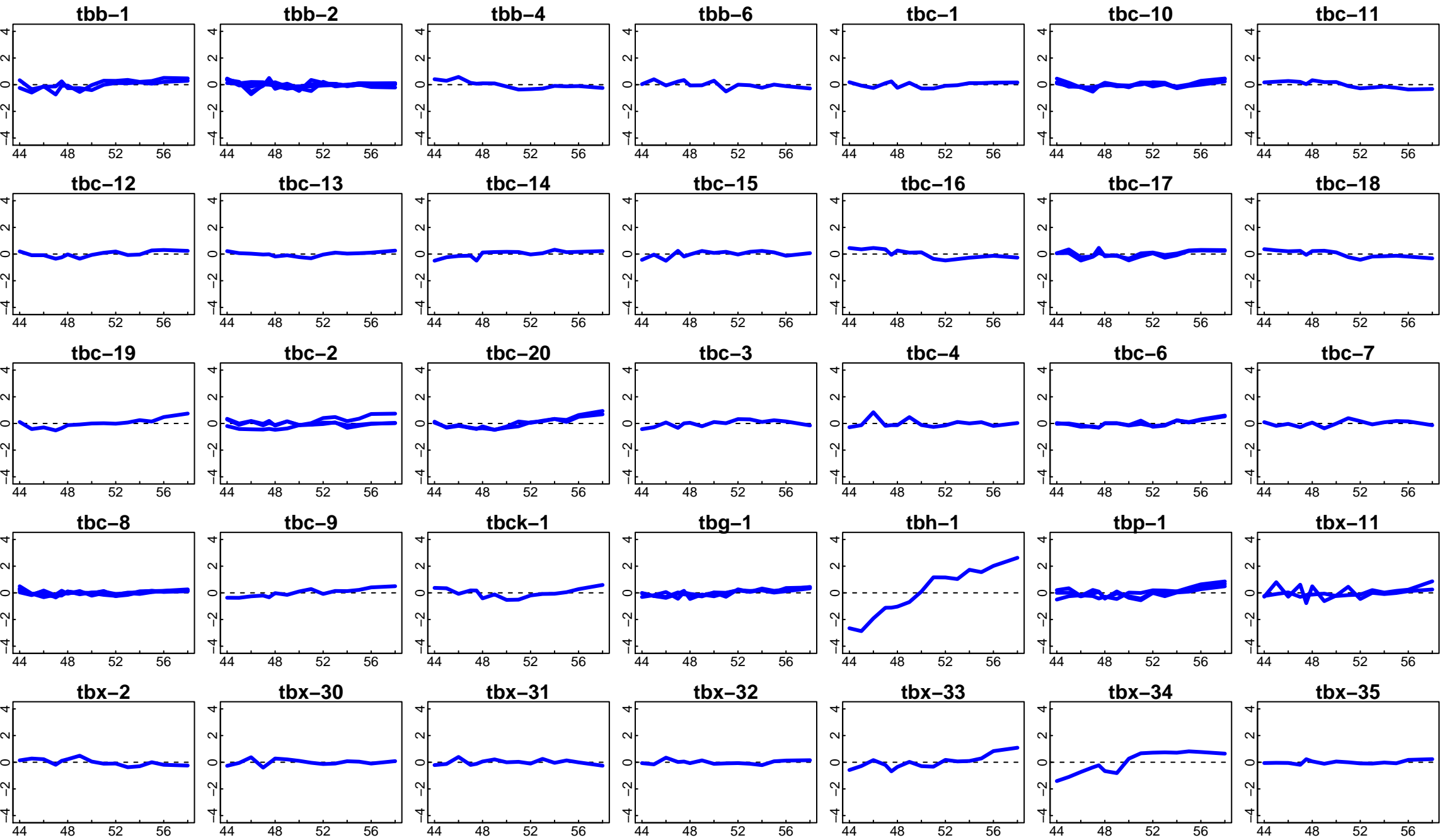


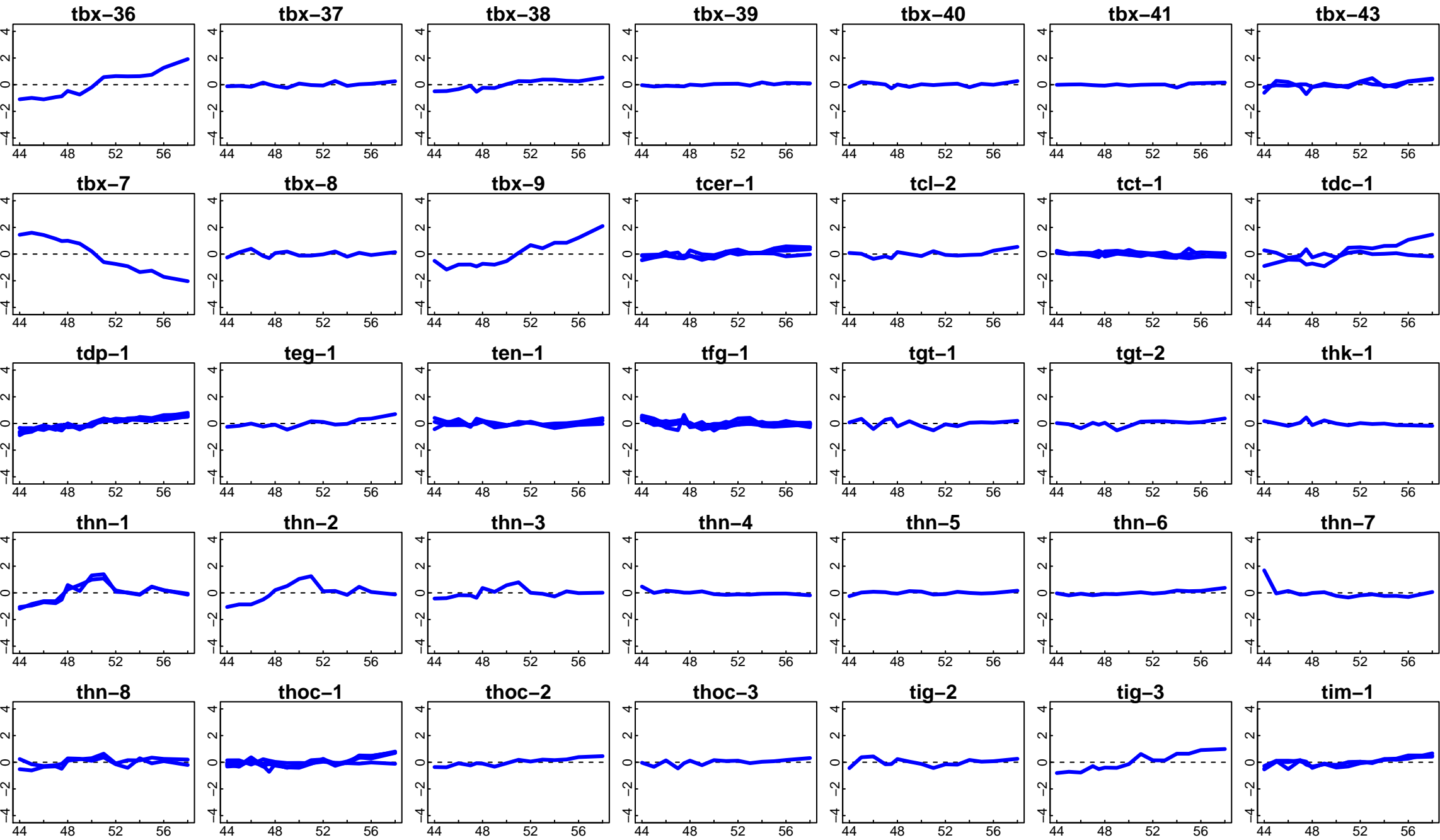


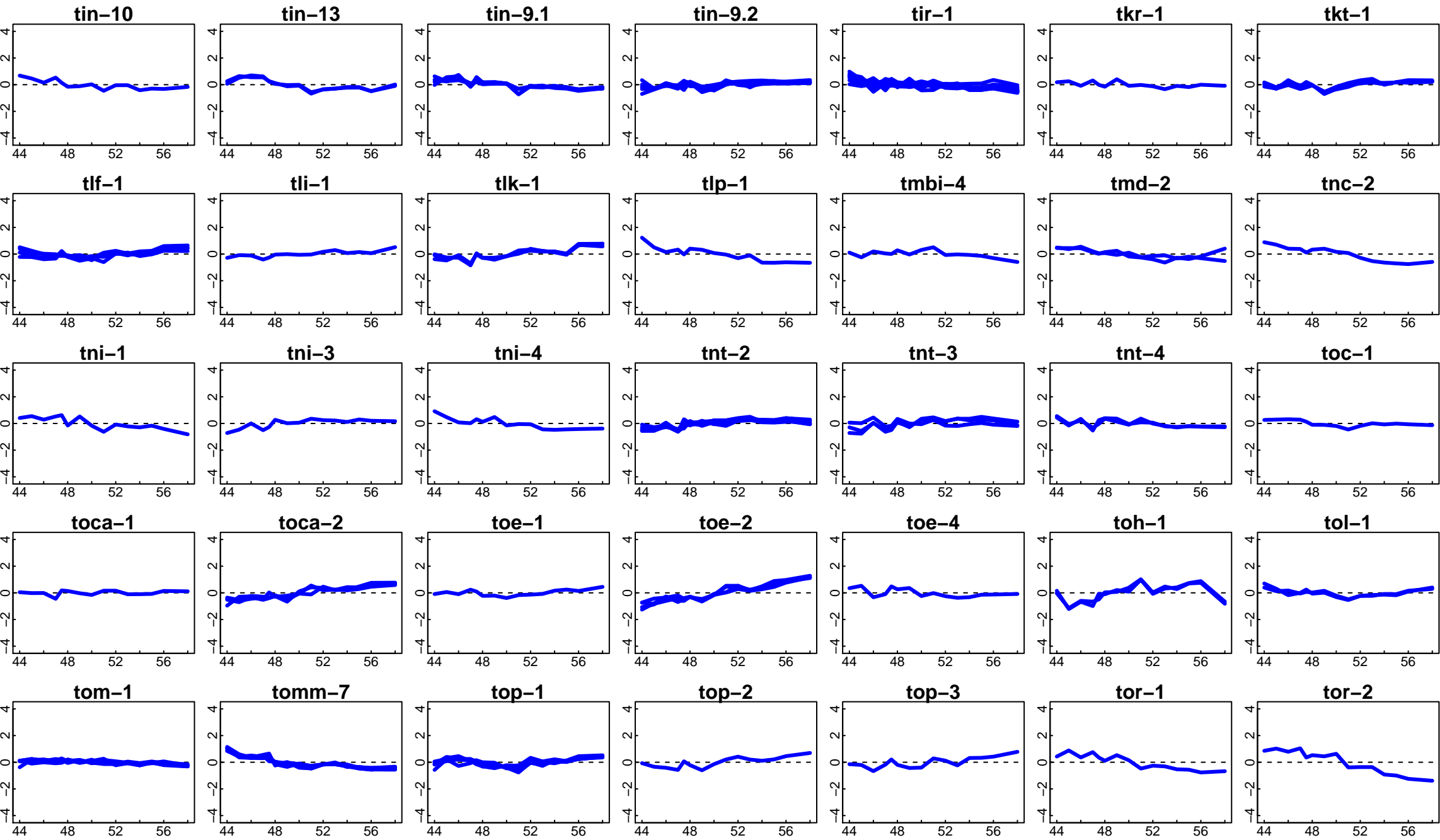


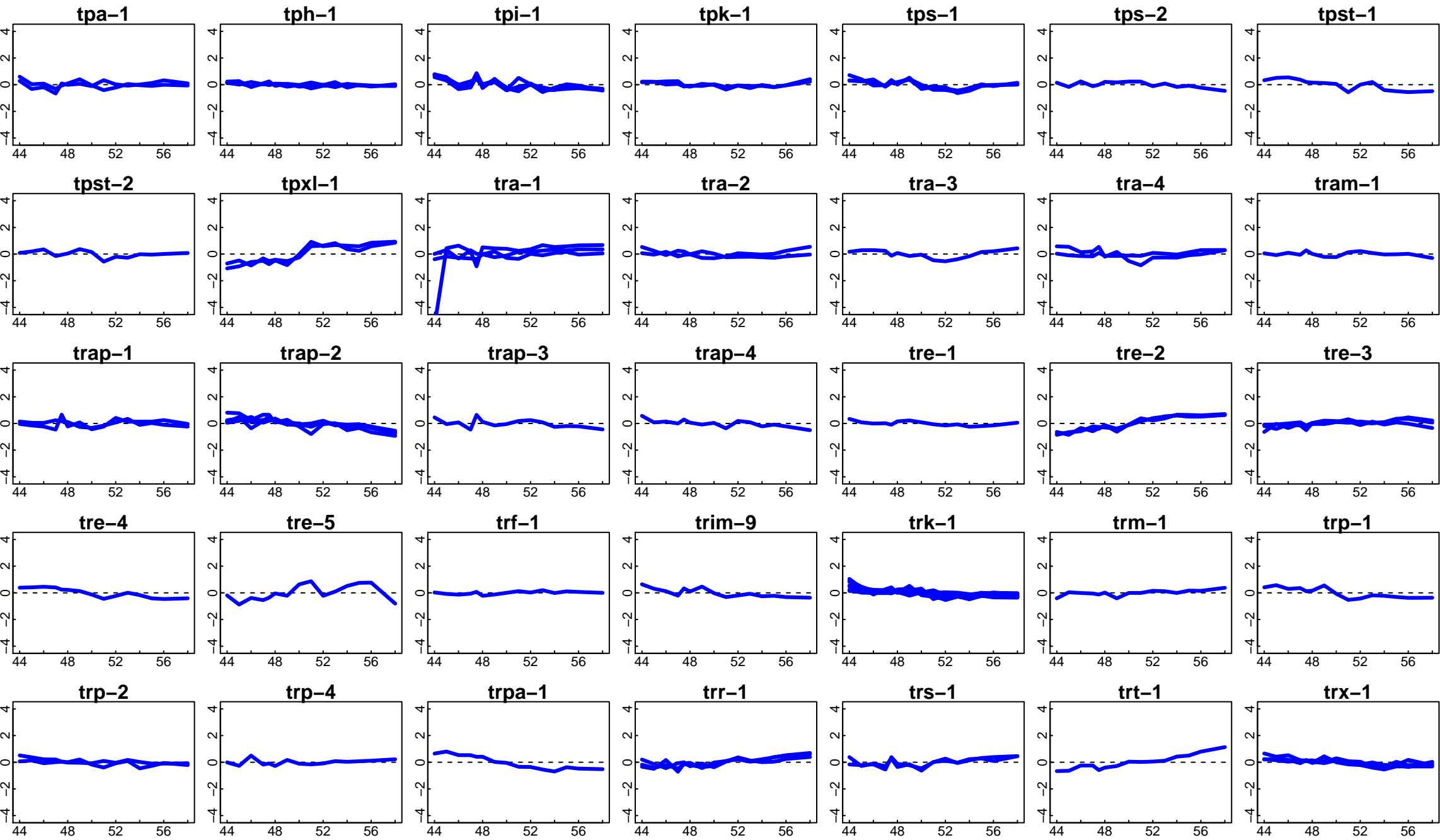


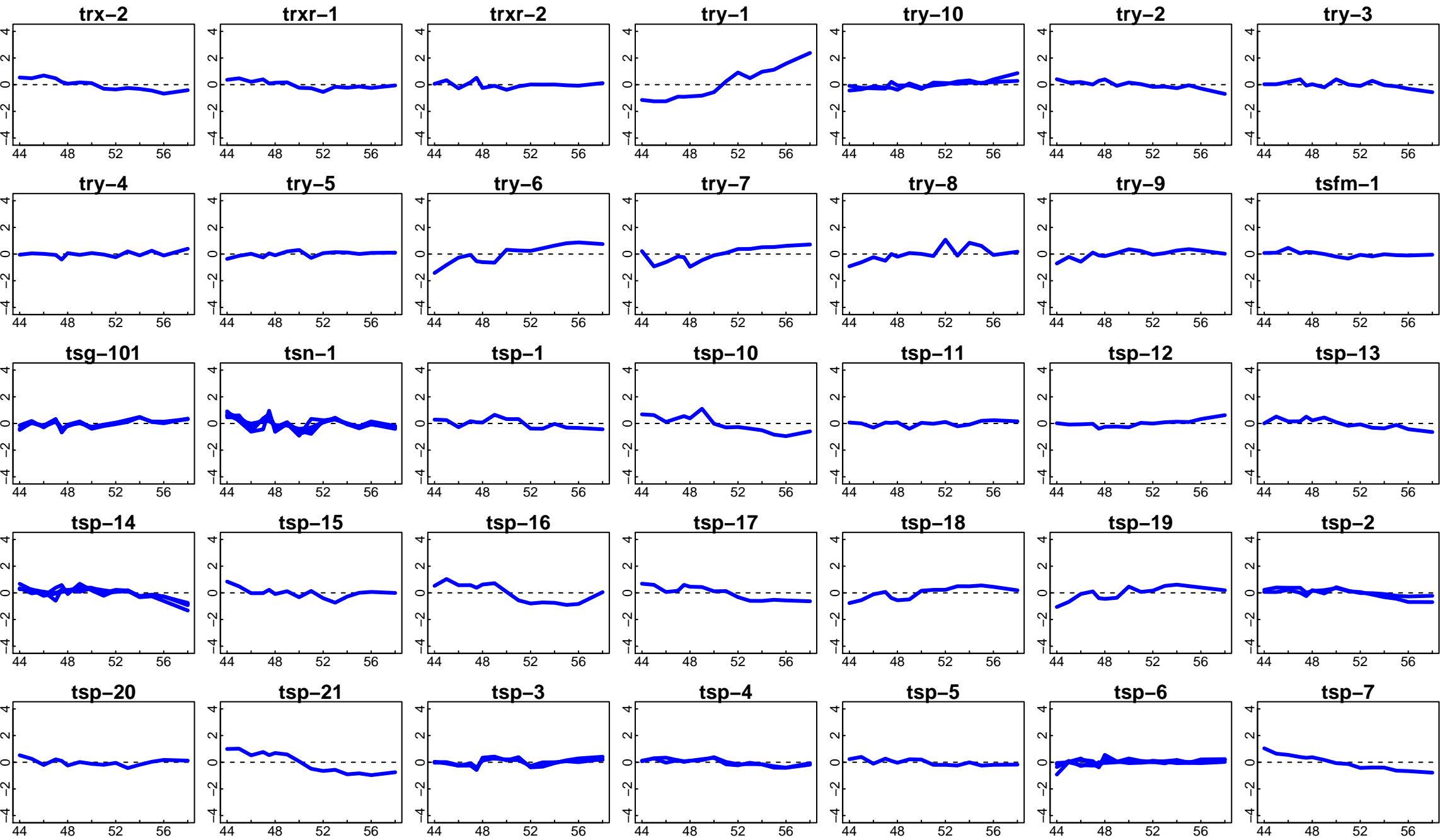


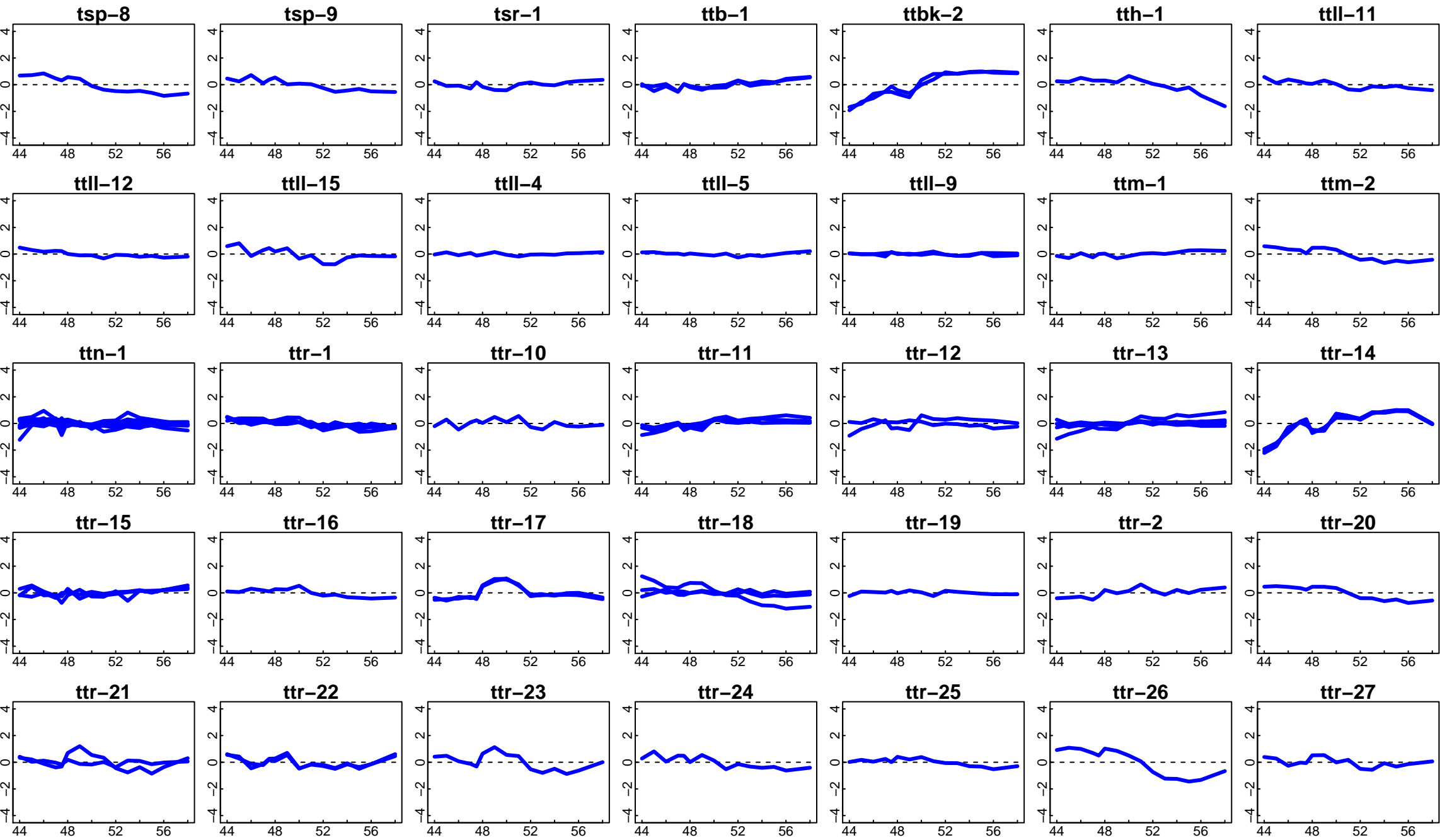


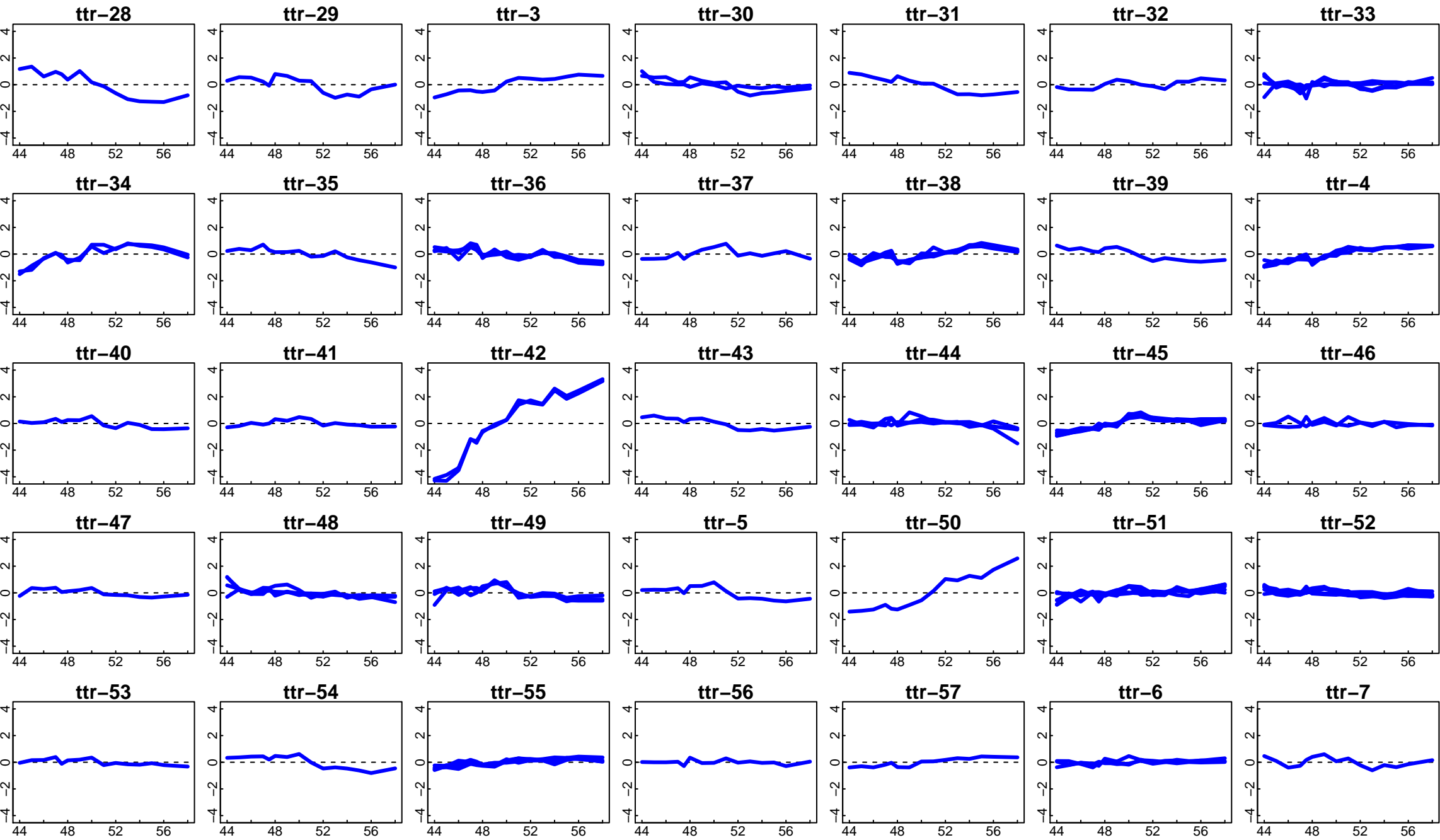


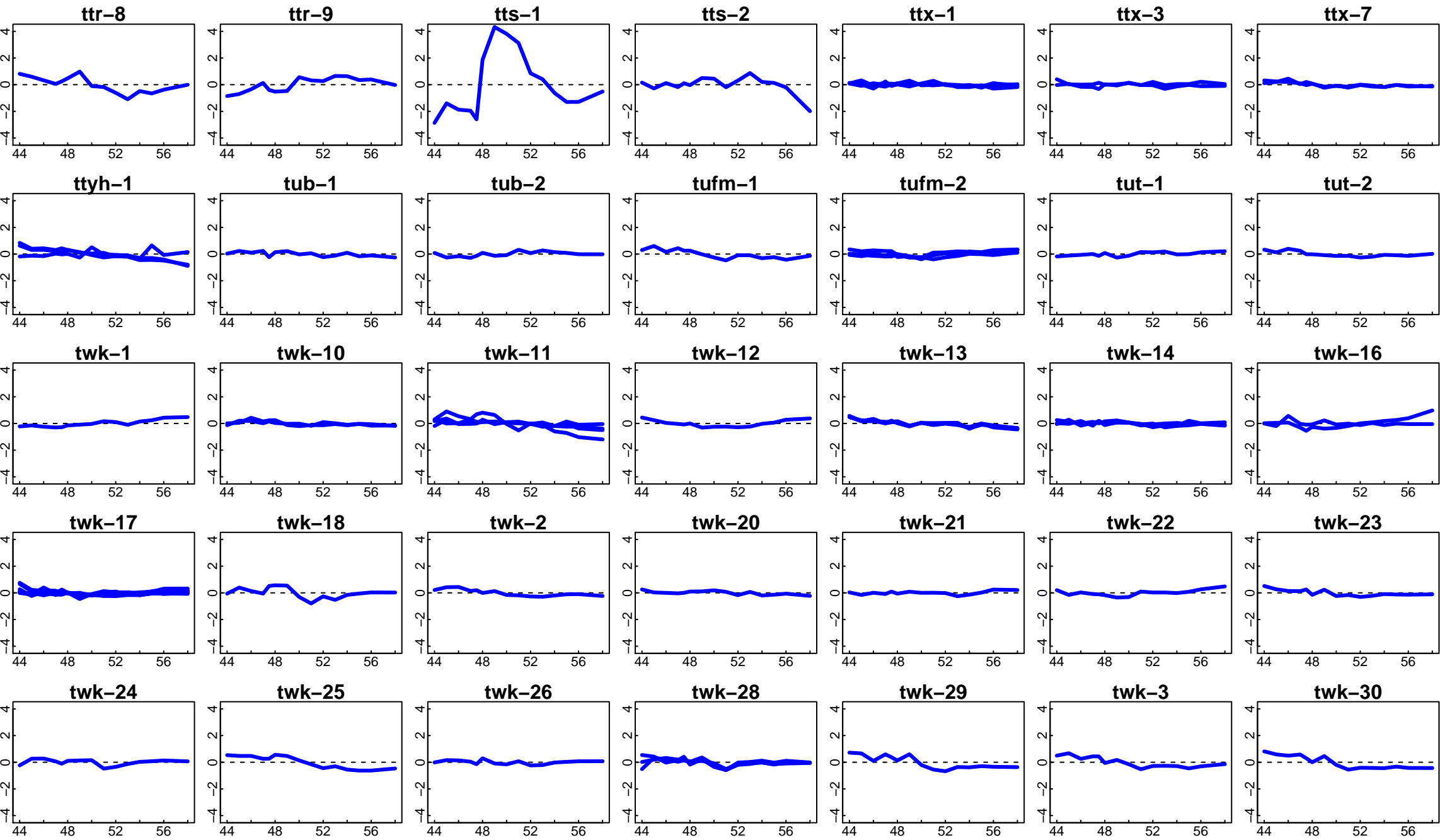


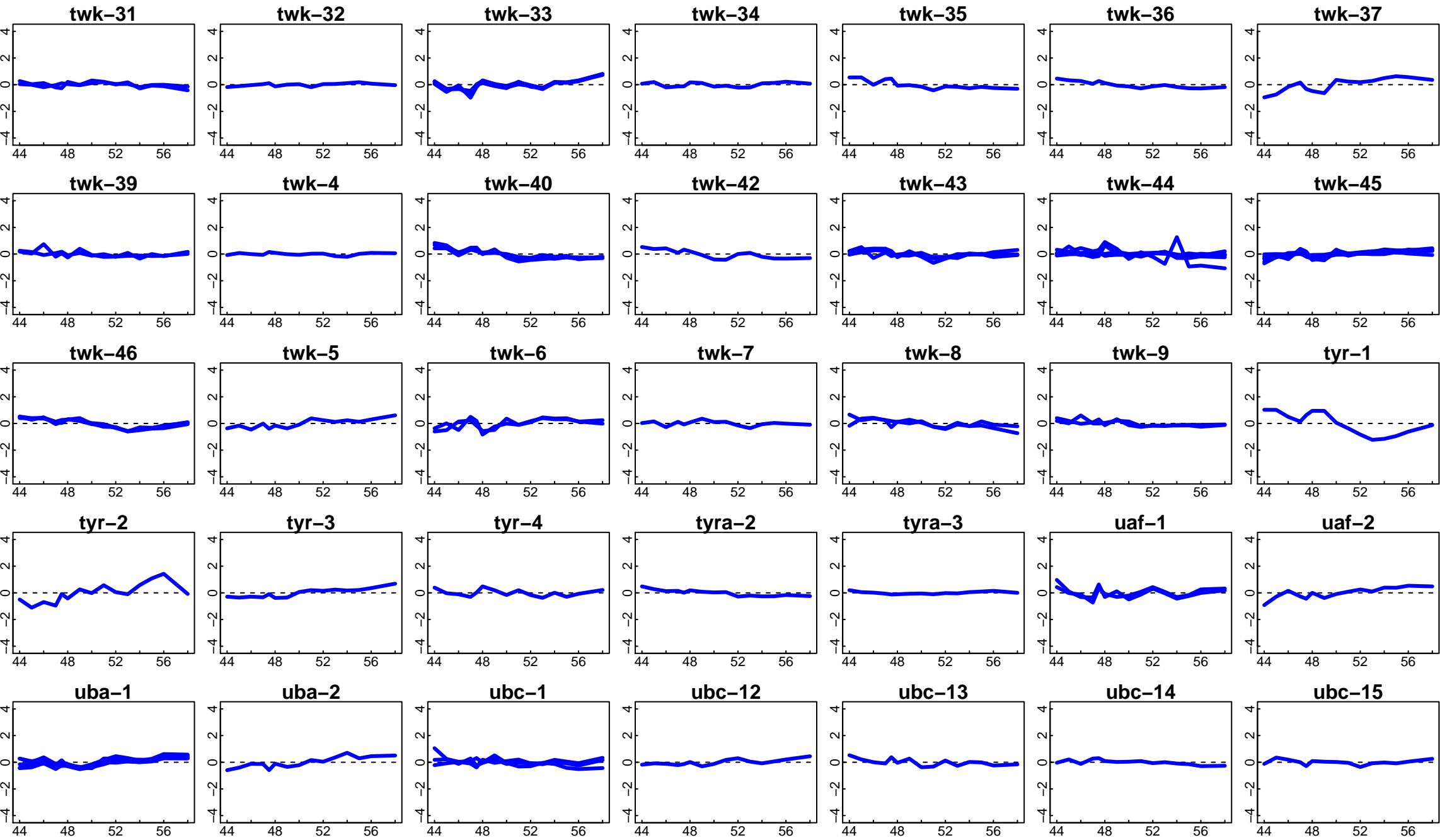


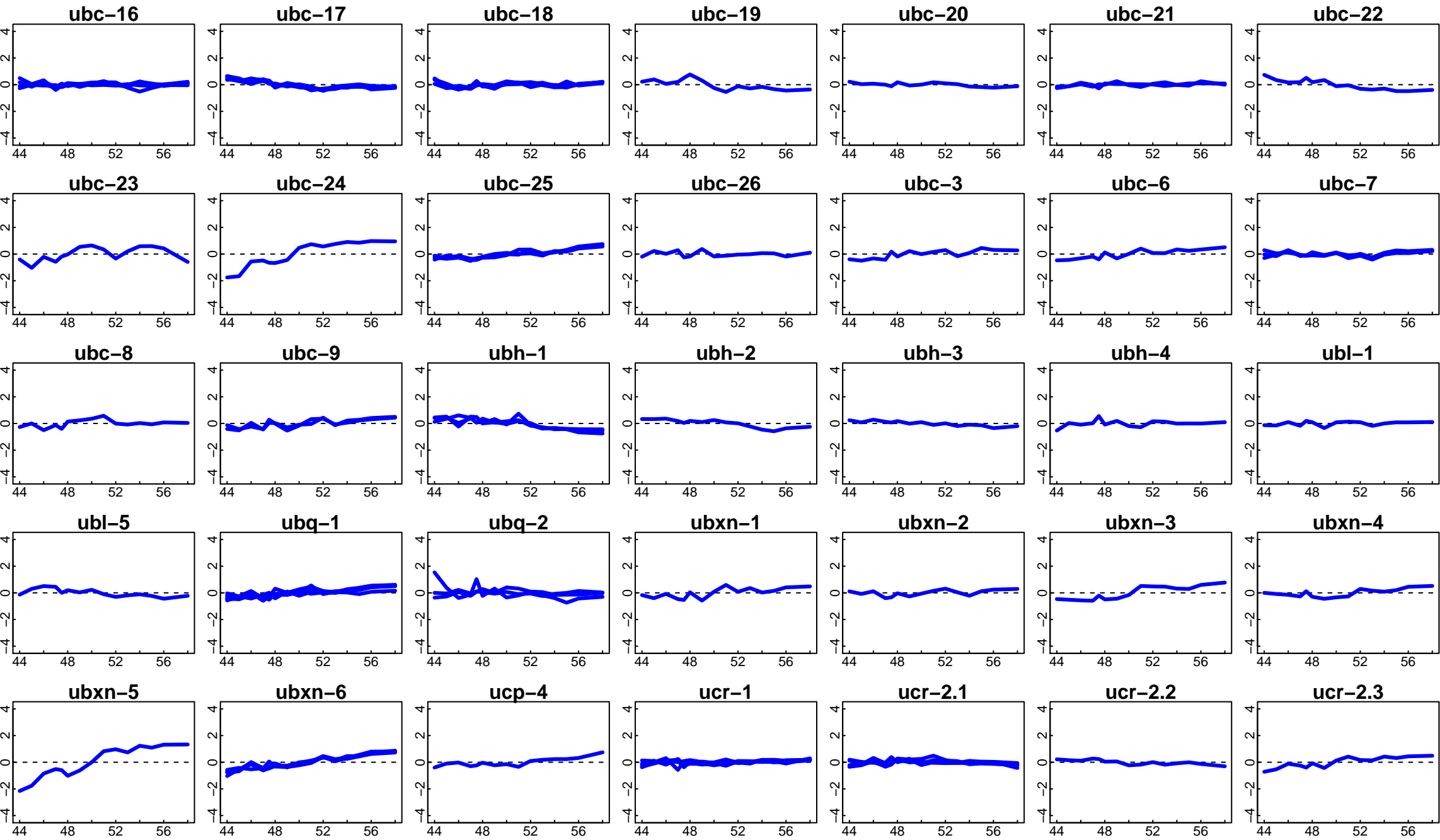


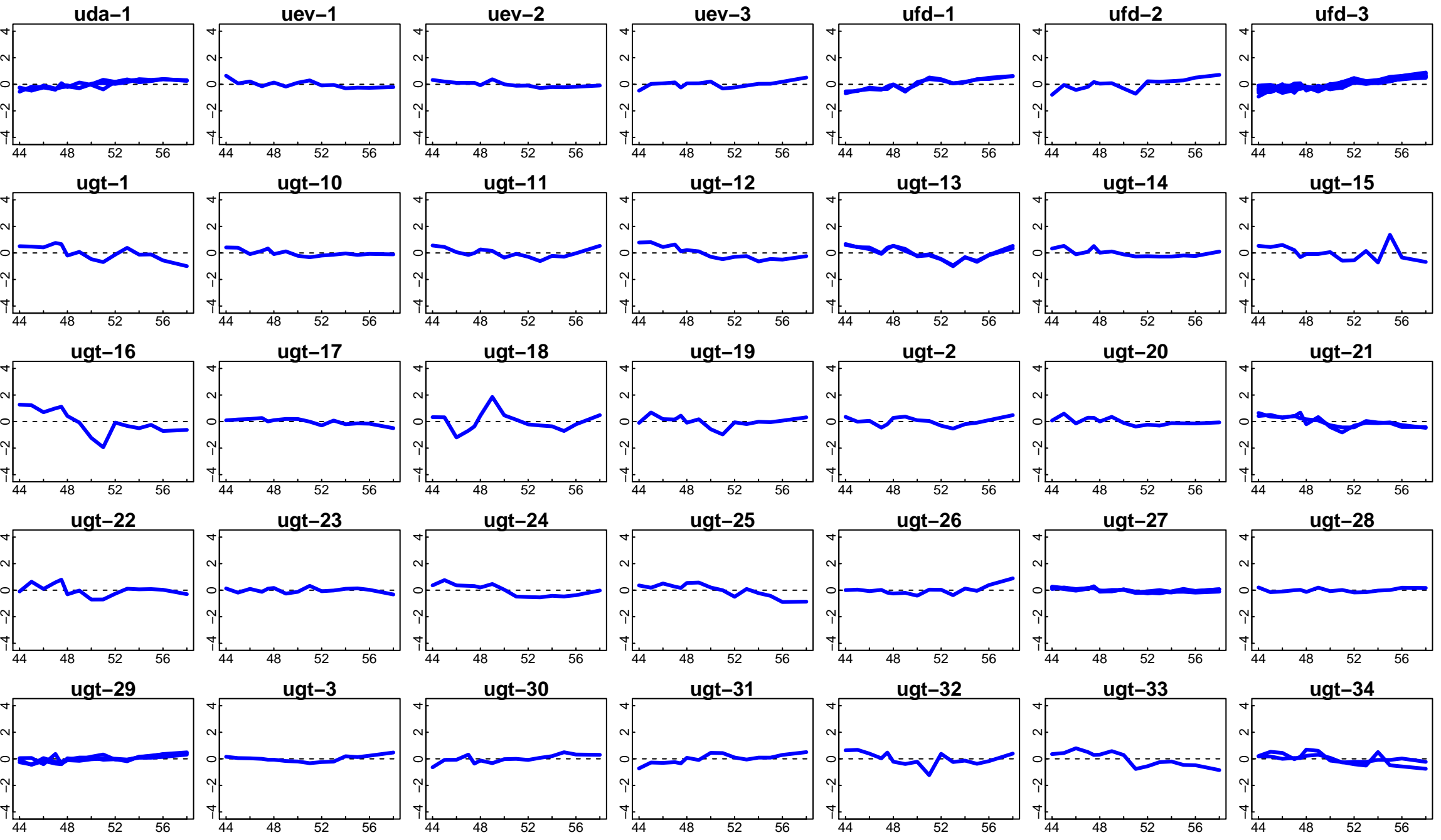


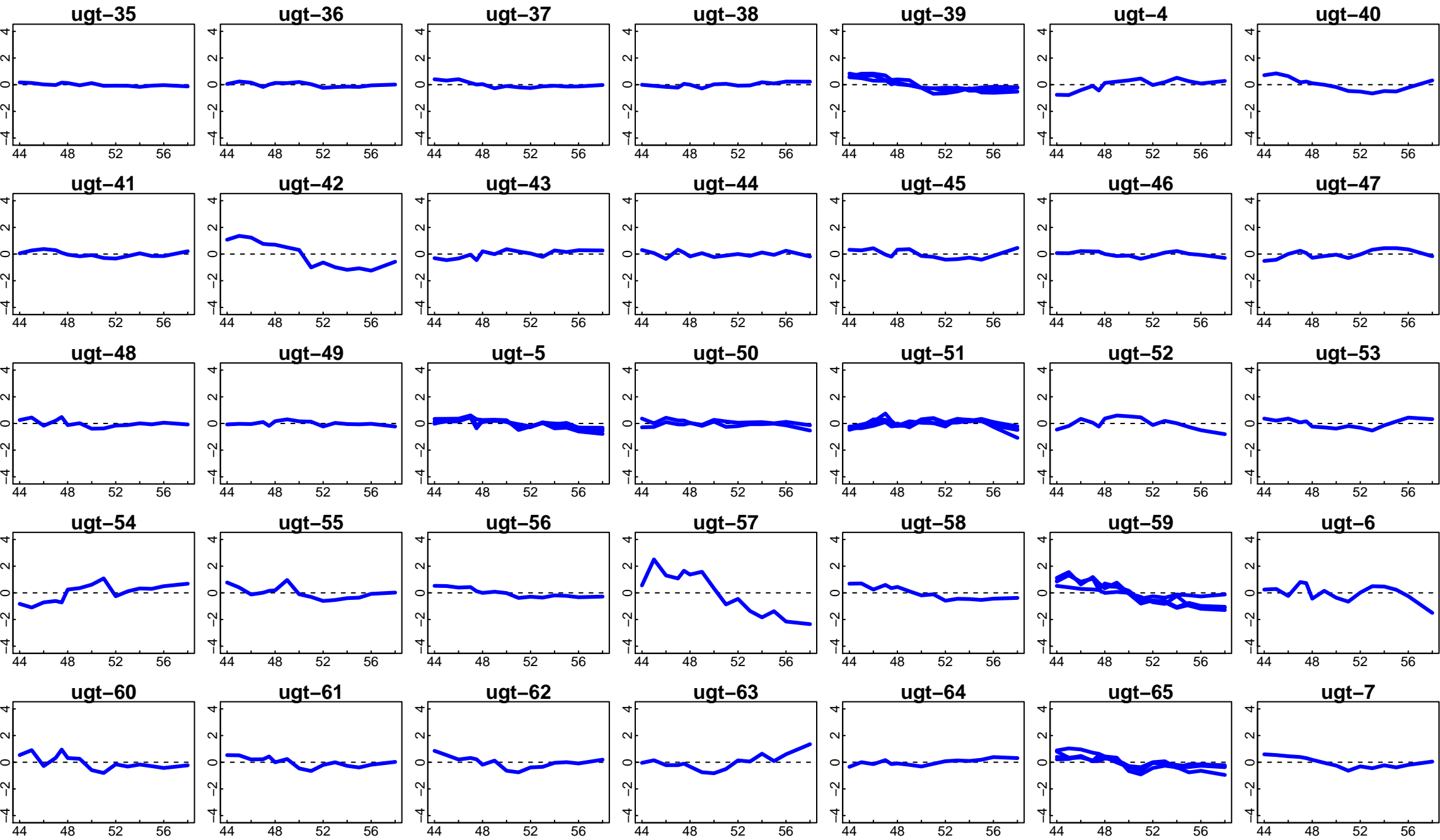


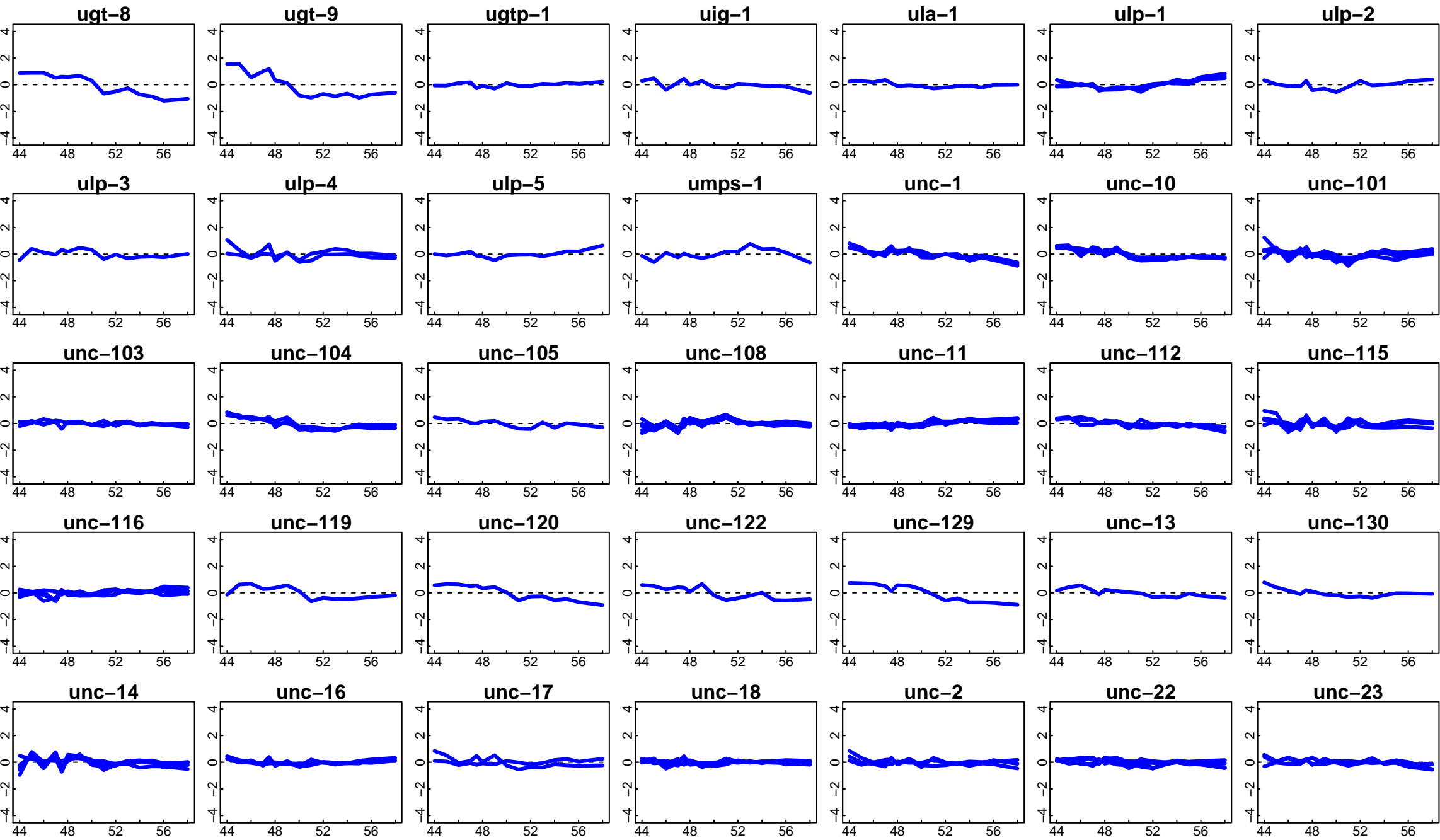


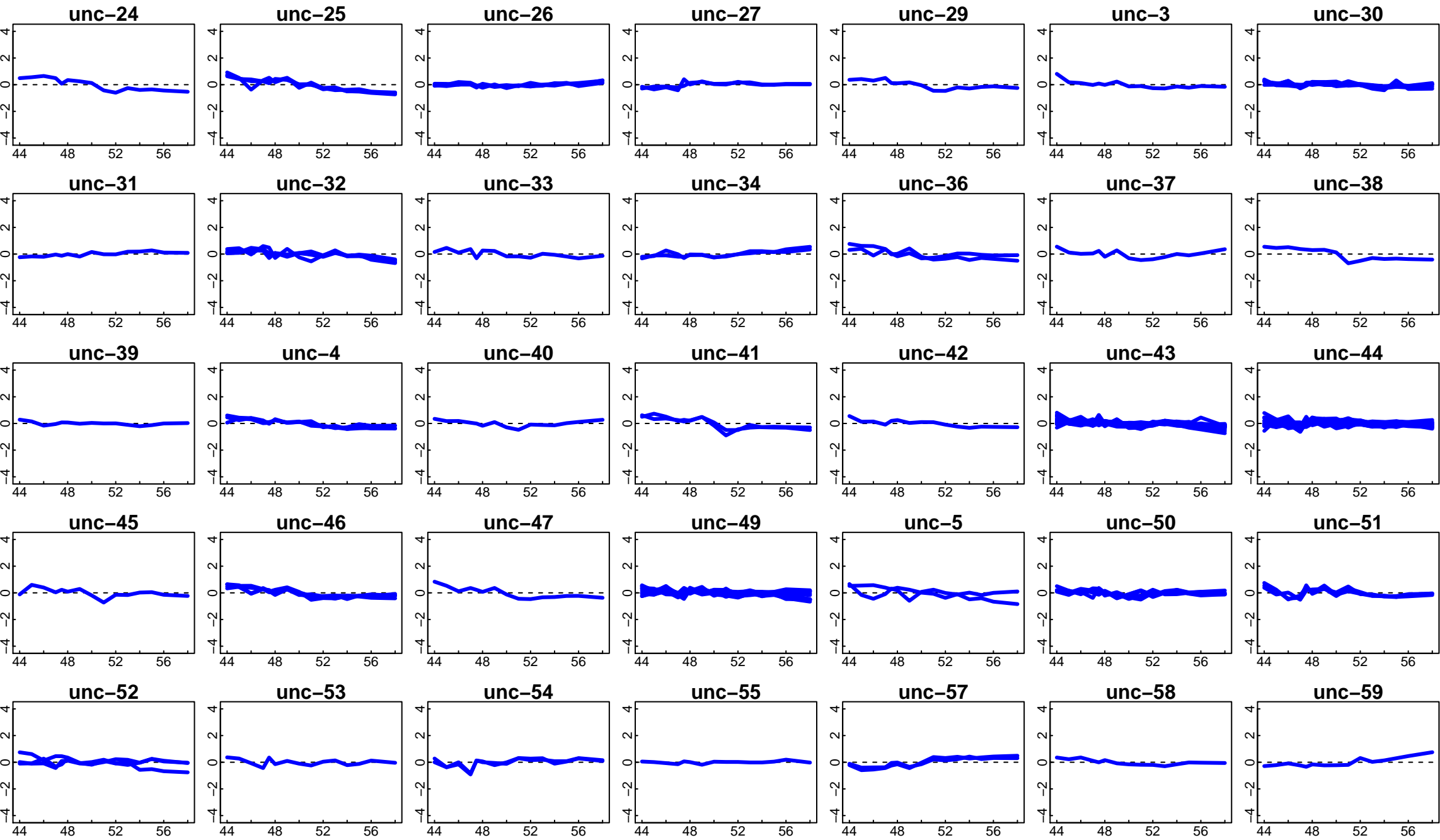


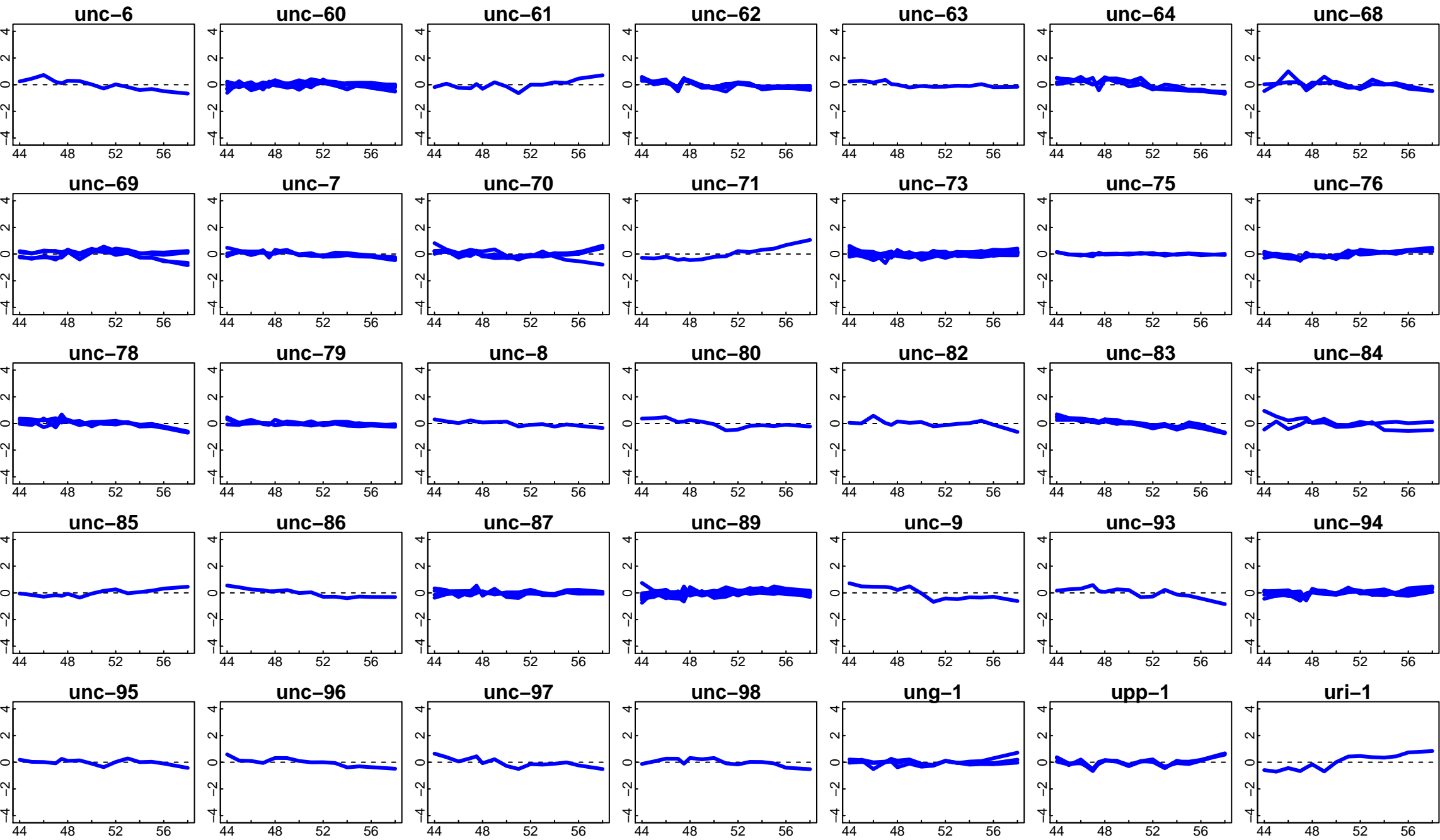


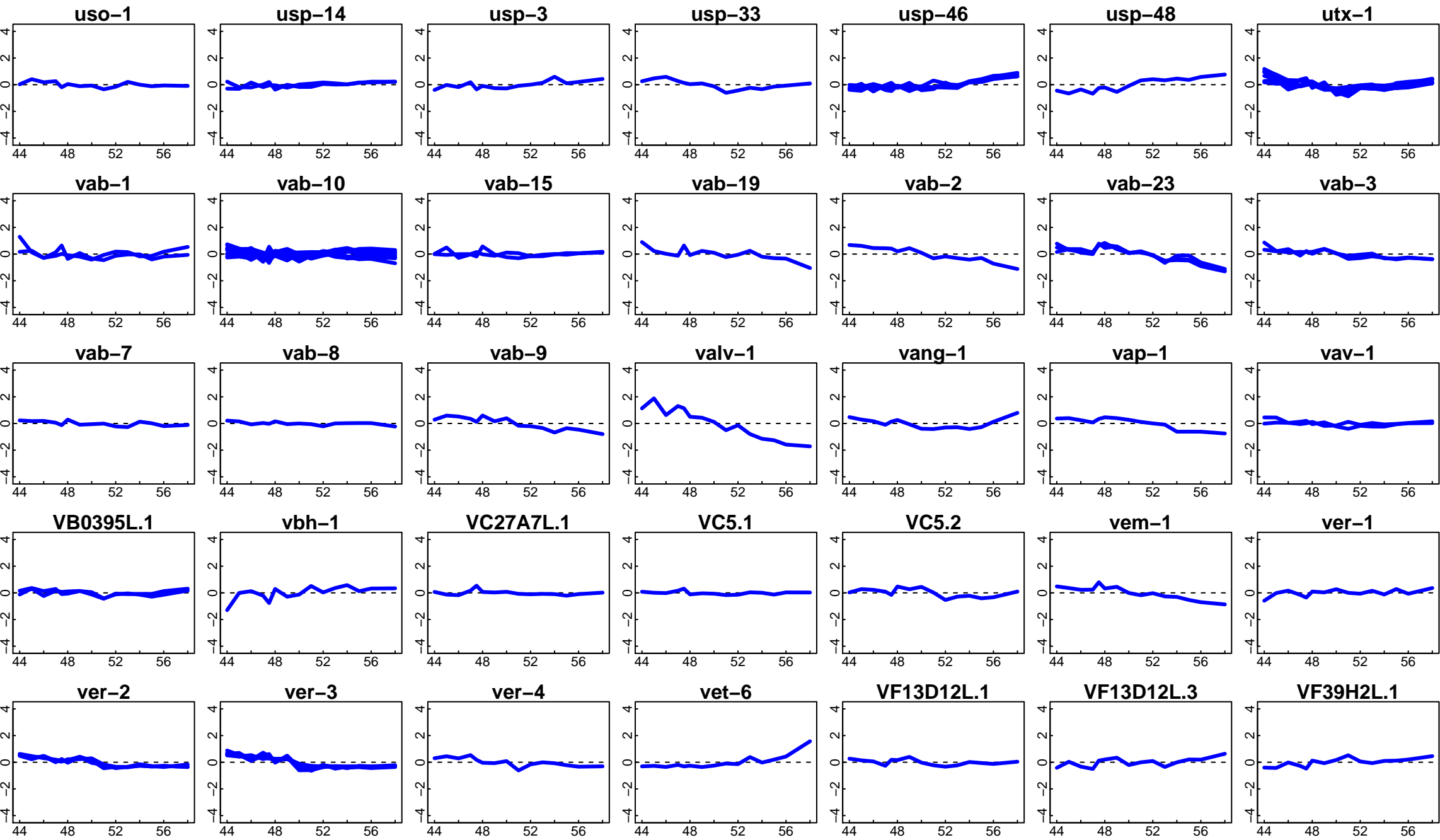


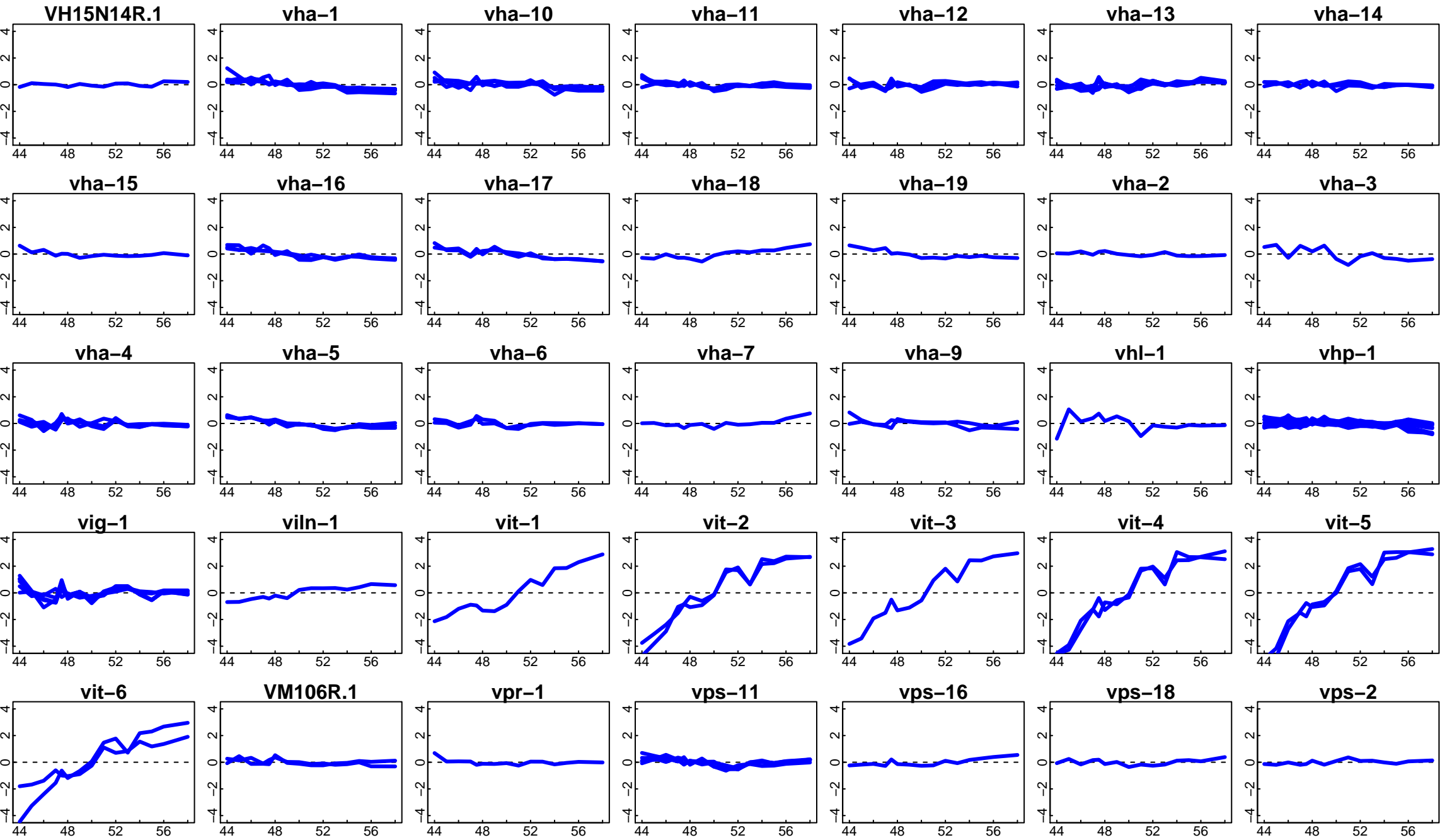


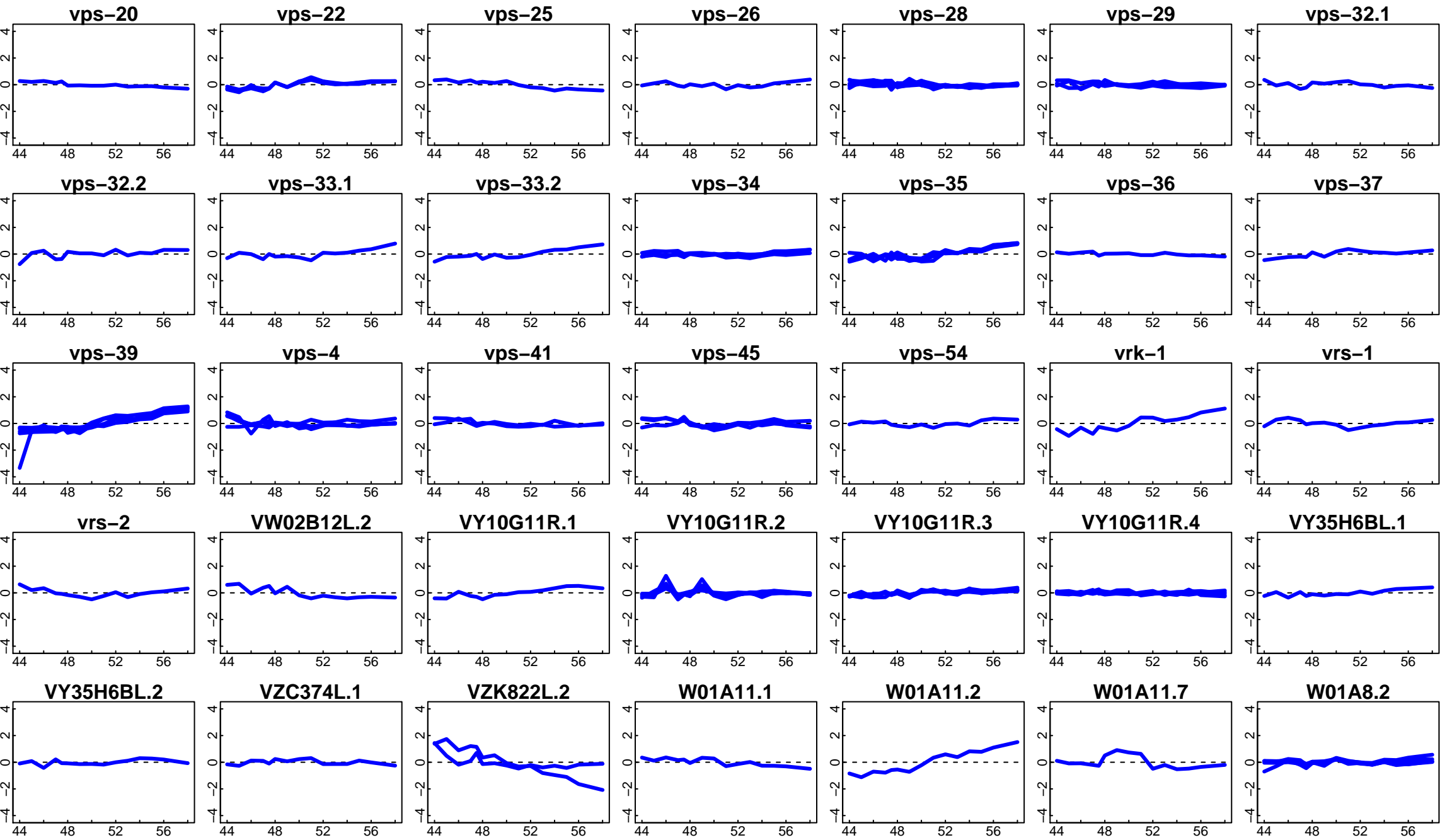


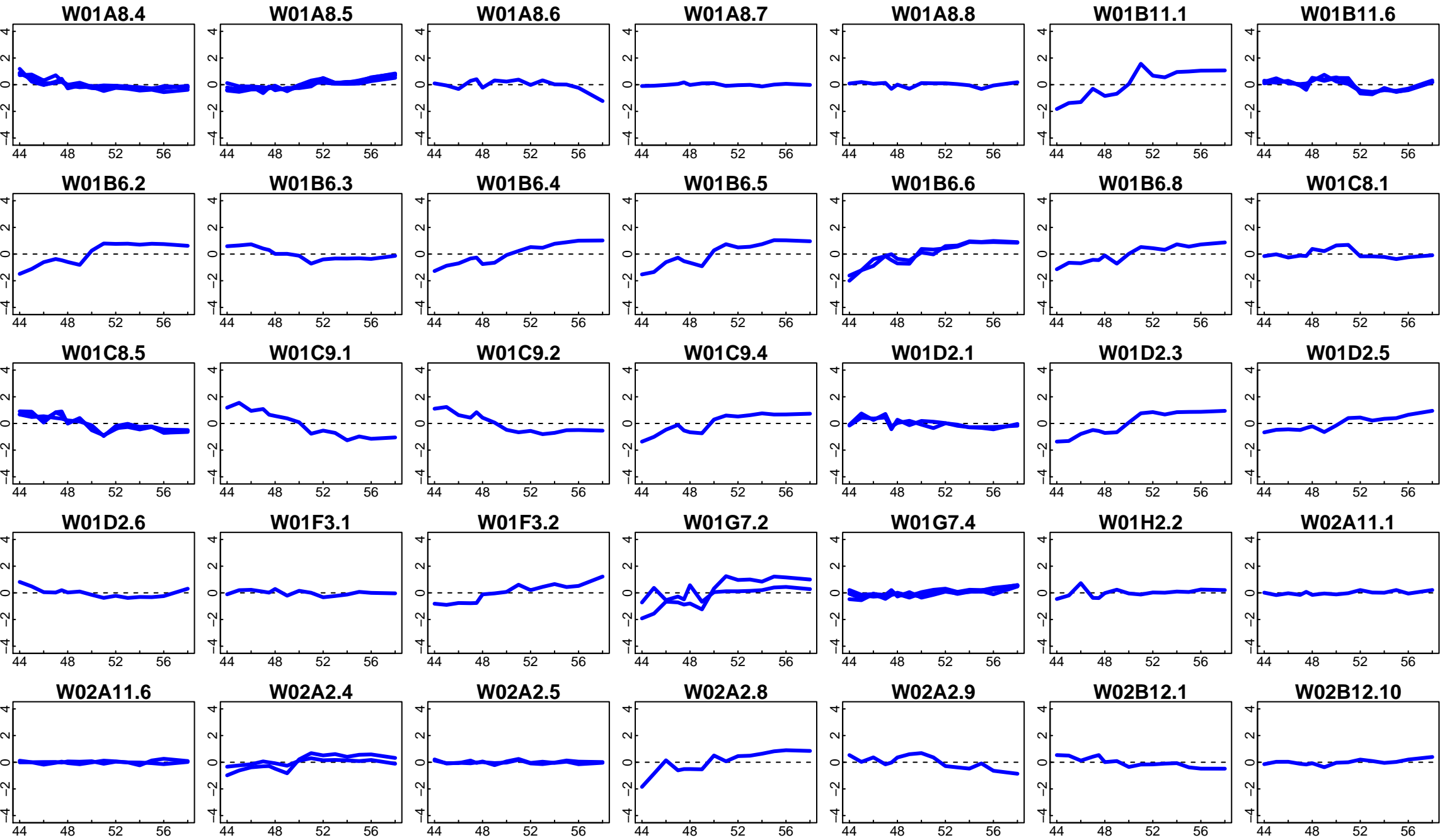


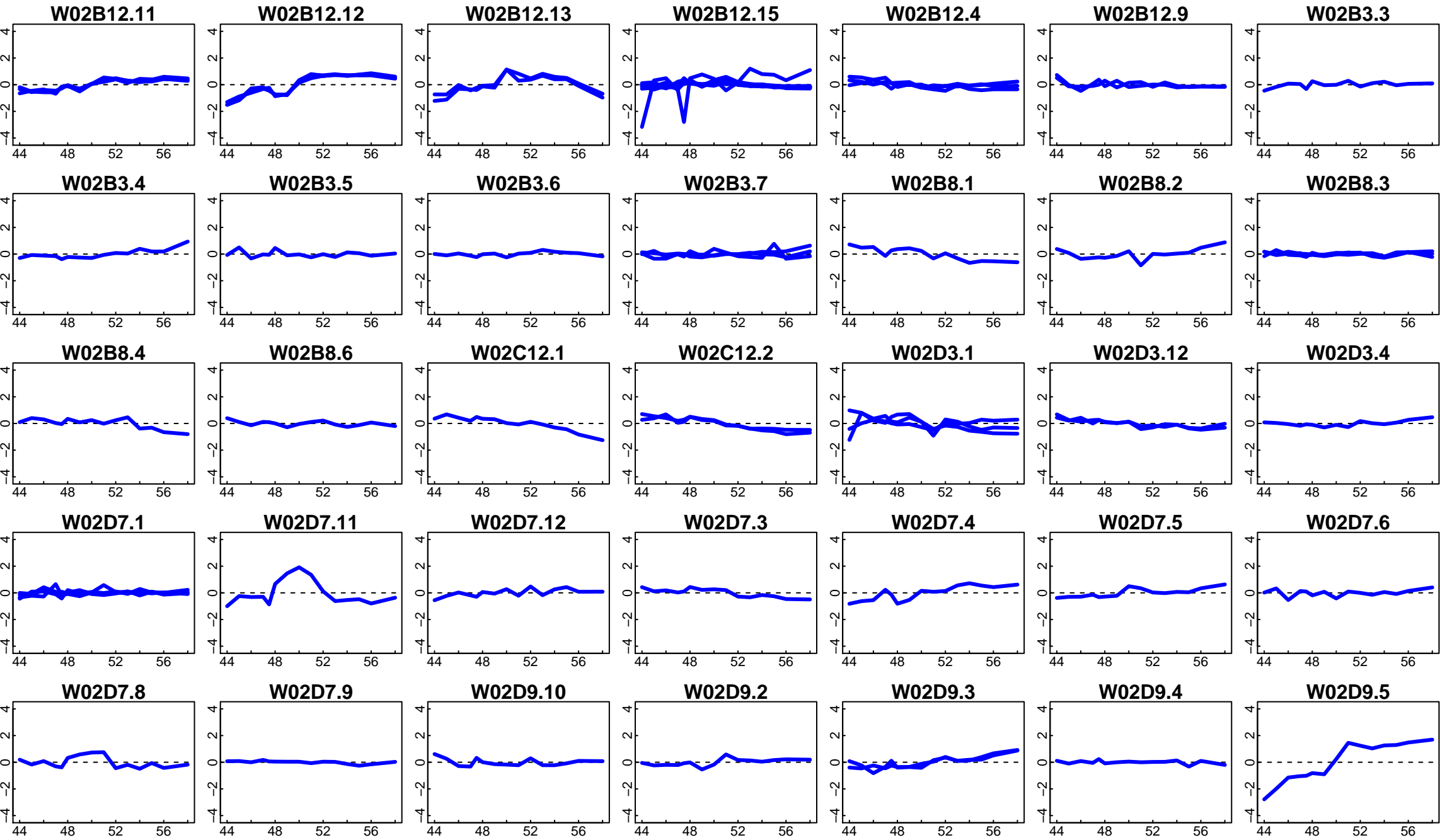


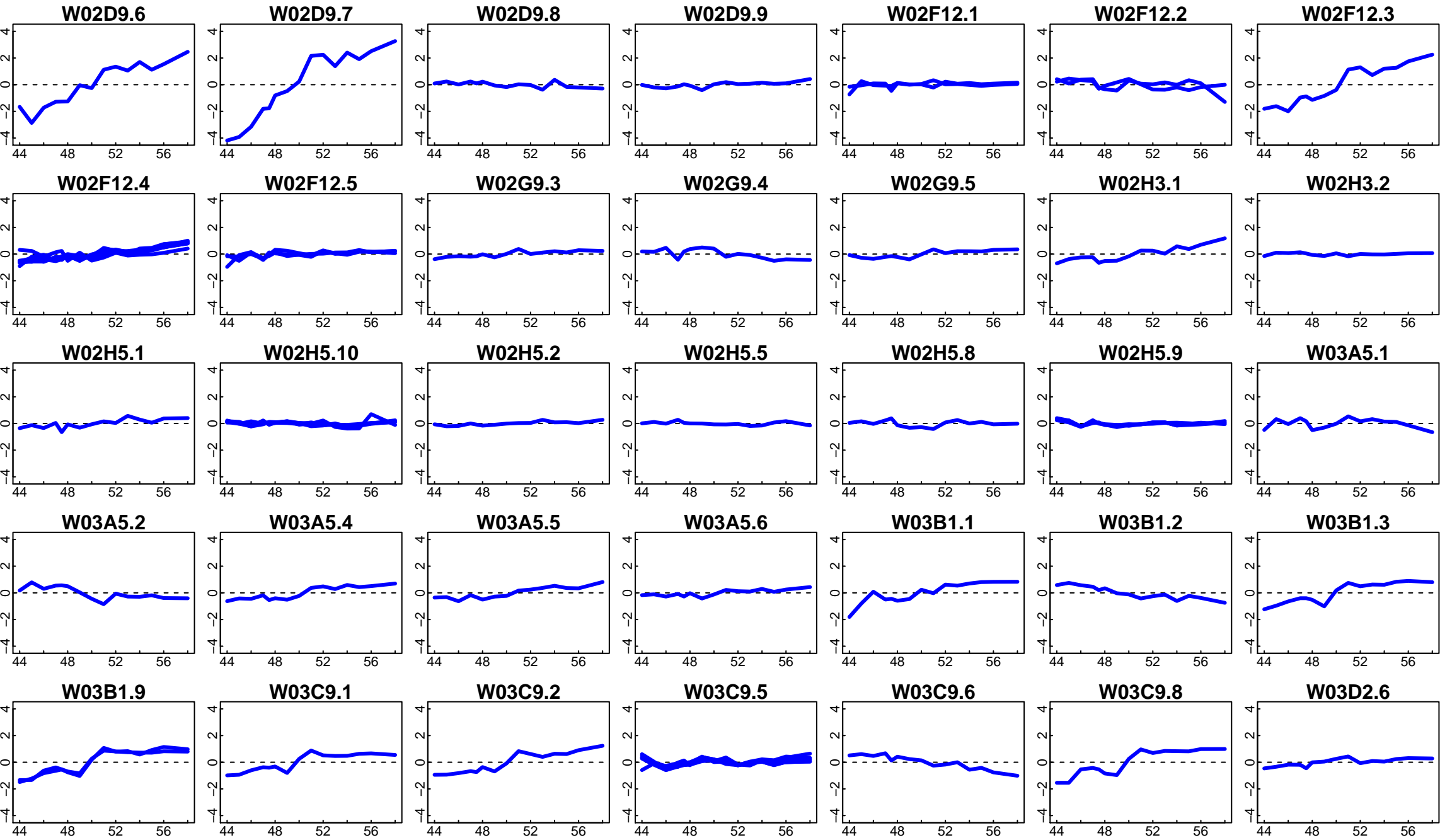


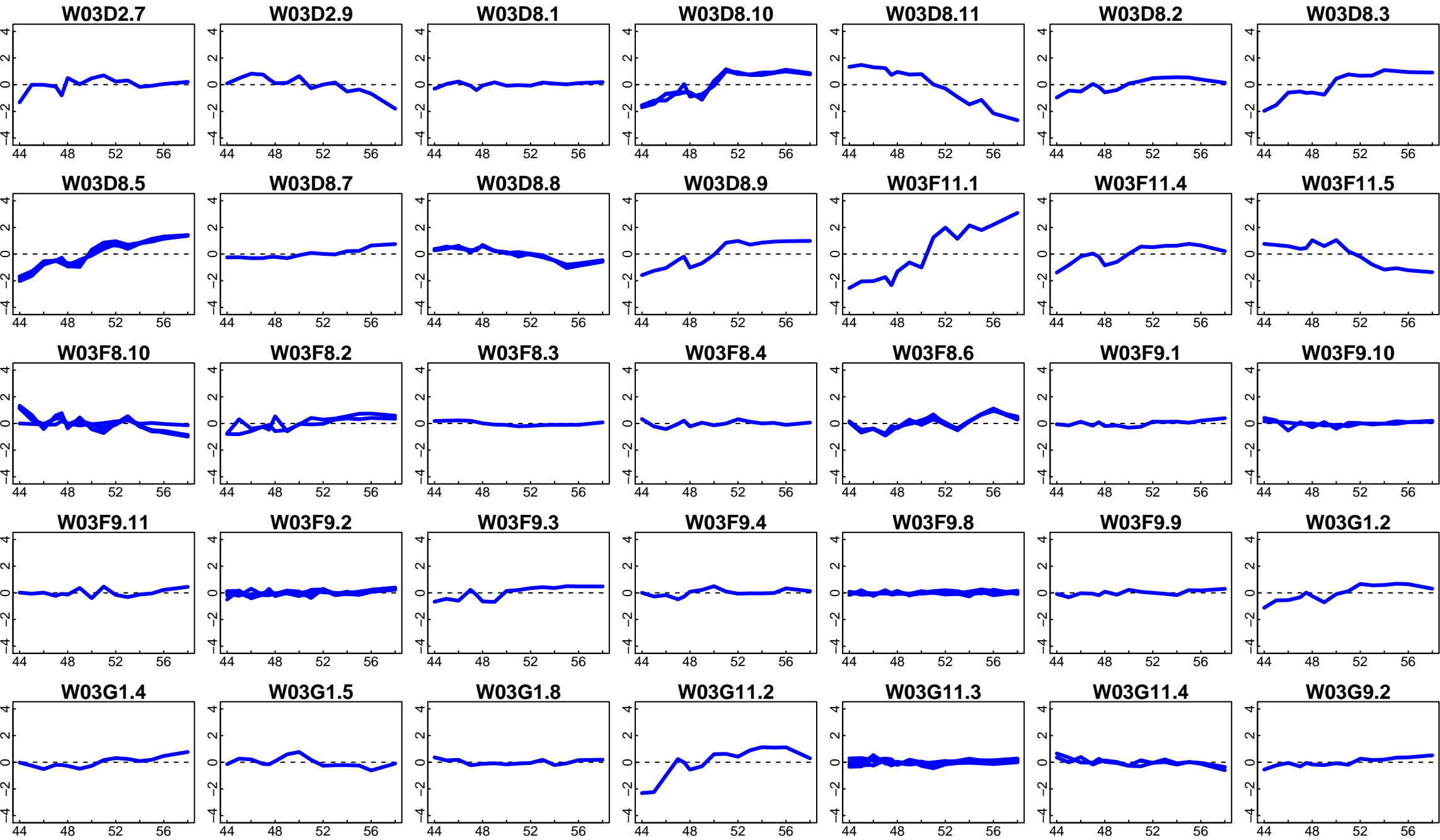


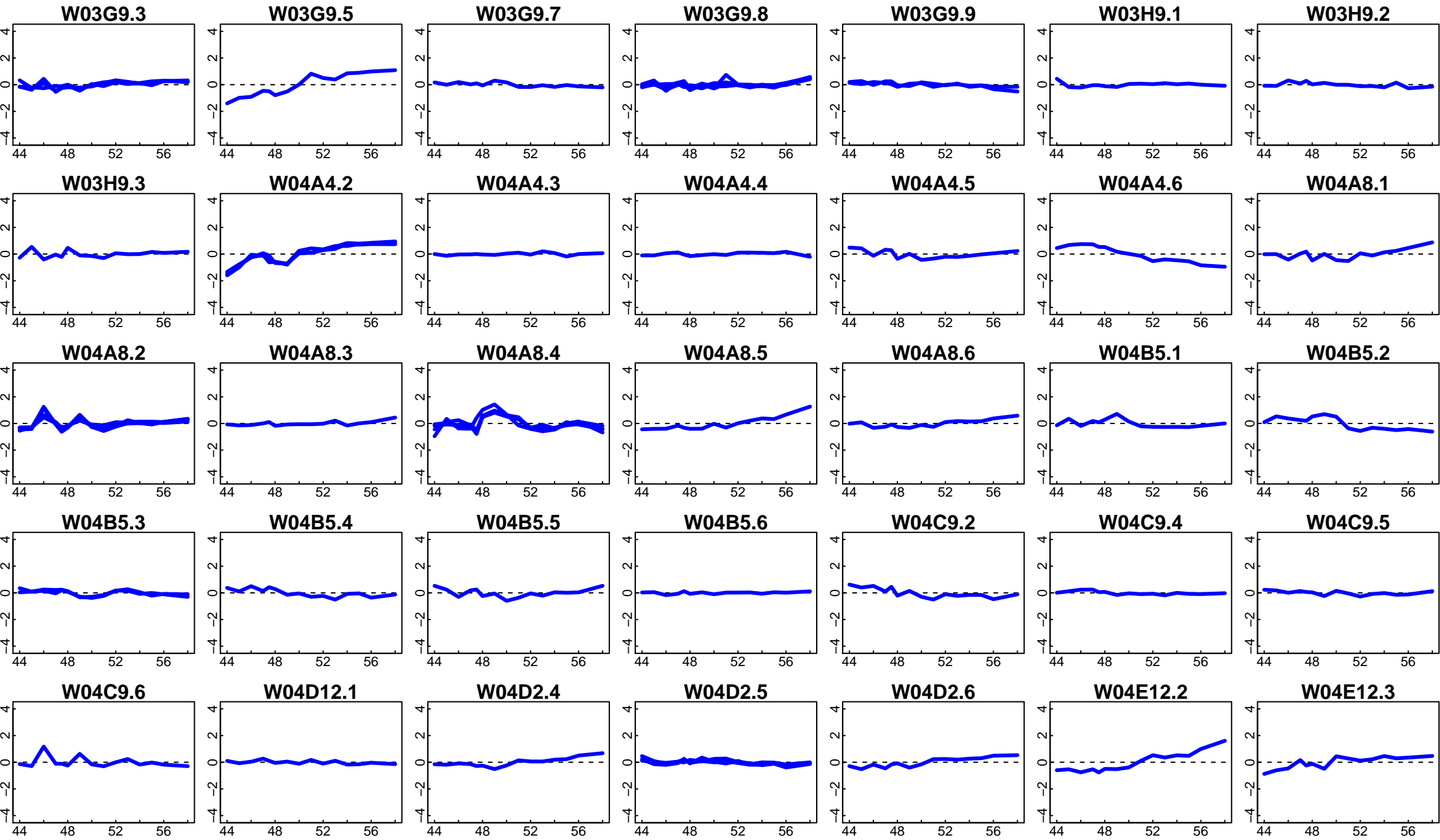


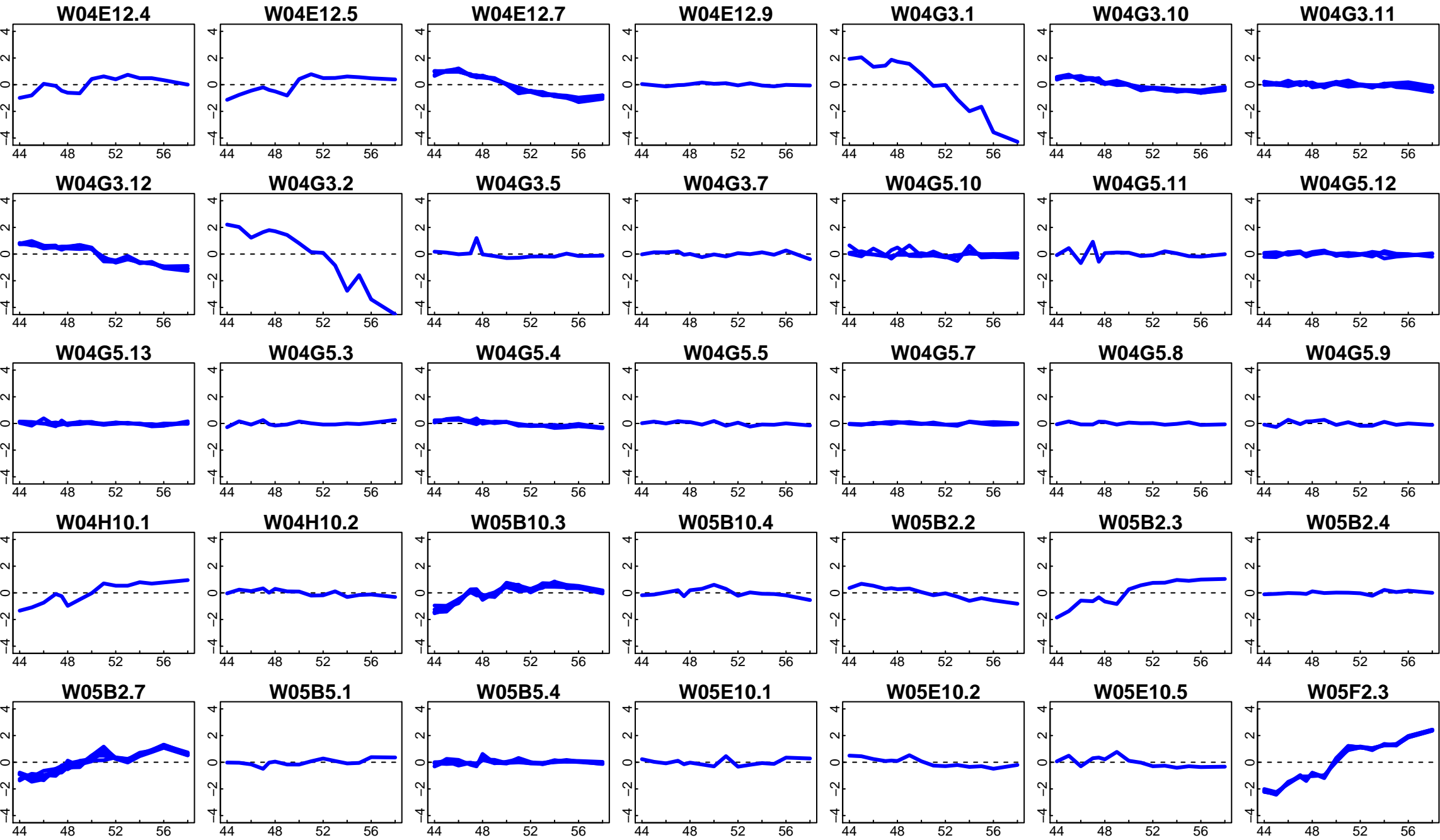


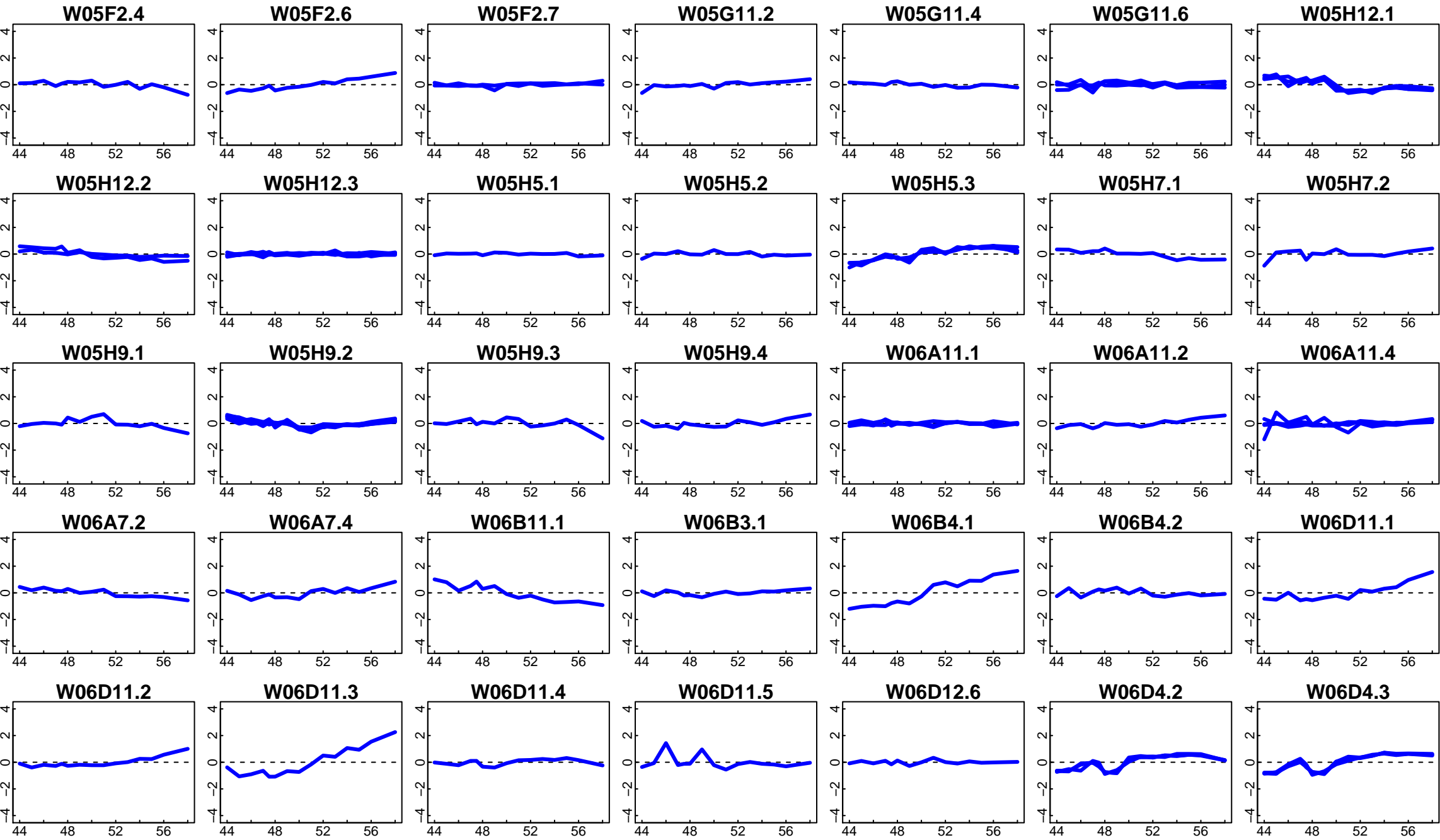


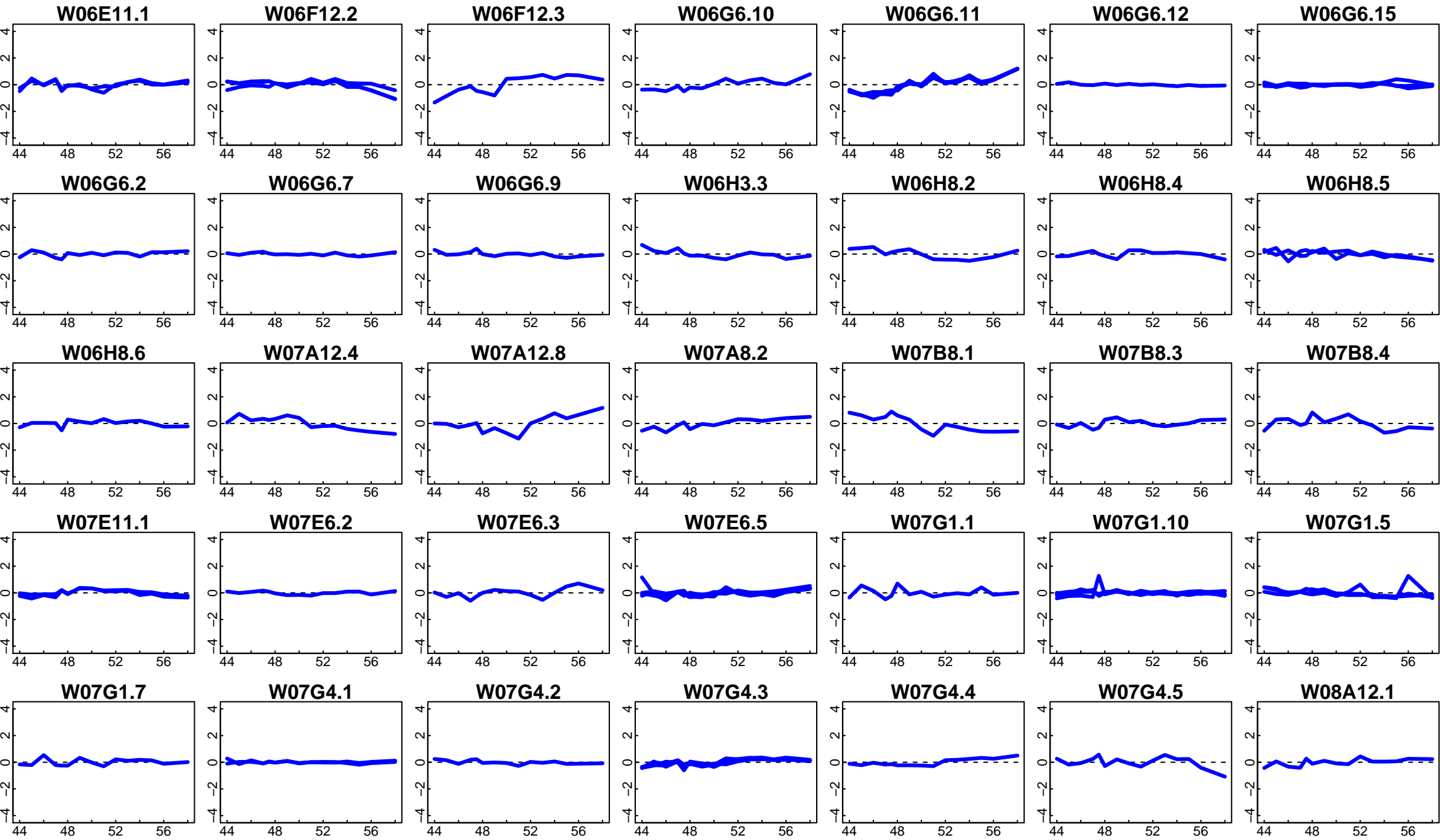


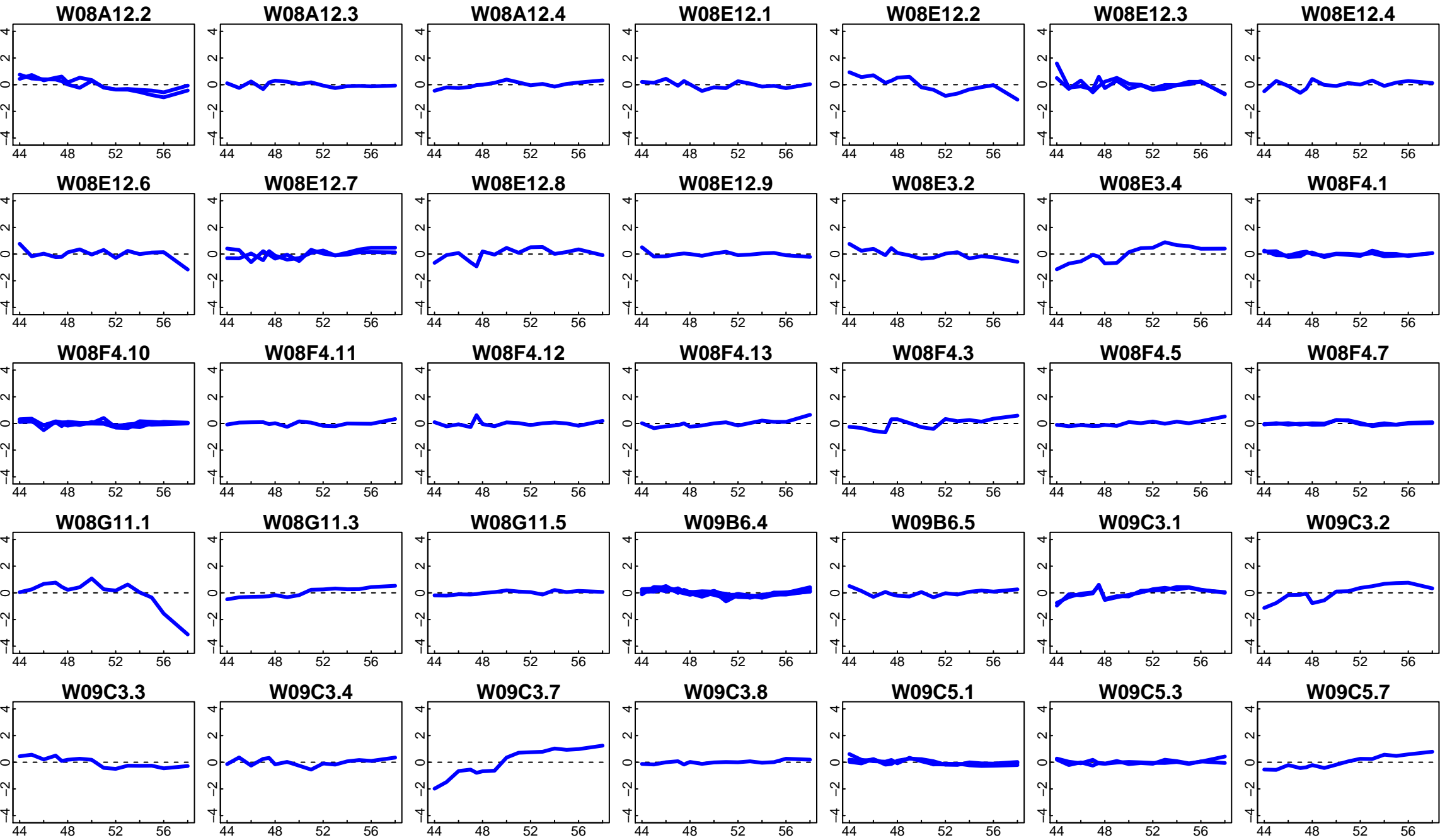


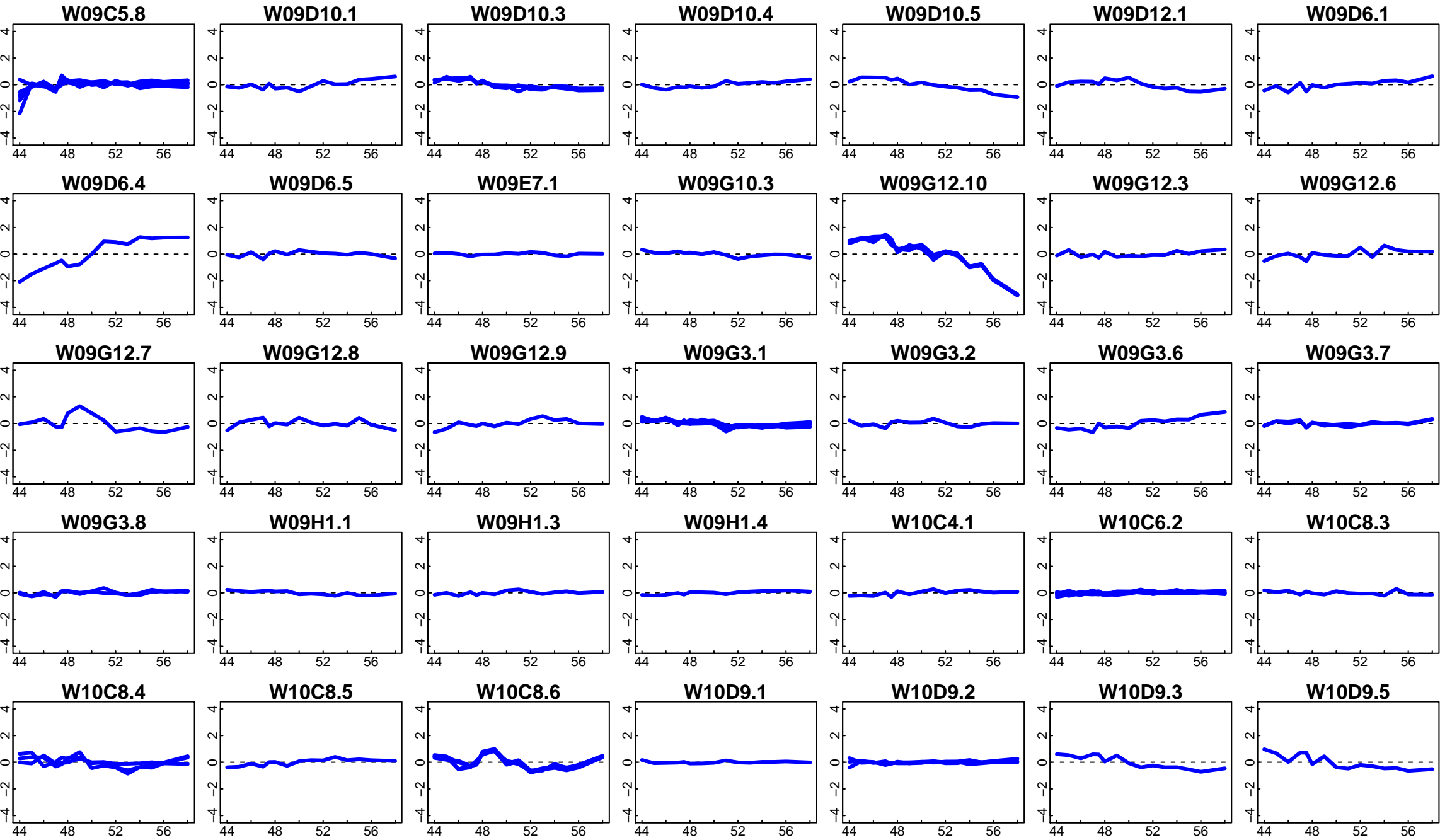


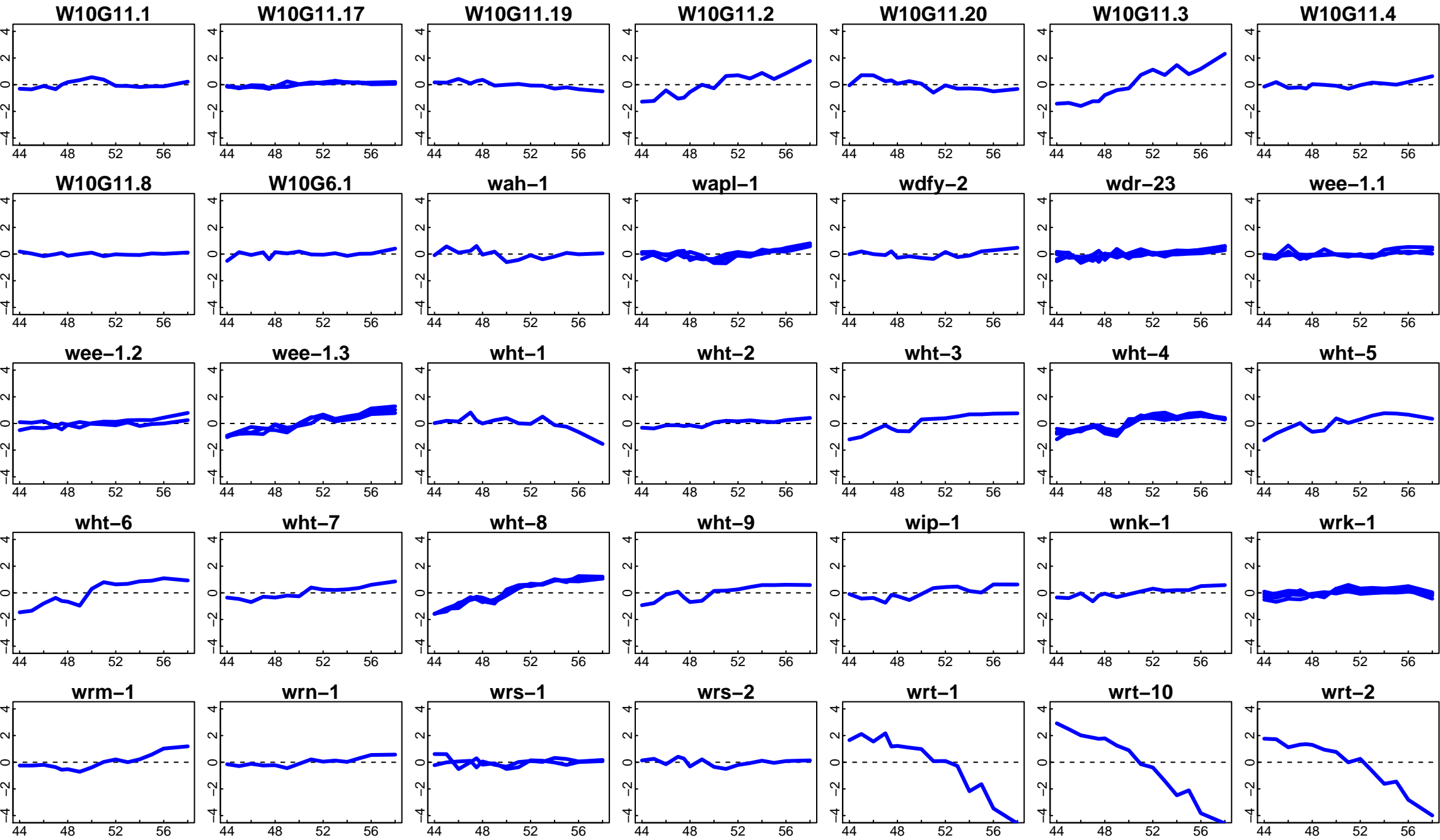


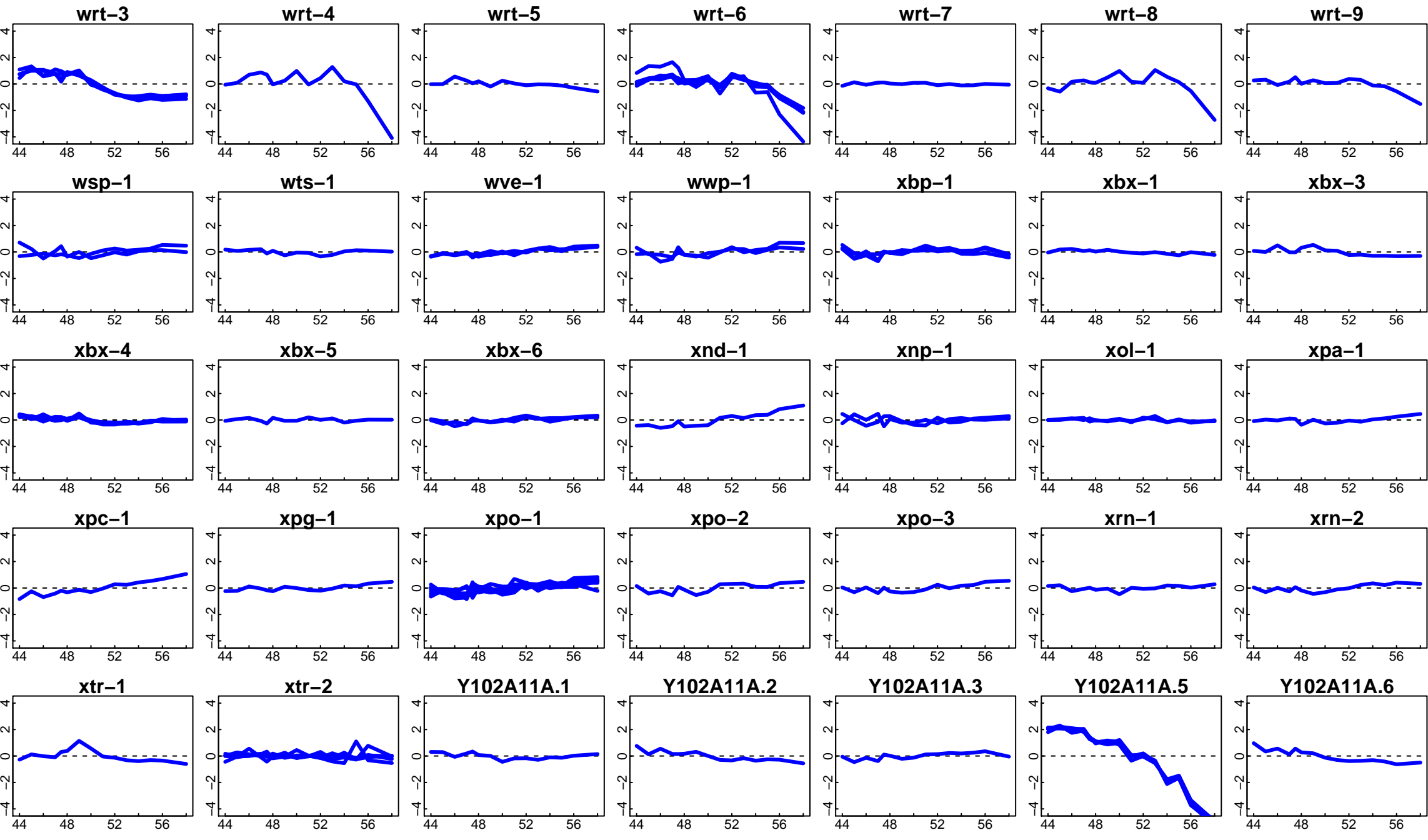


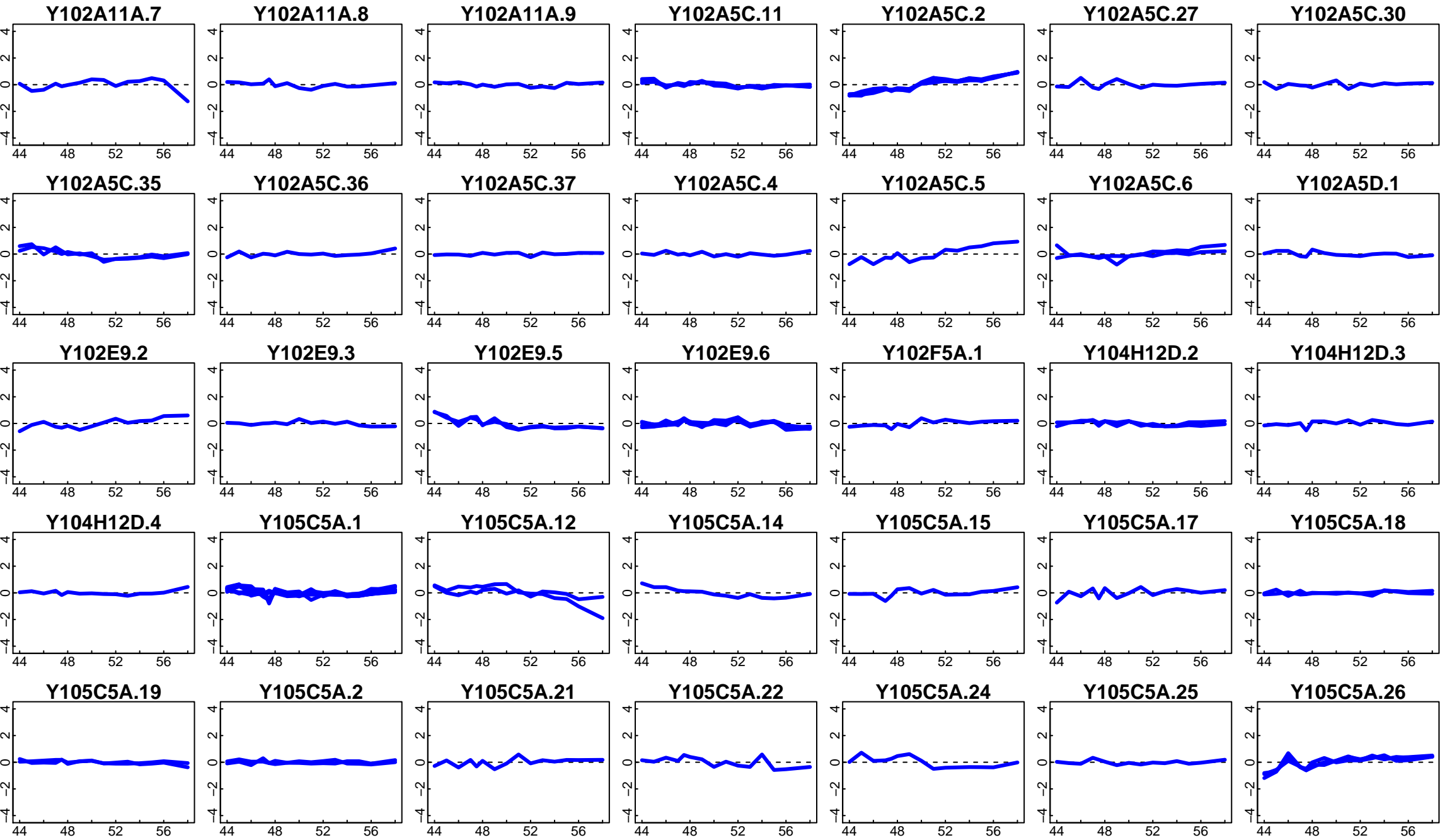


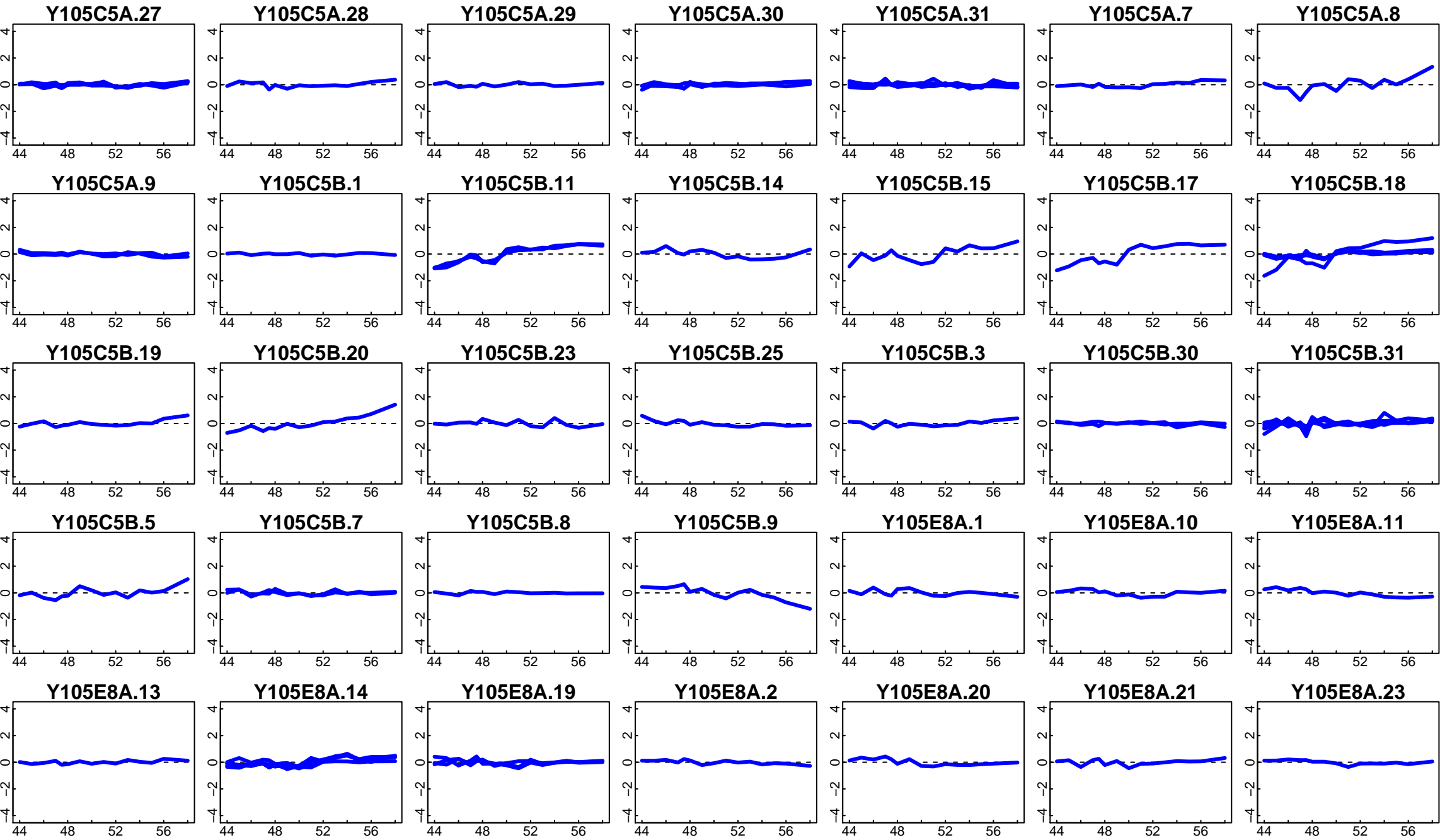


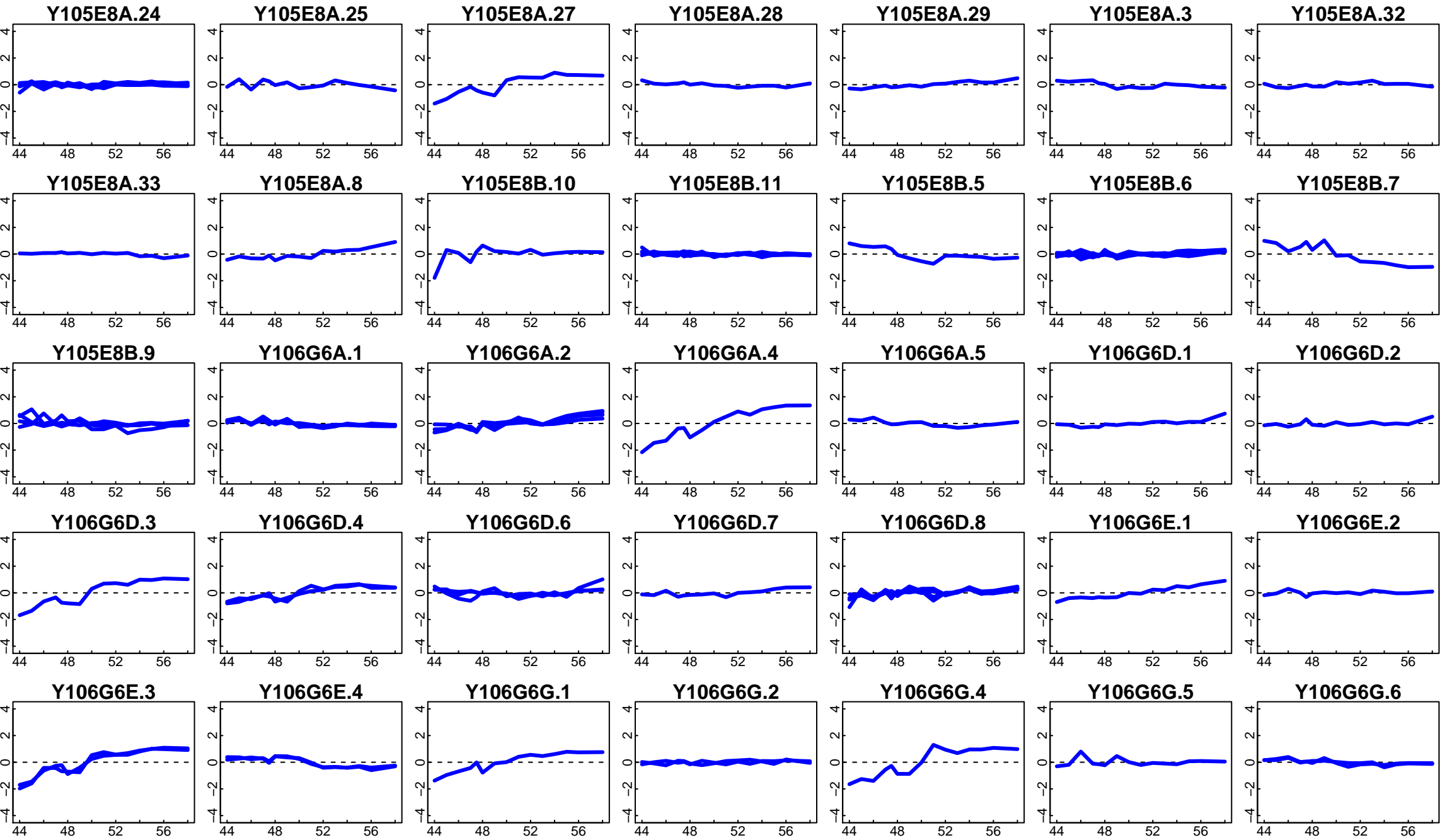


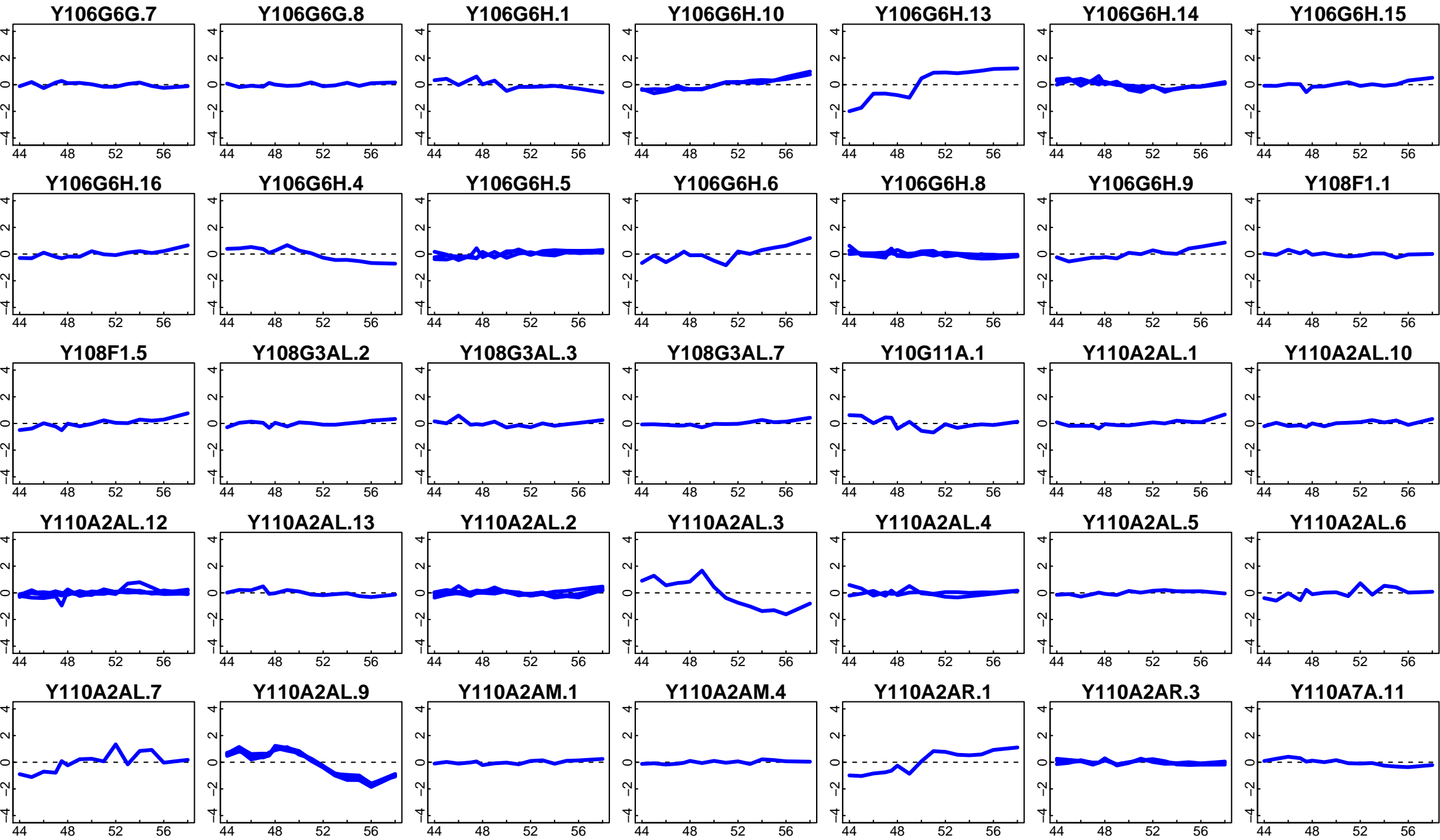


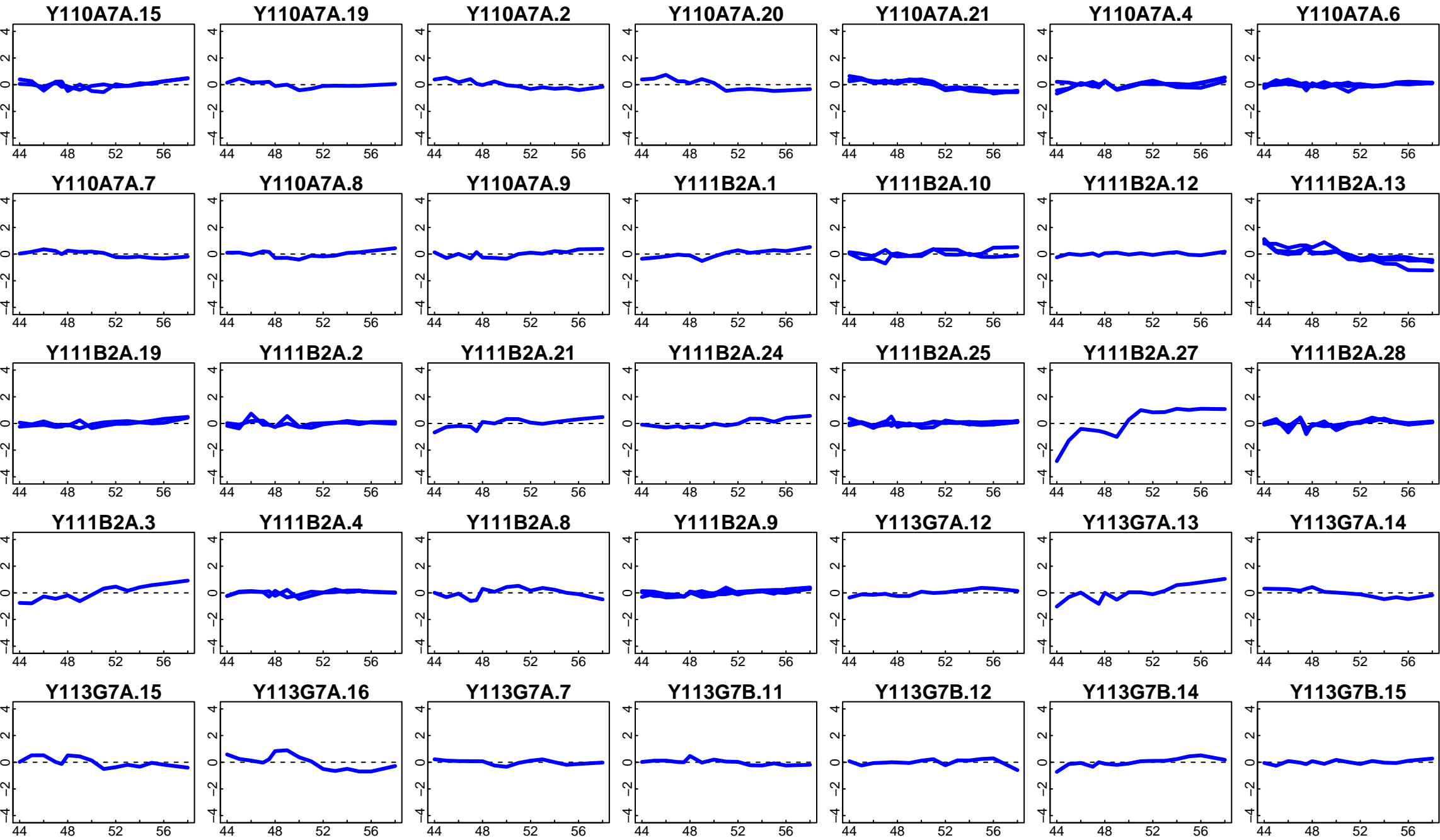


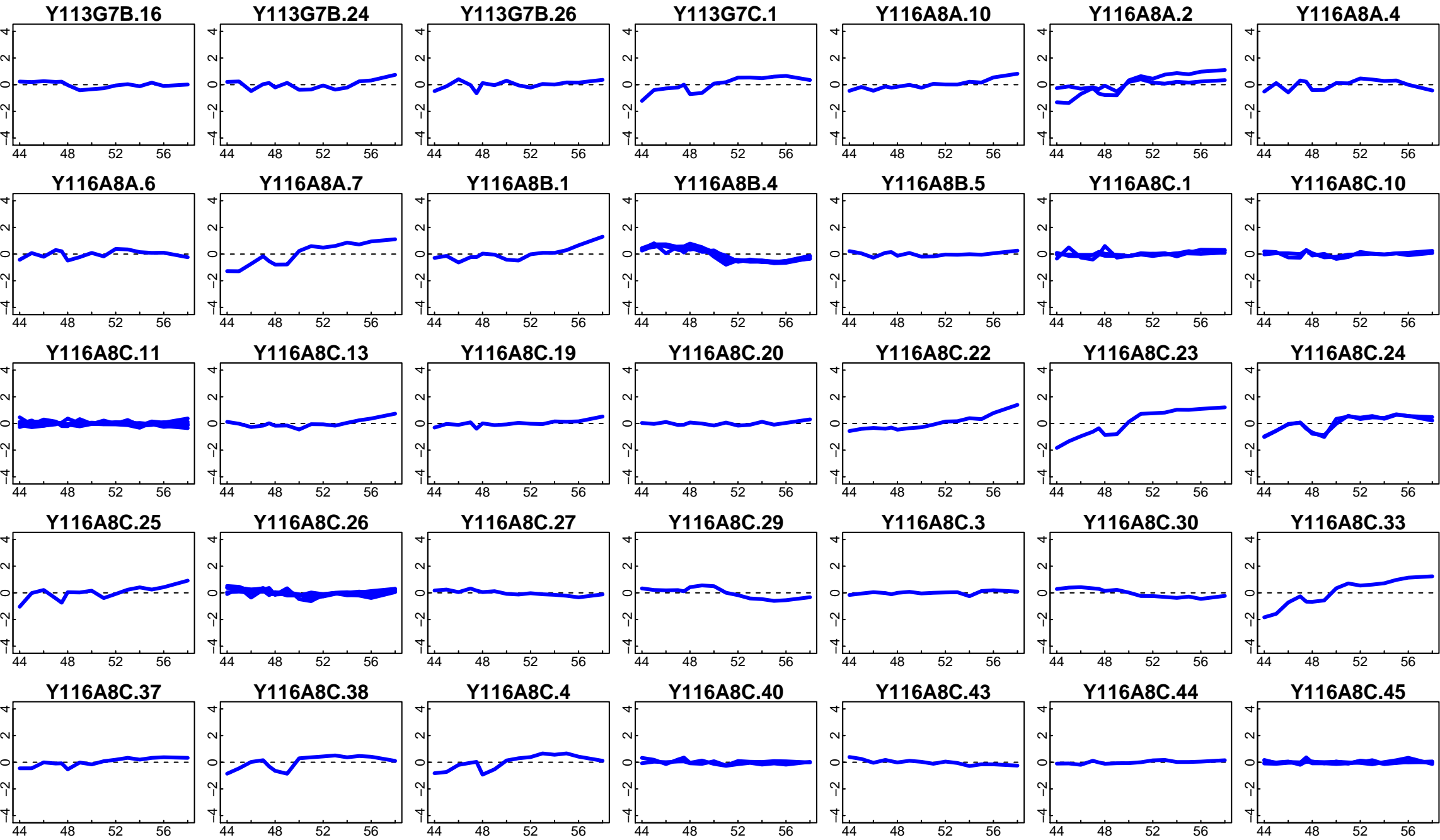


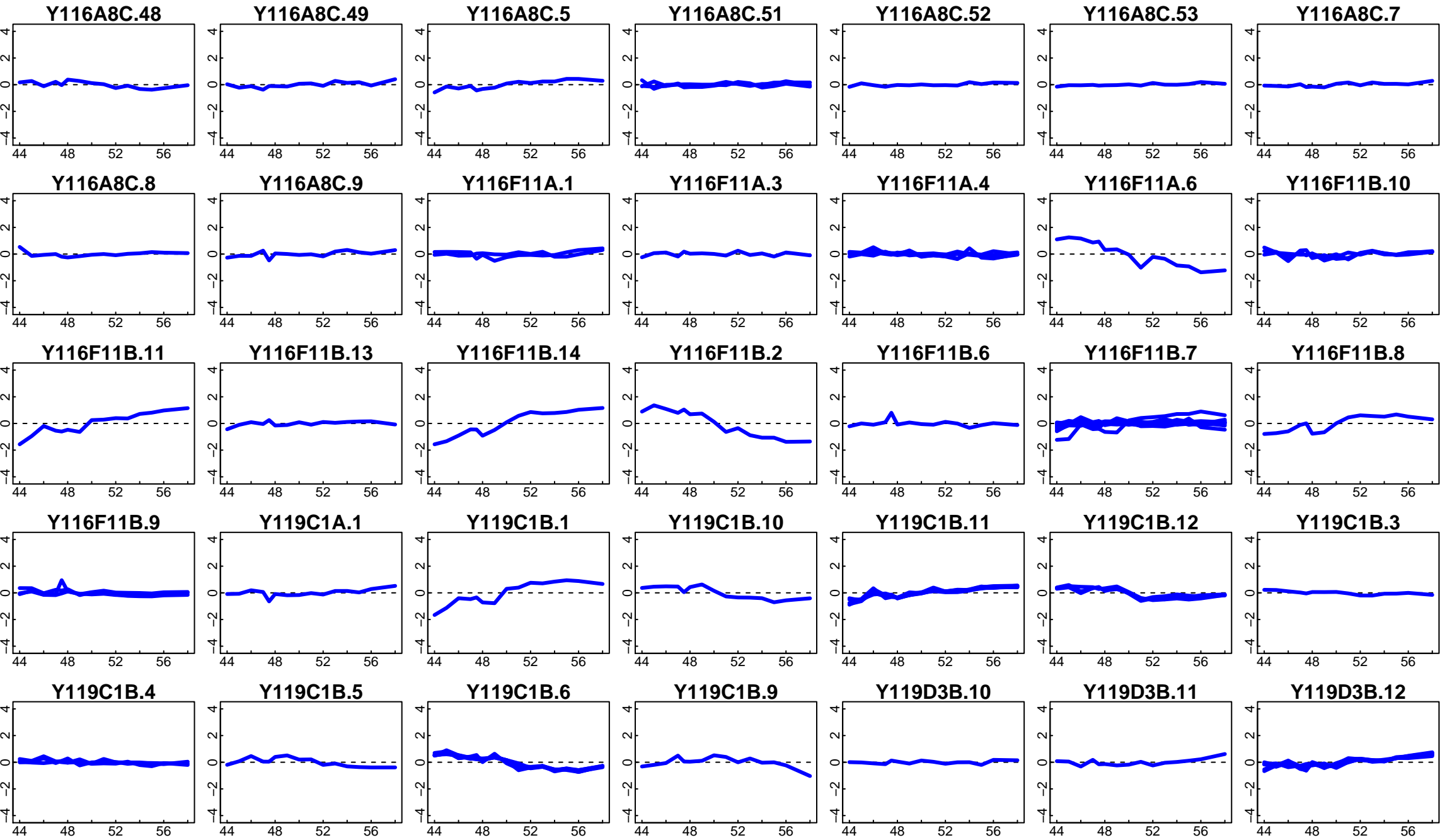


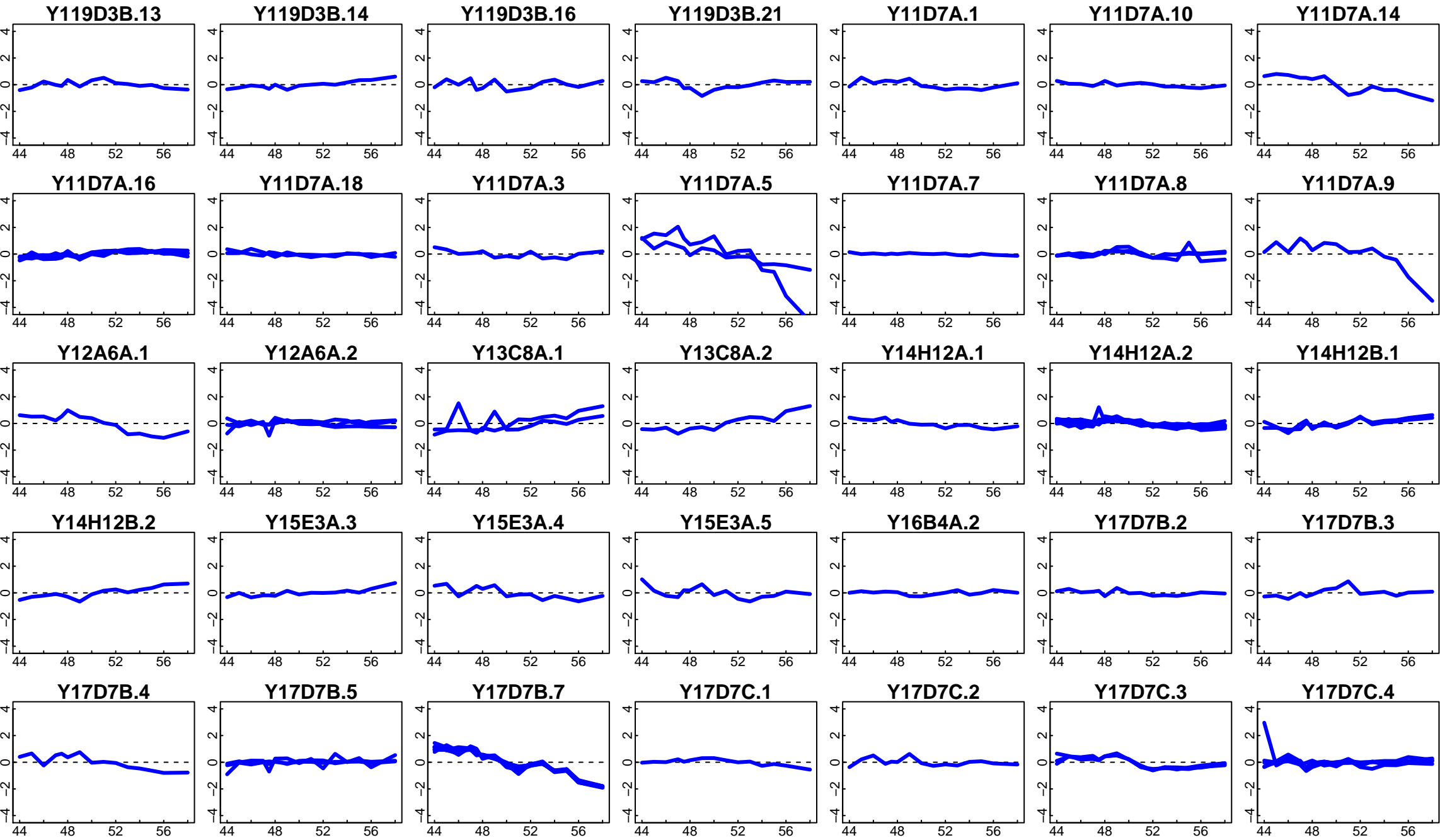


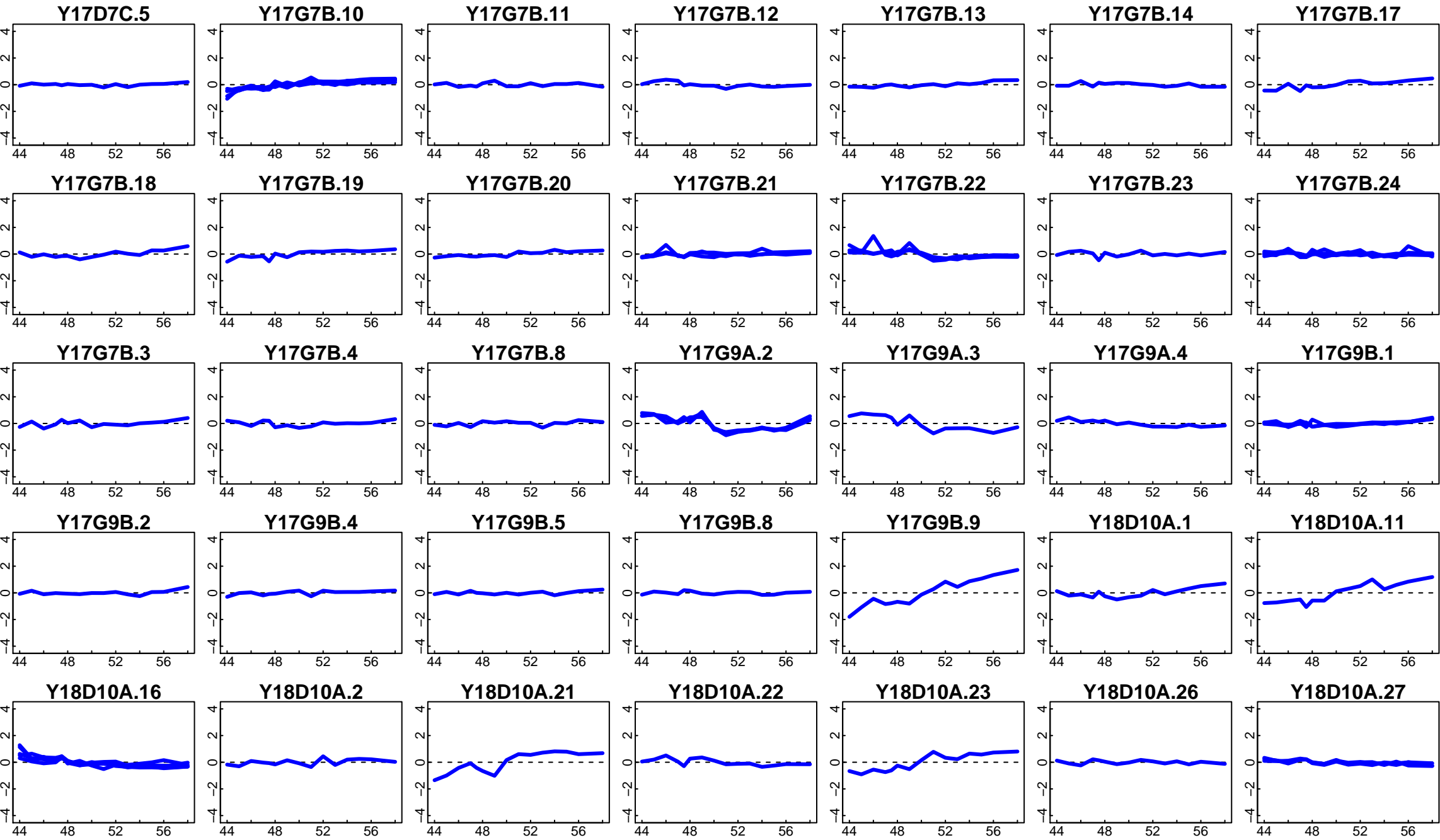


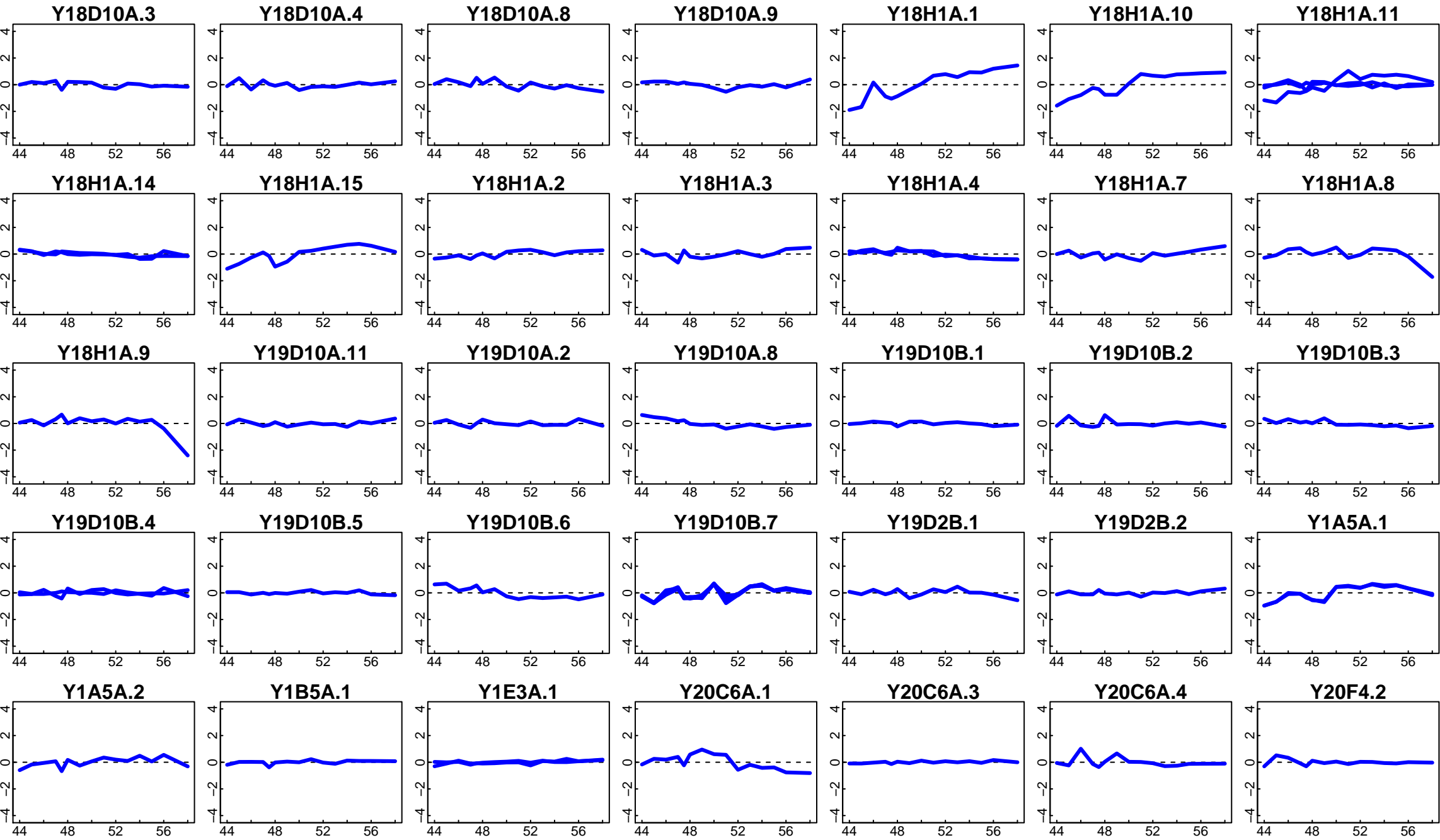


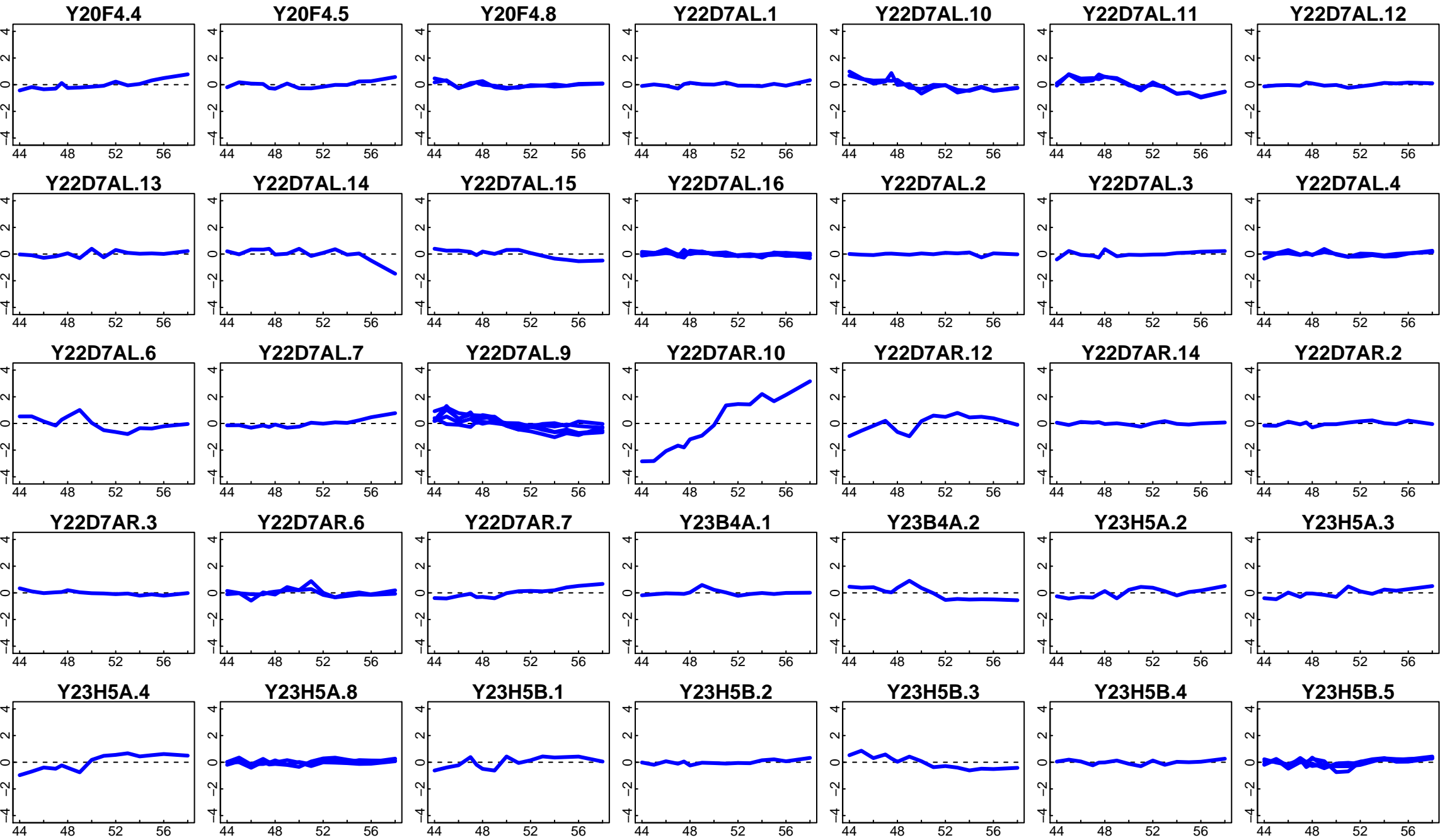


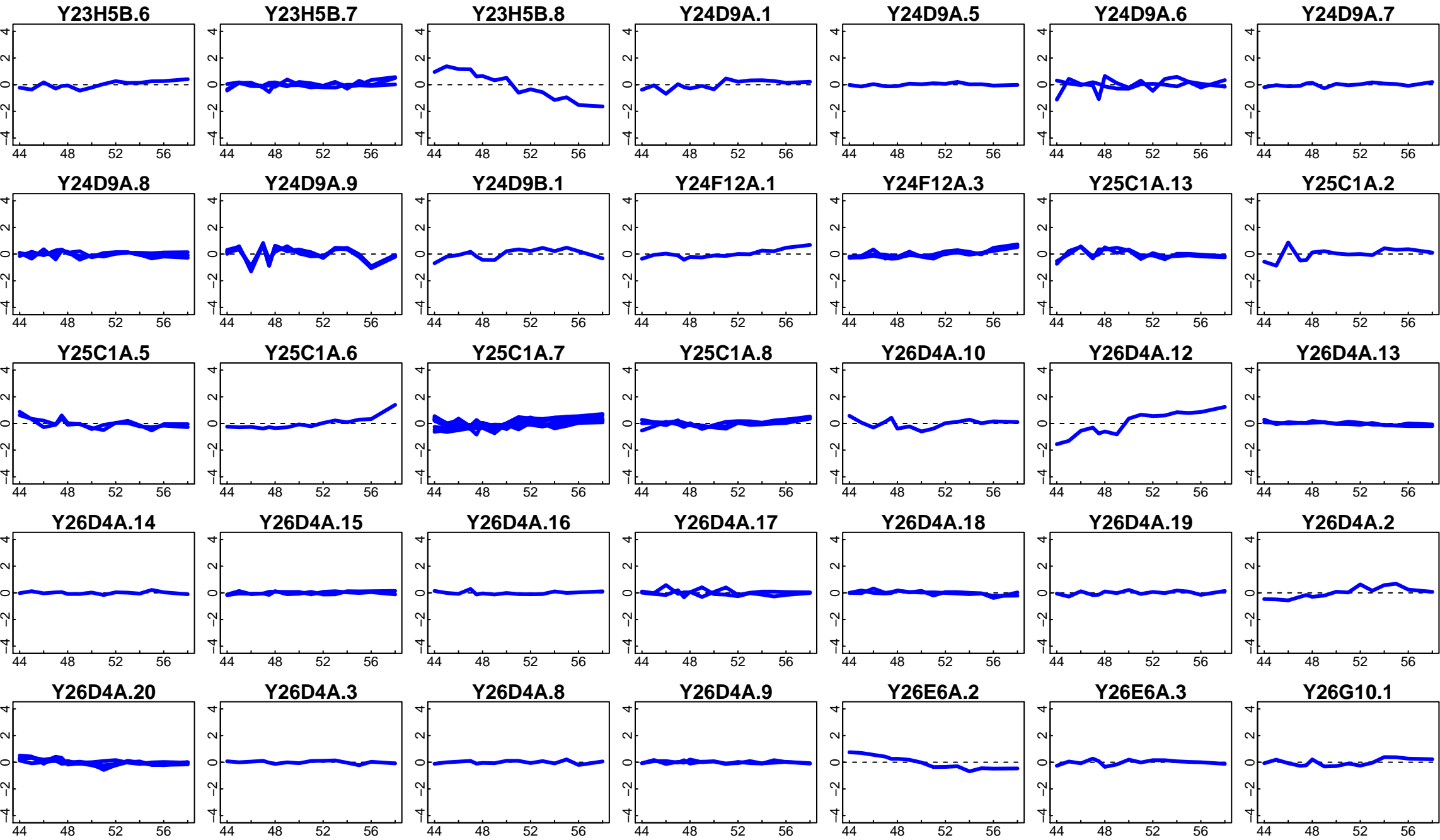


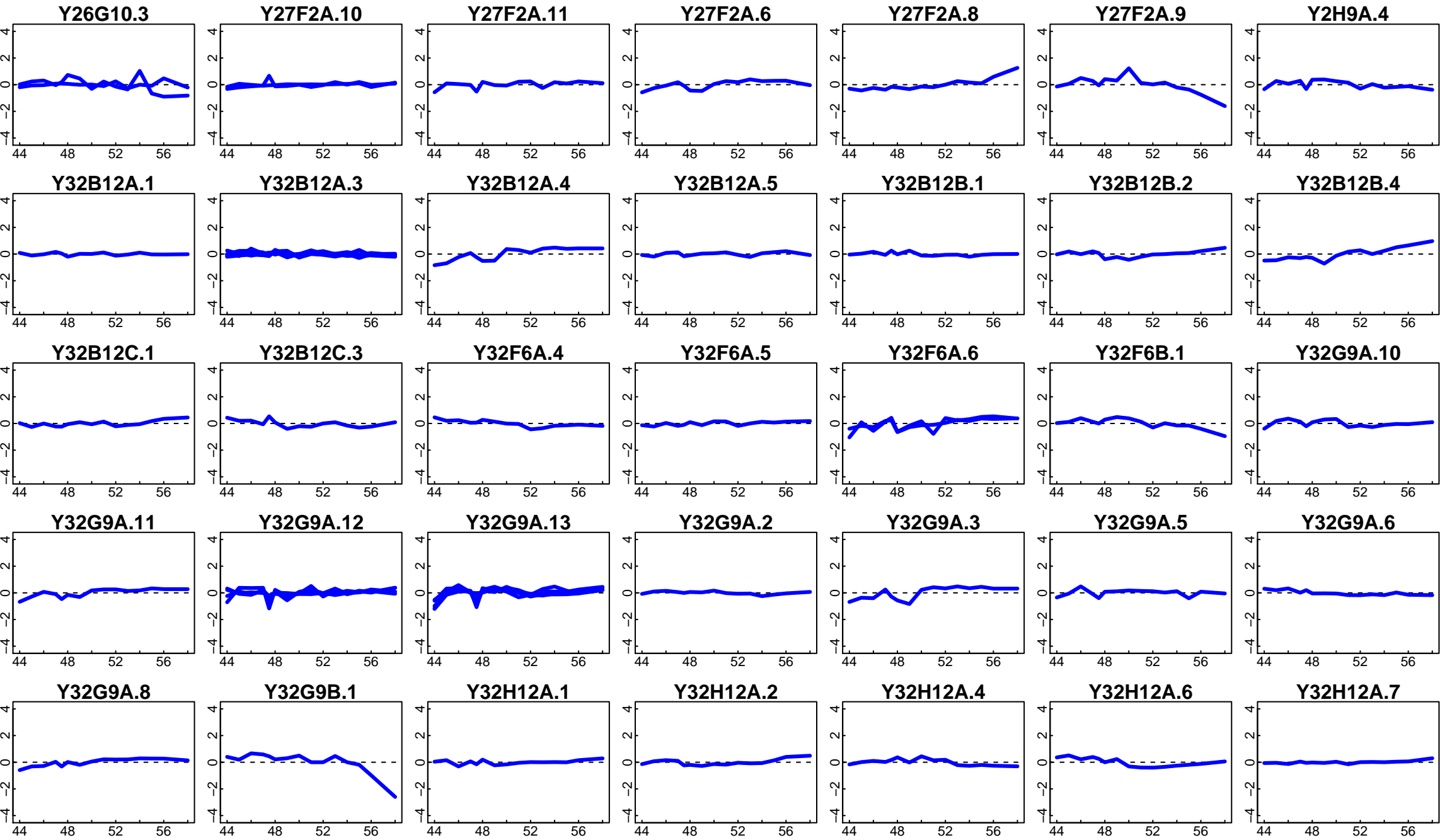


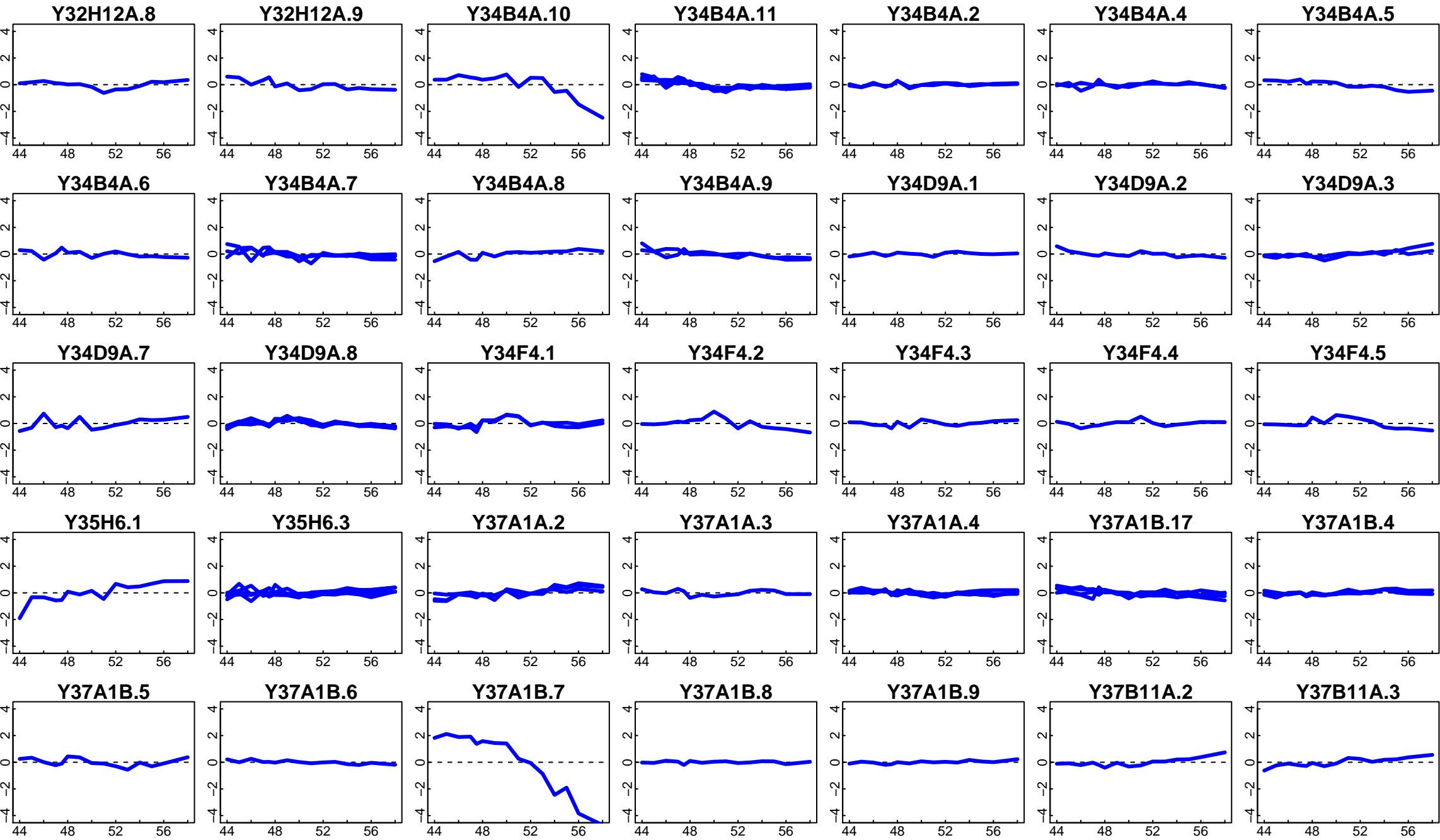


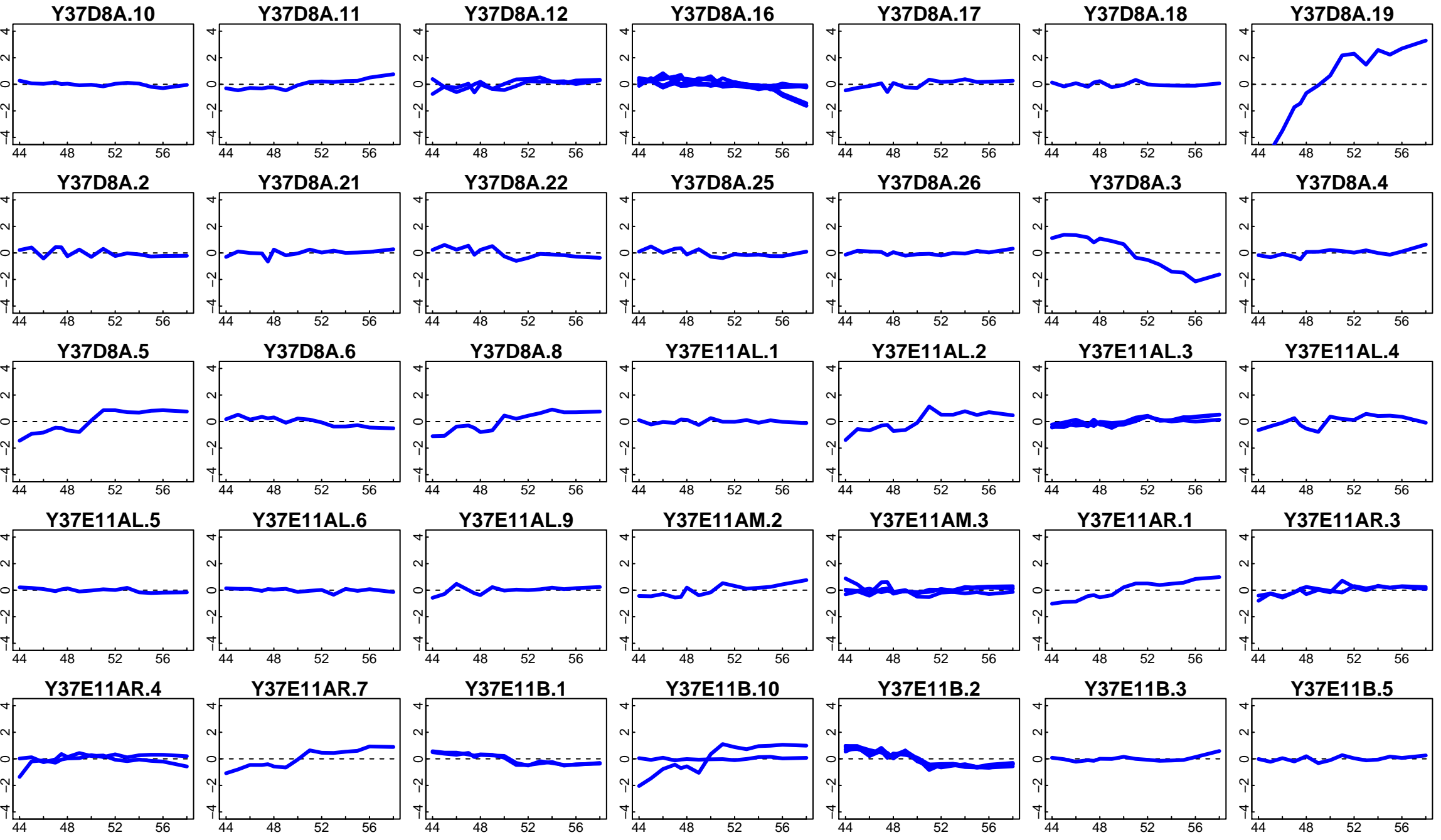


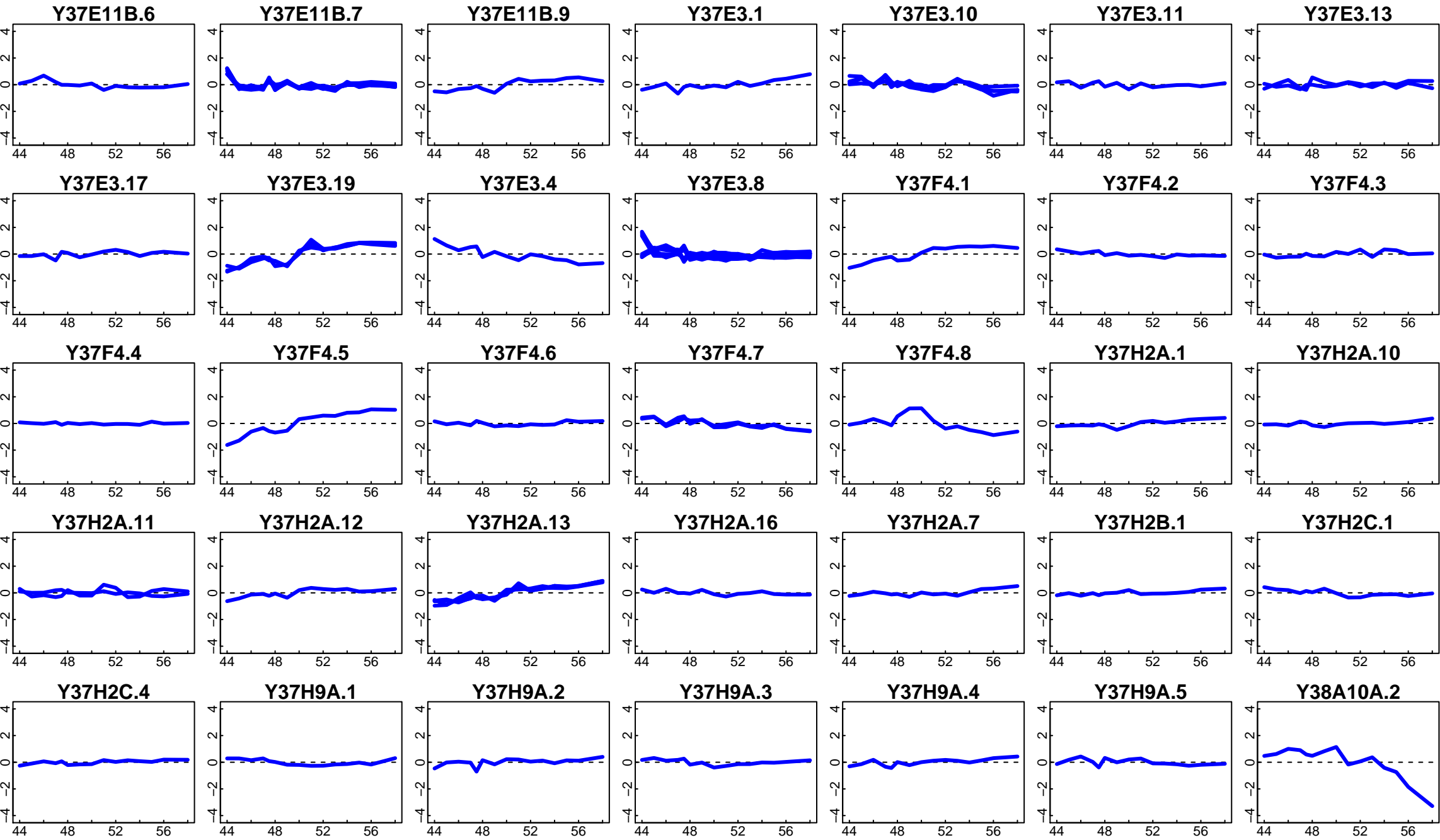


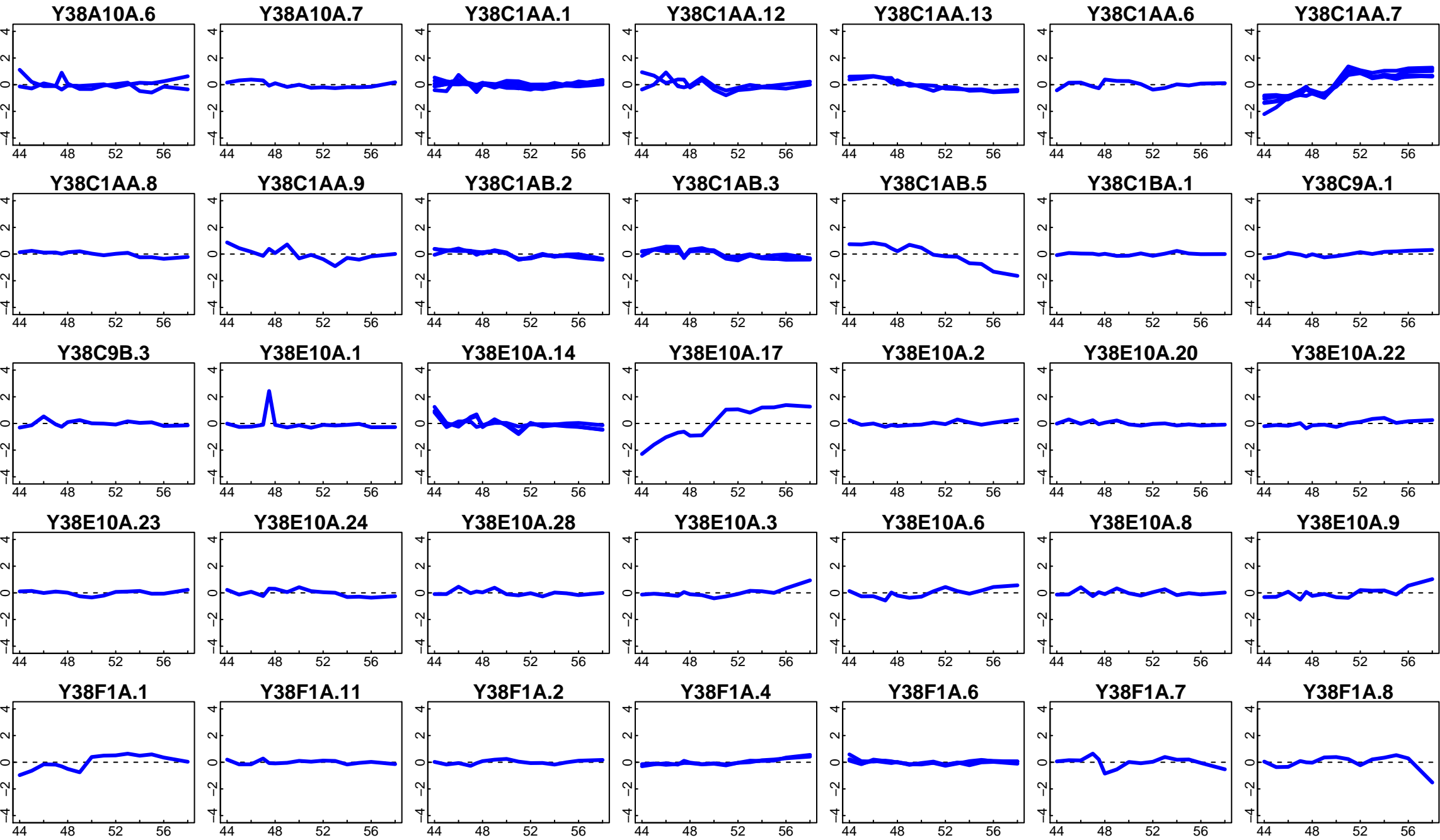


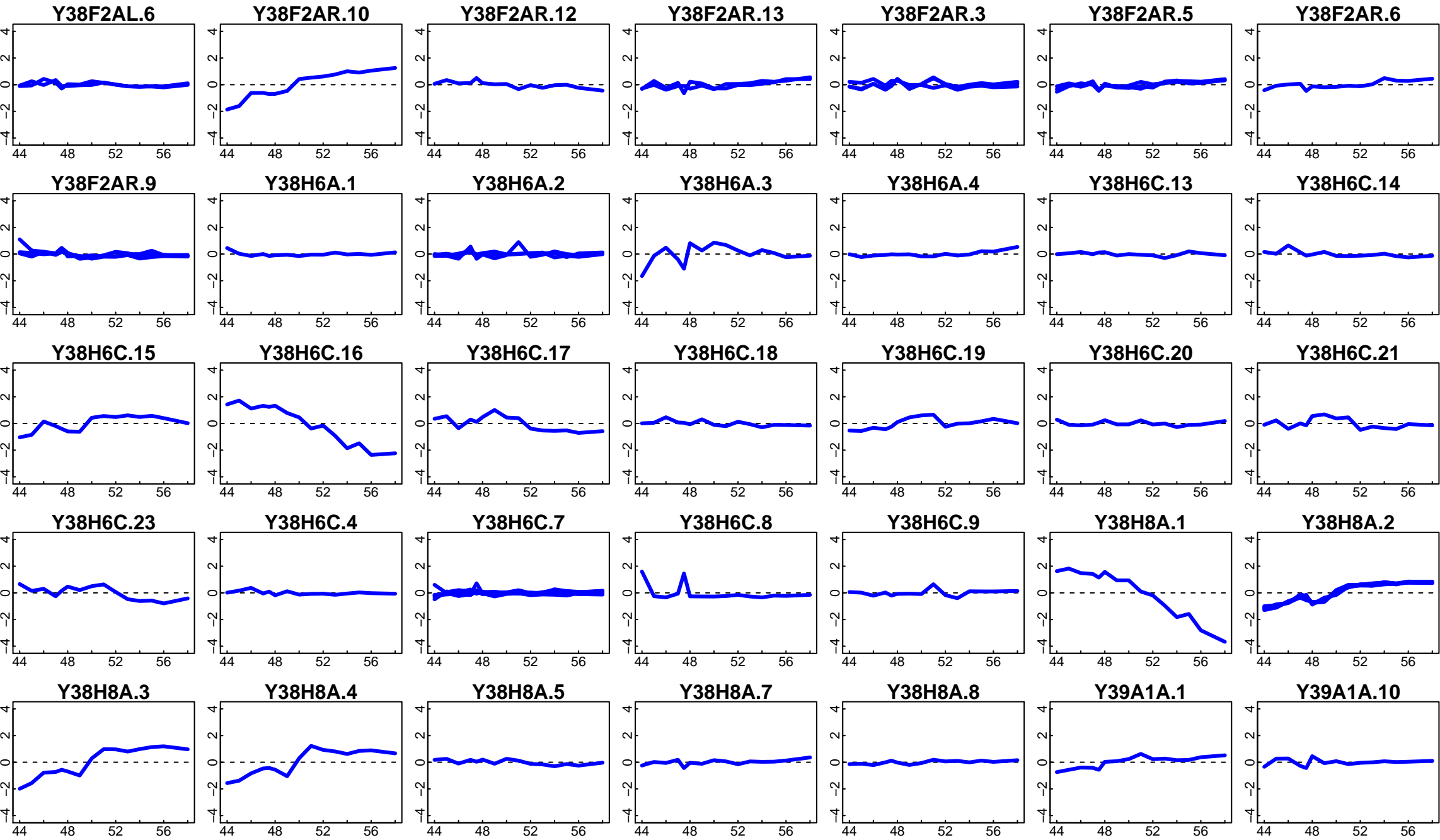


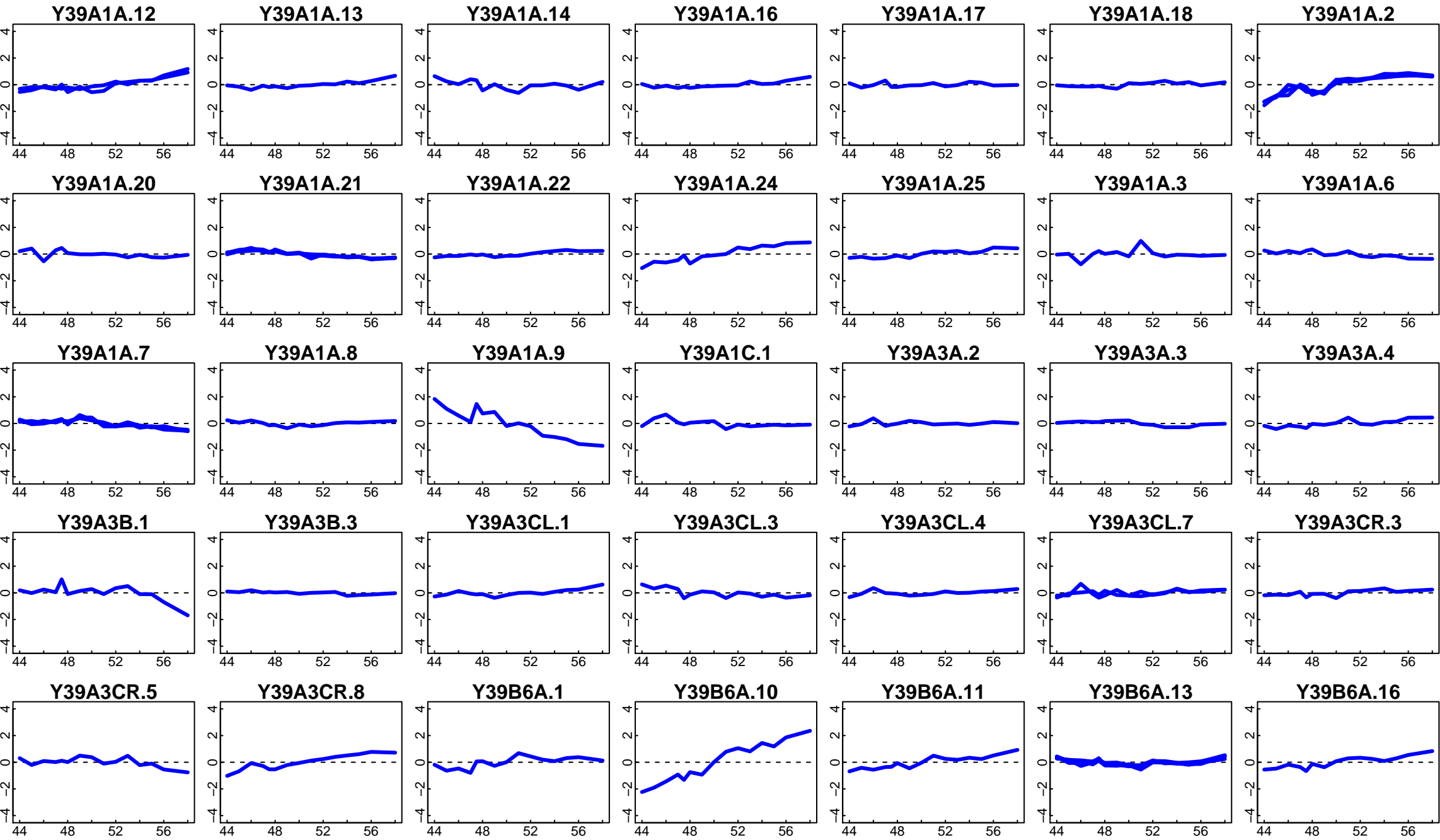


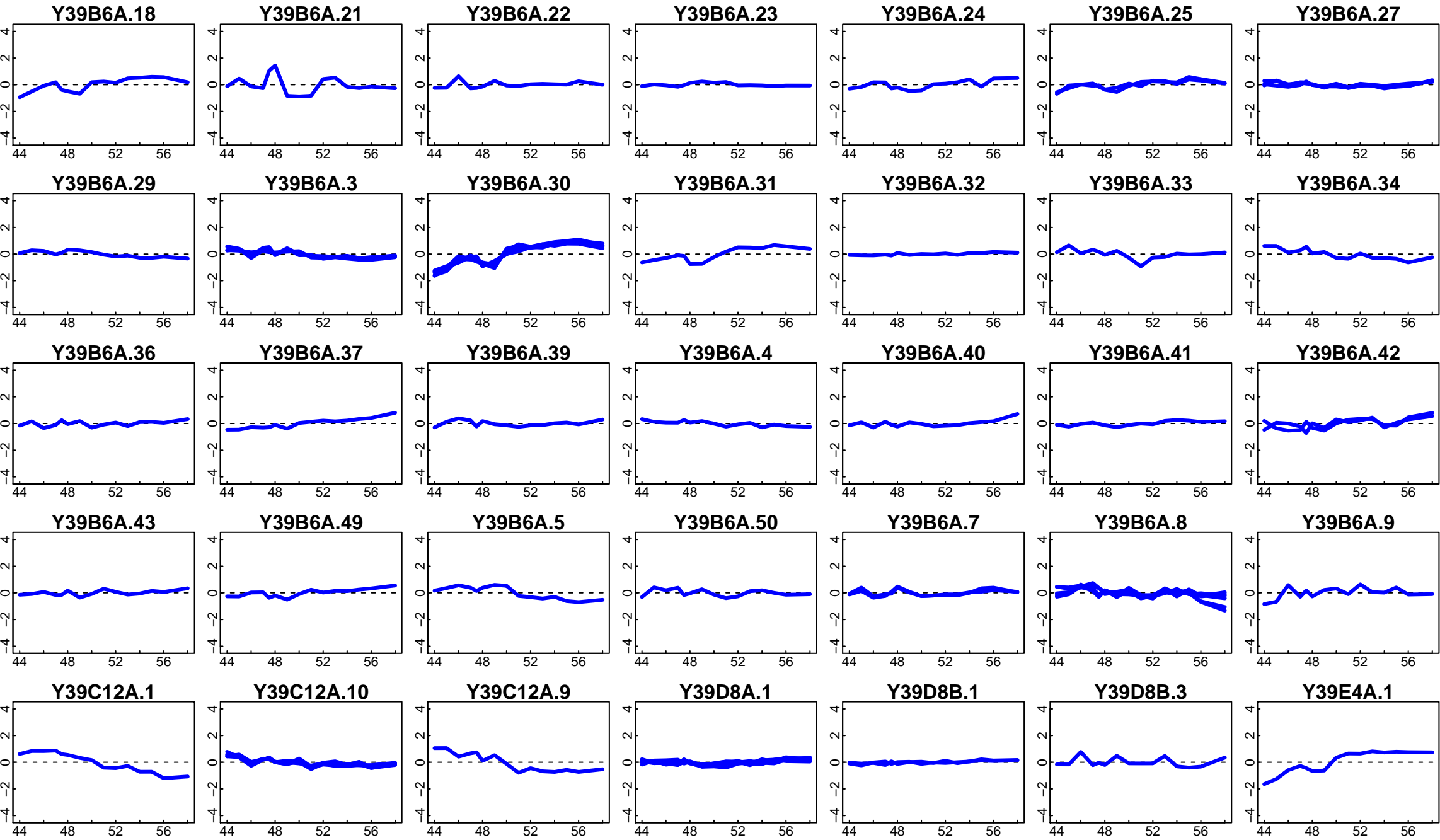


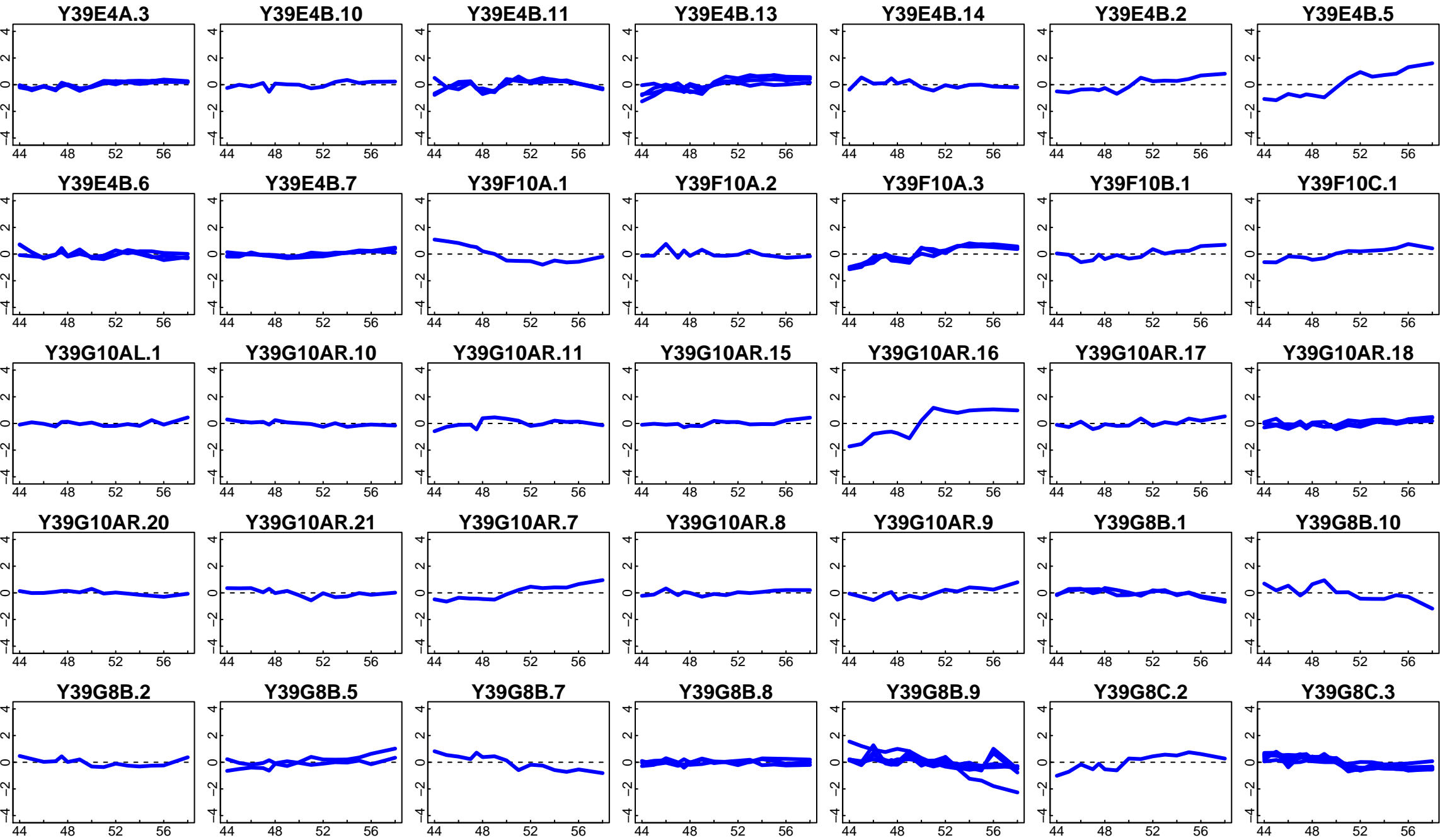


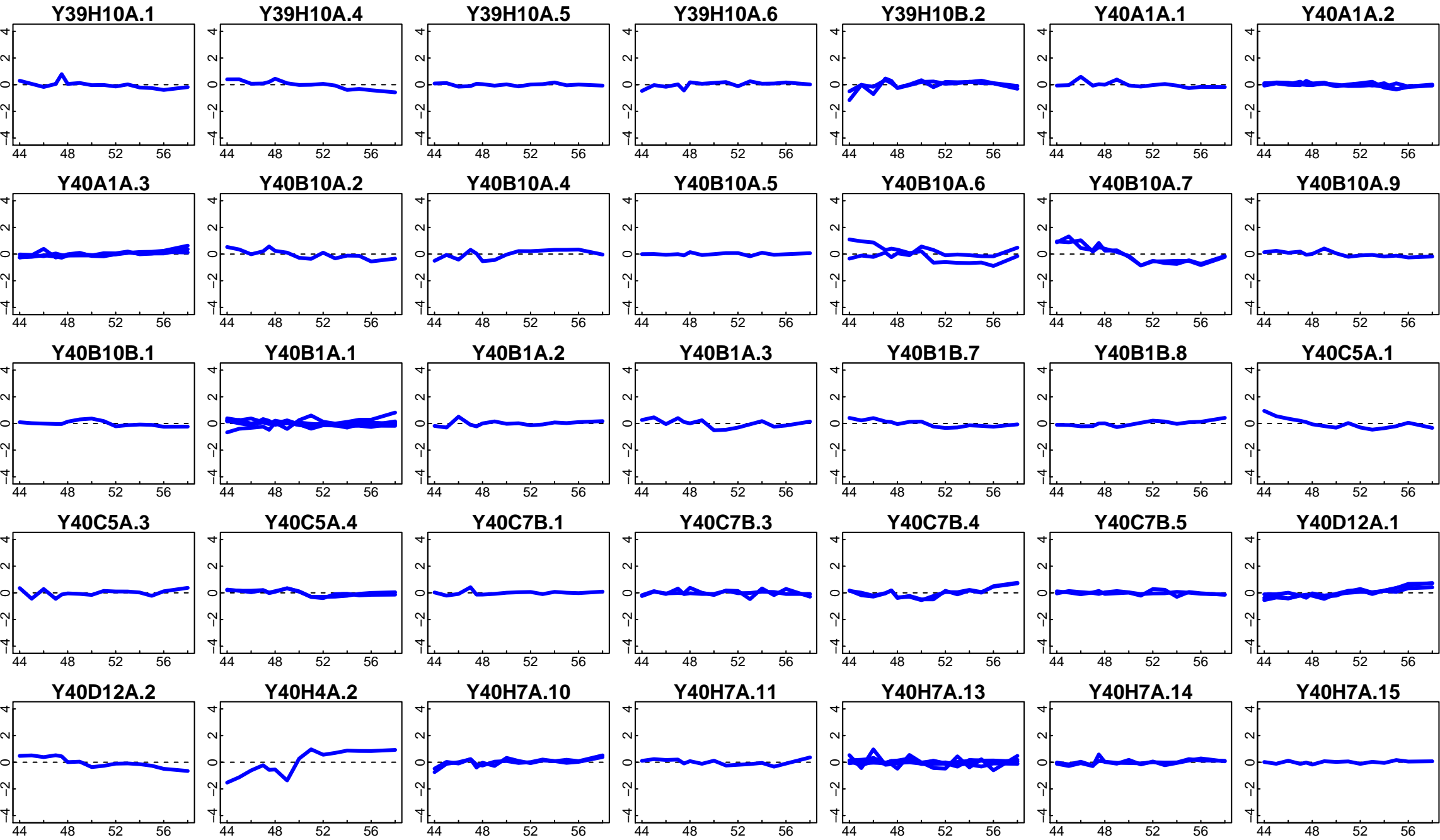


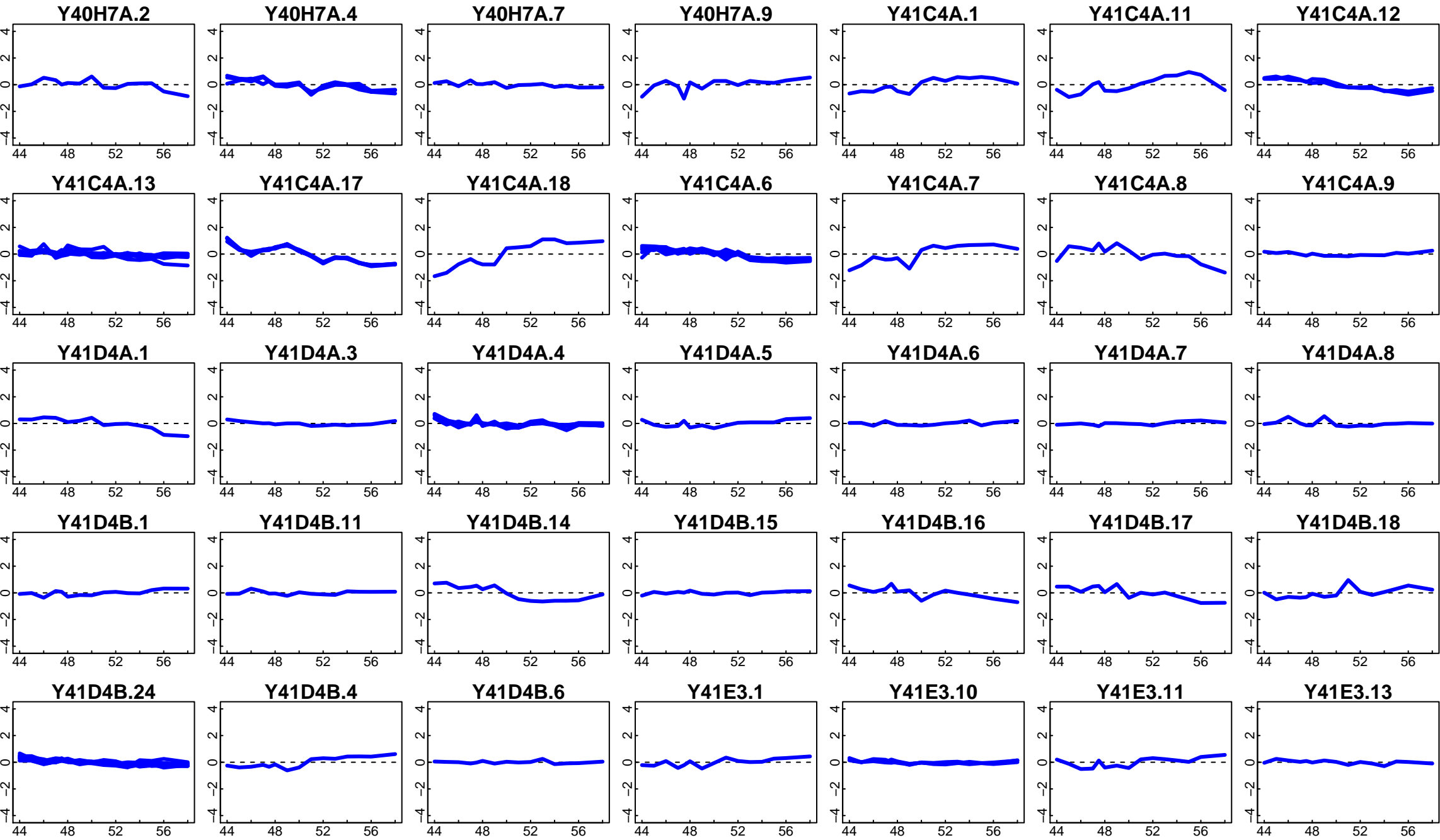


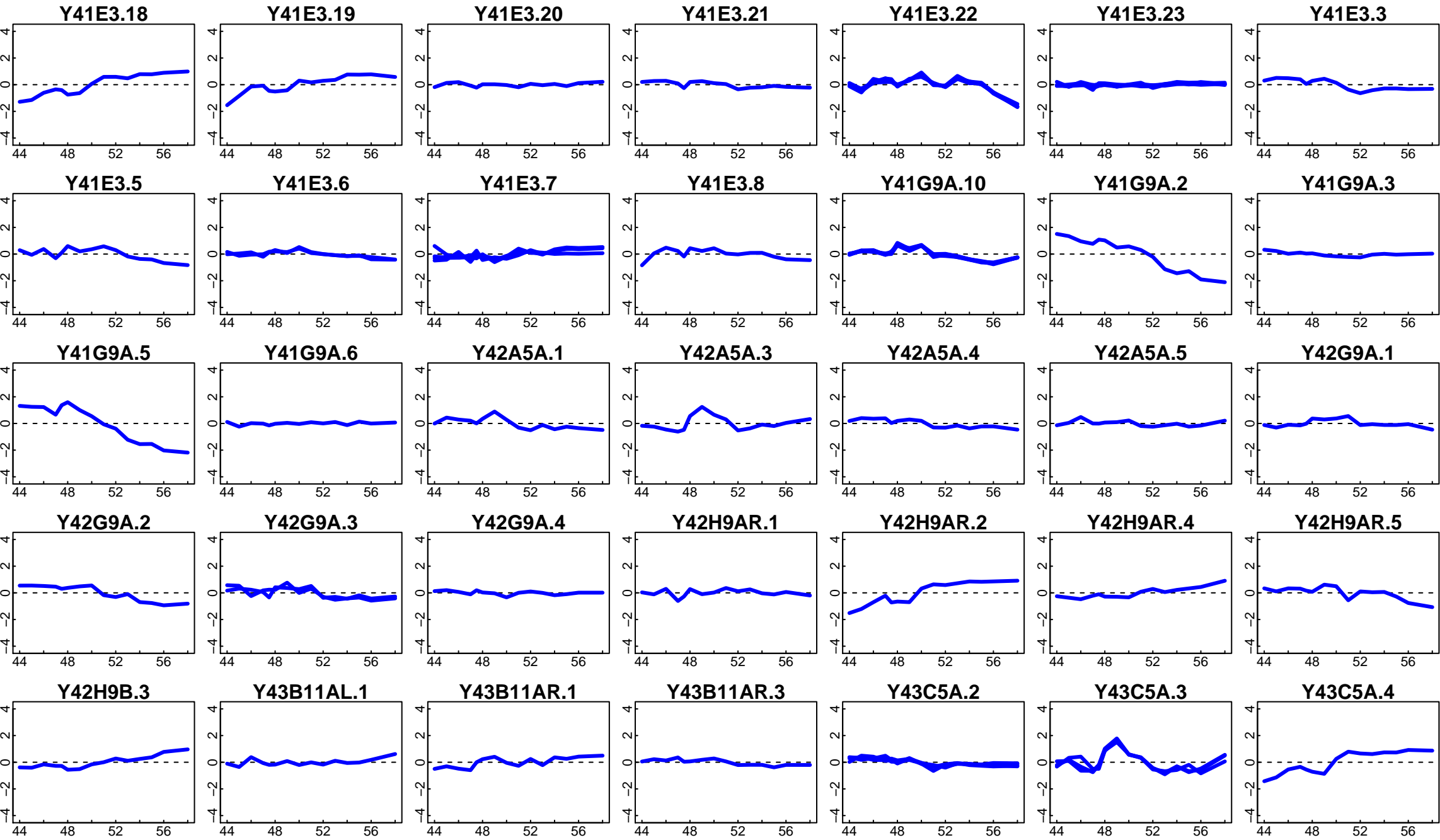


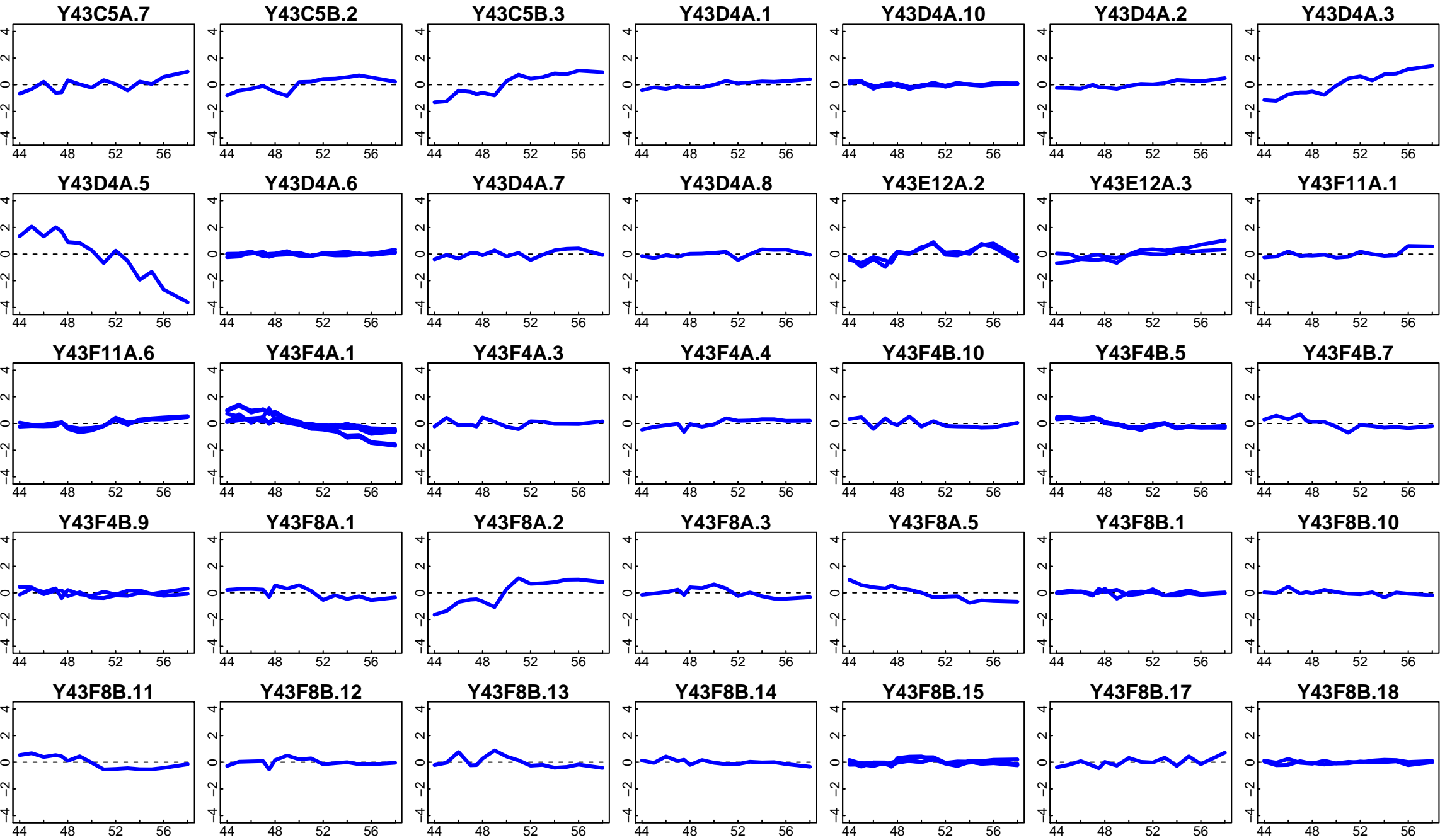


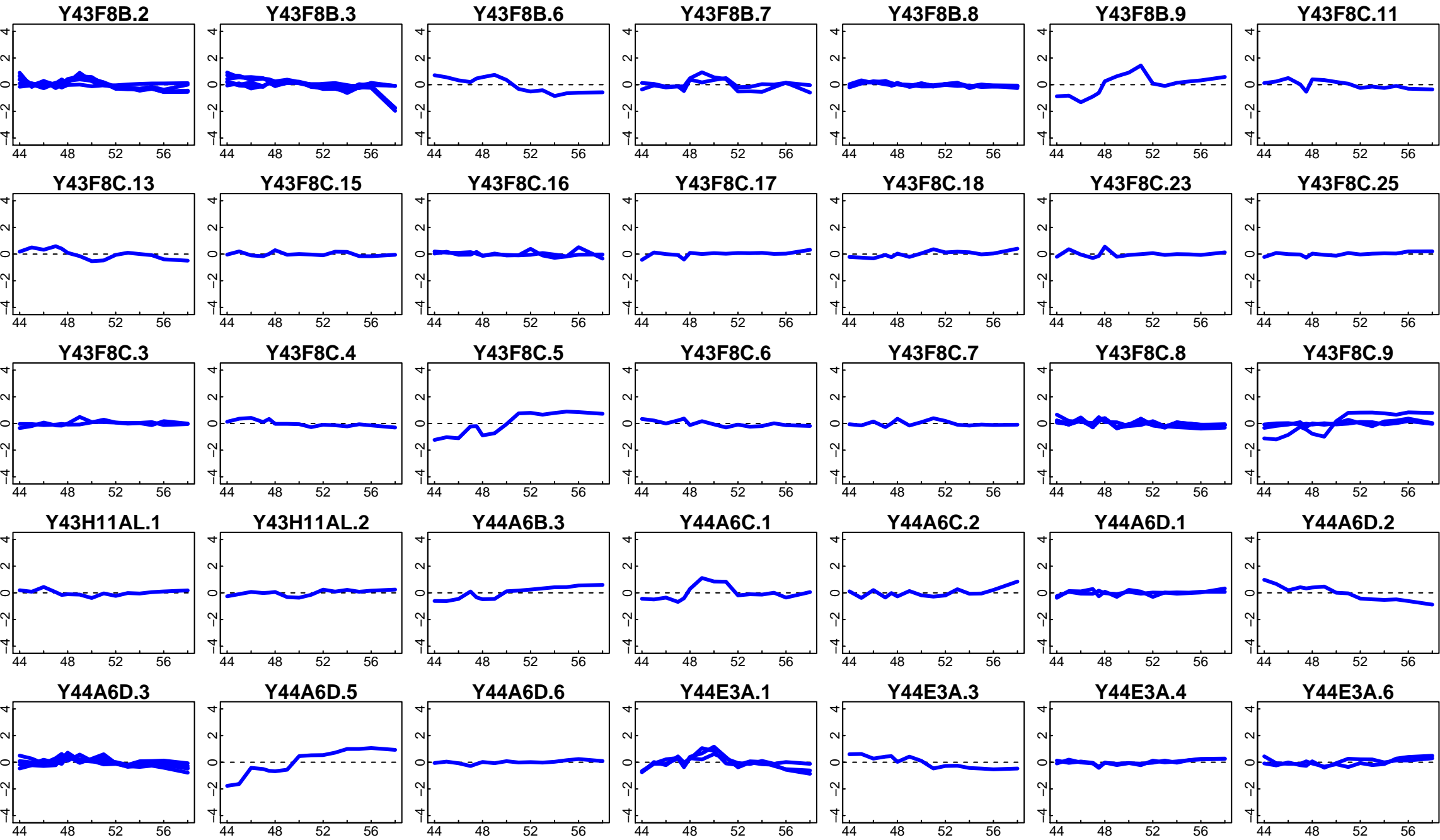


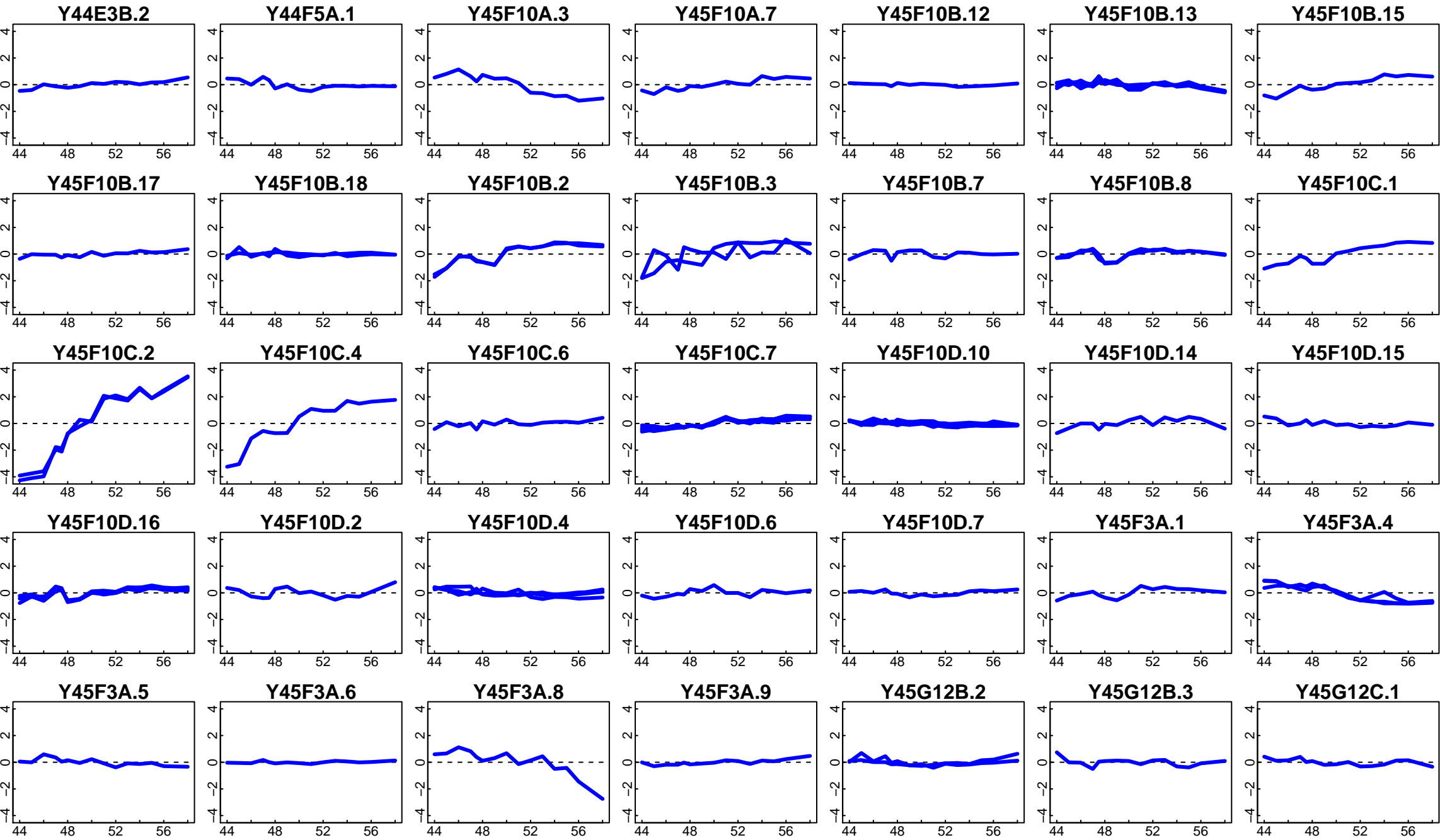


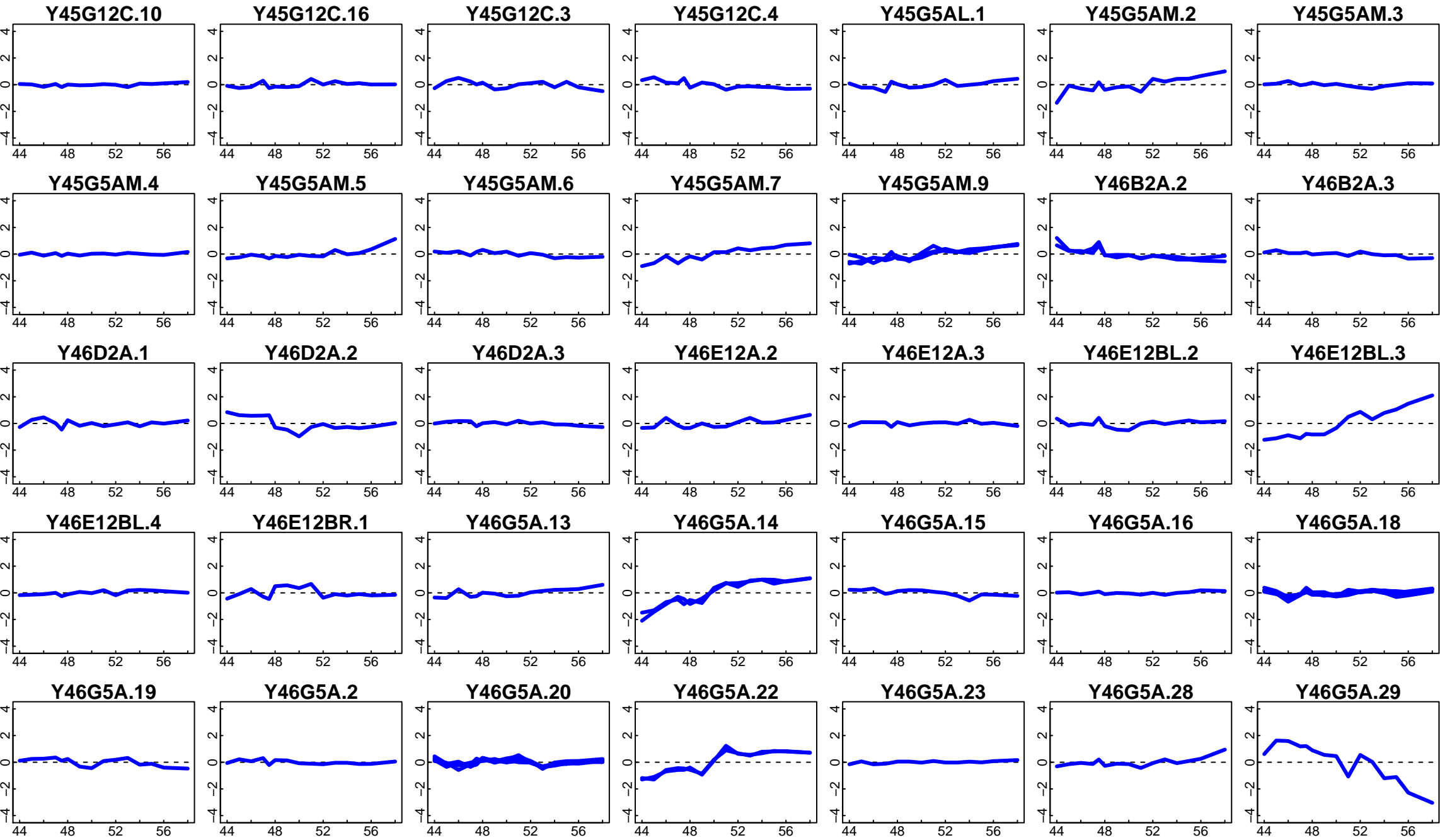


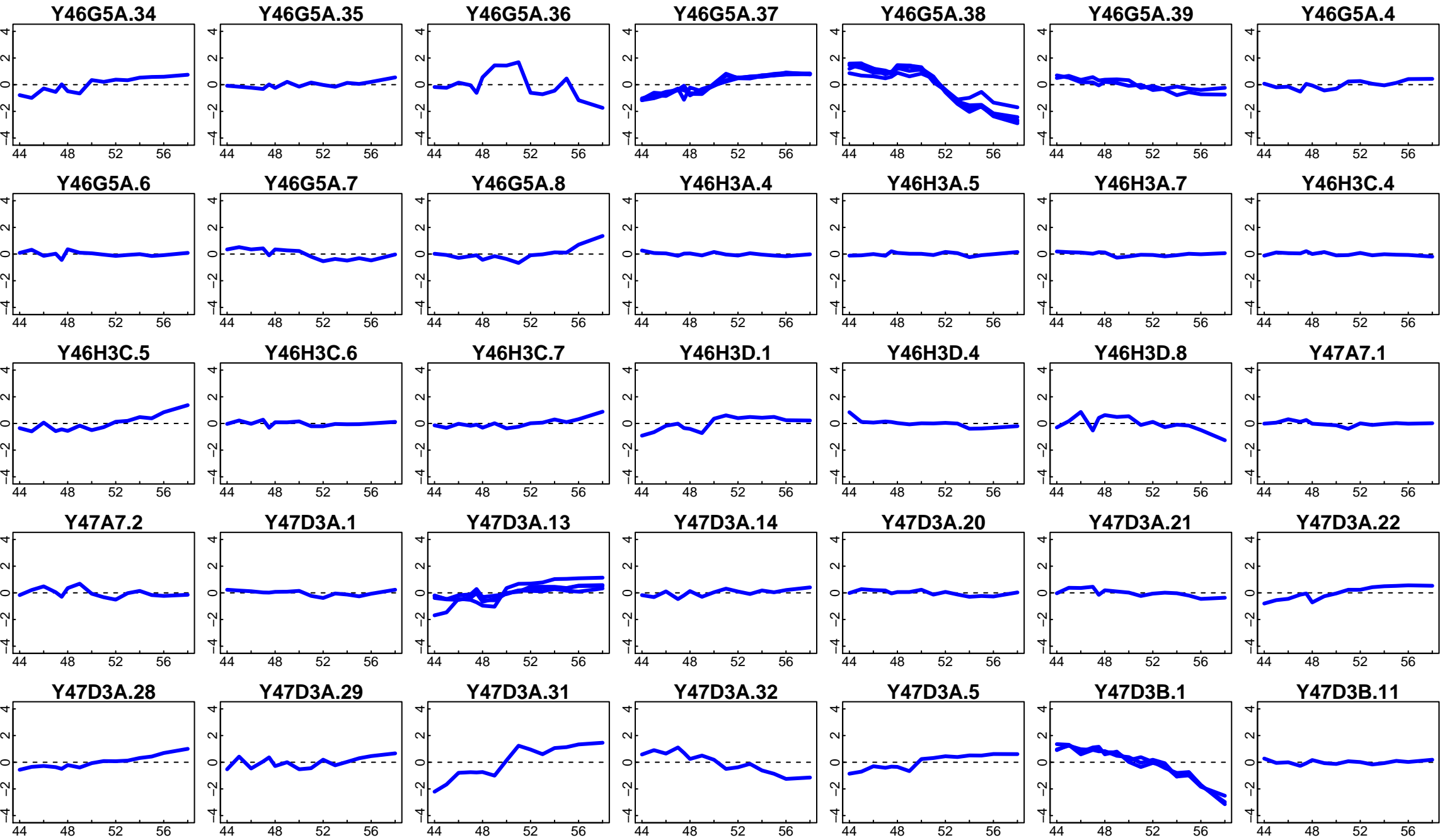


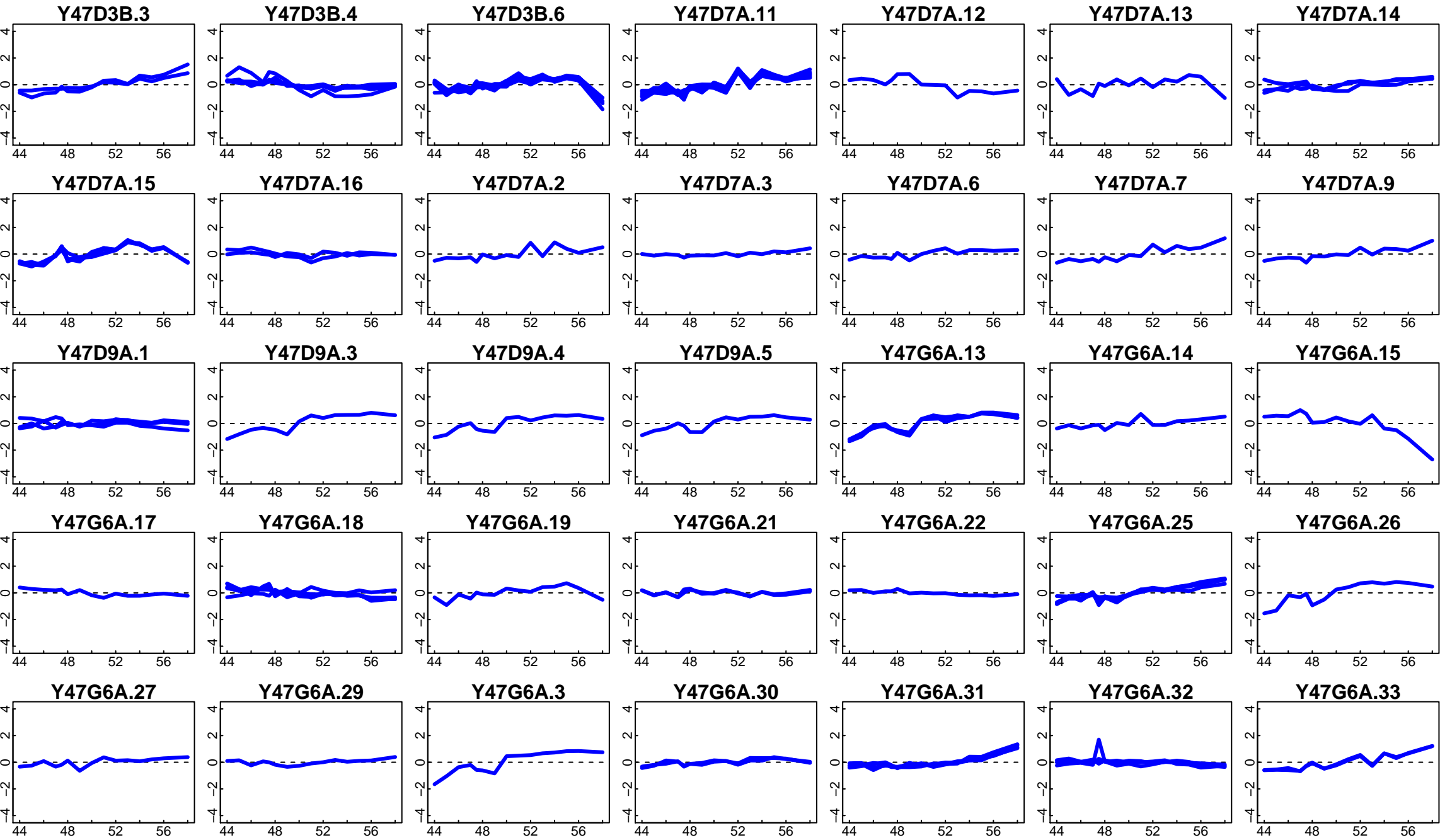


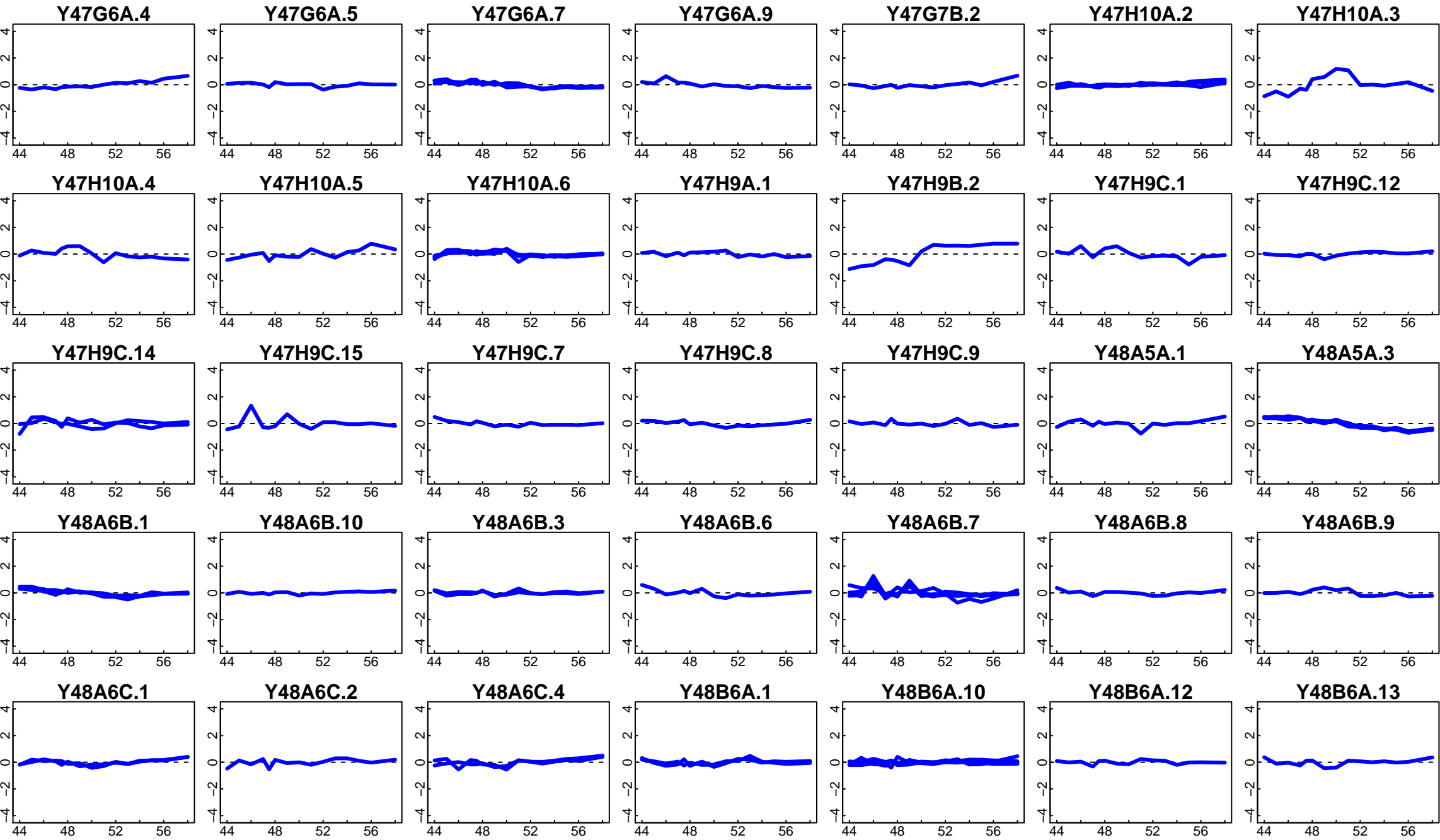


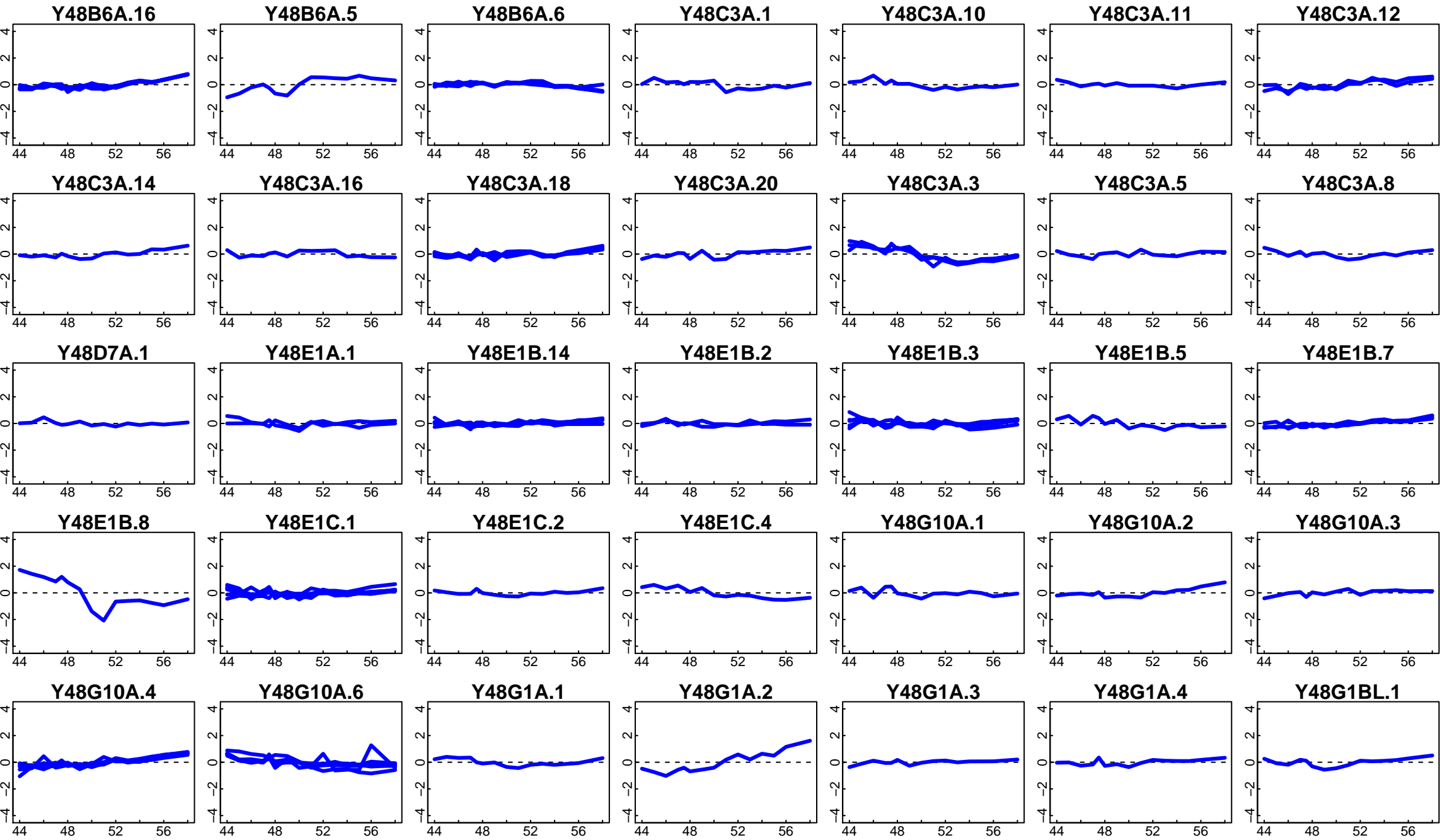


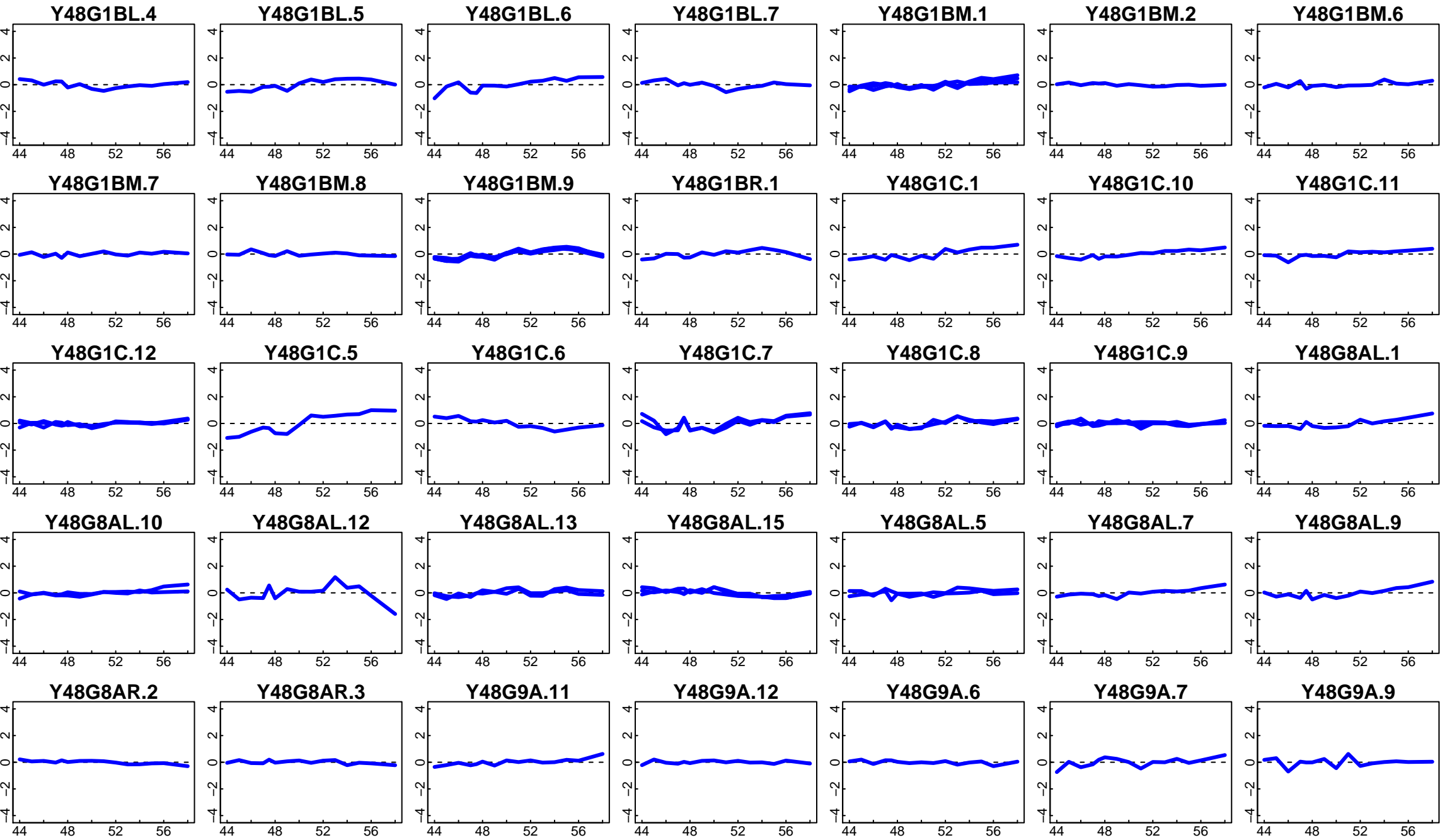


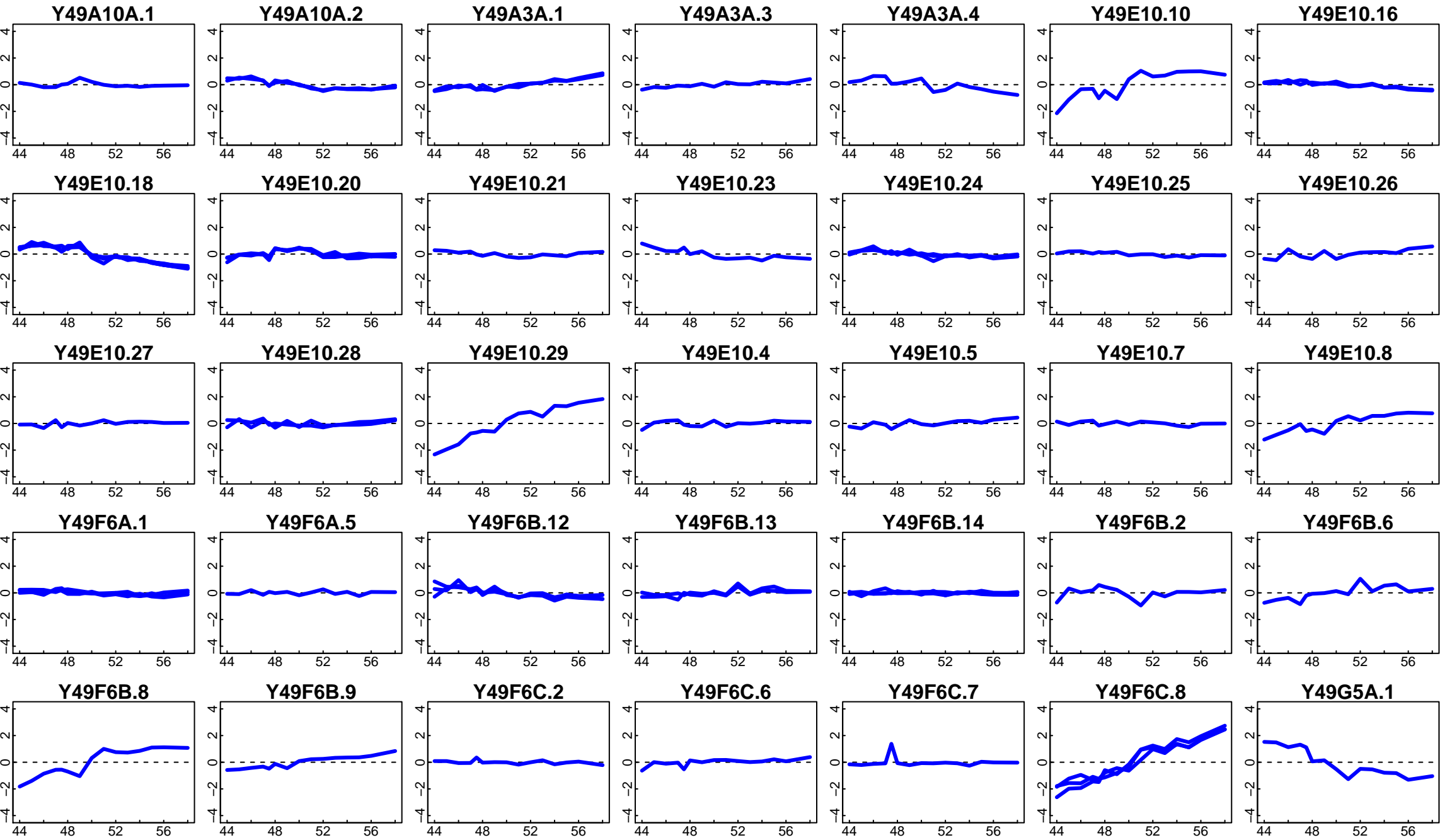


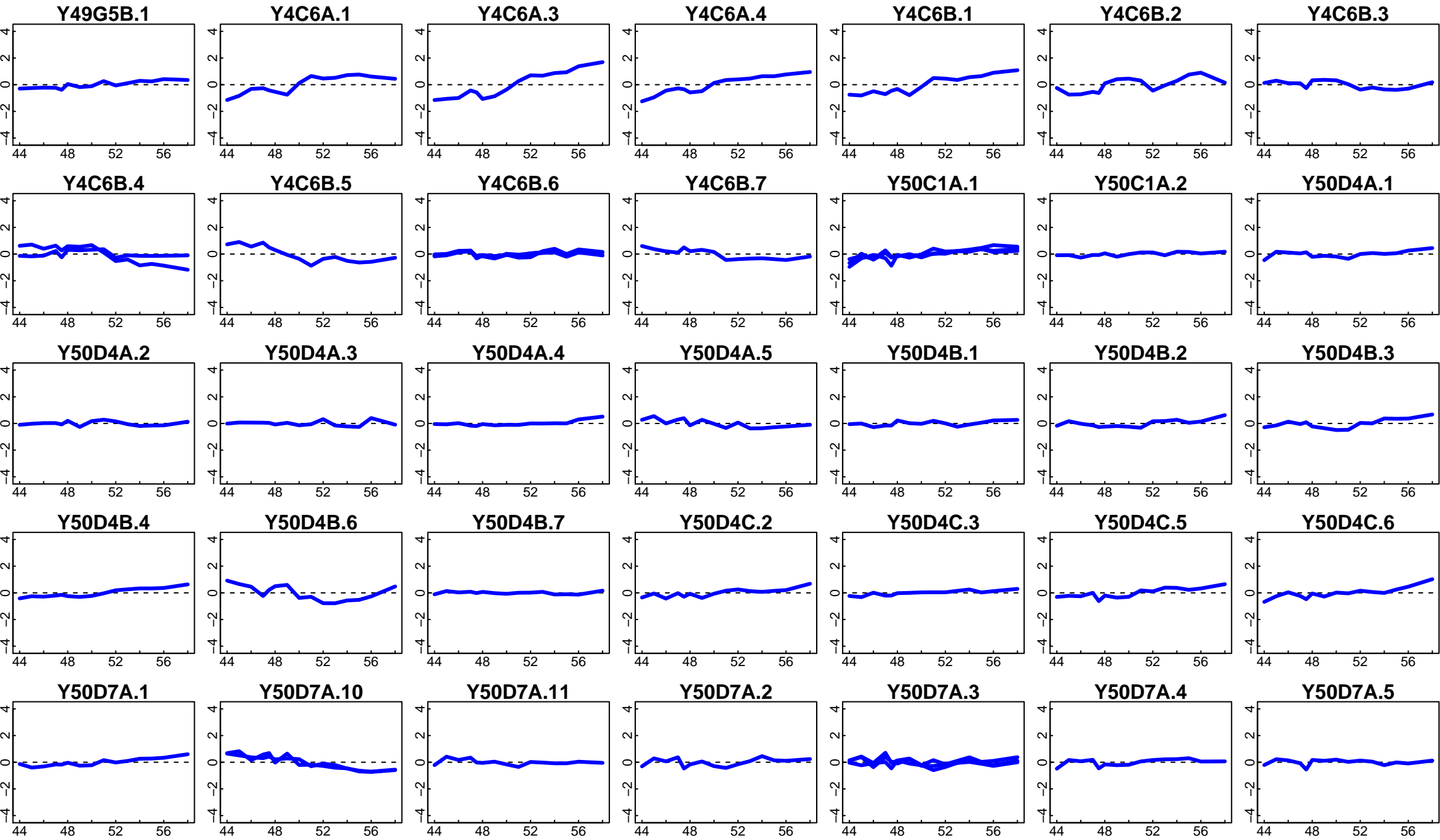


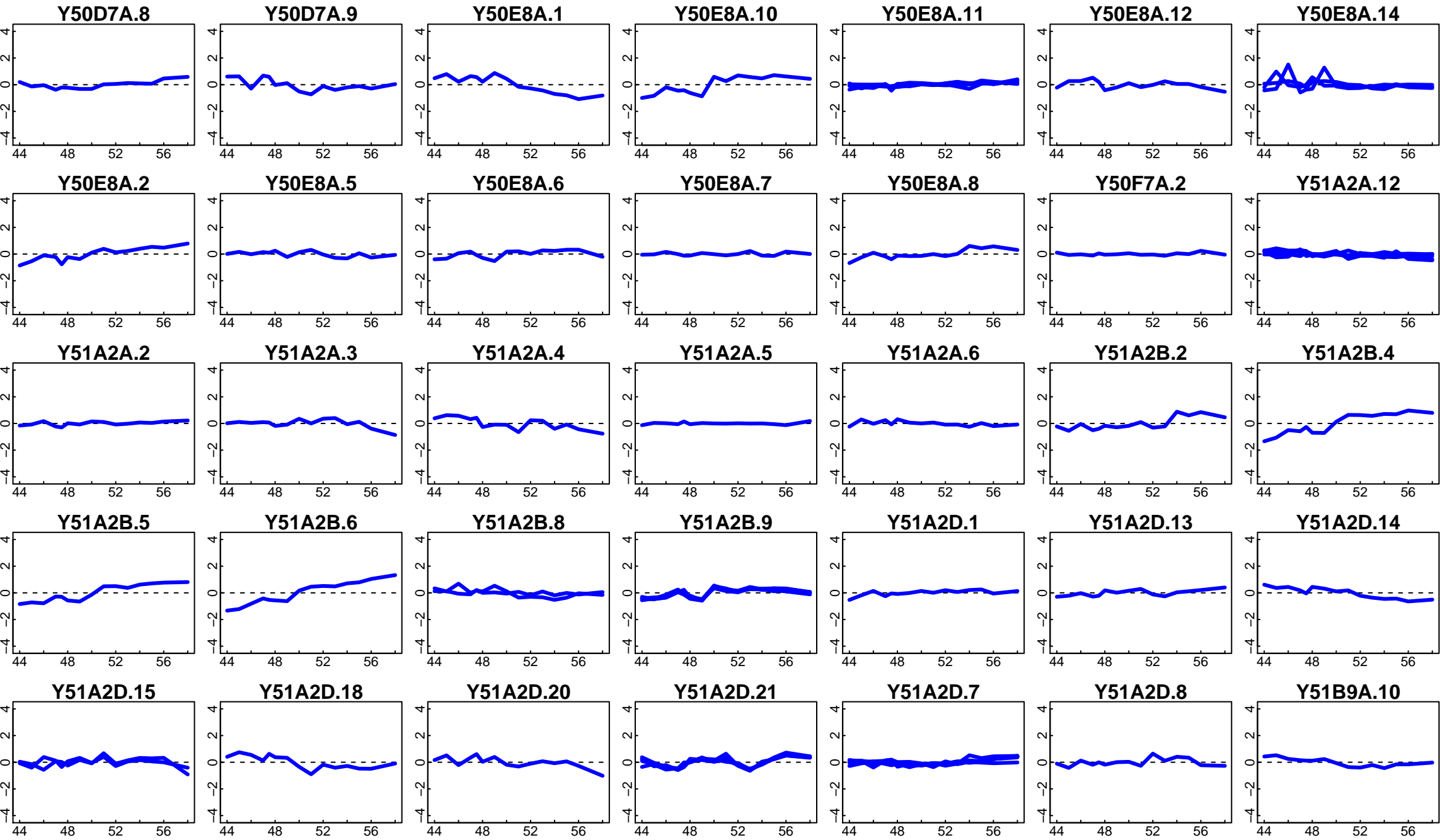


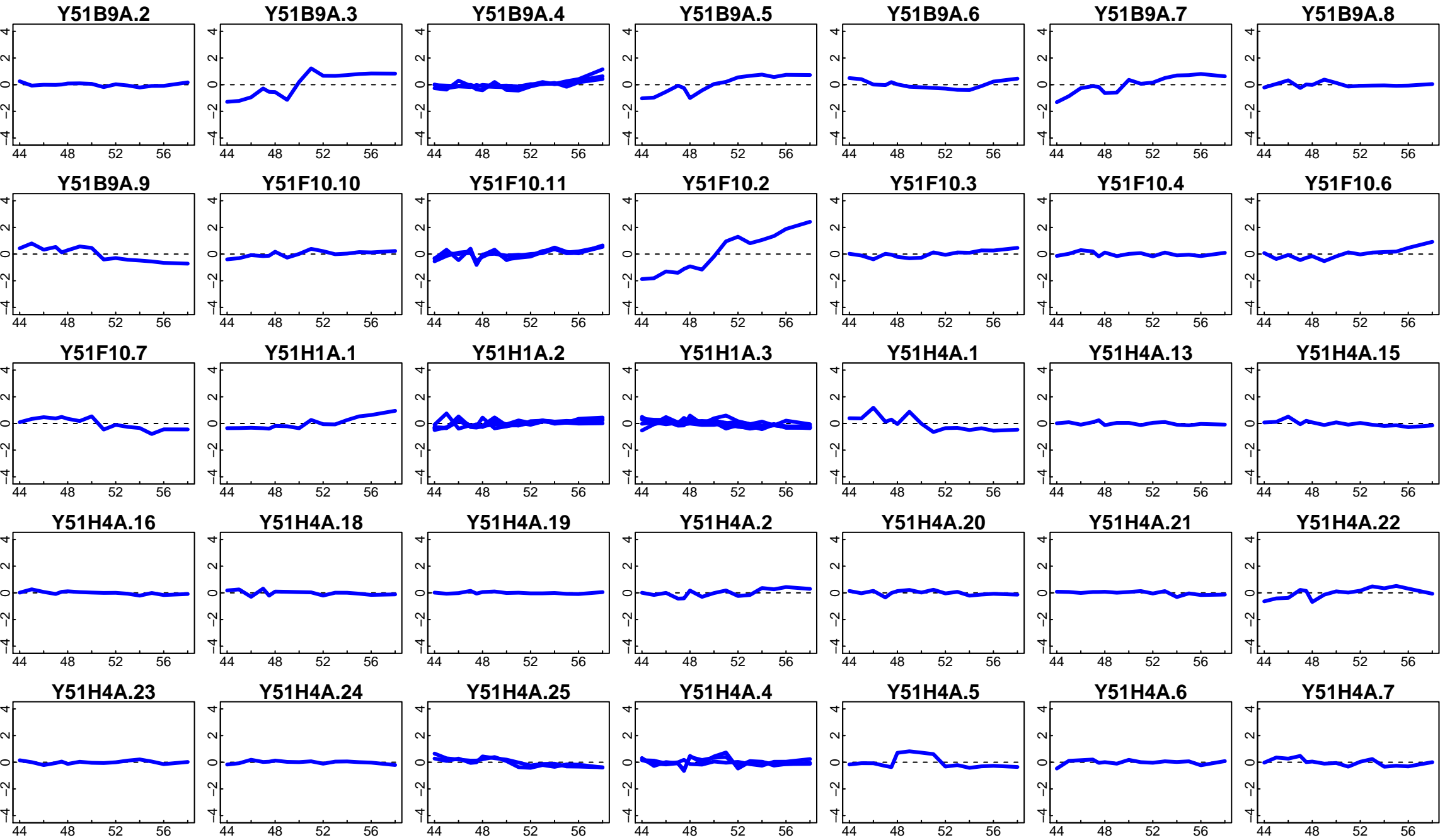


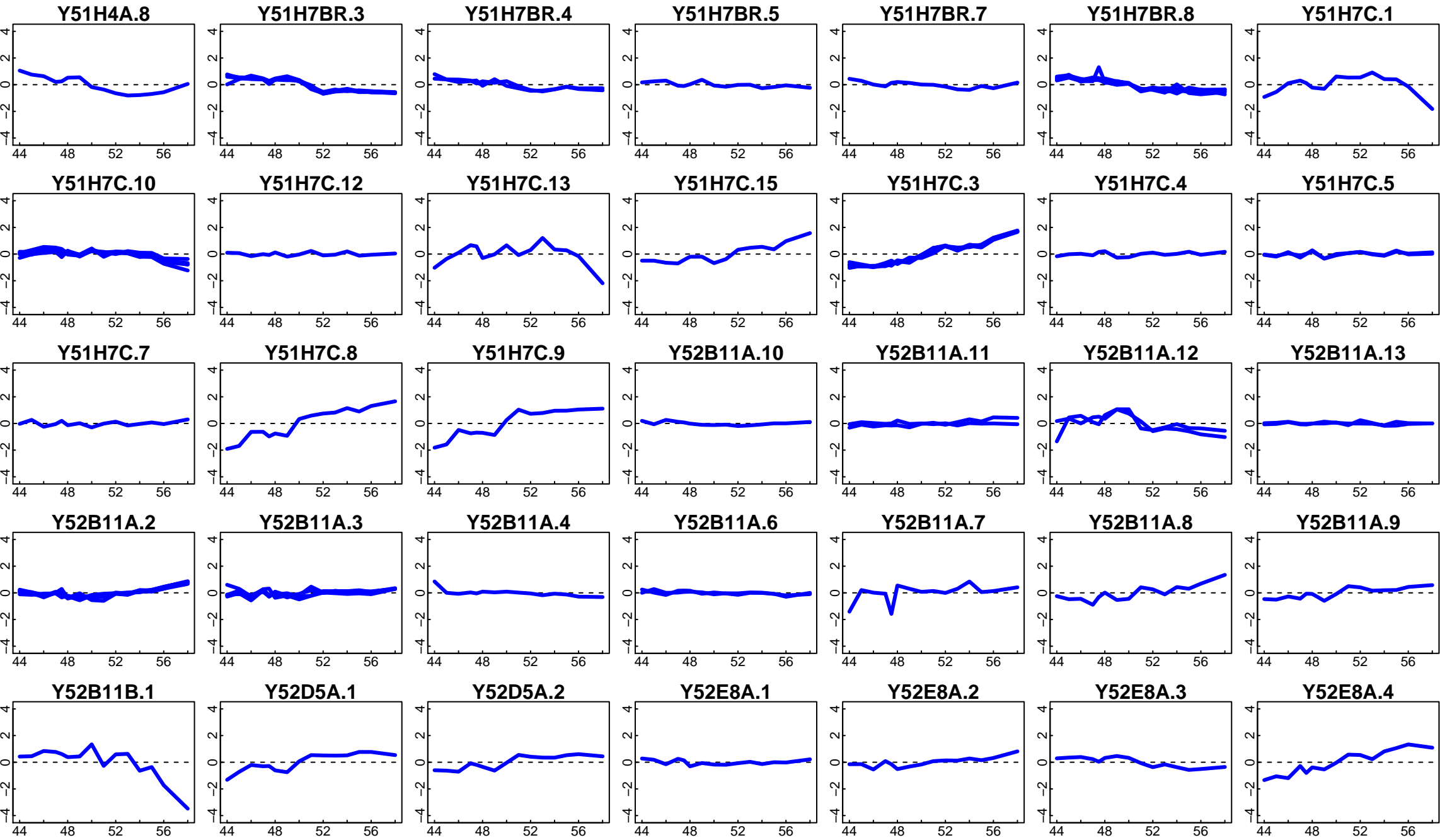


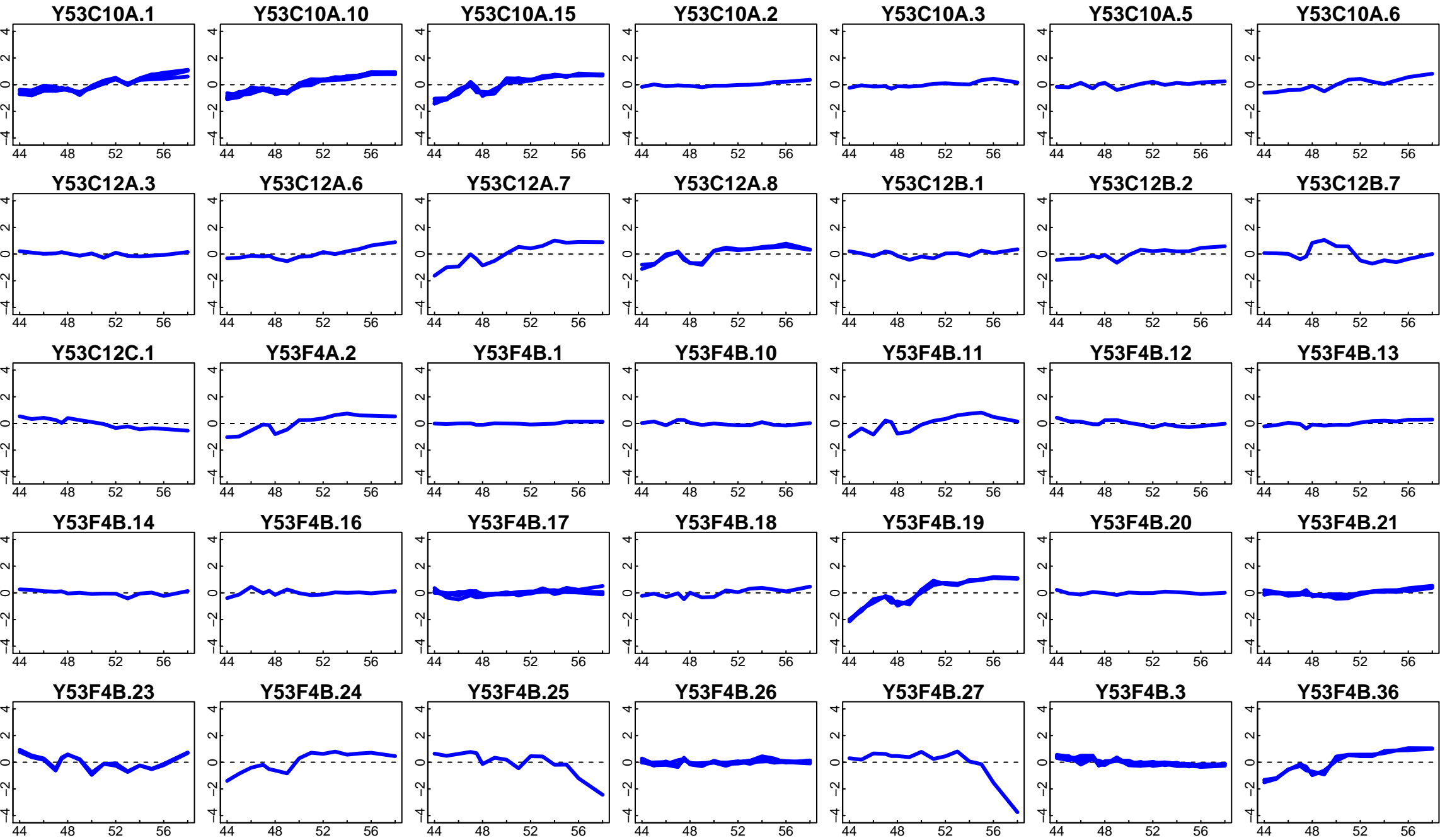


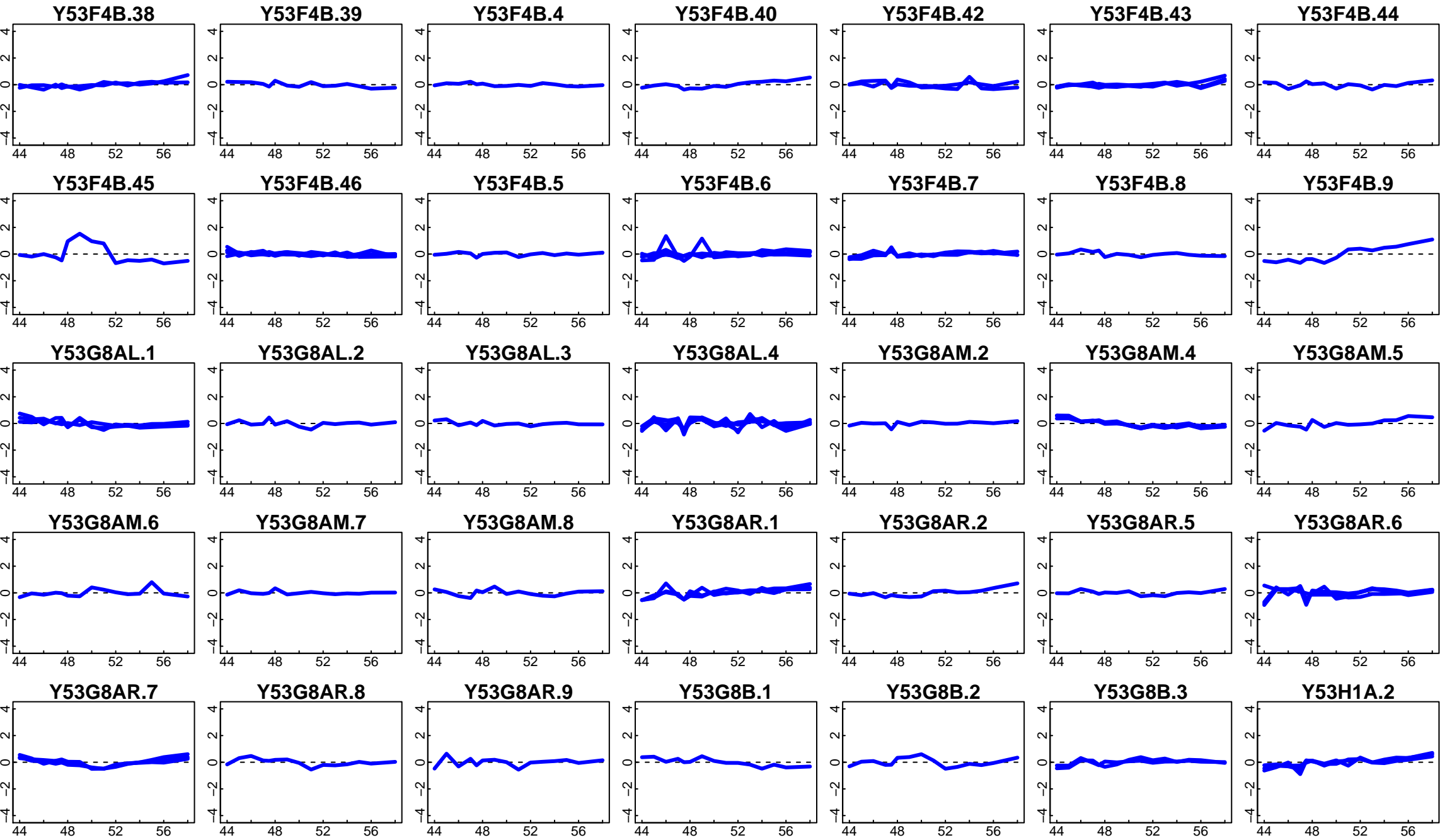


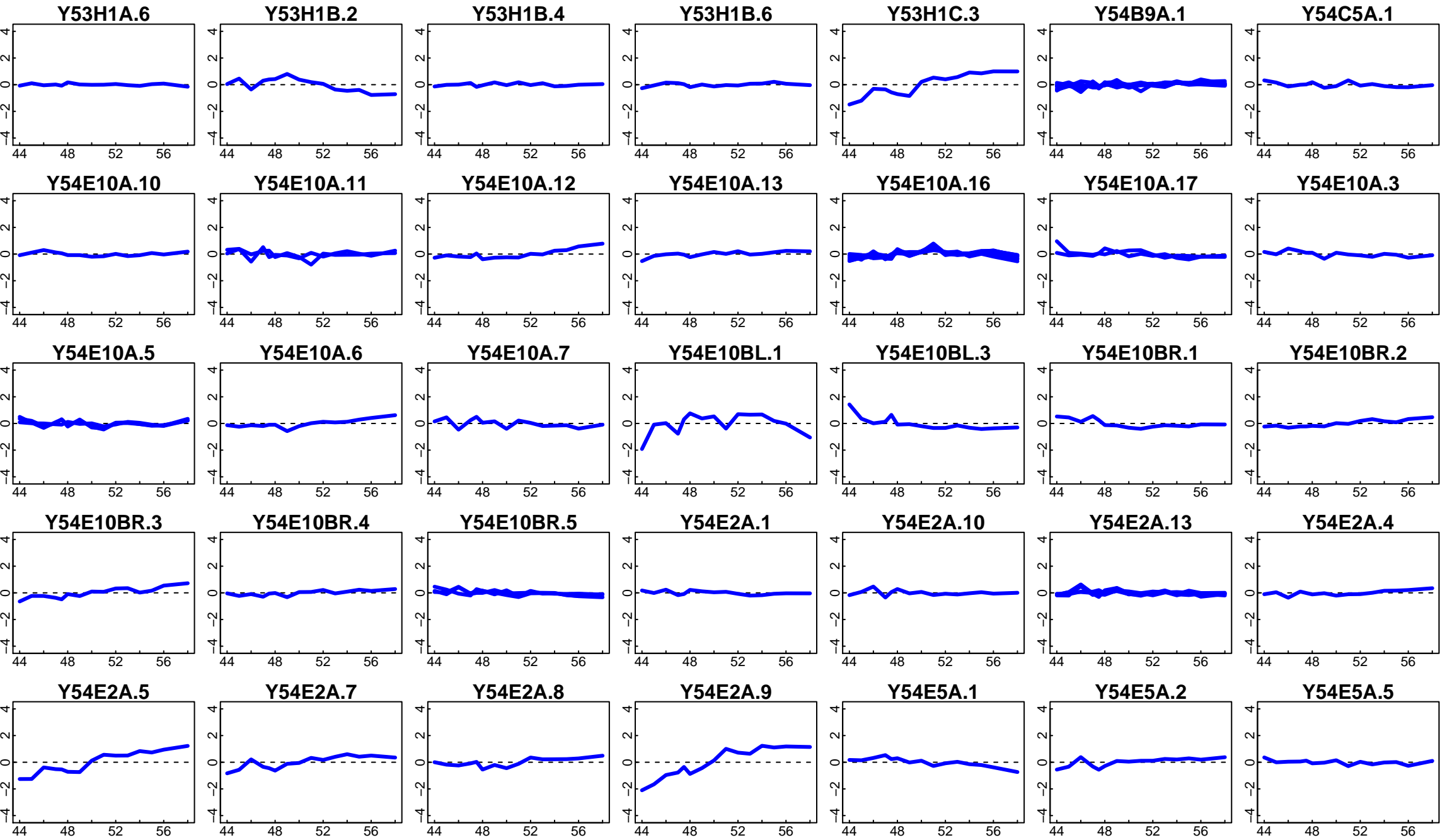


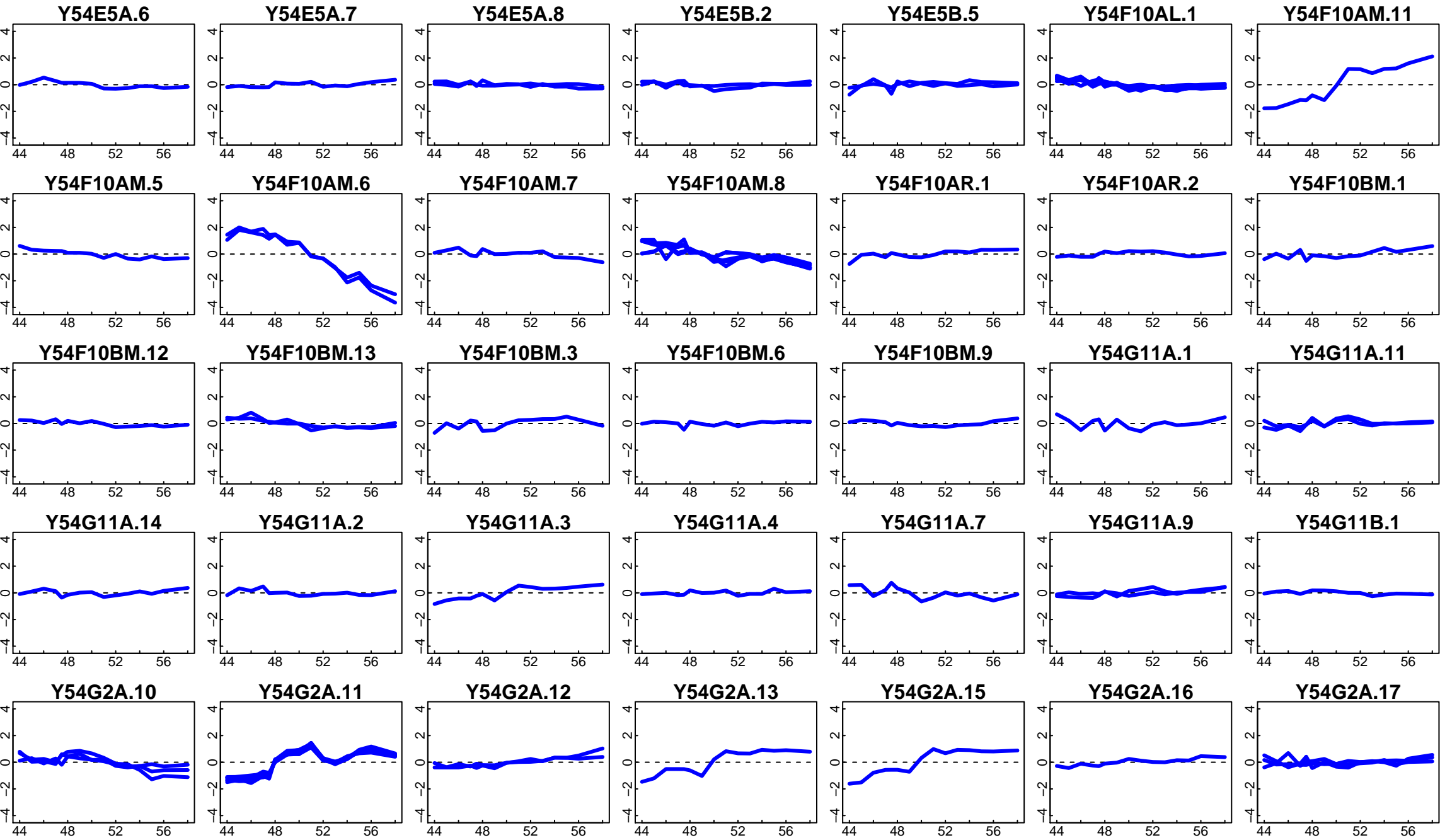


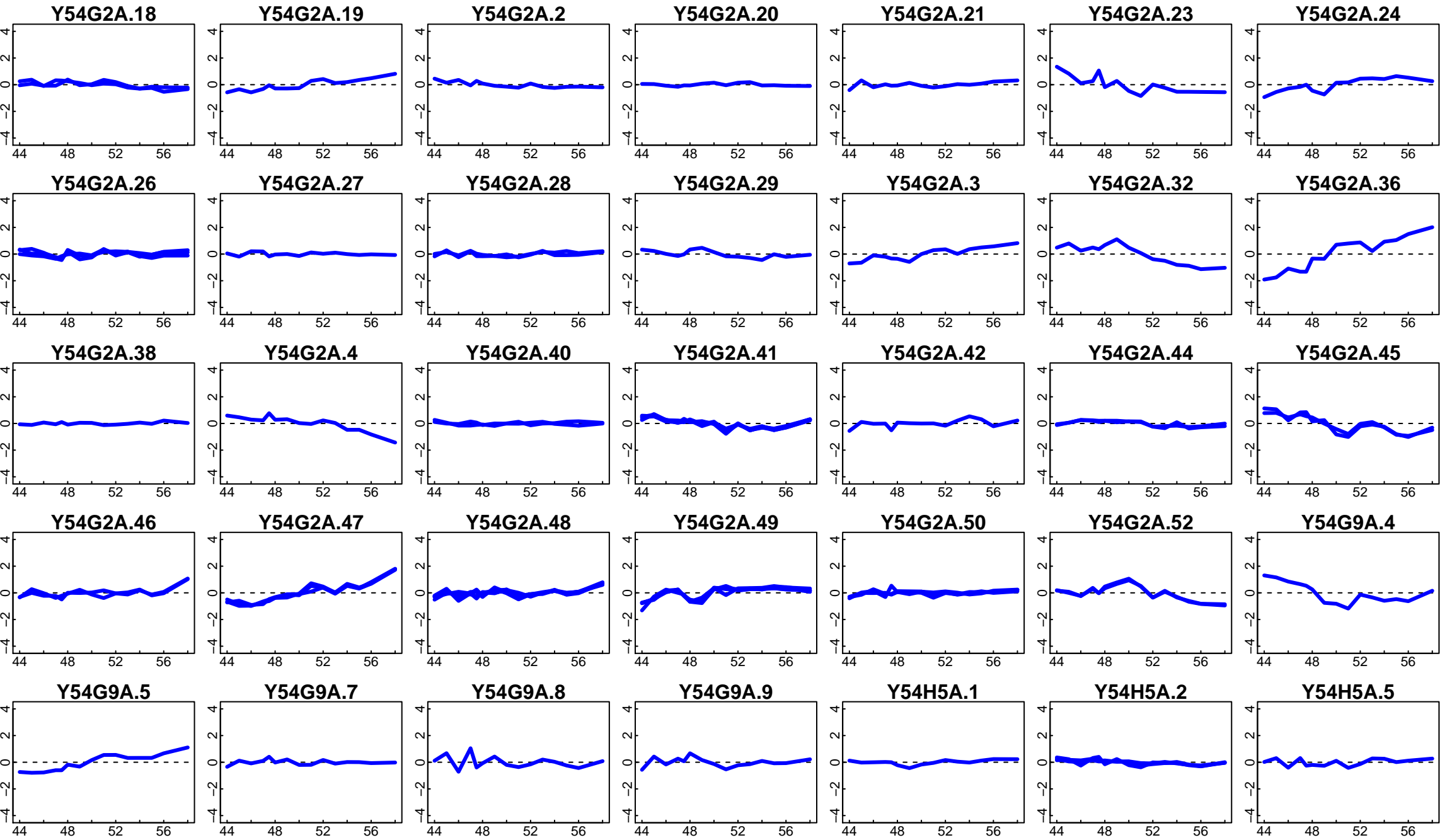


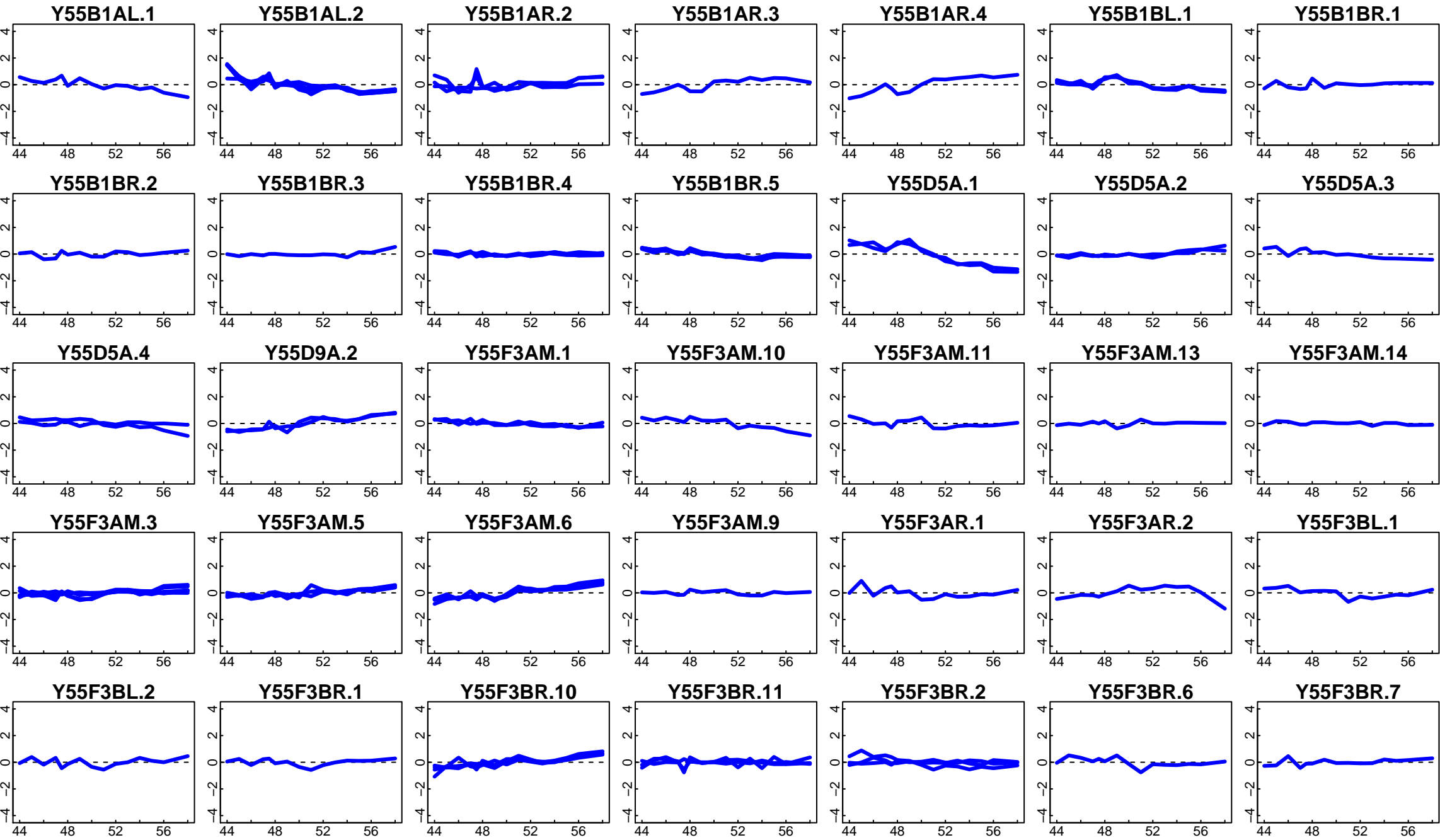


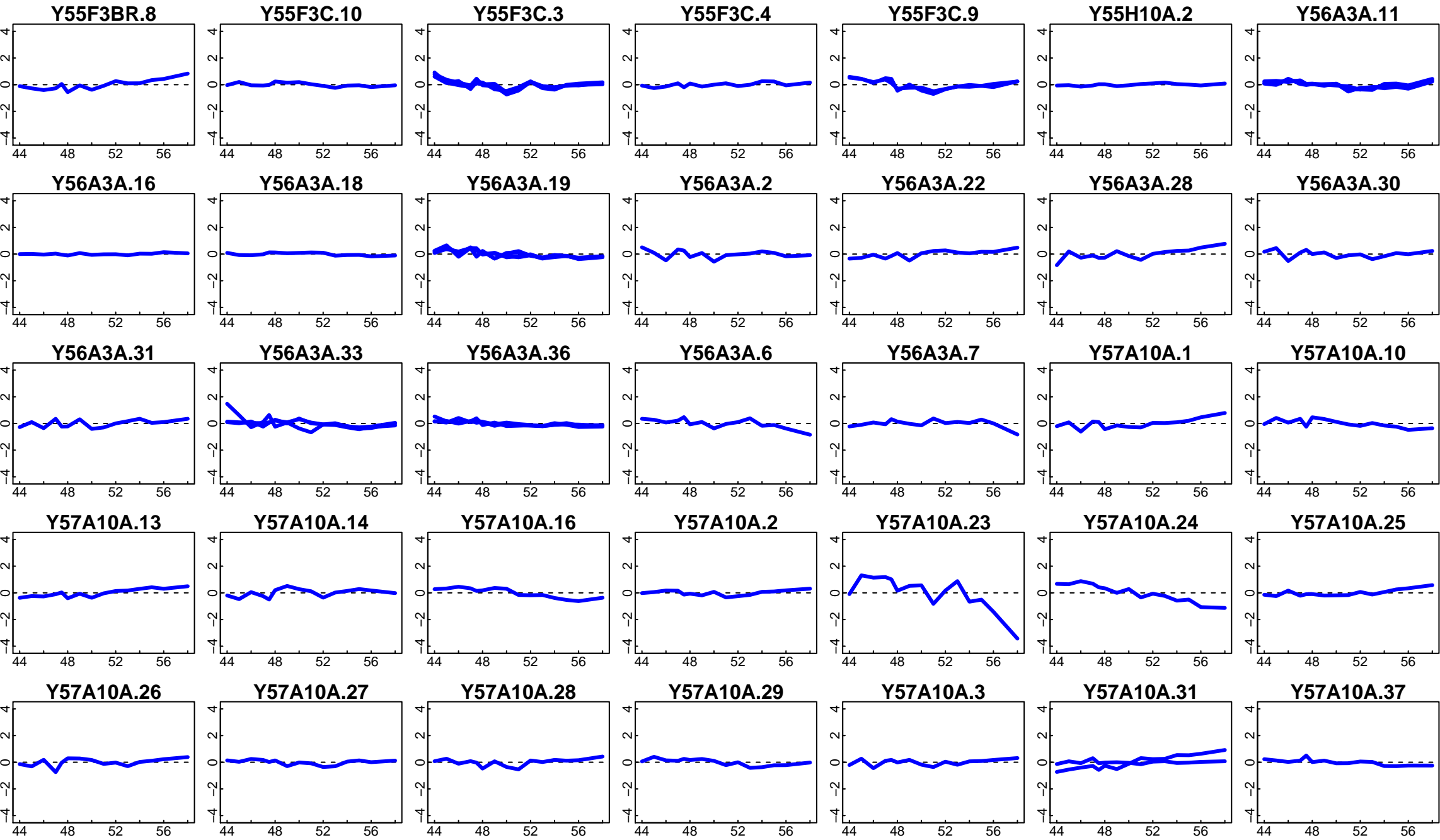


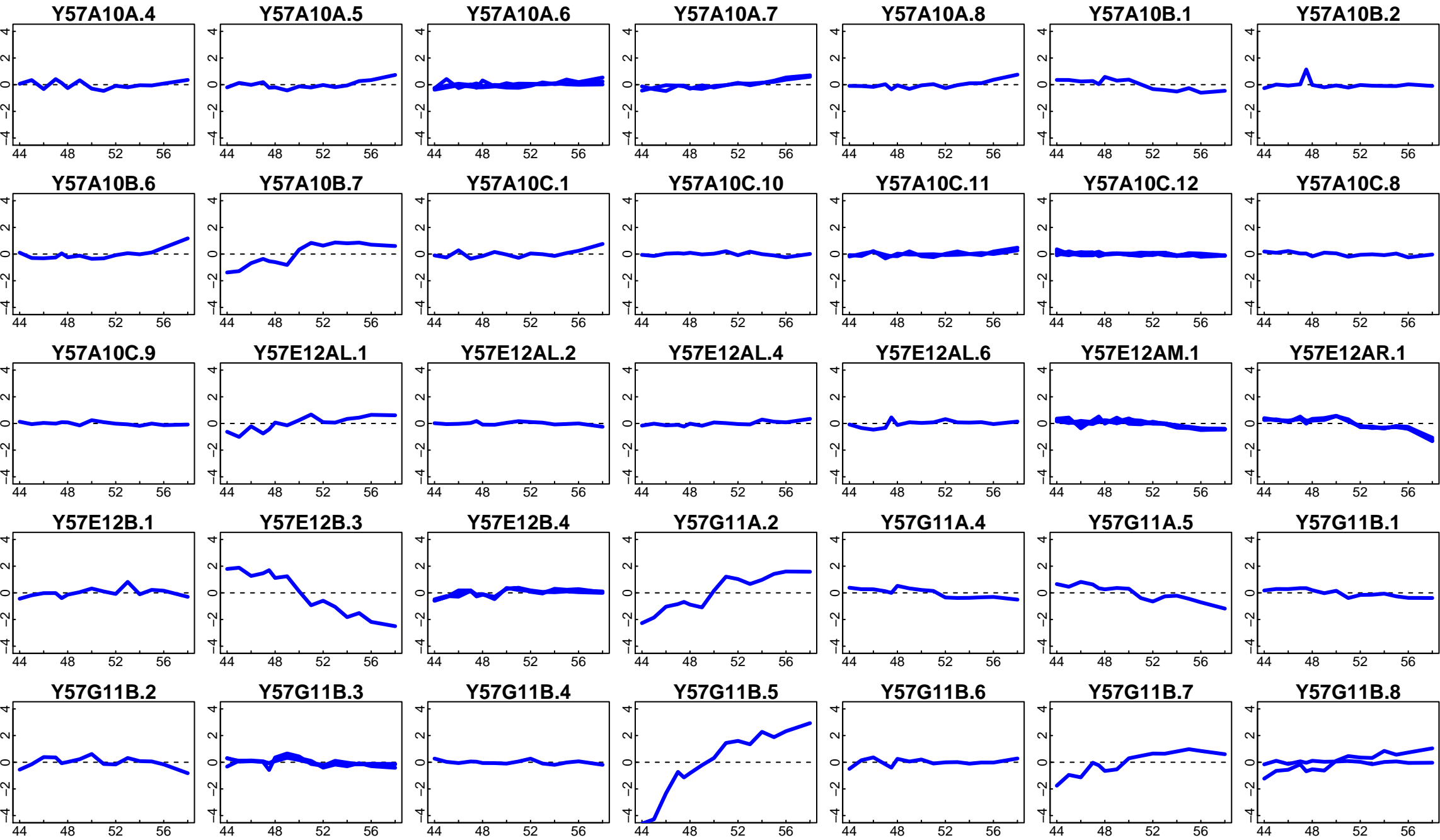


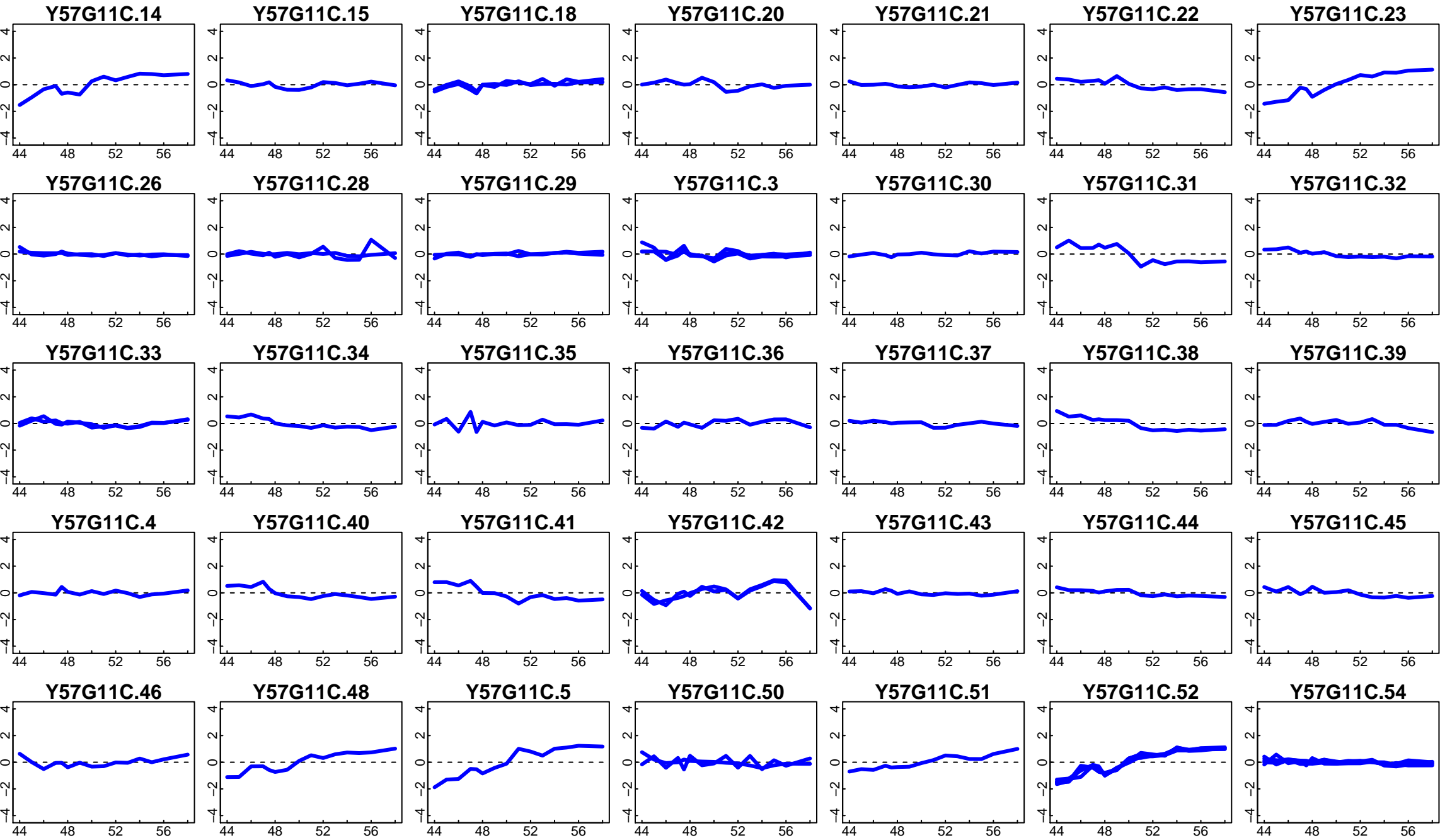


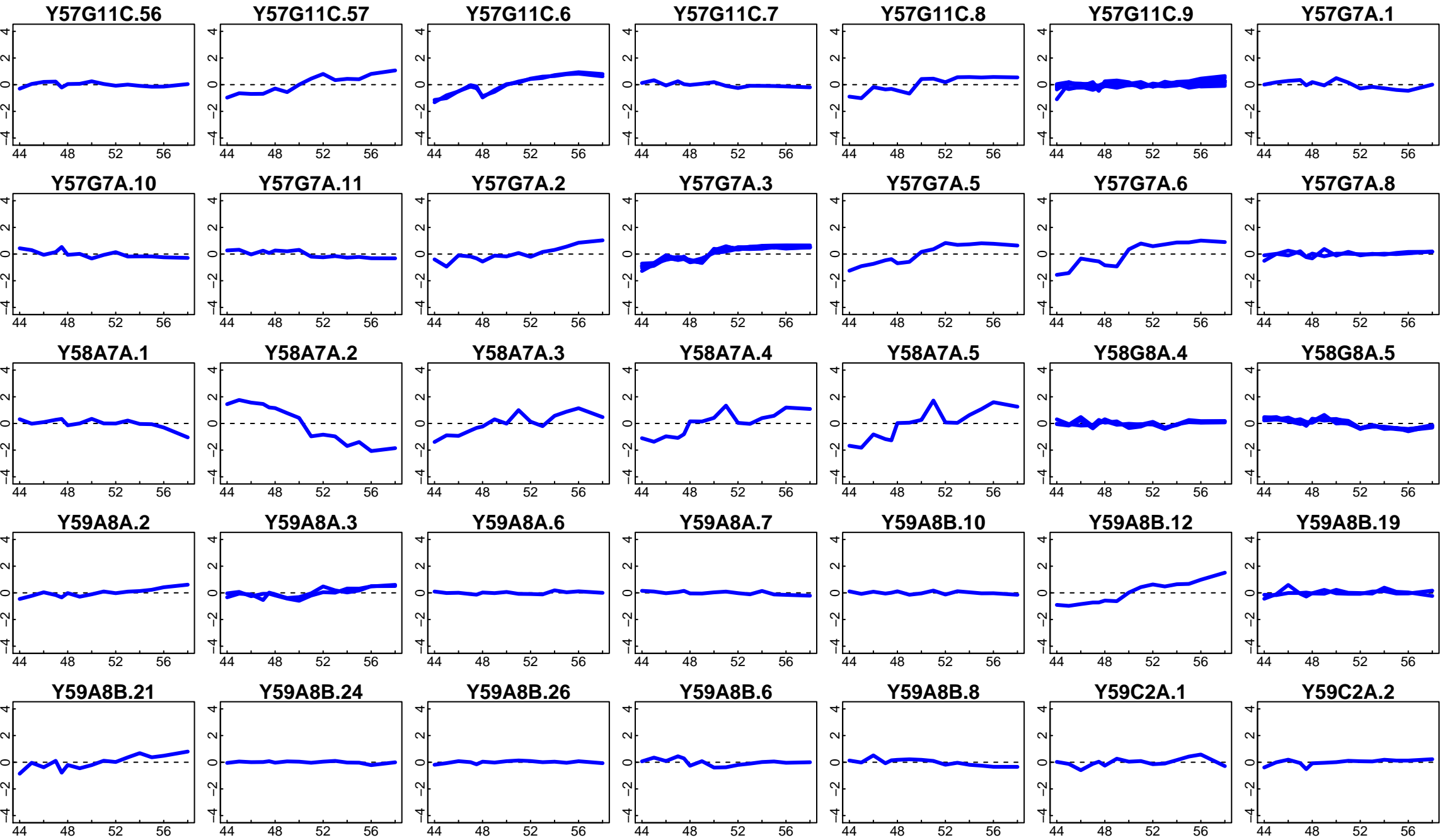


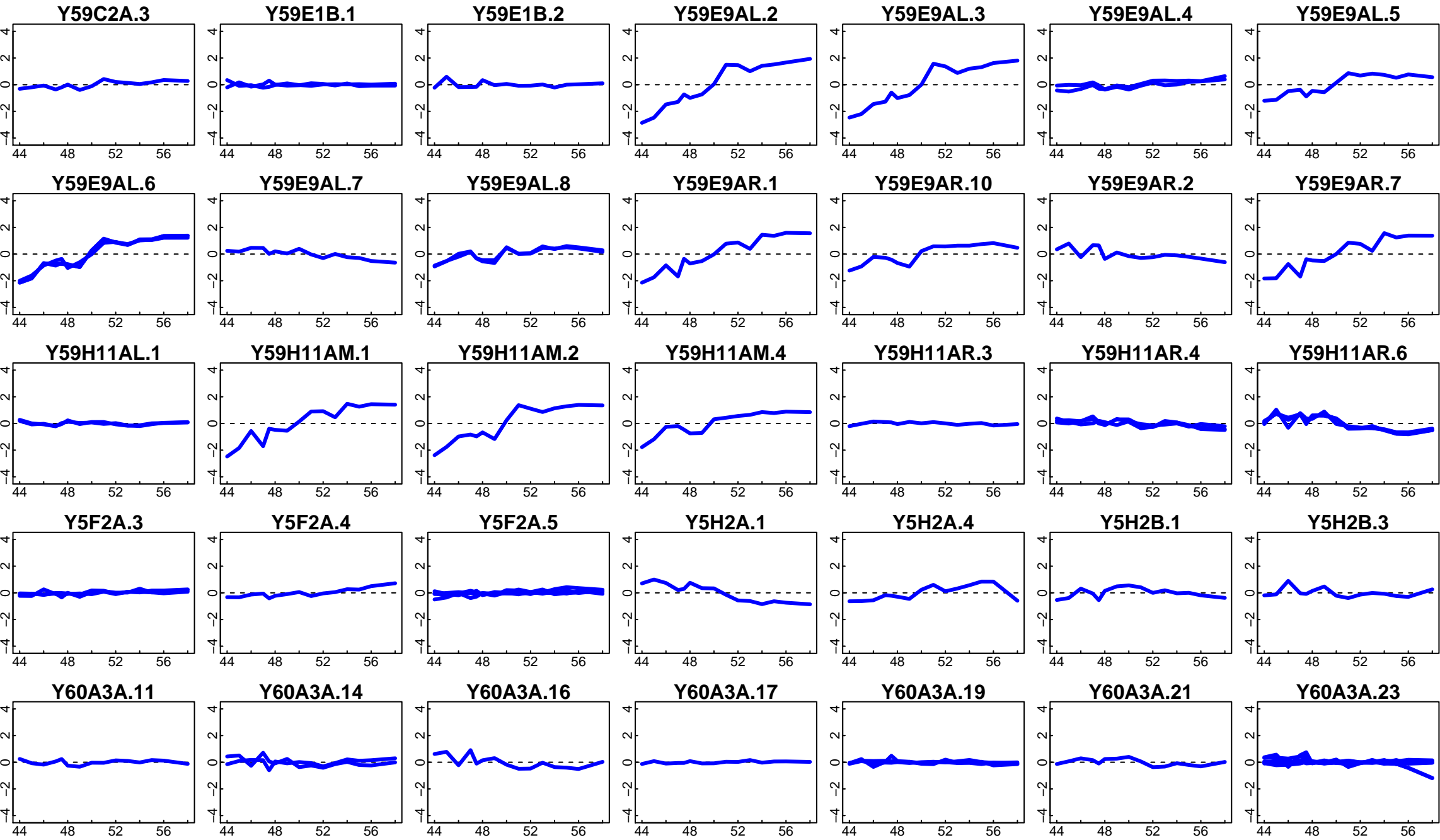


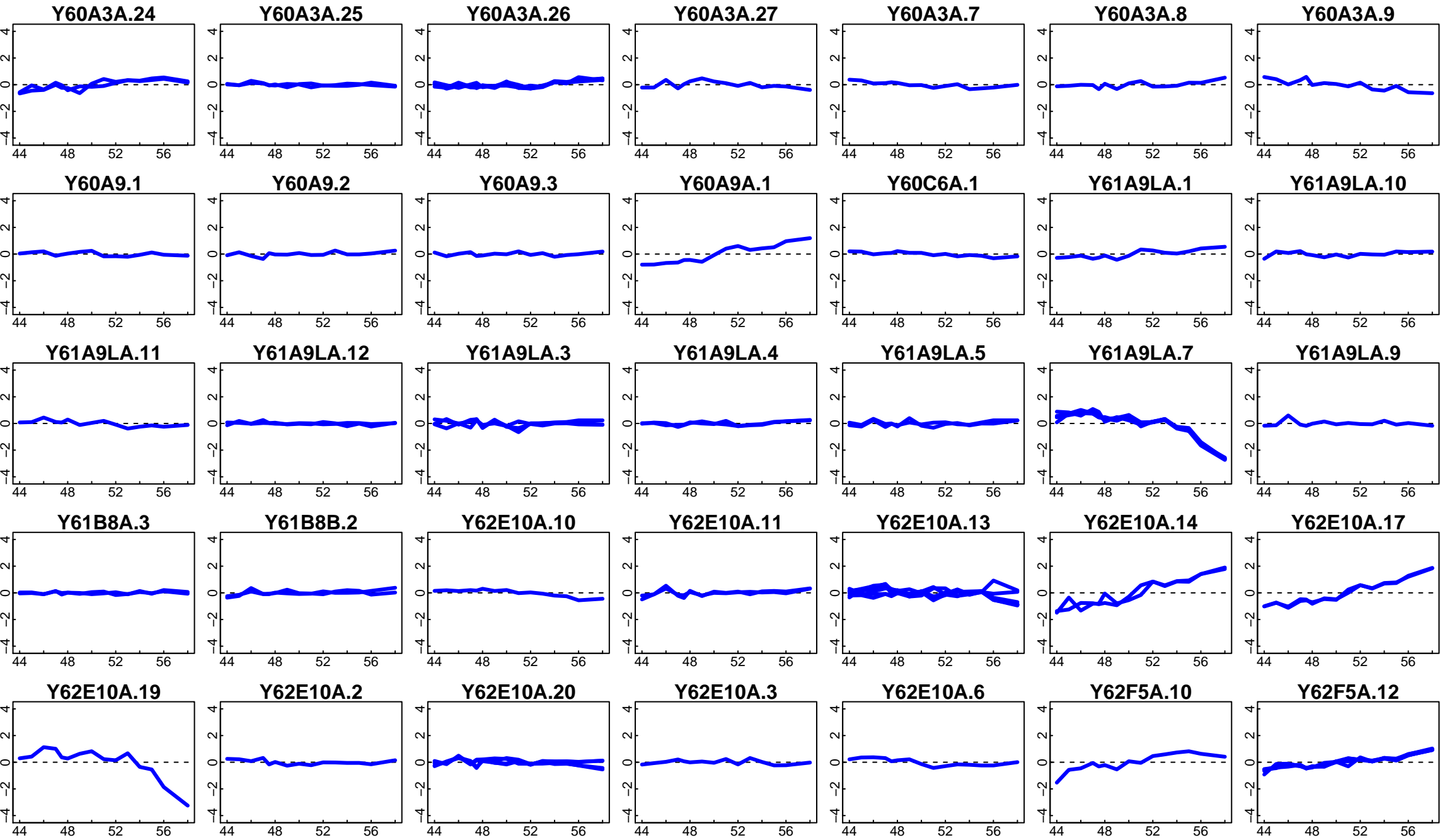


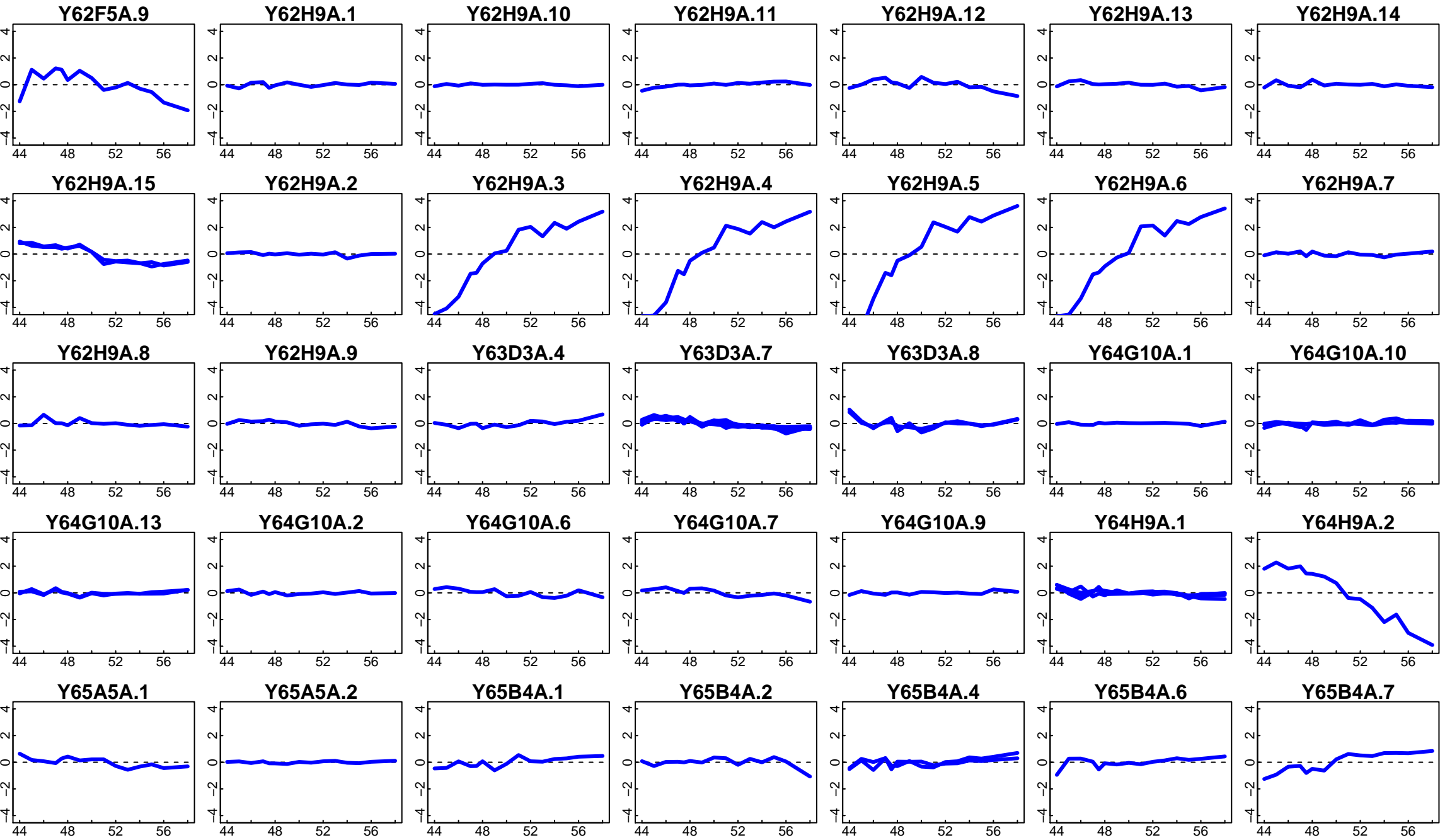


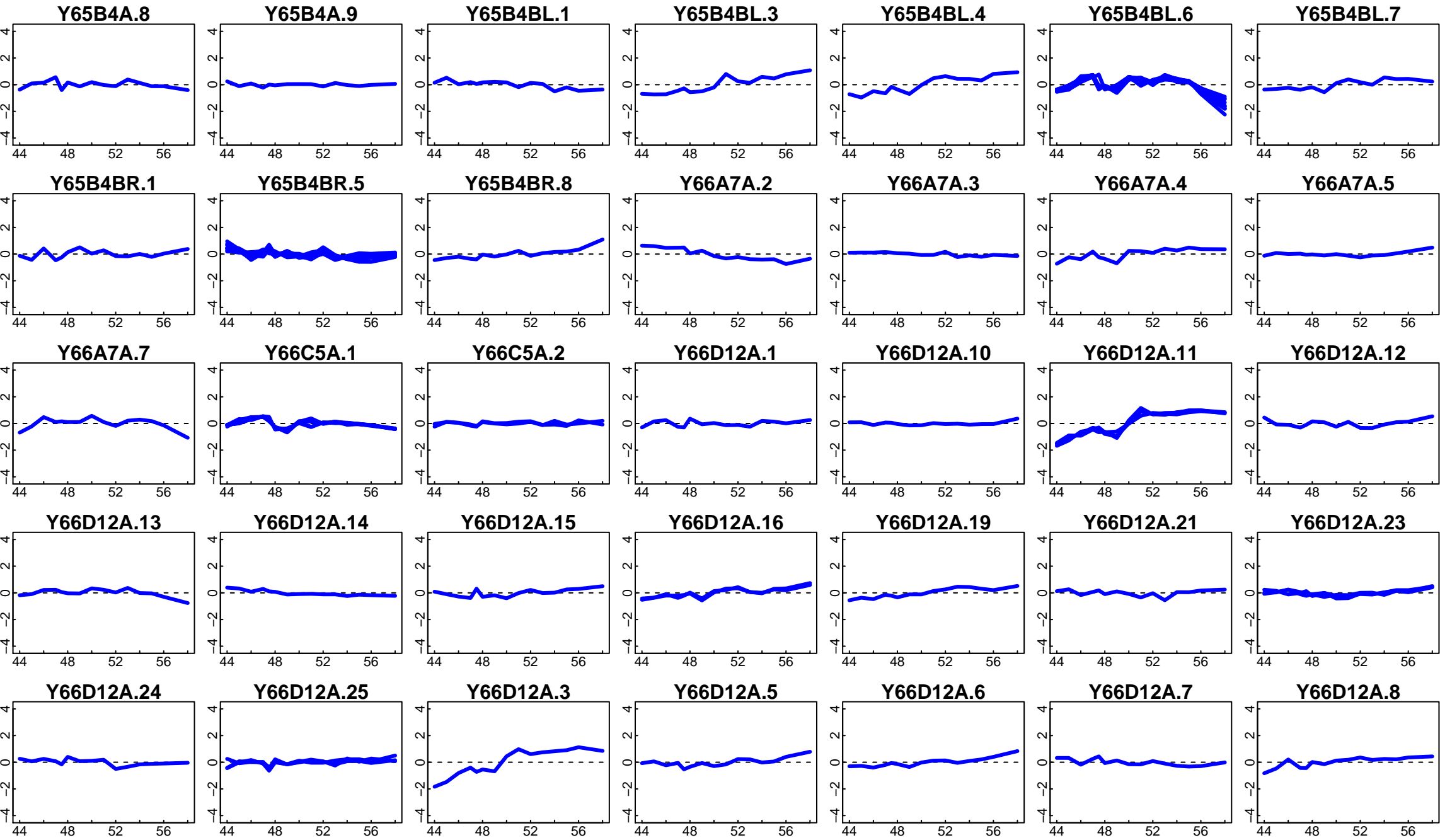


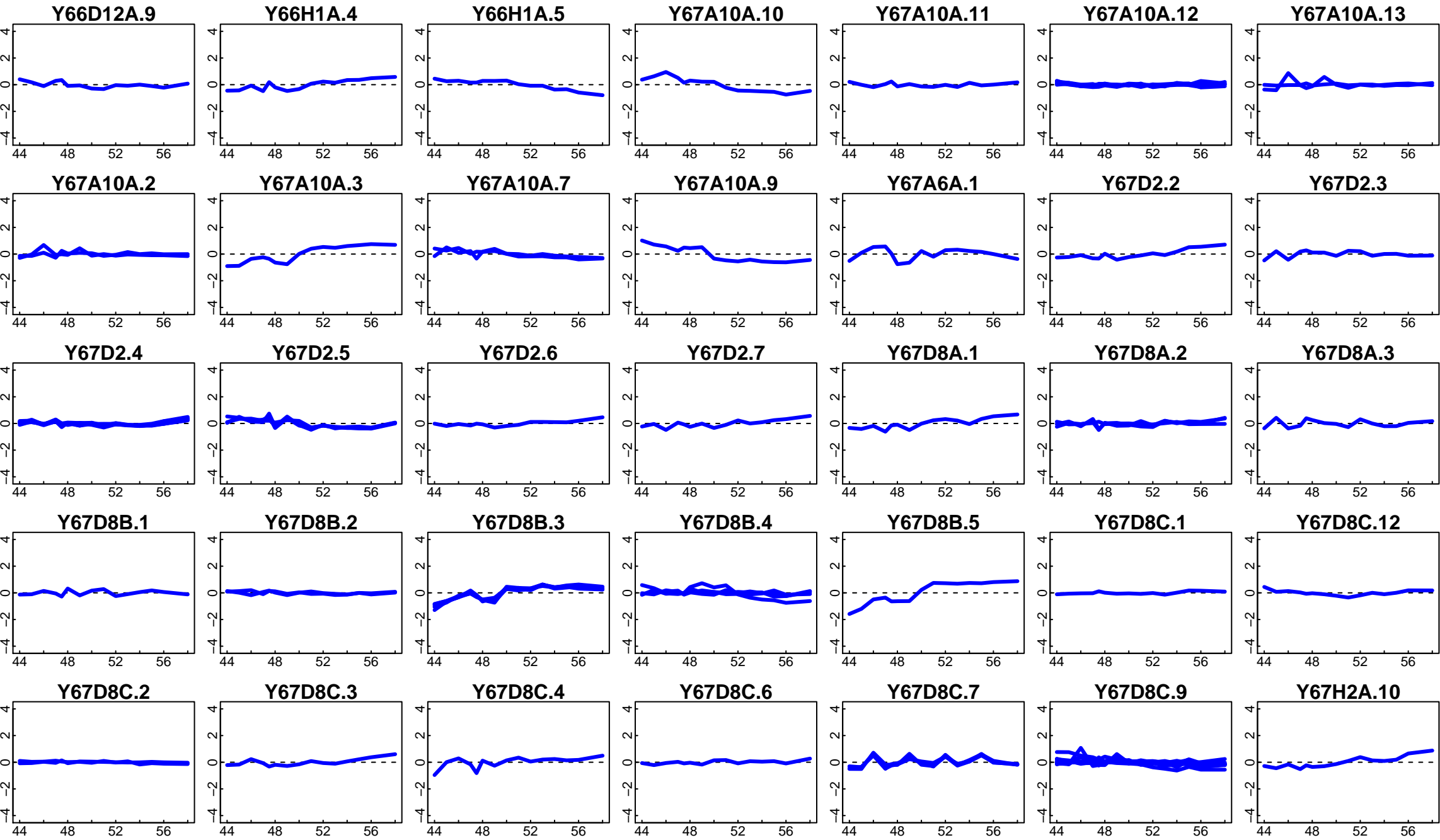


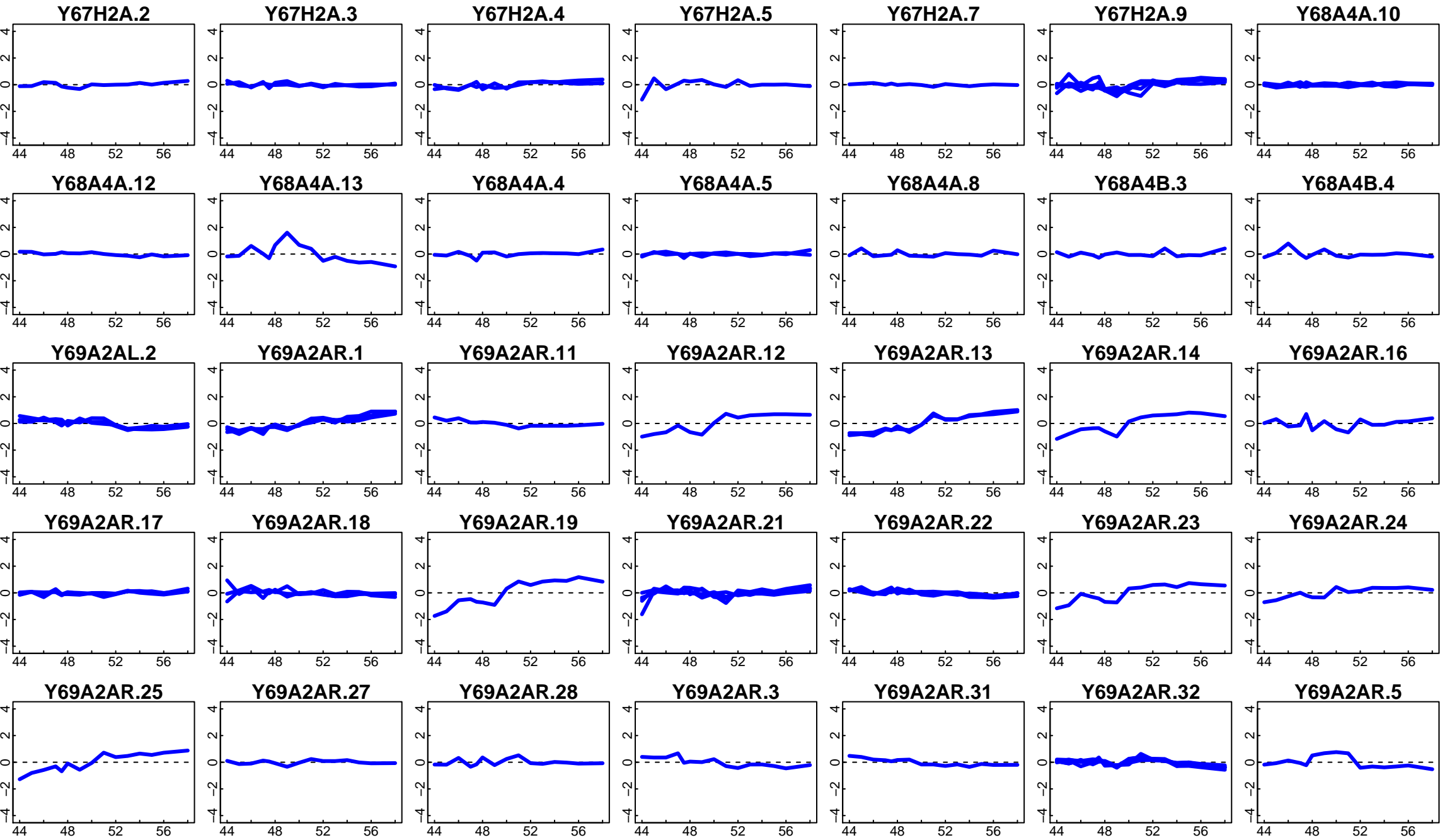


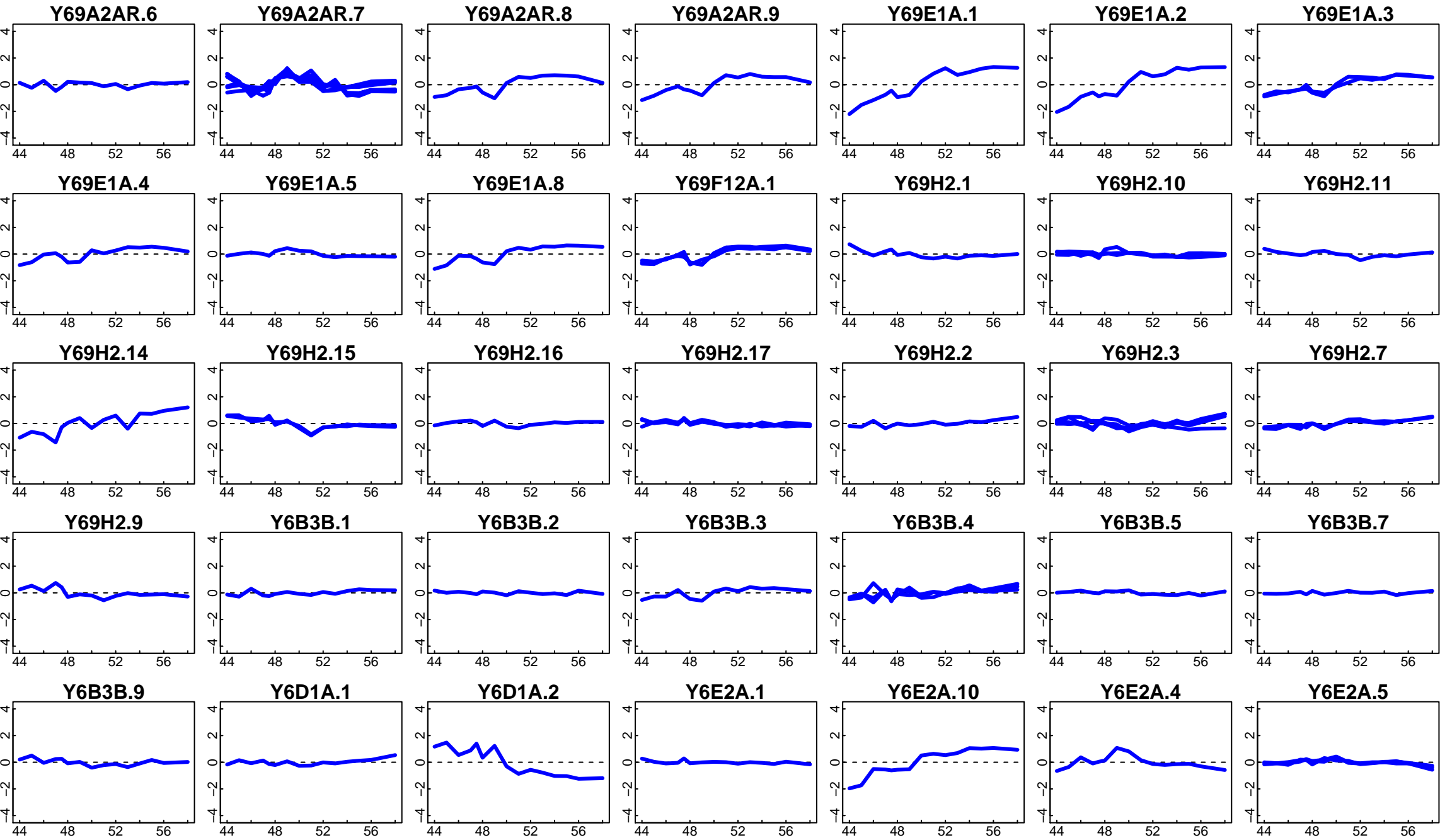


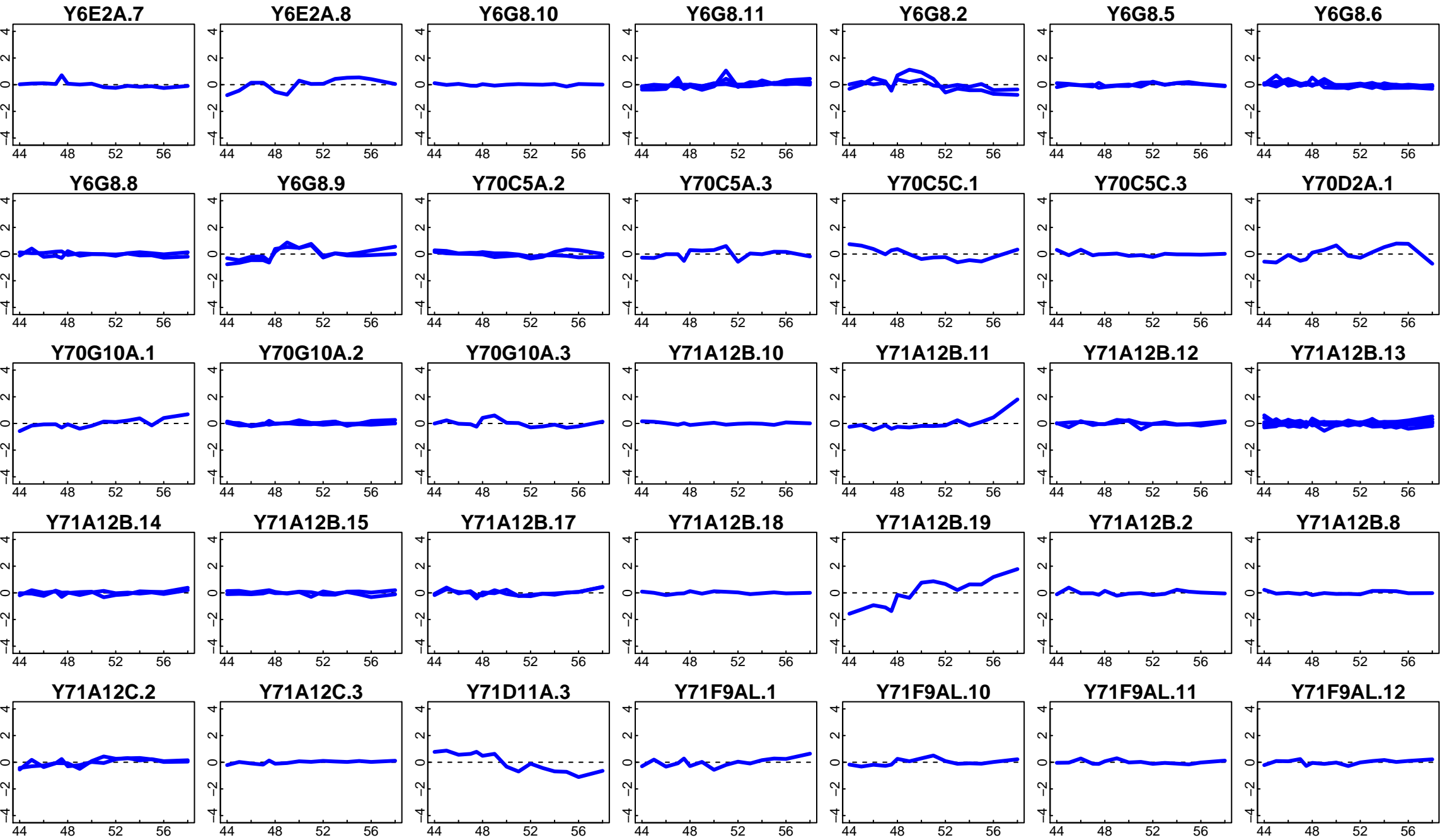


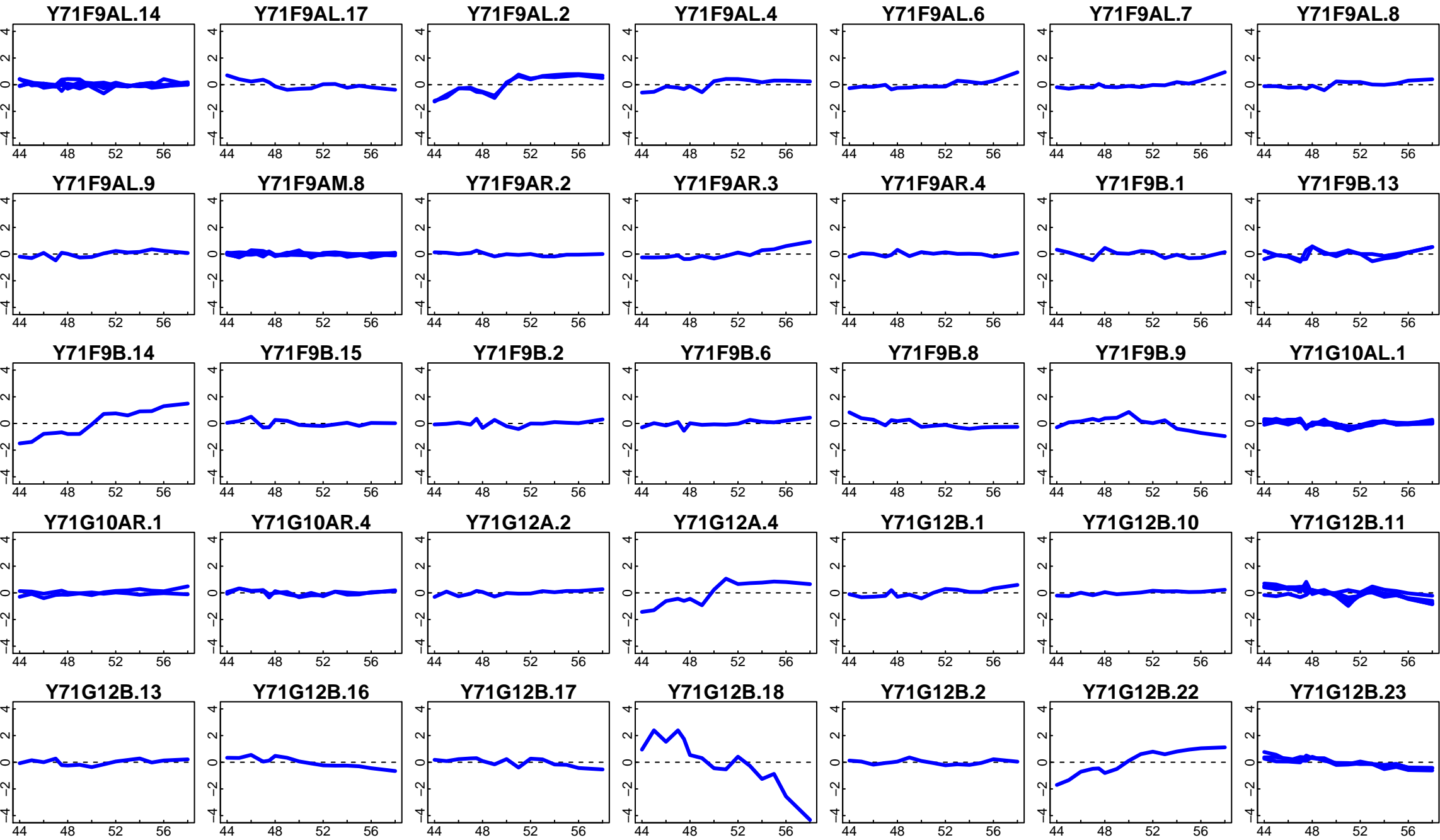


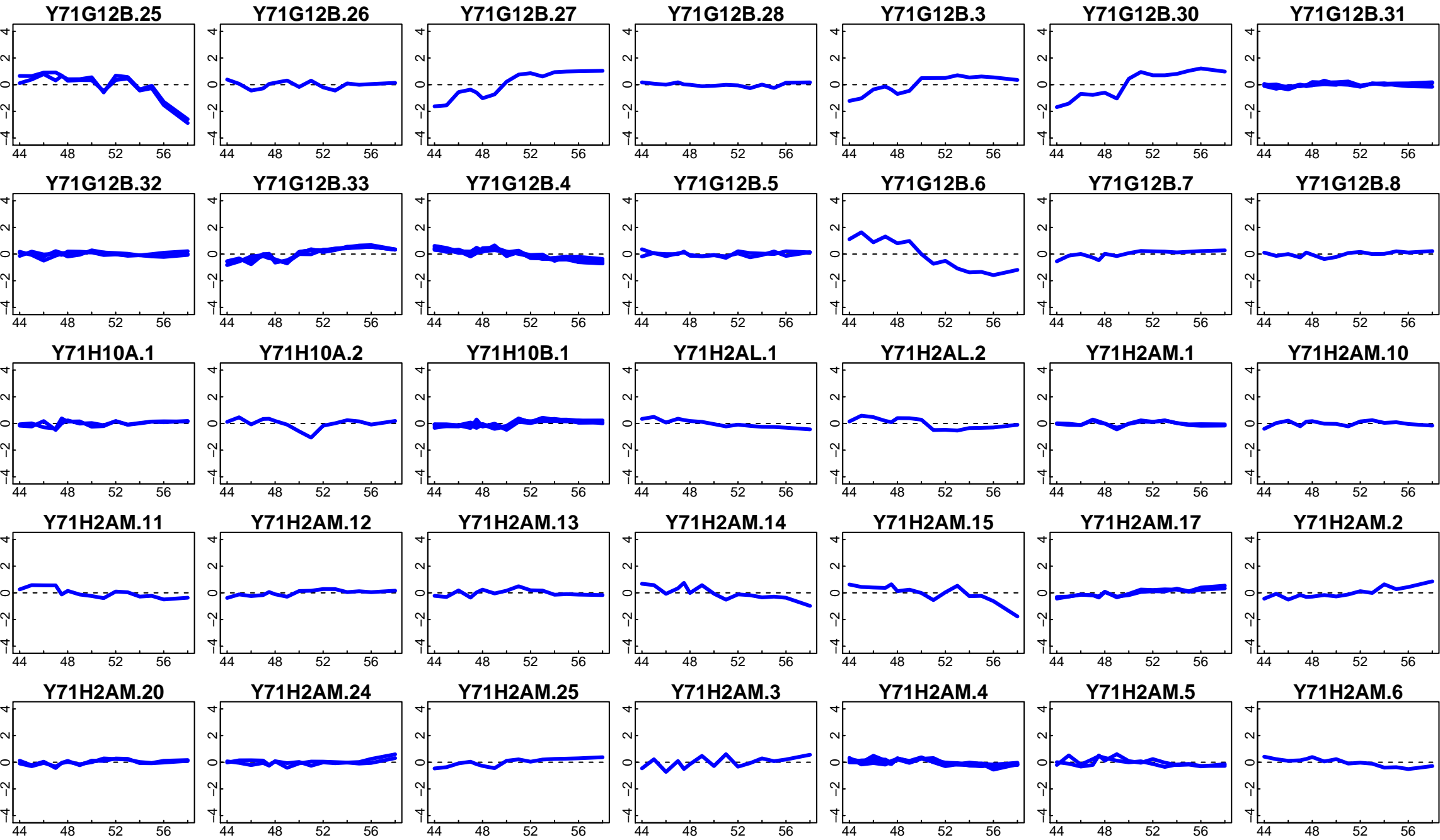


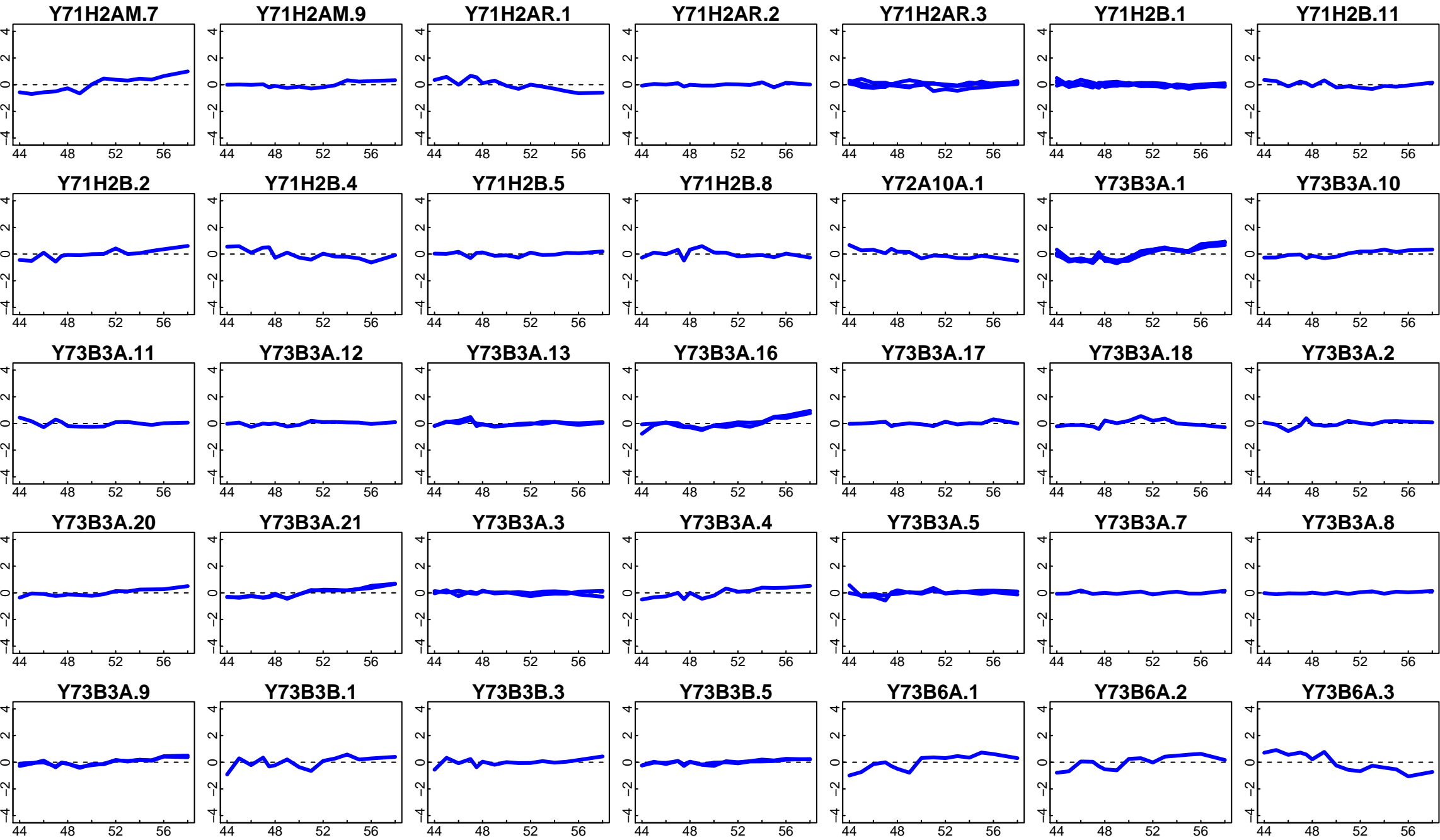


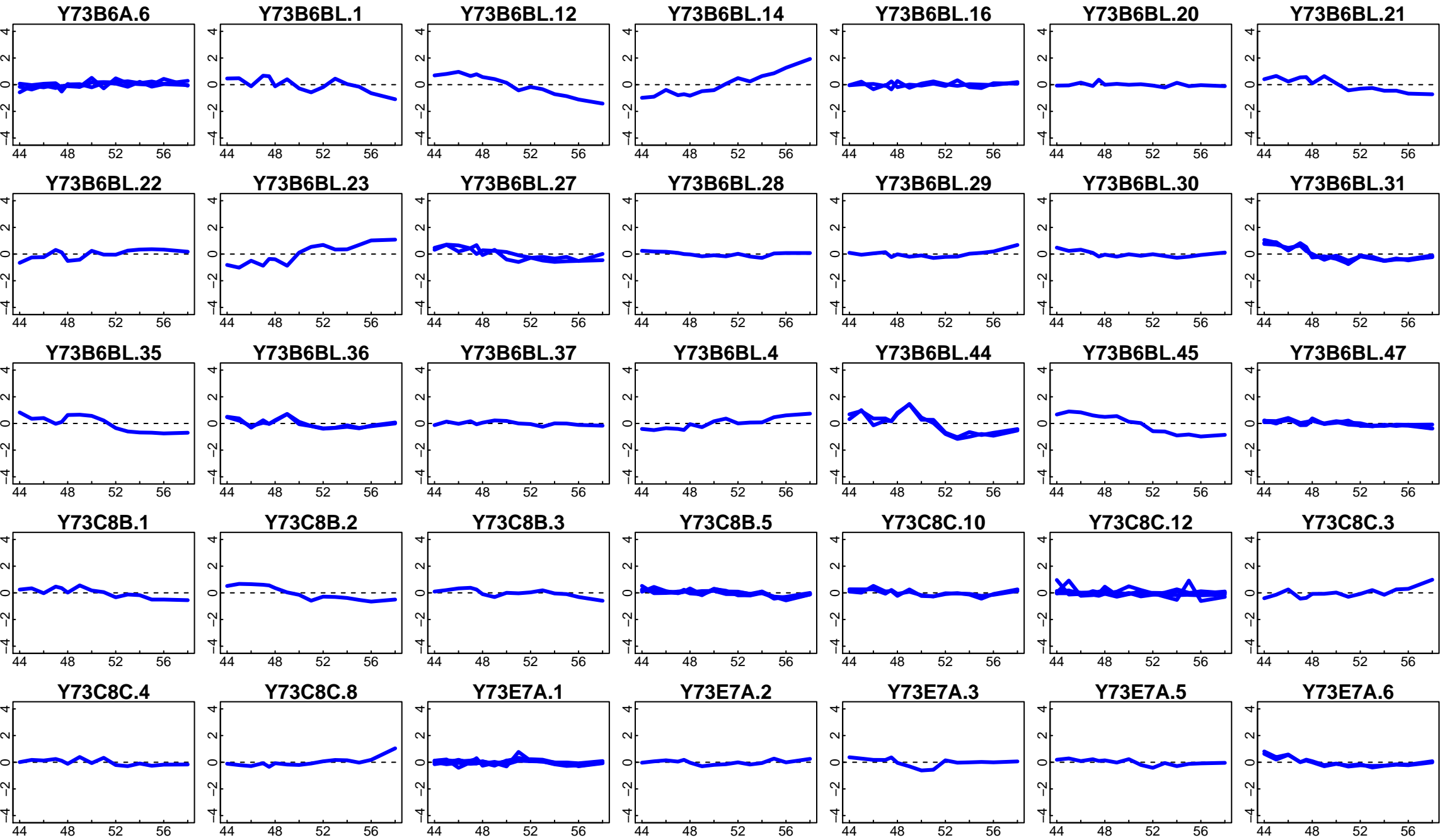


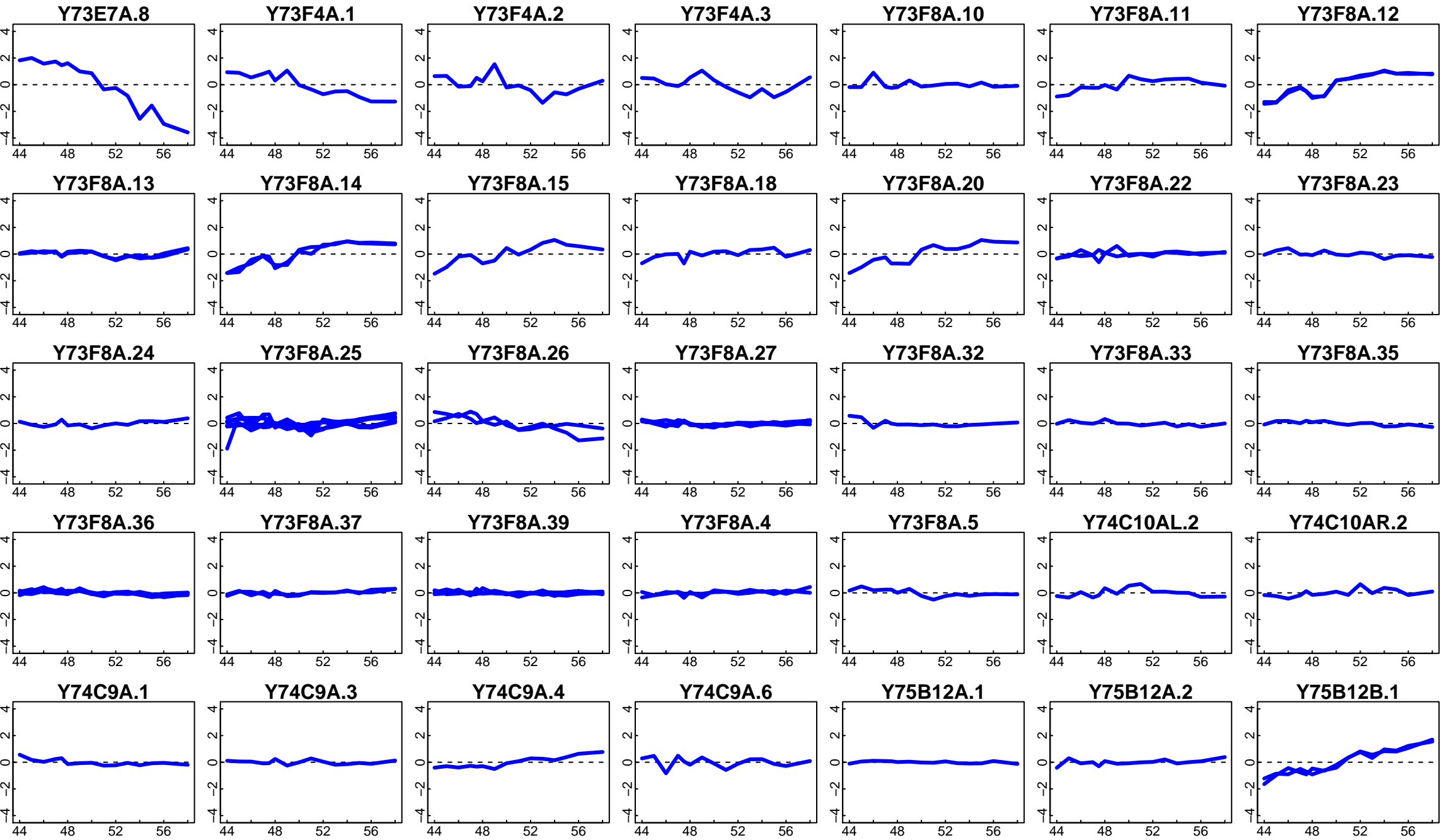


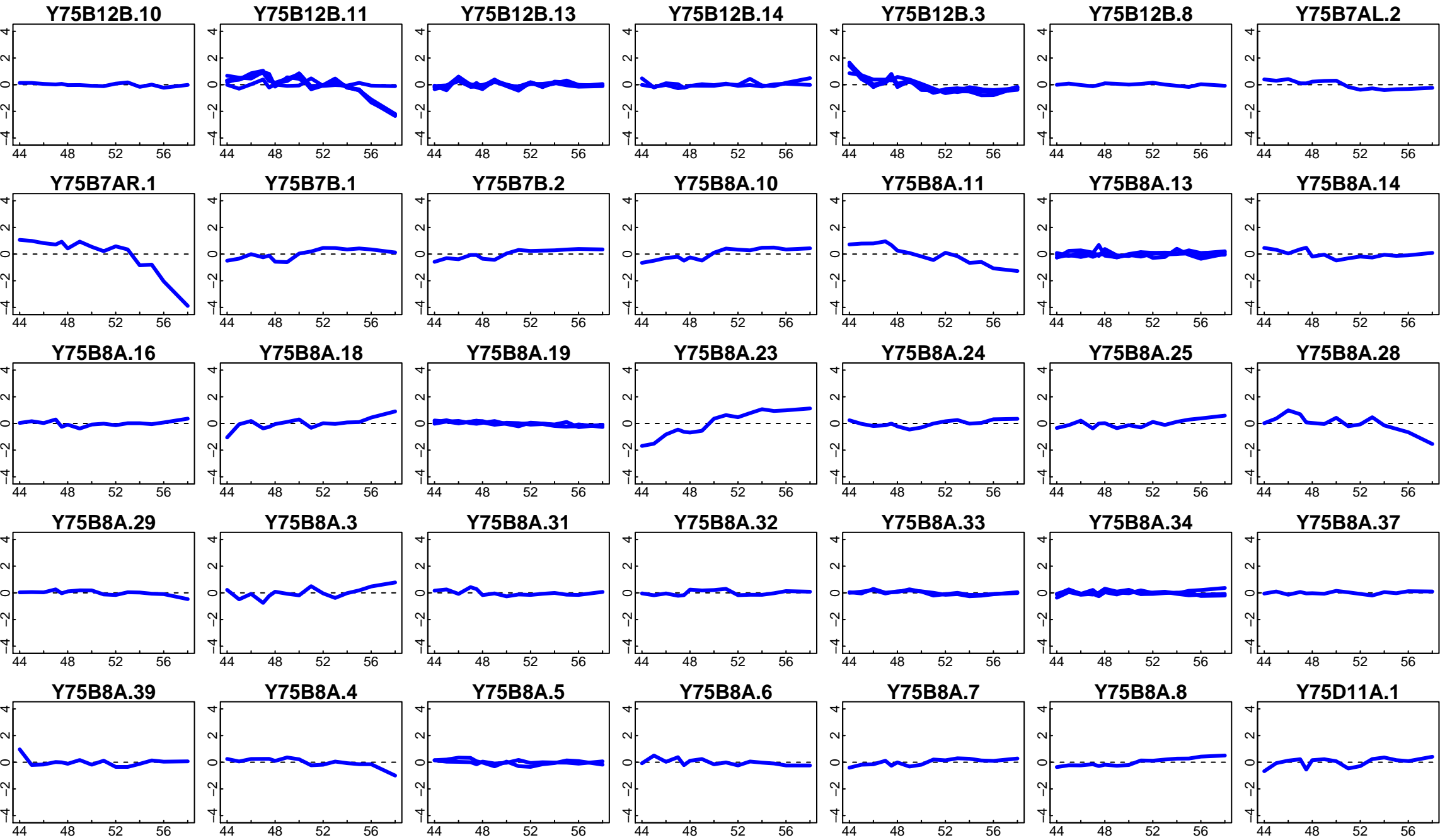


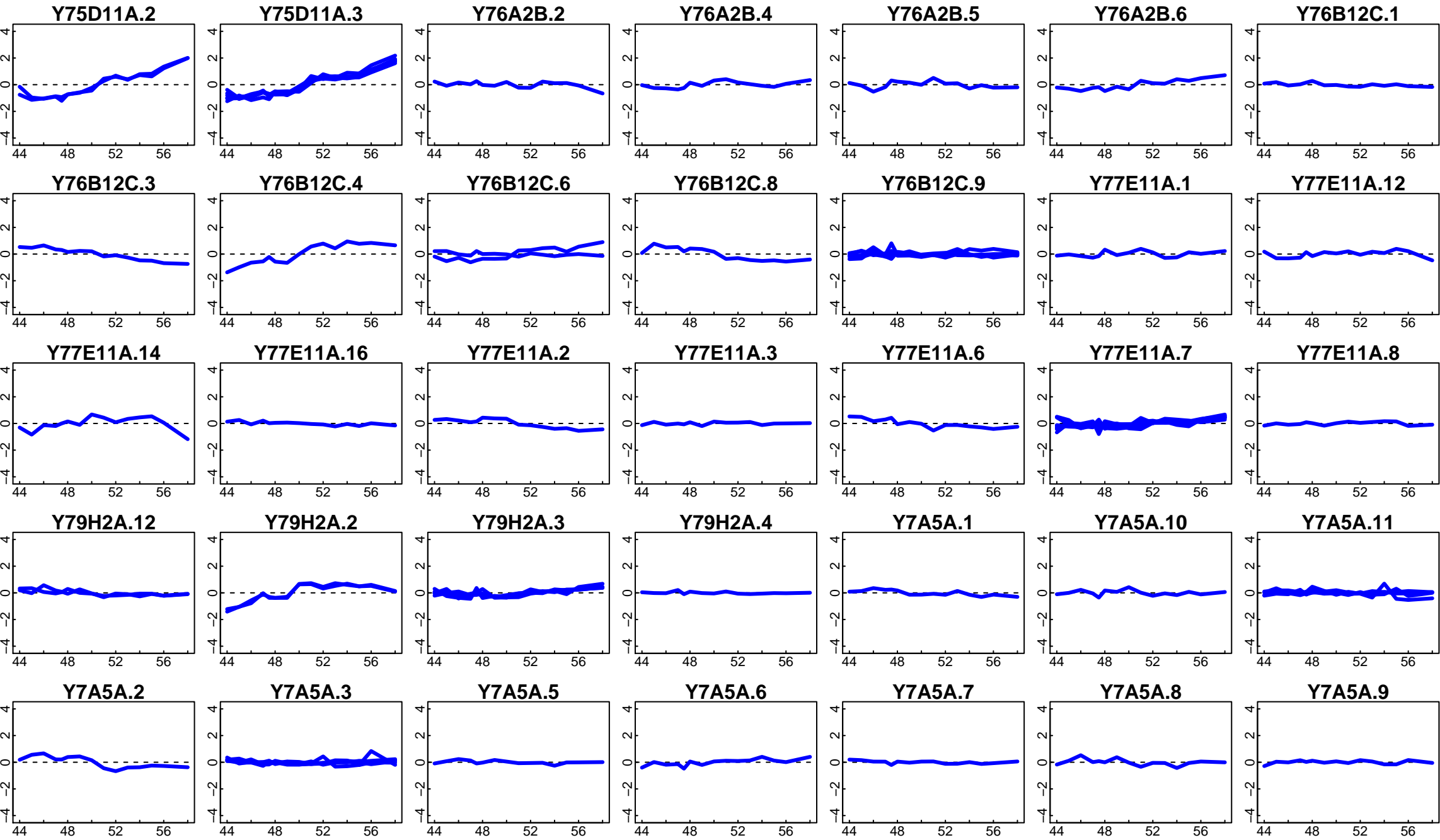


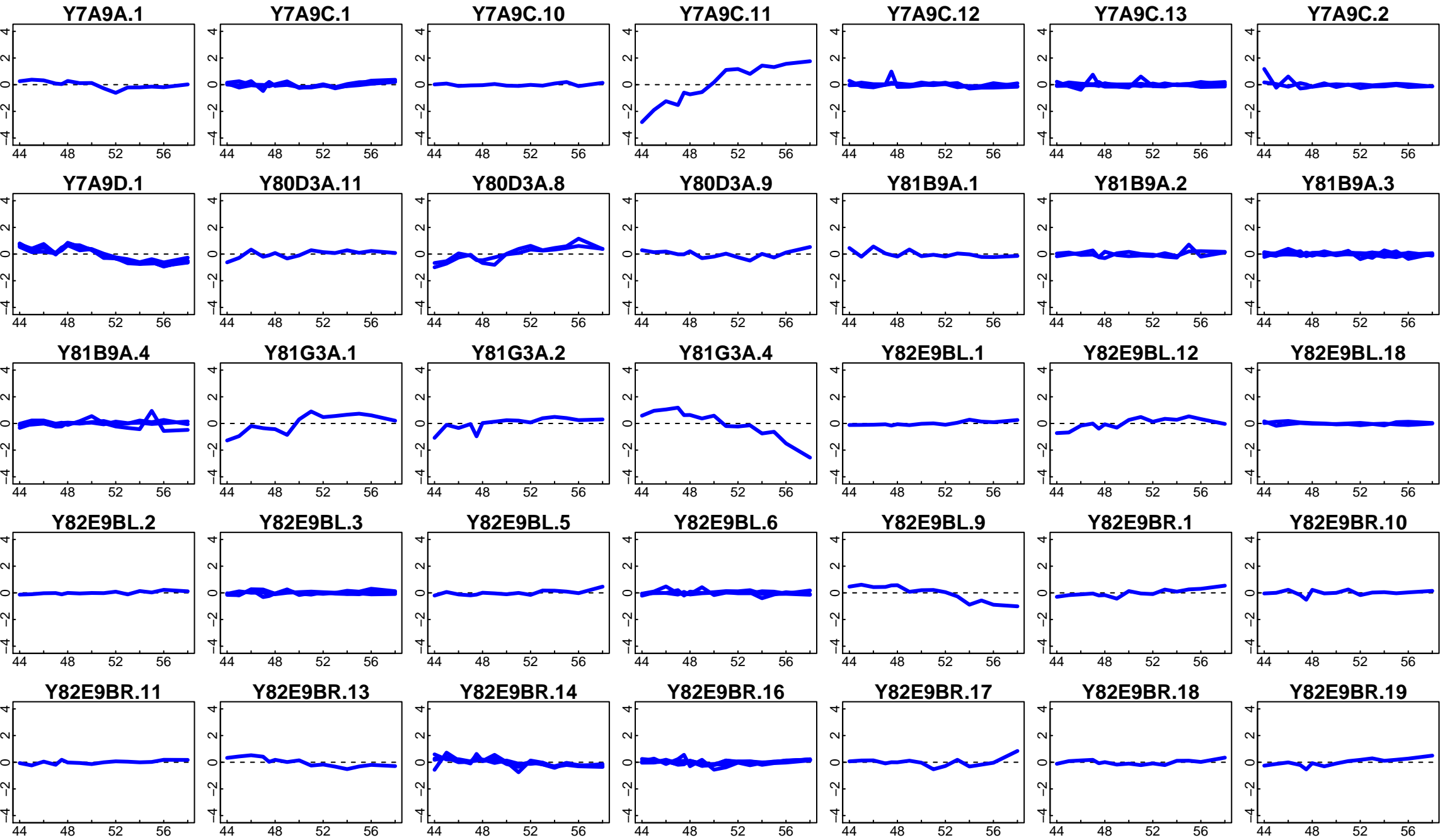


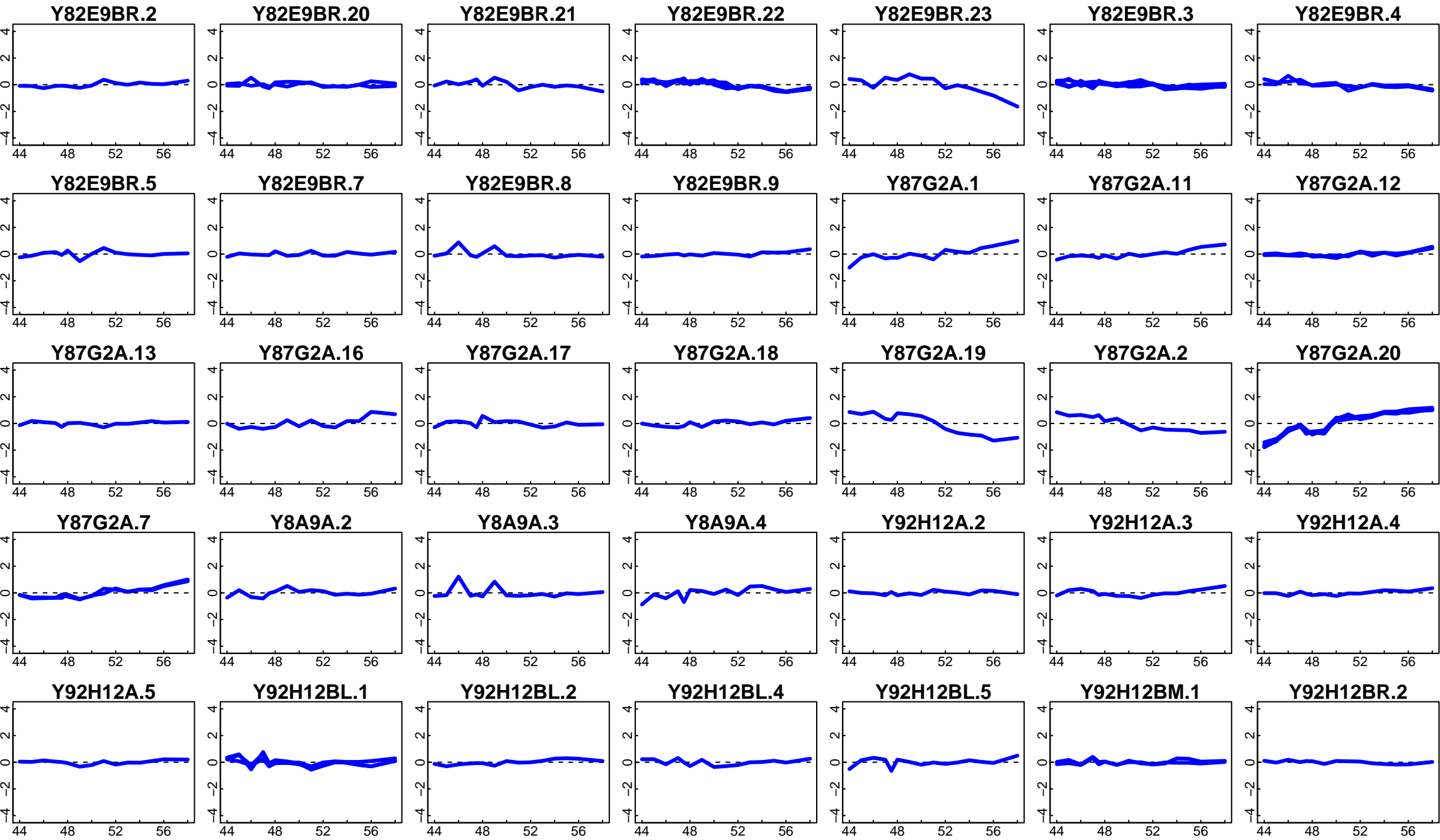


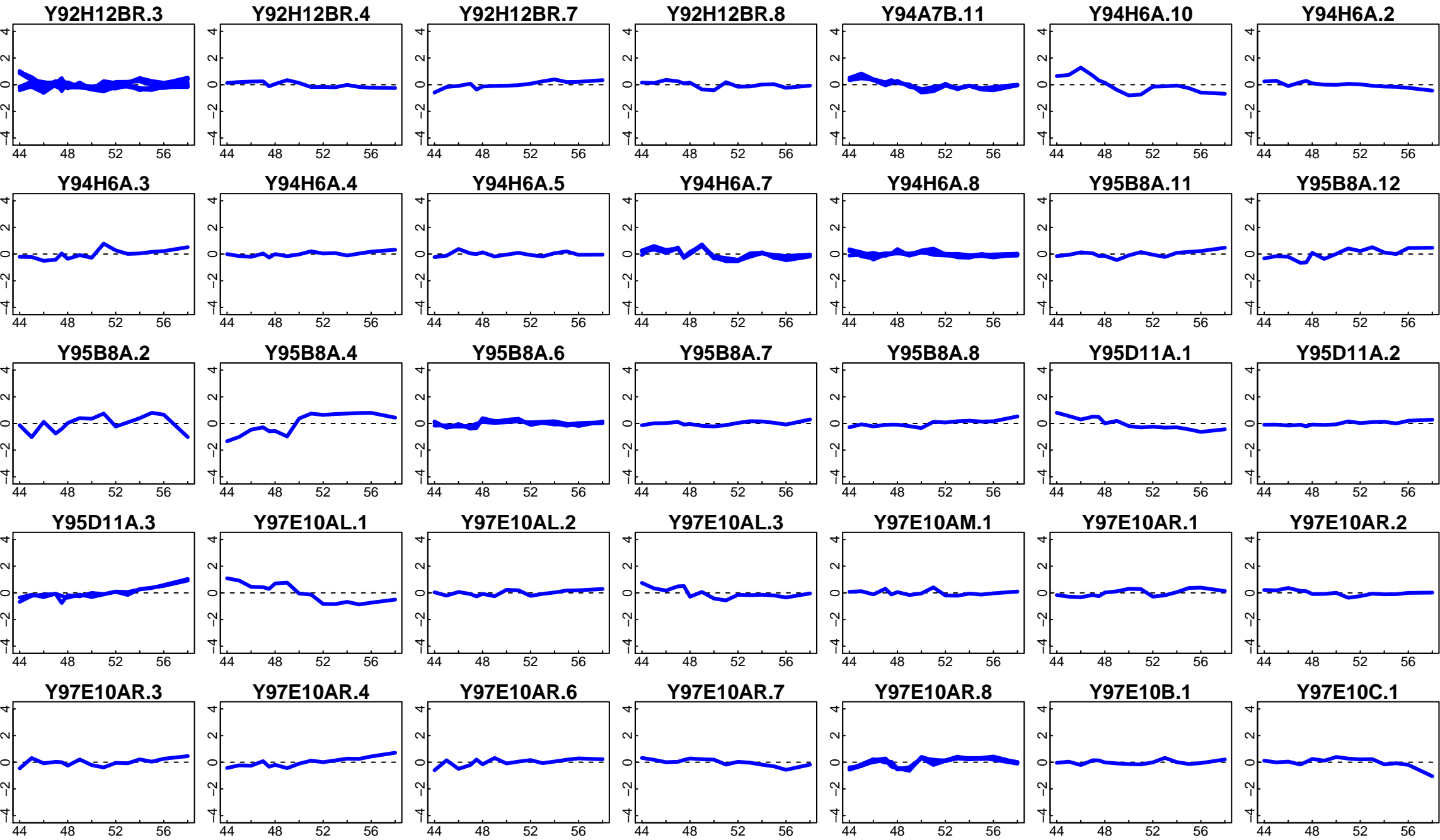


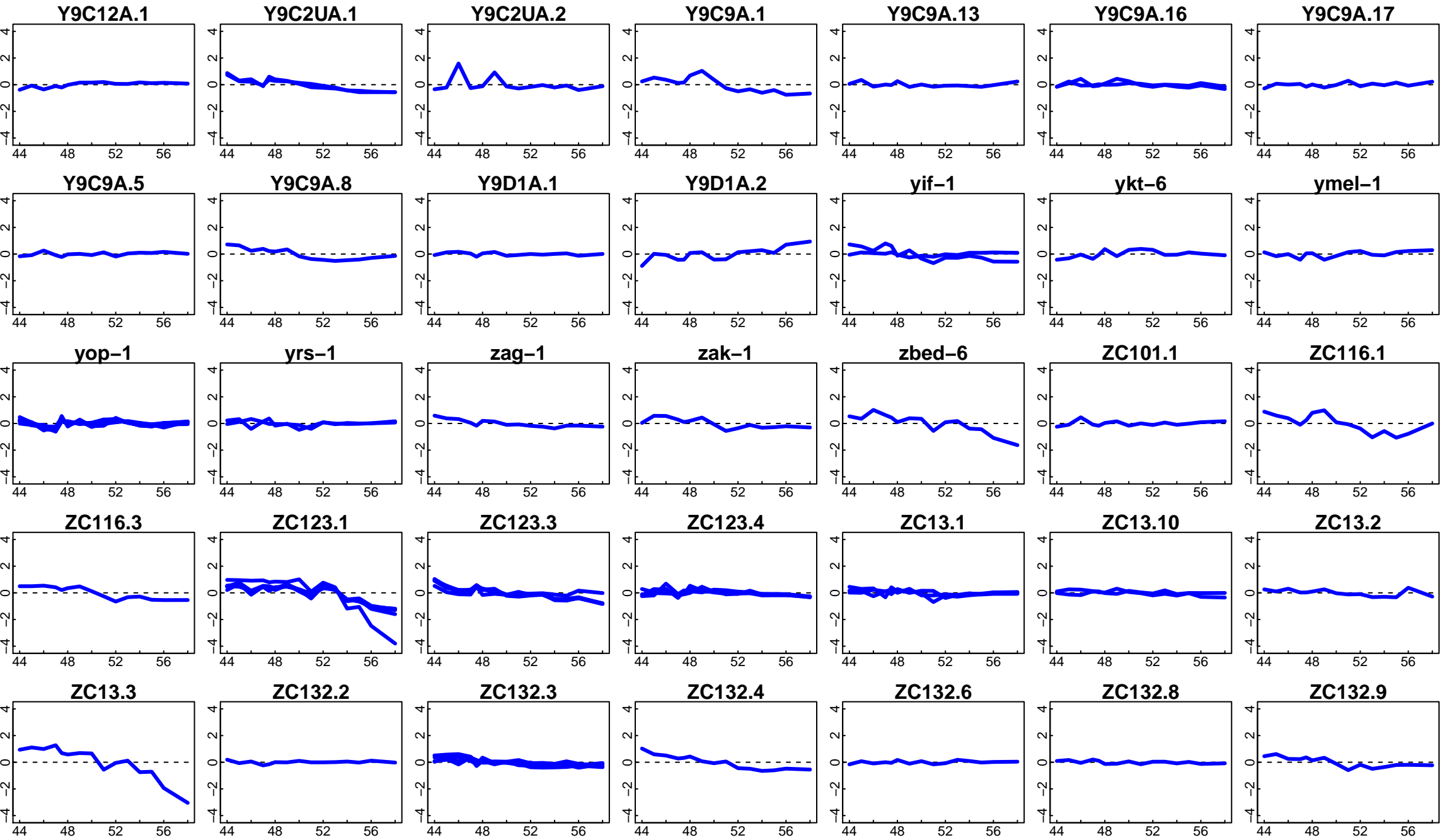


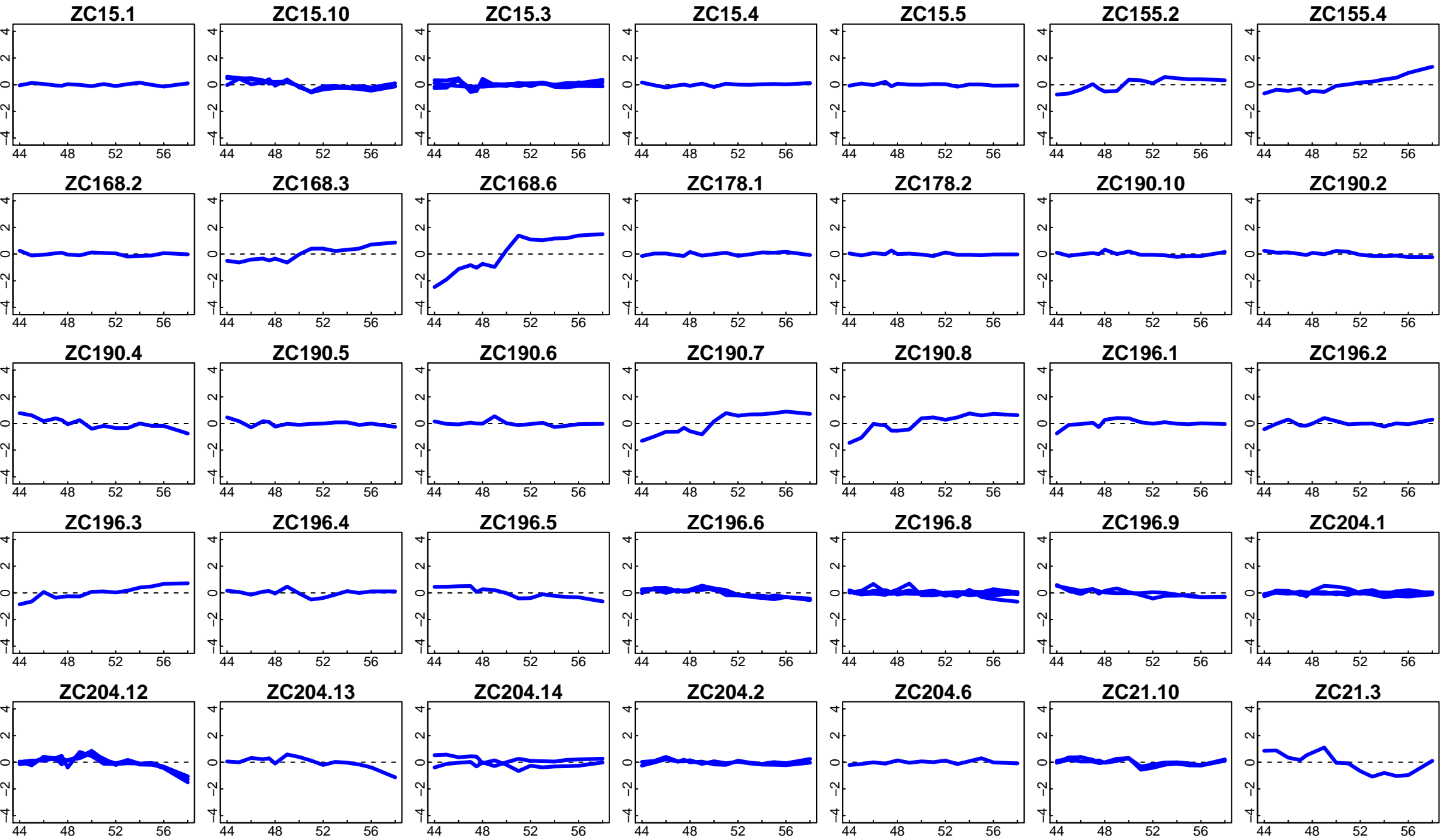


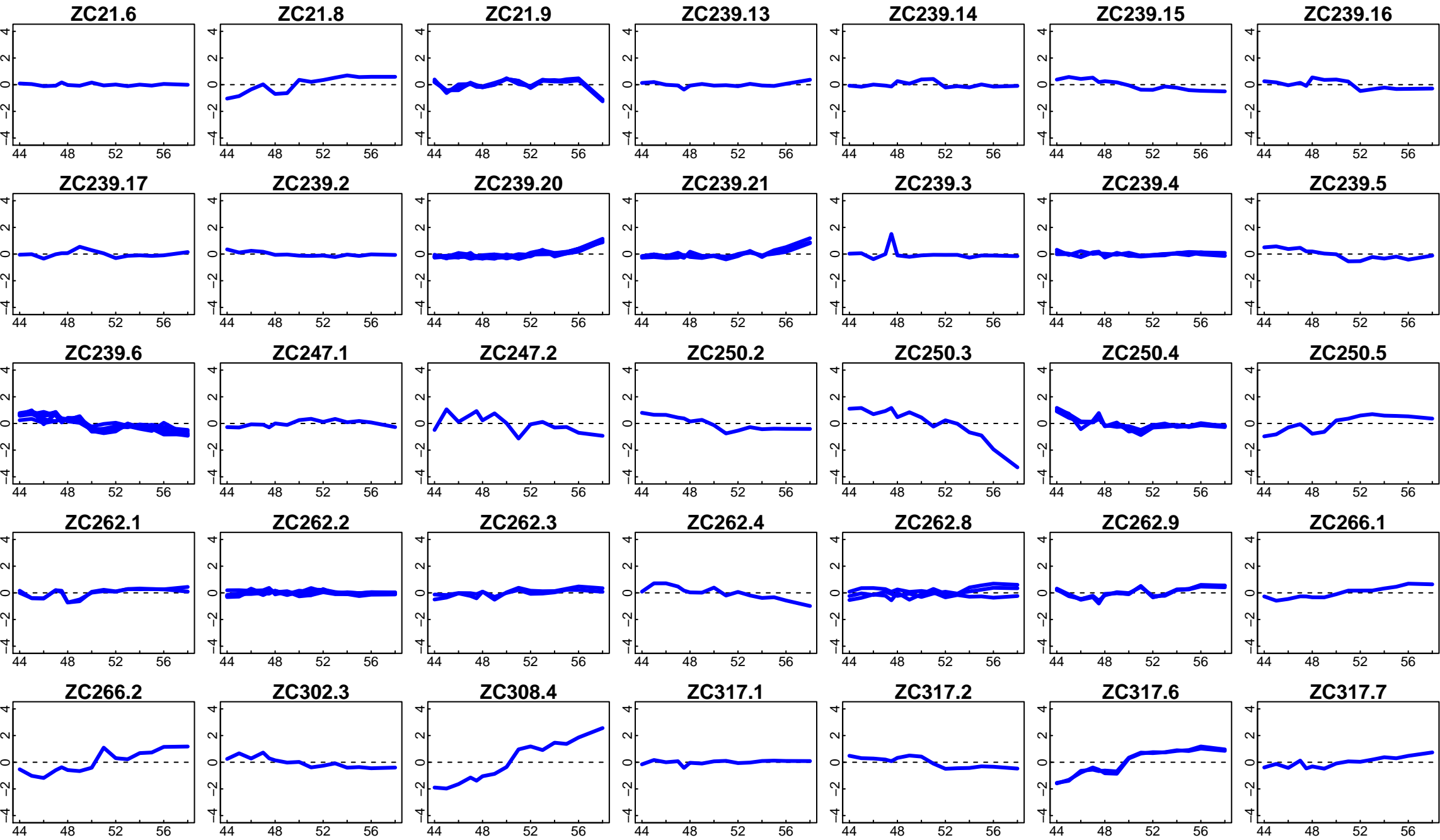


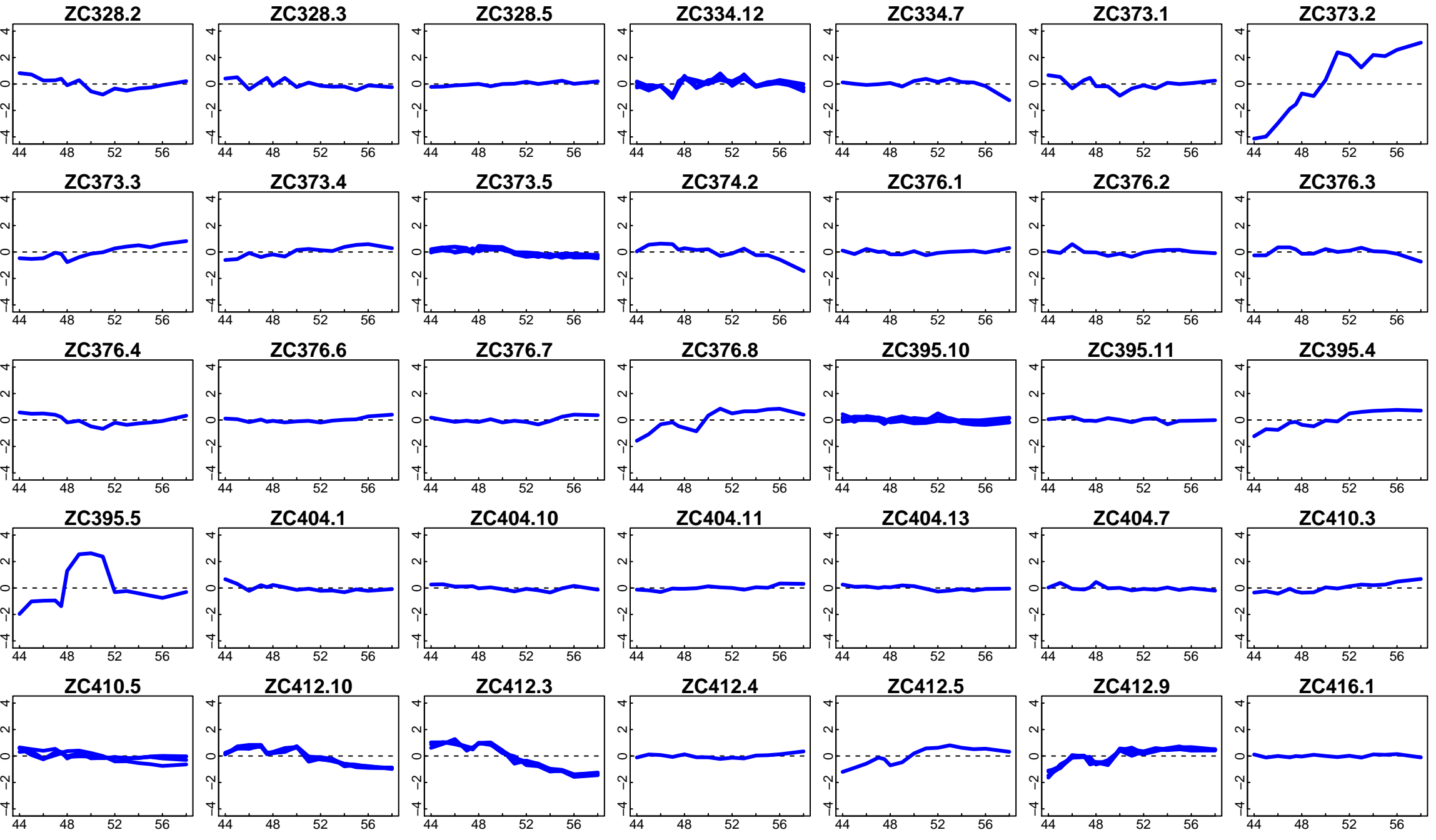


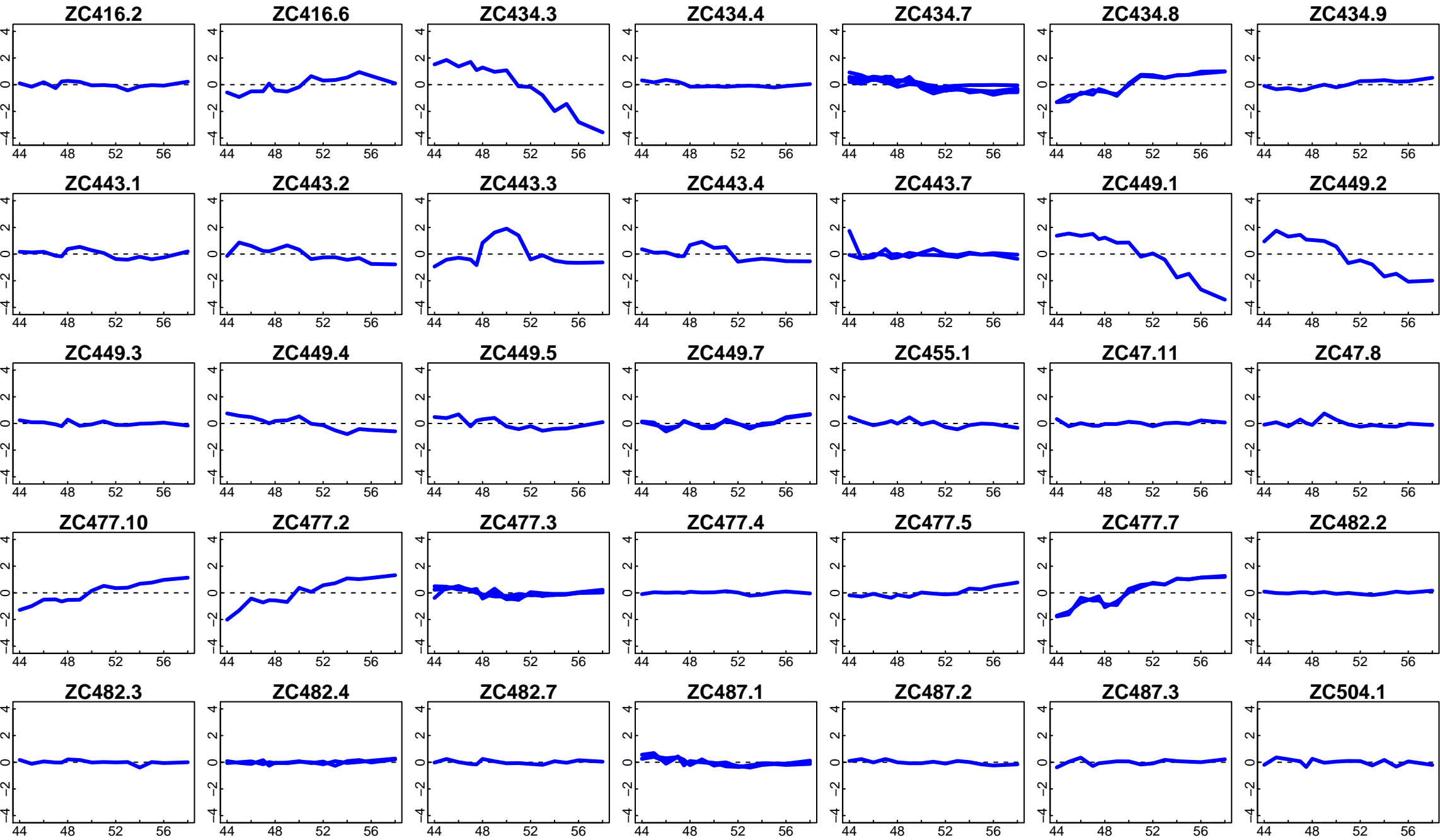


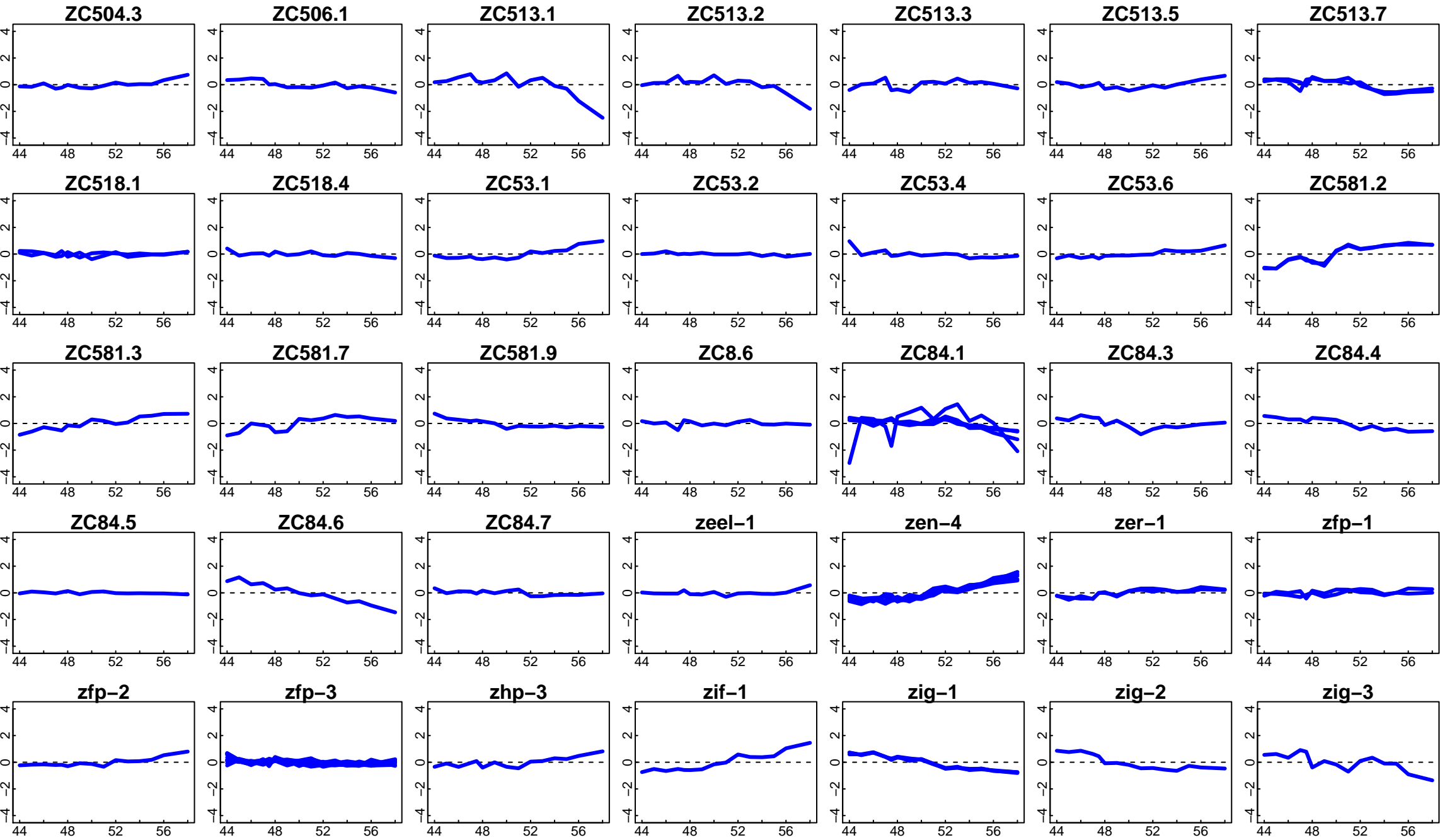


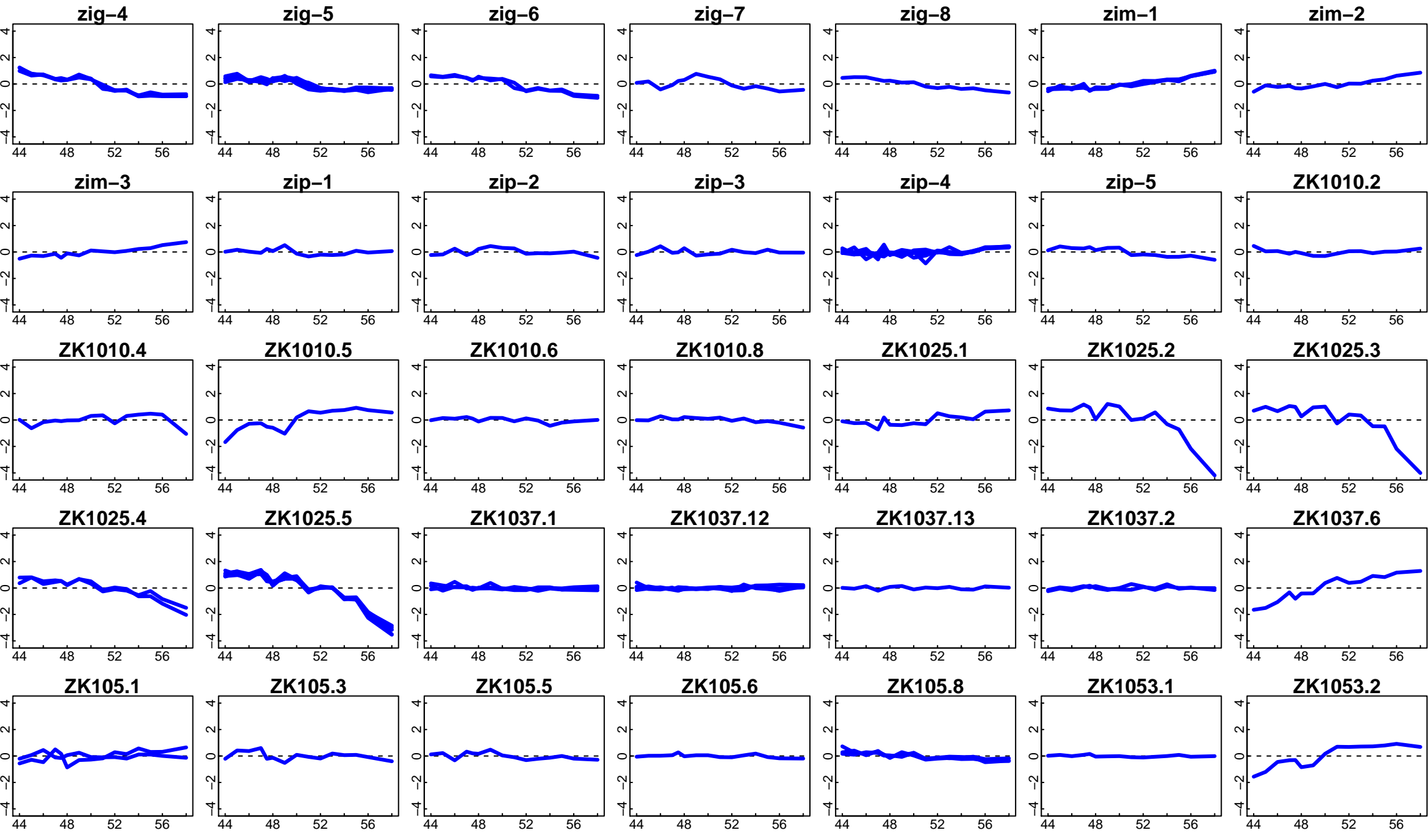


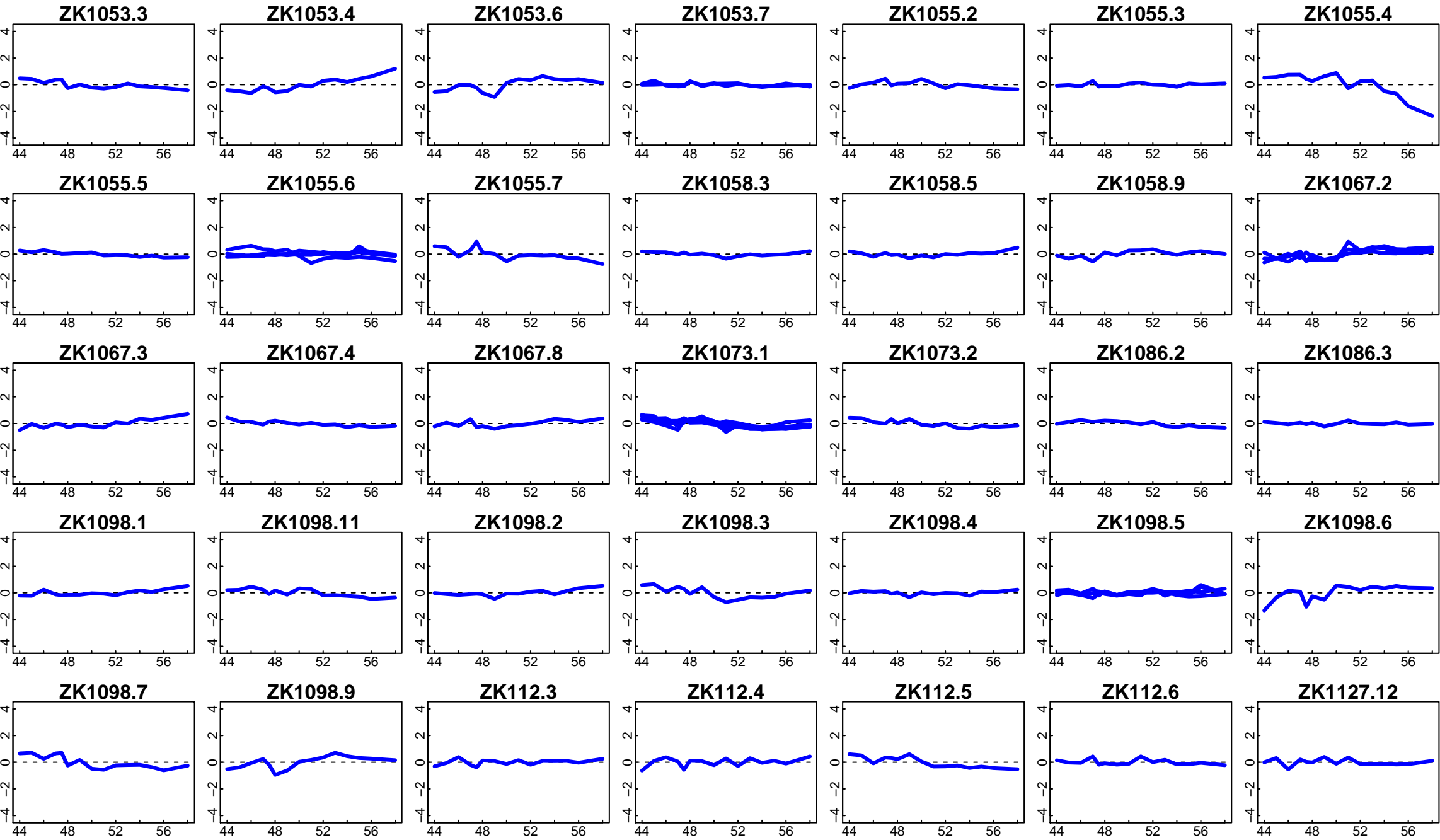


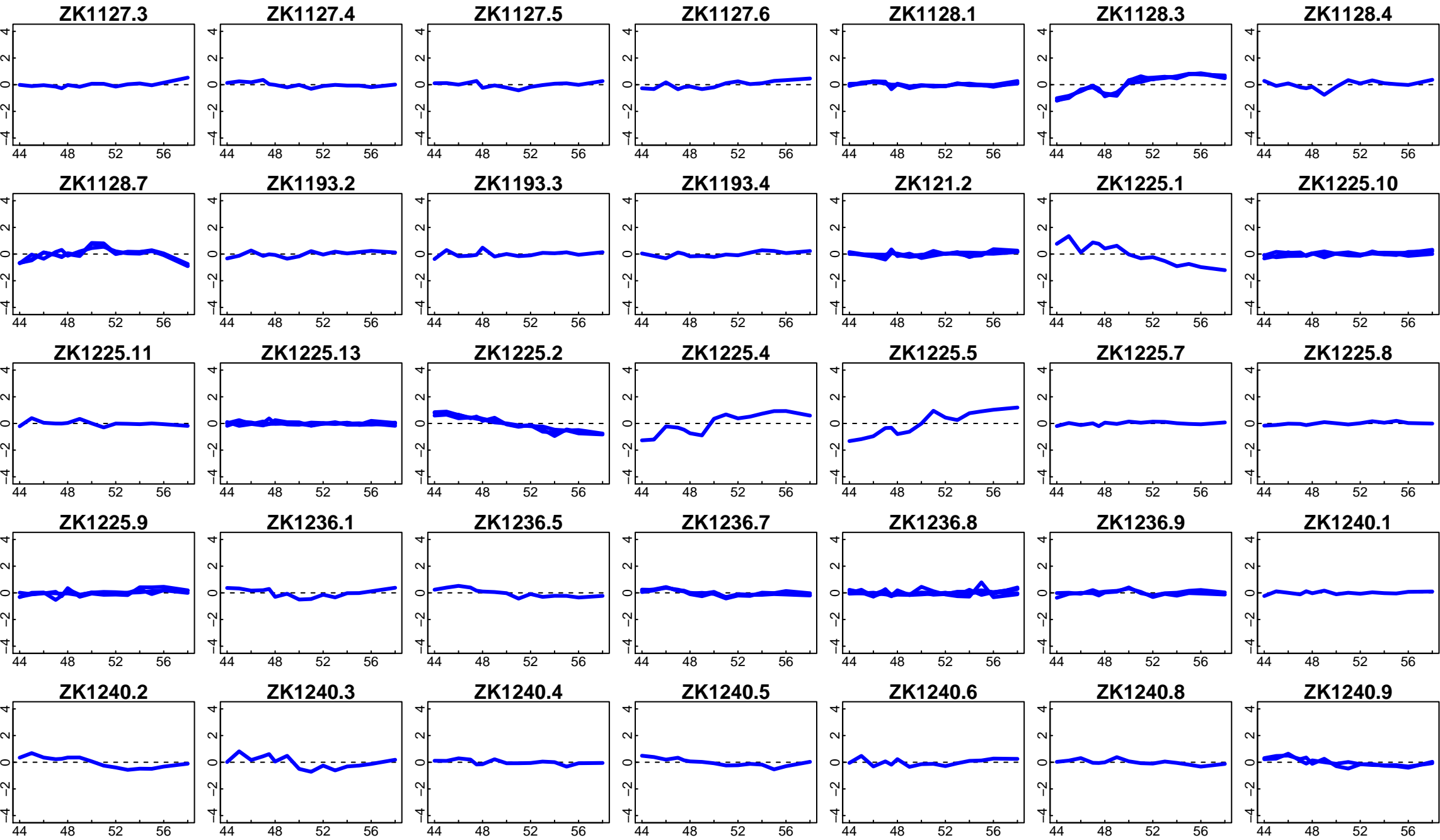


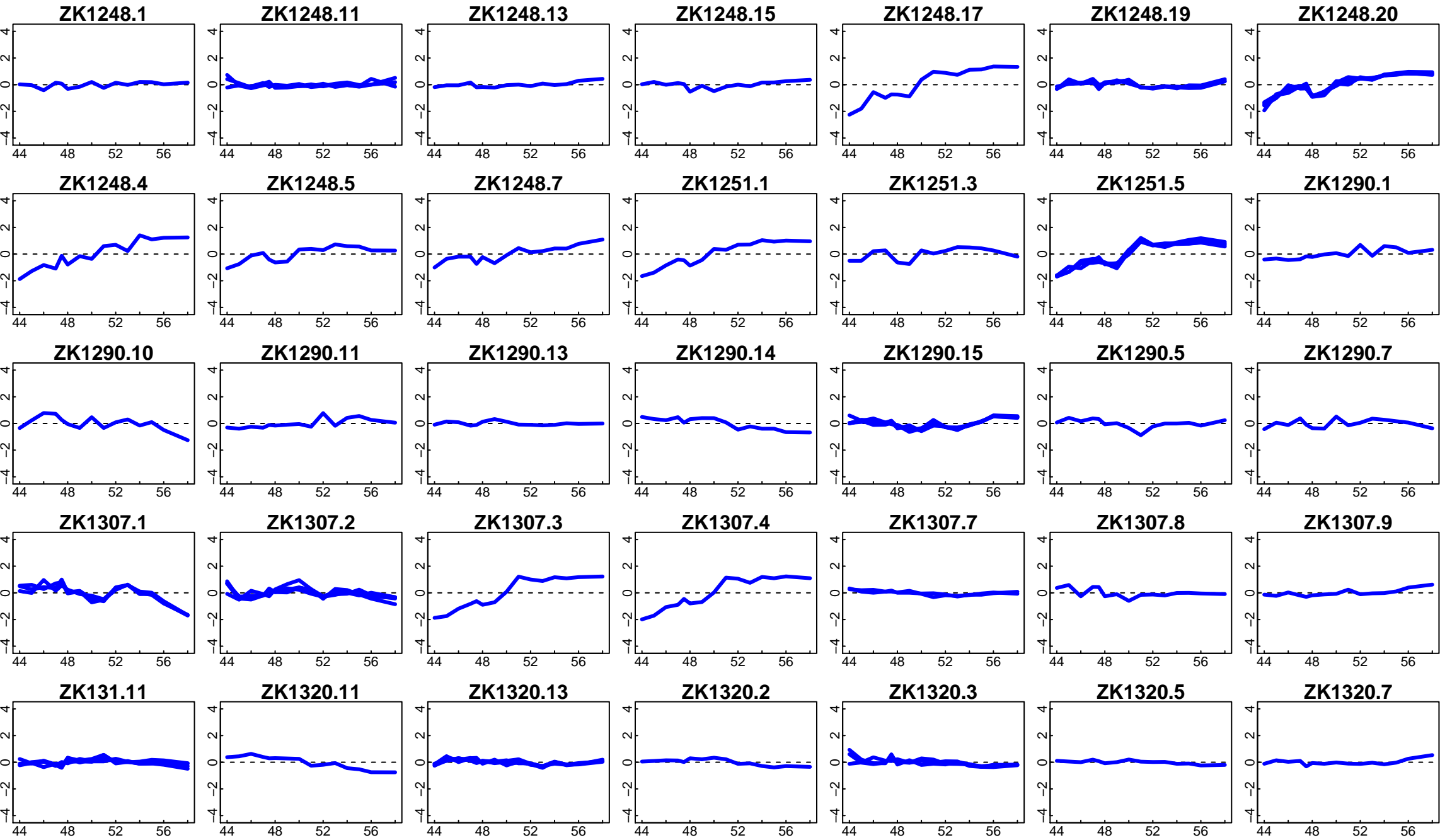


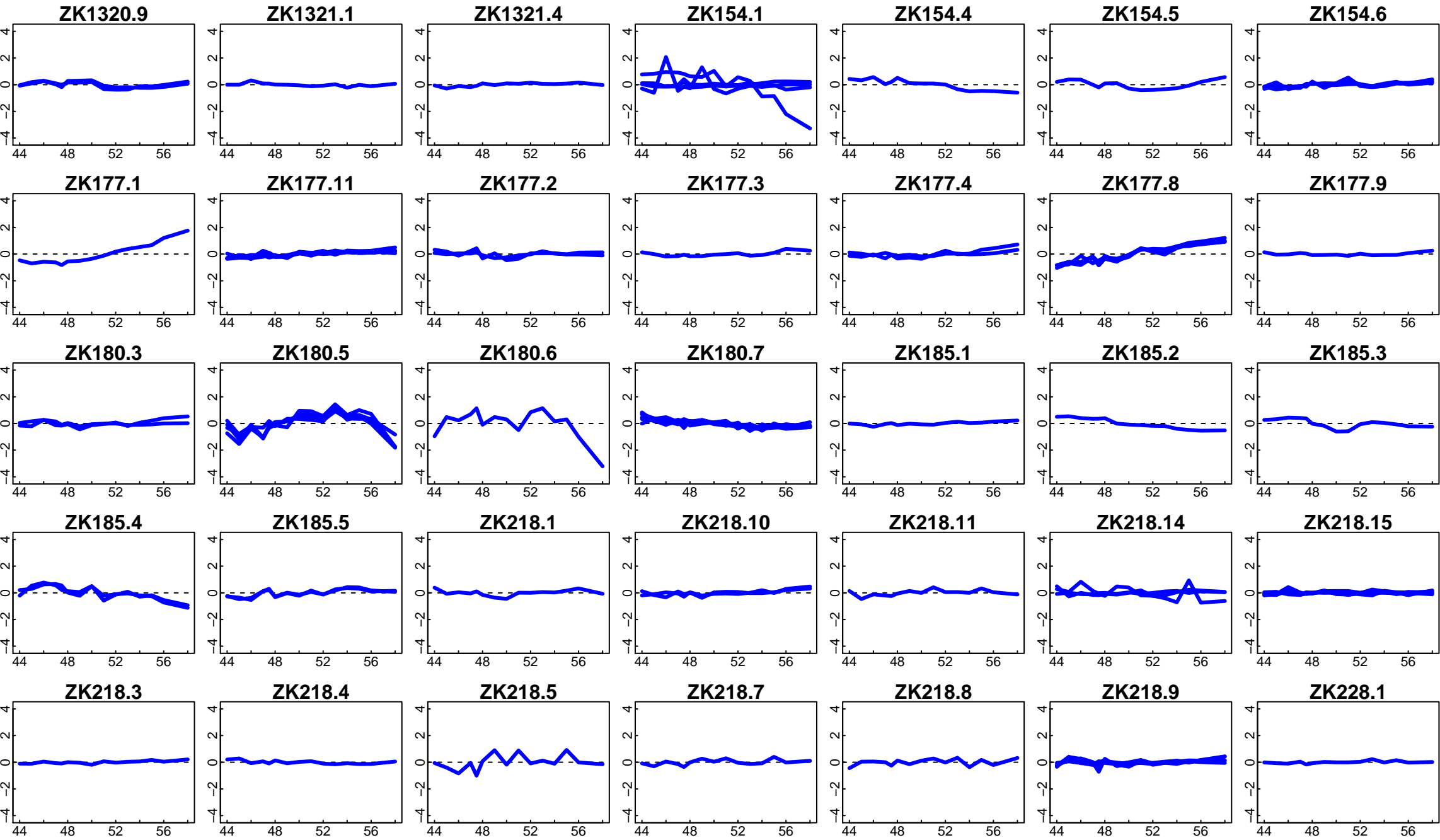


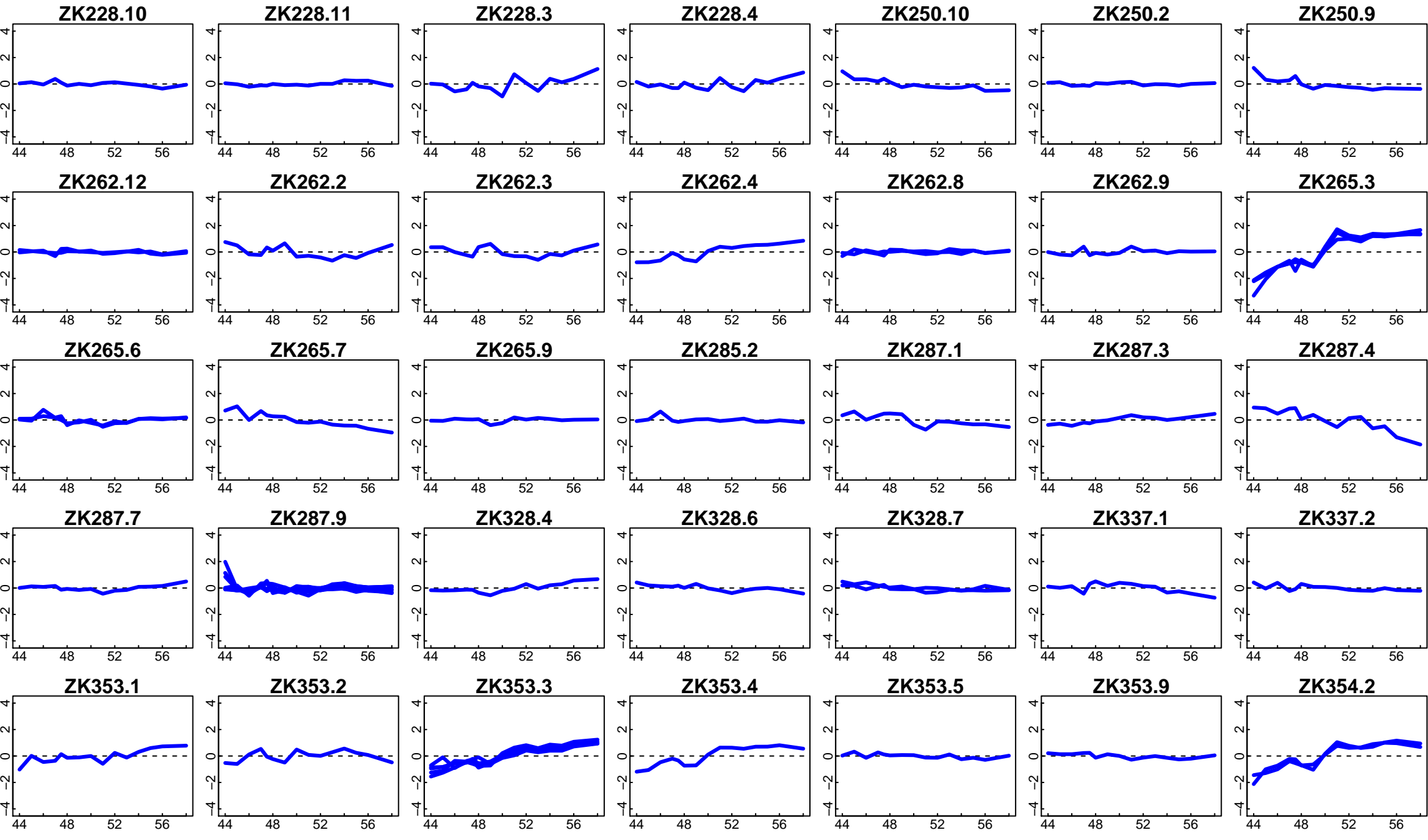


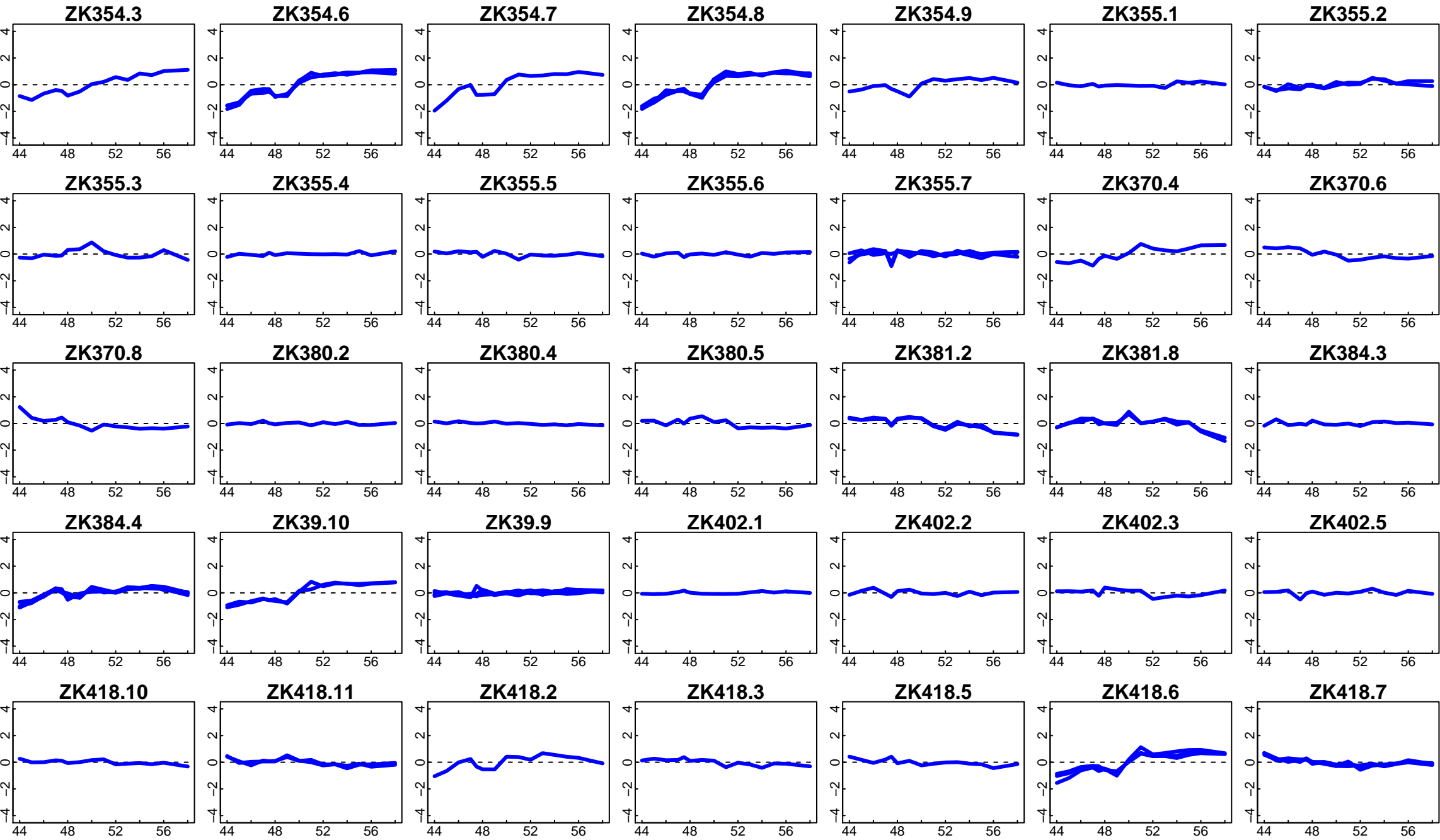


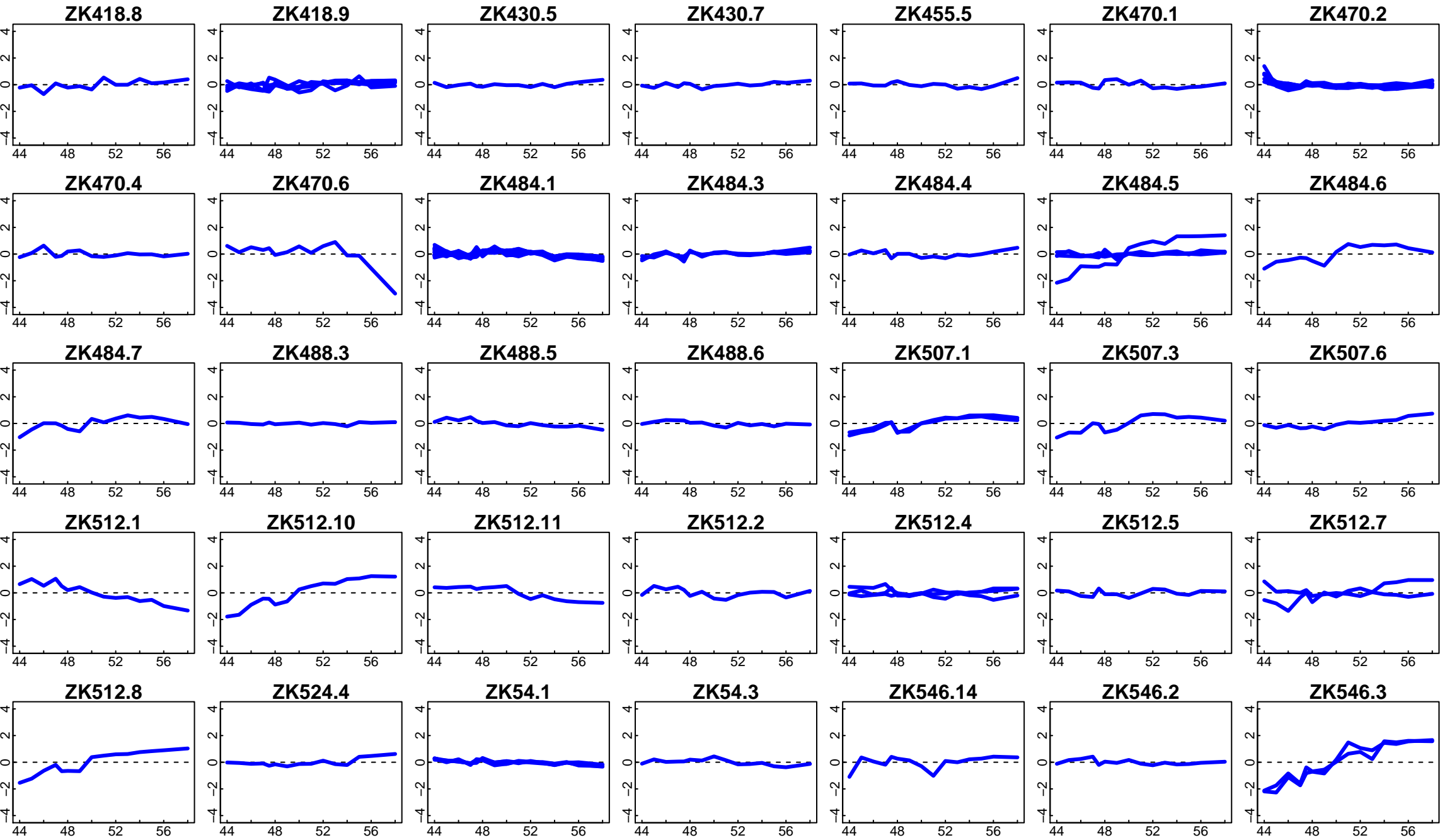


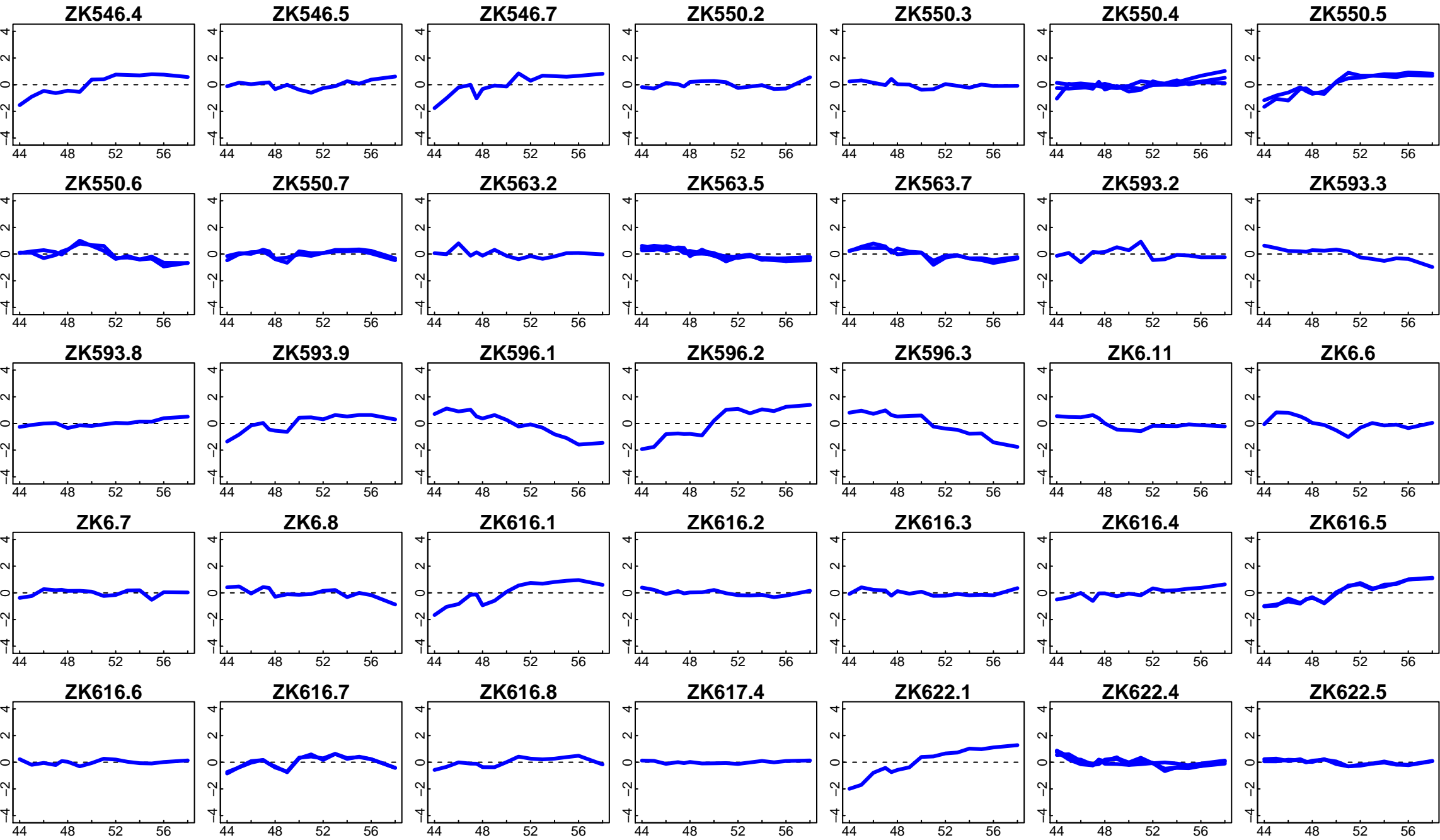


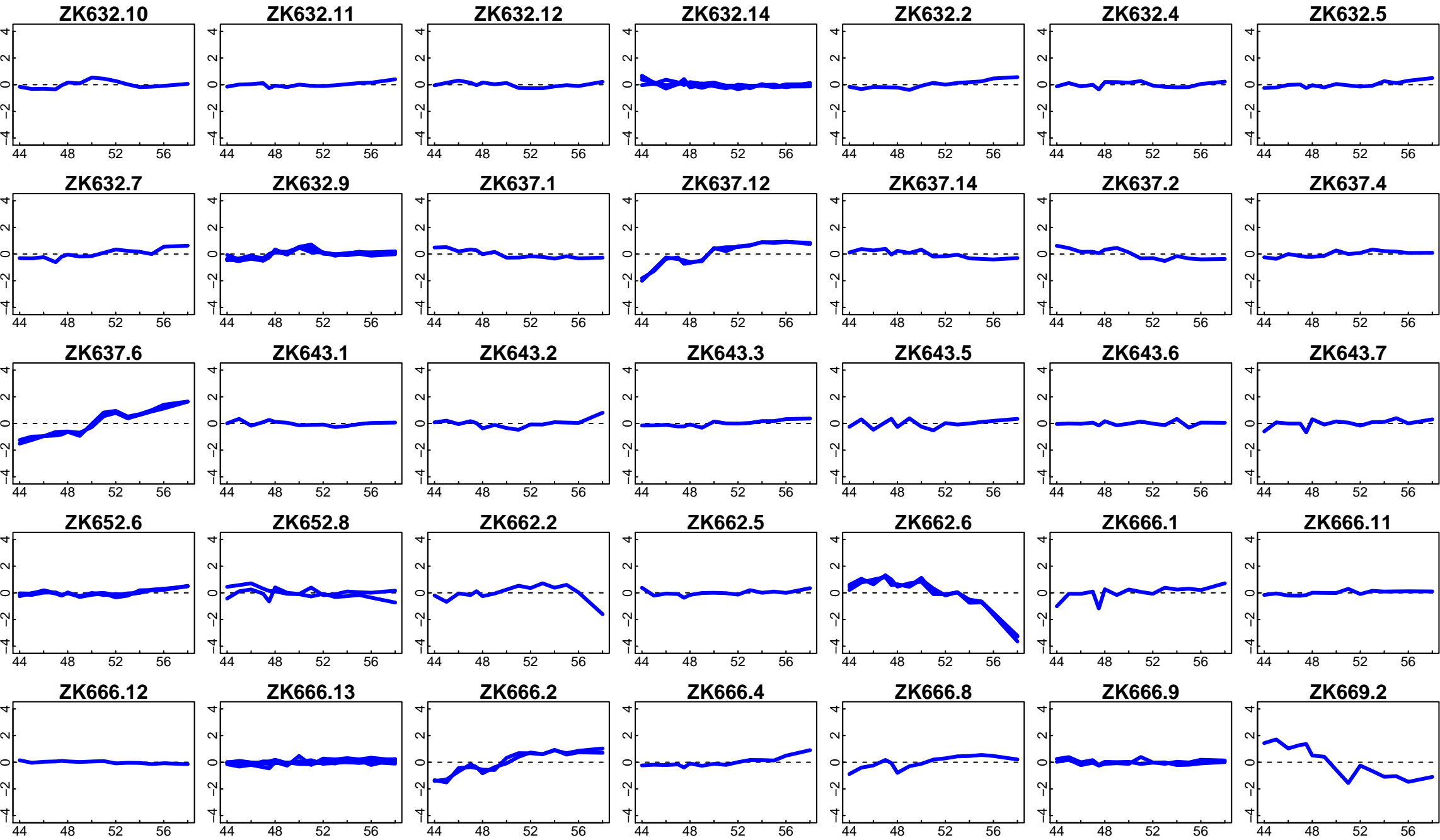


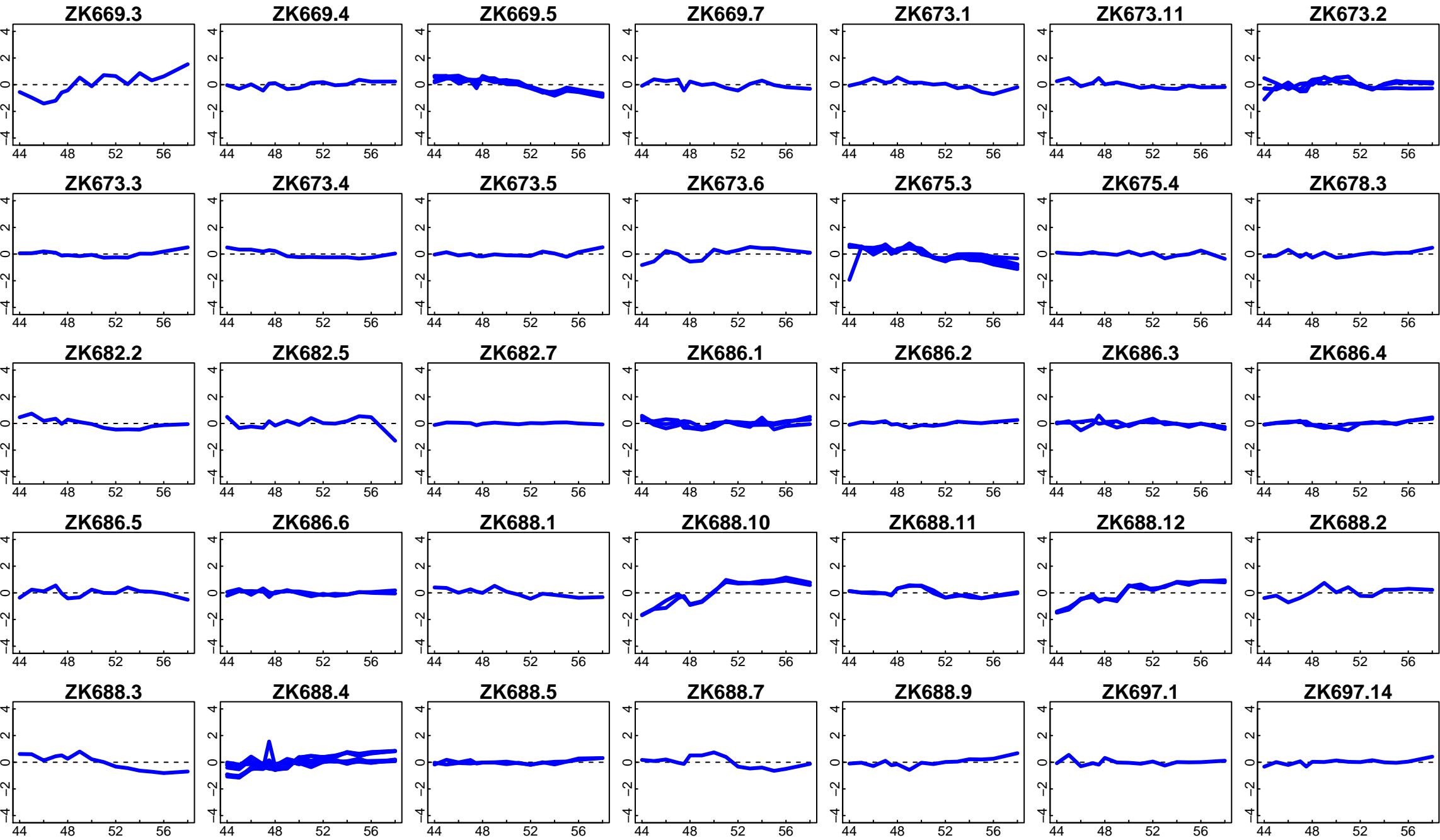


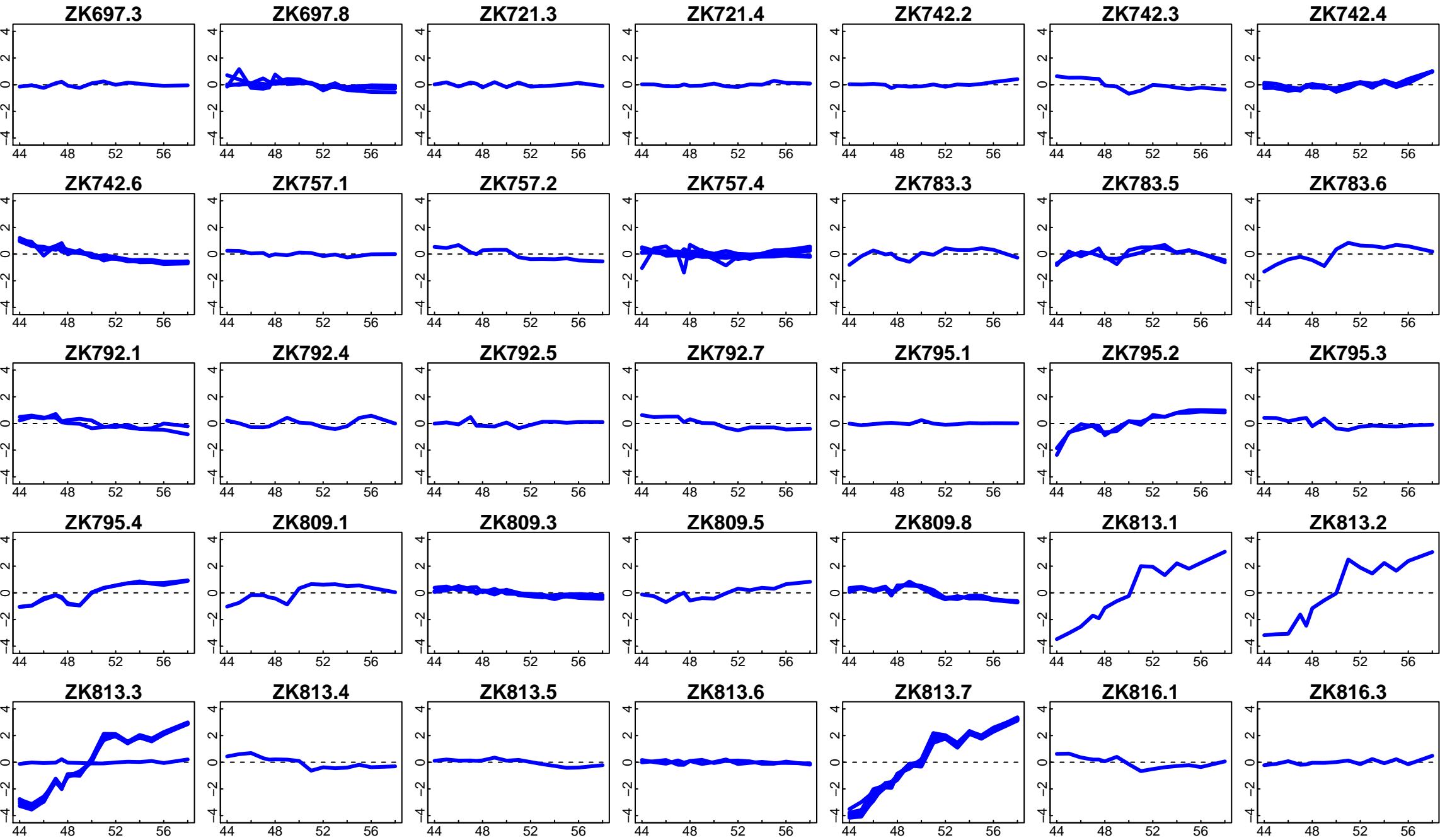


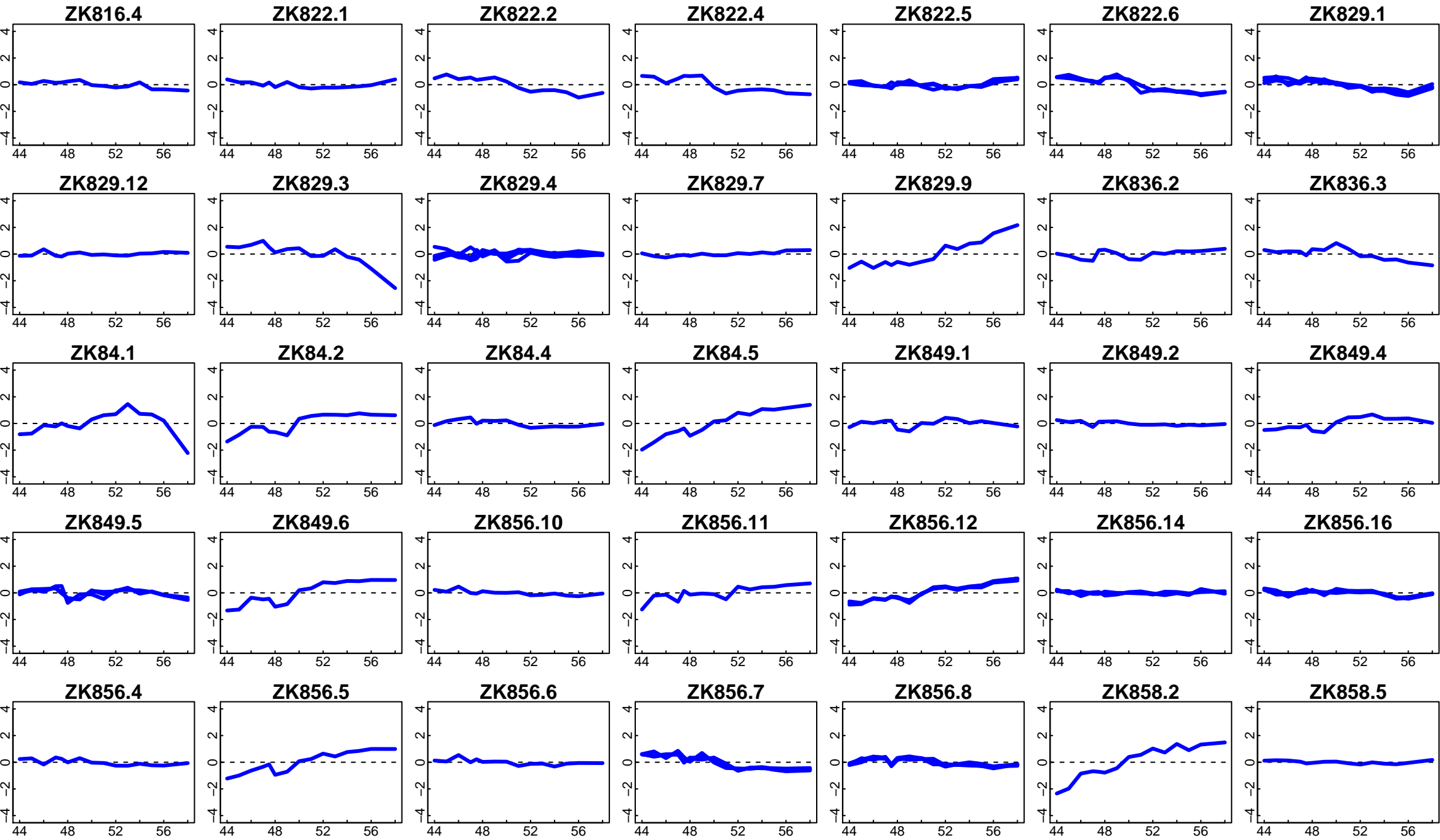


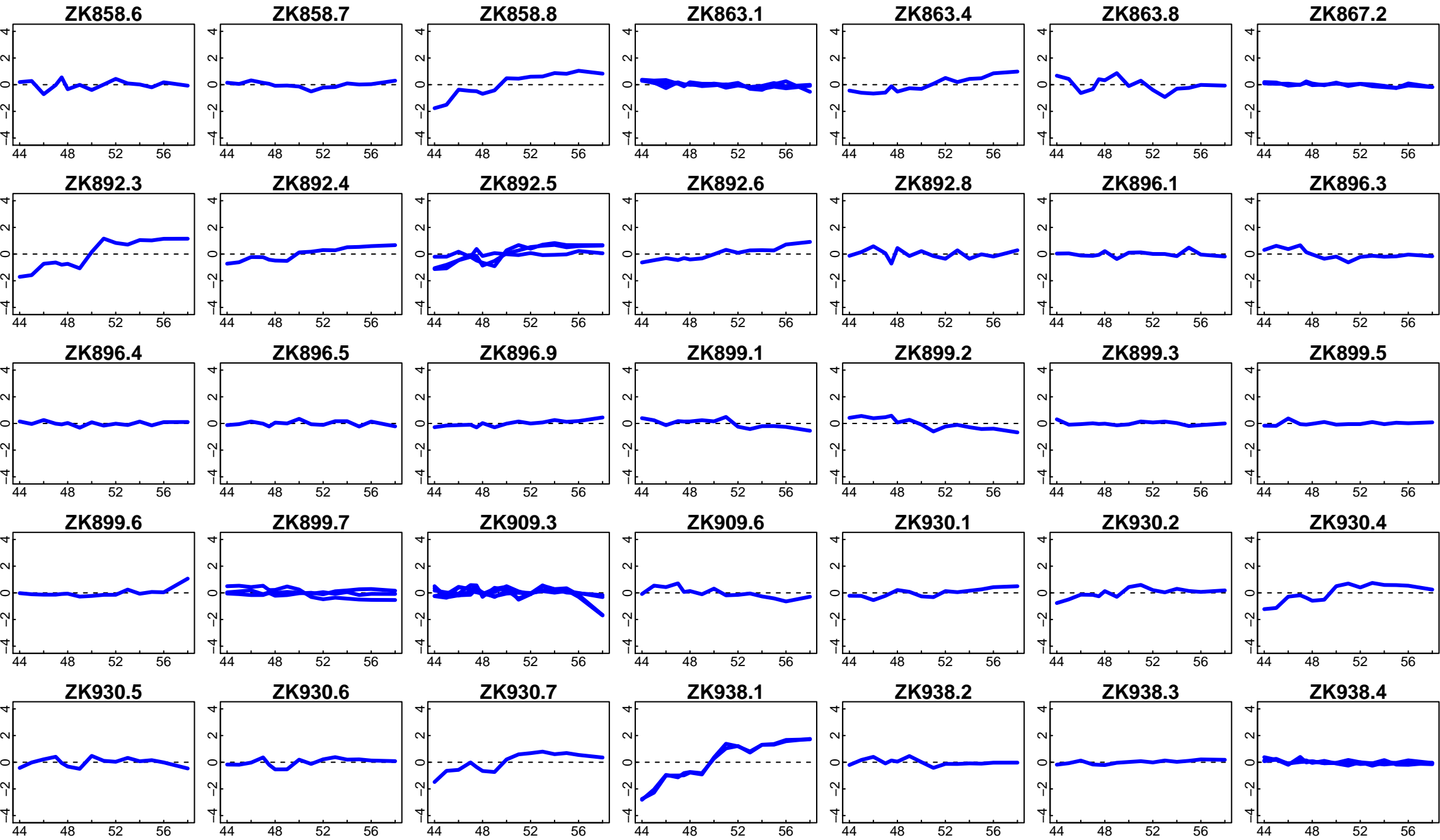


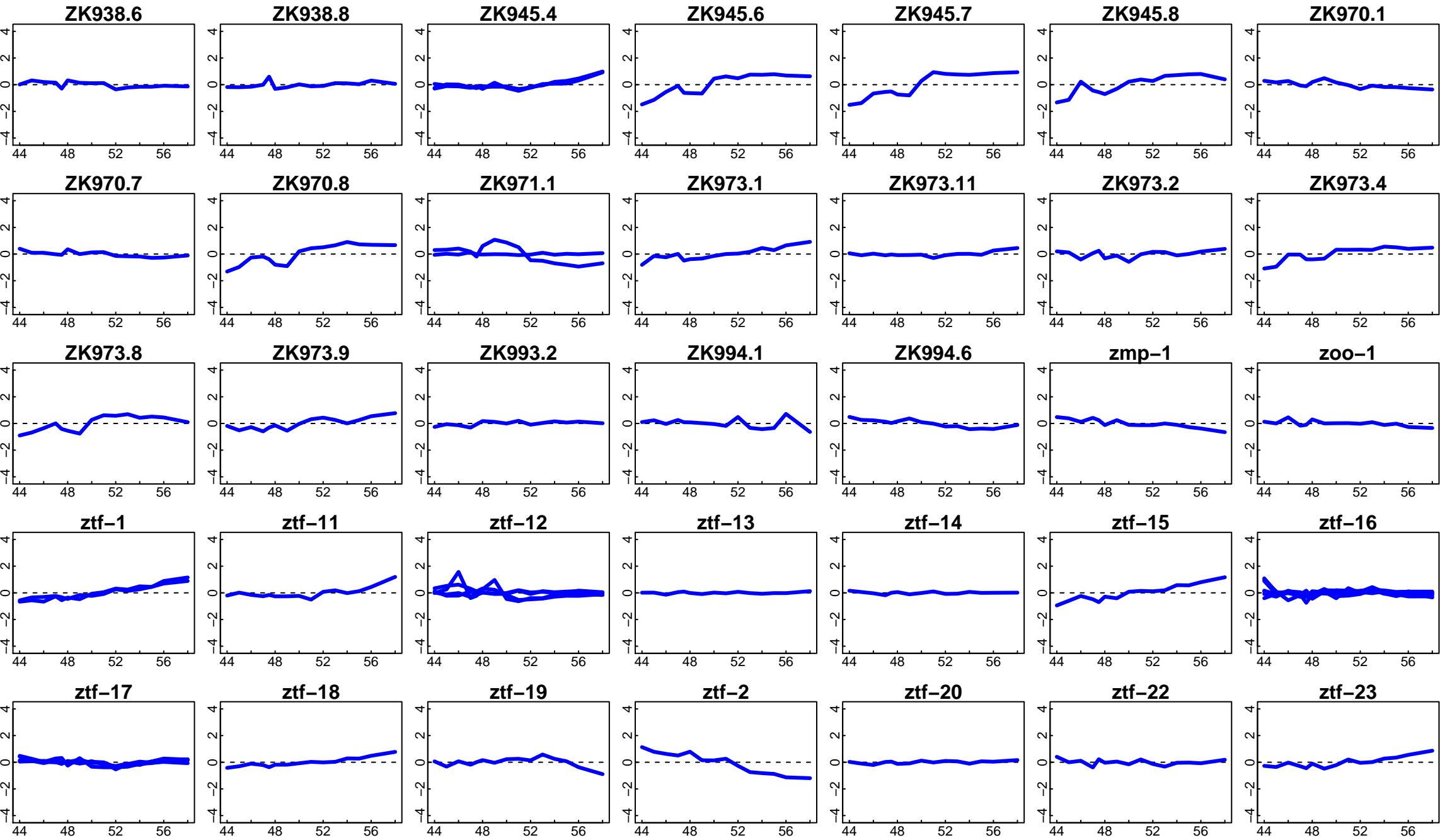


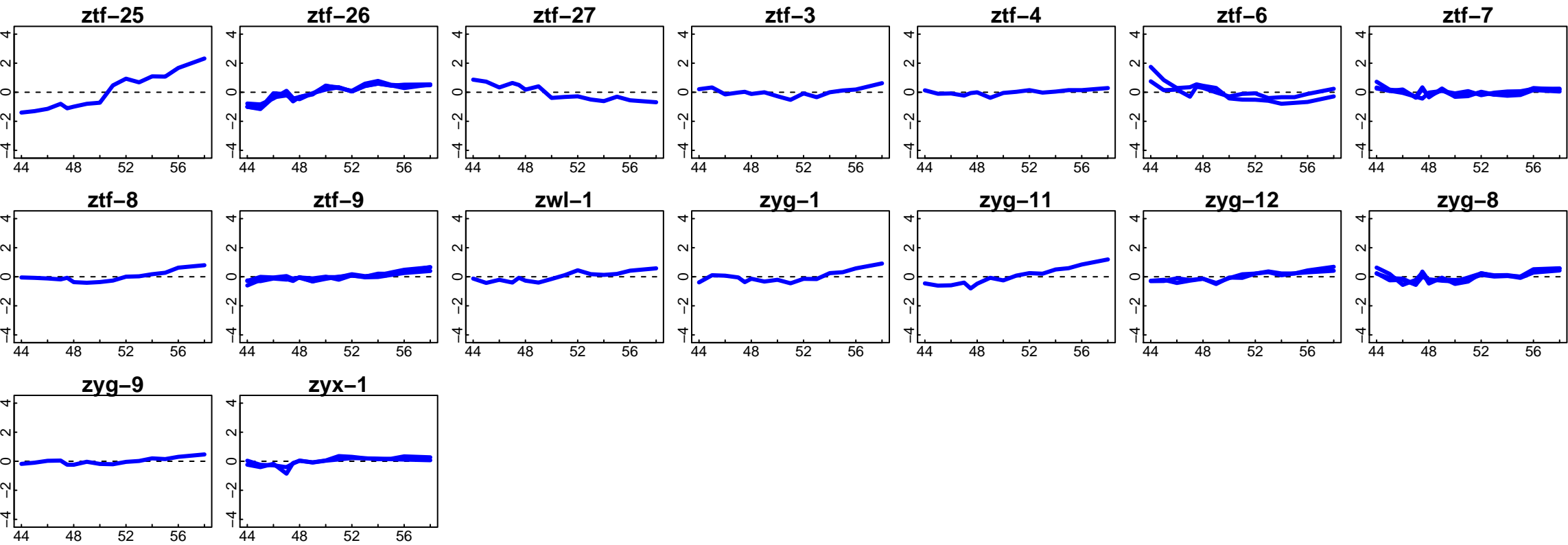








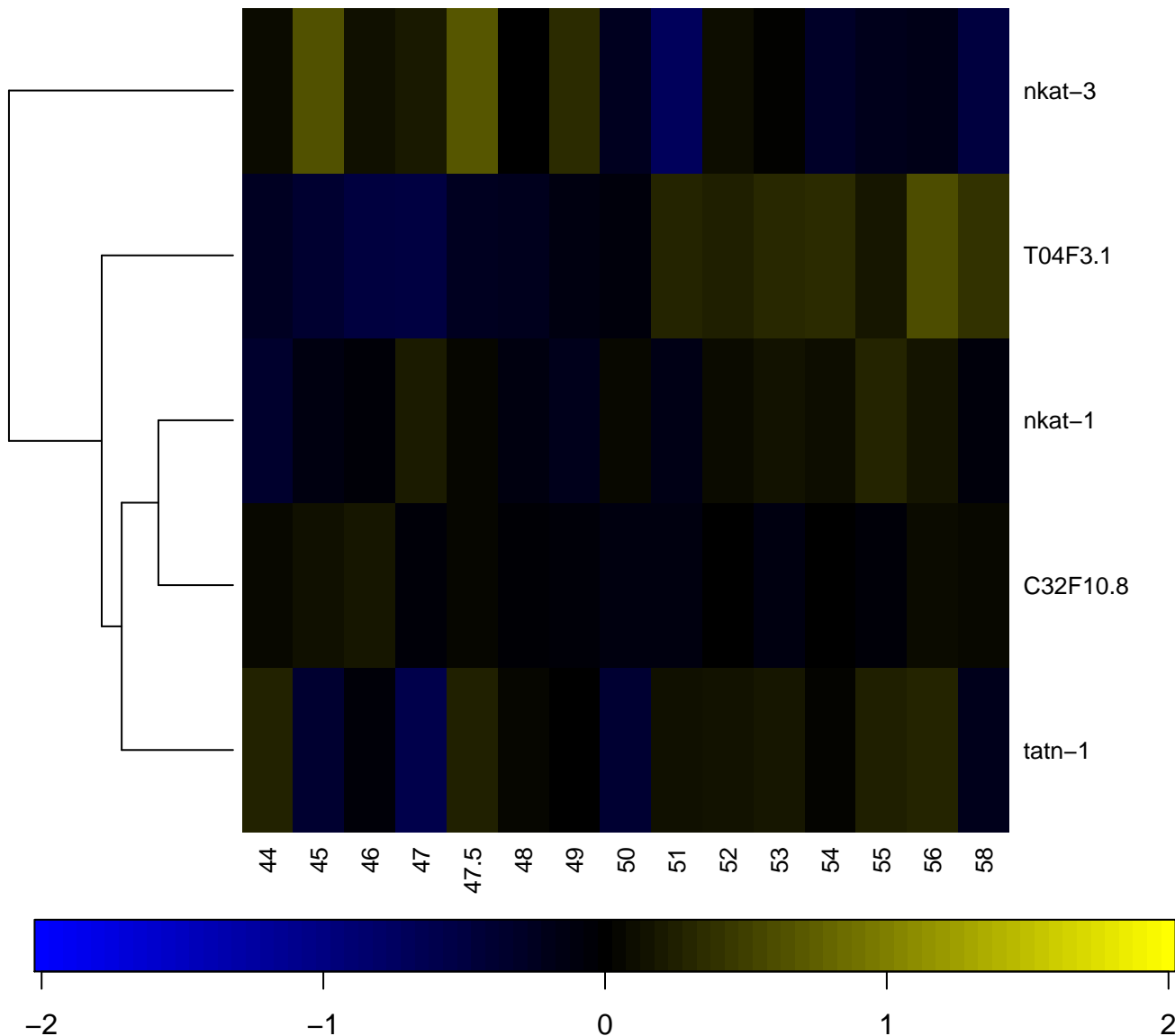




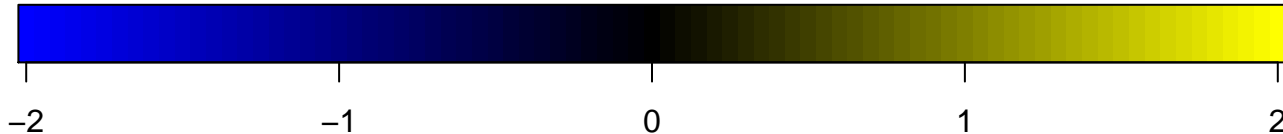
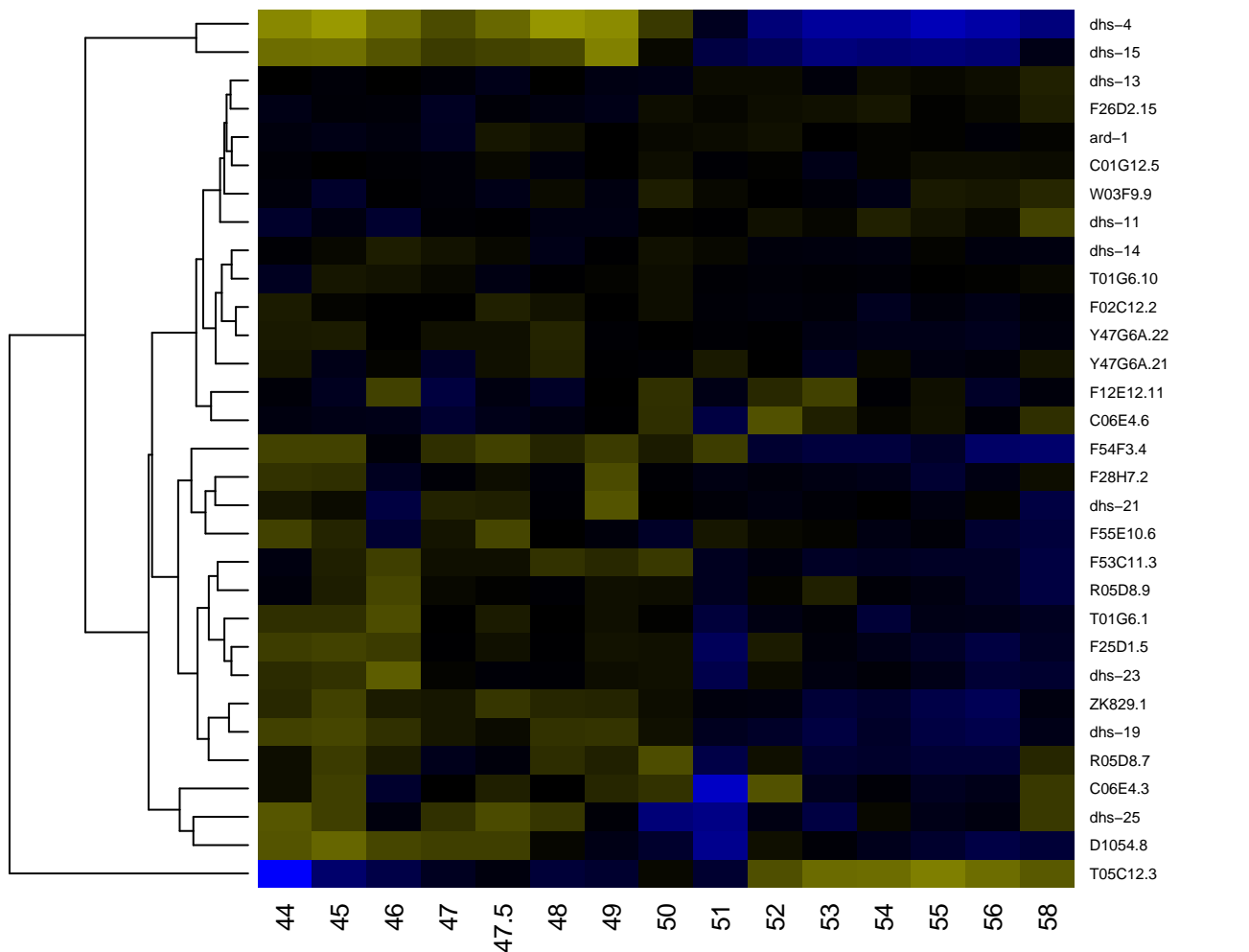
Supplementary file D | Dynamic gene expression patterns of all the GO-annotation terms.

The “heatmap” function of “R” was used to cluster genes of each individual GO-term according to their expression pattern. Annotation name is shown per page as figure title. The time in hours is shown on the x-axis. Gene names are shown on the y-axis. The scale bar shows the log₂ ratio with the mean for each time-point. Blue is lower than the mean and yellow is higher than the mean.

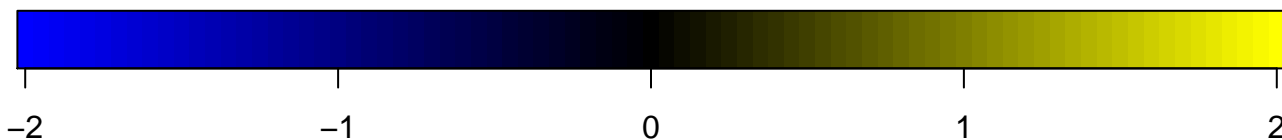
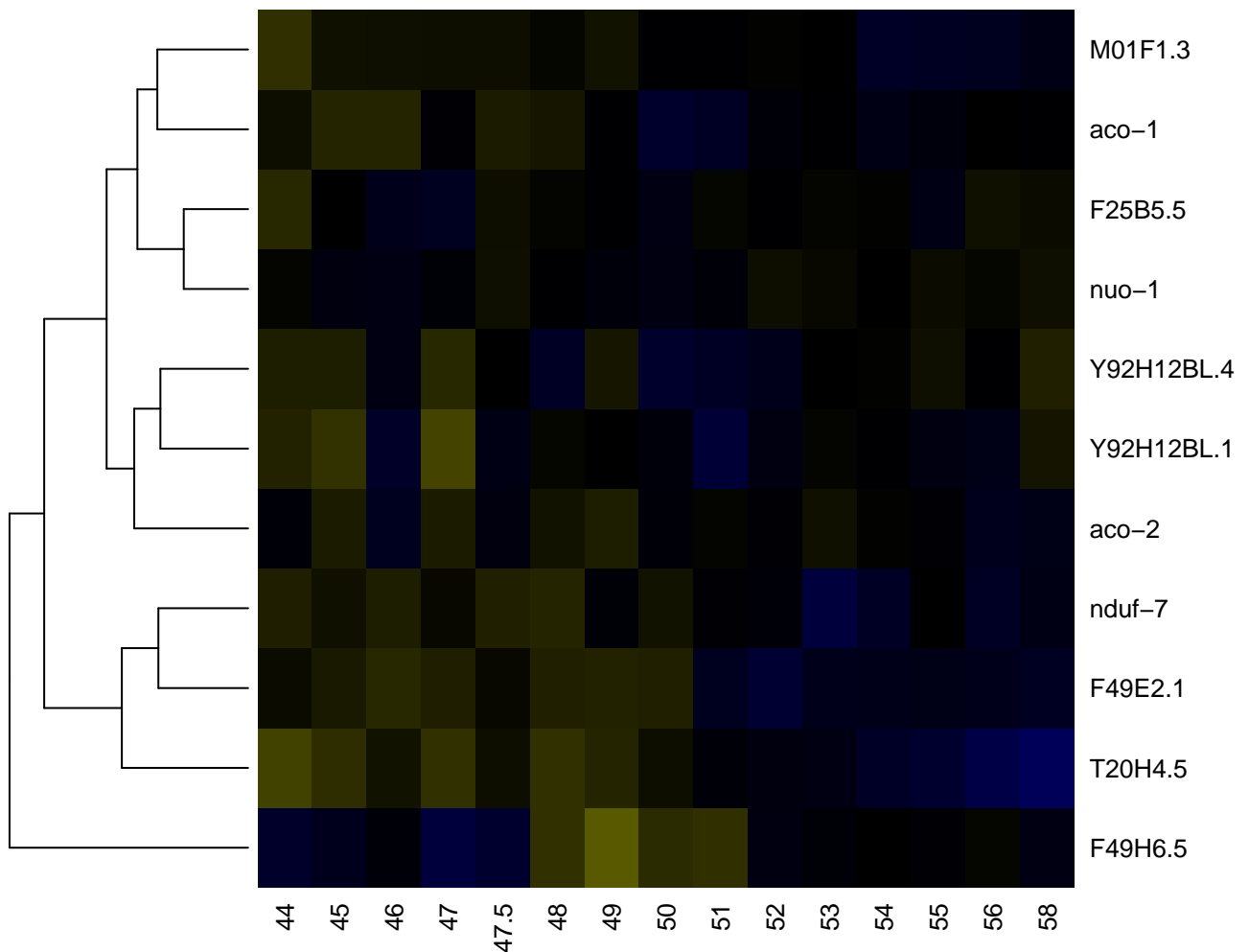
1-aminocyclopropane-1-carboxylate synthase activity



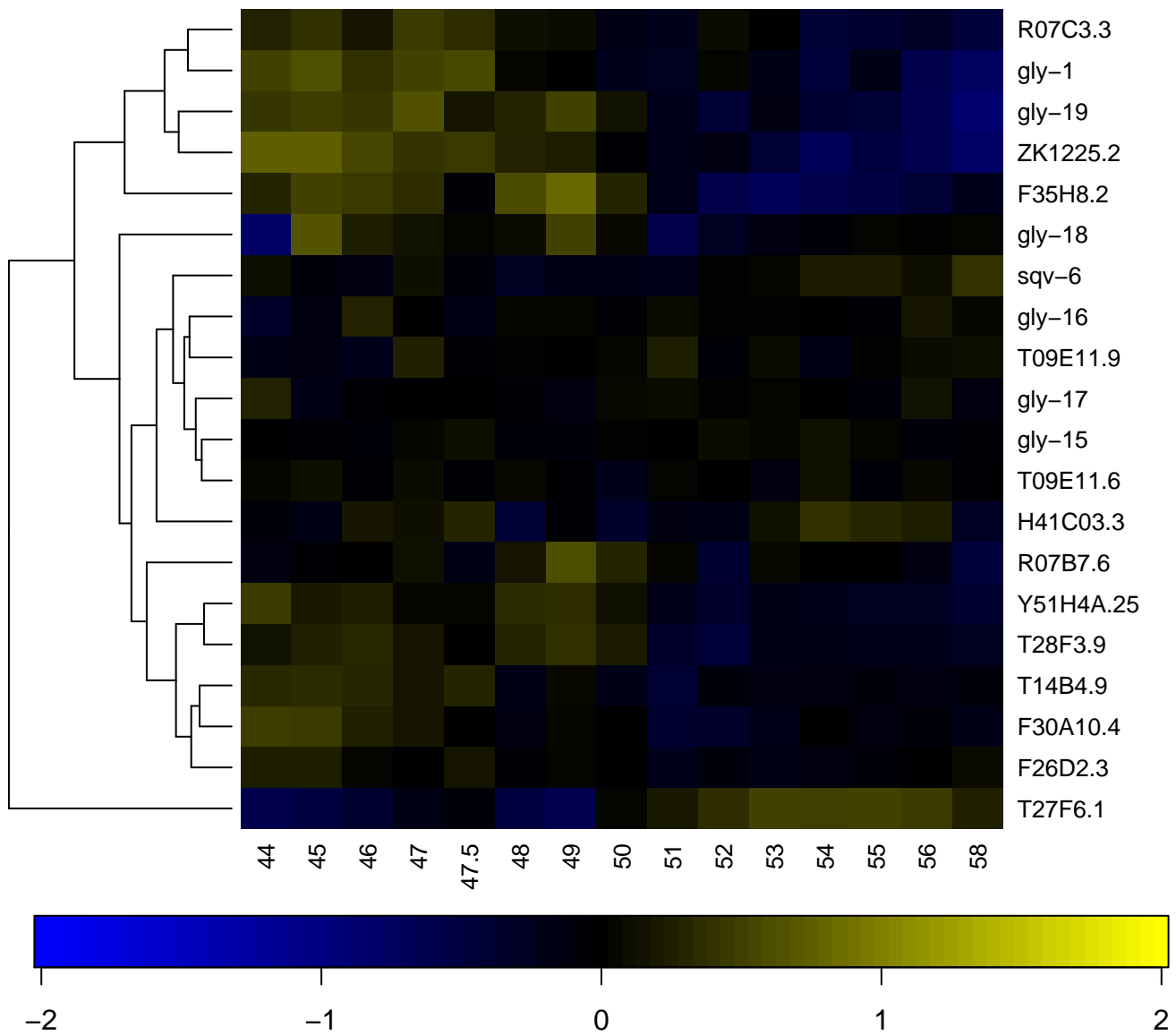
2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase activity



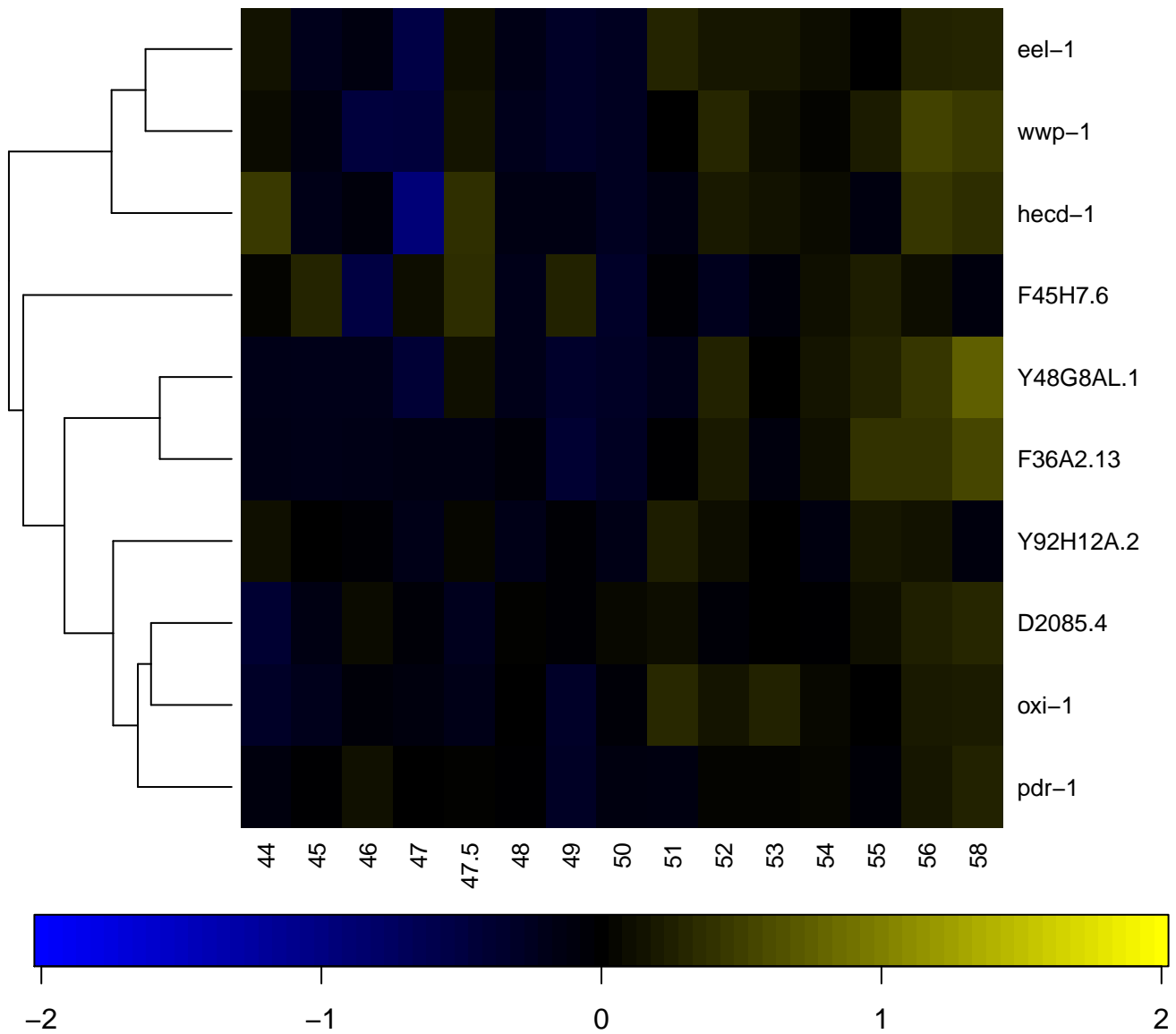
4 iron, 4 sulfur cluster binding



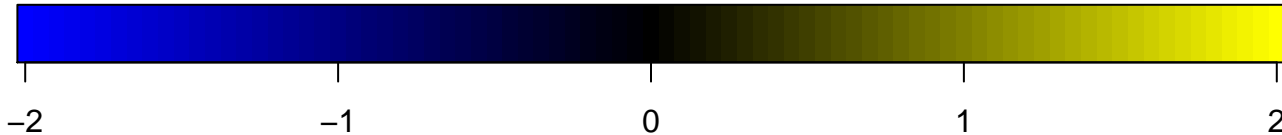
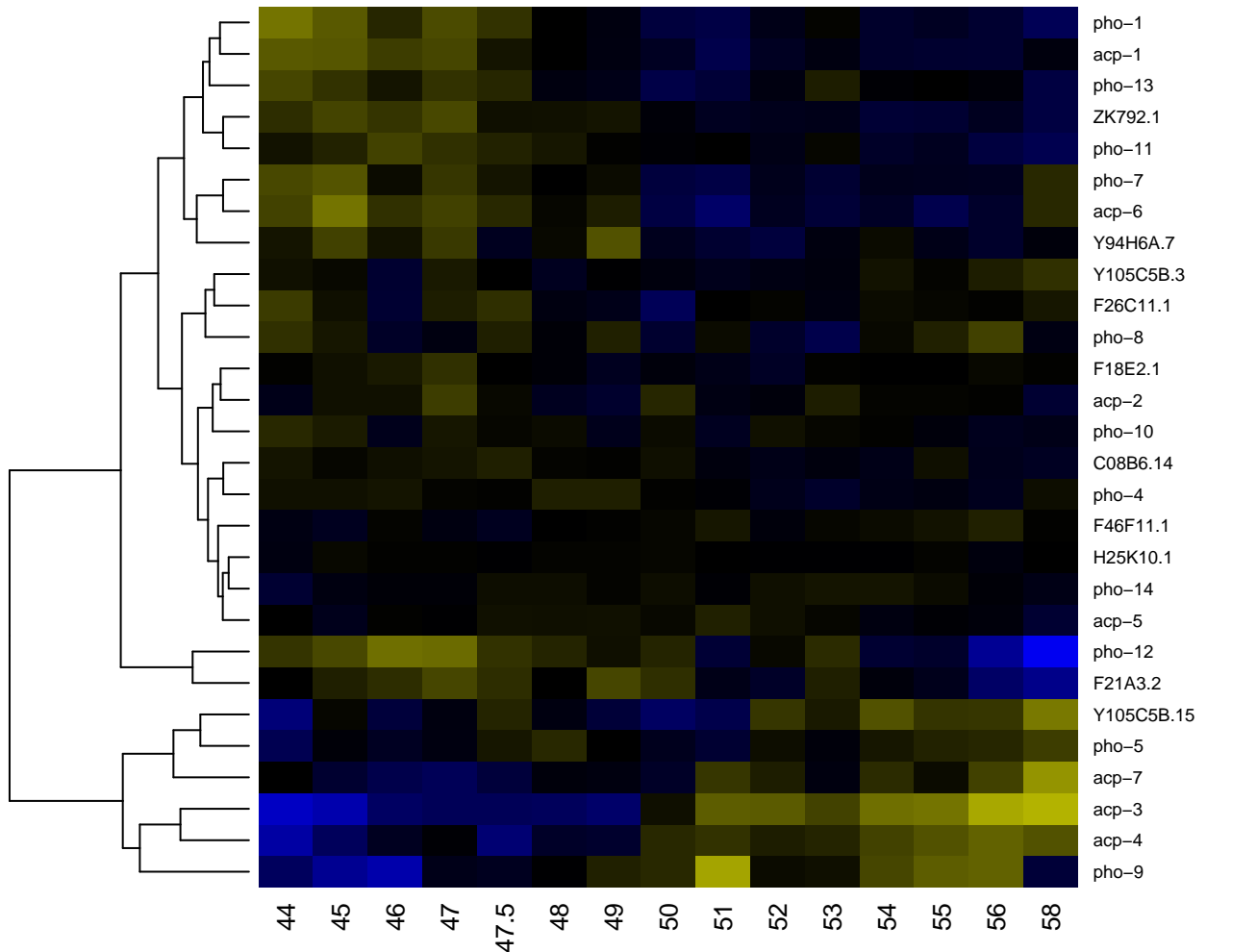
acetylglucosaminyltransferase activity



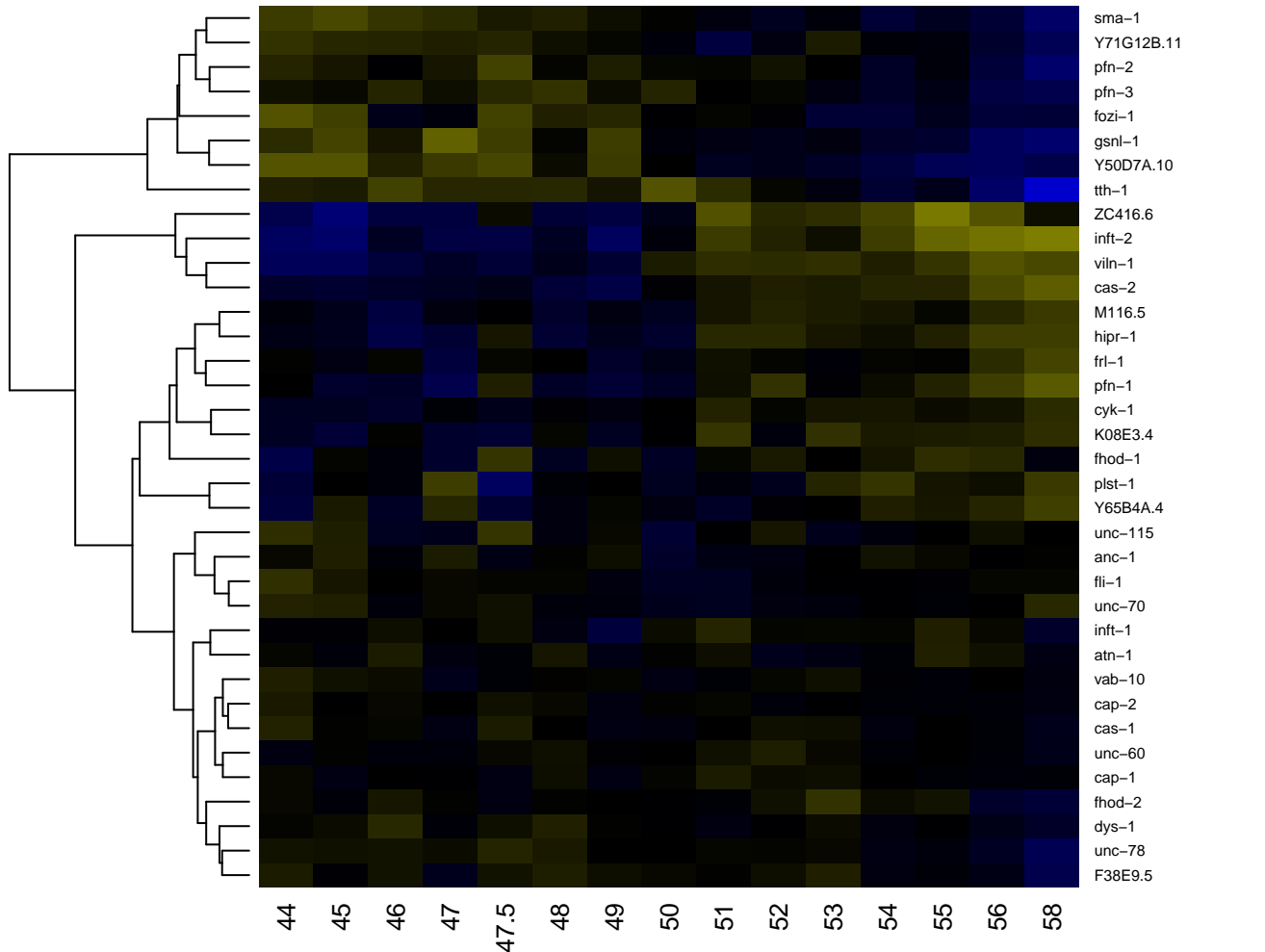
acid-amino acid ligase activity



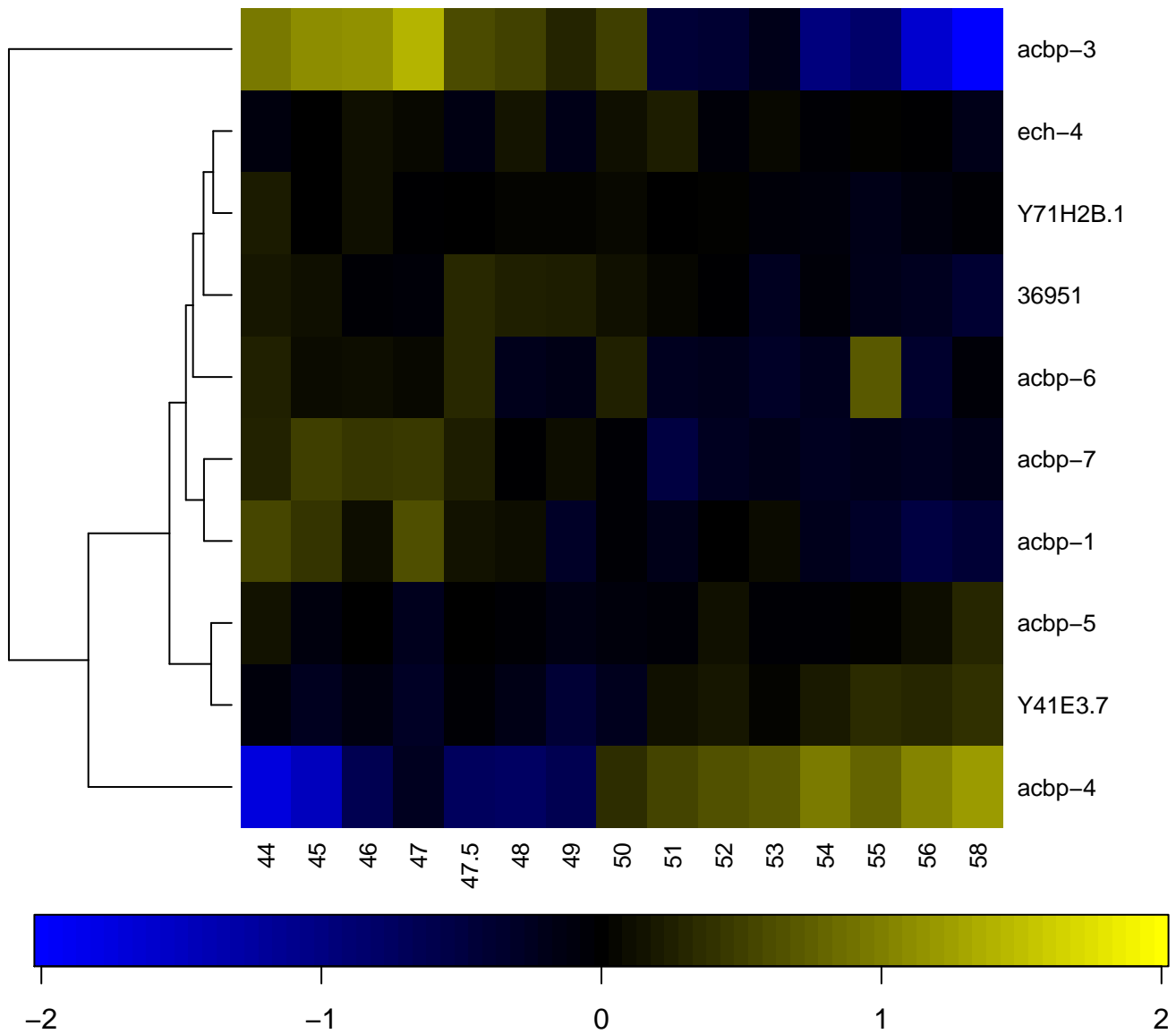
acid phosphatase activity



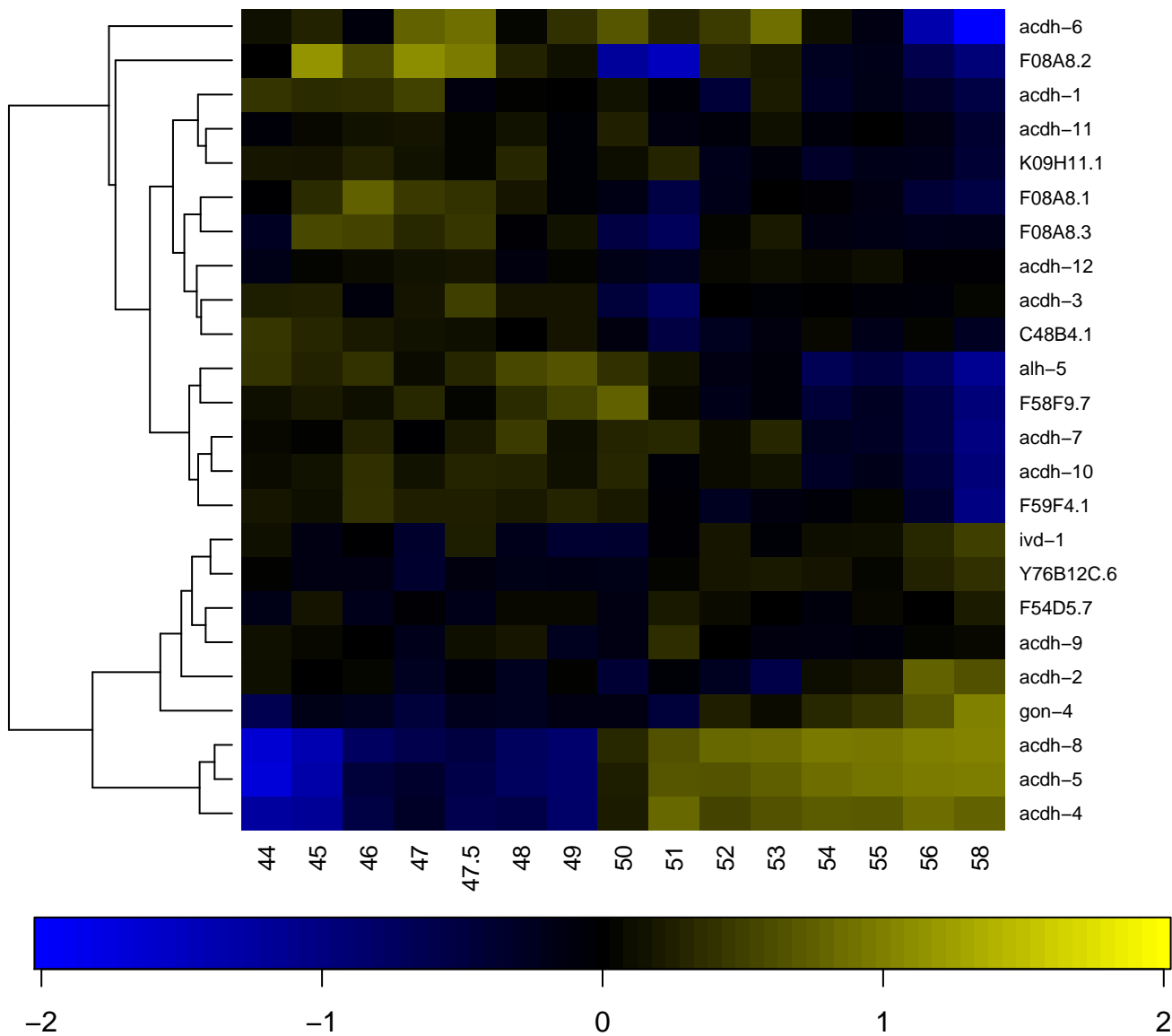
actin binding



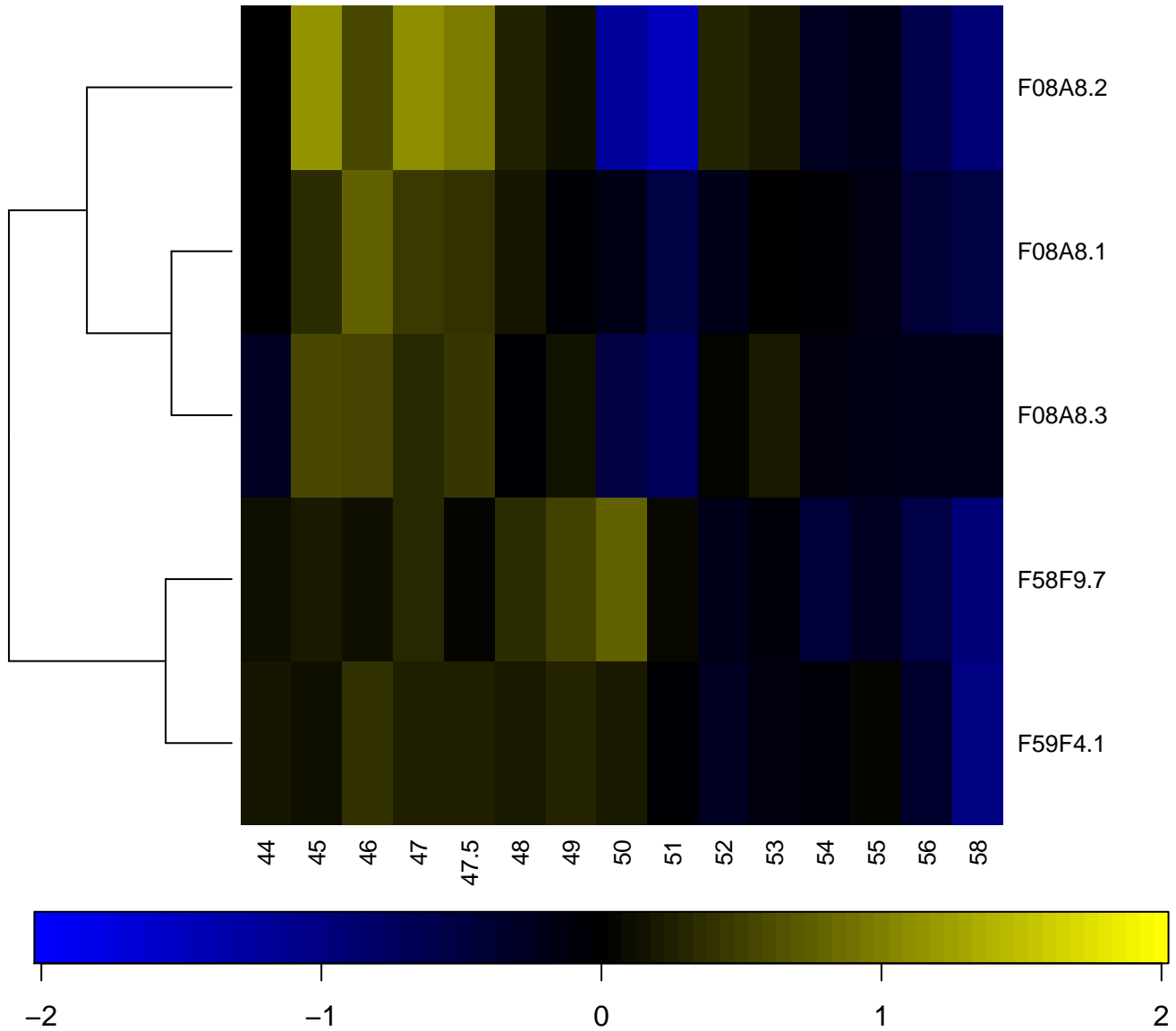
acyl-CoA binding



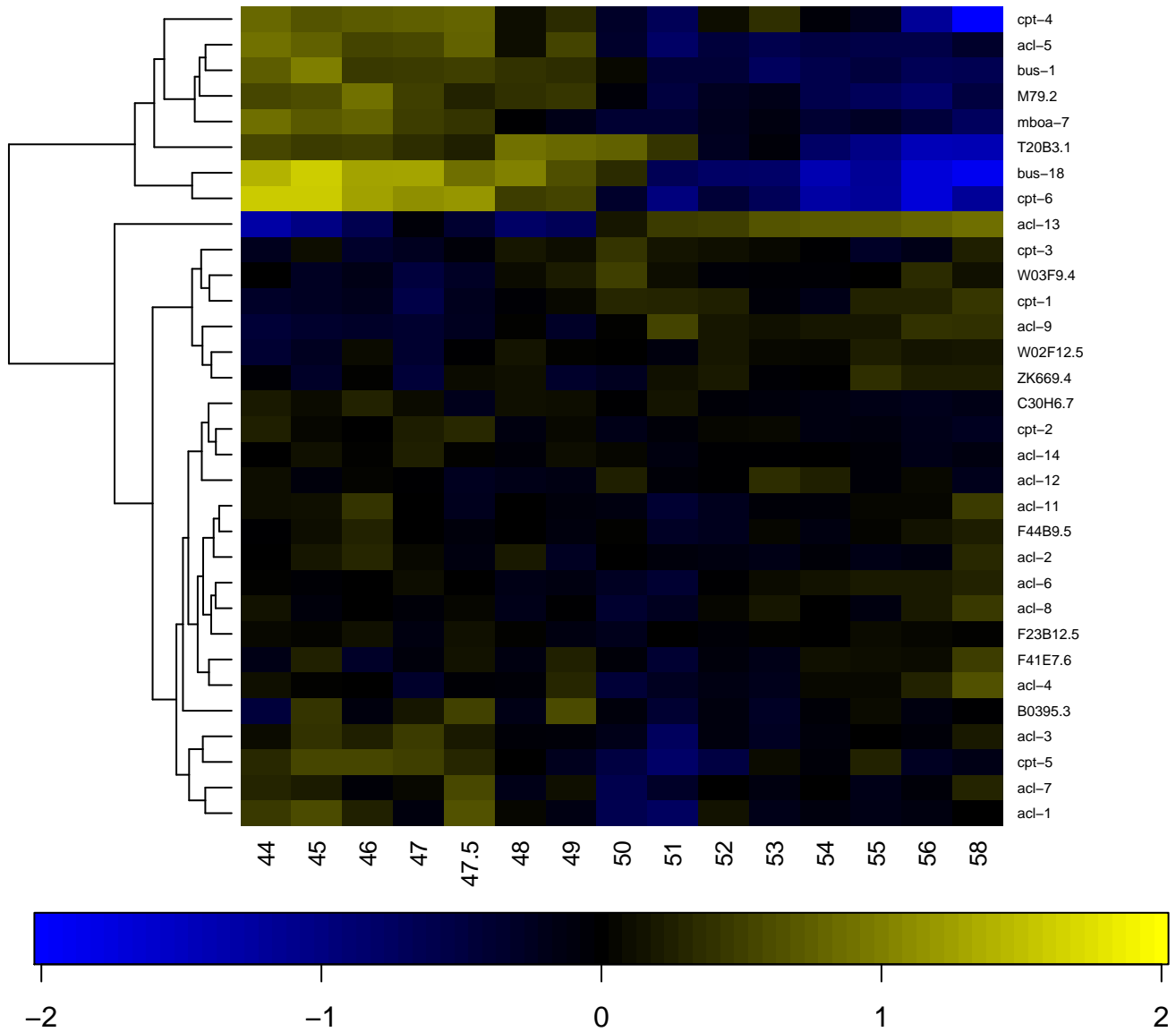
acyl-CoA dehydrogenase activity



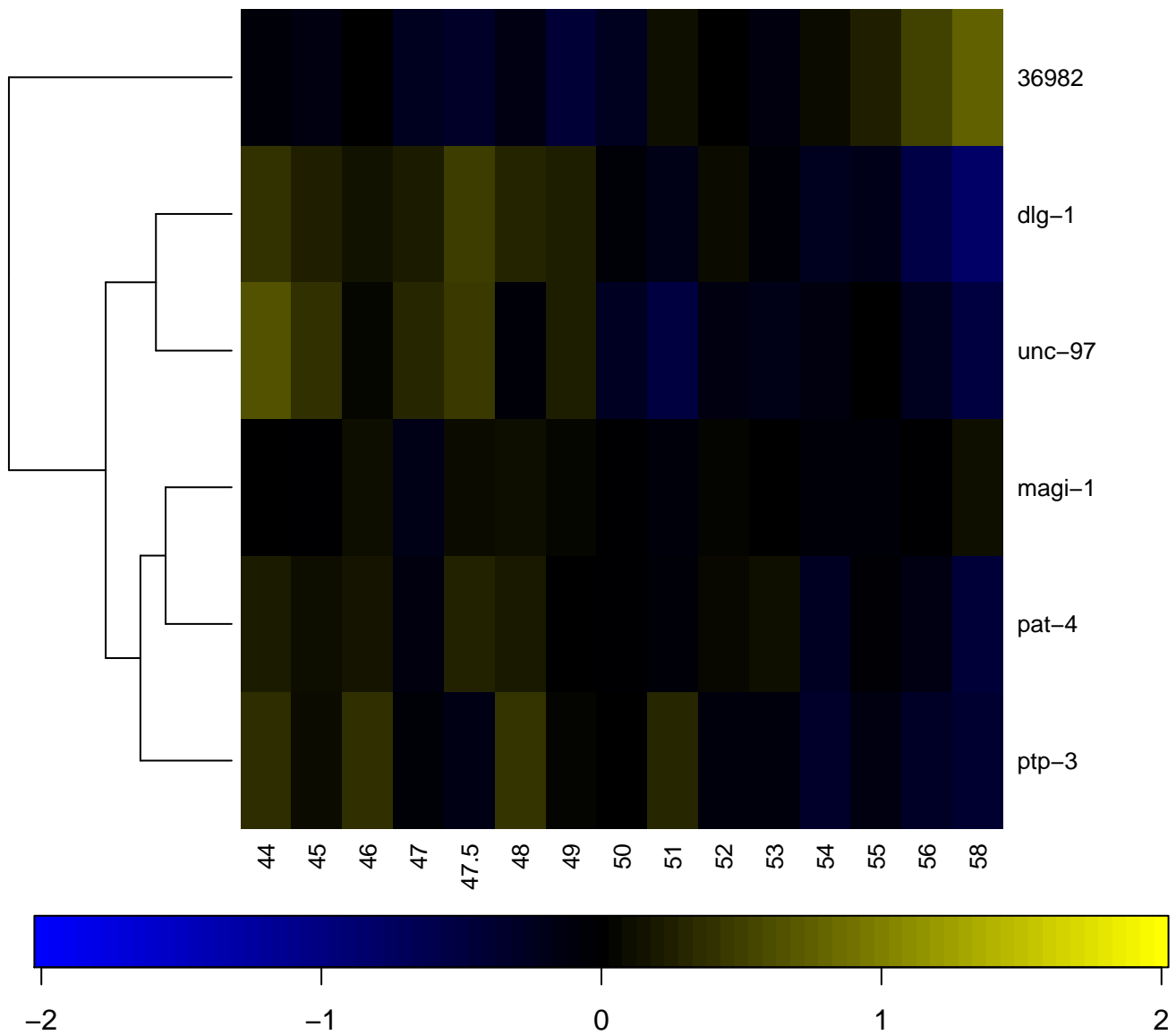
acyl-CoA oxidase activity



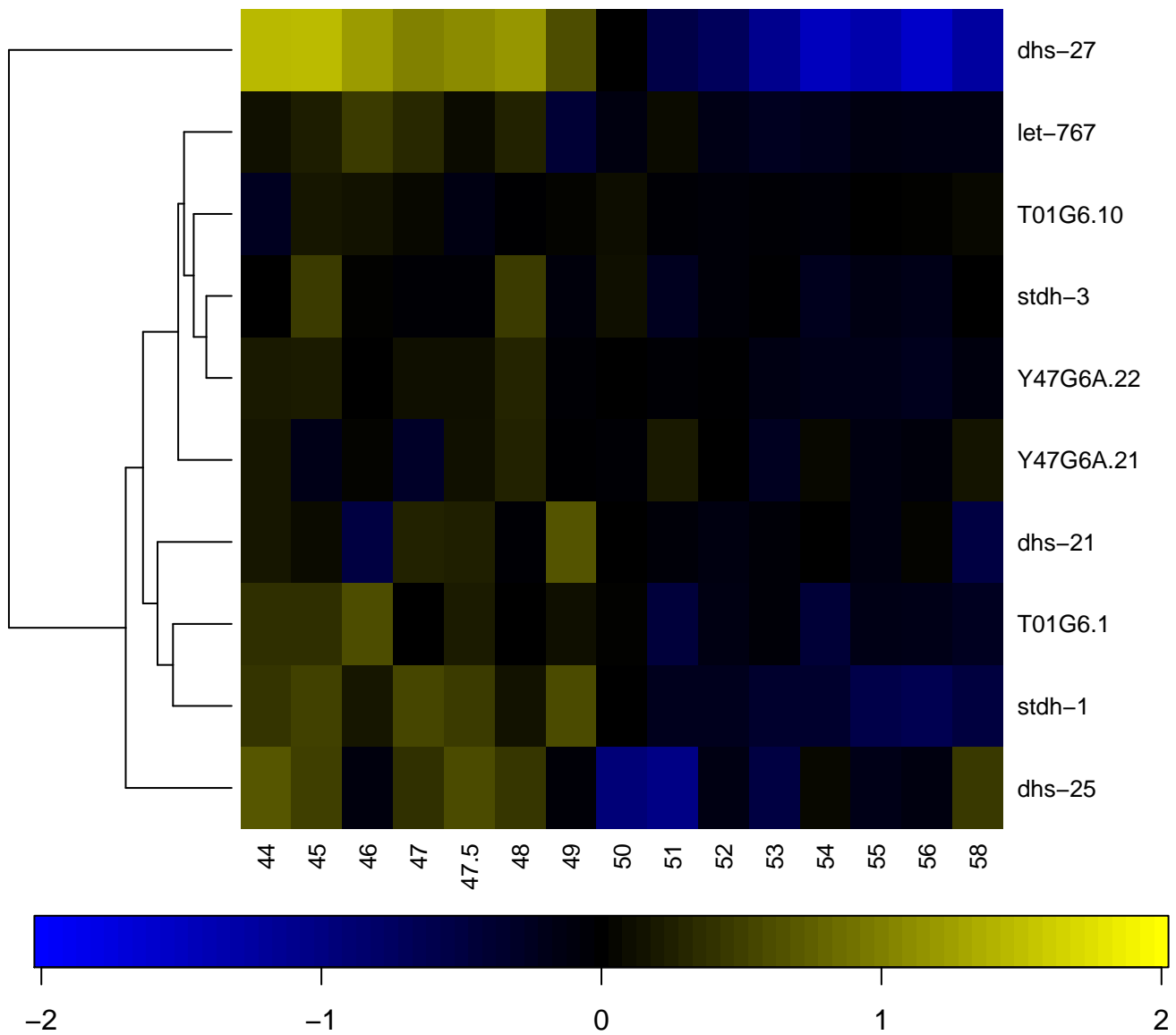
acyltransferase activity



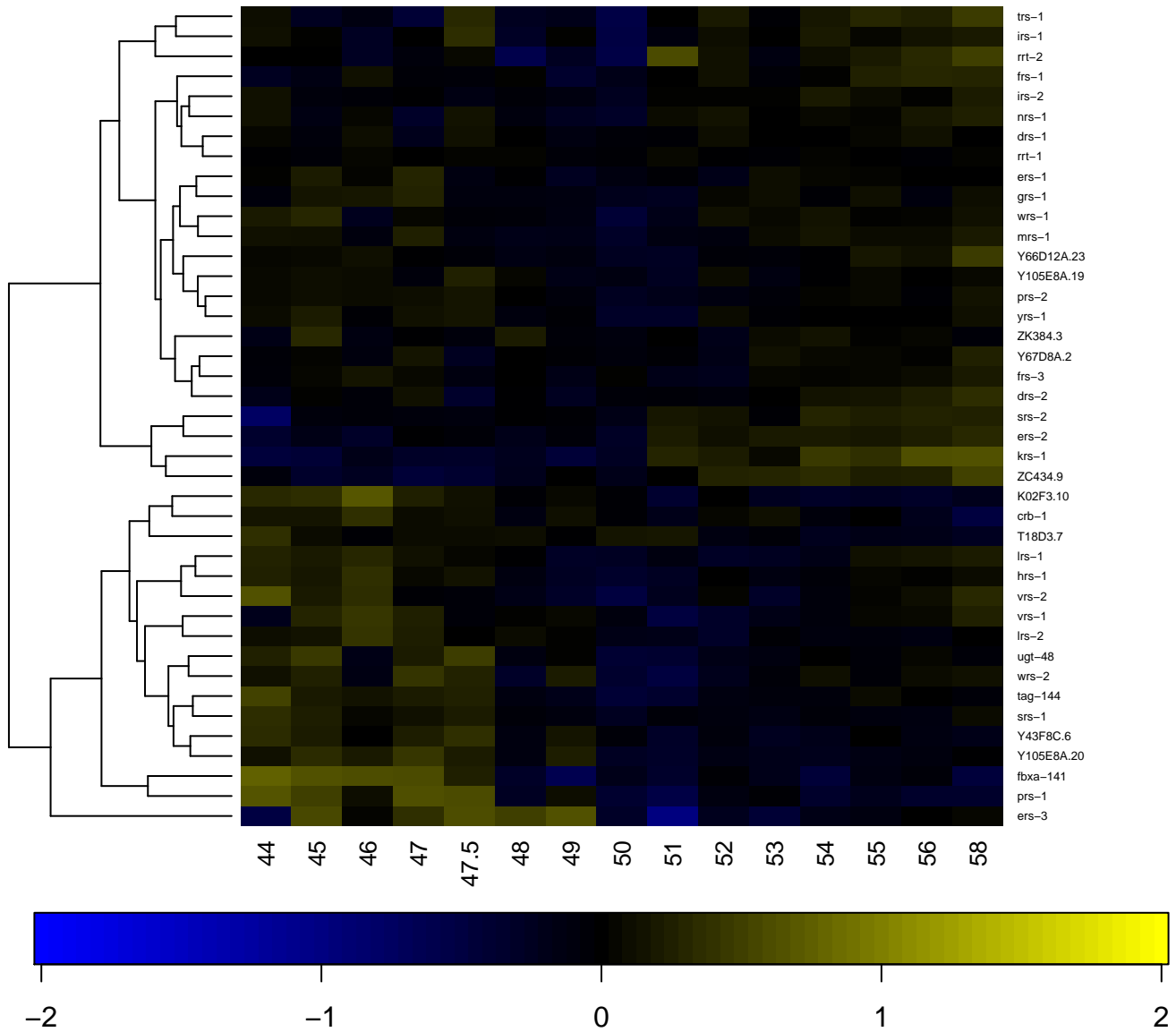
adherens junction



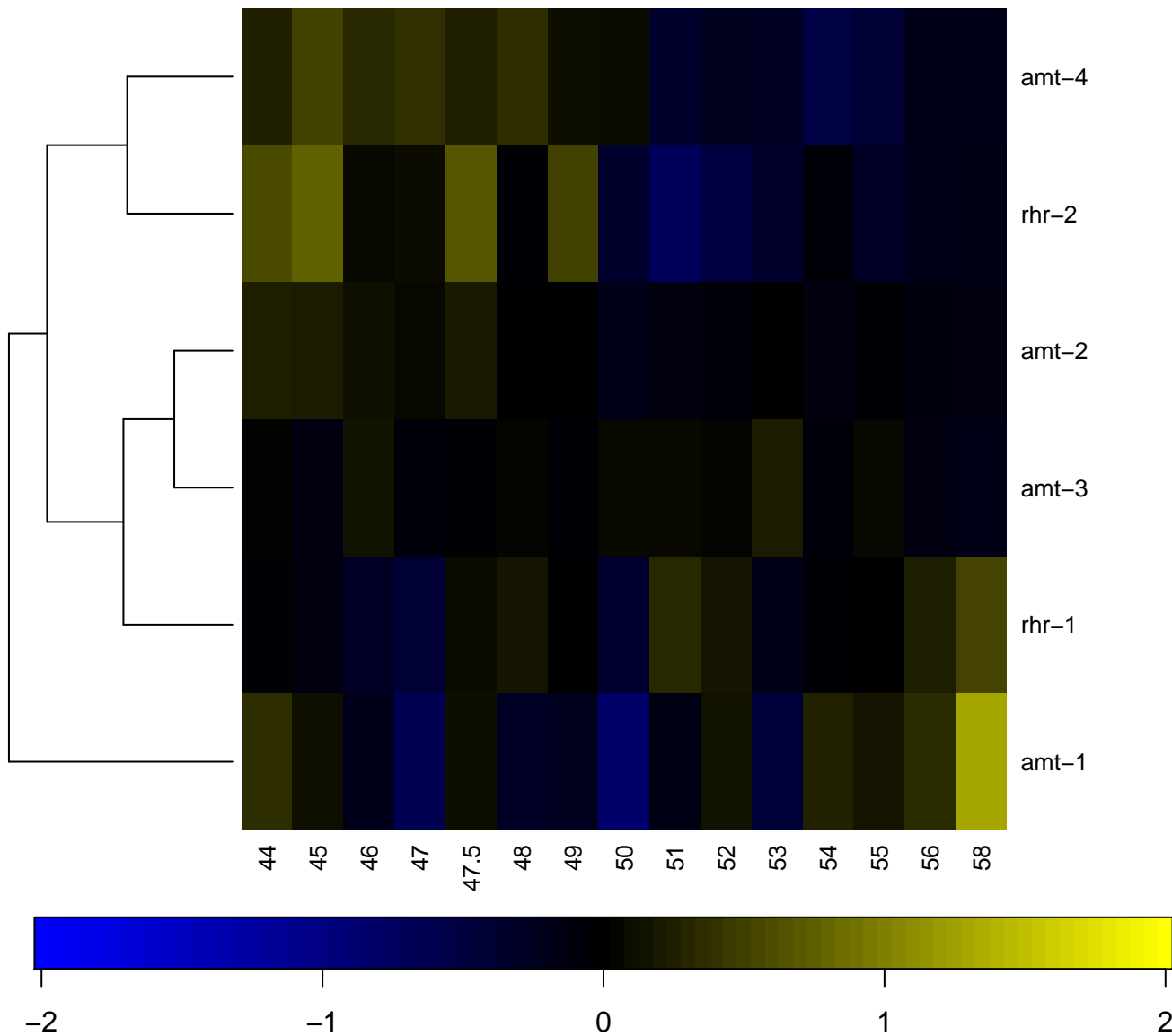
alcohol dehydrogenase (NAD) activity



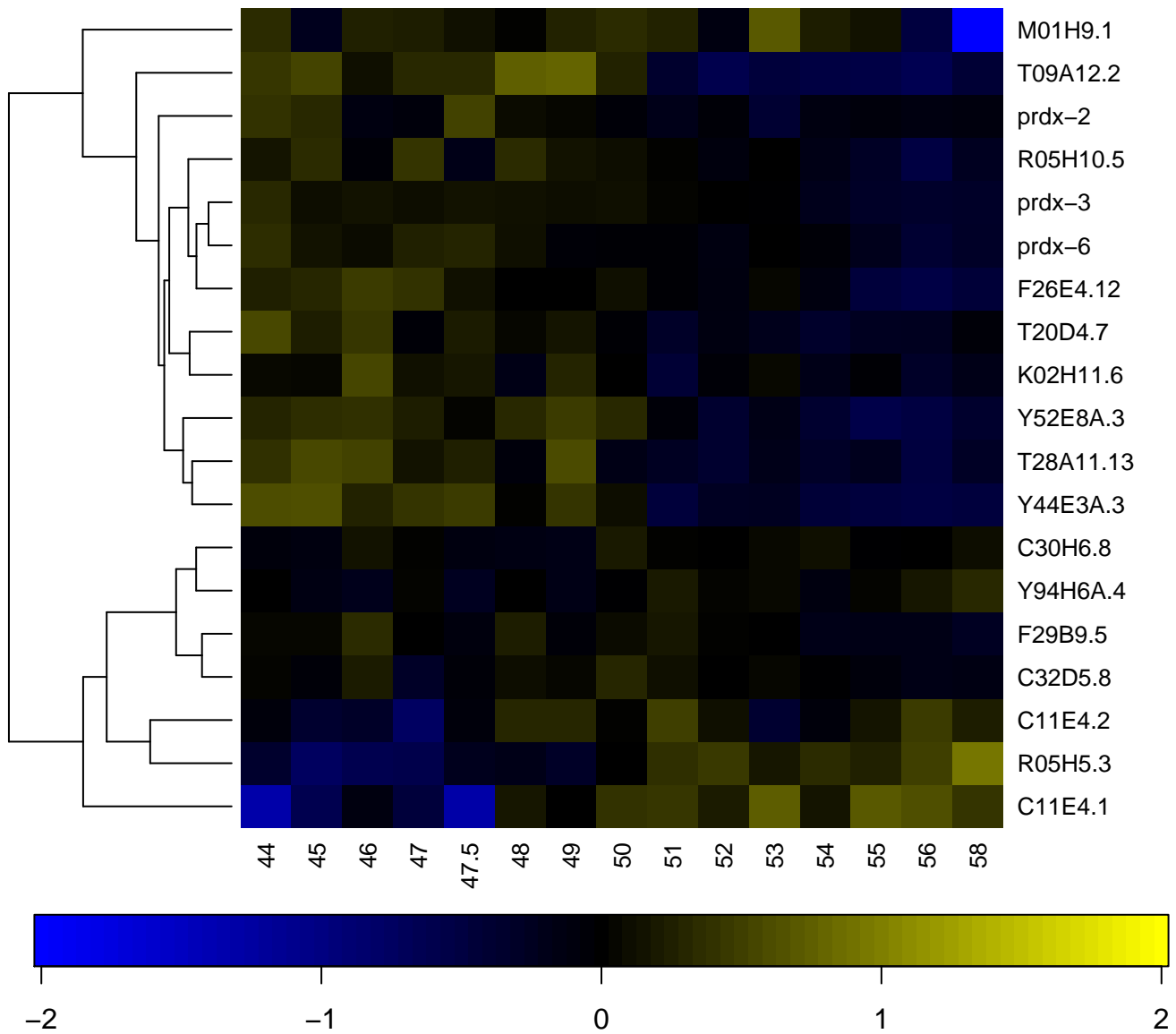
aminoacyl-tRNA ligase activity



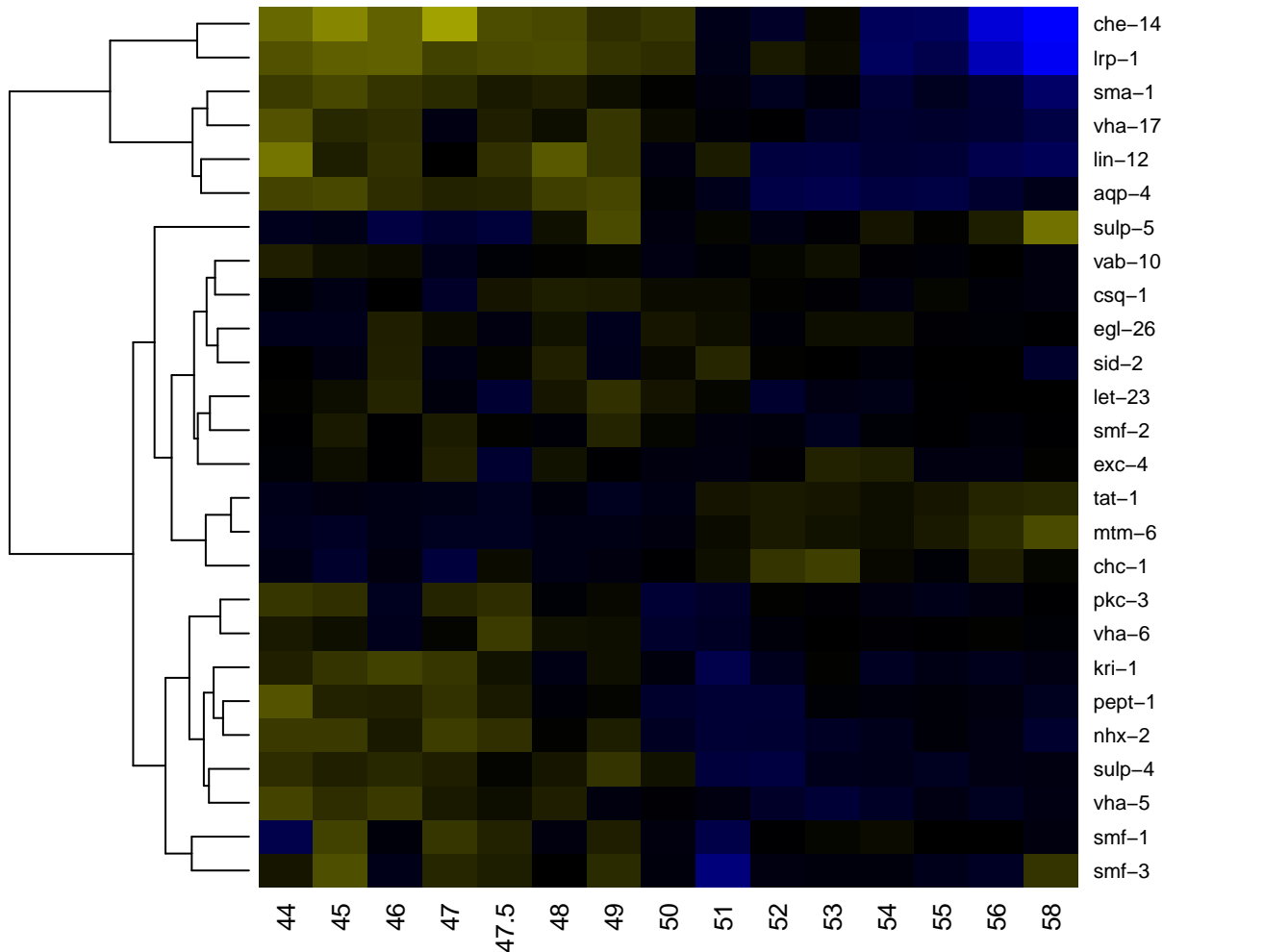
ammonium transmembrane transporter activity



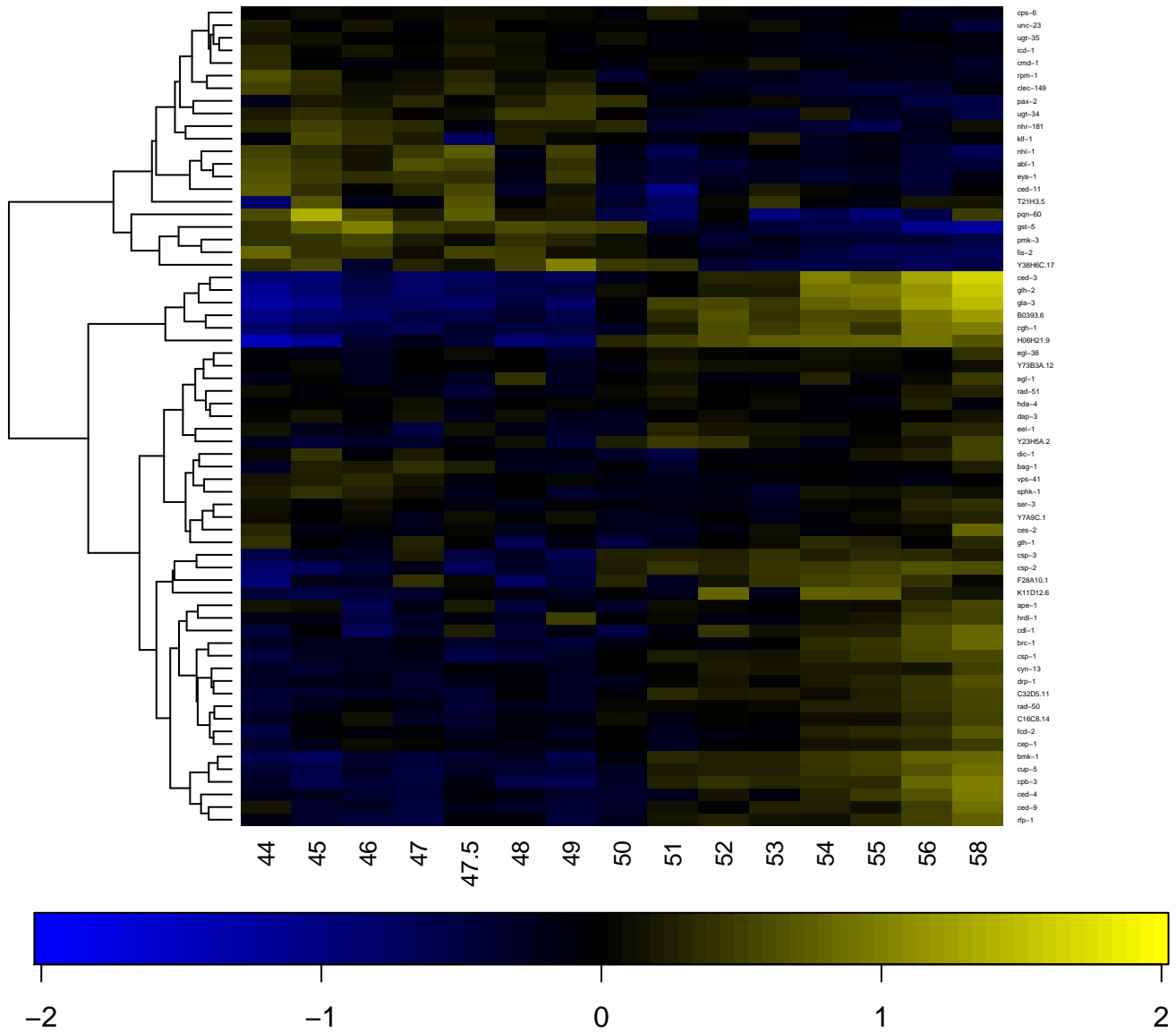
antioxidant activity



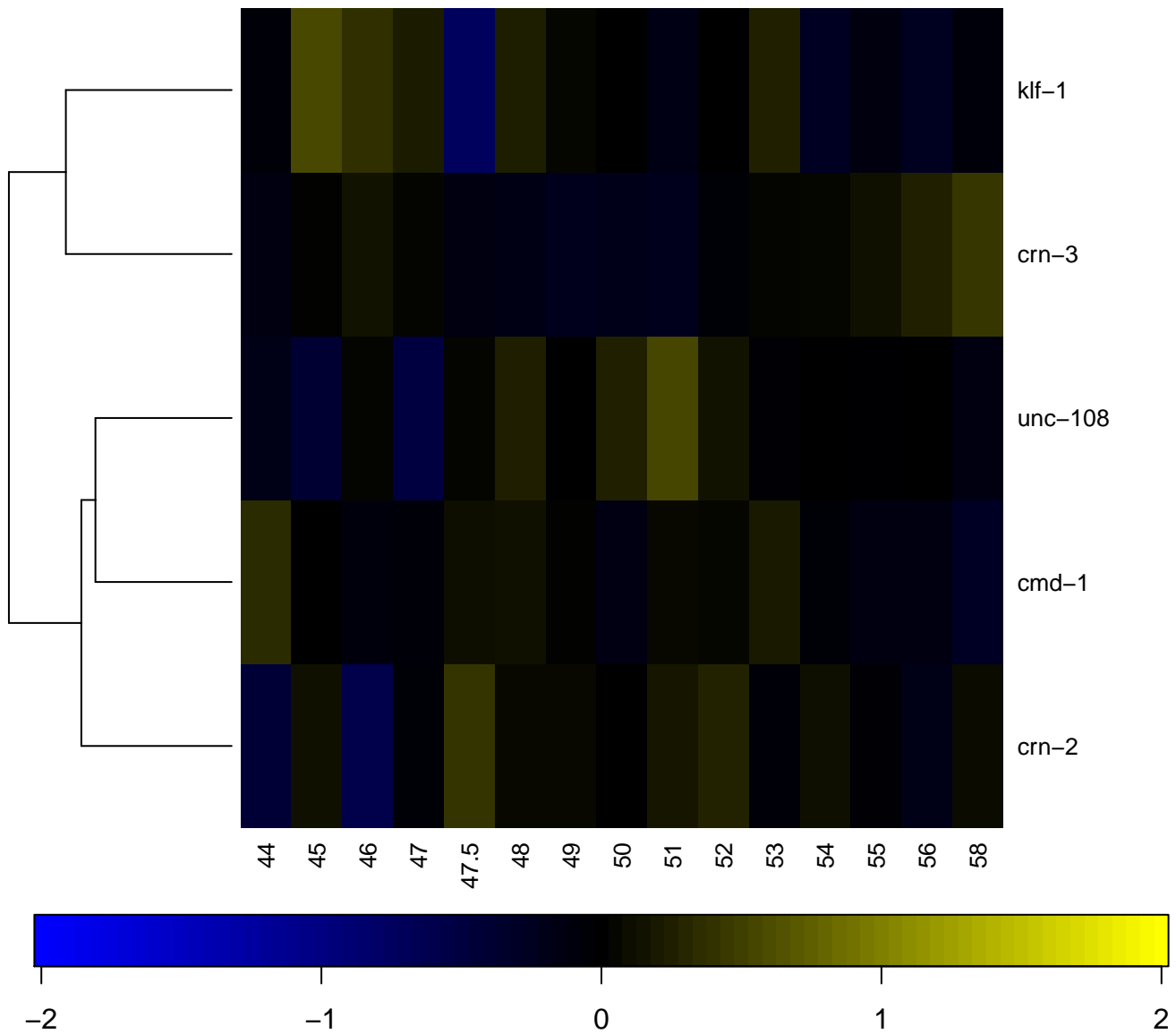
apical plasma membrane



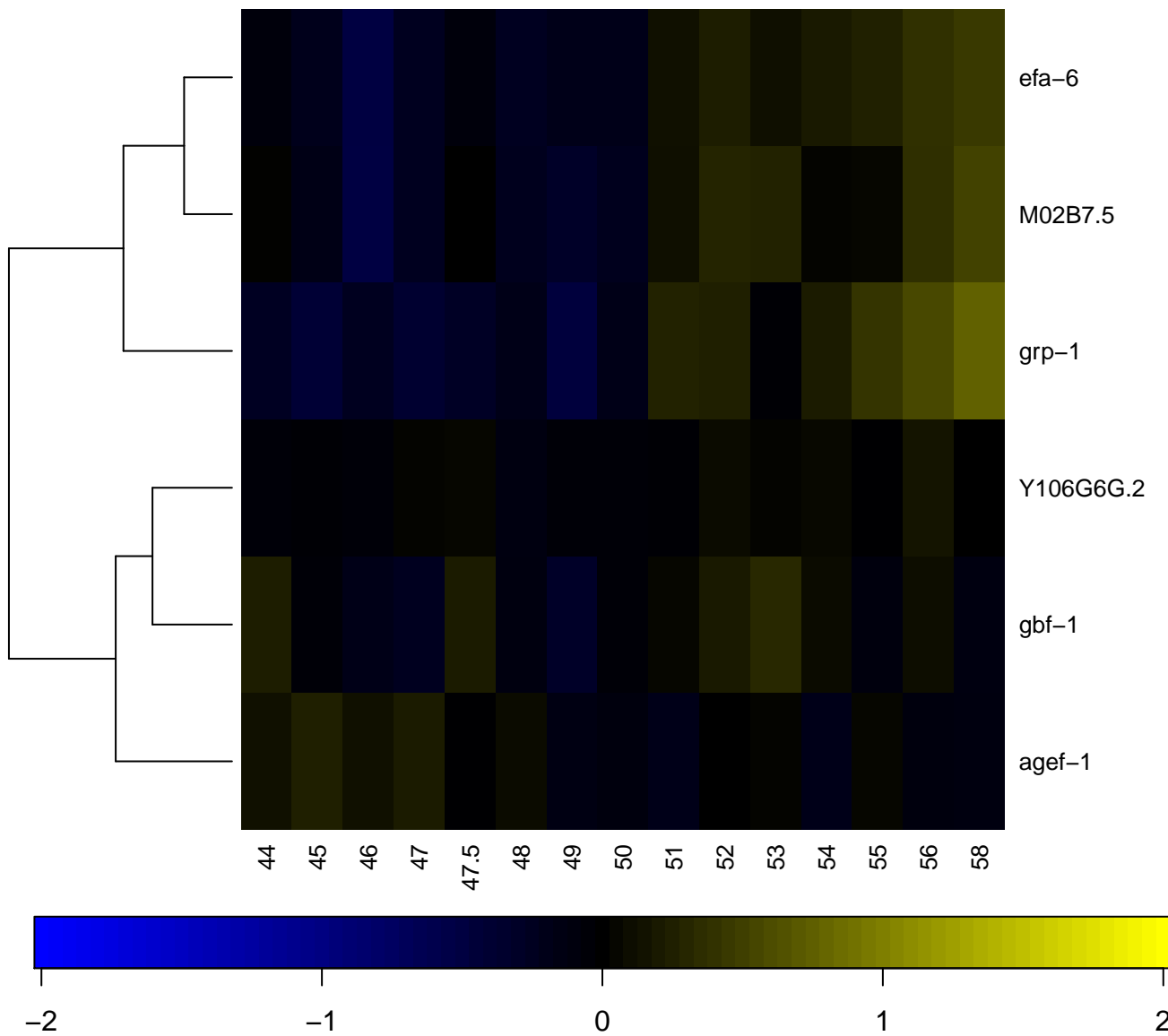
apoptosis



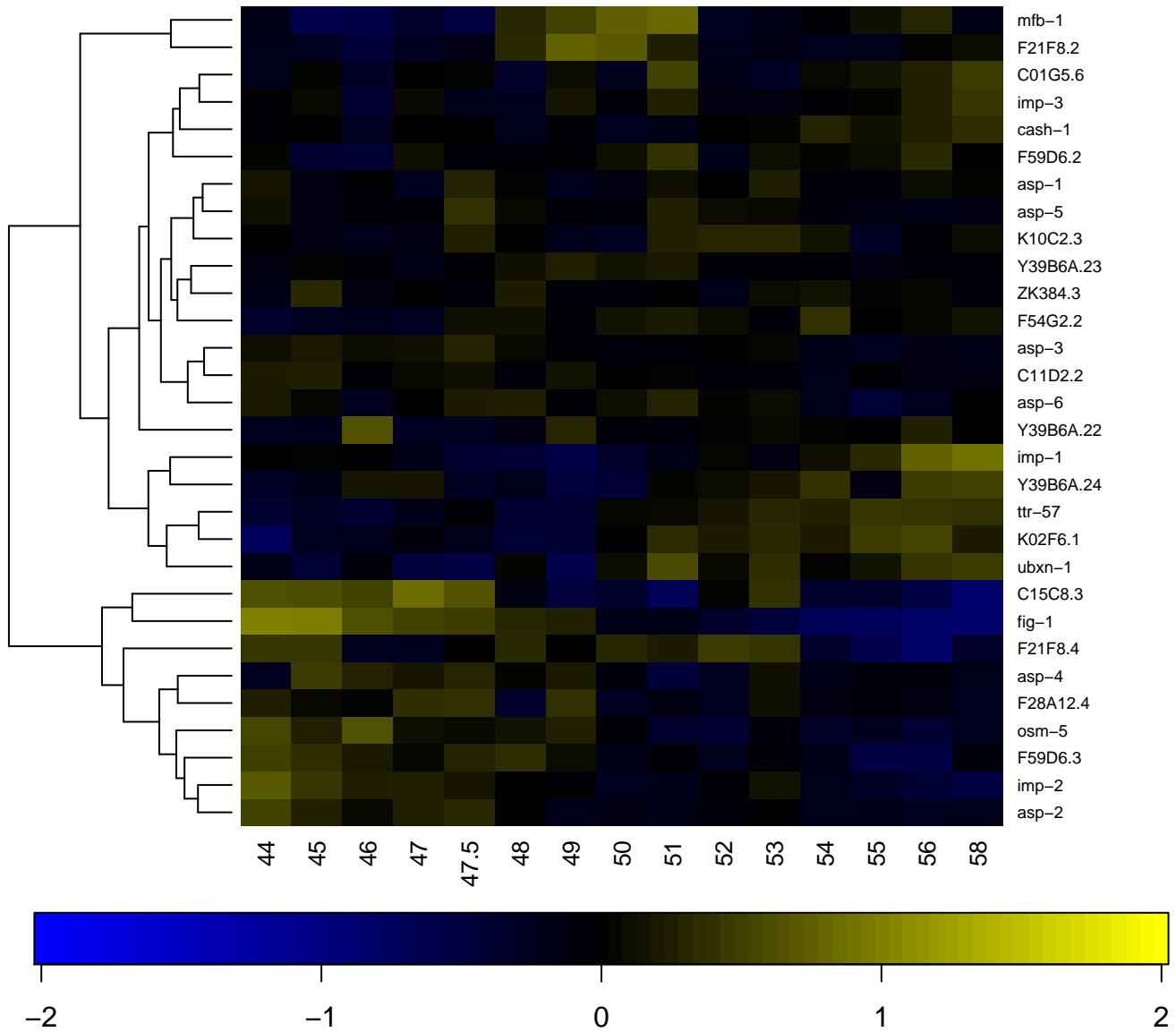
apoptotic cell clearance



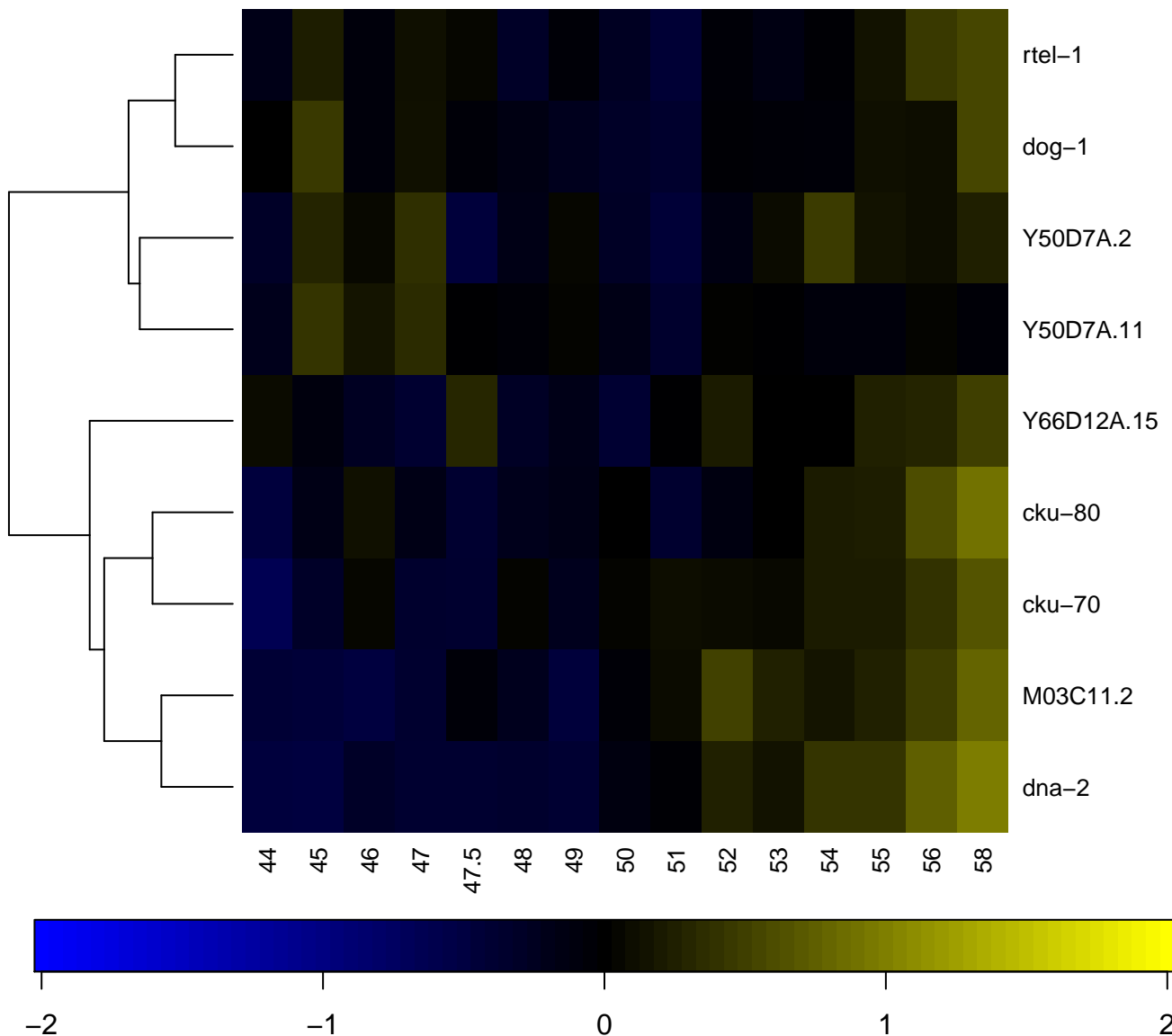
ARF guanyl–nucleotide exchange factor activity



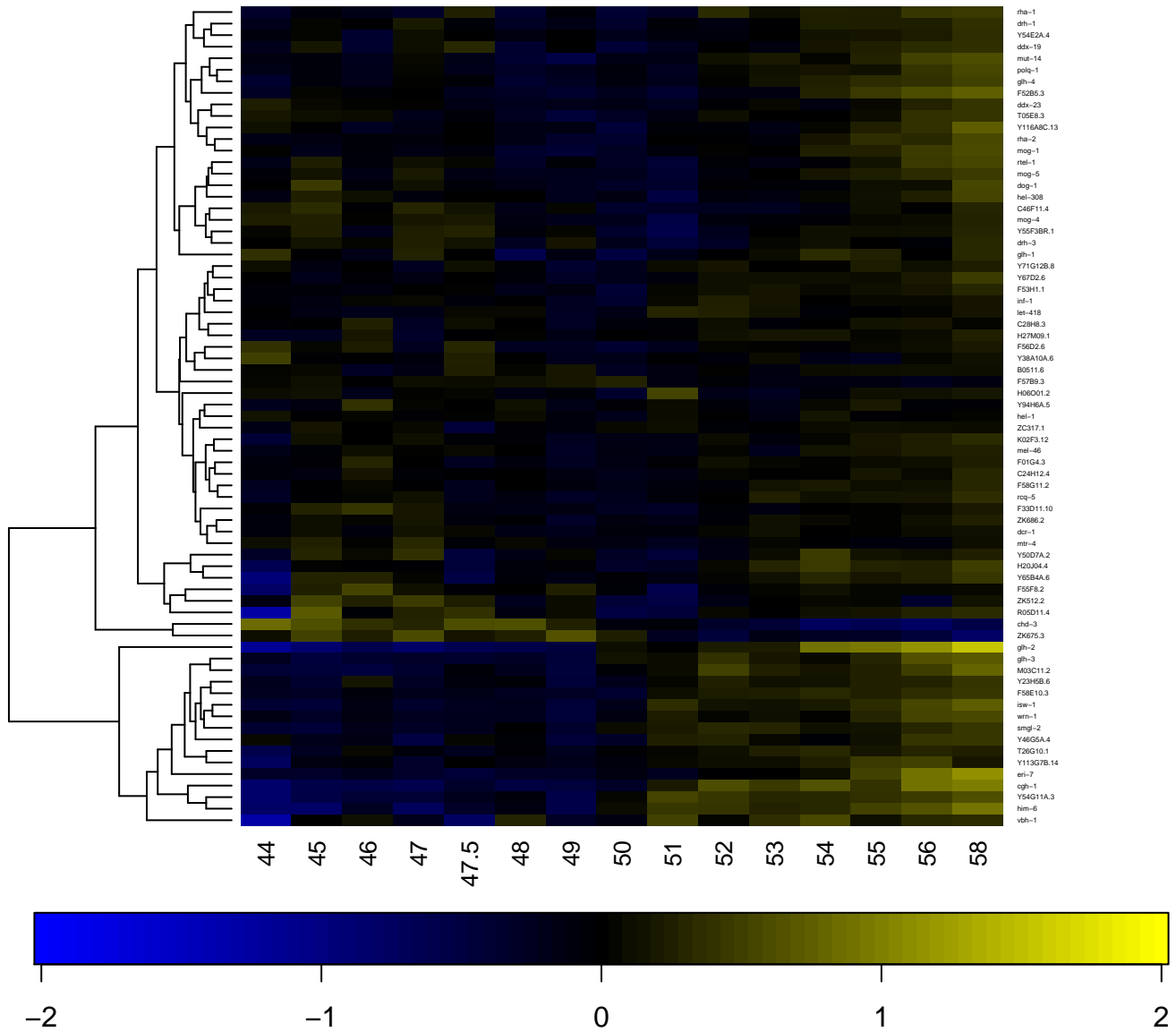
aspartic-type endopeptidase activity



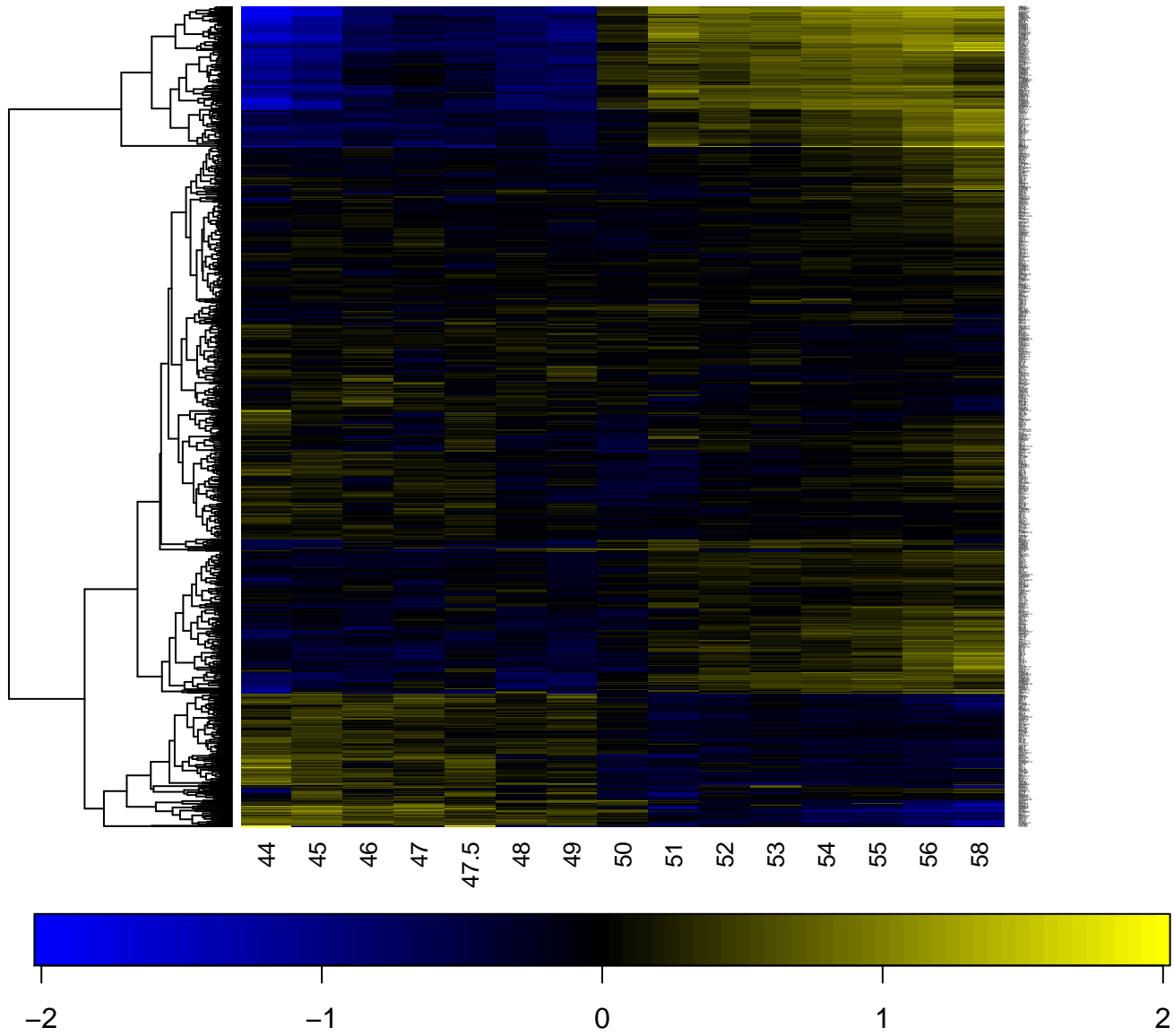
ATP-dependent DNA helicase activity



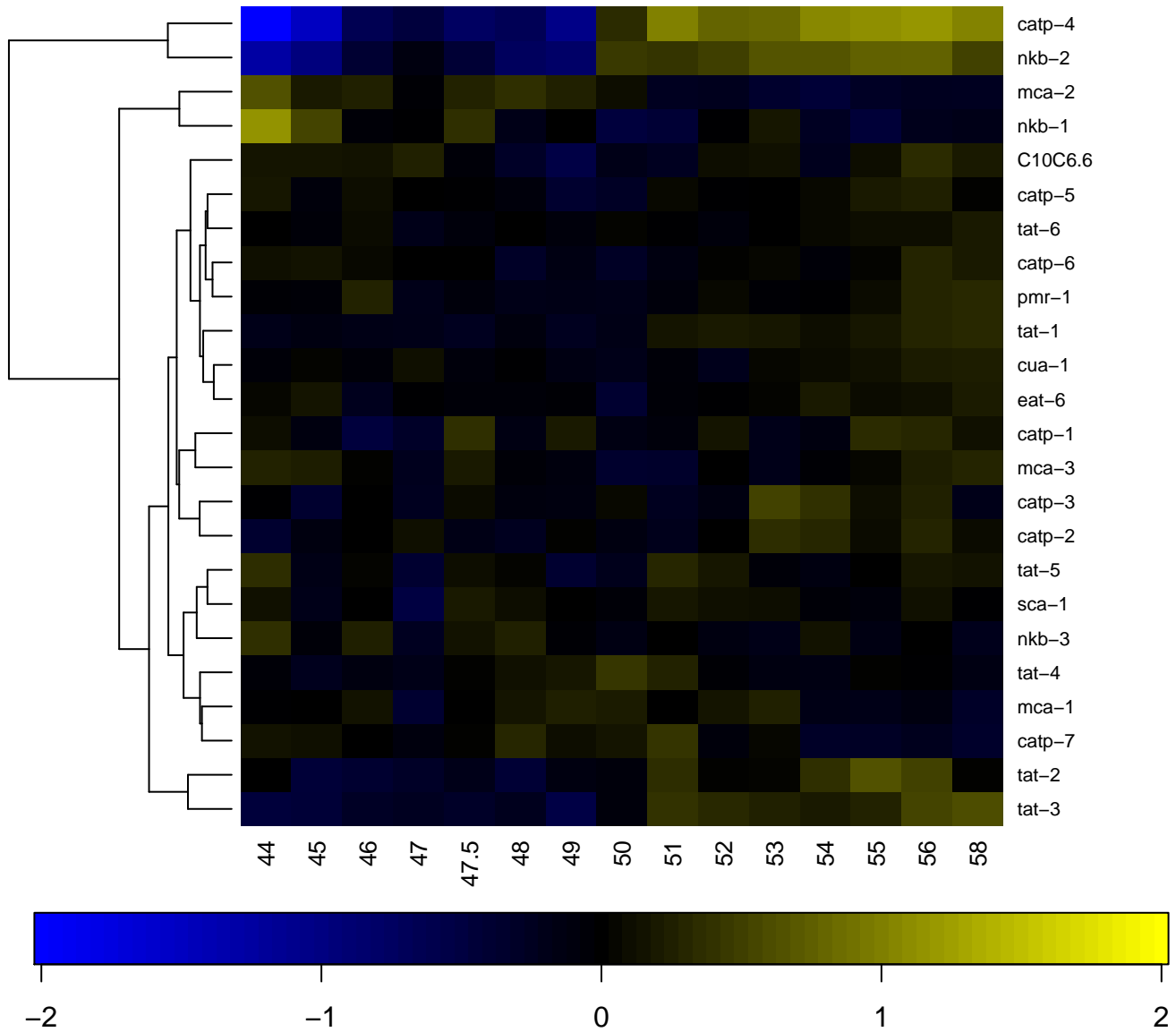
ATP-dependent helicase activity



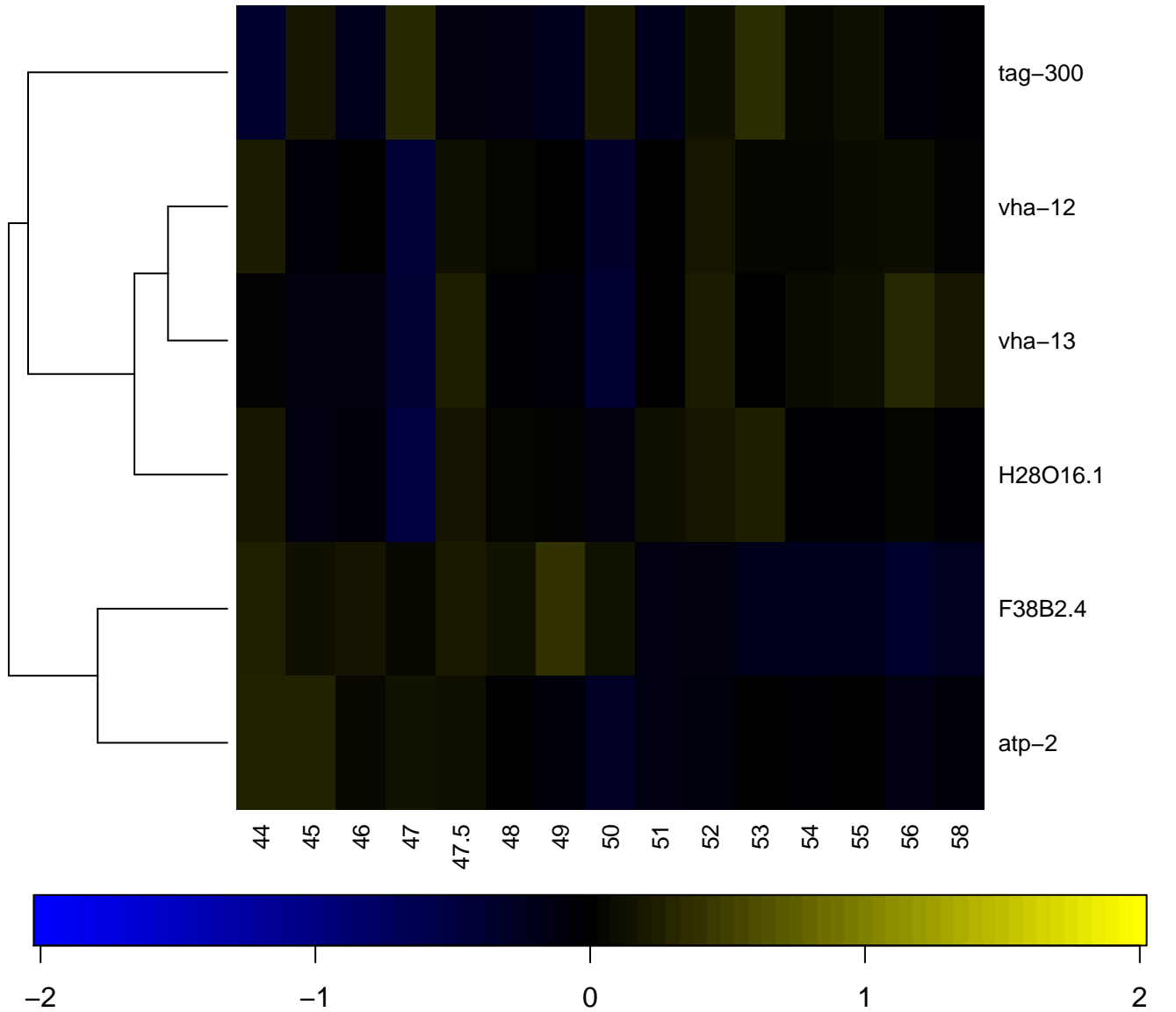
ATP binding



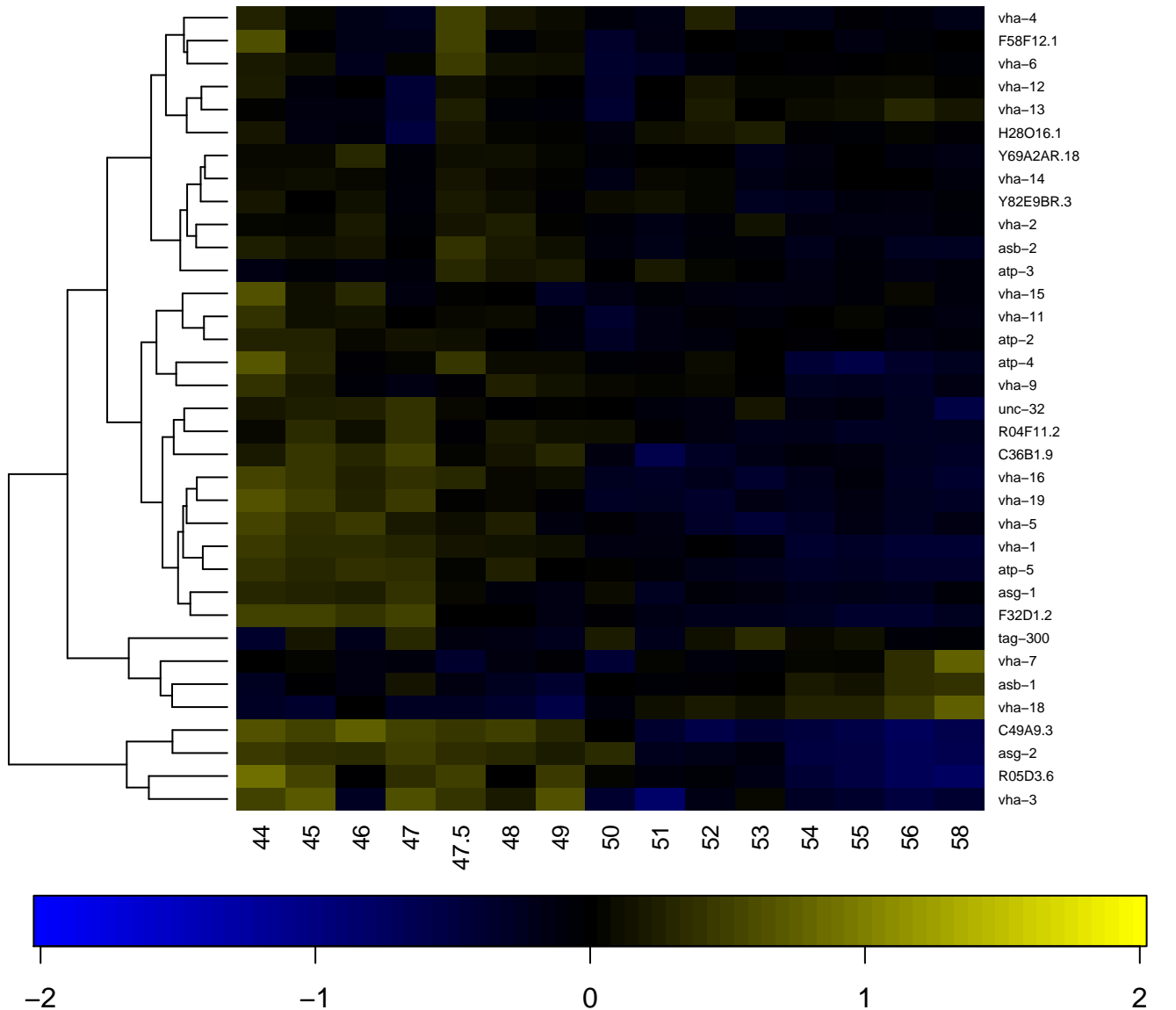
ATP biosynthetic process



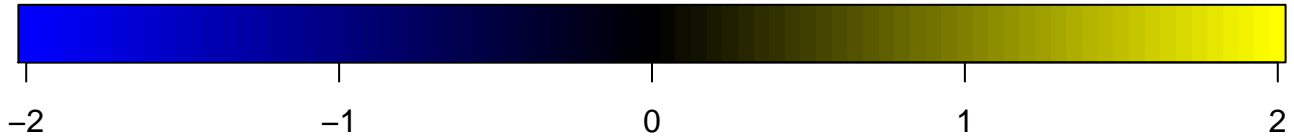
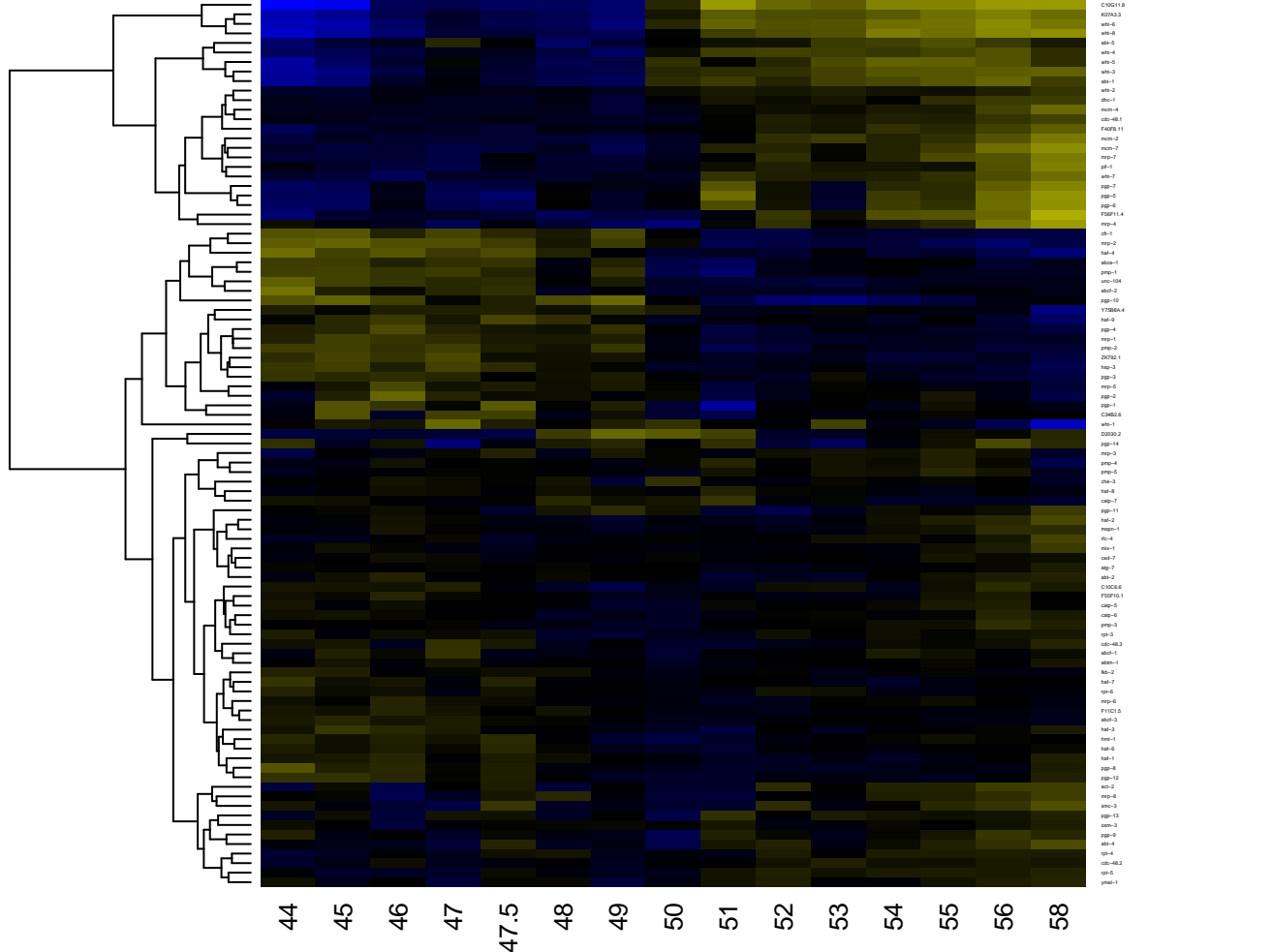
ATP metabolic process



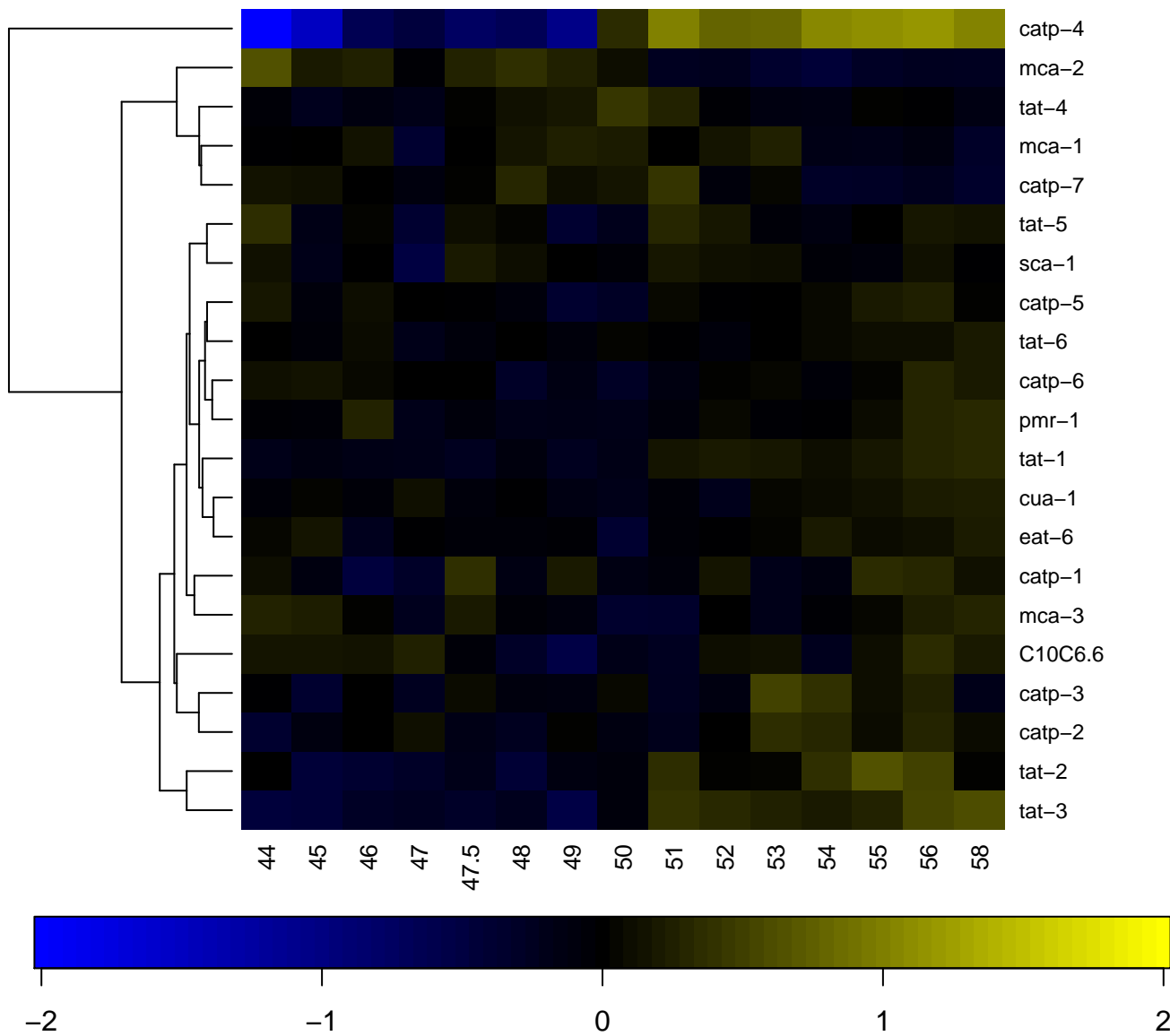
ATP synthesis coupled proton transport



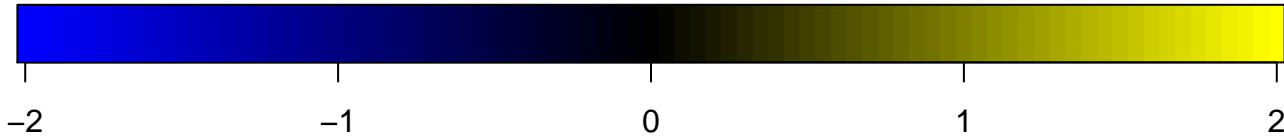
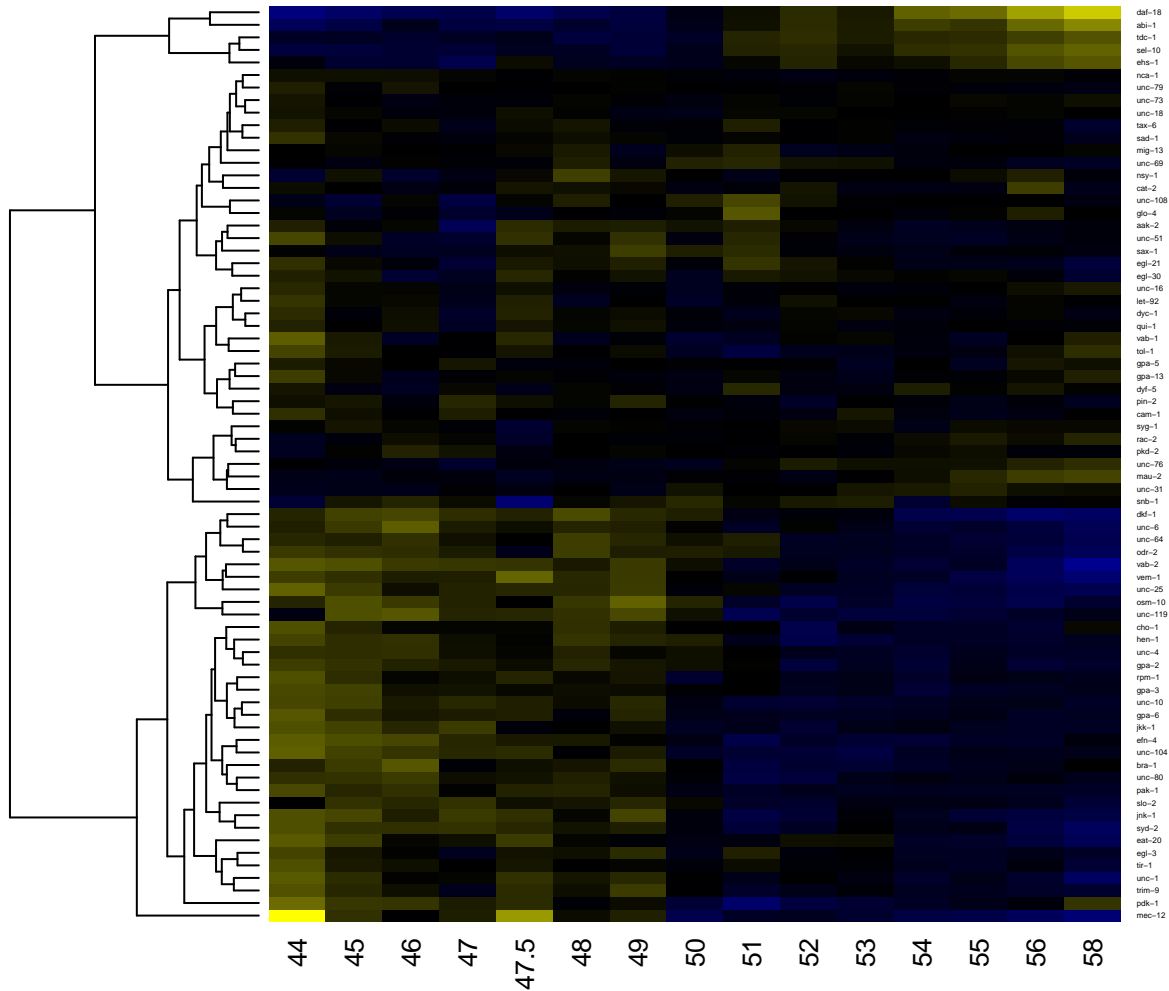
ATPase activity



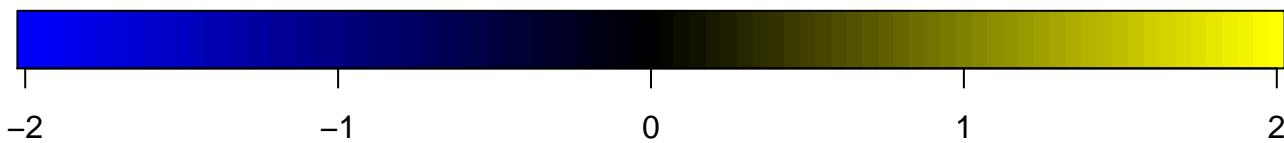
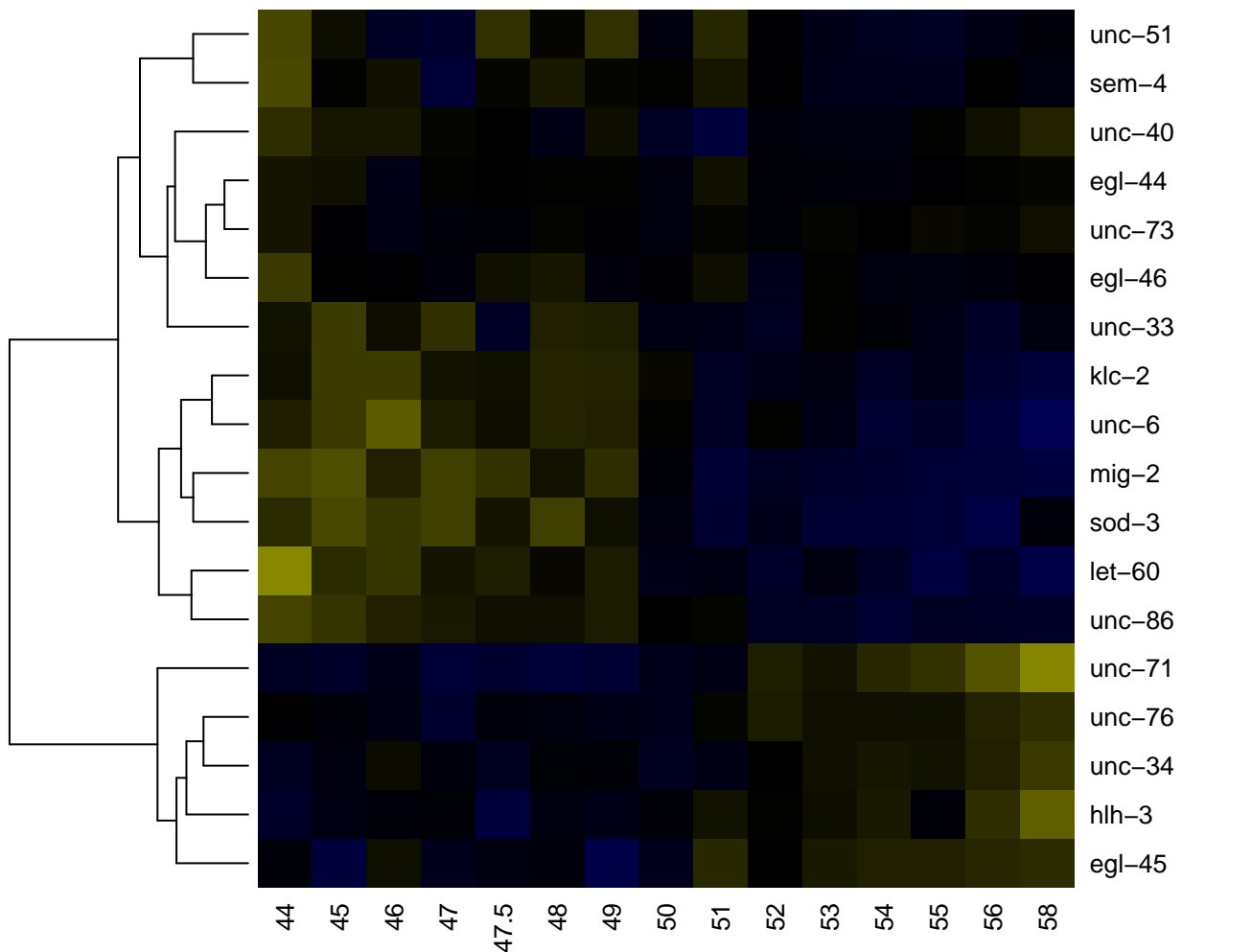
, coupled to transmembrane movement of ions, phosphoryl



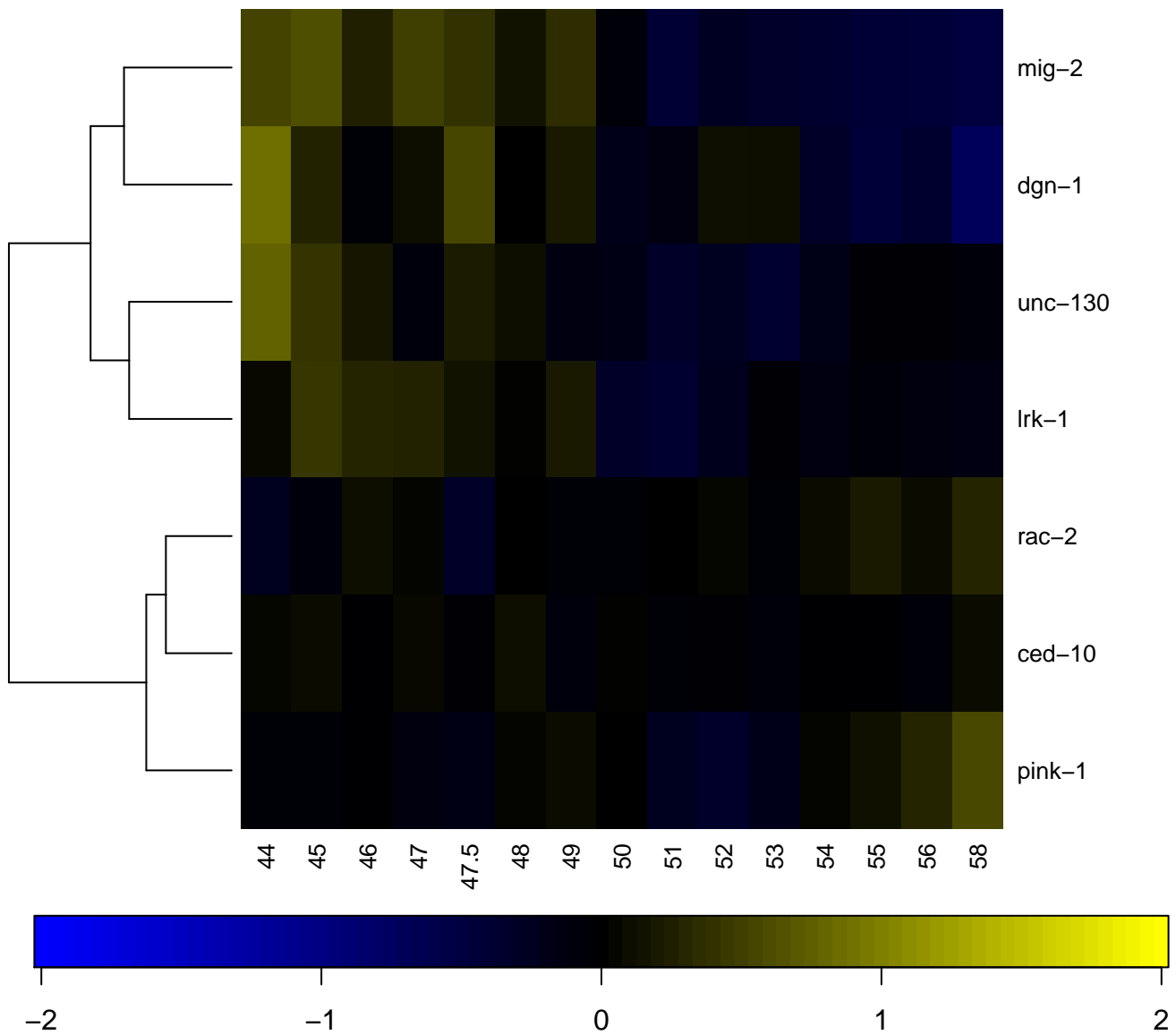
axon



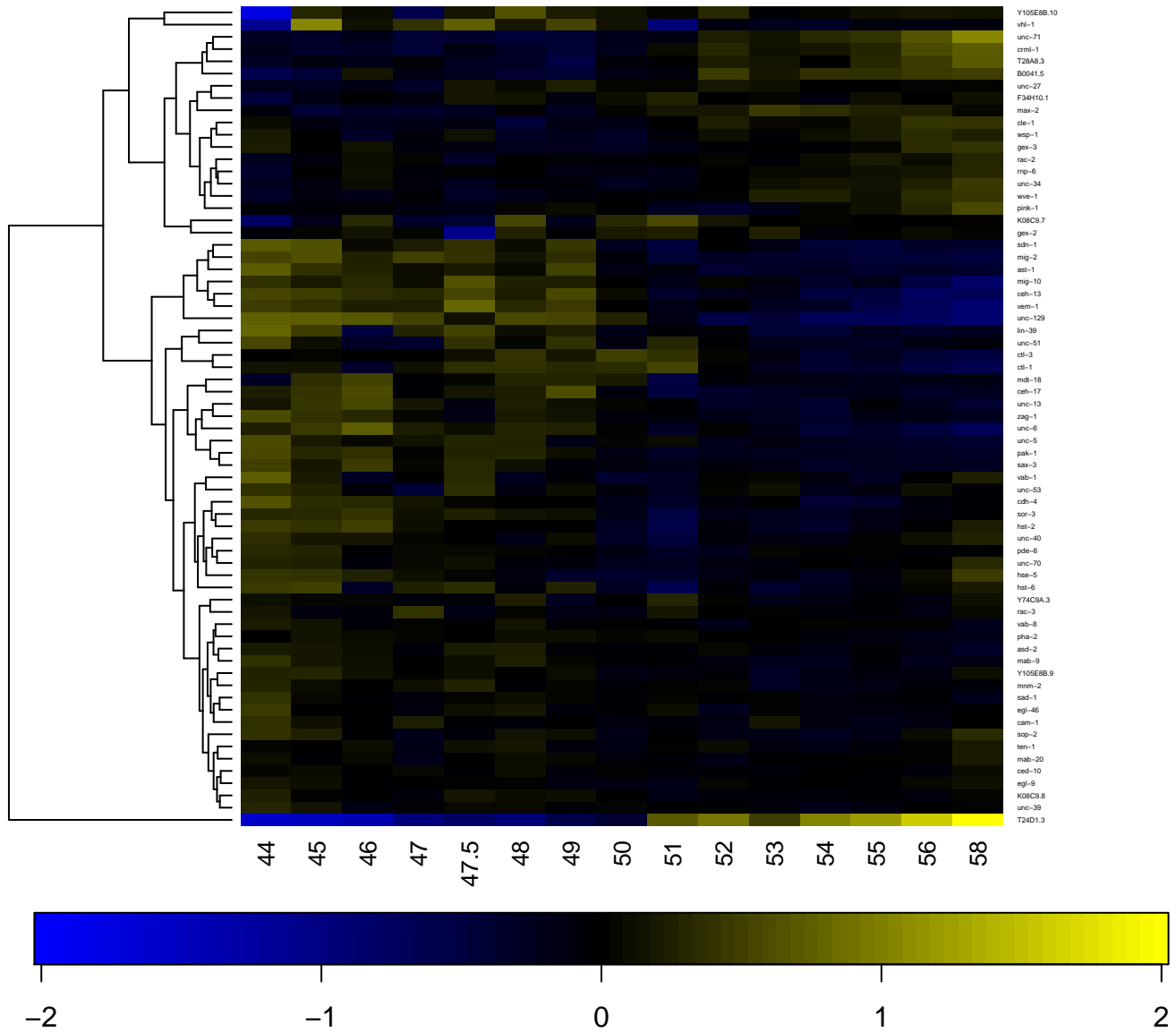
axon extension



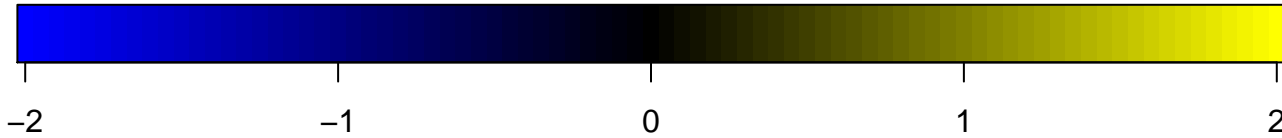
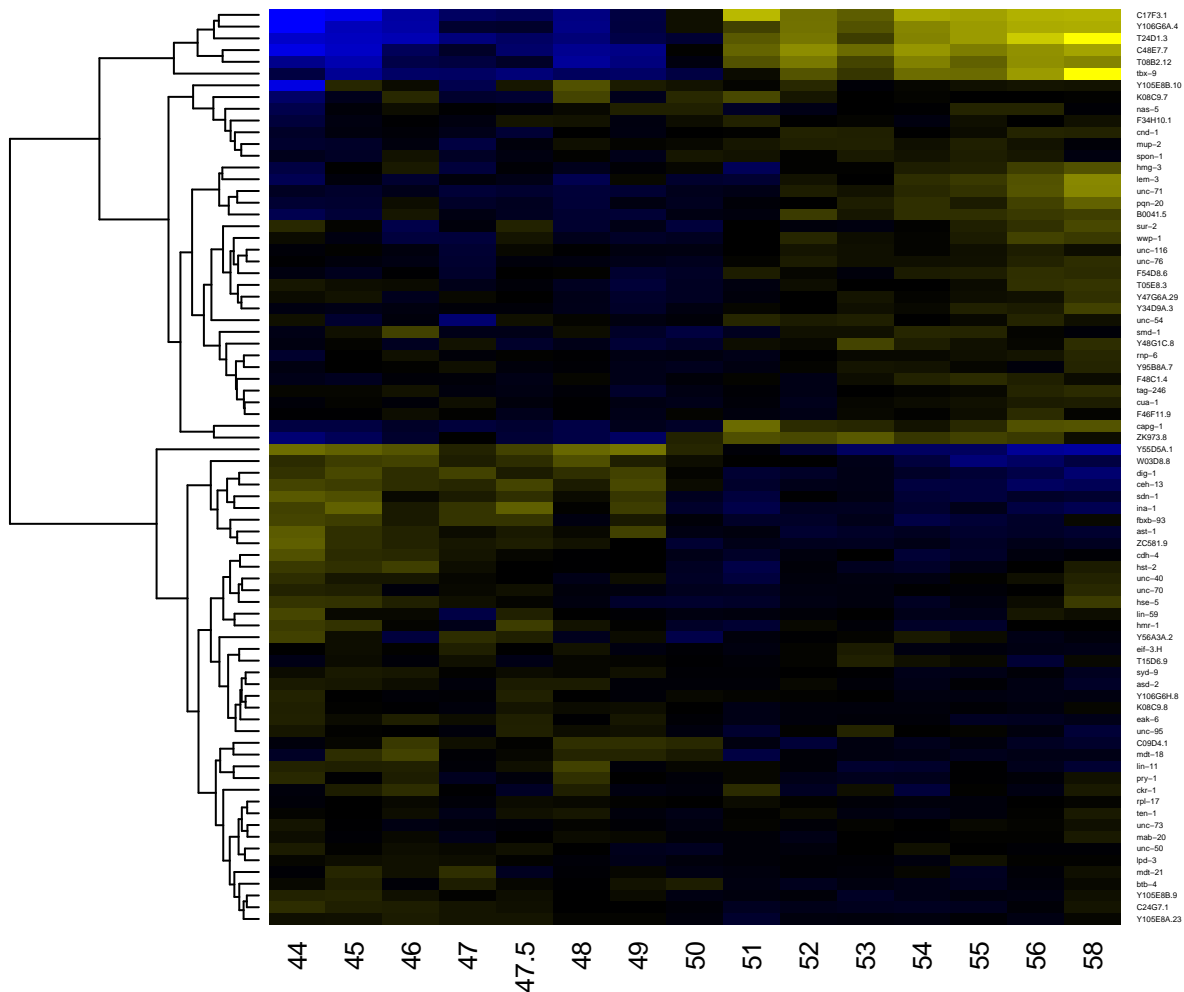
axon extension involved in axon guidance



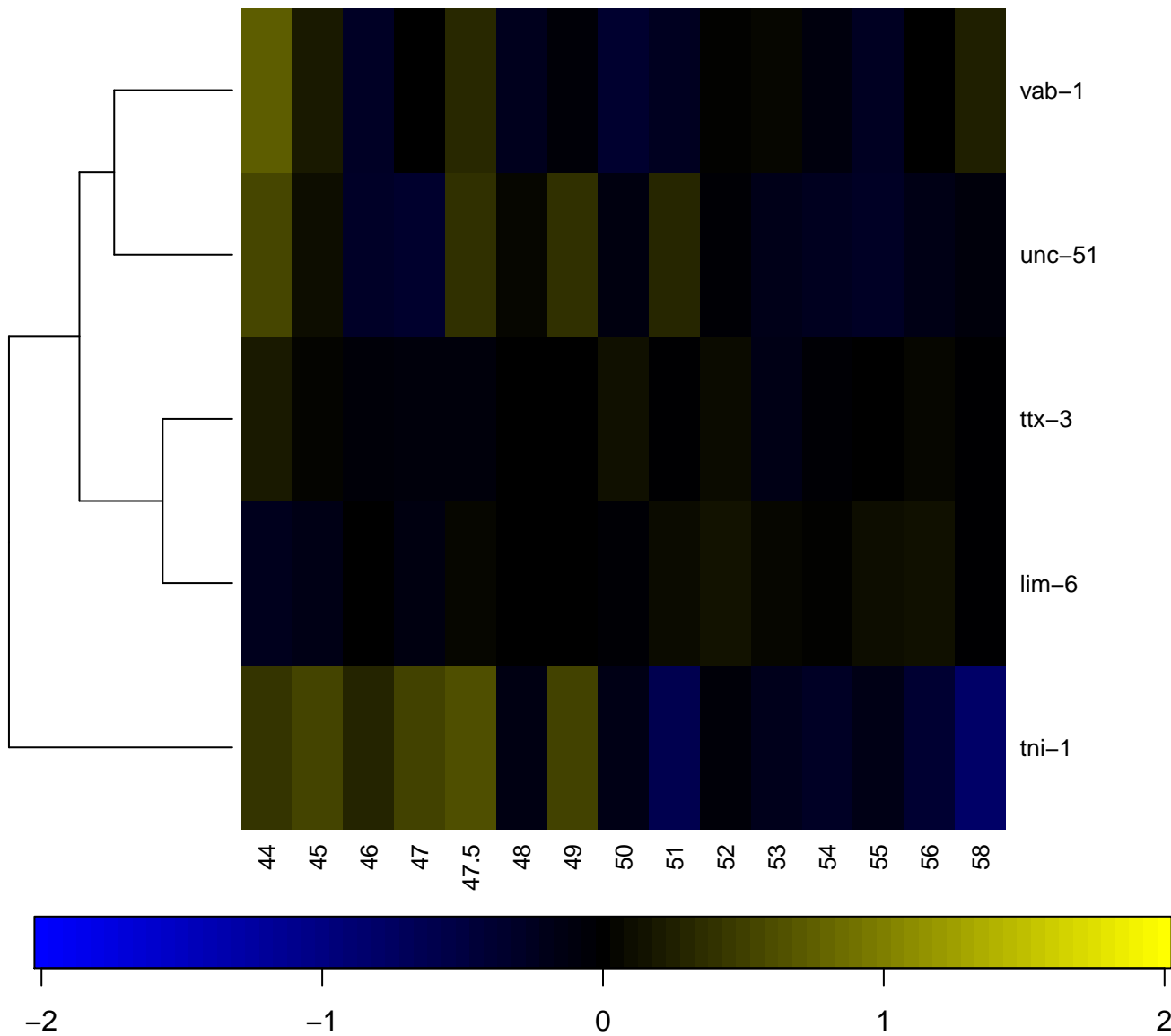
axon guidance



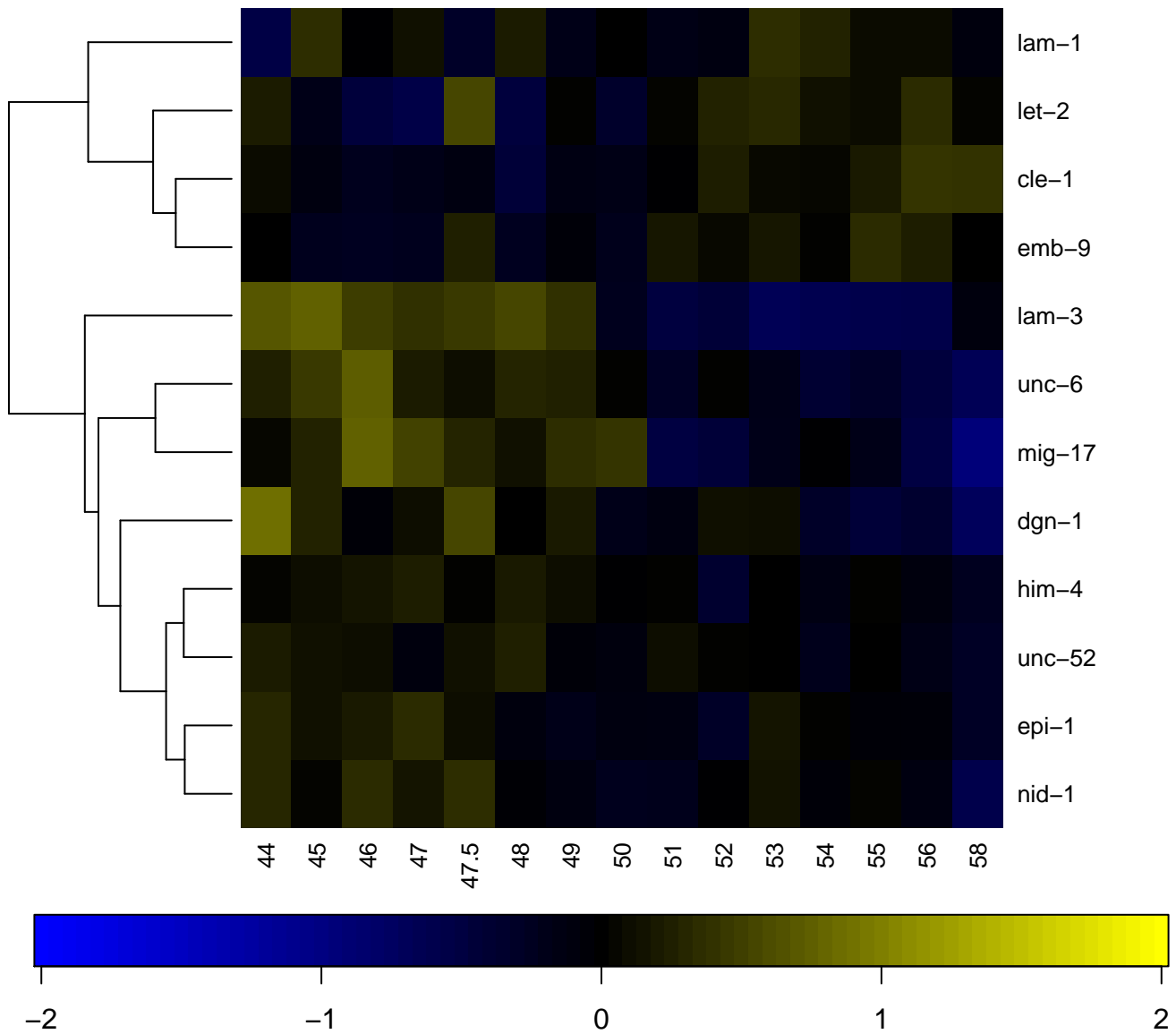
axonal fasciculation



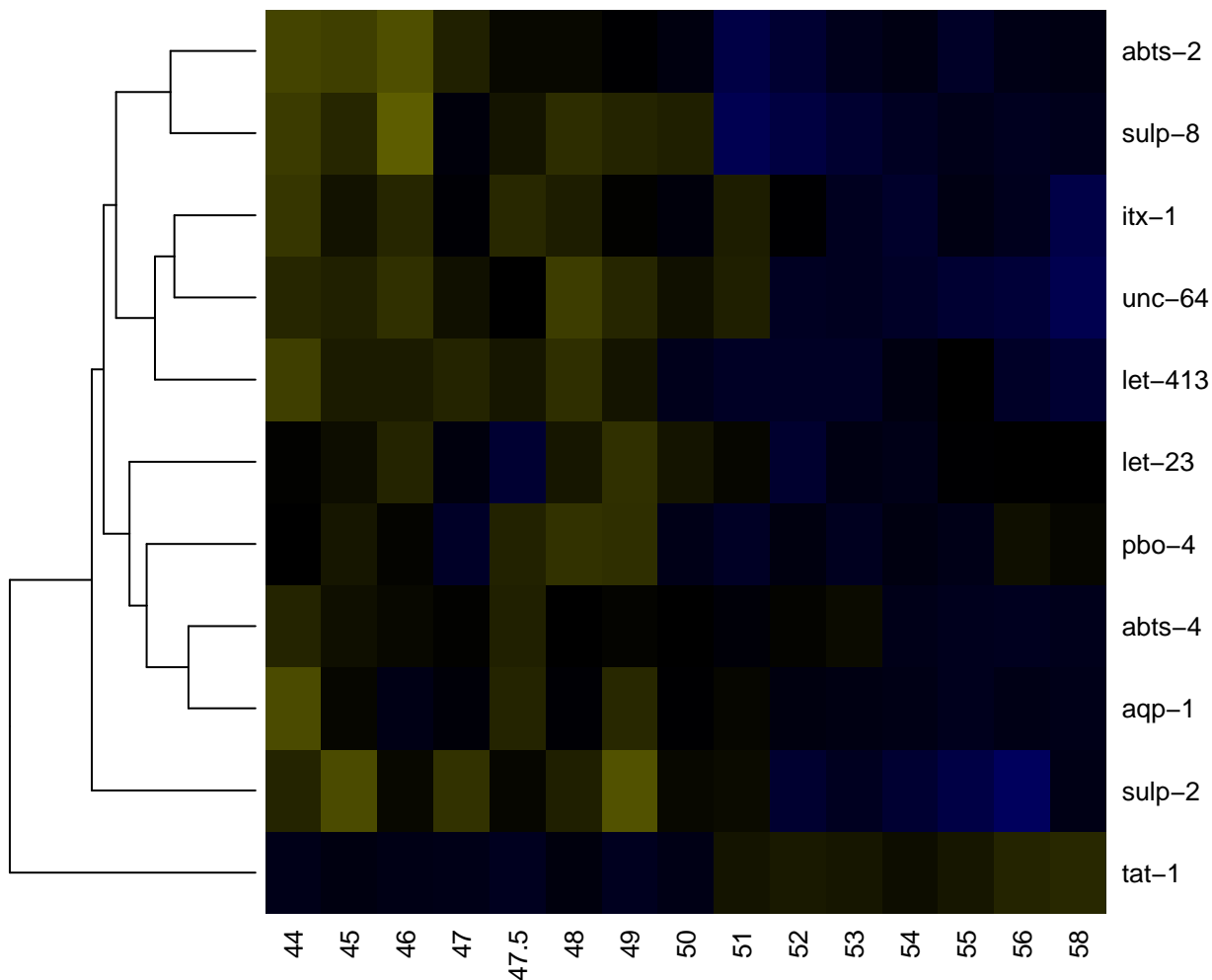
axonogenesis



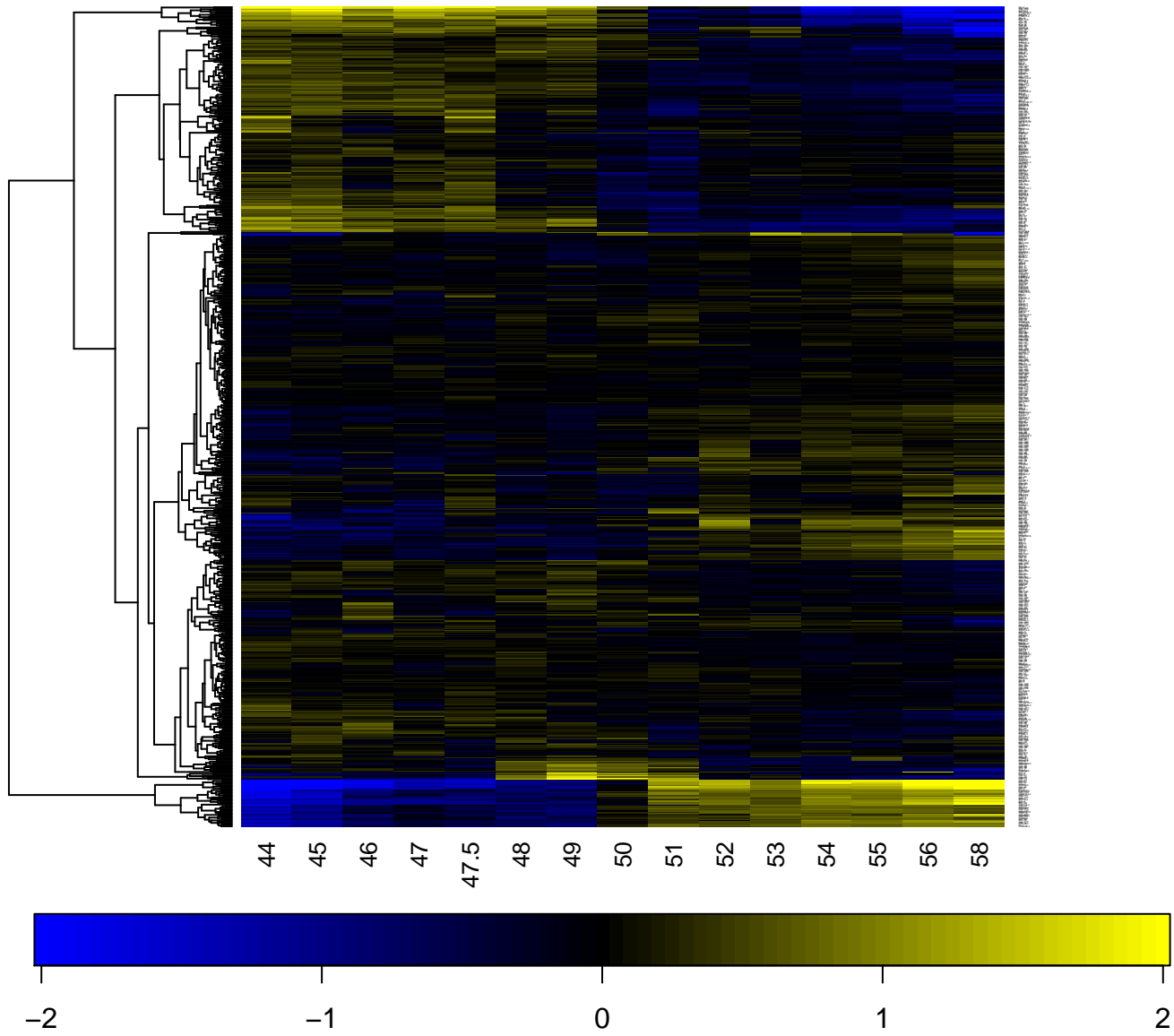
basement membrane



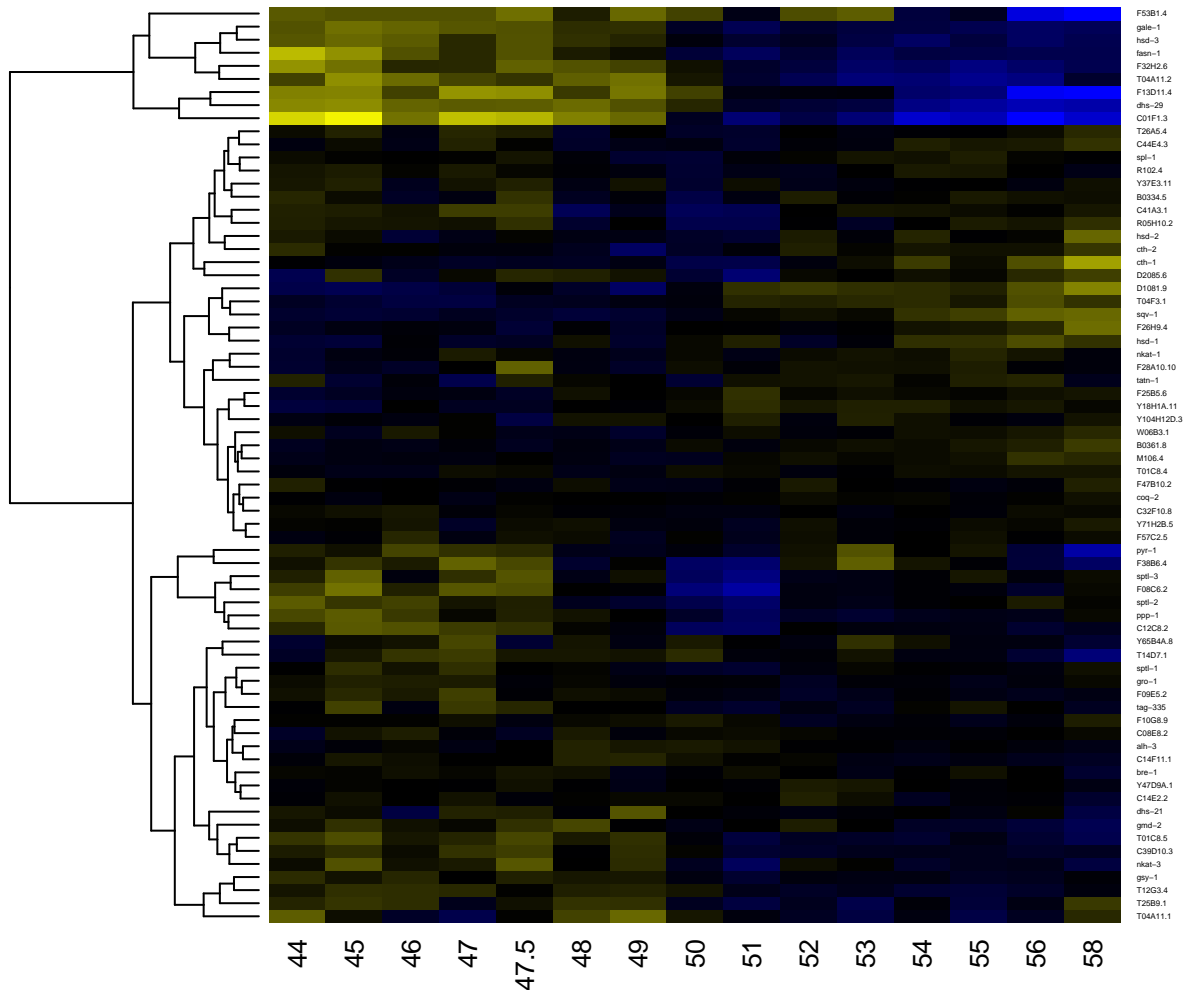
basolateral plasma membrane



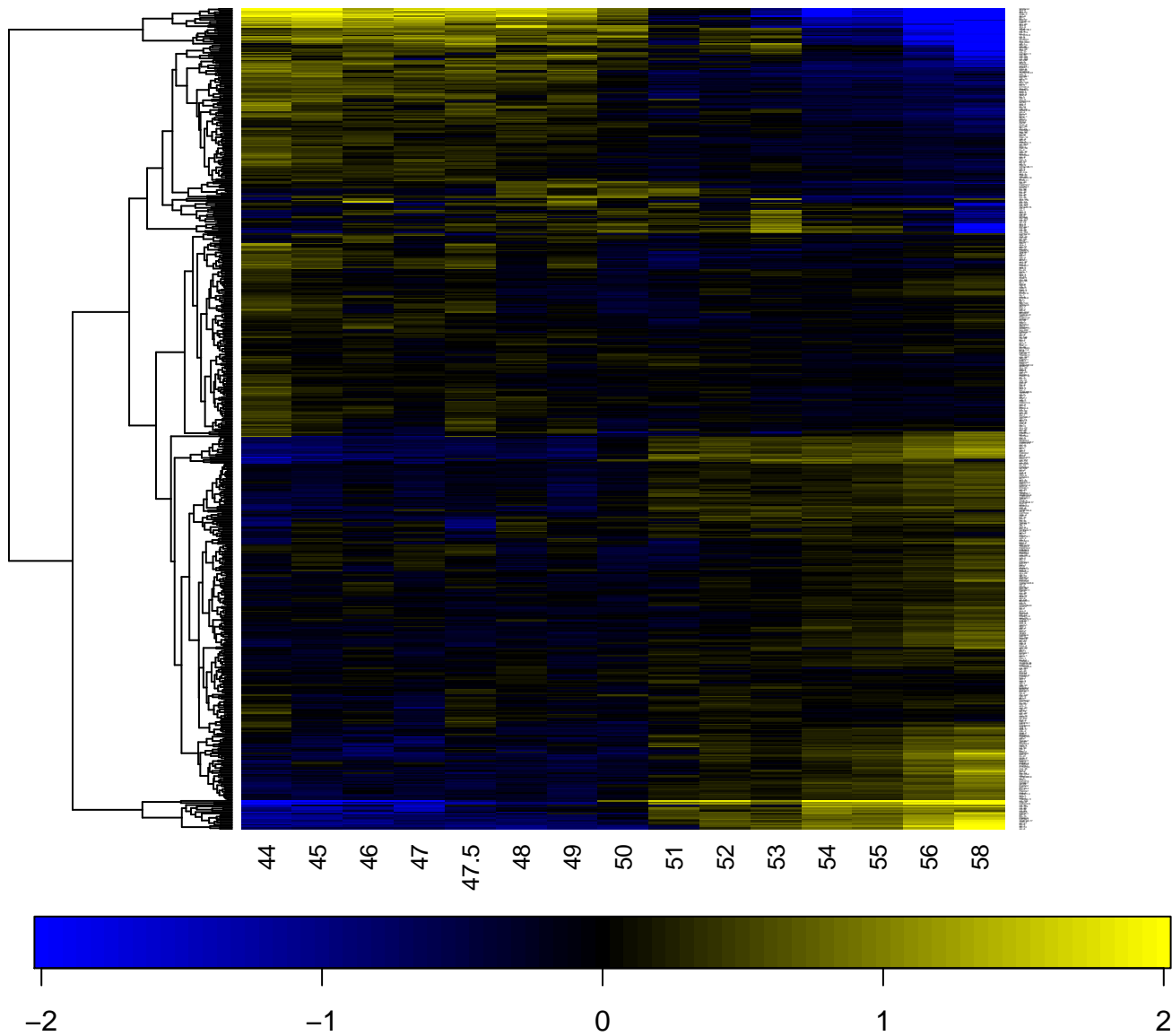
binding



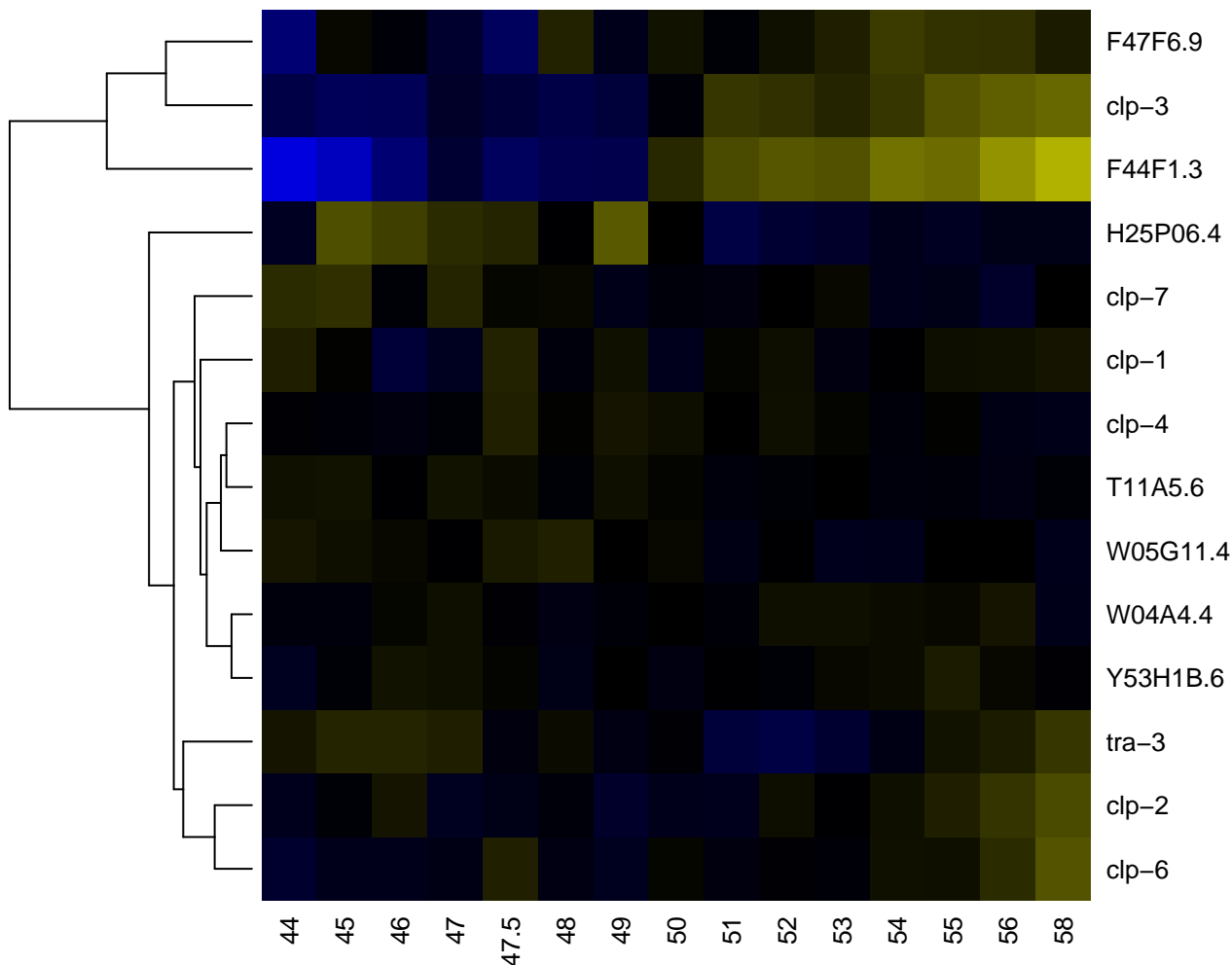
biosynthetic process



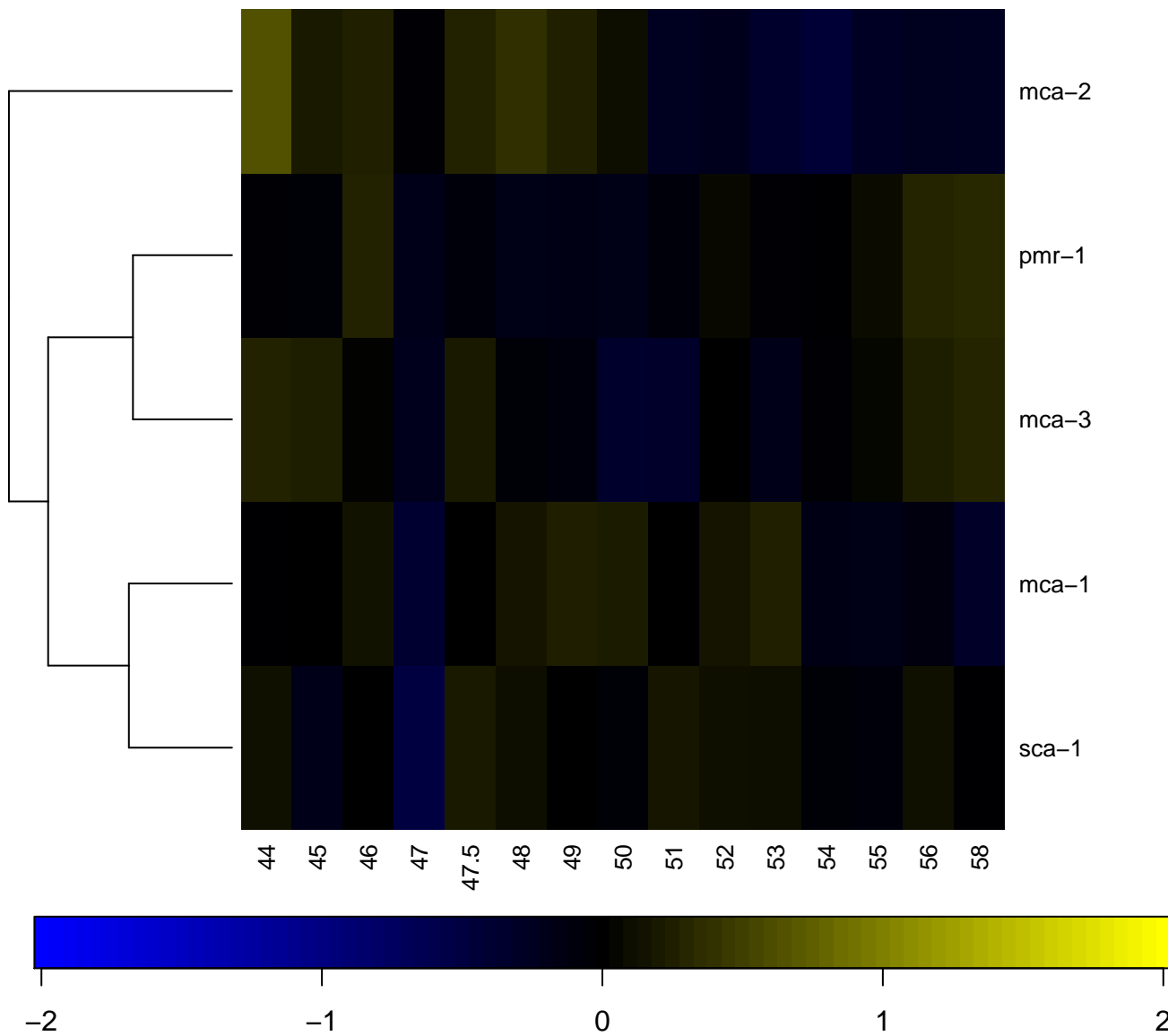
body morphogenesis



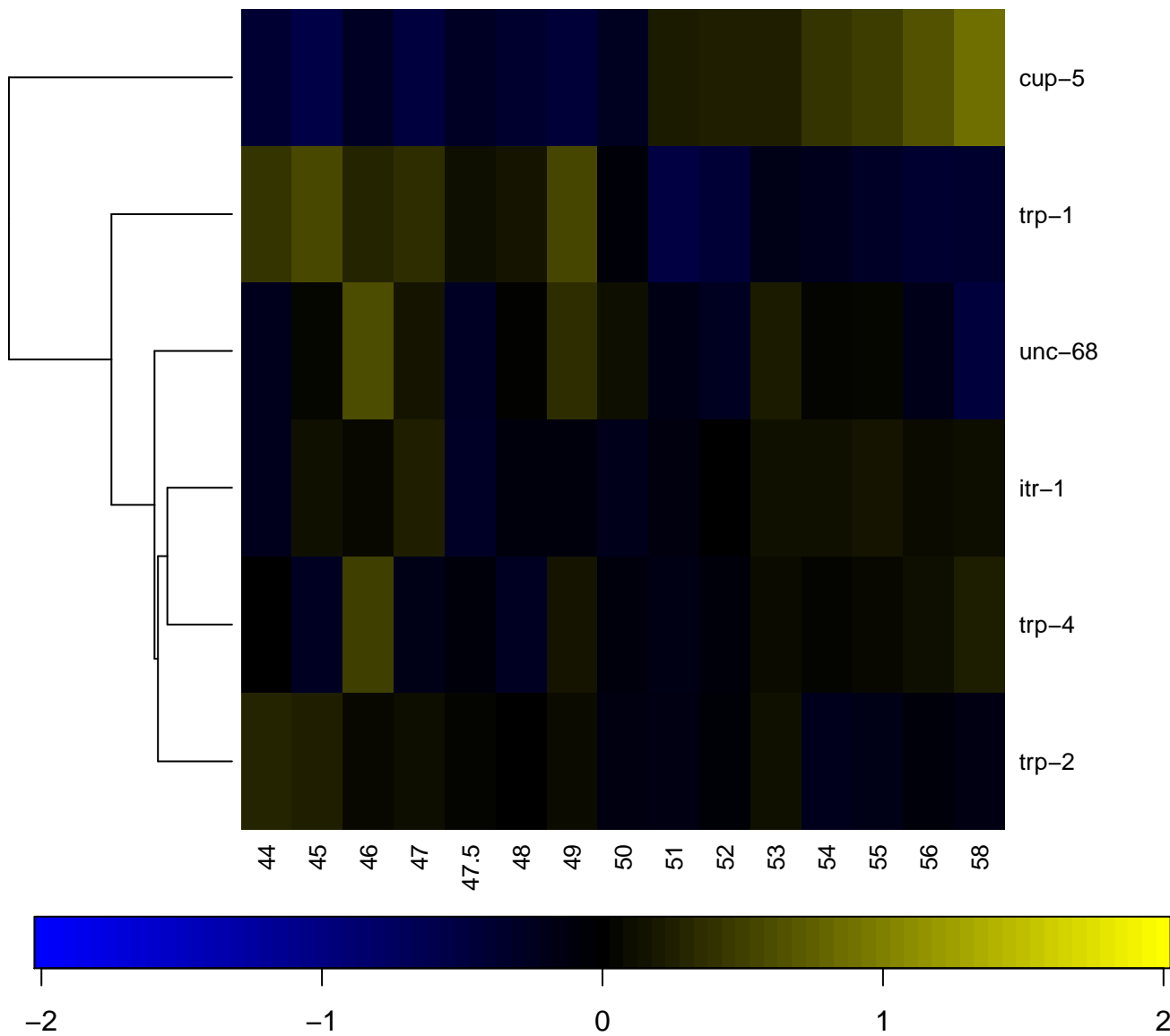
calcium-dependent cysteine-type endopeptidase activity



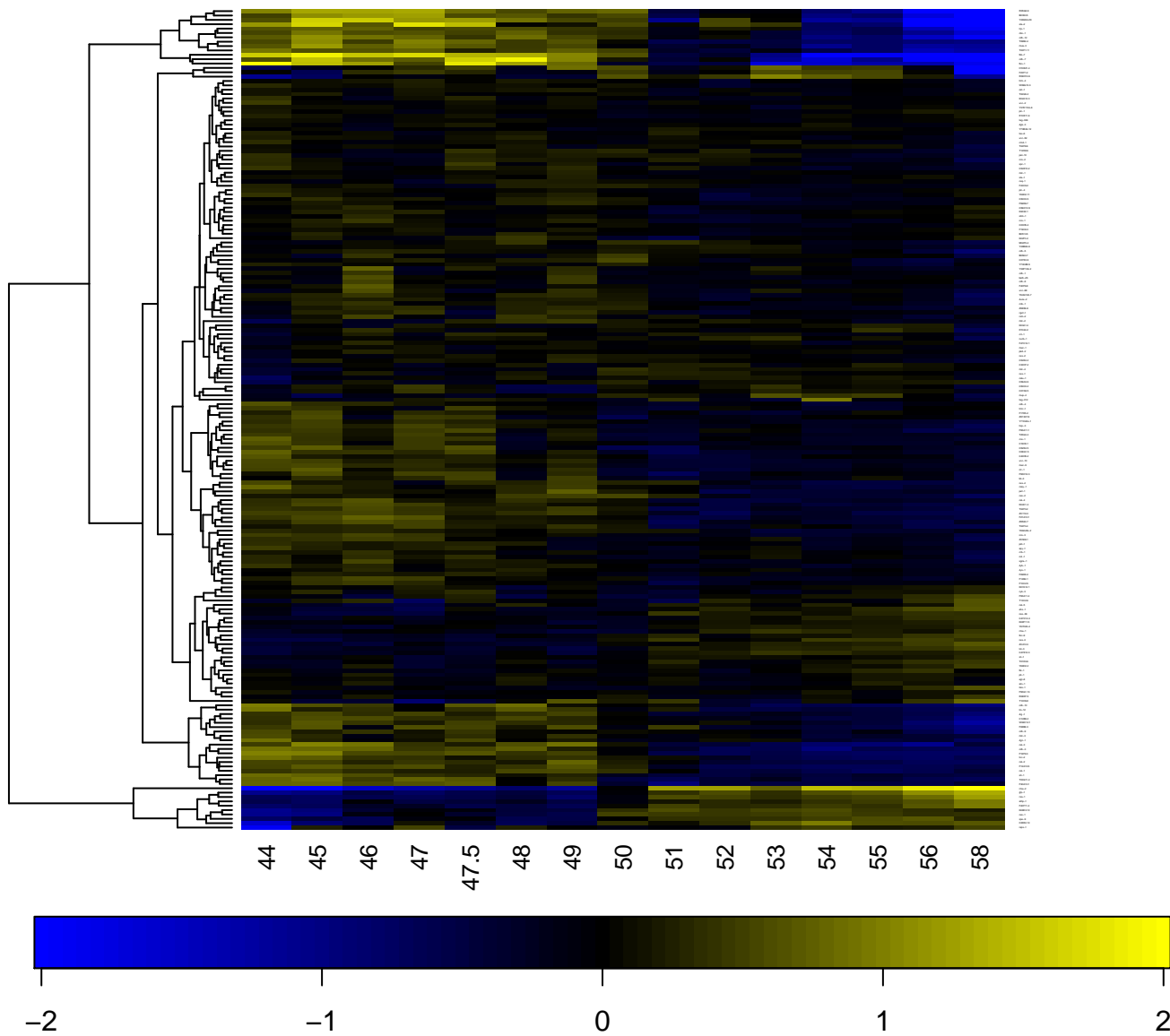
calcium-transporting ATPase activity



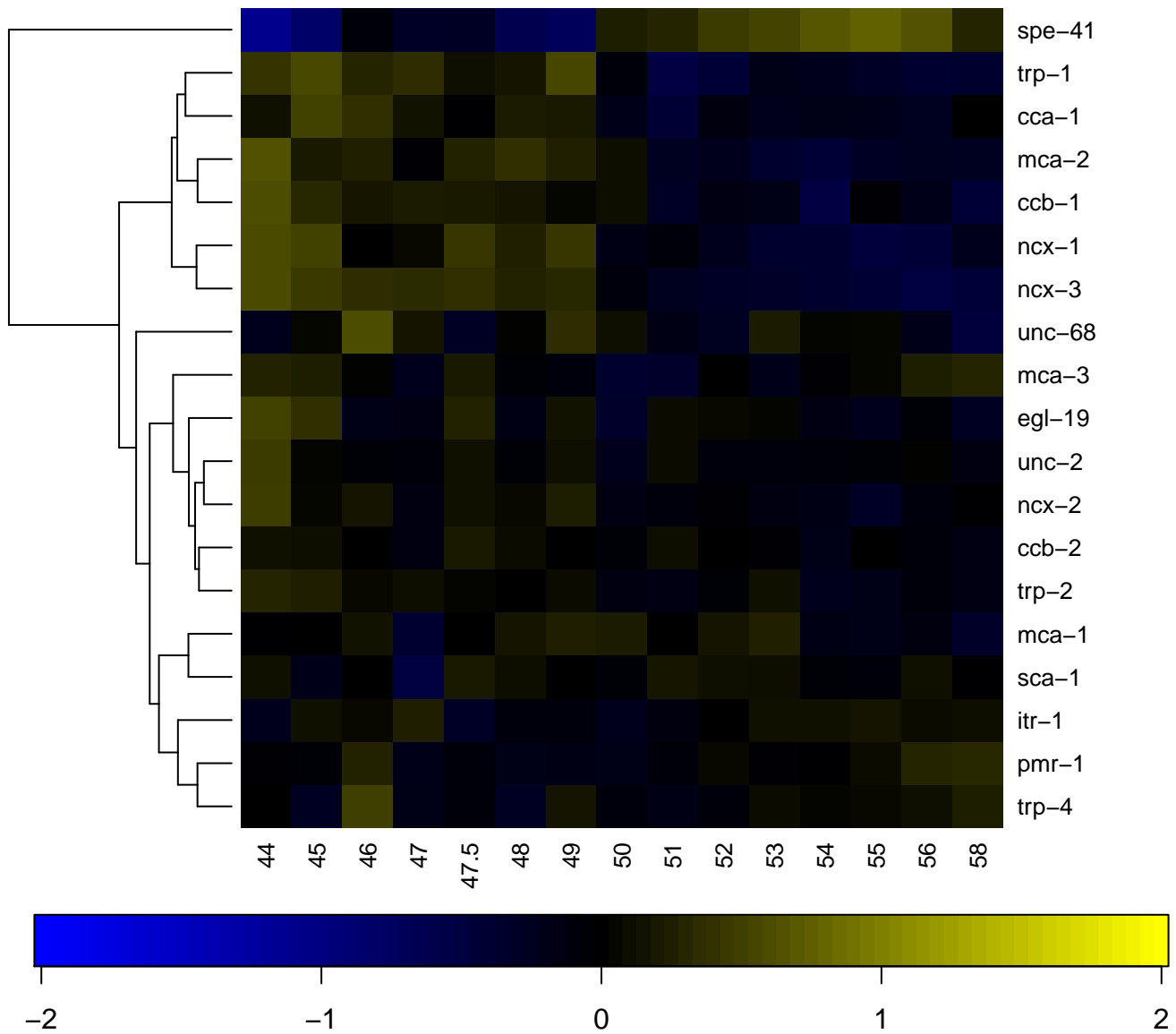
calcium channel activity



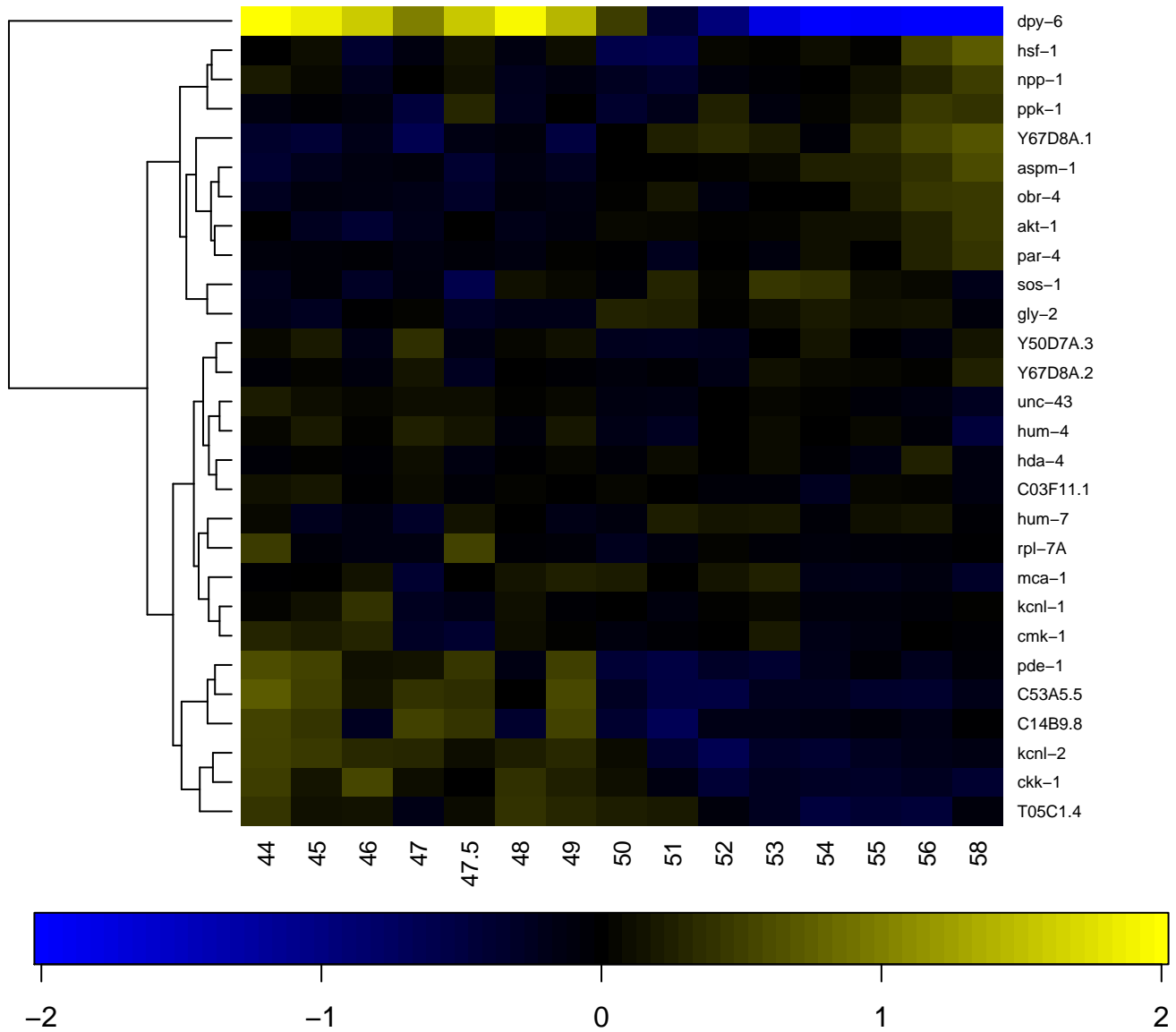
calcium ion binding



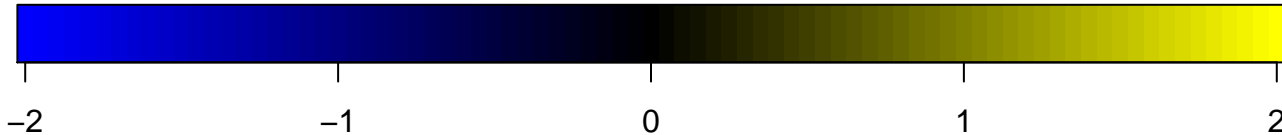
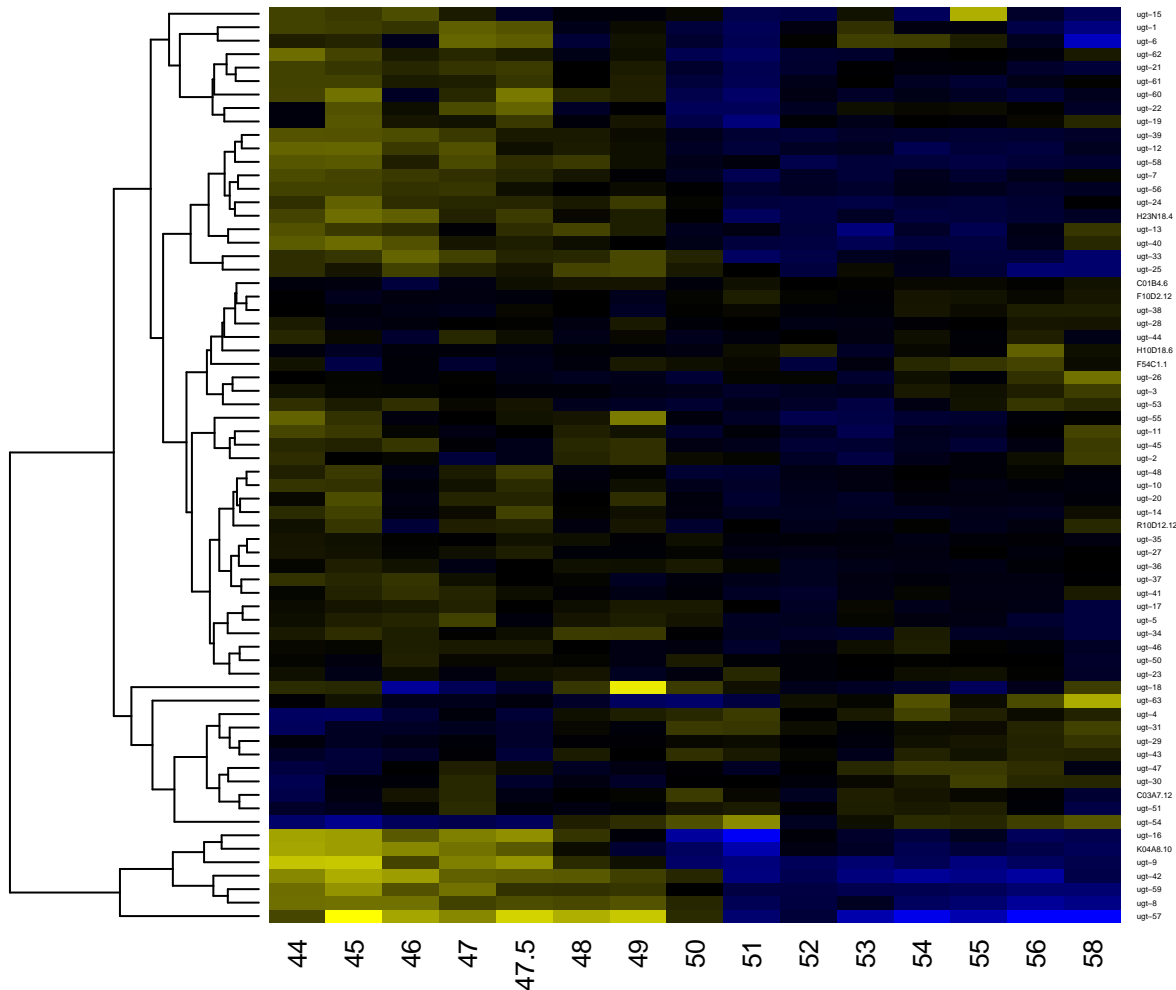
calcium ion transport



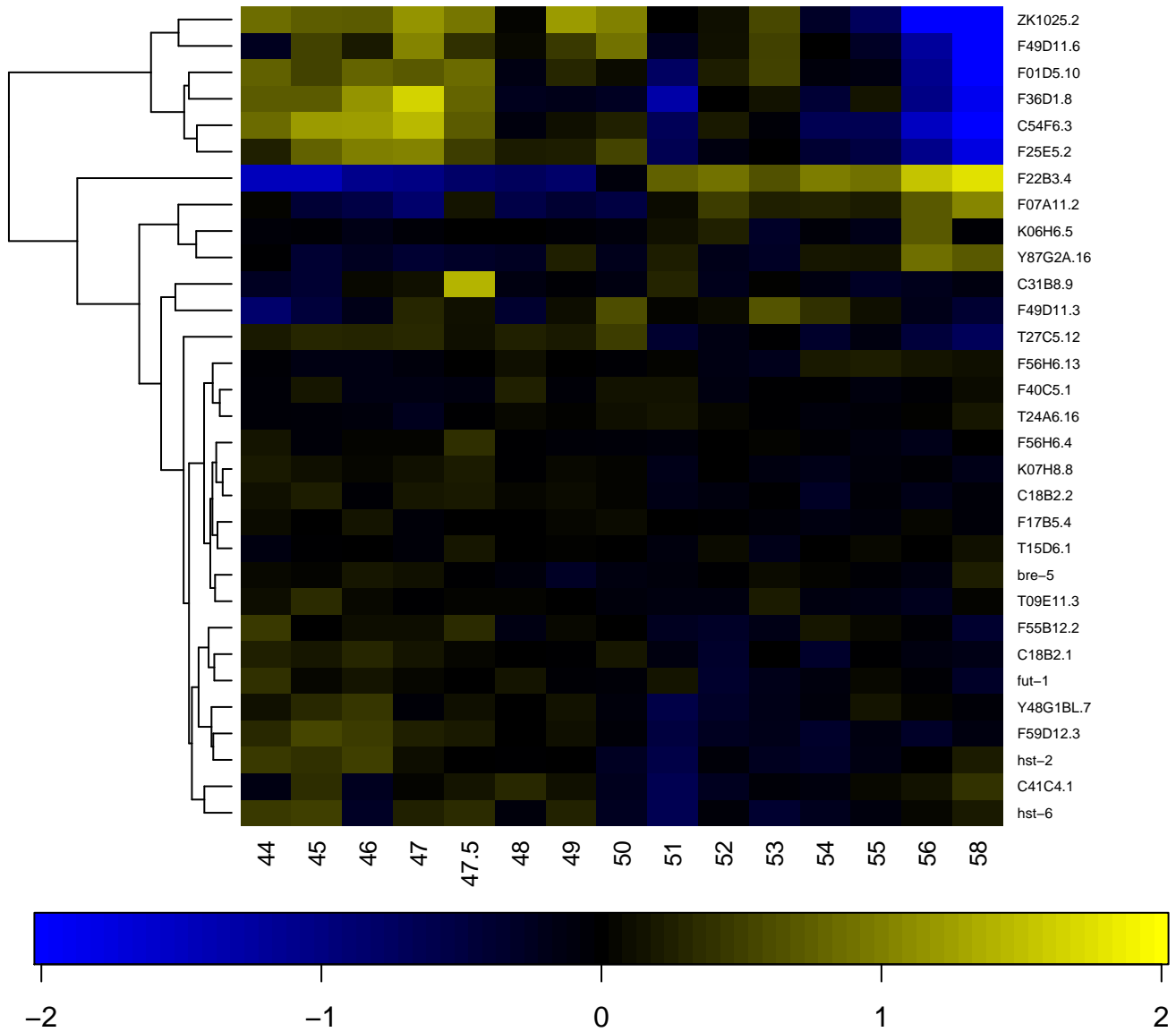
calmodulin binding



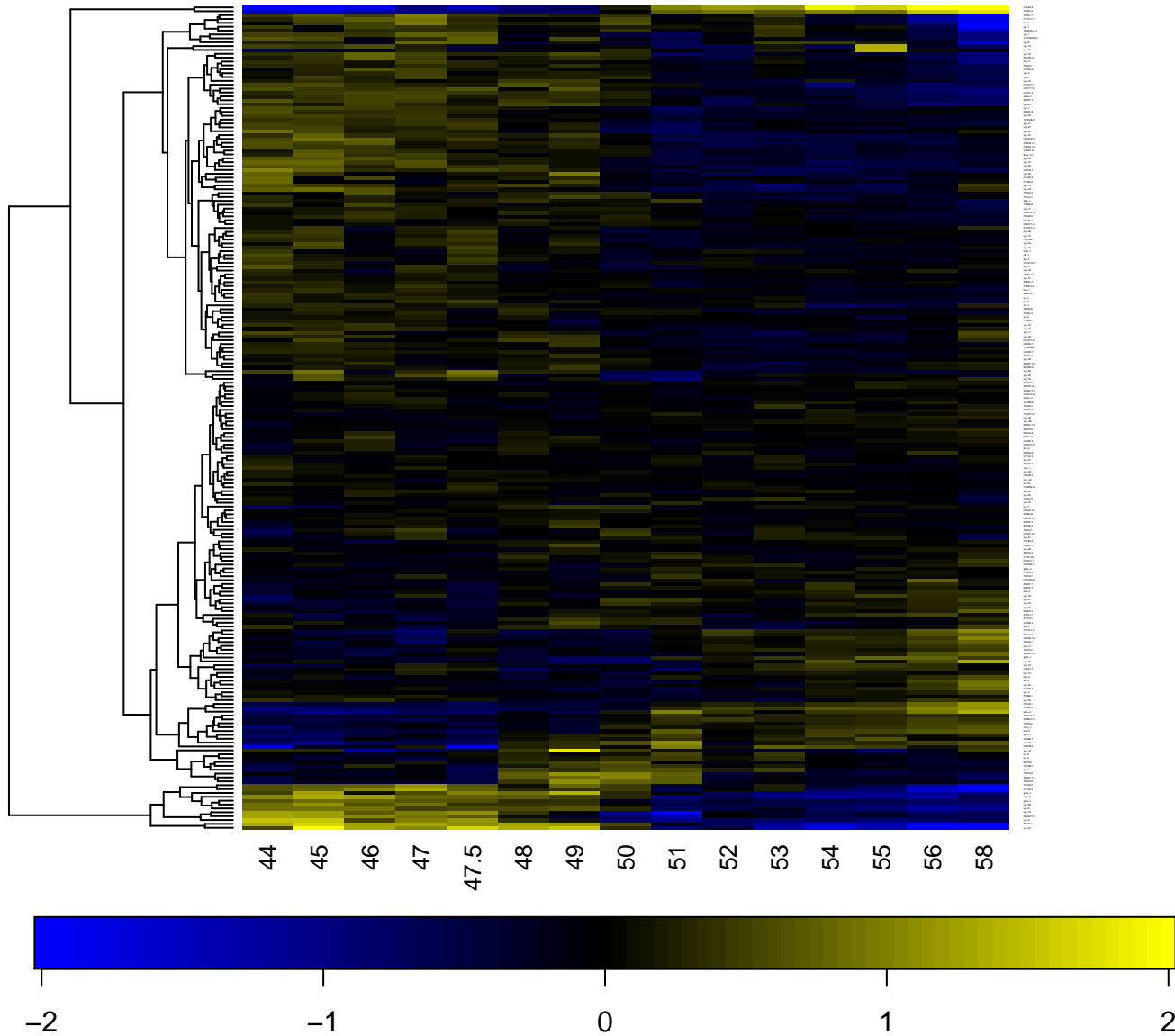
carbohydrate binding



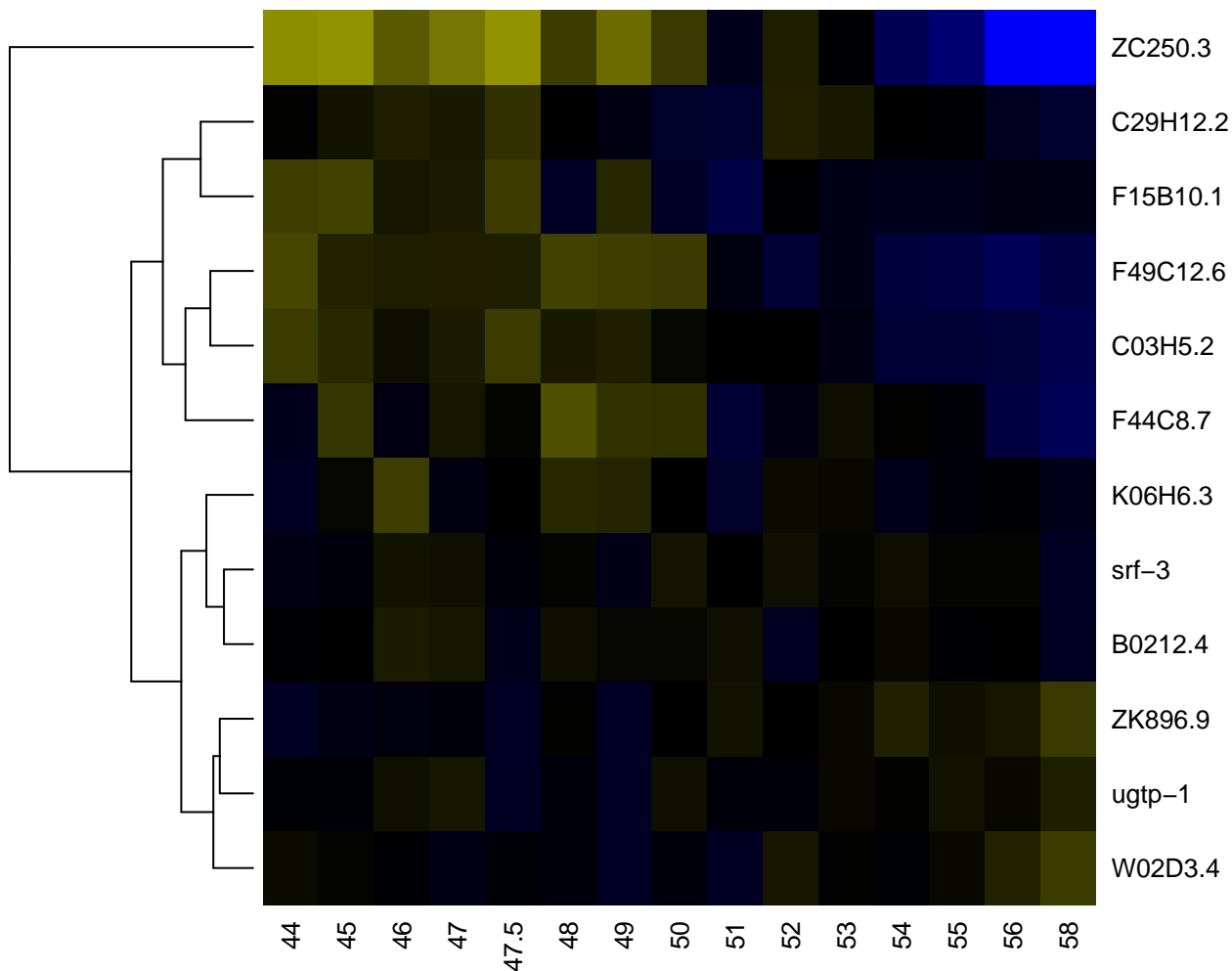
carbohydrate biosynthetic process



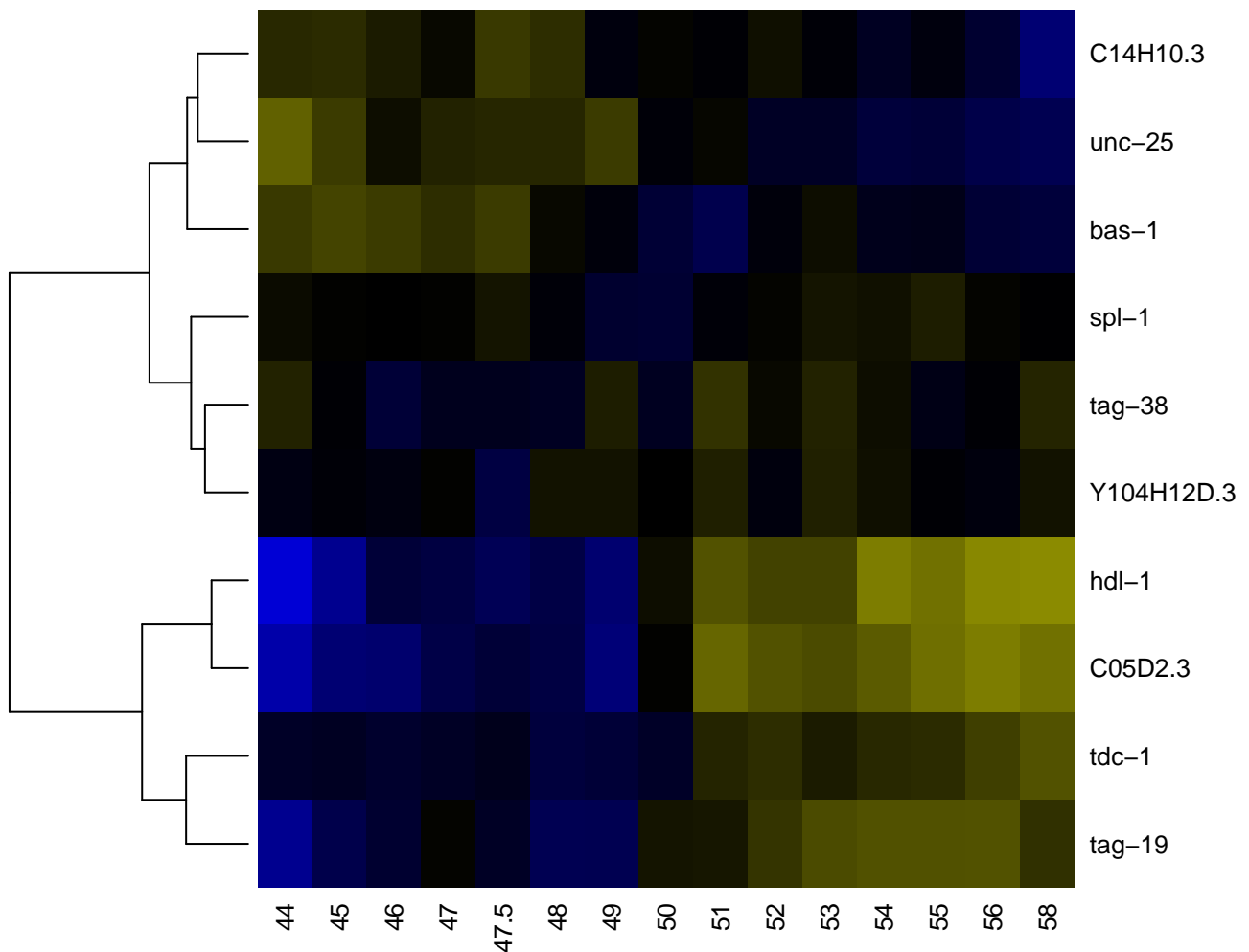
carbohydrate metabolic process



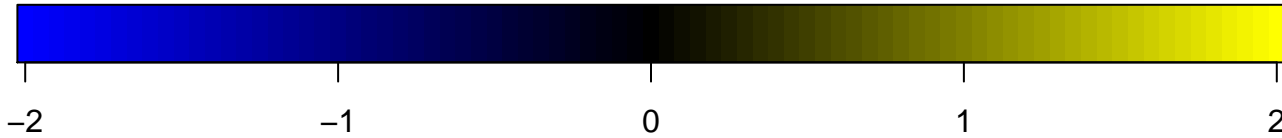
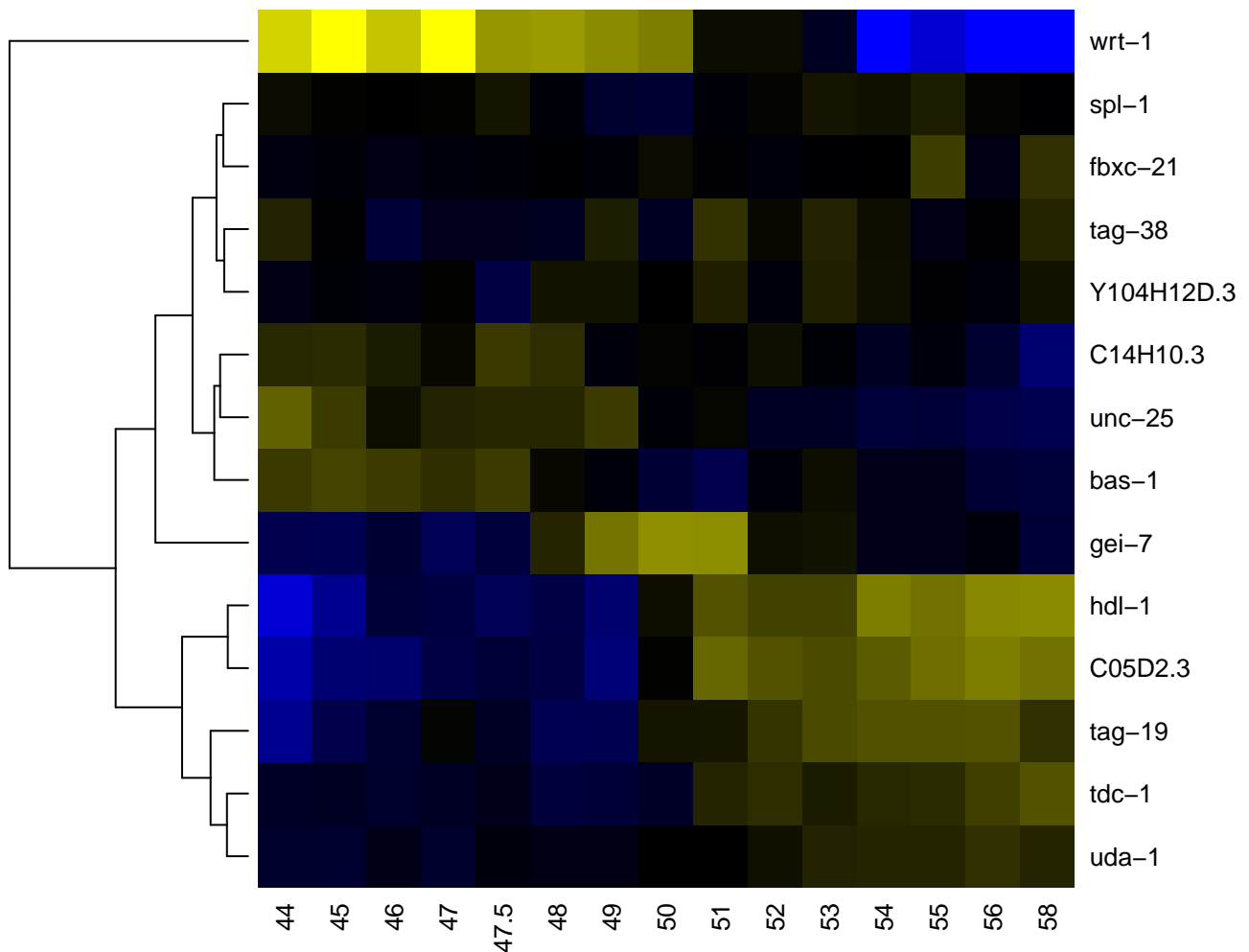
carbohydrate transport



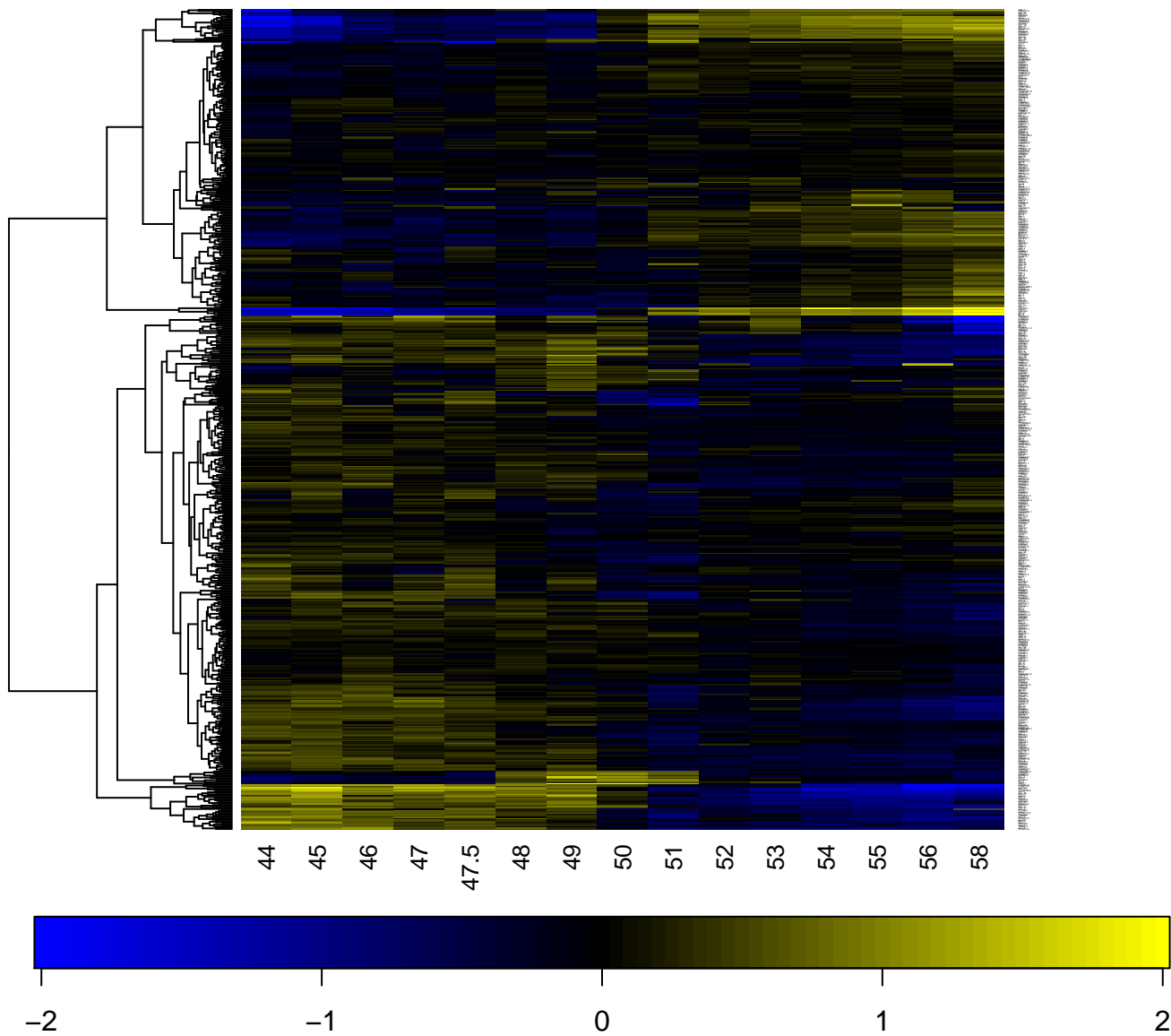
carboxy-lyase activity



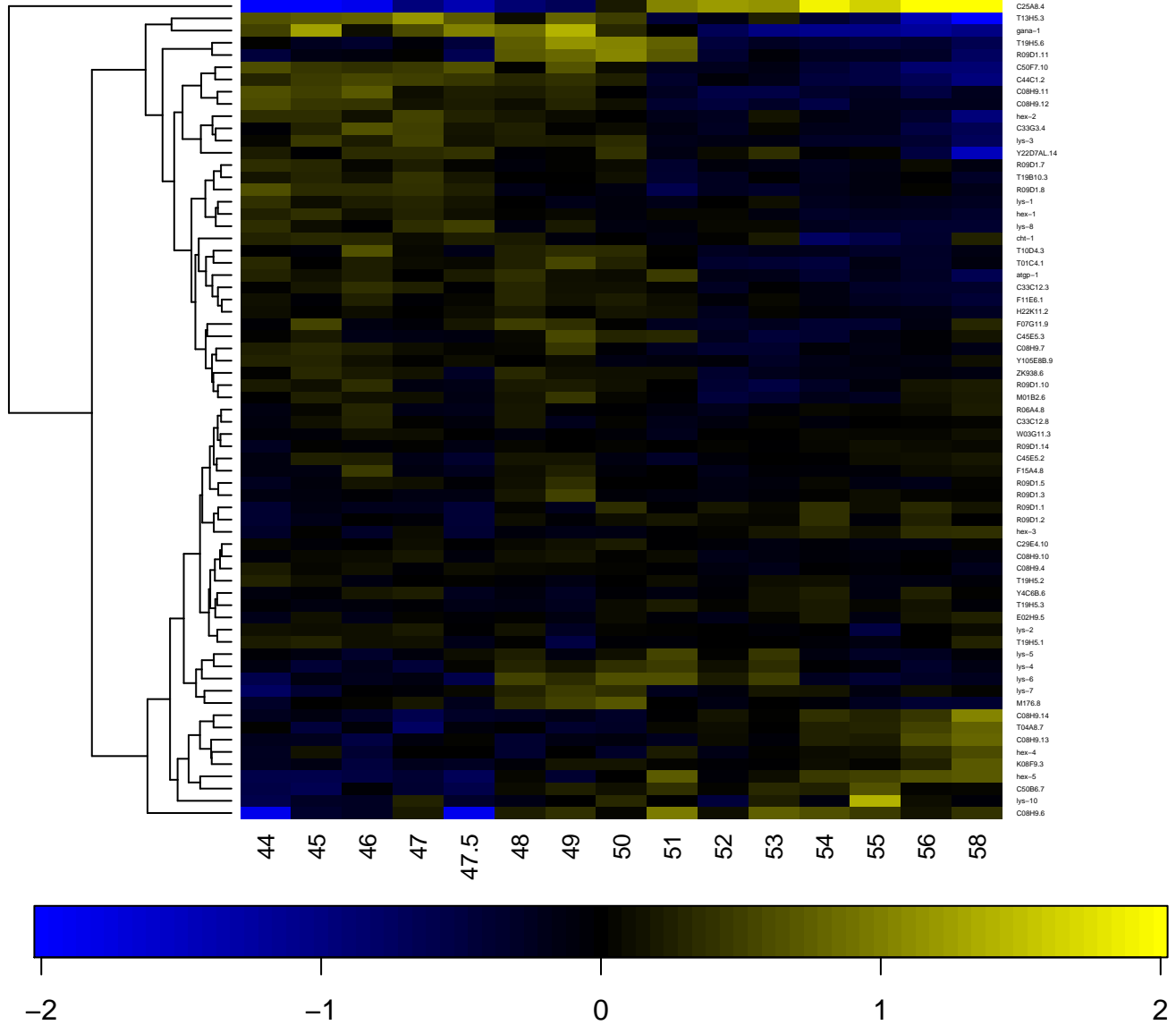
carboxylic acid metabolic process



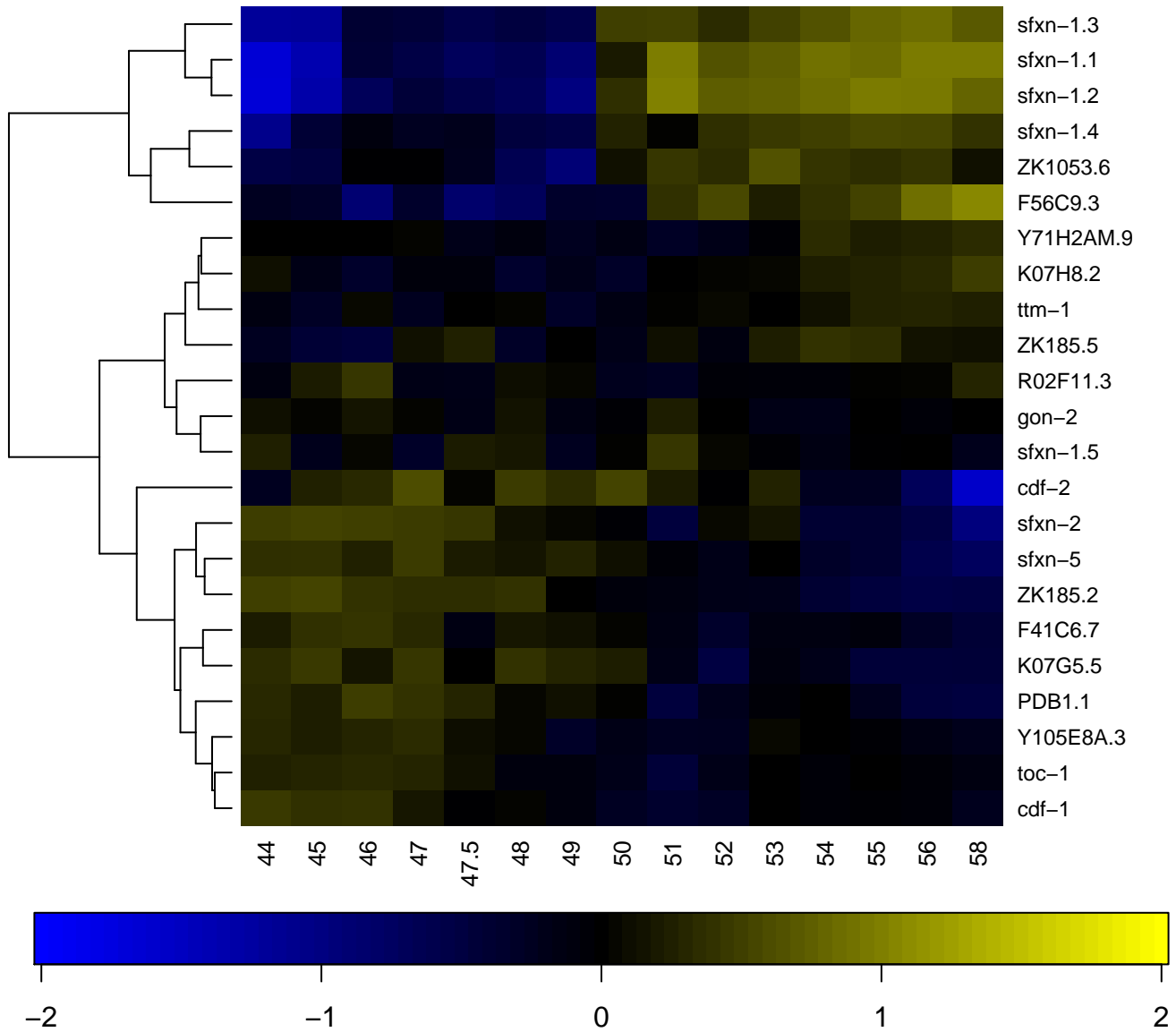
catalytic activity



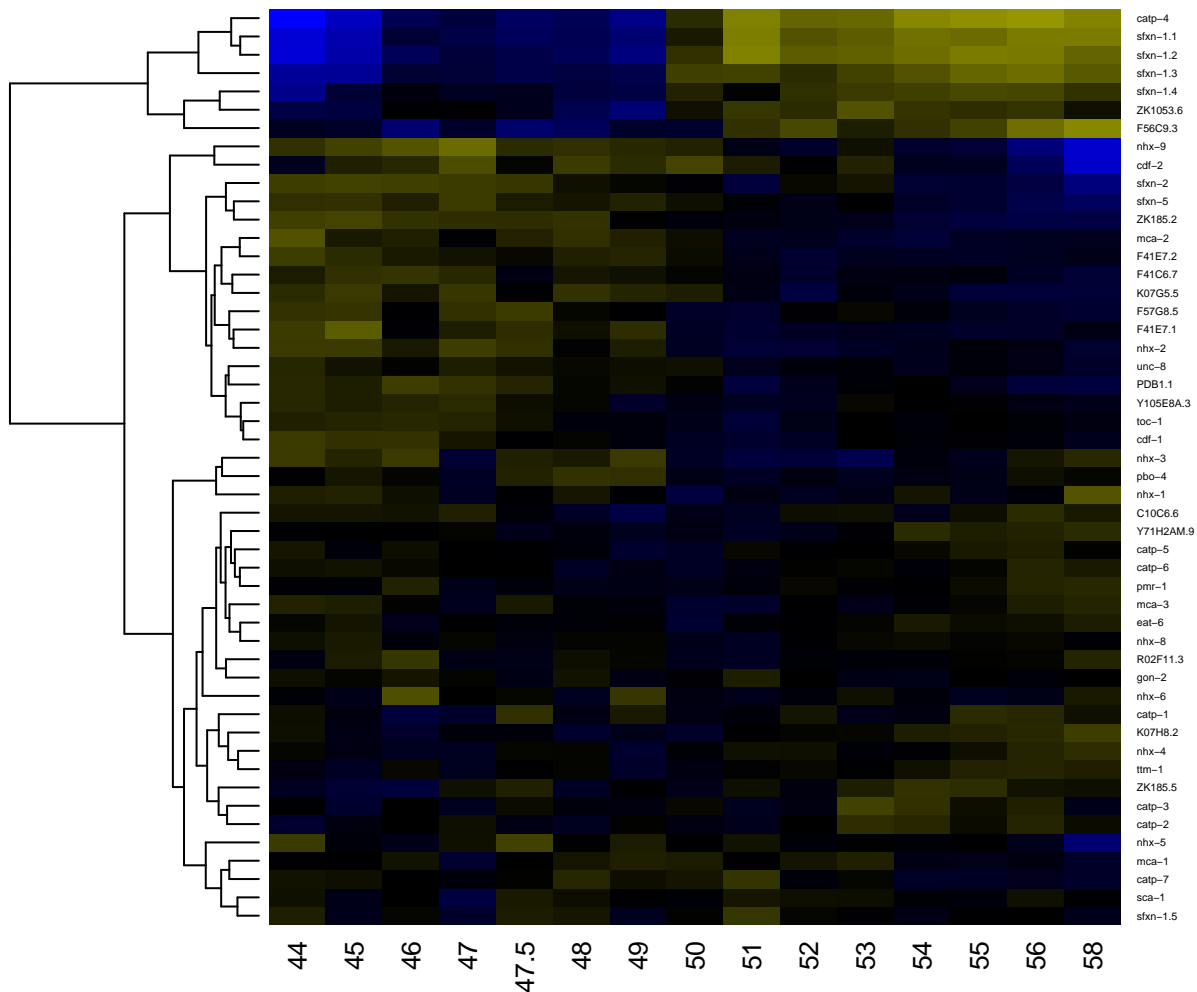
cation binding



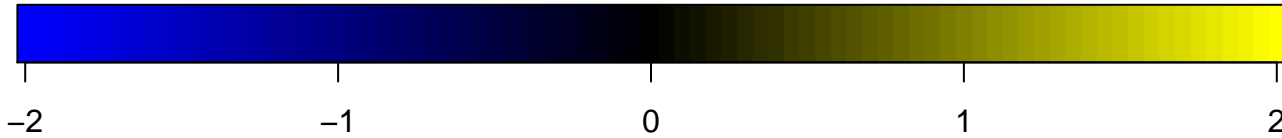
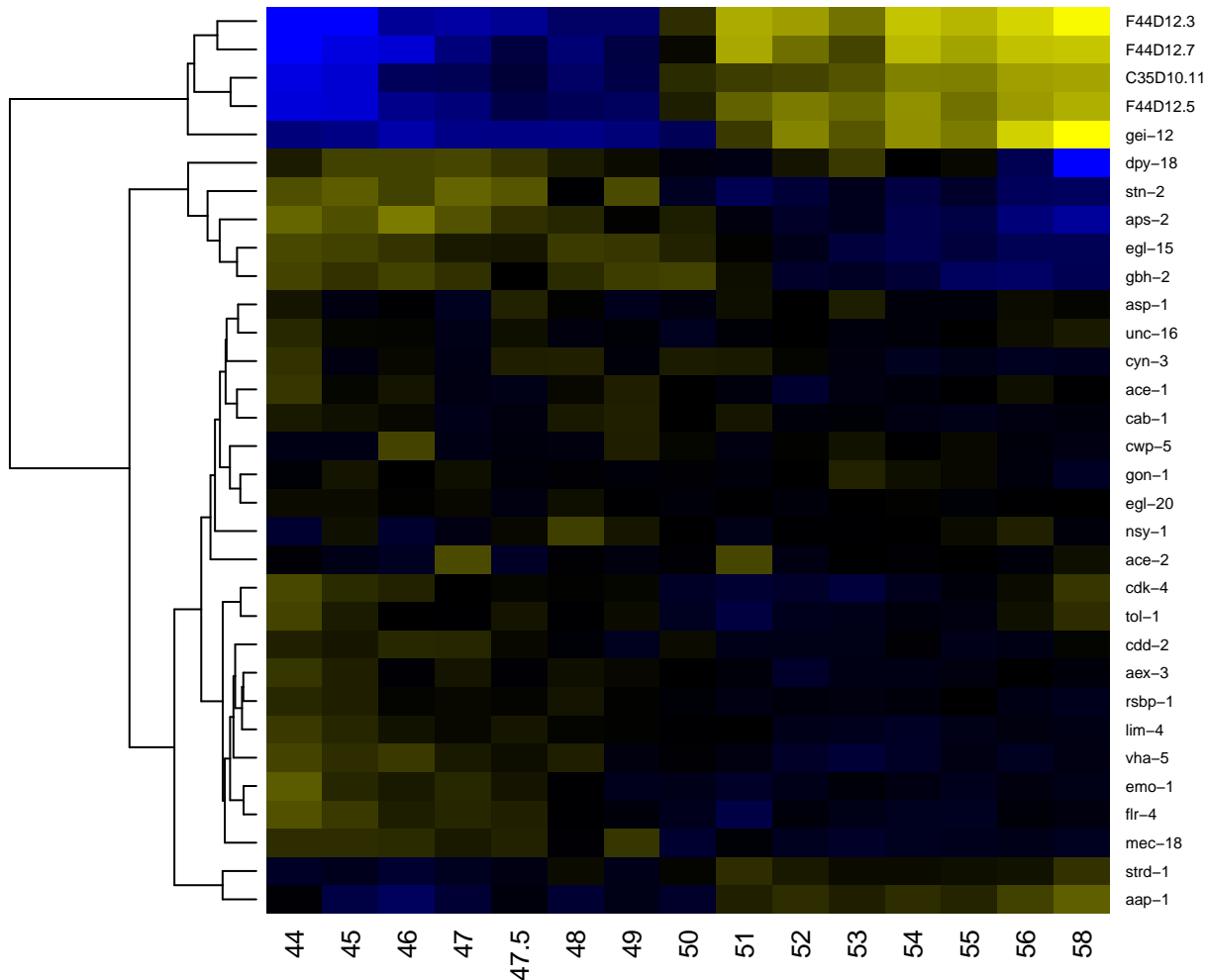
cation transmembrane transporter activity



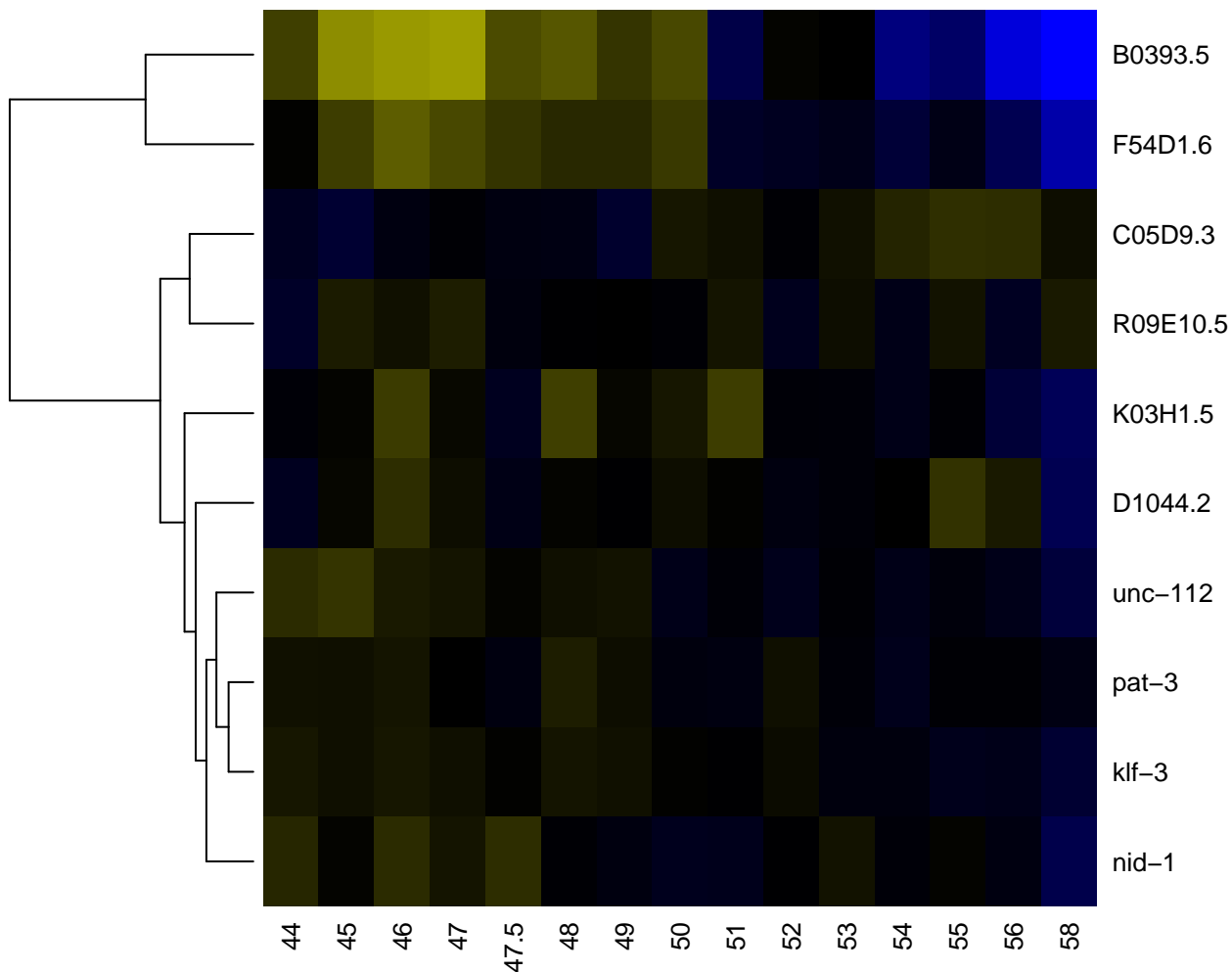
cation transport



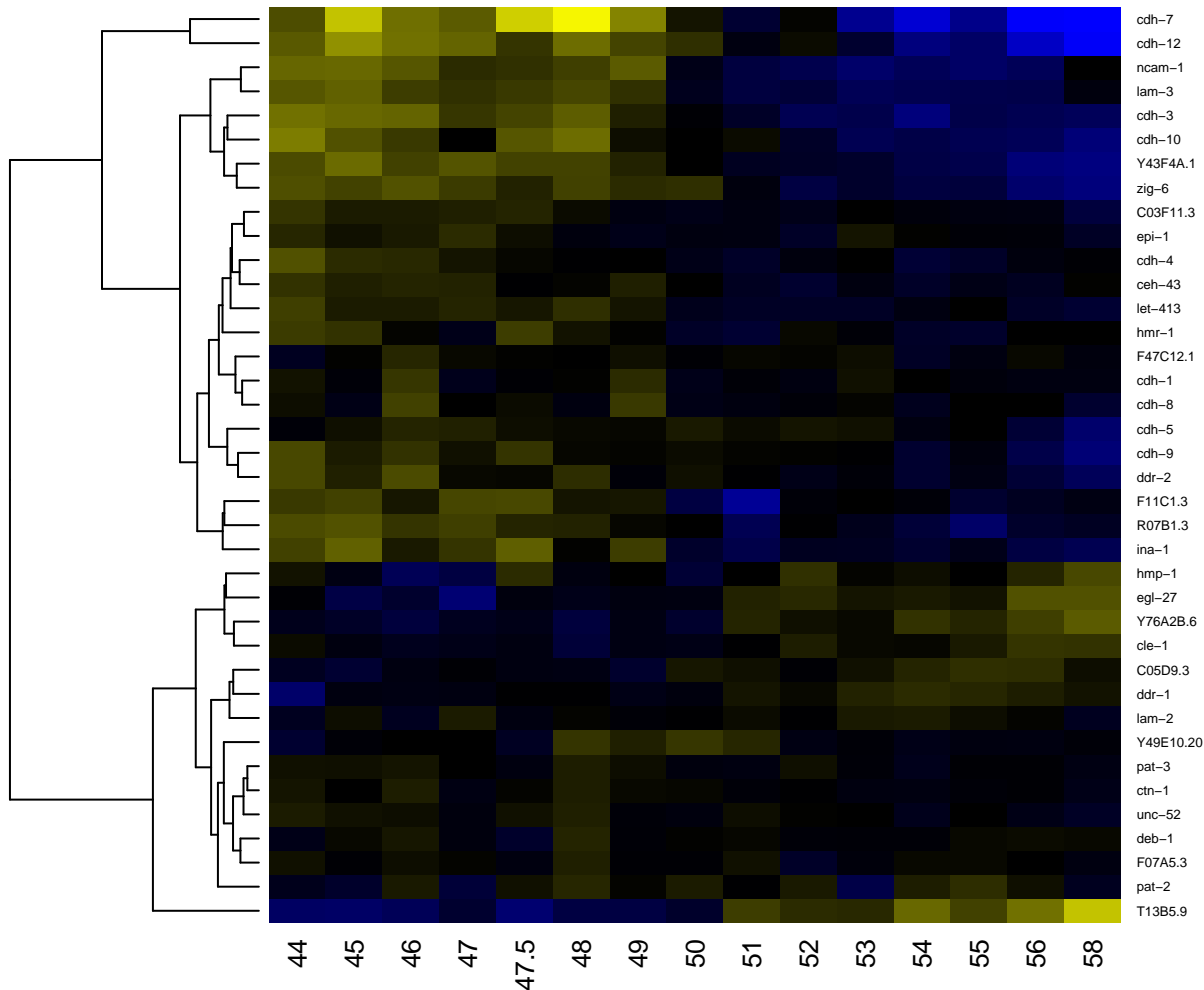
cell



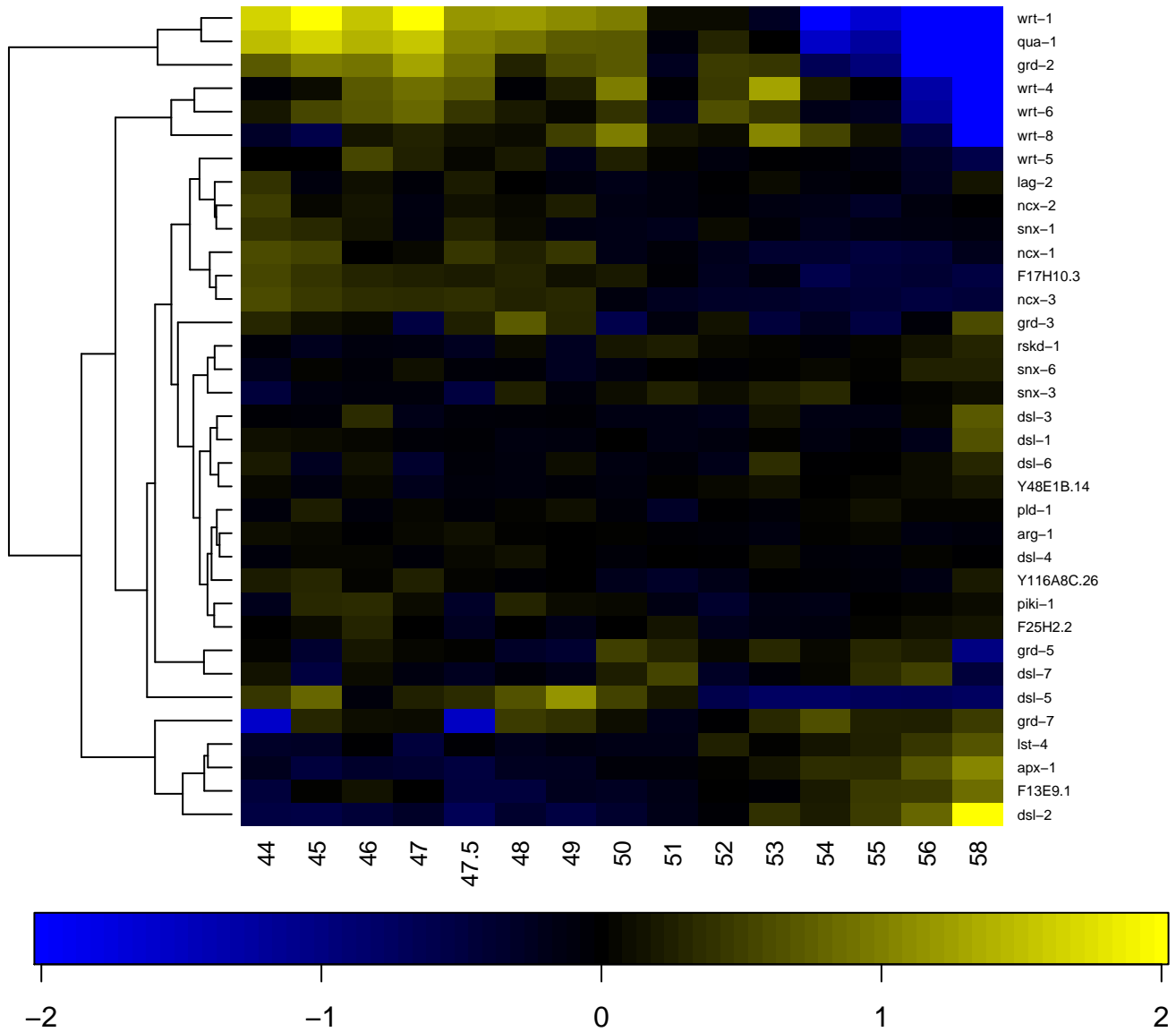
cell-matrix adhesion



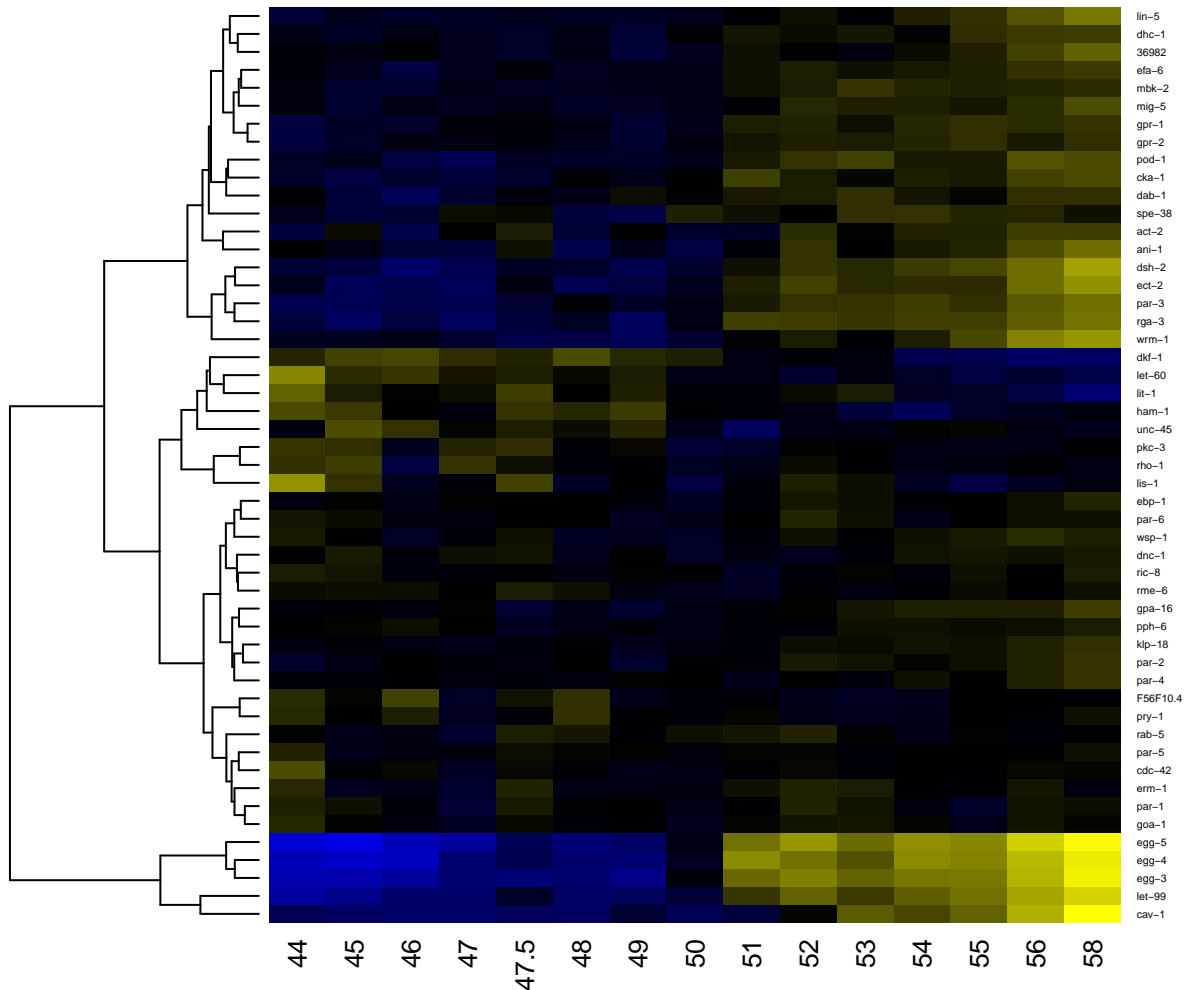
cell adhesion



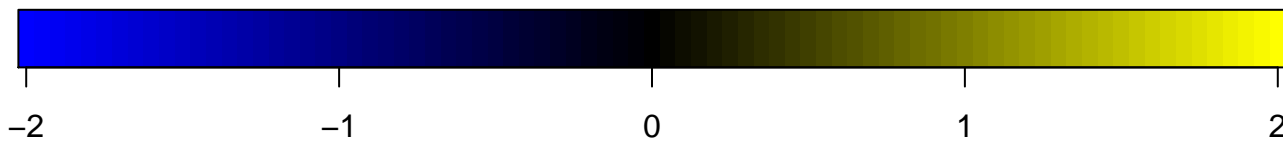
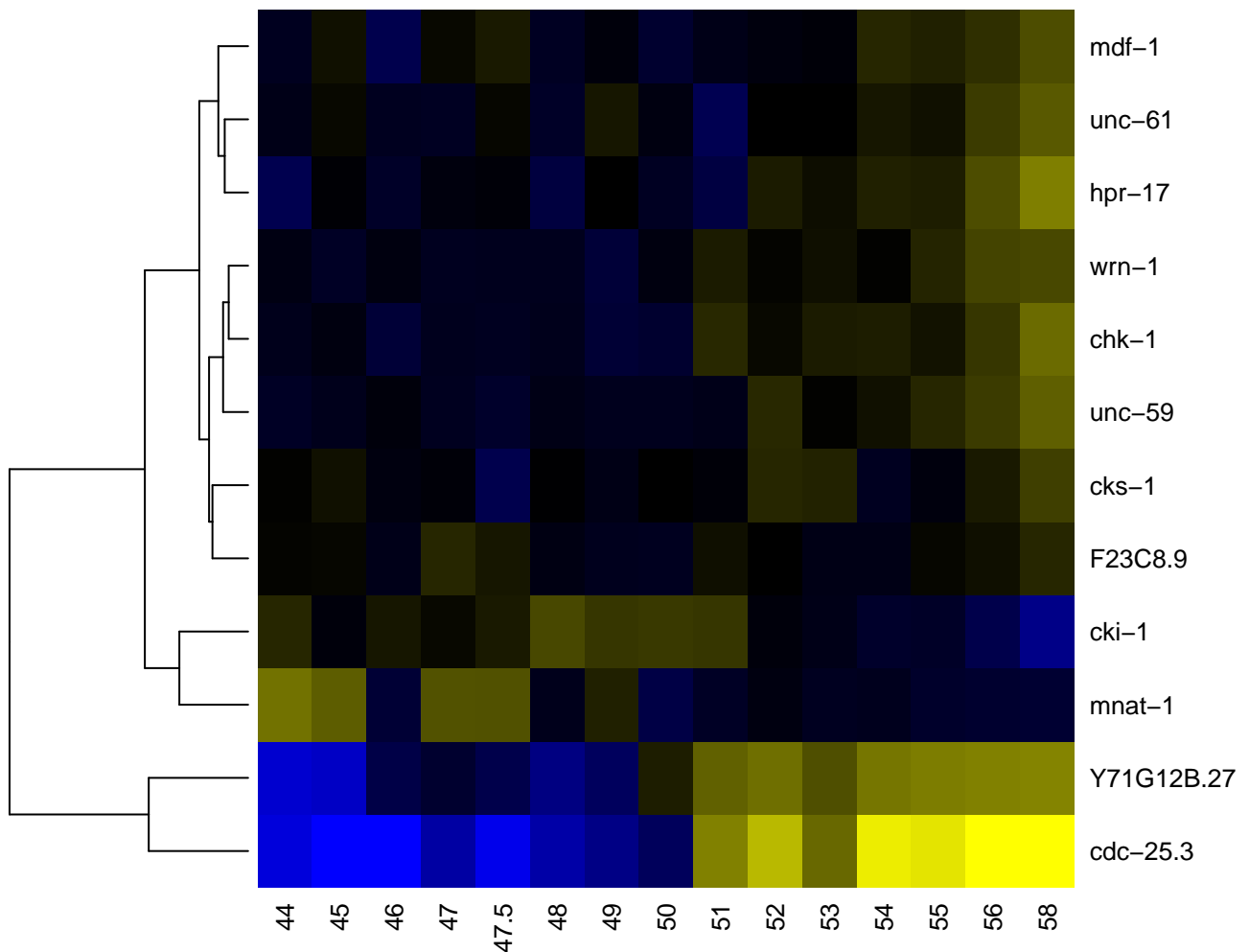
cell communication



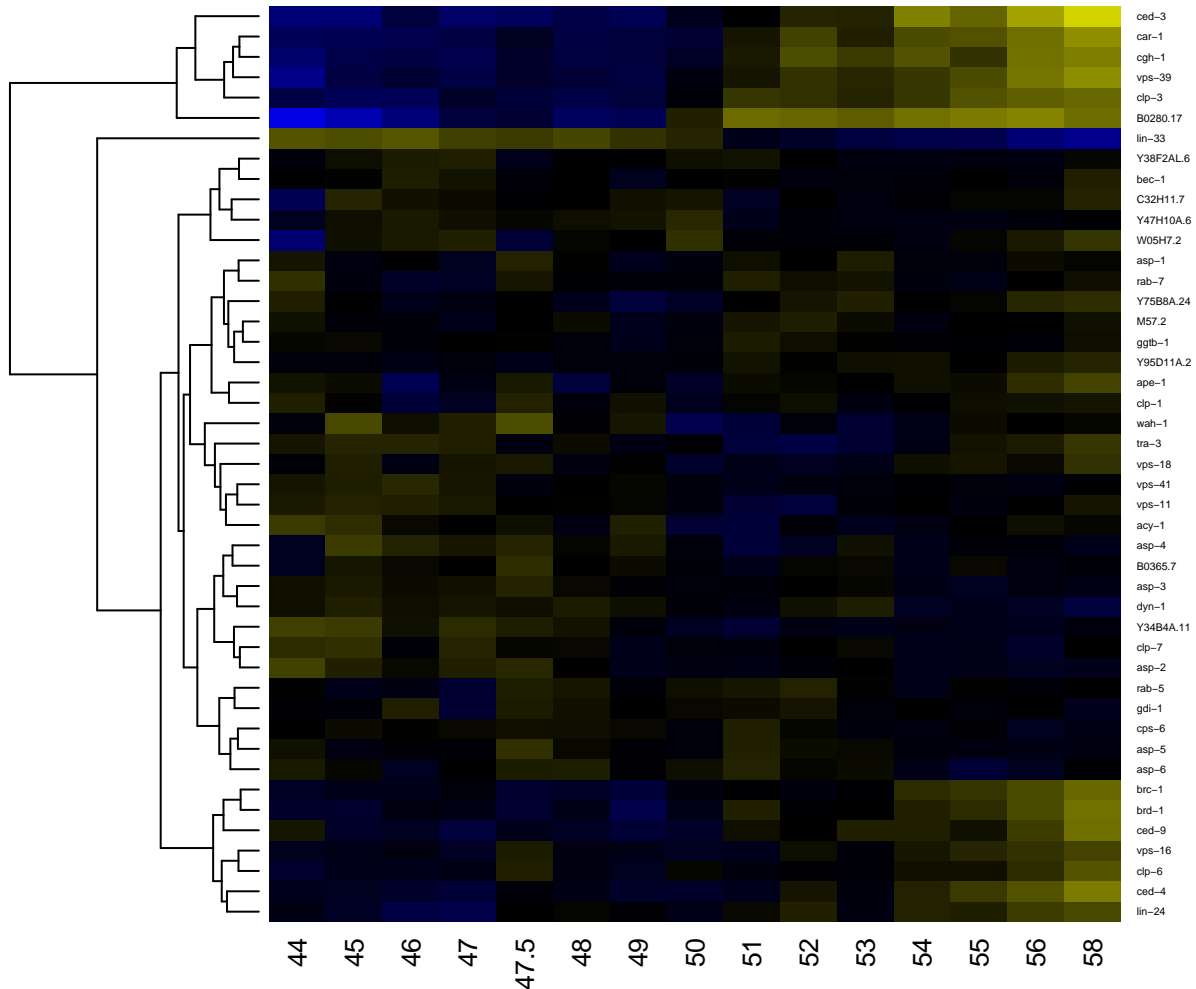
cell cortex



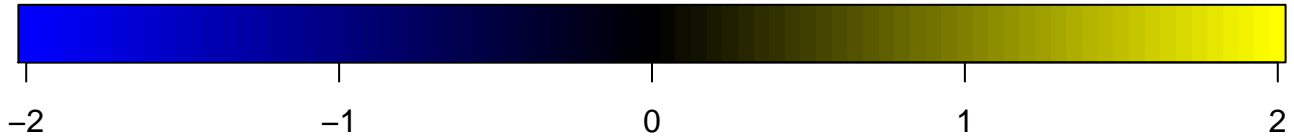
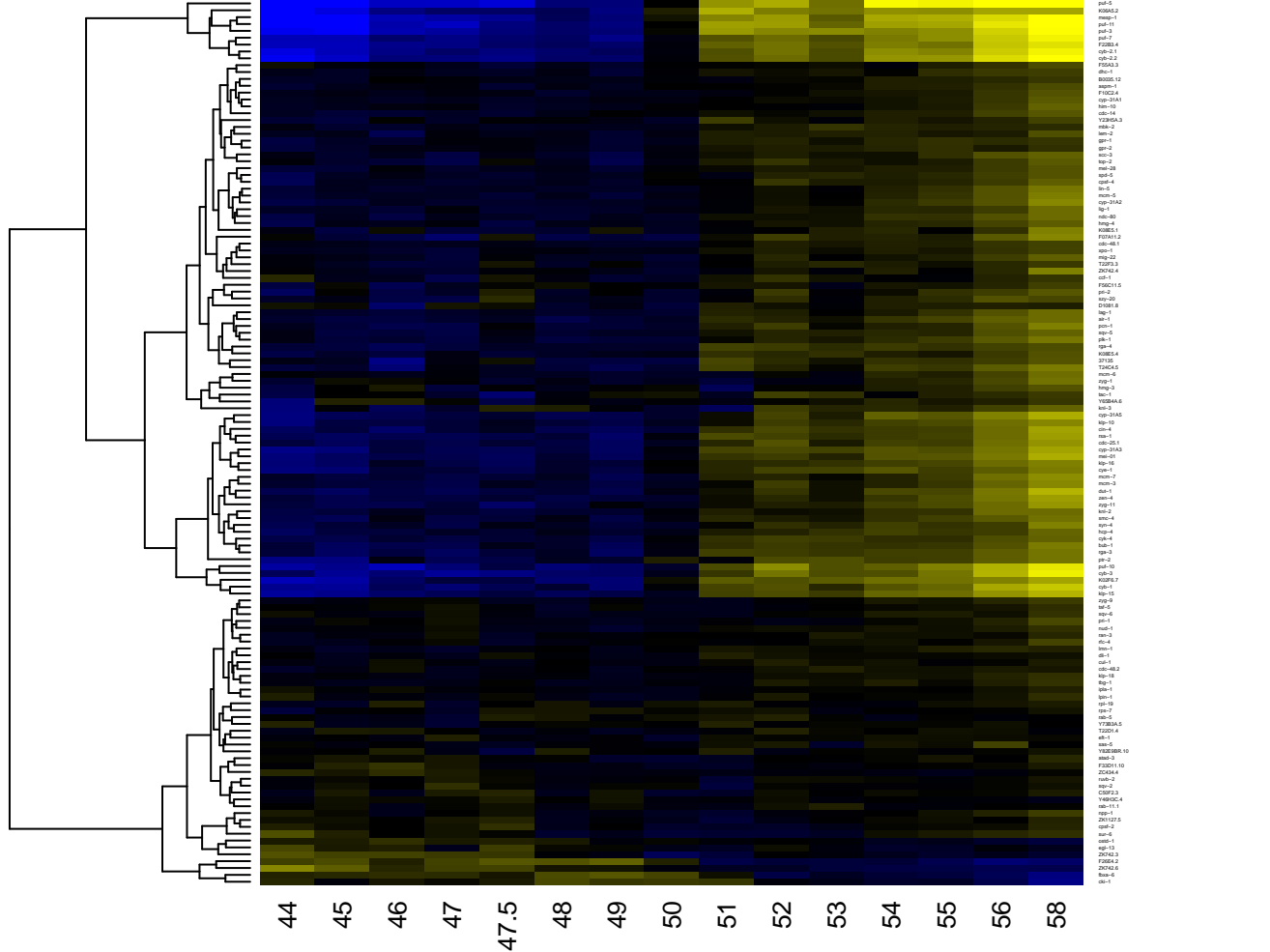
cell cycle



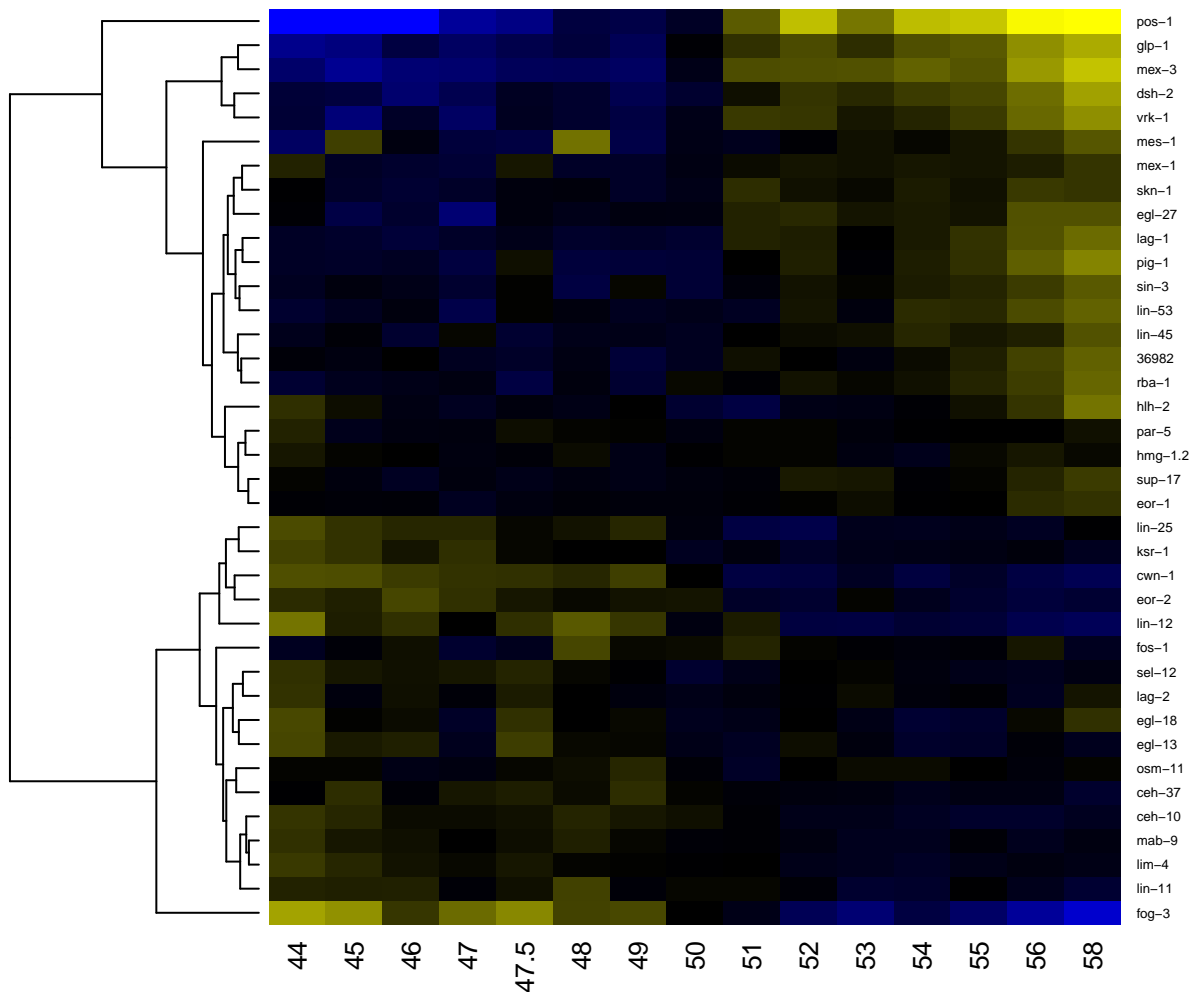
cell death



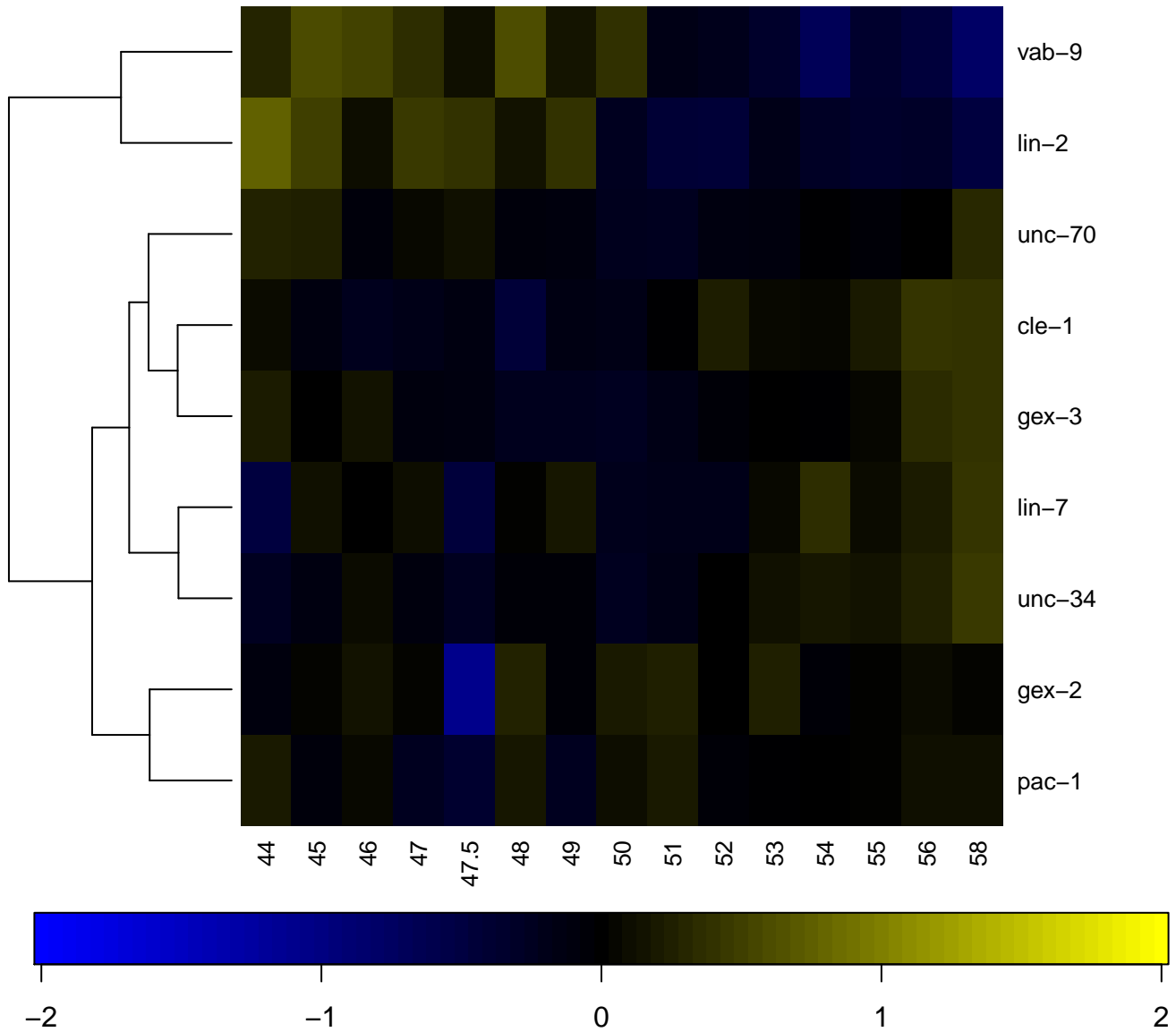
cell division



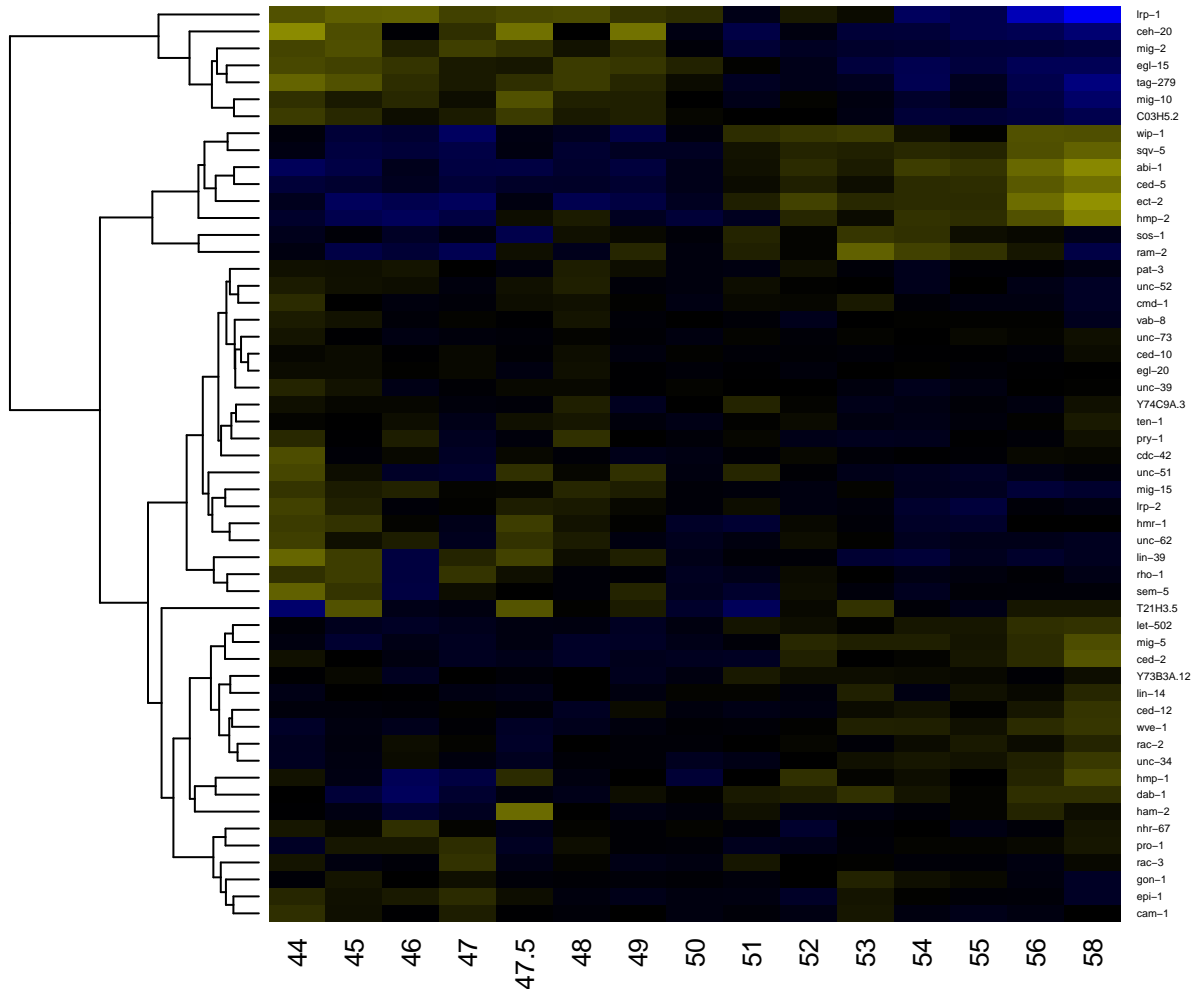
cell fate specification



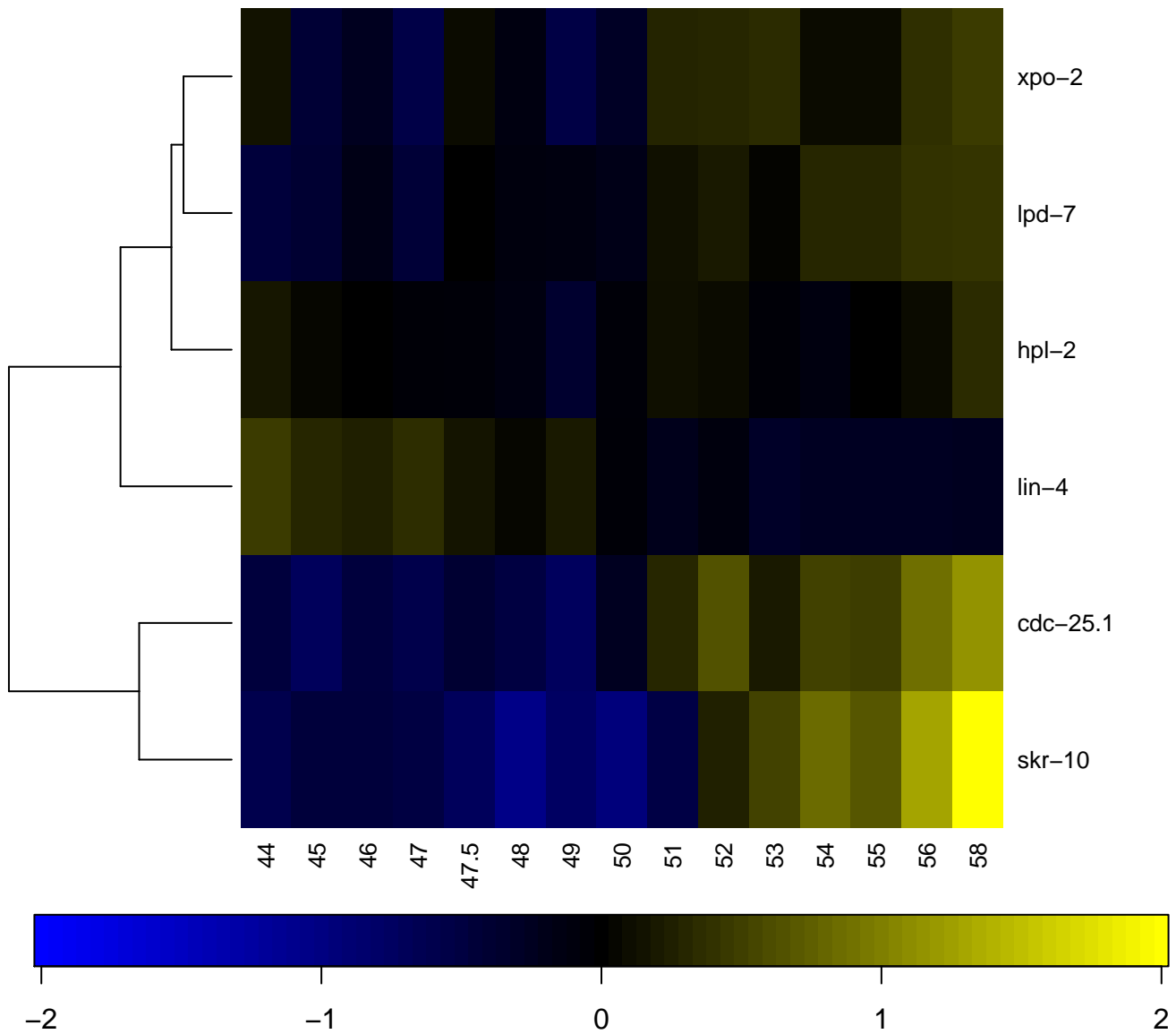
cell junction



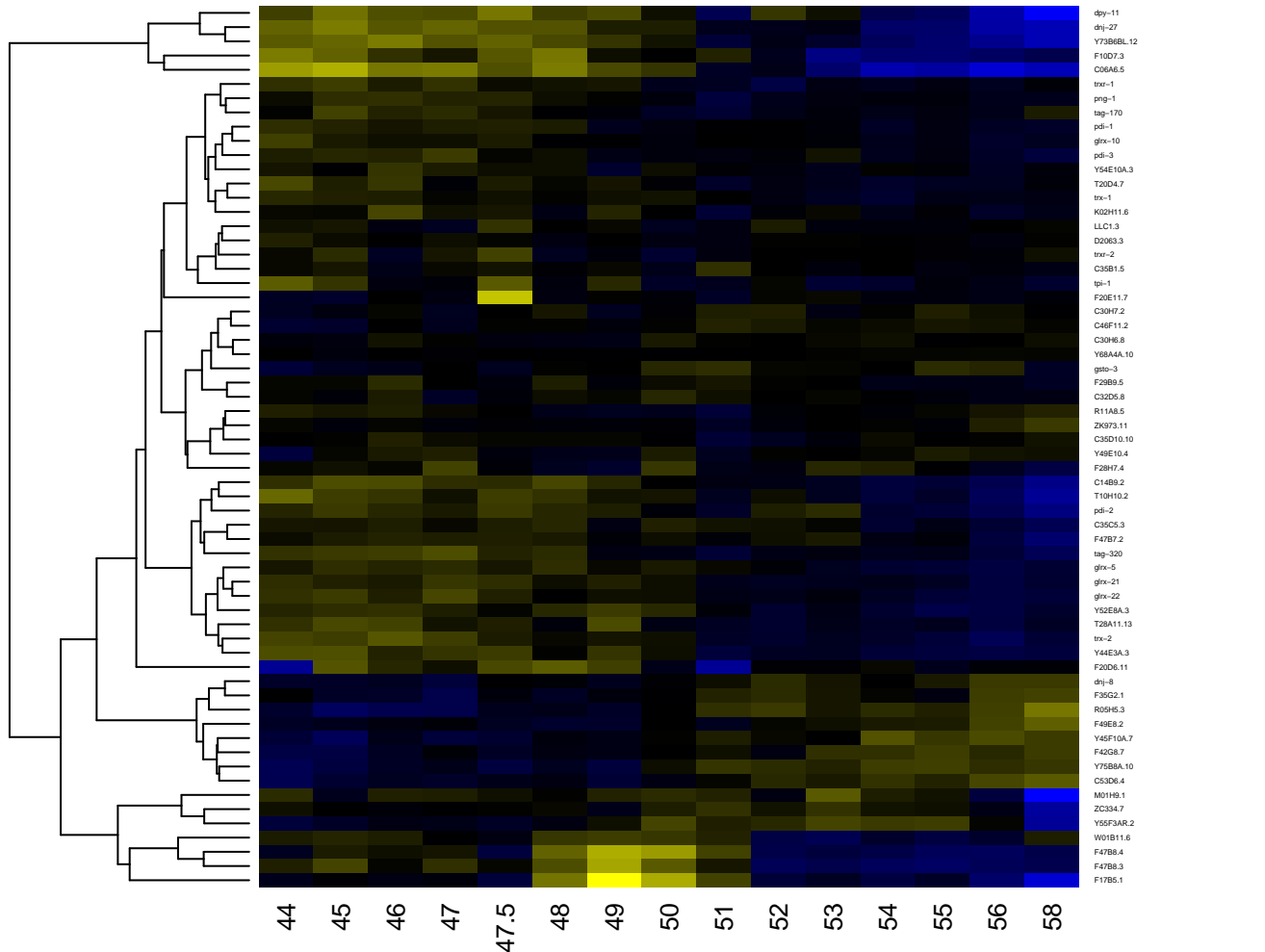
cell migration



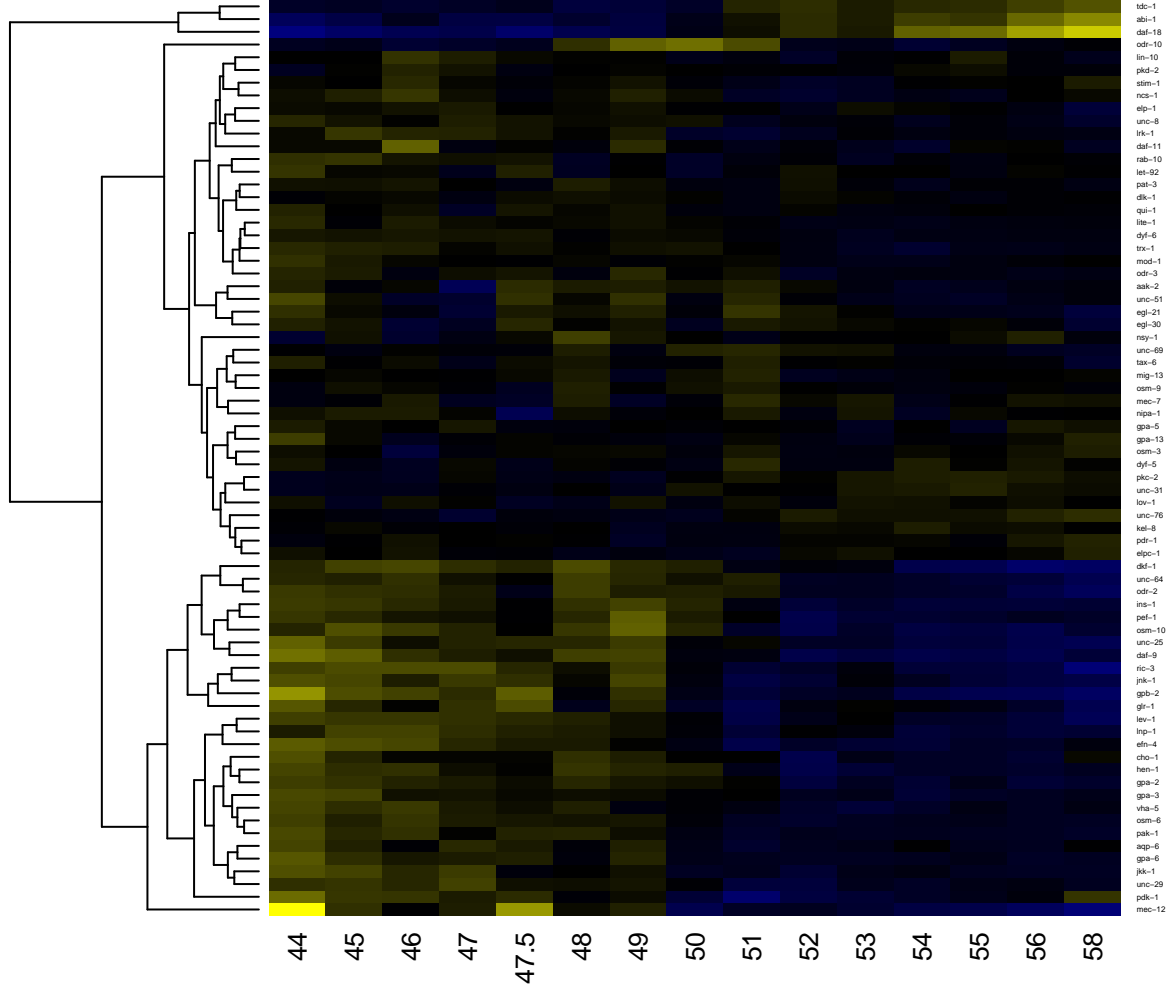
cell proliferation



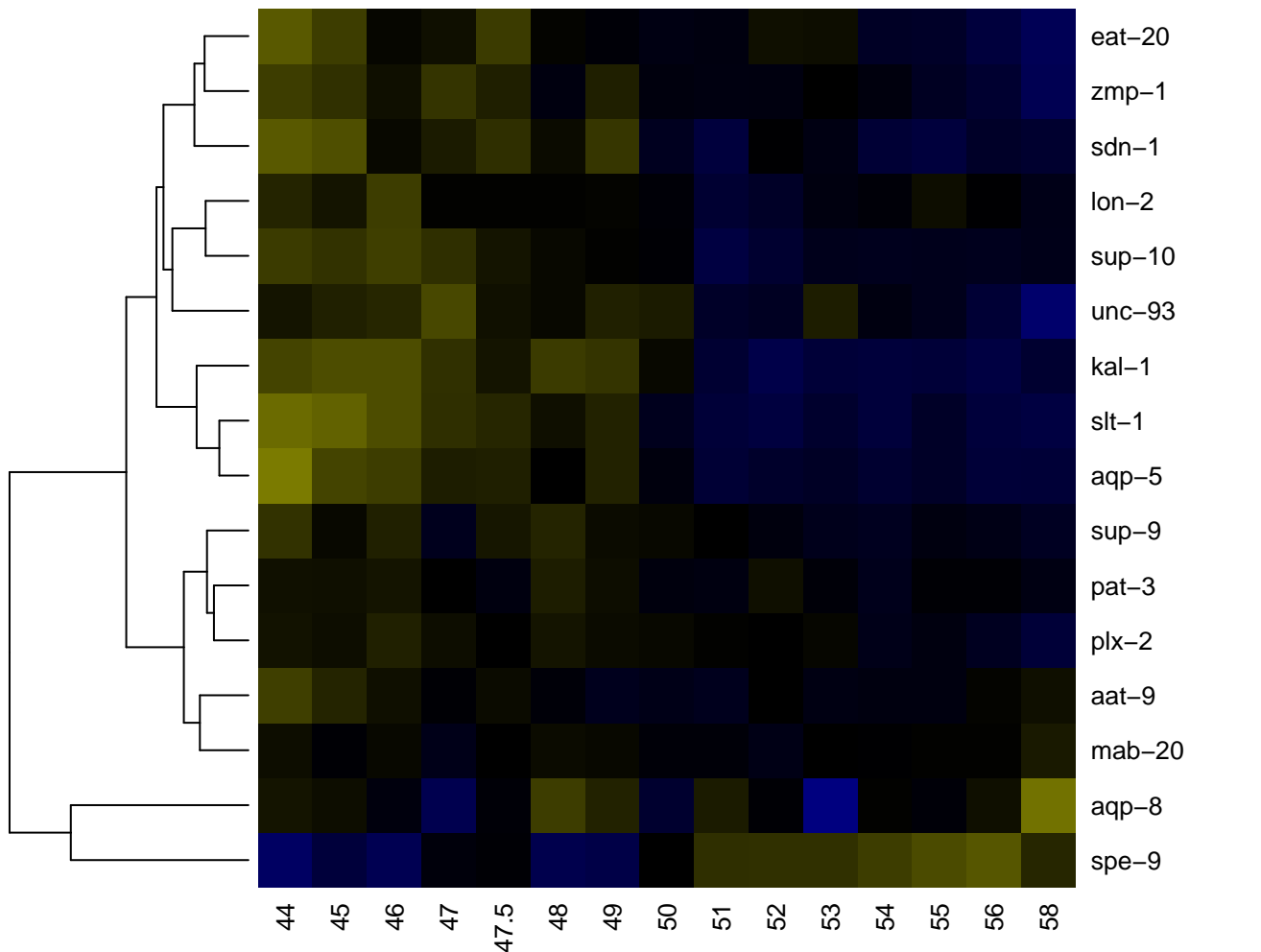
cell redox homeostasis



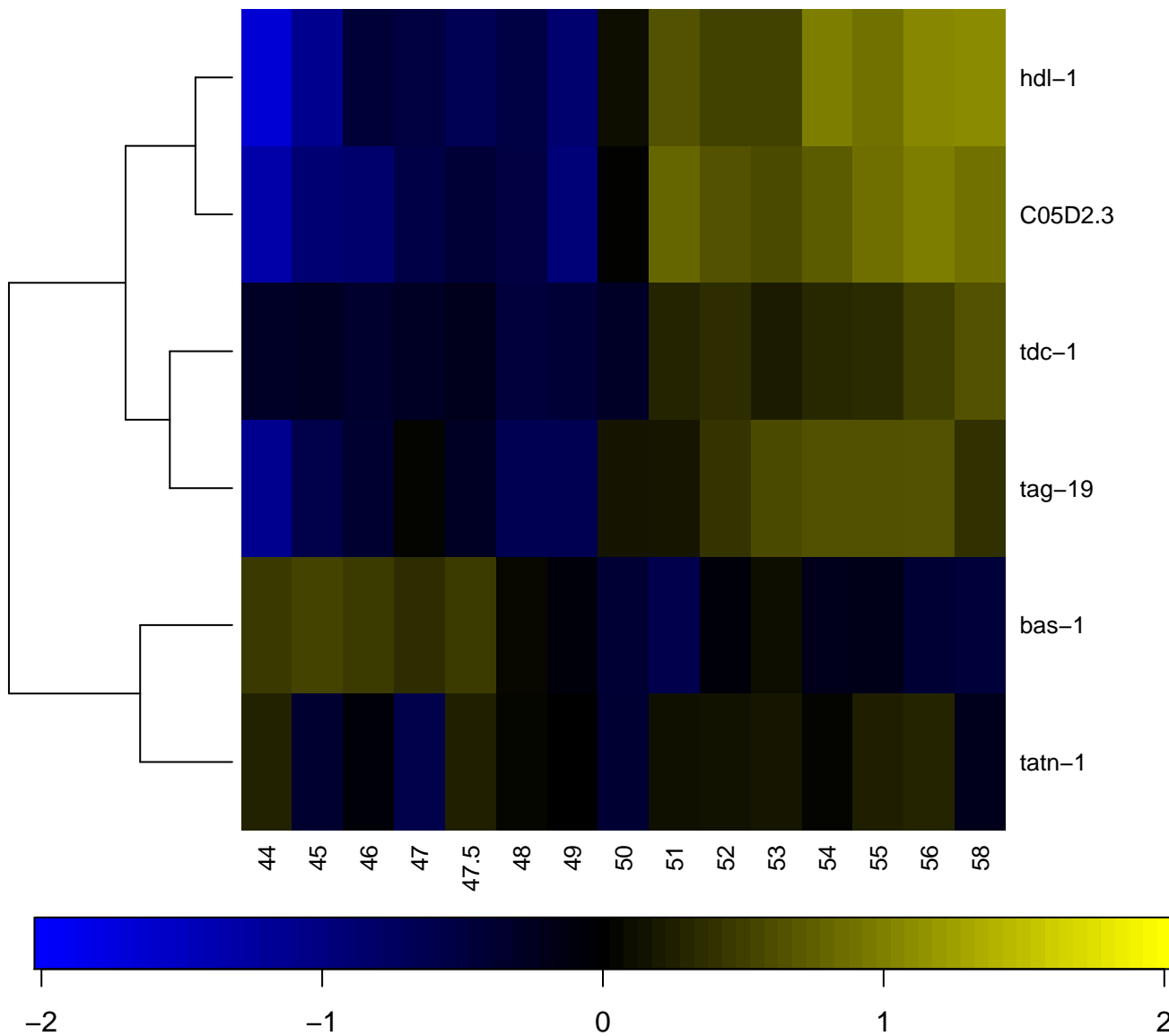
cell soma



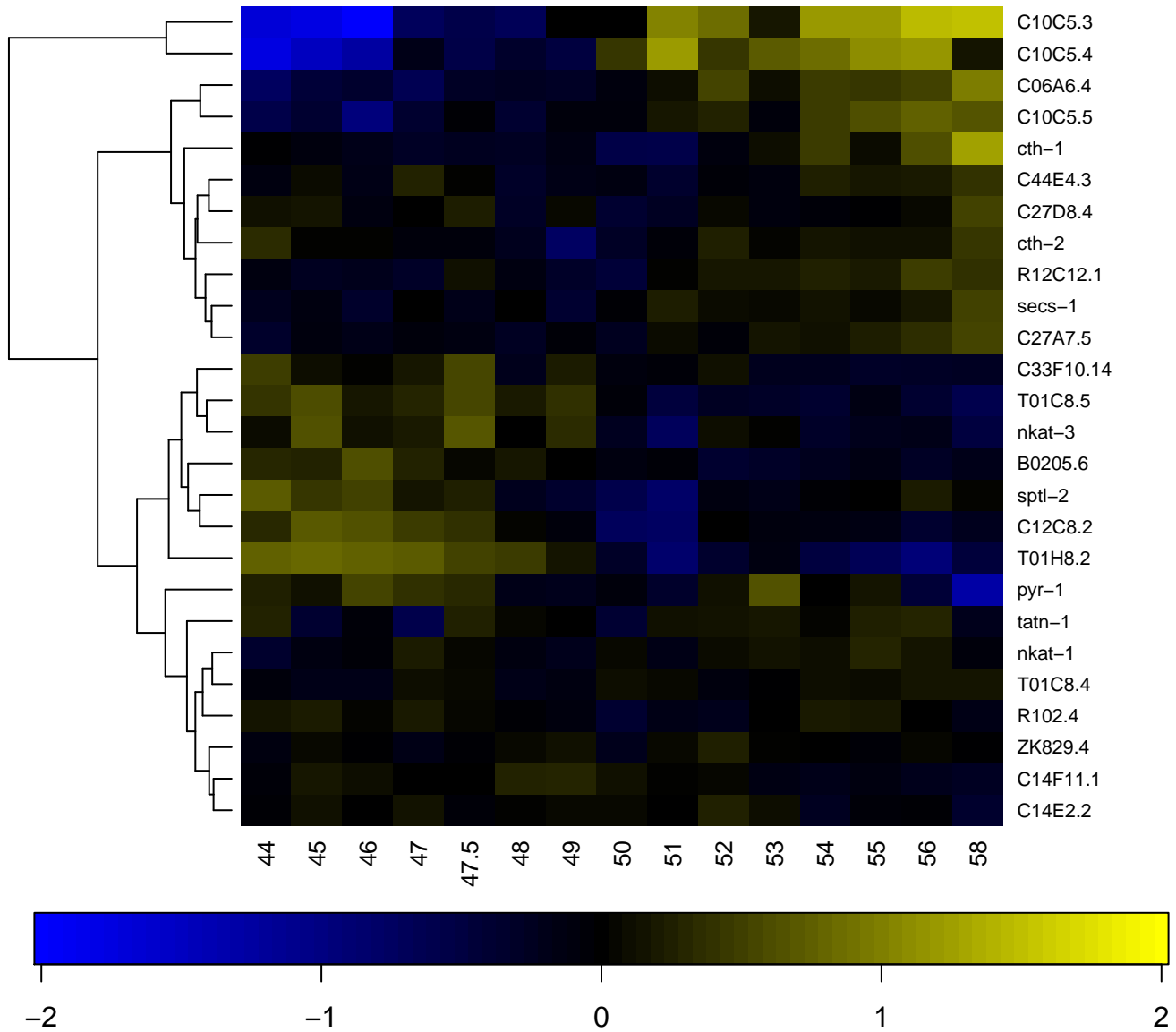
cell surface



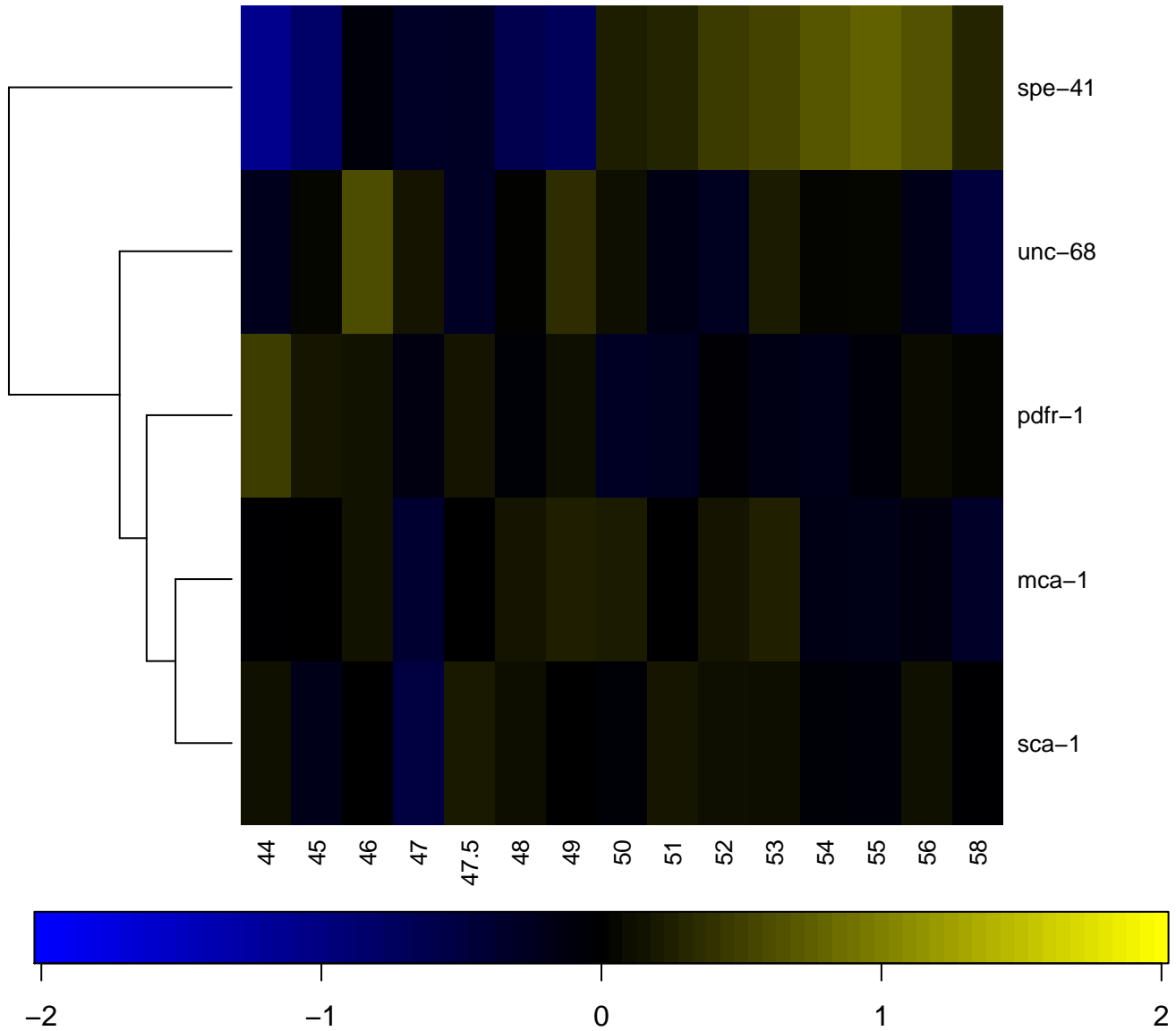
cellular amino acid and derivative metabolic process



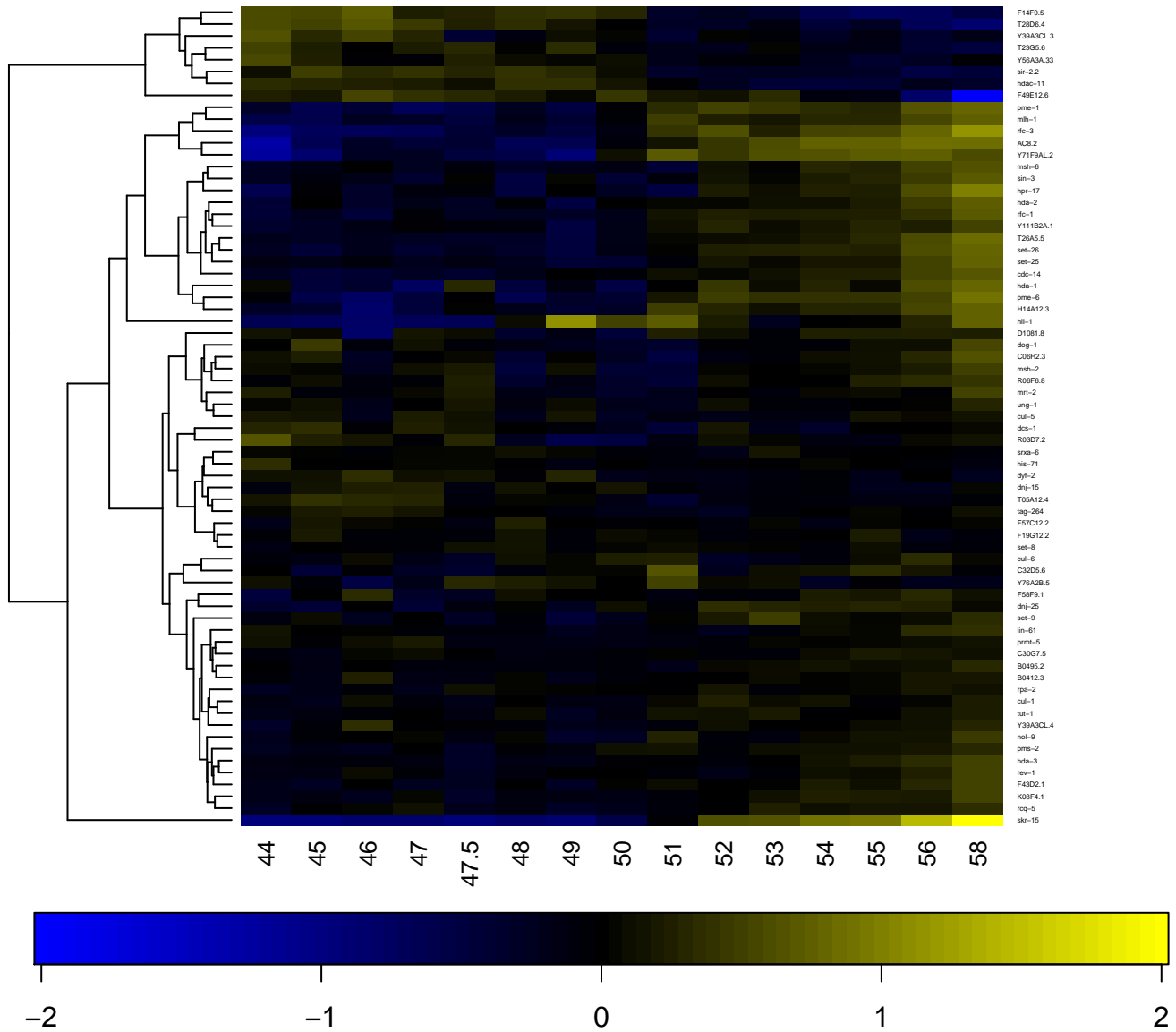
cellular amino acid metabolic process



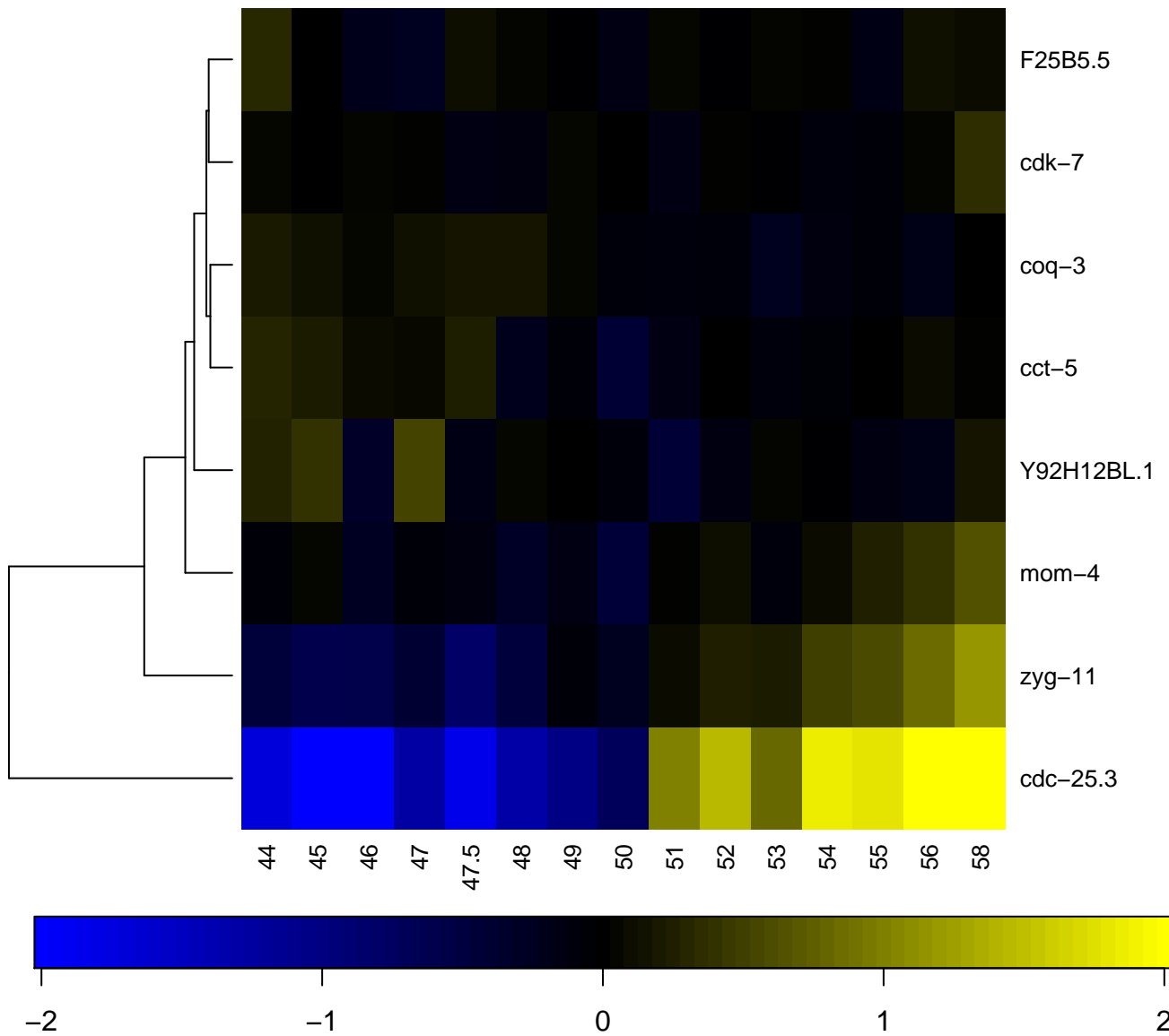
cellular calcium ion homeostasis



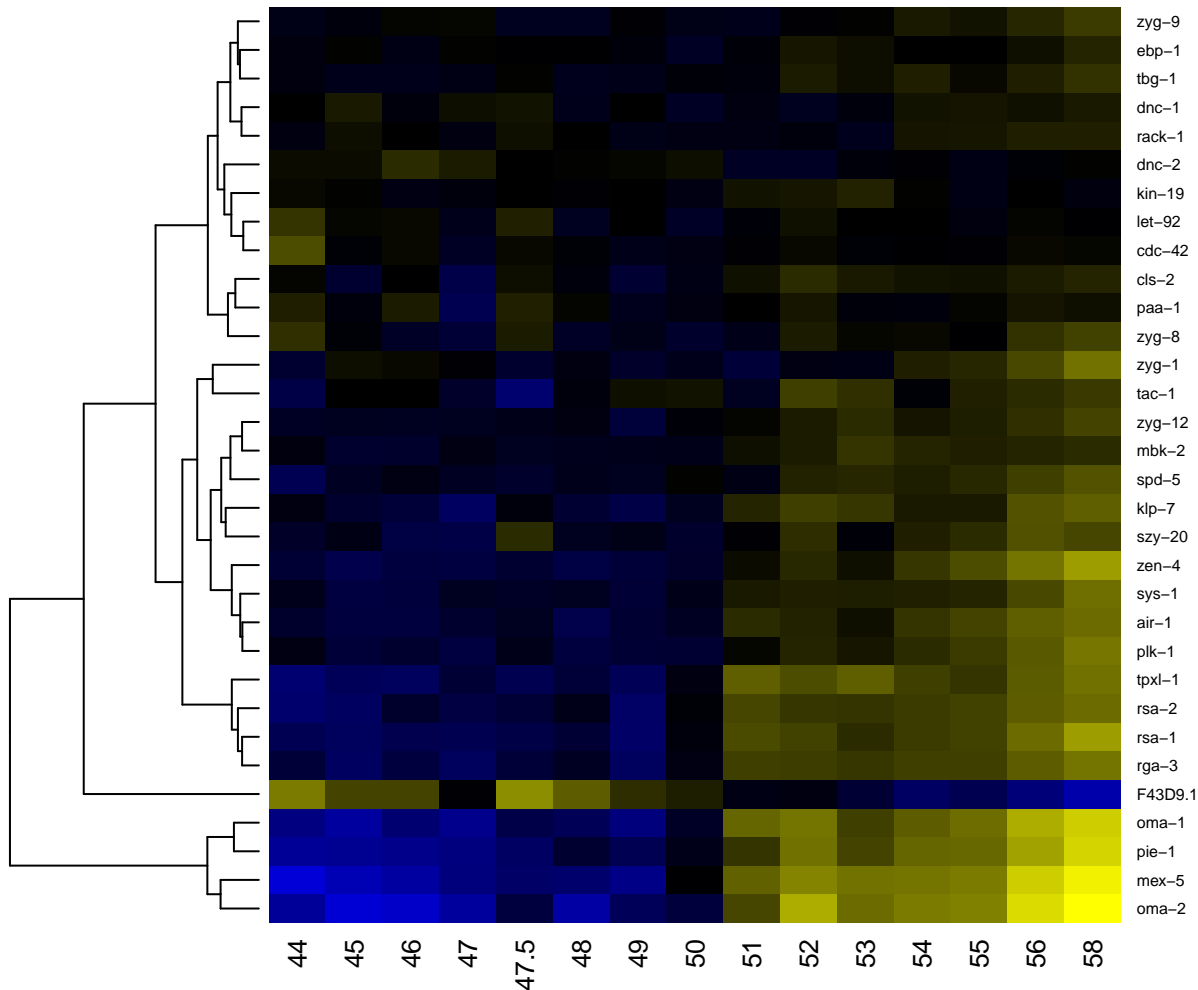
cellular response to DNA damage stimulus



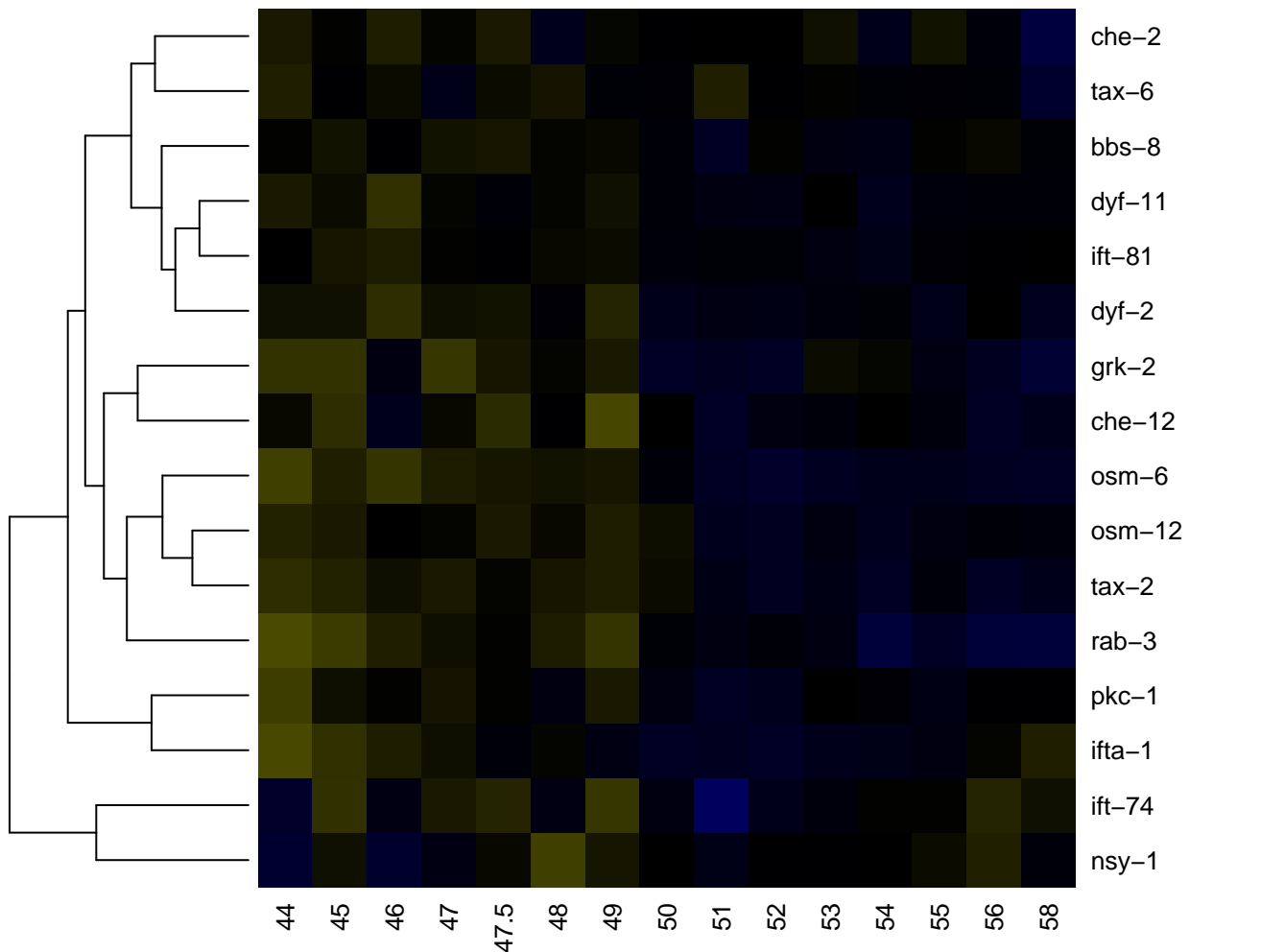
cellular_component



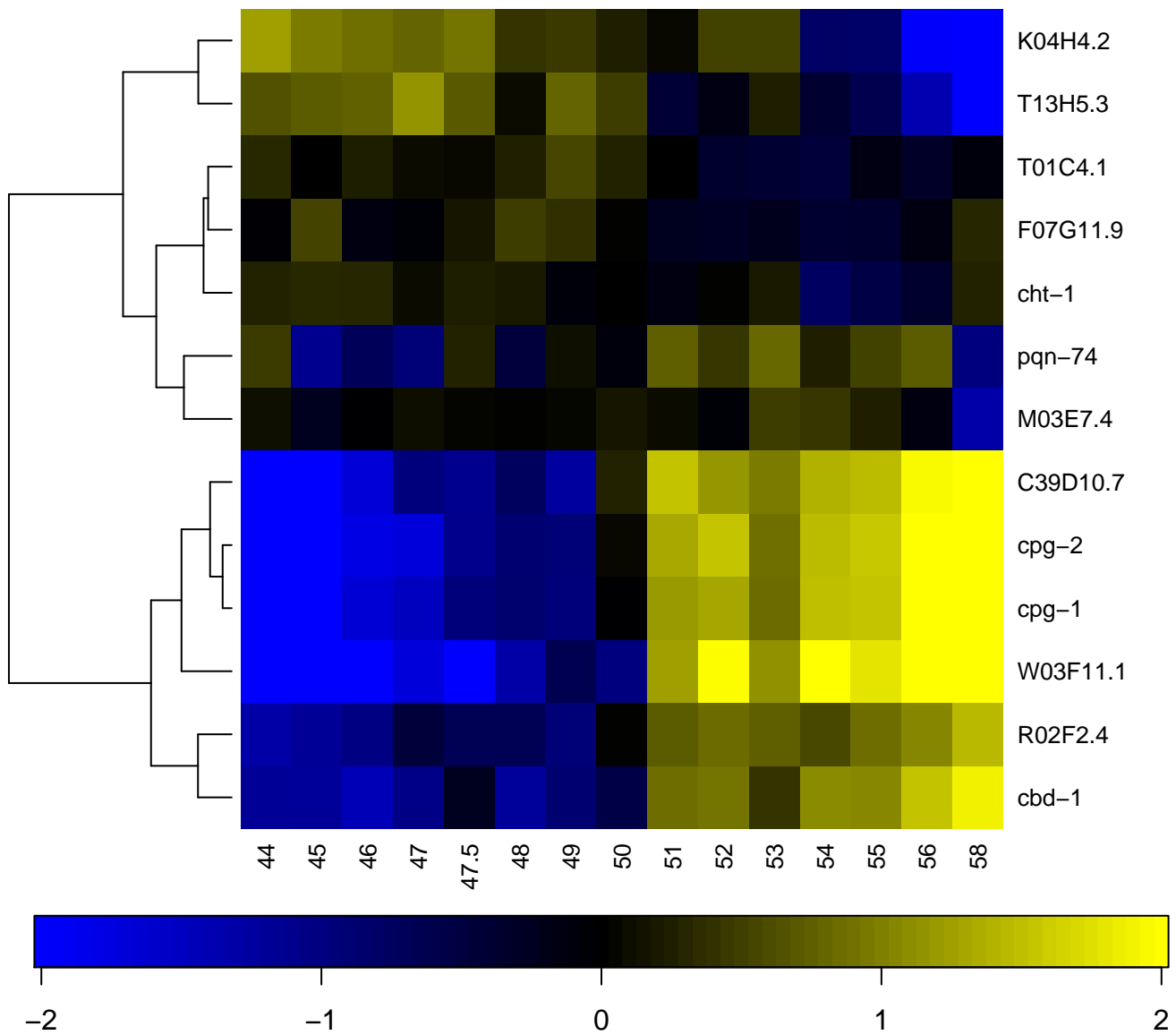
centrosome



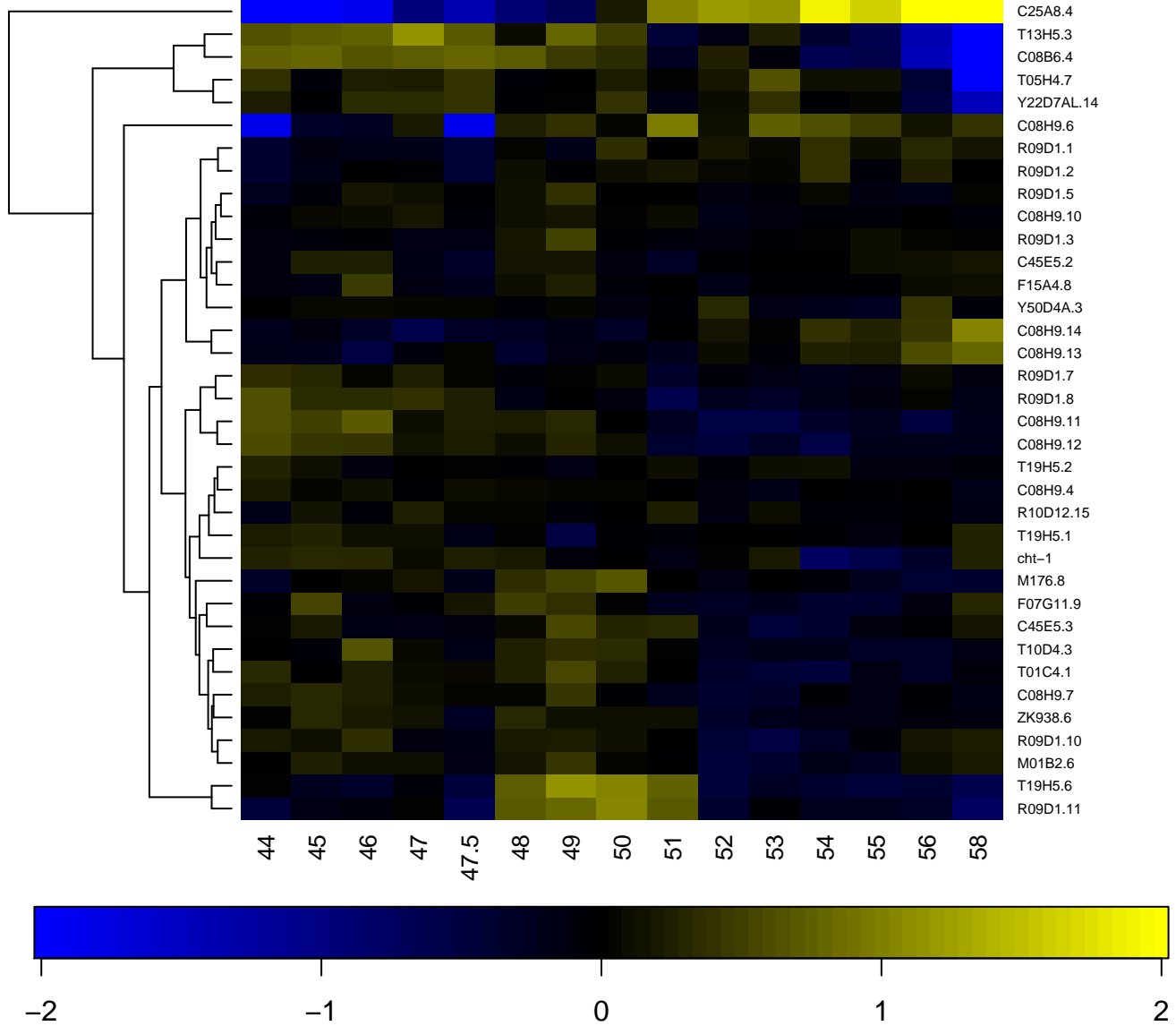
chemotaxis



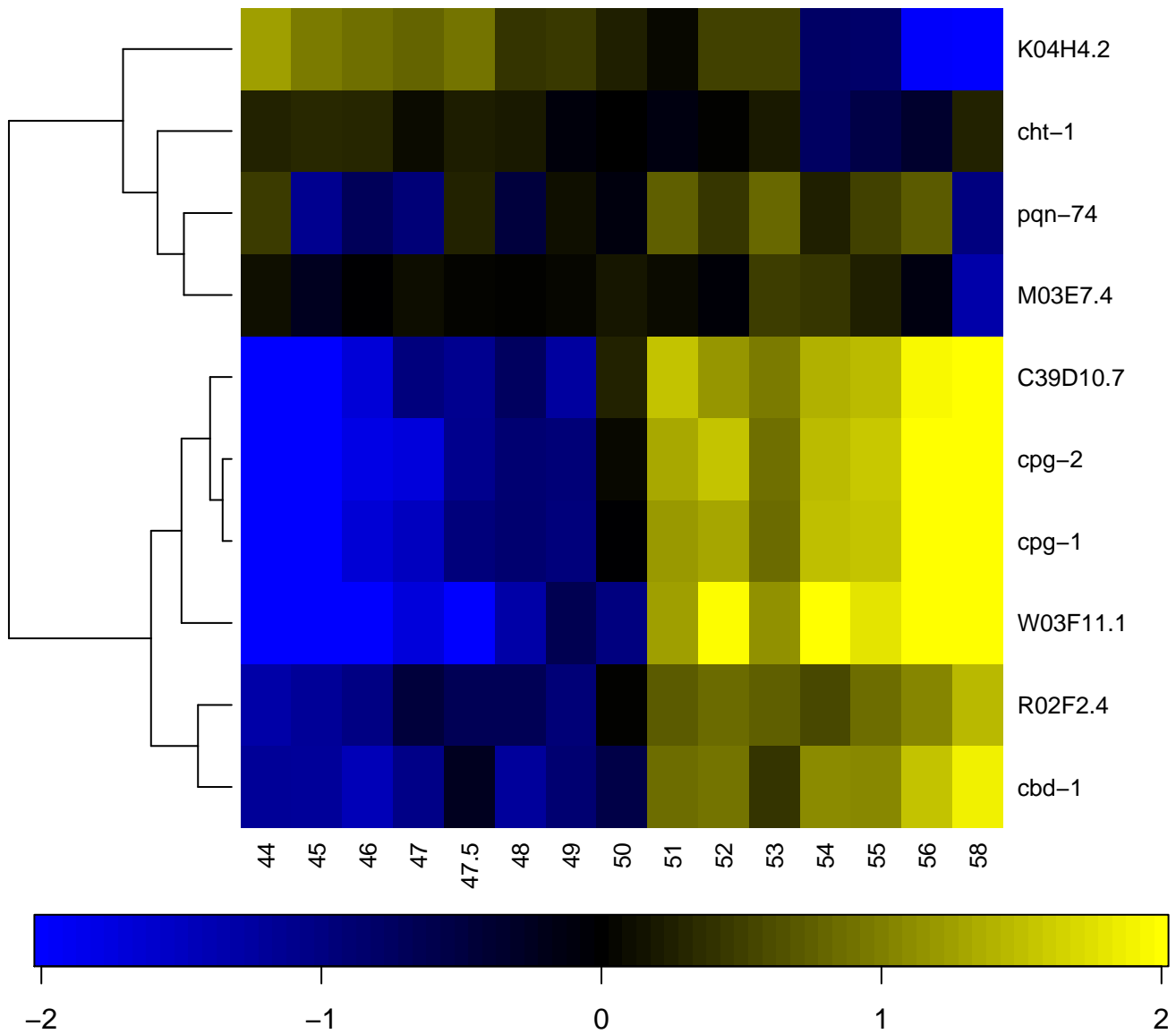
chitin binding



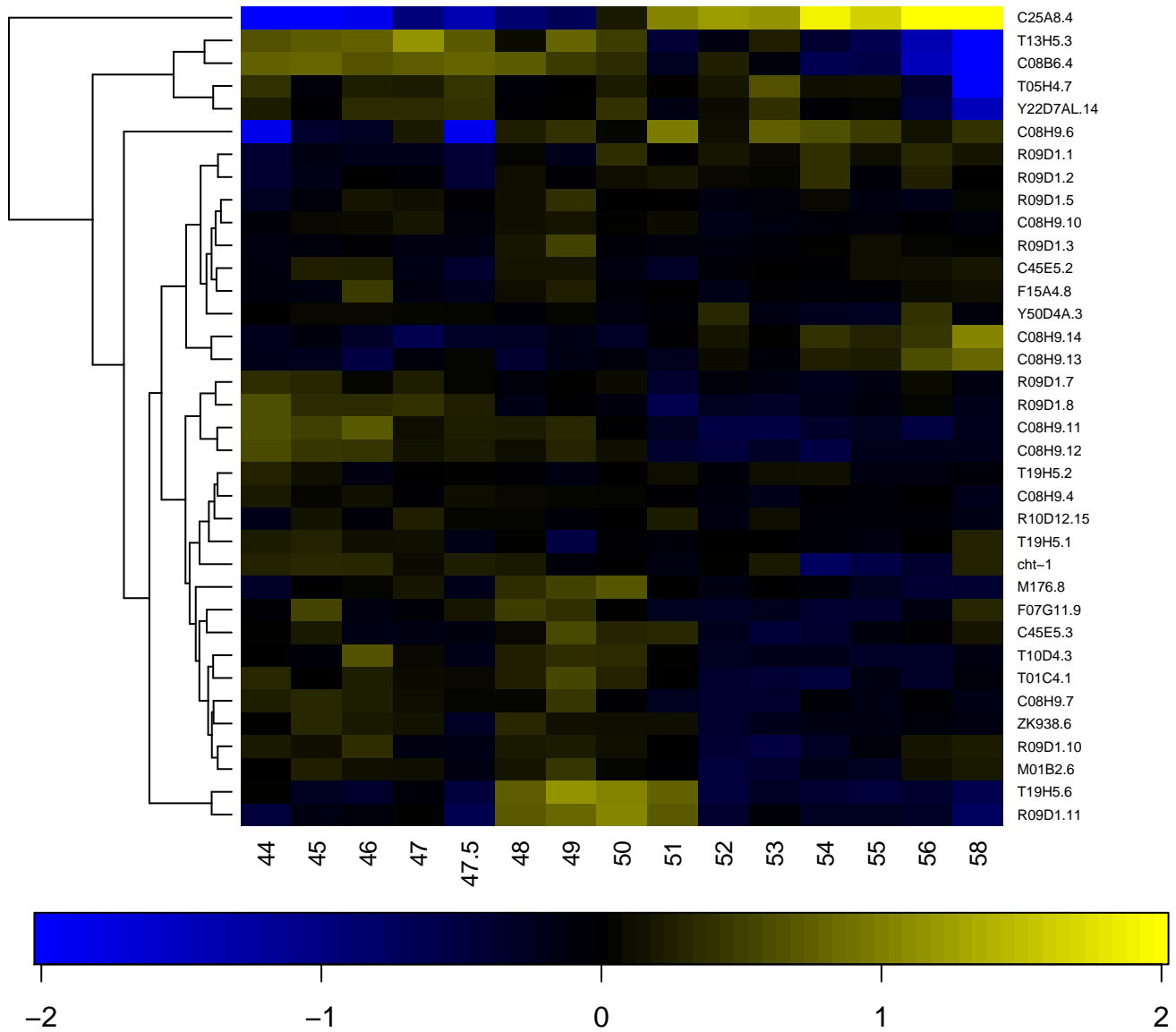
chitin catabolic process



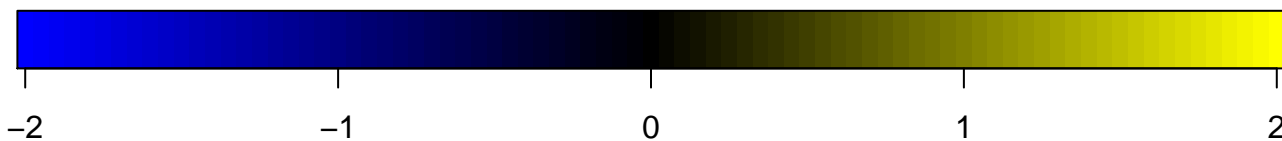
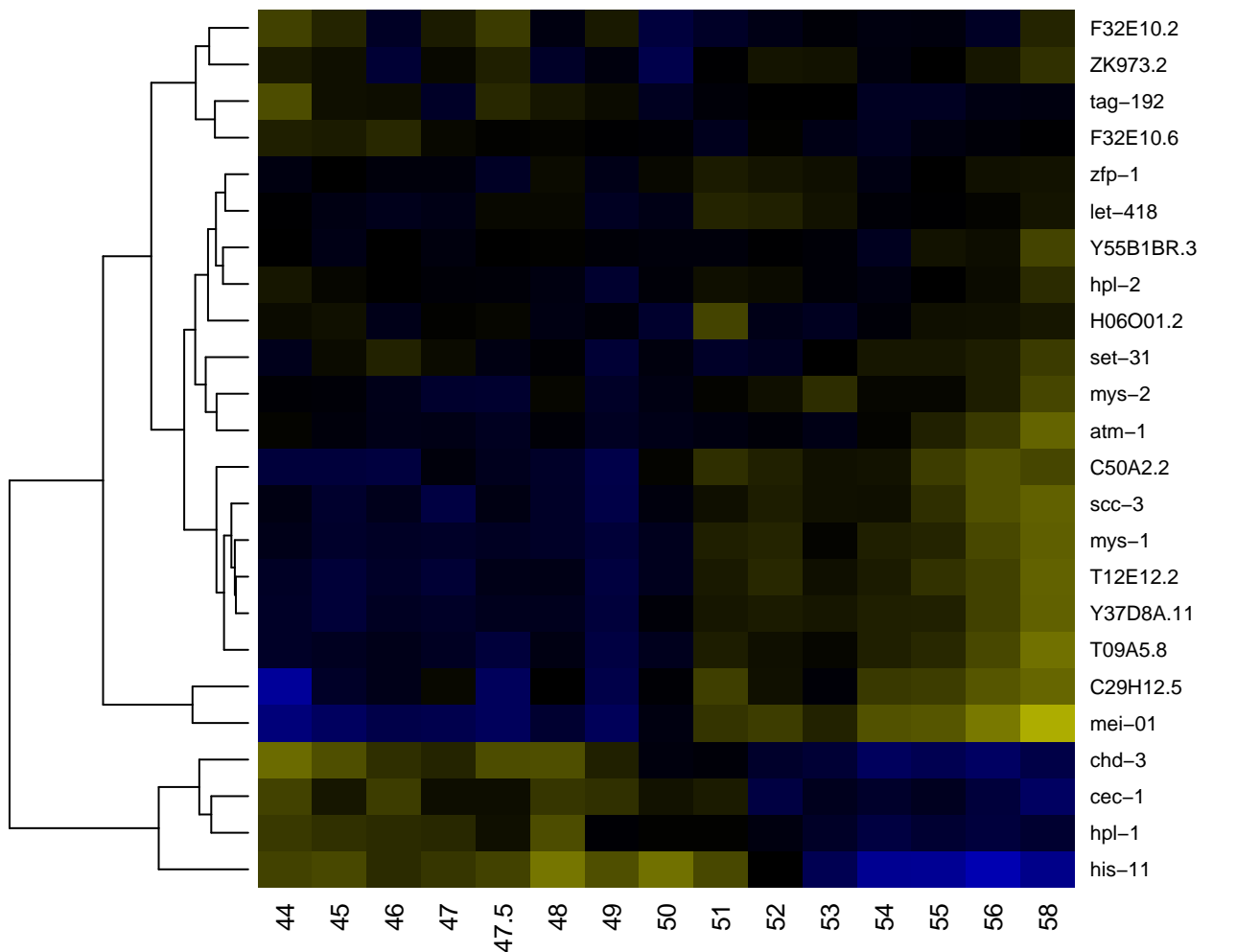
chitin metabolic process



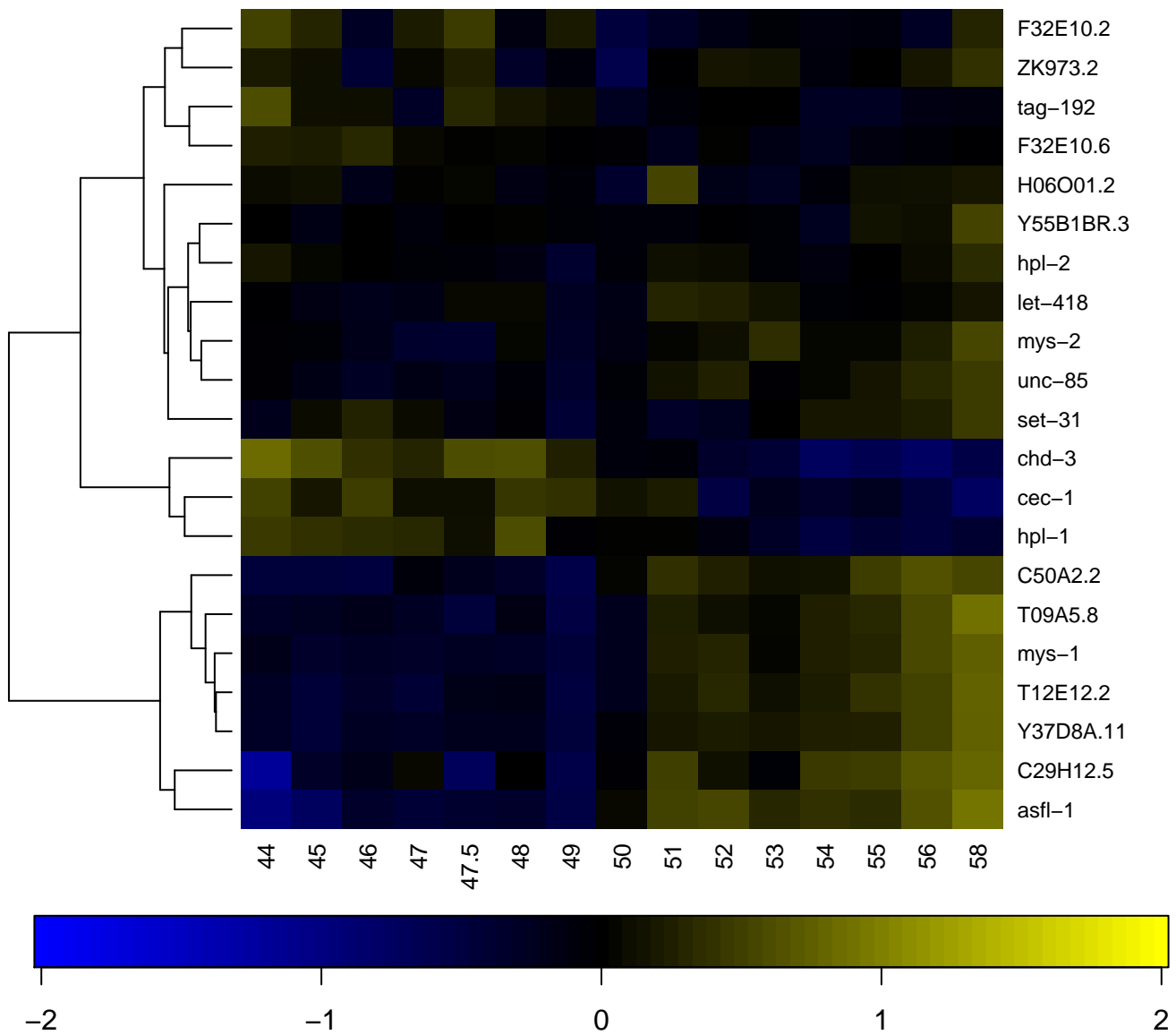
chitinase activity



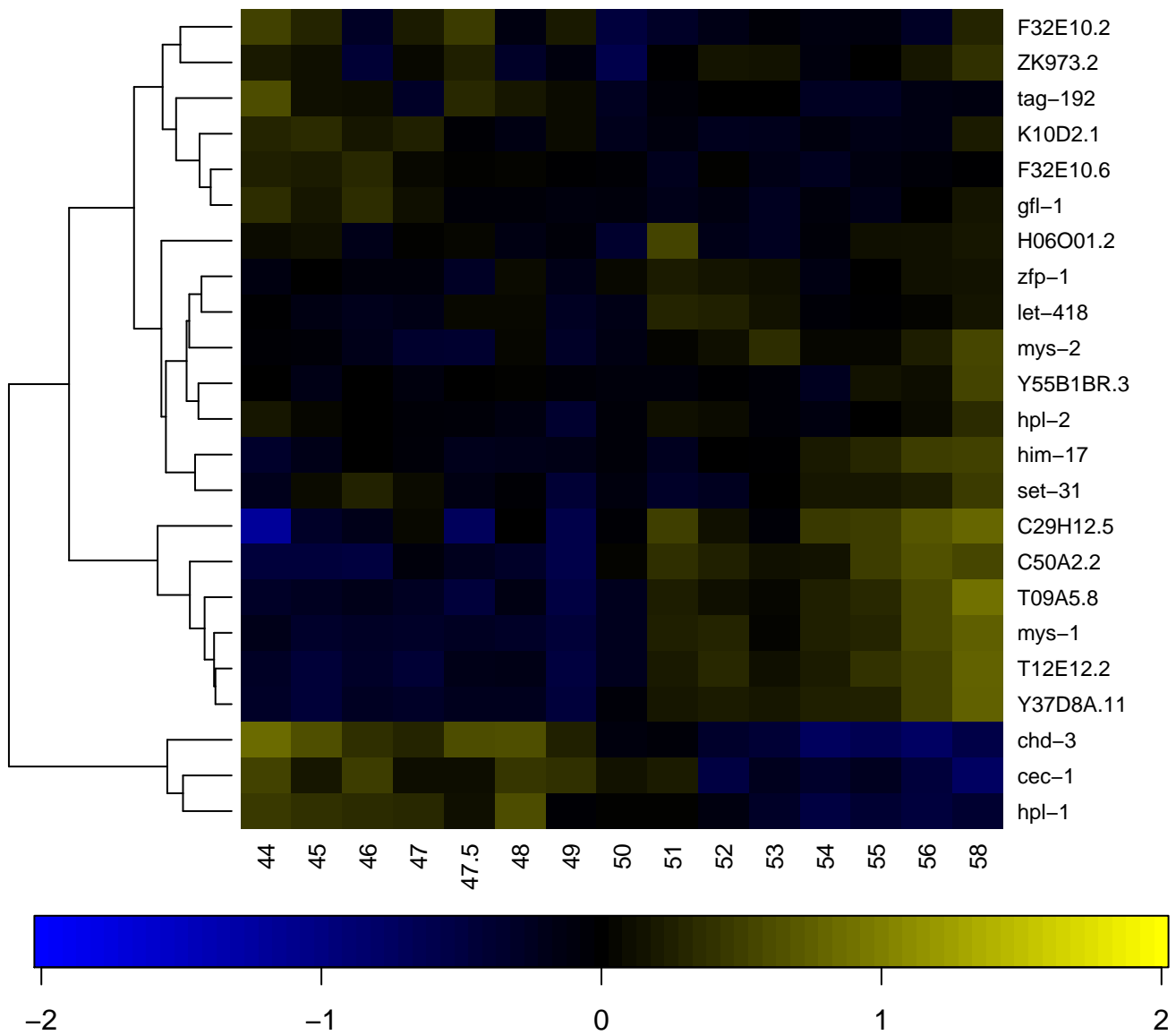
chromatin



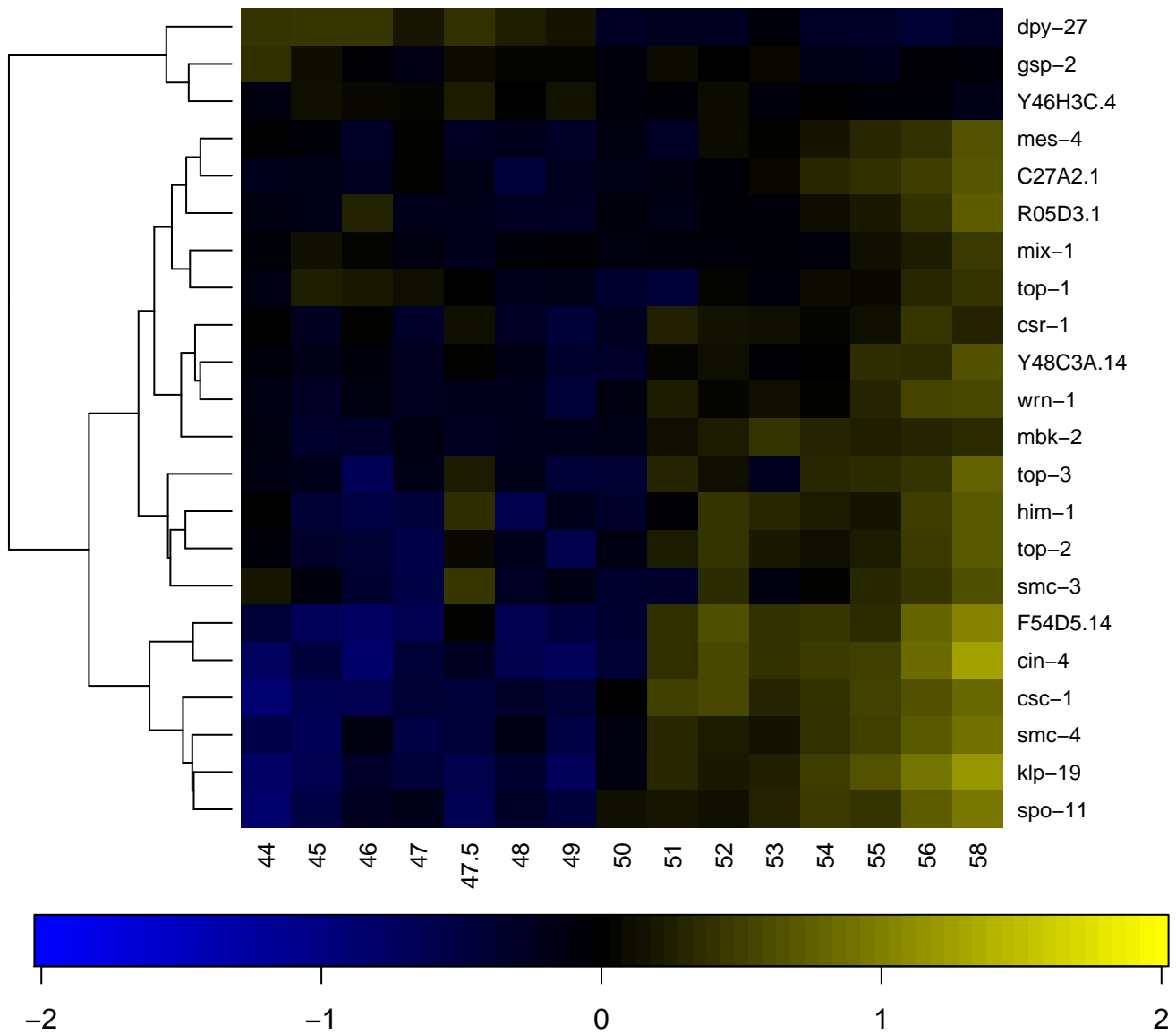
chromatin assembly or disassembly



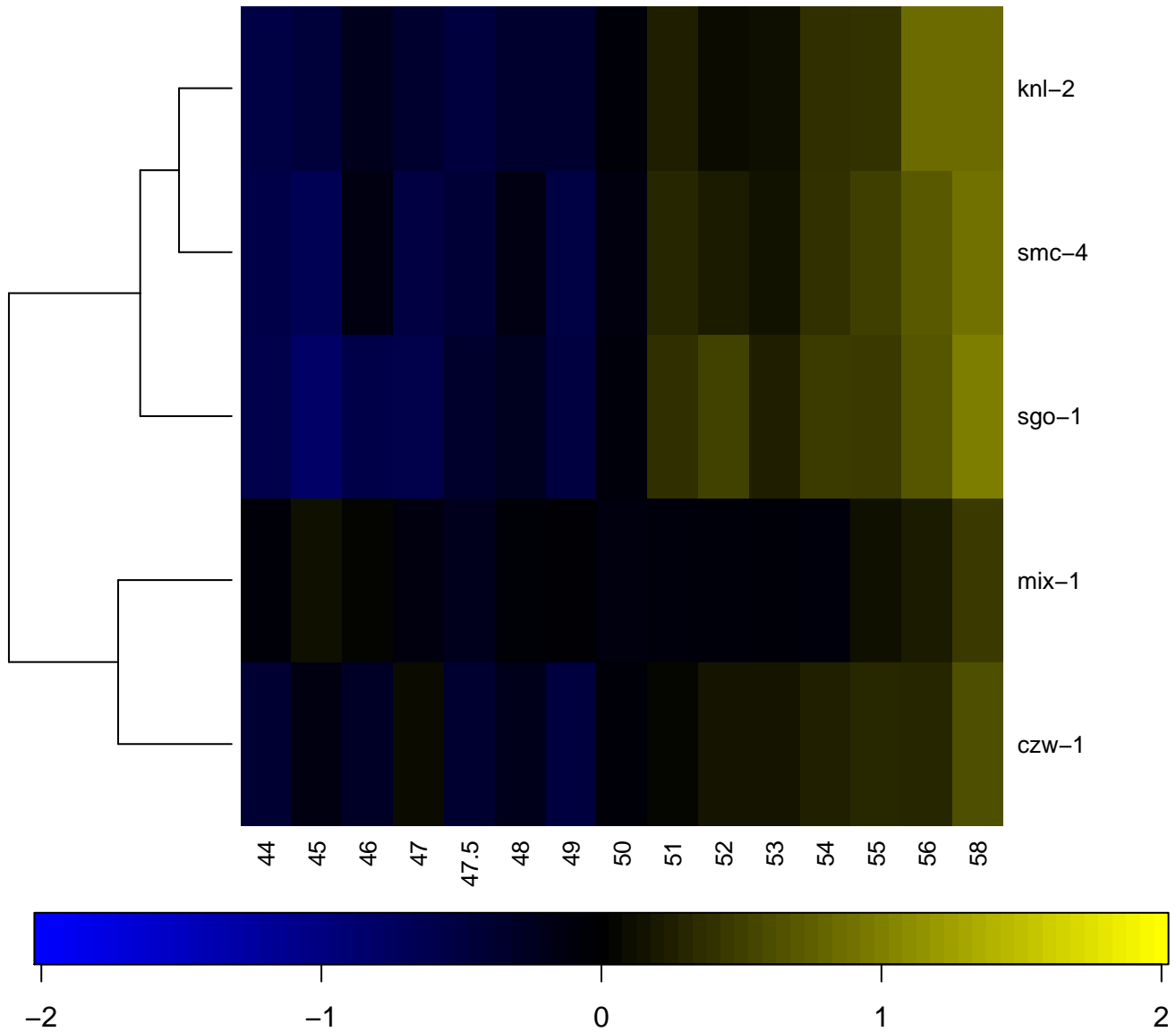
chromatin binding



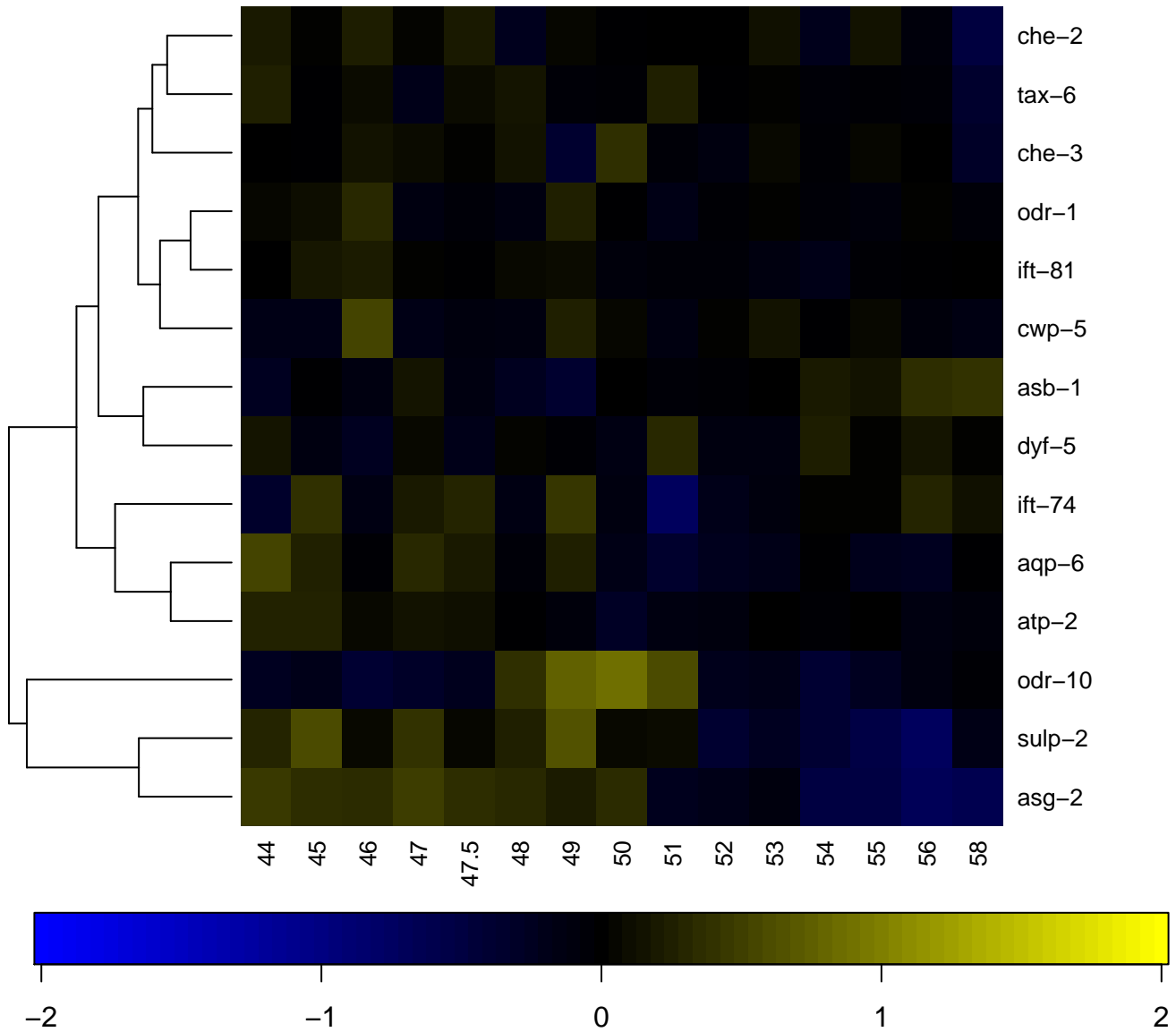
chromosome



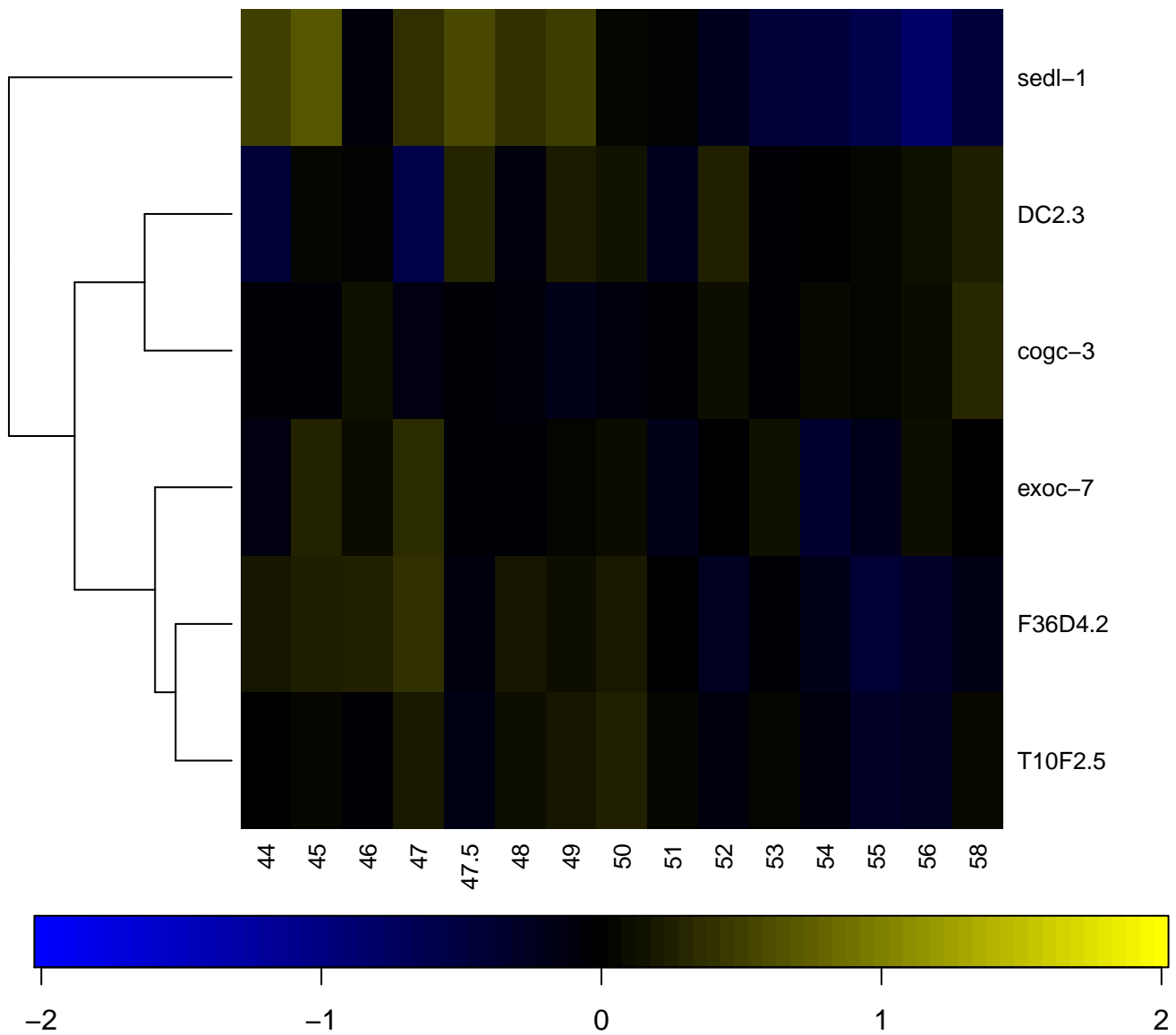
chromosome, centromeric region



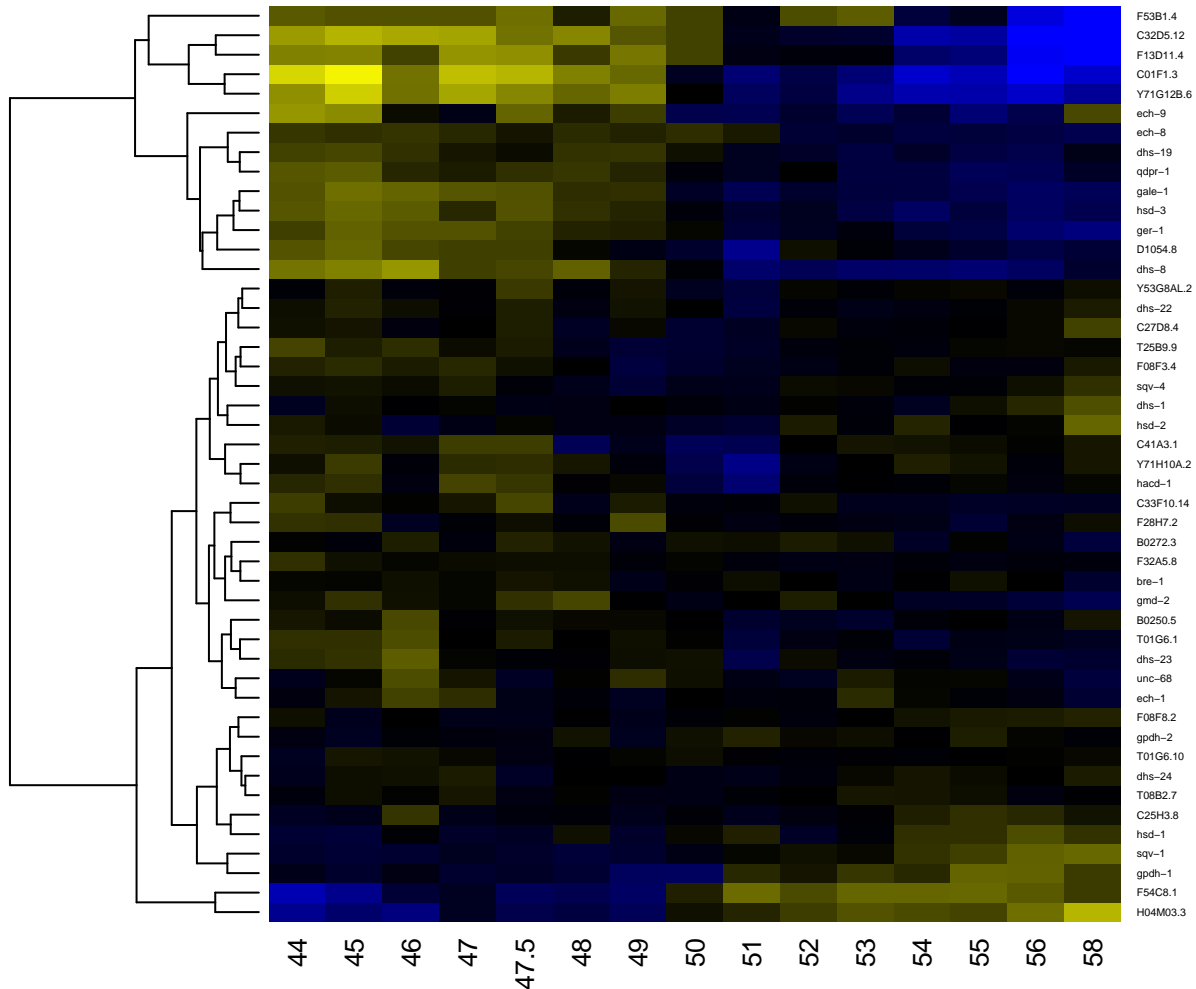
cilium



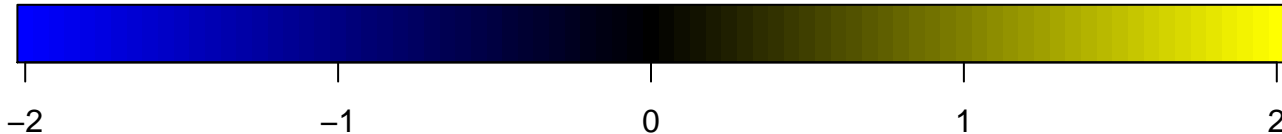
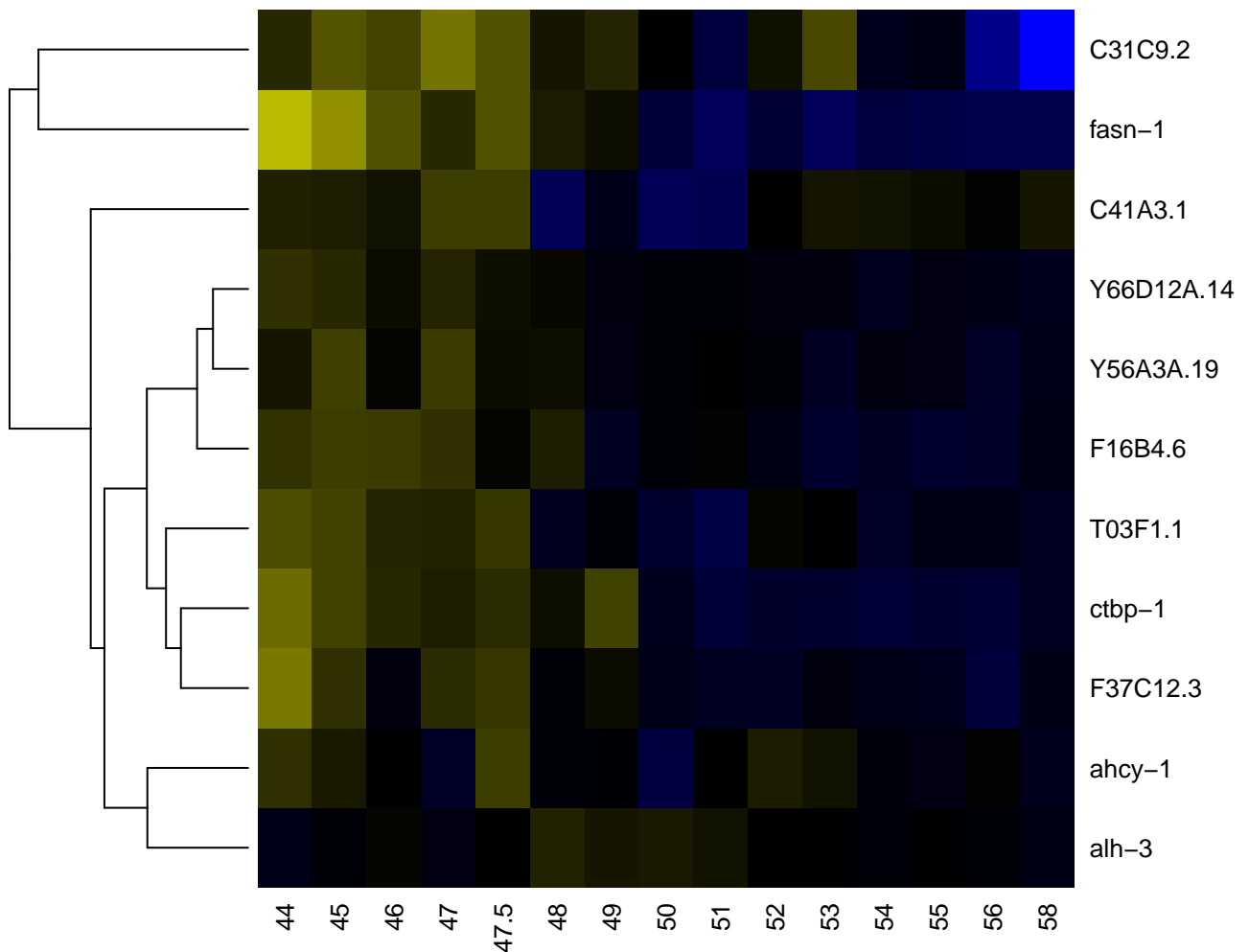
cis-Golgi network



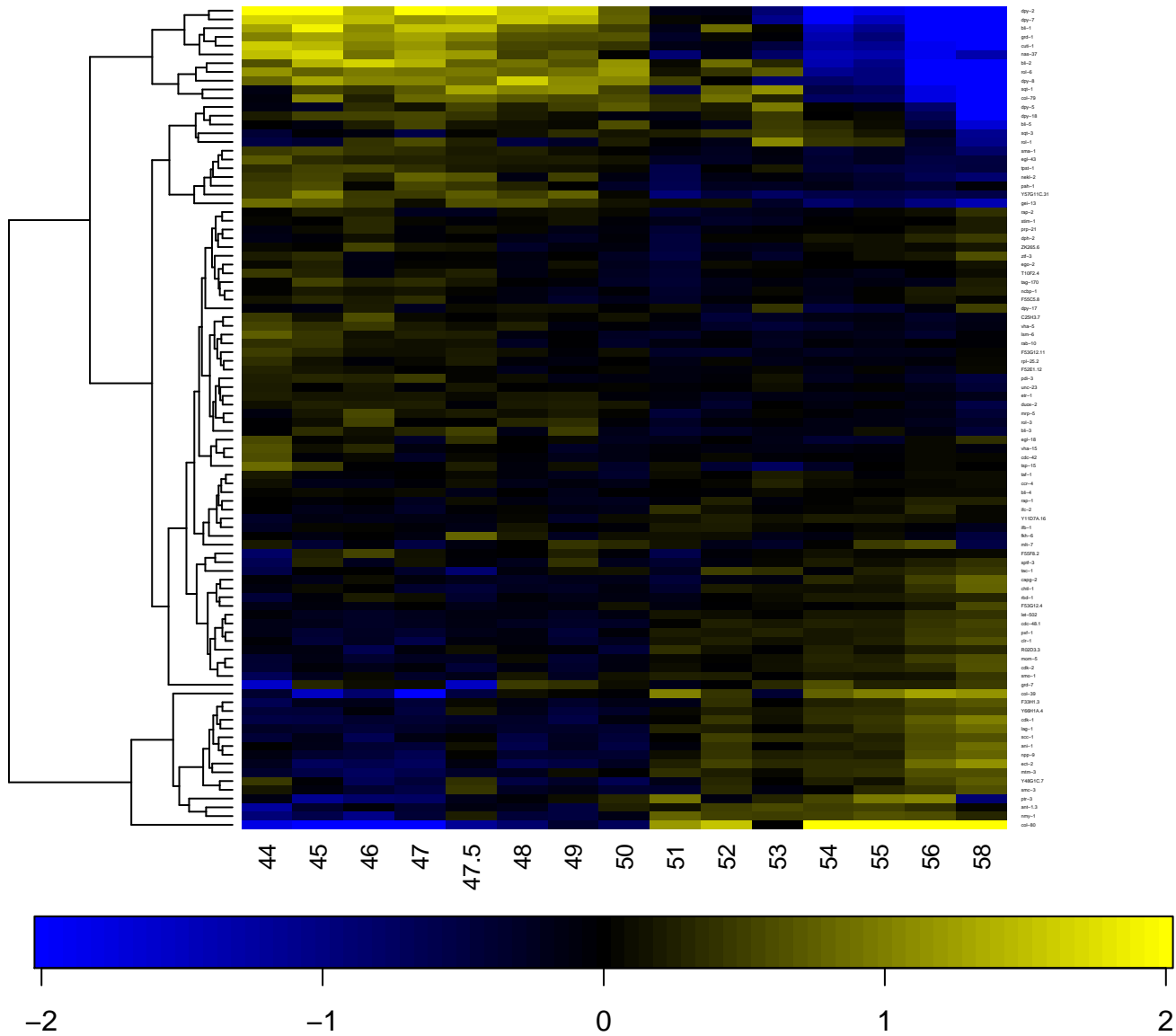
coenzyme binding



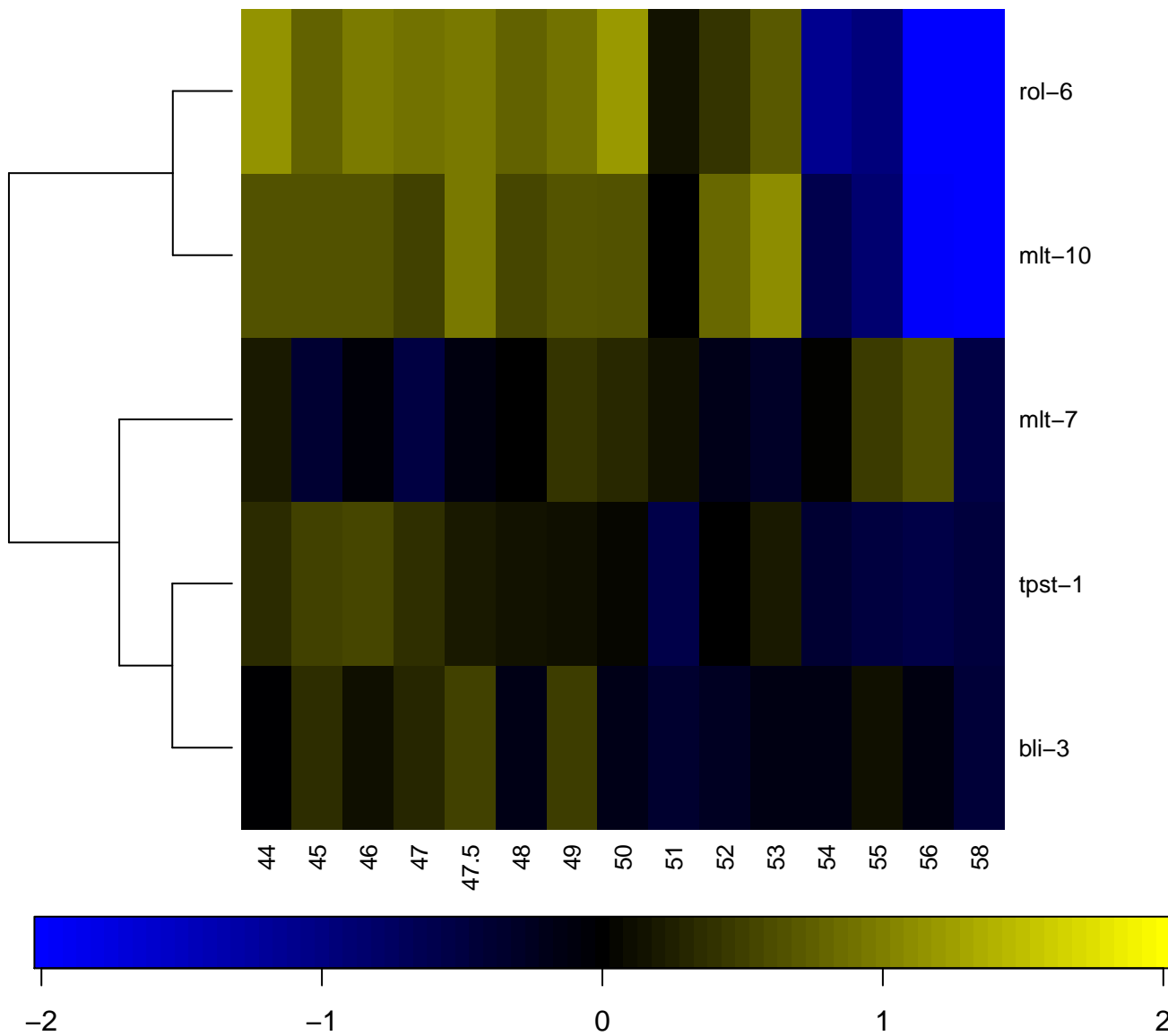
cofactor binding



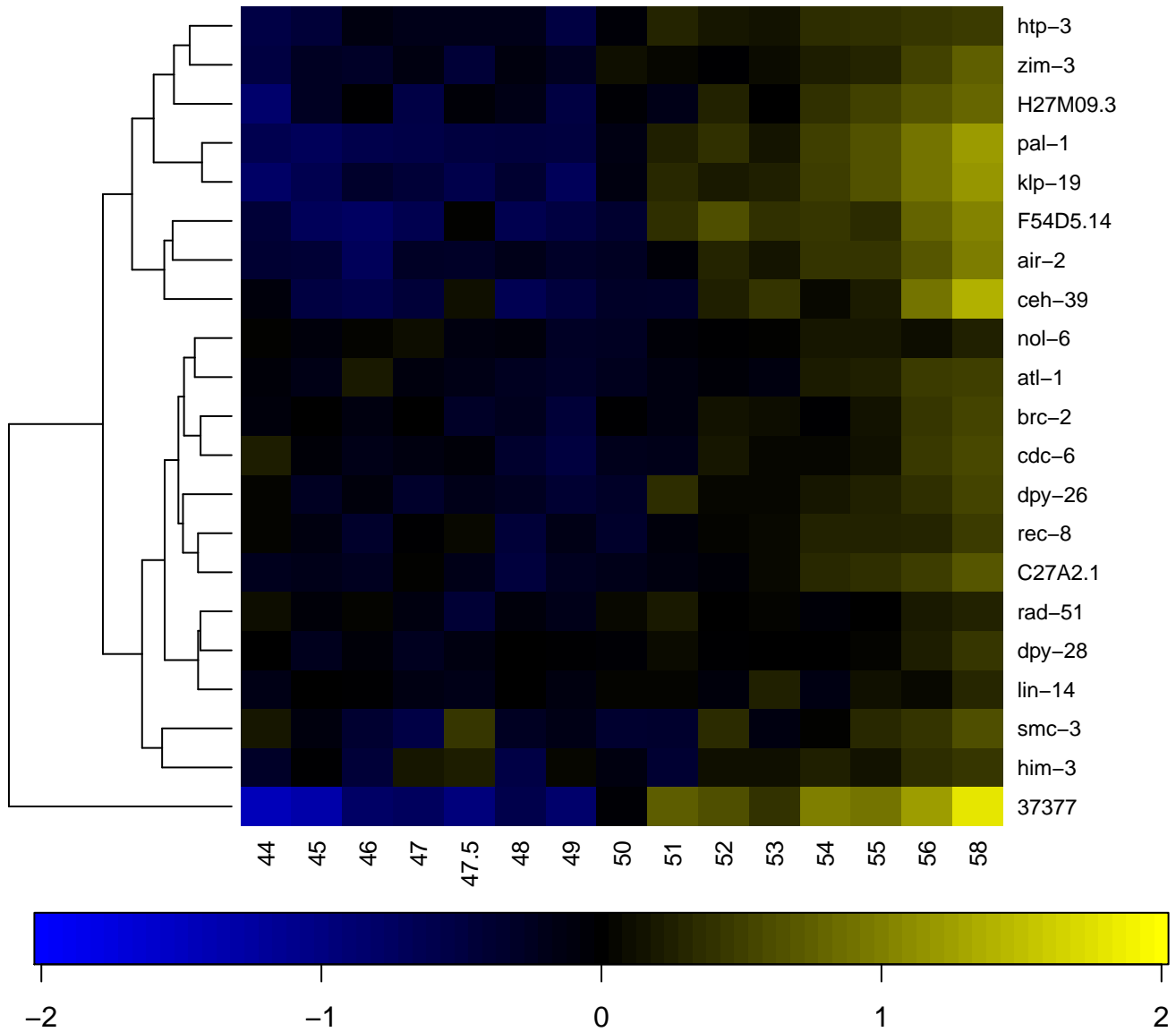
collagen and cuticulin-based cuticle development



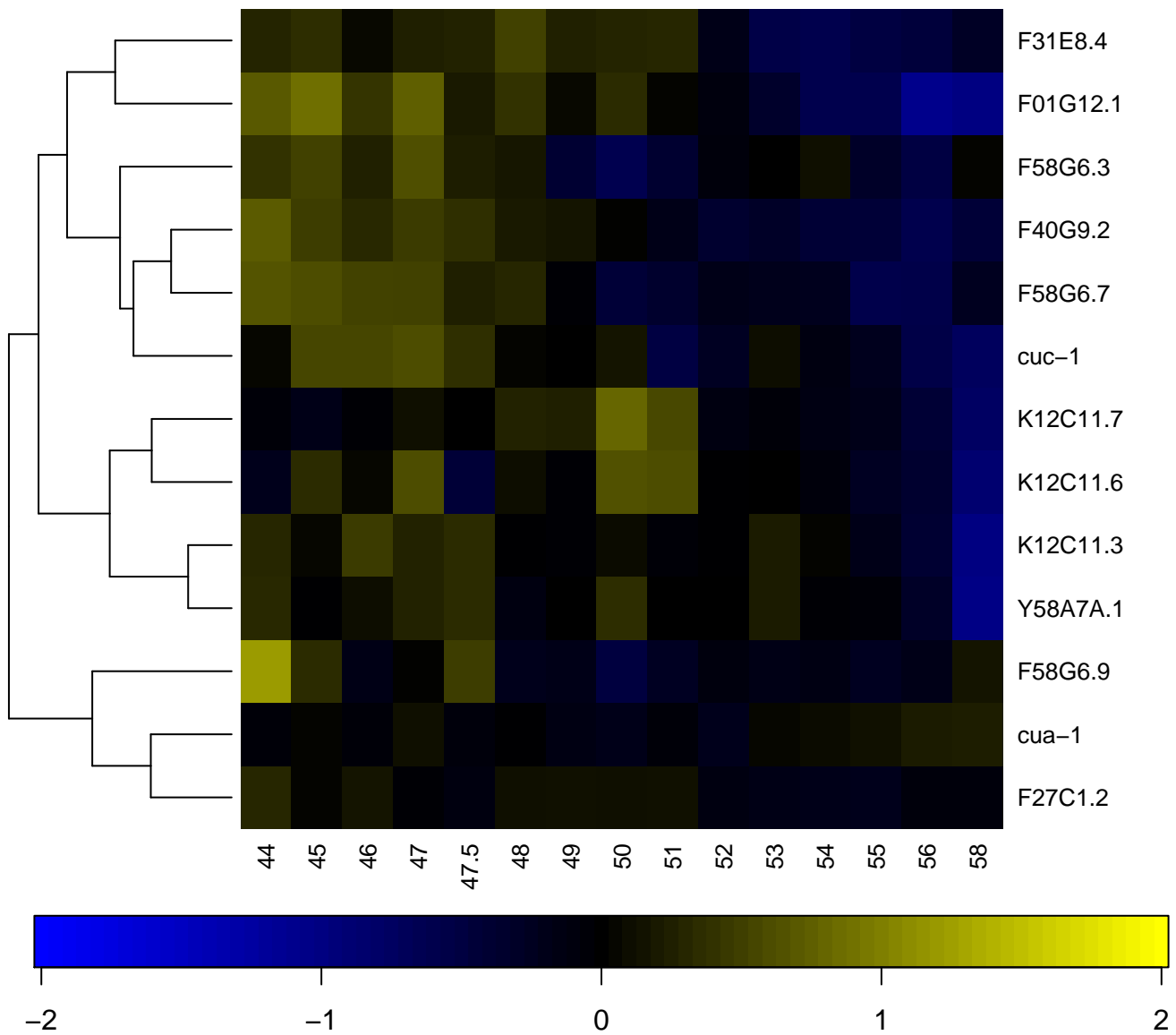
Collagen and cuticulin-based cuticle development during molting



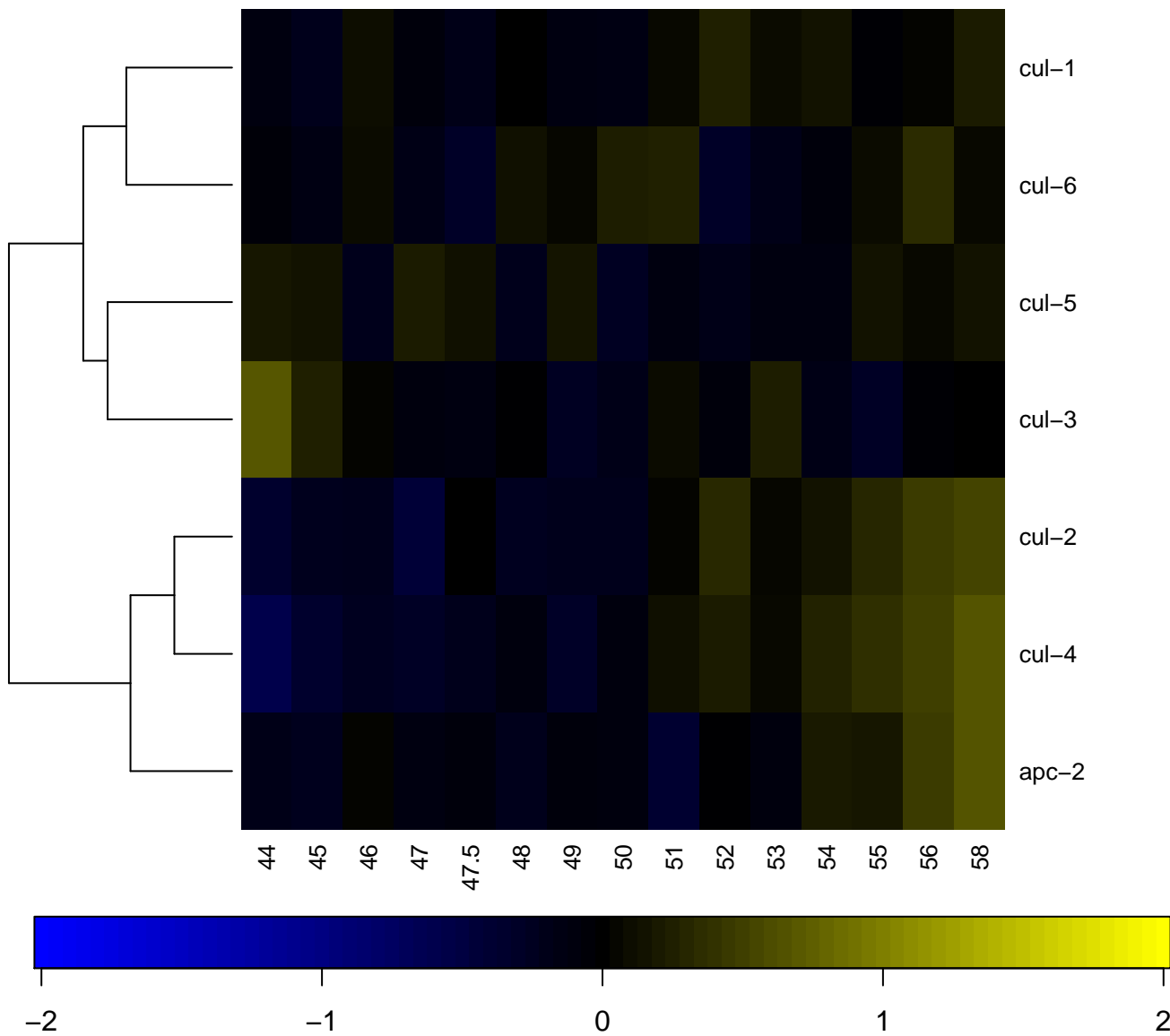
condensed nuclear chromosome



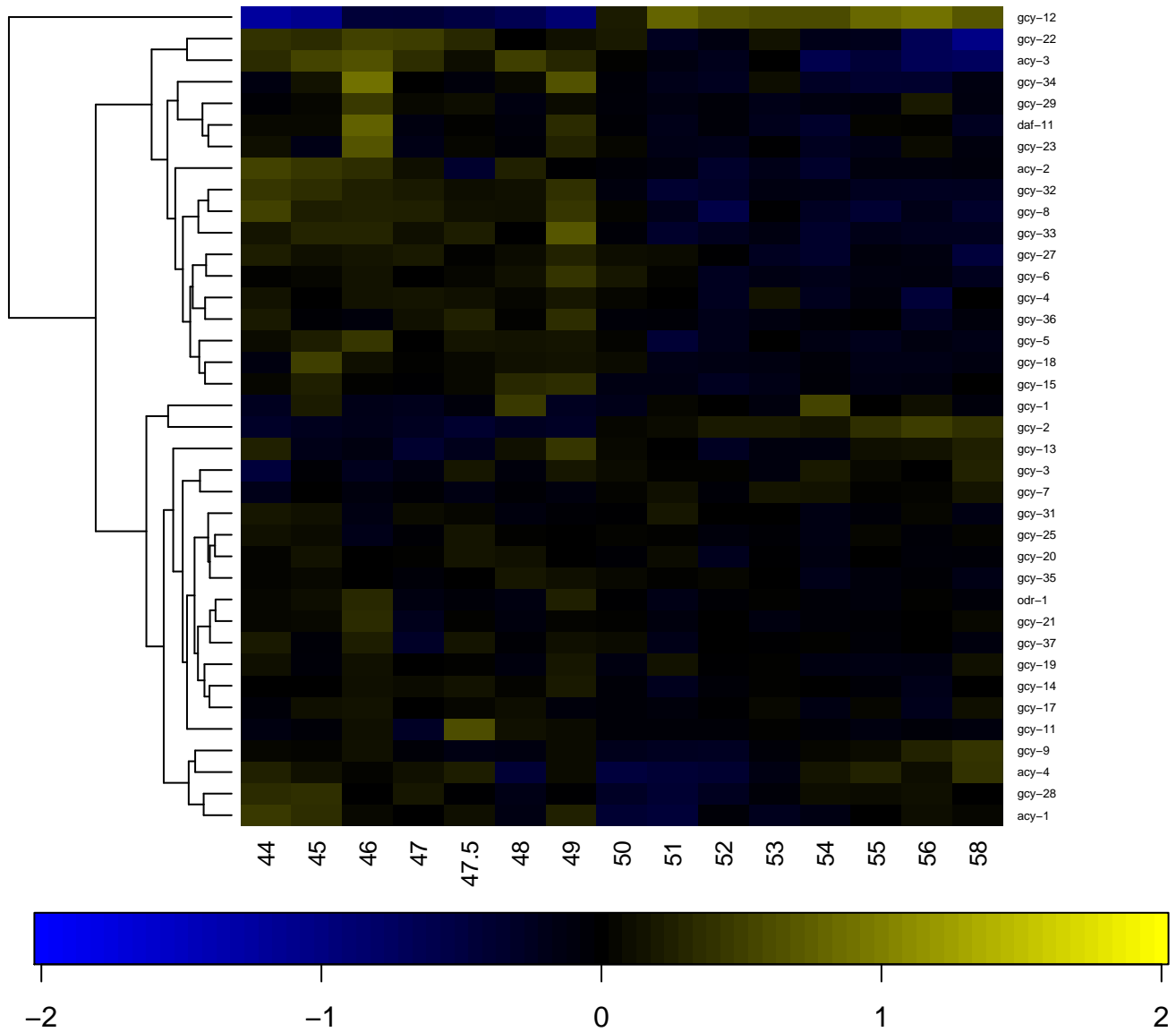
copper ion transport



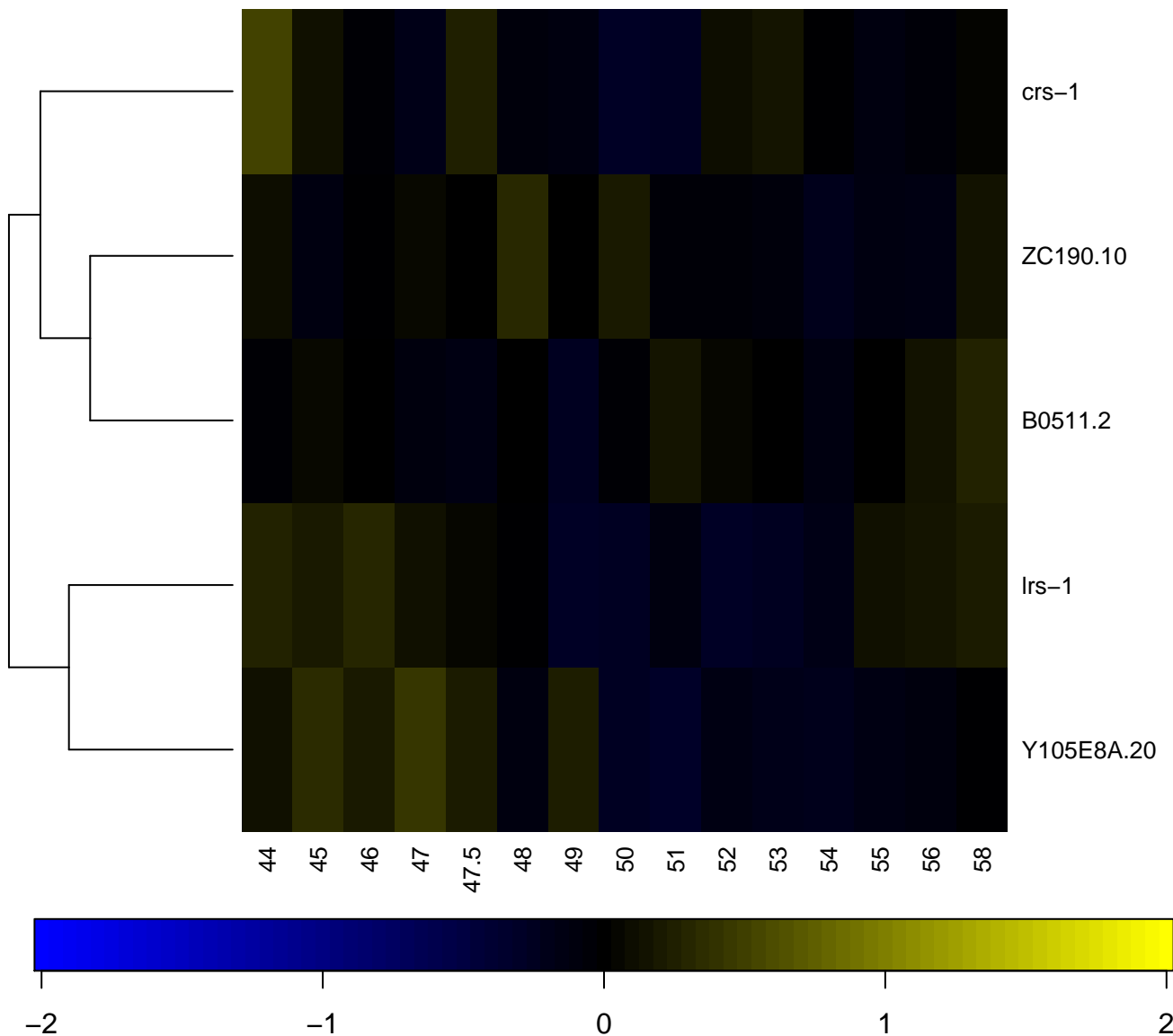
cullin-RING ubiquitin ligase complex



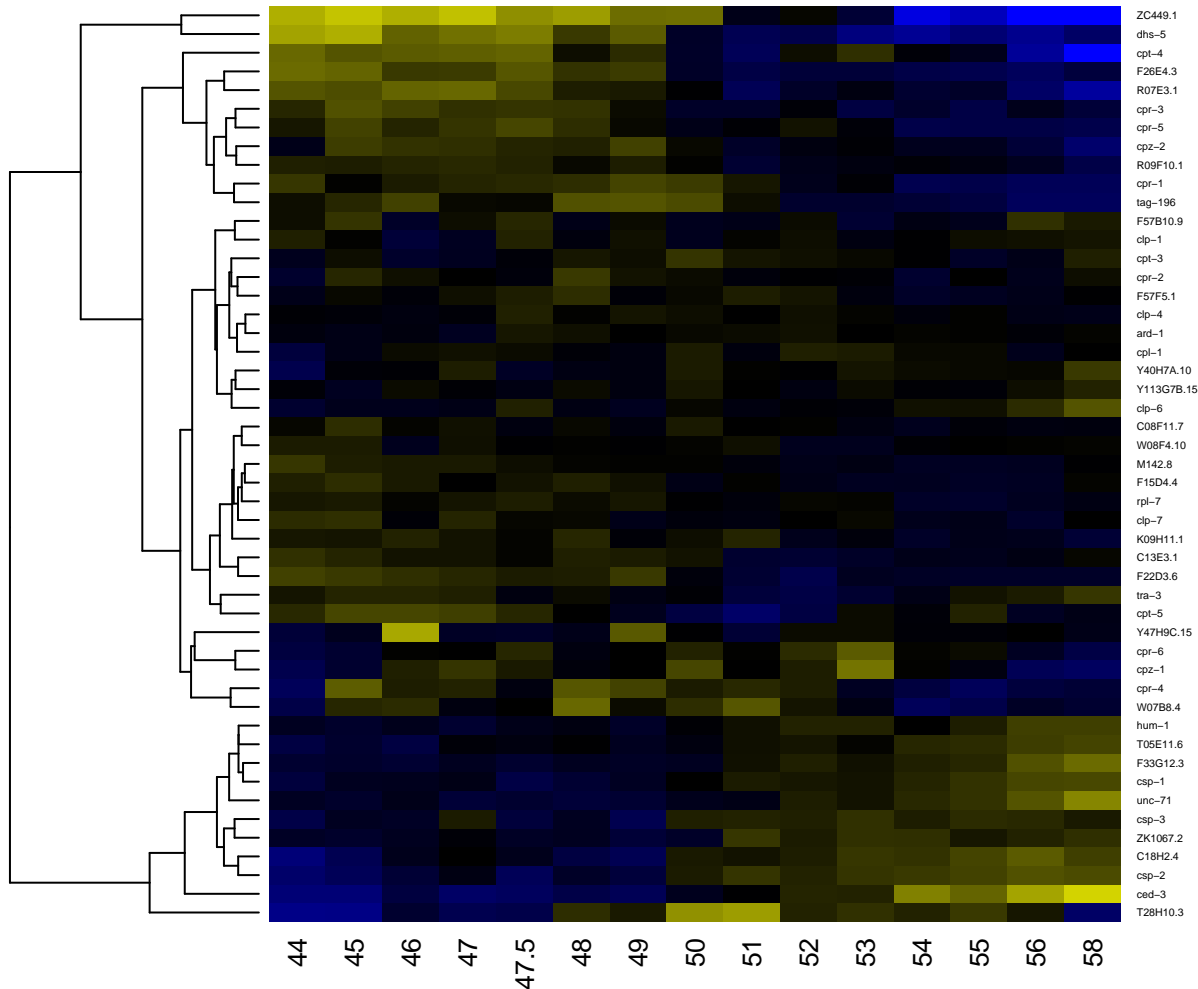
cyclic nucleotide biosynthetic process



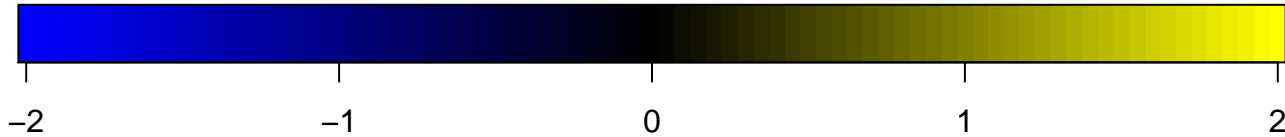
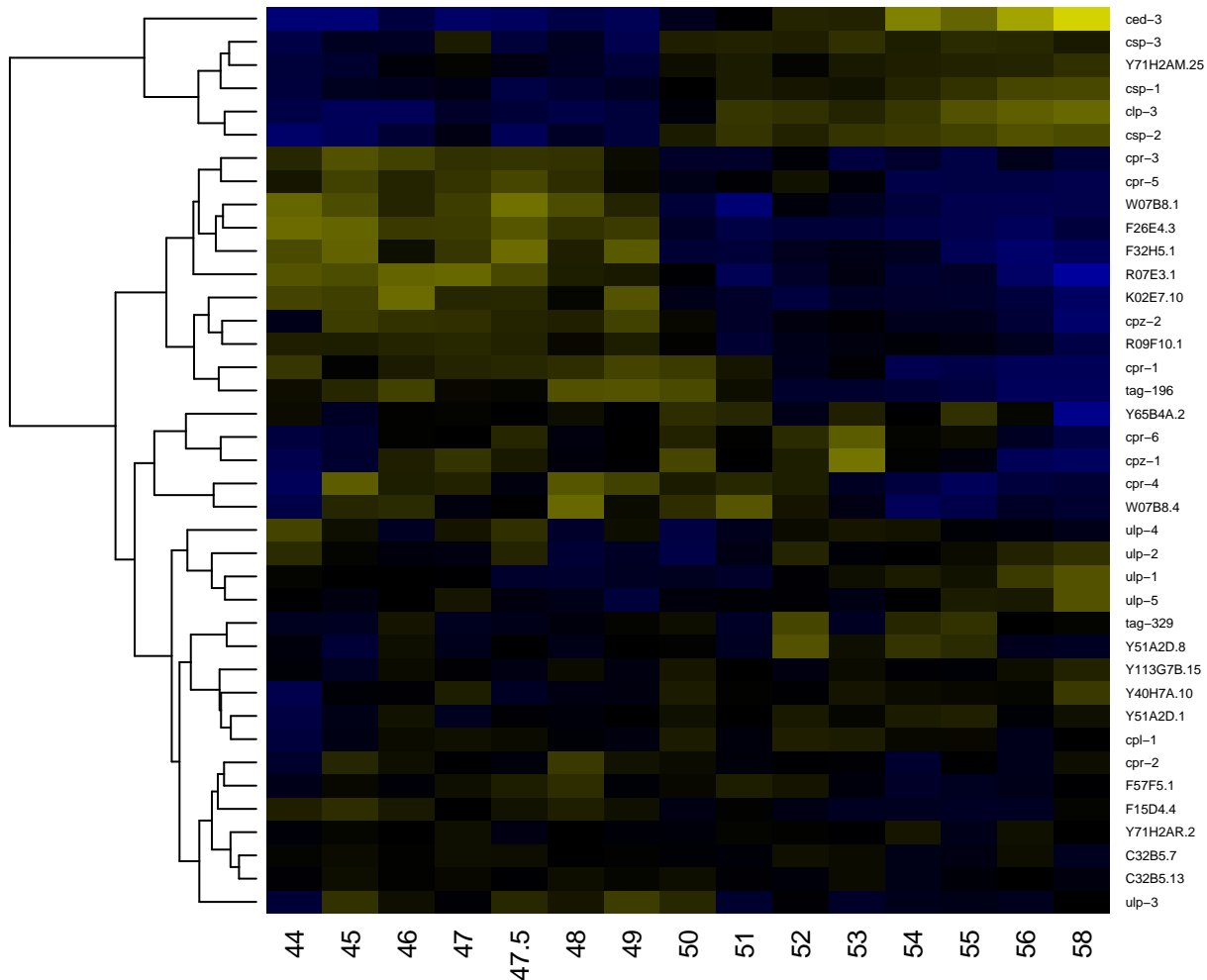
cysteine-tRNA ligase activity



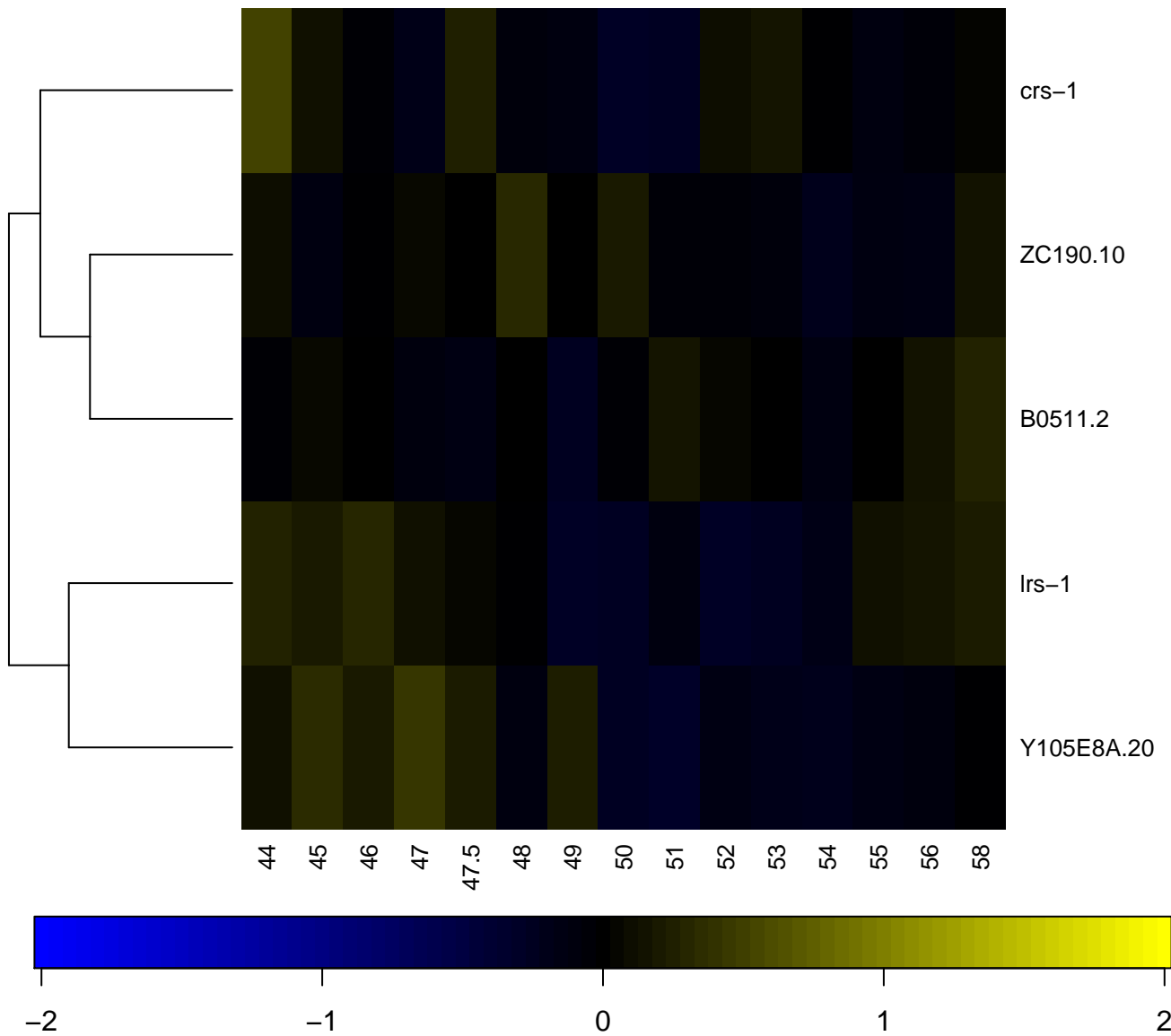
cysteine-type endopeptidase activity



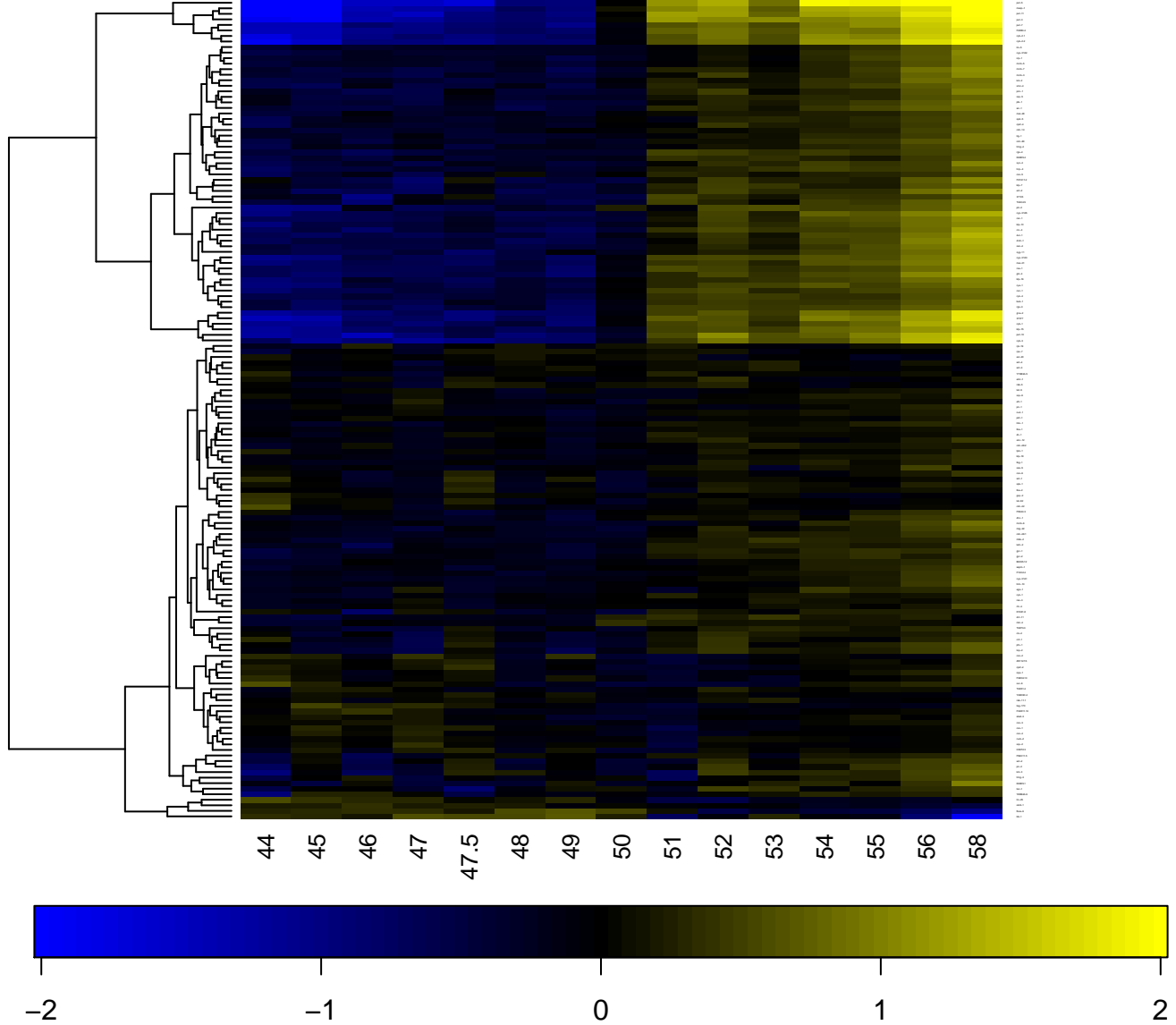
cysteine-type peptidase activity



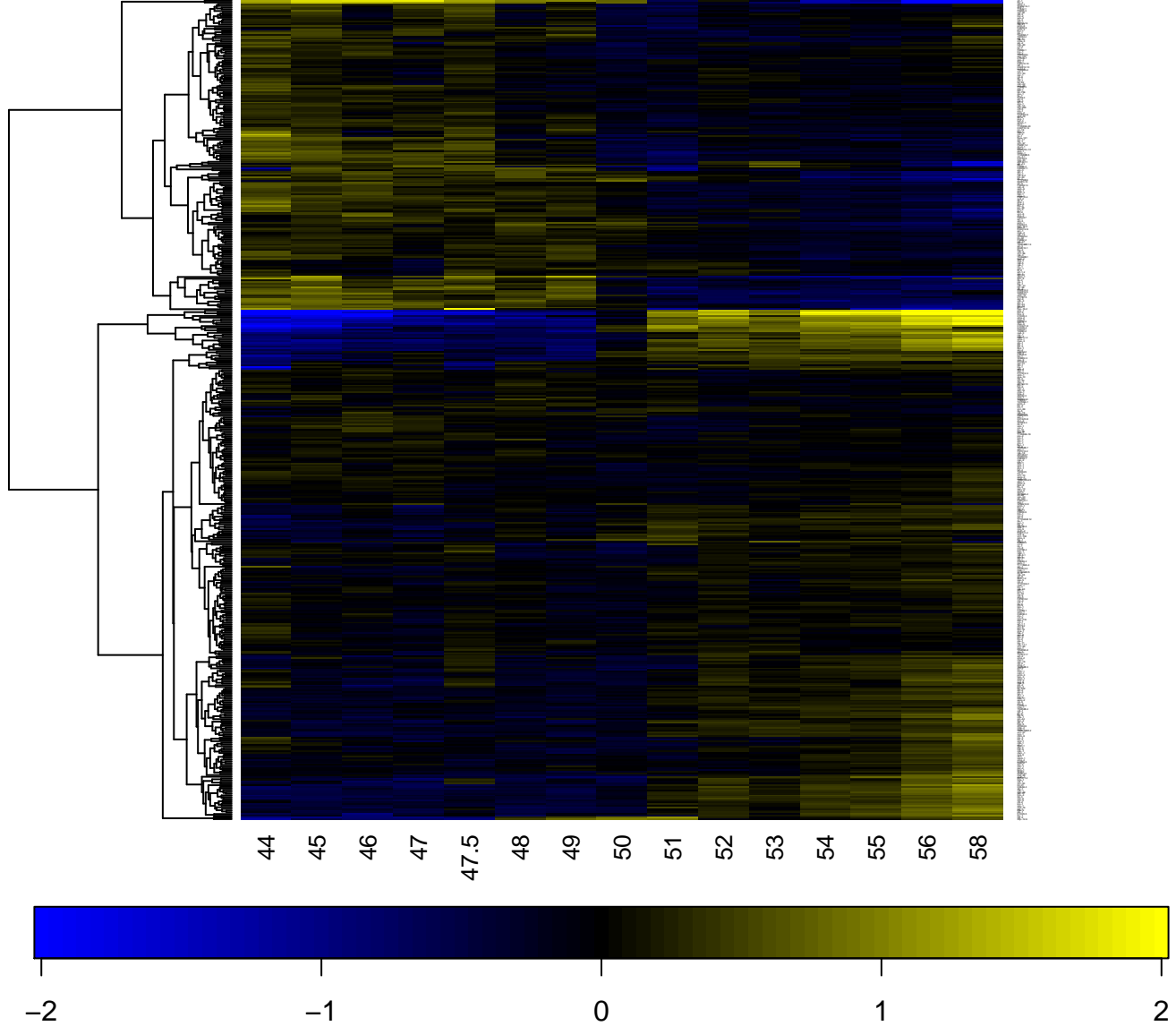
cysteinyI-tRNA aminoacylation



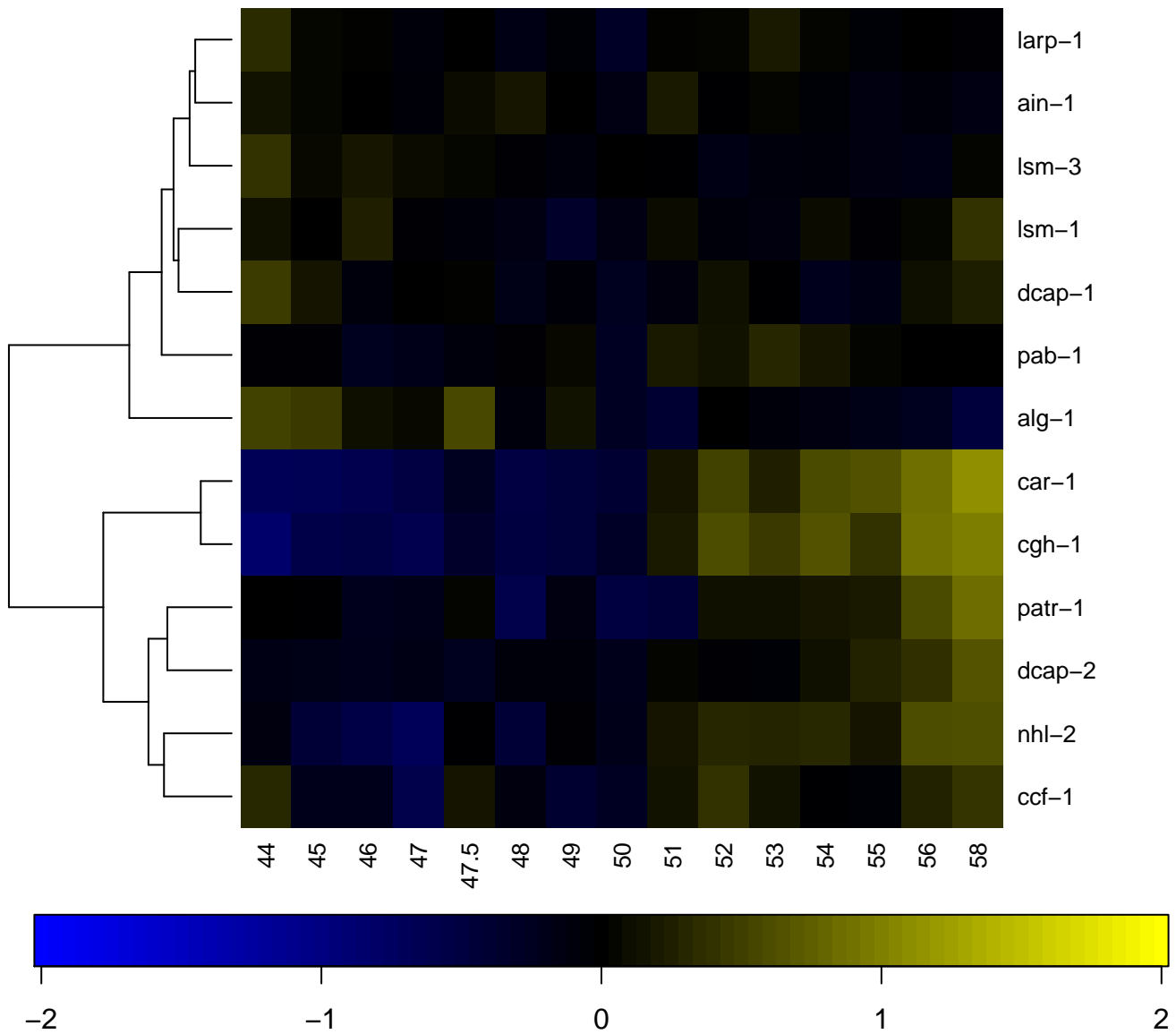
cytokines



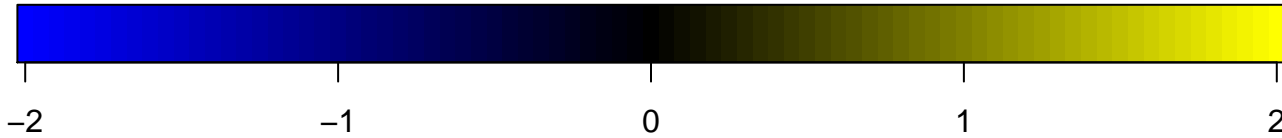
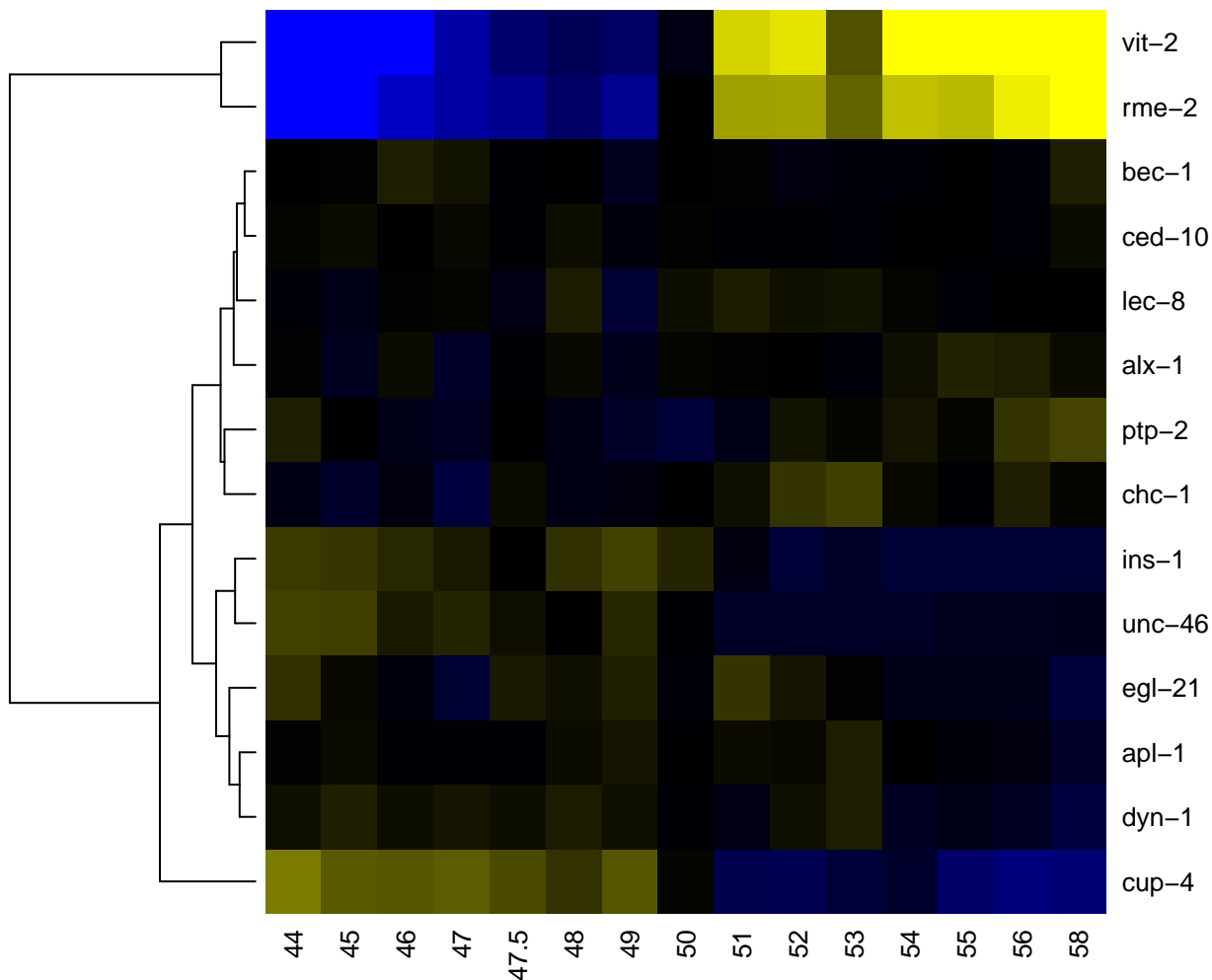
cytoplasm



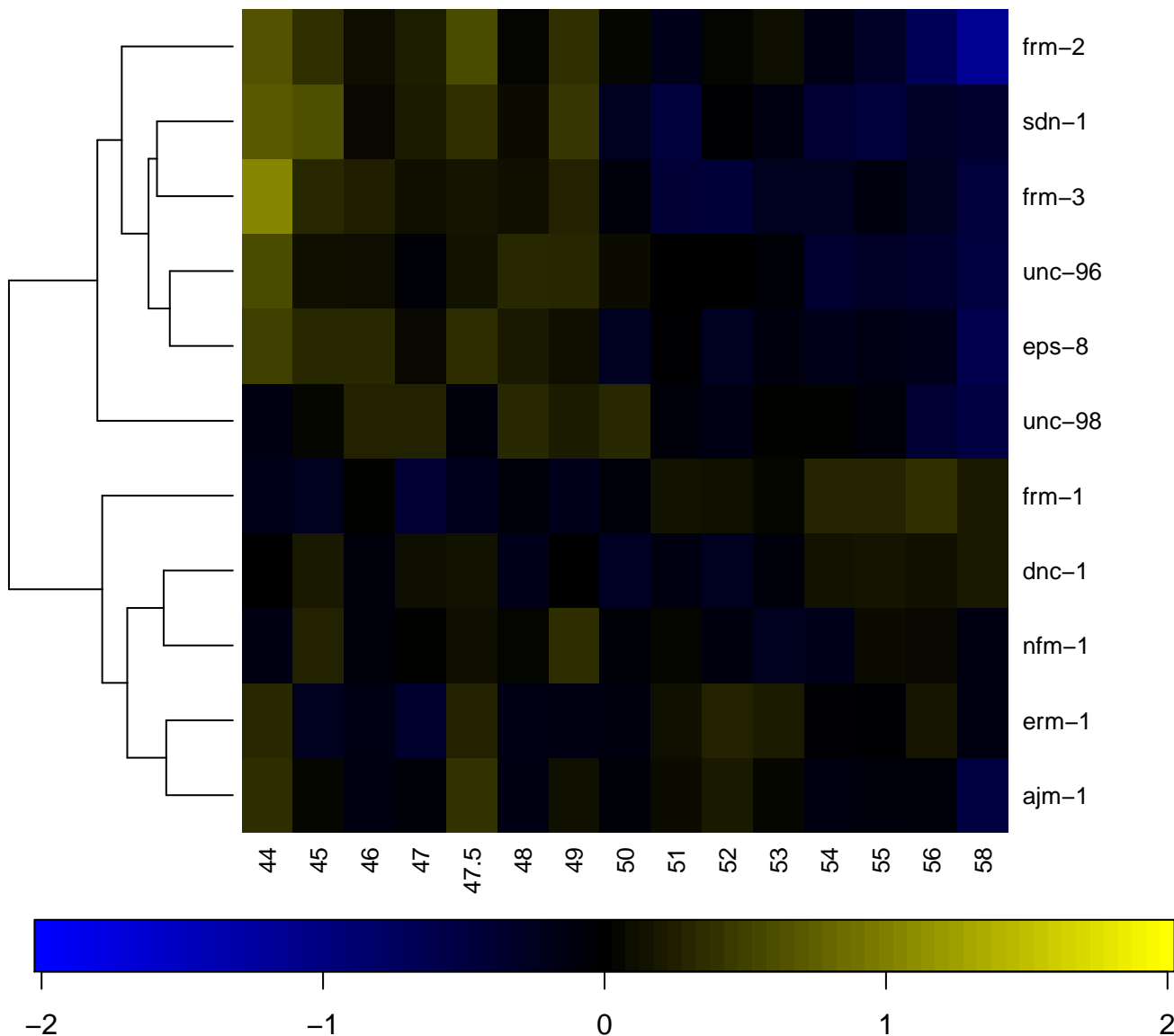
cytoplasmic mRNA processing body



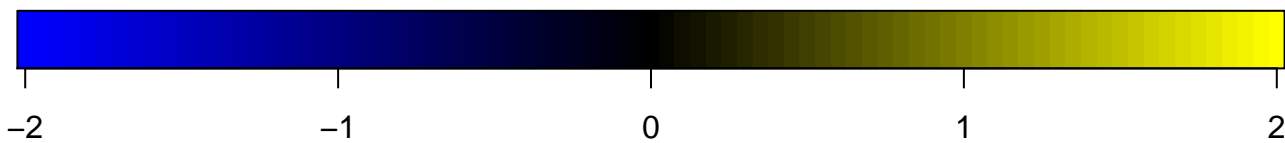
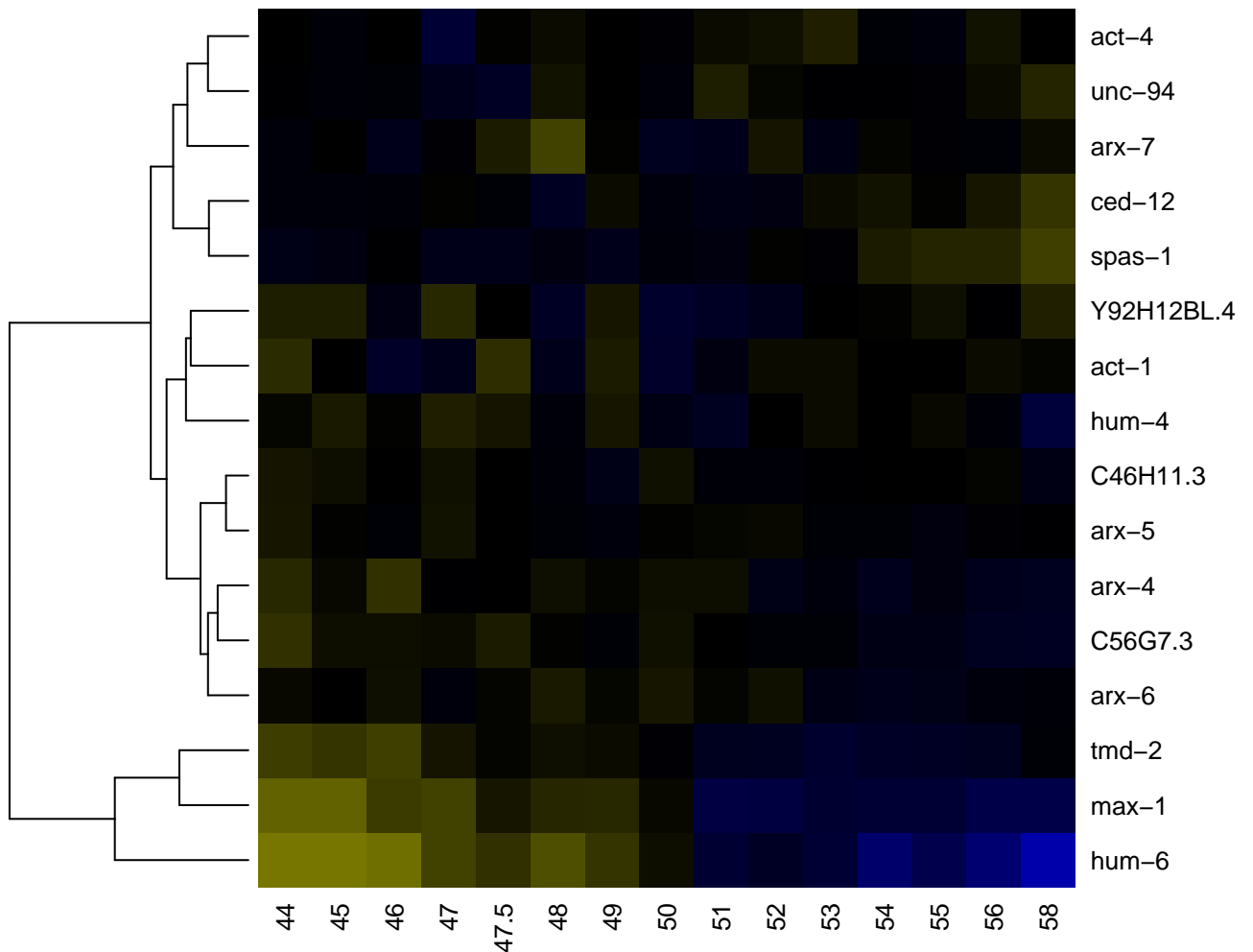
cytoplasmic vesicle



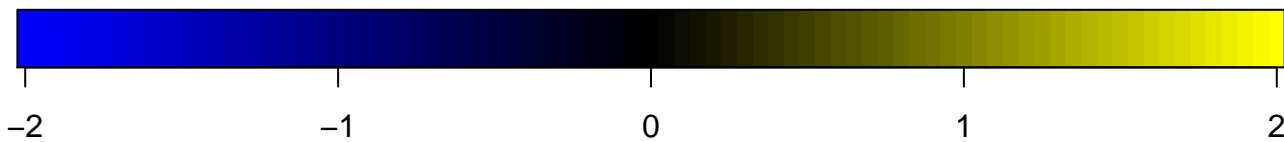
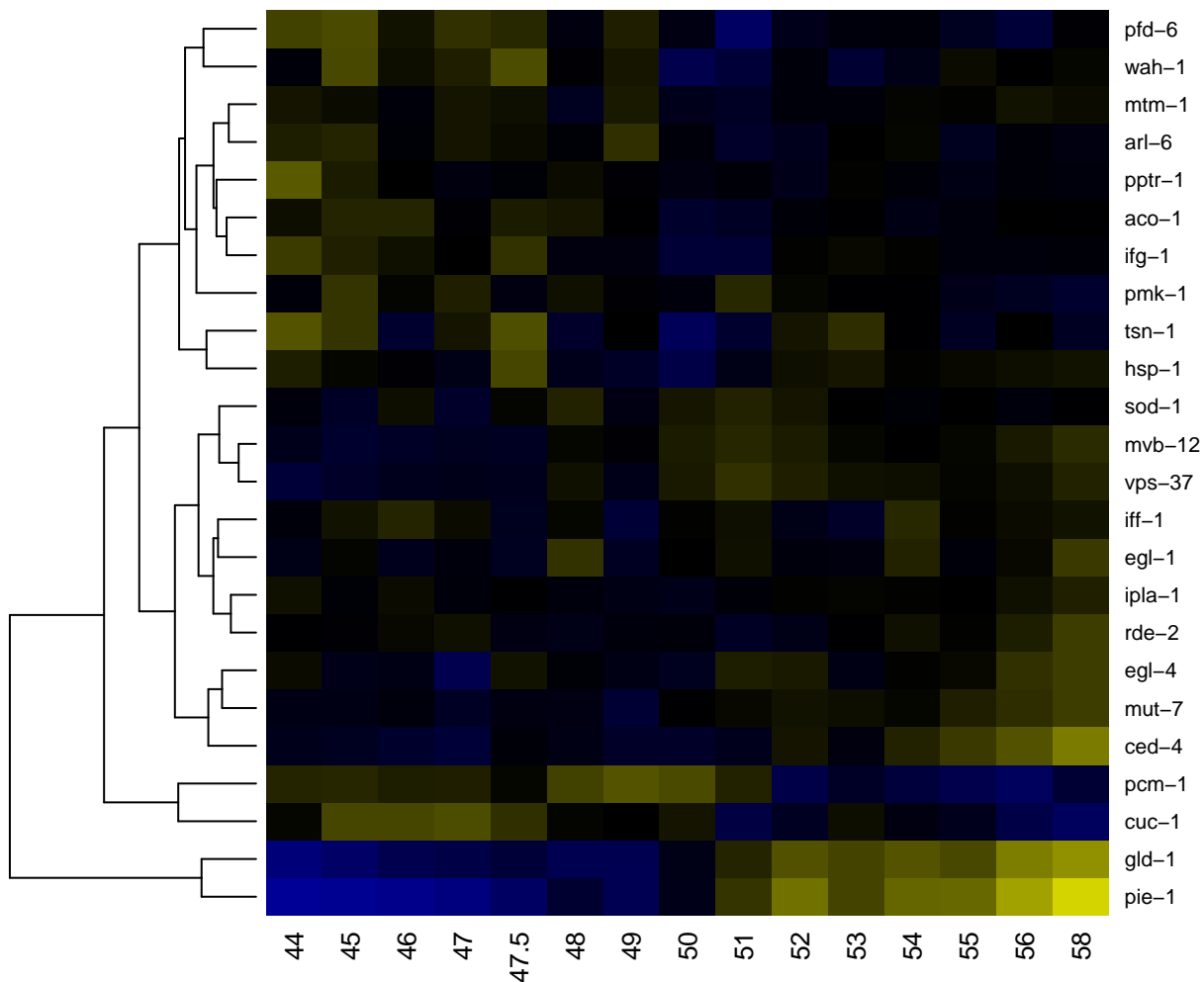
cytoskeletal protein binding



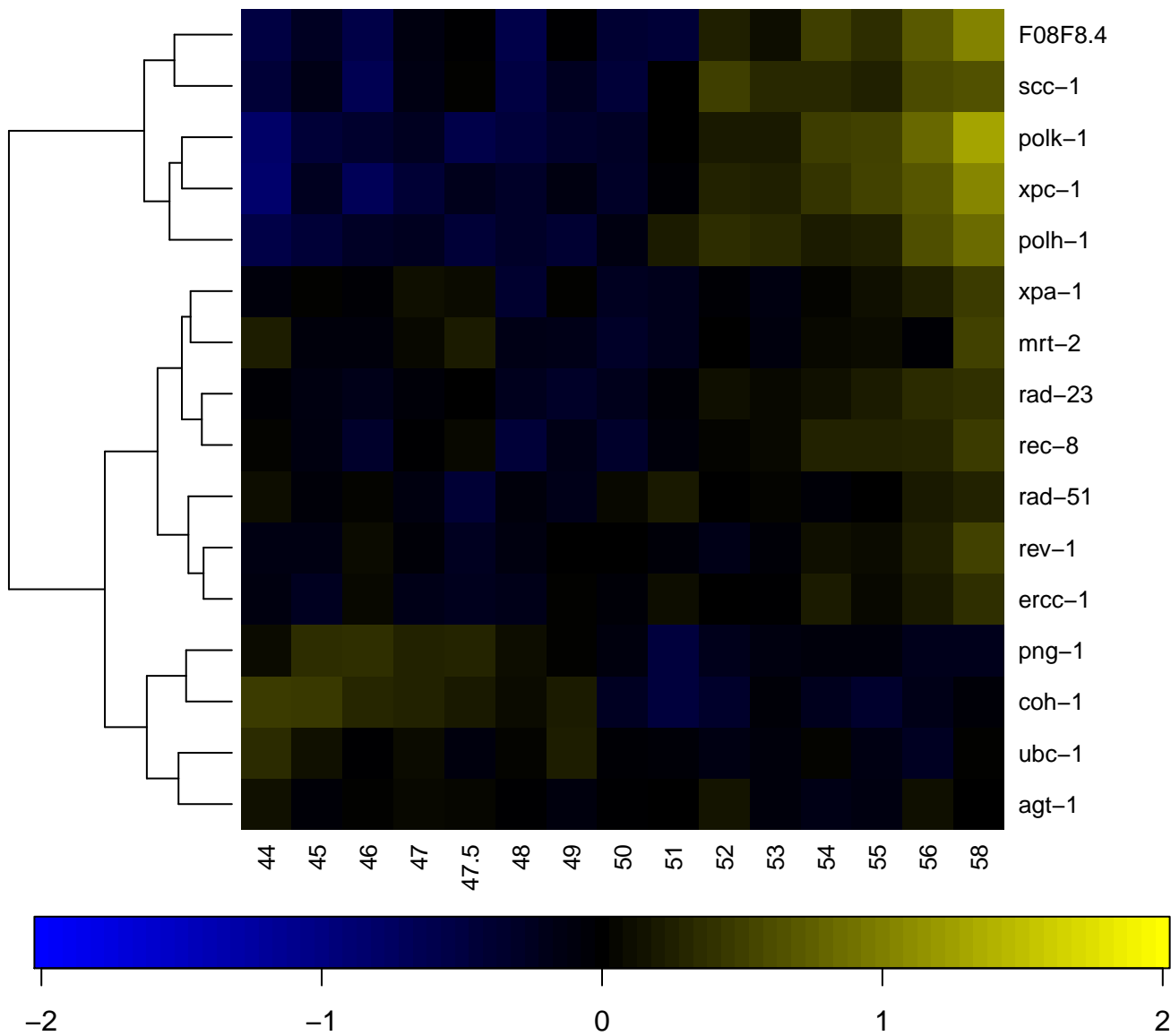
cytoskeleton



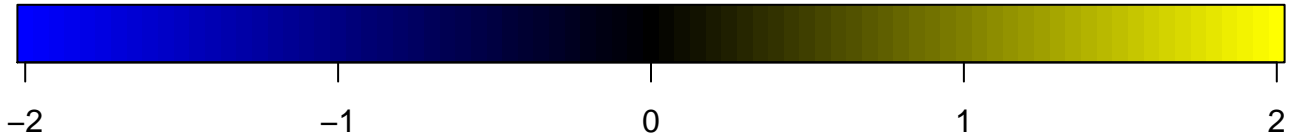
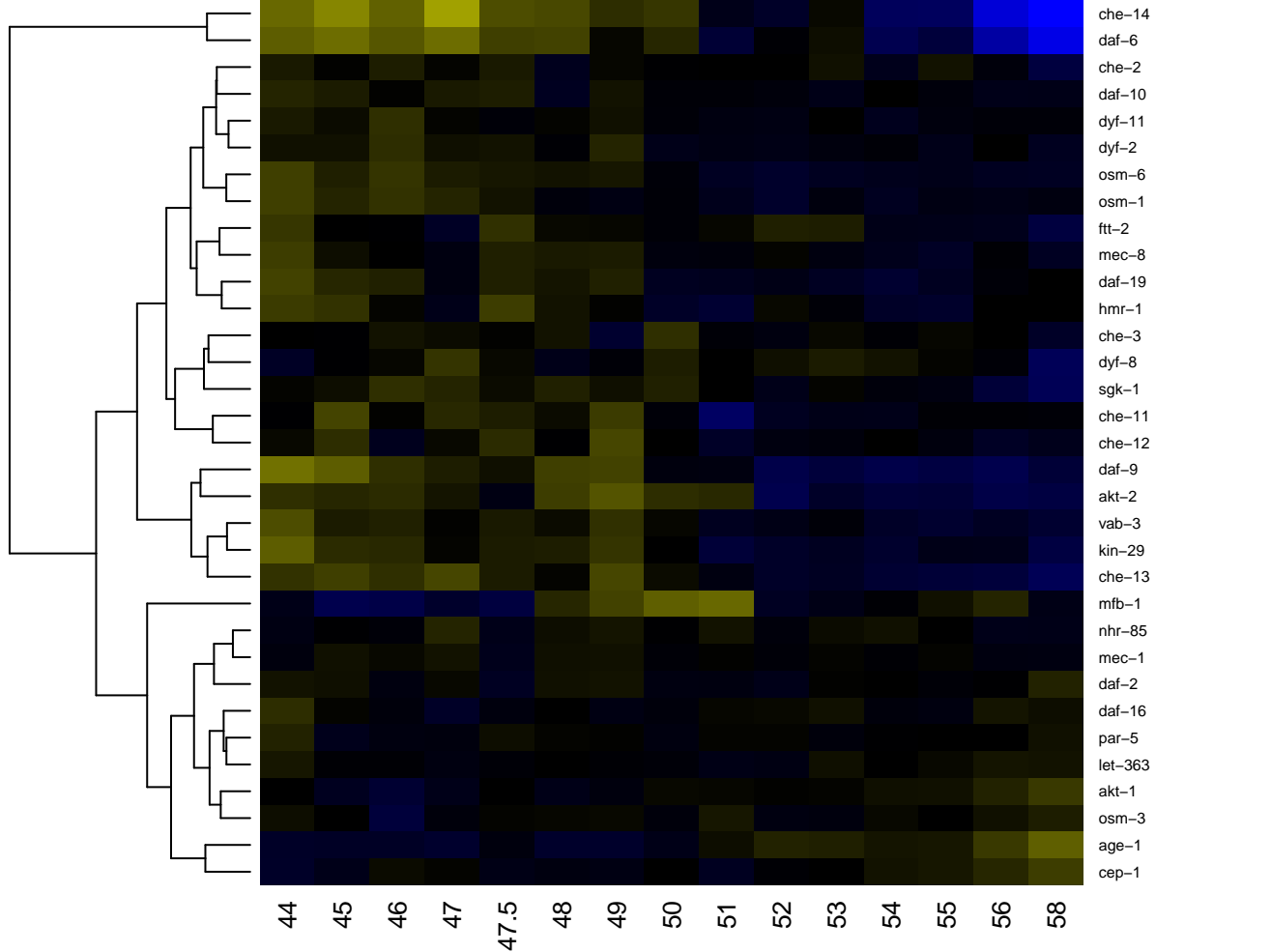
cytosol



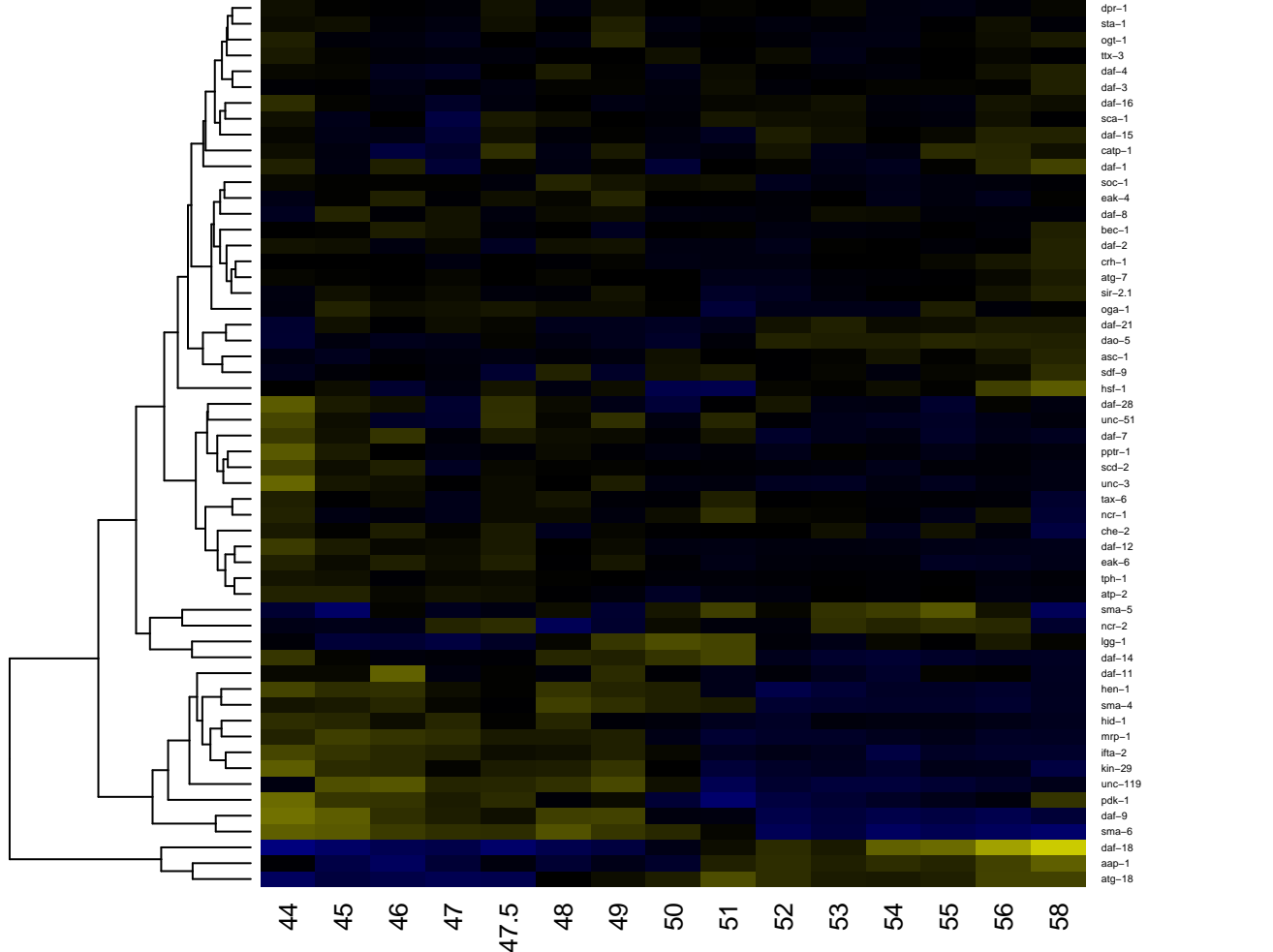
damaged DNA binding



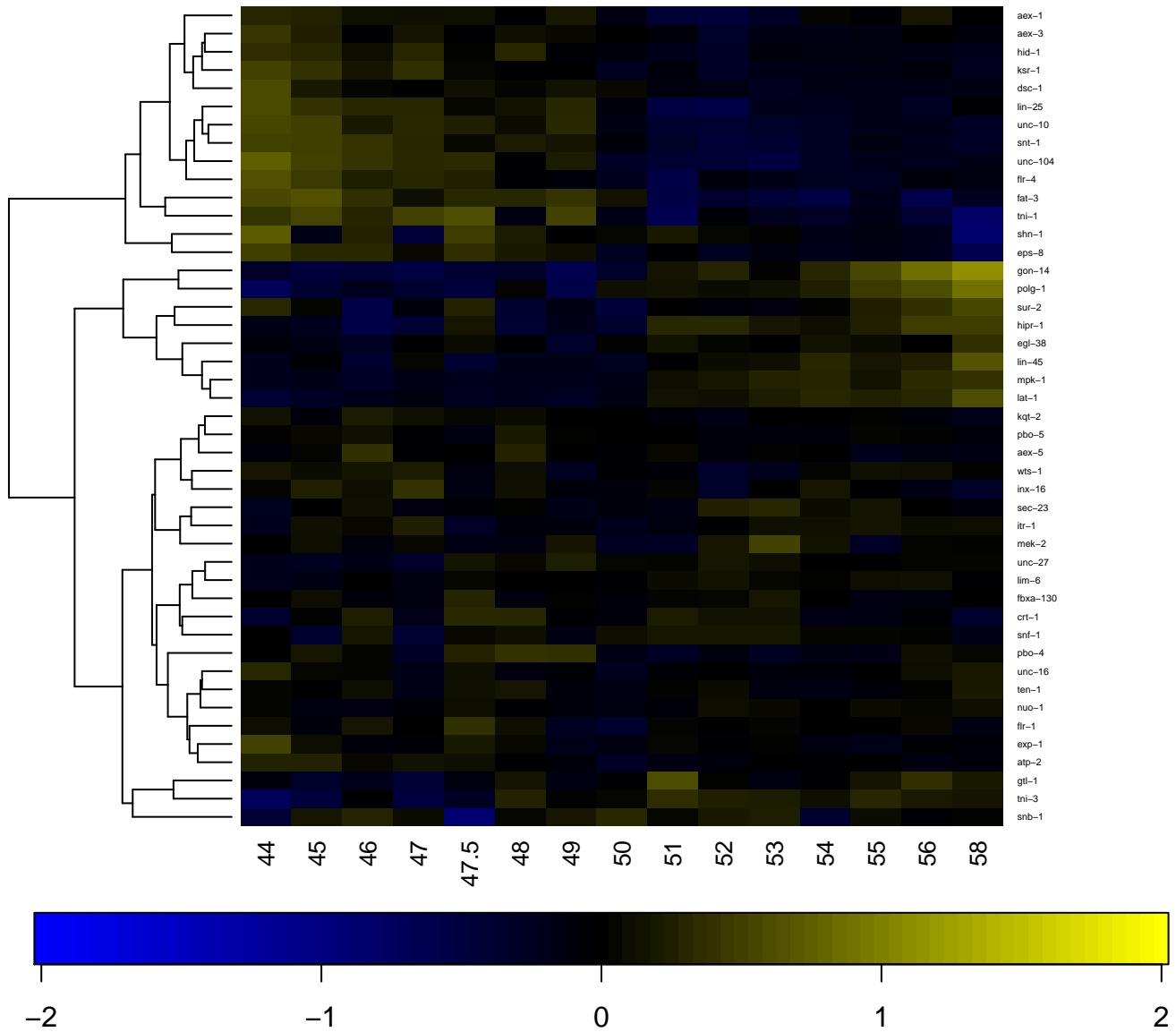
dauer entry



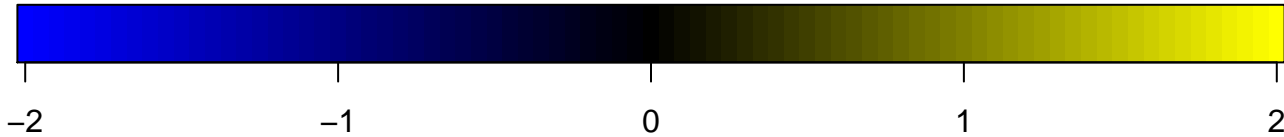
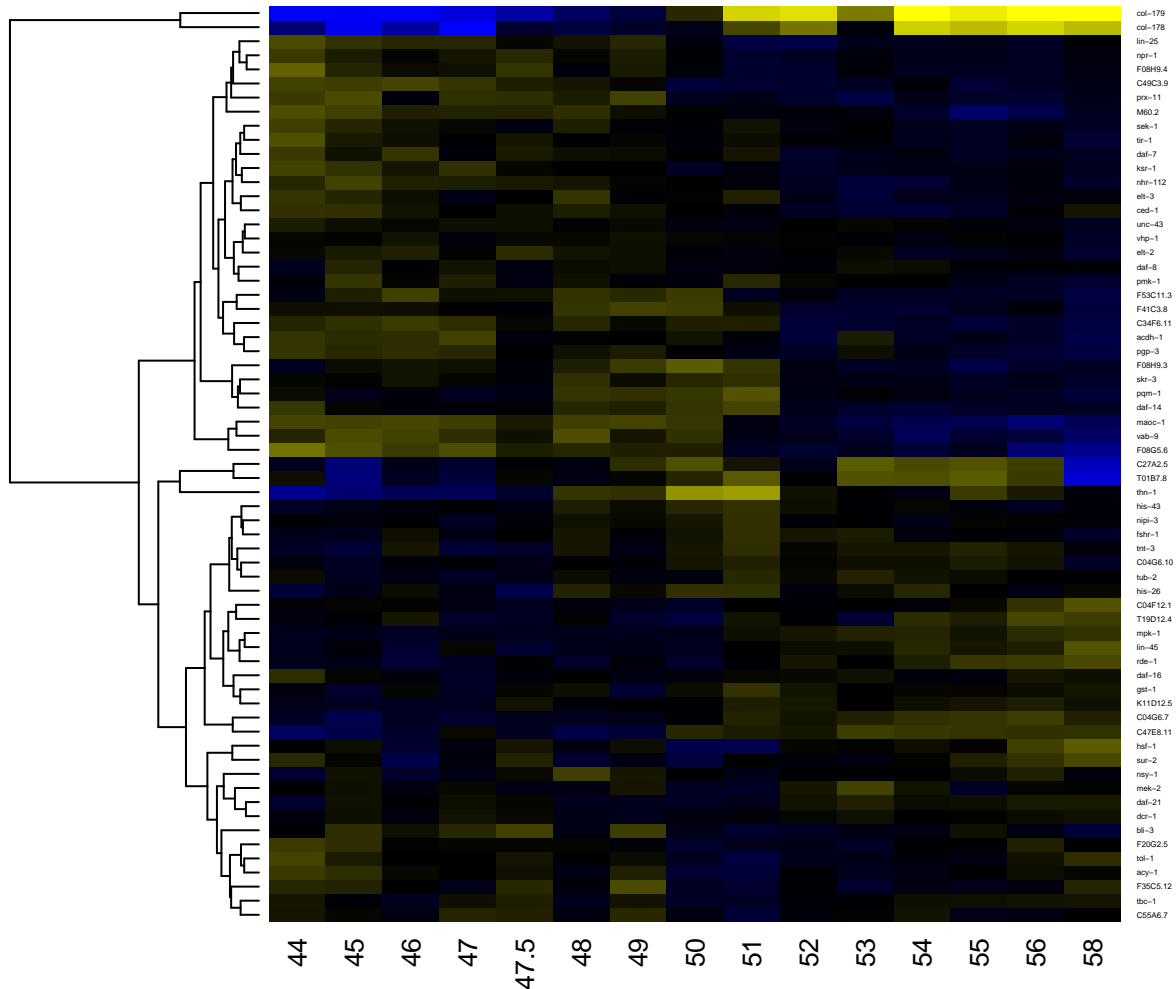
dauer larval development



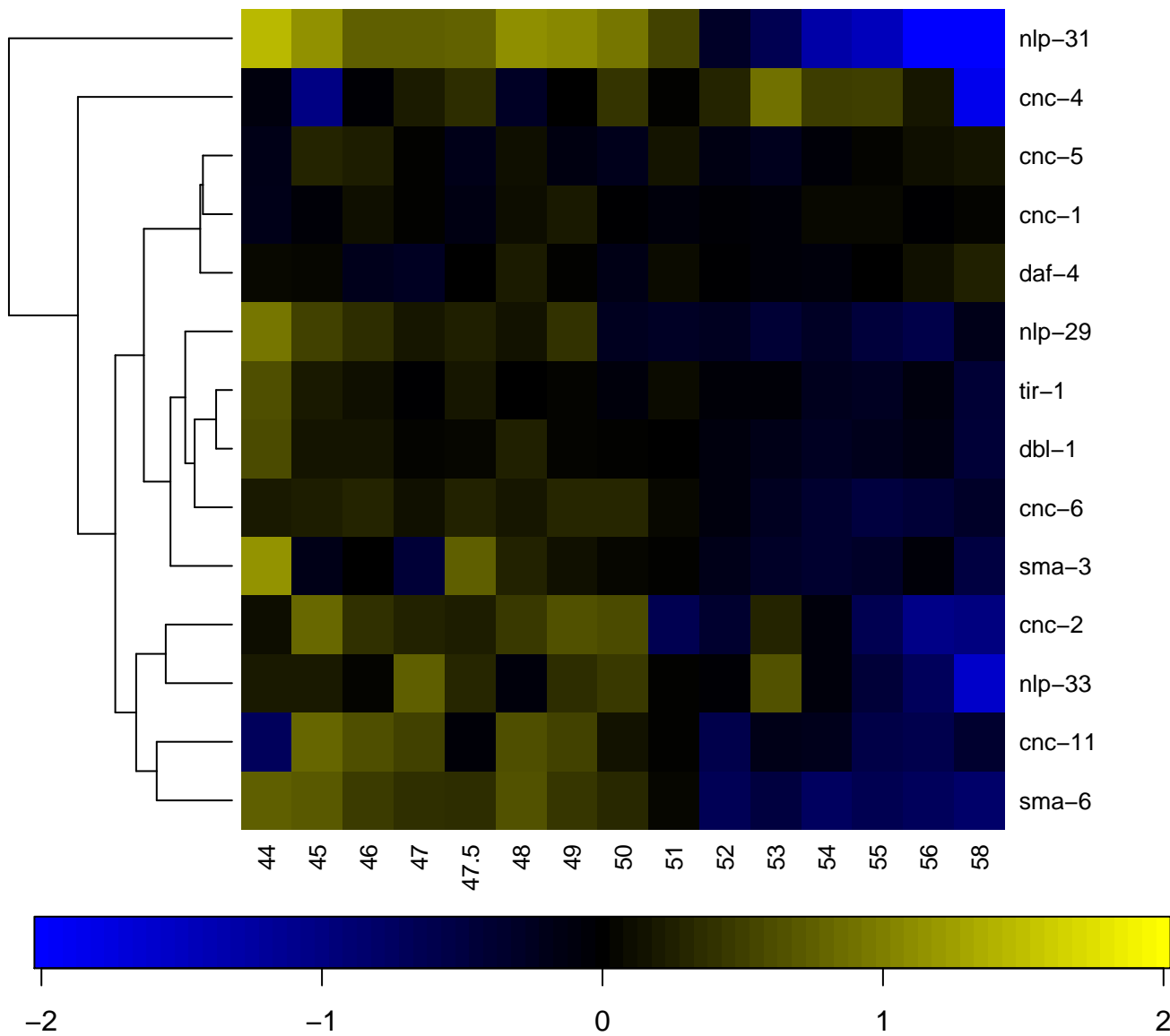
defecation



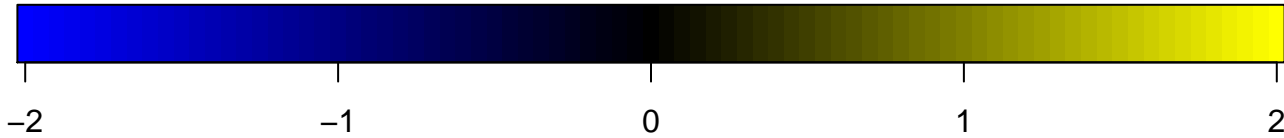
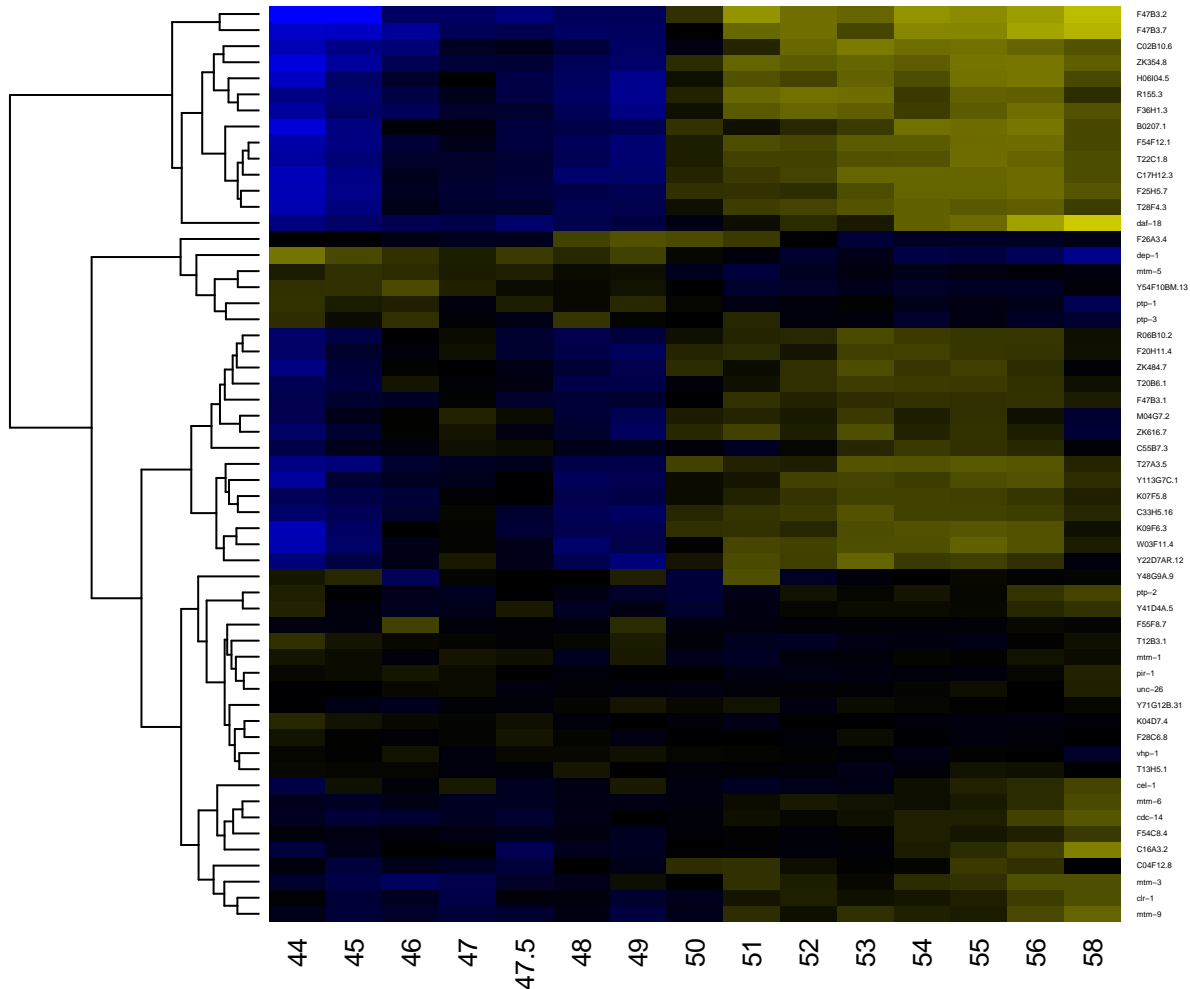
defense response



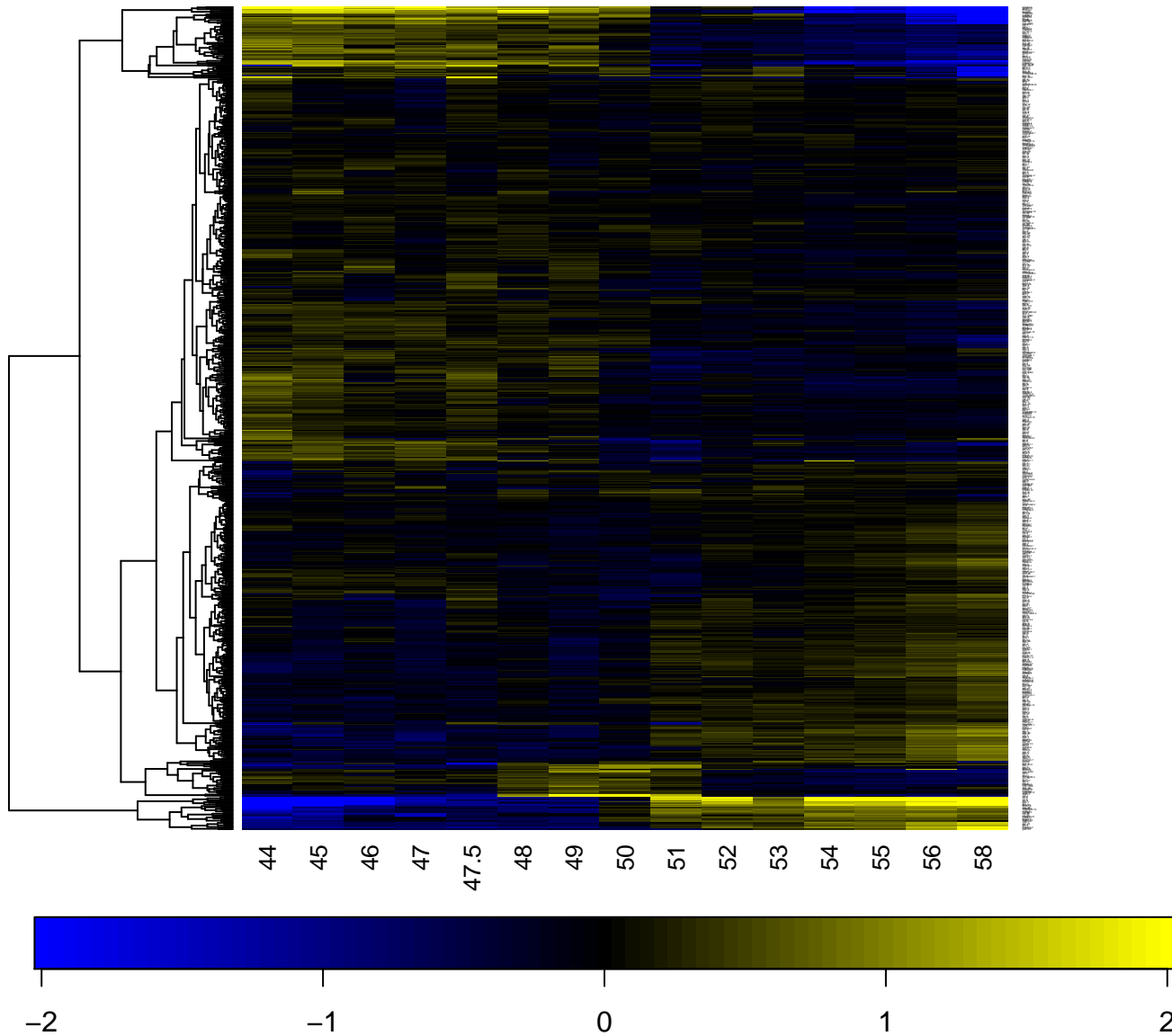
defense response to fungus



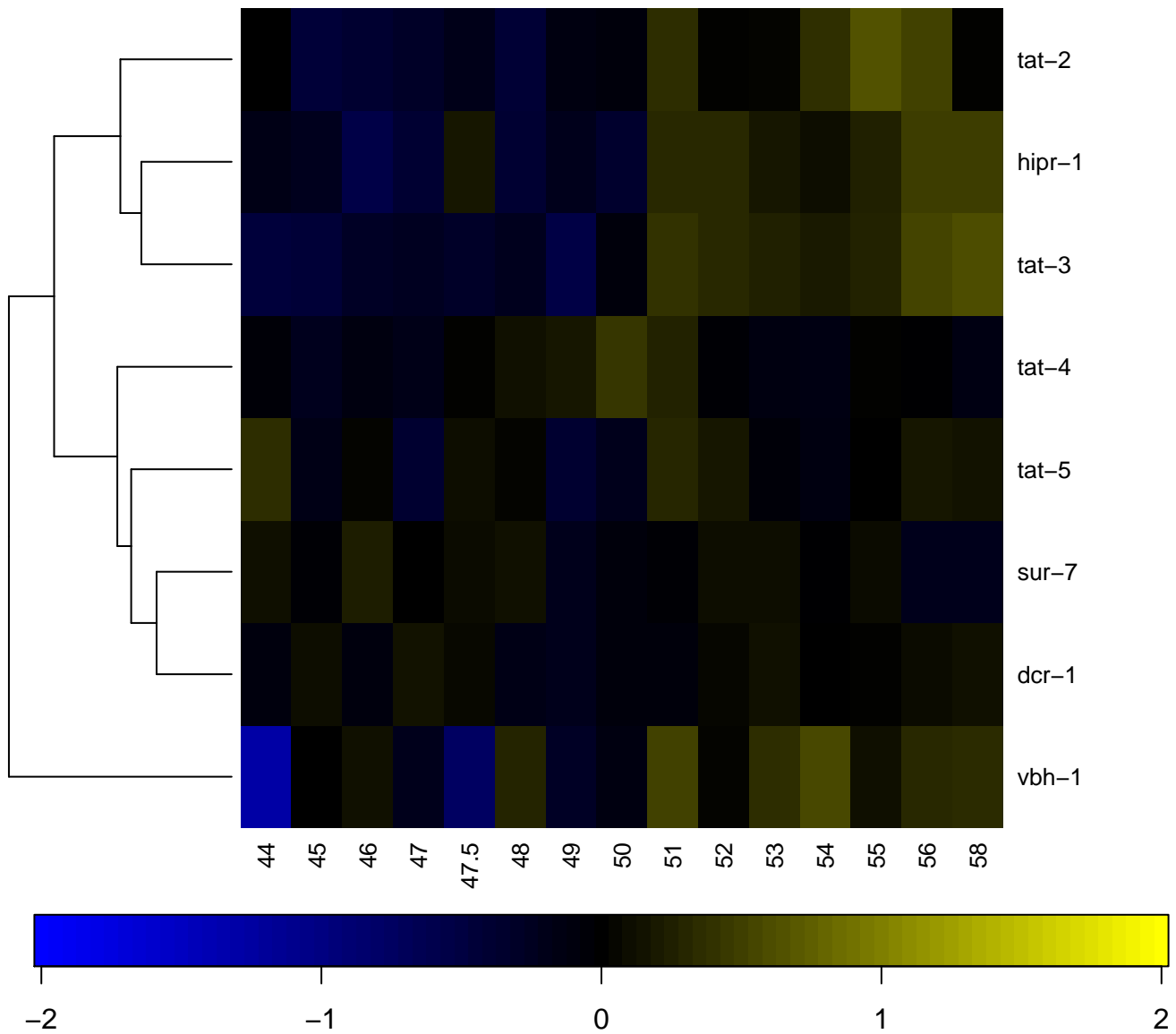
dephosphorylation



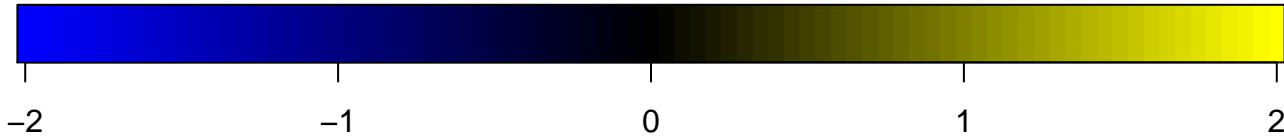
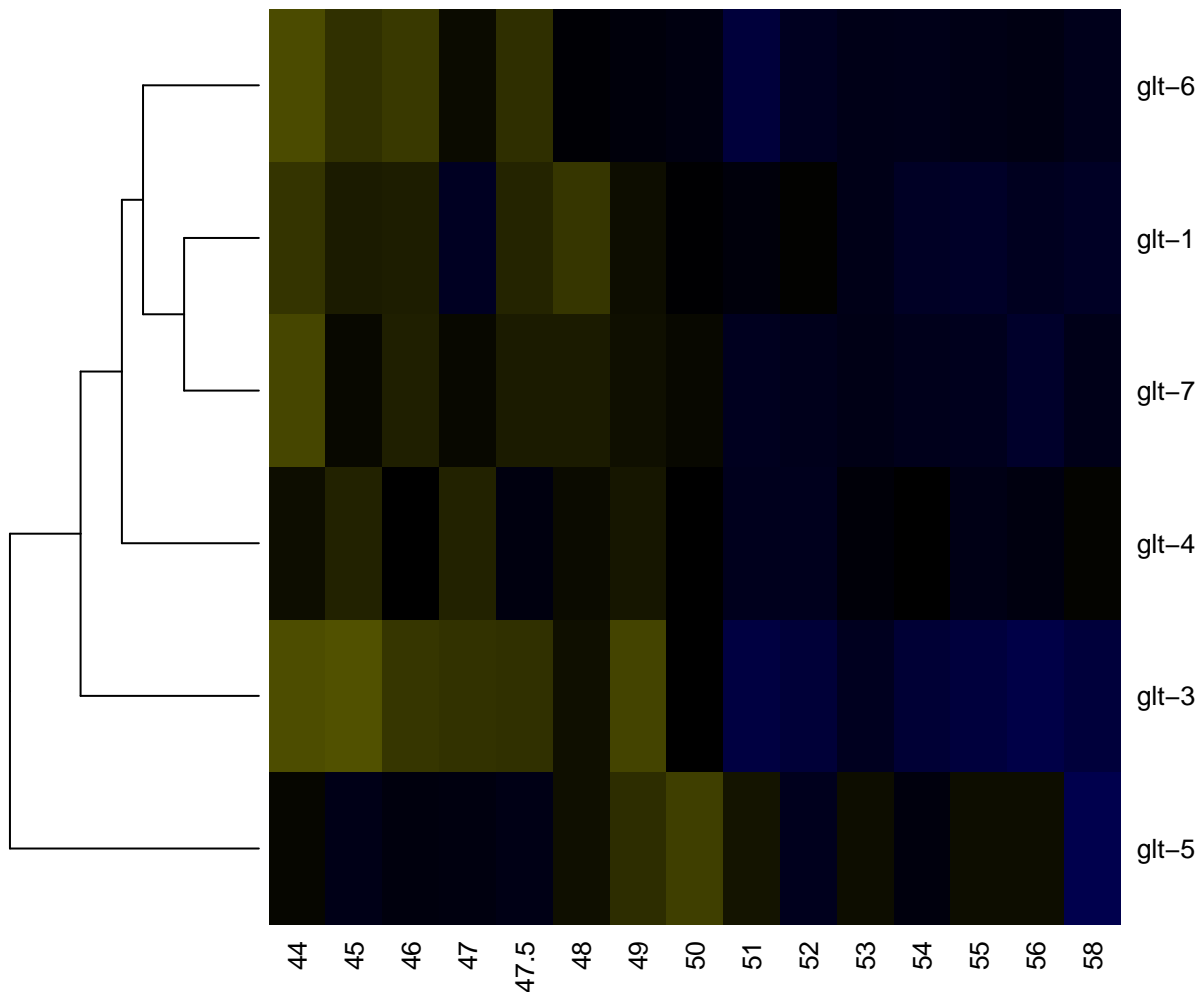
determination of adult life span



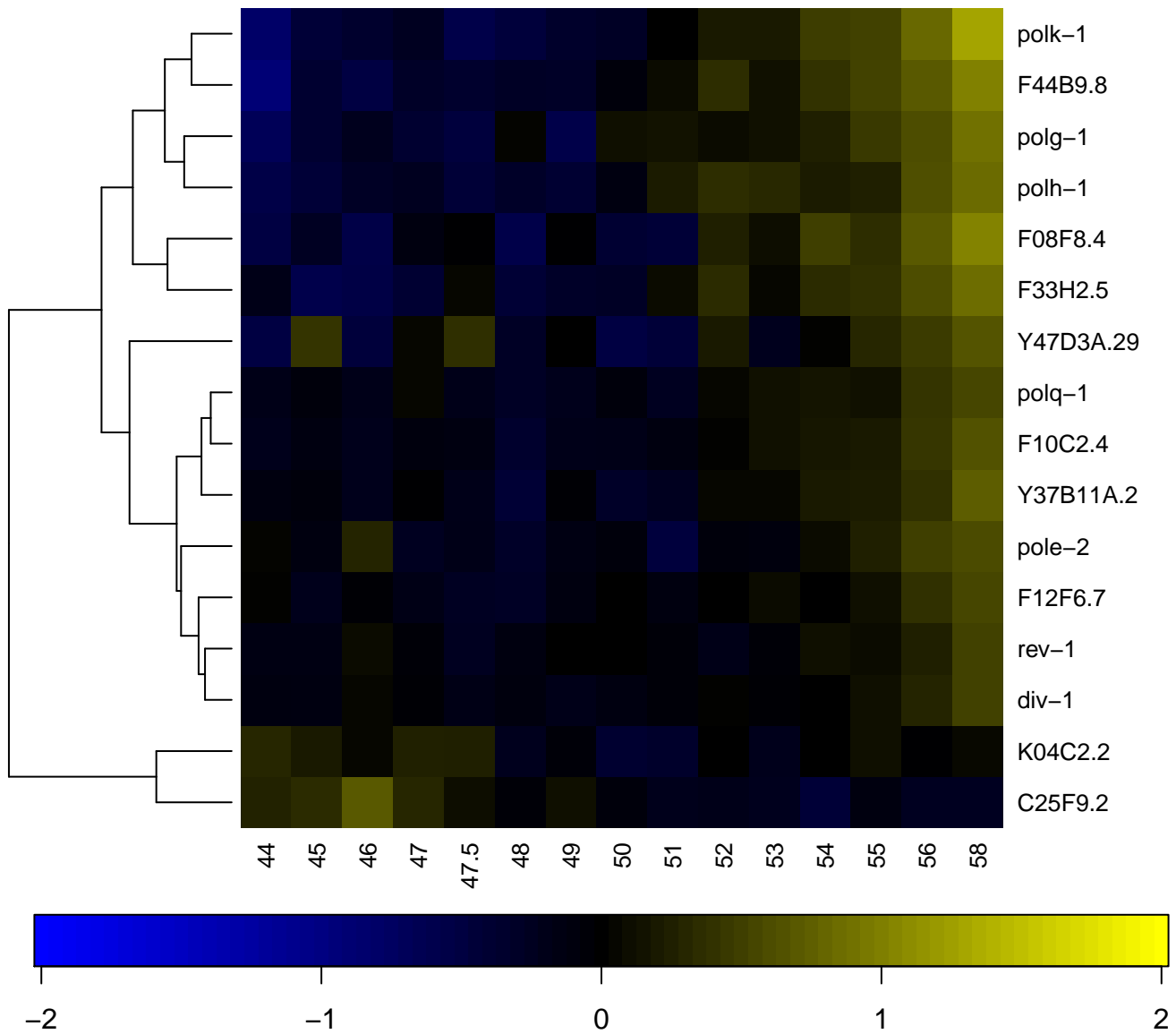
developmental process



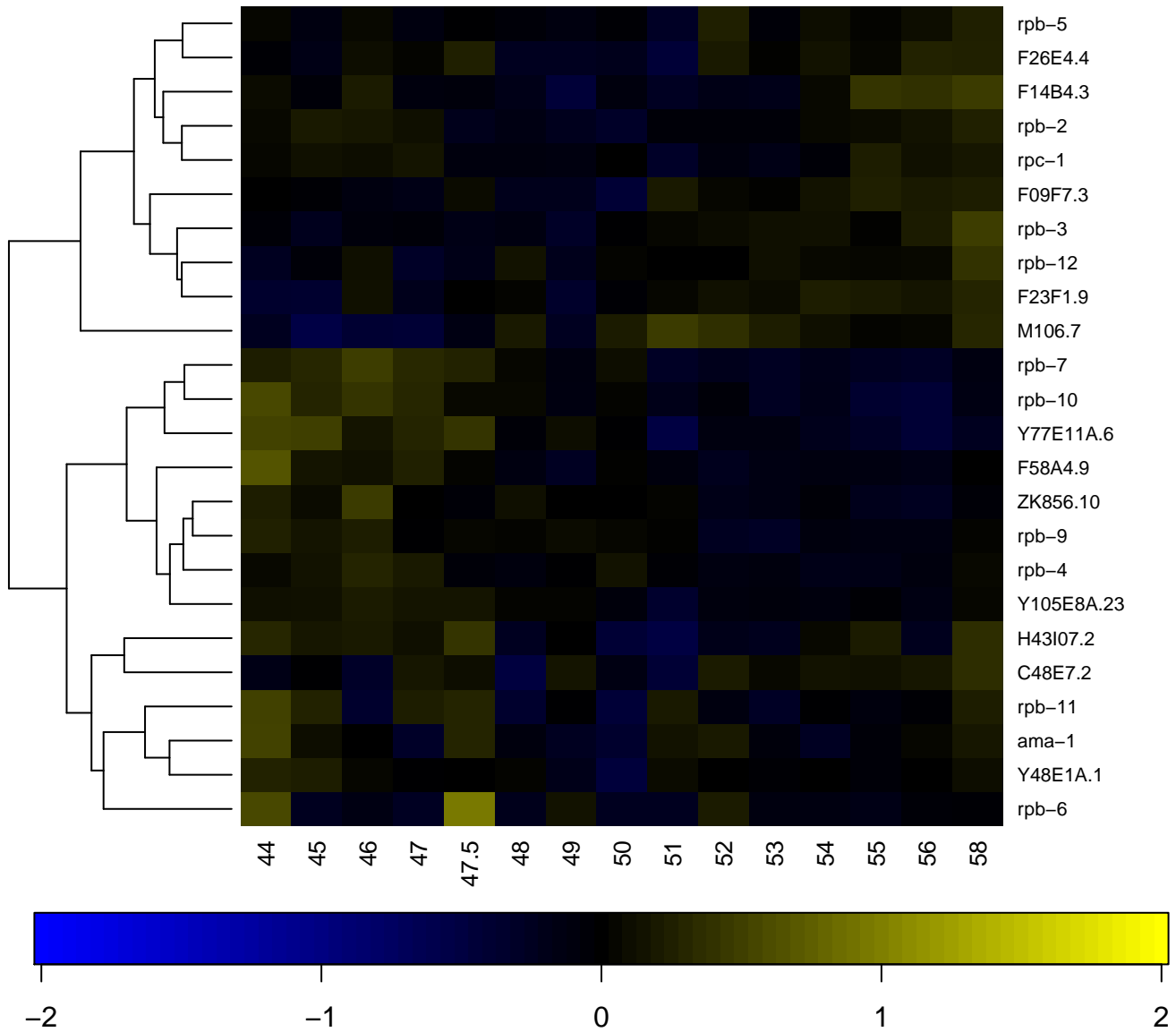
dicarboxylic acid transport



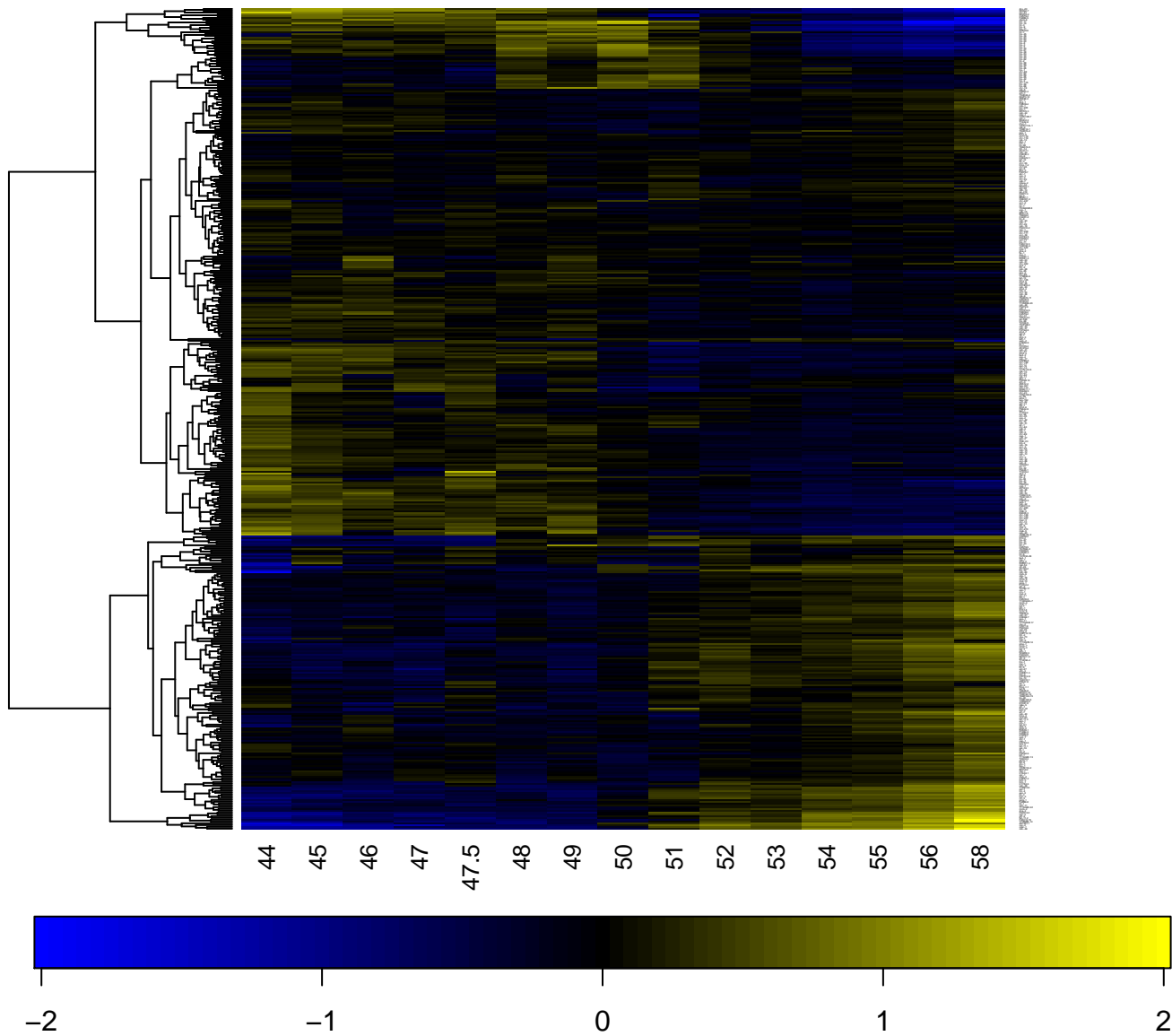
DNA-directed DNA polymerase activity



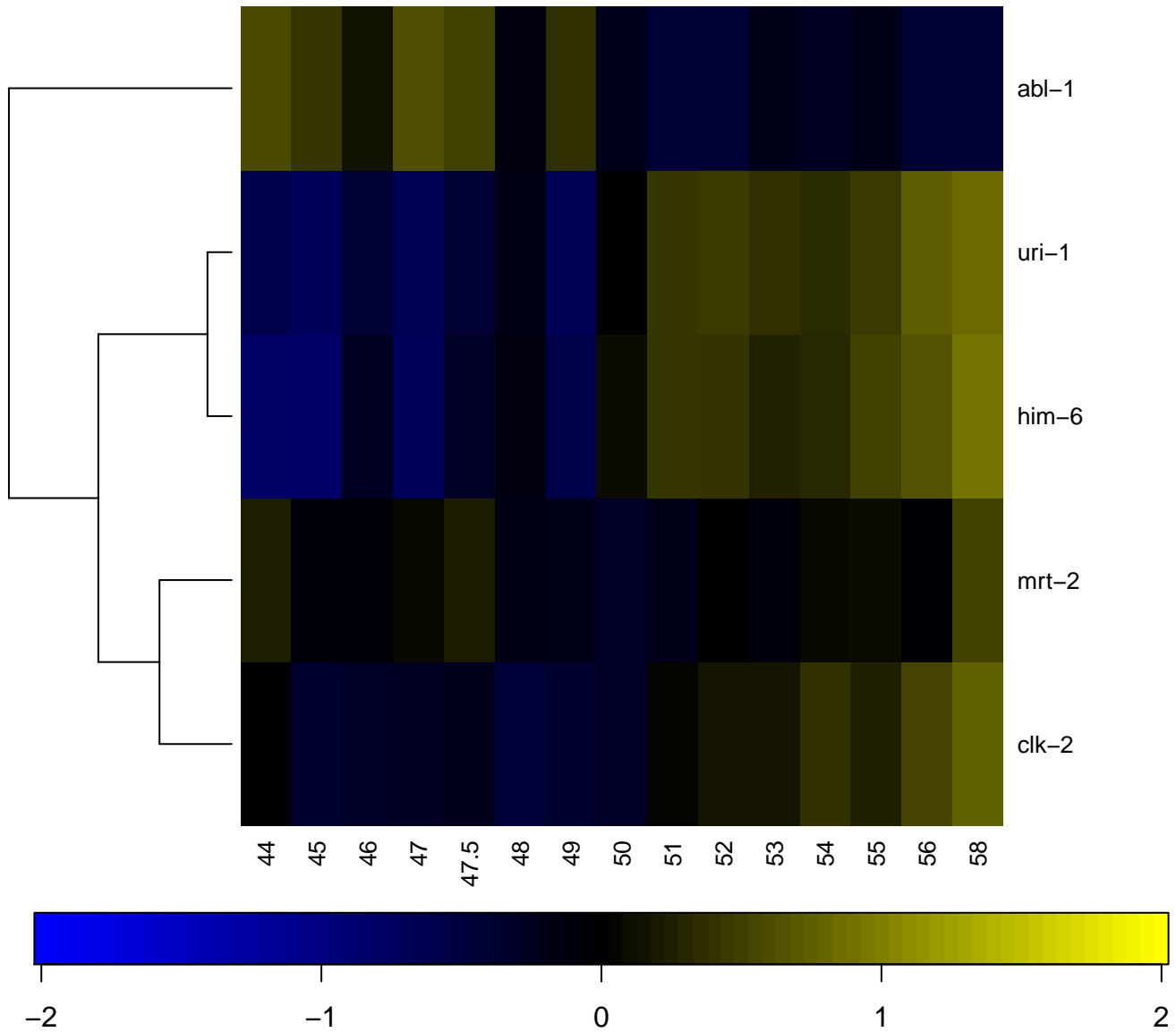
DNA-directed RNA polymerase activity



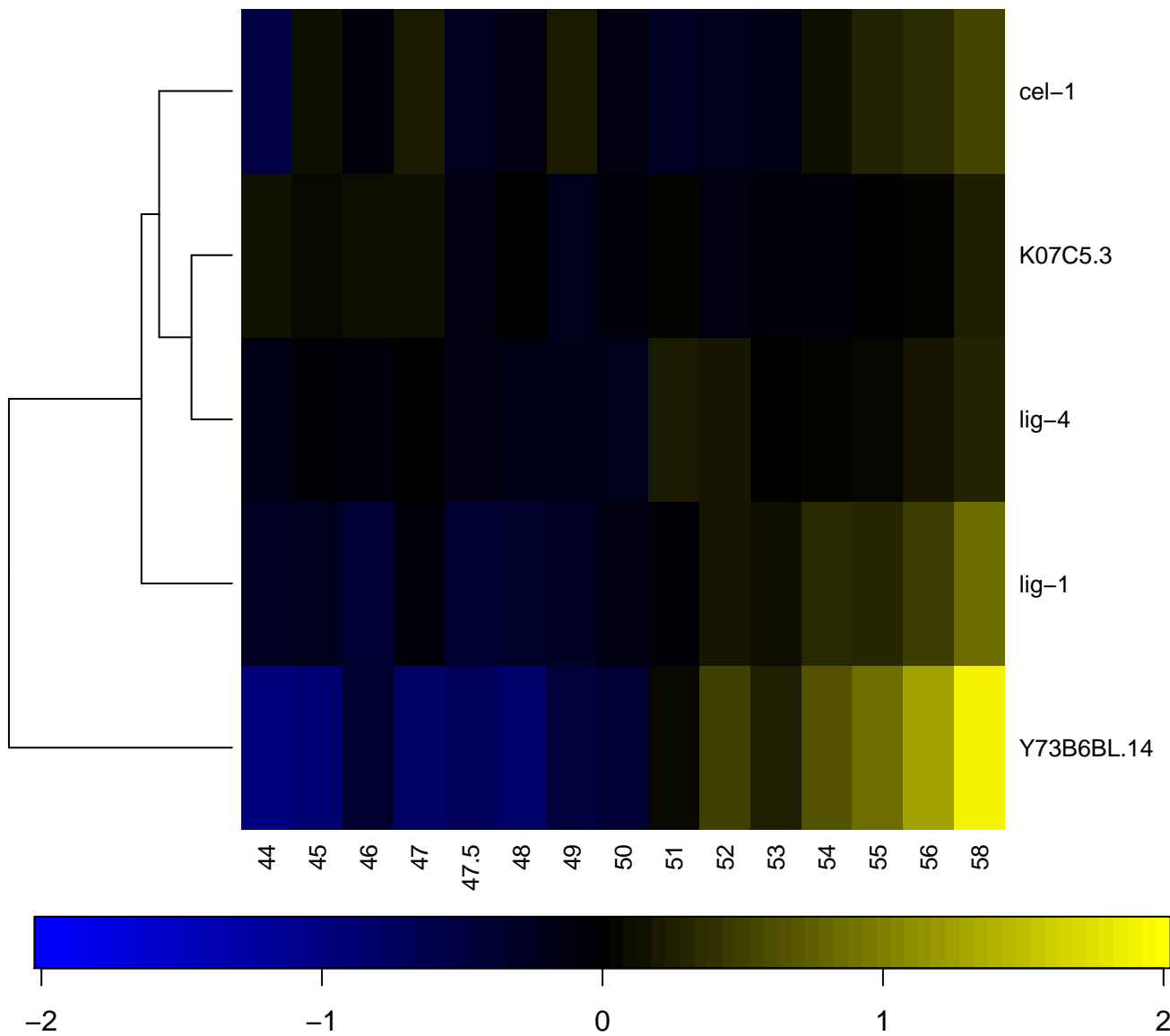
DNA binding



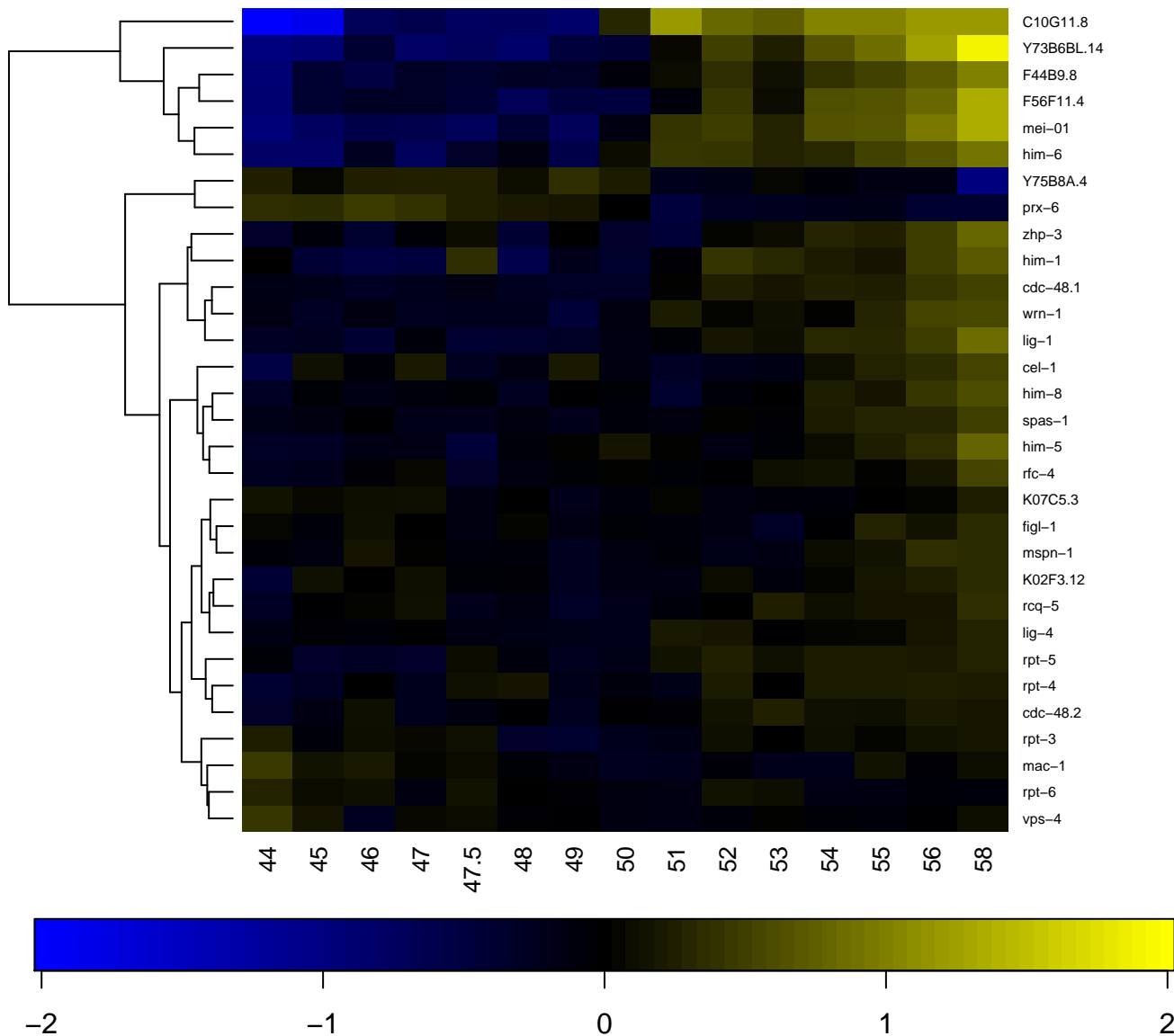
DNA damage checkpoint



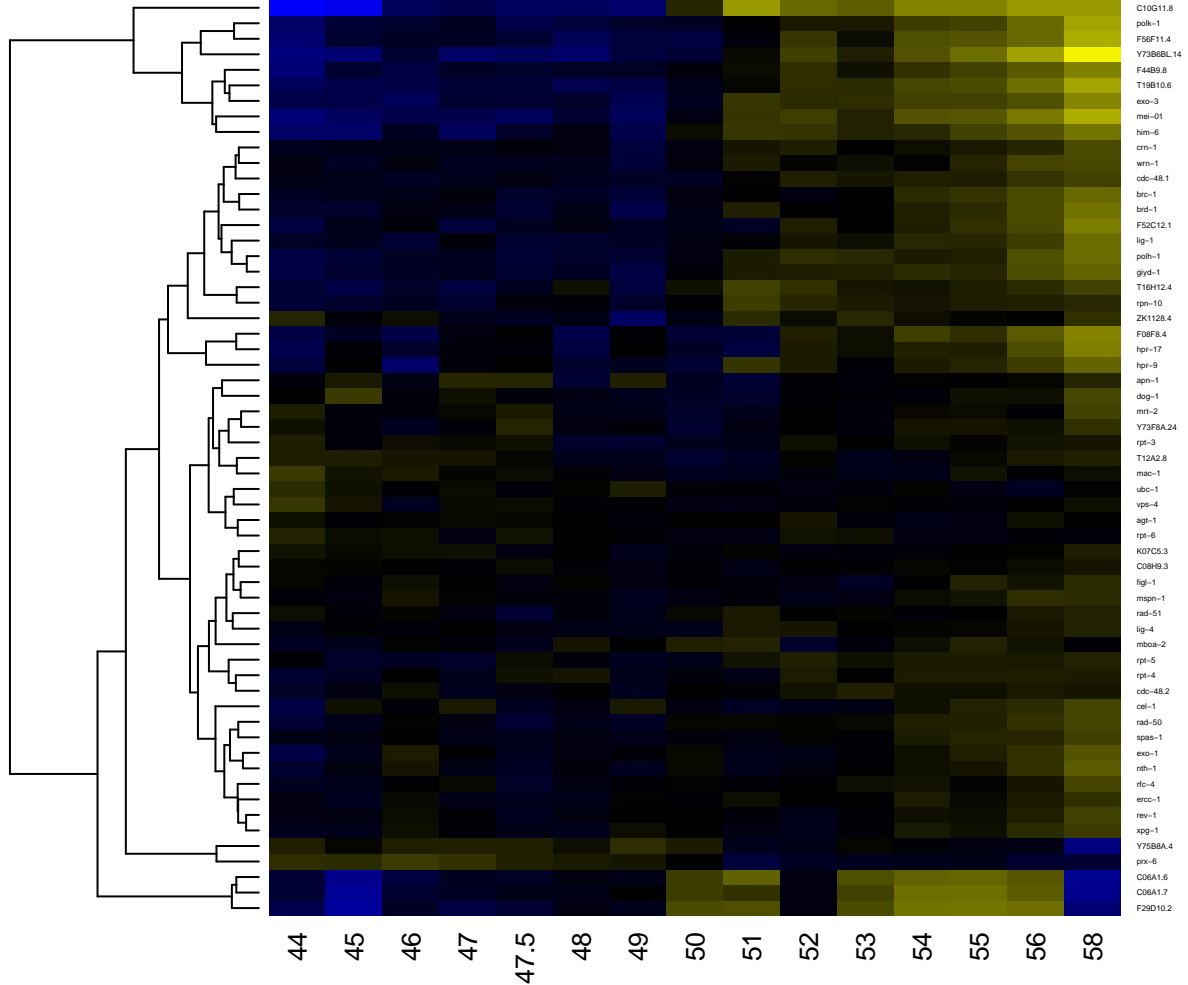
DNA ligase (ATP) activity



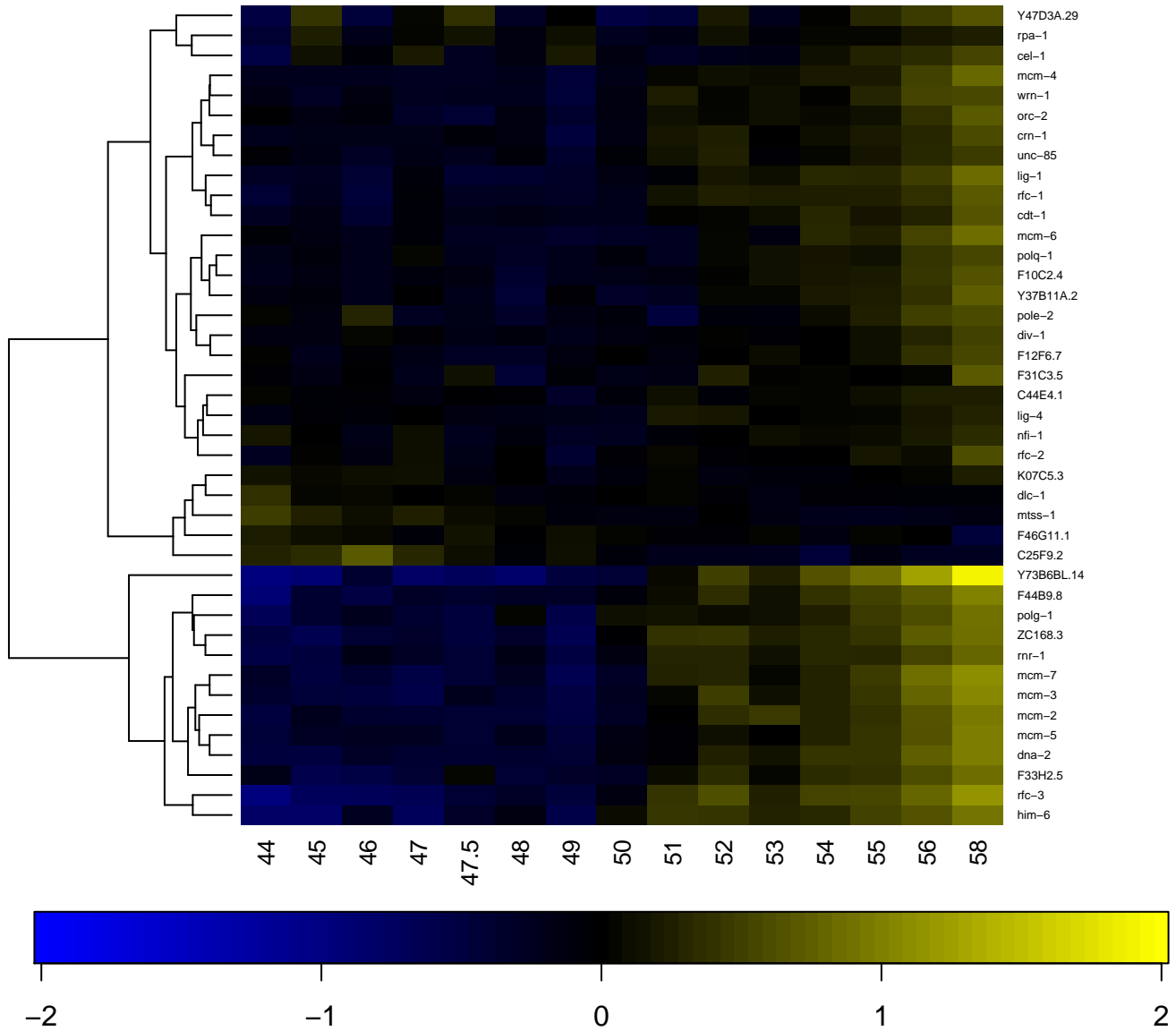
DNA recombination



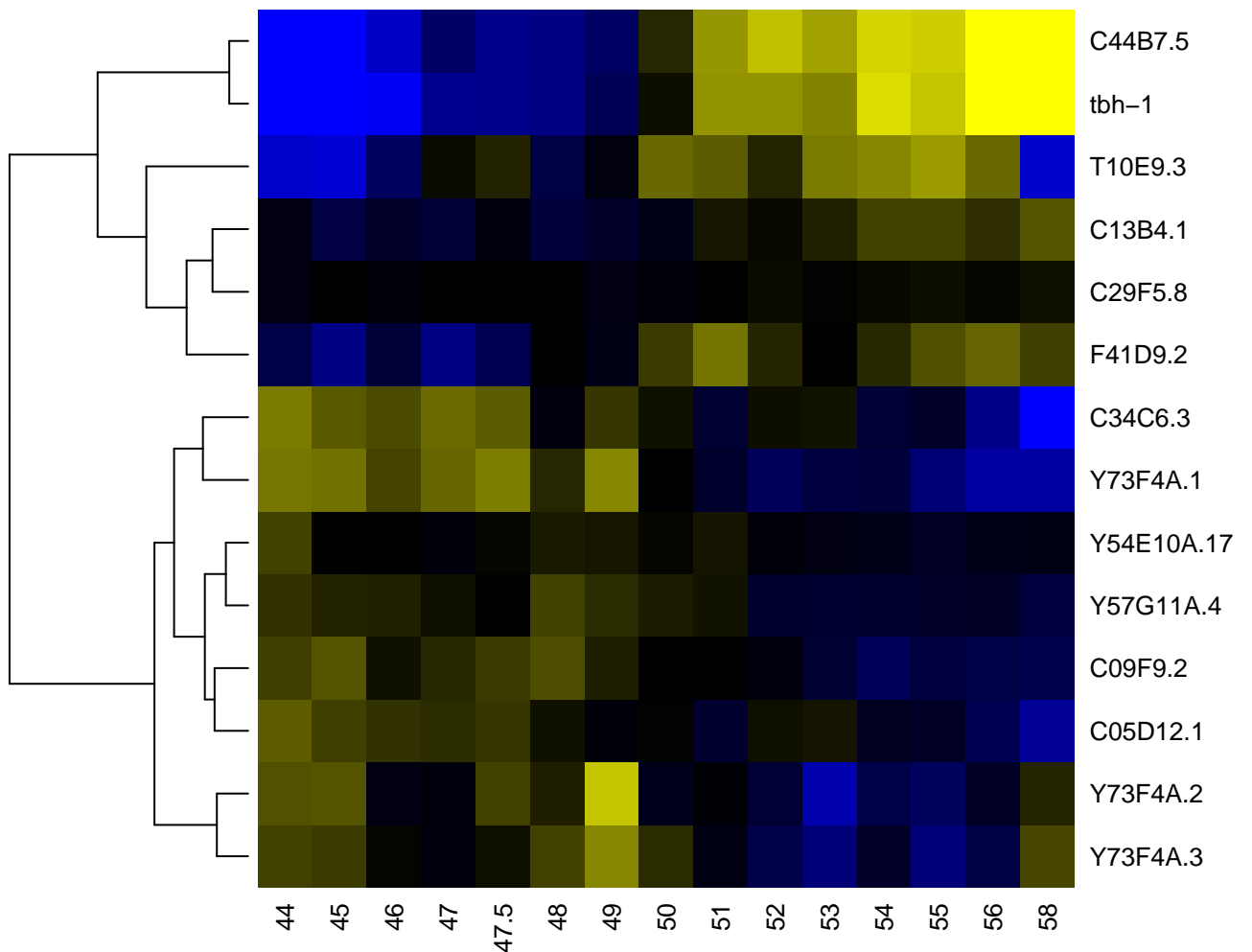
DNA repair



DNA replication



dopamine beta-monooxygenase activity



-2

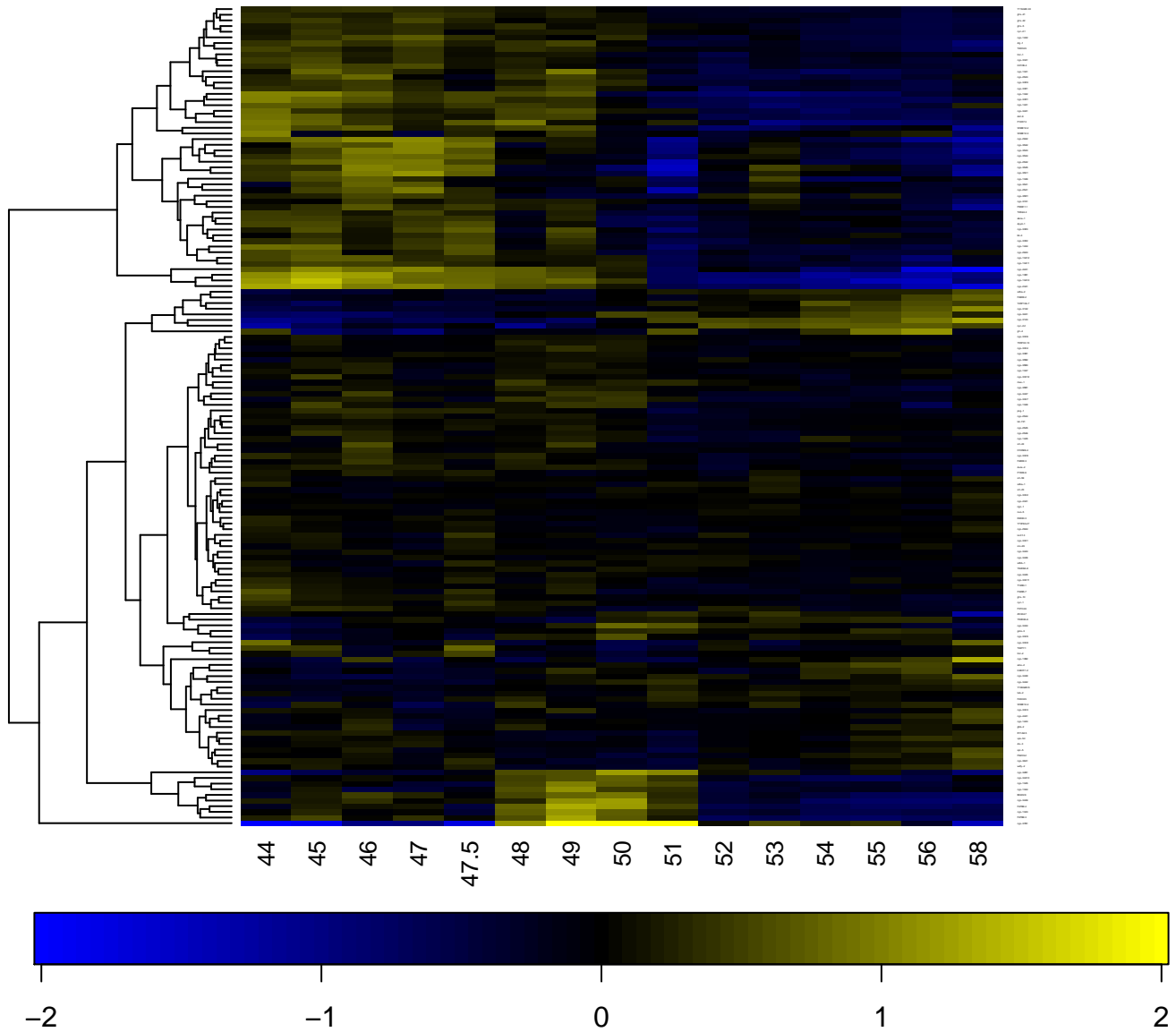
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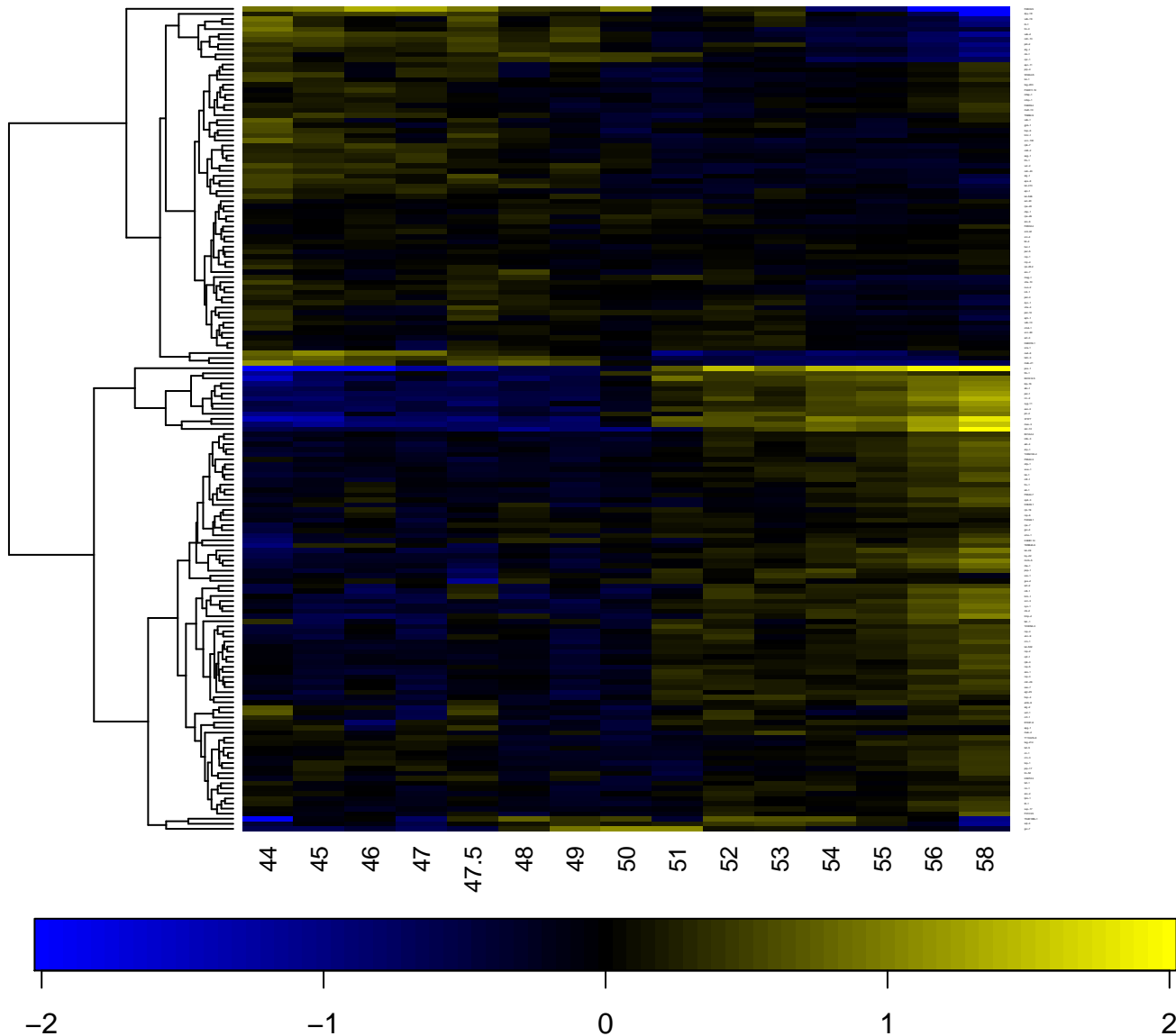
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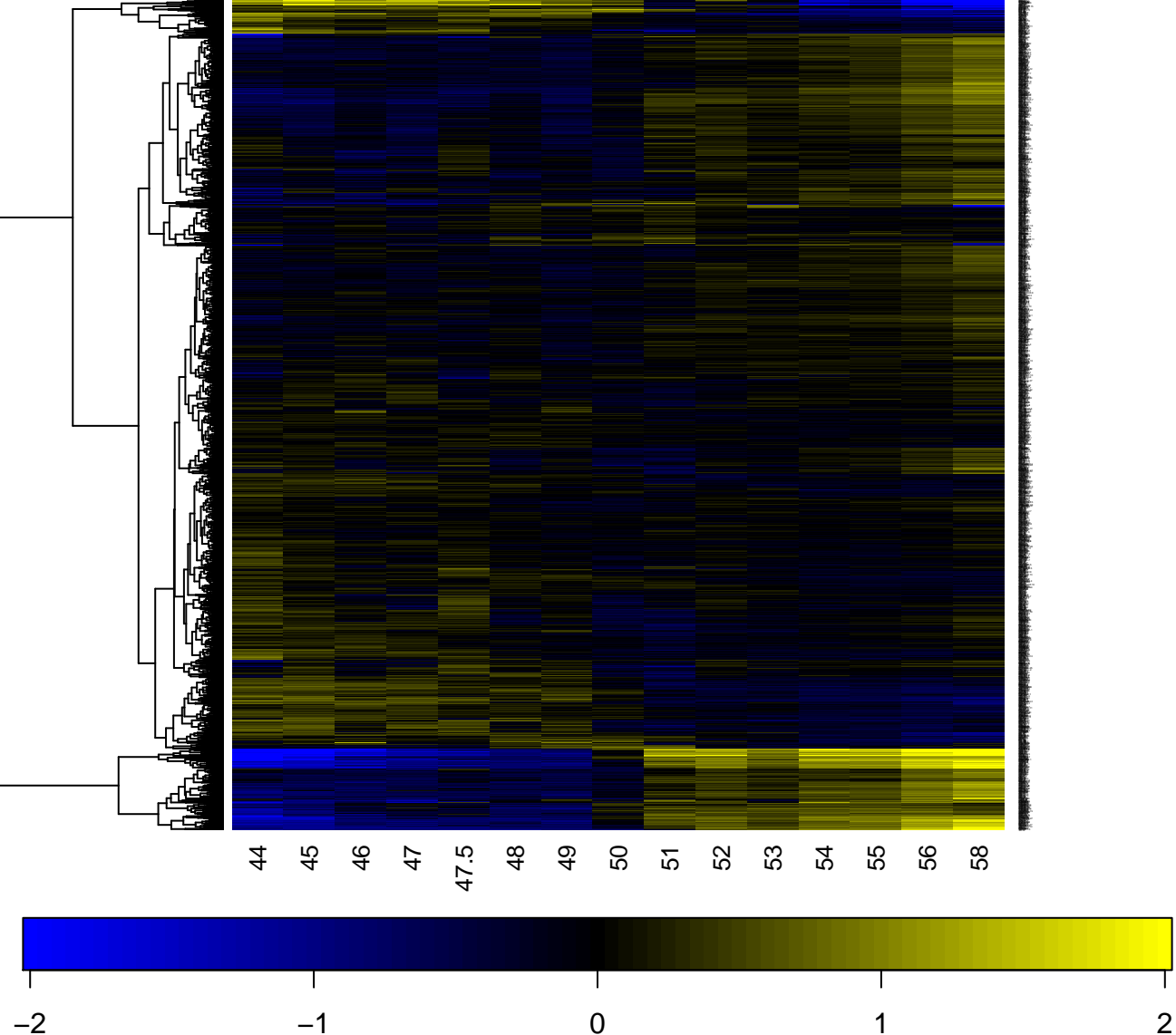
electron carrier activity



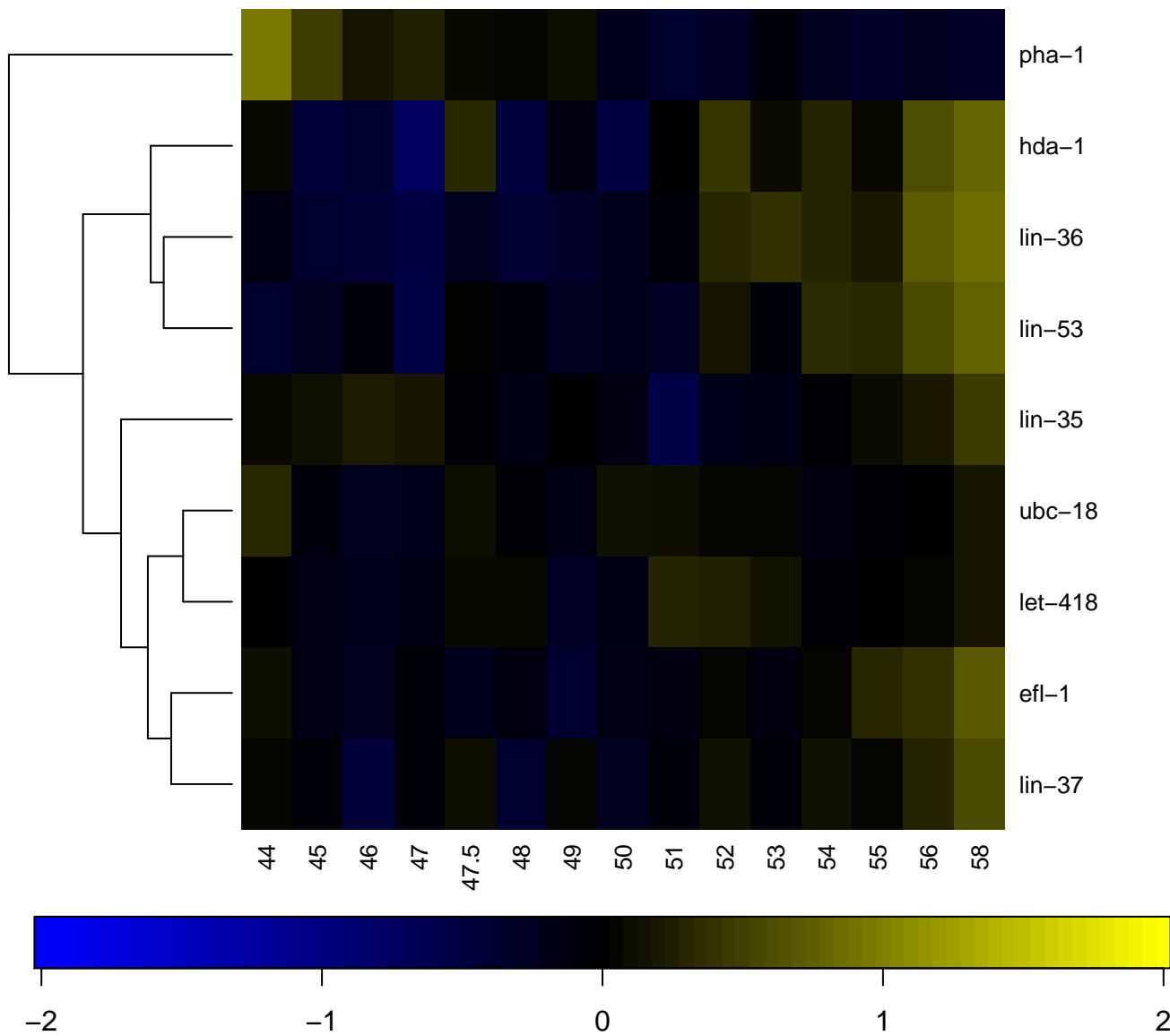
embryonic development



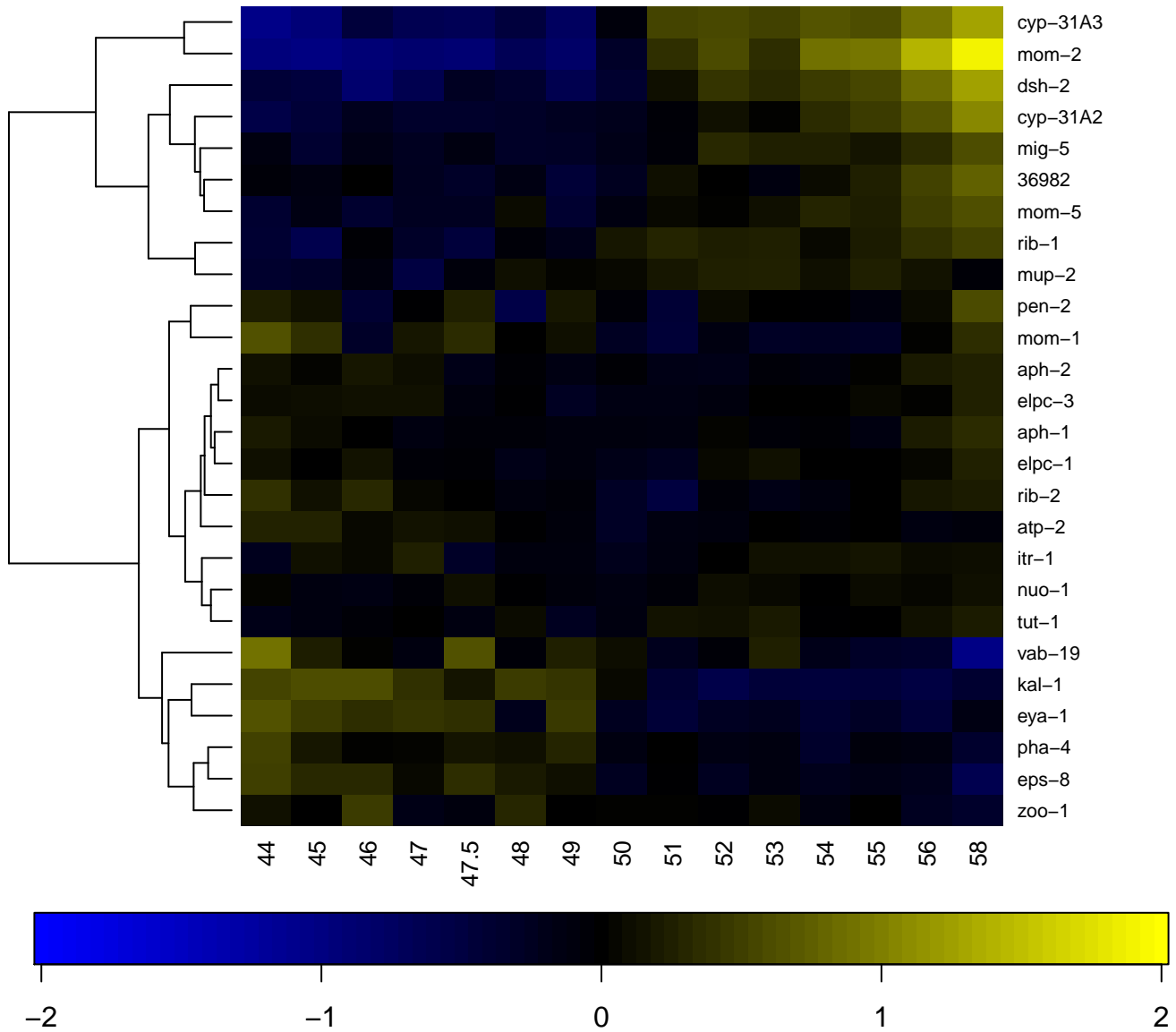
embryonic development ending in birth or egg hatching



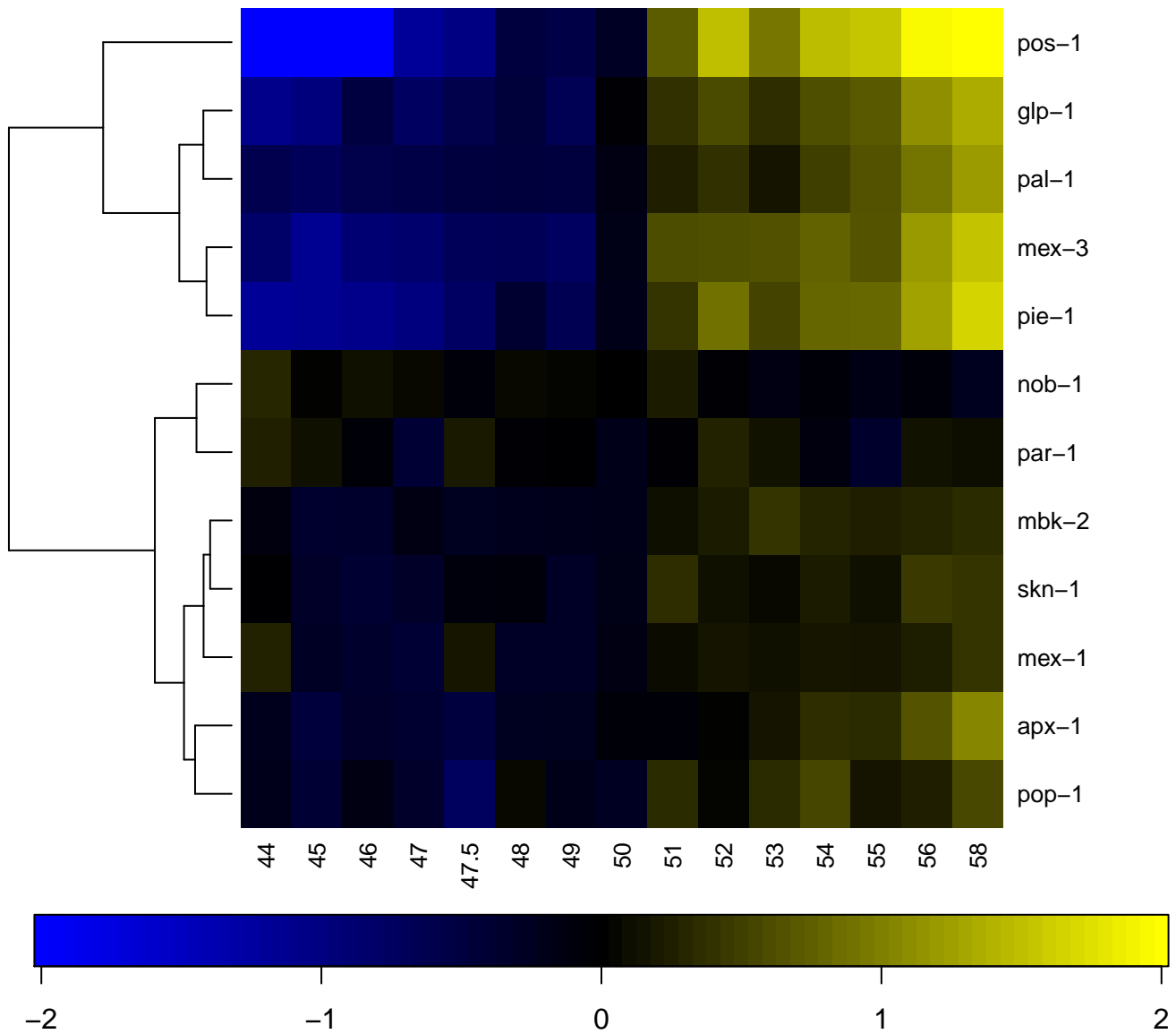
embryonic digestive tract morphogenesis



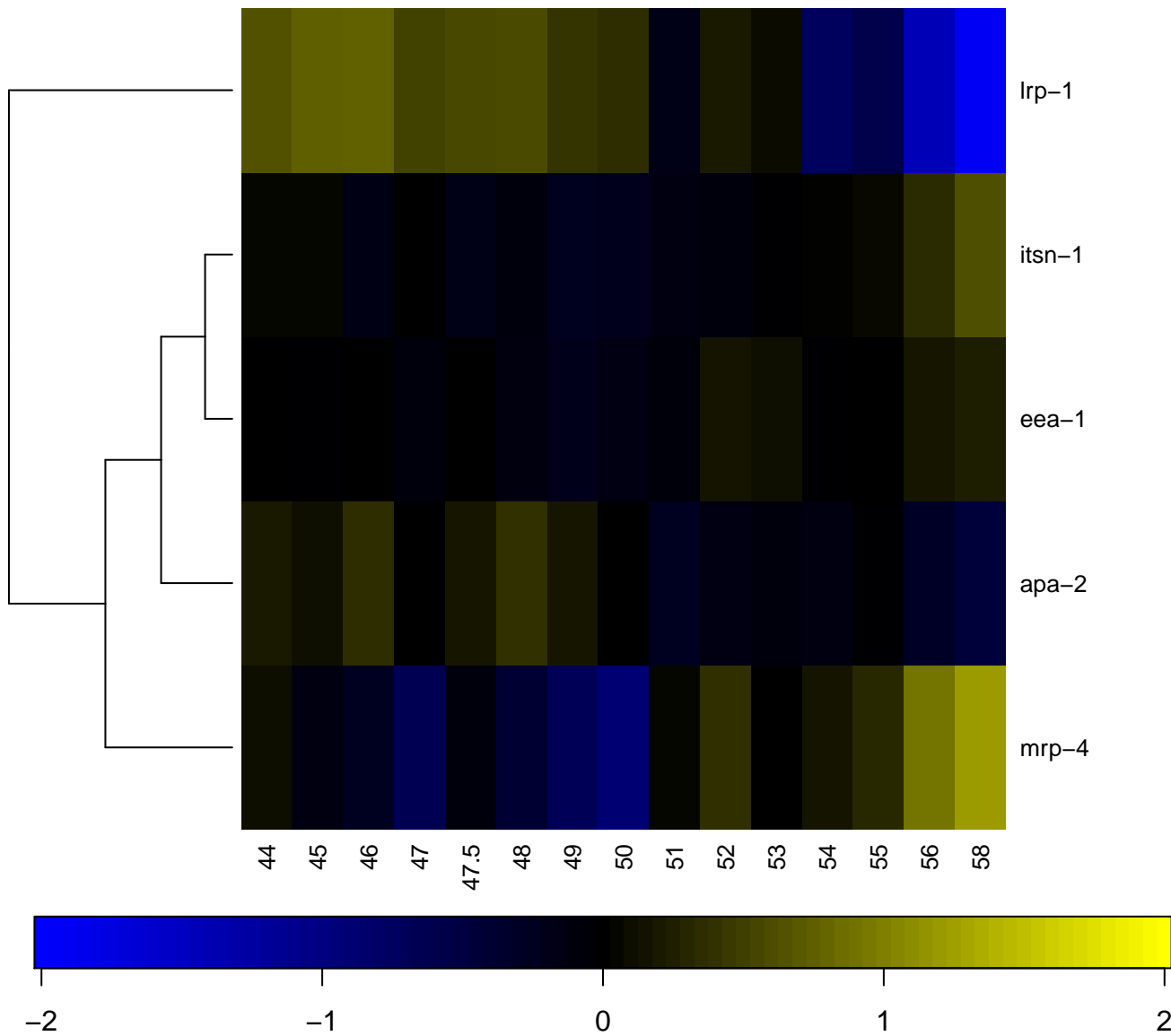
embryonic morphogenesis



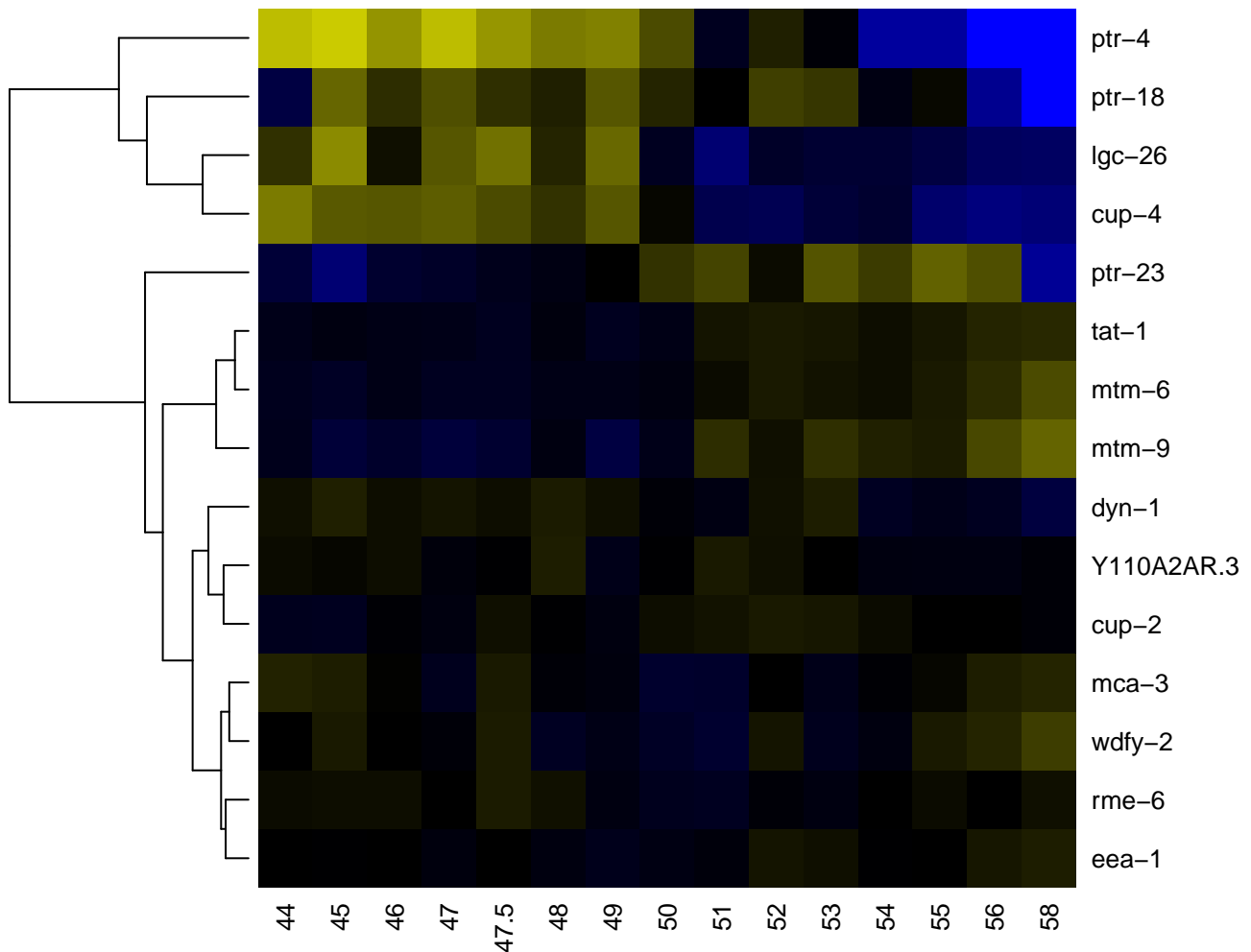
embryonic pattern specification



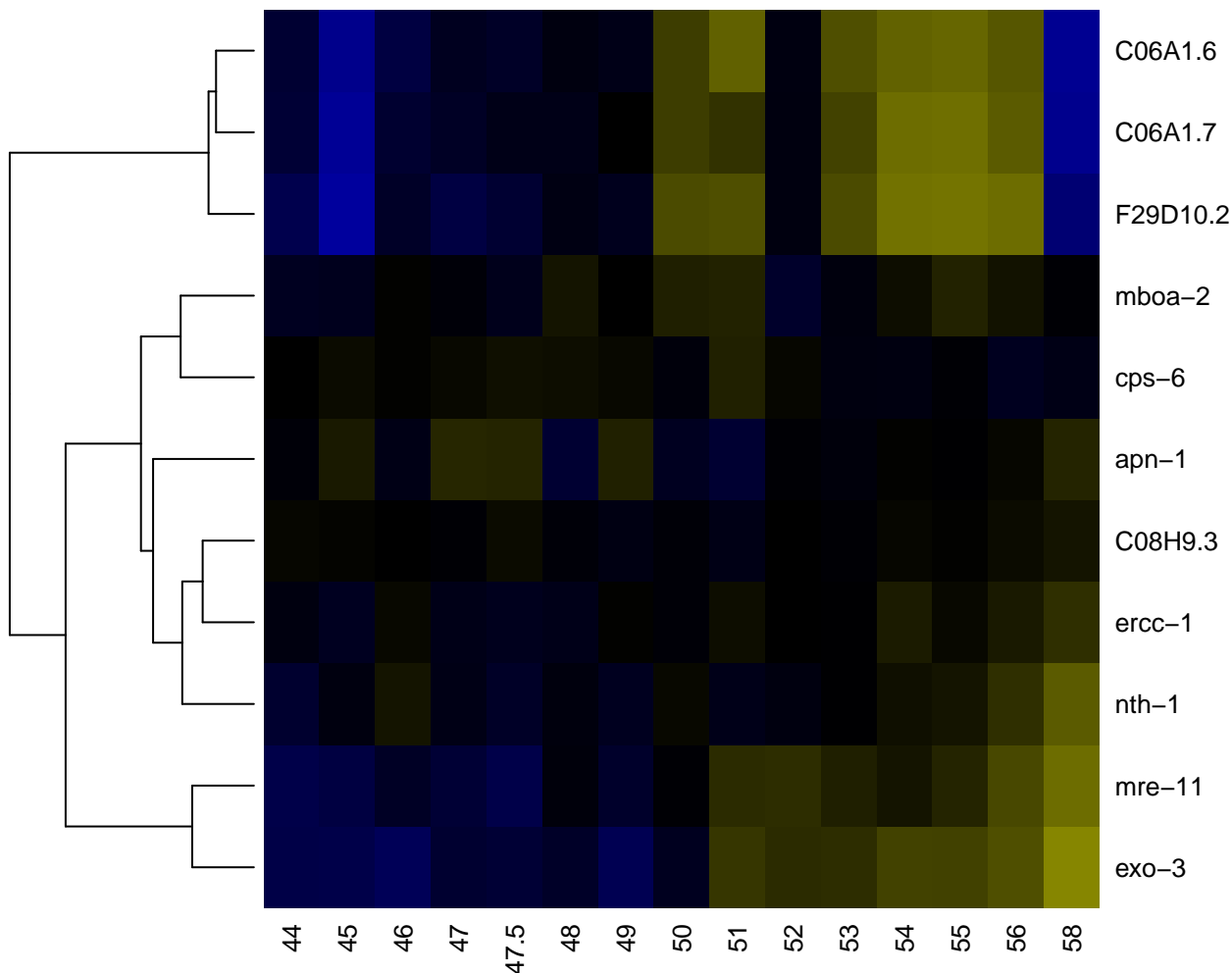
endocytic vesicle



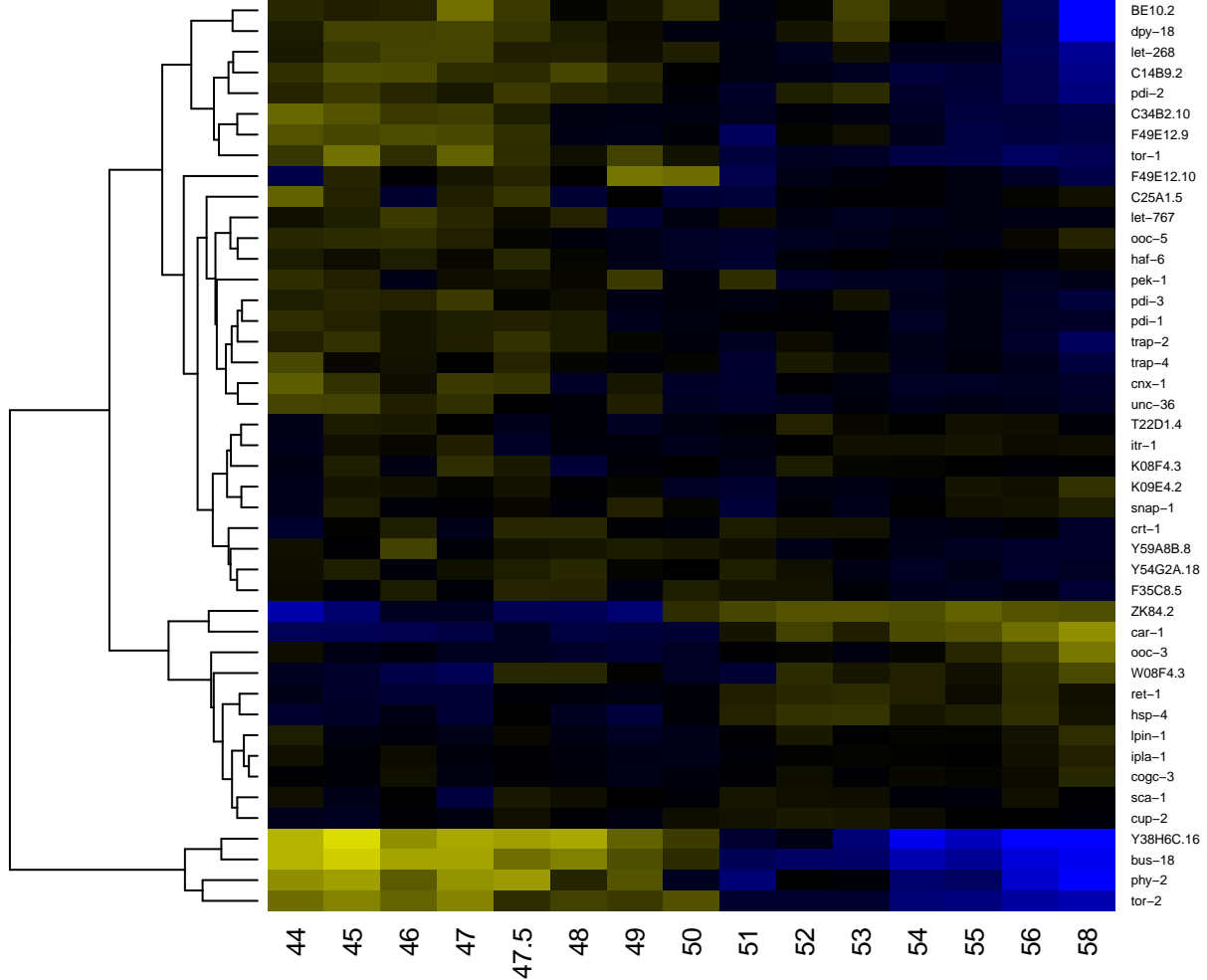
endocytosis



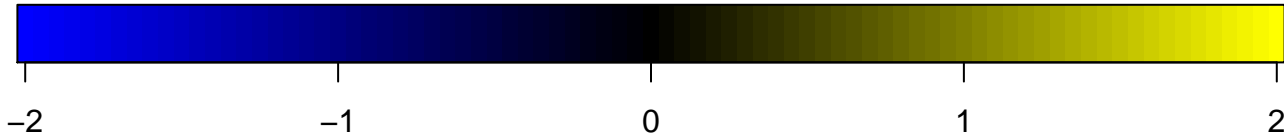
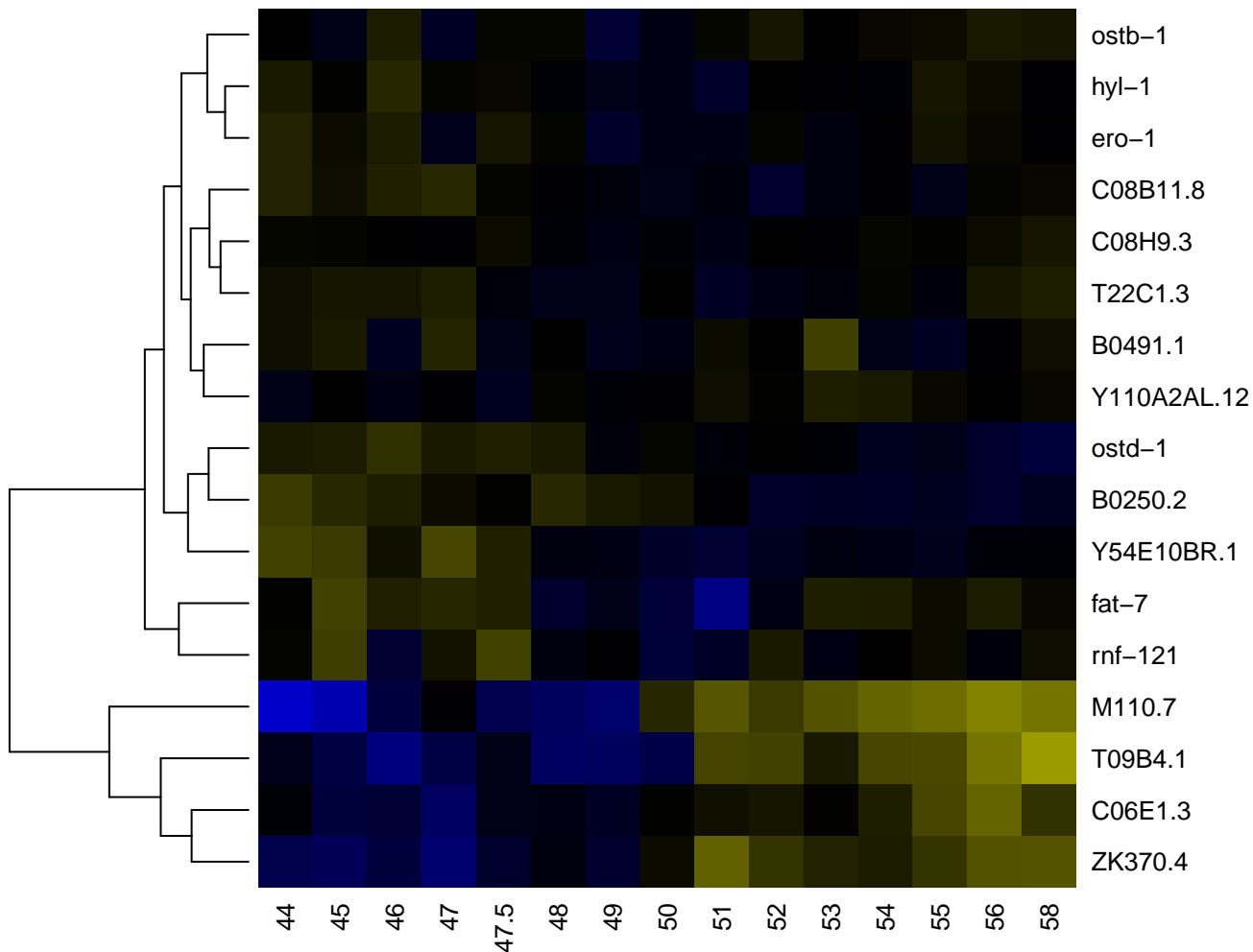
endonuclease activity



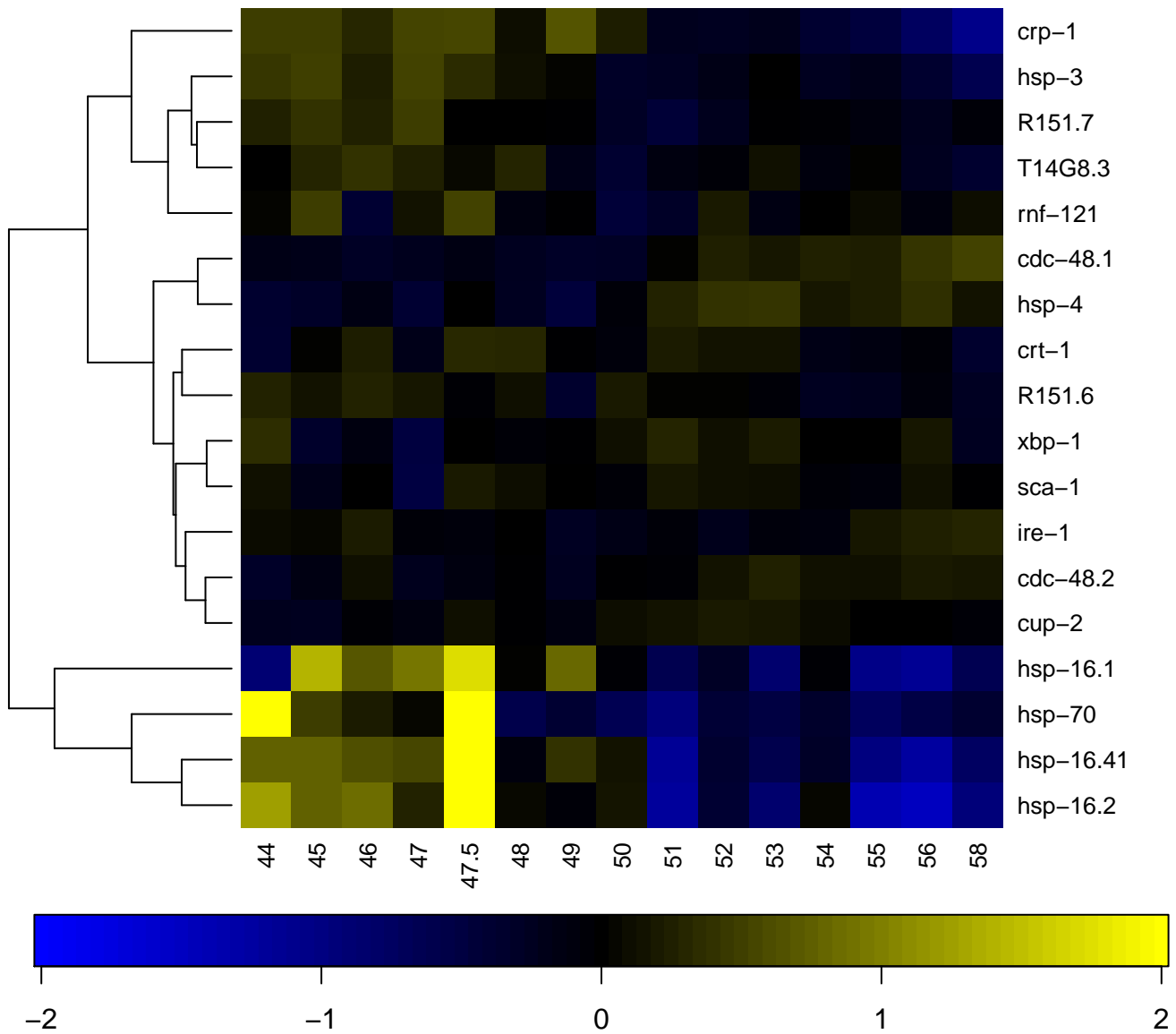
endoplasmic reticulum



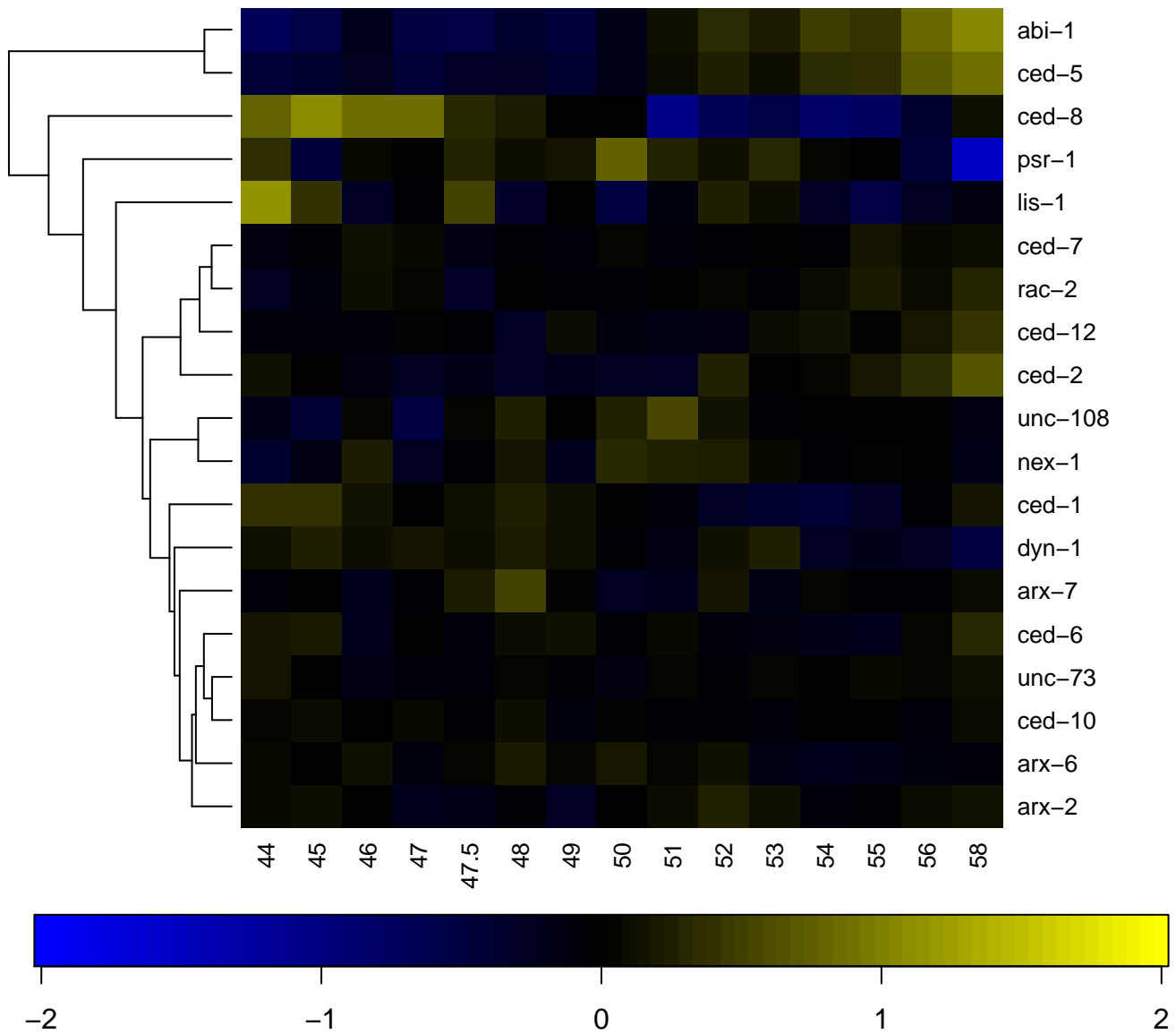
endoplasmic reticulum membrane



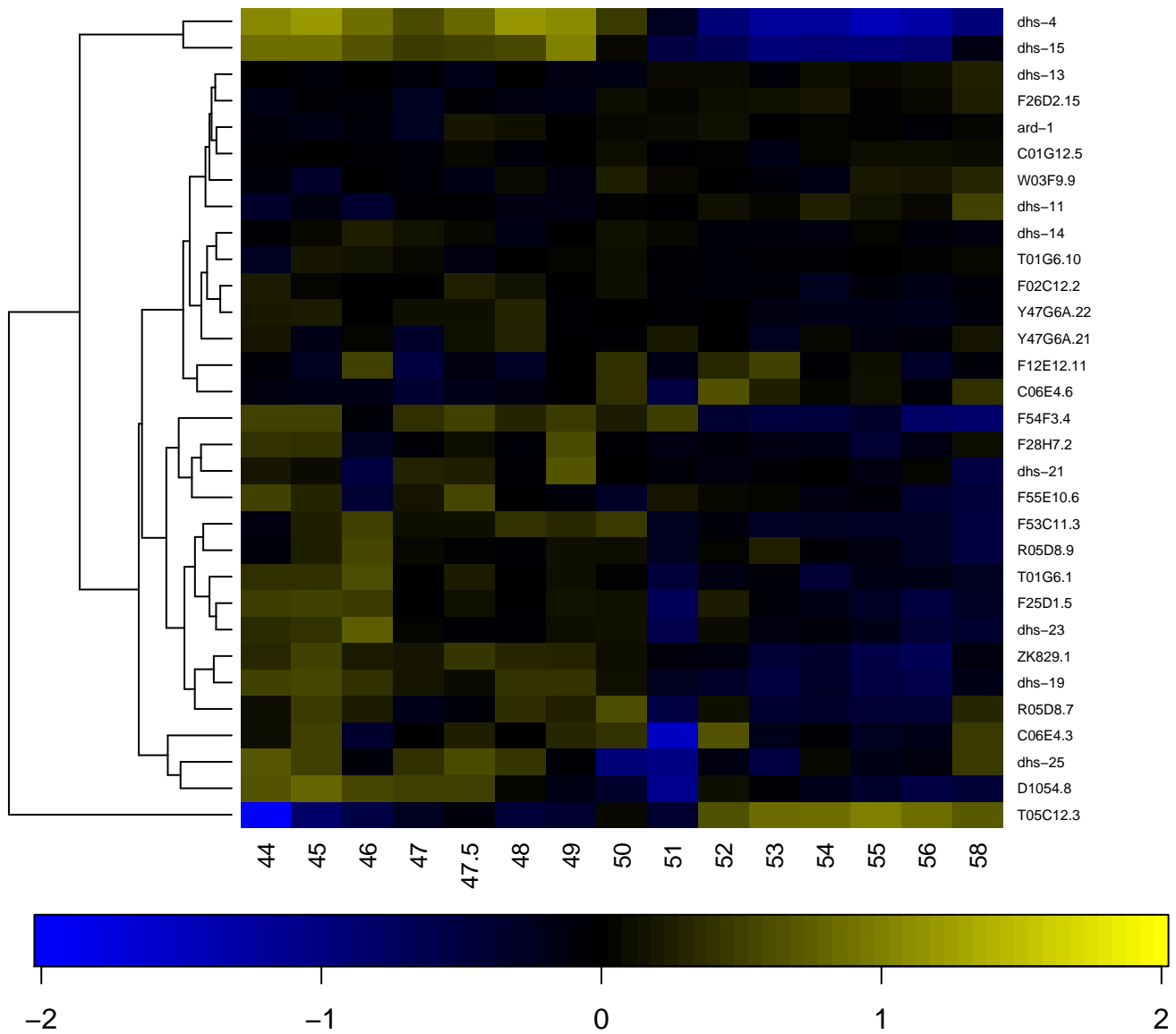
endoplasmic reticulum unfolded protein response



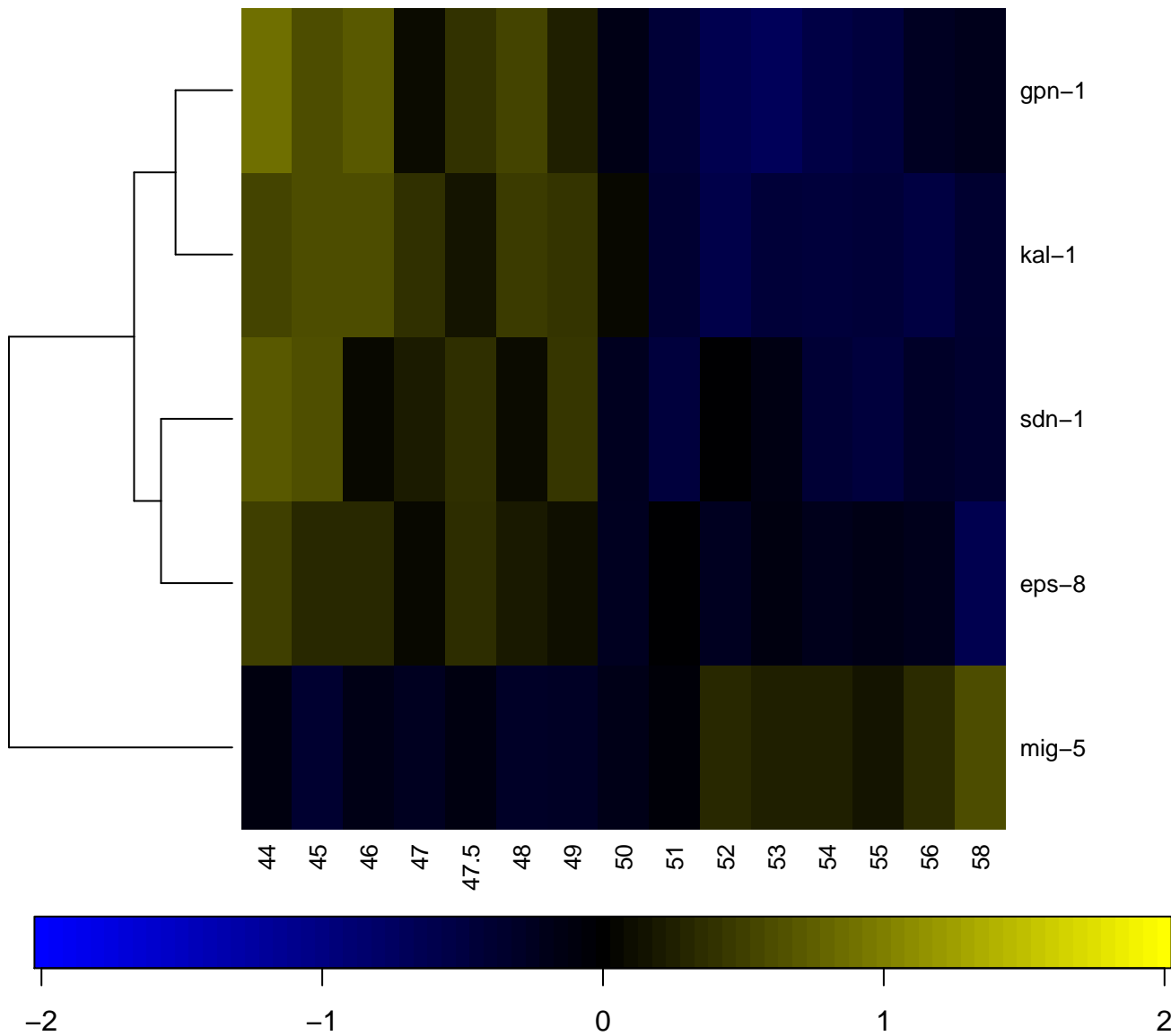
engulfment of apoptotic cell



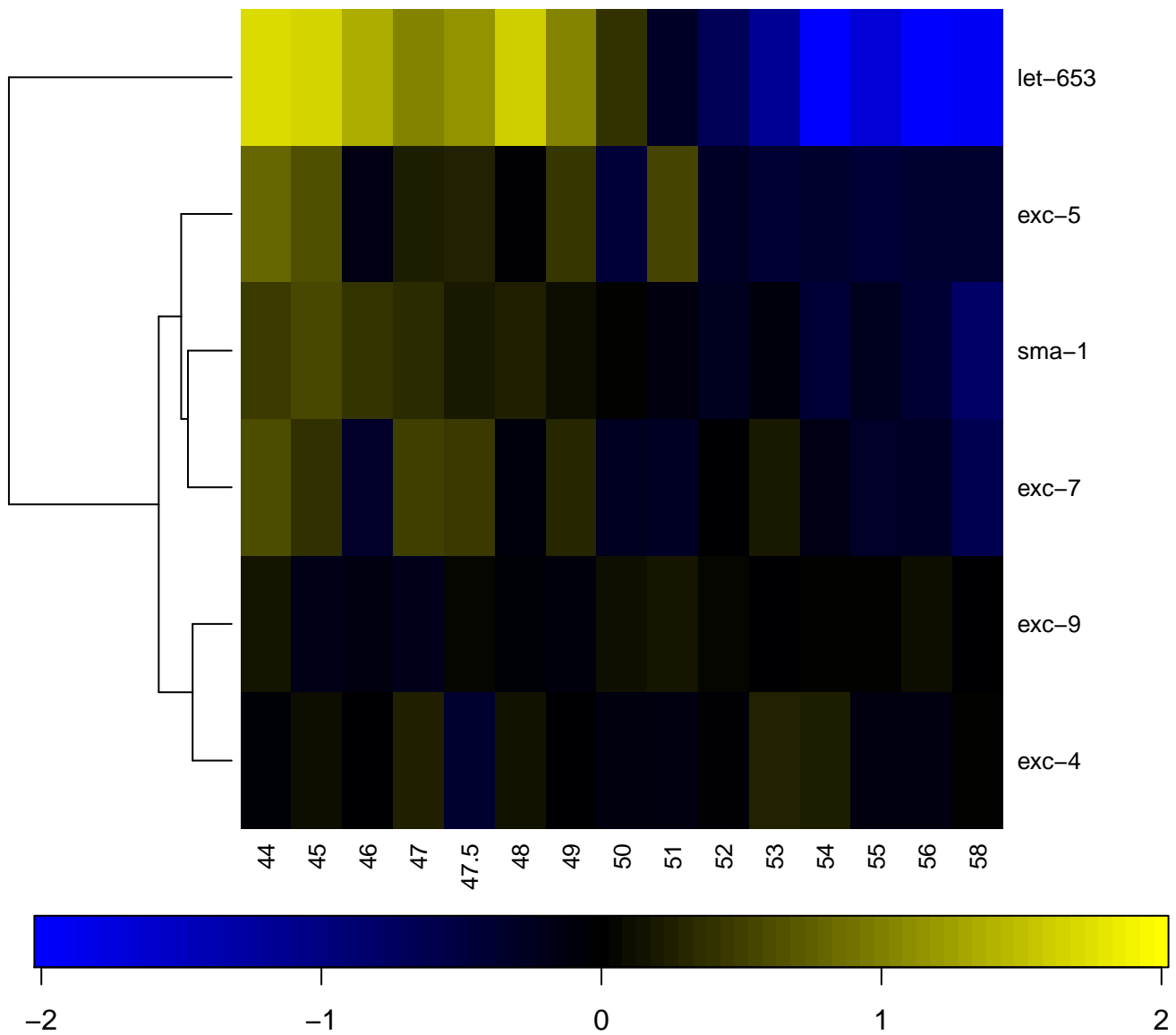
enterobactin biosynthetic process



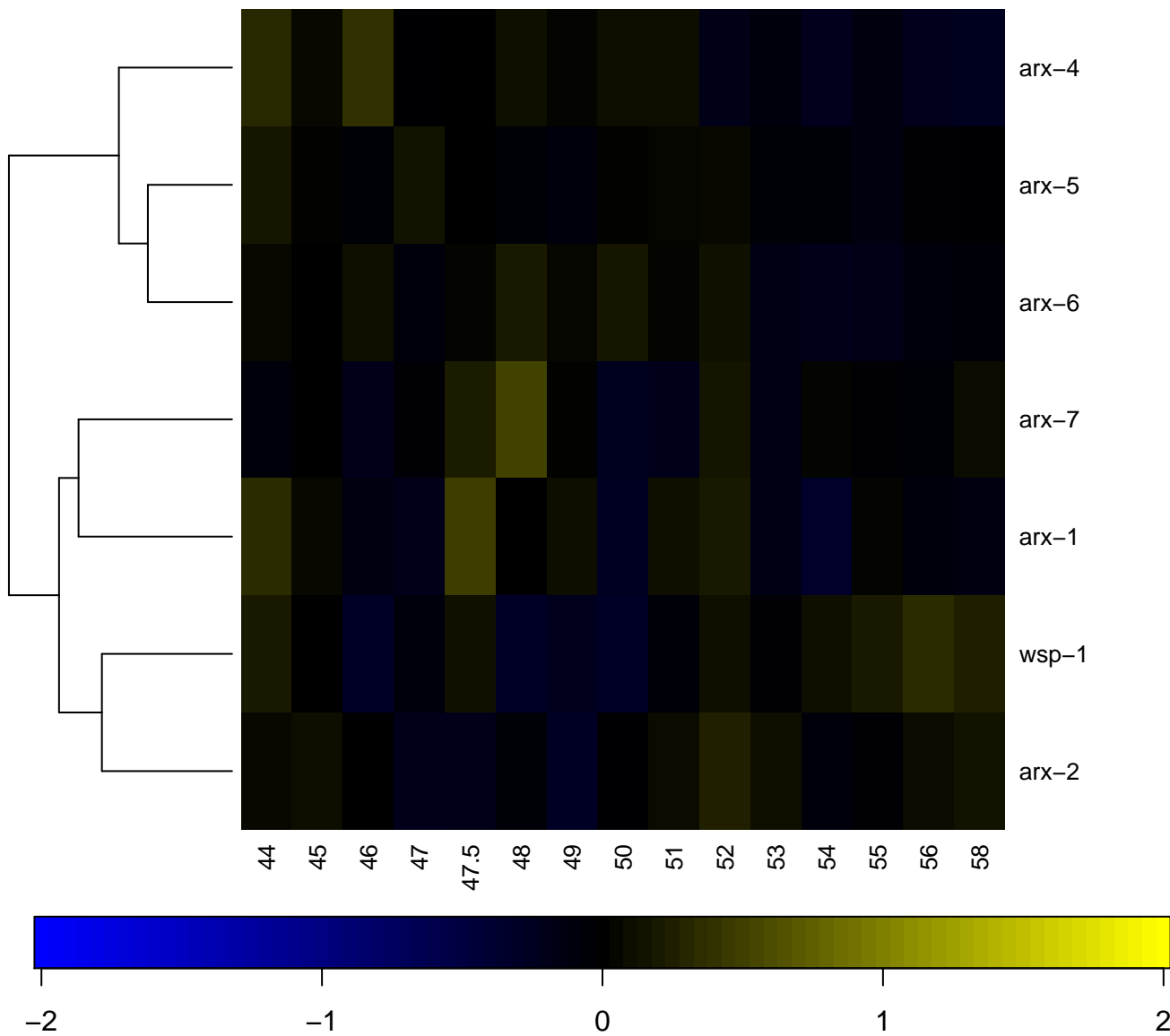
epidermis morphogenesis



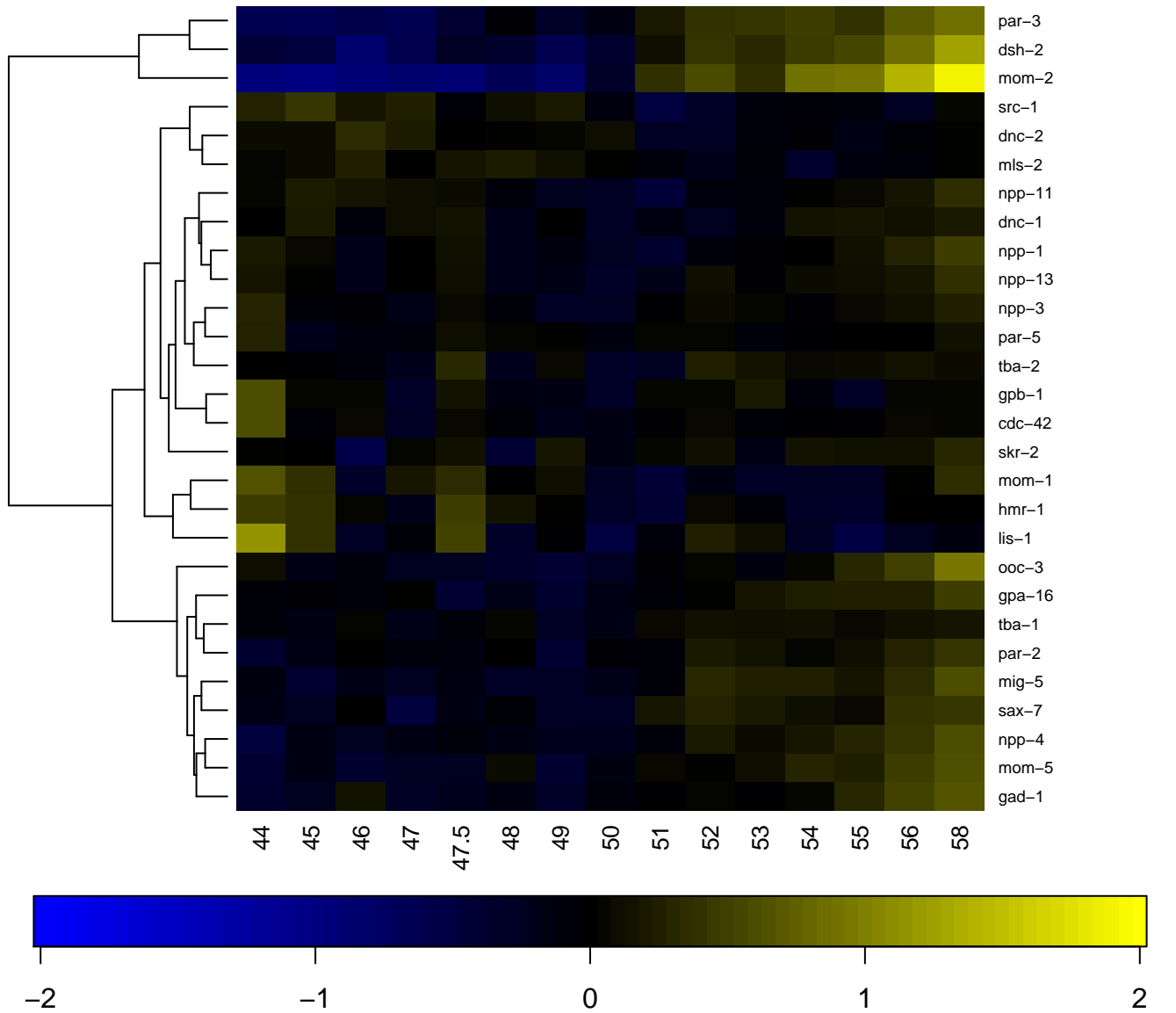
epithelial cell development



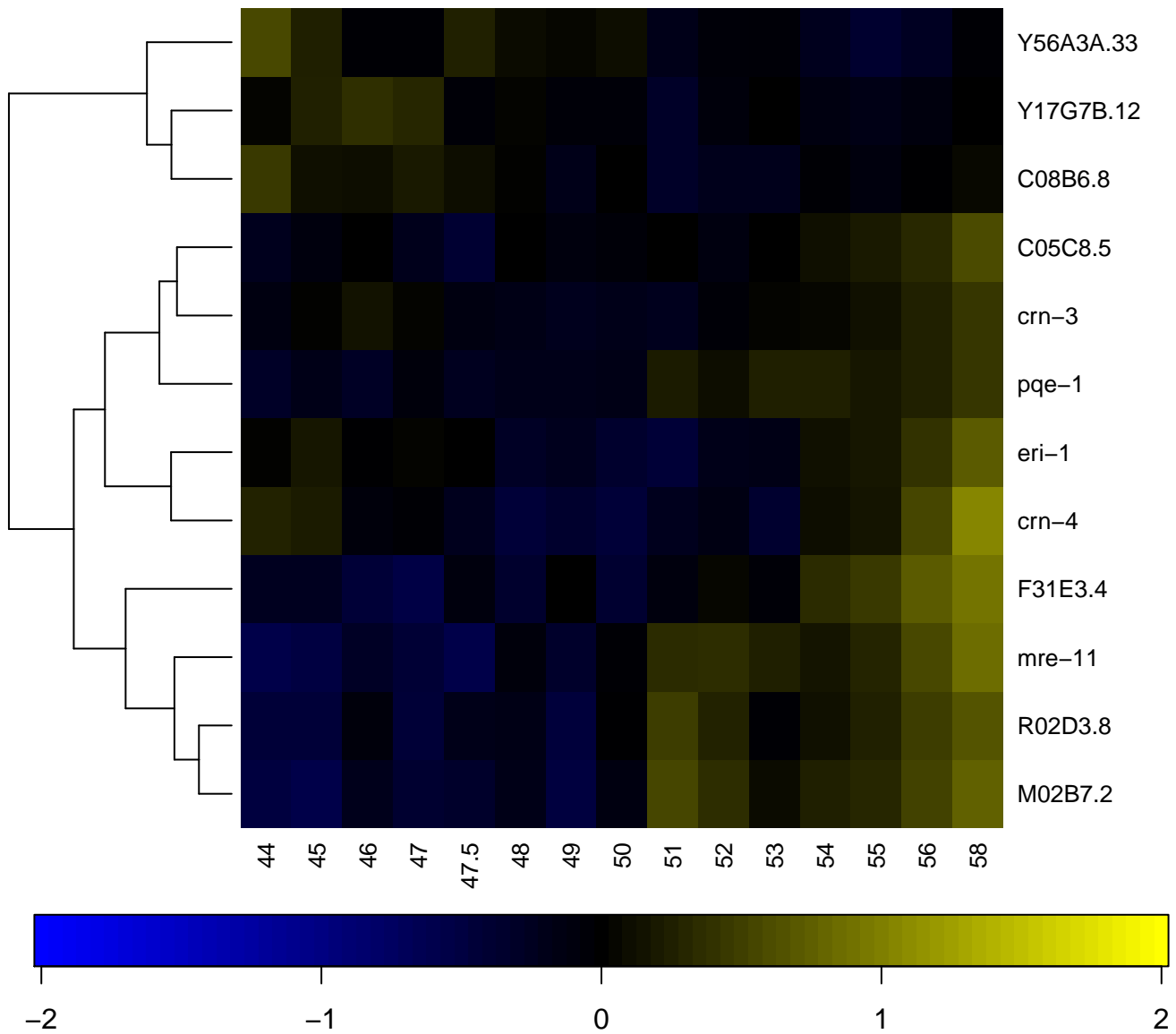
epithelial cell migration



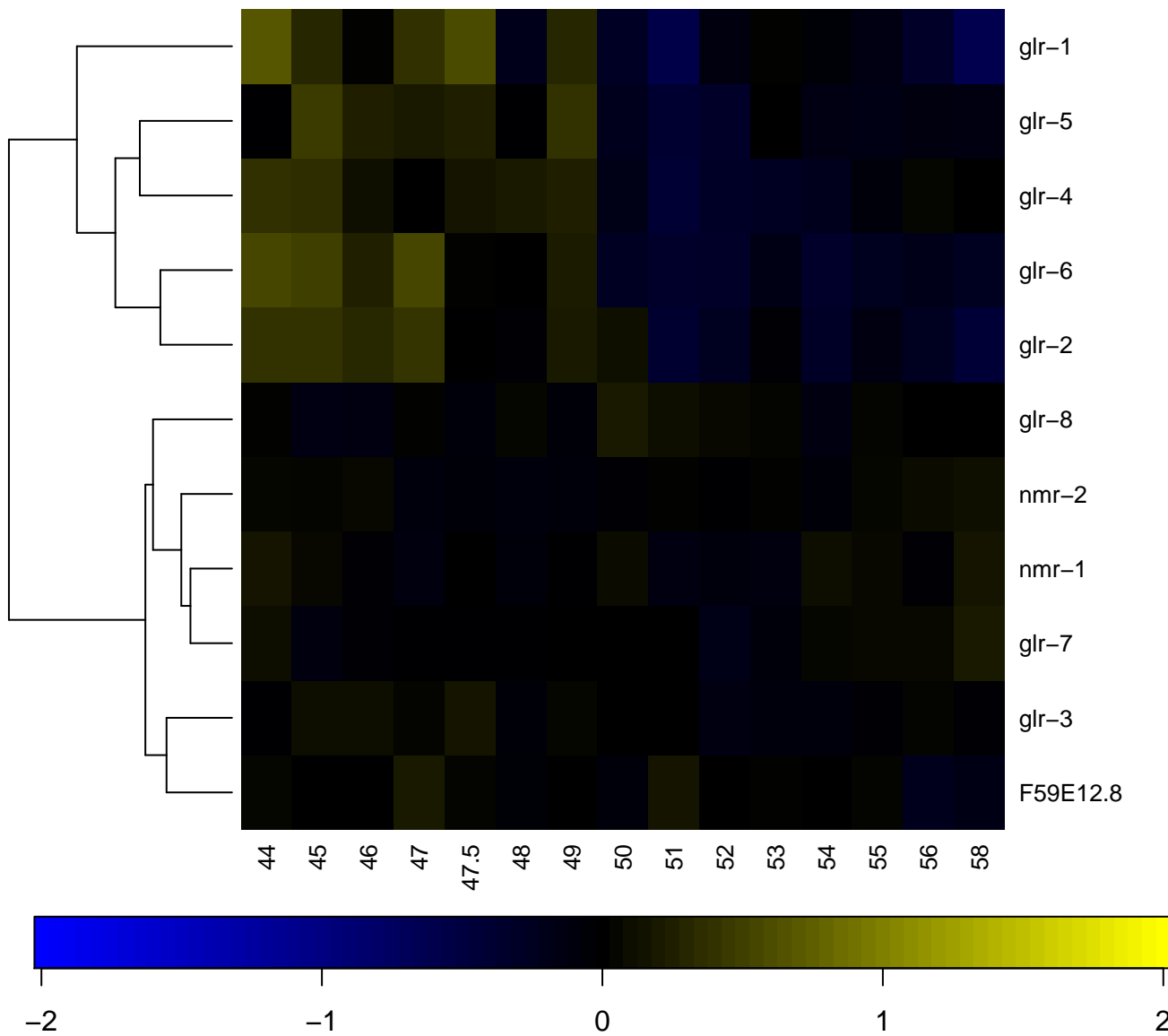
establishment of mitotic spindle orientation



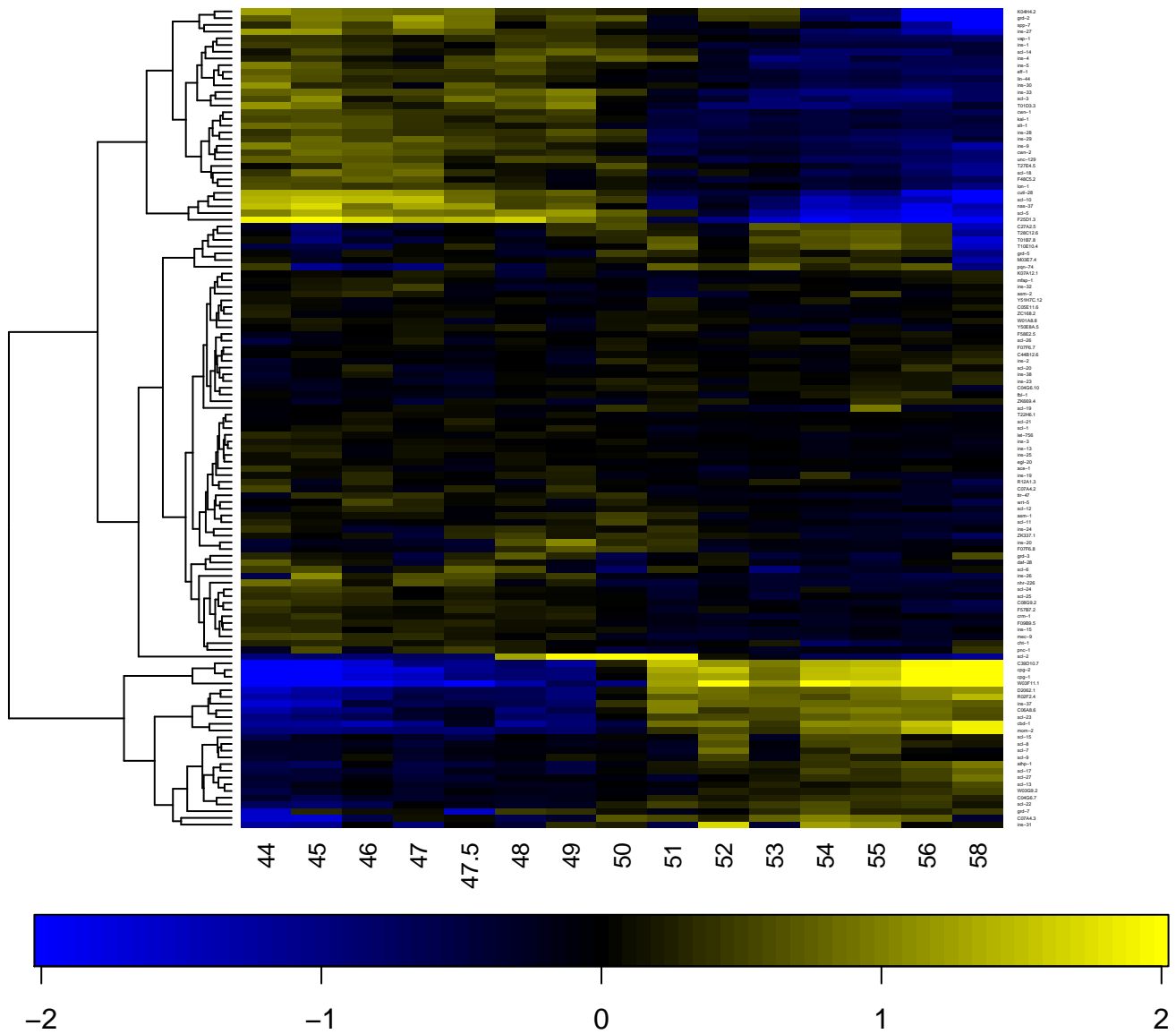
exonuclease activity



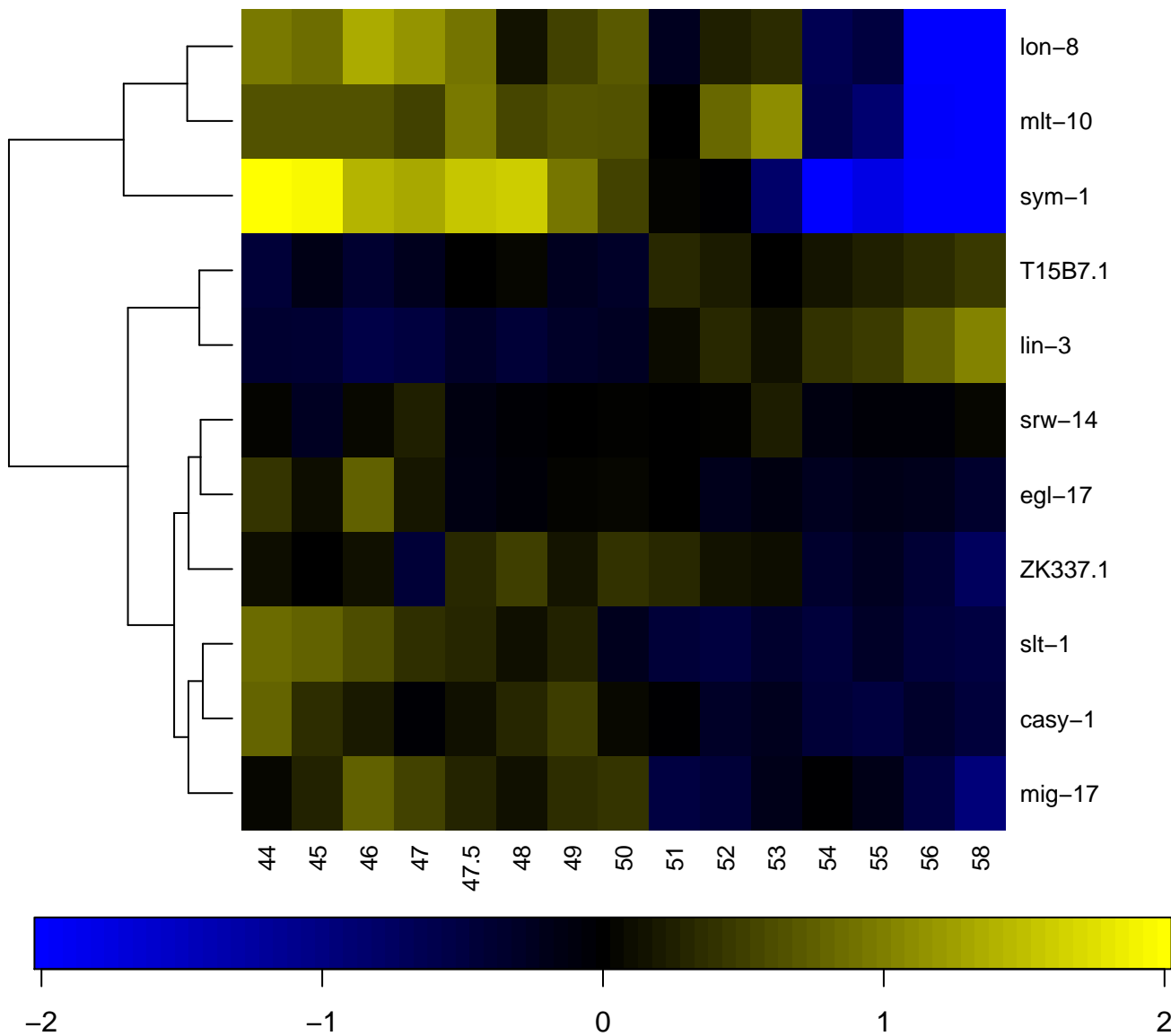
extracellular-glutamate-gated ion channel activity



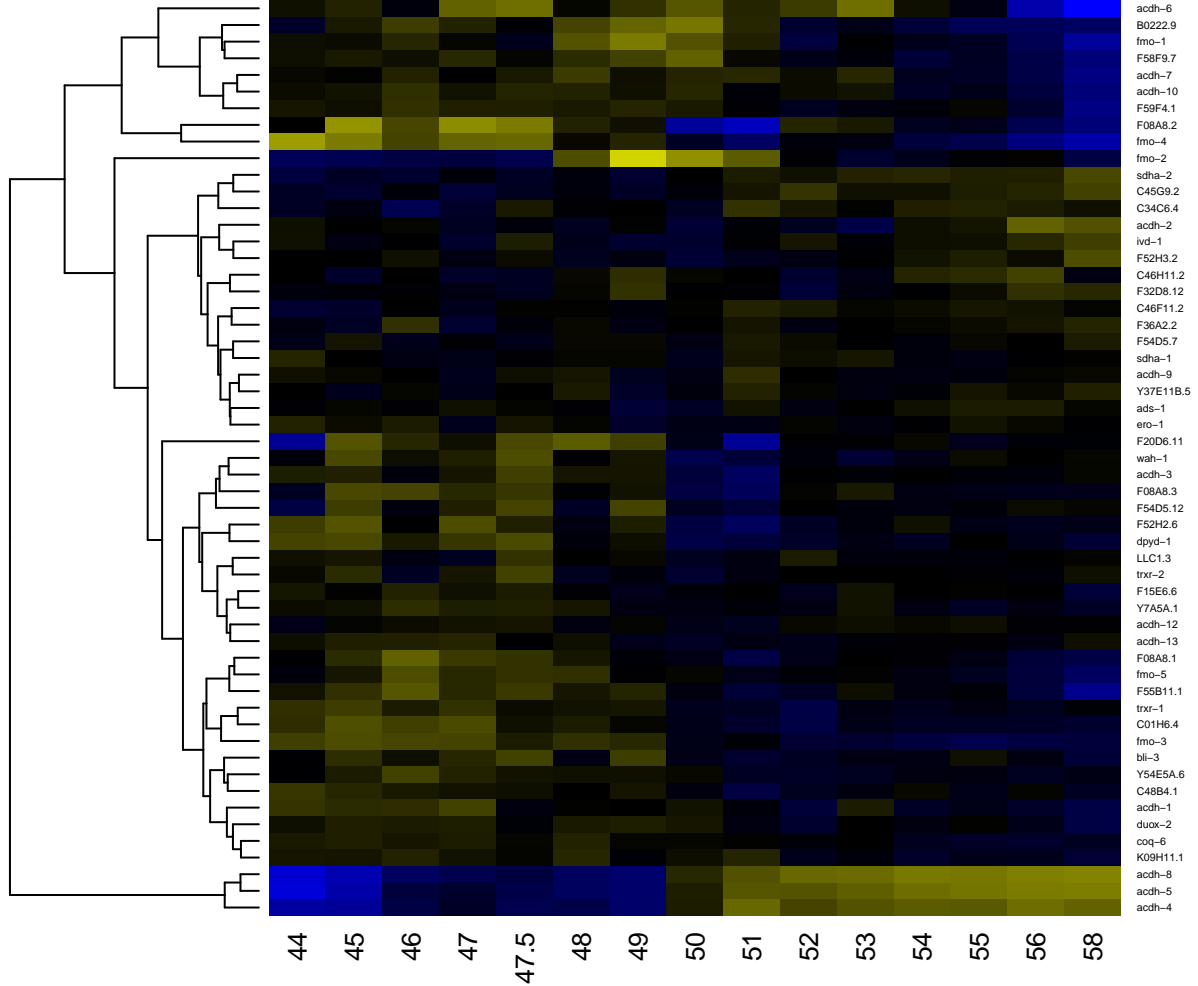
extracellular region



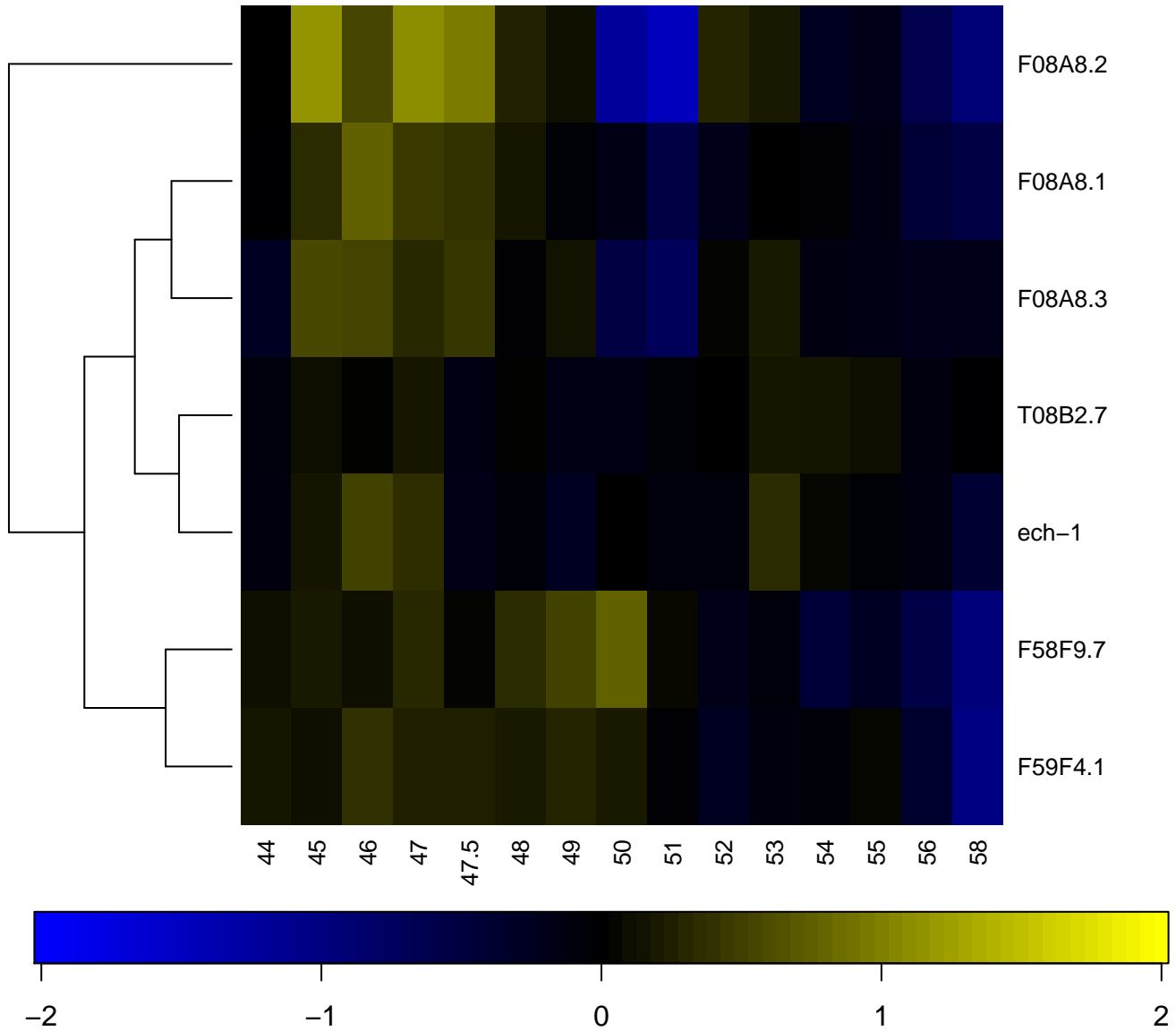
extracellular space



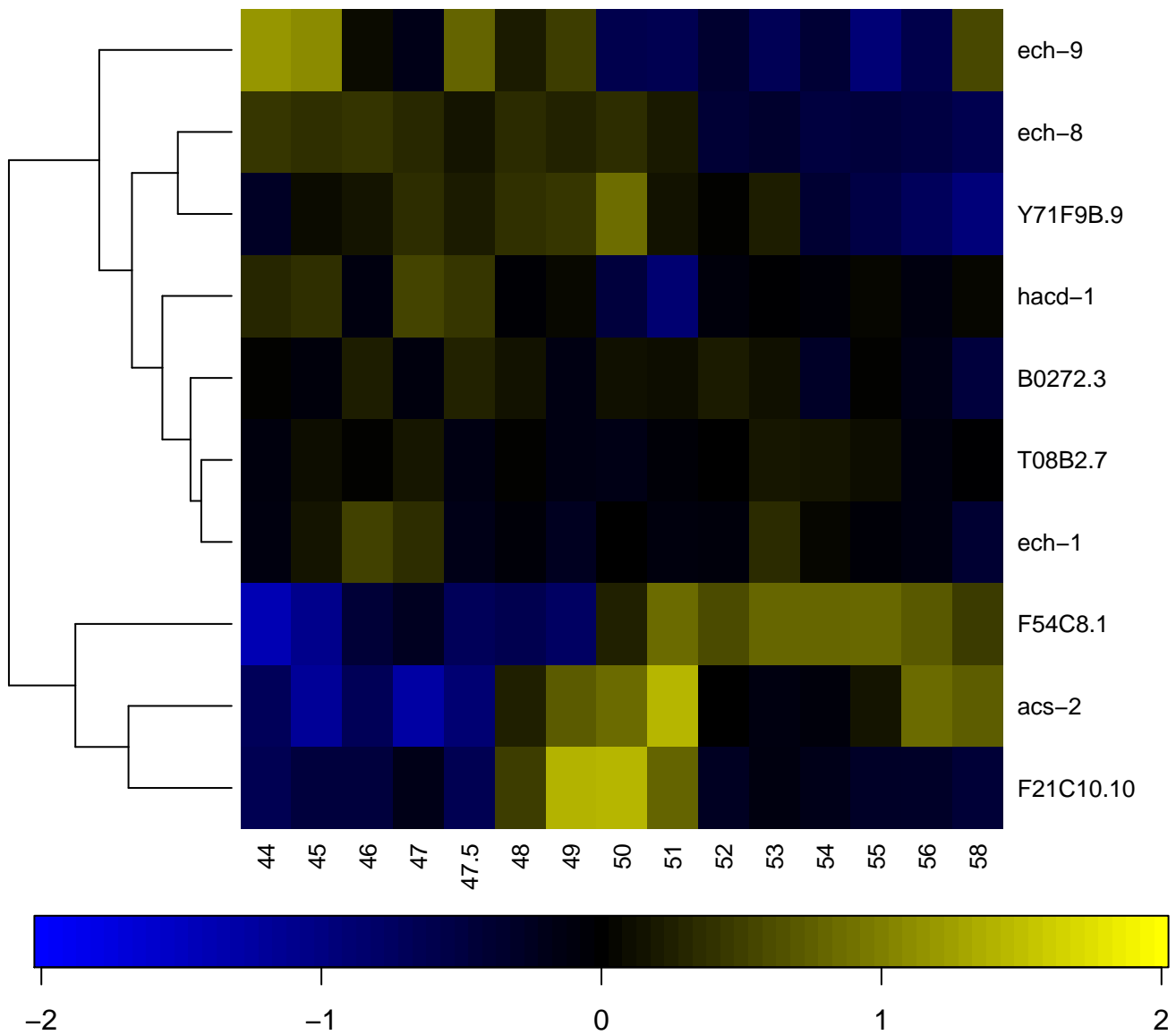
FAD binding



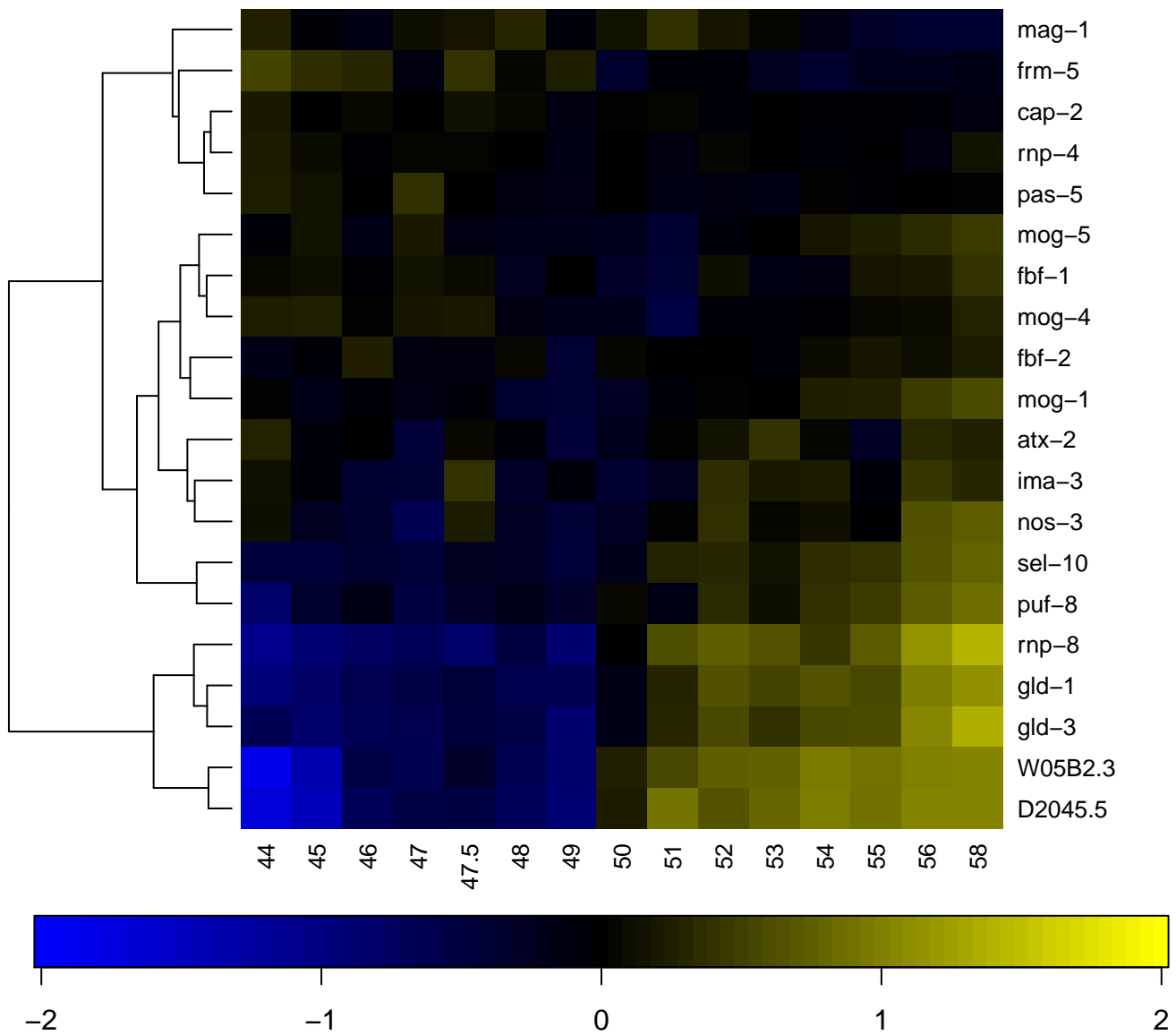
fatty acid beta-oxidation



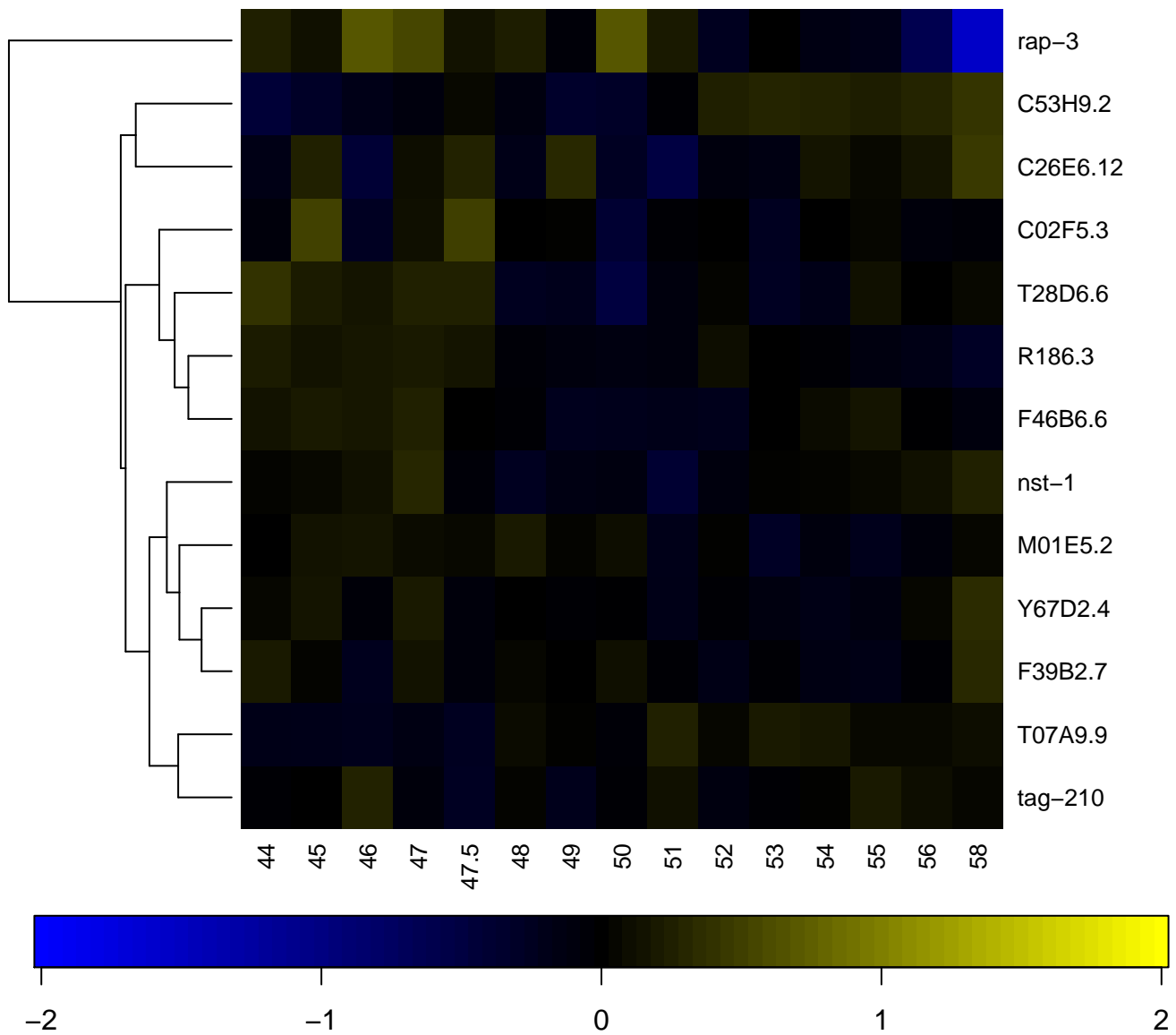
fatty acid metabolic process



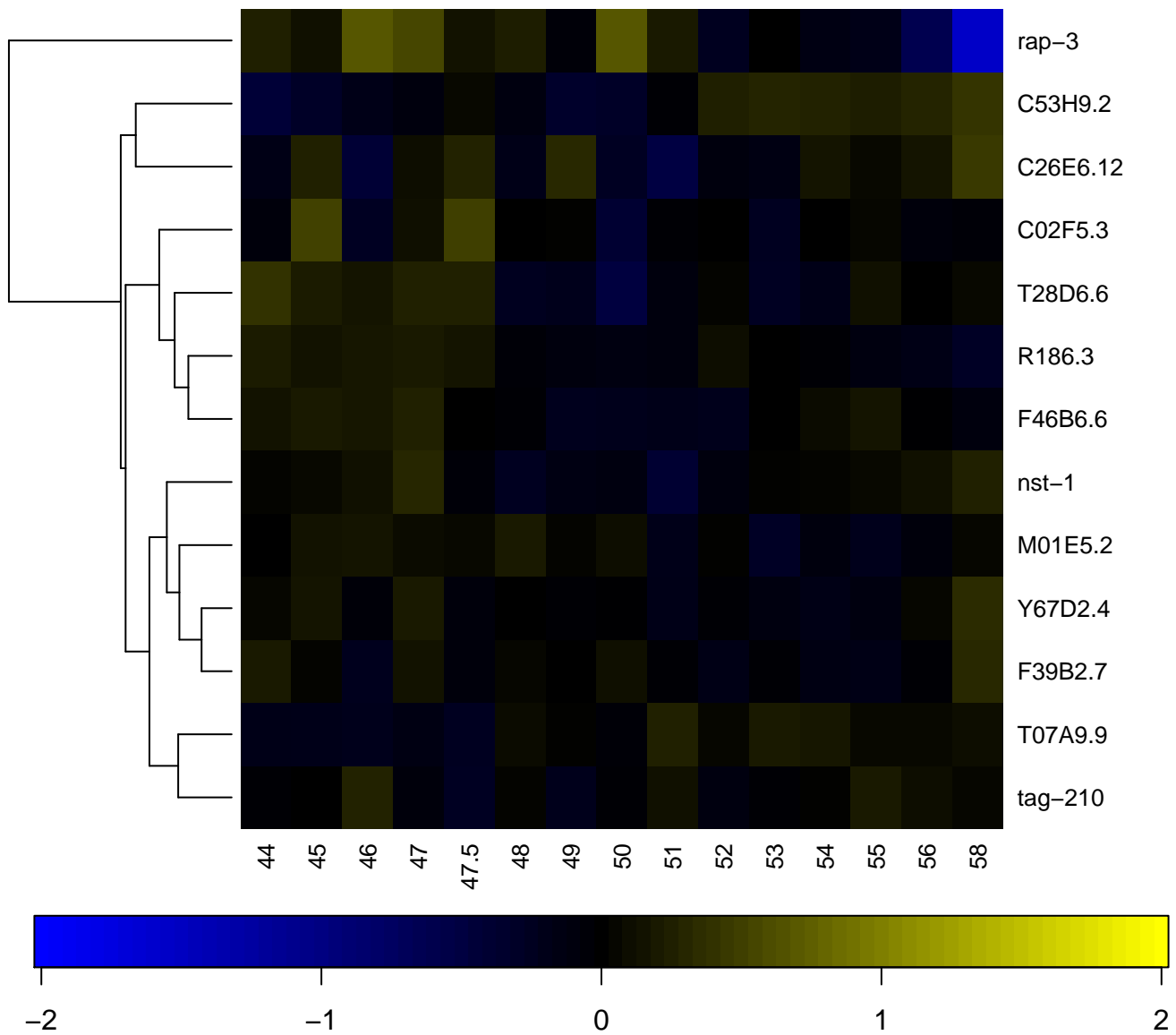
feminization of hermaphroditic germ-line



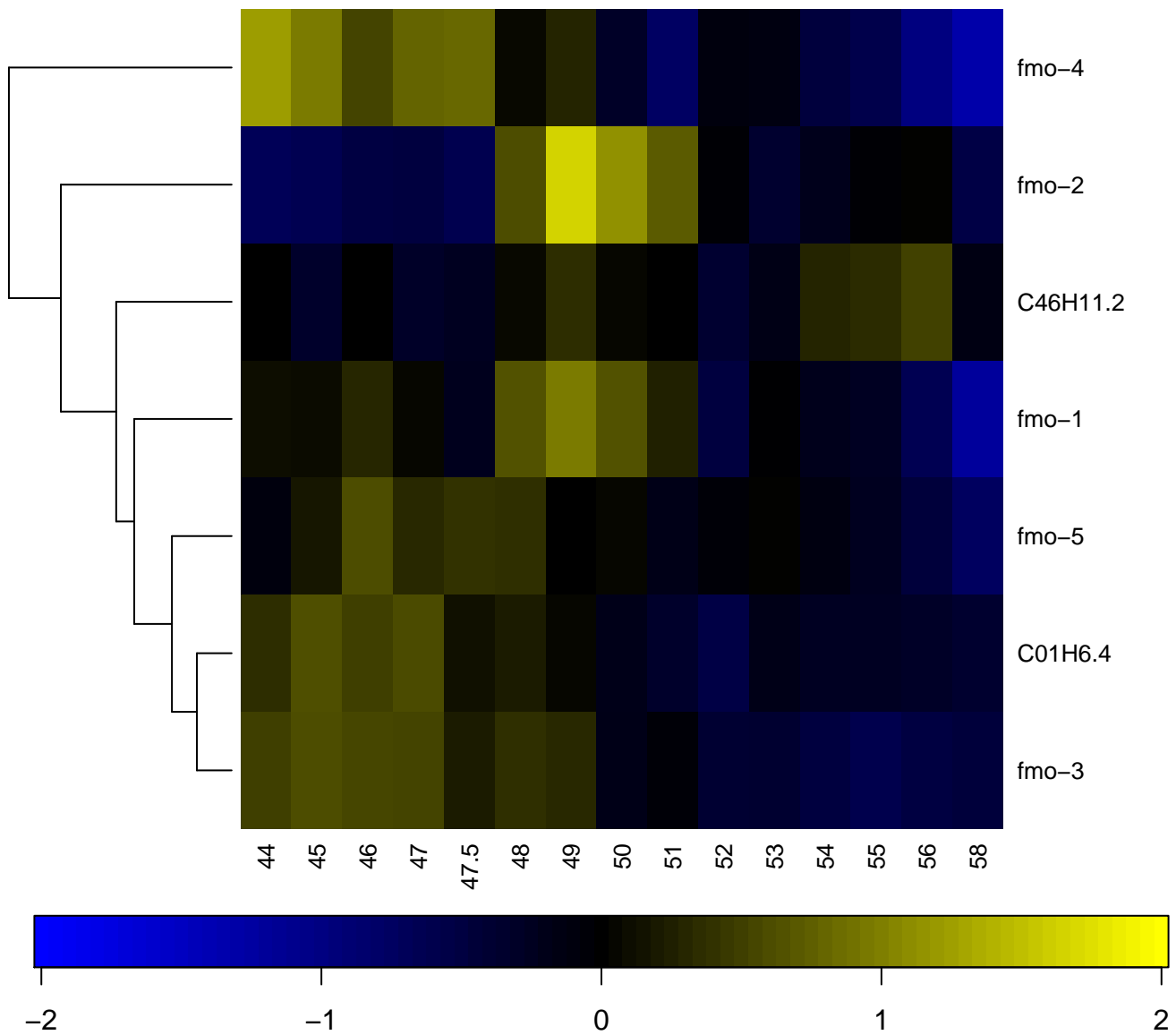
ferrous iron transmembrane transporter activity



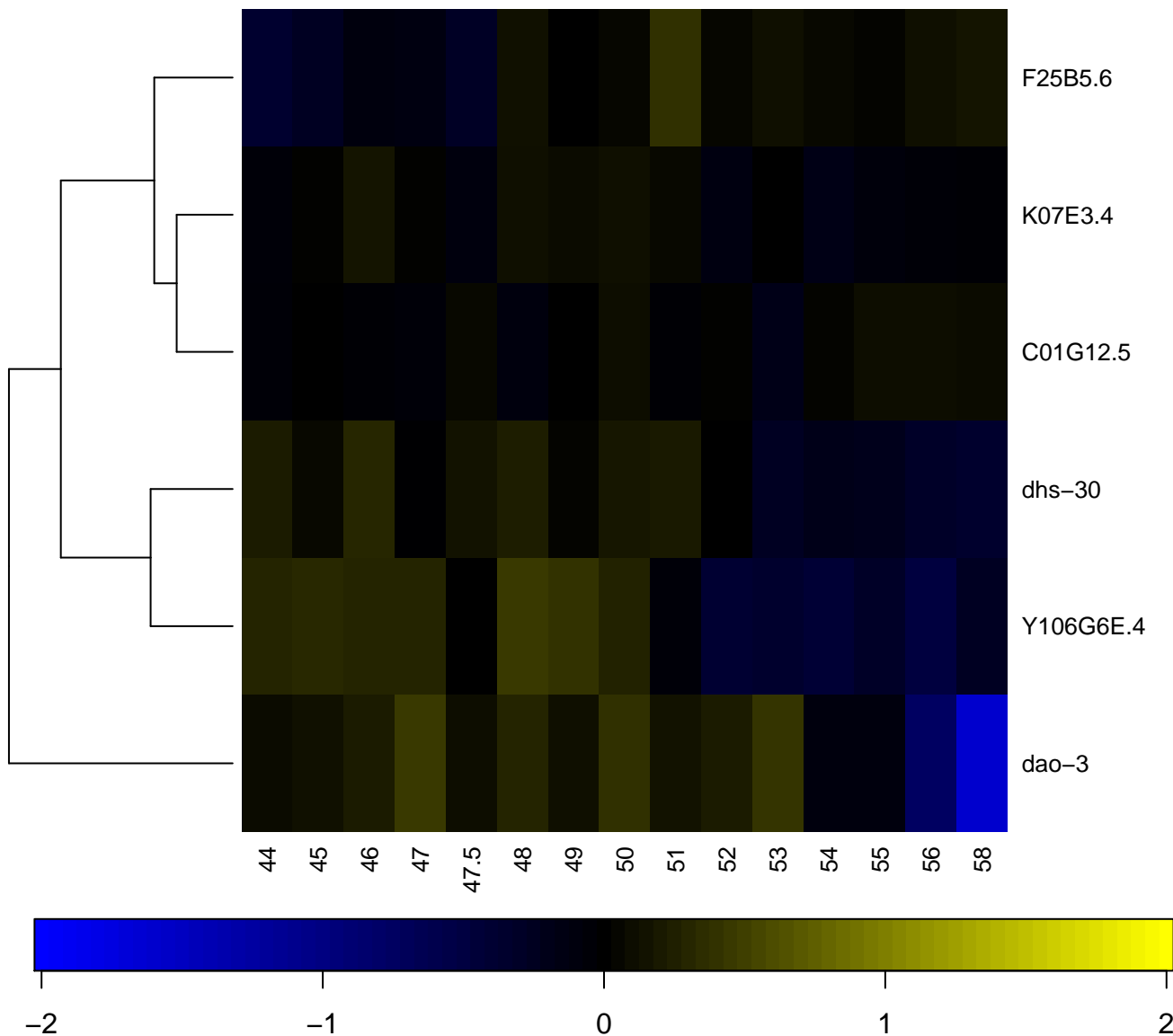
ferrous iron transport



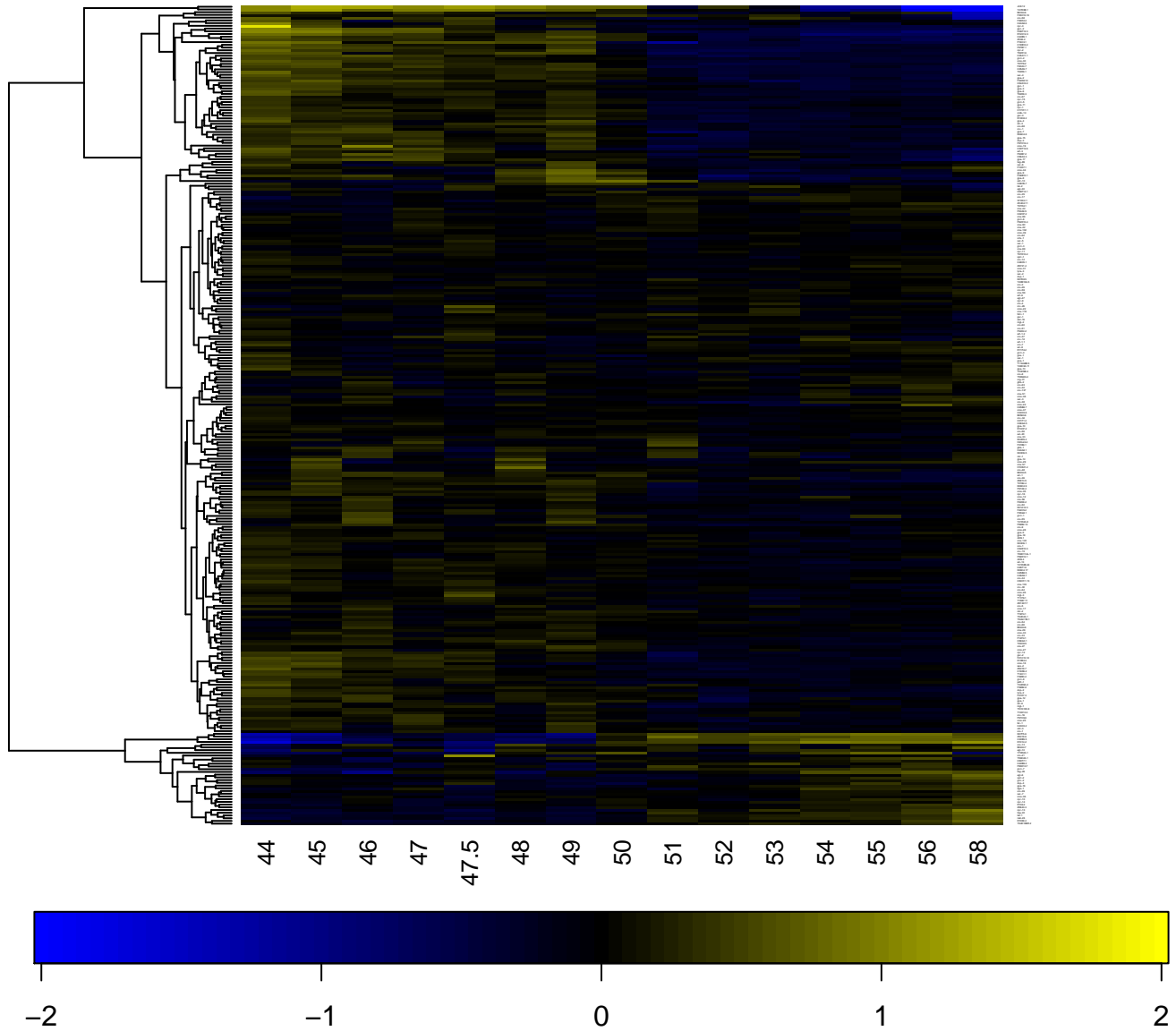
flavin-containing monooxygenase activity



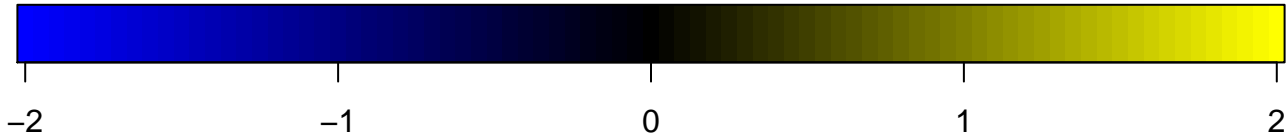
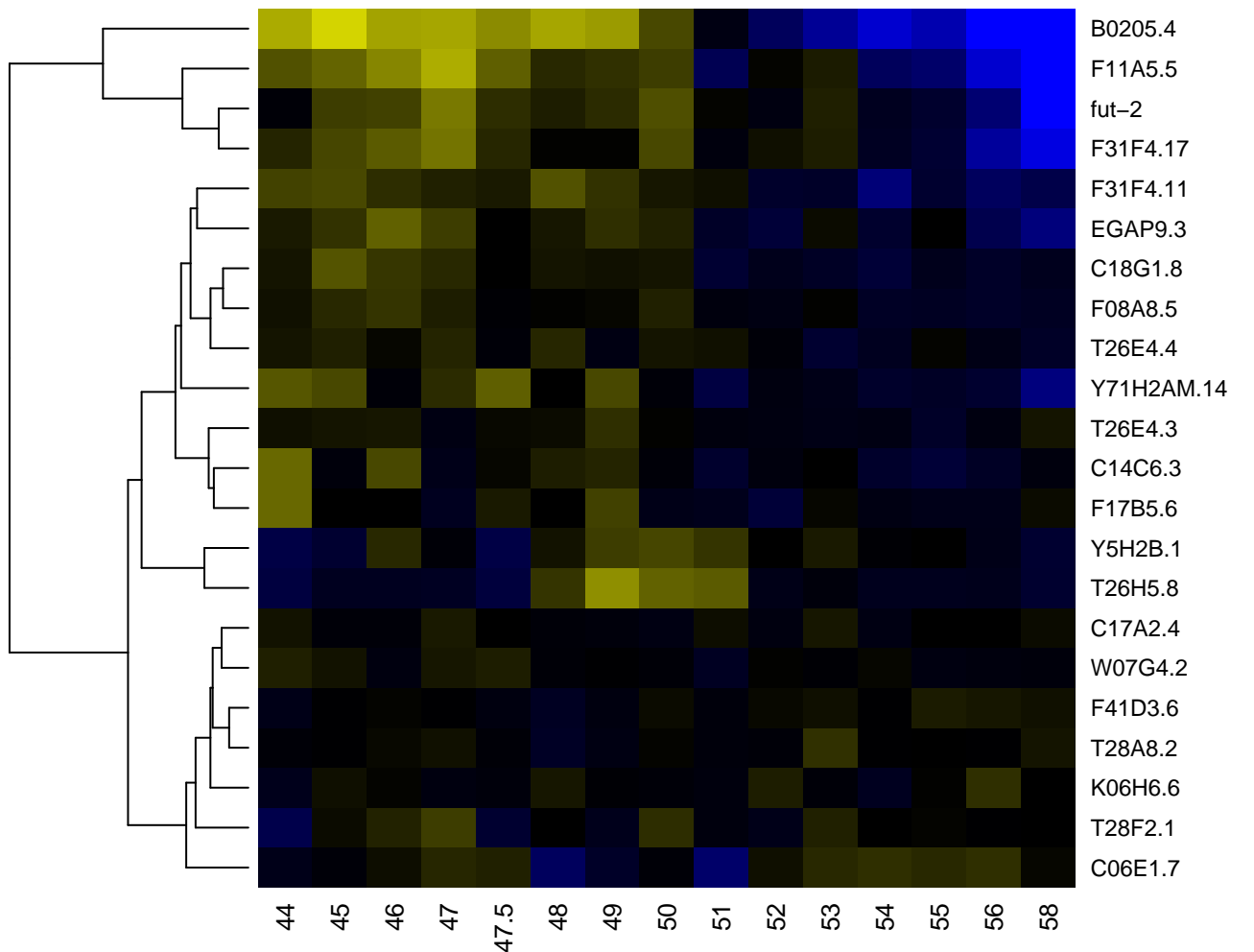
folic acid and derivative biosynthetic process



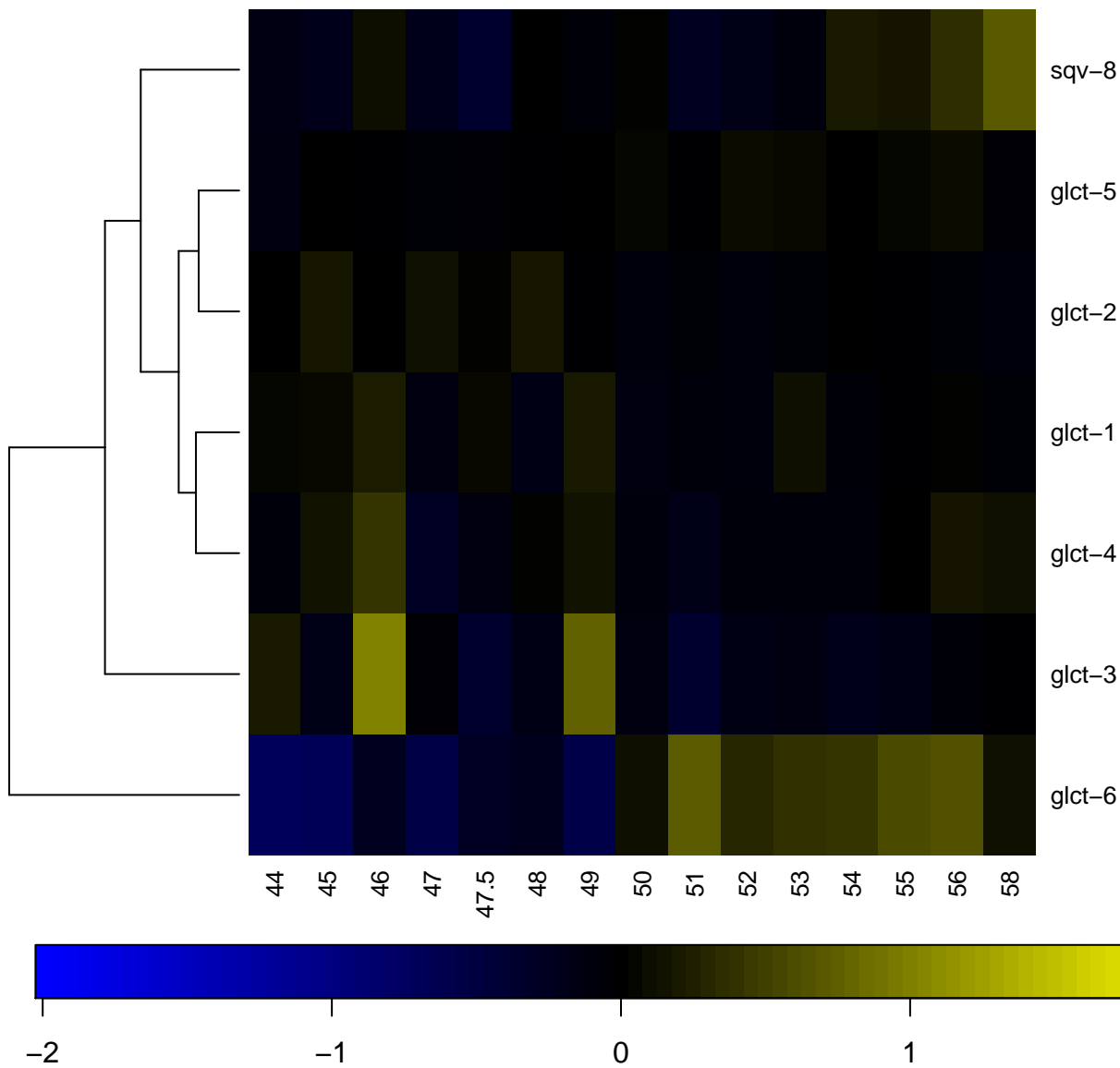
G-protein coupled receptor protein signaling pathway



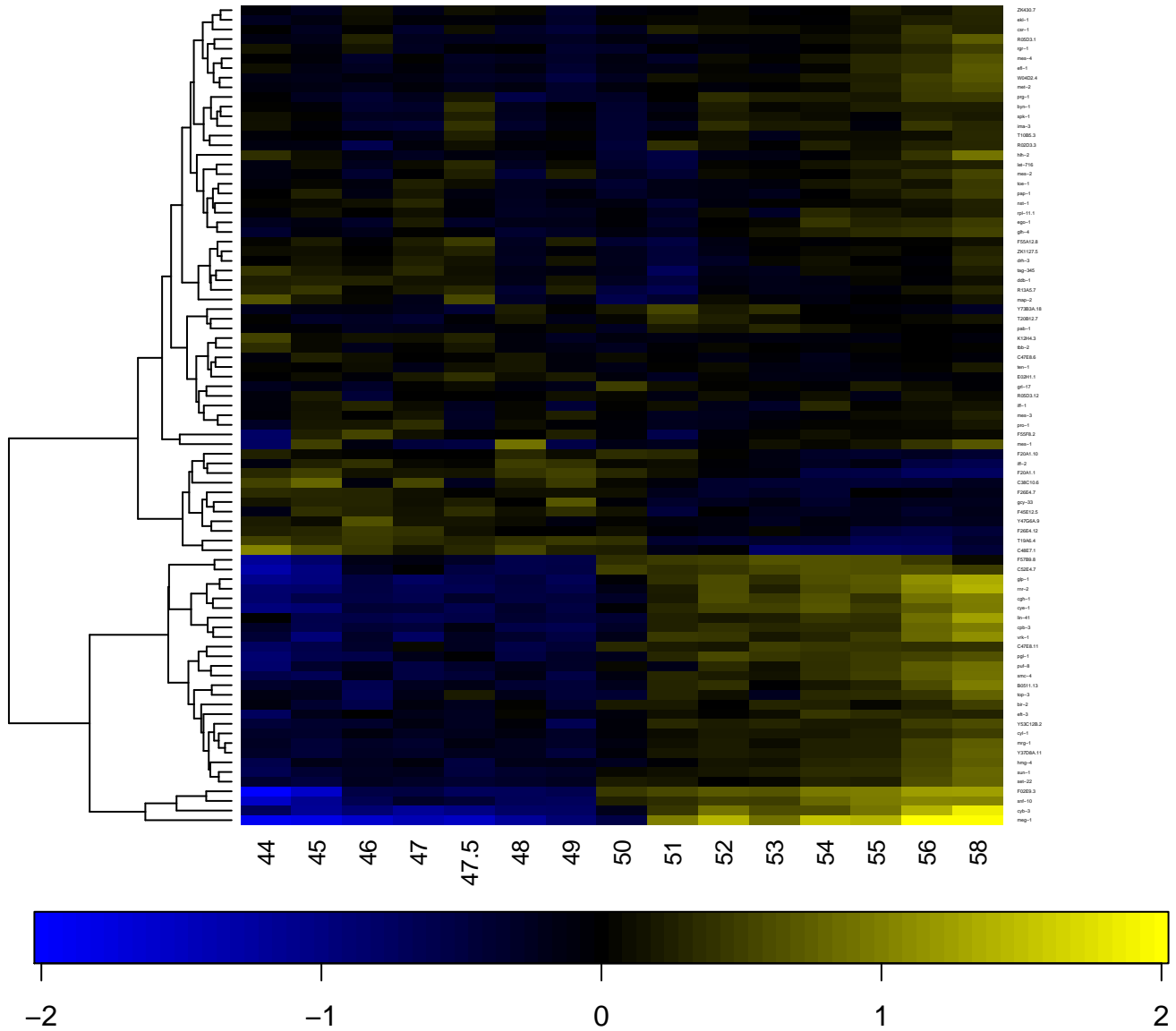
galactoside 2-alpha-L-fucosyltransferase activity



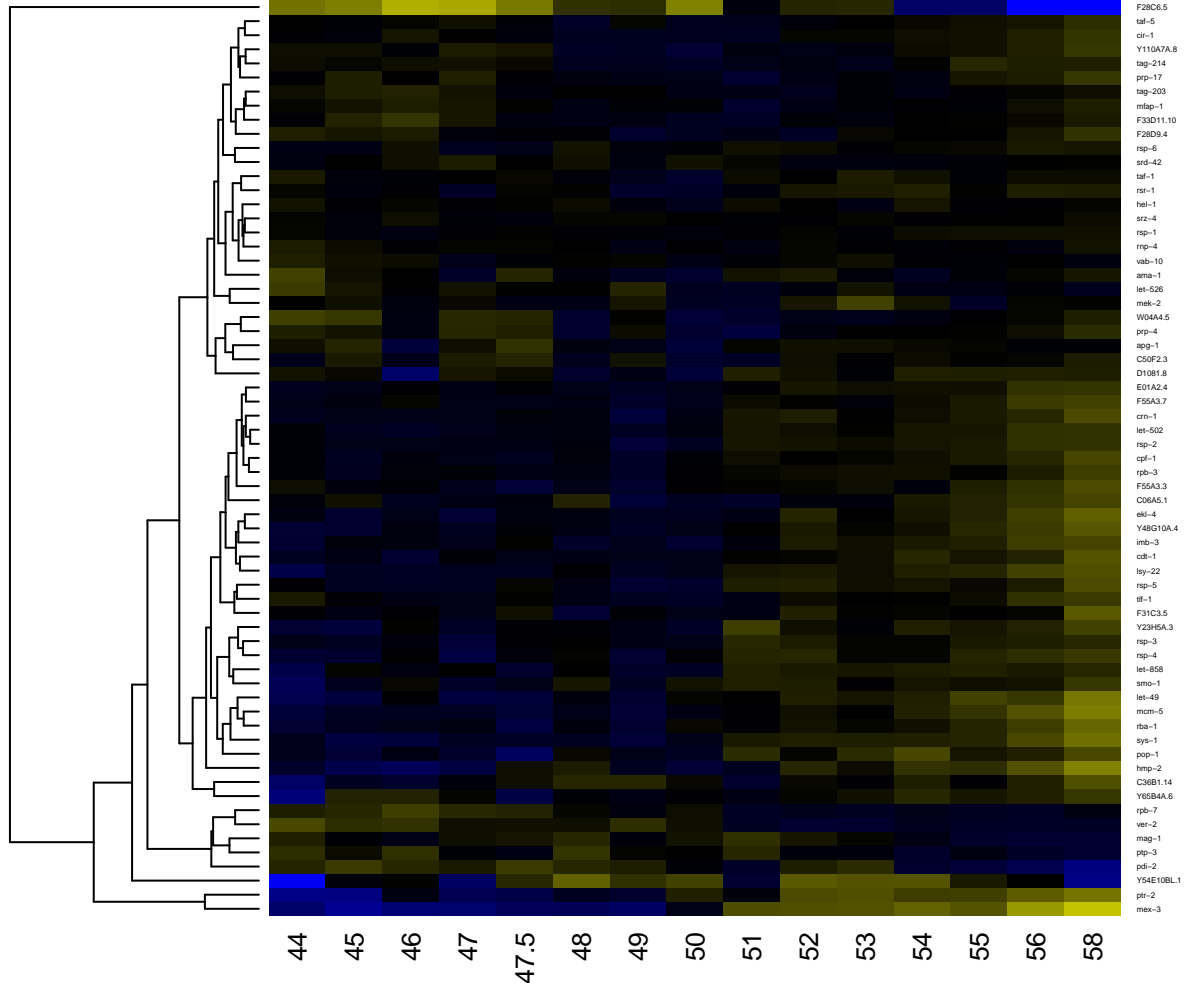
sylgalactosylxylosylprotein 3-beta-glucuronosyltransferase



gamete generation



gastrulation



-2

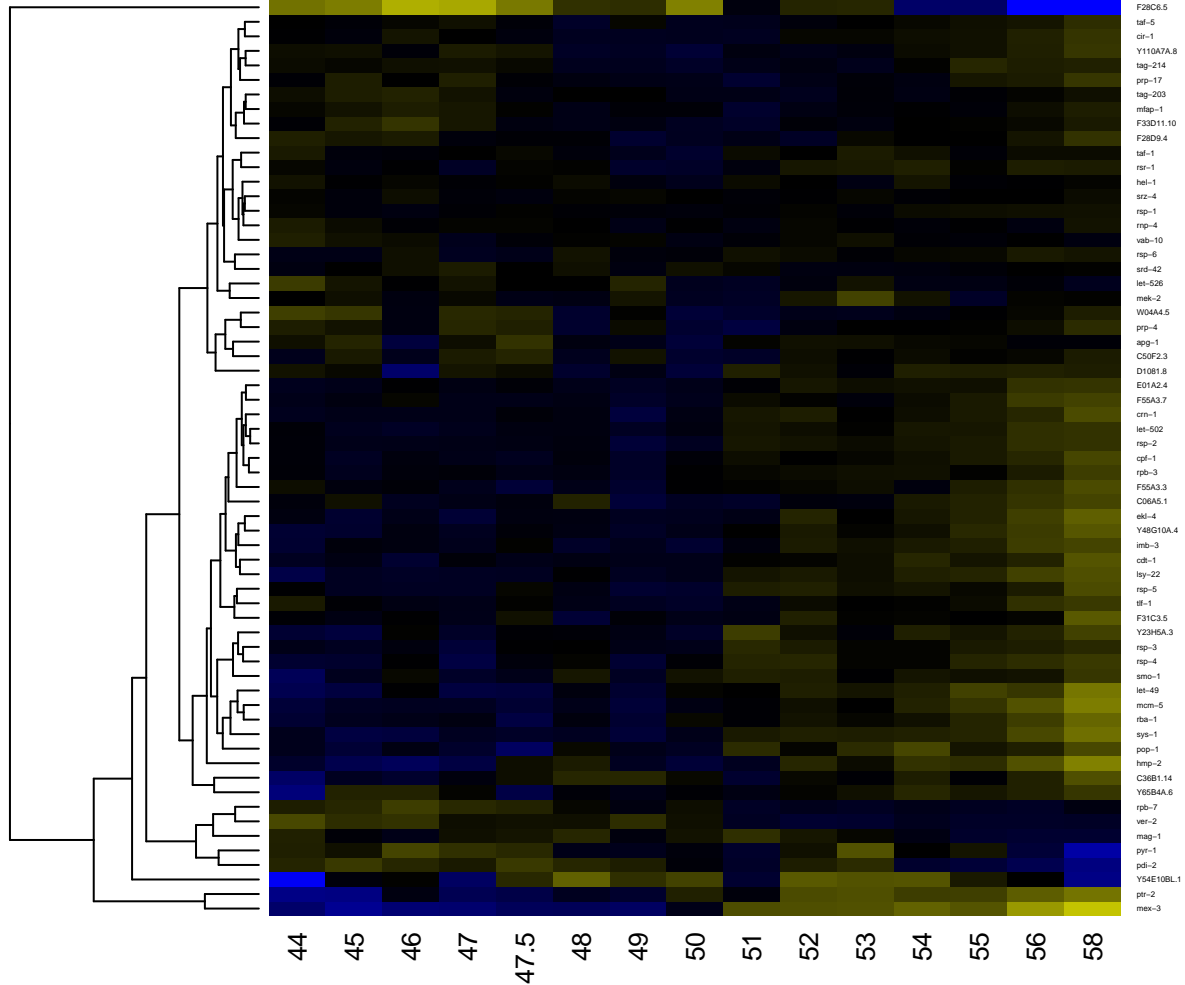
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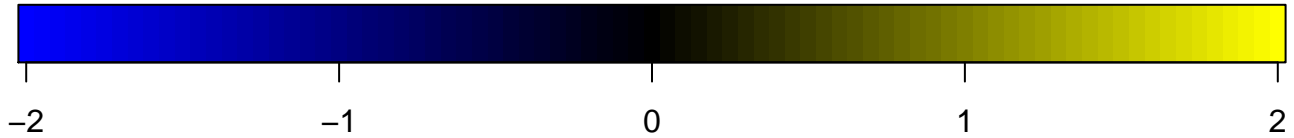
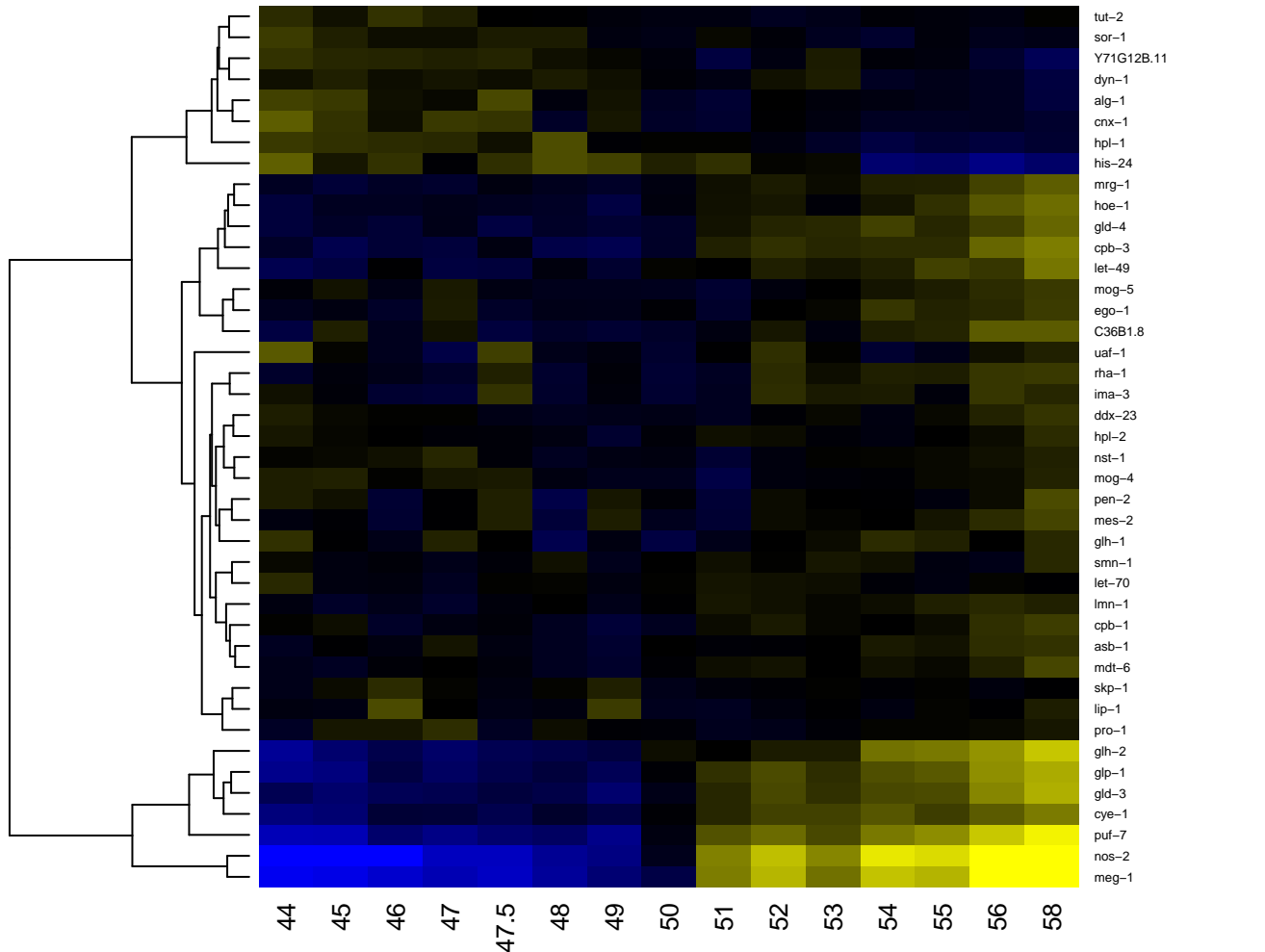
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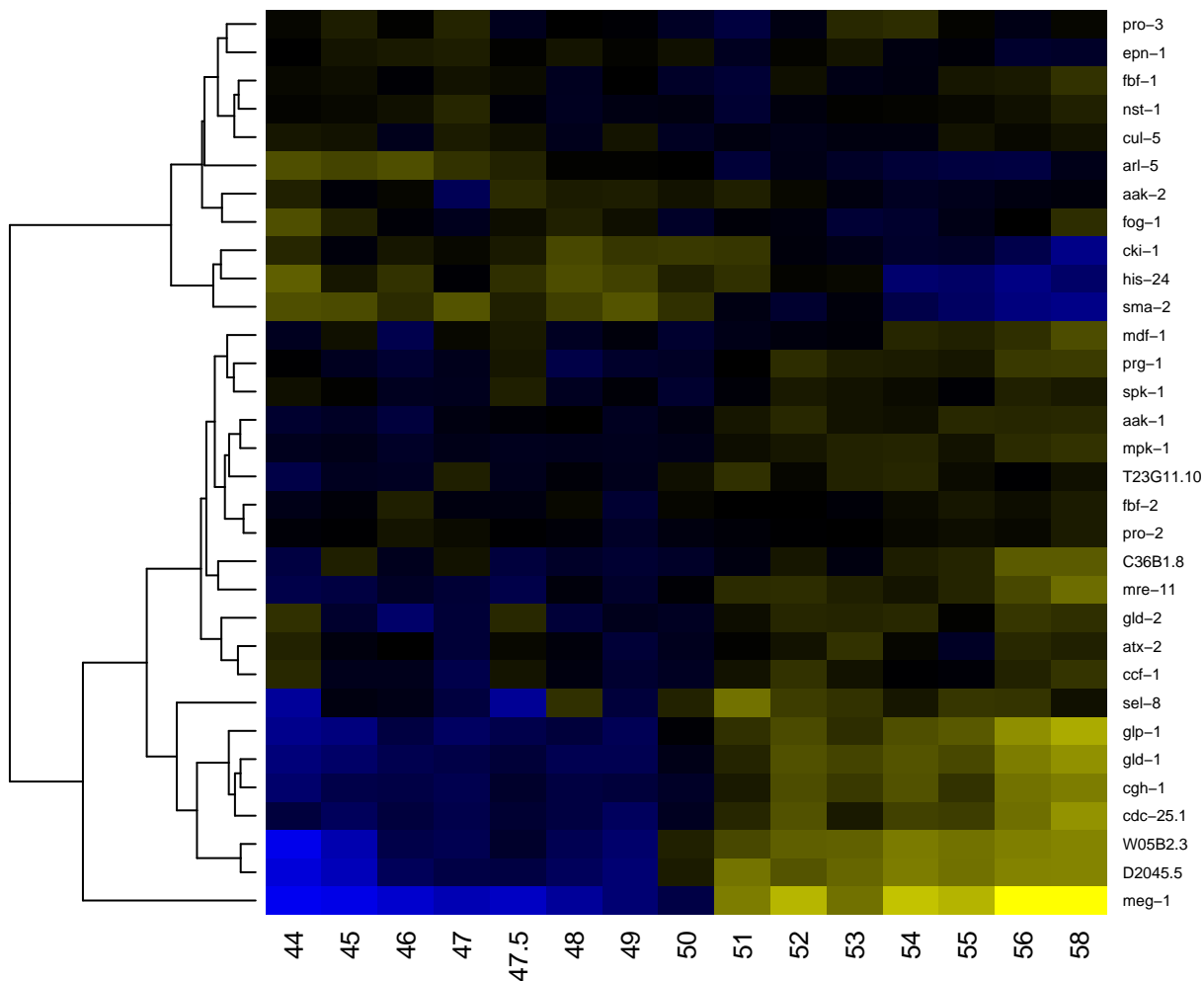
gastrulation with mouth forming first



germ cell development



germline cell cycle switching, mitotic to meiotic cell cycle



-2

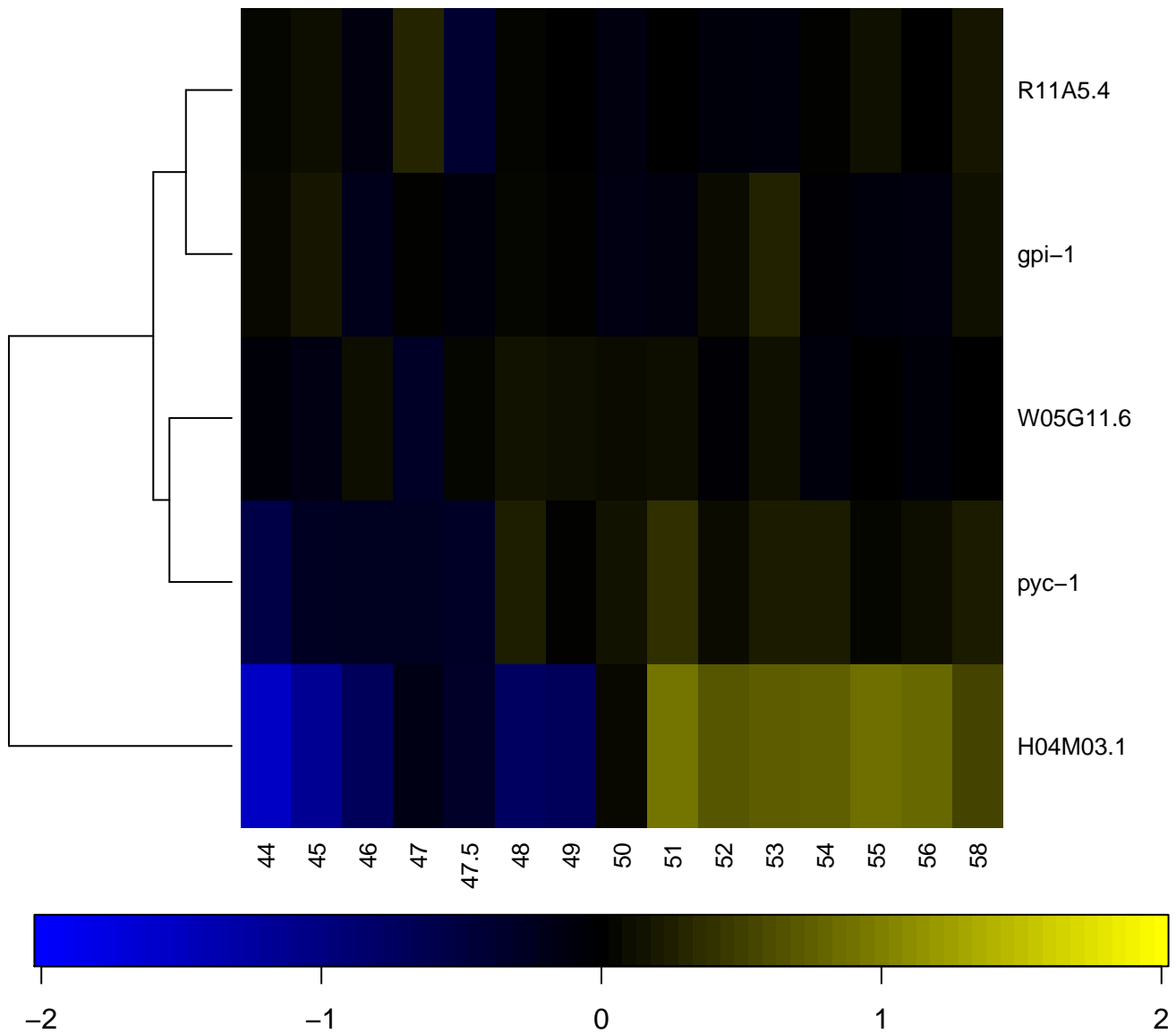
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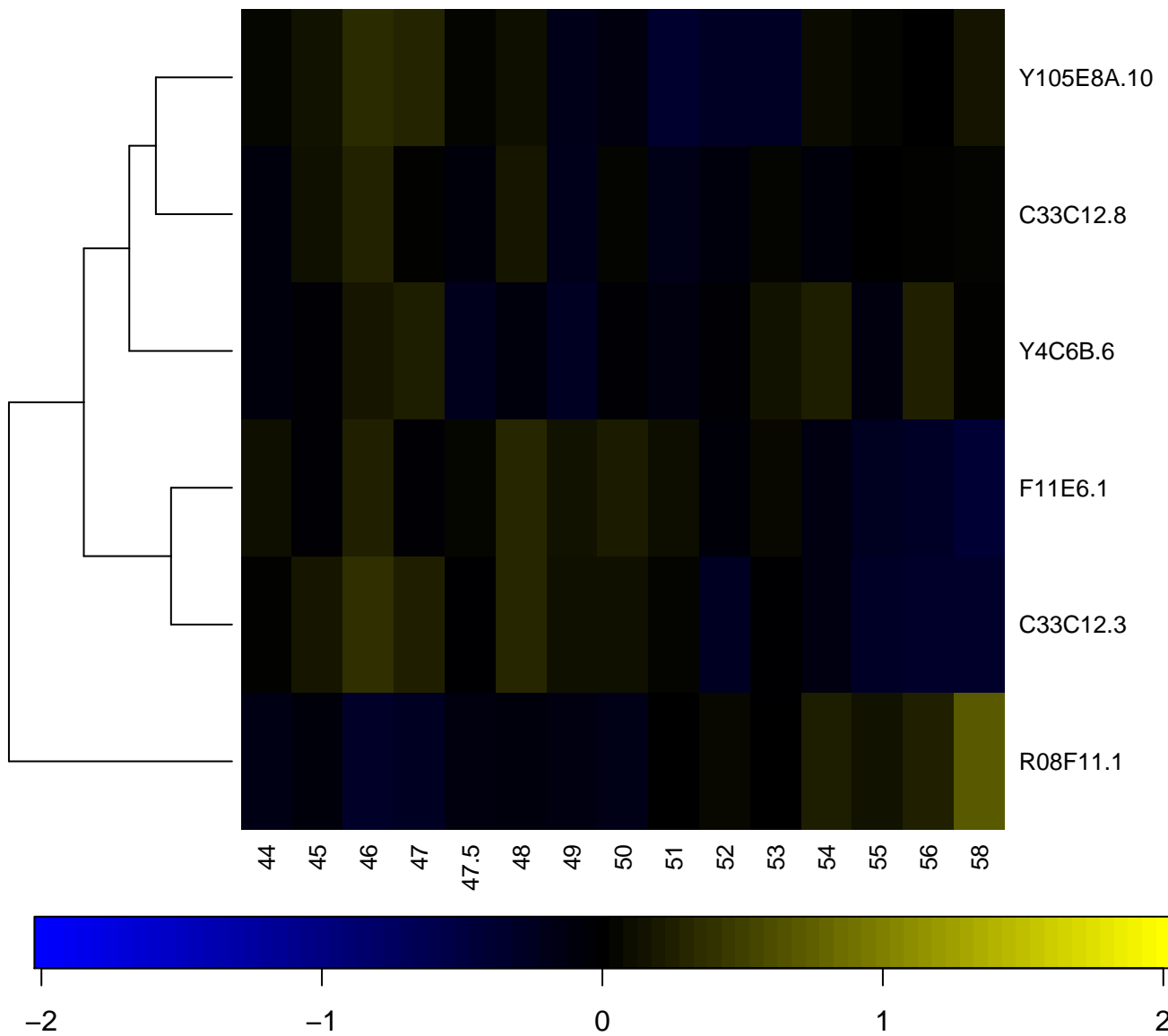
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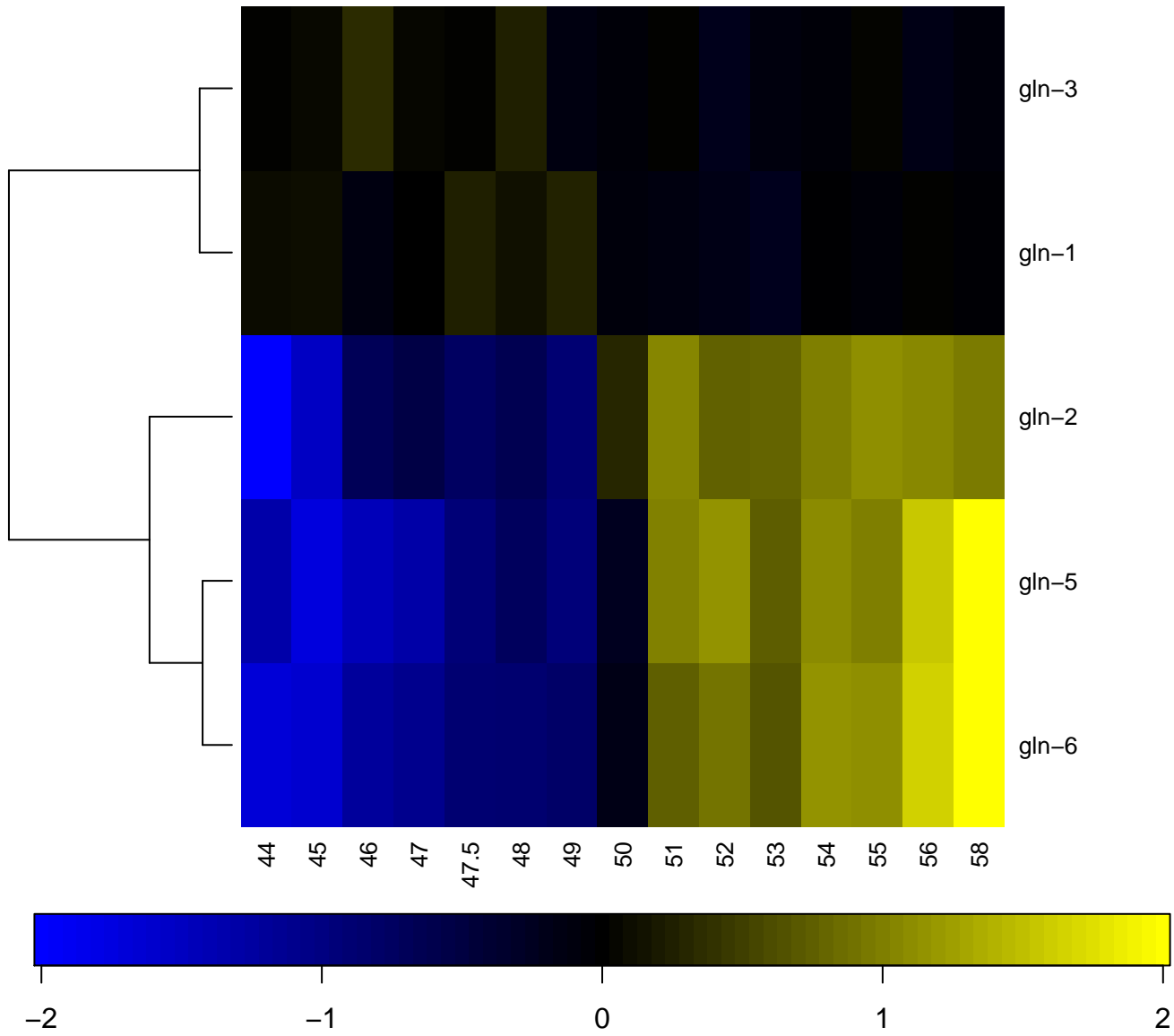
gluconeogenesis



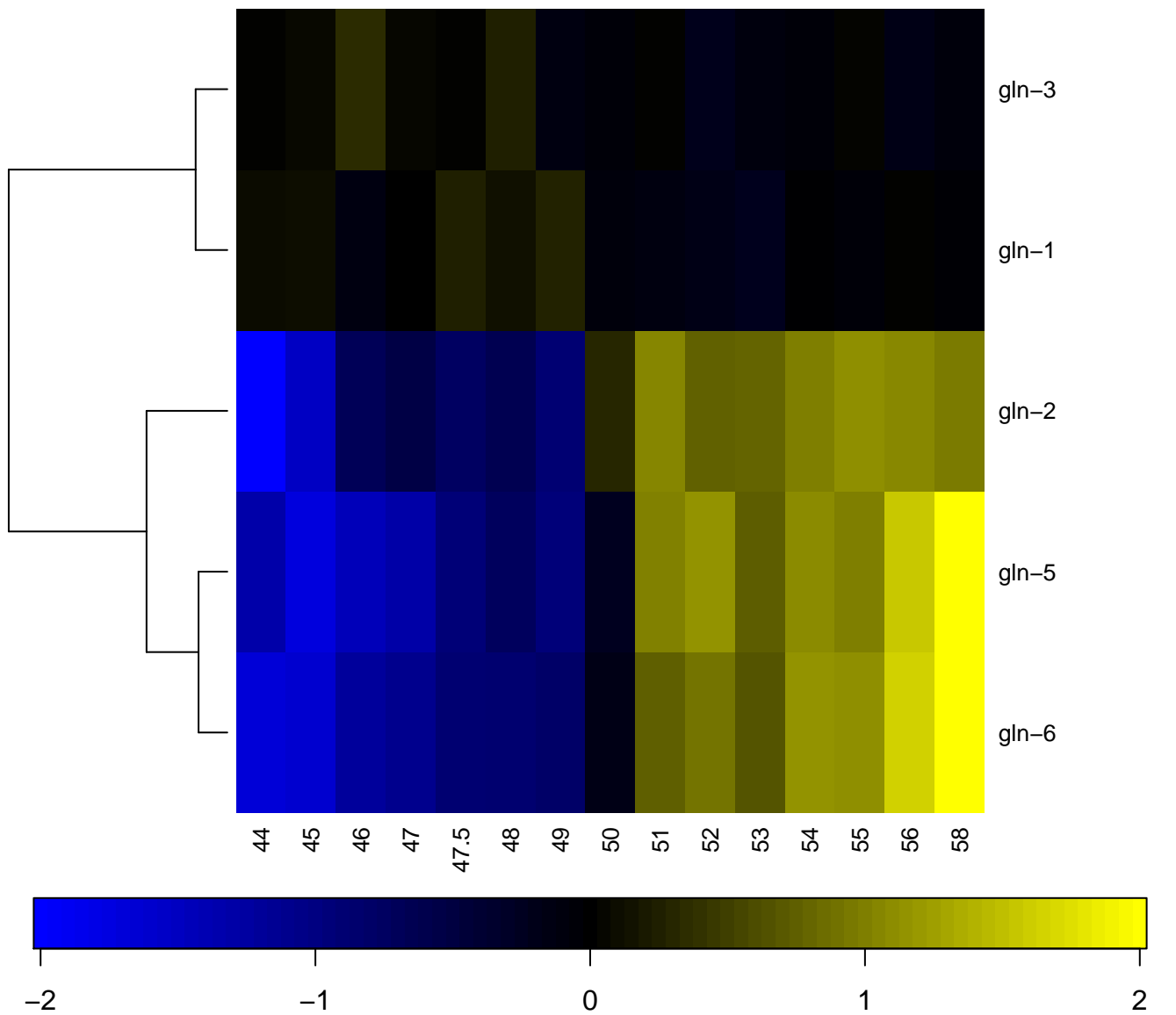
glucosylceramidase activity



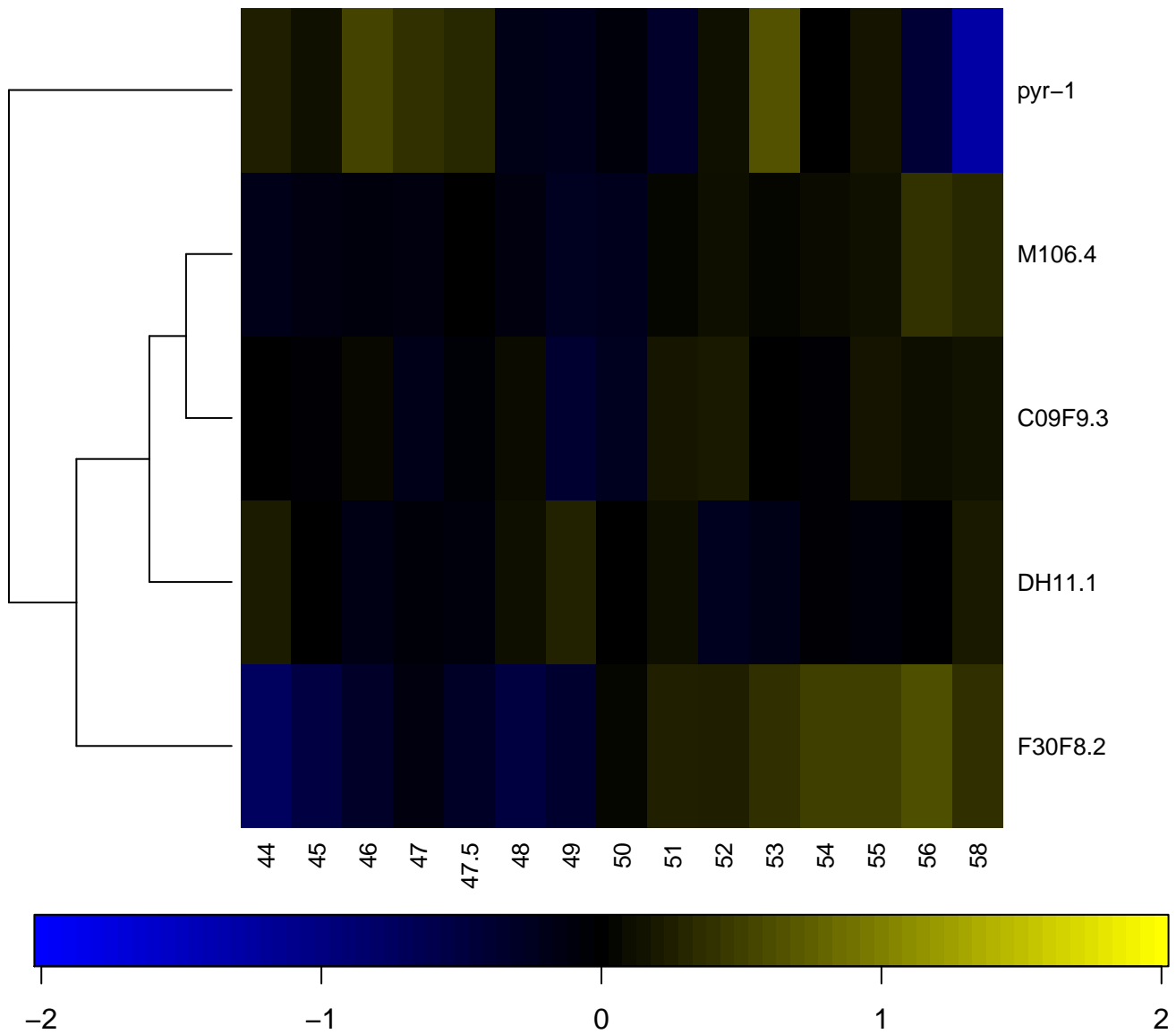
glutamate-ammonia ligase activity



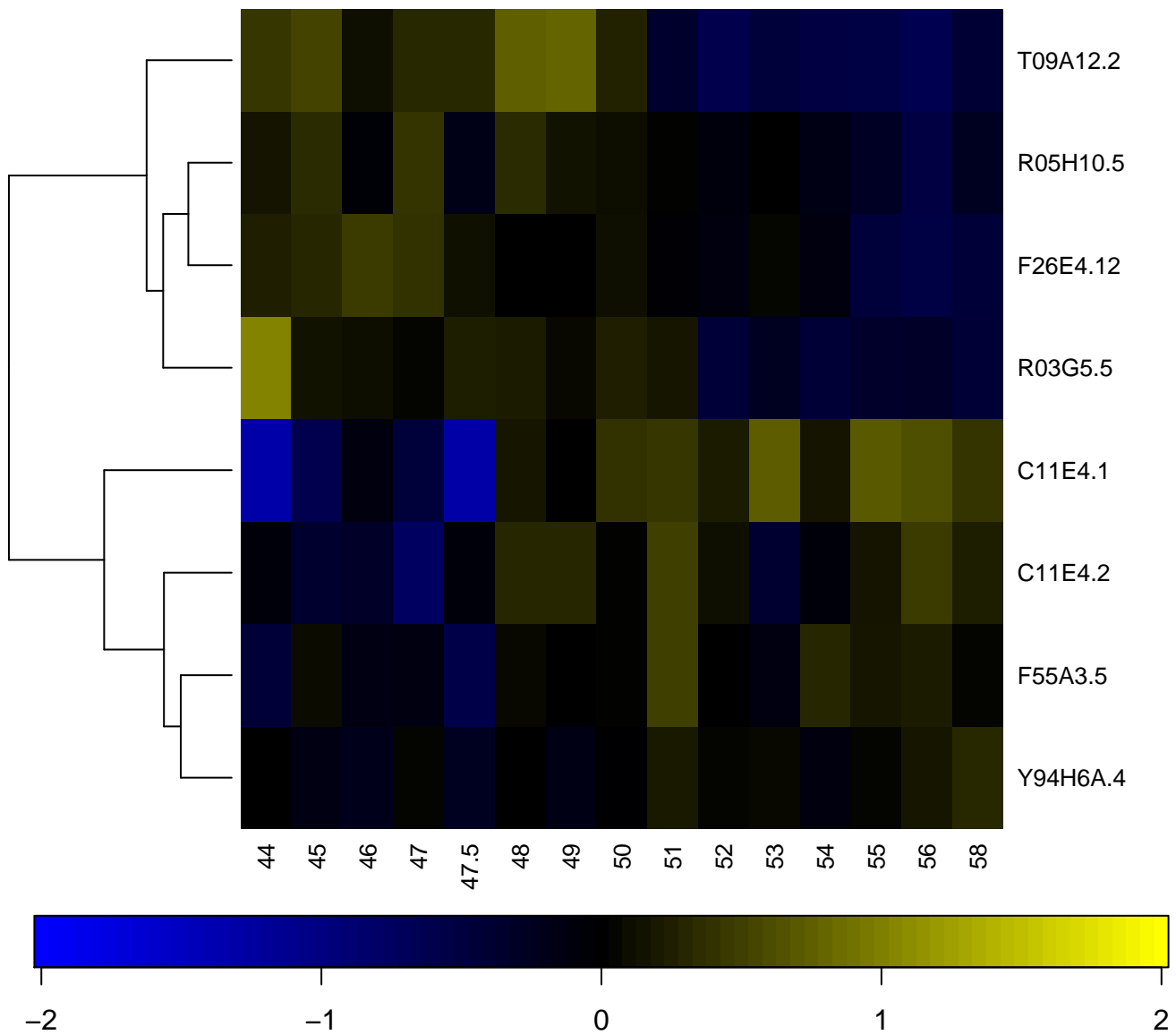
glutamine biosynthetic process



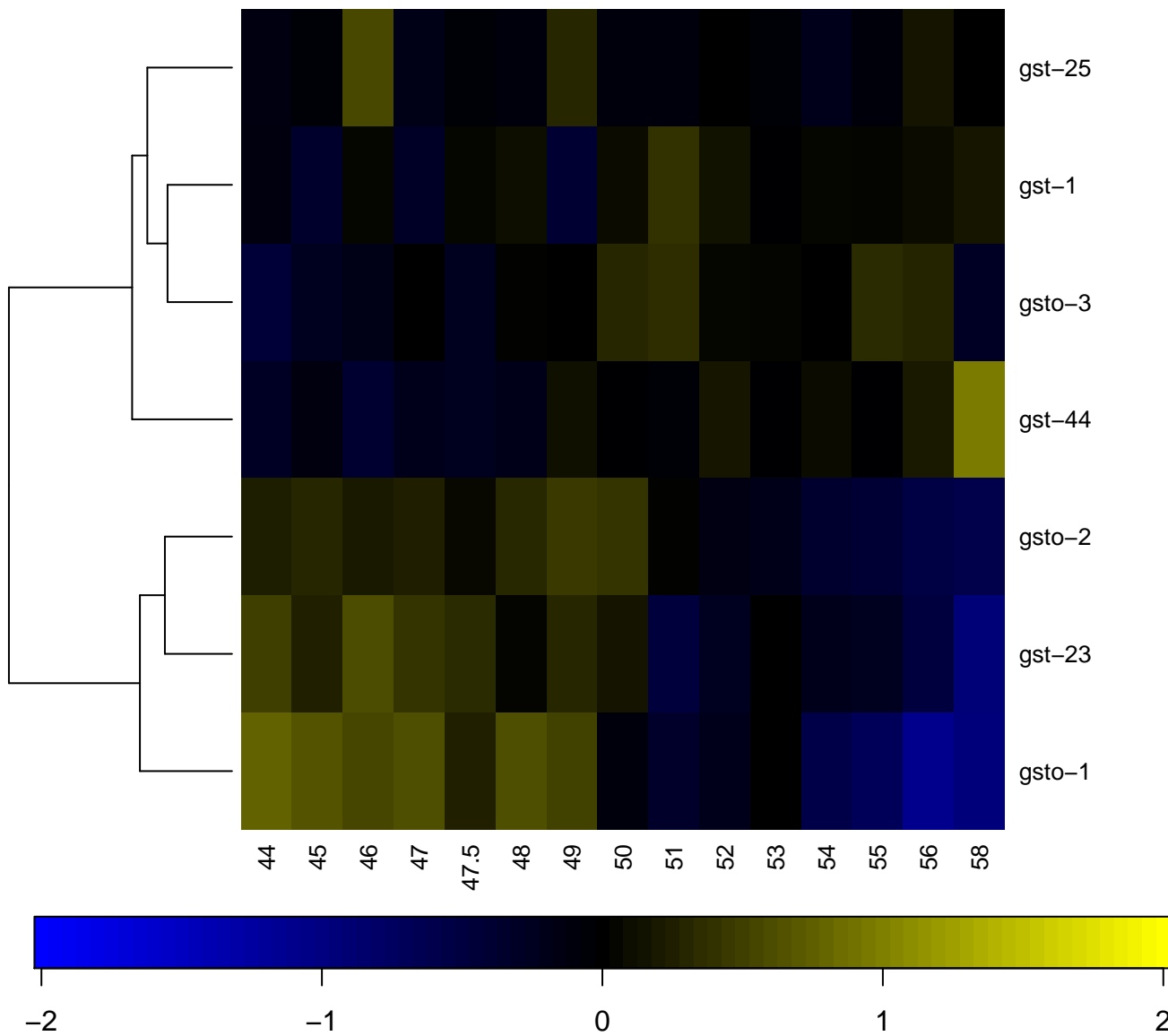
glutamine metabolic process



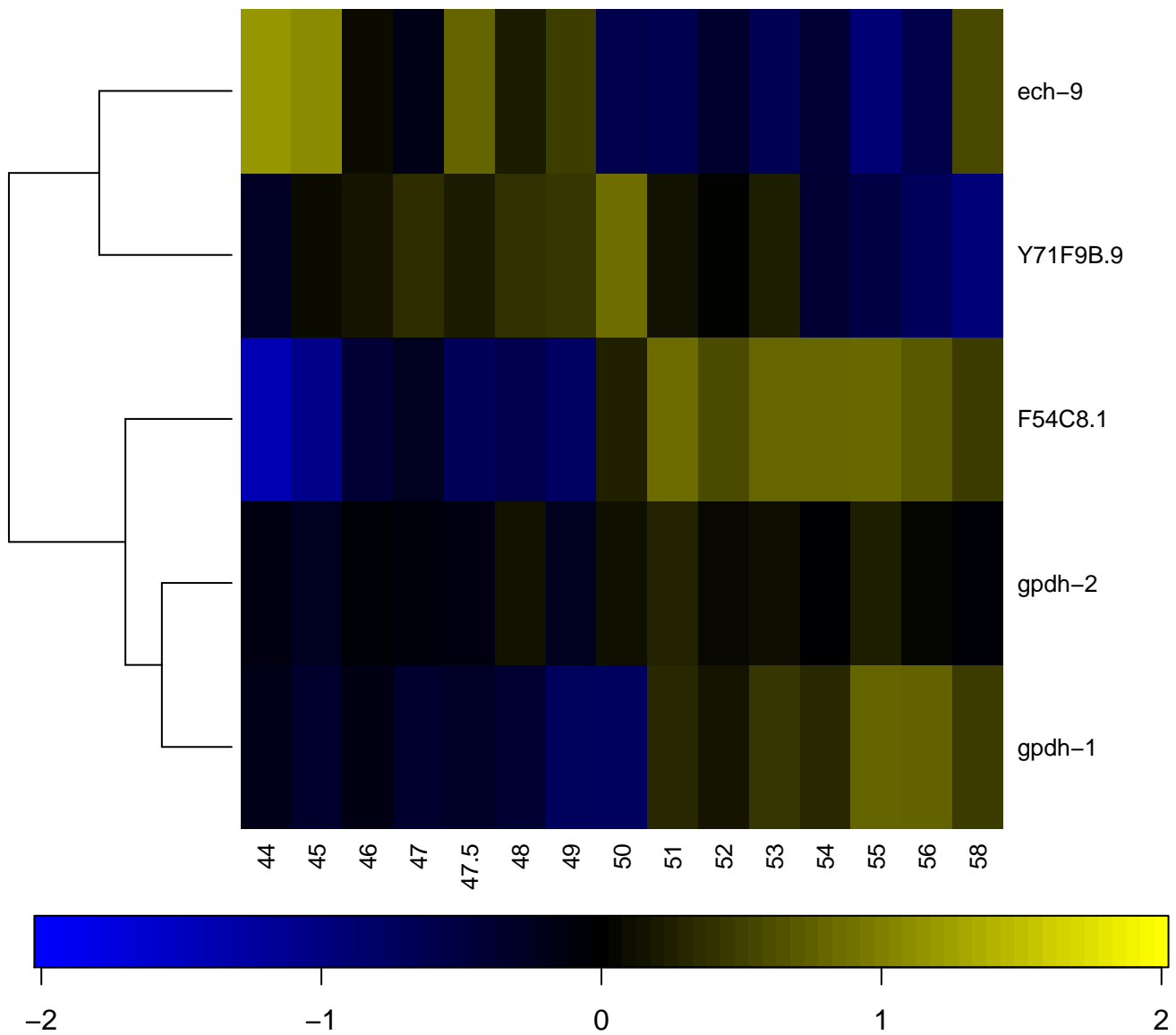
glutathione peroxidase activity



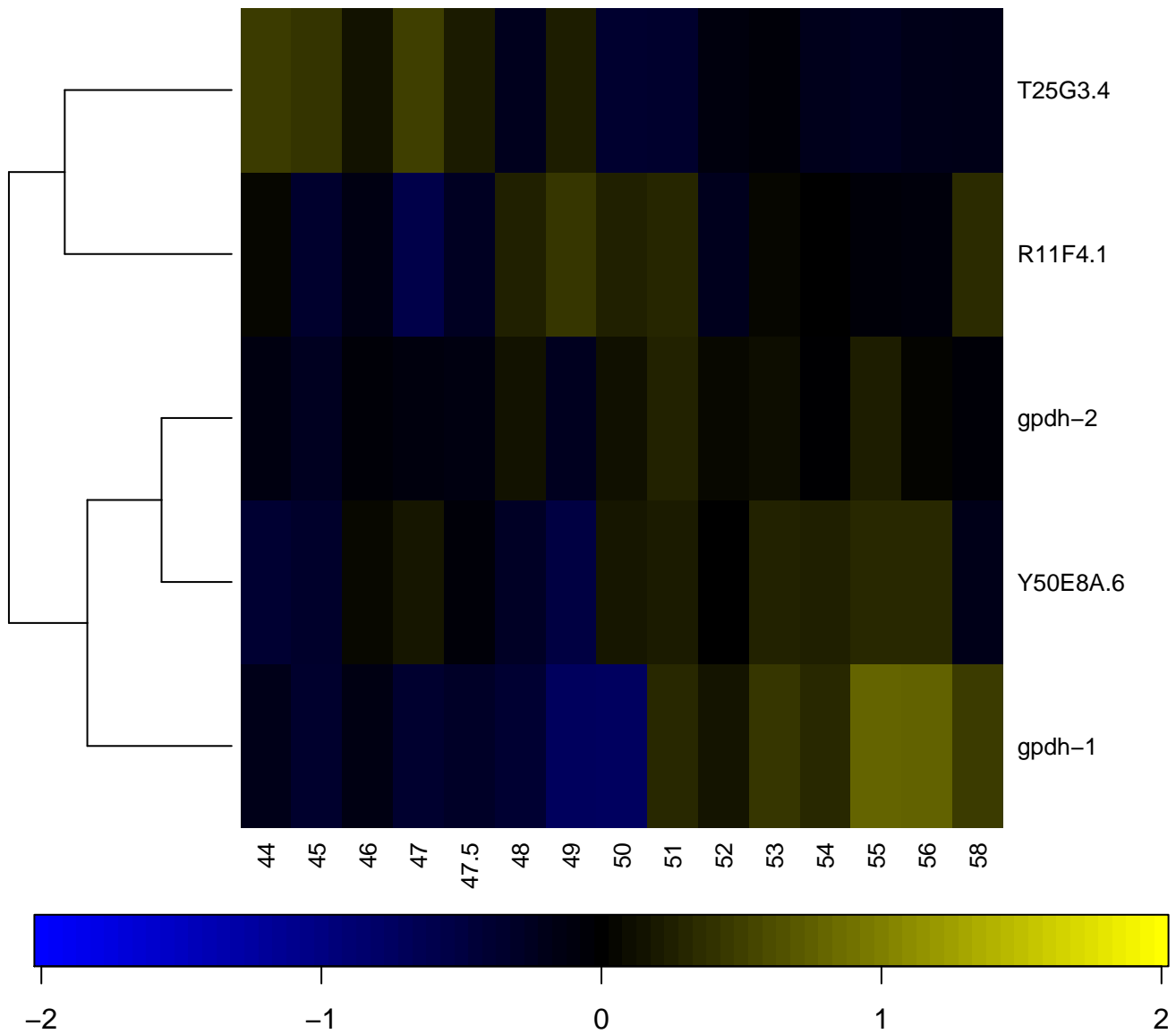
glutathione transferase activity



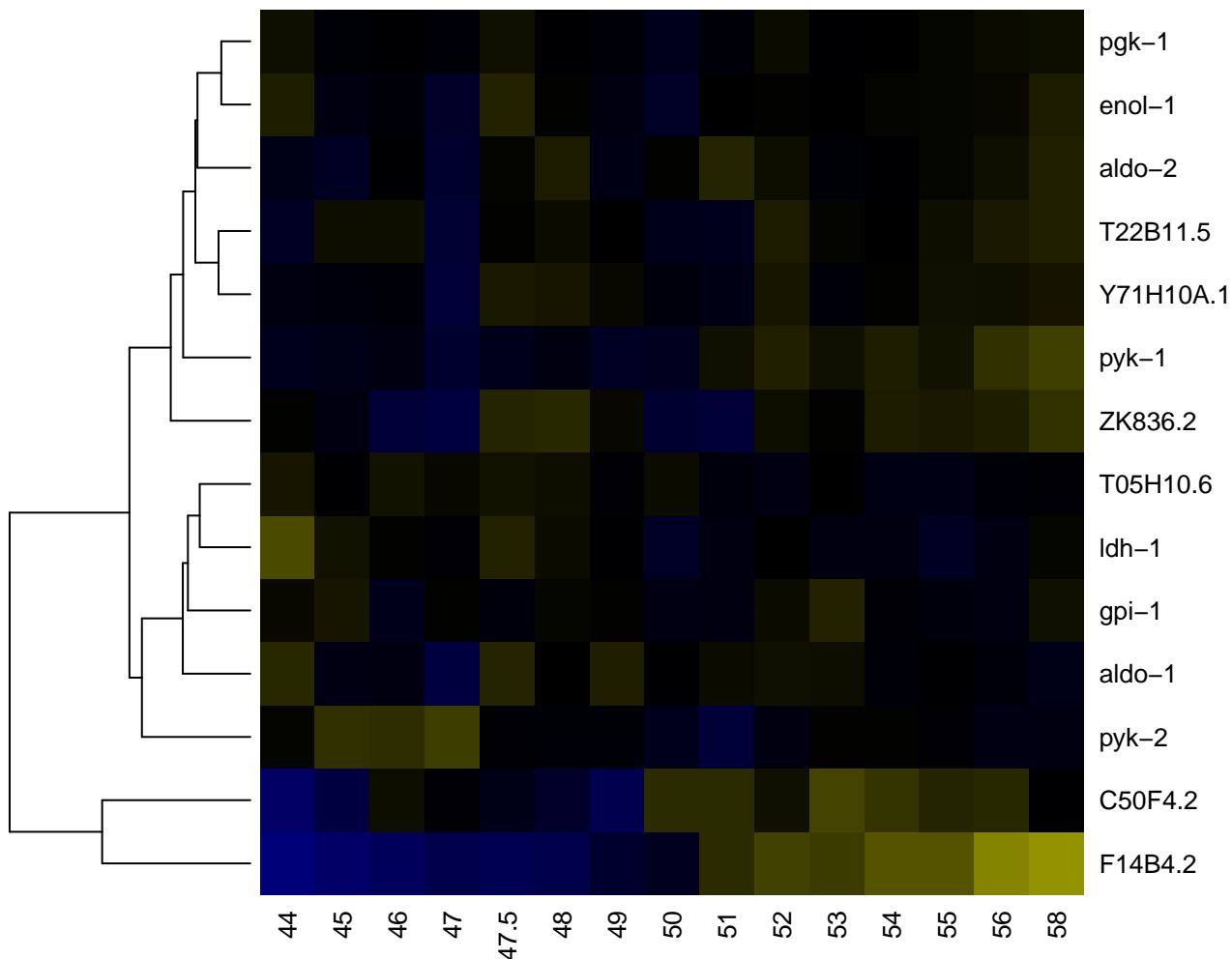
glycerol-3-phosphate catabolic process



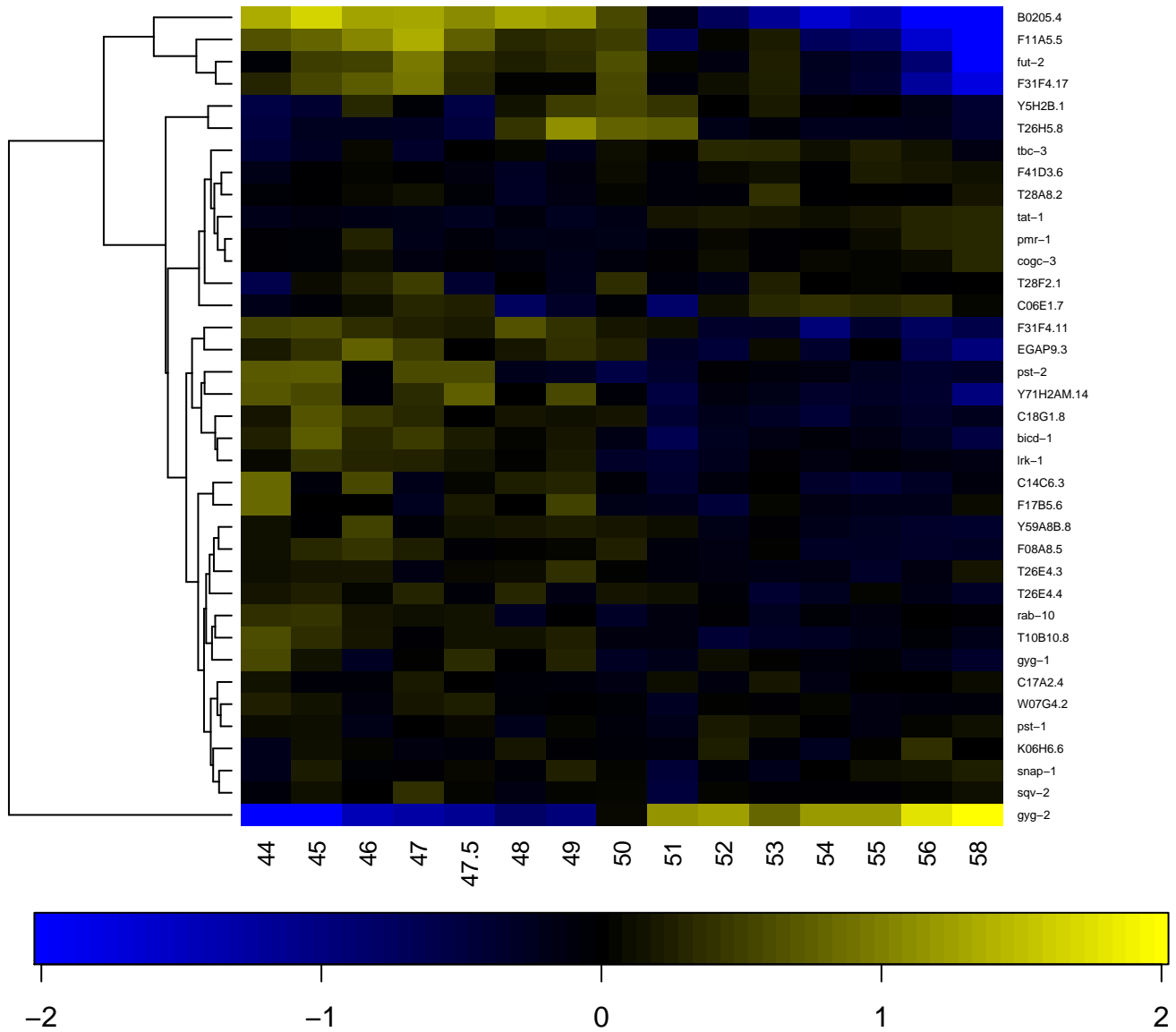
glycerol-3-phosphate metabolic process



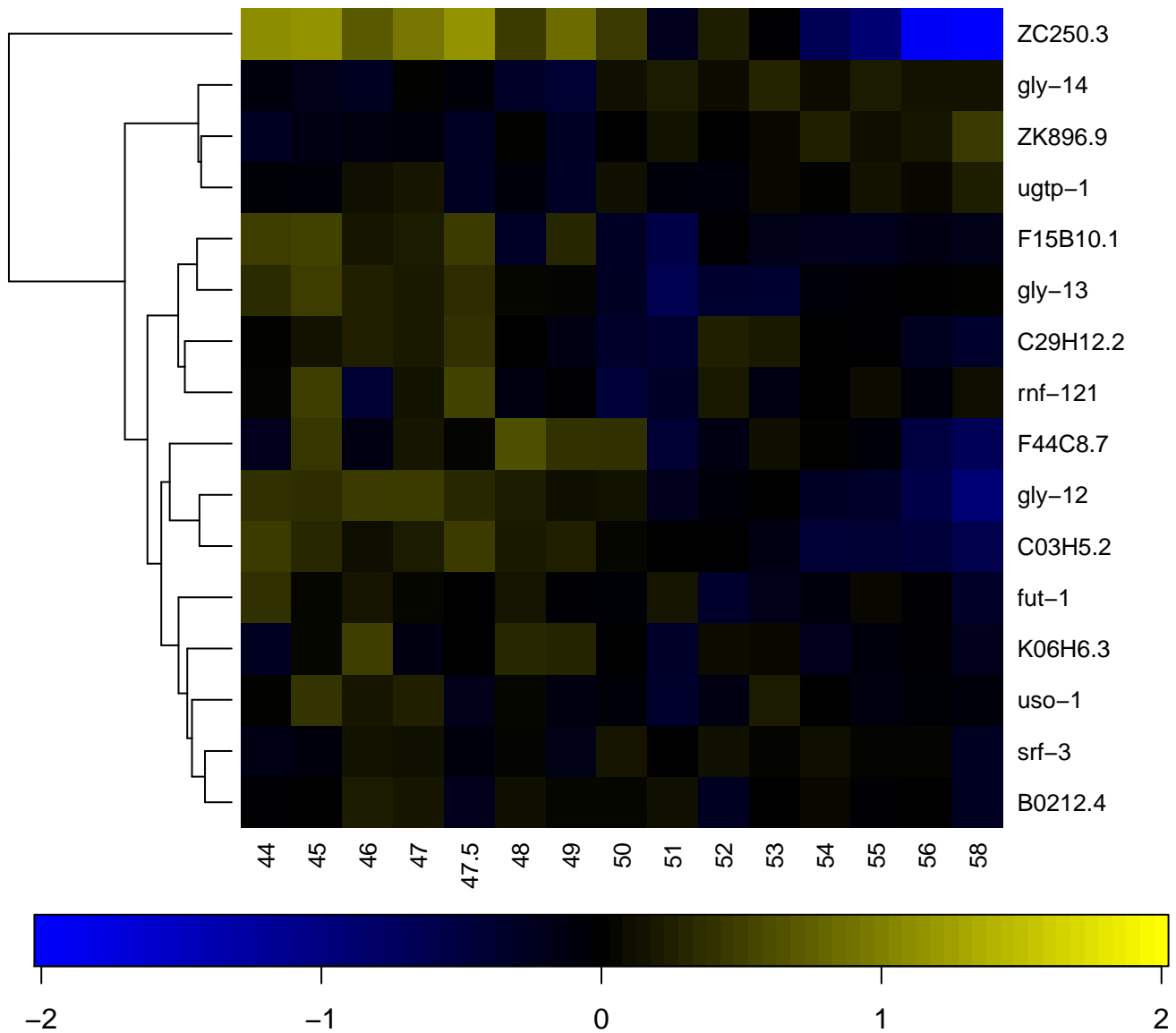
glycolysis



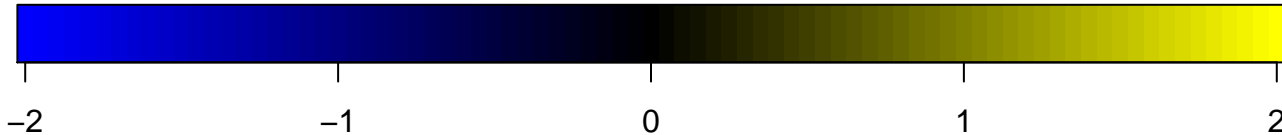
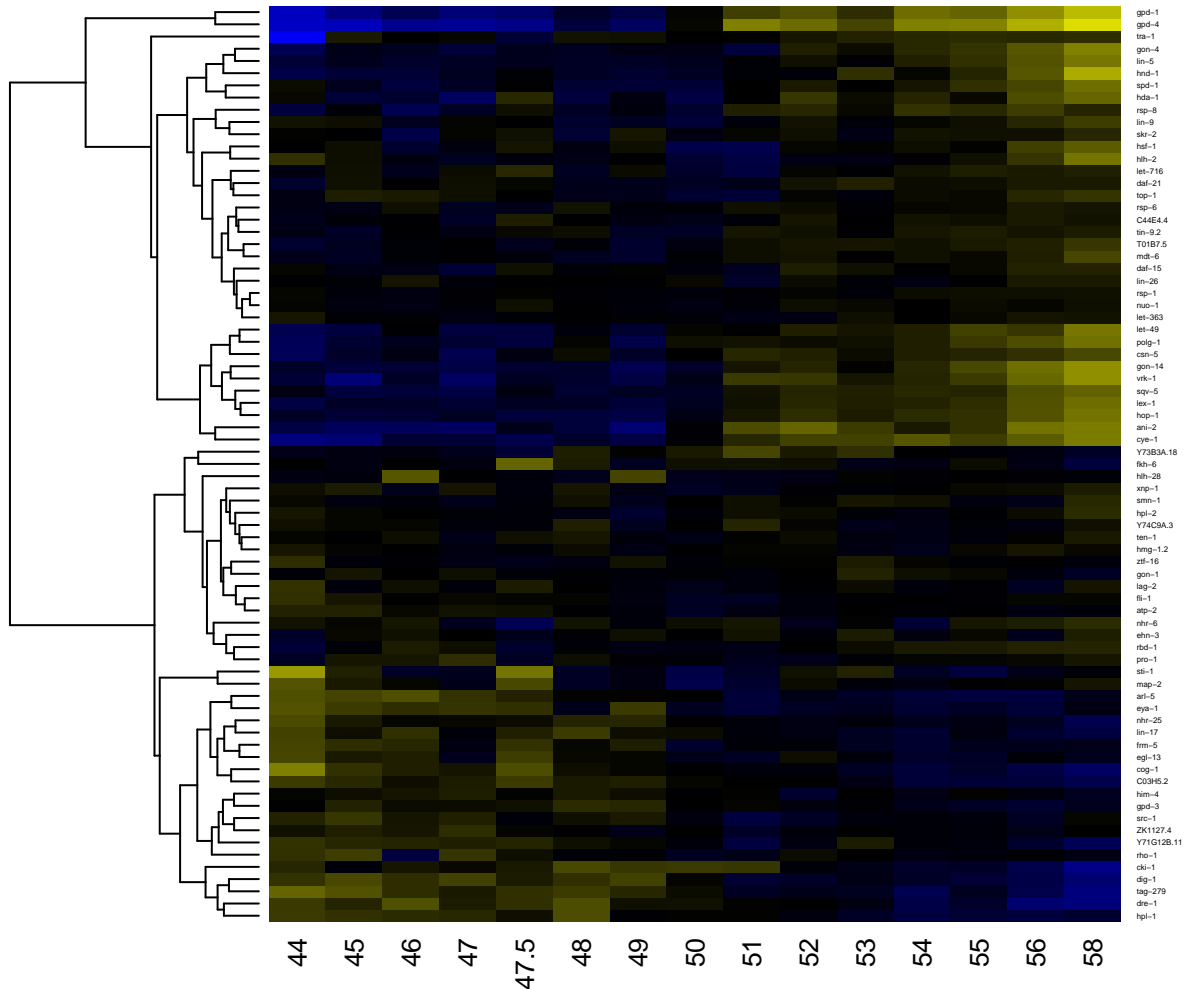
Golgi apparatus



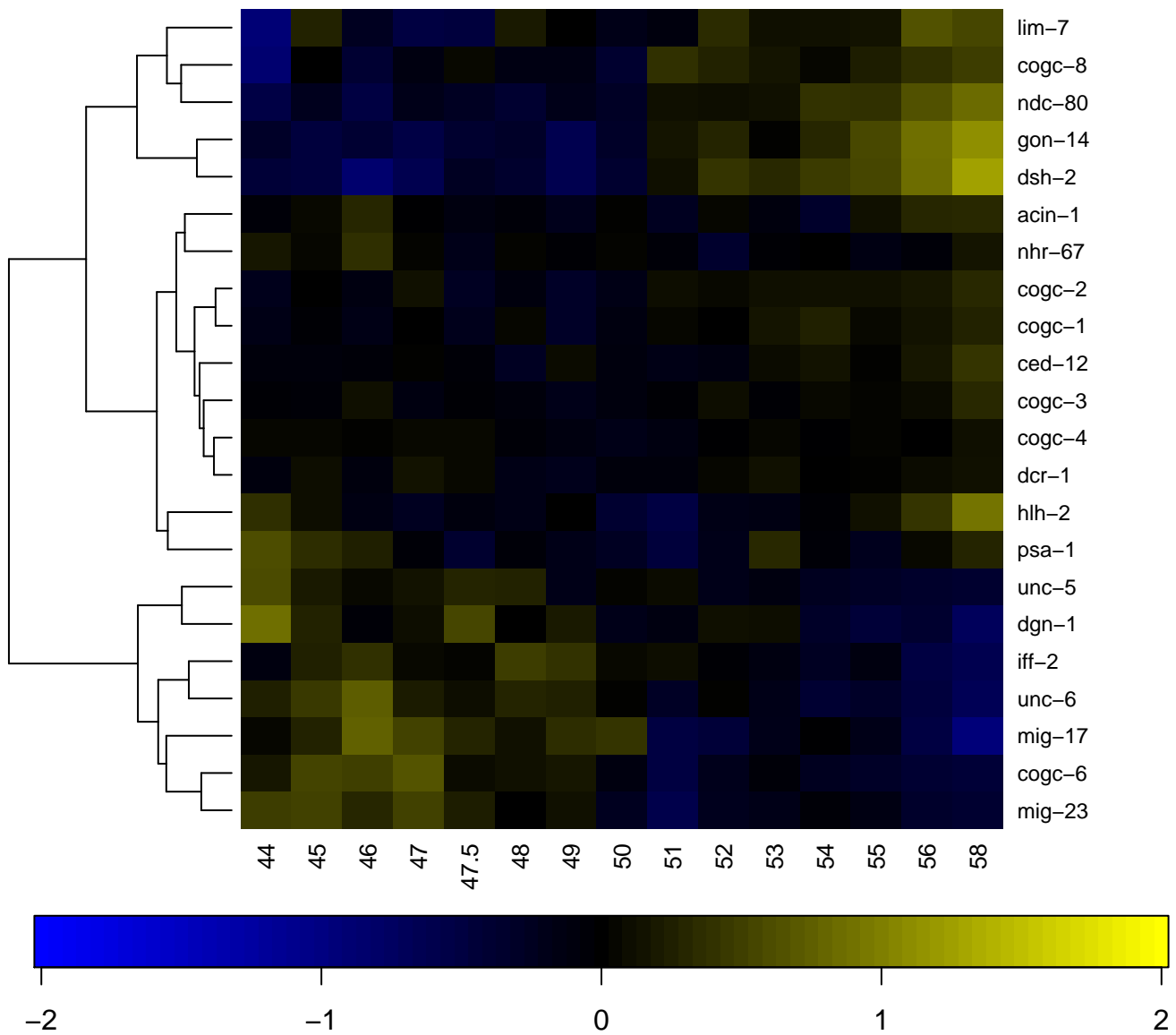
Golgi membrane



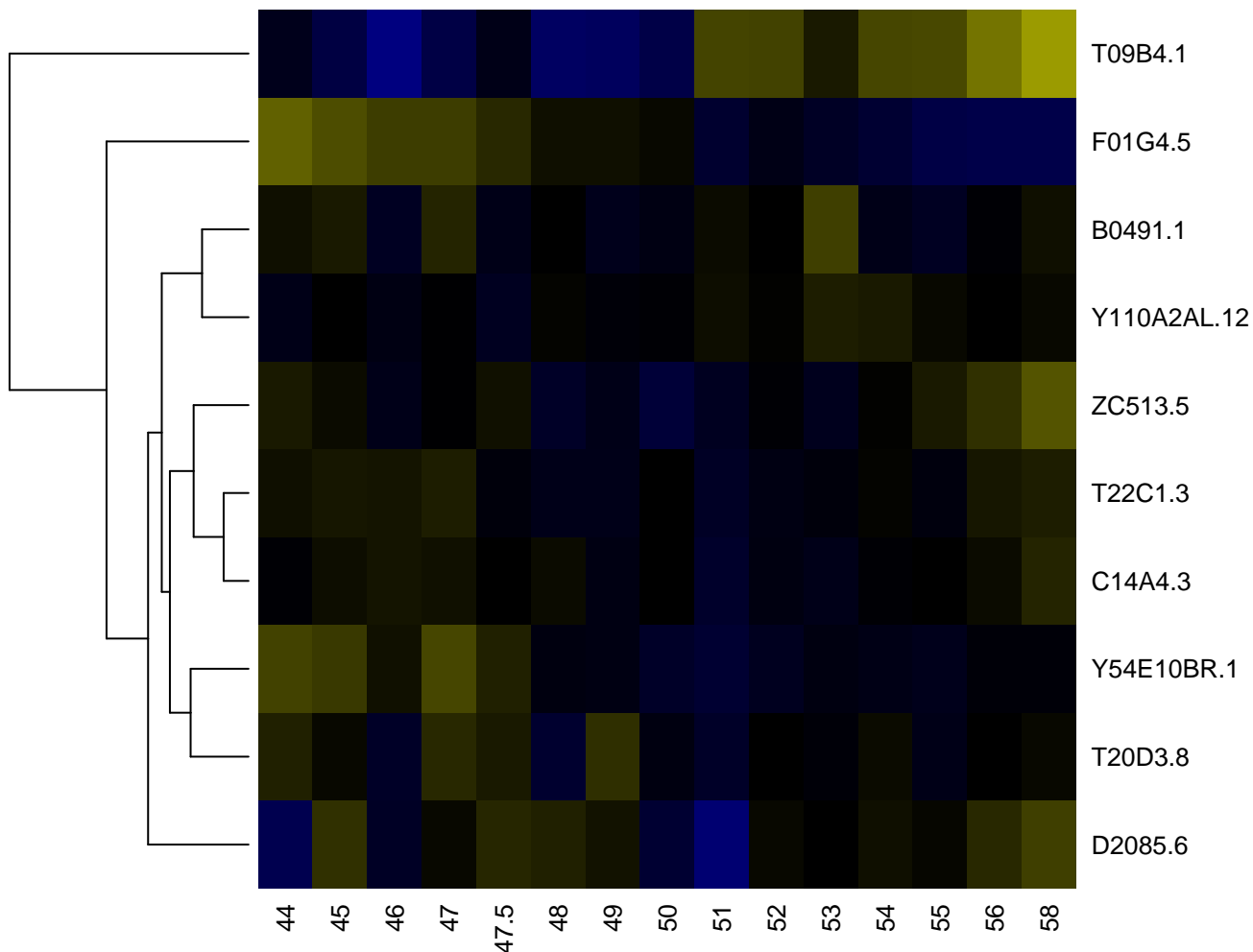
gonad development



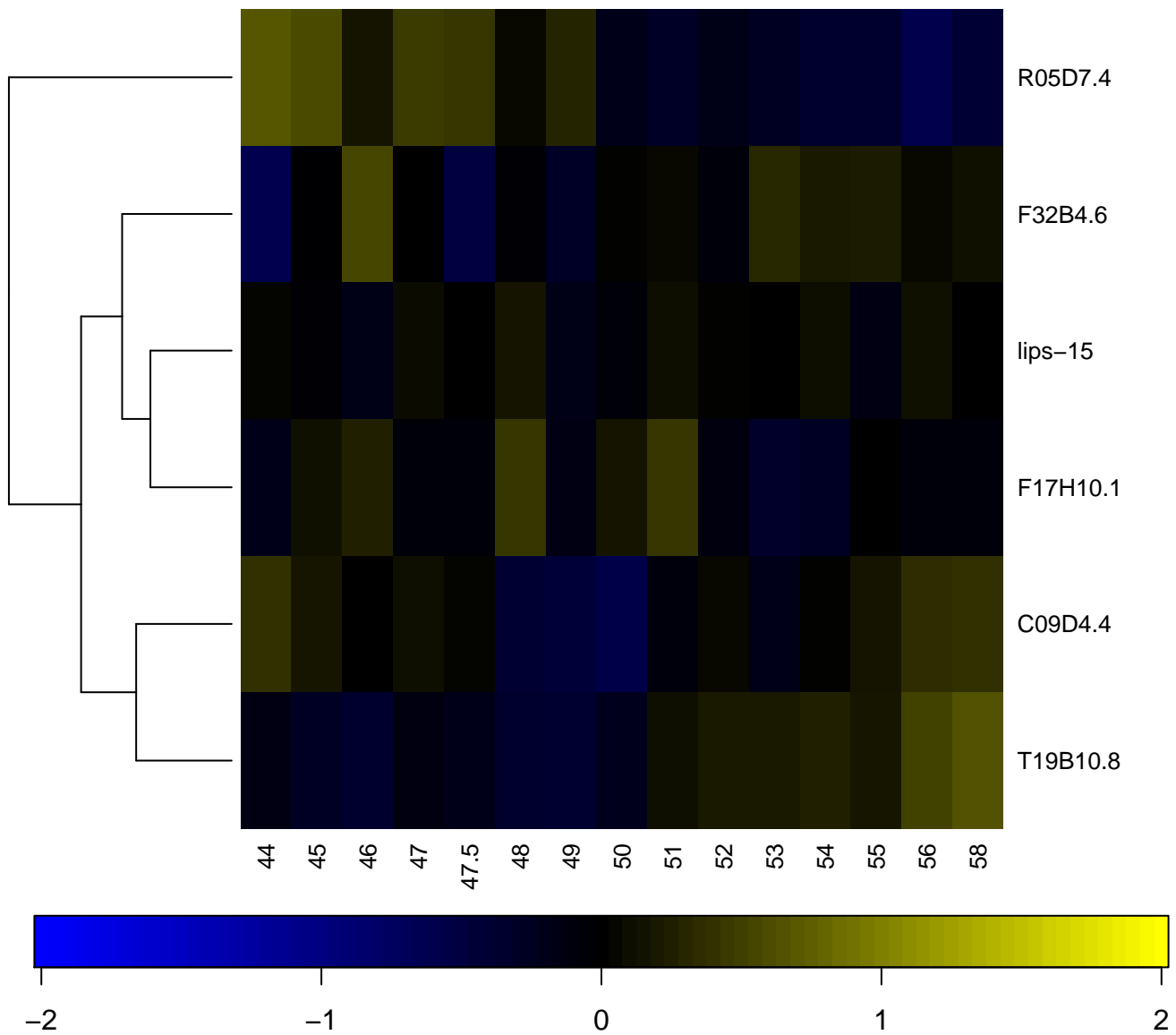
gonad morphogenesis



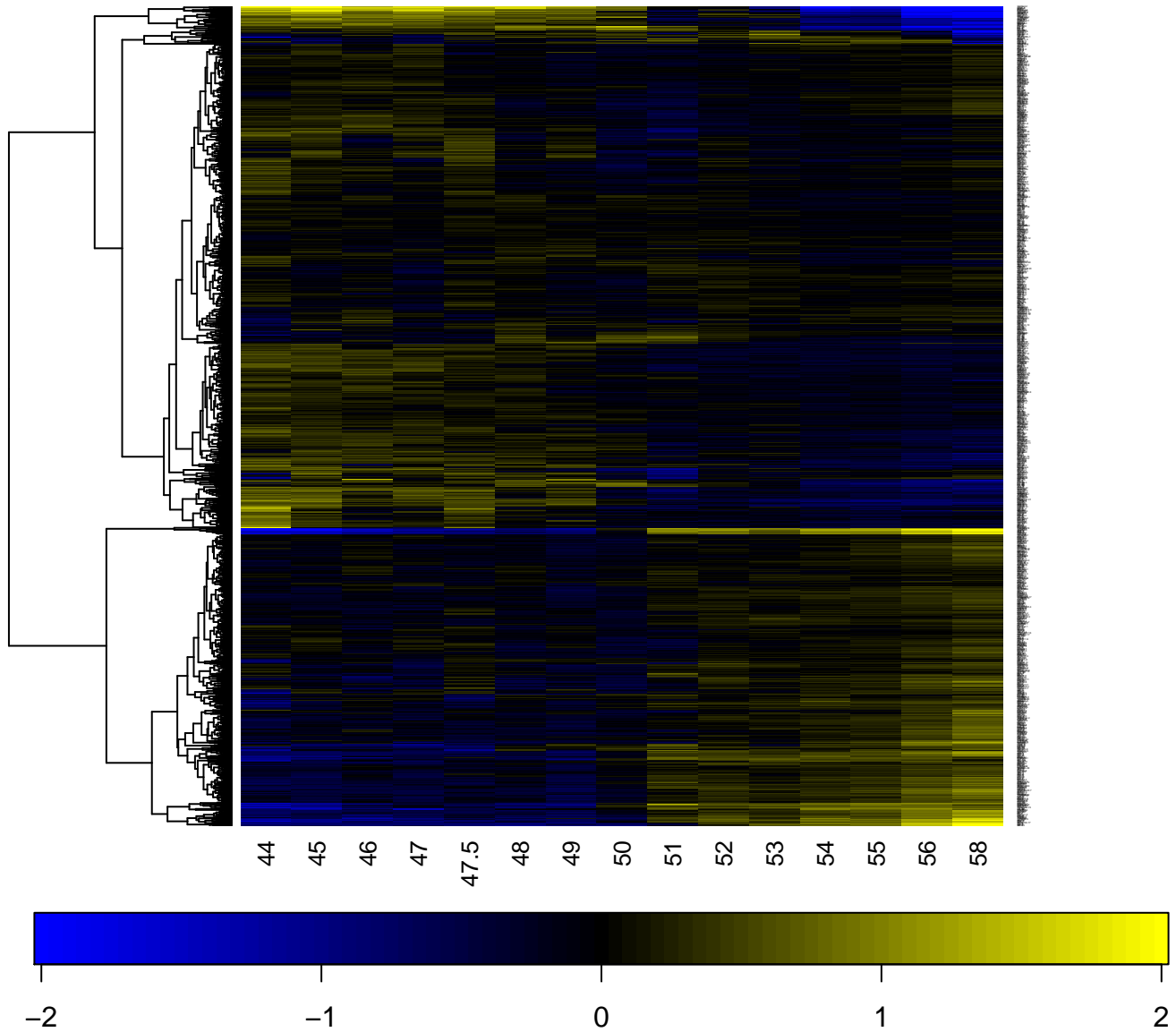
GPI anchor biosynthetic process



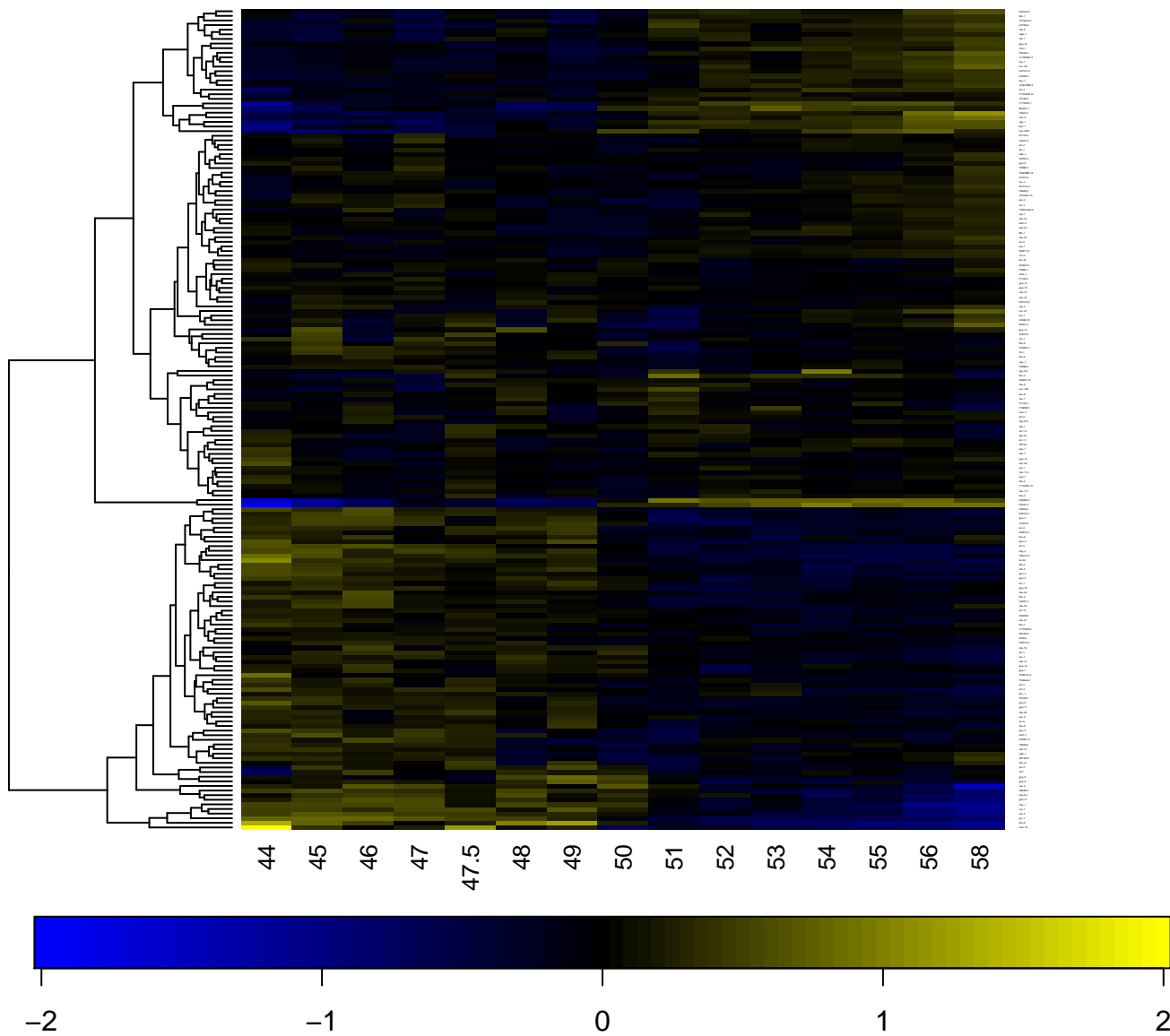
GPI anchor metabolic process



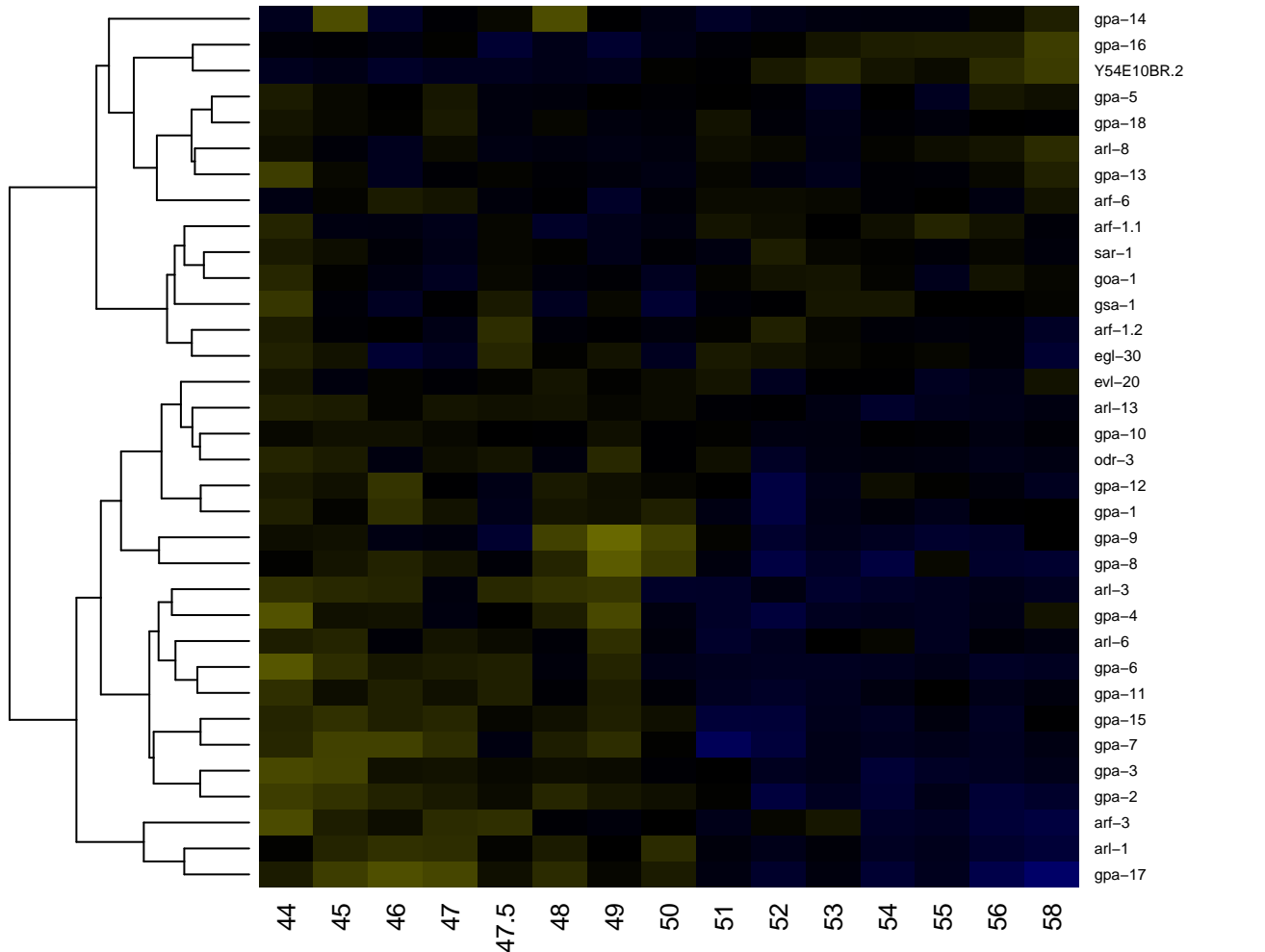
growth



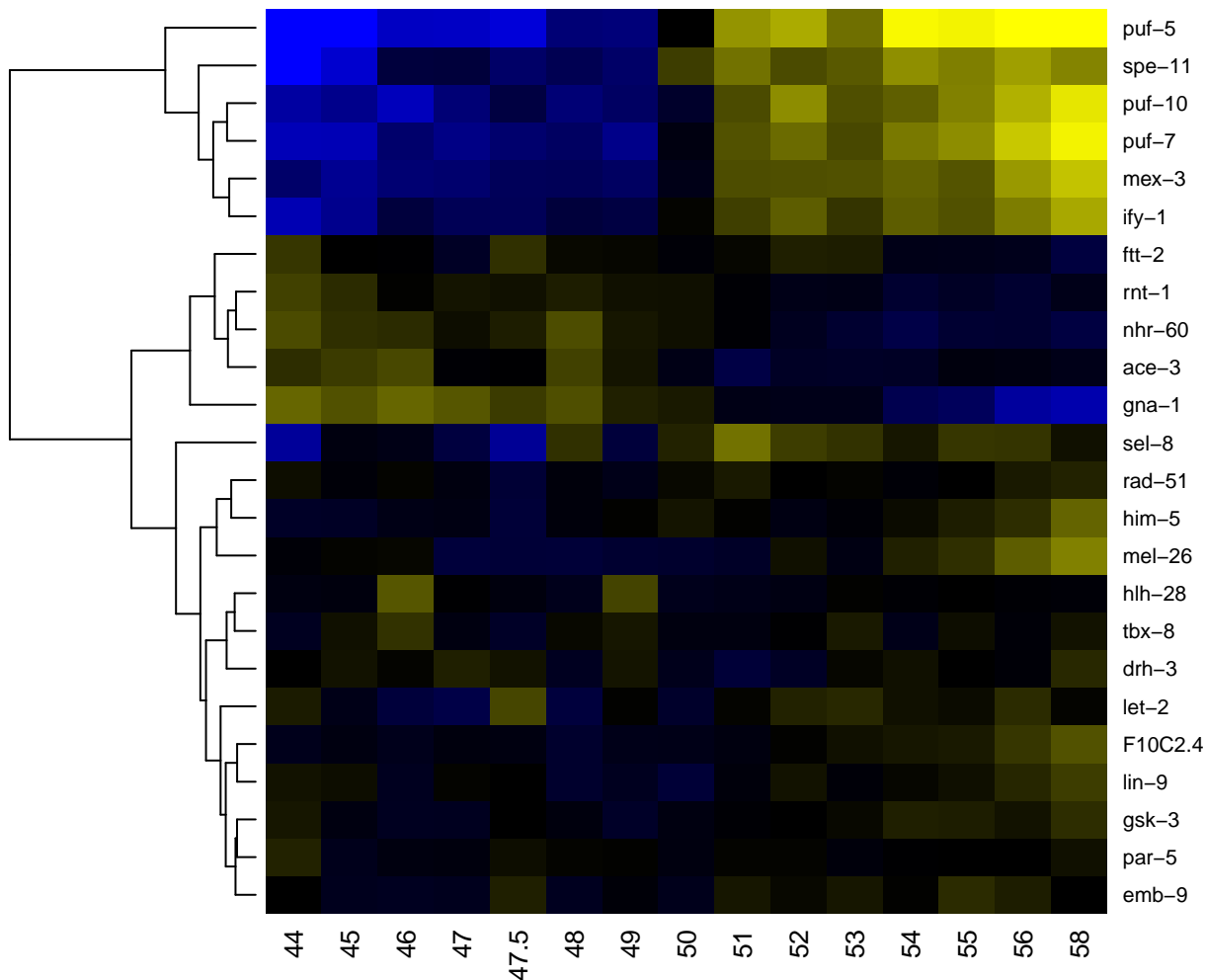
GTP binding



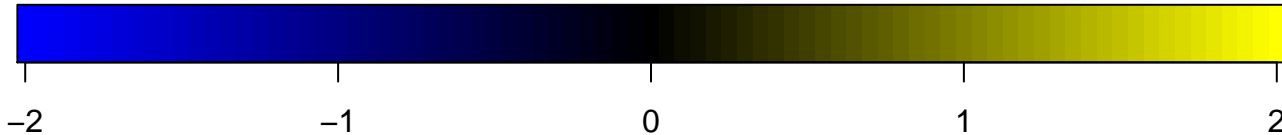
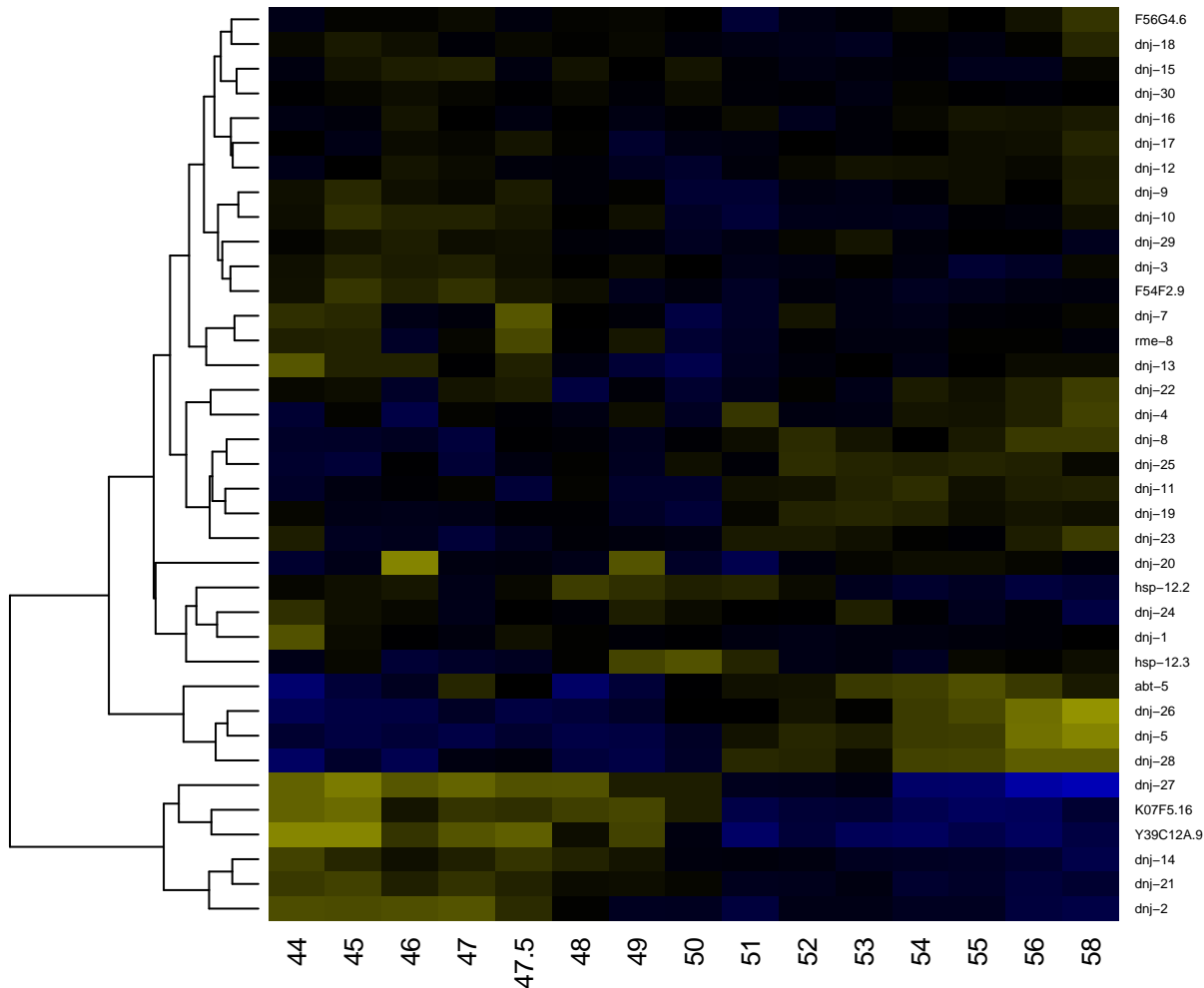
guanyl nucleotide binding



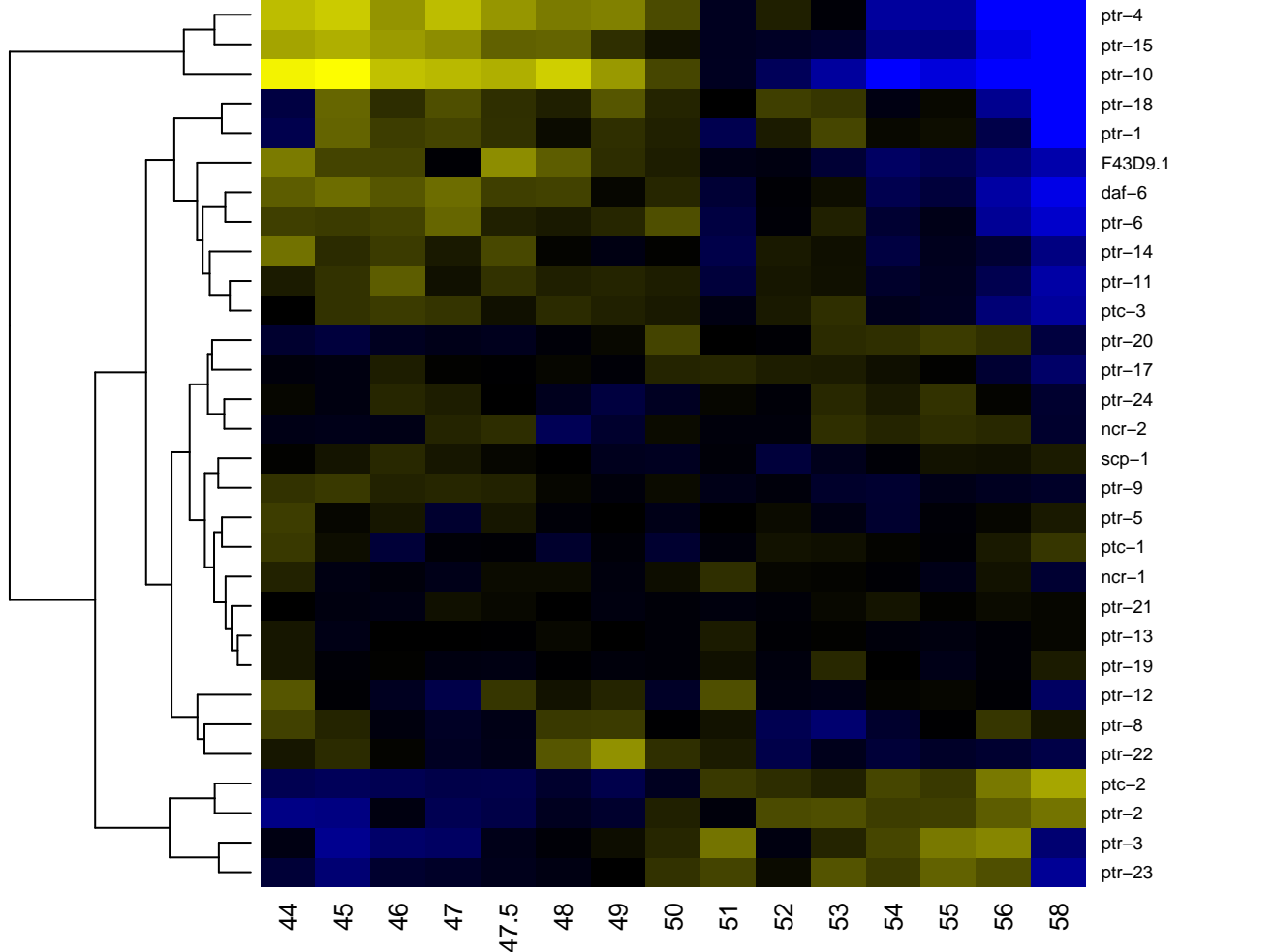
hatching



heat shock protein binding



hedgehog receptor activity



-2

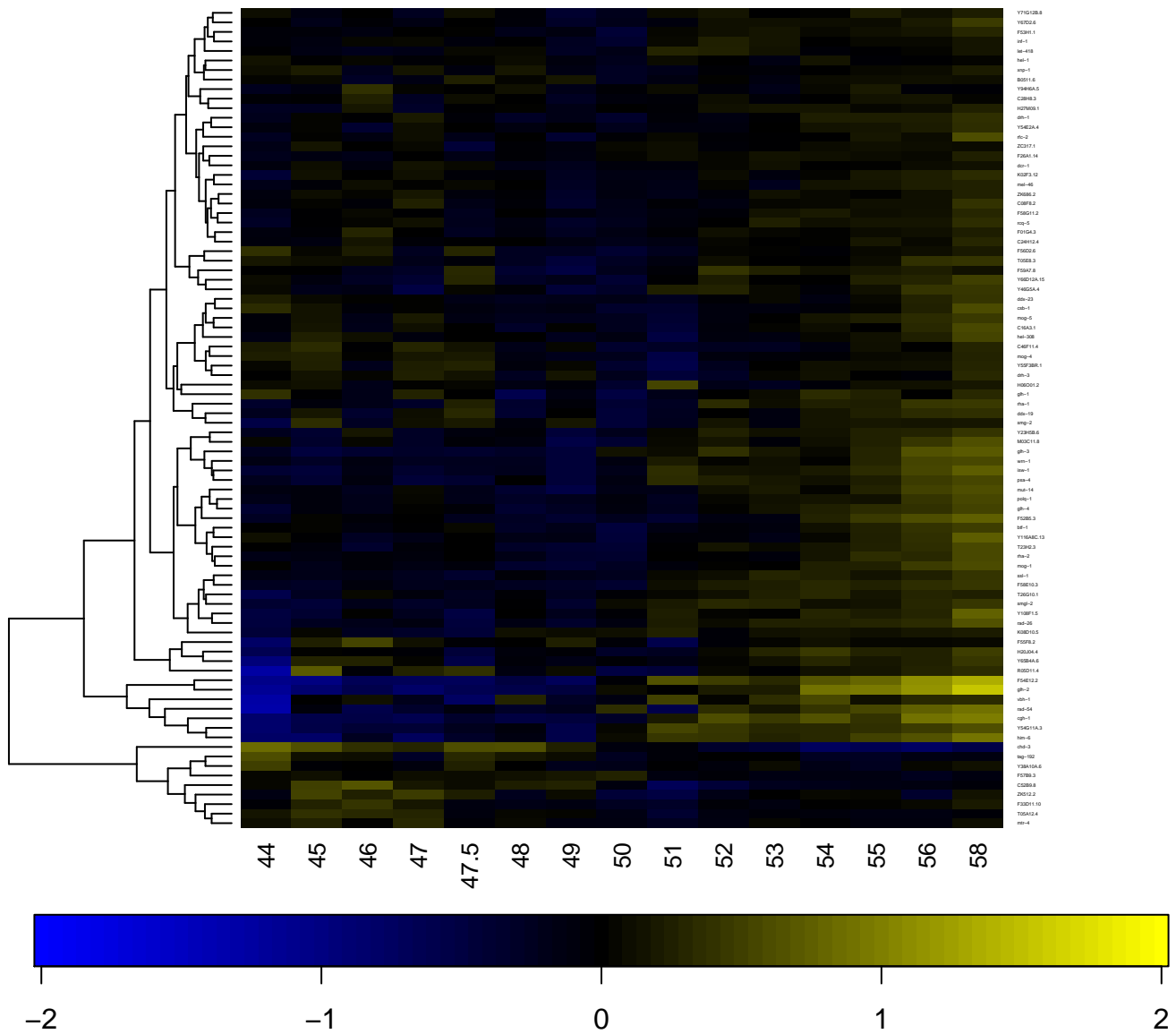
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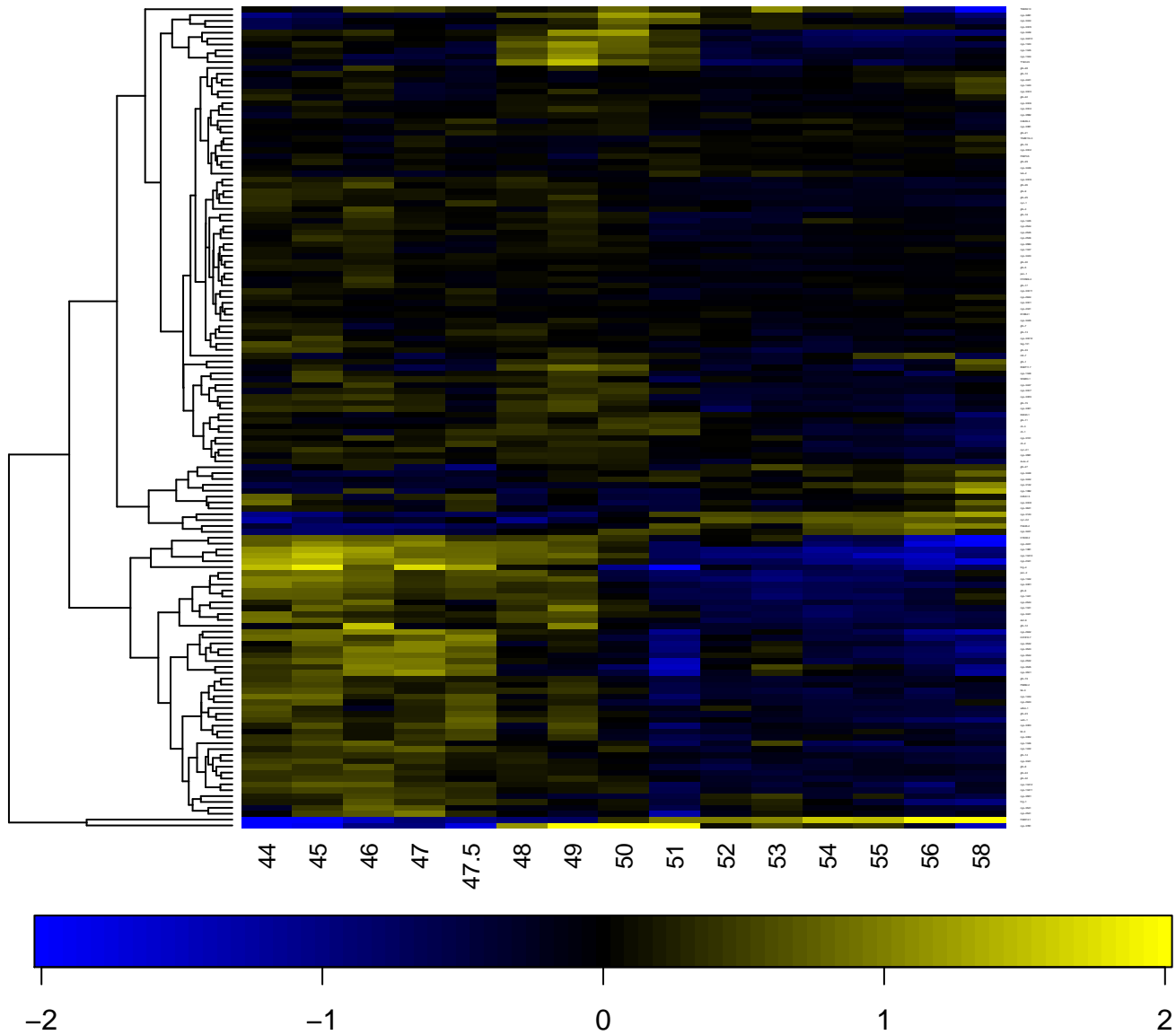
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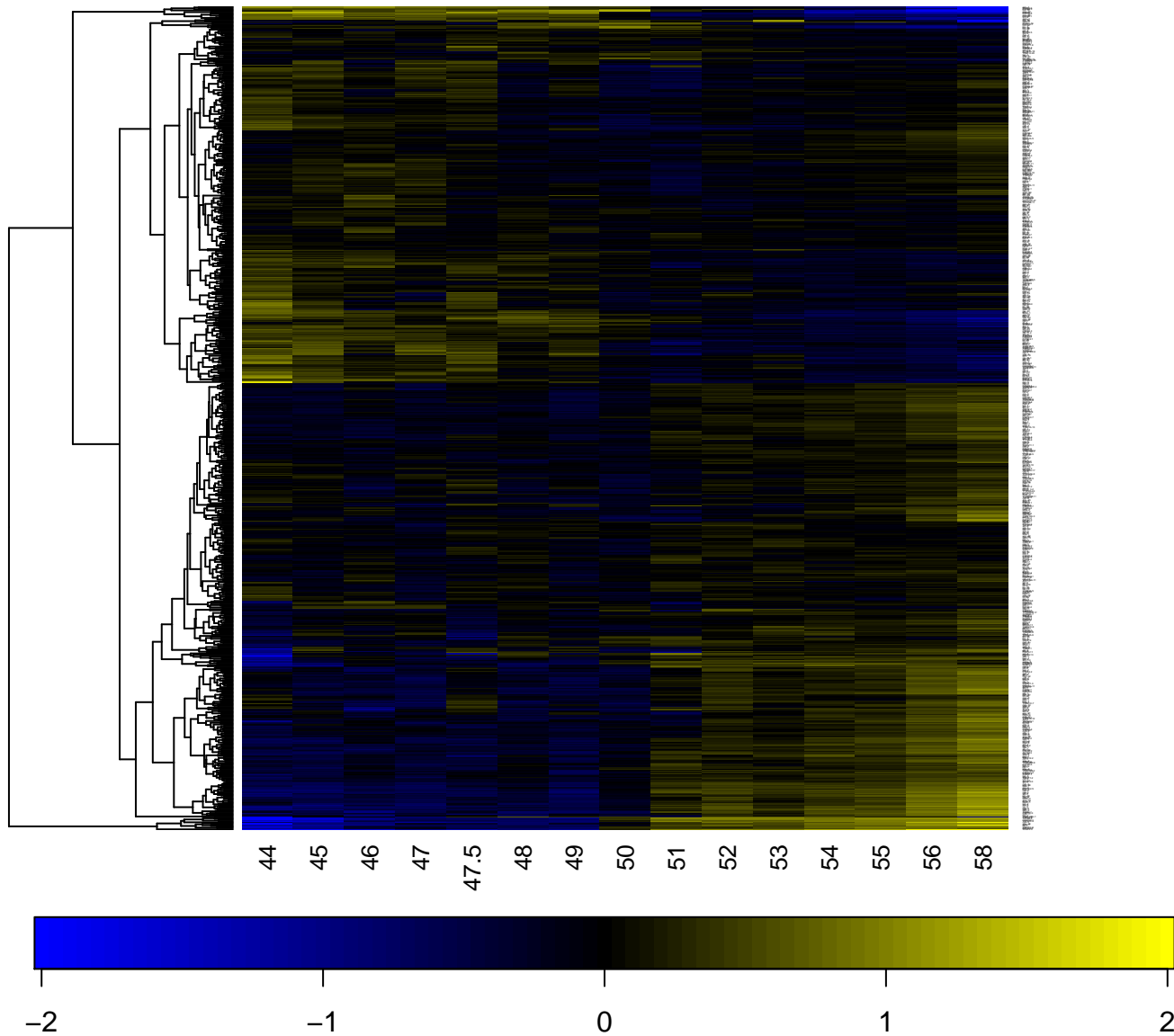
helicase activity



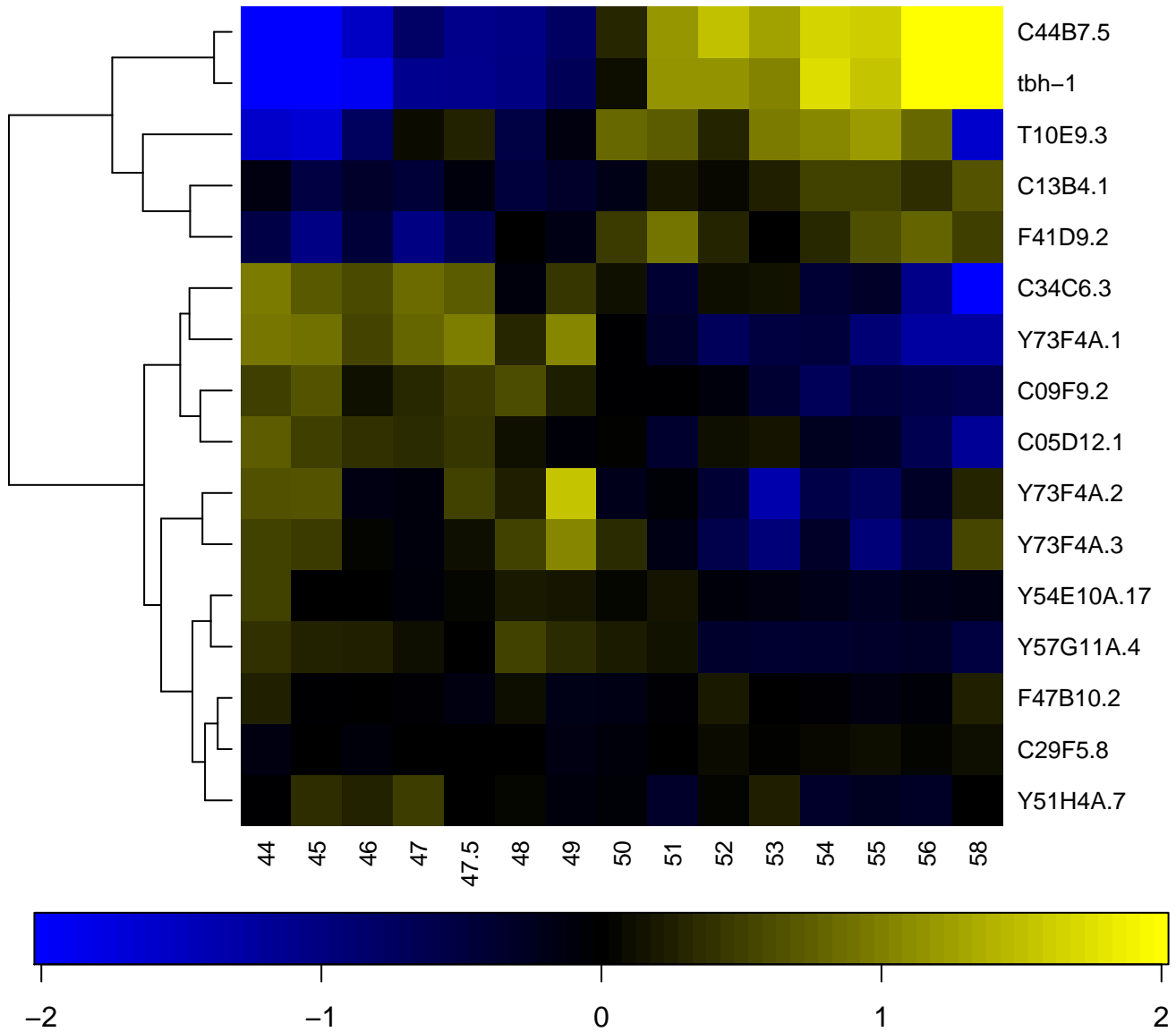
heme binding



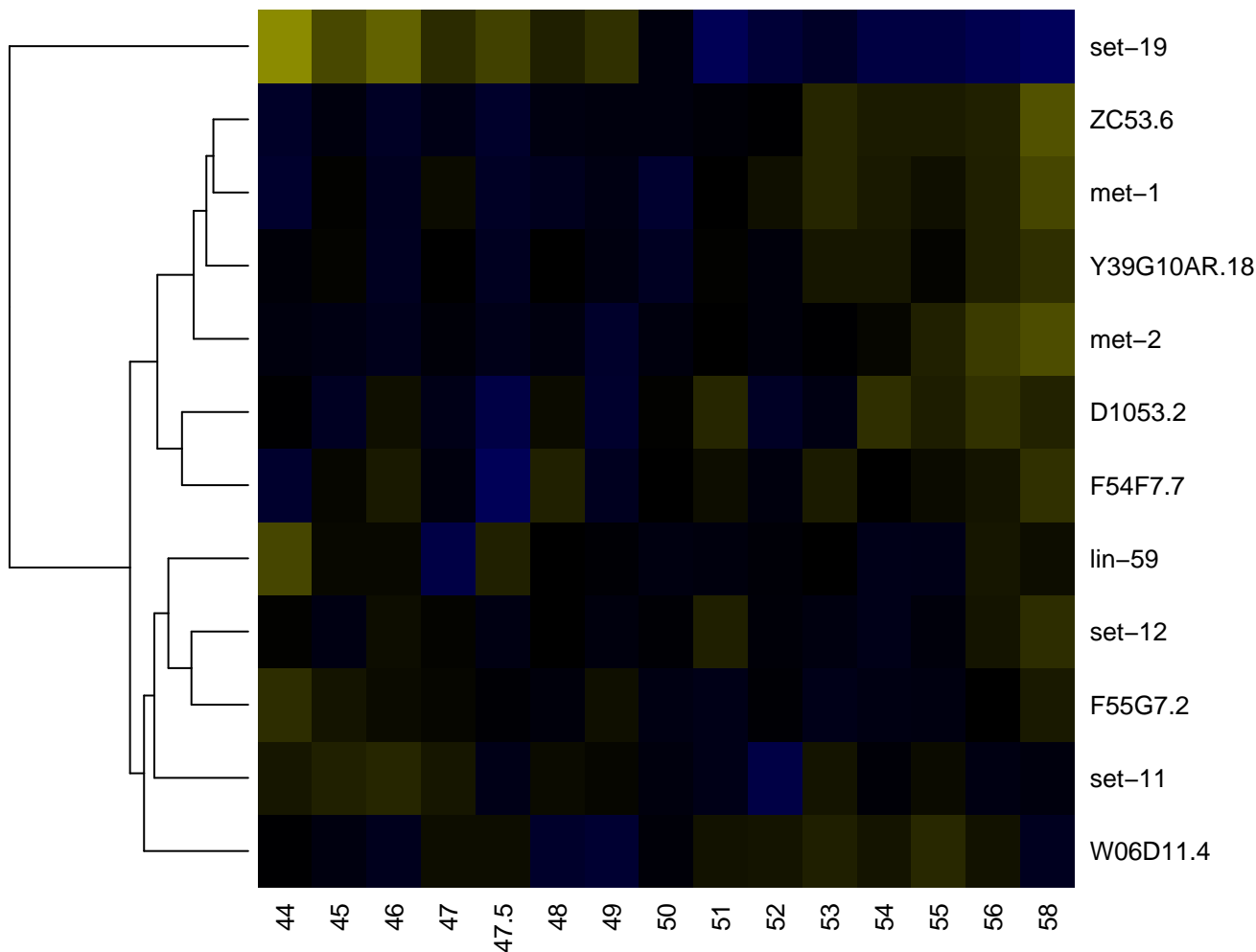
hermaphrodite genitalia development



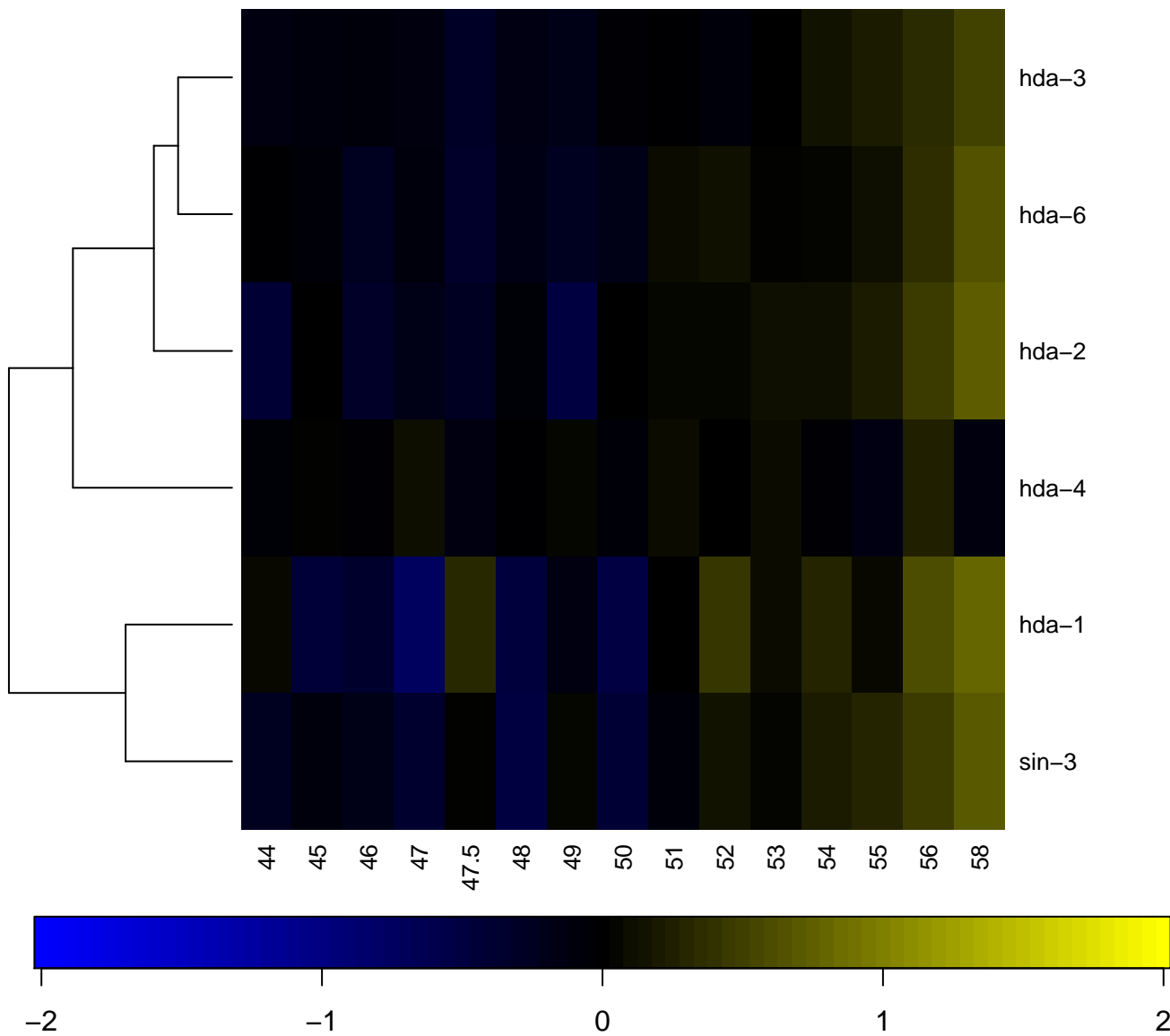
histidine catabolic process



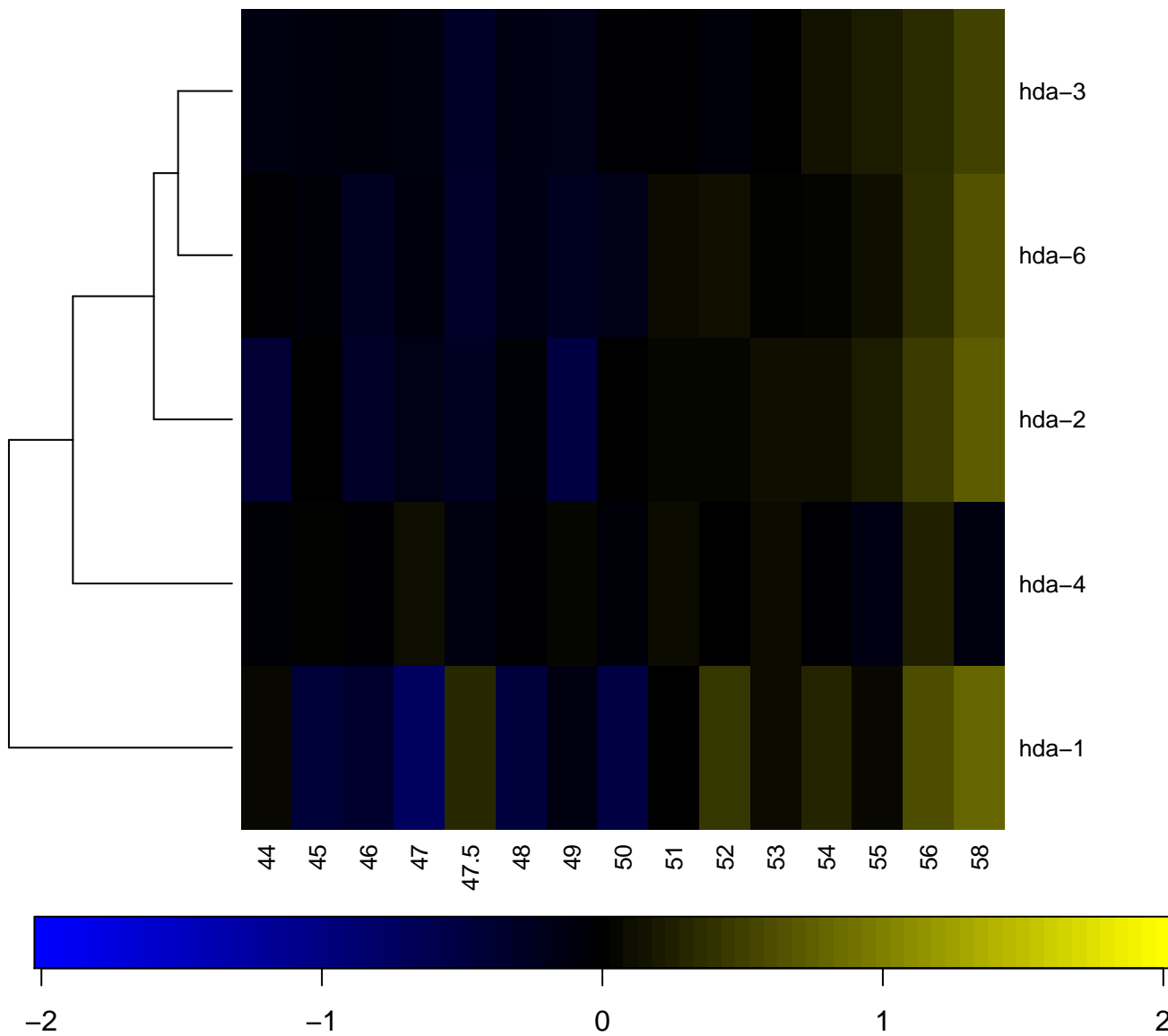
histone-lysine N-methyltransferase activity



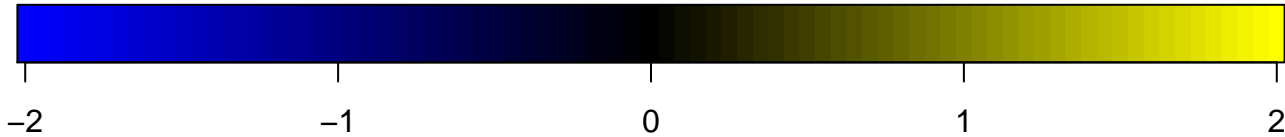
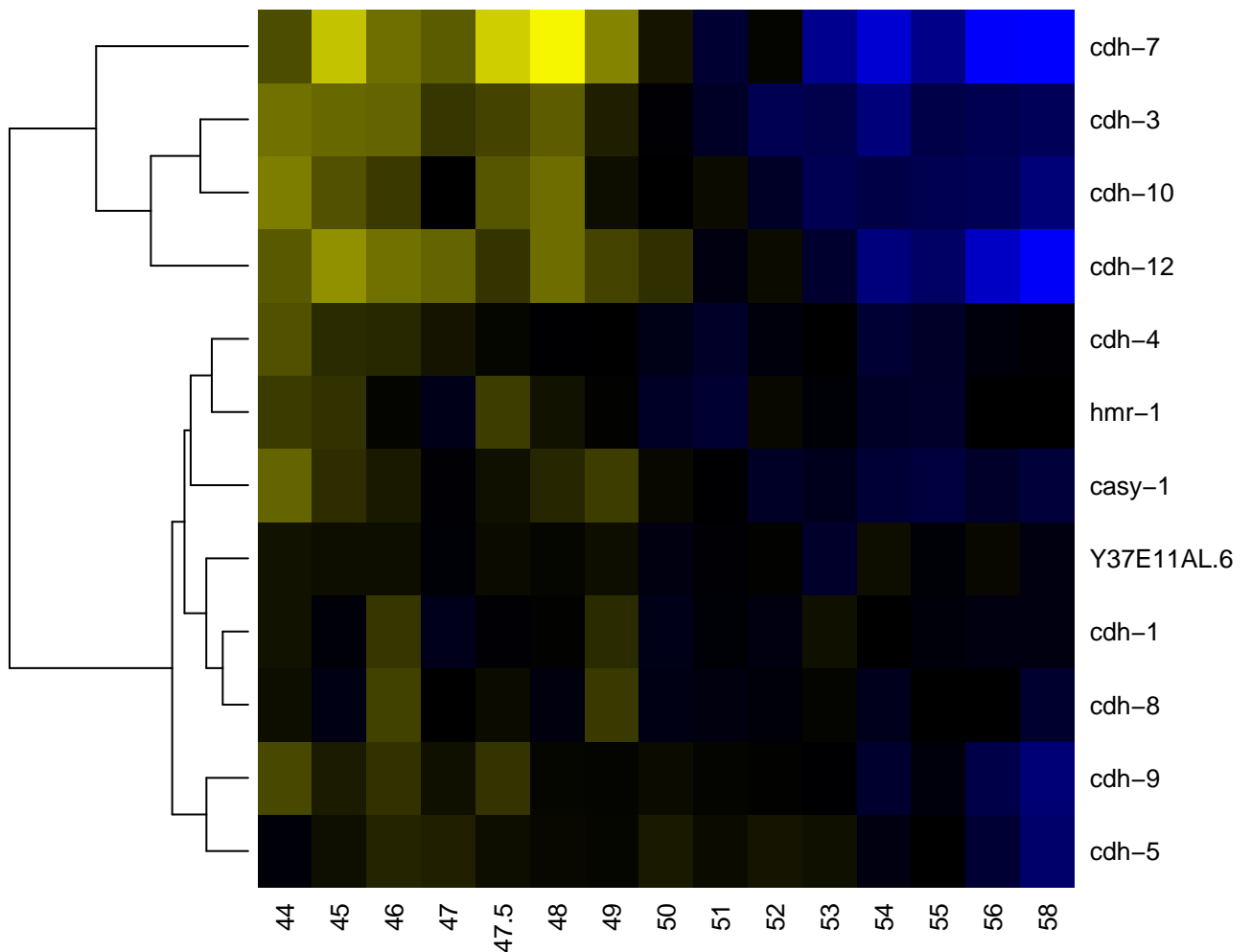
histone deacetylase activity



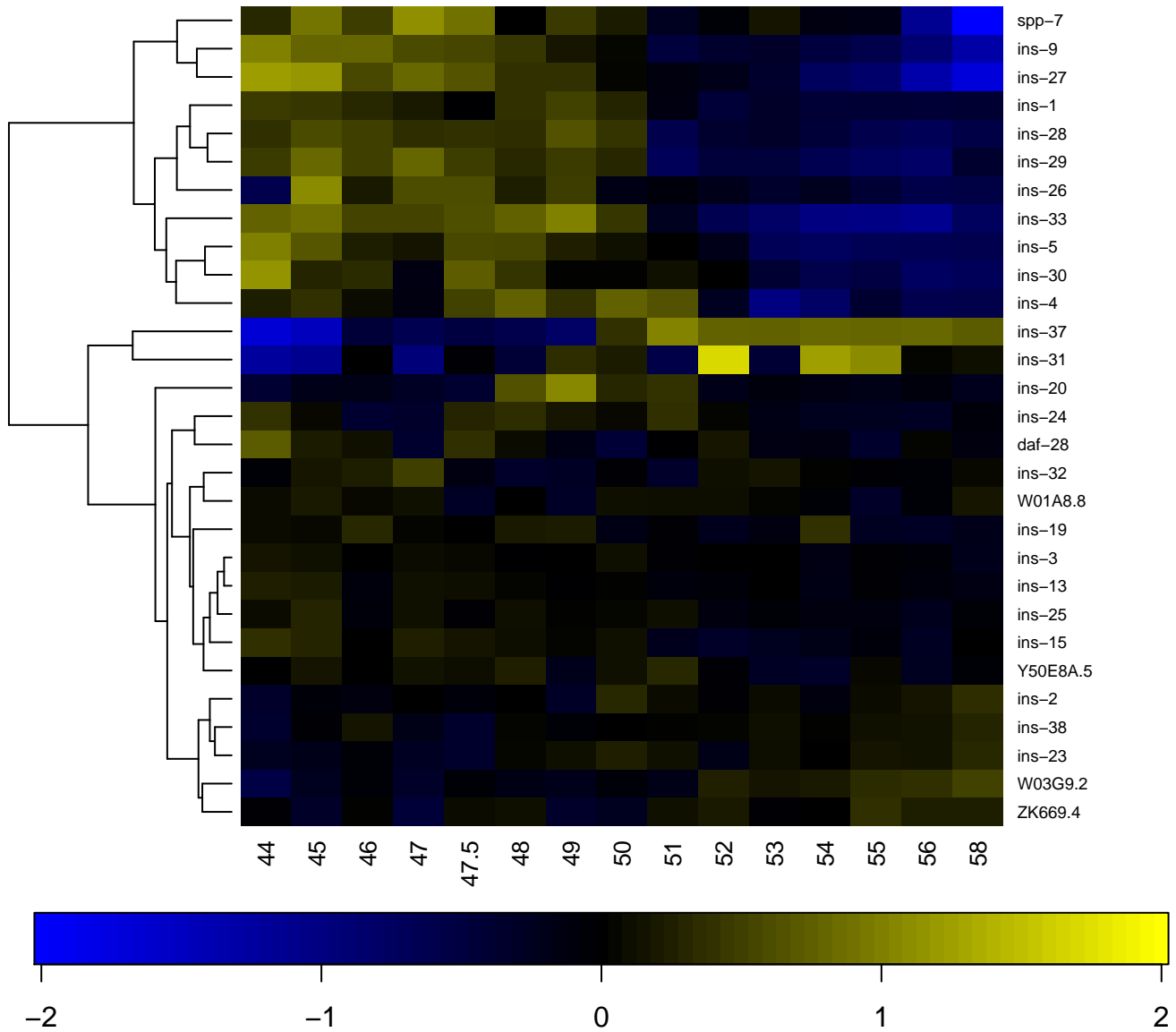
histone deacetylation



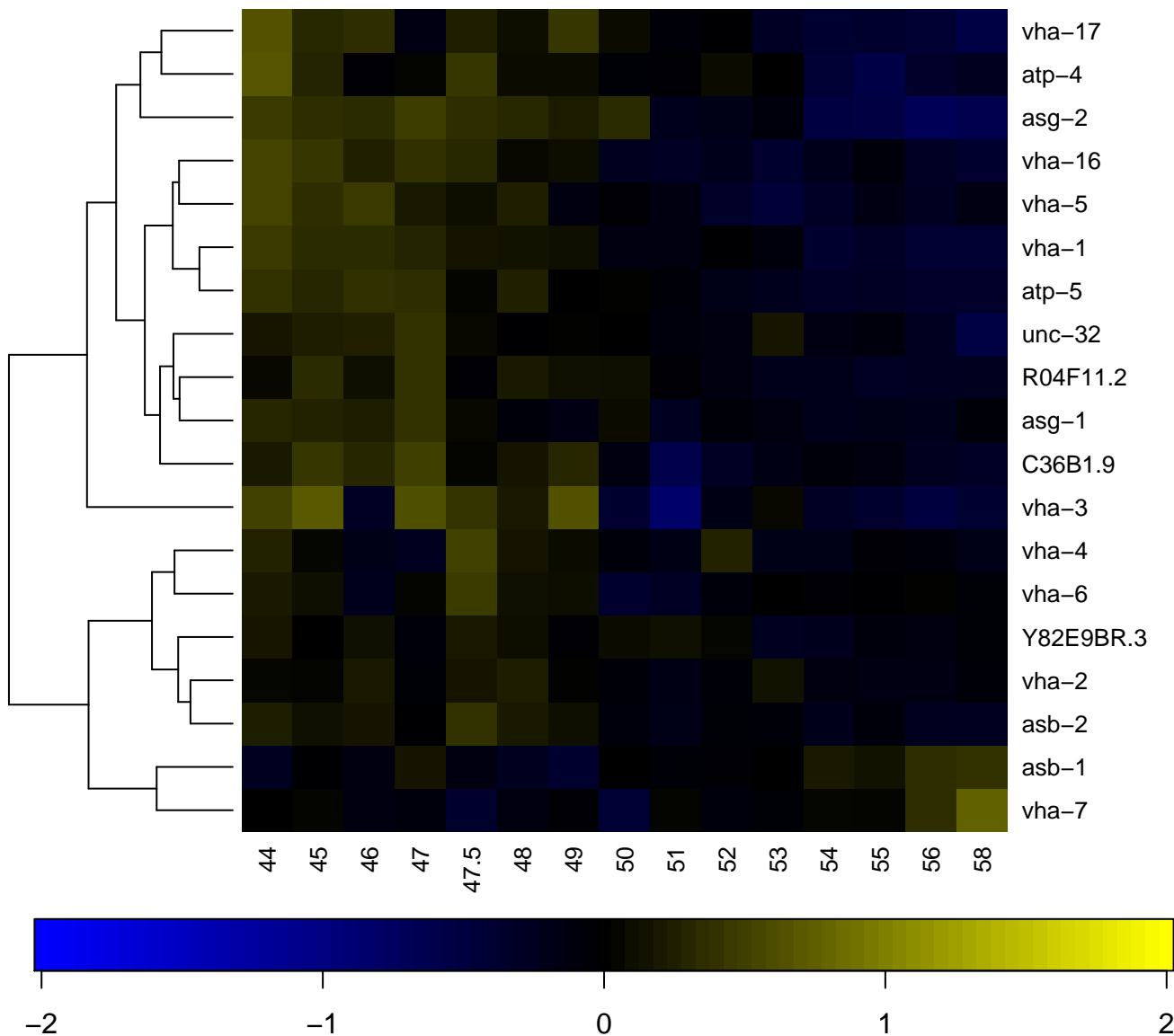
homophilic cell adhesion



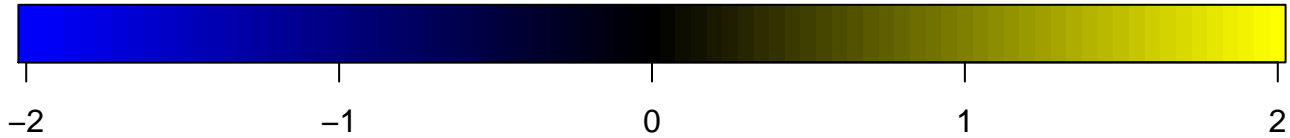
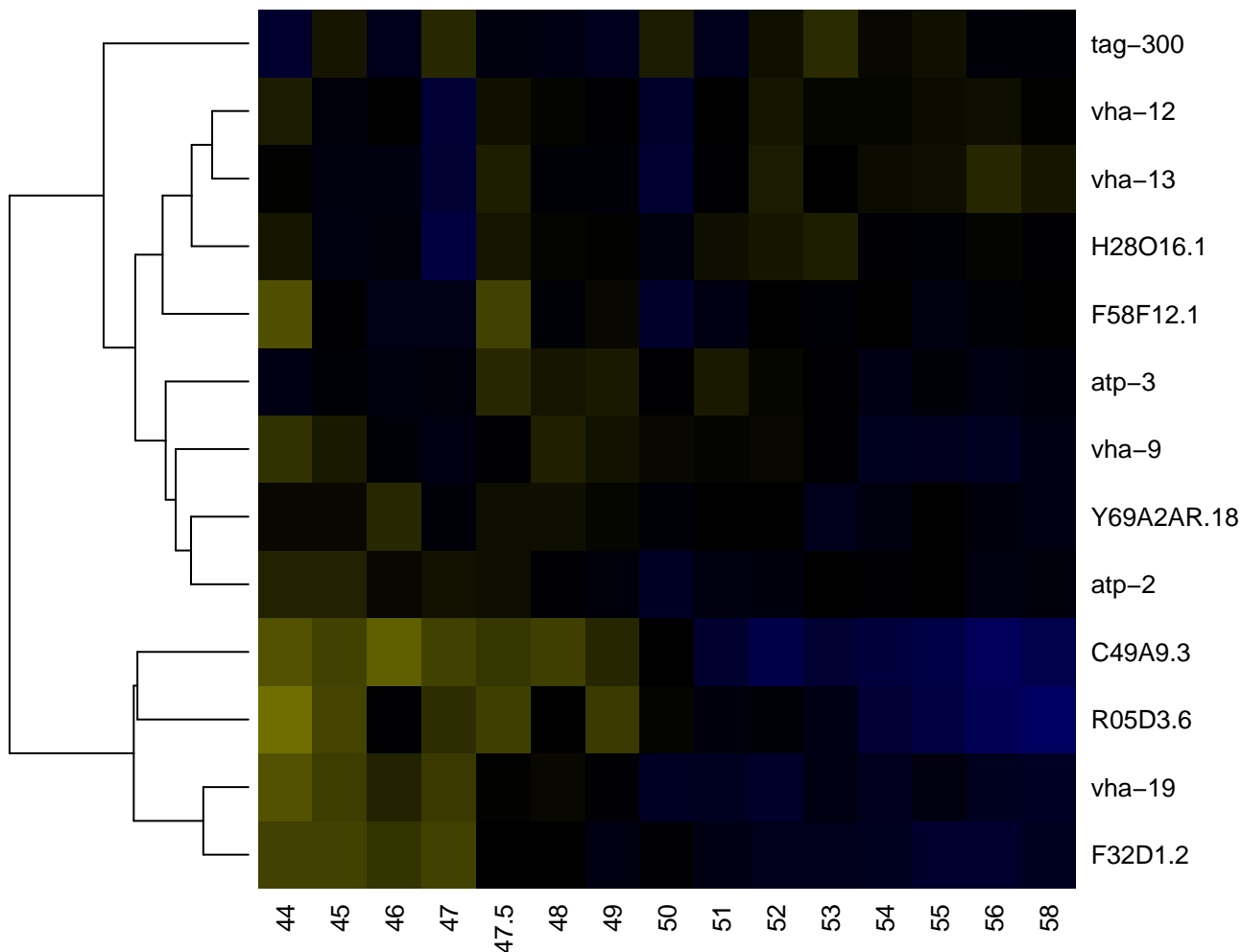
hormone activity



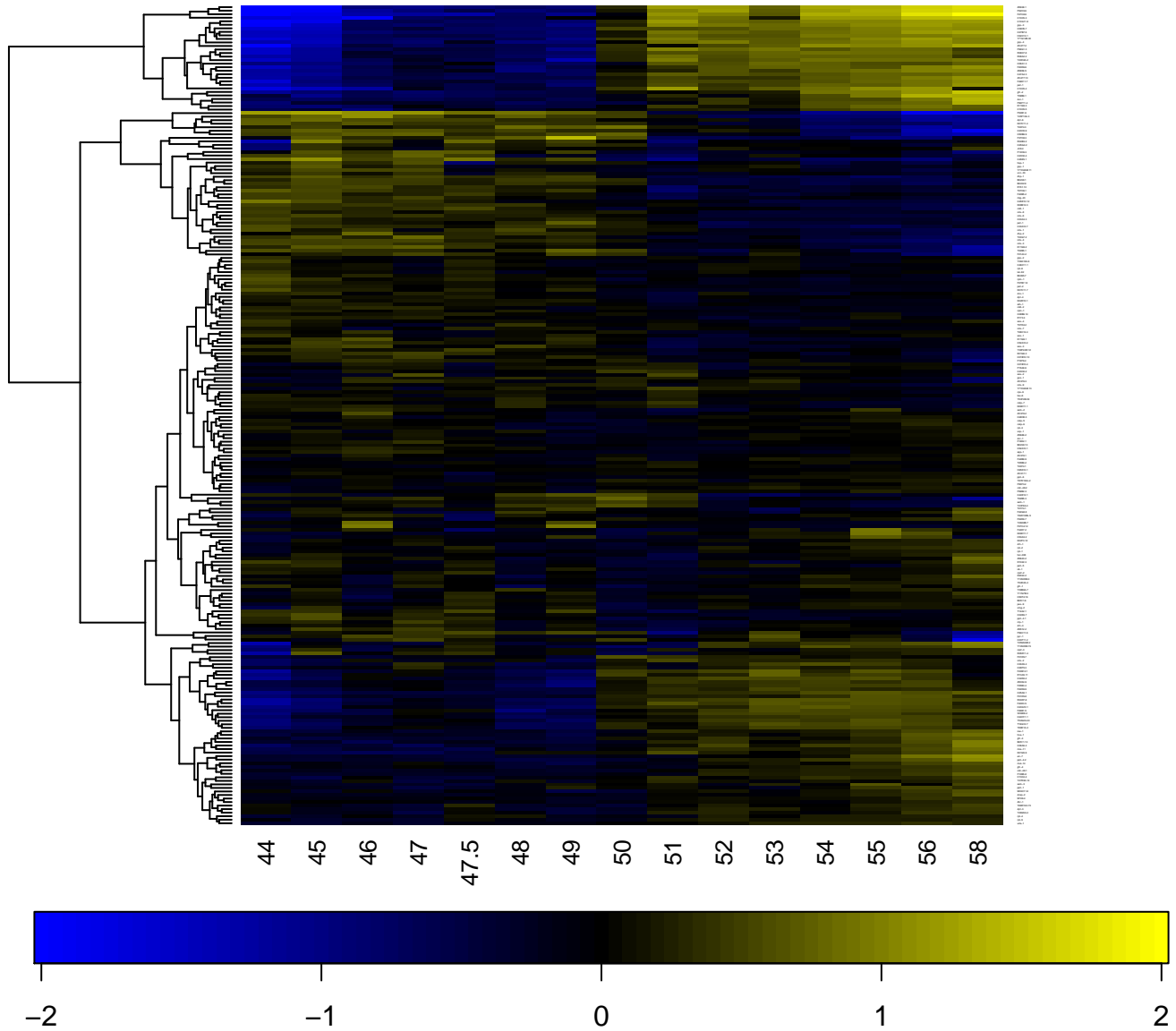
hydrogen ion transmembrane transporter activity



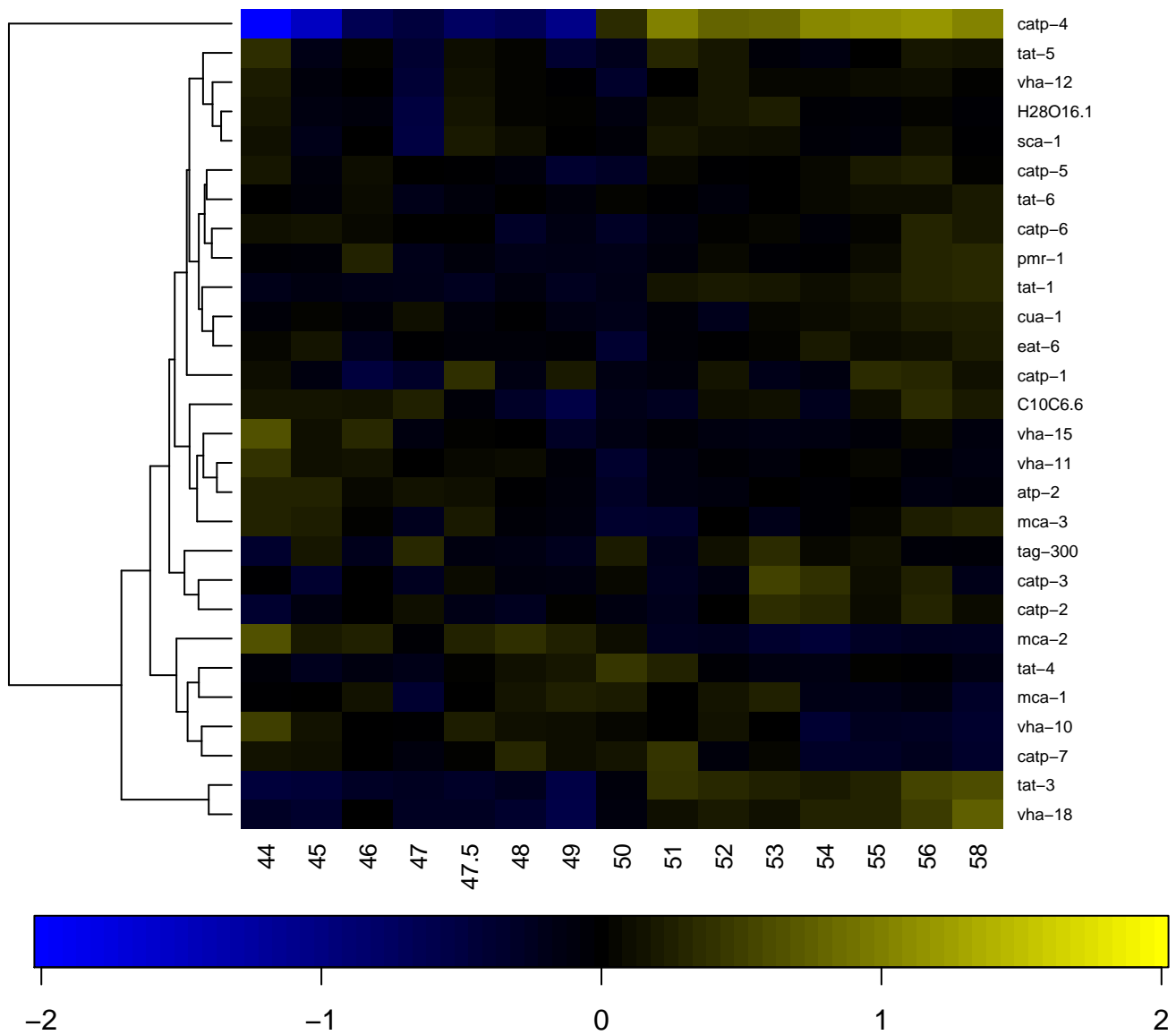
Proton ion transporting ATP synthase activity, rotational mec



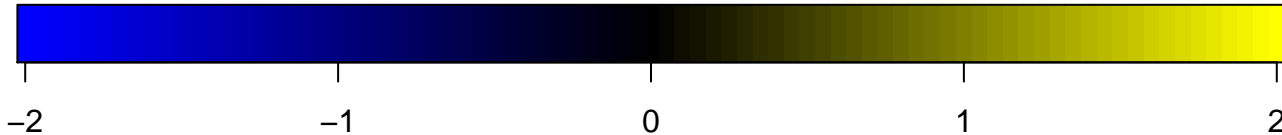
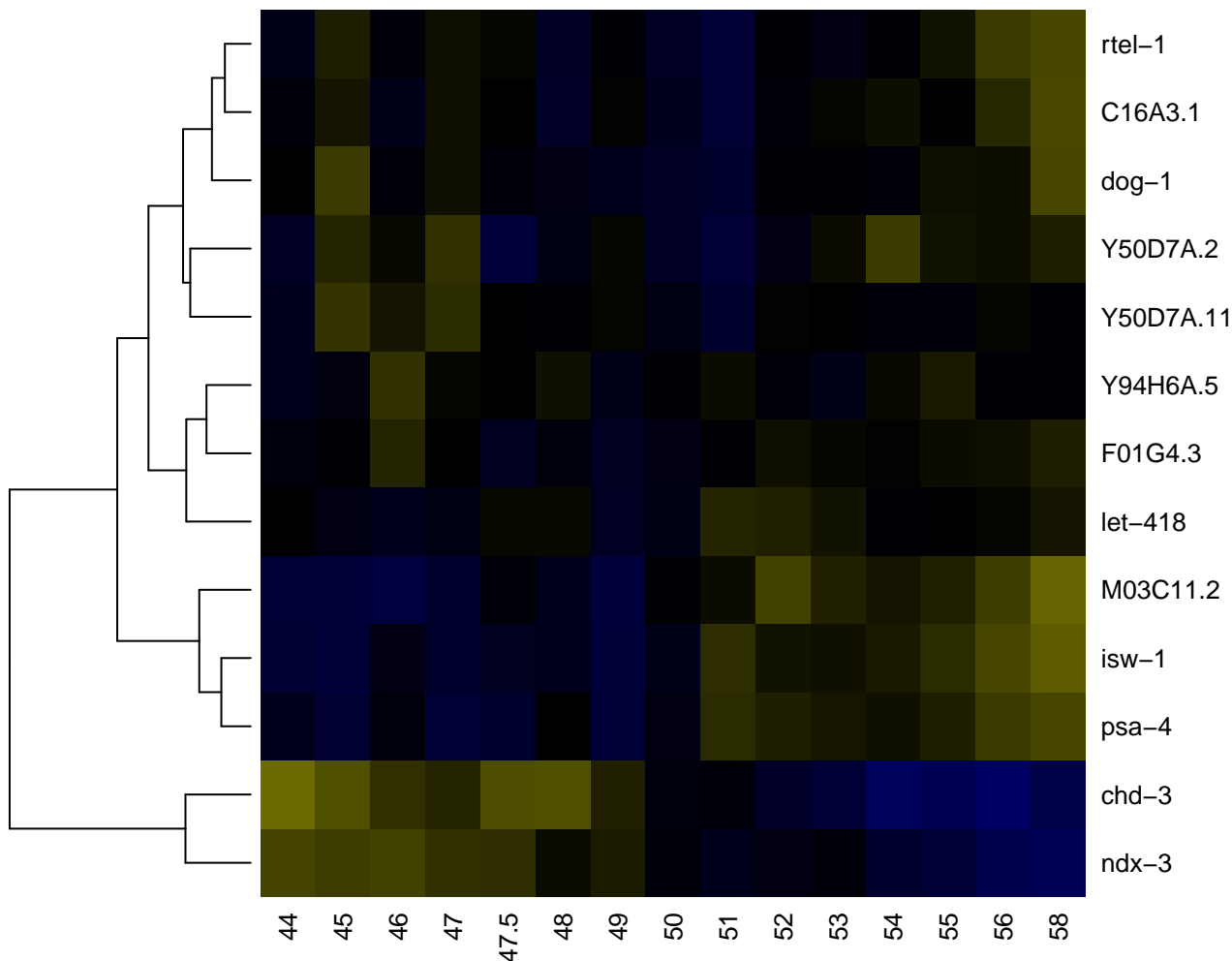
hydrolase activity



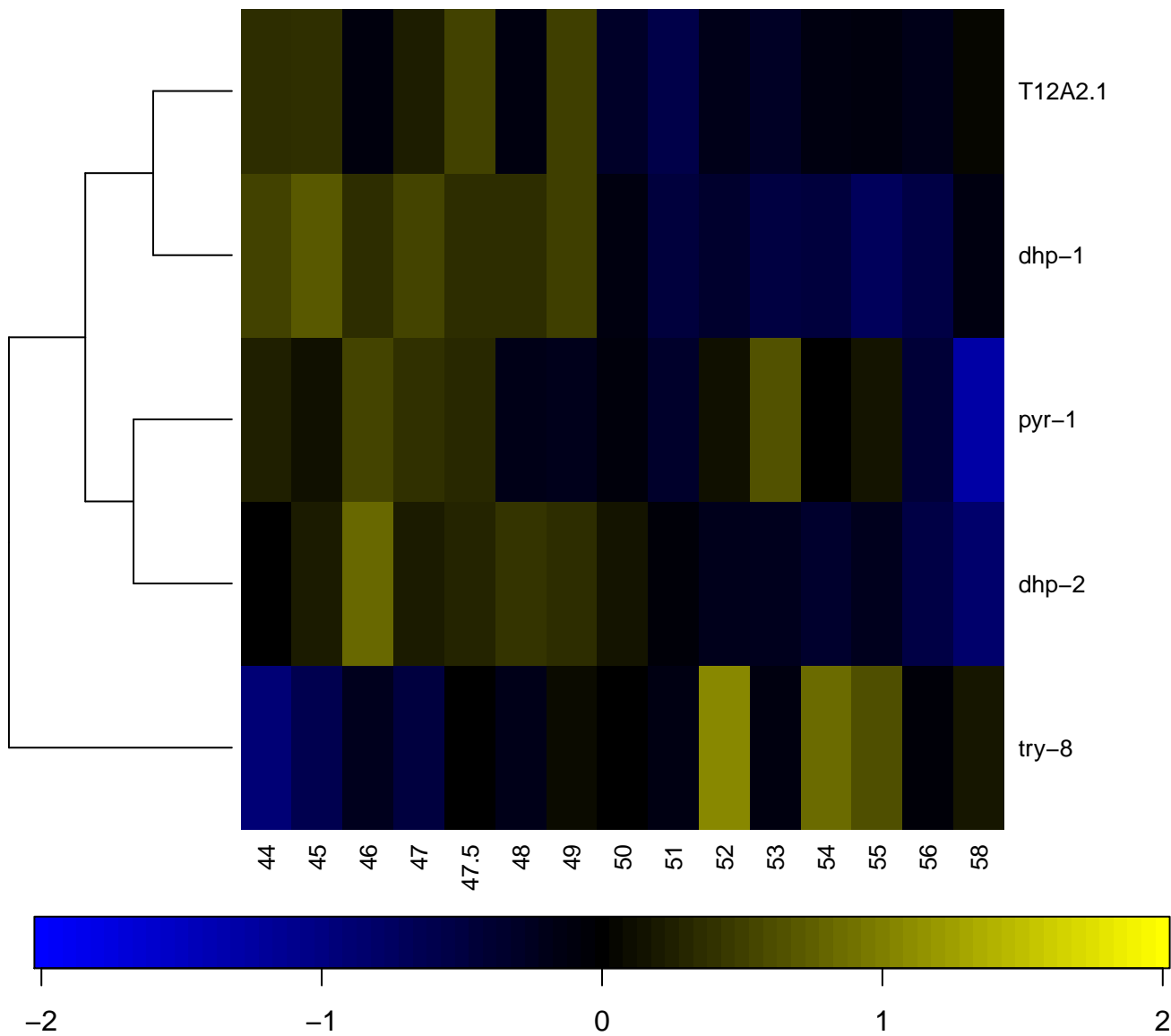
acting on acid anhydrides, catalyzing transmembrane move



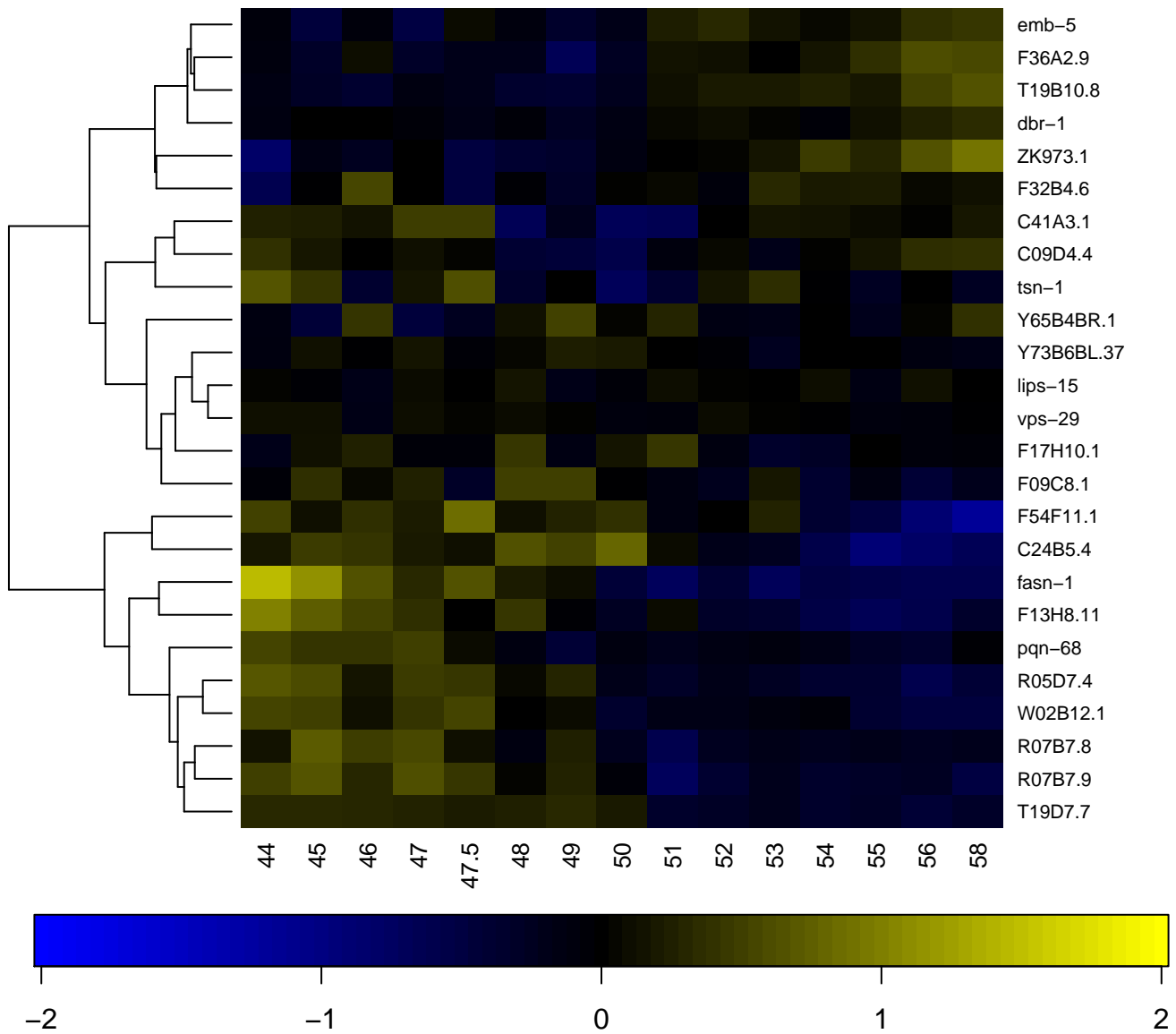
activity, acting on acid anhydrides, in phosphorus-containing



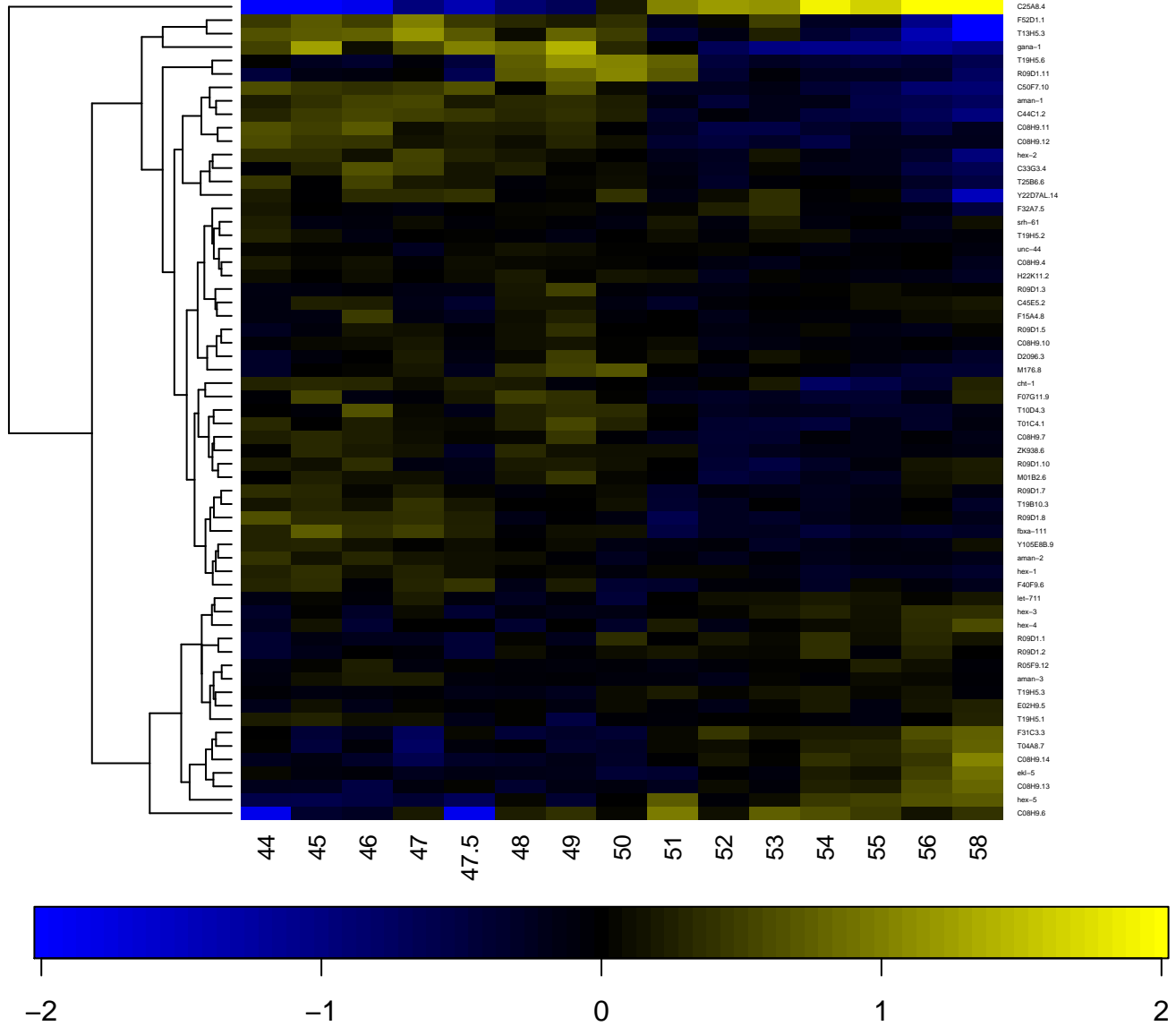
activity, acting on carbon–nitrogen (but not peptide) bonds, in



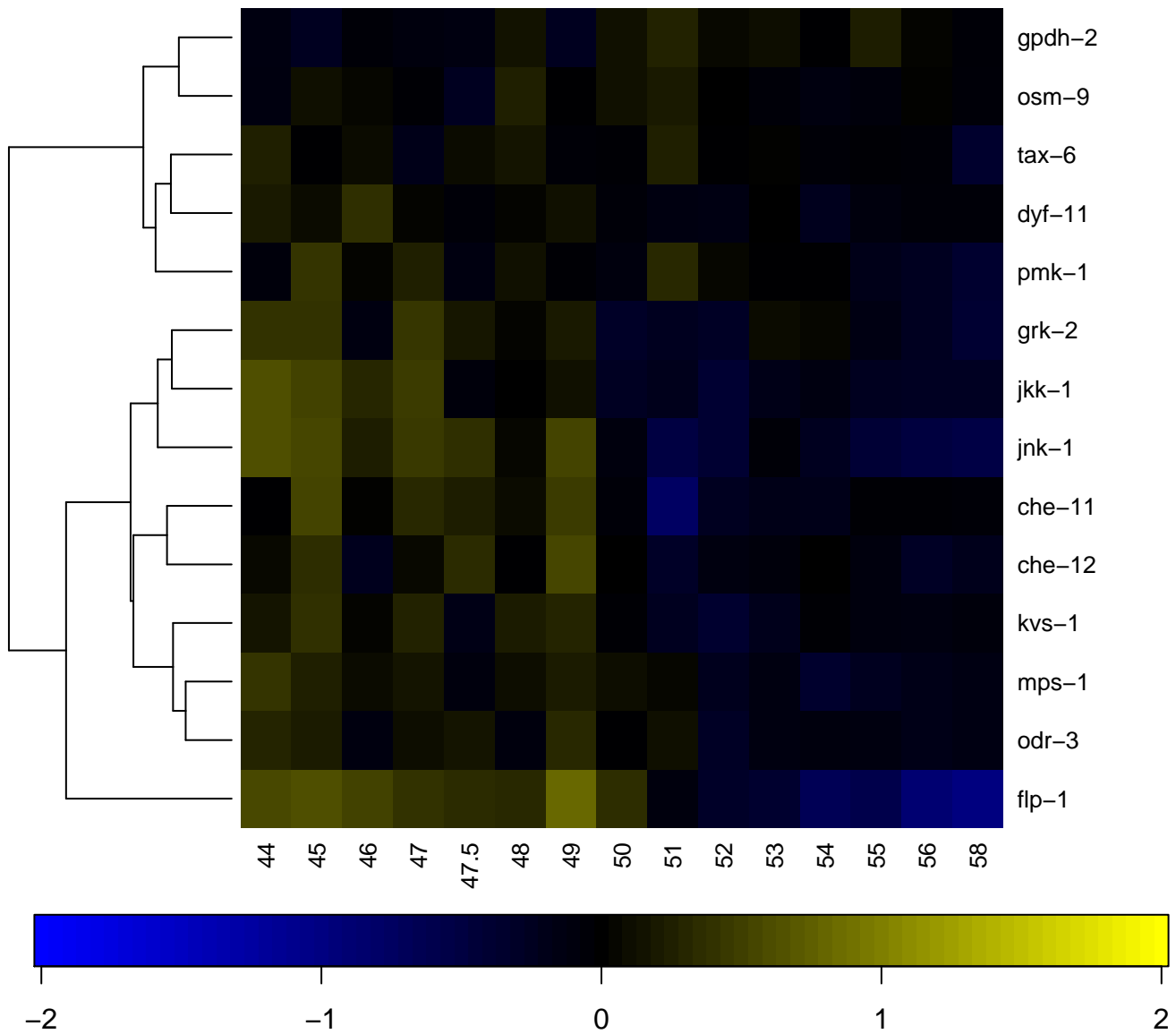
hydrolase activity, acting on ester bonds



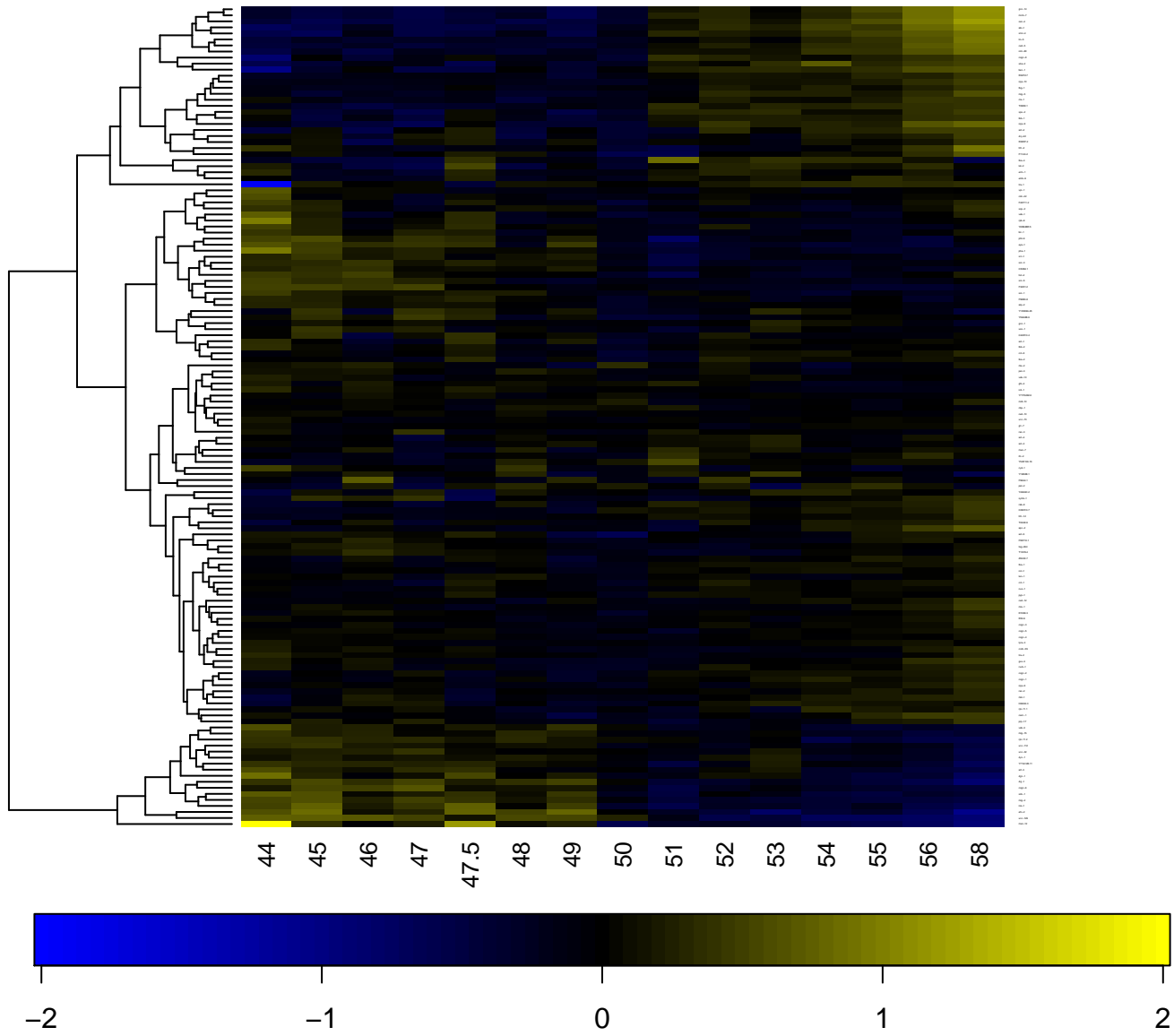
hydrolase activity, hydrolyzing O-glycosyl compounds



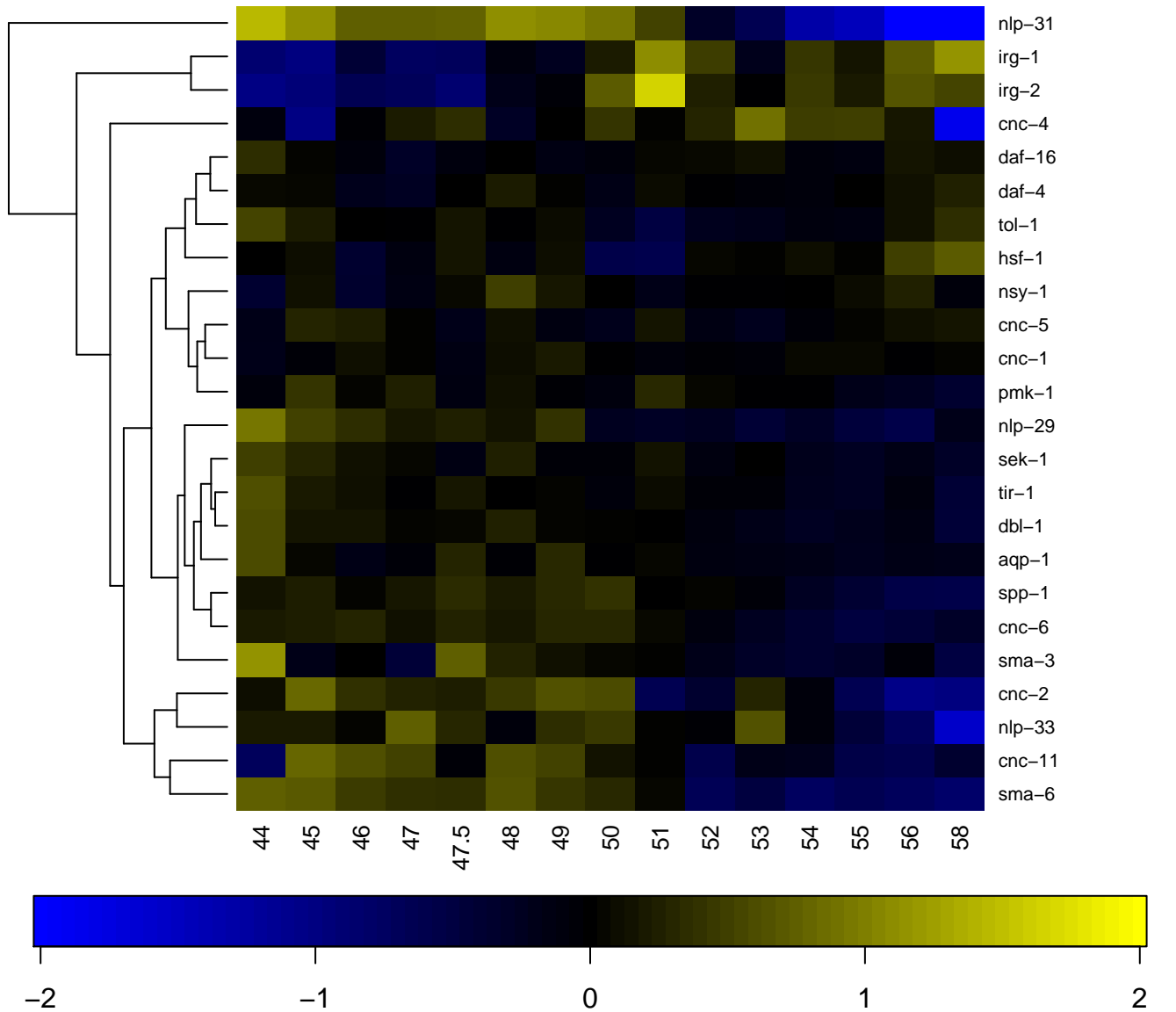
hyperosmotic response



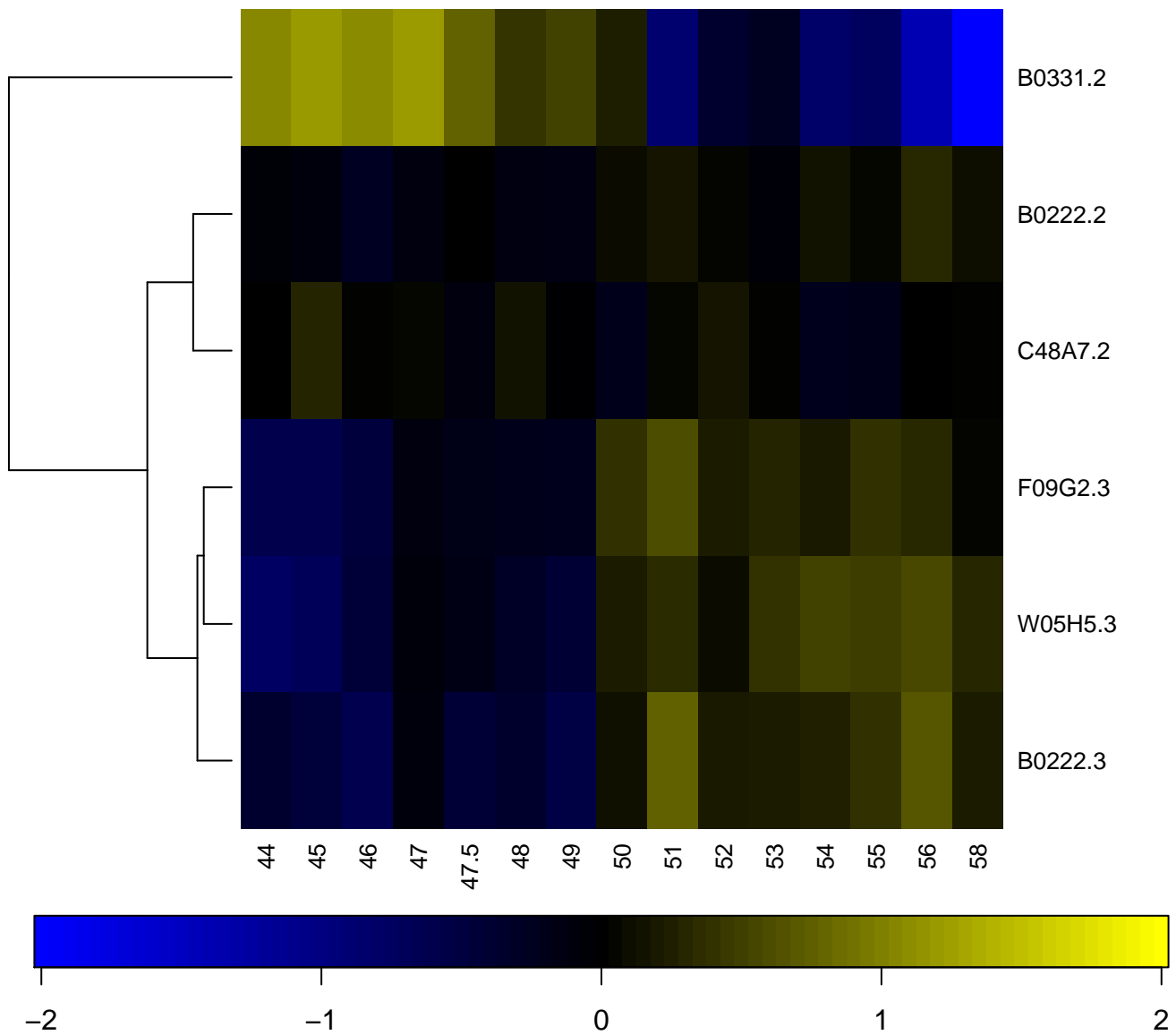
inductive cell migration



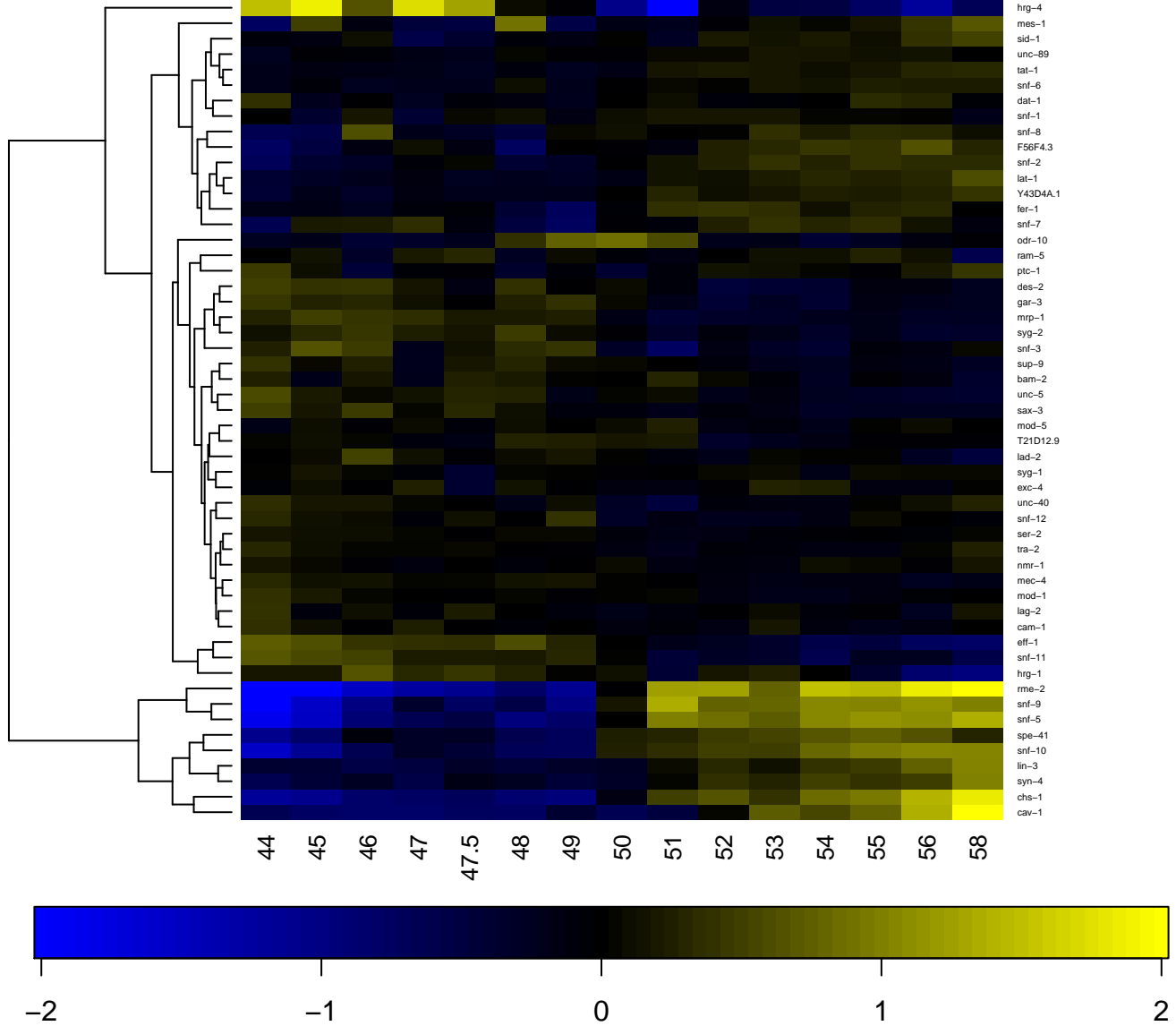
innate immune response



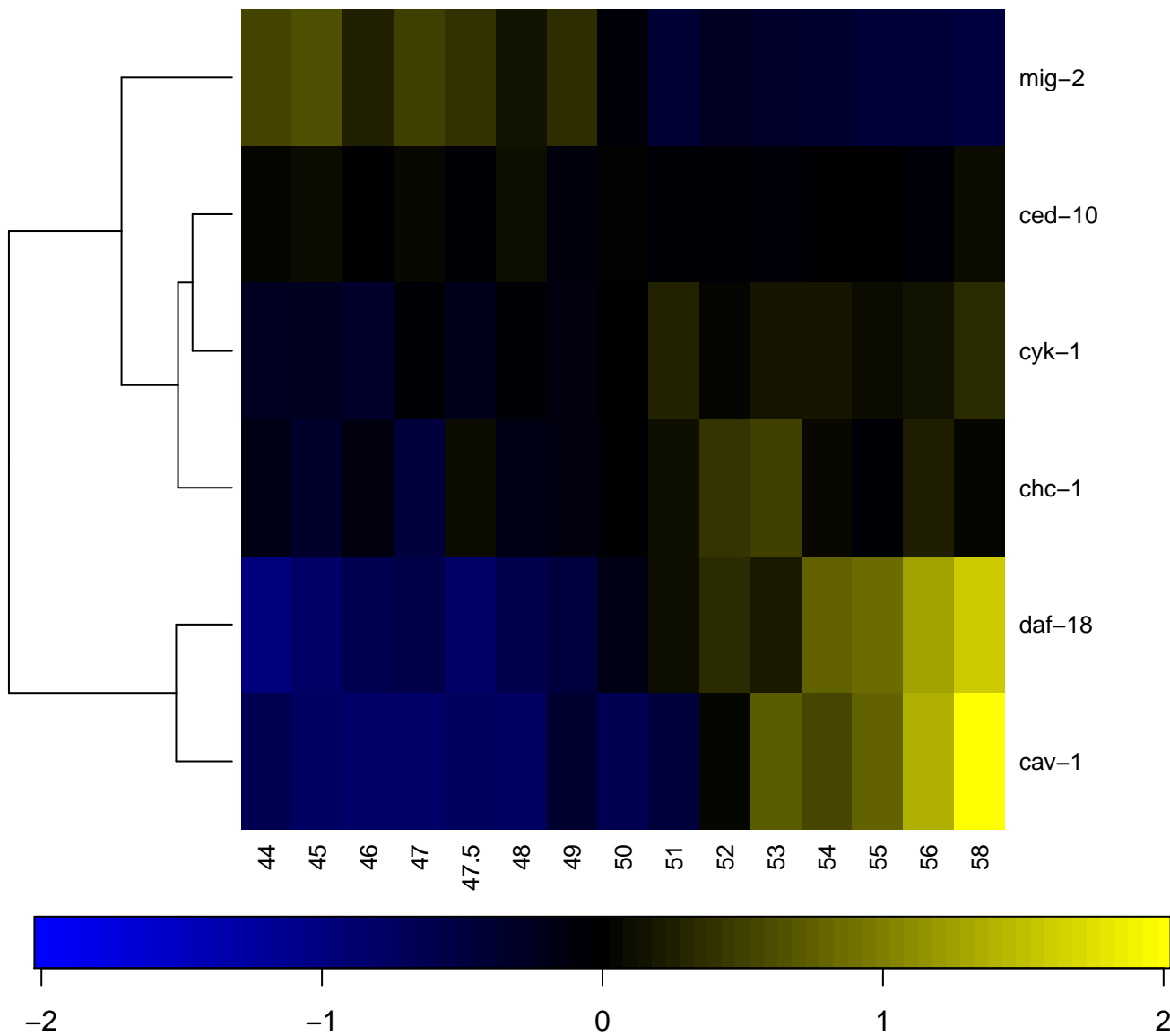
inorganic phosphate transmembrane transporter activity



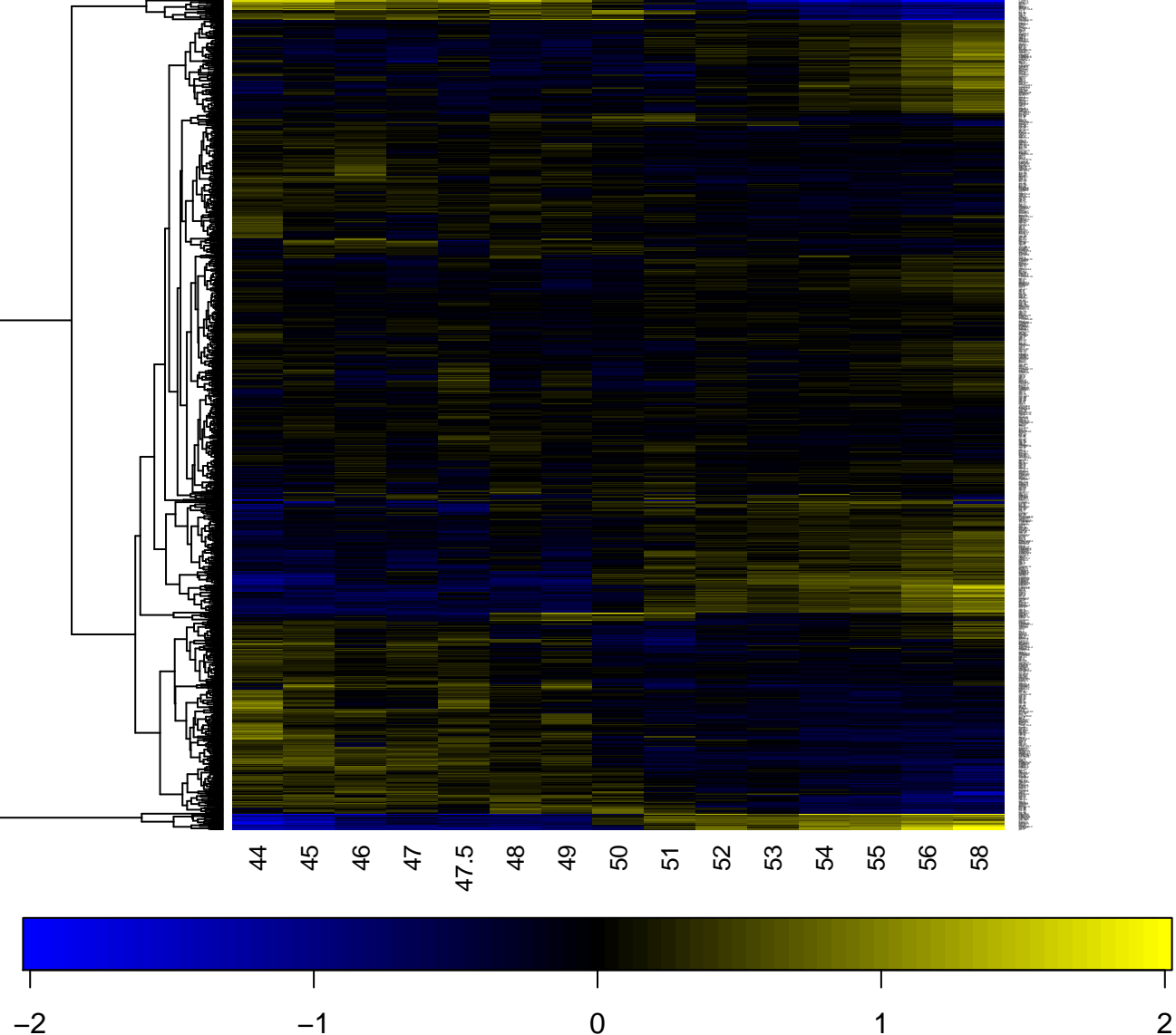
integral to plasma membrane



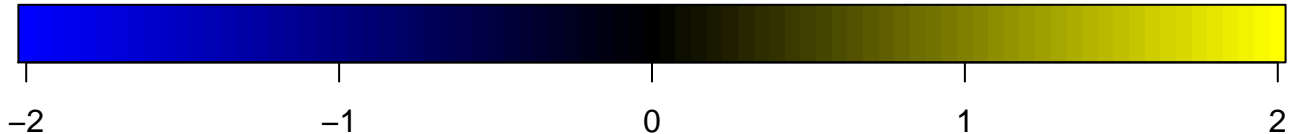
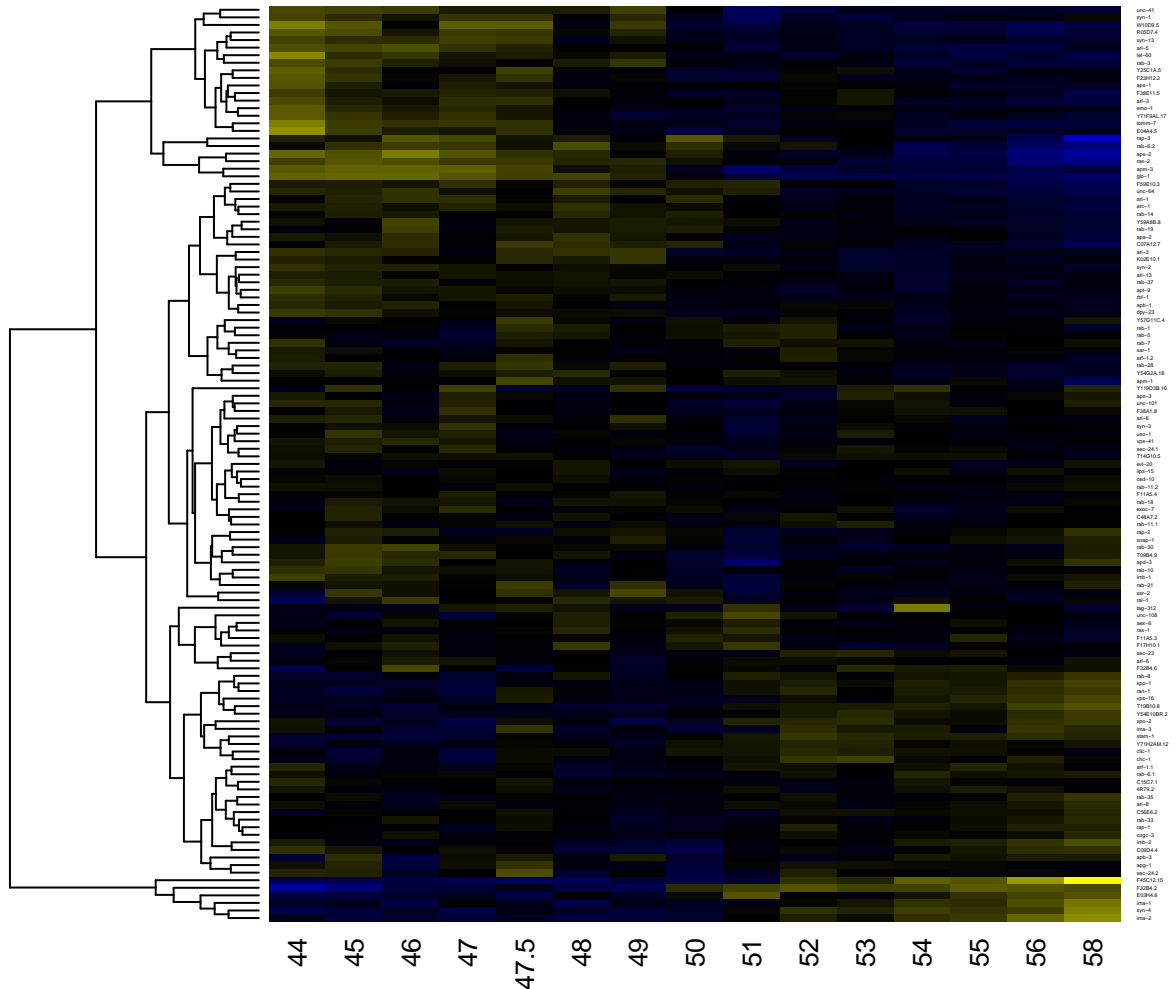
internal side of plasma membrane



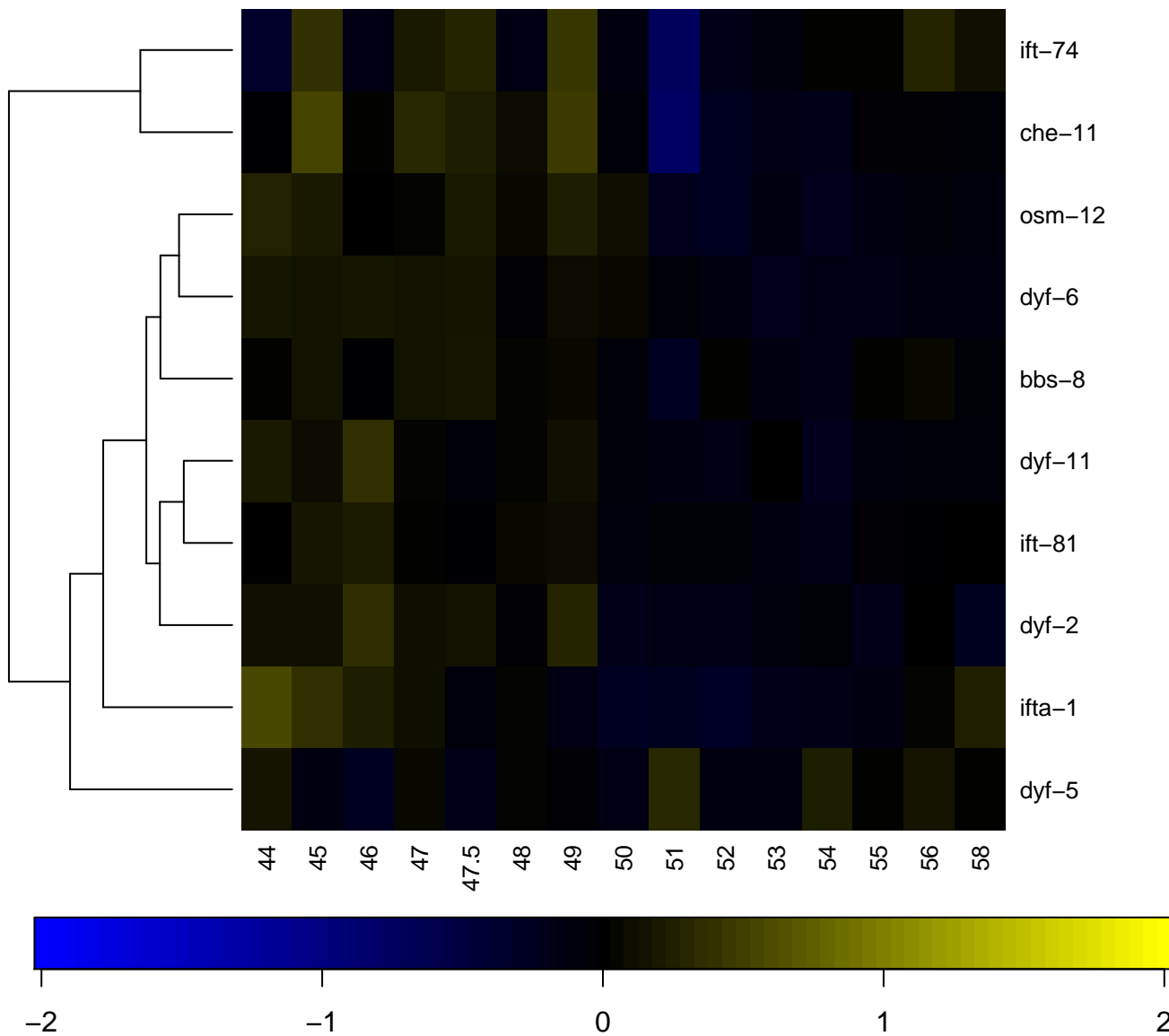
intracellular



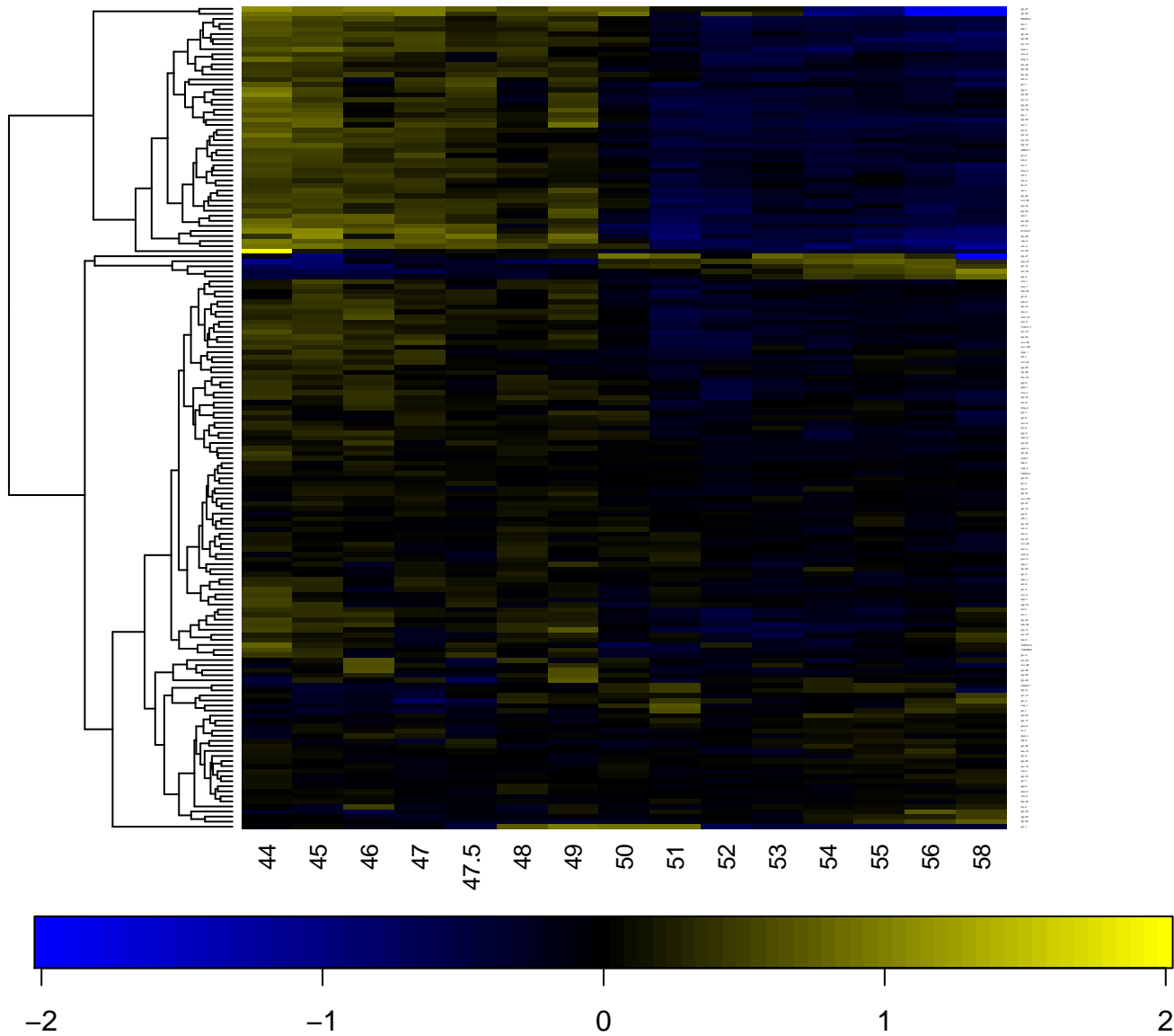
intracellular protein transport



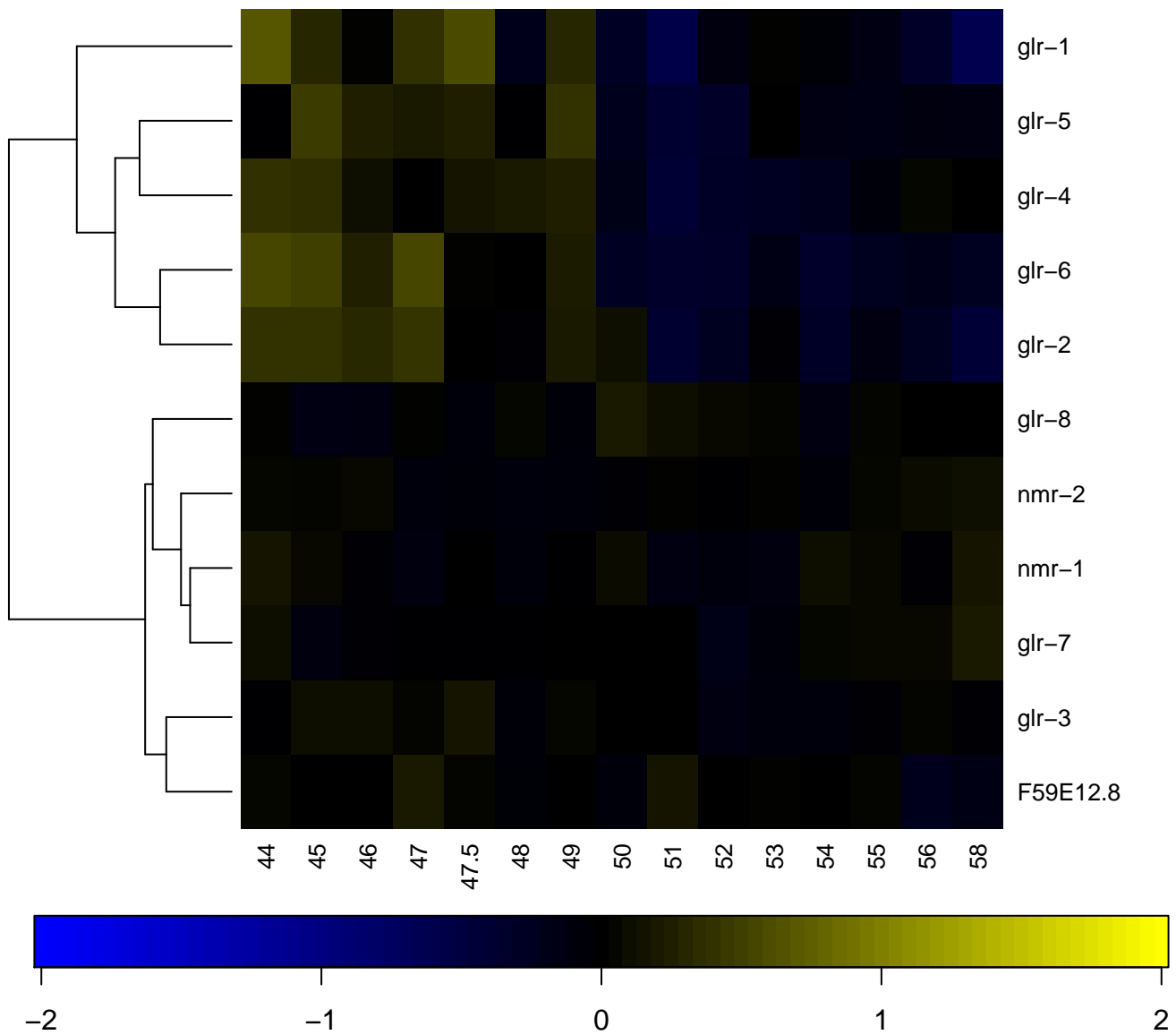
intraflagellar transport



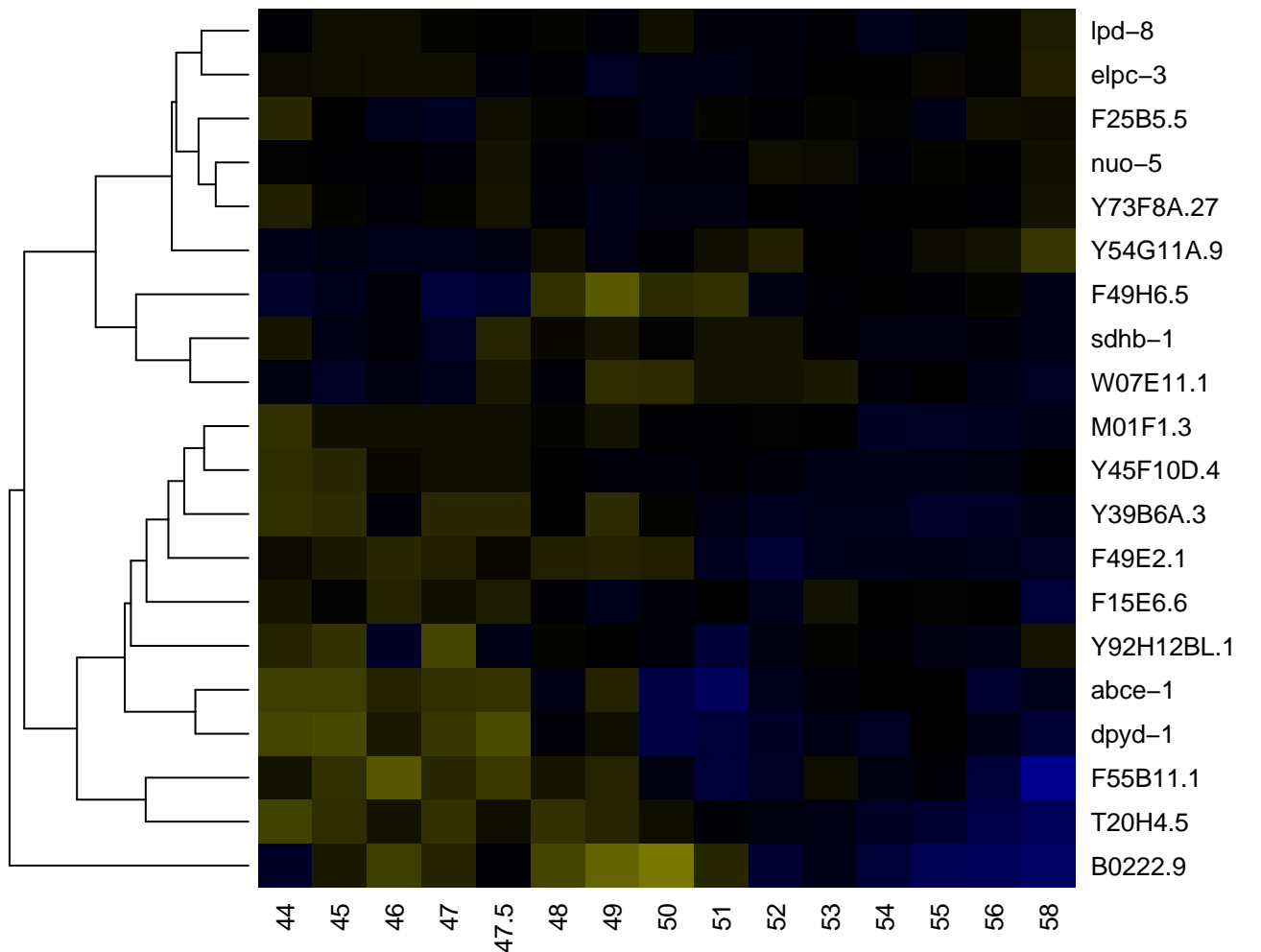
ion transport



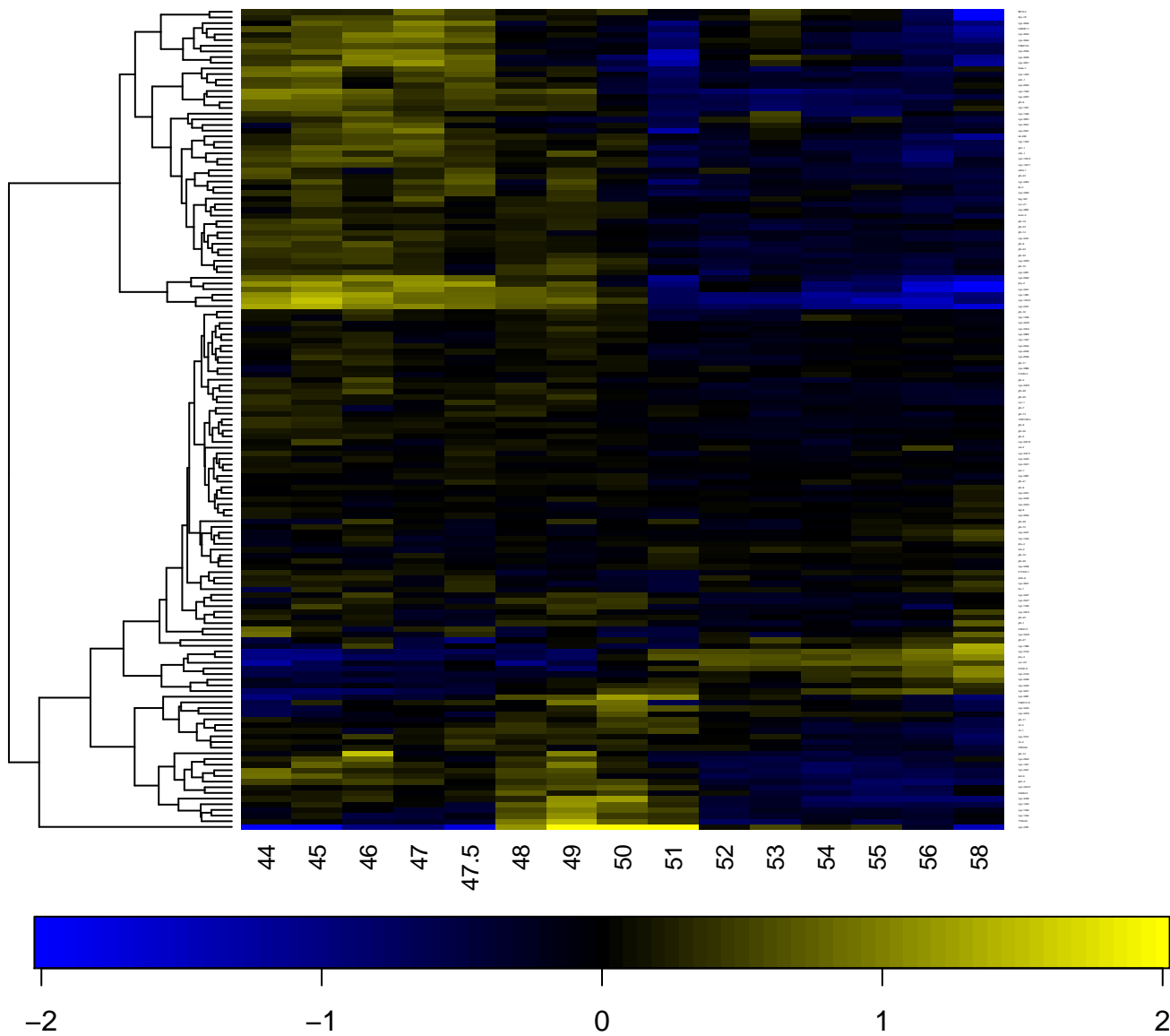
ionotropic glutamate receptor activity



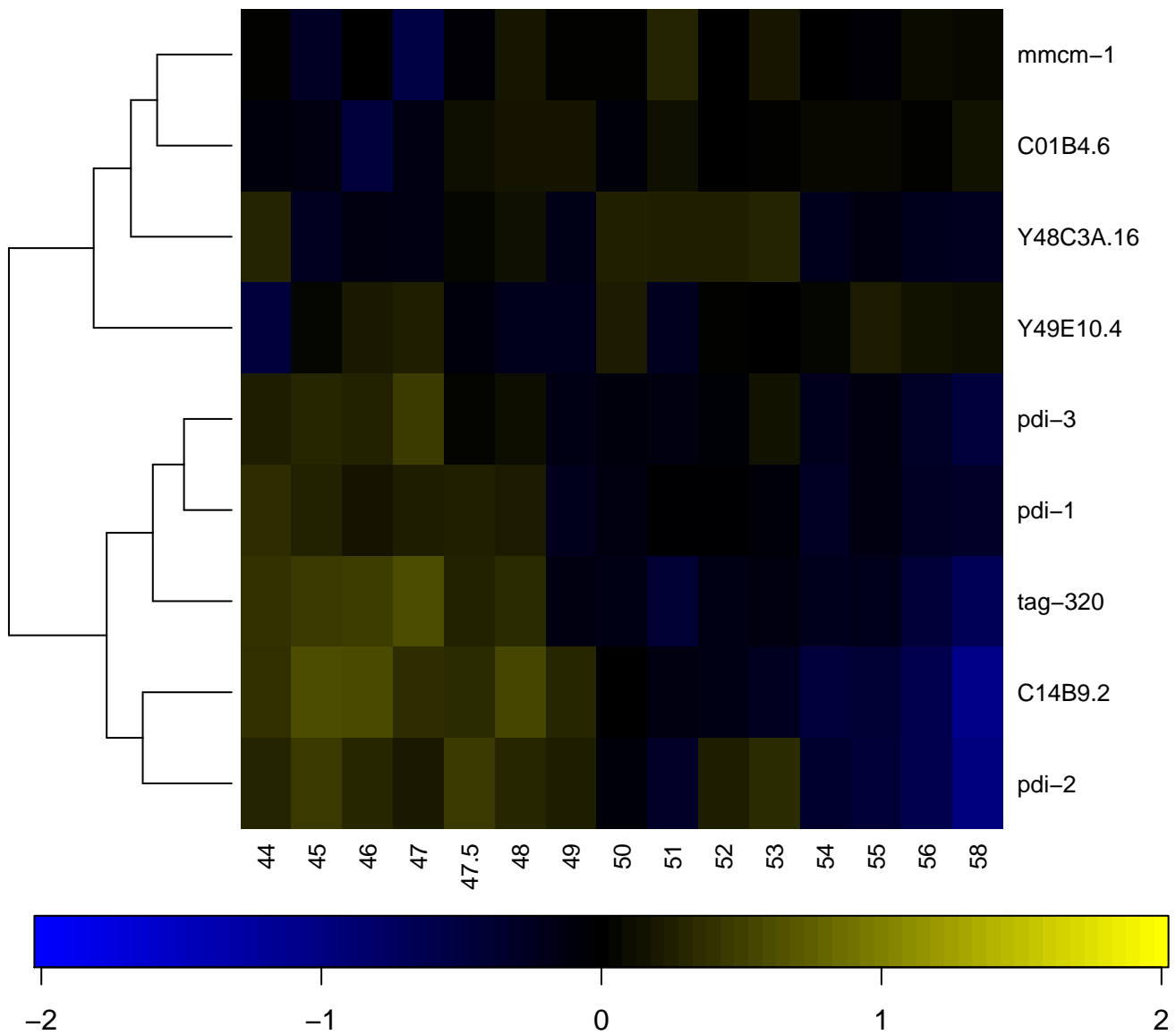
iron-sulfur cluster binding



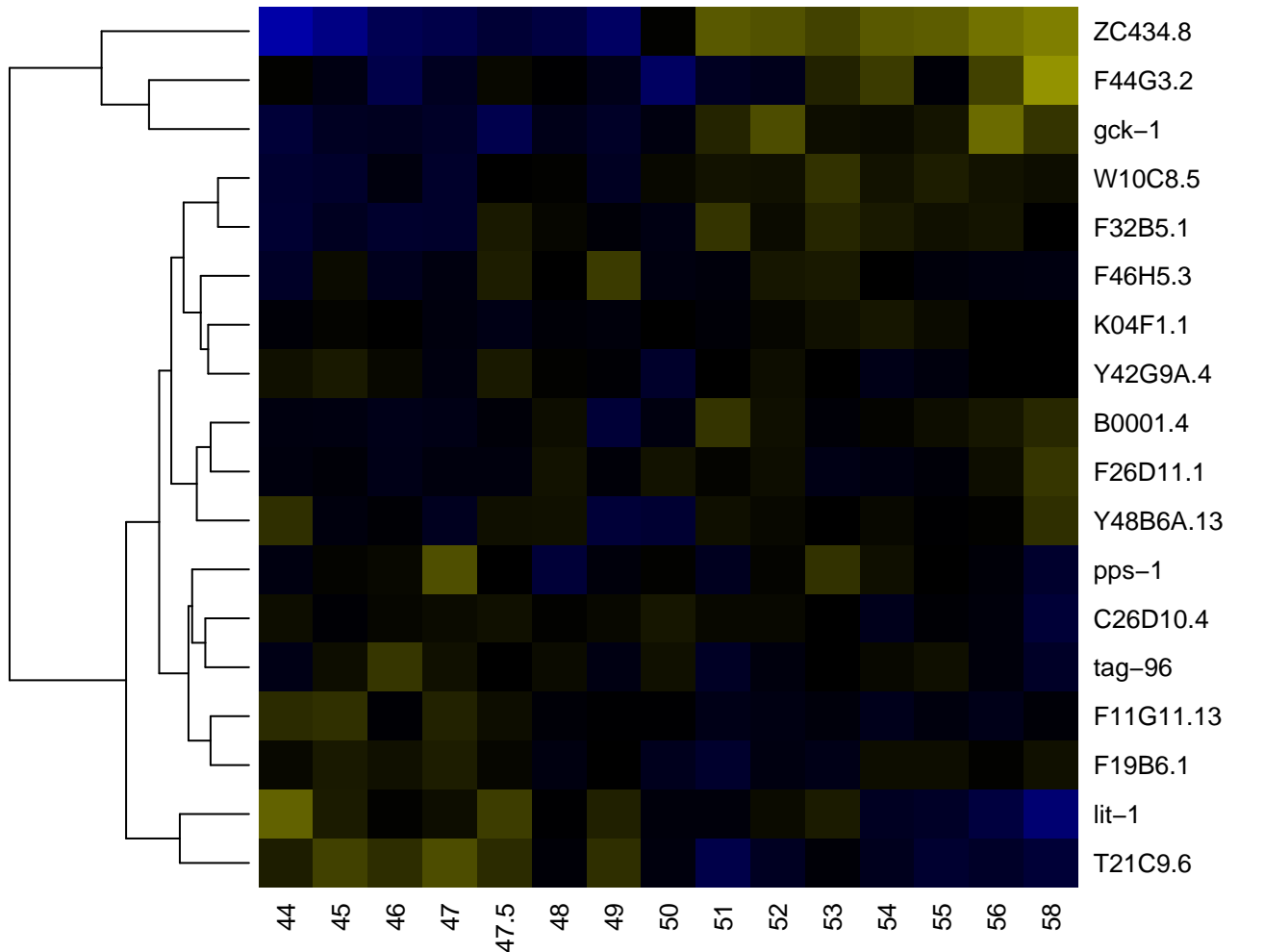
iron ion binding



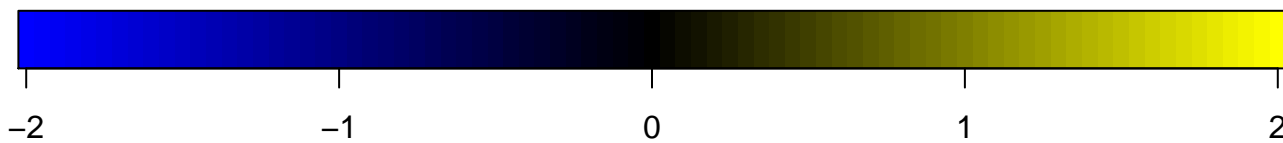
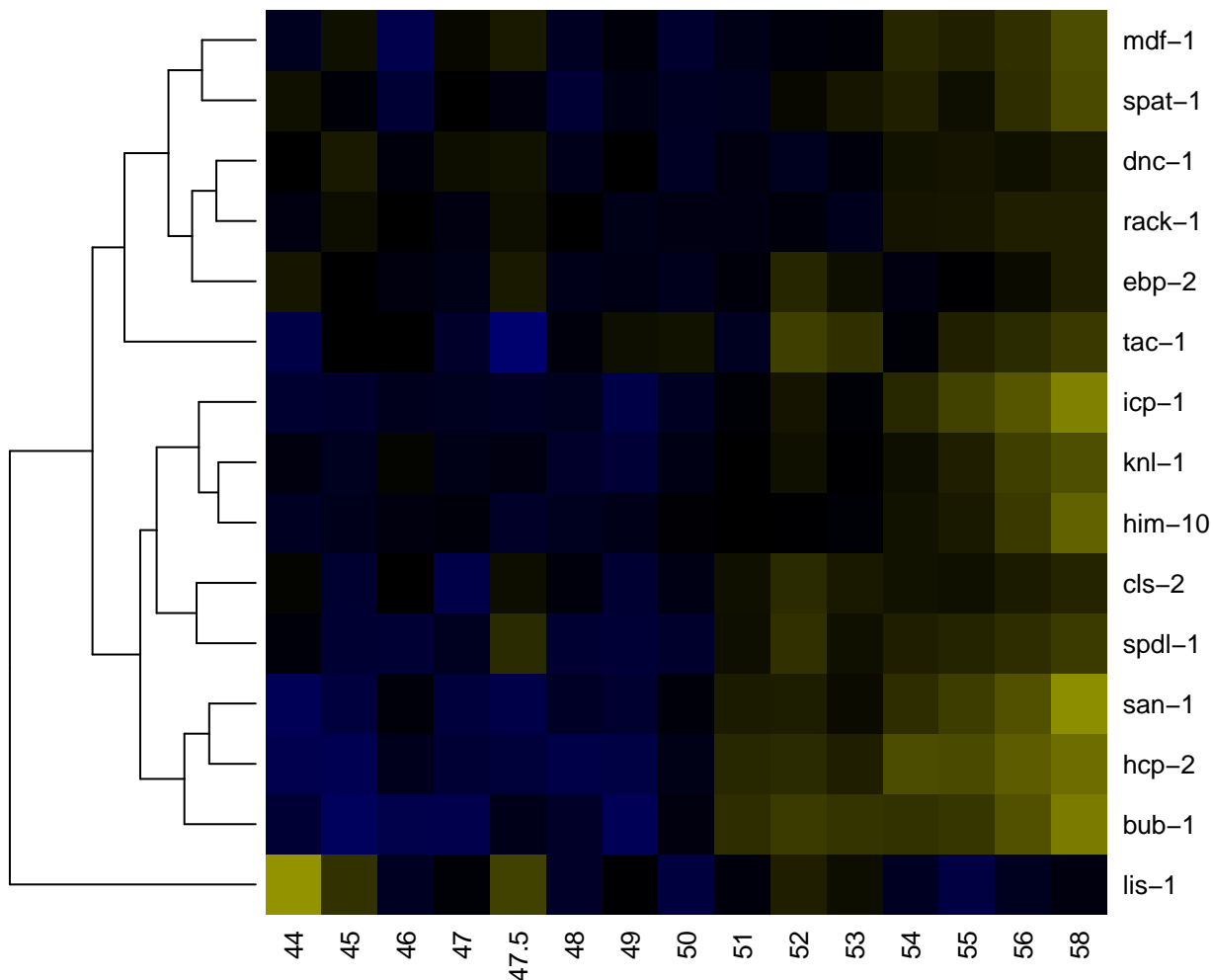
isomerase activity



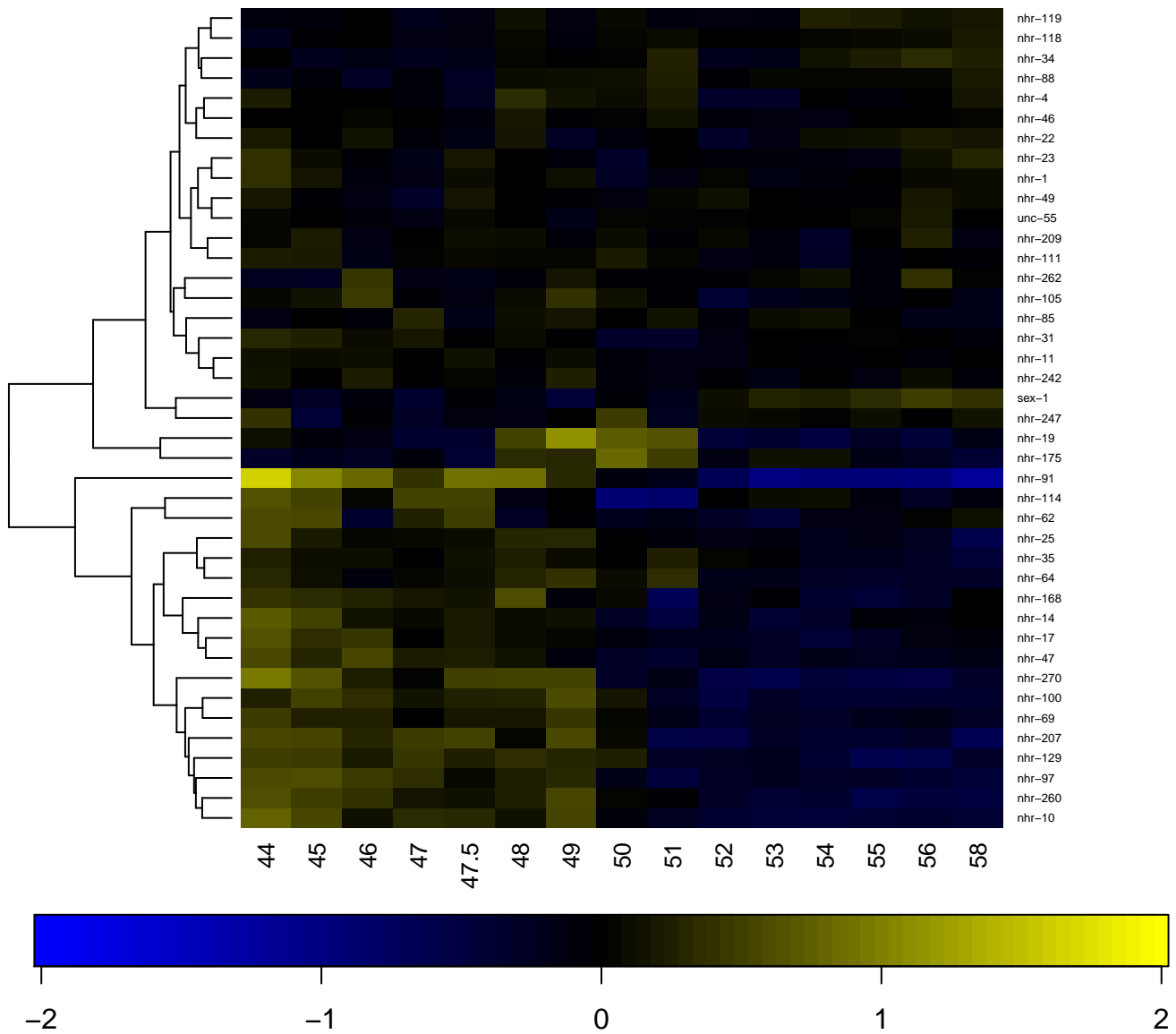
kinase activity



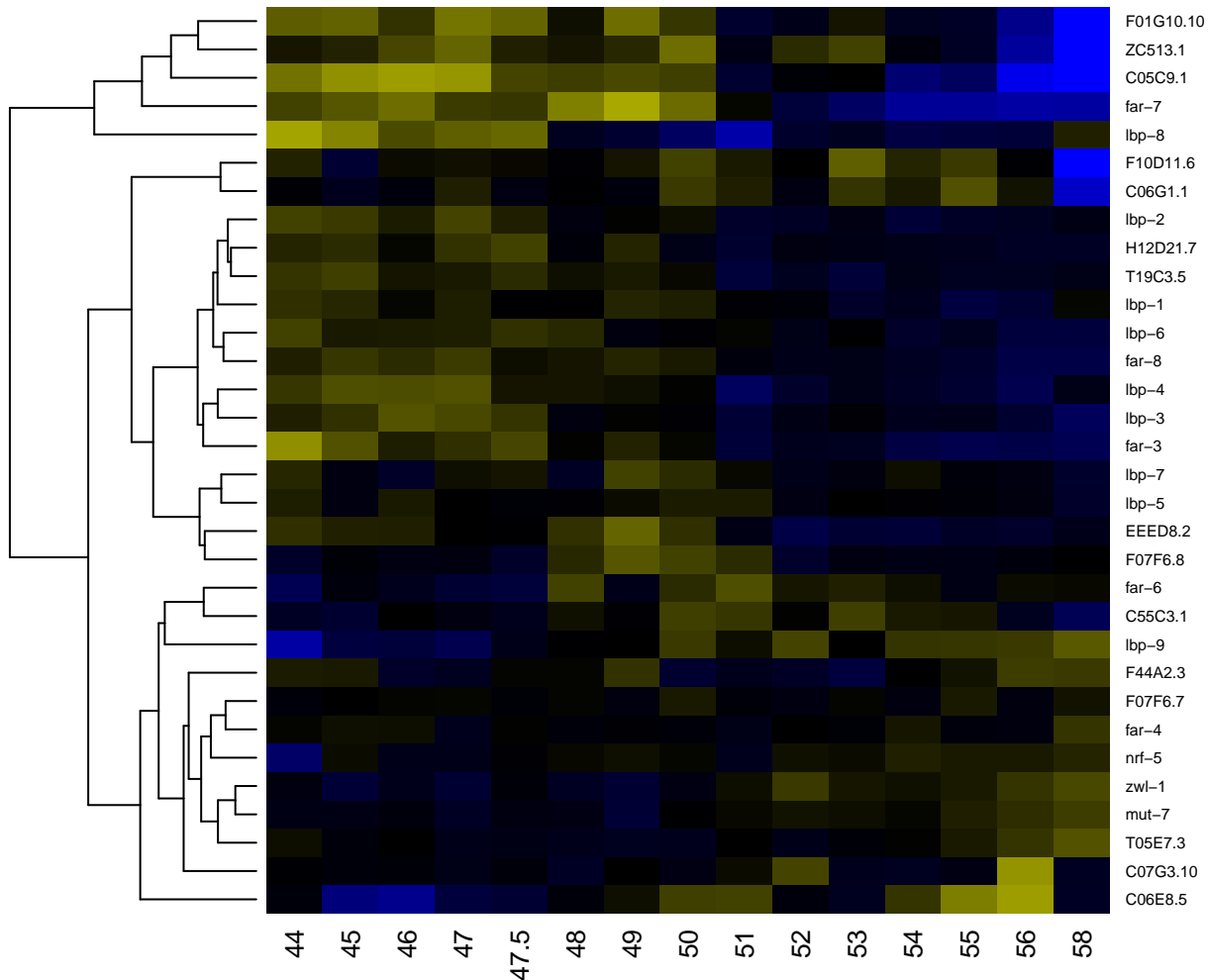
kinetochore



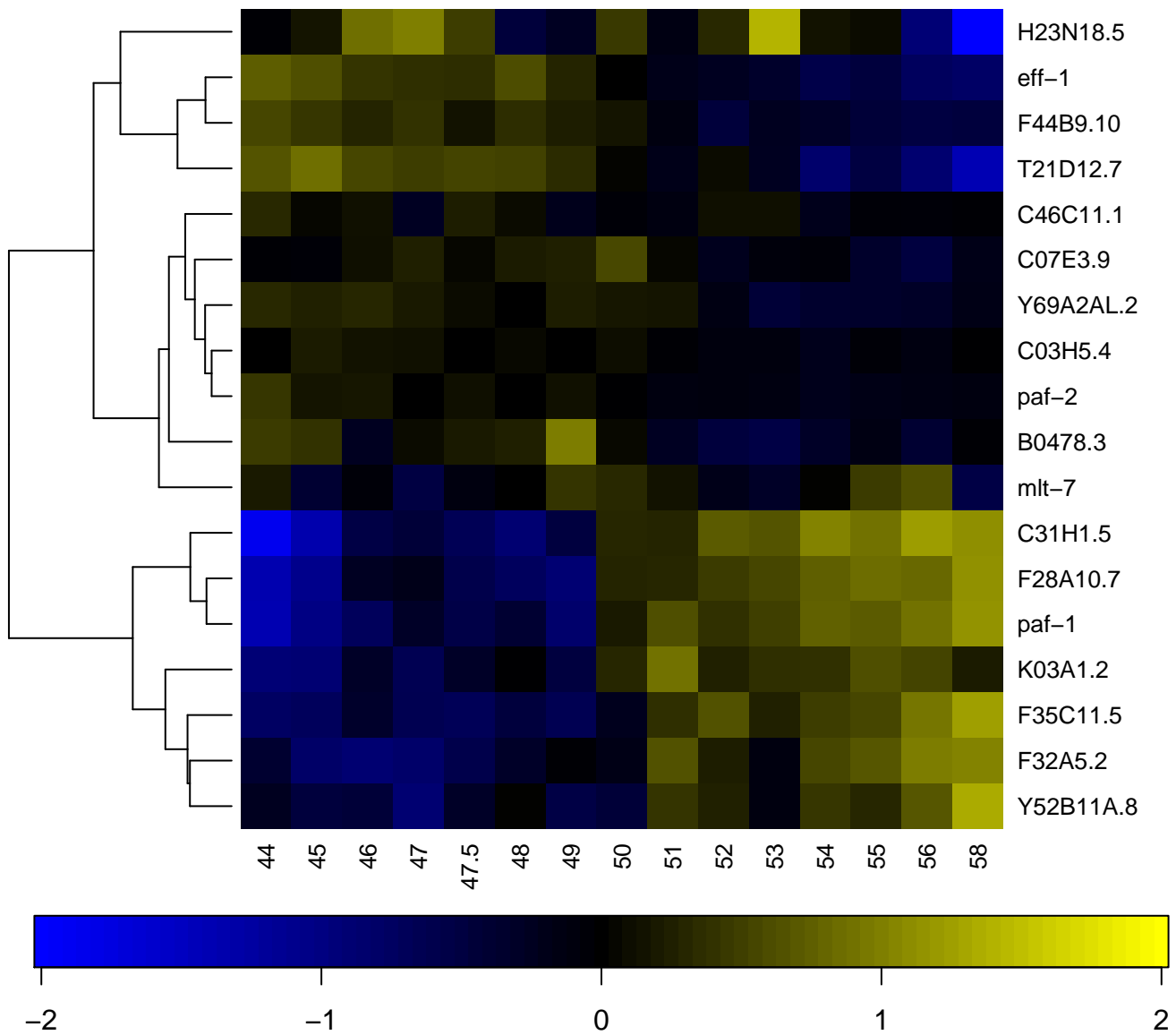
ligand-dependent nuclear receptor activity



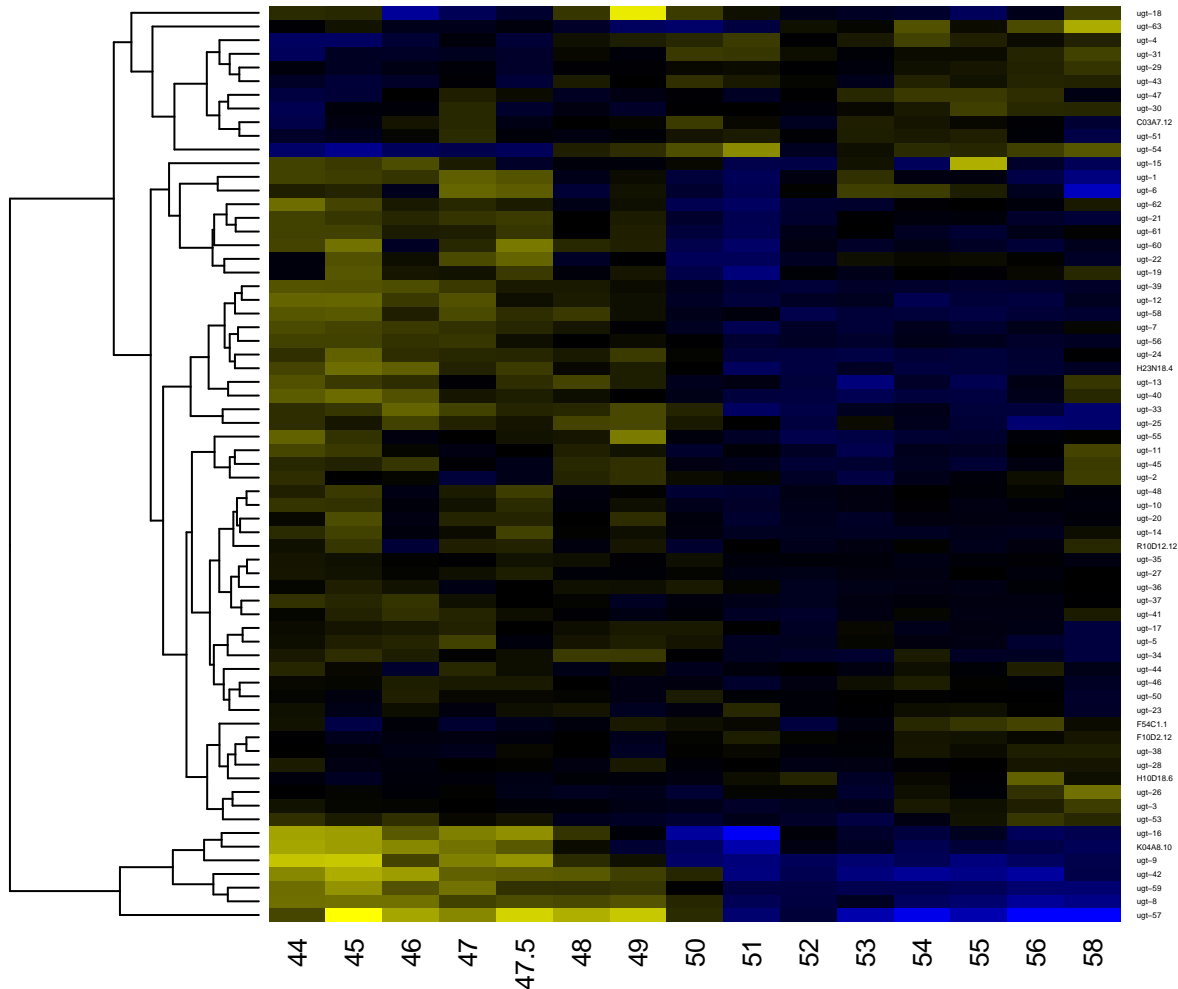
lipid binding



lipid catabolic process



lipid glycosylation



-2

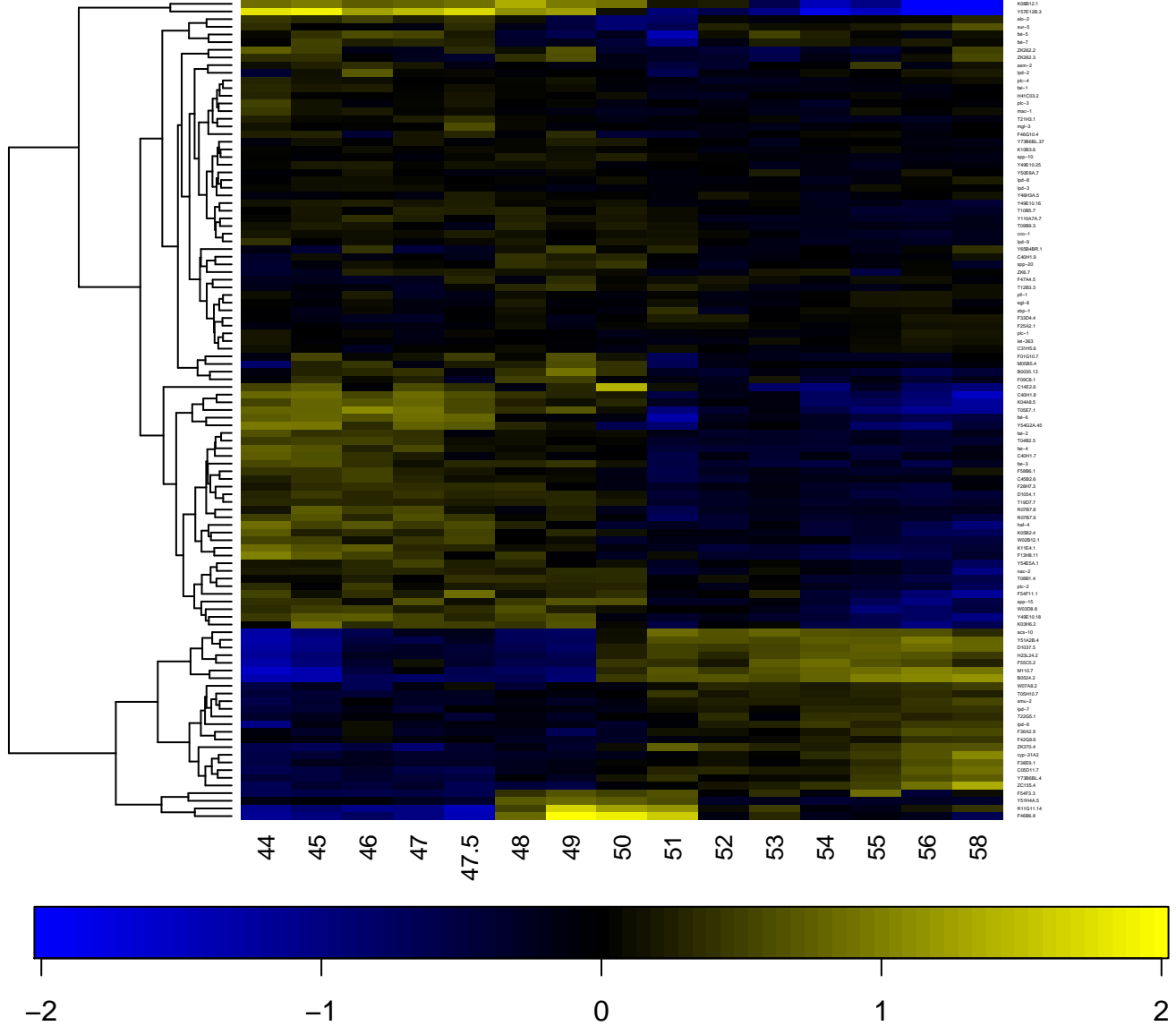
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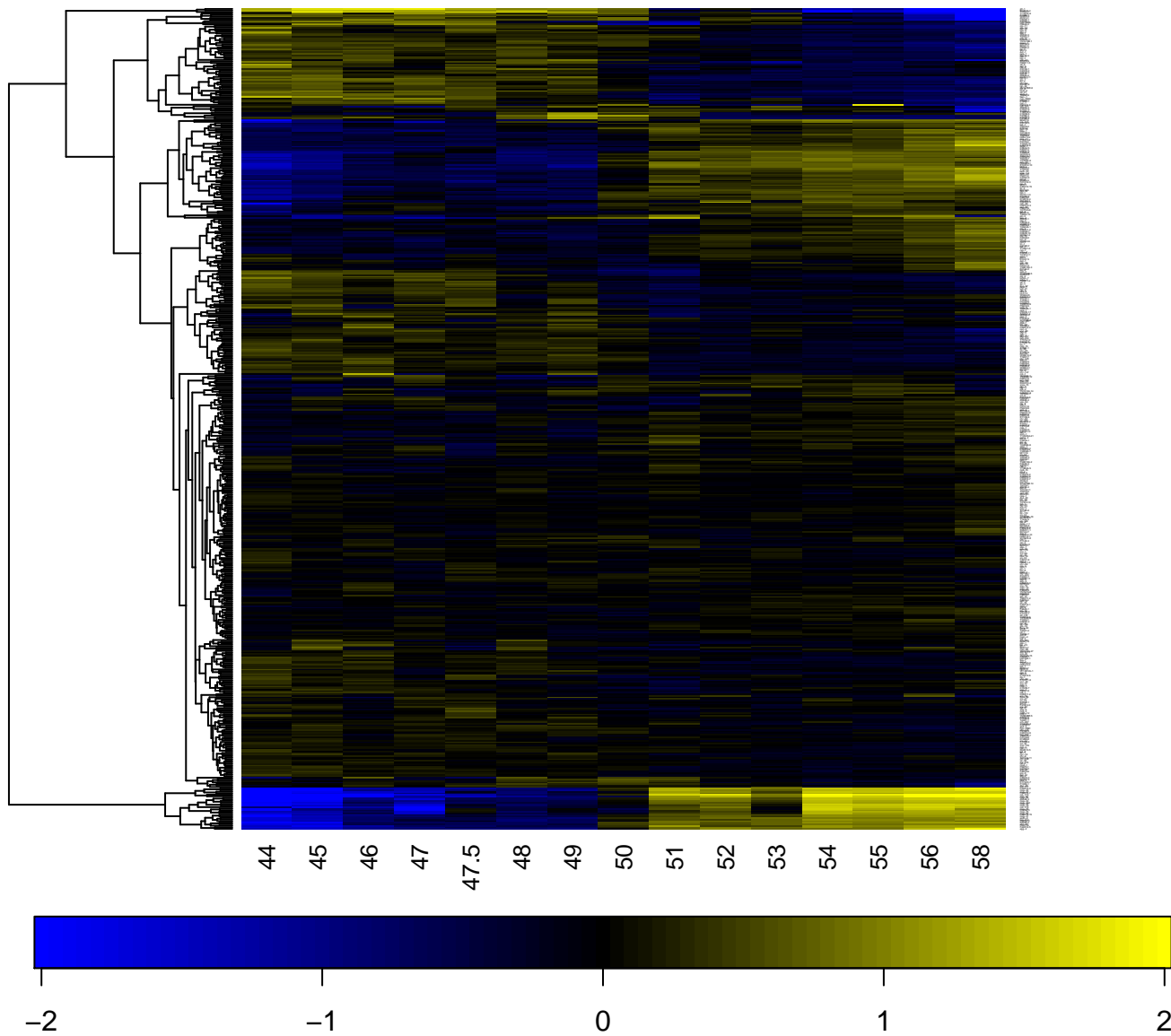
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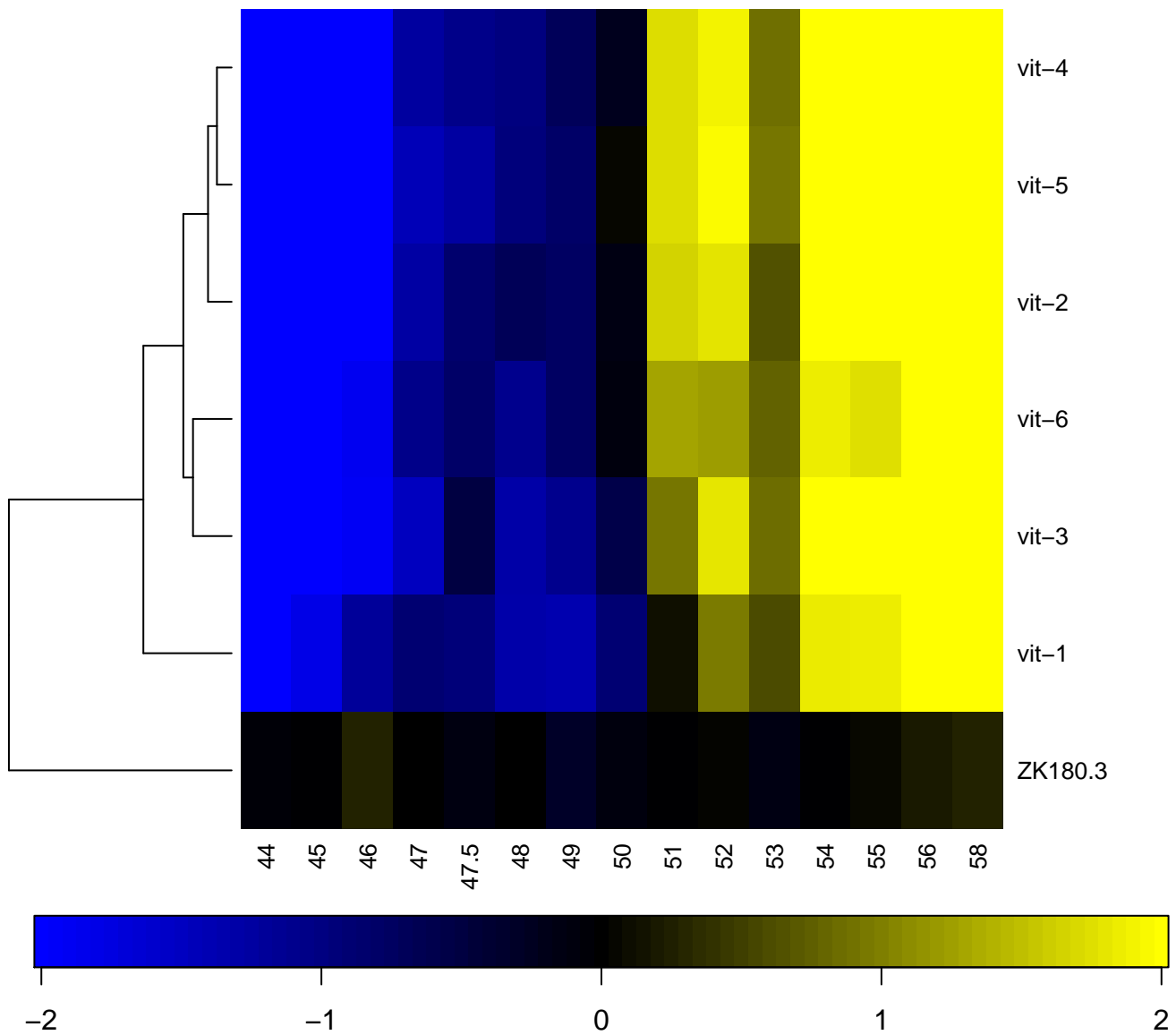
lipid metabolic process



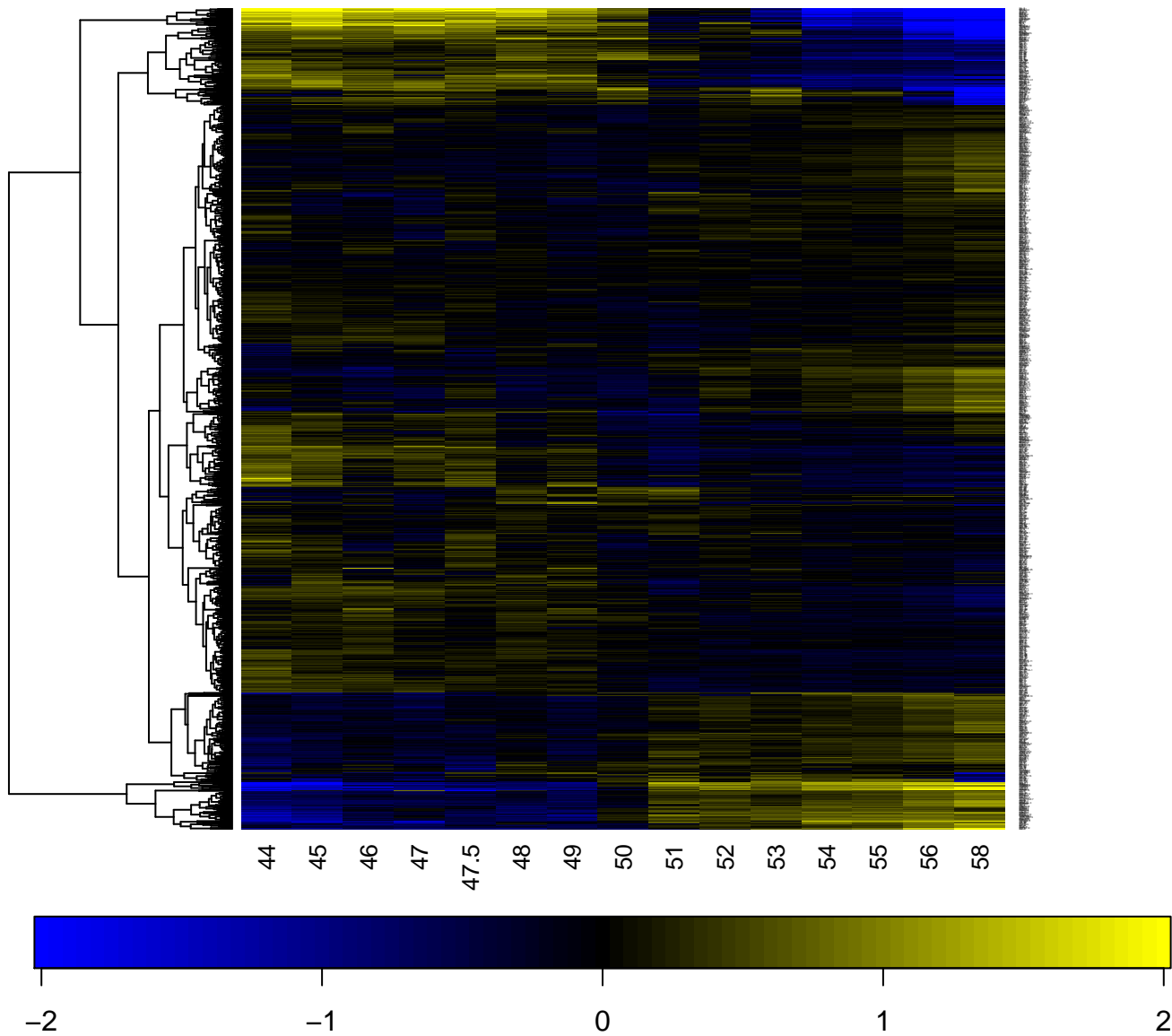
lipid storage



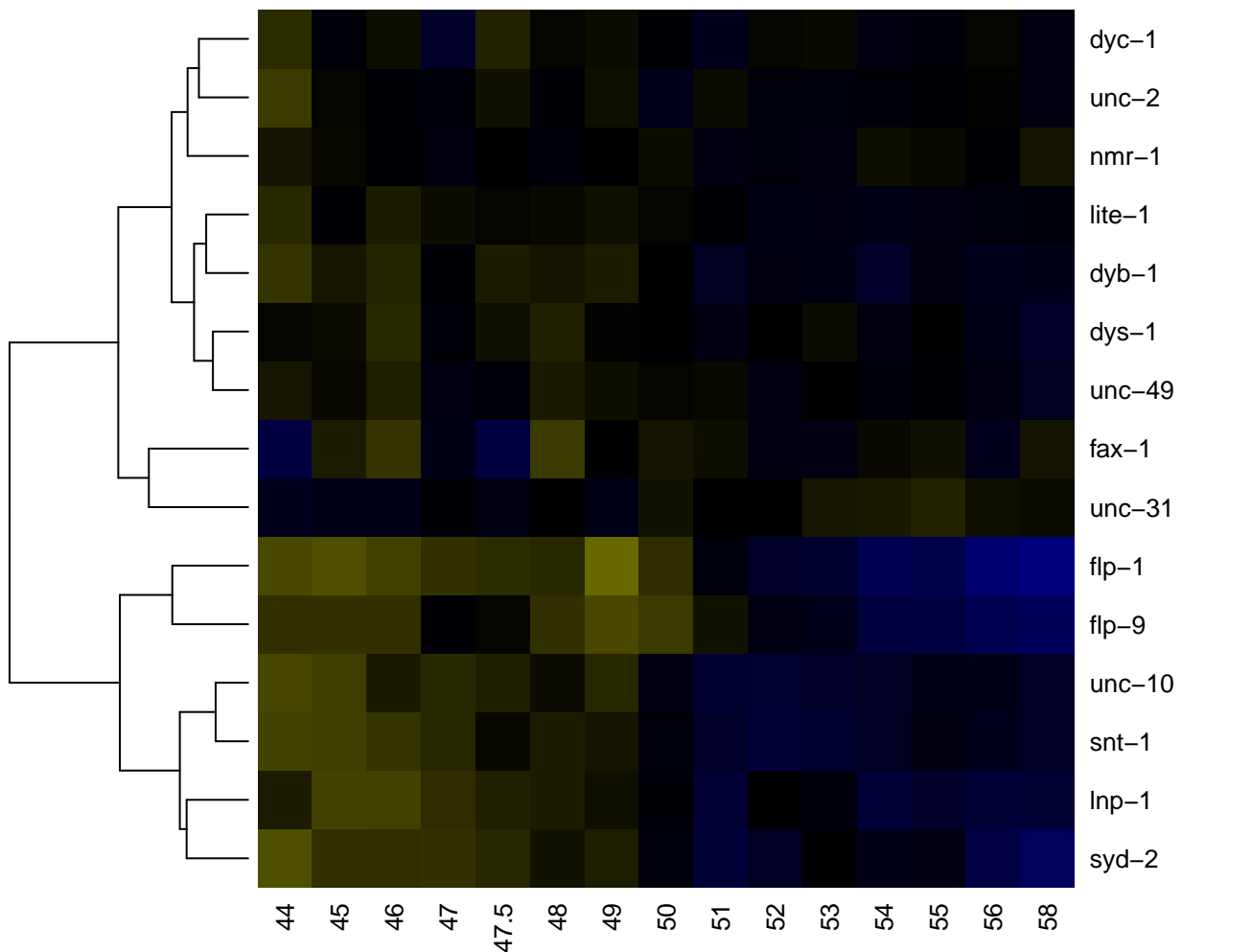
lipid transporter activity



locomotion



locomotory behavior



-2

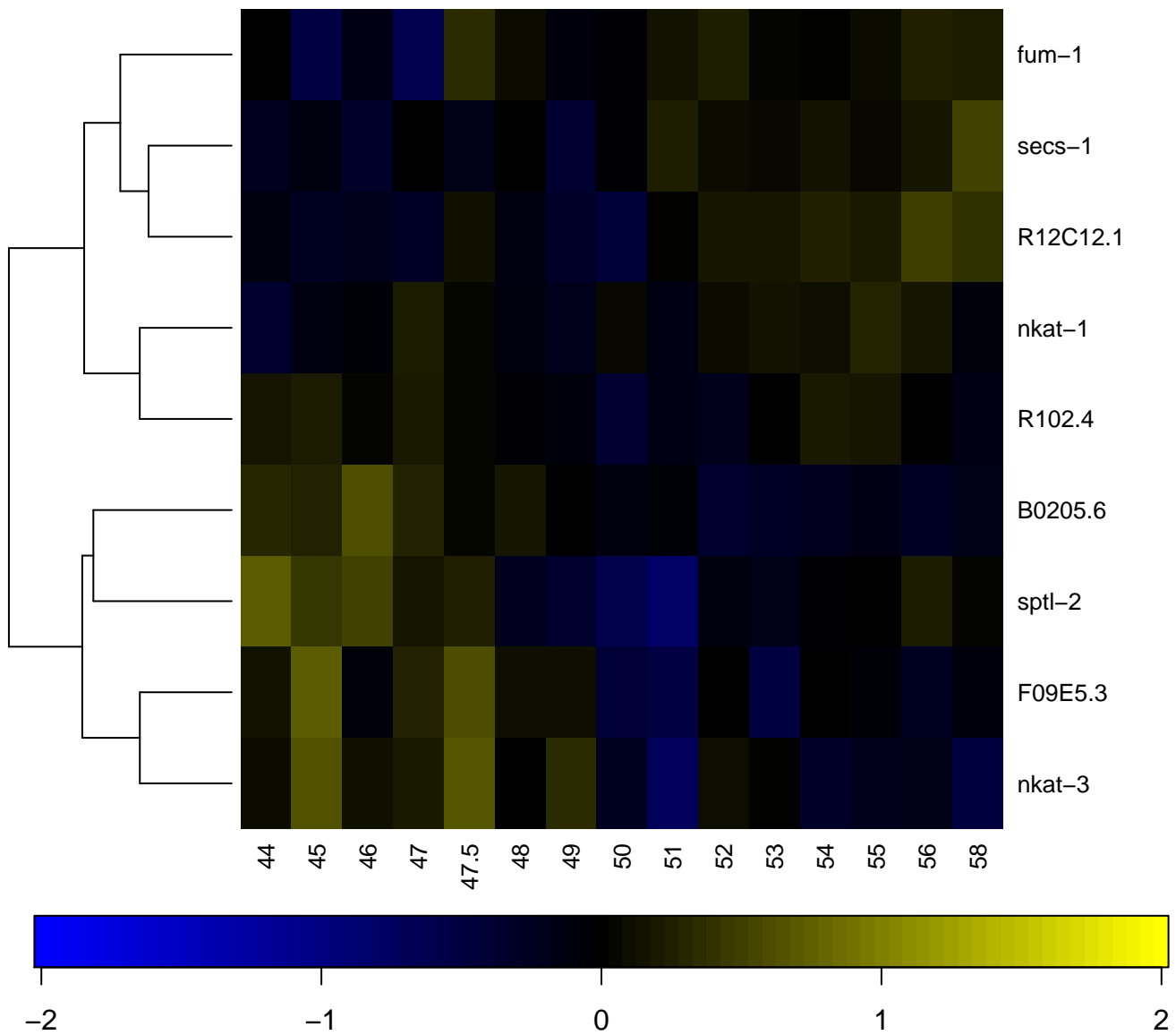
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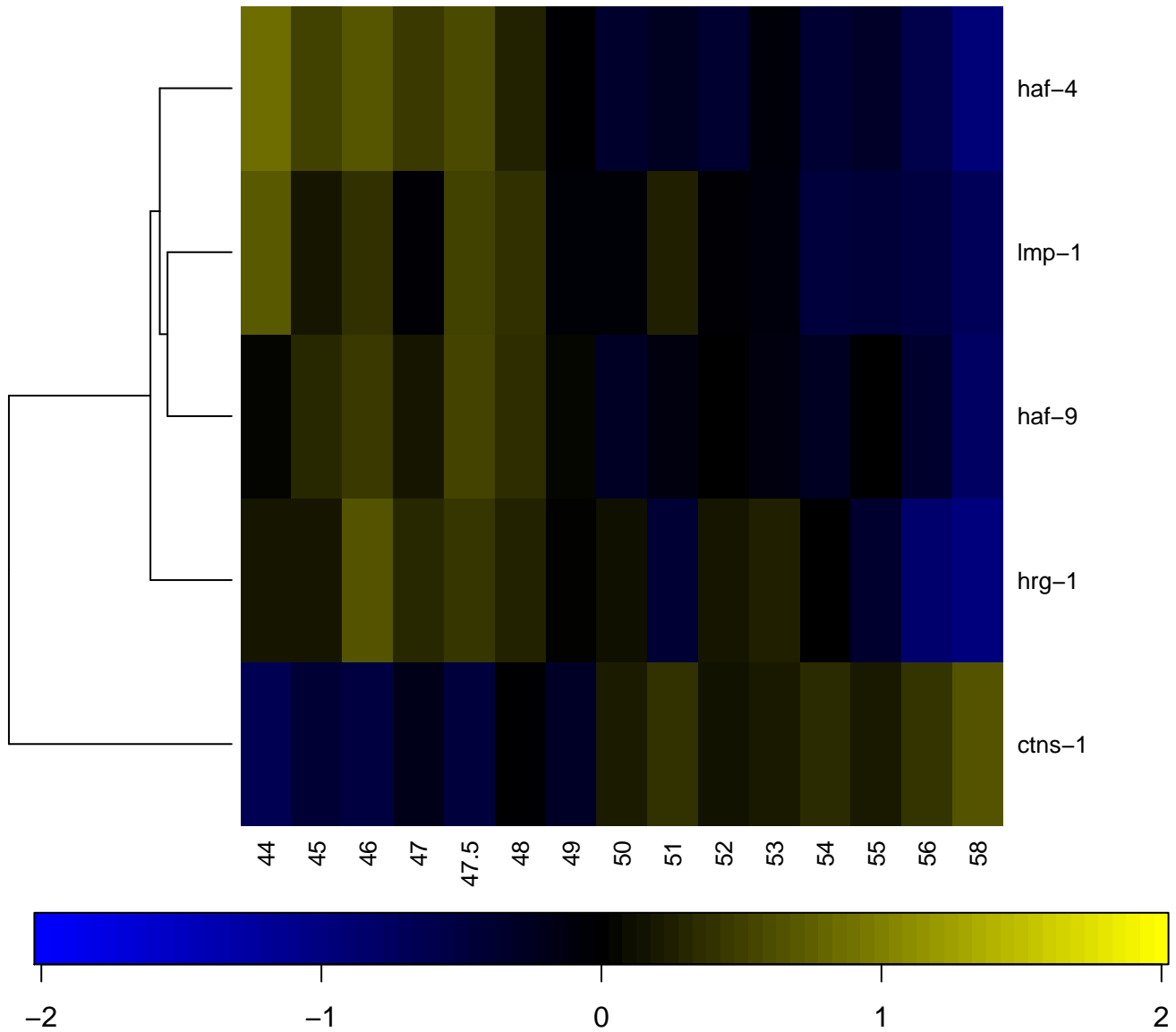
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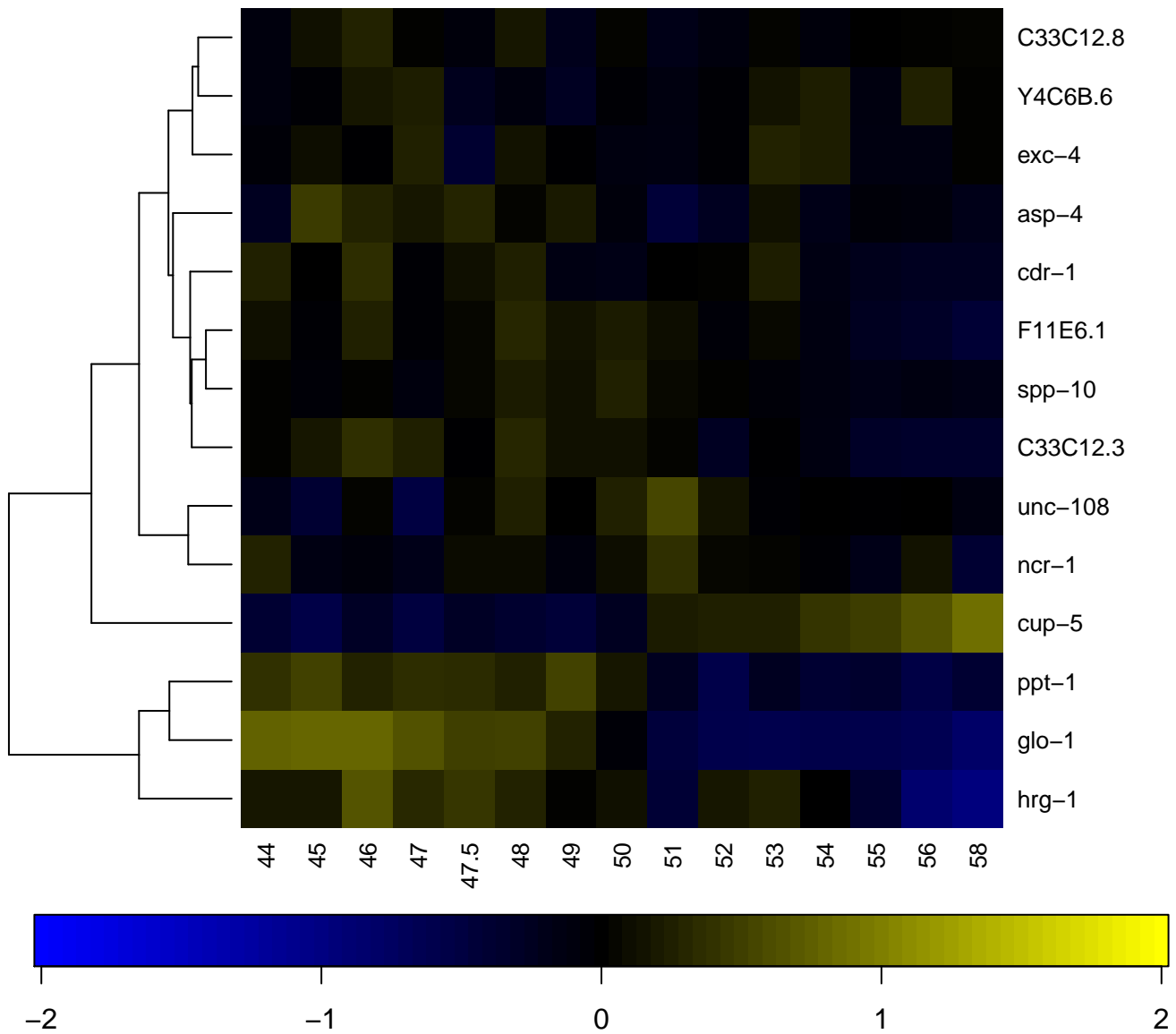
lyase activity



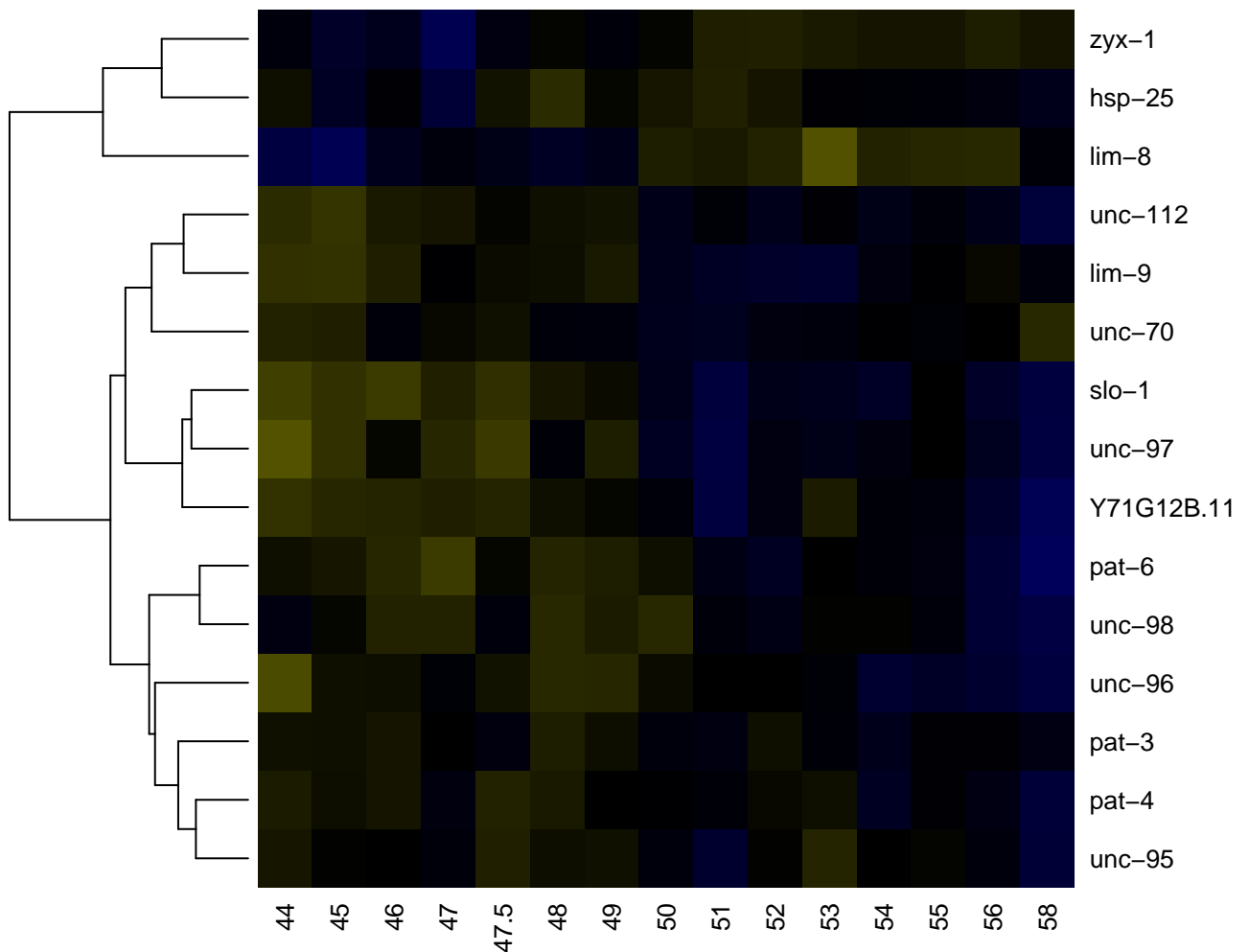
lysosomal membrane



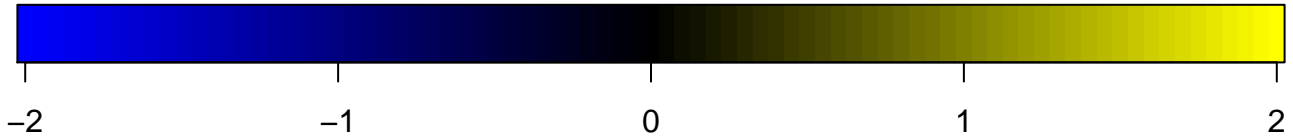
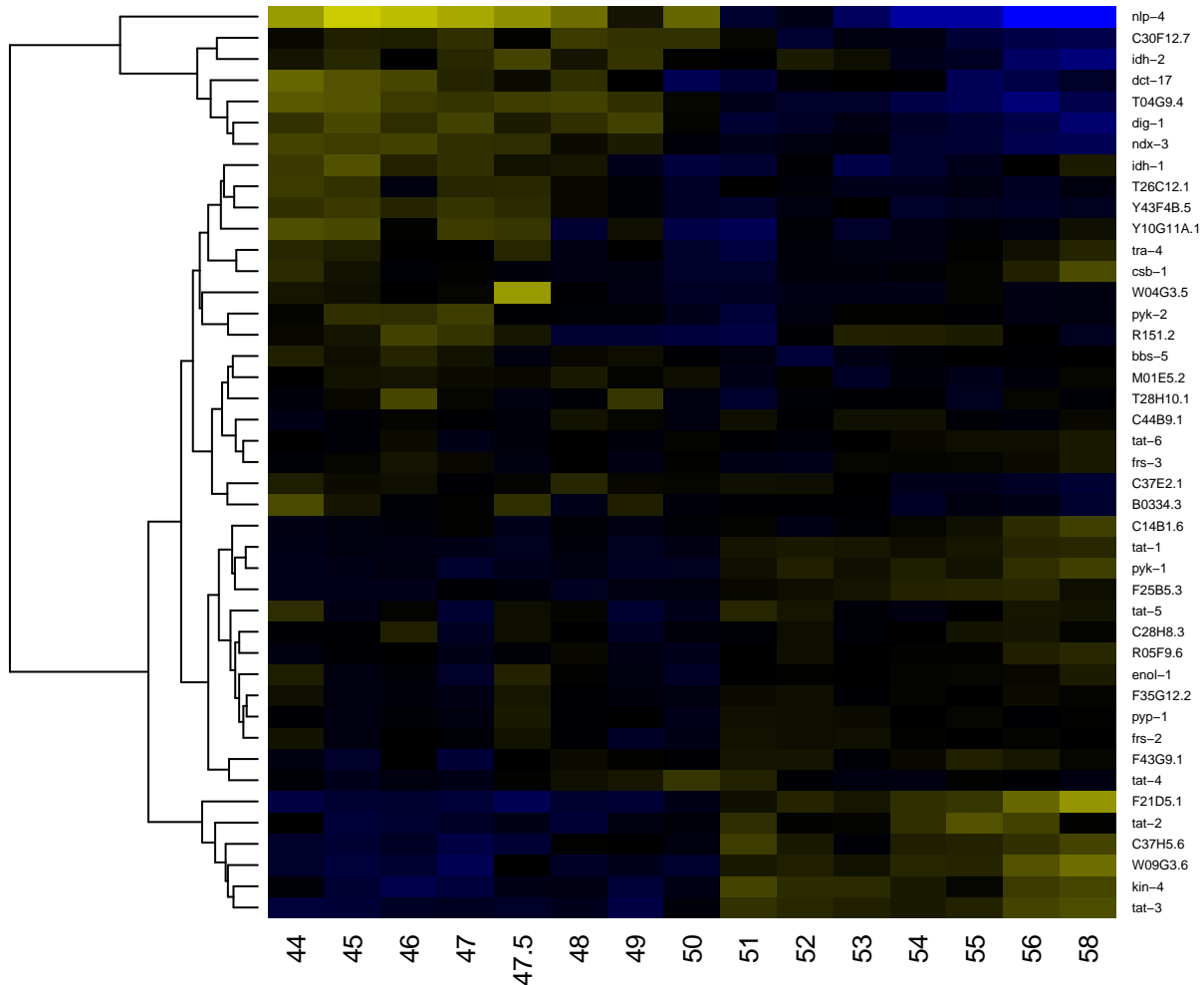
lysosome



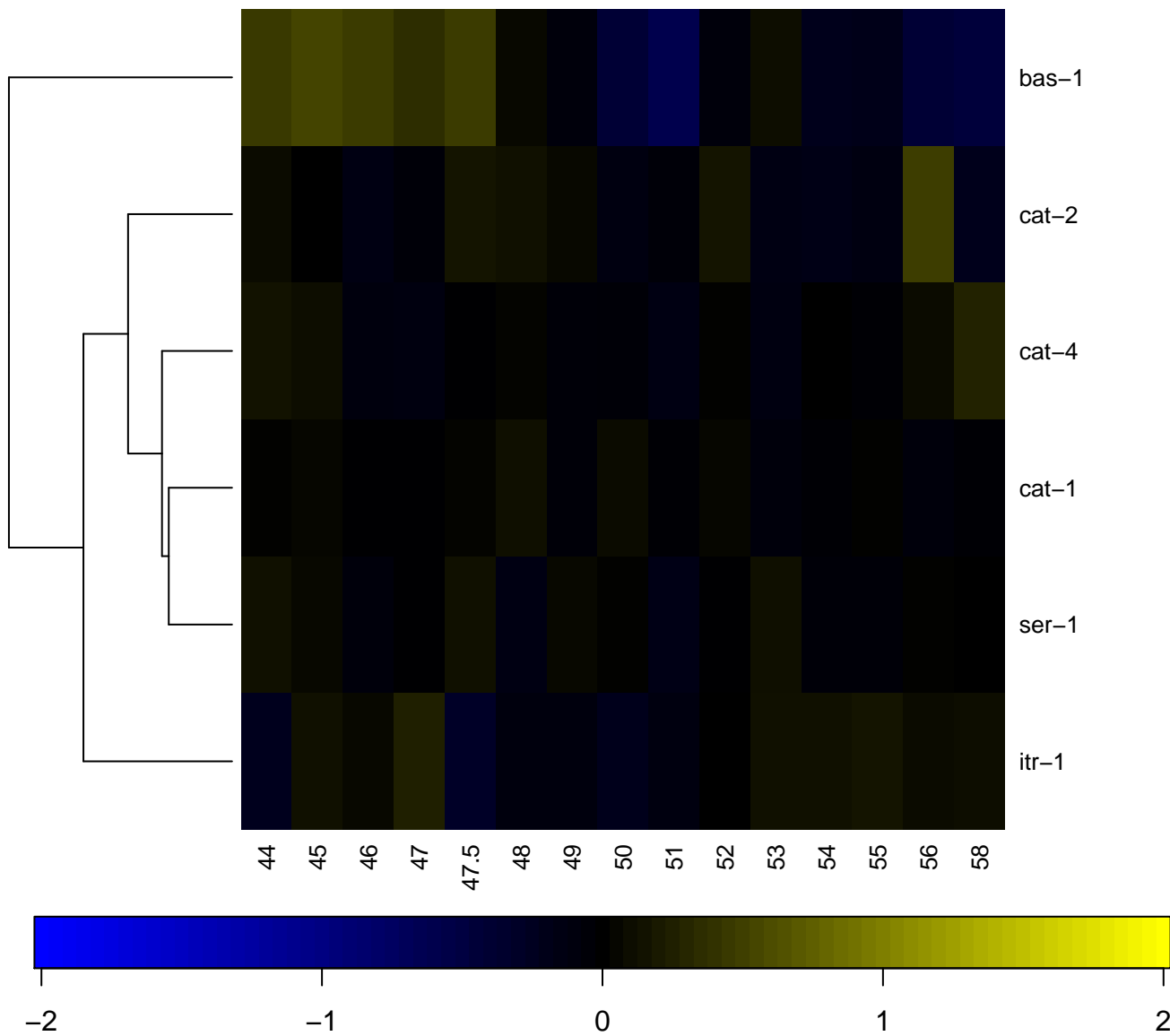
M band



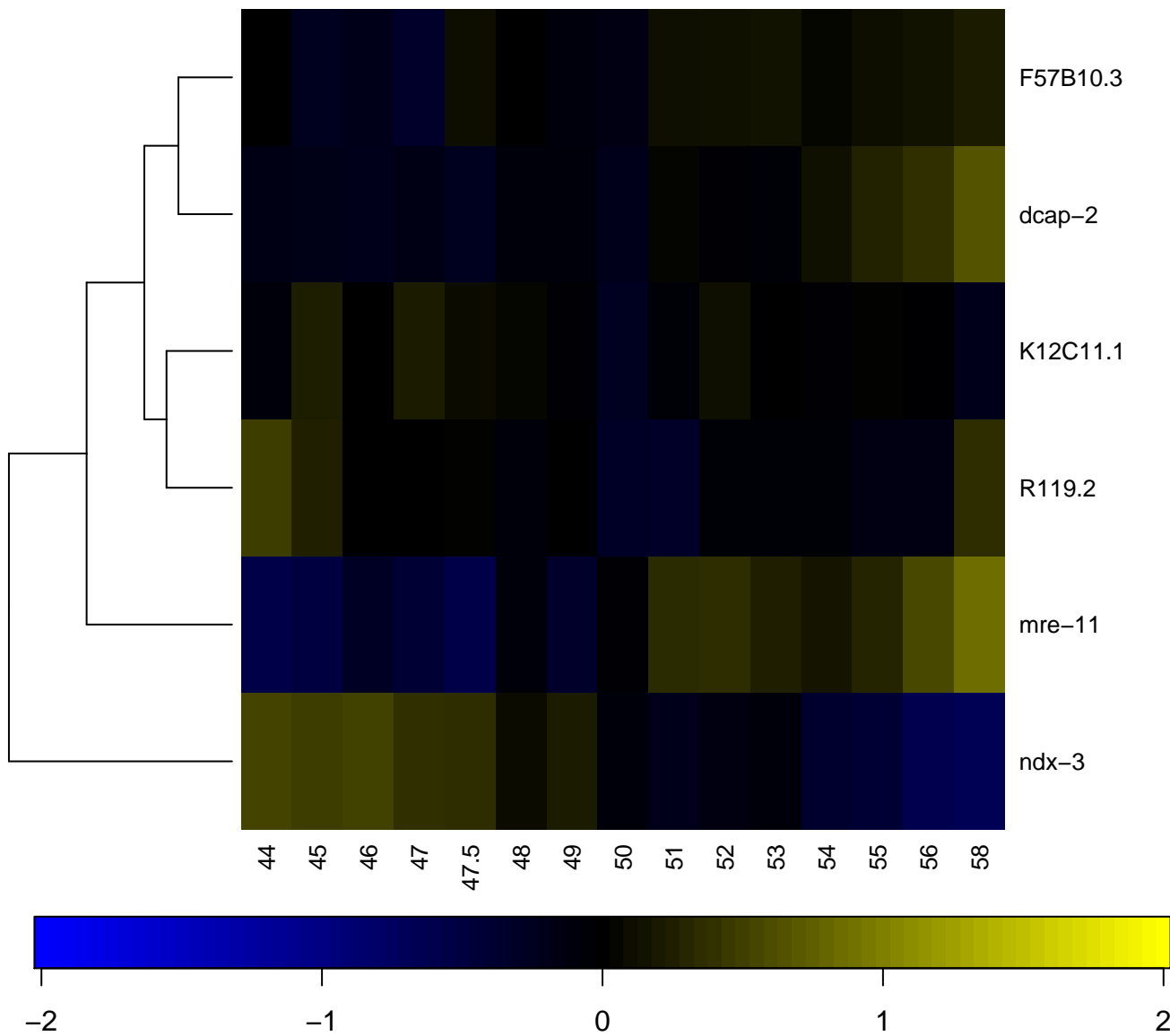
magnesium ion binding



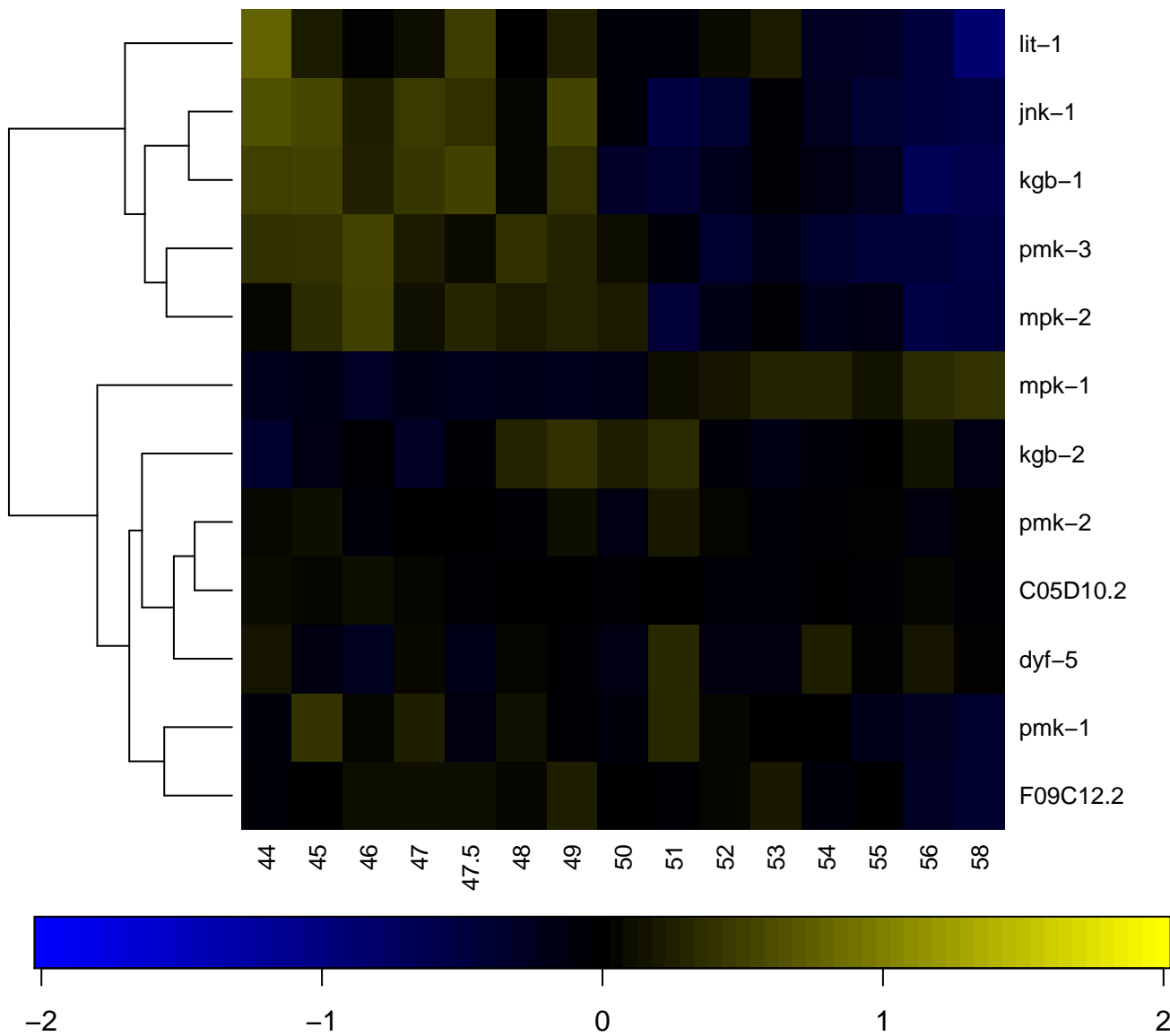
male mating behavior



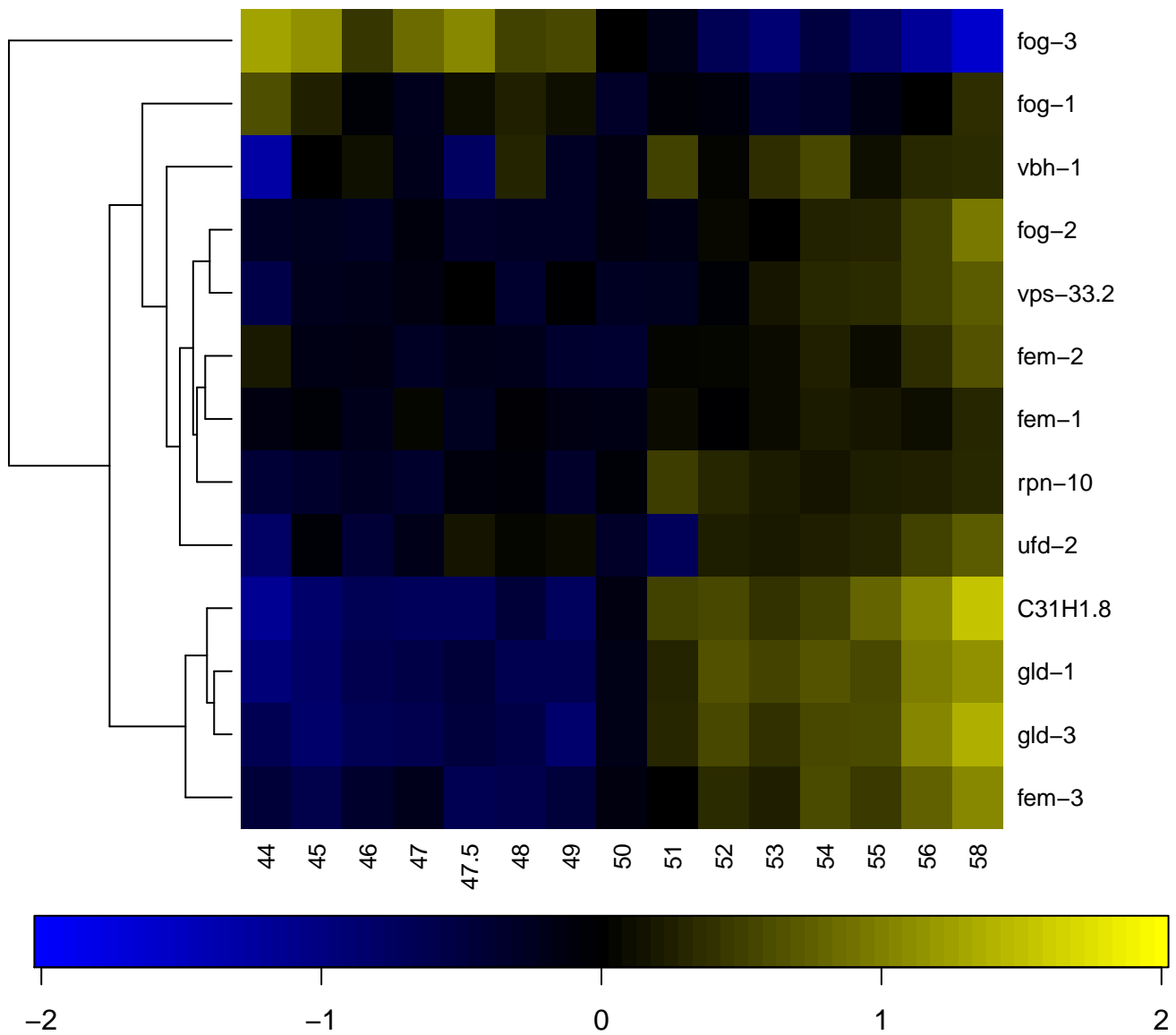
manganese ion binding



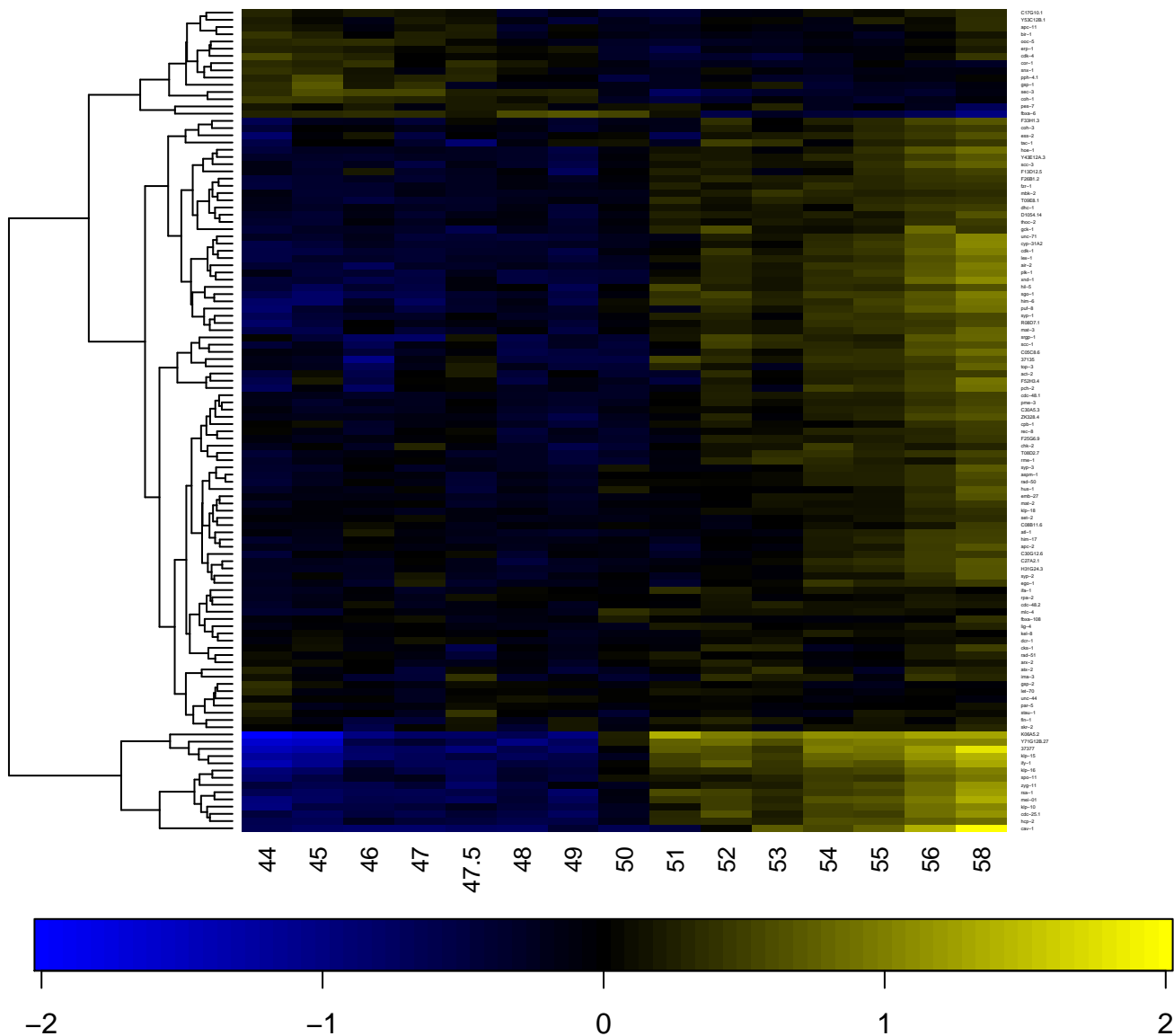
MAP kinase activity



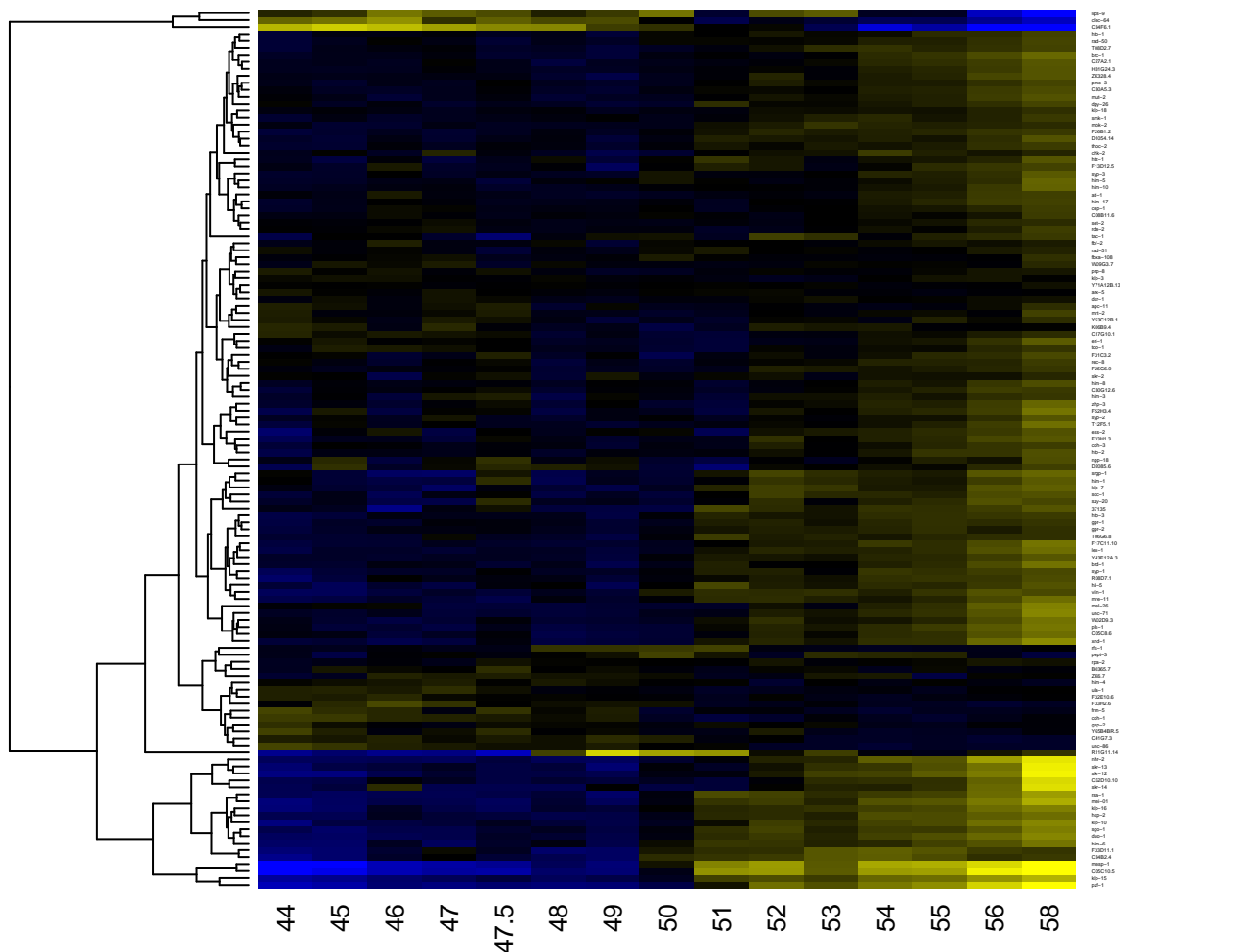
masculinization of hermaphroditic germ-line



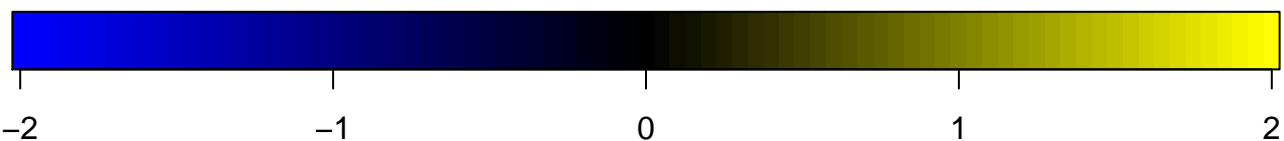
meiosis



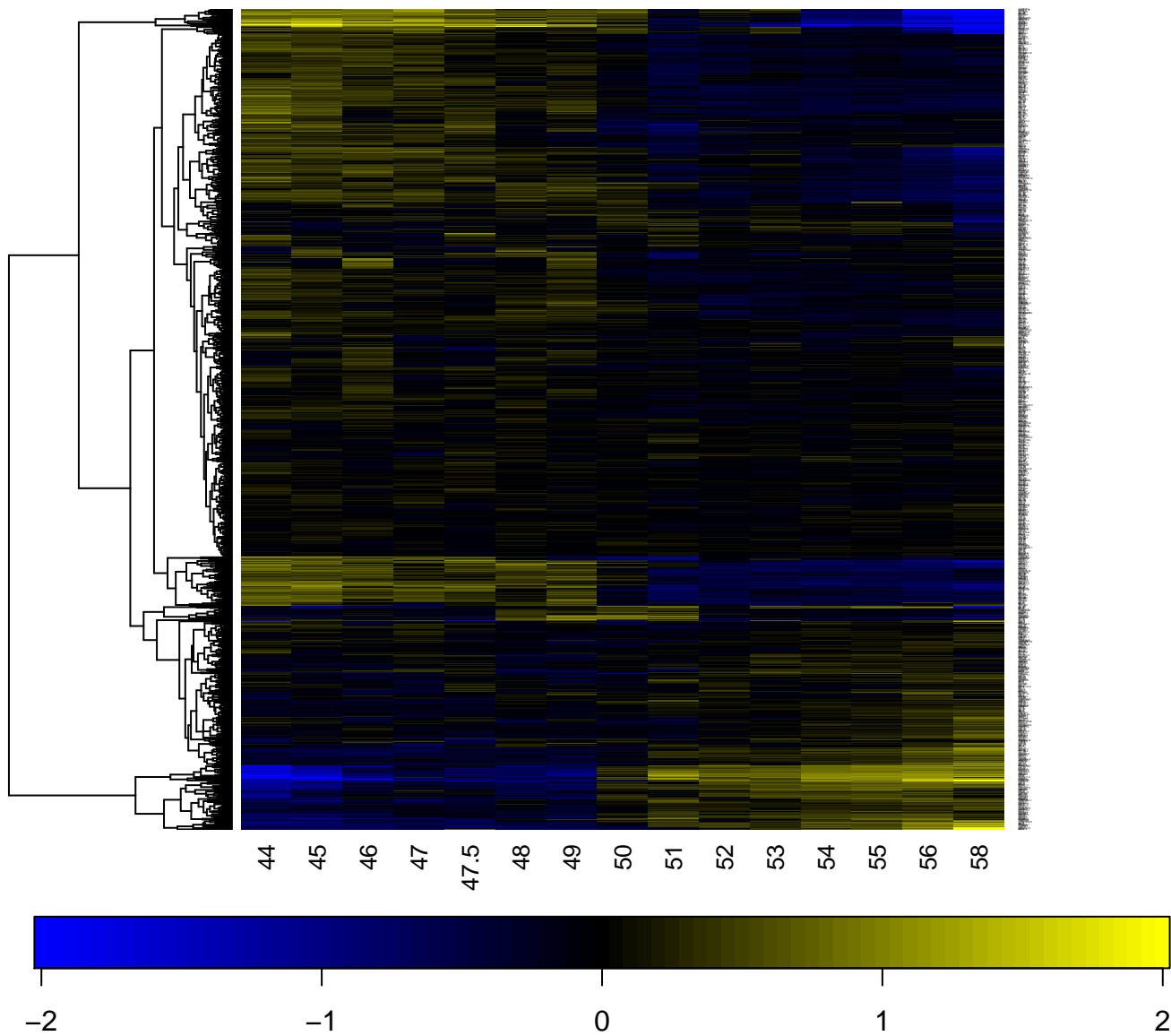
meiotic chromosome segregation



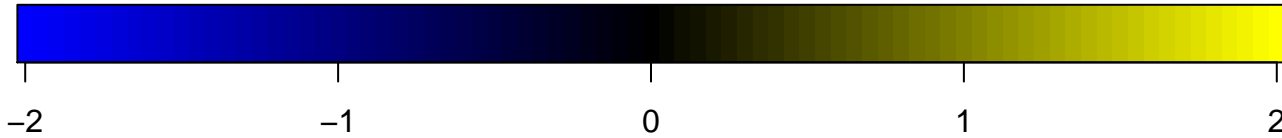
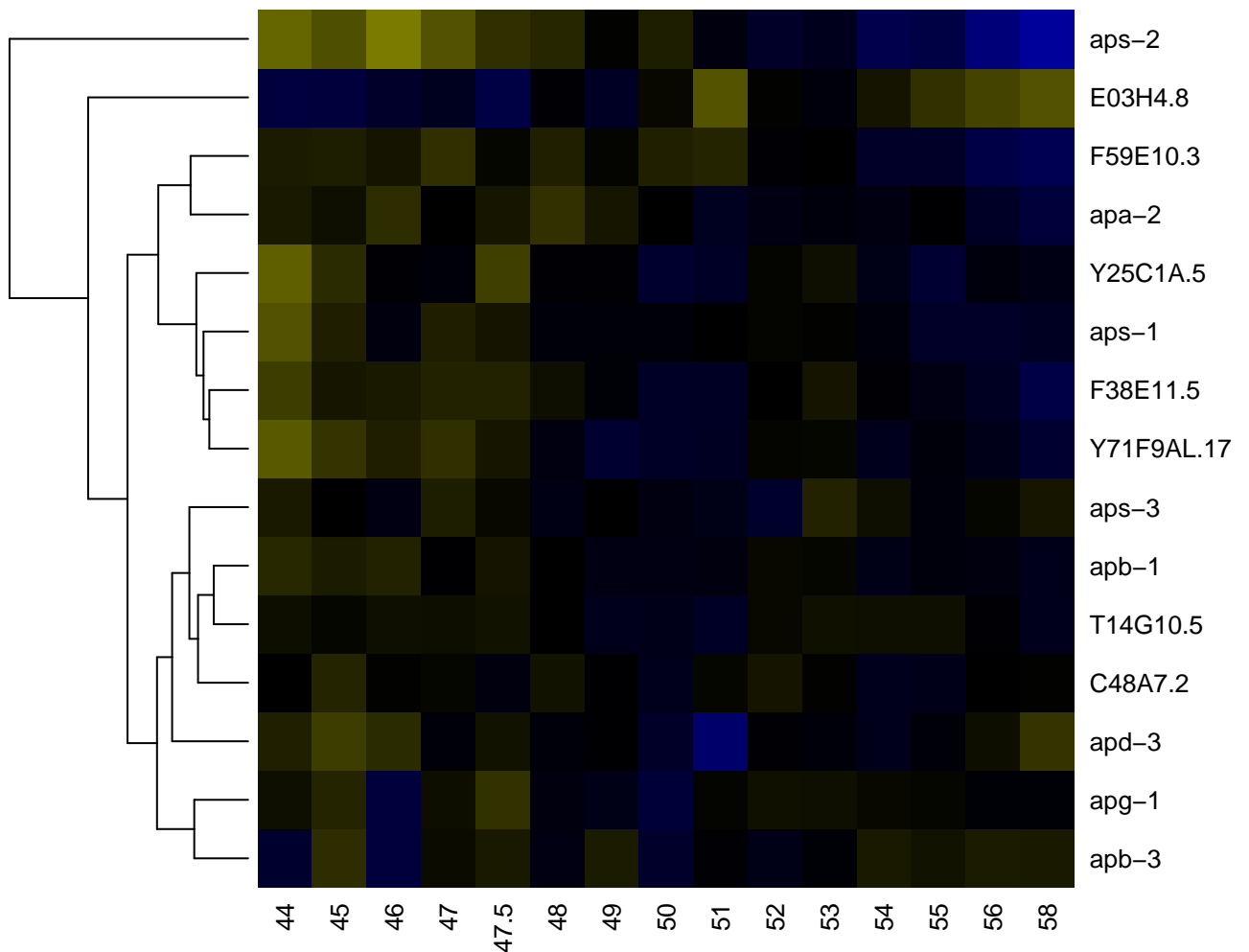
9p-9
PAC9.4
CAP9.1
RAD50
TRIO2
SPO1
C17orf11
RIZ2A3
C20orf4
PRM2
C16orf3
ME1
SPY2
ME1
FMR2
FMR14
ME2
ME3
SPO1
SPO2
SPO3
SPO4
SPO5
SPO6
SPO7
SPO8
SPO9
SPO10
SPO11
SPO12
SPO13
SPO14
SPO15
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SPO17
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SPO109
SPO110



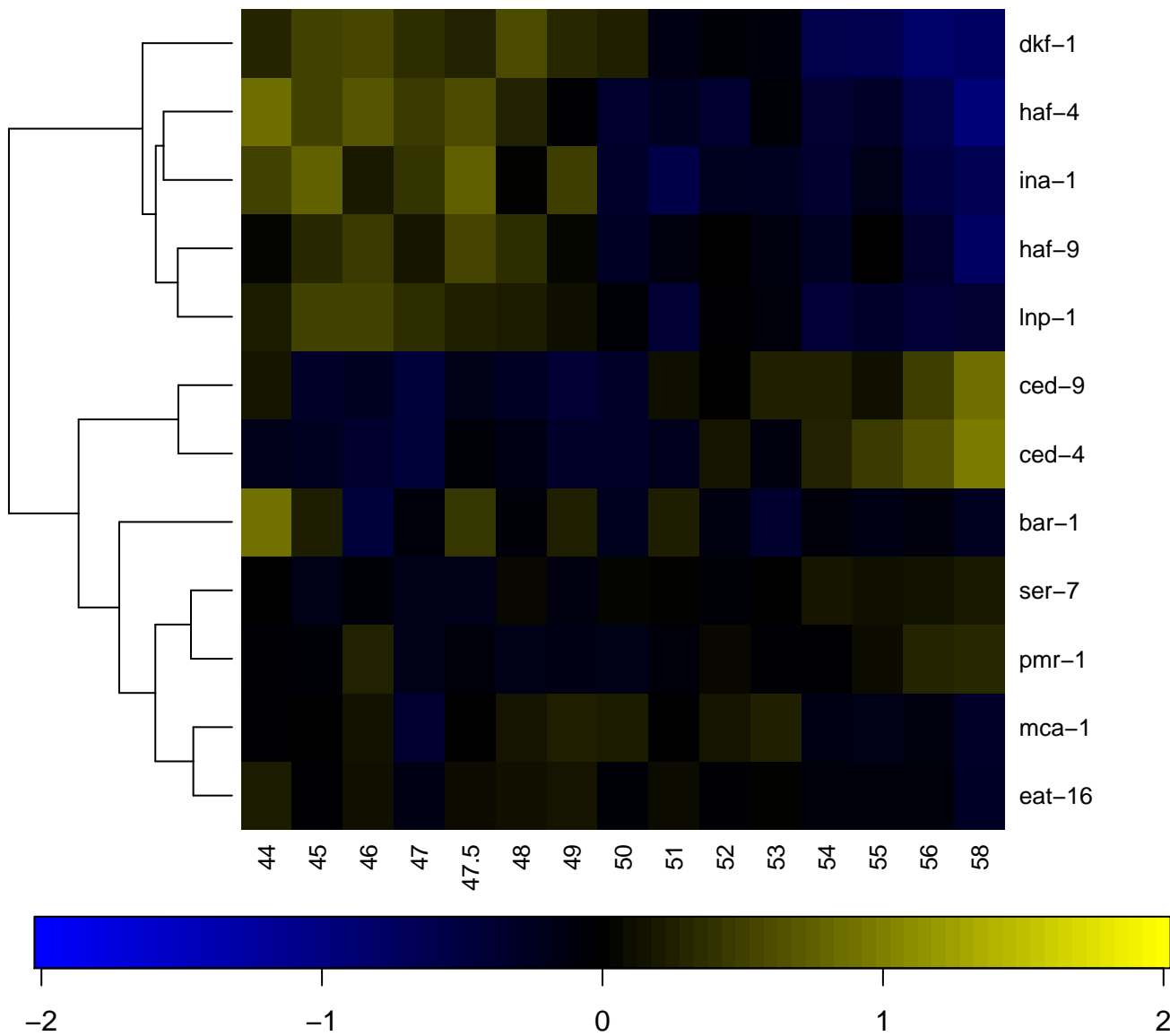
membrane



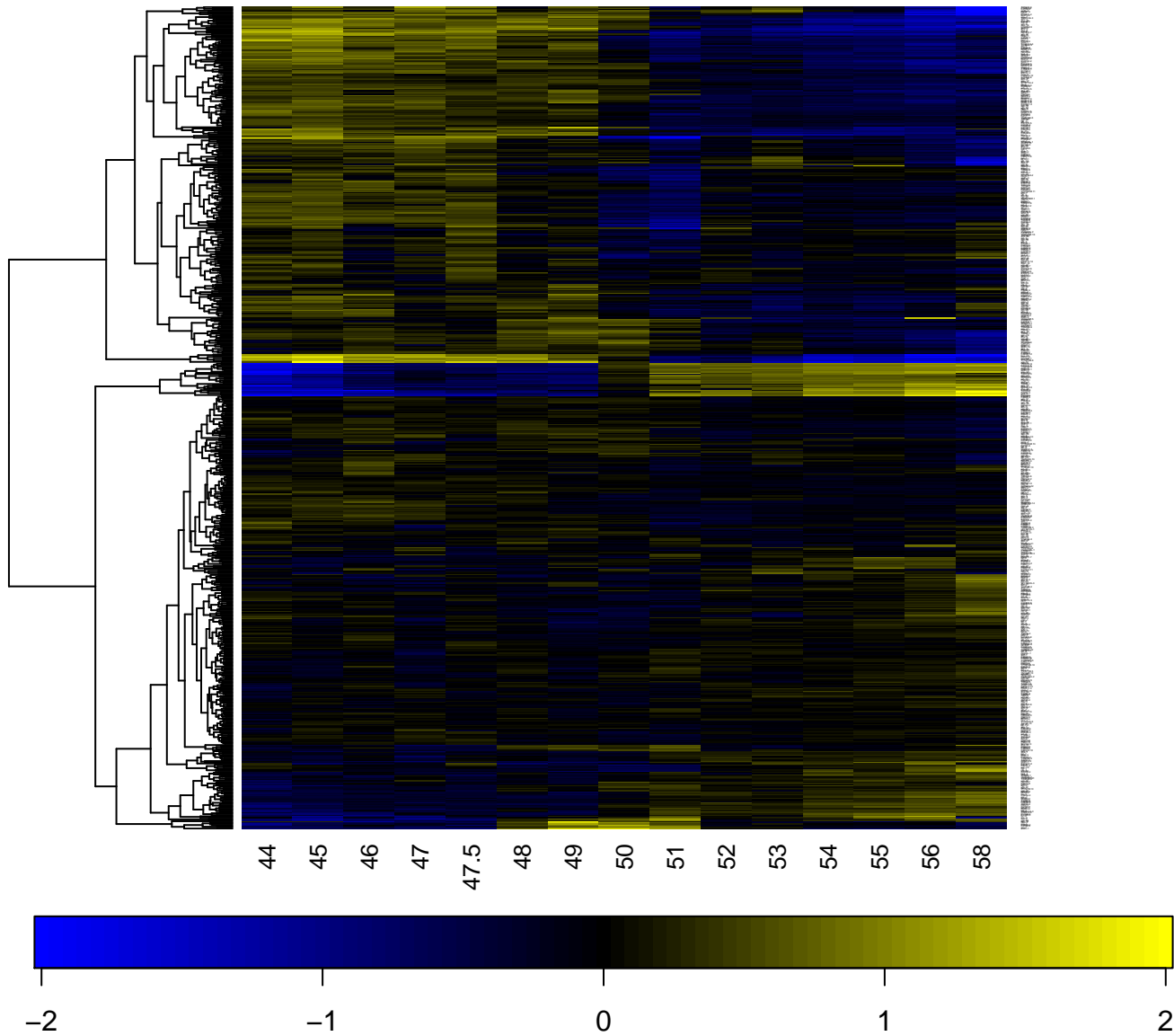
membrane coat



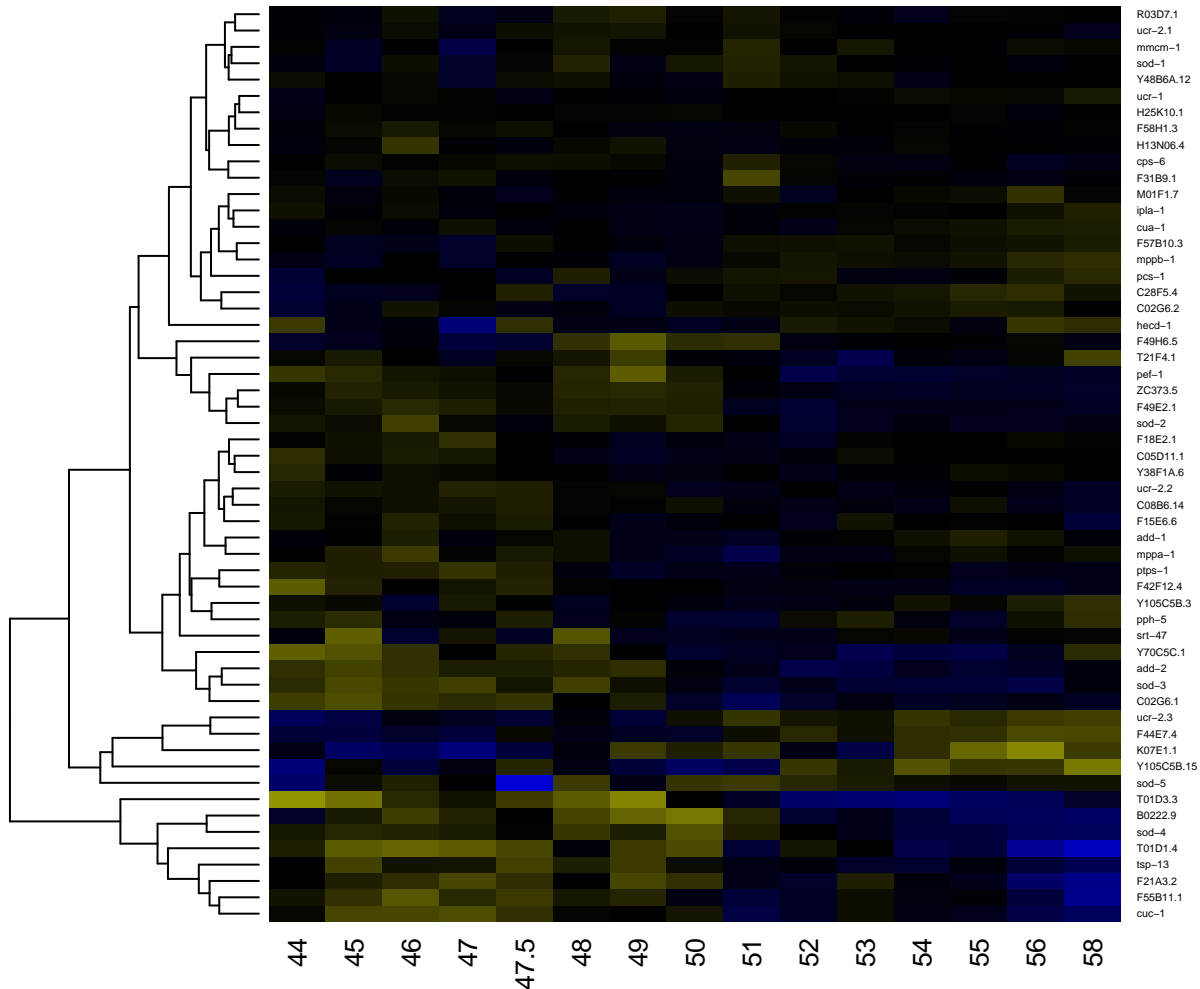
membrane fraction



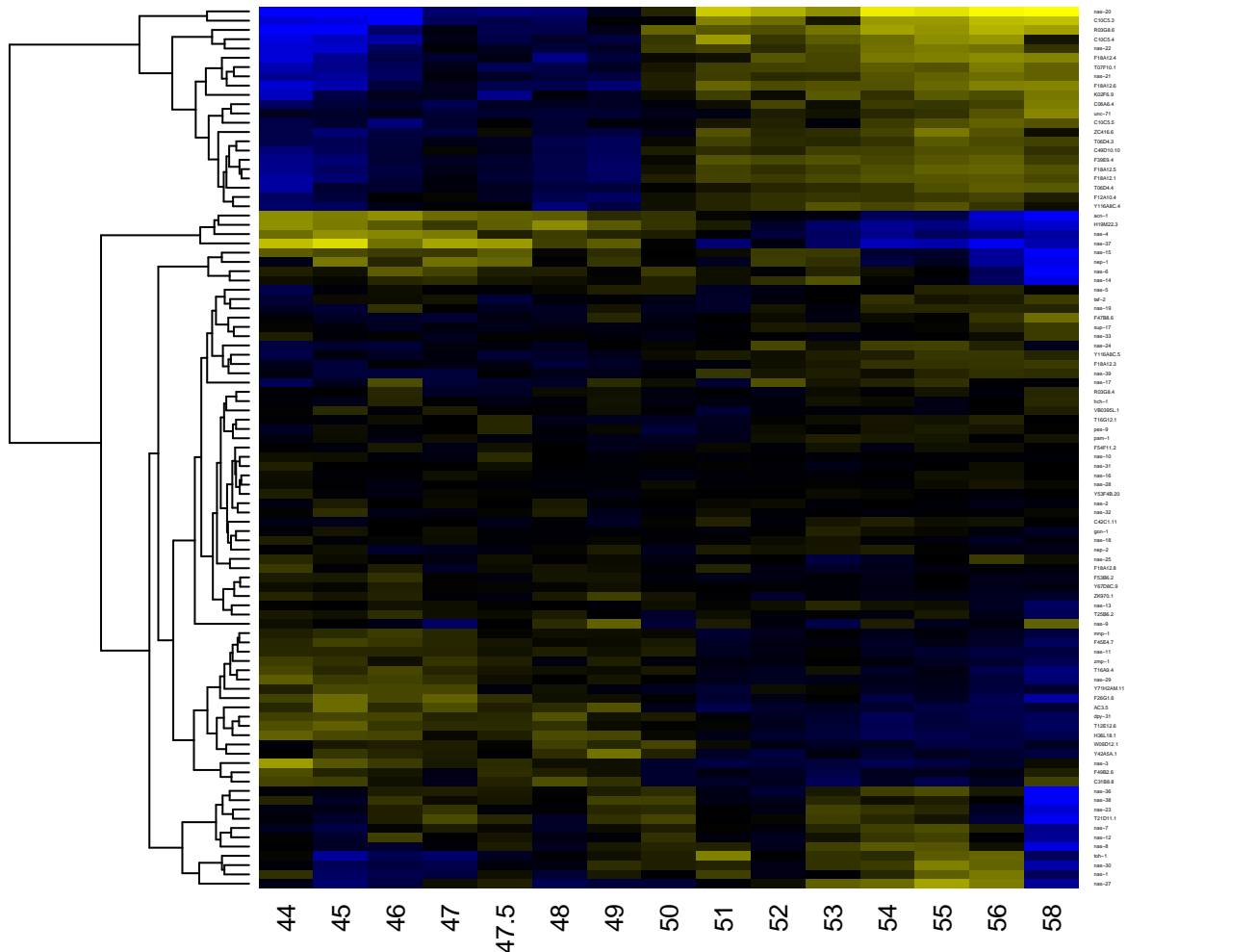
metabolic process



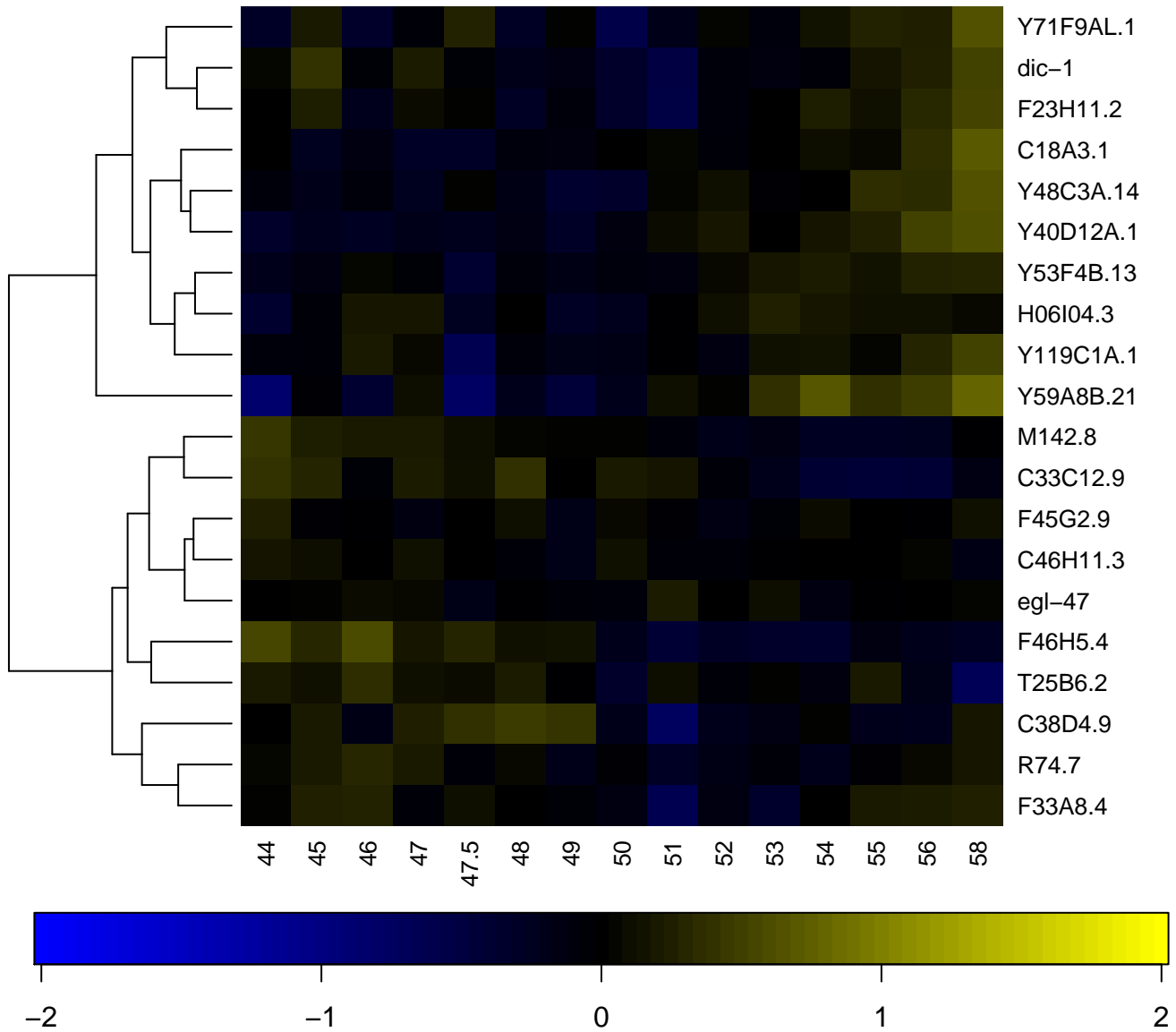
metal ion binding



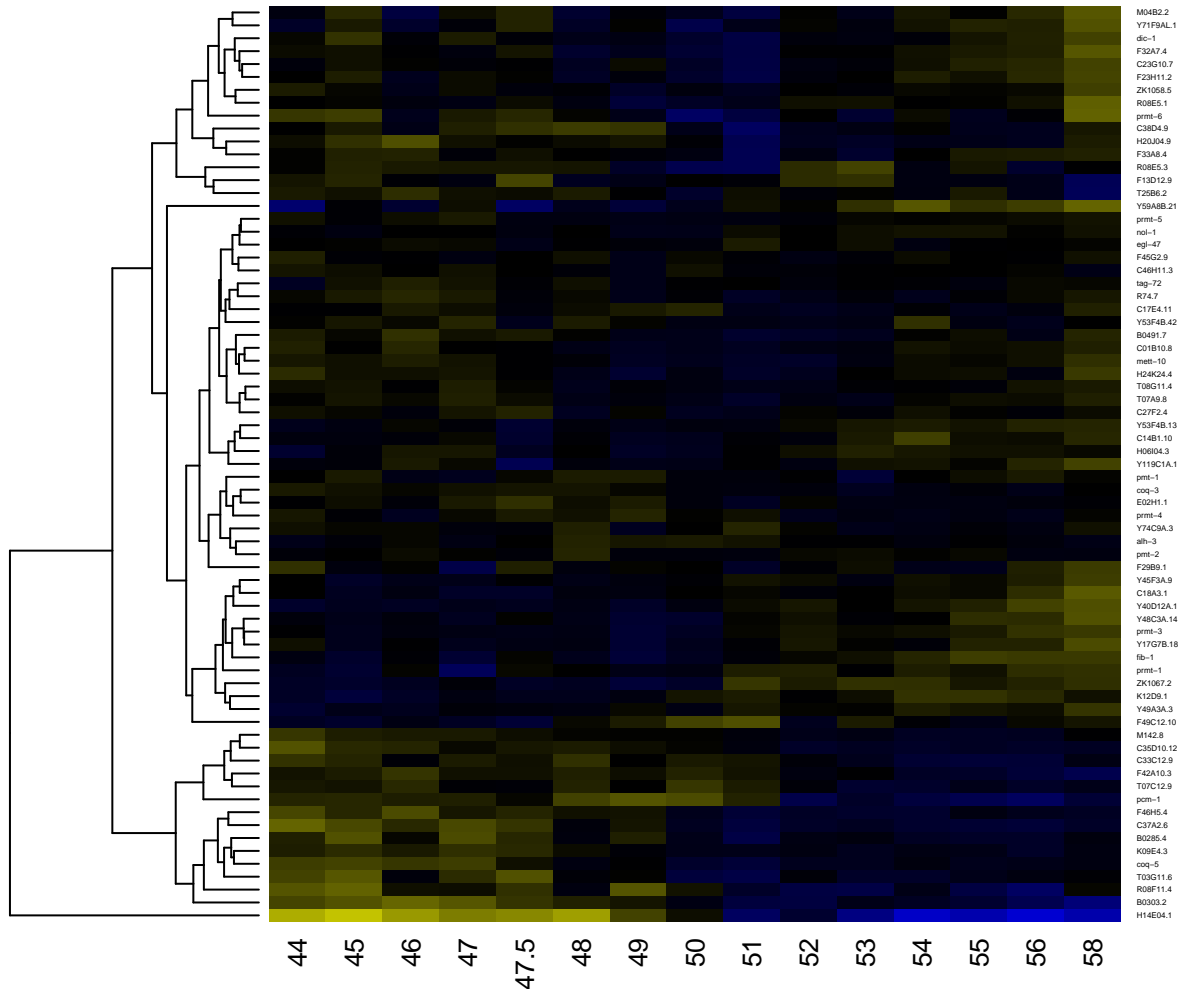
metallopeptidase activity



methylation



methyltransferase activity



-2

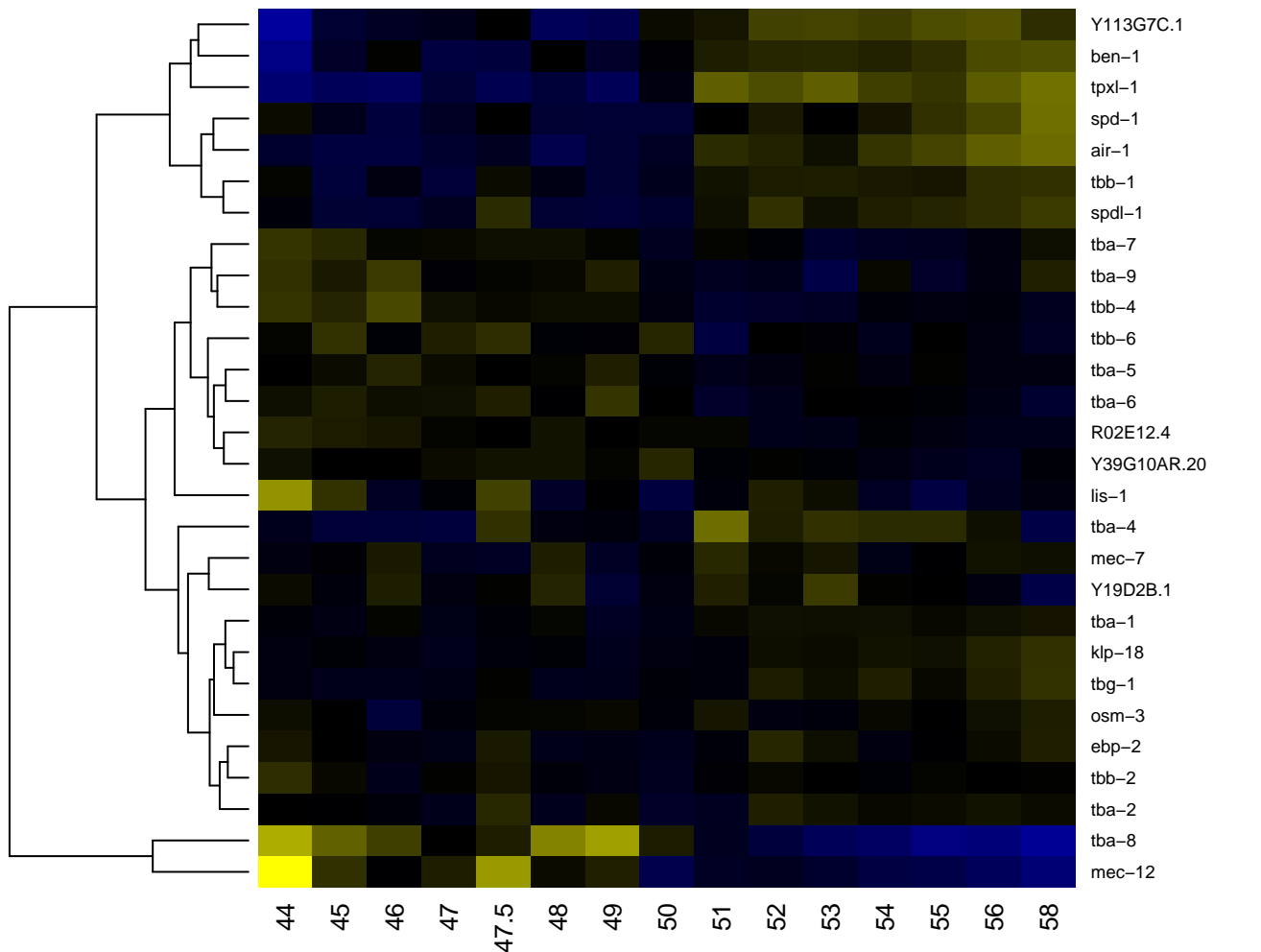
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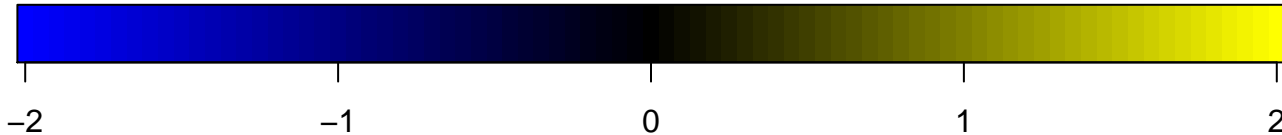
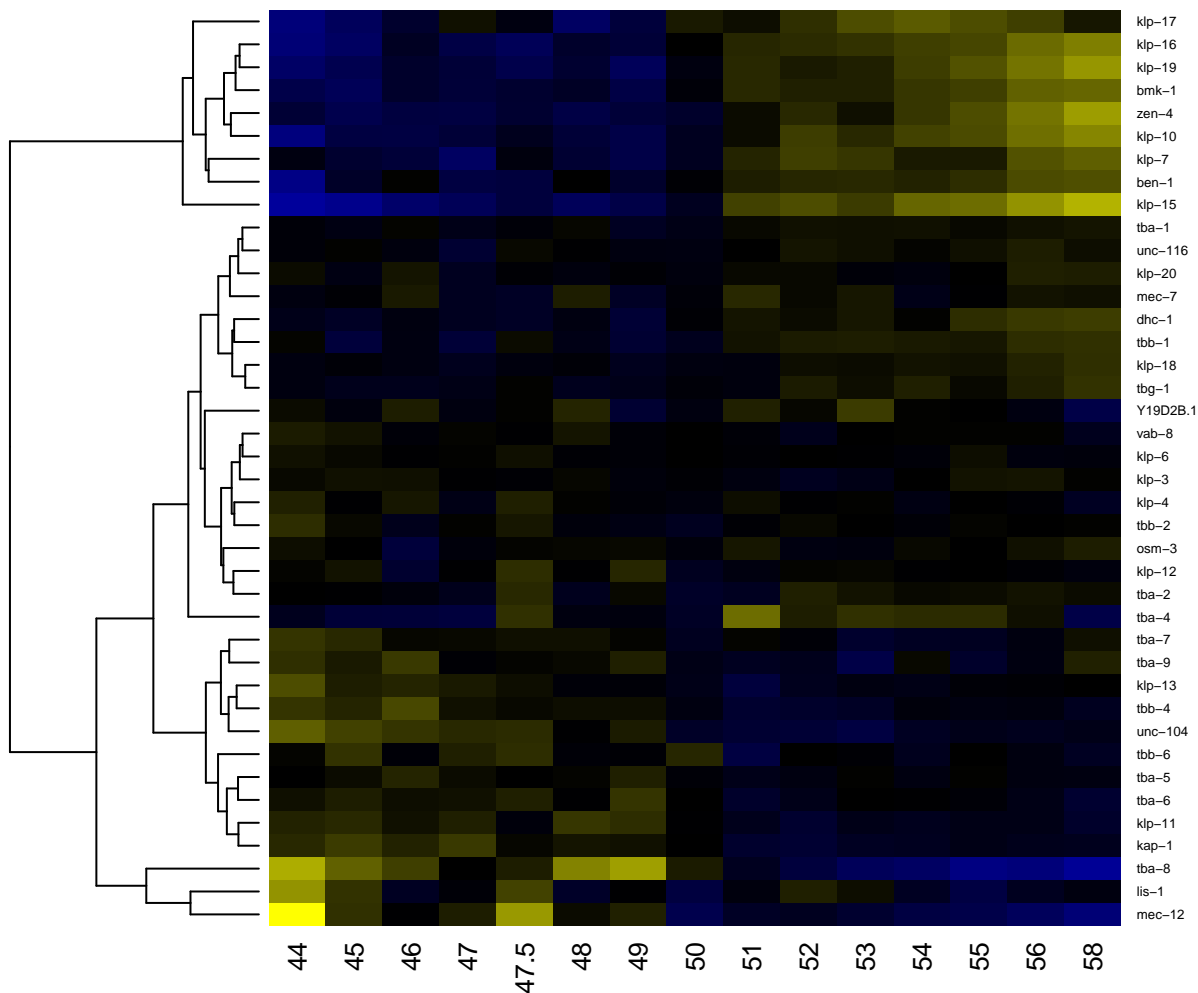
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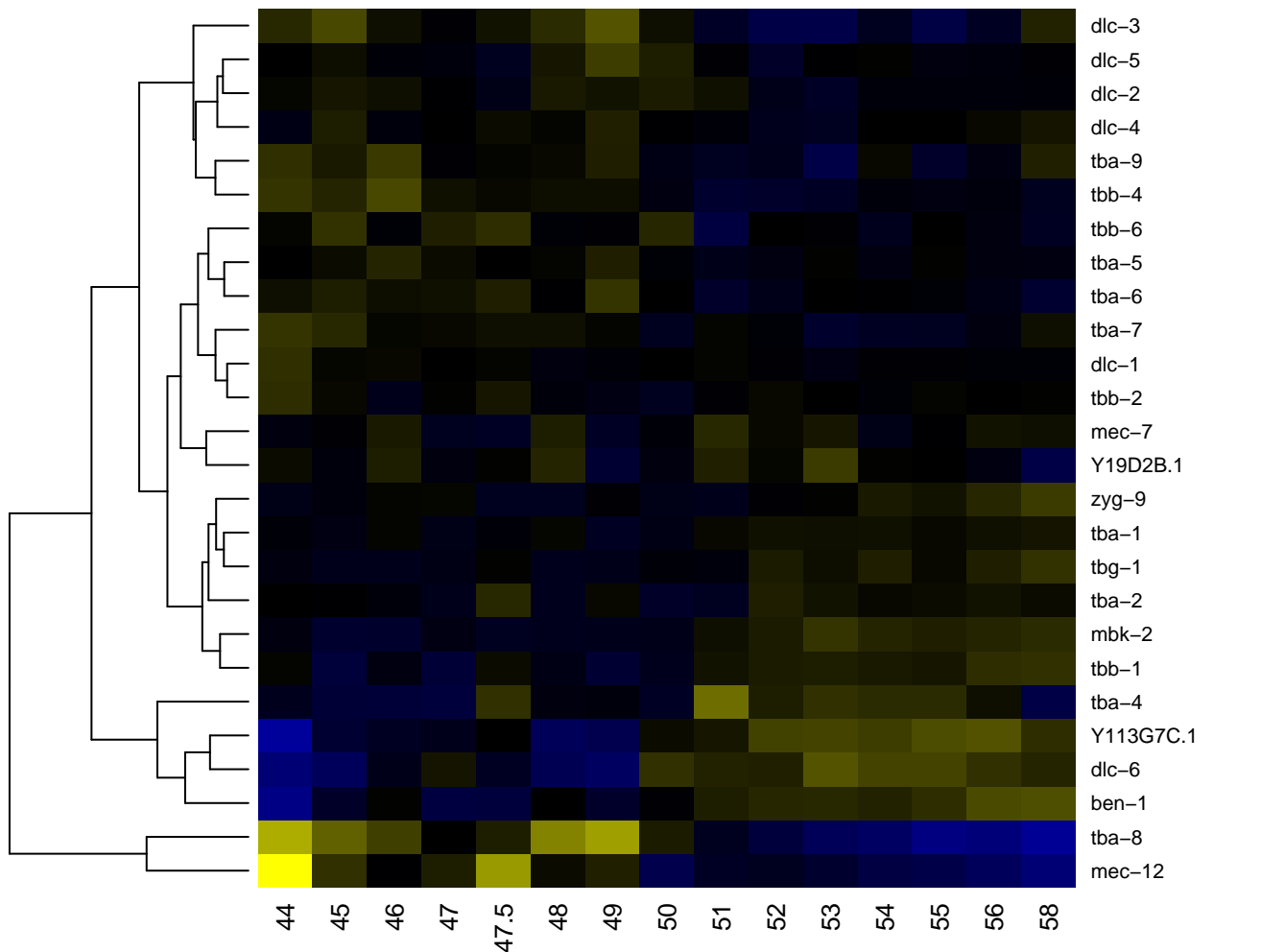
microtubule



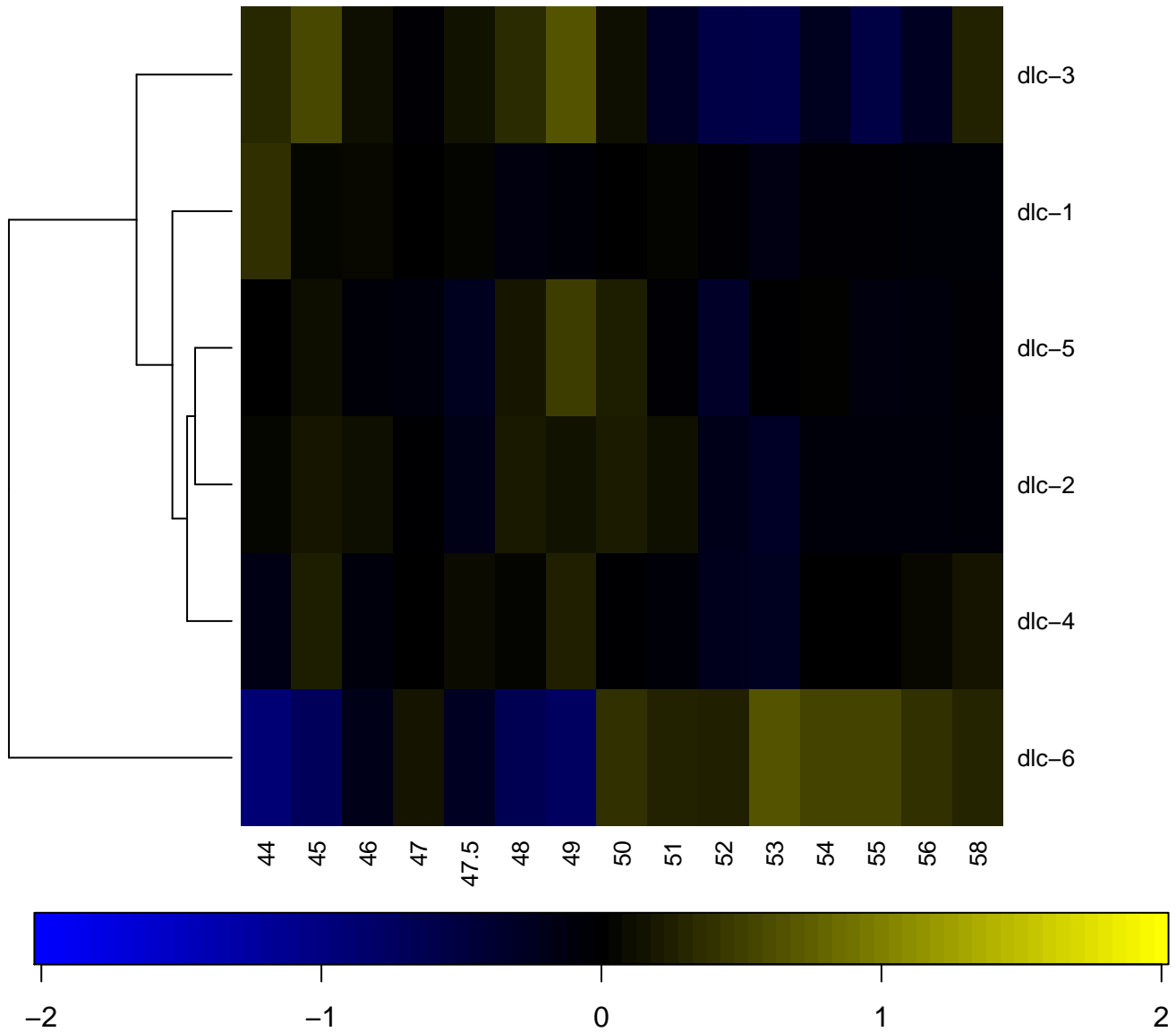
microtubule-based movement



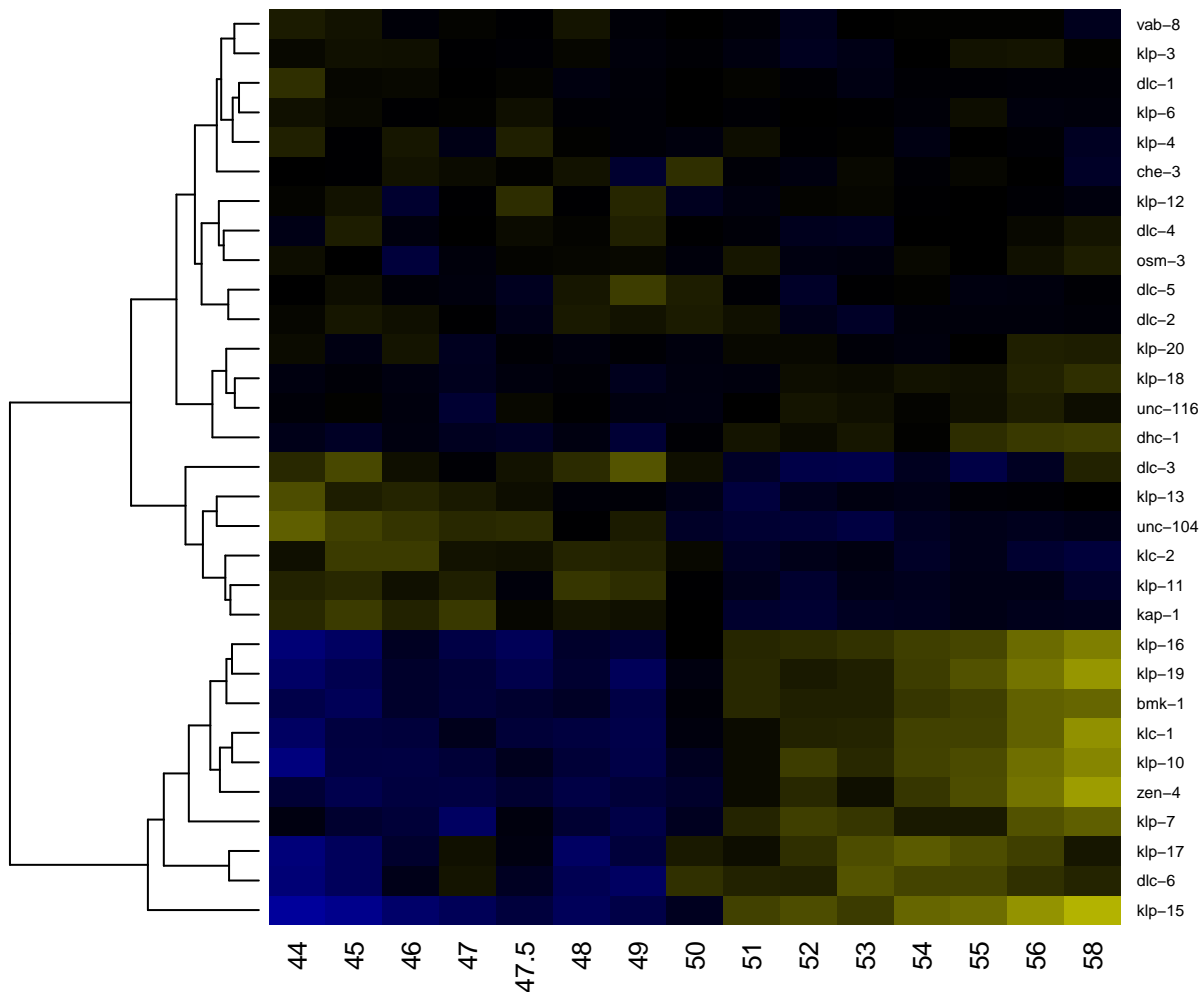
microtubule-based process



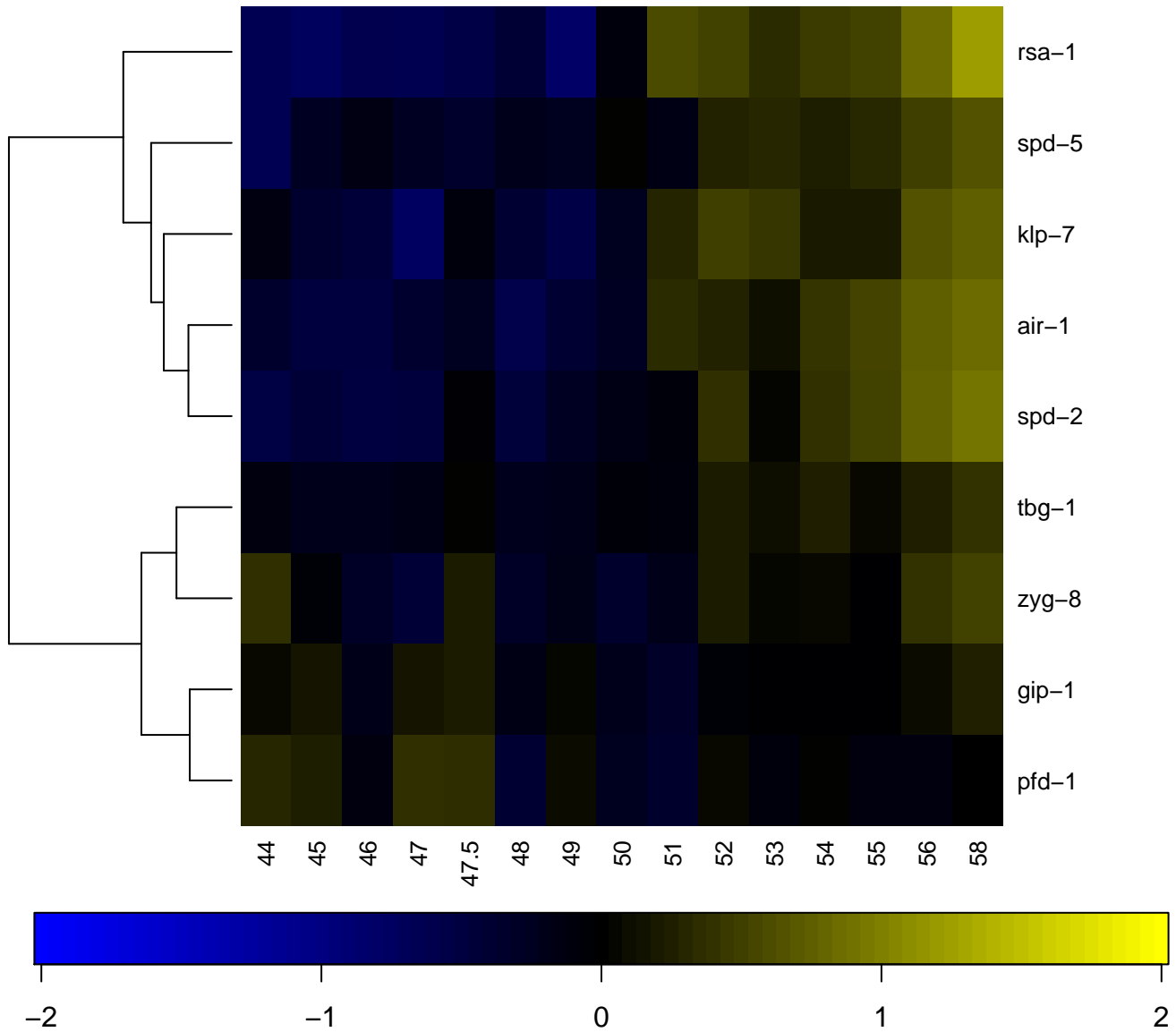
microtubule associated complex



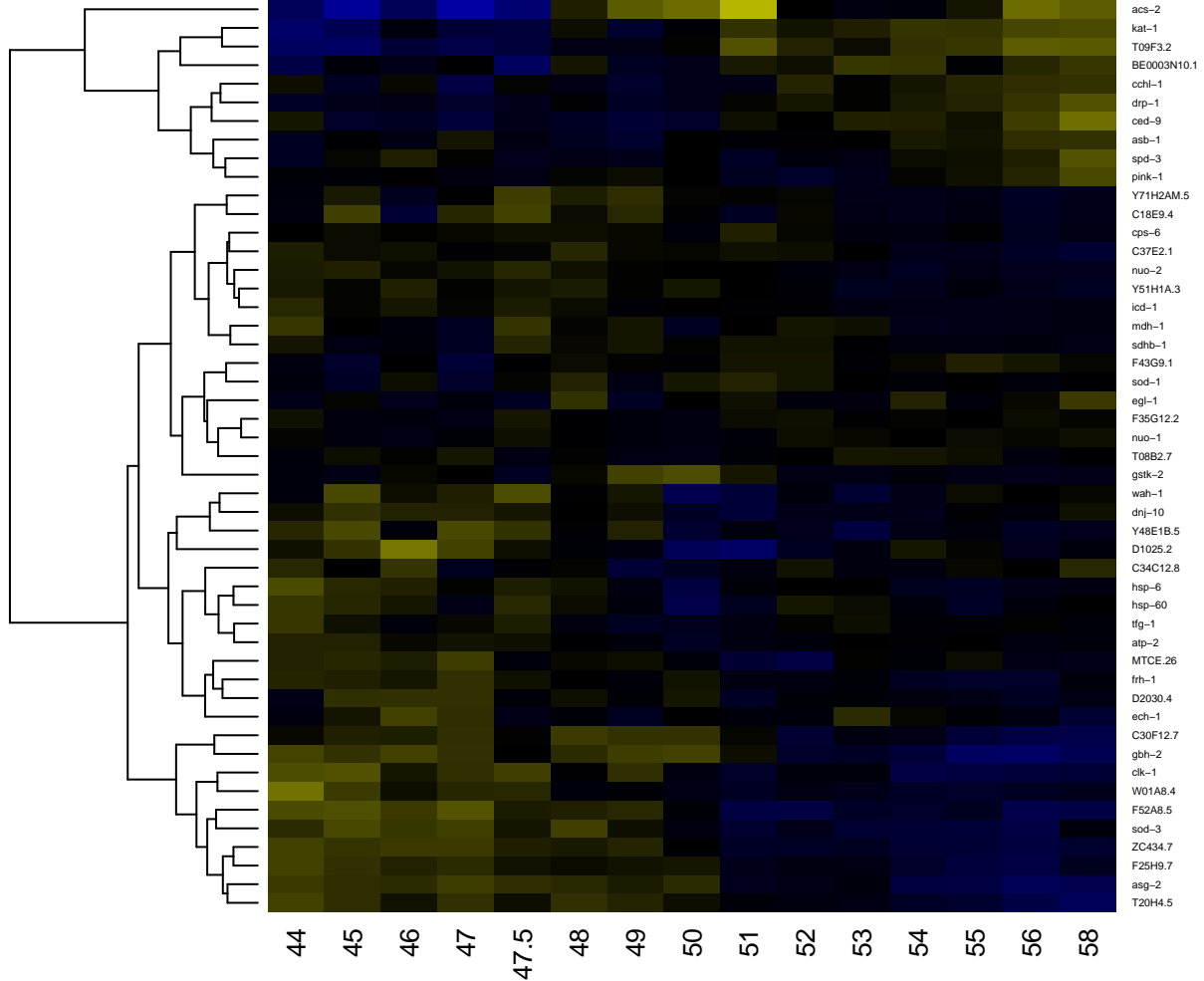
microtubule motor activity



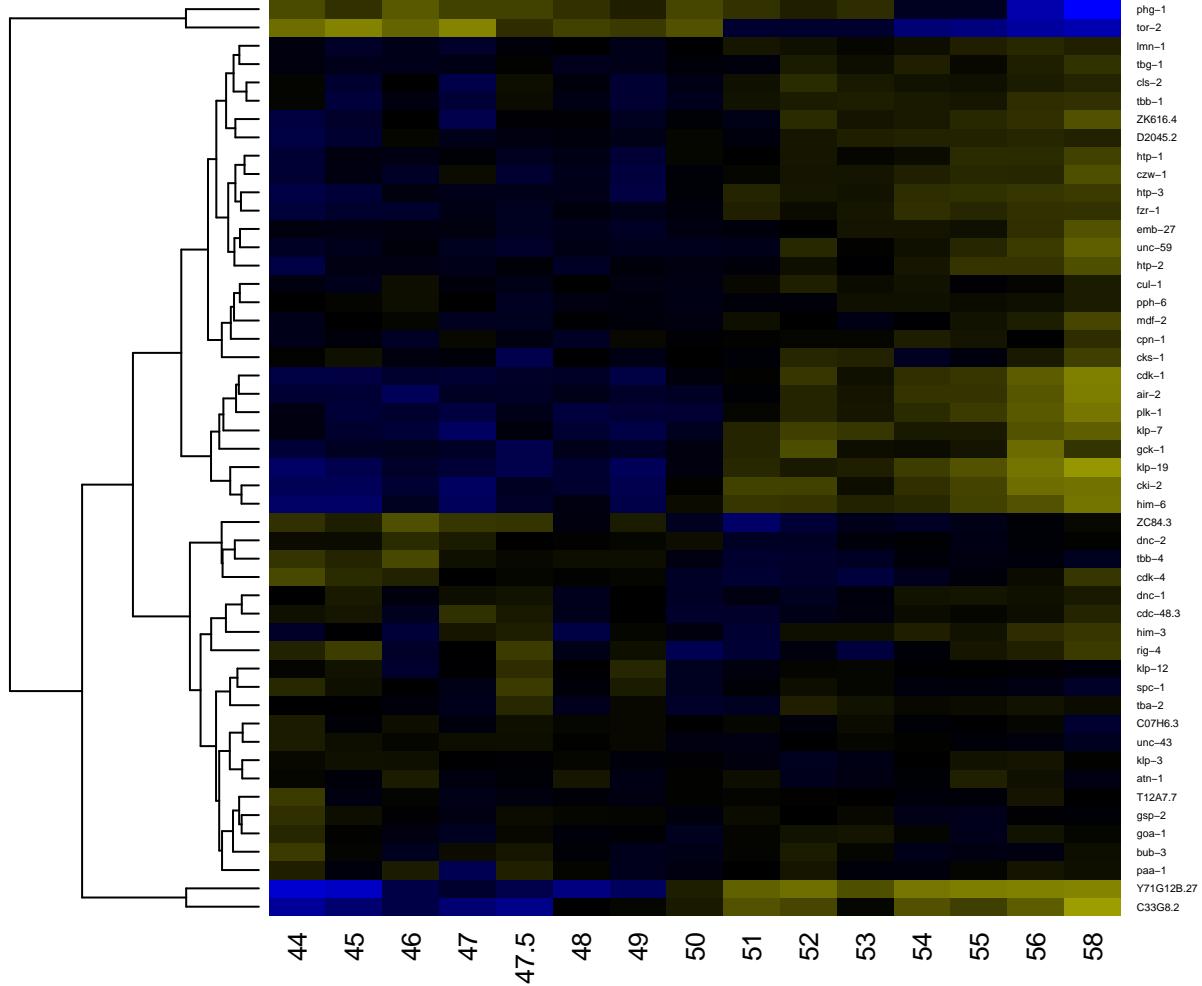
microtubule nucleation



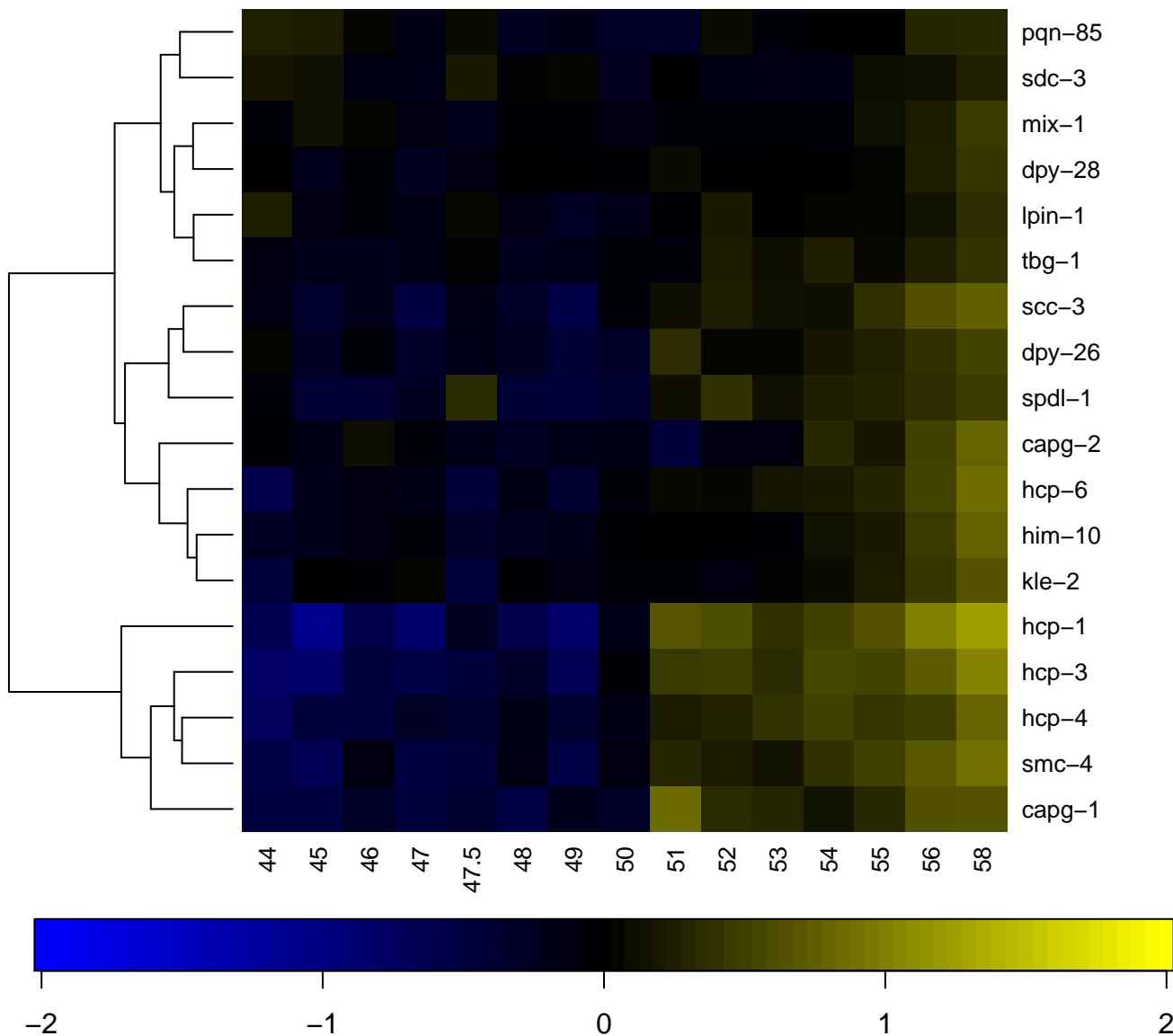
mitochondrion



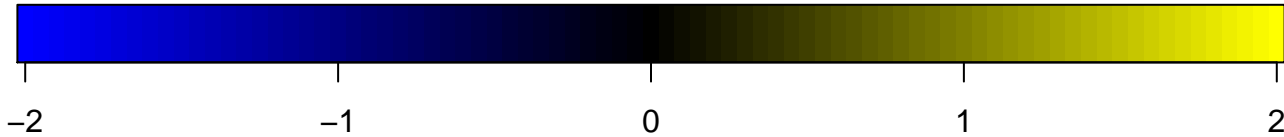
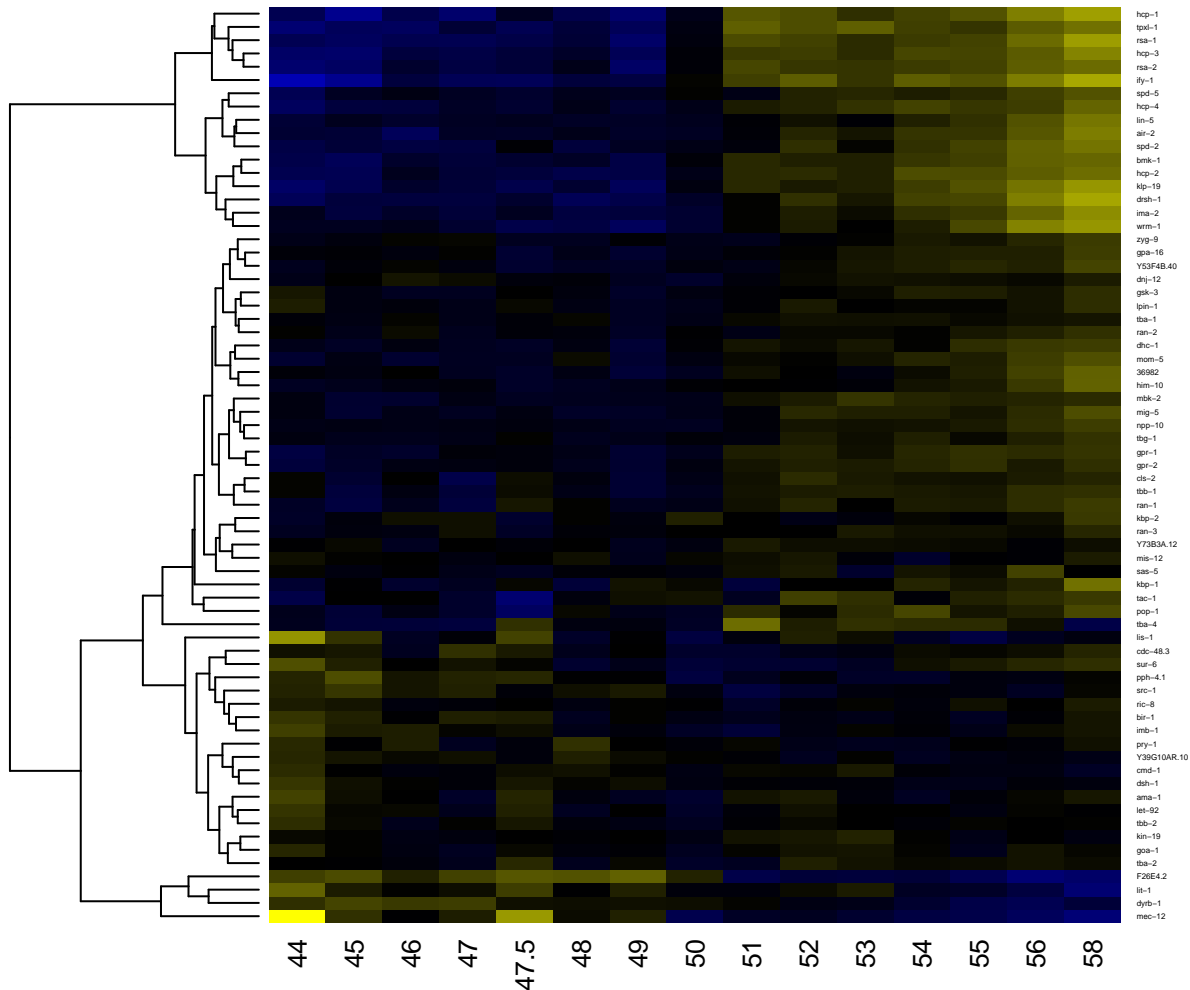
mitosis



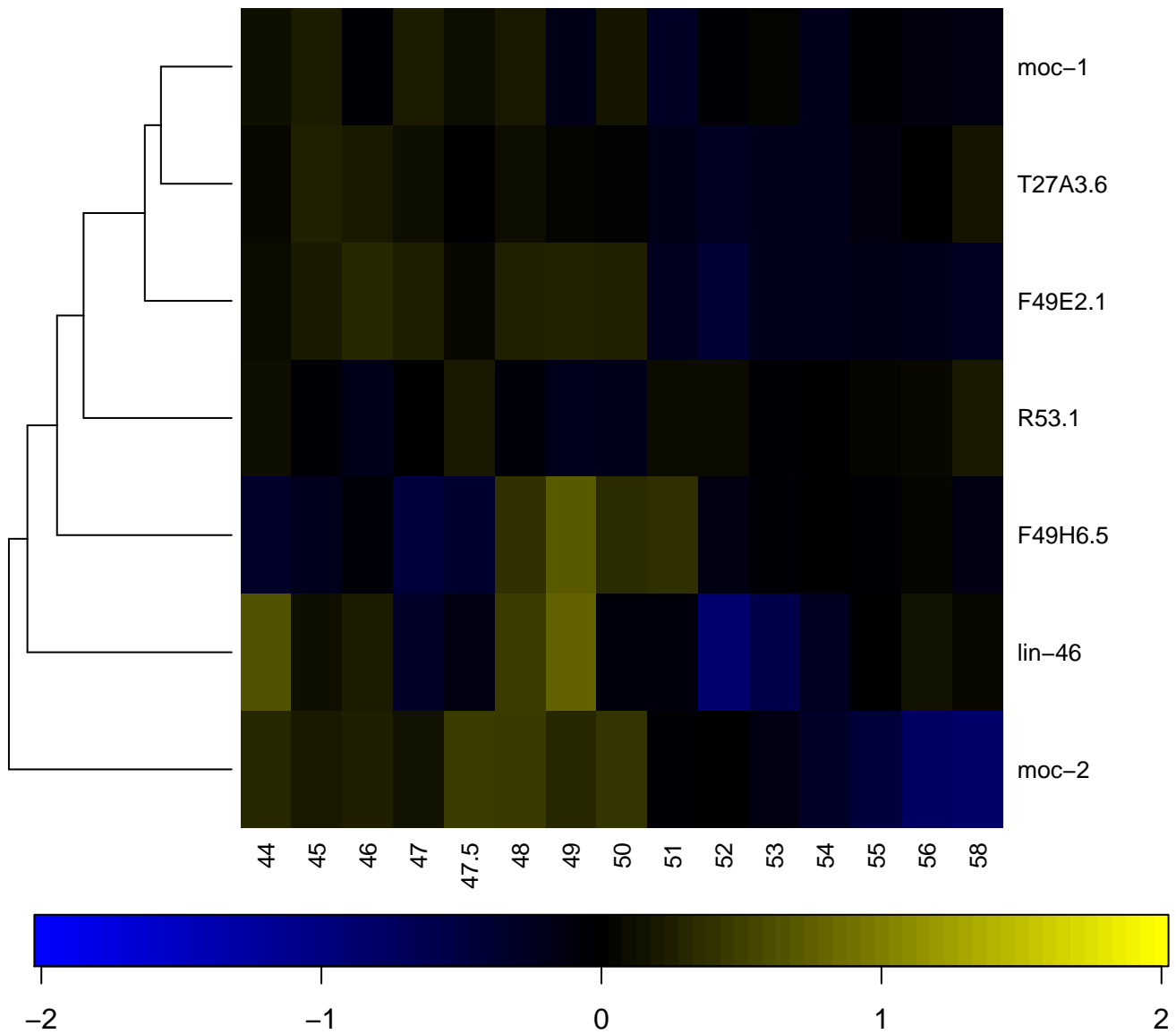
mitotic sister chromatid segregation



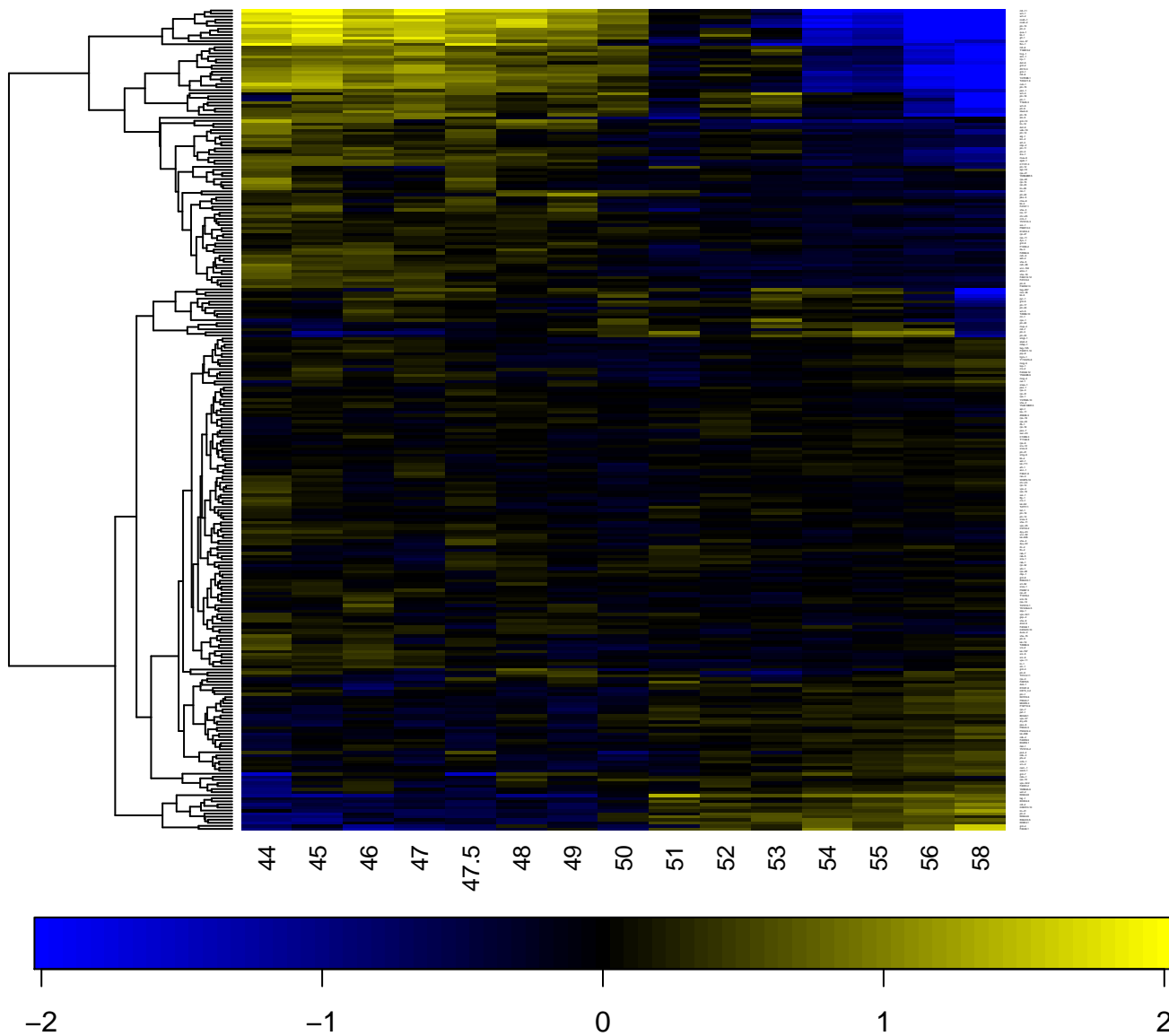
mitotic spindle organization



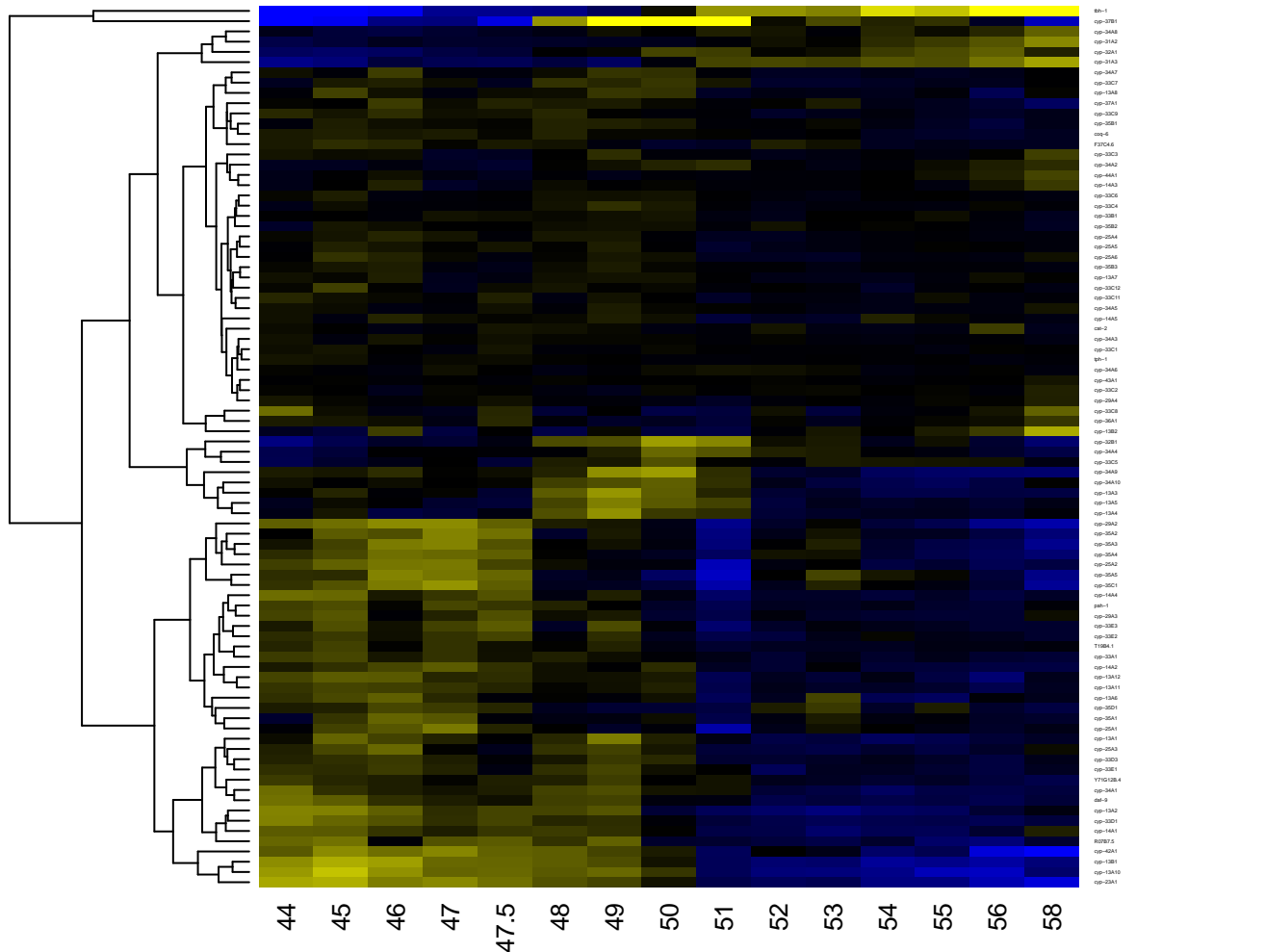
Mo-molybdopterin cofactor biosynthetic process



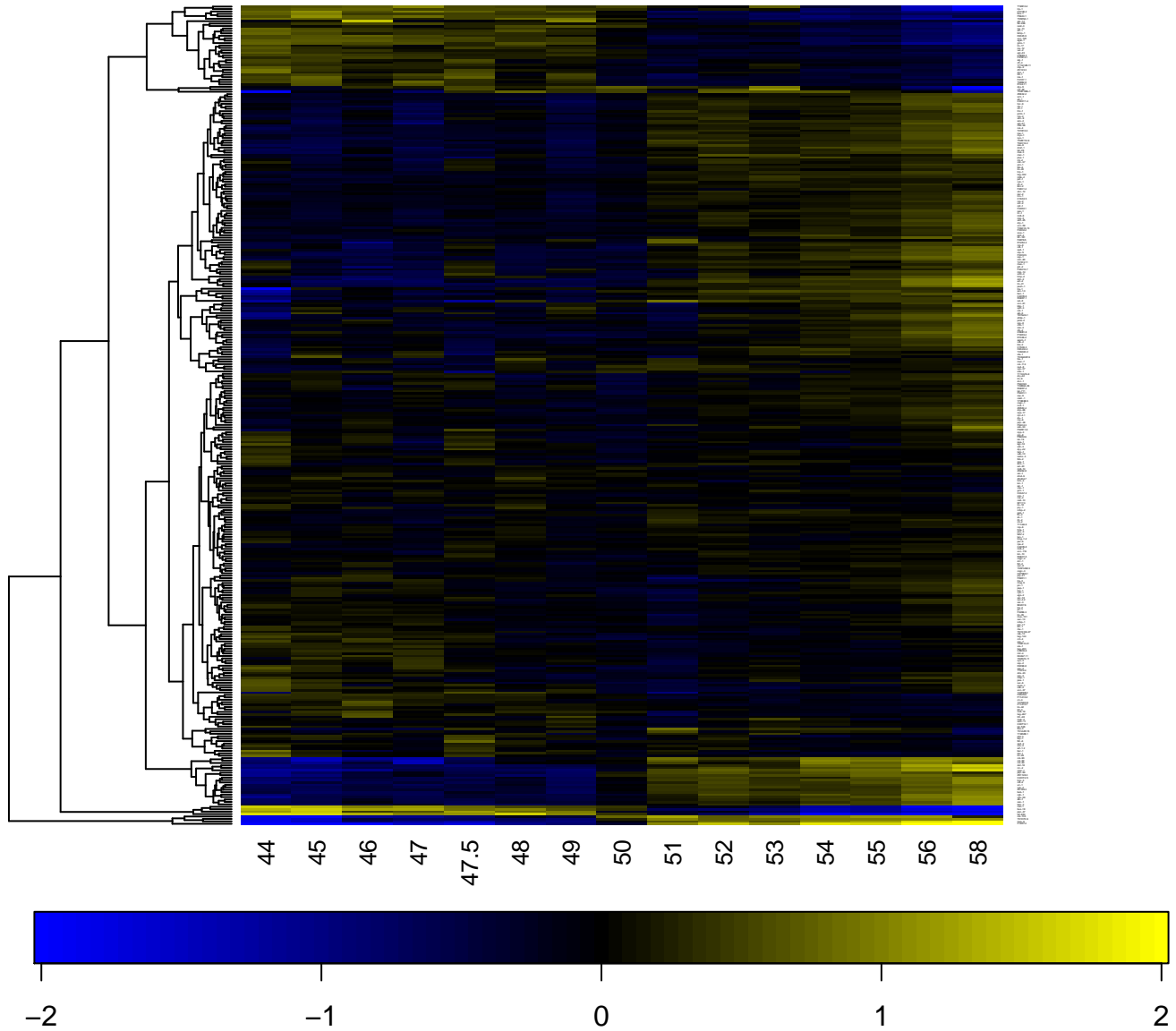
molting cycle, collagen and cuticulin-based cuticle



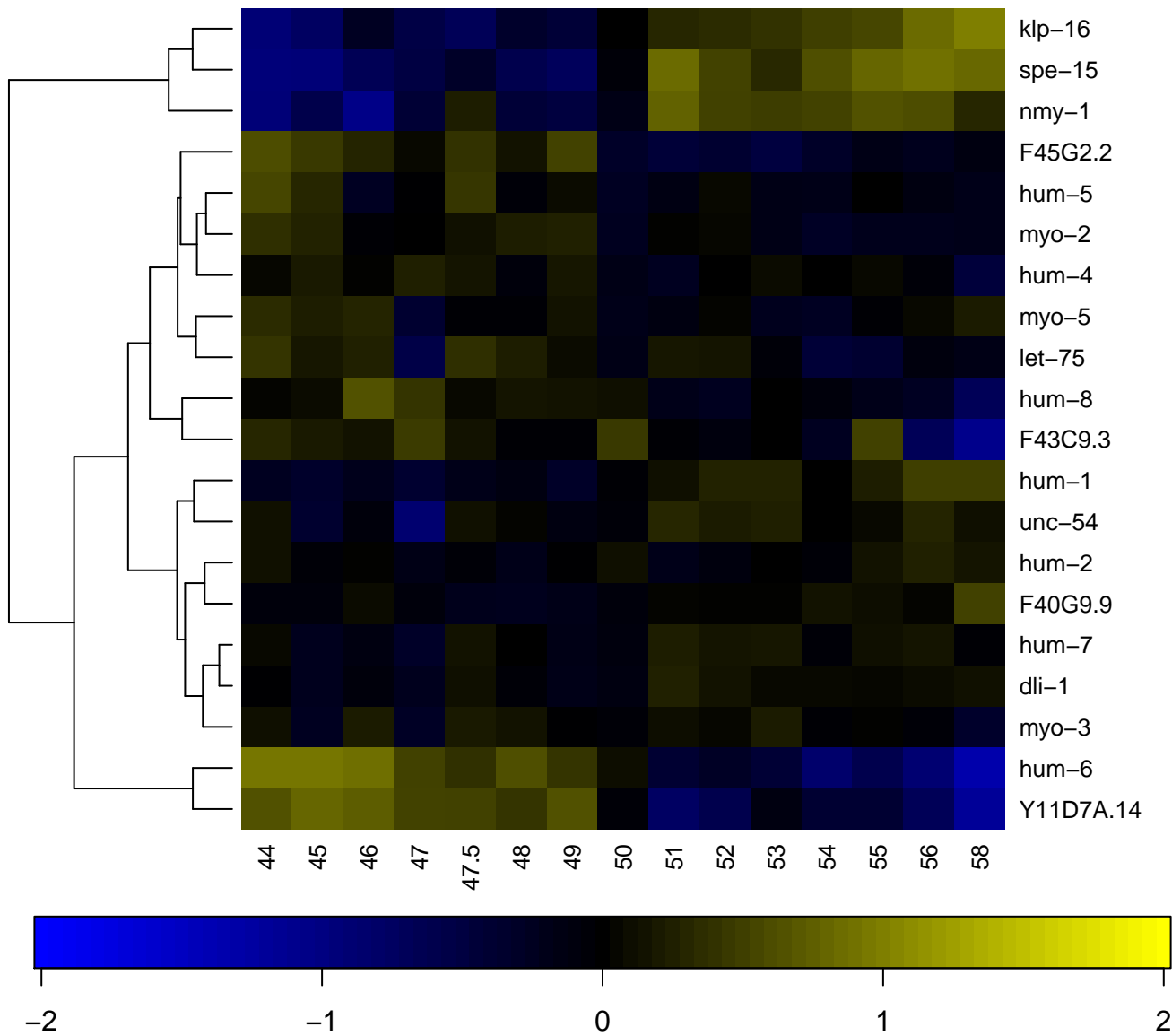
monooxygenase activity



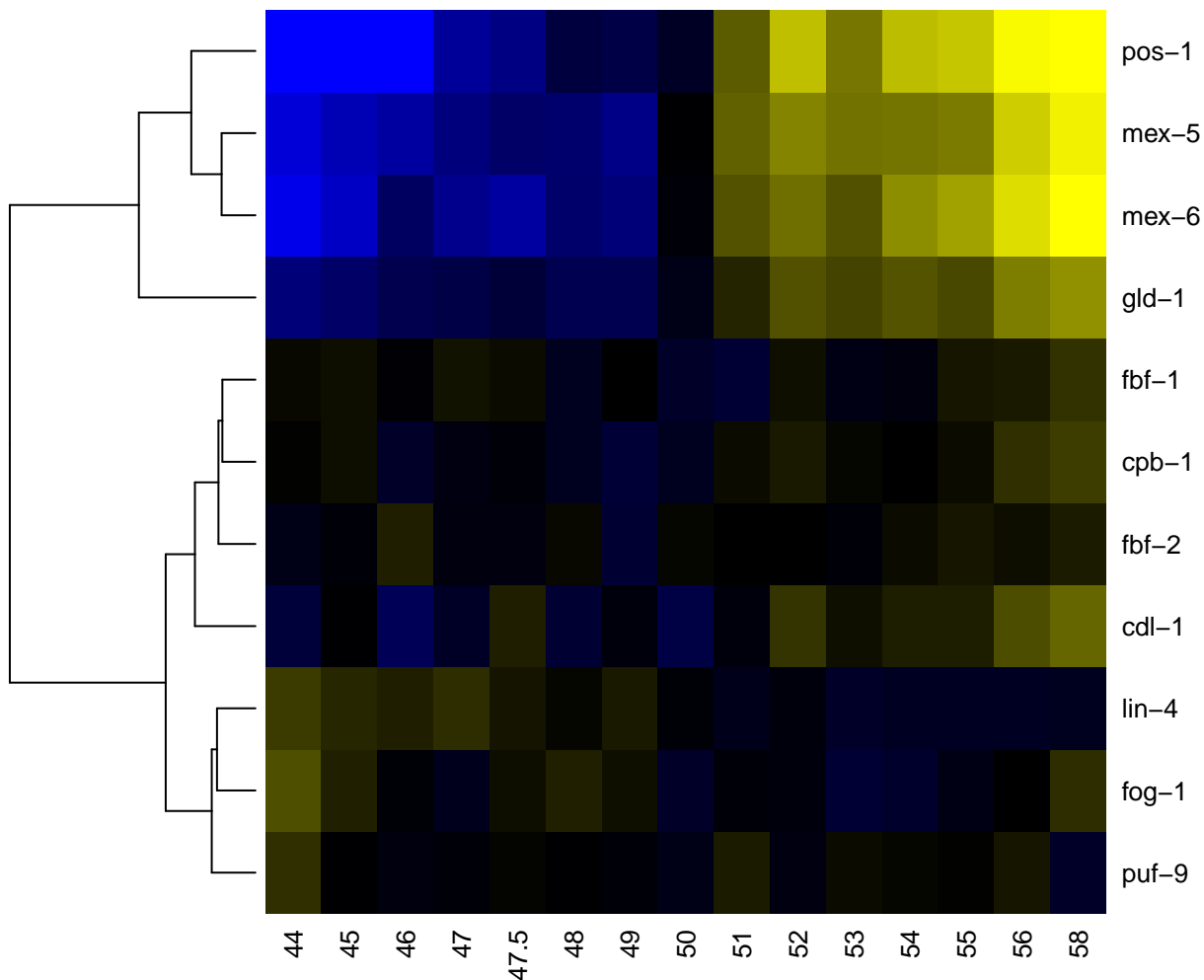
morphogenesis of an epithelium



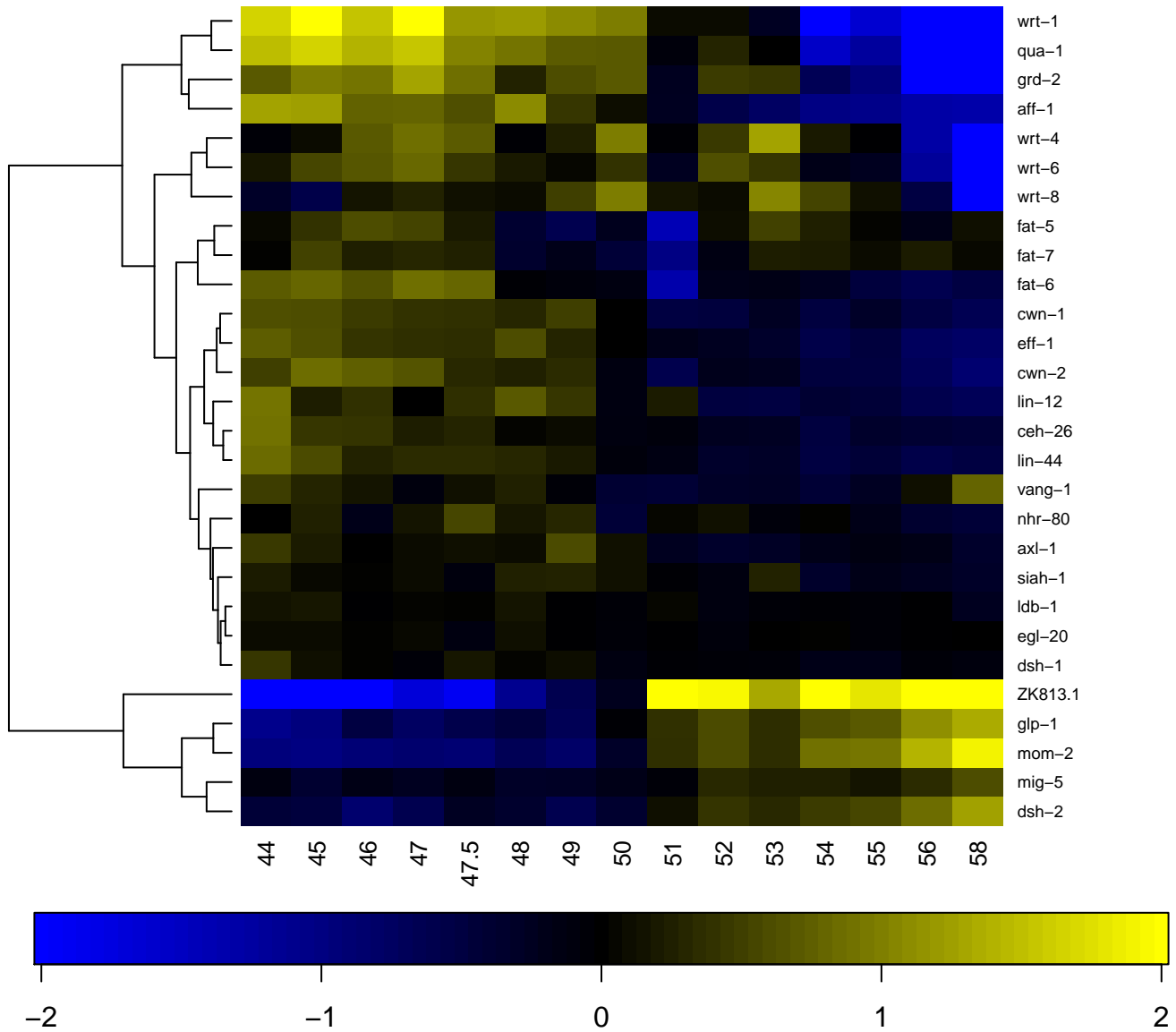
motor activity



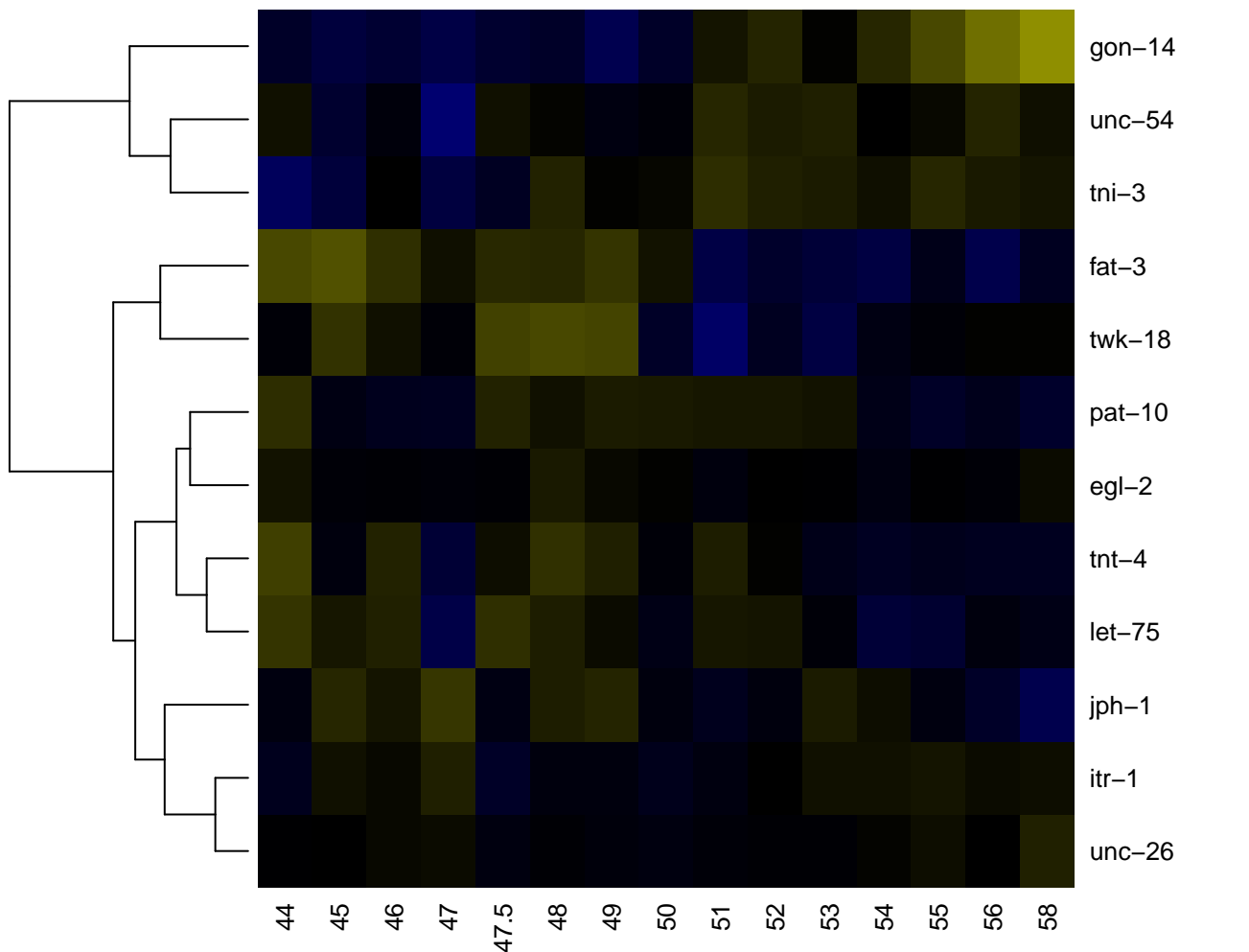
mRNA 3'-UTR binding



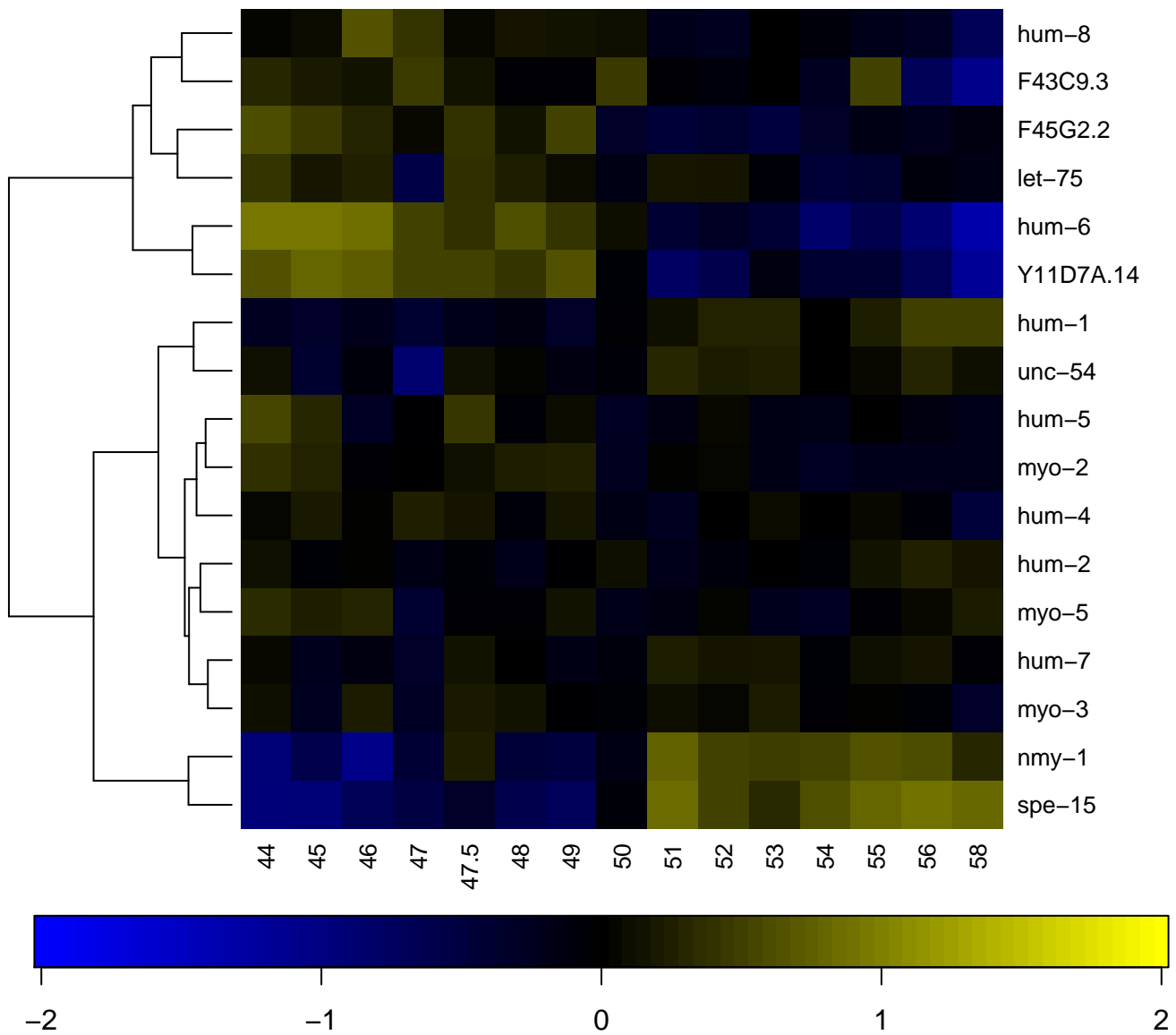
multicellular organismal development



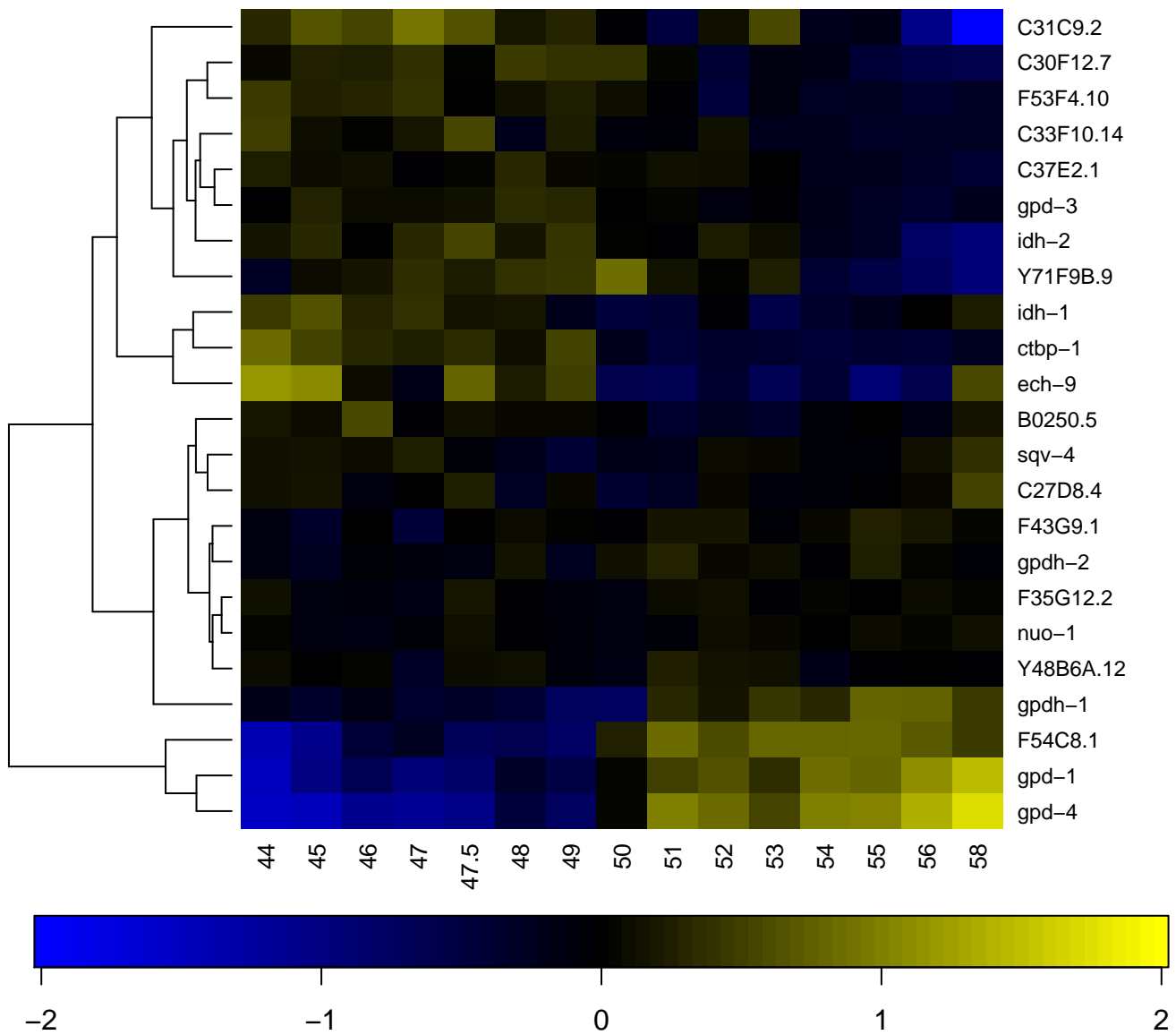
muscle contraction



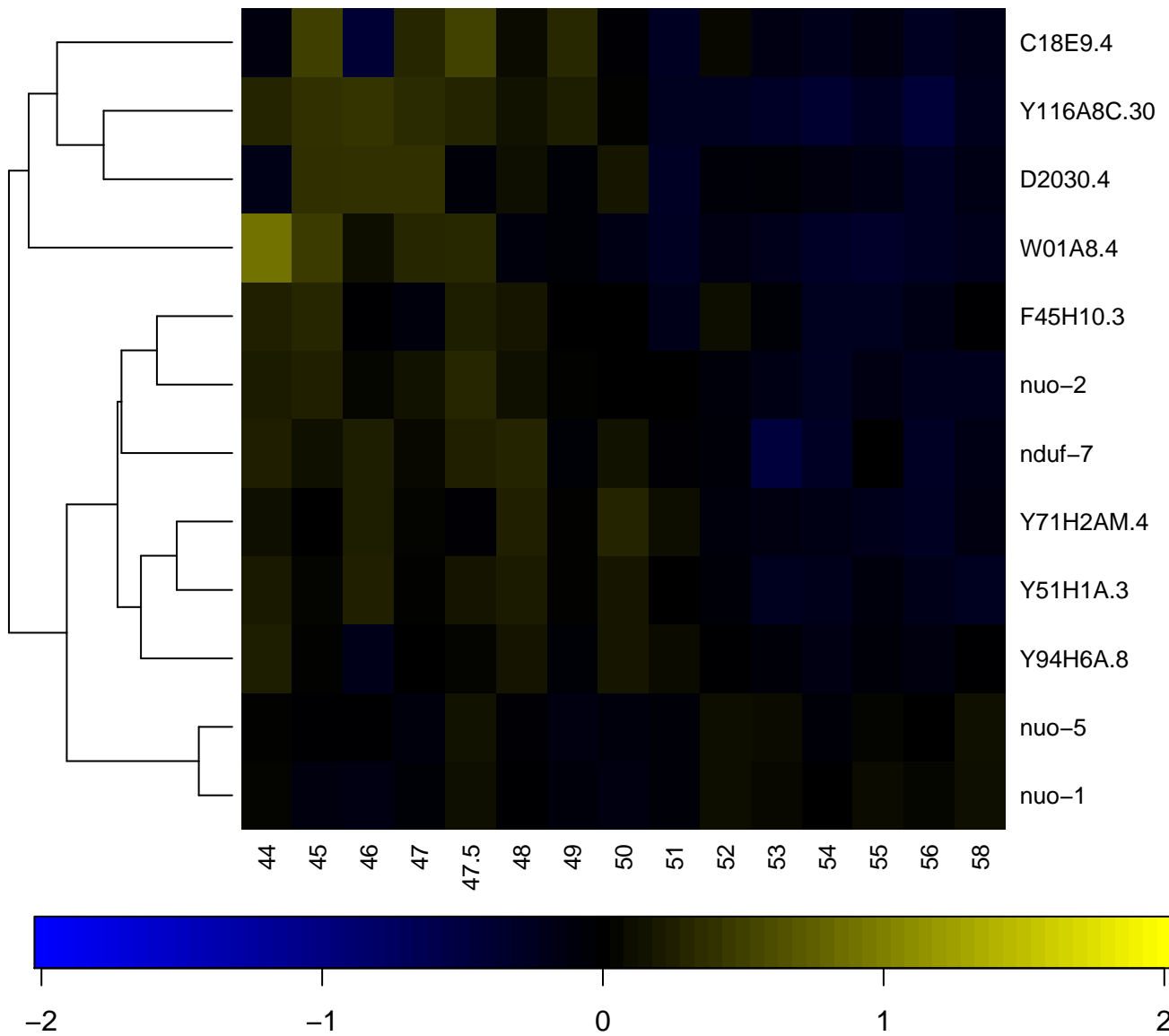
myosin complex



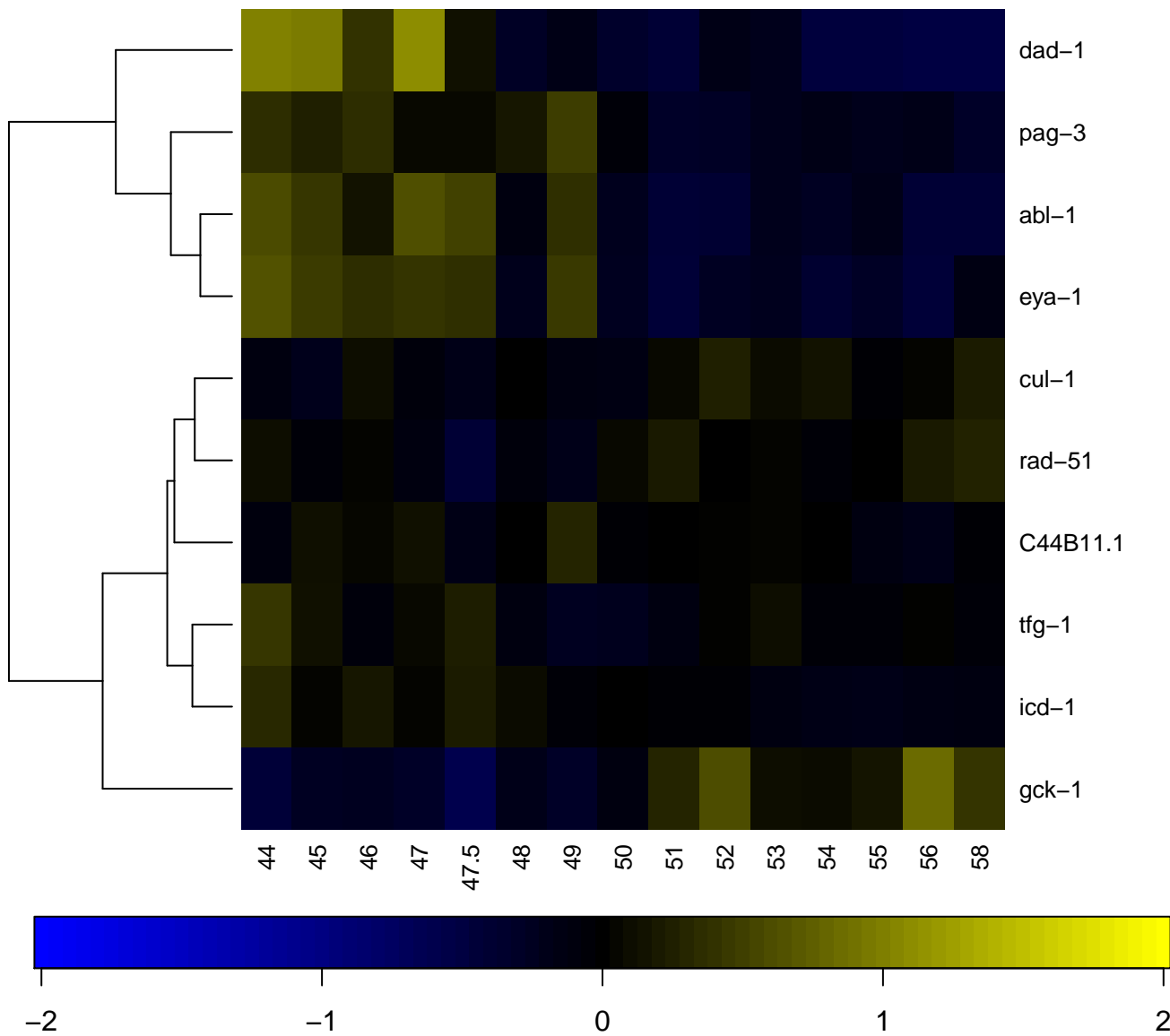
NAD or NADH binding



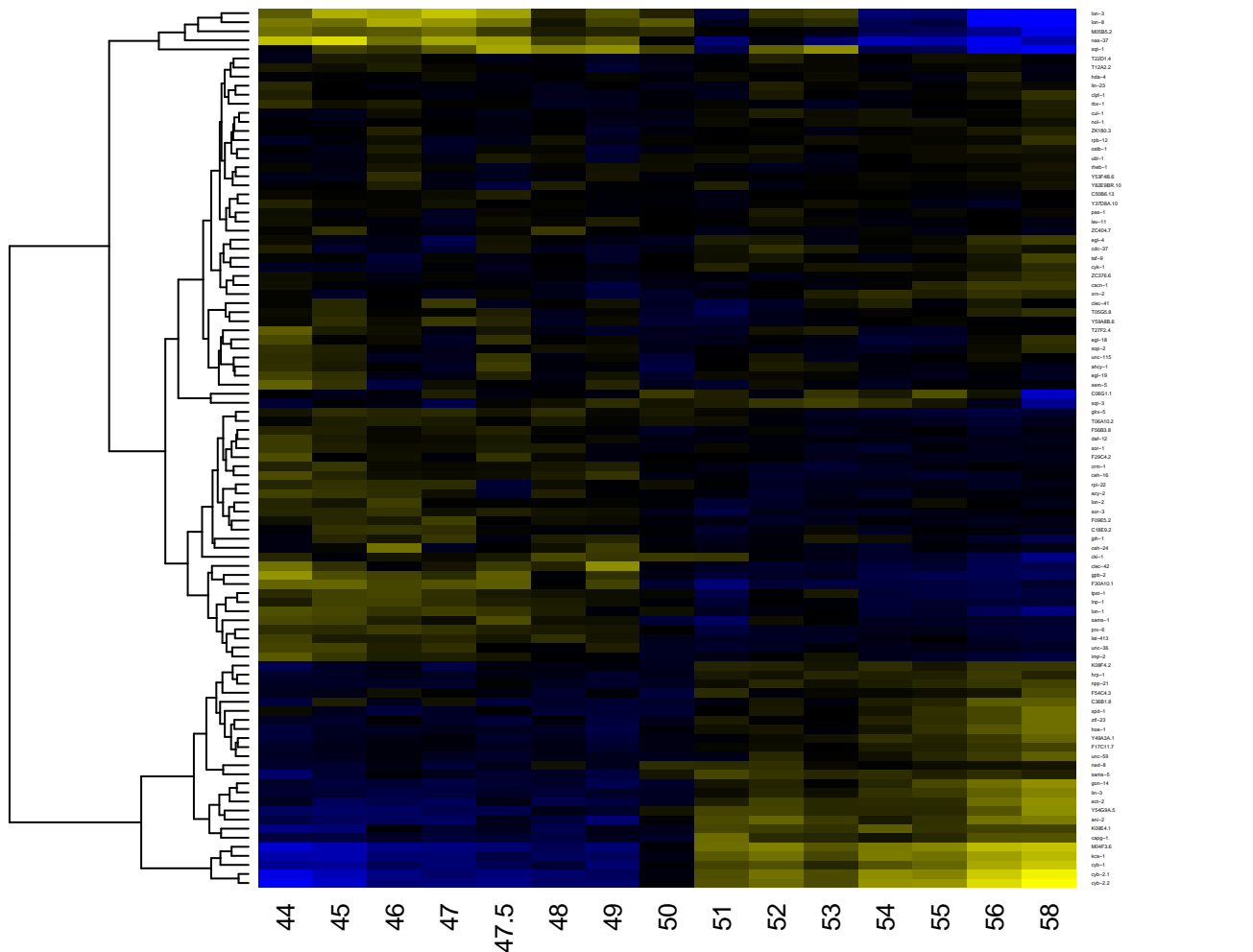
NADH dehydrogenase (ubiquinone) activity



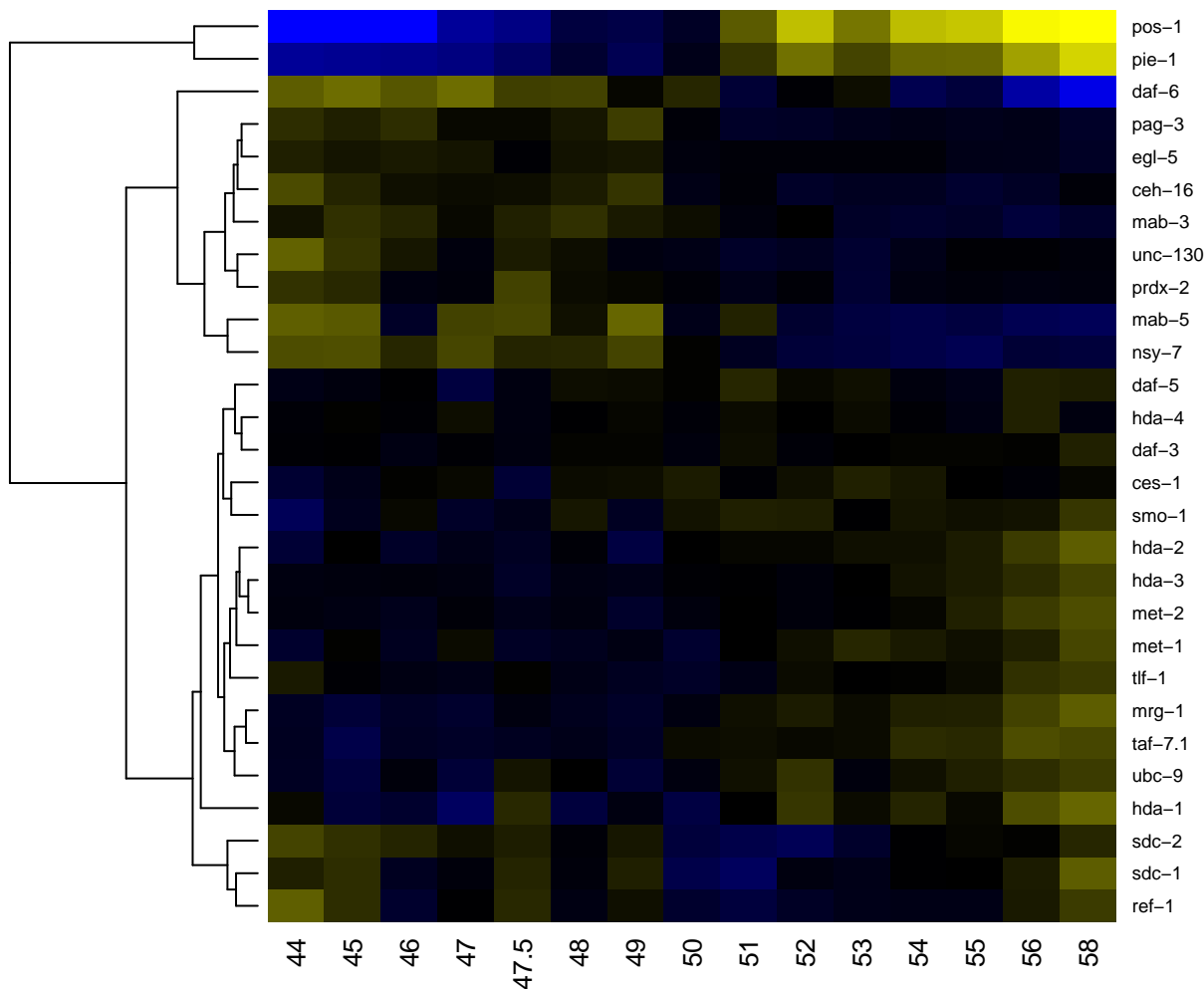
negative regulation of apoptosis



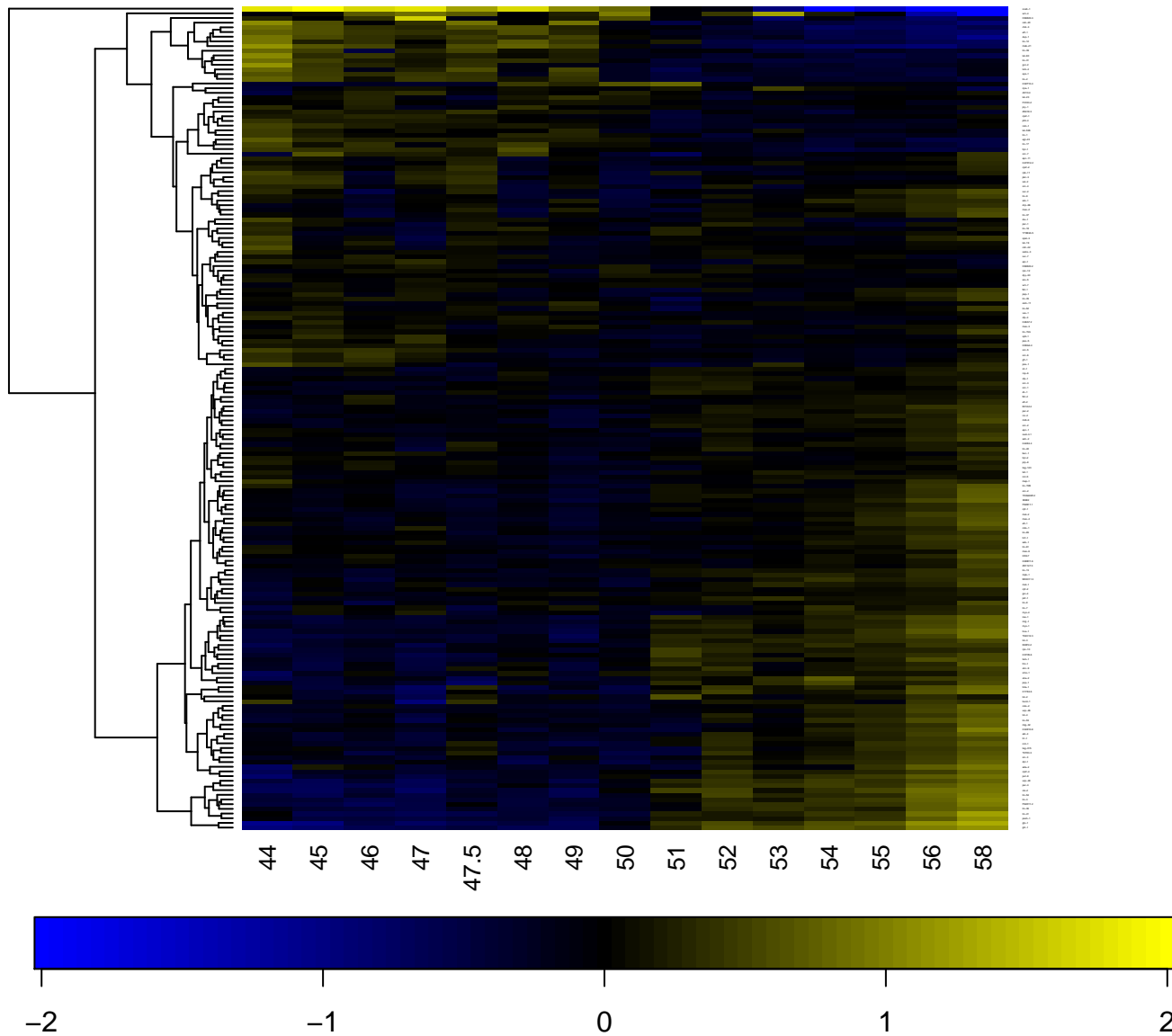
negative regulation of multicellular organism growth



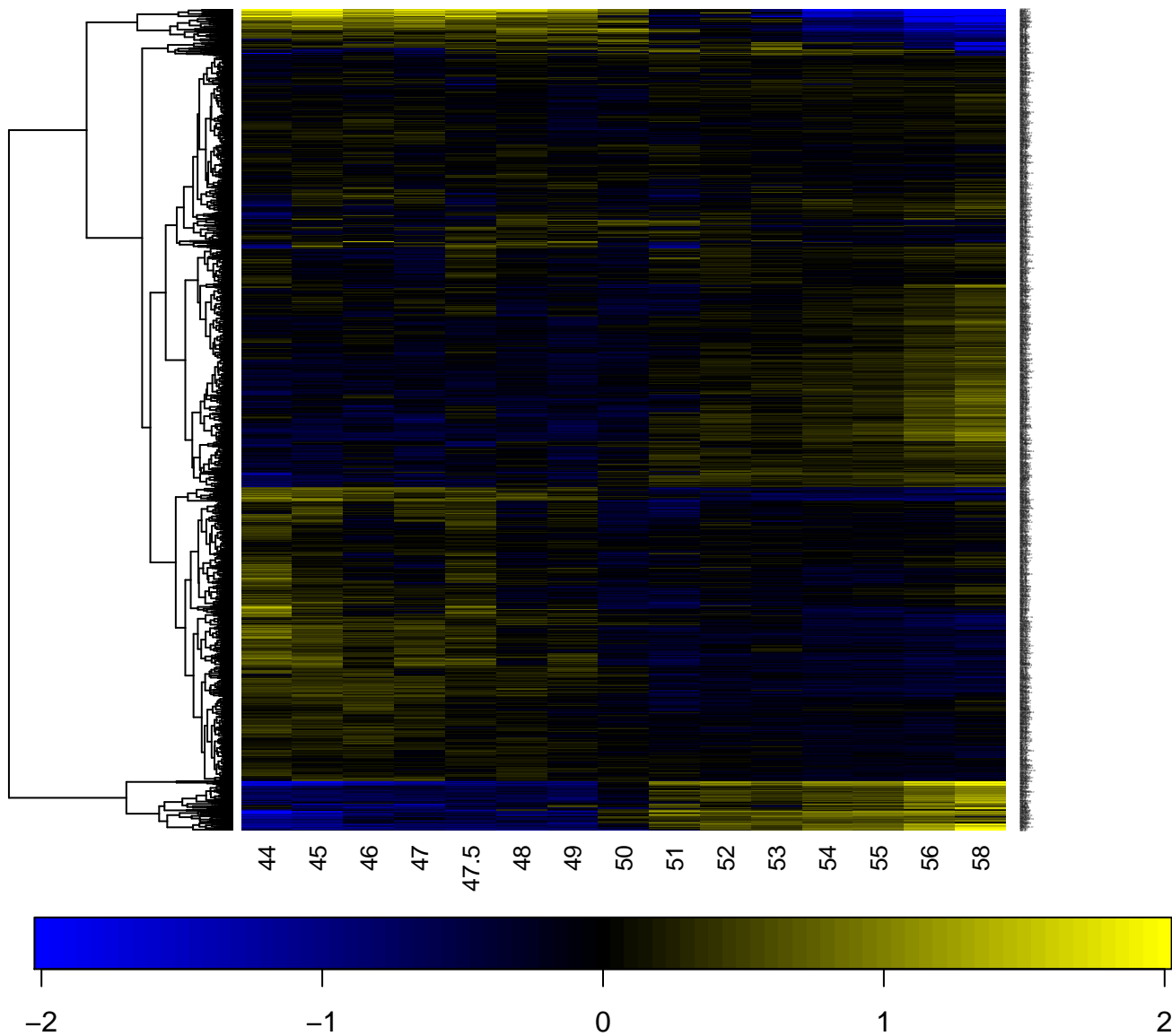
Alternative regulation of transcription from RNA polymerase II promoter



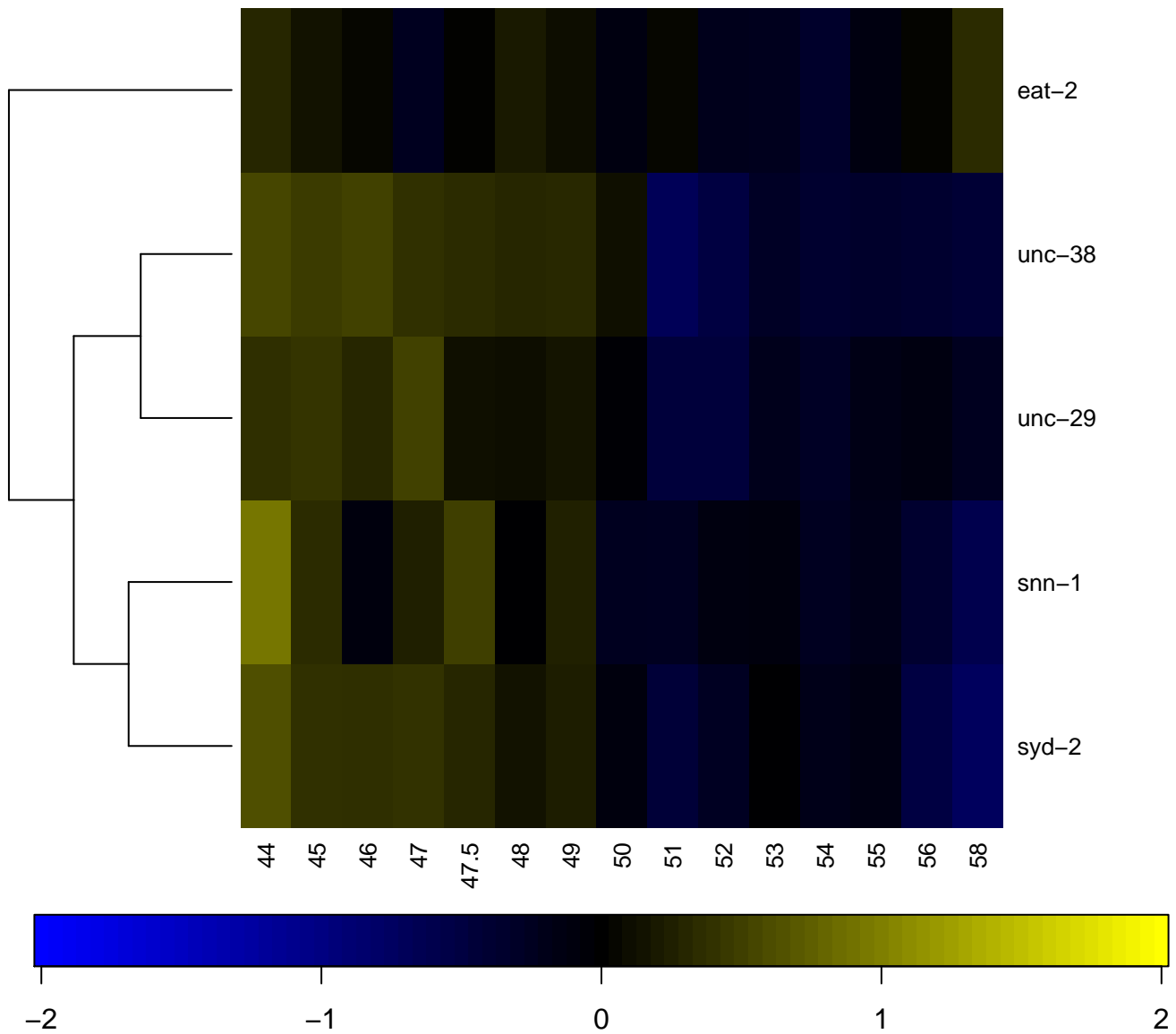
negative regulation of vulval development



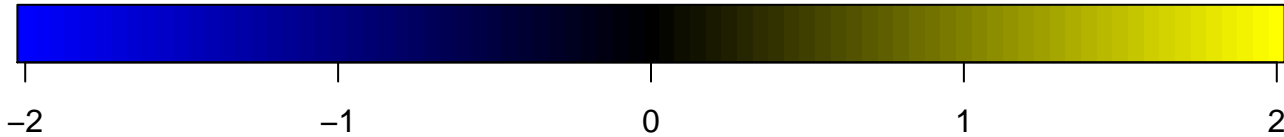
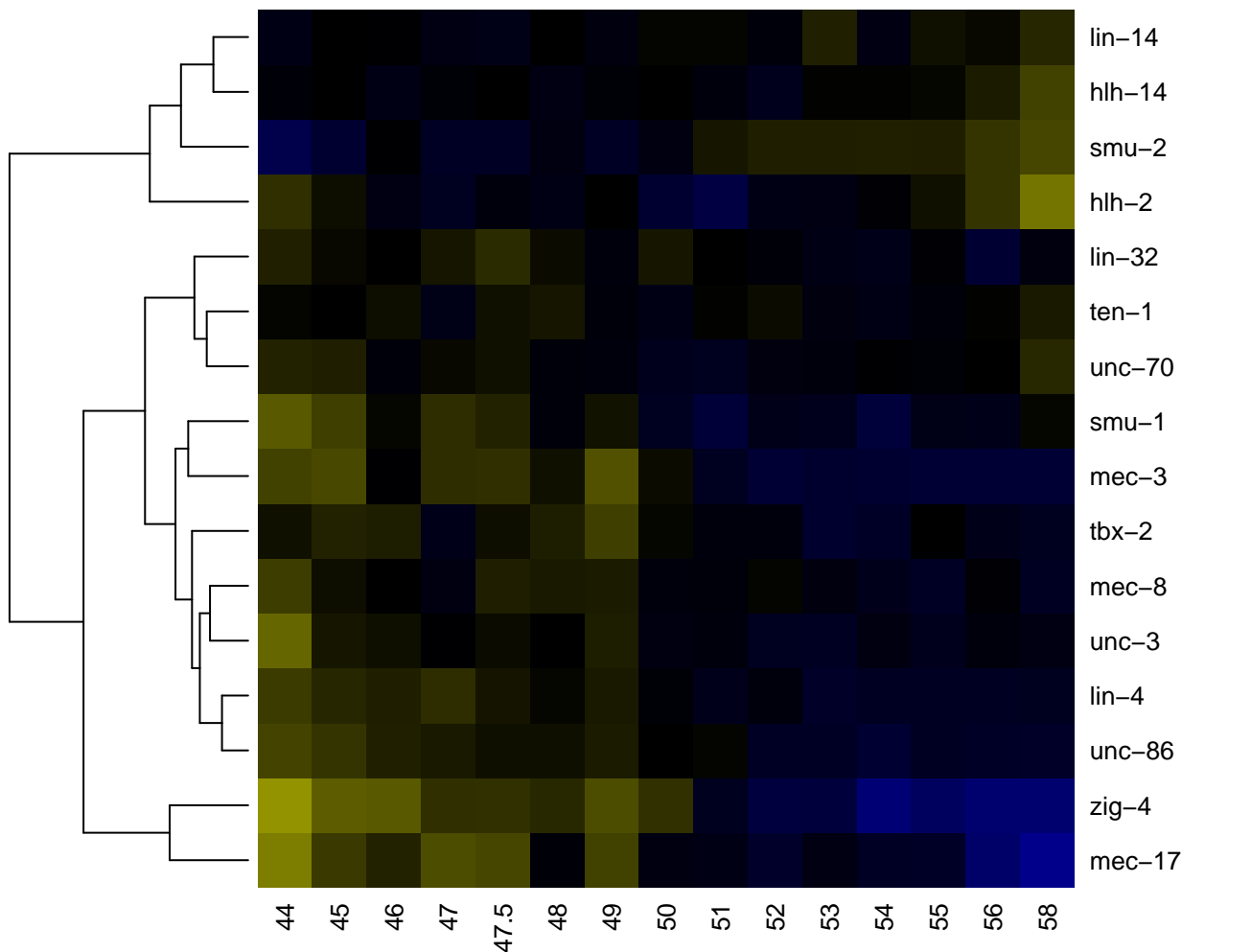
nematode larval development



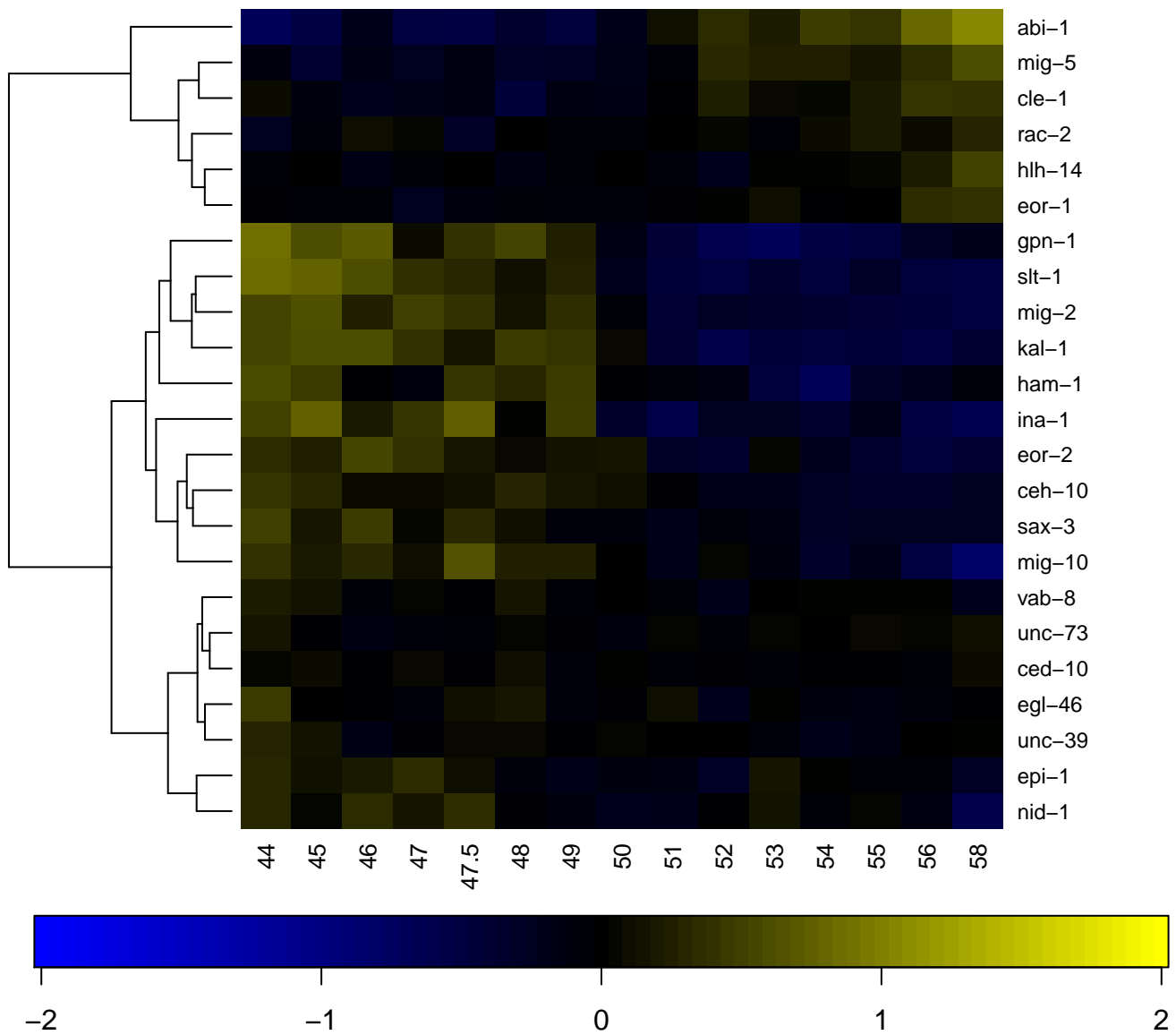
neuromuscular synaptic transmission



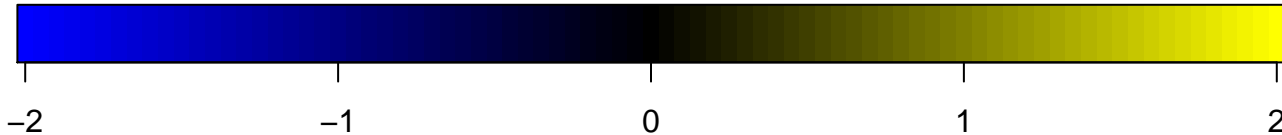
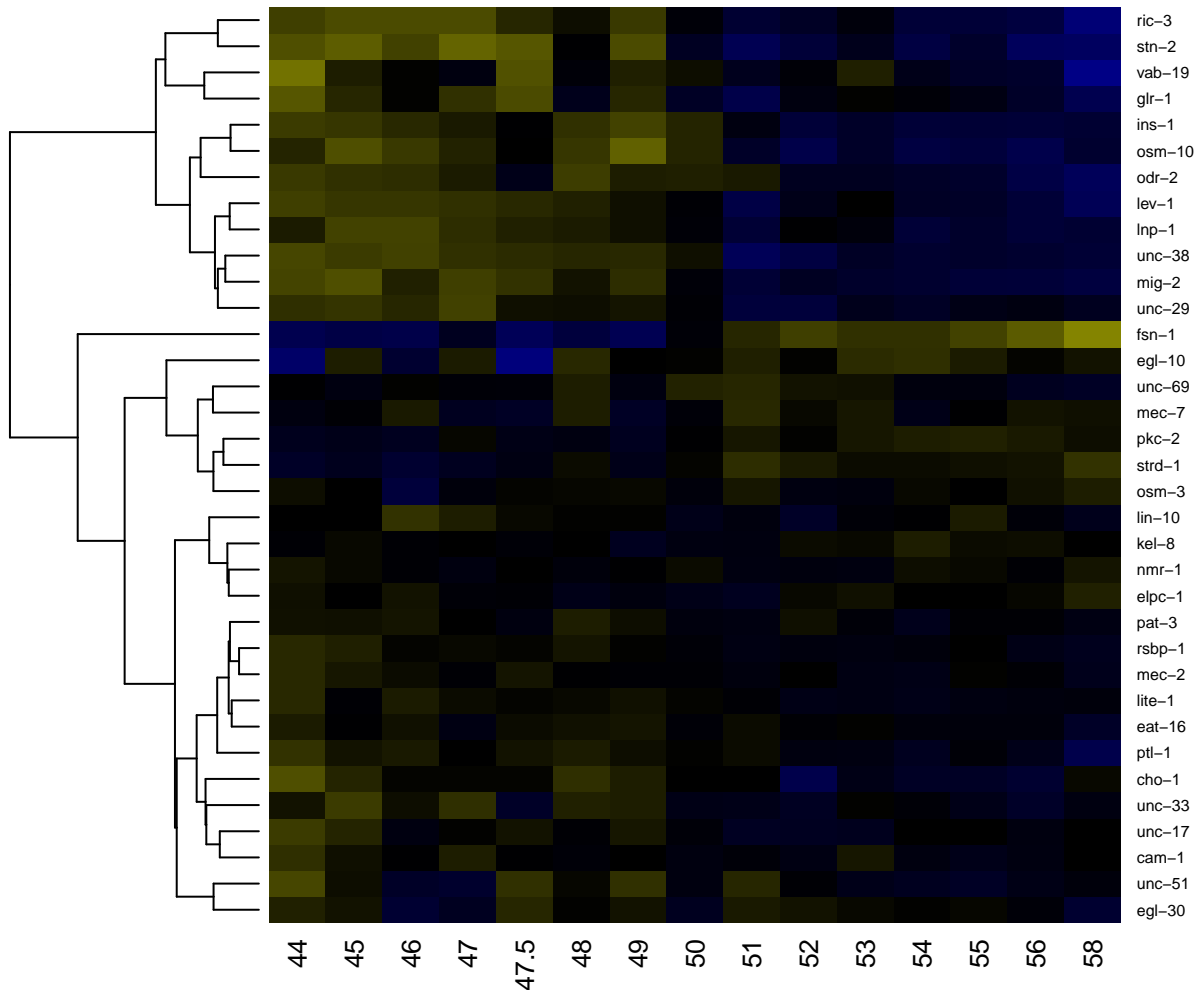
neuron development



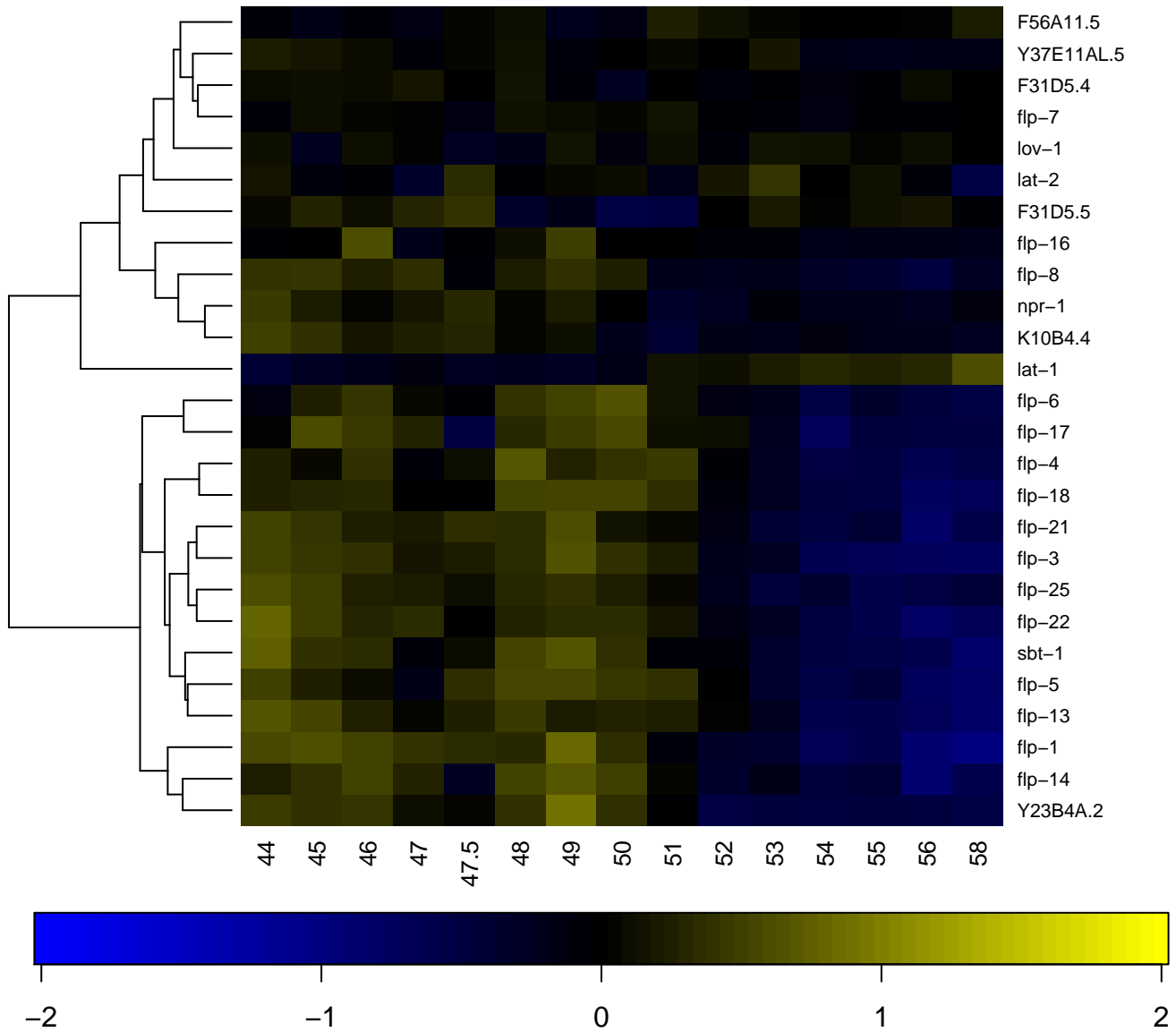
neuron migration



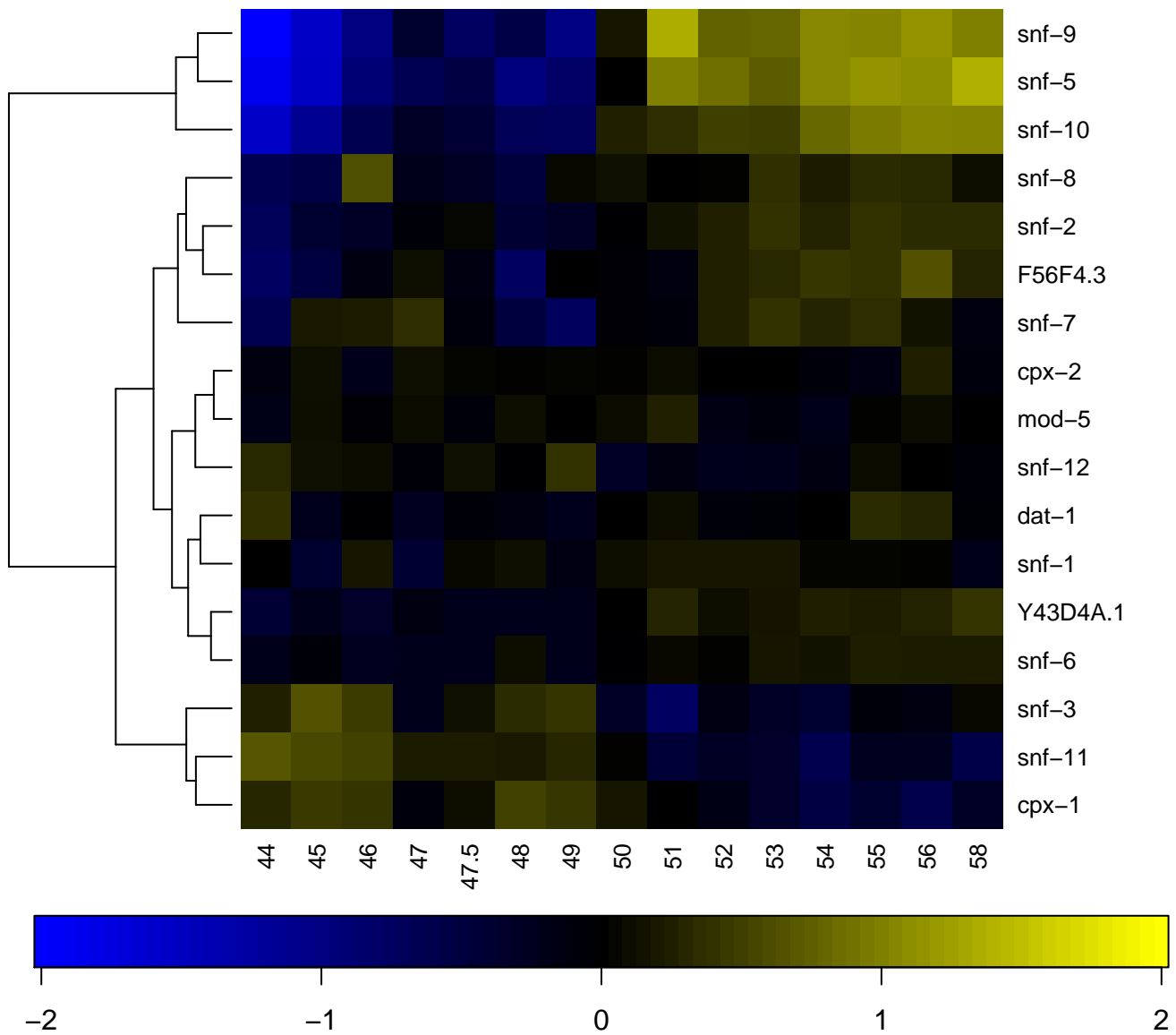
neuron projection



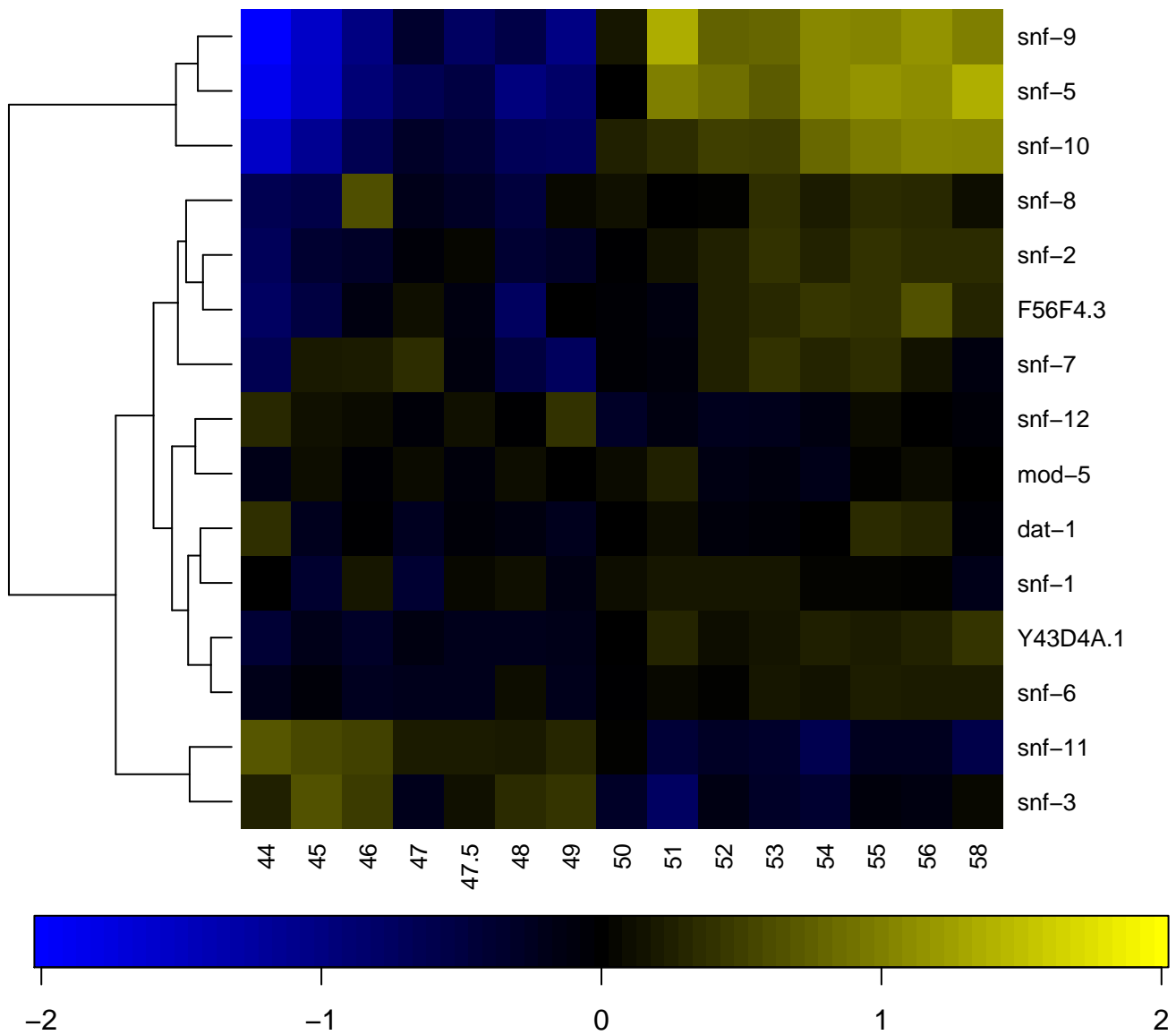
neuropeptide signaling pathway



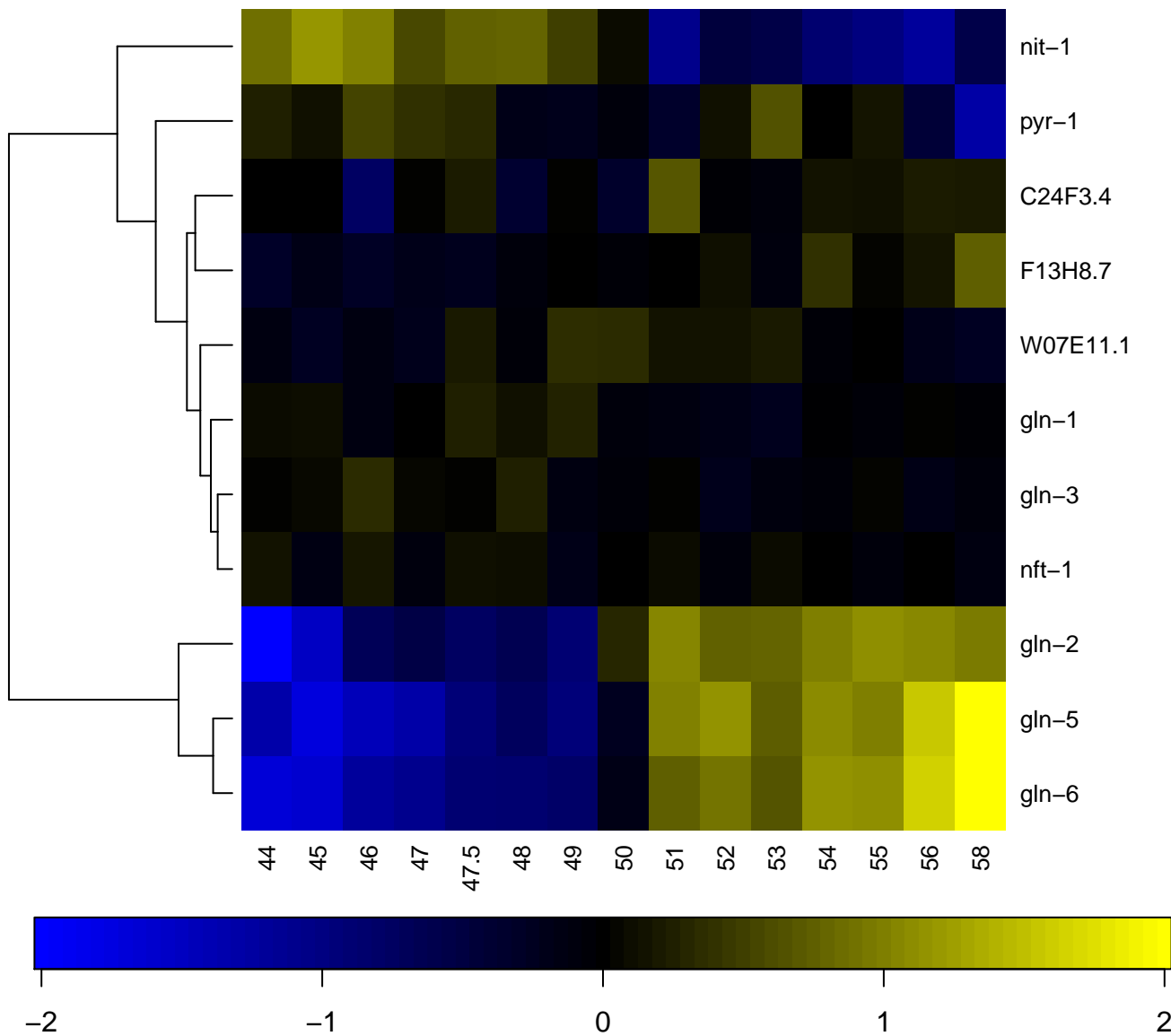
neurotransmitter transport



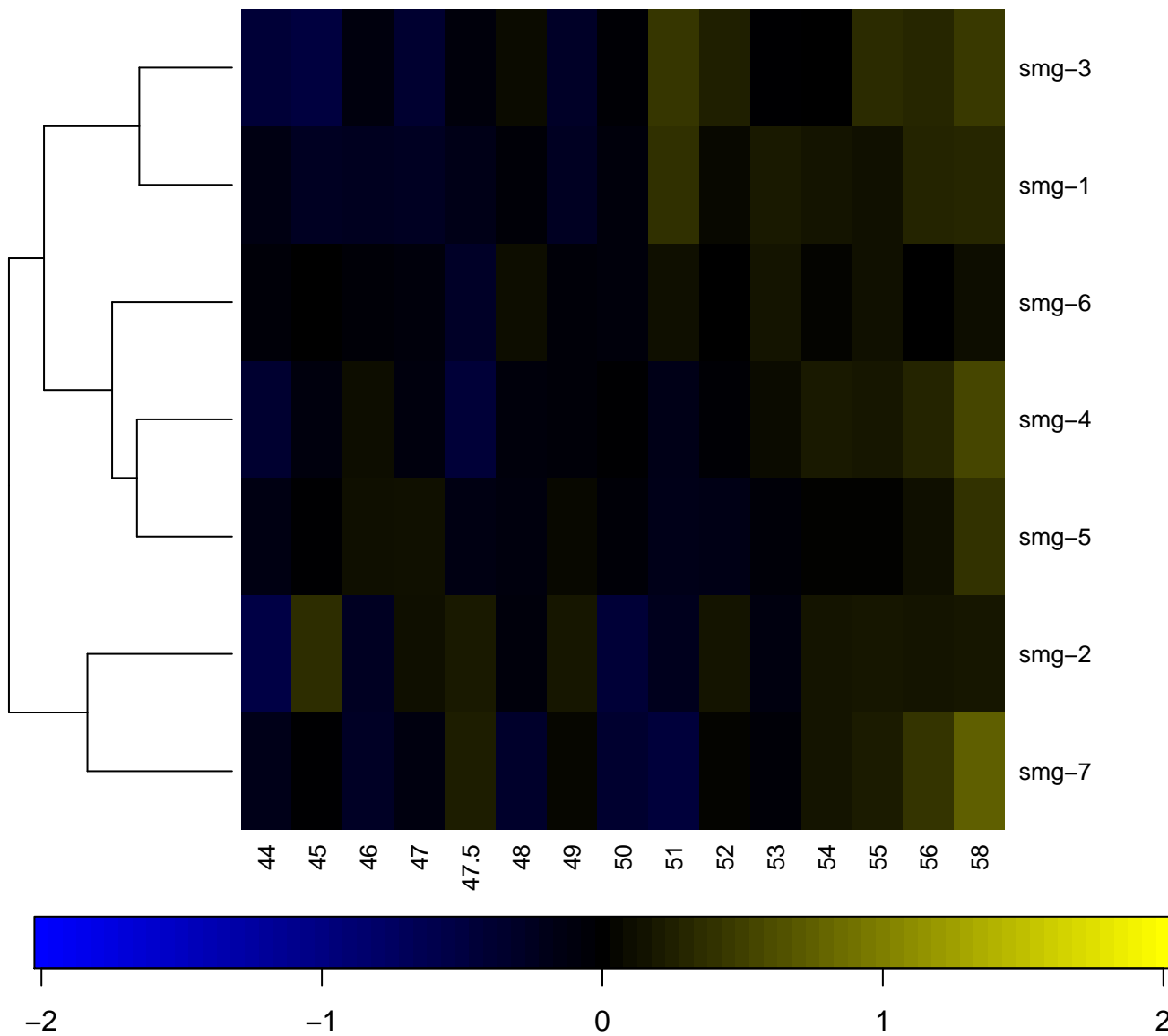
neurotransmitter:sodium symporter activity



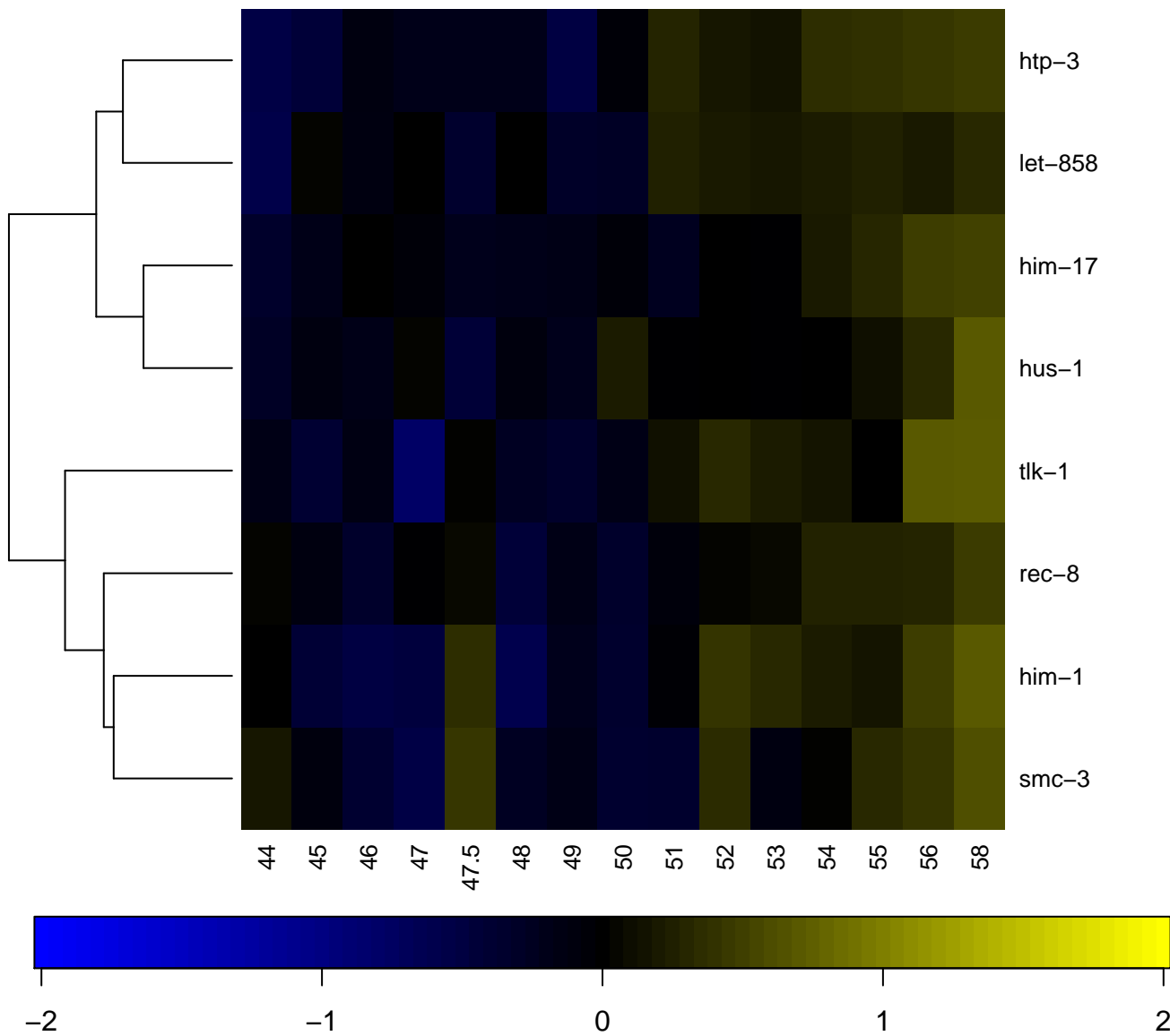
nitrogen compound metabolic process



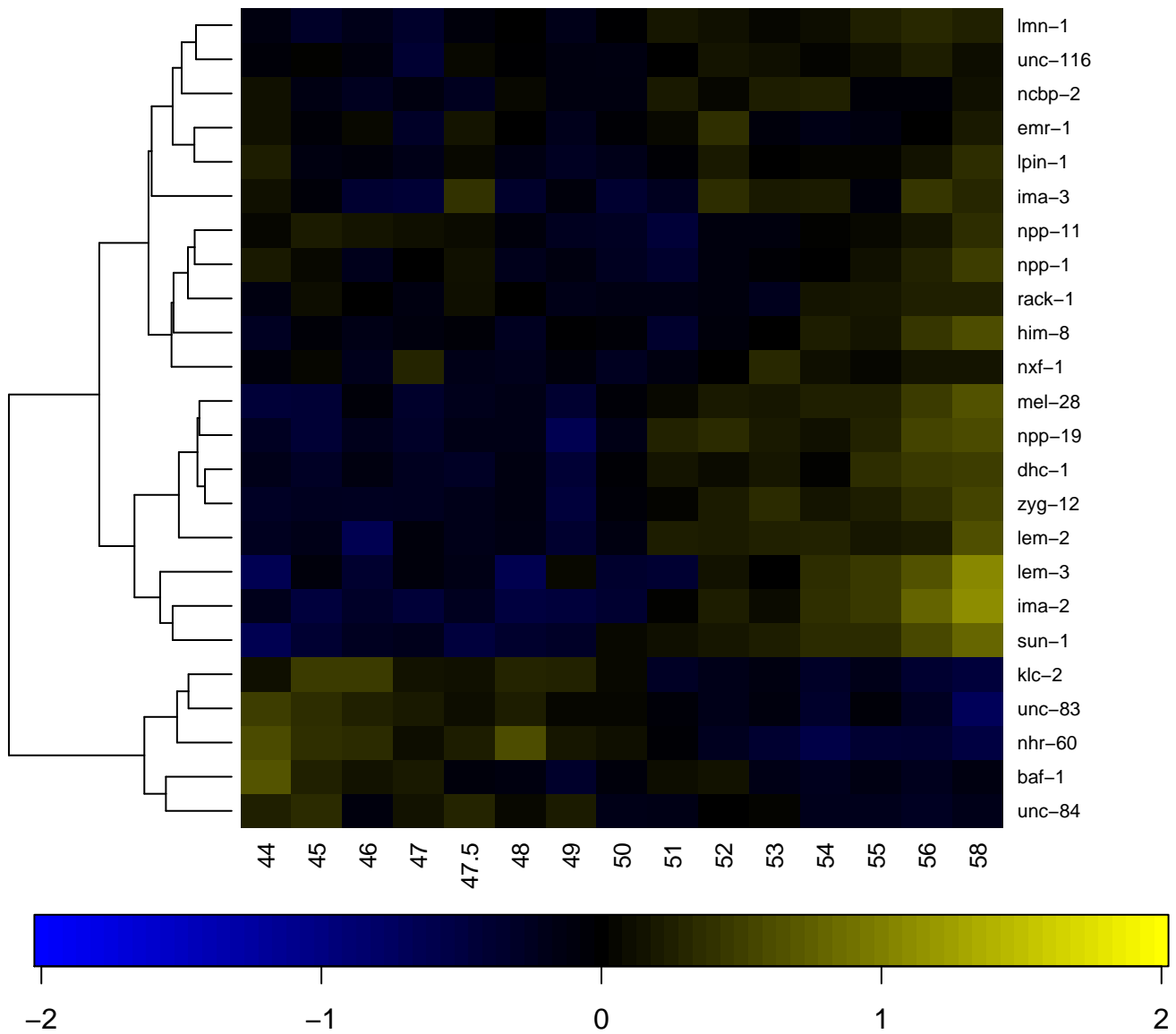
ar-transcribed mRNA catabolic process, nonsense-mediate



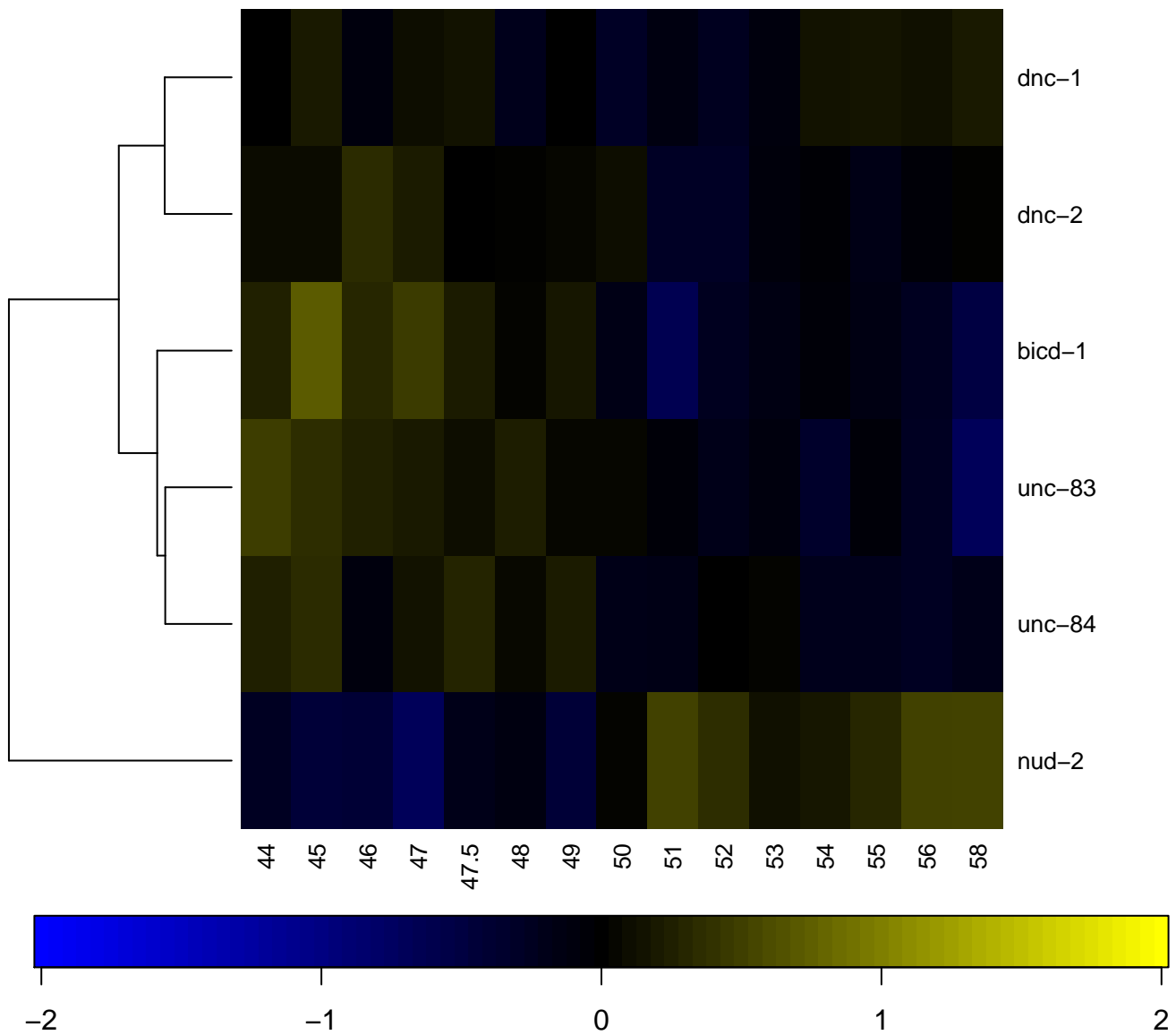
nuclear chromatin



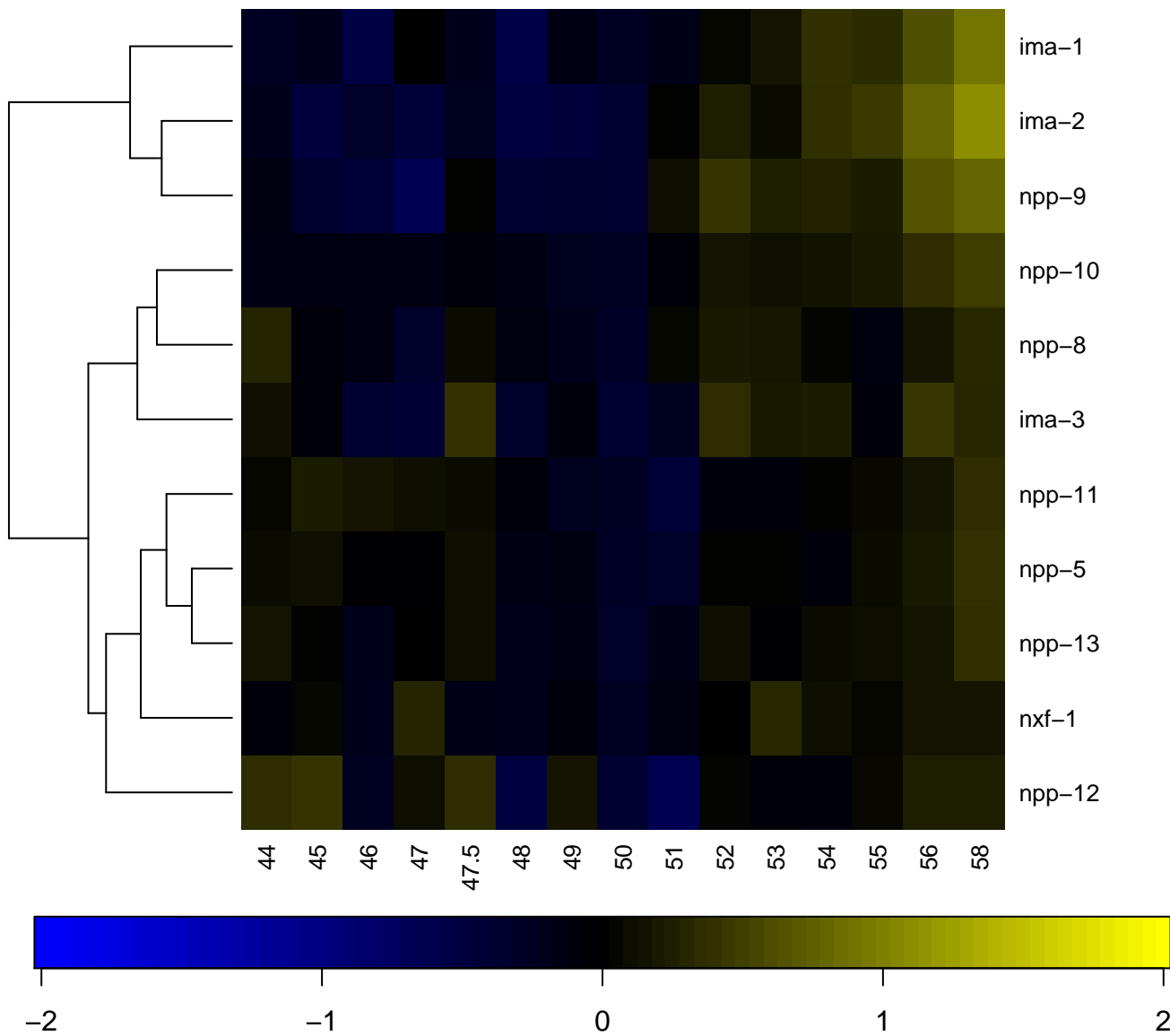
nuclear envelope



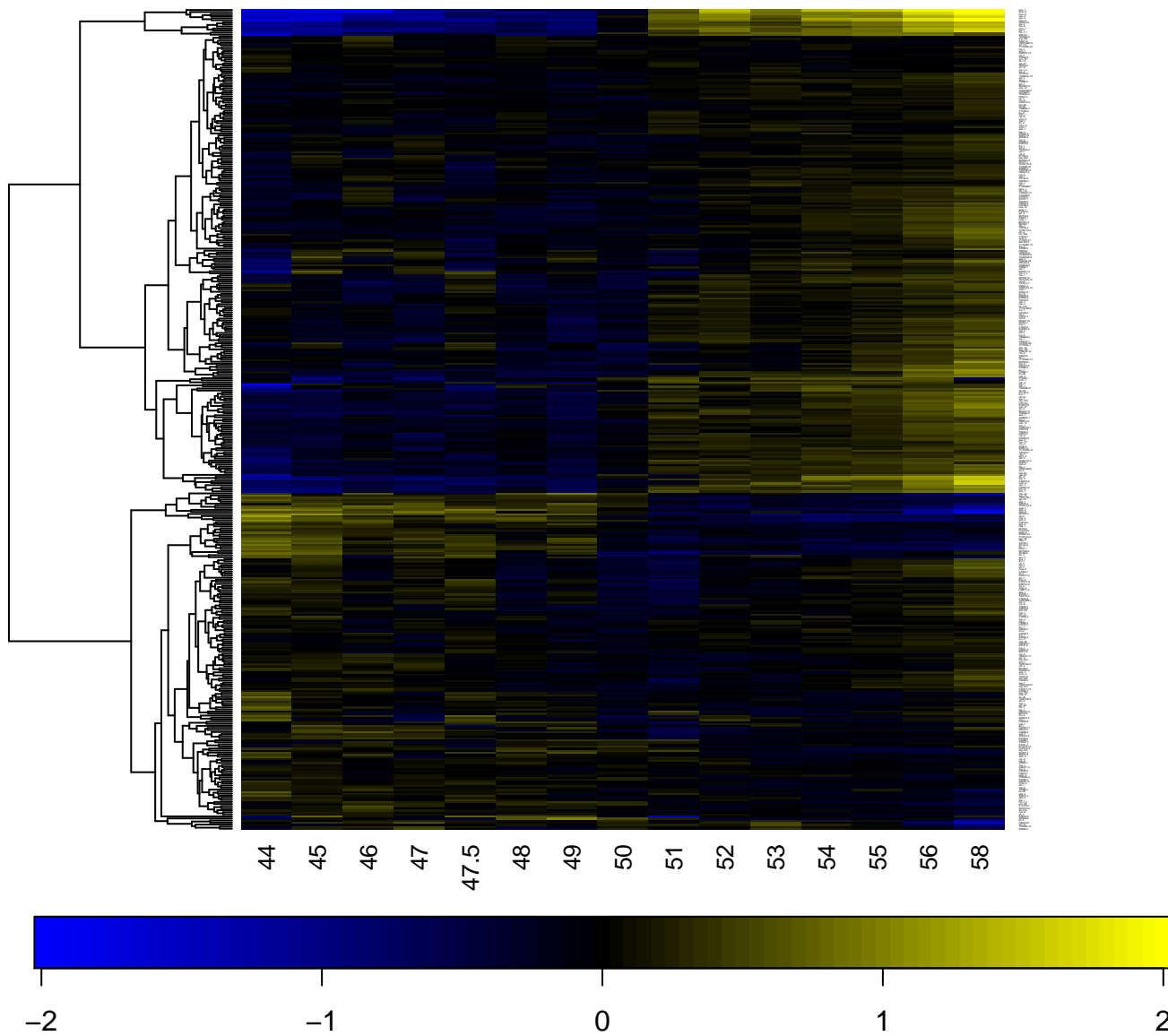
nuclear migration



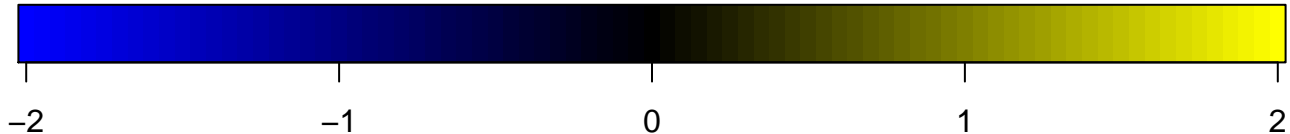
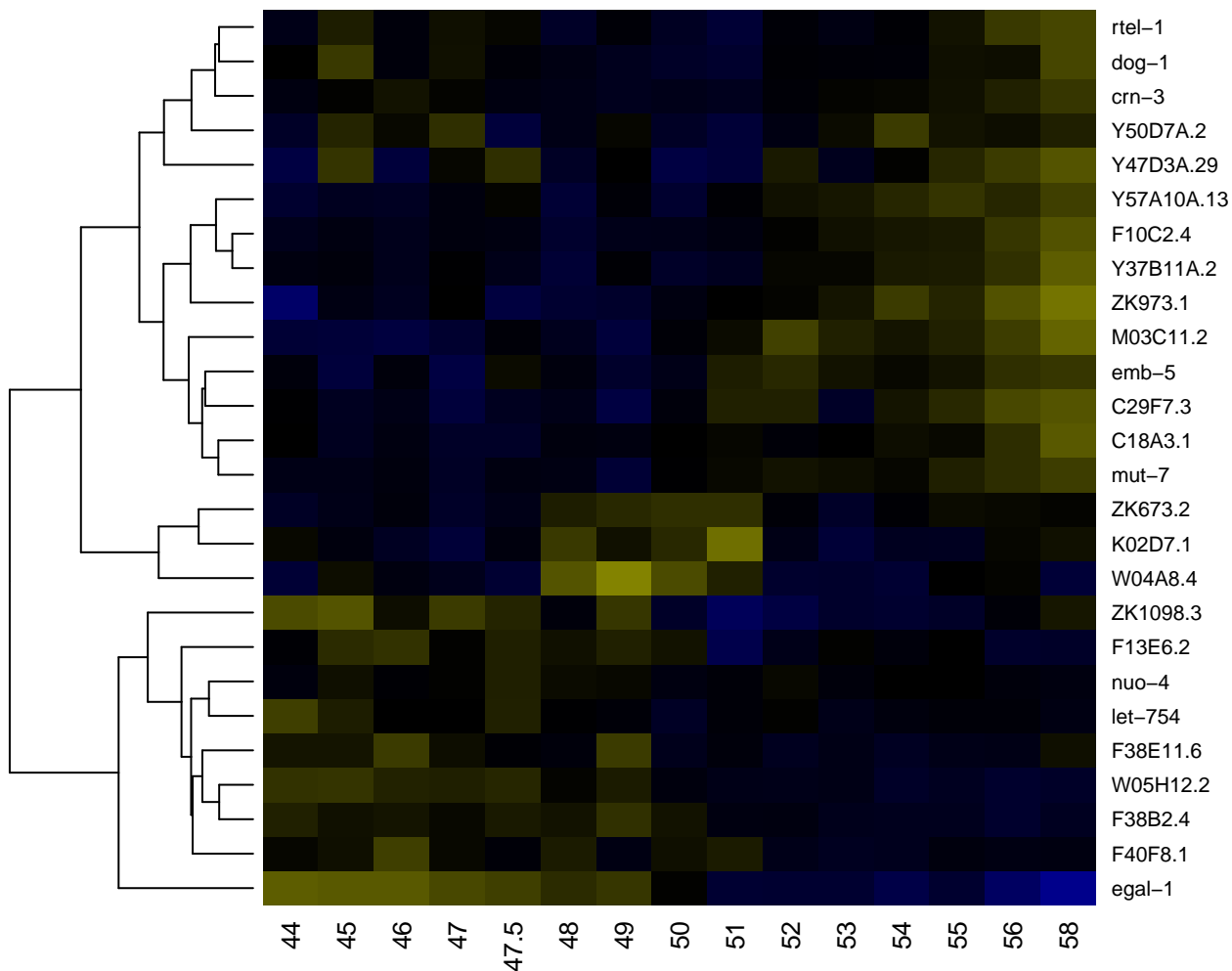
nuclear pore



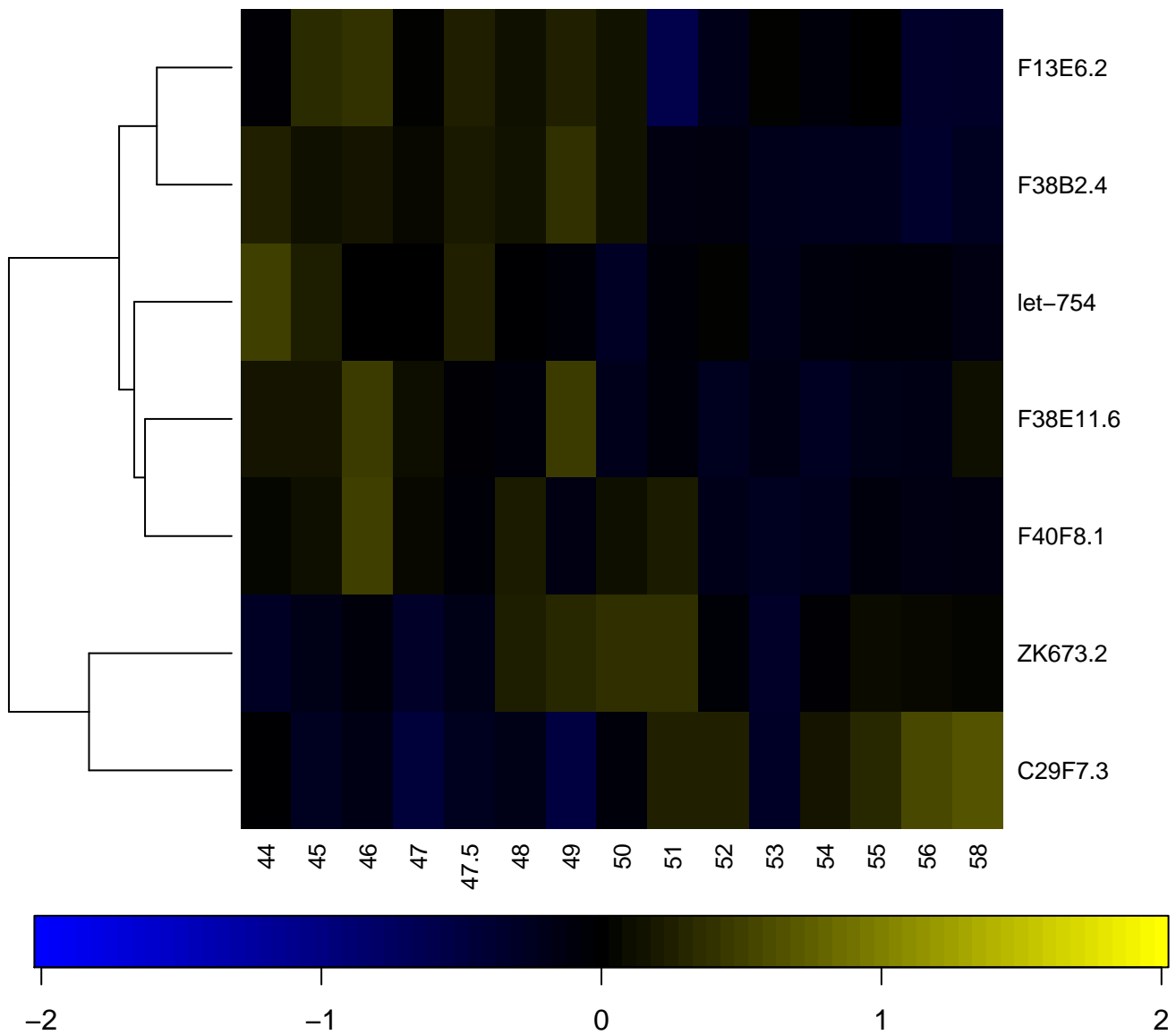
nucleic acid binding



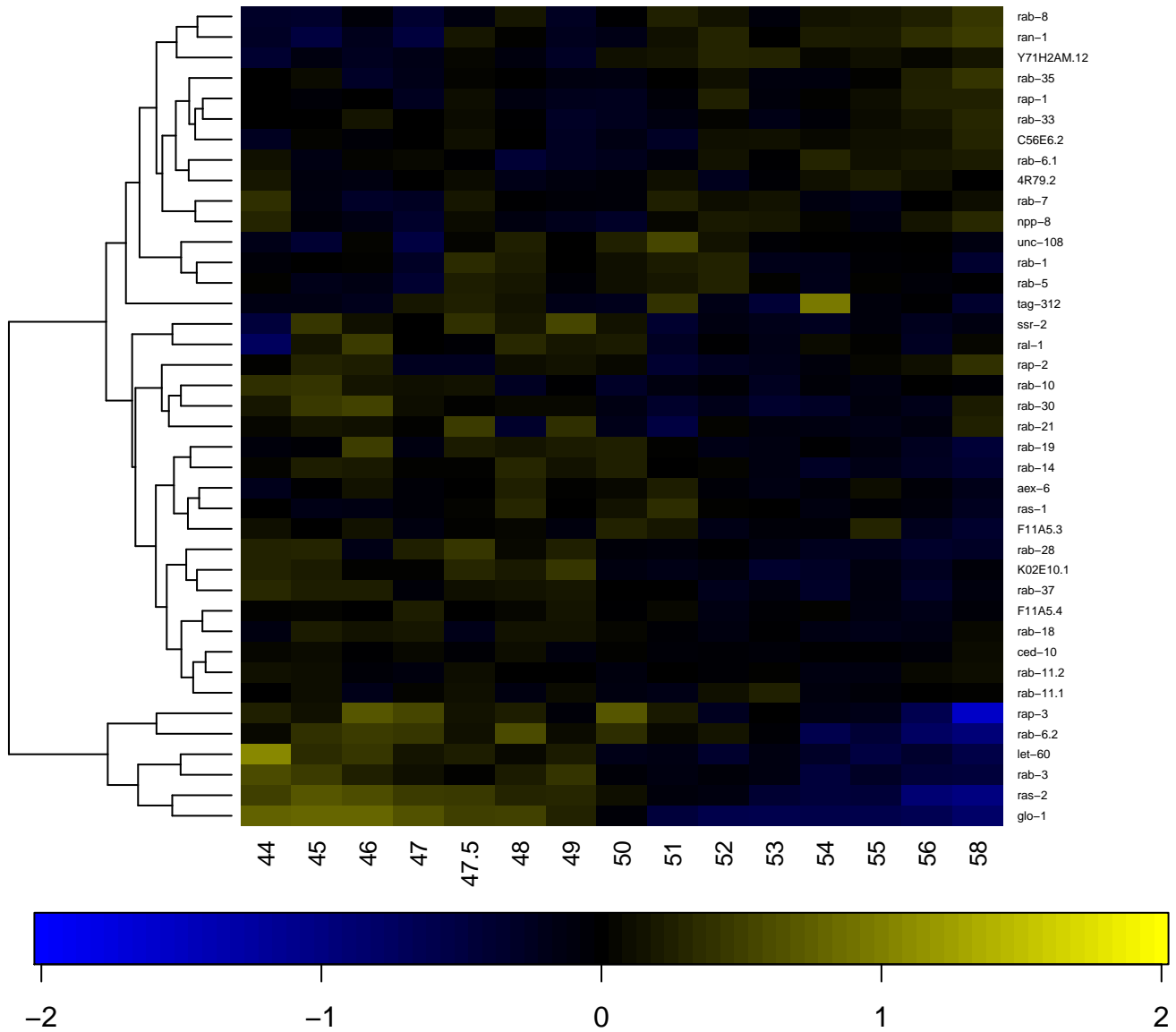
Probase, nucleoside, nucleotide and nucleic acid metabolic p



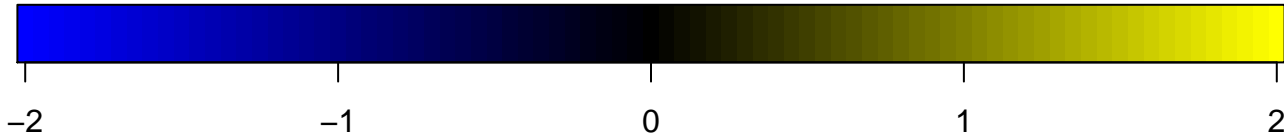
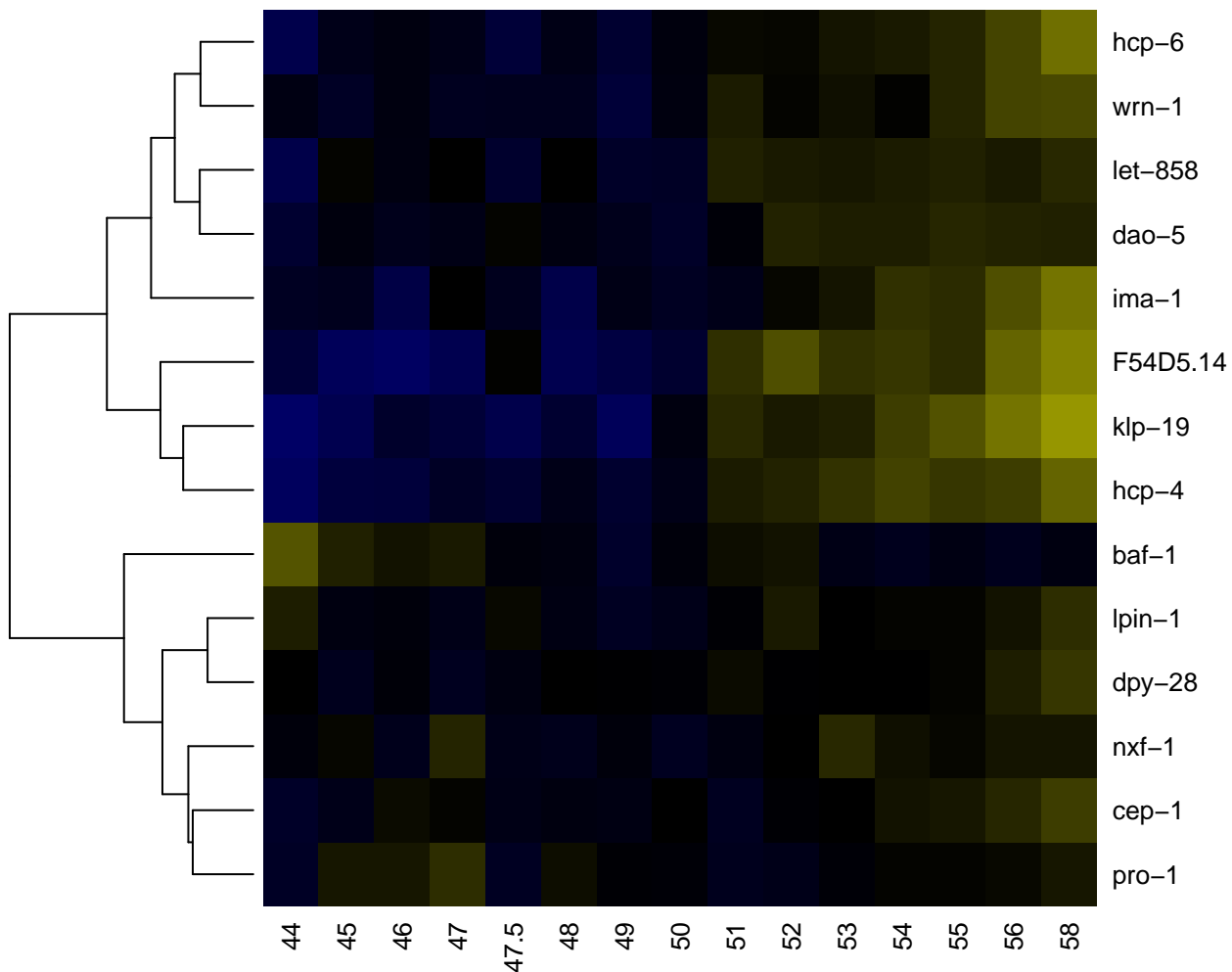
nucleobase, nucleoside, nucleotide kinase activity



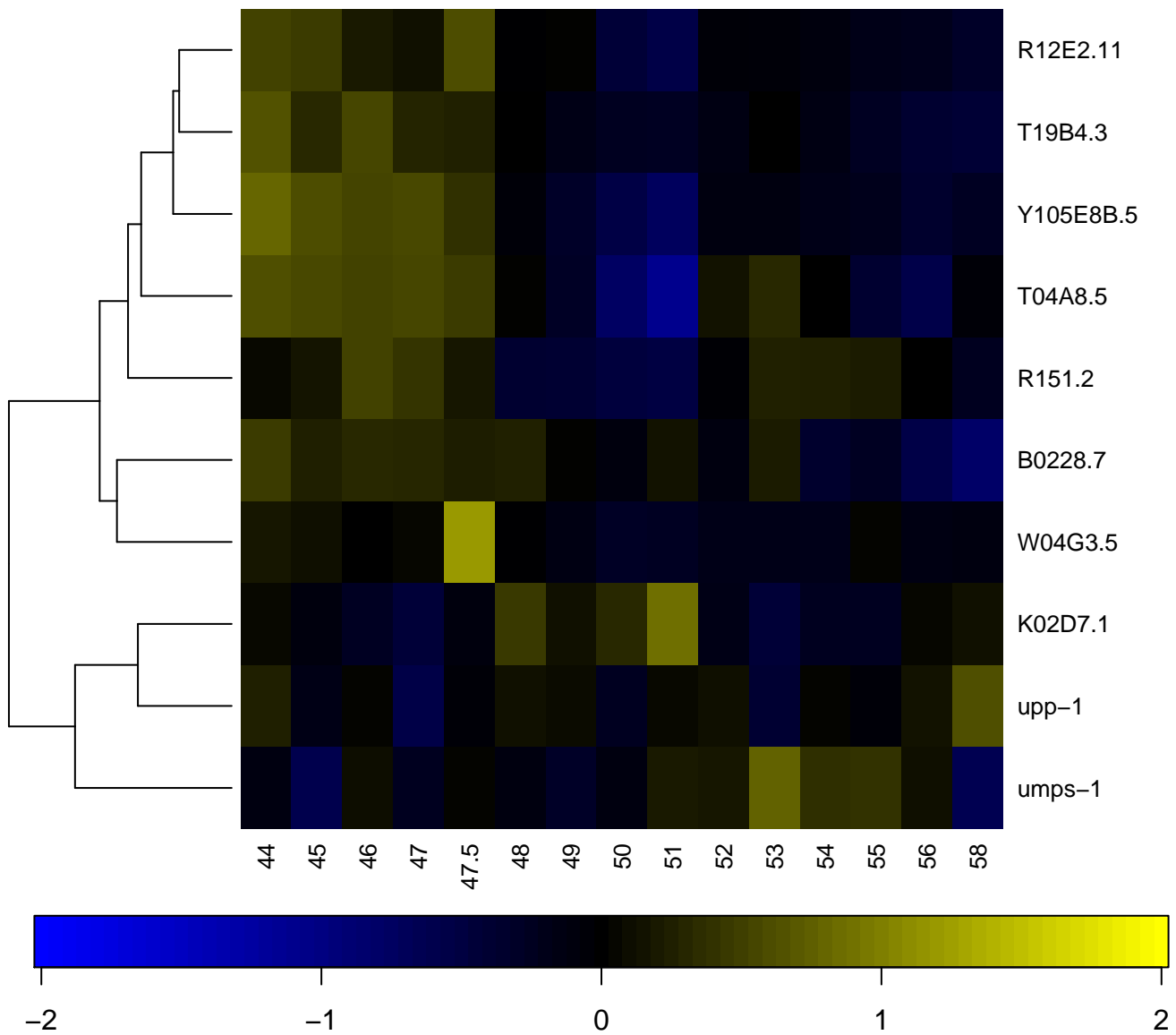
nucleocytoplasmic transport



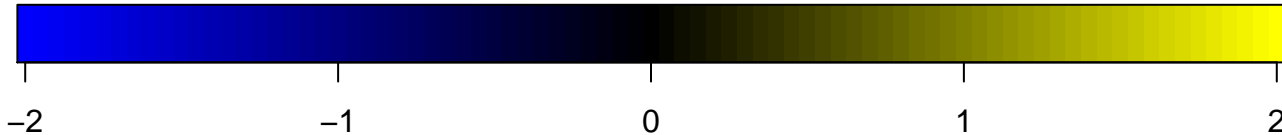
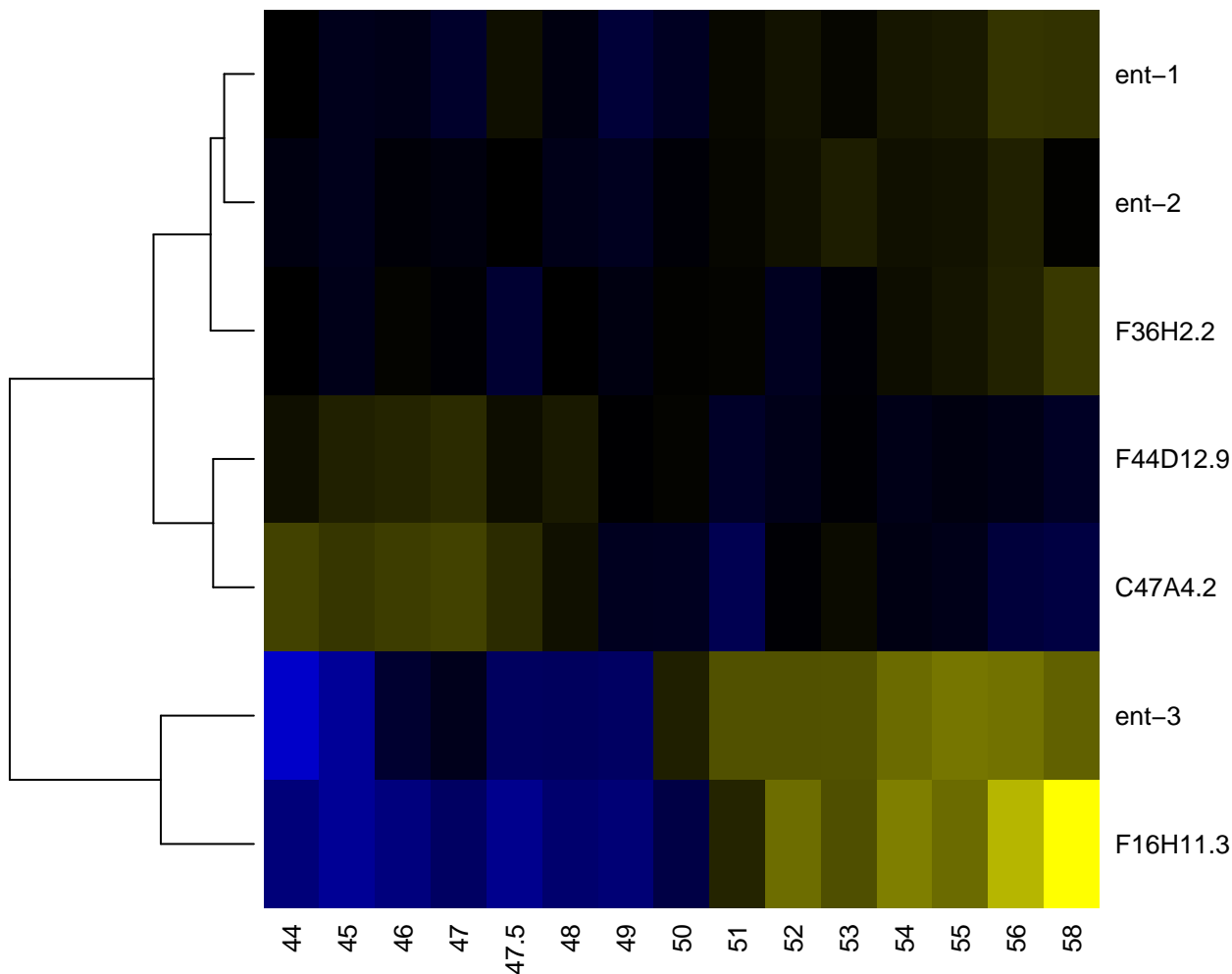
nucleoplasm



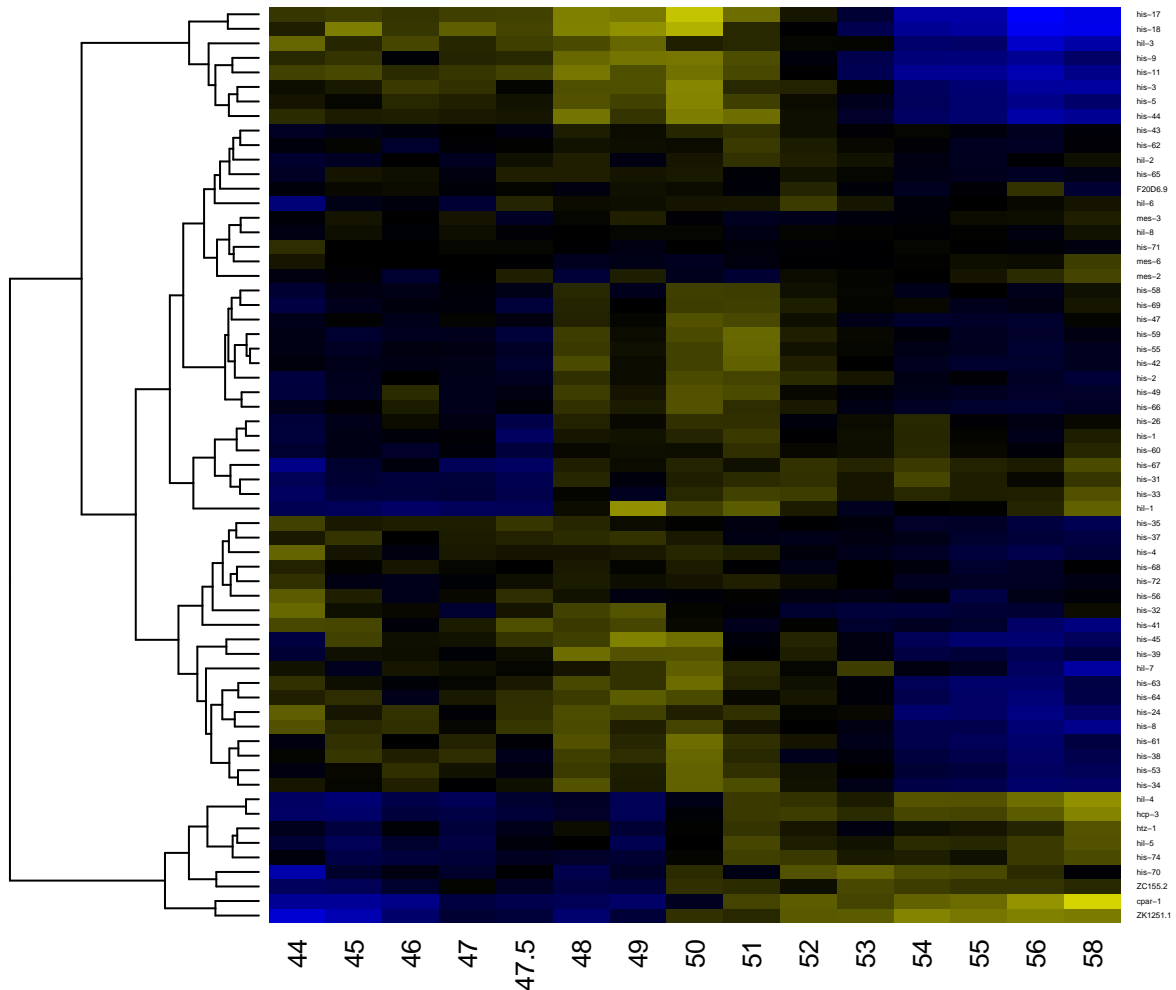
nucleoside metabolic process



nucleoside transmembrane transporter activity



nucleosome



-2

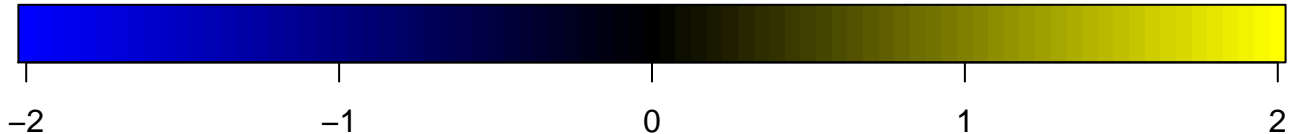
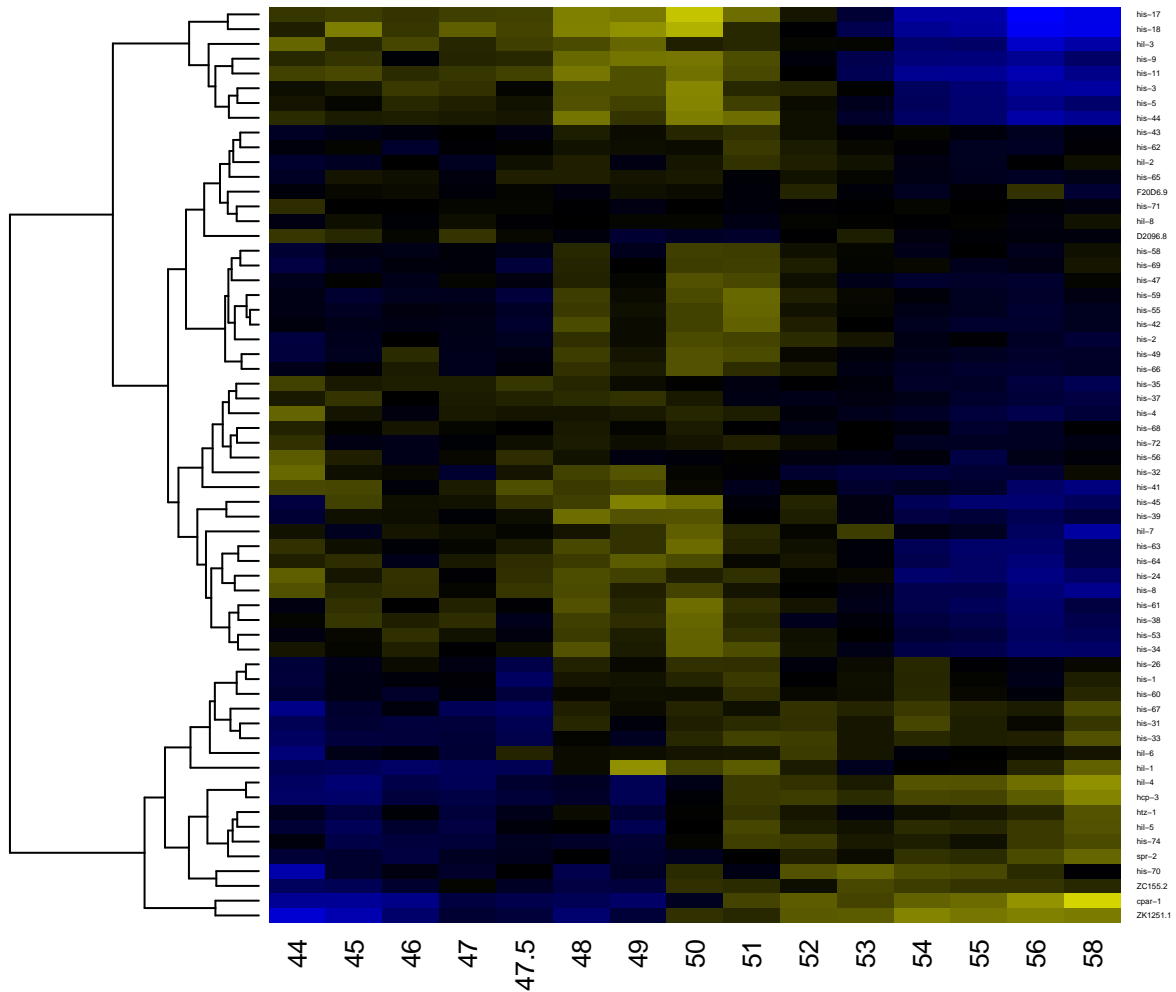
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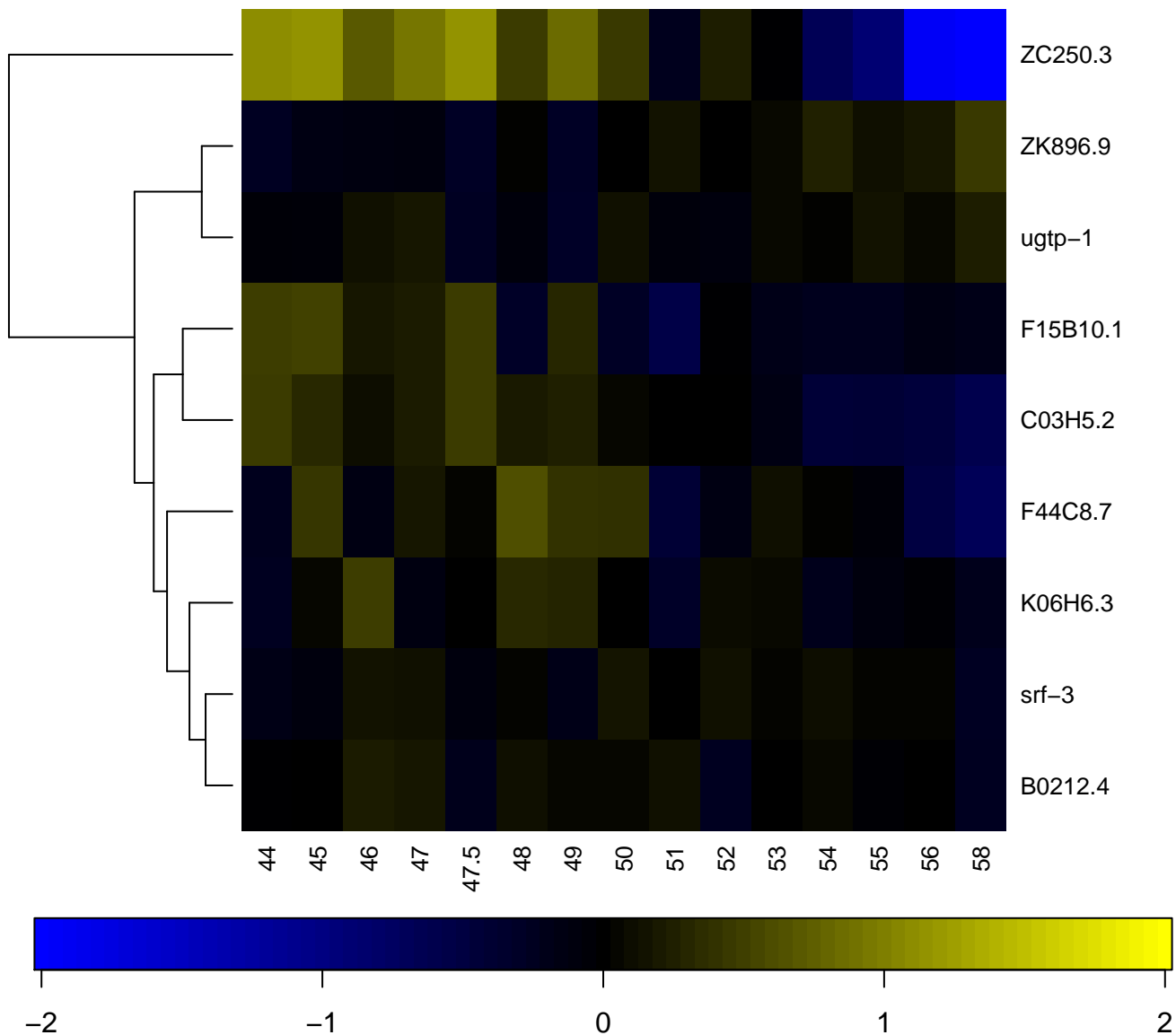
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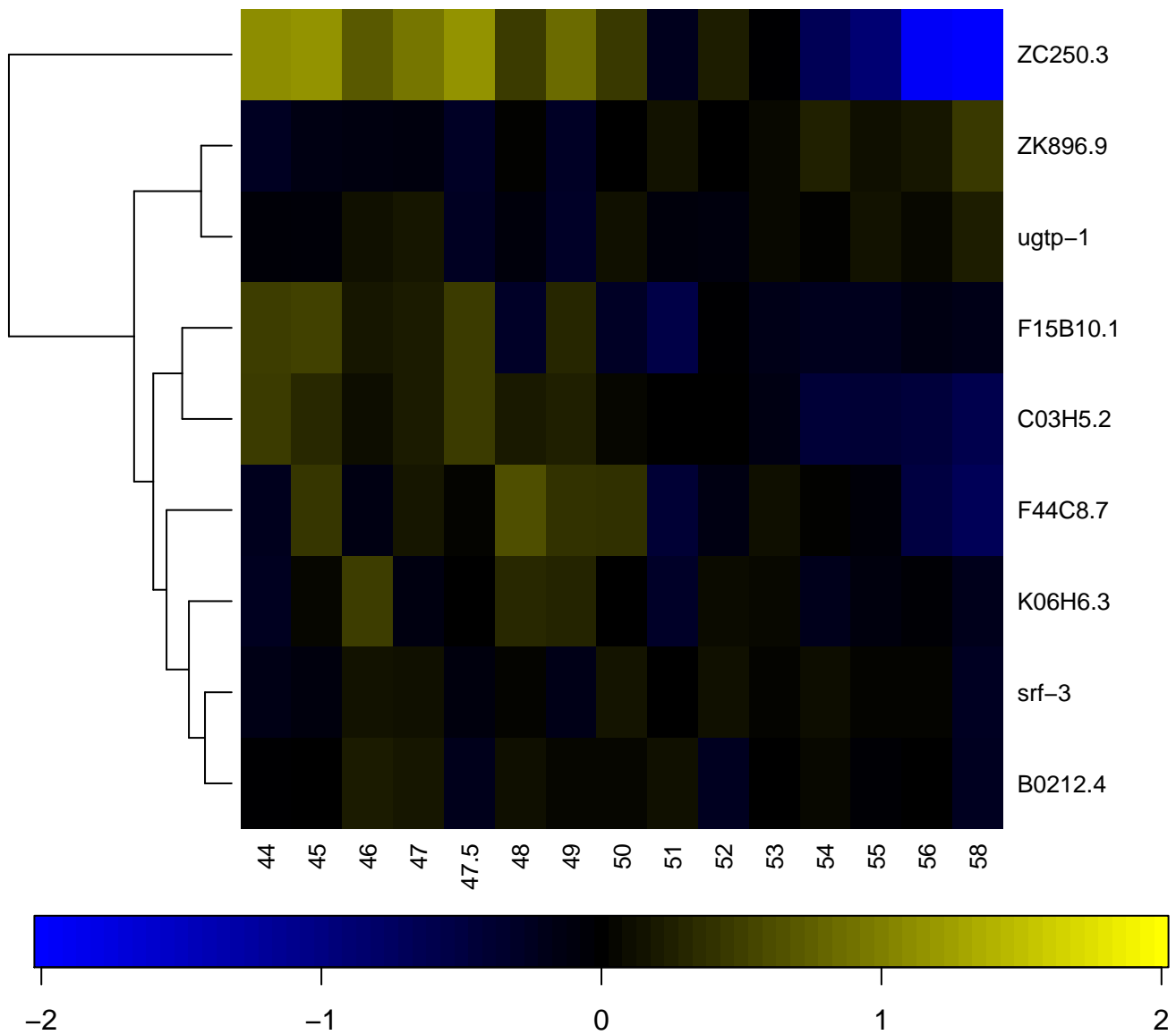
nucleosome assembly



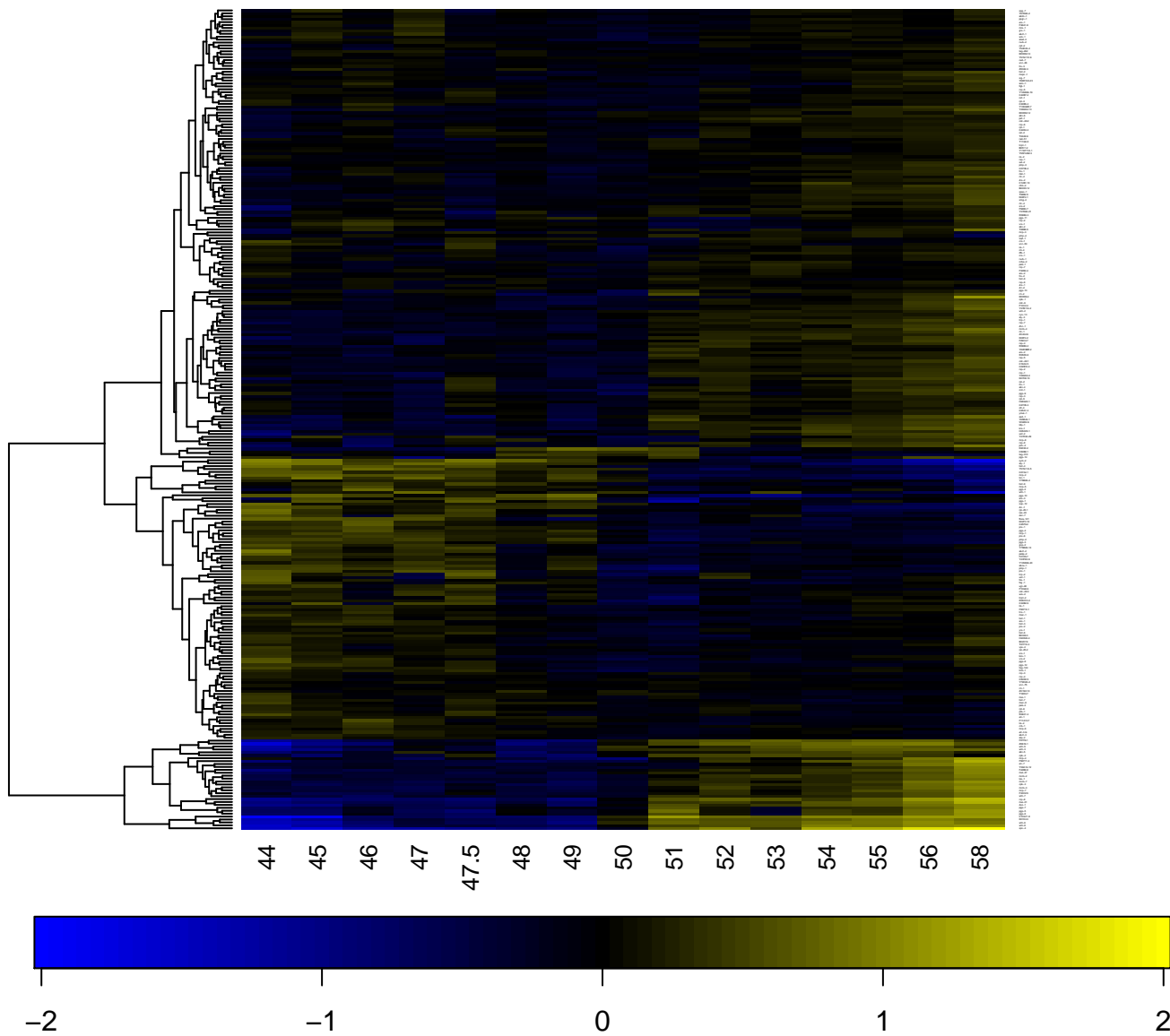
nucleotide-sugar transmembrane transporter activity



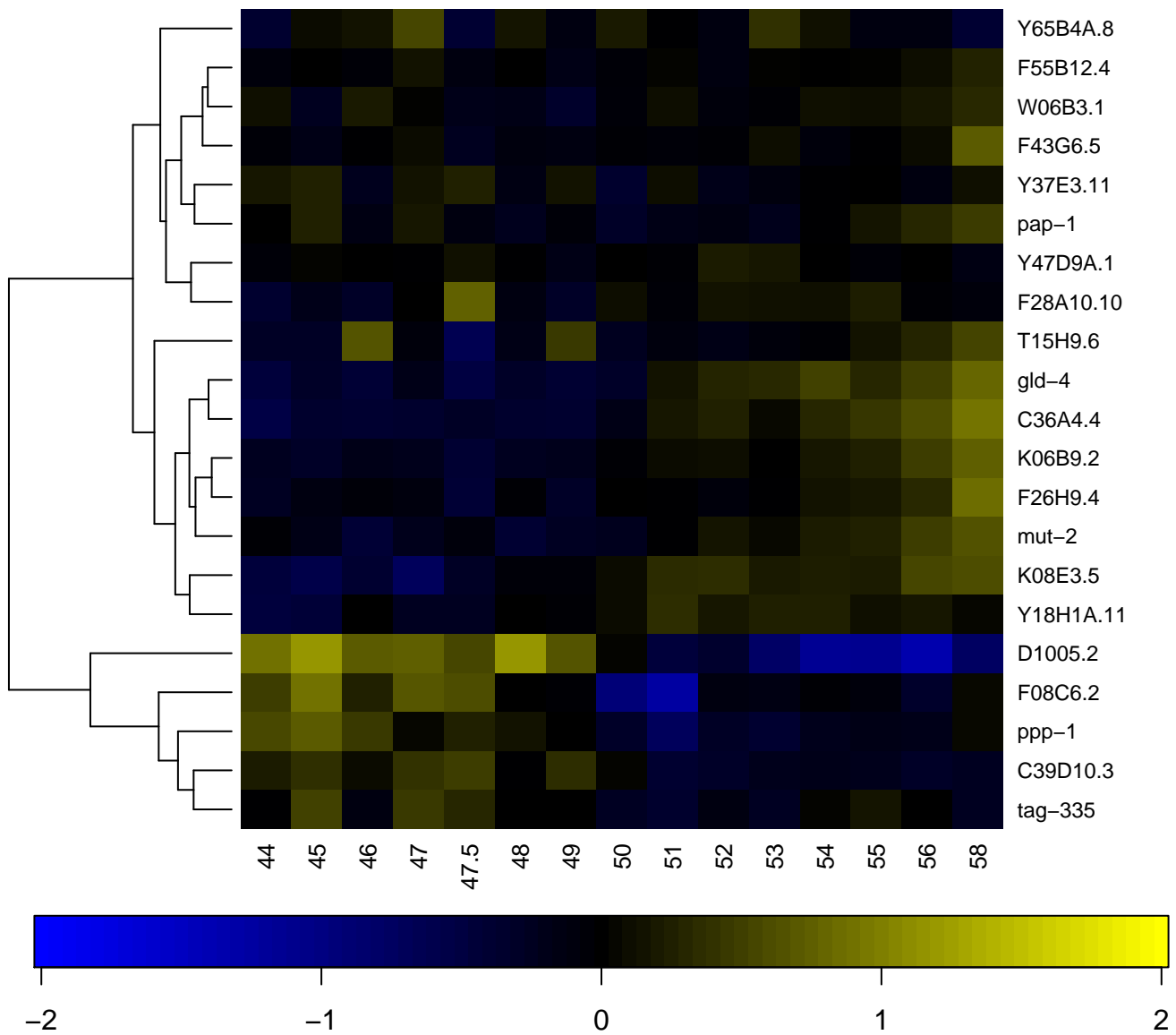
nucleotide-sugar transport



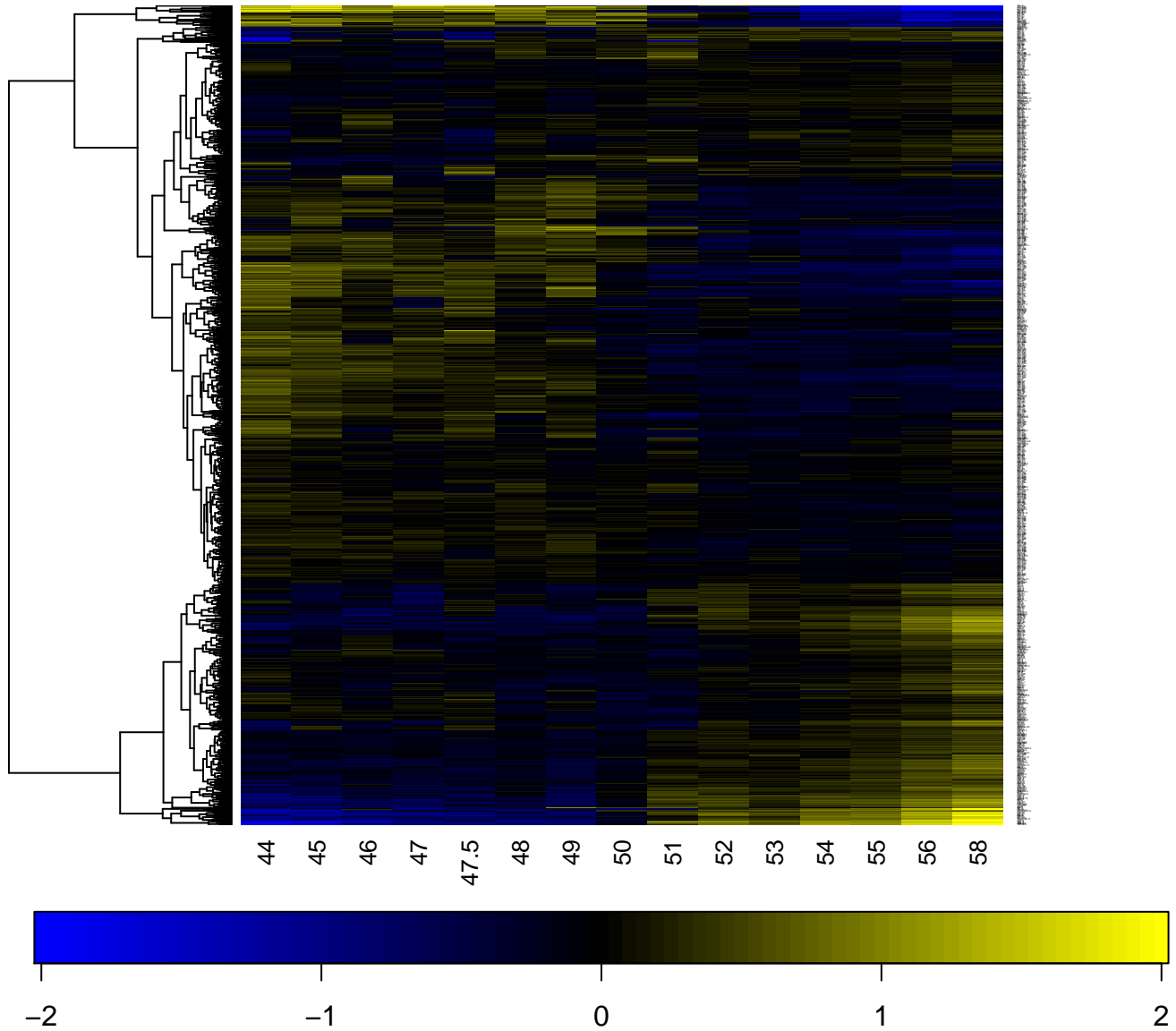
nucleotide binding



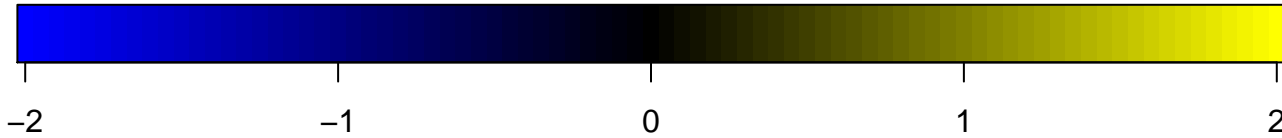
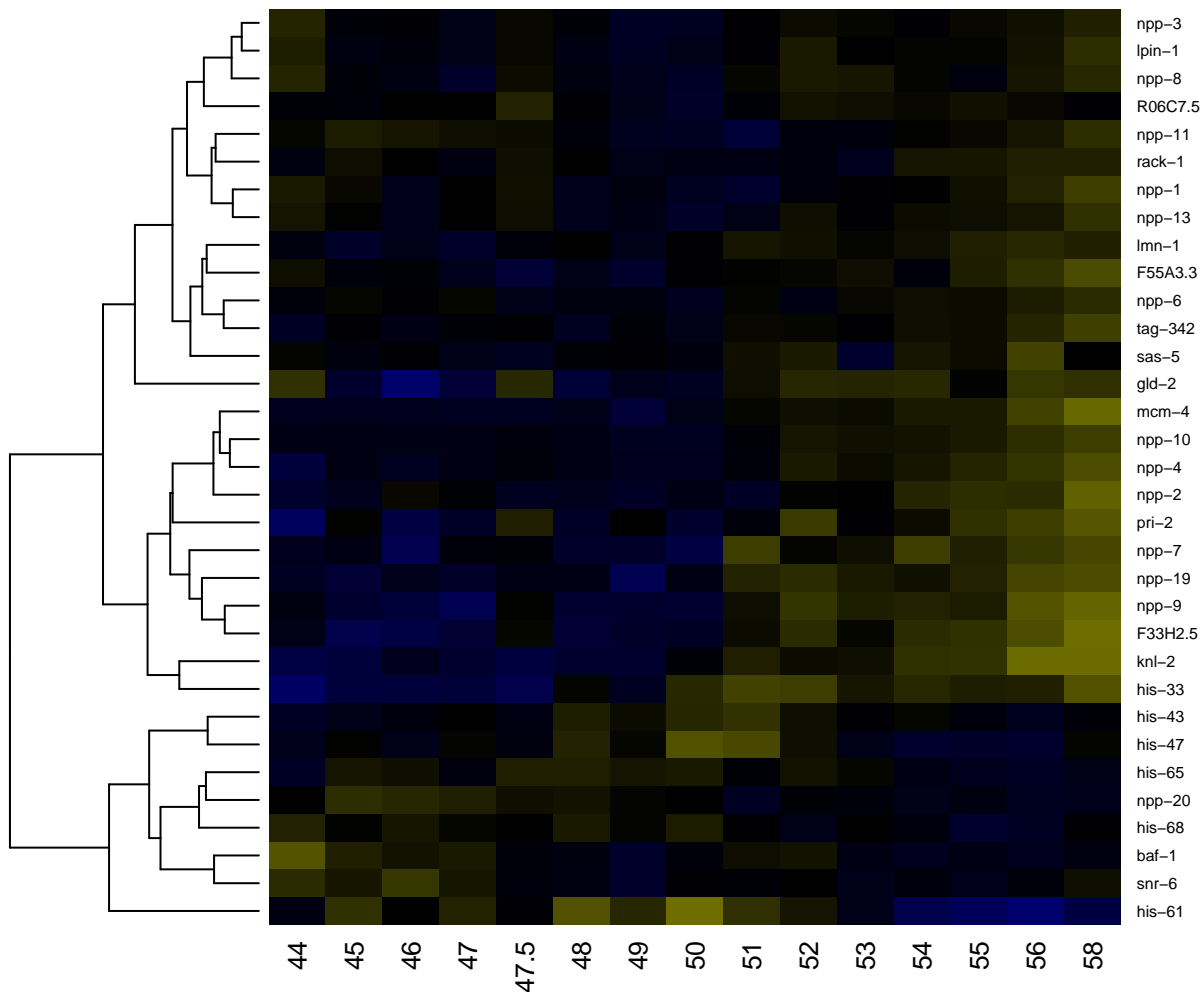
nucleotidyltransferase activity



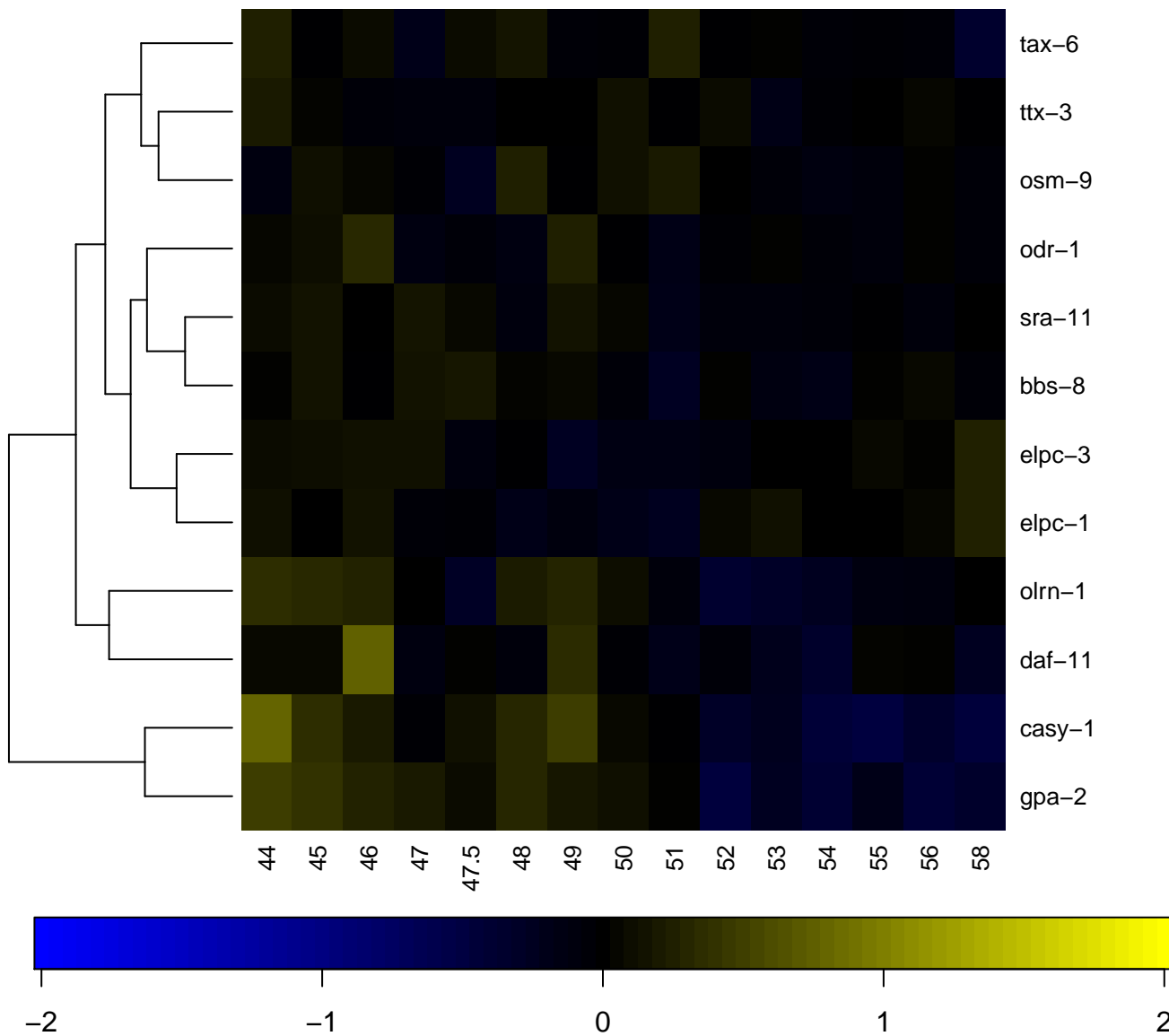
nucleus



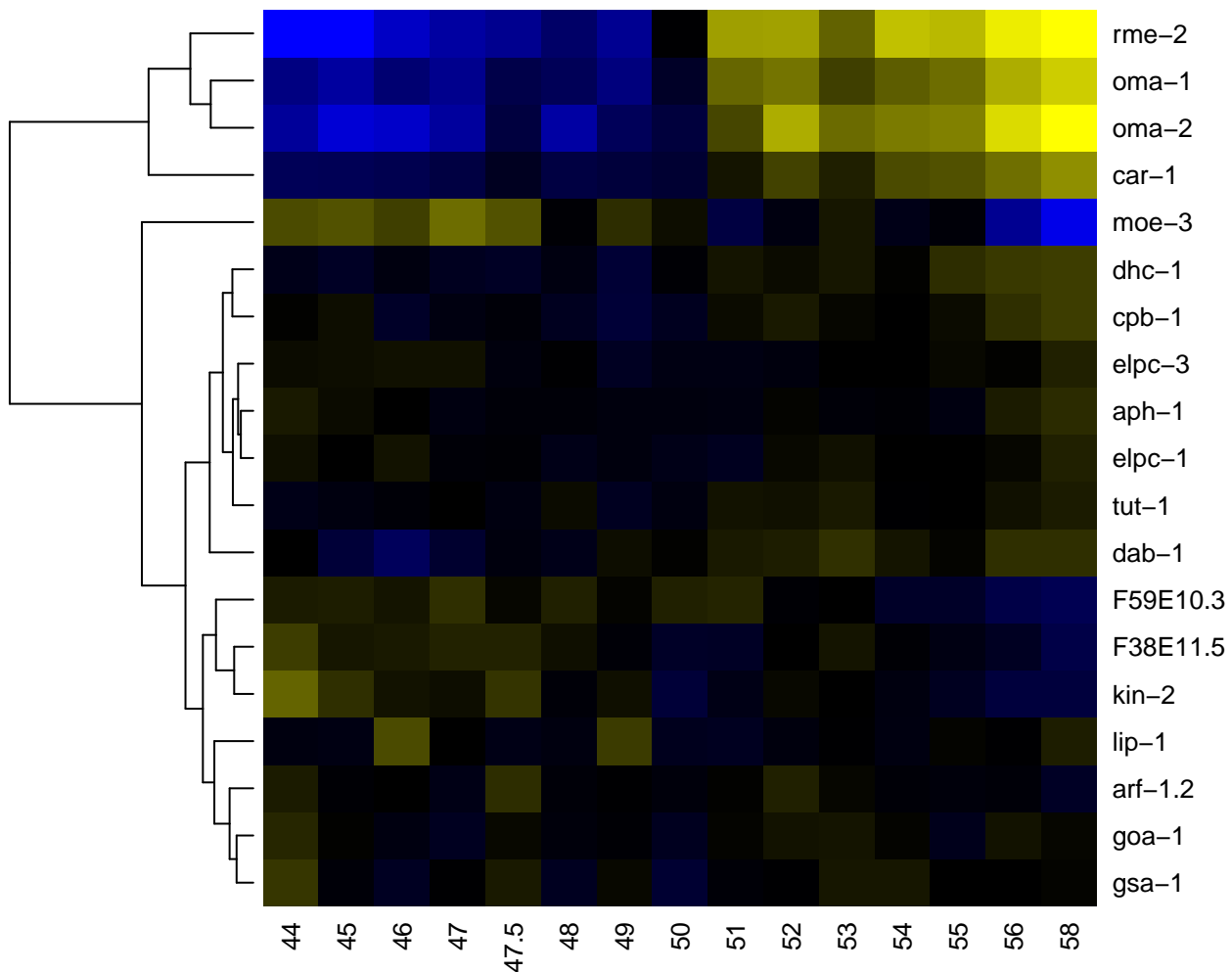
nucleus organization



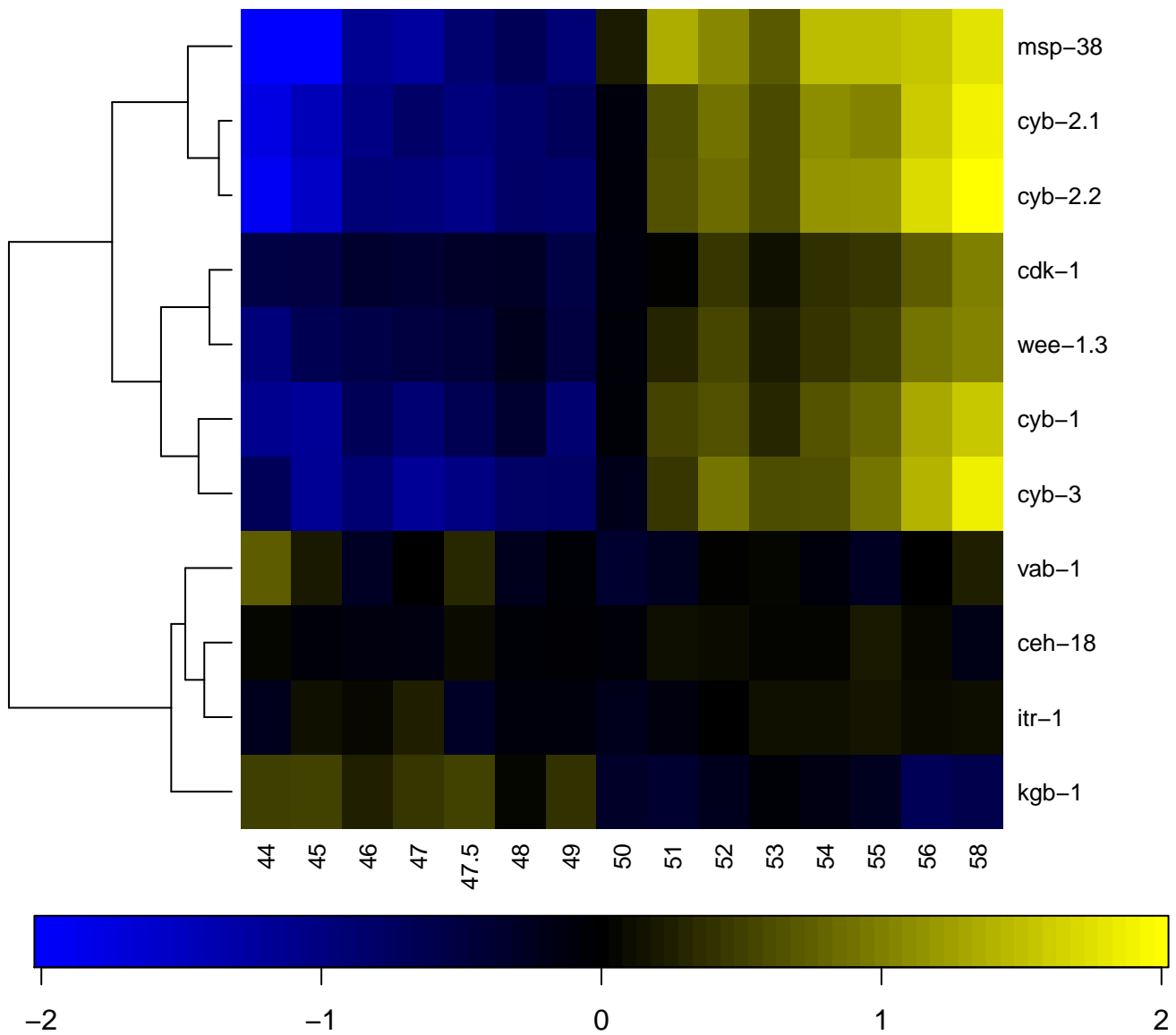
olfactory learning



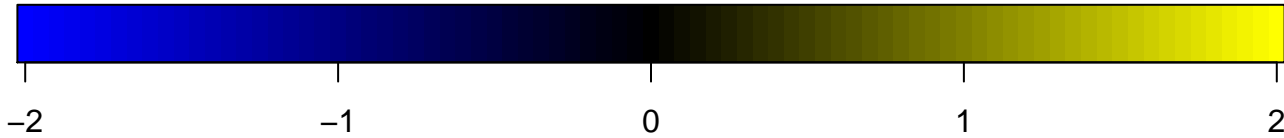
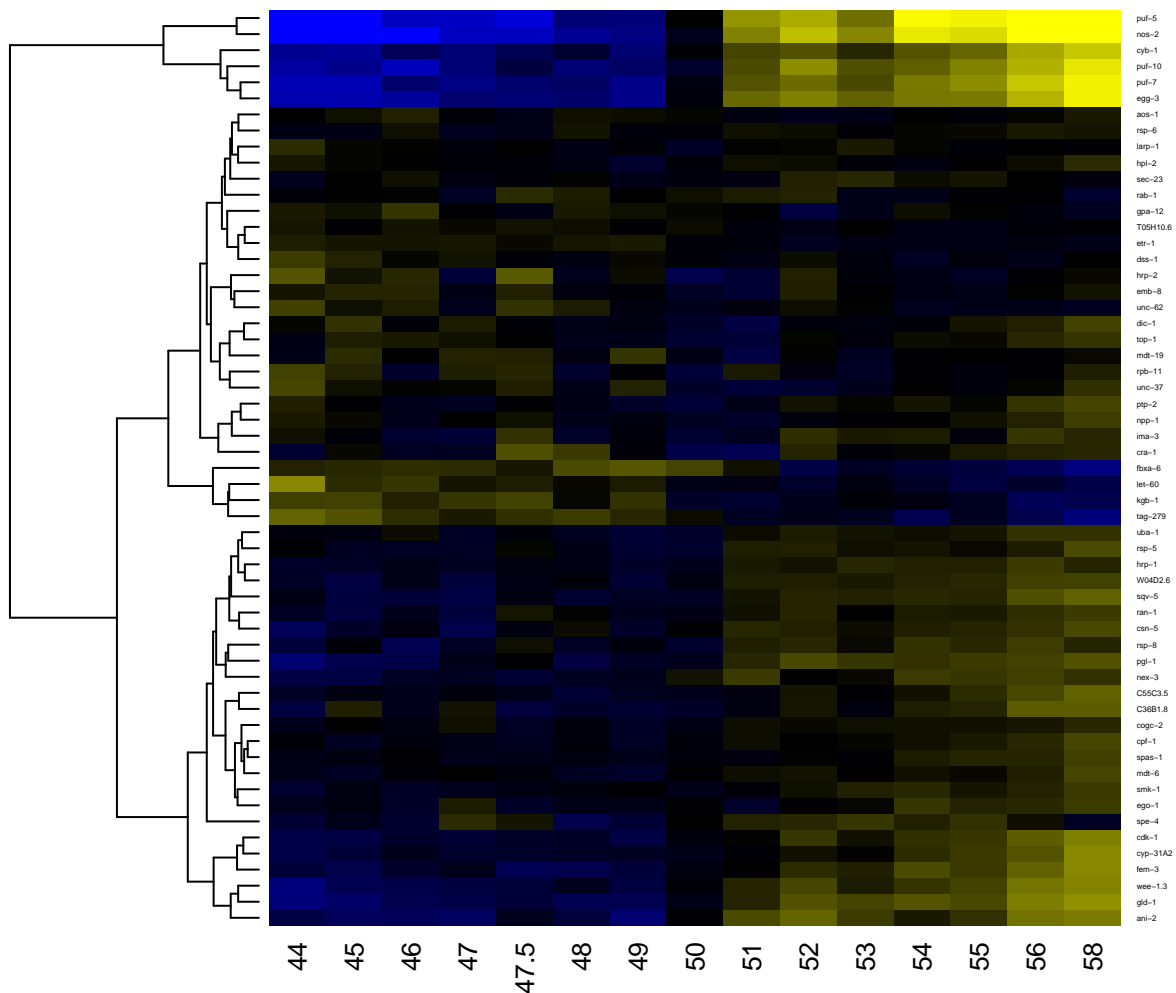
oocyte development



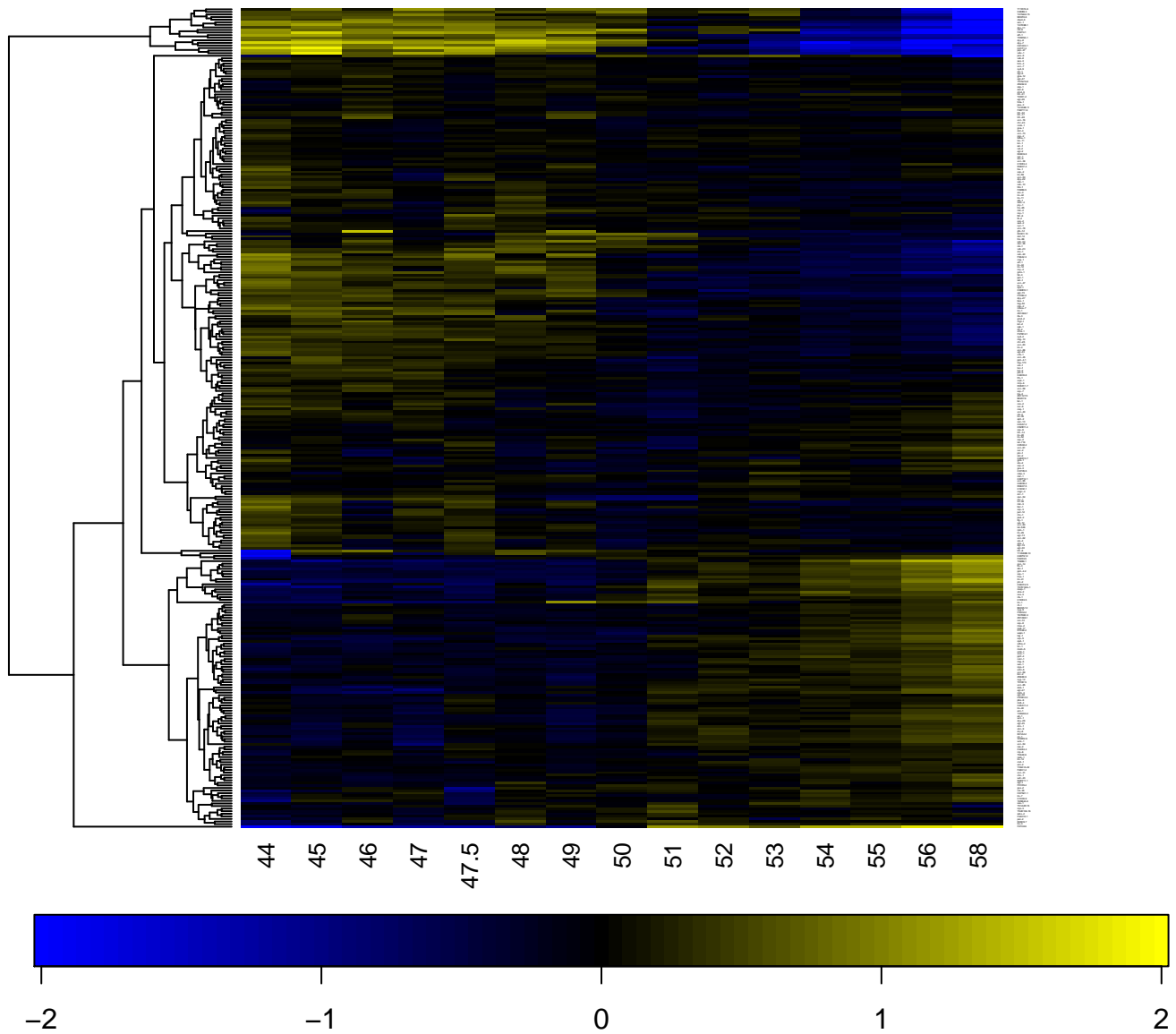
oocyte maturation



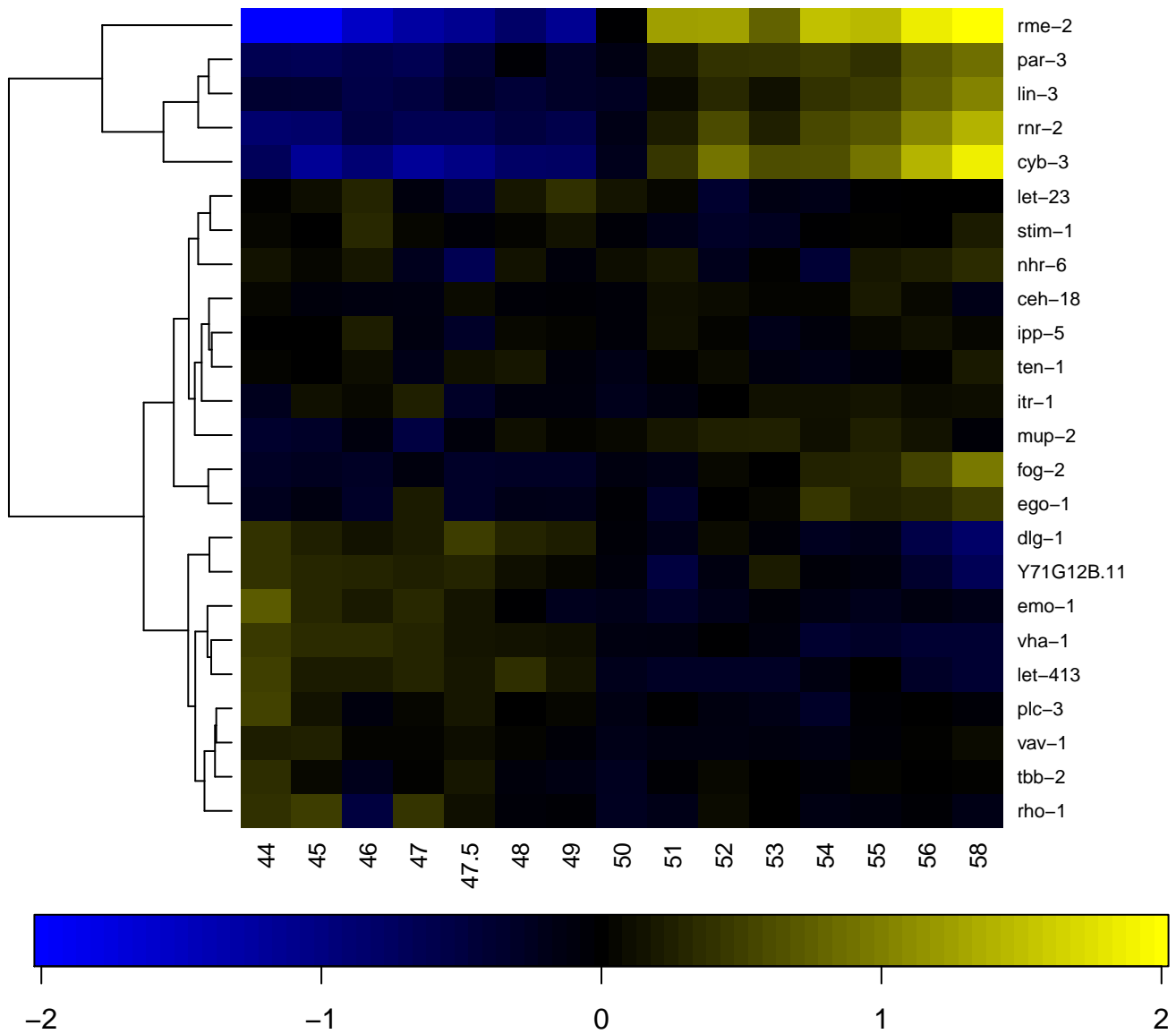
oogenesis



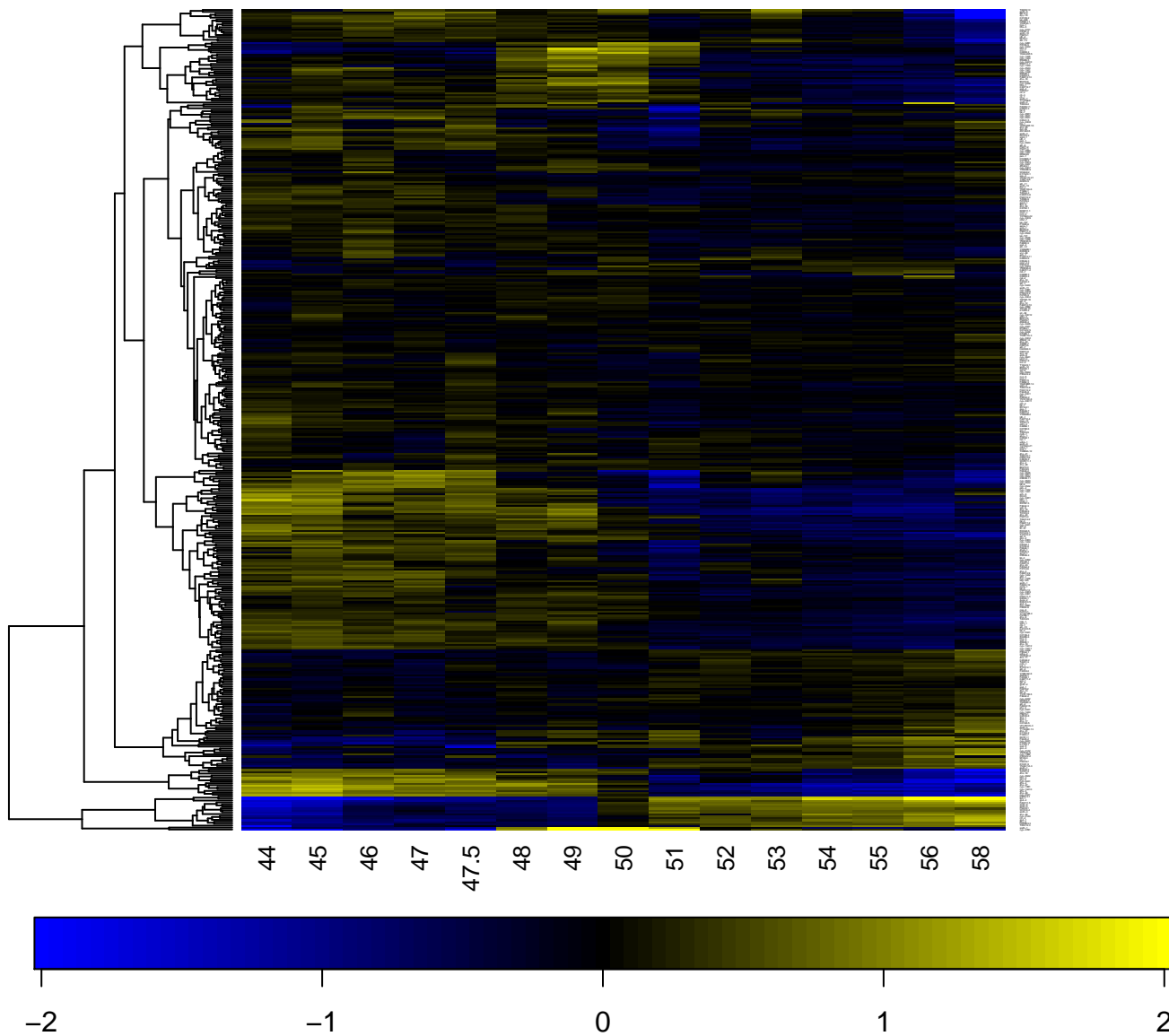
oviposition



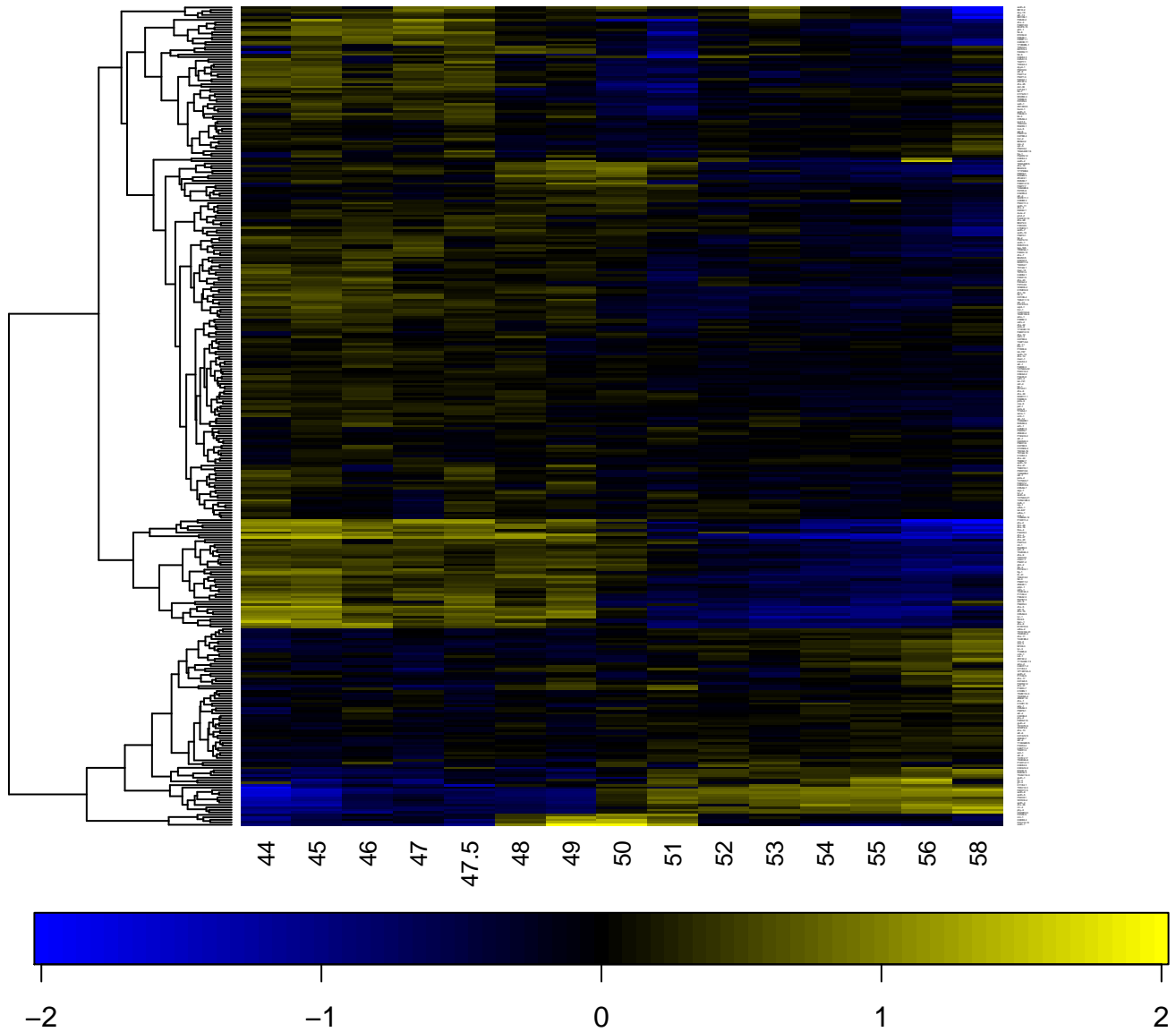
ovulation



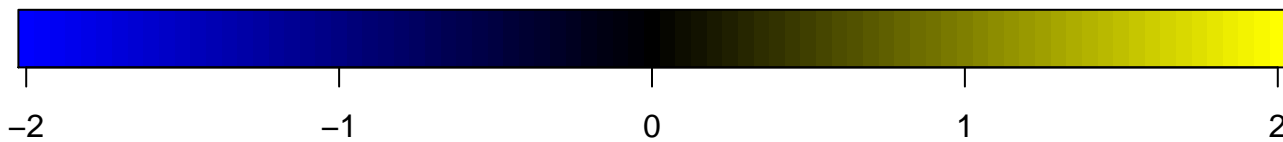
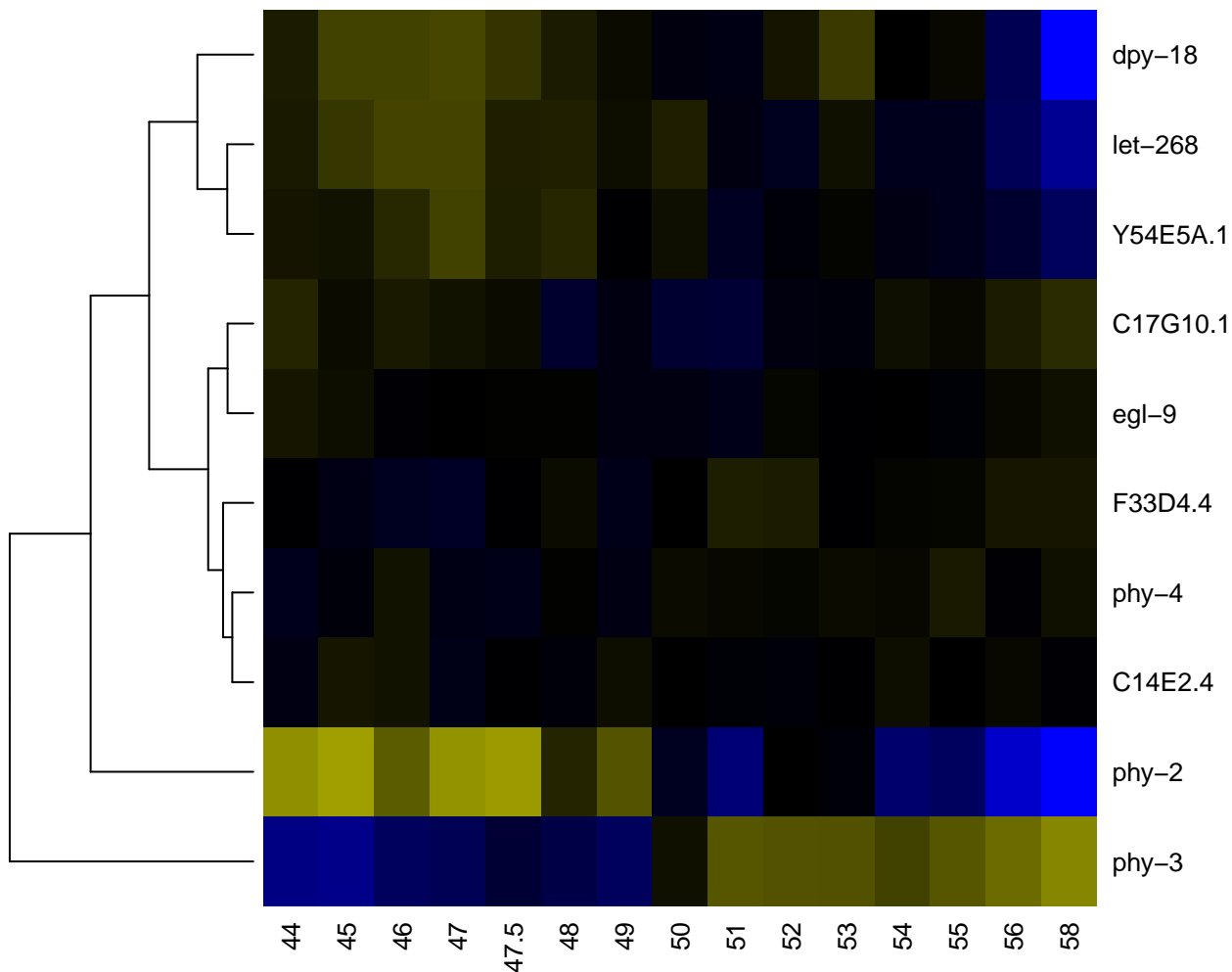
oxidation reduction



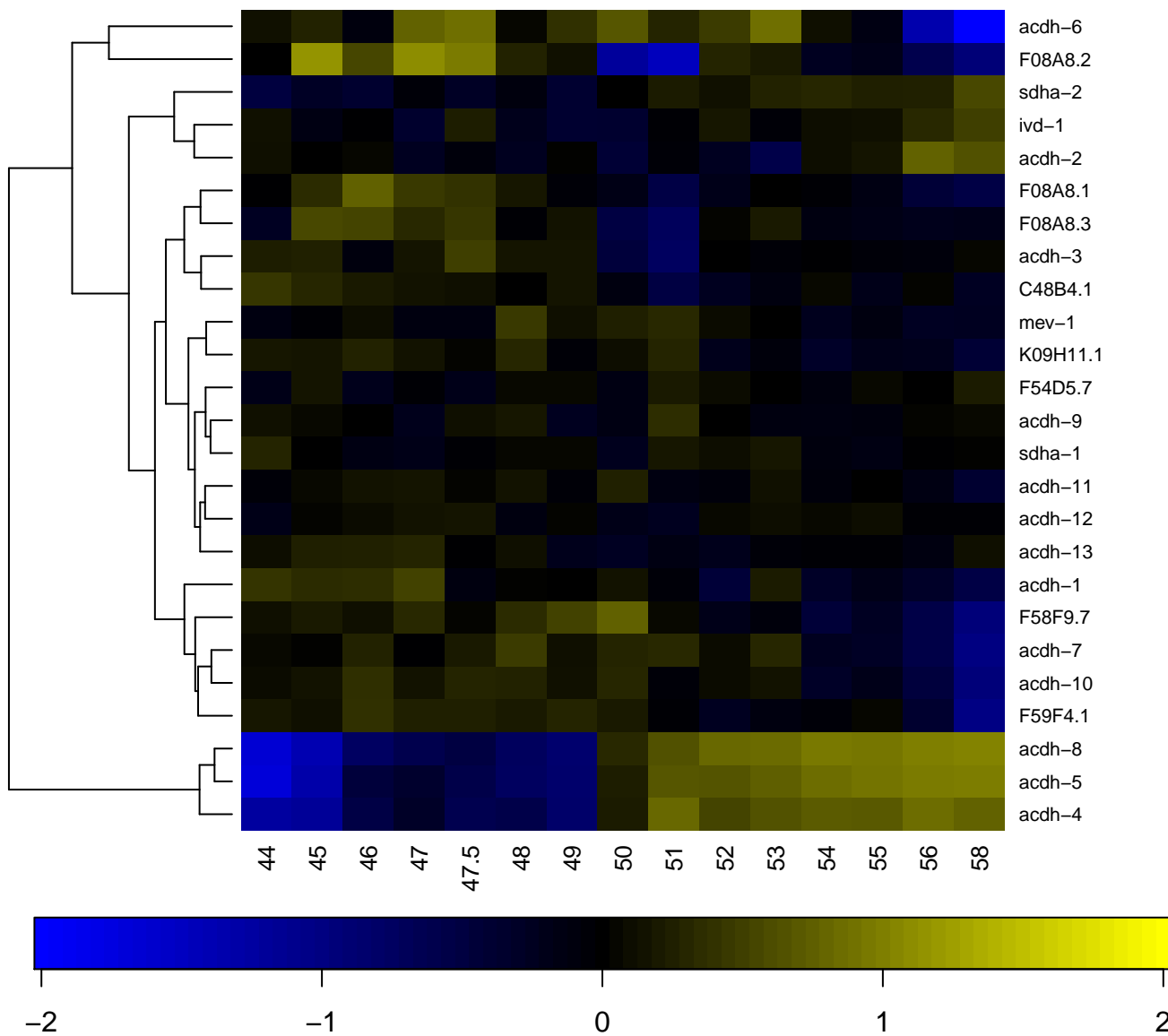
oxidoreductase activity



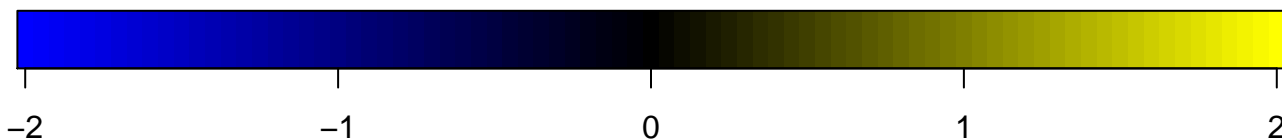
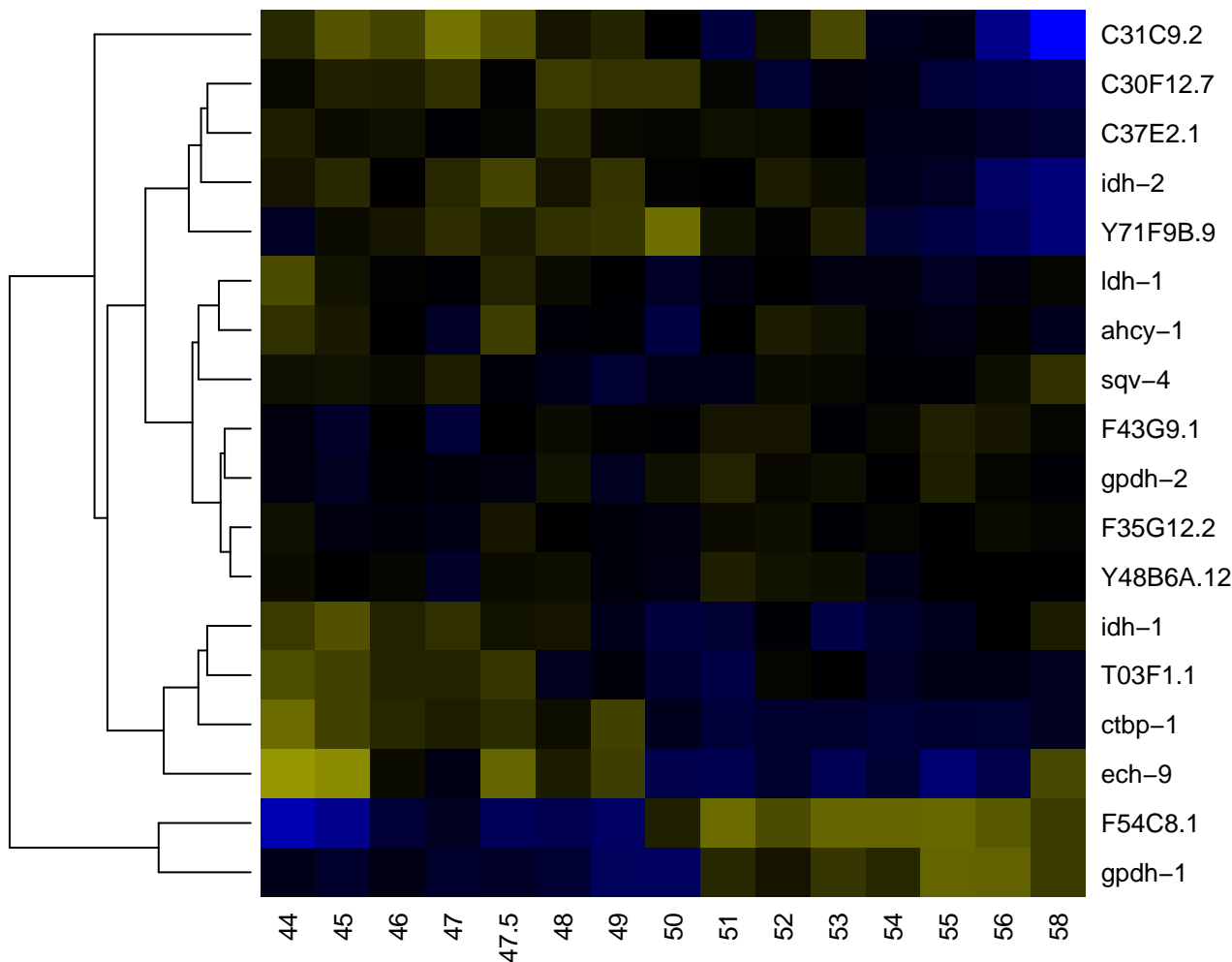
activity, acting on paired donors, with incorporation or reduction



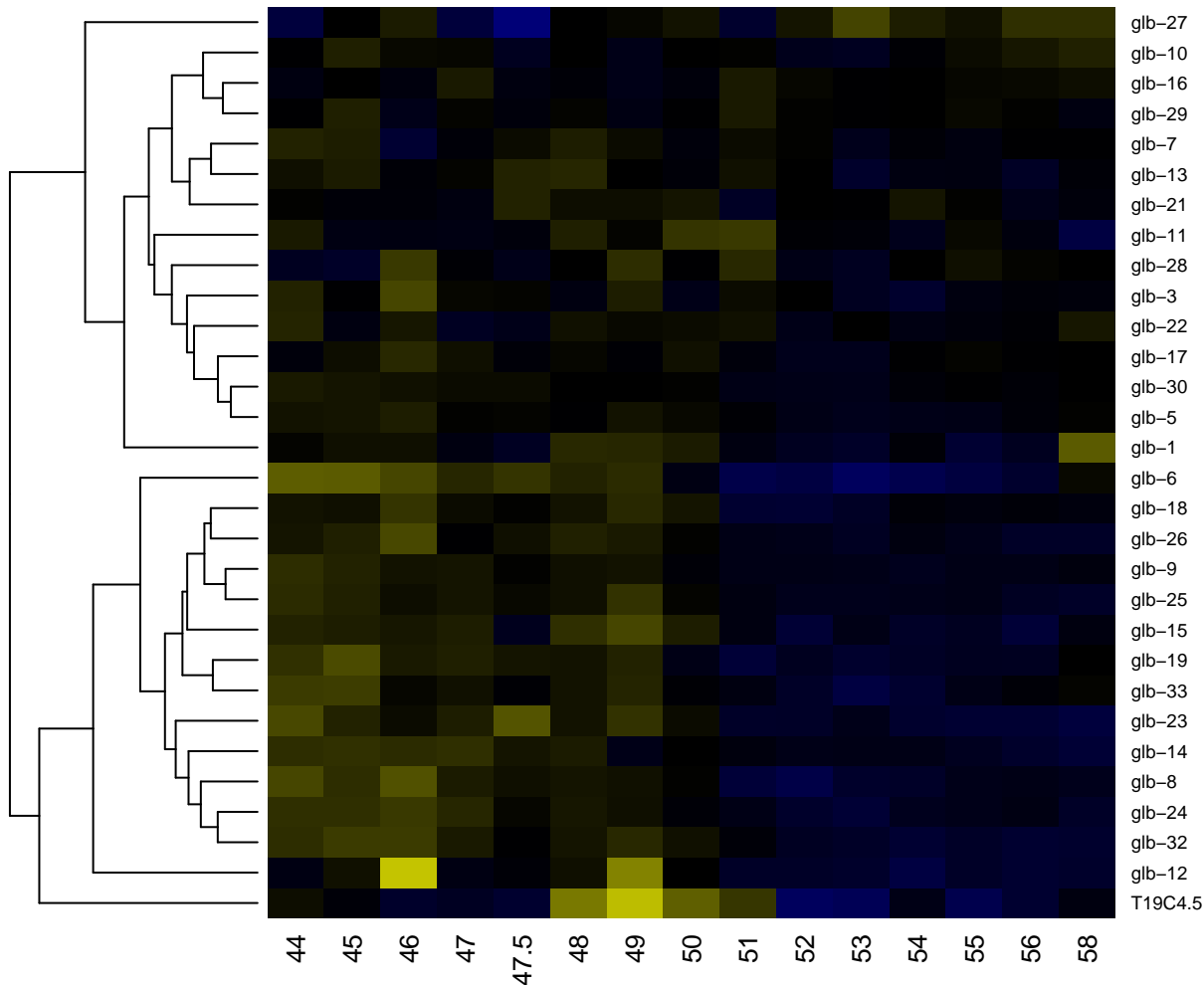
oxidoreductase activity, acting on the CH-CH group of donc



Activity, acting on the CH-OH group of donors, NAD or NADP



oxygen binding



-2

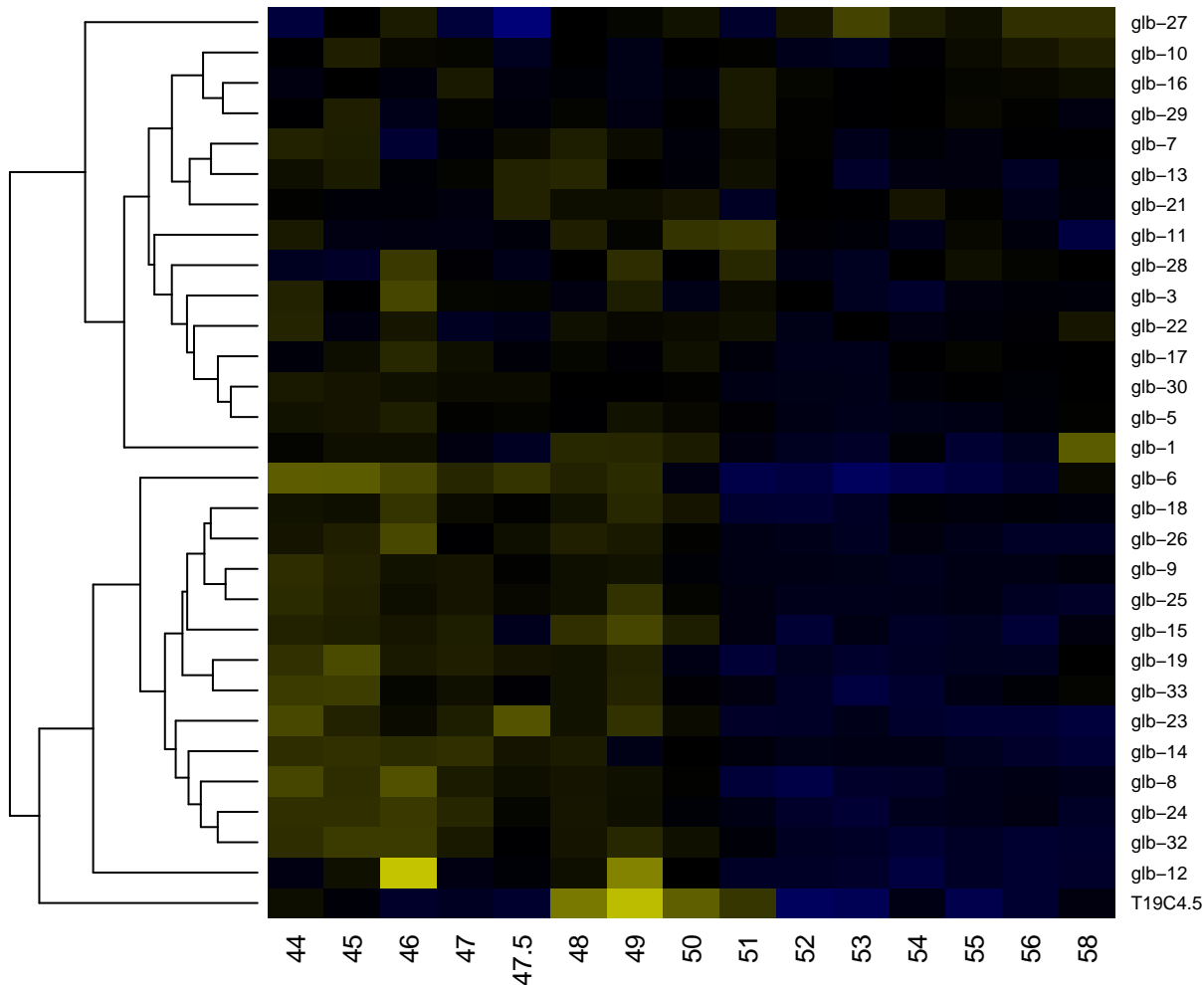
-1

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oxygen transport



-2

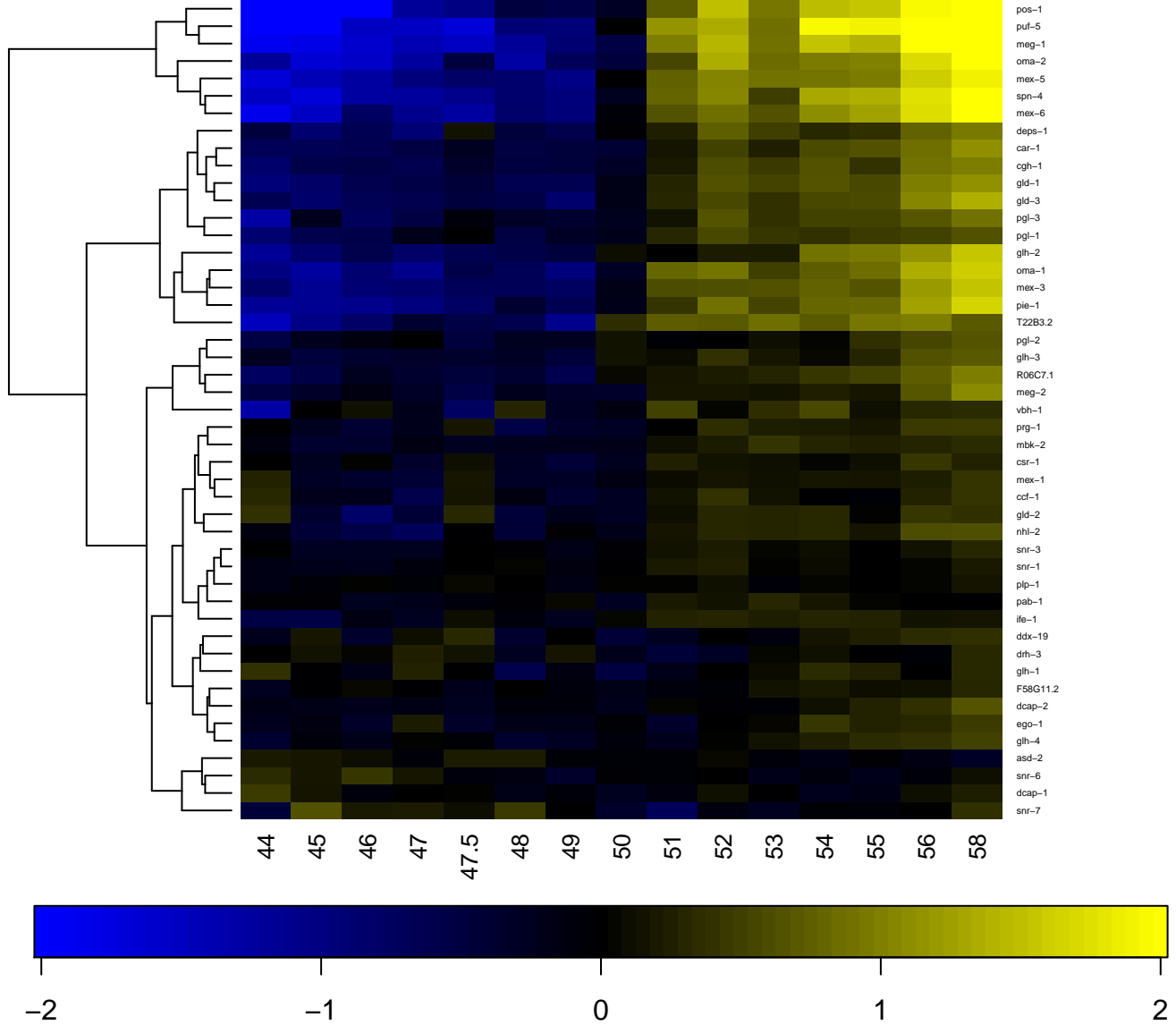
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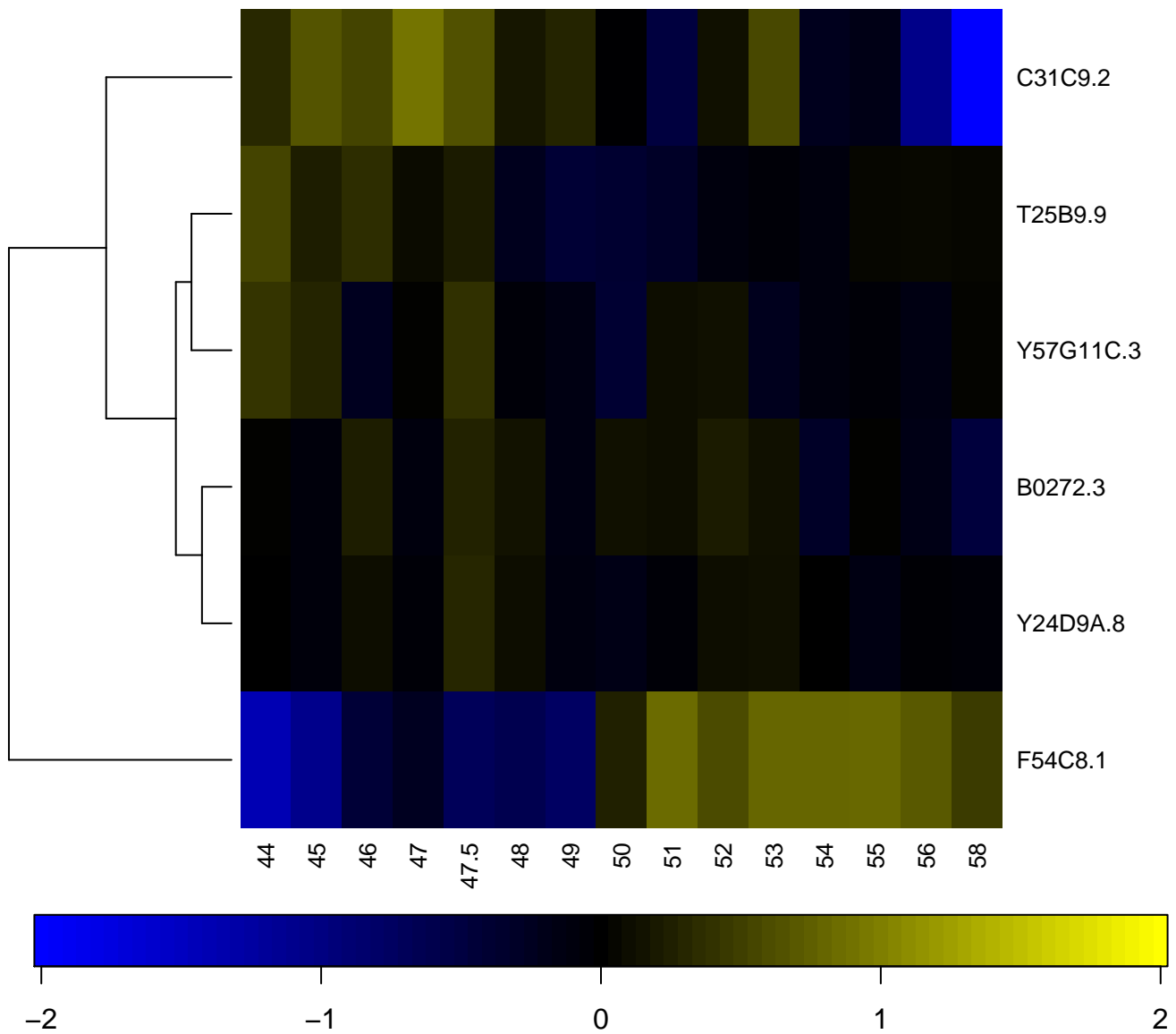
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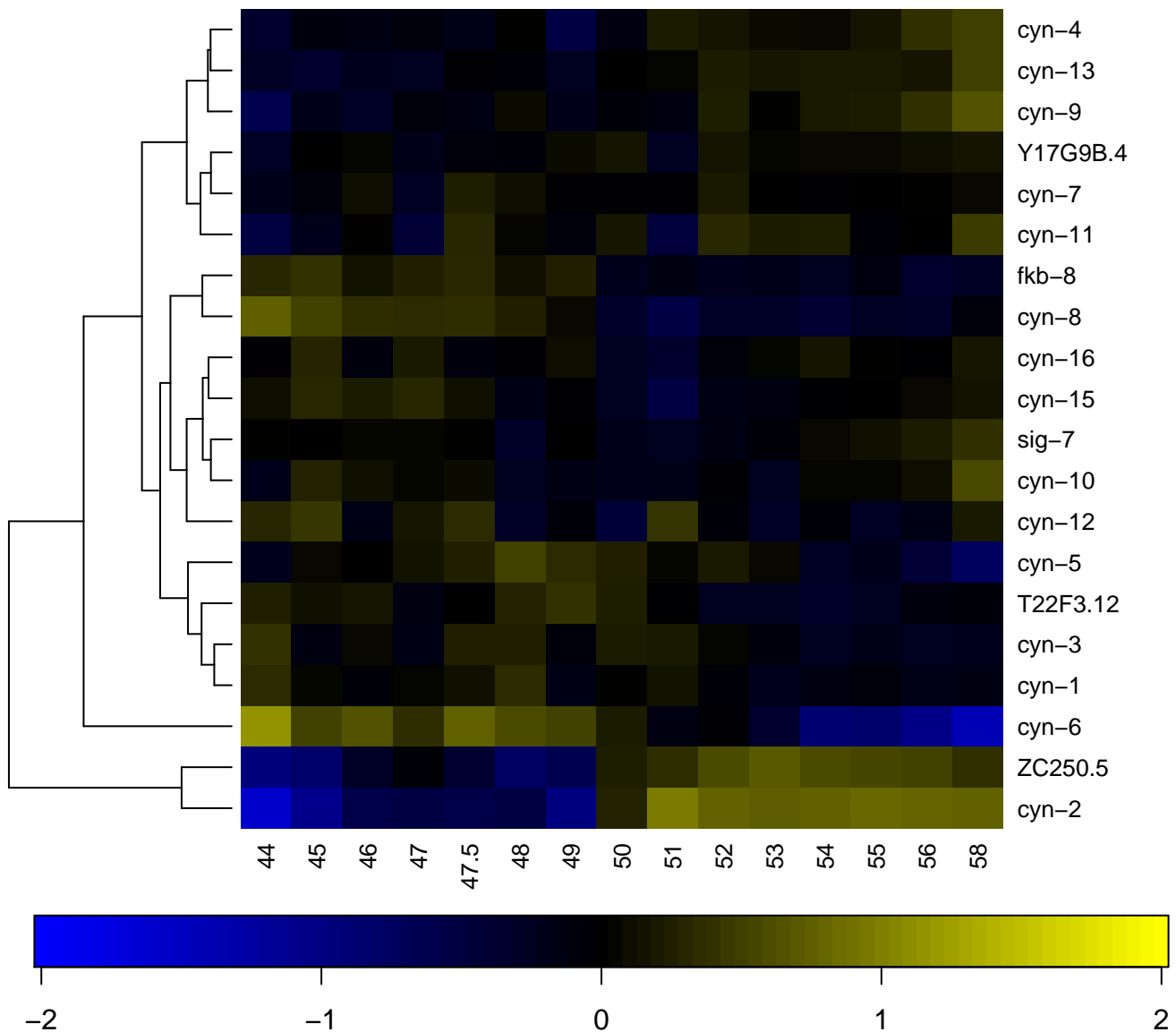
P granule



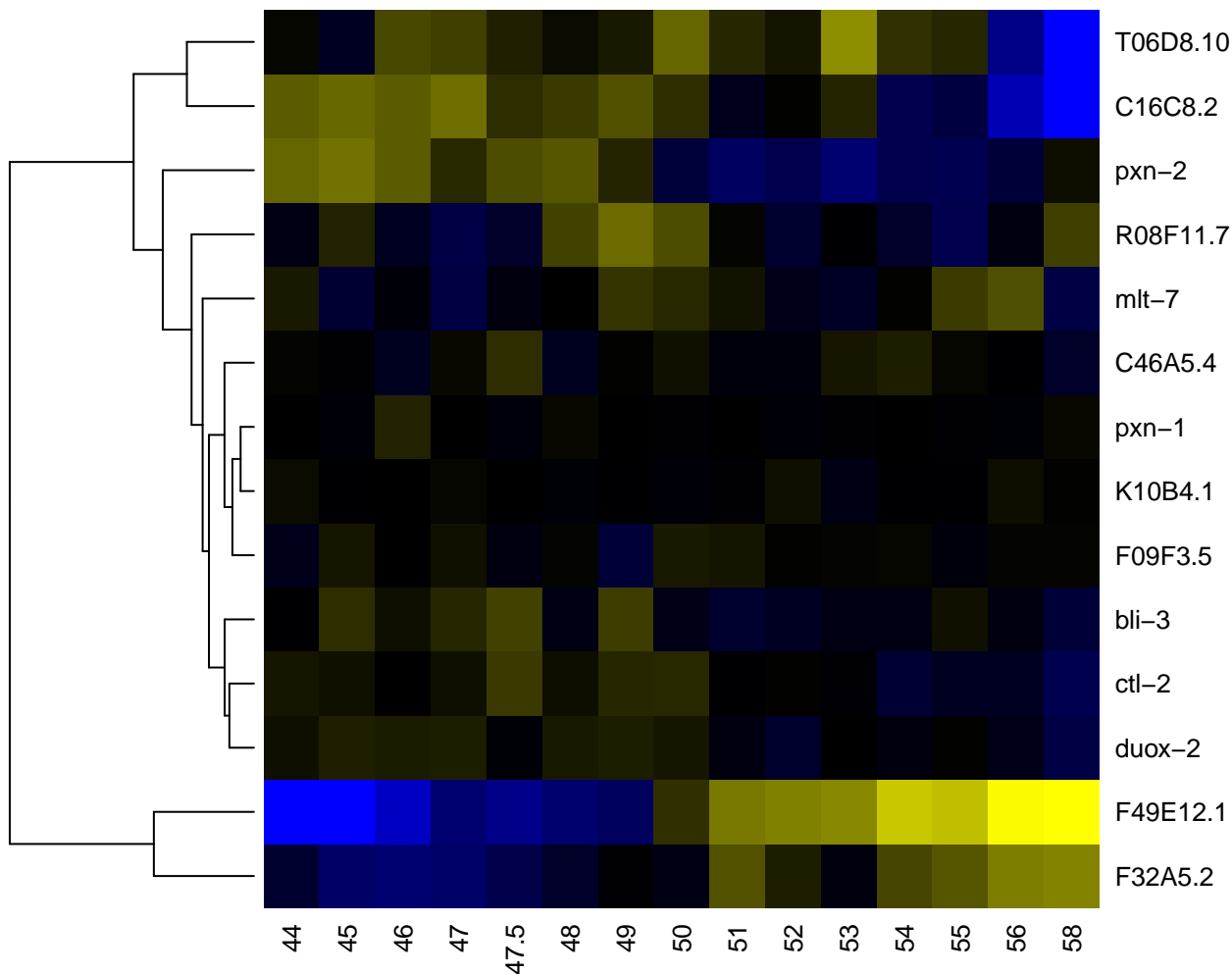
pentose-phosphate shunt



peptidyl-prolyl cis-trans isomerase activity



peroxidase activity



-2

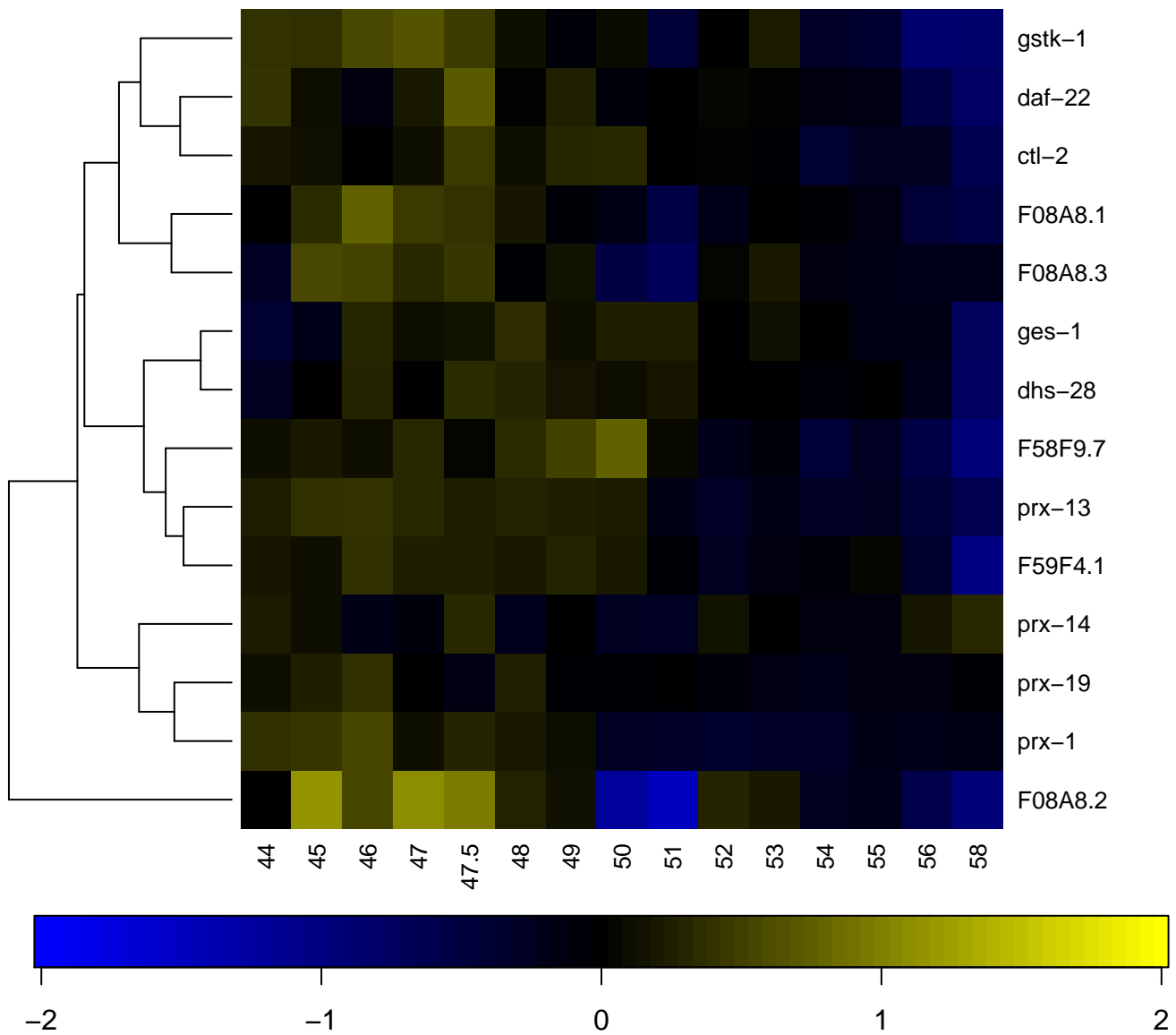
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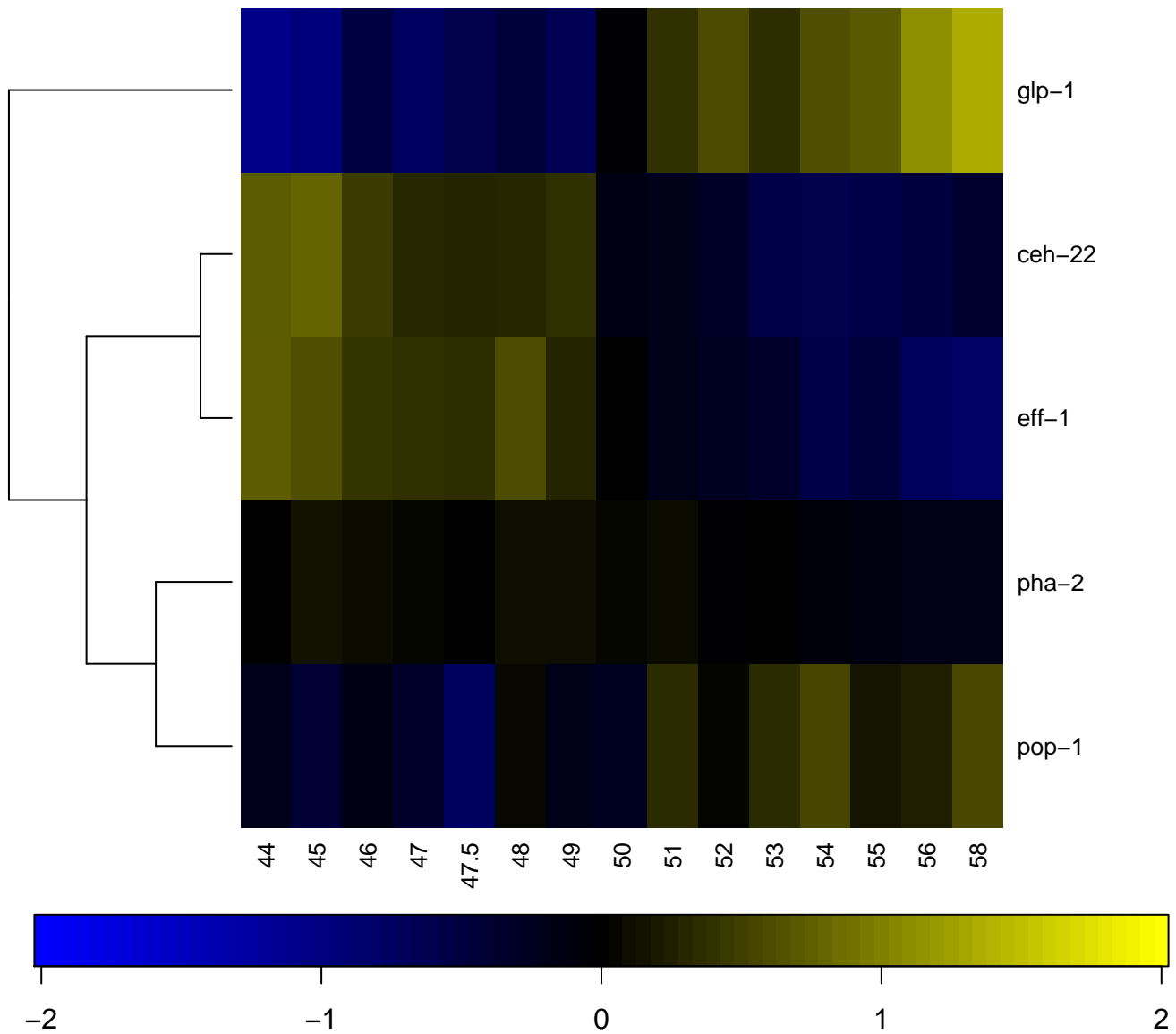
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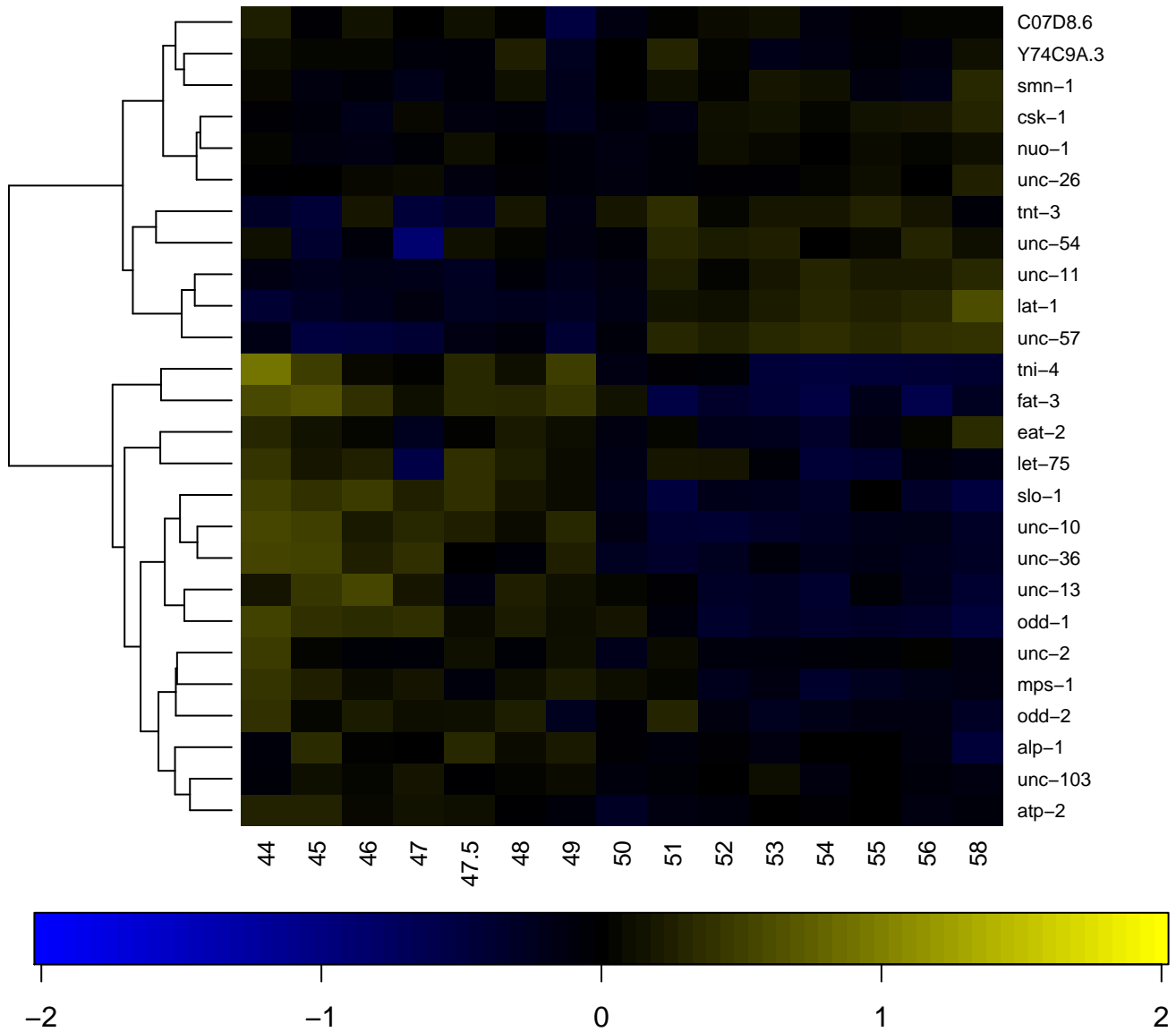
peroxisome



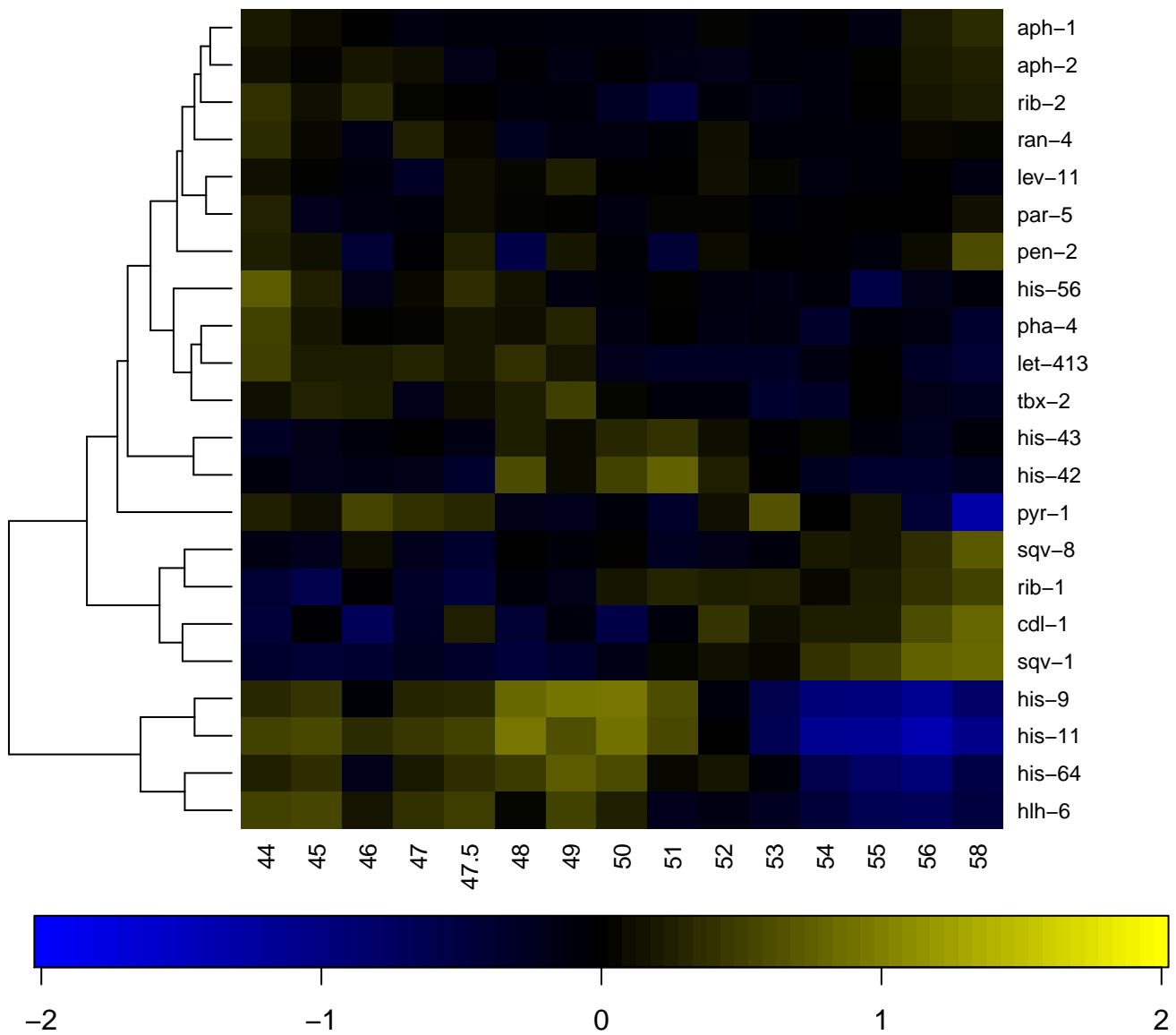
pharyngeal muscle development



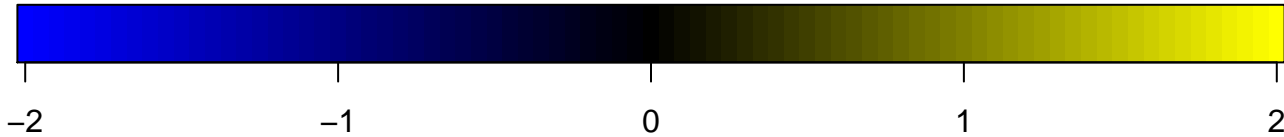
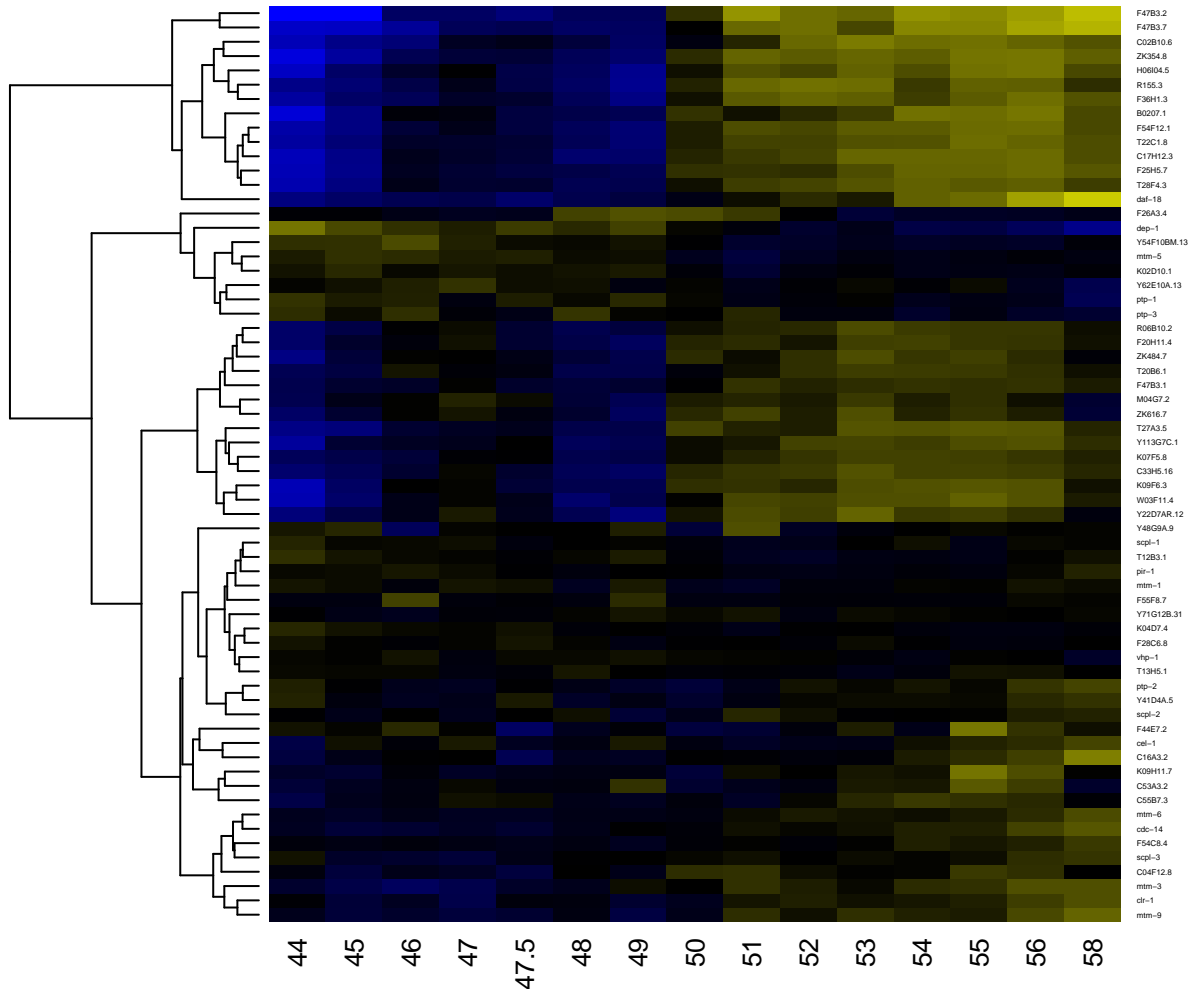
pharyngeal pumping



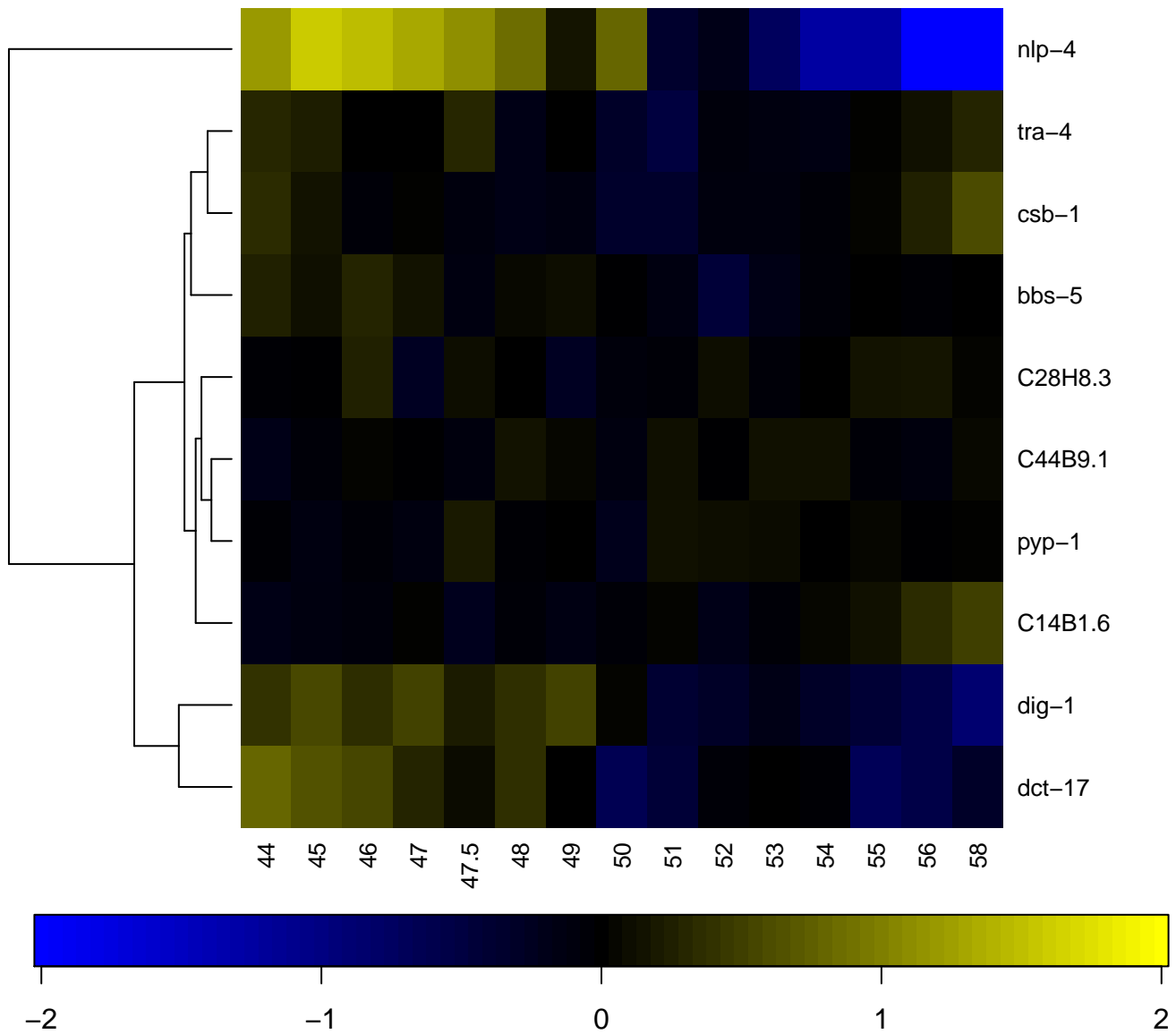
pharynx development



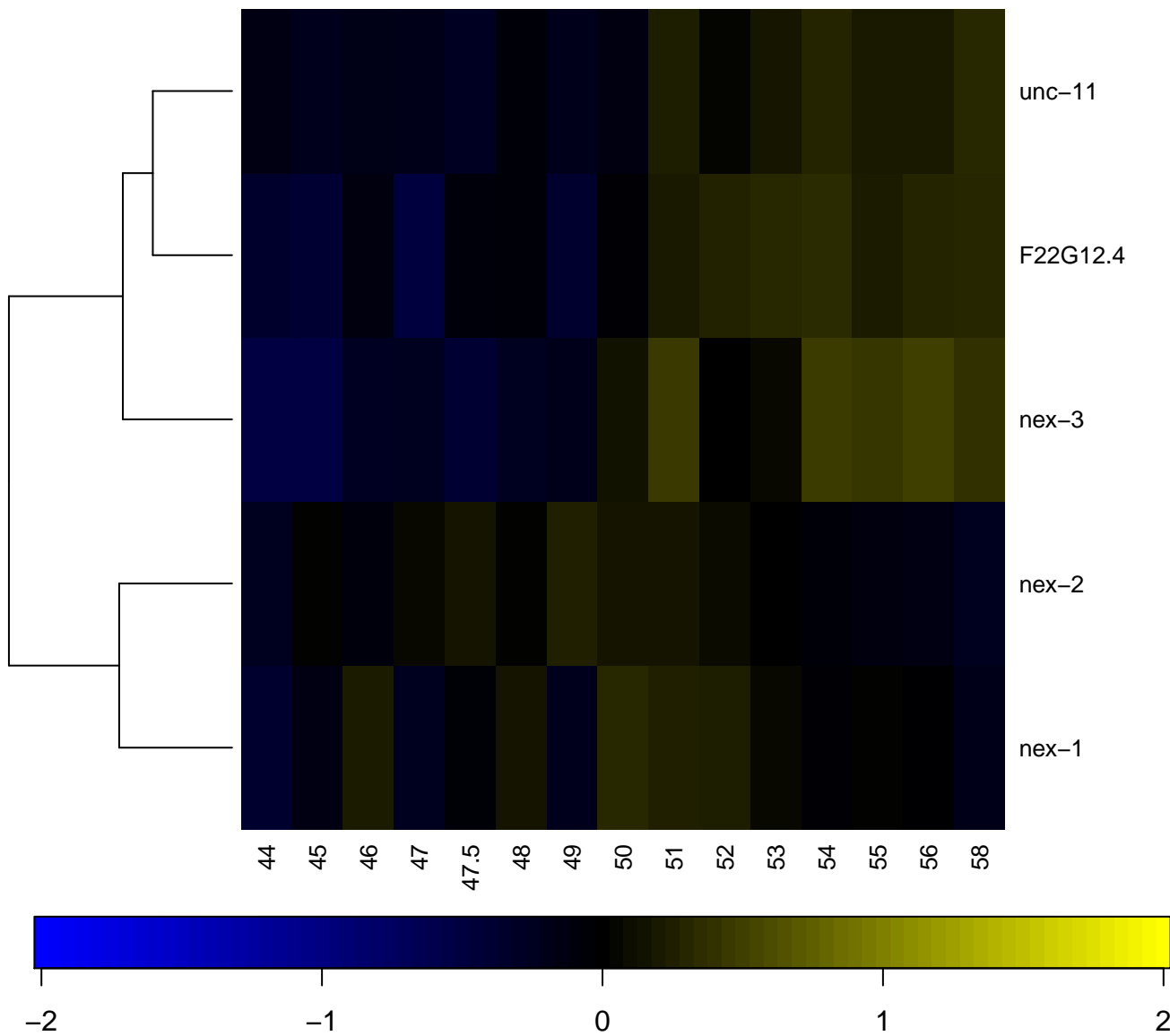
phosphatase activity



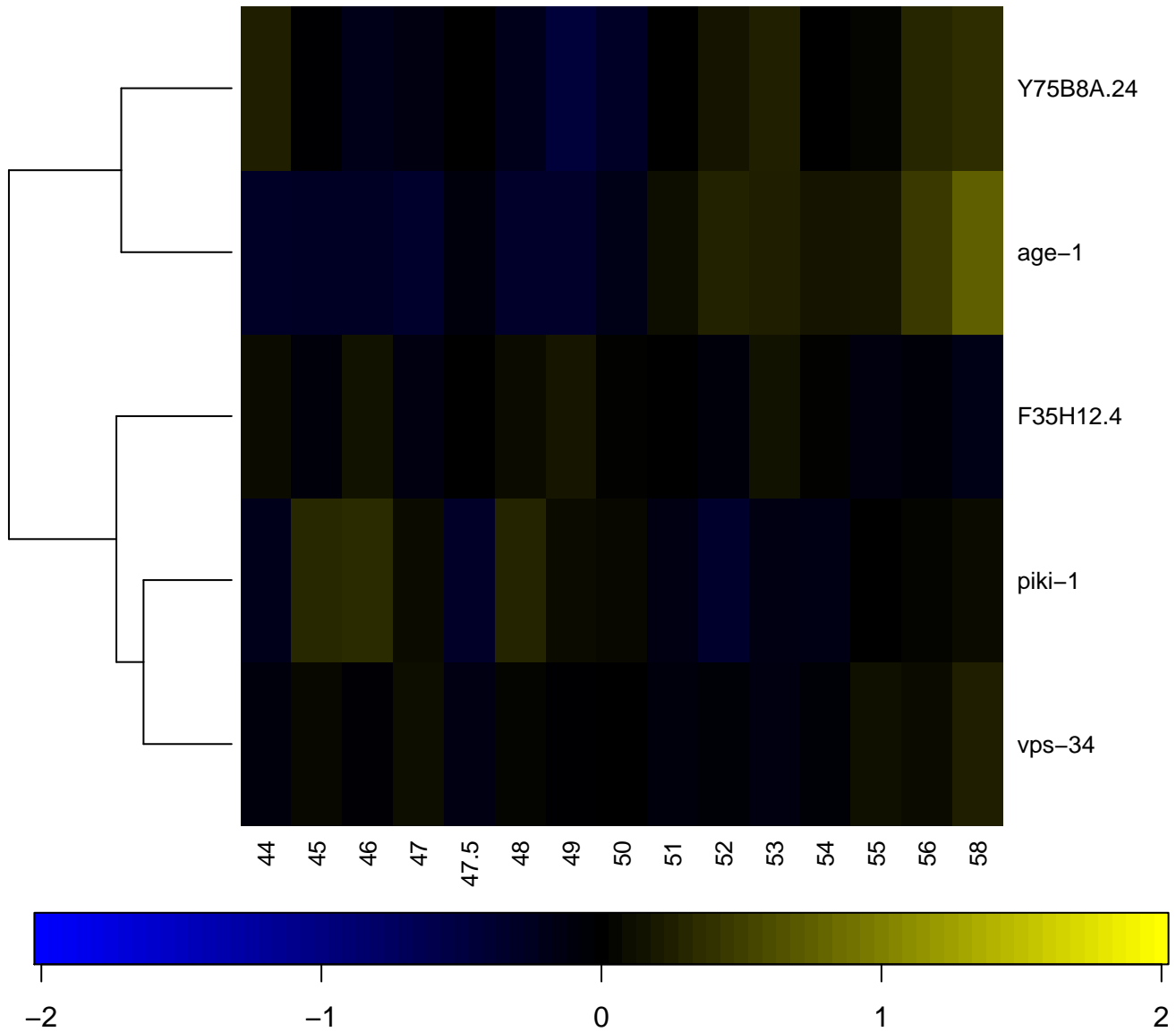
phosphate metabolic process



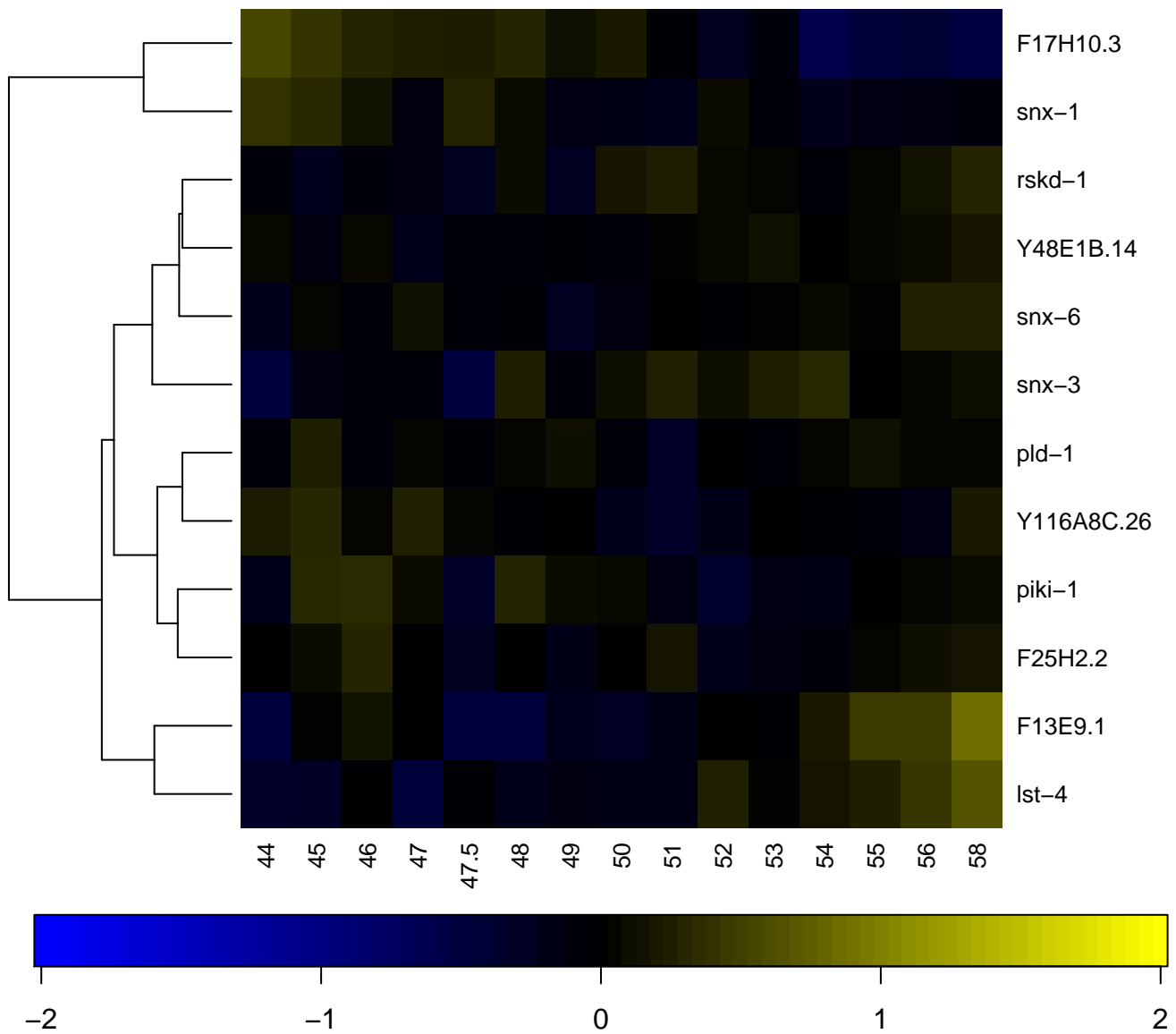
phosphatidylinositol binding



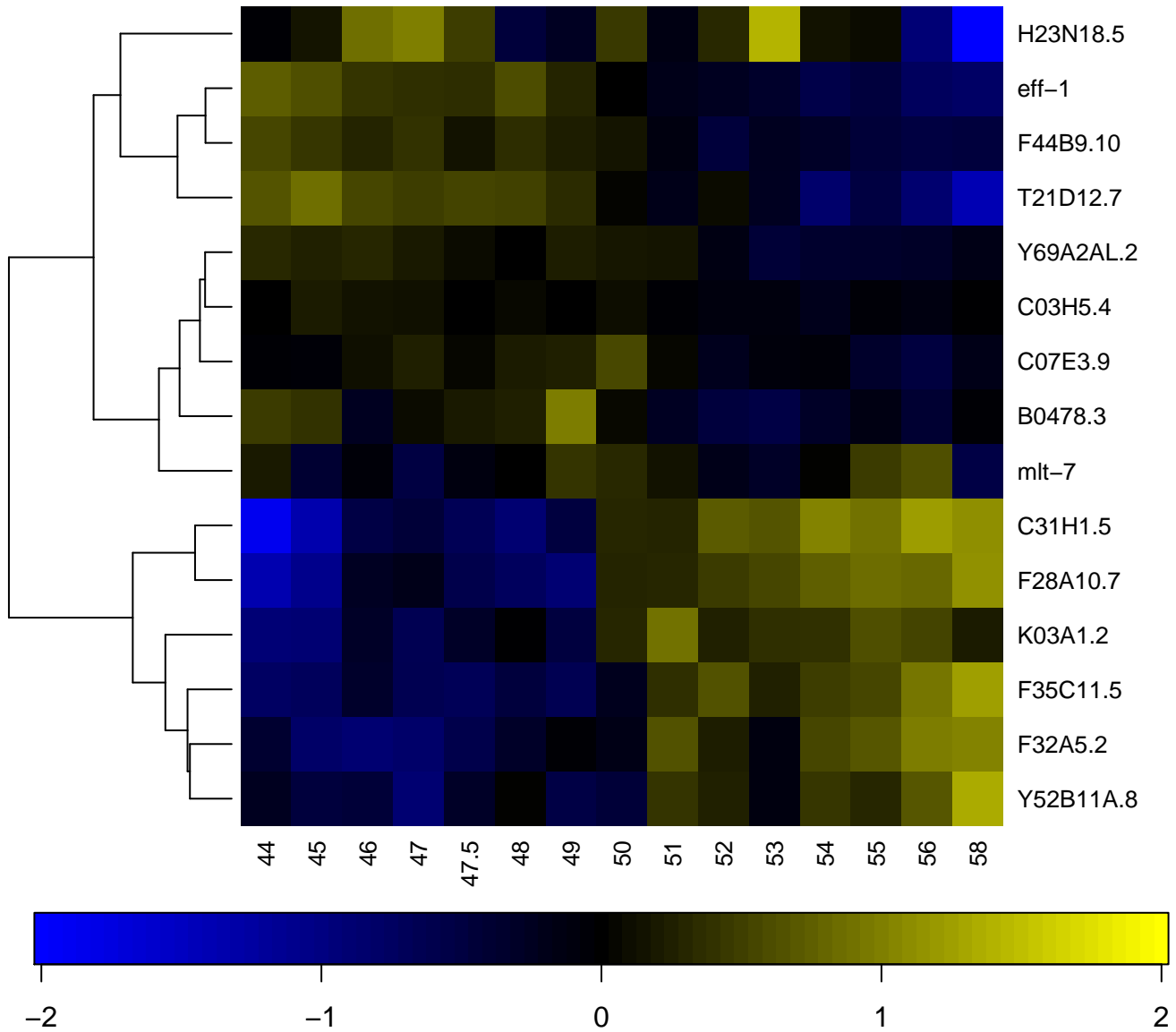
phosphoinositide-mediated signaling



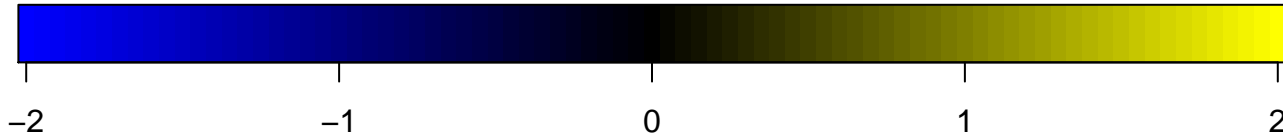
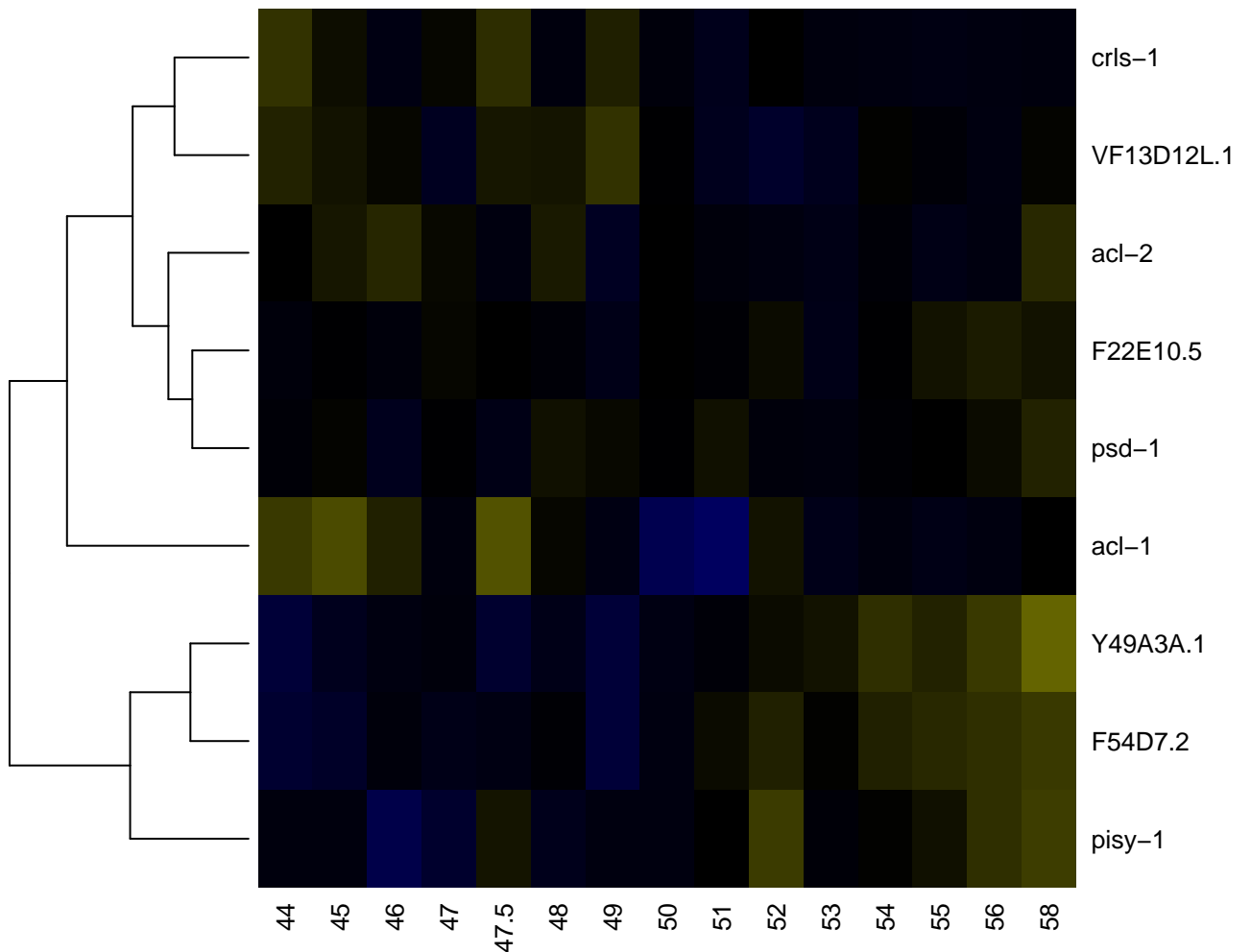
phosphoinositide binding



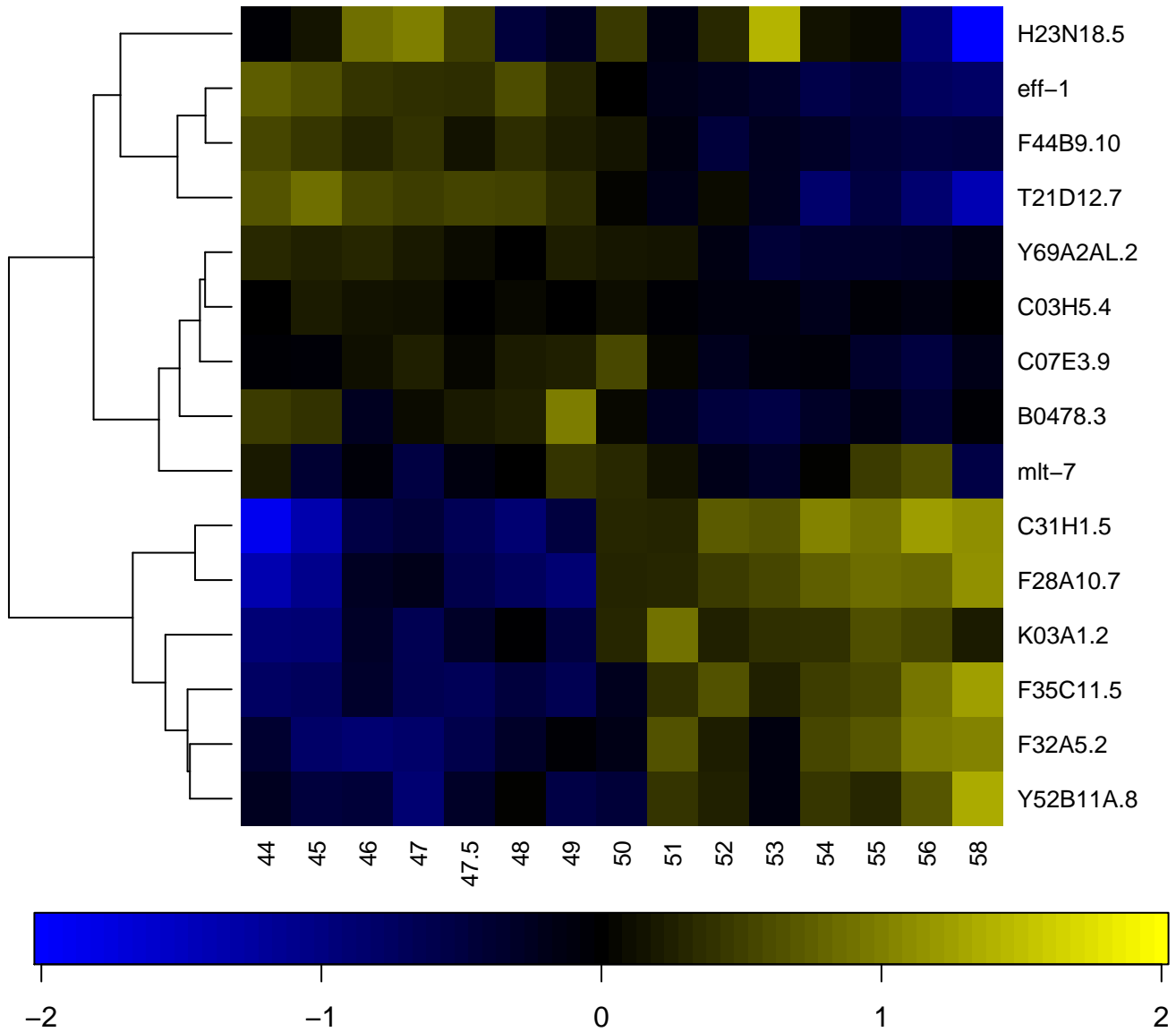
phospholipase A2 activity



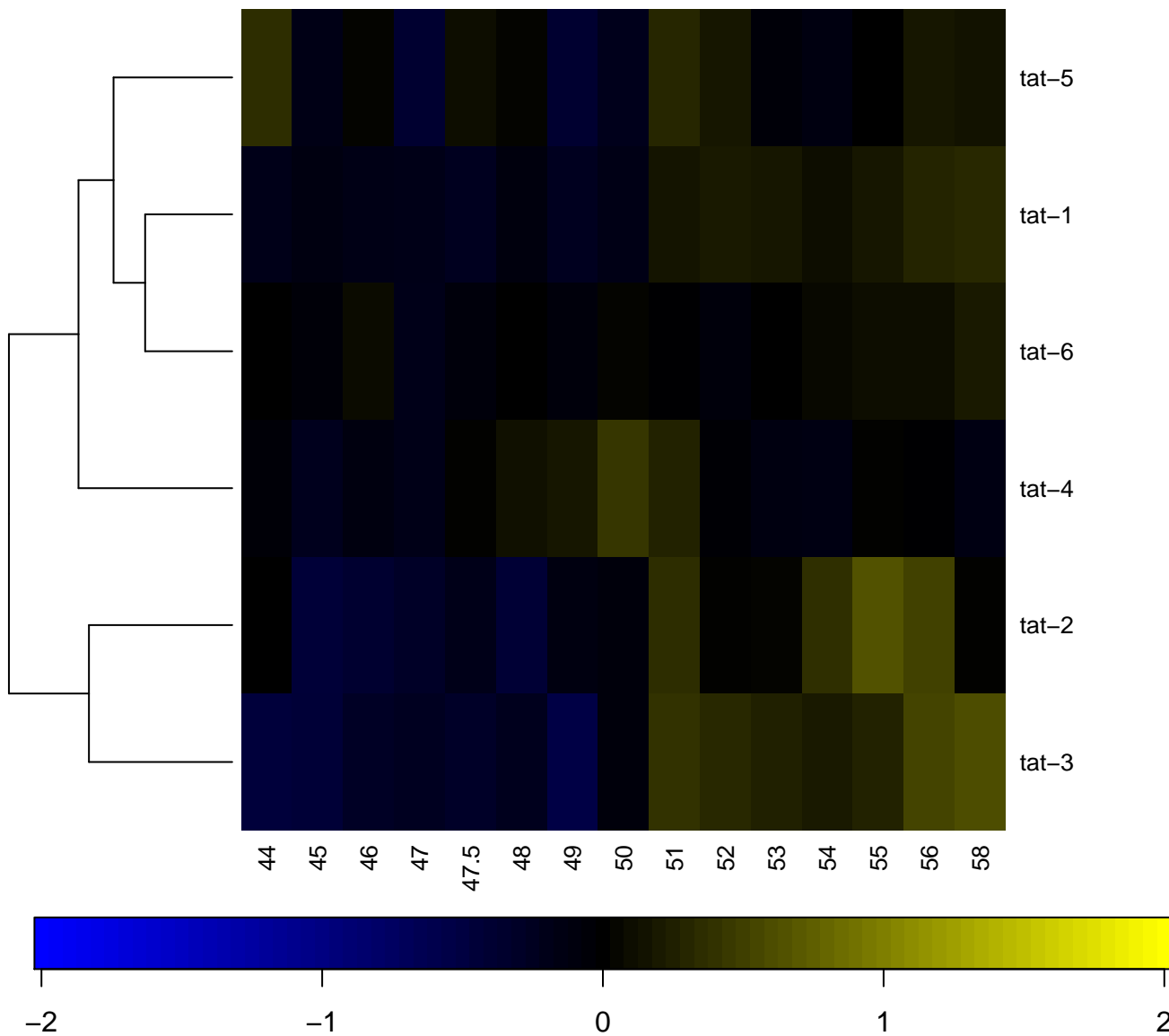
phospholipid biosynthetic process



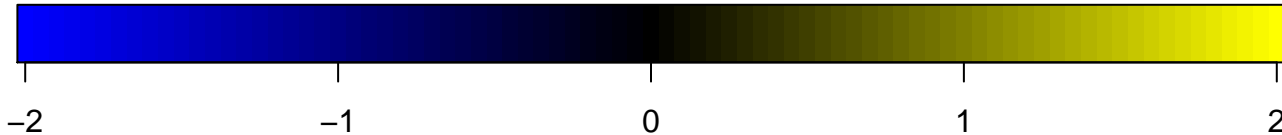
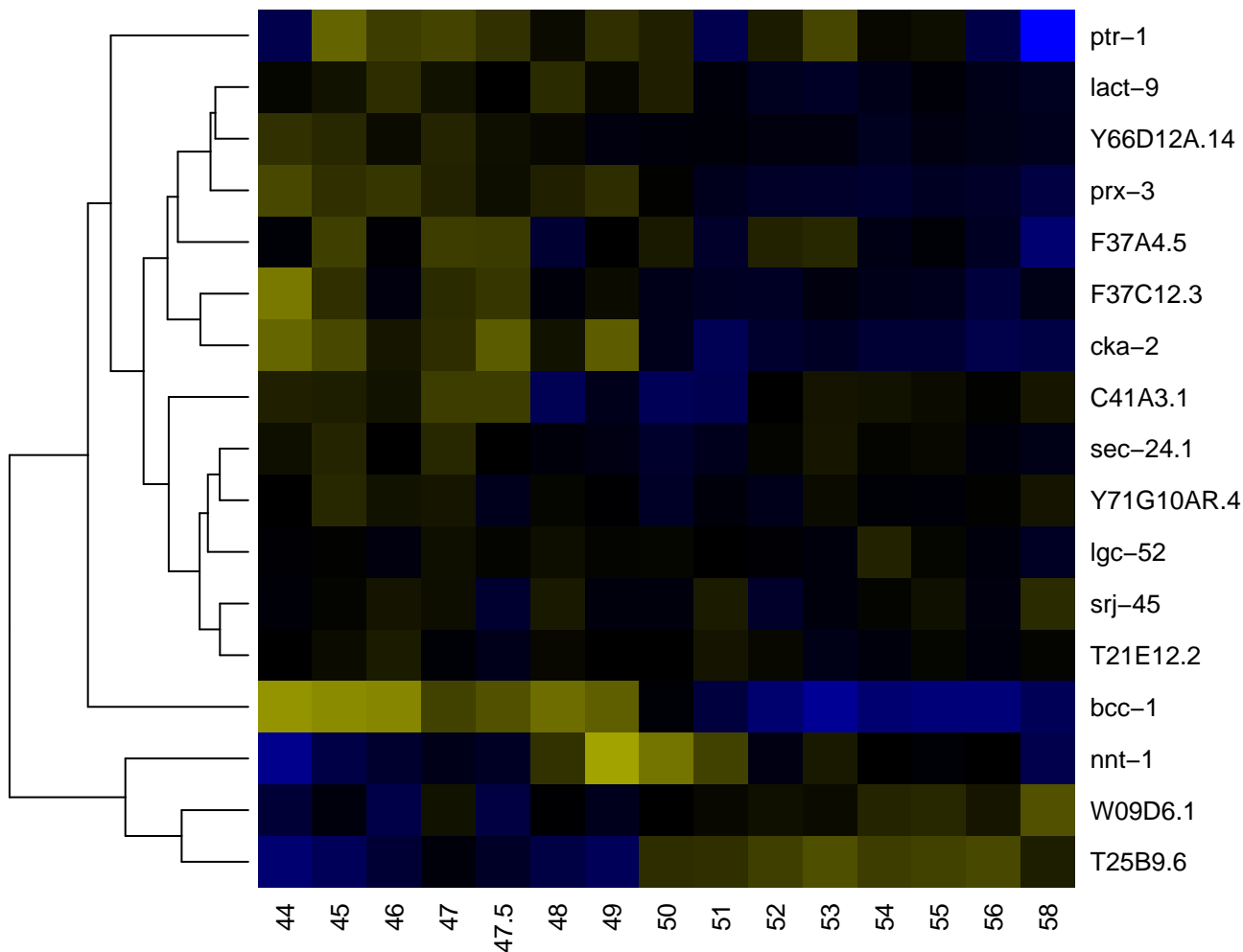
phospholipid metabolic process



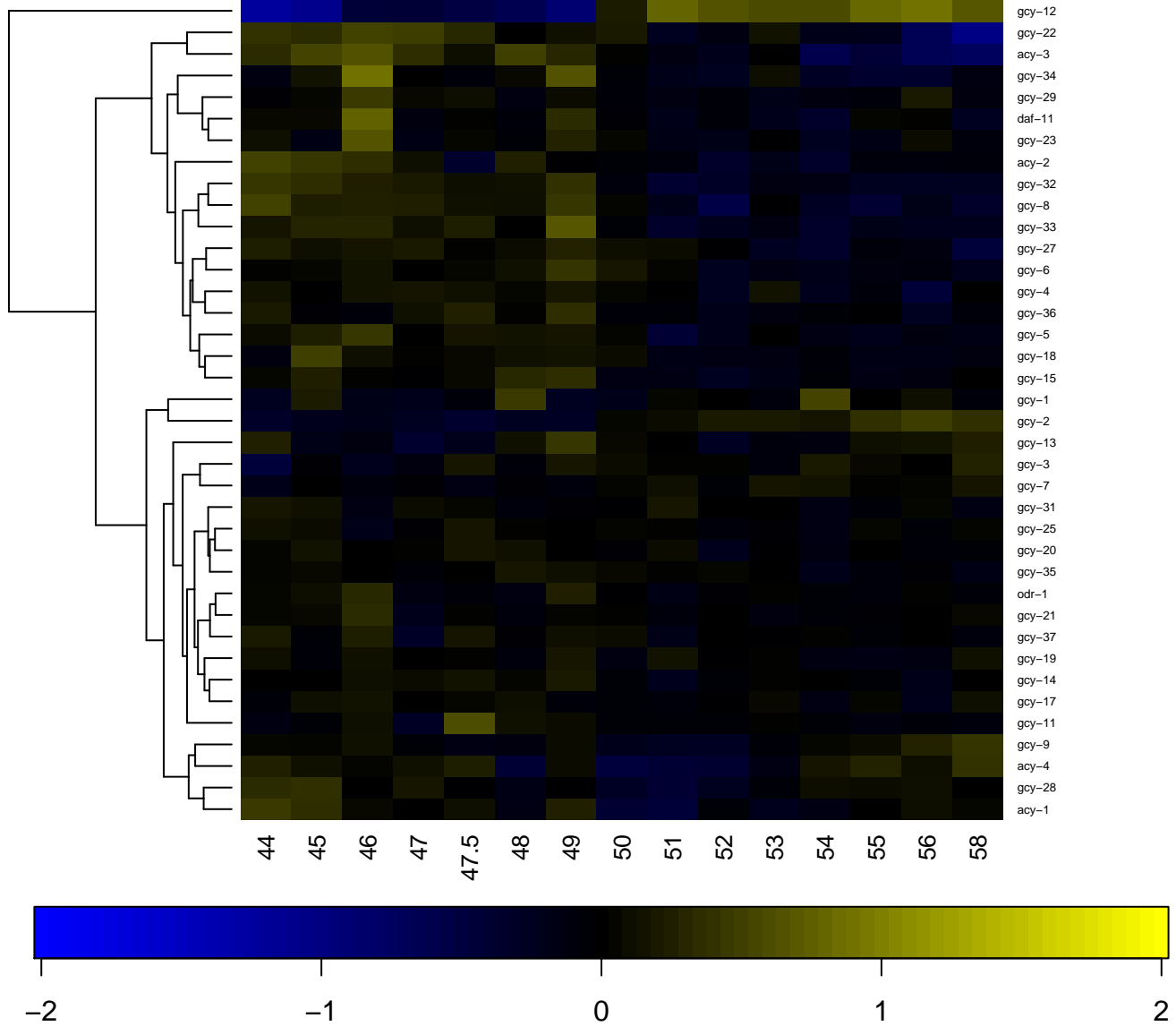
phospholipid transport



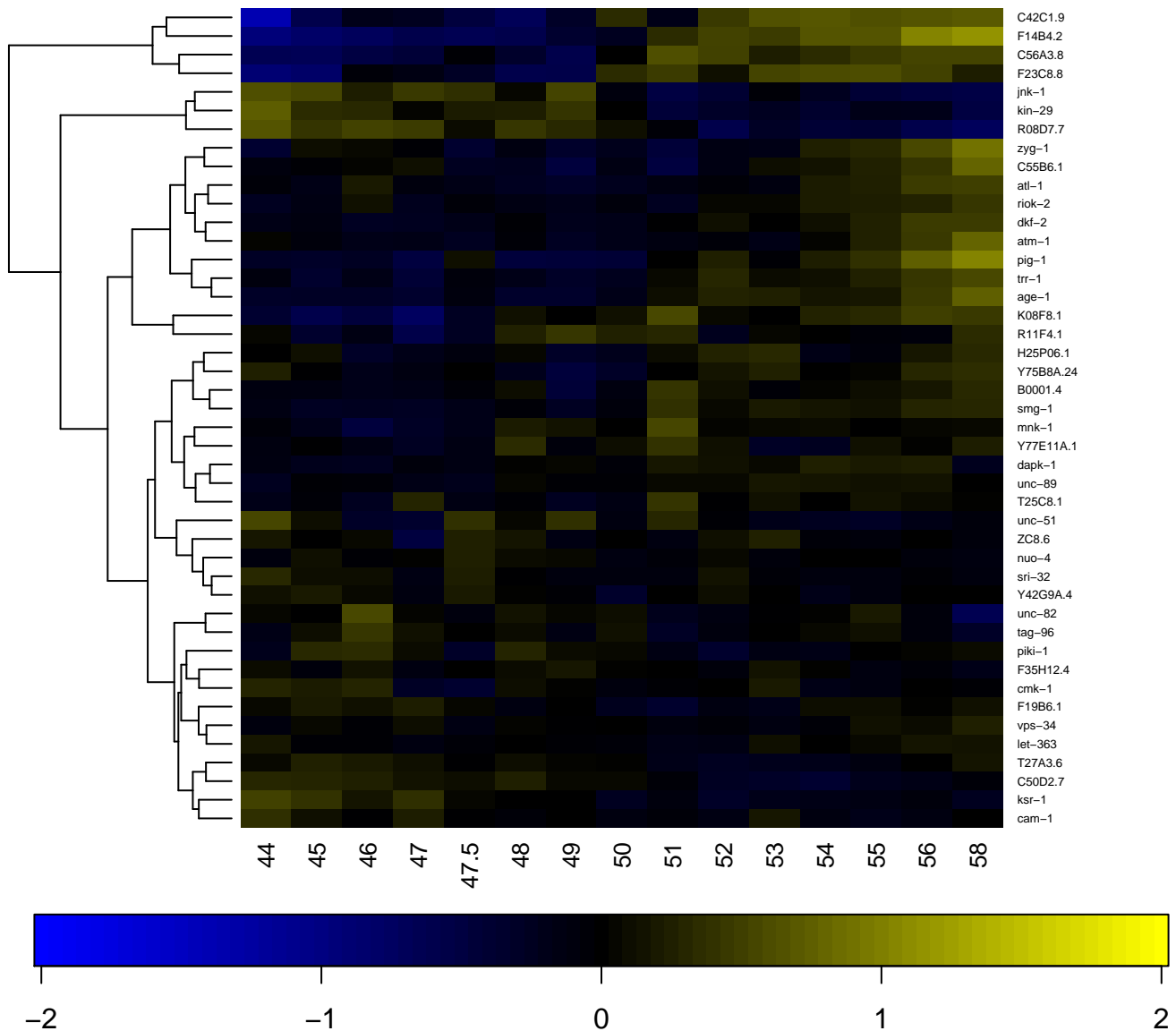
phosphopantetheine binding



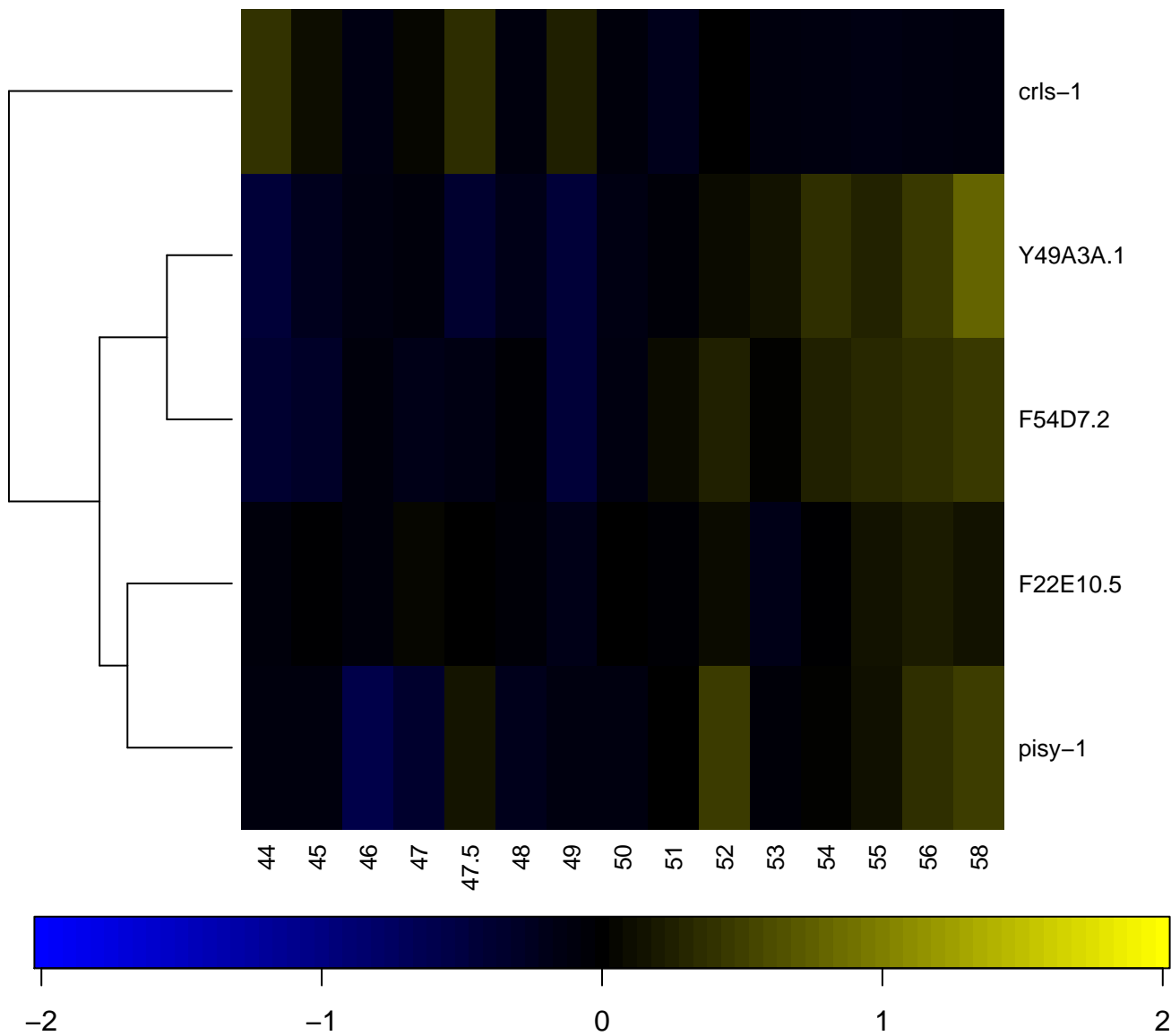
phosphorus-oxygen lyase activity



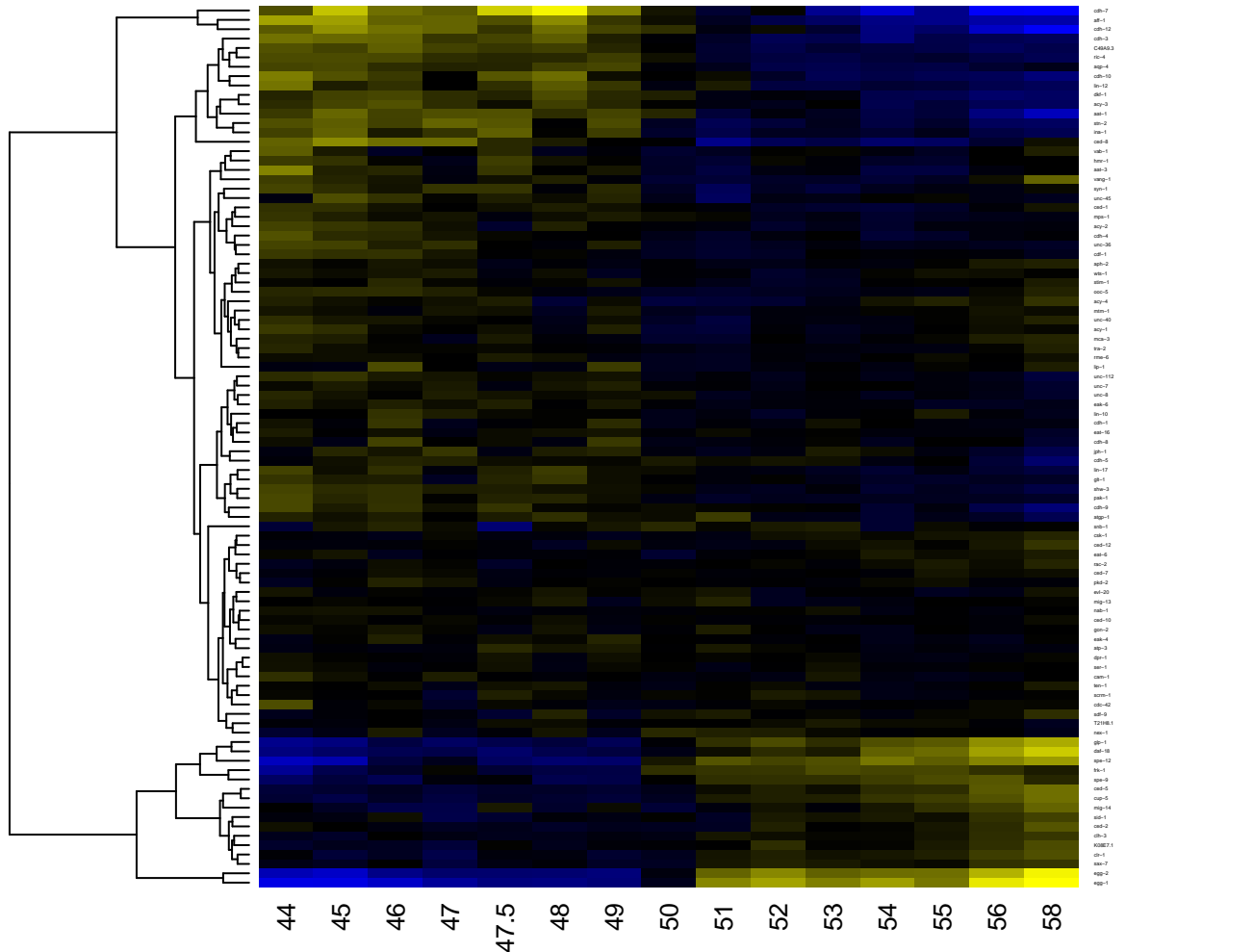
phosphotransferase activity, alcohol group as acceptor



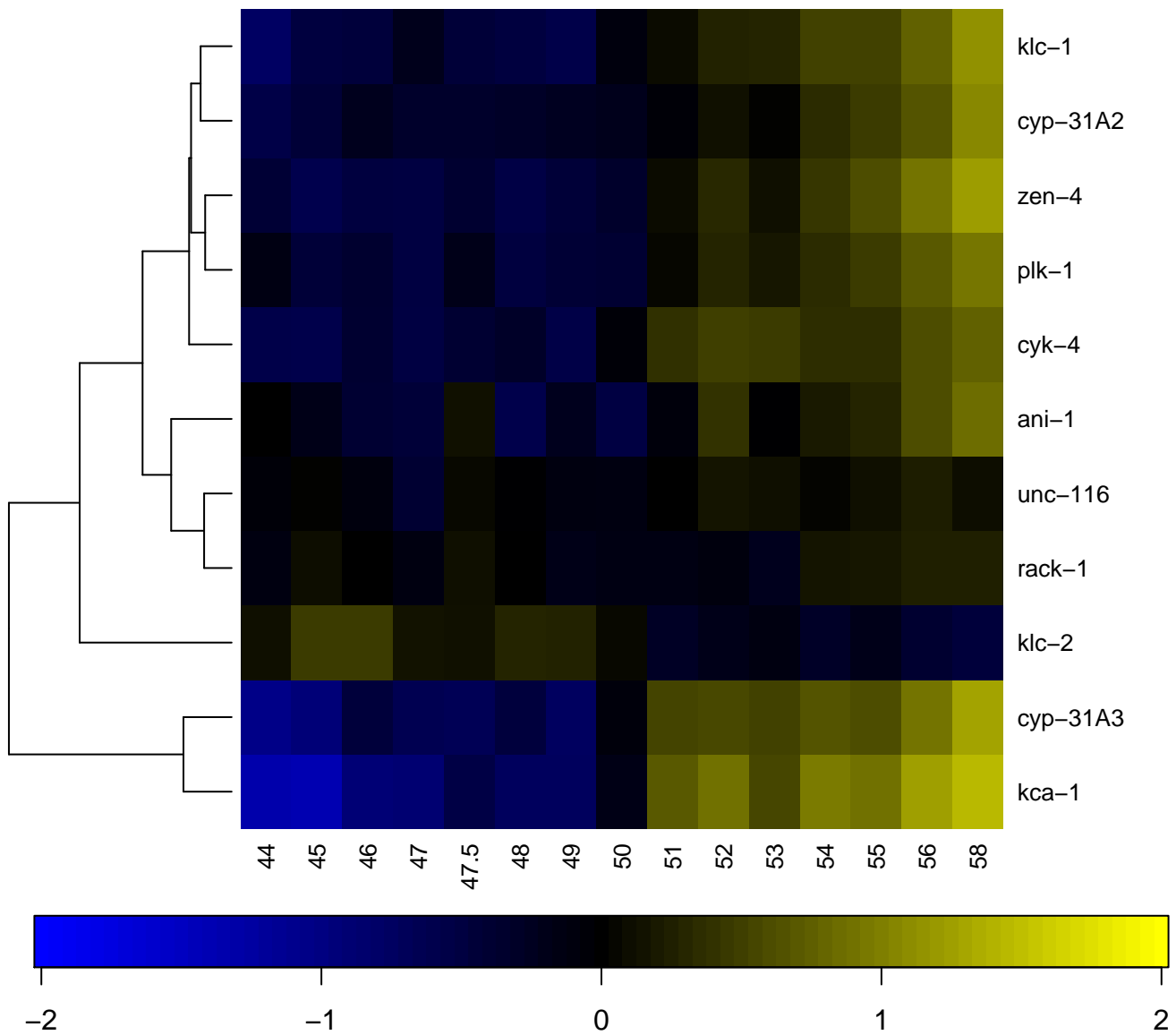
phosphotransferase activity, for other substituted phosphate g



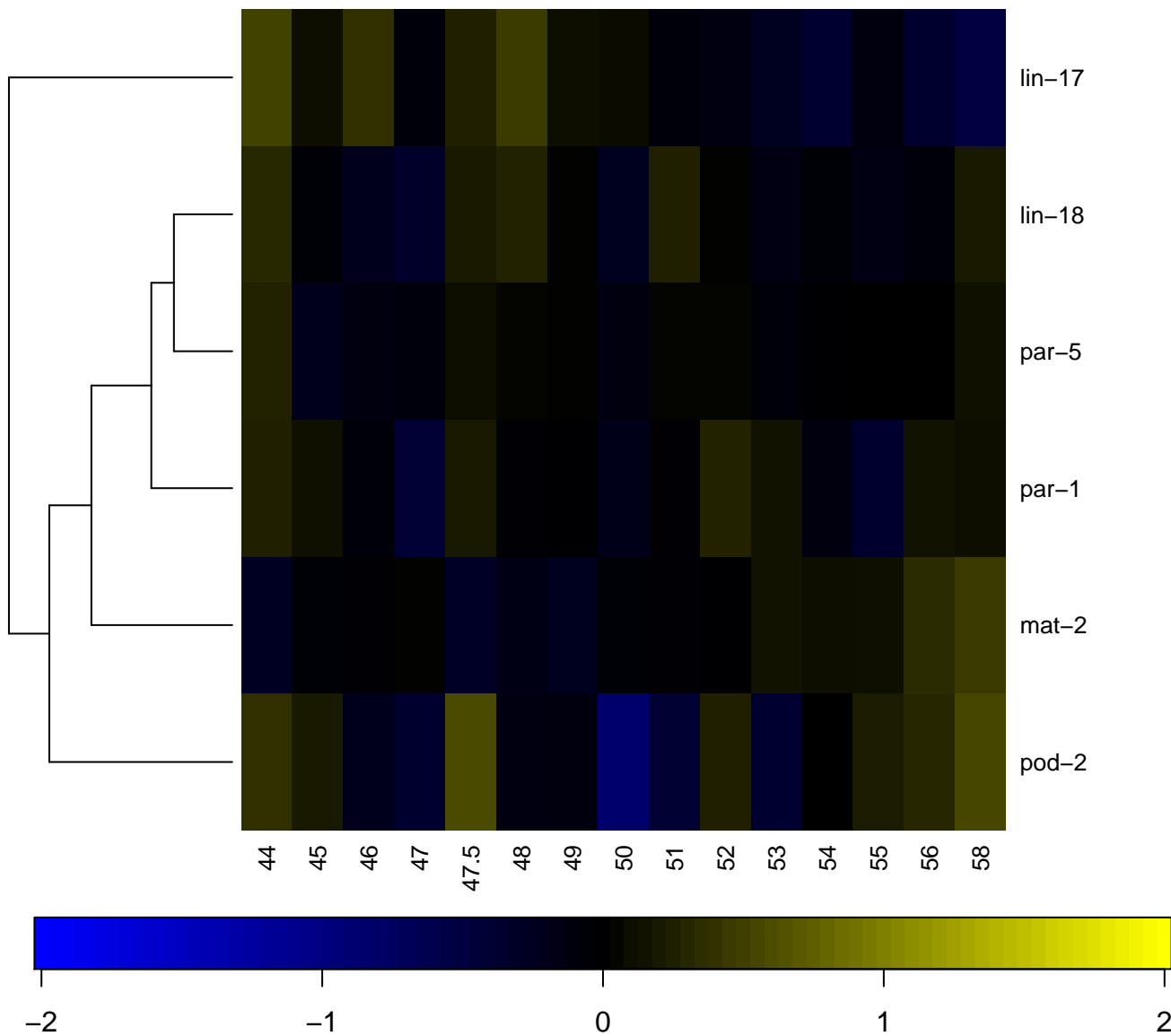
plasma membrane



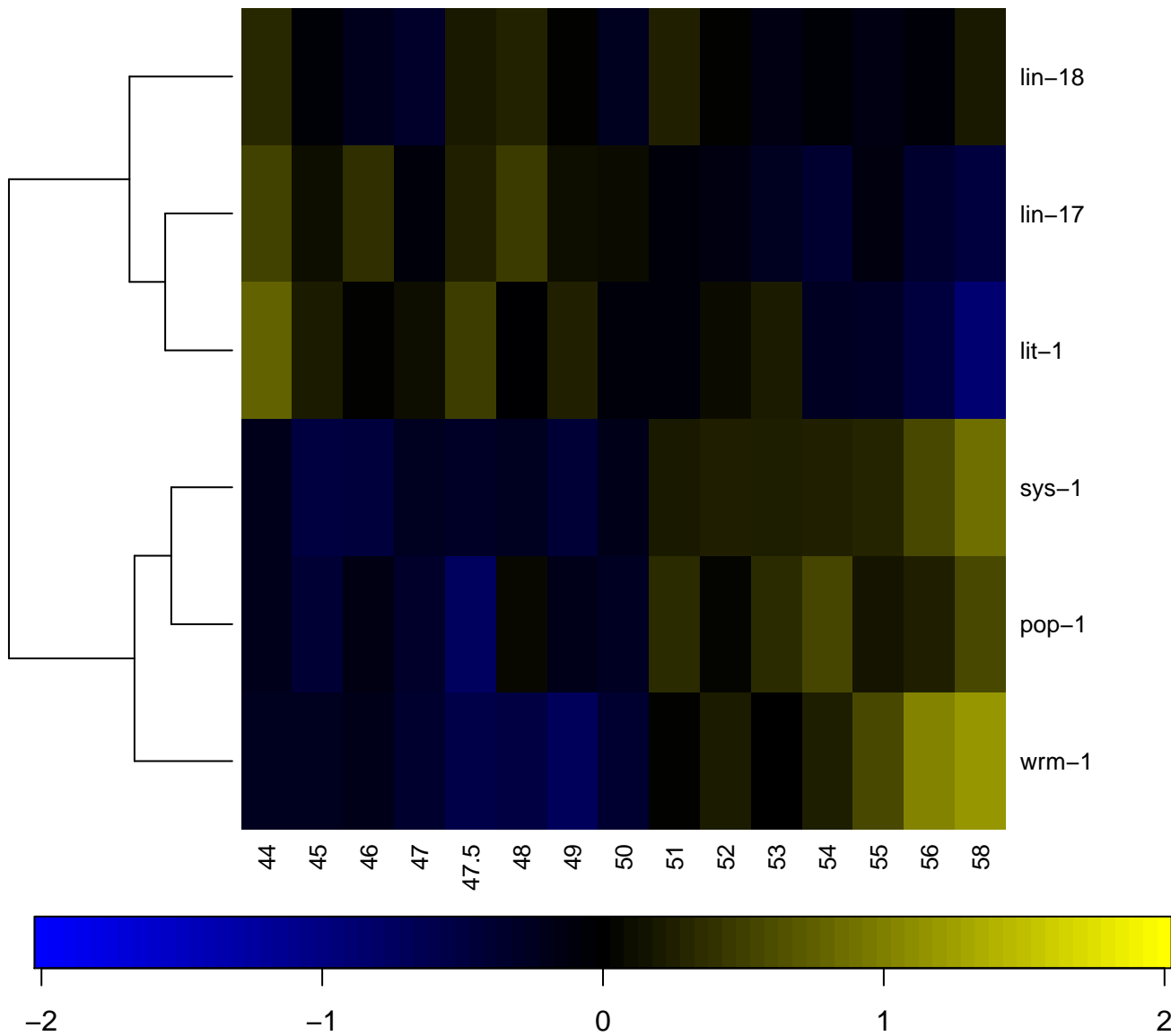
polar body extrusion after meiotic divisions



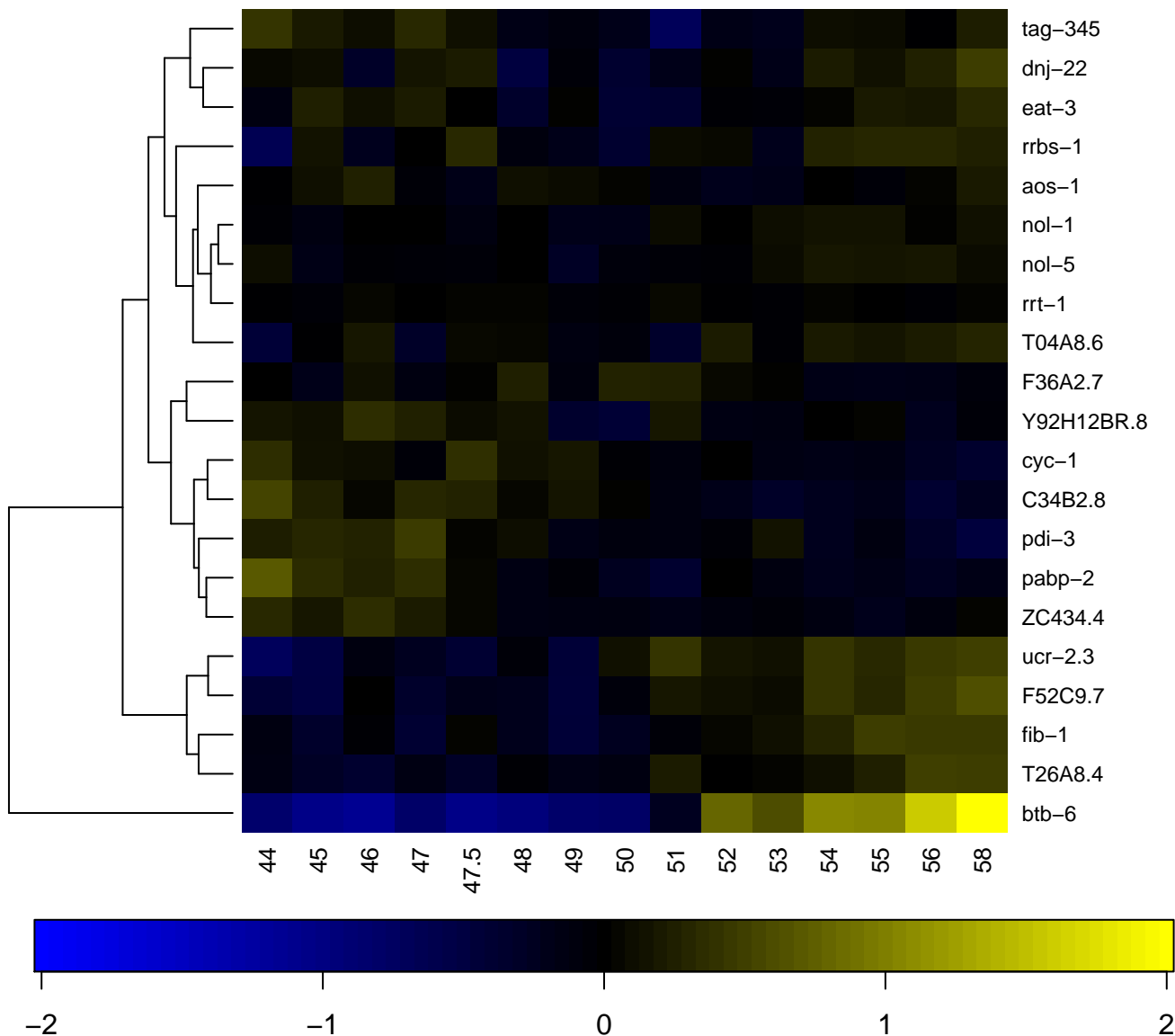
polarity specification of anterior/posterior axis



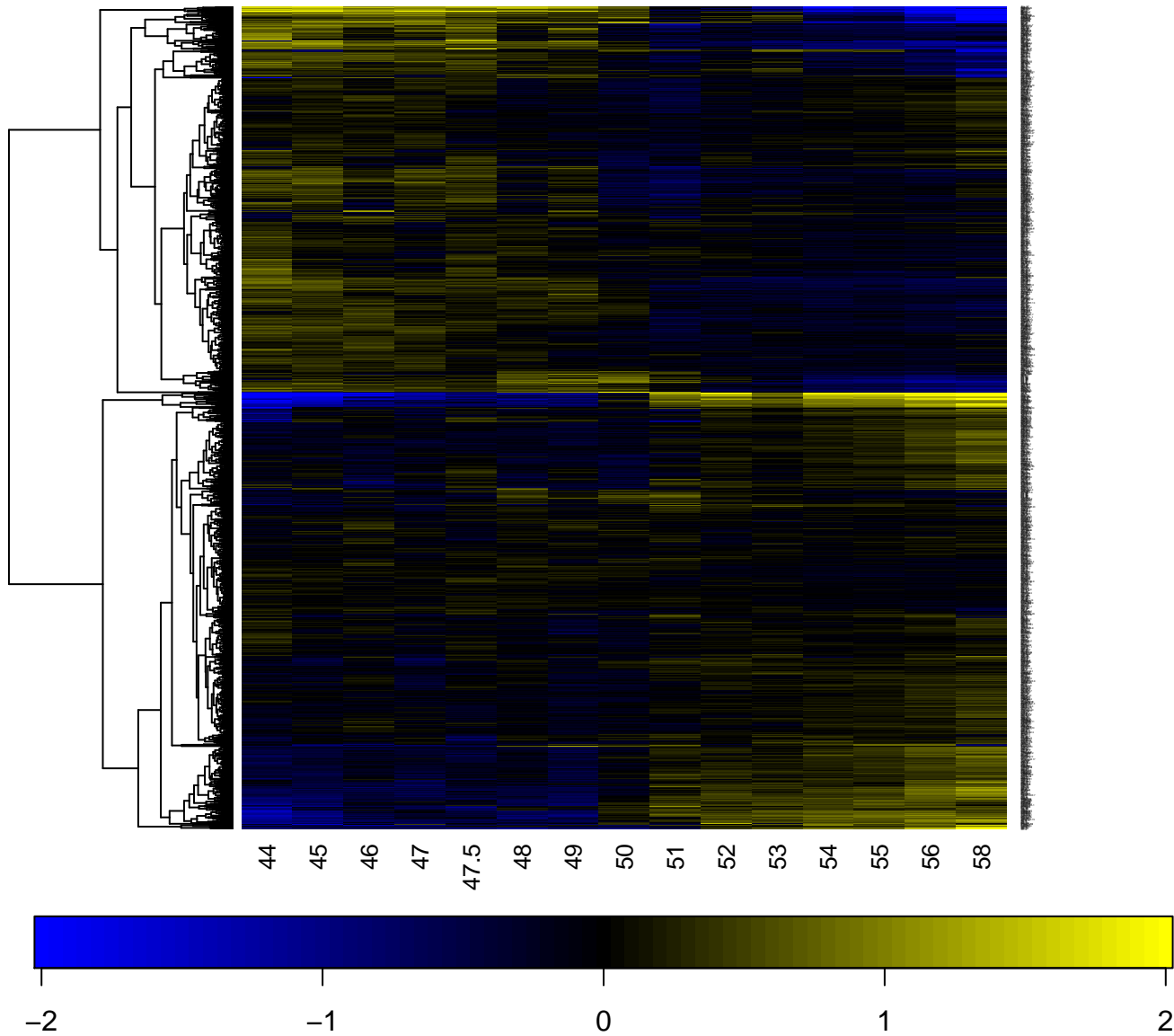
polarity specification of proximal/distal axis



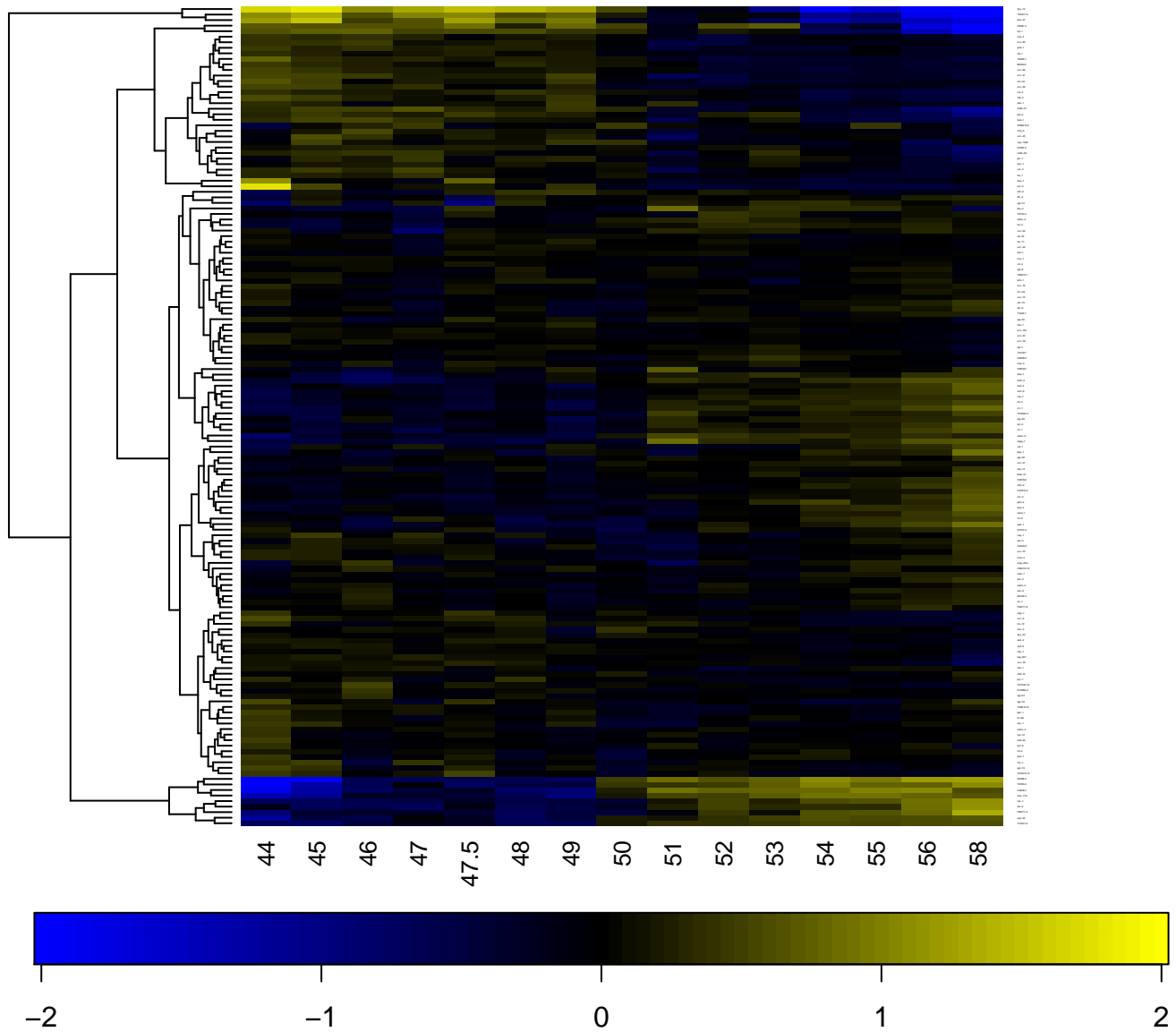
positive regulation of embryonic development



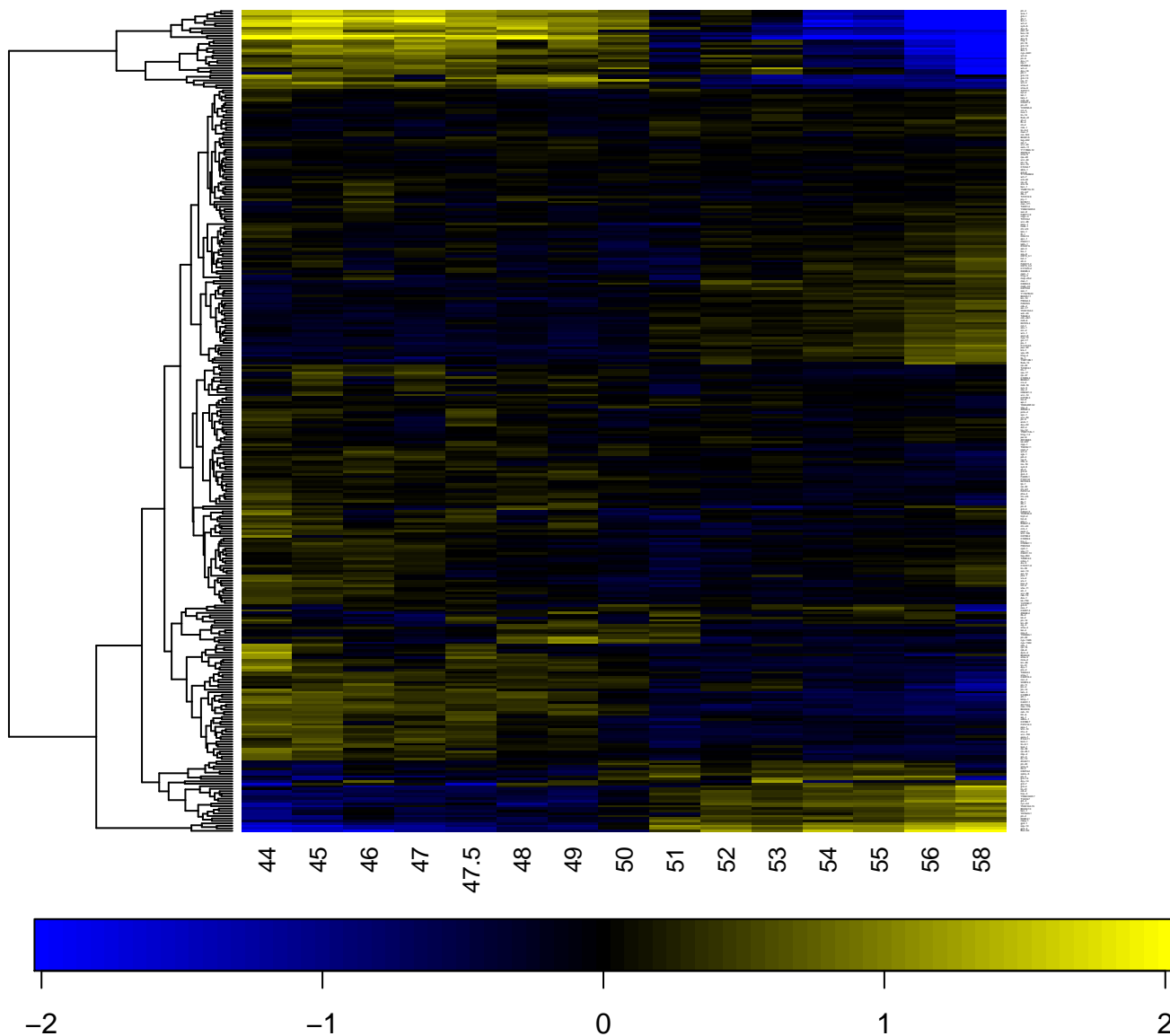
positive regulation of growth rate



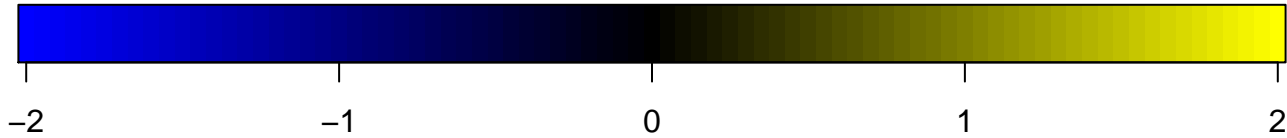
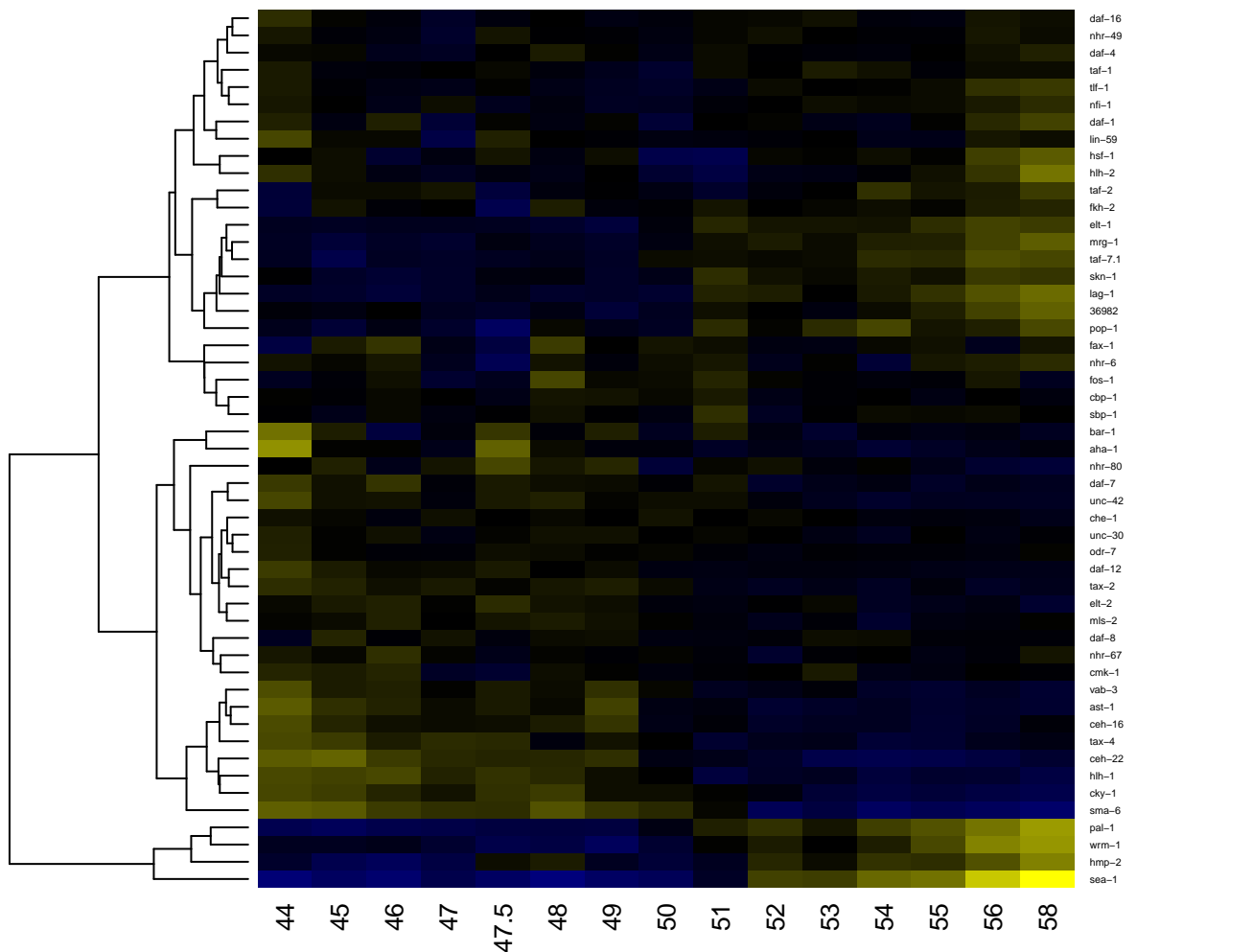
positive regulation of locomotion



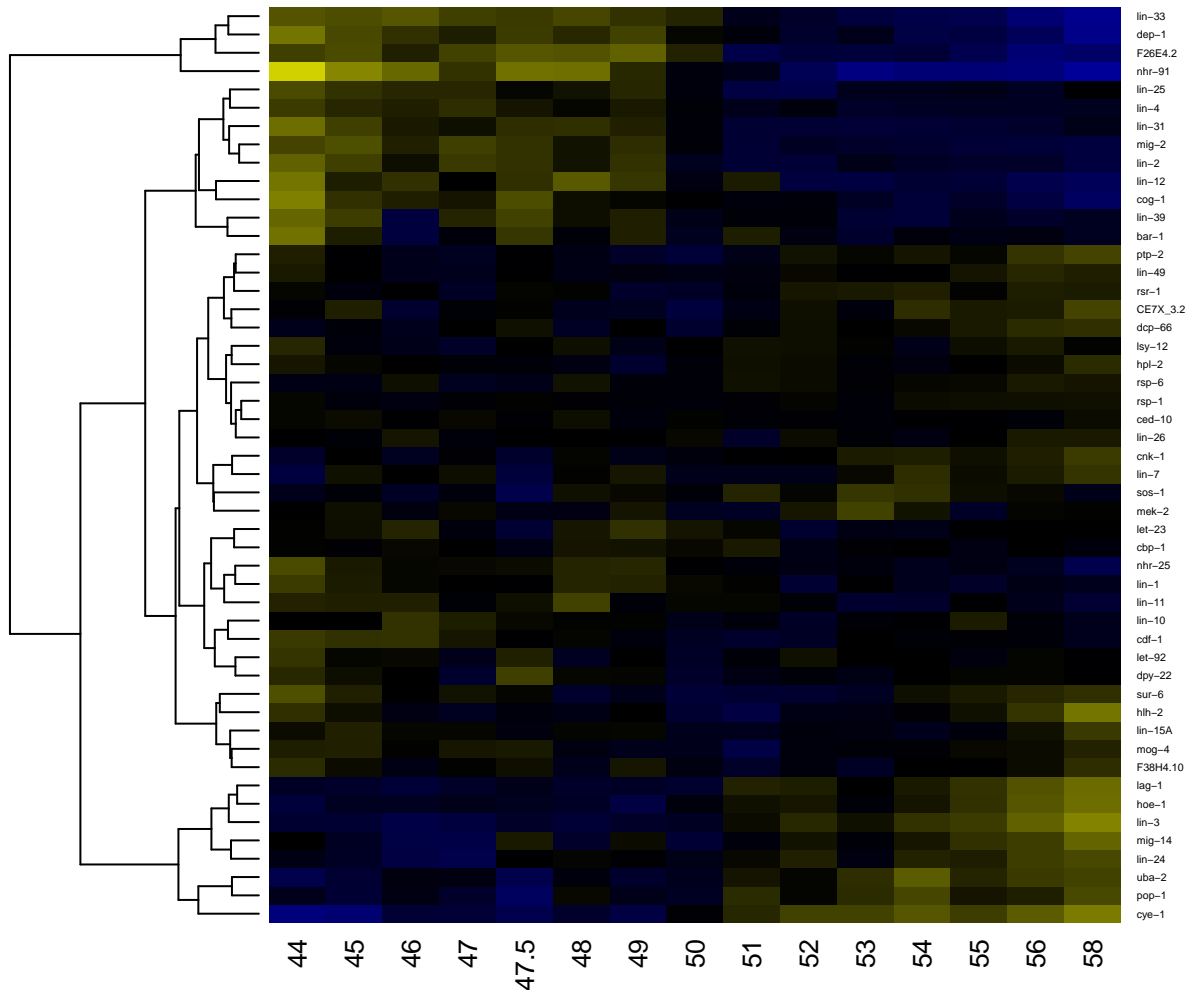
positive regulation of multicellular organism growth



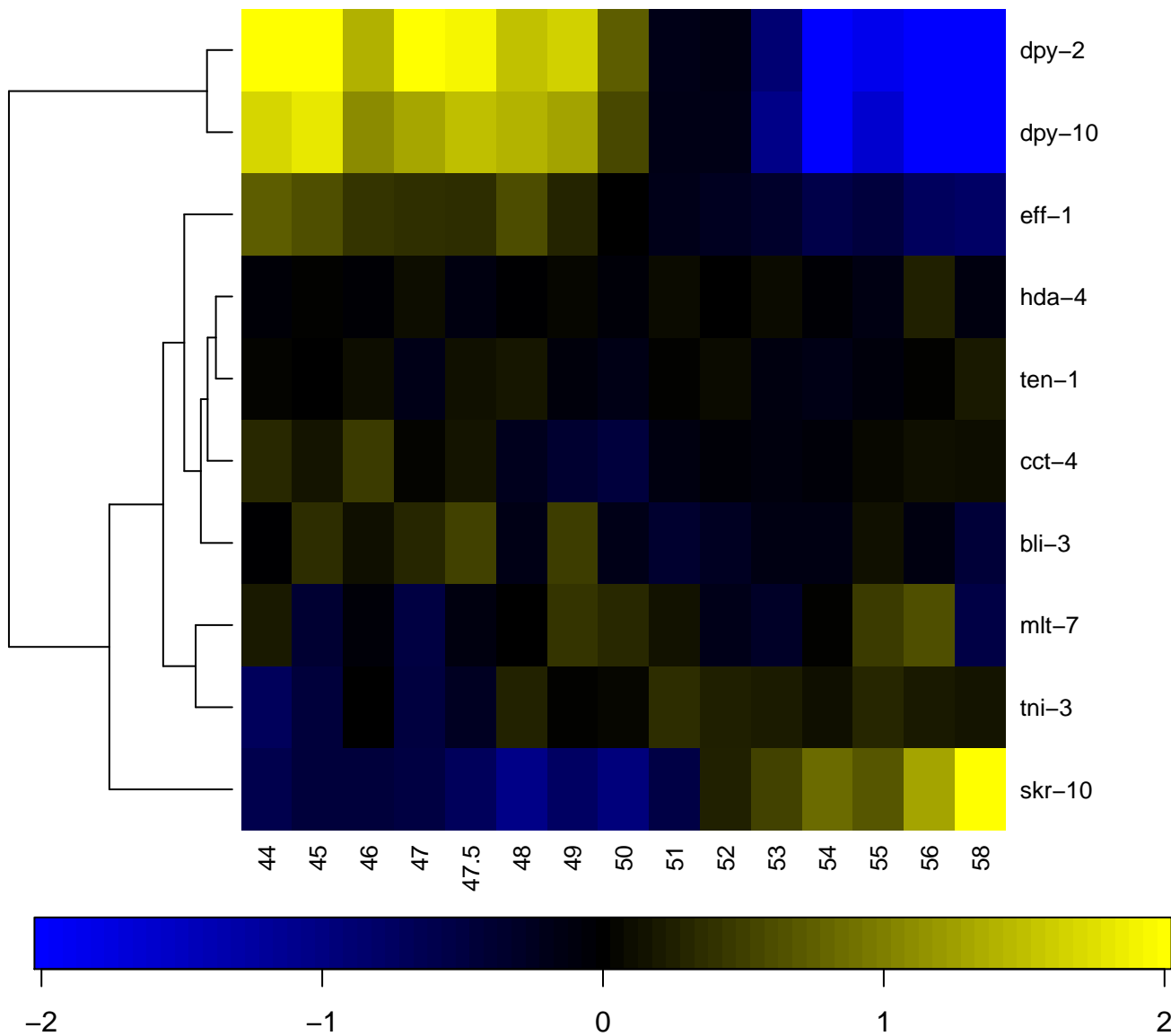
Positive regulation of transcription from RNA polymerase II promoter



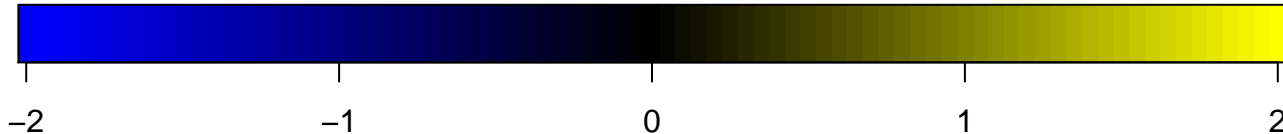
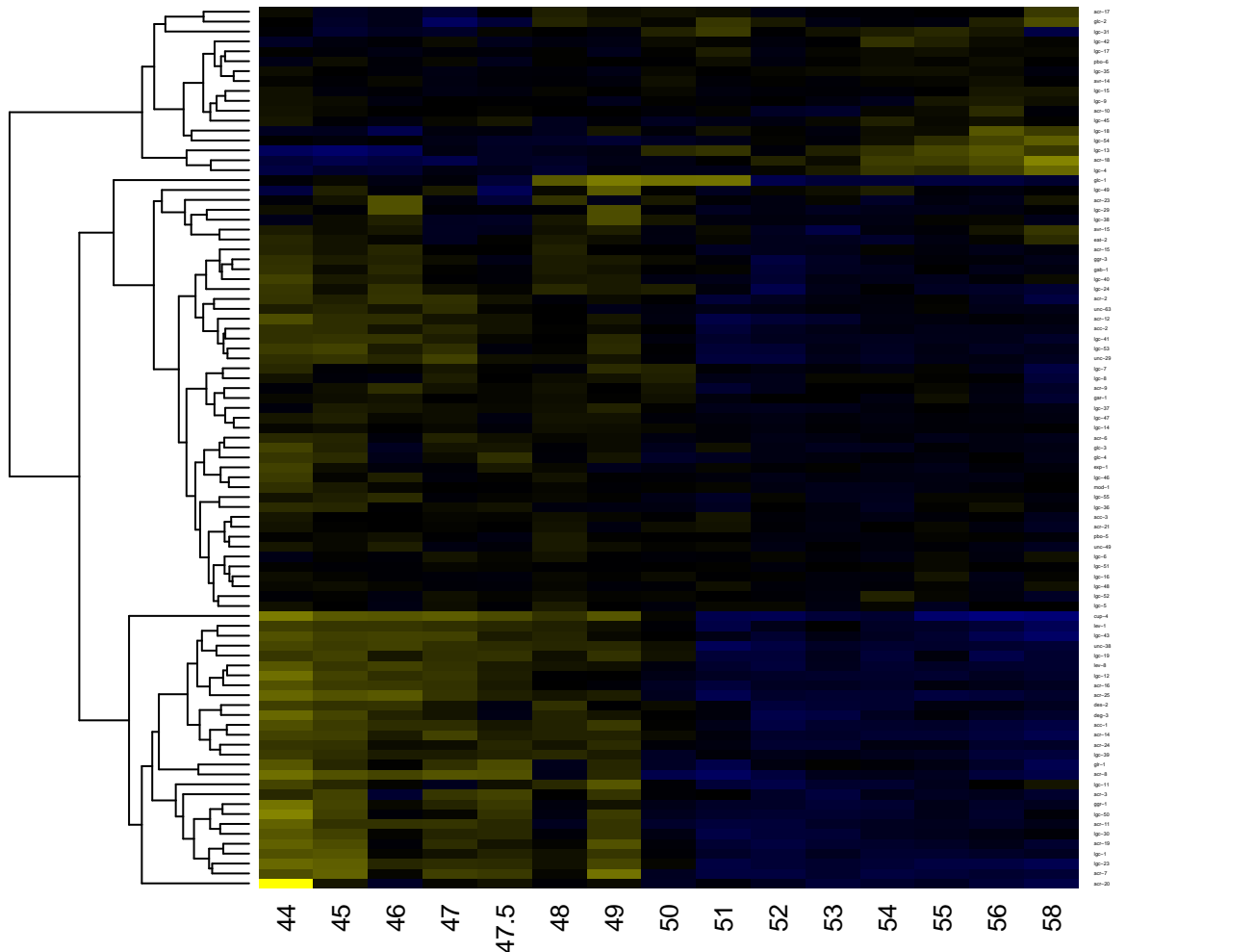
positive regulation of vulval development



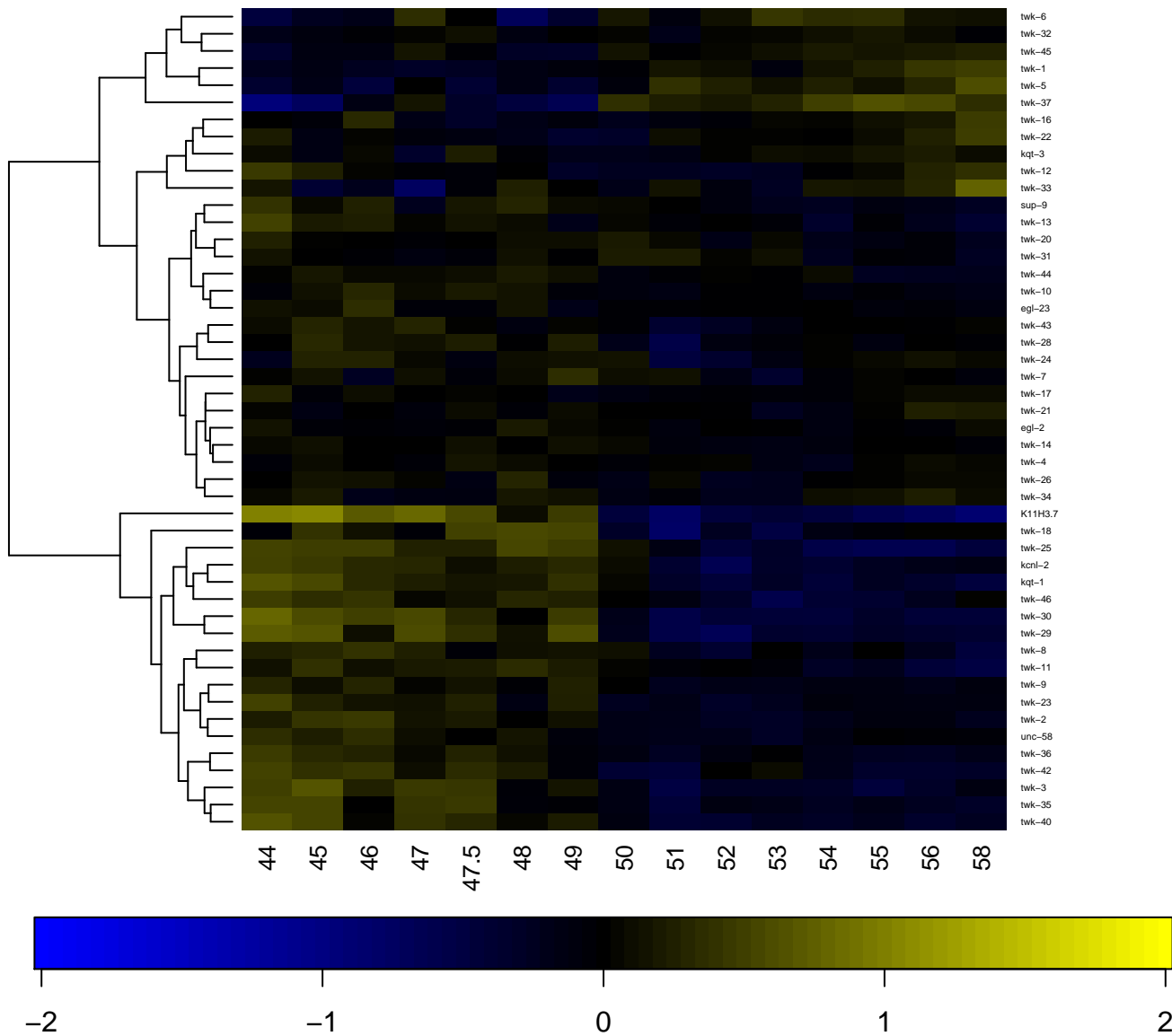
post-embryonic body morphogenesis



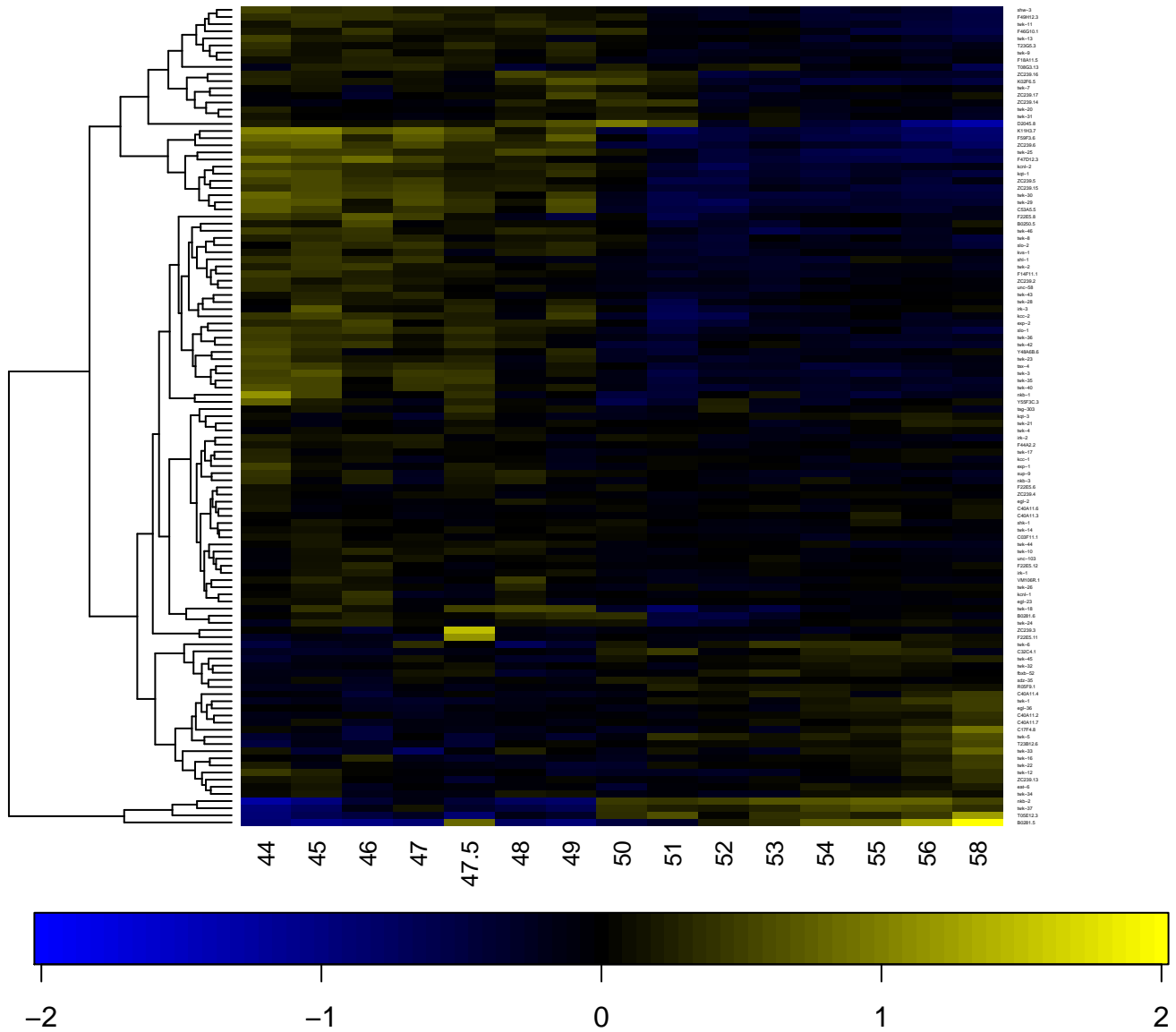
postsynaptic membrane



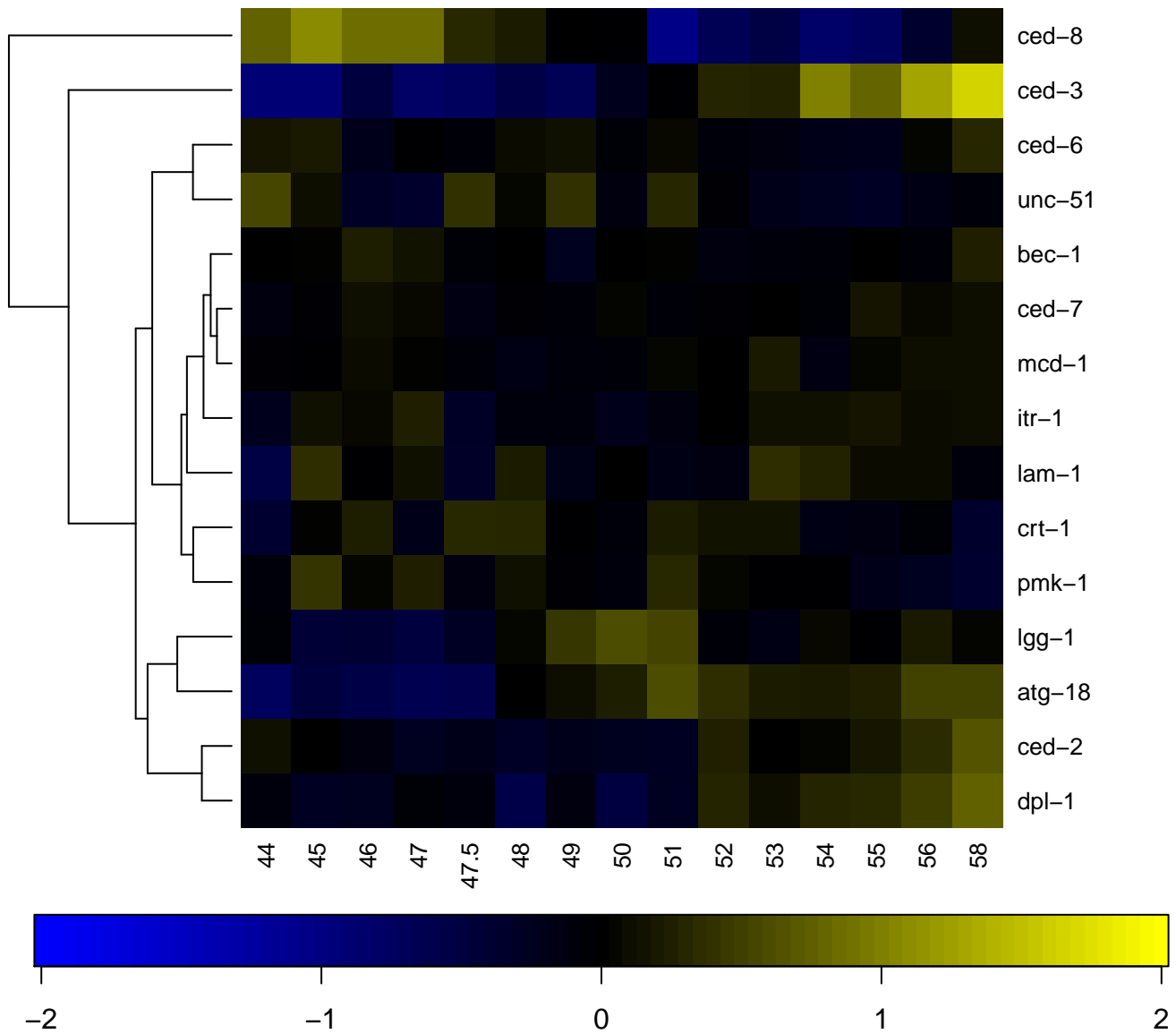
potassium channel activity



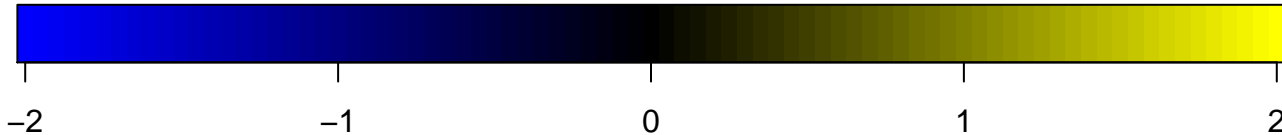
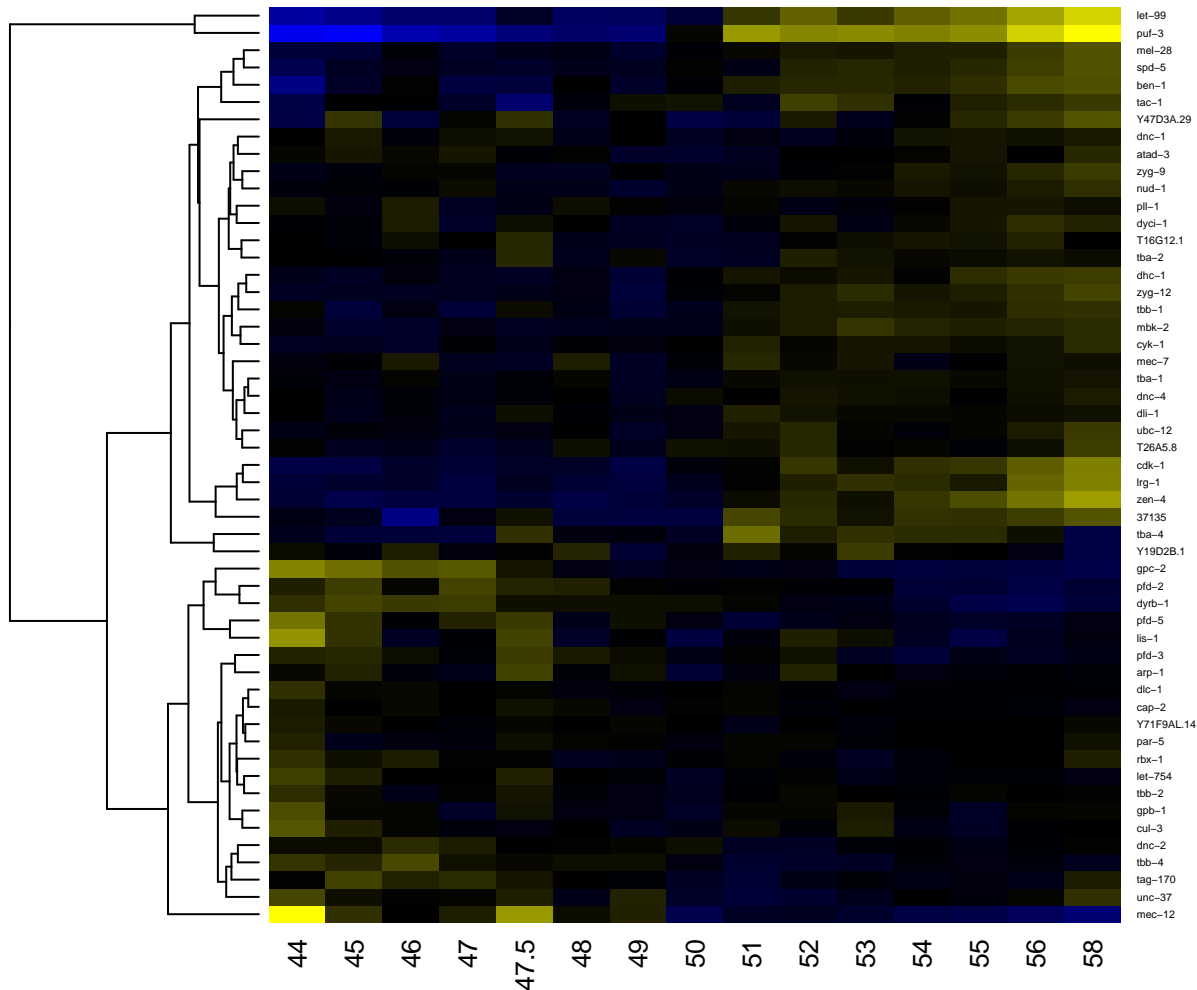
potassium ion transport



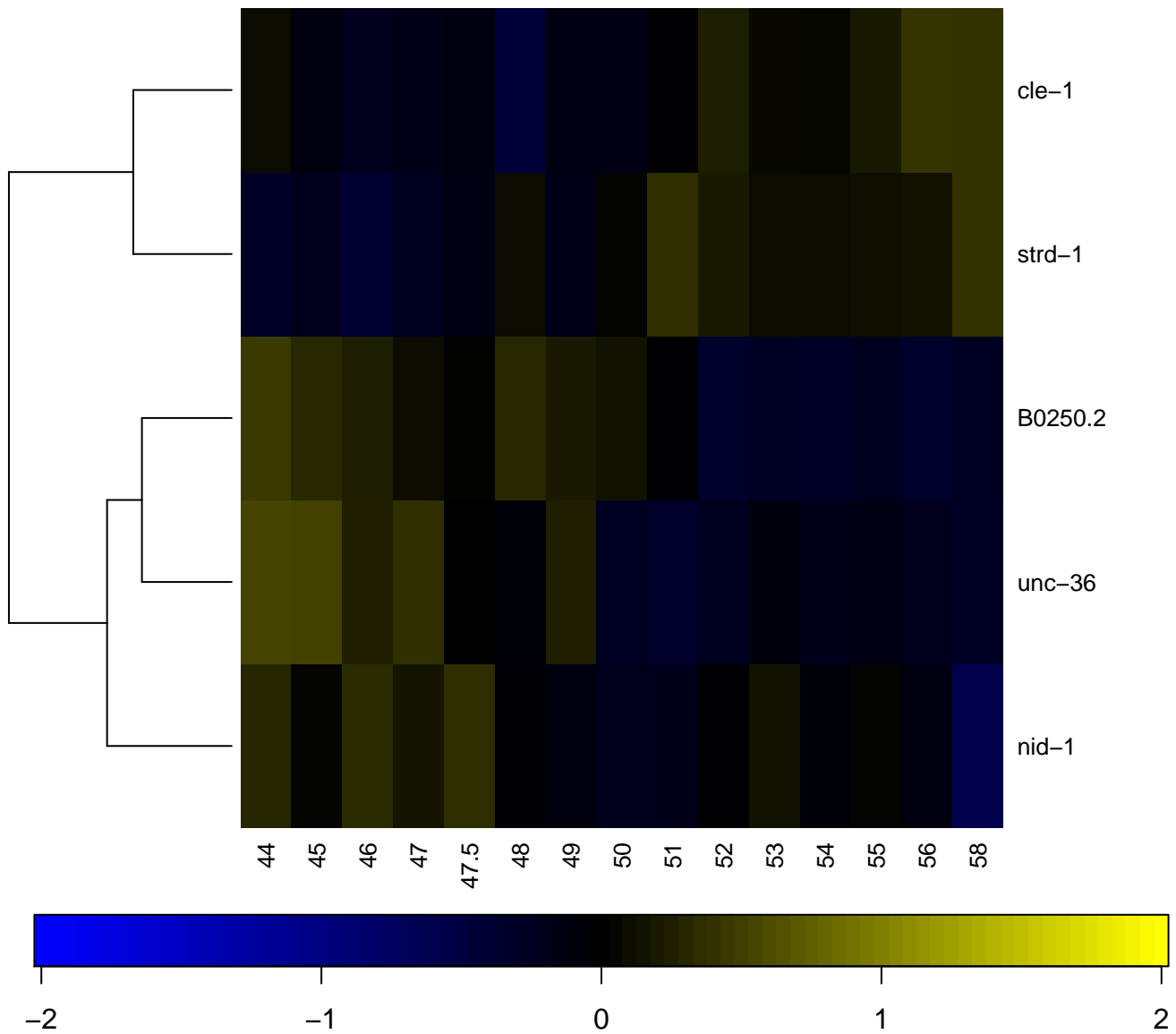
programmed cell death



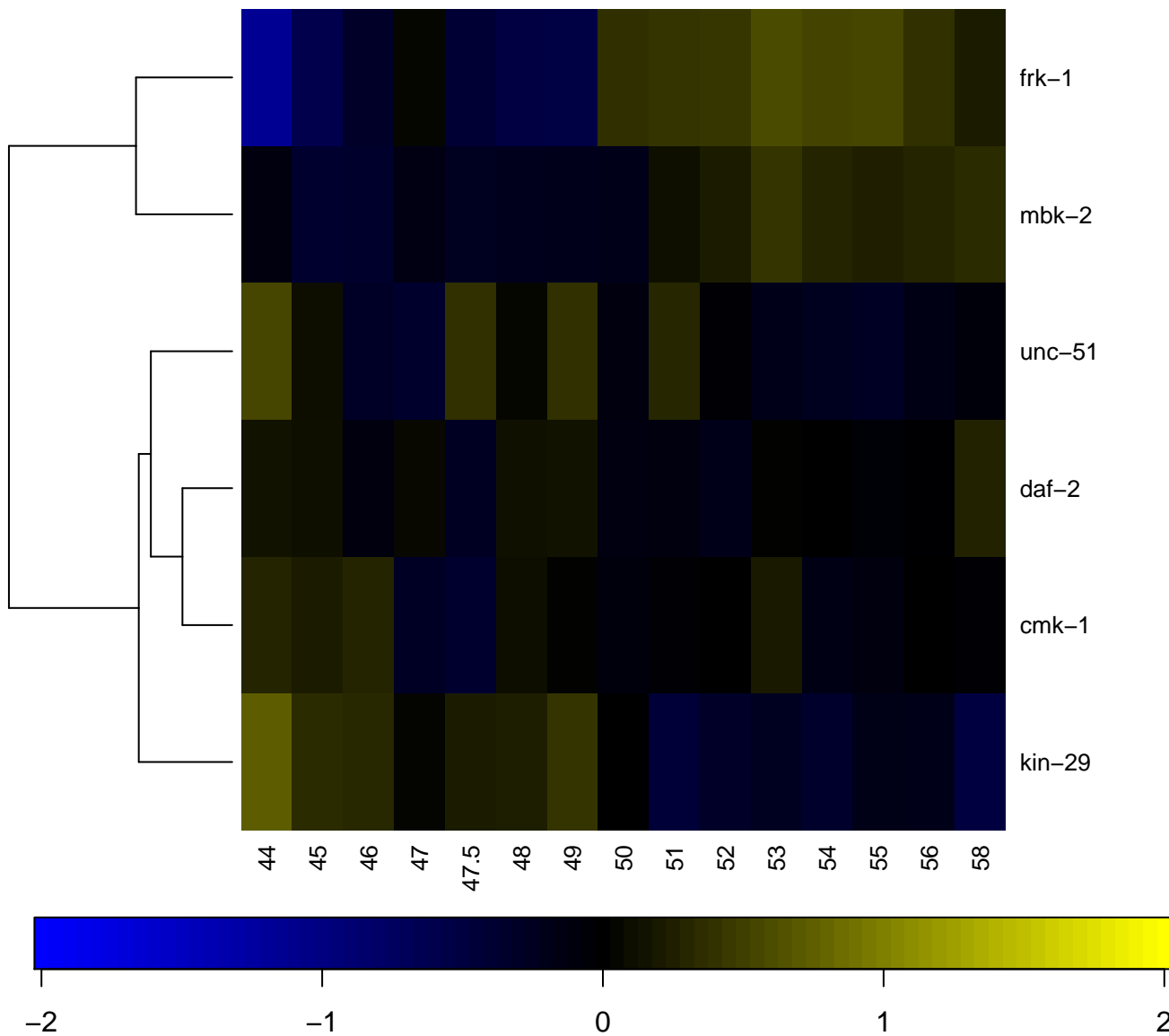
pronuclear migration



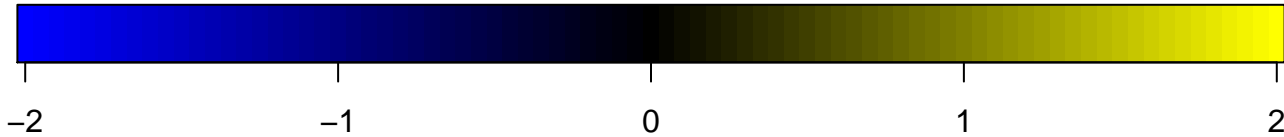
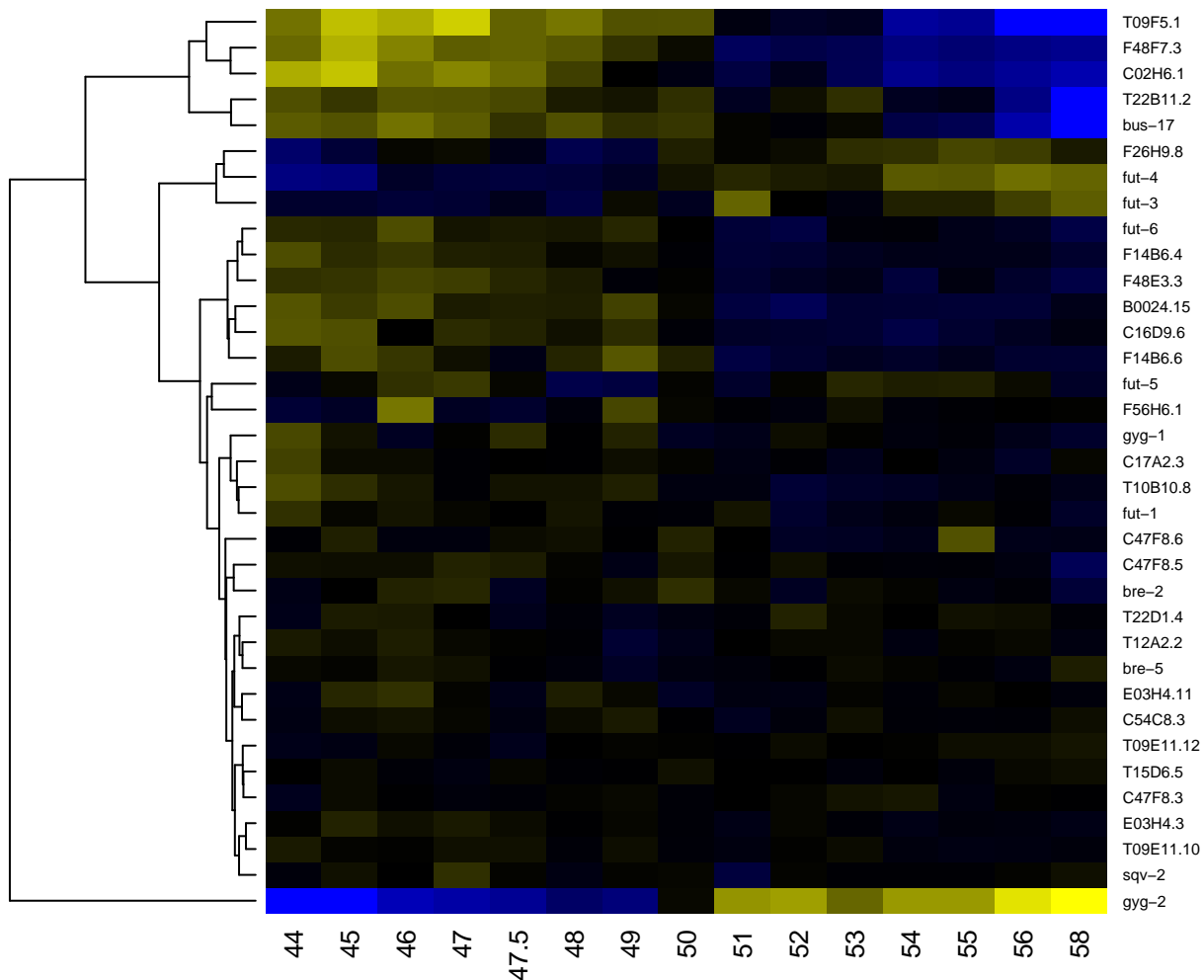
protein



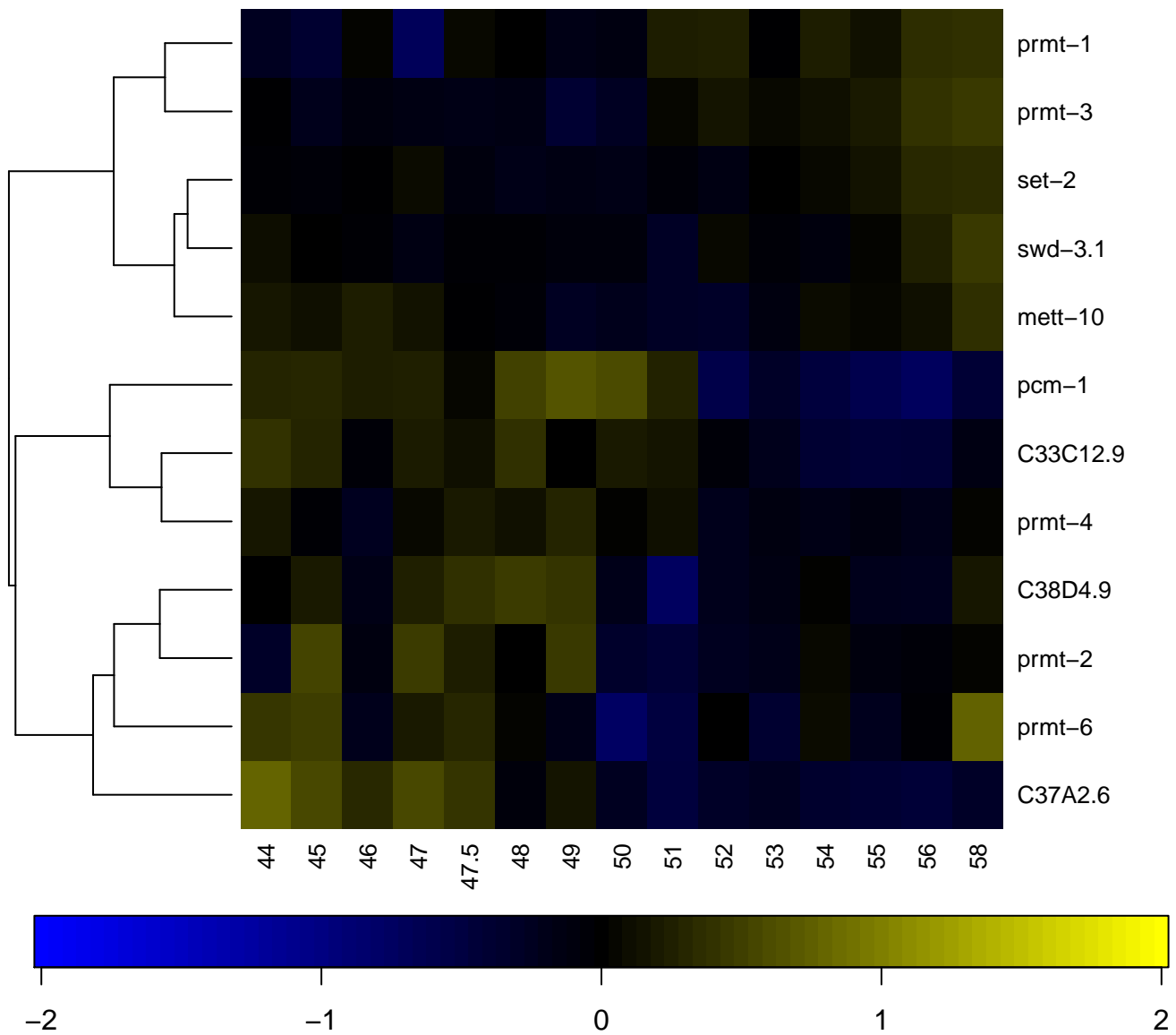
protein amino acid autophosphorylation



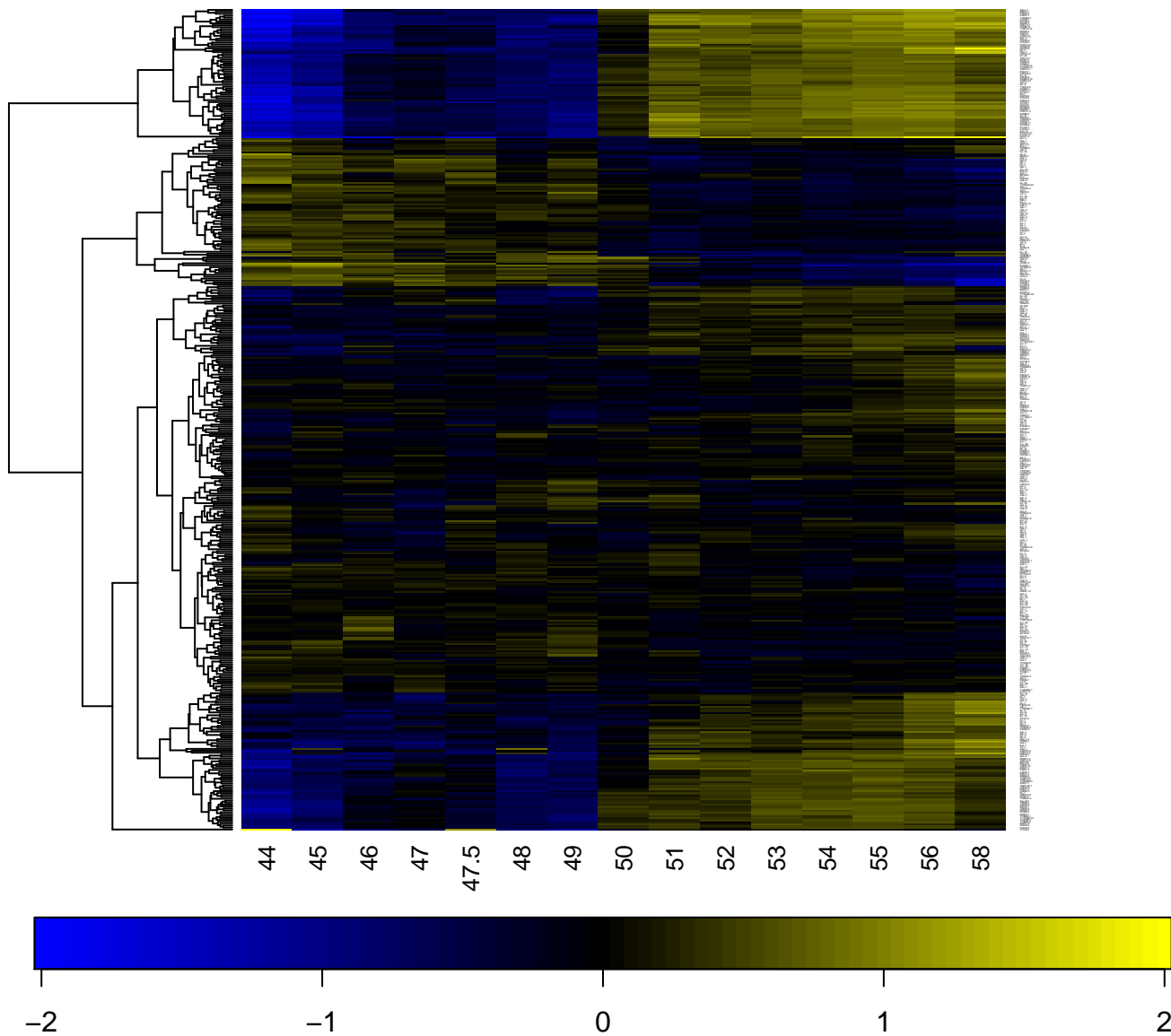
protein amino acid glycosylation



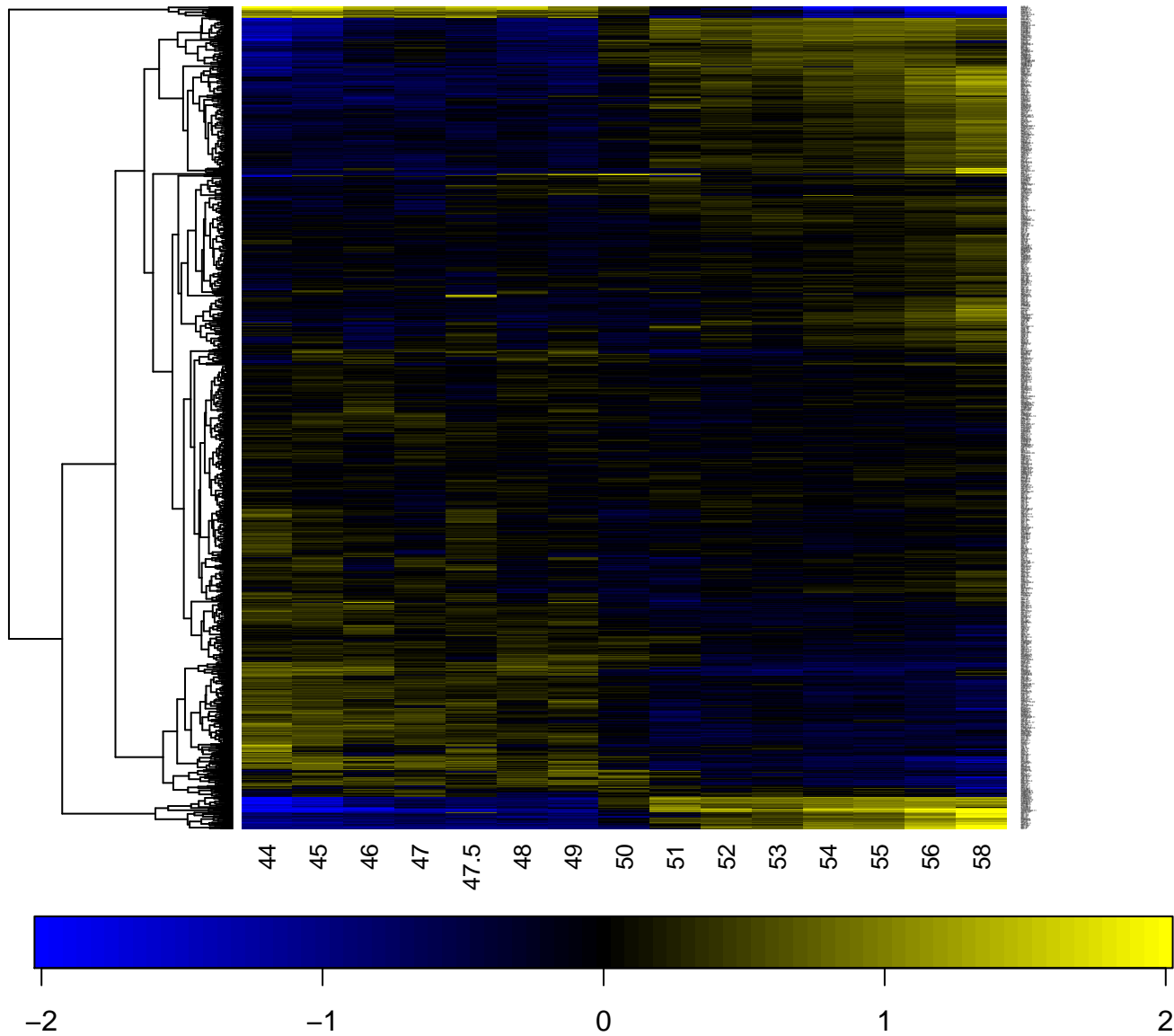
protein amino acid methylation



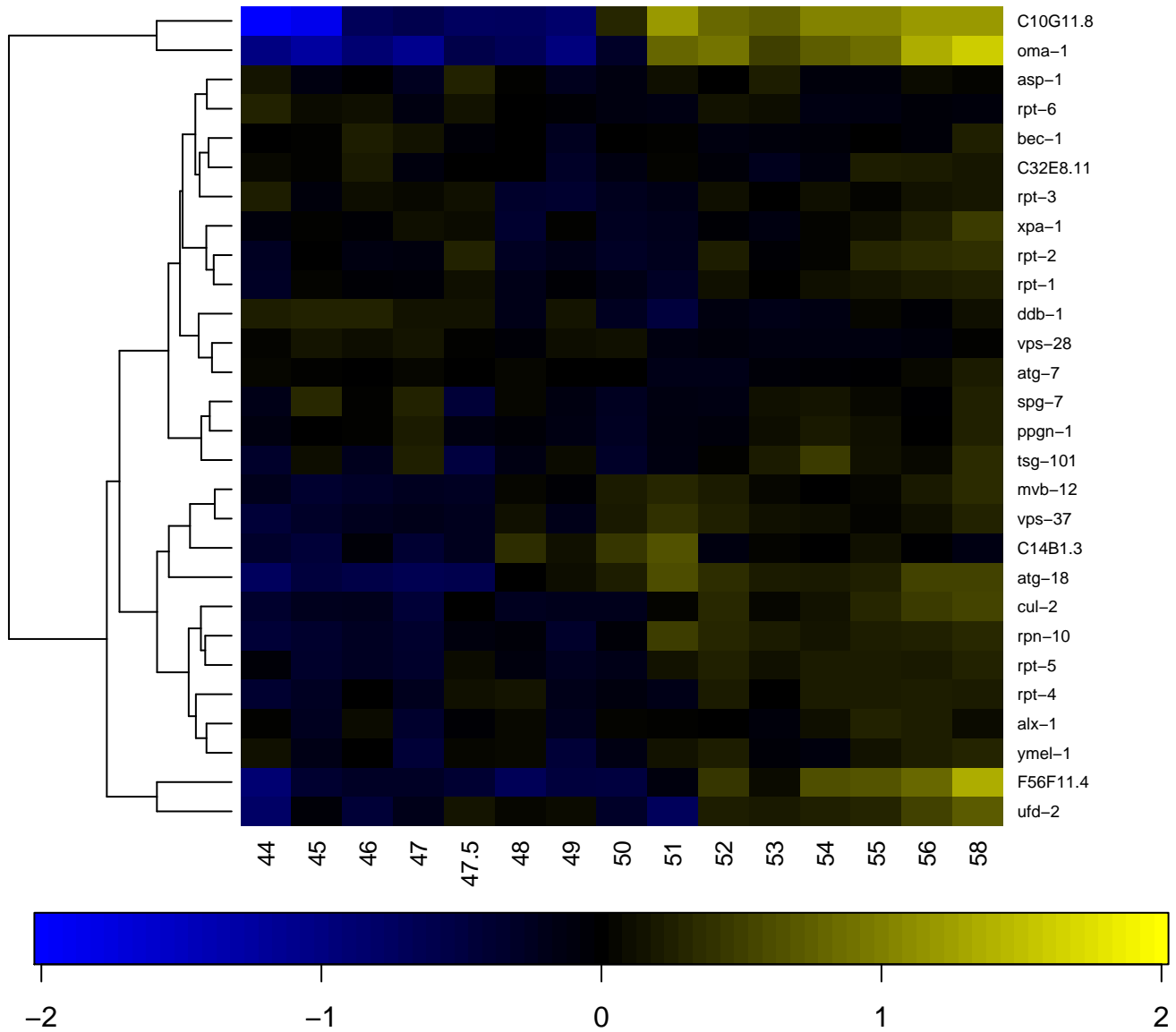
protein amino acid phosphorylation



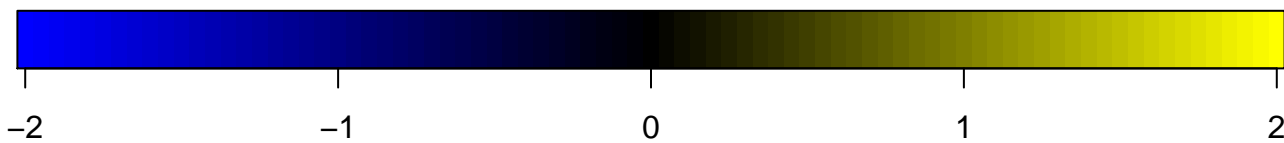
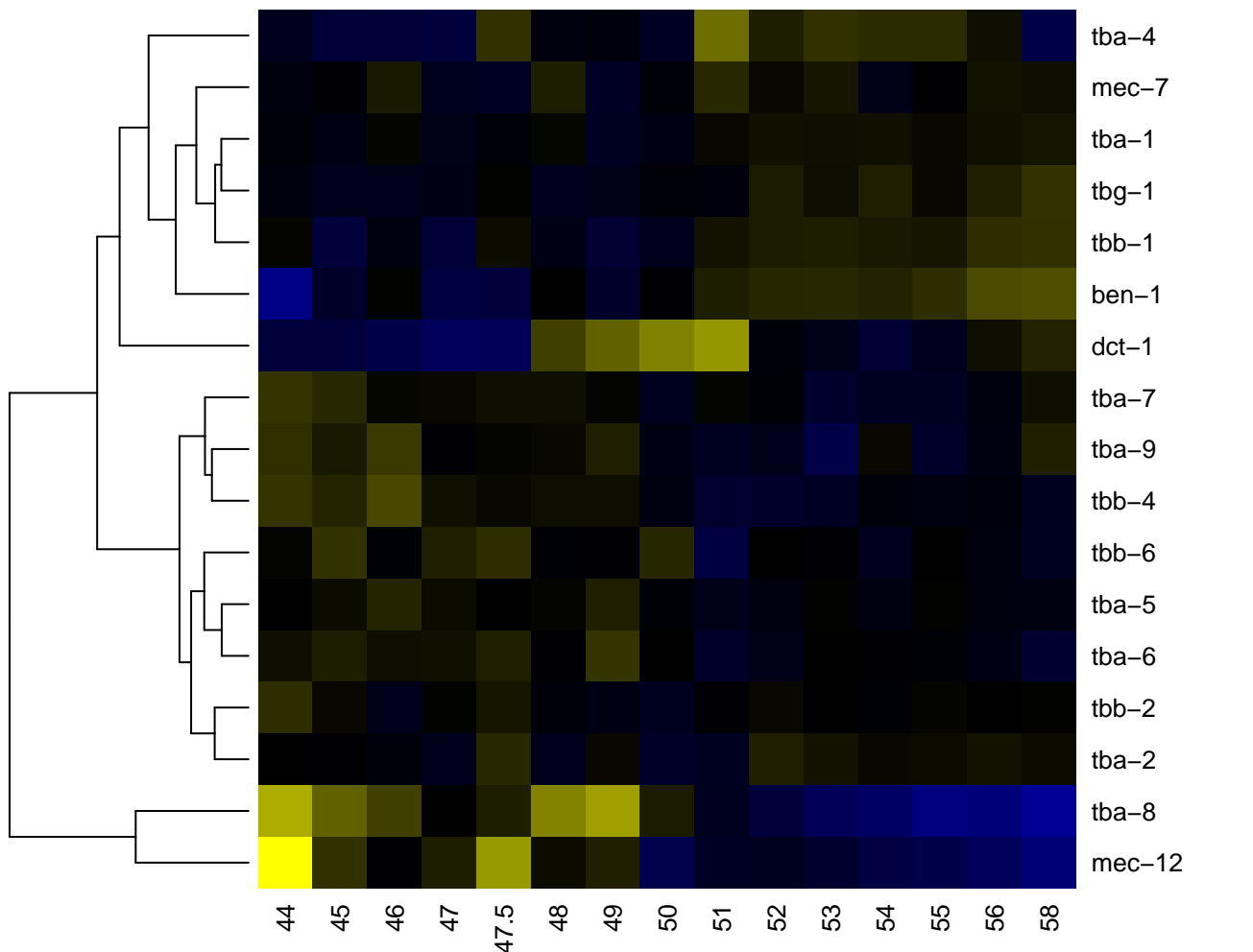
protein binding



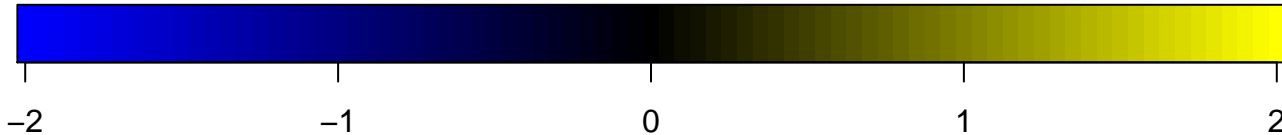
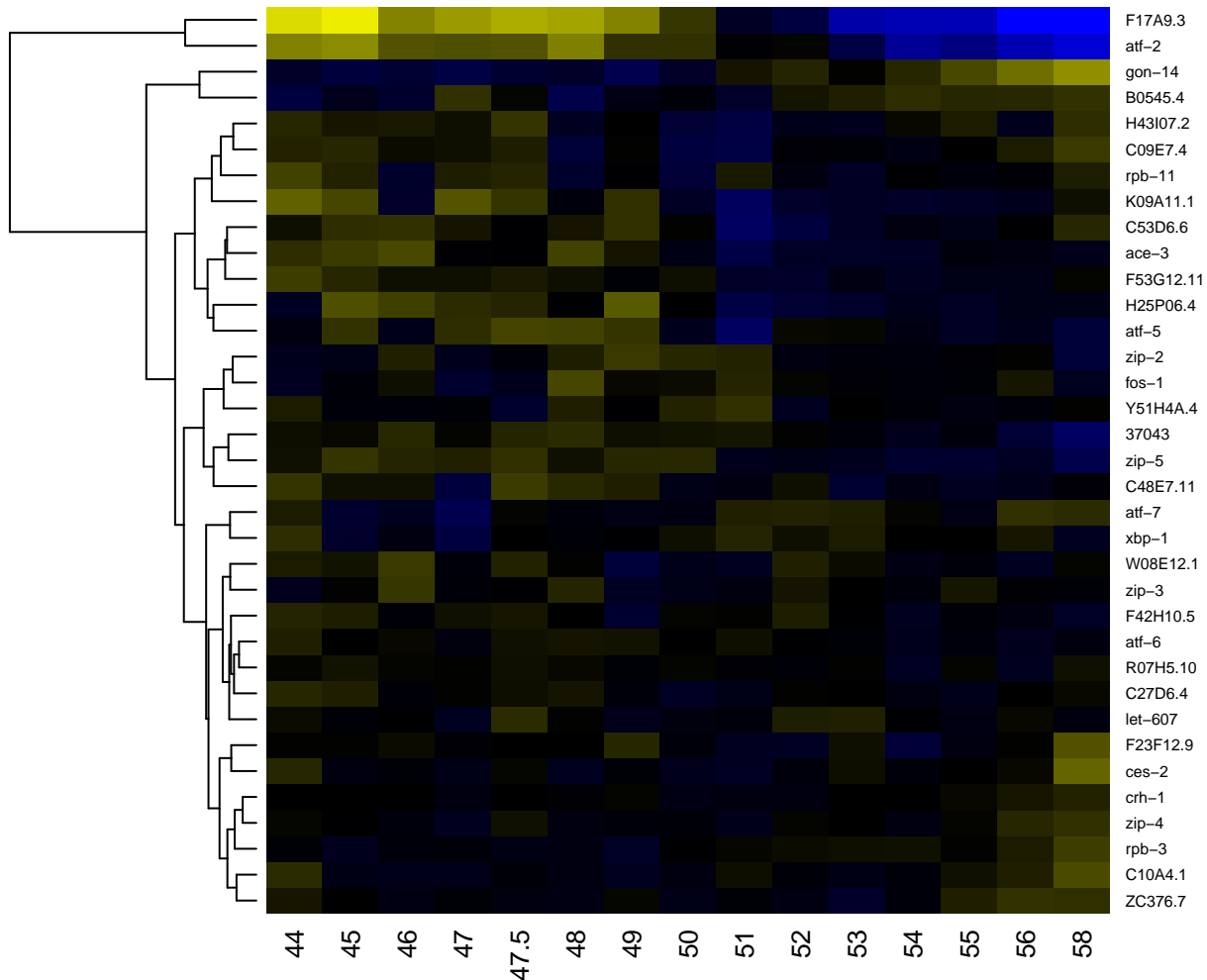
protein catabolic process



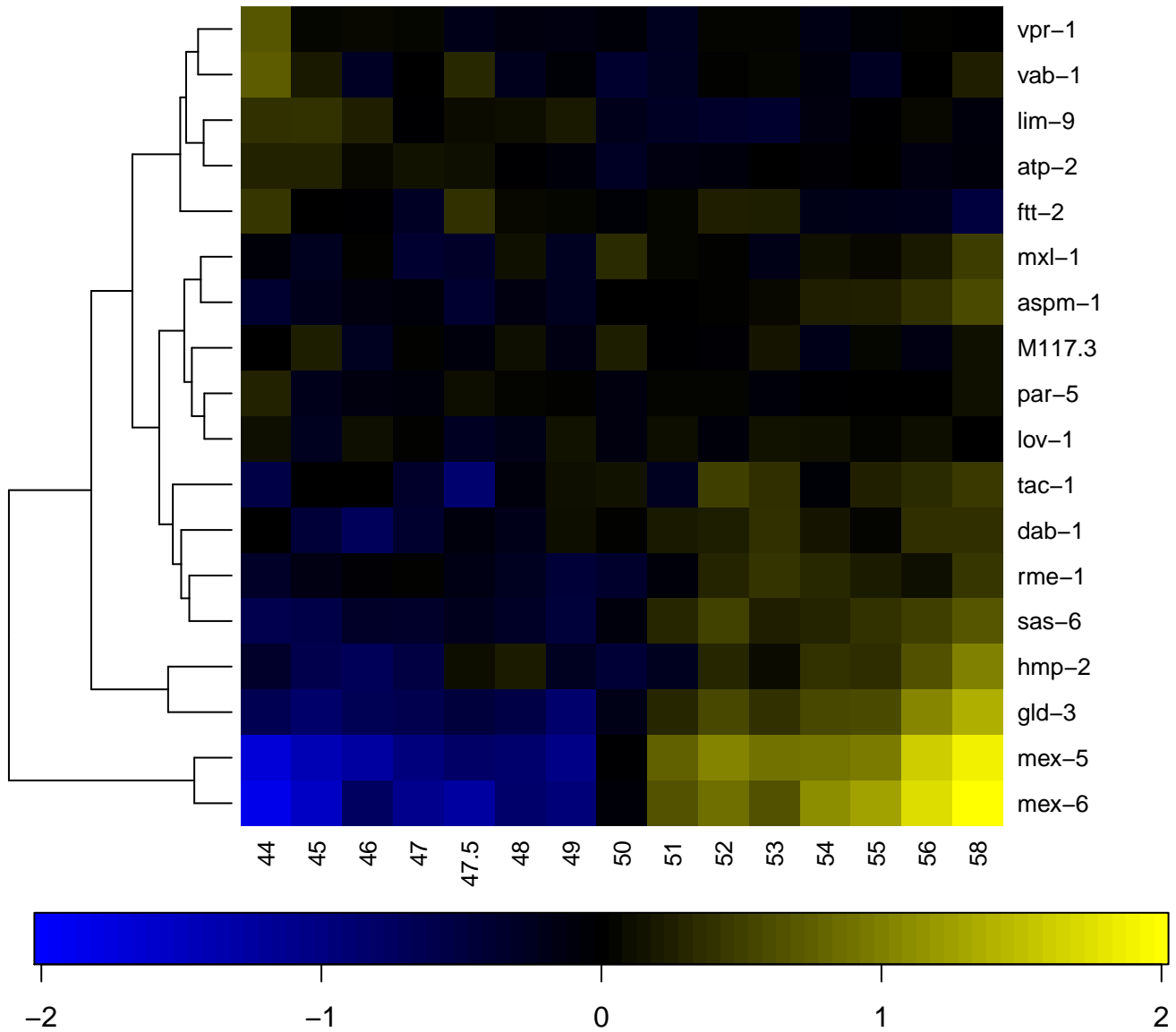
protein complex



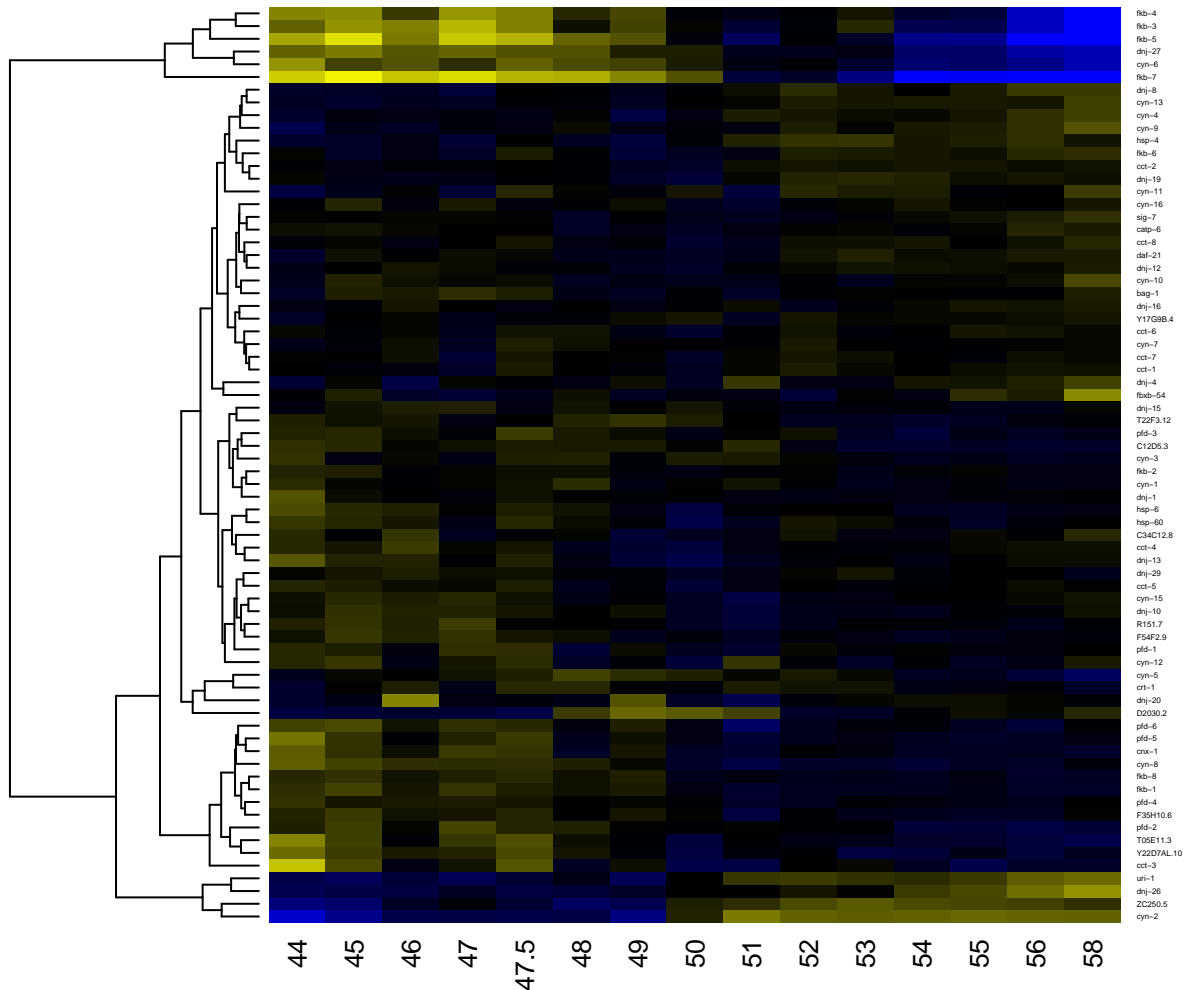
protein dimerization activity



protein domain specific binding



protein folding



-2

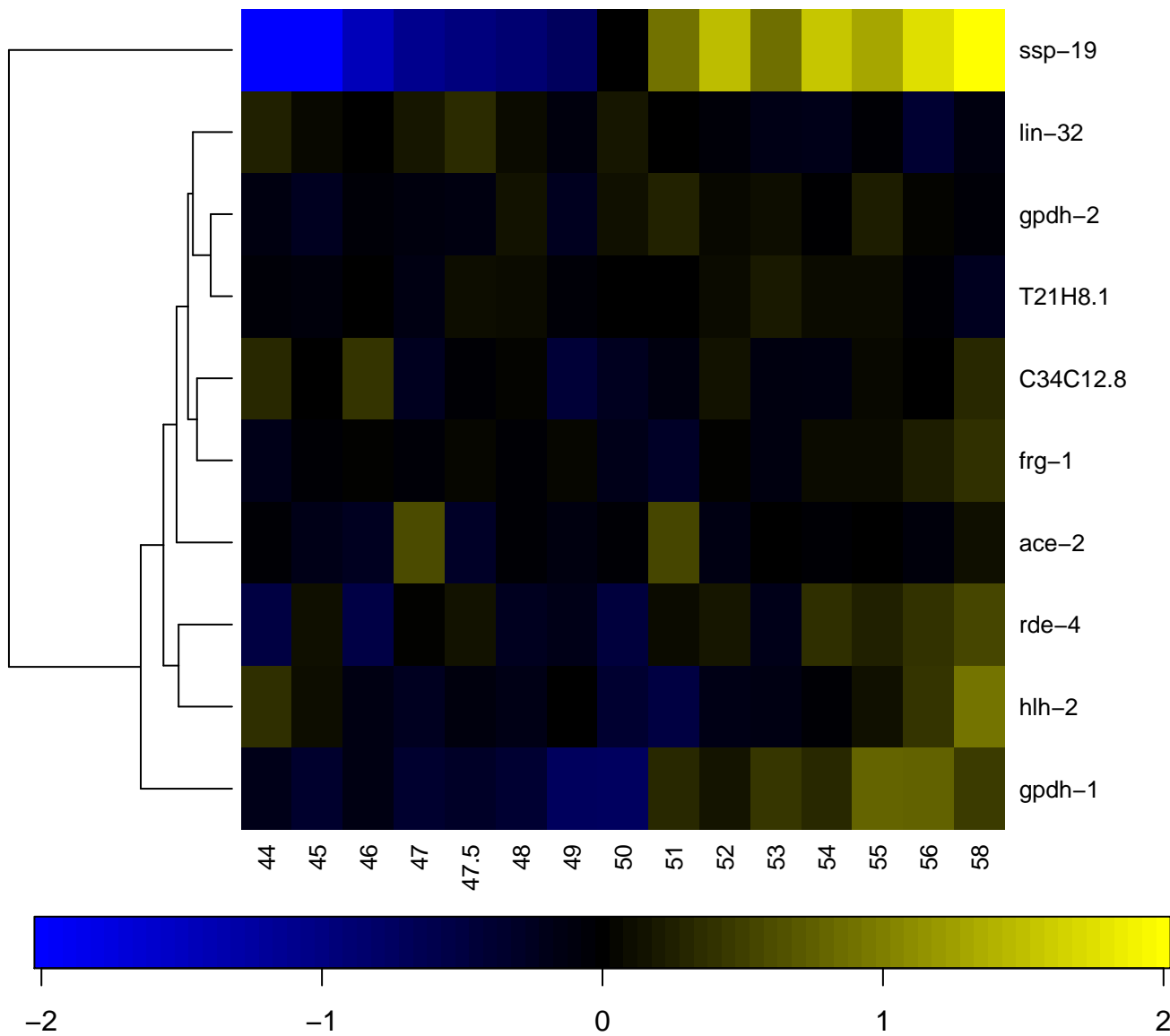
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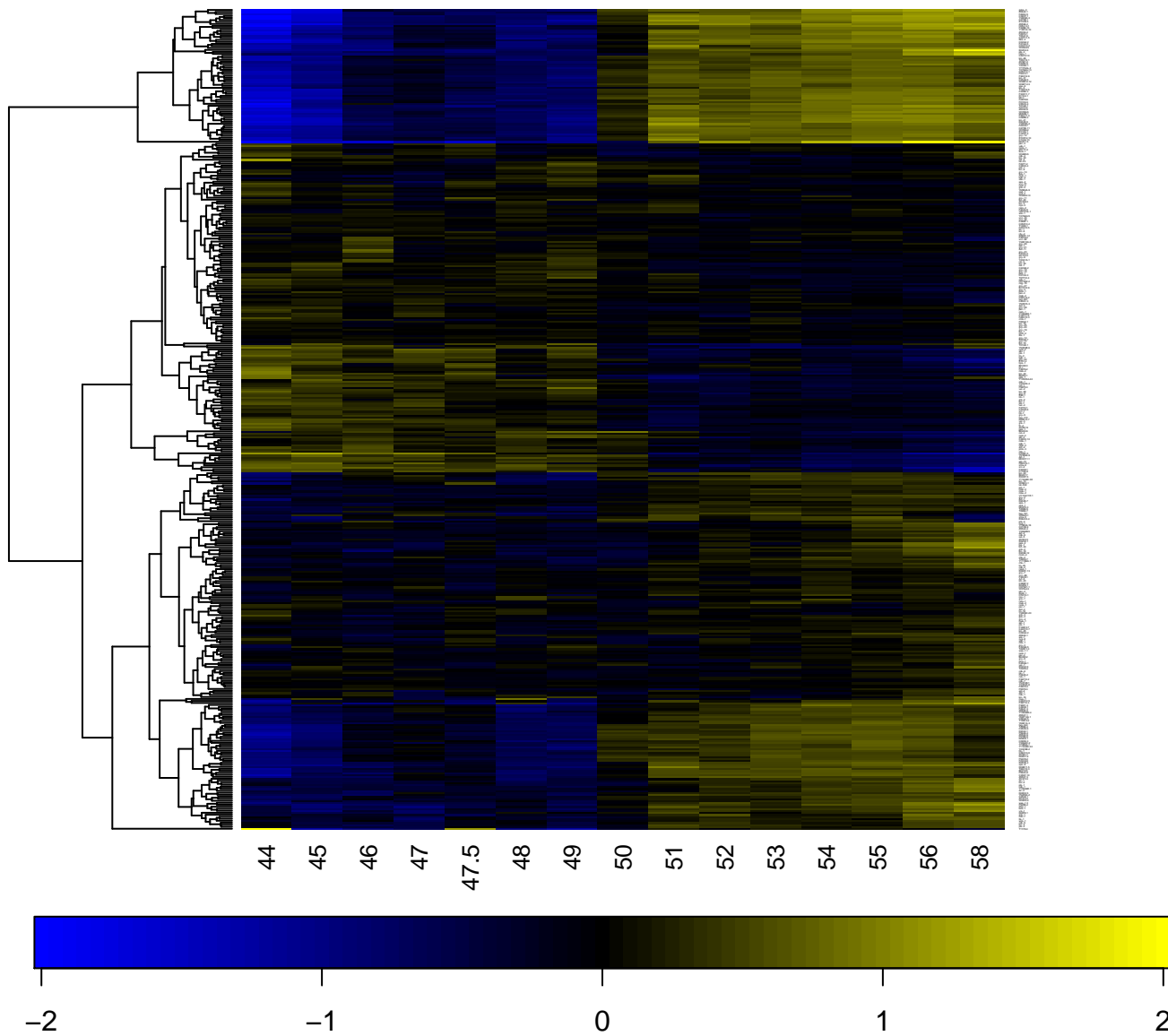
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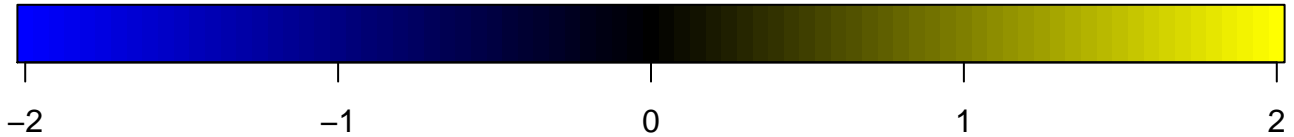
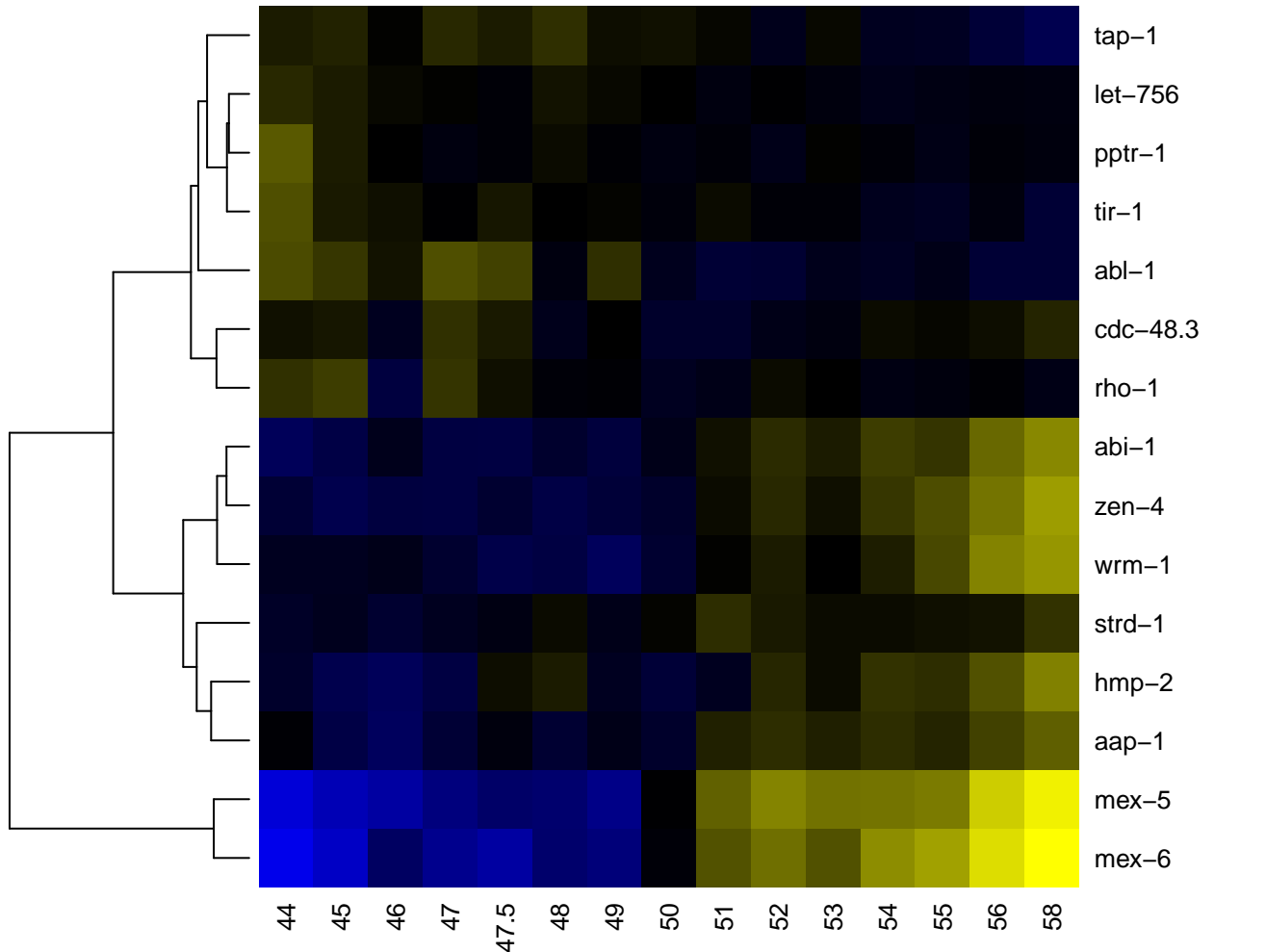
protein homodimerization activity



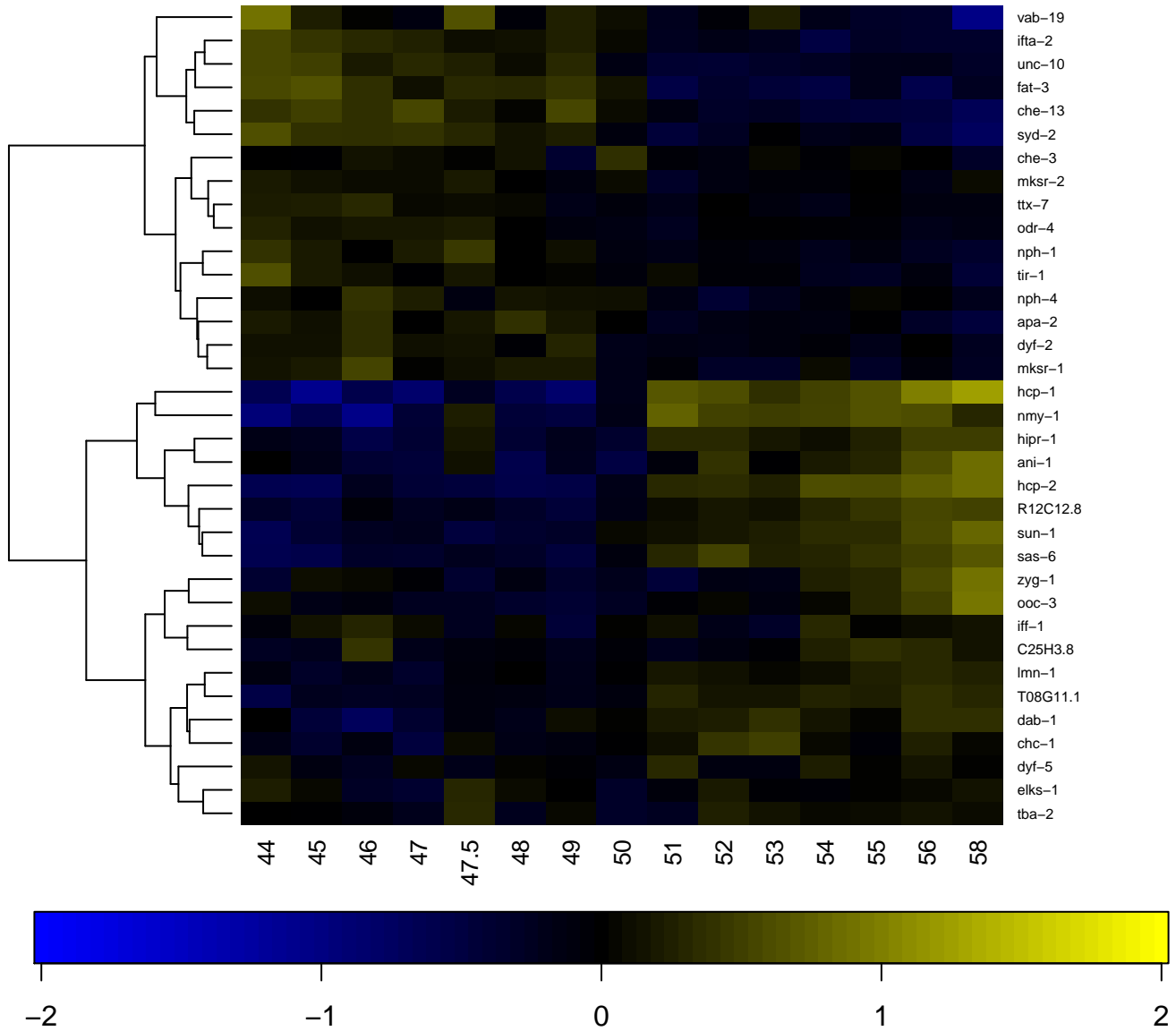
protein kinase activity



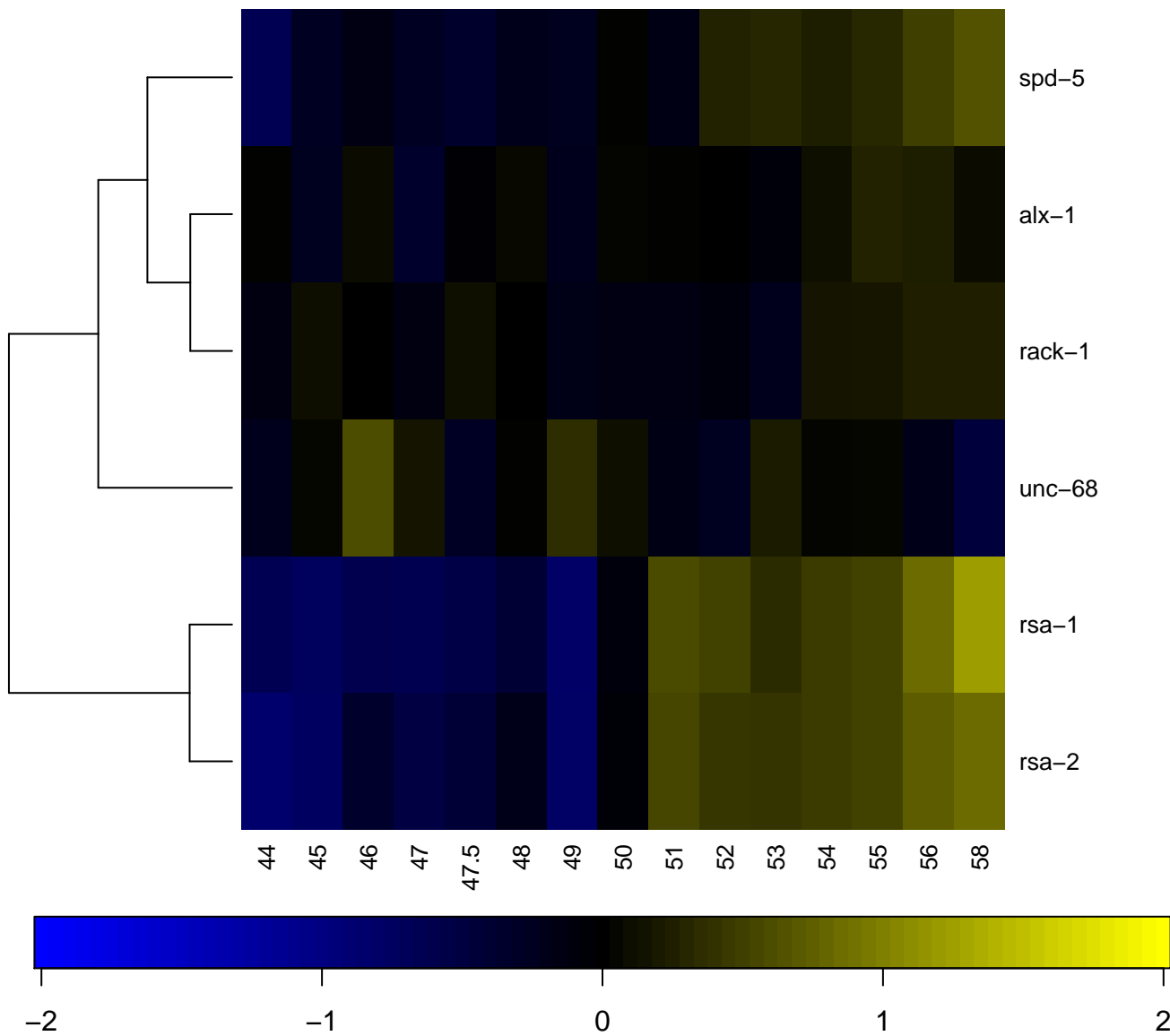
protein kinase binding



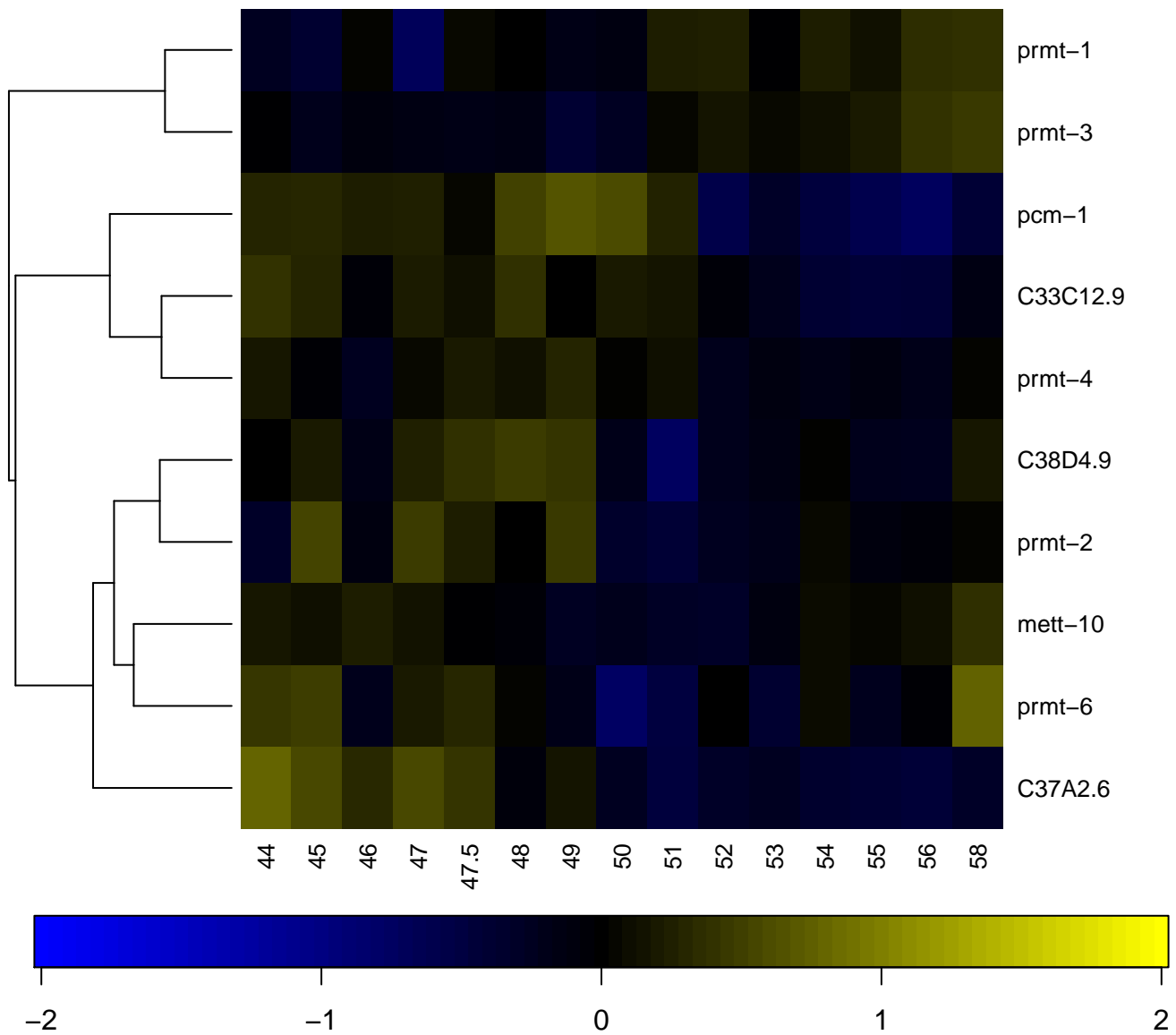
protein localization



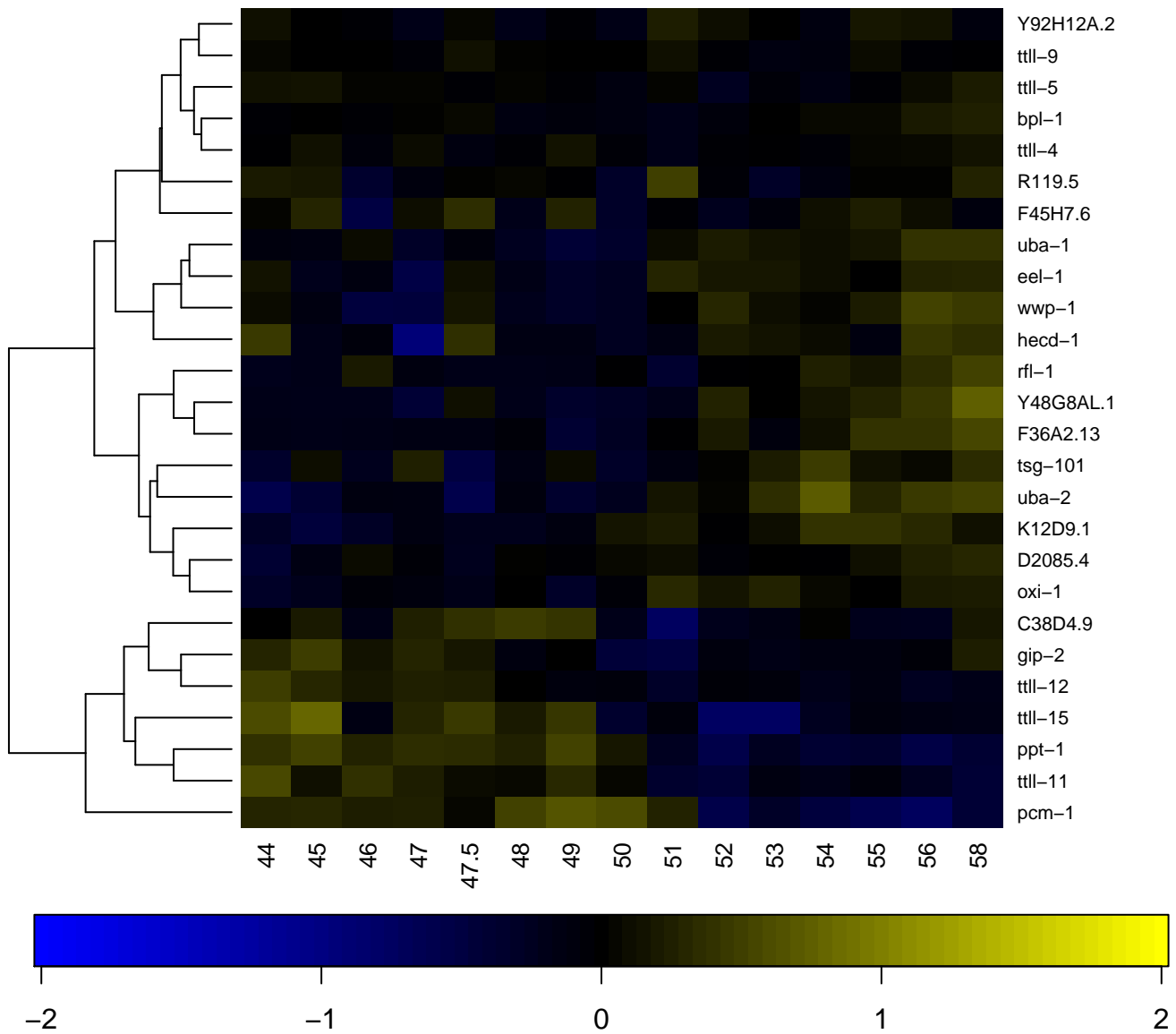
protein localization in organelle



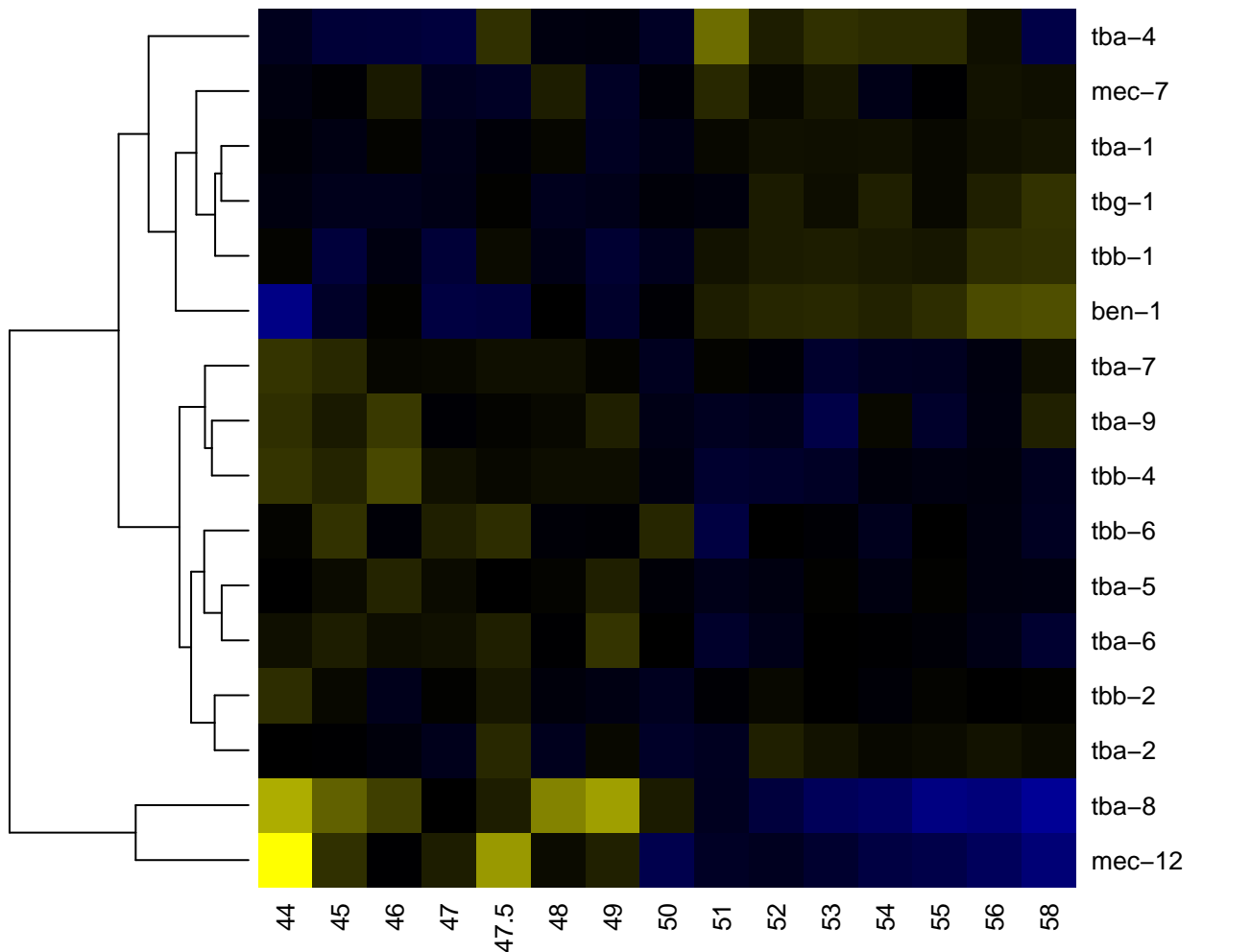
protein methyltransferase activity



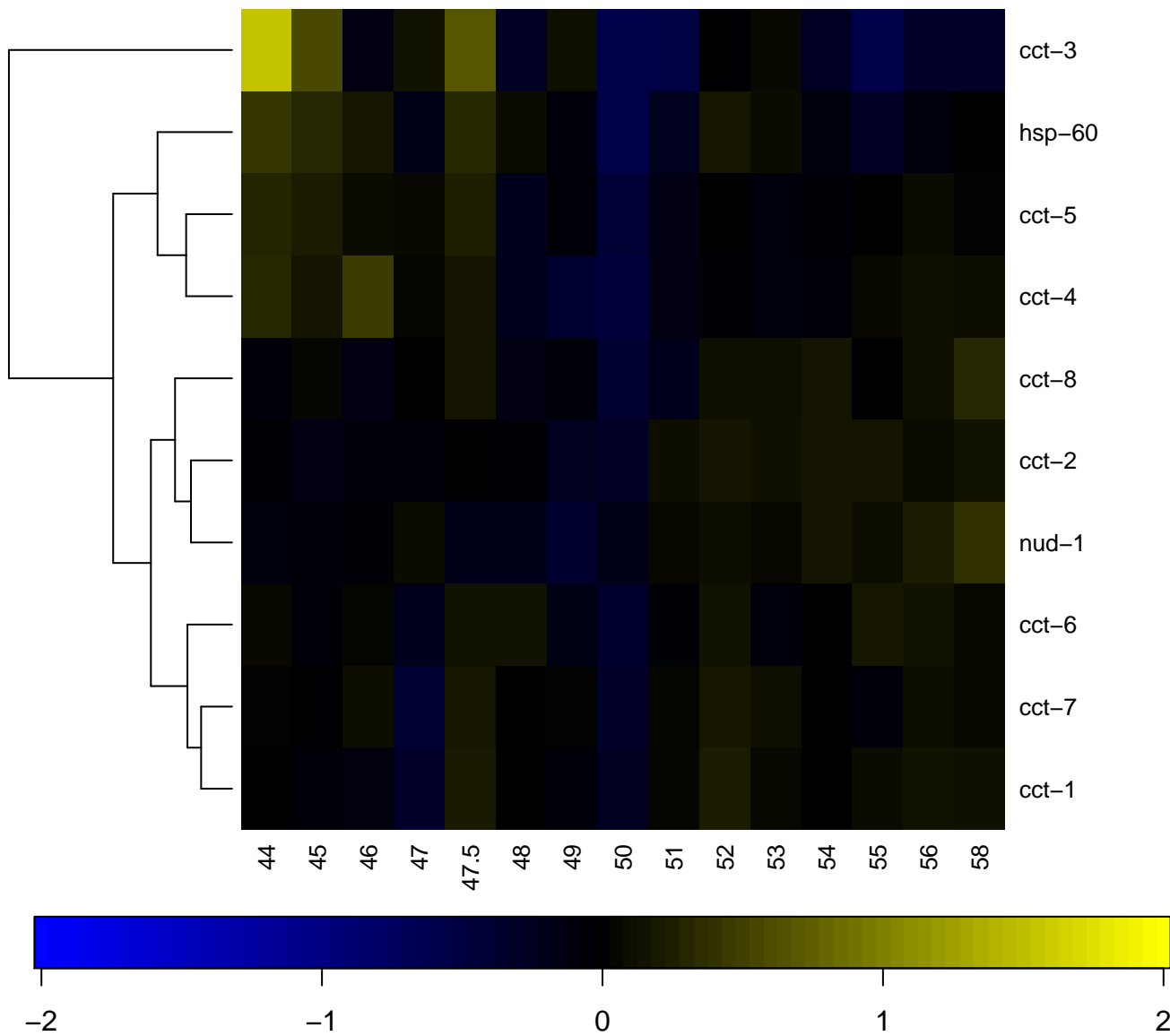
protein modification process



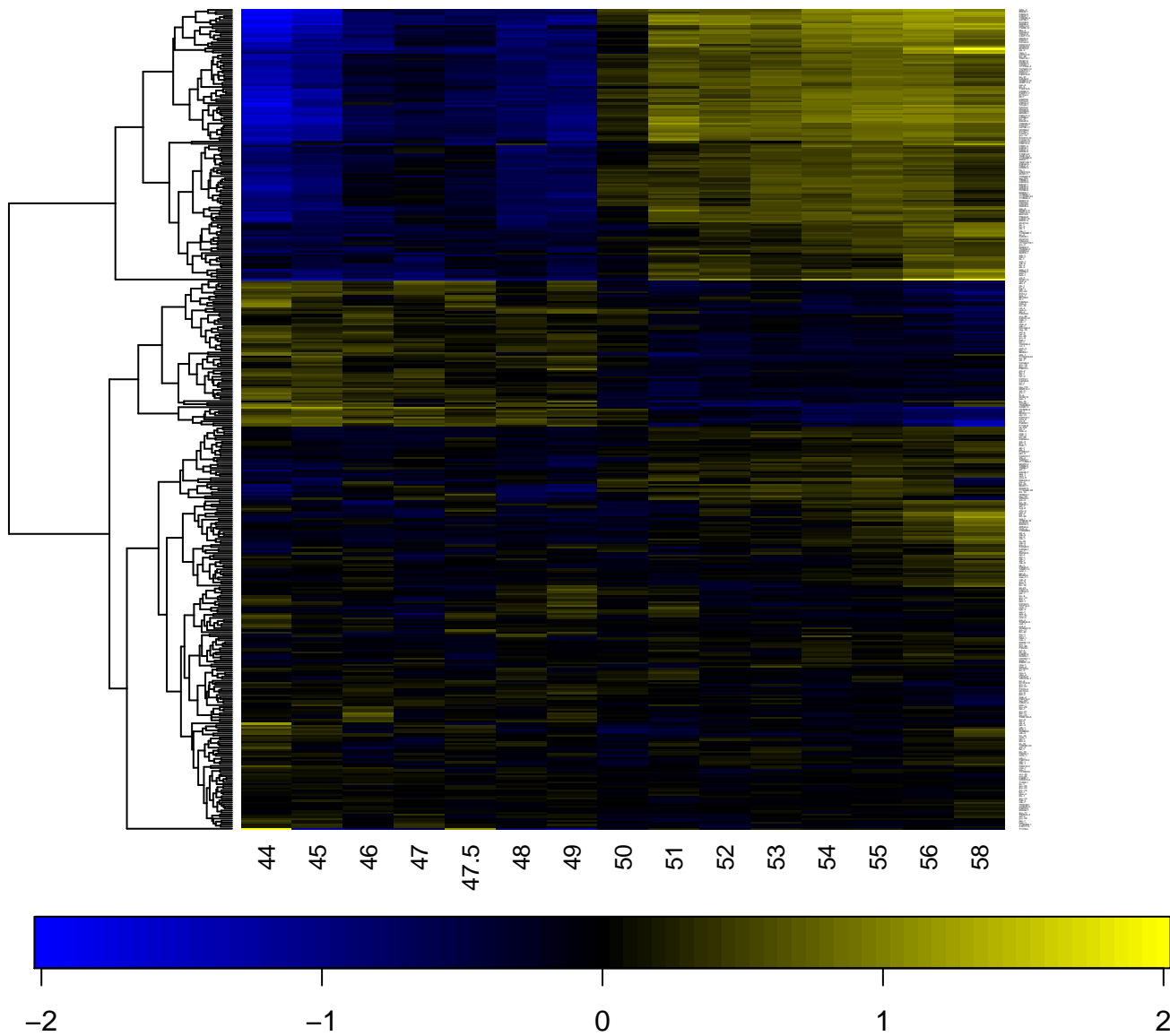
protein polymerization



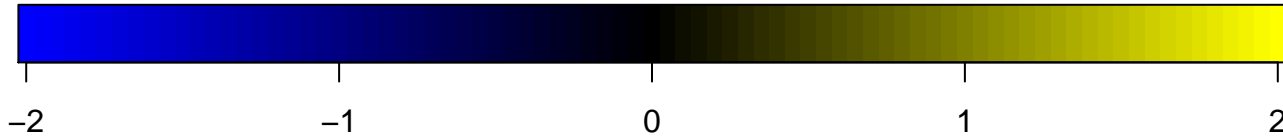
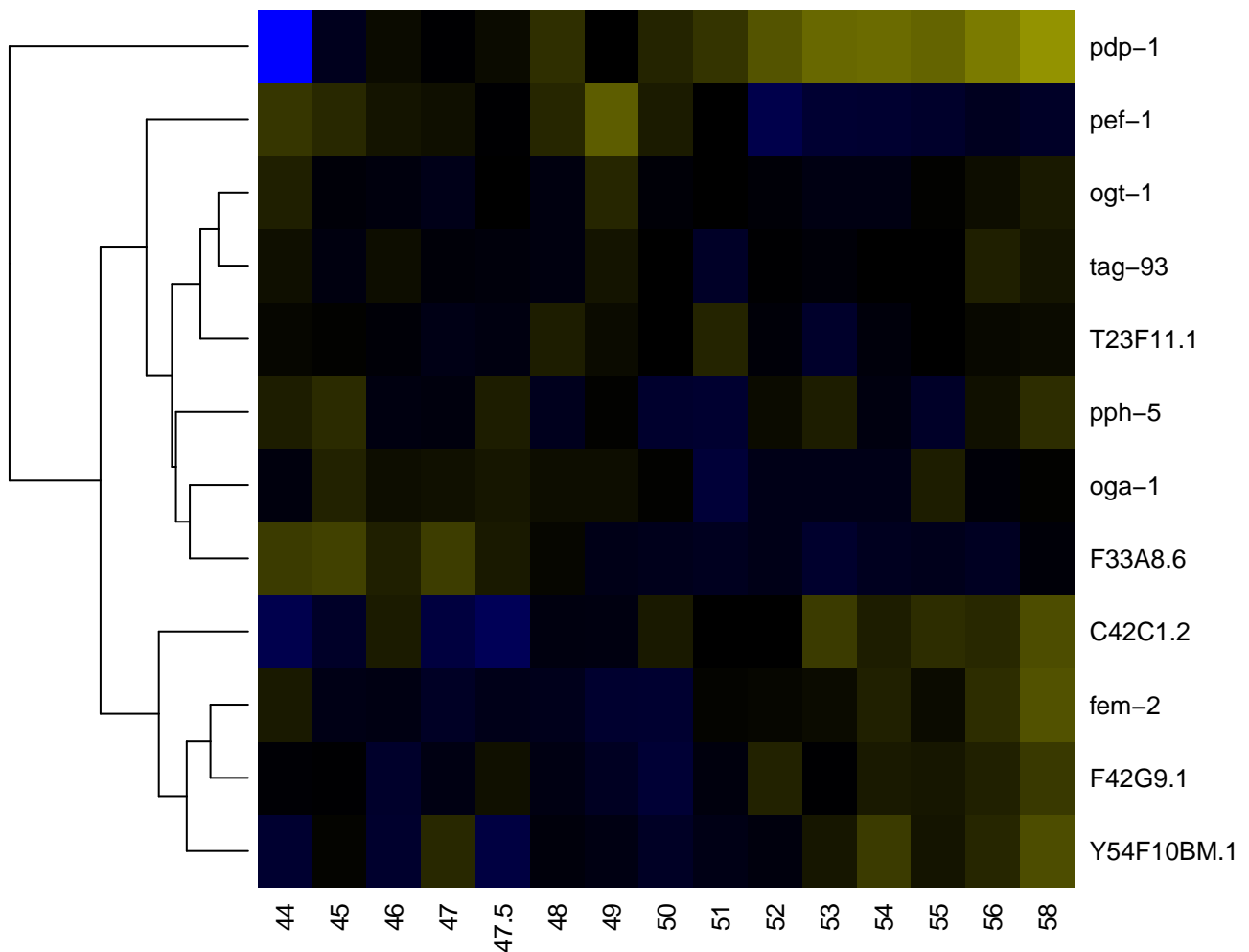
protein refolding



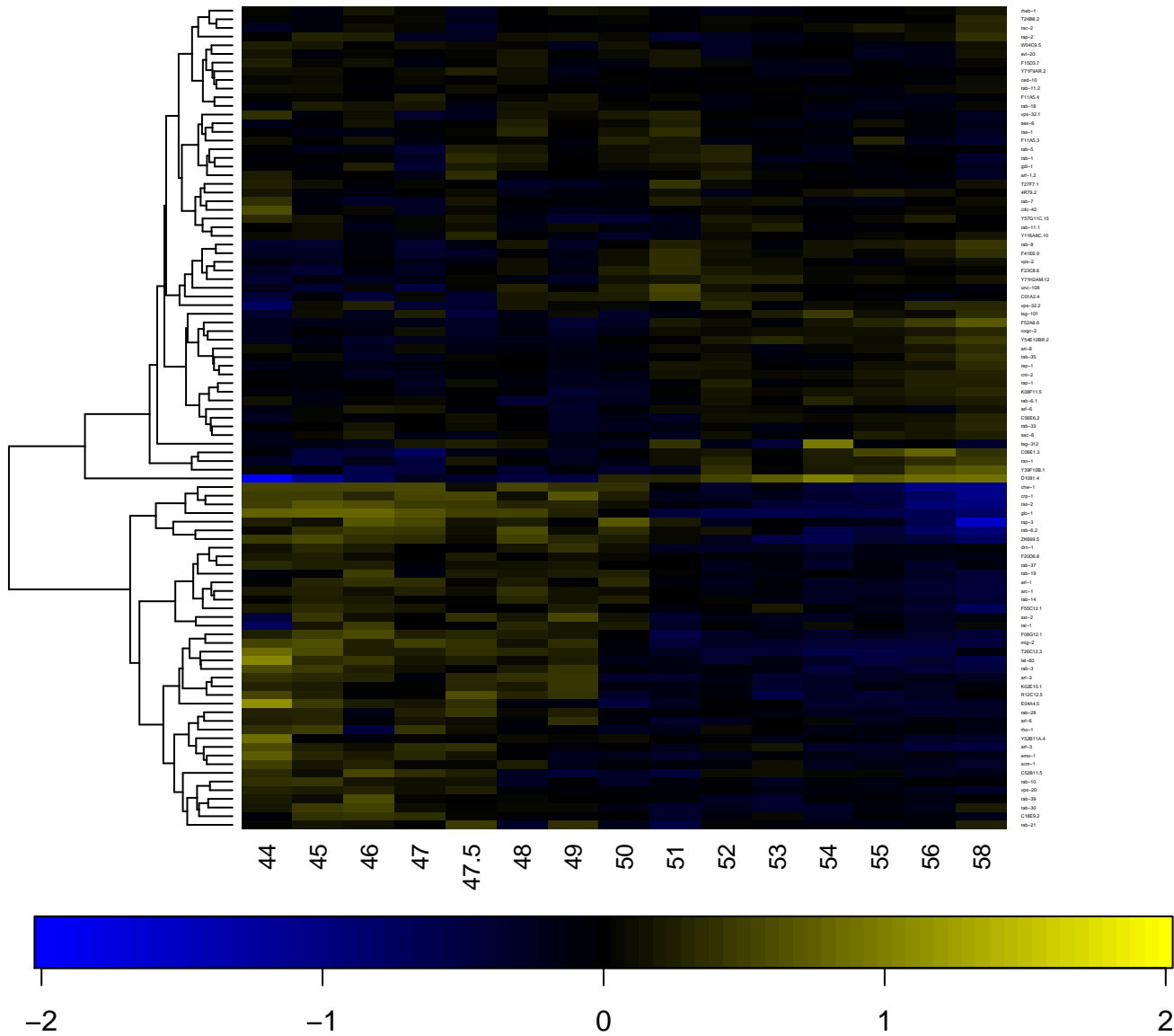
protein serine/threonine kinase activity



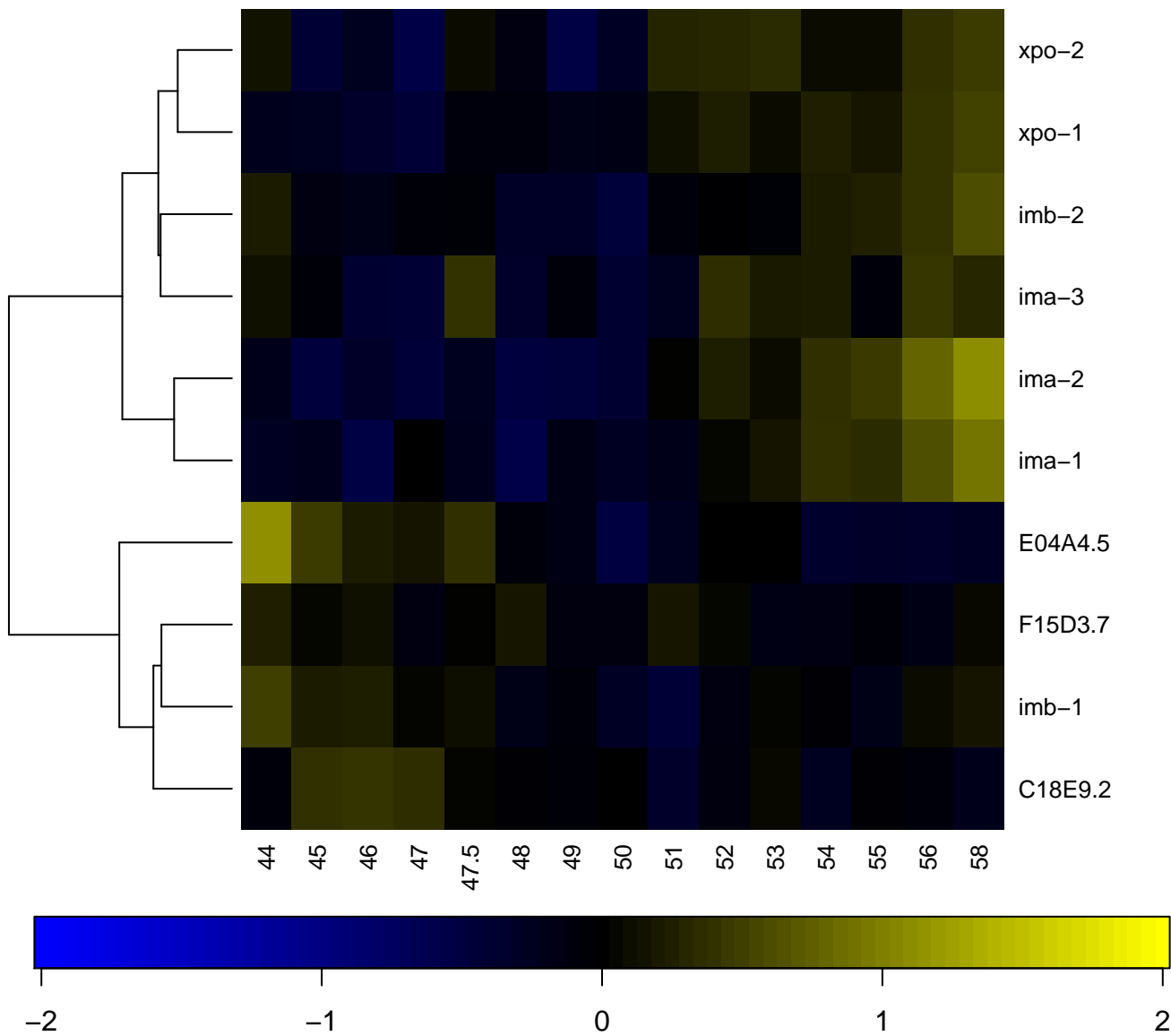
protein serine/threonine phosphatase activity



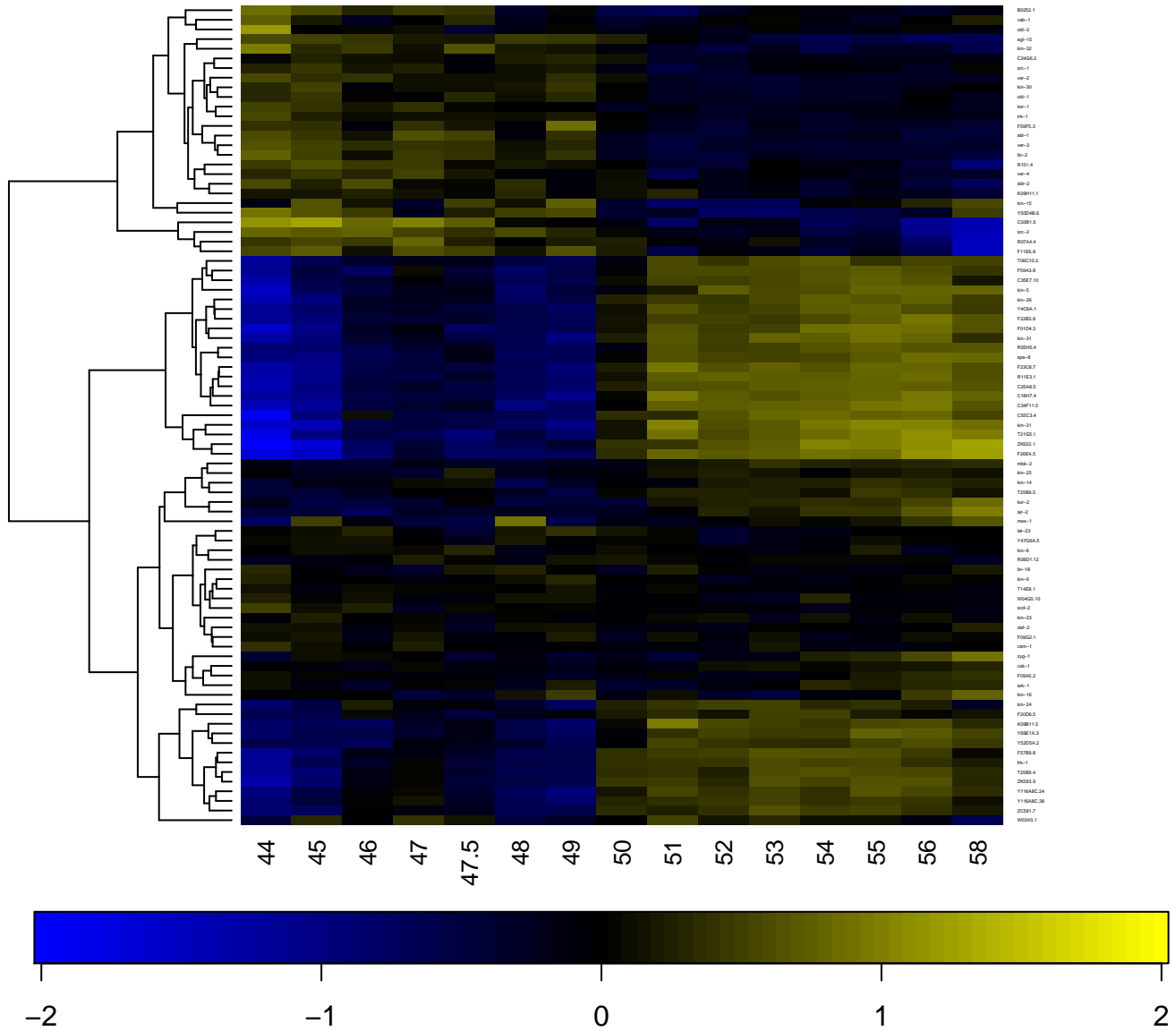
protein transport



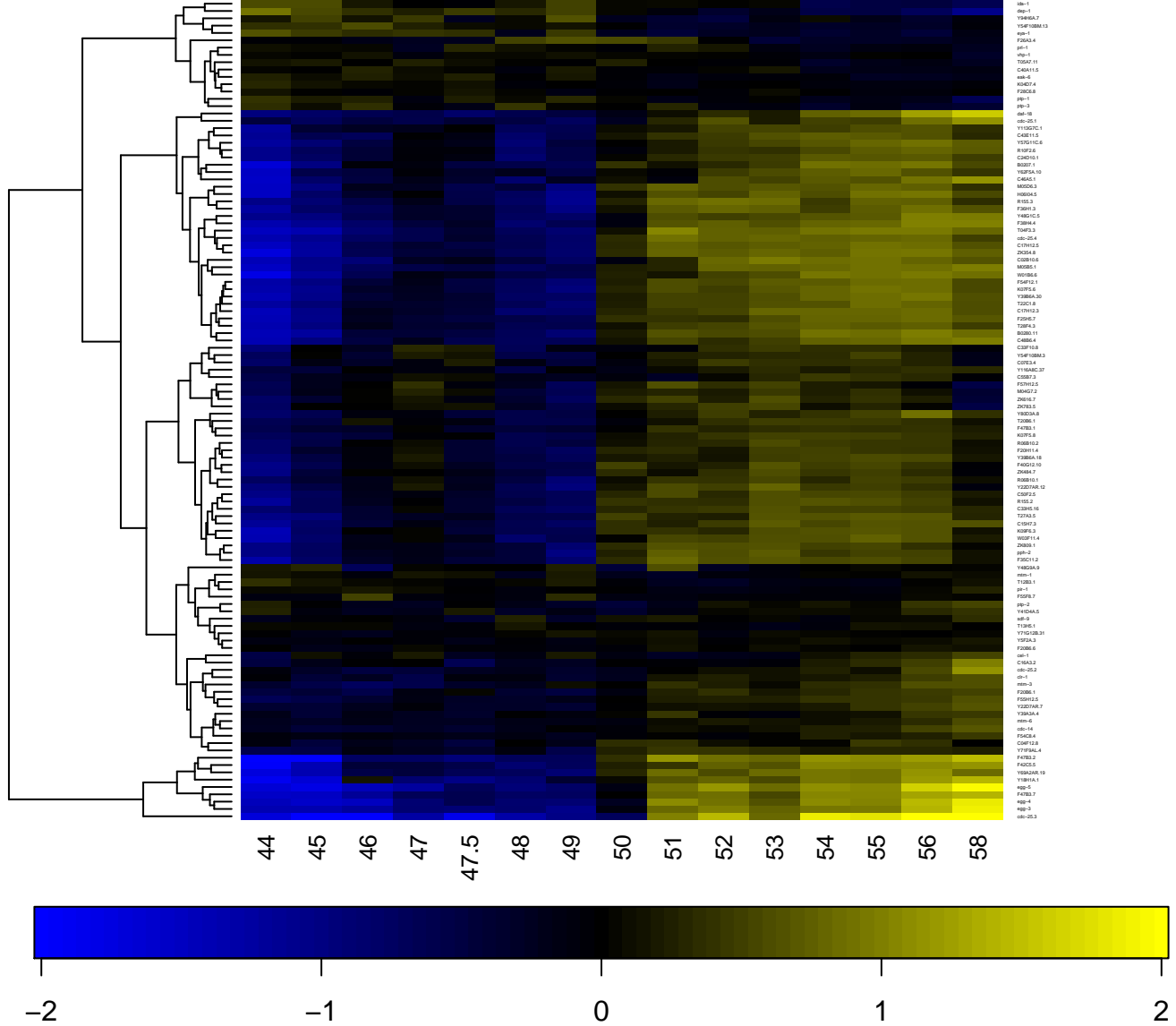
protein transporter activity



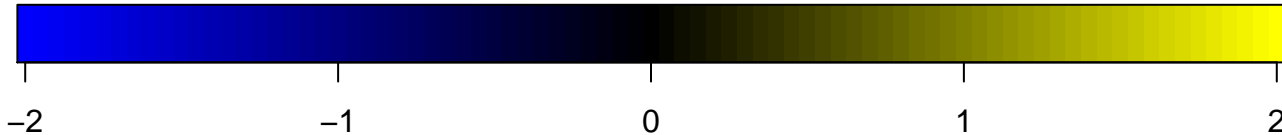
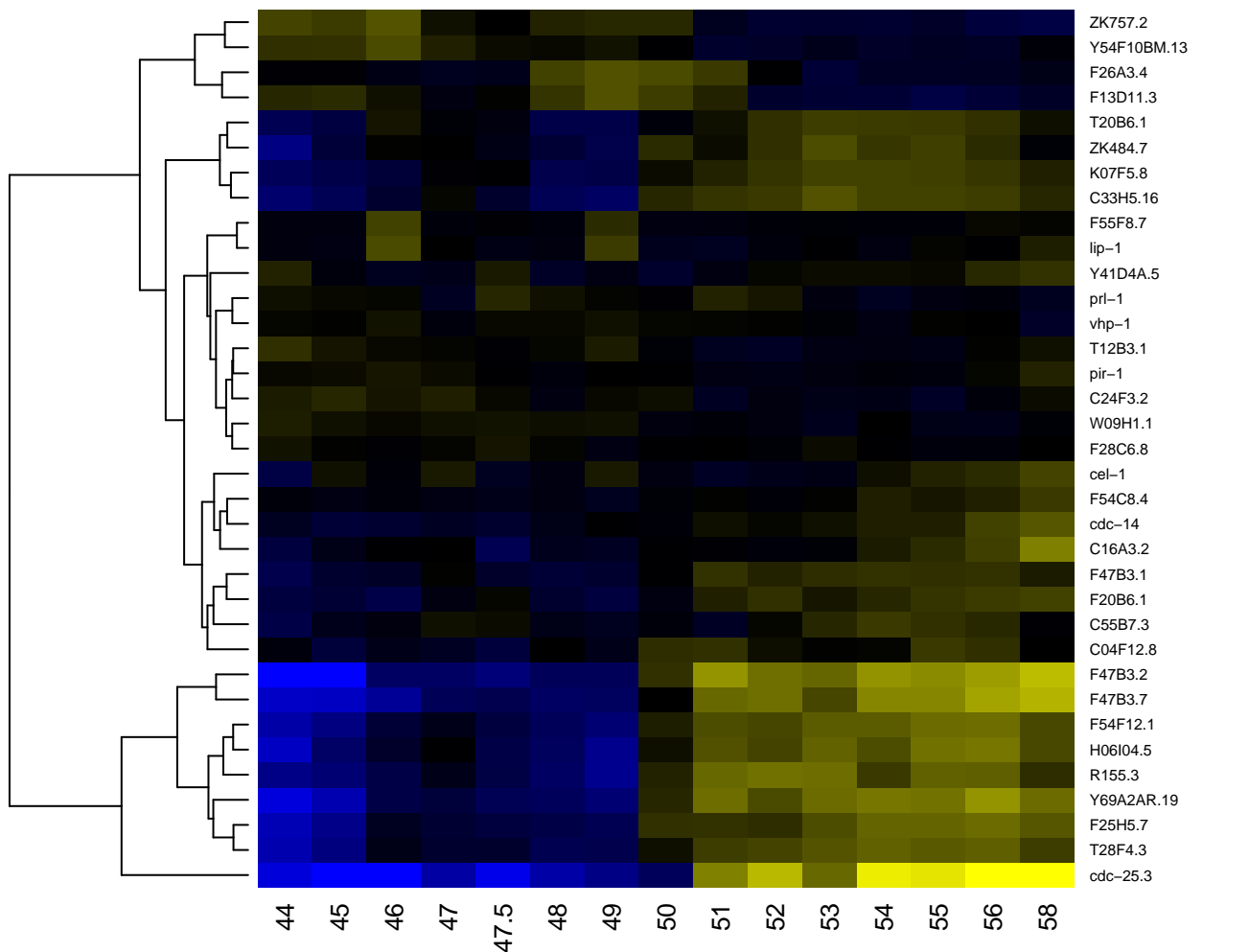
protein tyrosine kinase activity



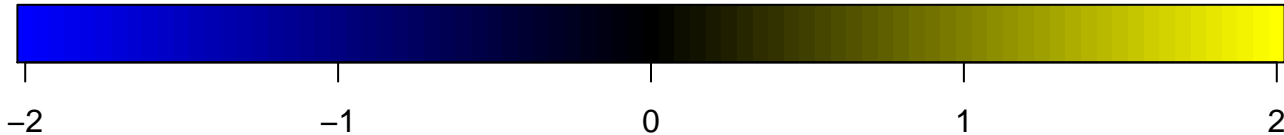
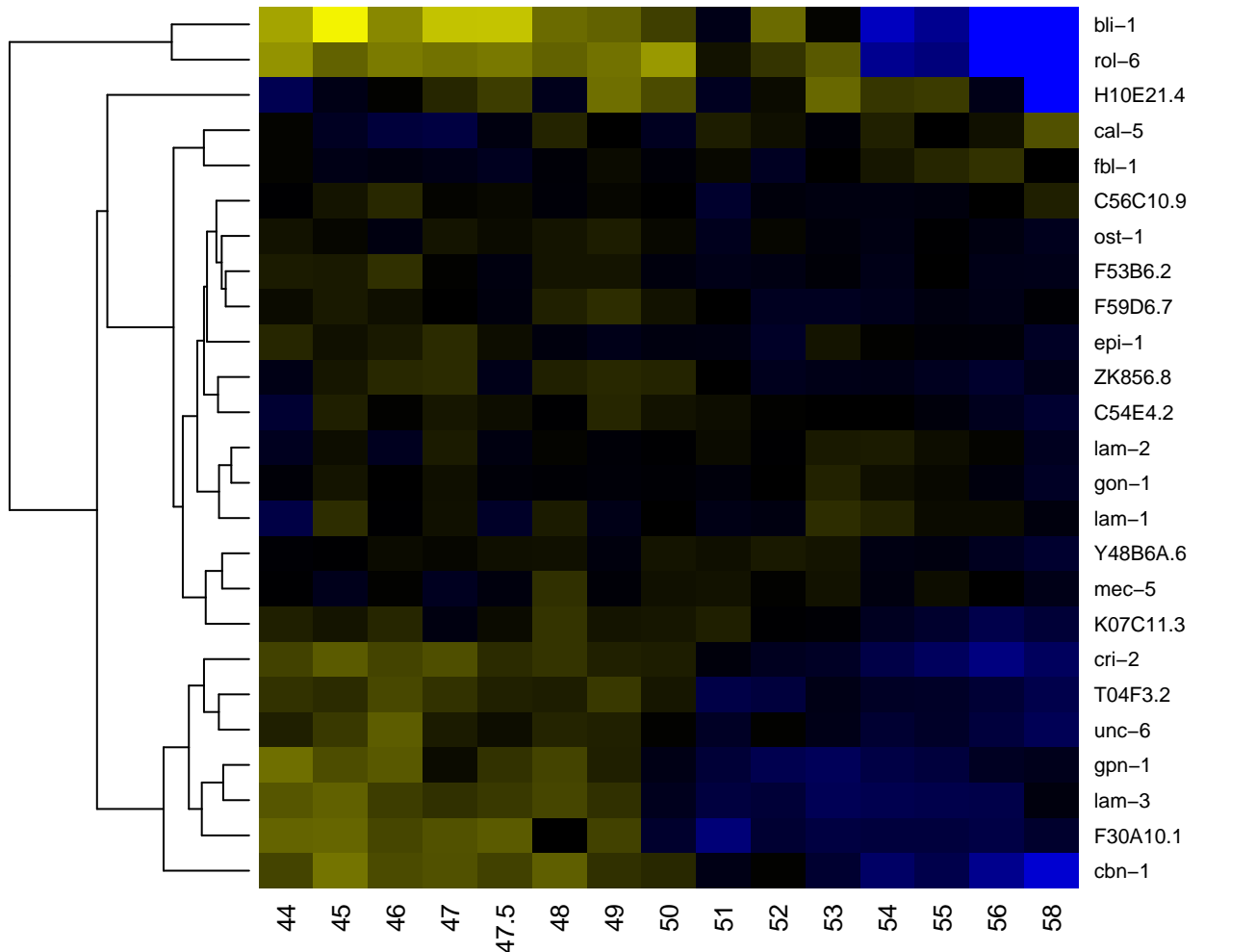
protein tyrosine phosphatase activity



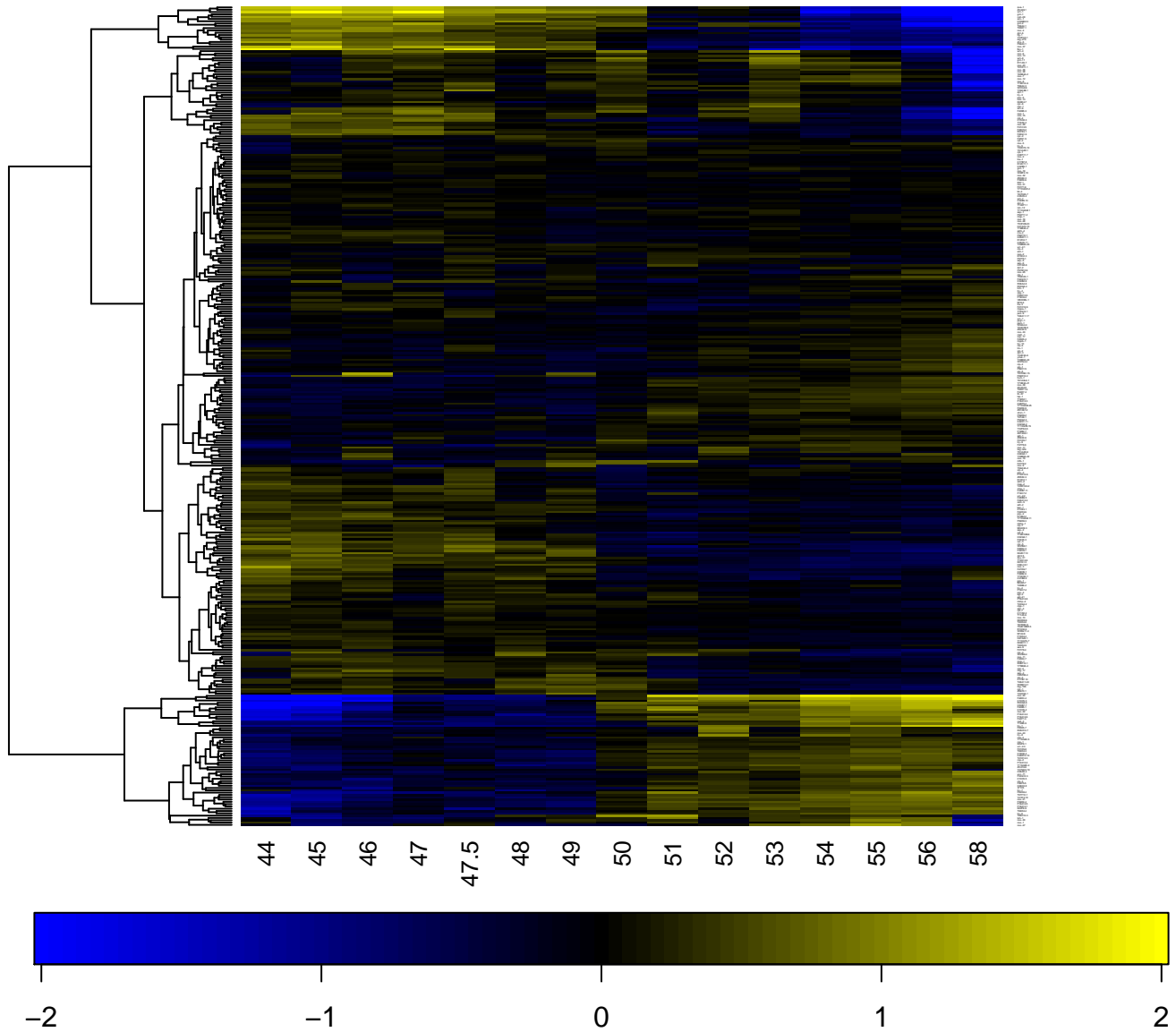
protein tyrosine/serine/threonine phosphatase activity



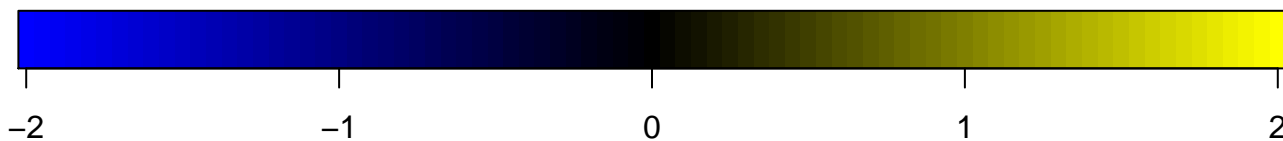
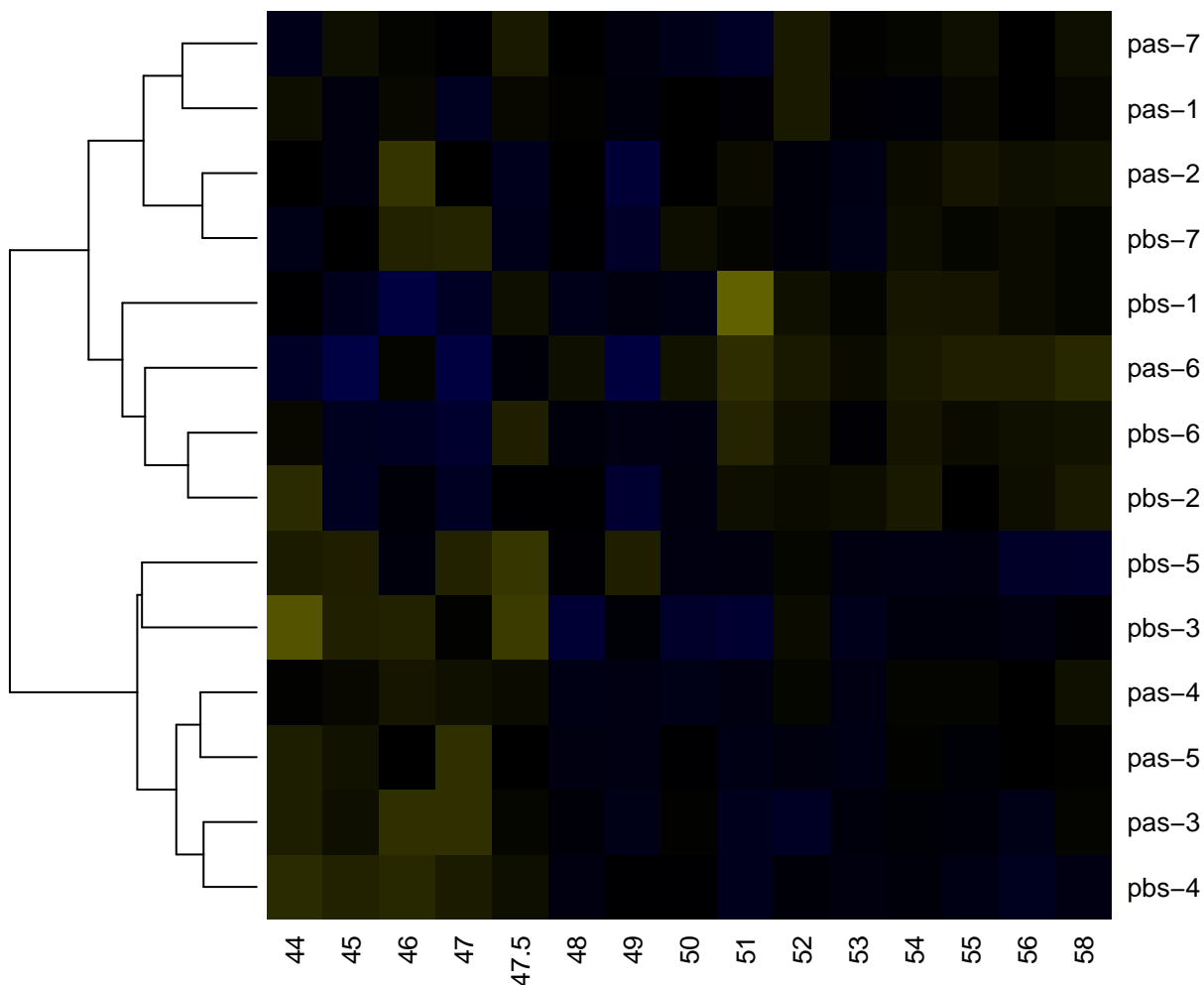
proteinaceous extracellular matrix



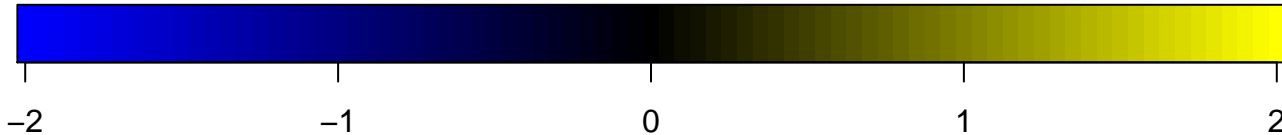
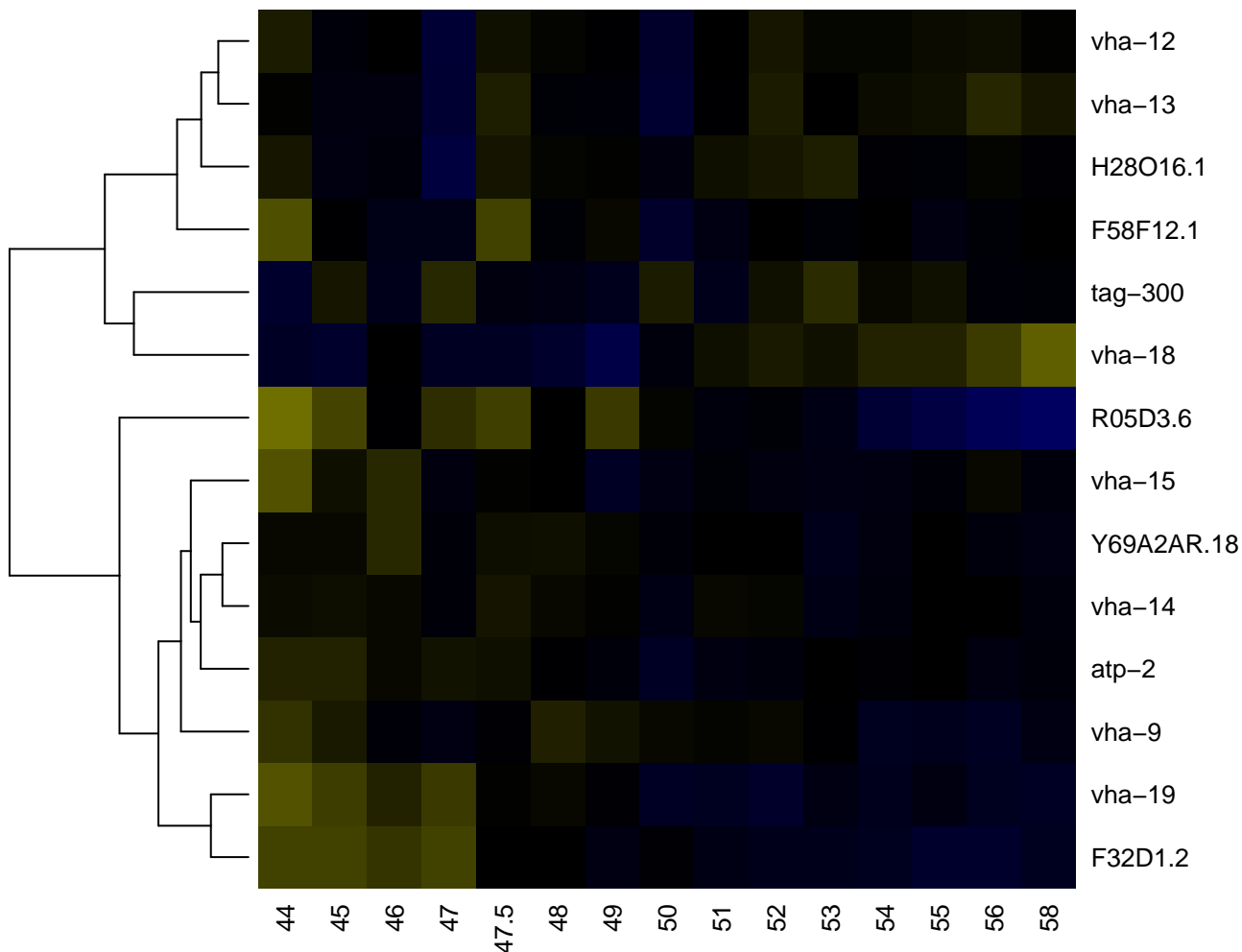
proteolysis



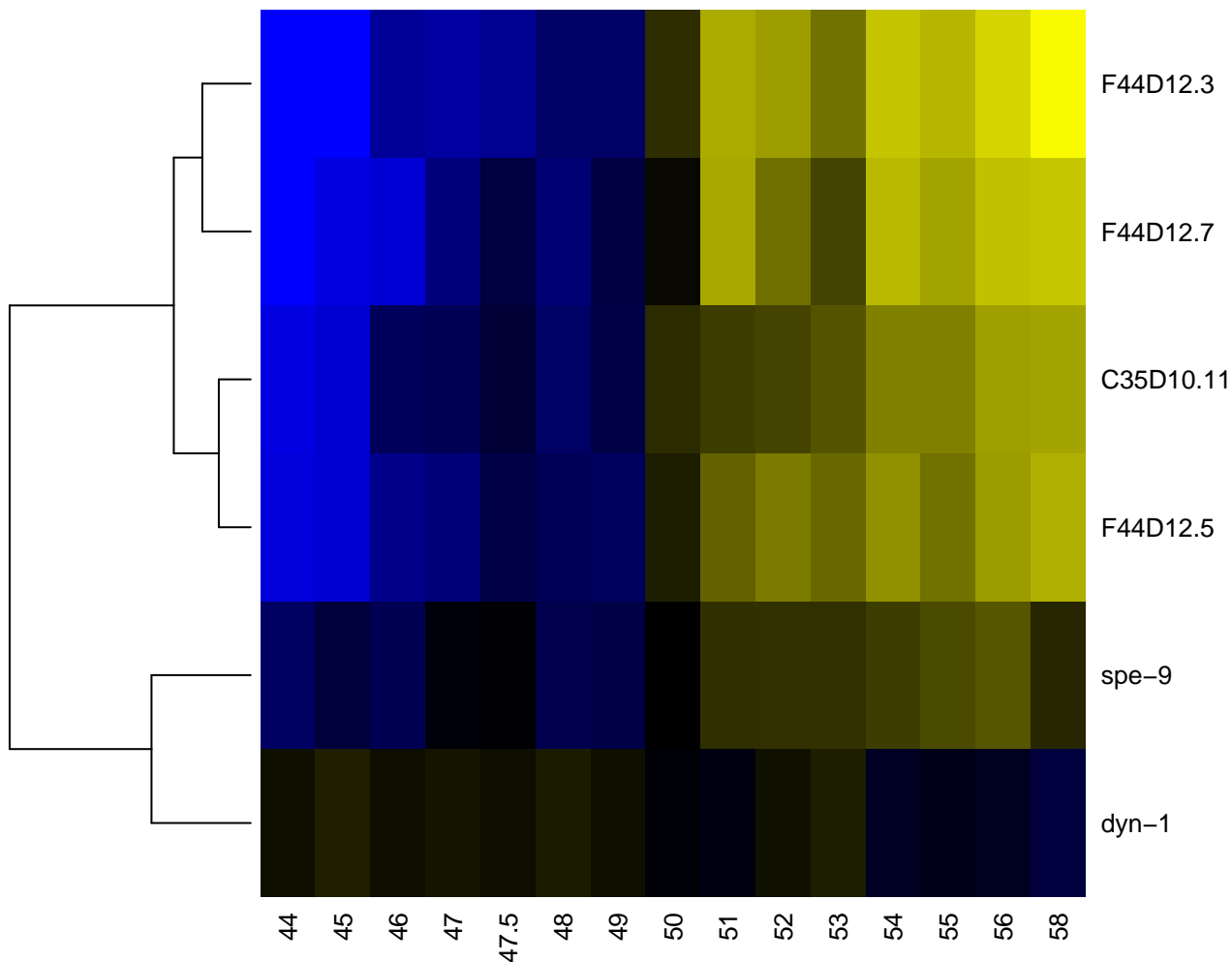
proteolysis involved in cellular protein catabolic process



proton-transporting ATPase activity, rotational mechanism



pseudopodium



-2

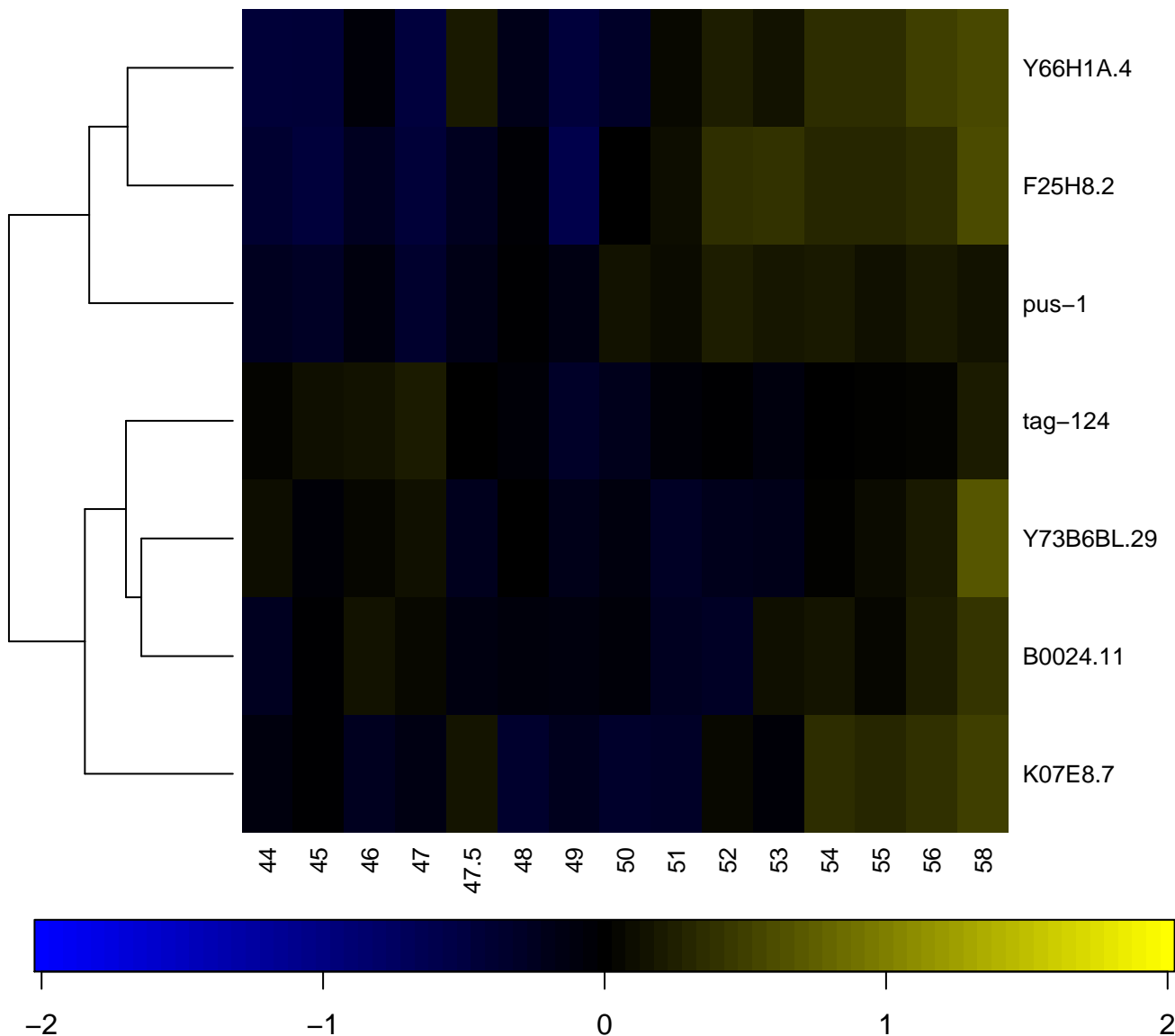
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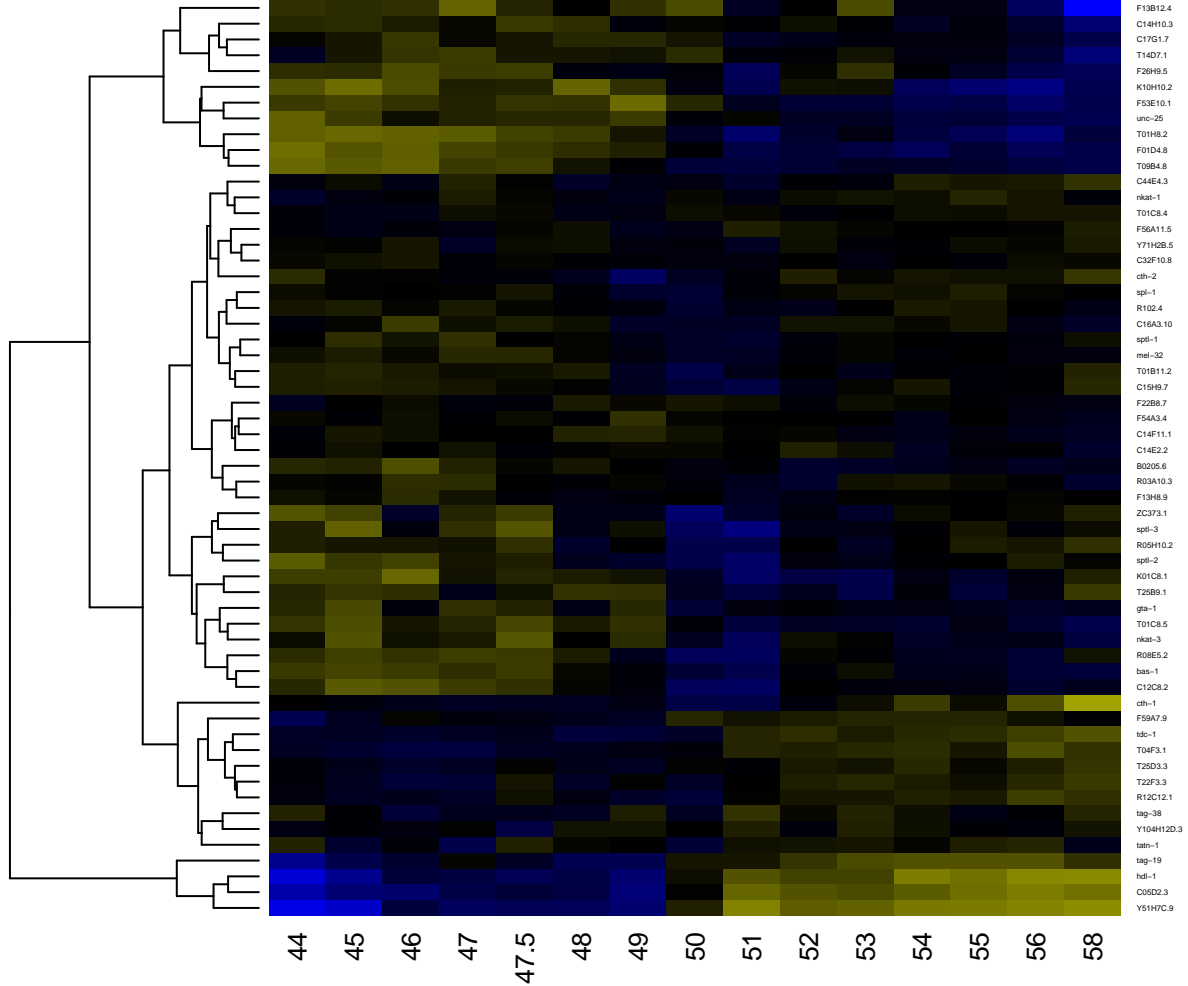
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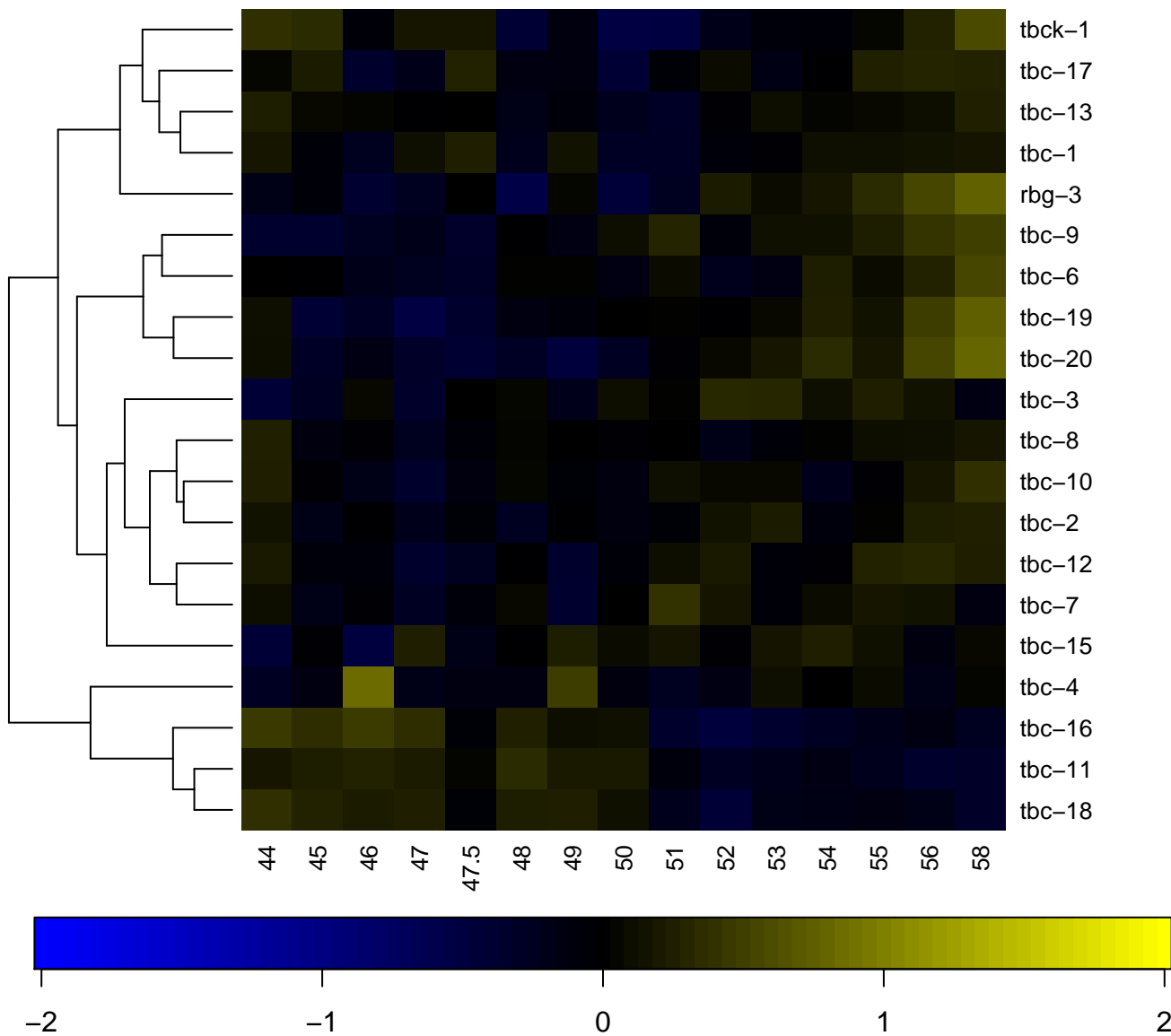
pseudouridine synthase activity



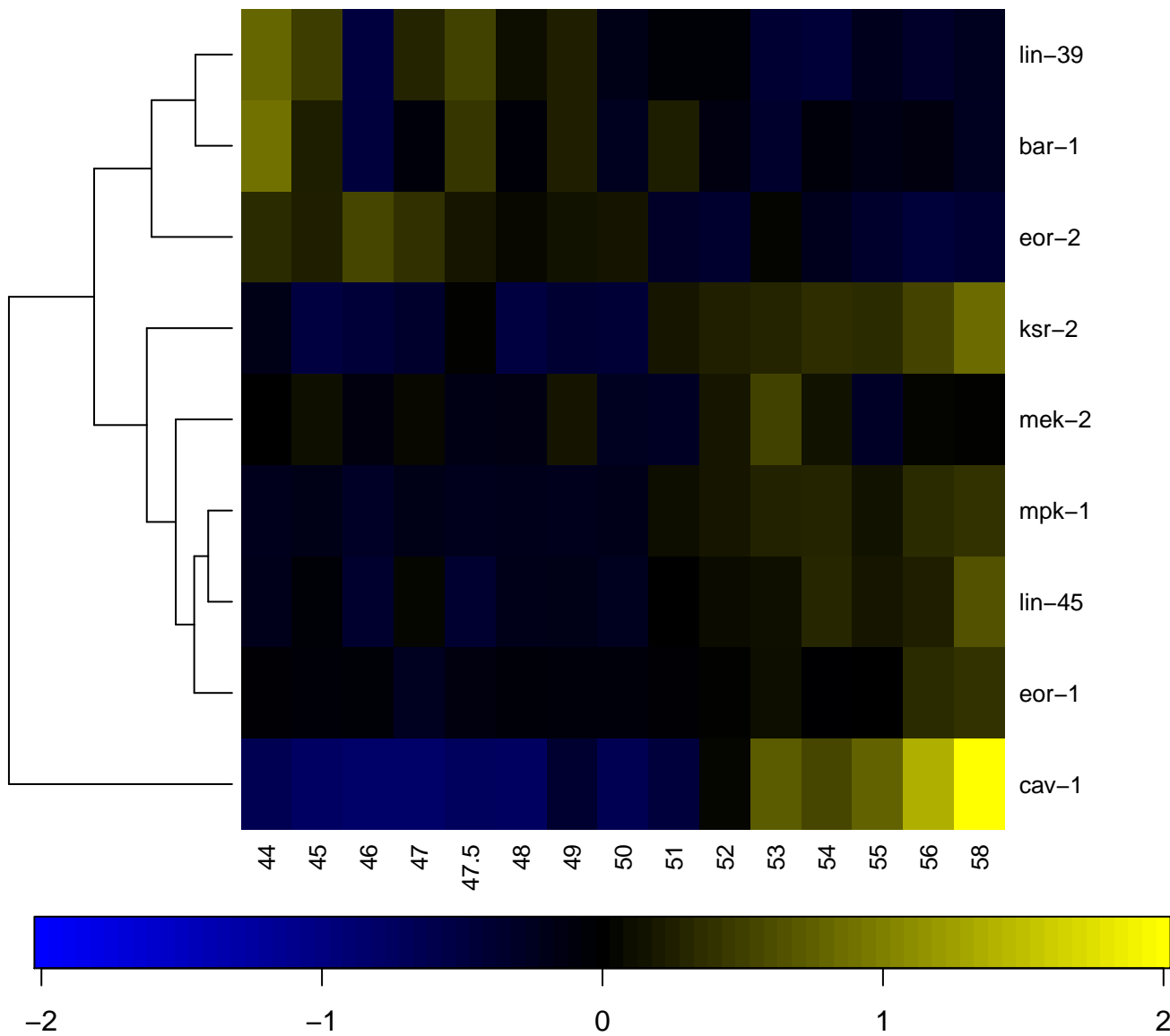
pyridoxal phosphate binding



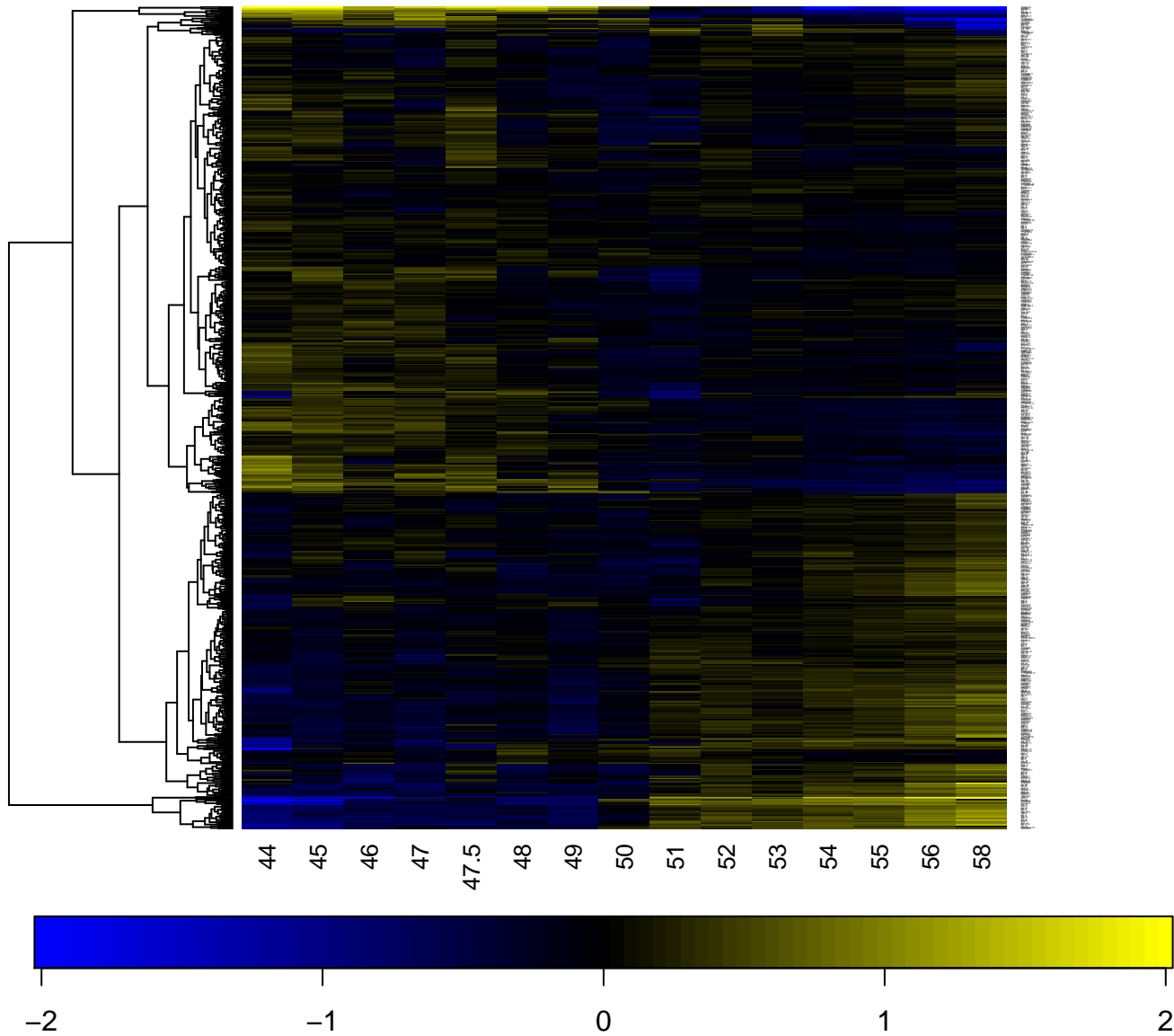
Rab GTPase activator activity



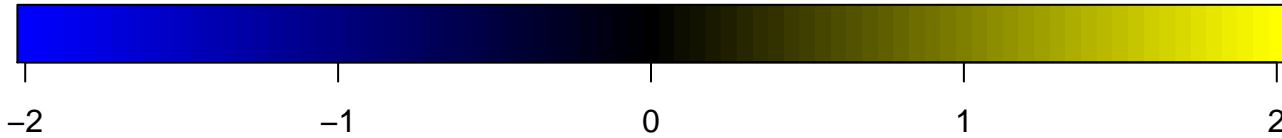
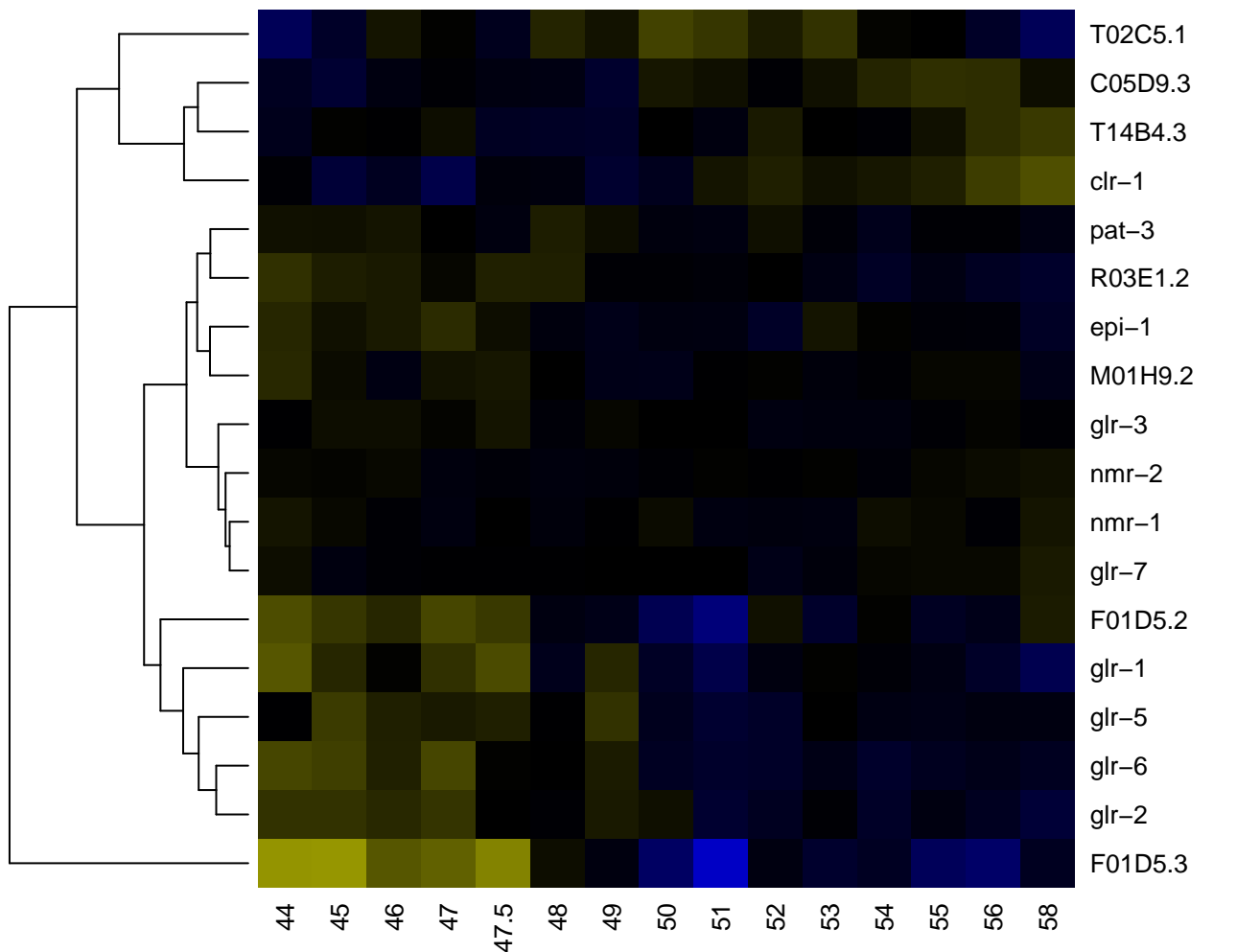
Ras protein signal transduction



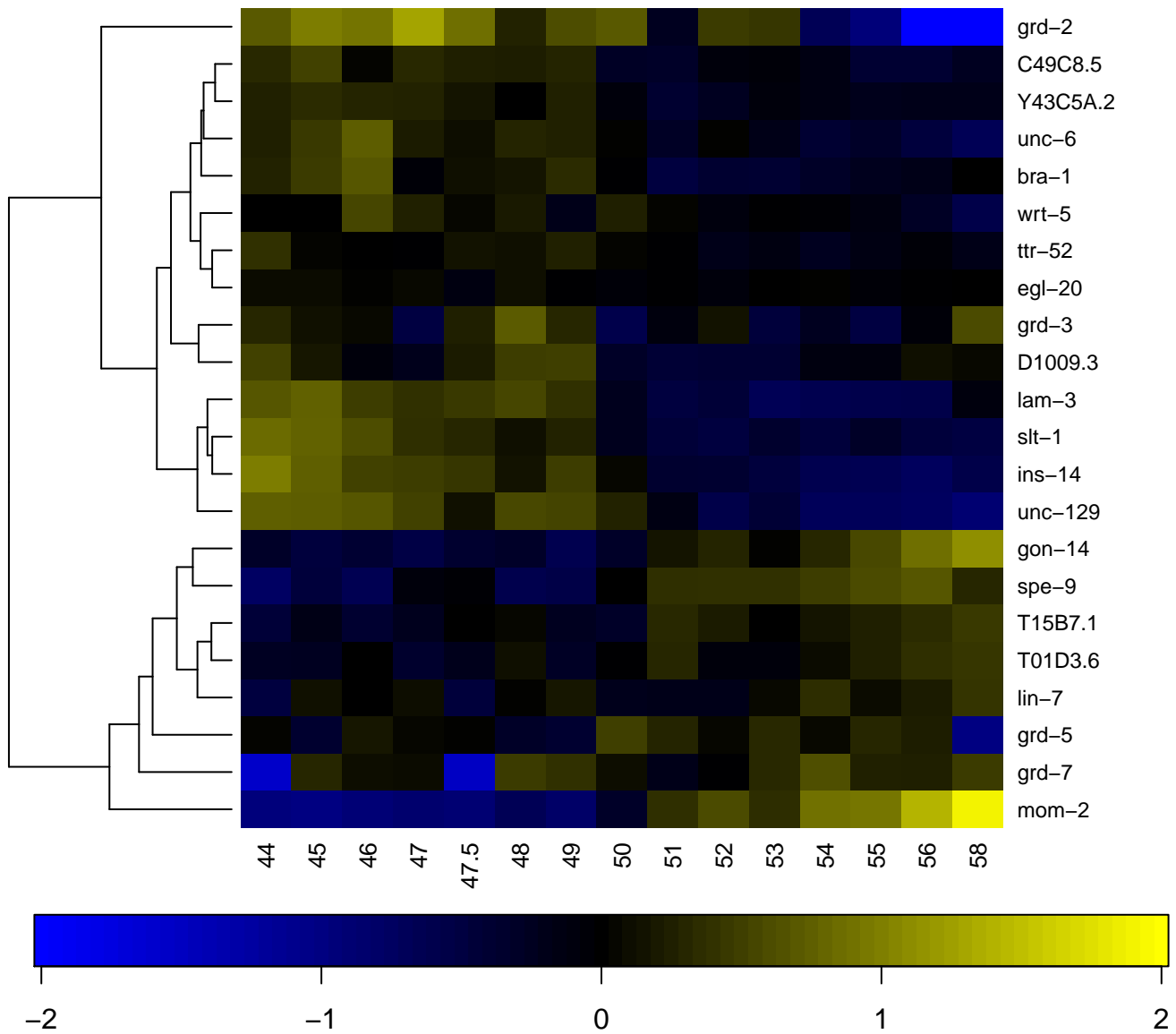
receptor-mediated endocytosis



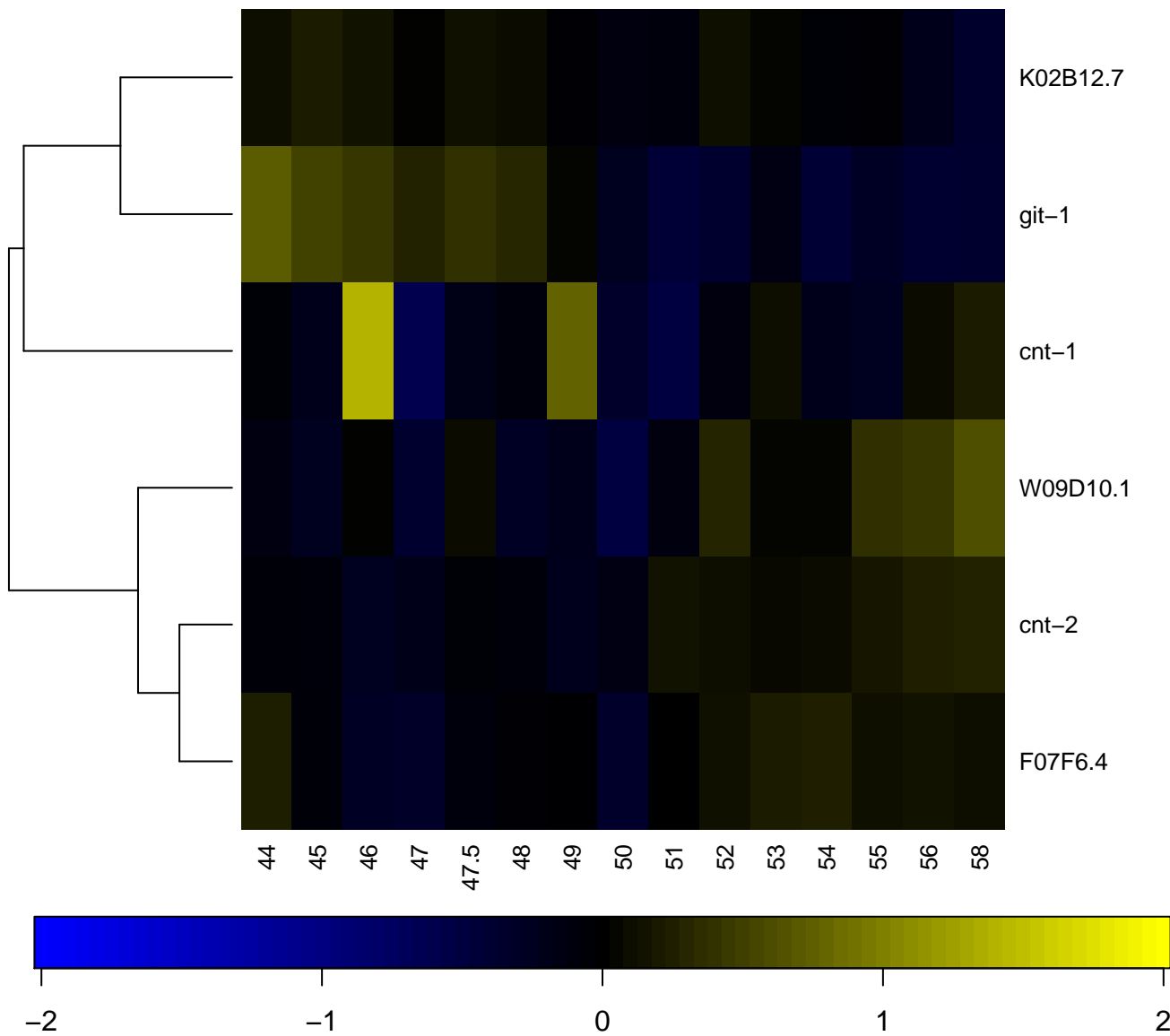
receptor activity



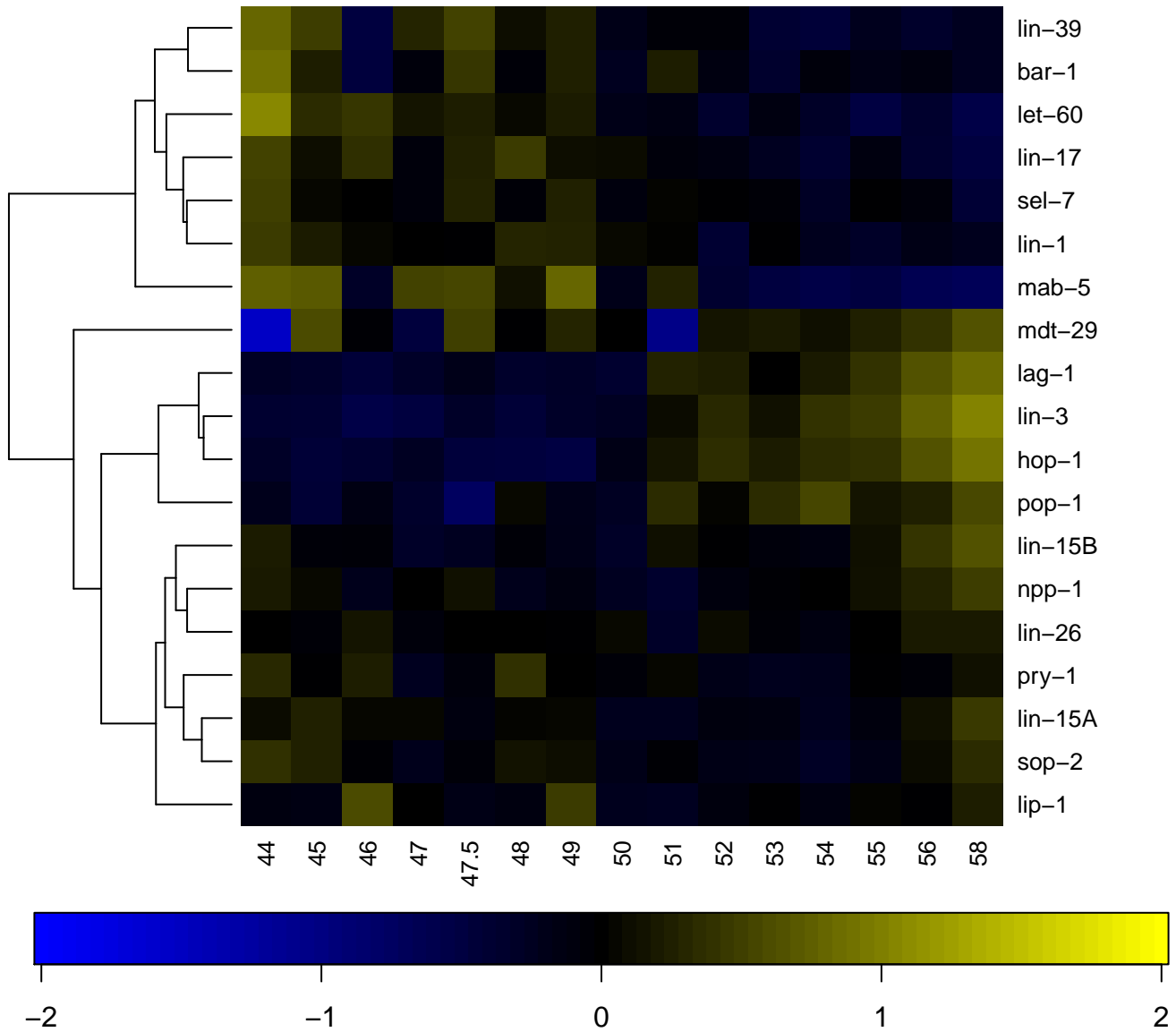
receptor binding



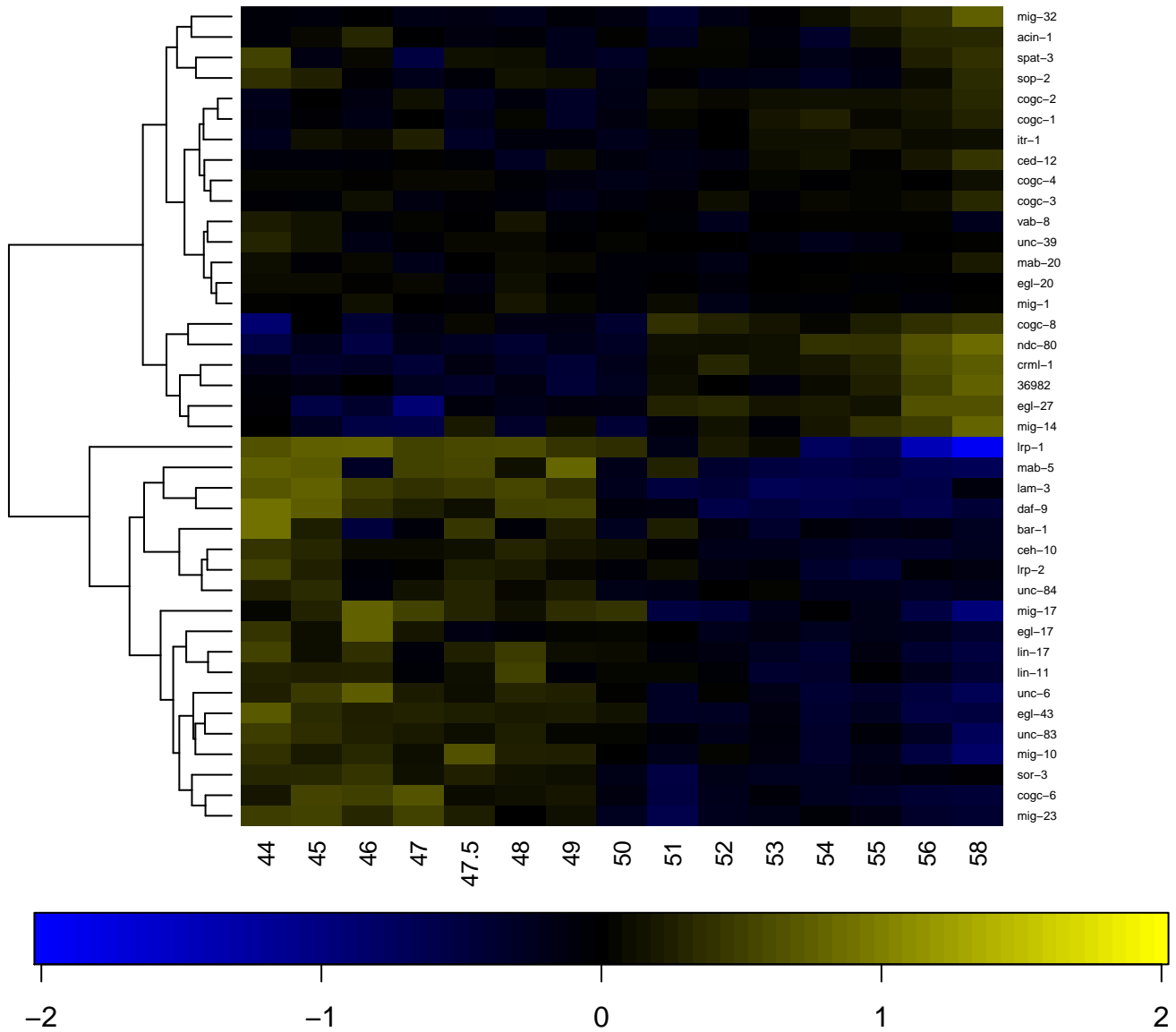
regulation of ARF GTPase activity



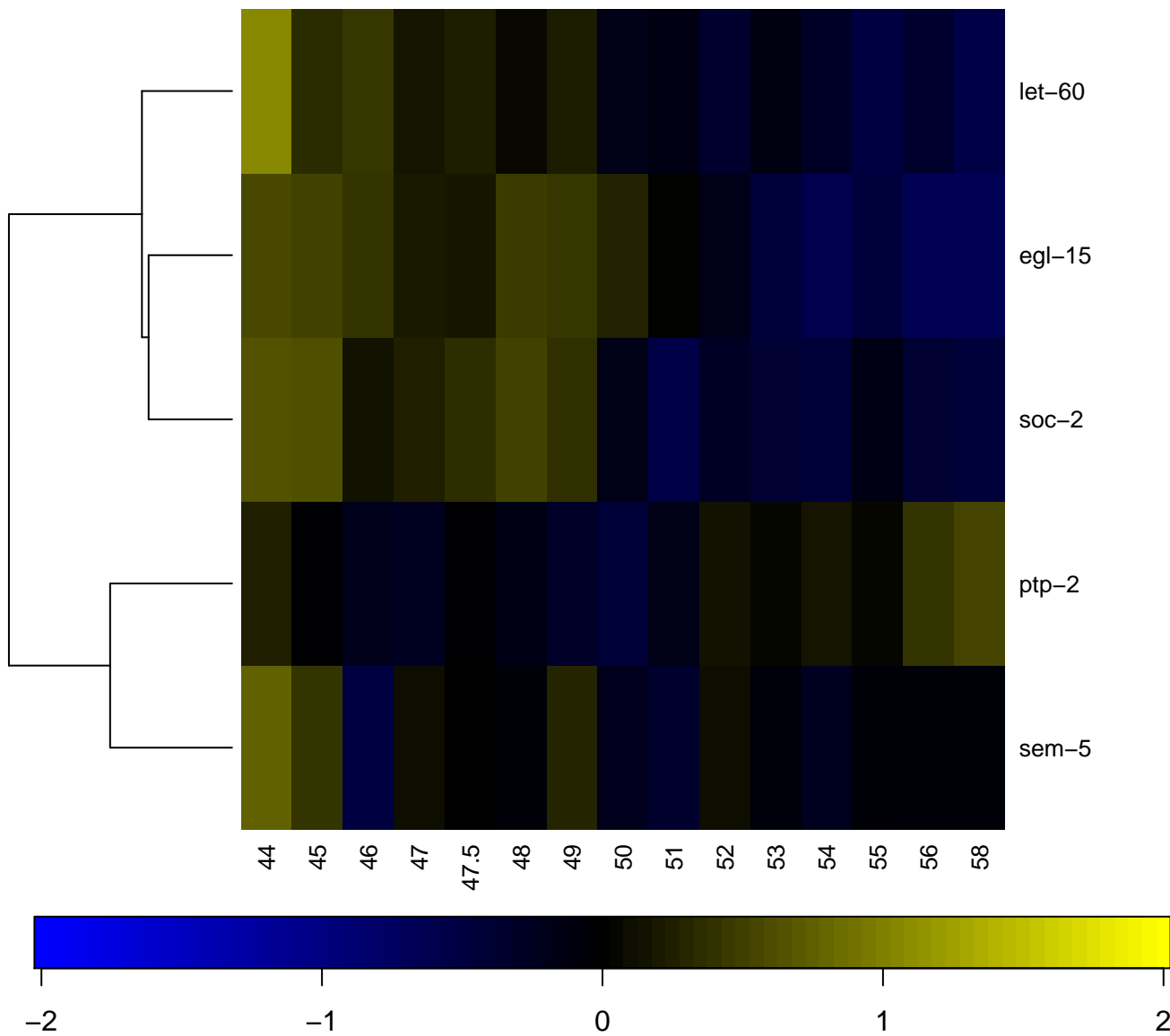
regulation of cell fate specification



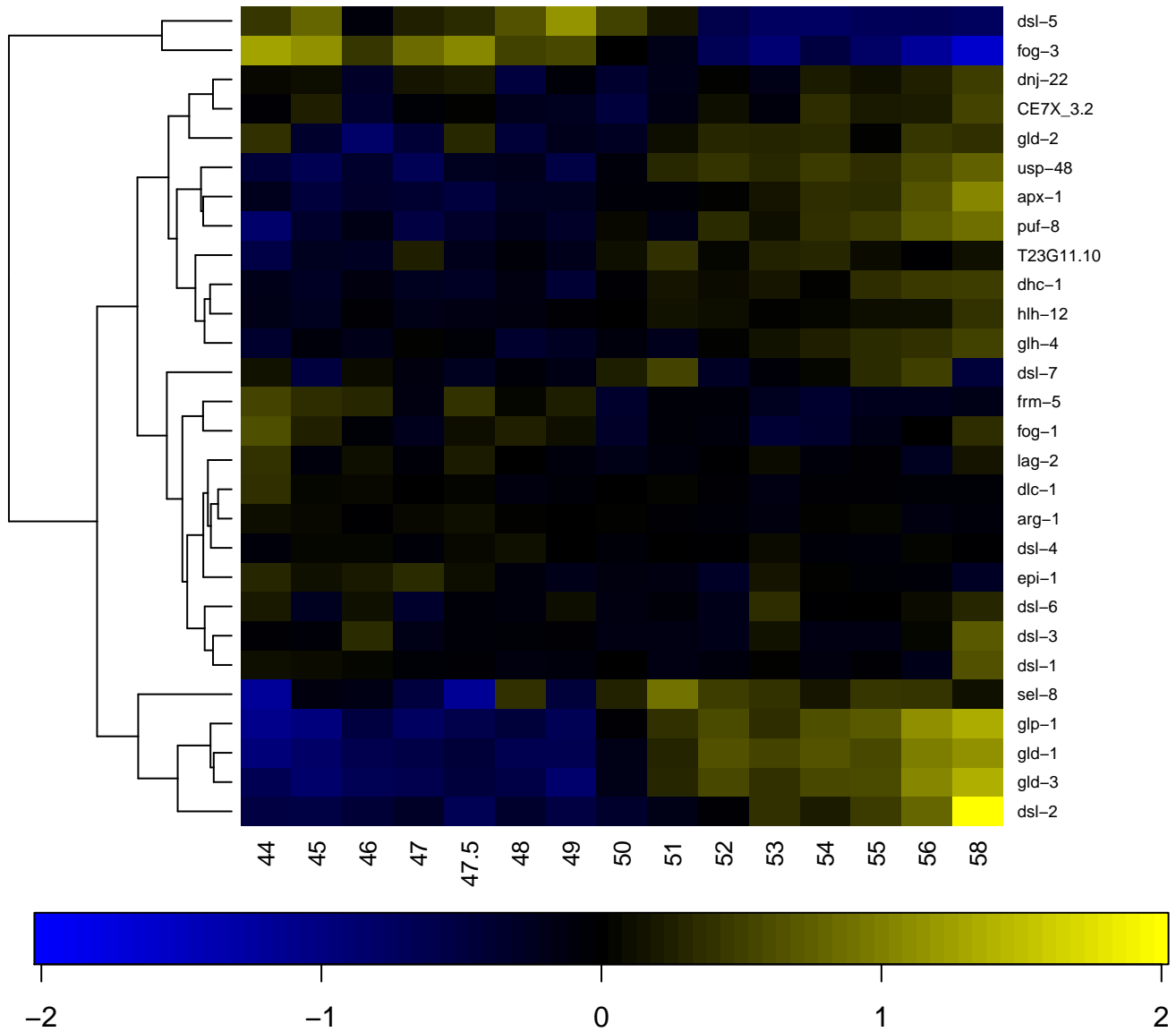
regulation of cell migration



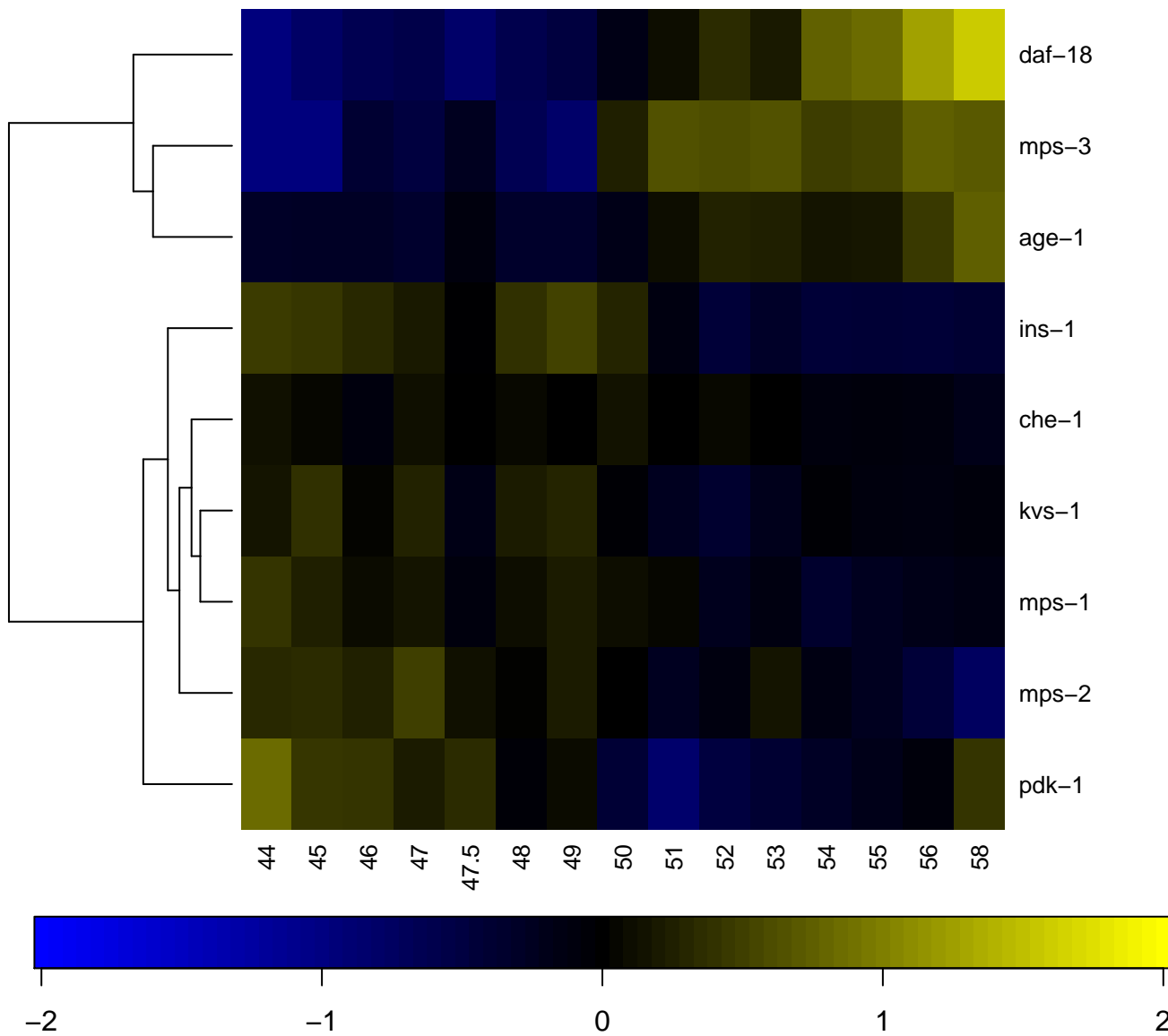
regulation of cell projection organization



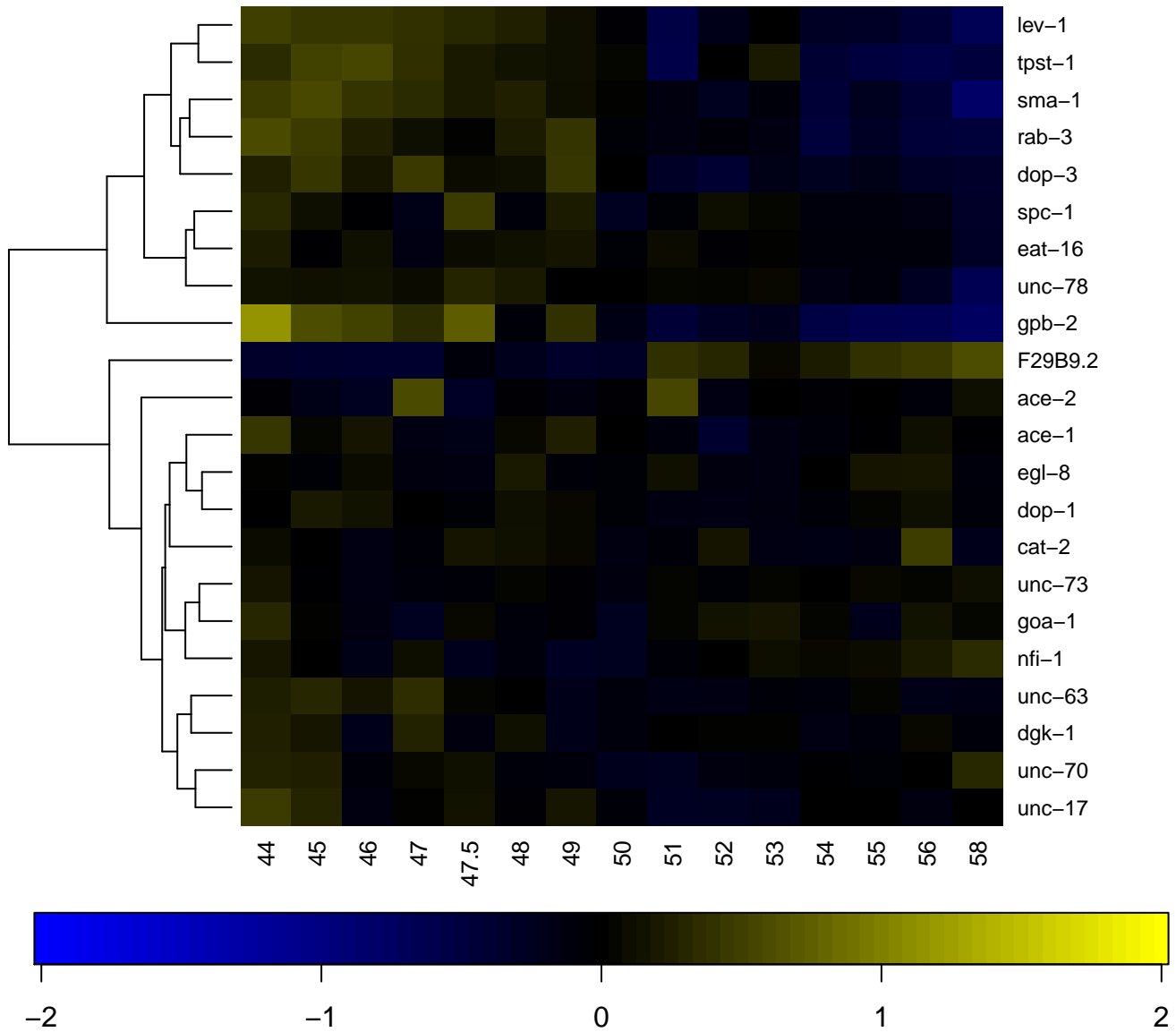
regulation of cell proliferation



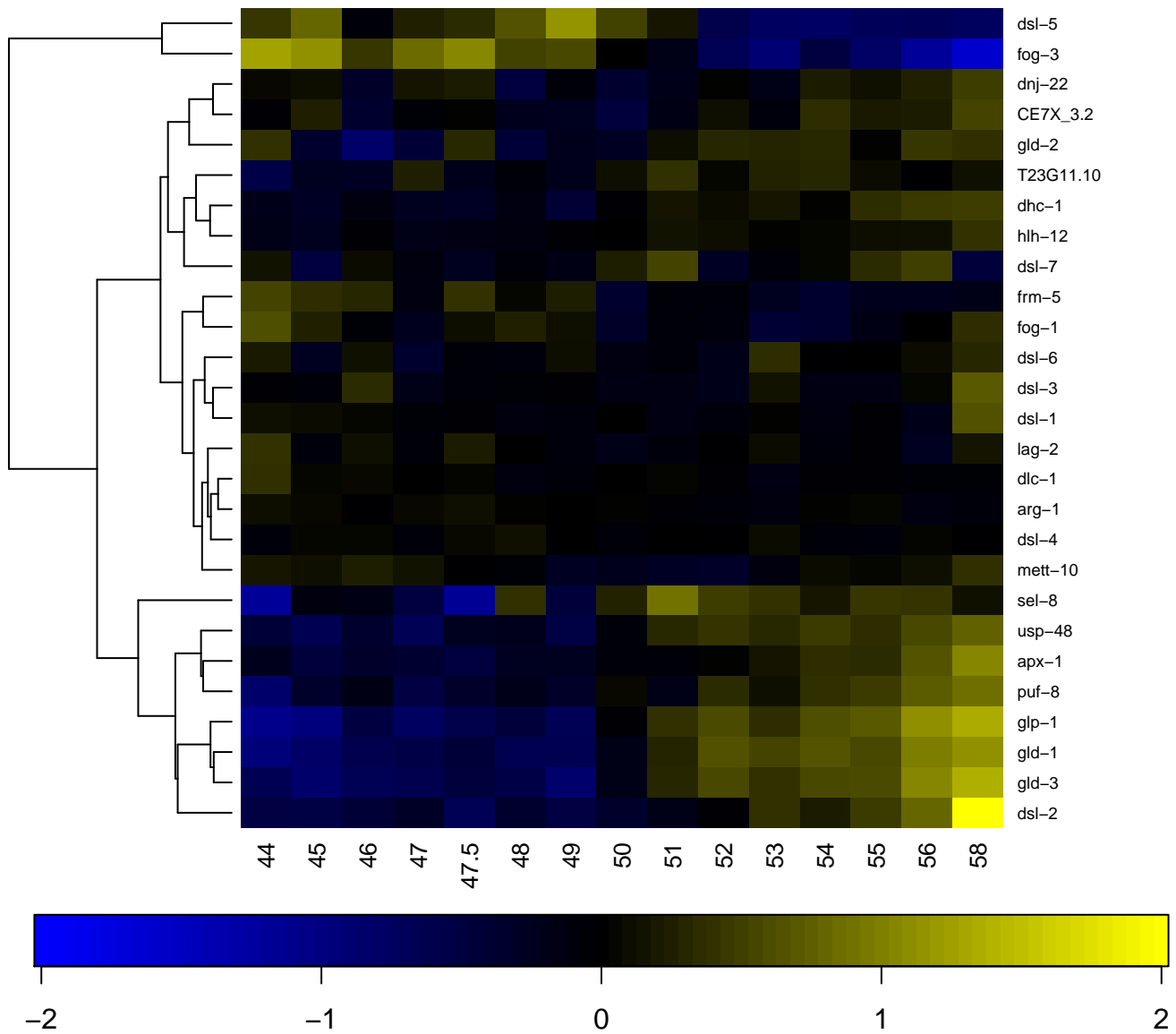
regulation of chemotaxis



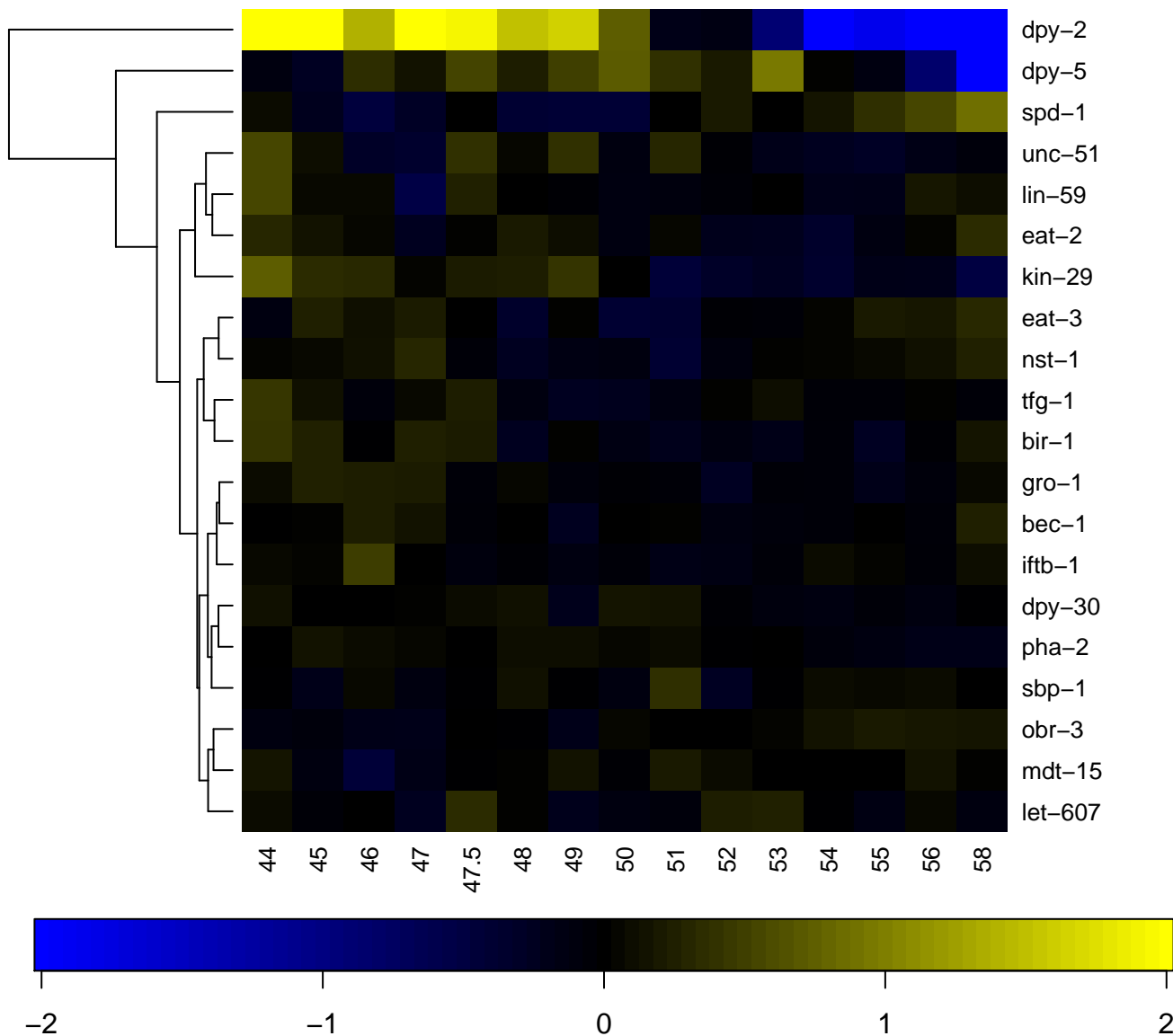
regulation of locomotion



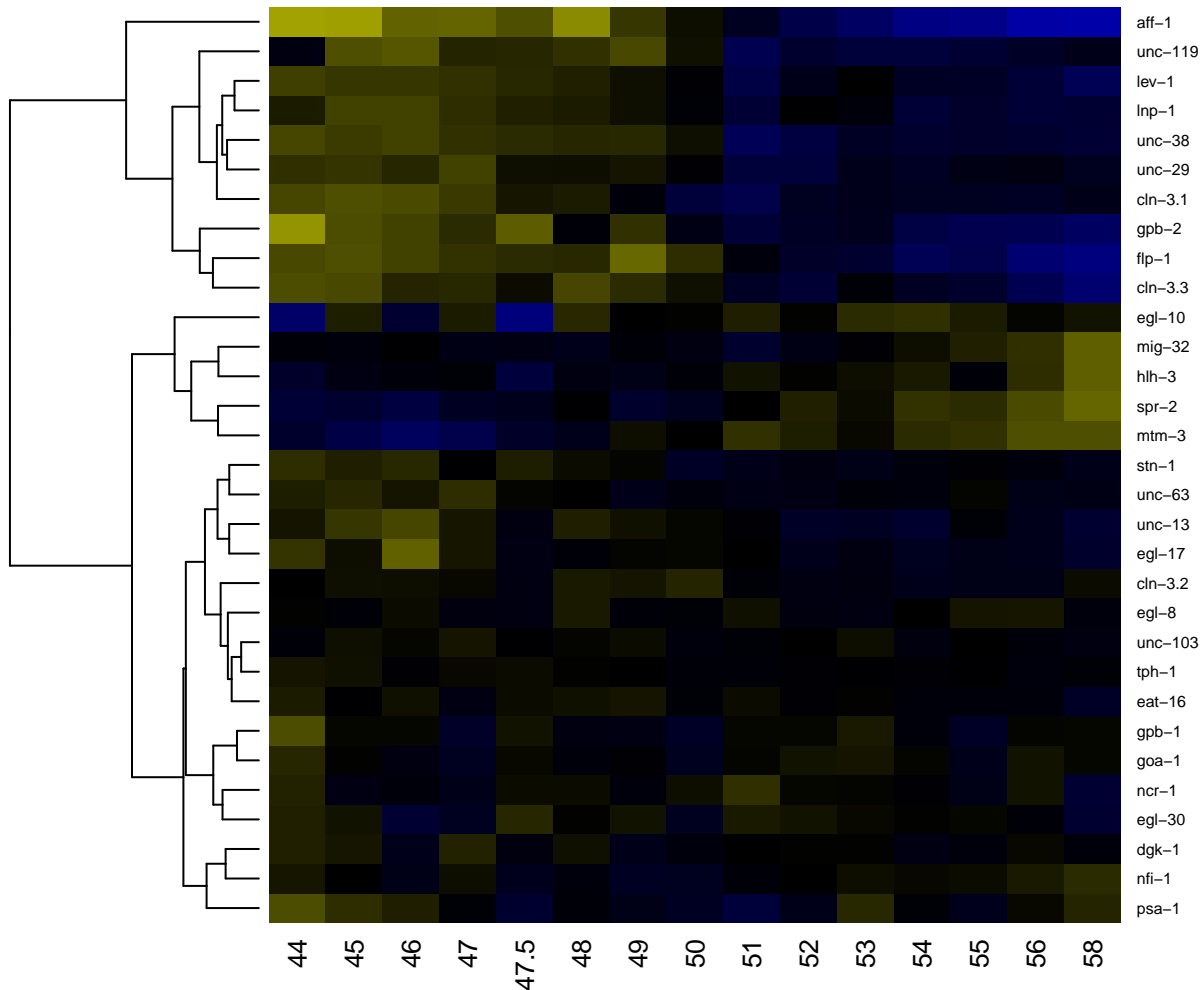
regulation of meiosis



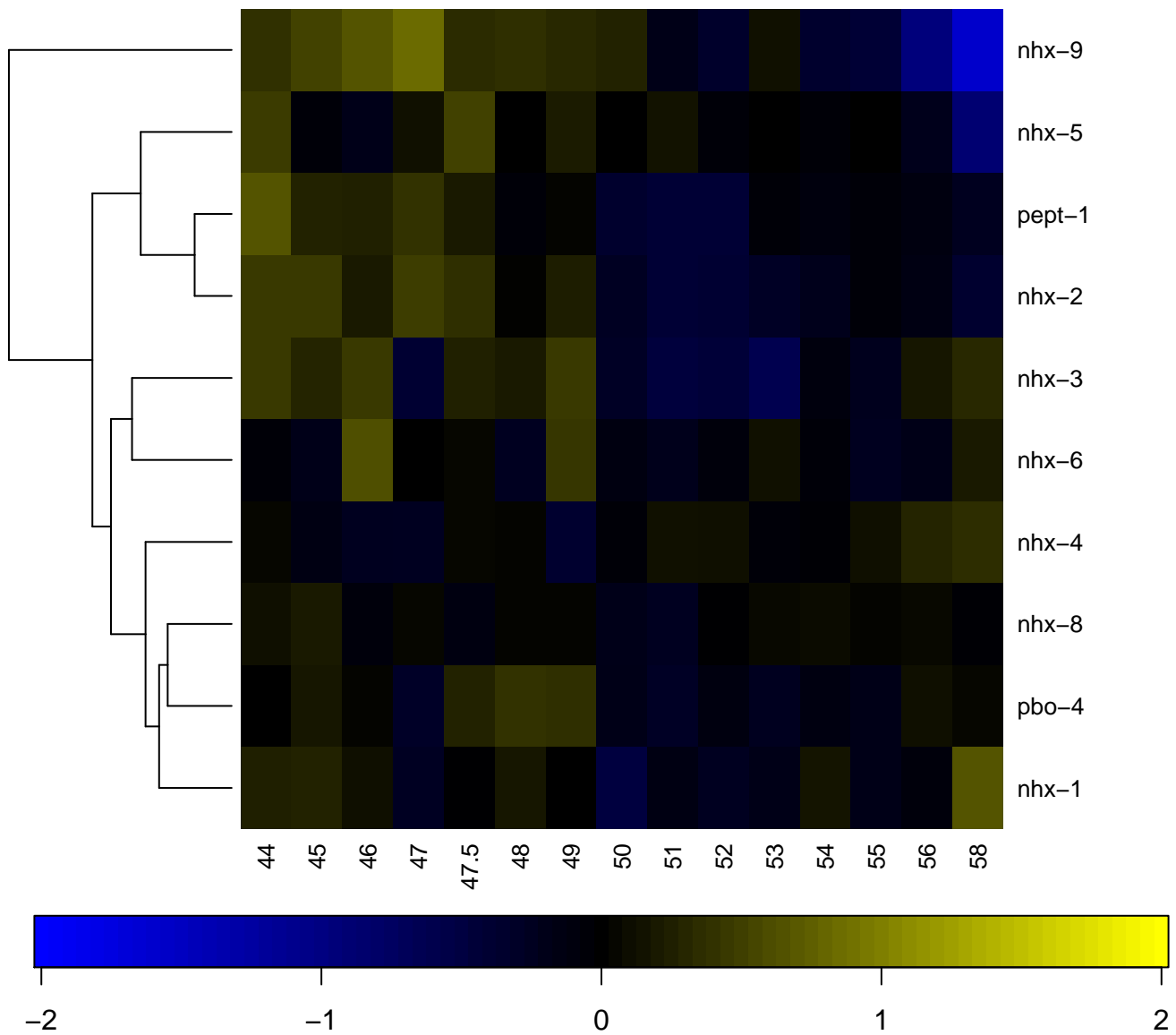
regulation of multicellular organism growth



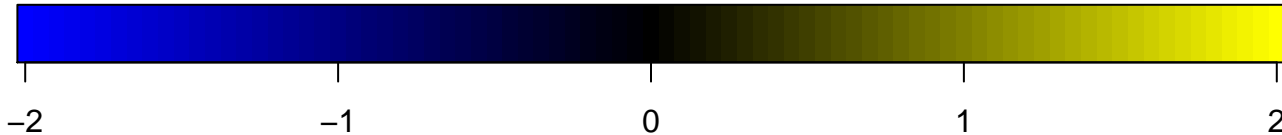
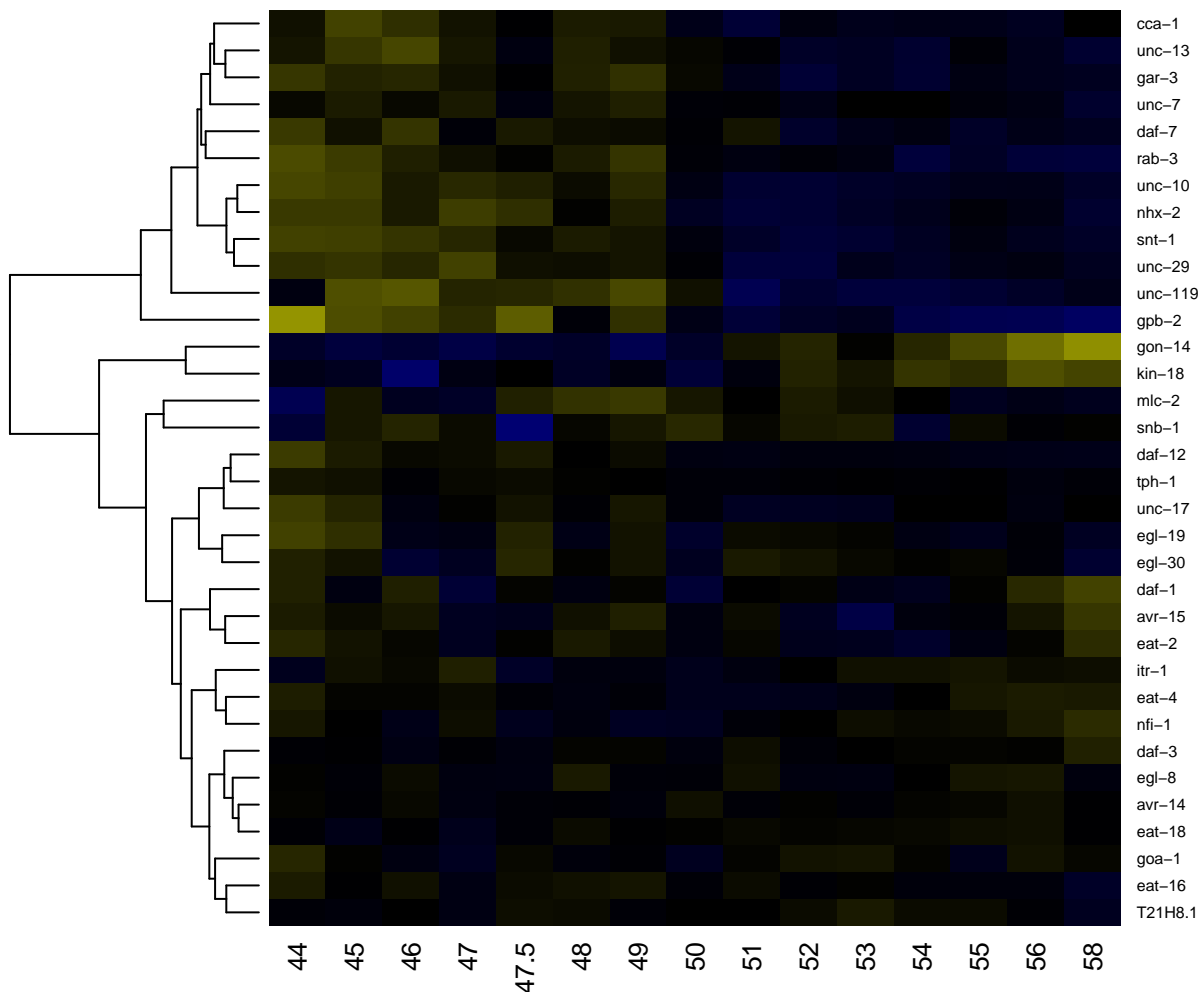
regulation of oviposition



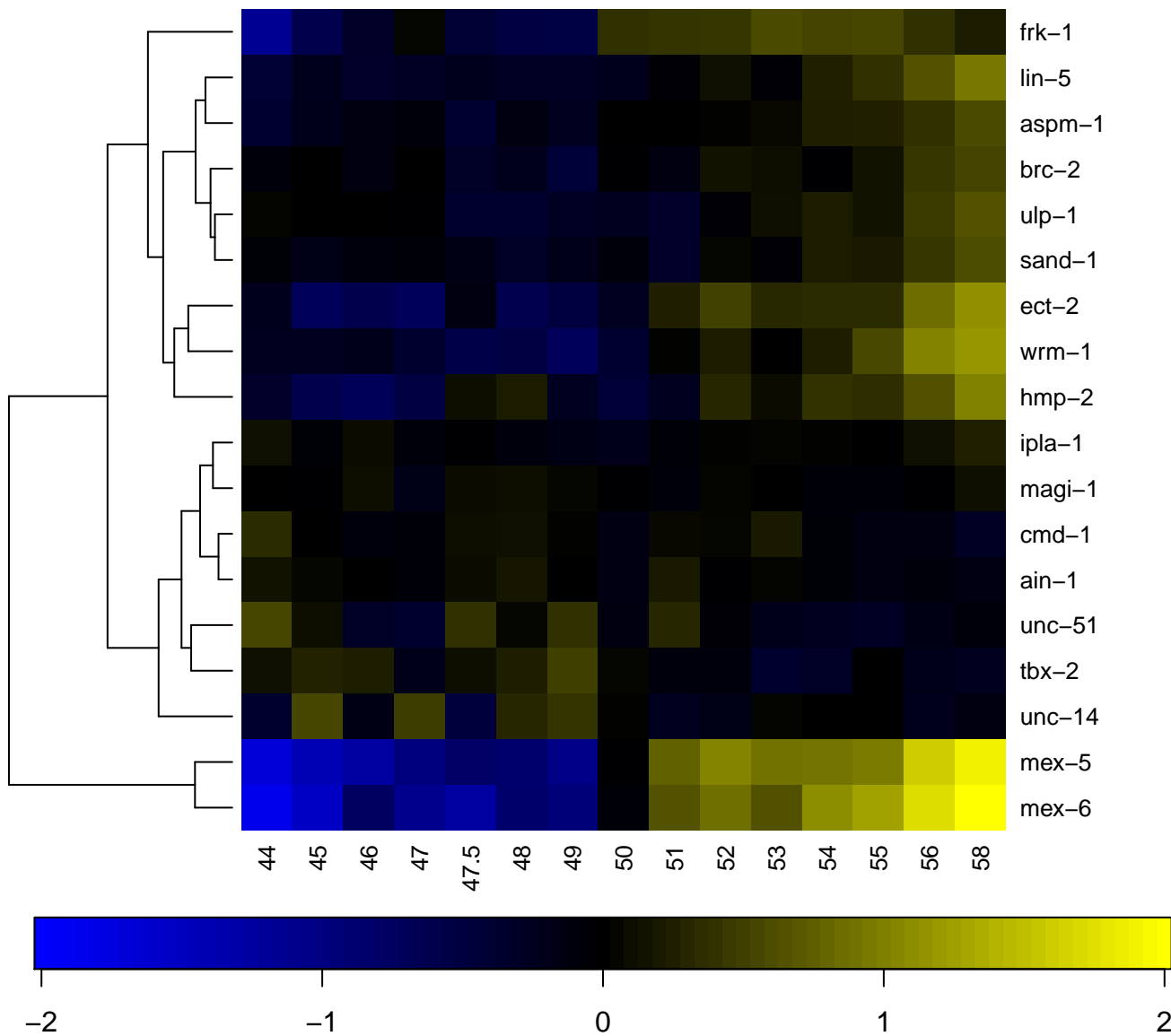
regulation of pH



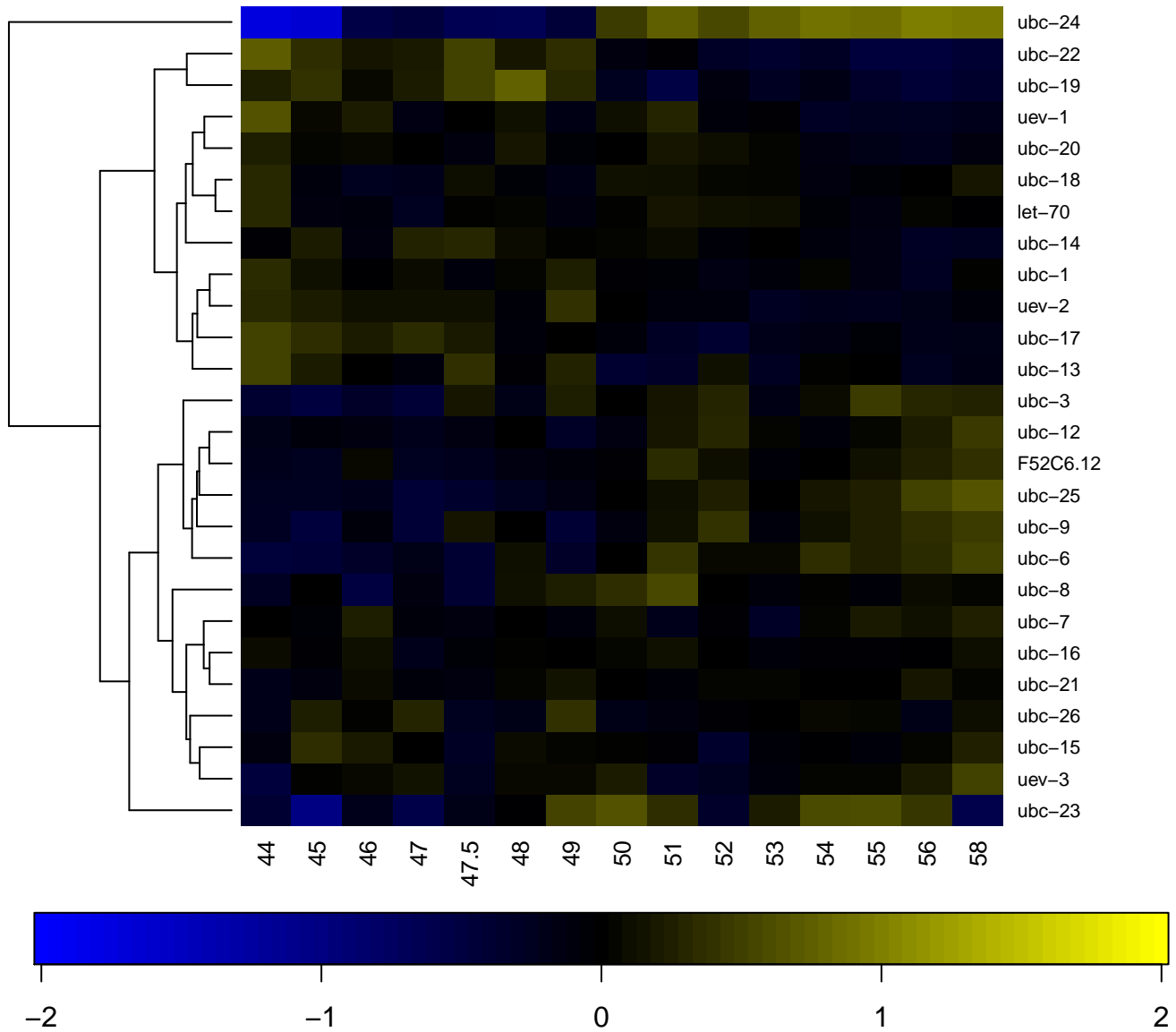
regulation of pharyngeal pumping



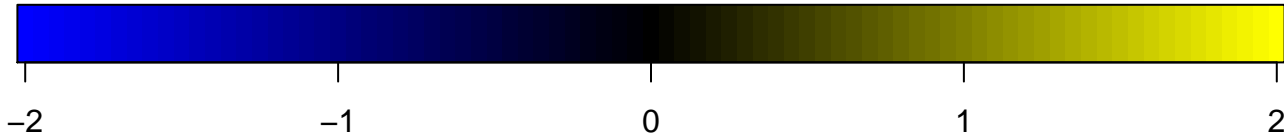
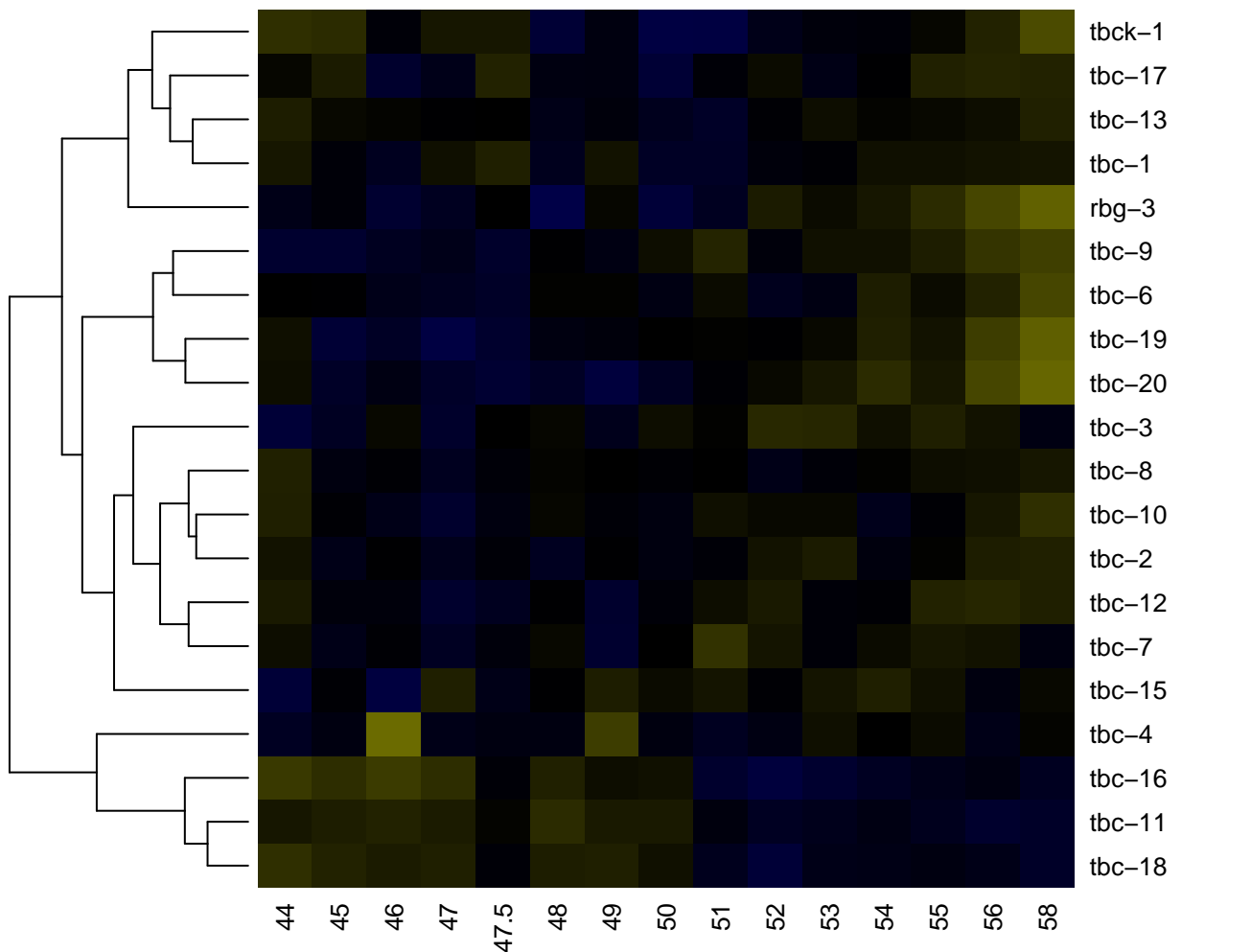
regulation of protein localization



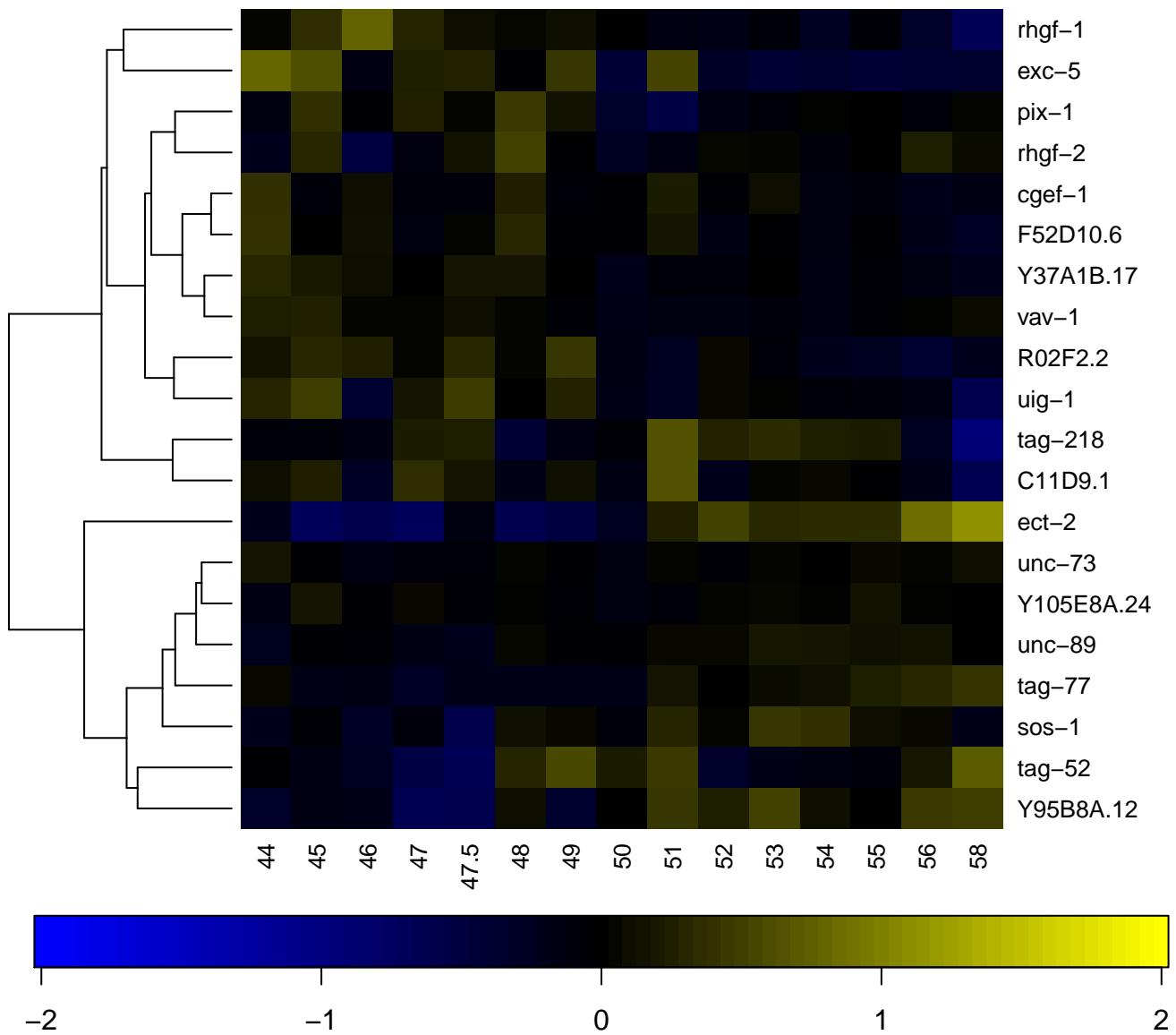
regulation of protein metabolic process



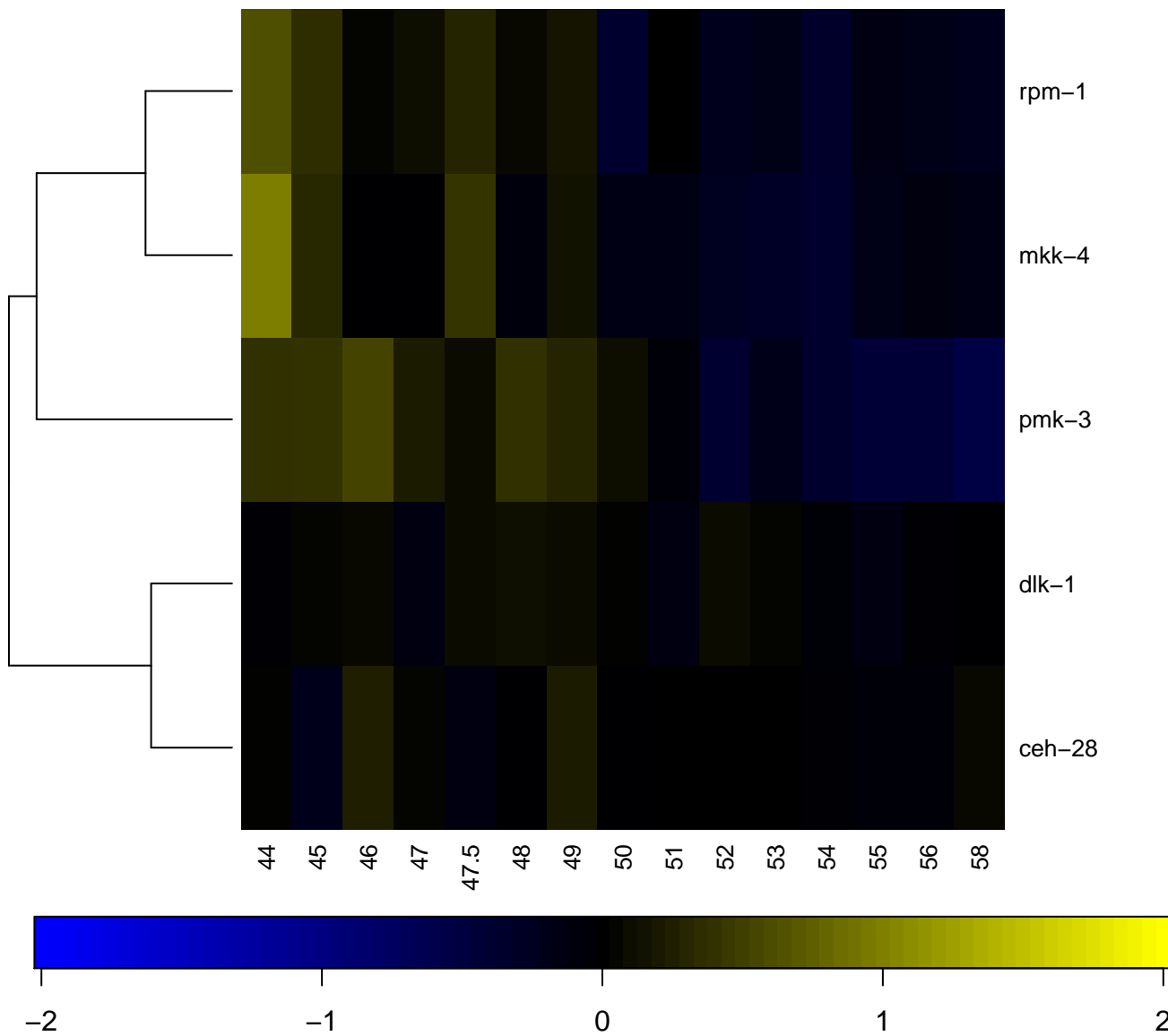
regulation of Rab GTPase activity



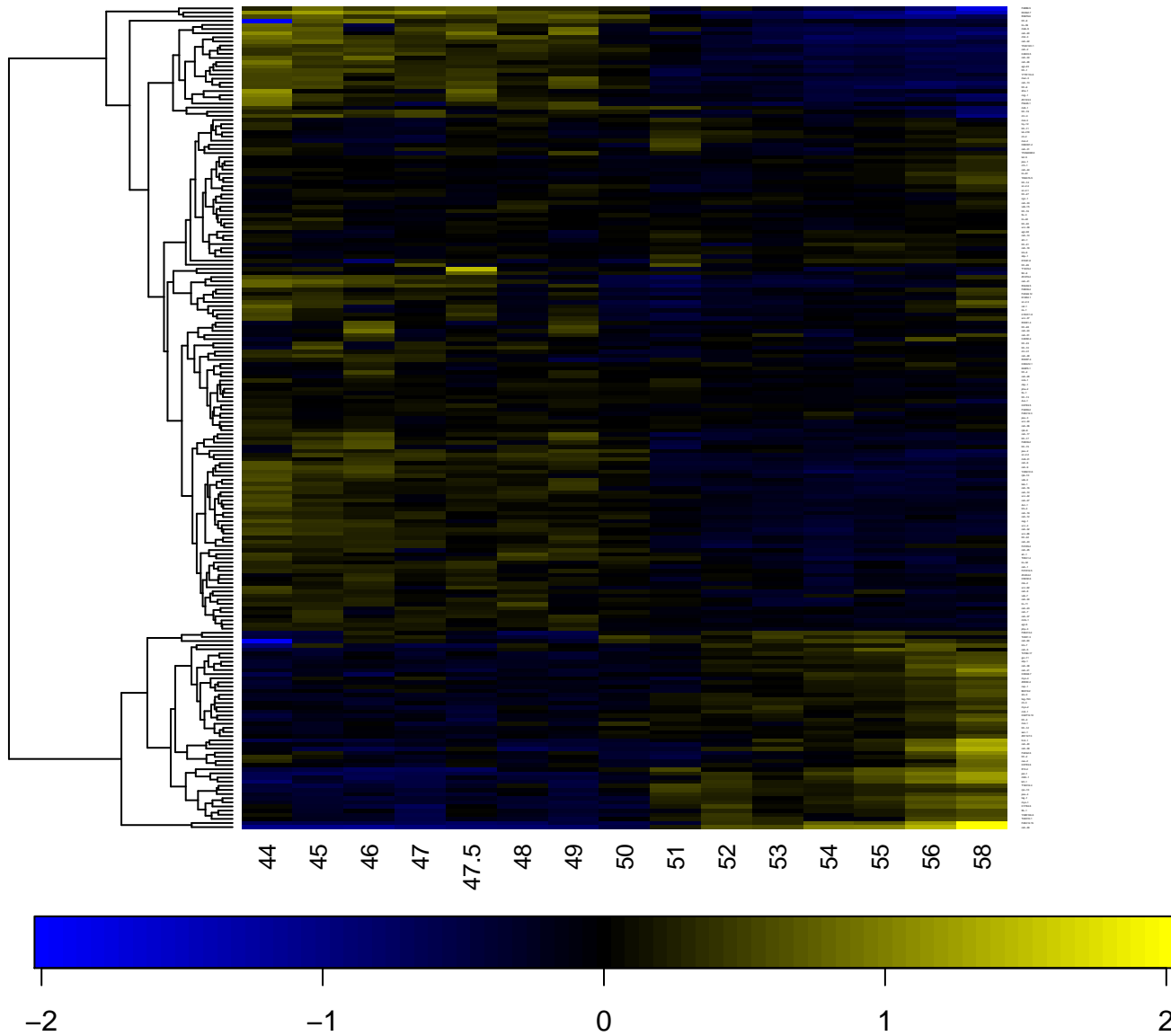
regulation of Rho protein signal transduction



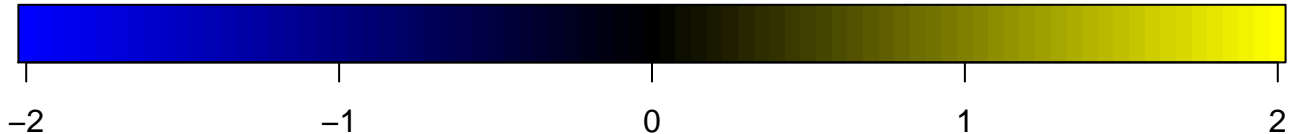
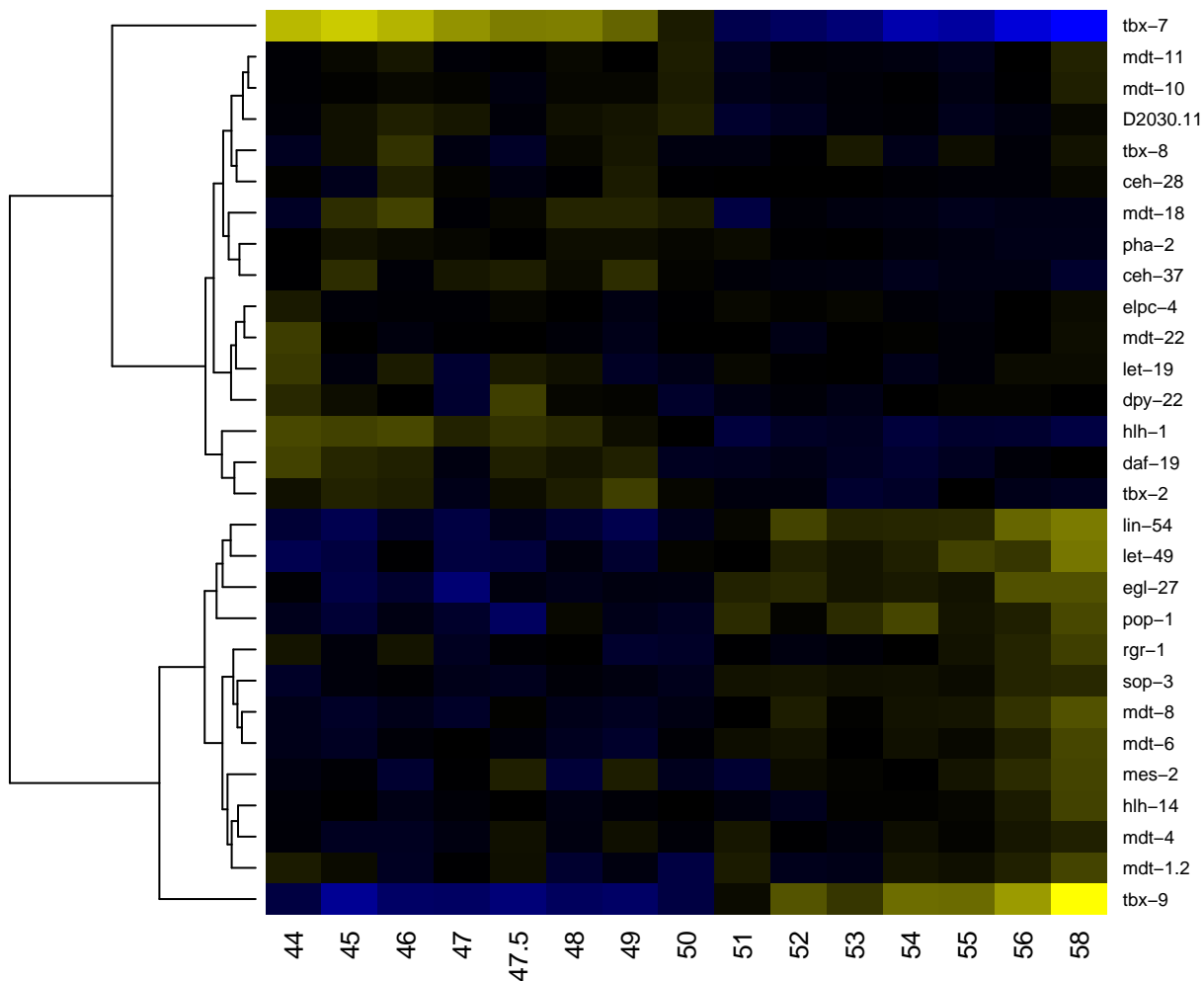
regulation of synapse organization



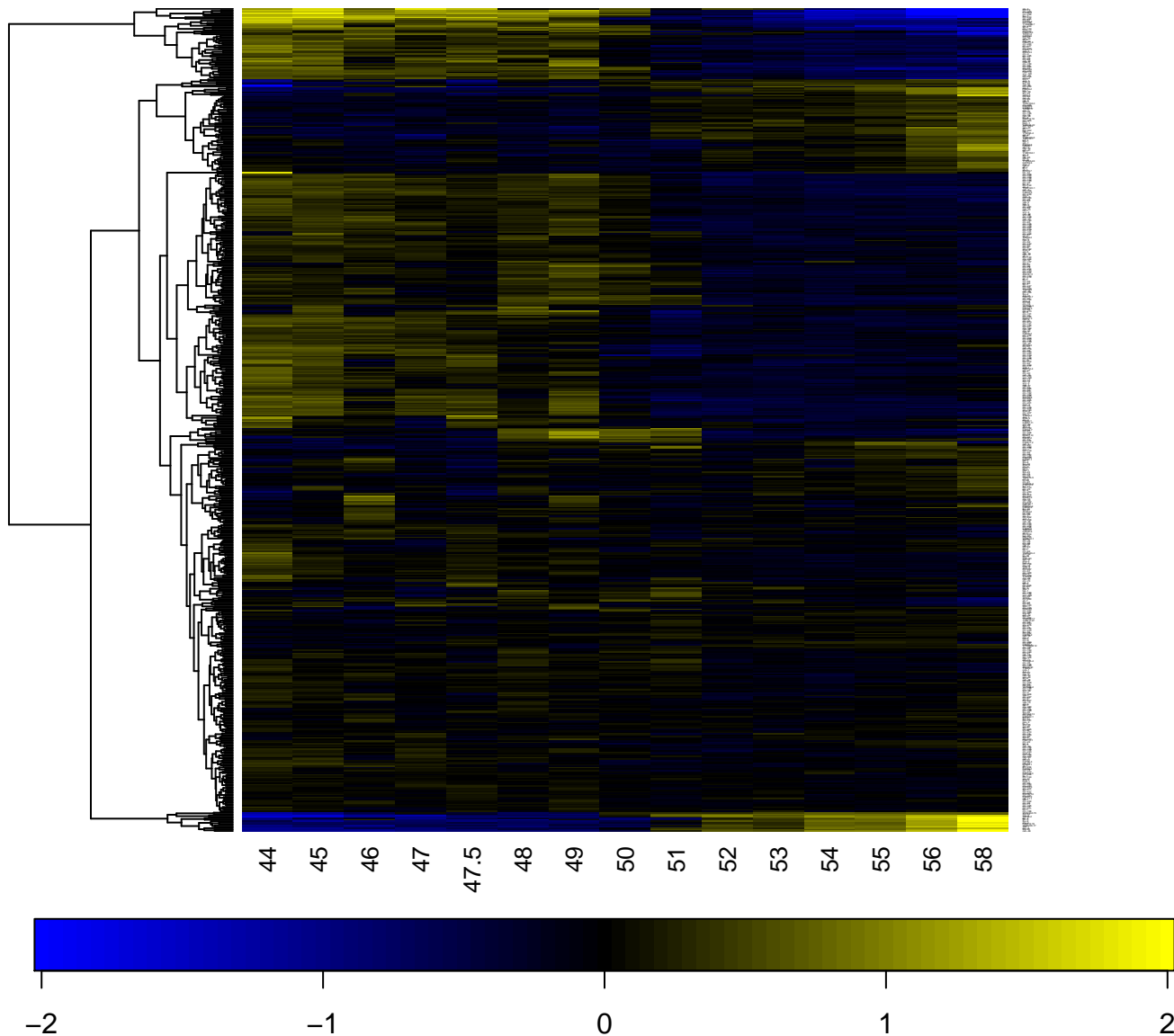
regulation of transcription



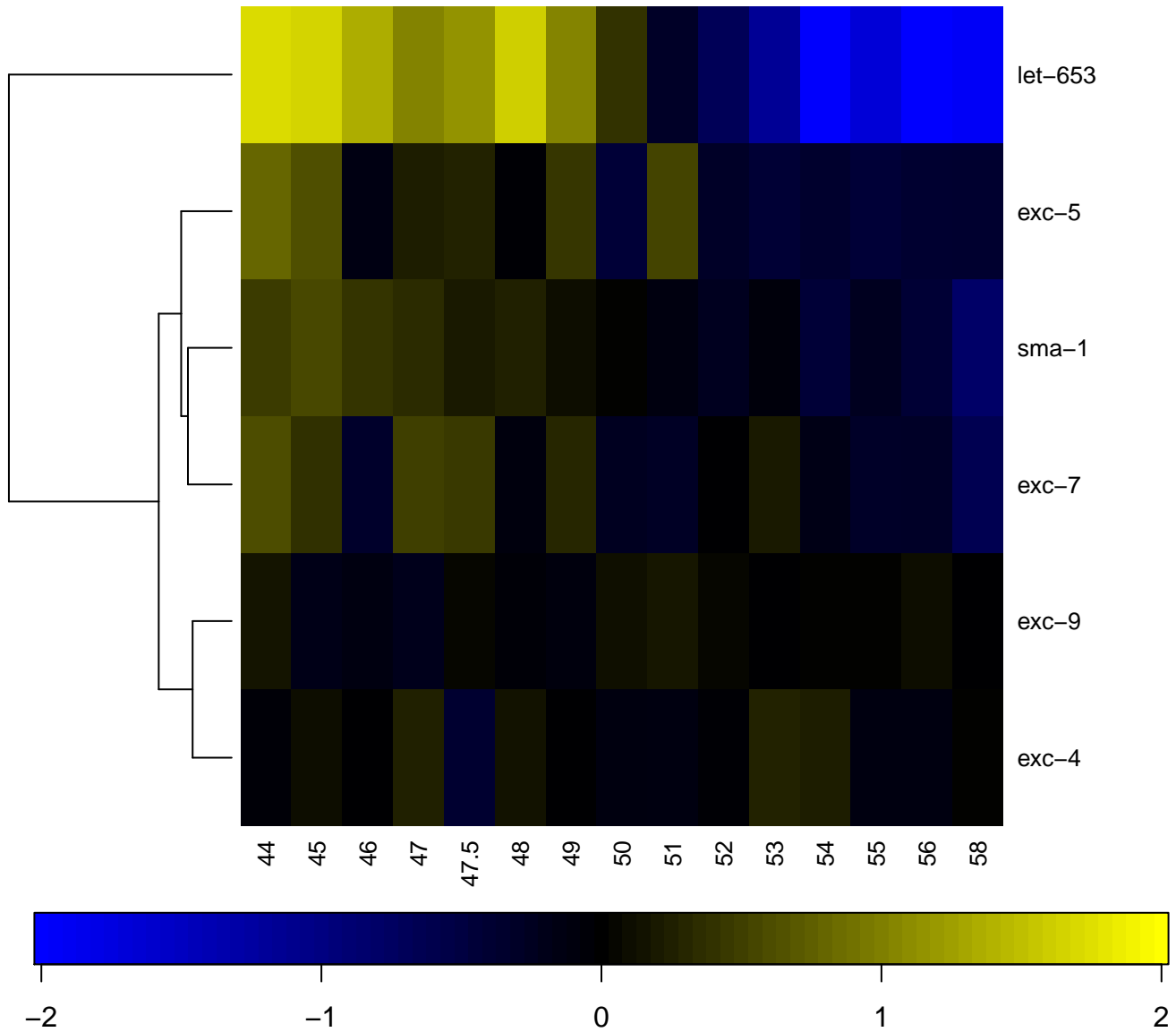
regulation of transcription from RNA polymerase II promot



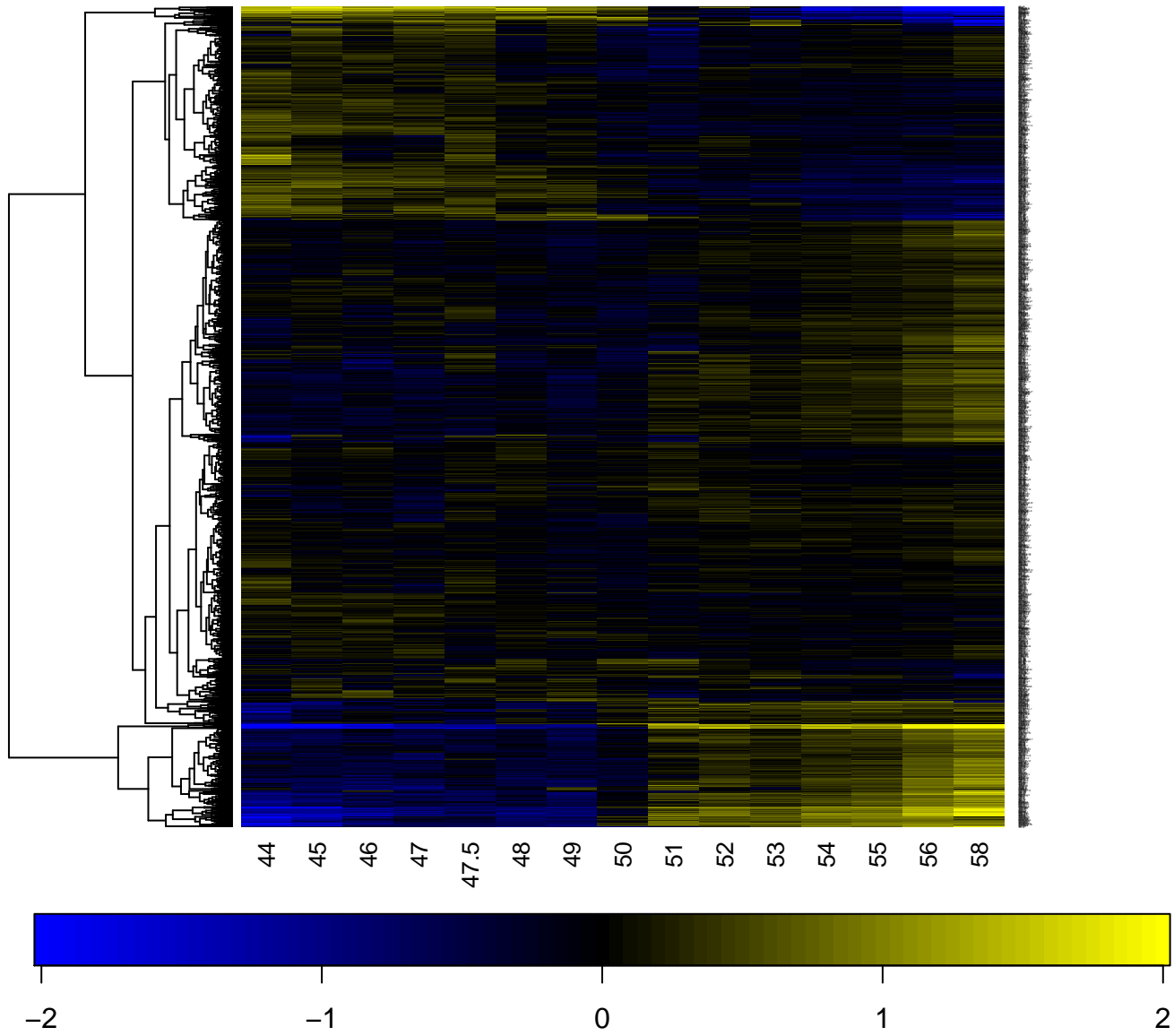
regulation of transcription, DNA-dependent



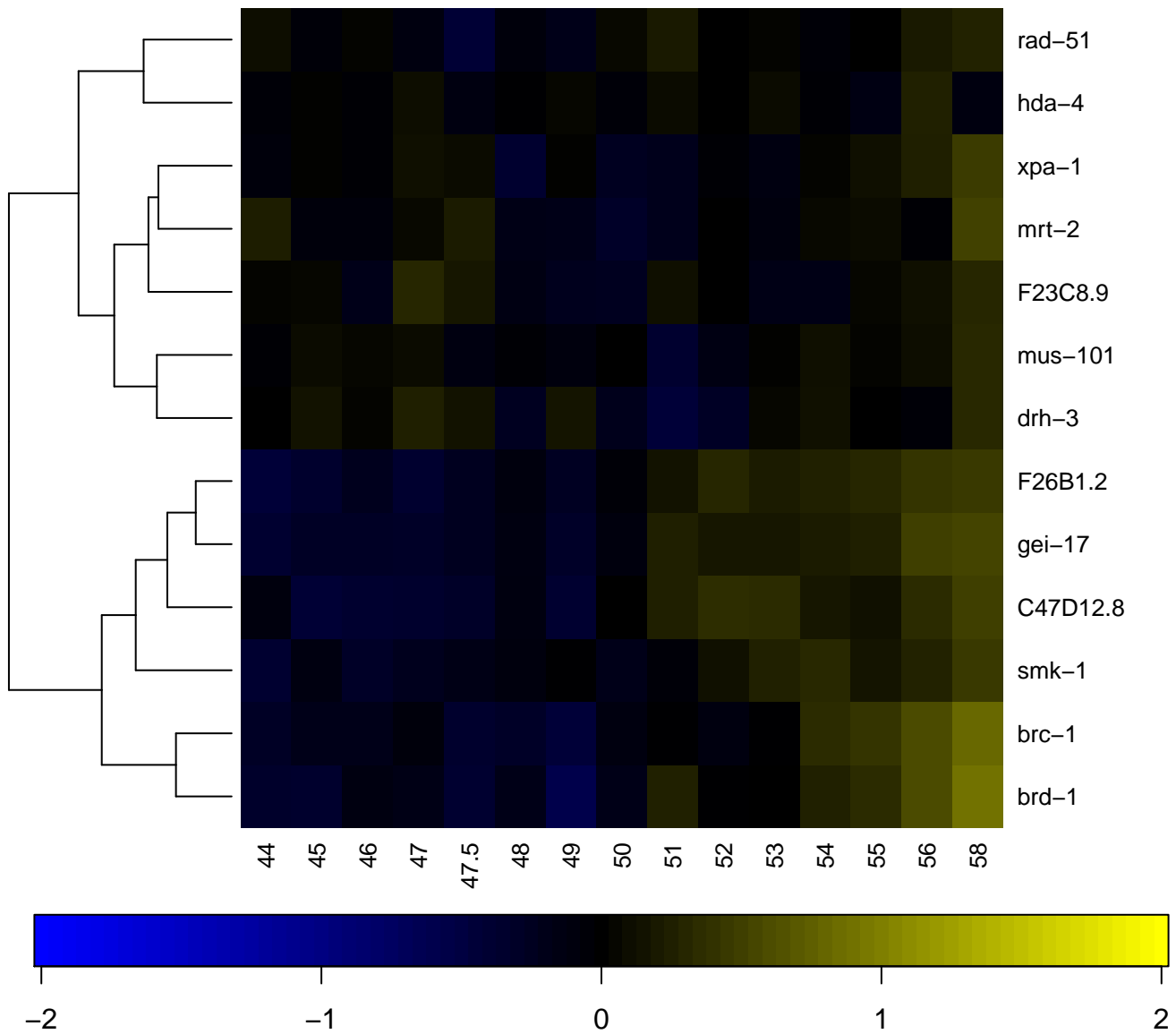
regulation of tube size



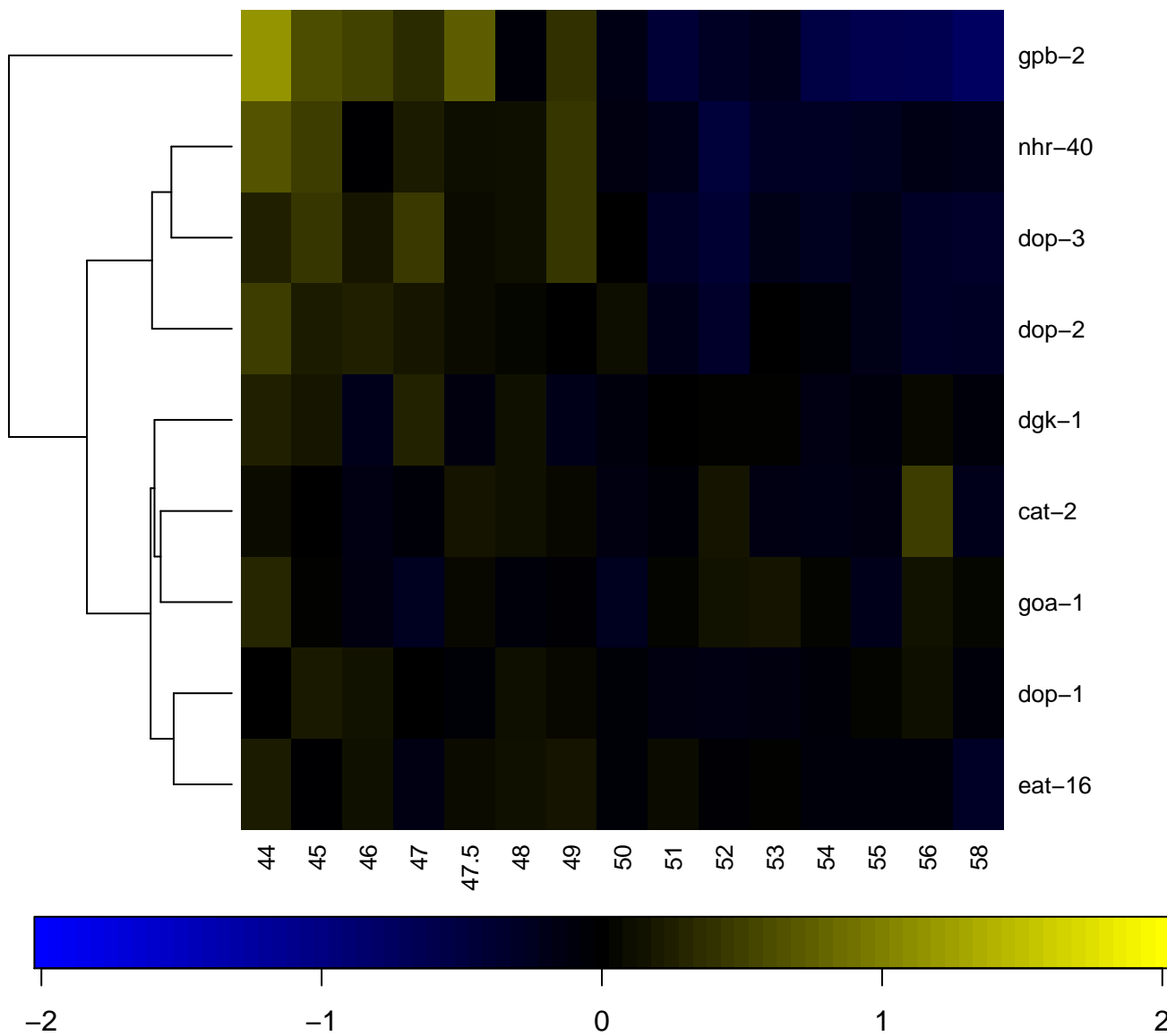
reproduction



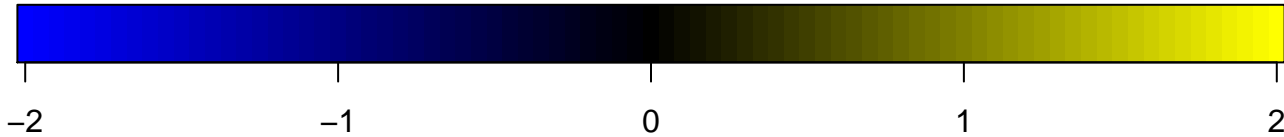
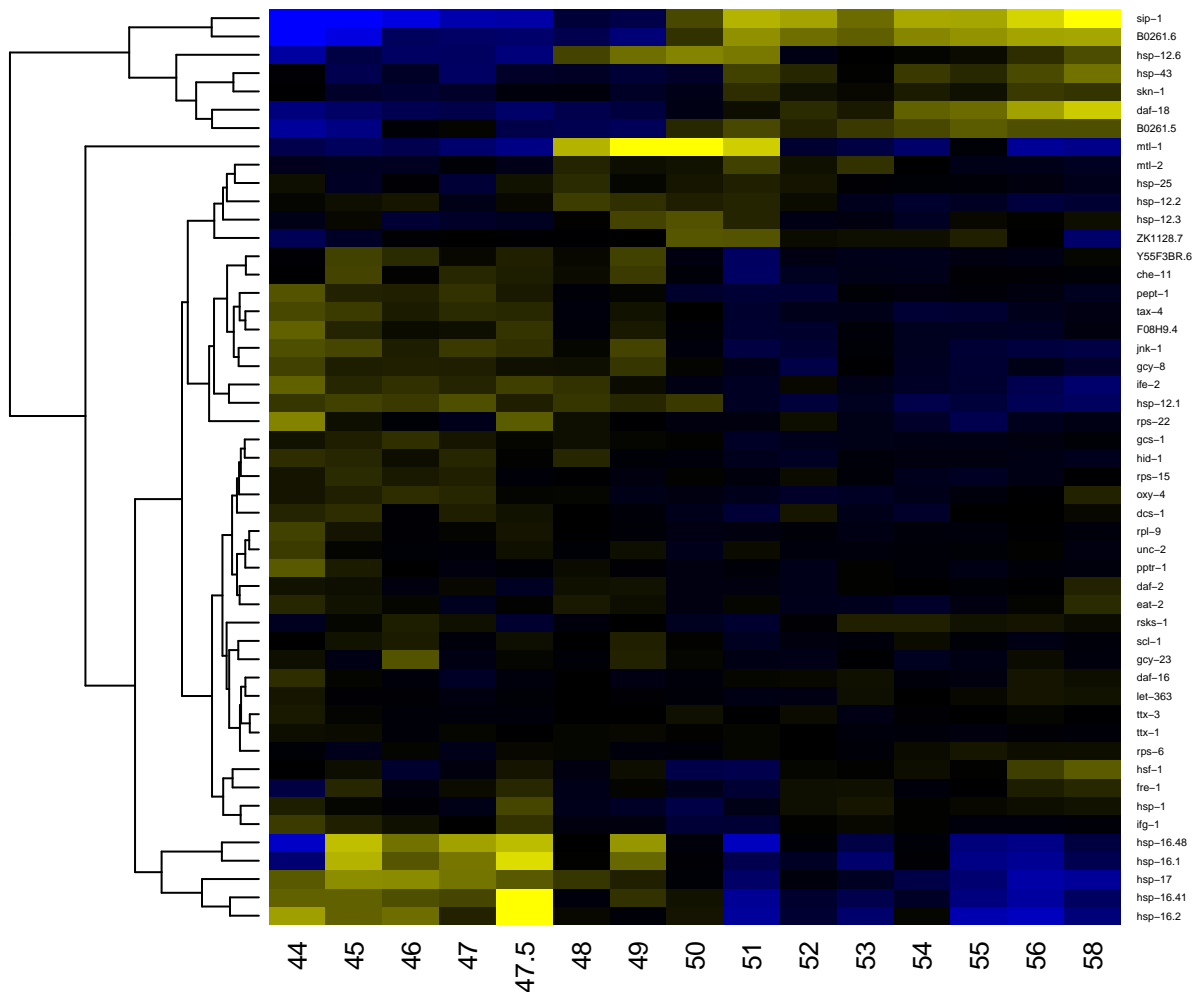
response to DNA damage stimulus



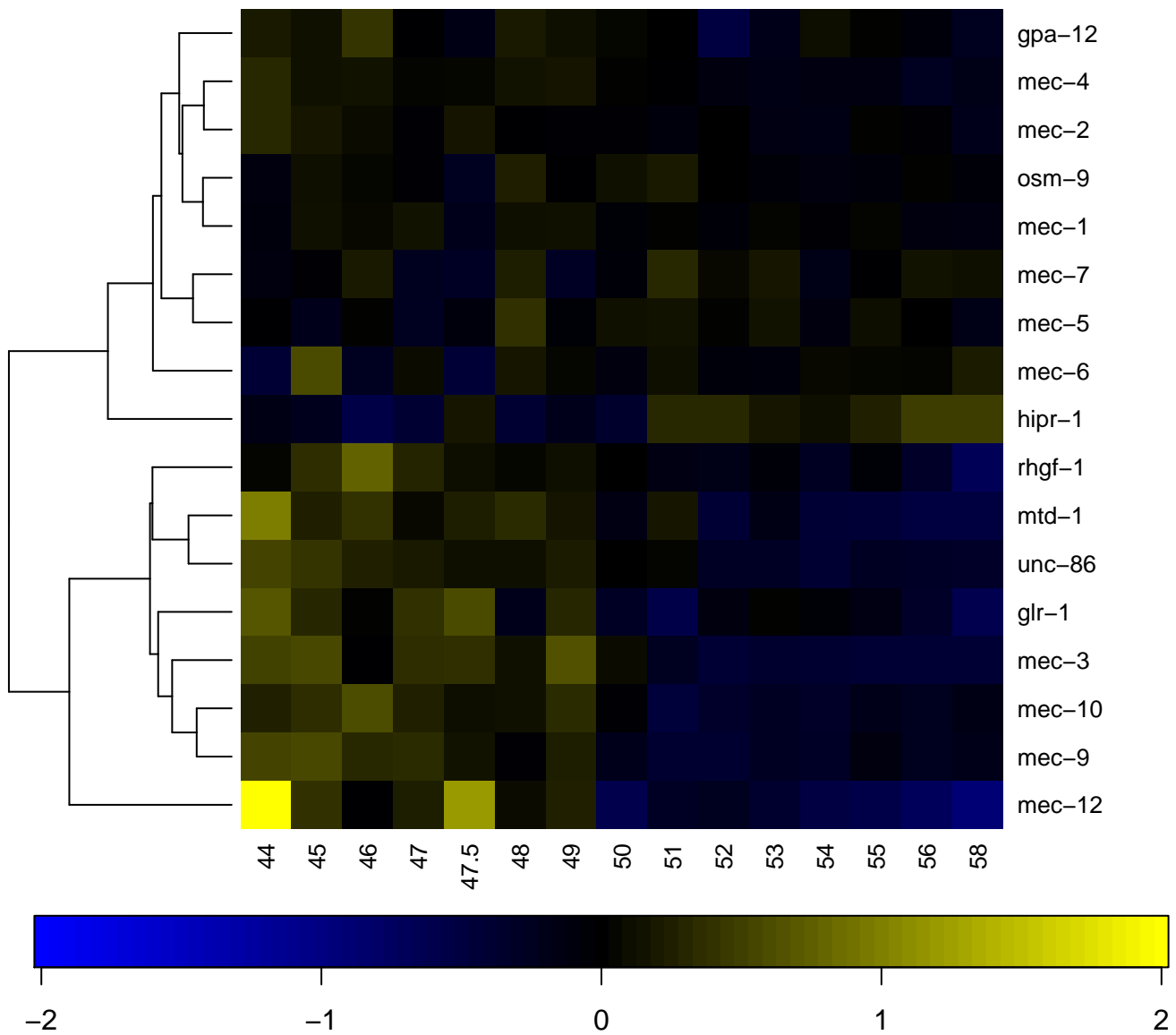
response to food



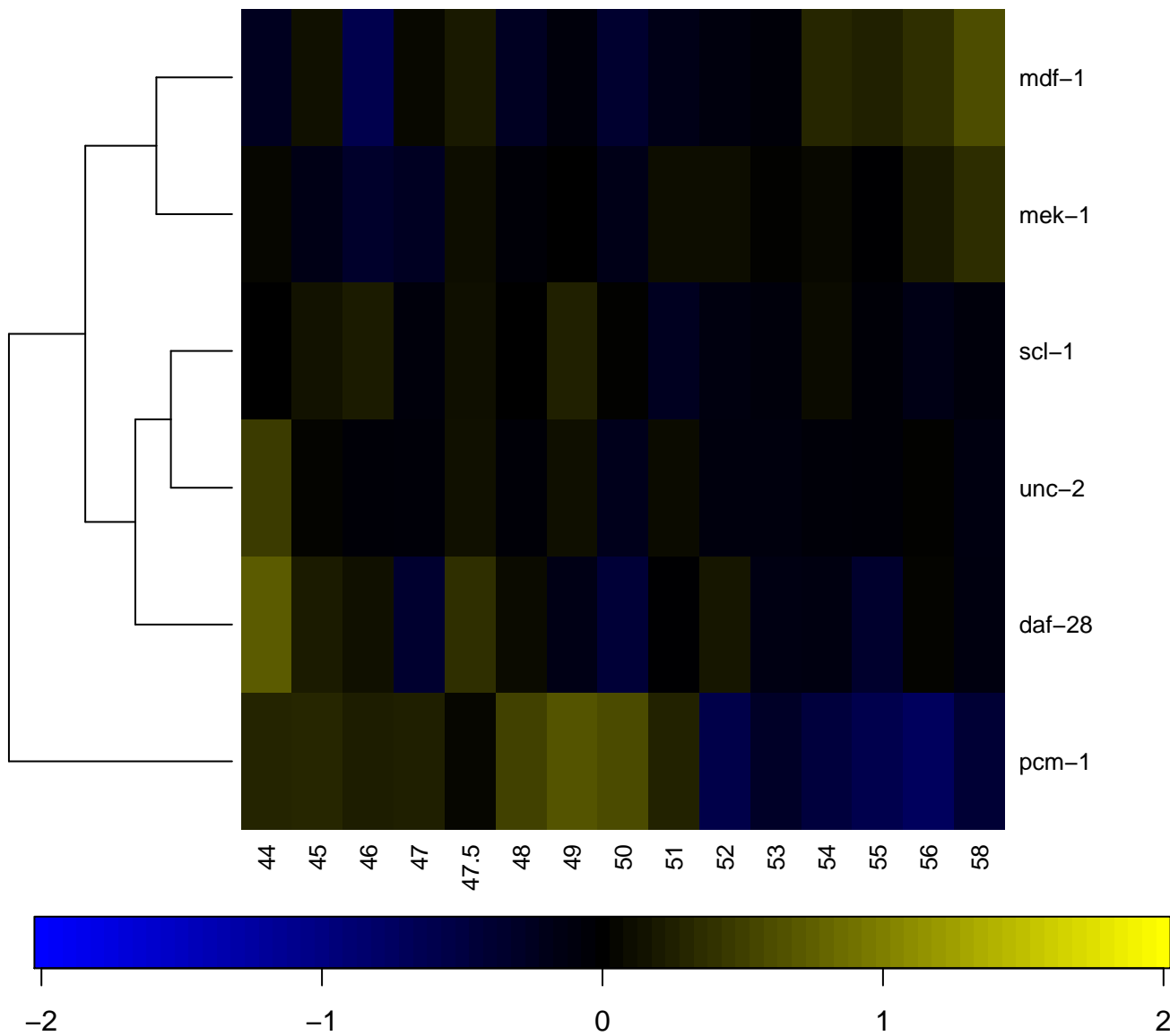
response to heat



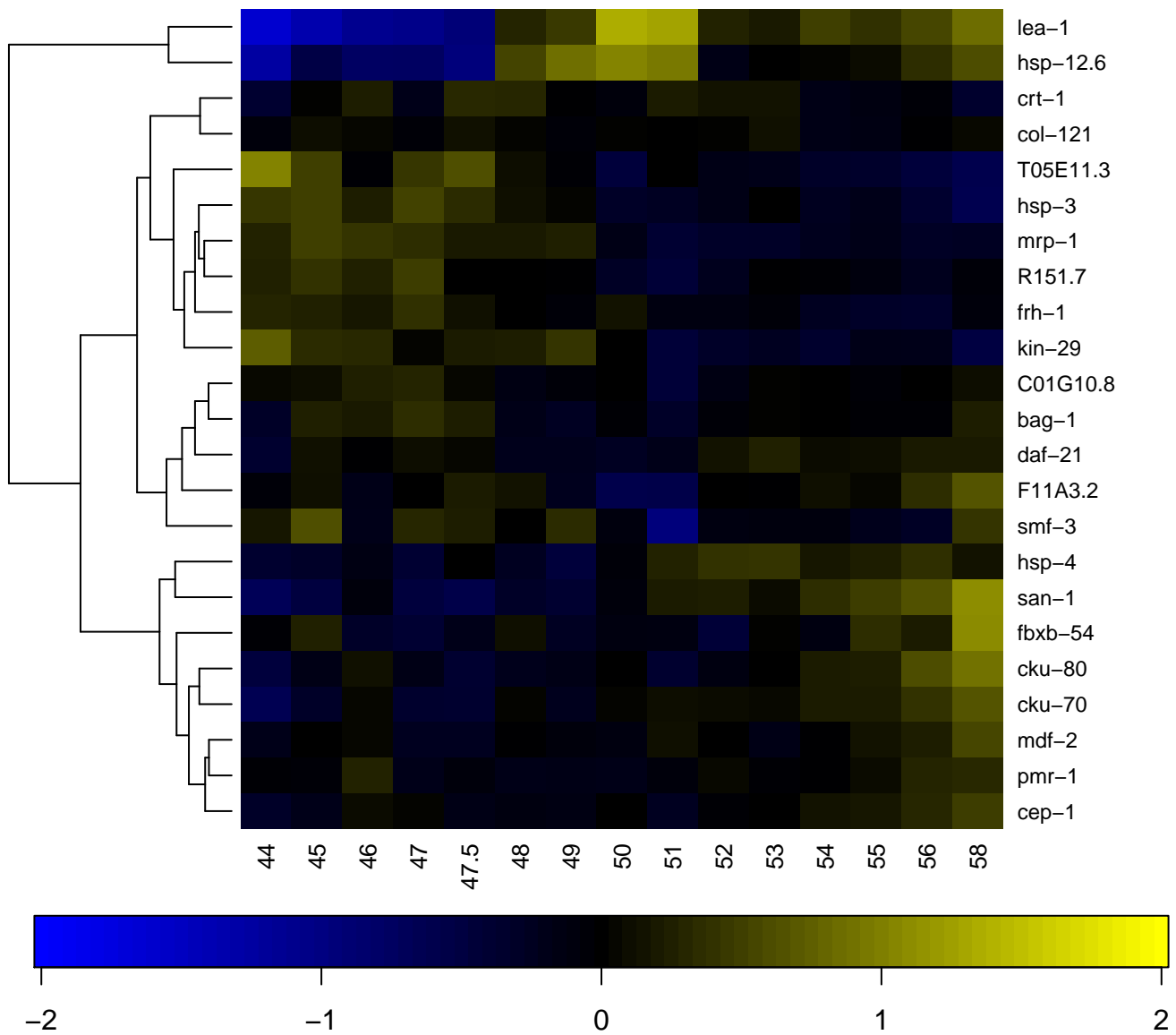
response to mechanical stimulus



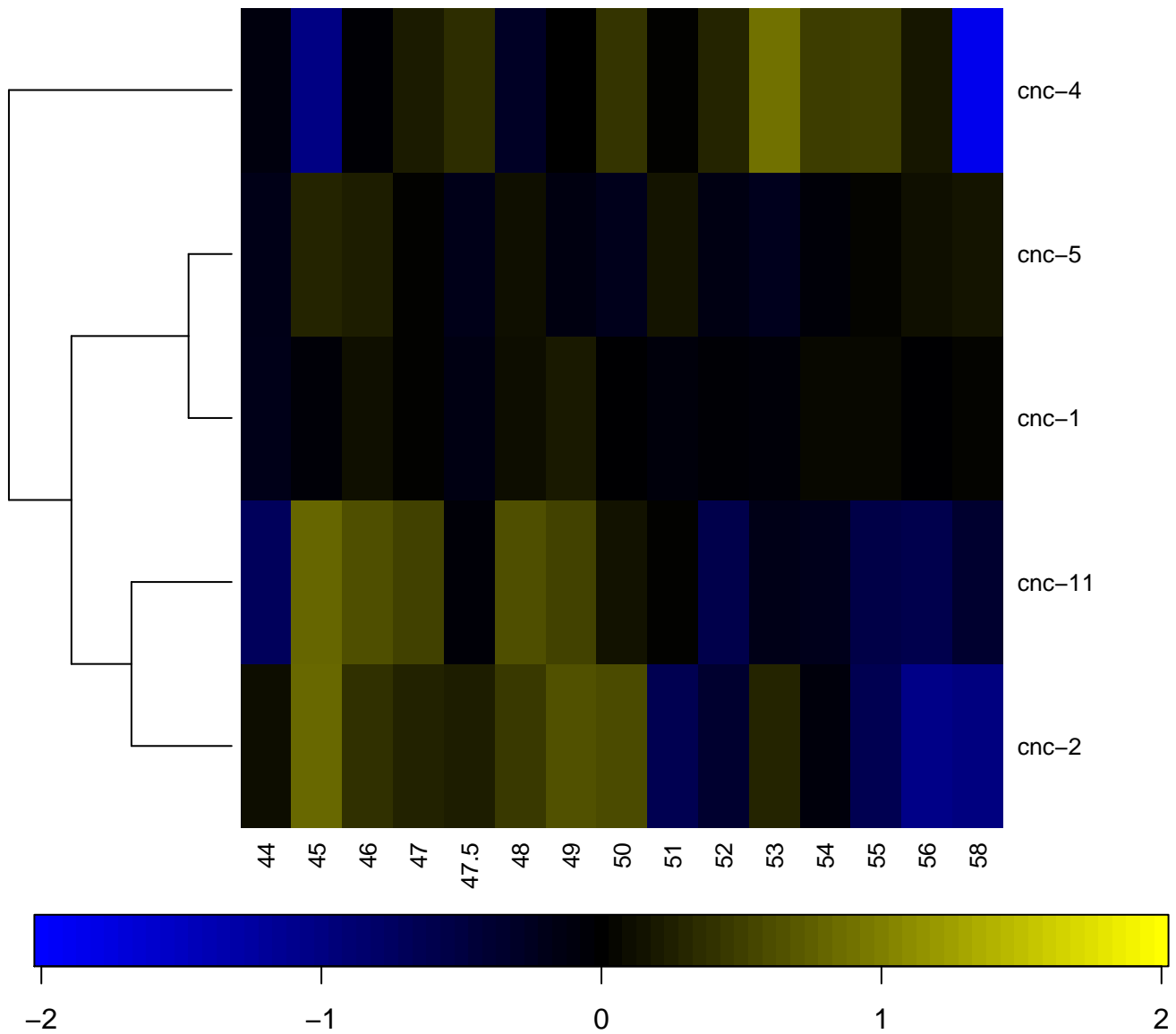
response to starvation



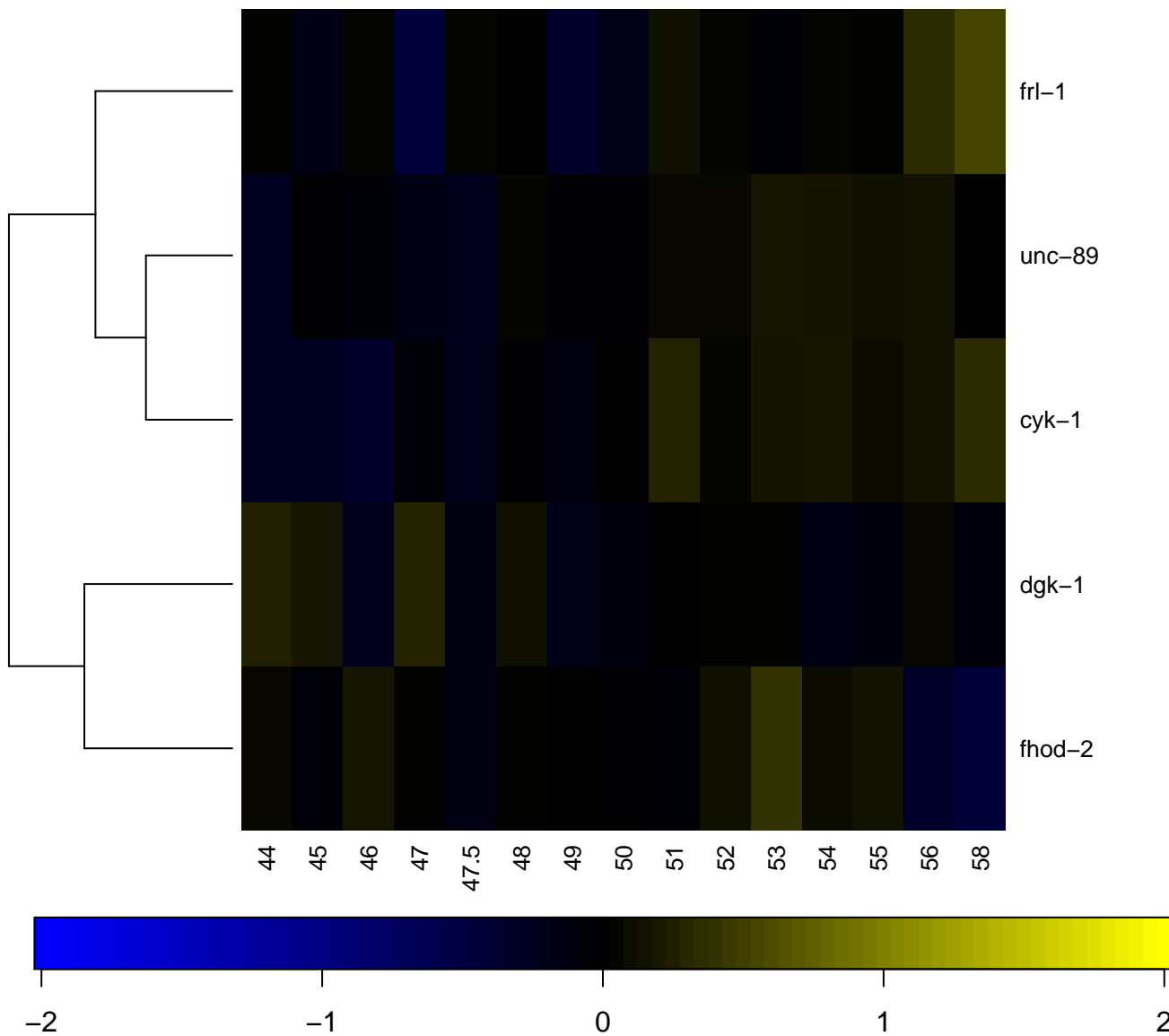
response to stress



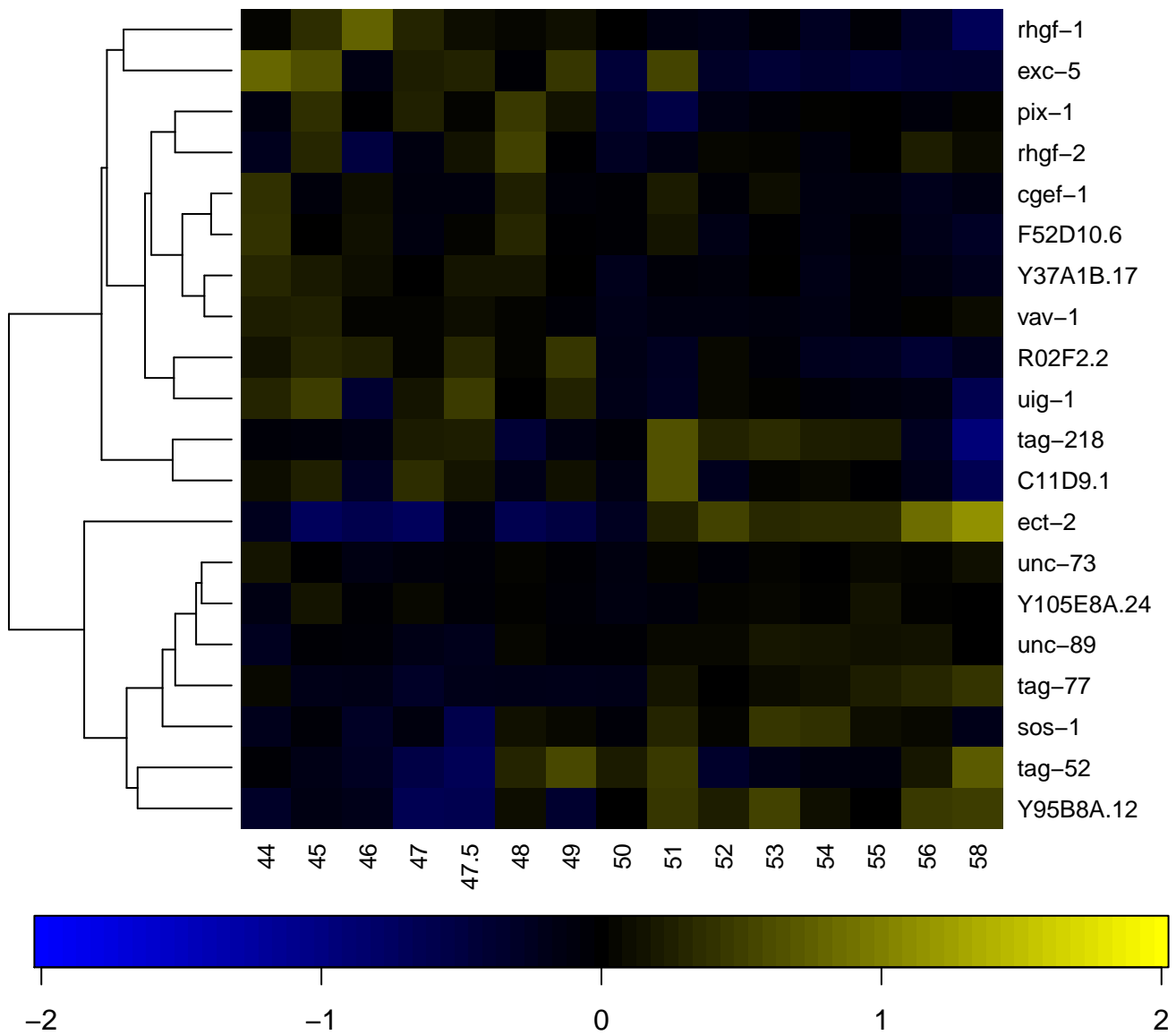
response to wounding



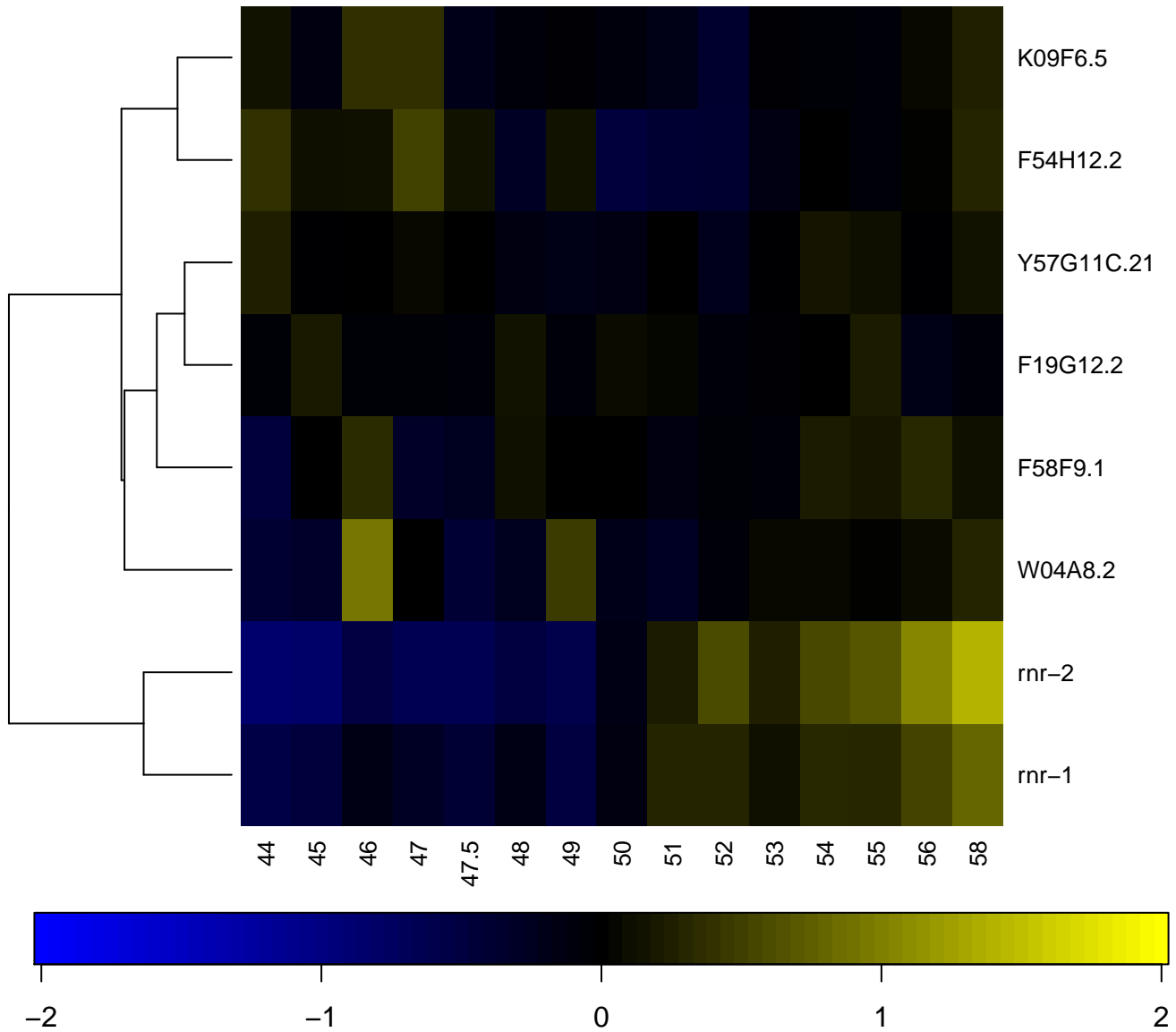
Rho GTPase binding



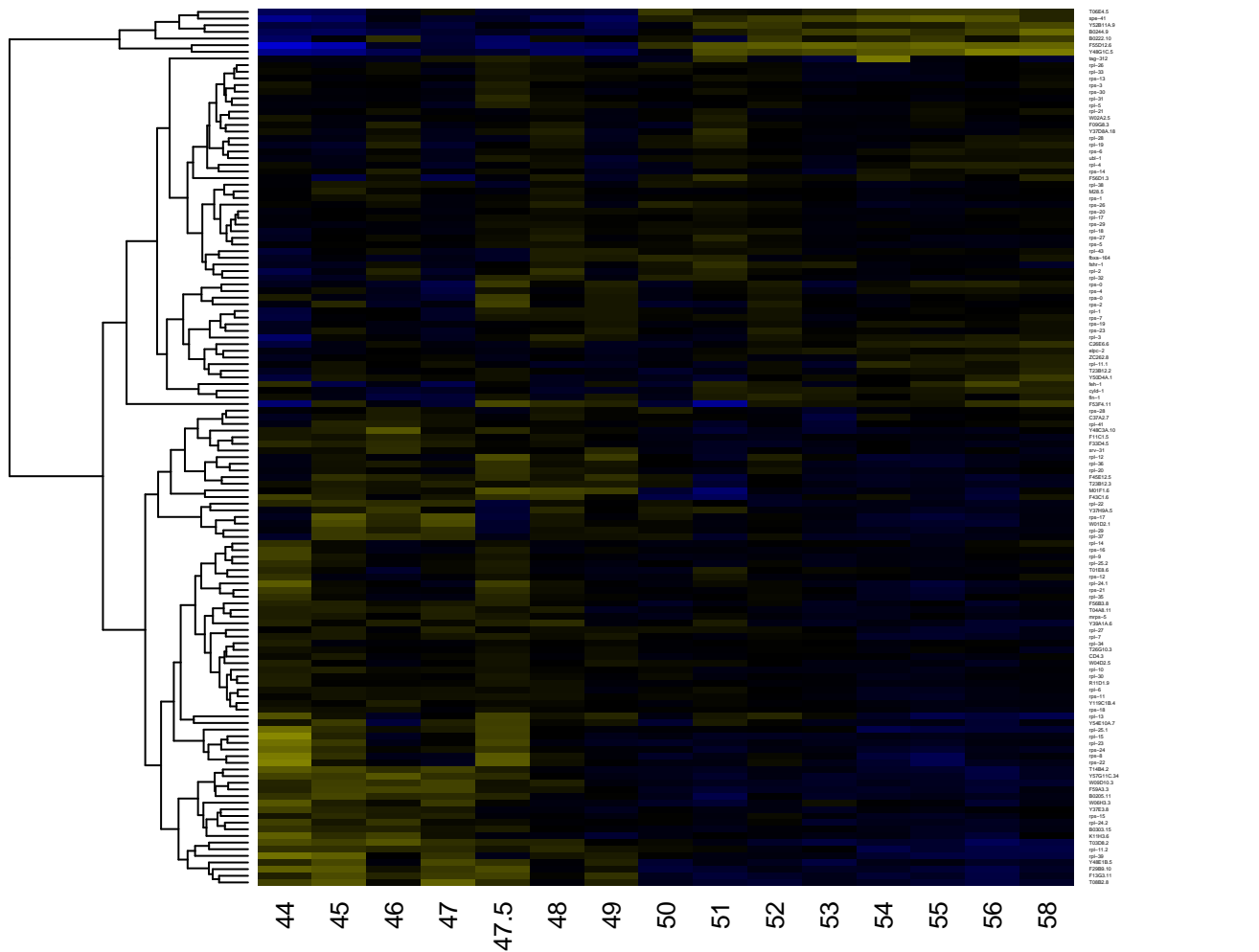
Rho guanyl–nucleotide exchange factor activity



ribonucleoside-diphosphate reductase activity



ribosome



-2

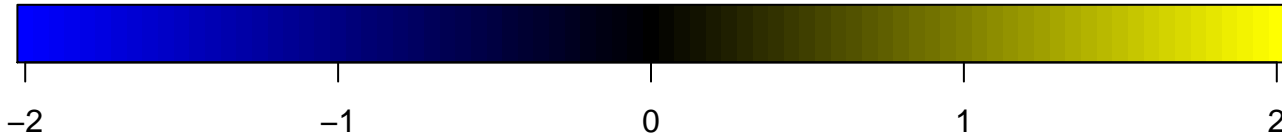
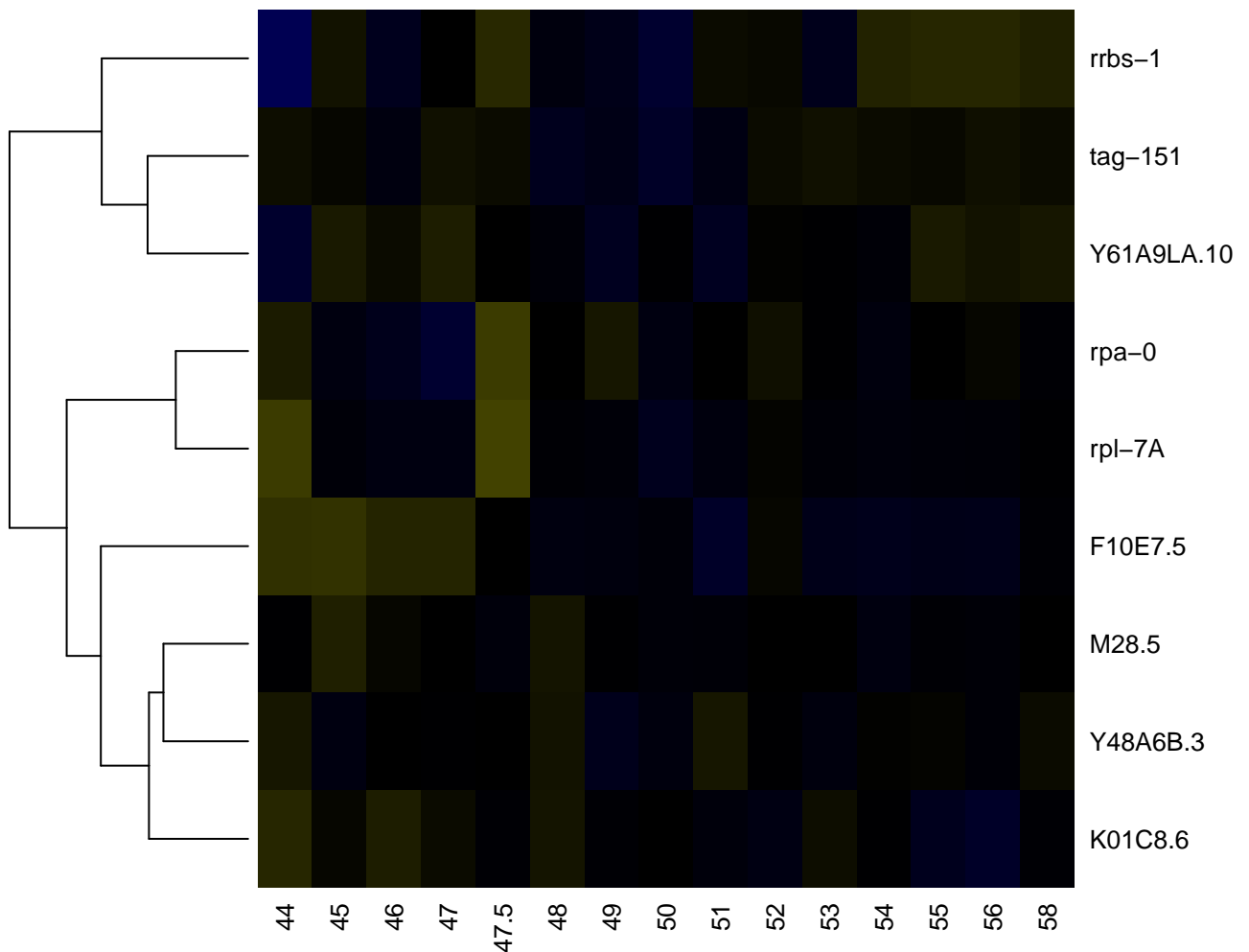
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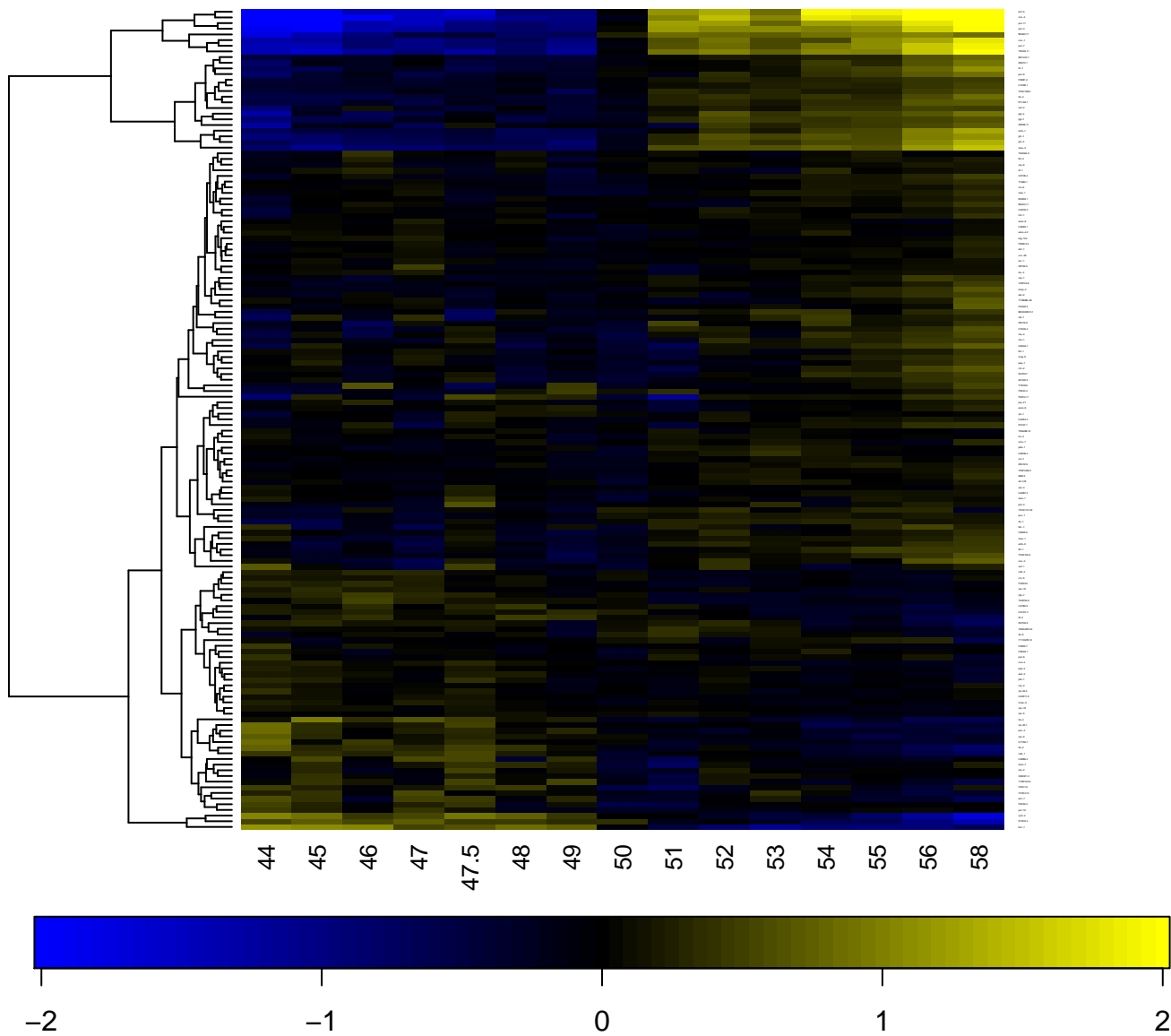
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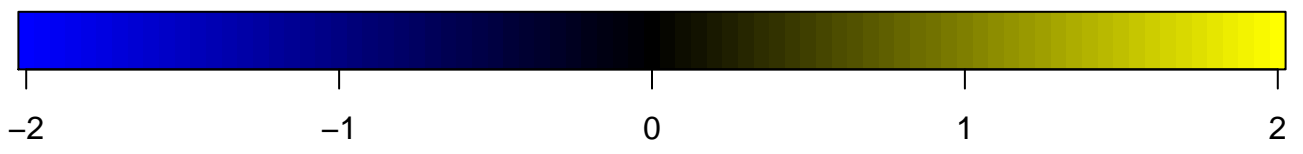
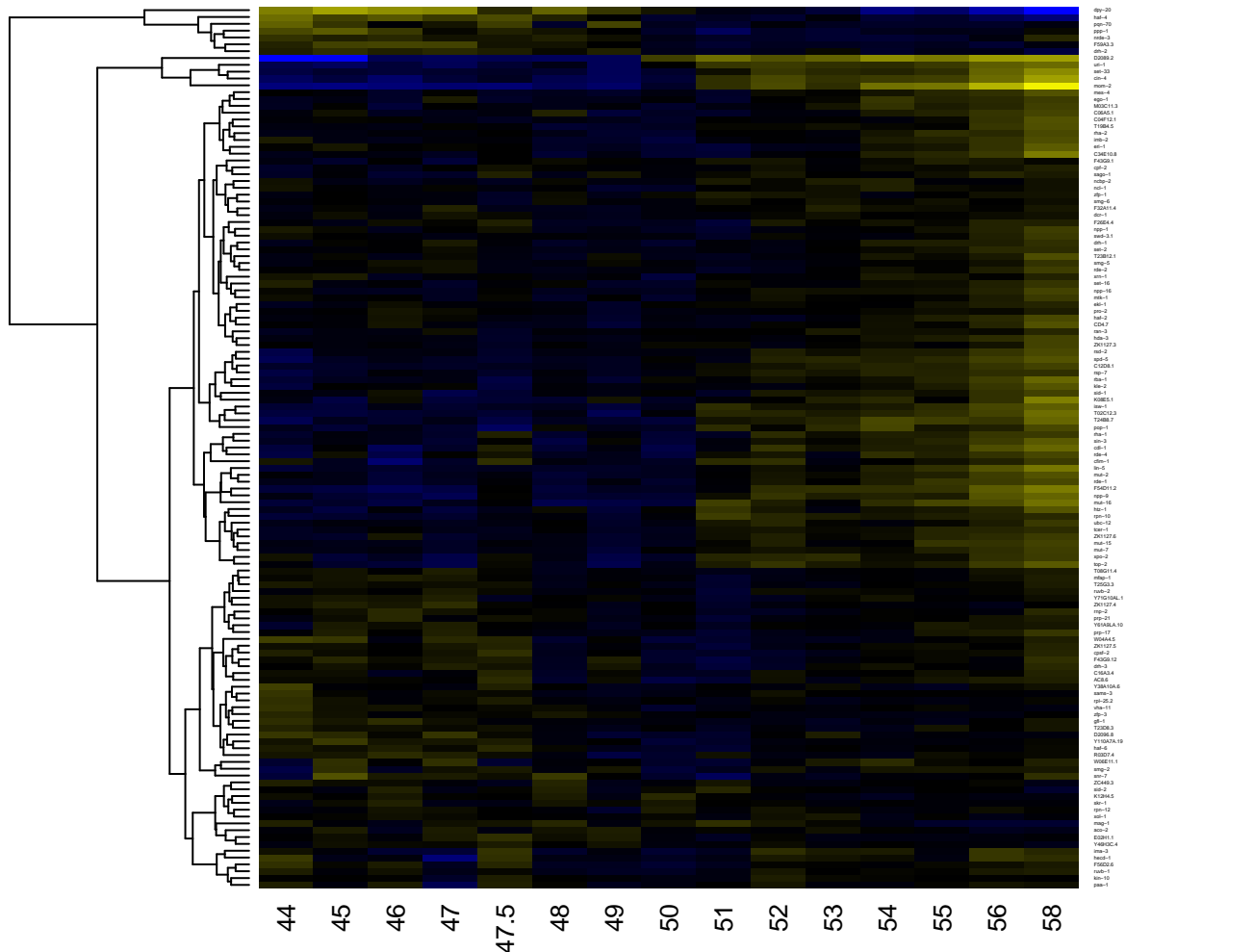
ribosome biogenesis



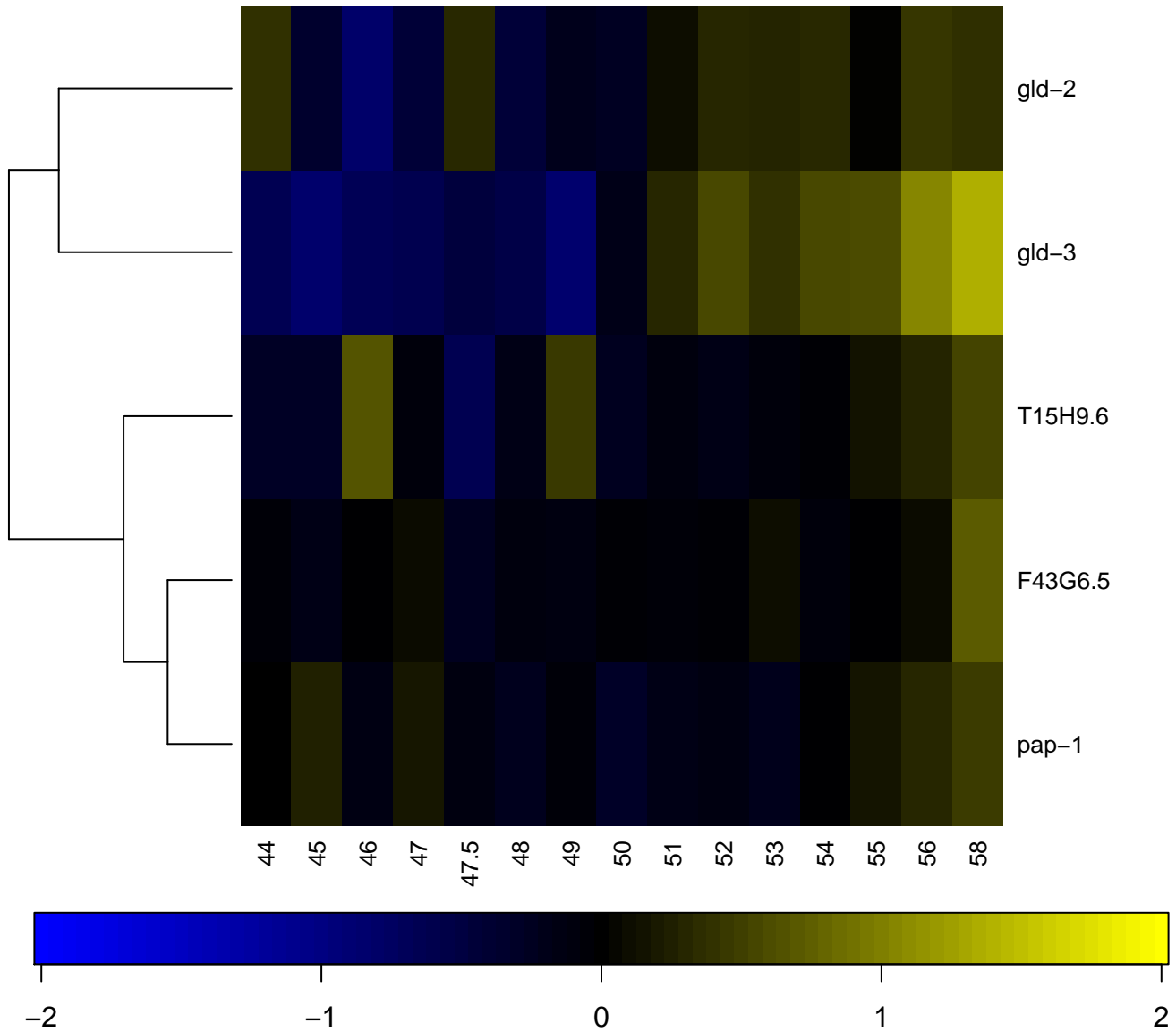
RNA binding



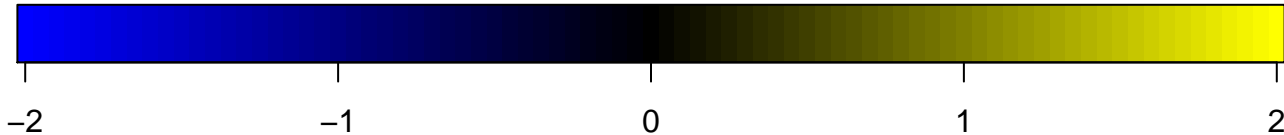
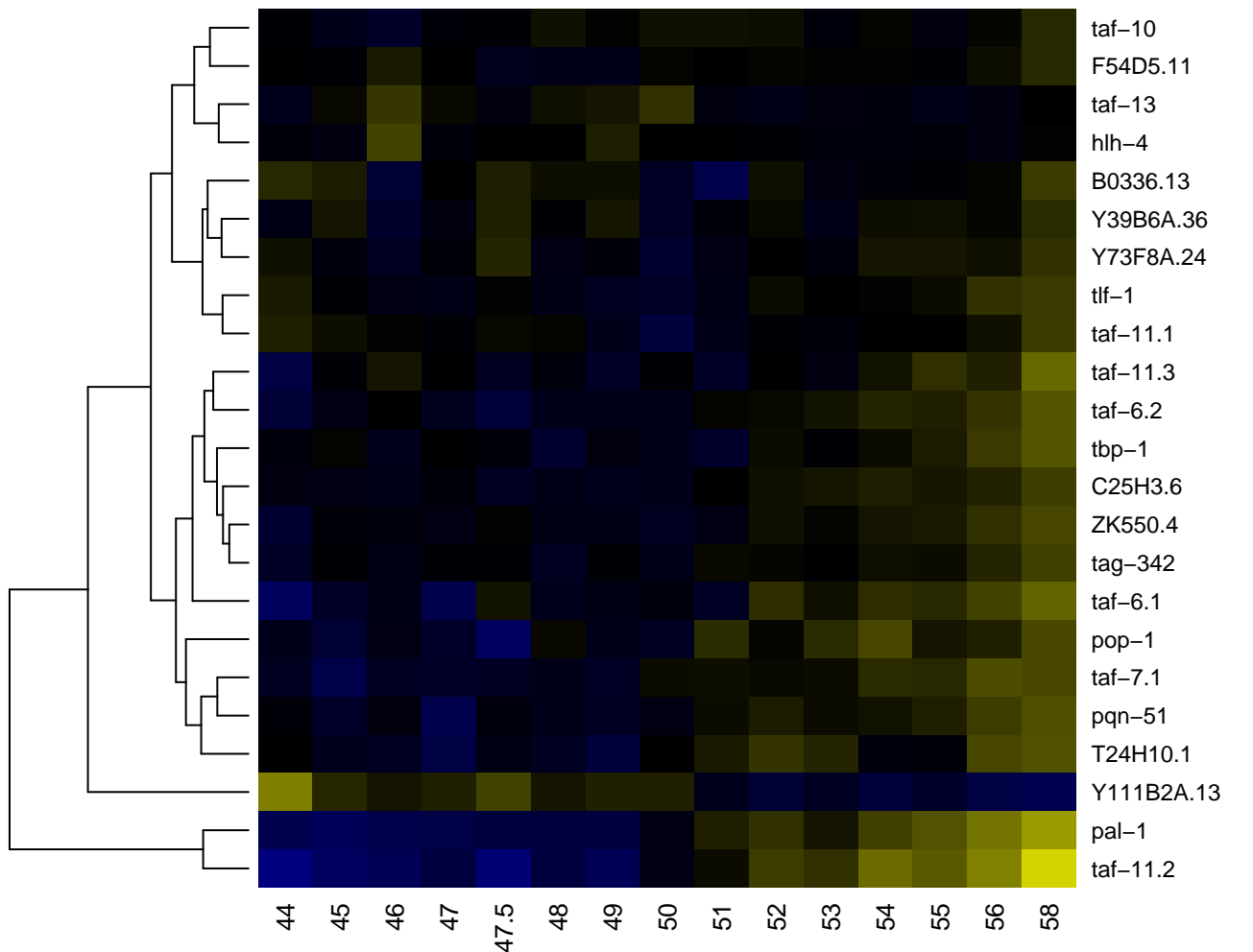
RNA interference



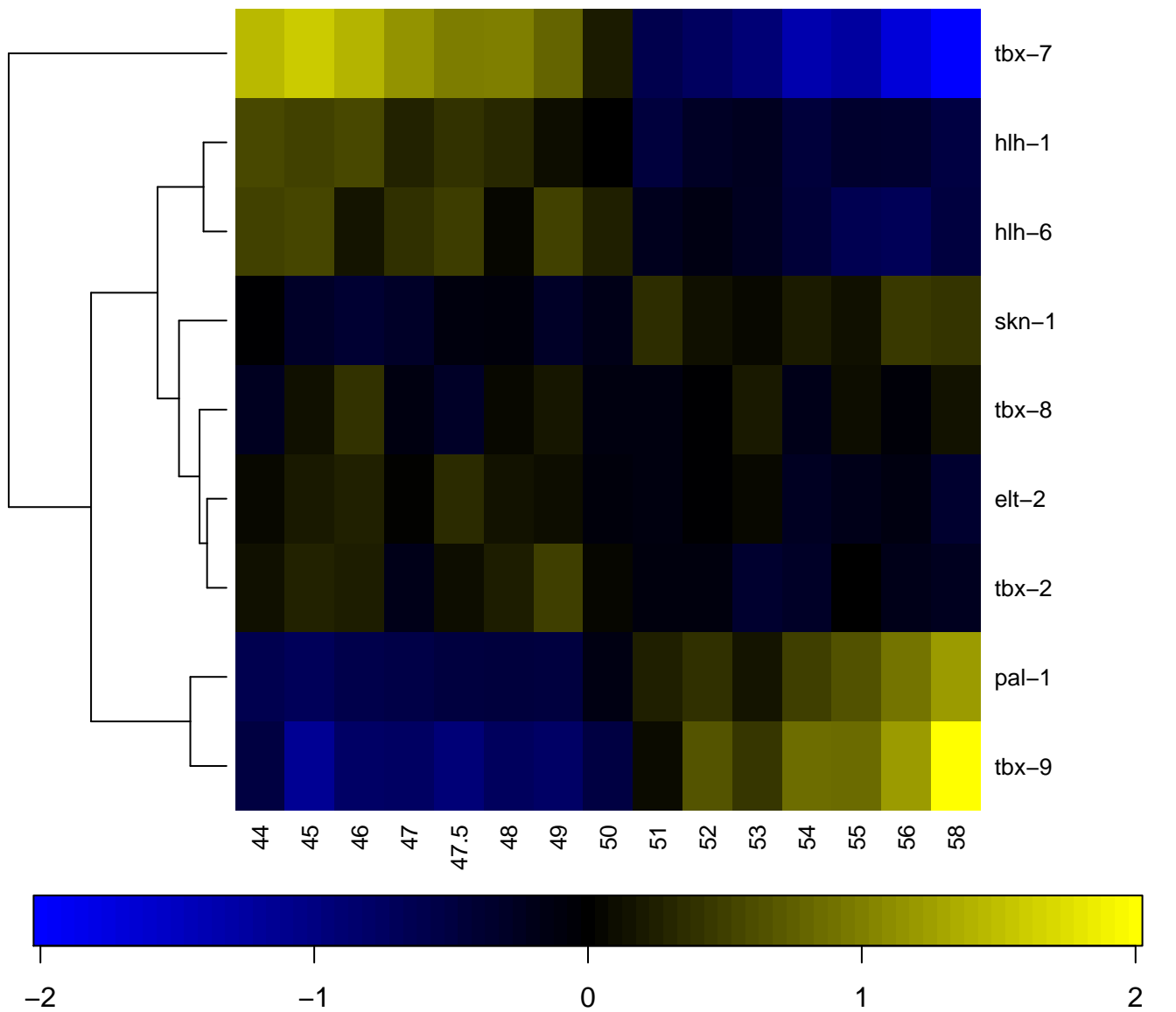
RNA polyadenylation



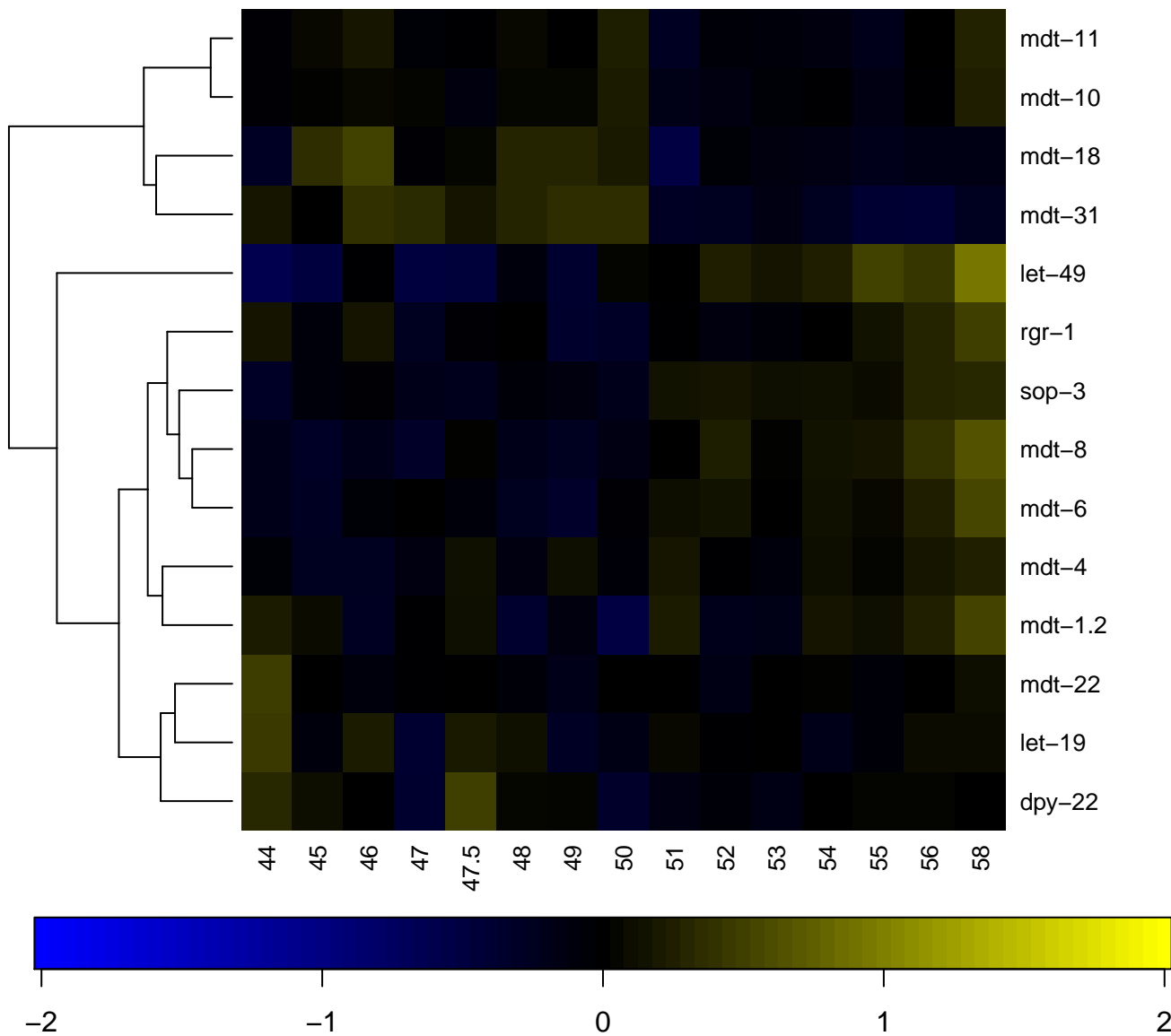
RNA polymerase II transcription factor activity



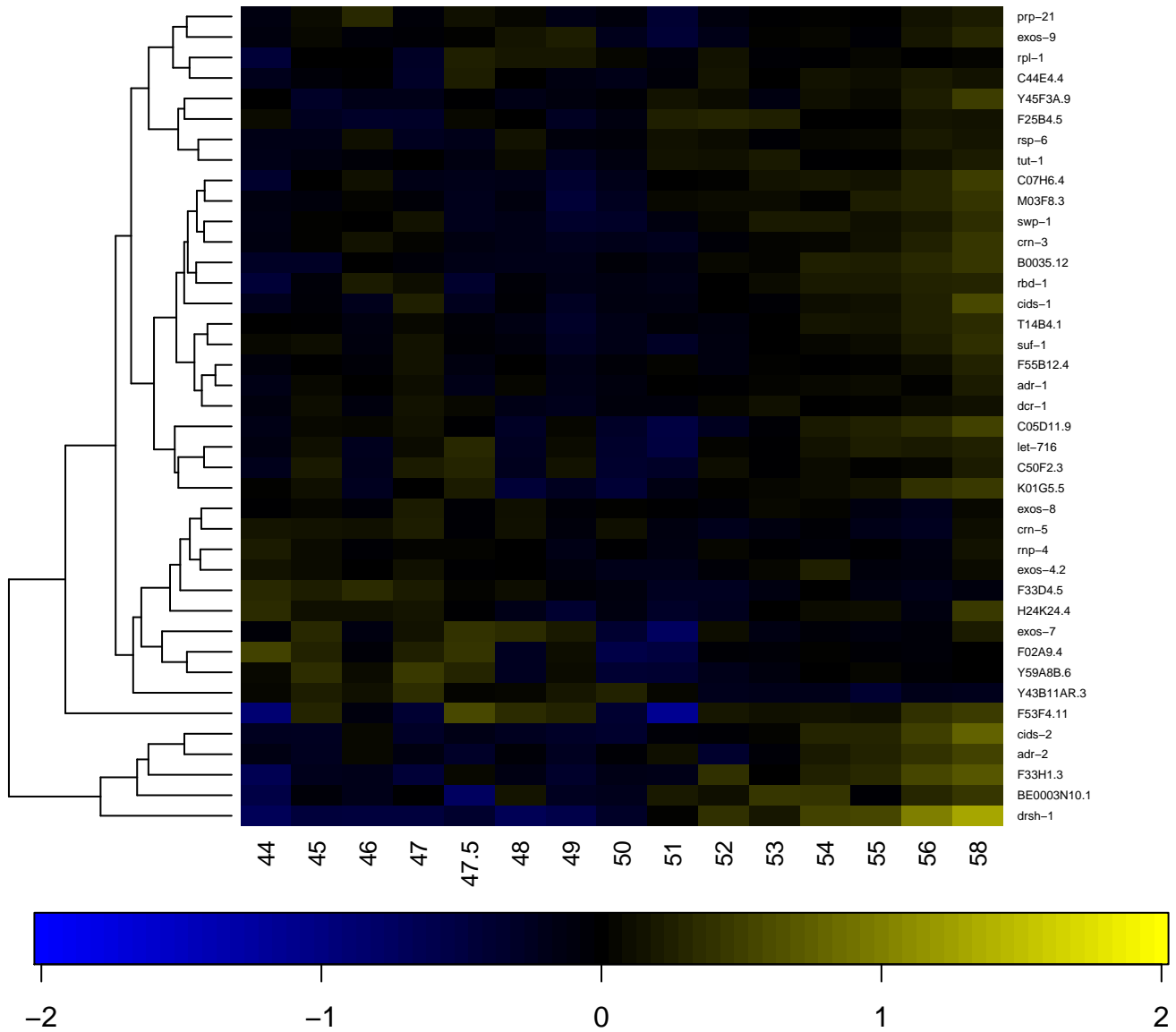
NA polymerase II transcription factor activity, enhancer binding



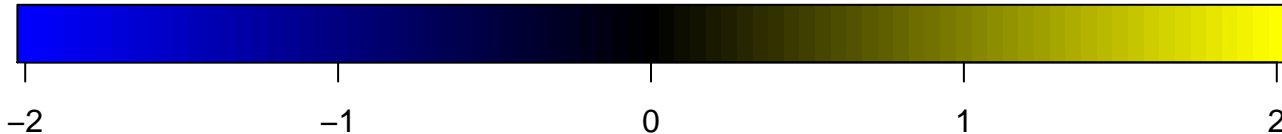
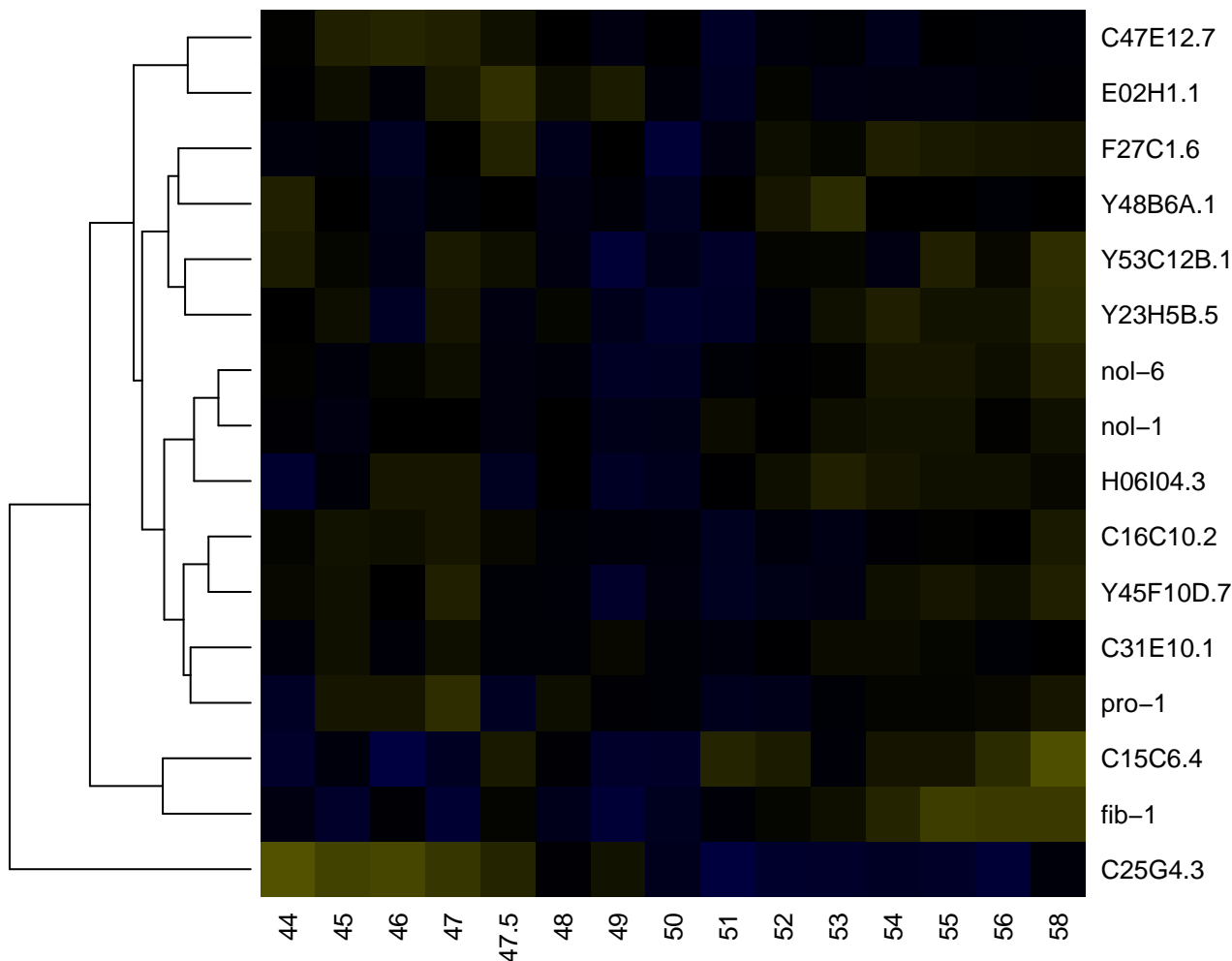
RNA polymerase II transcription mediator activity



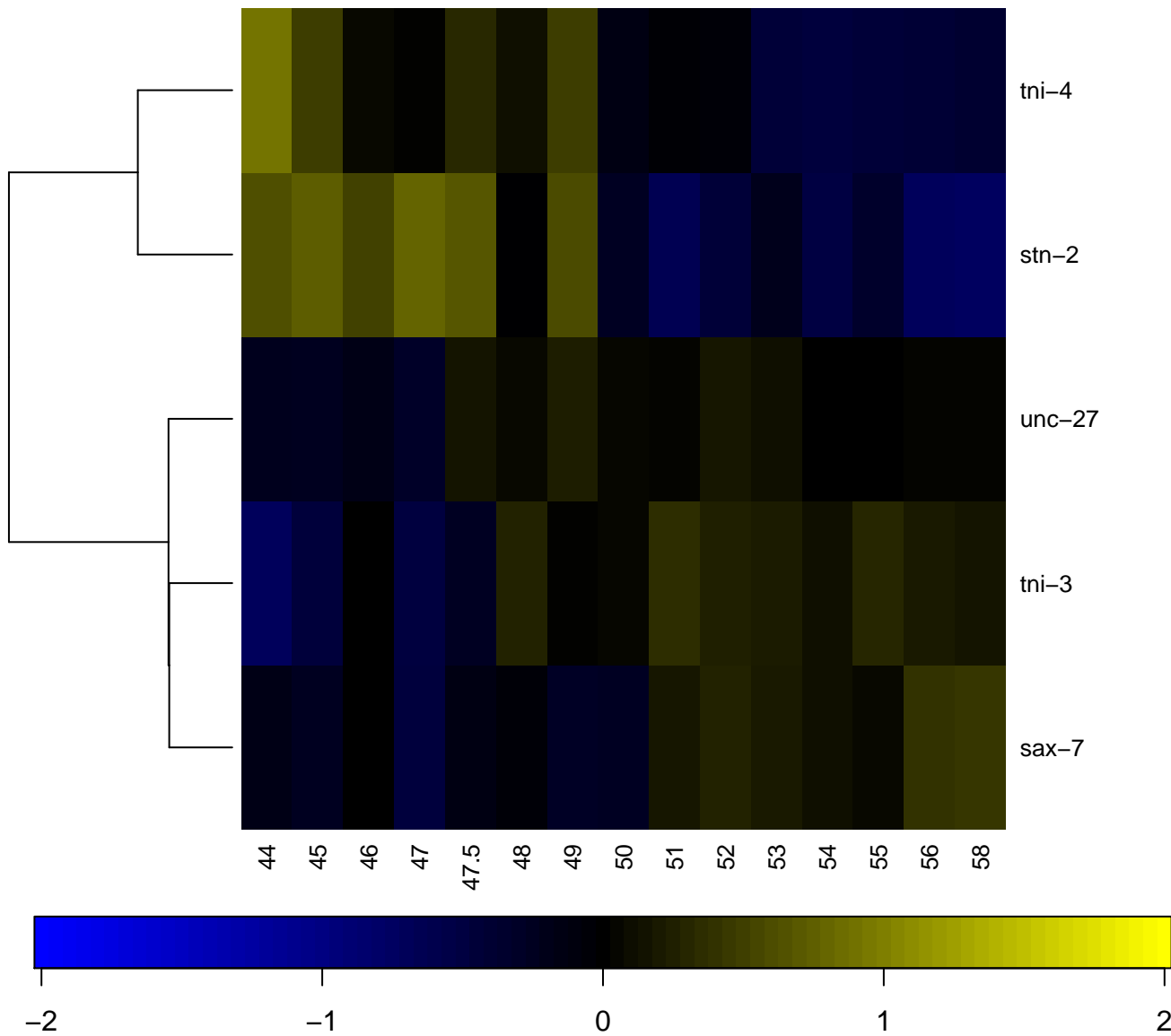
RNA processing



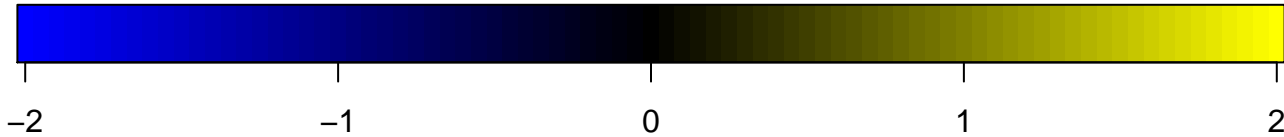
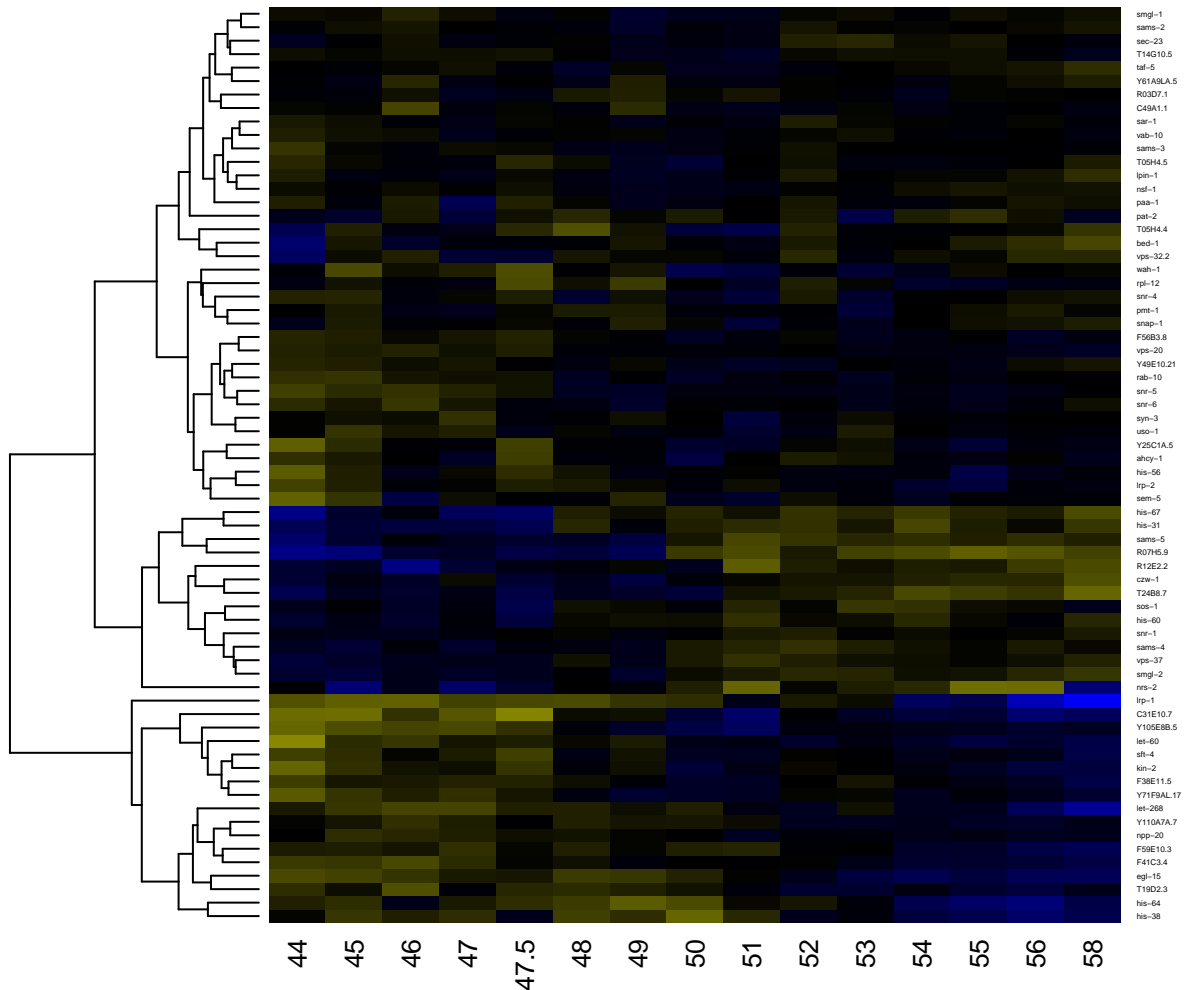
rRNA processing



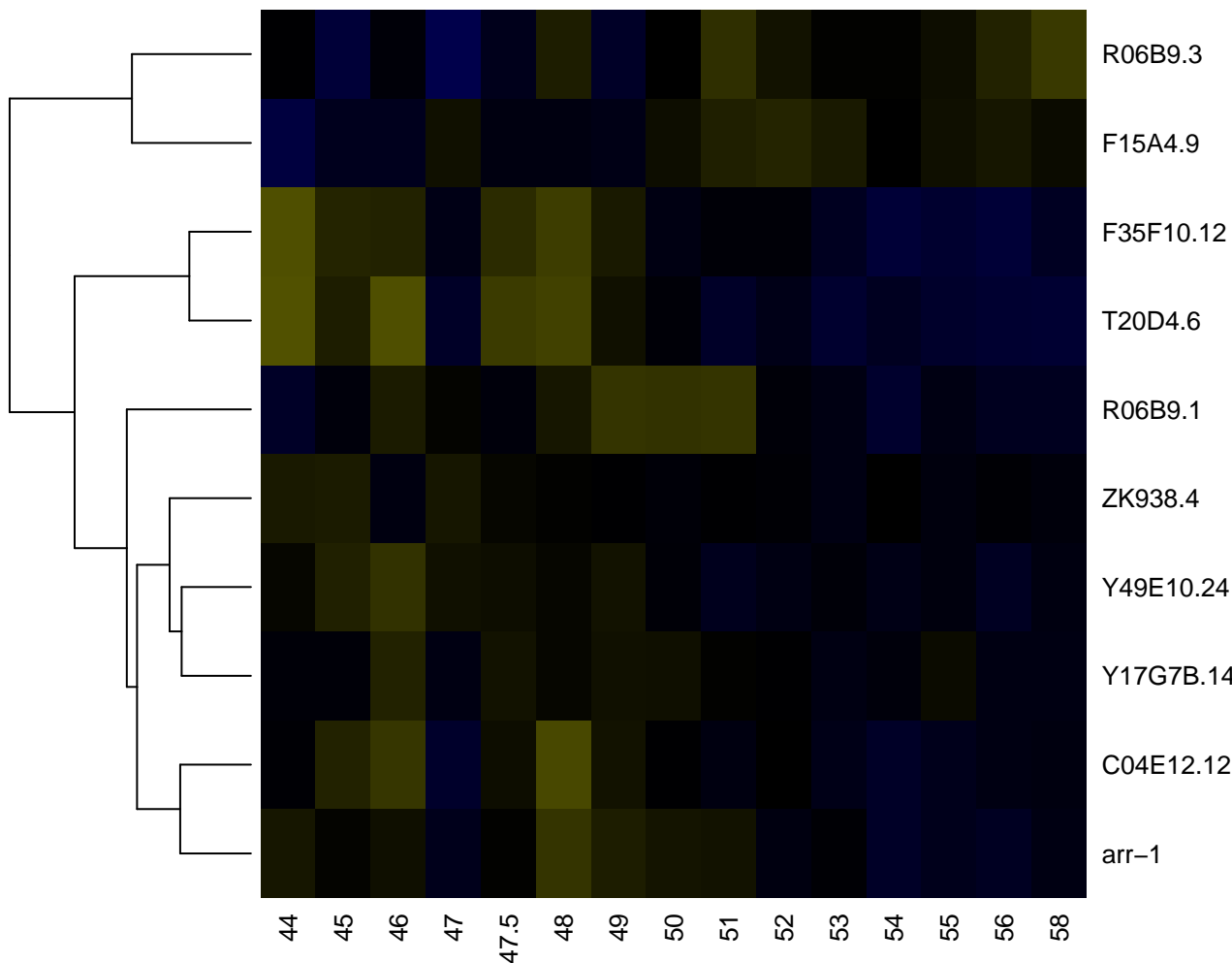
sarcomere



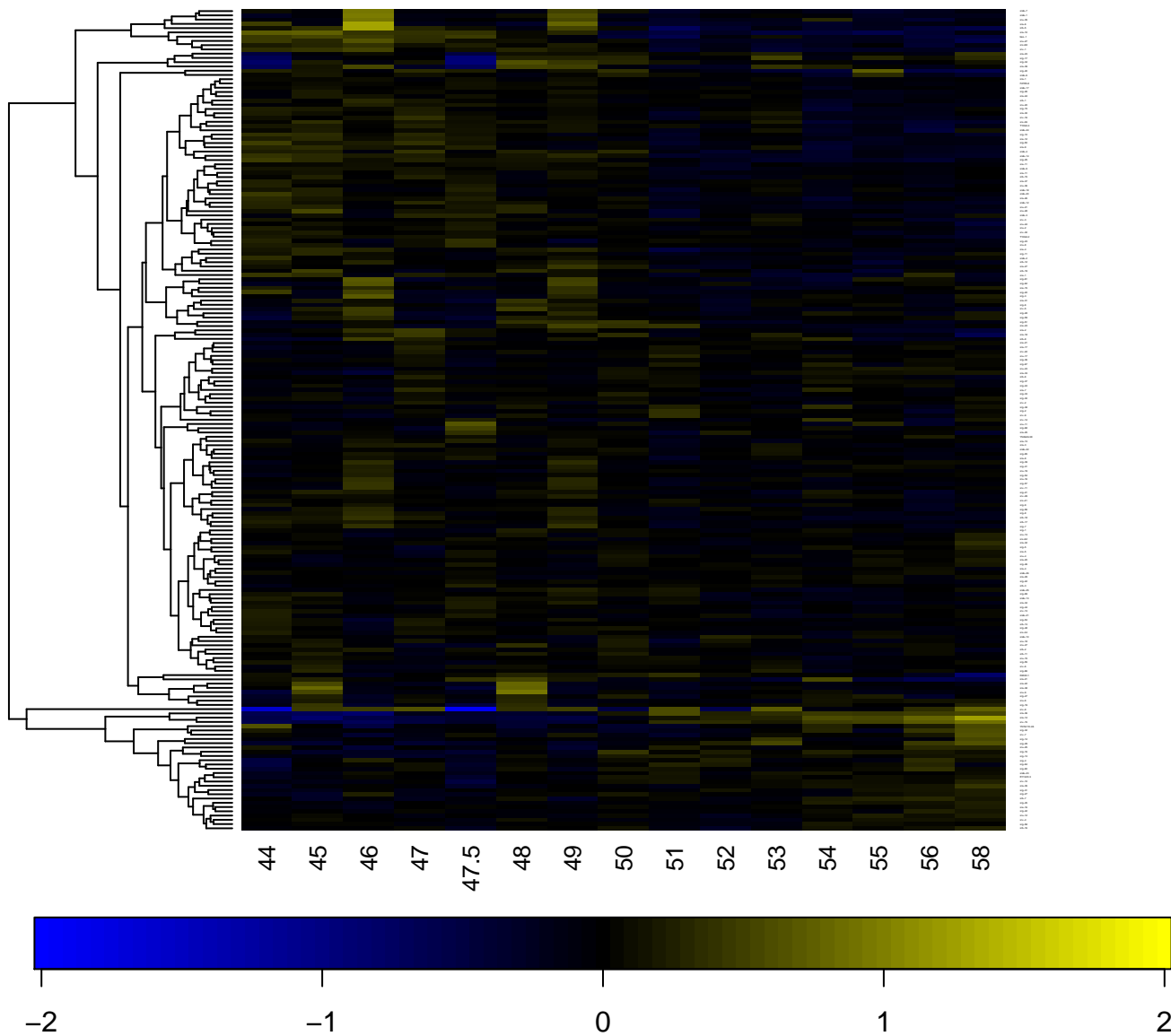
secretion by cell



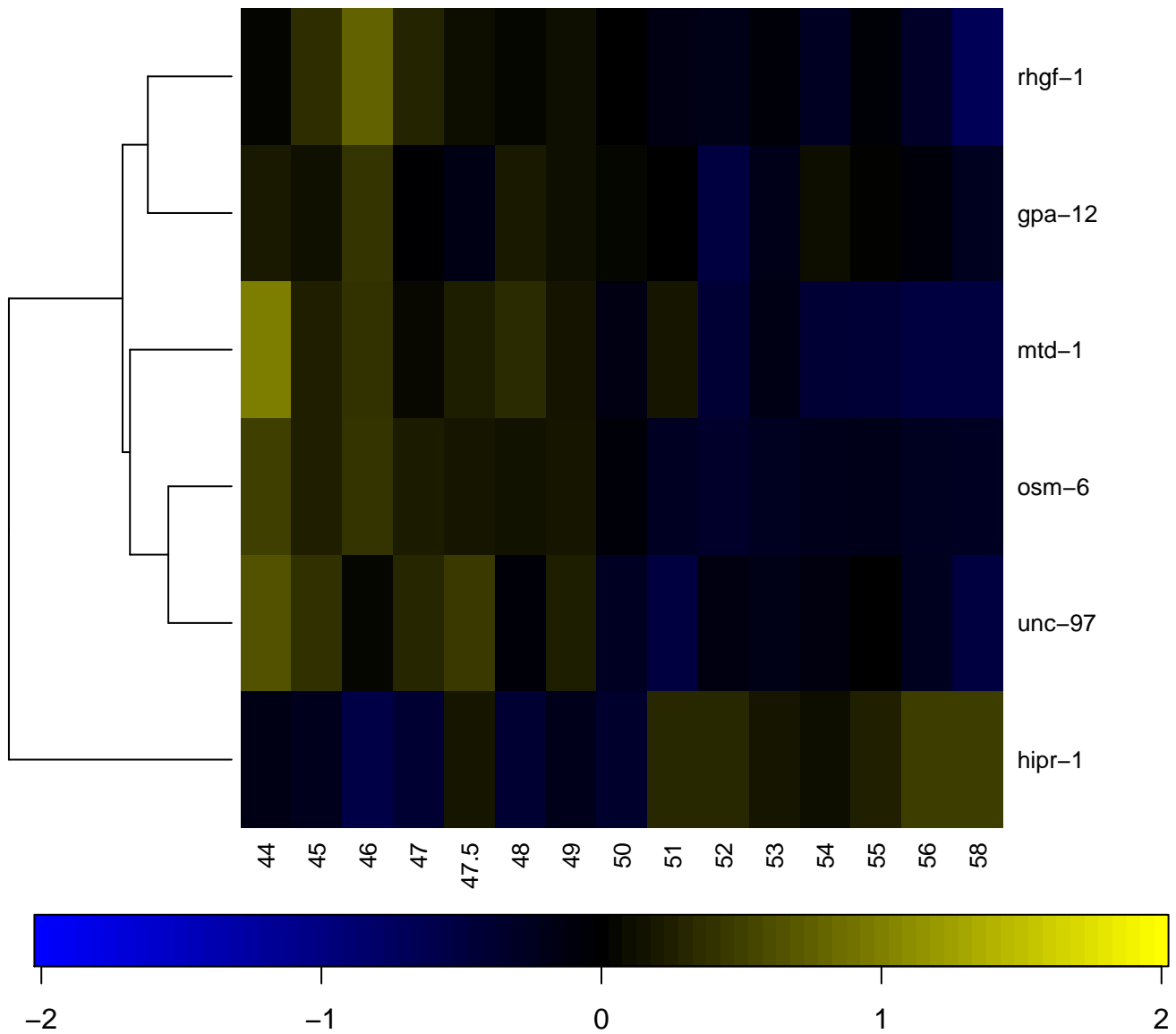
sensory perception



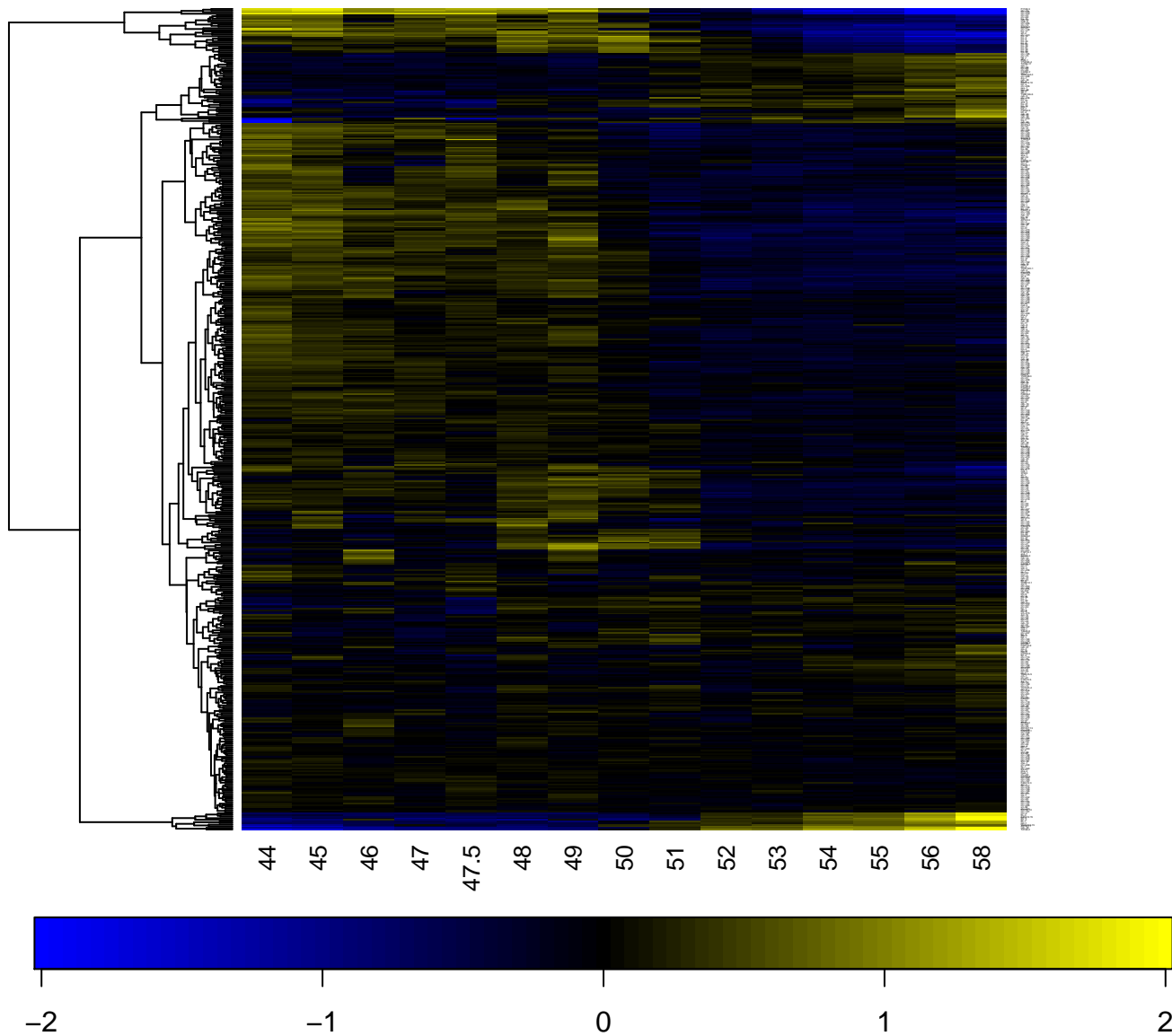
sensory perception of chemical stimulus



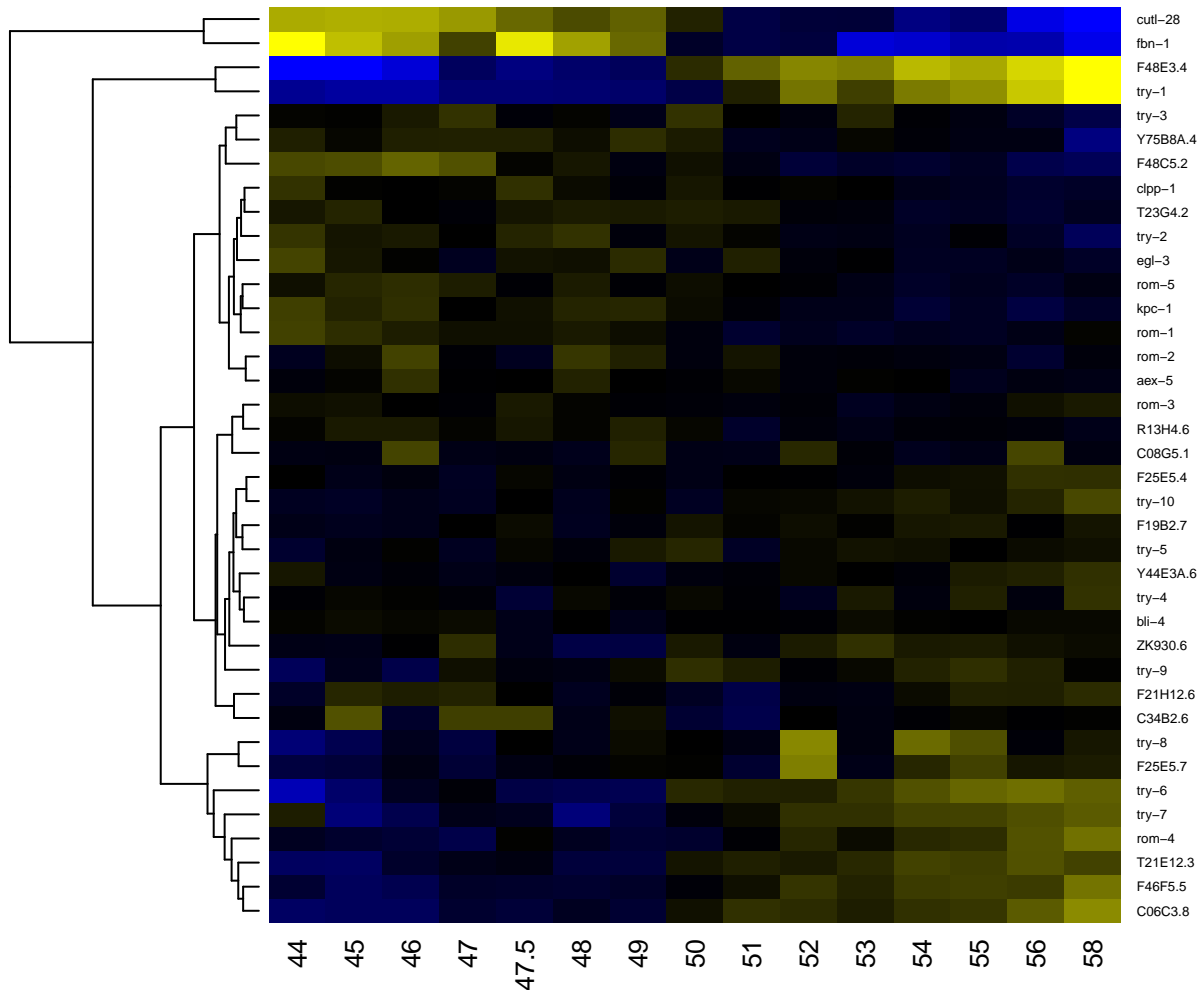
sensory perception of mechanical stimulus



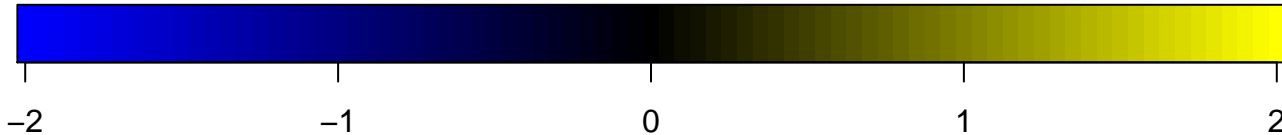
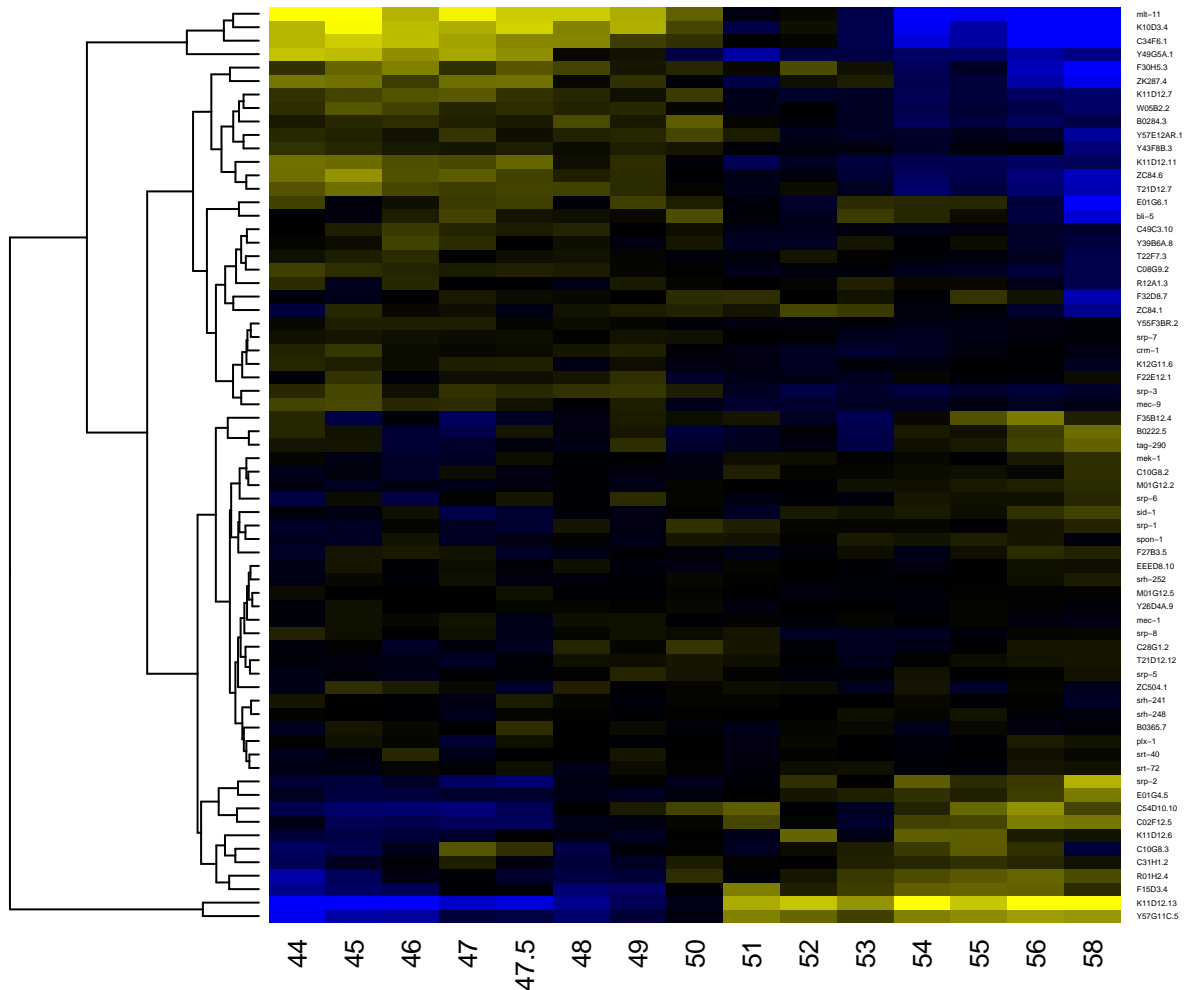
sequence-specific DNA binding



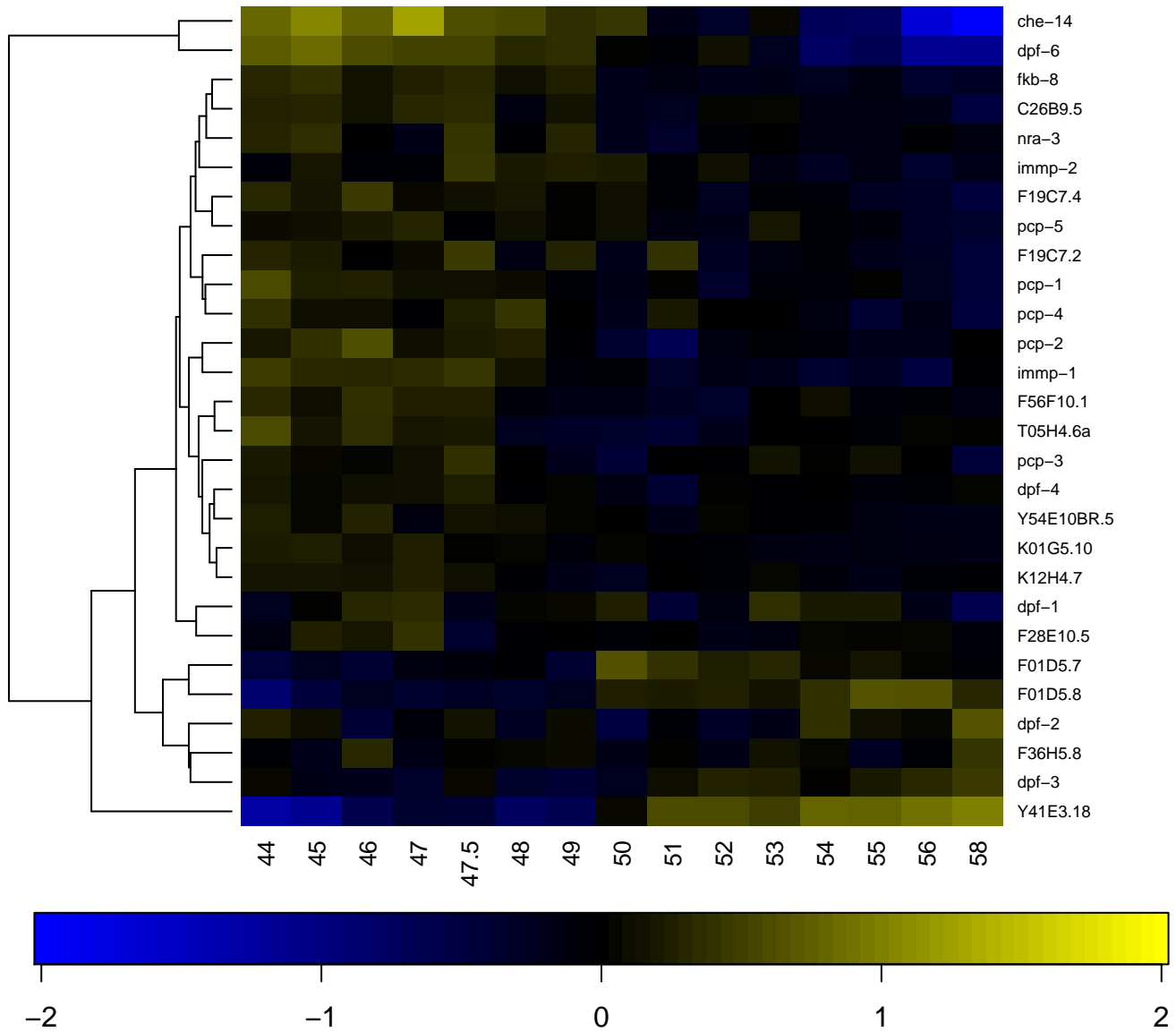
serine-type endopeptidase activity



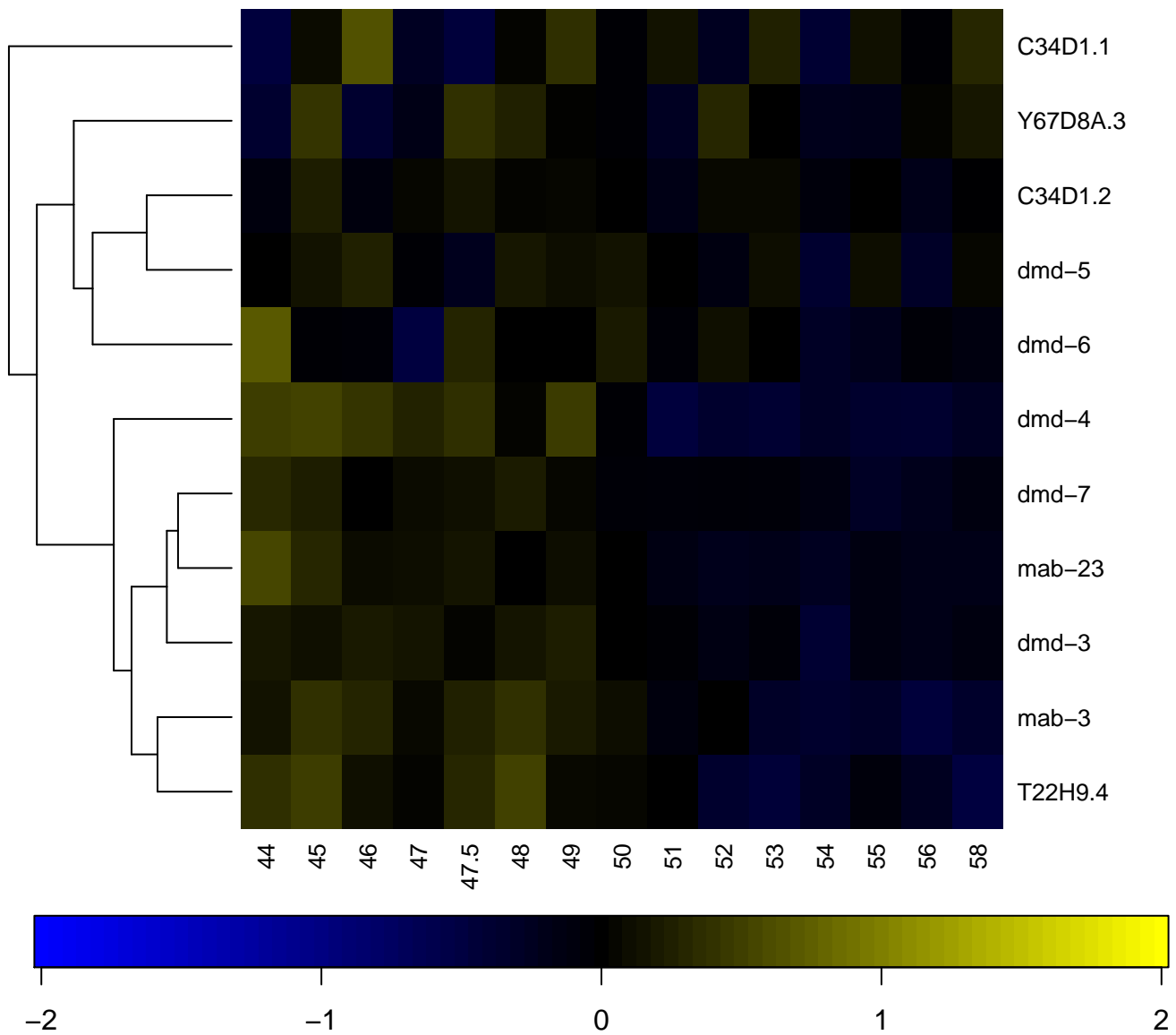
serine-type endopeptidase inhibitor activity



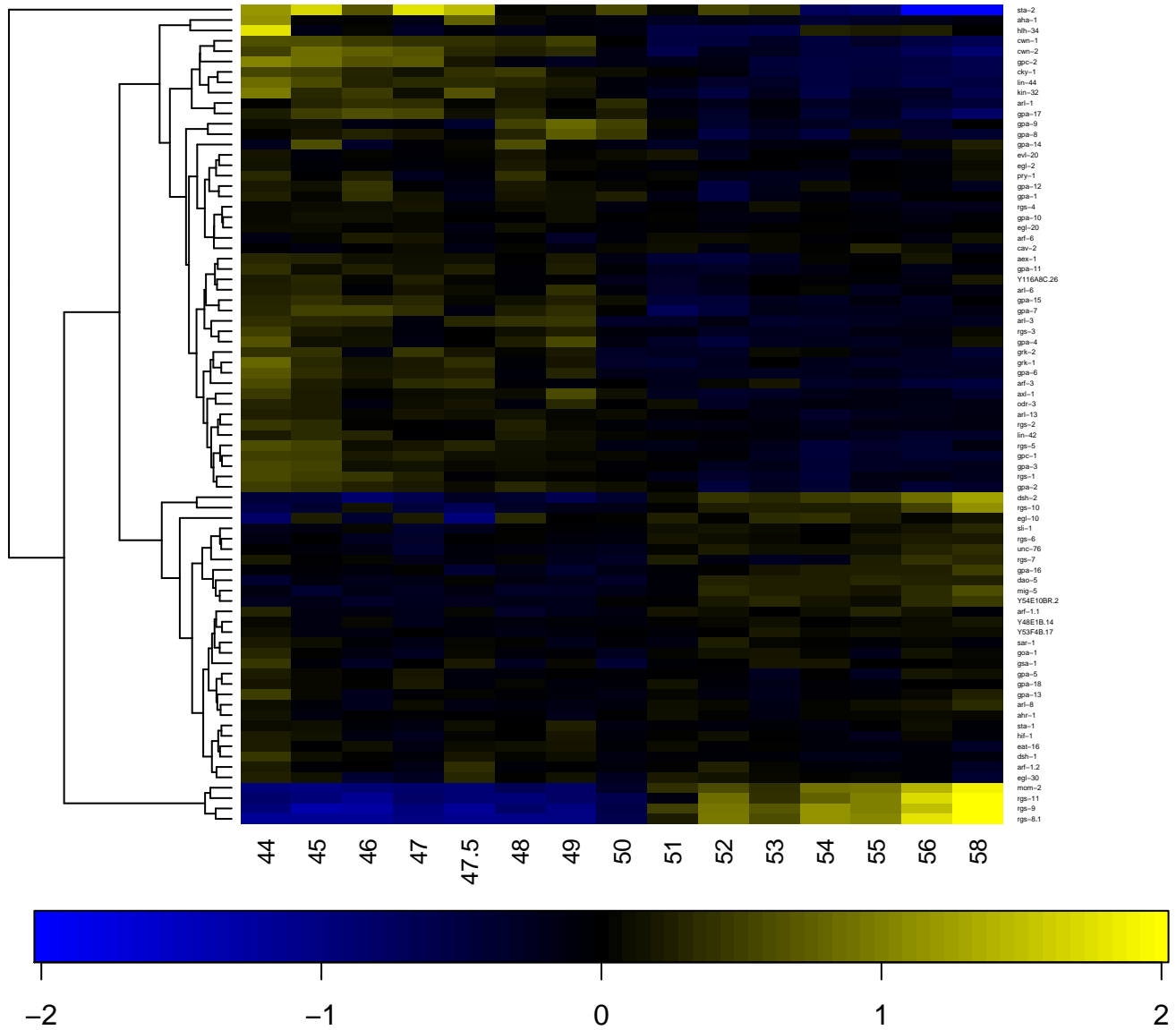
serine-type peptidase activity



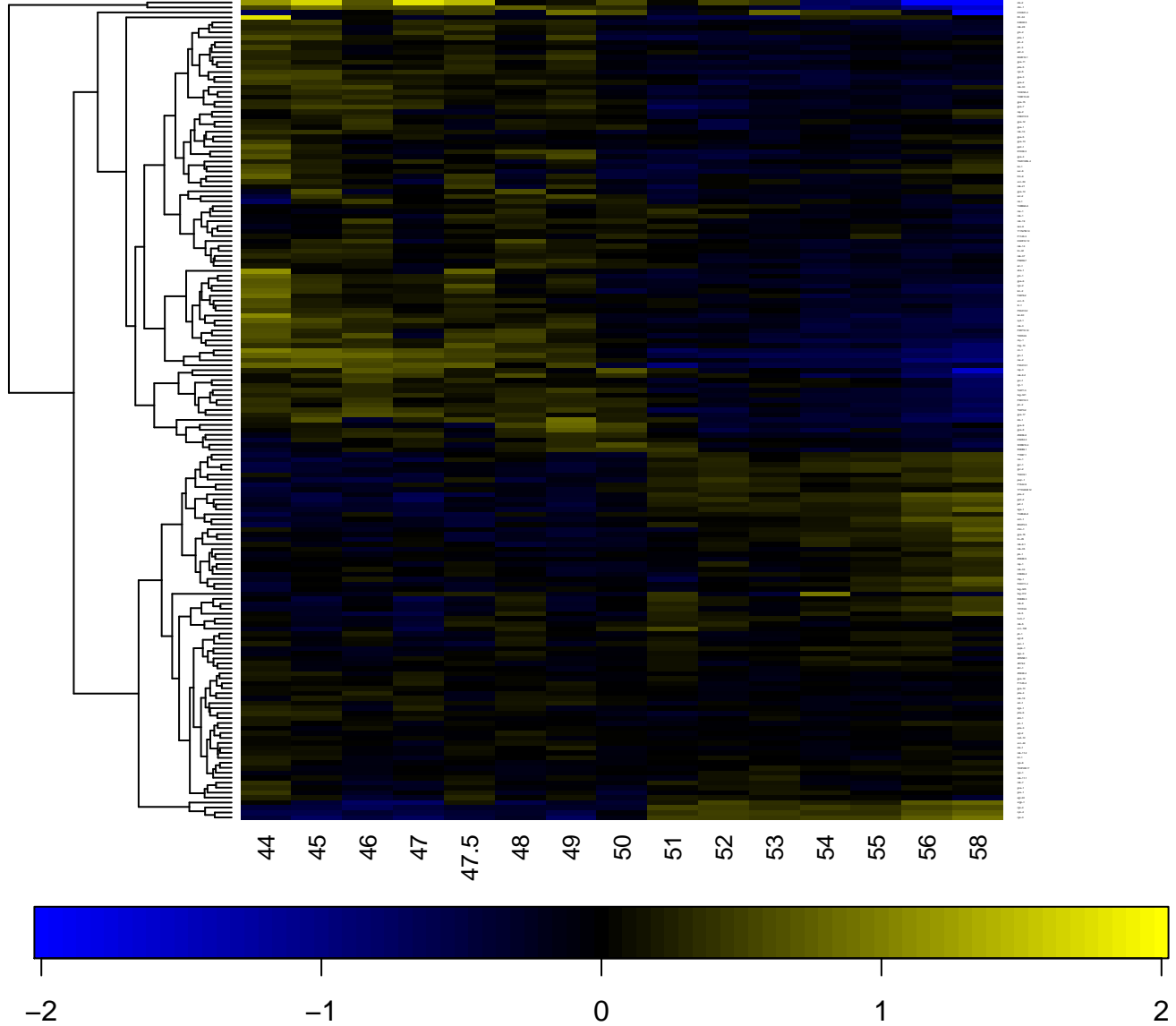
sex differentiation



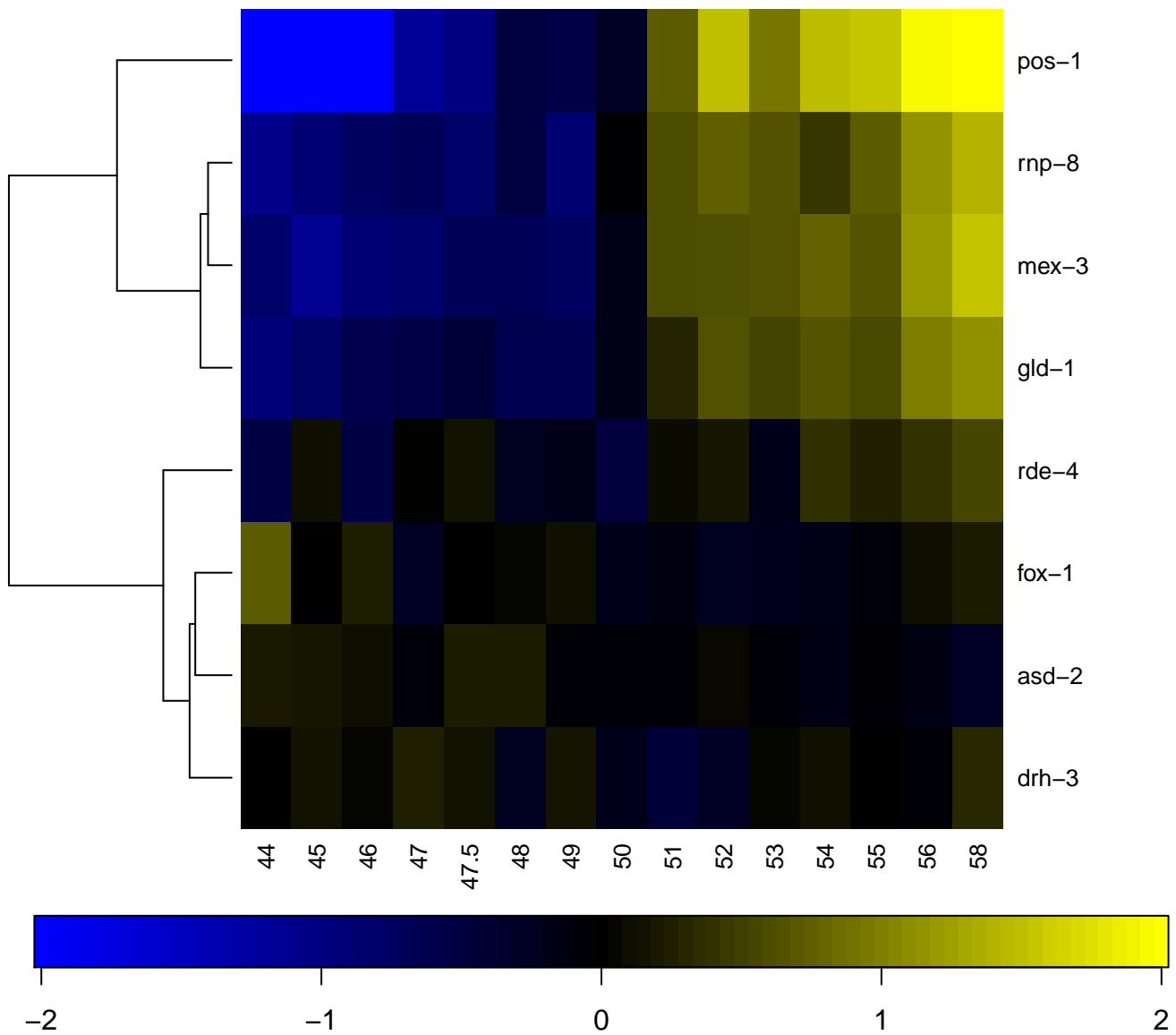
signal transducer activity



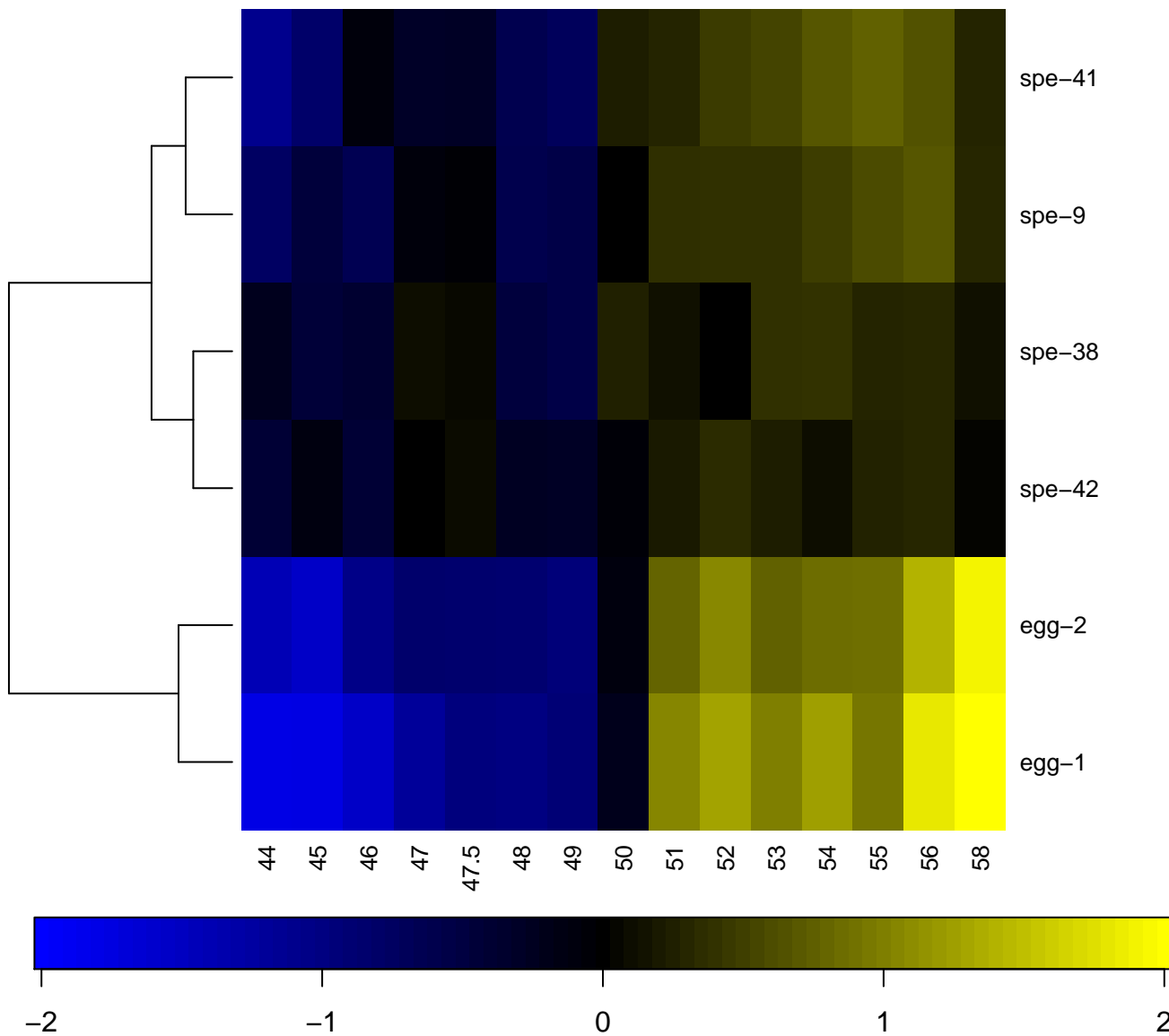
signal transduction



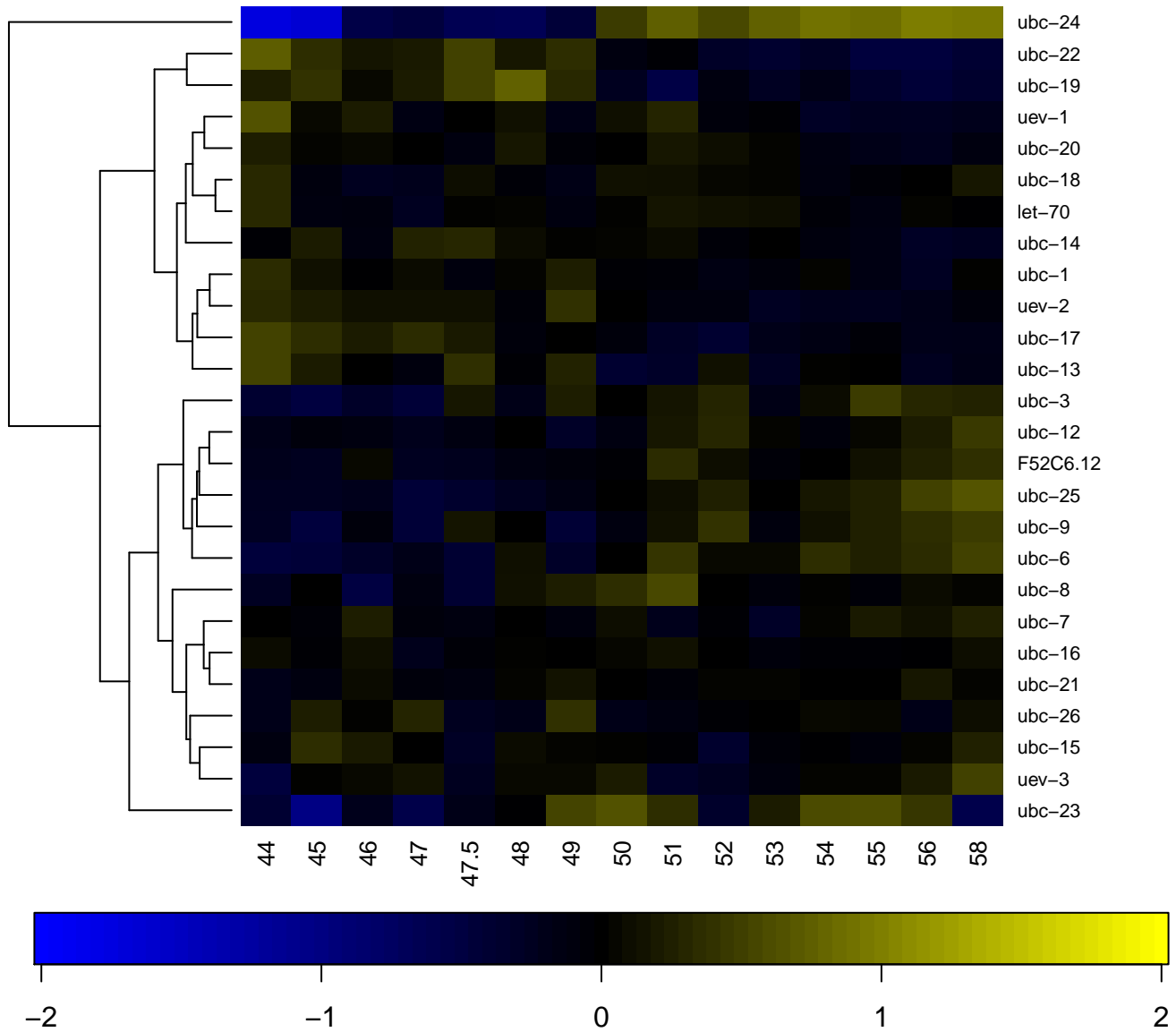
single-stranded RNA binding



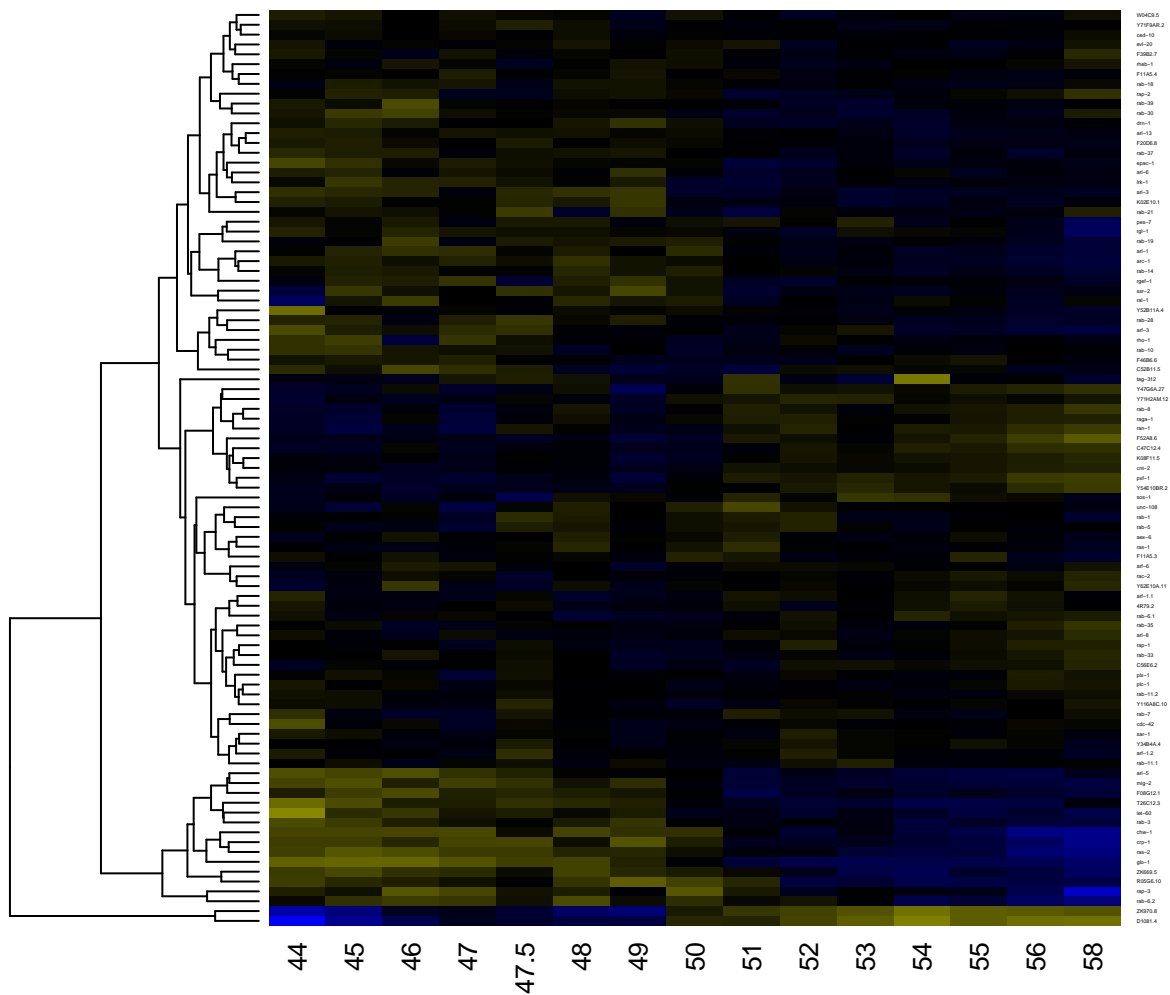
single fertilization



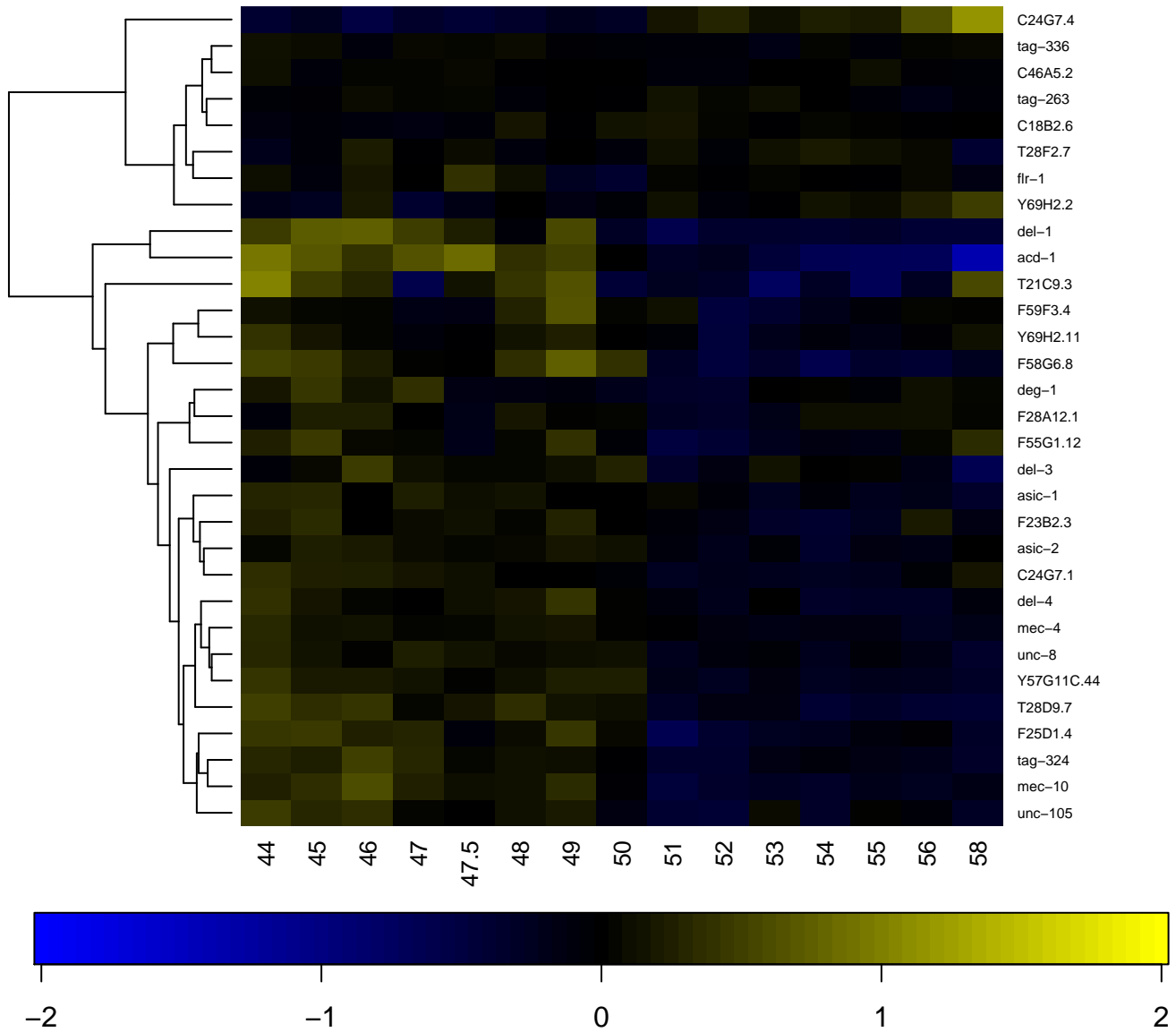
small conjugating protein ligase activity



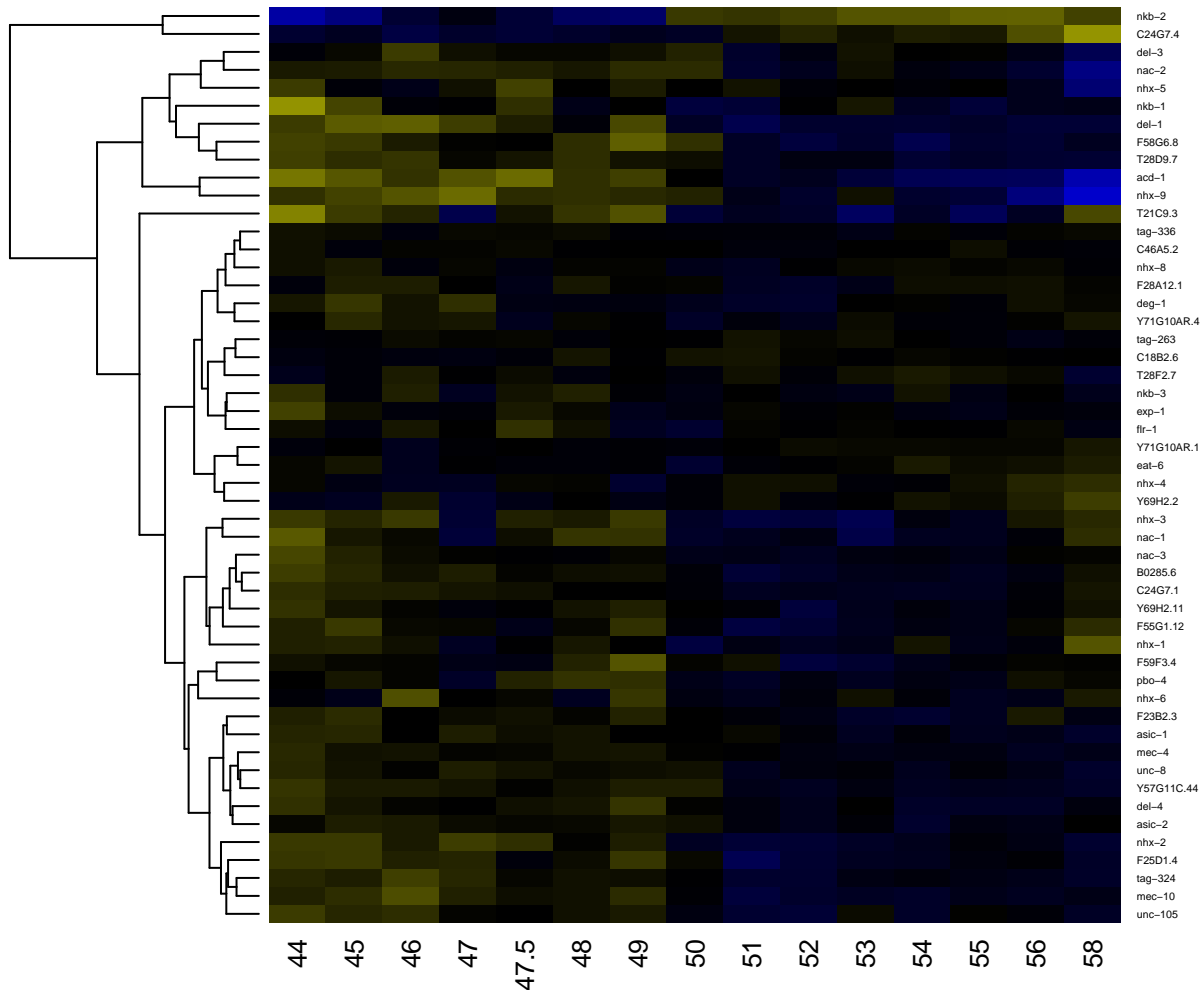
small GTPase mediated signal transduction



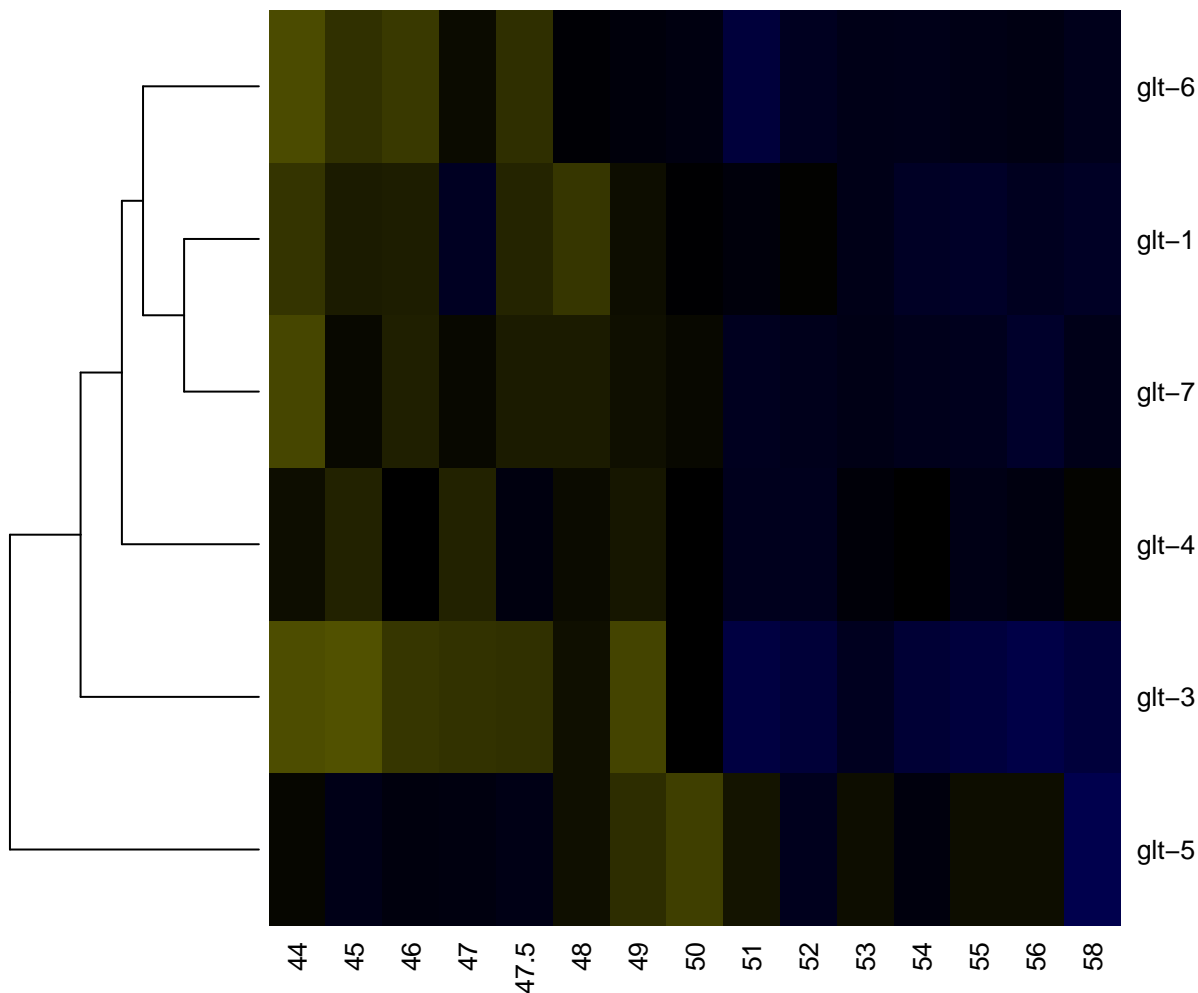
sodium channel activity



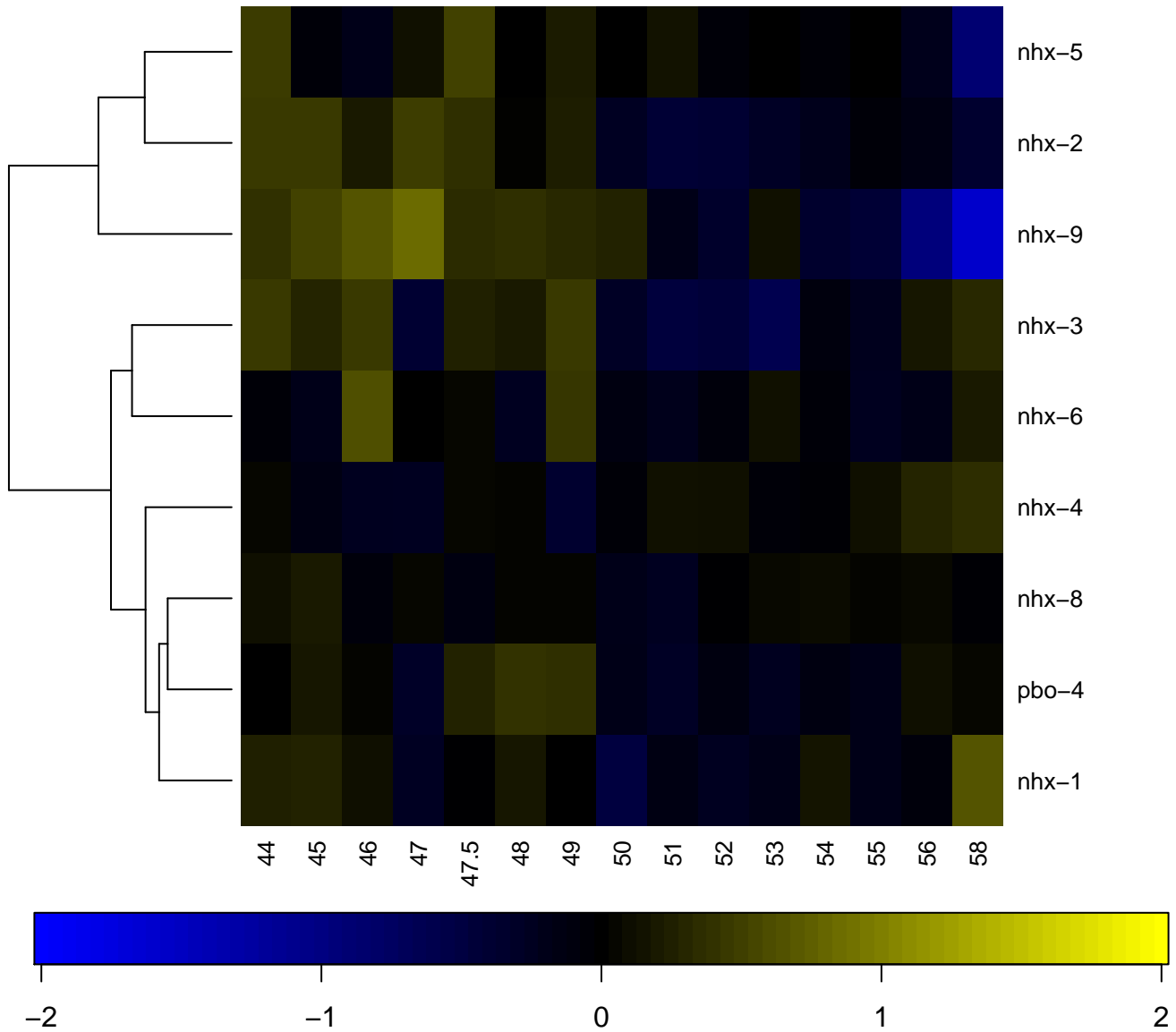
sodium ion transport



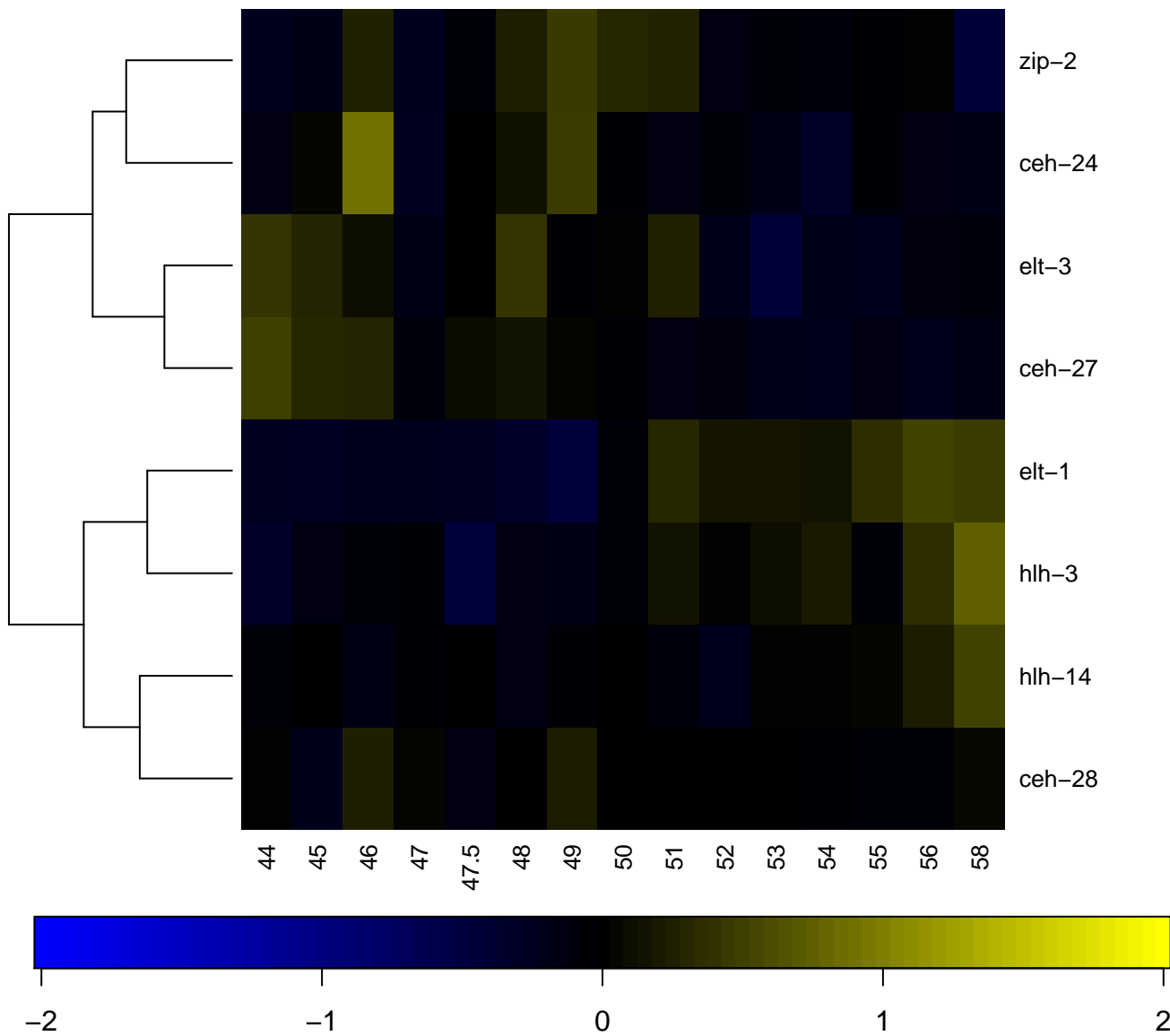
sodium:dicarboxylate symporter activity



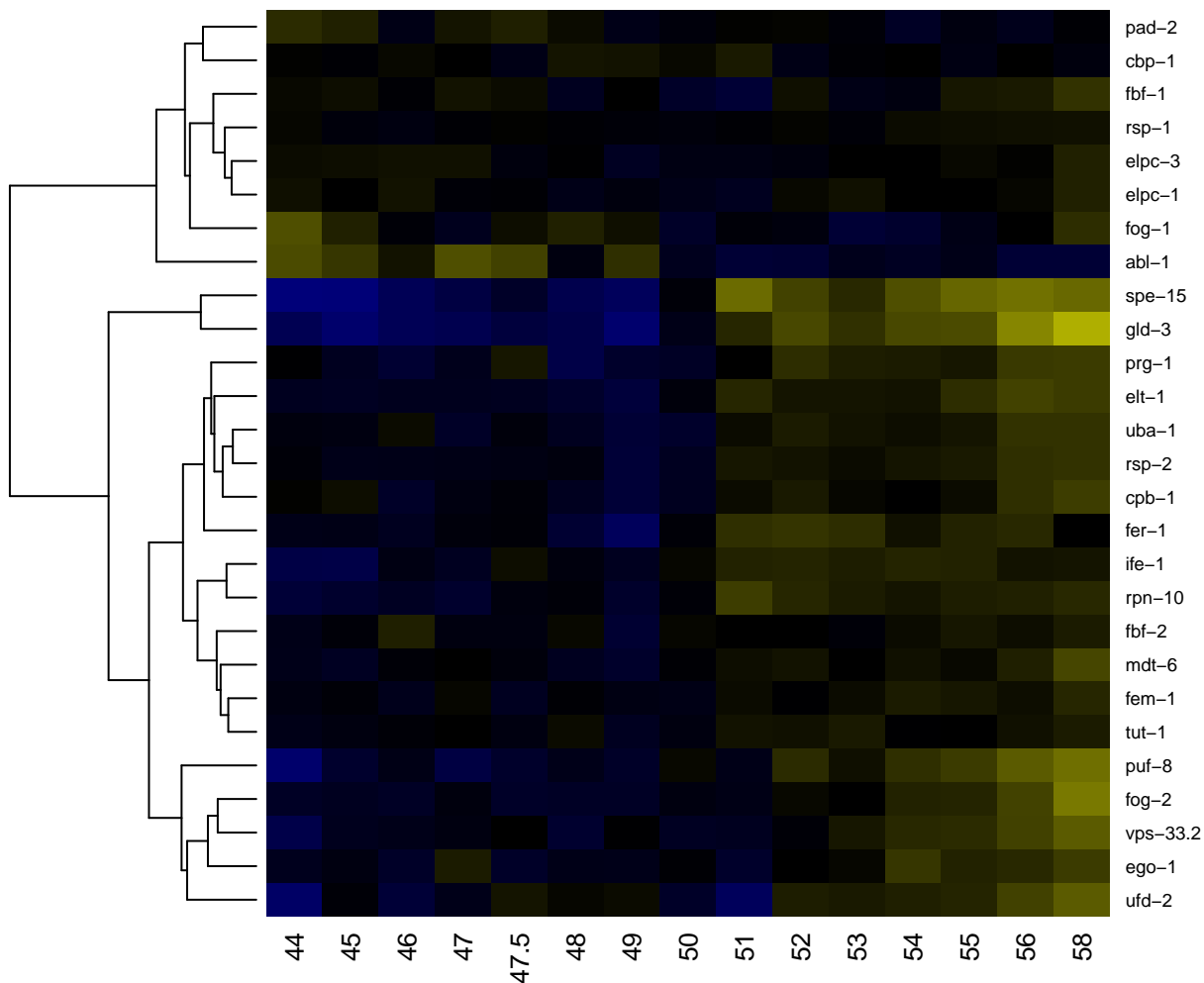
sodium:hydrogen antiporter activity



specific RNA polymerase II transcription factor activity



spermatogenesis



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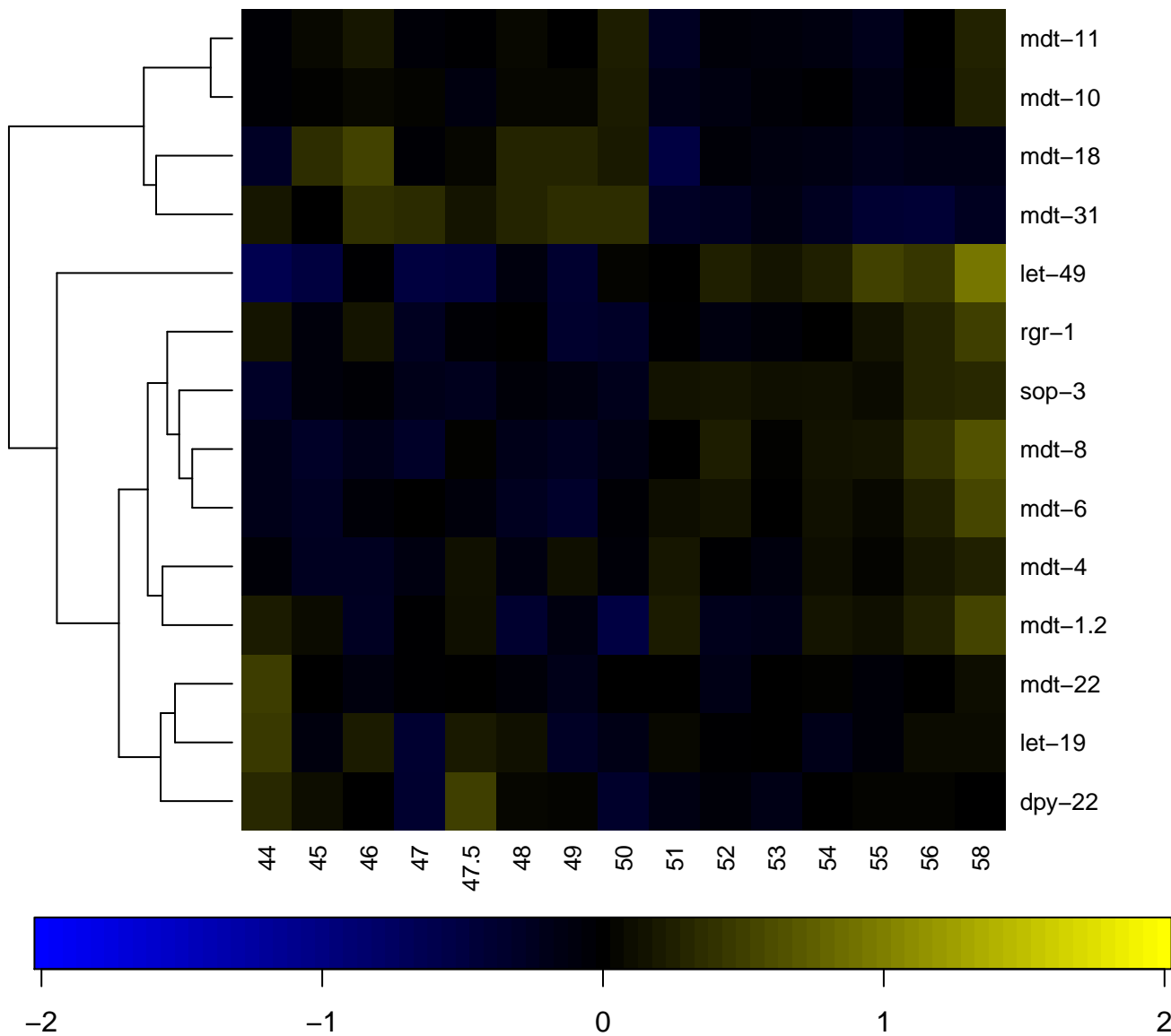
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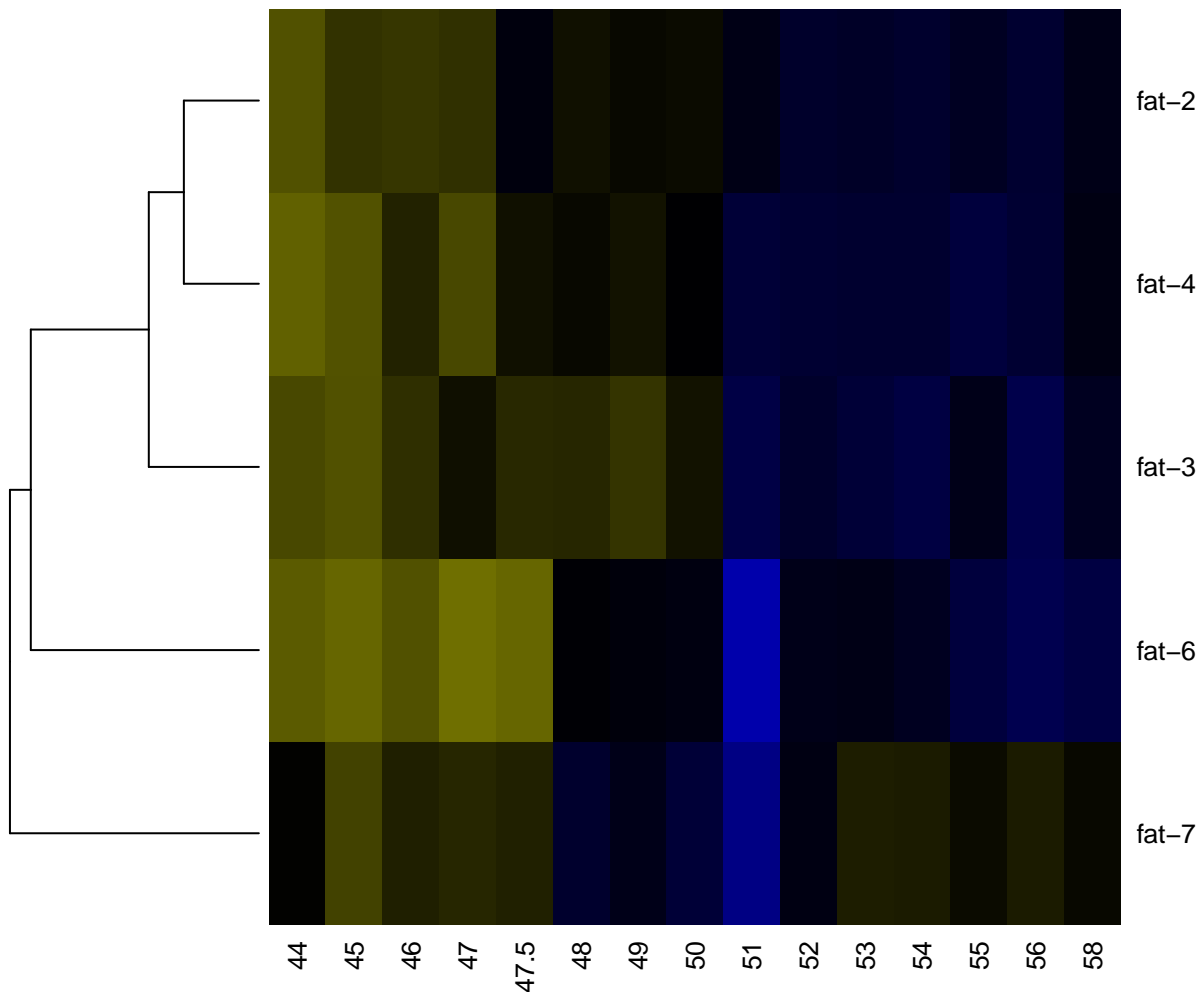
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Srb-mediator complex



stearoyl-CoA 9-desaturase activity



-2

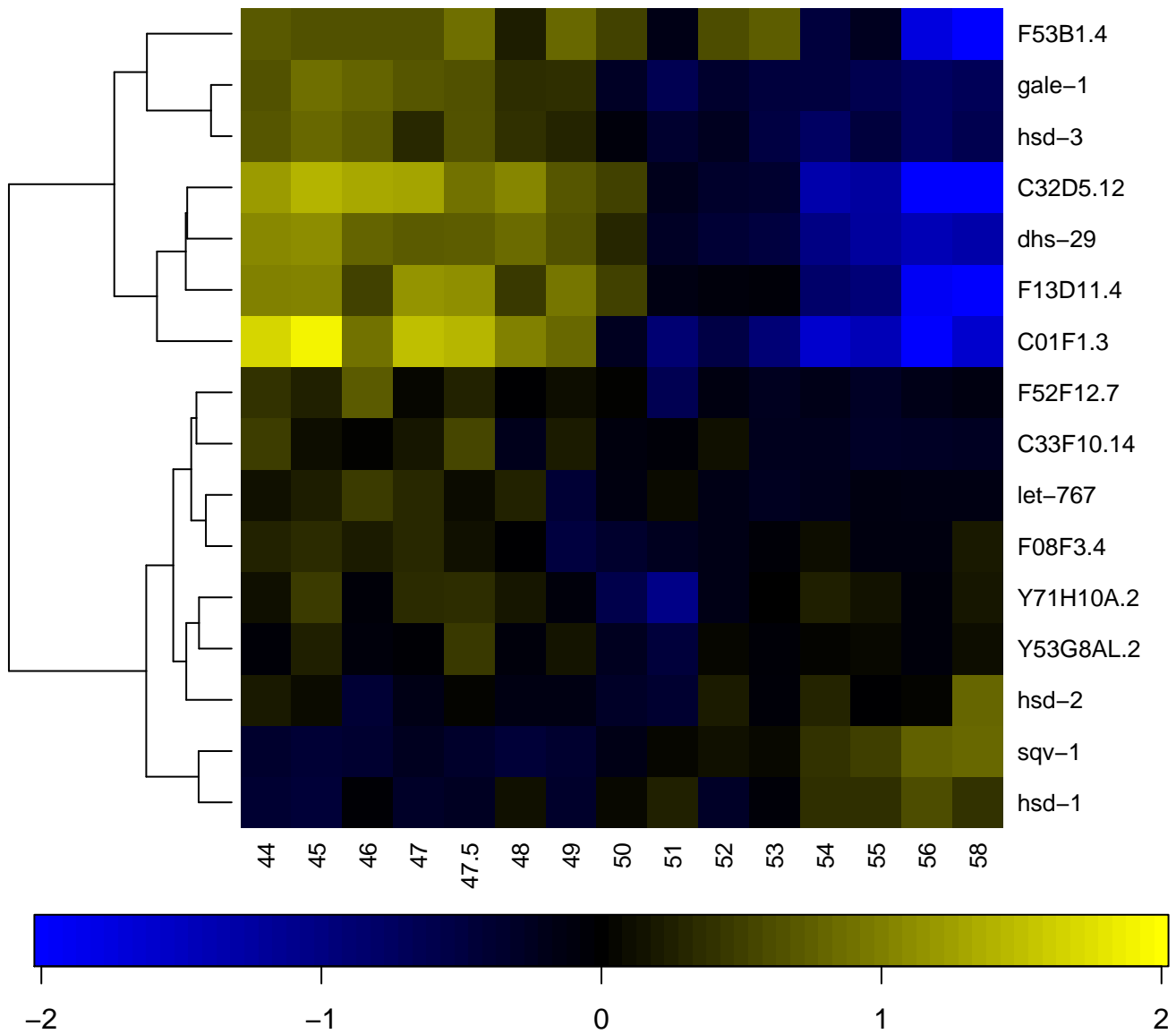
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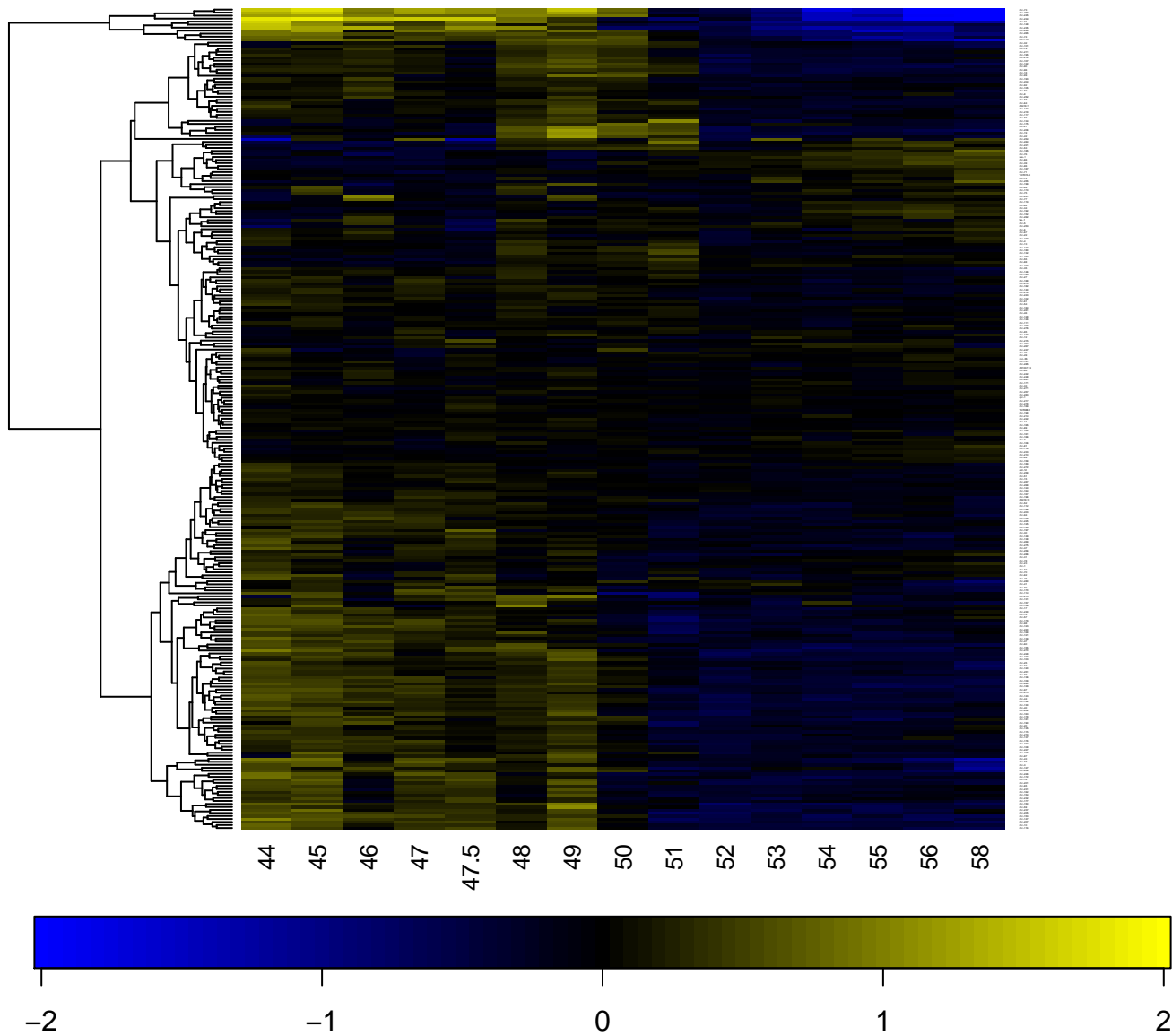
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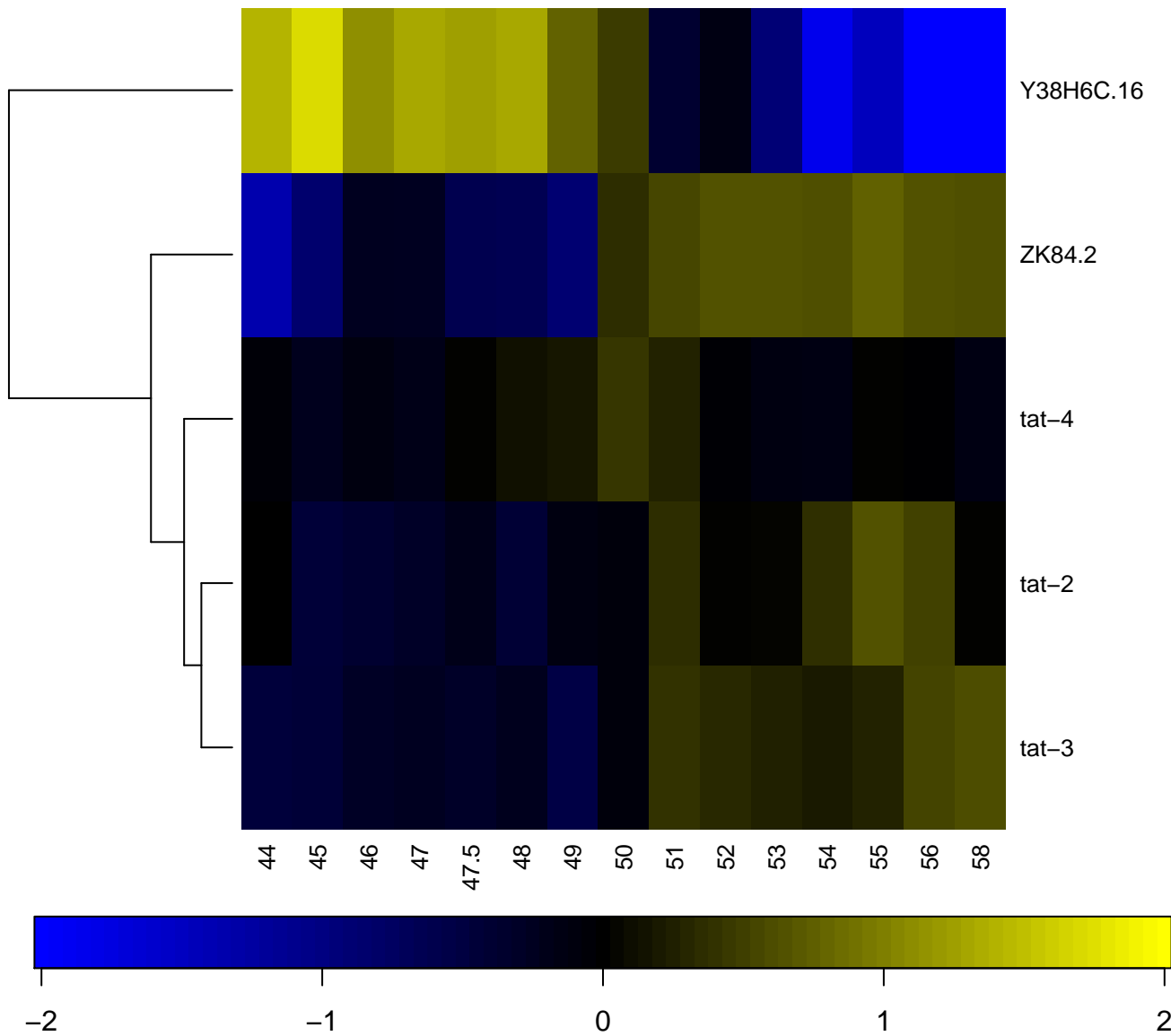
steroid biosynthetic process



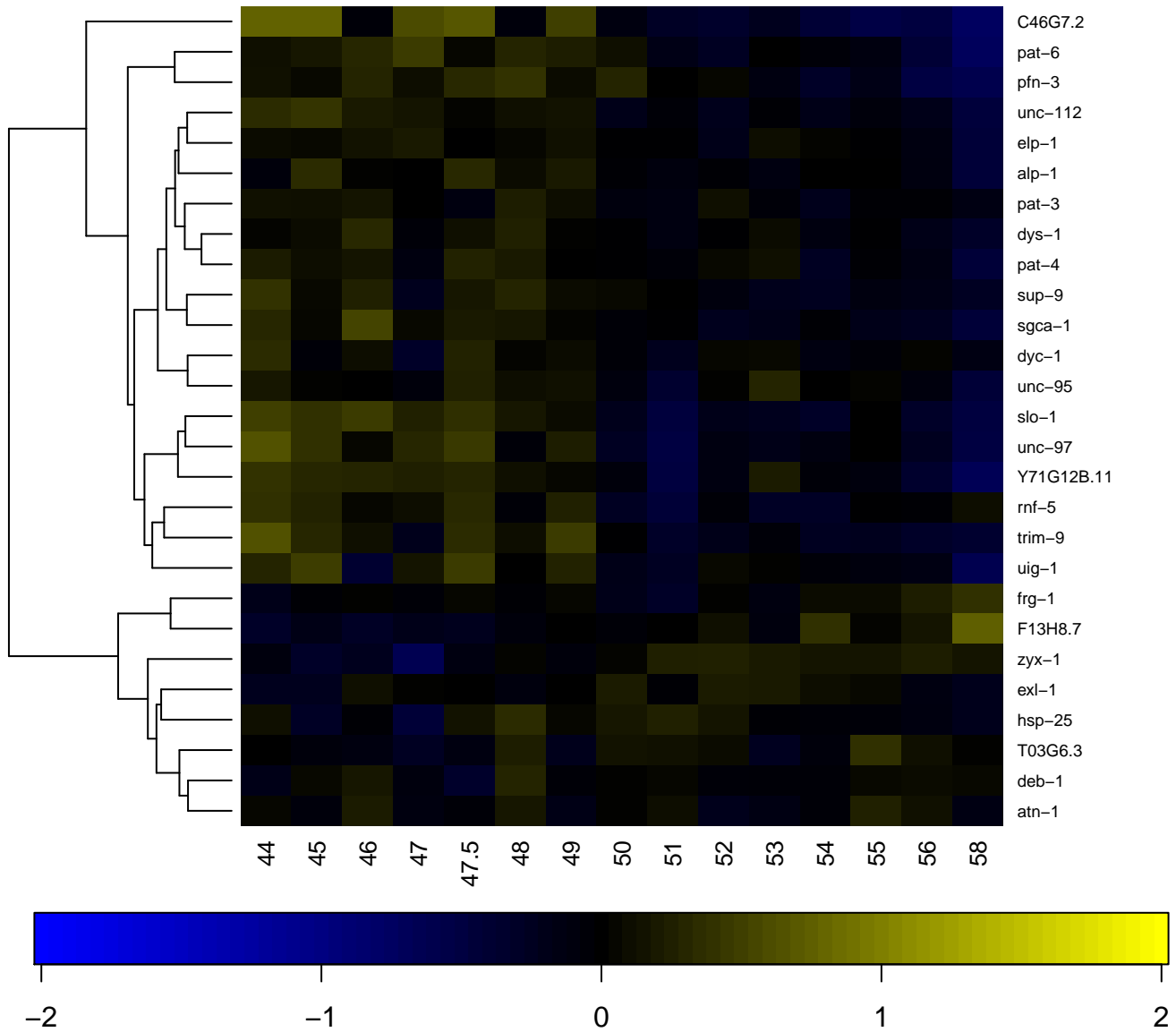
steroid hormone receptor activity



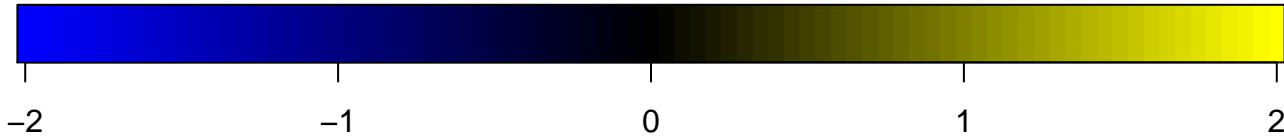
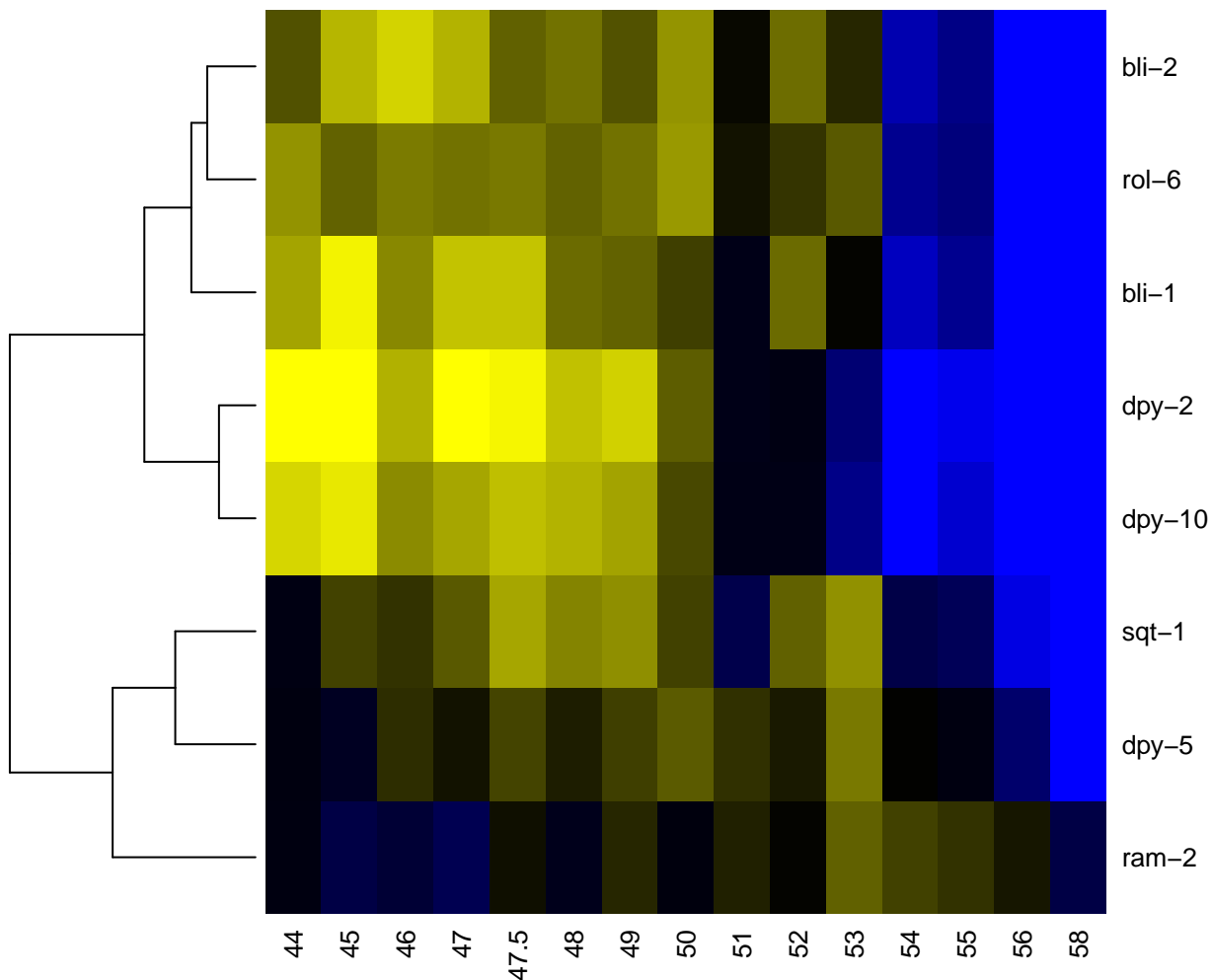
sterol metabolic process



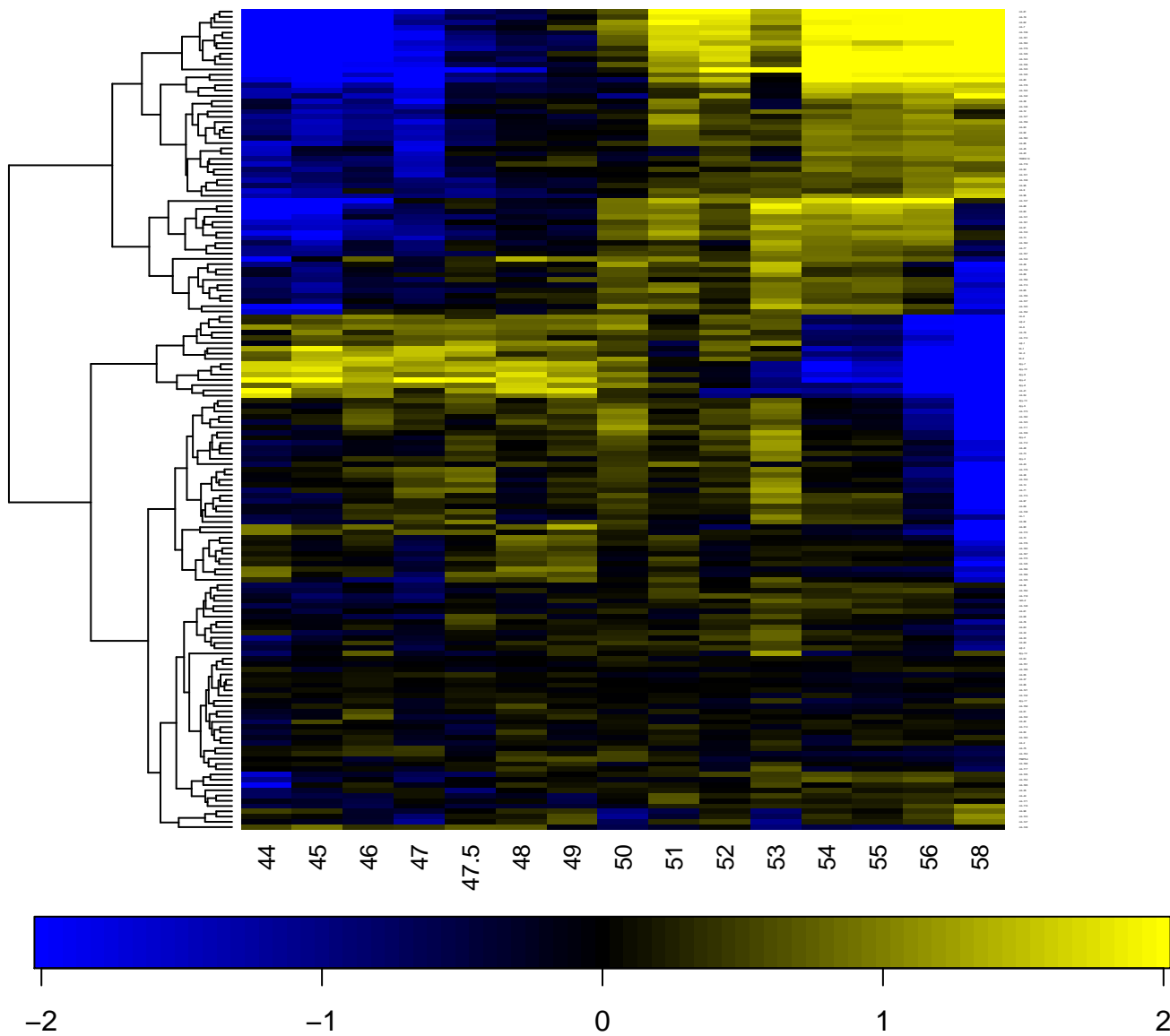
striated muscle dense body



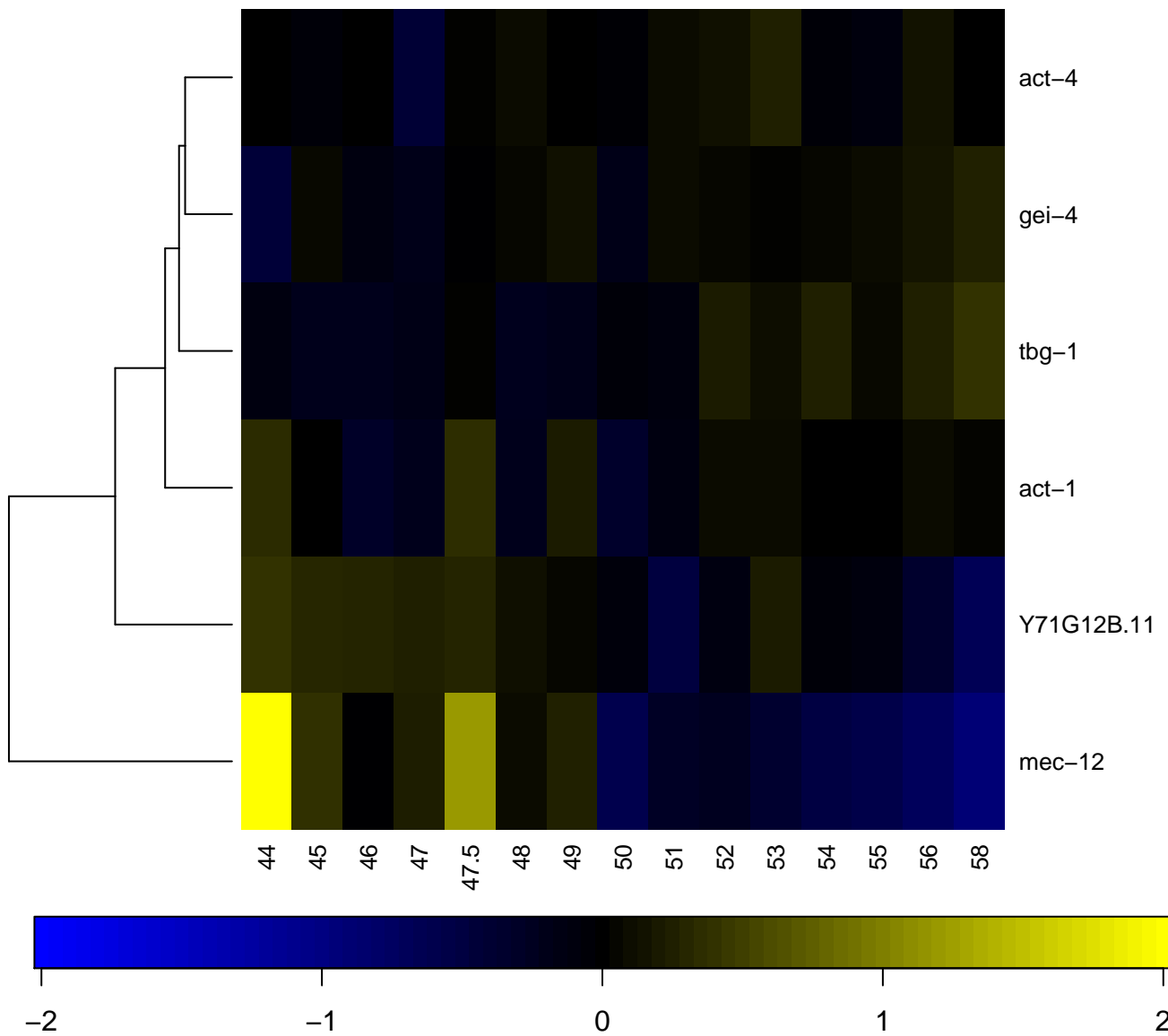
structural constituent of collagen and cuticulin-based cuticle



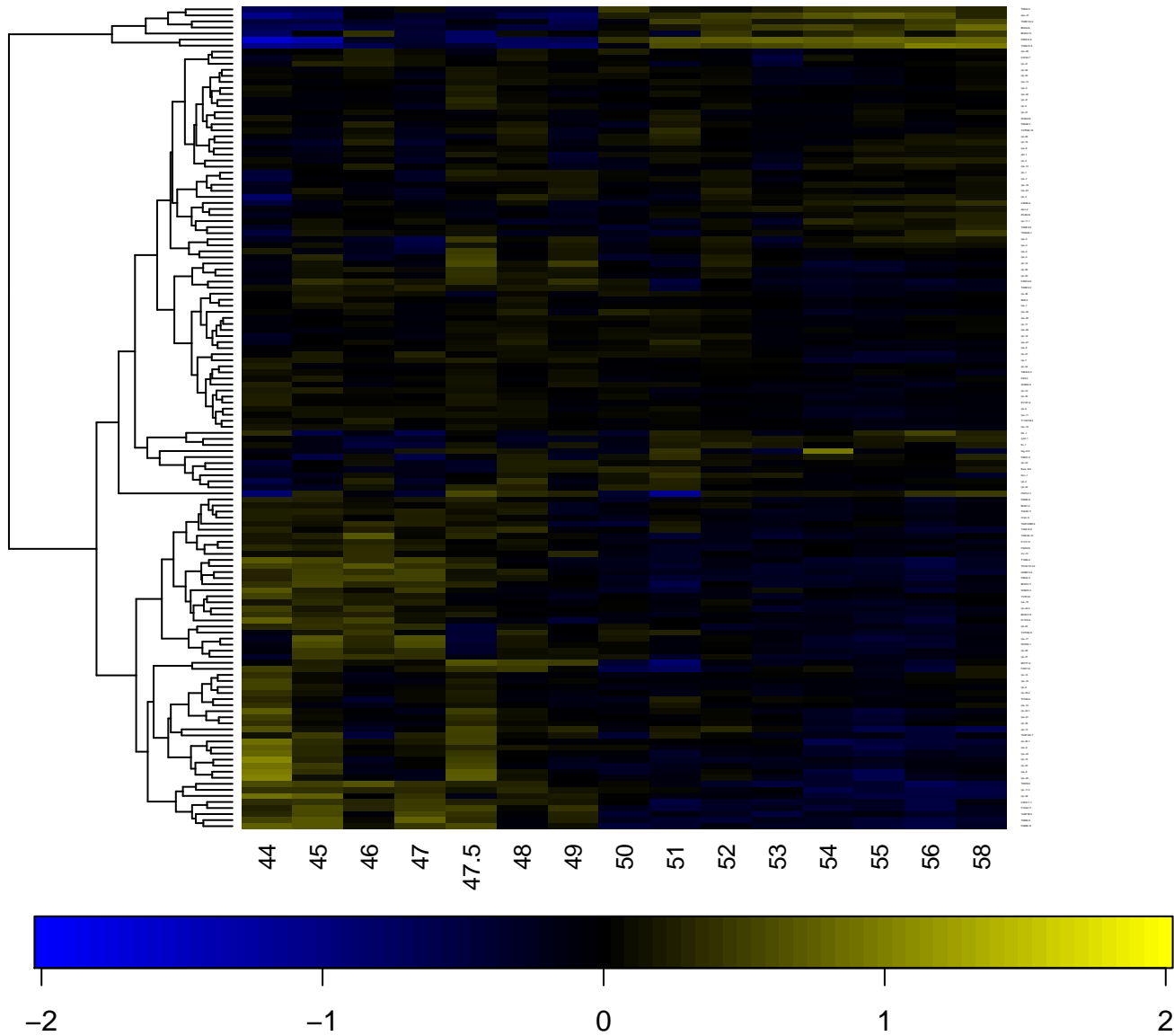
structural constituent of cuticle



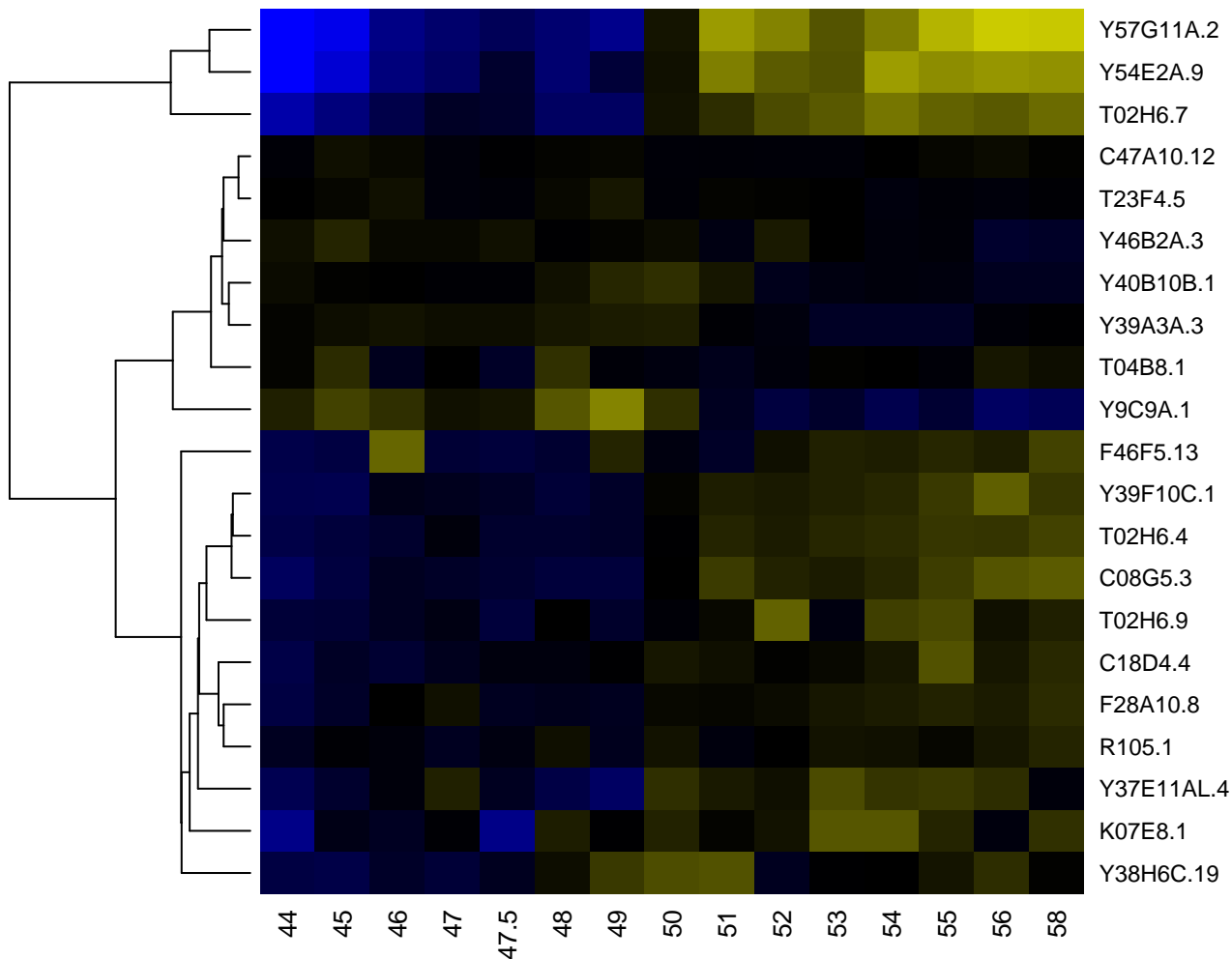
structural constituent of cytoskeleton



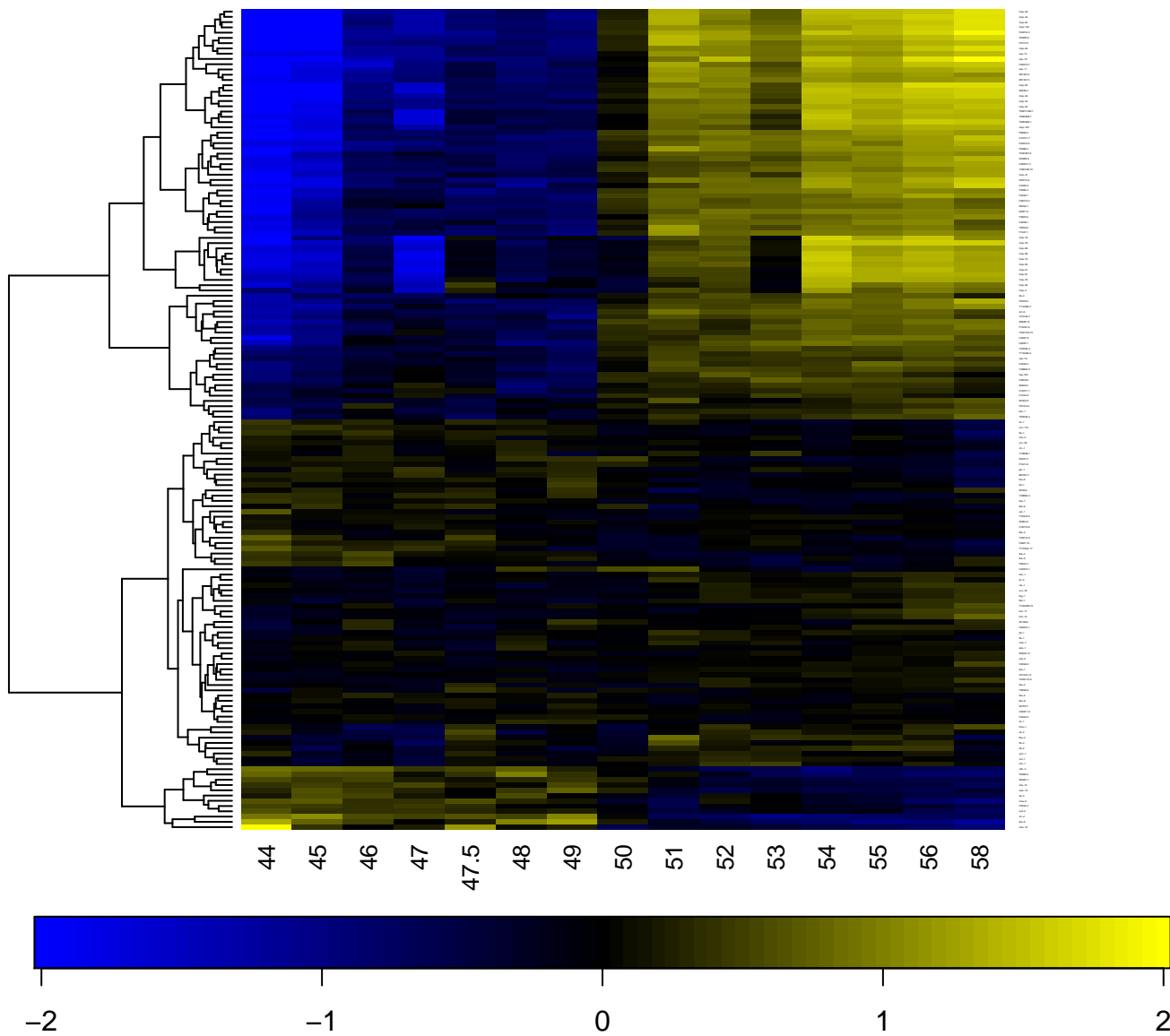
structural constituent of ribosome



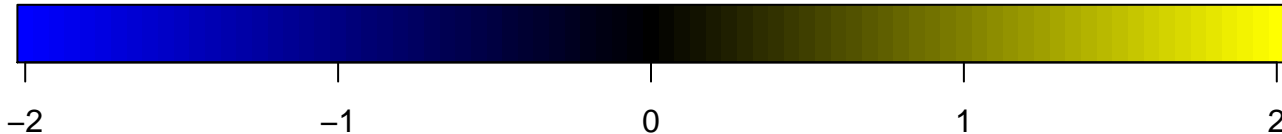
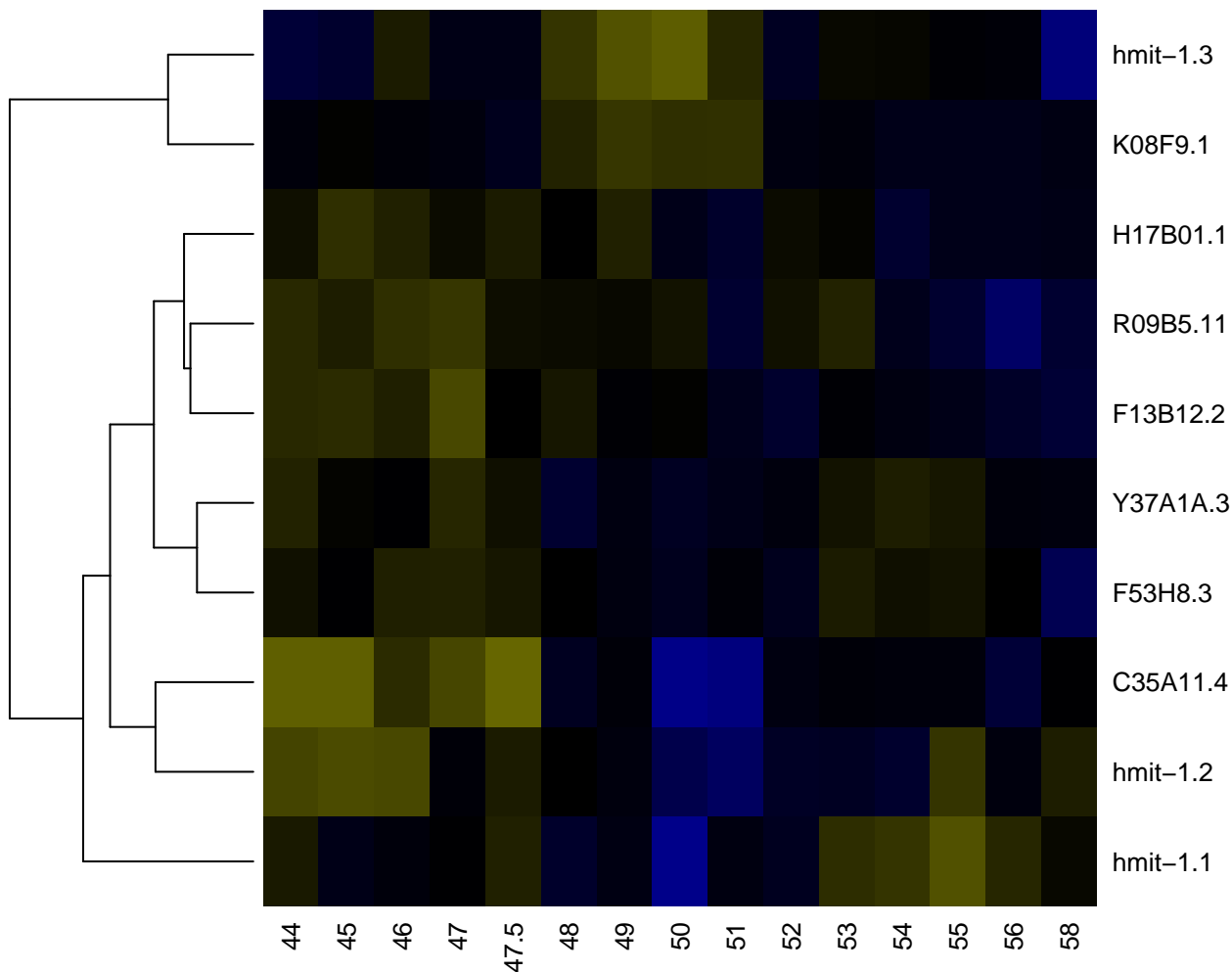
structural constituent of vitelline membrane



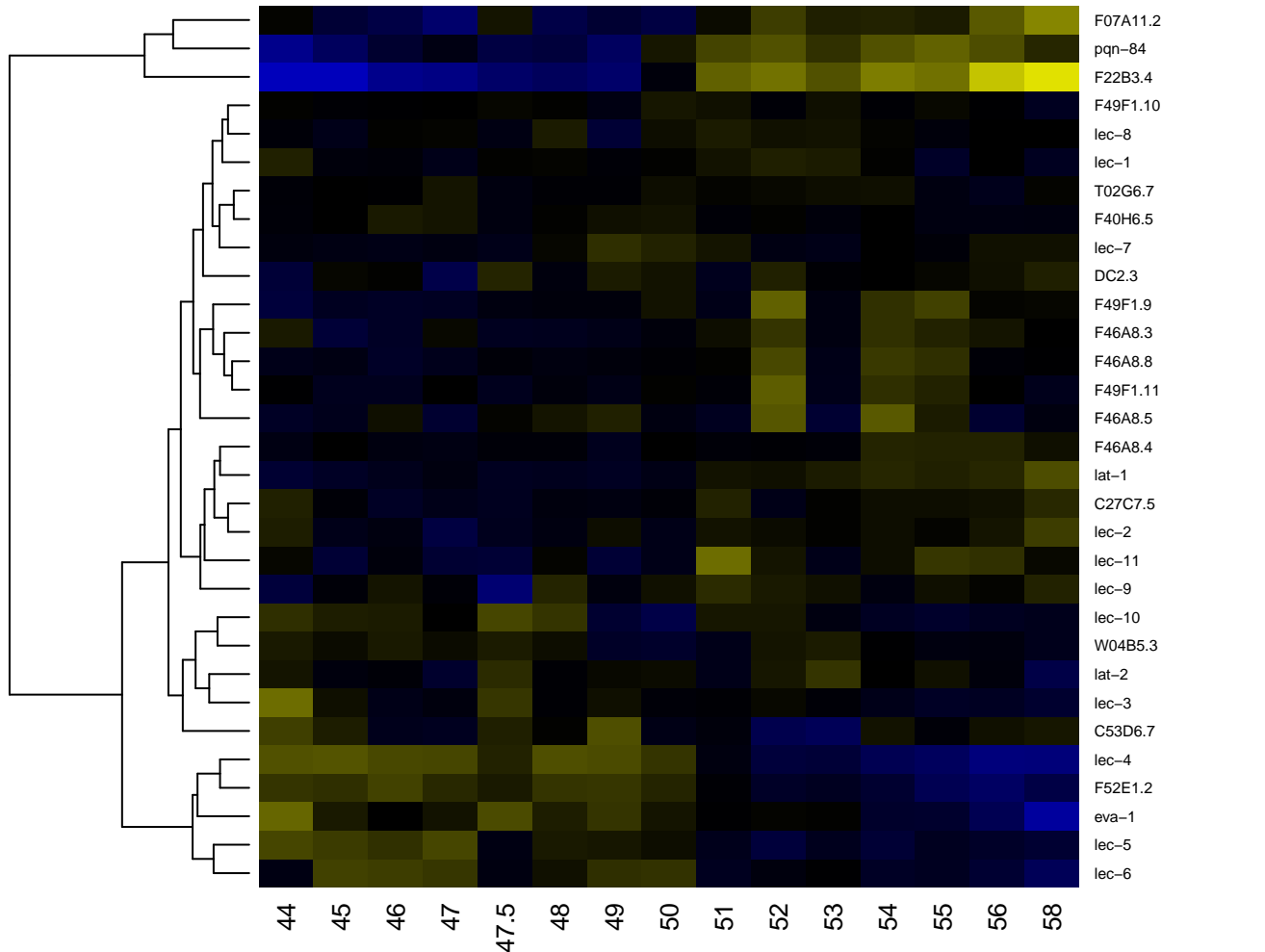
structural molecule activity



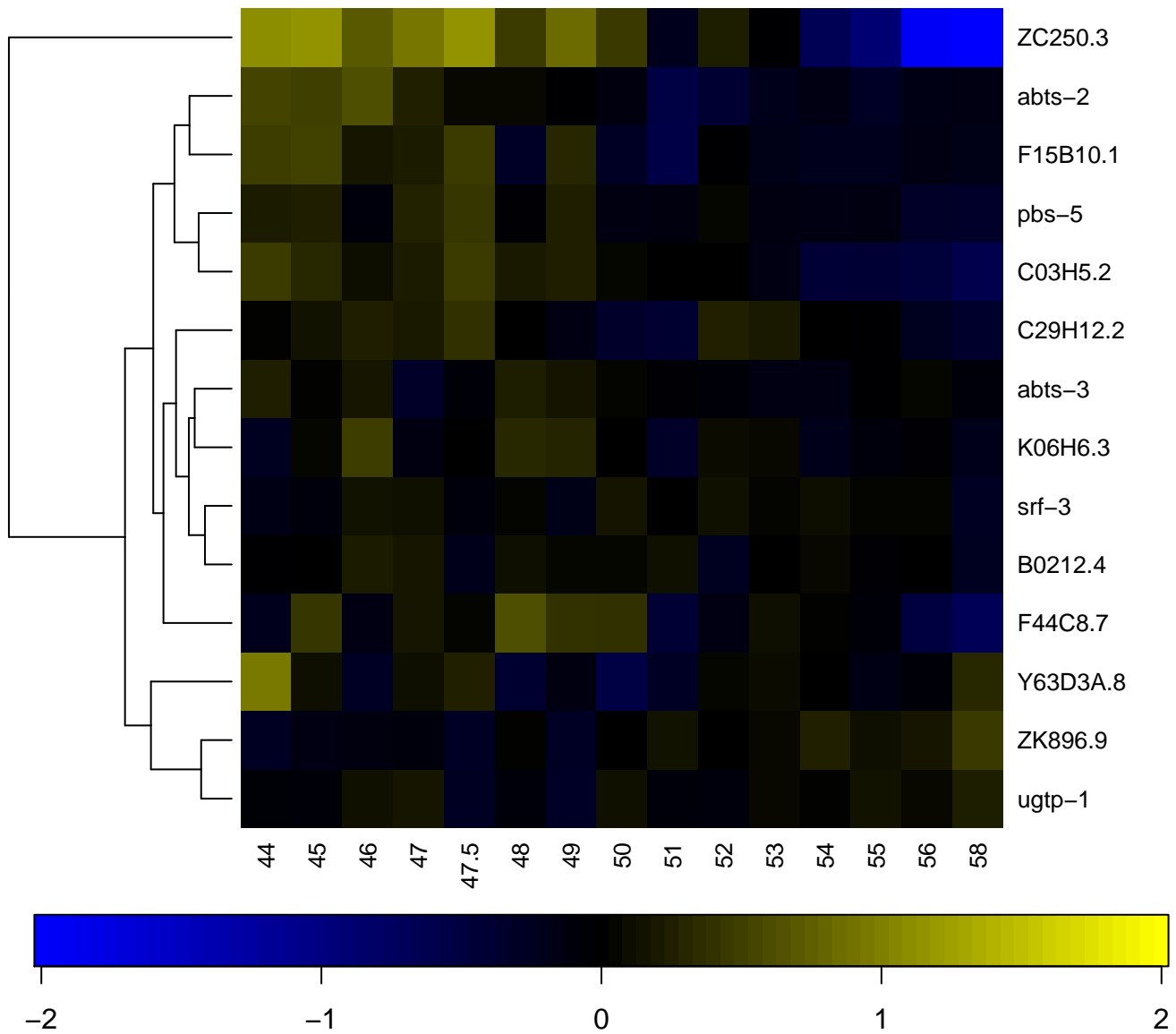
substrate-specific transmembrane transporter activity



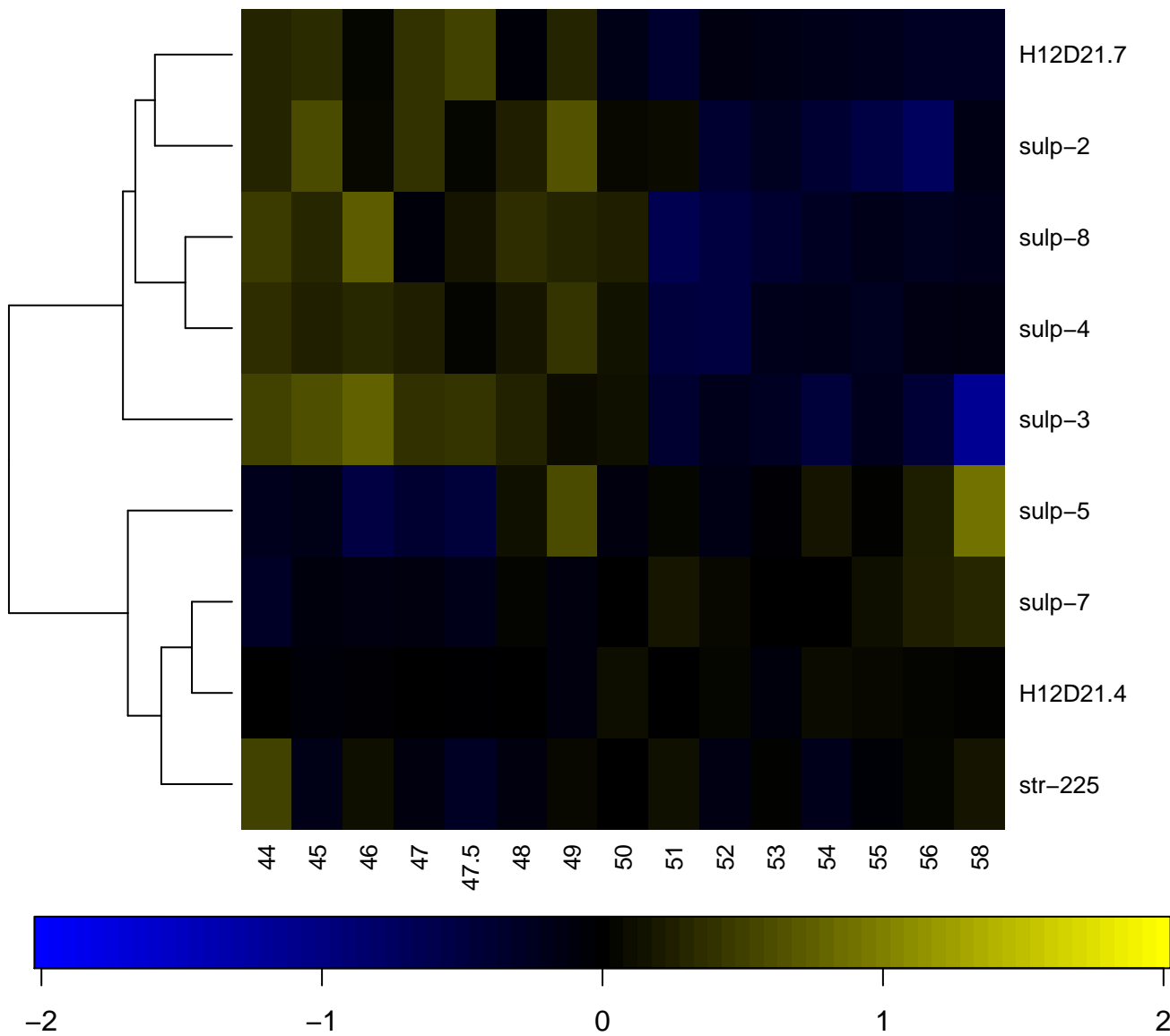
sugar binding



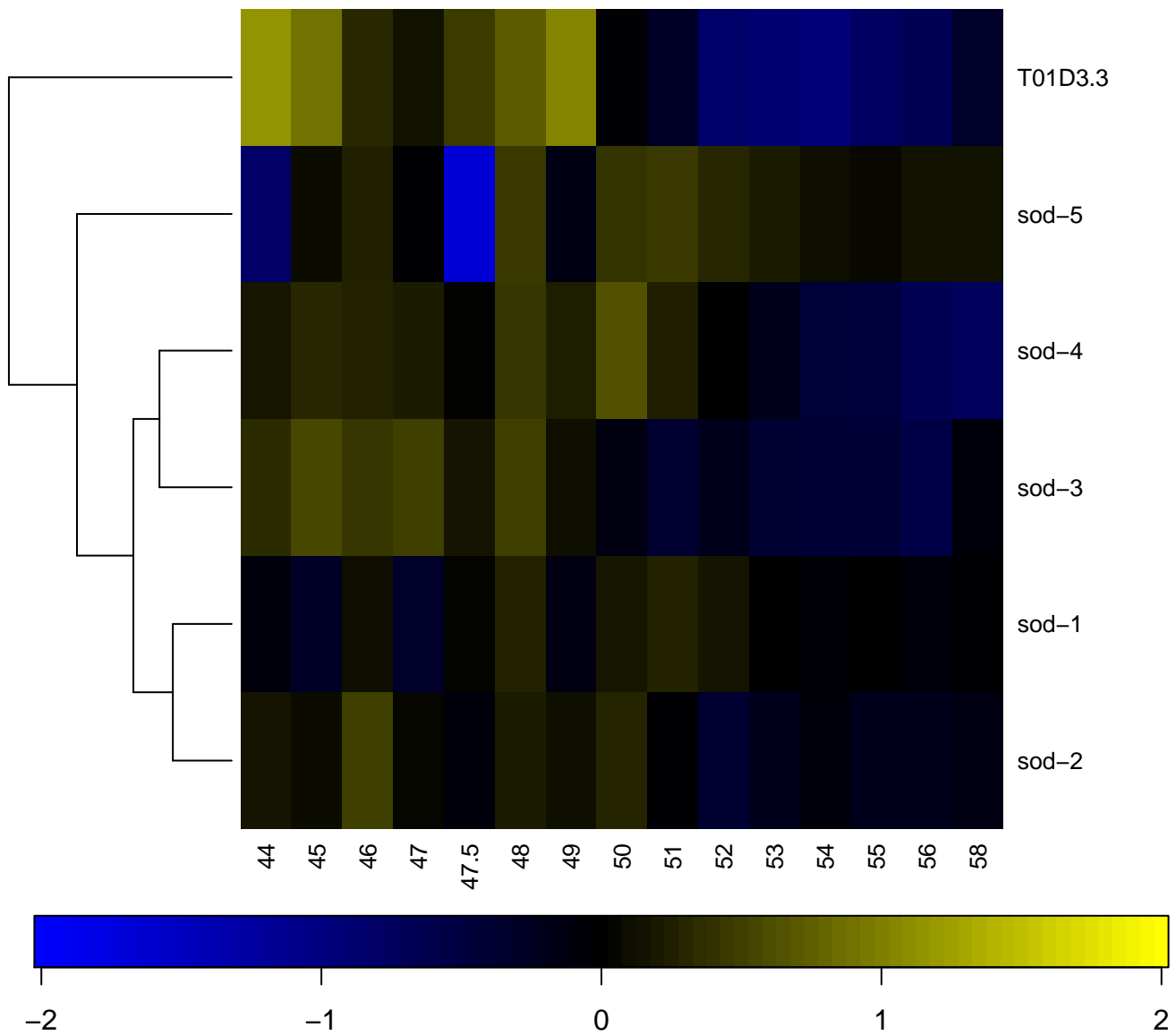
sugar:hydrogen symporter activity



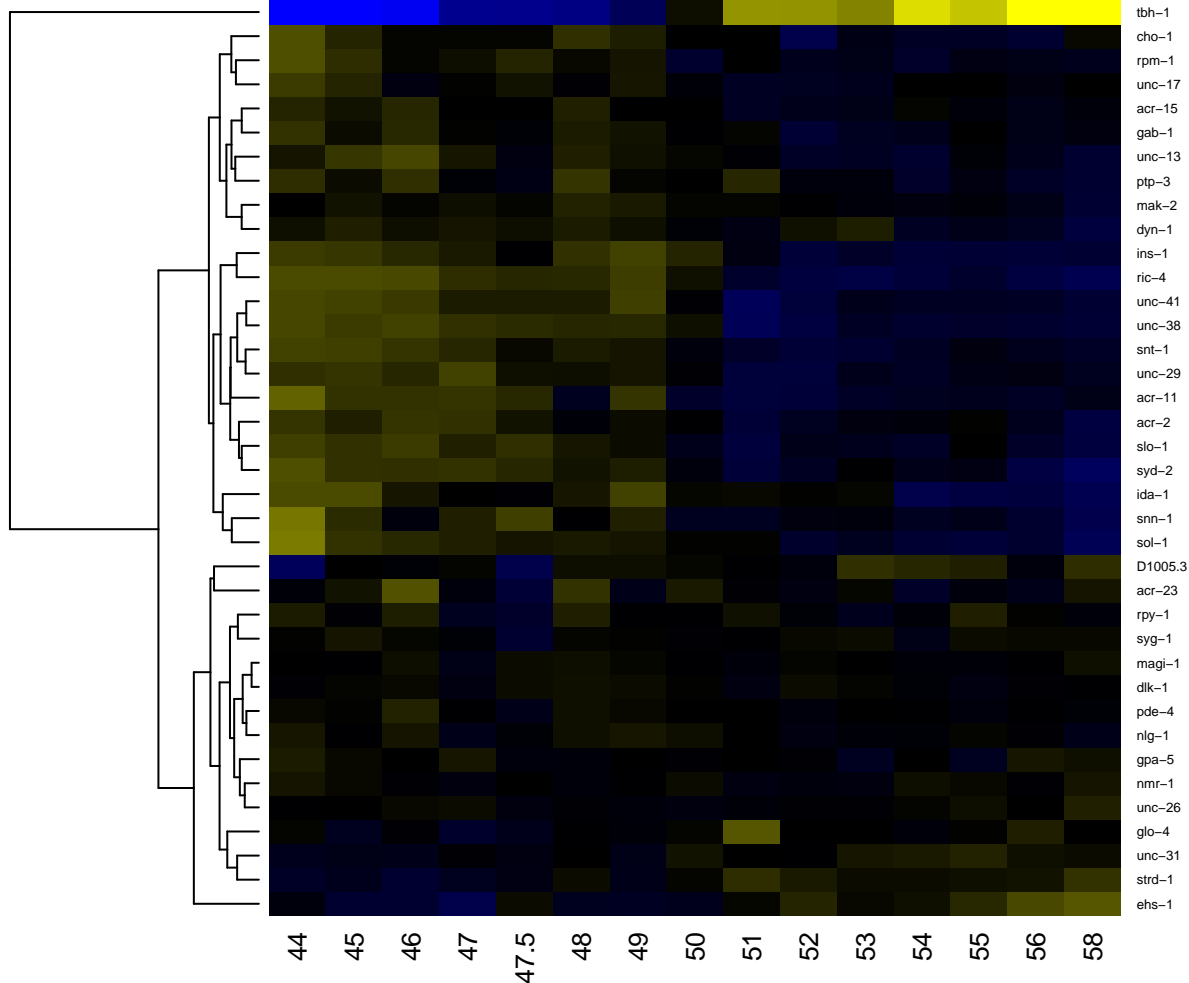
sulfate transport



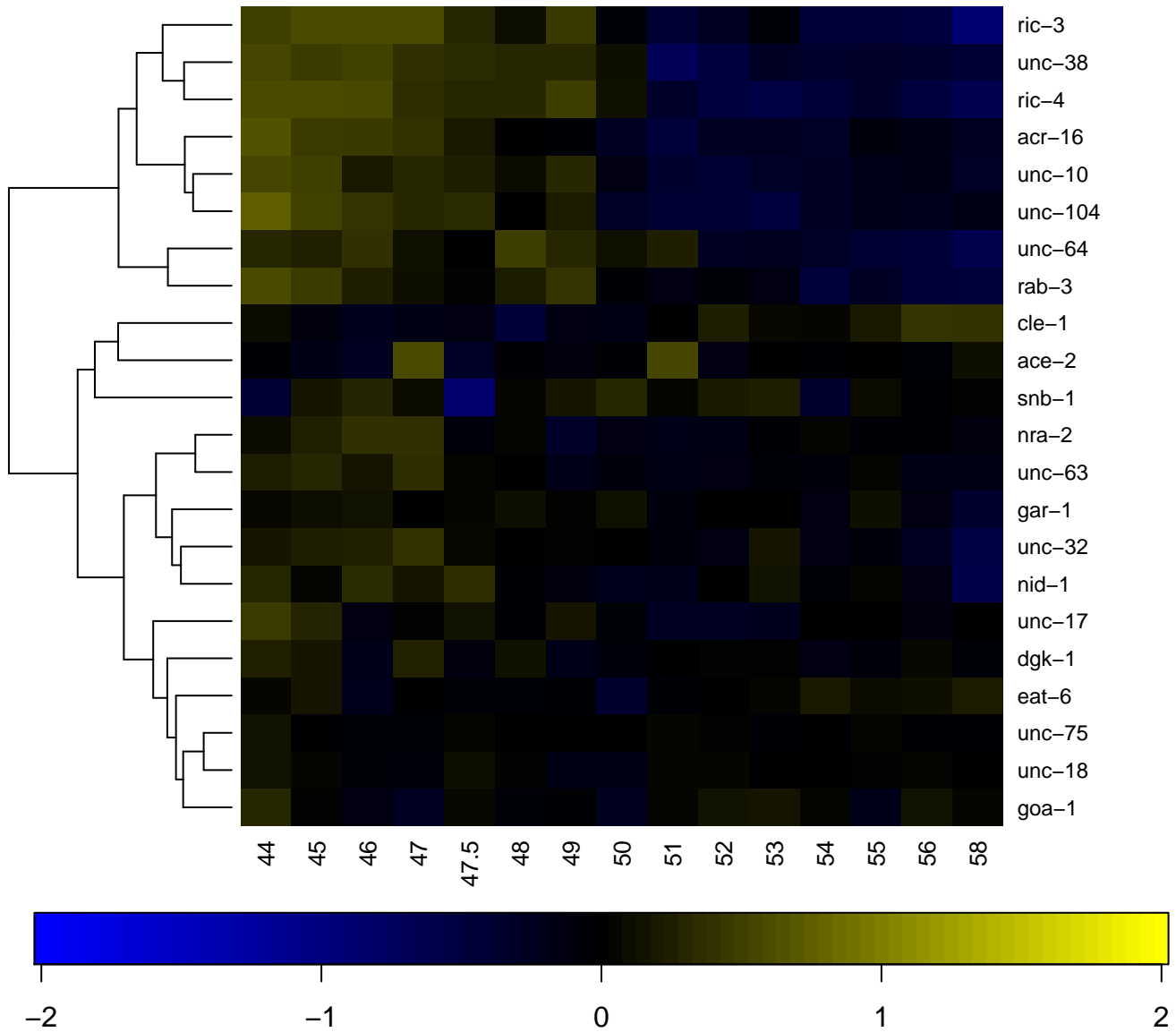
superoxide metabolic process



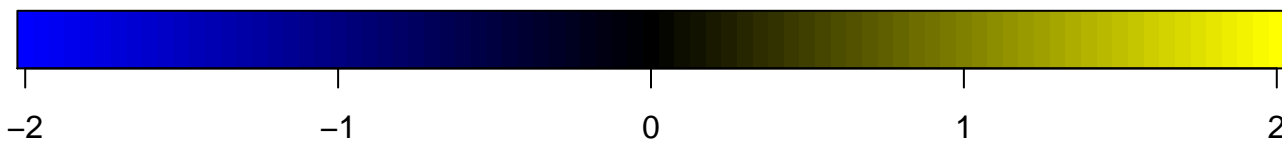
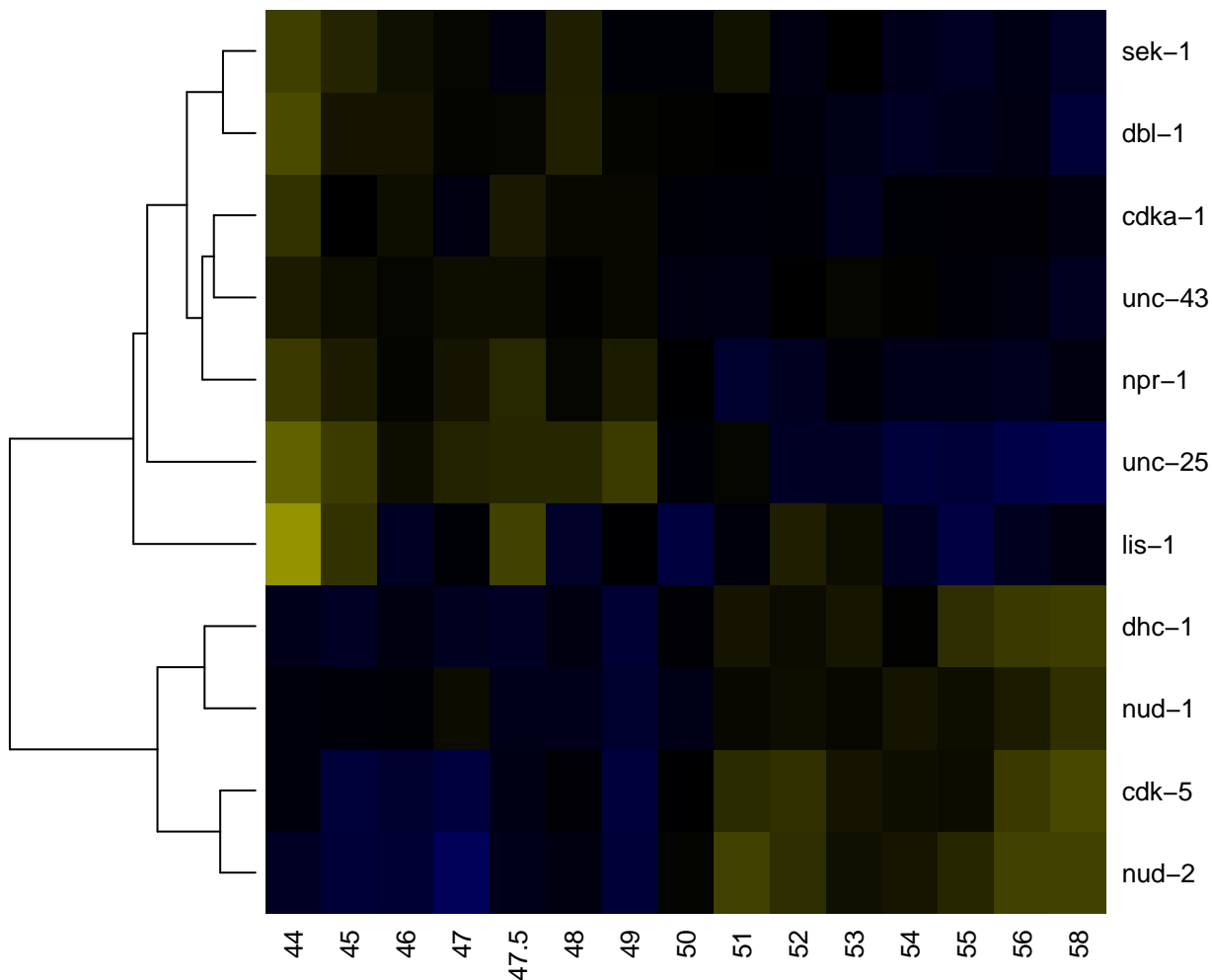
synapse



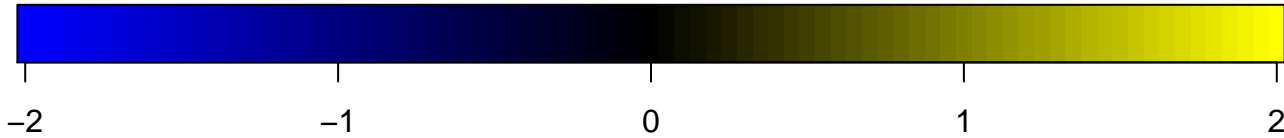
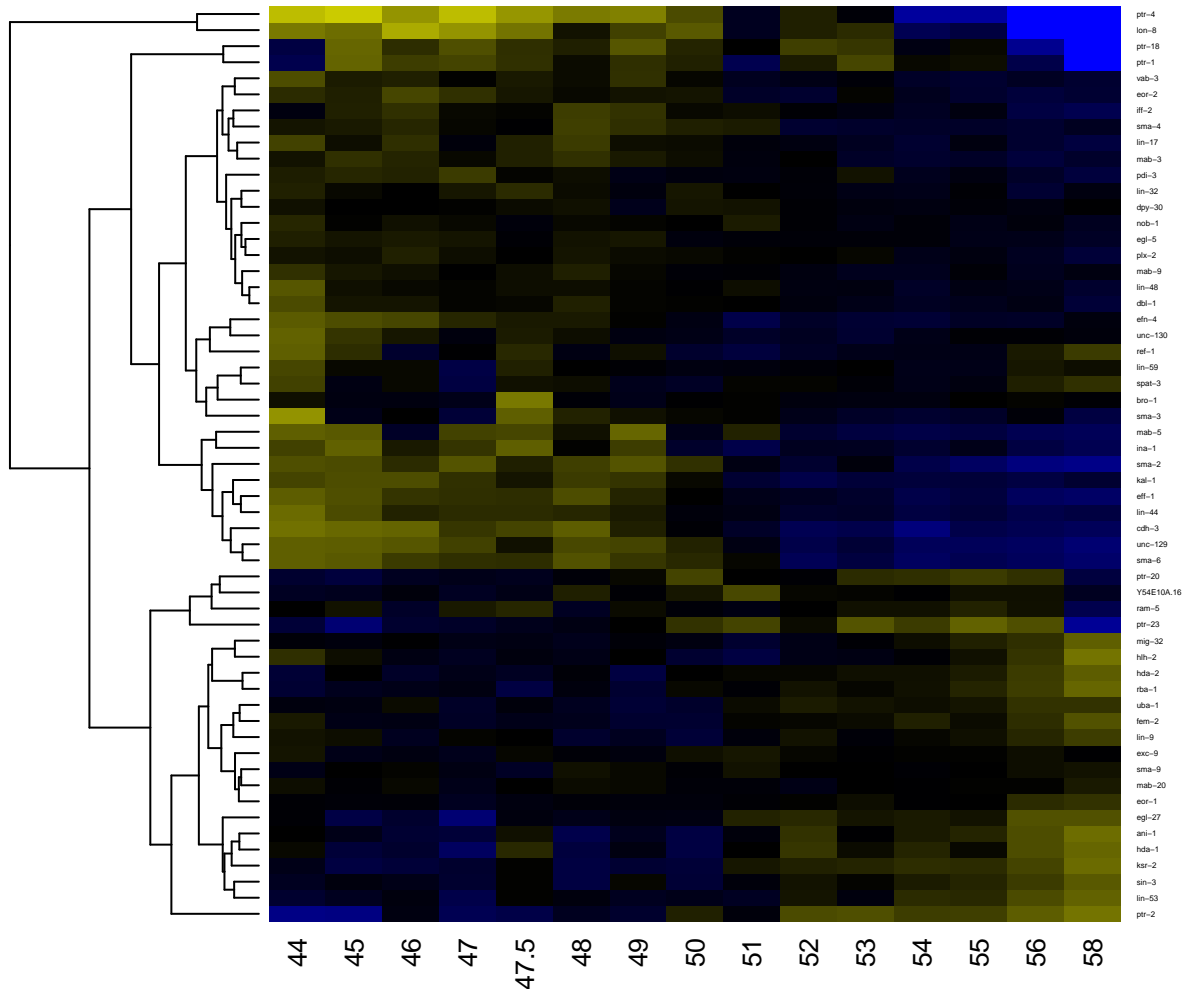
synaptic transmission, cholinergic



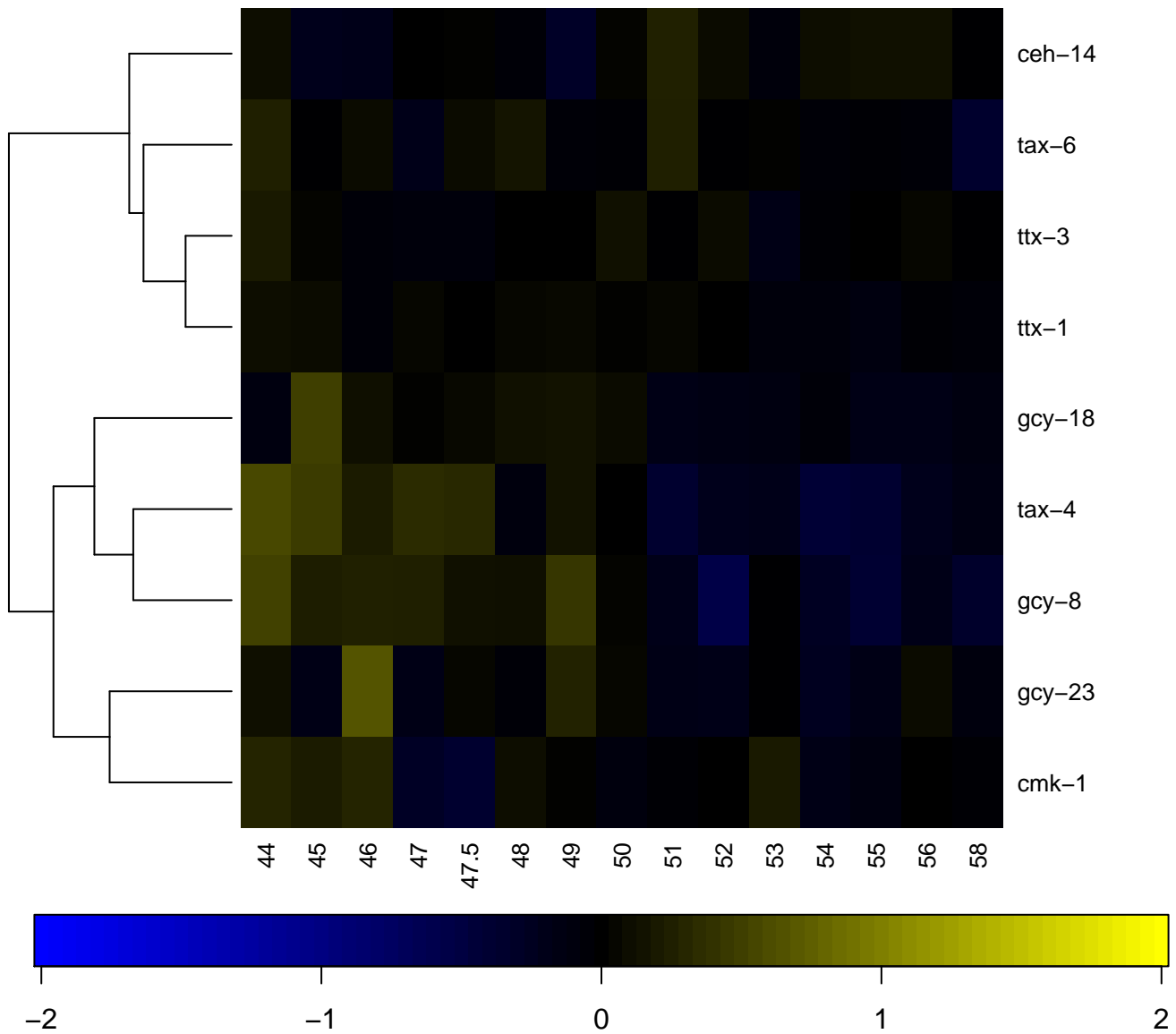
synaptic transmission, GABAergic



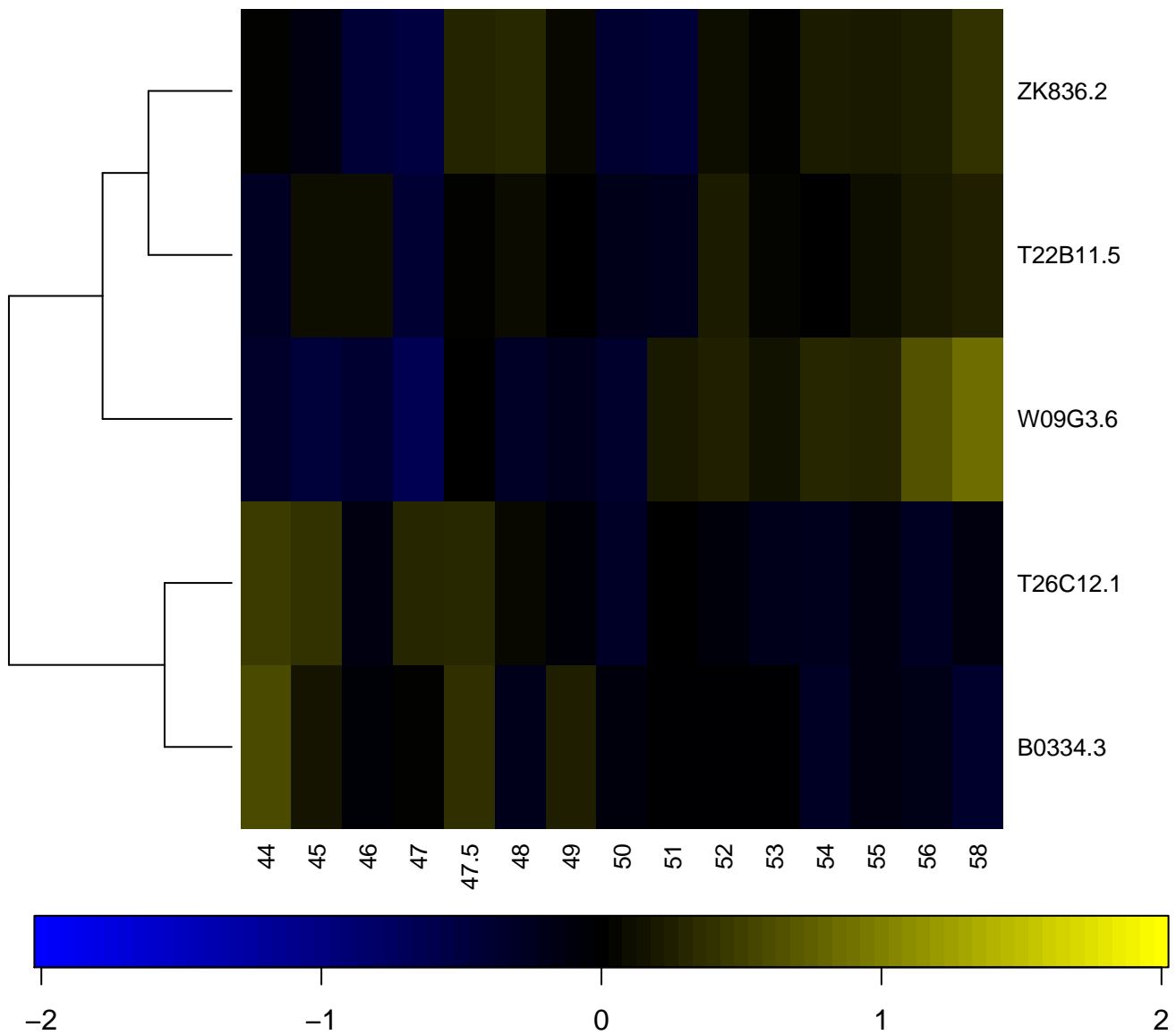
tail tip morphogenesis



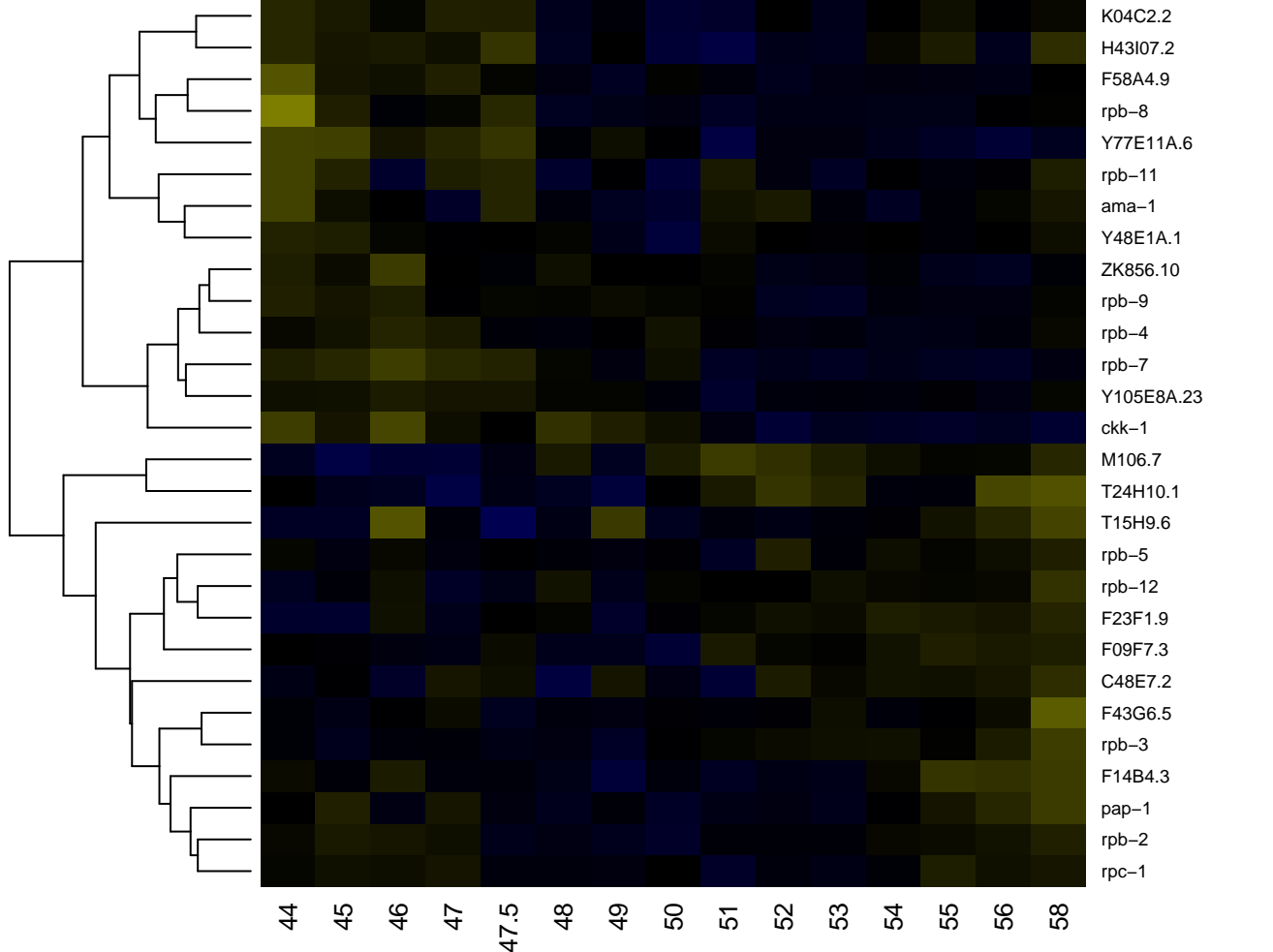
thermosensory behavior



thiamin pyrophosphate binding



transcription



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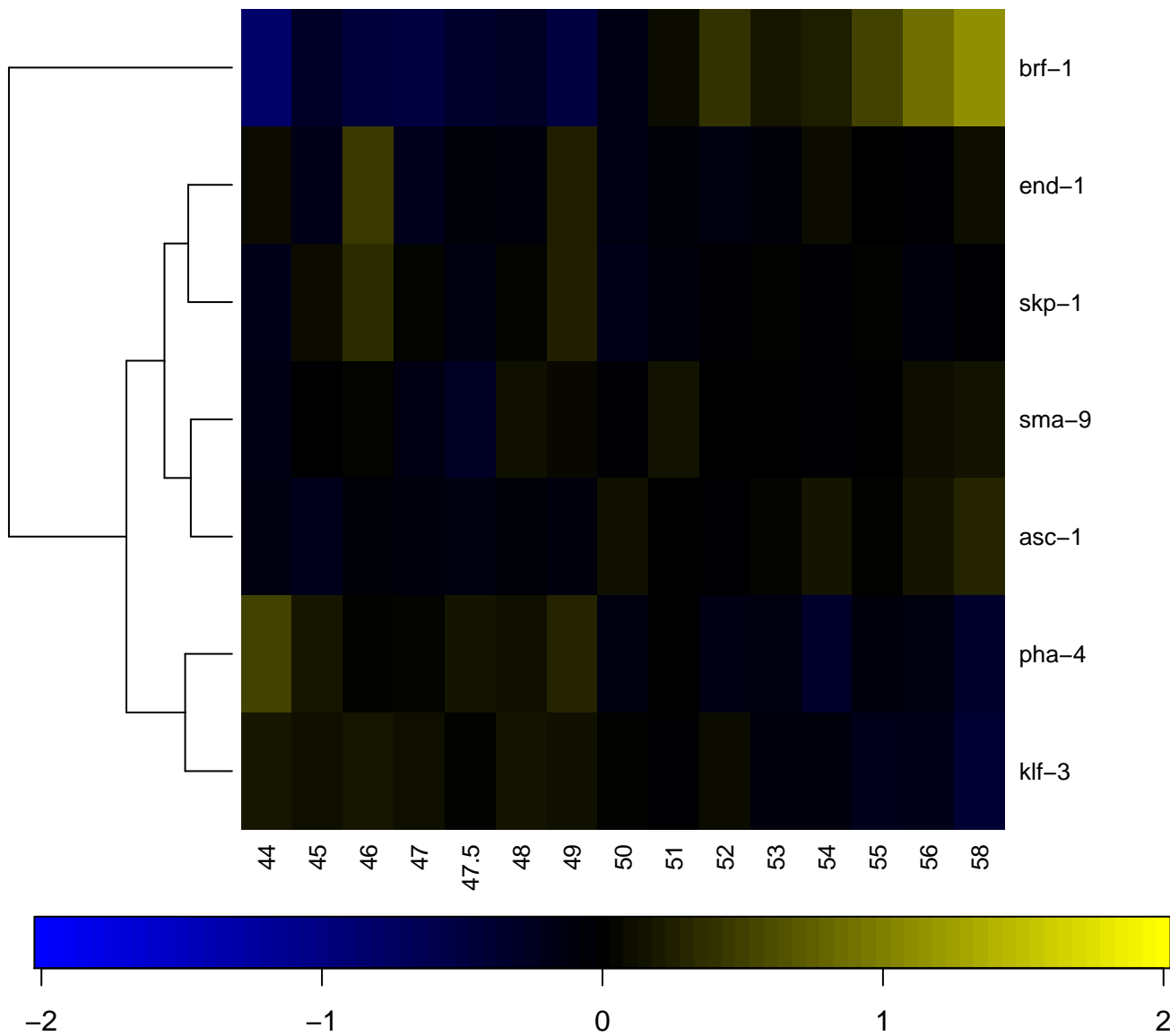
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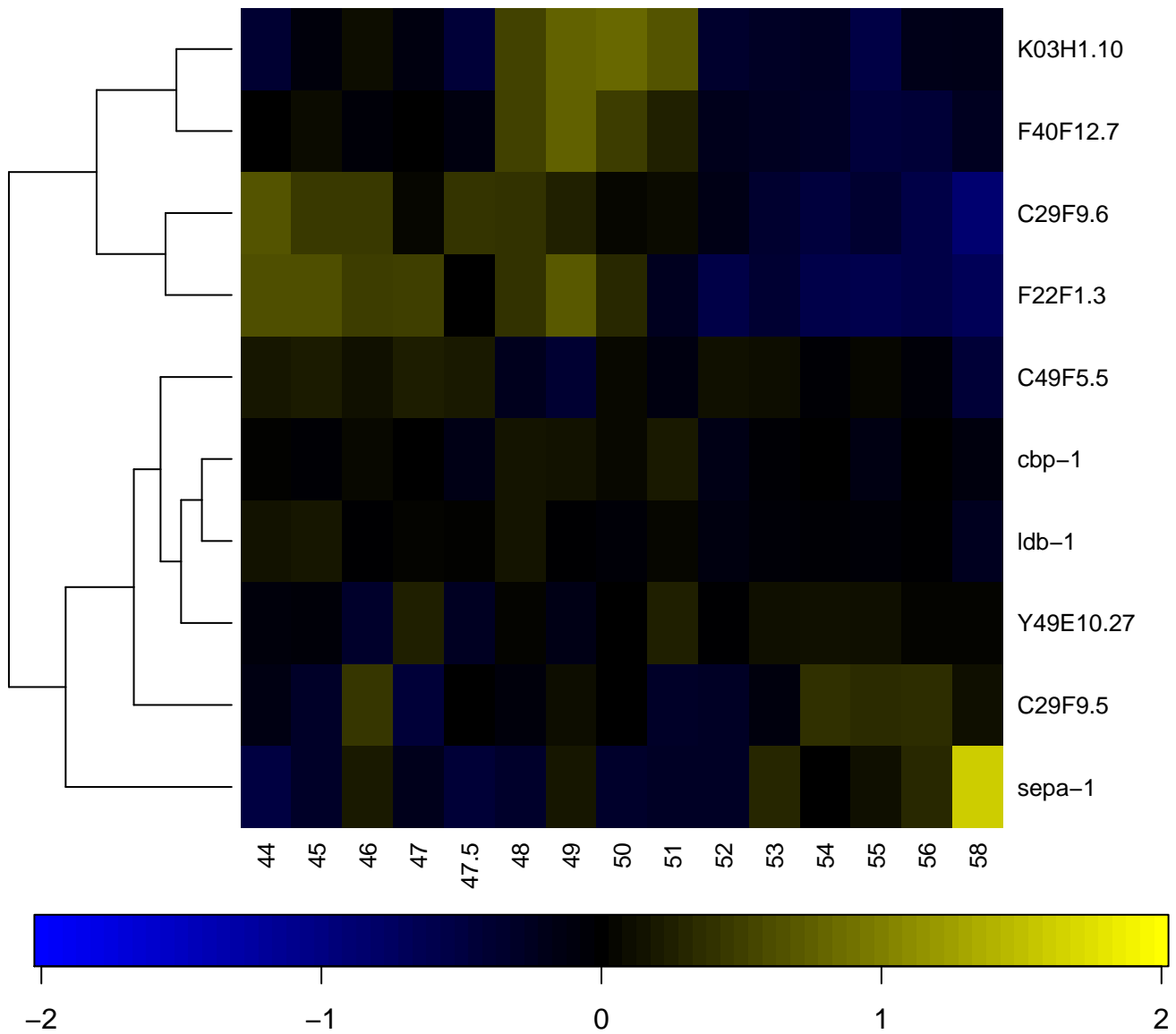
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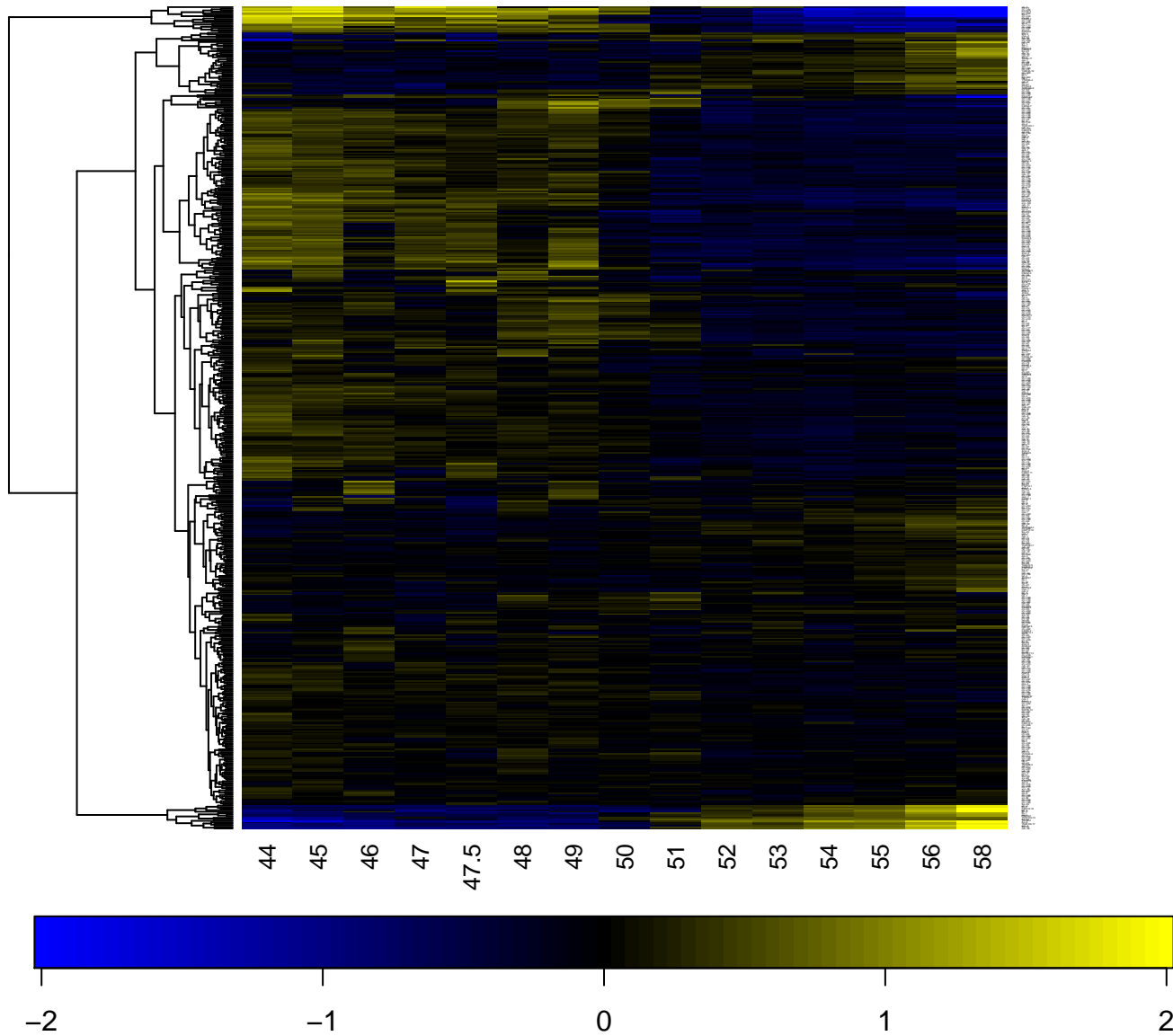
transcription activator activity



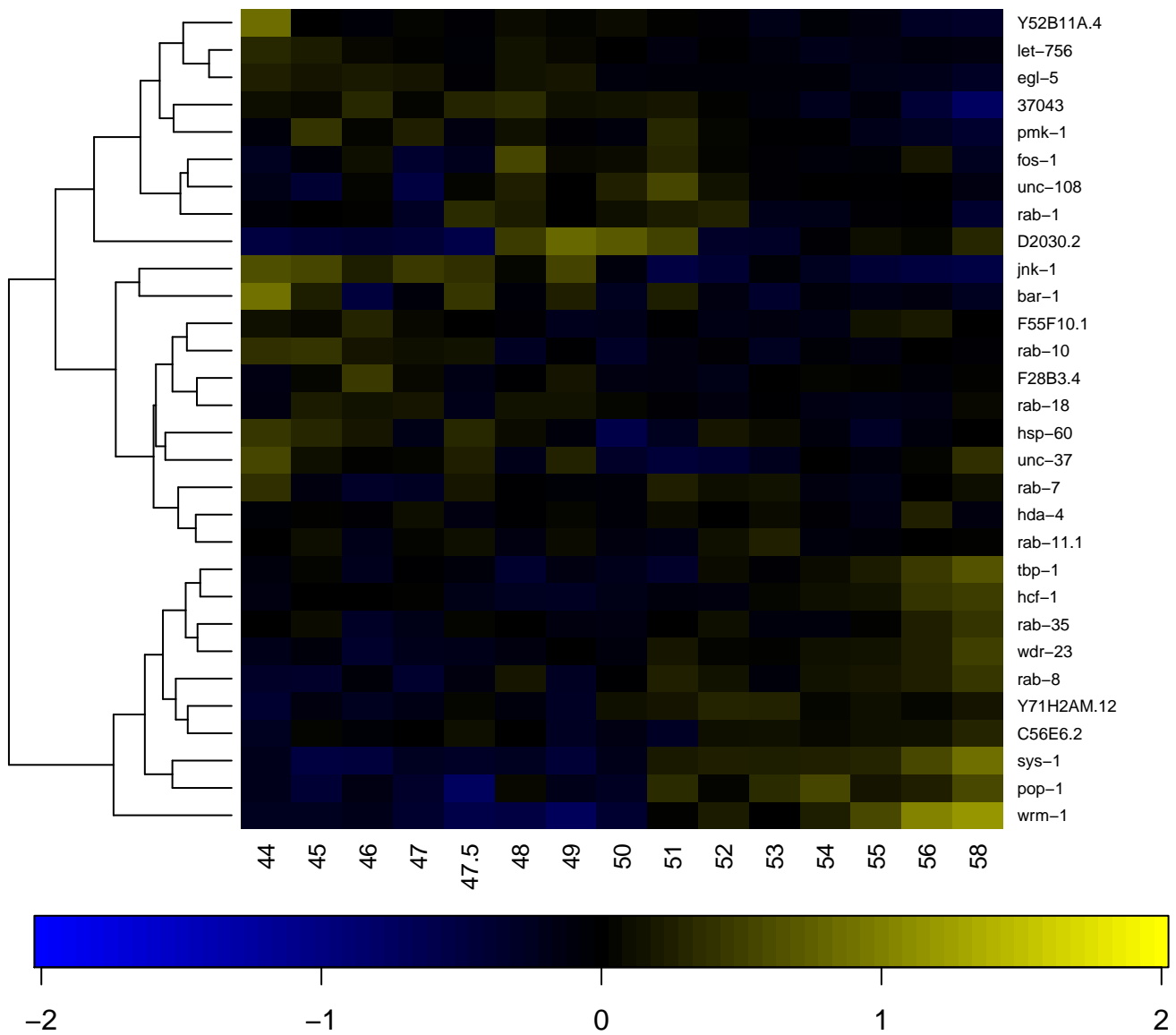
transcription cofactor activity



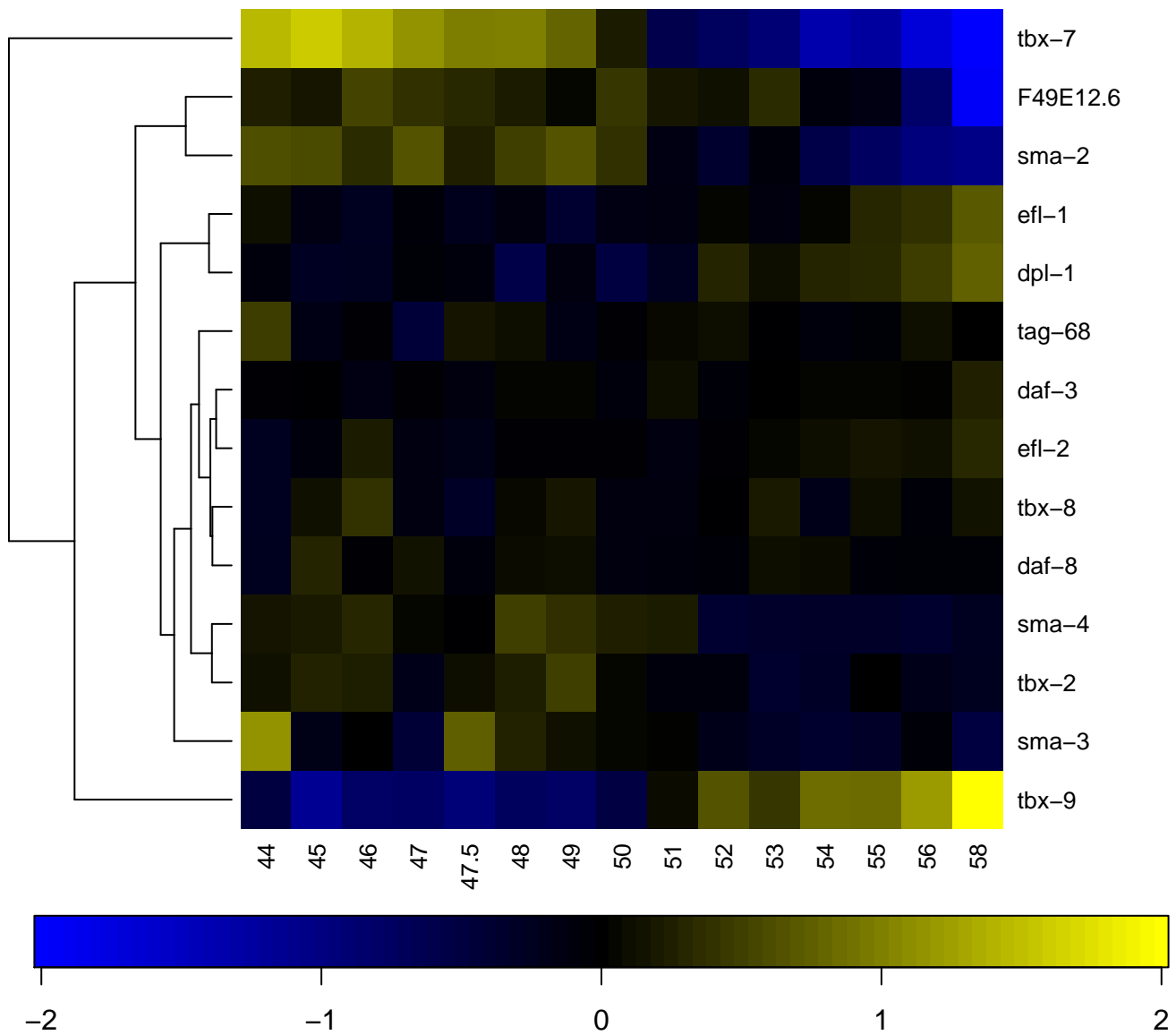
transcription factor activity



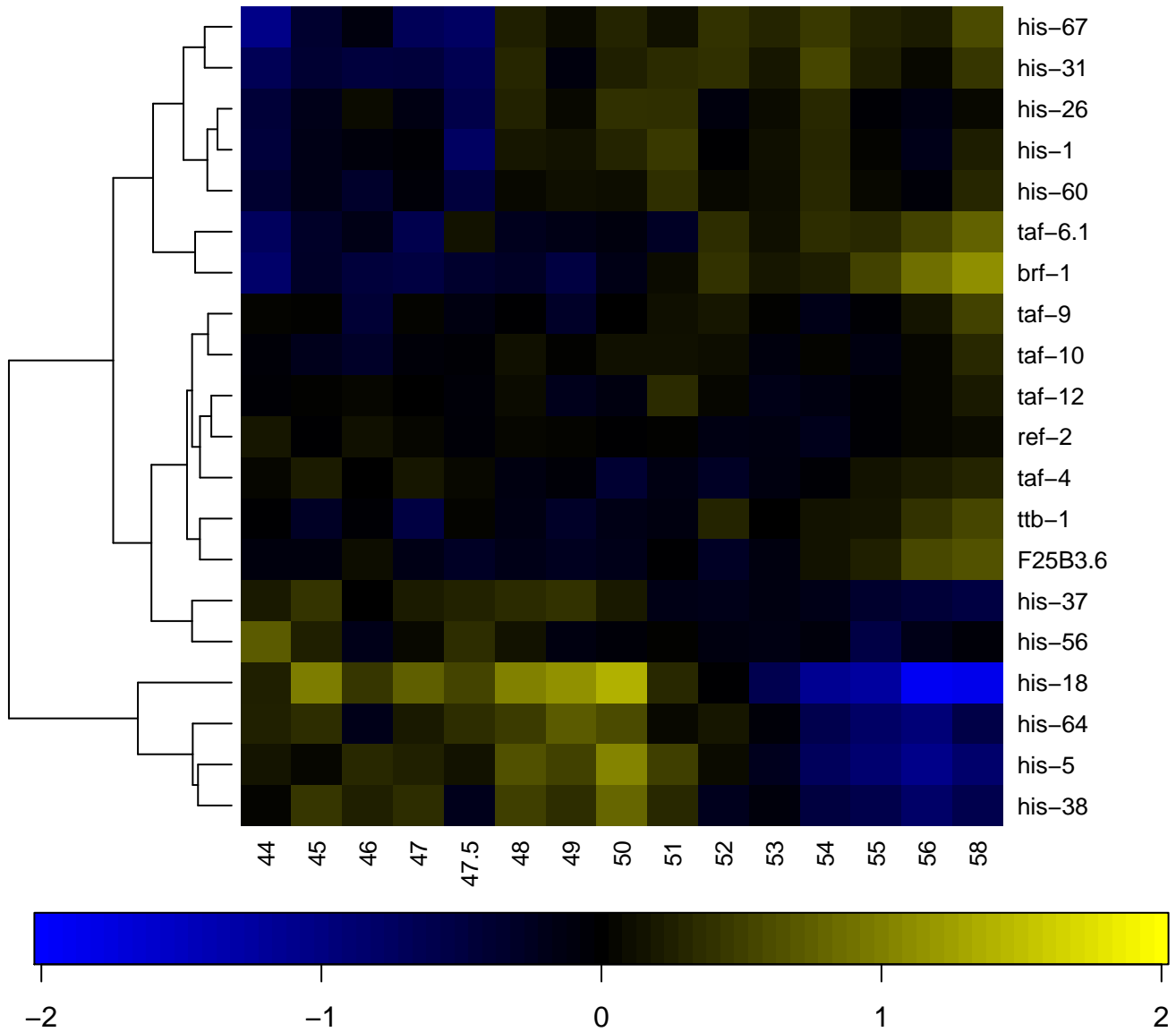
transcription factor binding



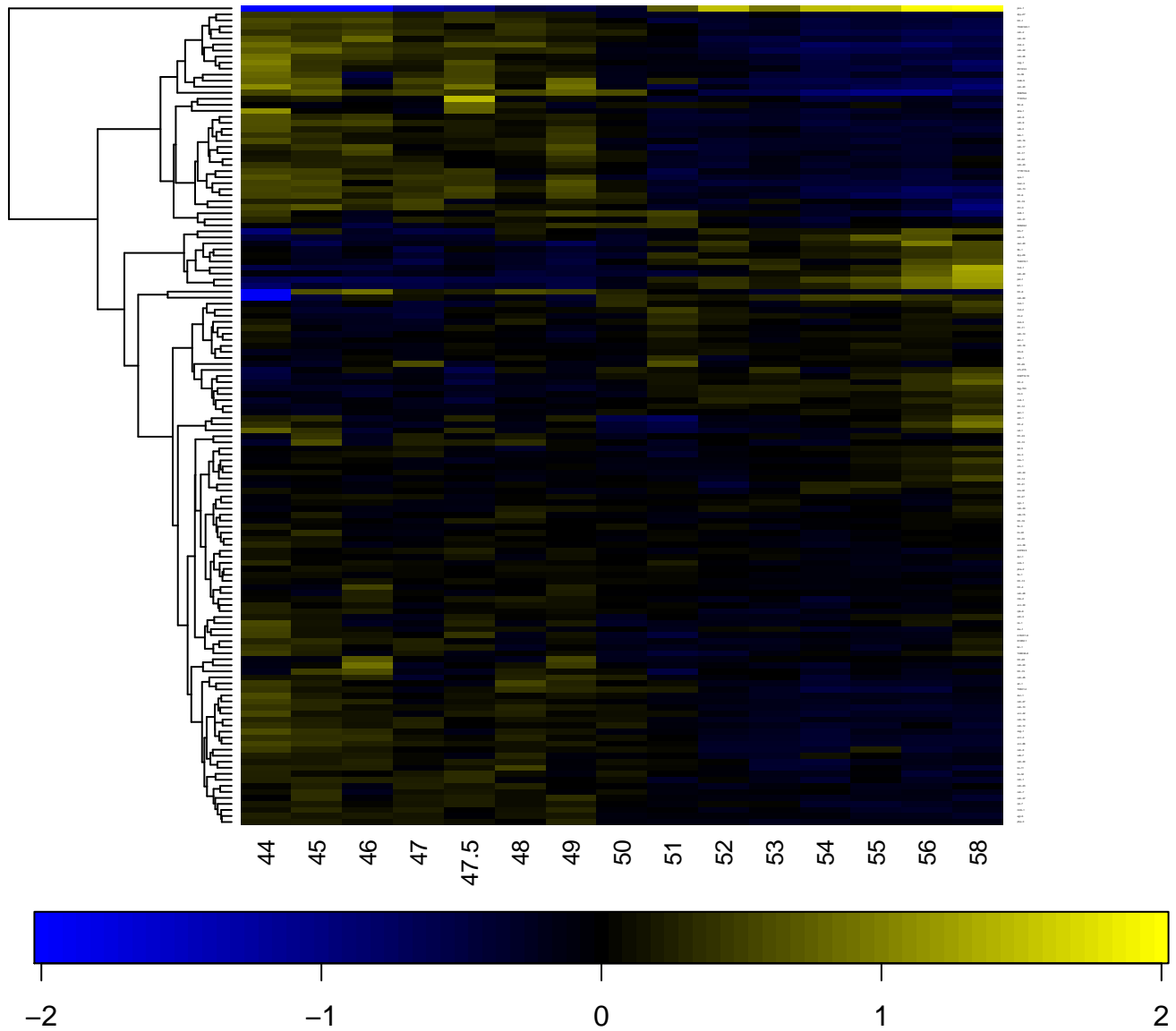
transcription factor complex



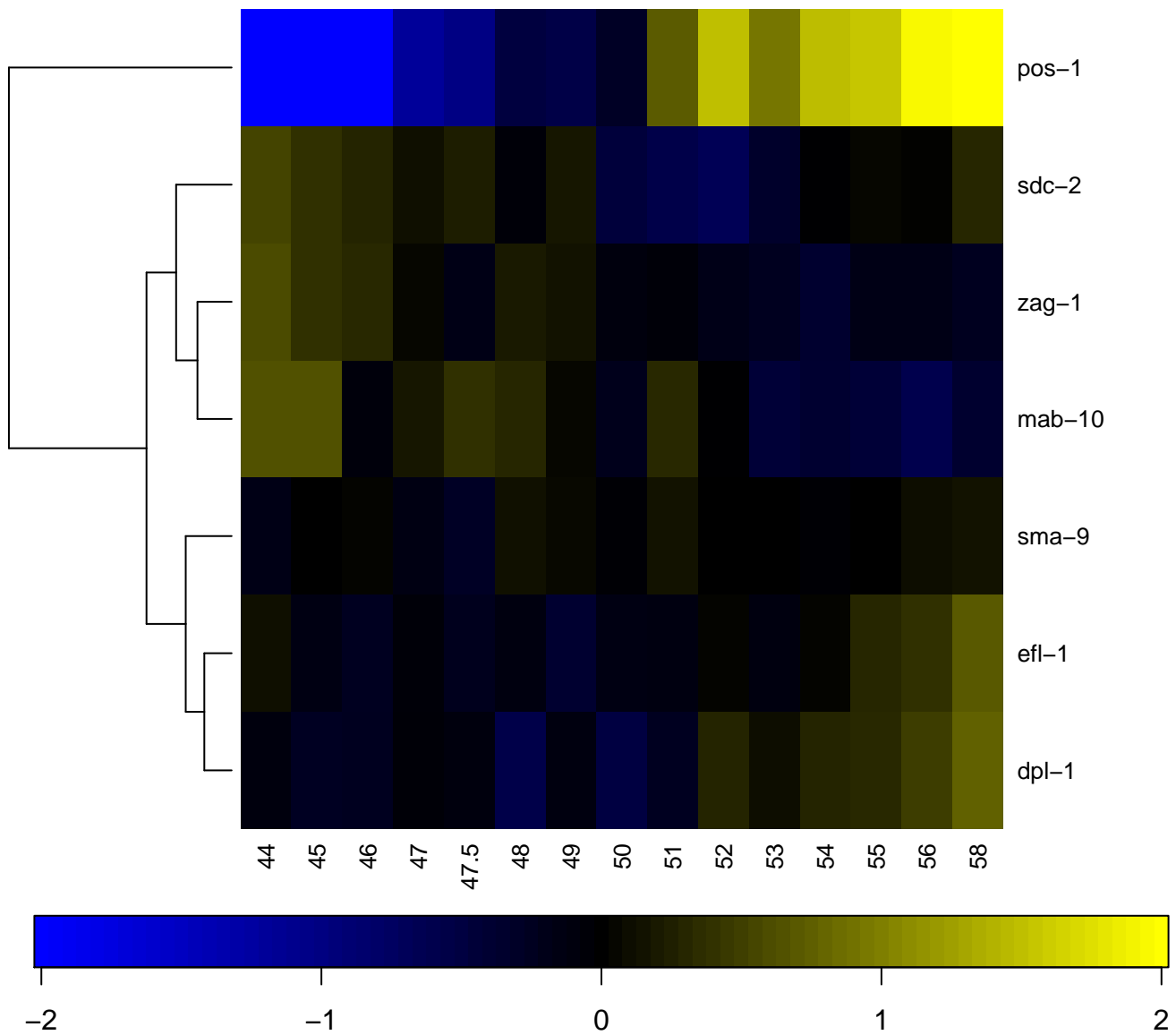
transcription initiation



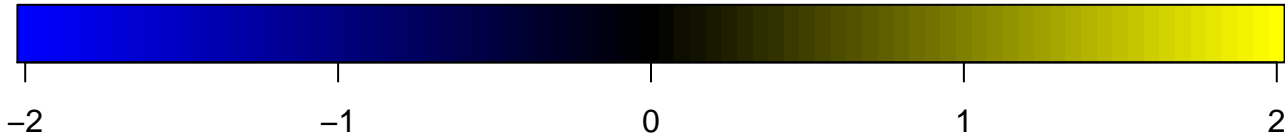
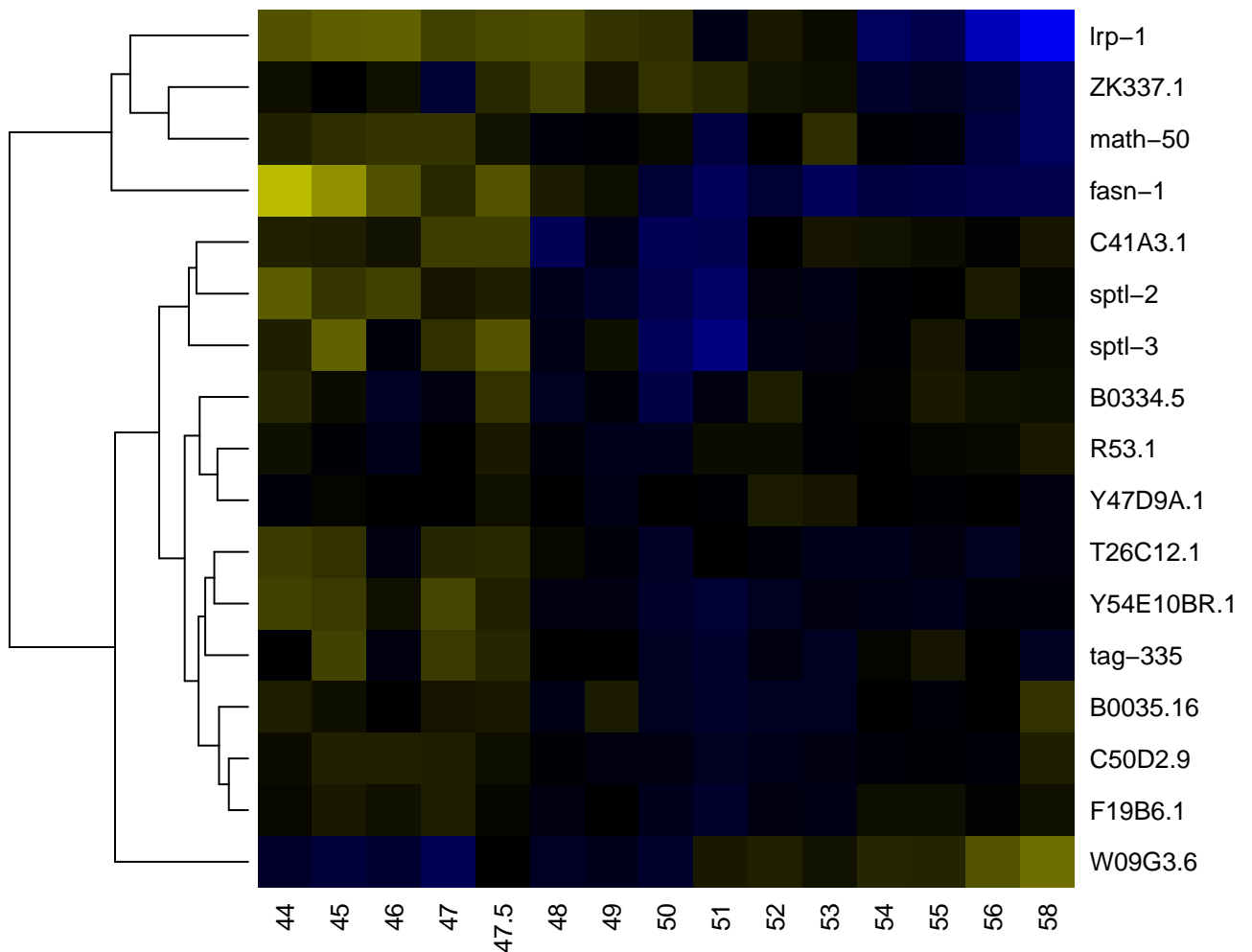
transcription regulator activity



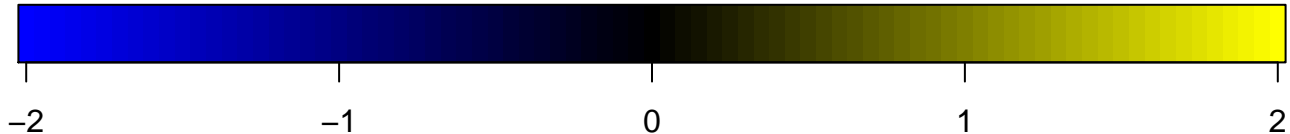
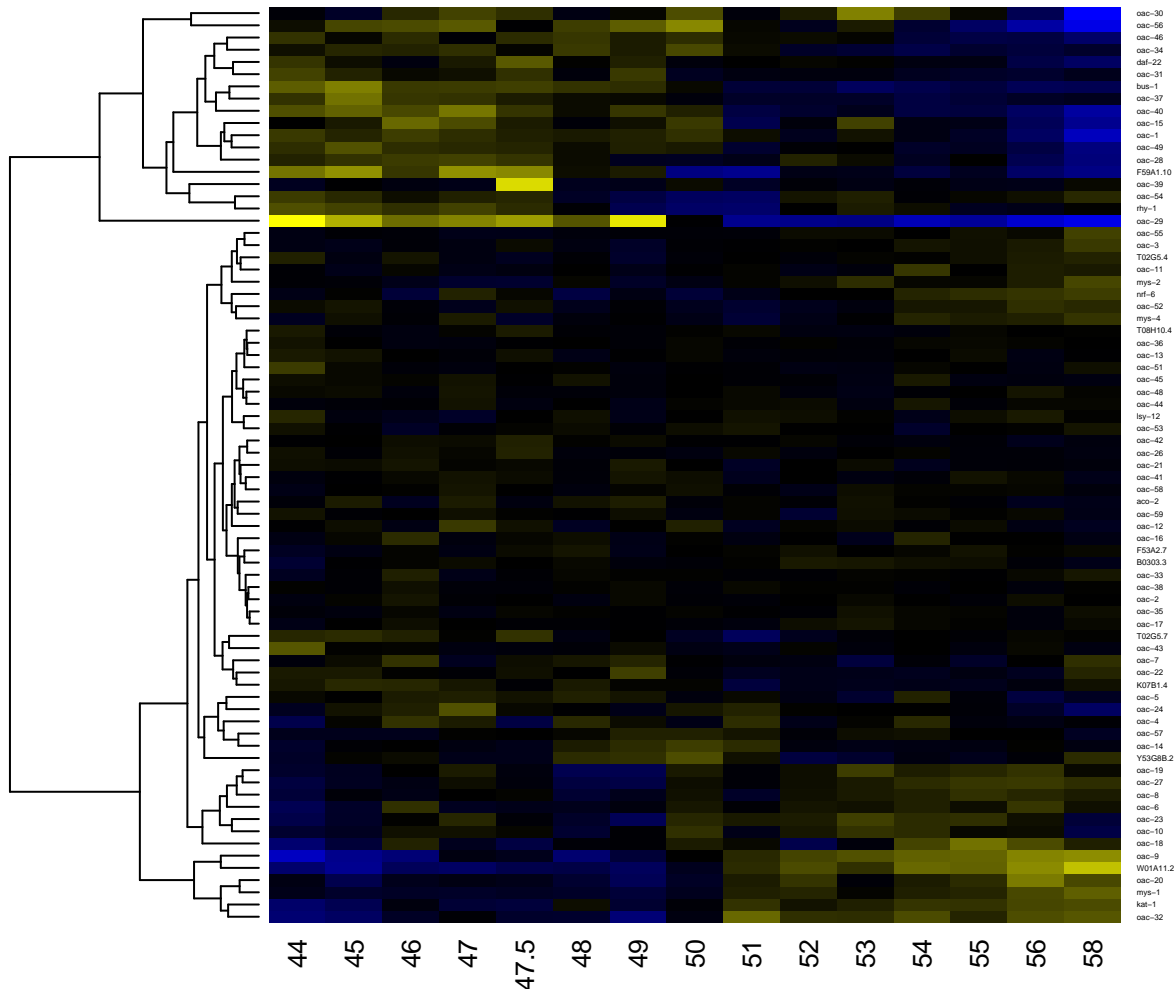
transcription repressor activity



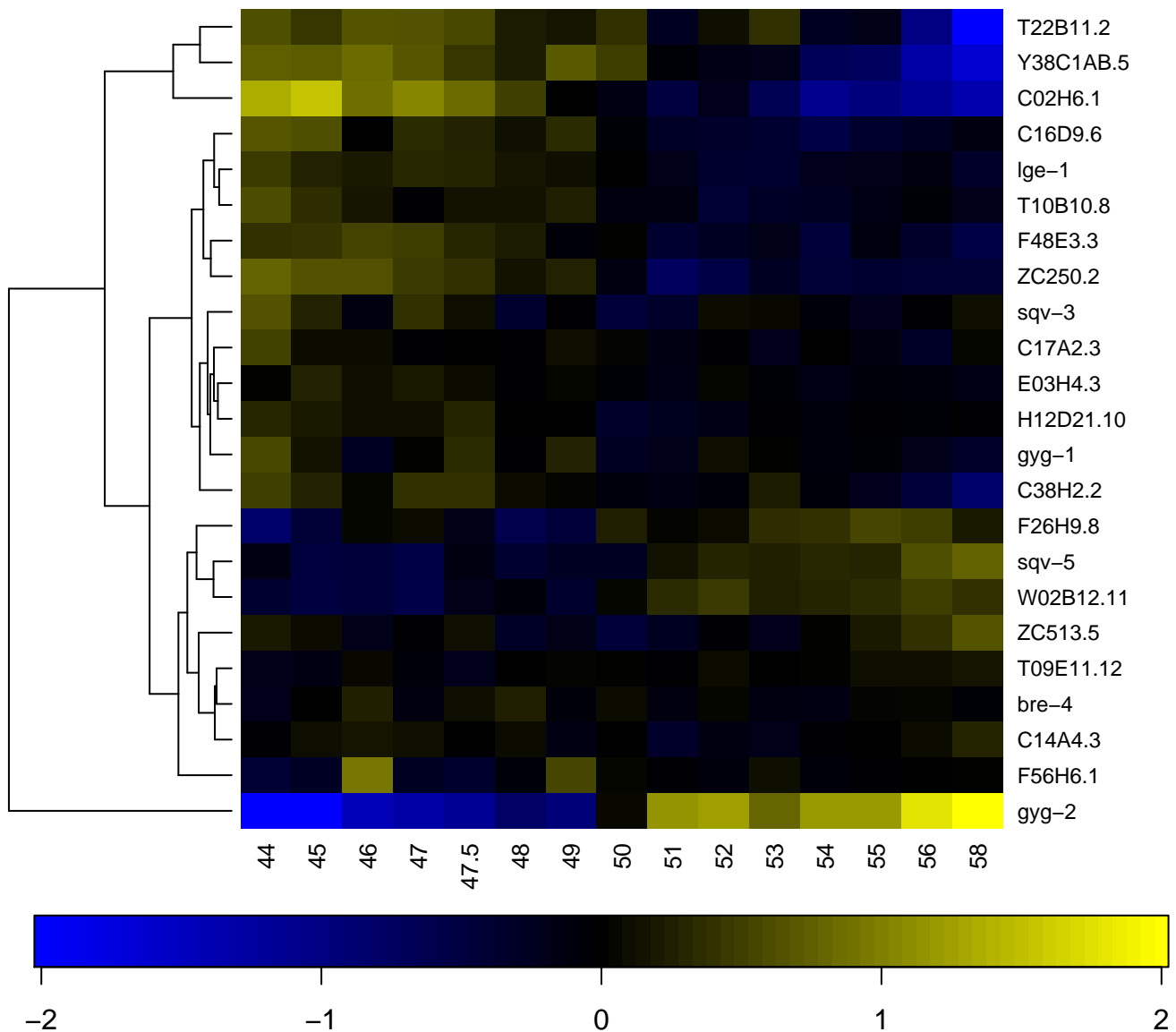
transferase activity



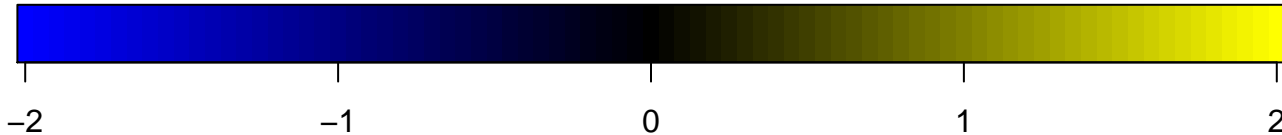
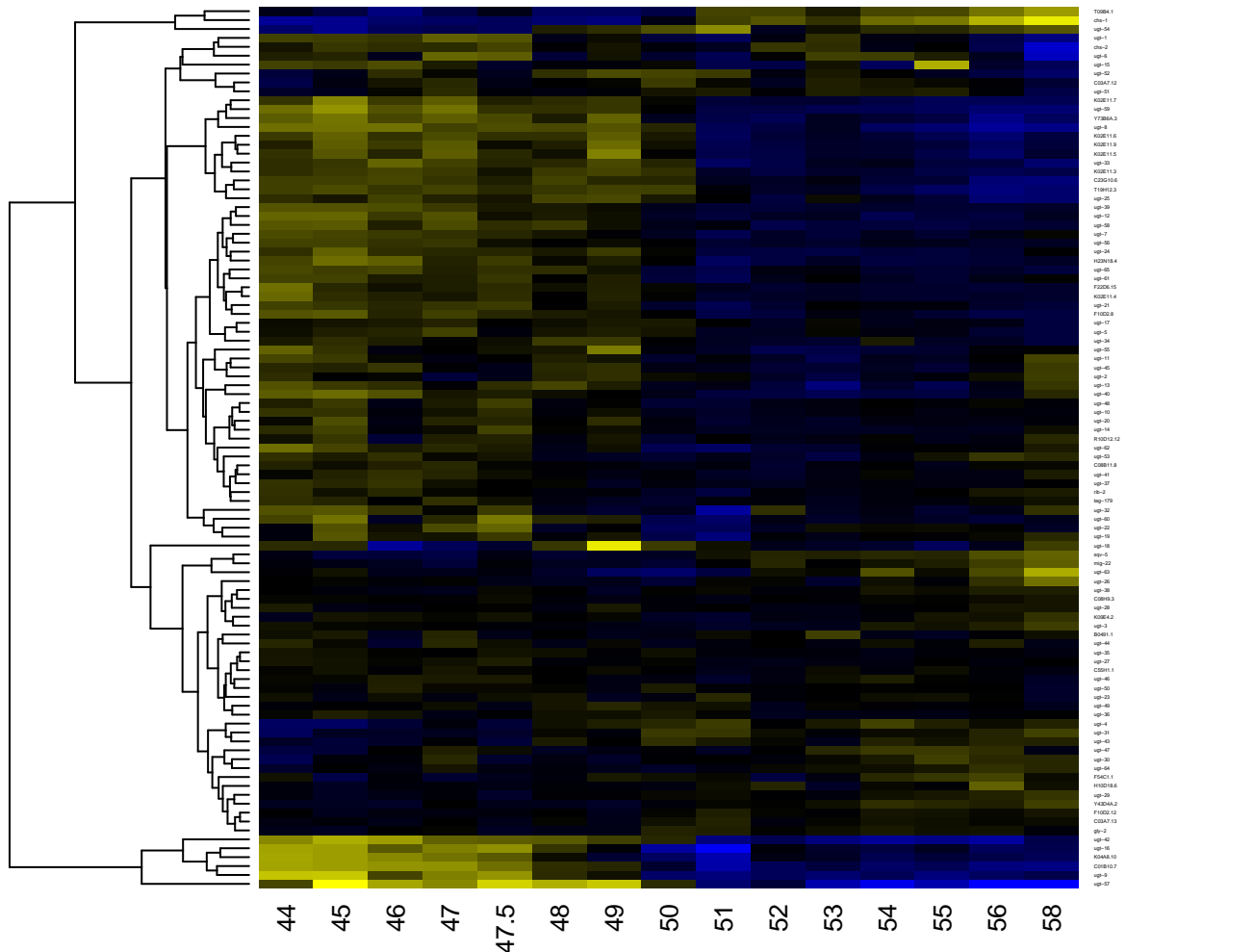
ase activity, transferring acyl groups other than amino-acyl



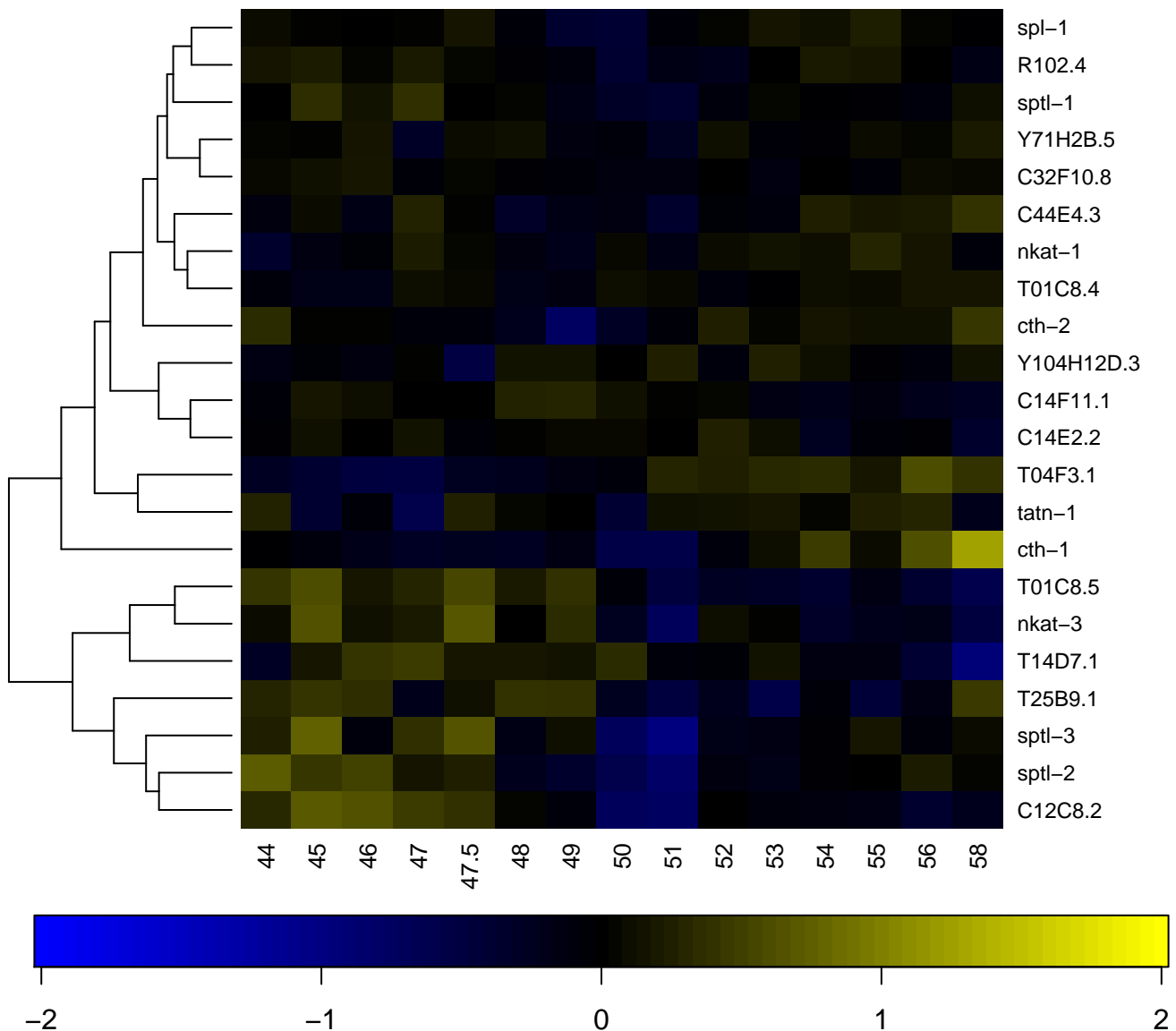
transferase activity, transferring glycosyl groups



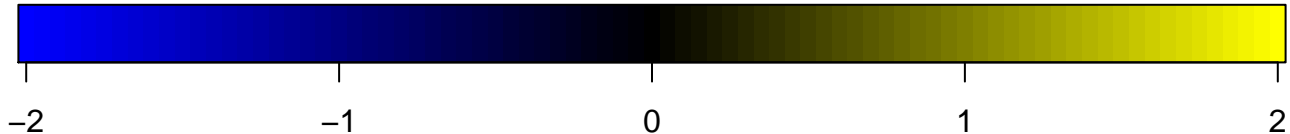
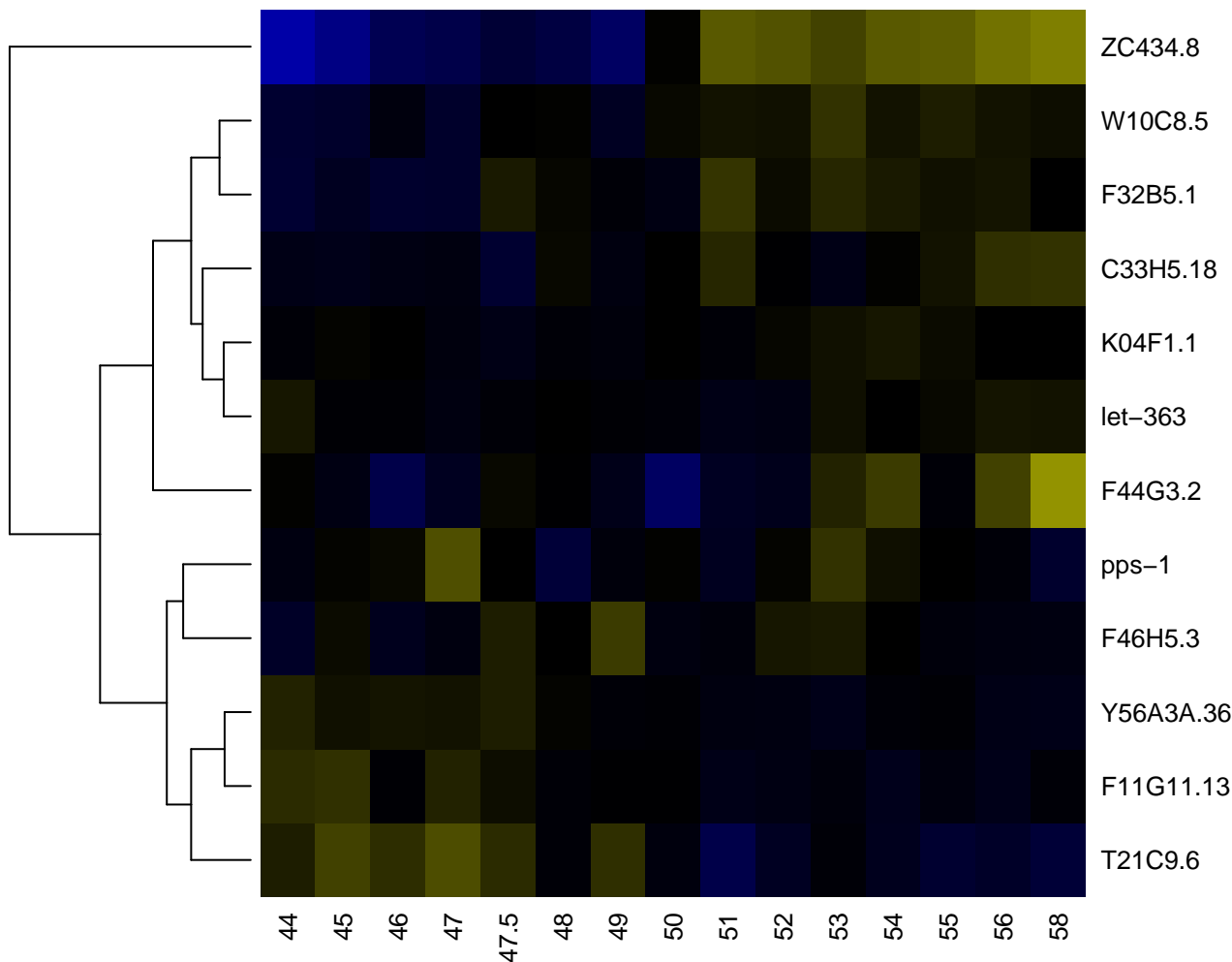
transferase activity, transferring hexosyl groups



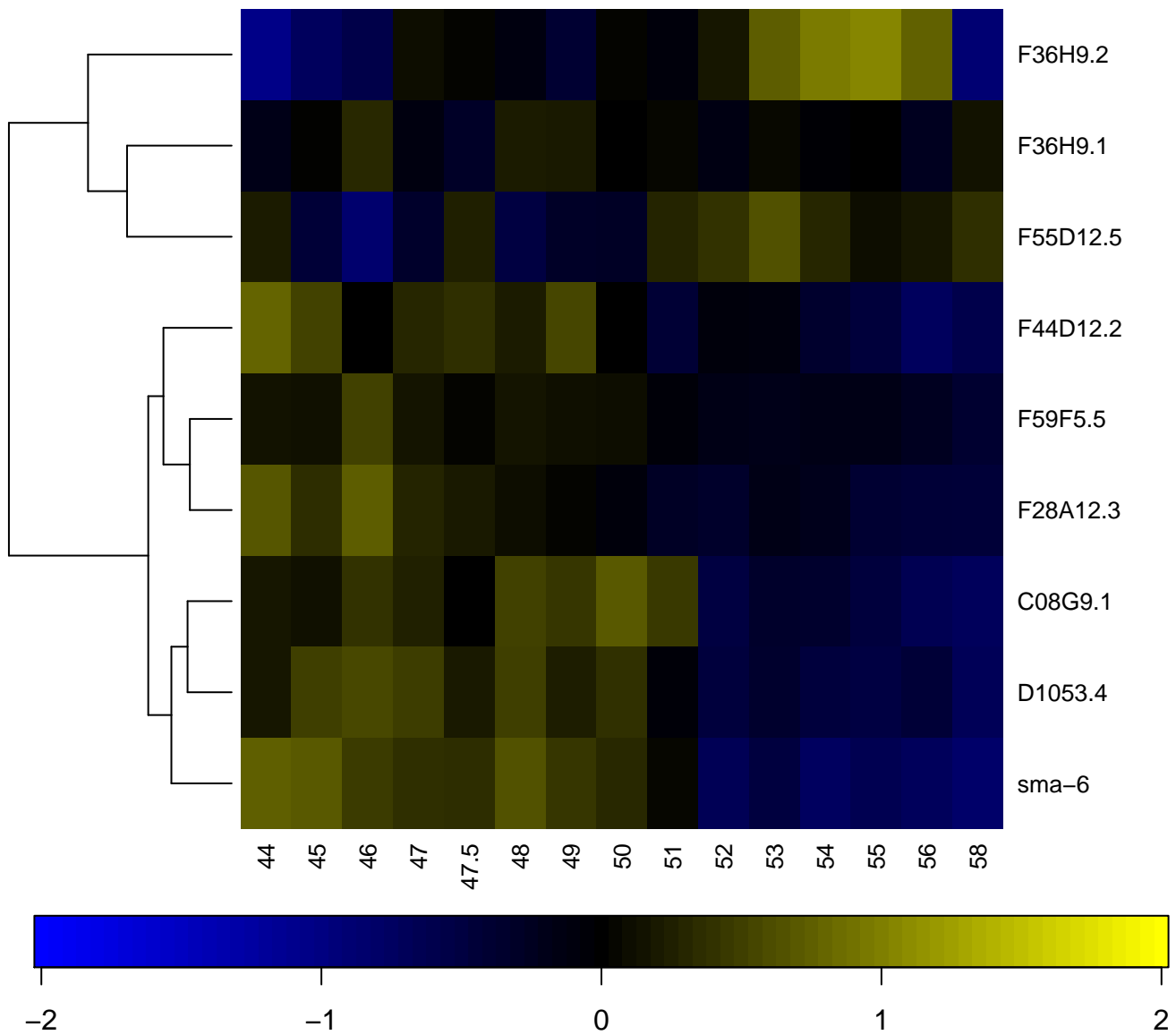
transferase activity, transferring nitrogenous groups



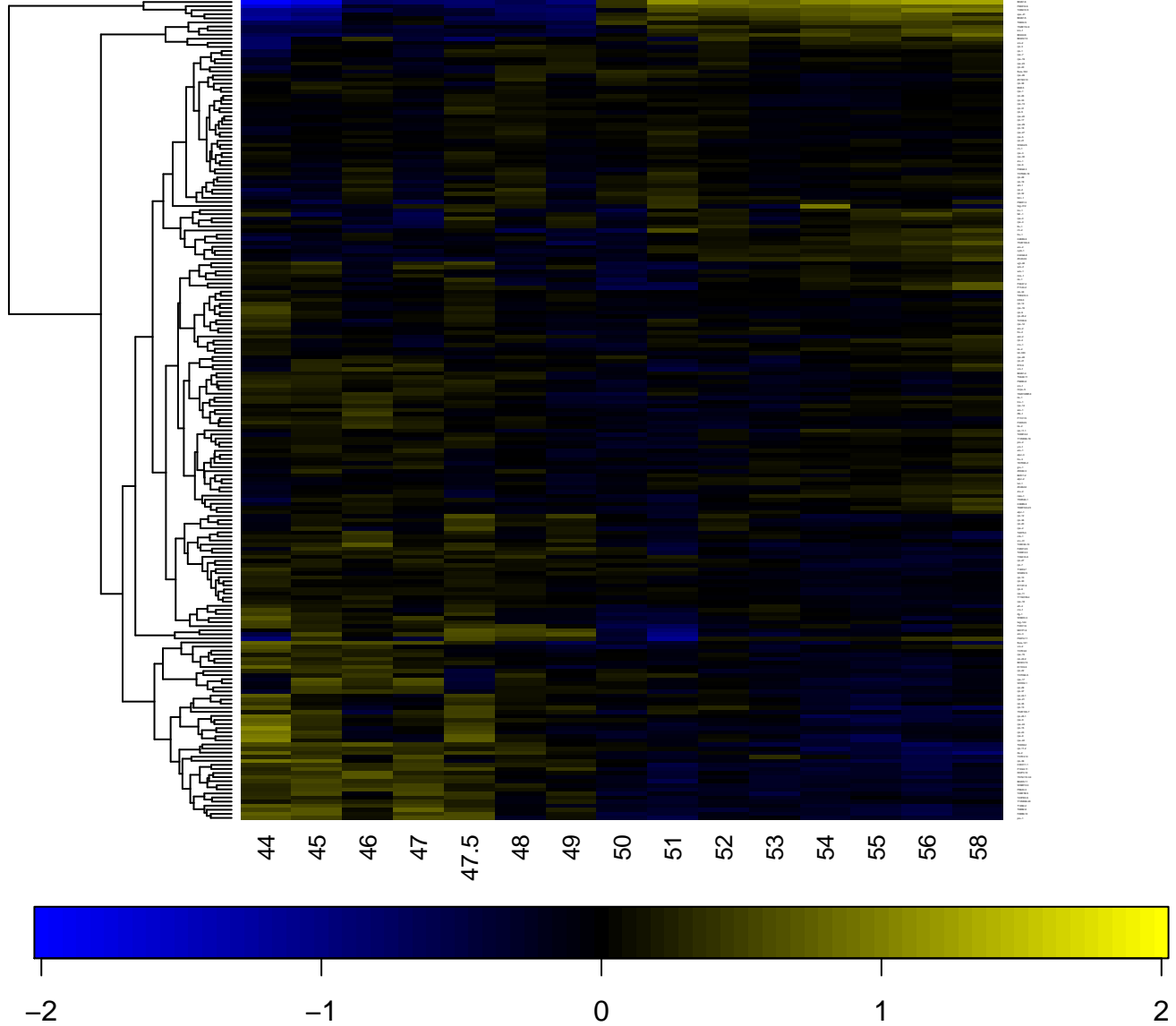
transferase activity, transferring phosphorus-containing gro



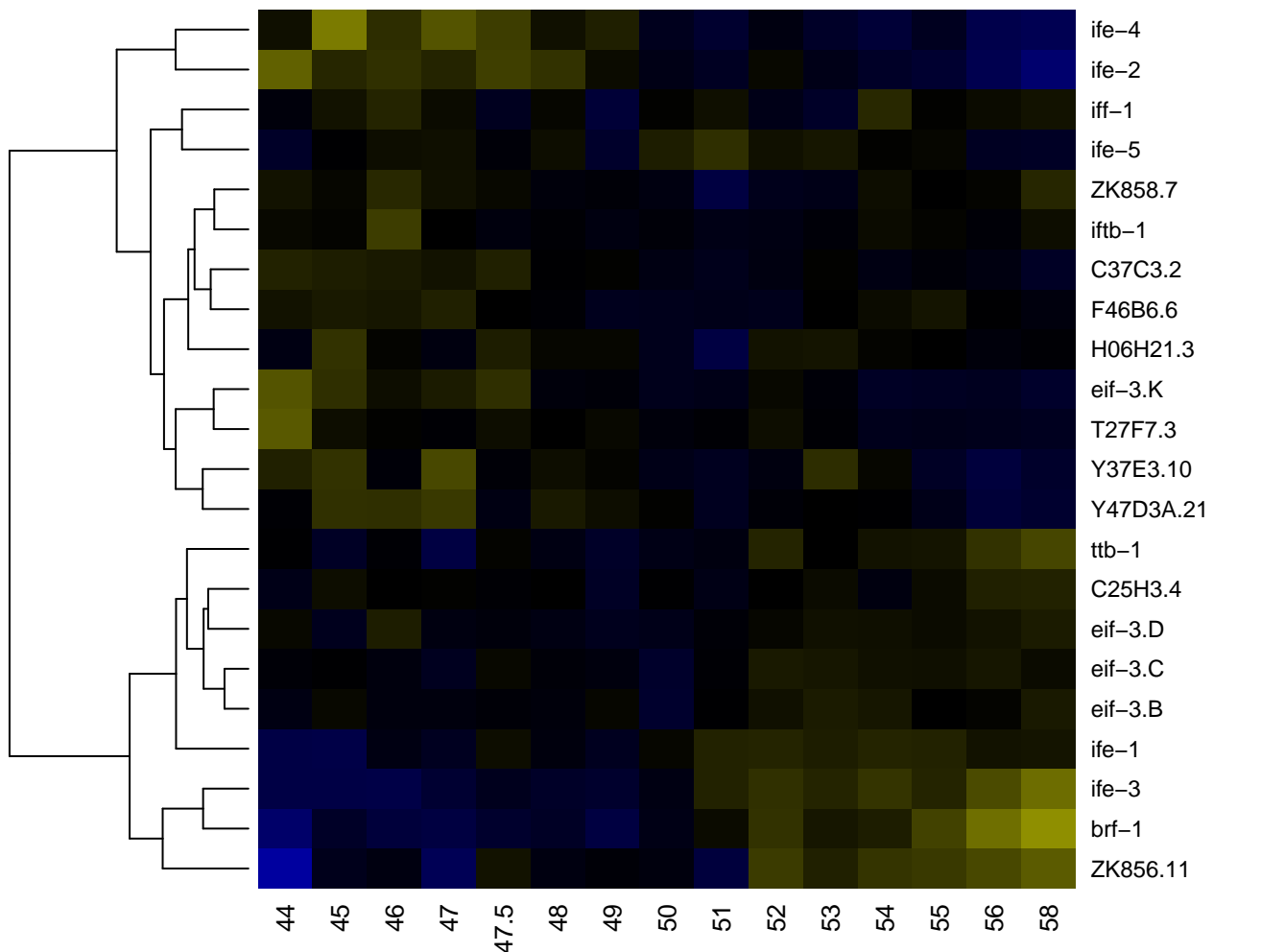
transforming growth factor beta receptor activity



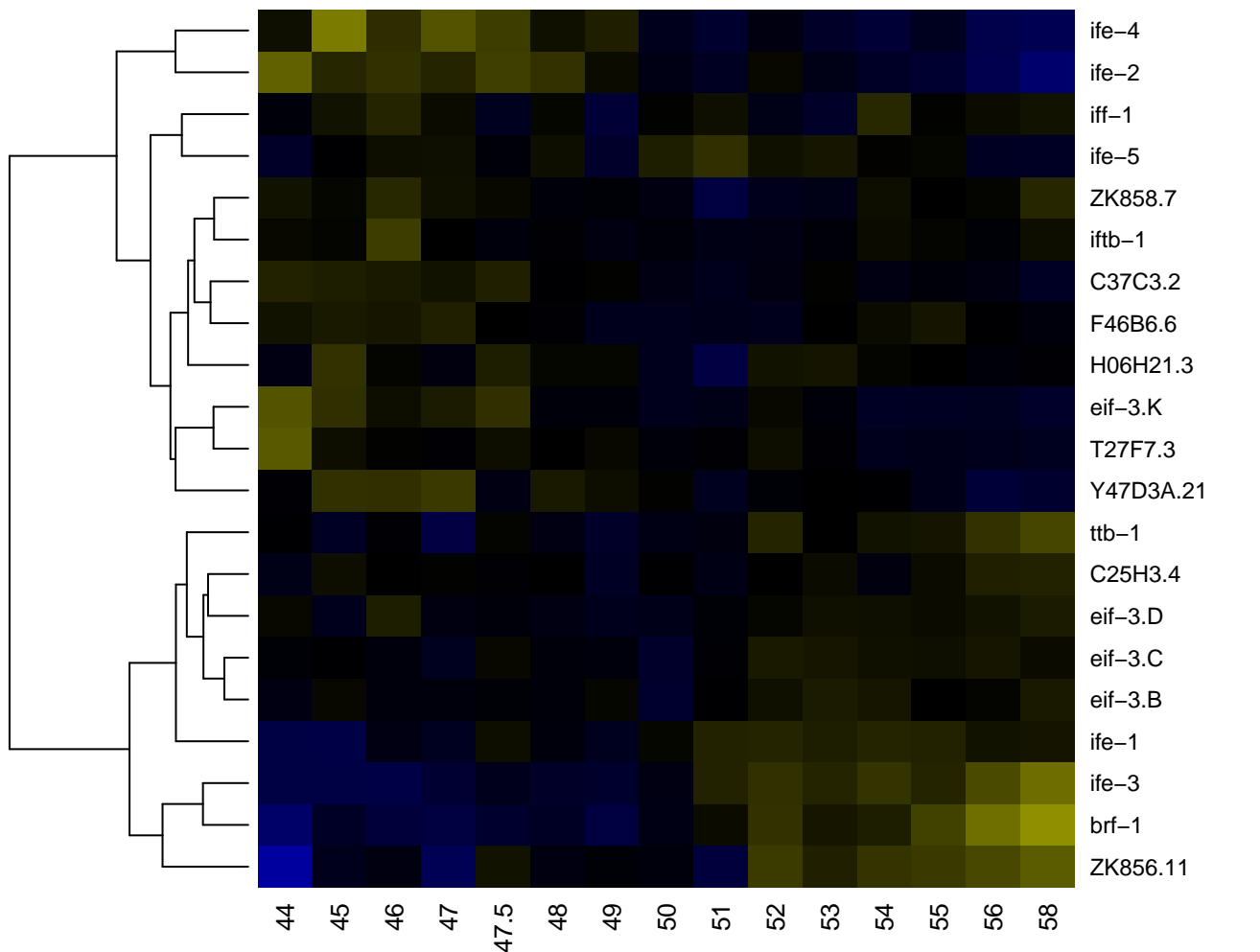
translation



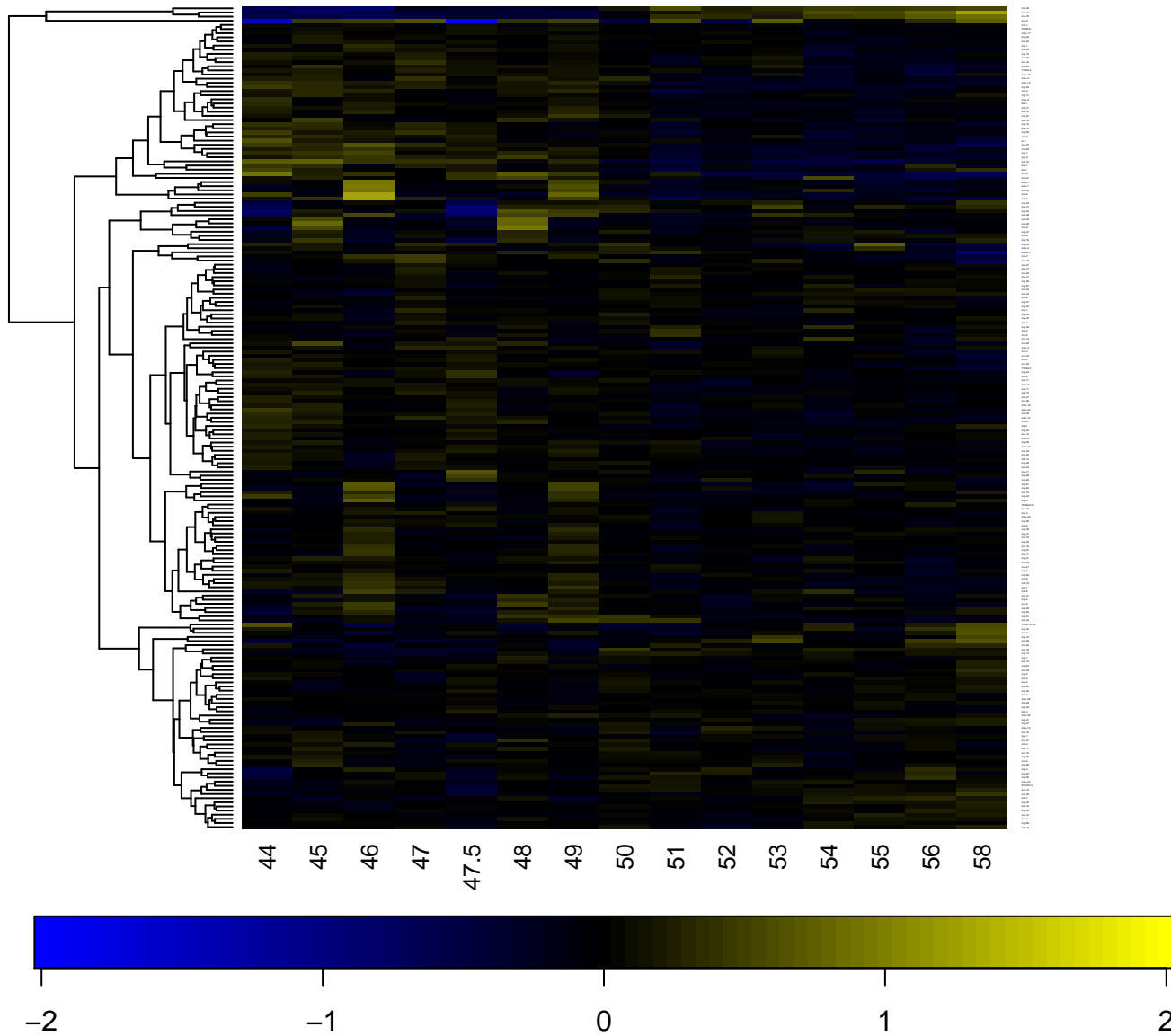
translation initiation factor activity



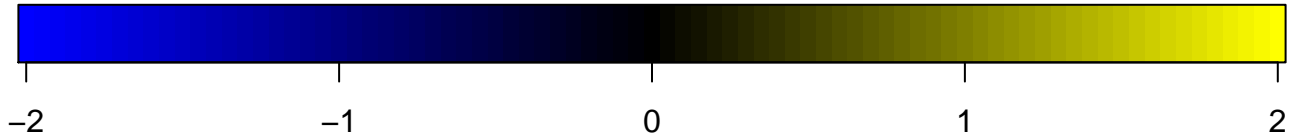
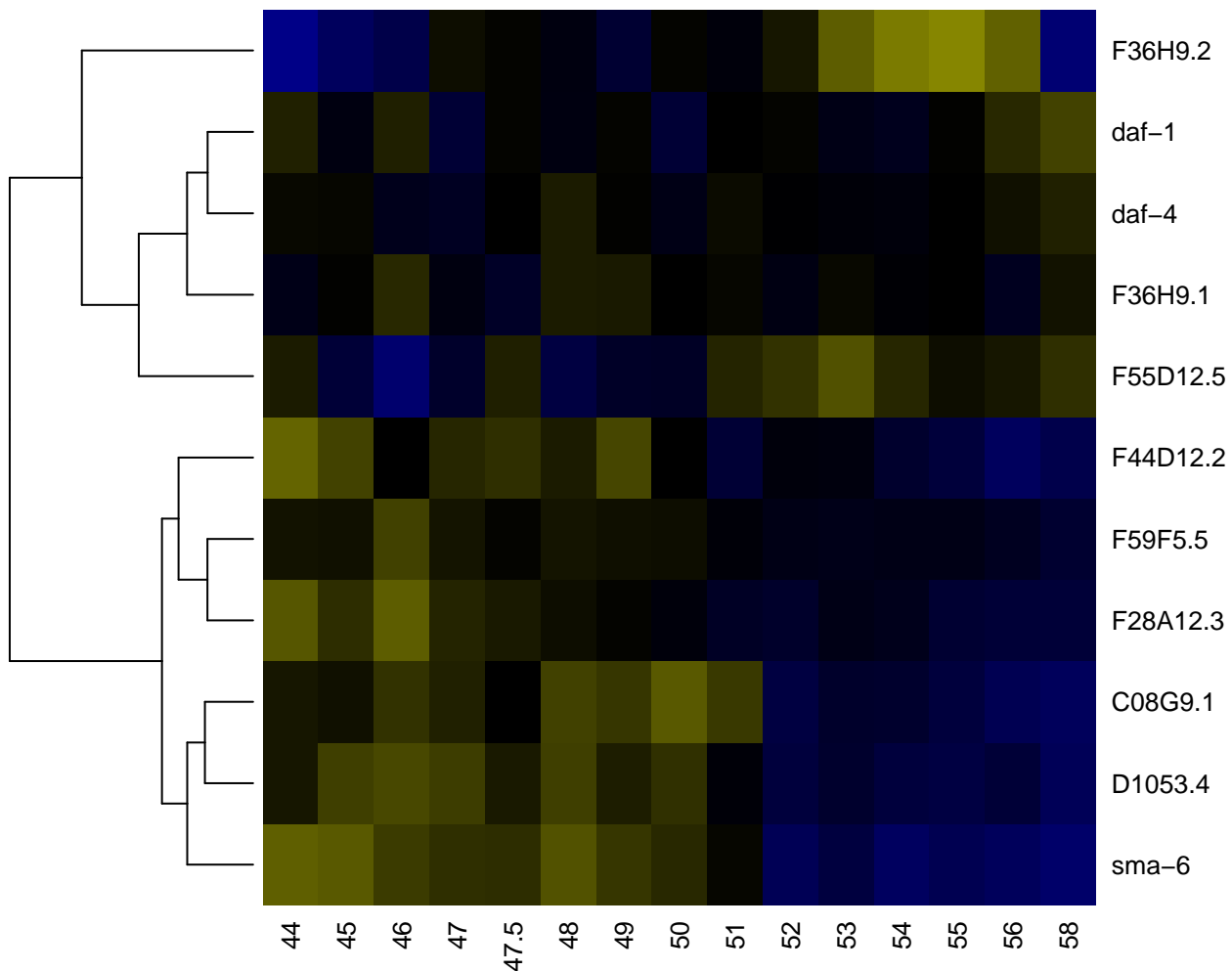
translational initiation



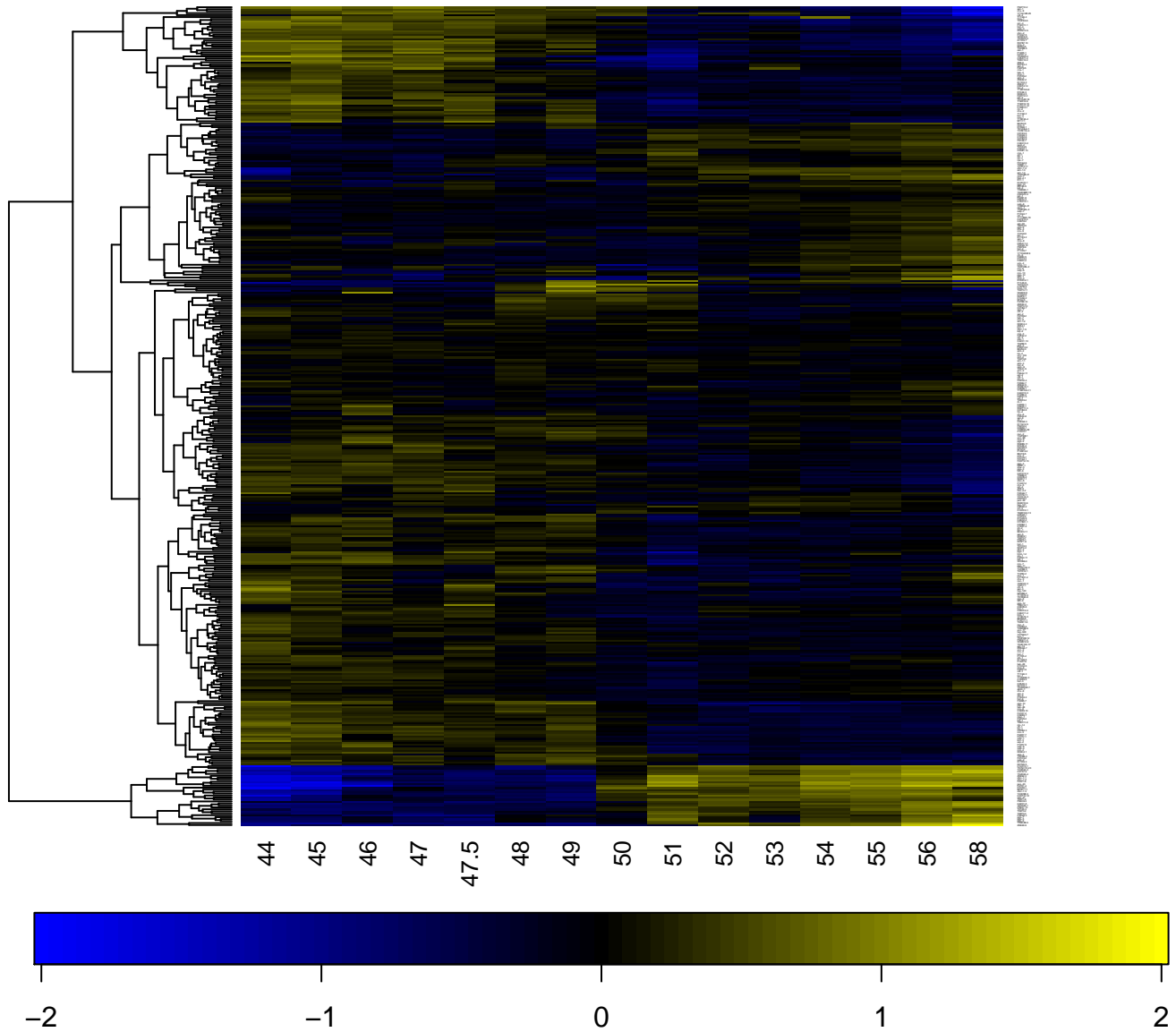
transmembrane receptor activity



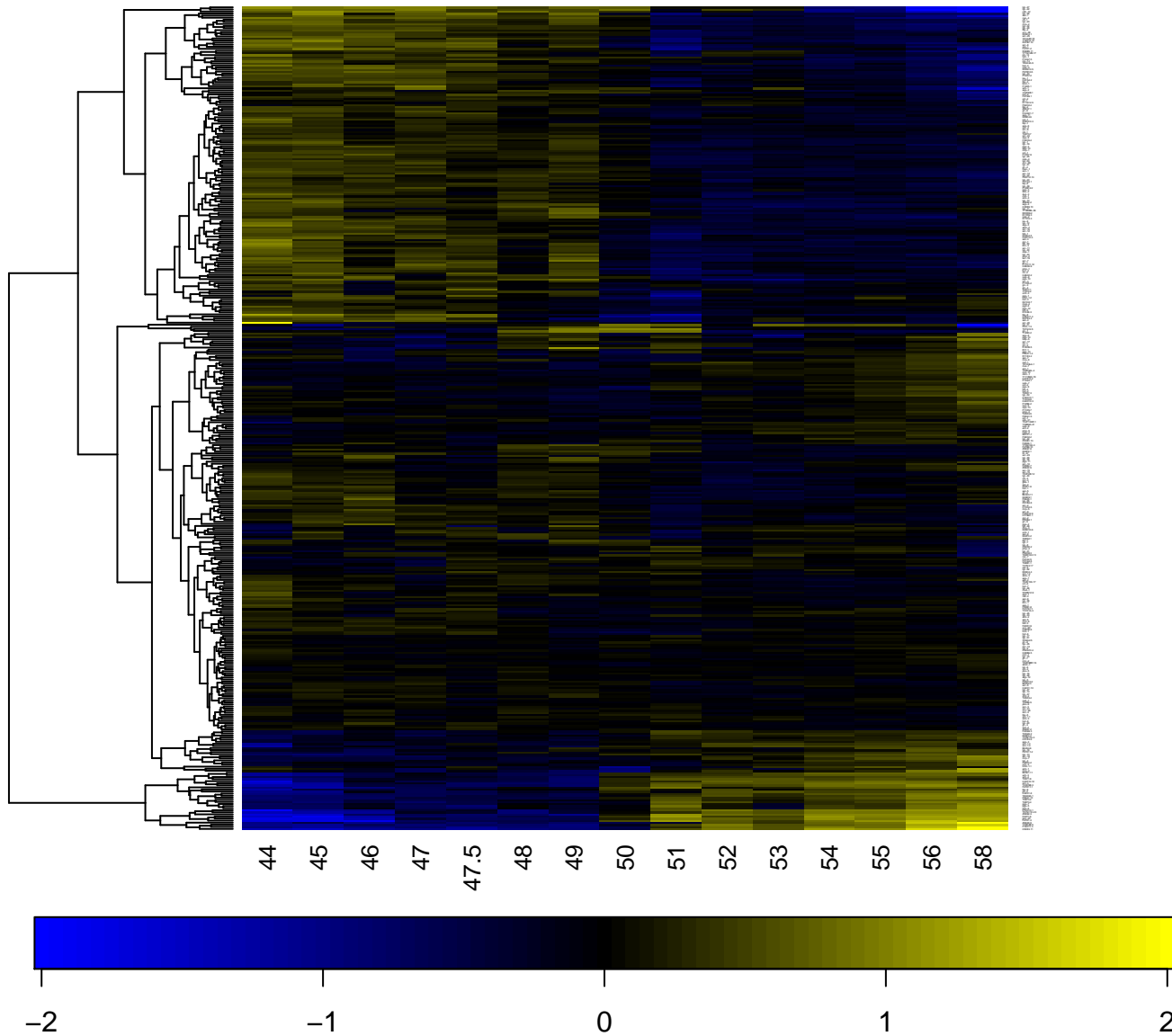
transmembrane receptor protein serine/threonine kinase acti



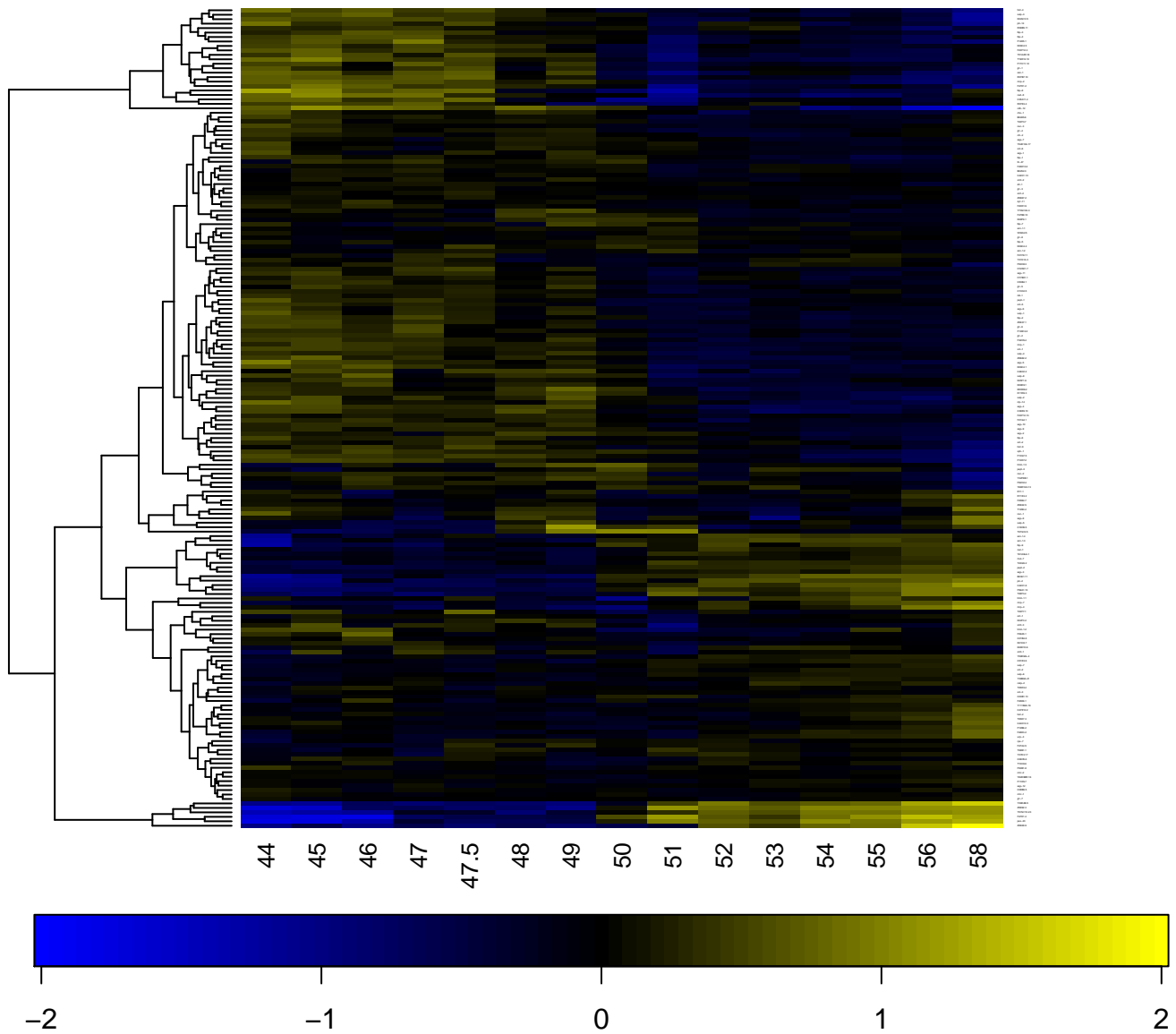
transmembrane transport



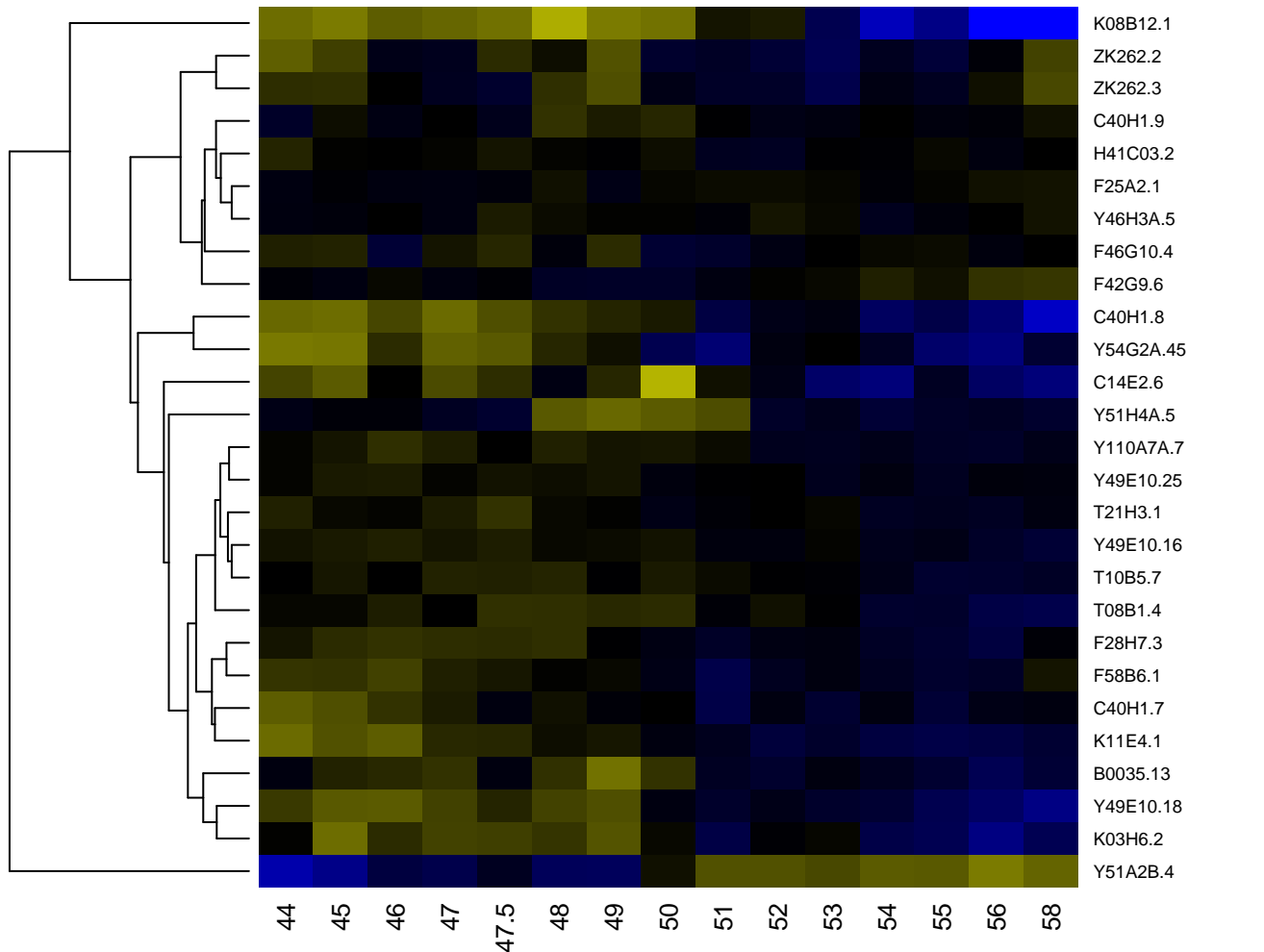
transport



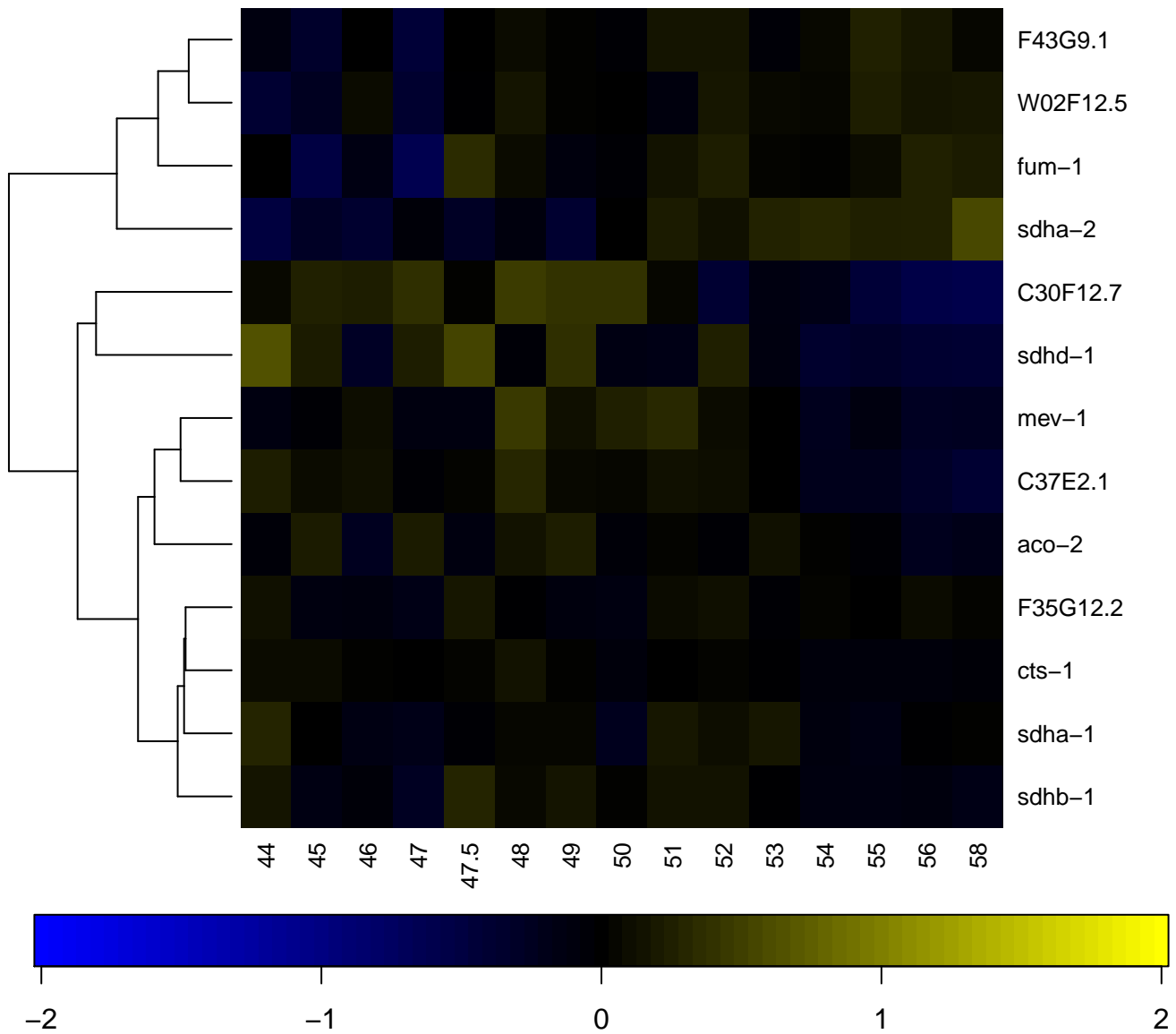
transporter activity



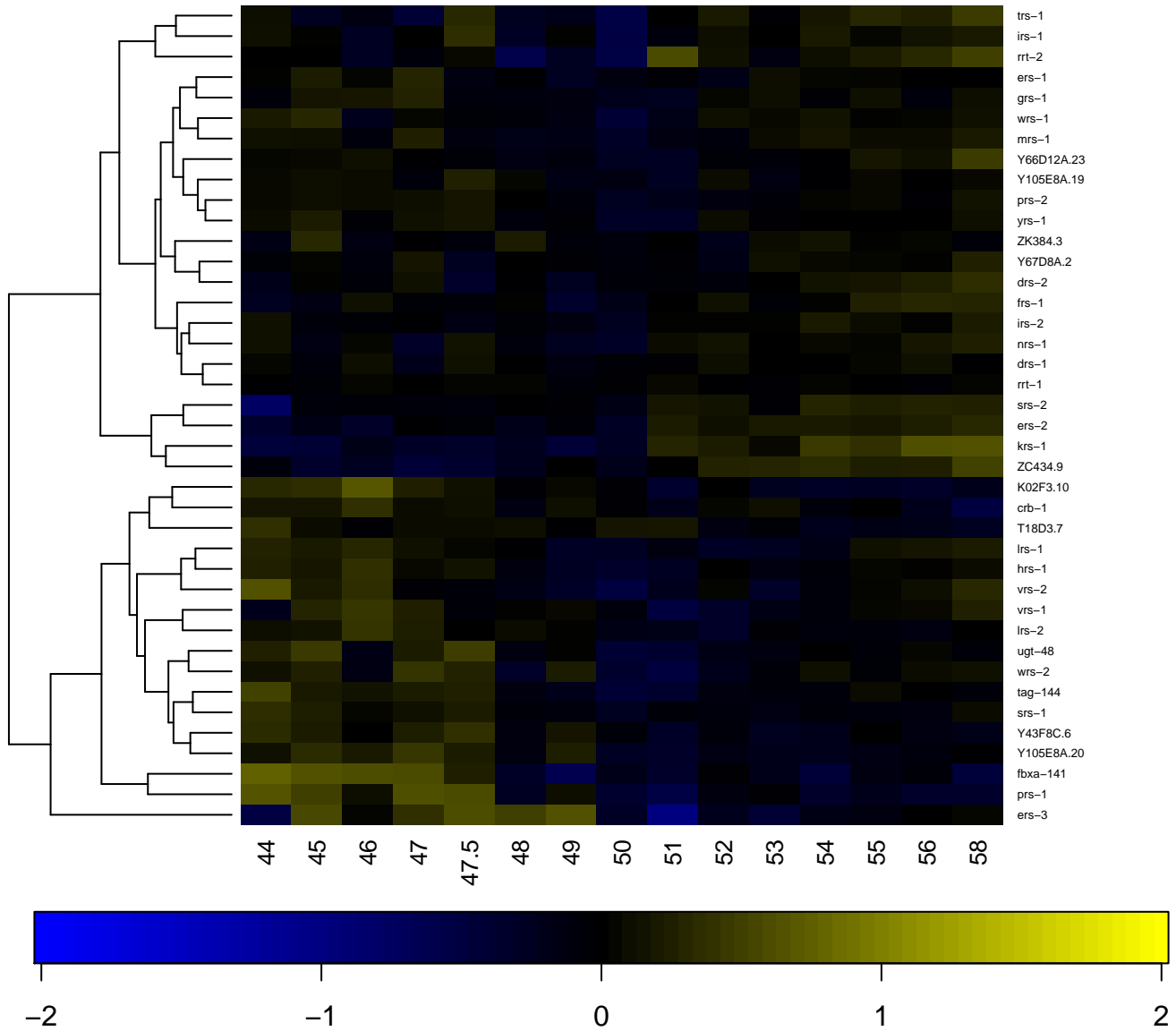
triacylglycerol lipase activity



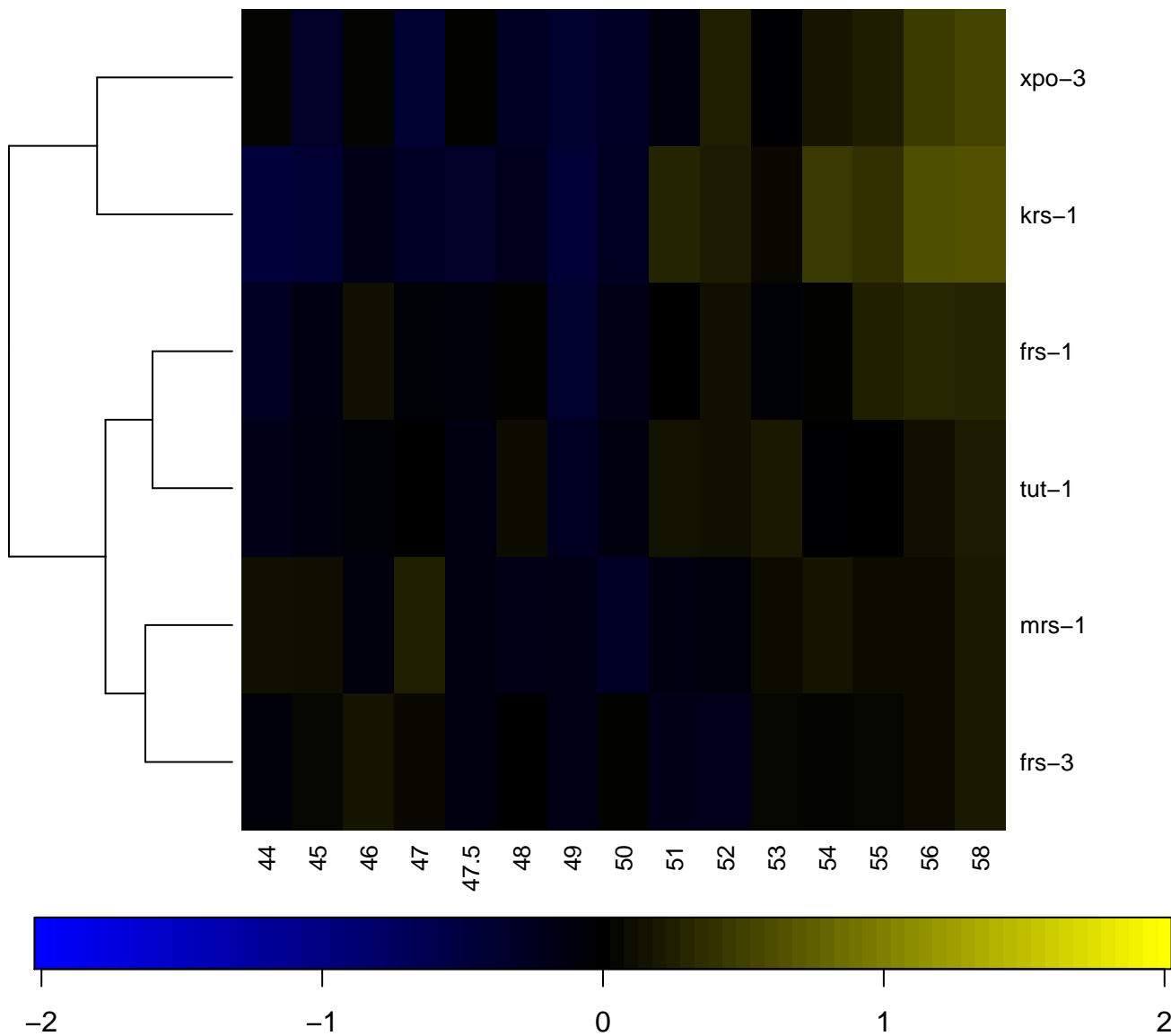
tricarboxylic acid cycle



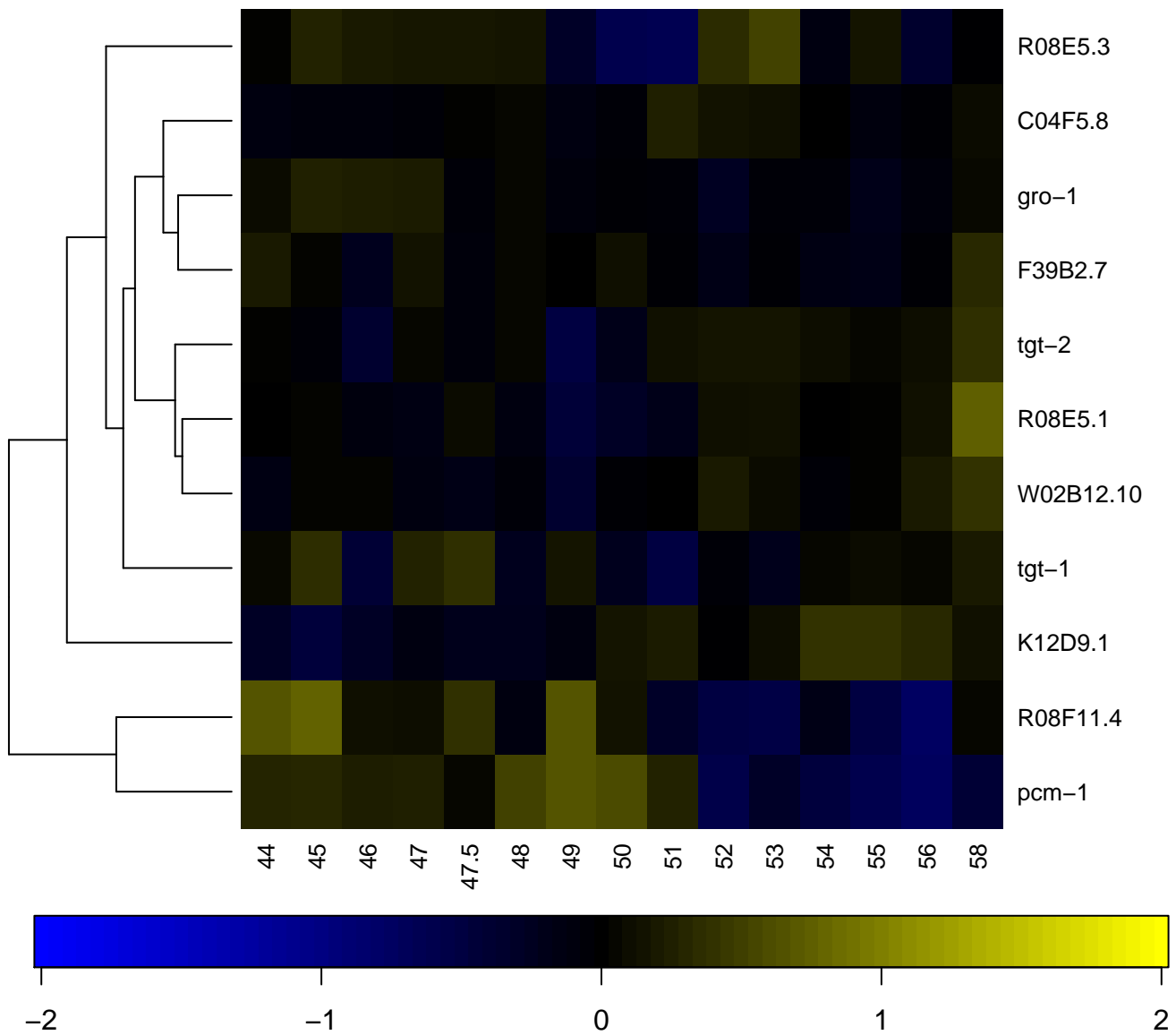
tRNA aminoacylation for protein translation



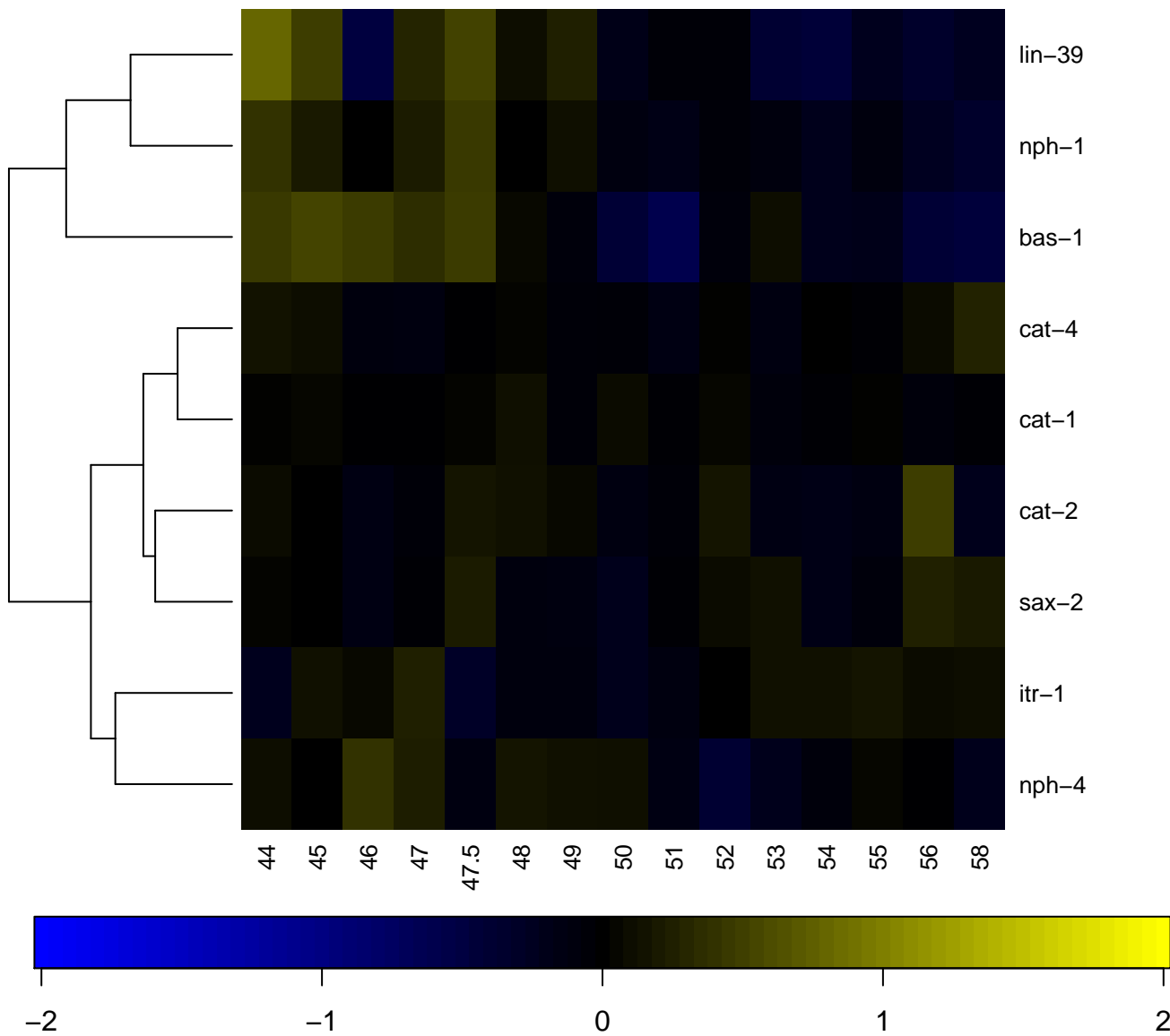
tRNA binding



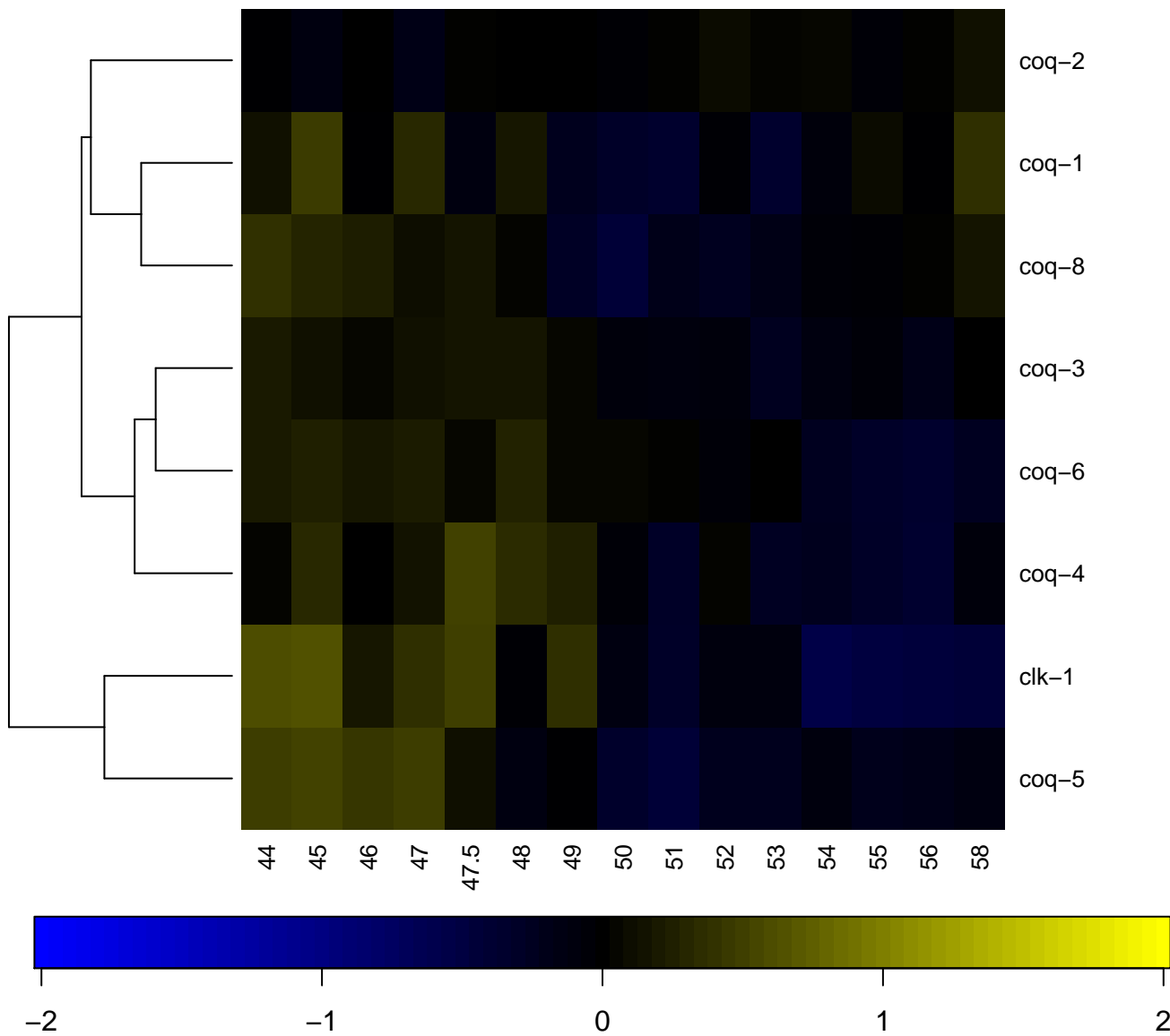
tRNA modification



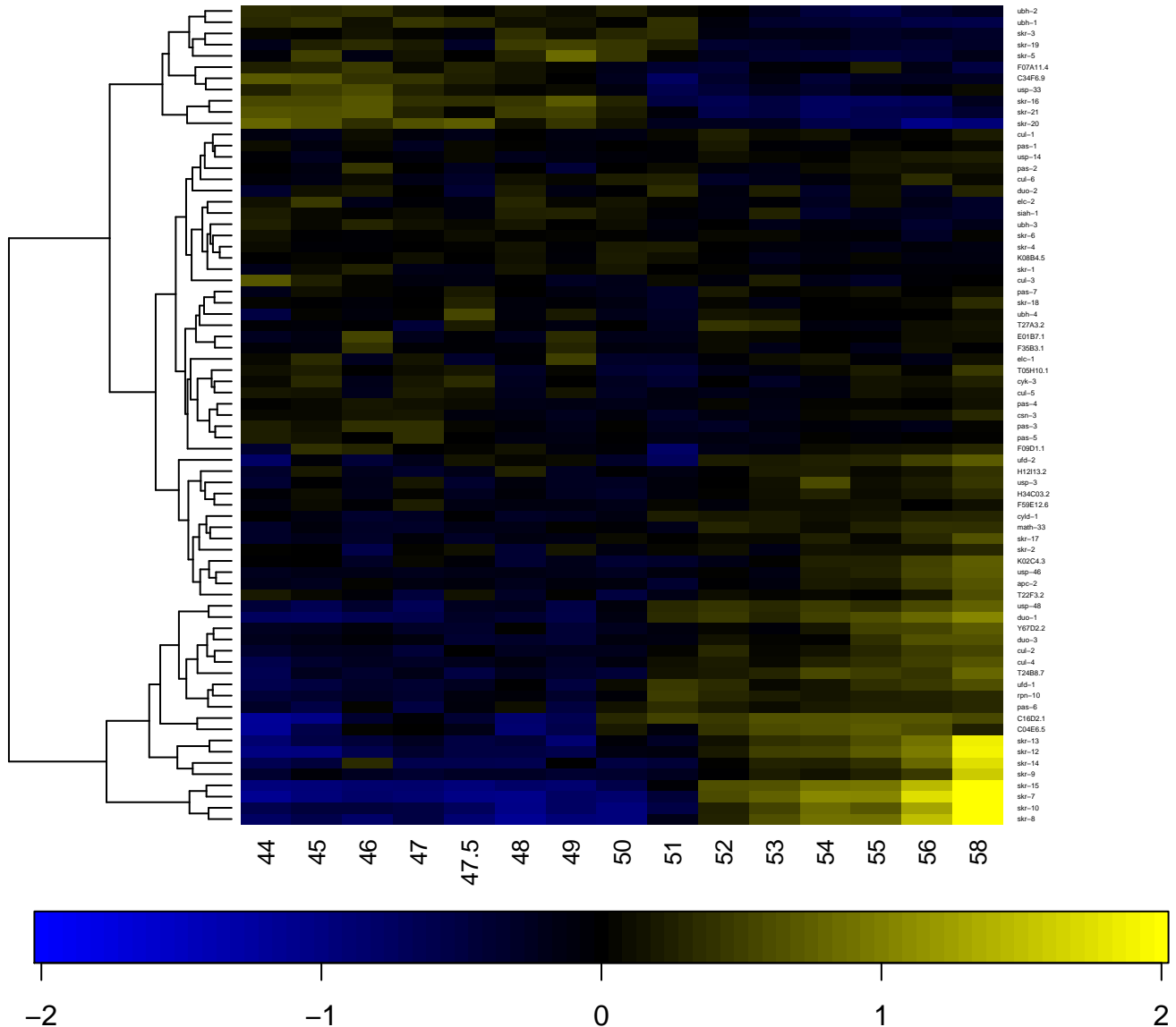
turning behavior involved in mating



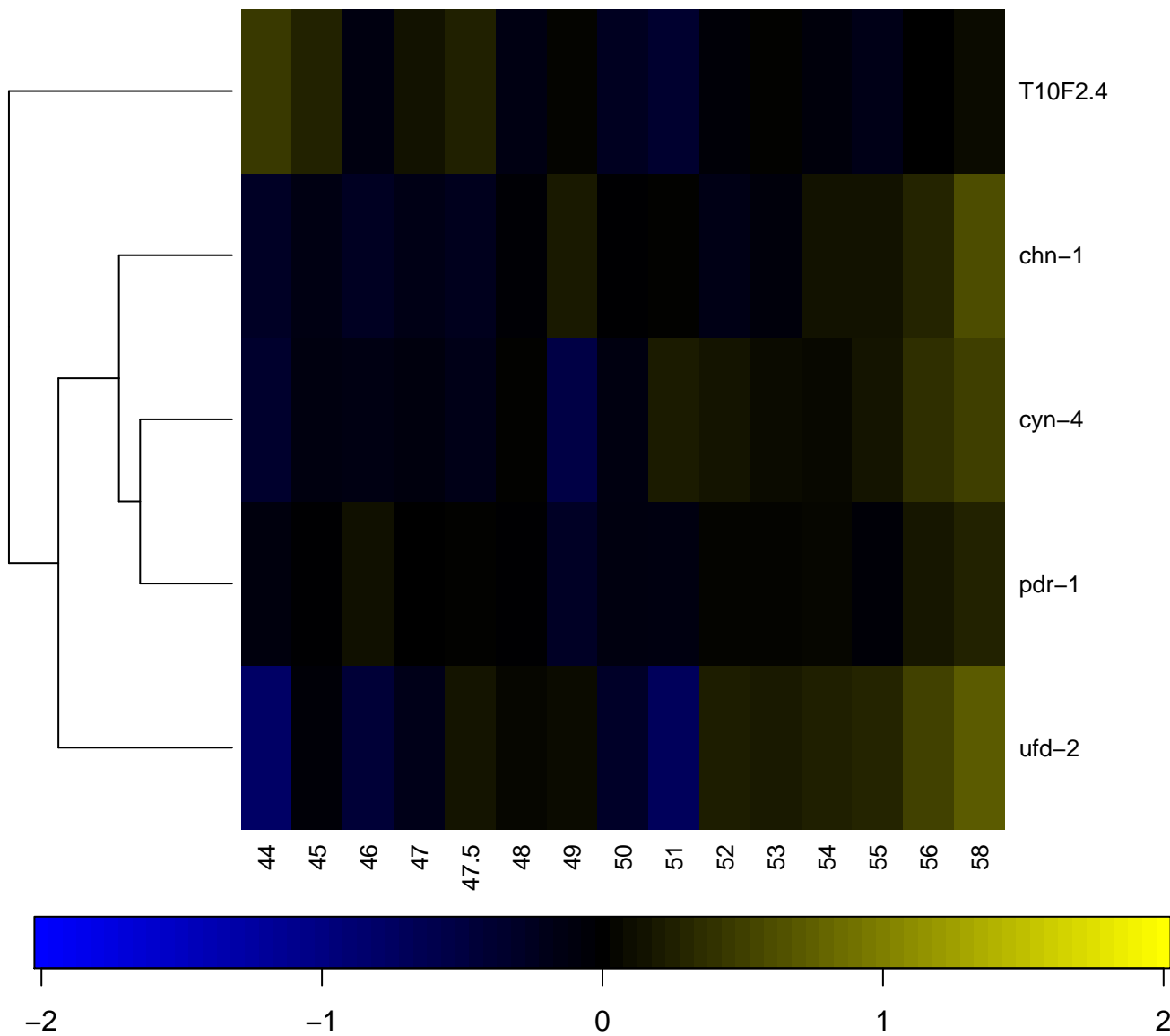
ubiquinone biosynthetic process



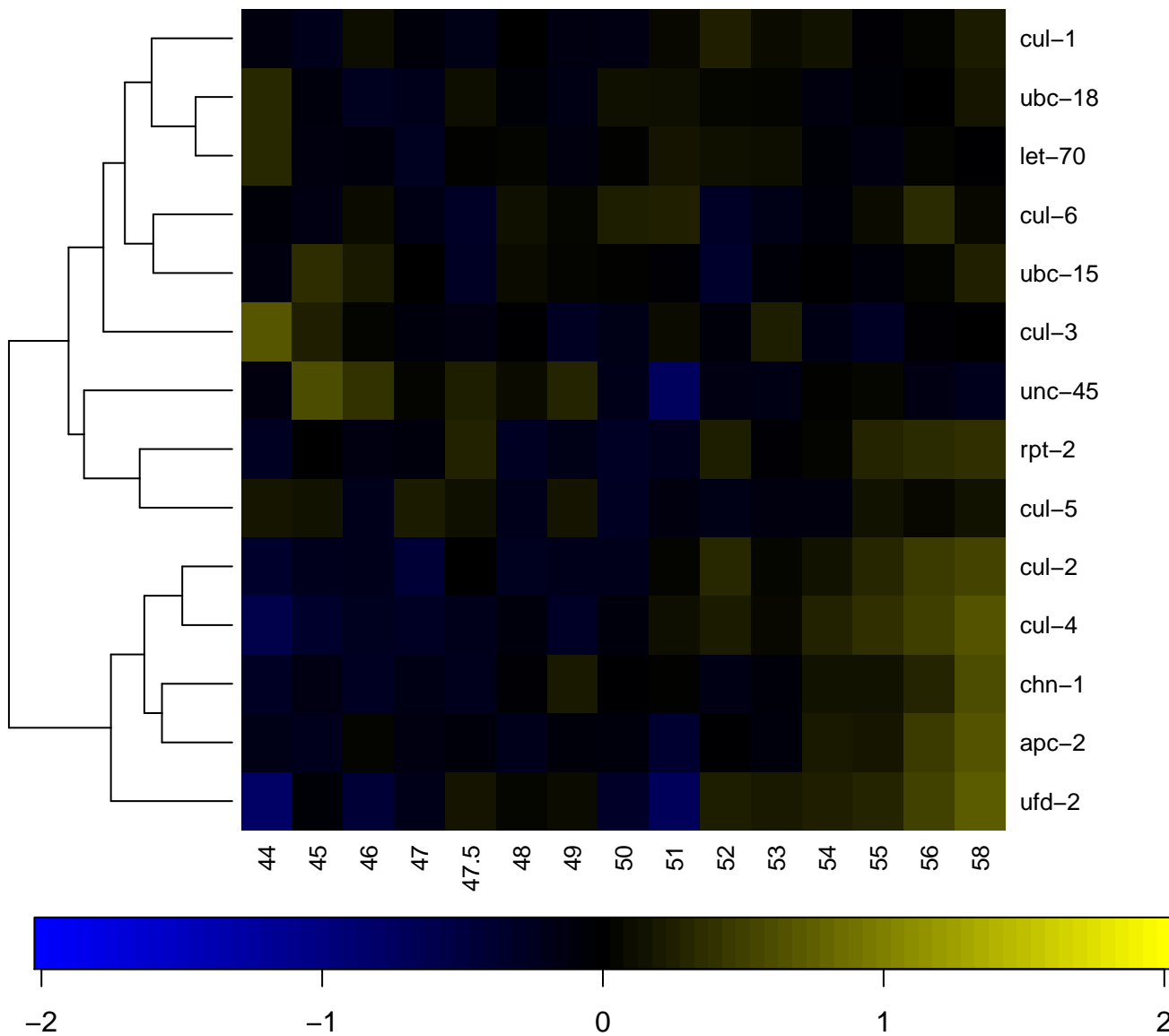
ubiquitin-dependent protein catabolic process



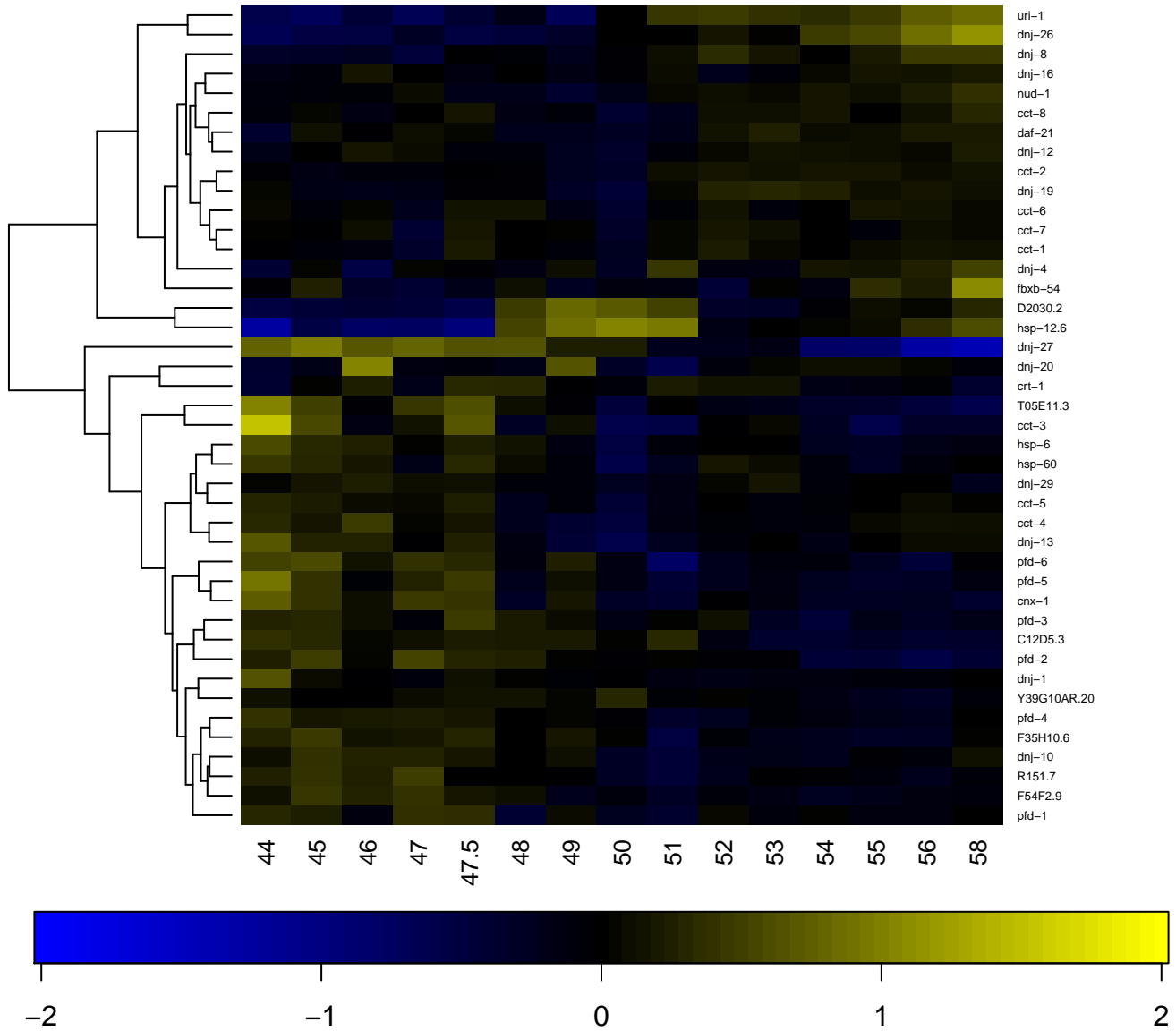
ubiquitin ligase complex



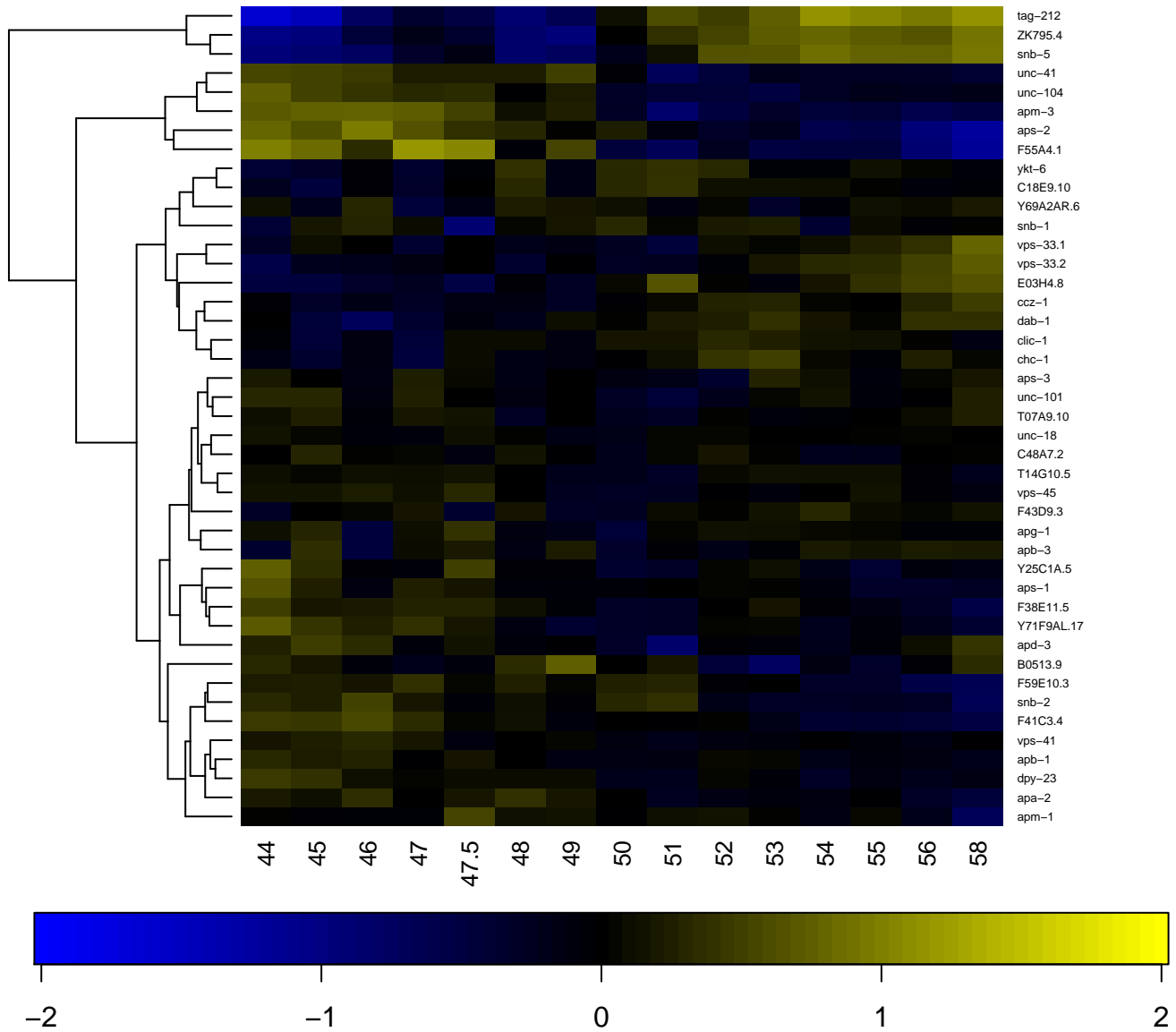
ubiquitin protein ligase binding



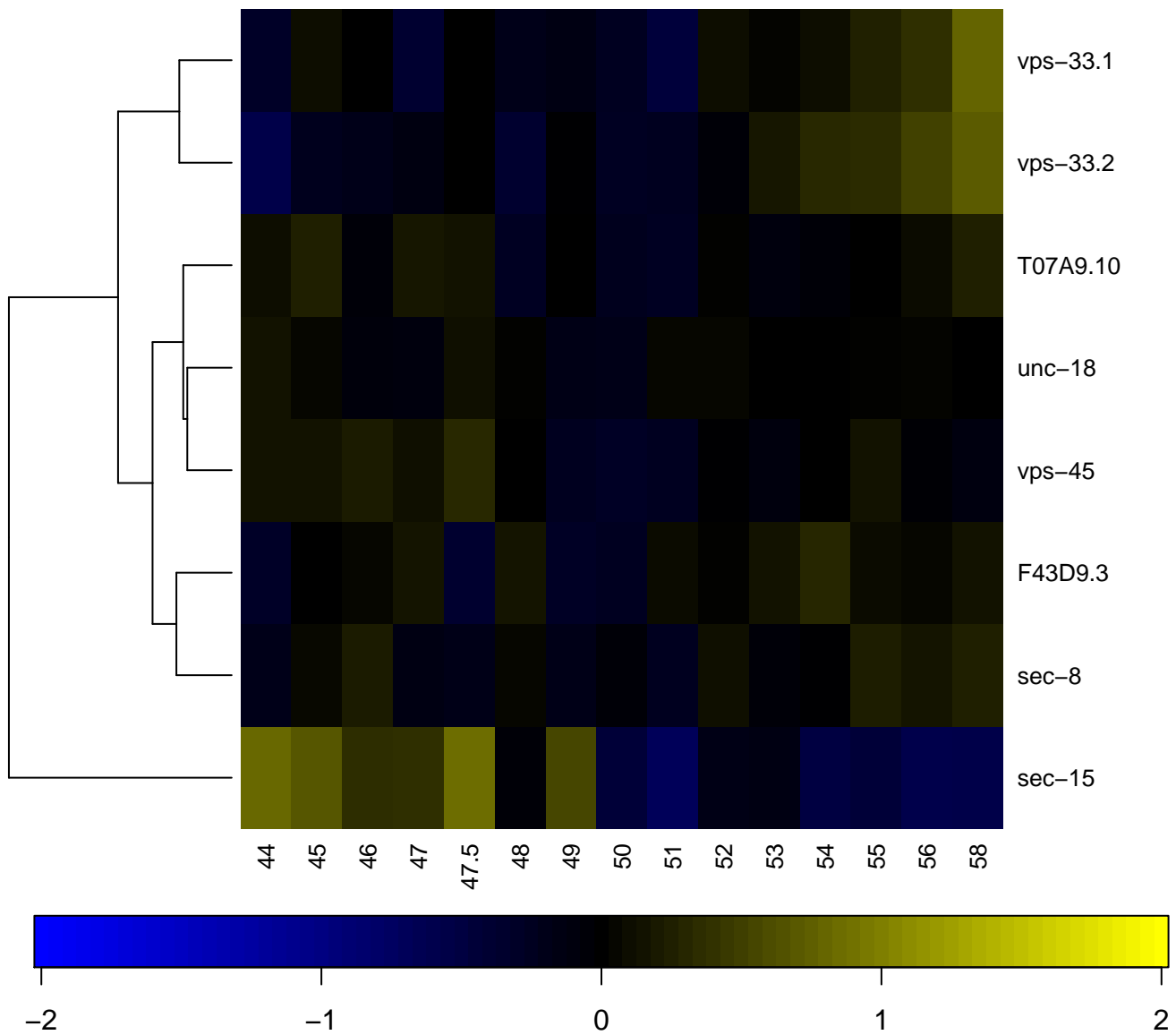
unfolded protein binding



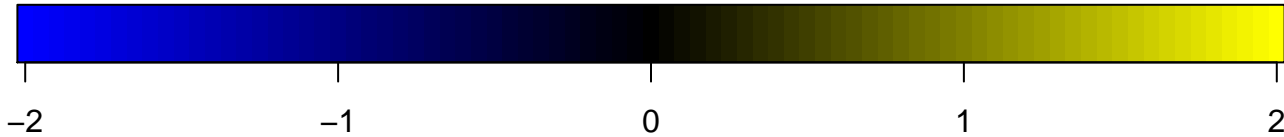
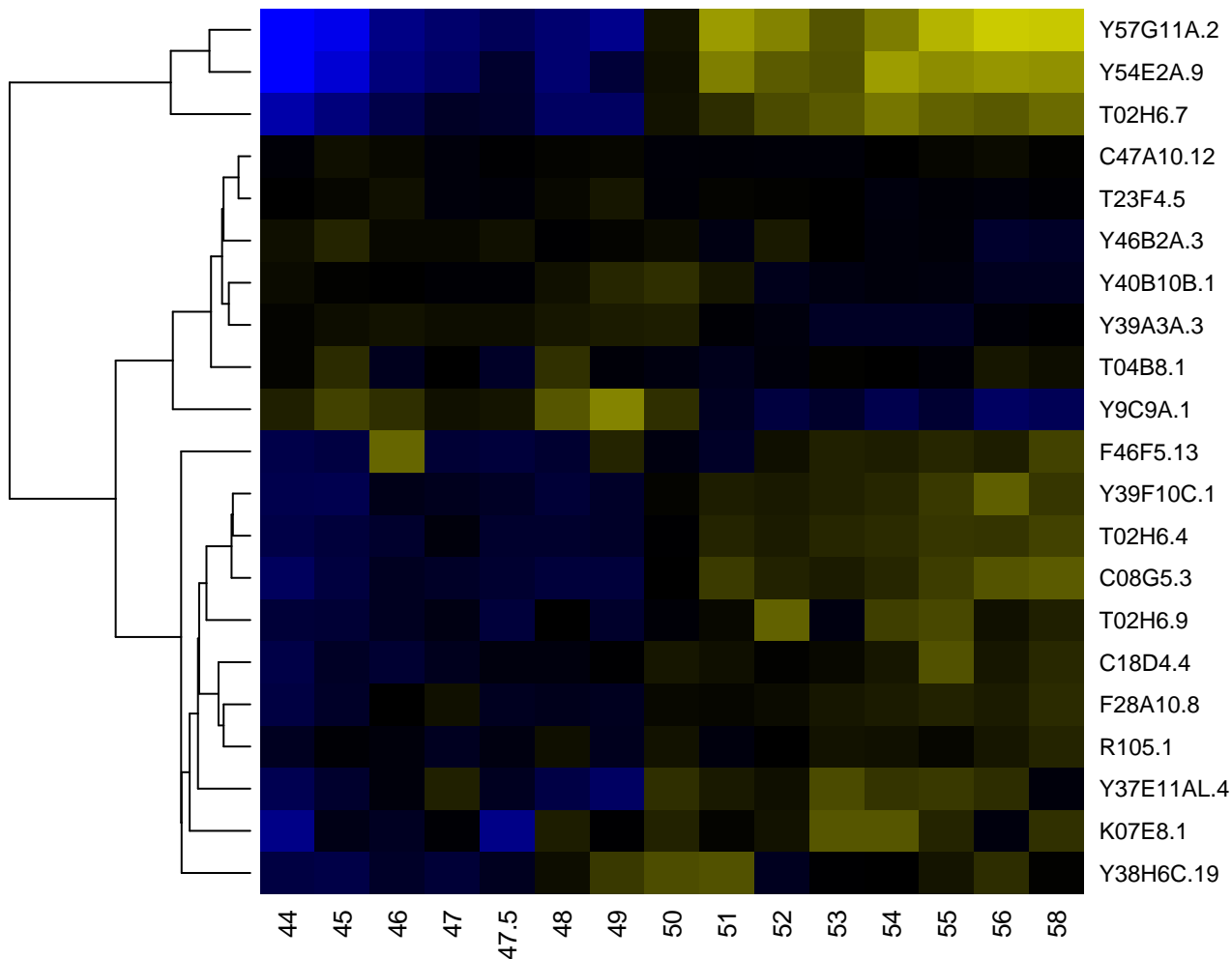
vesicle-mediated transport



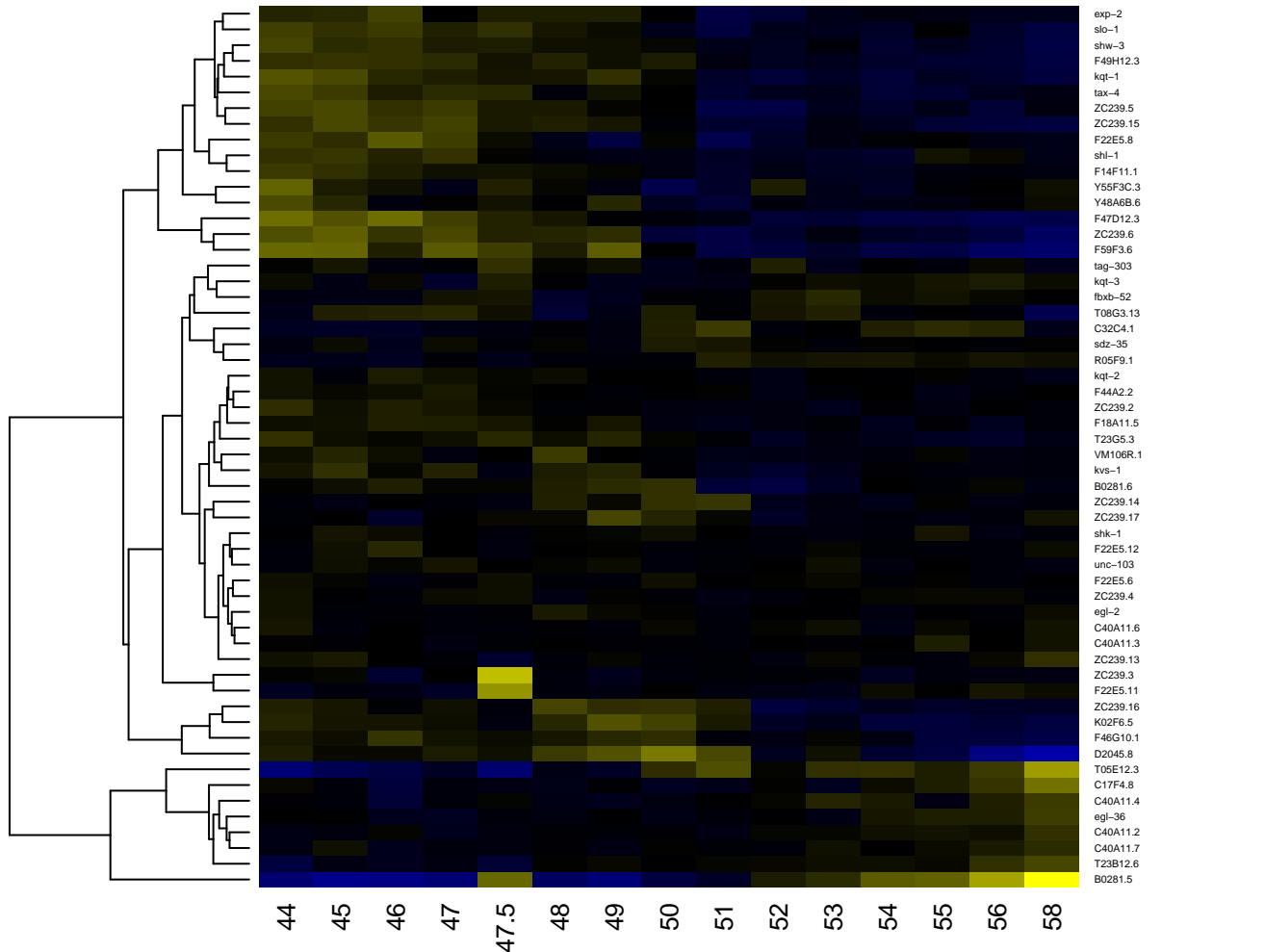
vesicle docking during exocytosis



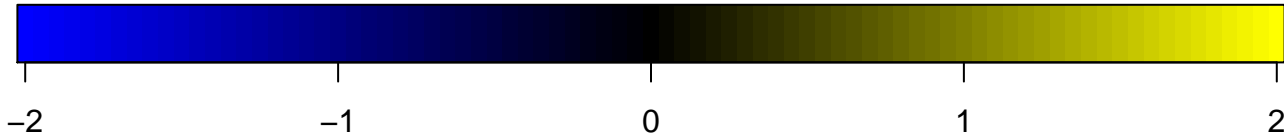
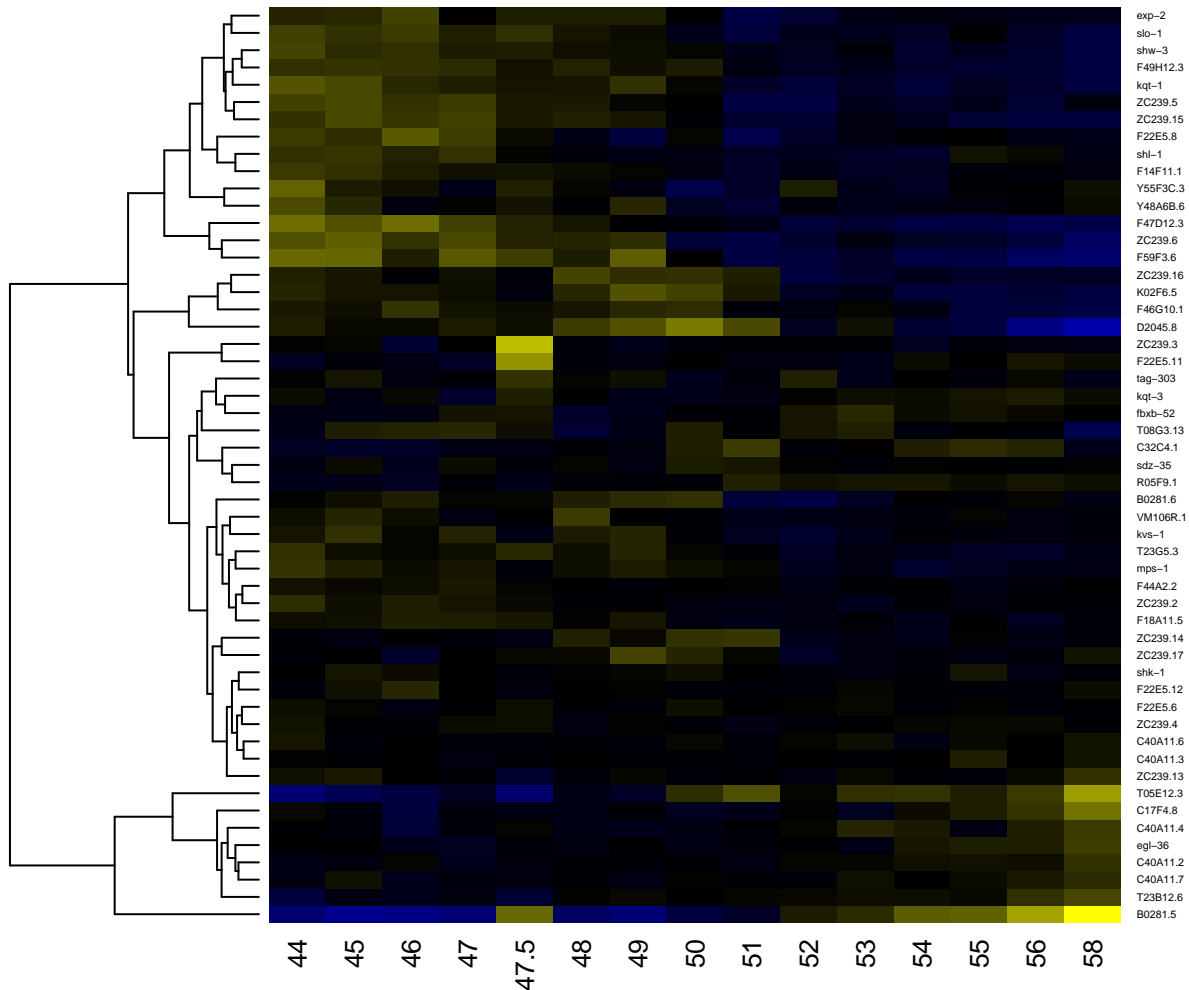
vitelline membrane formation



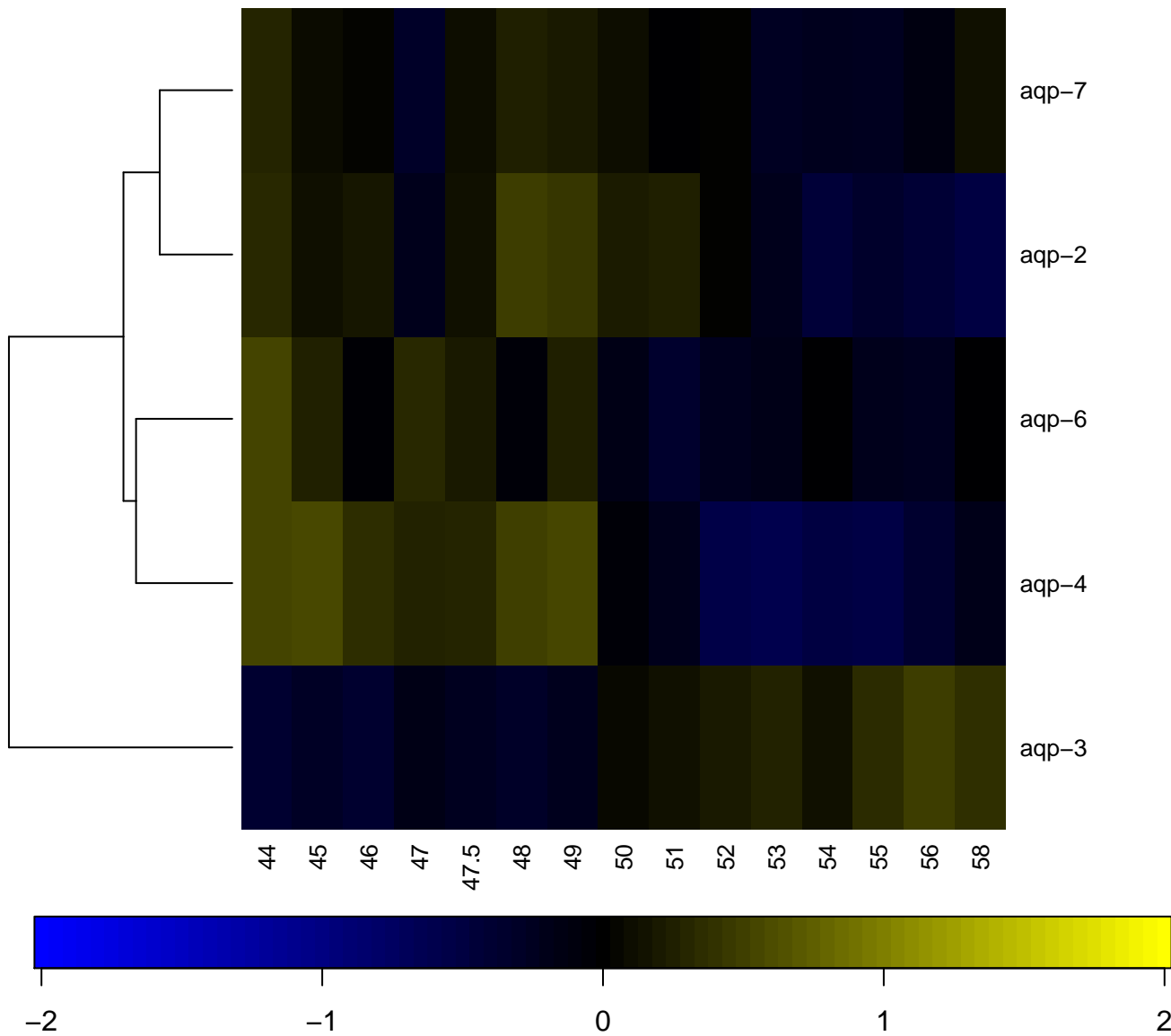
voltage-gated potassium channel activity



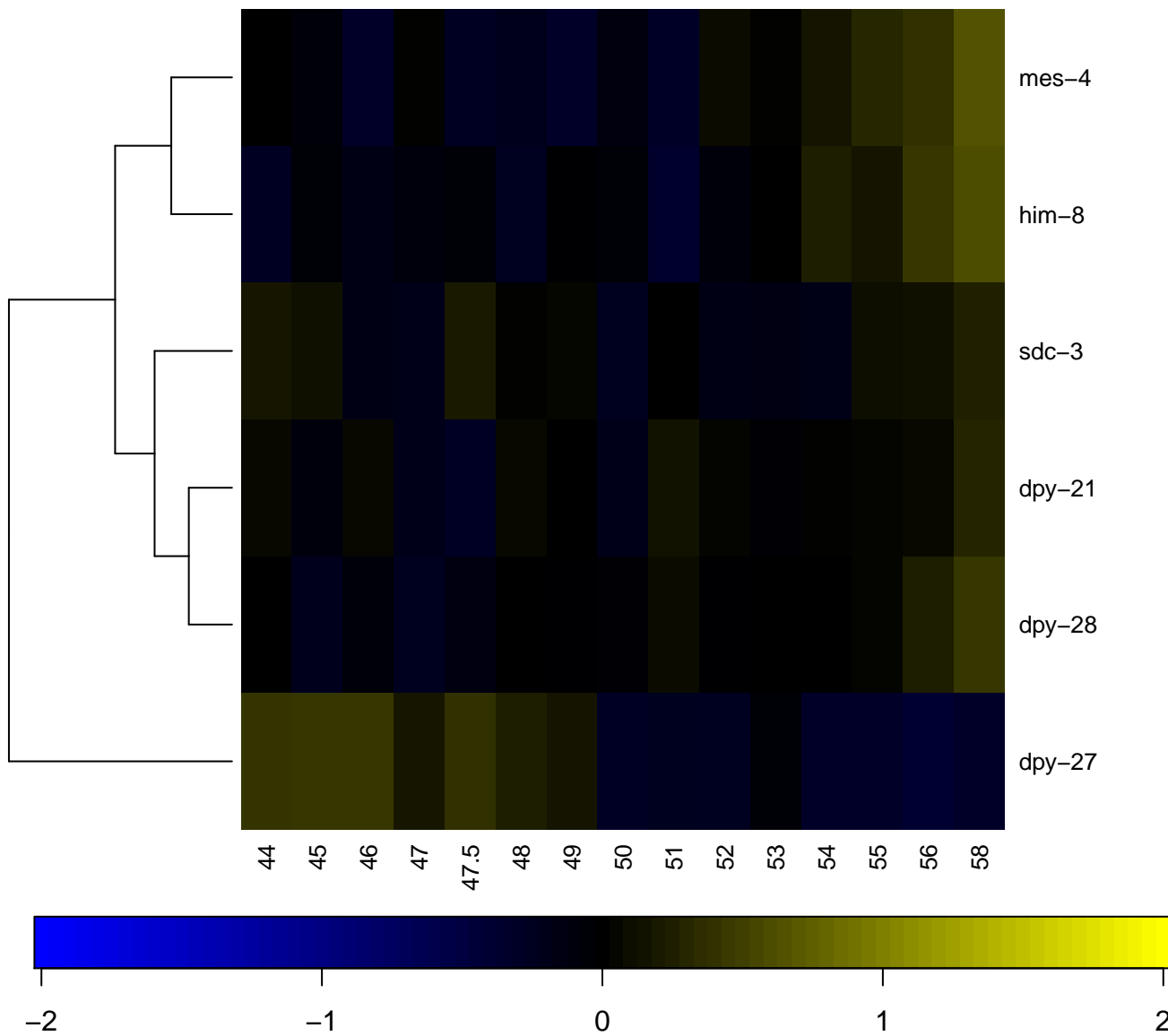
voltage-gated potassium channel complex



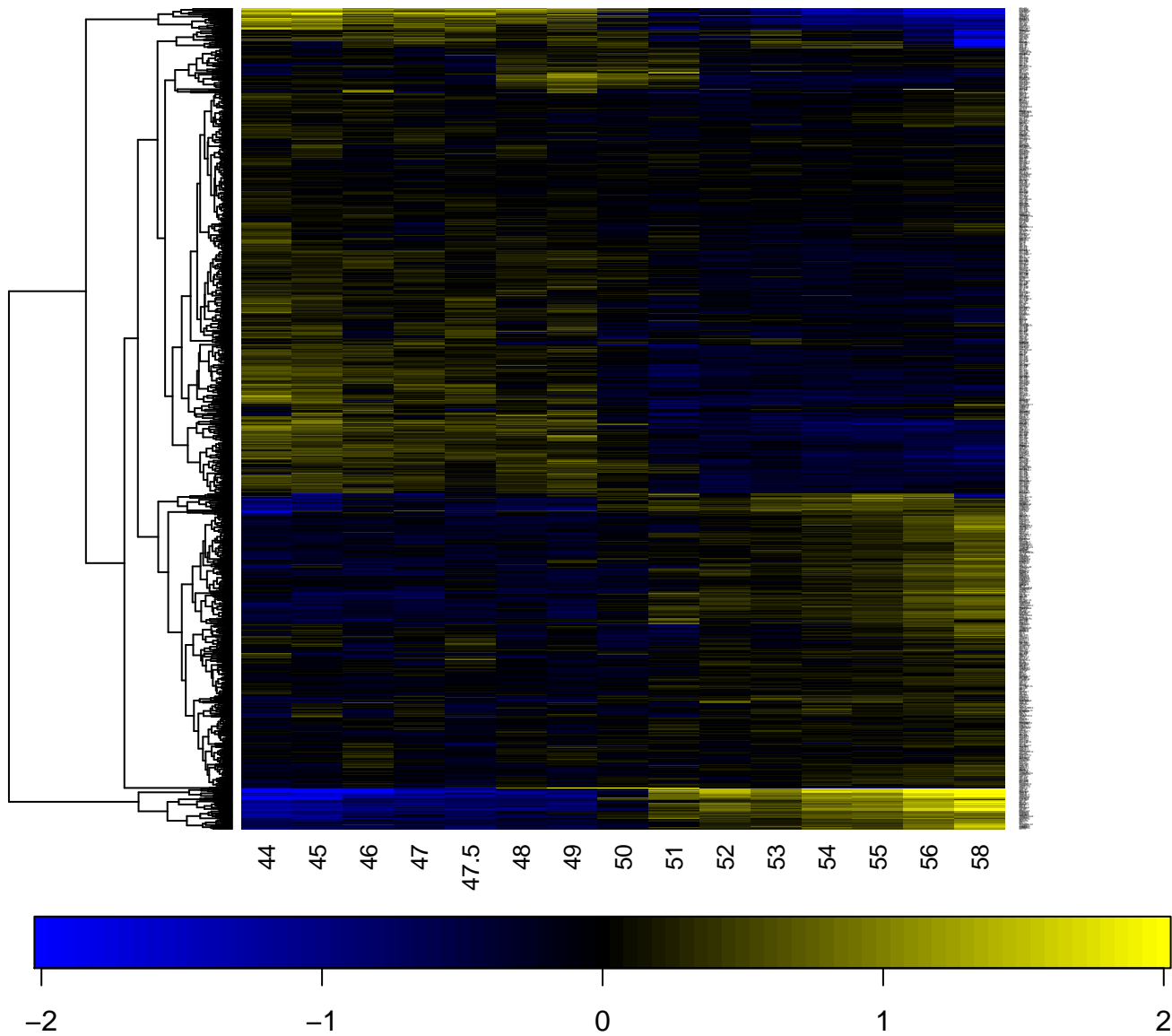
water transport



X chromosome

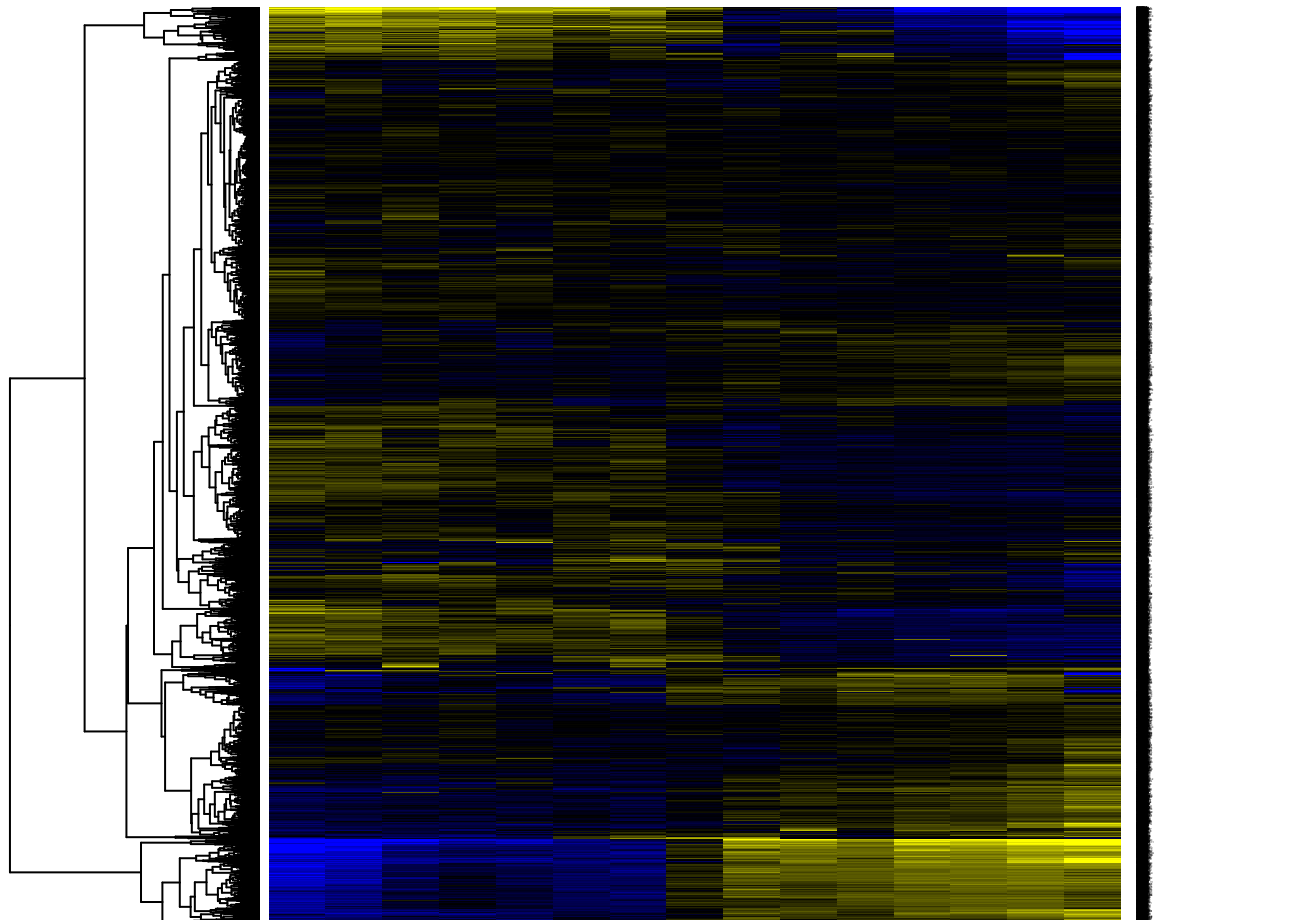


zinc ion binding

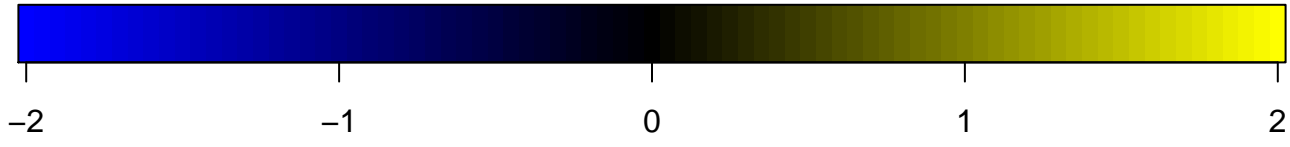


Supplementary file E | Dynamic gene expression patterns of all Gene Classes.

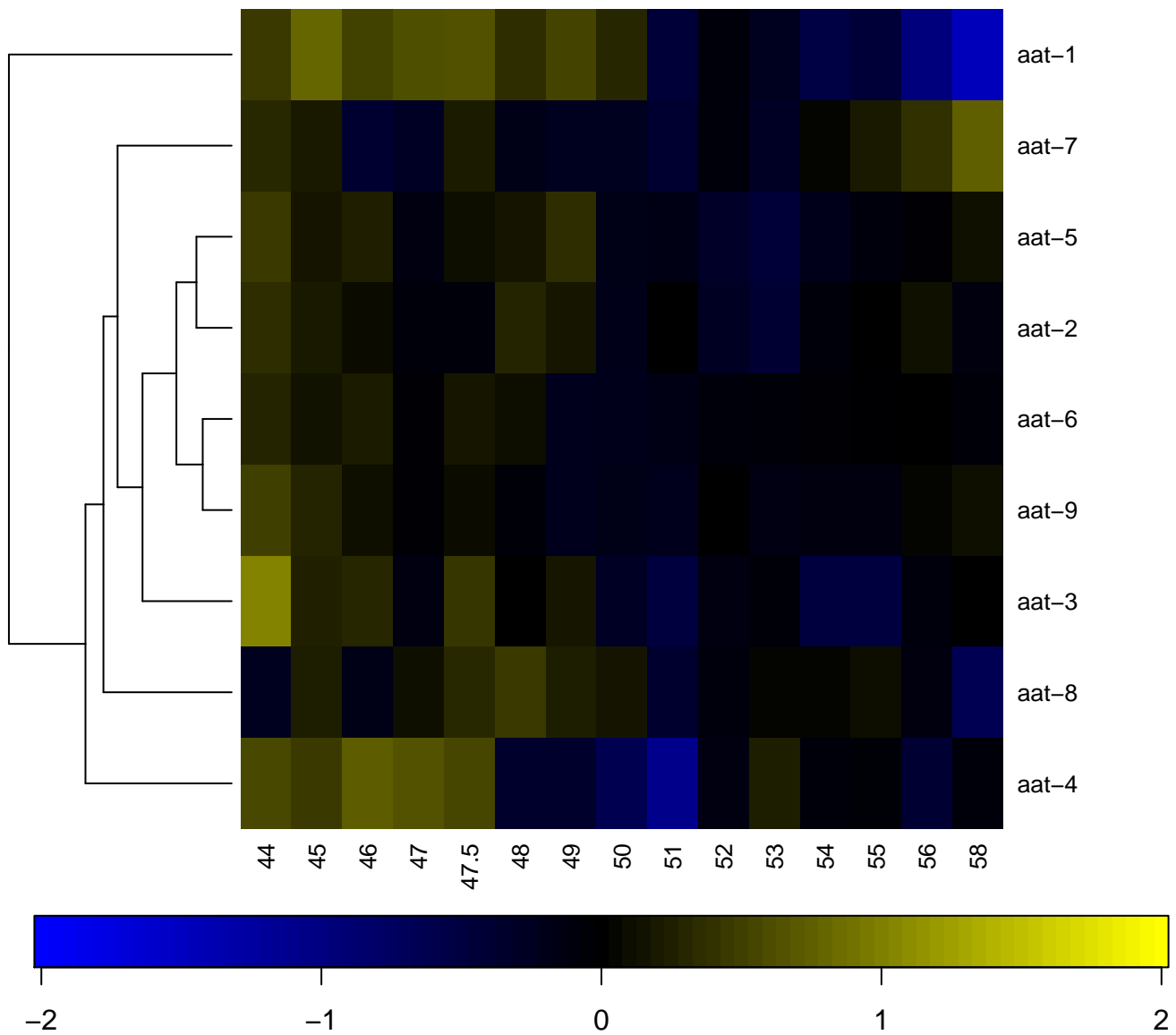
The “heatmap” function of “R” was used to cluster genes of each individual Gene Classes according to their expression pattern. Gene Class name is shown per page as figure title. The time in hours is shown on the x-axis. Gene names are shown on the y-axis. The scale bar shows the log₂ ratio with the mean for each time-point. Blue is lower than the mean and yellow is higher than the mean.



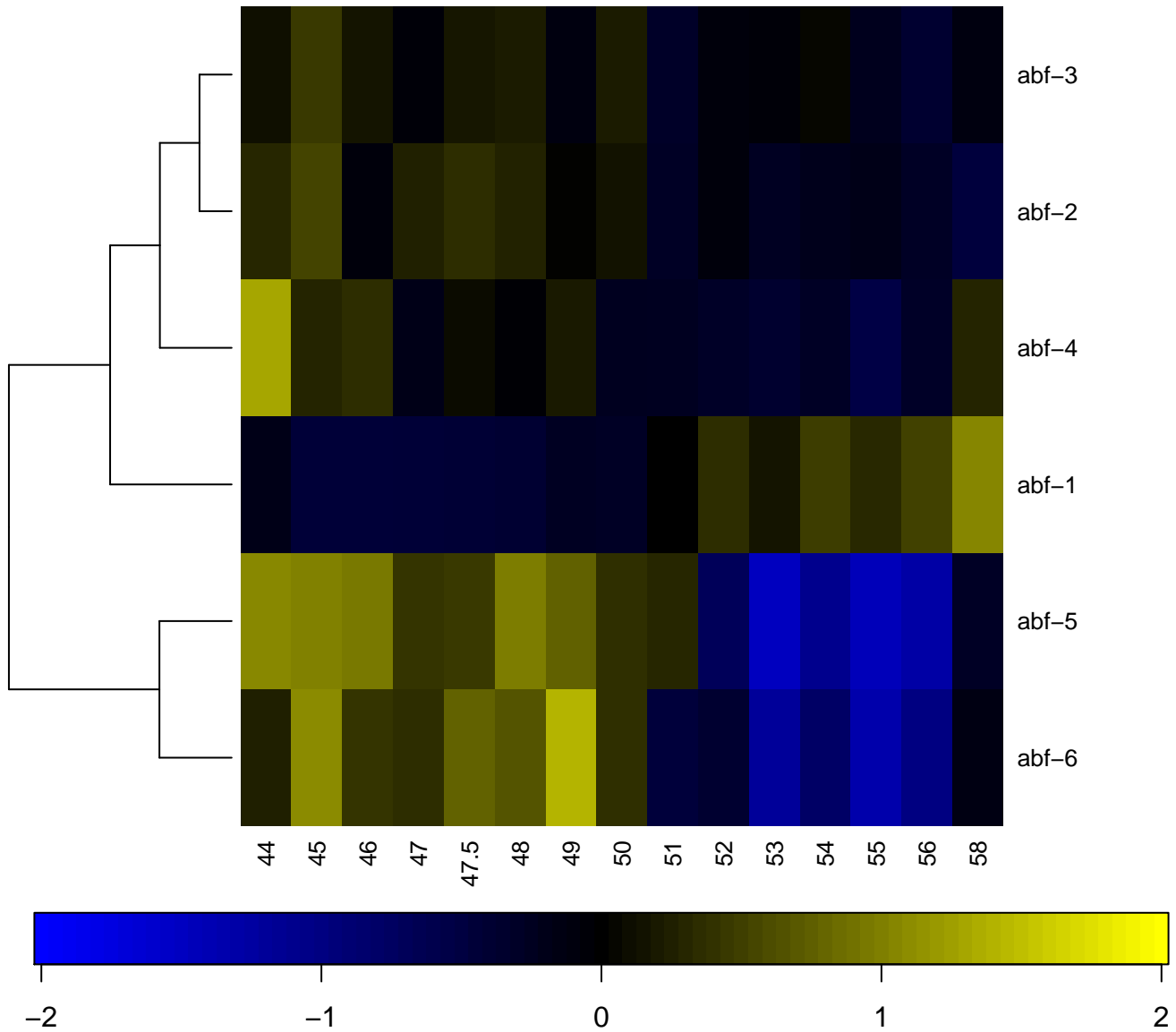
44 45 46 47 47.5 48 49 50 51 52 53 54 55 56 58



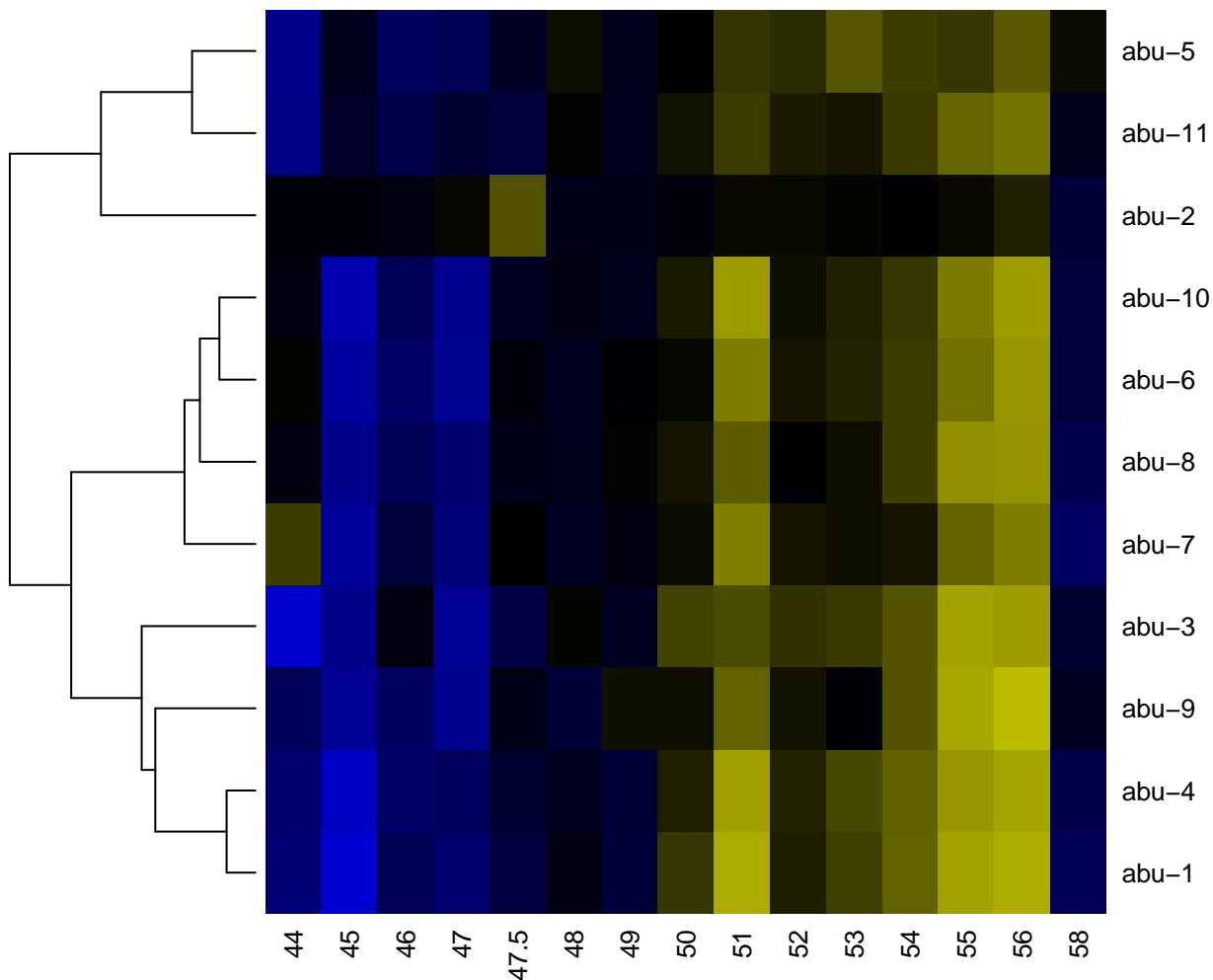
aat



abf



abu



-2

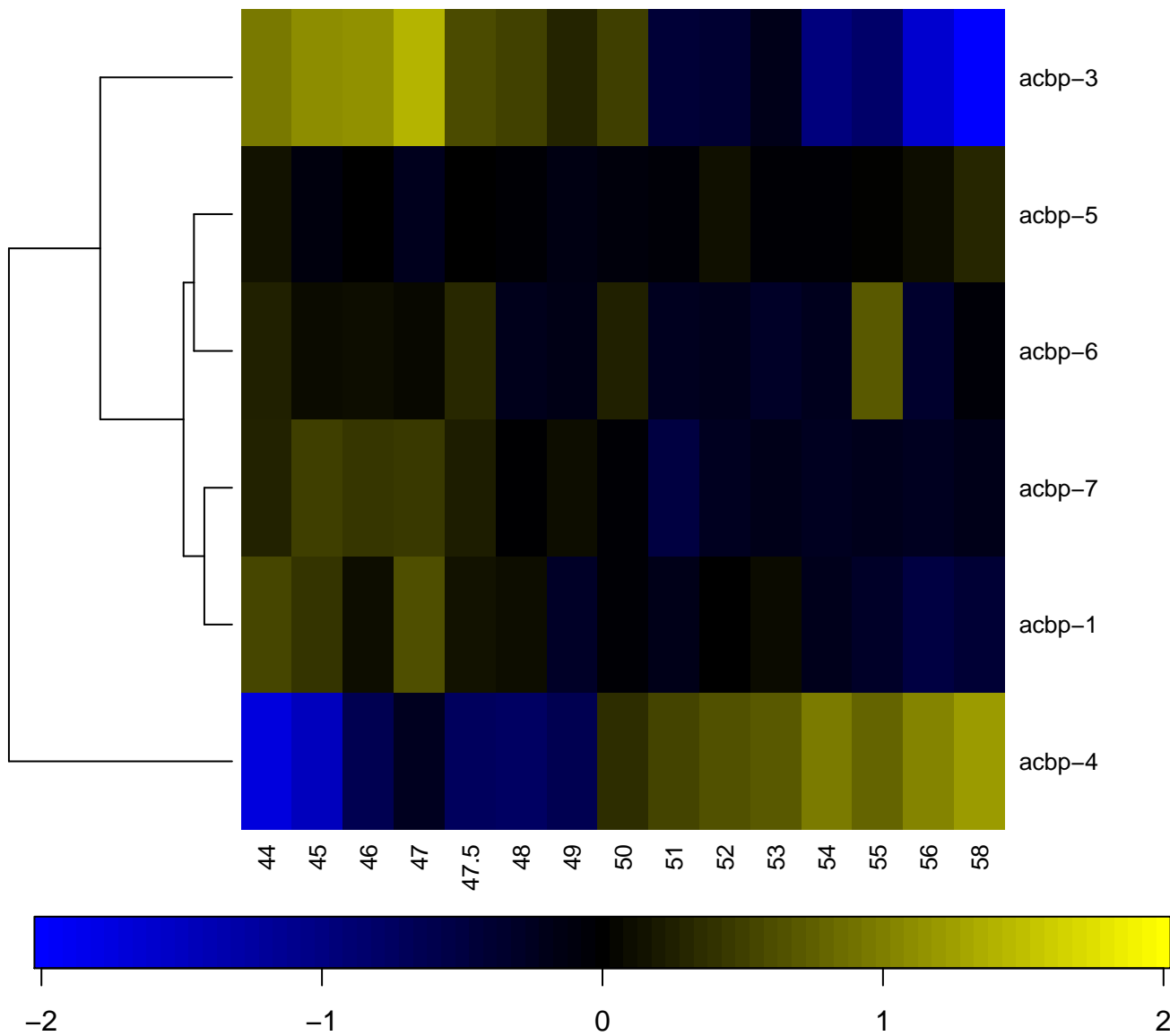
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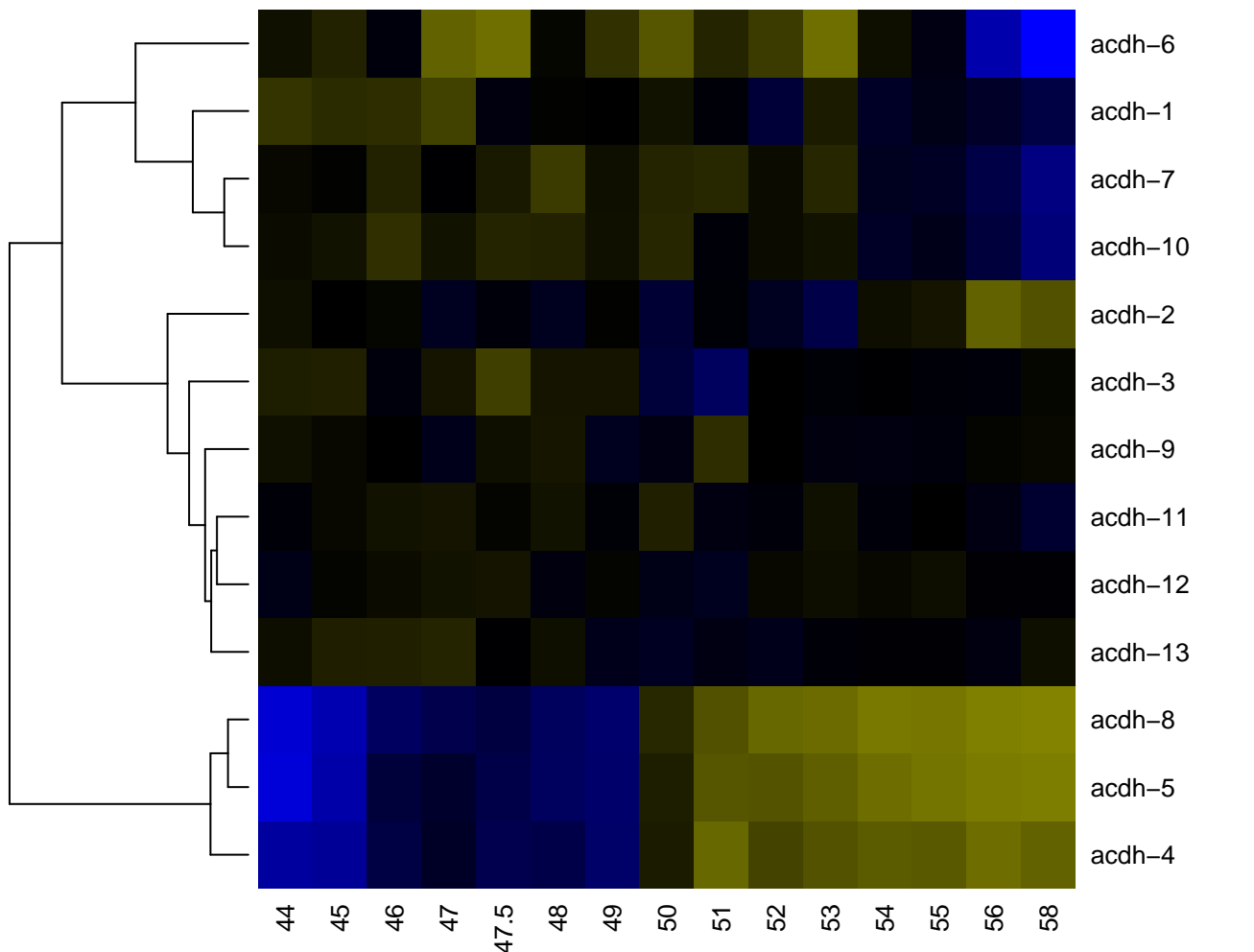
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acbp



acdH



-2

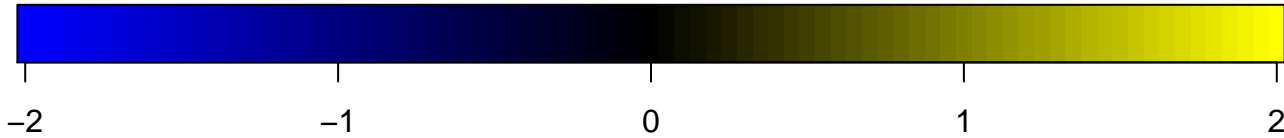
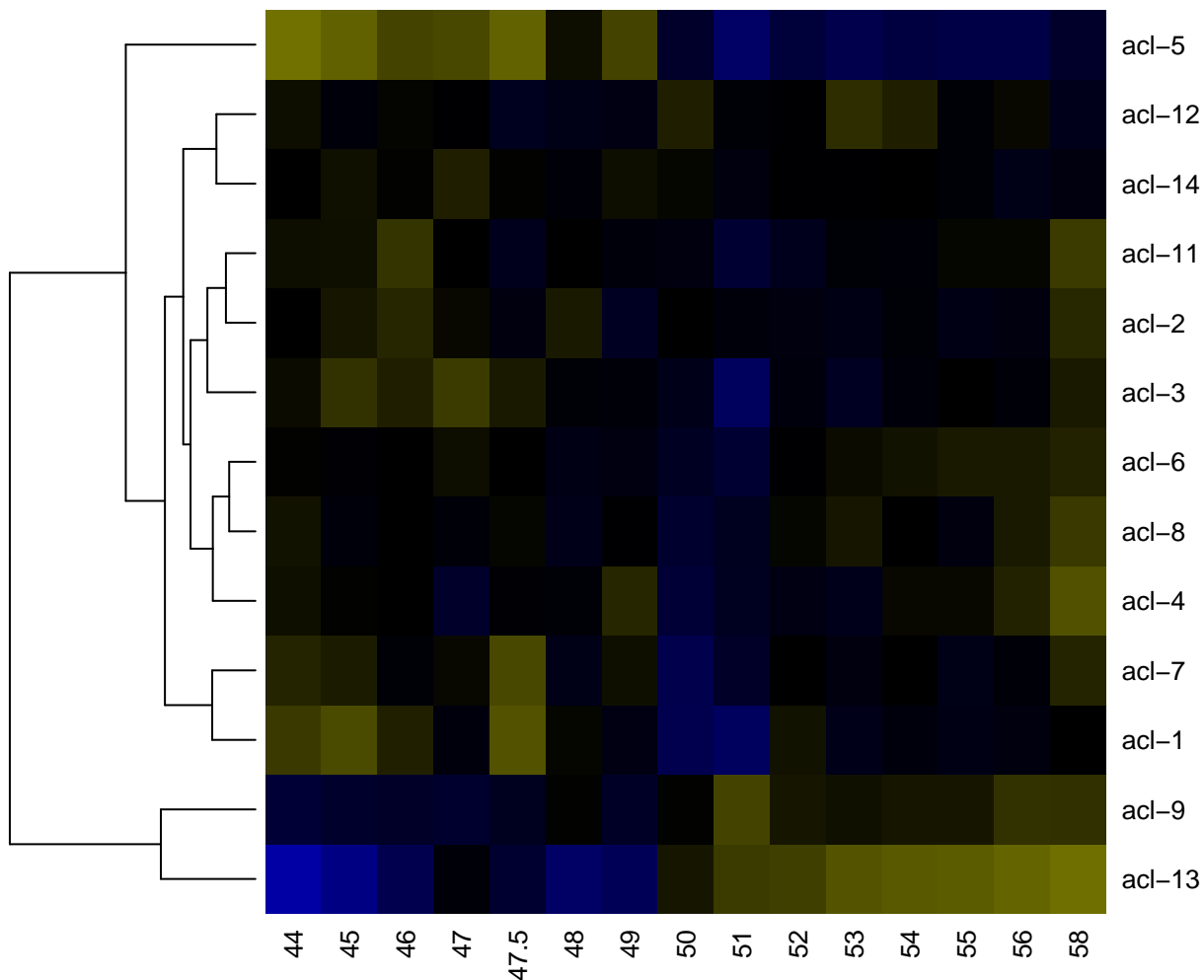
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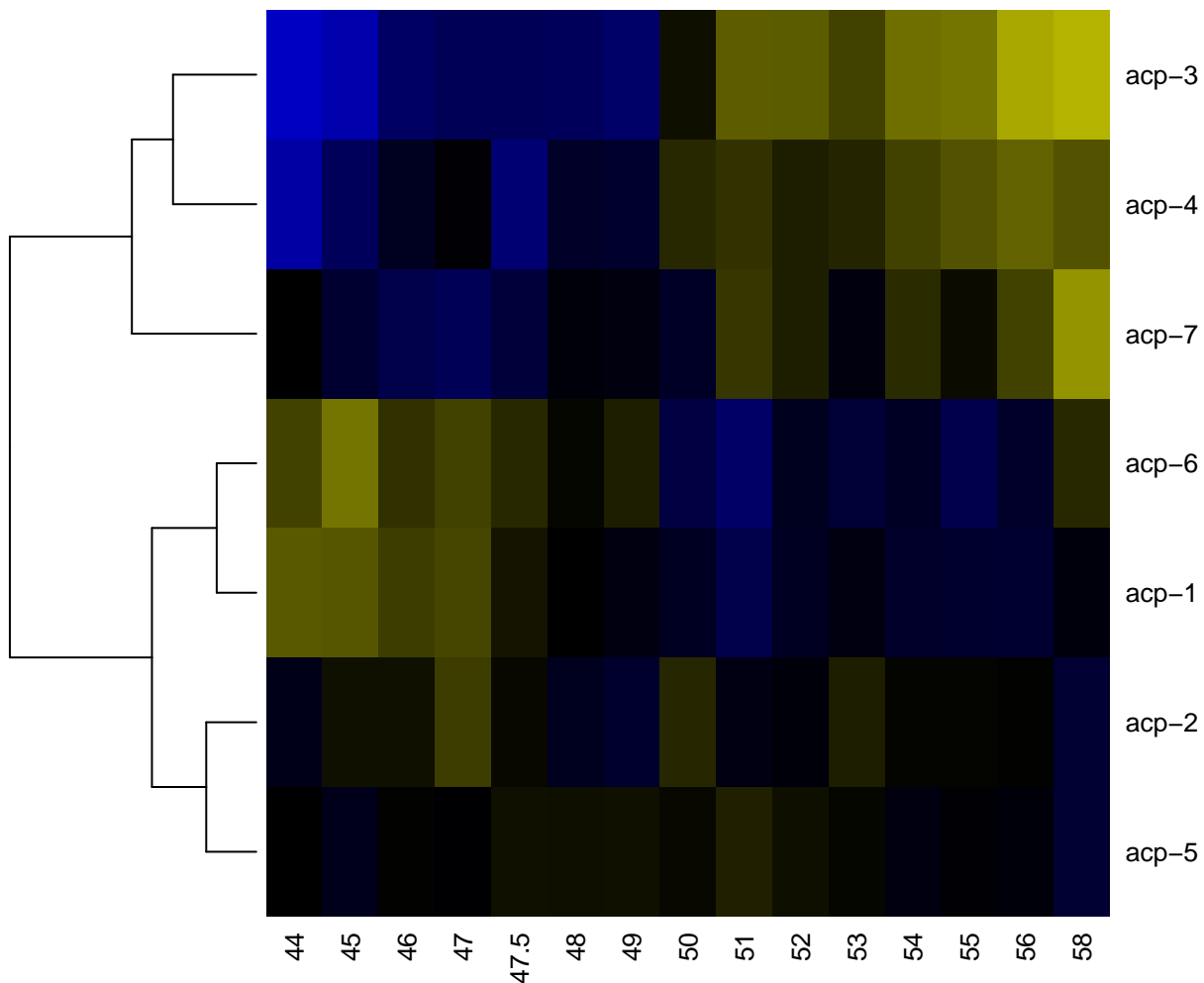
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acp



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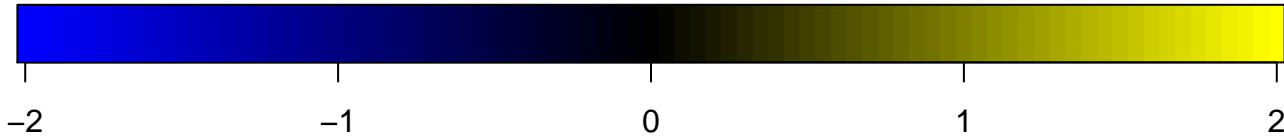
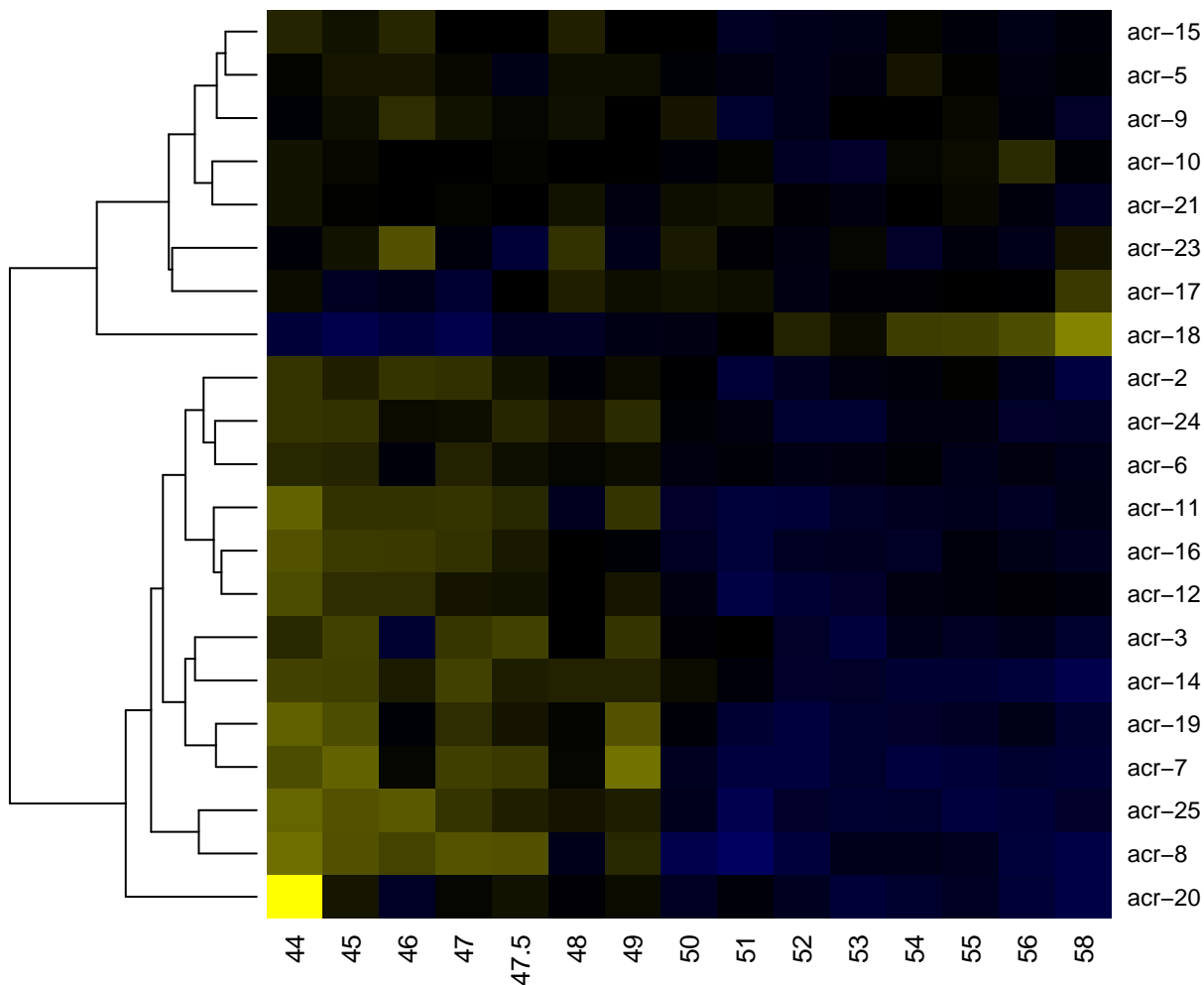
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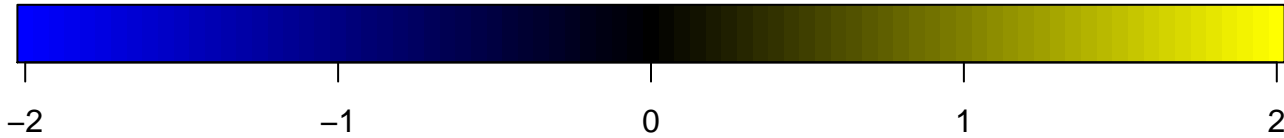
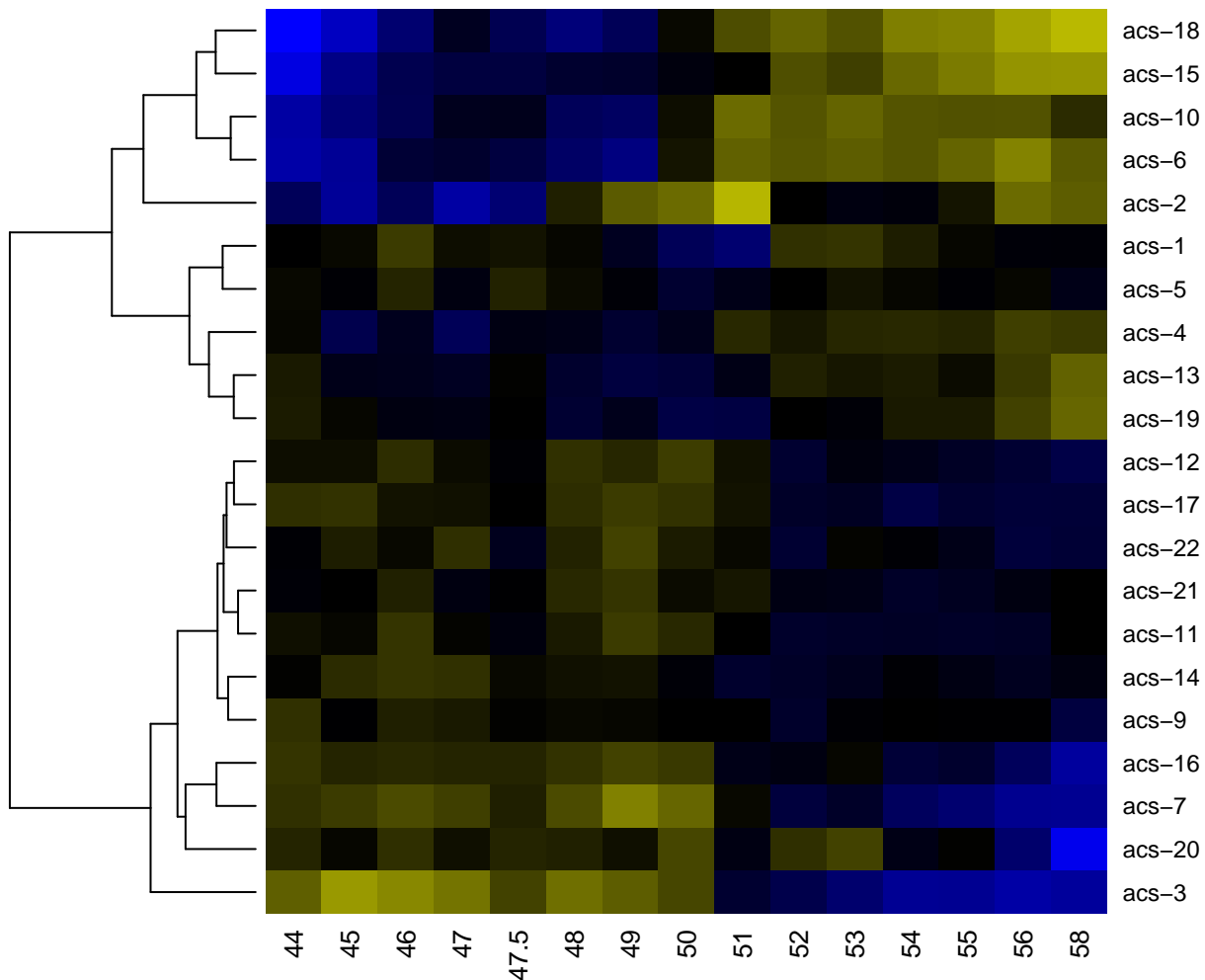
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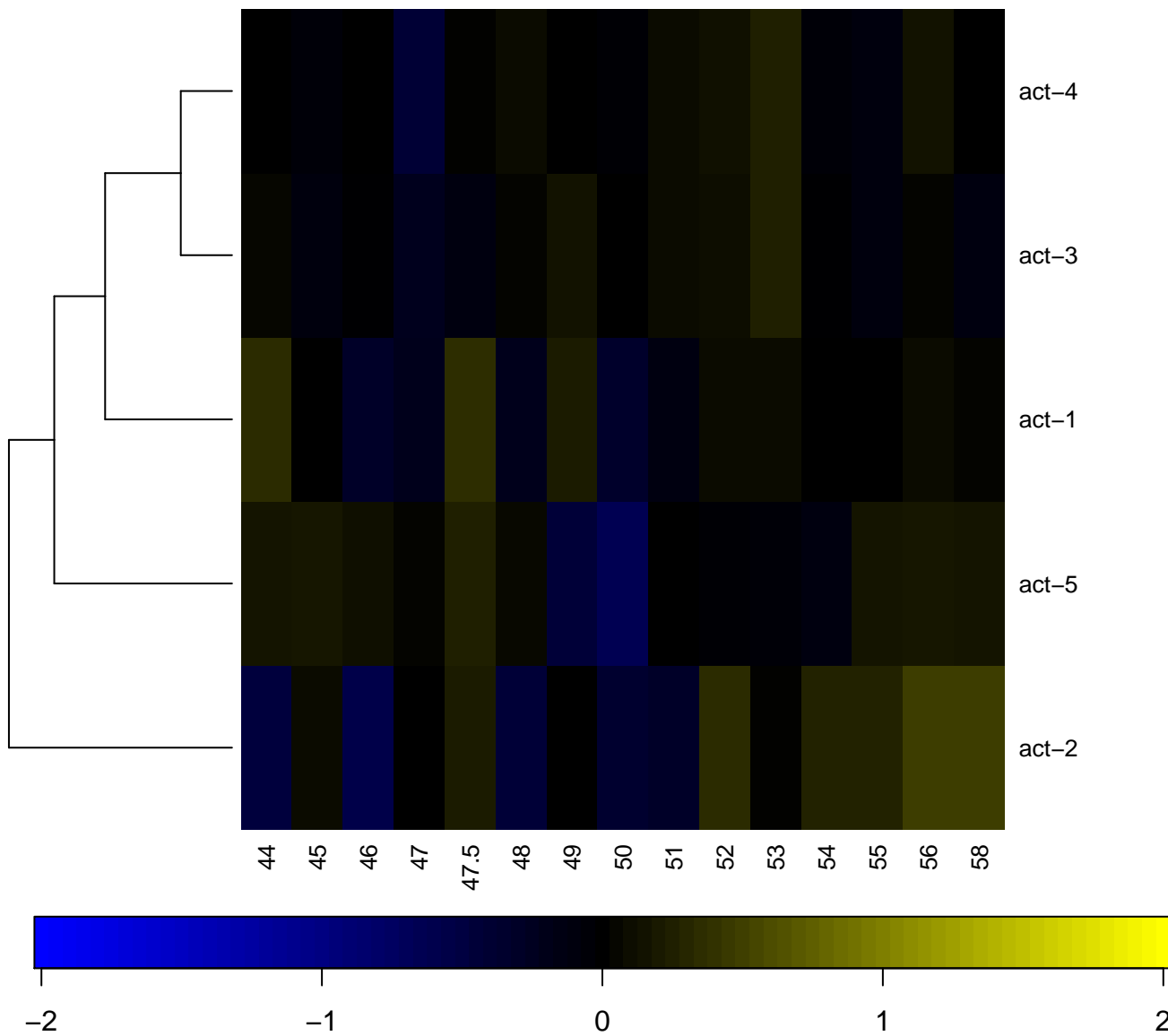
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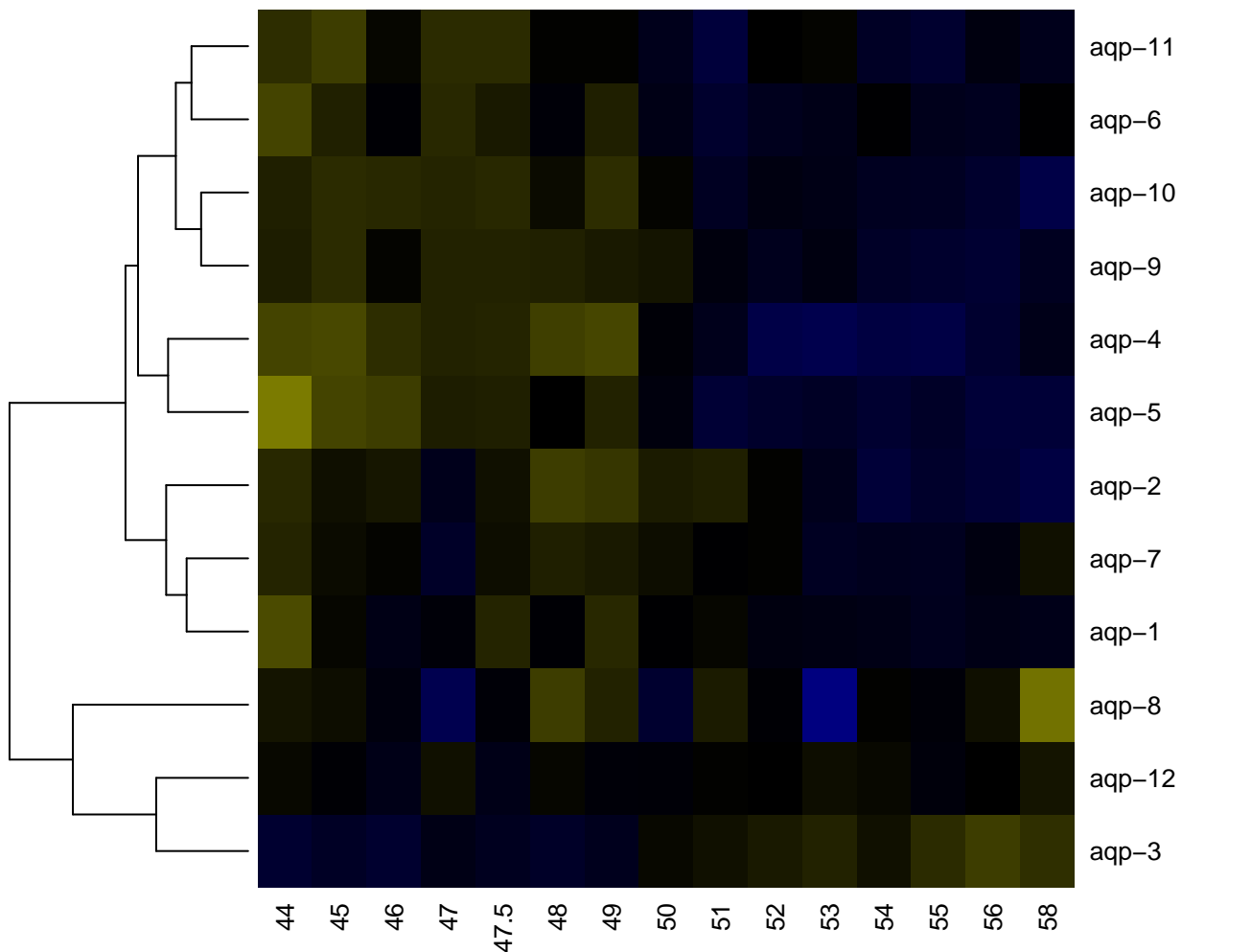
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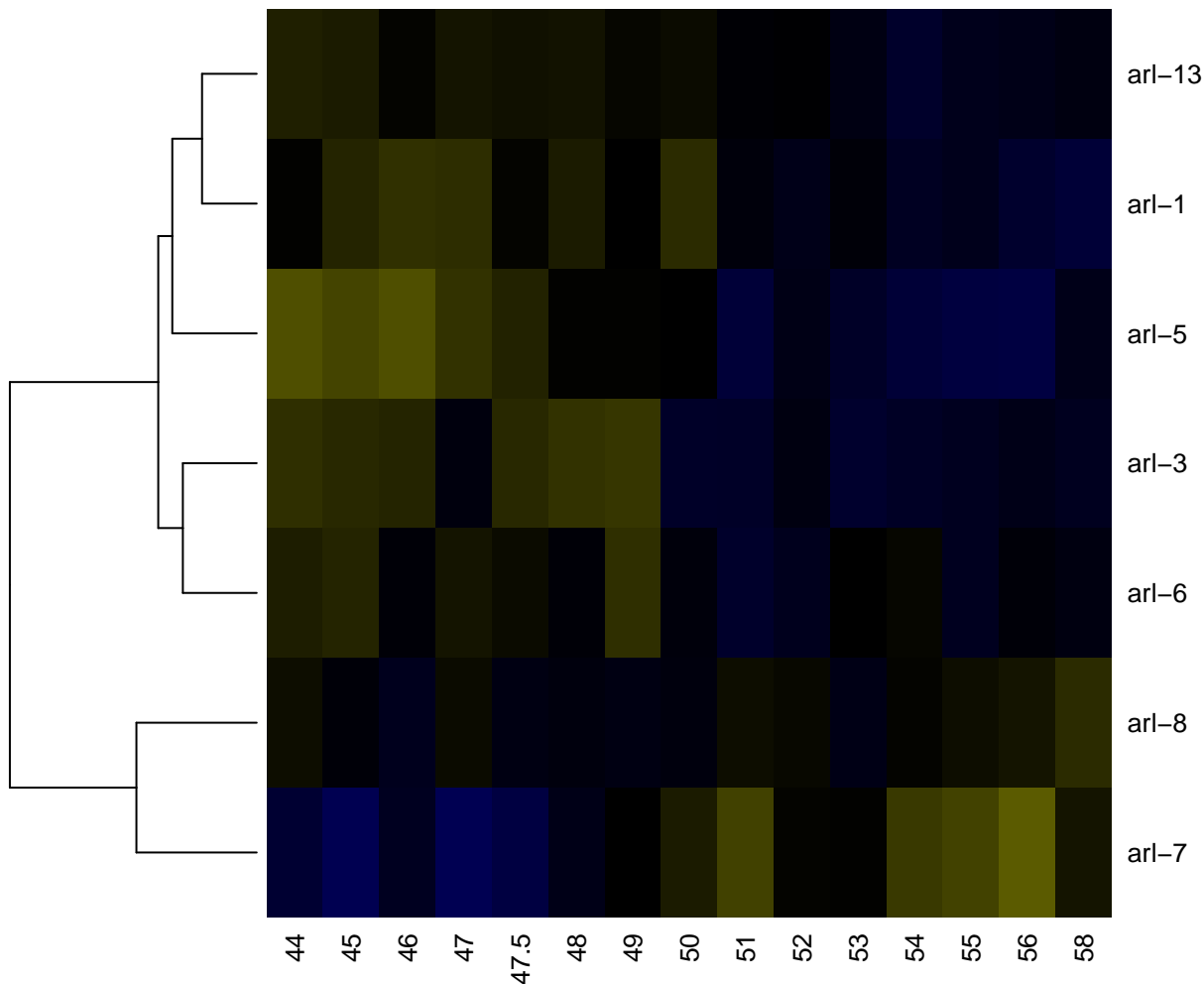
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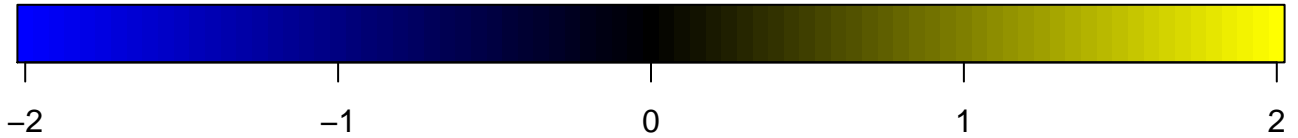
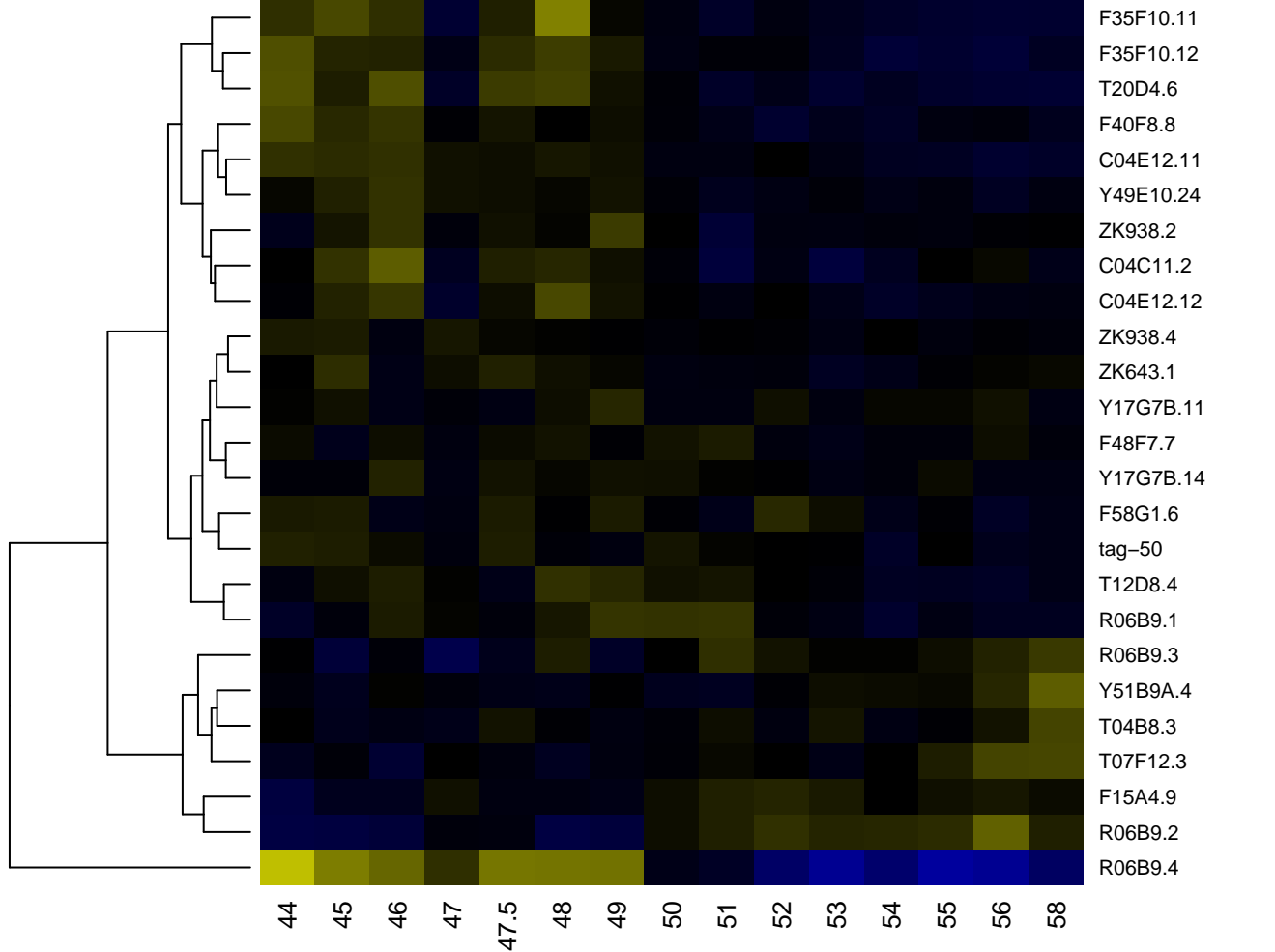
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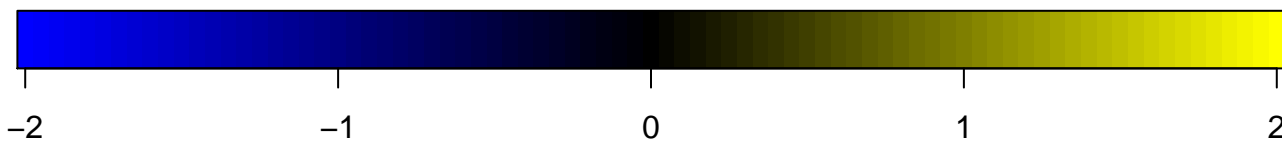
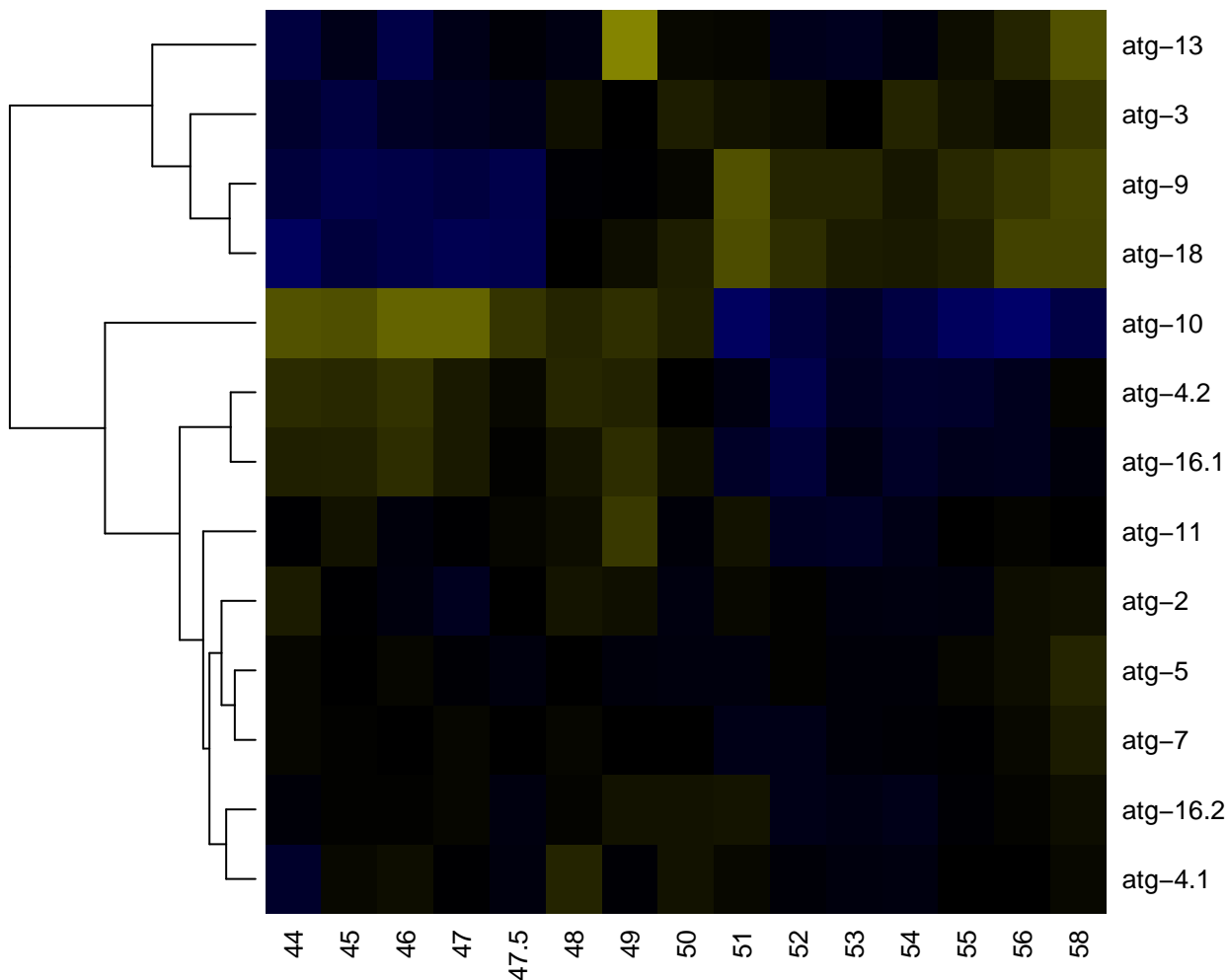
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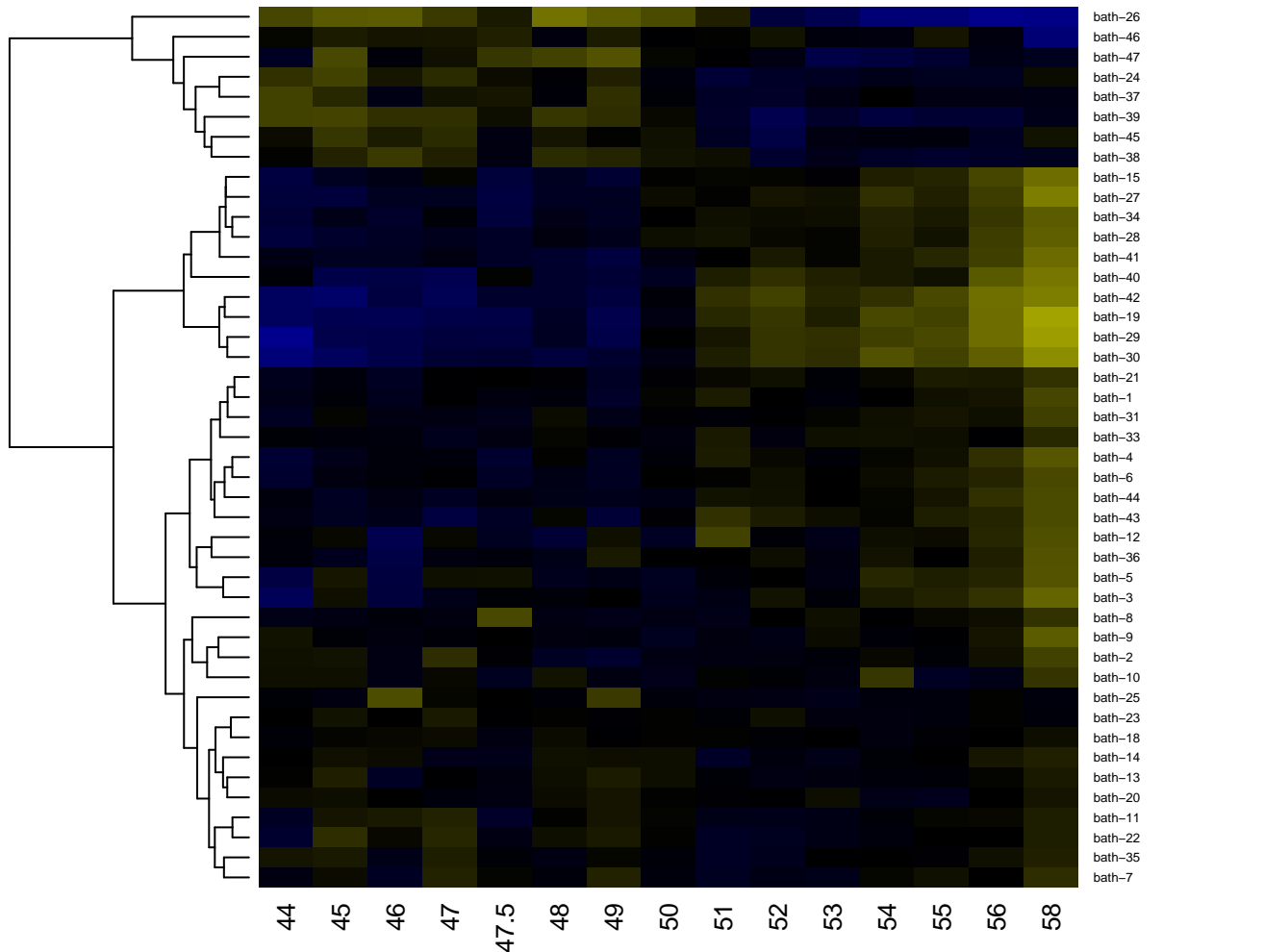
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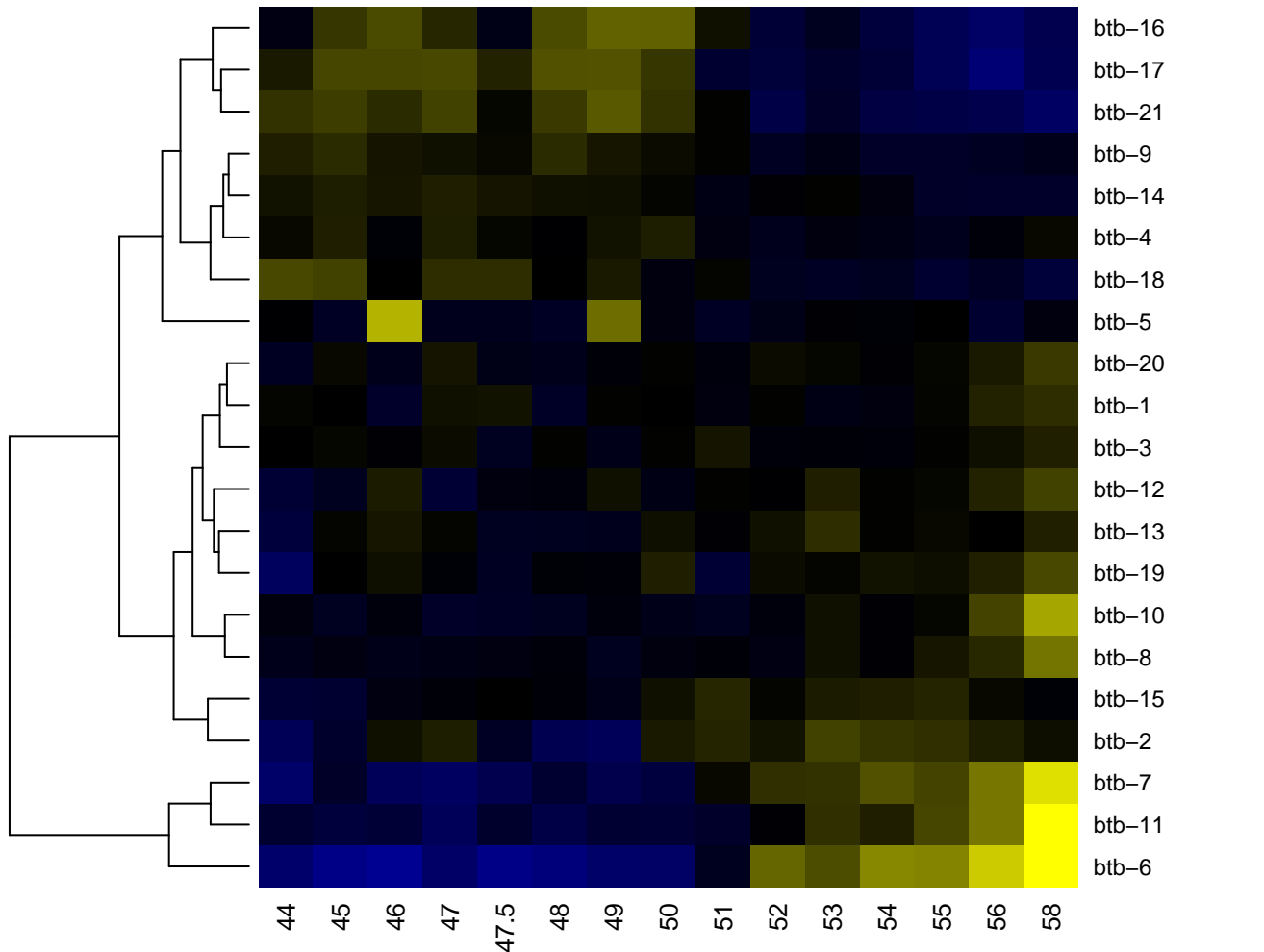
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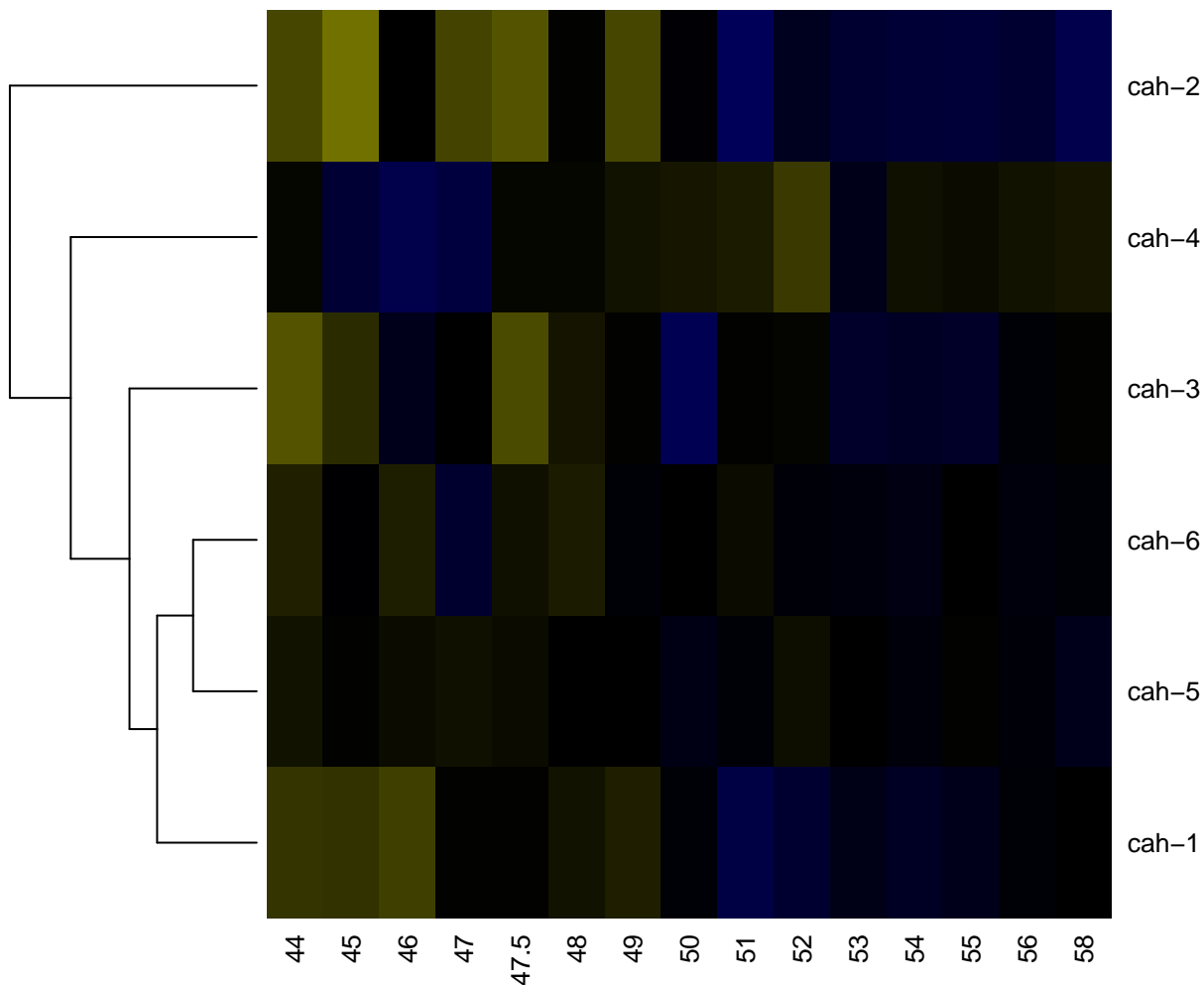
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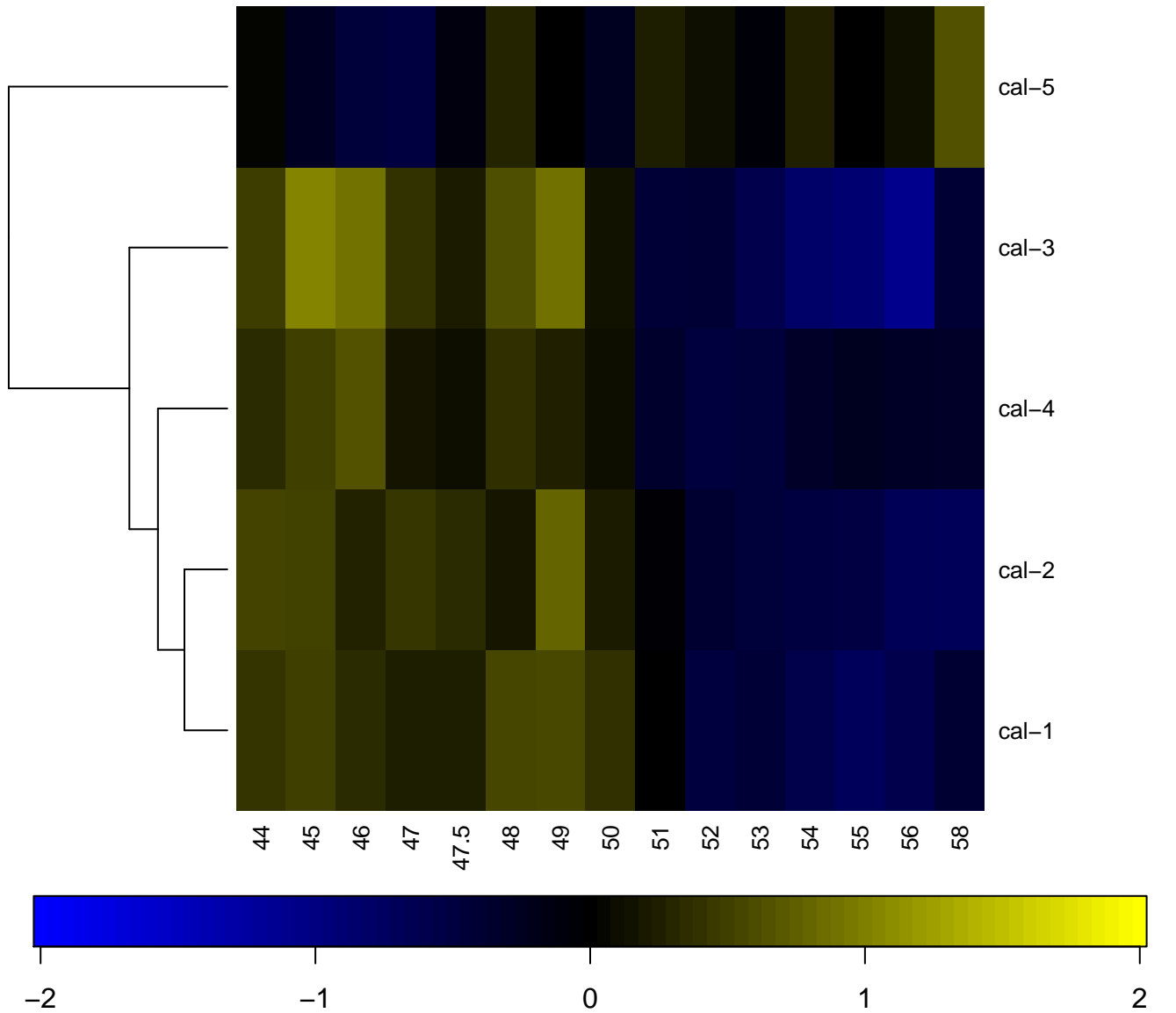
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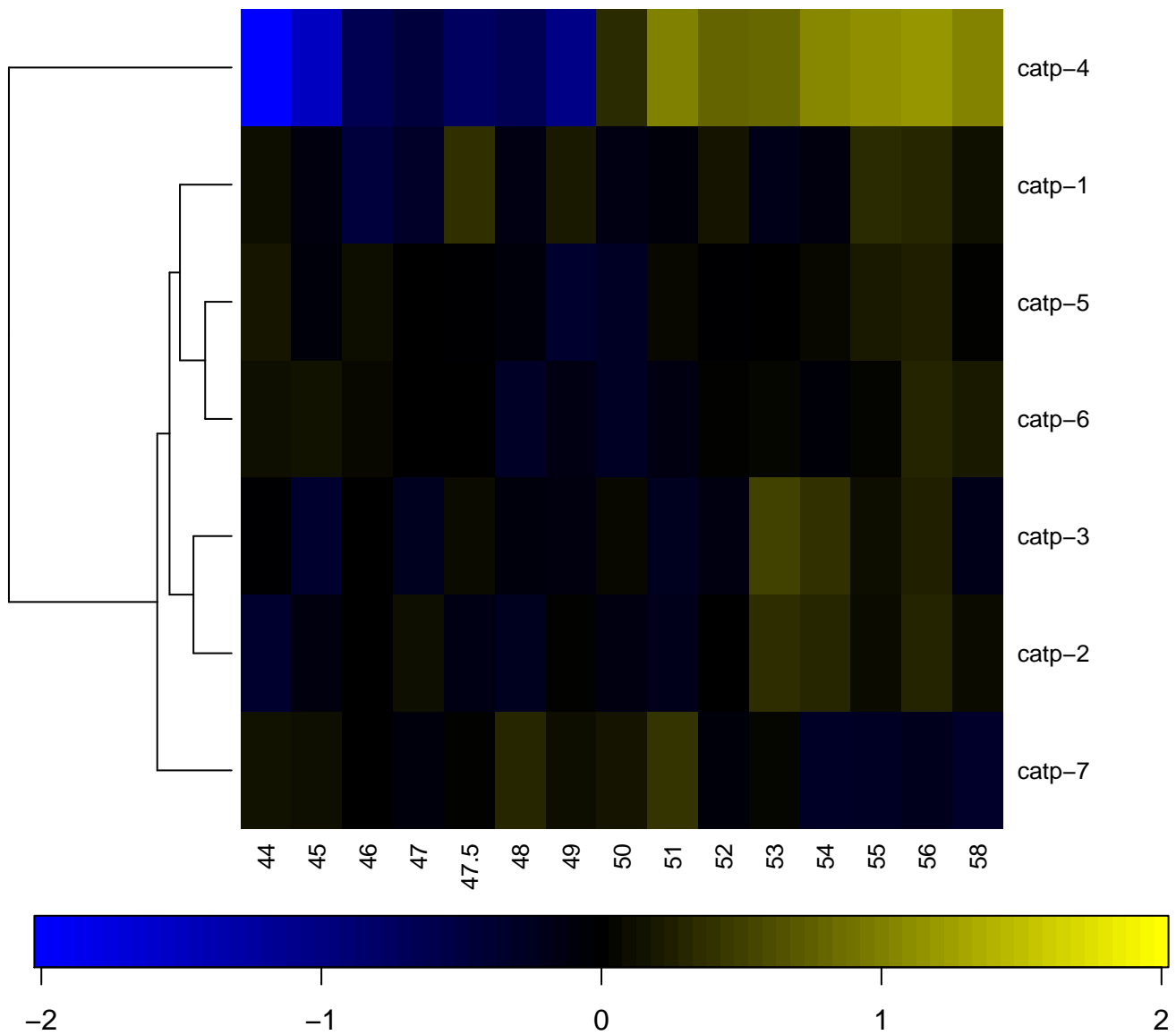
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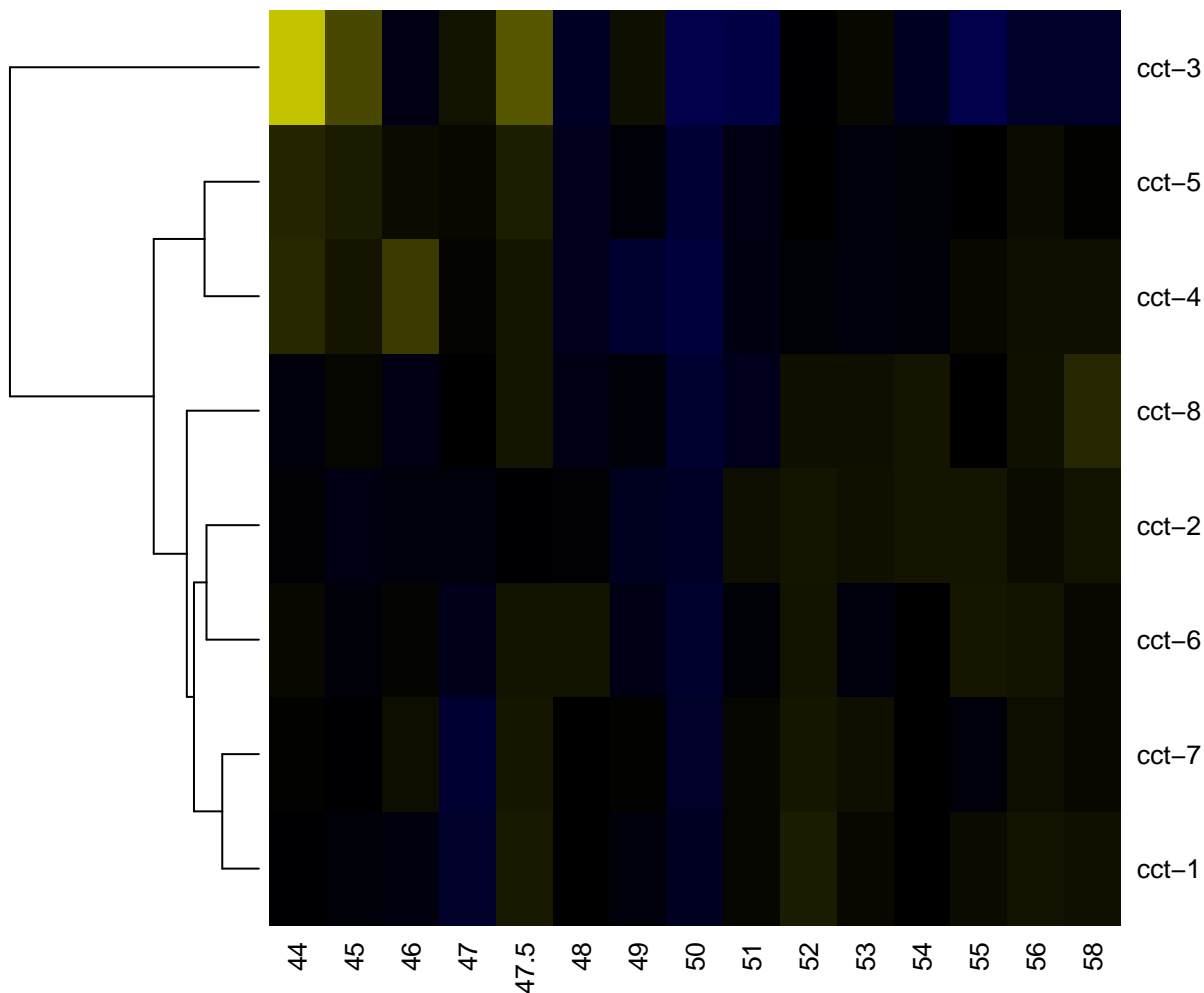
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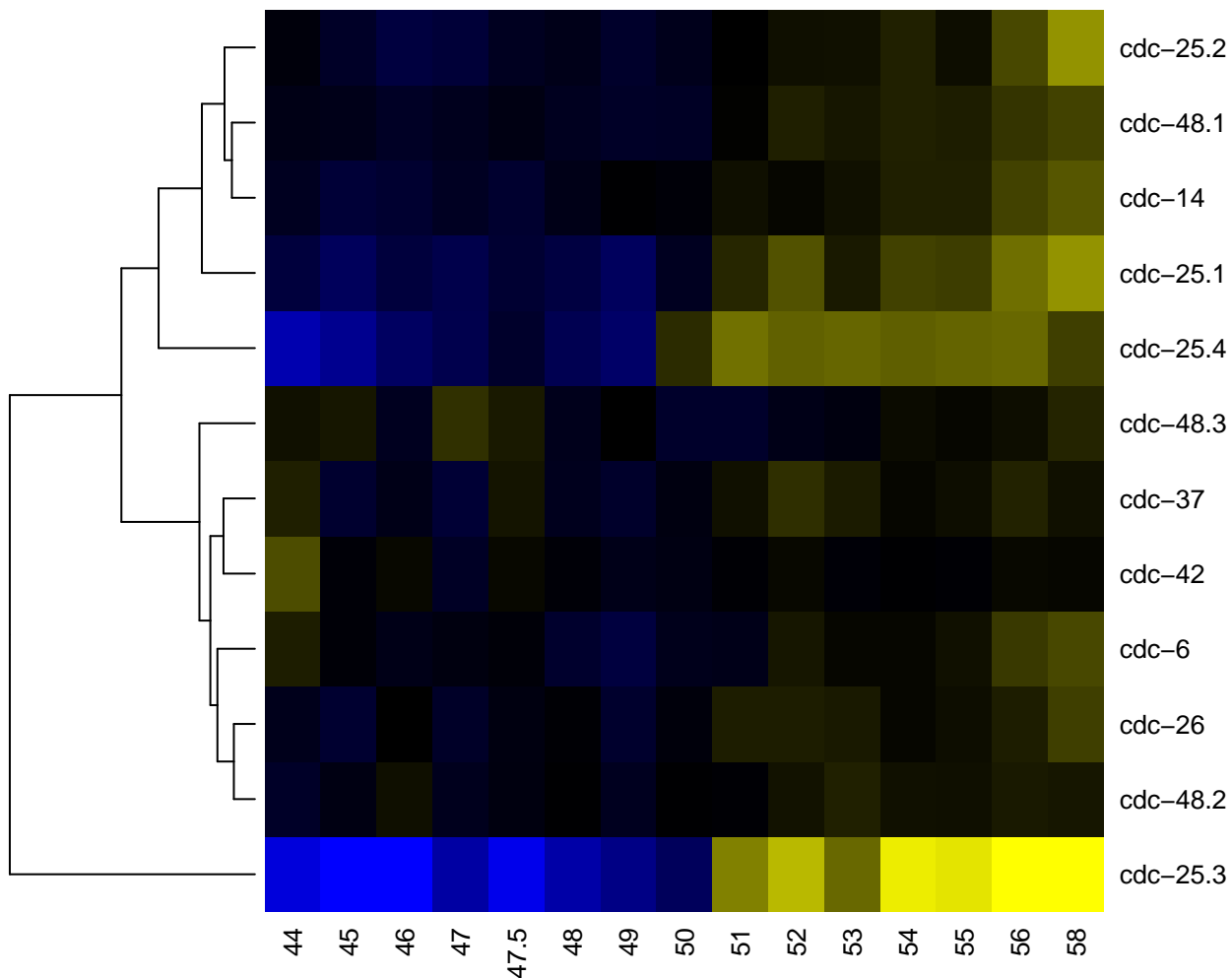
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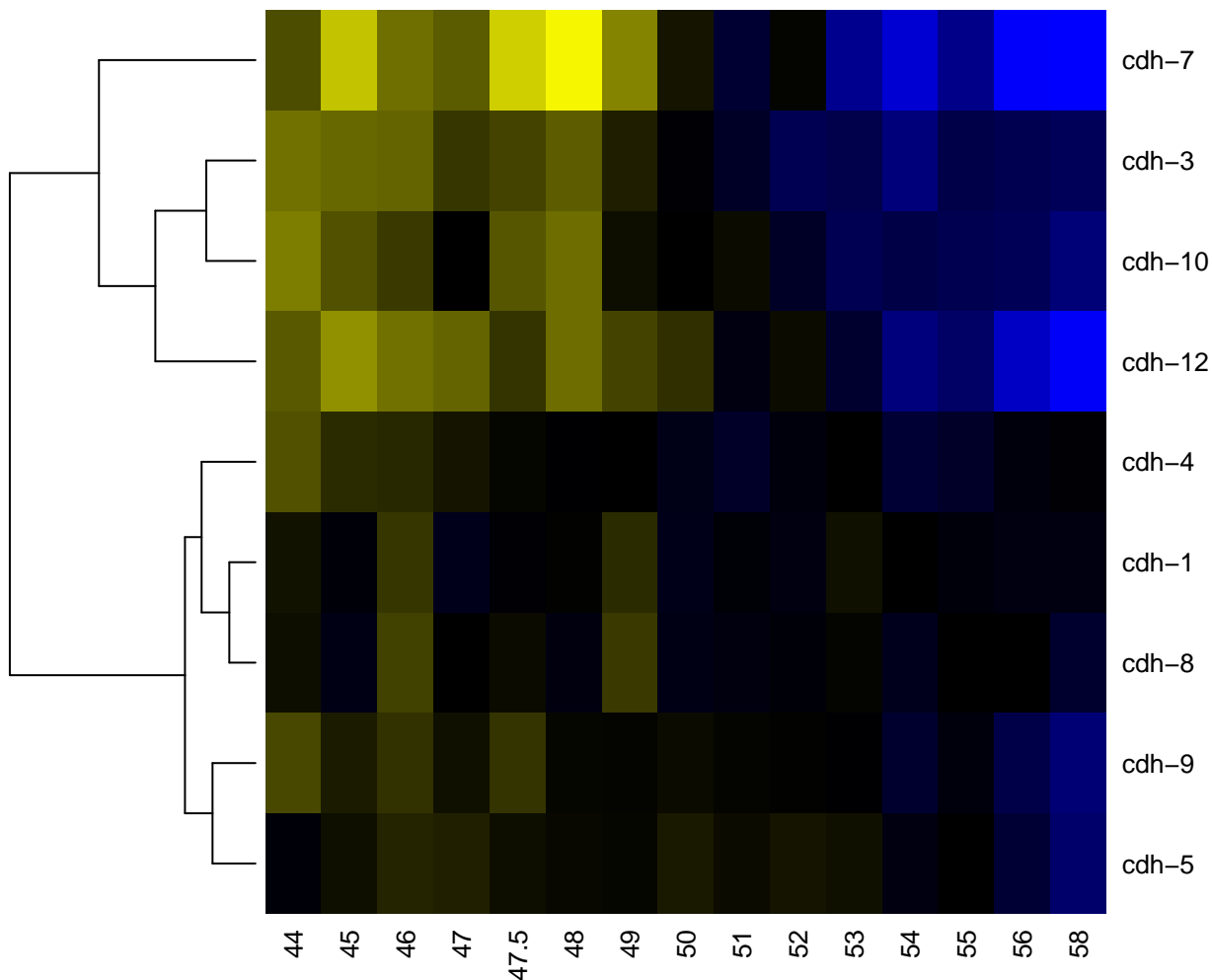
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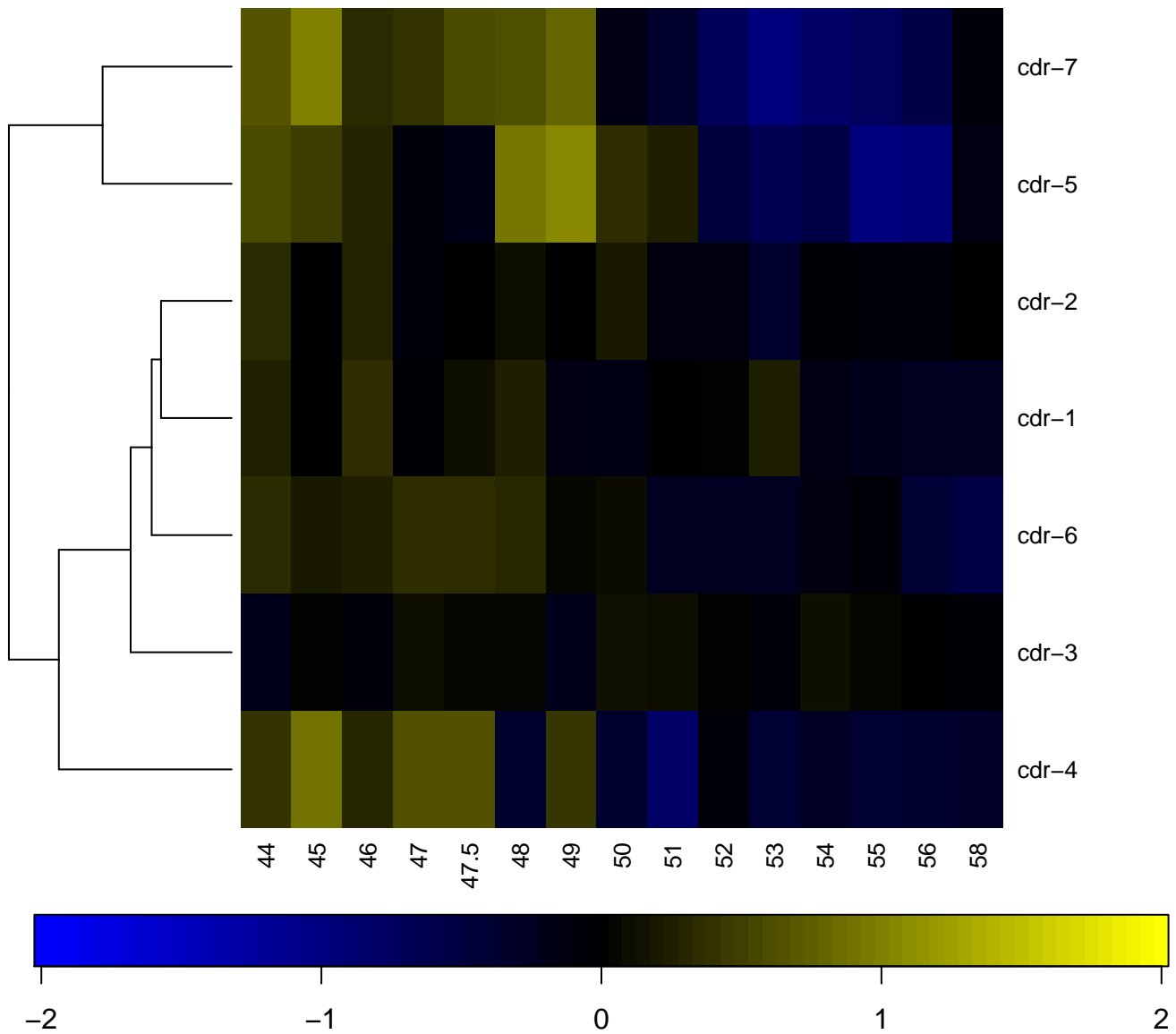
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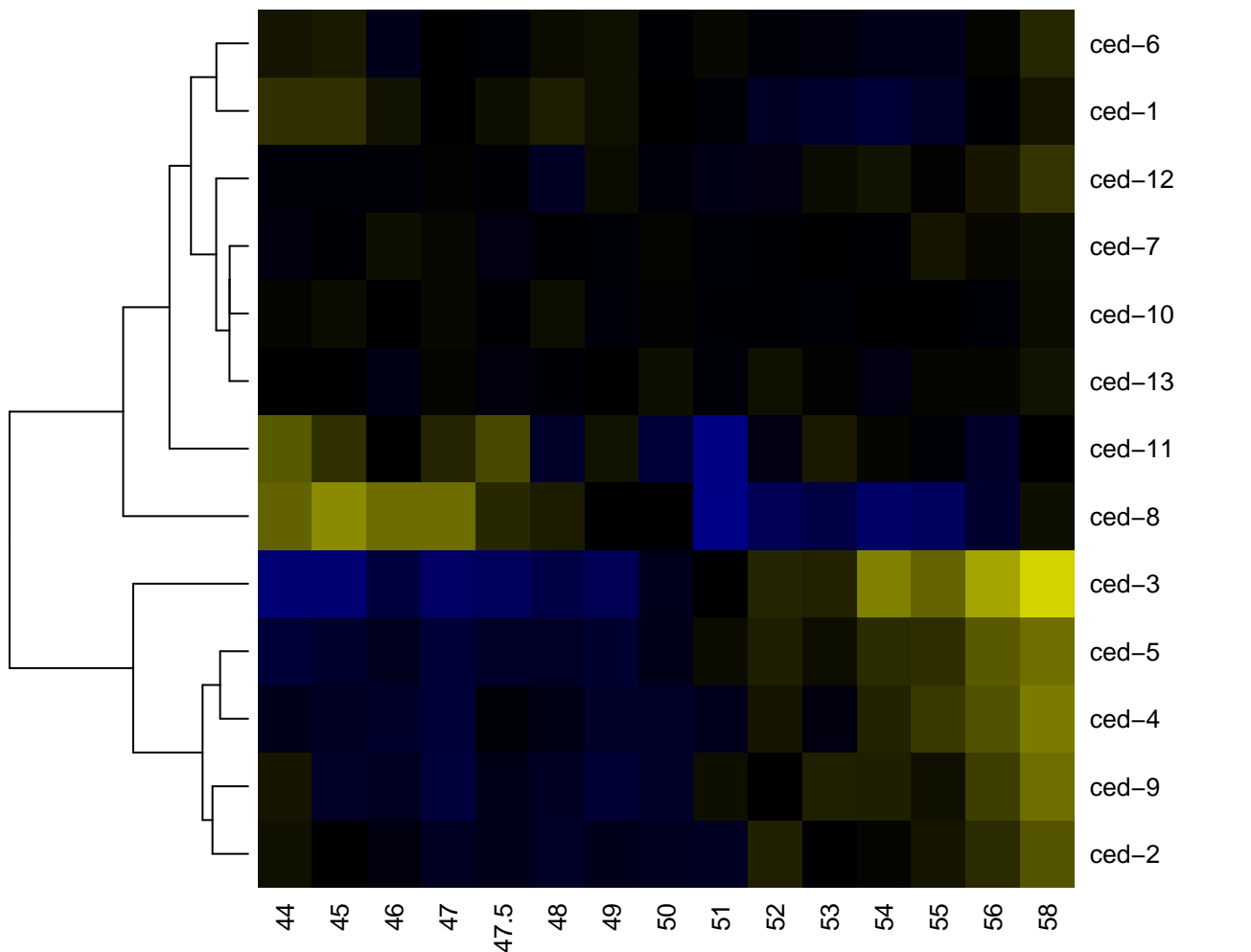
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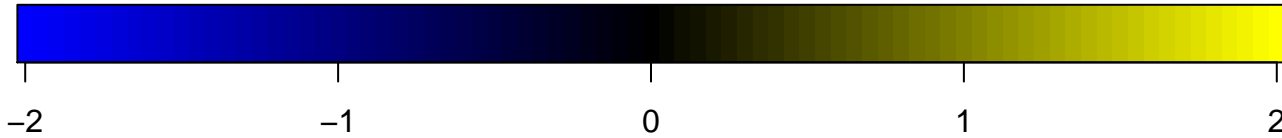
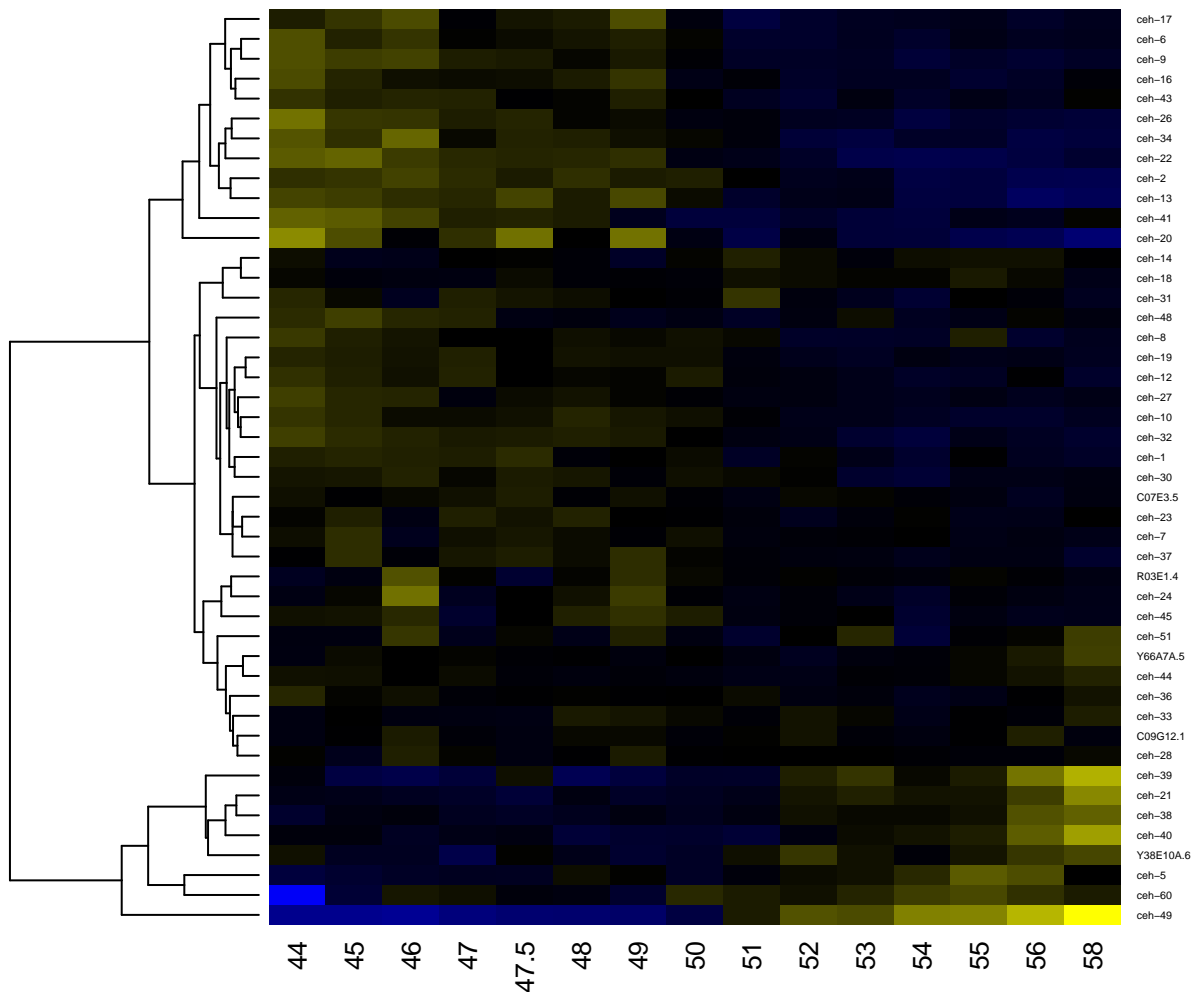
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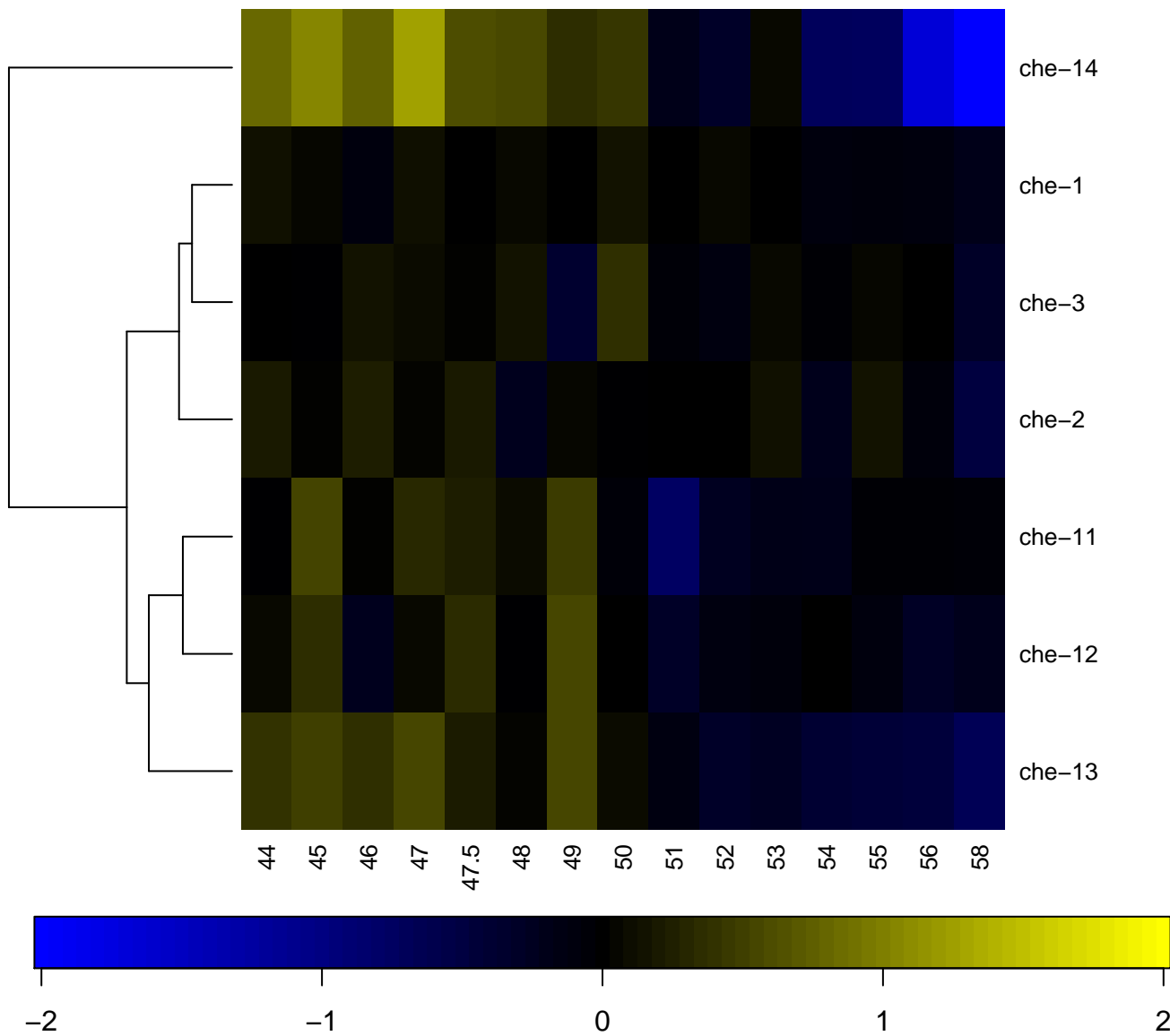
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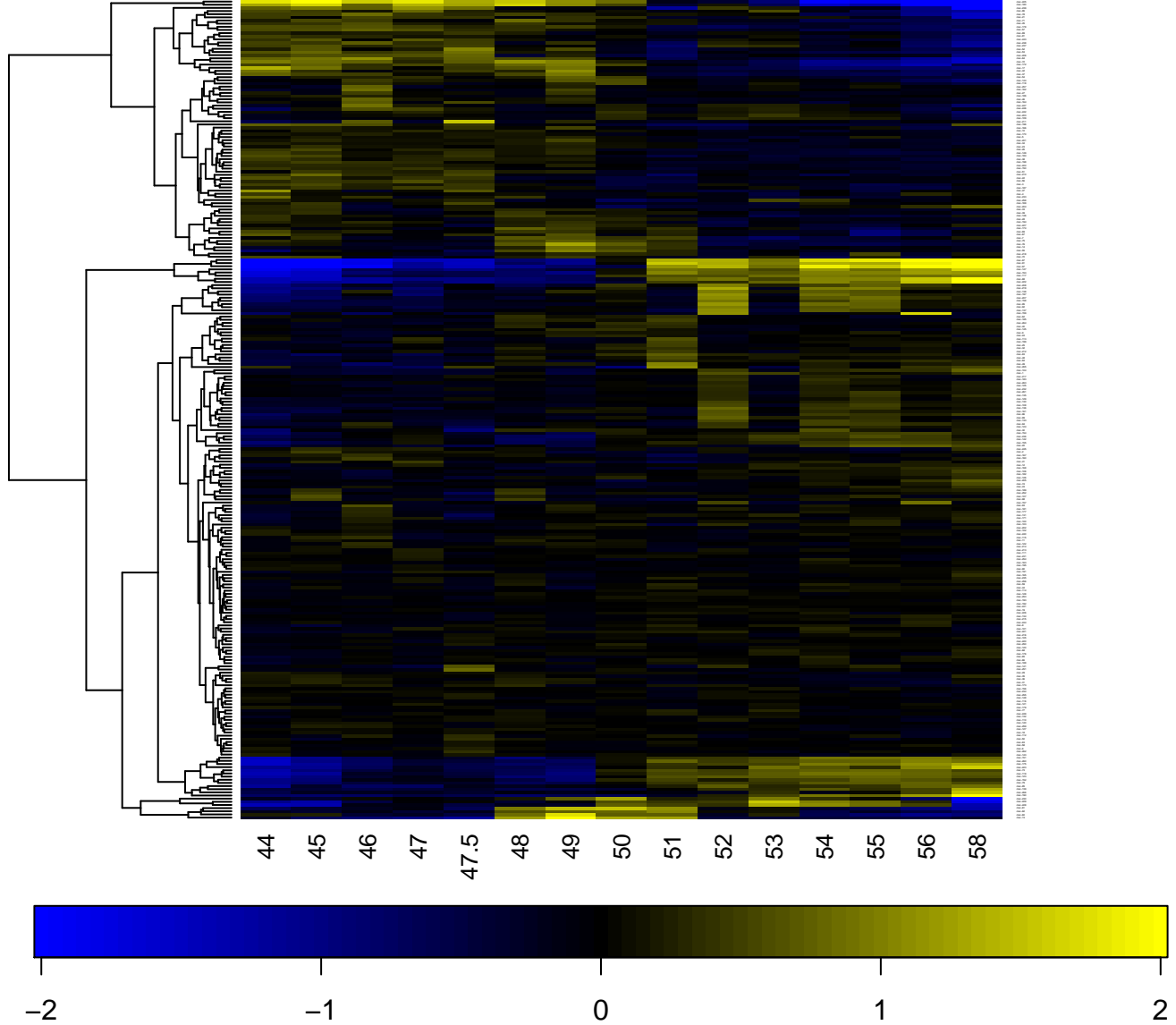
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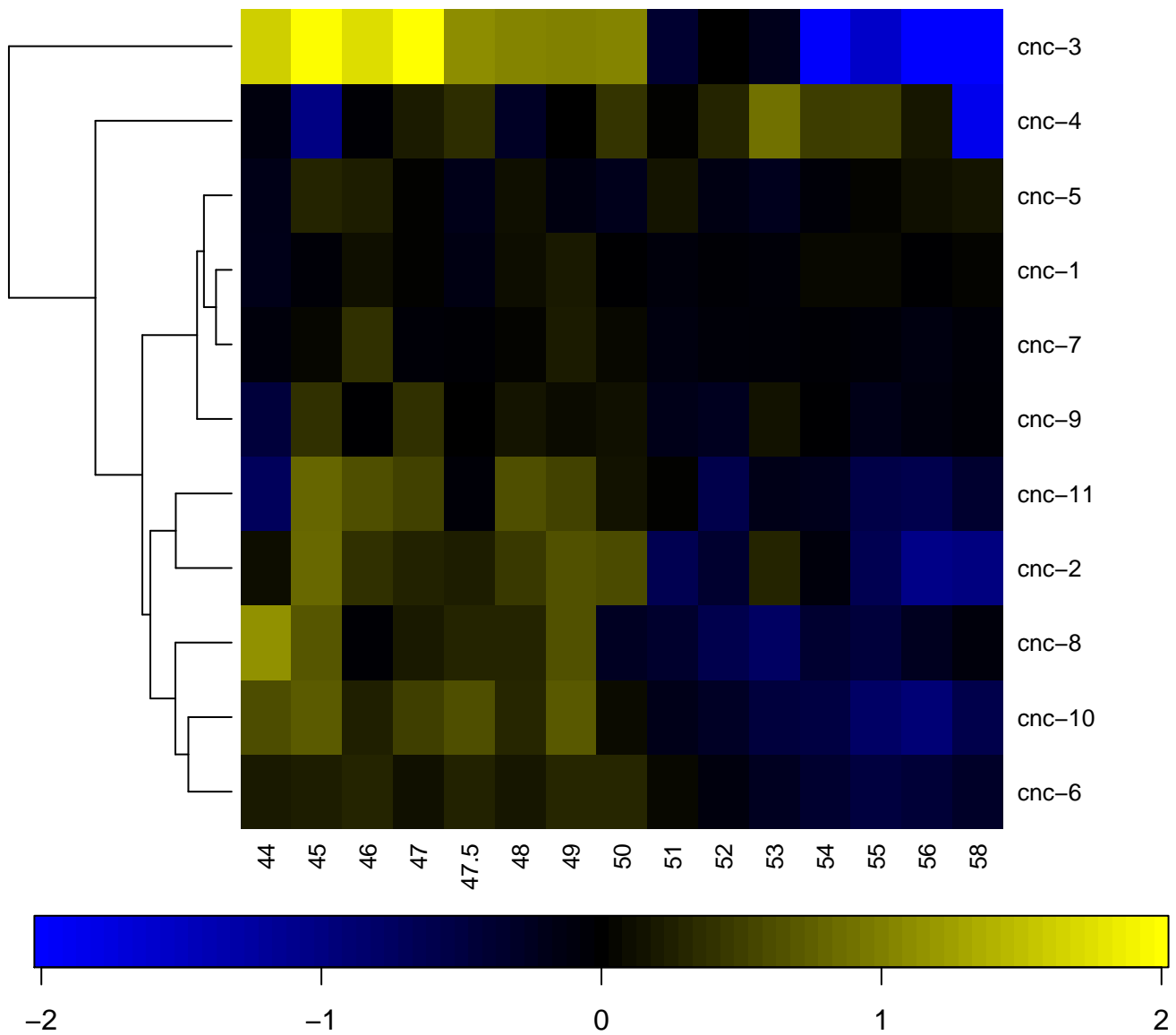
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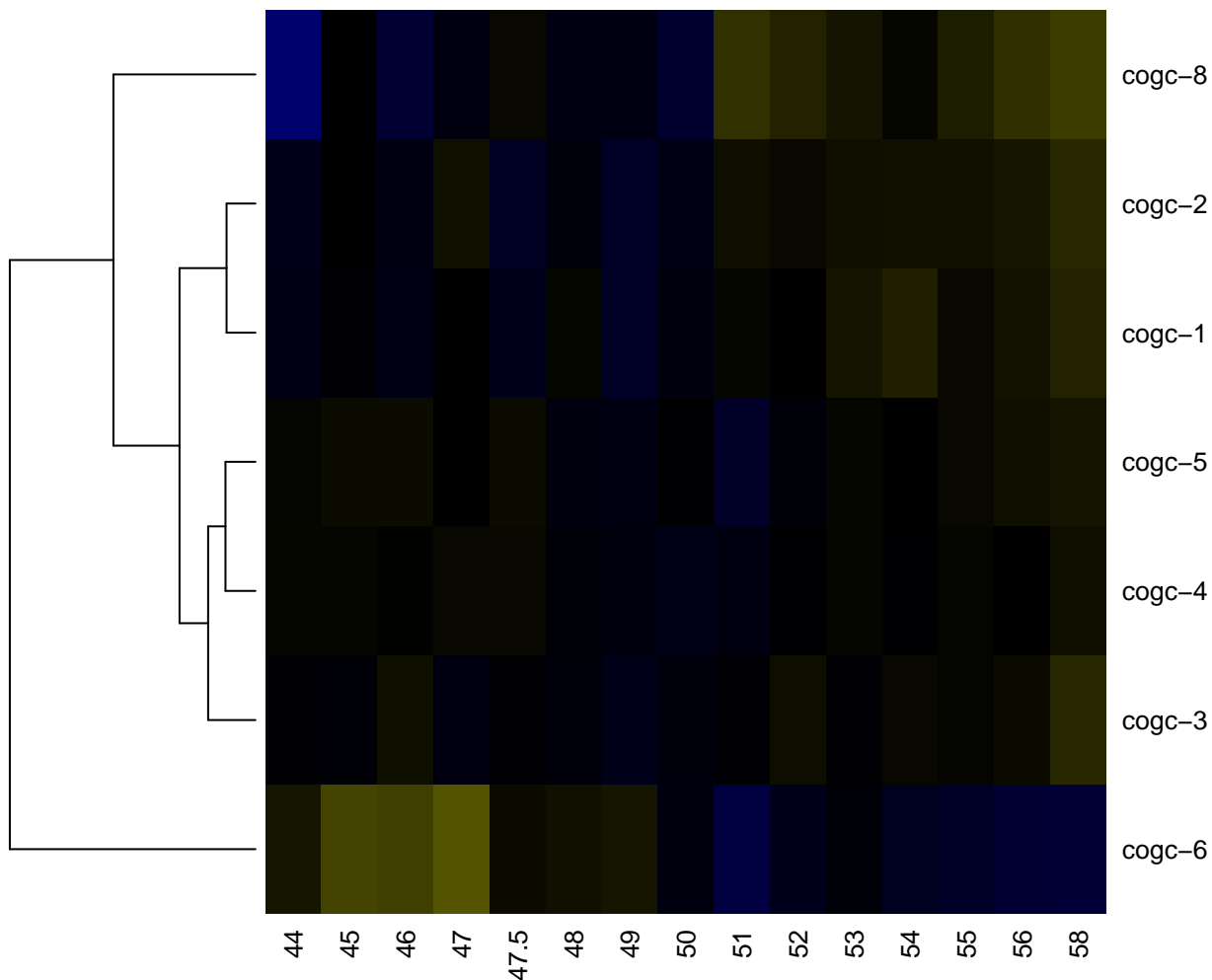
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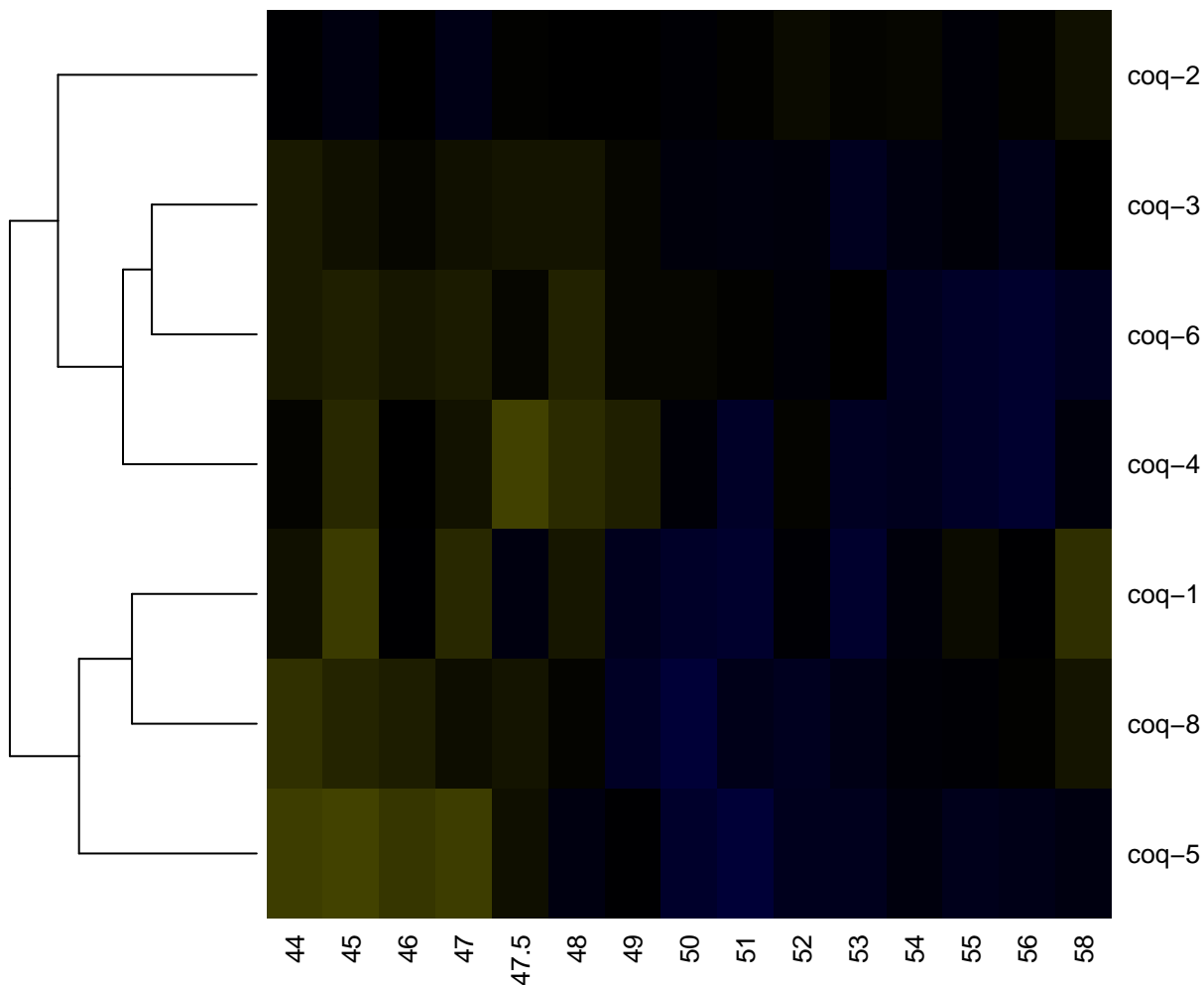
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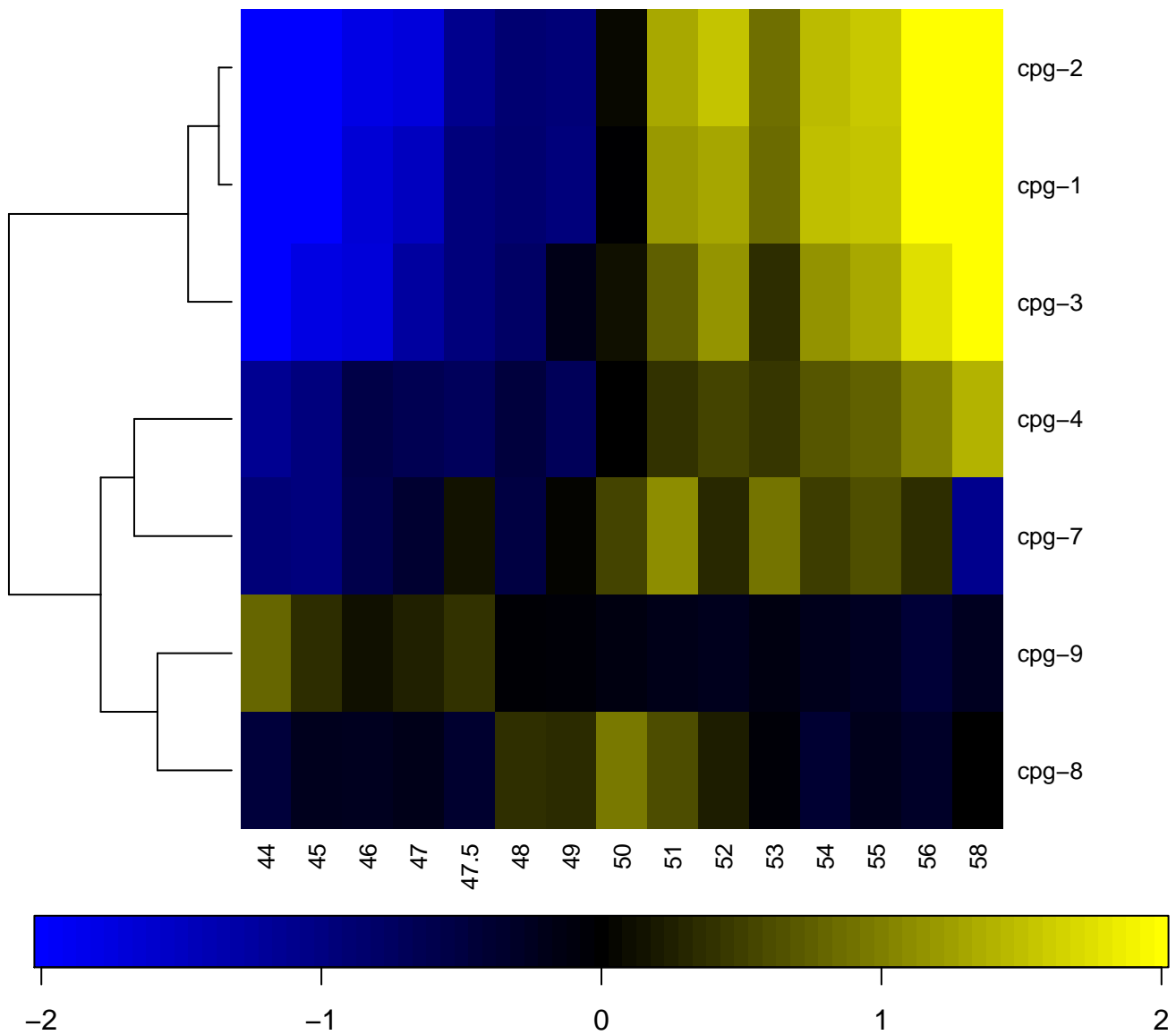
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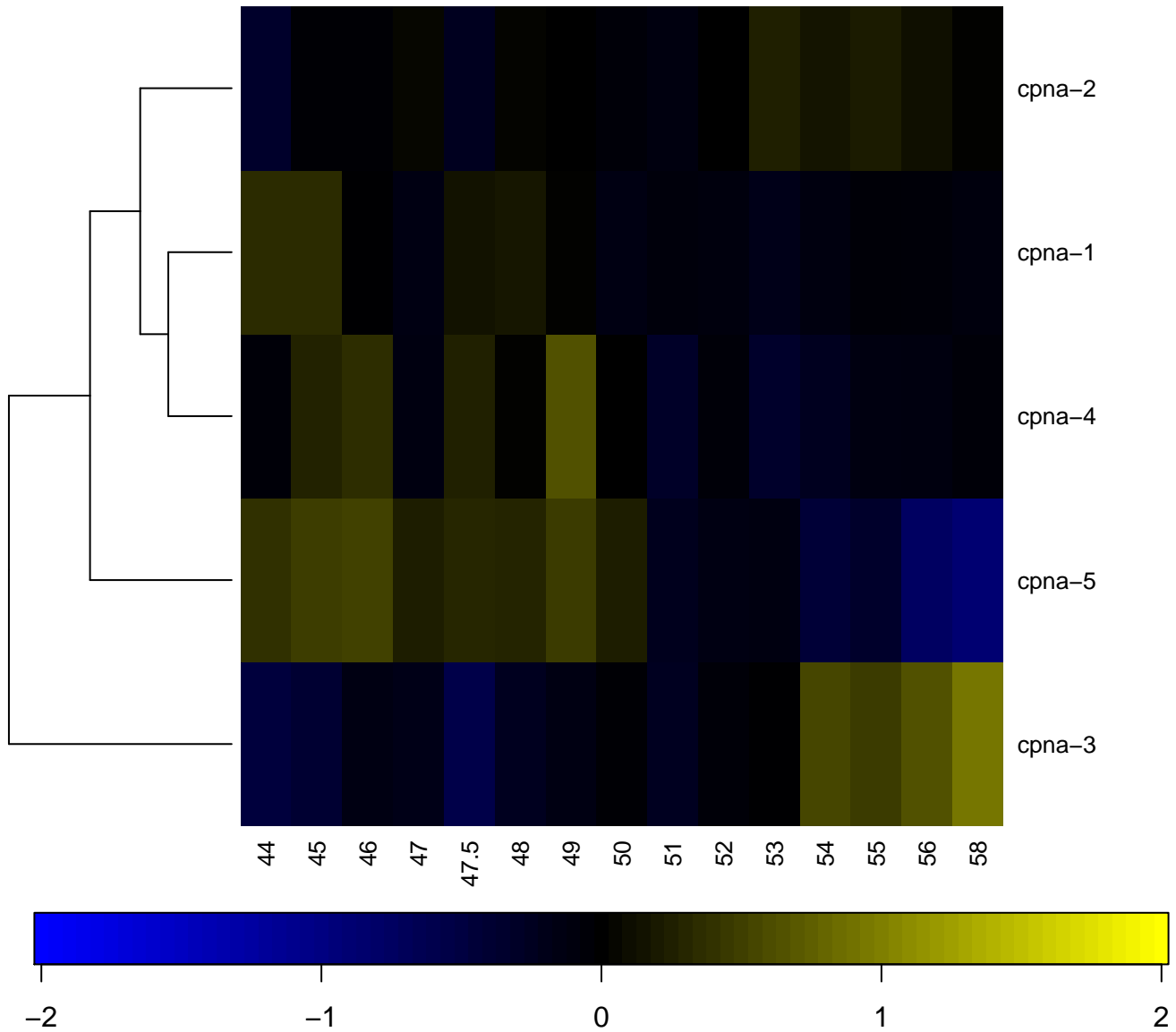
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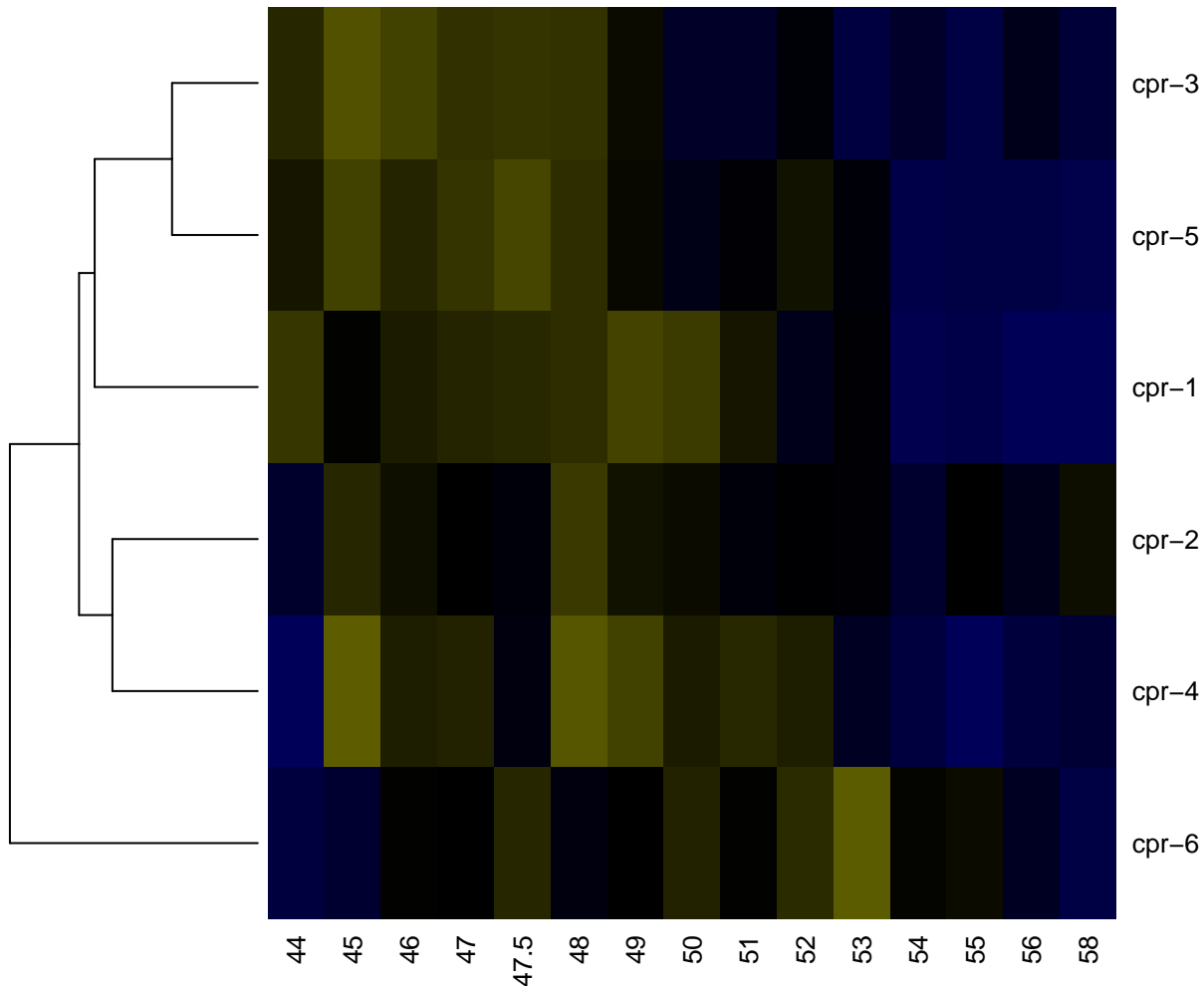
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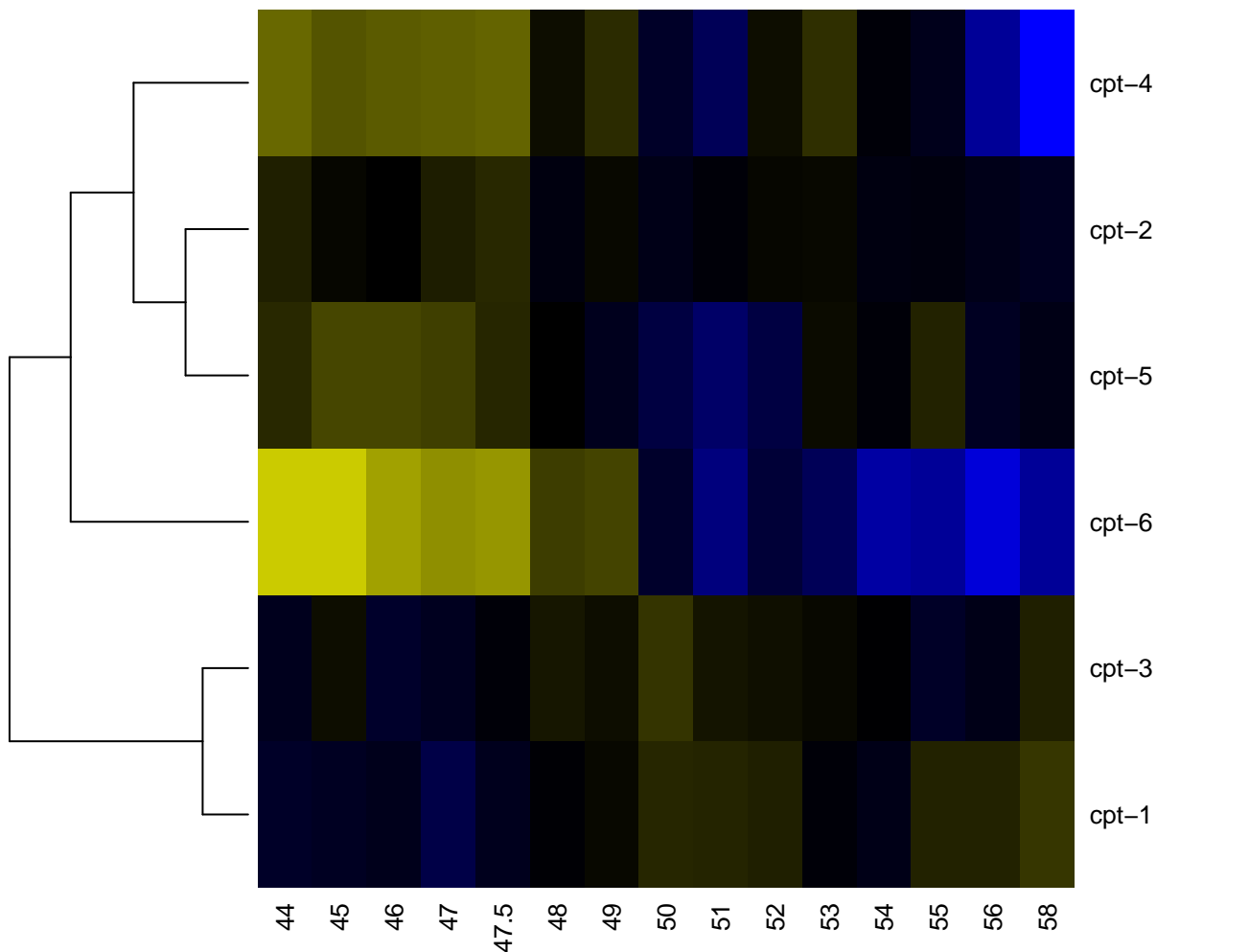
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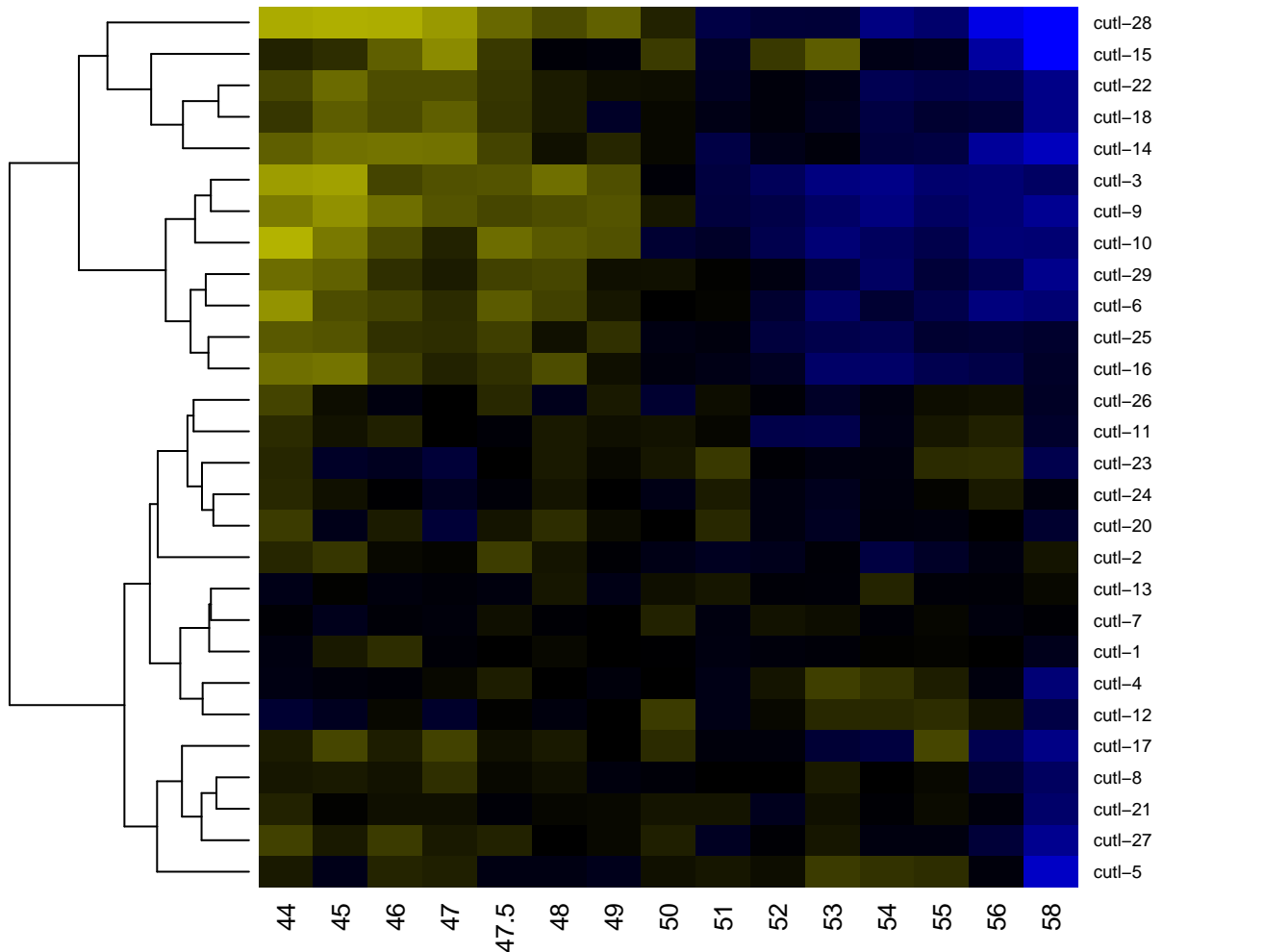
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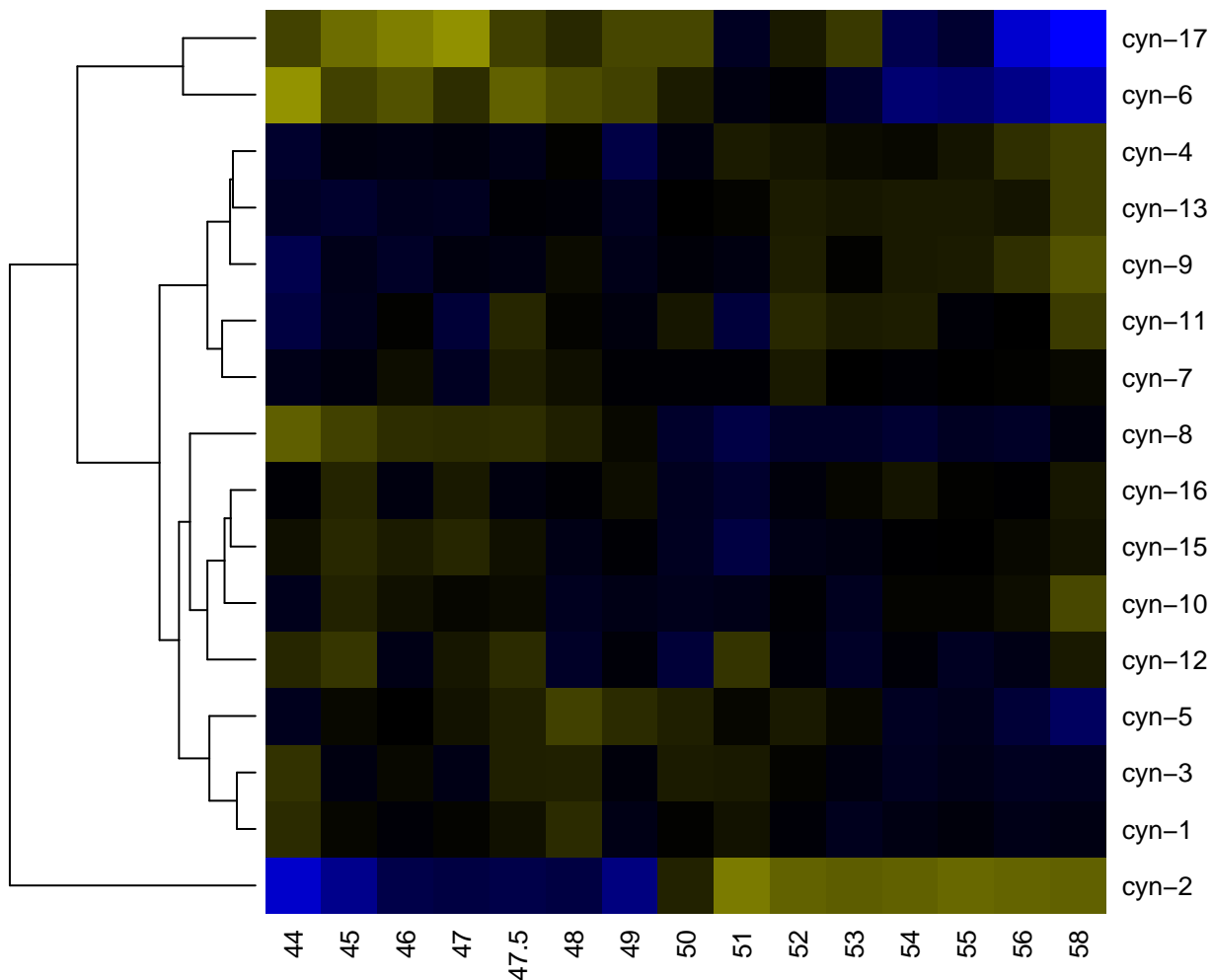
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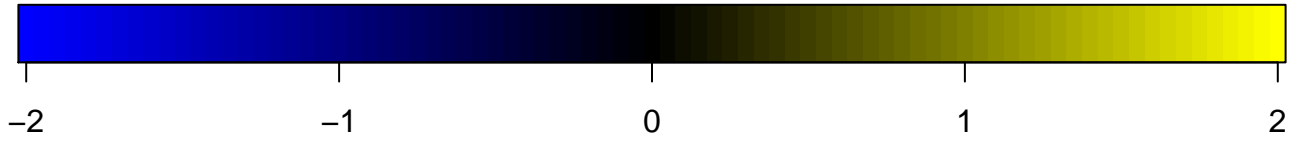
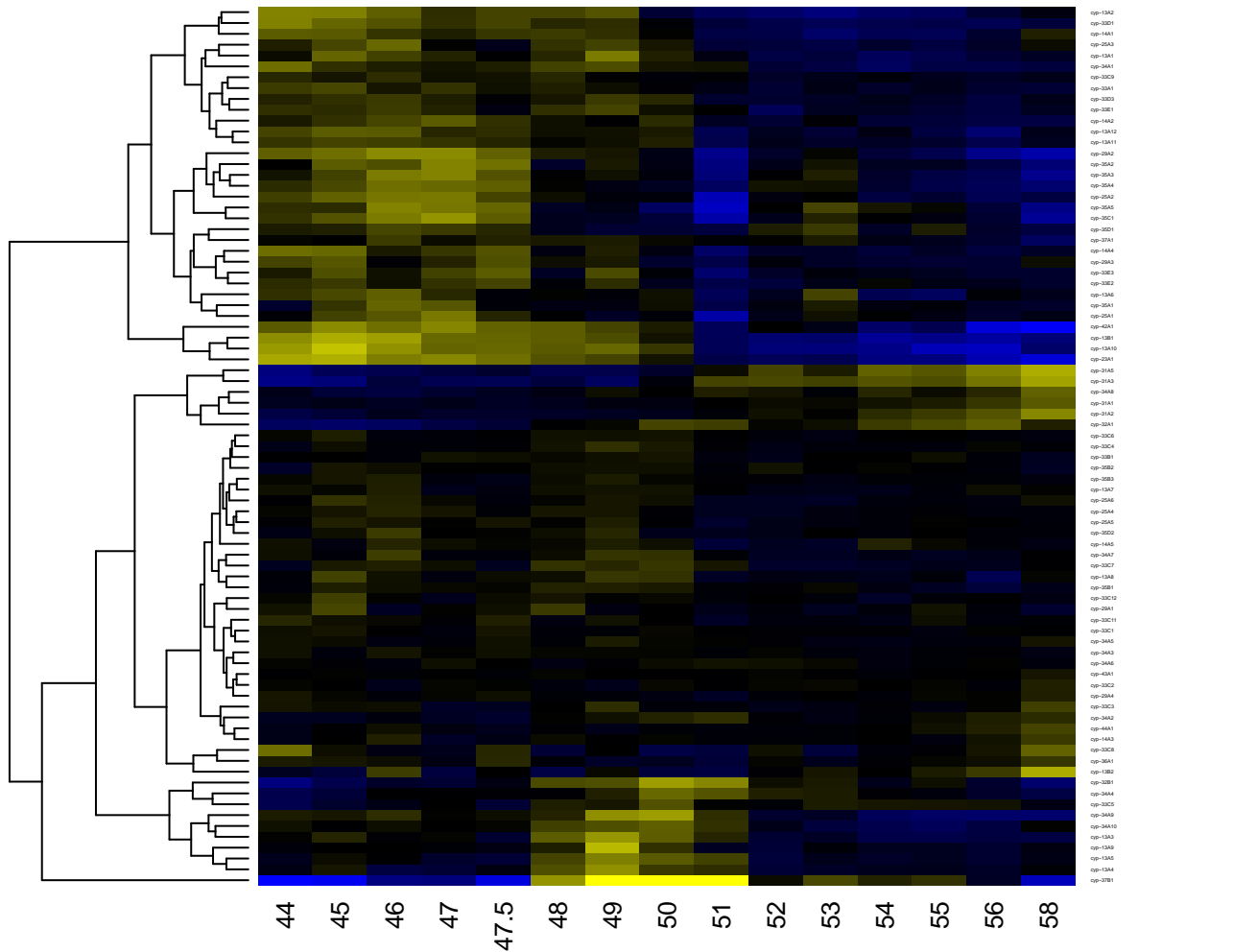
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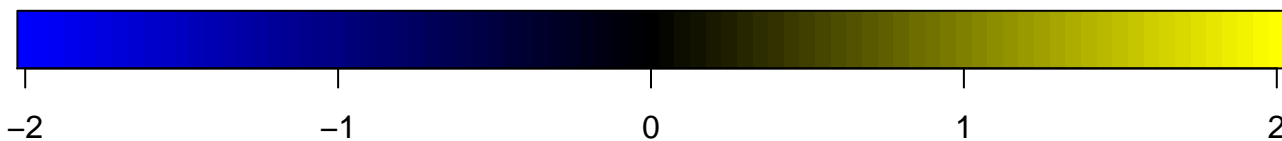
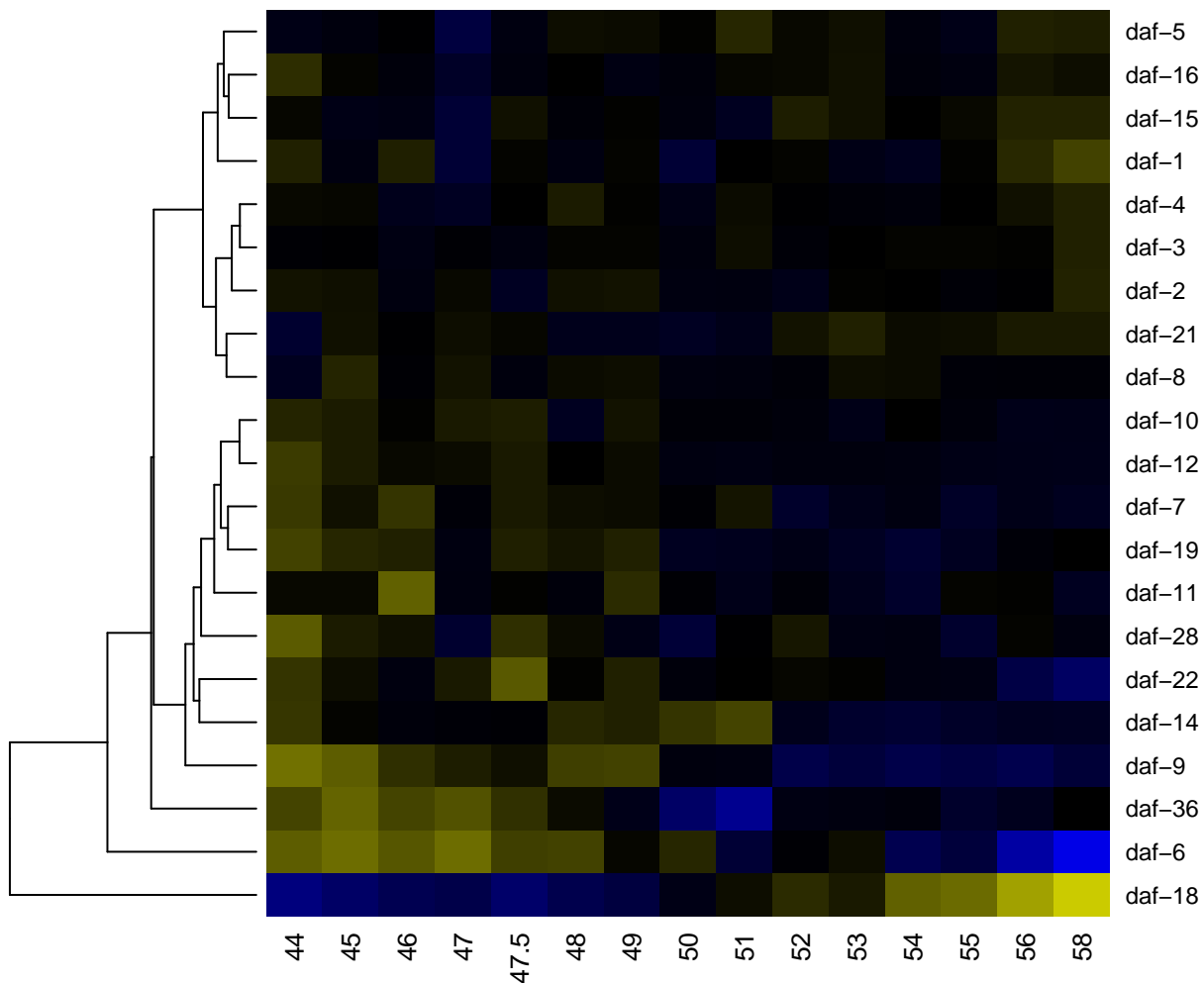
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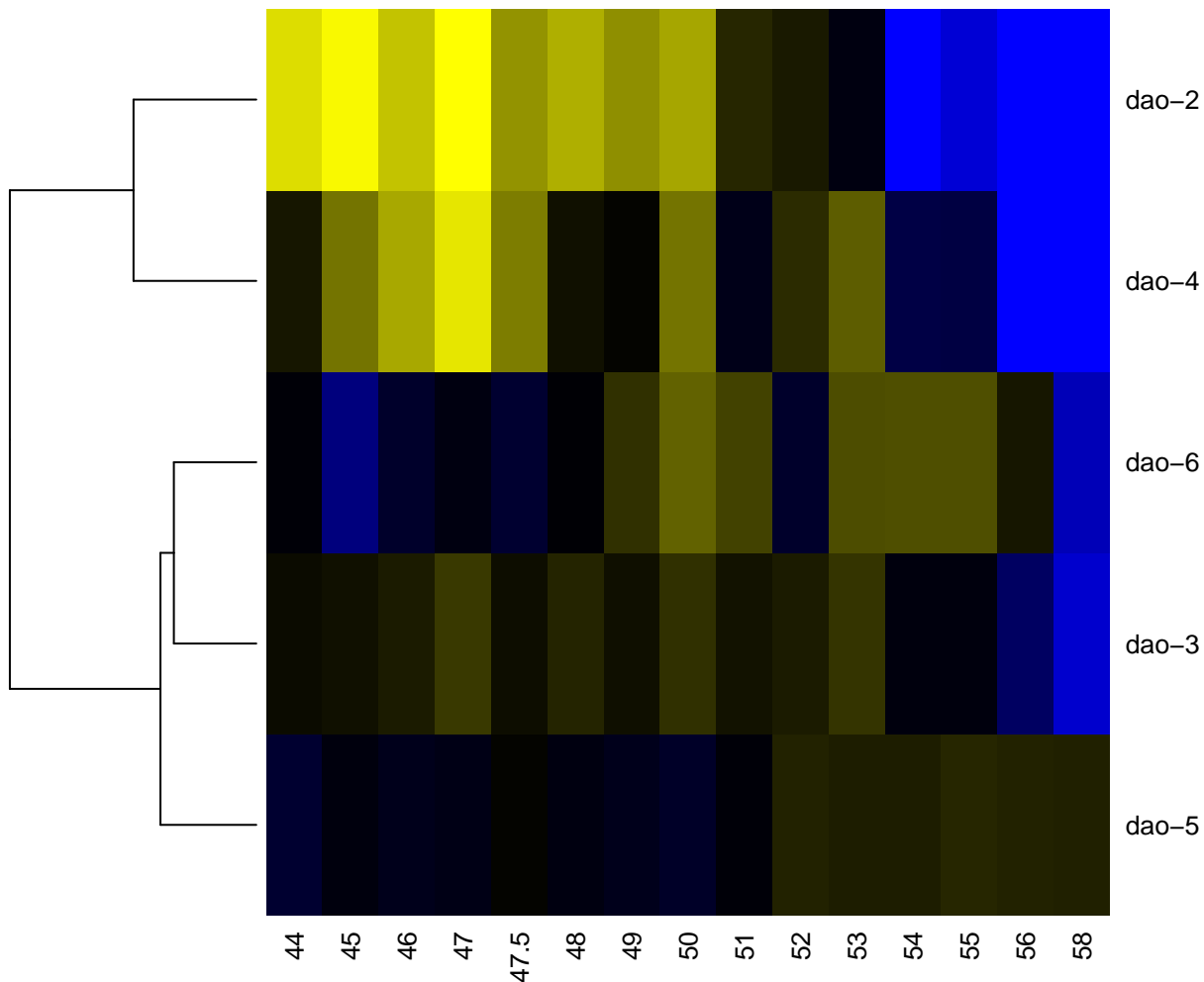
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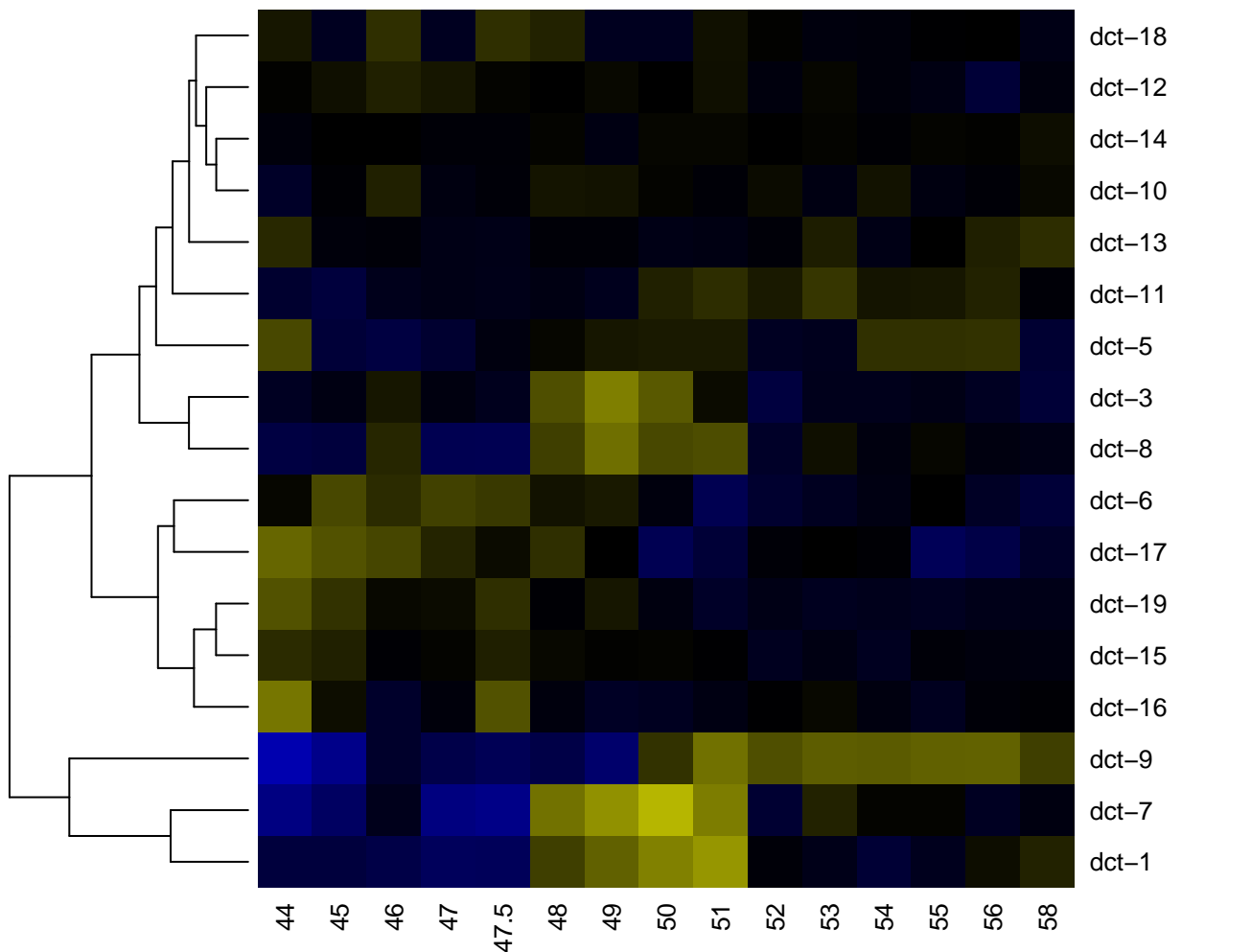
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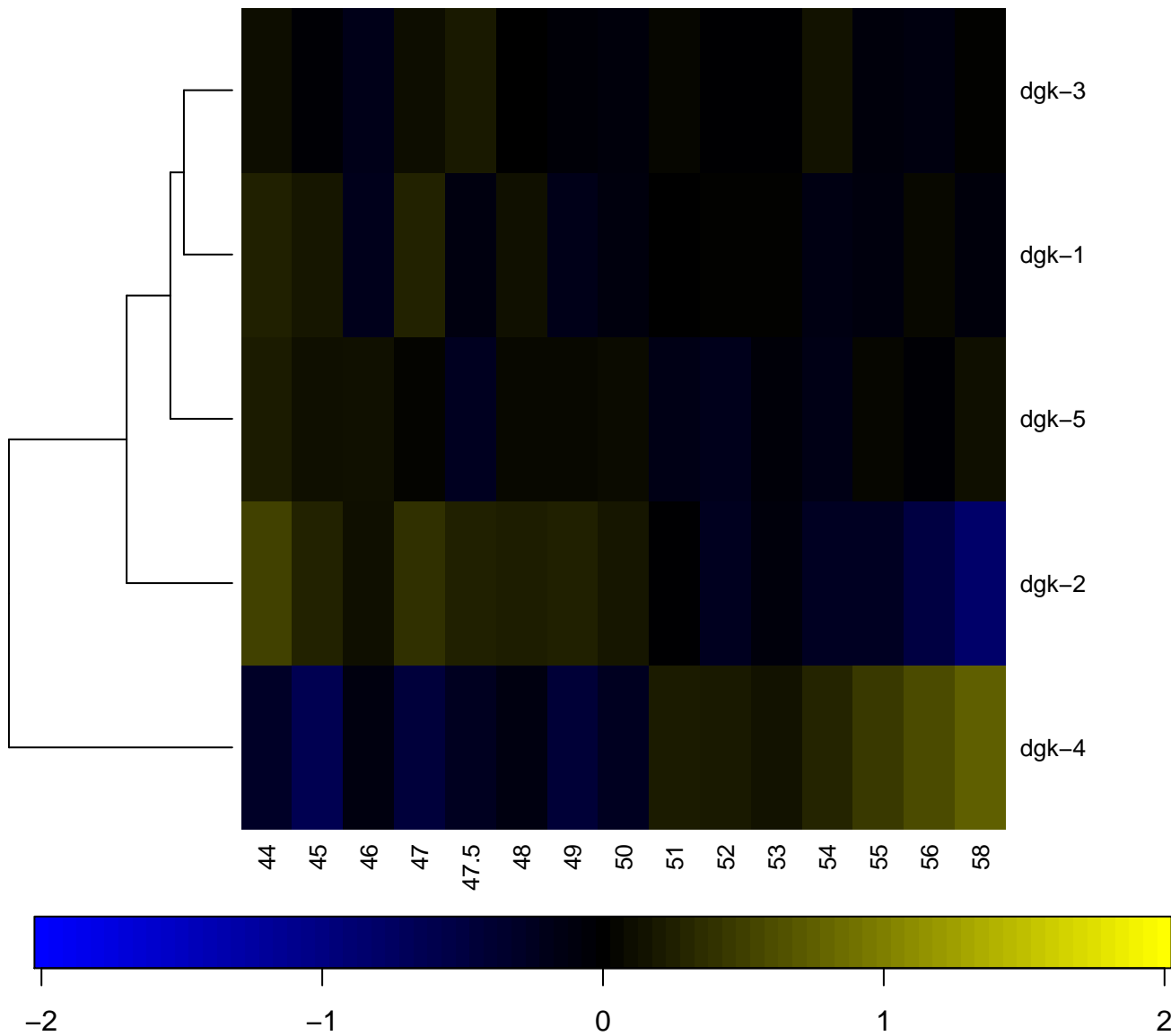
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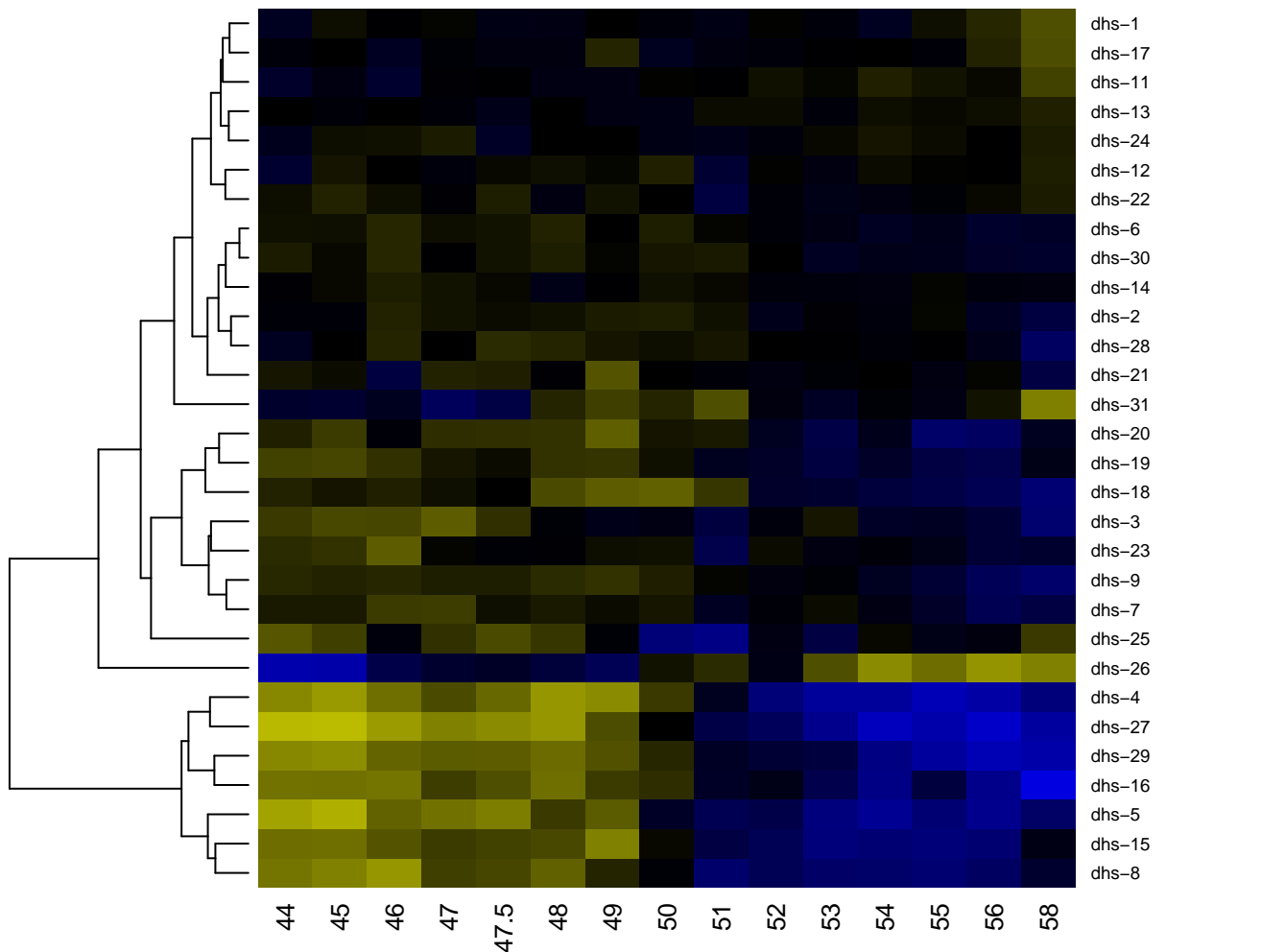
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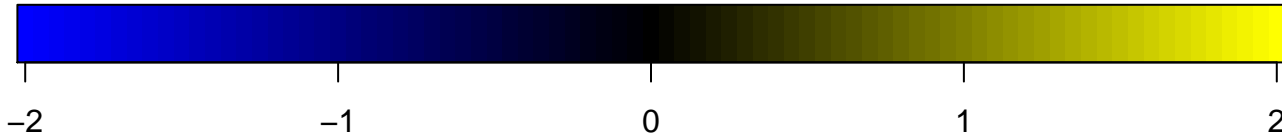
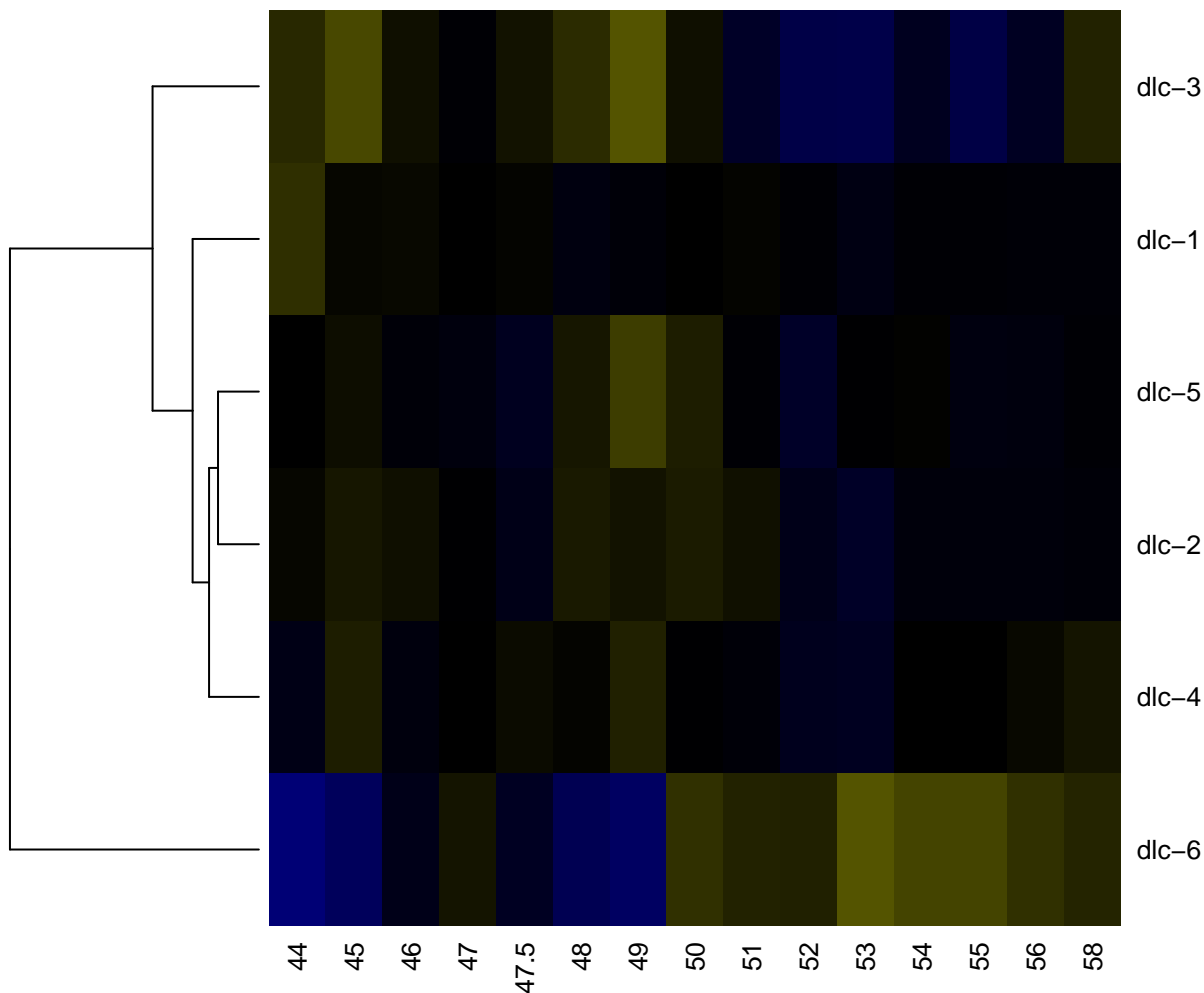
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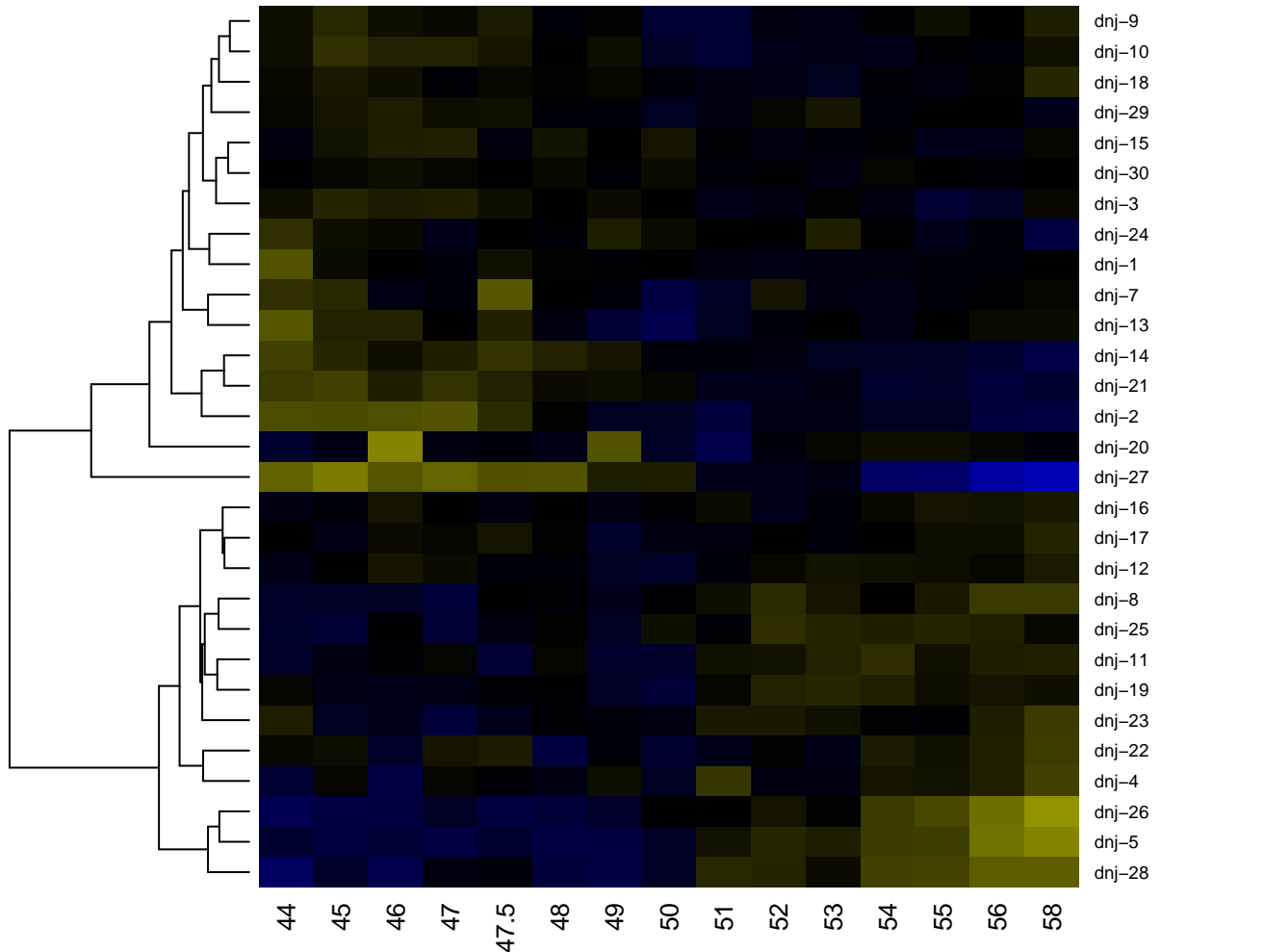
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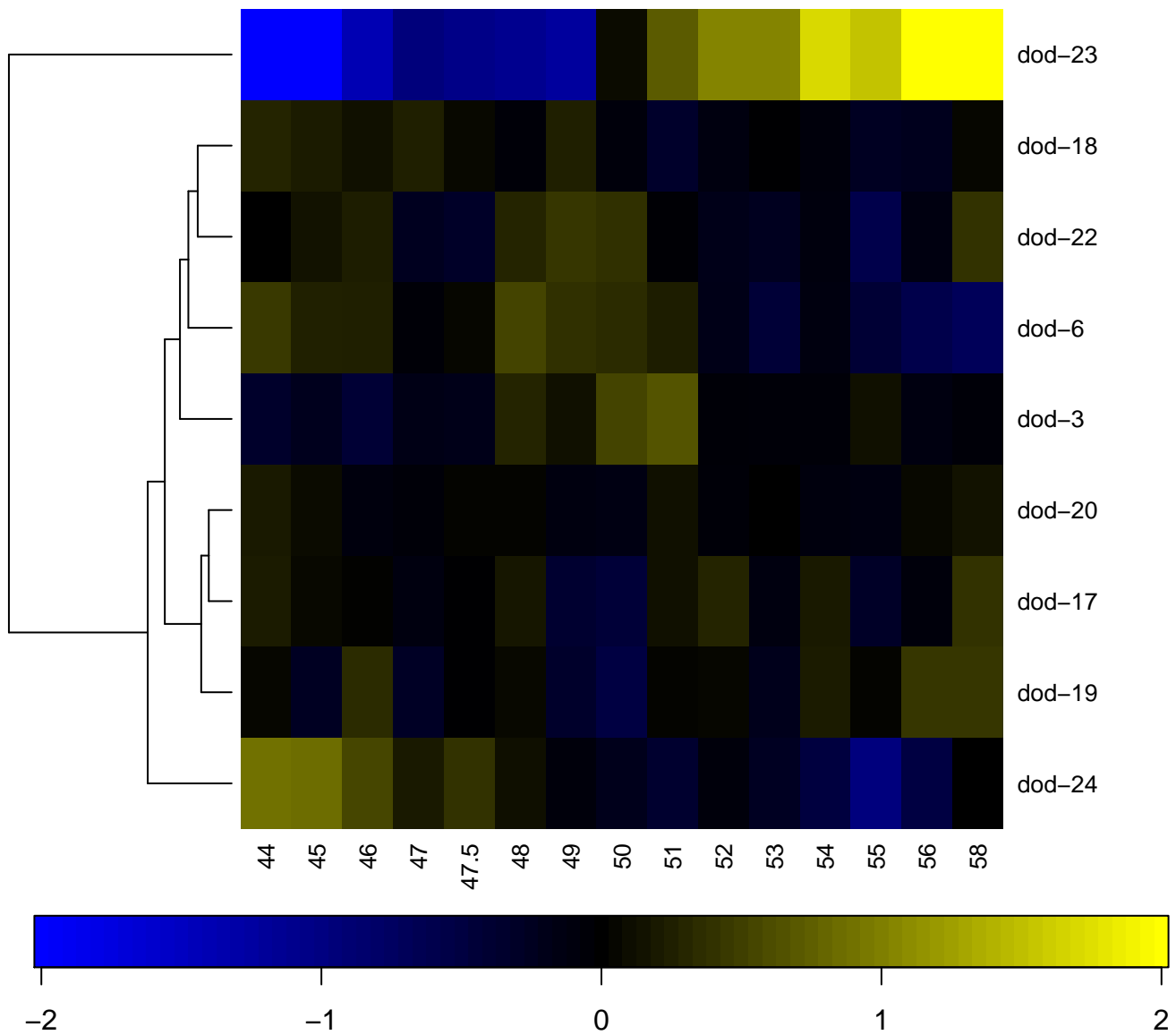
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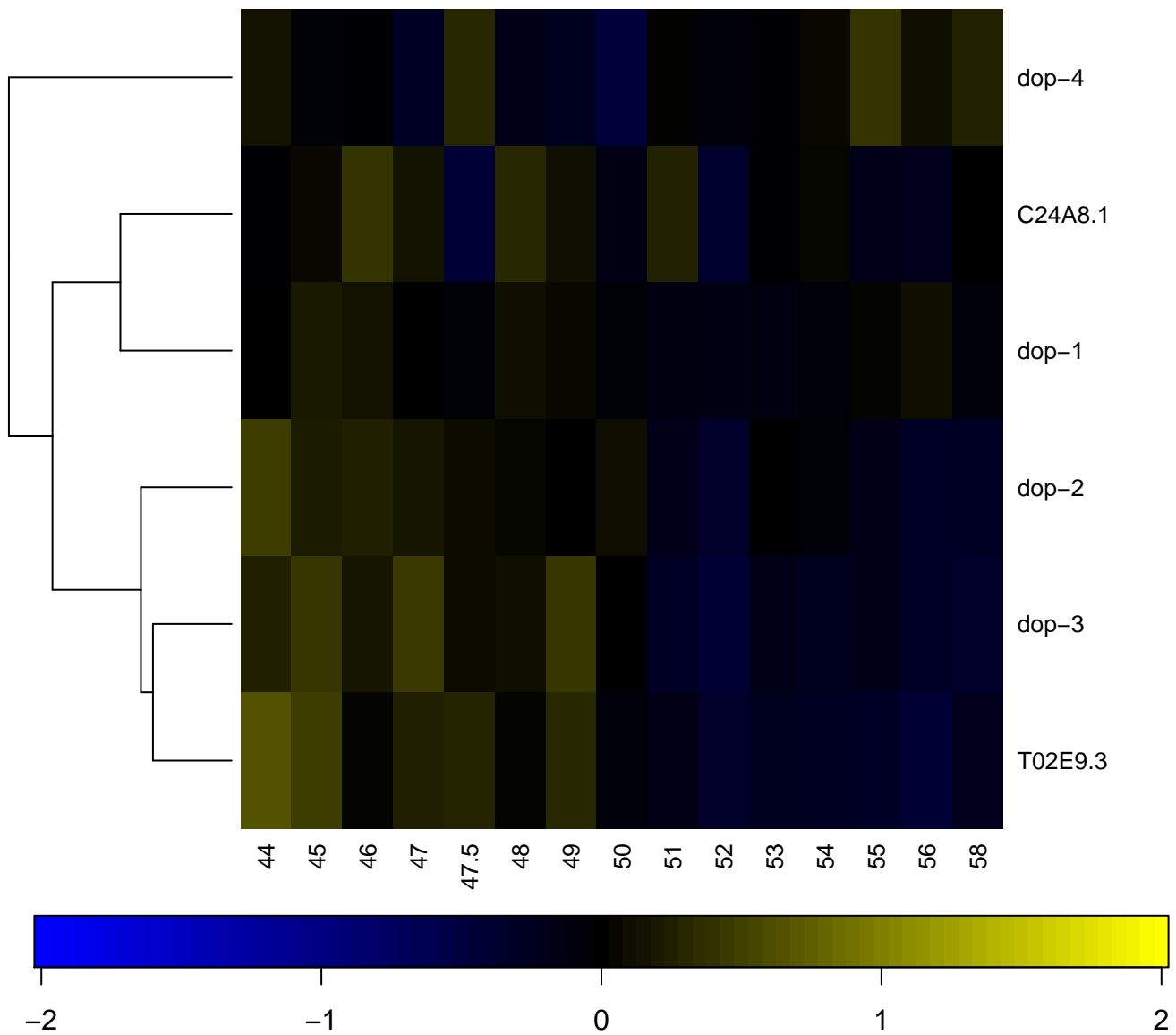
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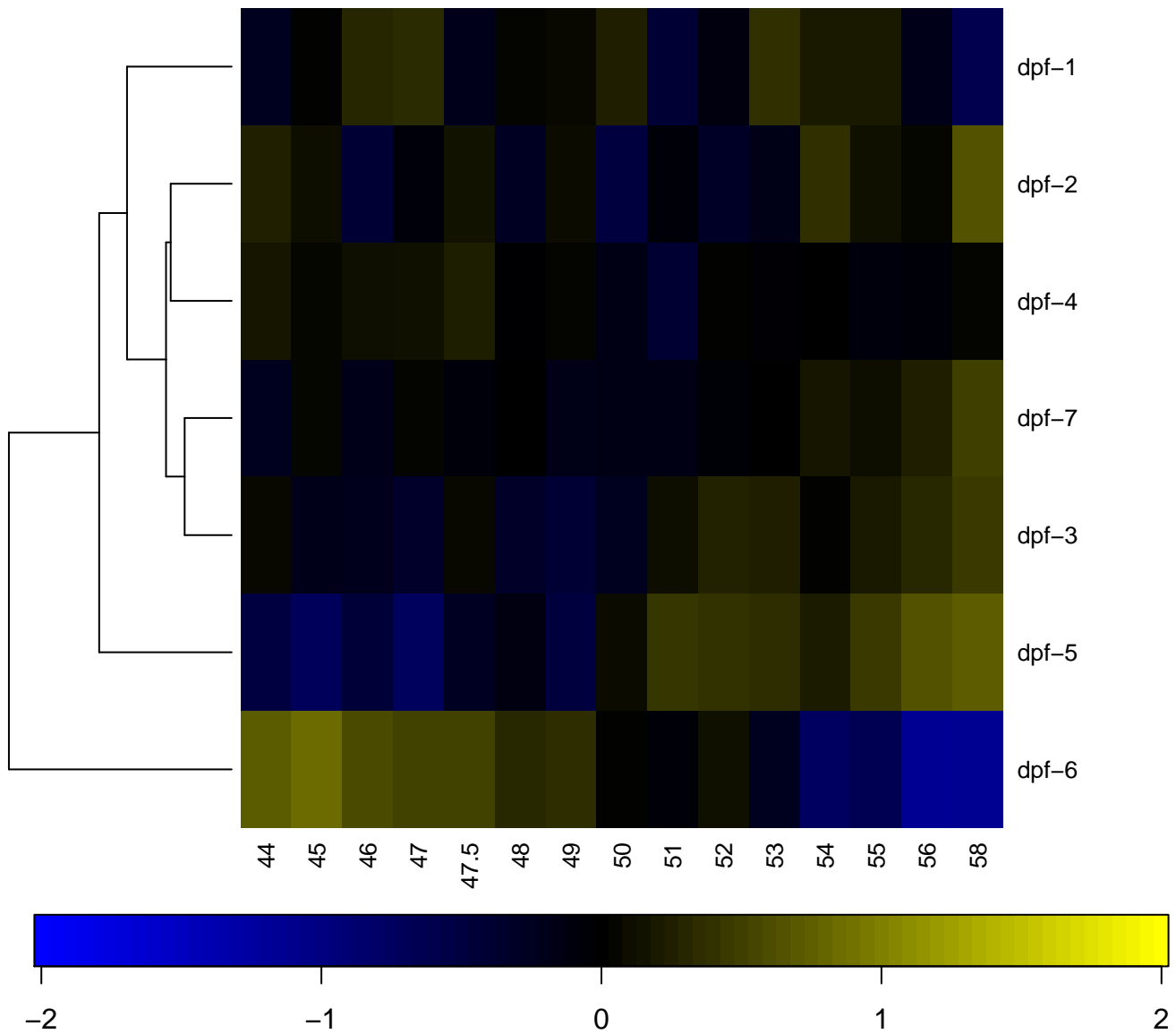
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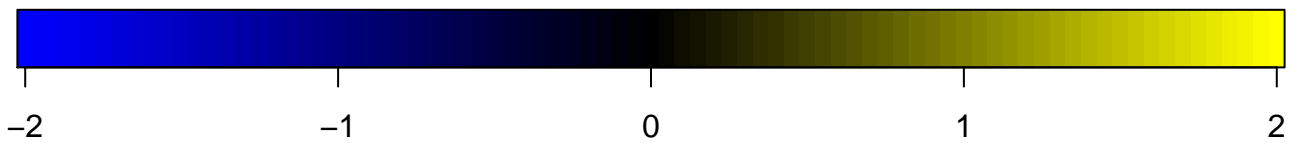
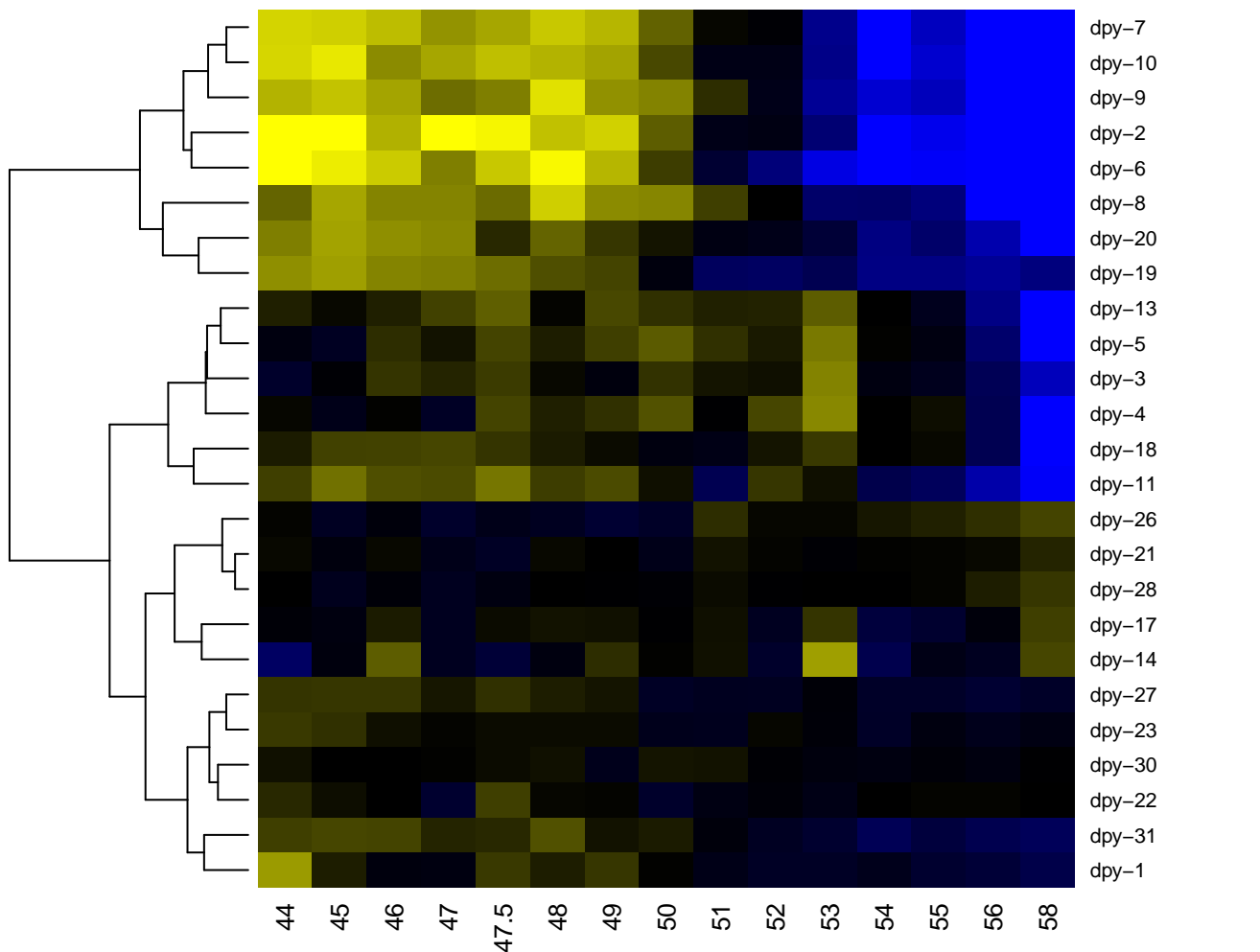
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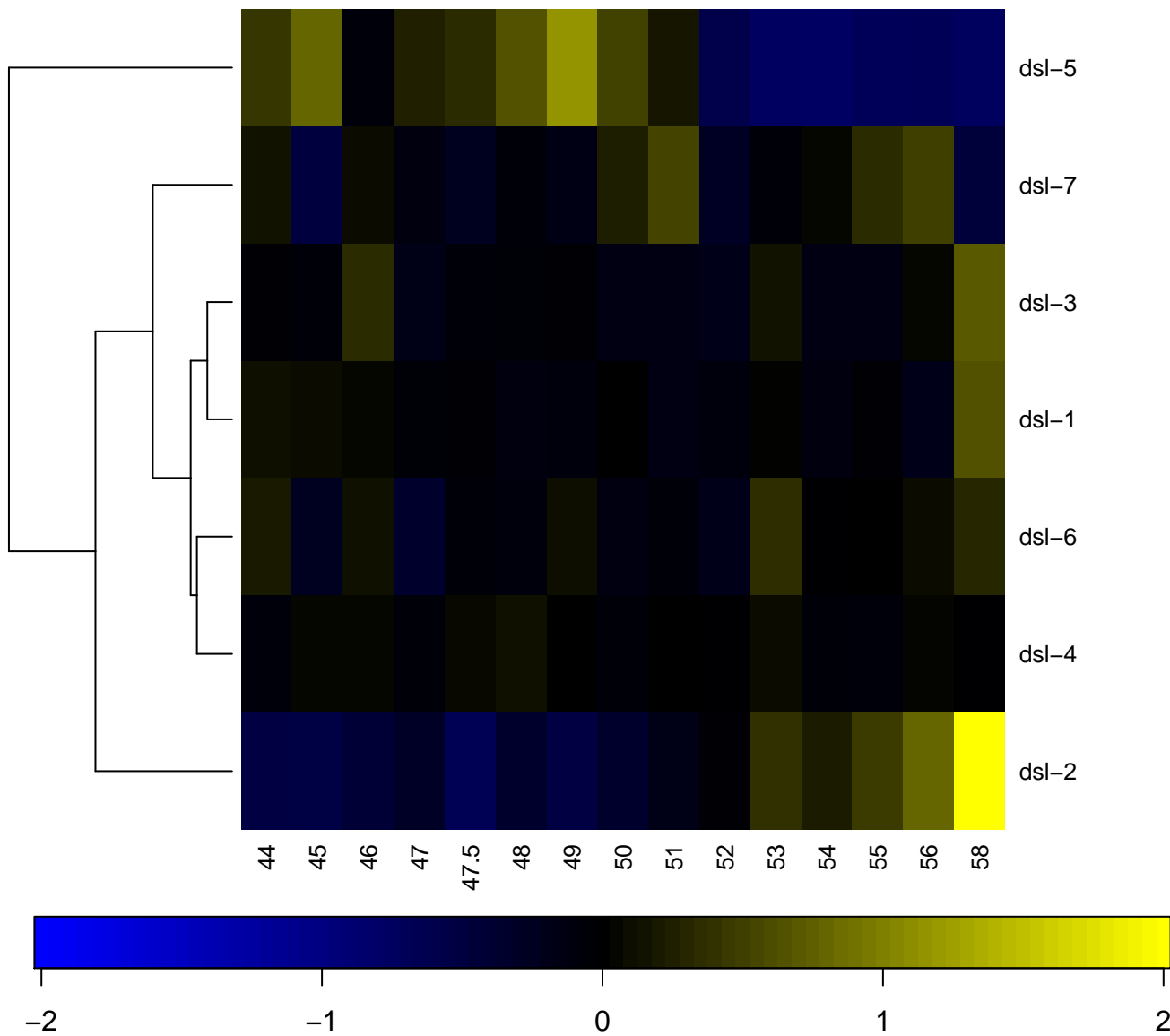
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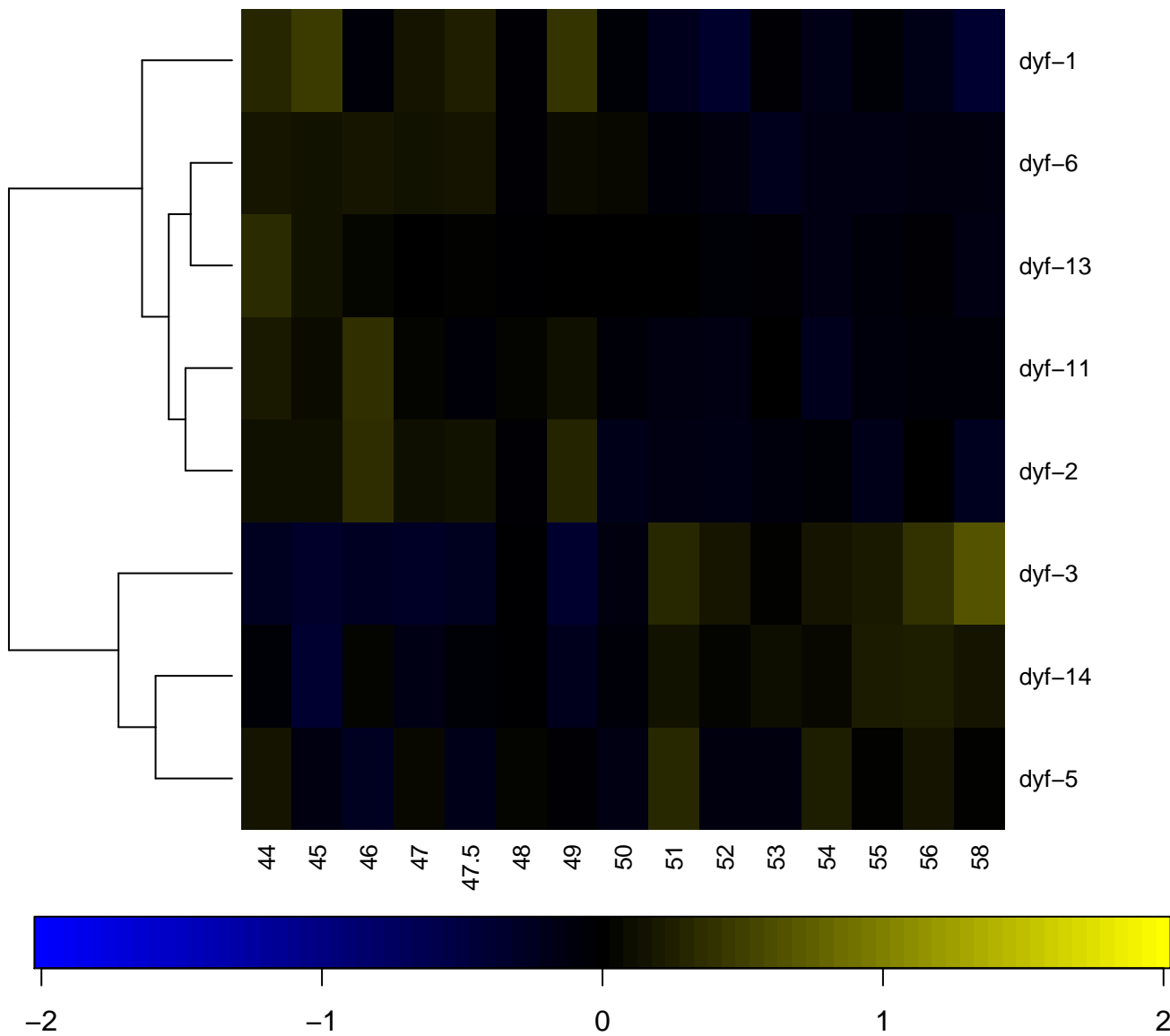
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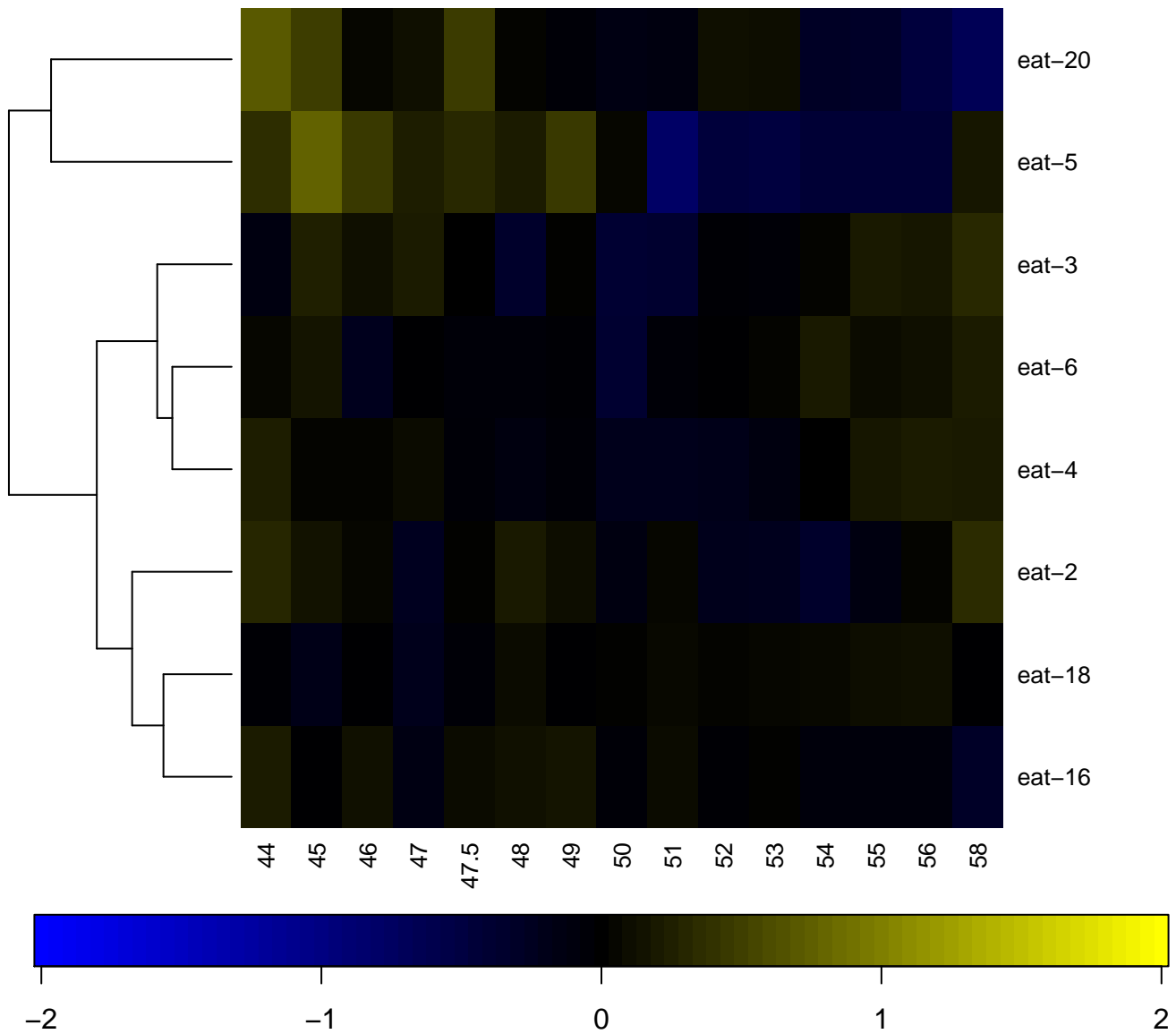
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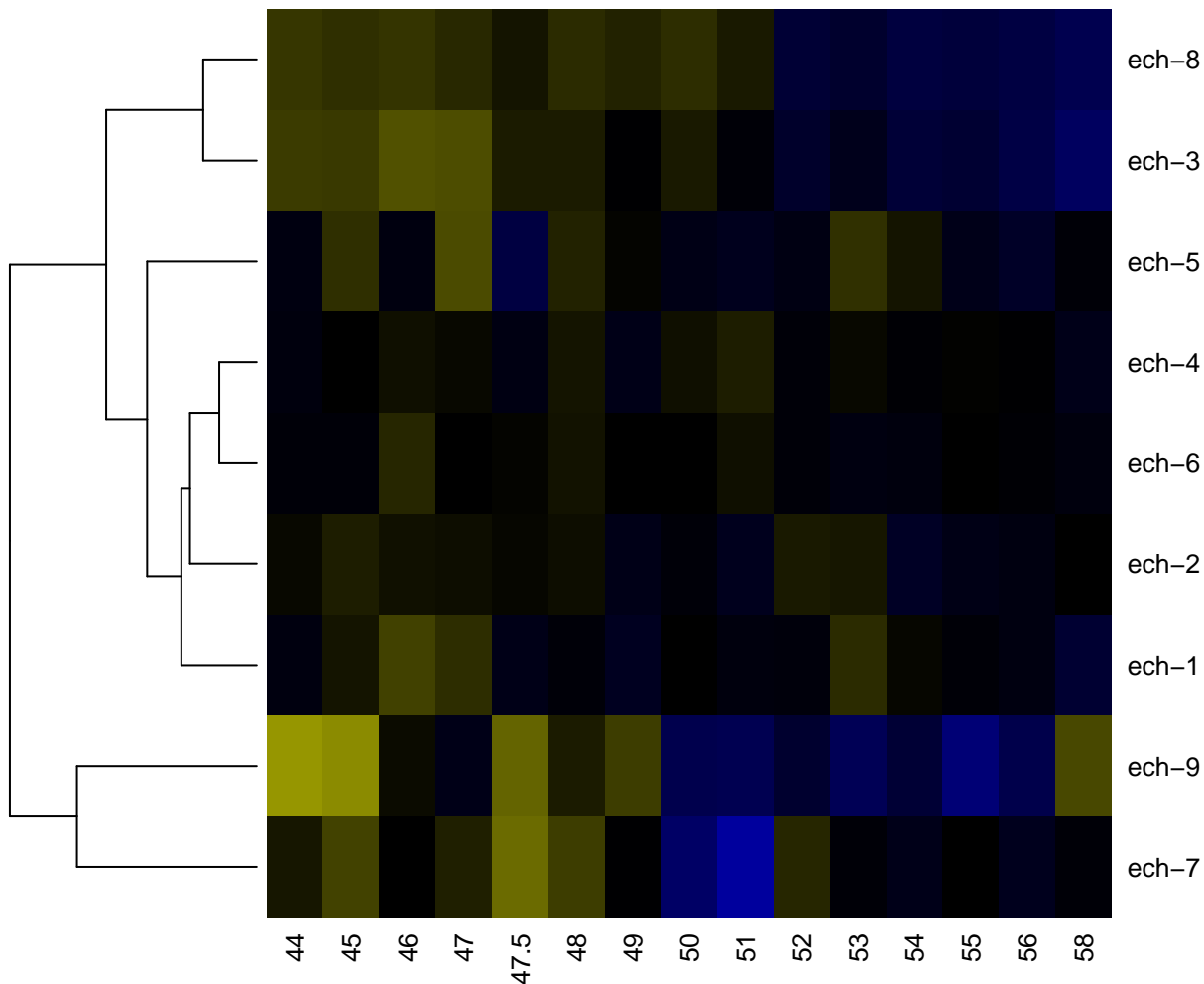
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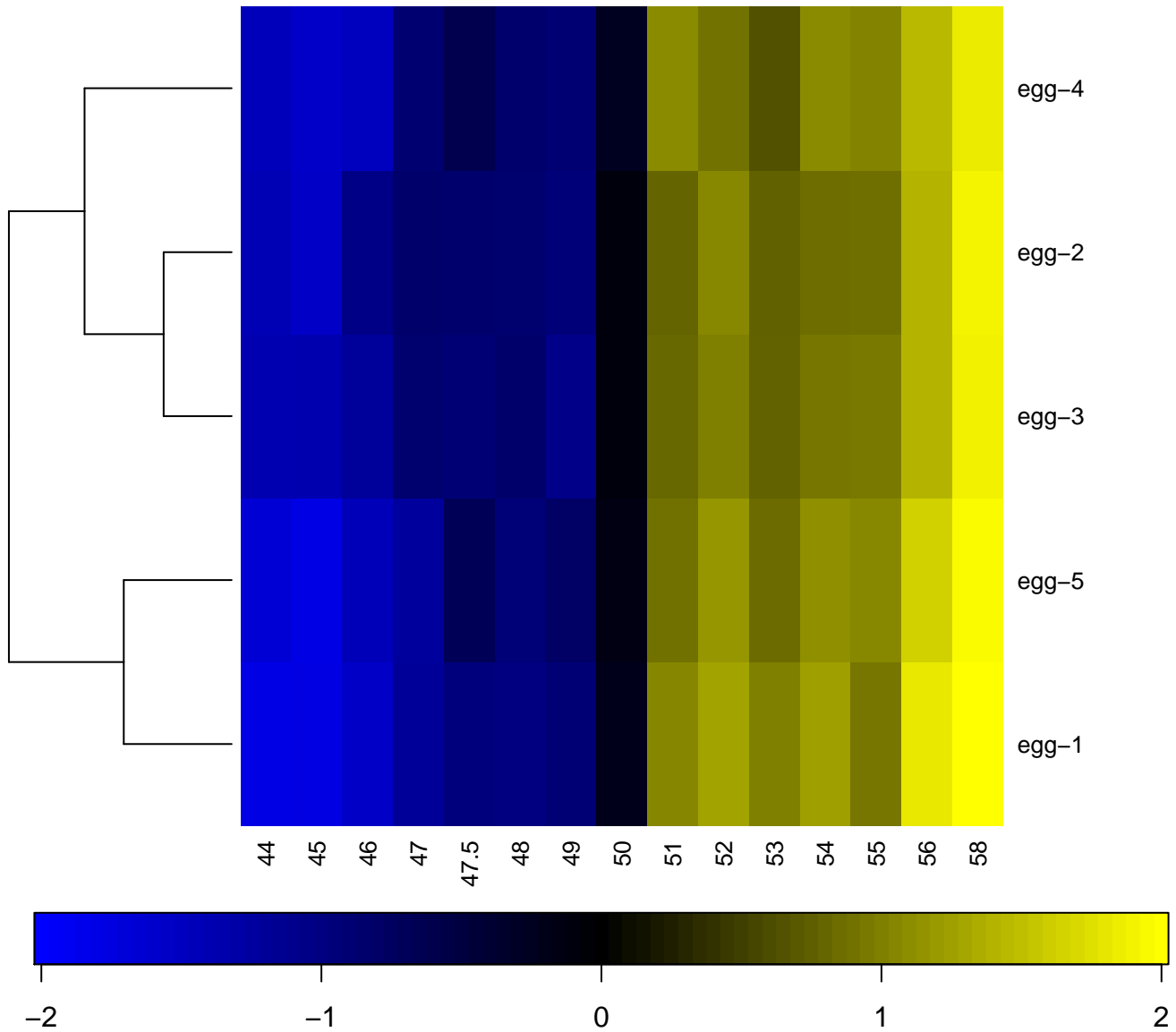
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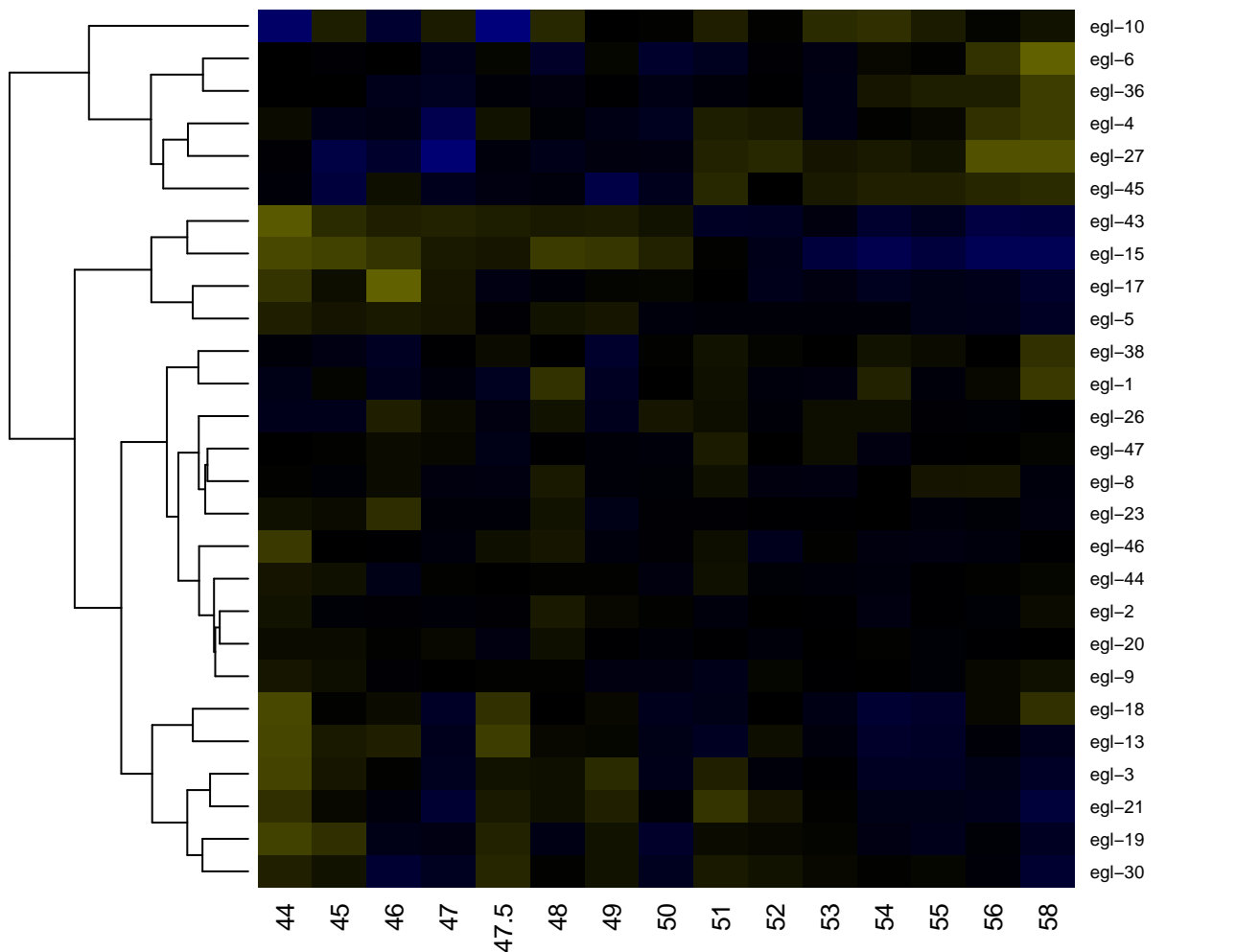
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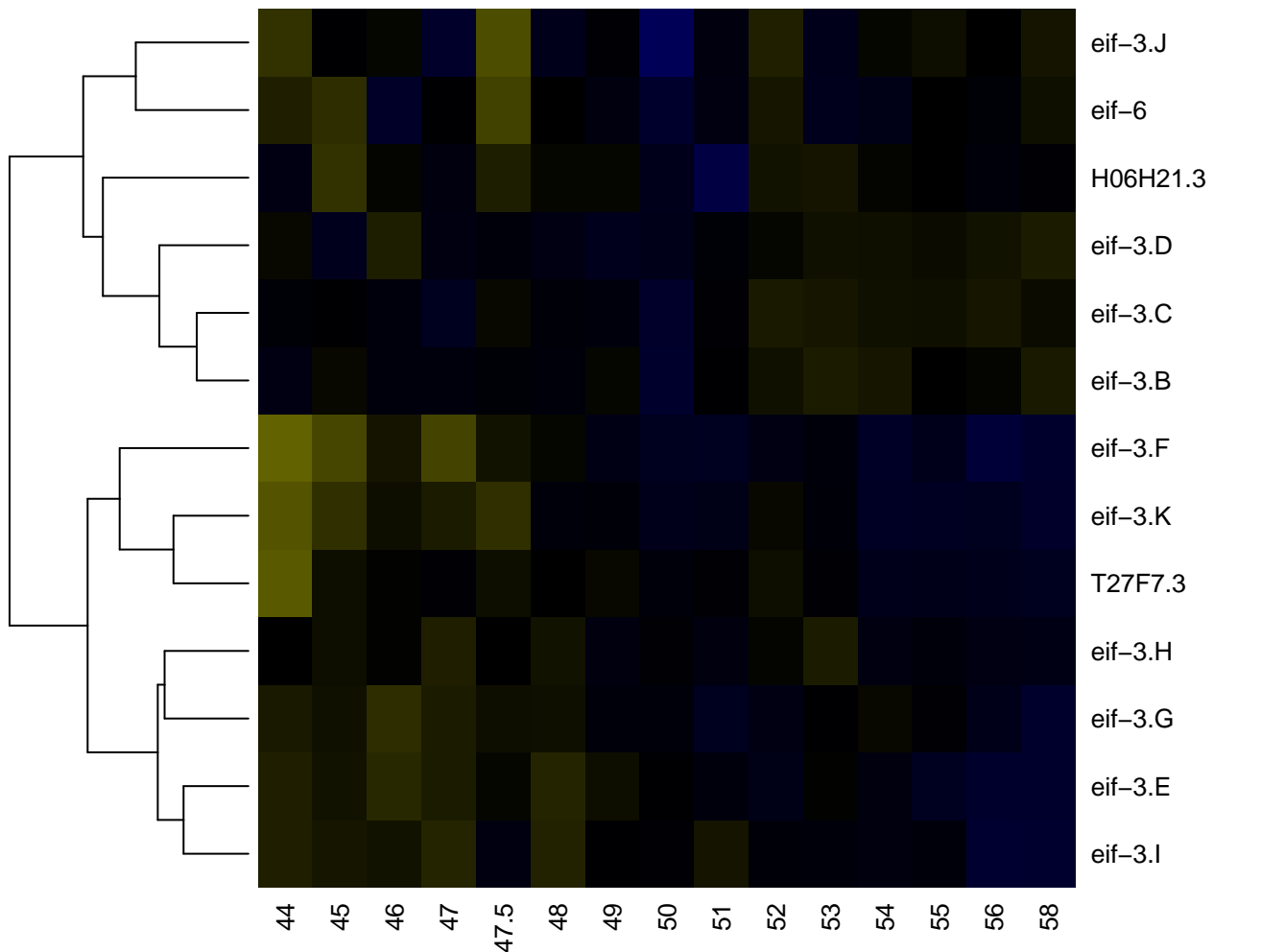
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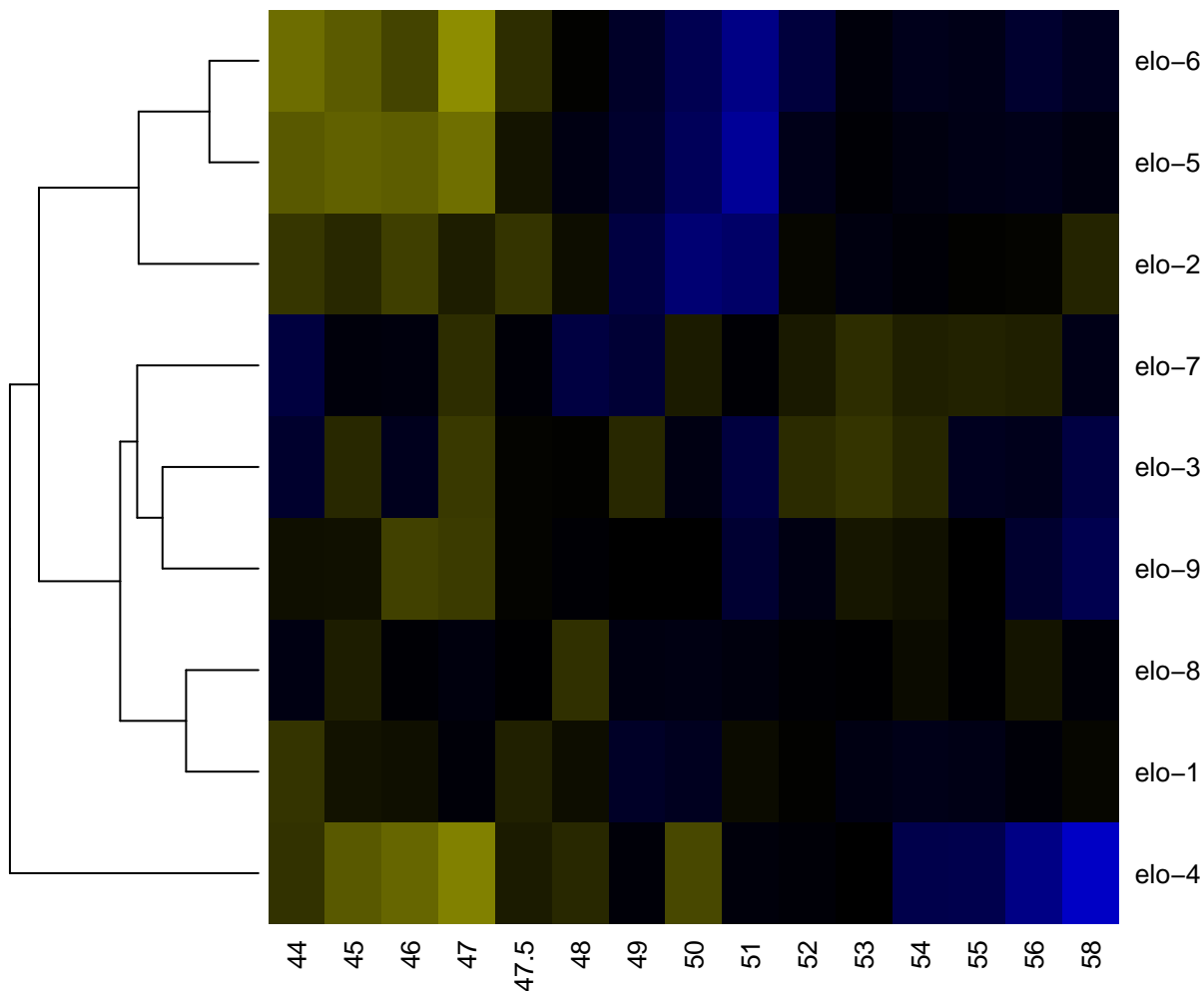
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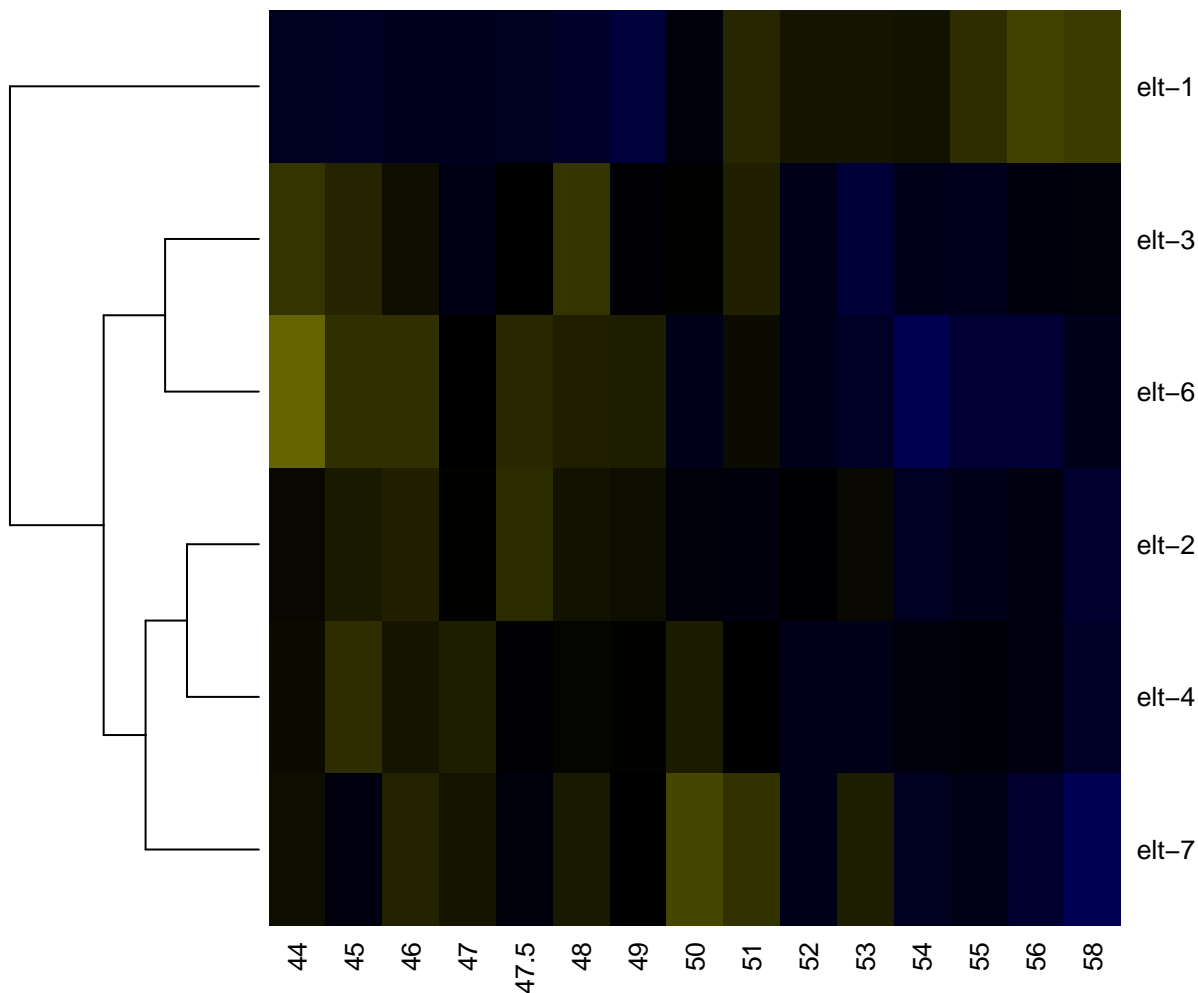
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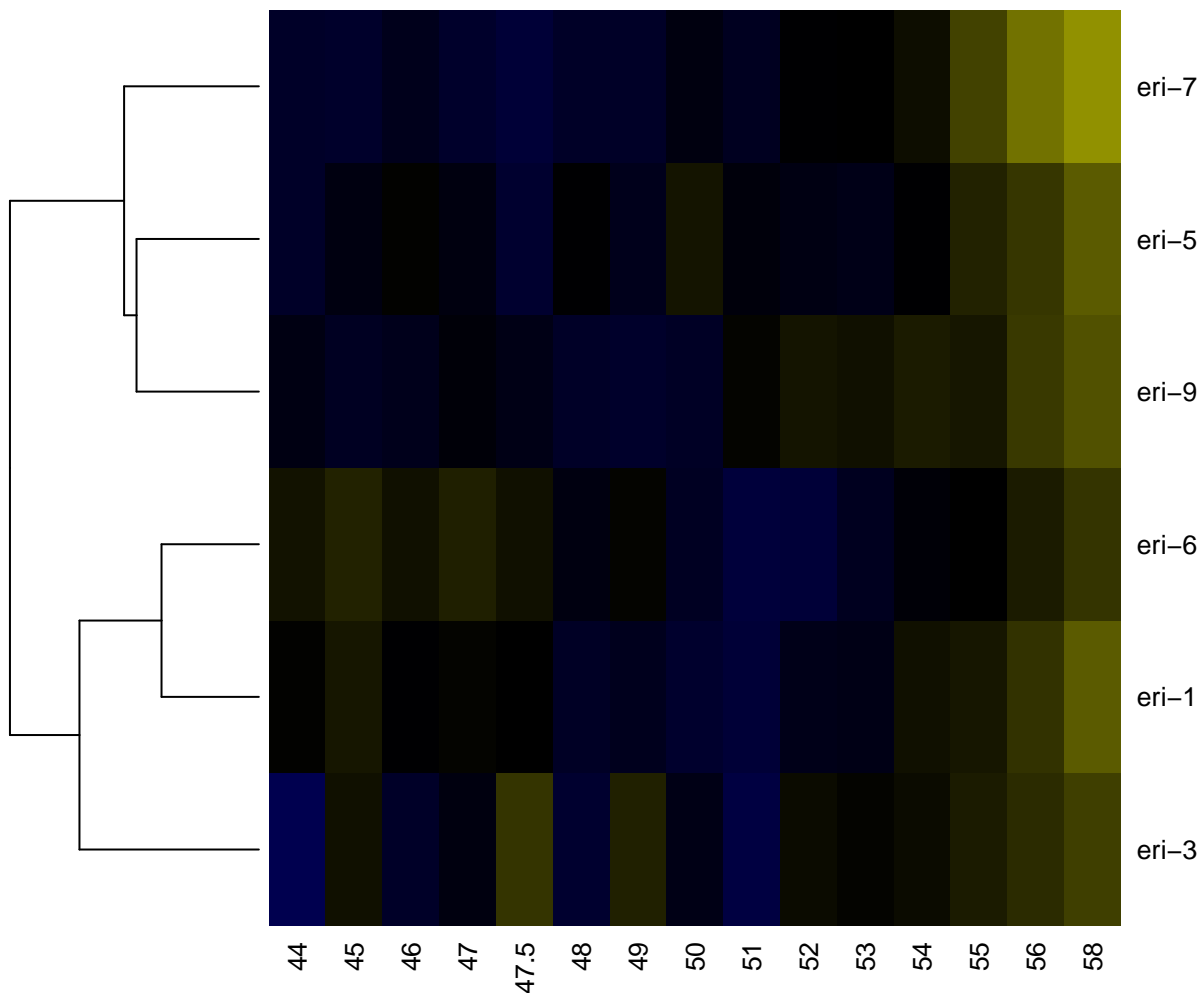
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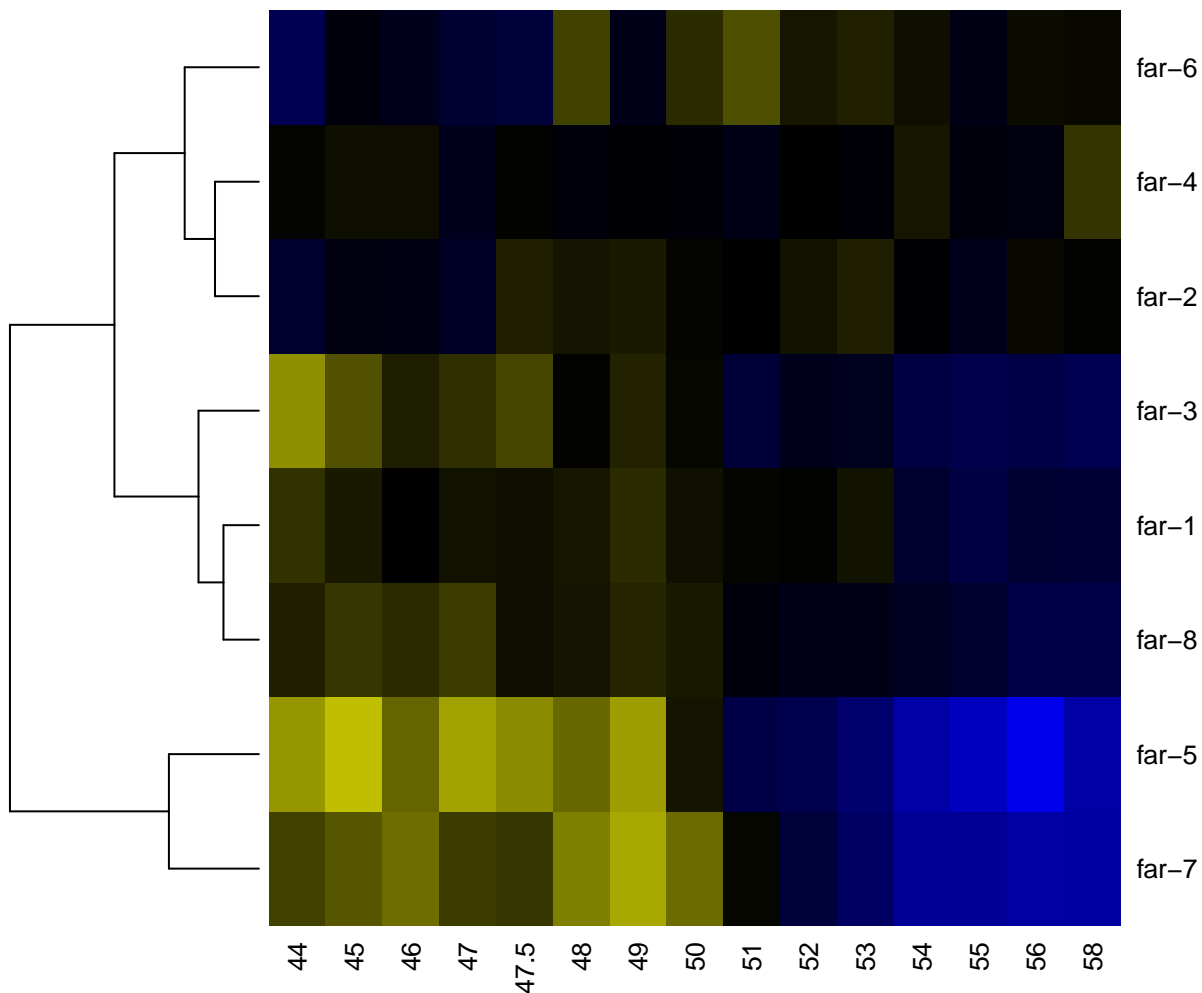
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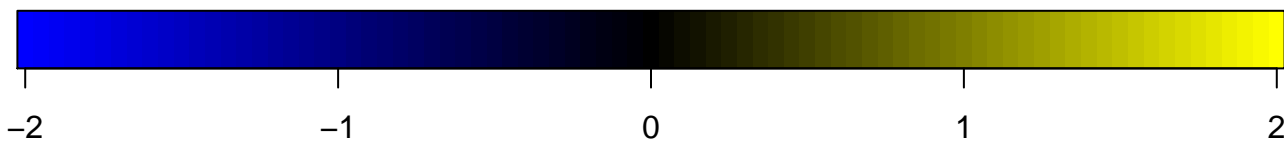
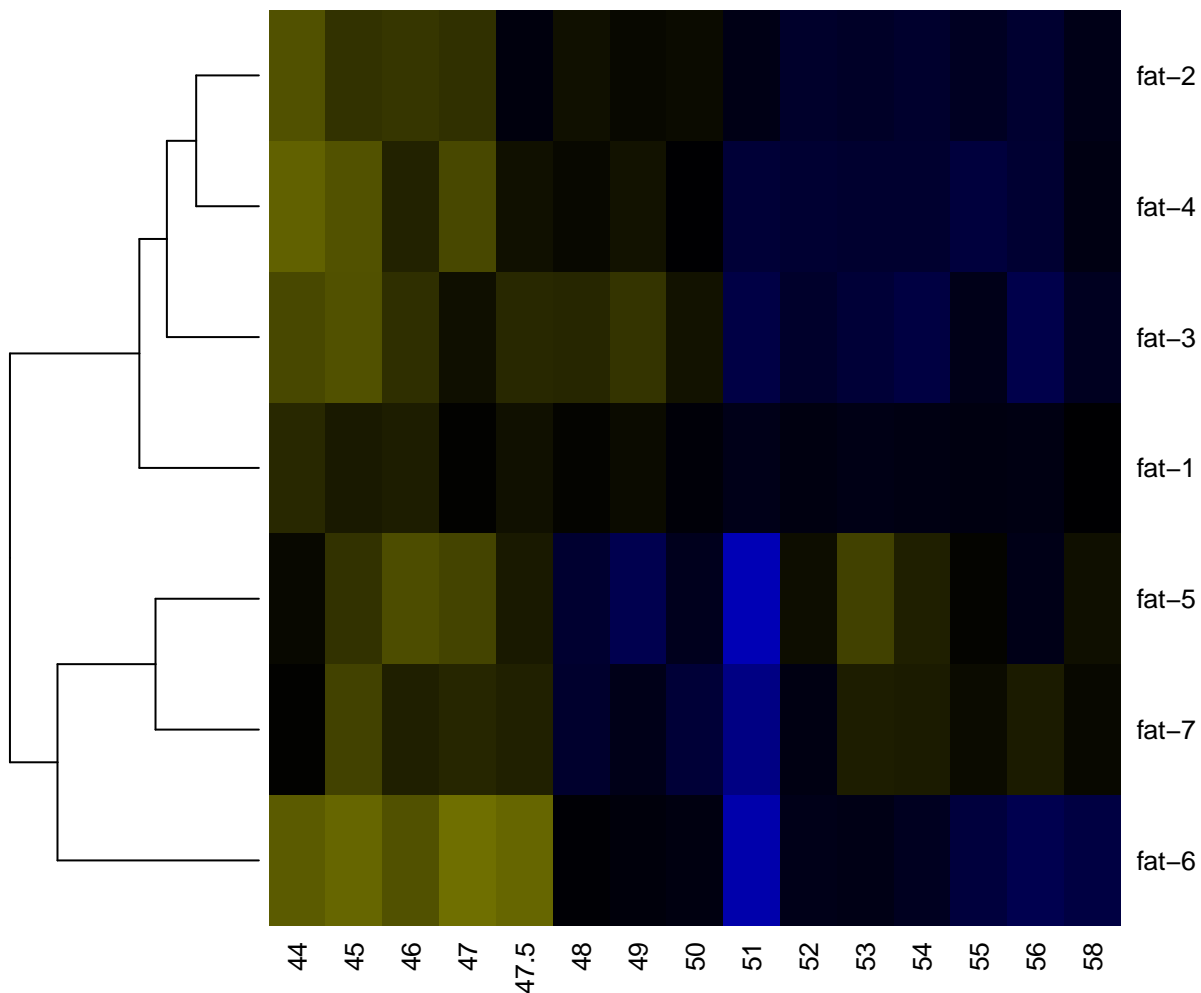
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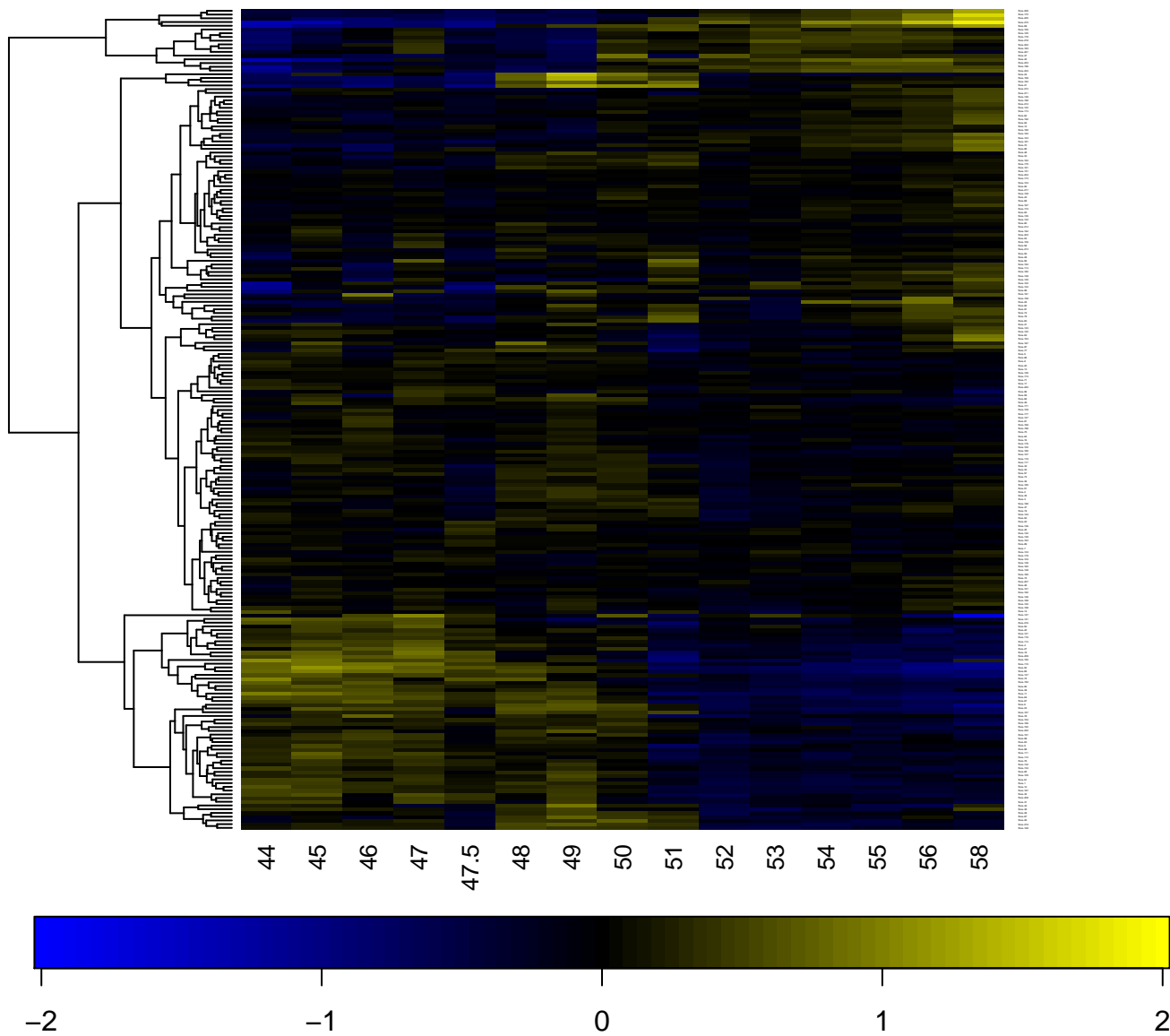
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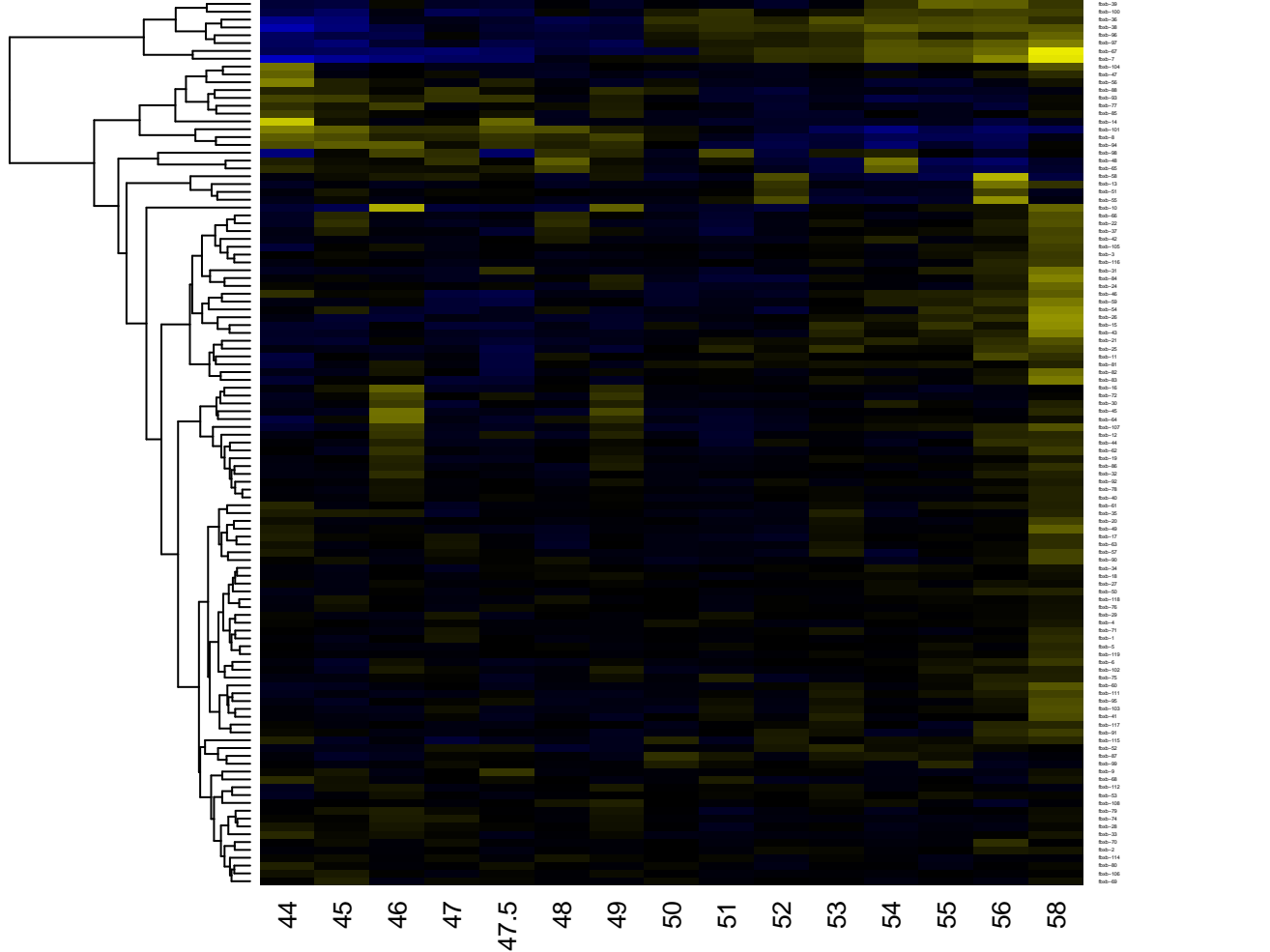
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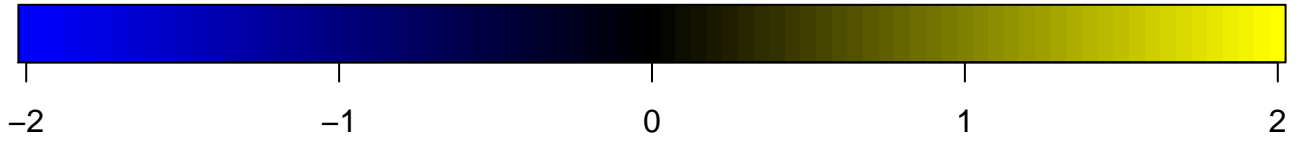


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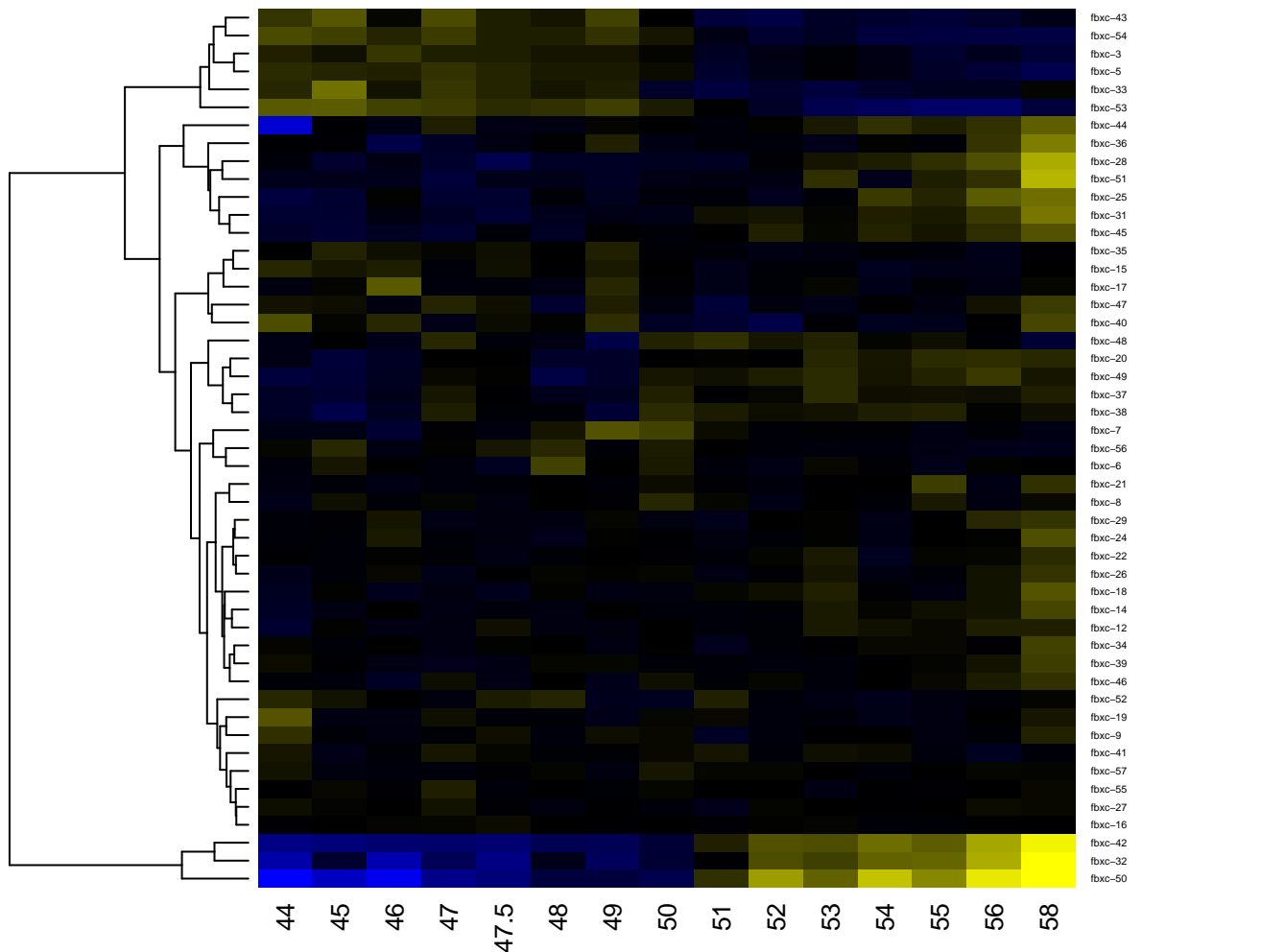


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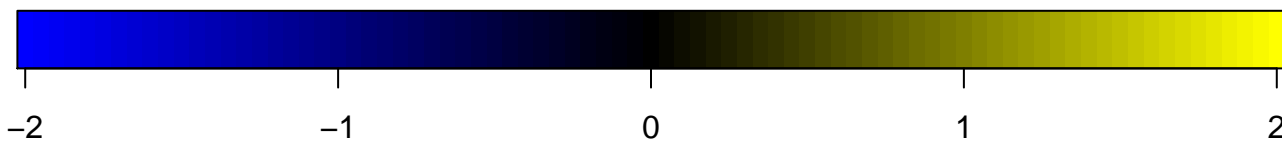
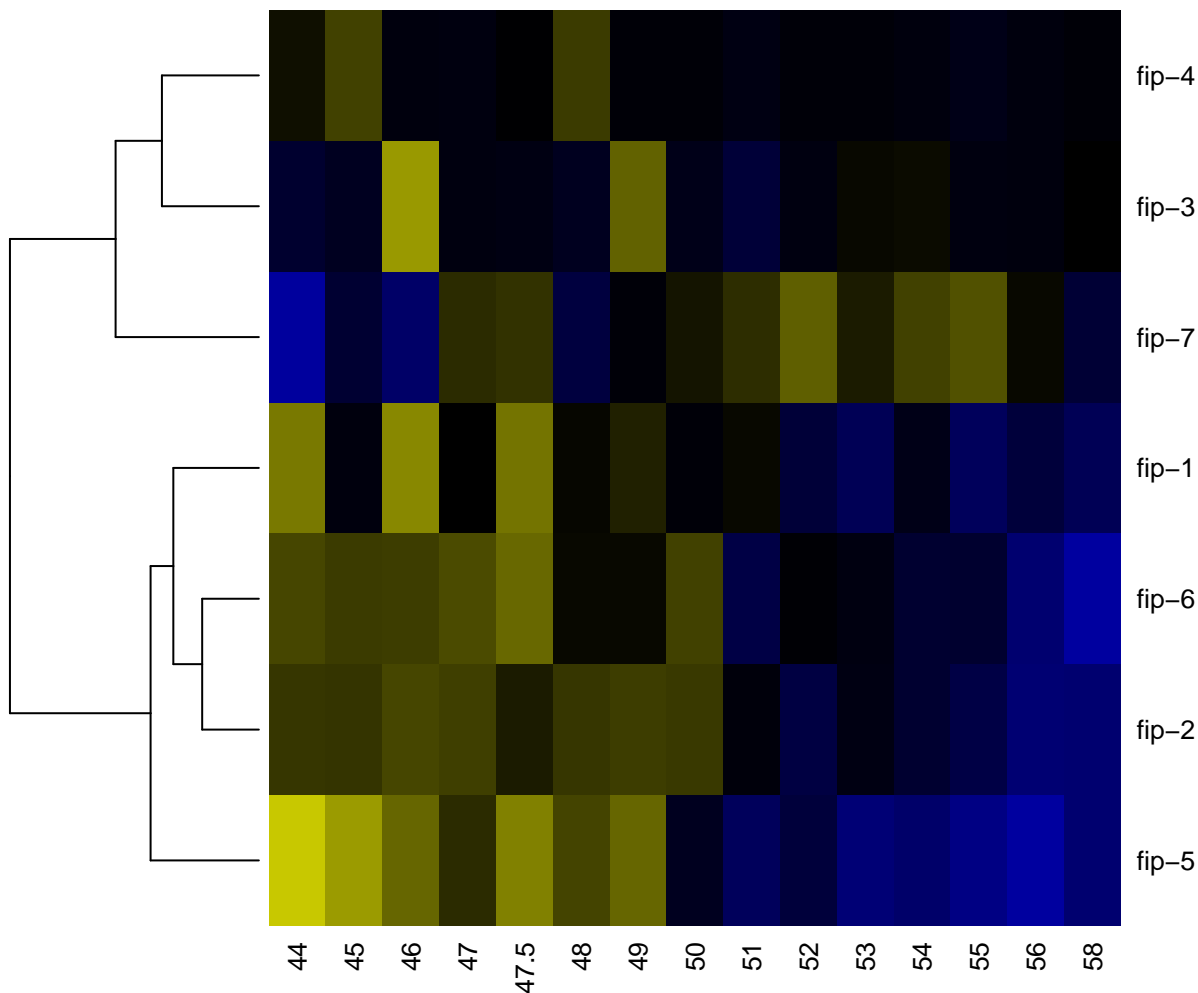
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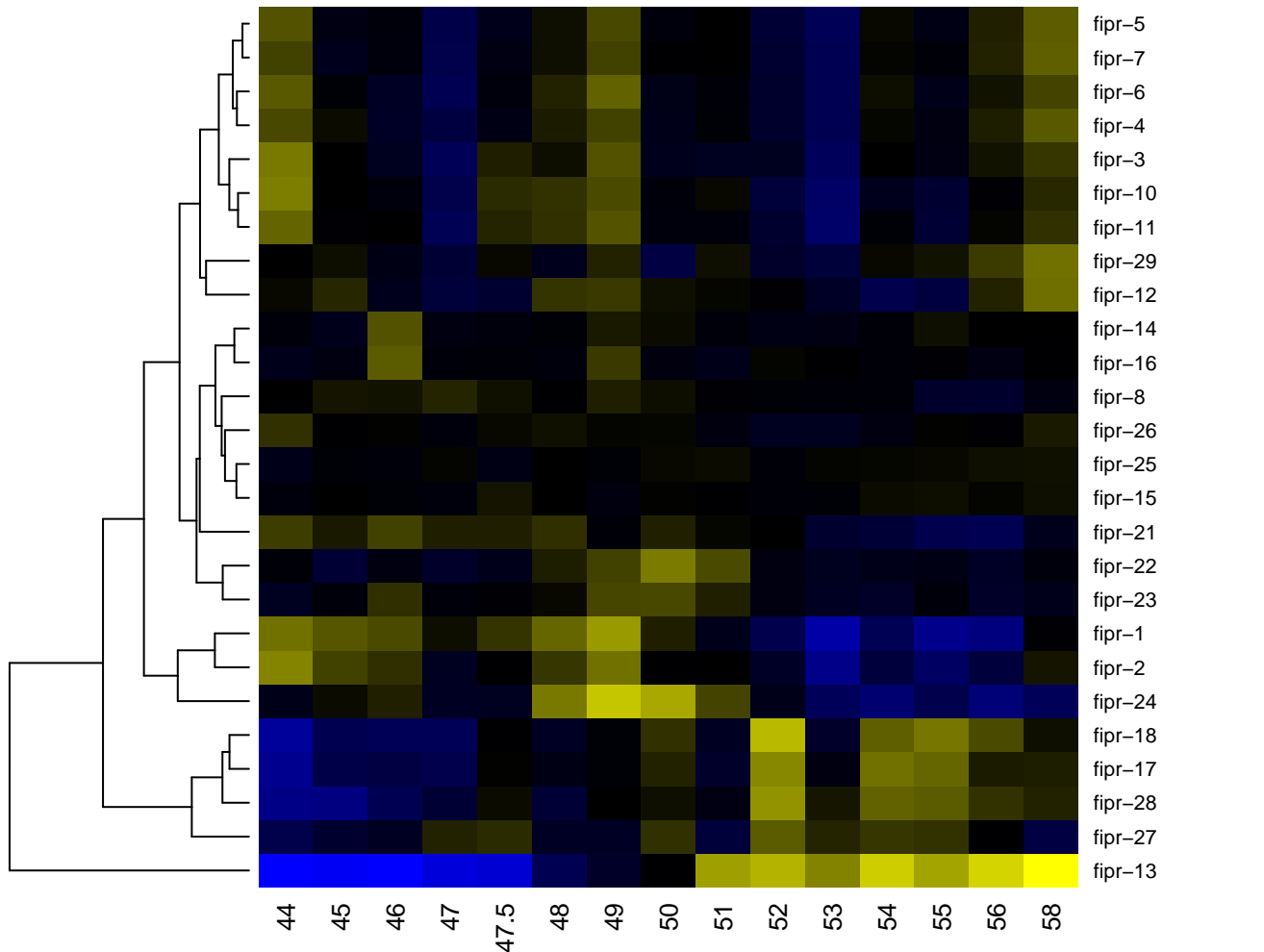
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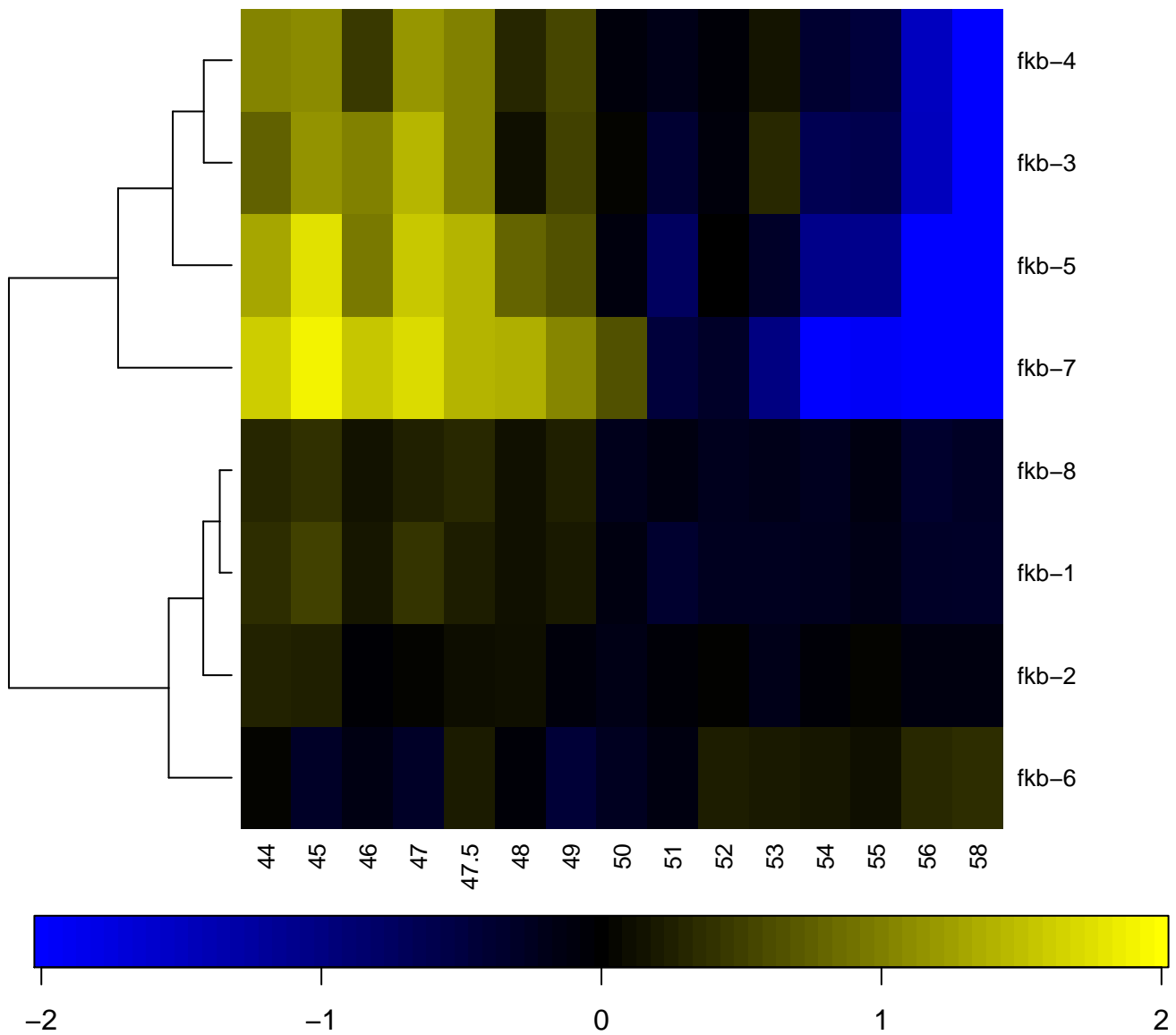
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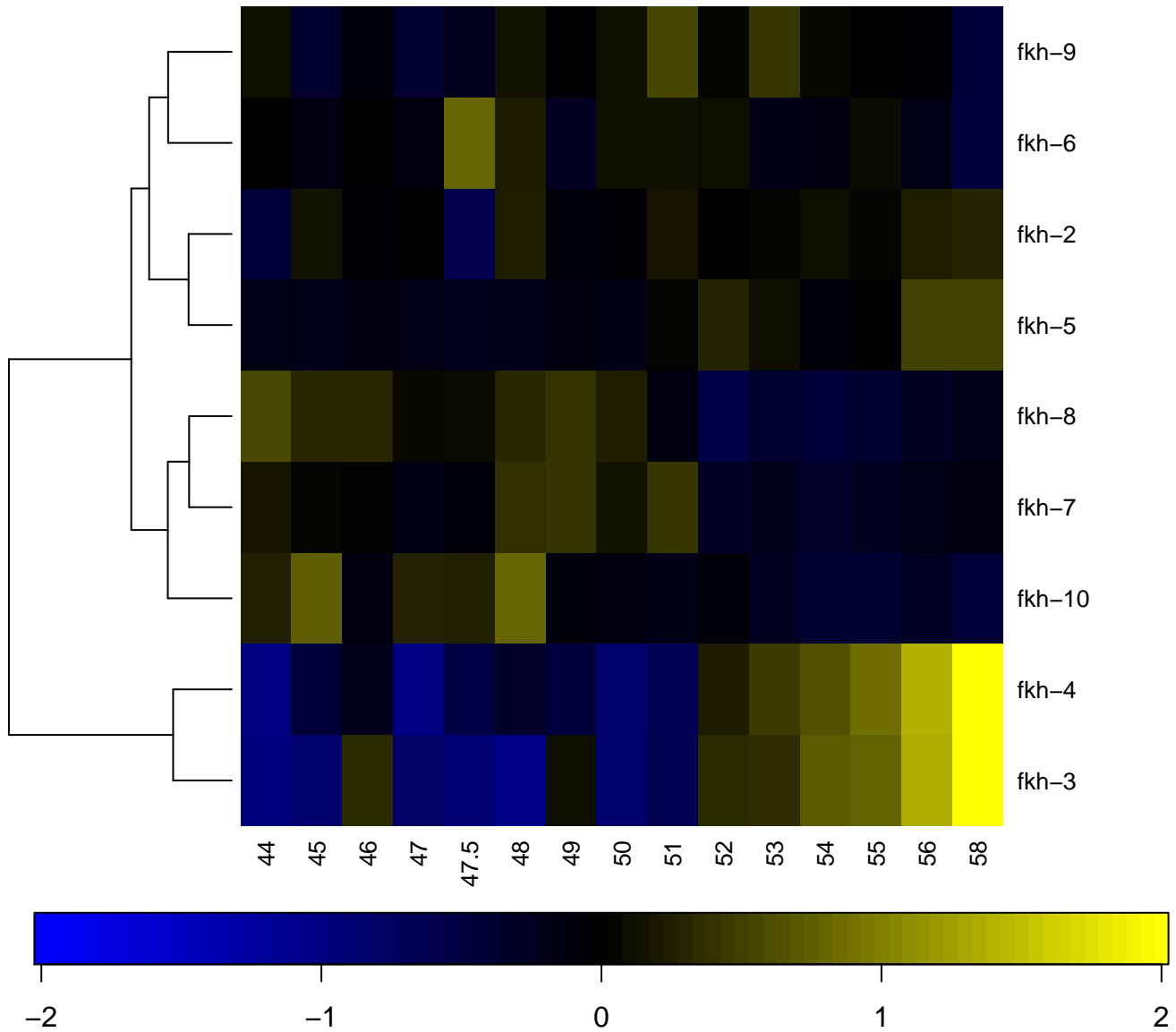
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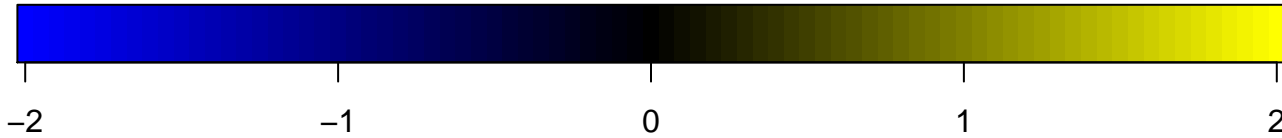
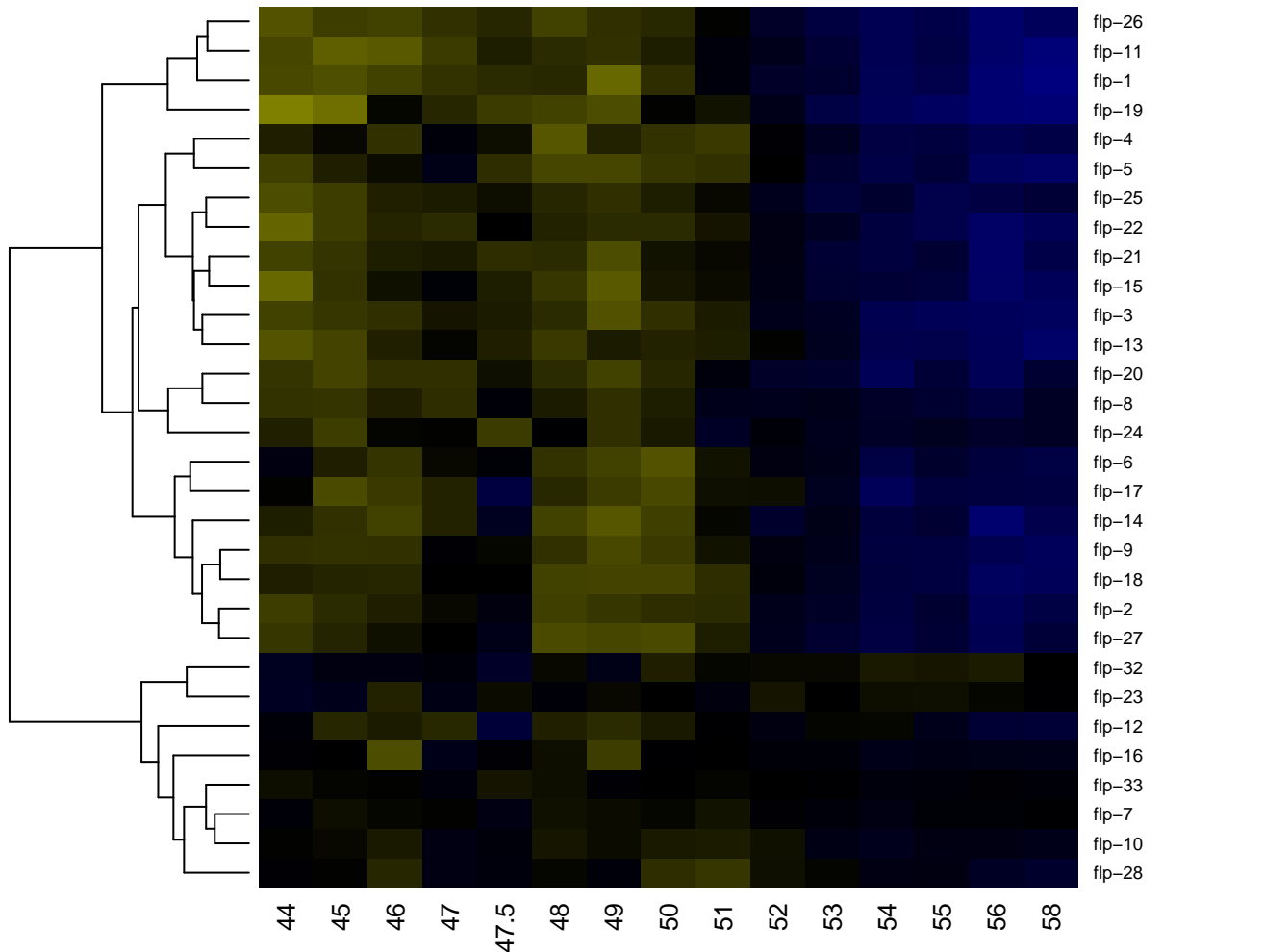
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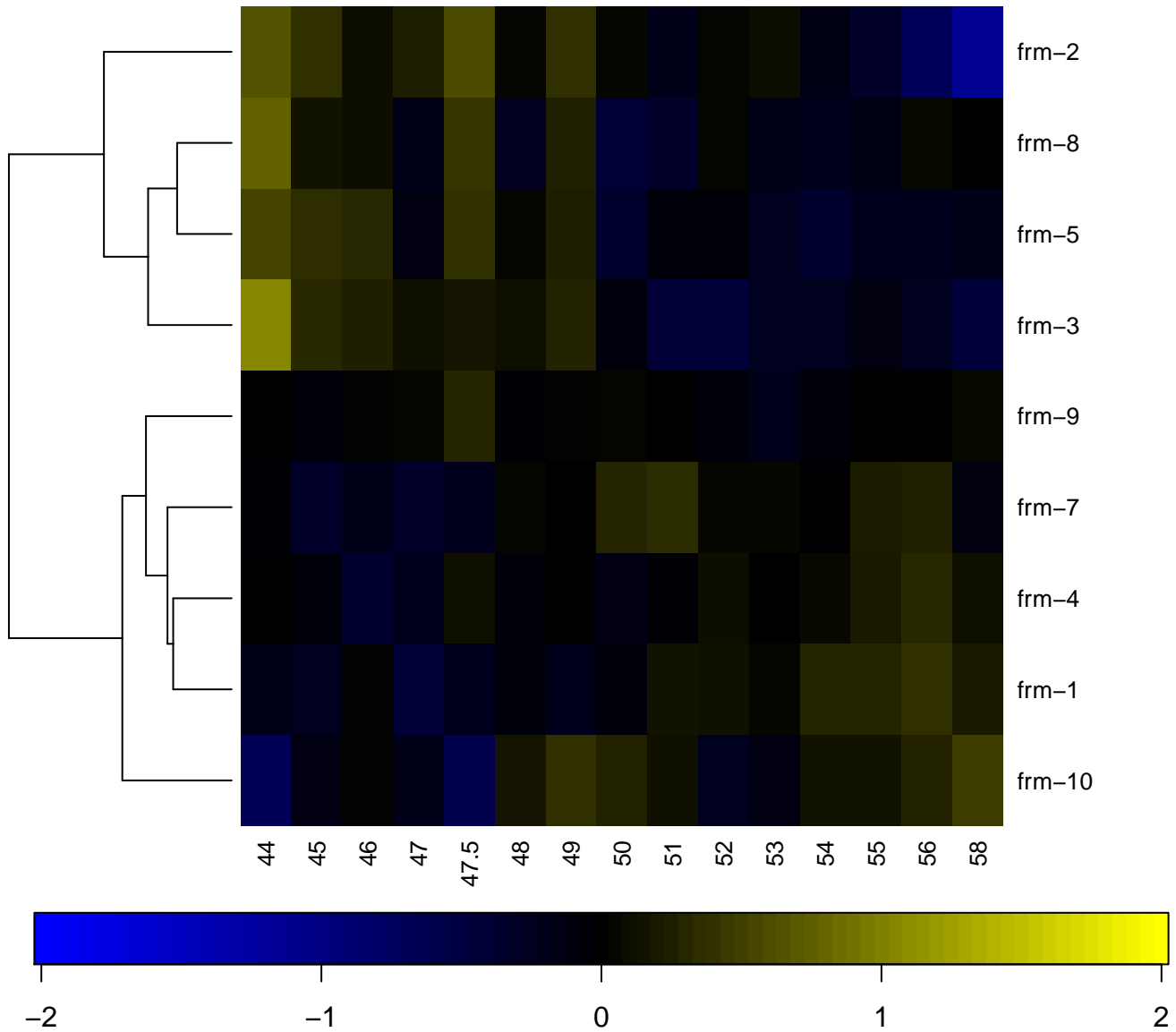
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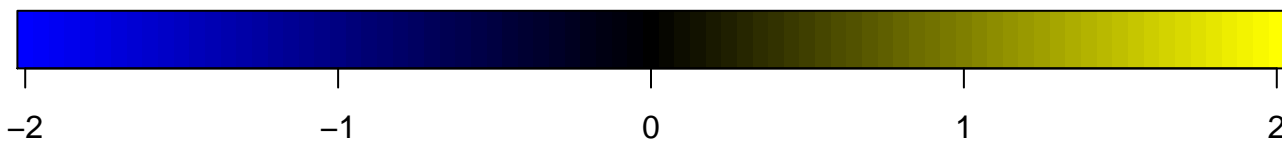
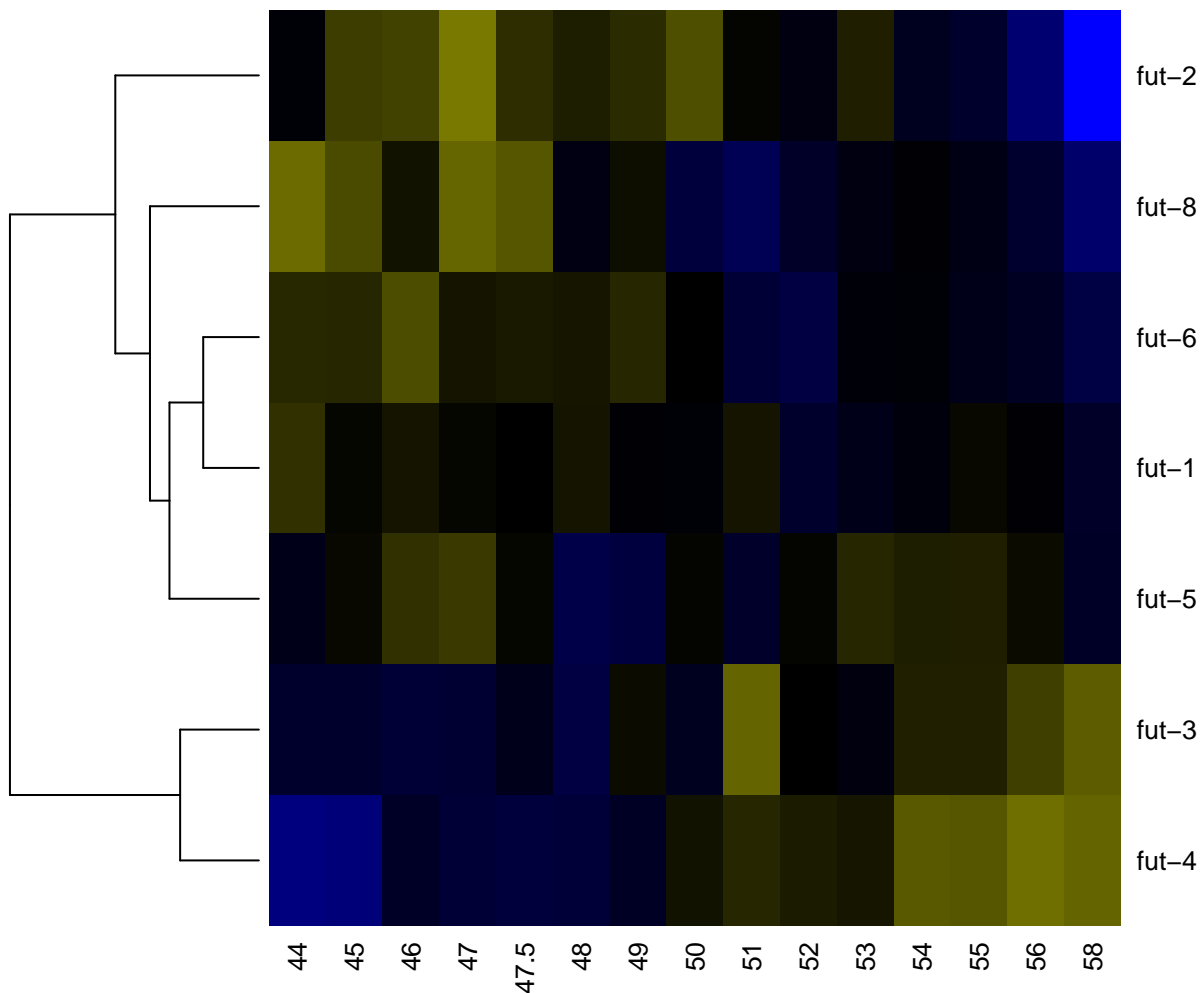
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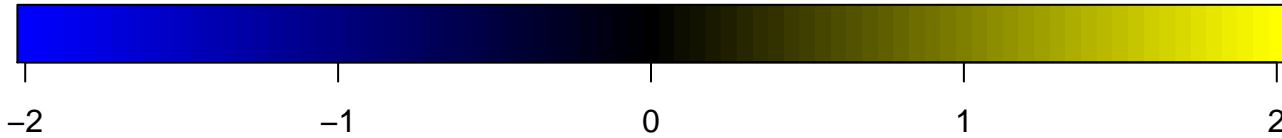
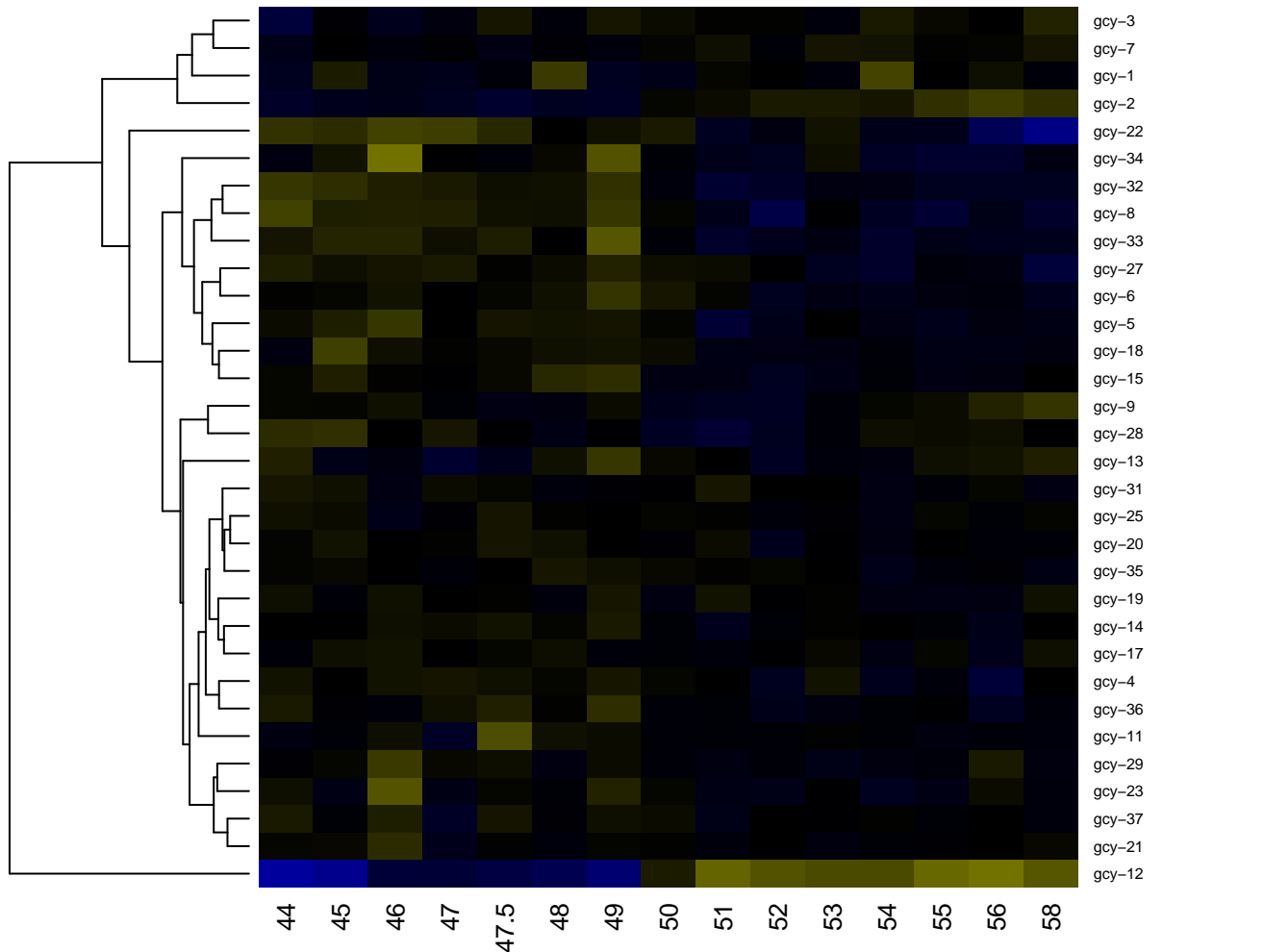
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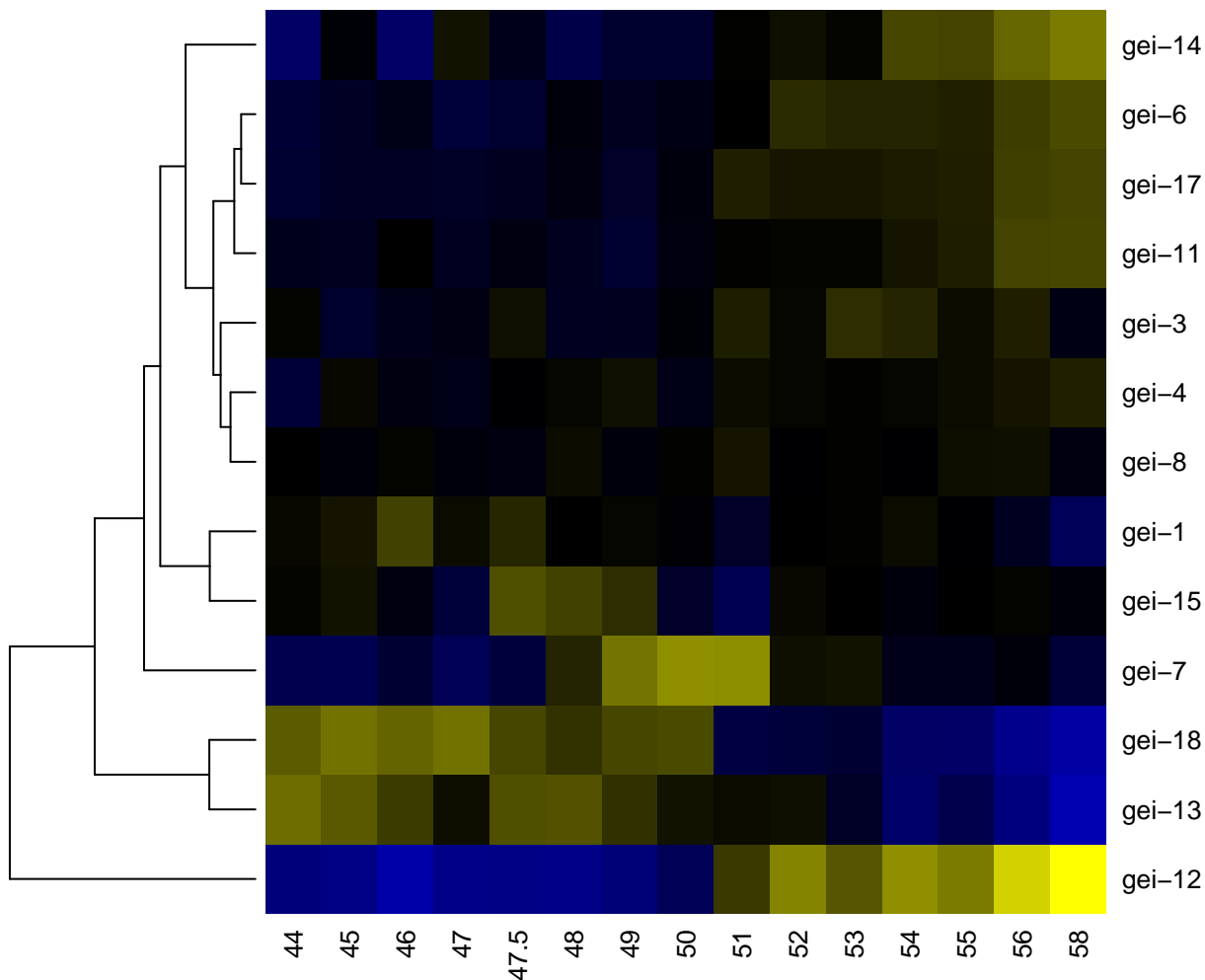
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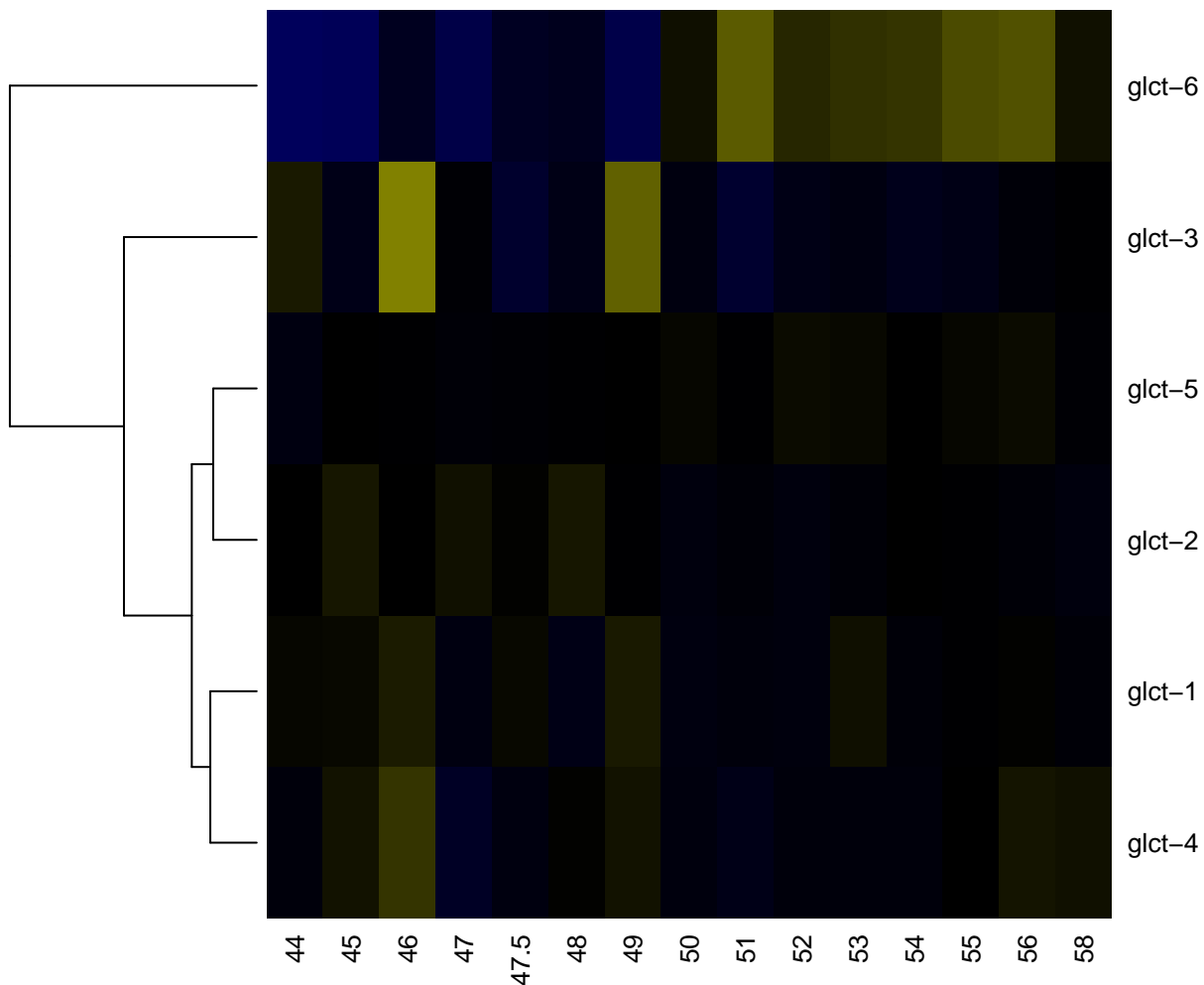
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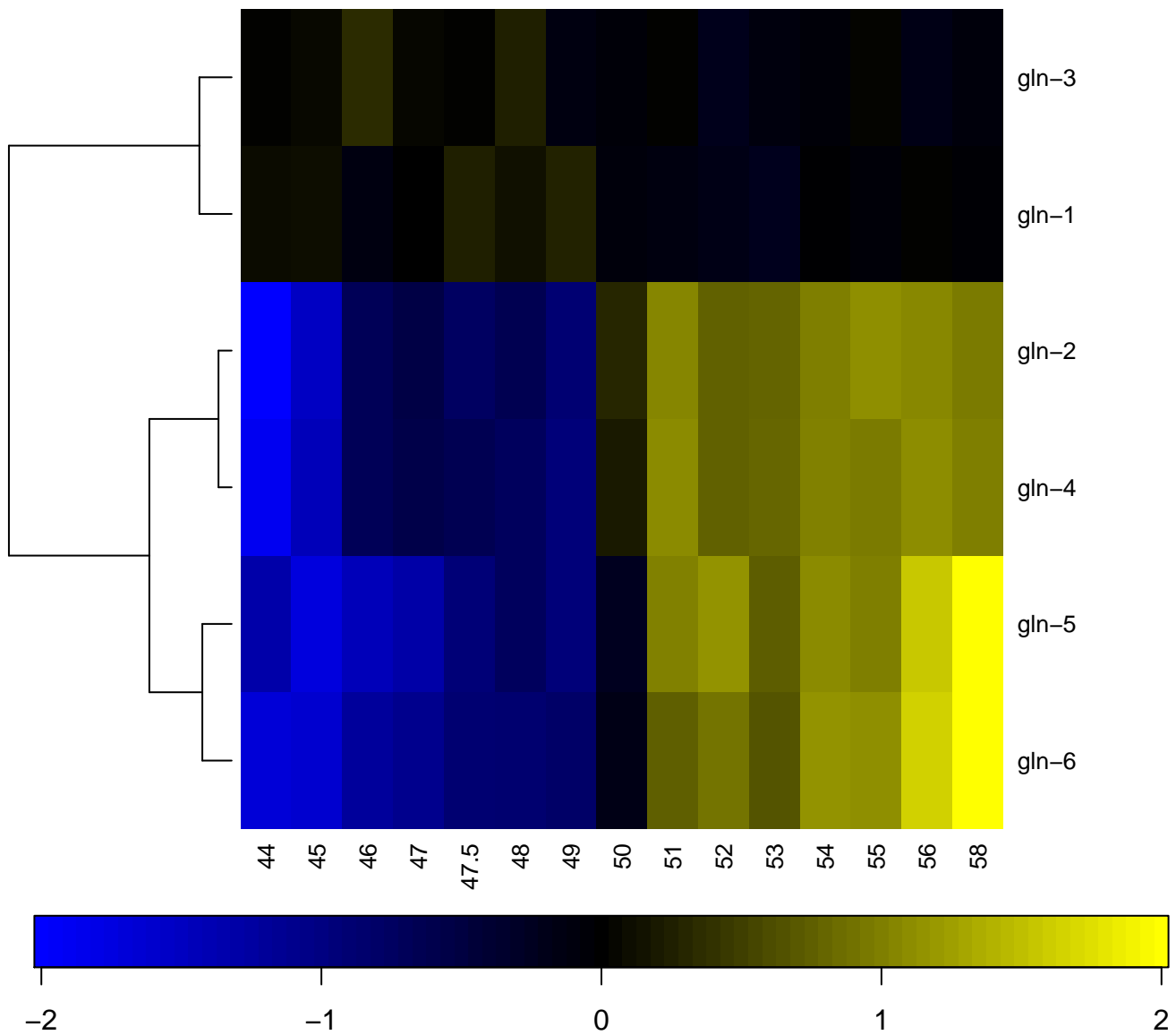
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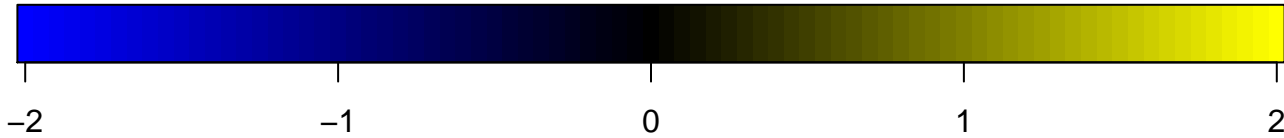
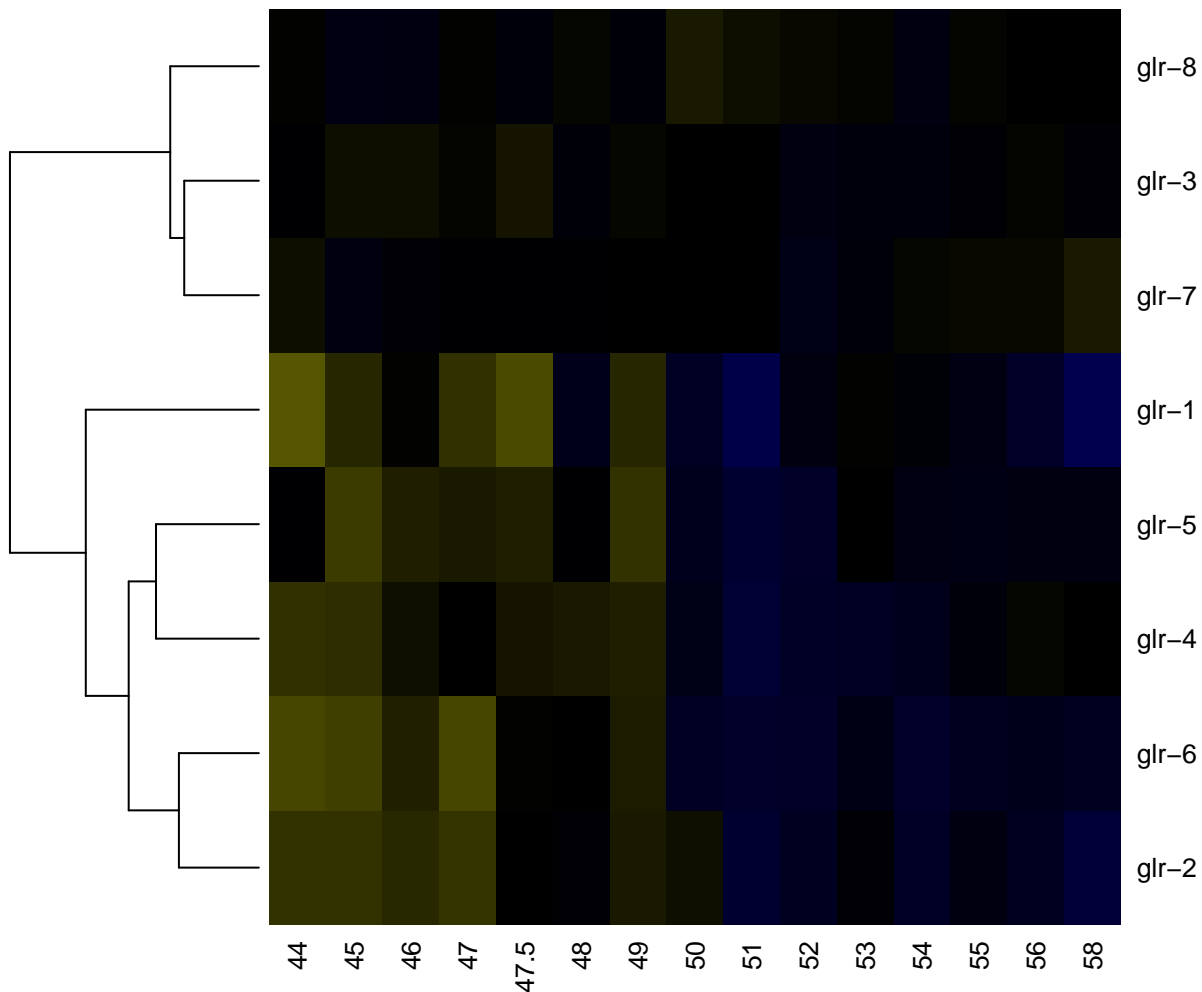
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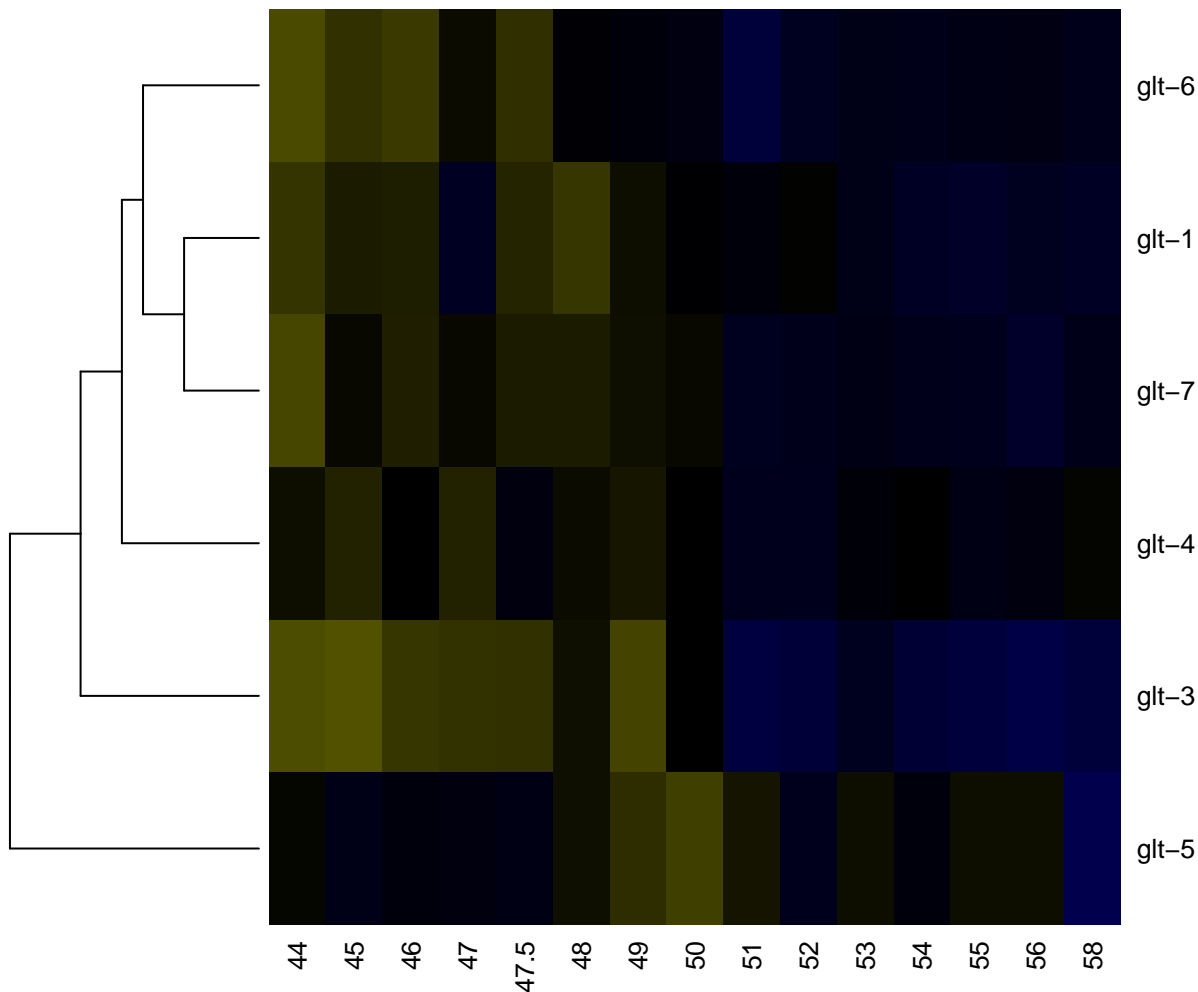
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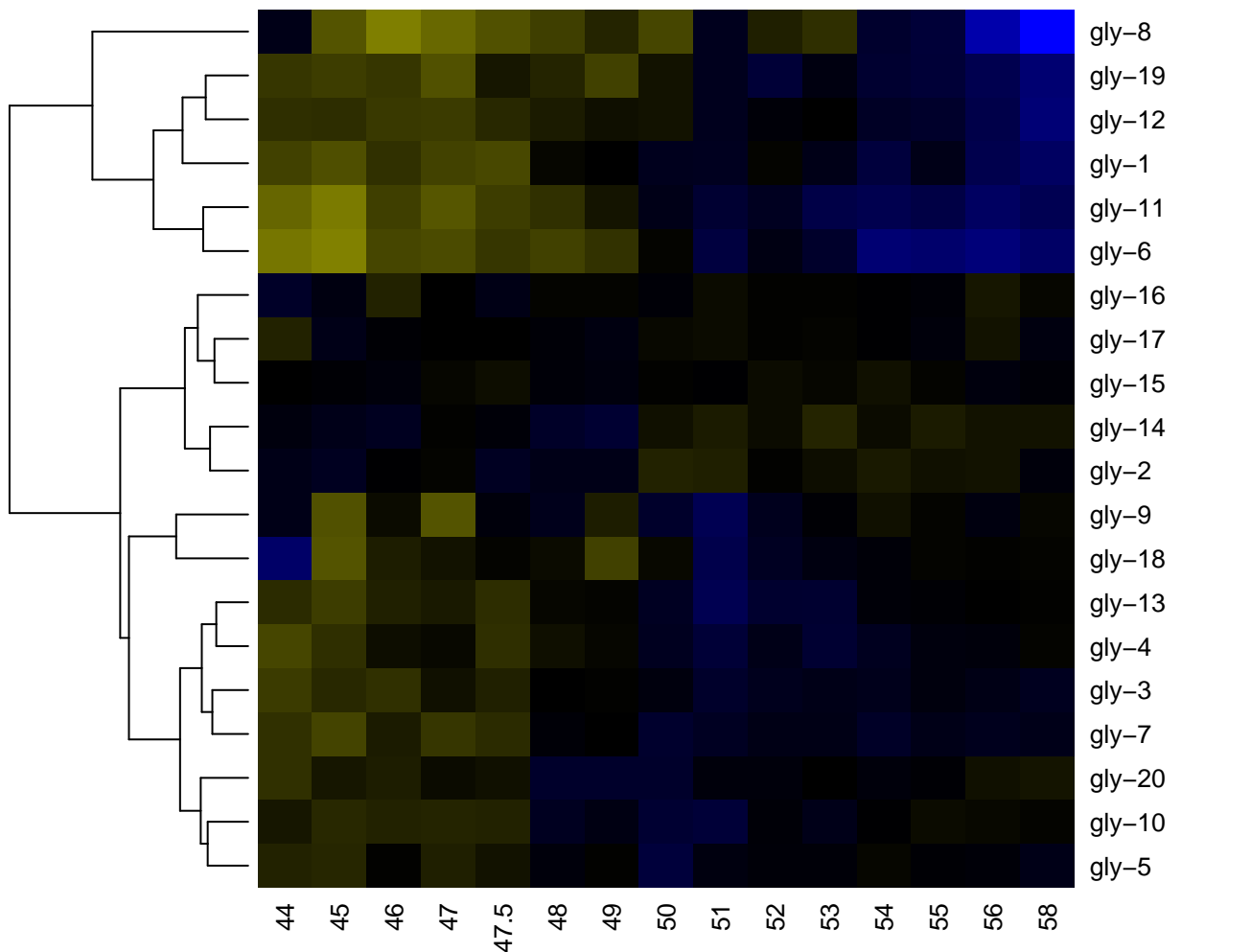
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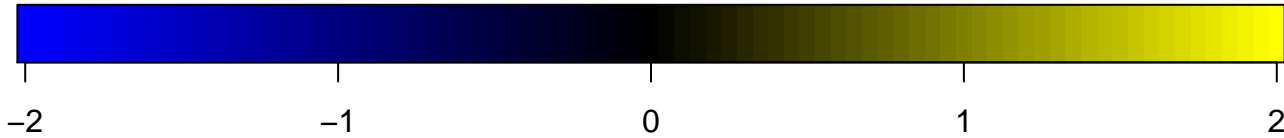
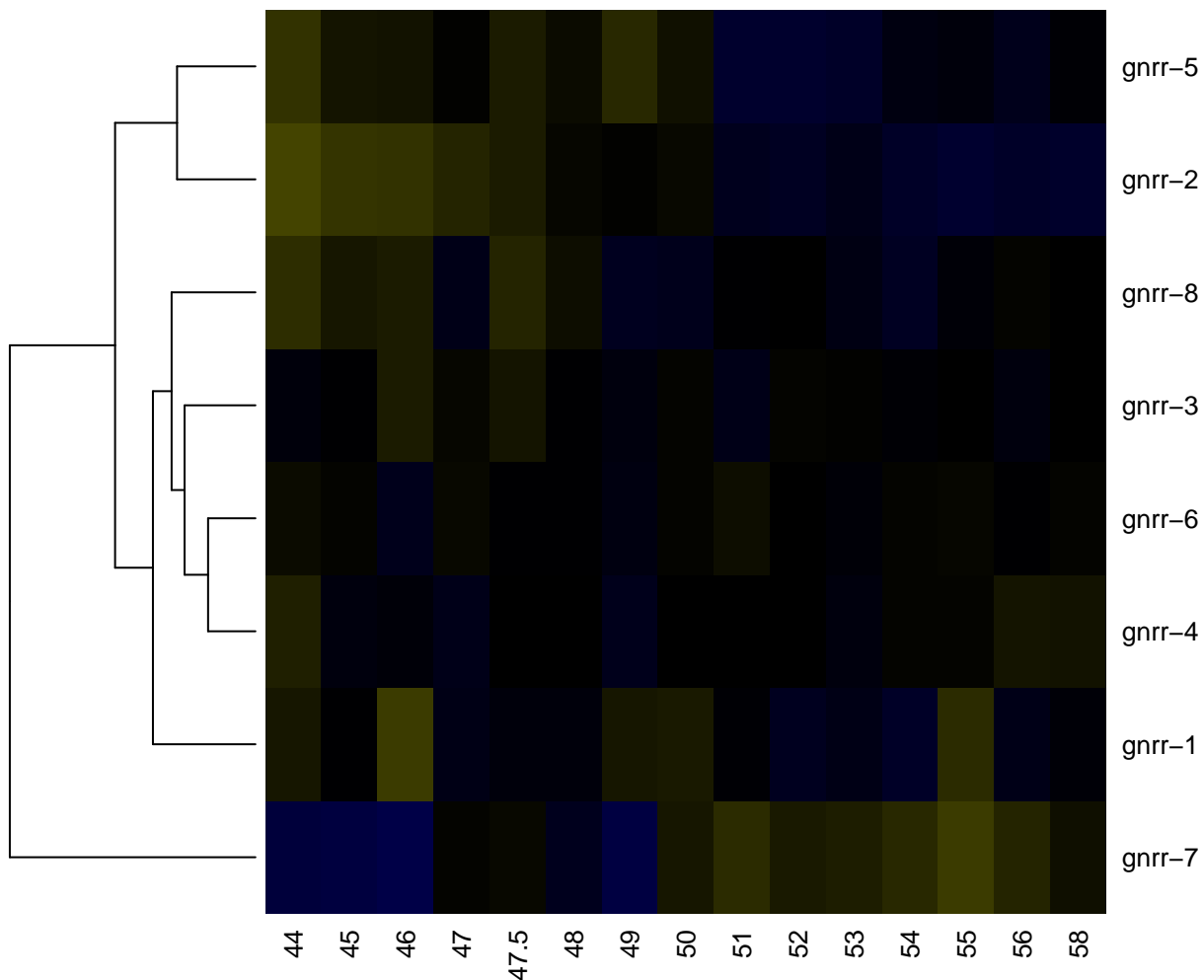
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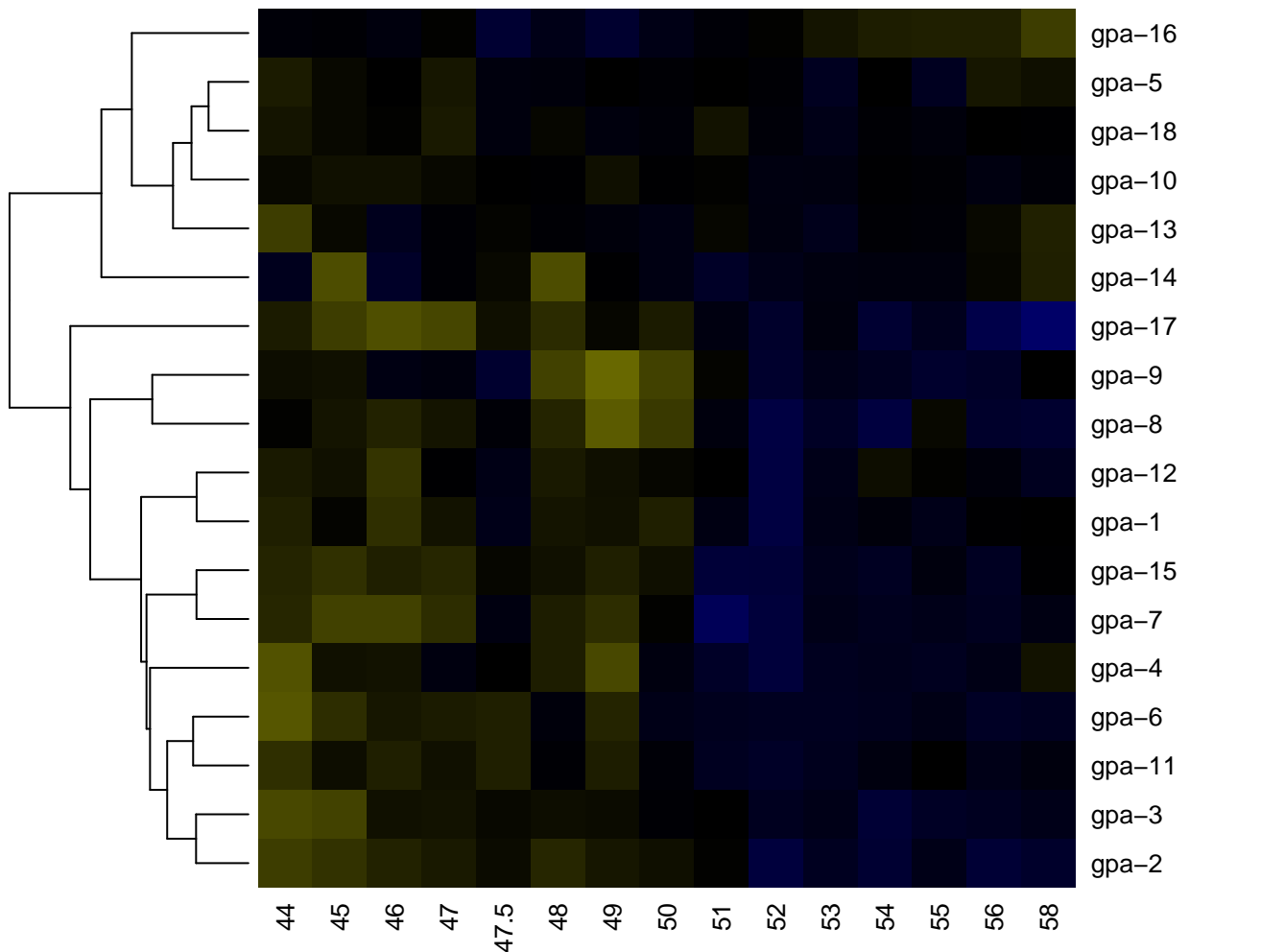
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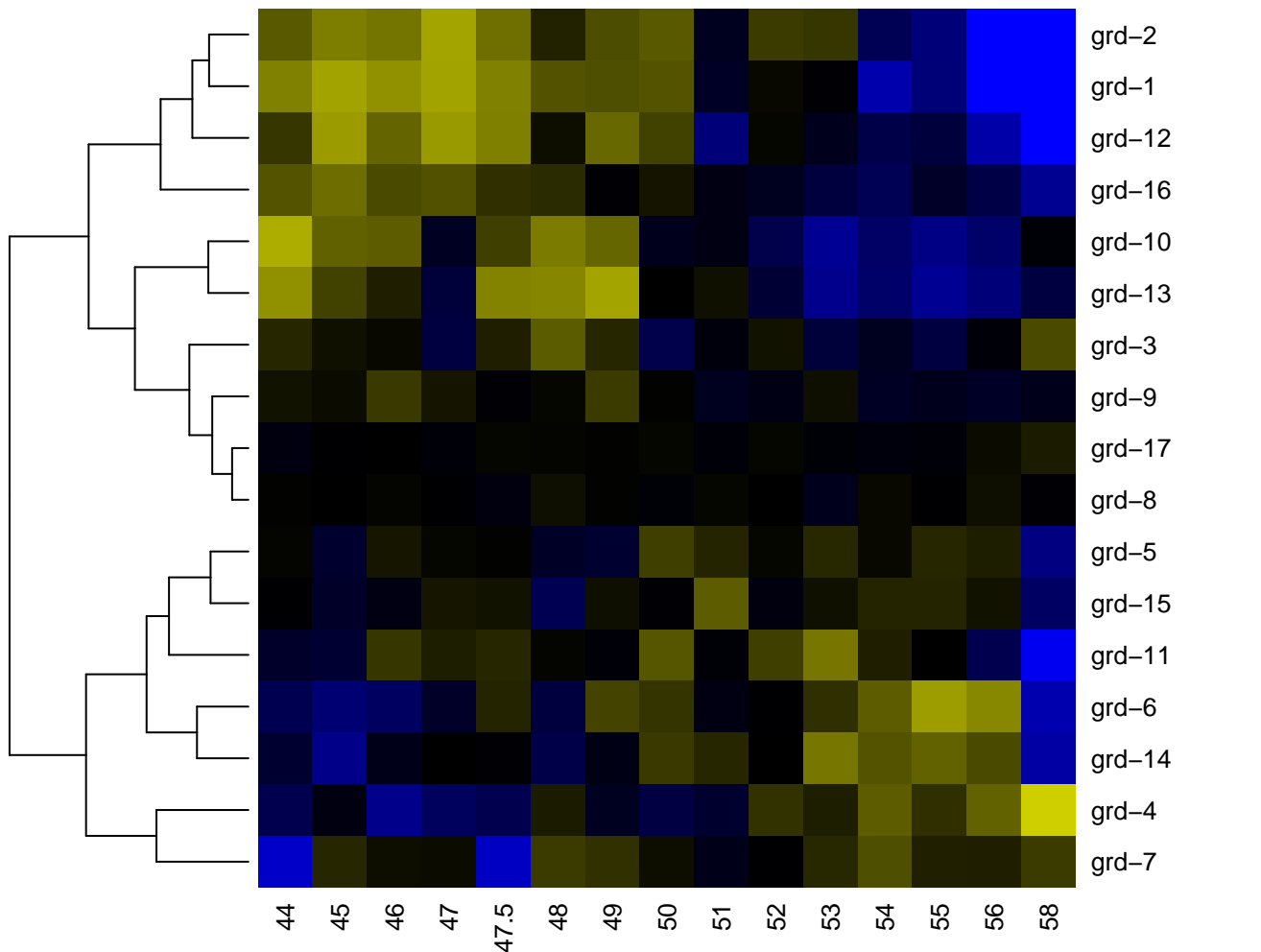
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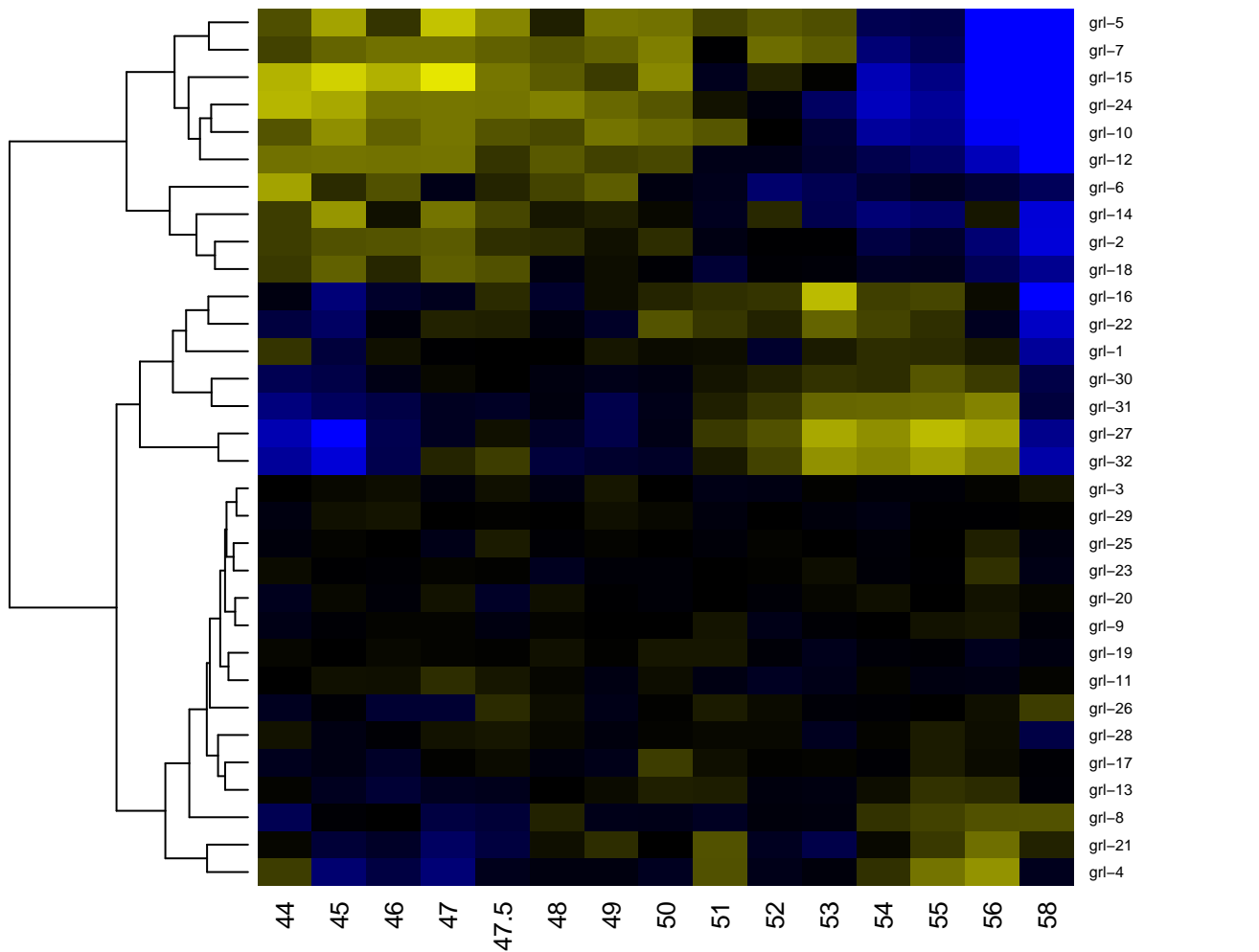
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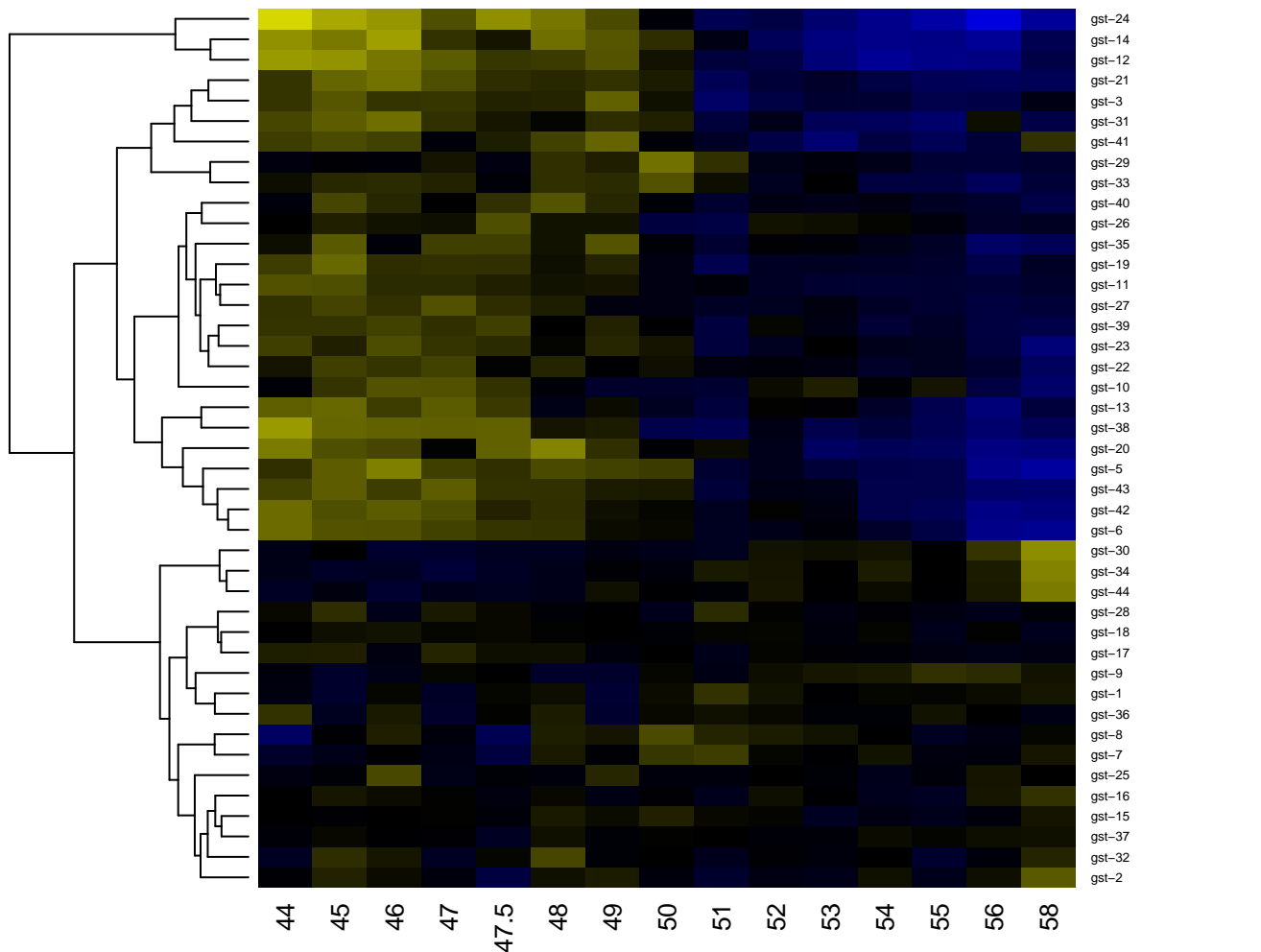
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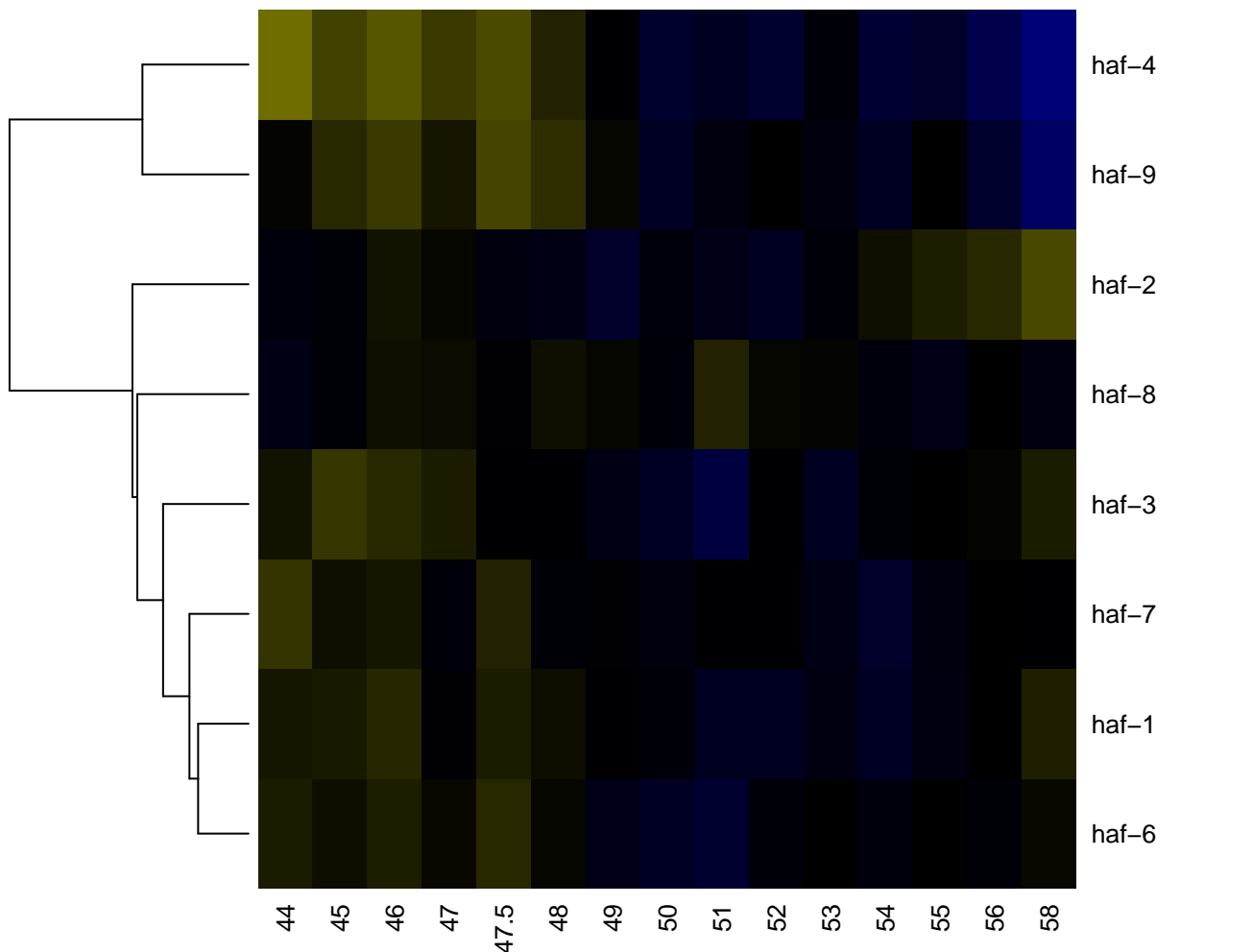
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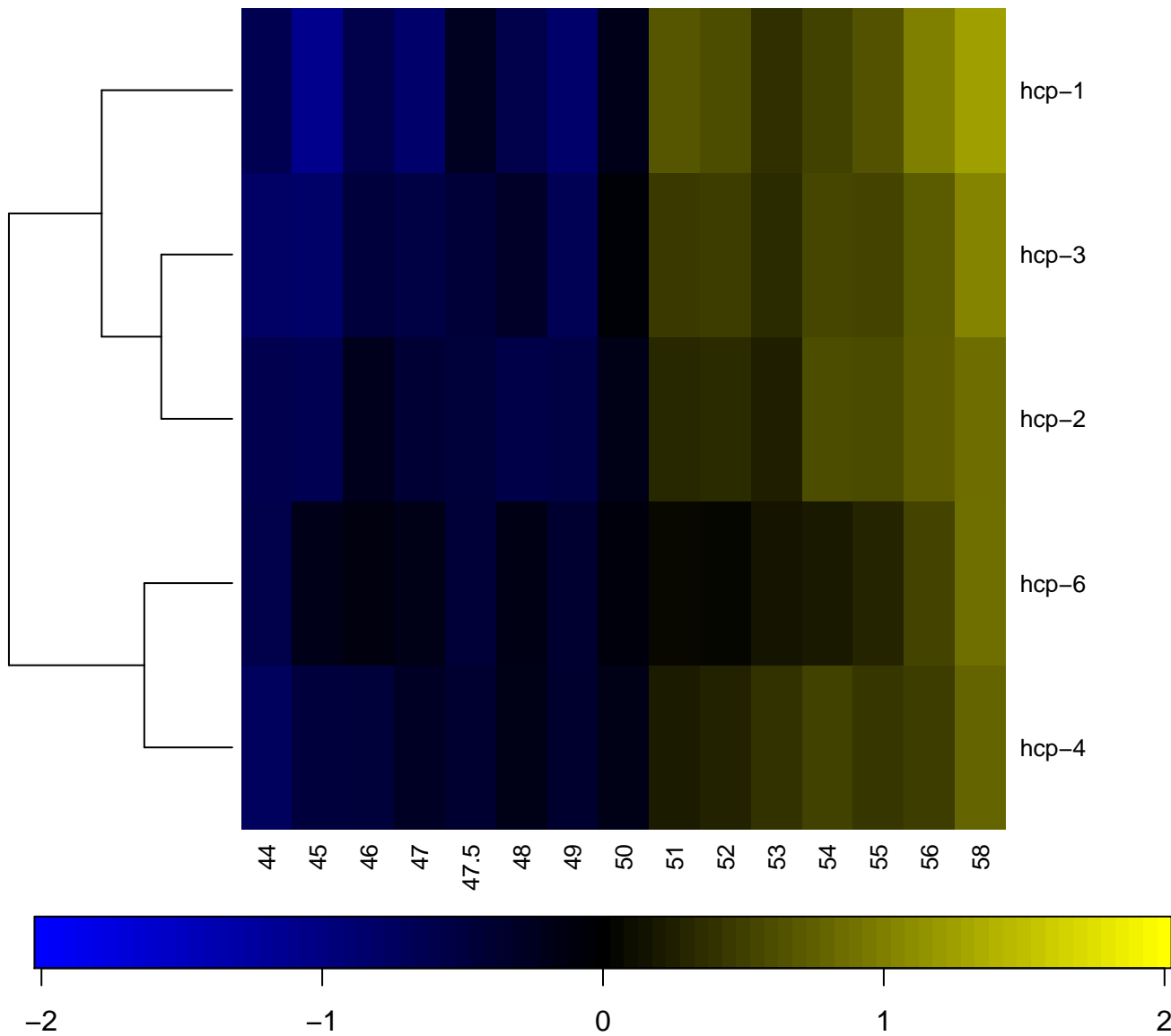
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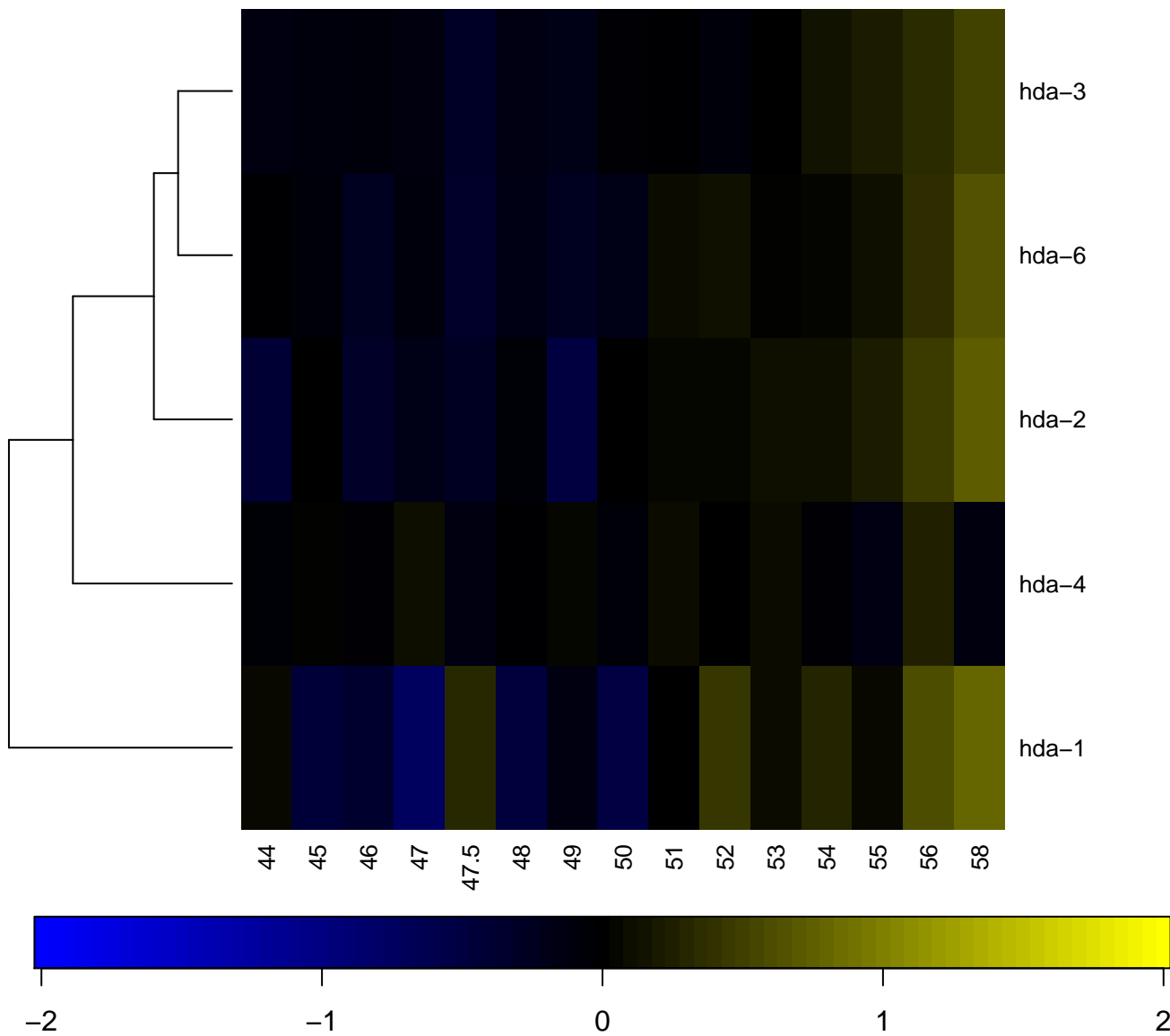
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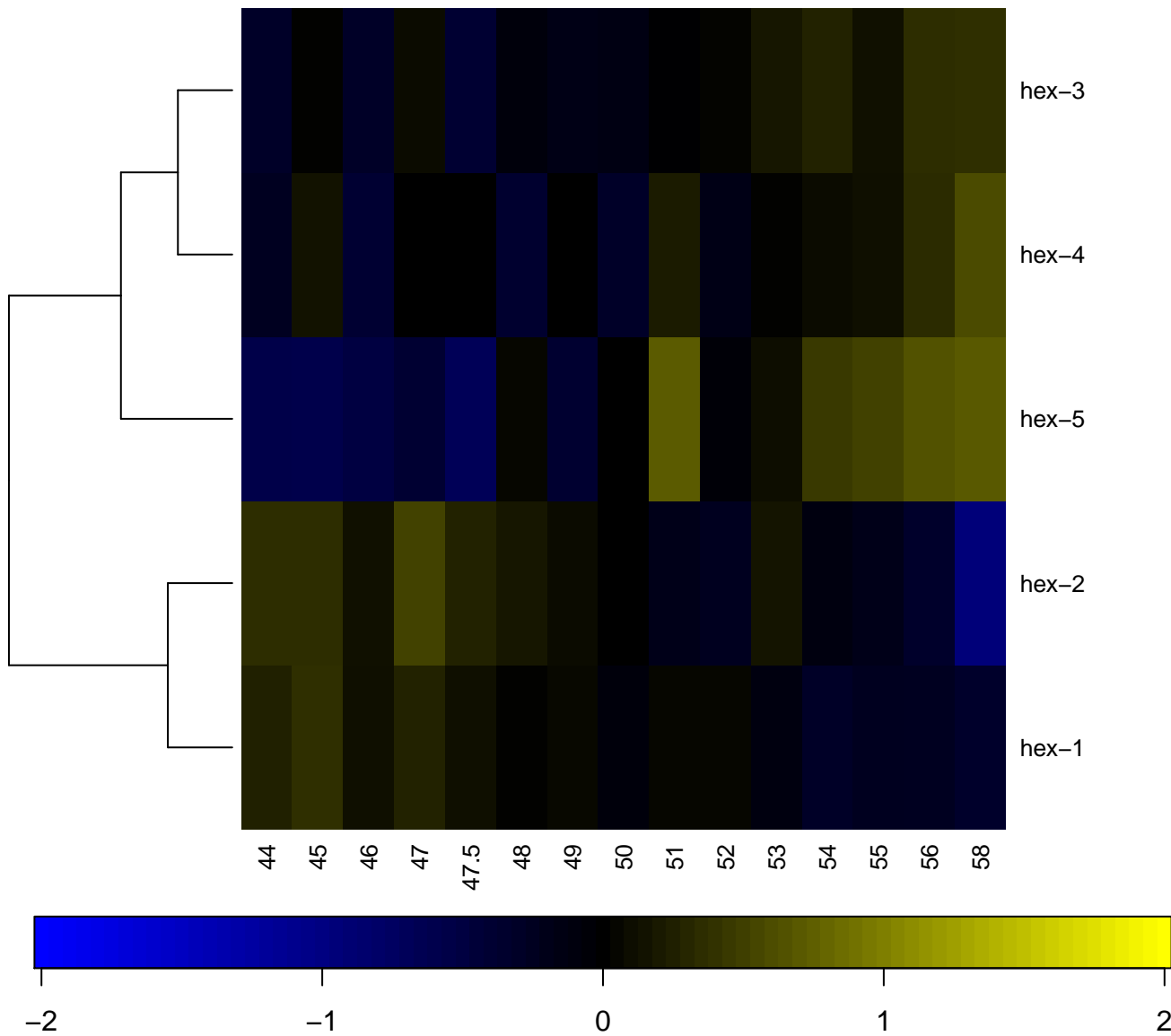
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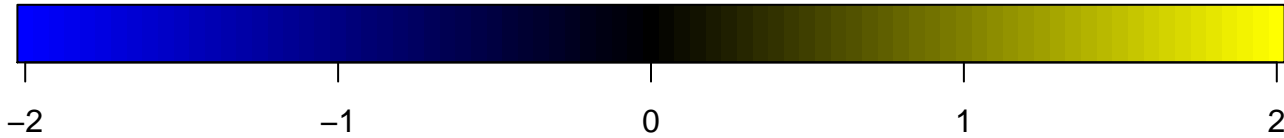
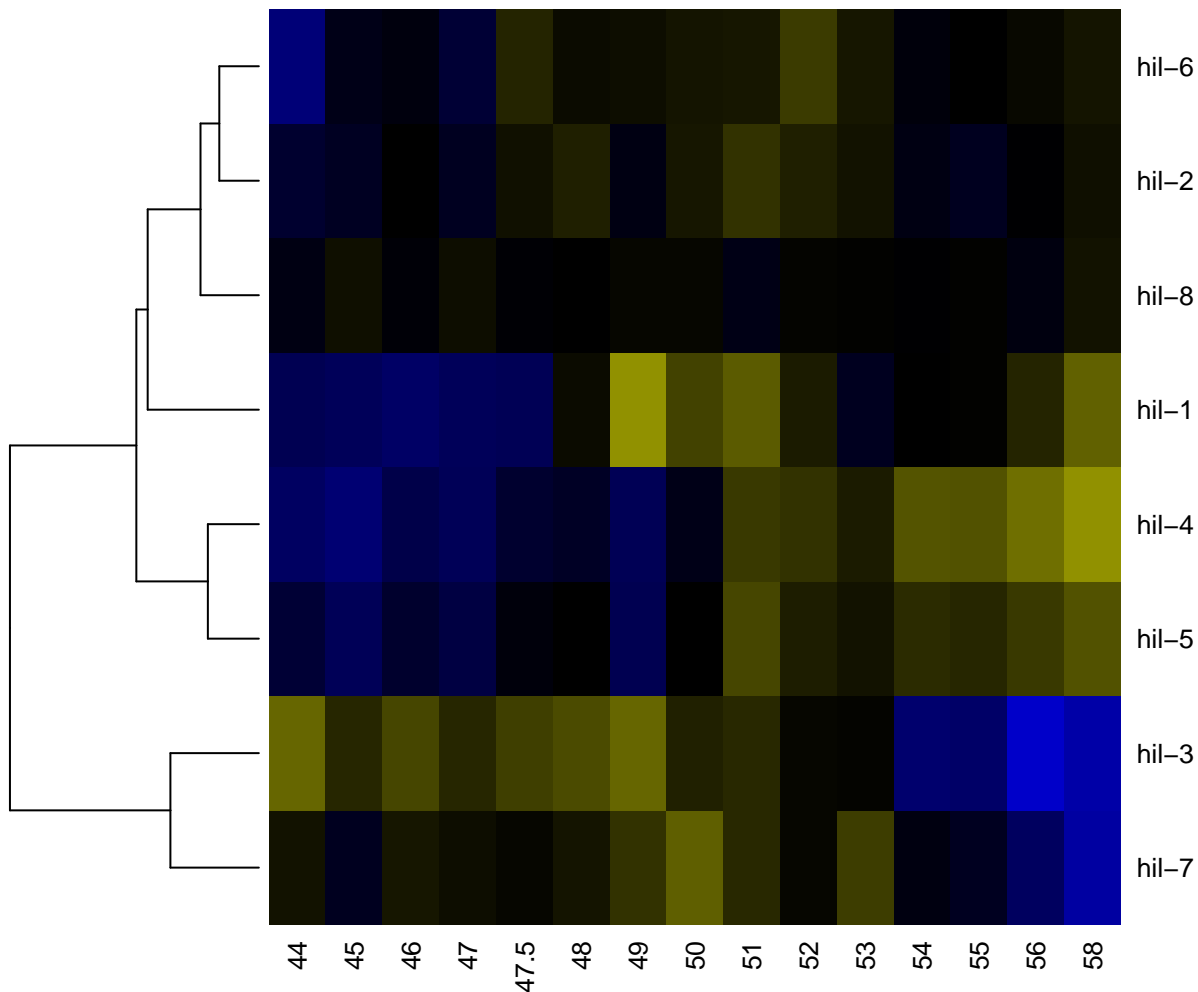
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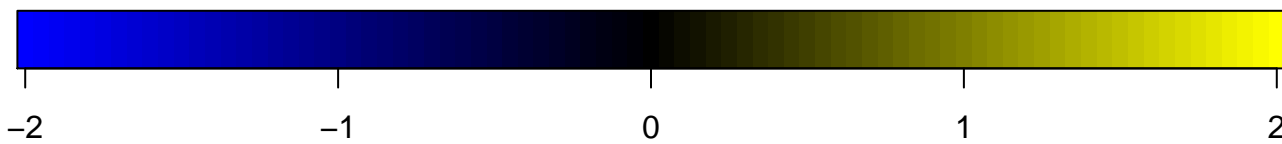
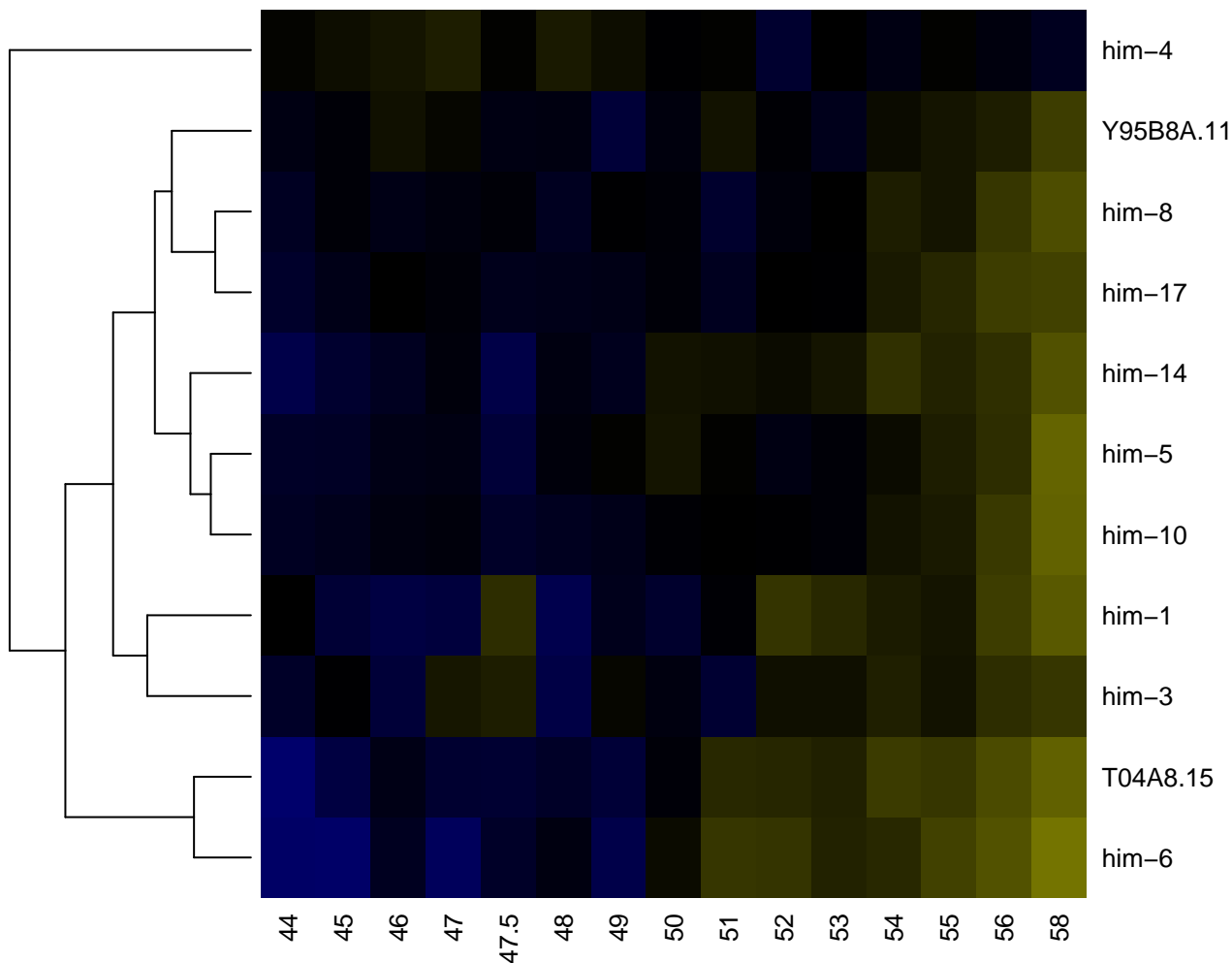
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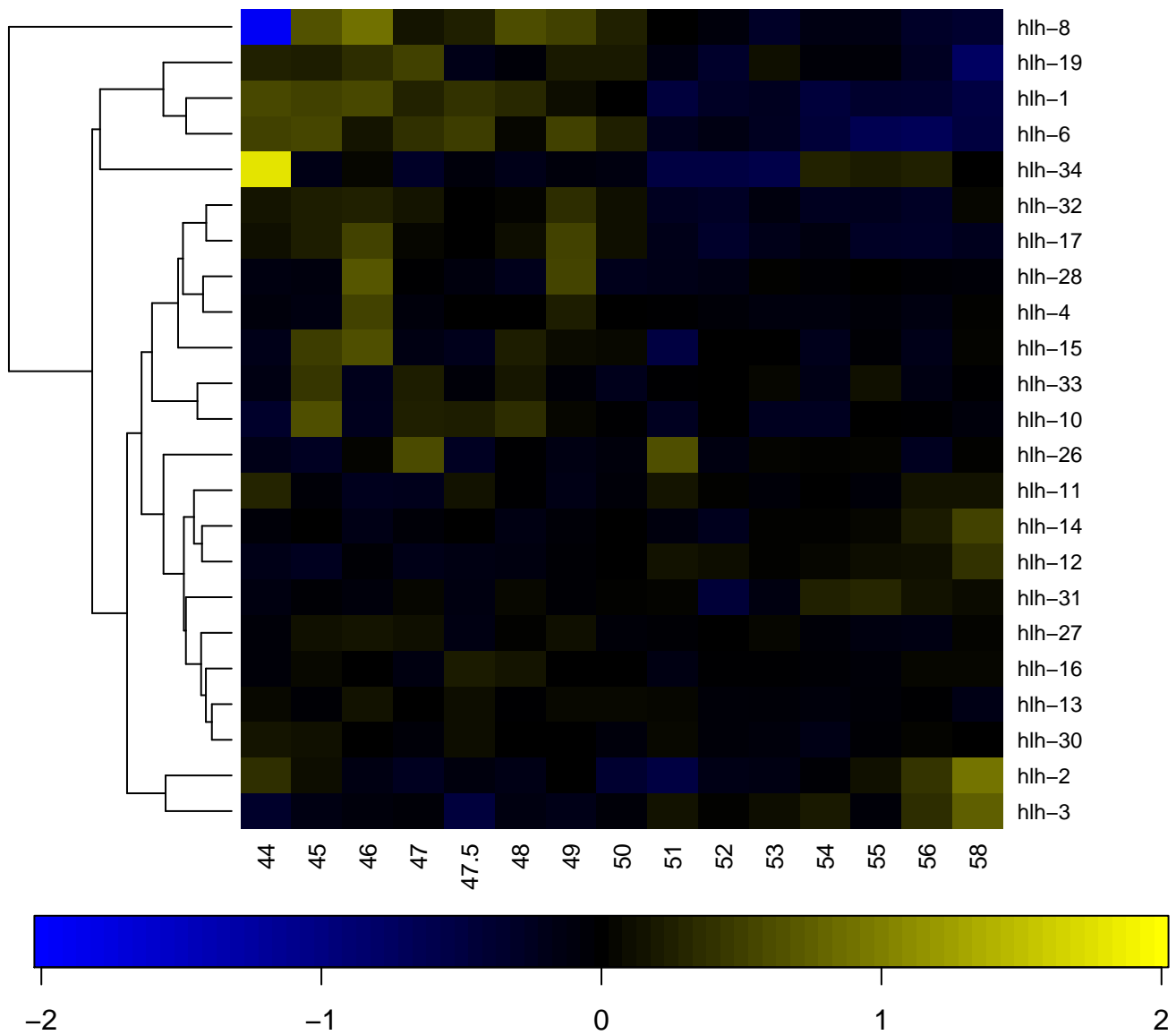
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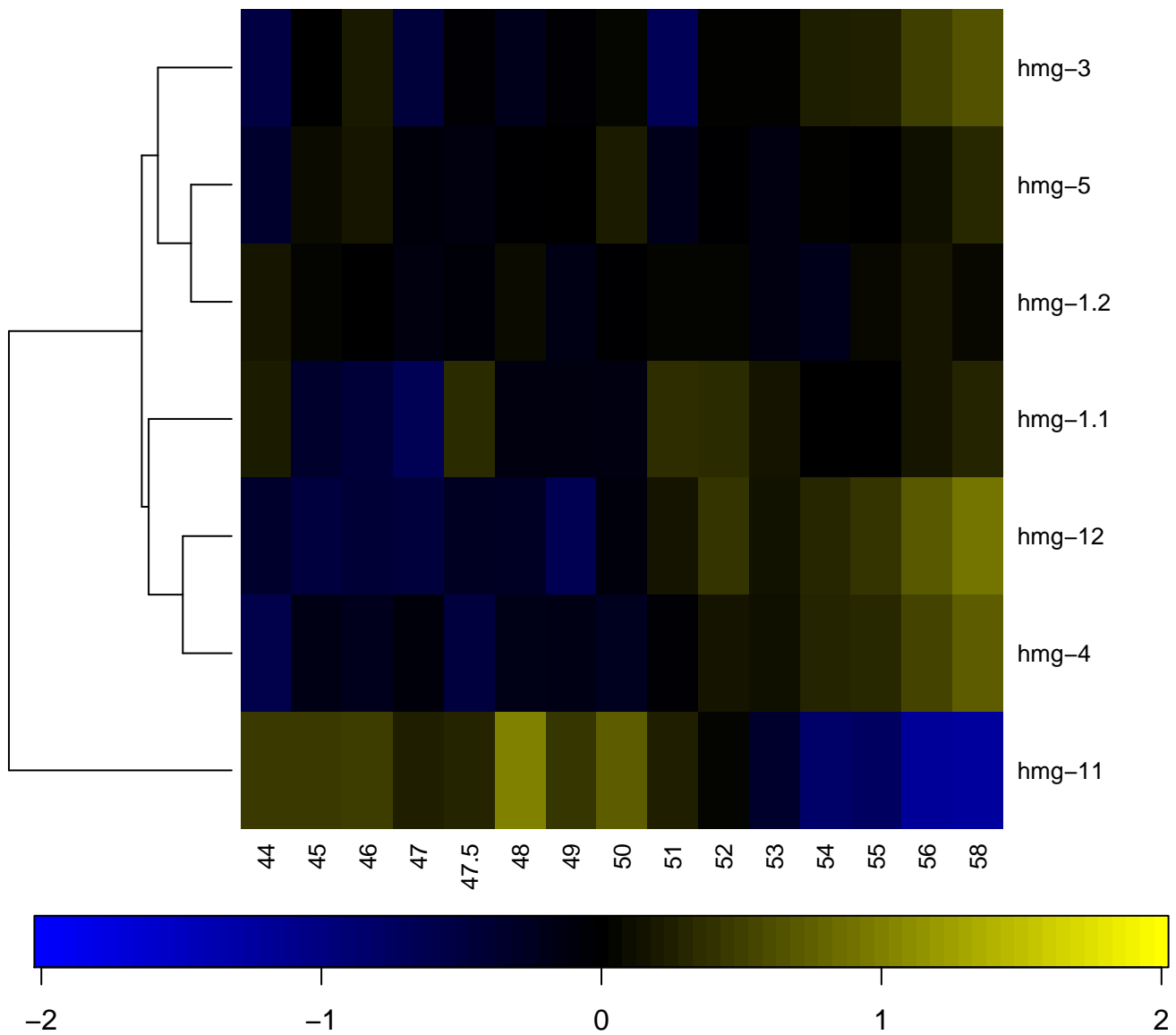
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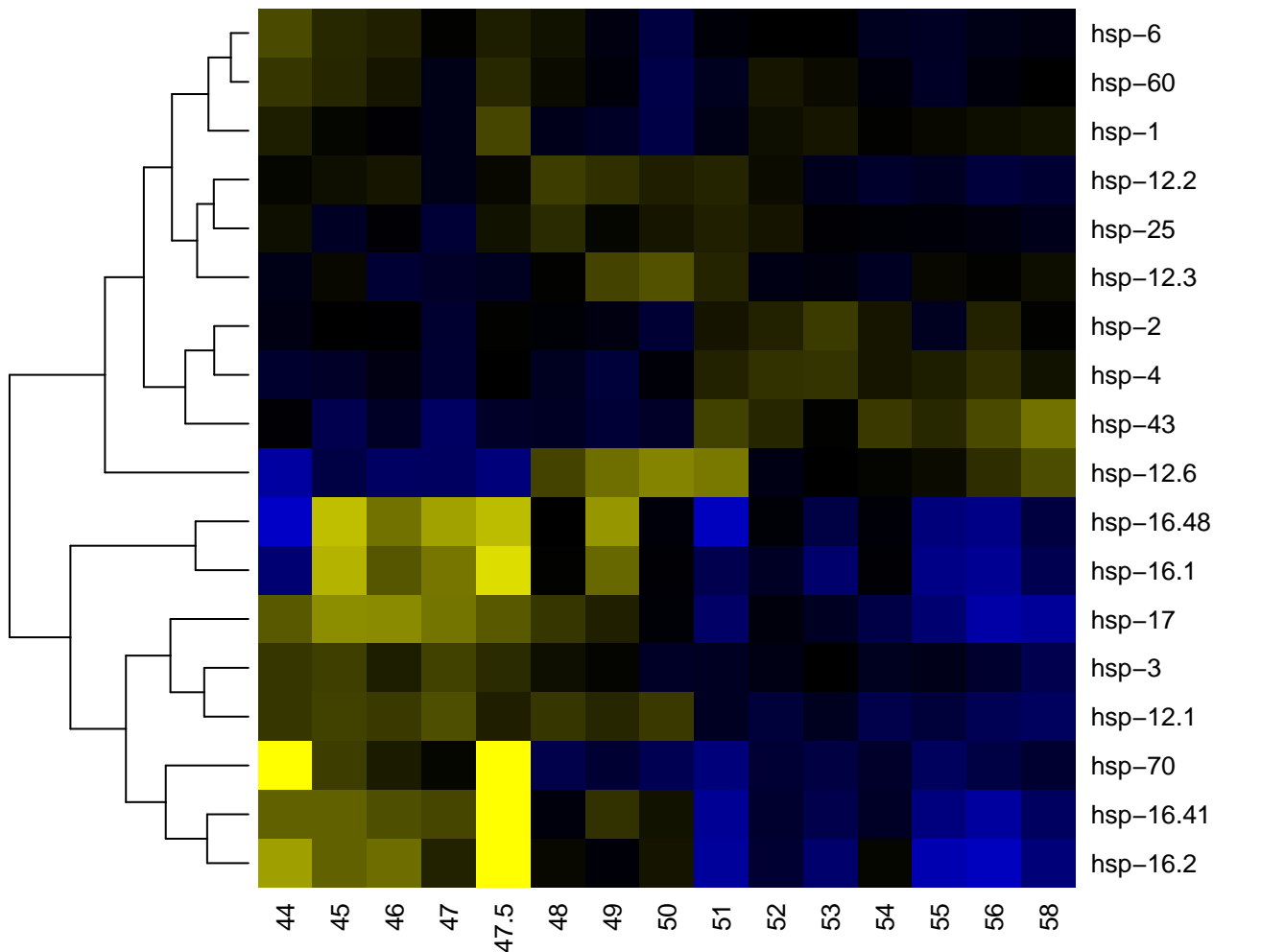
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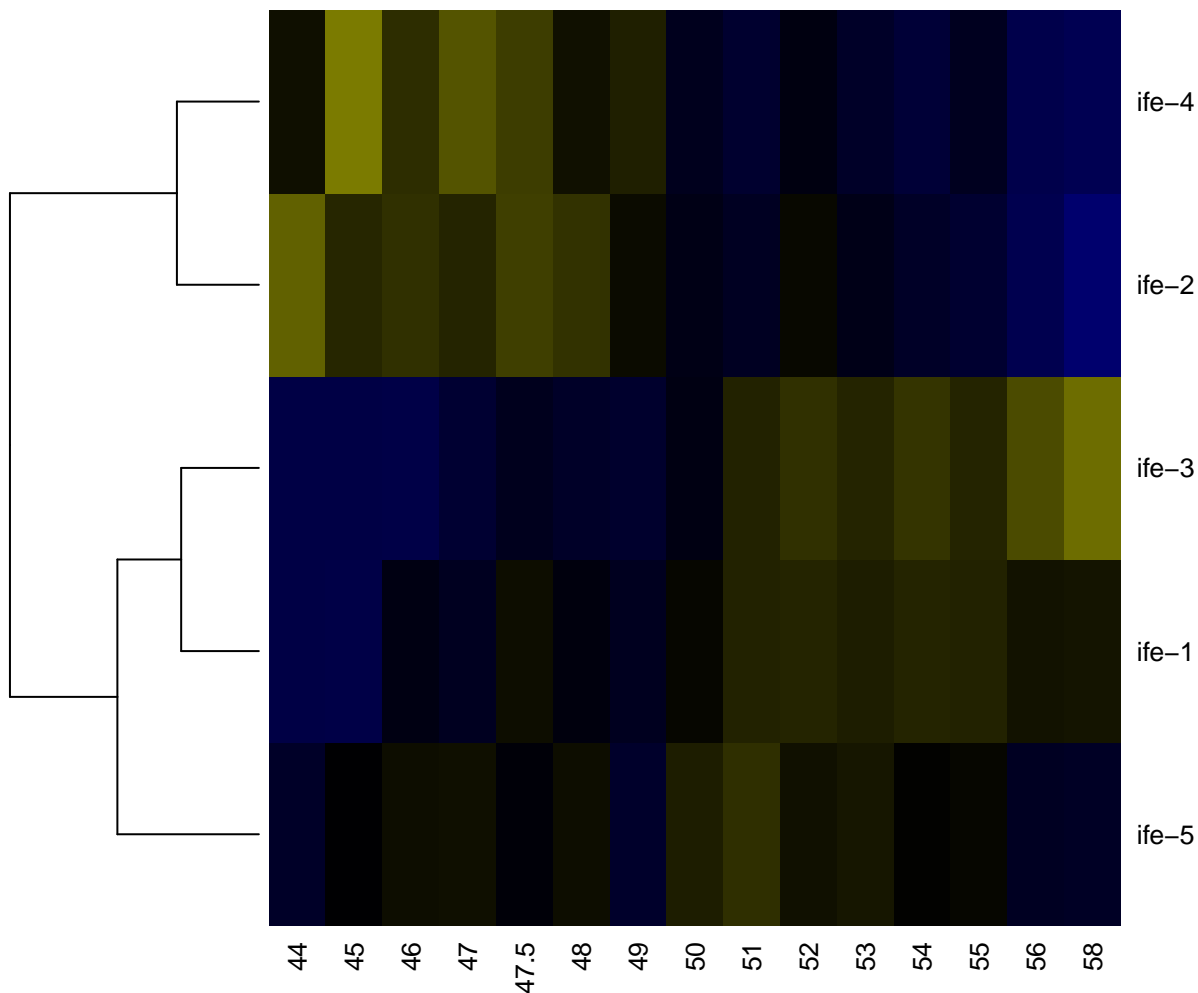
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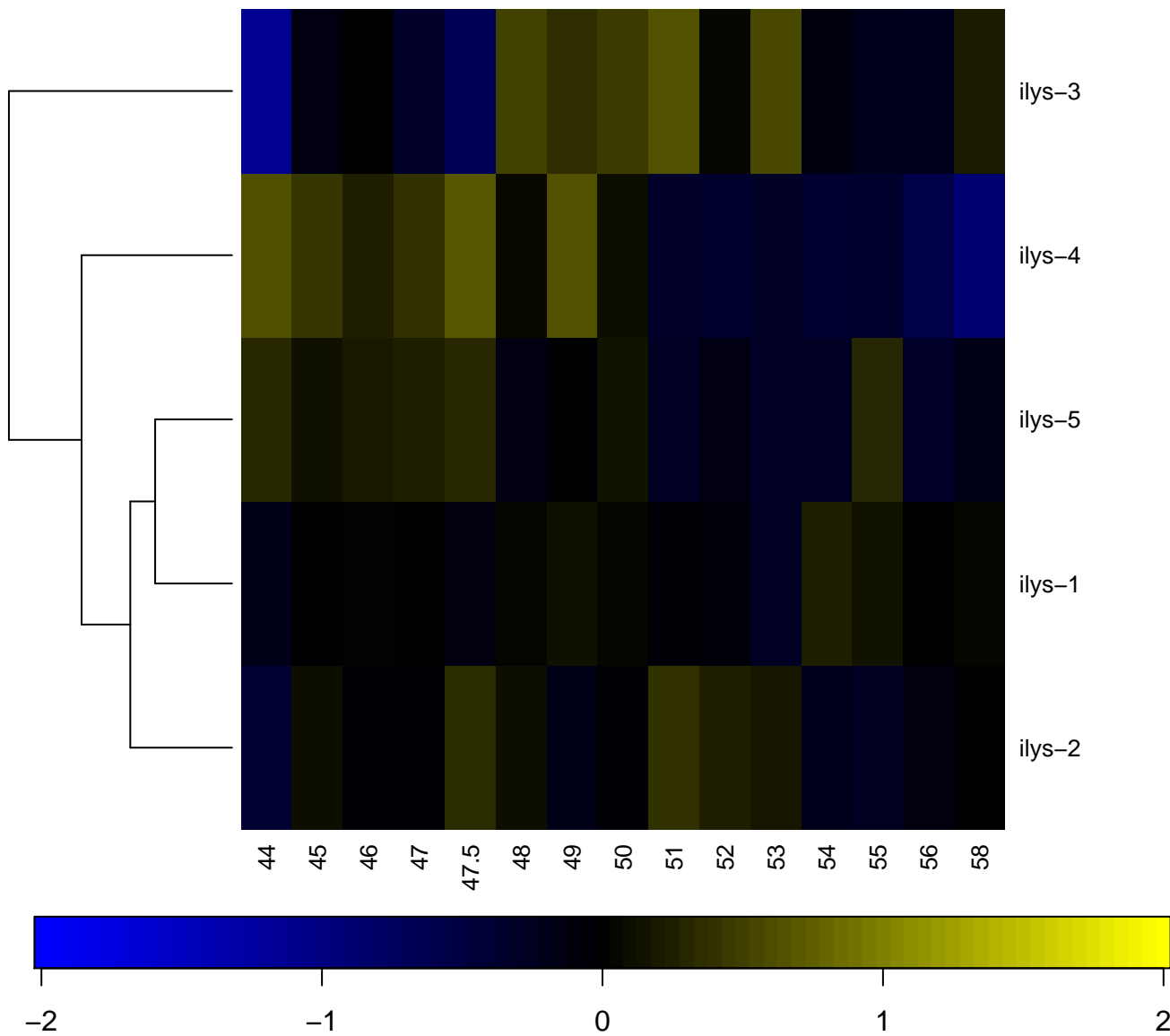
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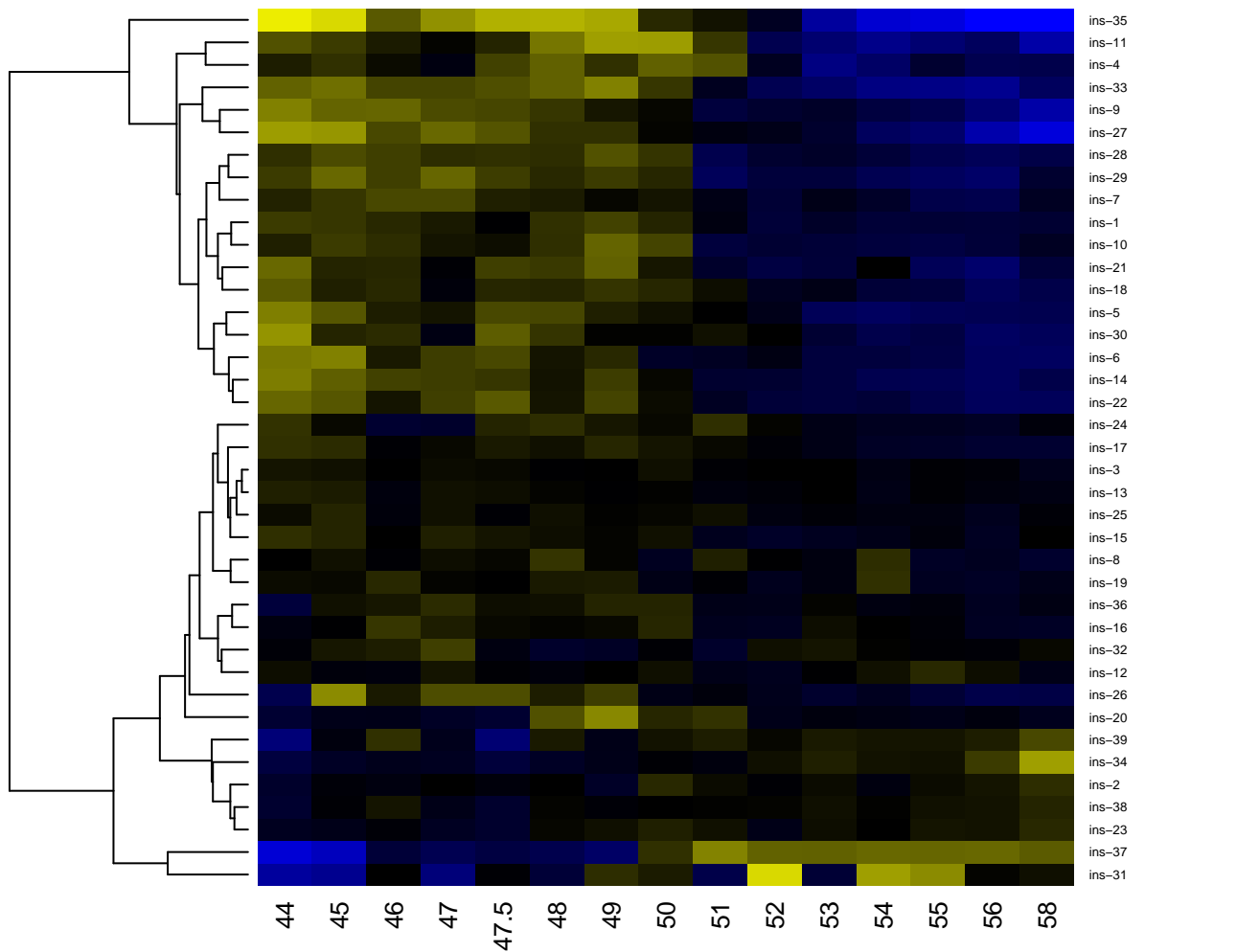
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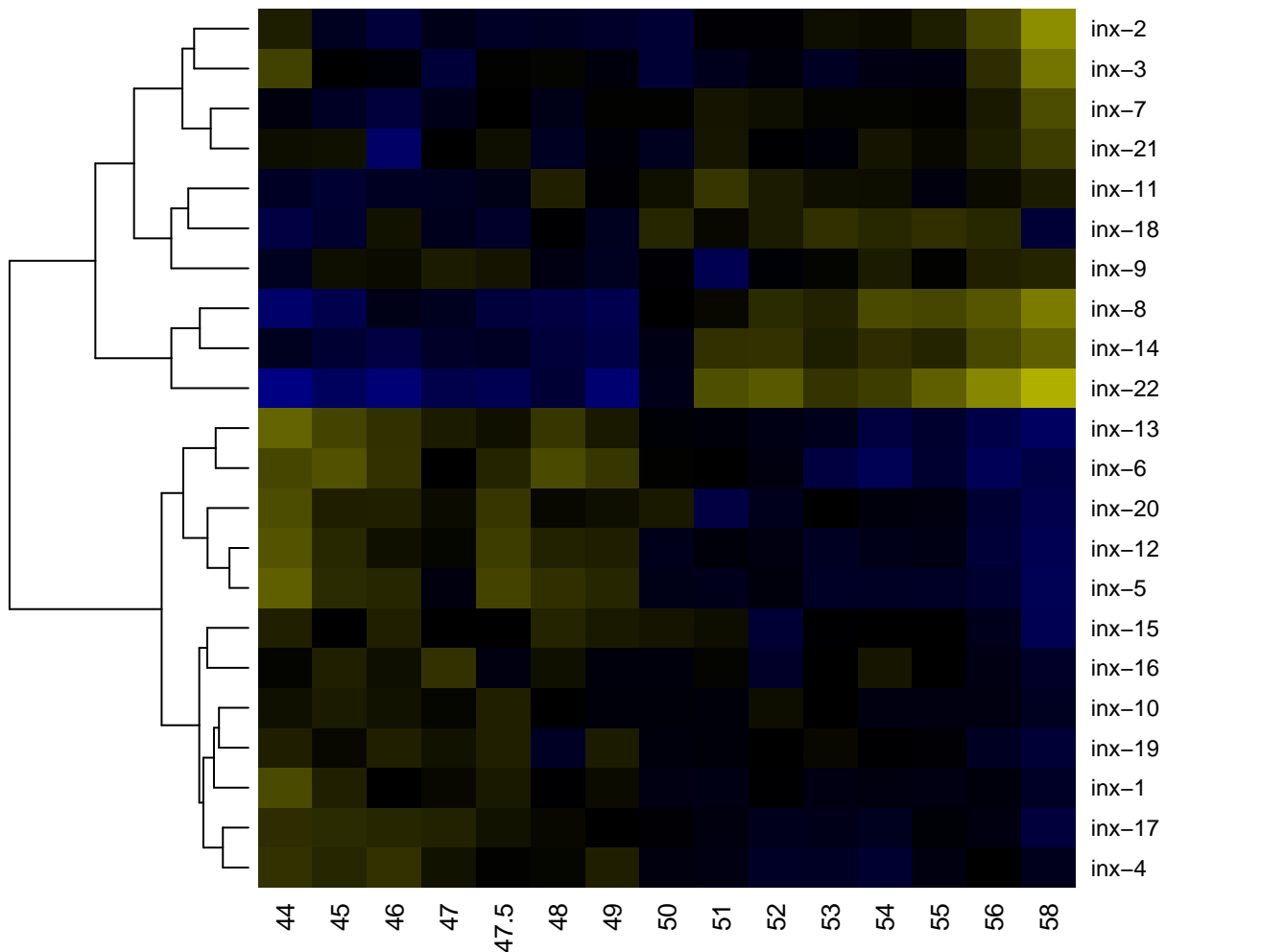
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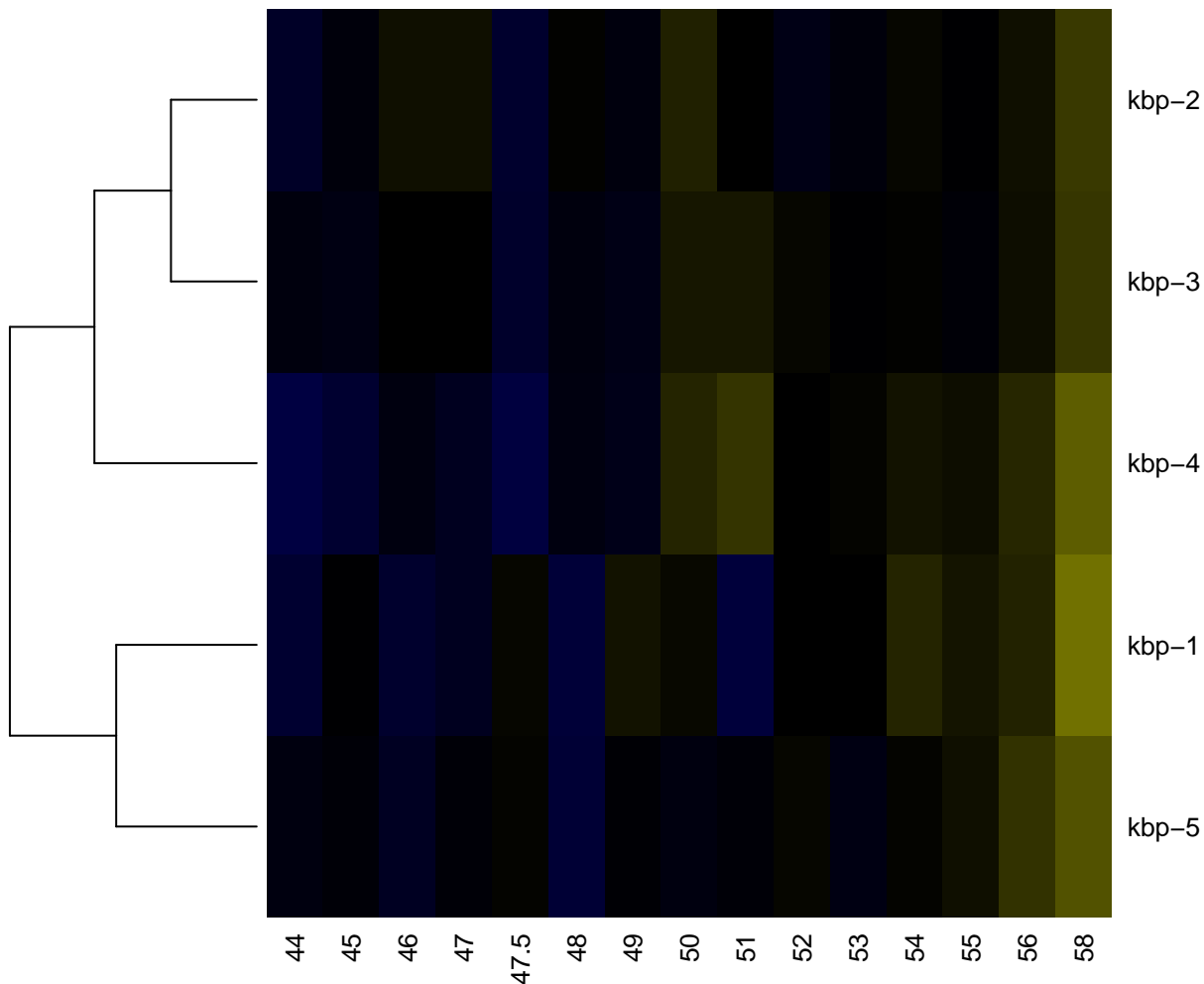
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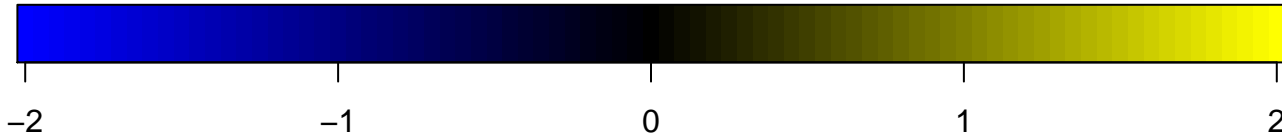
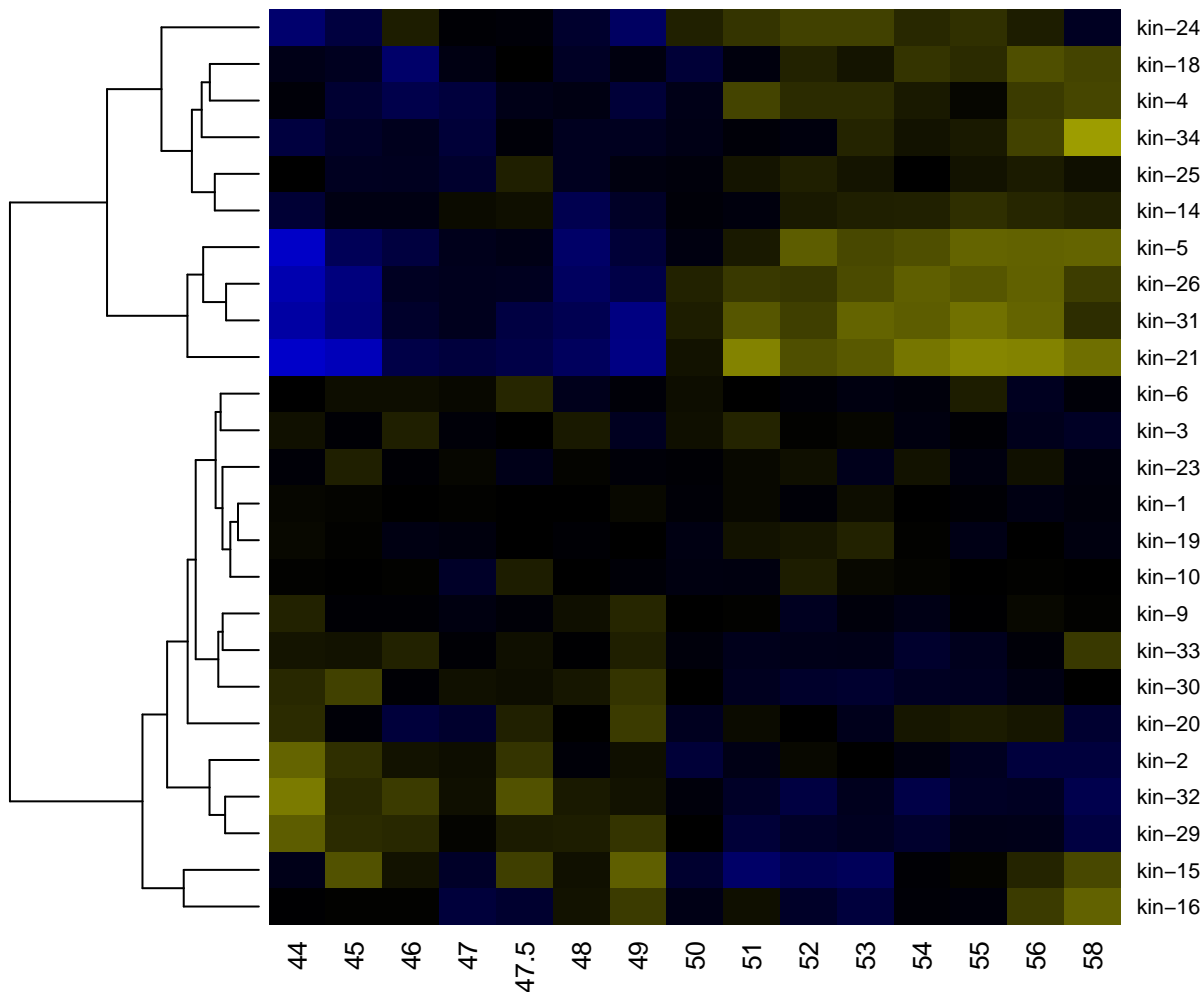
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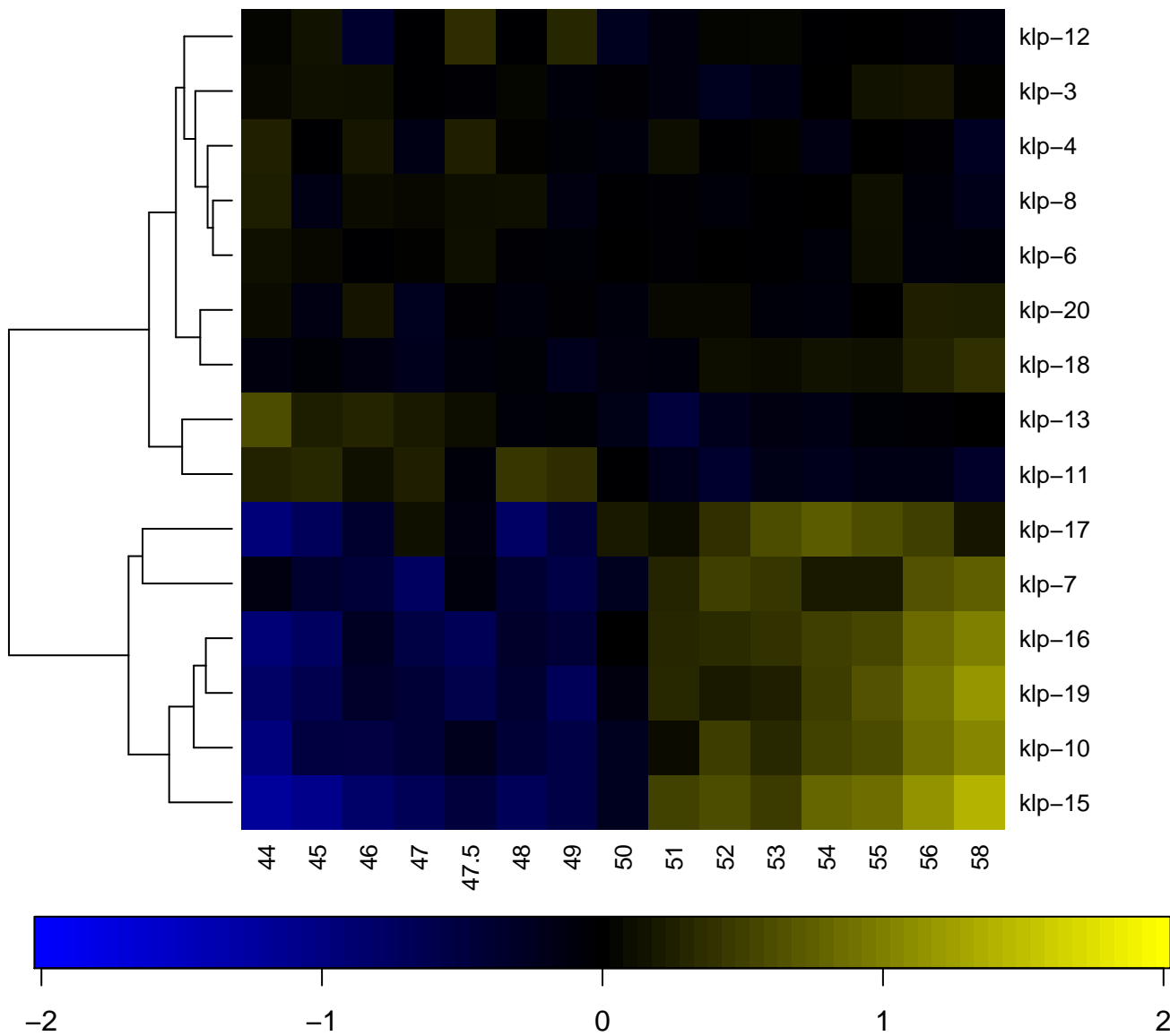
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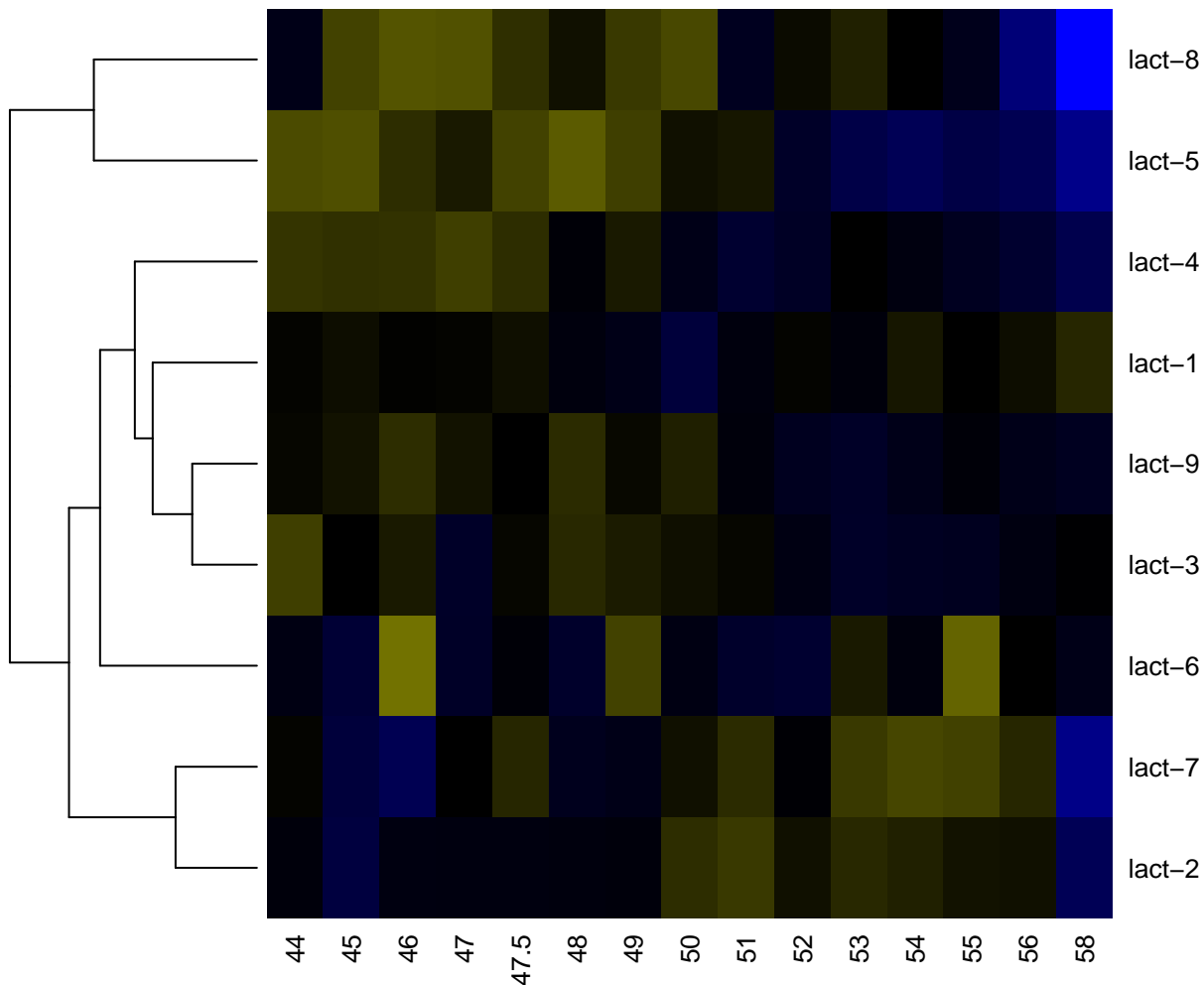
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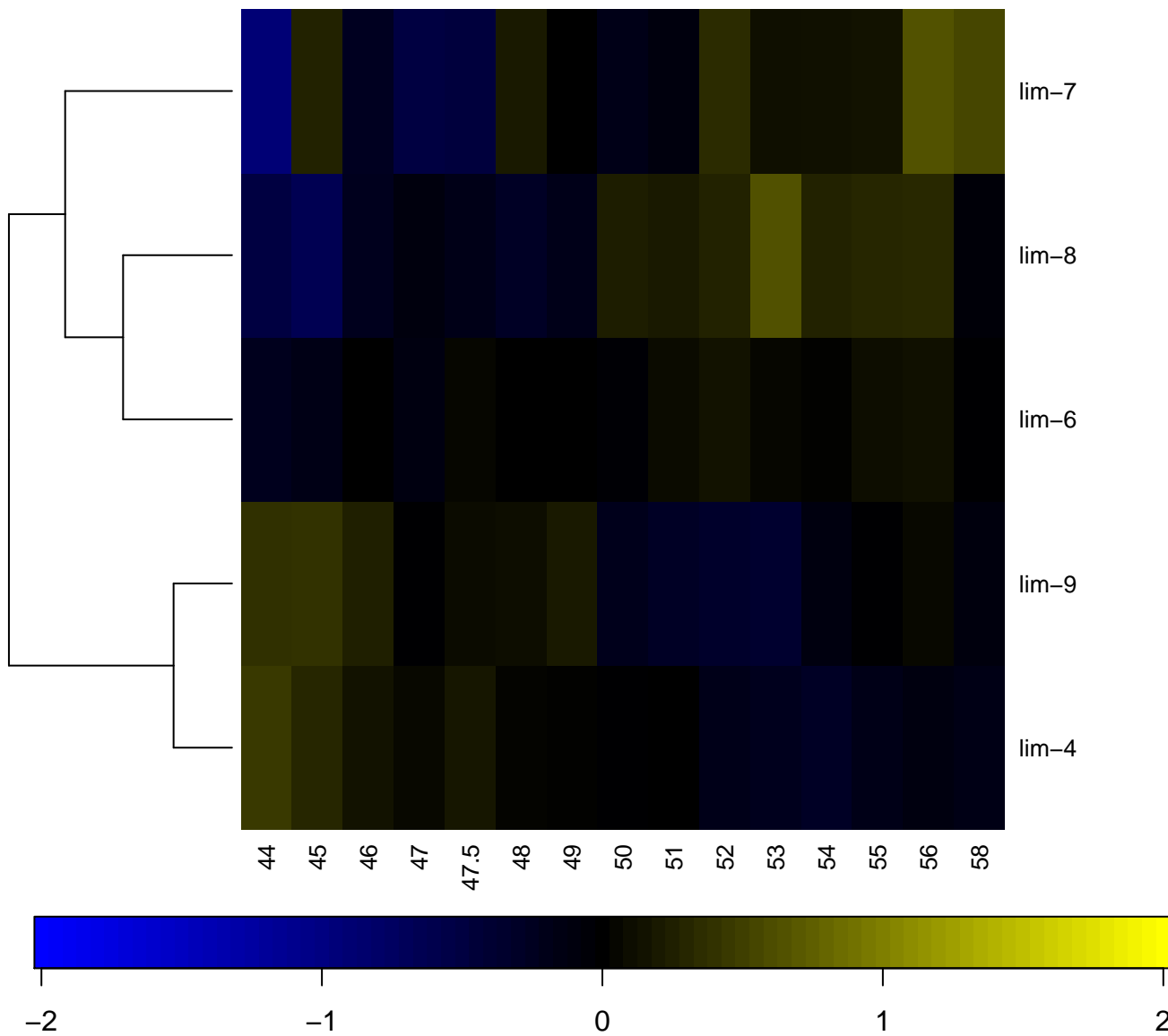
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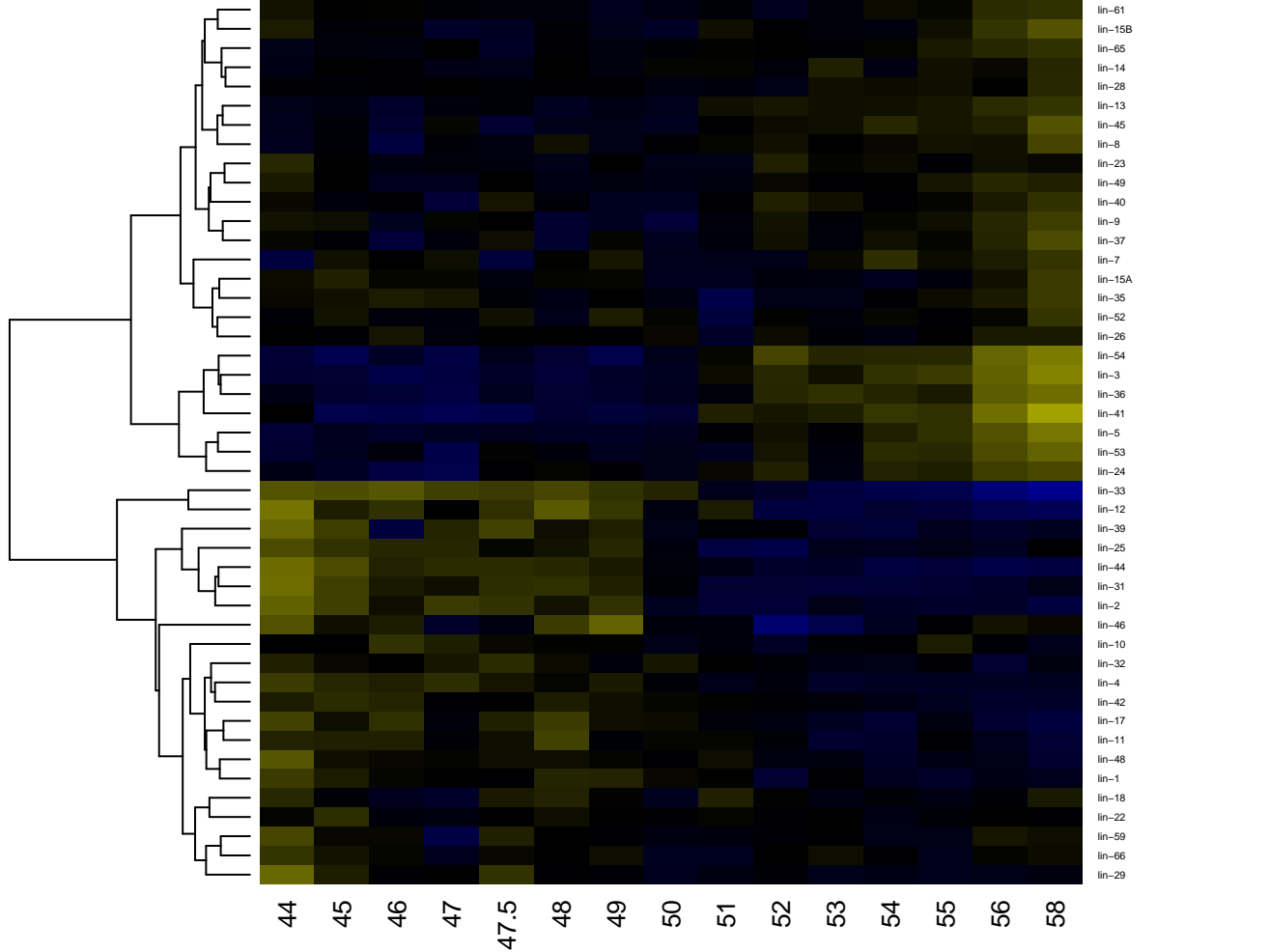
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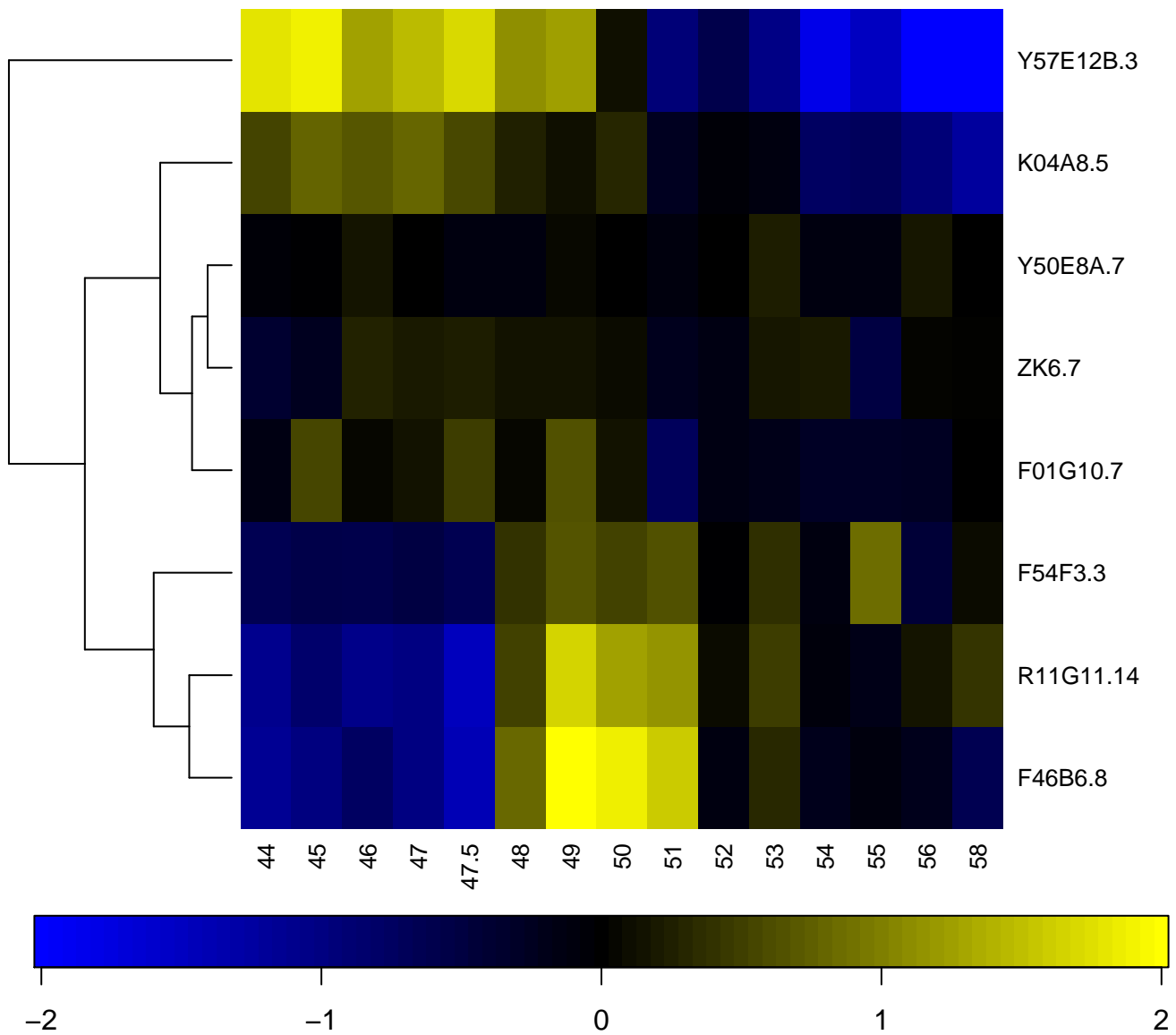
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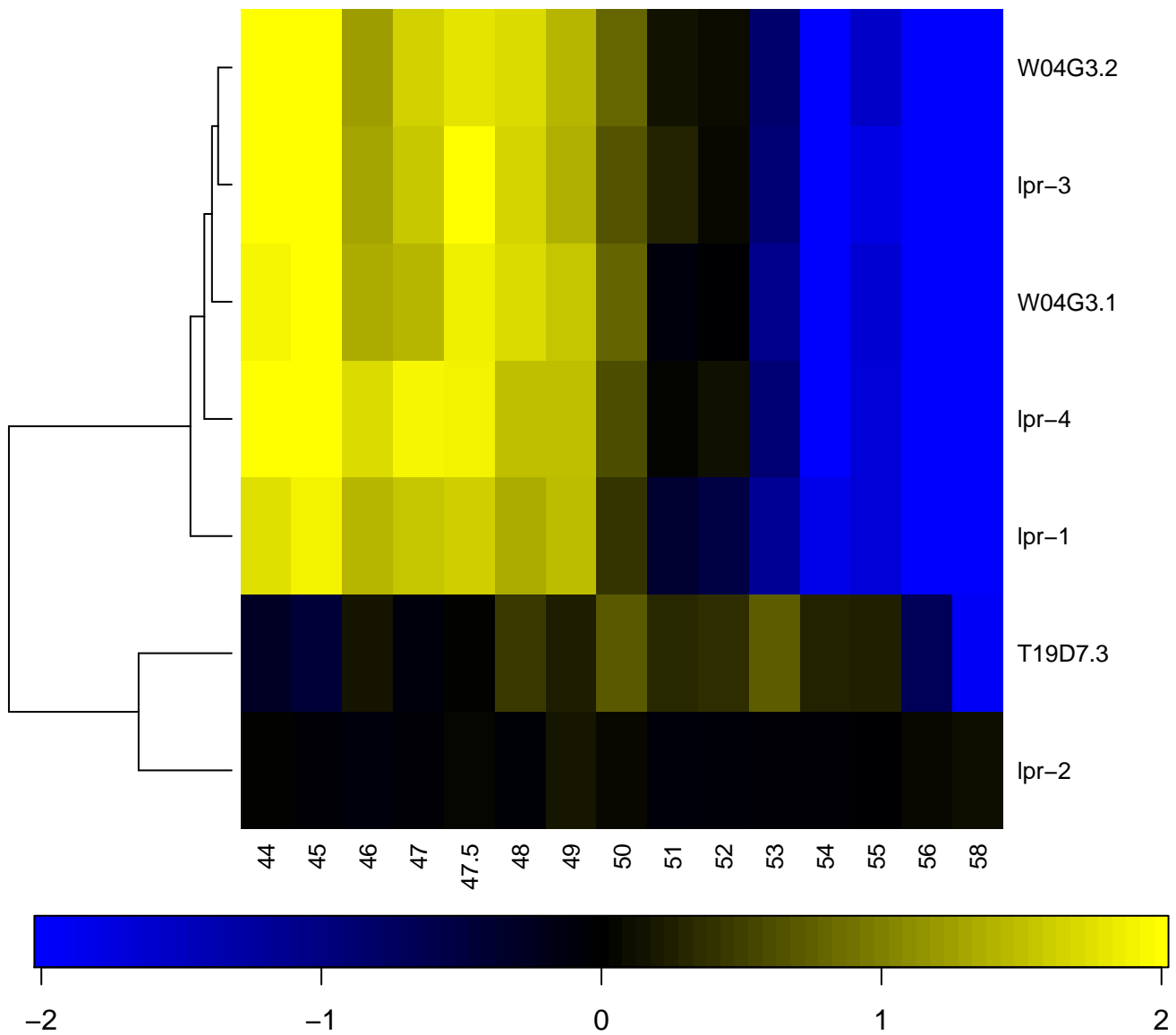
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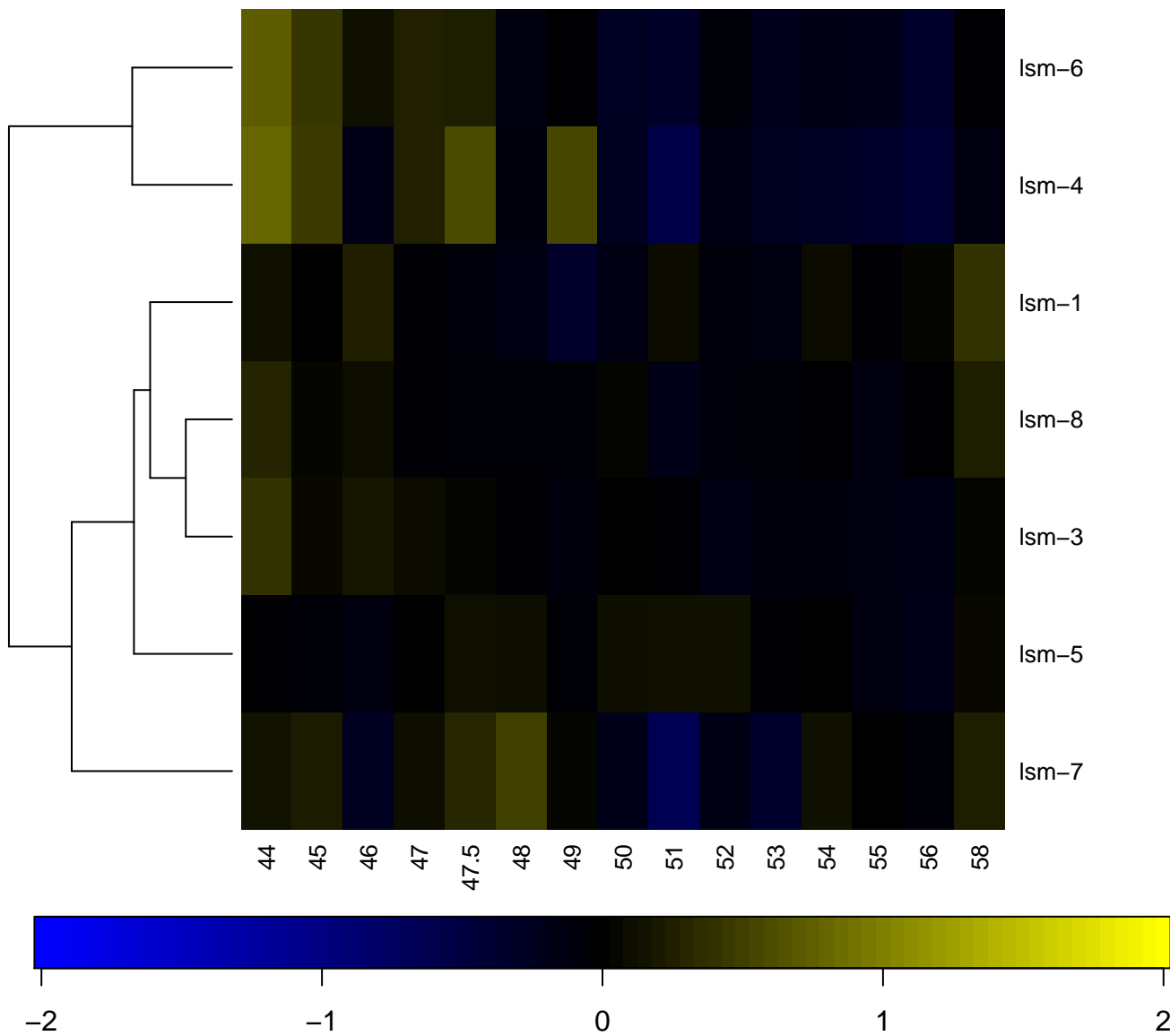
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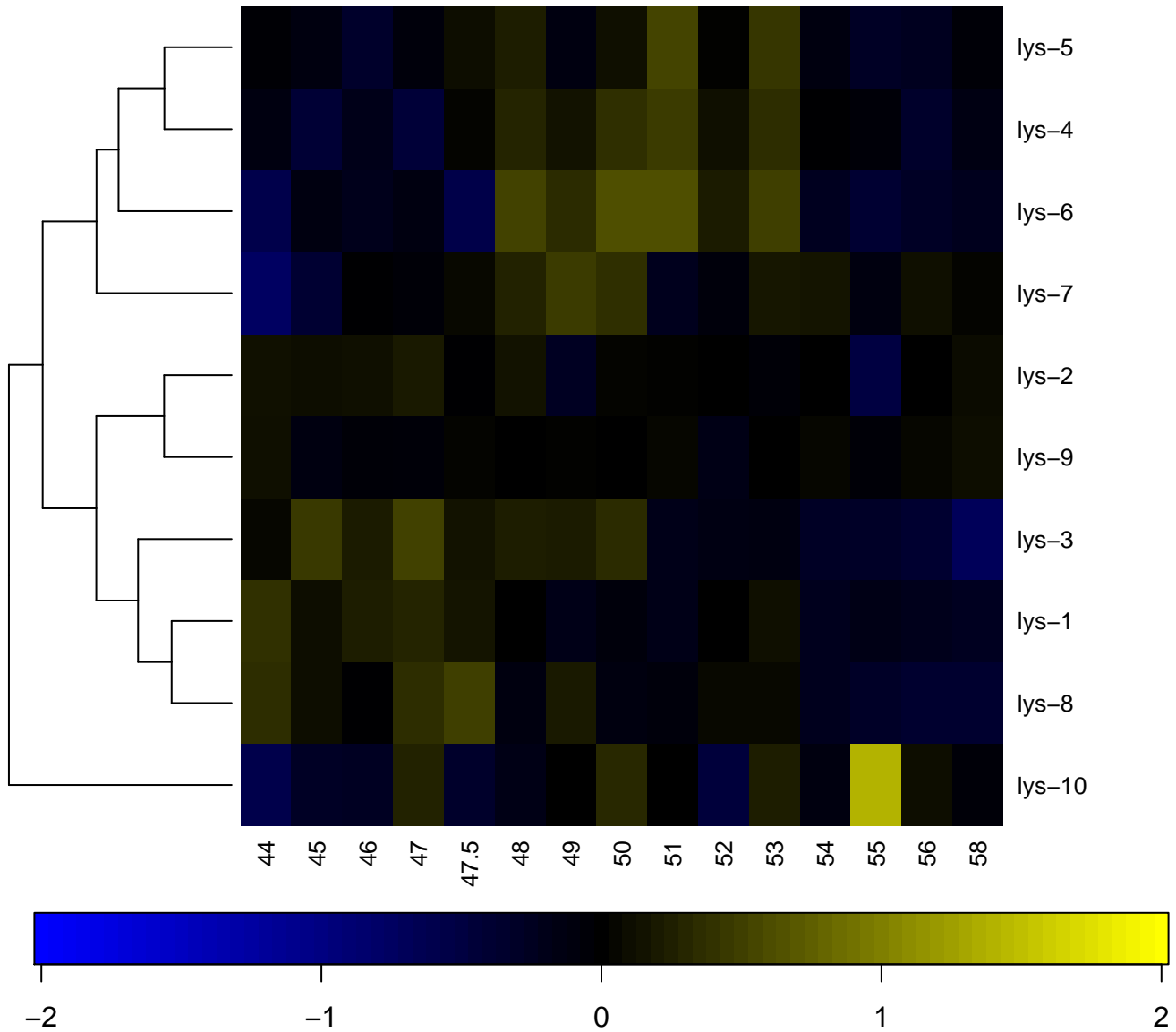
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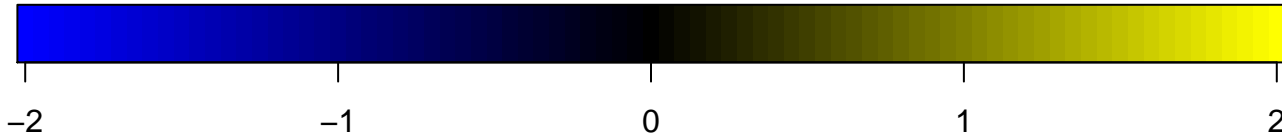
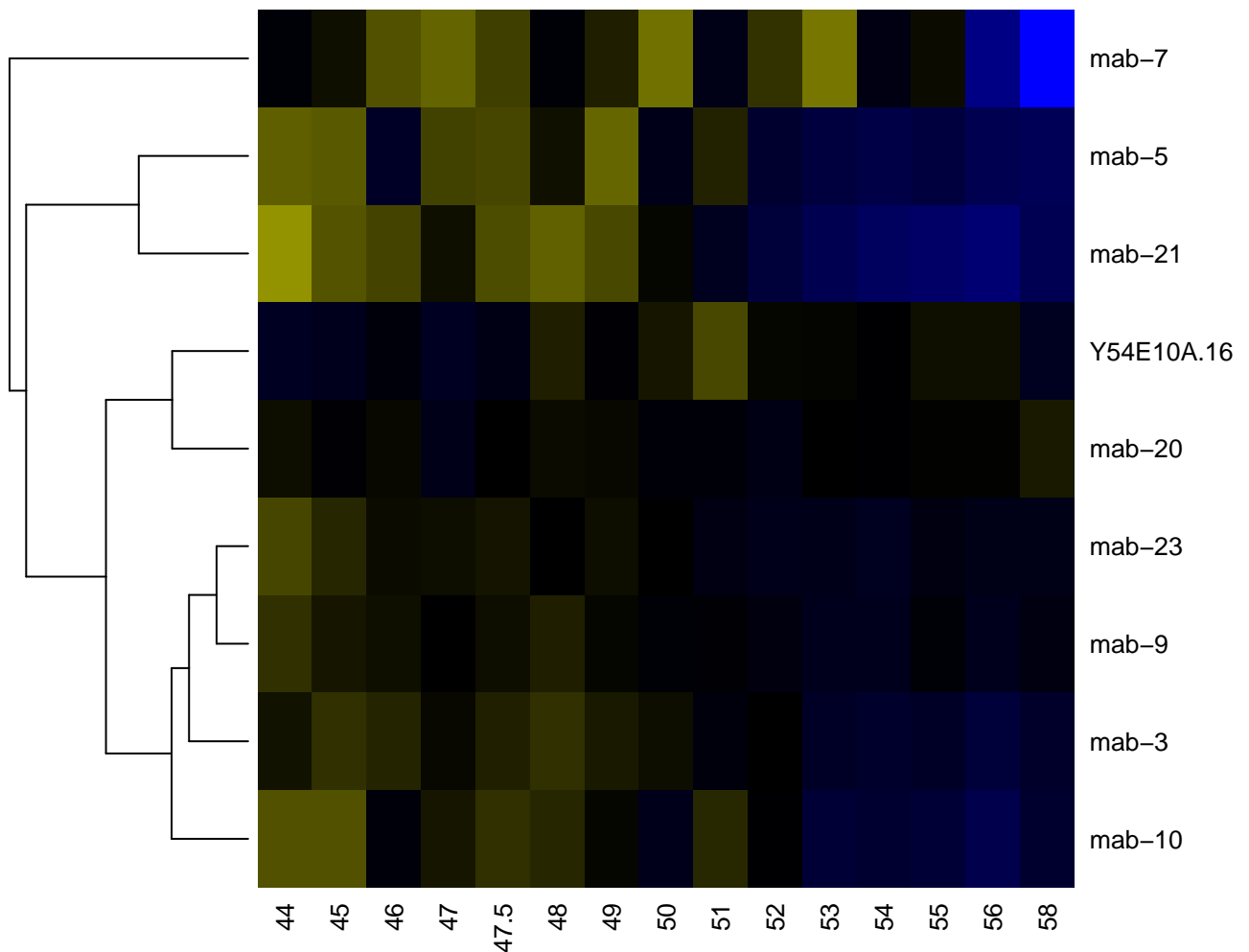
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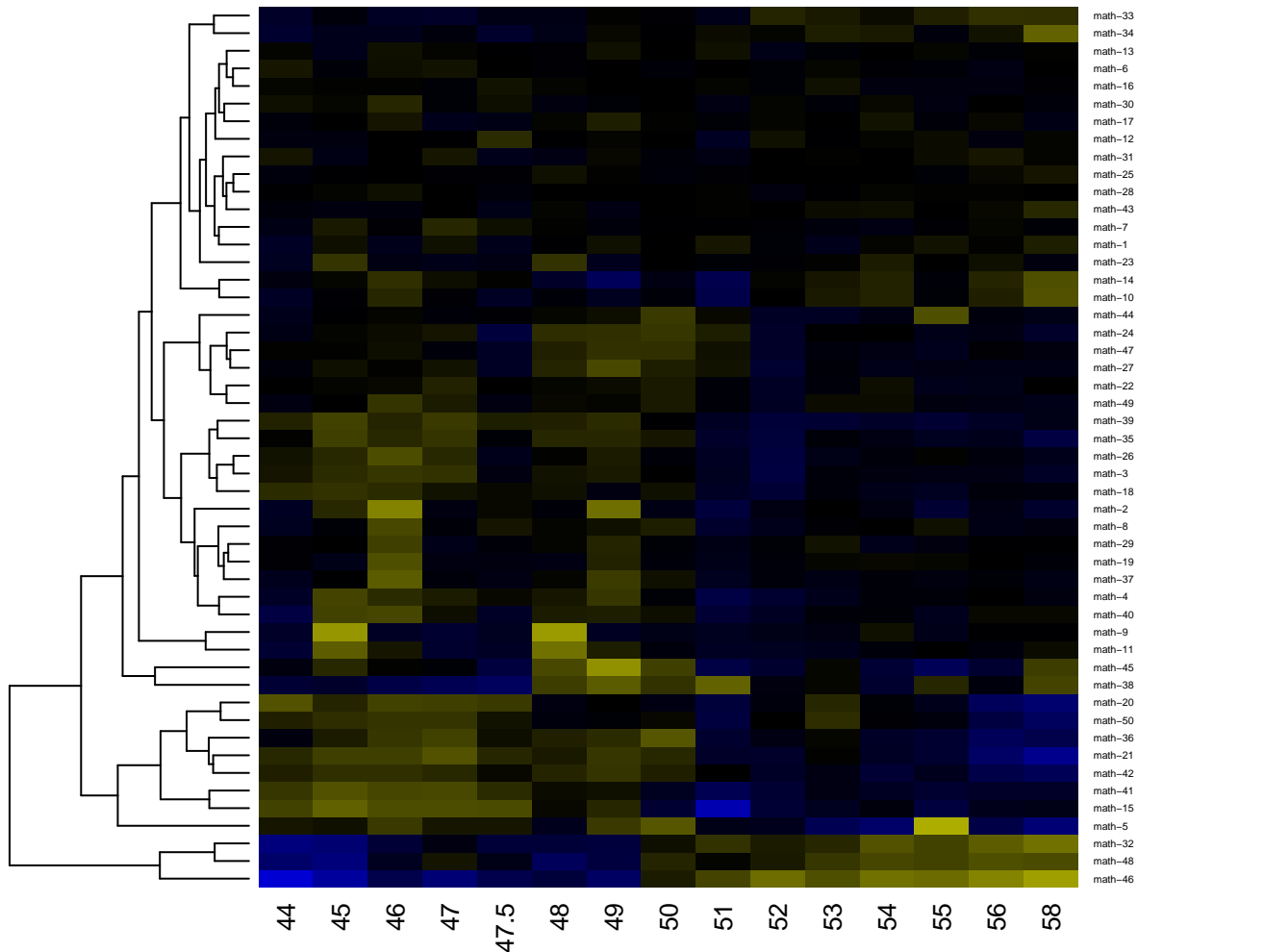
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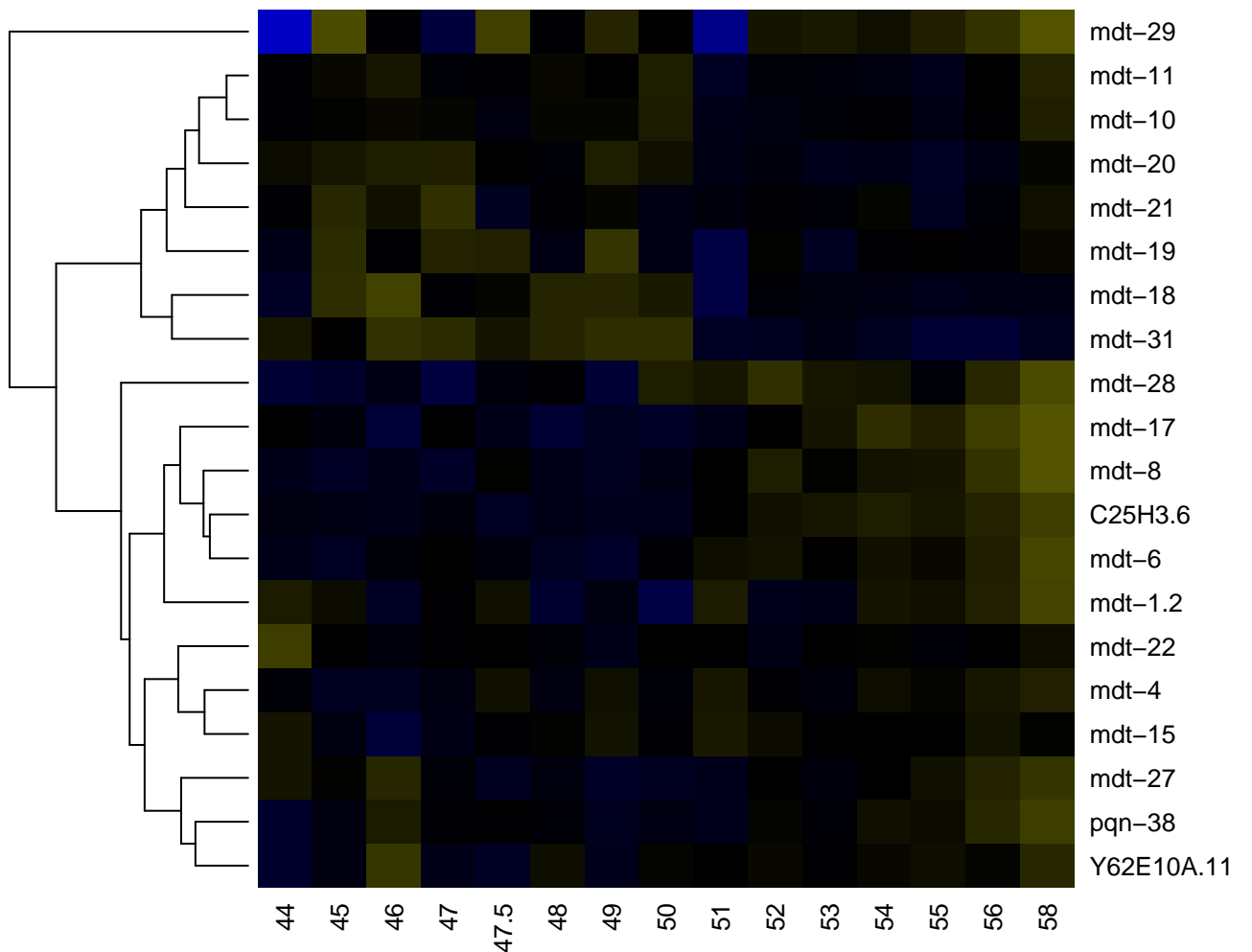
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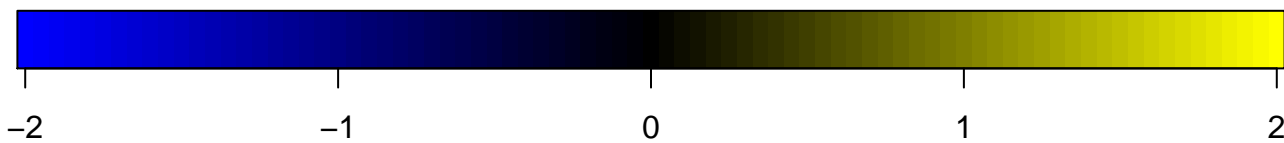
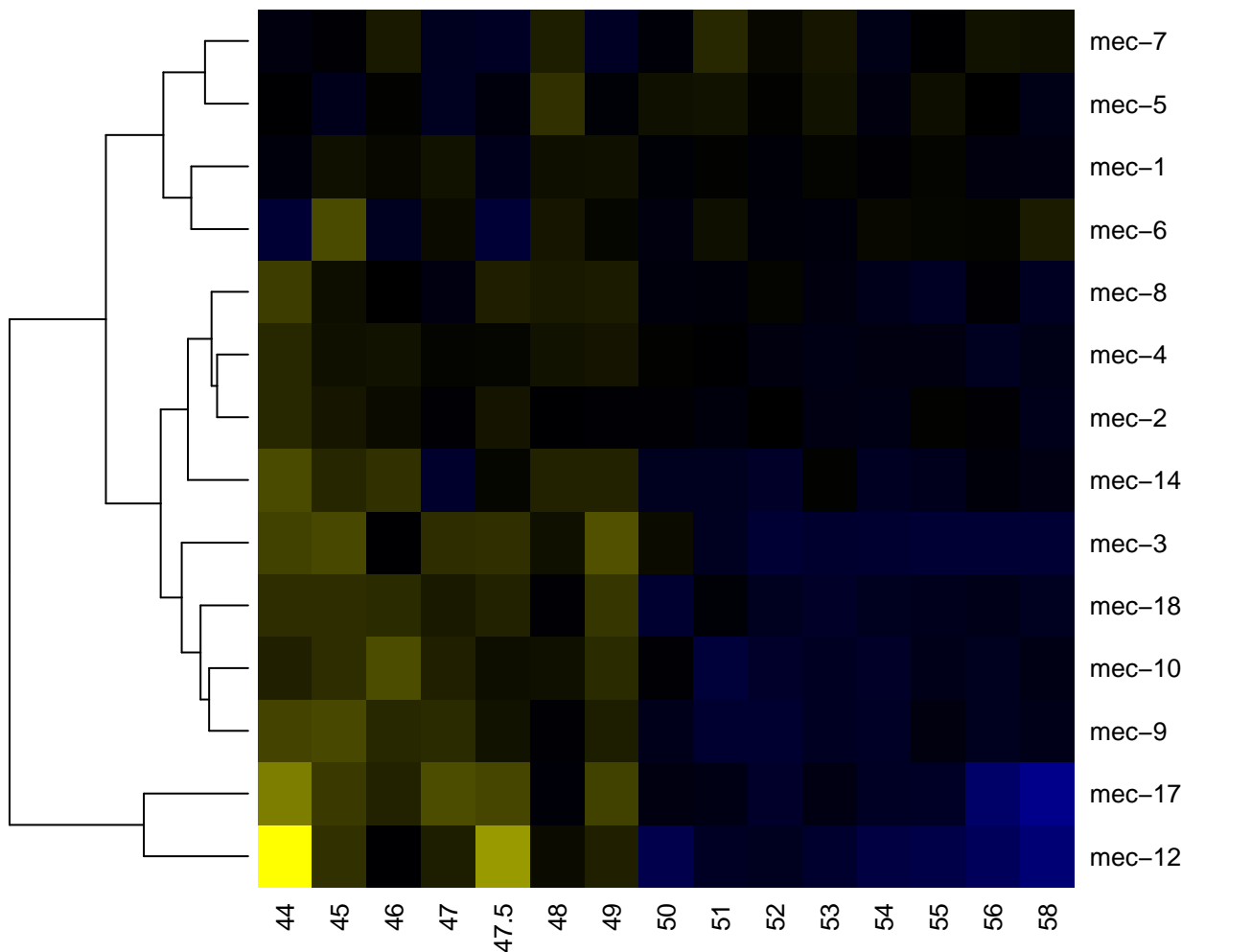
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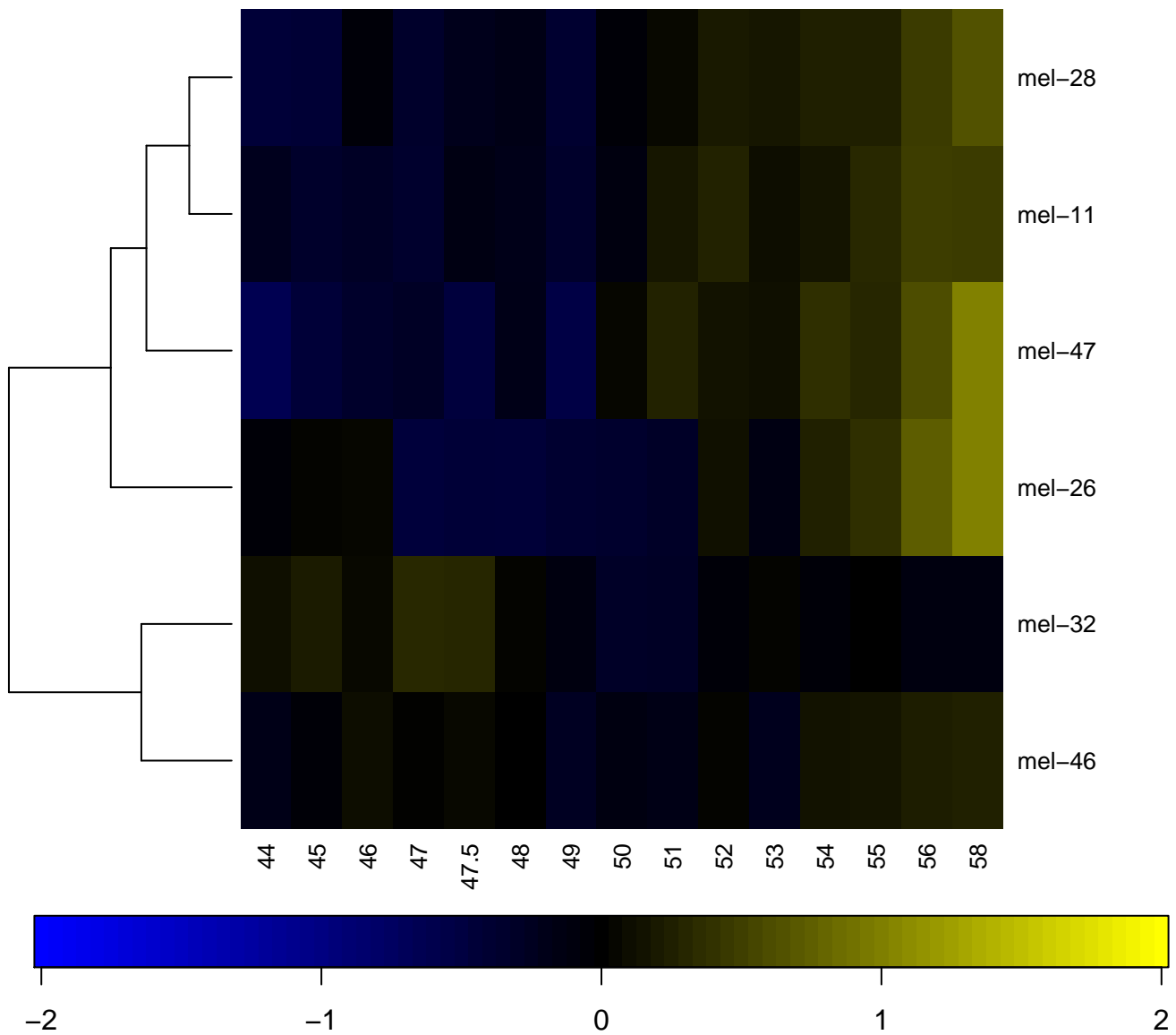
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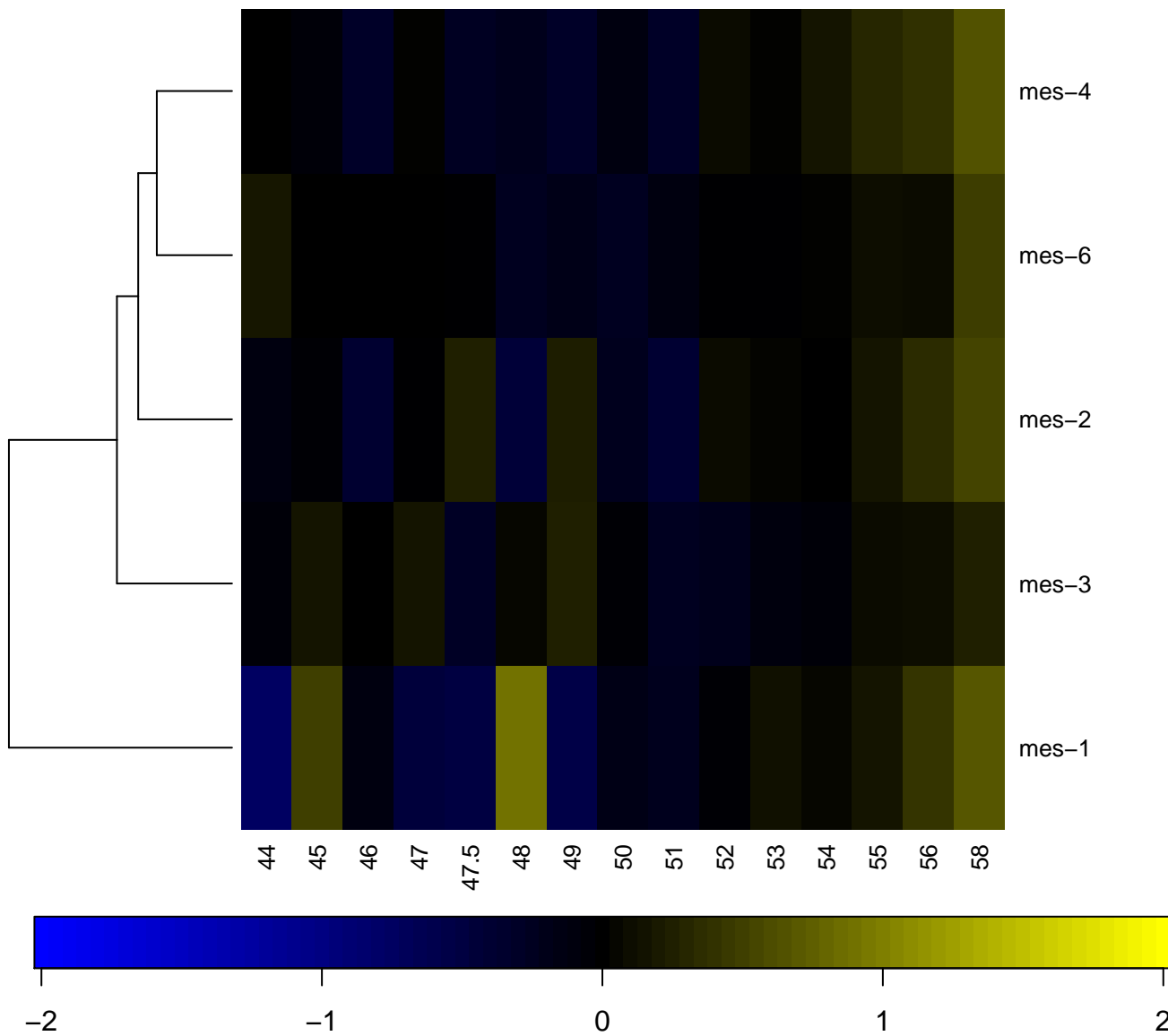
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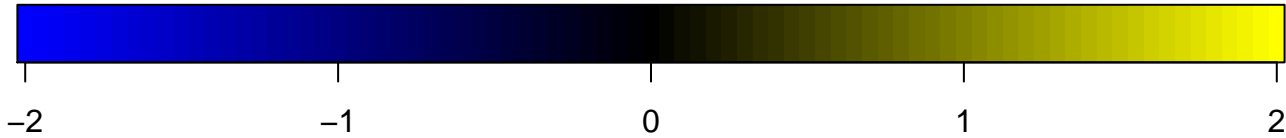
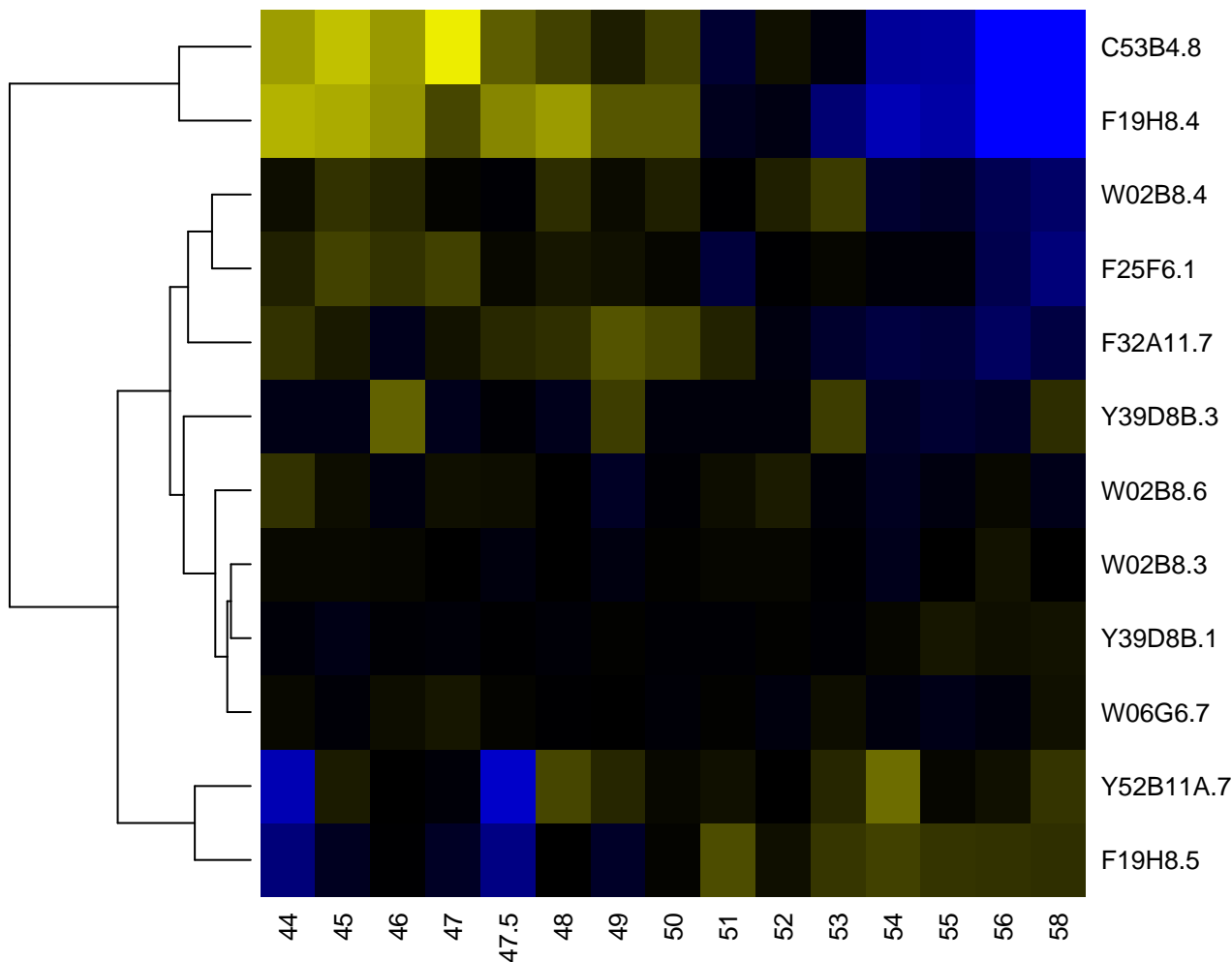
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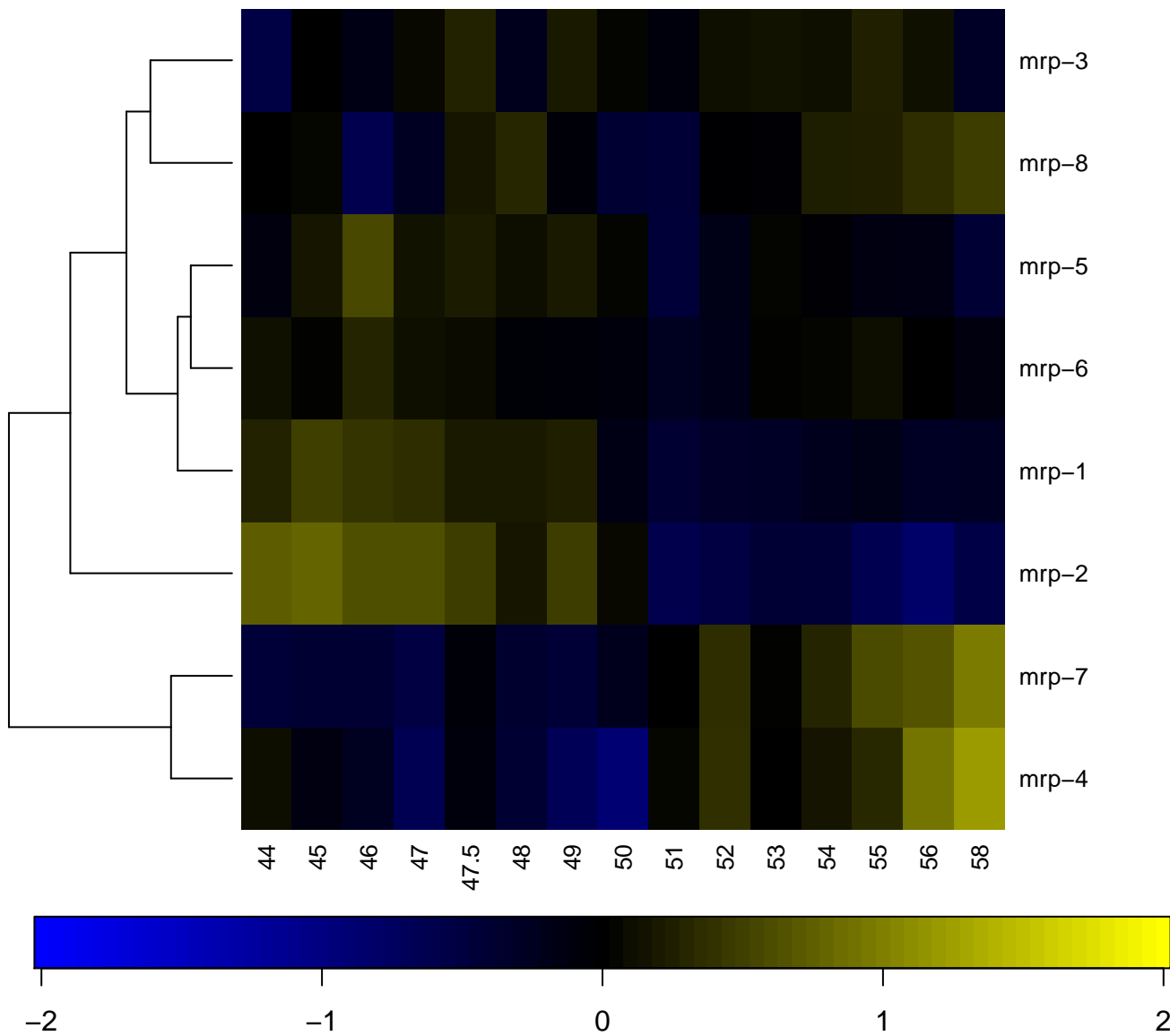
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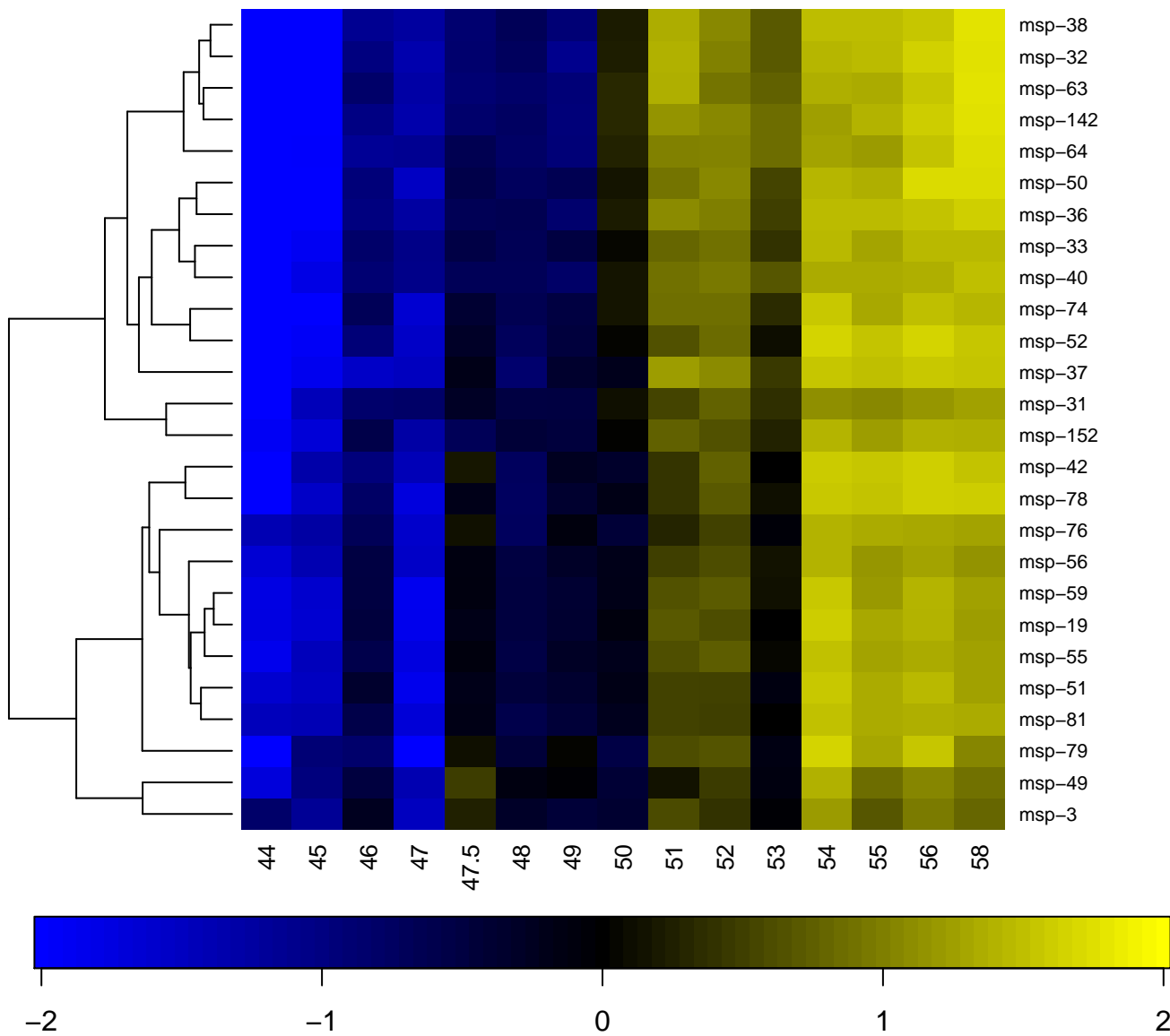
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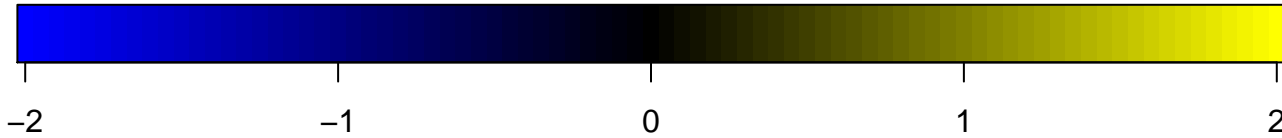
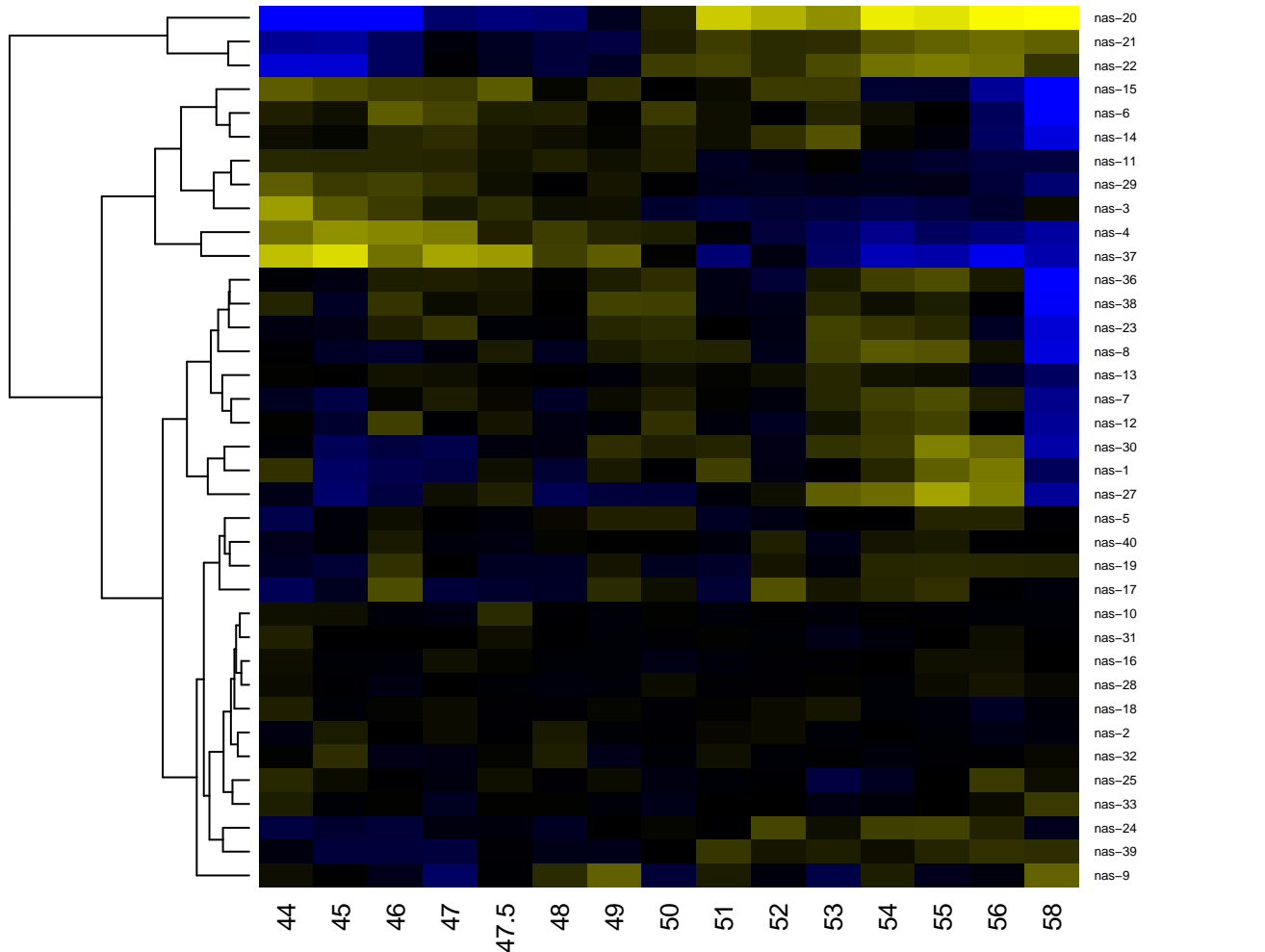
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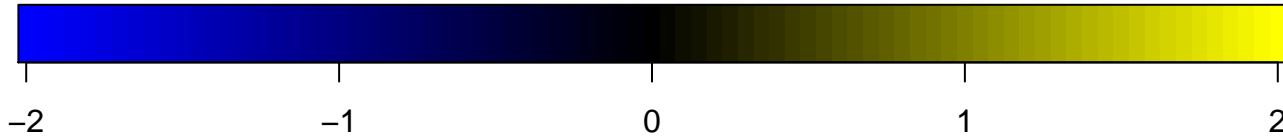
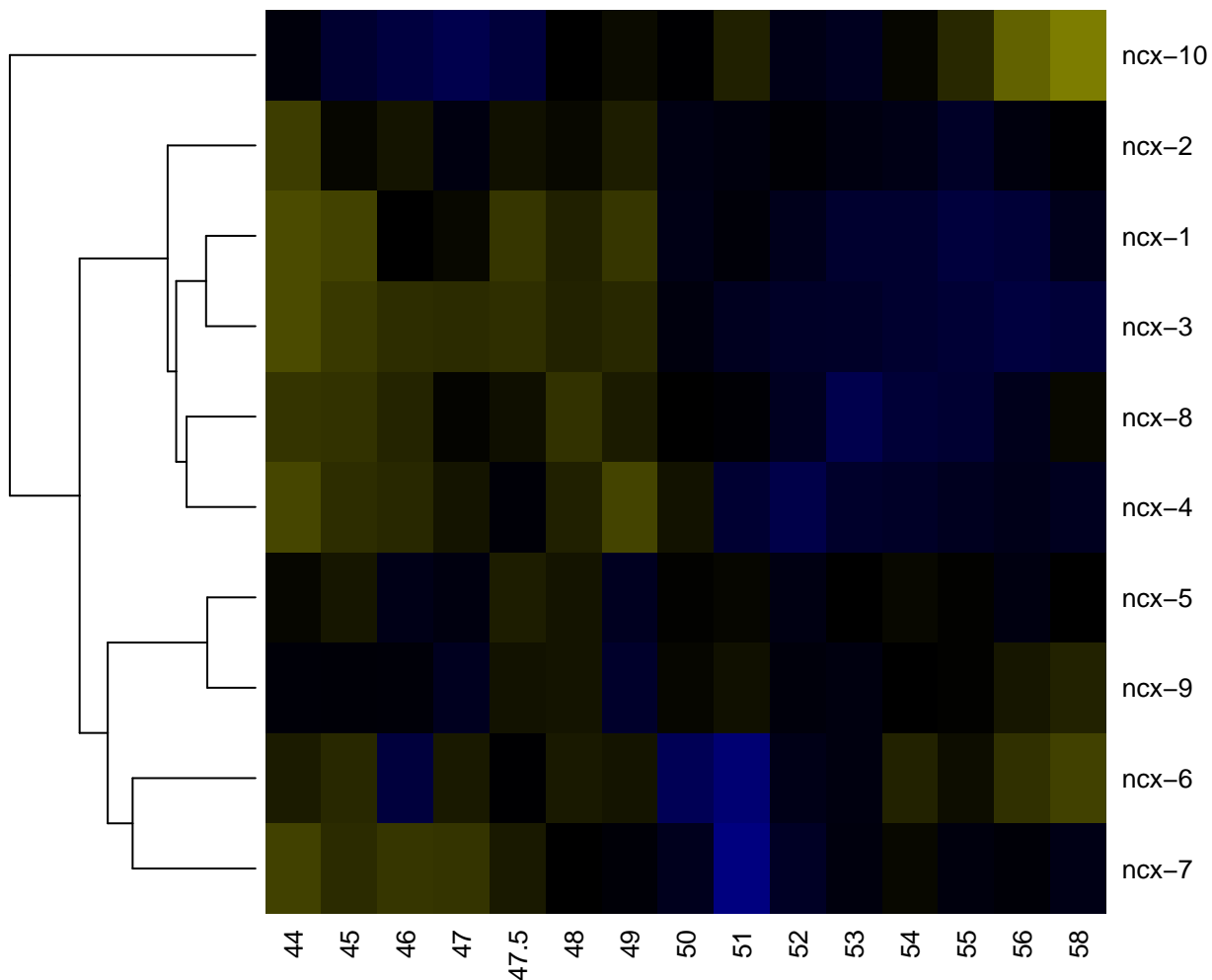
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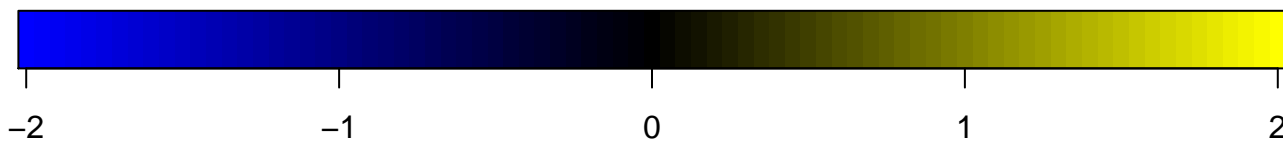
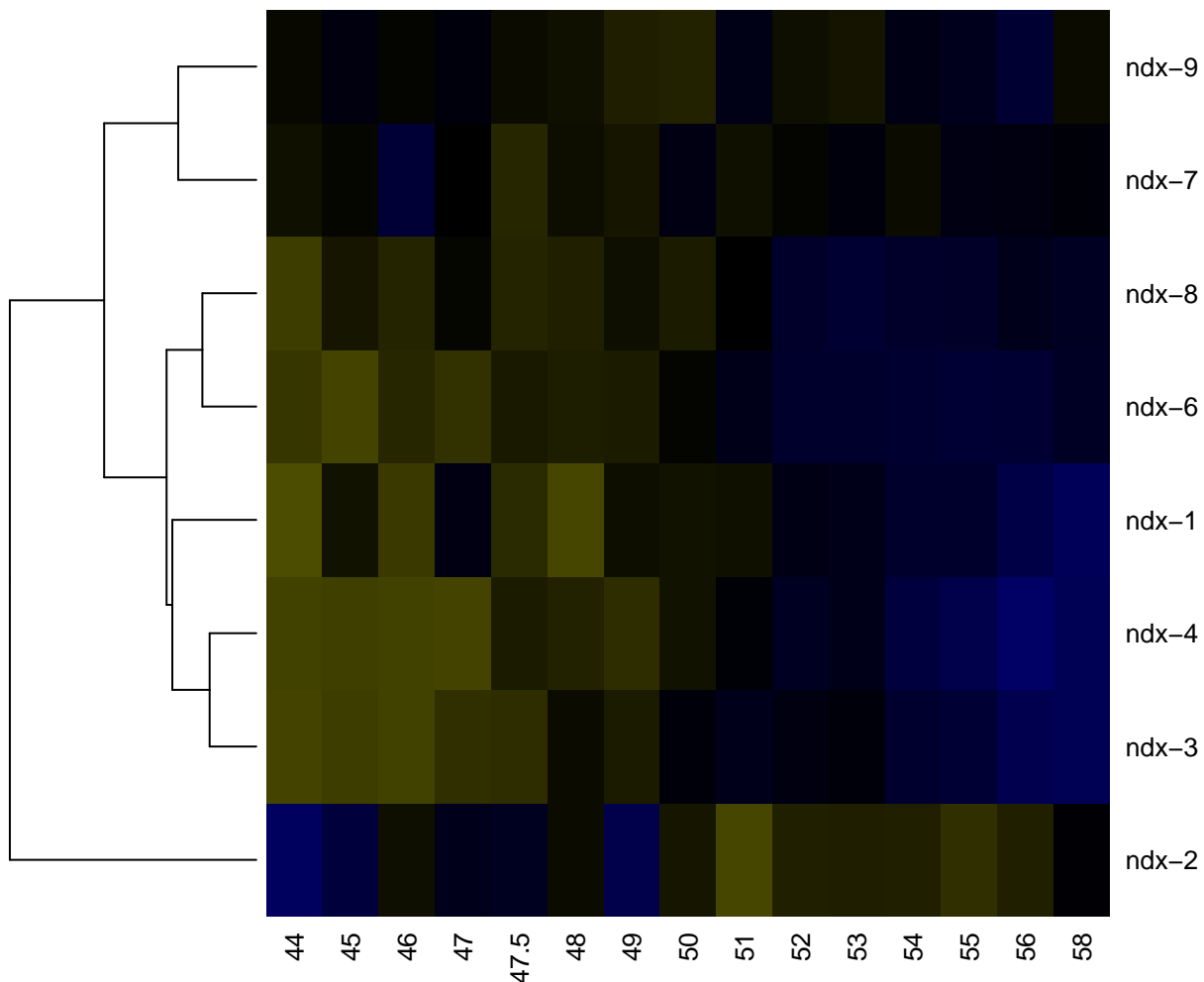
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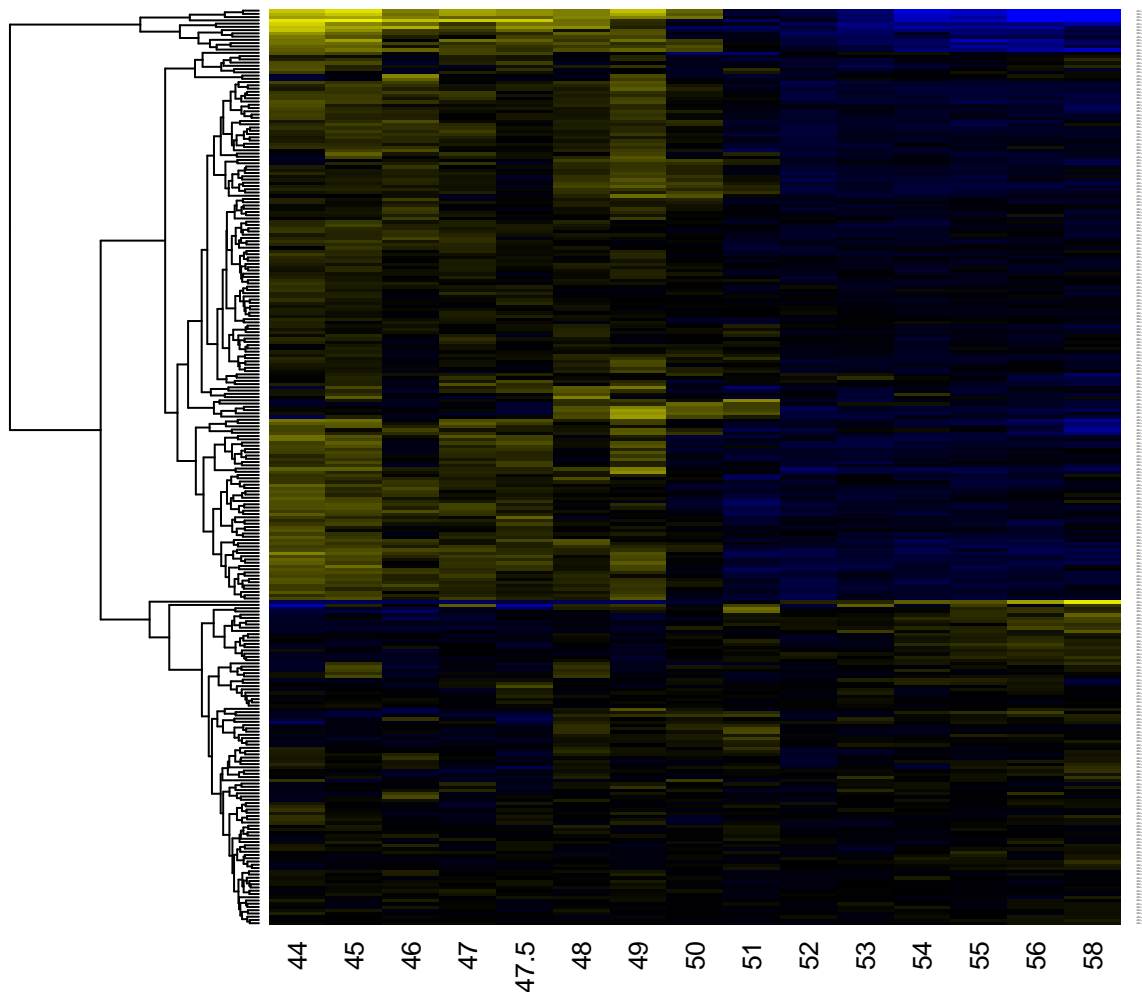
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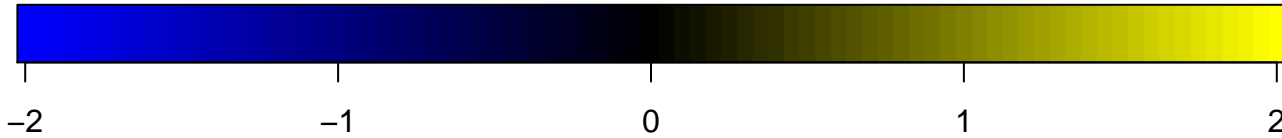
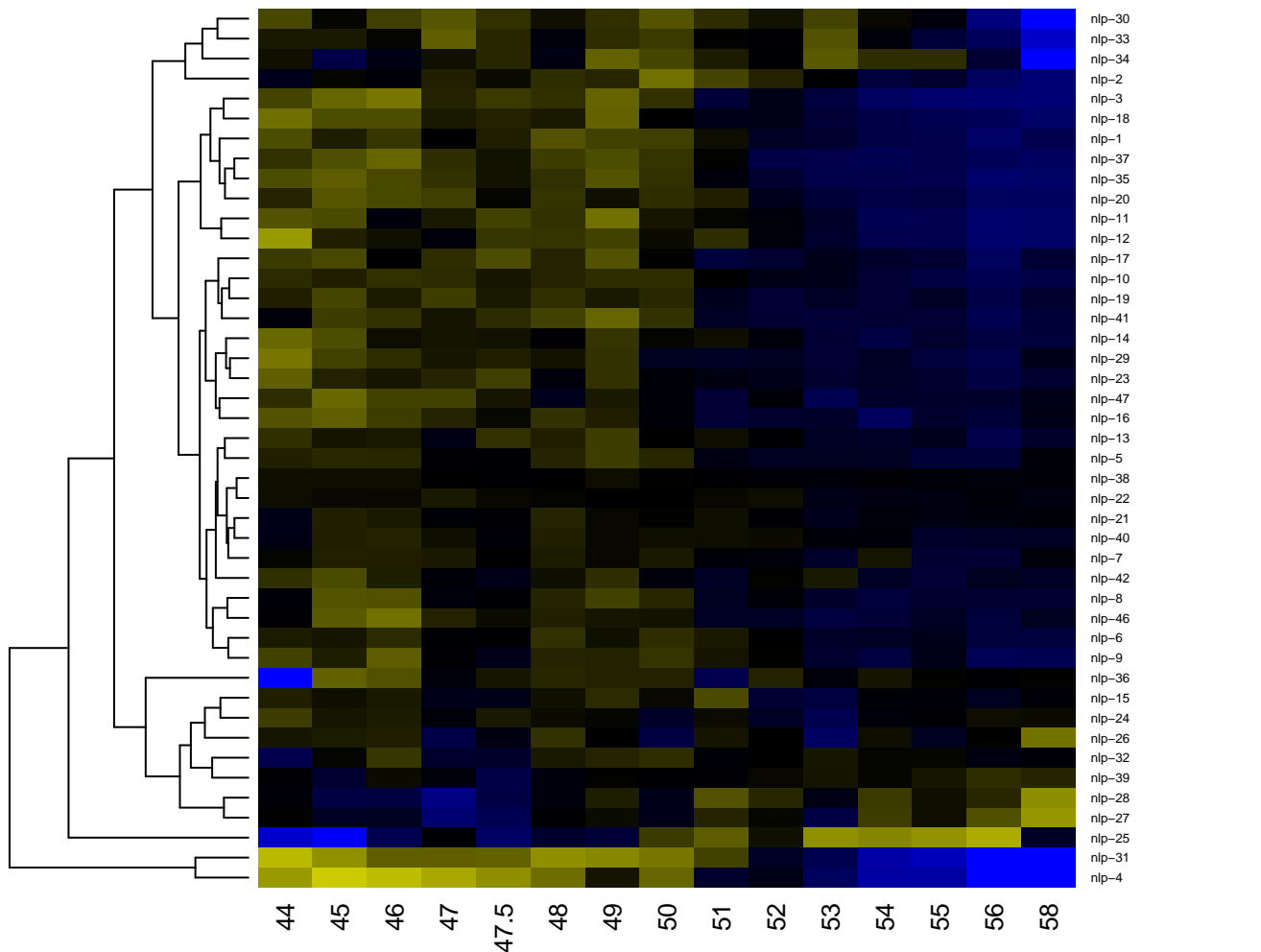
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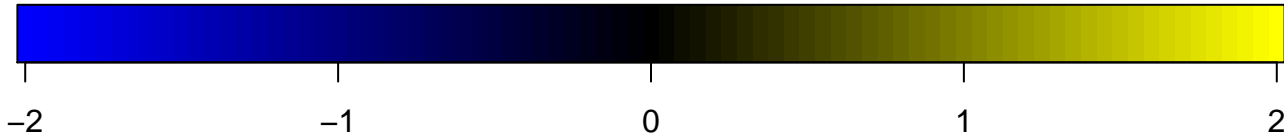
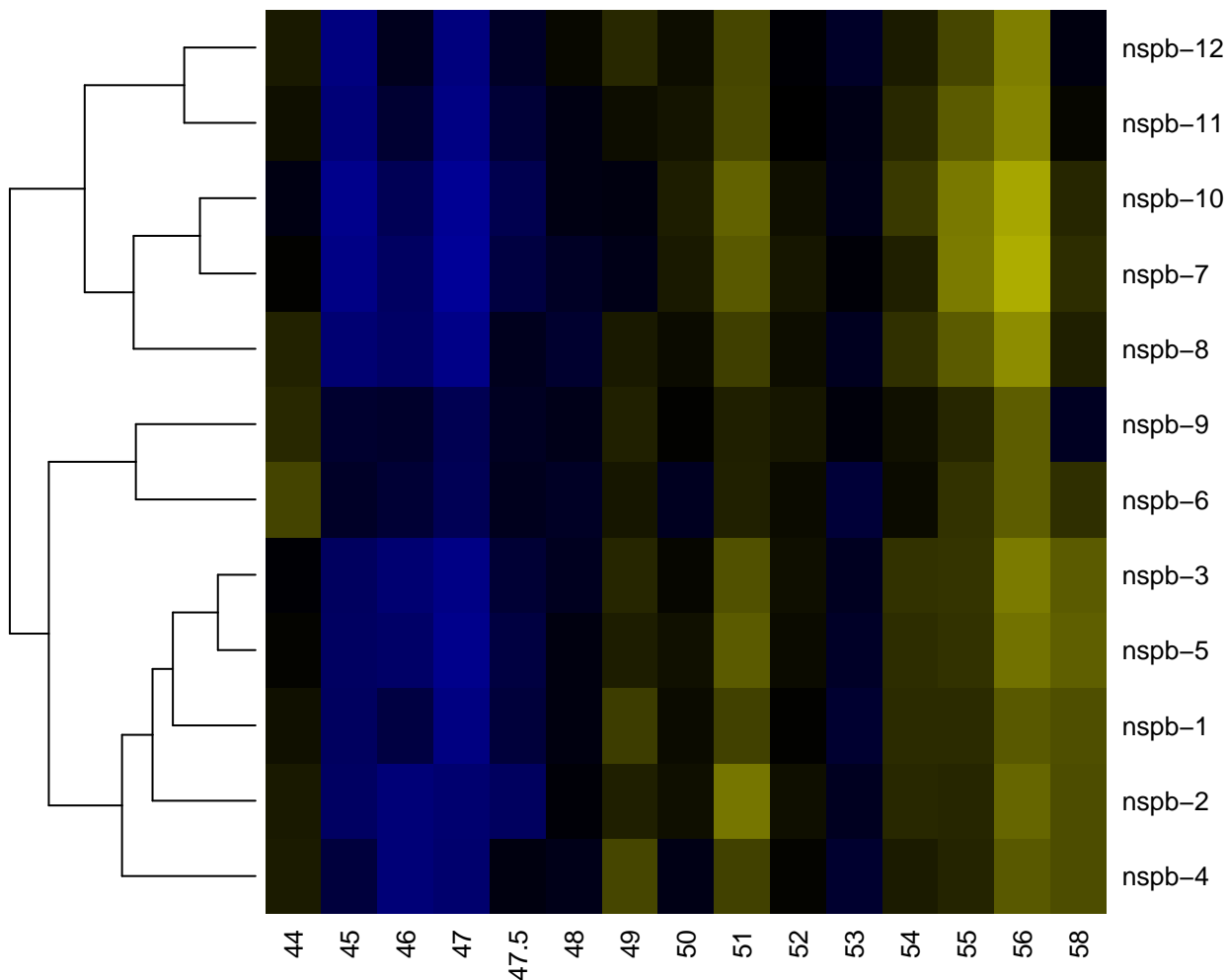
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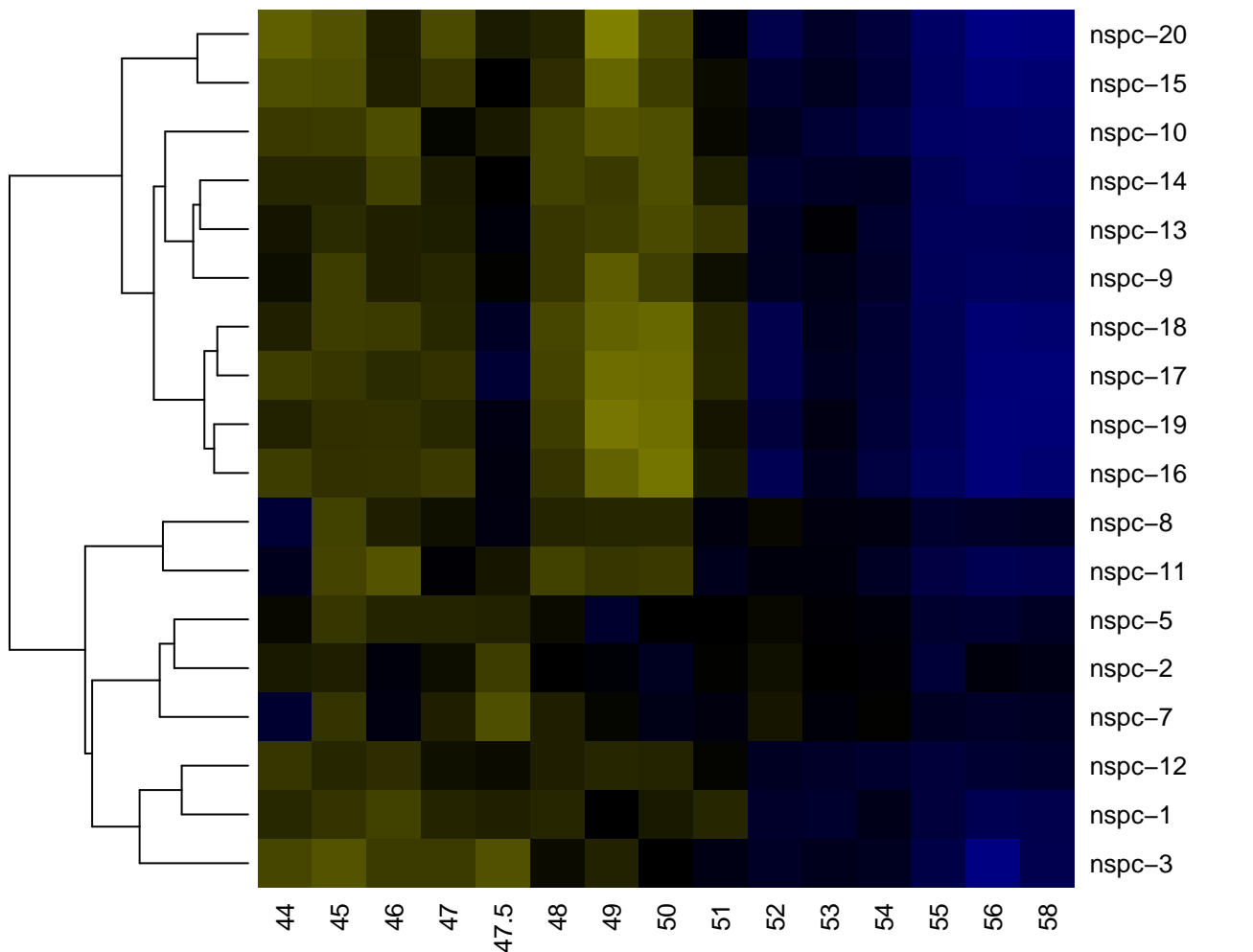
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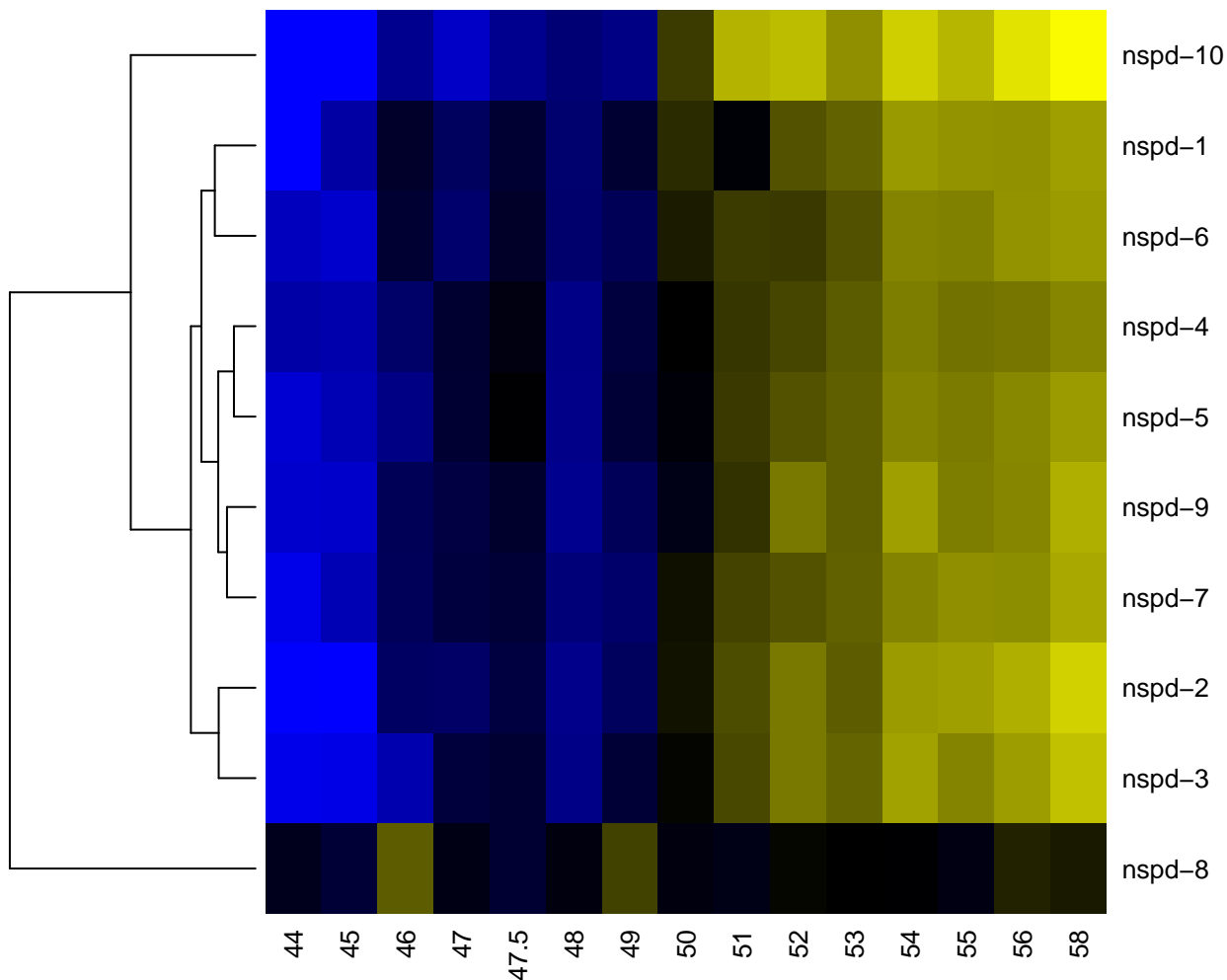
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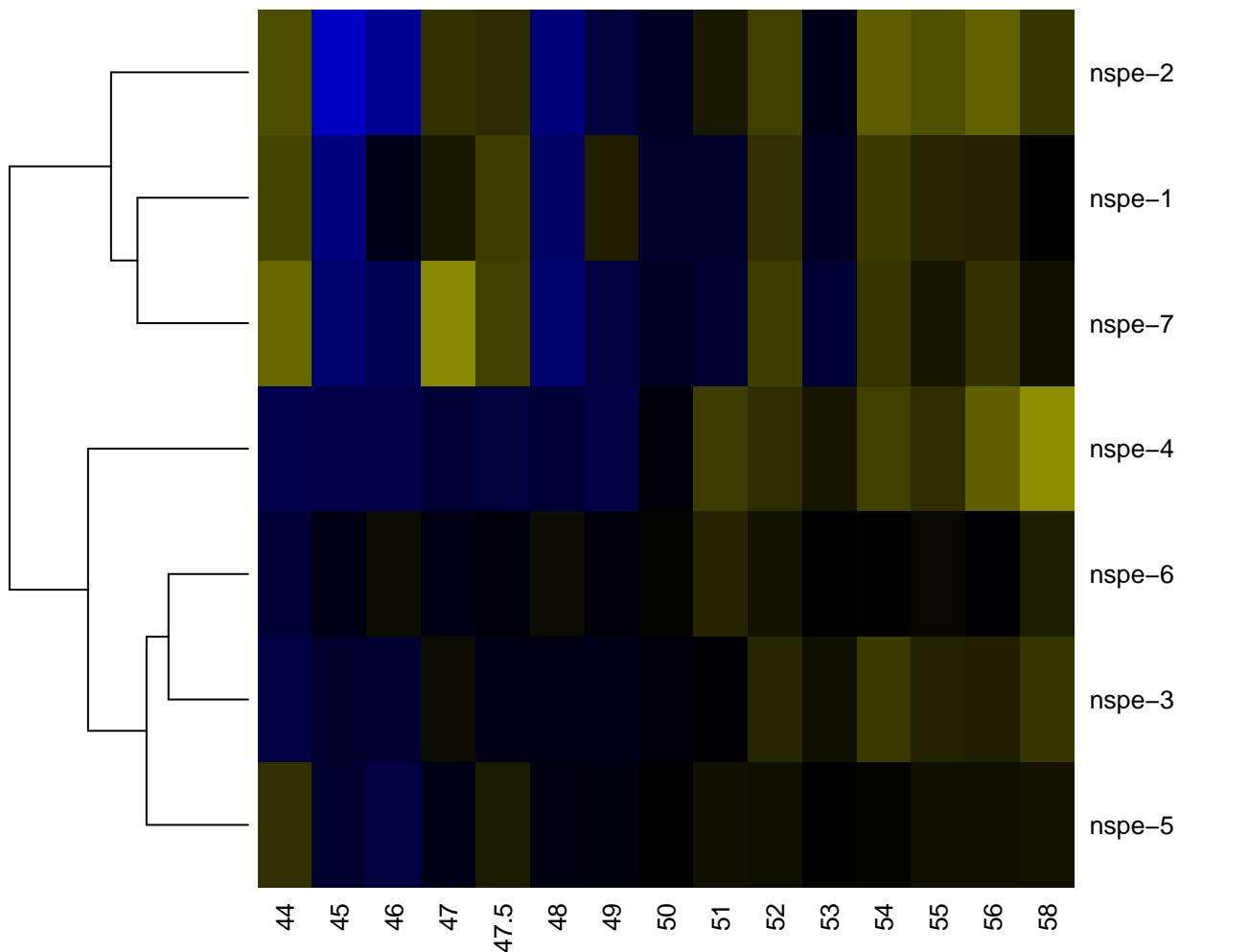
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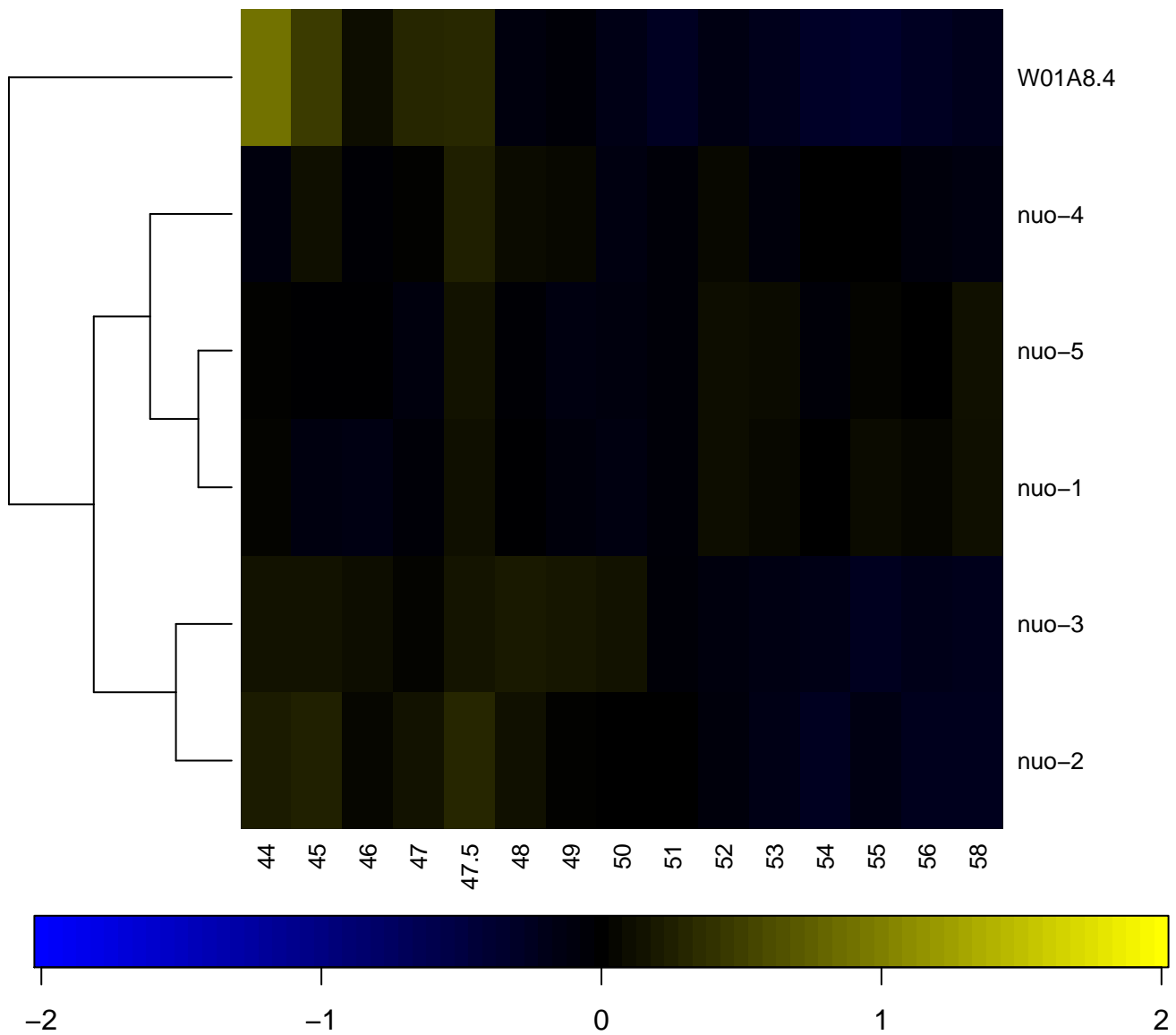
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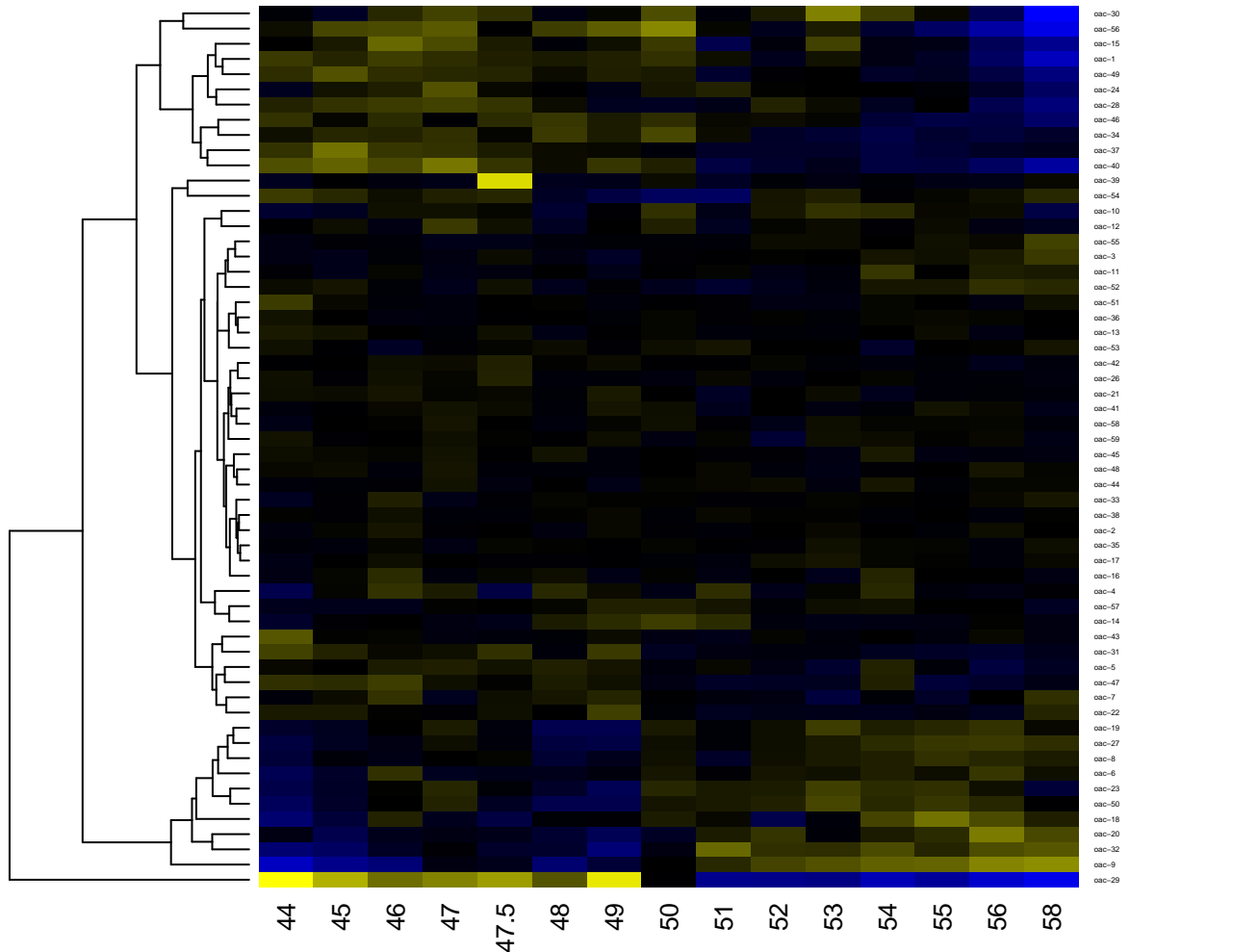
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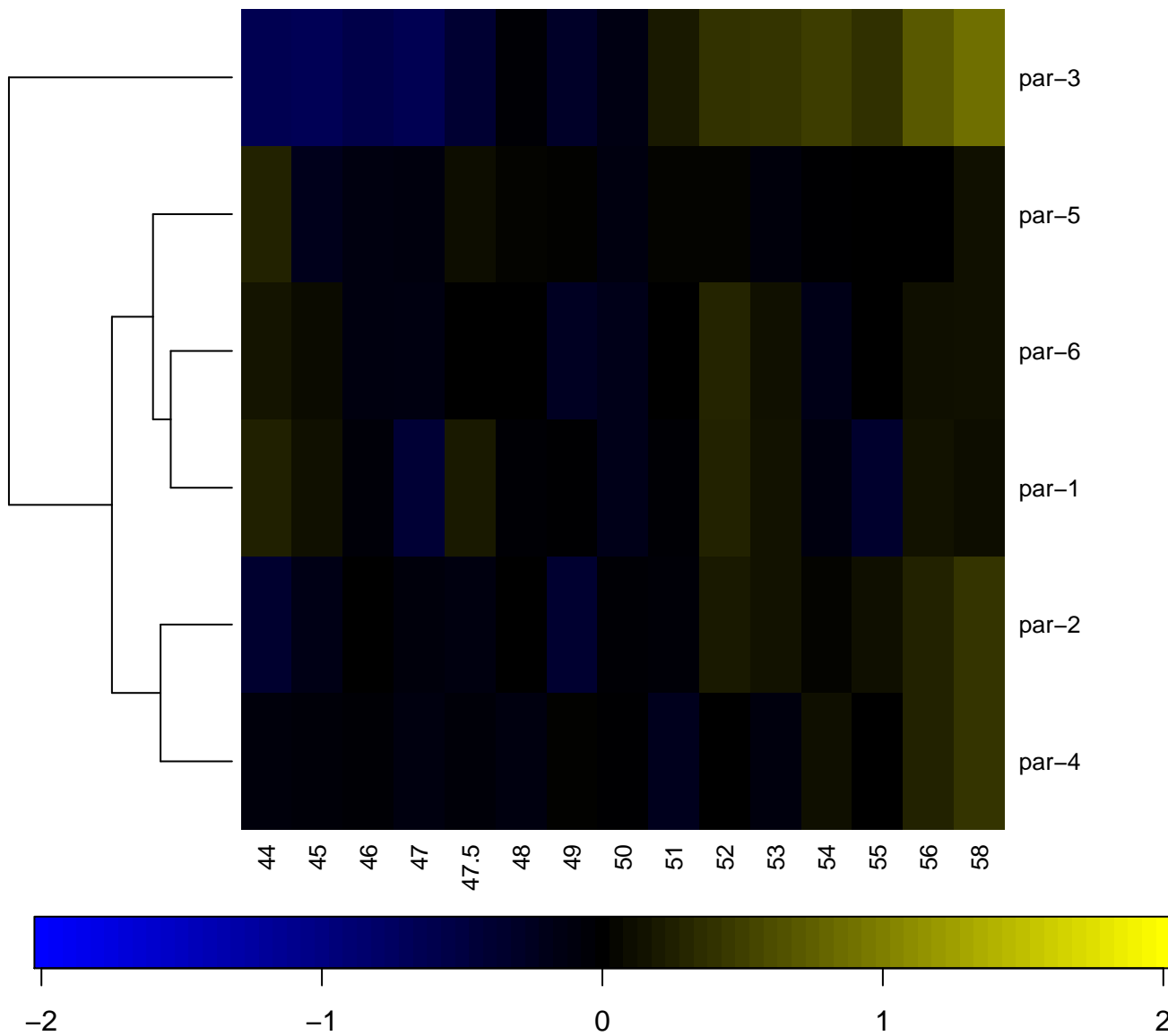
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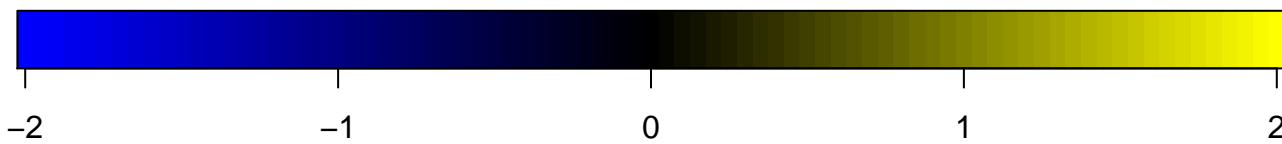
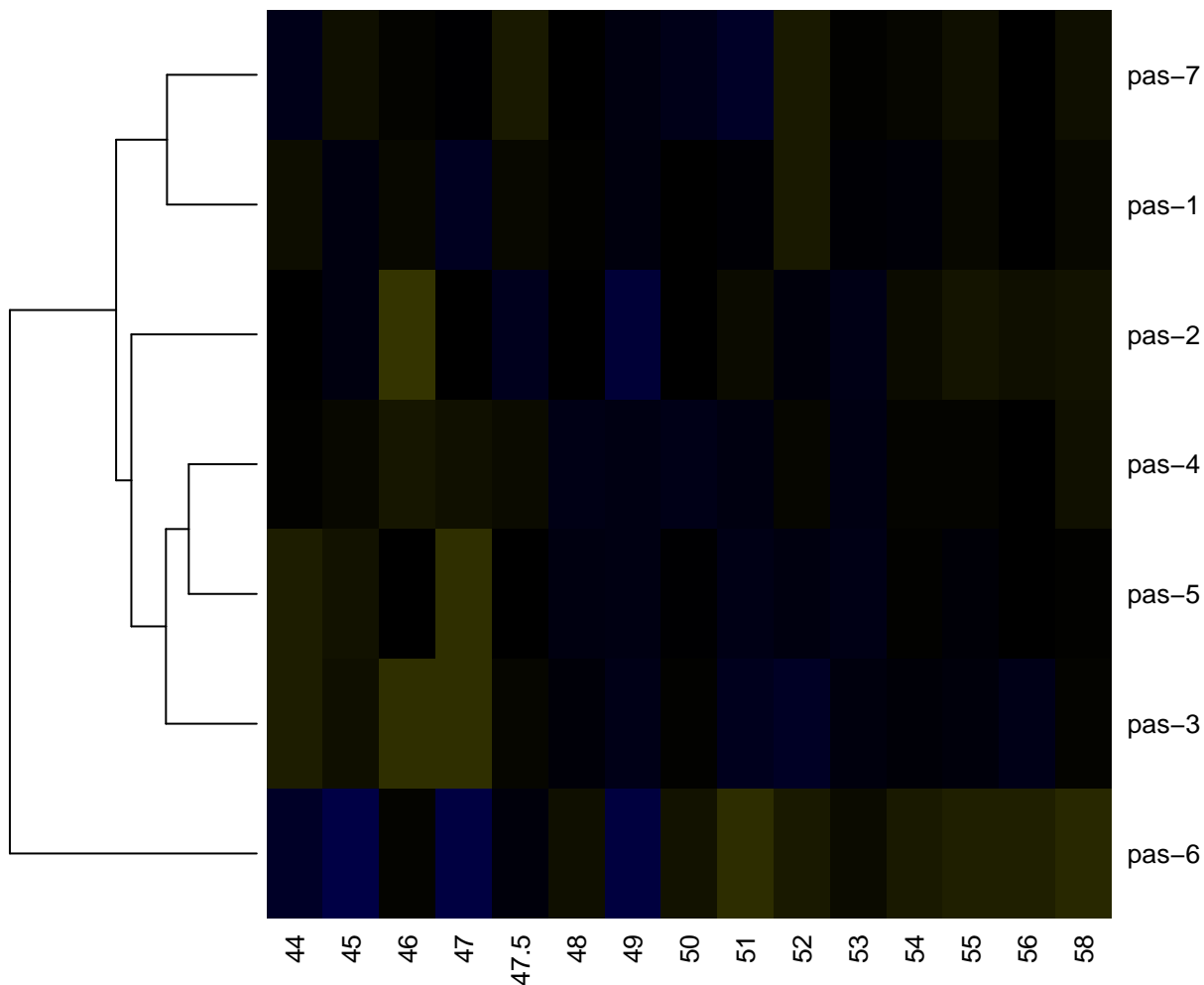
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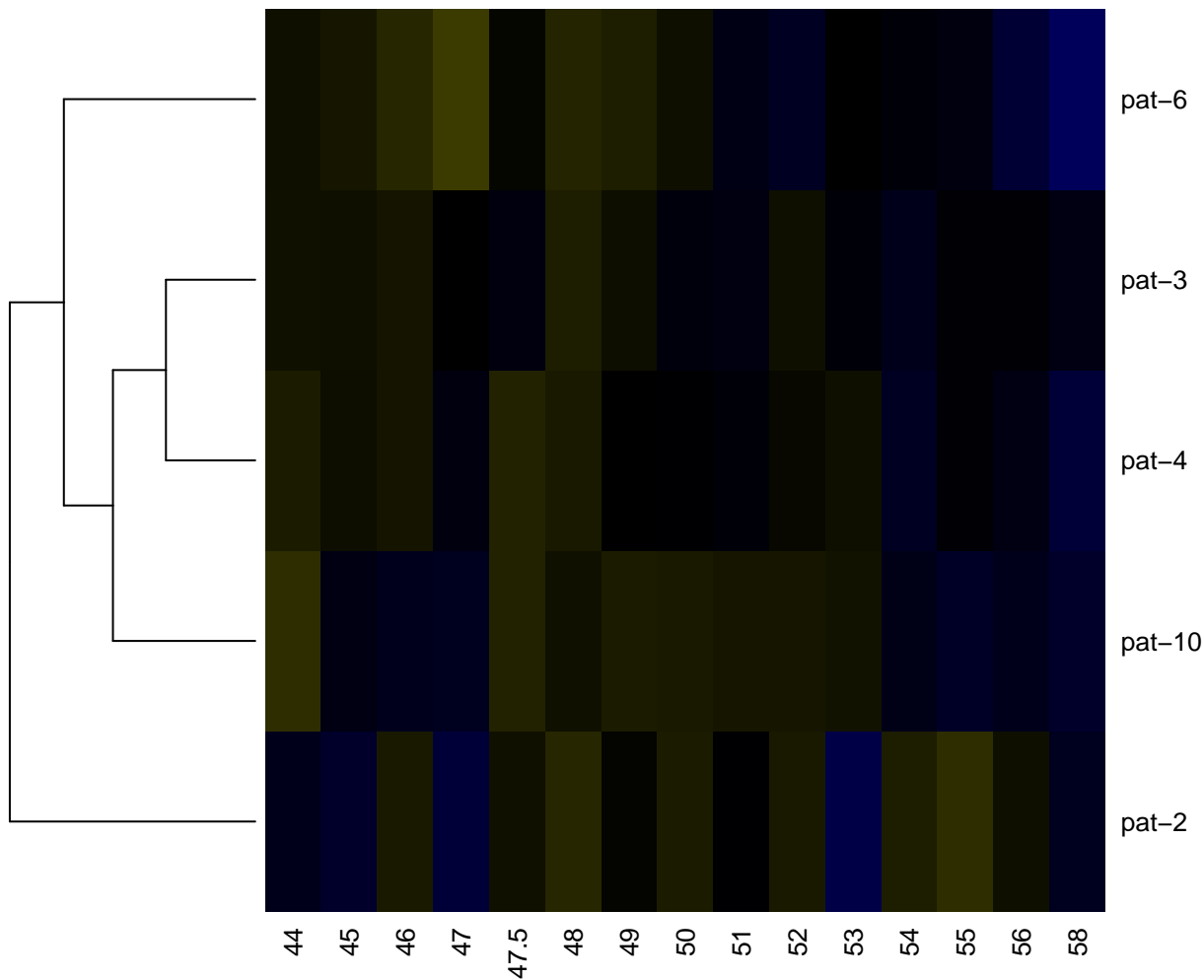
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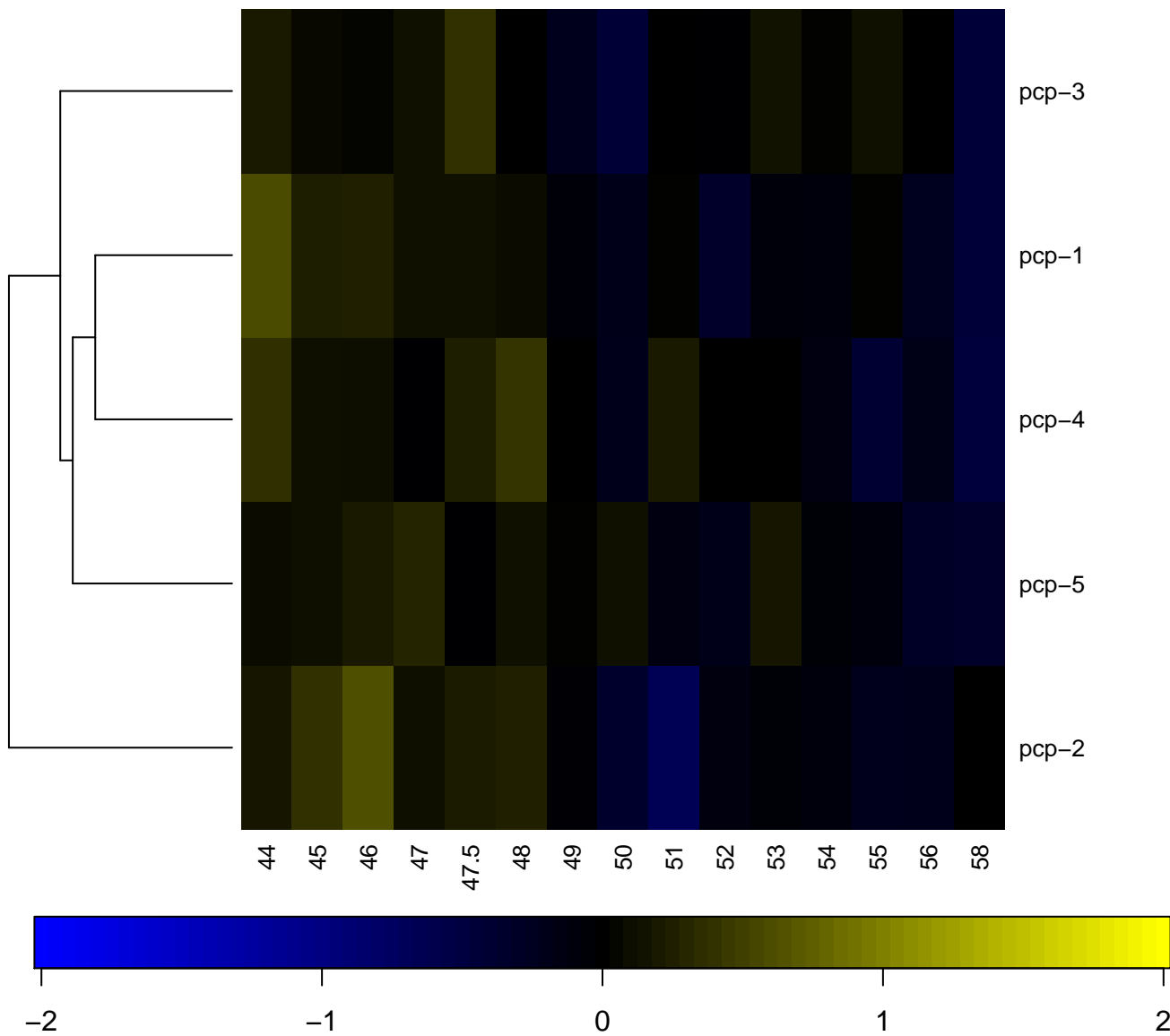
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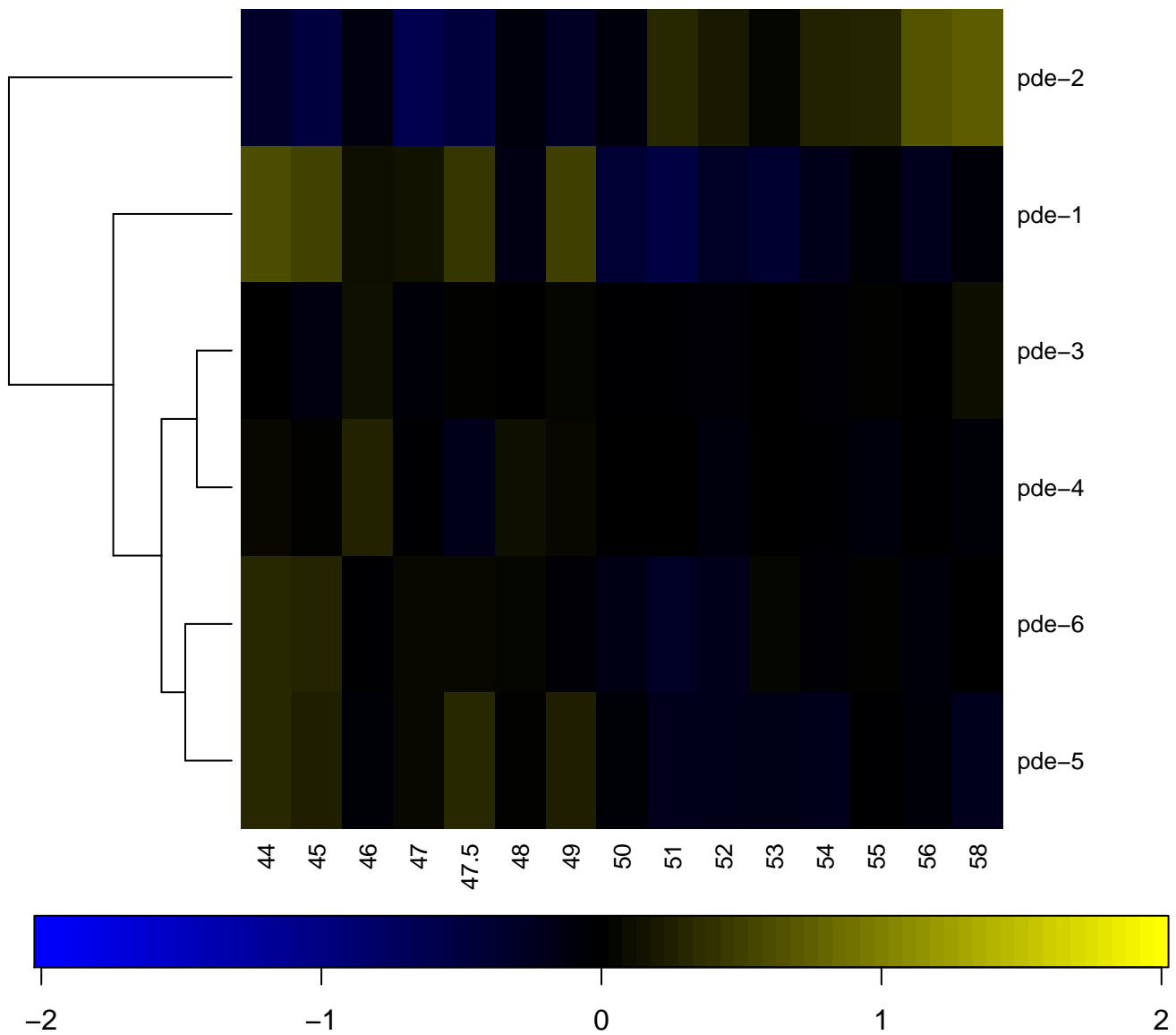
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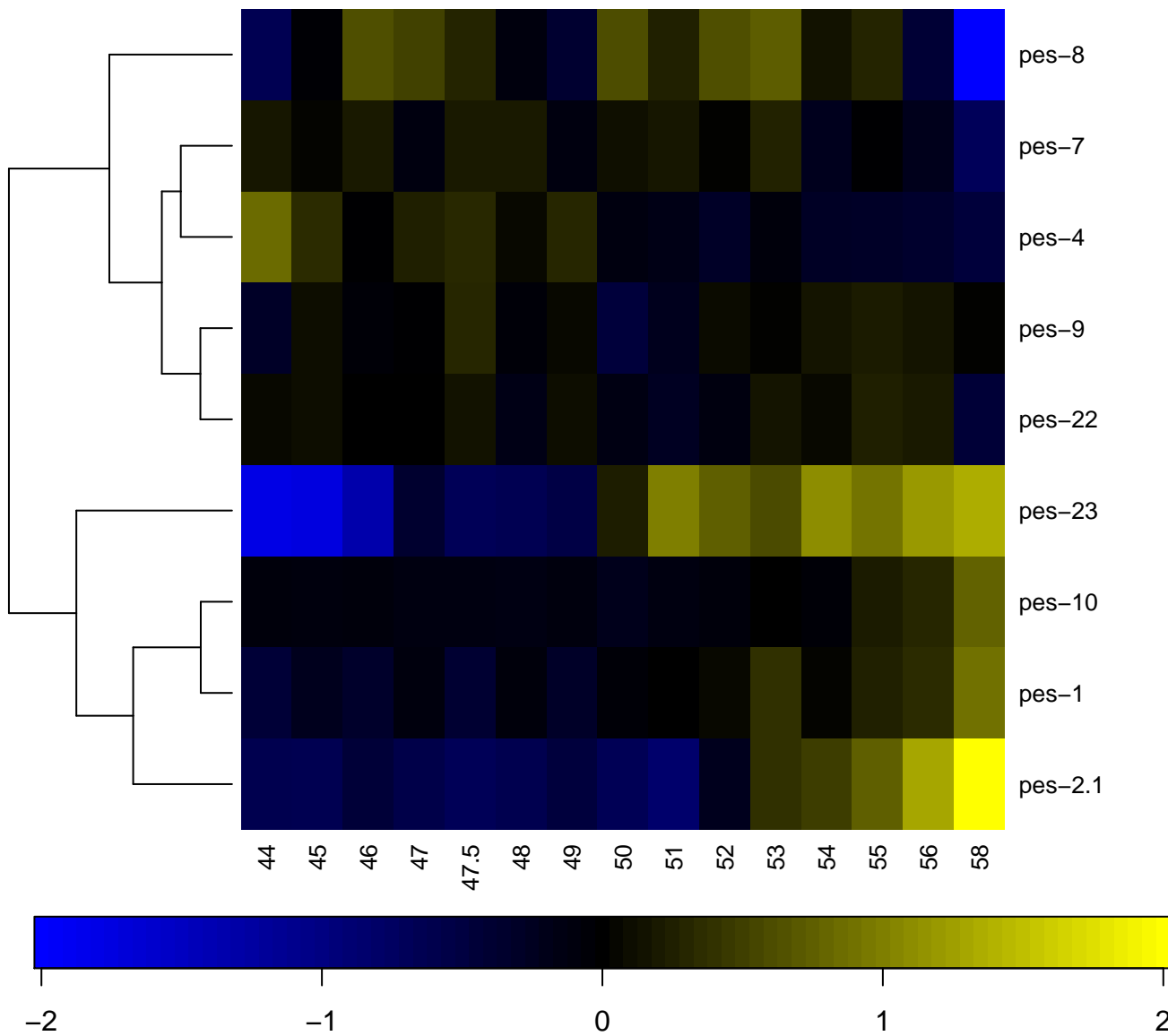
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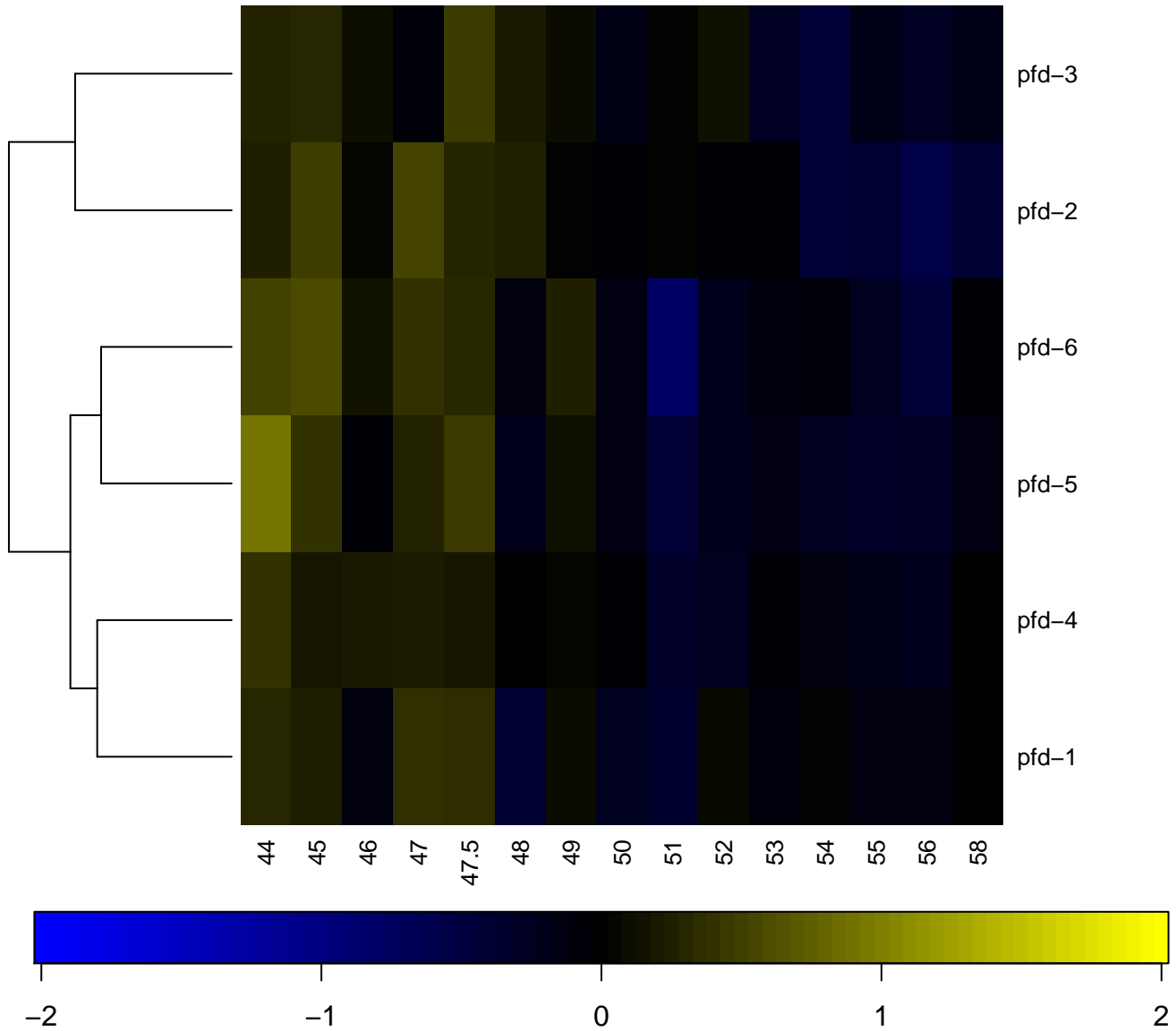
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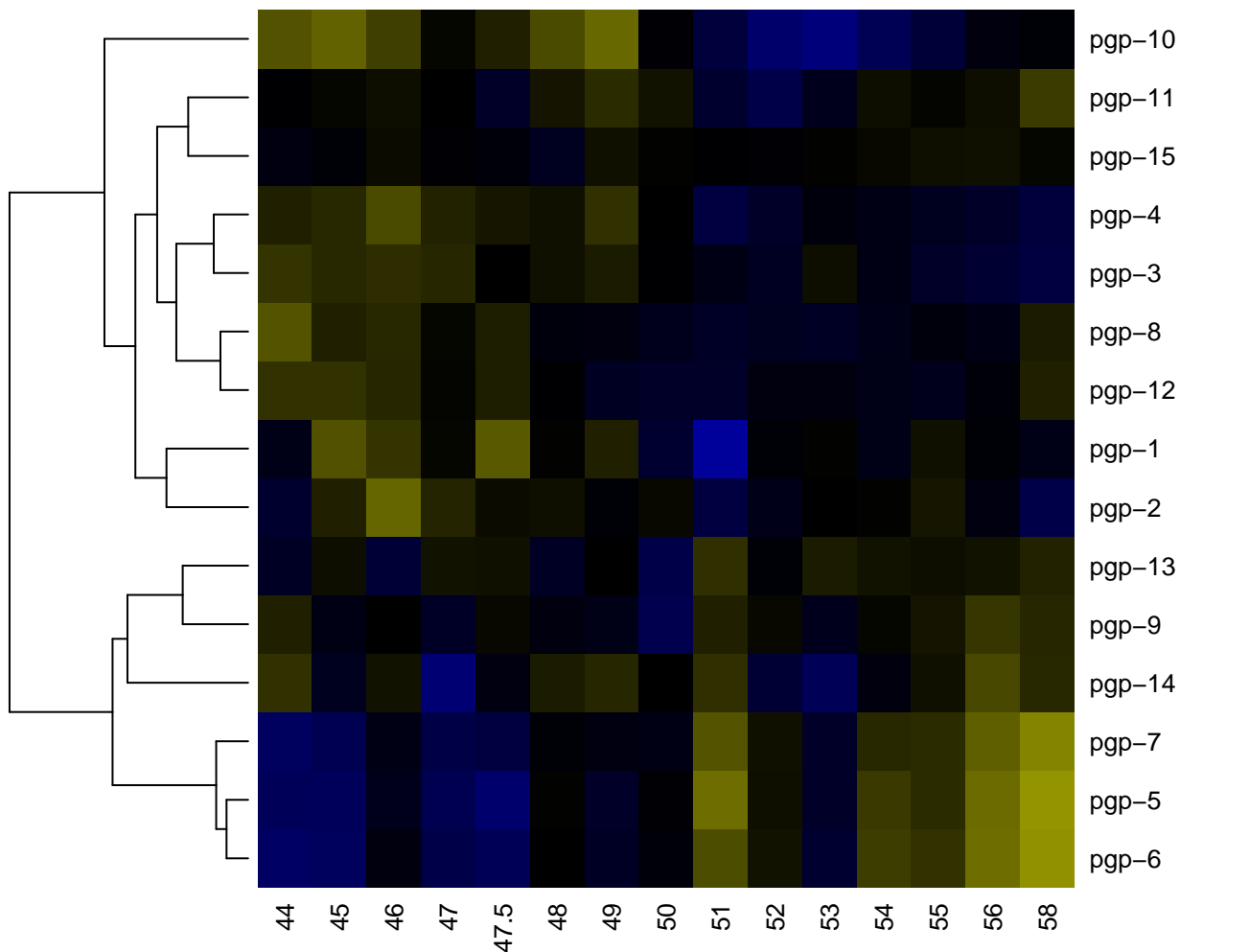
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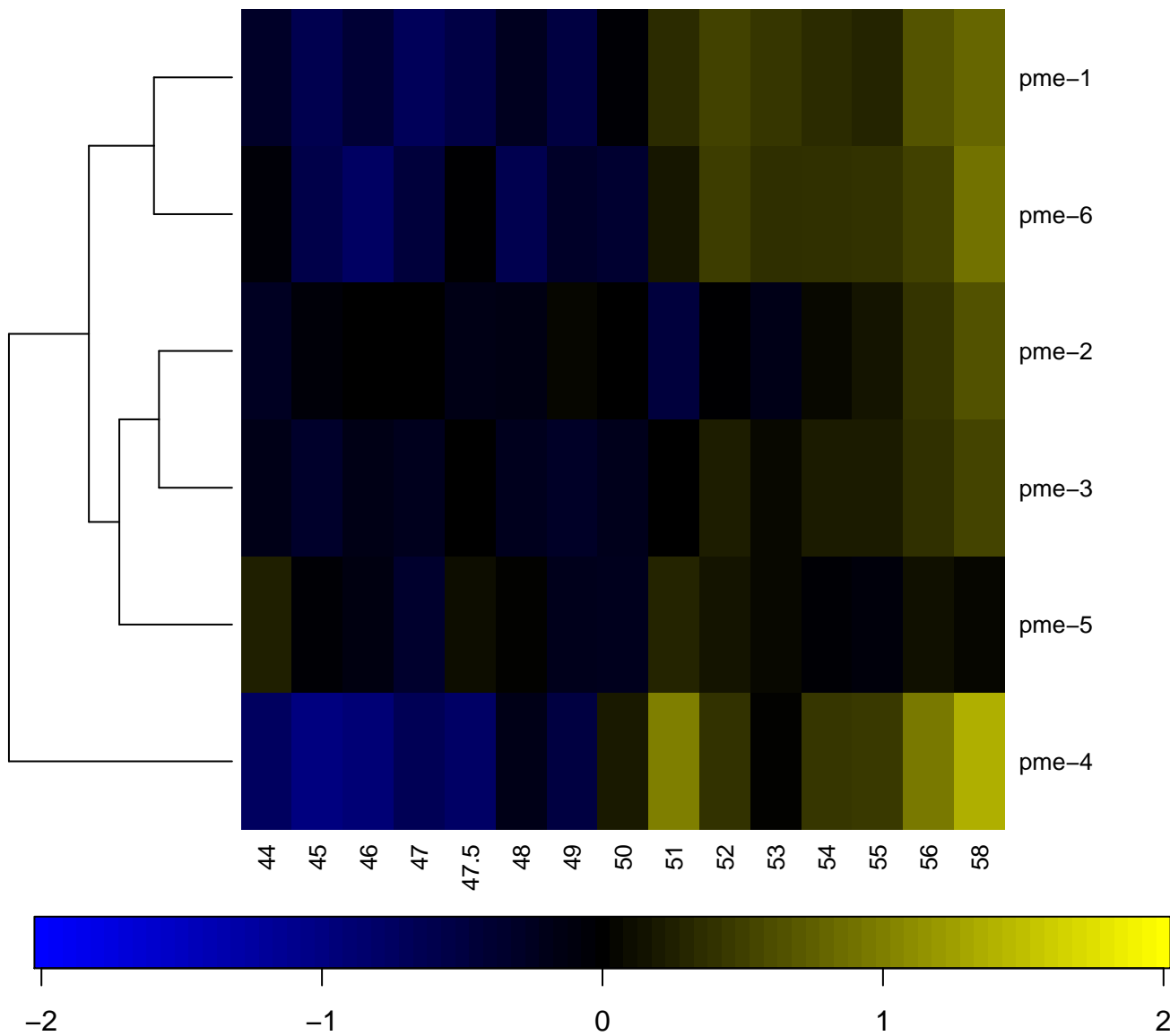
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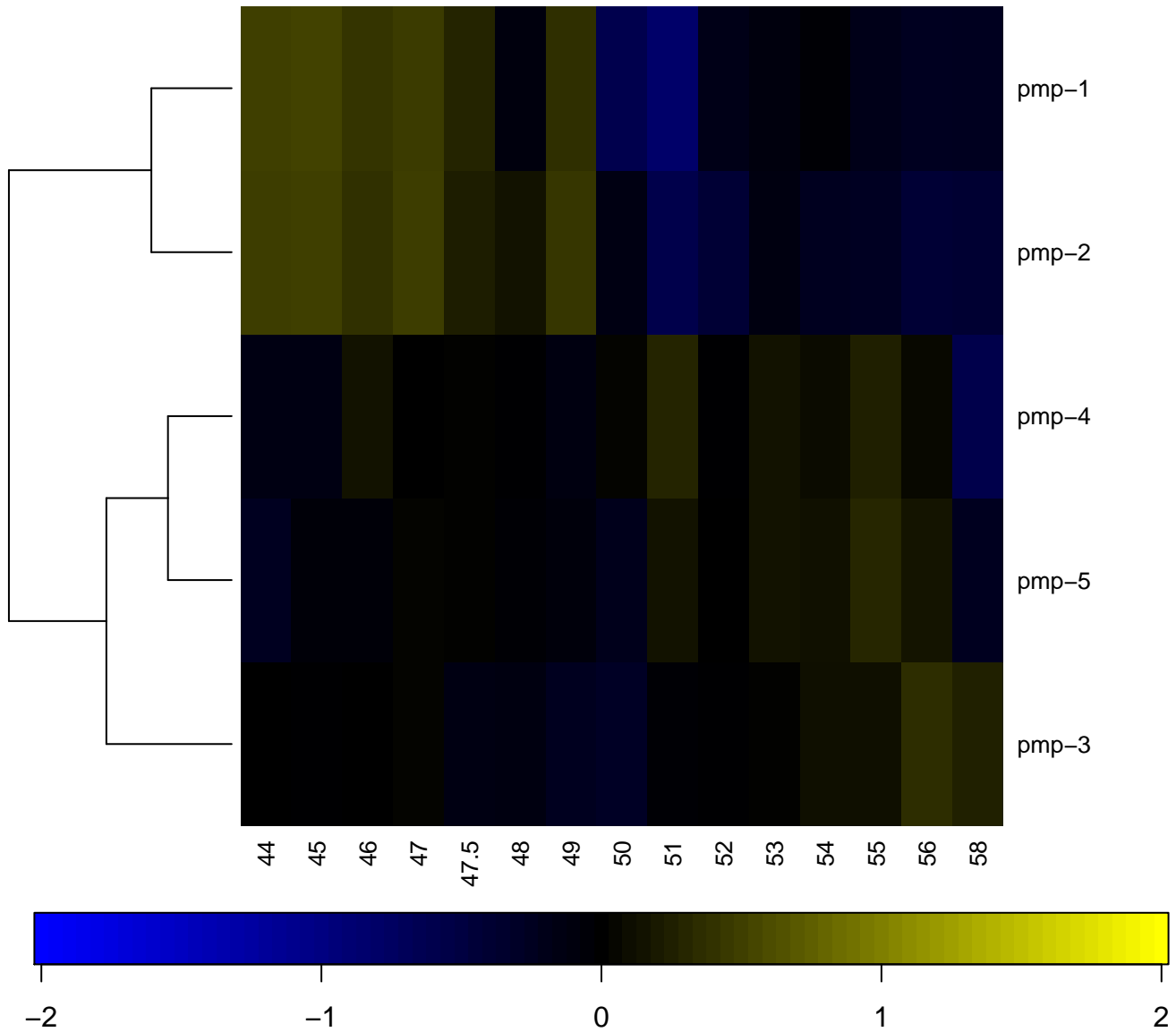
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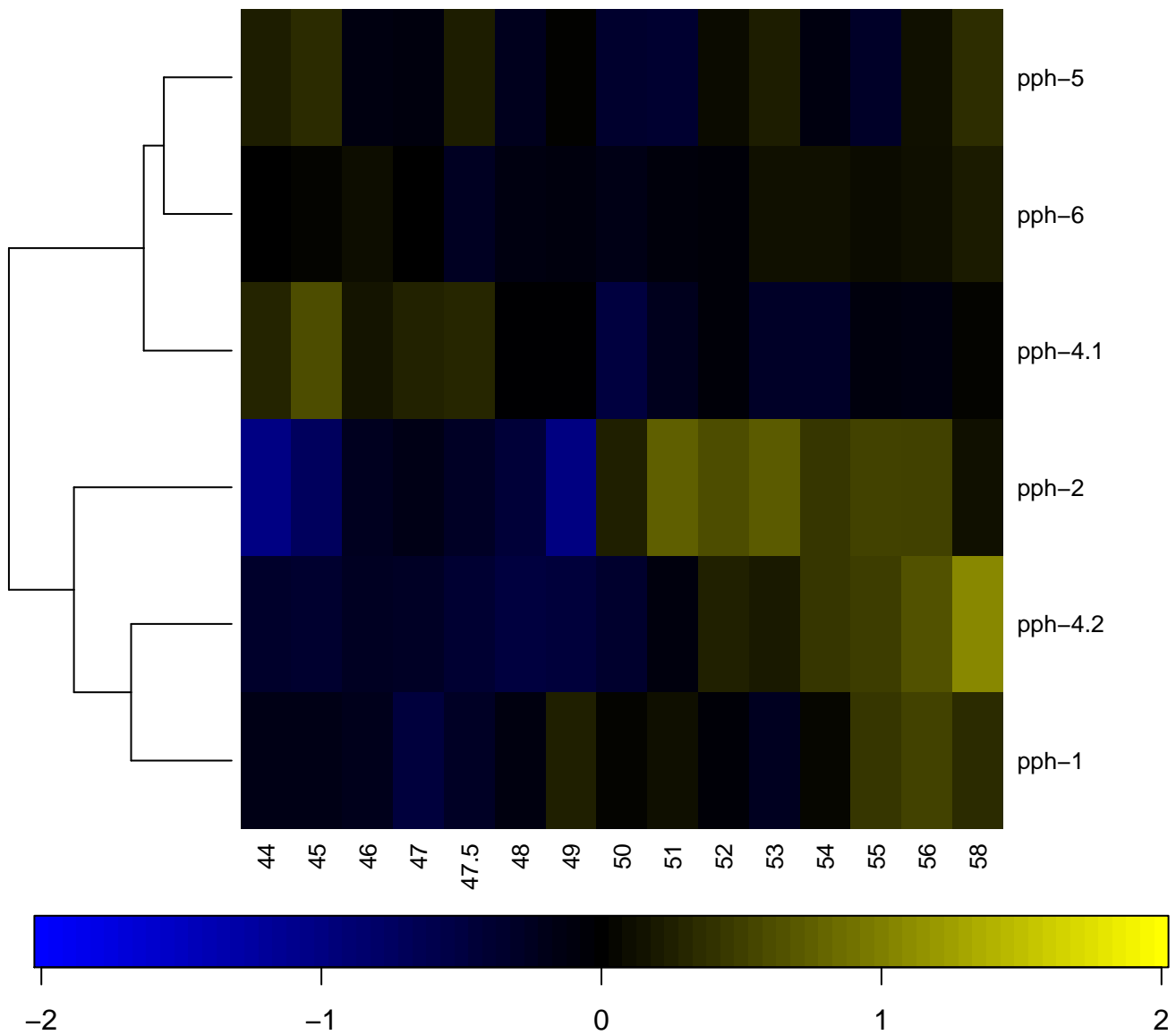
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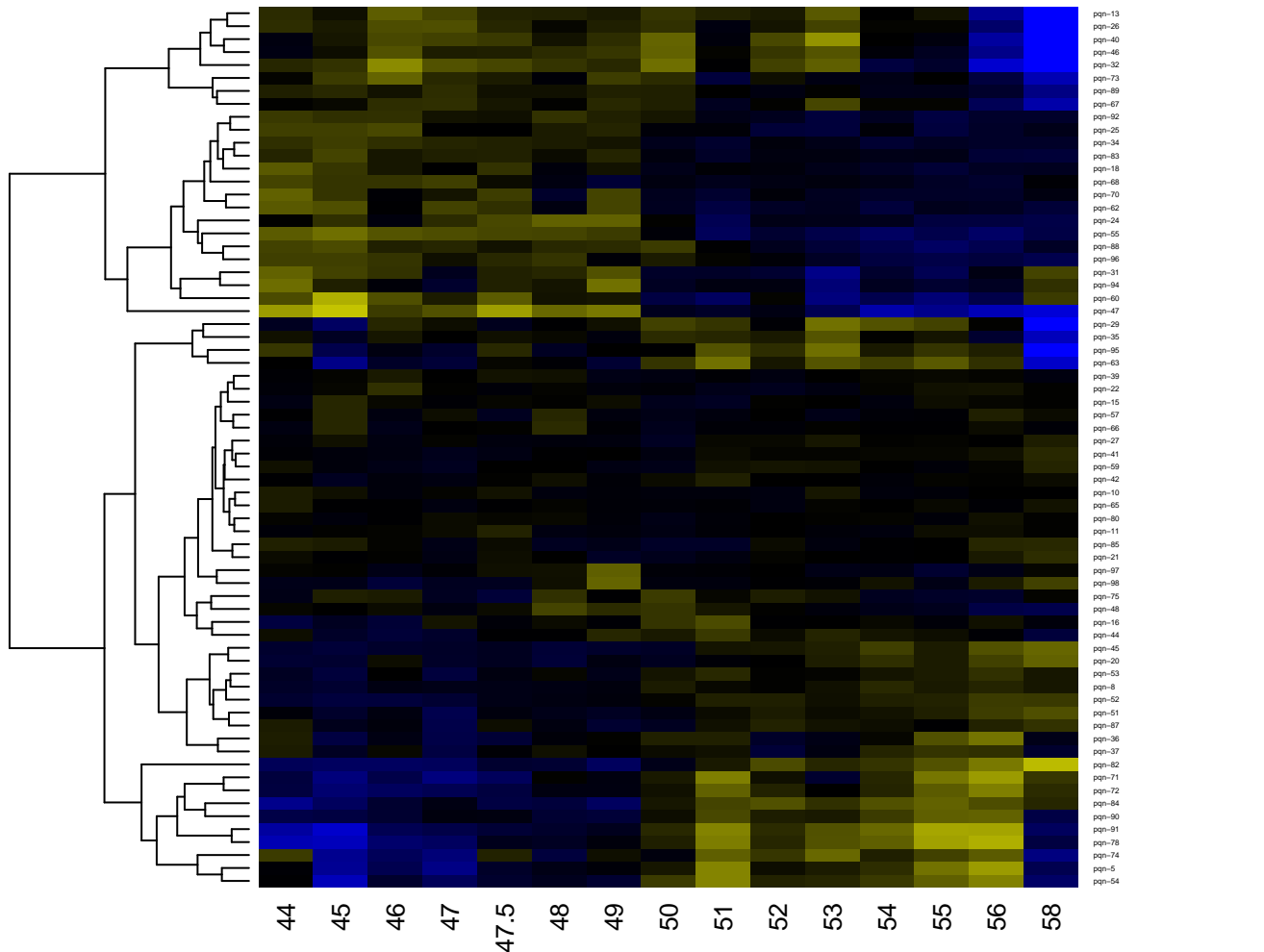
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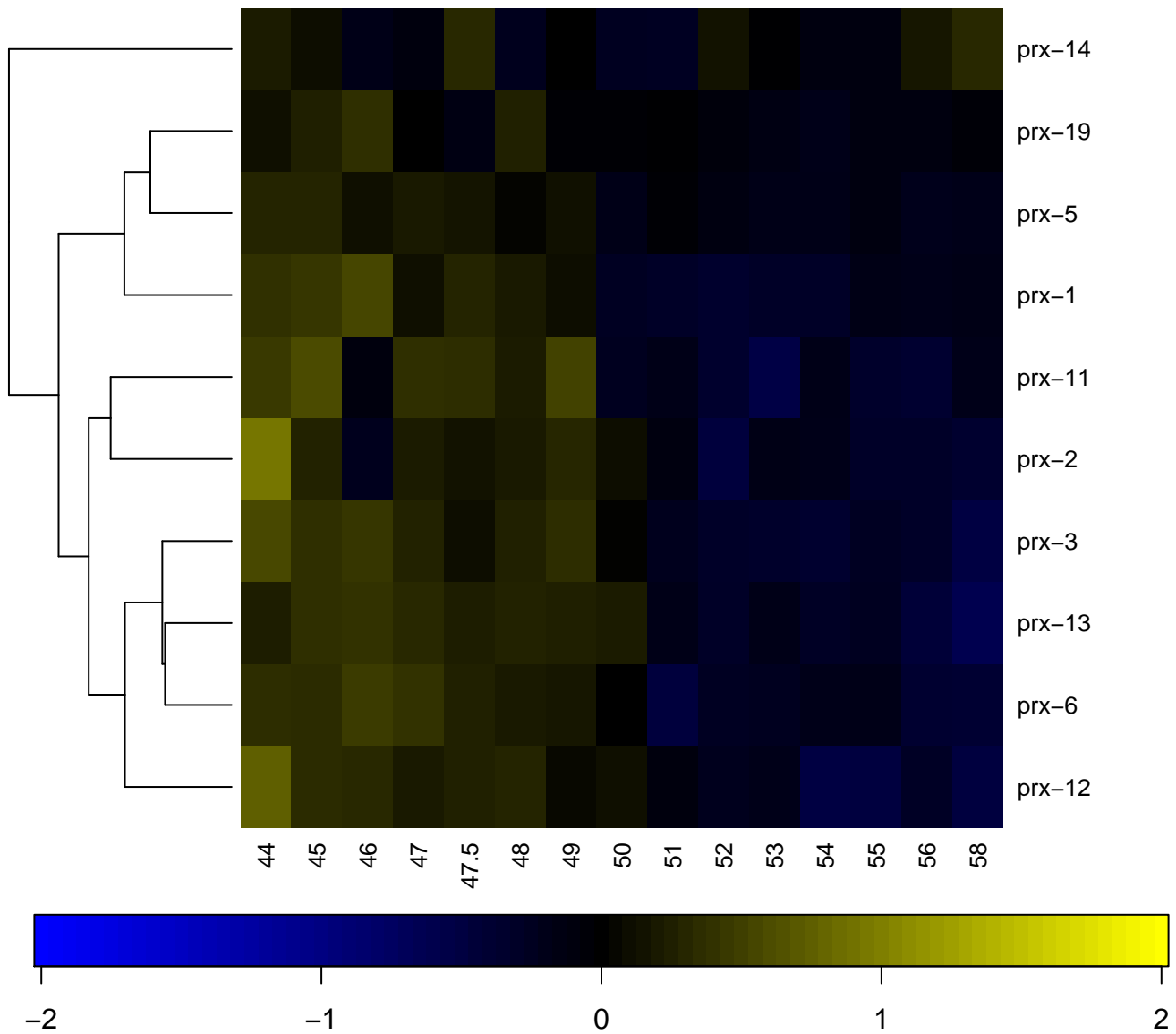
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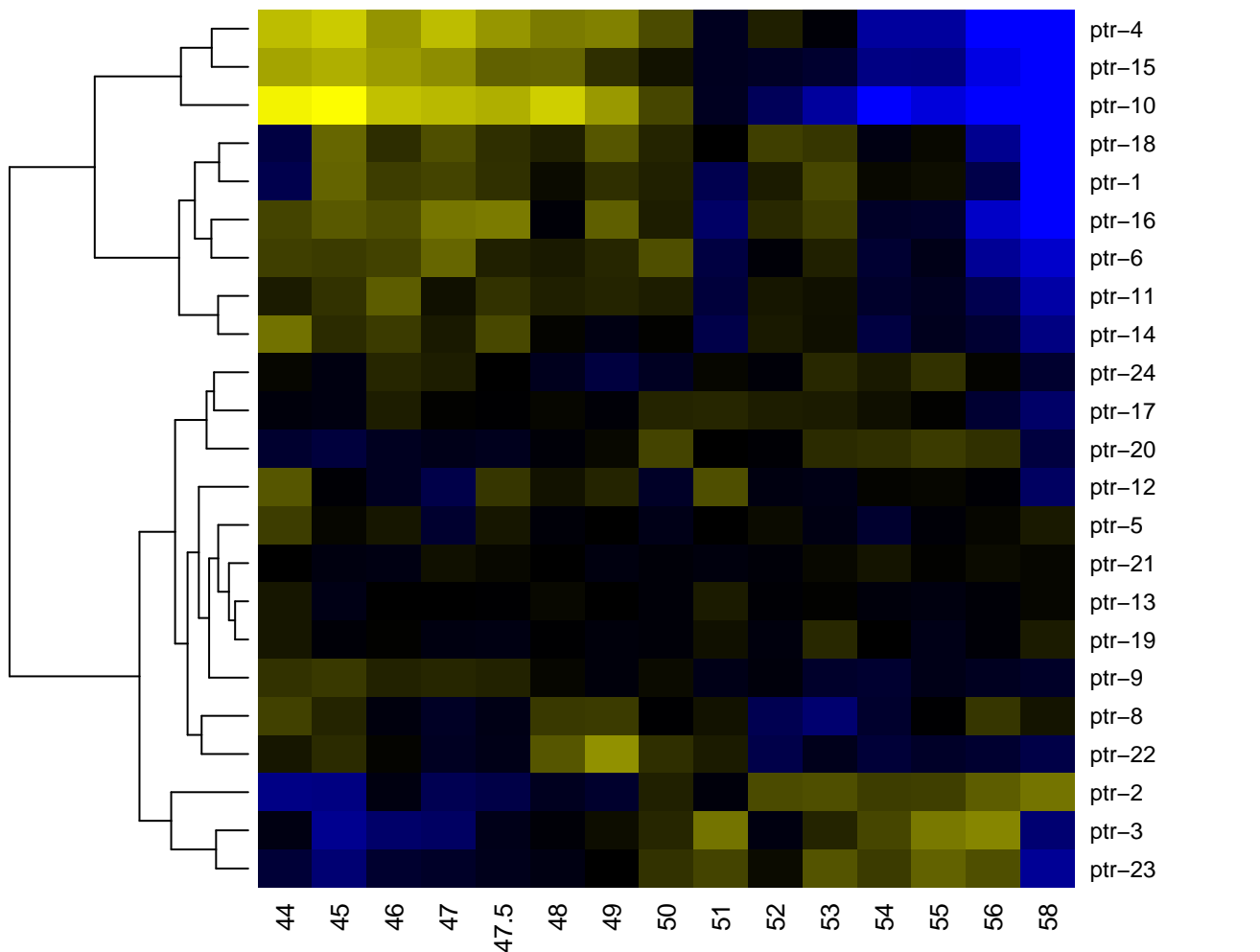
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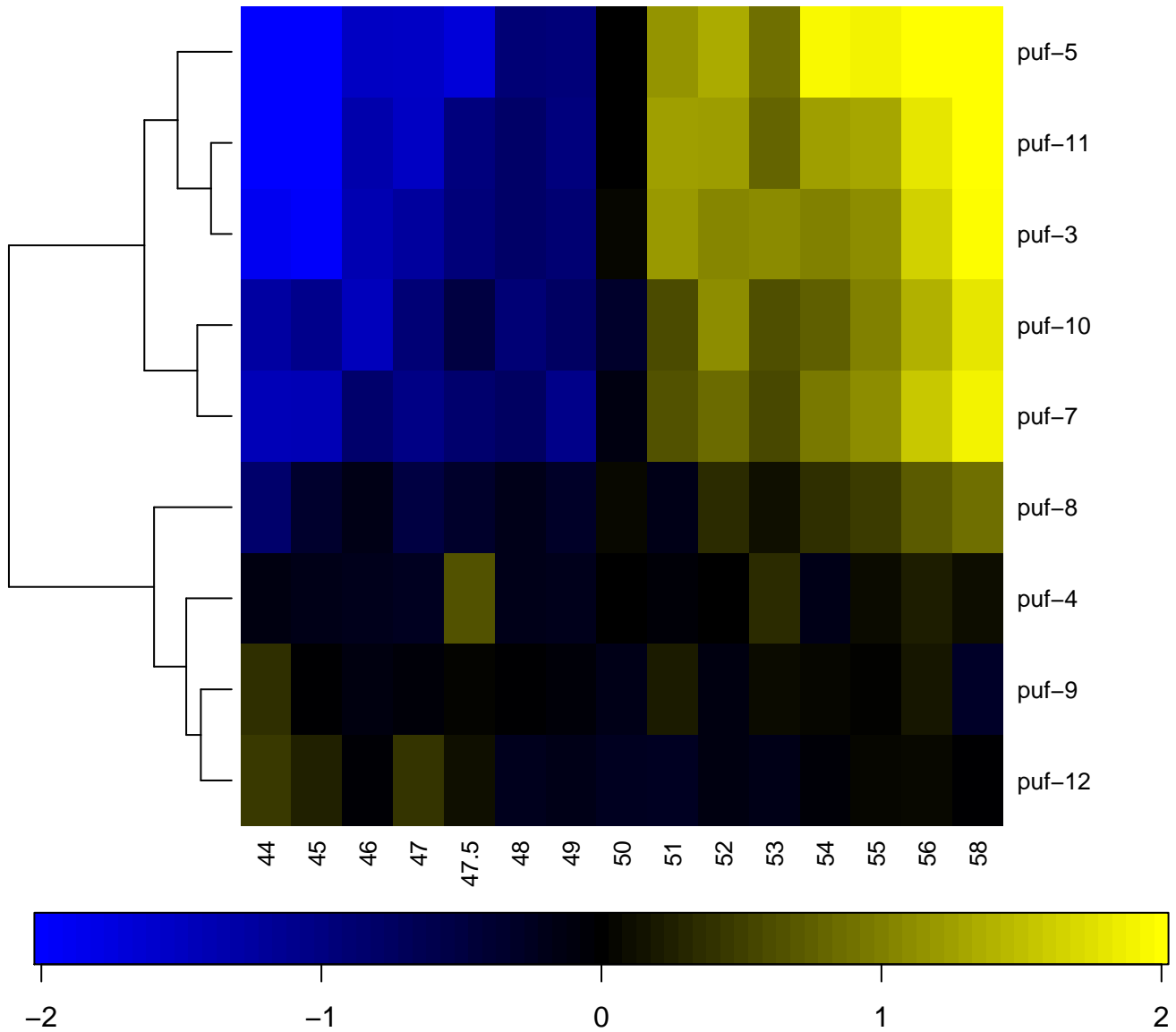
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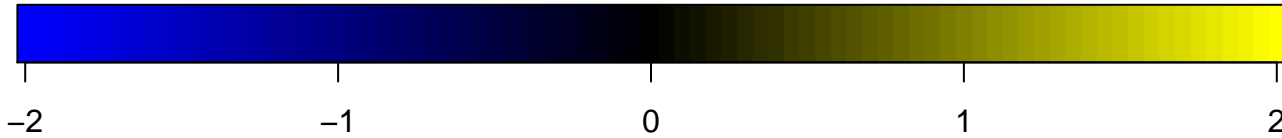
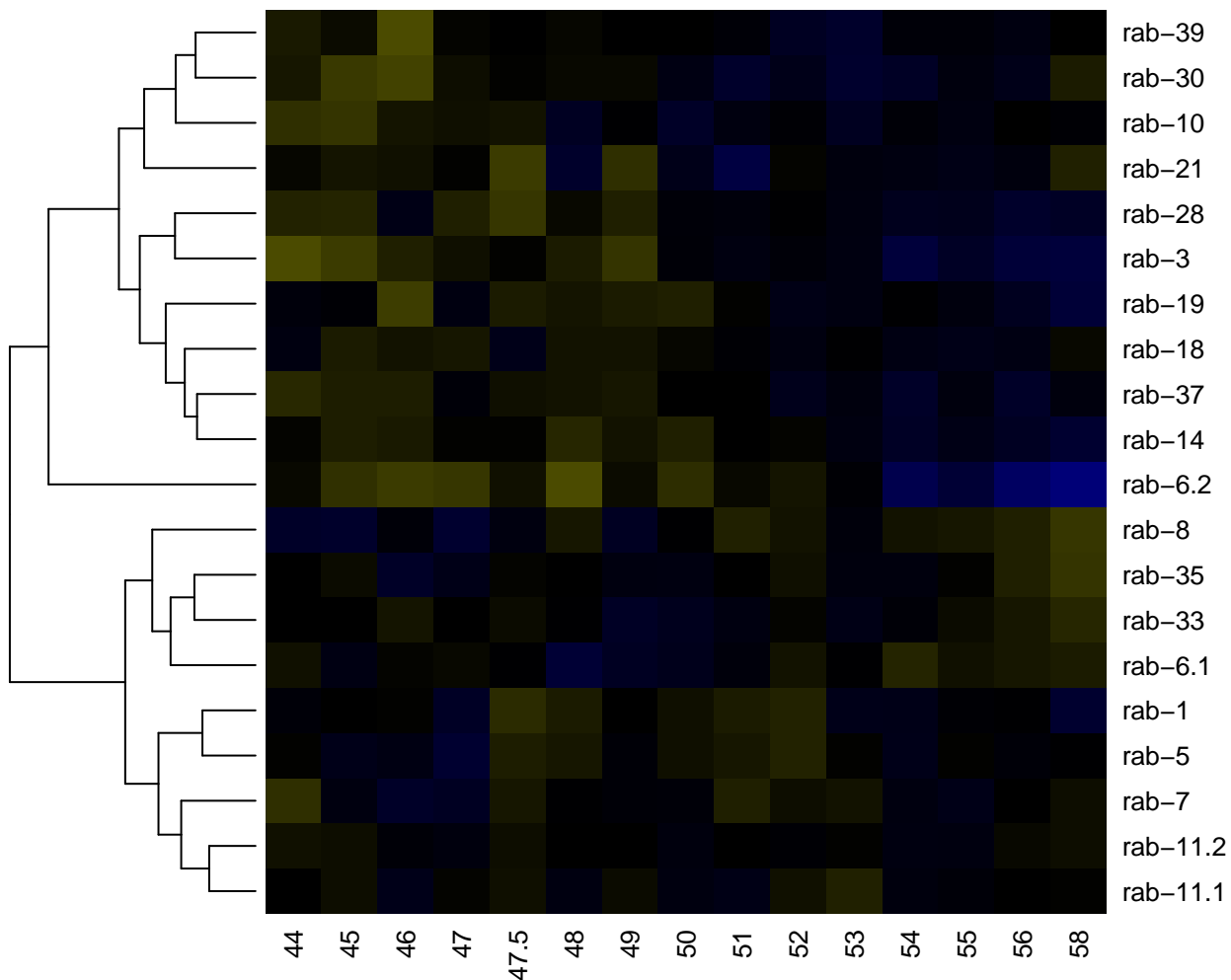
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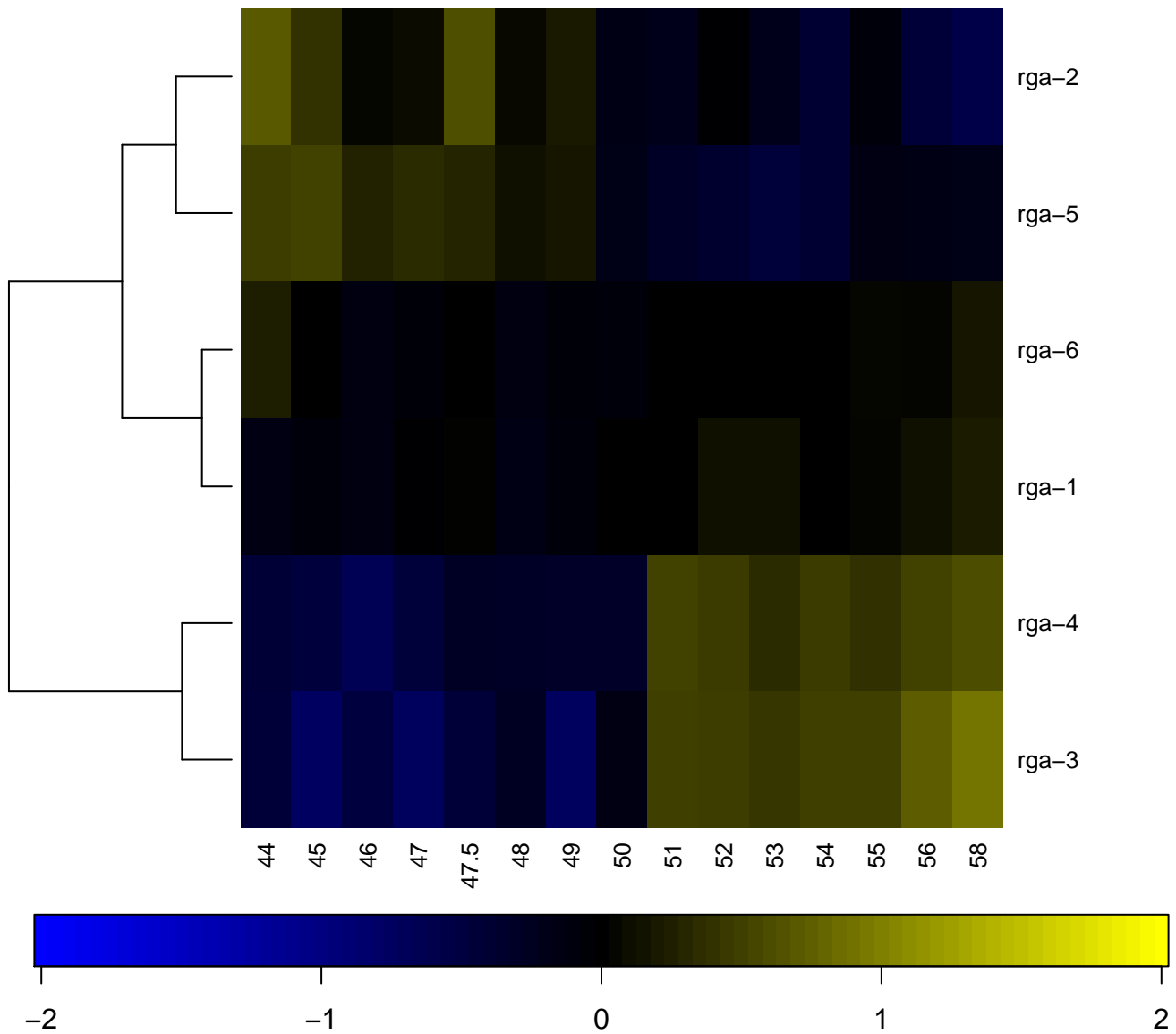
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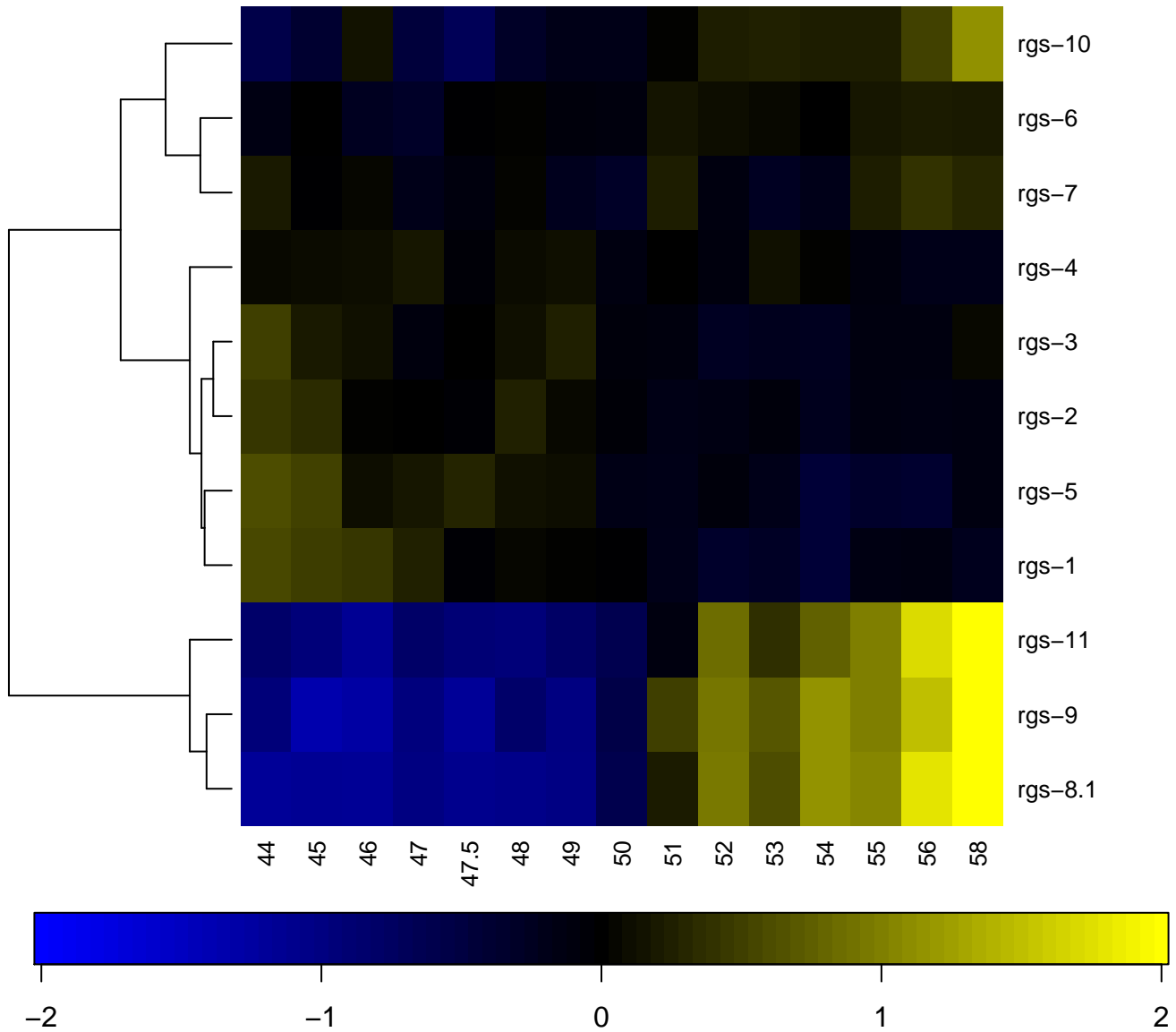
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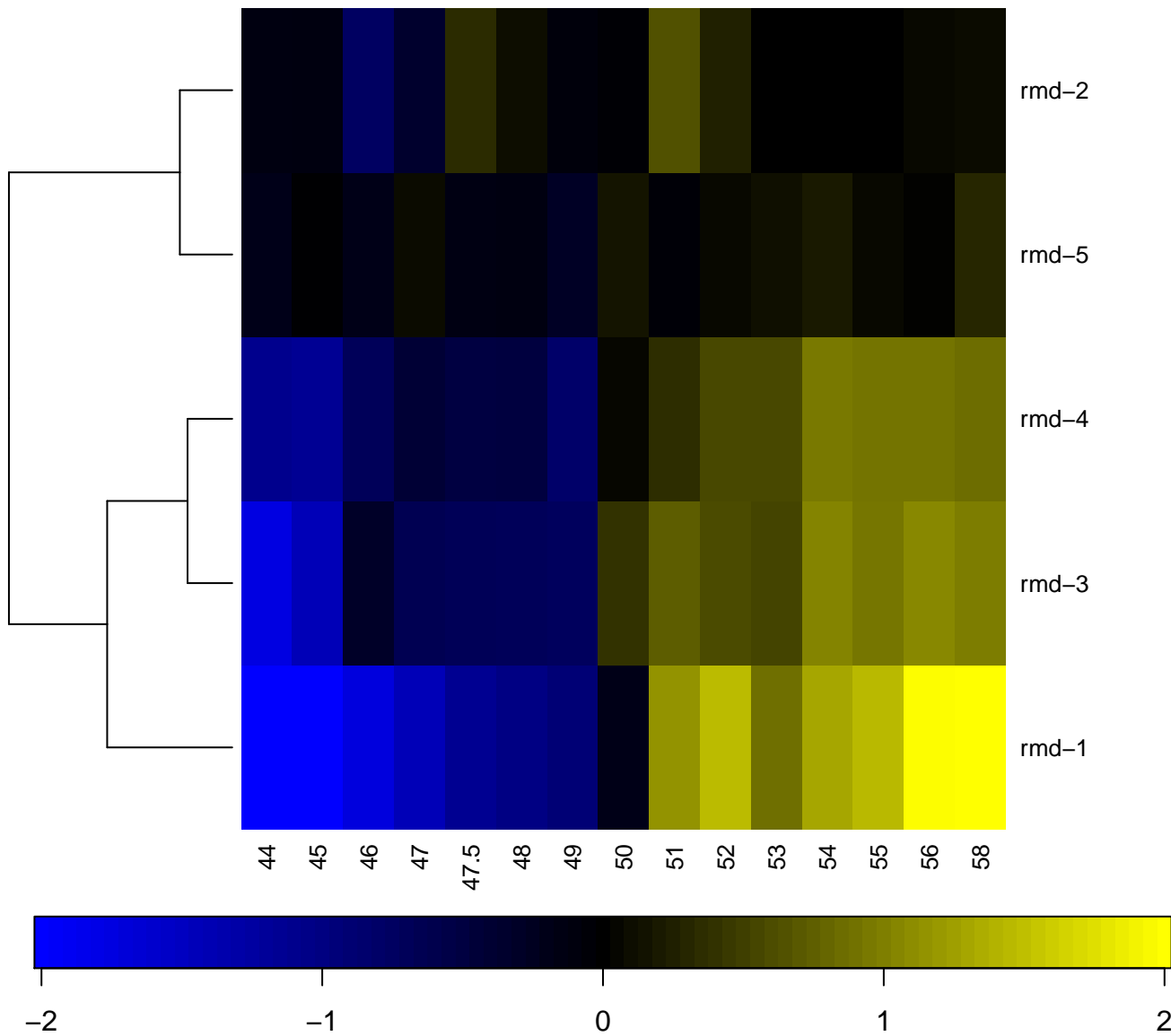
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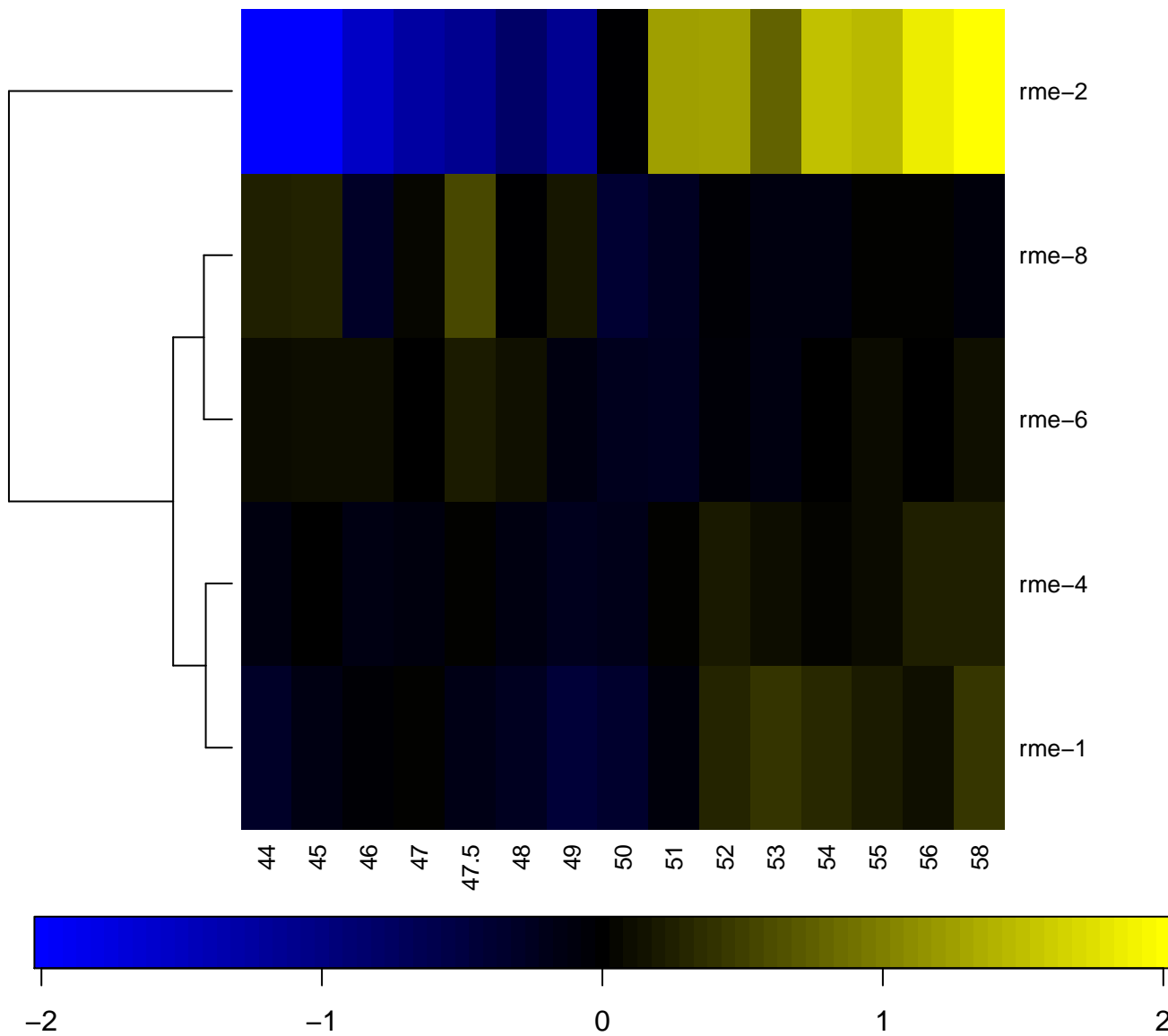
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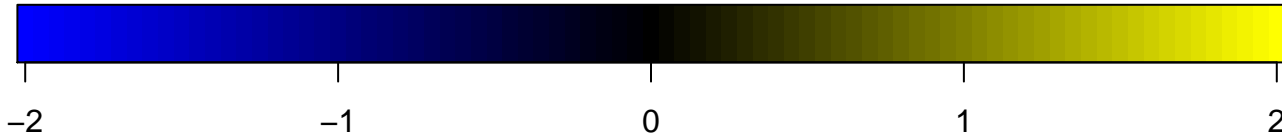
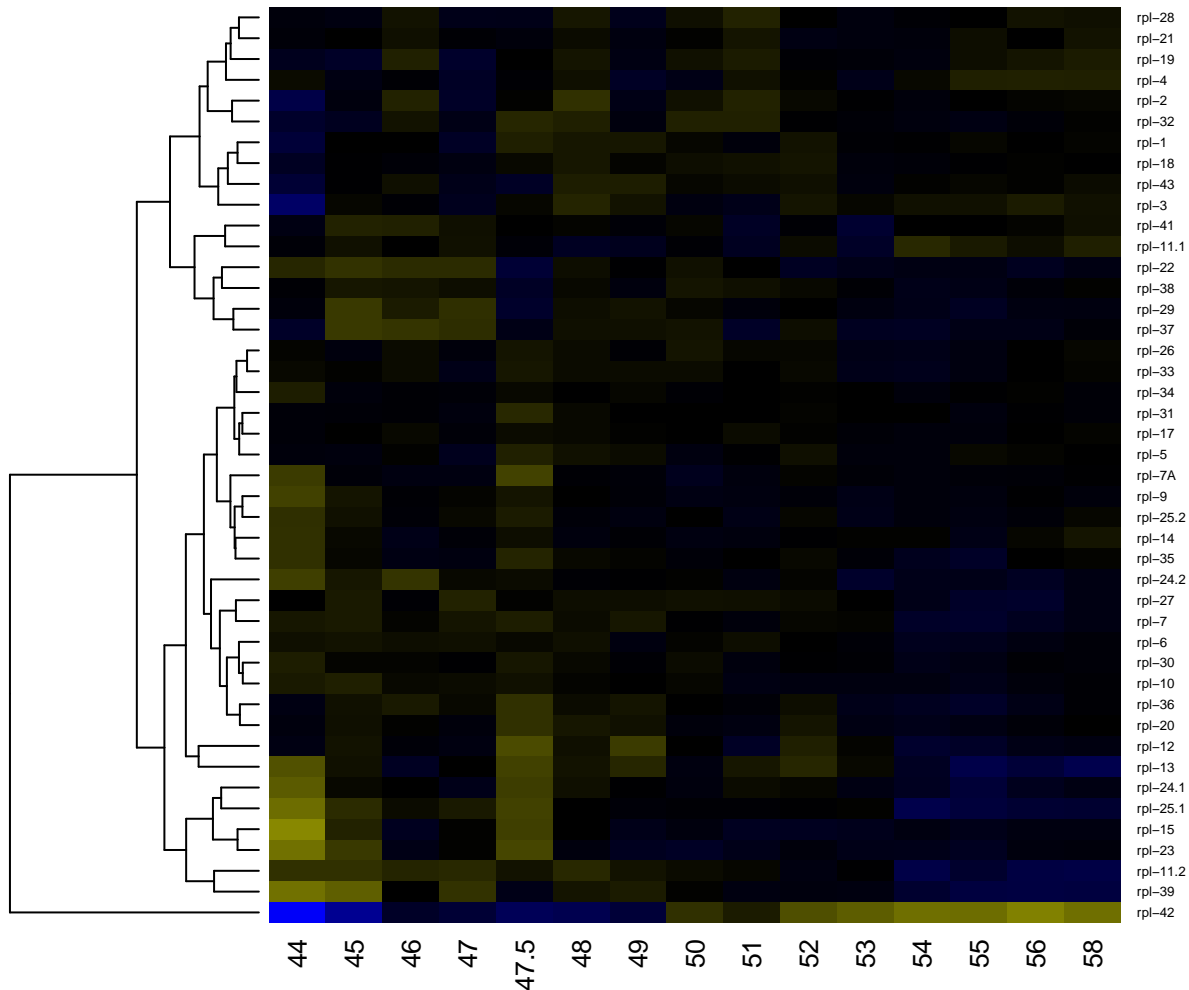
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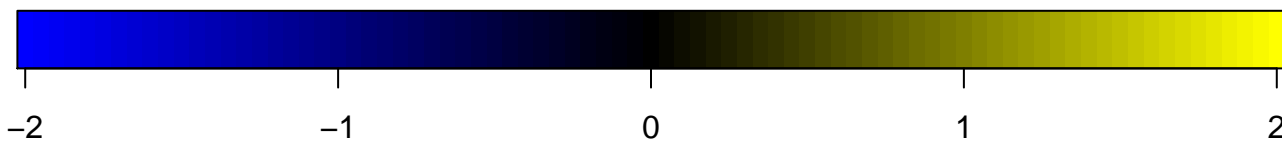
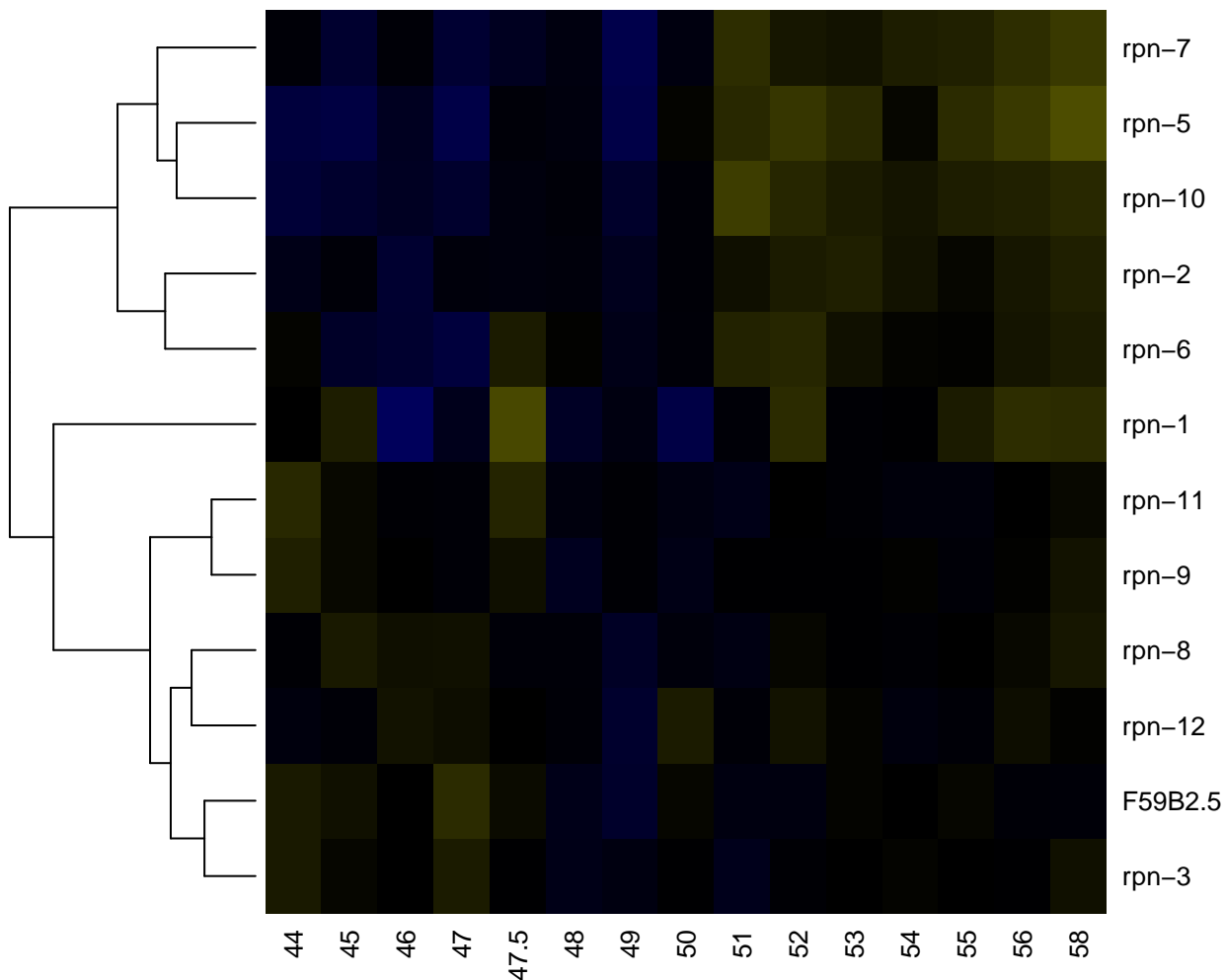
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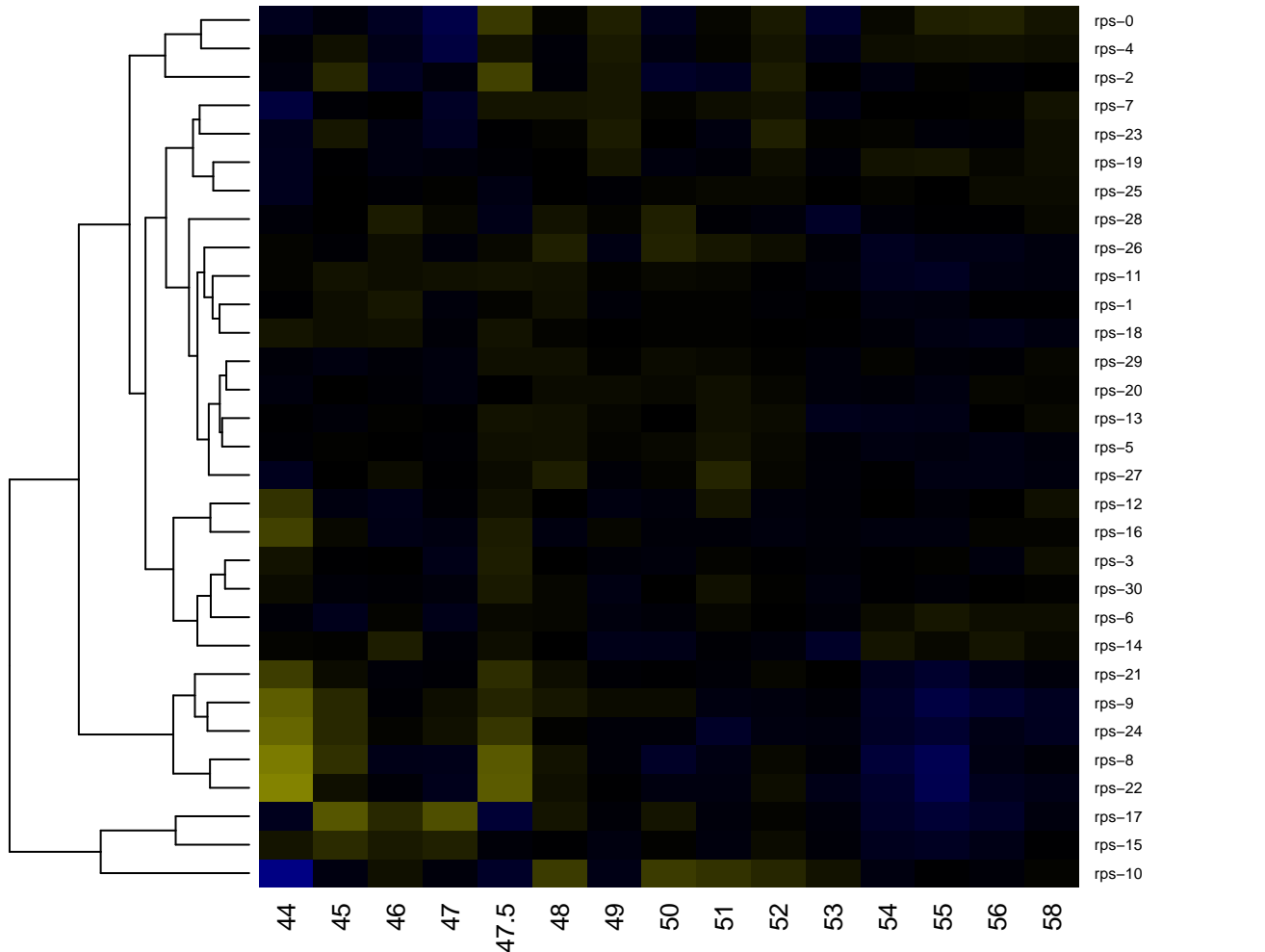
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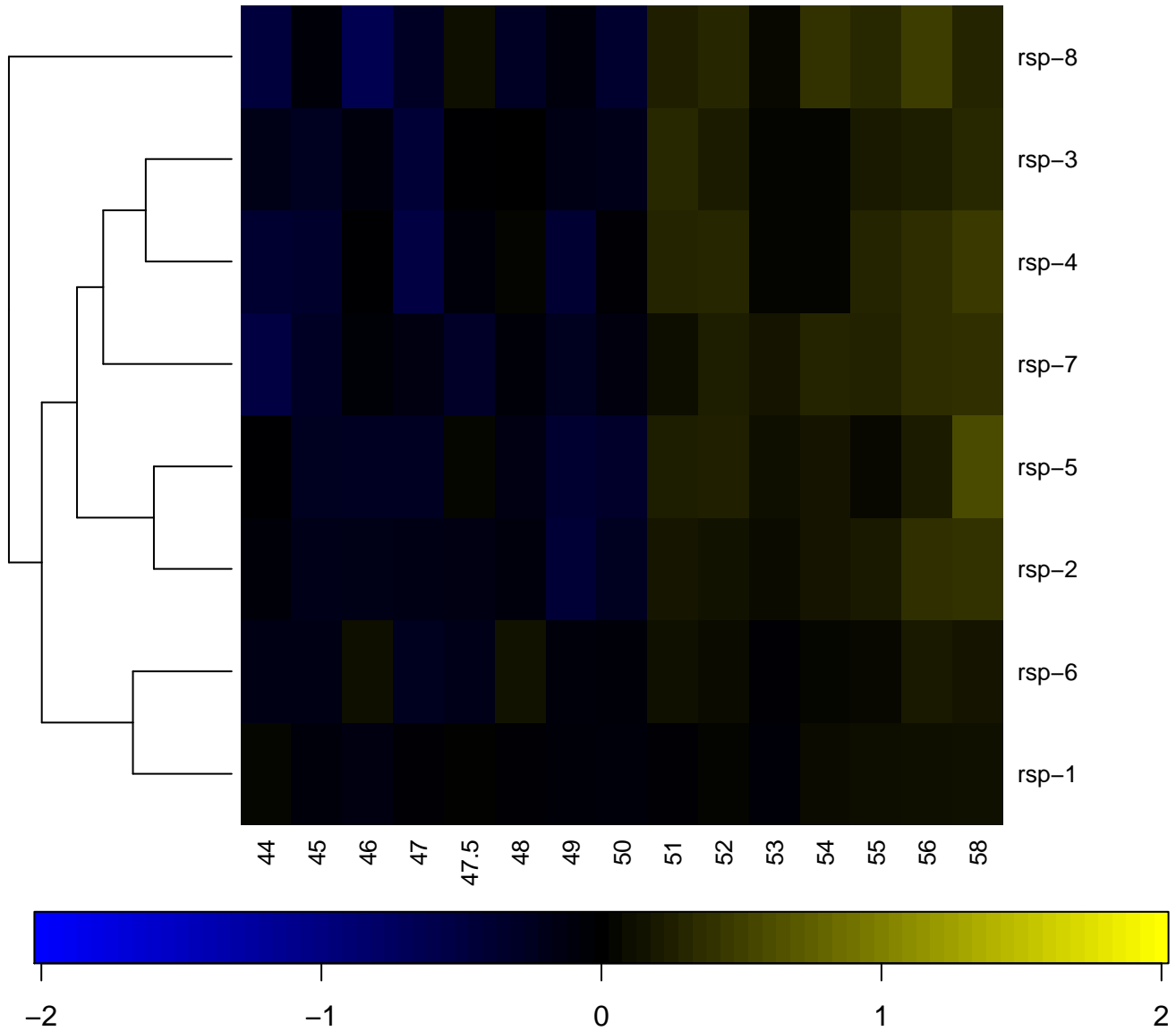
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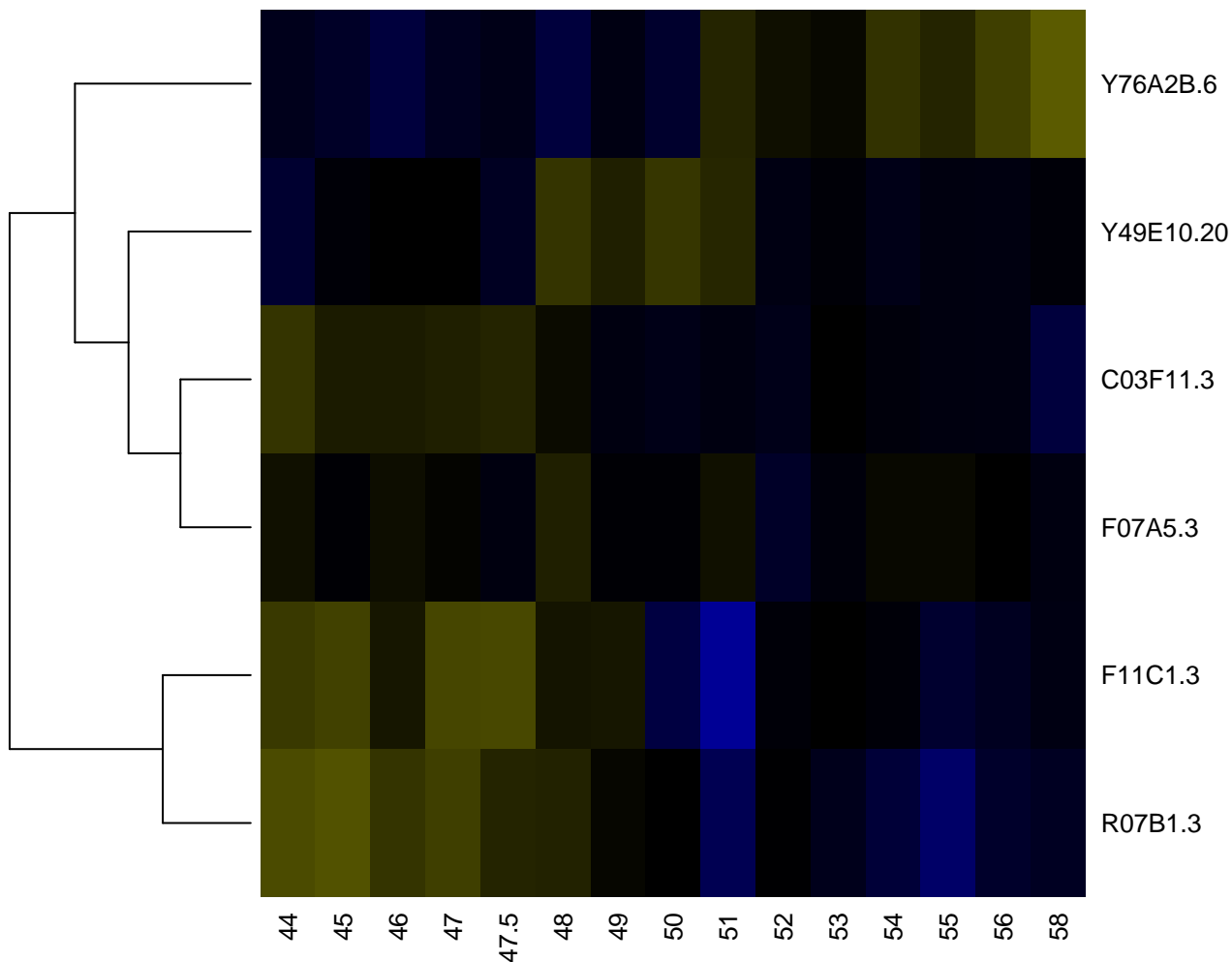
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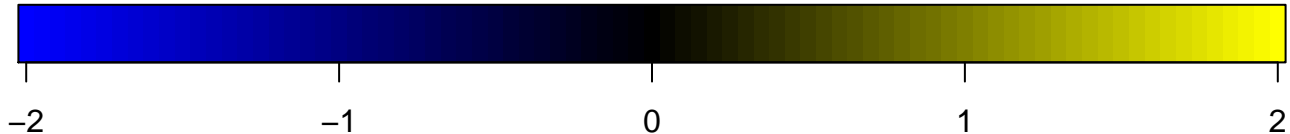
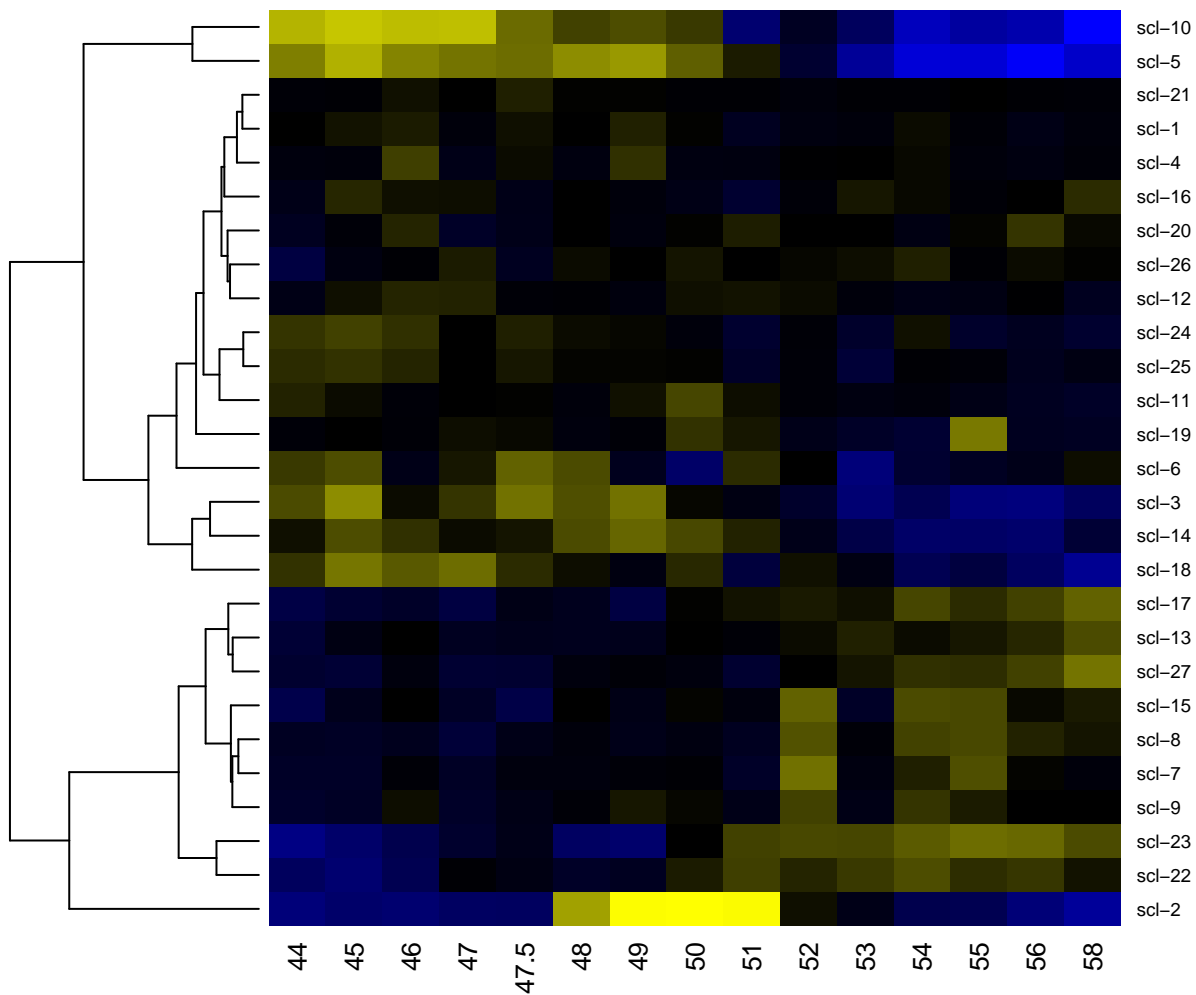
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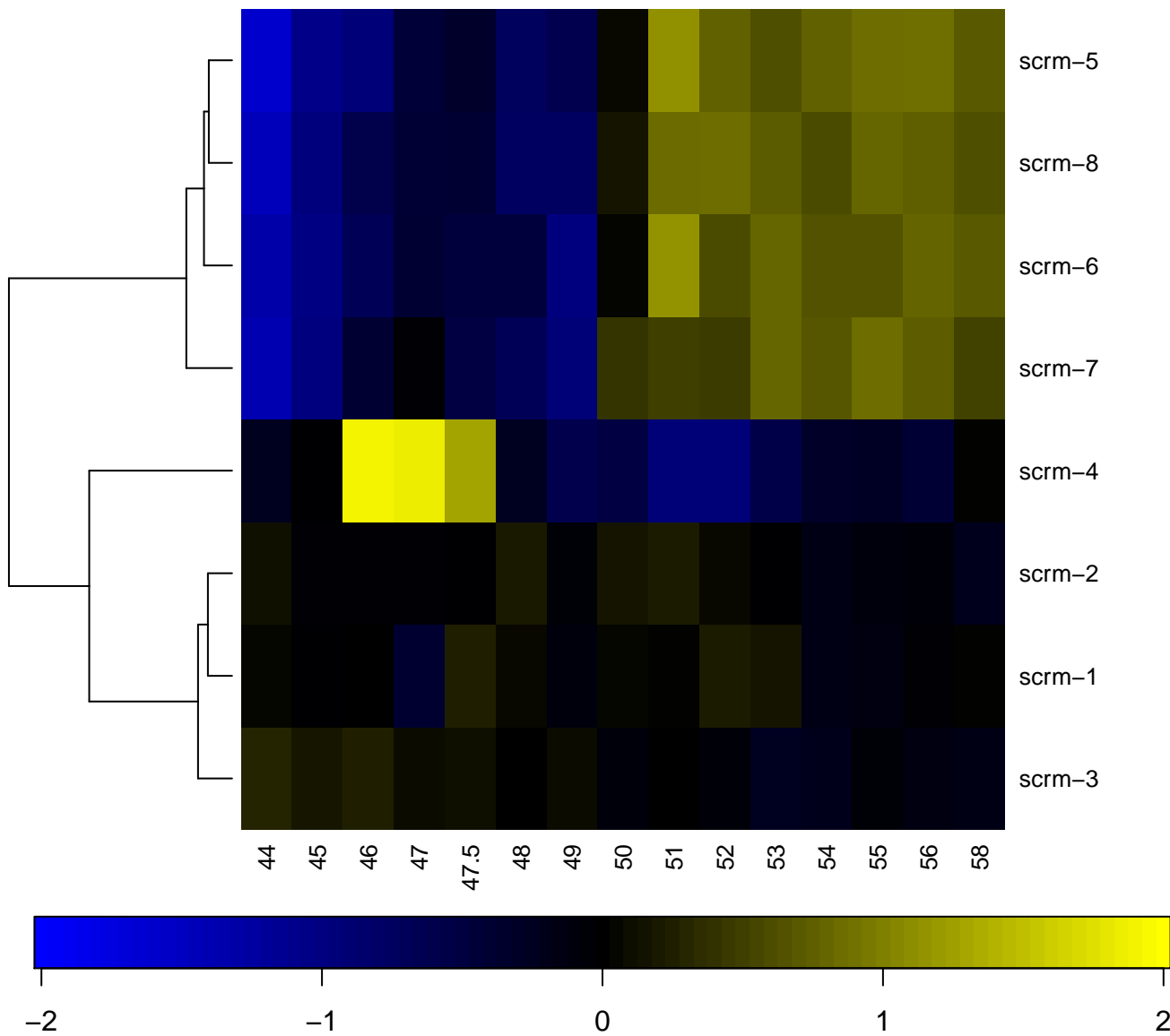
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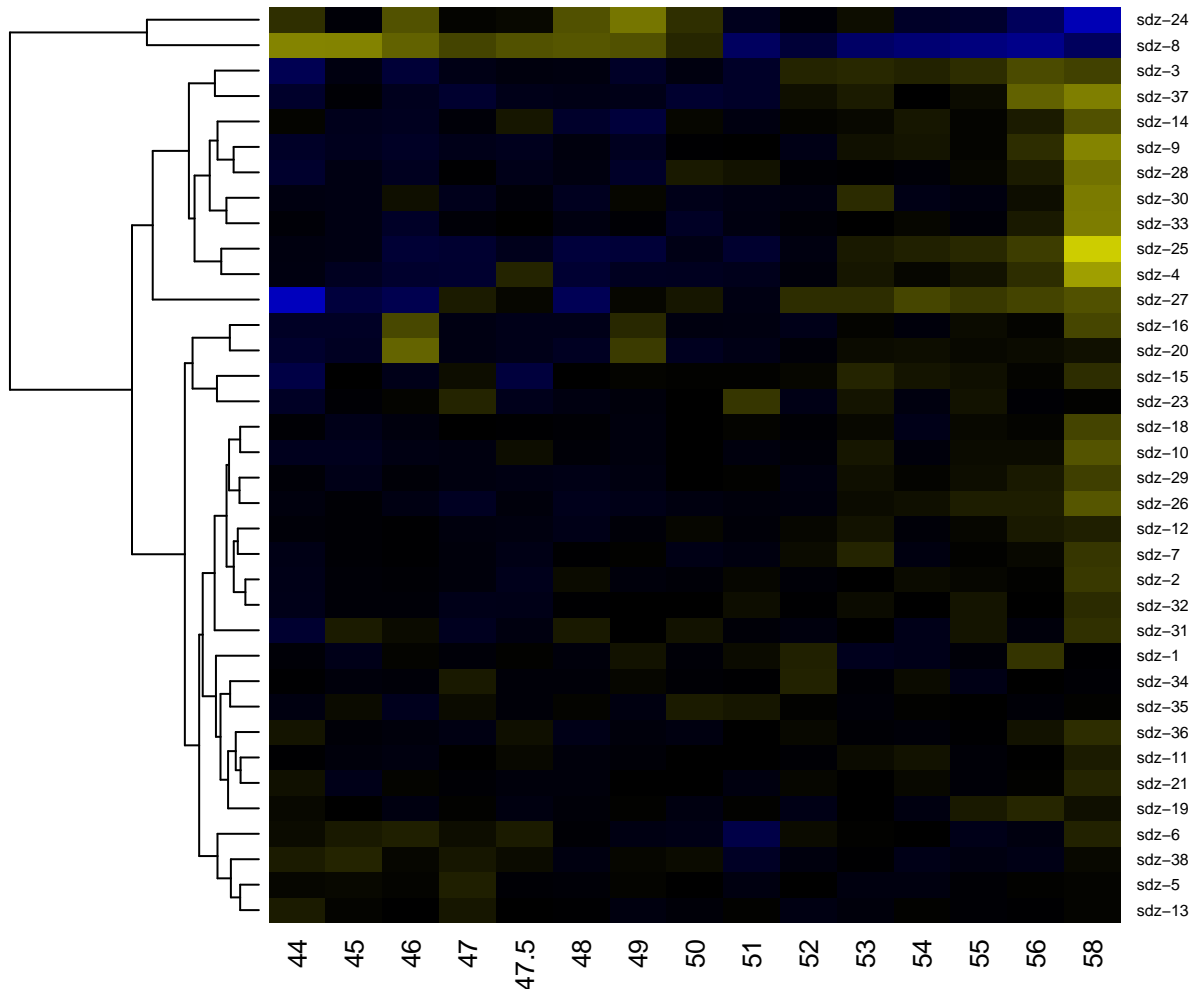
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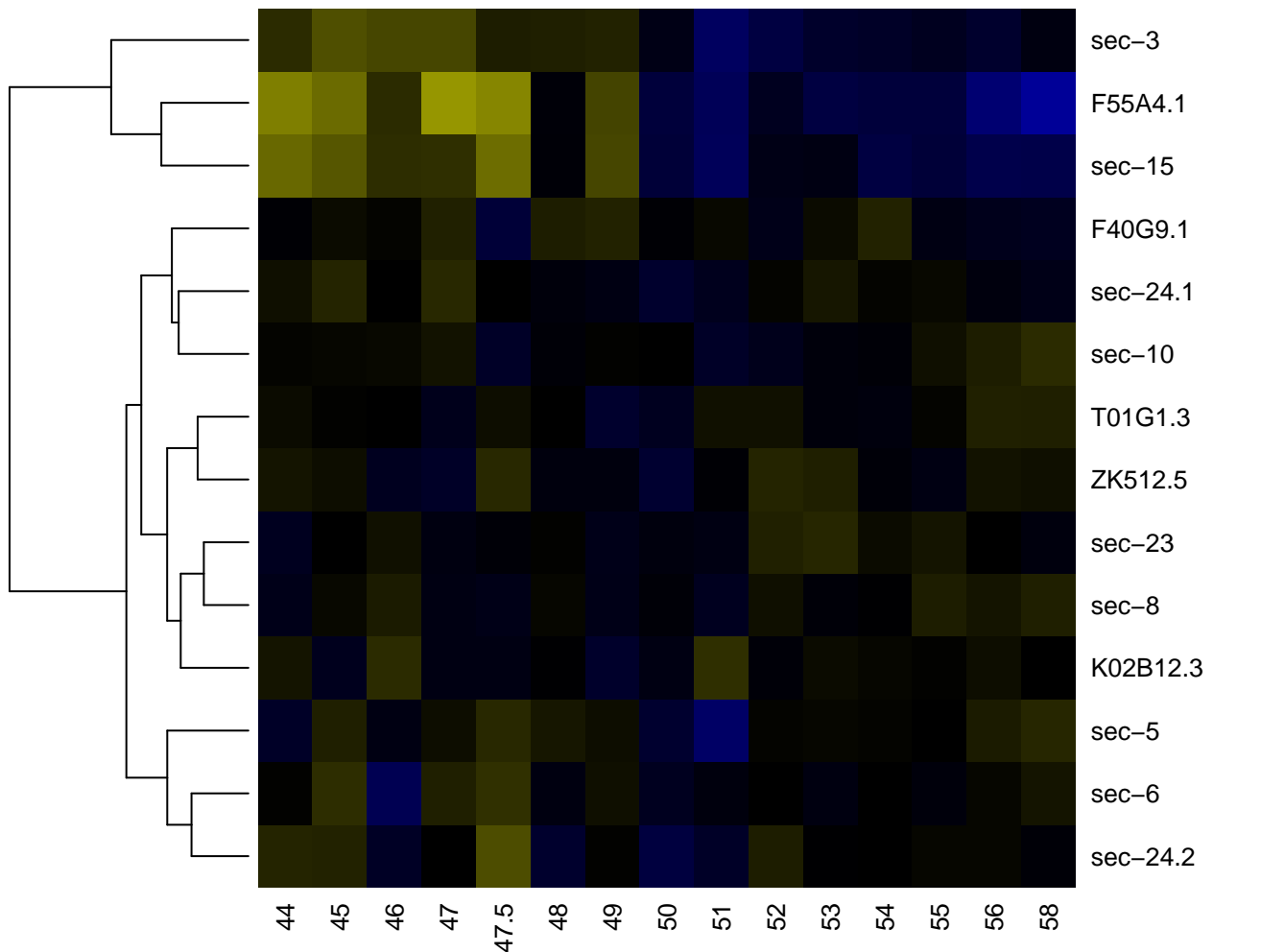
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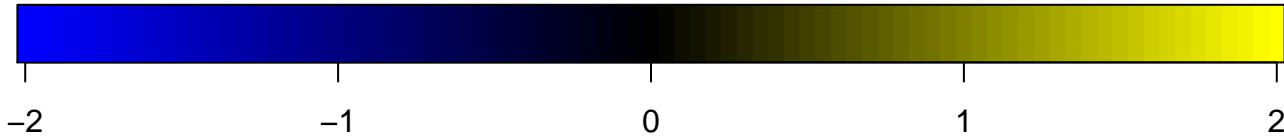
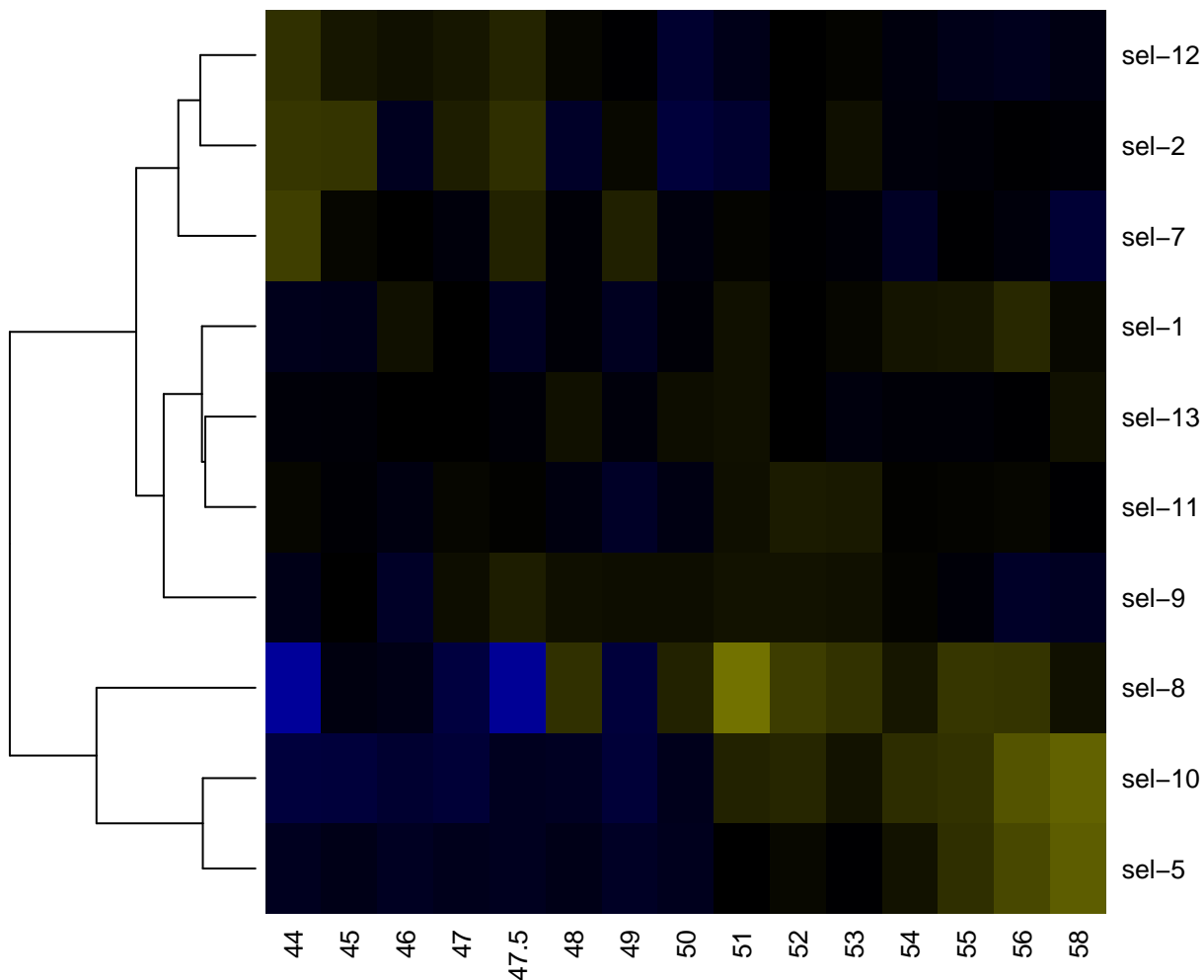
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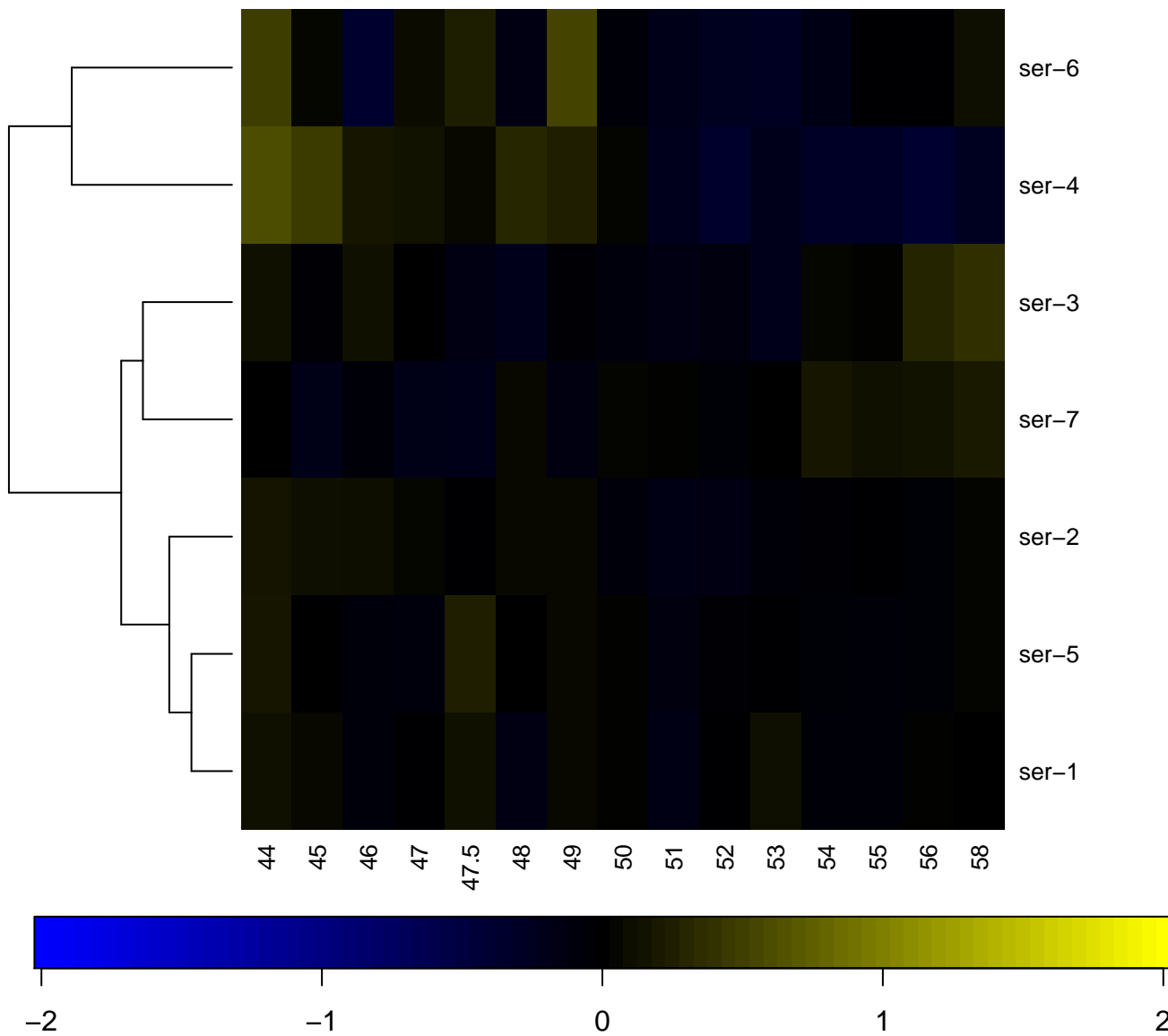
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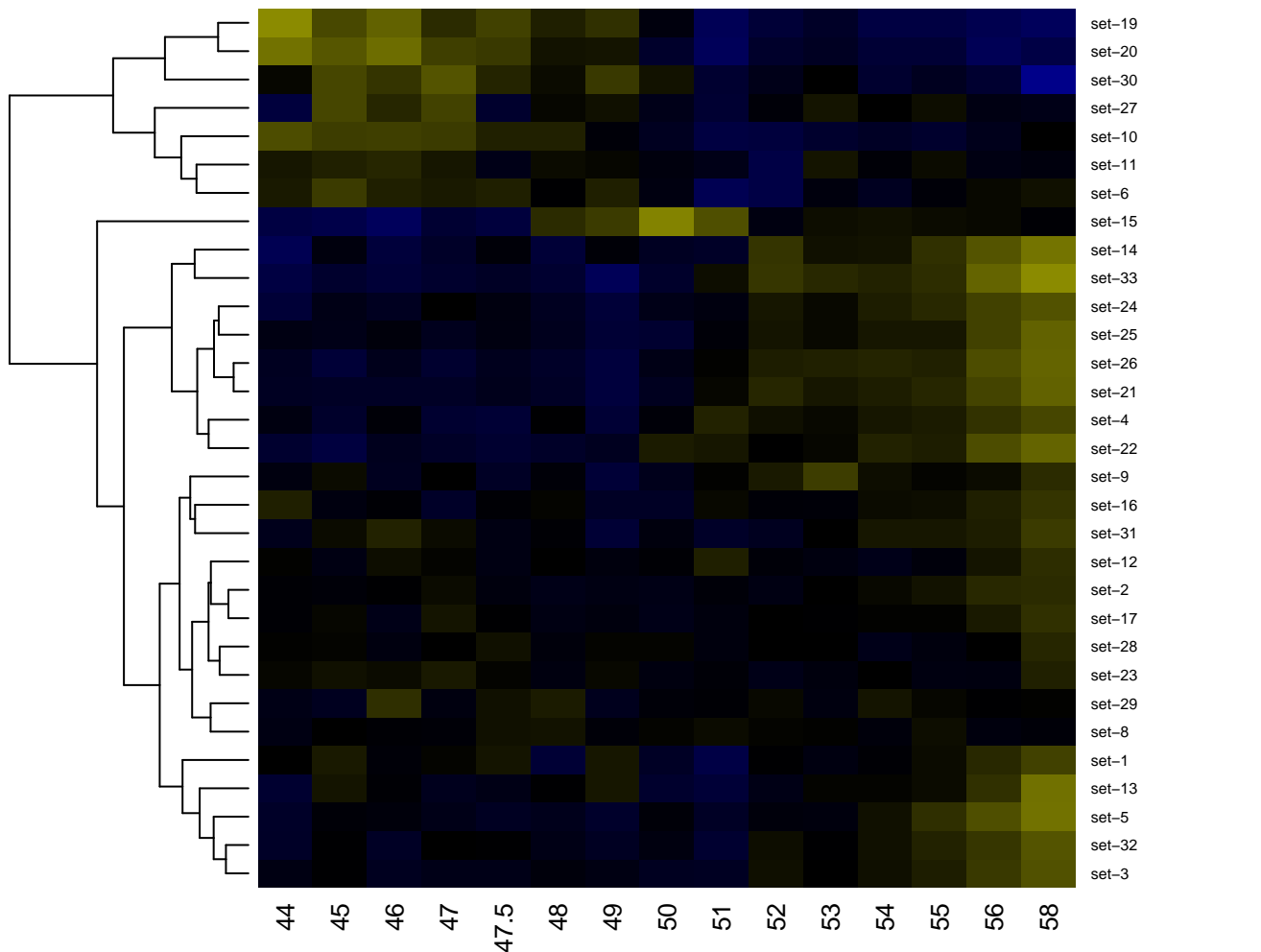
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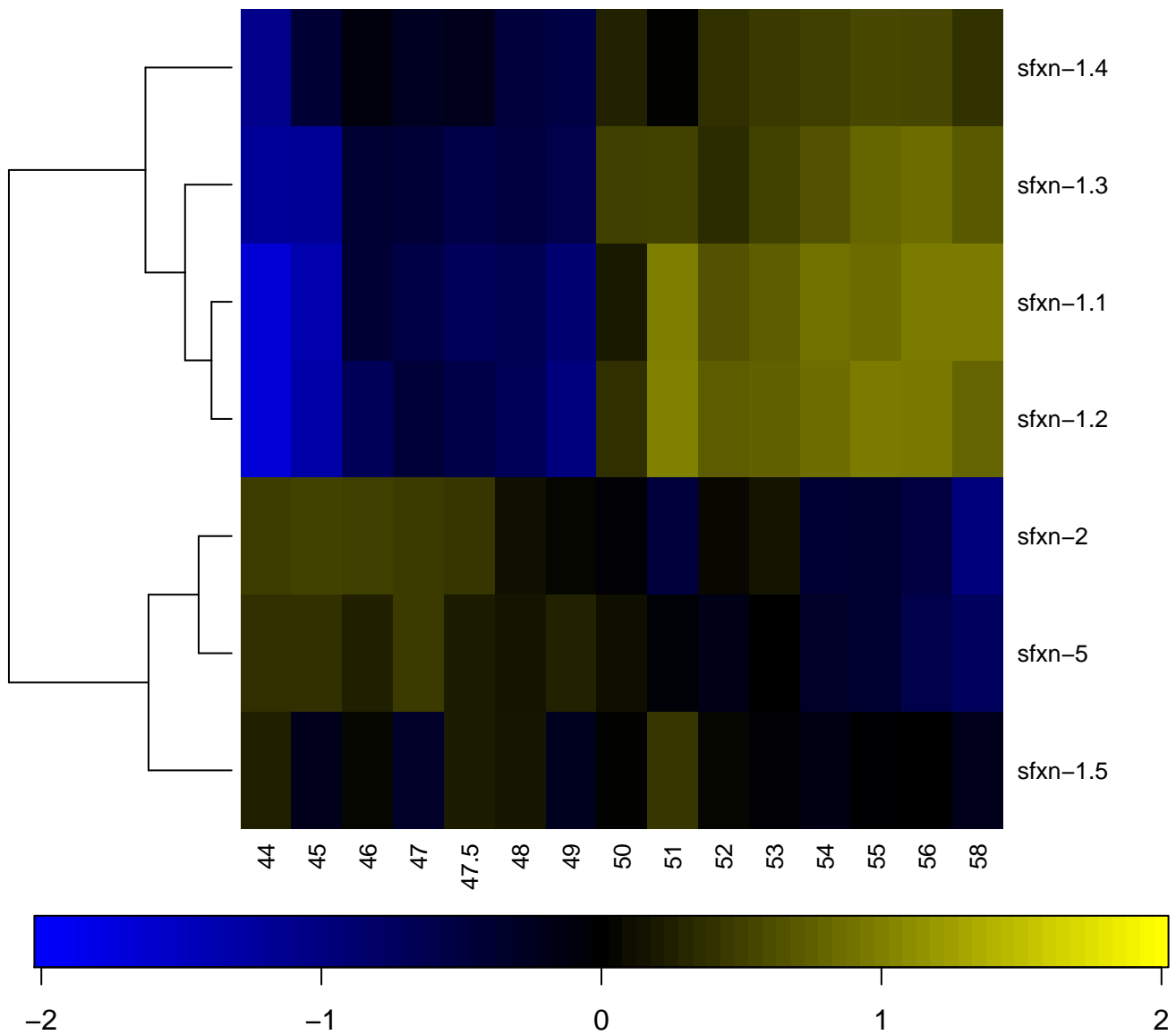
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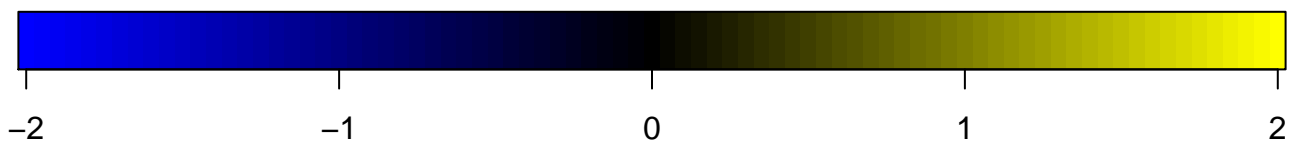
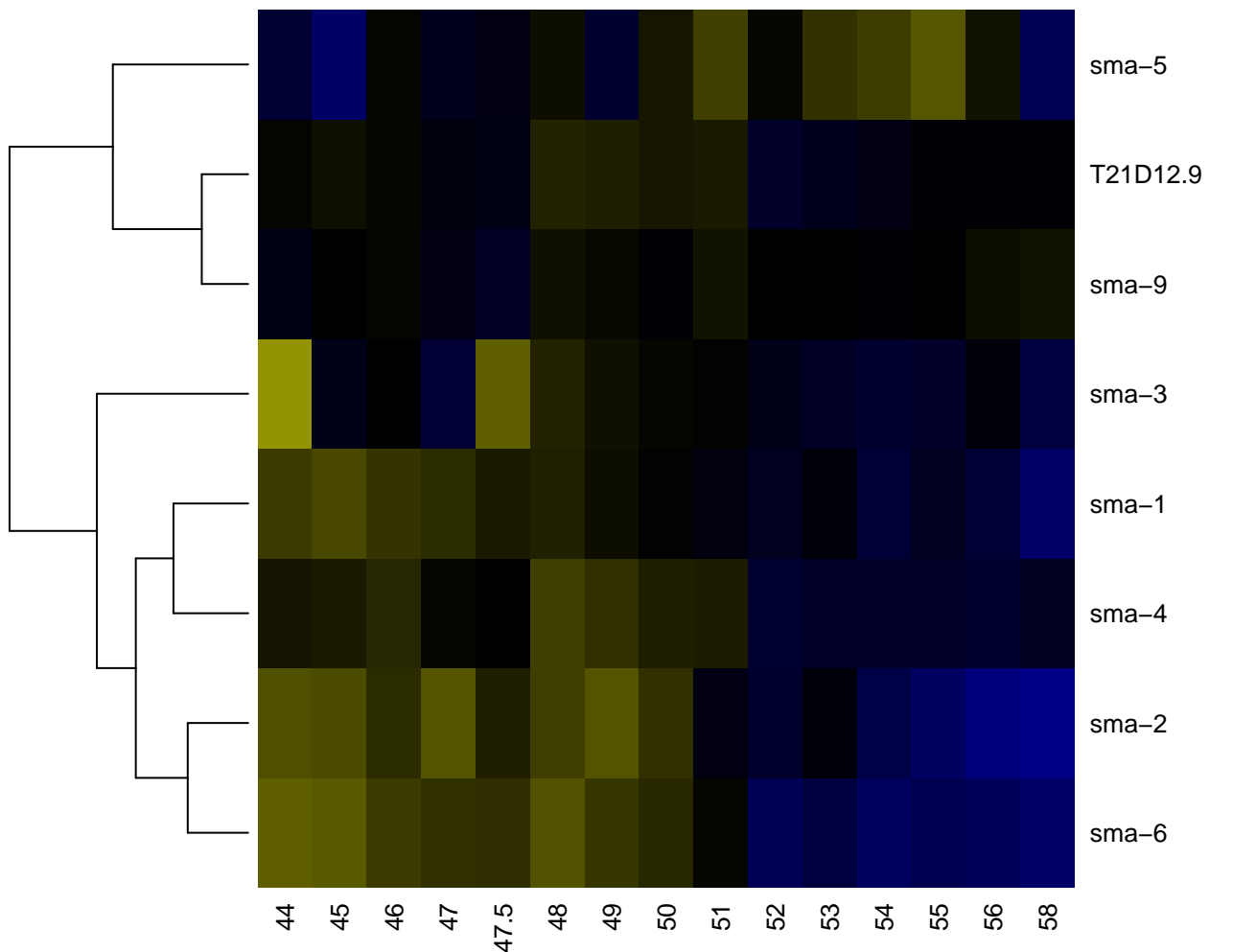
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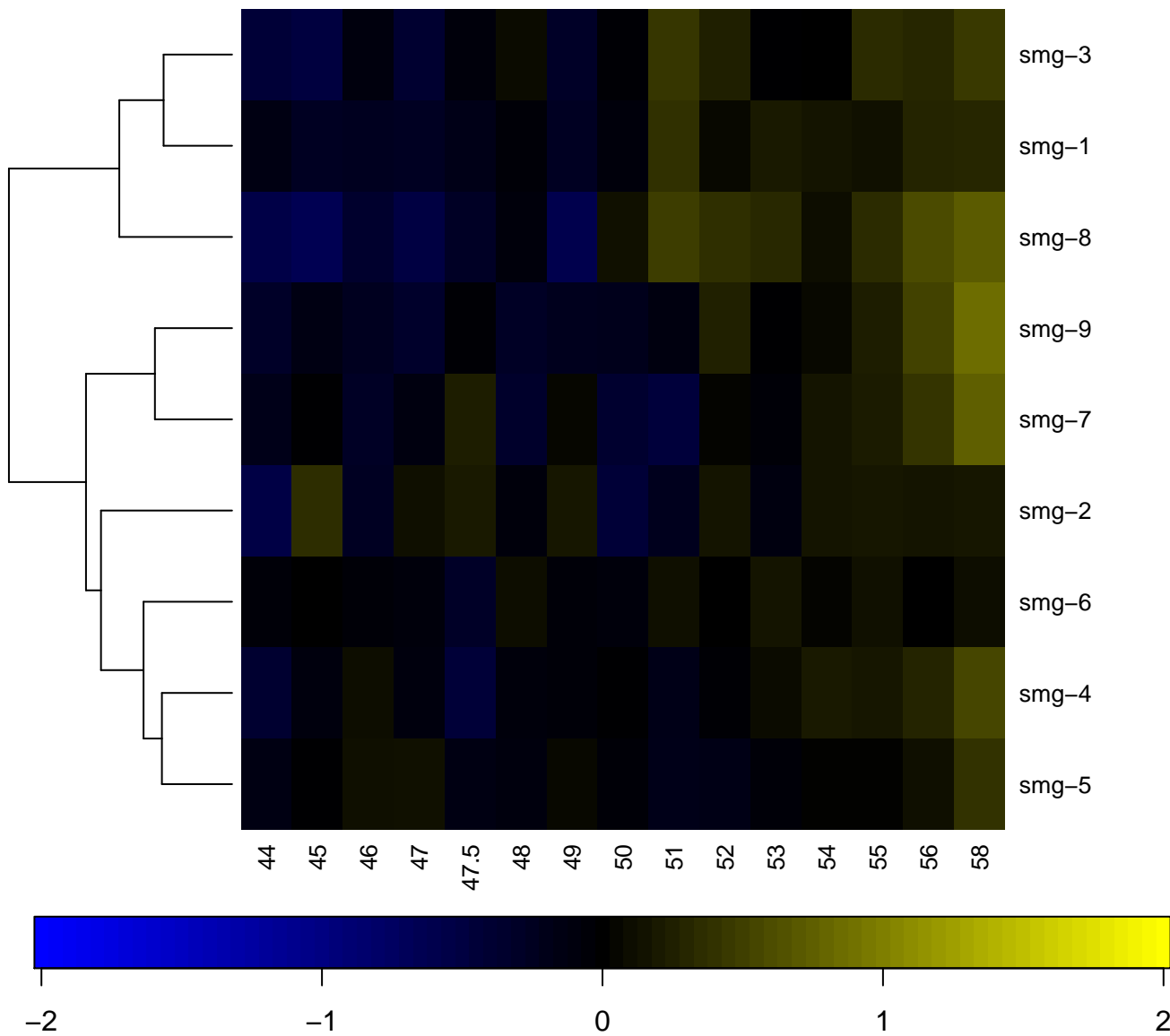
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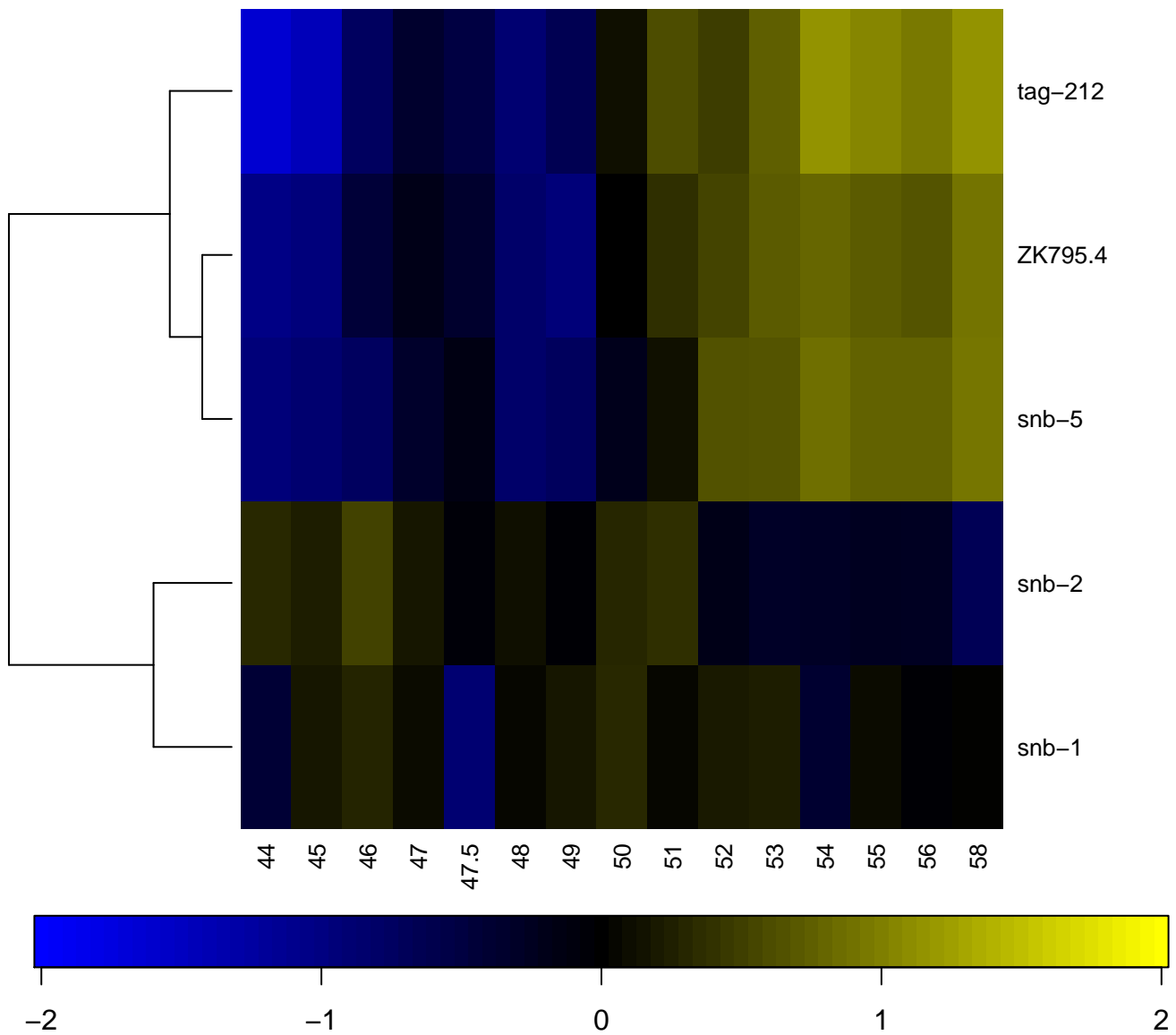
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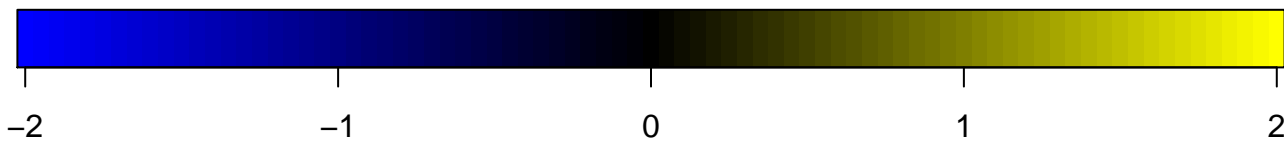
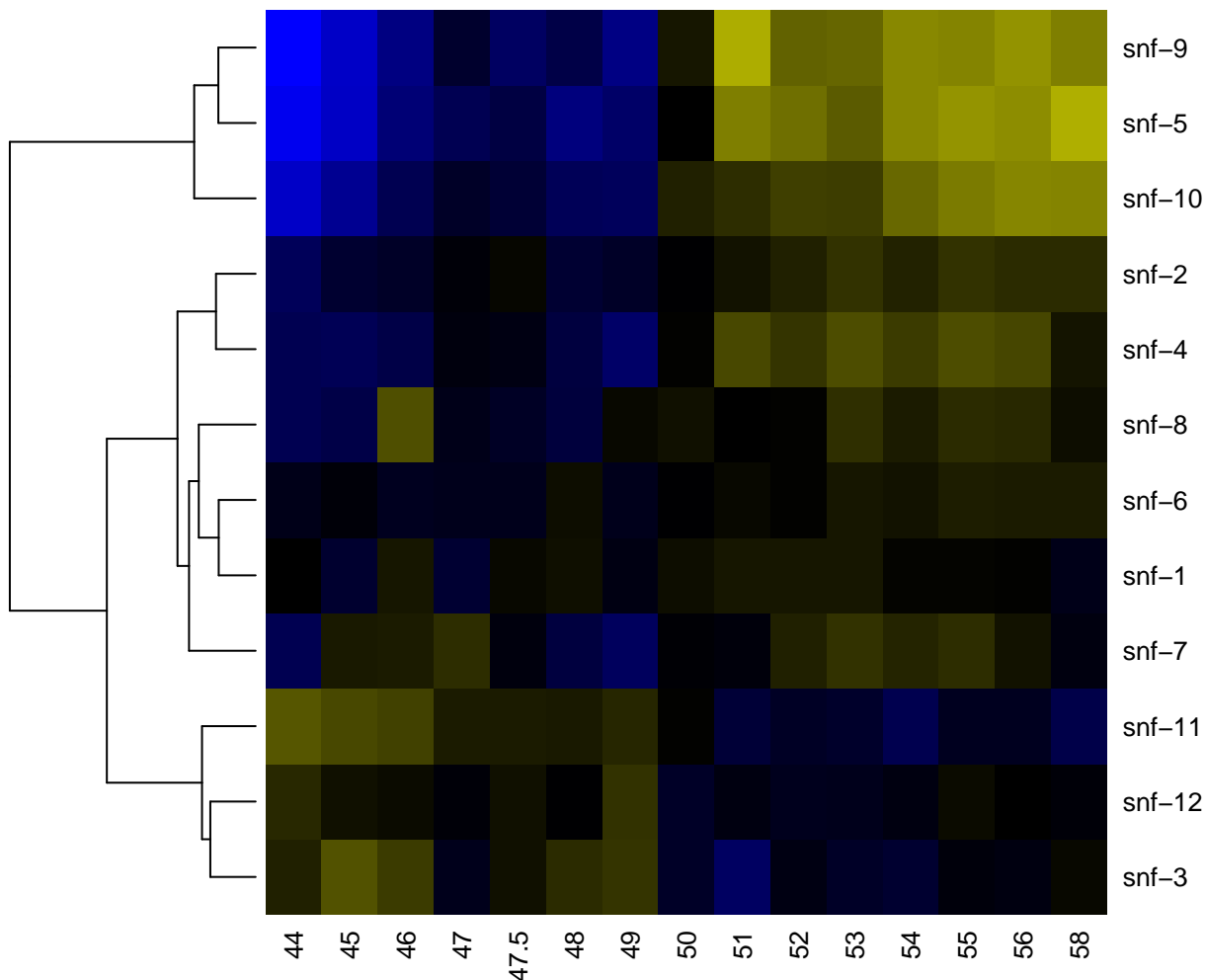
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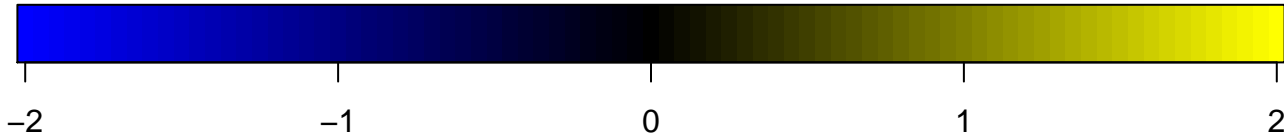
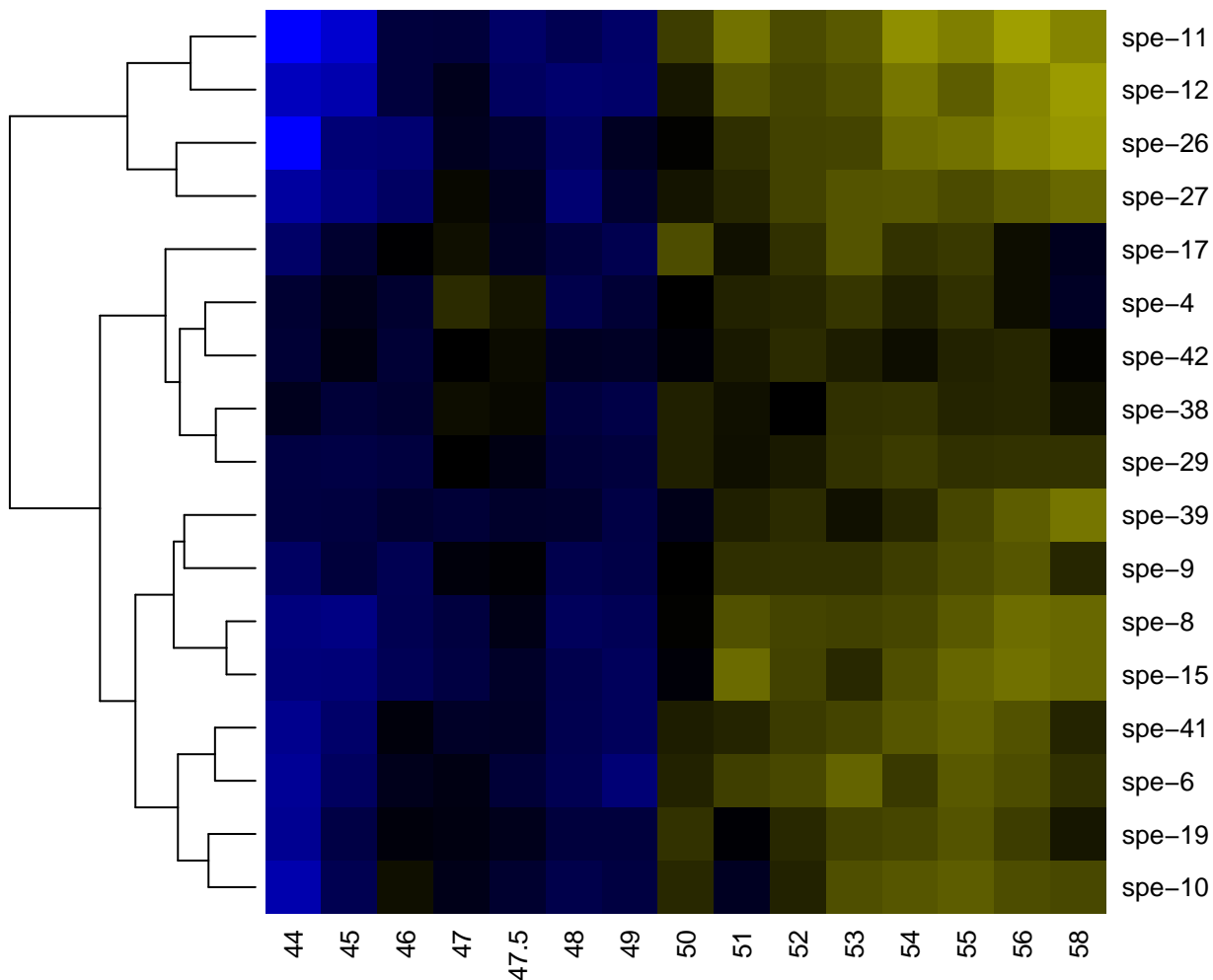
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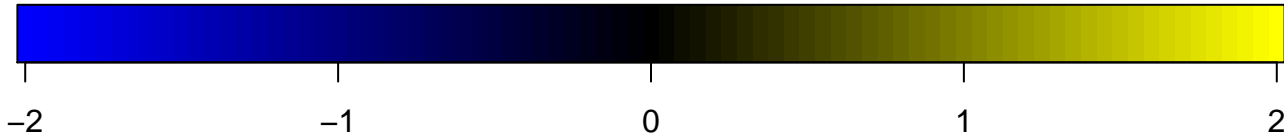
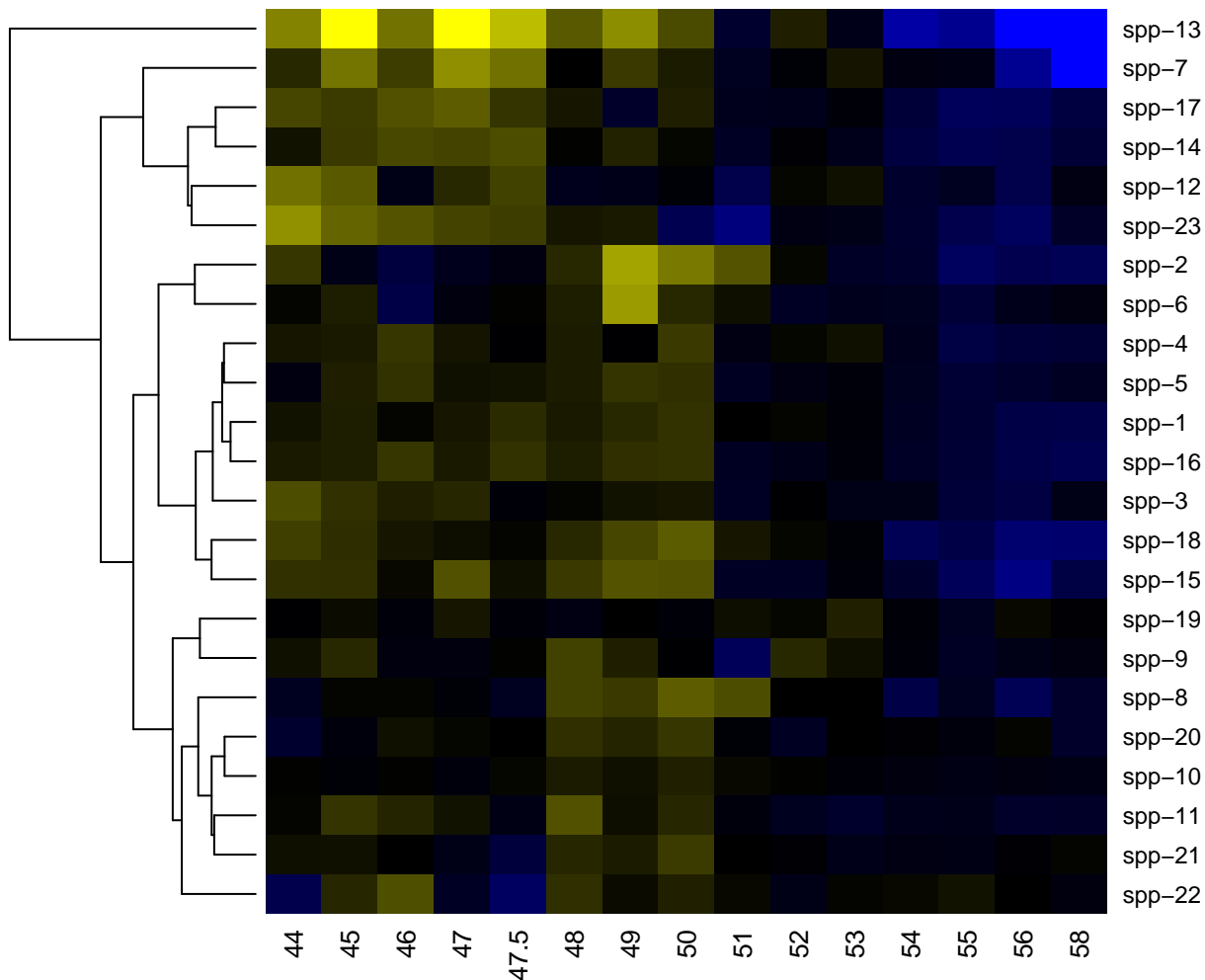
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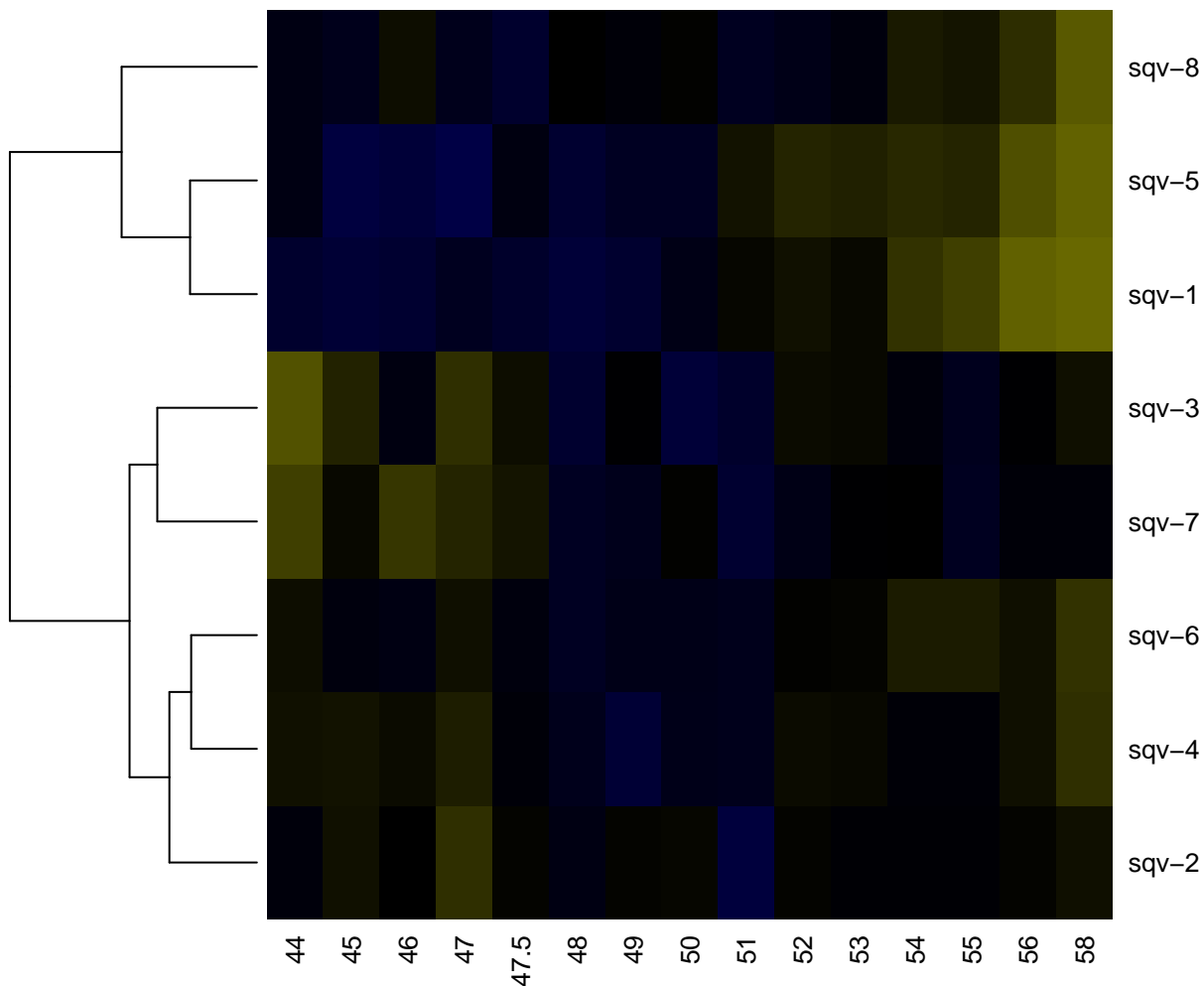
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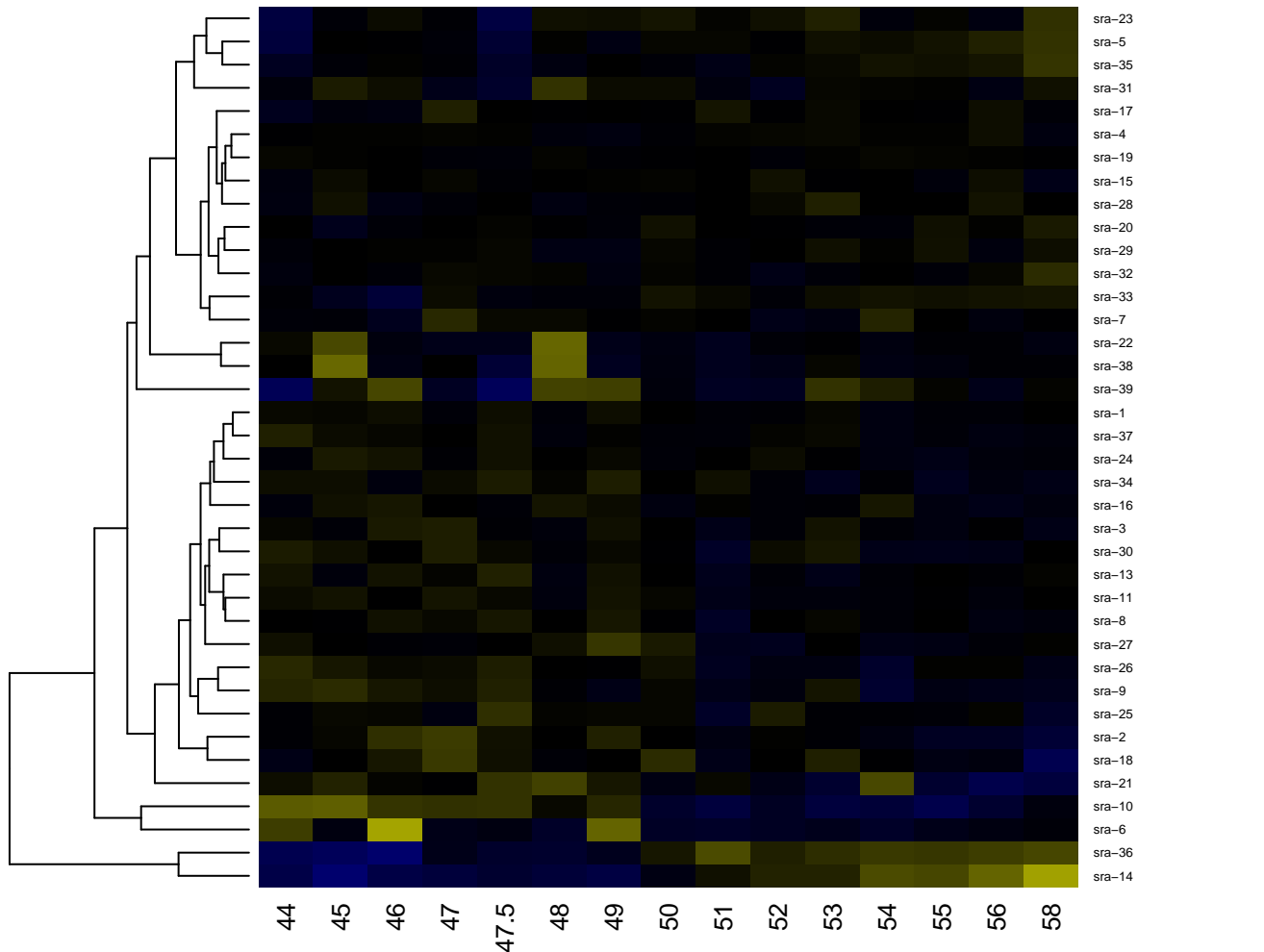
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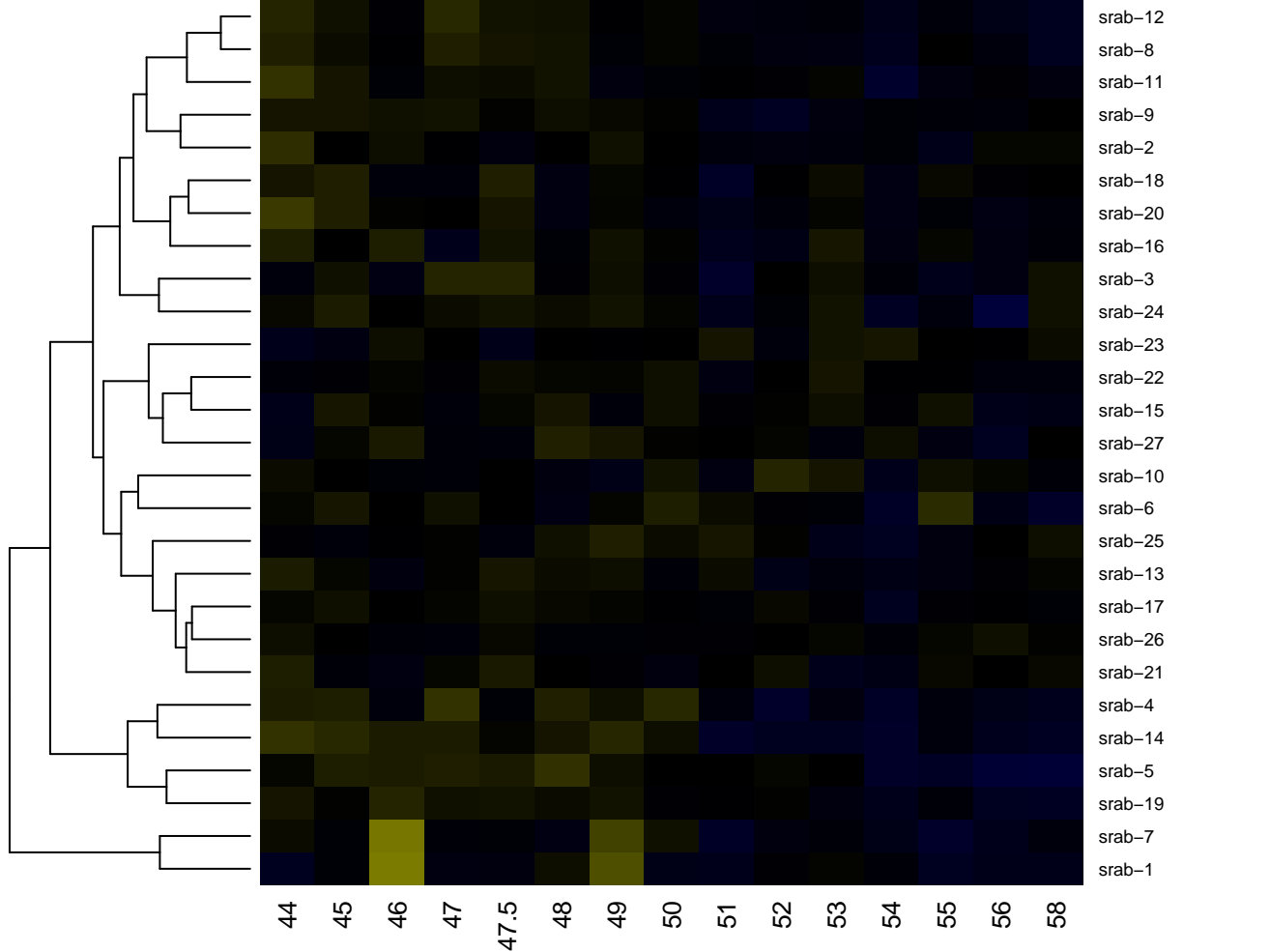
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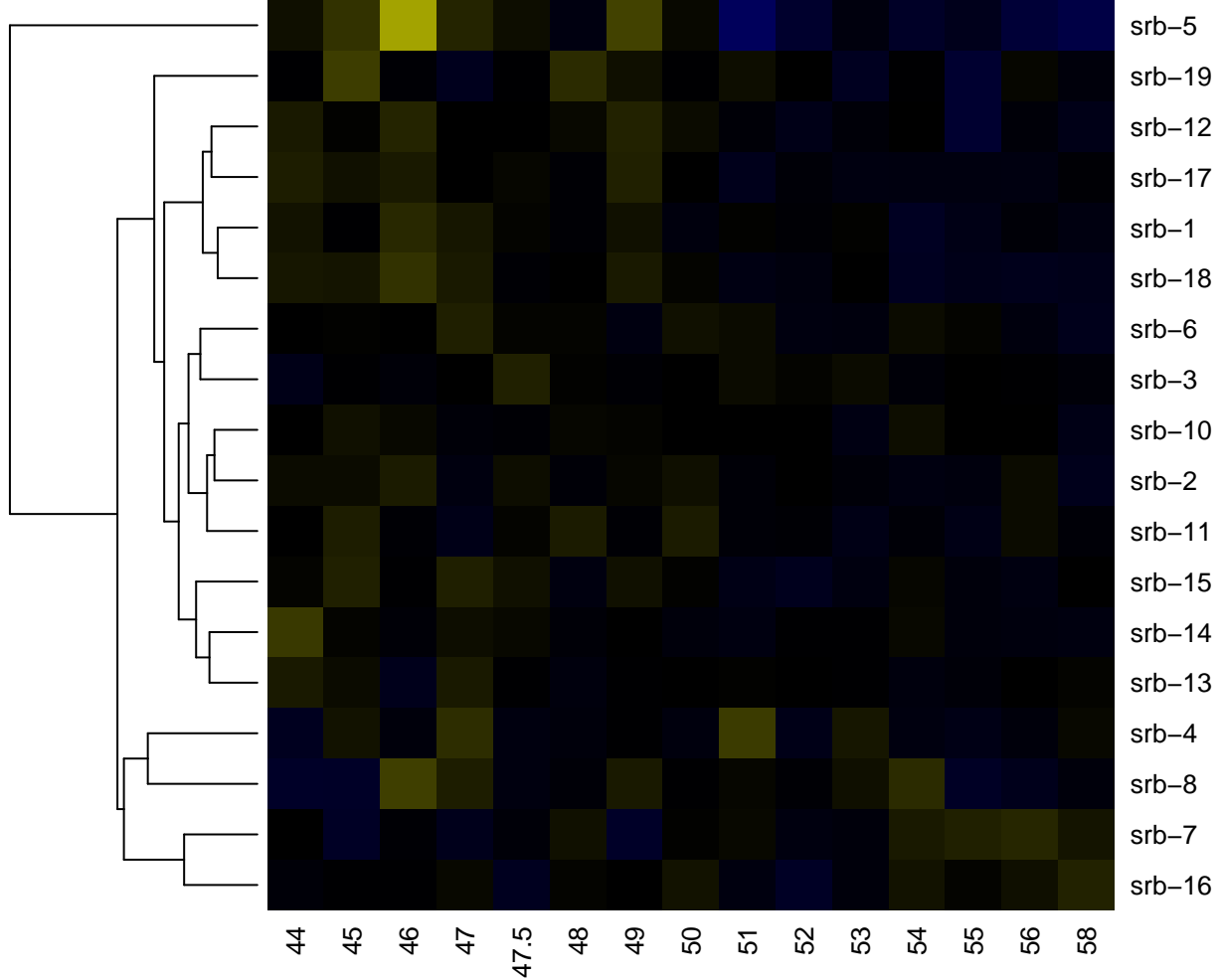
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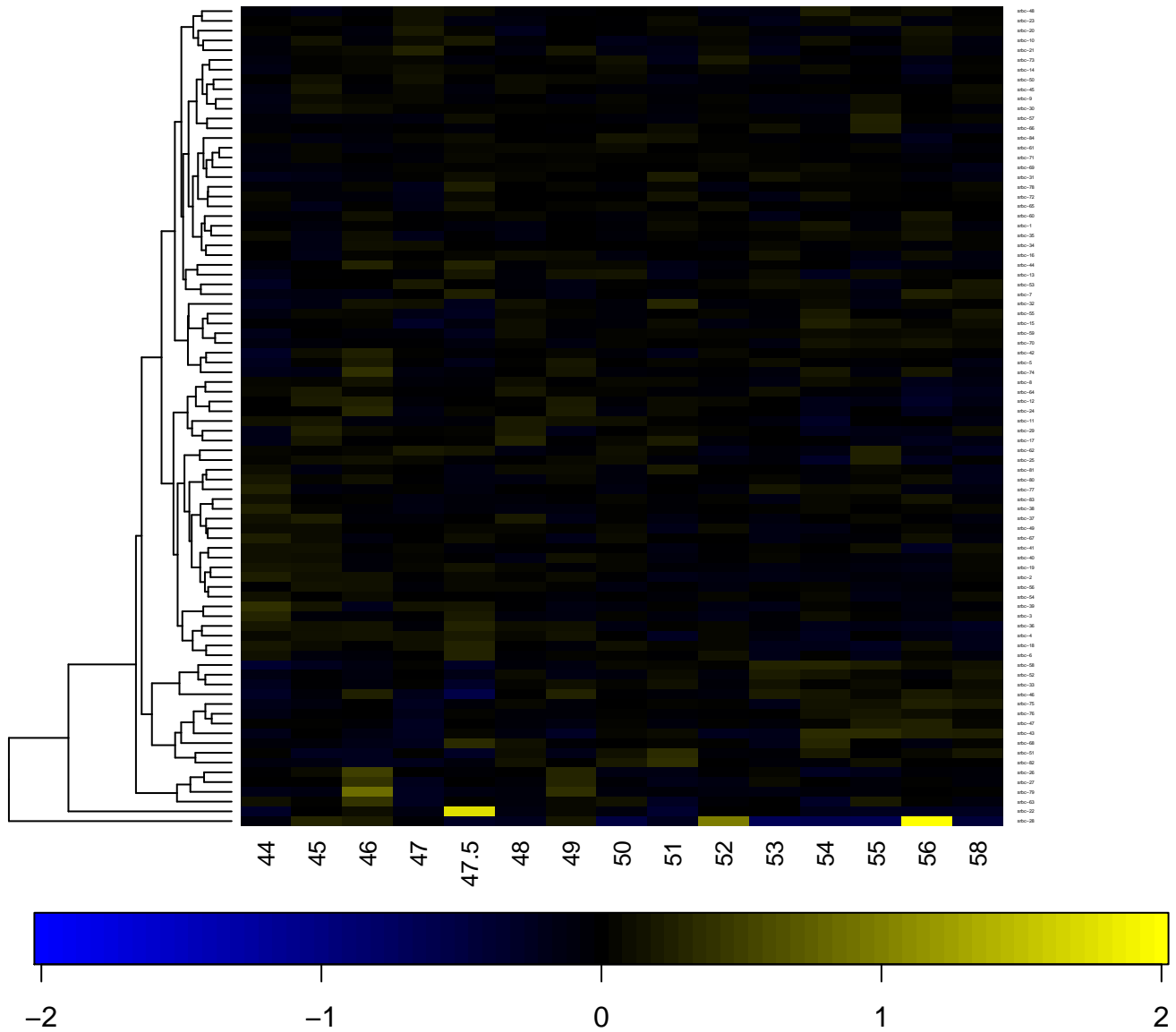
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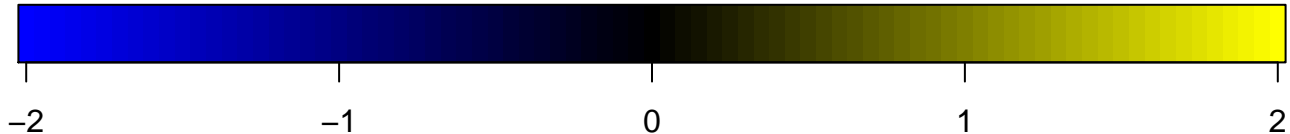
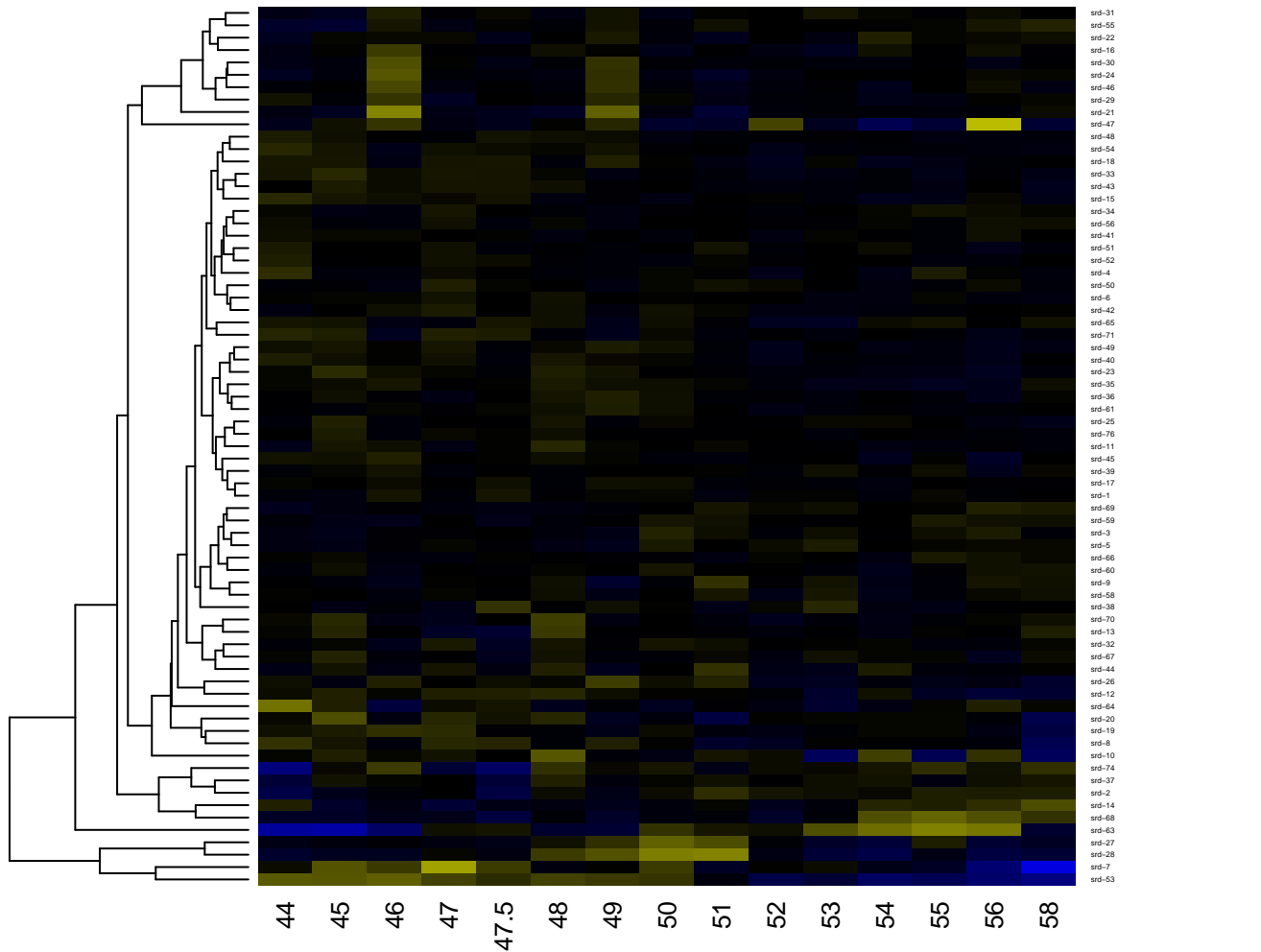
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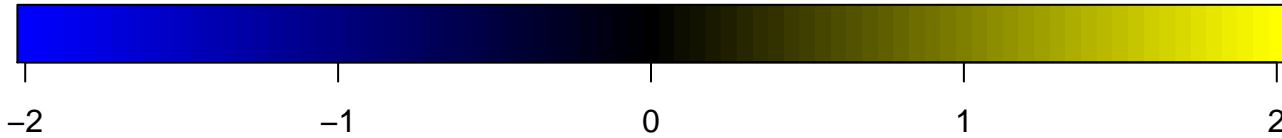
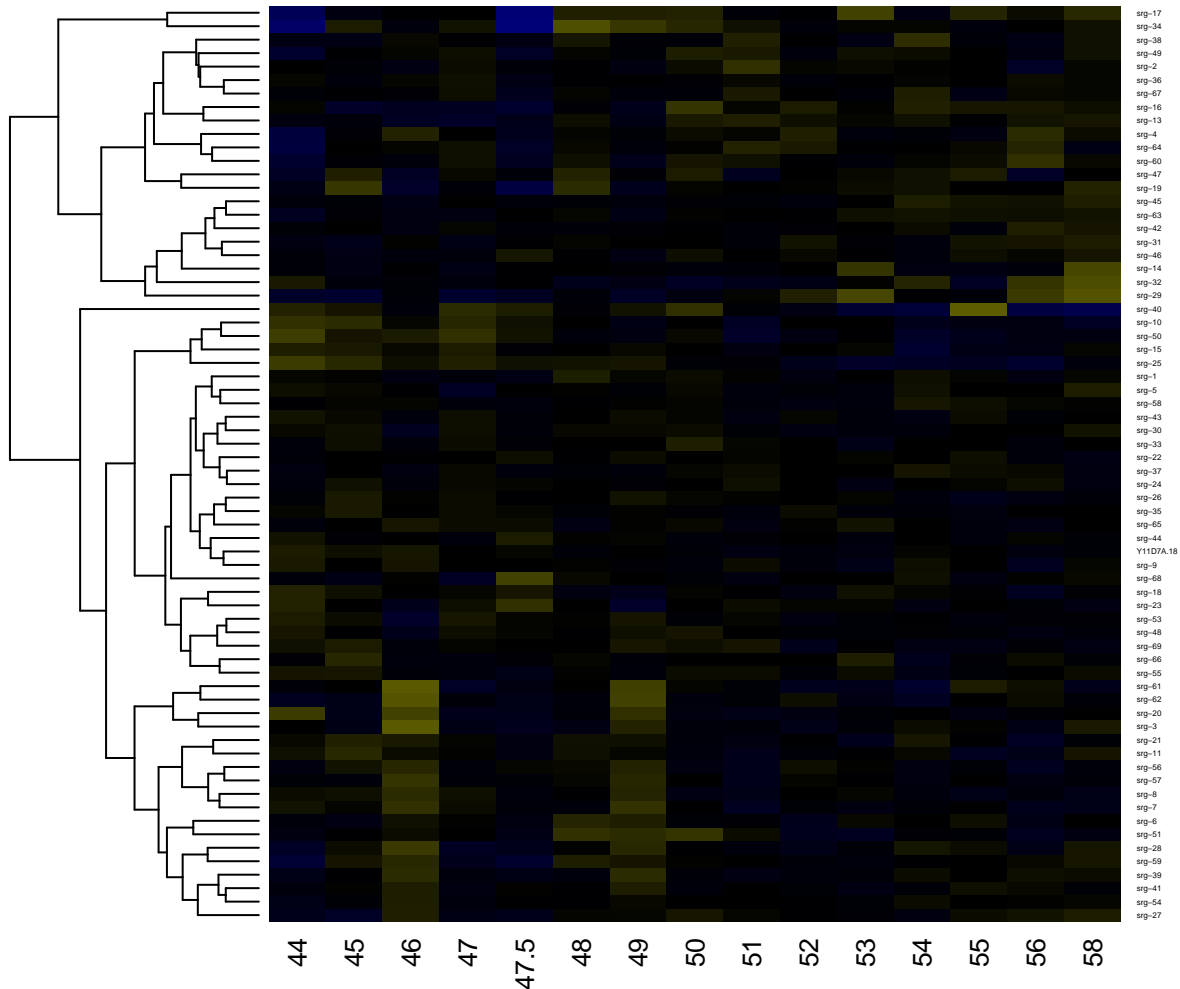
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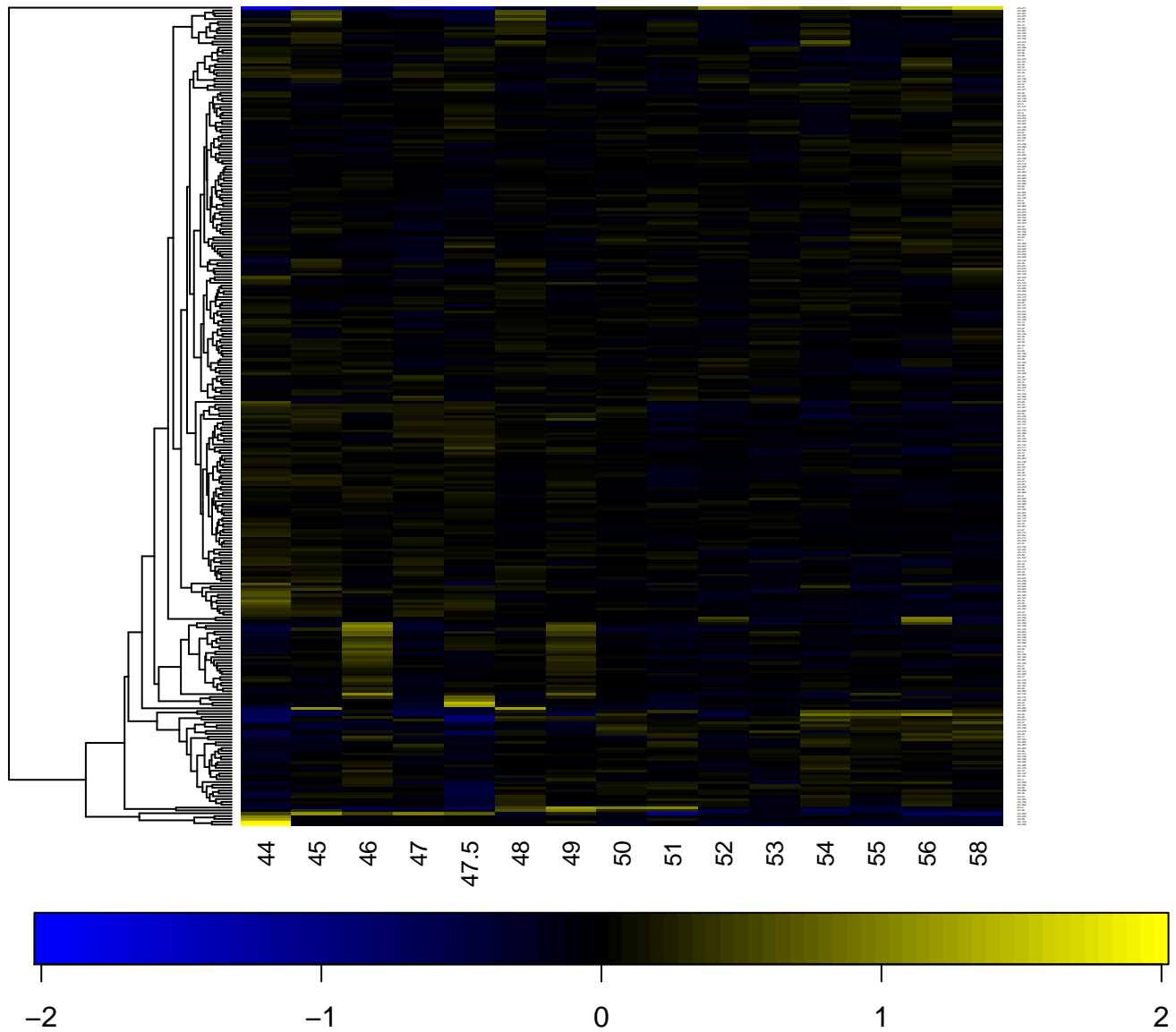
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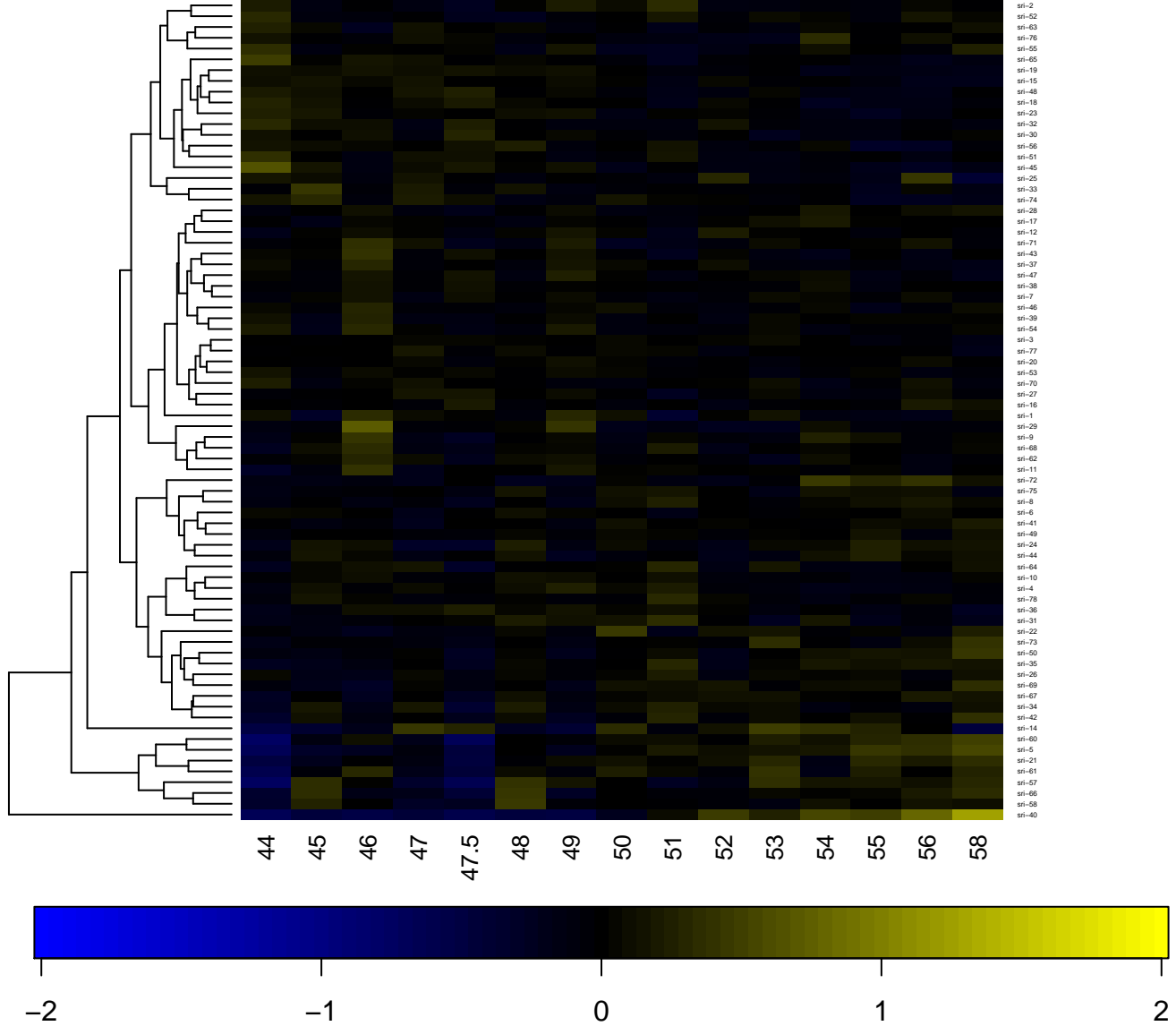
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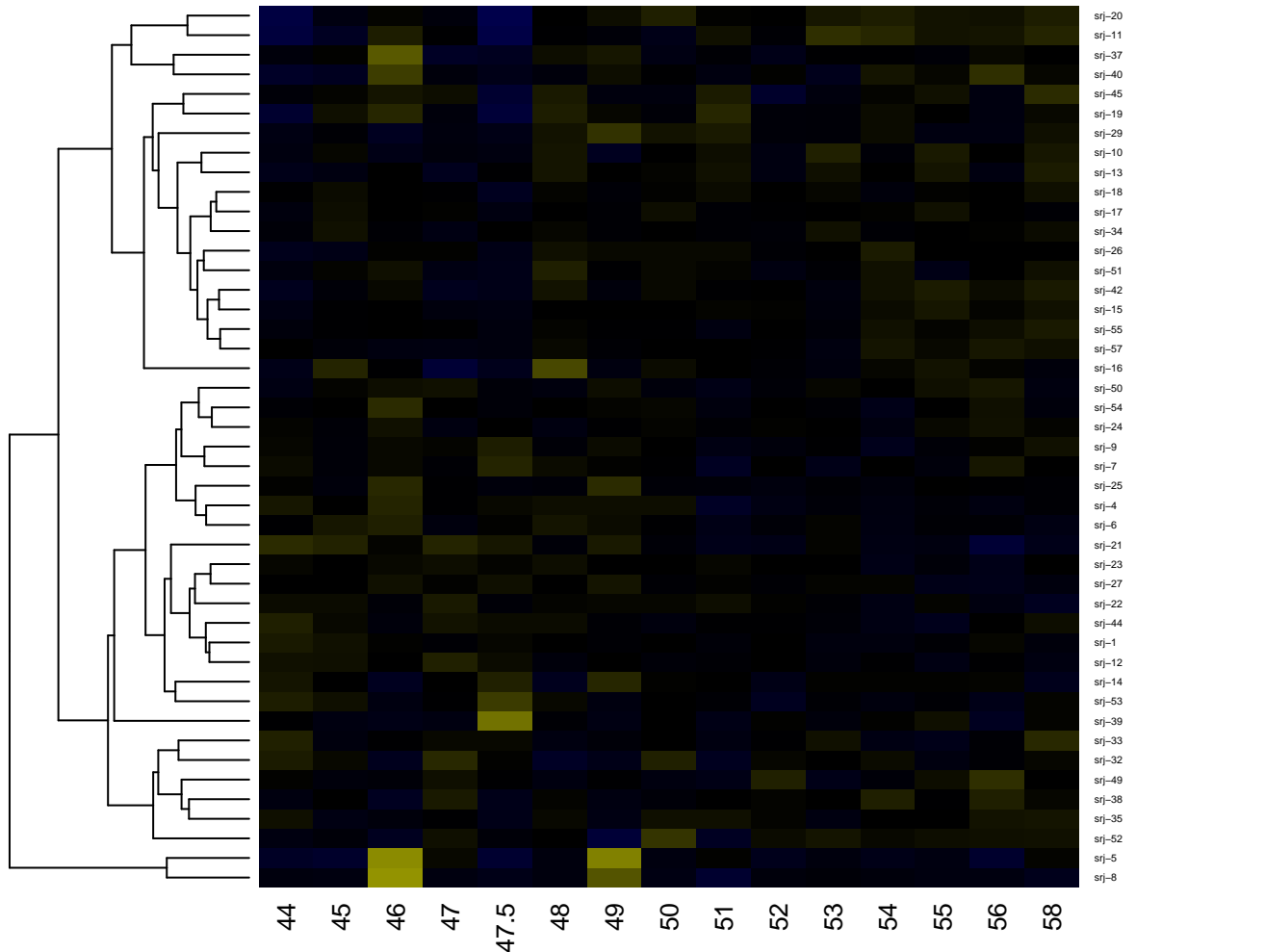
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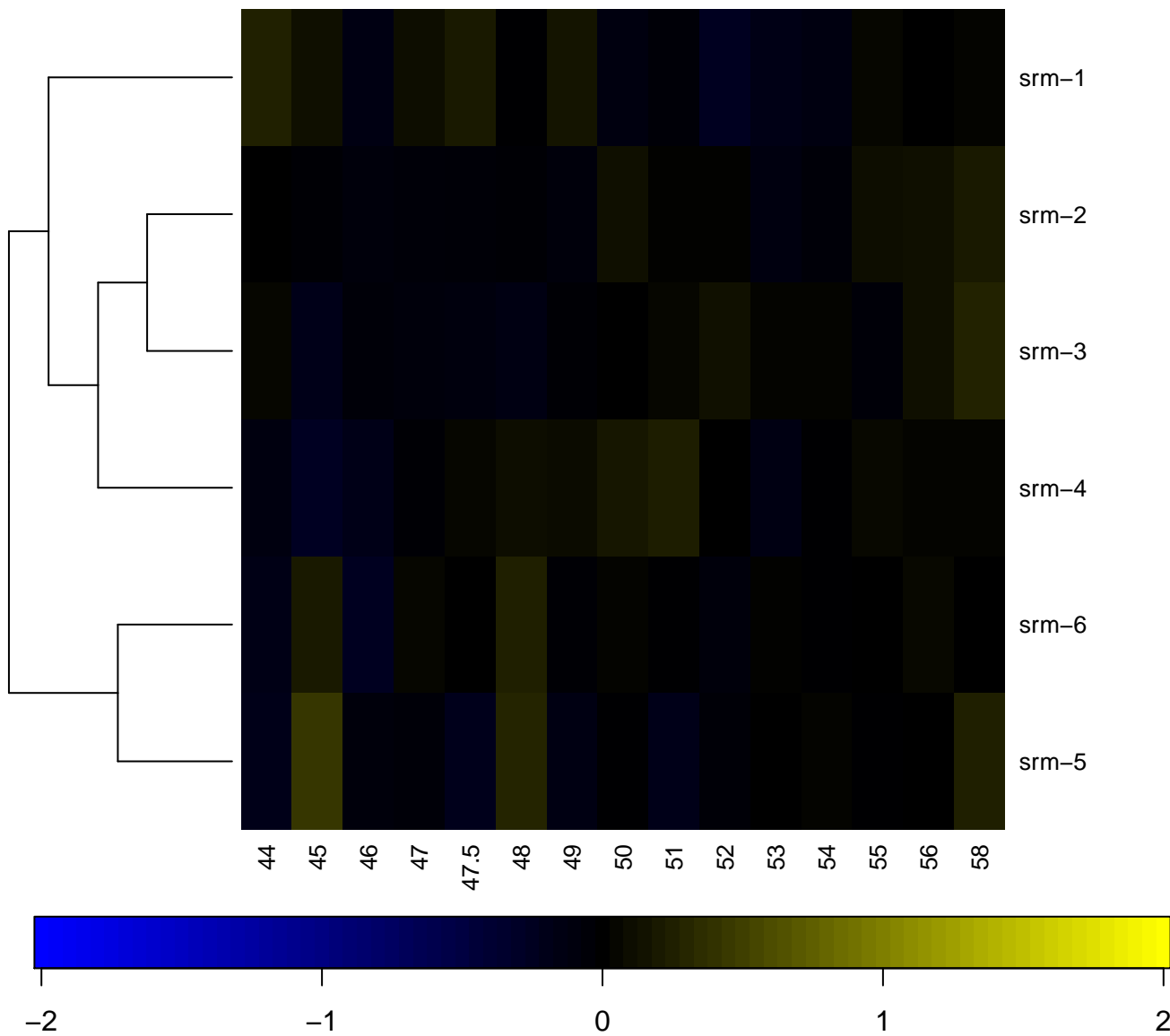
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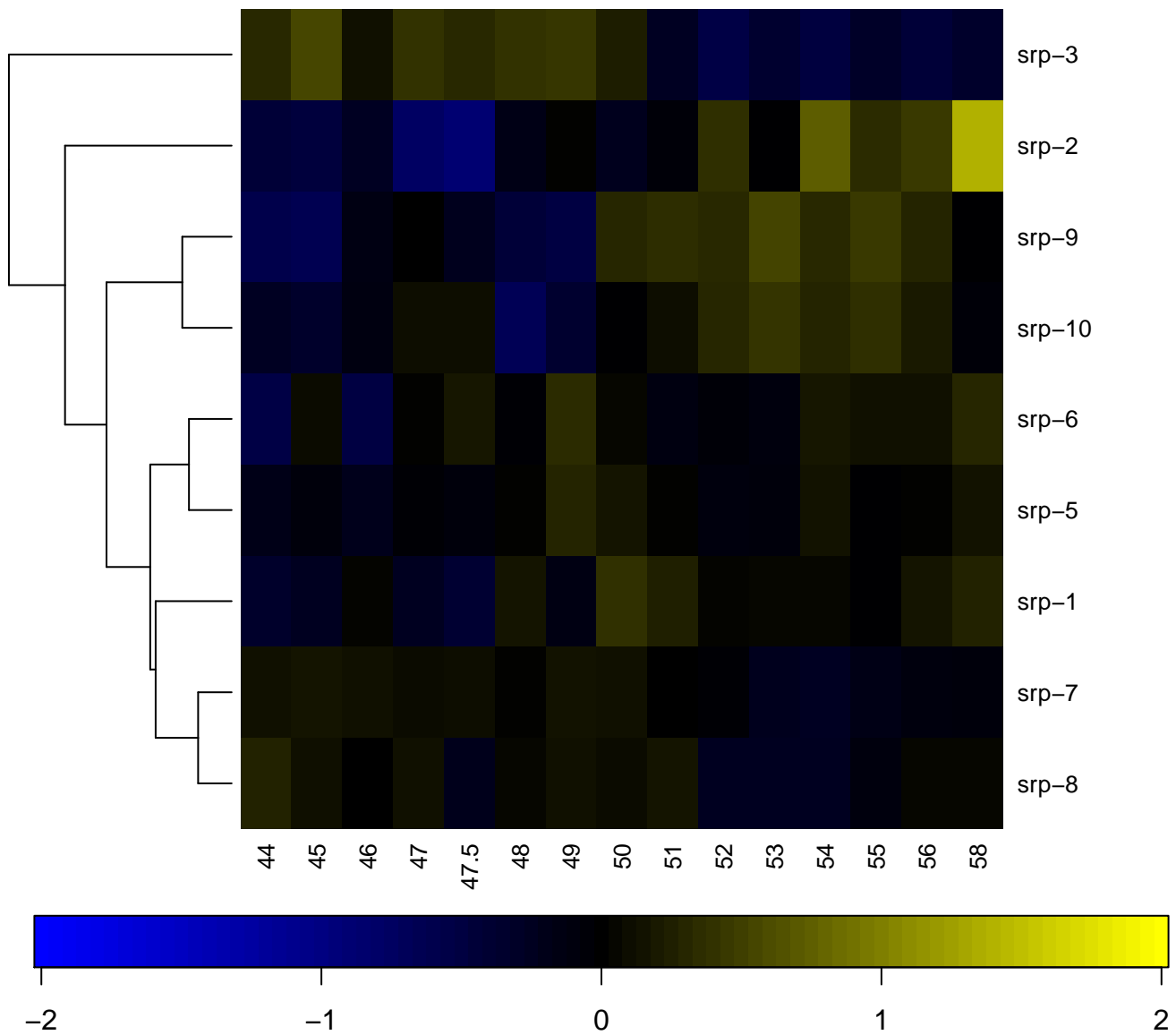
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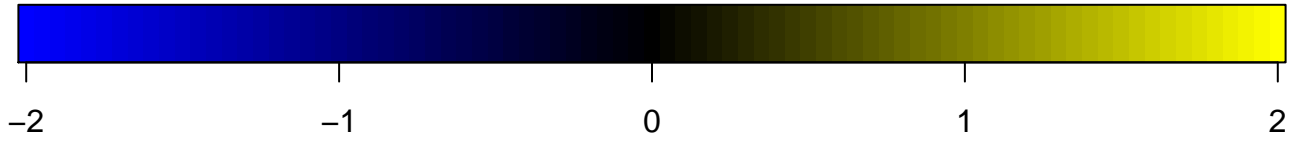
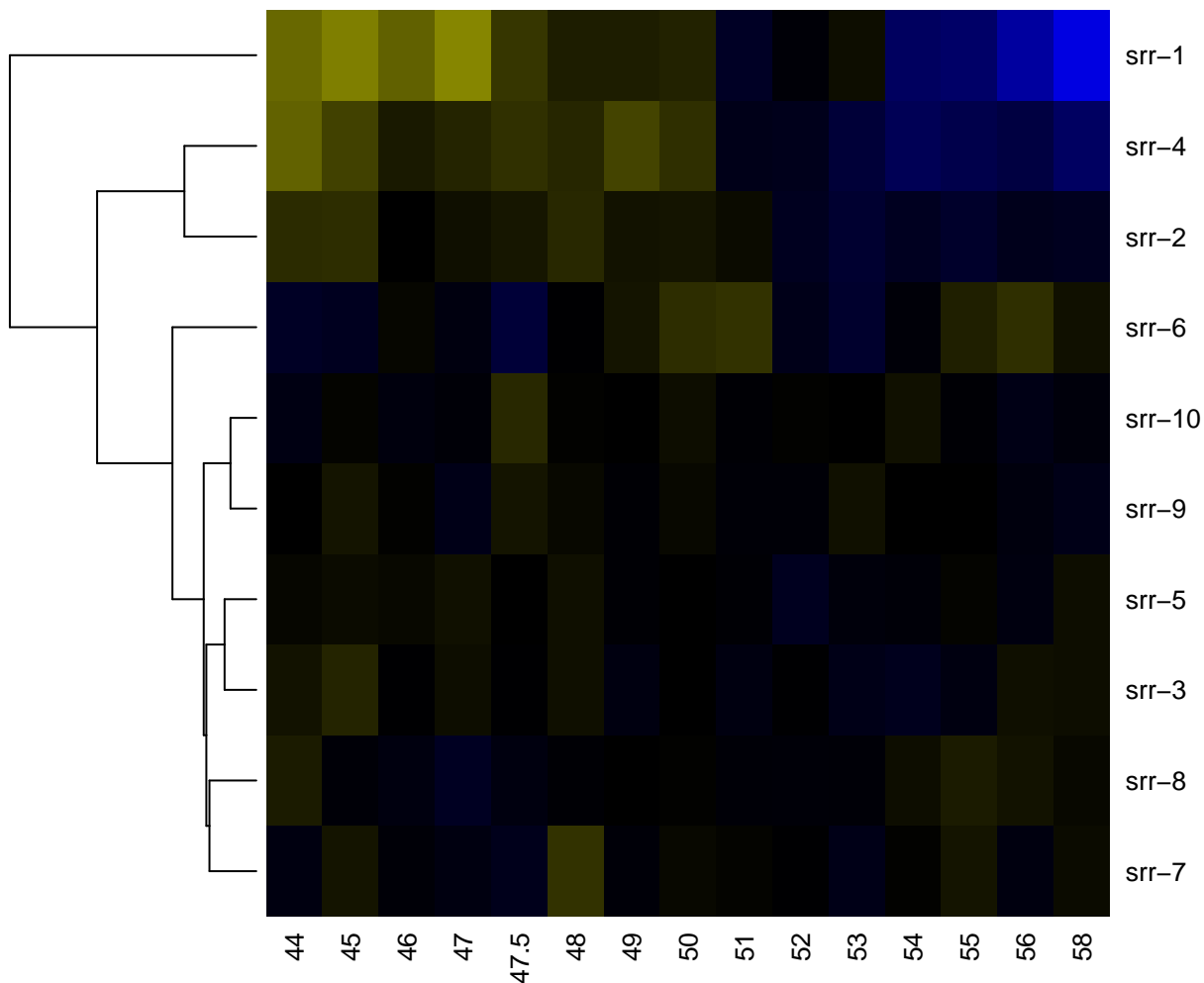
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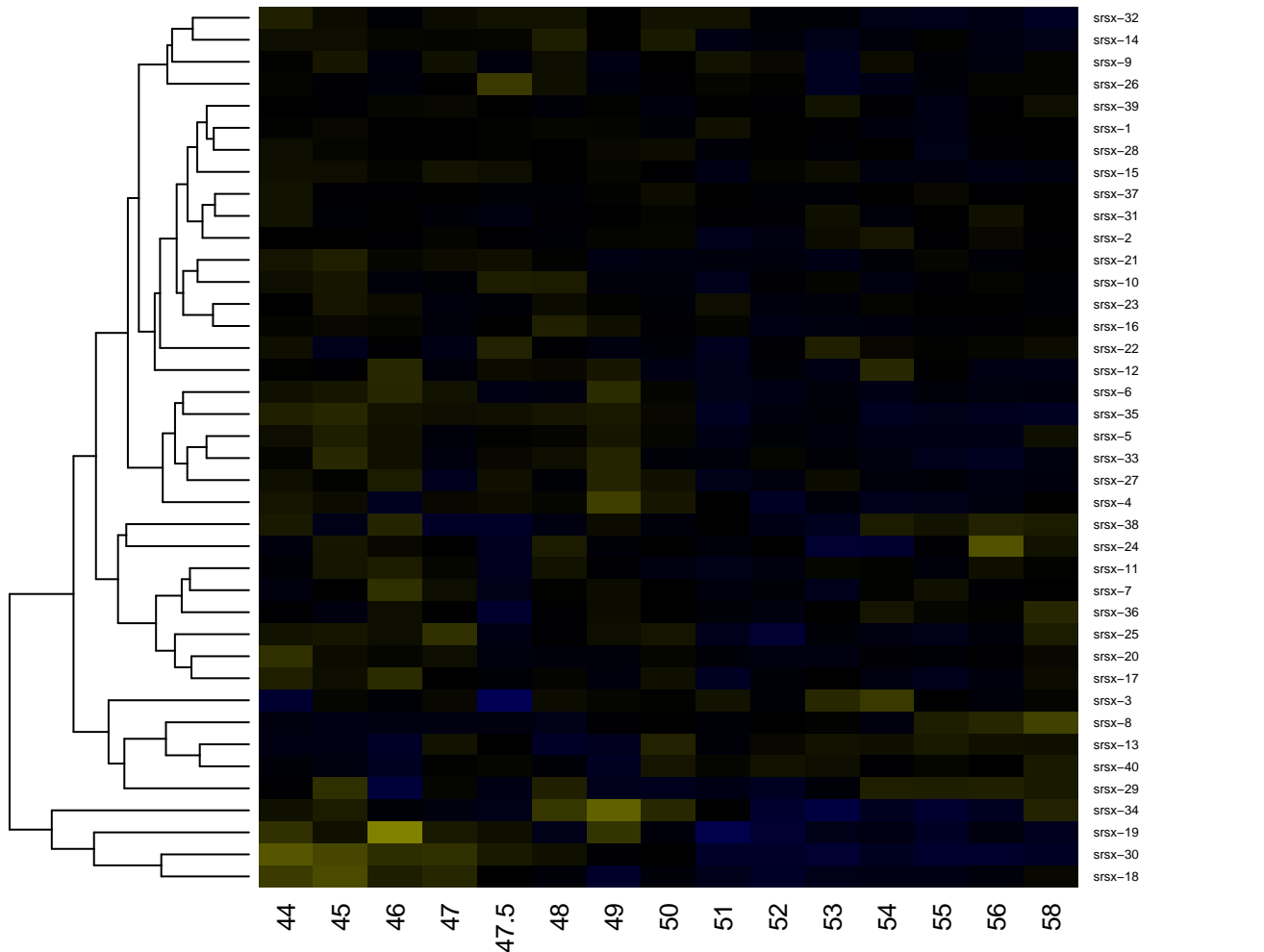
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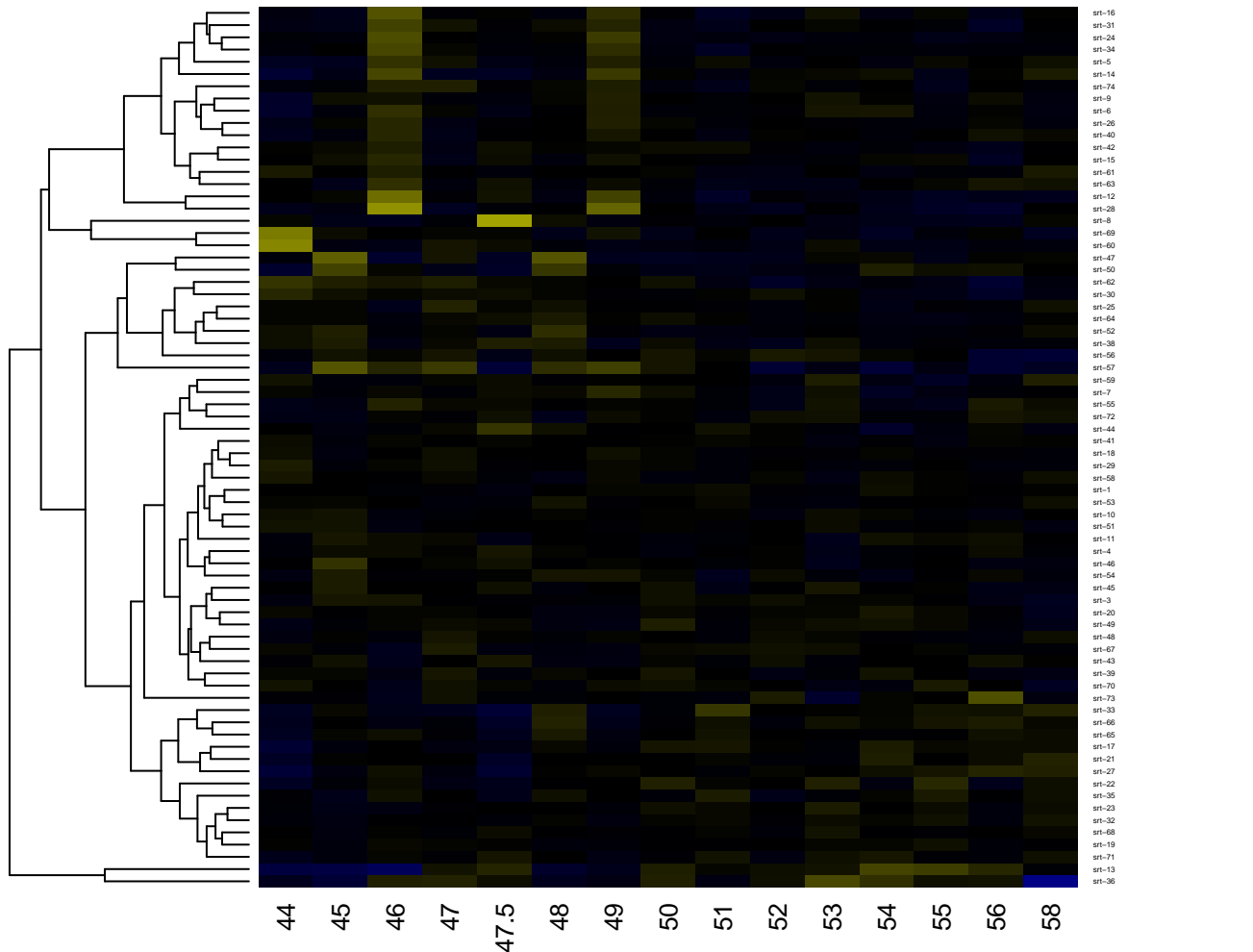
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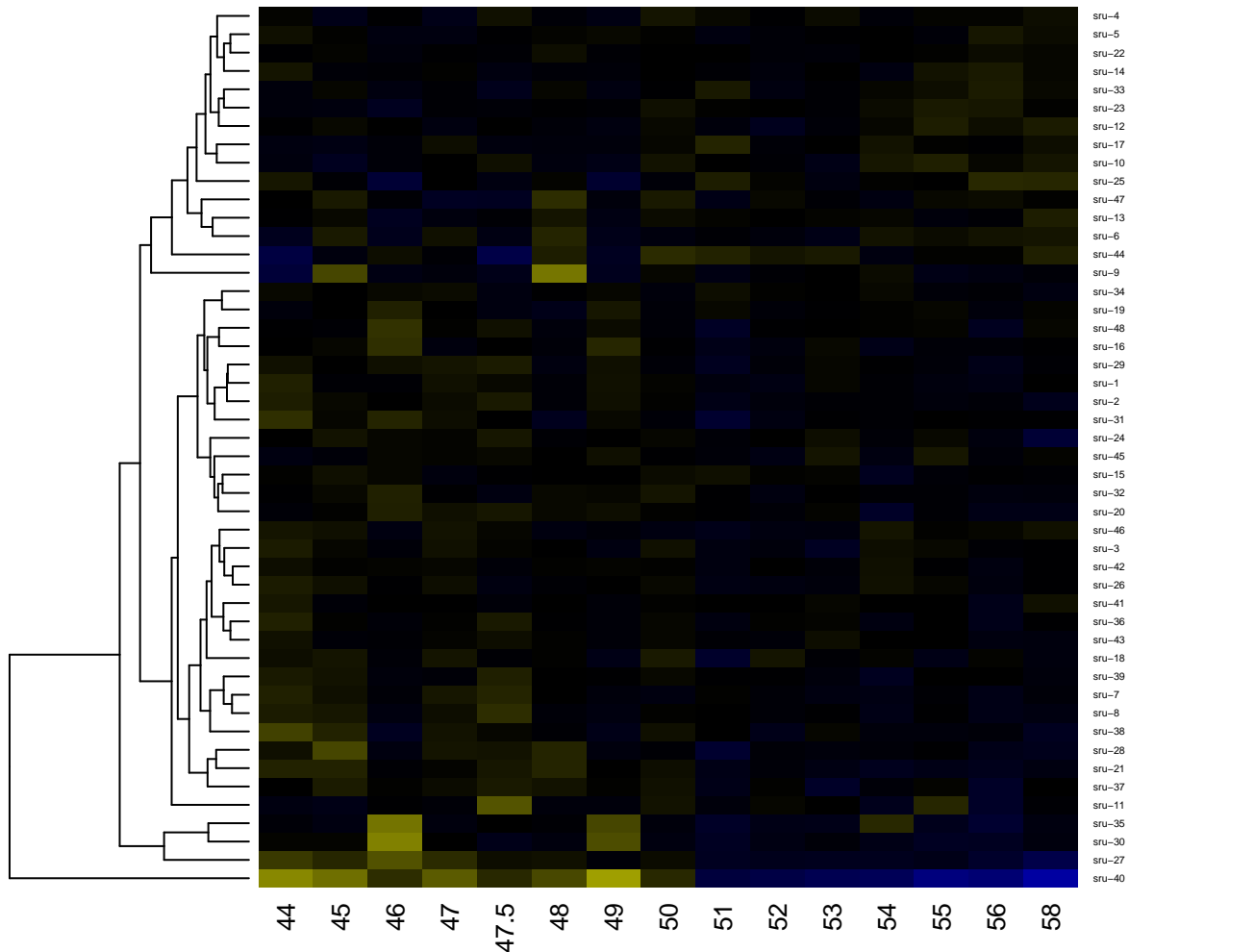
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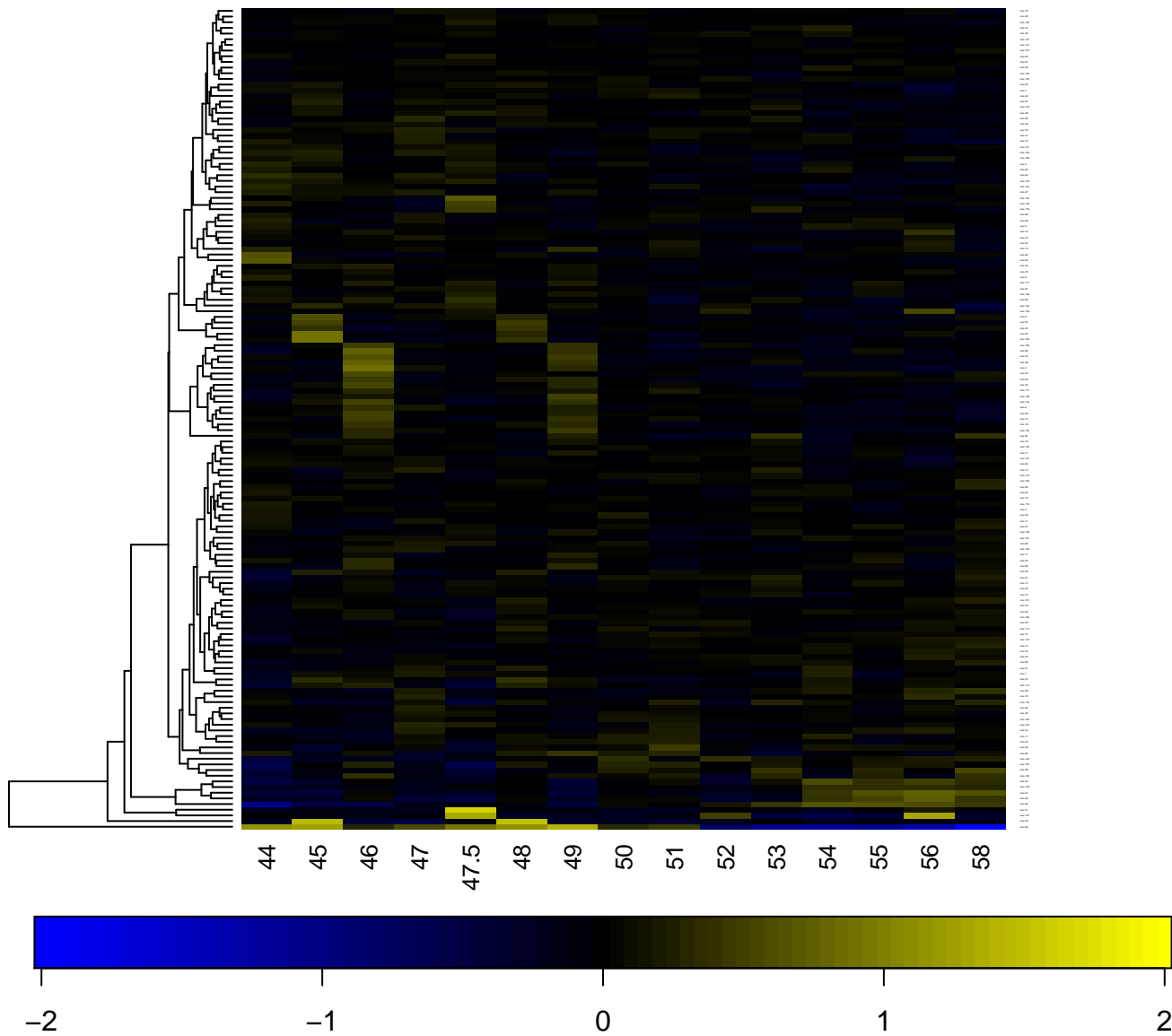
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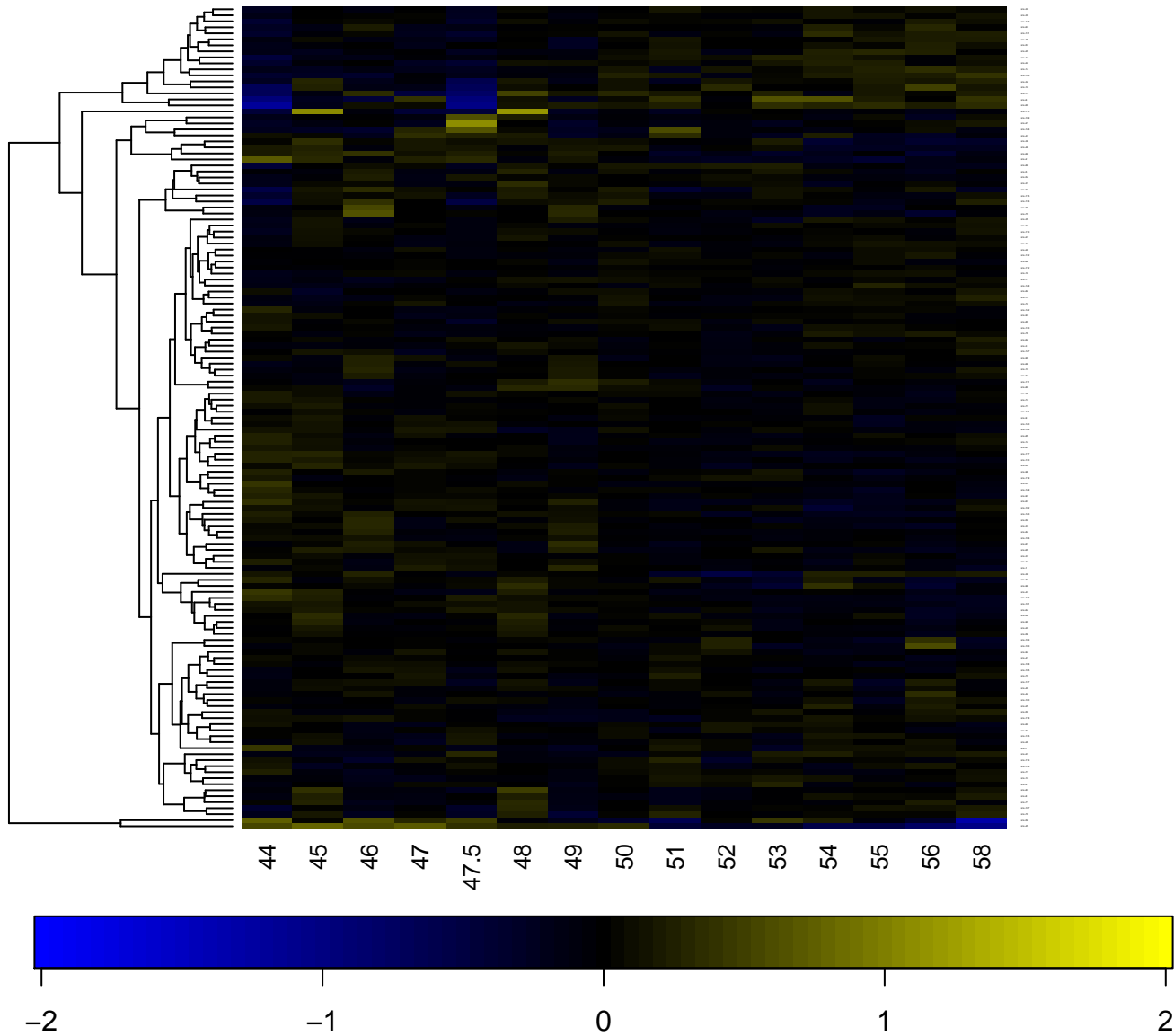
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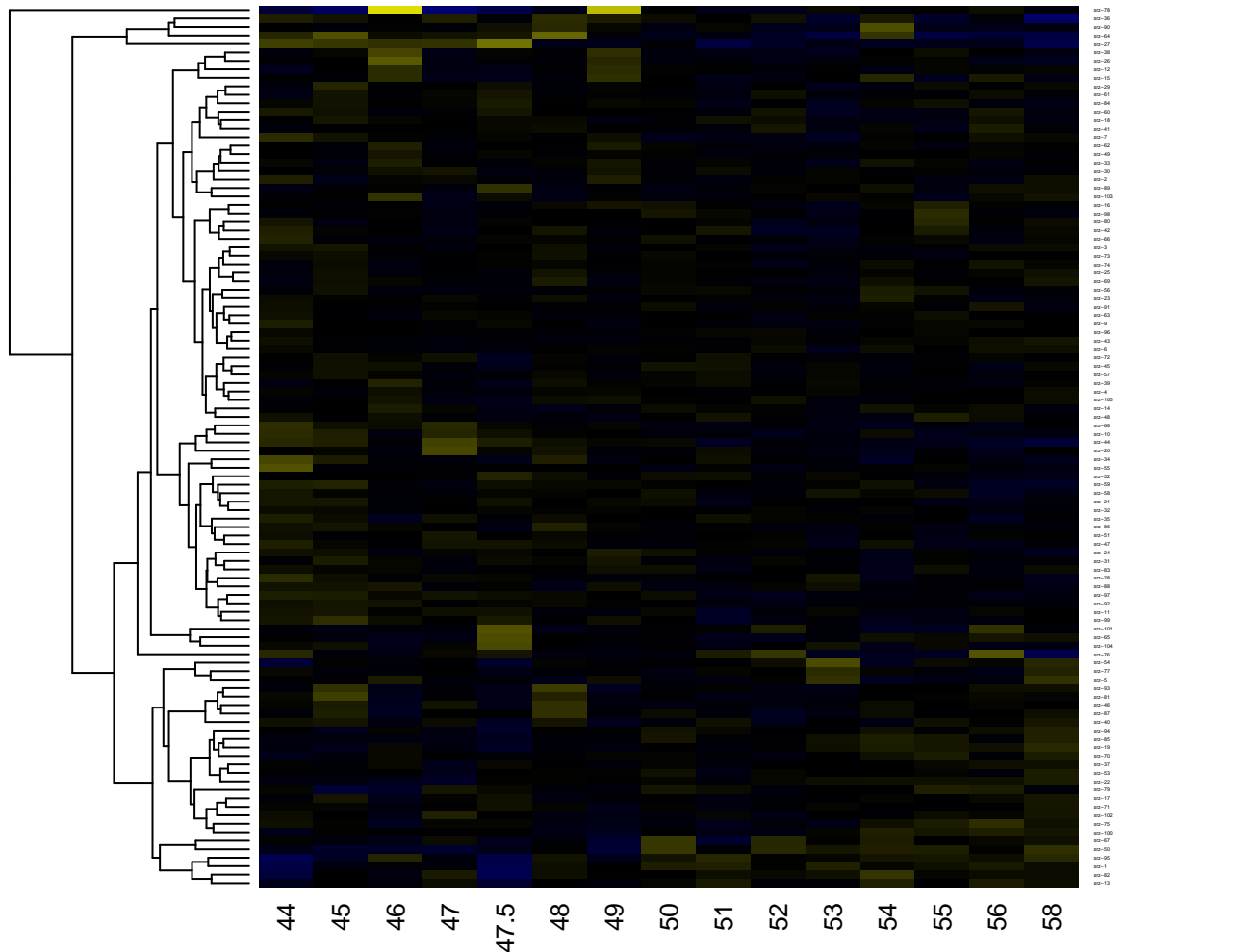
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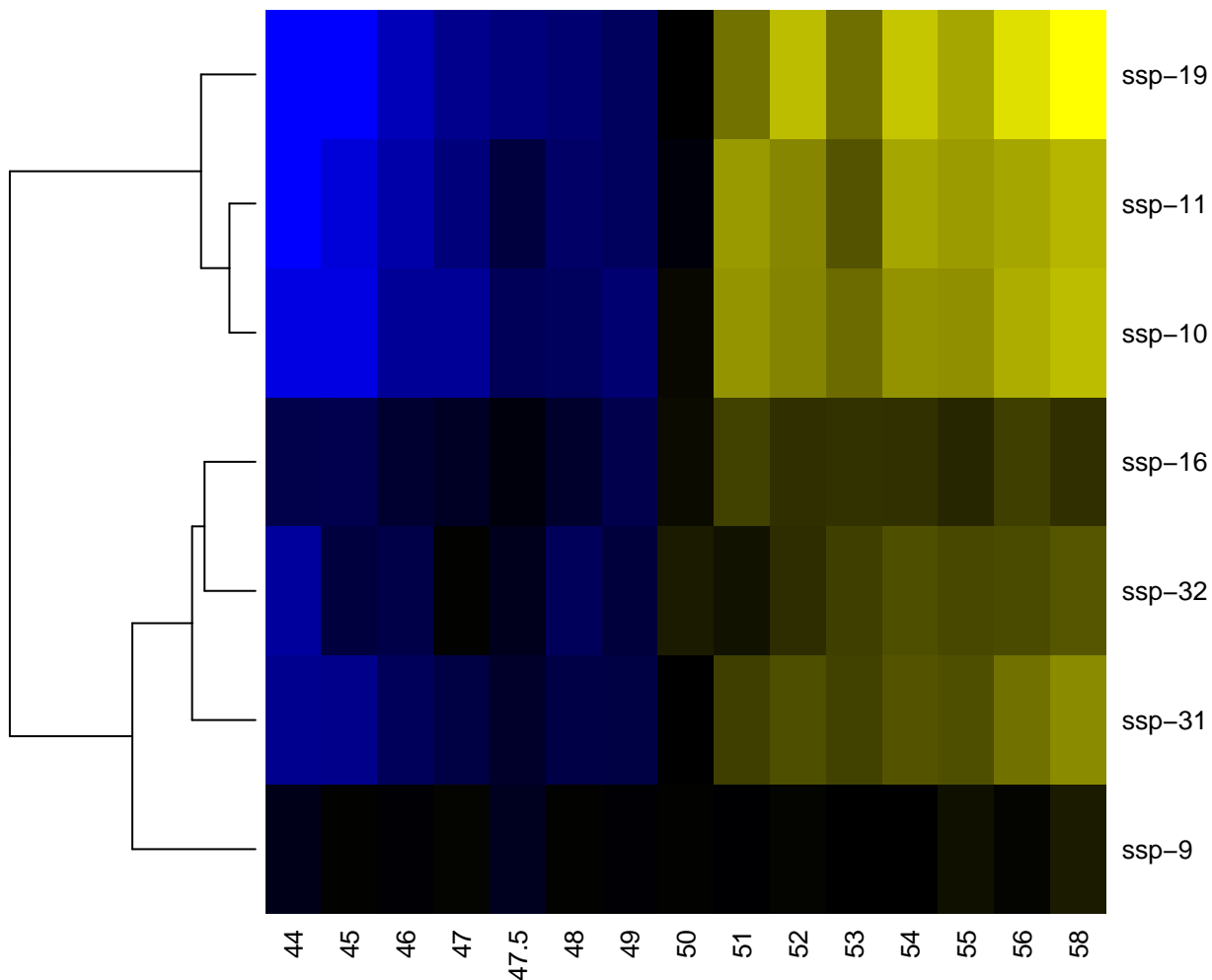
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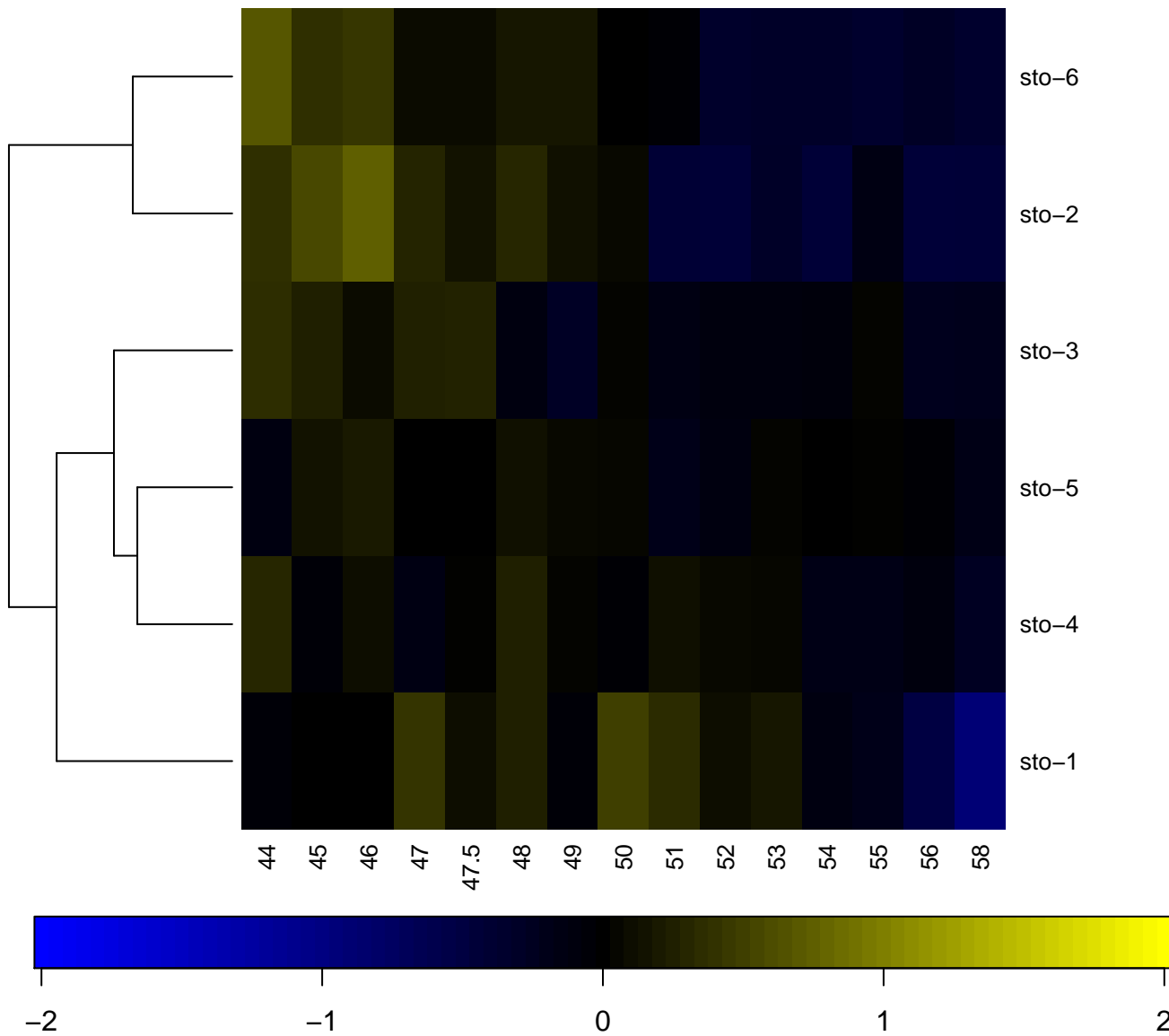
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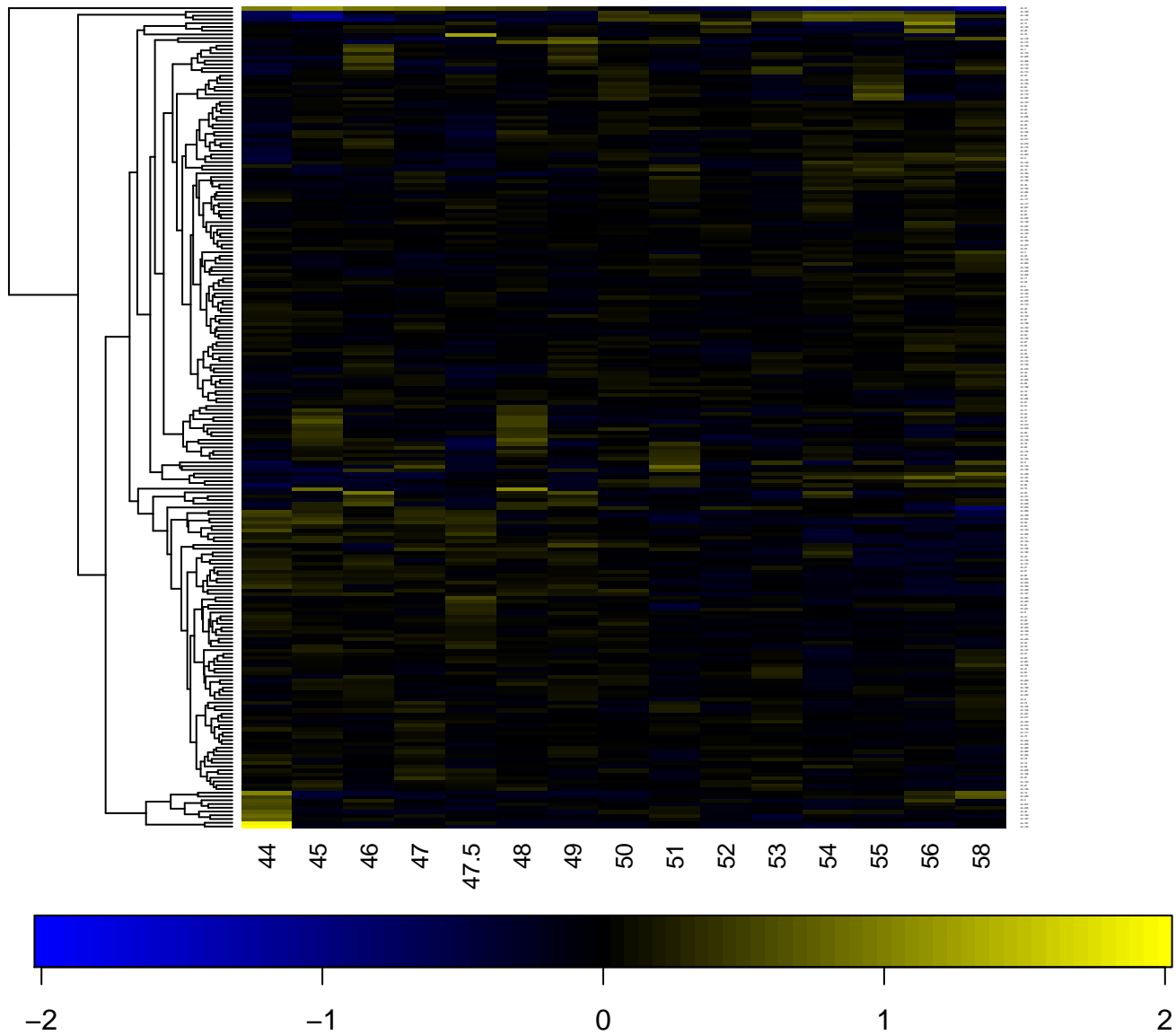
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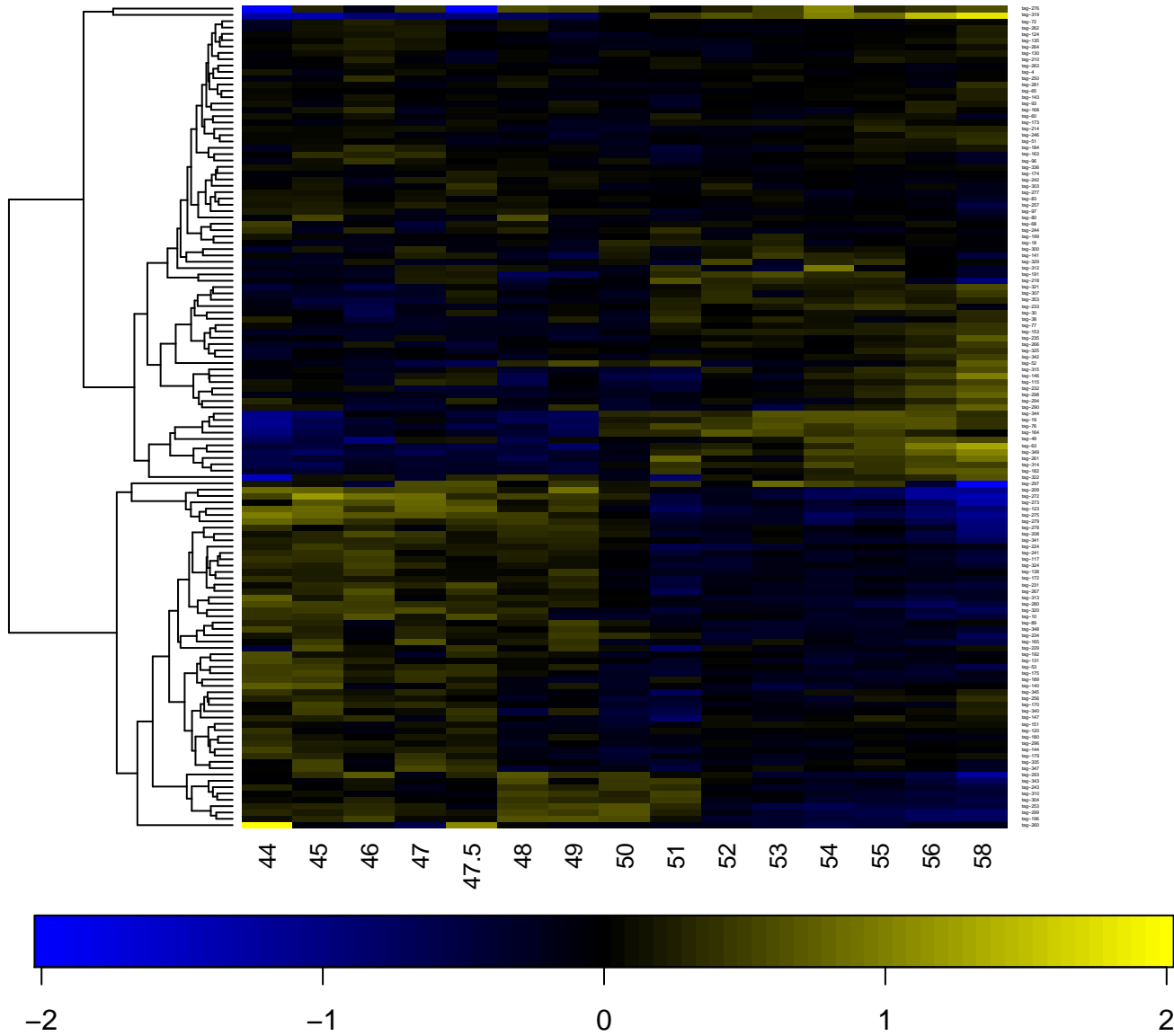
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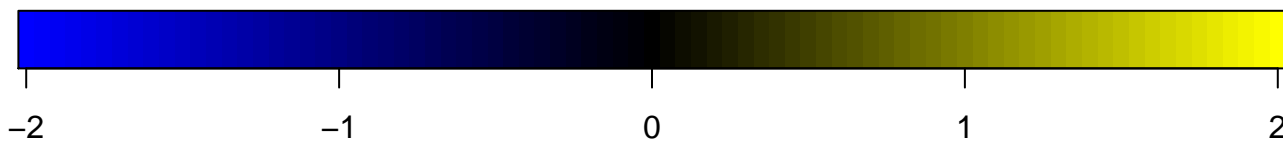
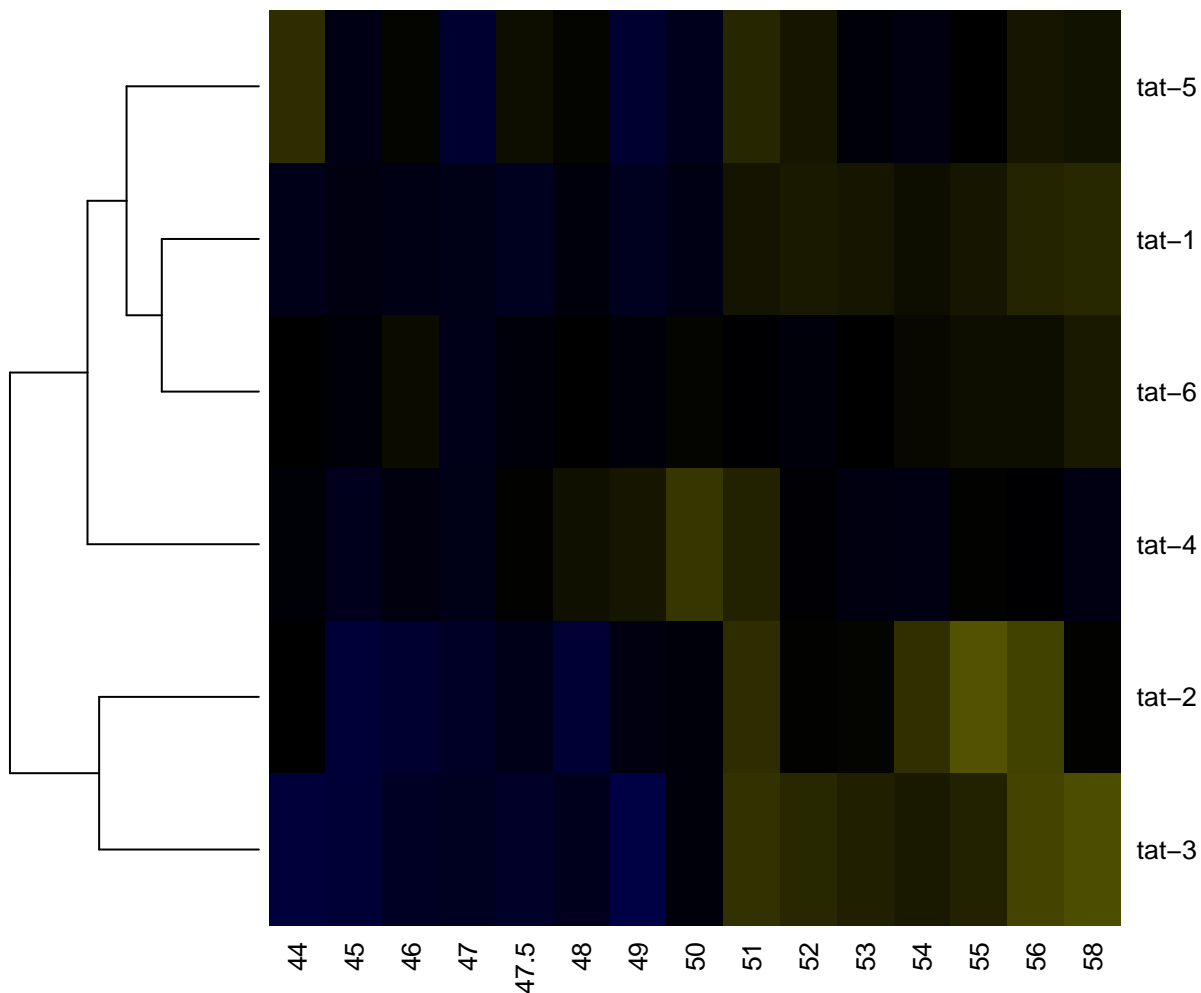
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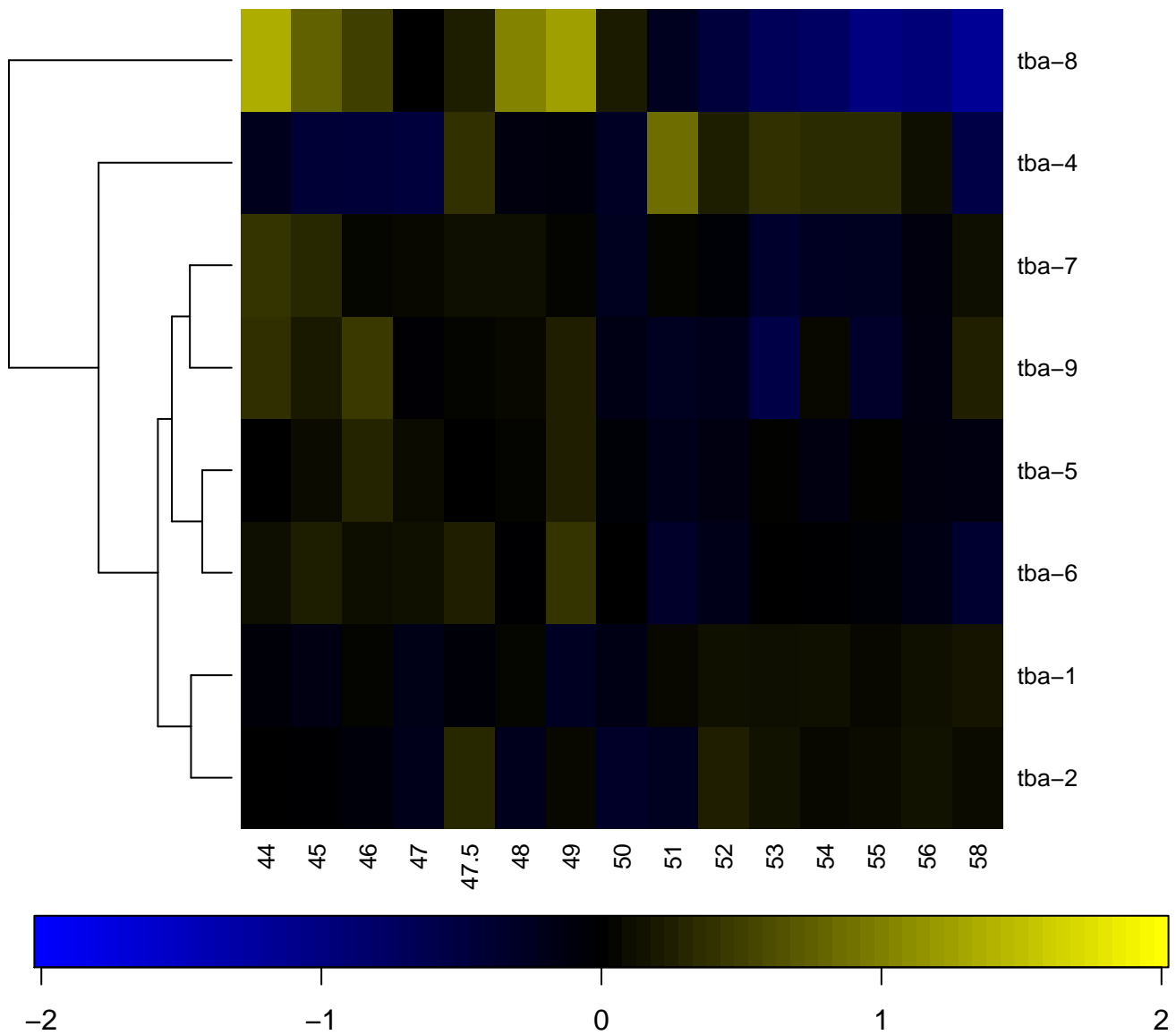
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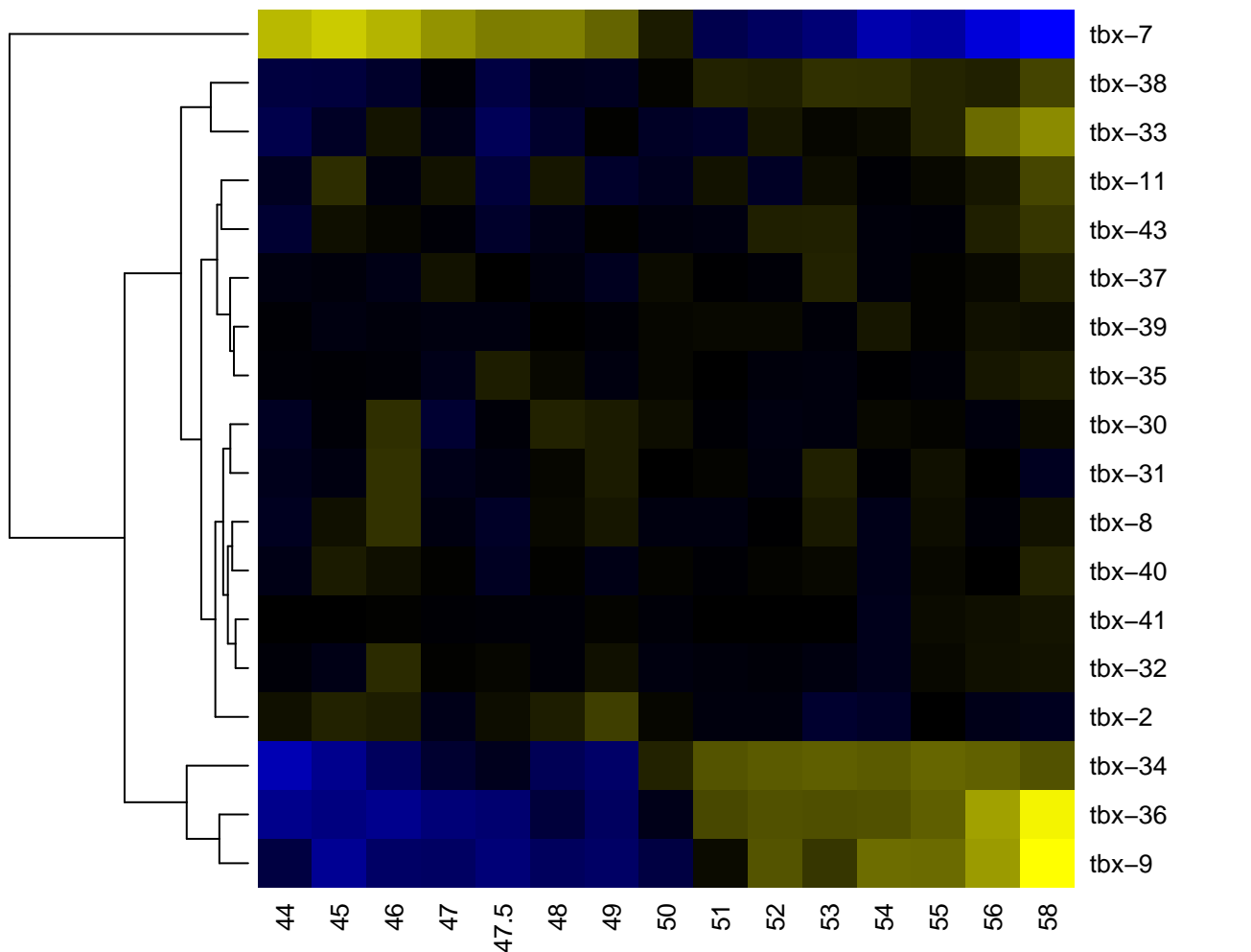
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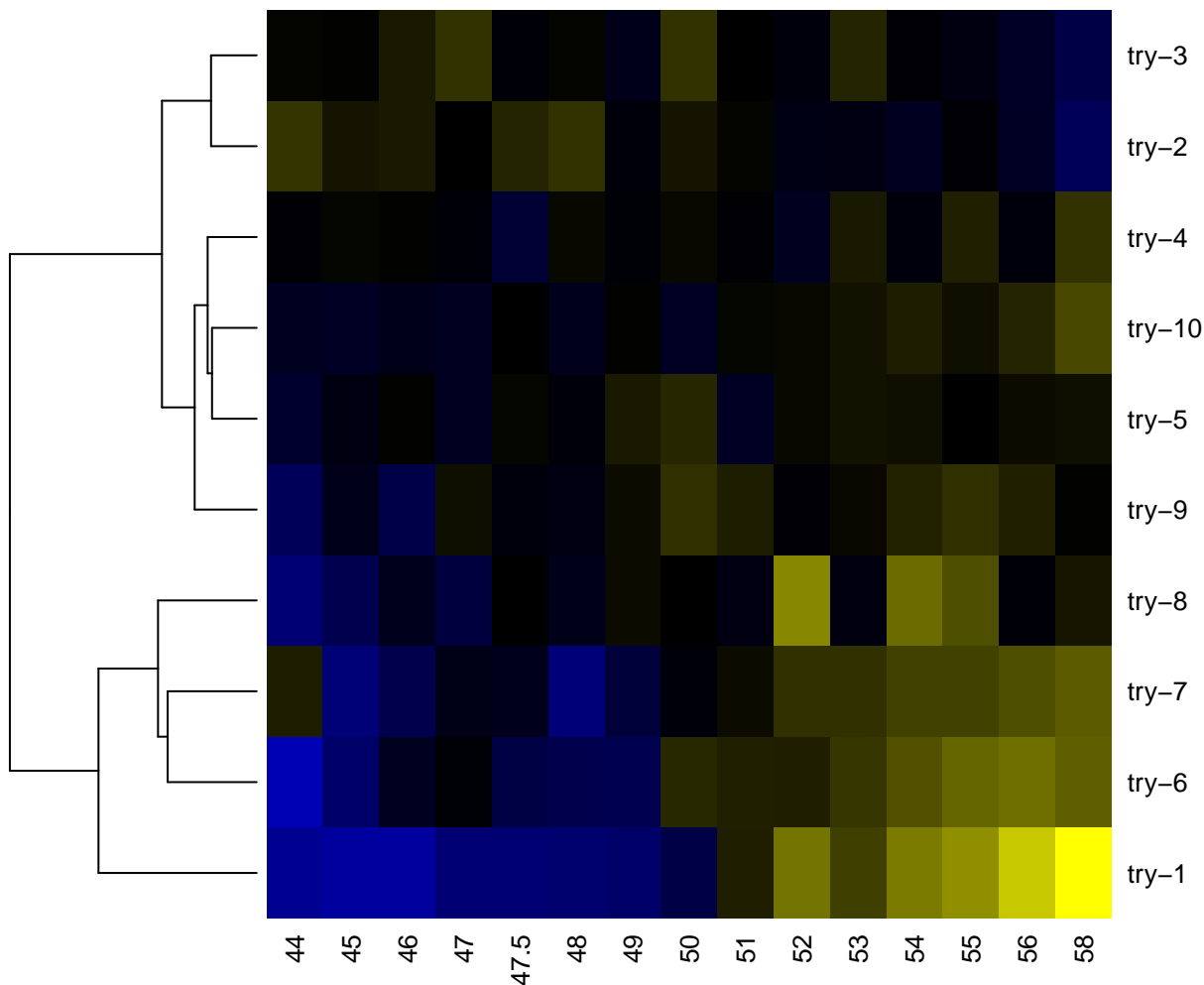
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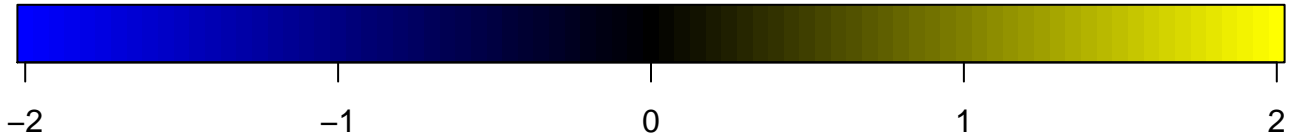
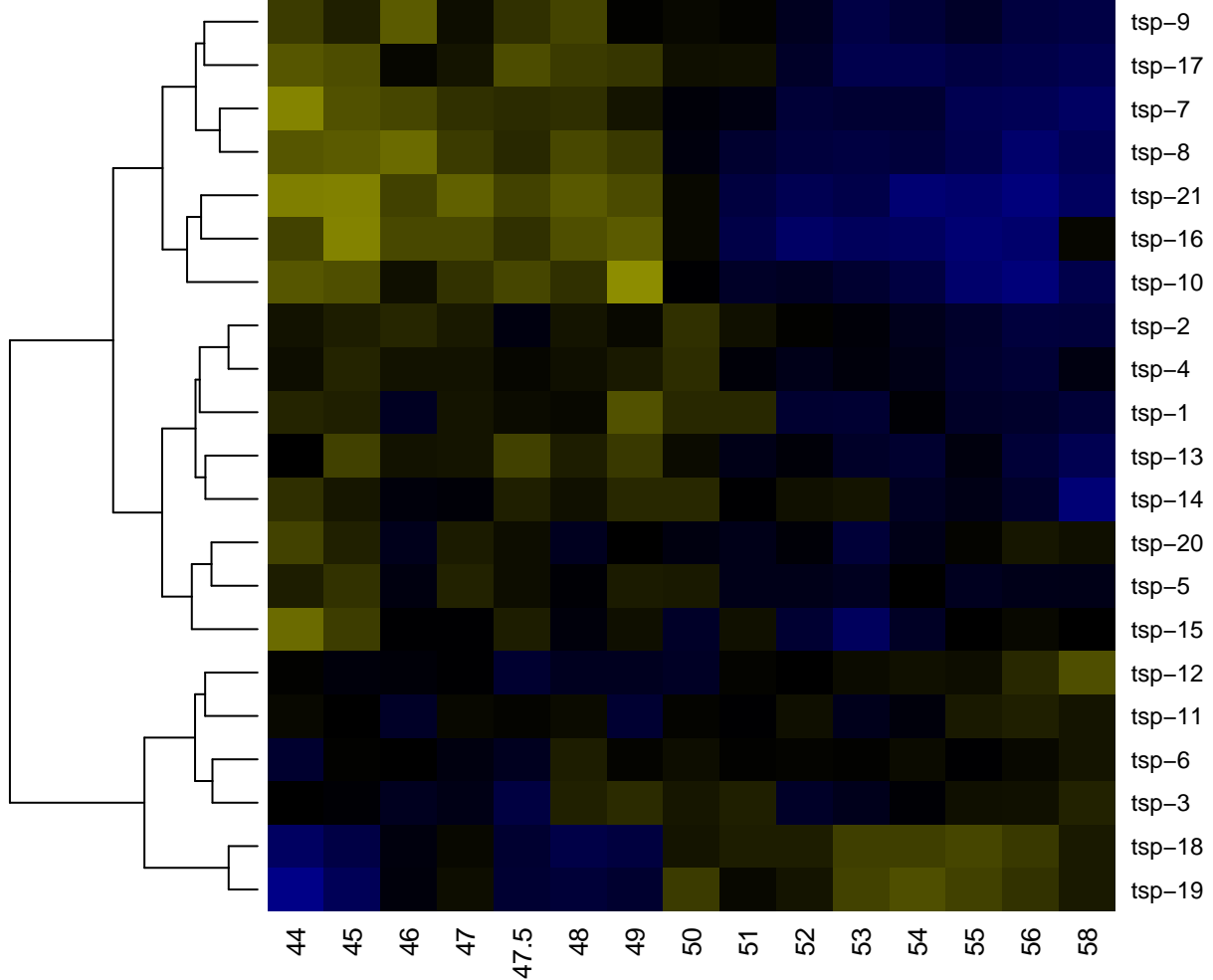
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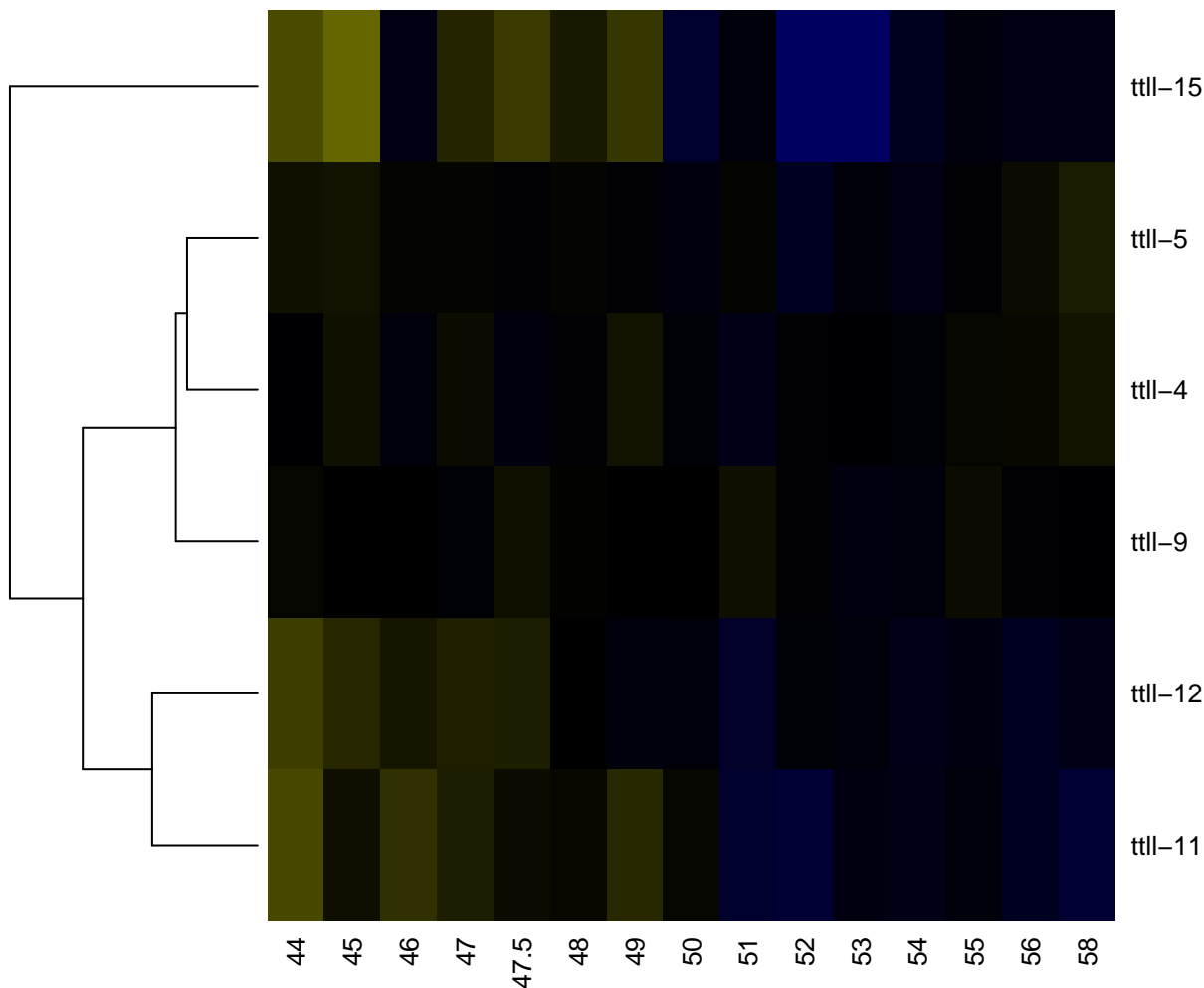
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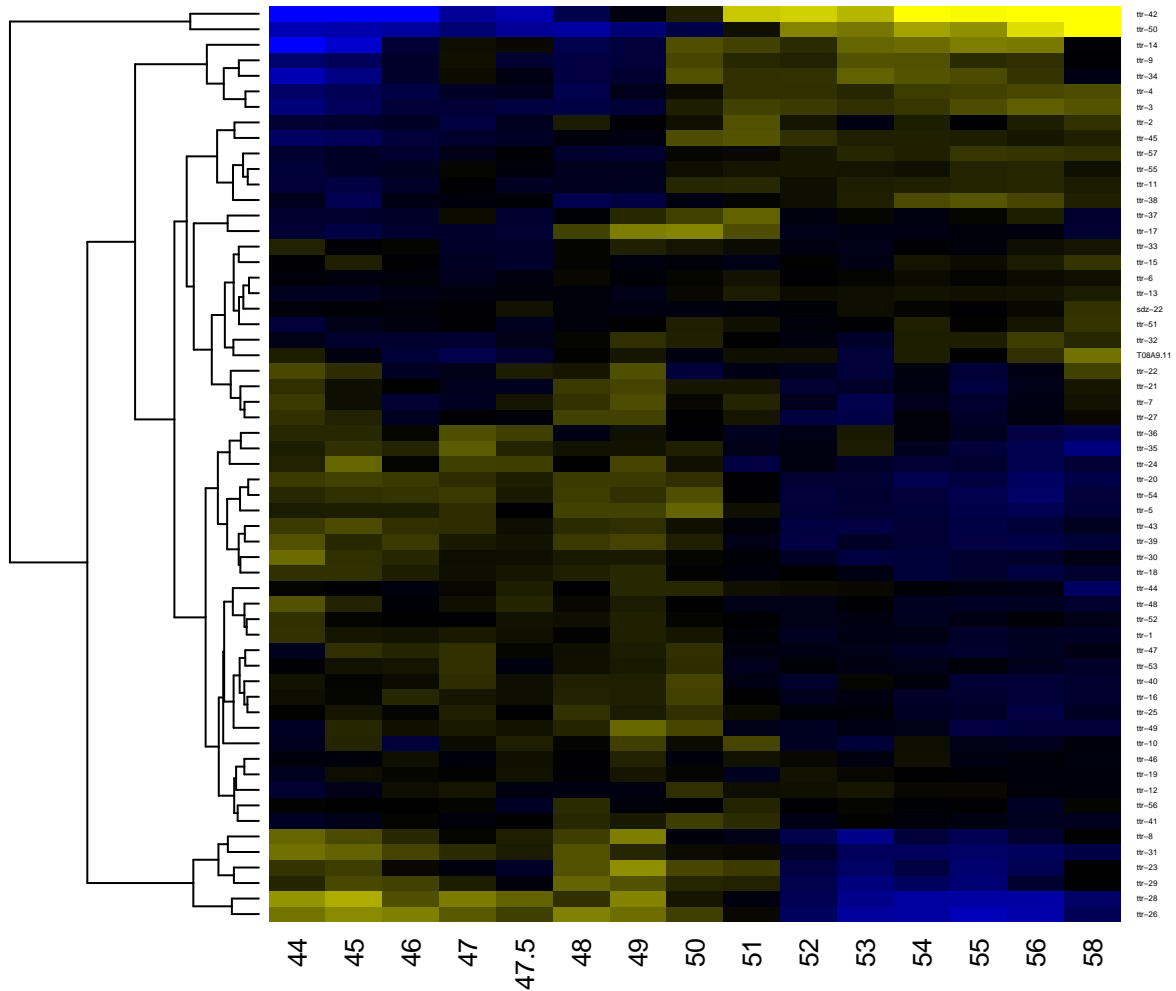
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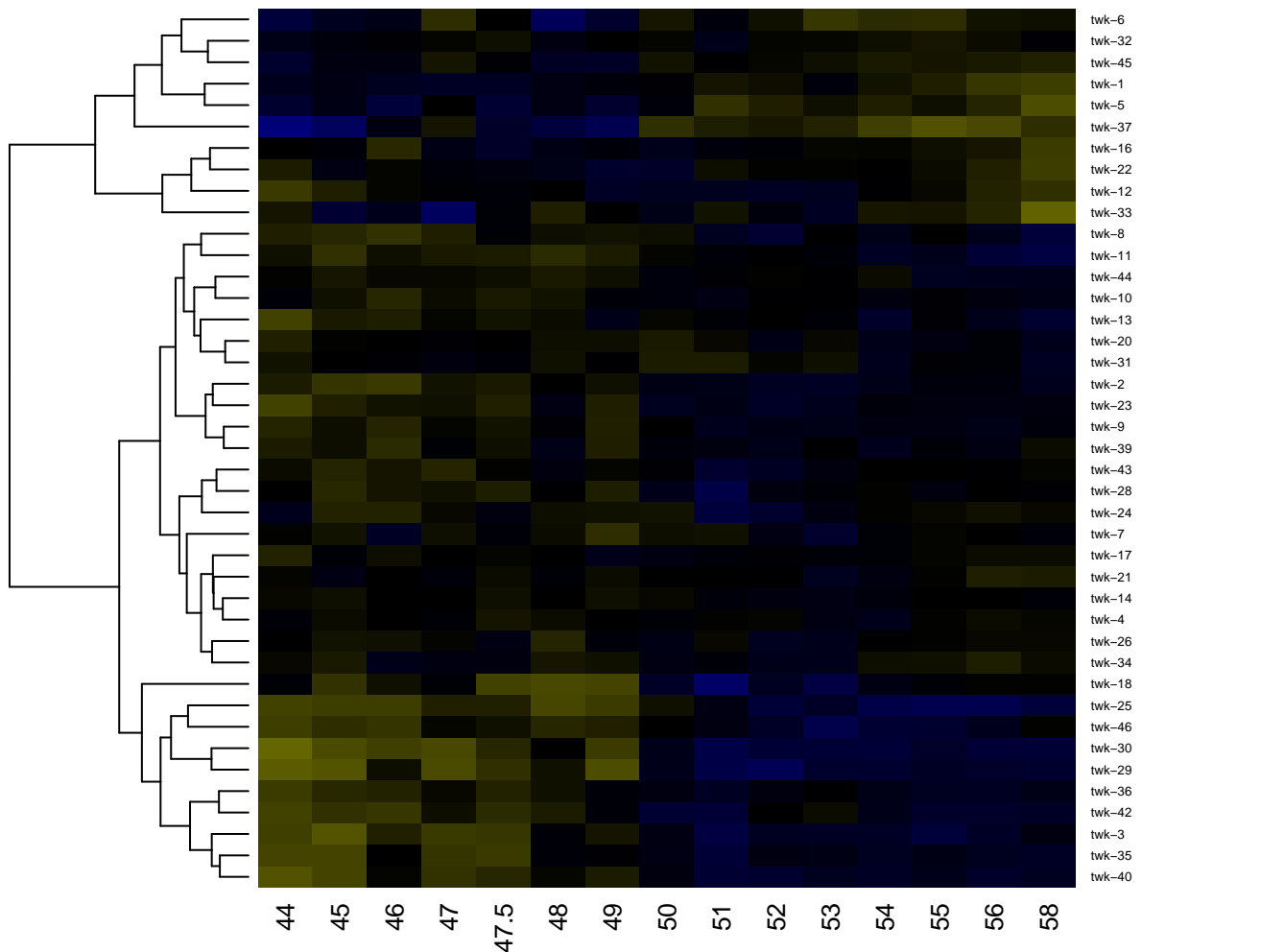
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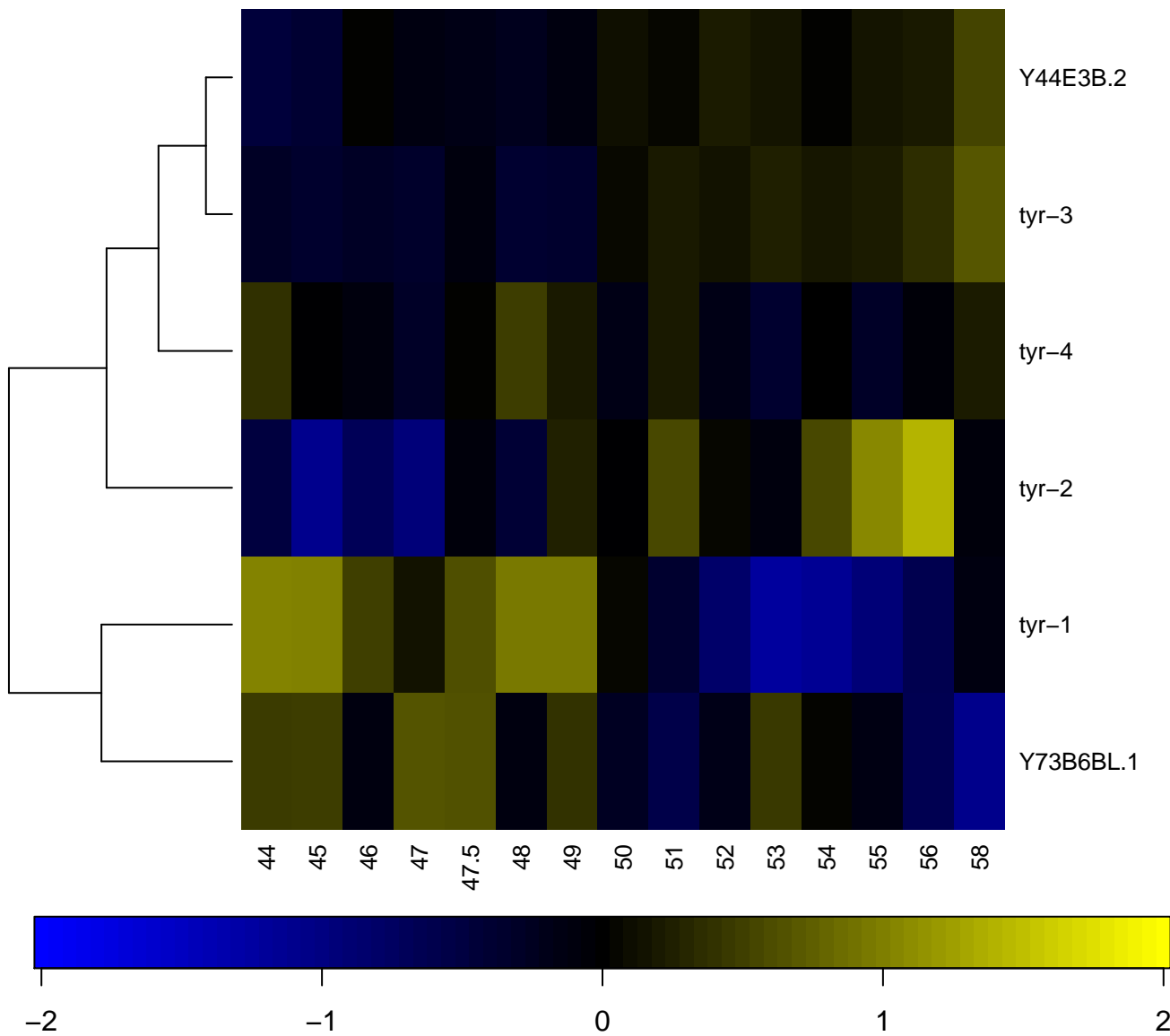
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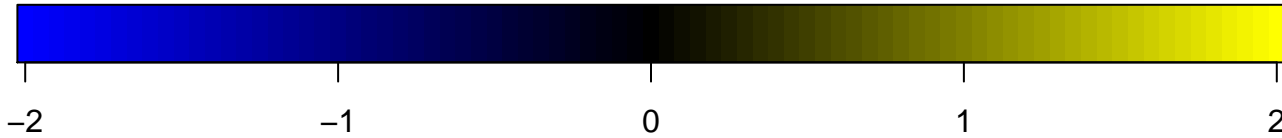
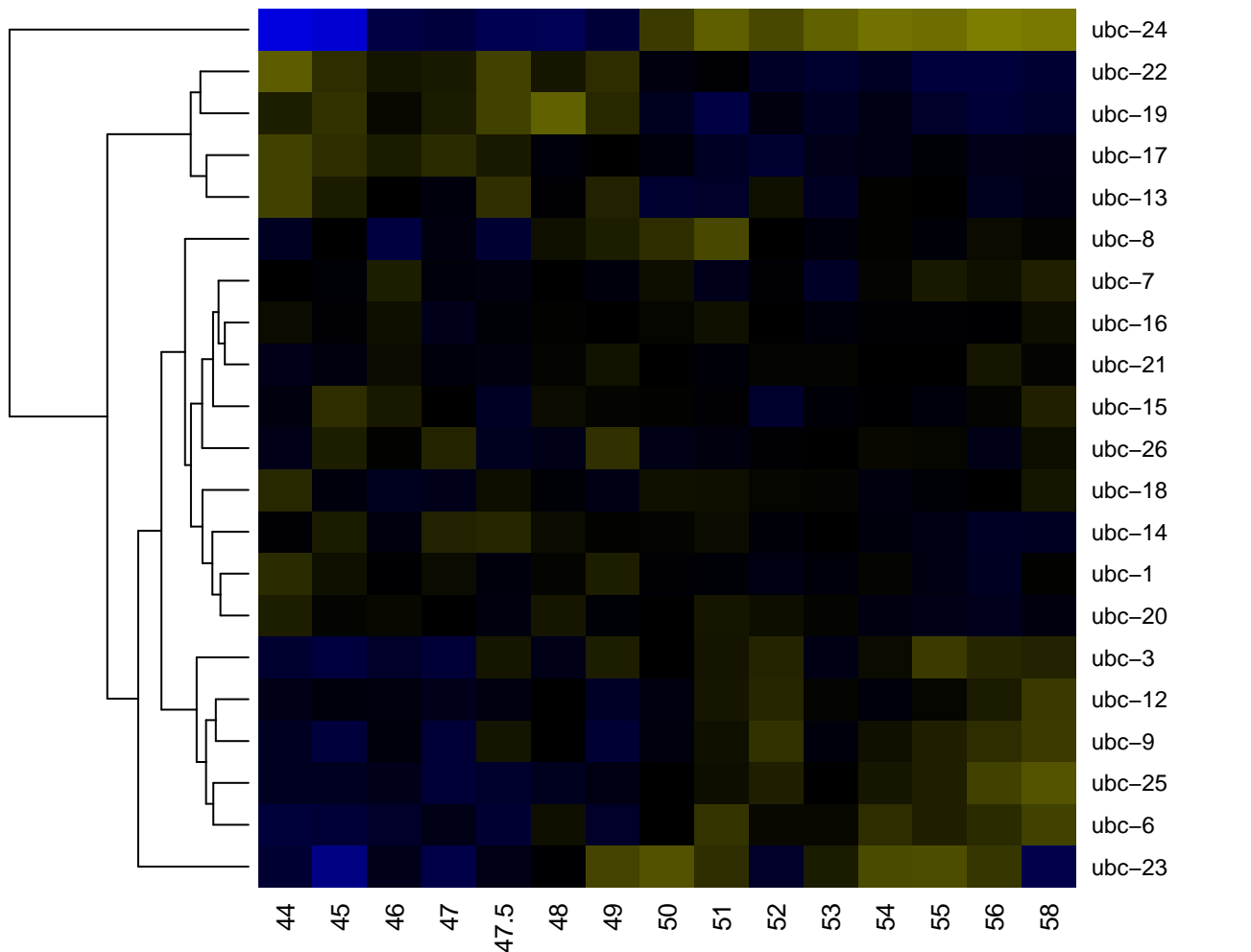
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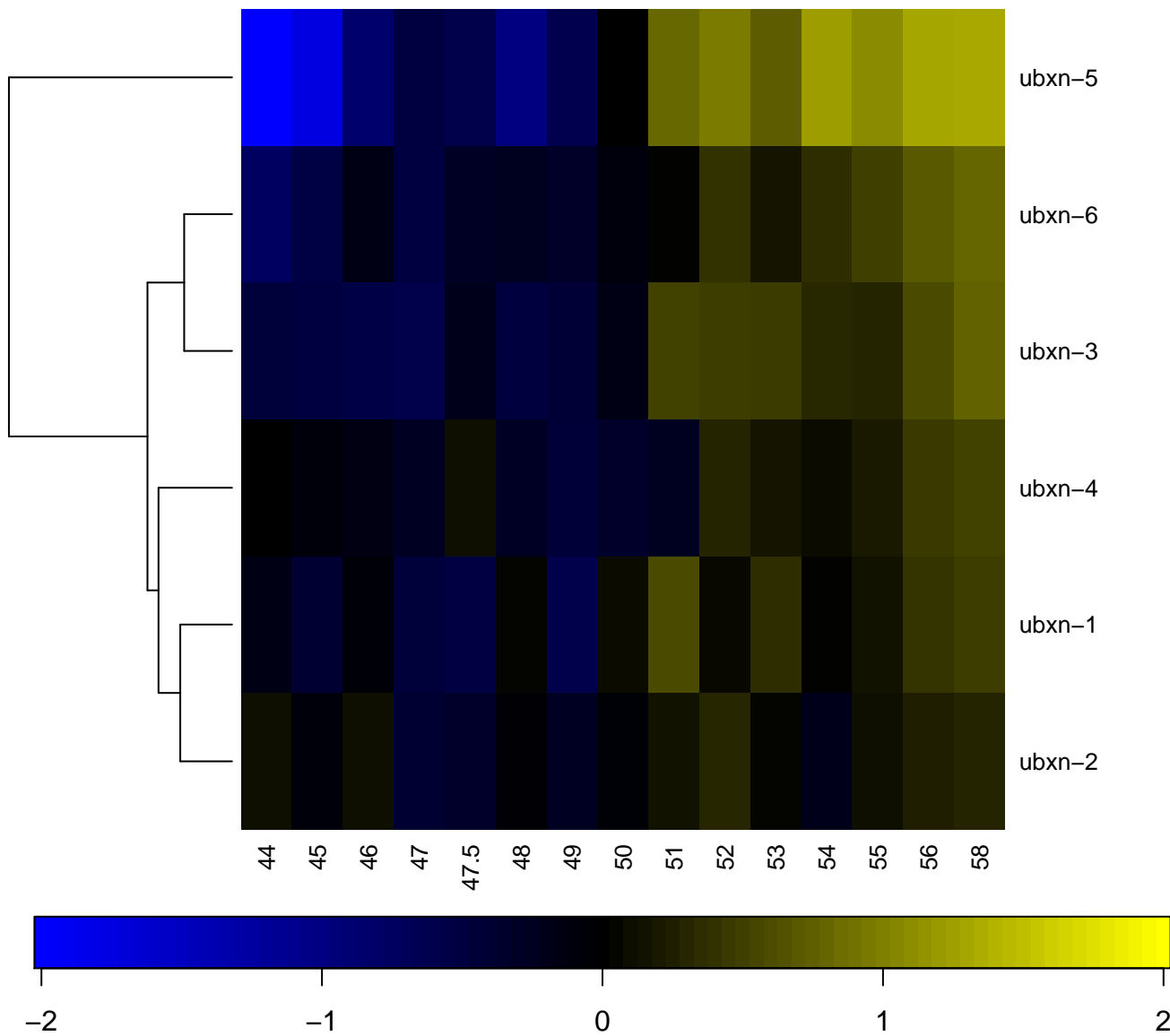
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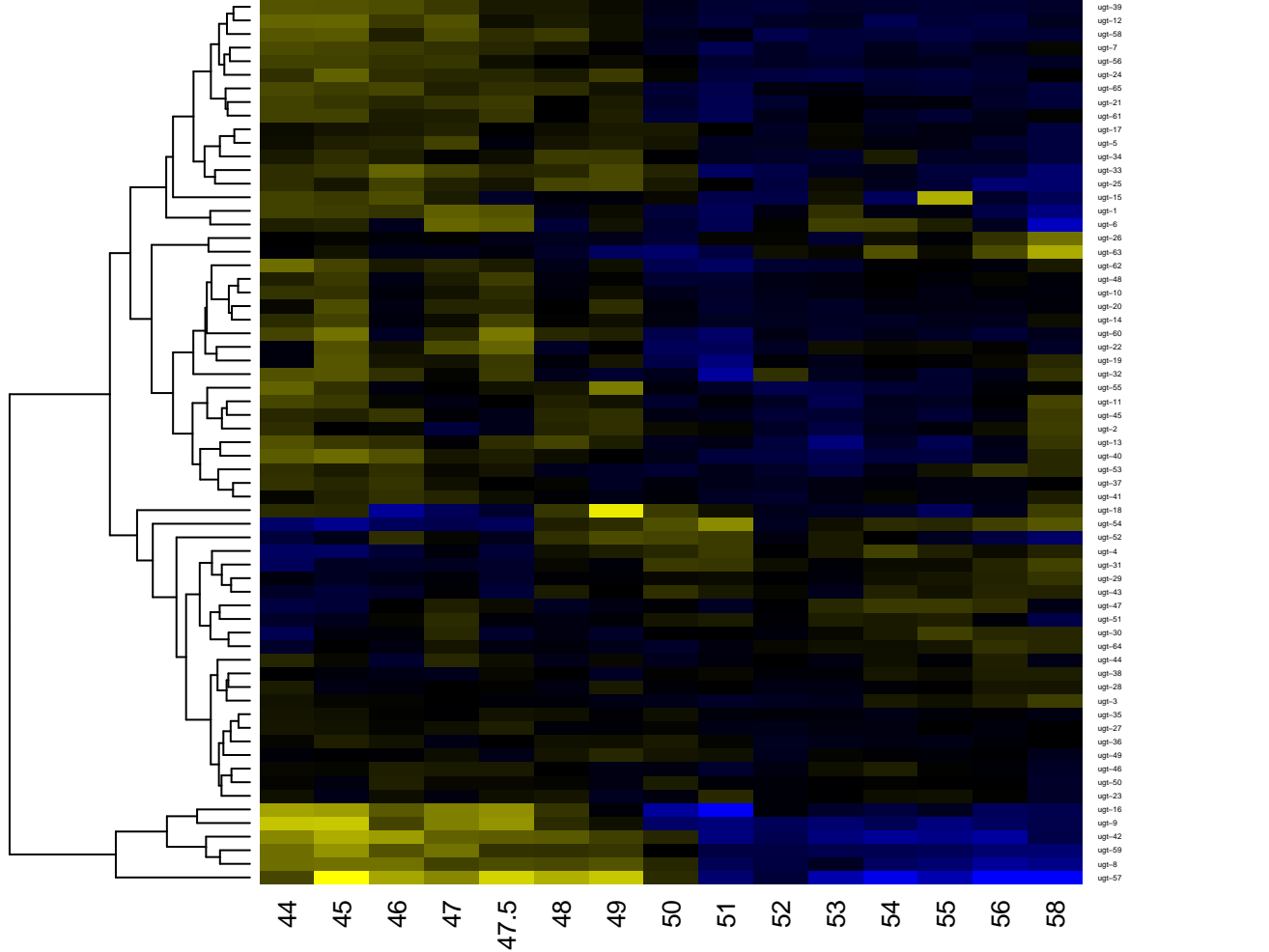
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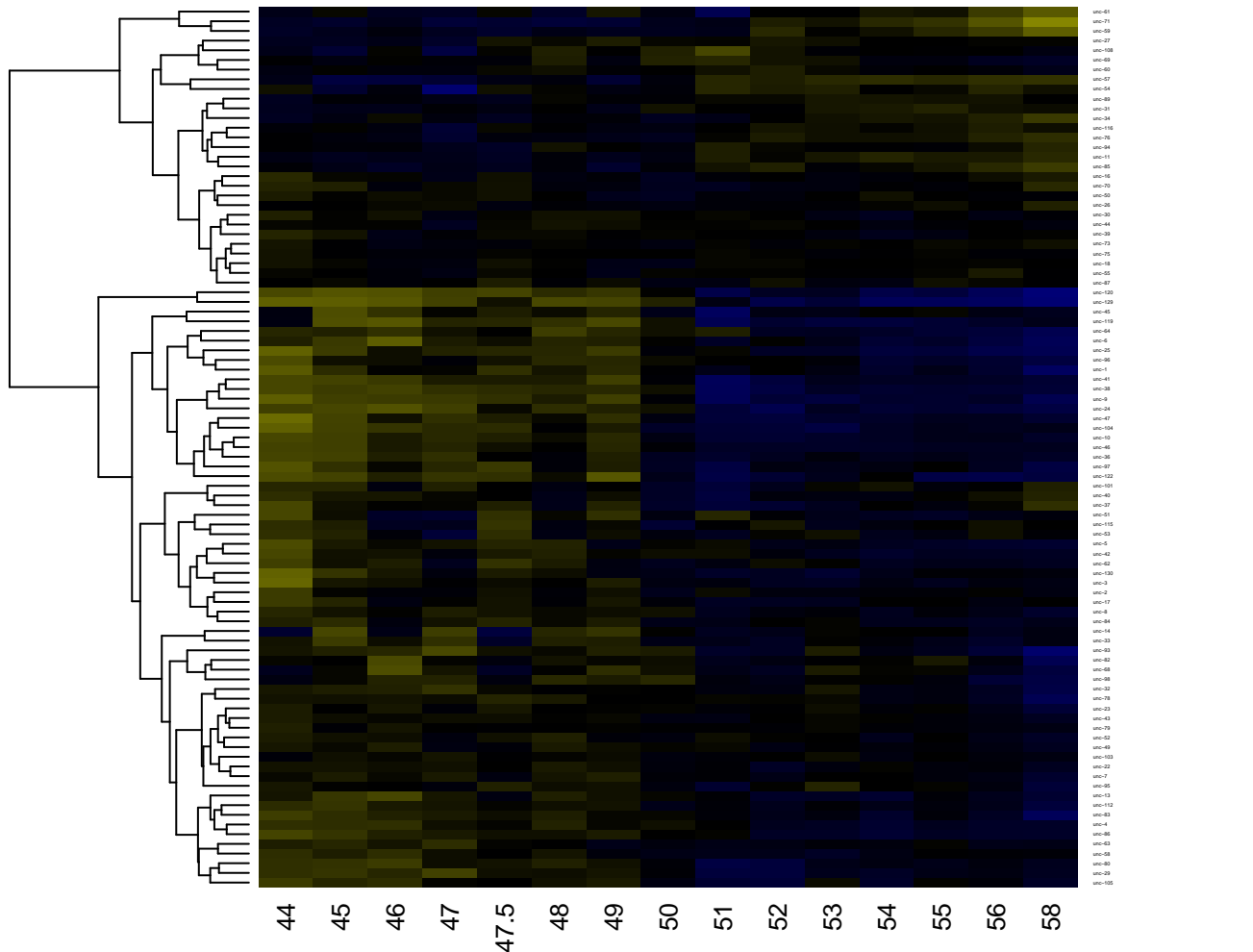
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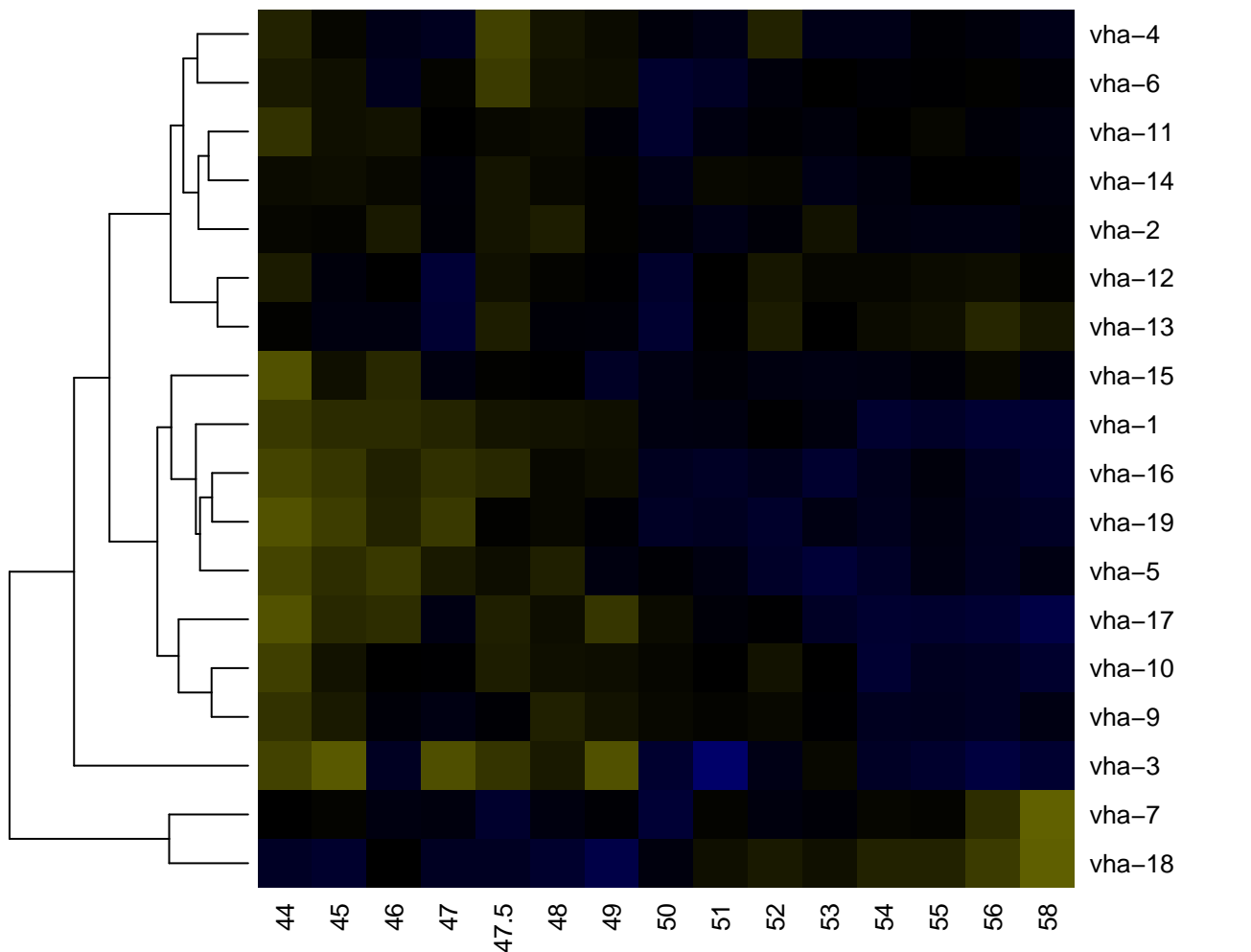
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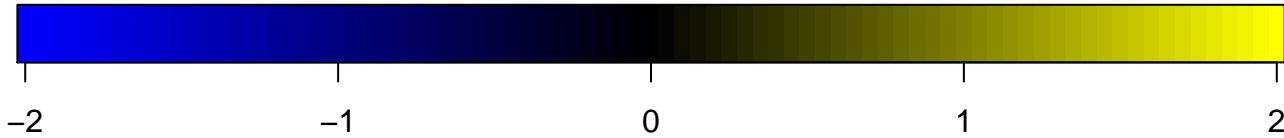
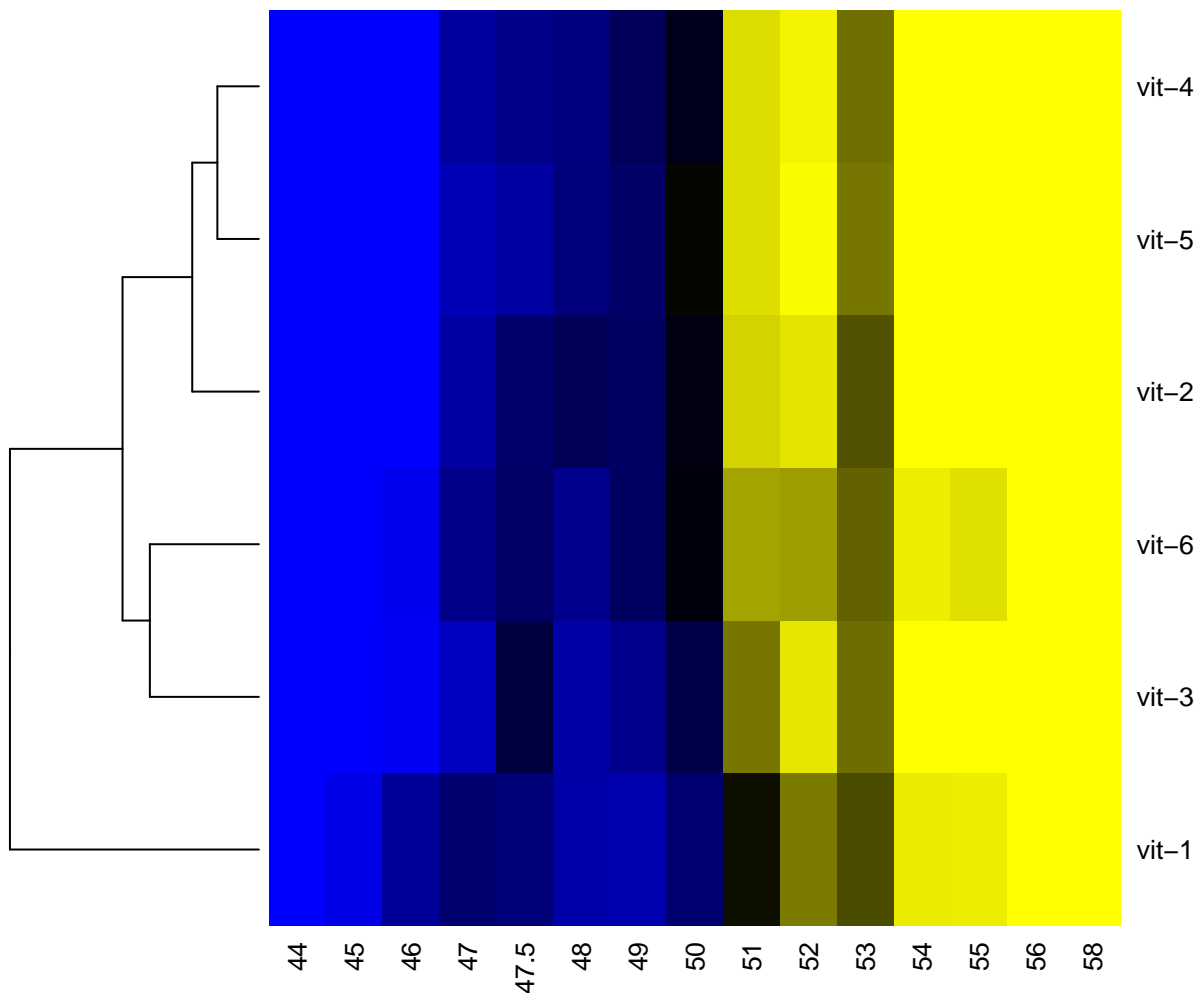
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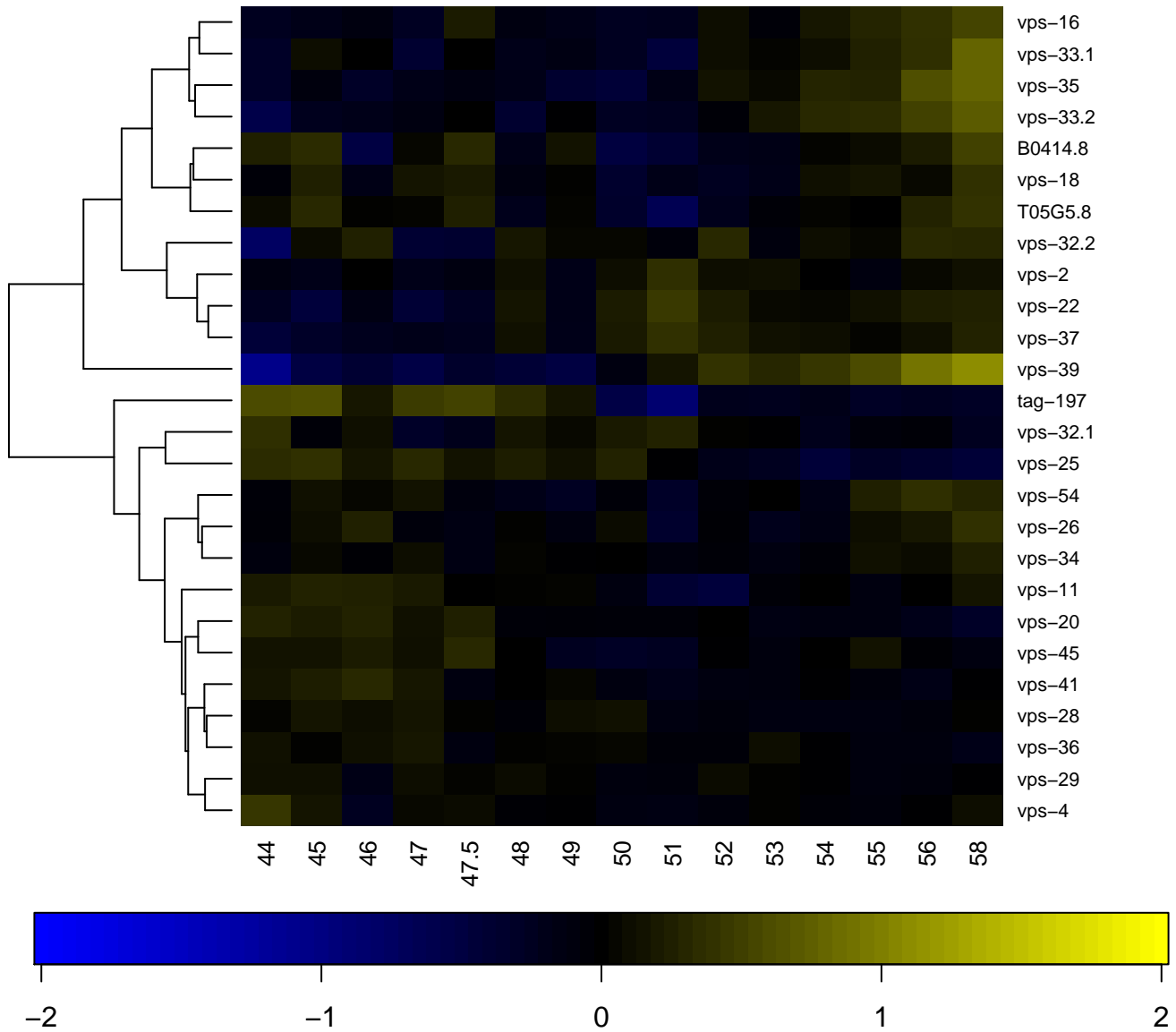
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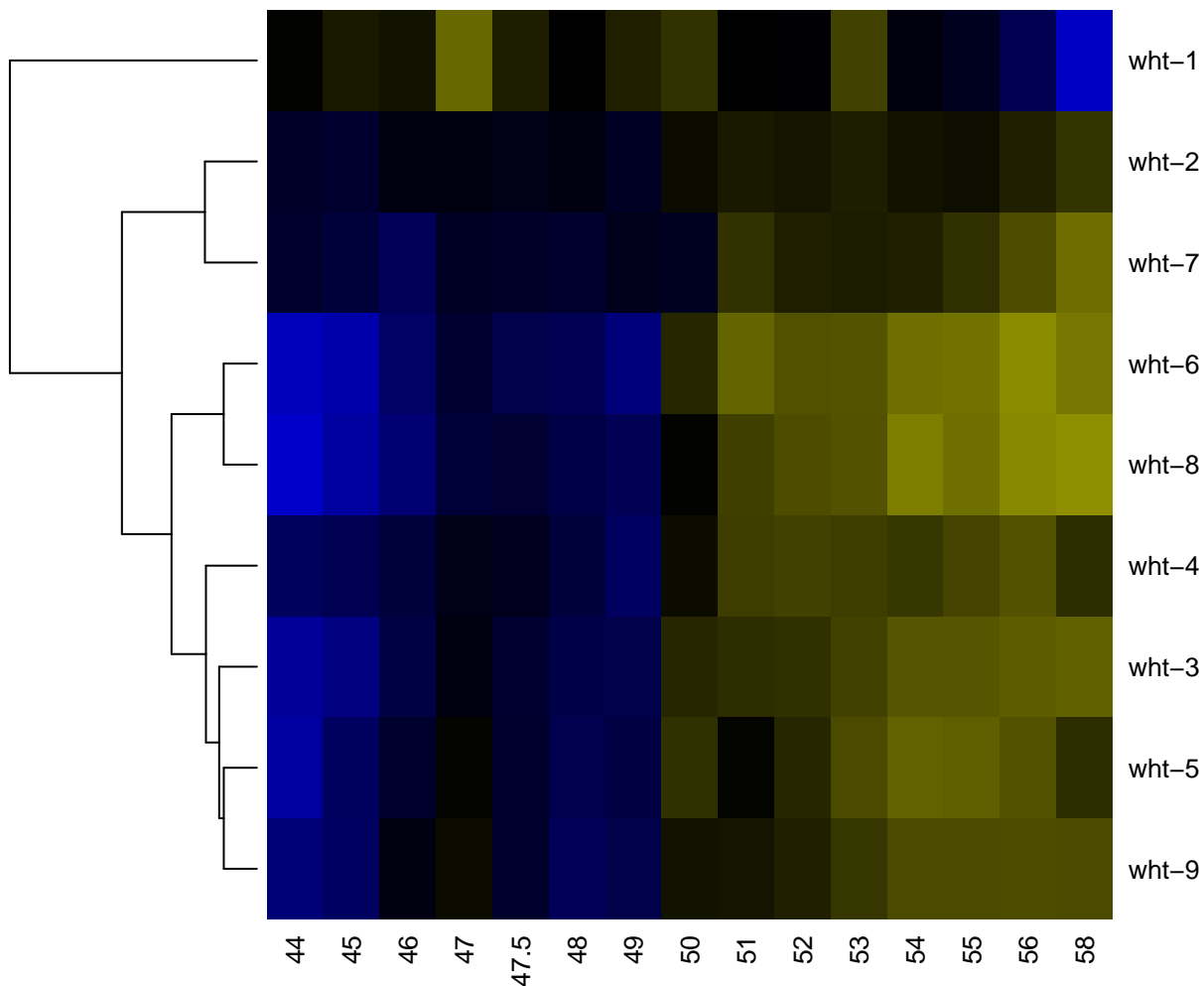
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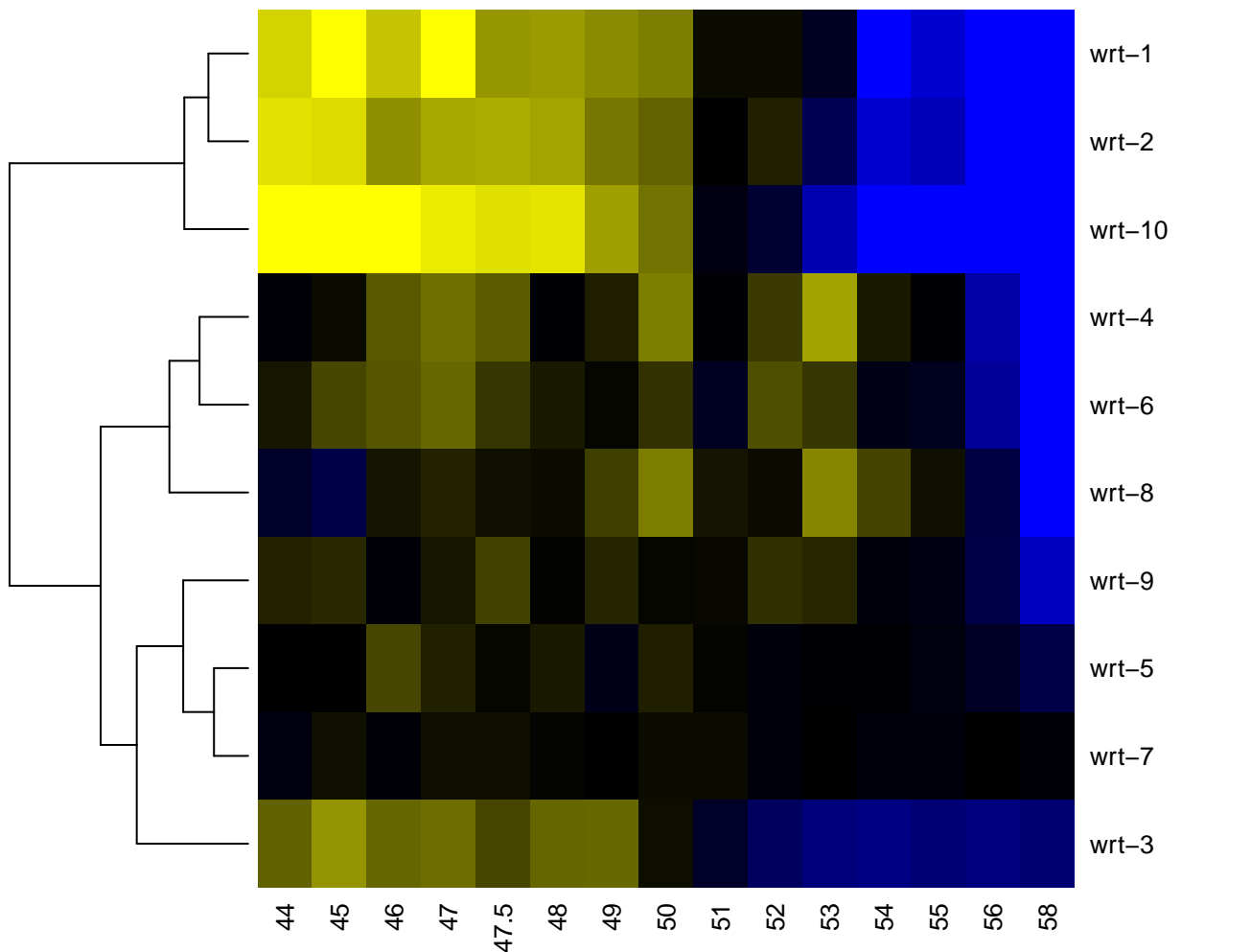
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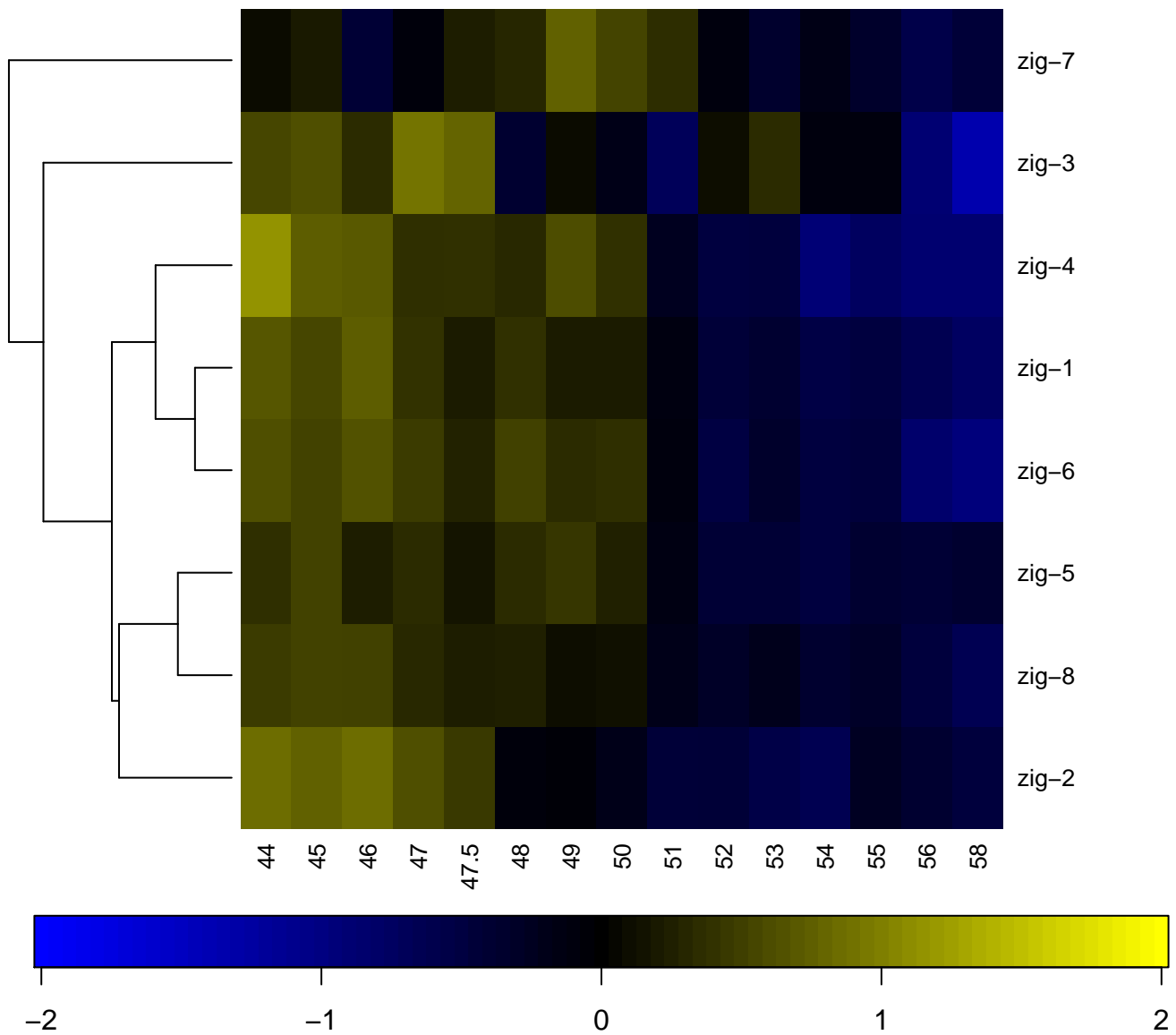
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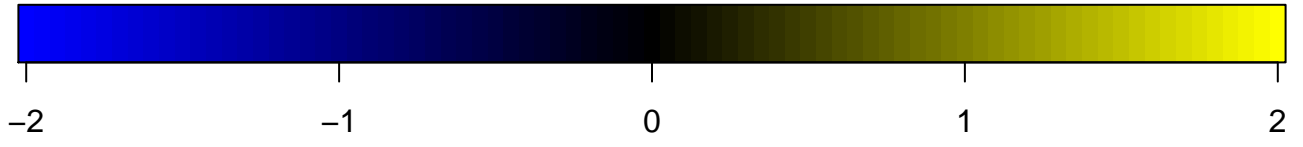
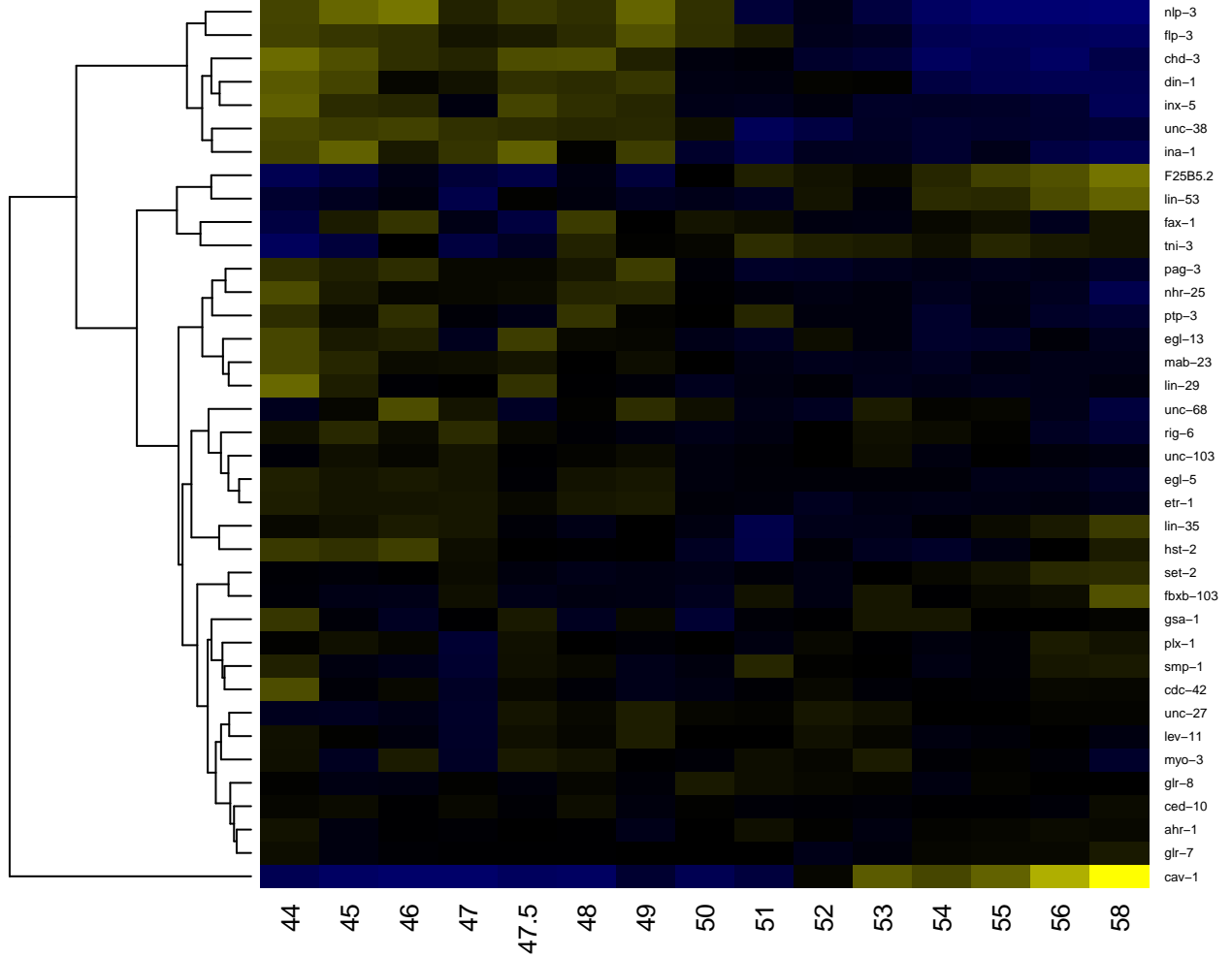
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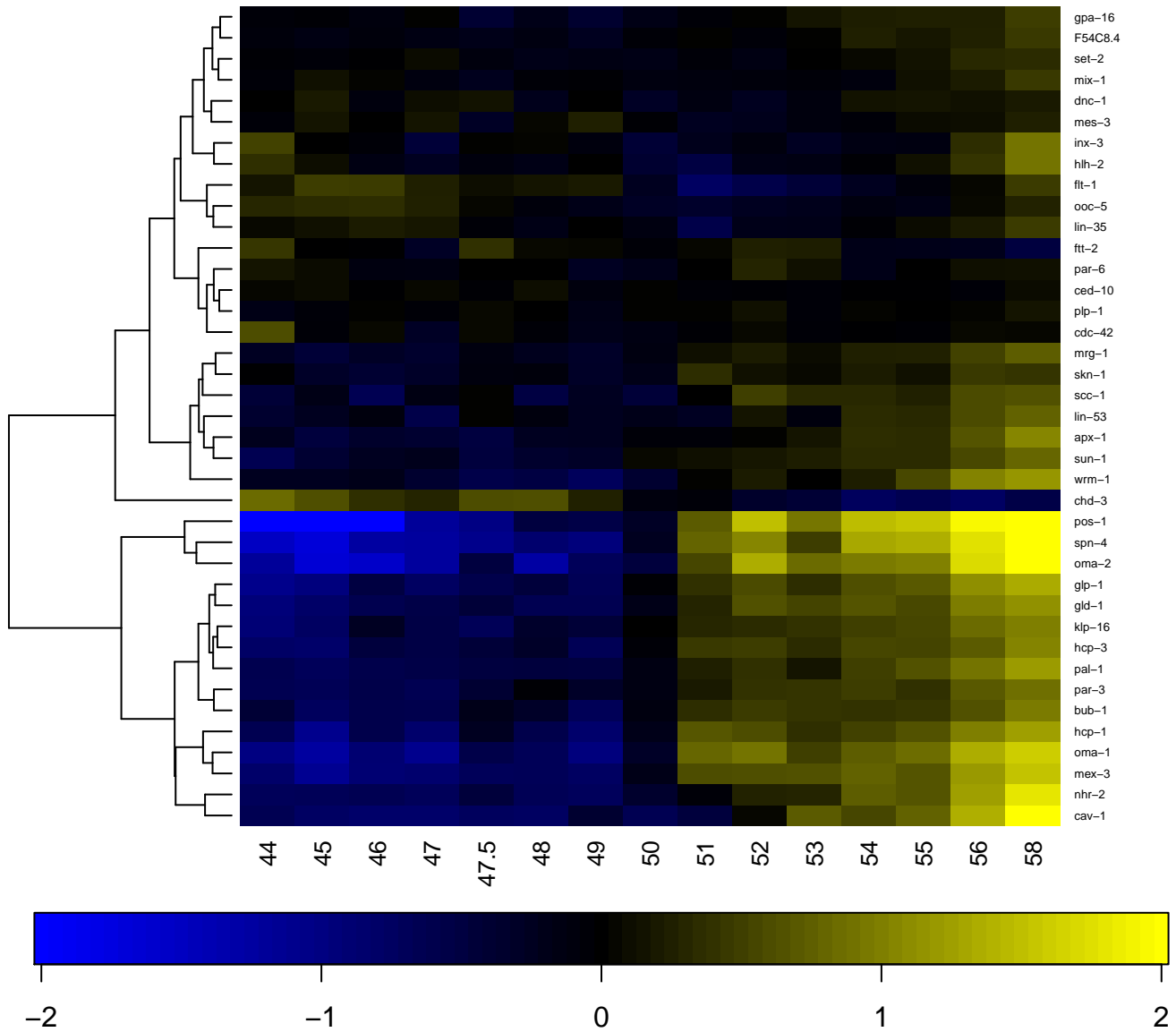


Supplementary file F | Dynamic gene expression patterns of all Anatomy terms.

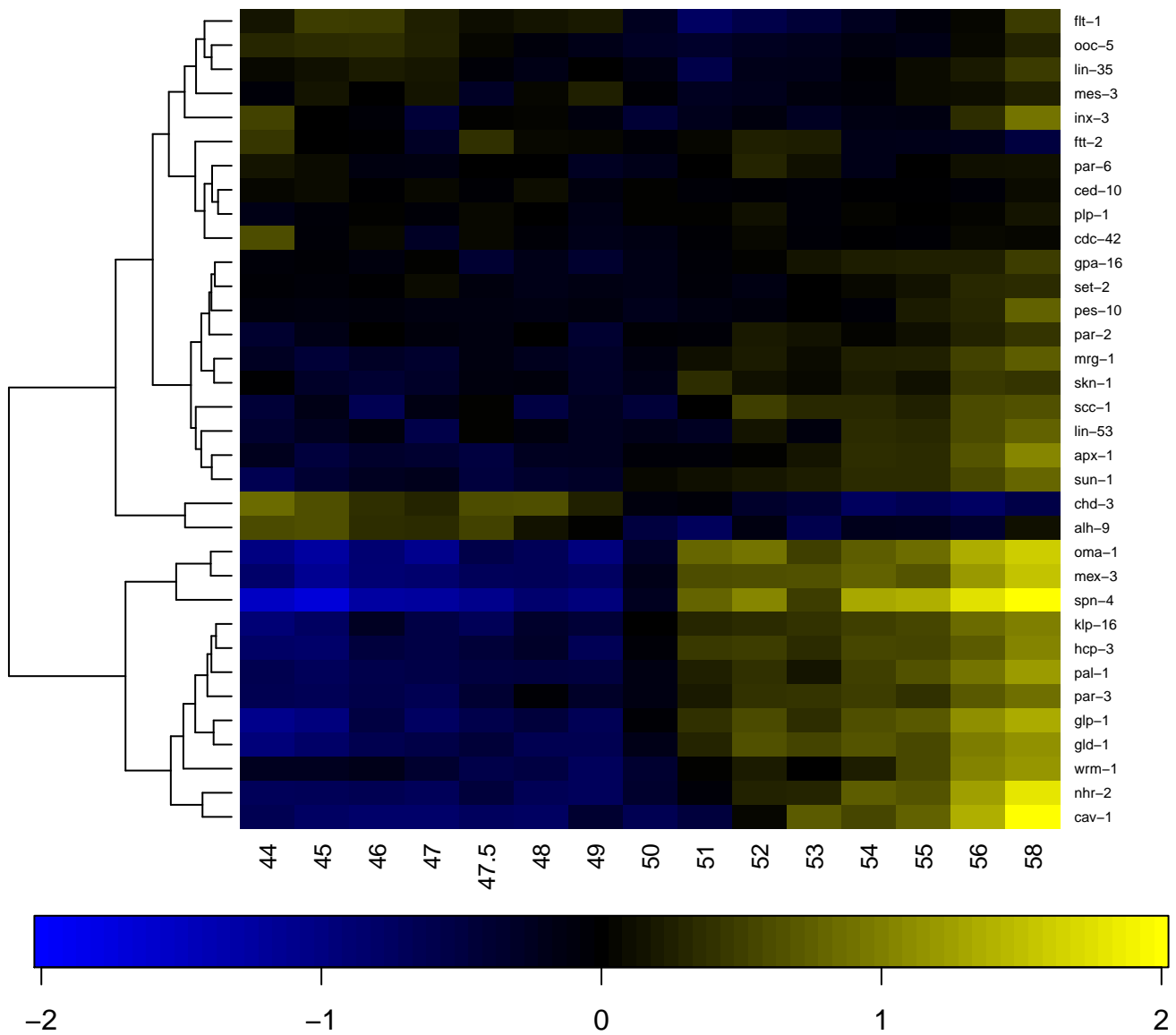
The “heatmap” function of “R” was used to cluster genes of each individual Anatomy terms according to their expression pattern. Anatomy term name is shown per page as figure title. The time in hours is shown on the x-axis. Gene names are shown on the y-axis. The scale bar shows the log₂ ratio with the mean for each time-point. Blue is lower than the mean and yellow is higher than the mean.



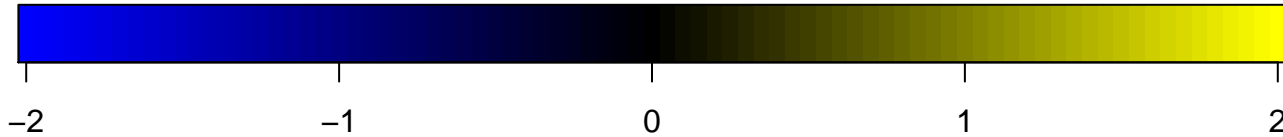
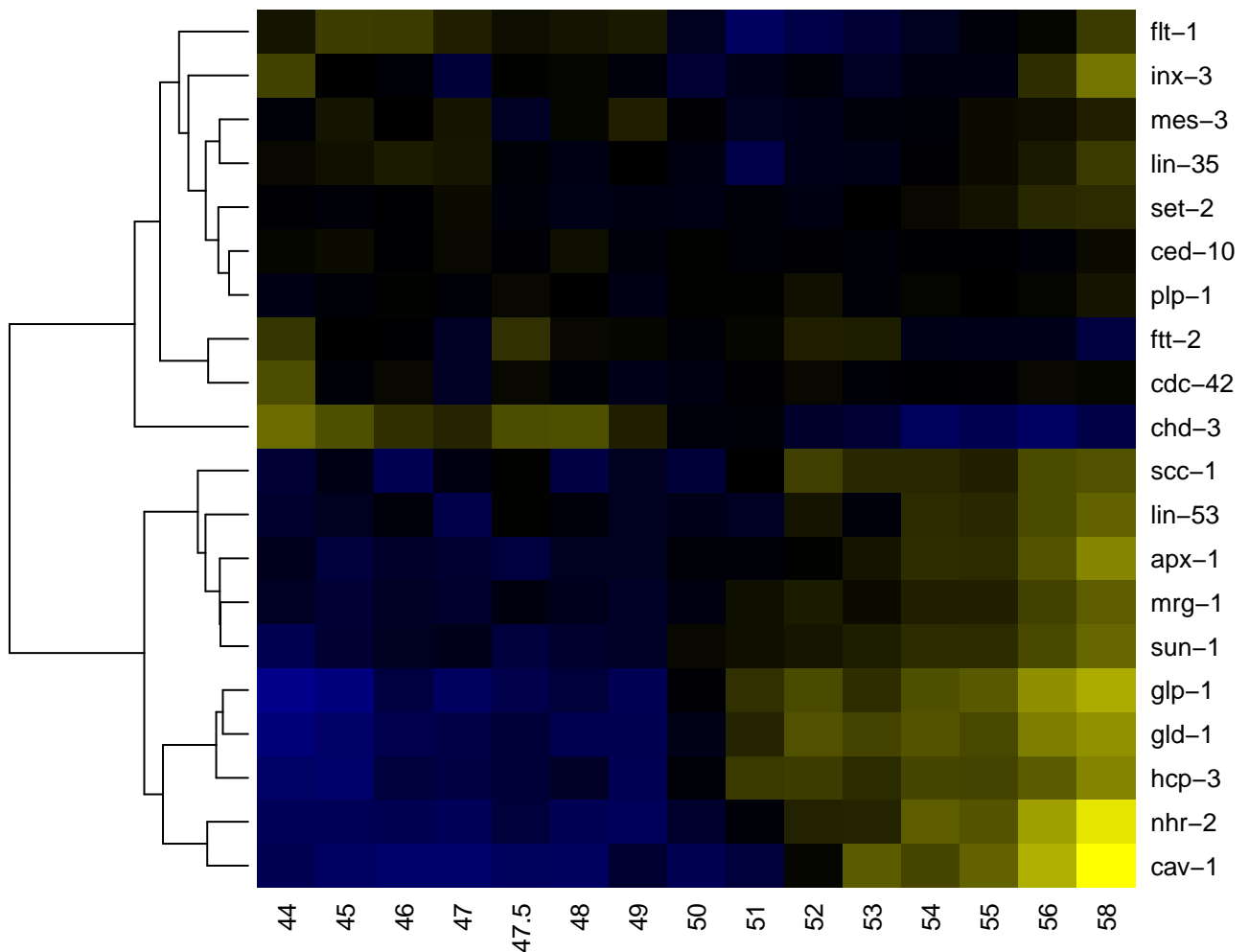
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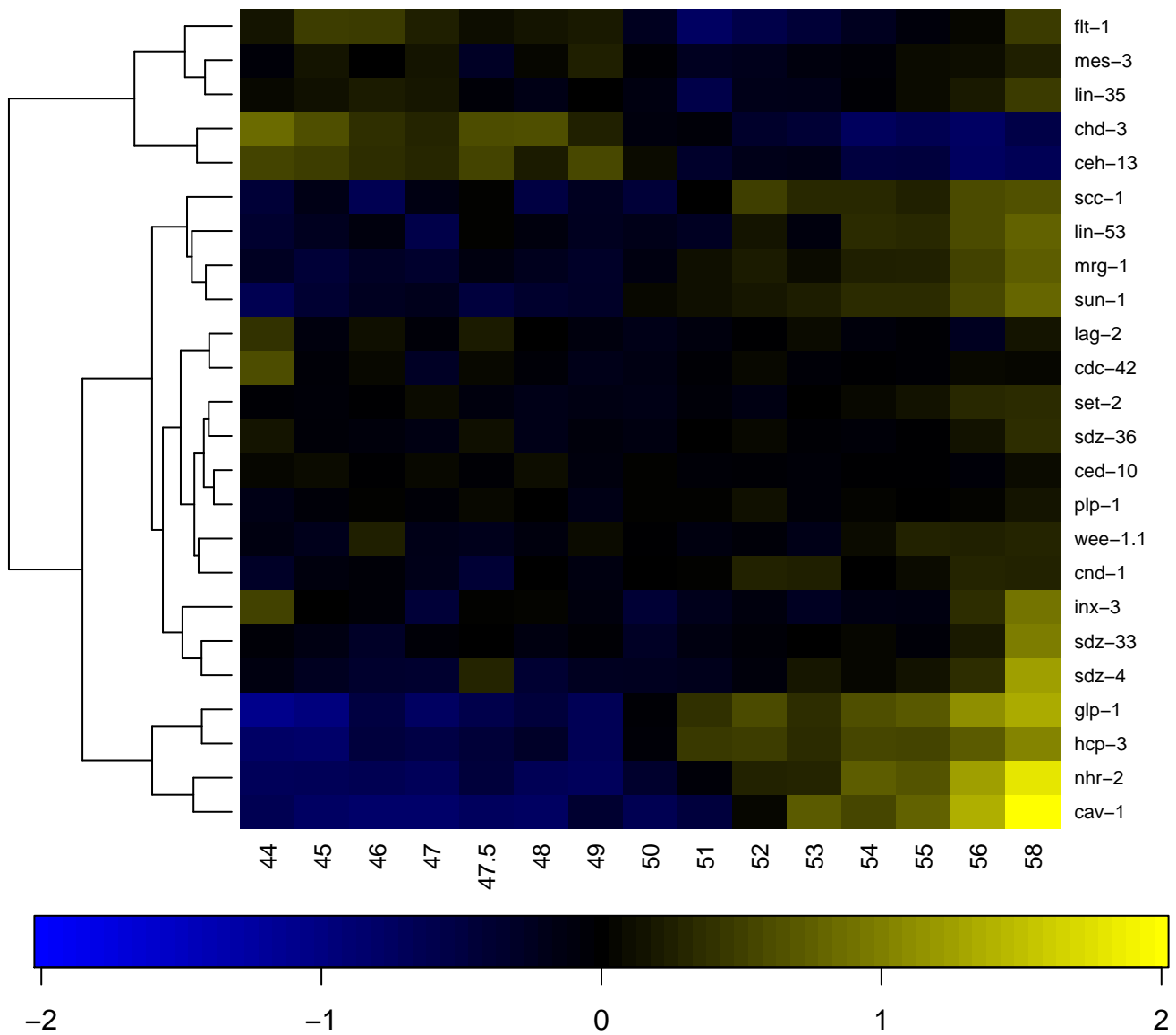
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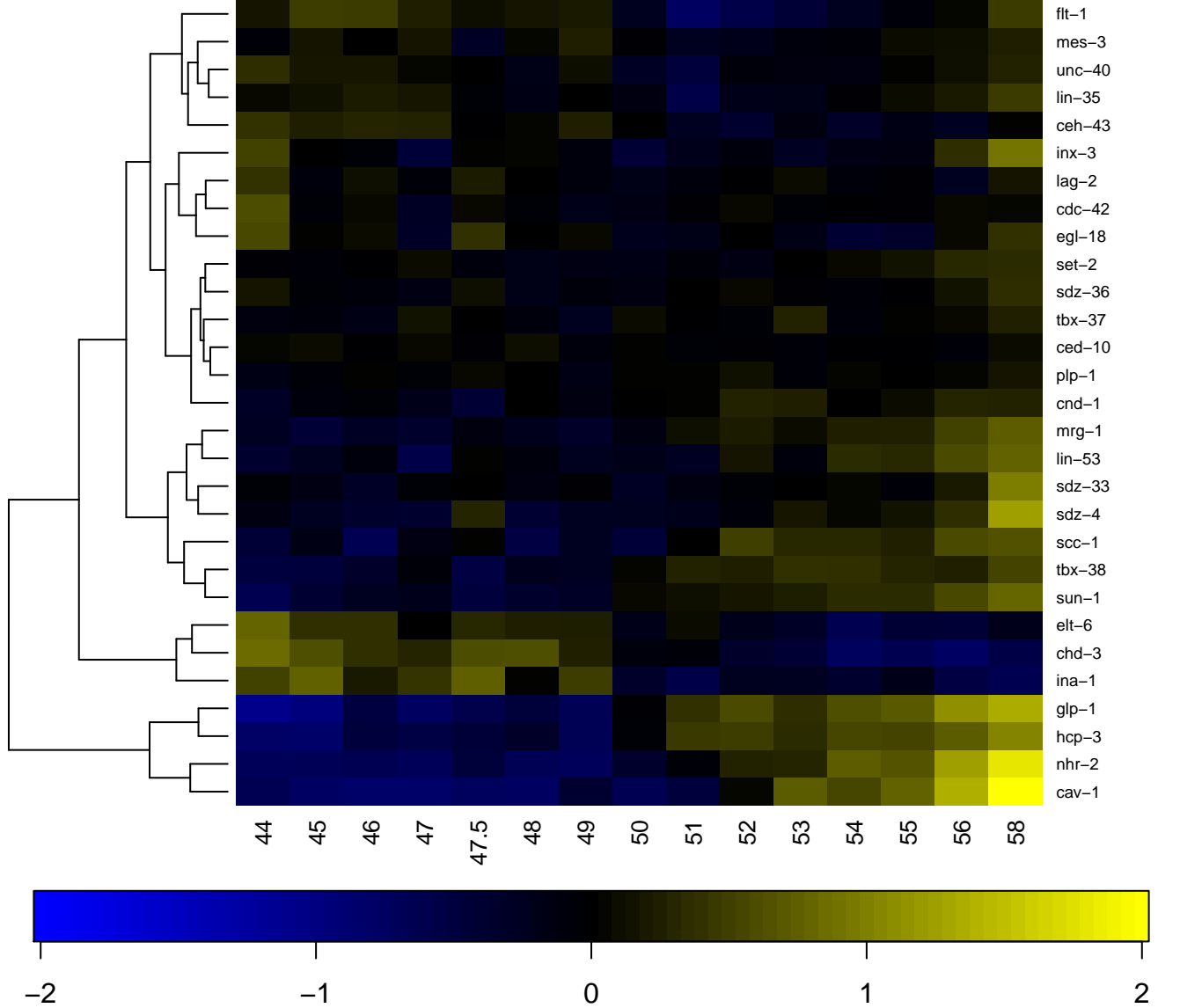
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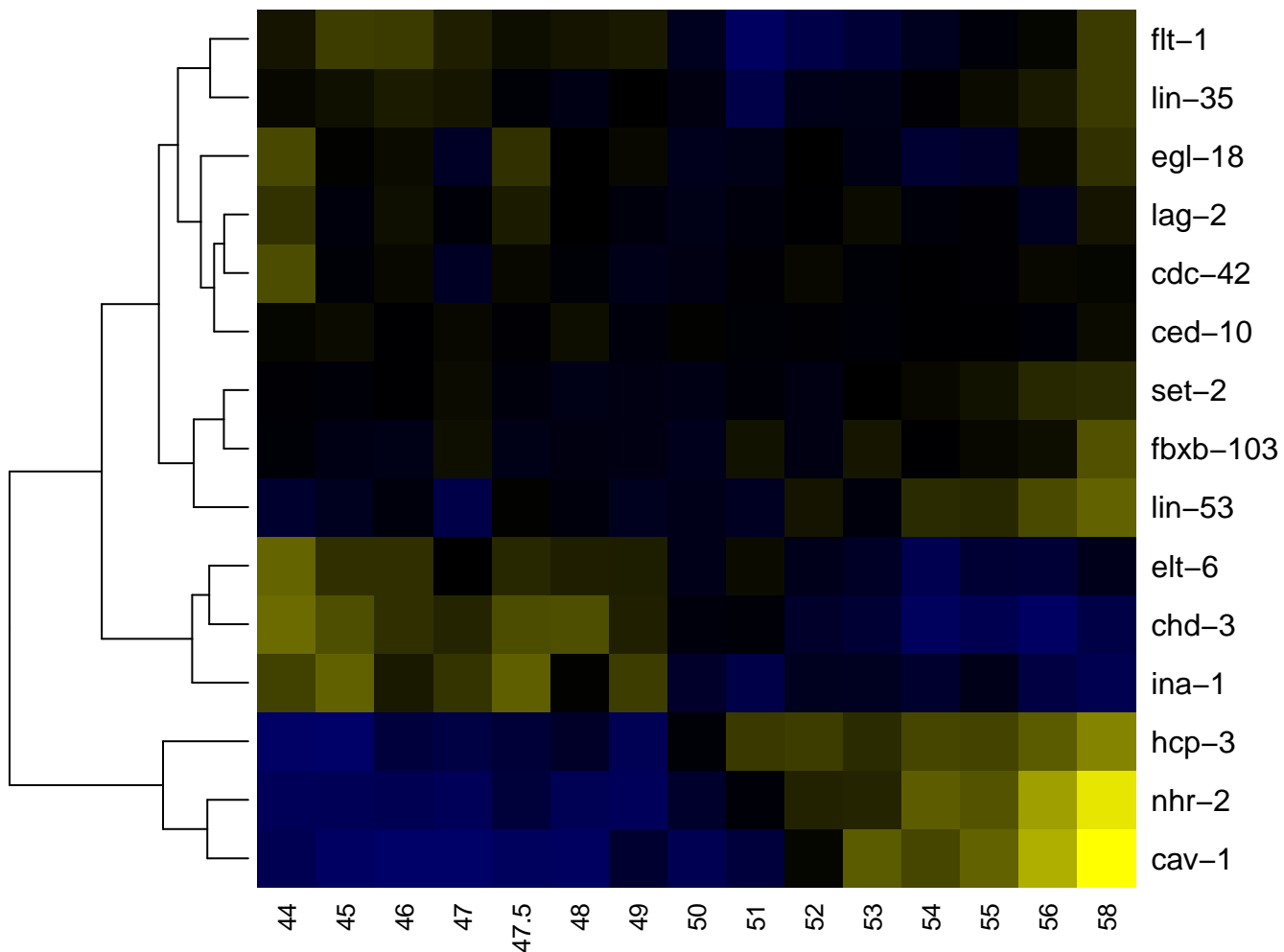
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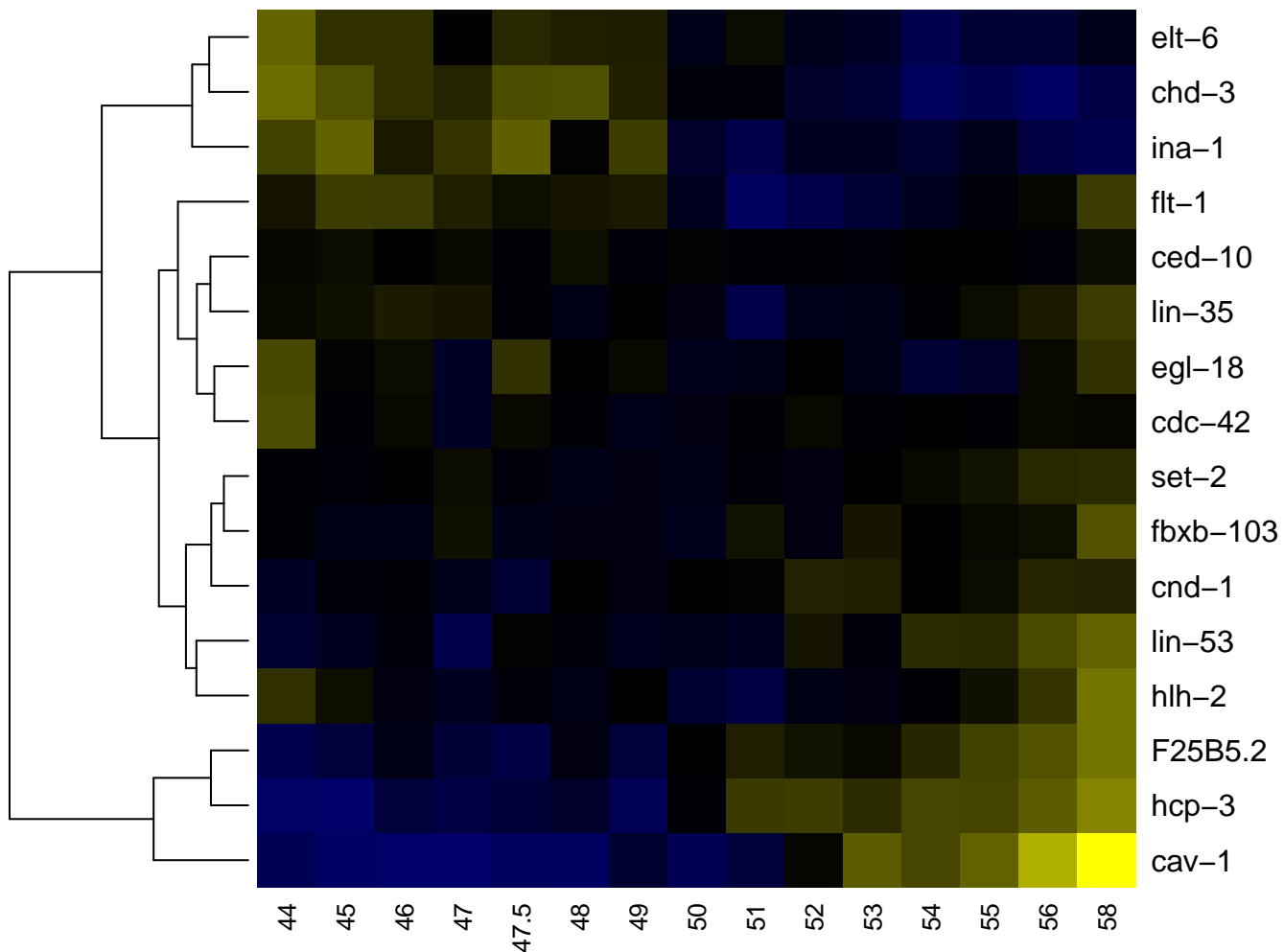
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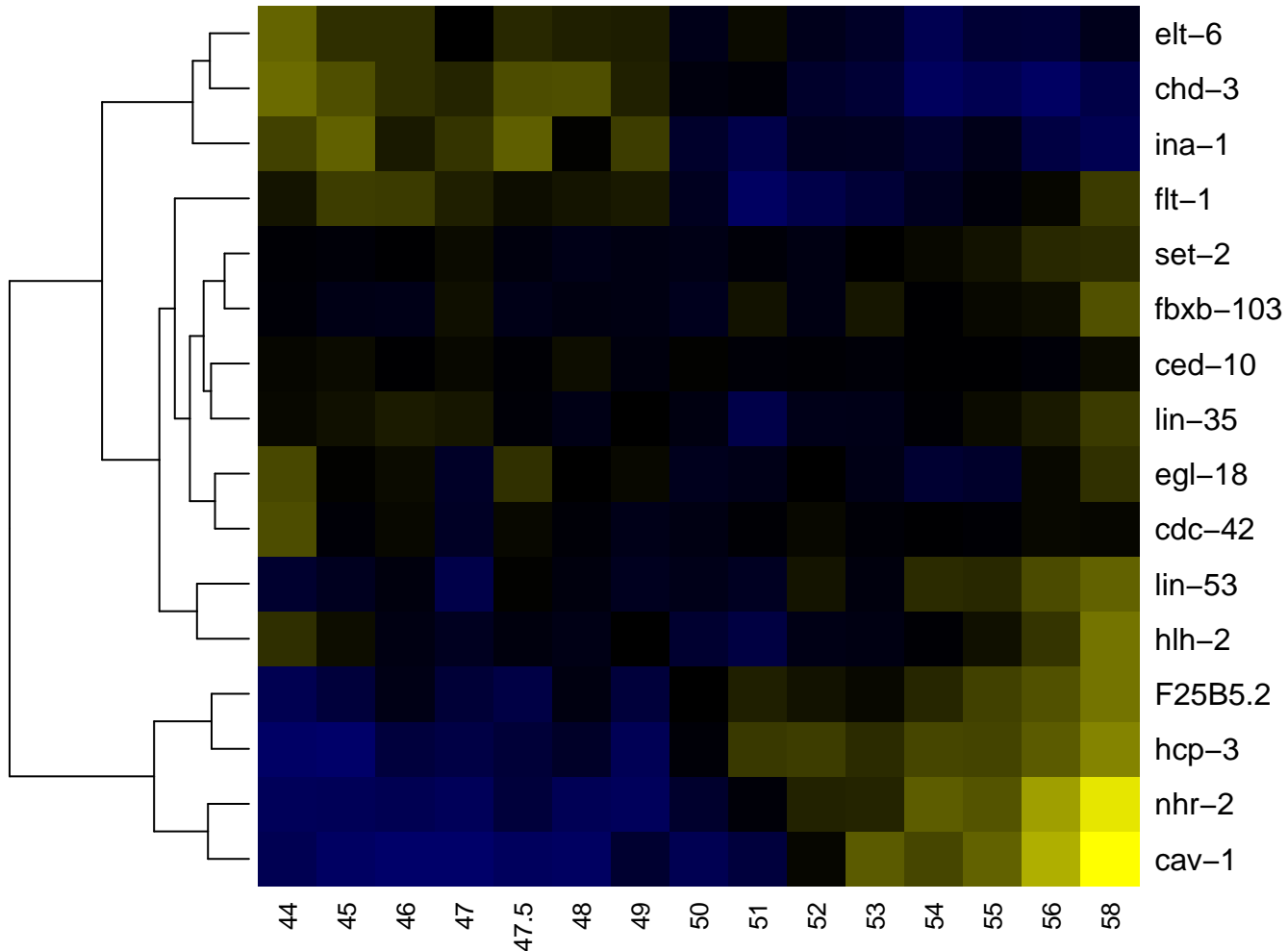
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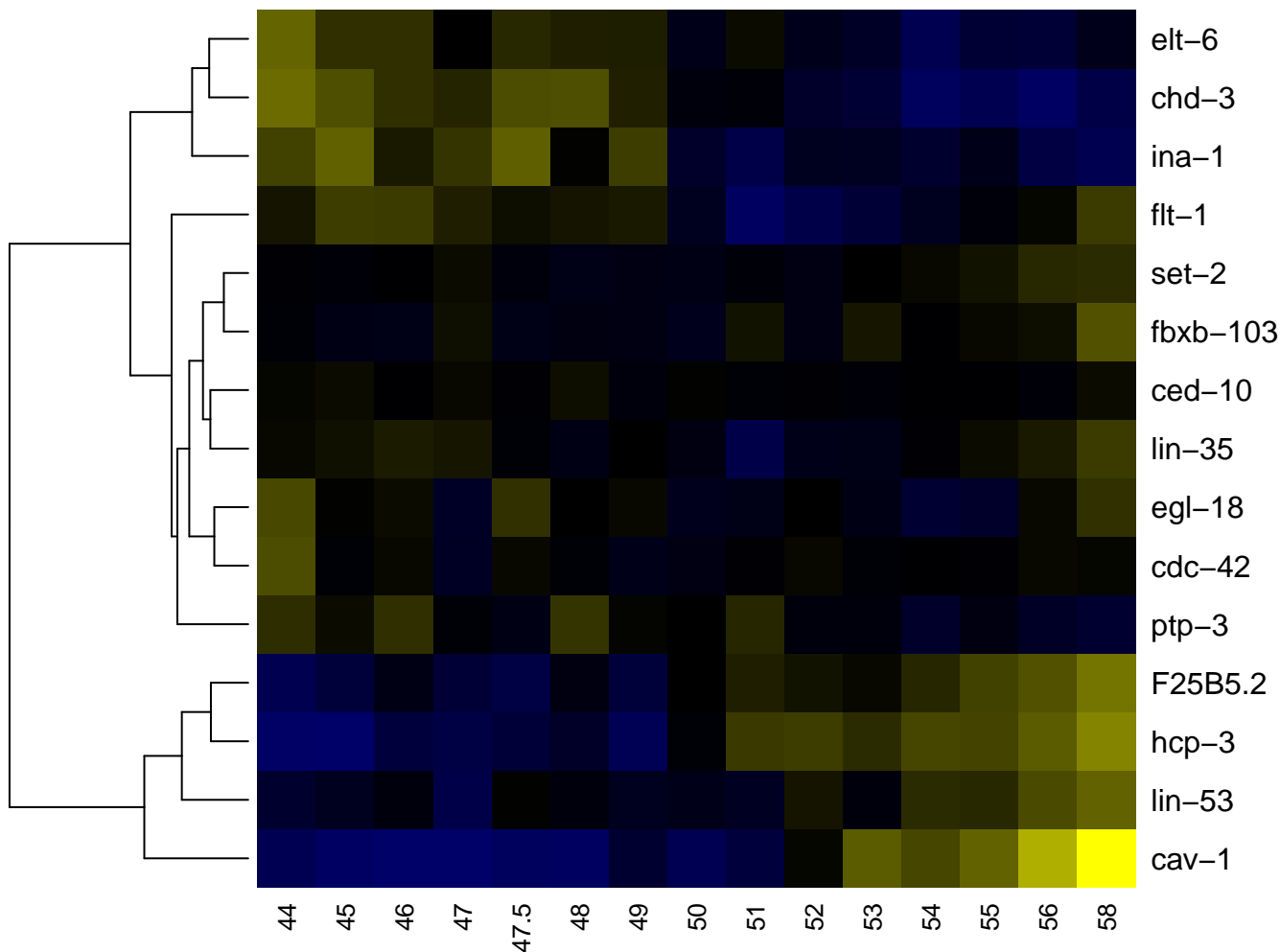
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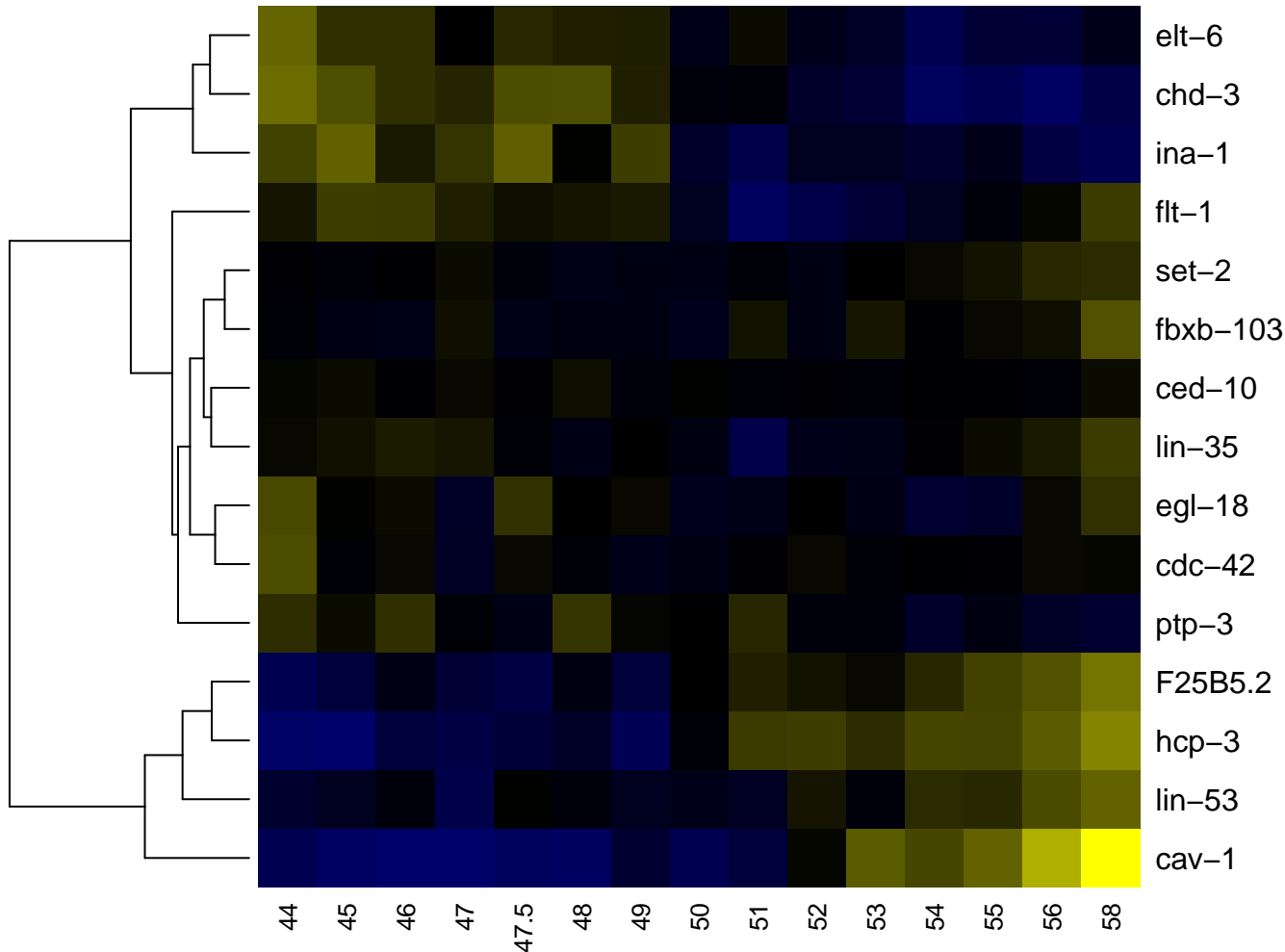
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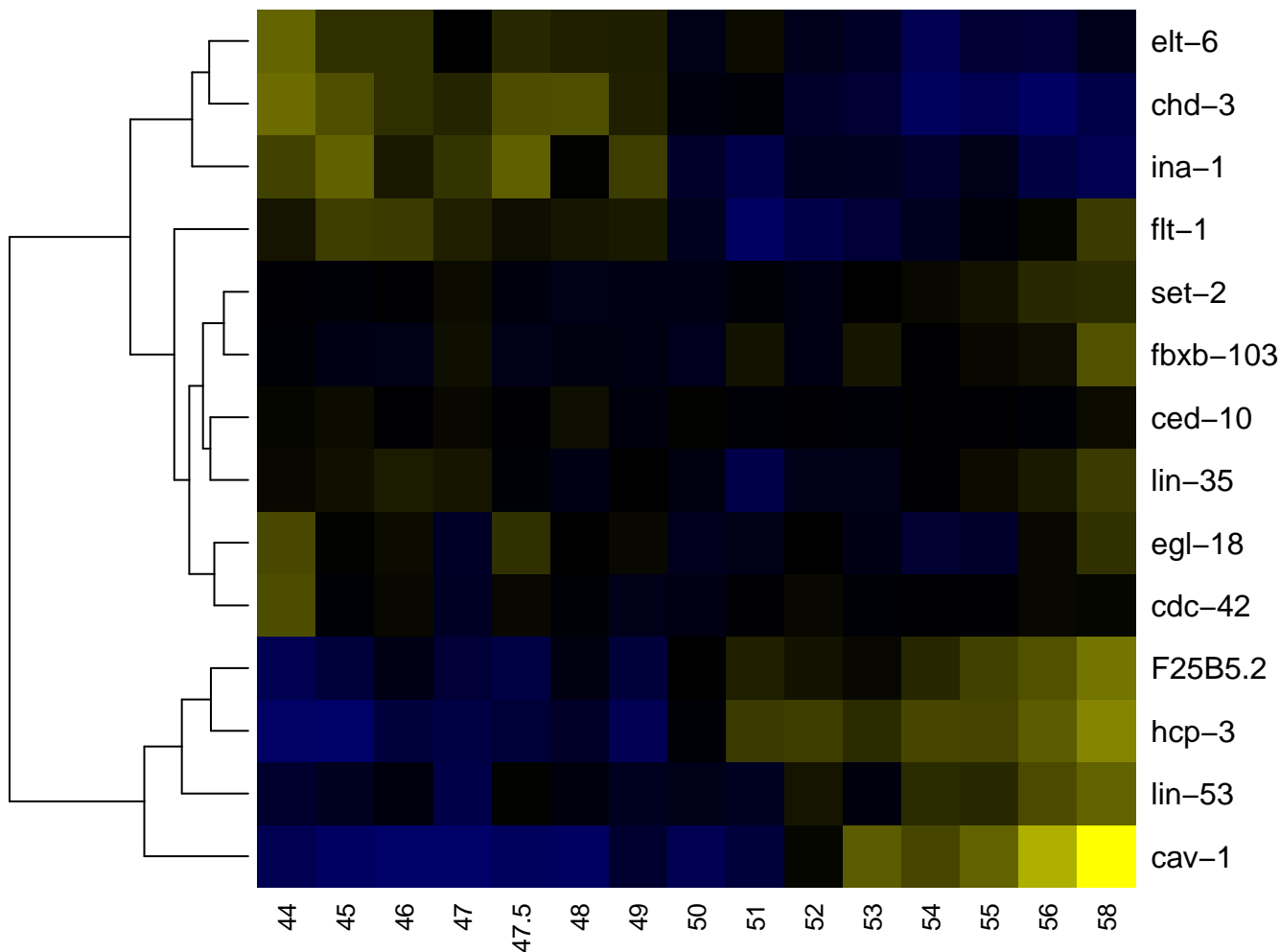
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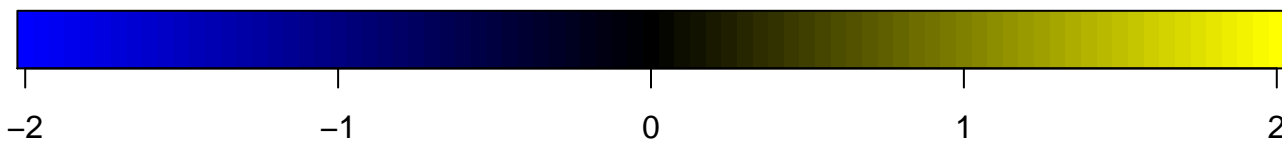
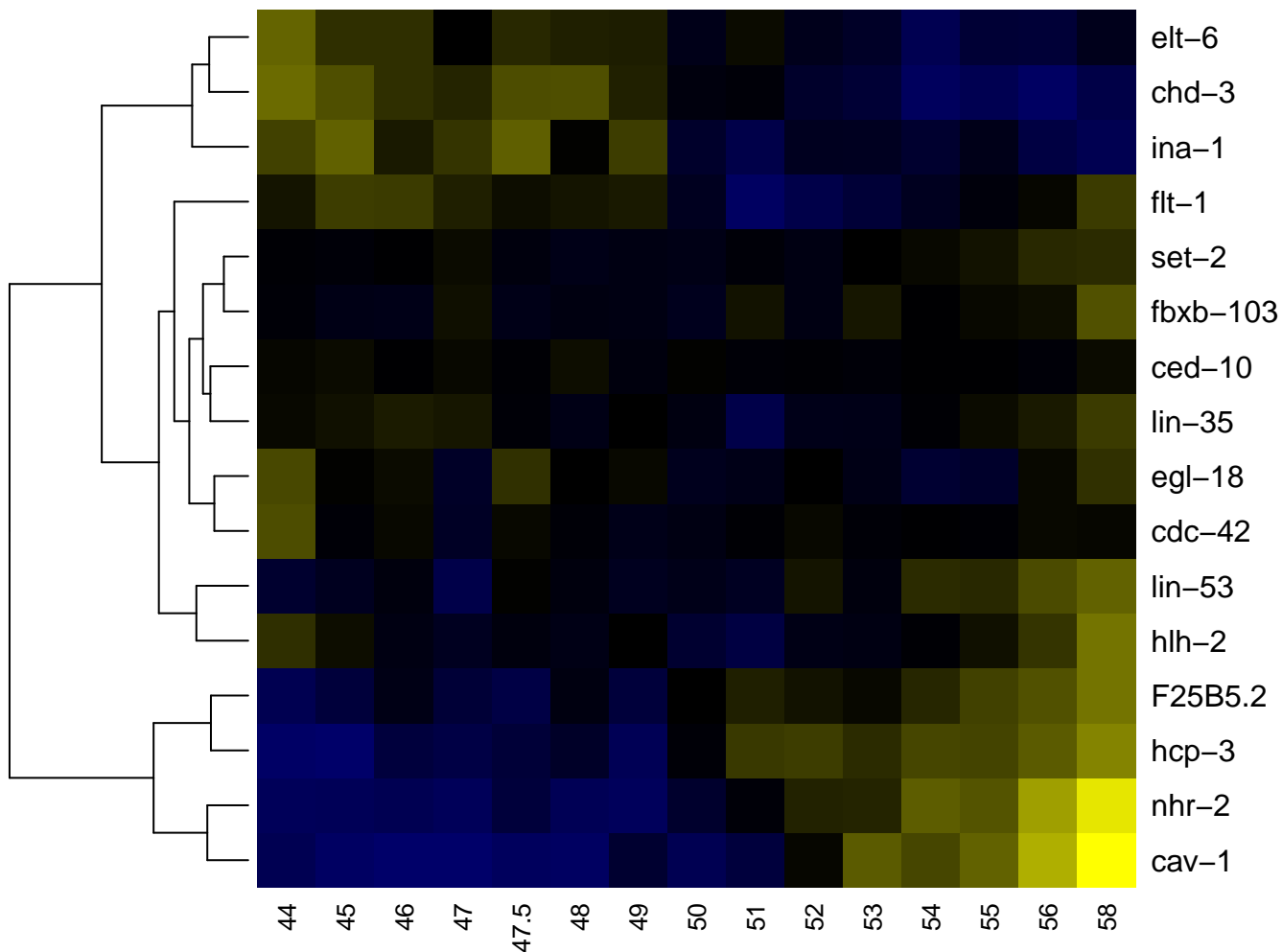
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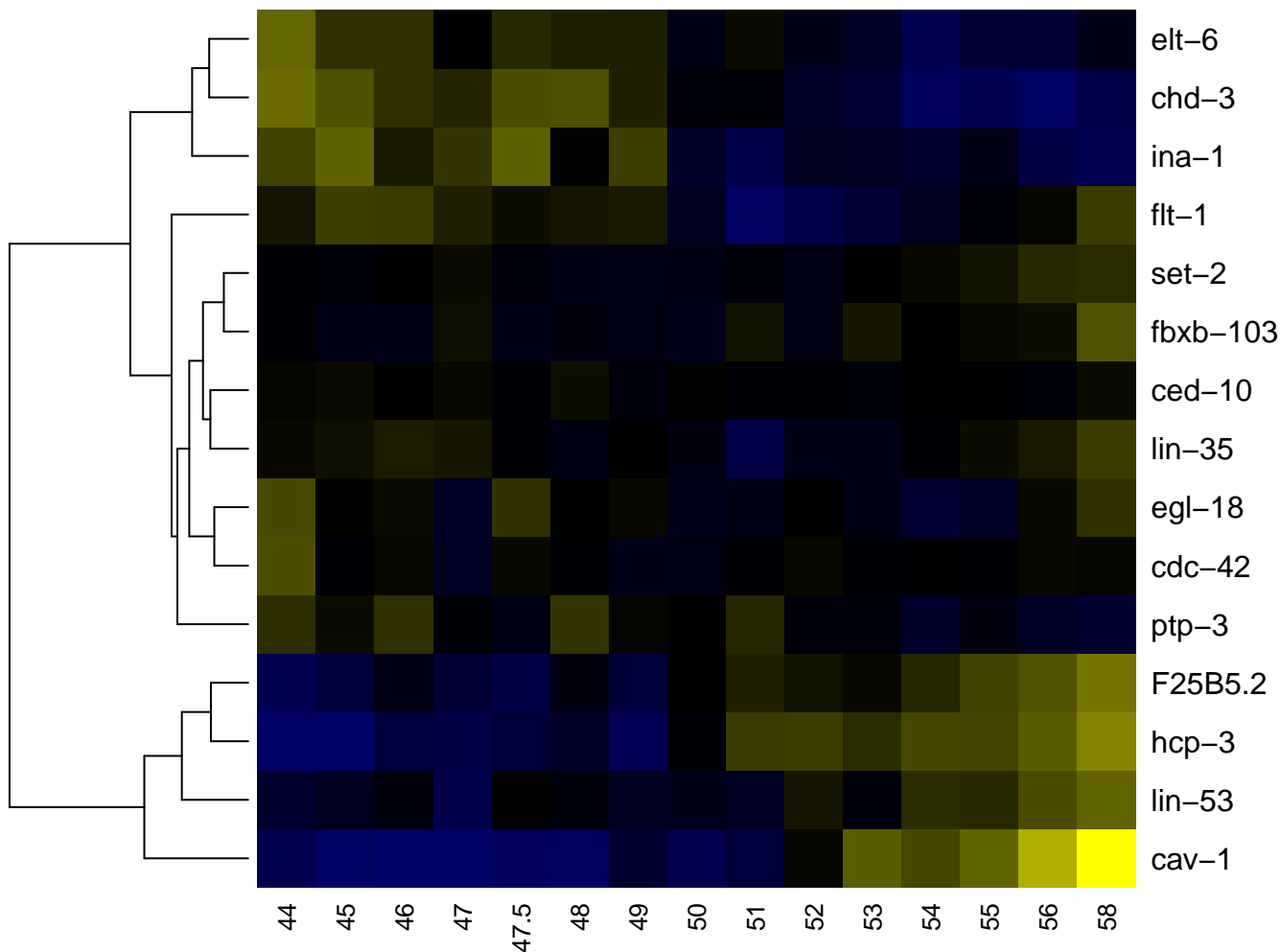
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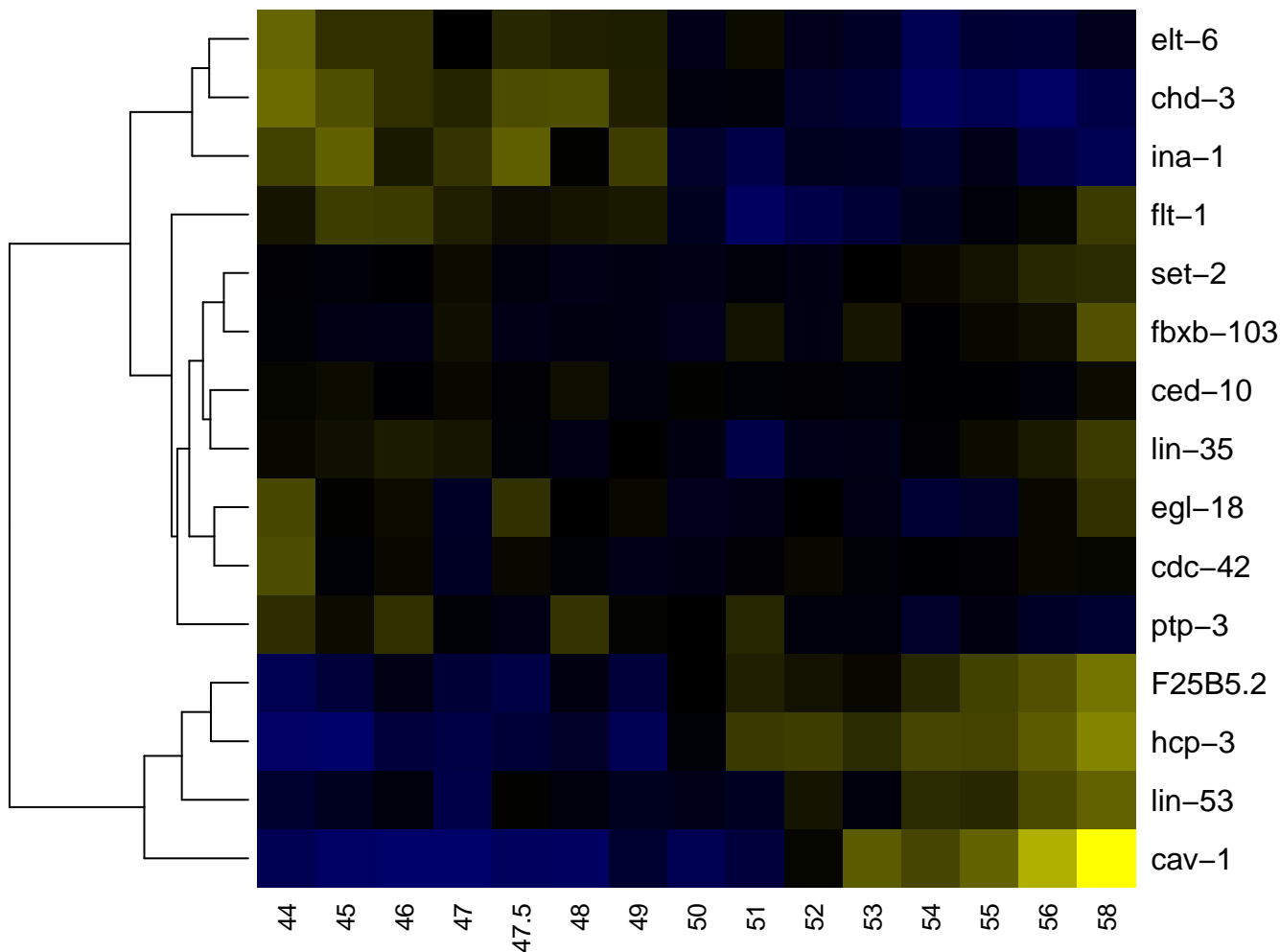
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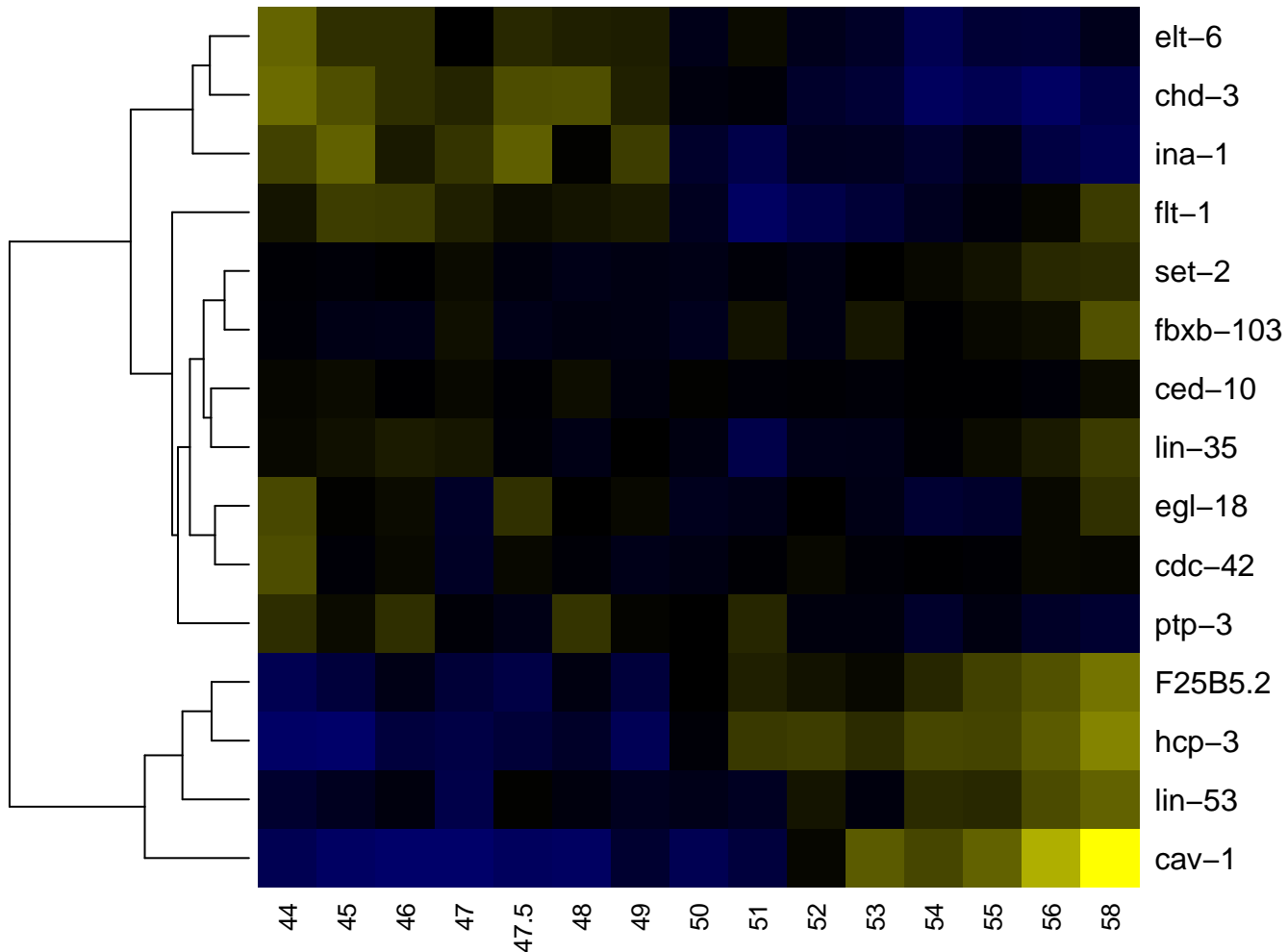
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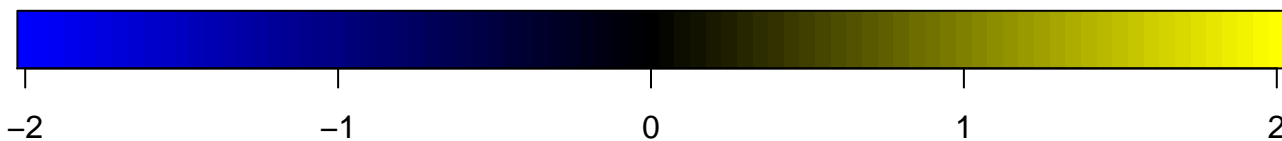
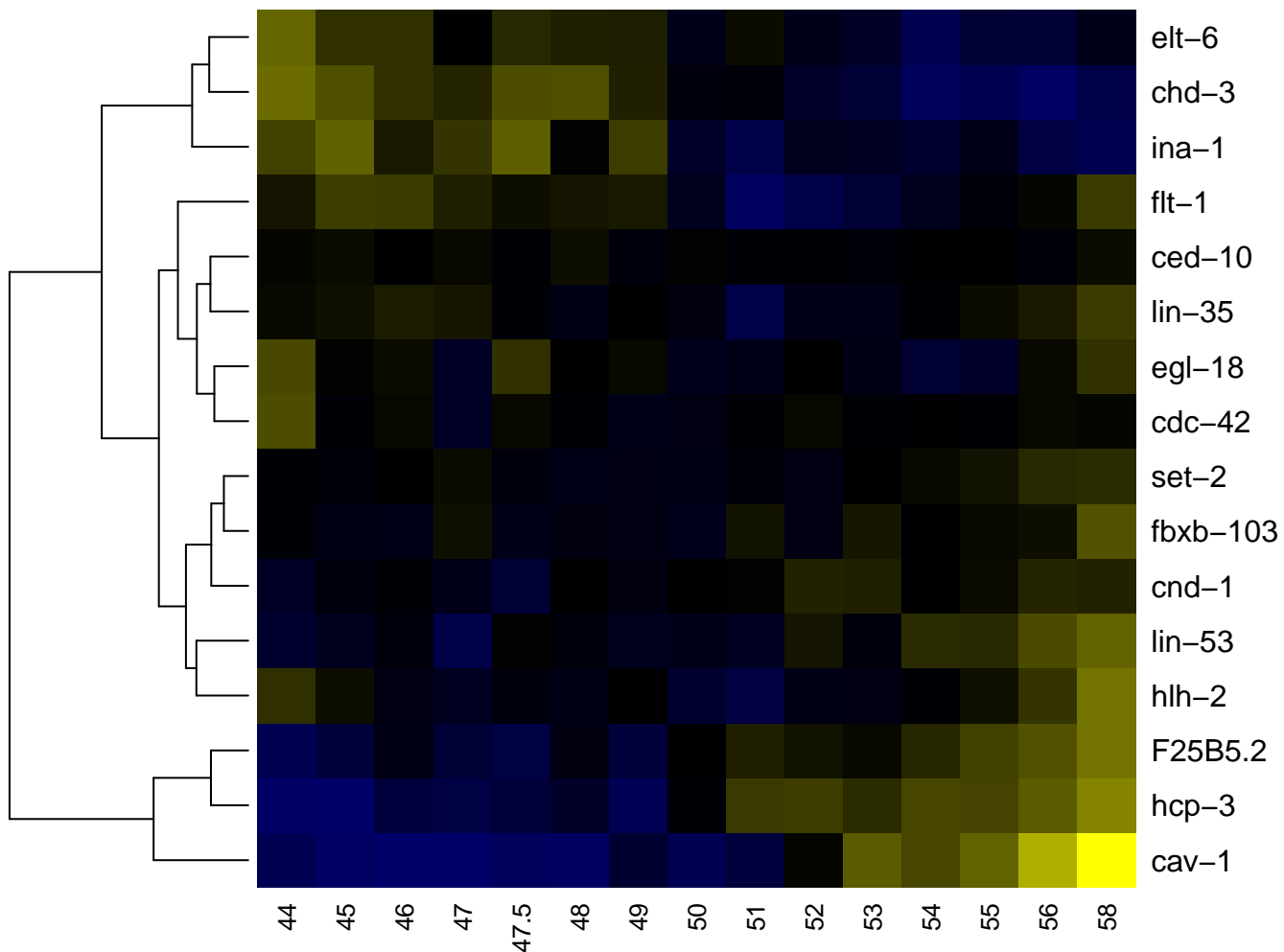
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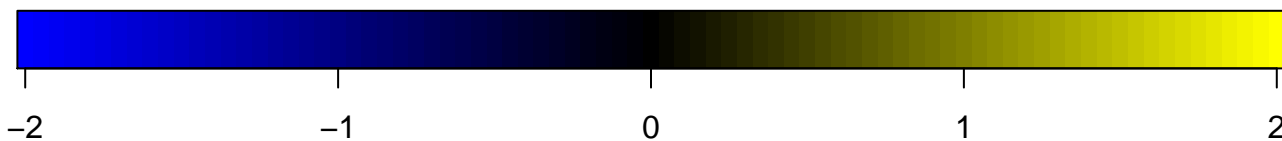
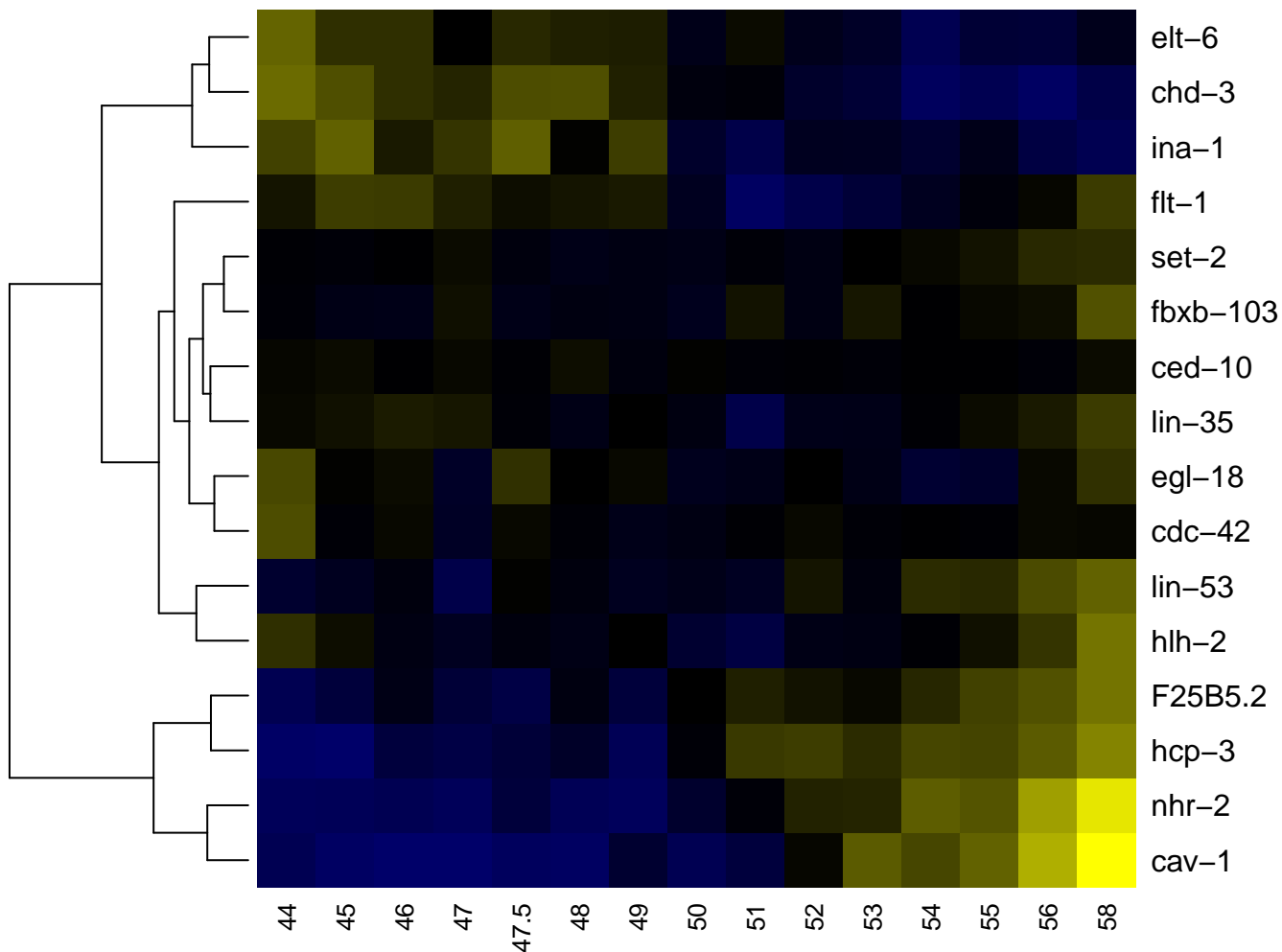
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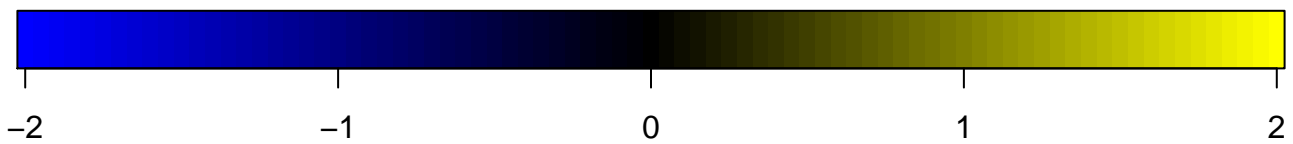
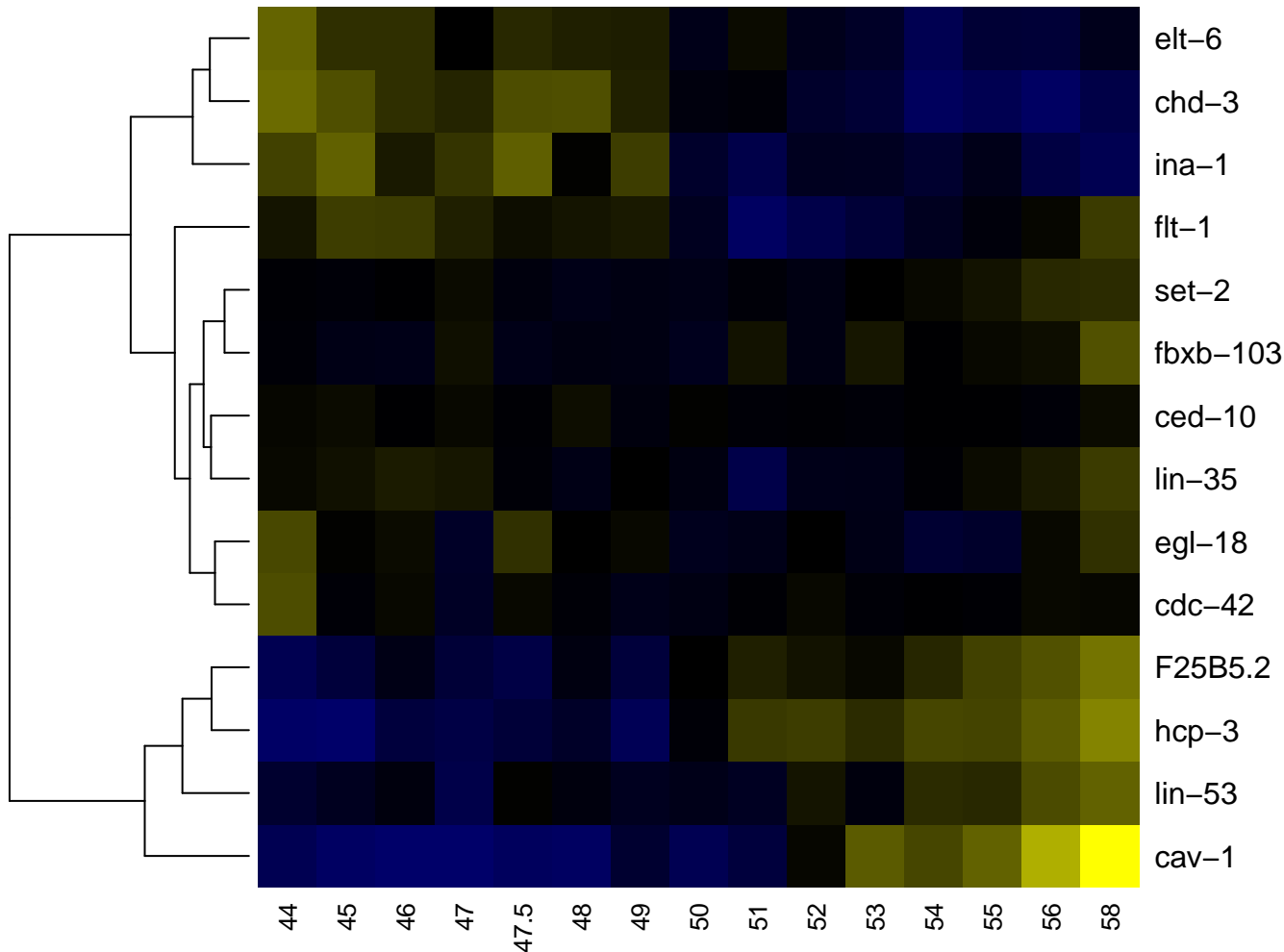
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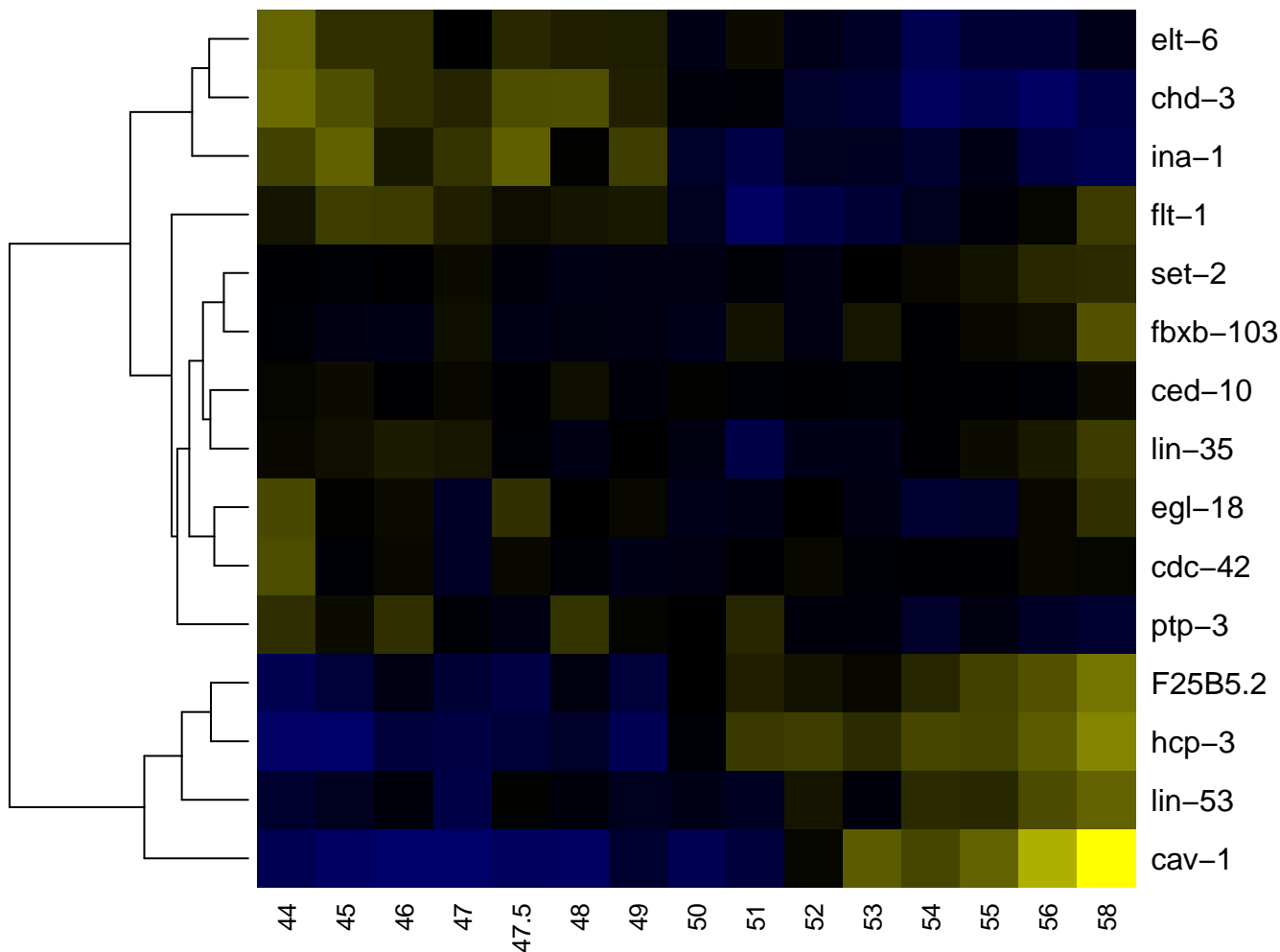
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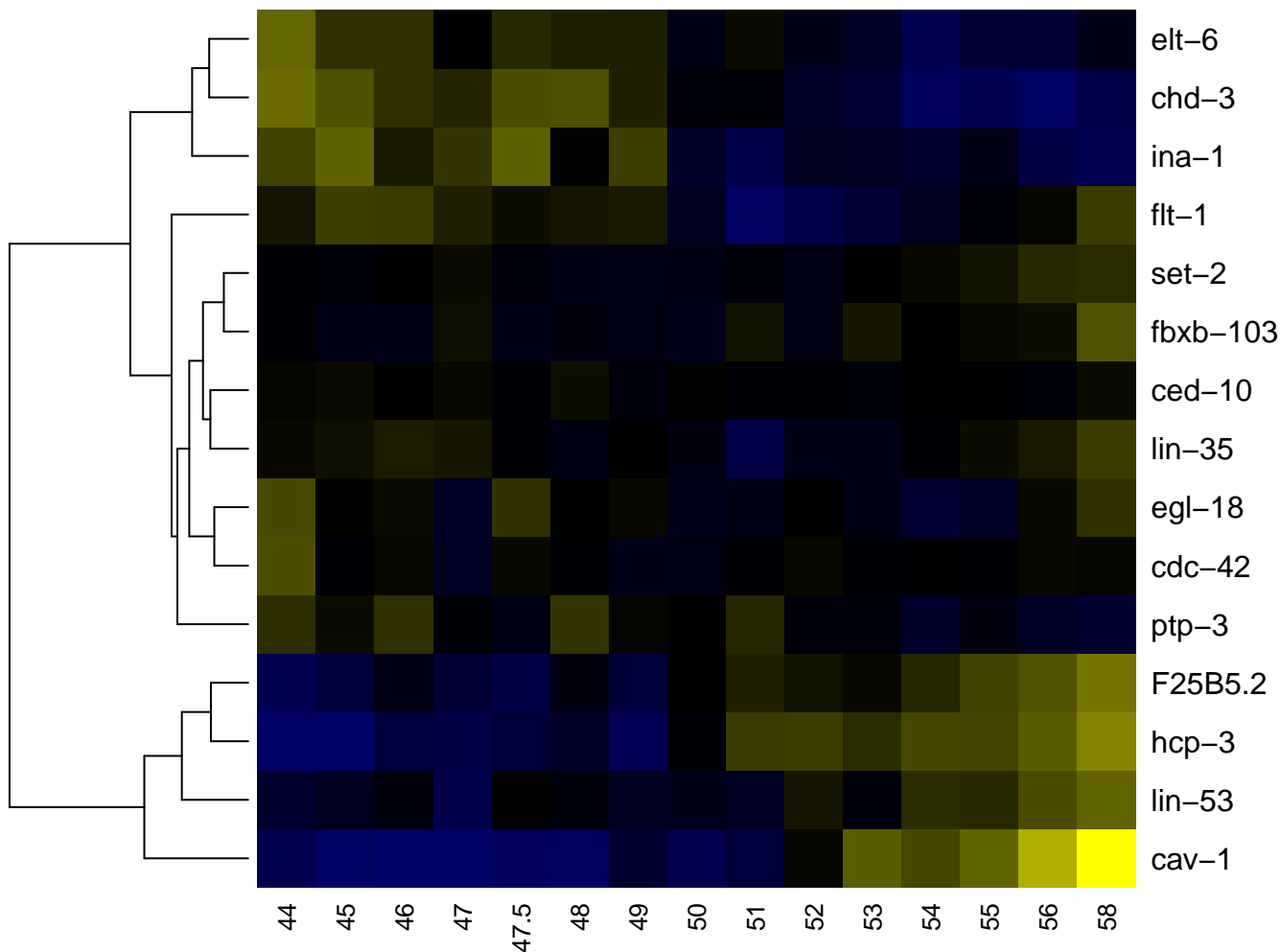
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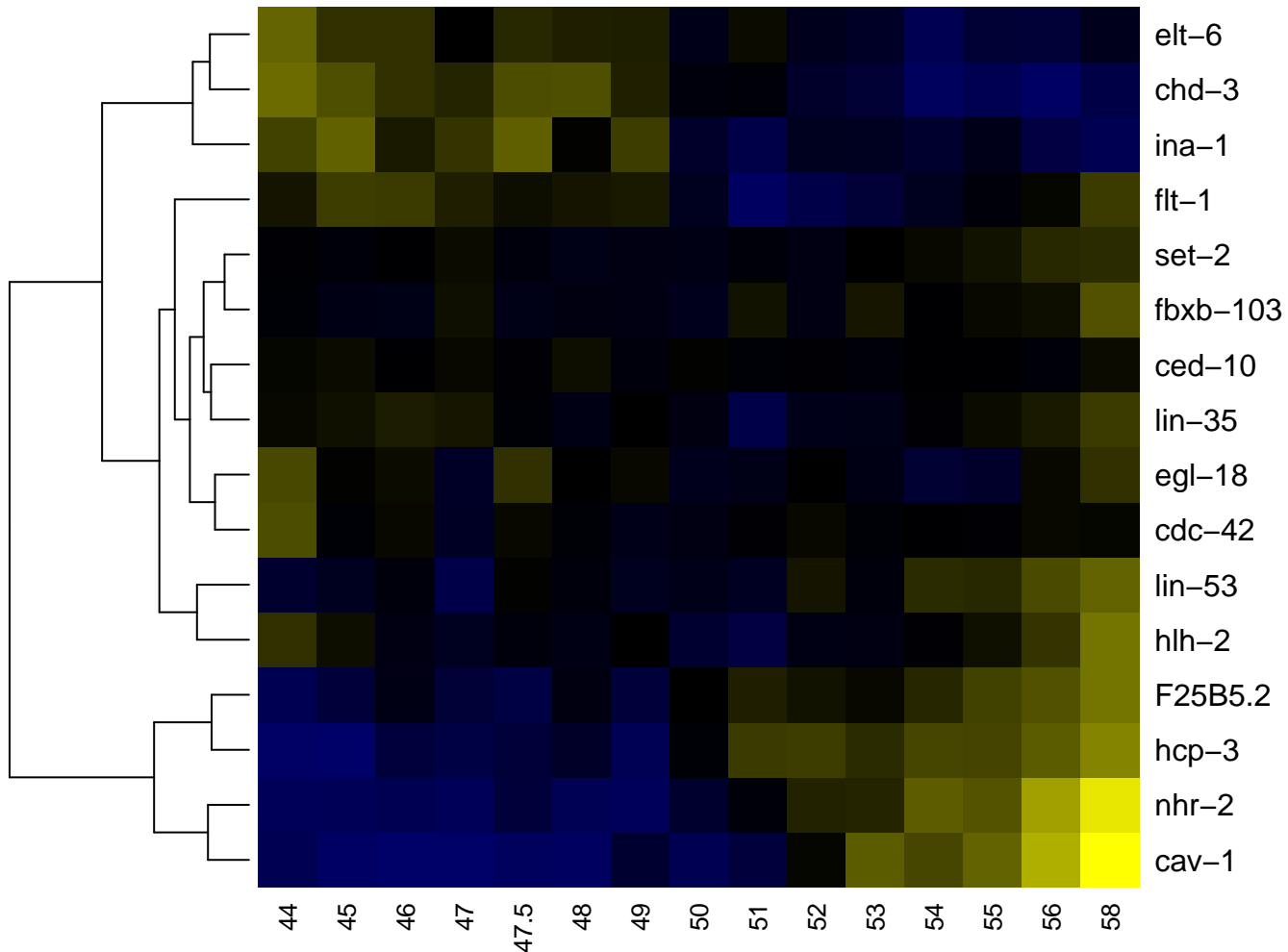
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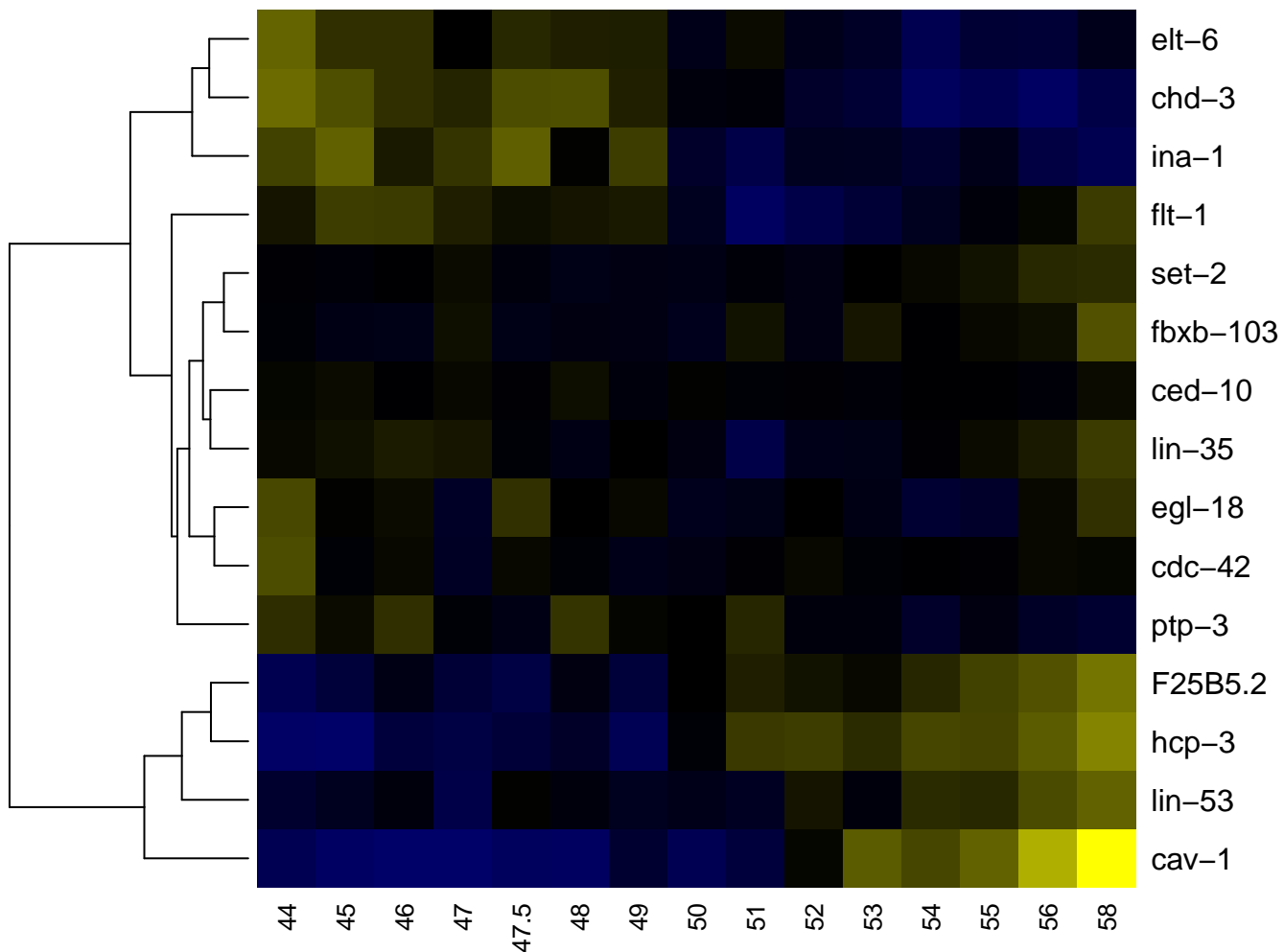
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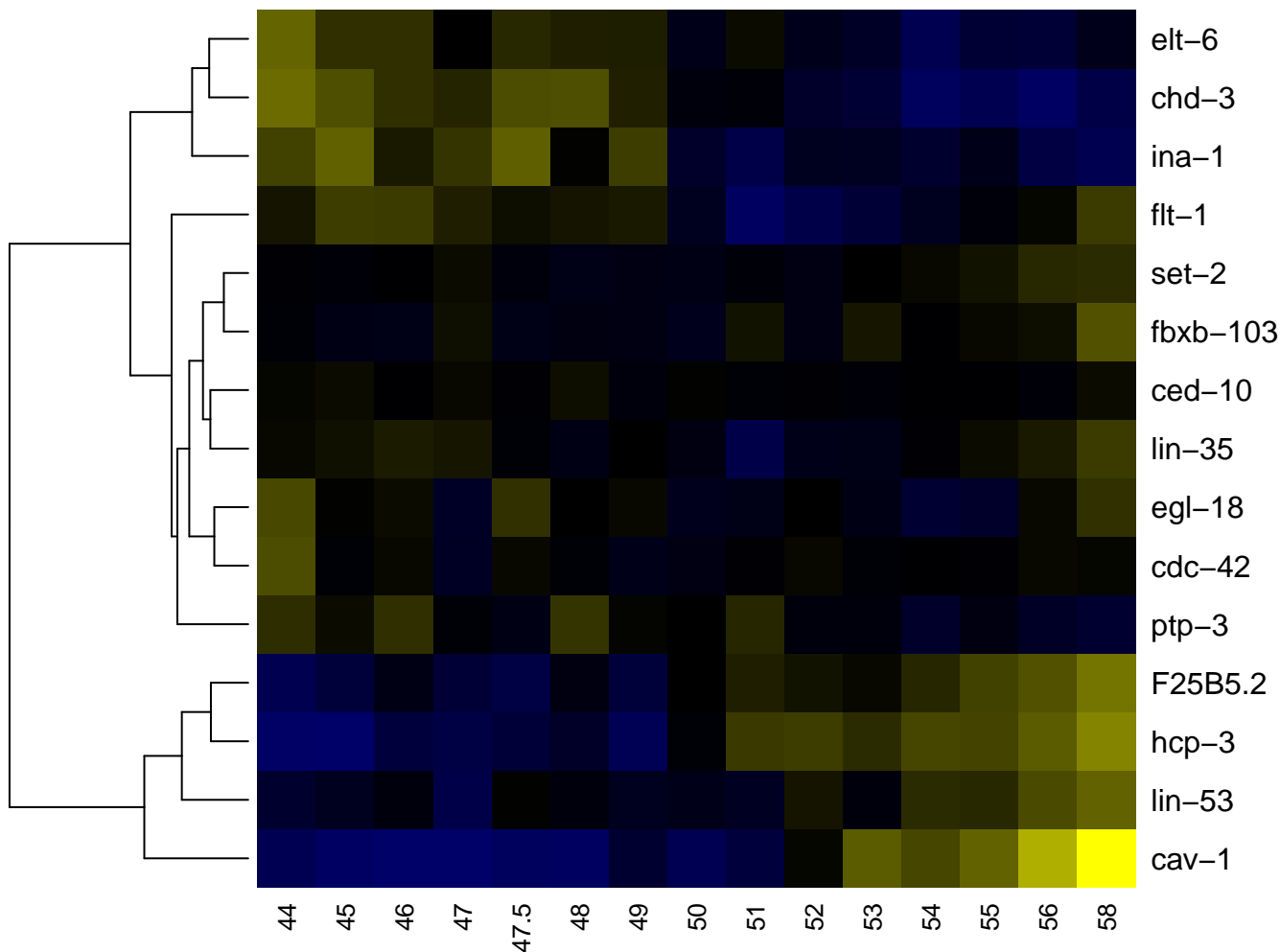
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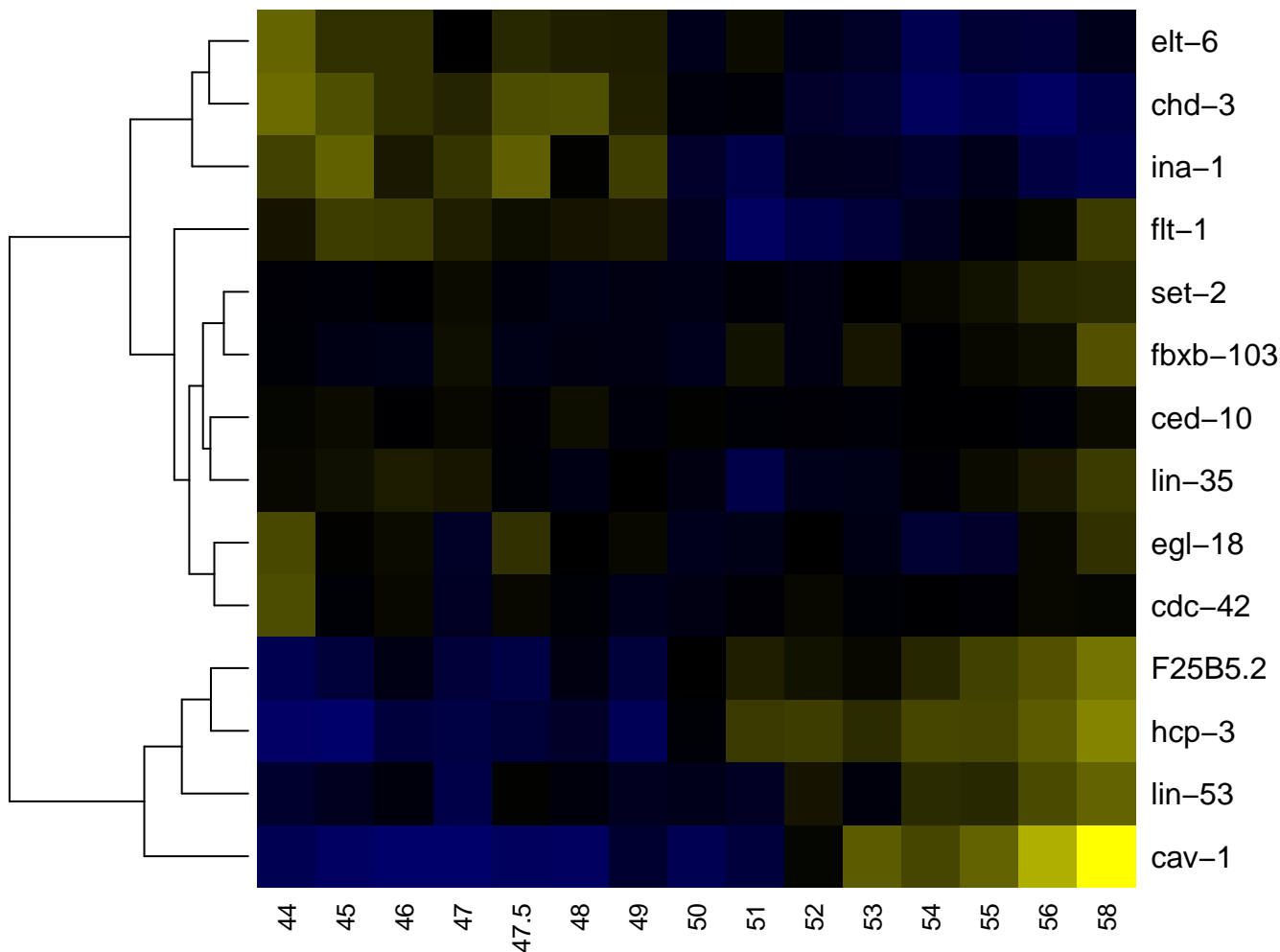
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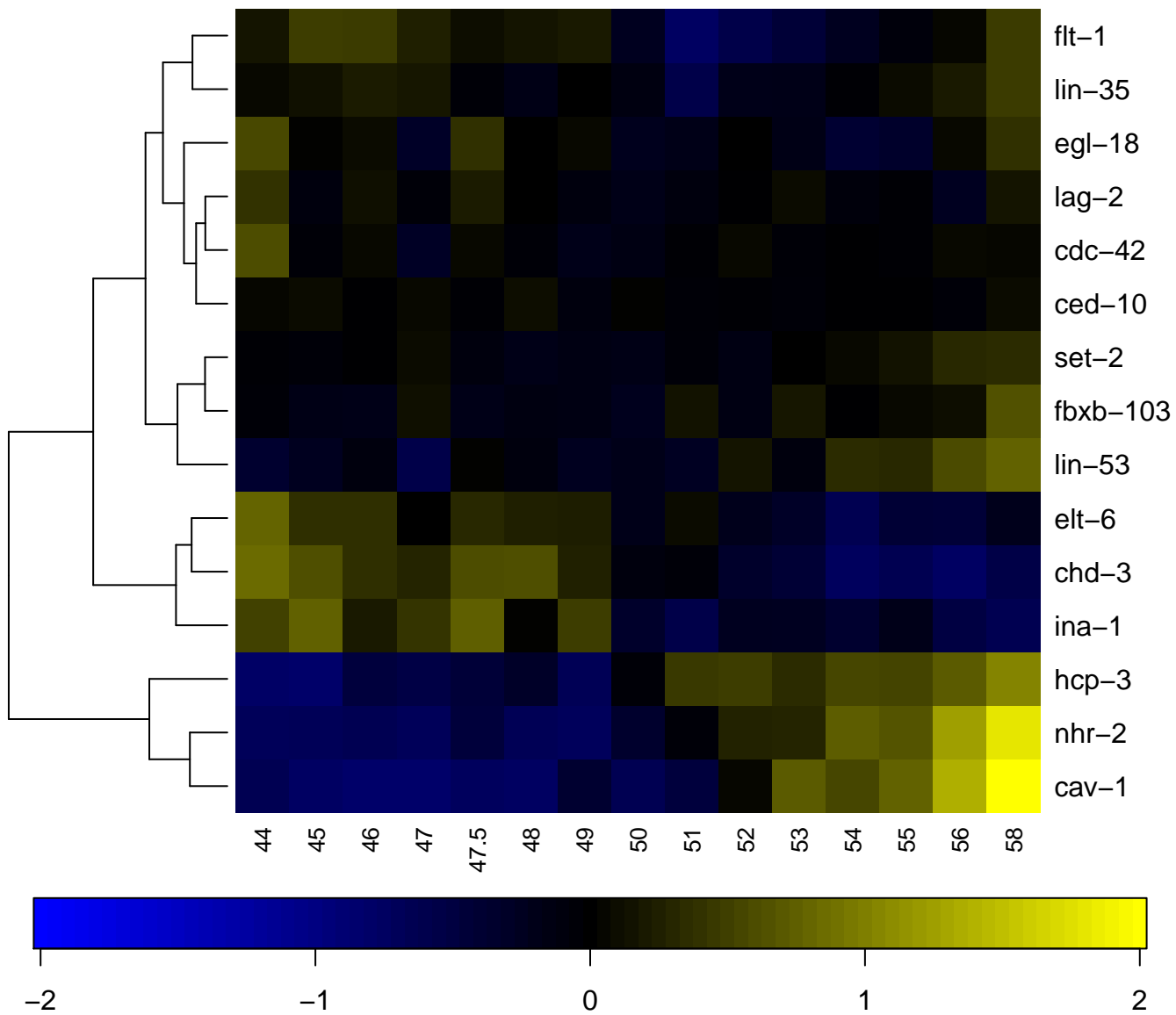
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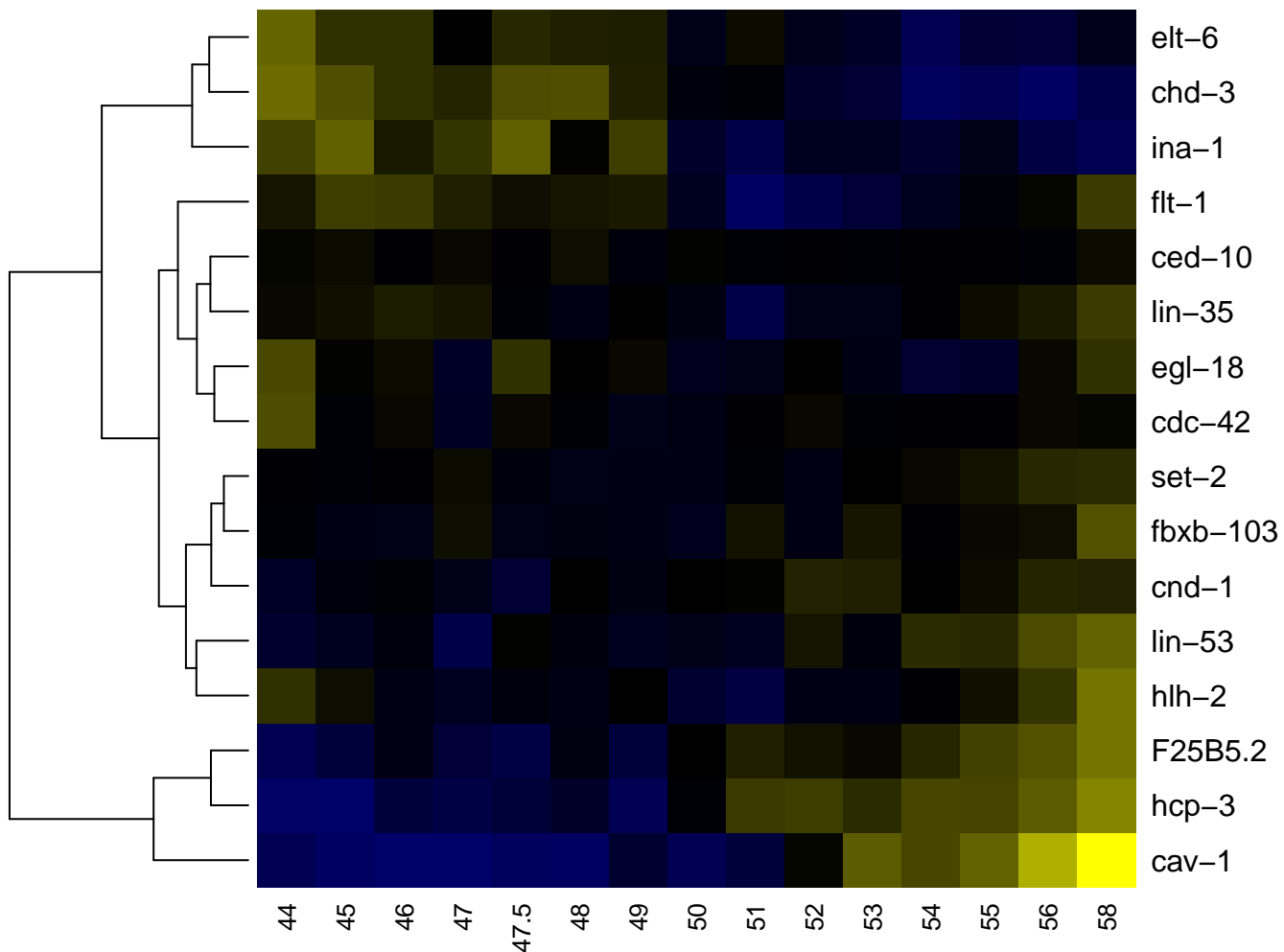
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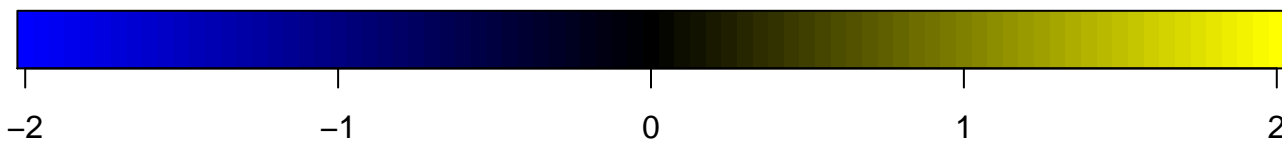
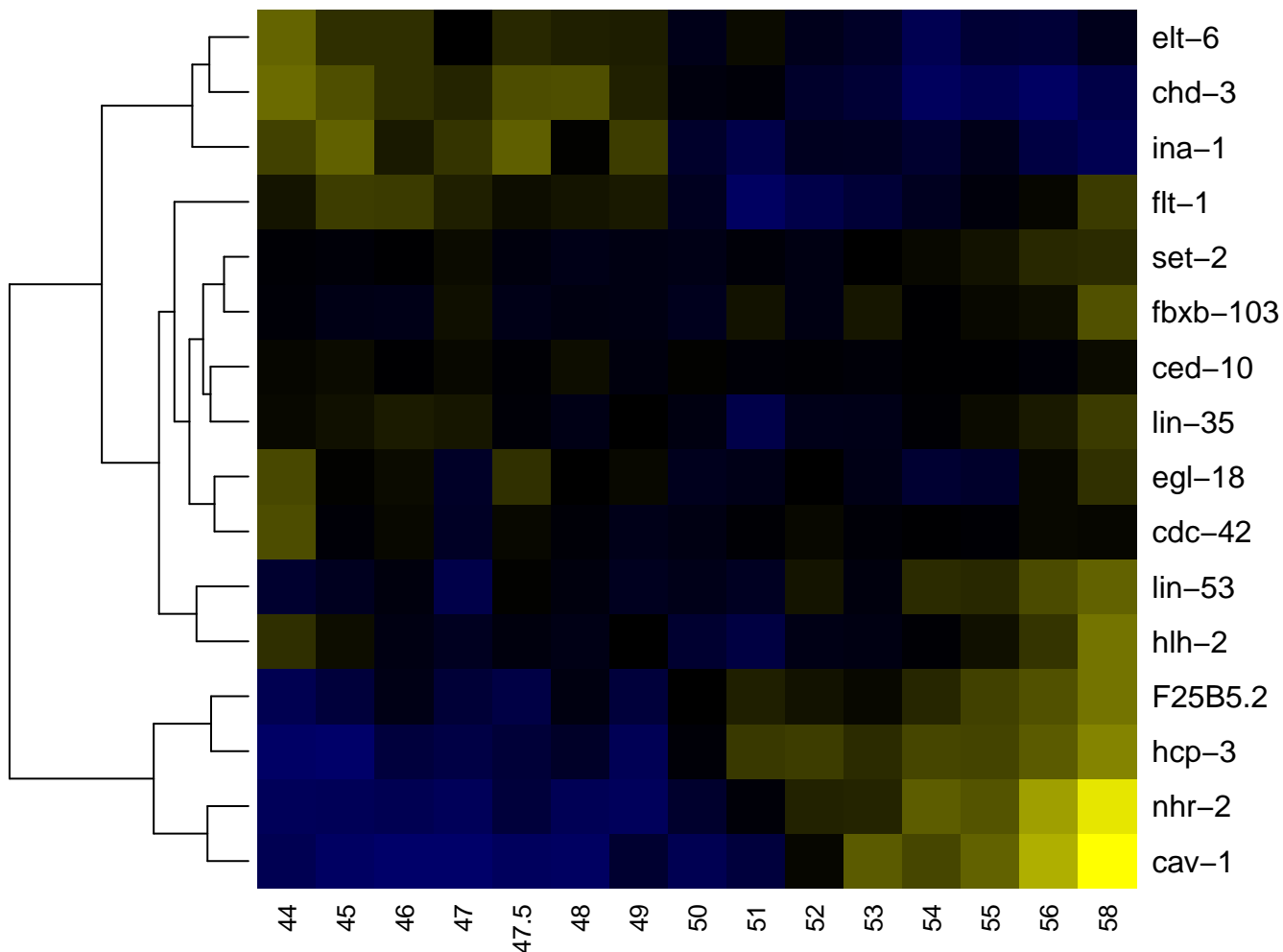
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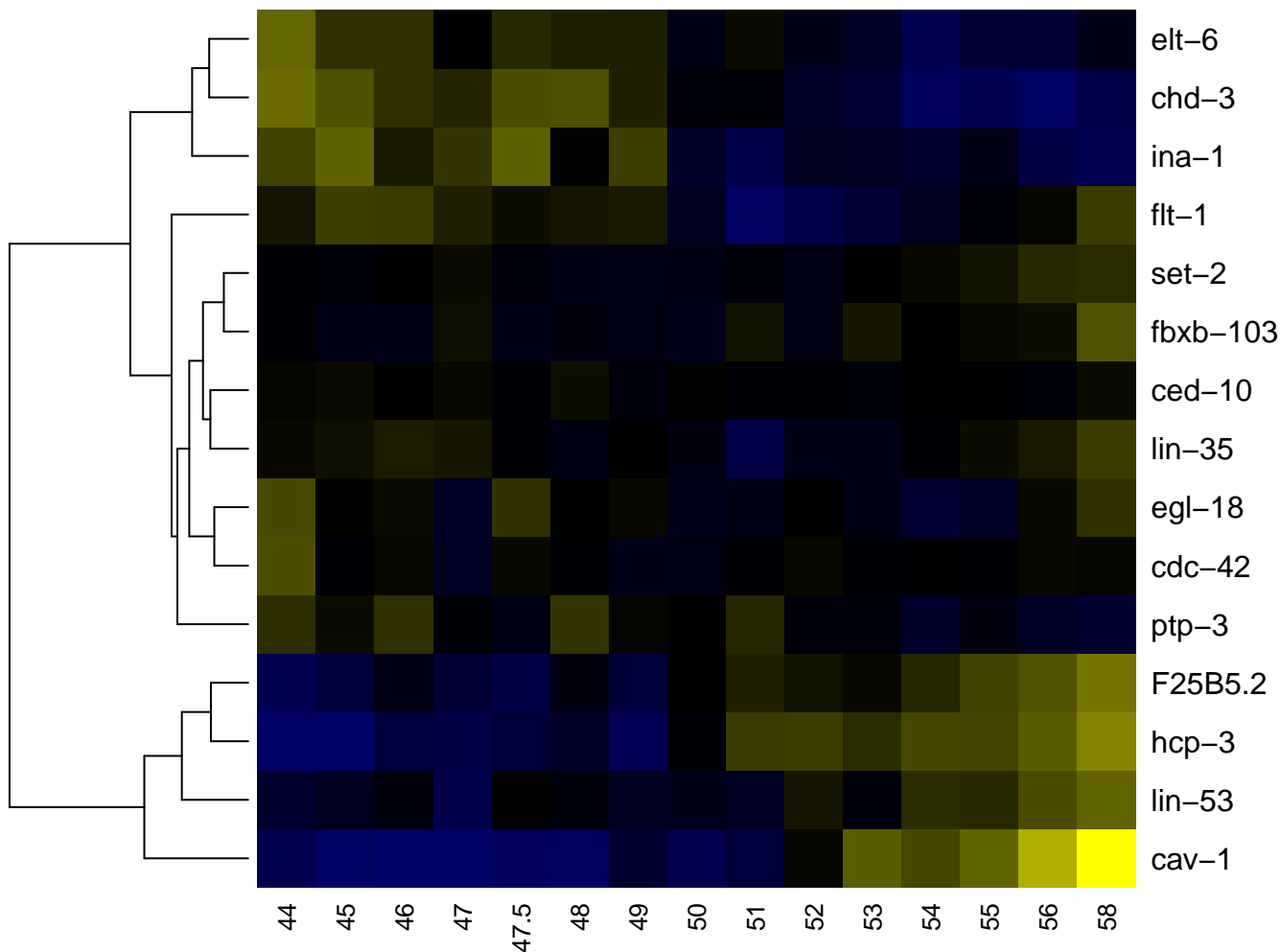
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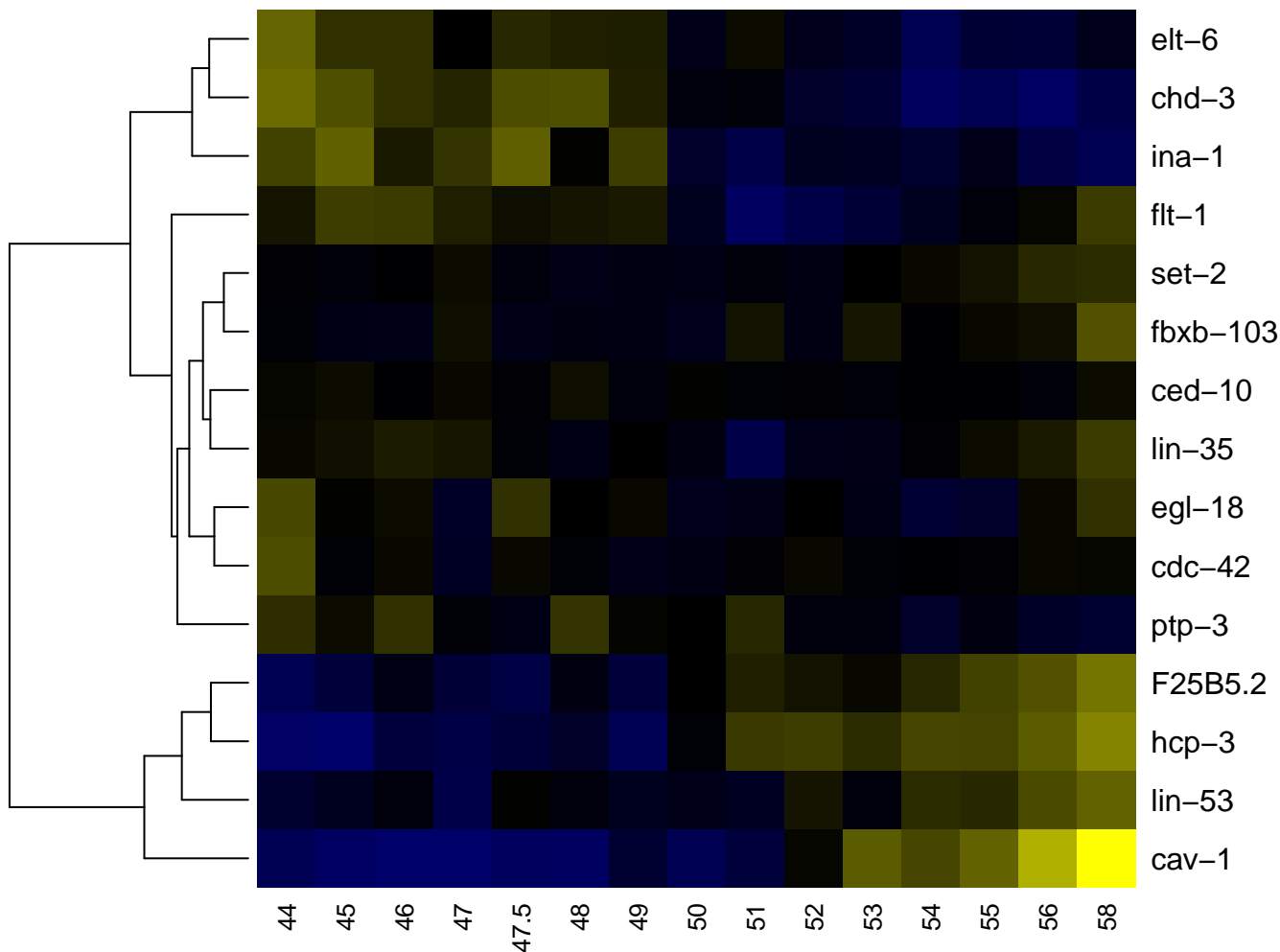
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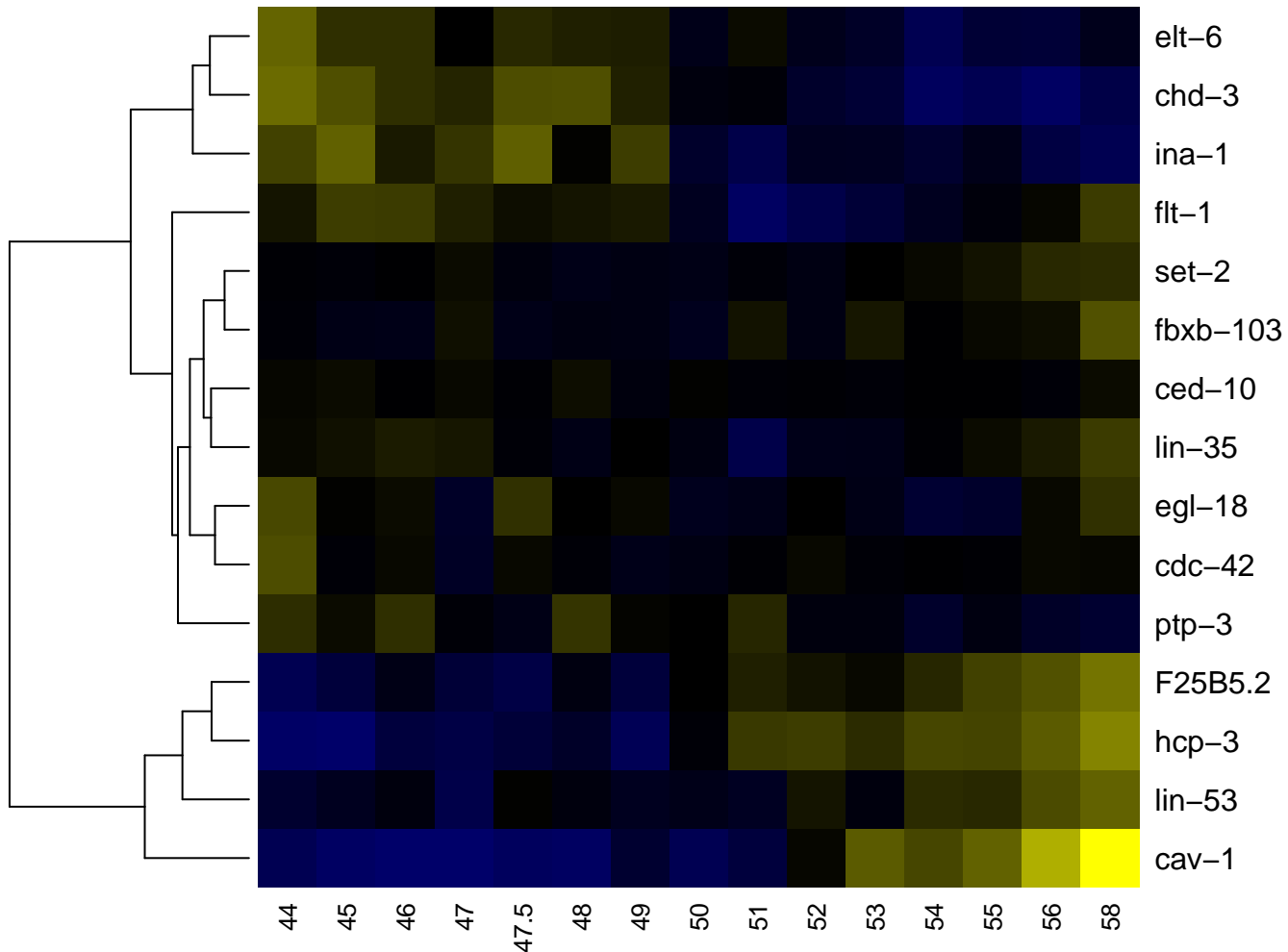
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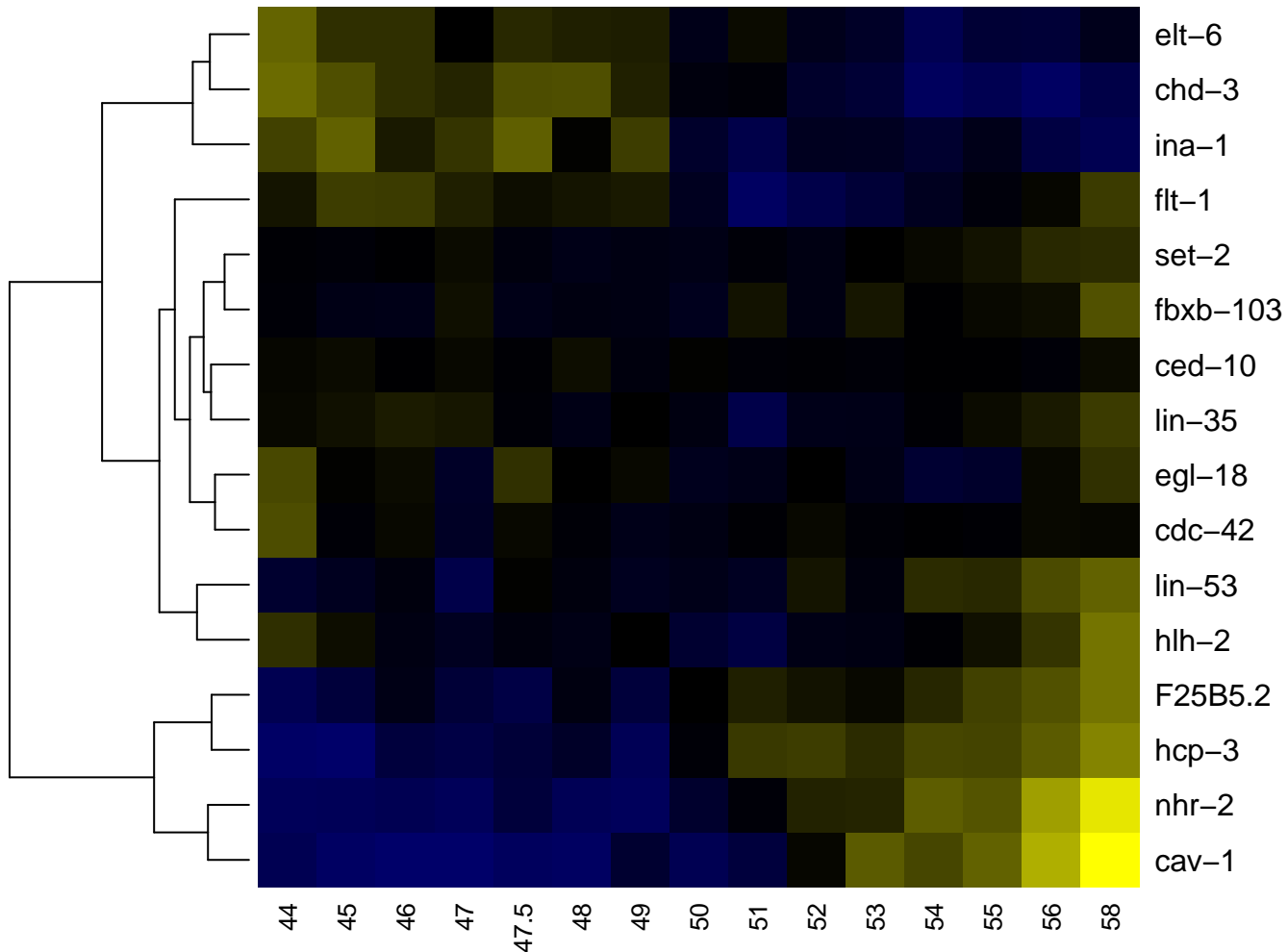
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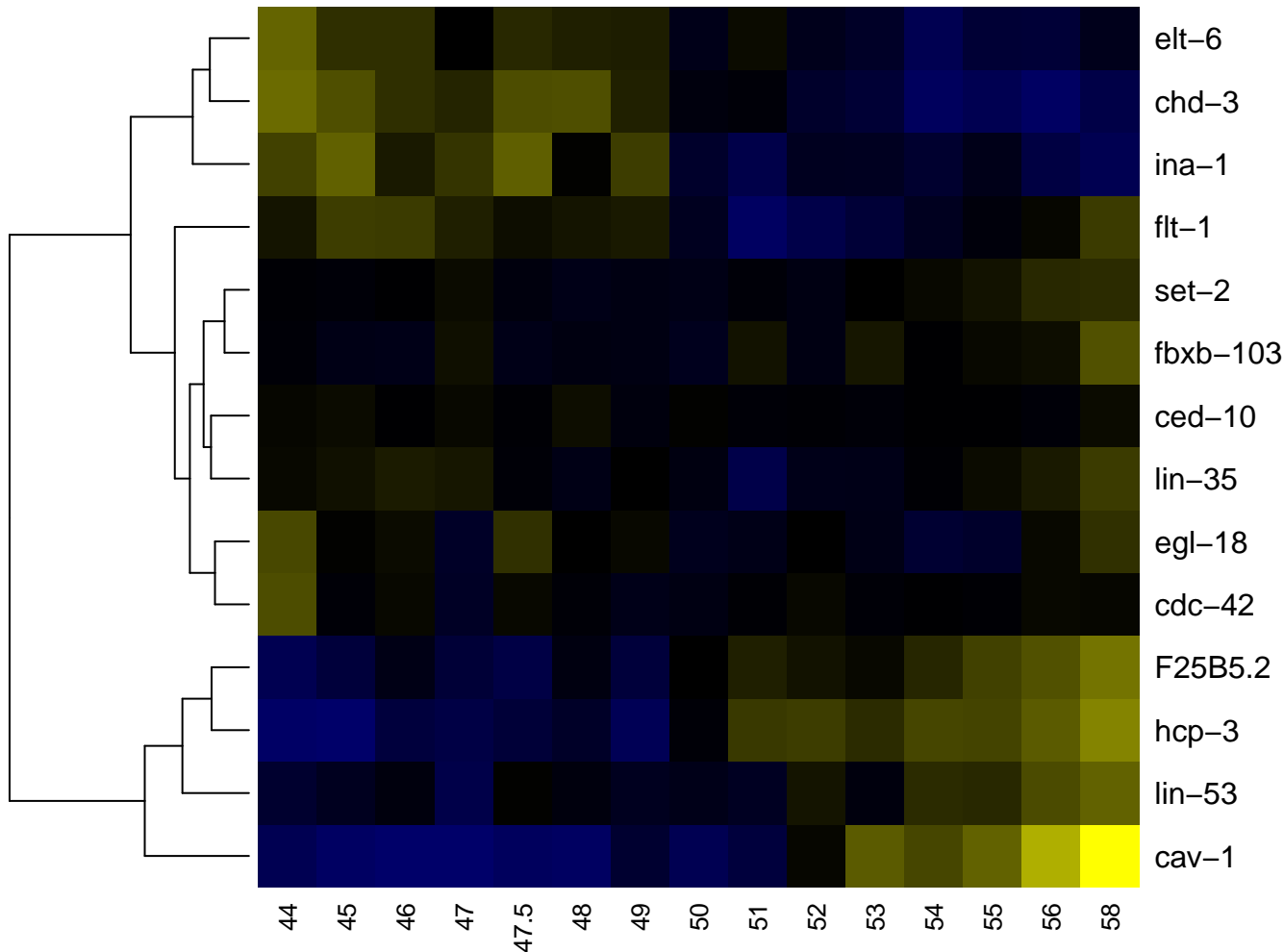
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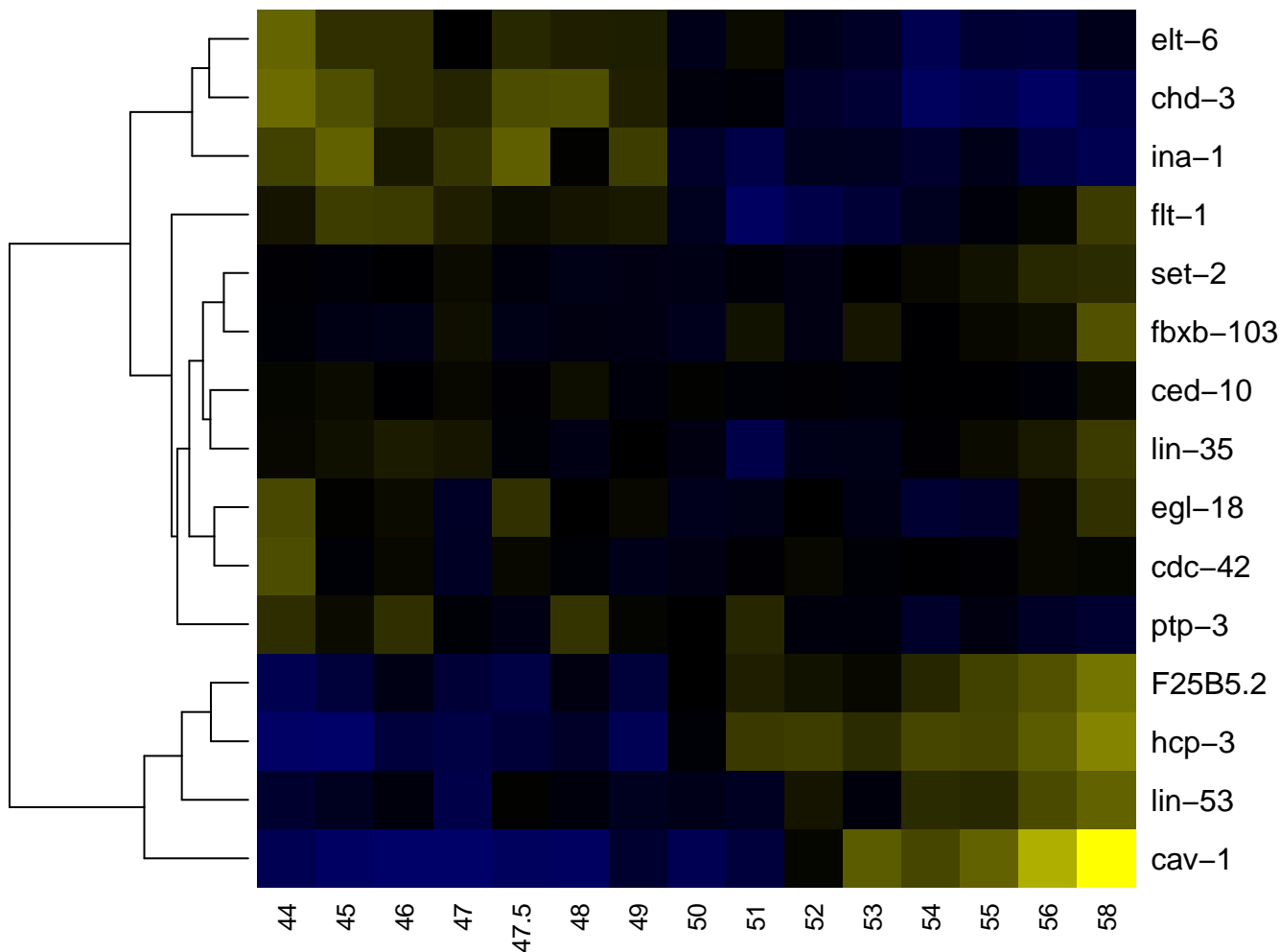
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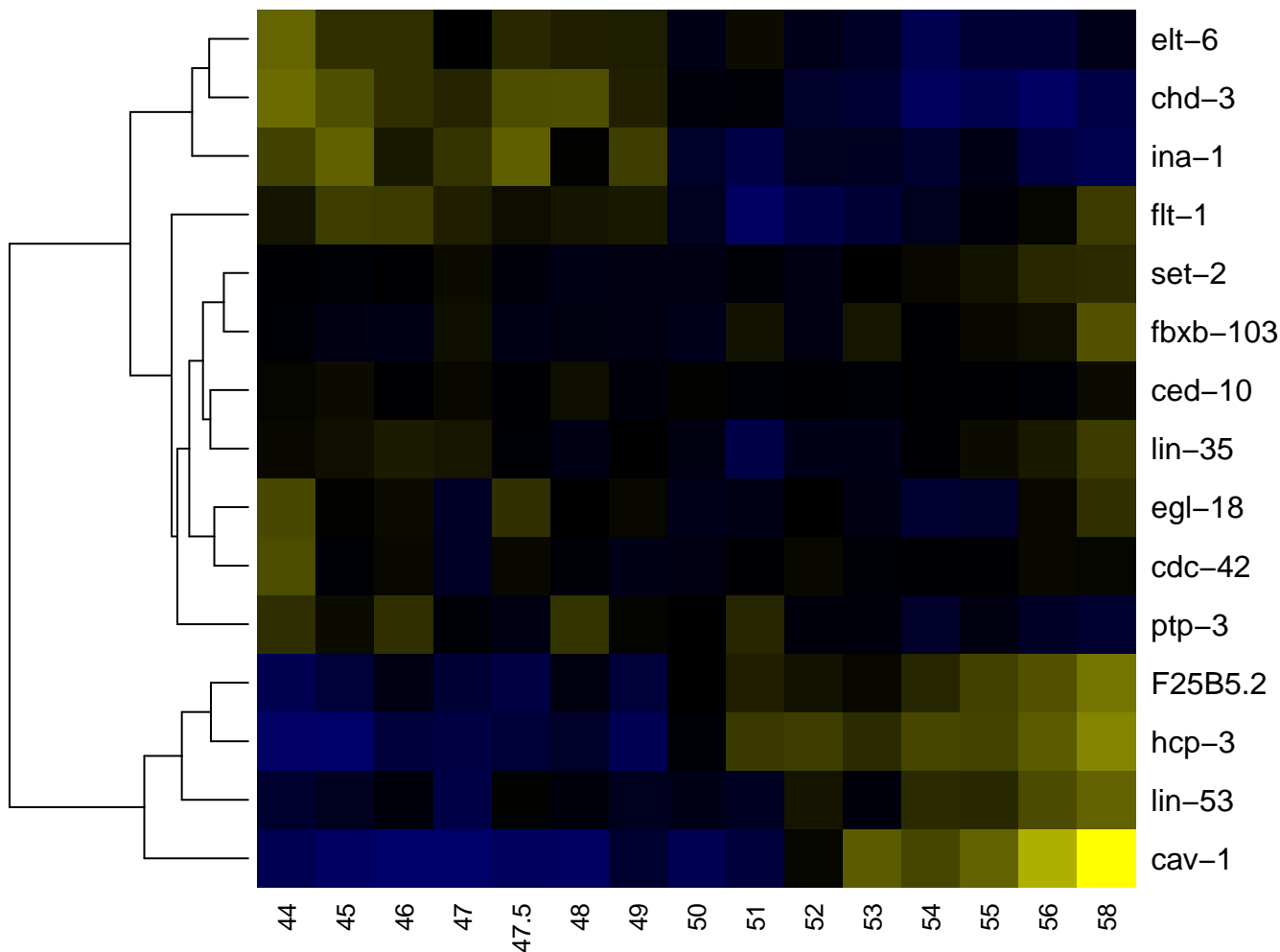
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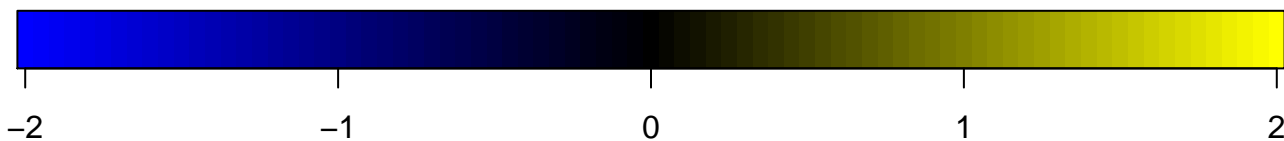
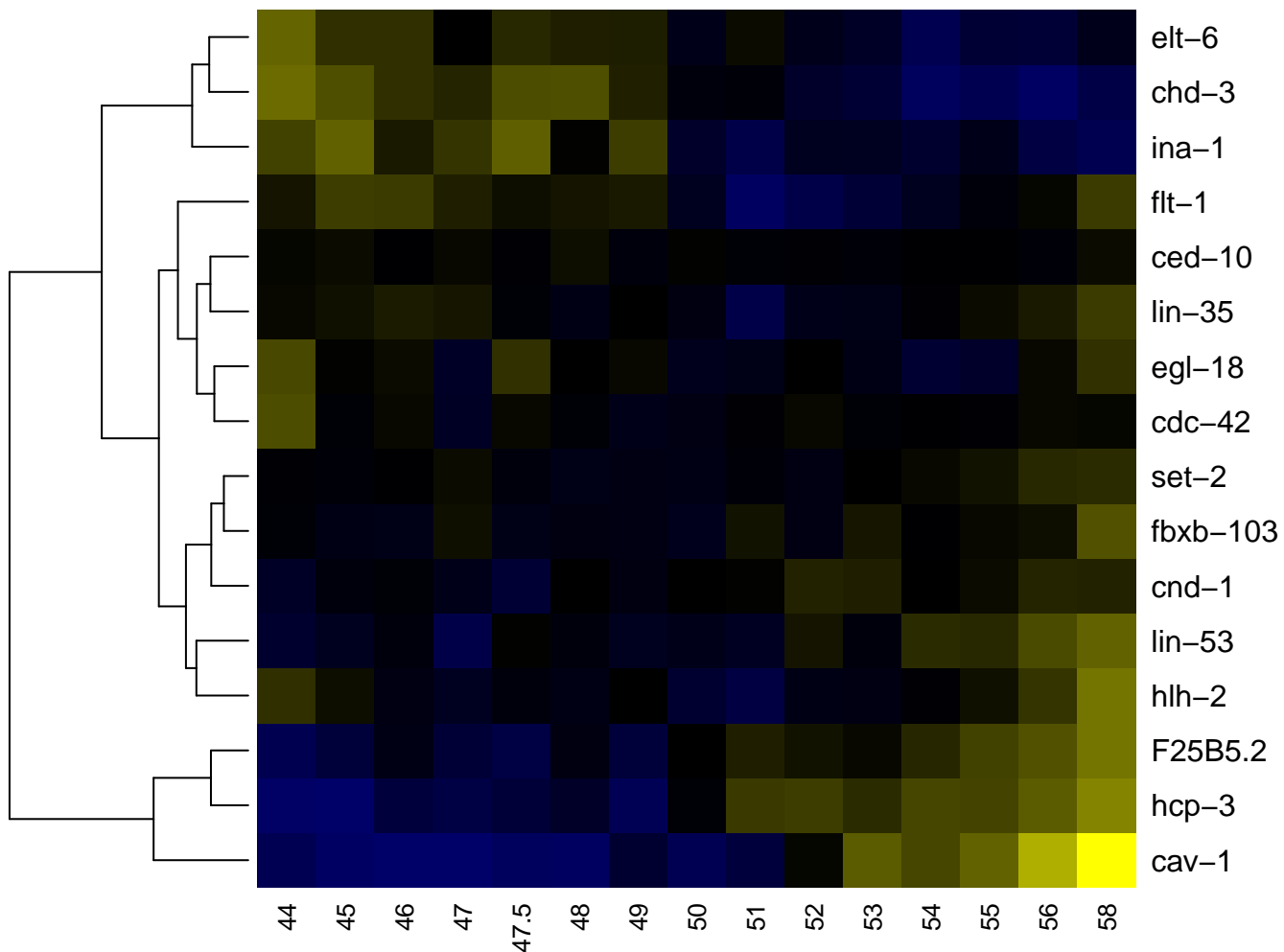
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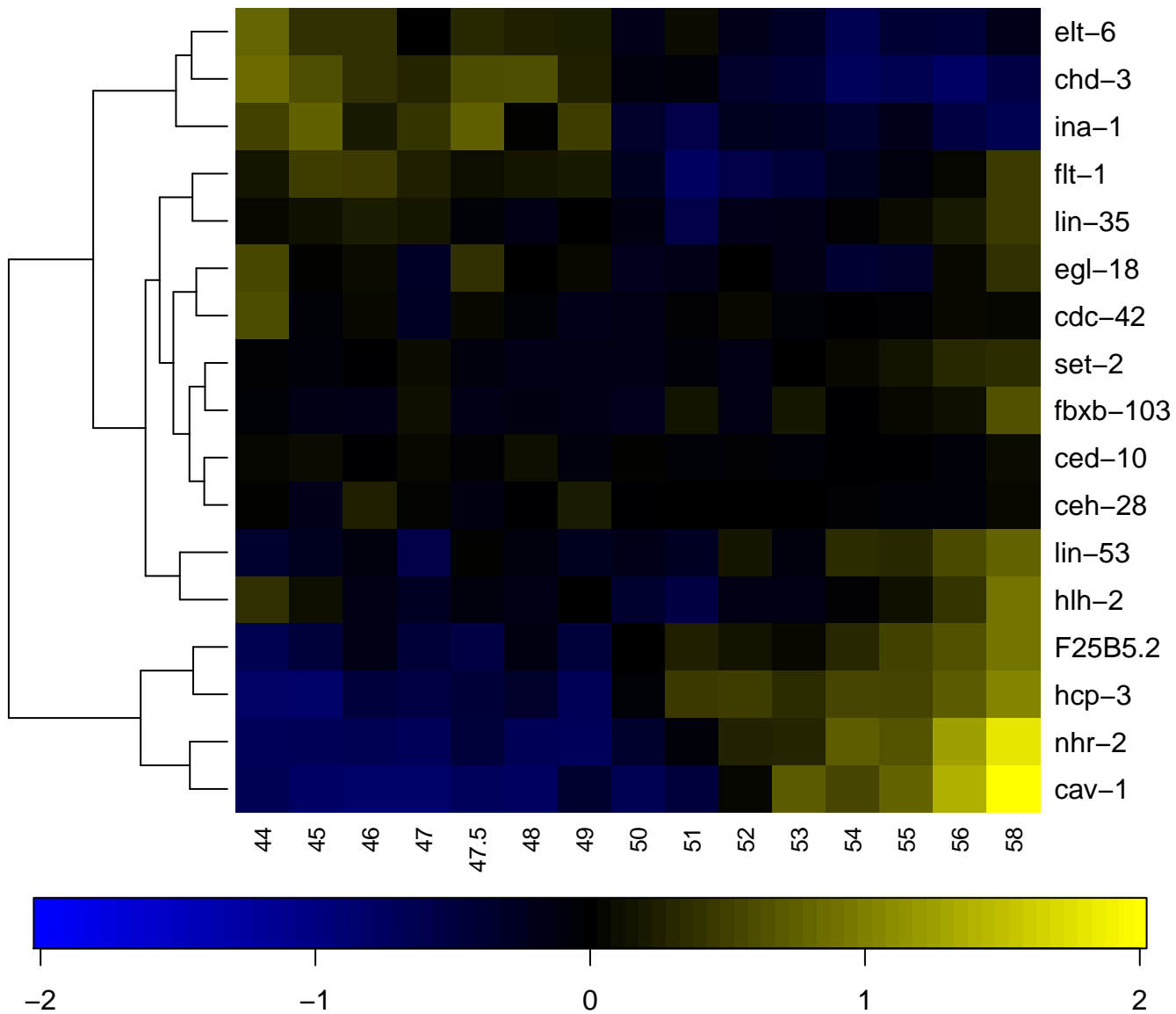
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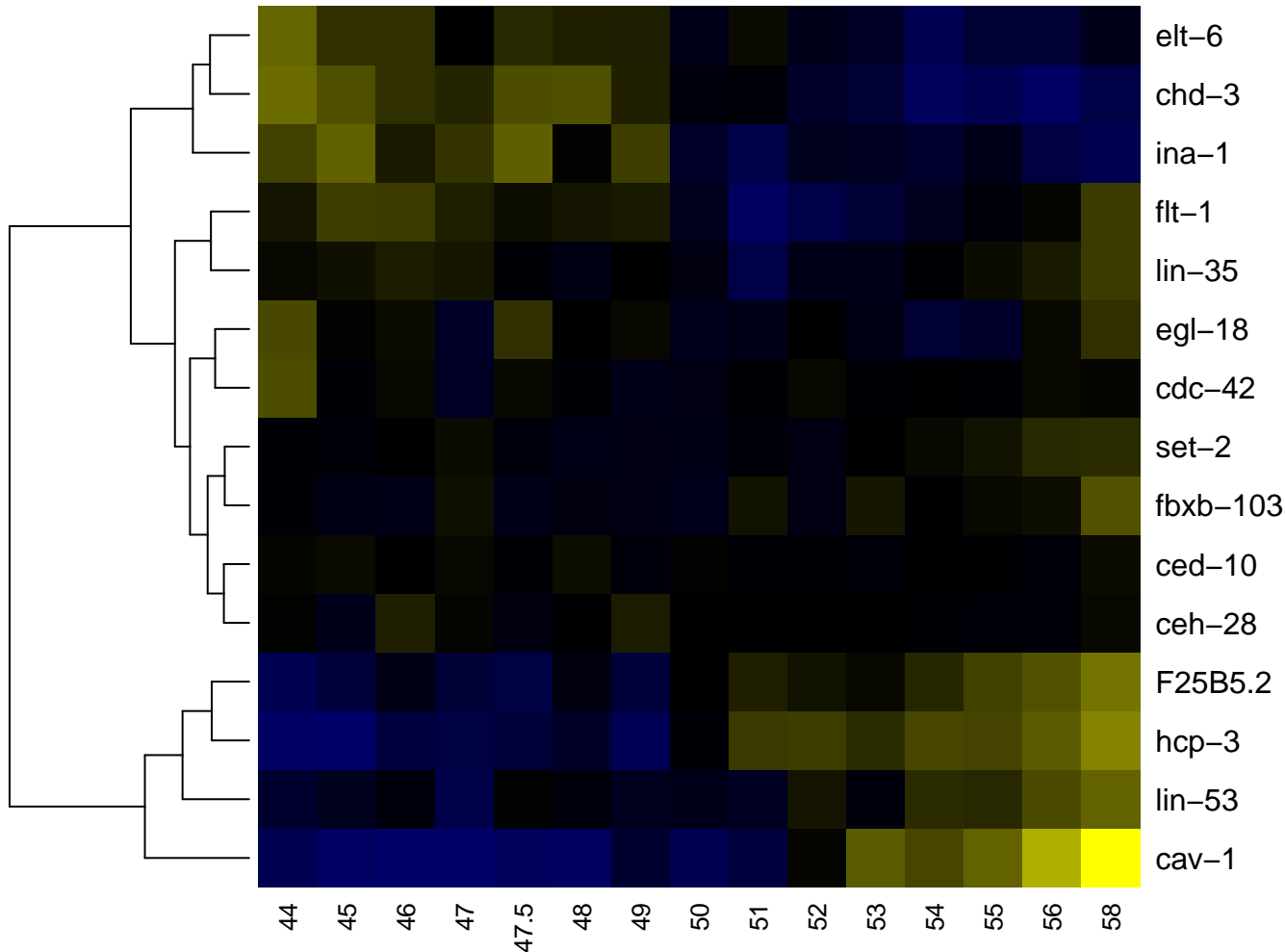
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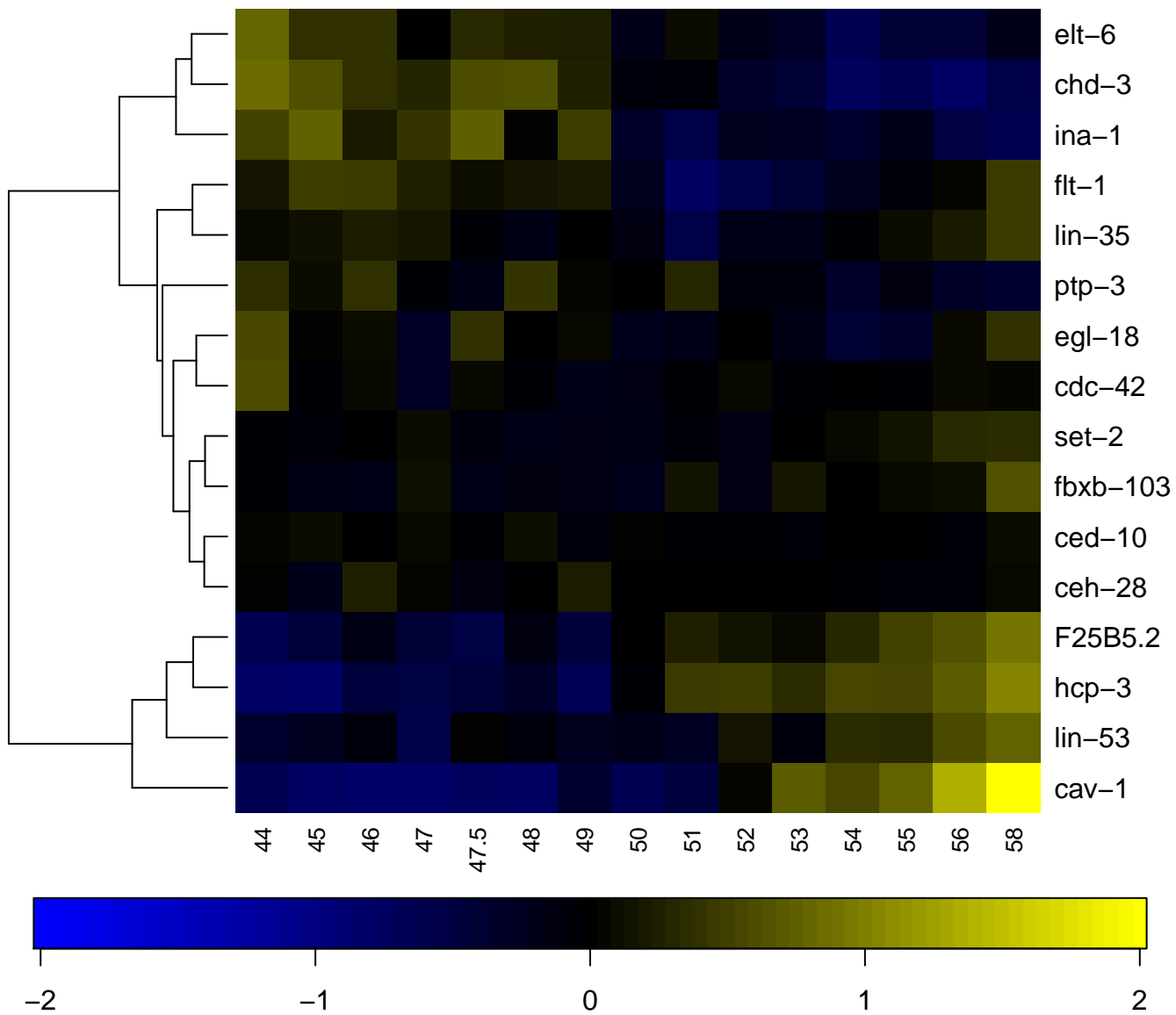
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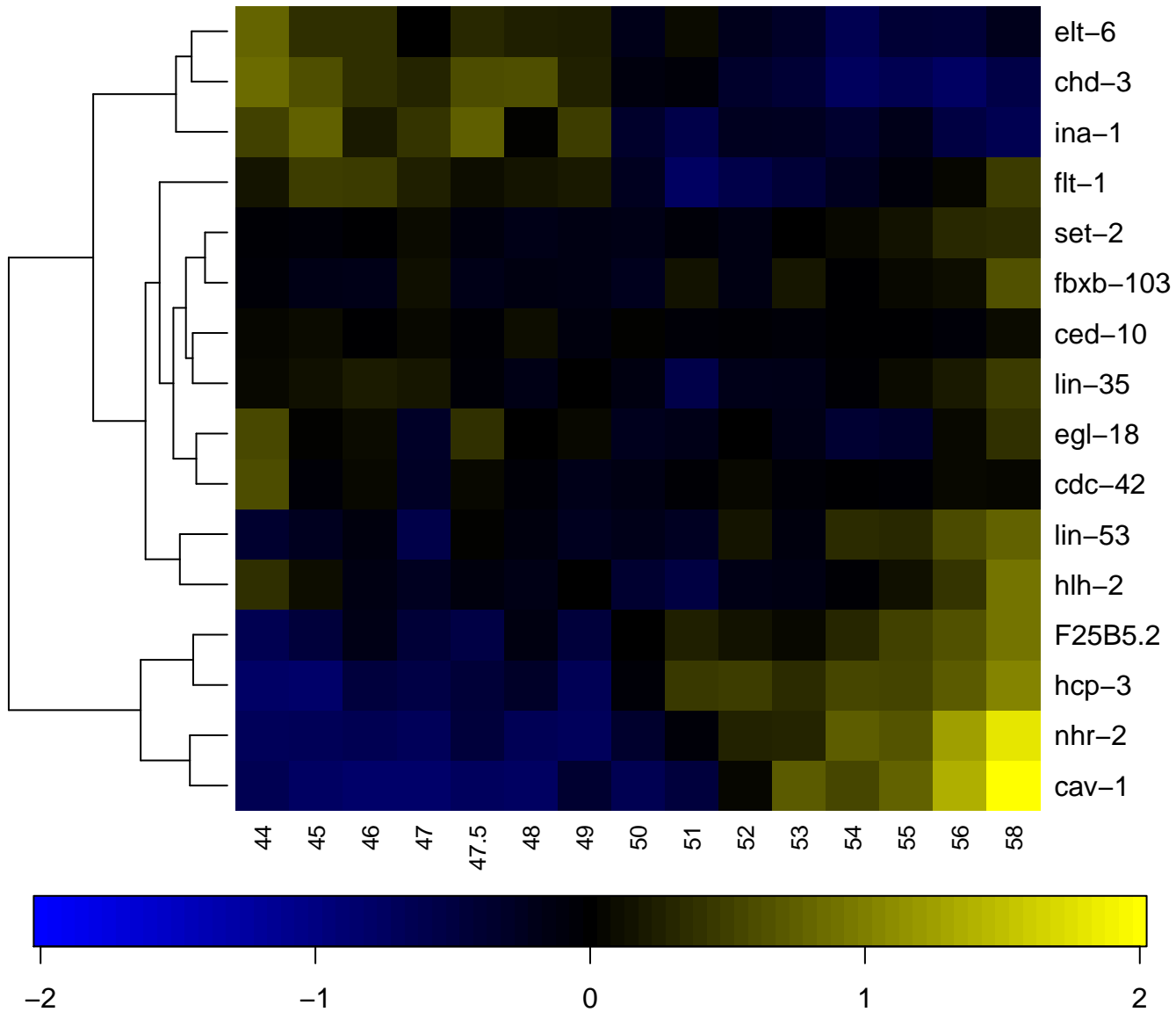
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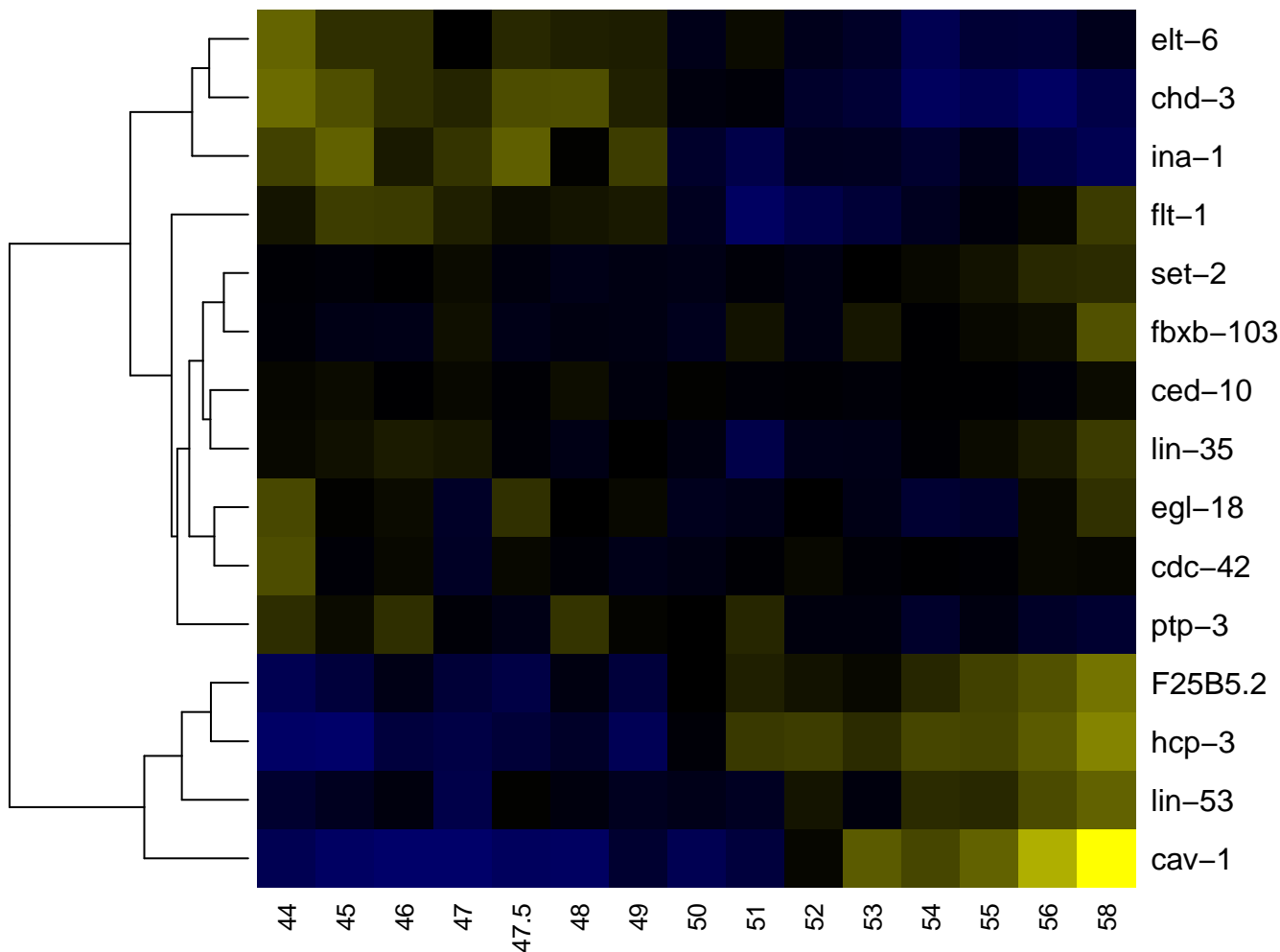
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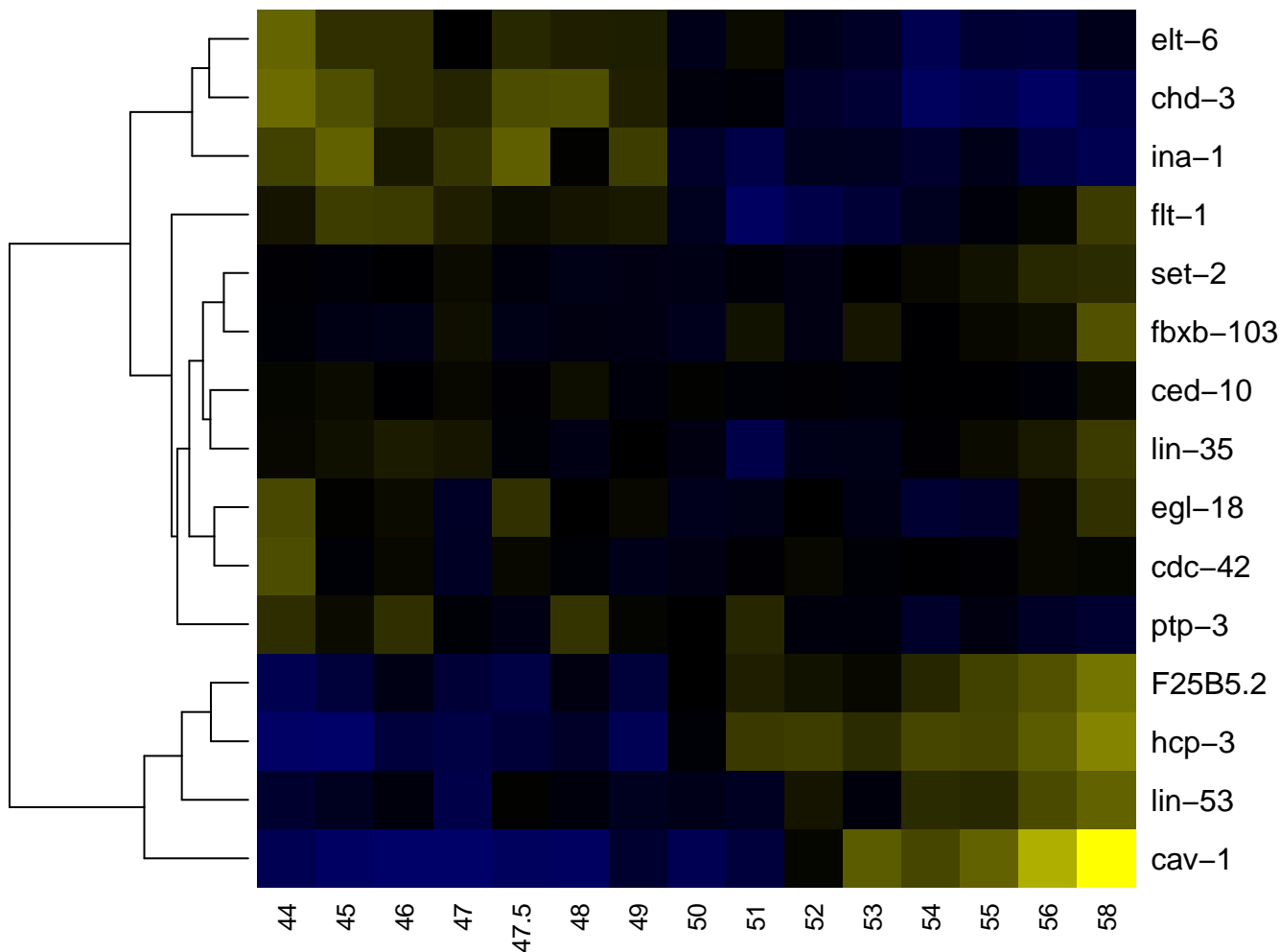
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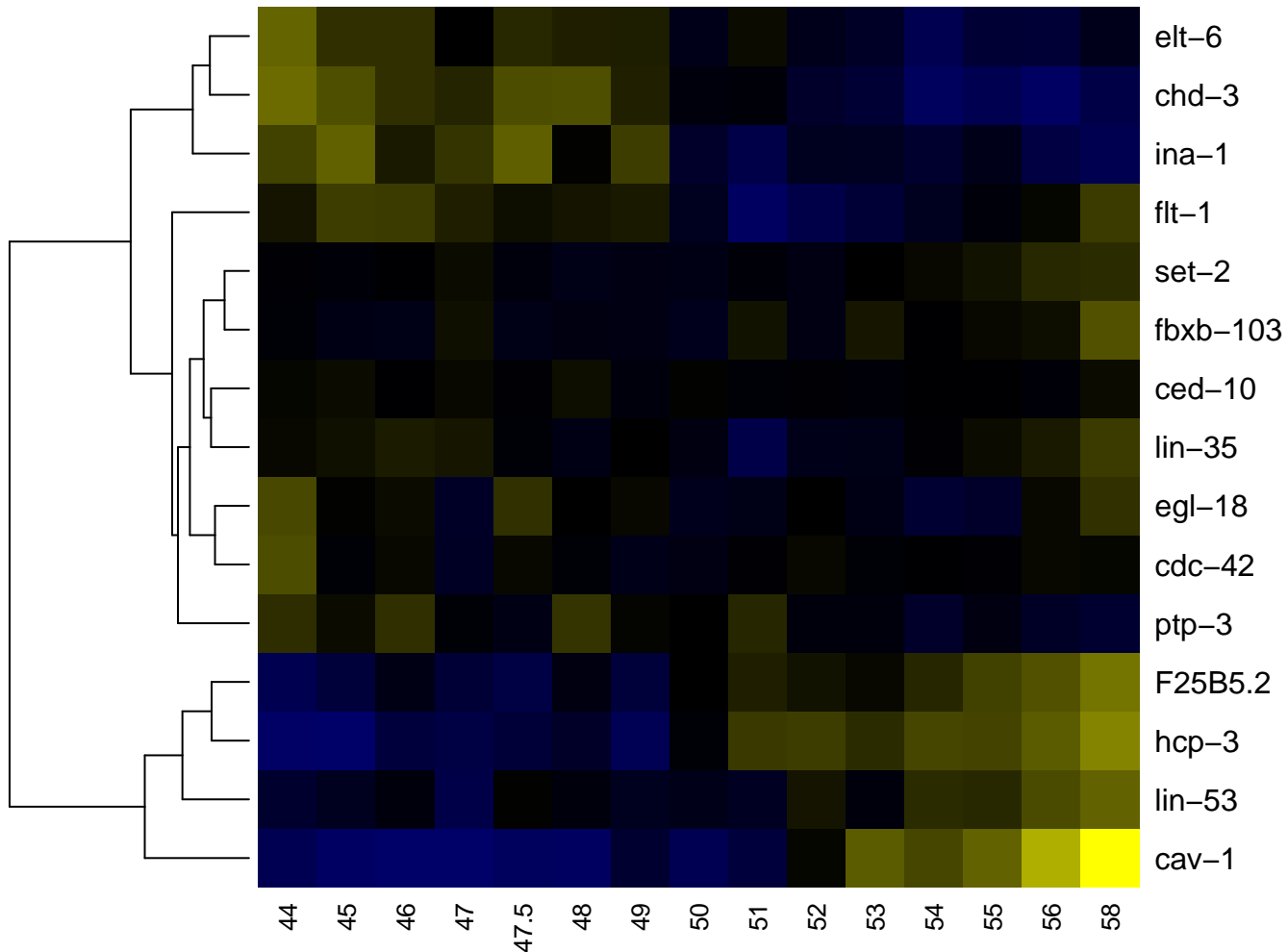
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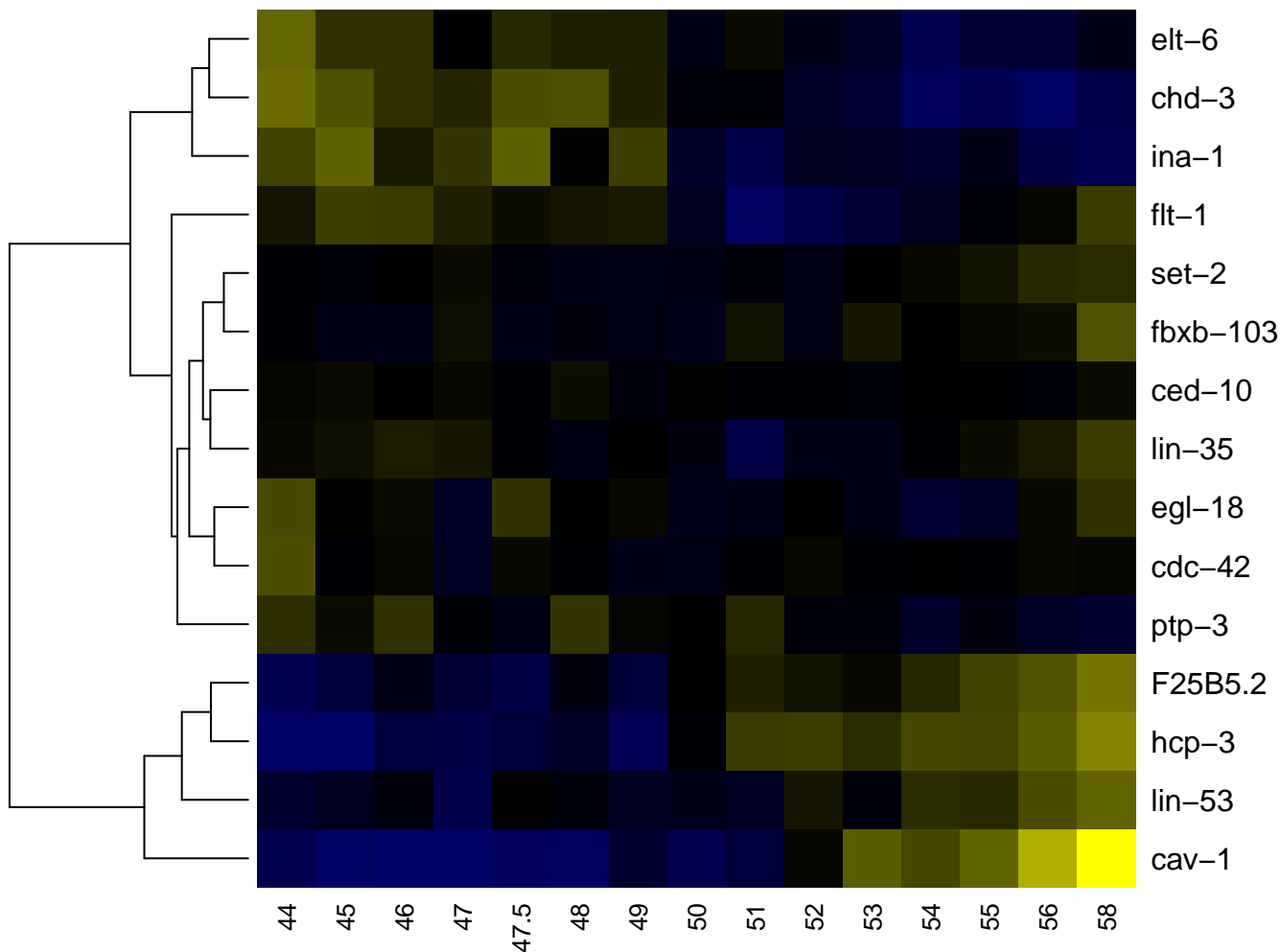
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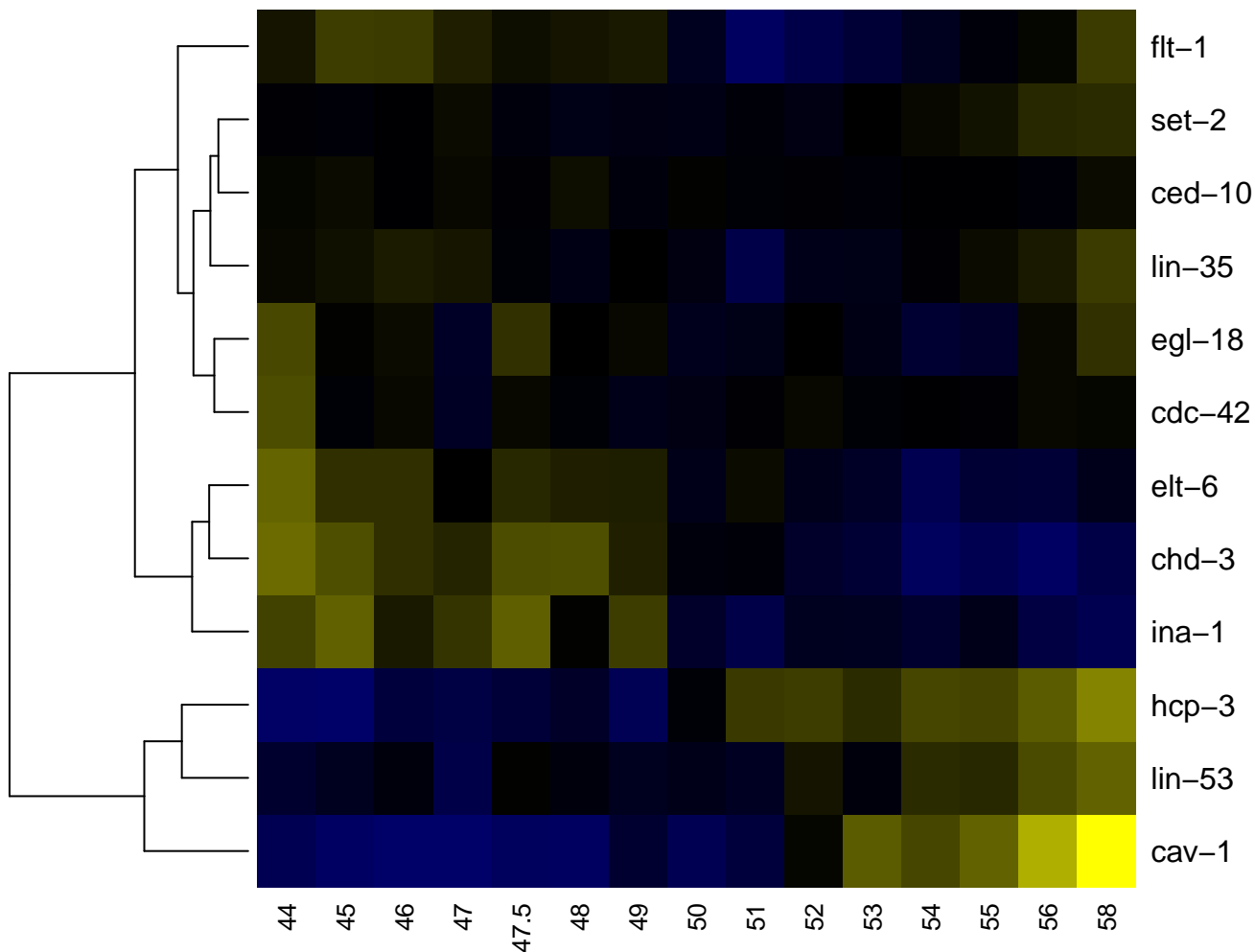
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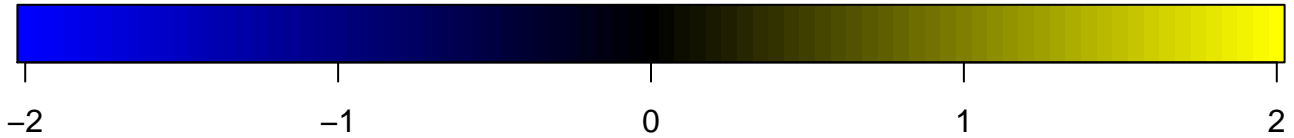
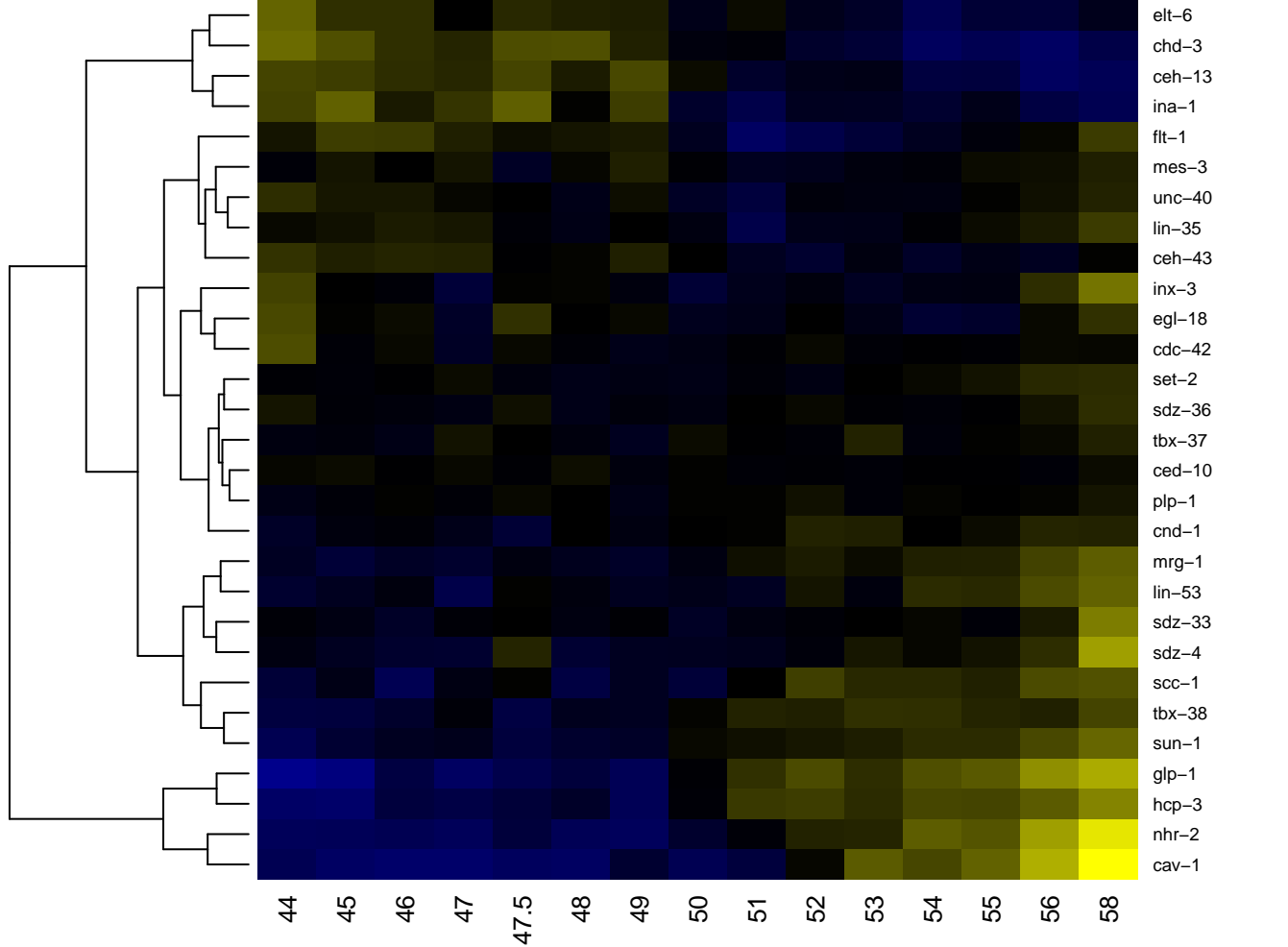
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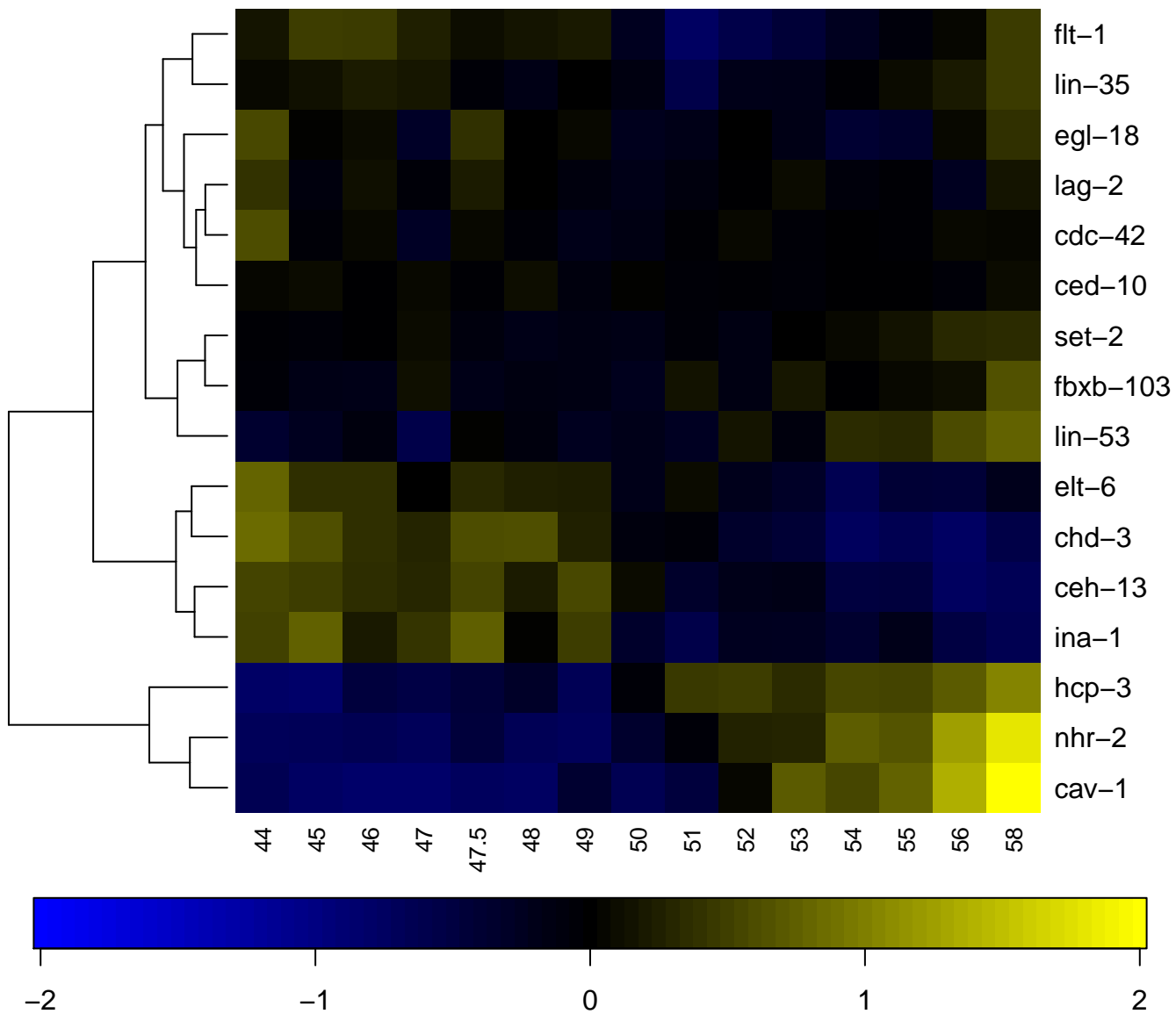
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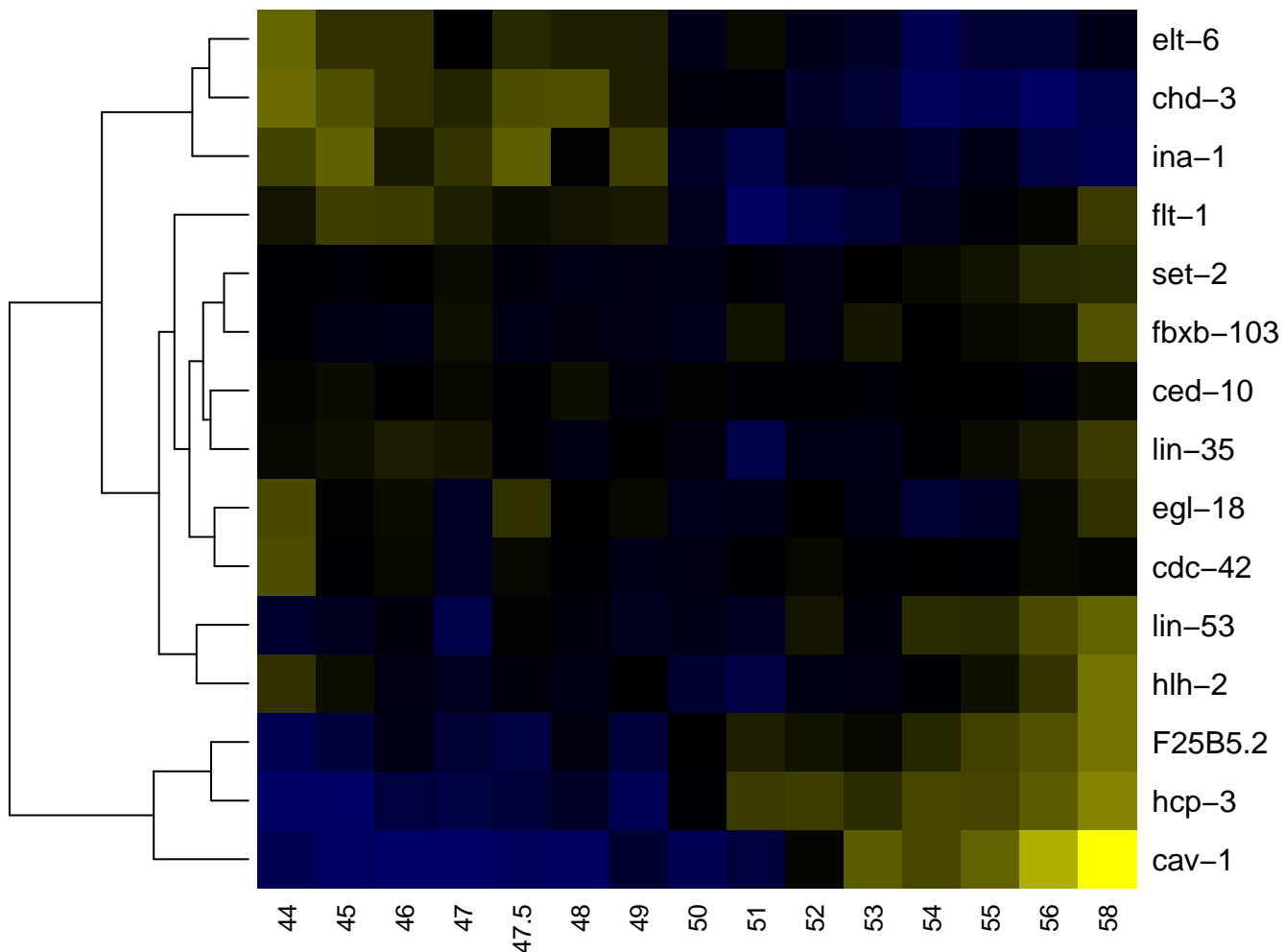
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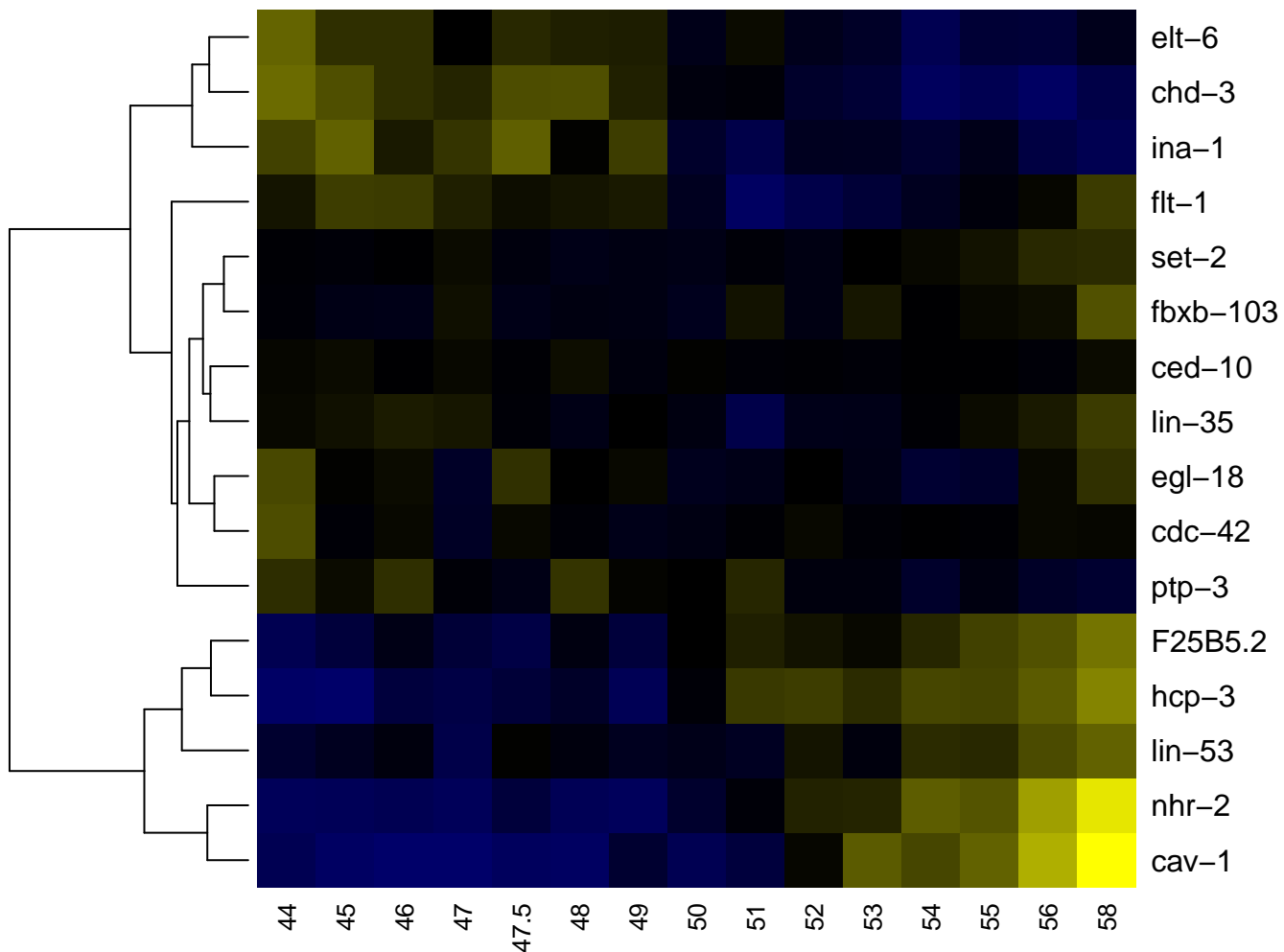
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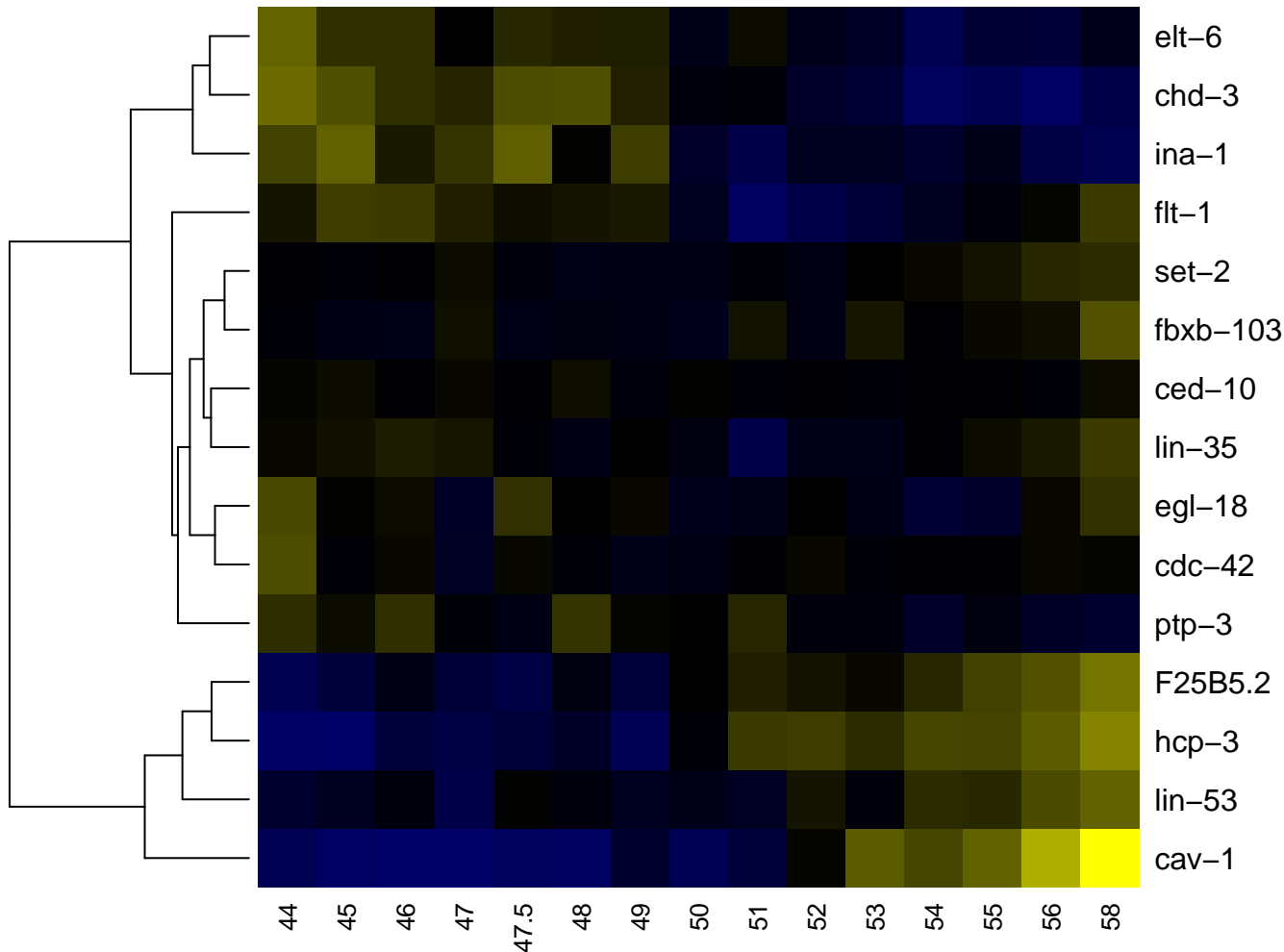
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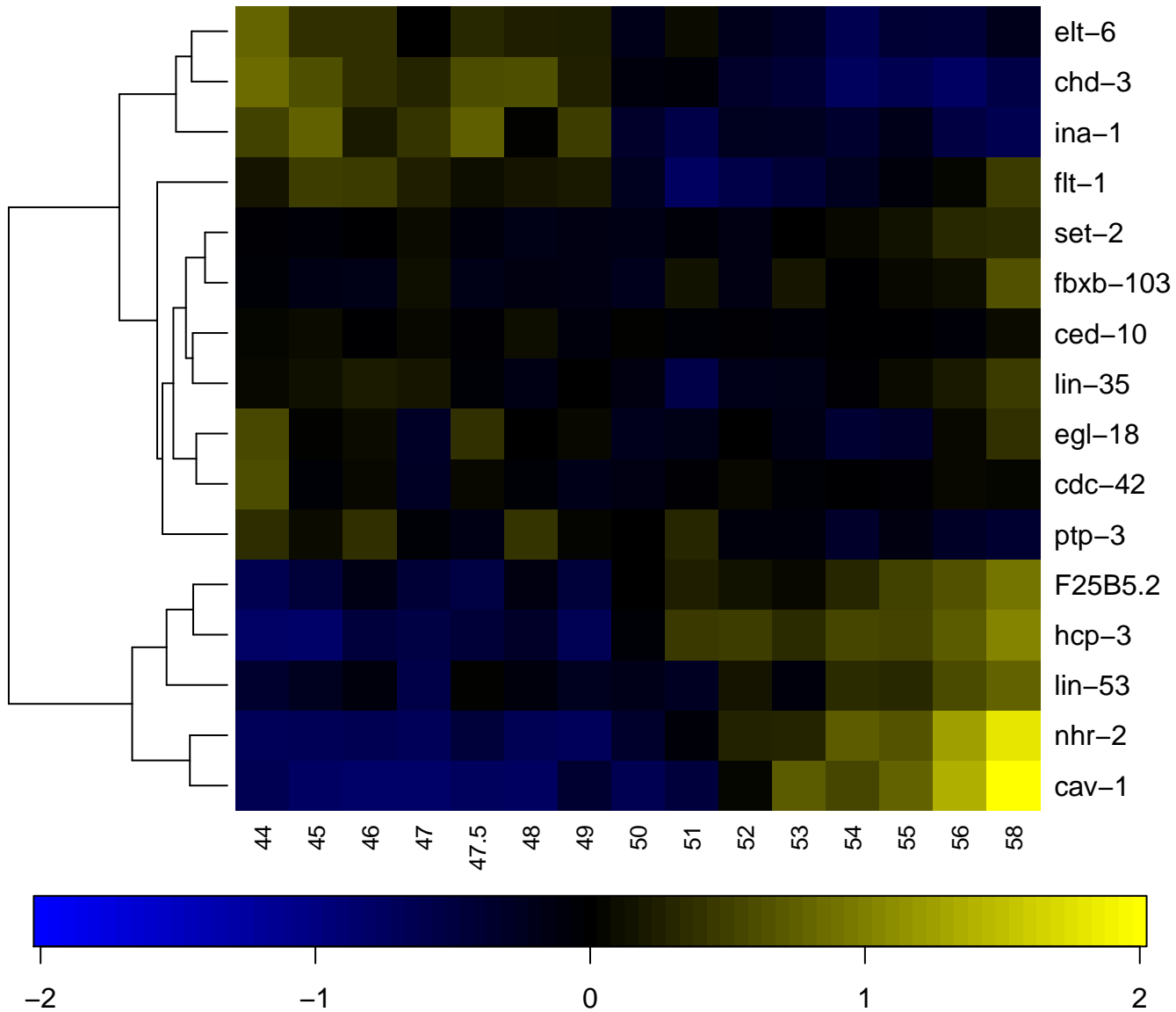
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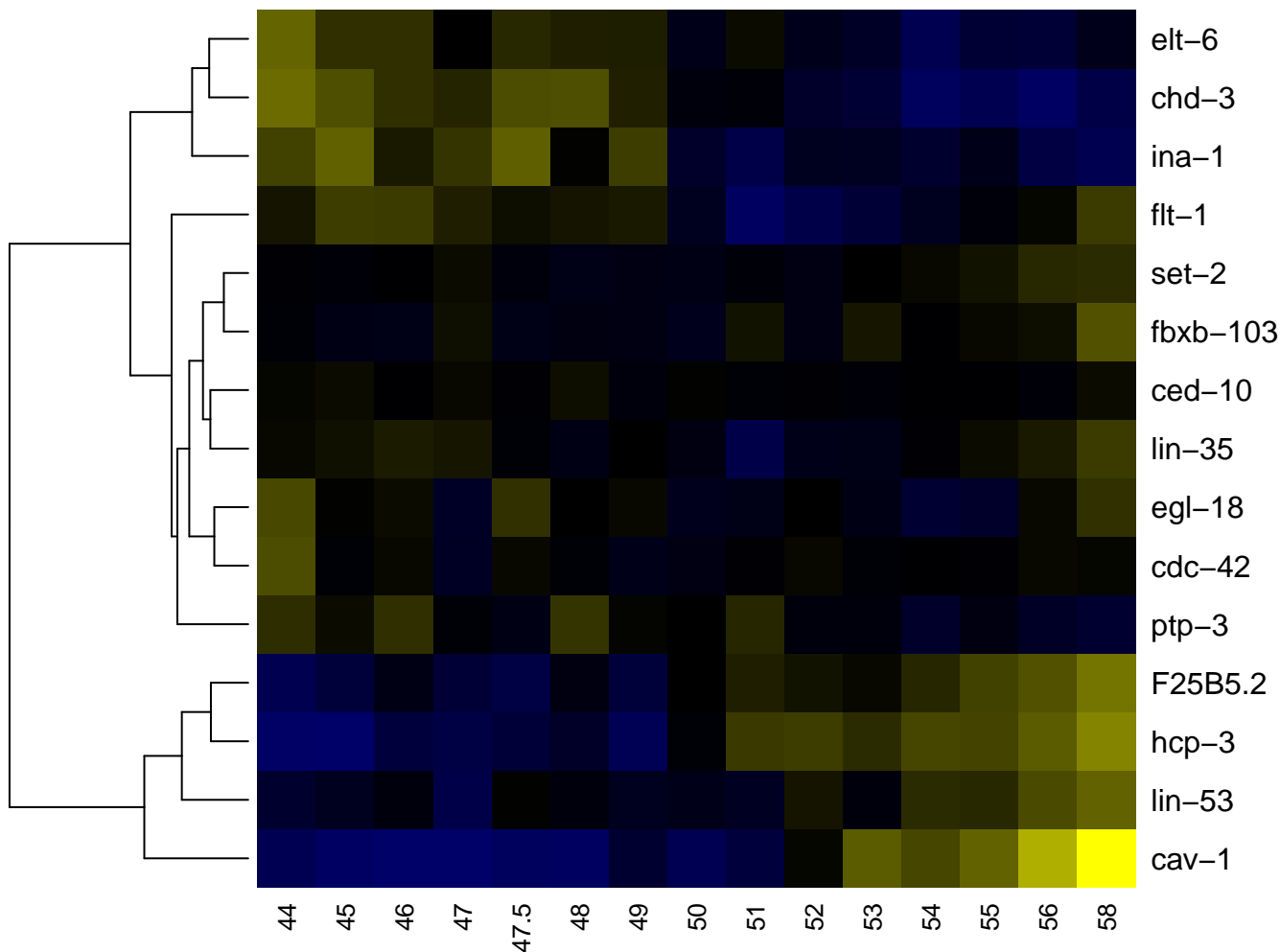
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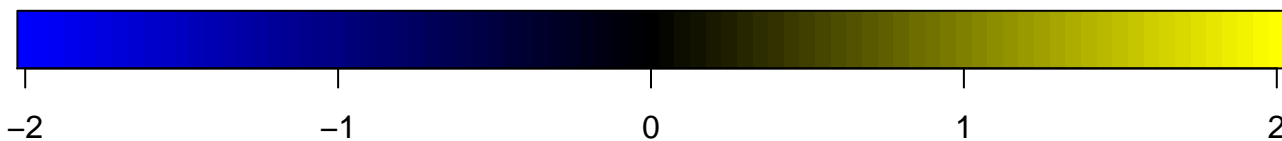
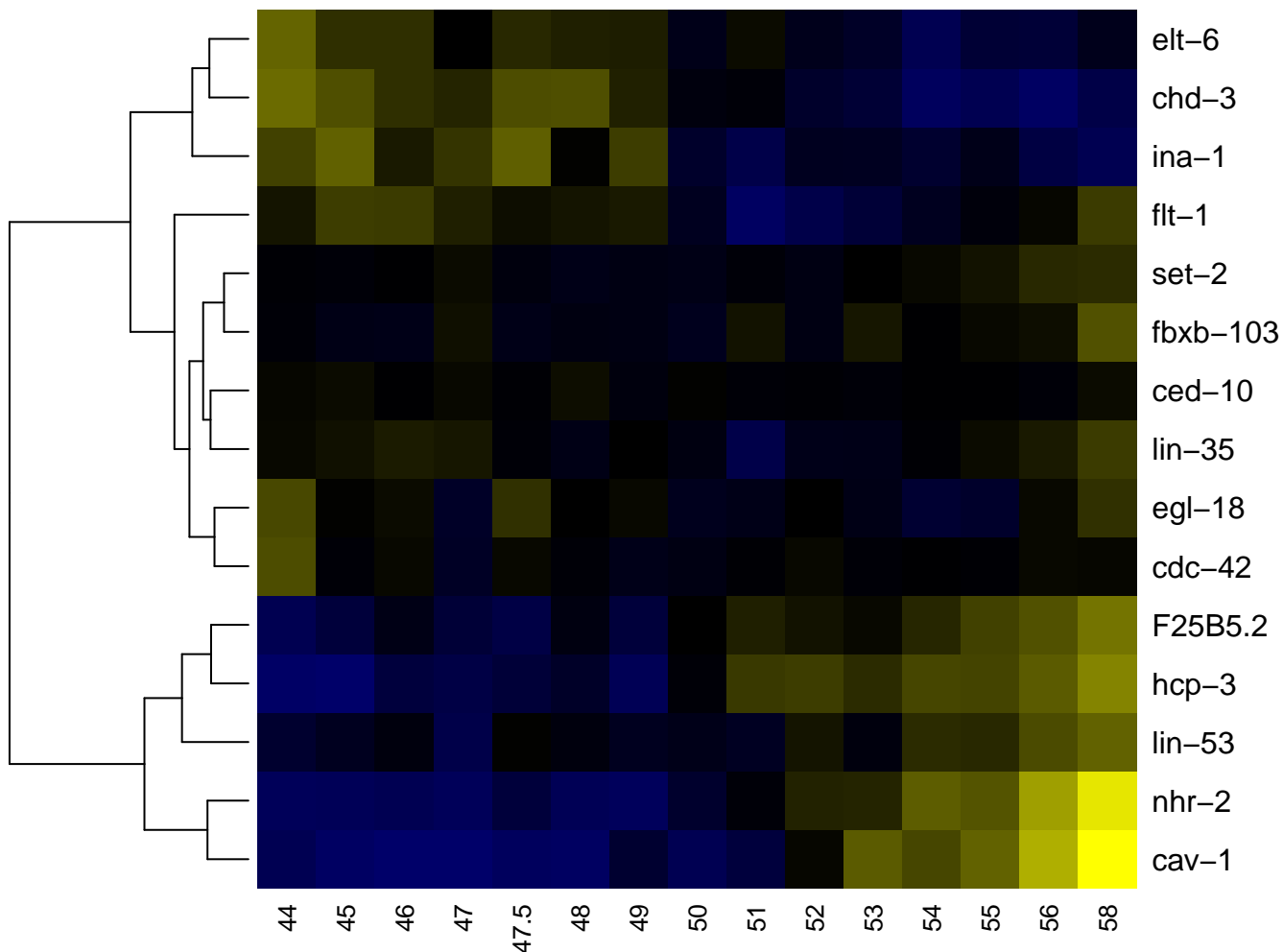
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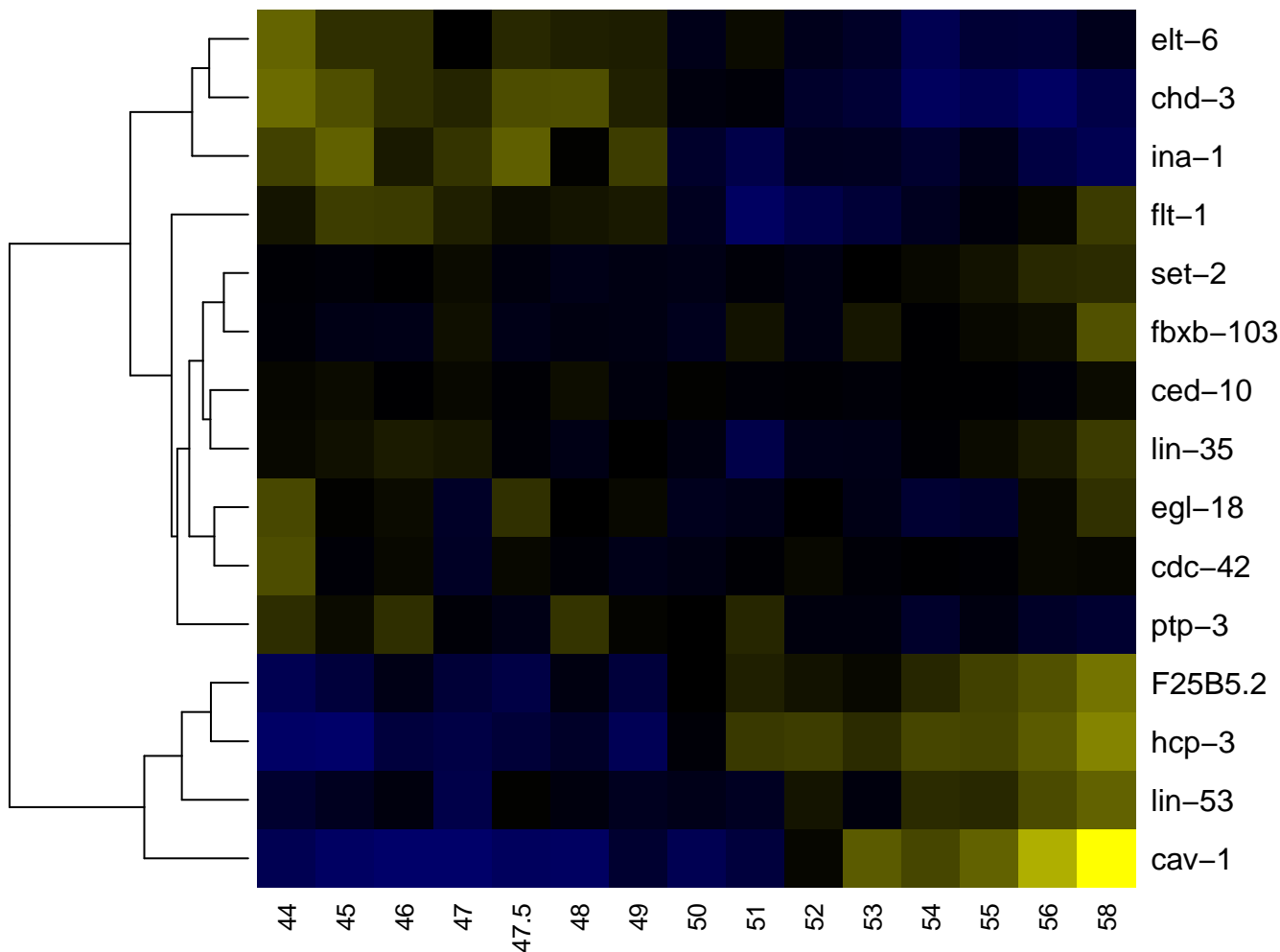
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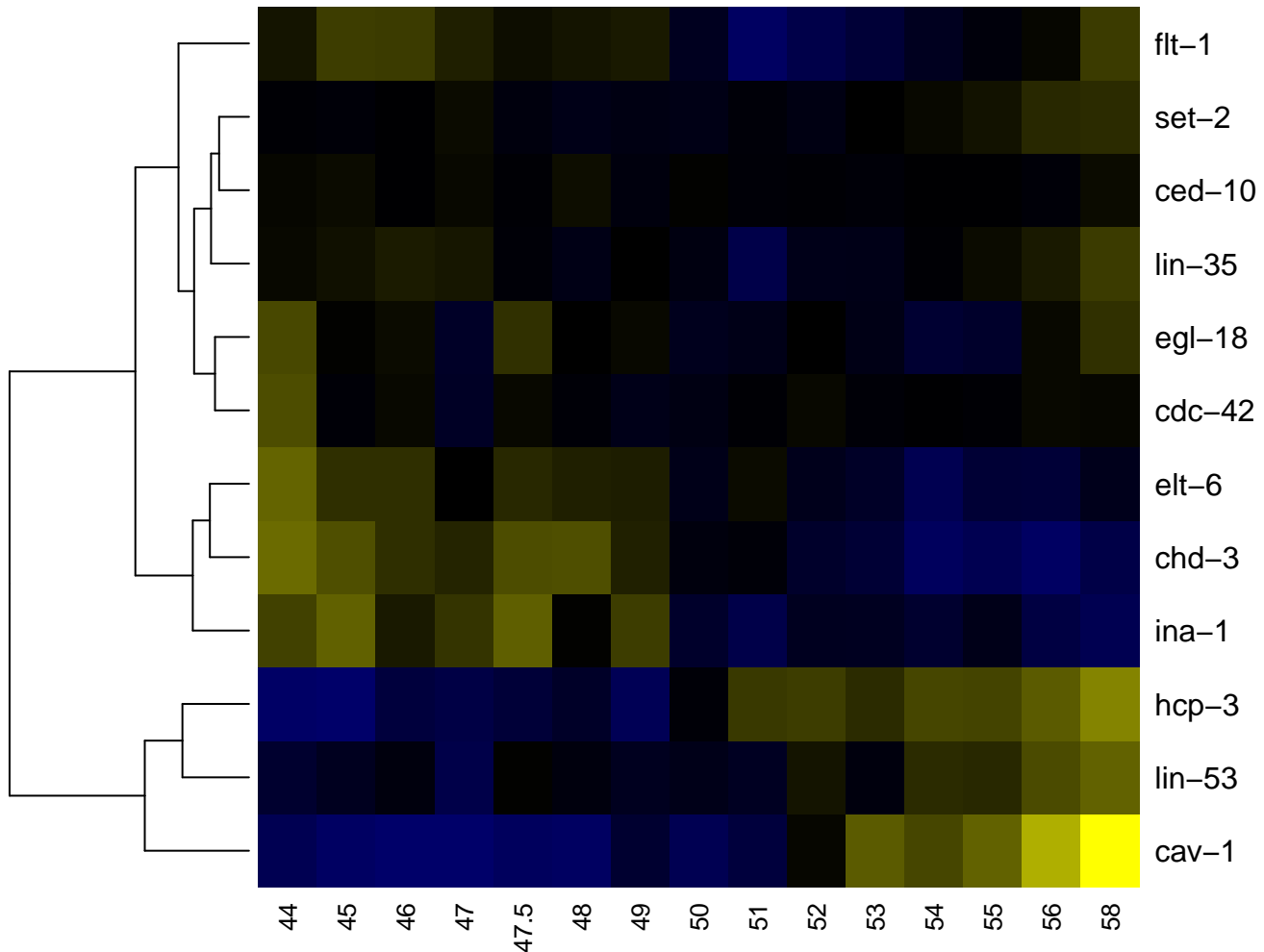
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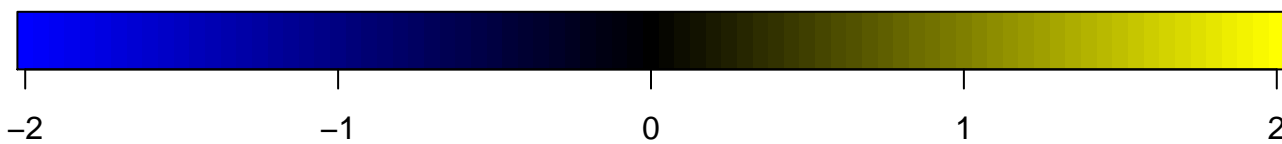
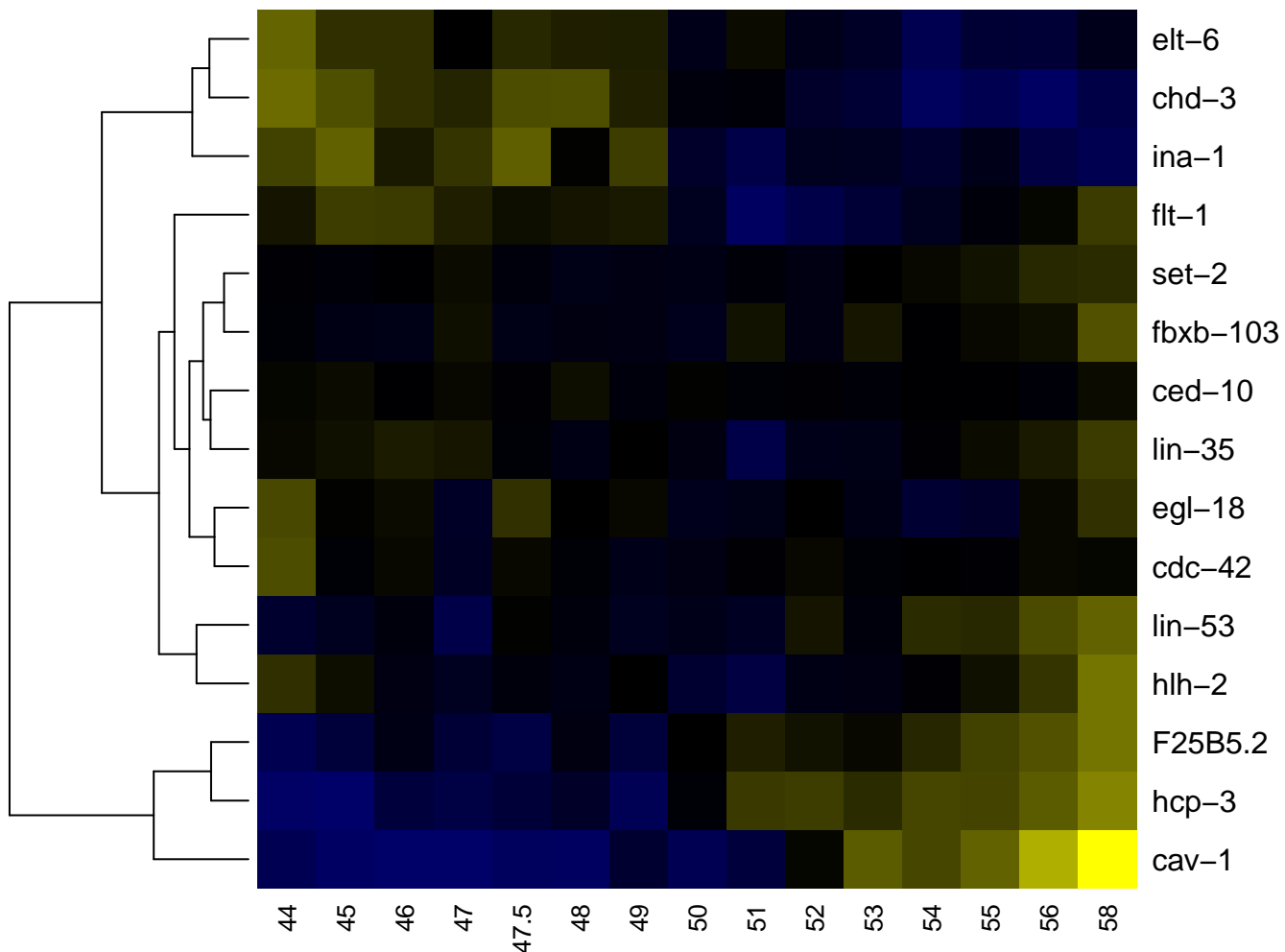
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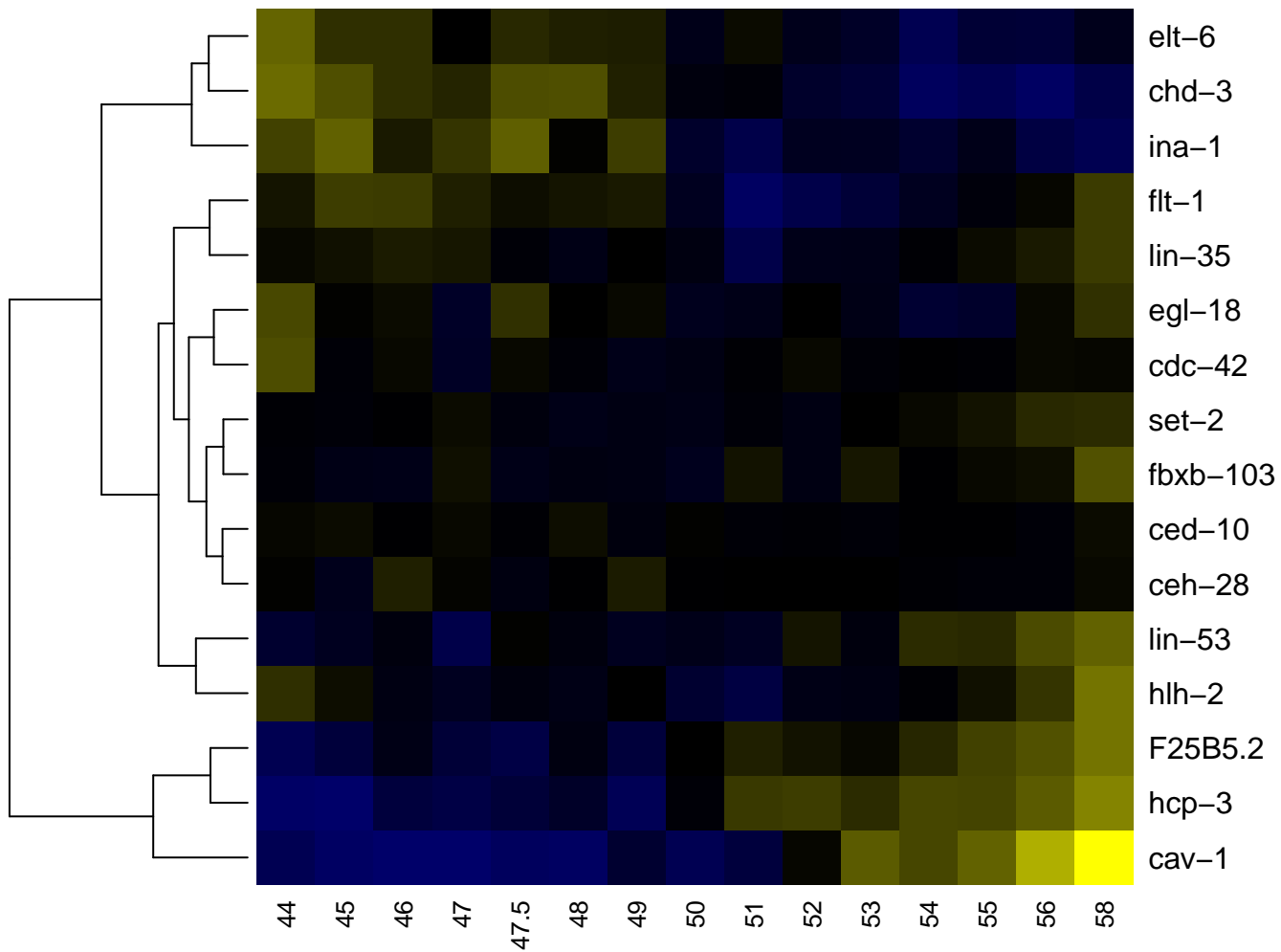
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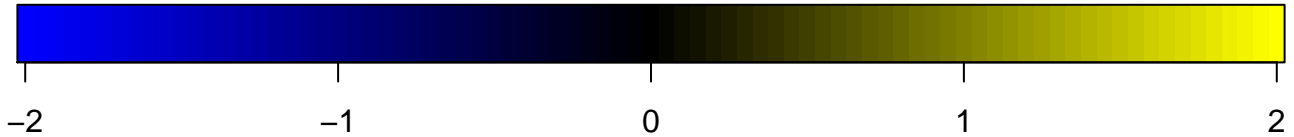
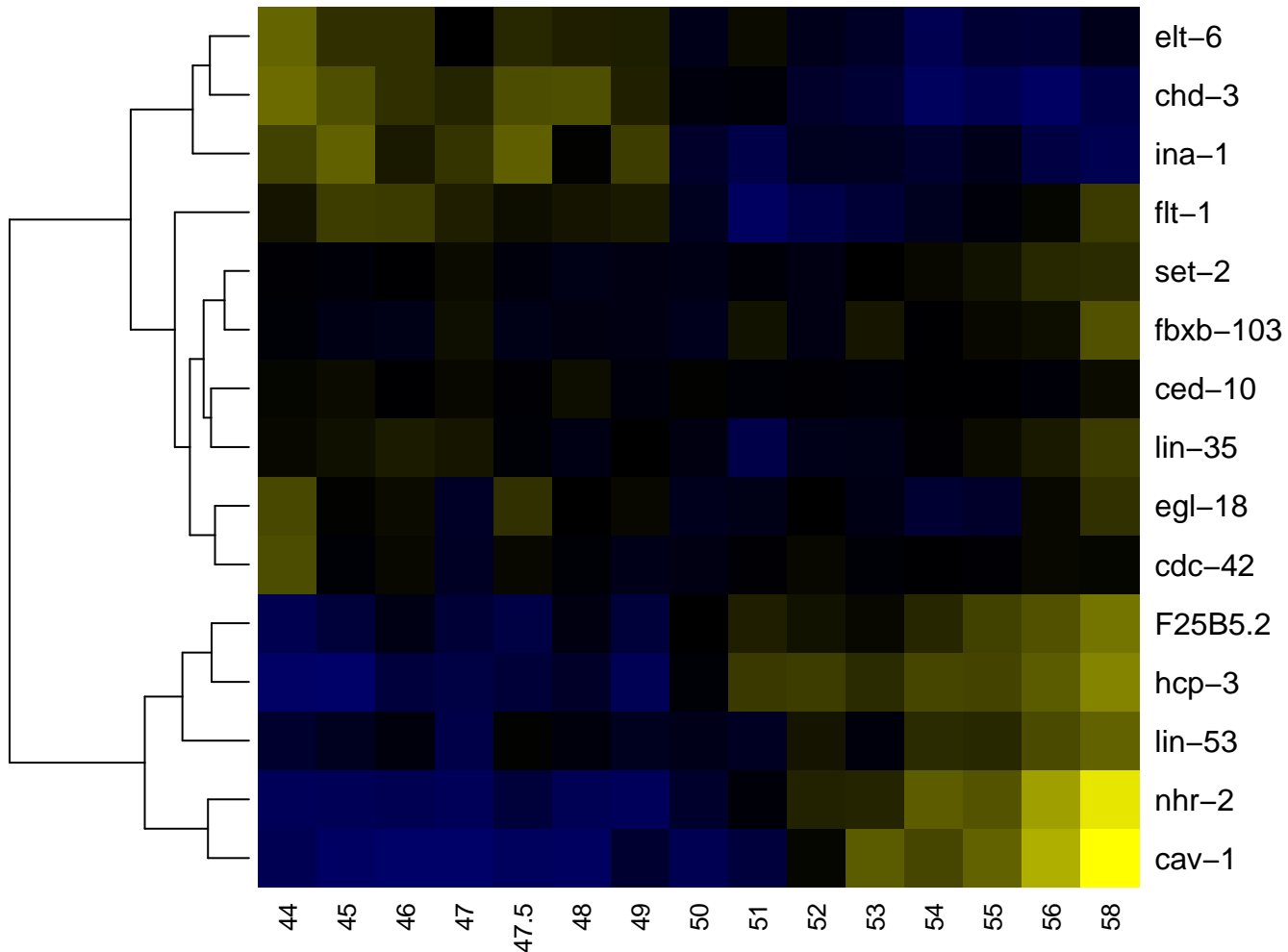
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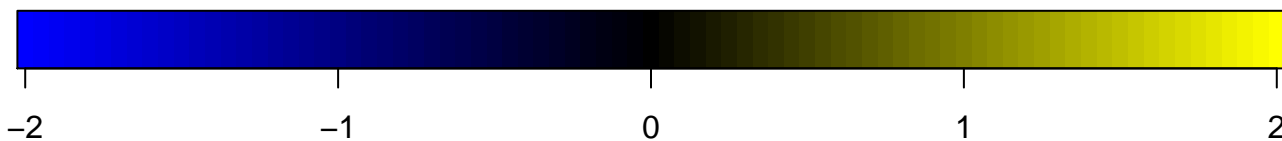
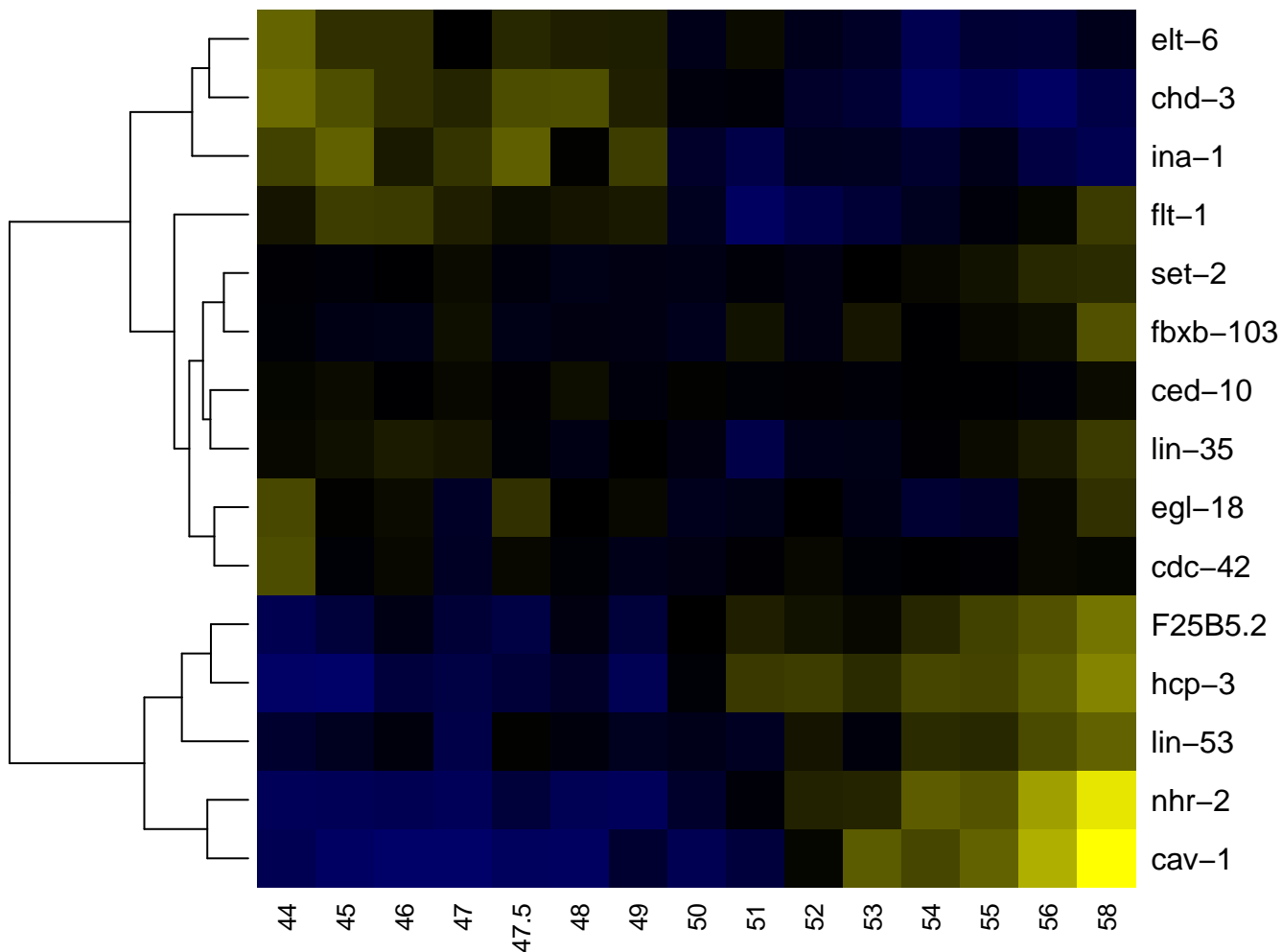
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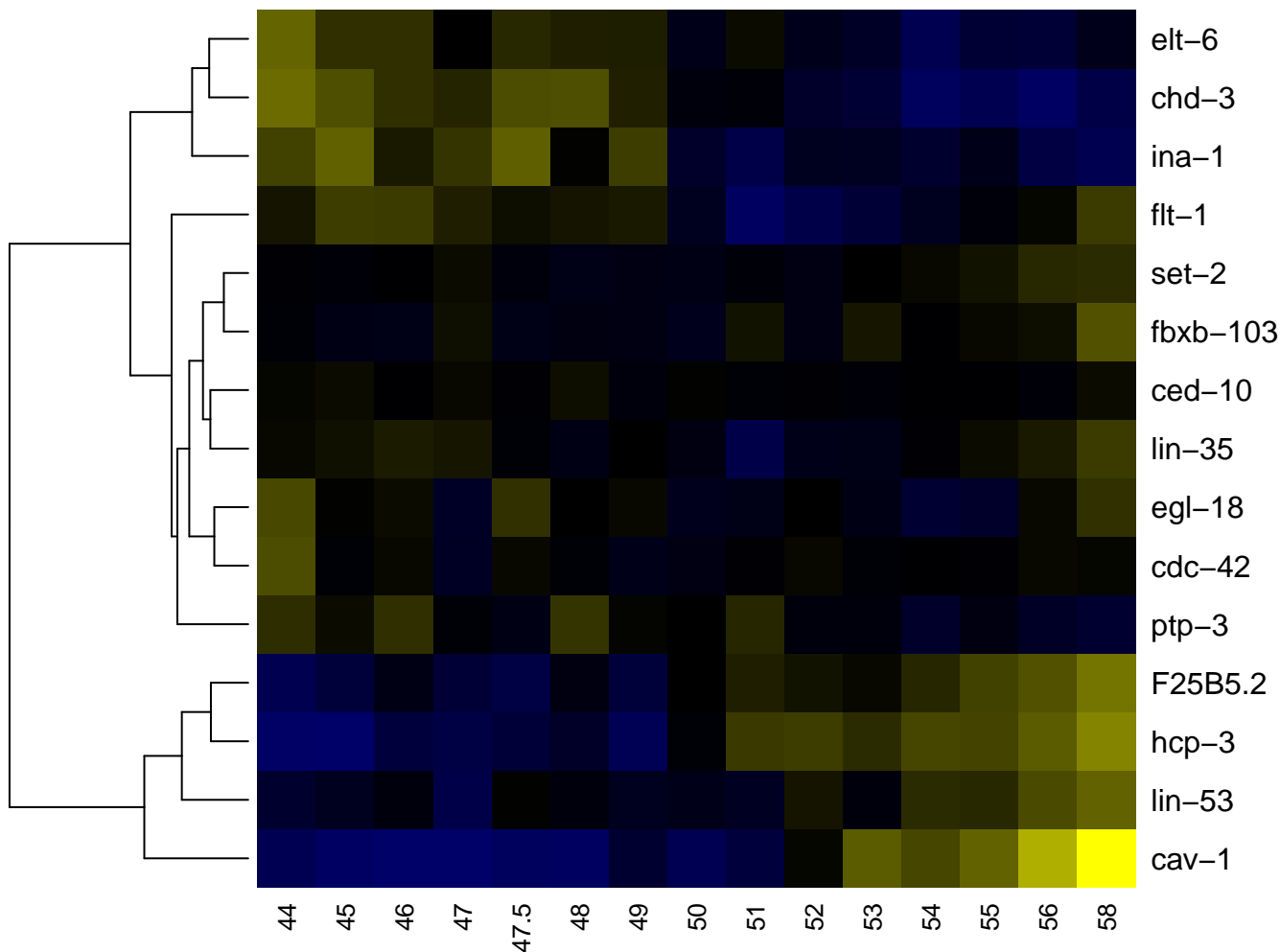
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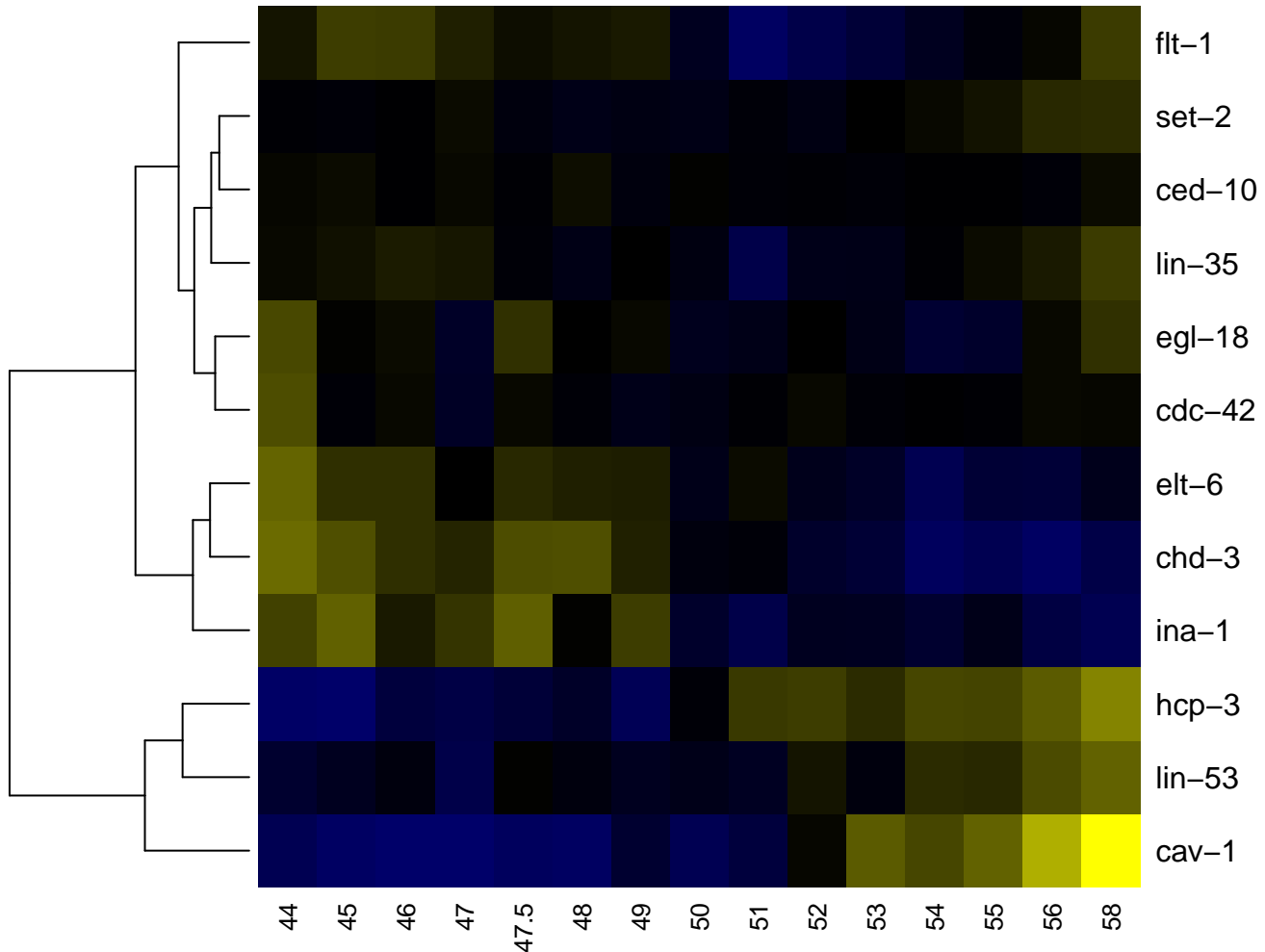
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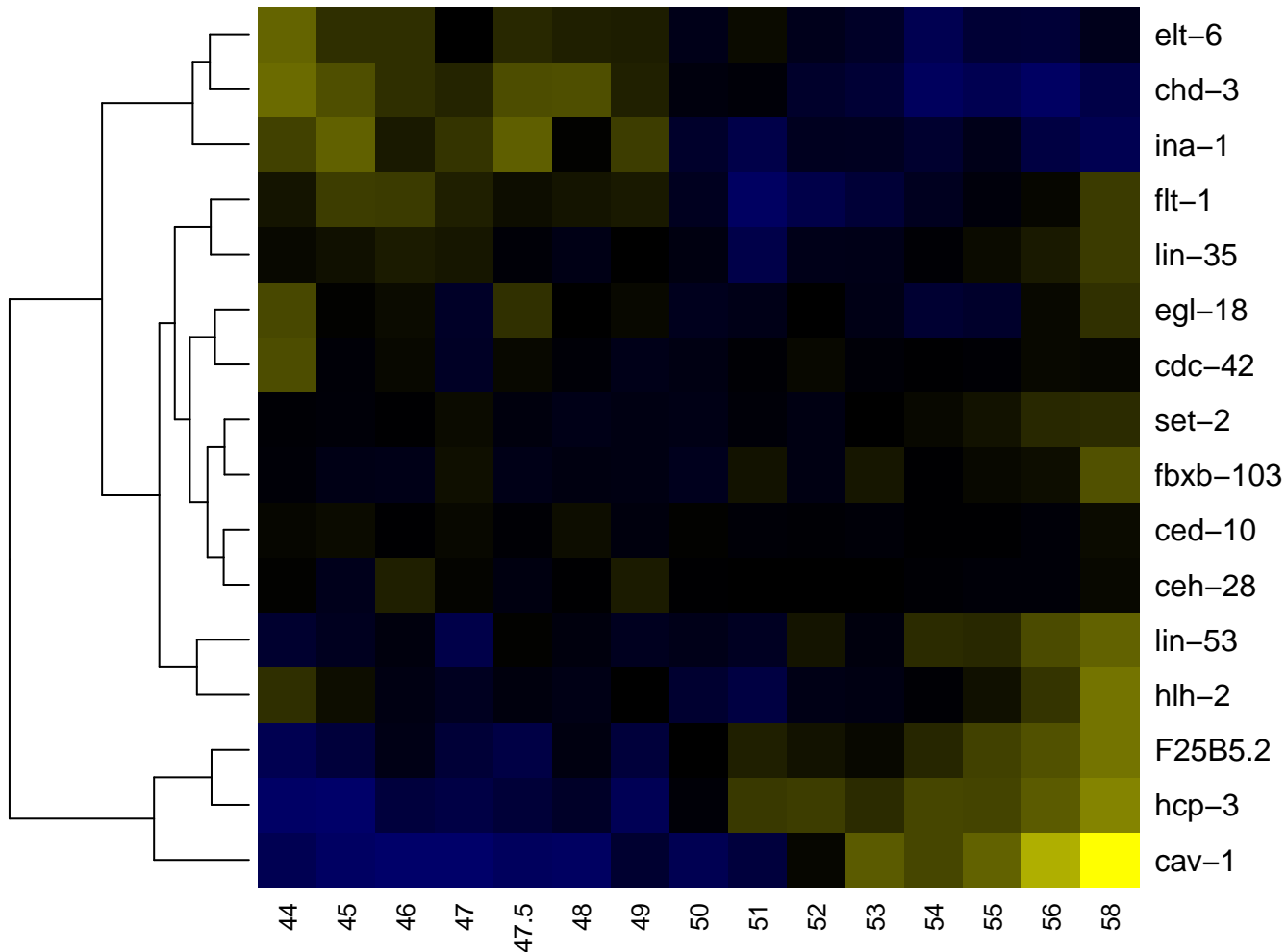
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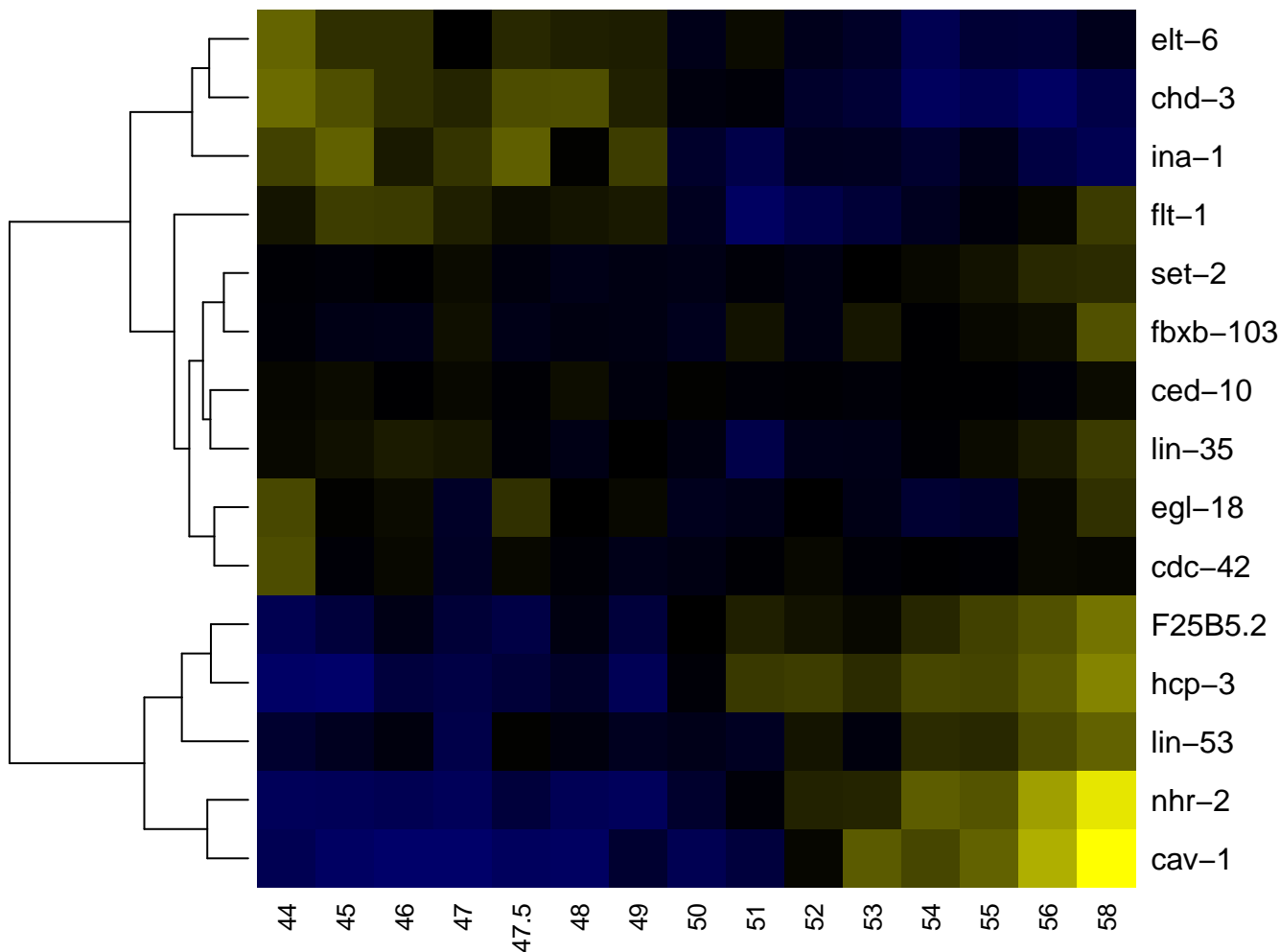
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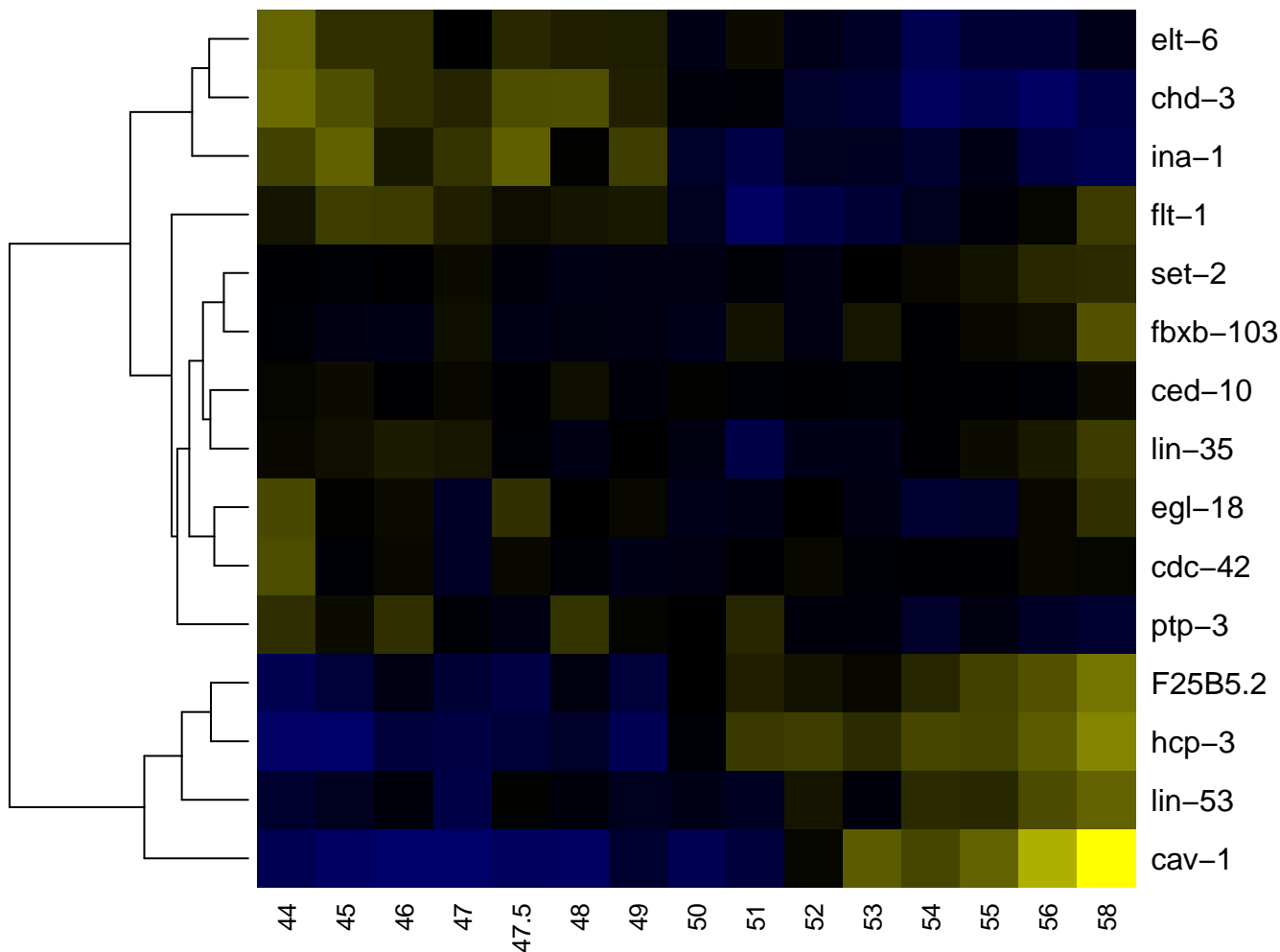
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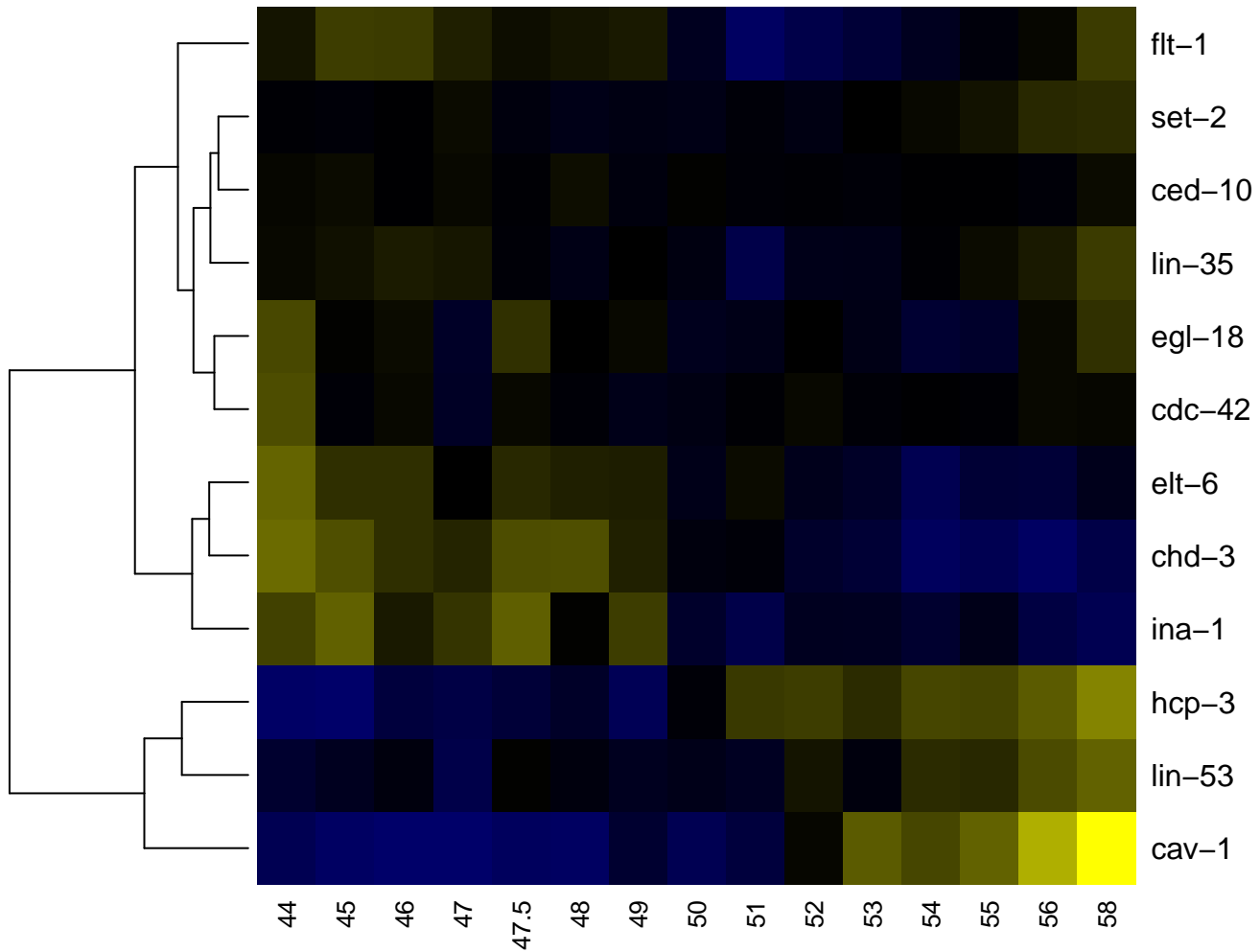
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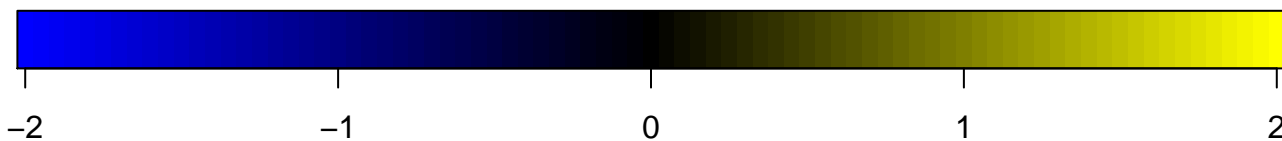
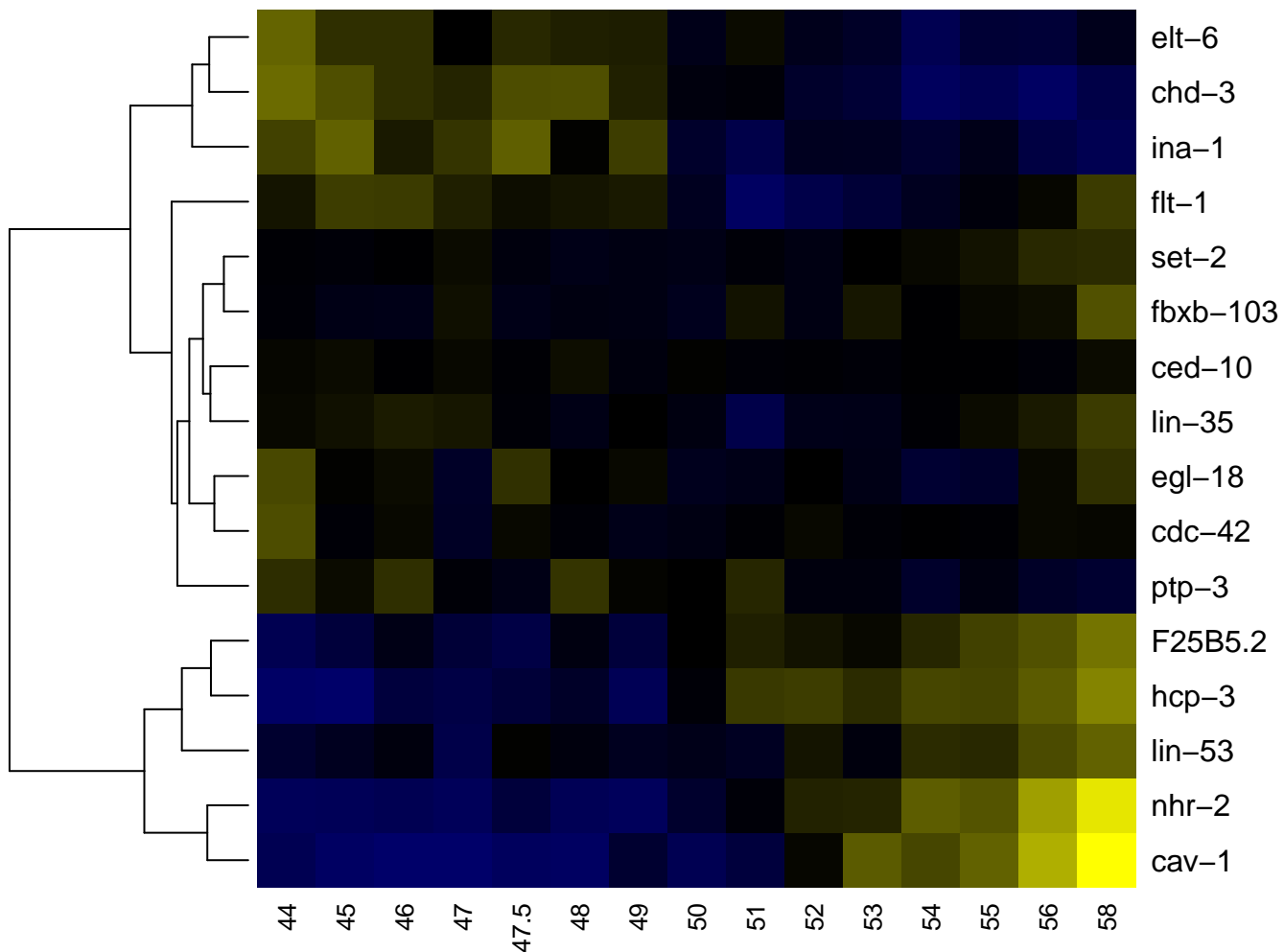
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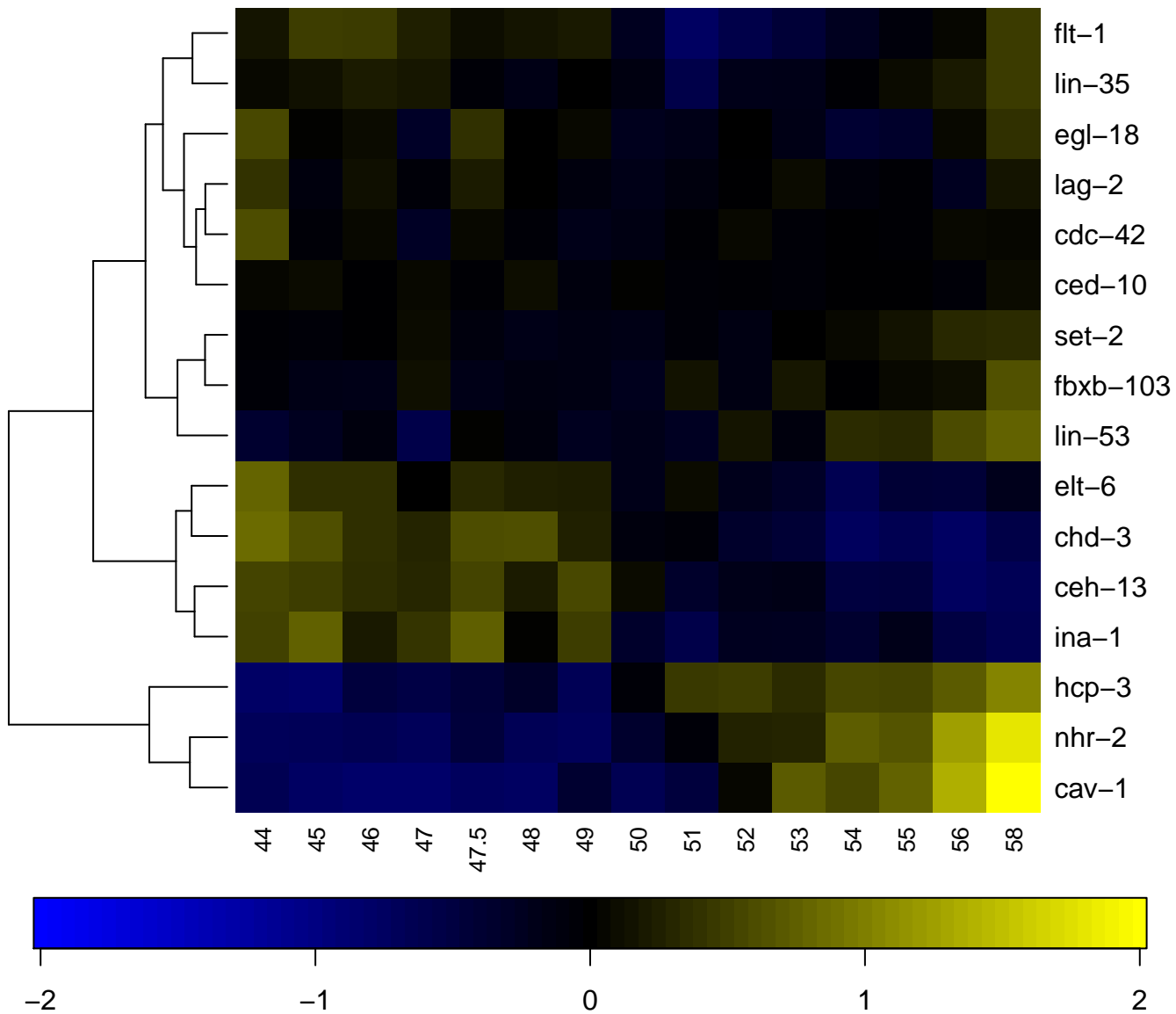
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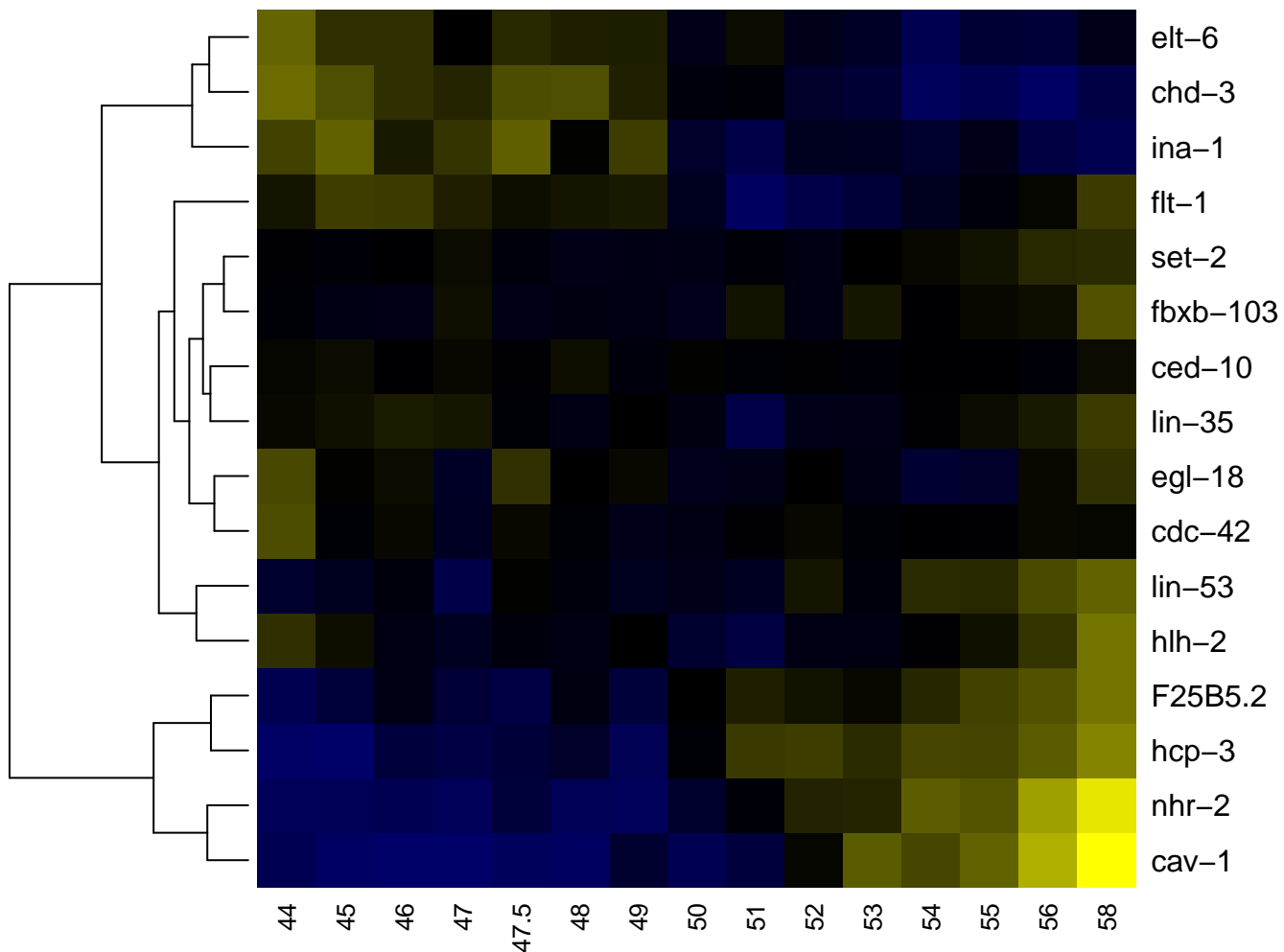
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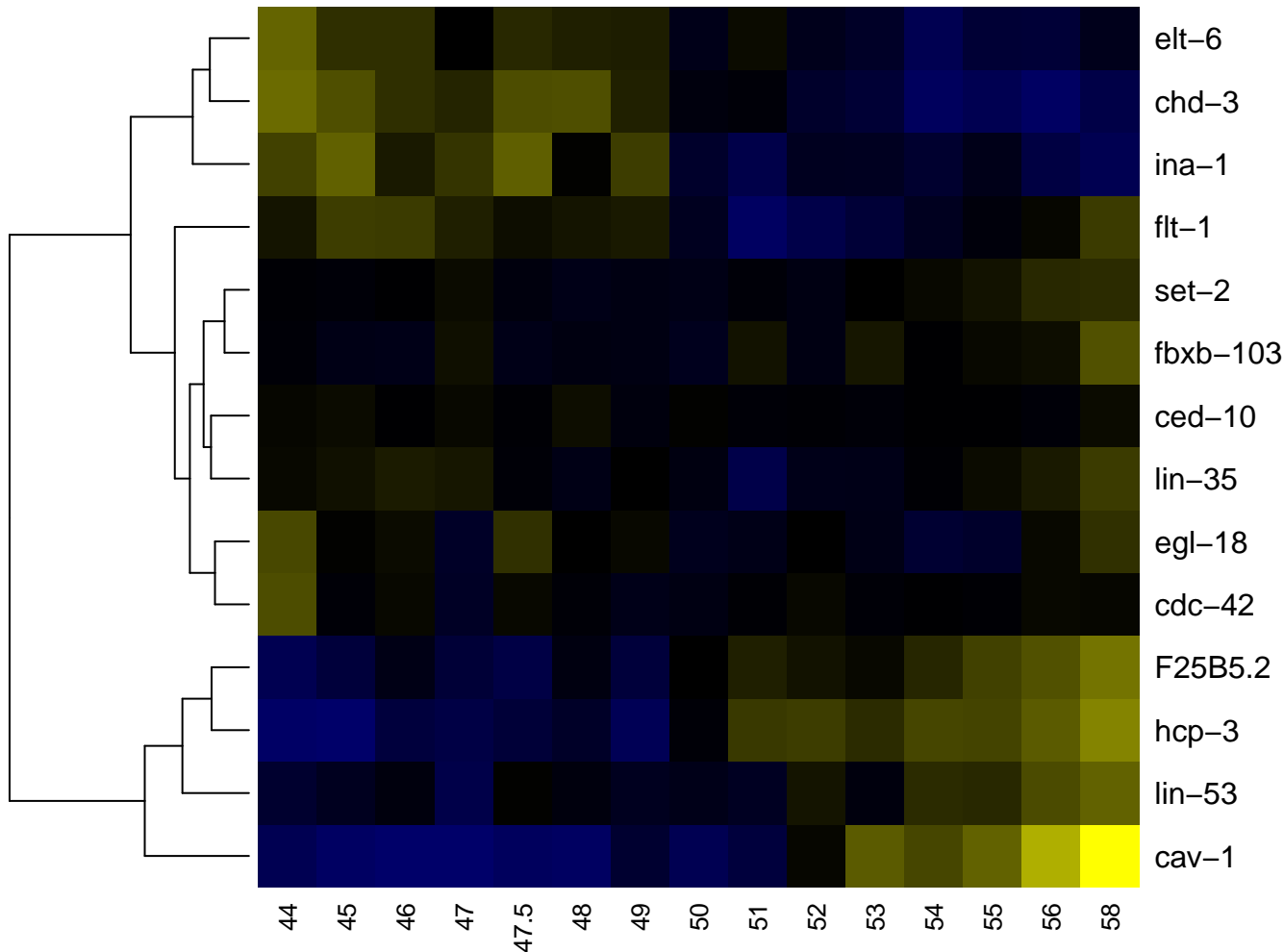
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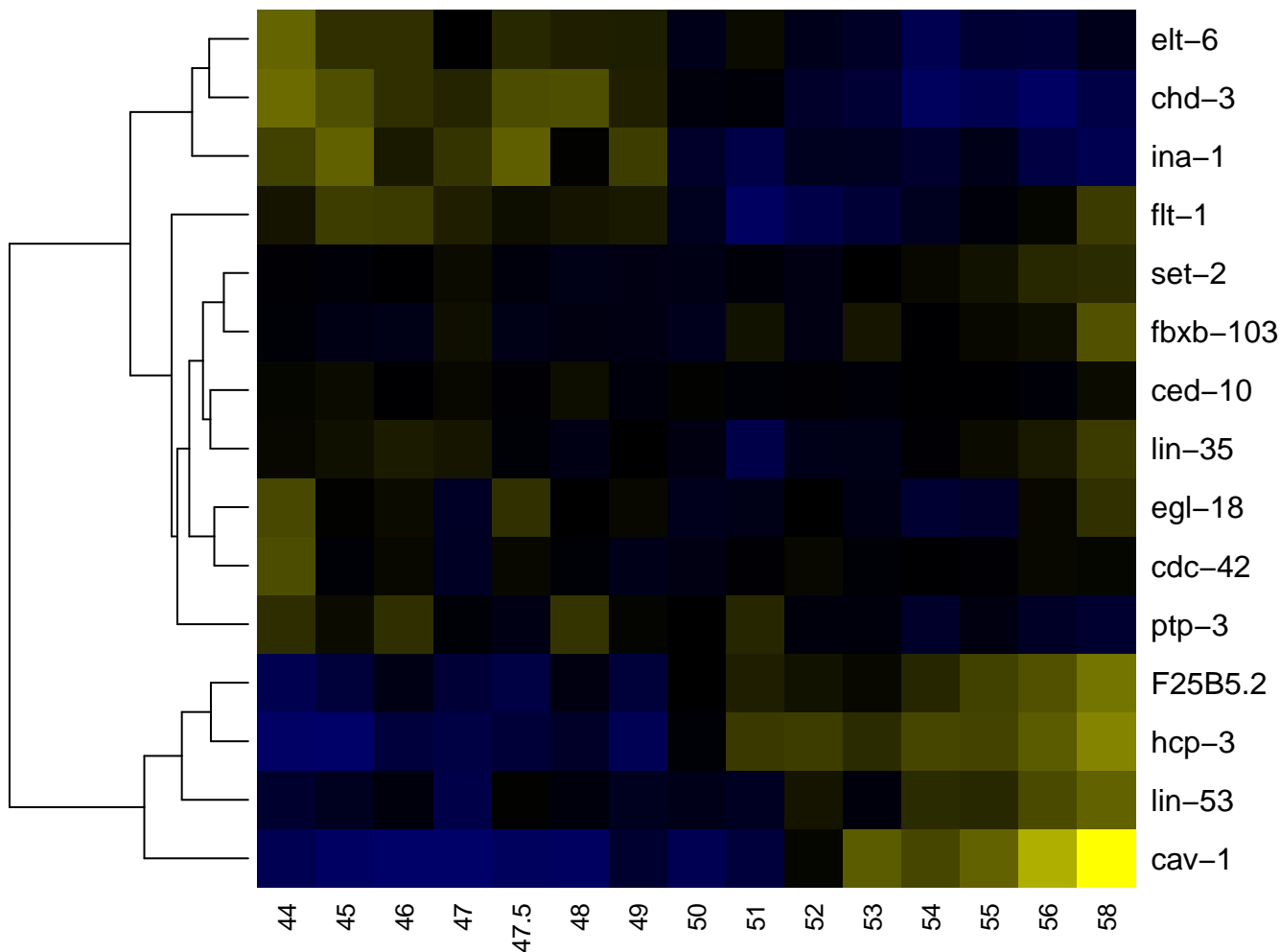
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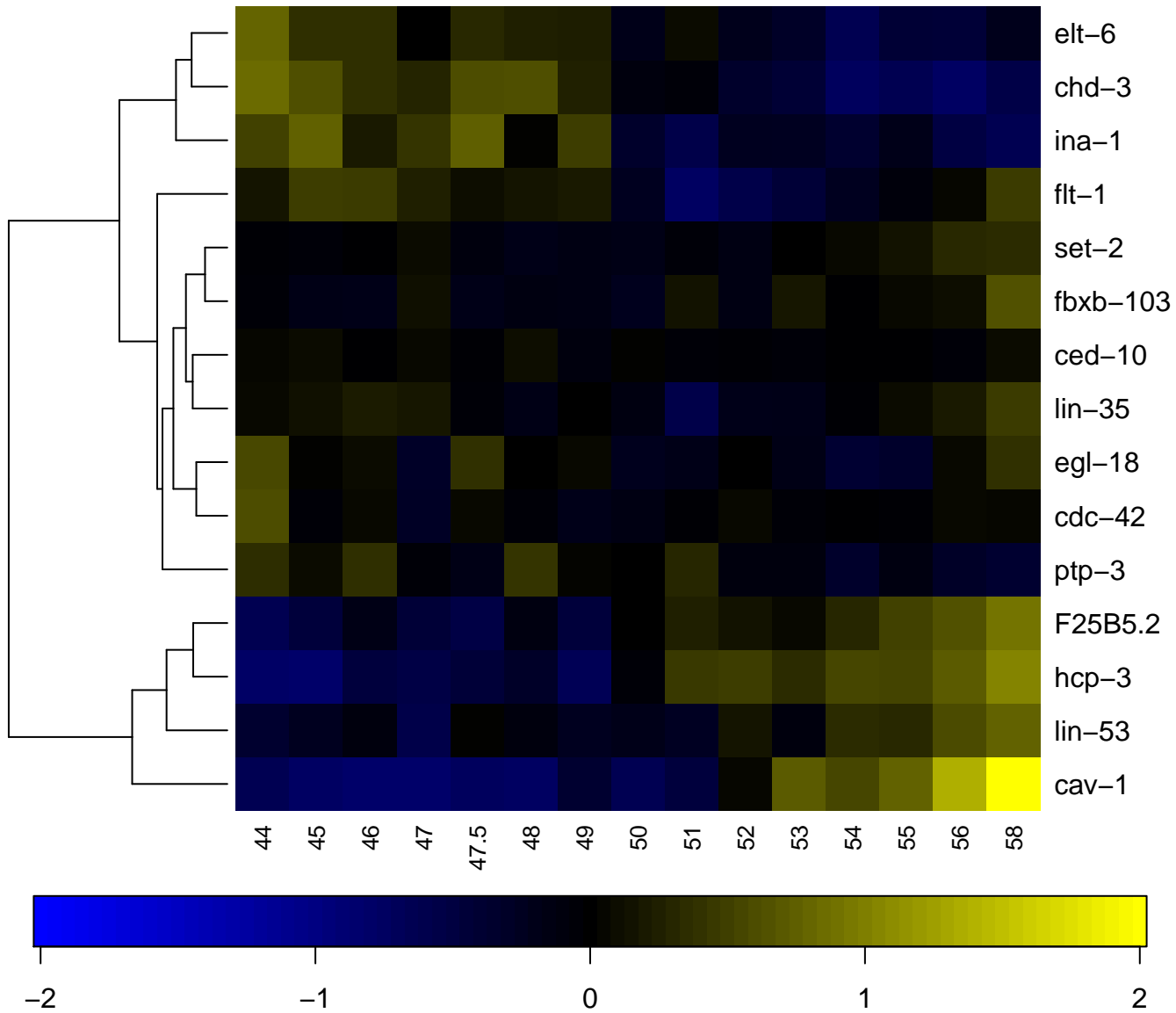
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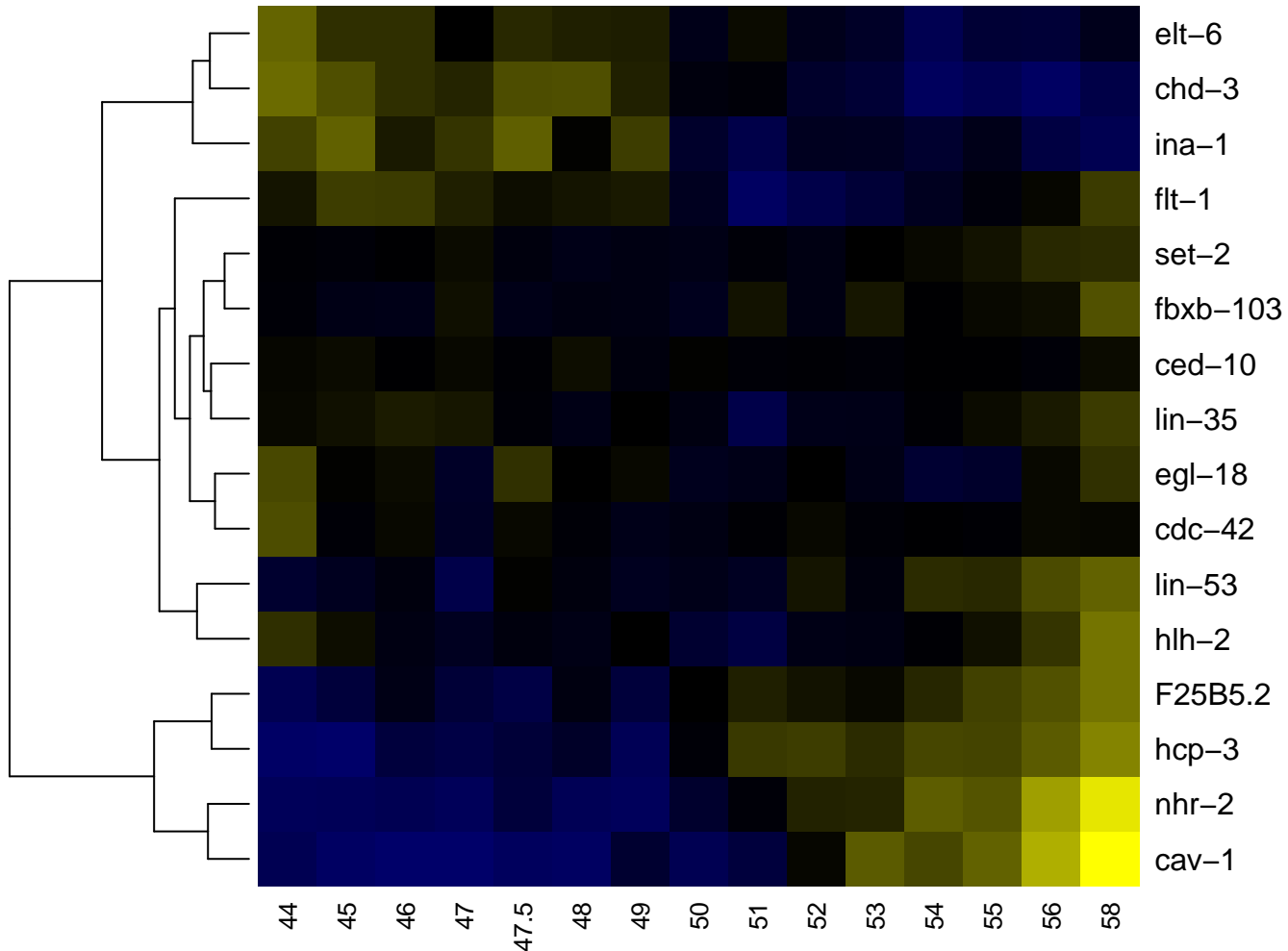
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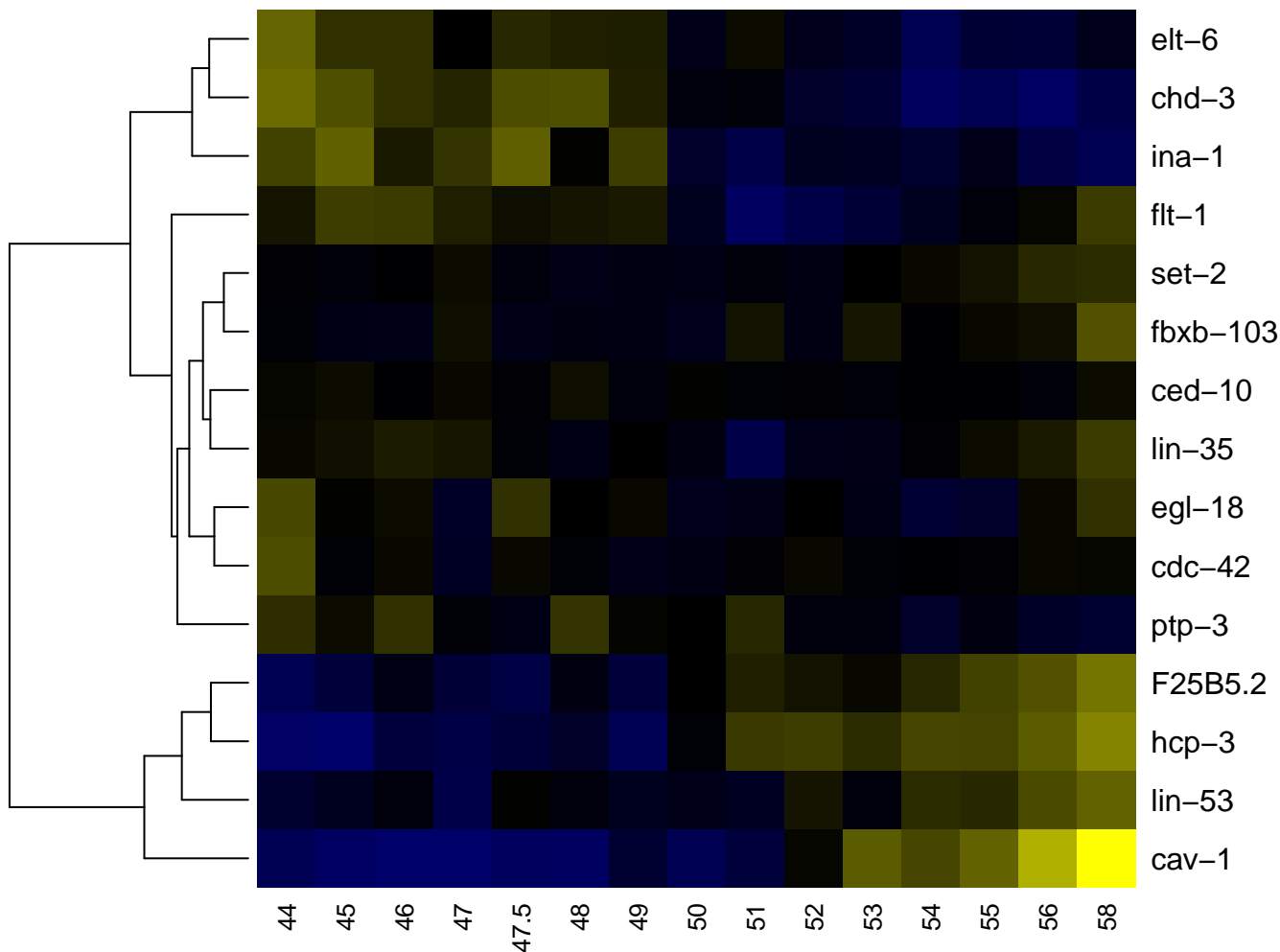
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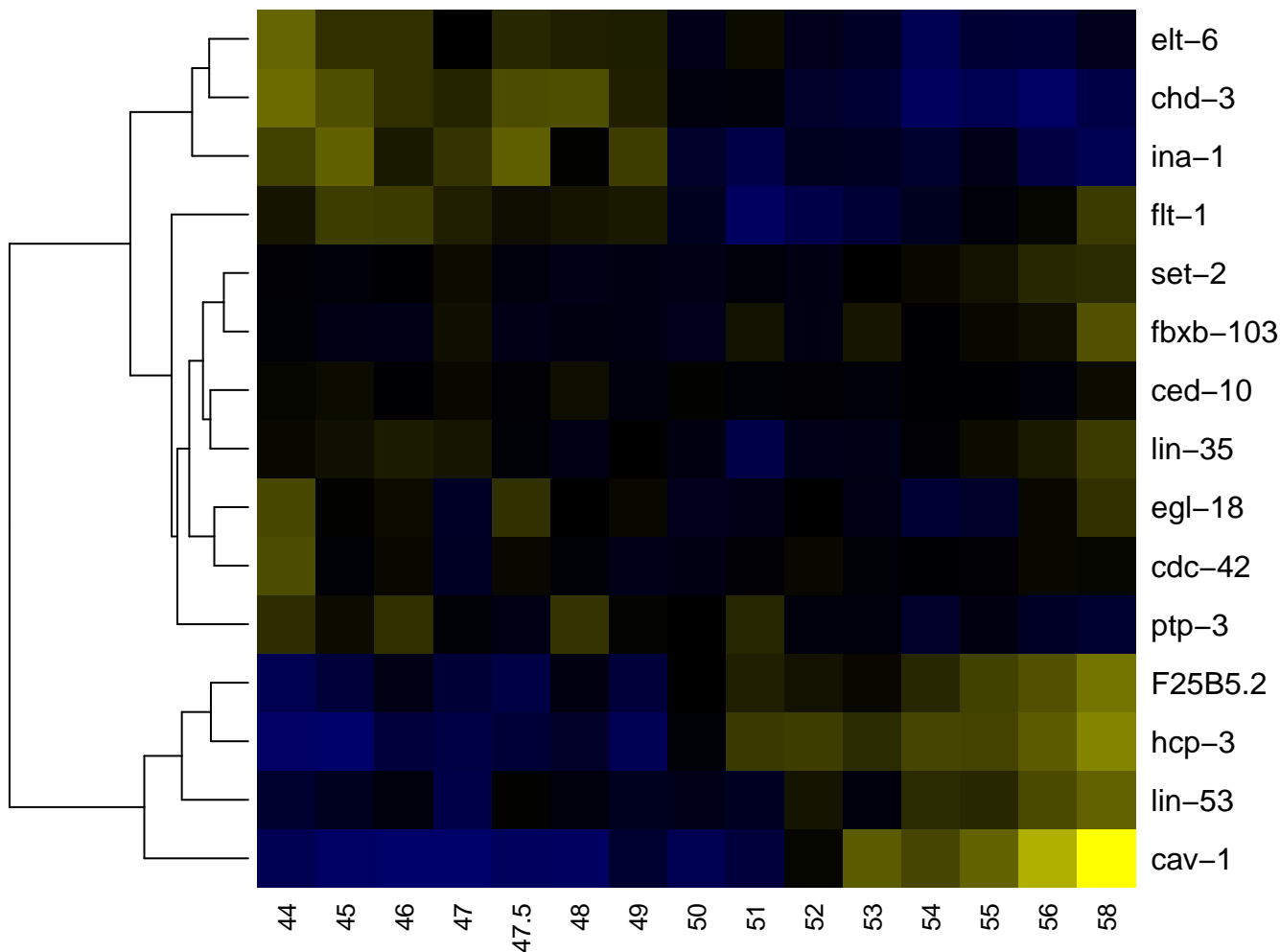
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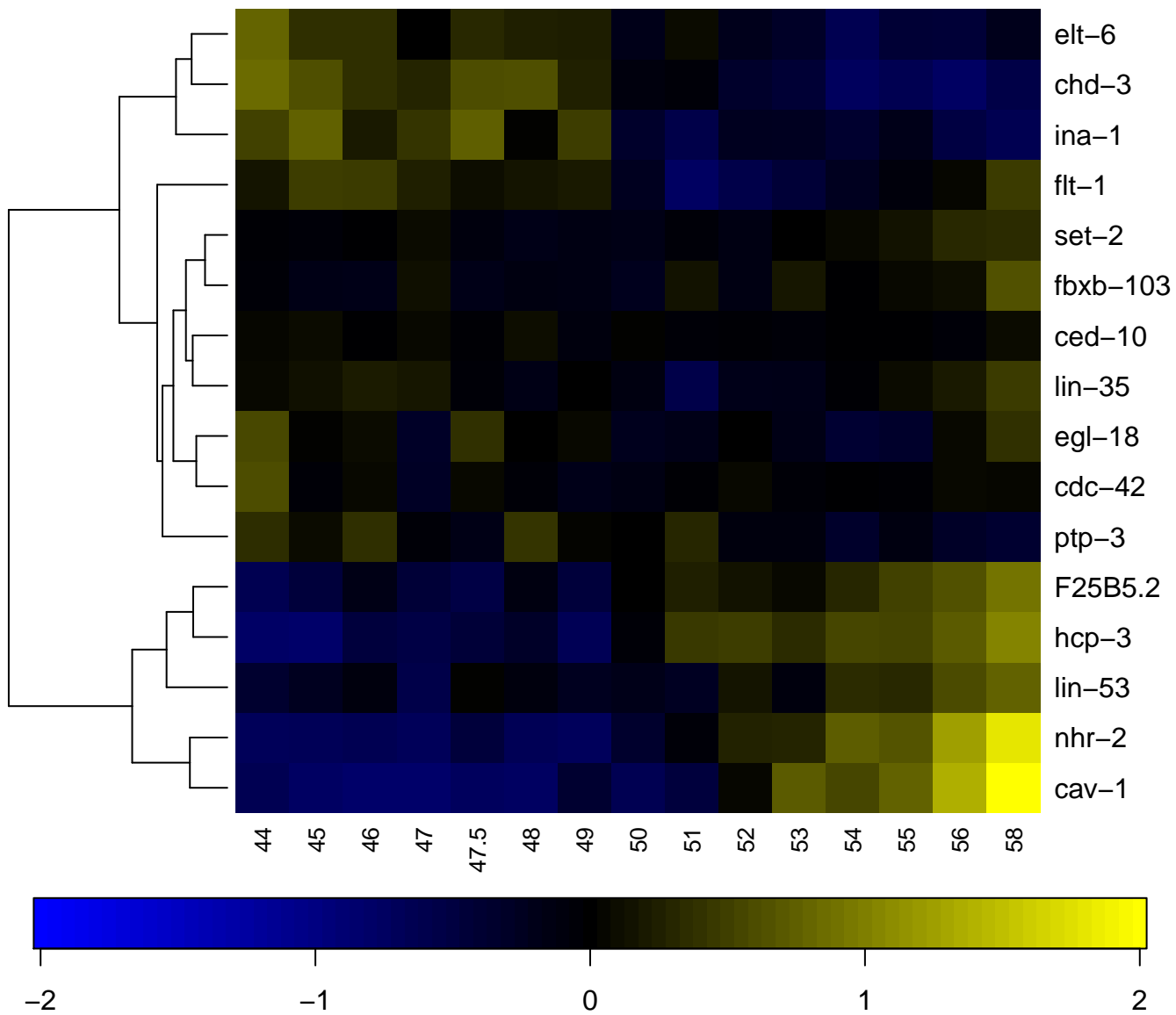
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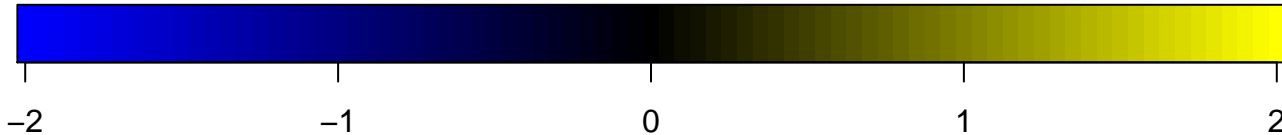
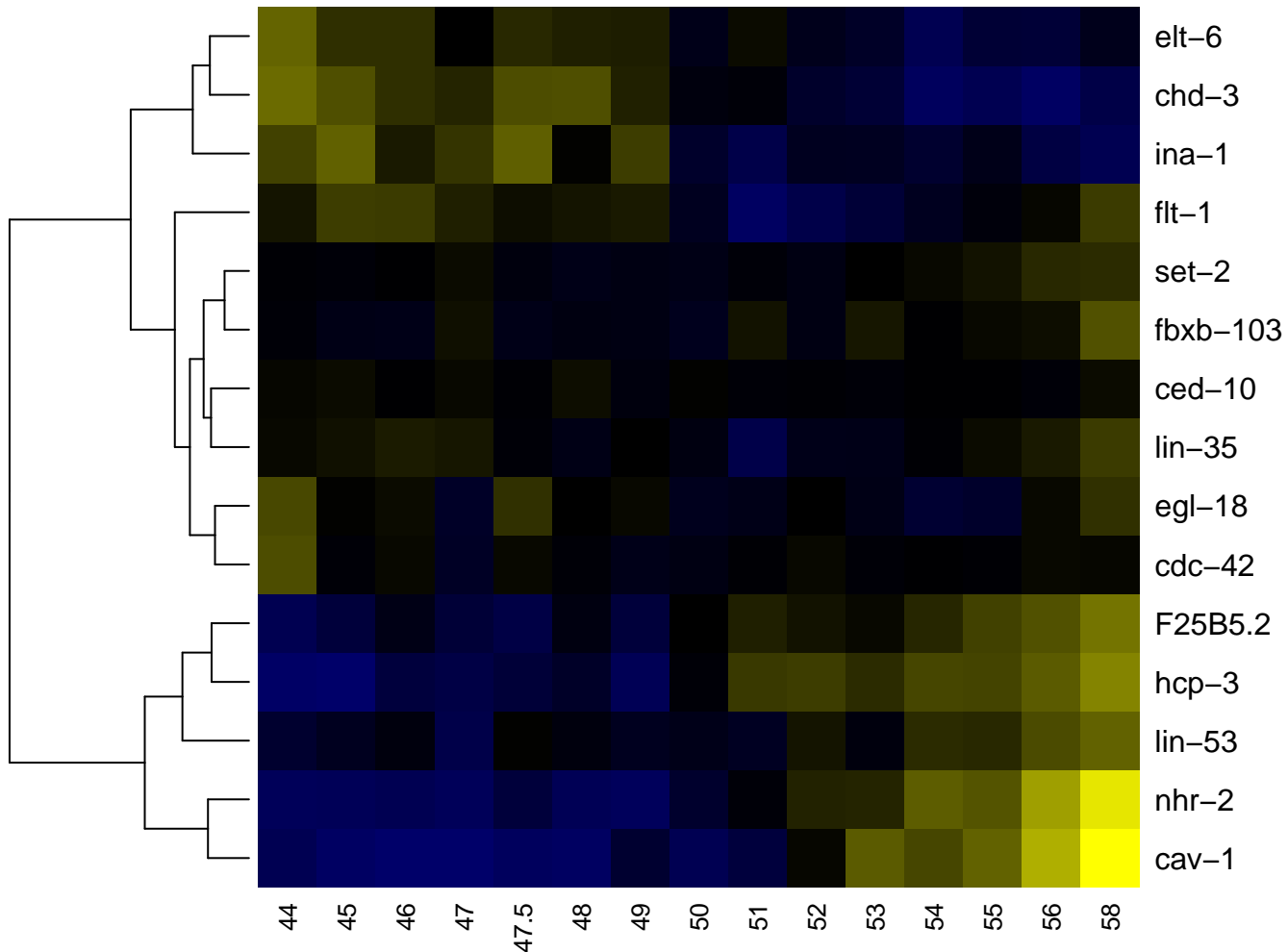
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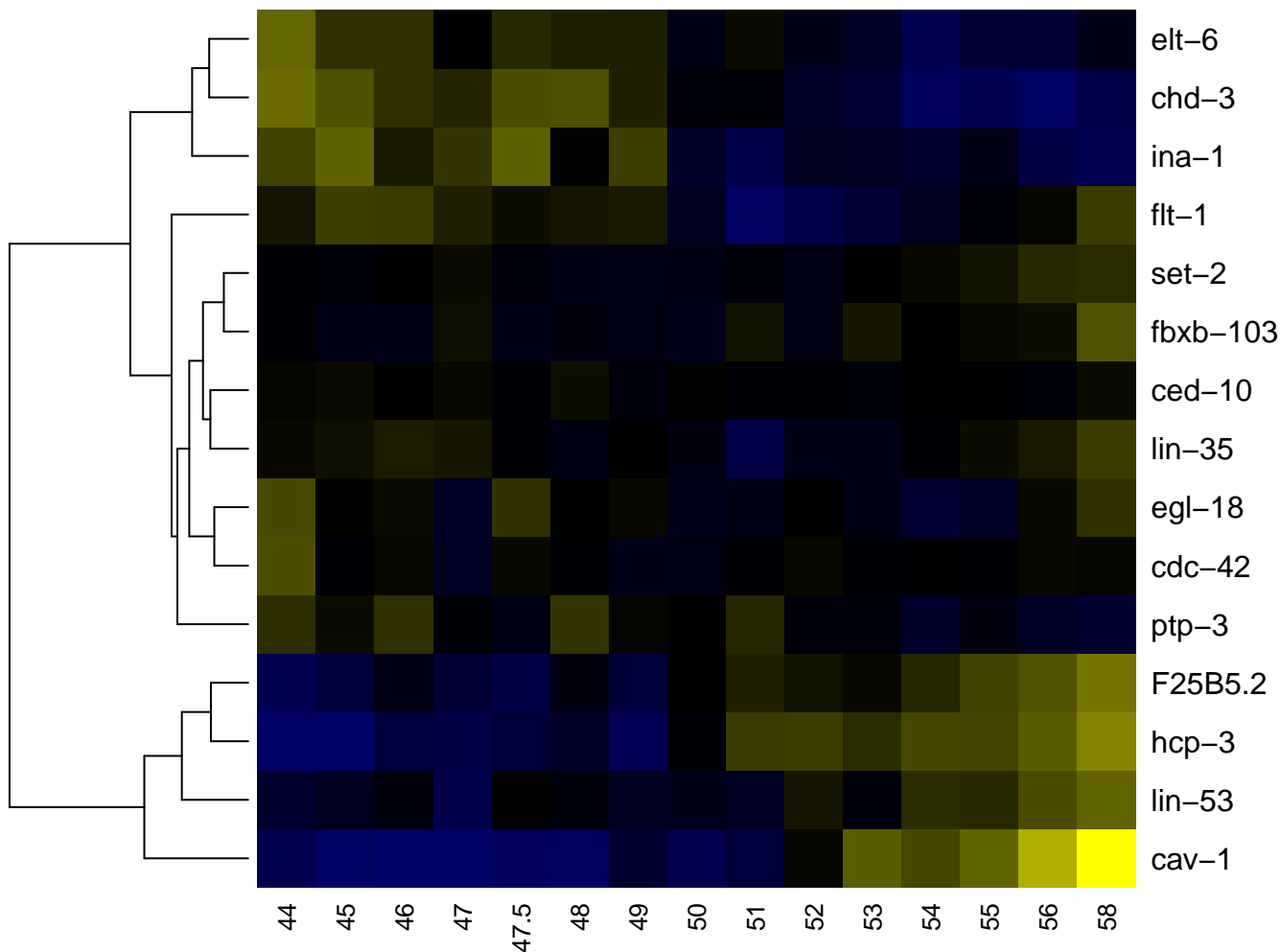
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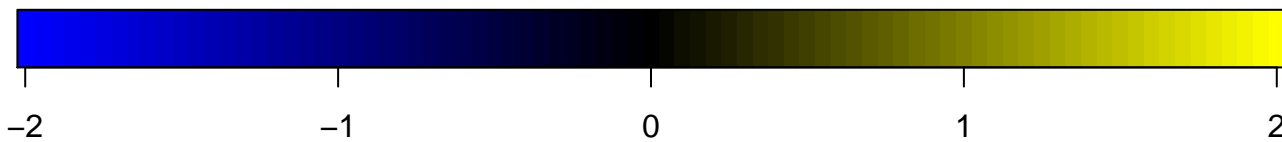
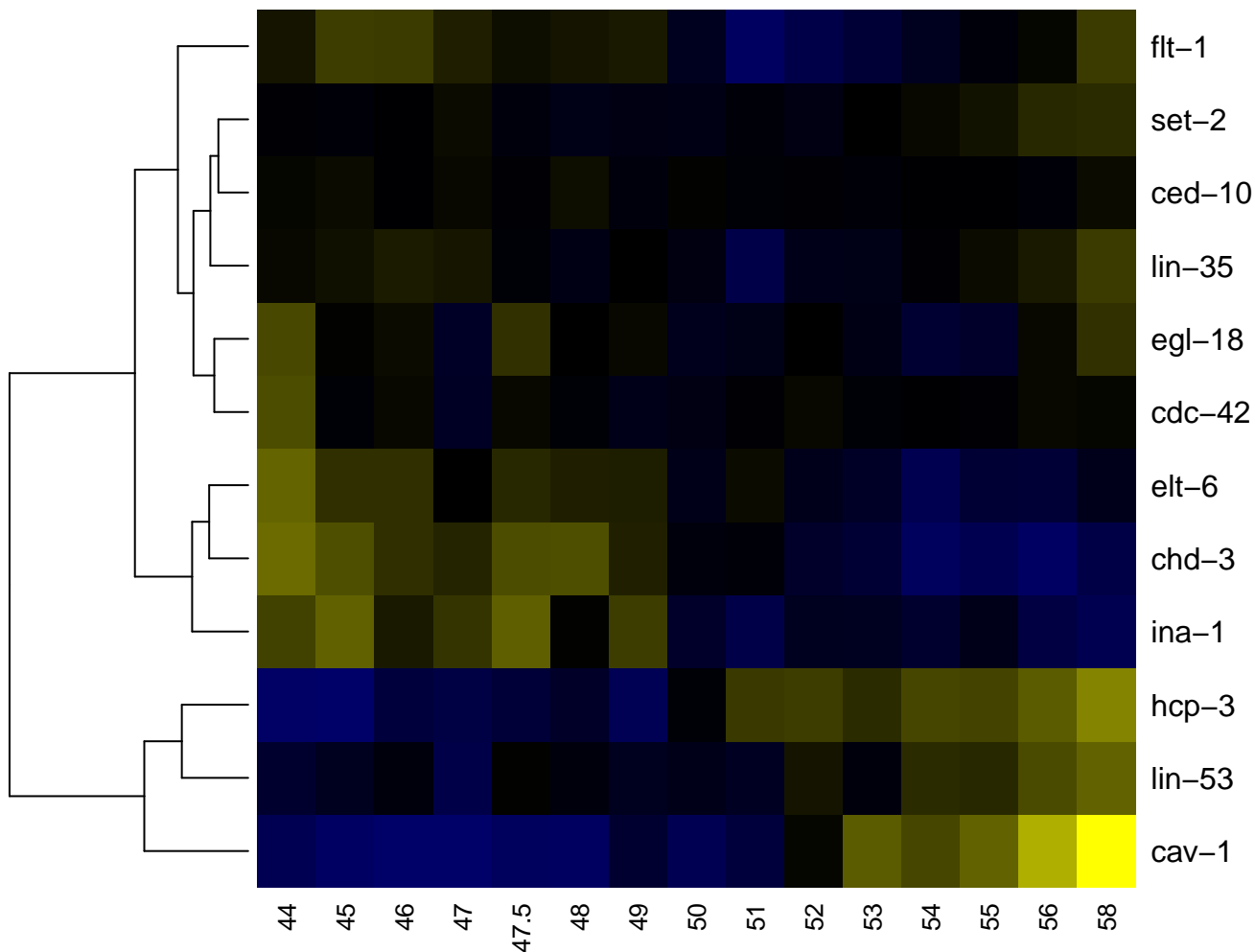
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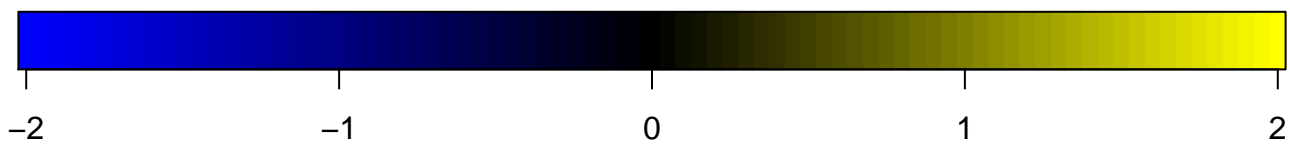
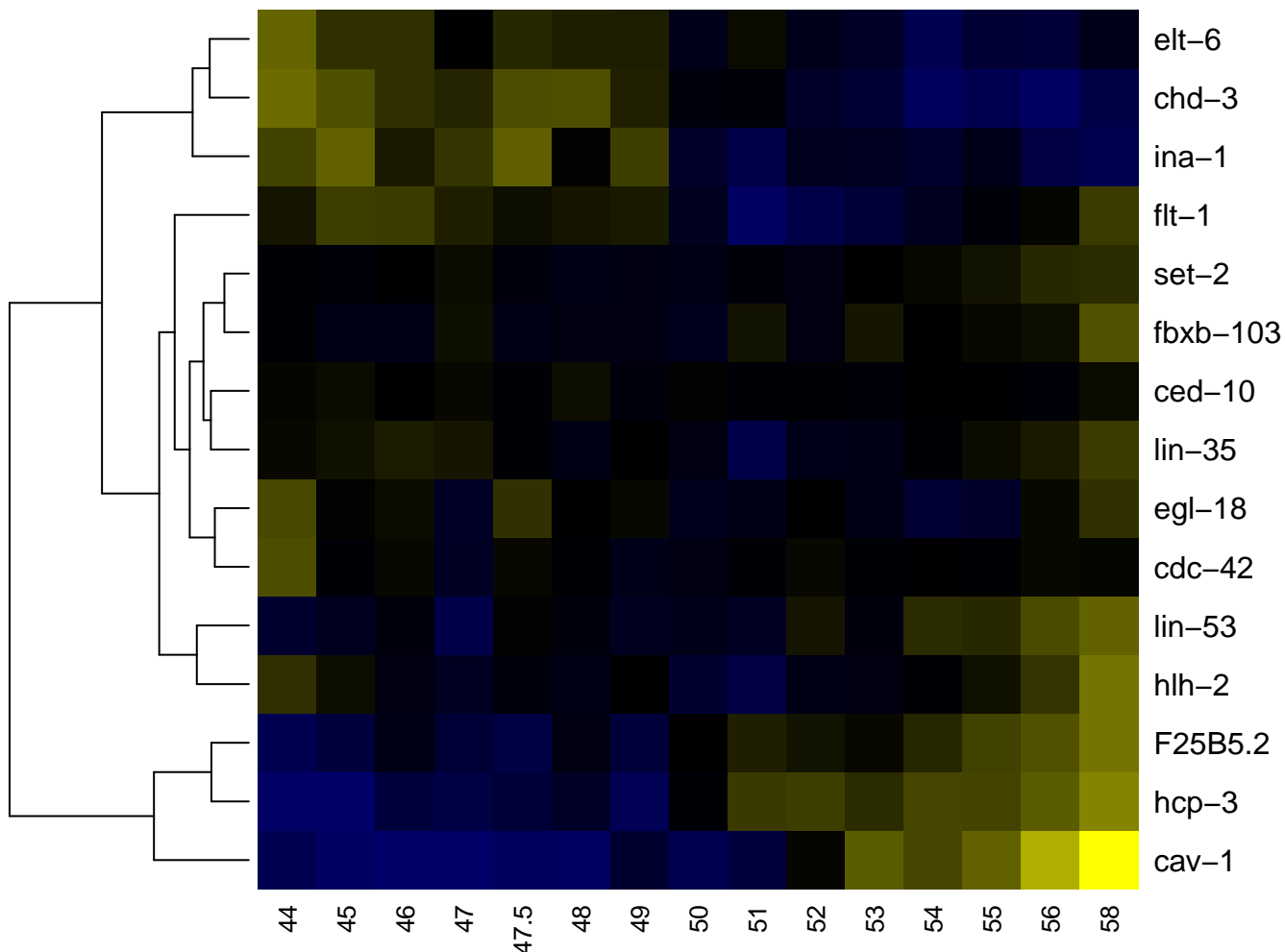
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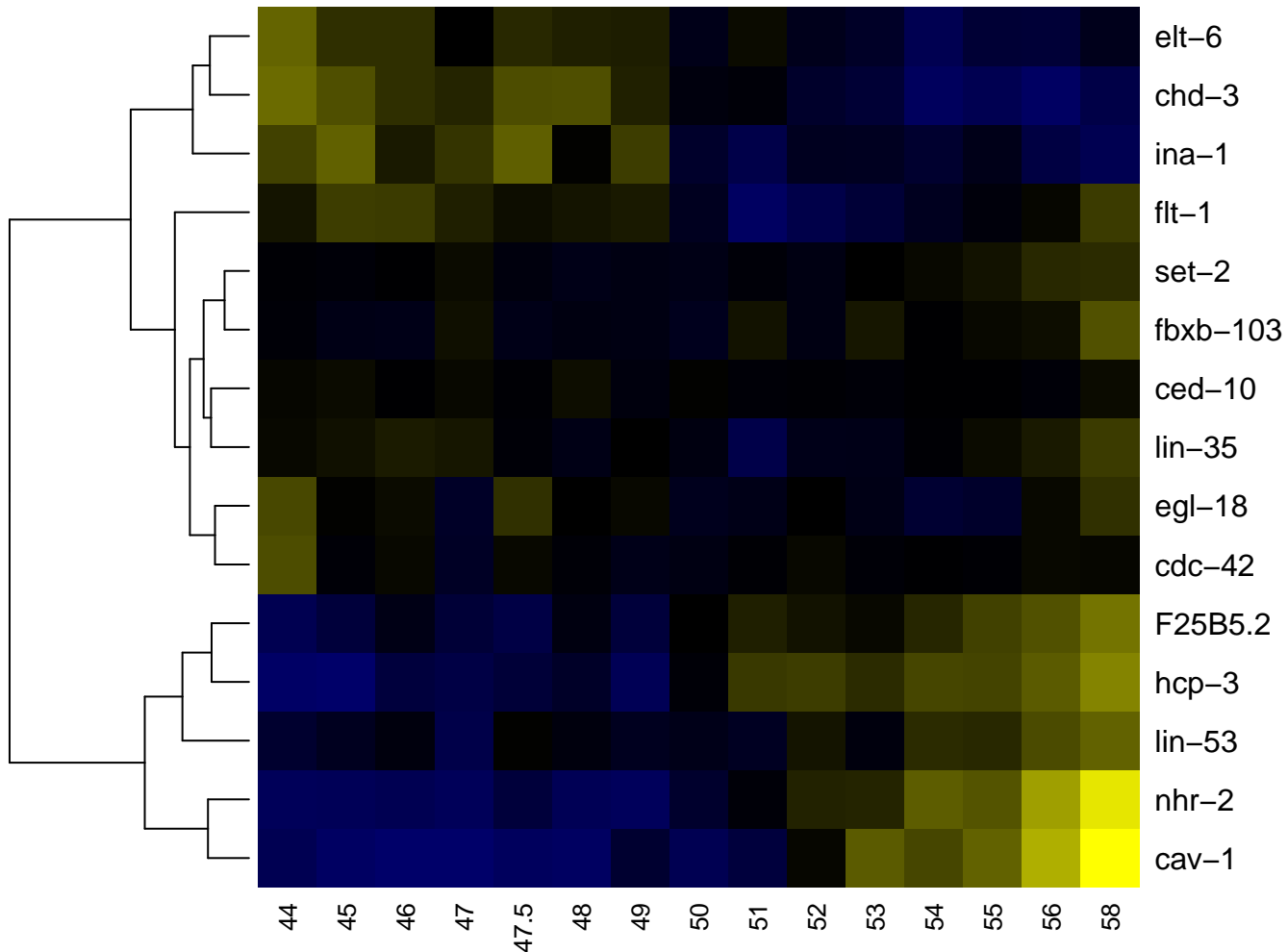
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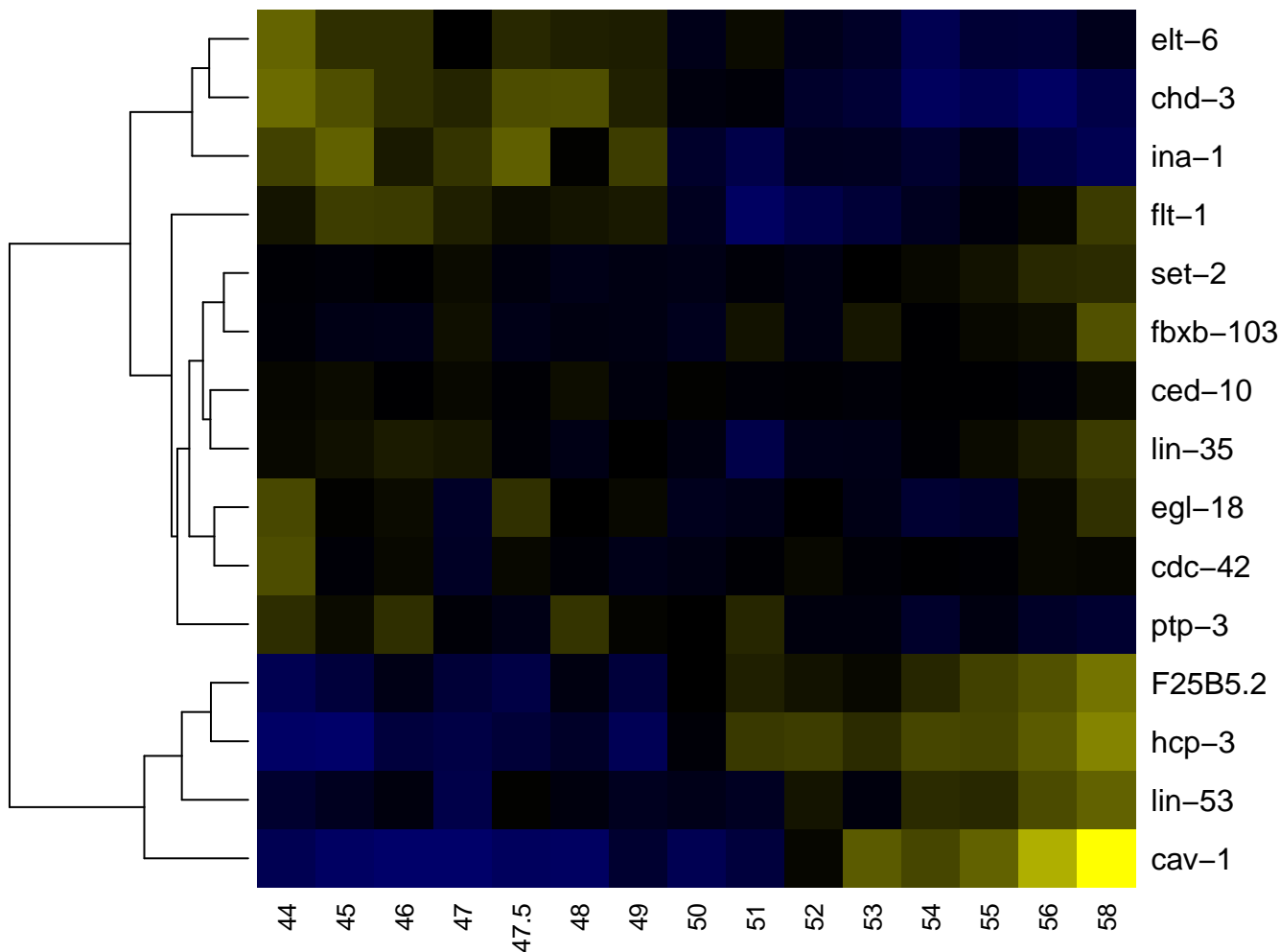
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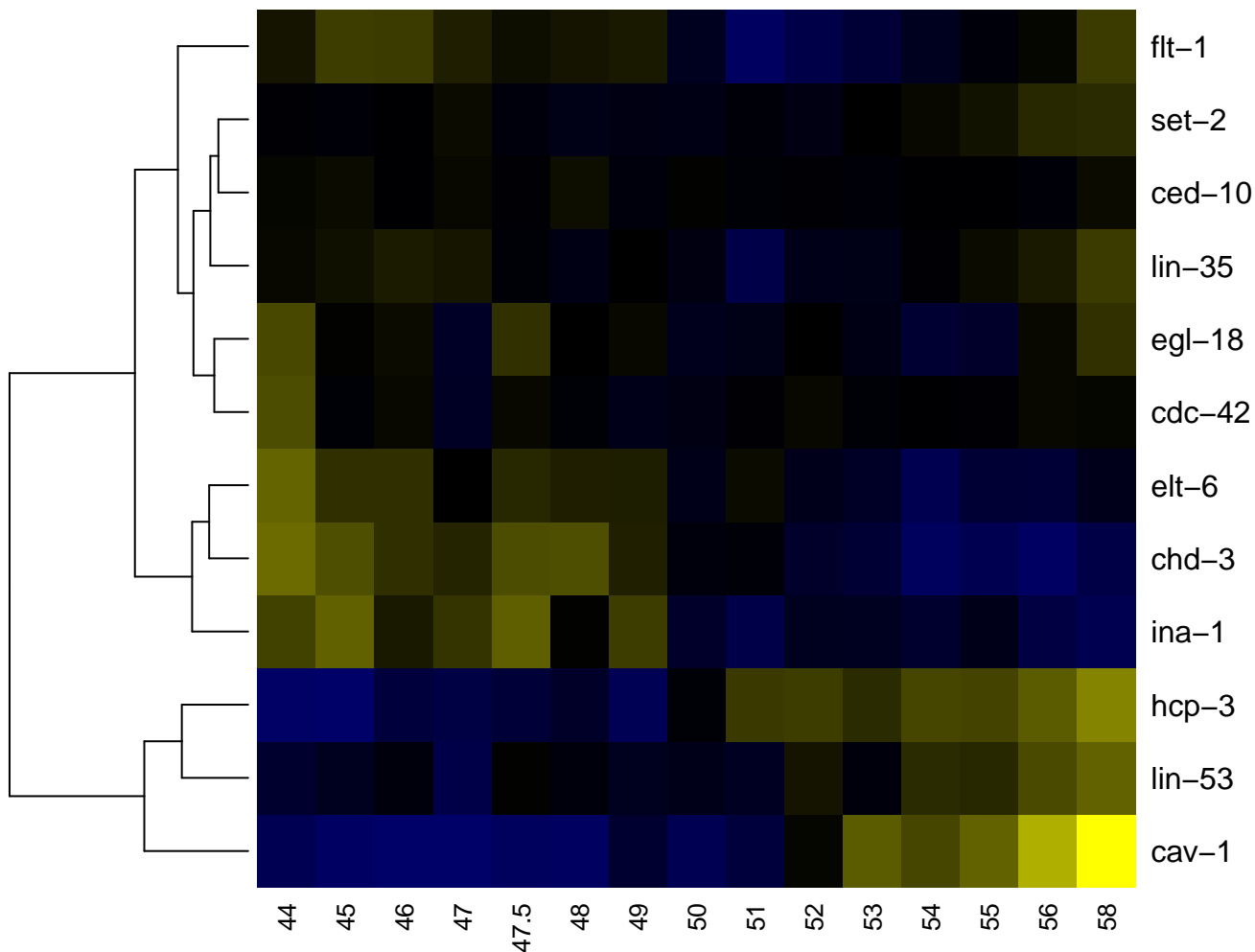
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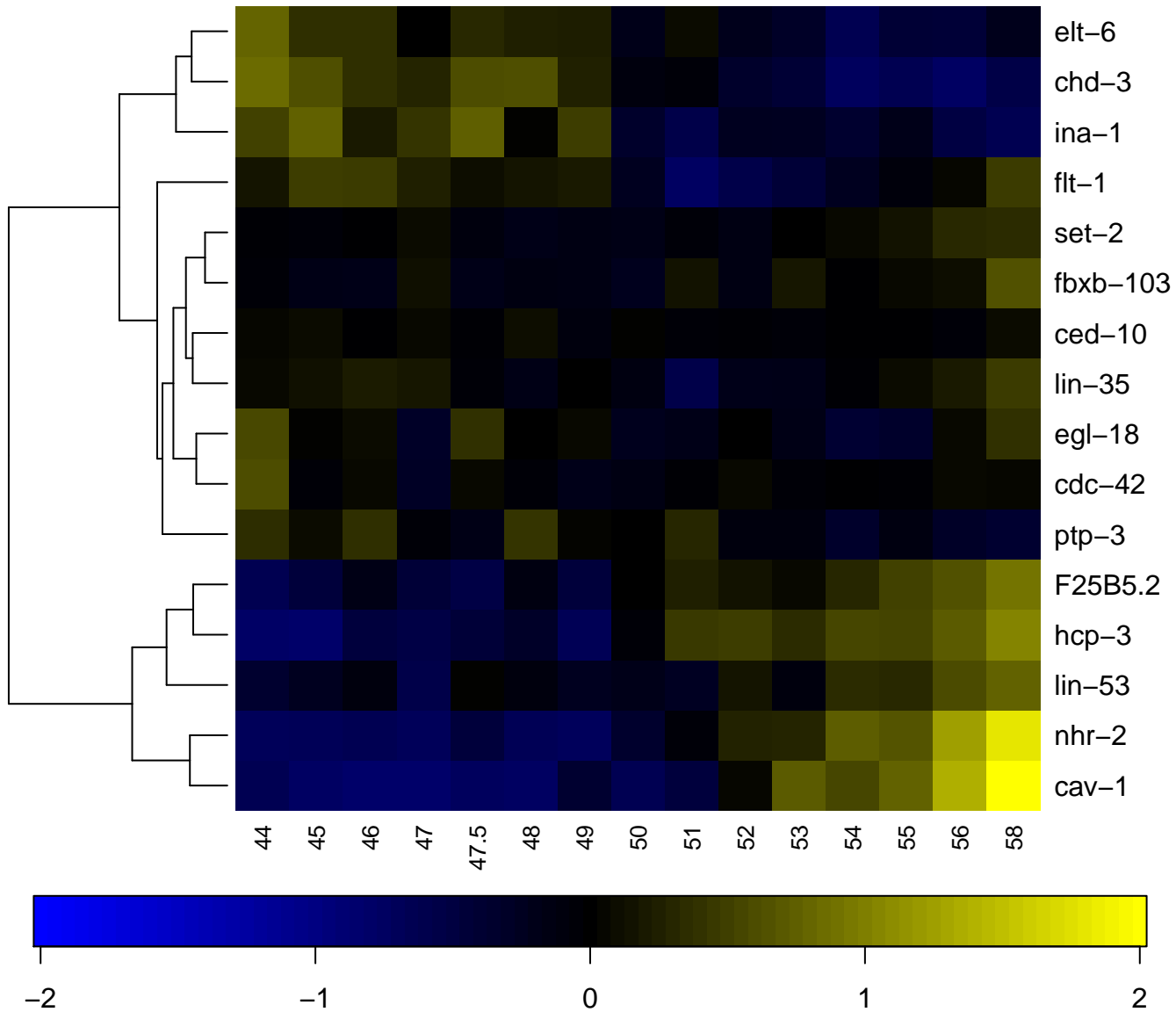
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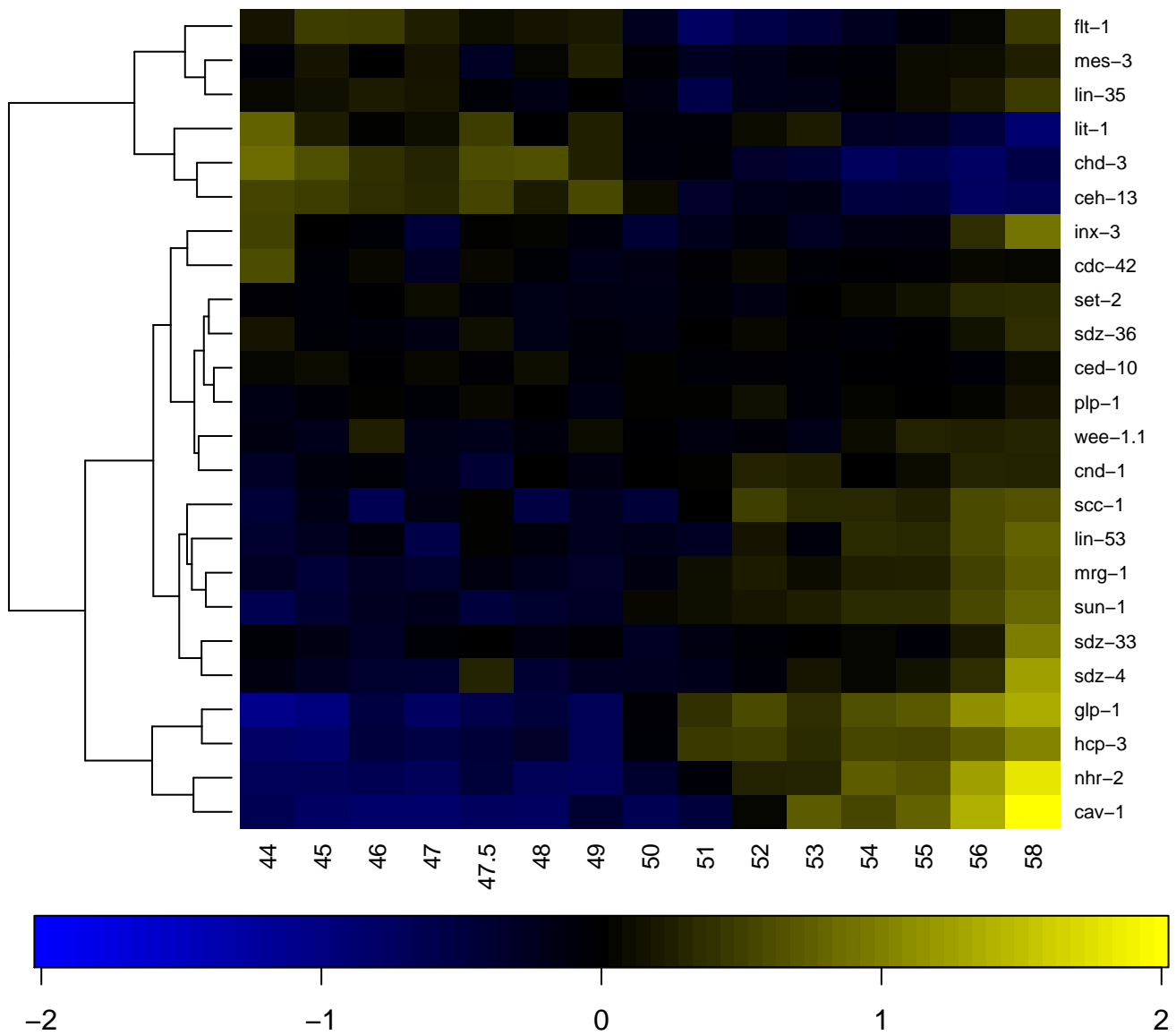
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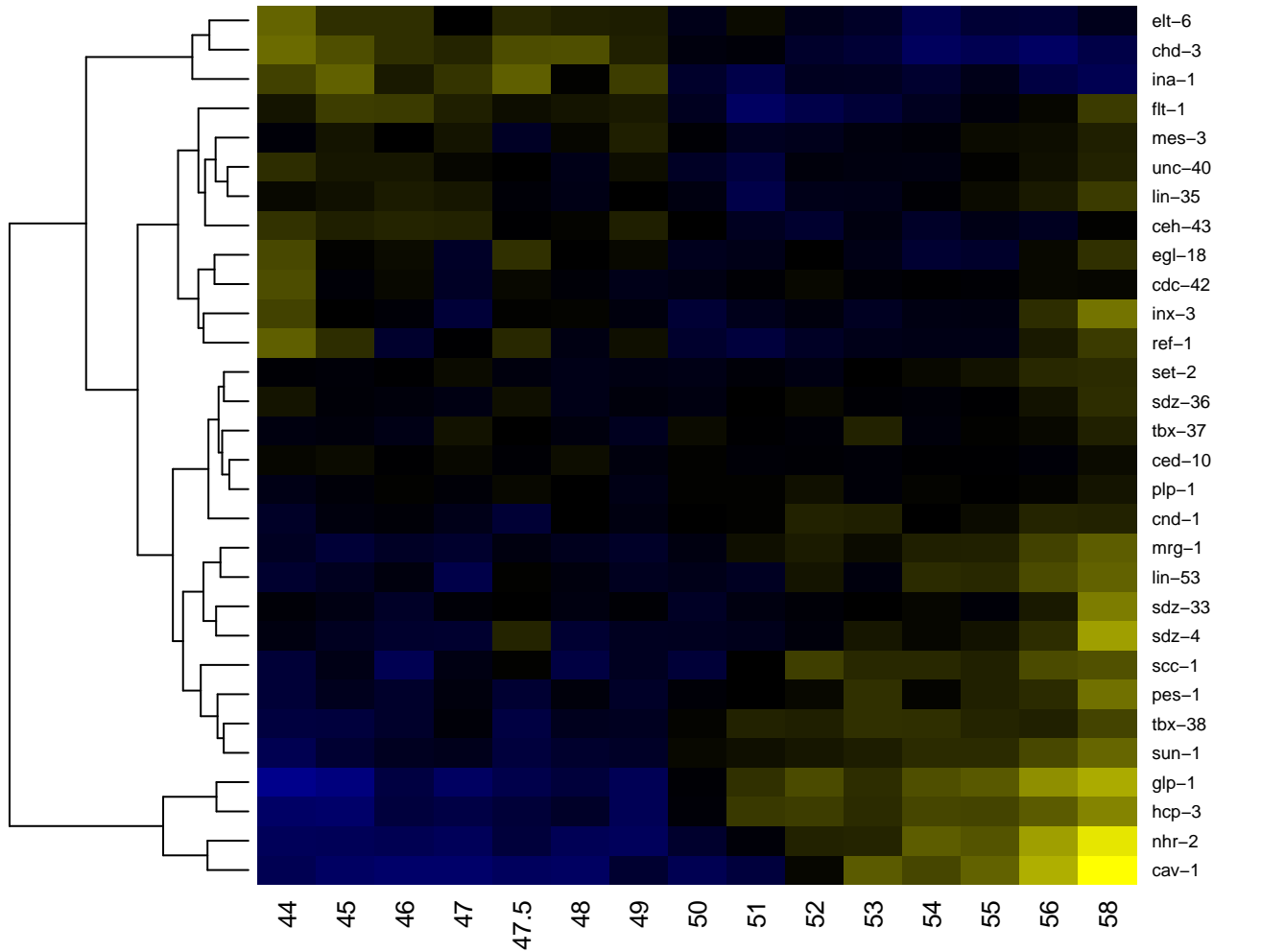
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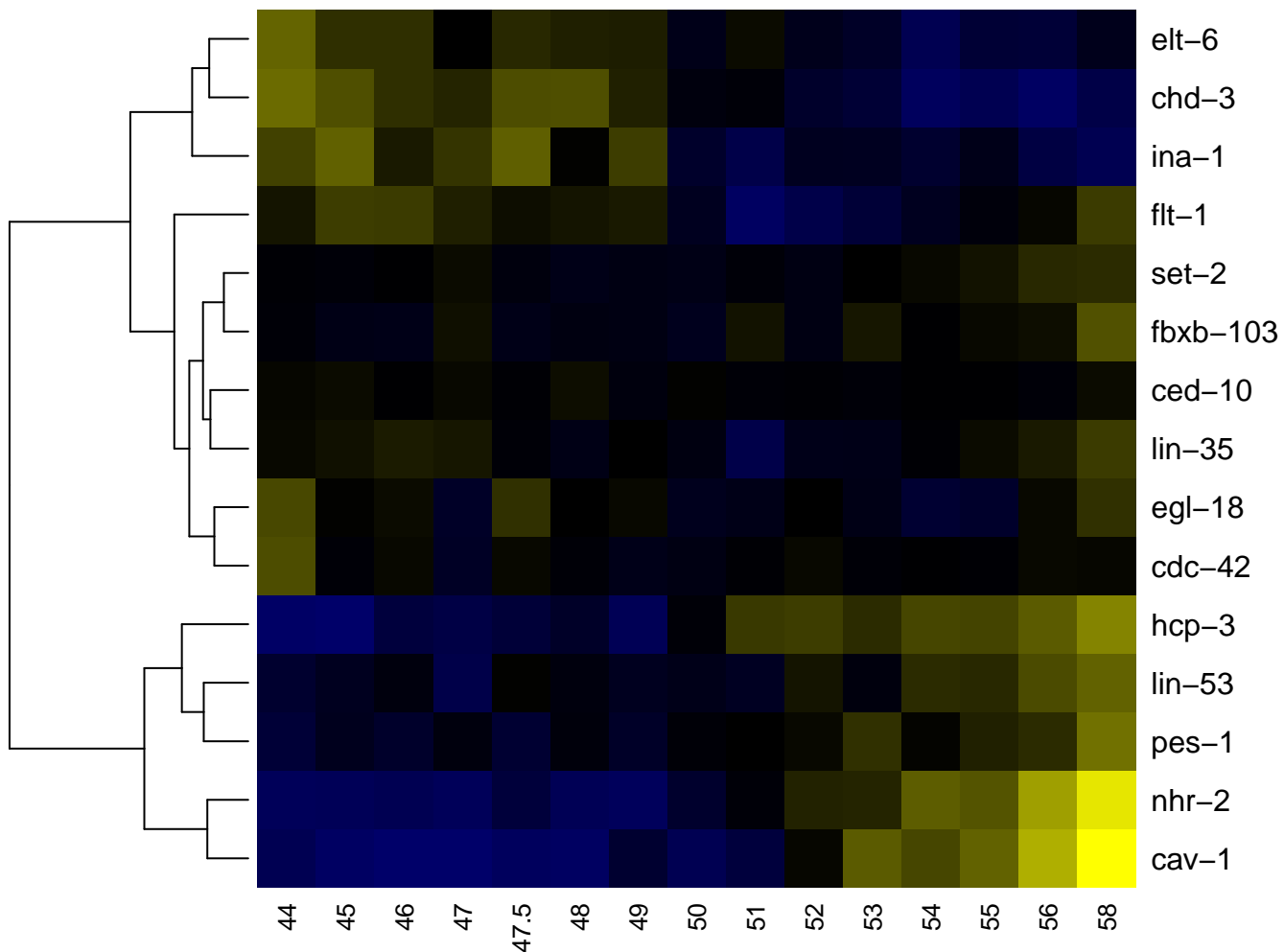
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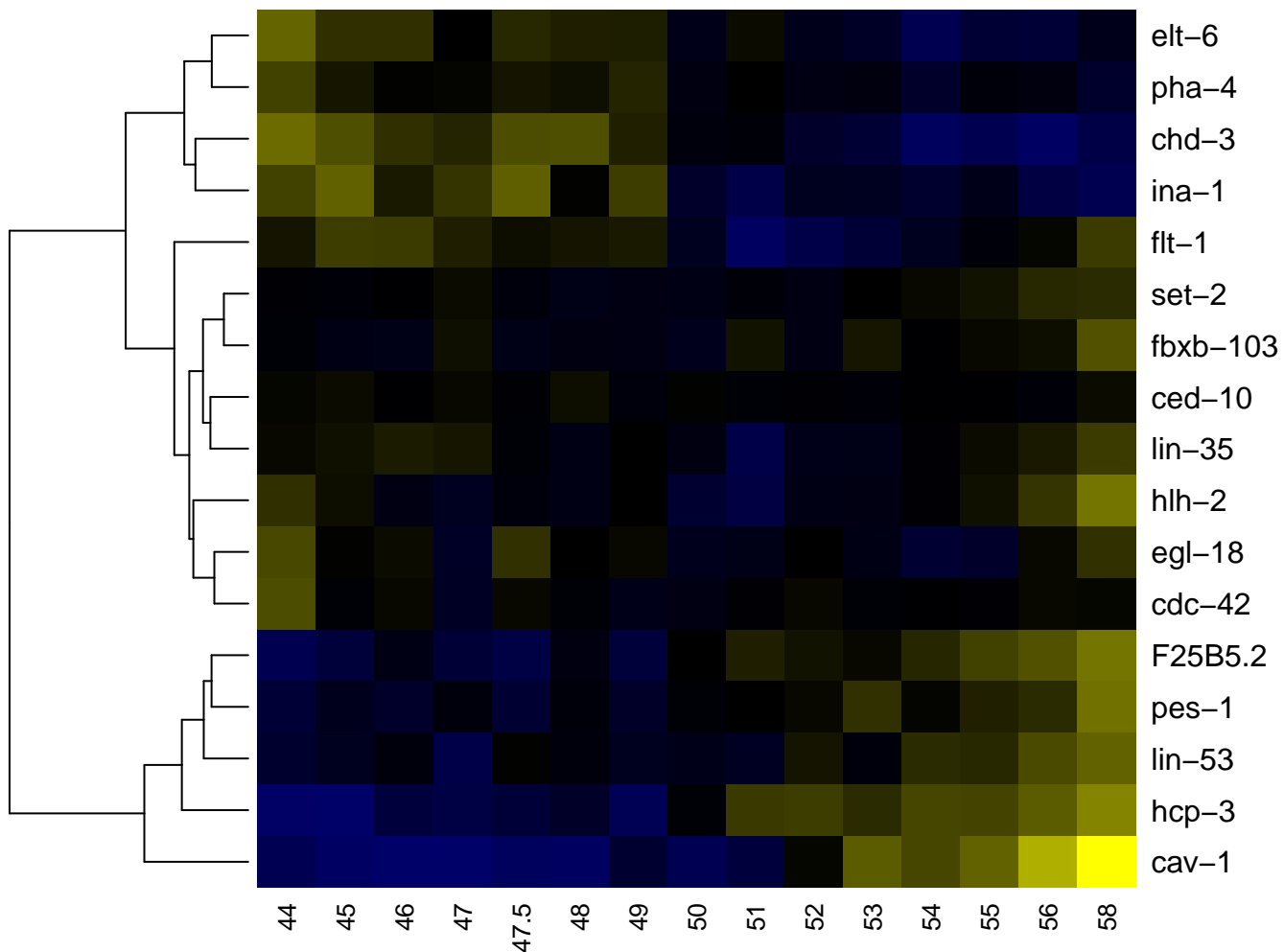
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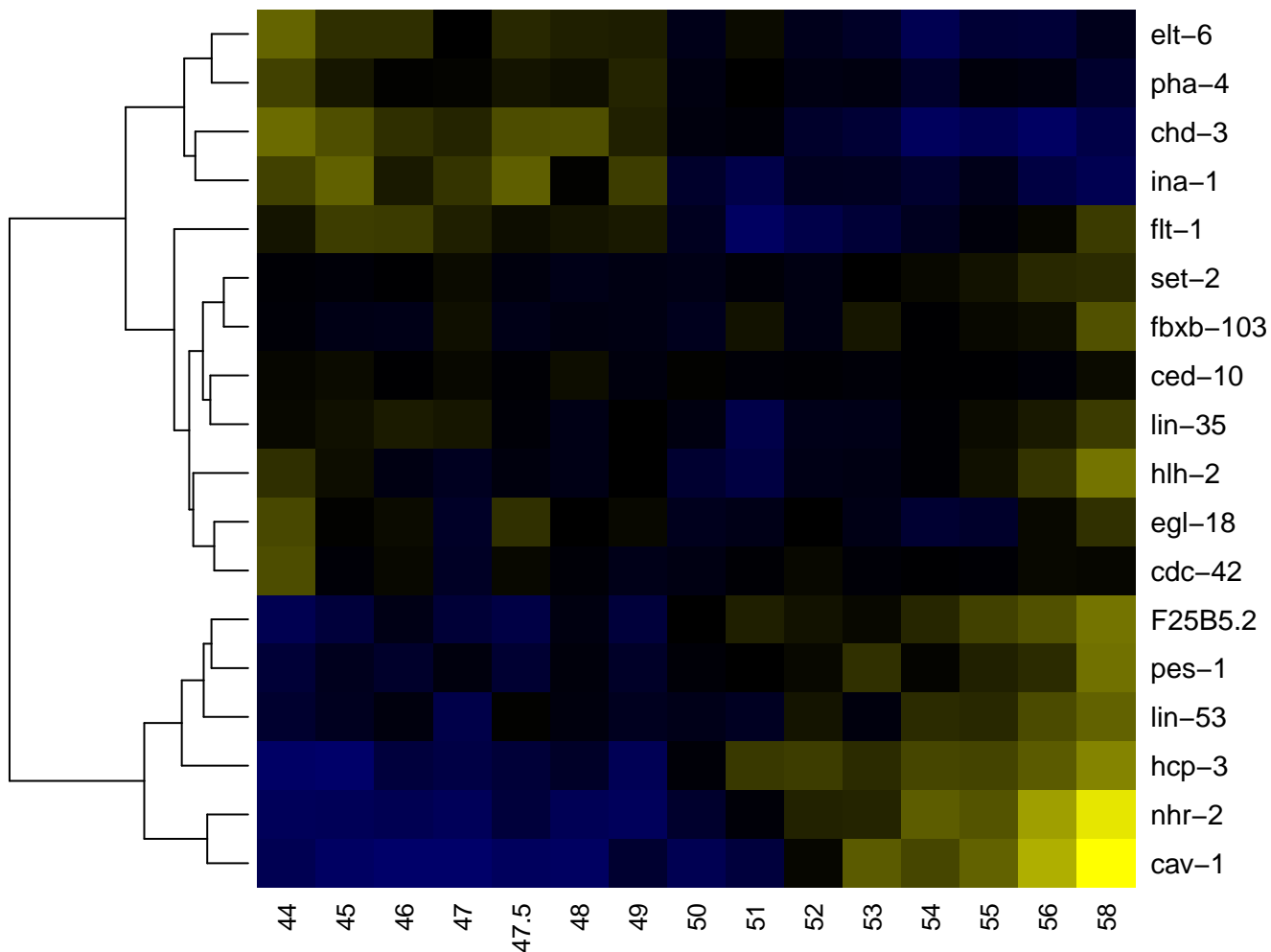
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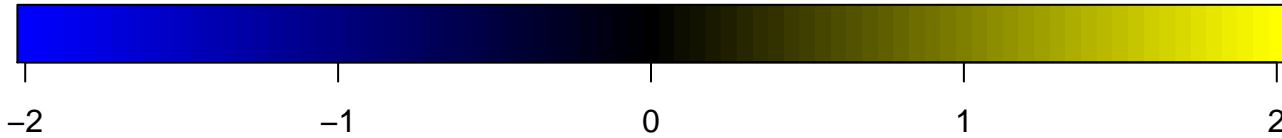
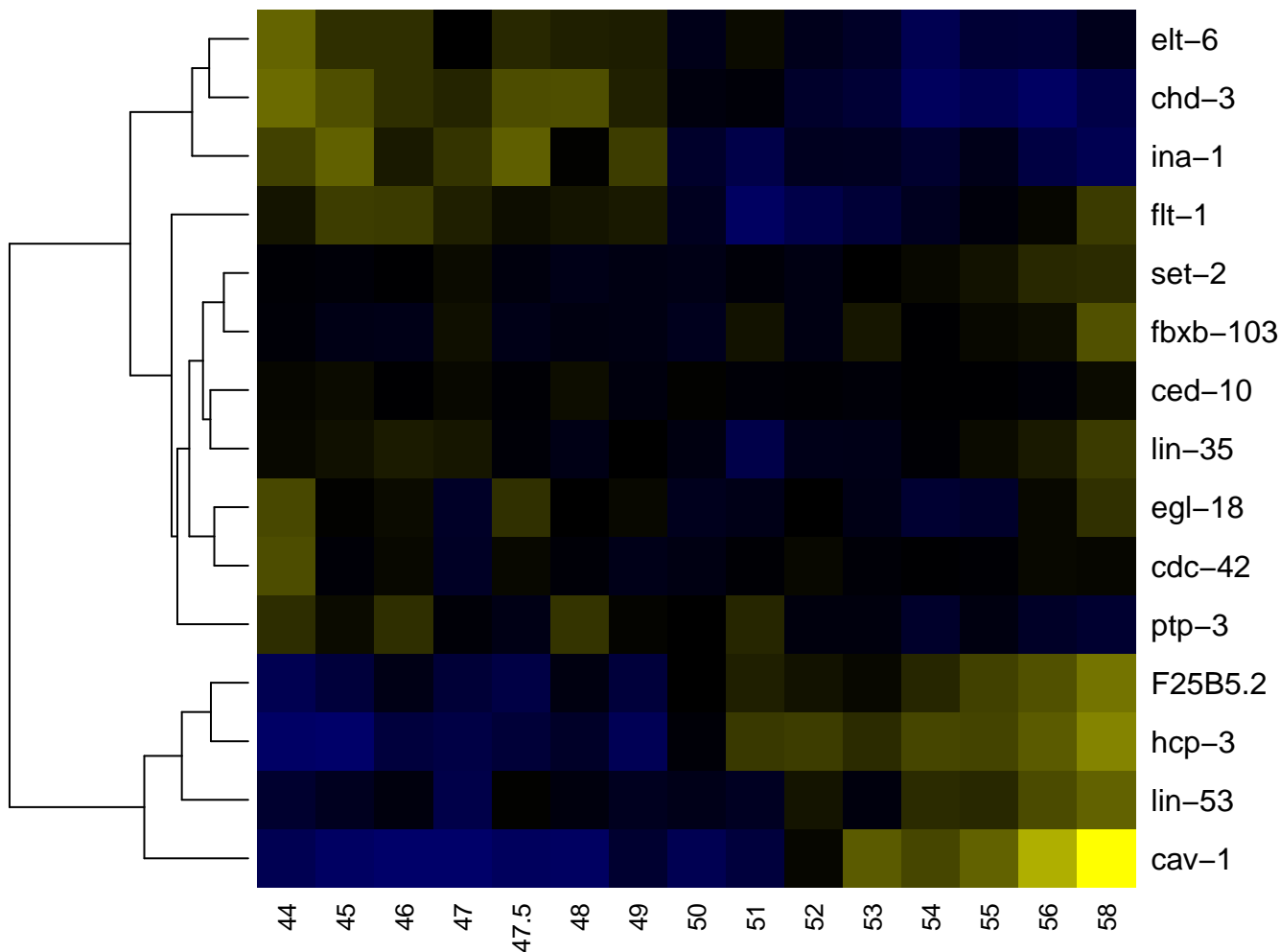
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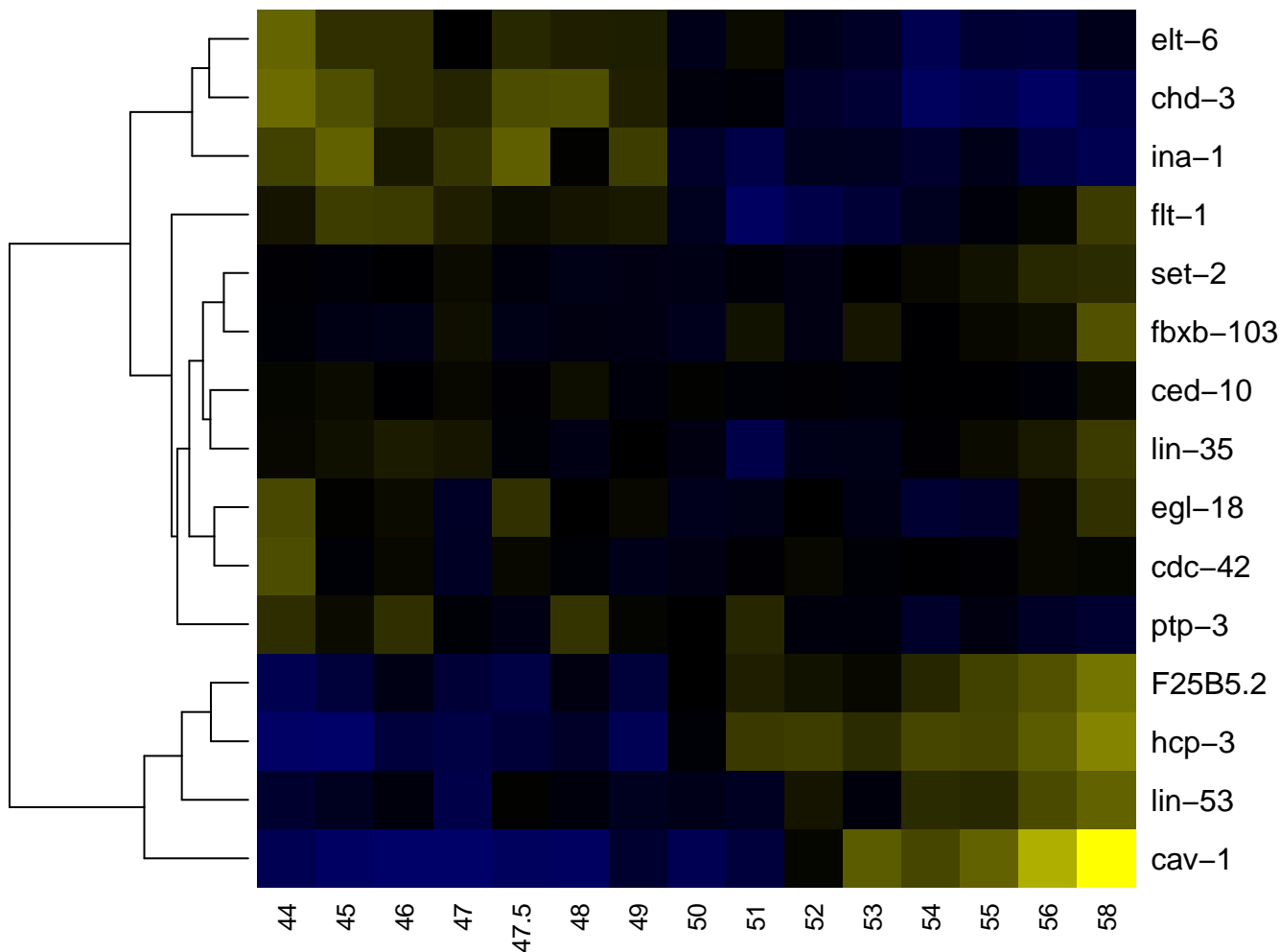
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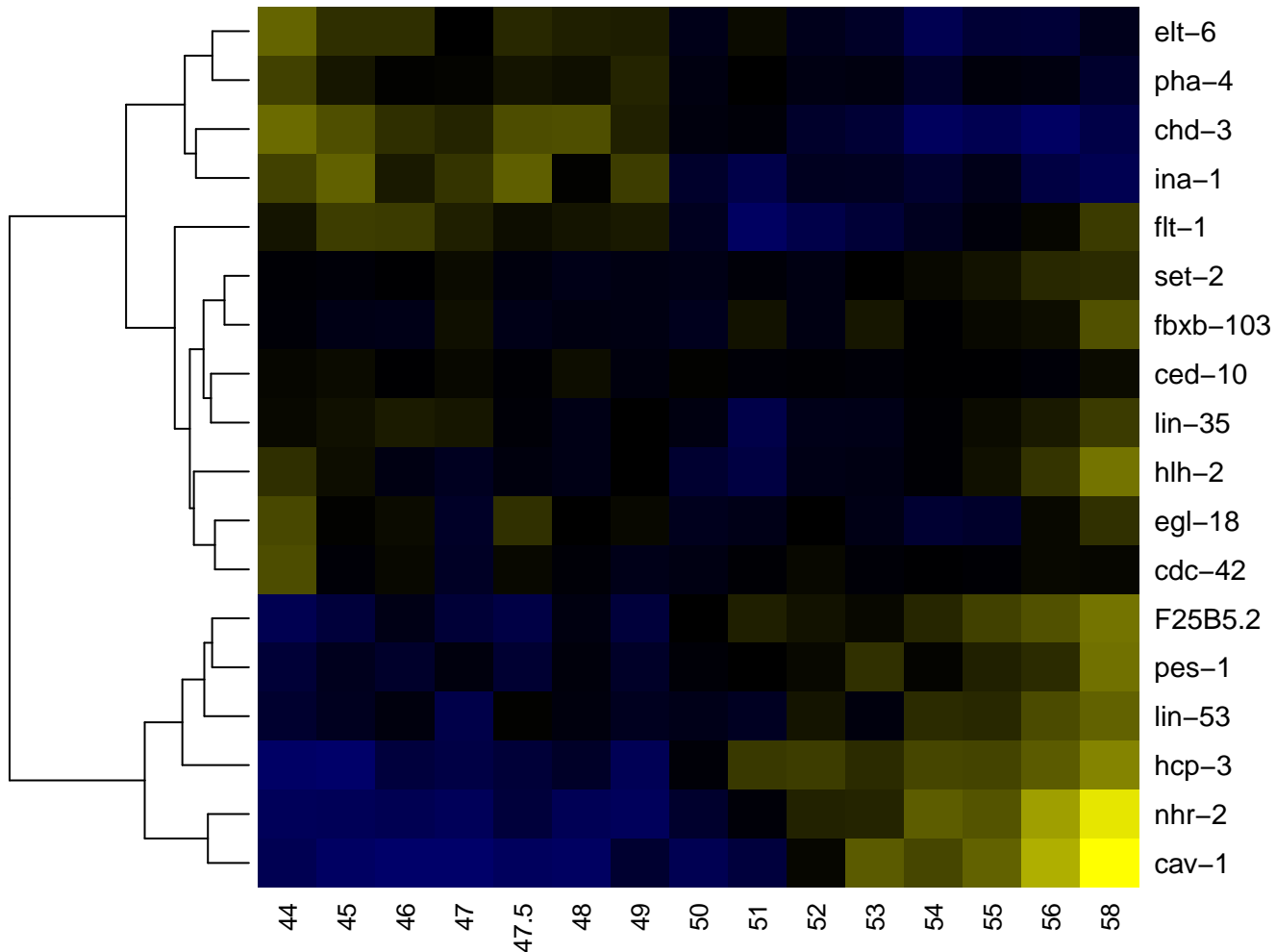
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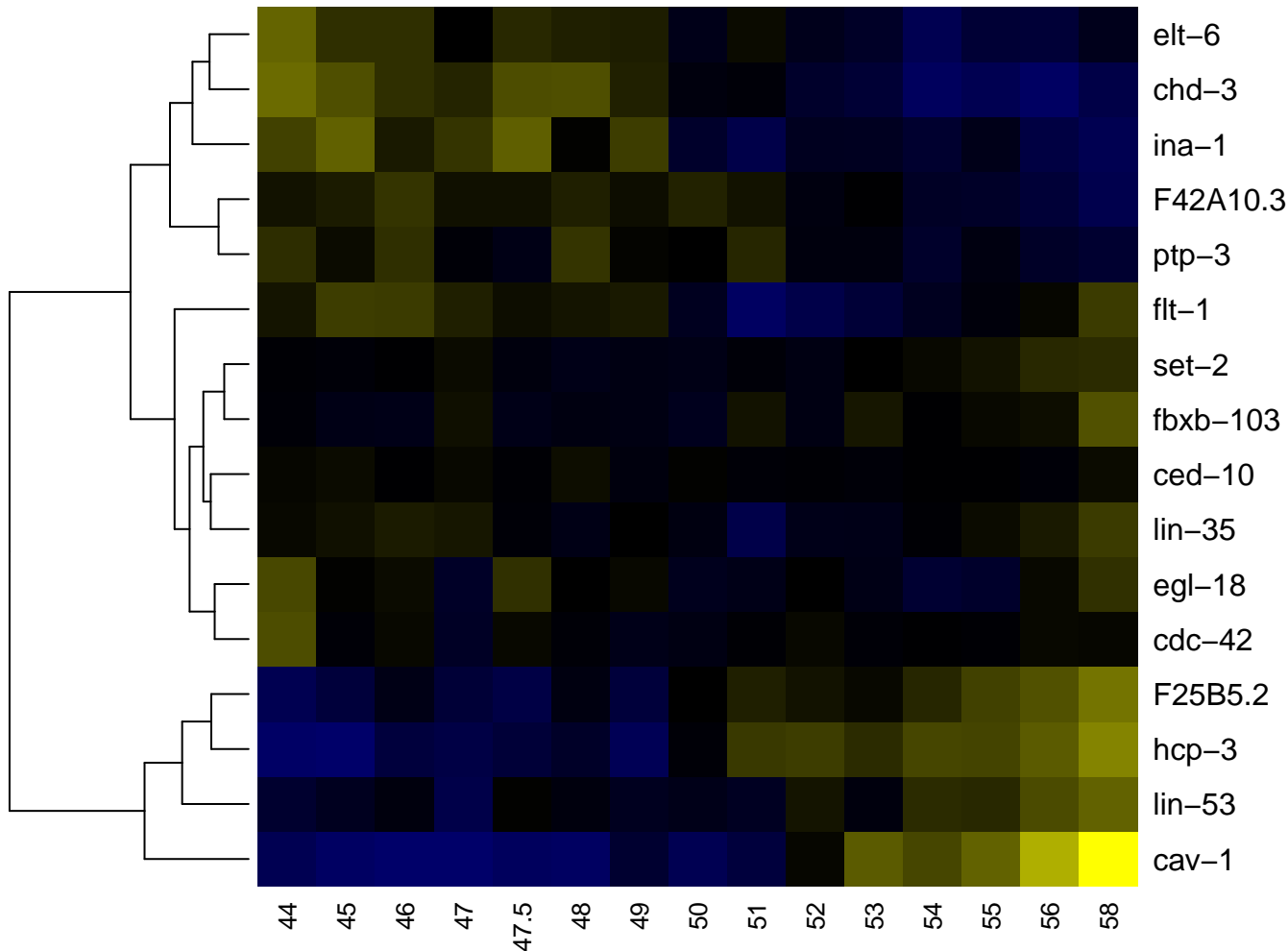
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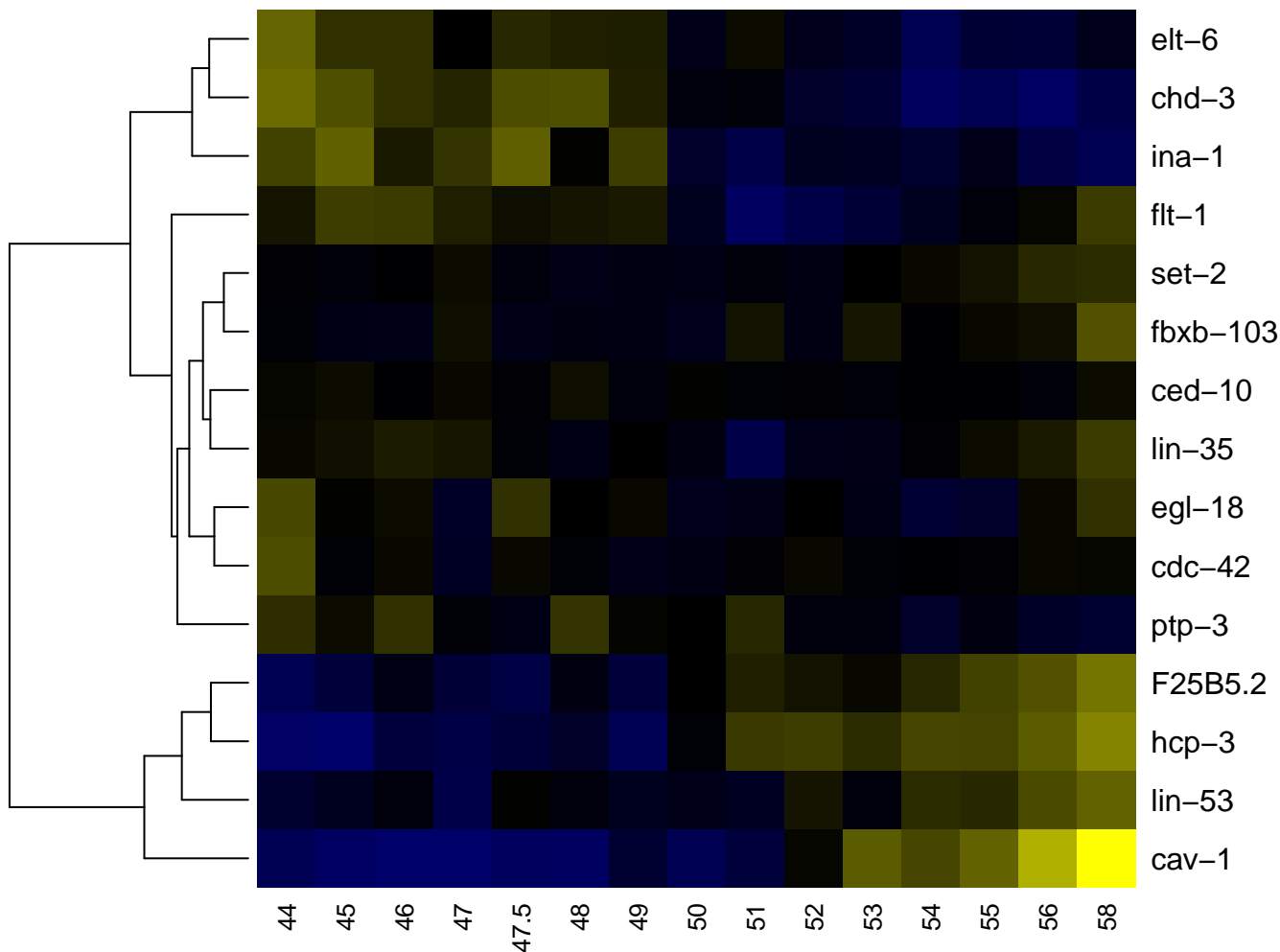
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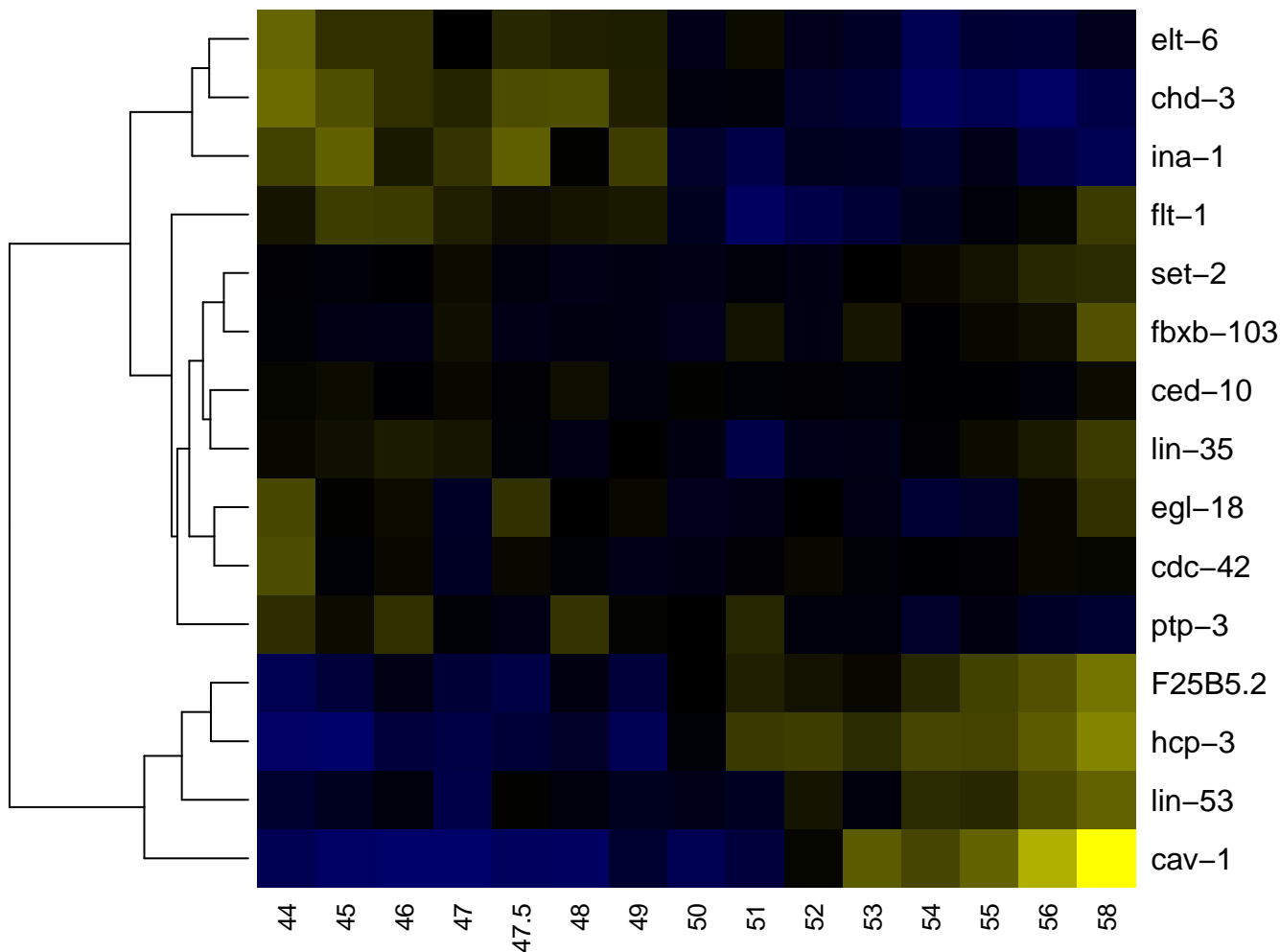
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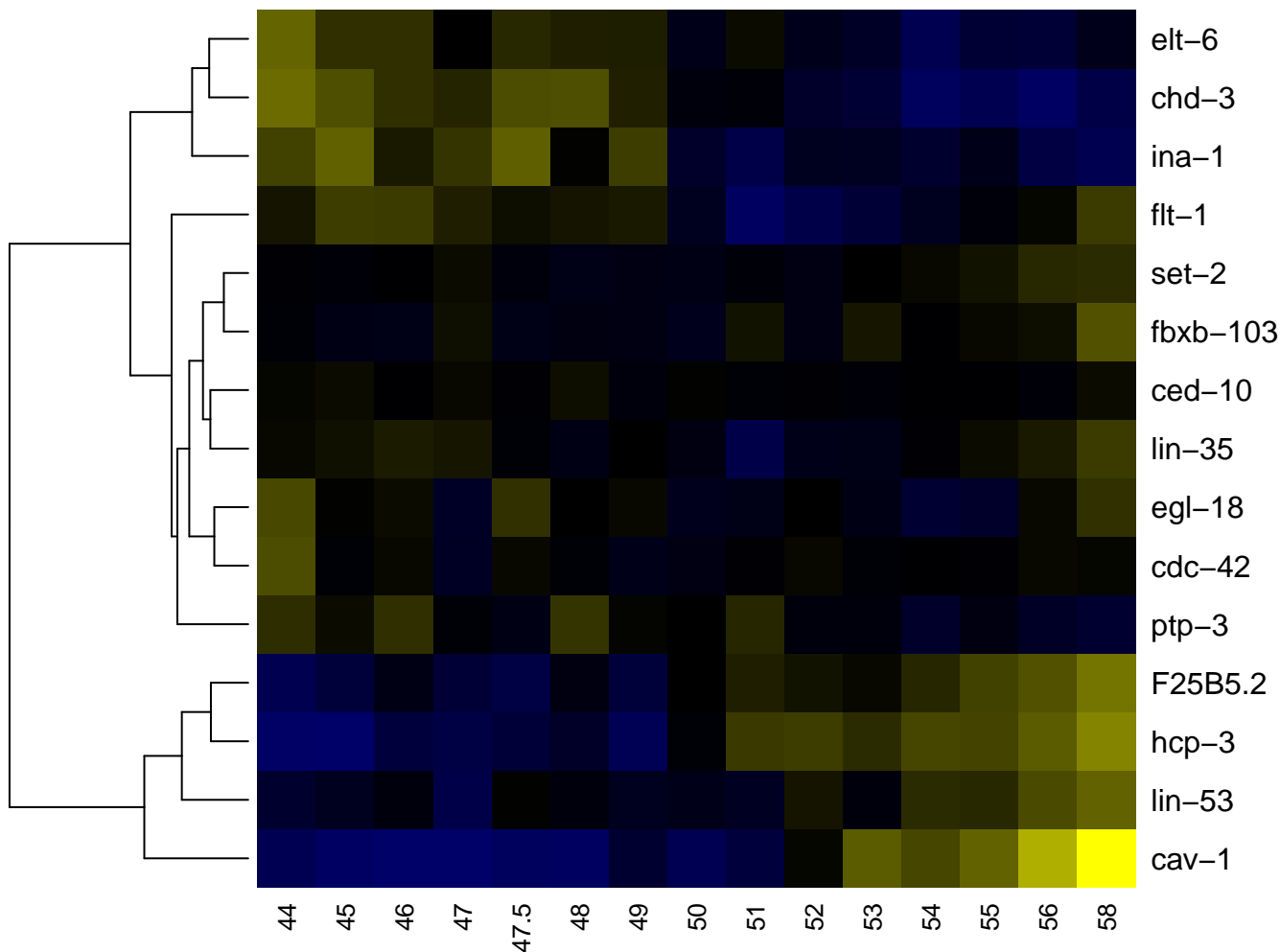
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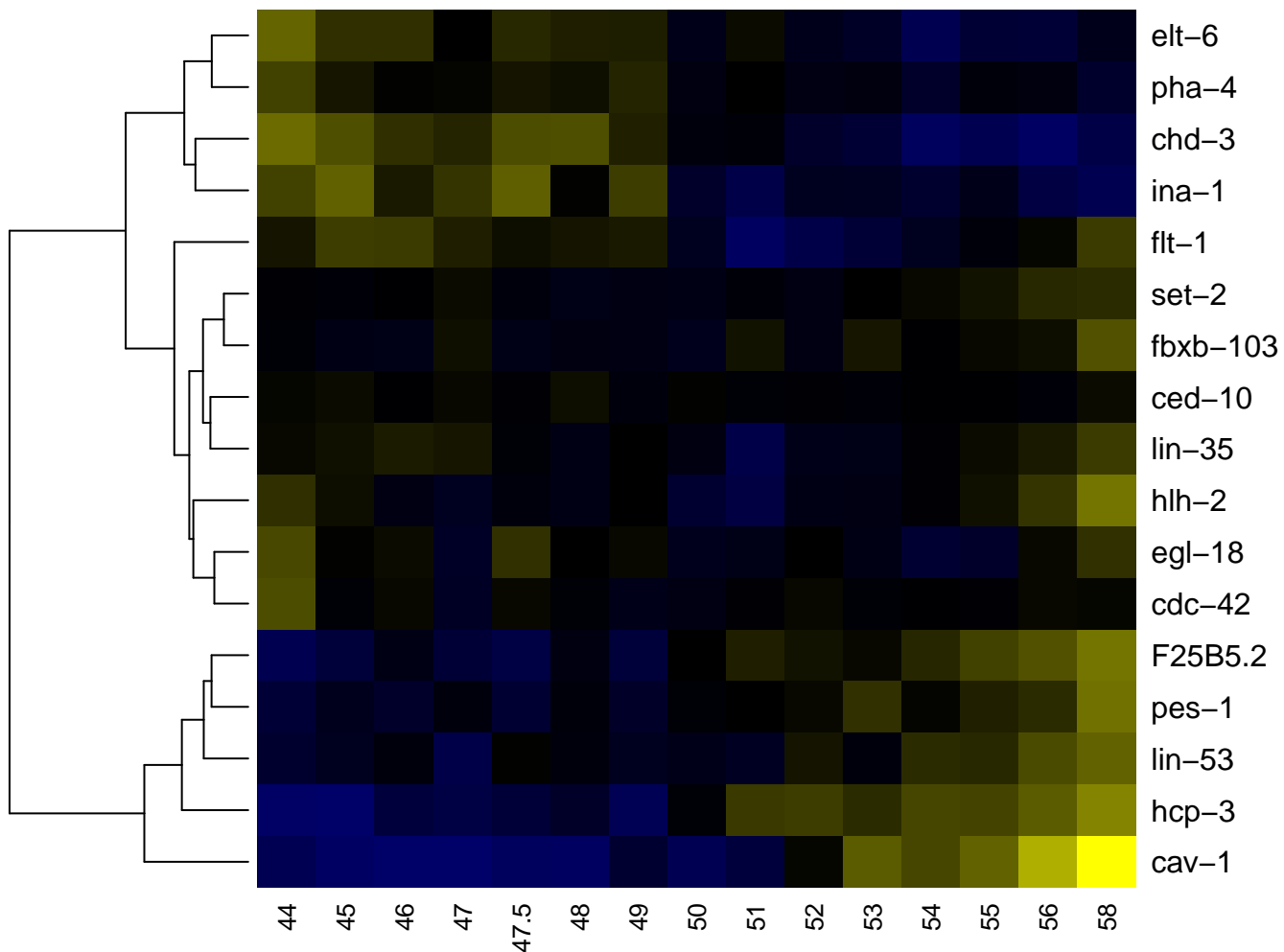
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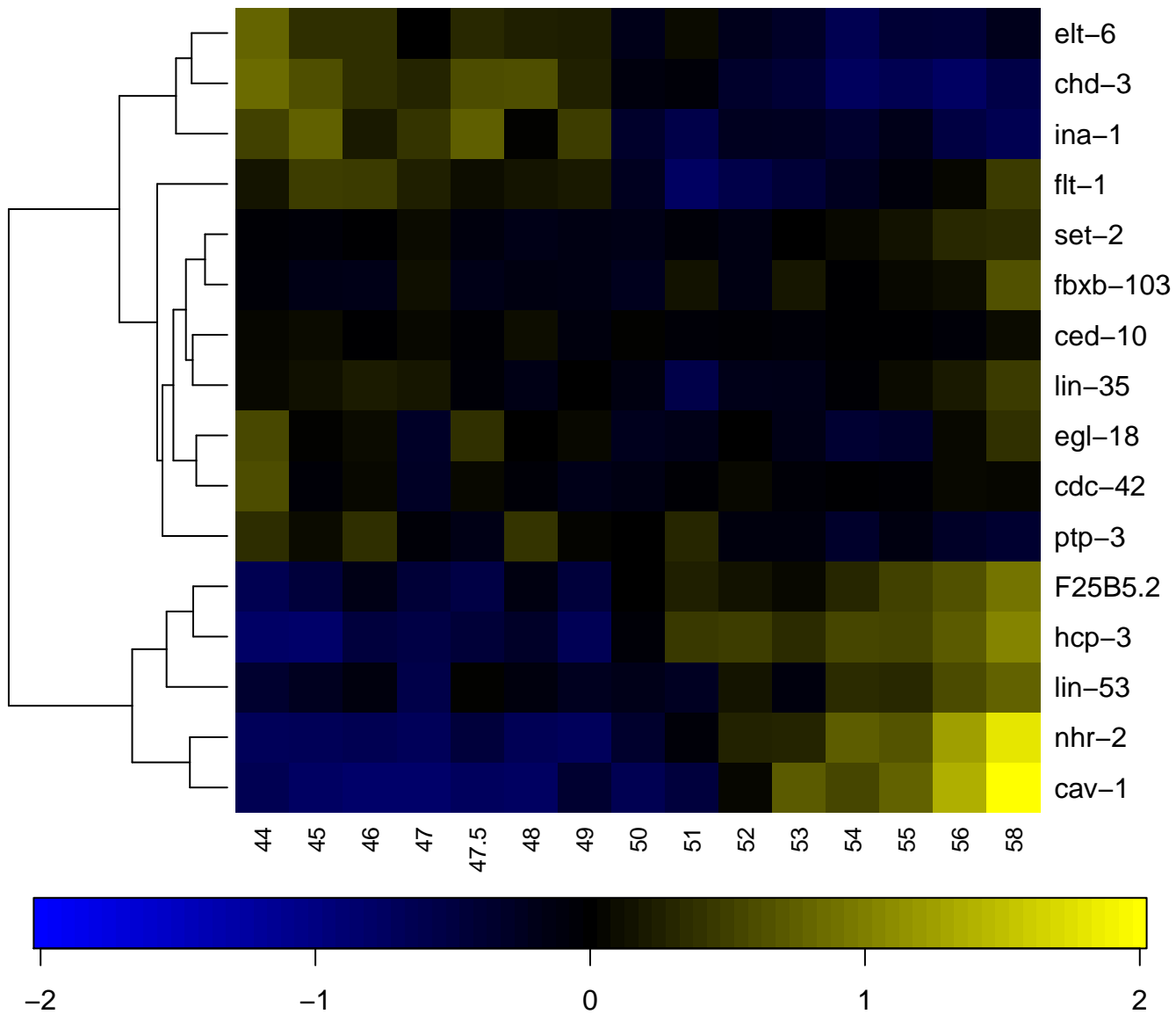
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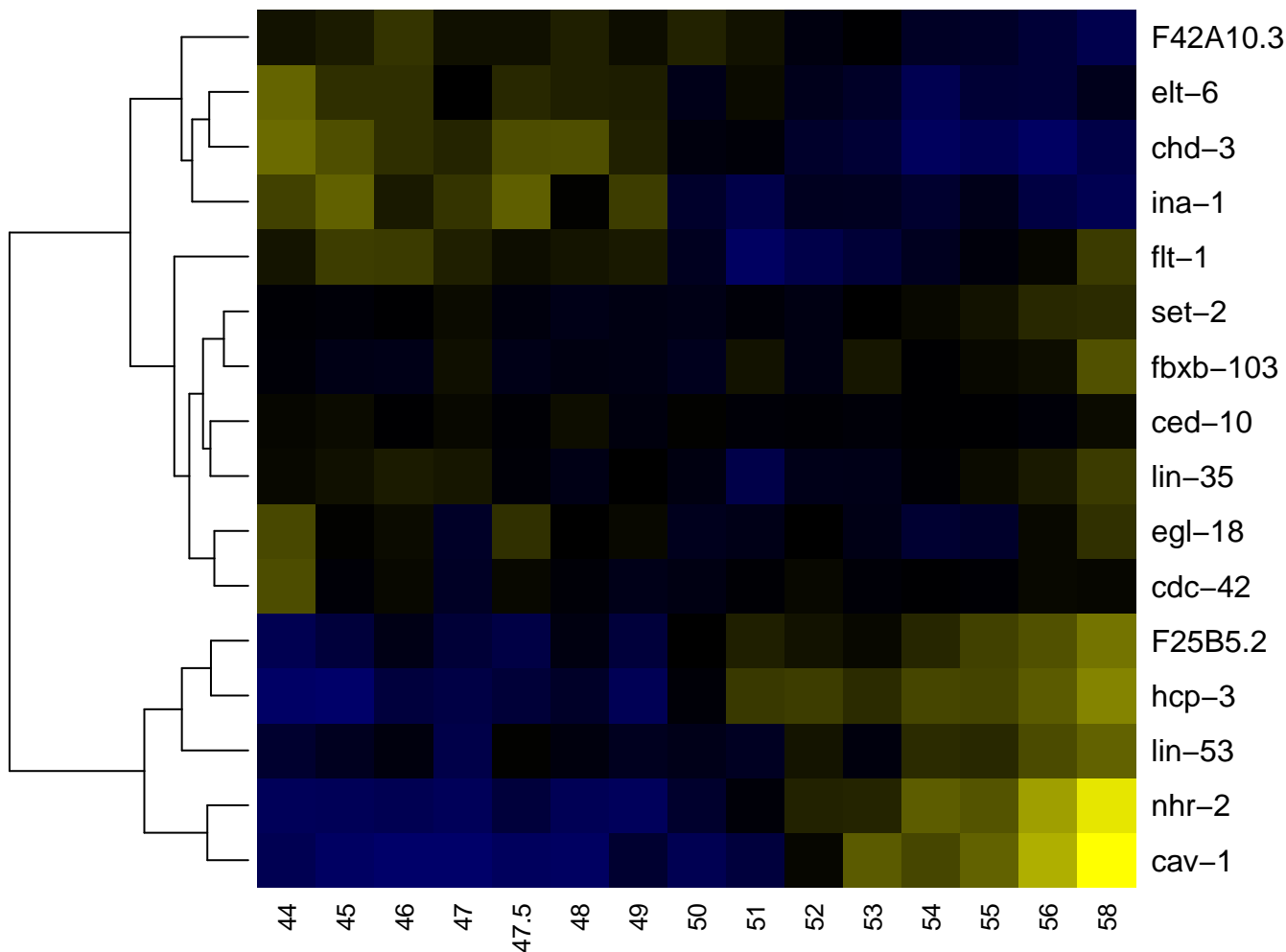
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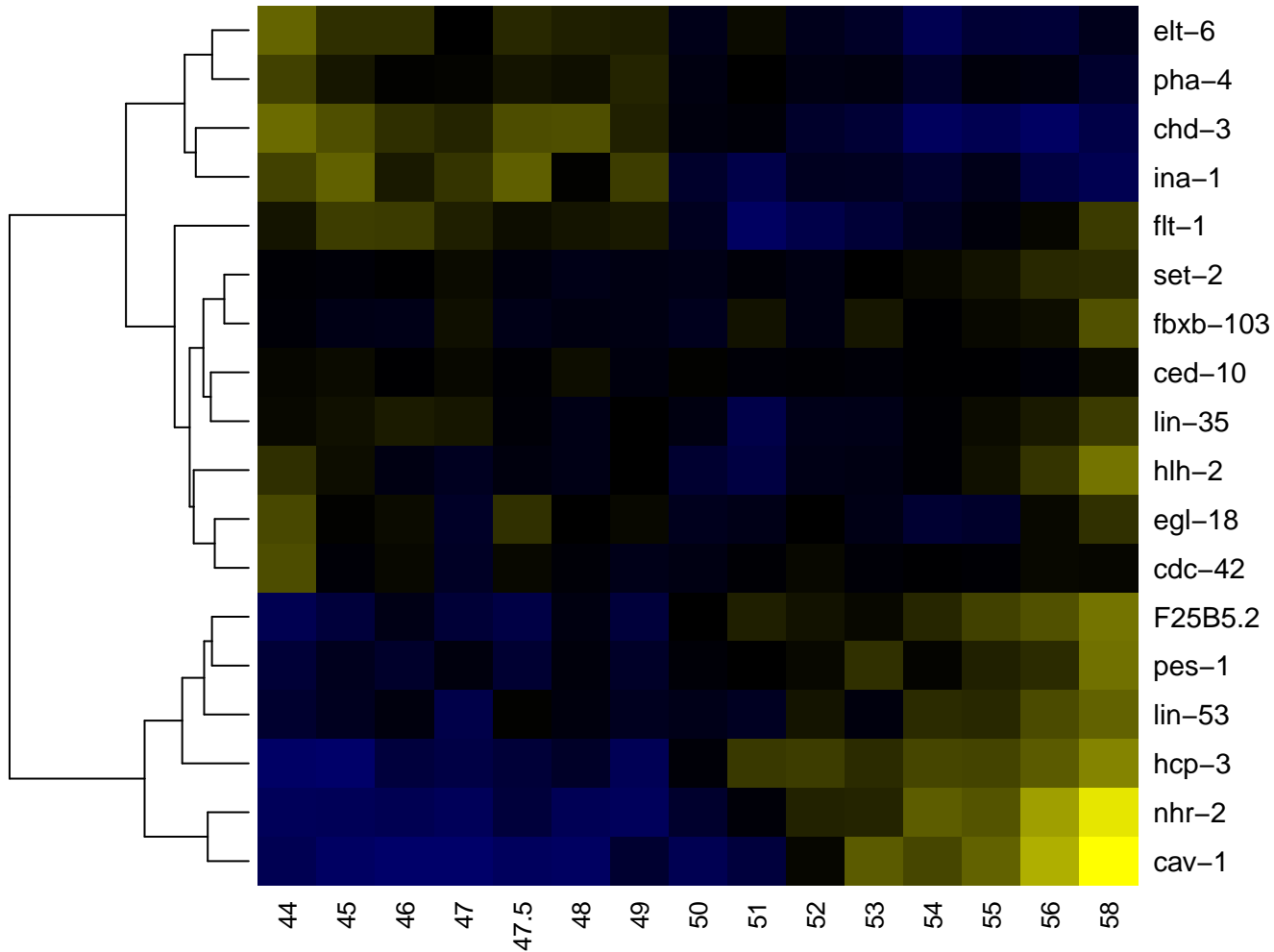
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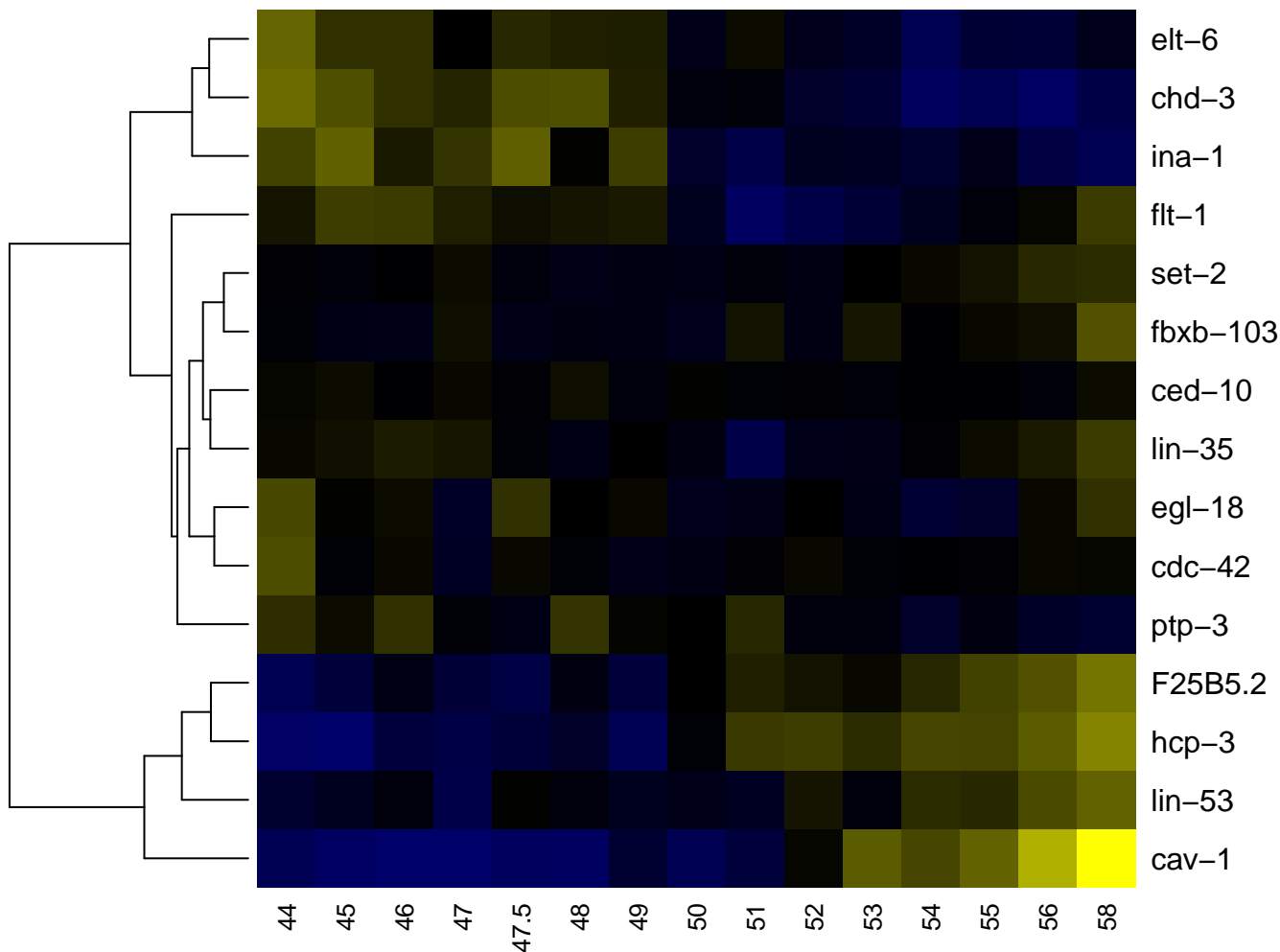
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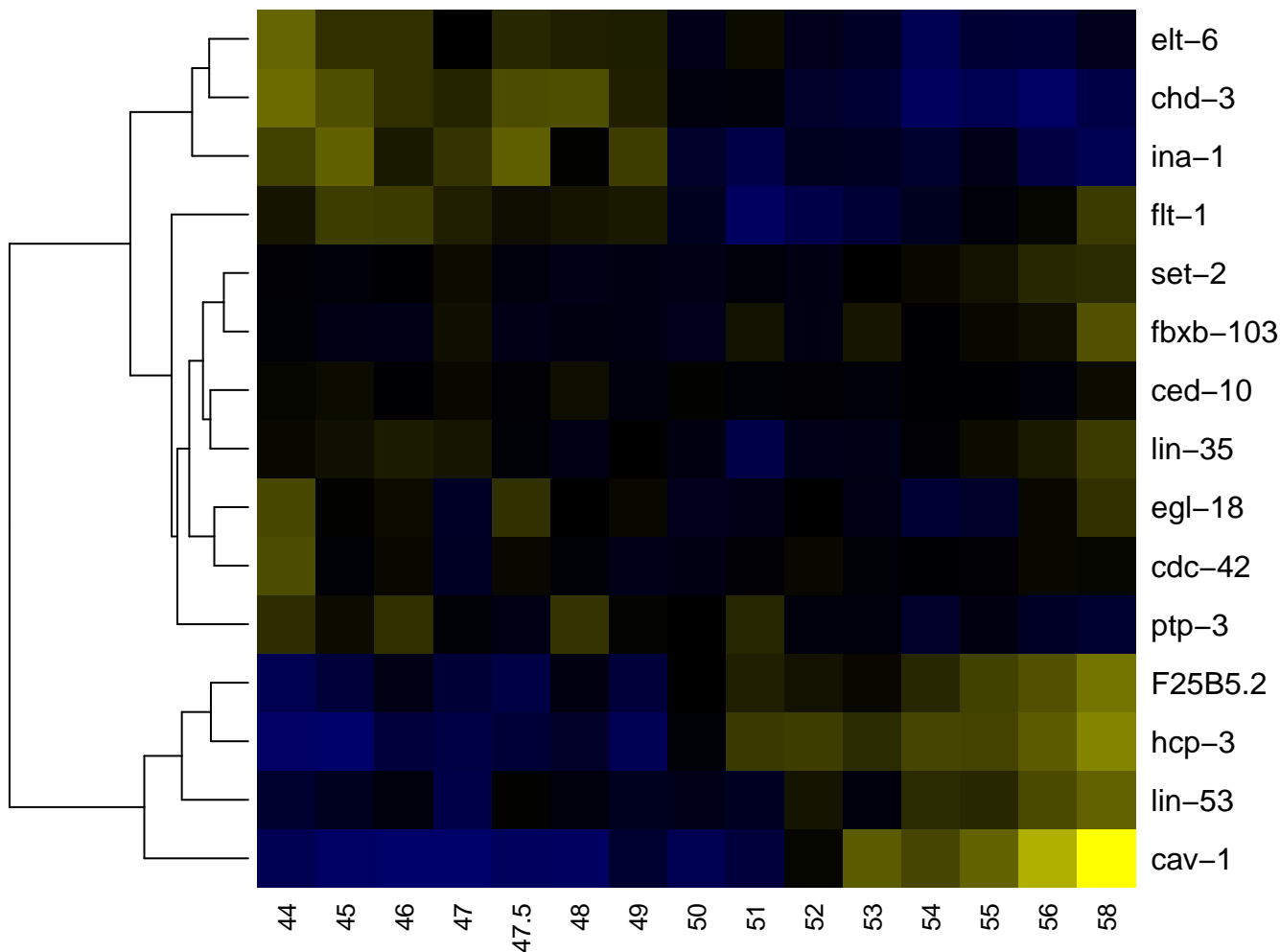
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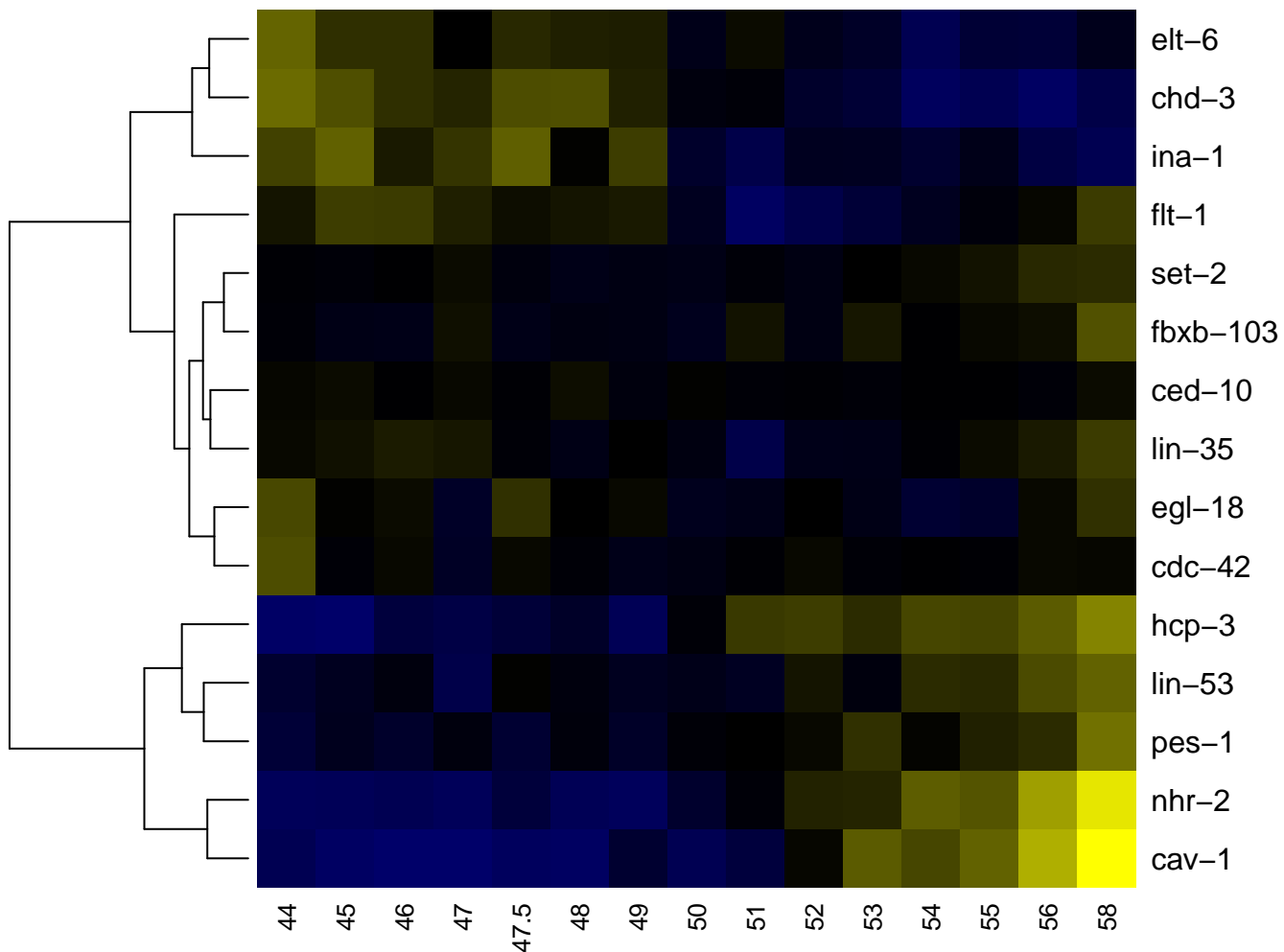
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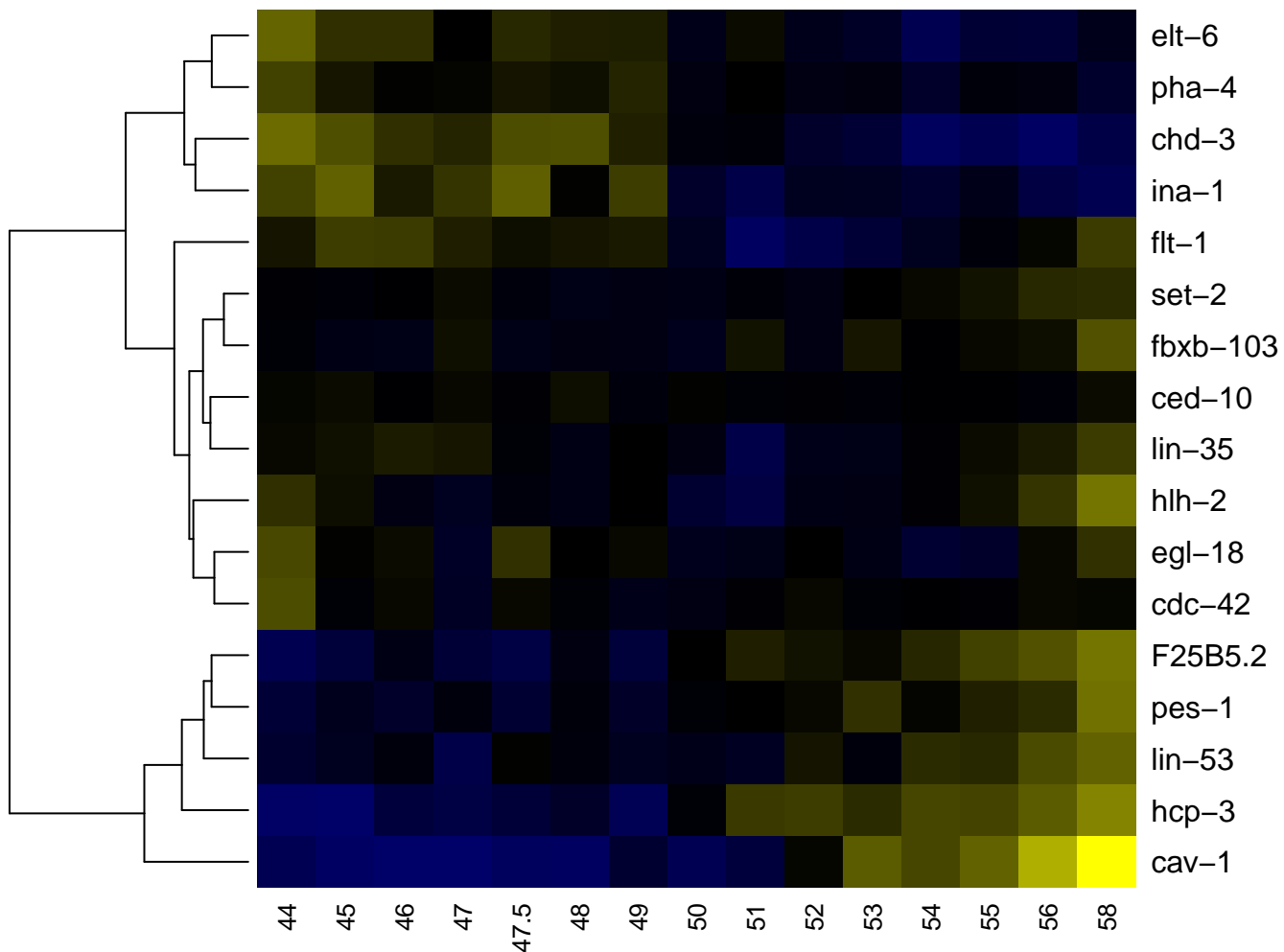
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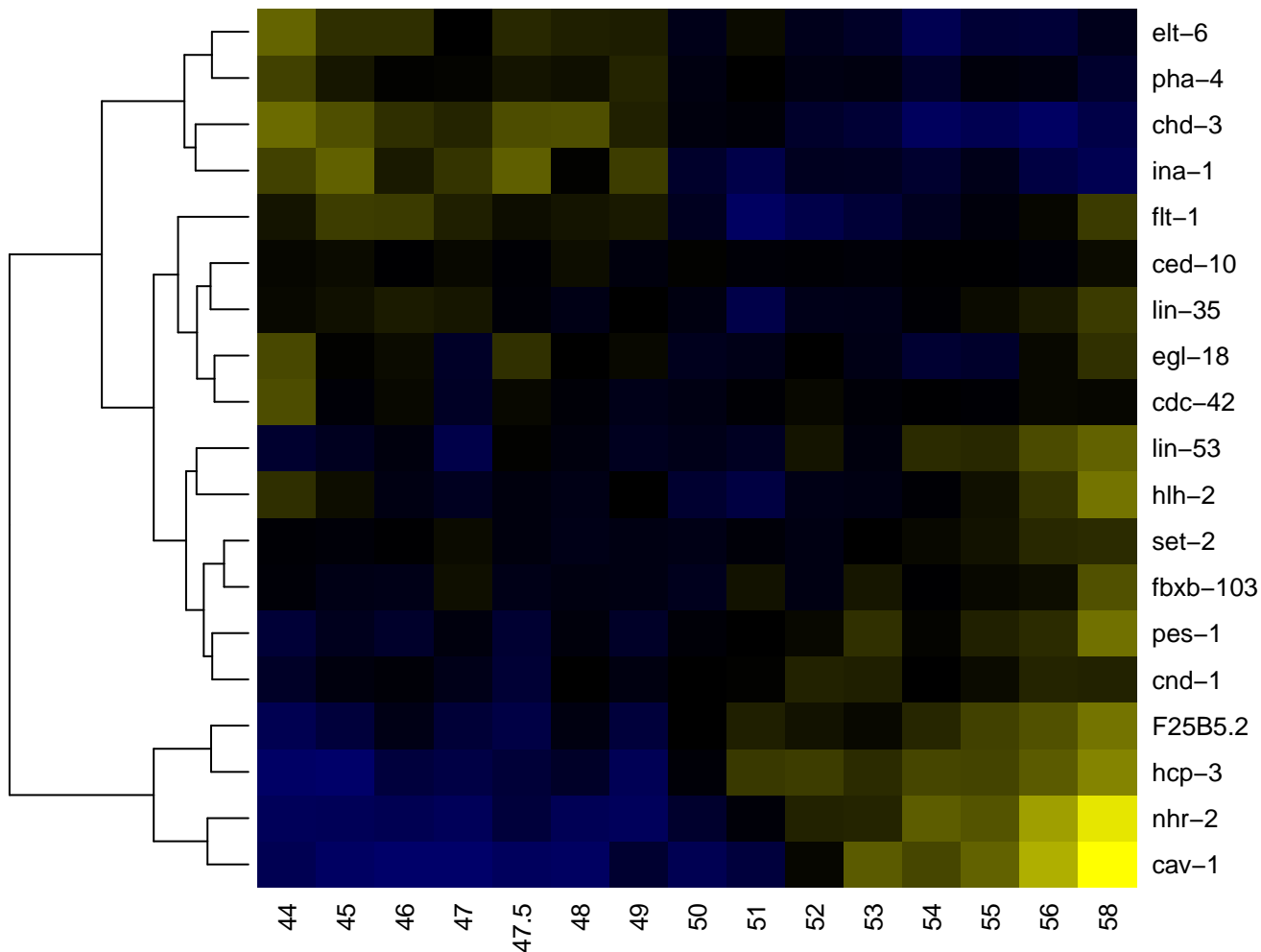
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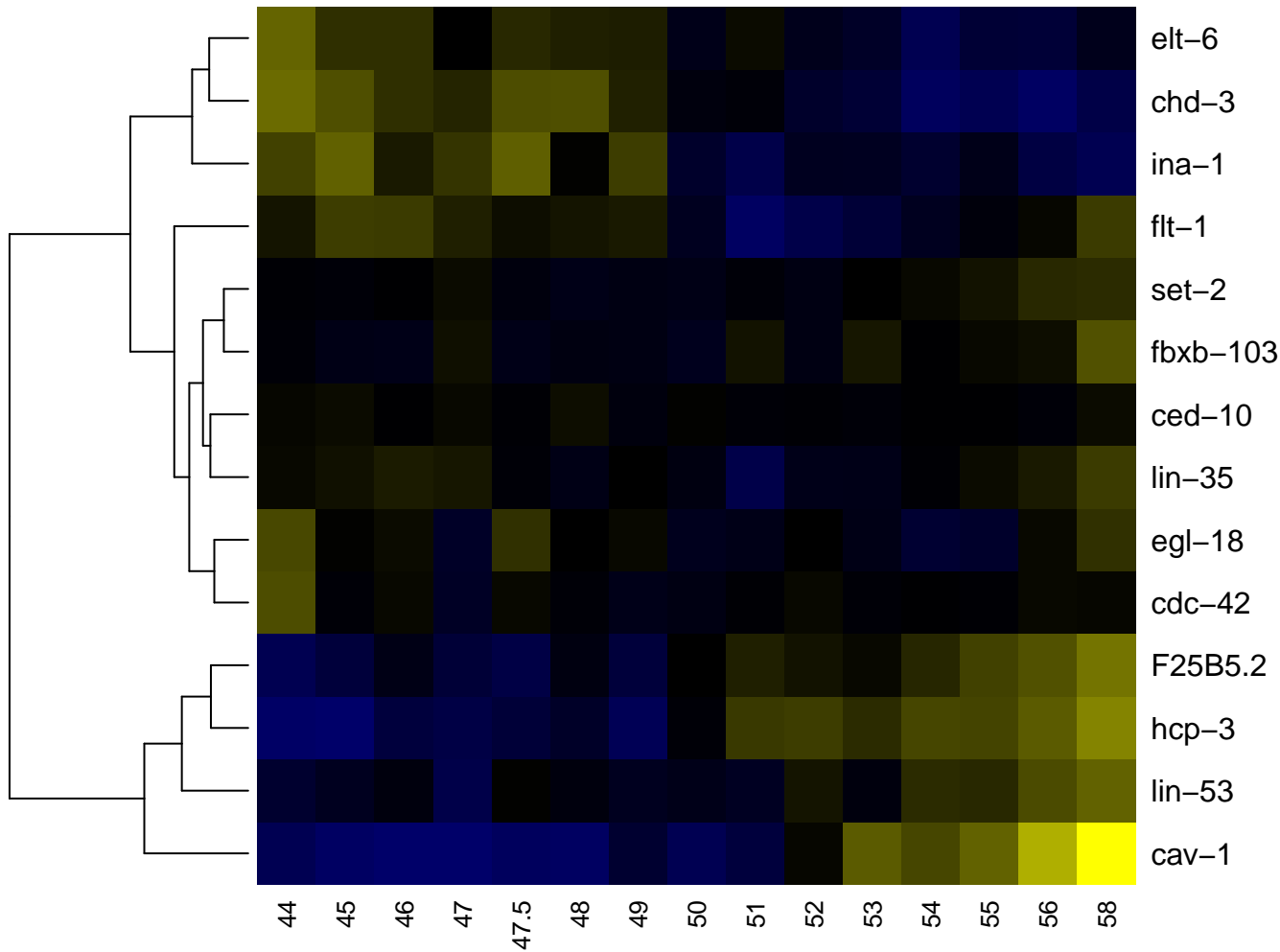
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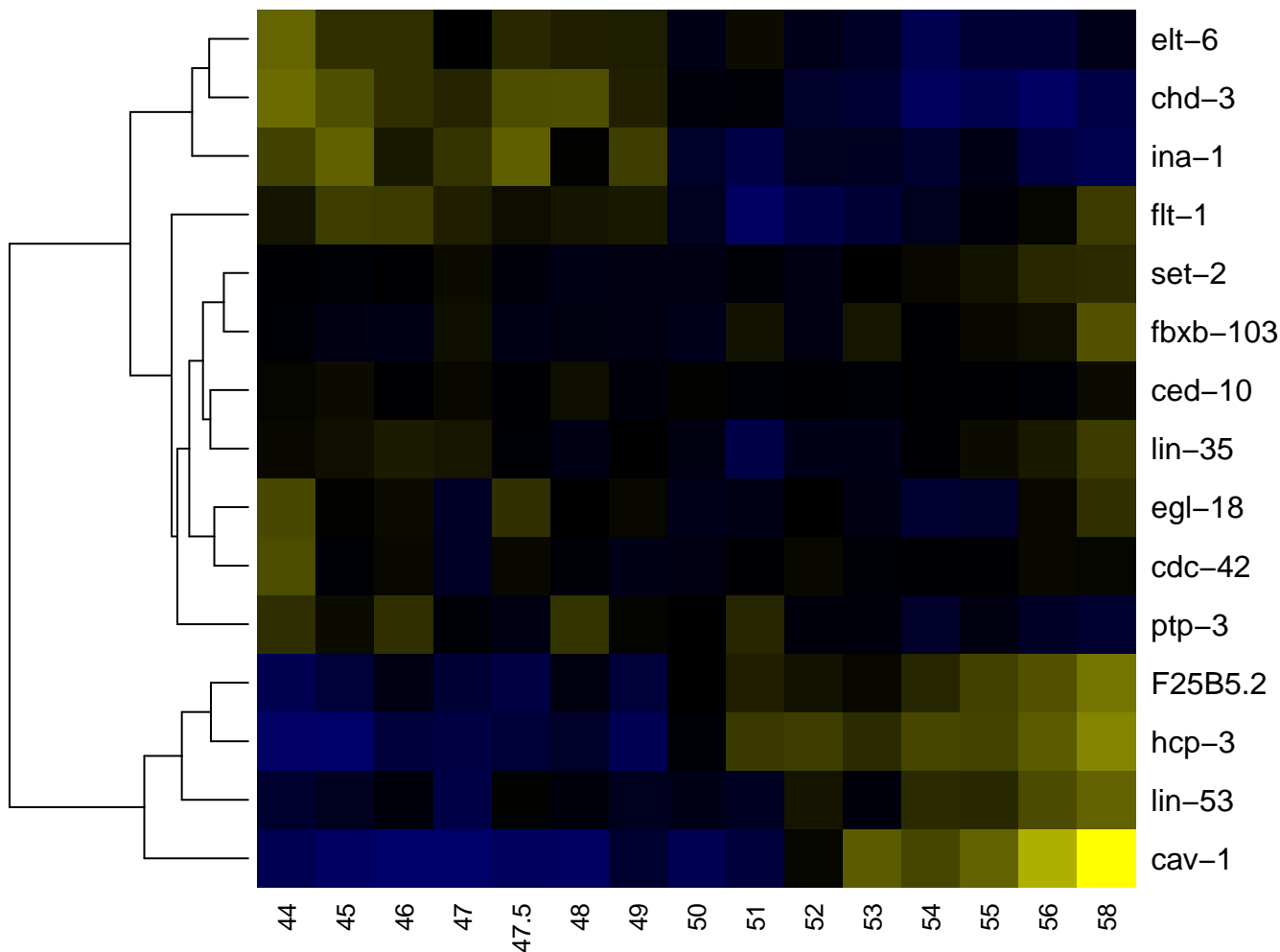
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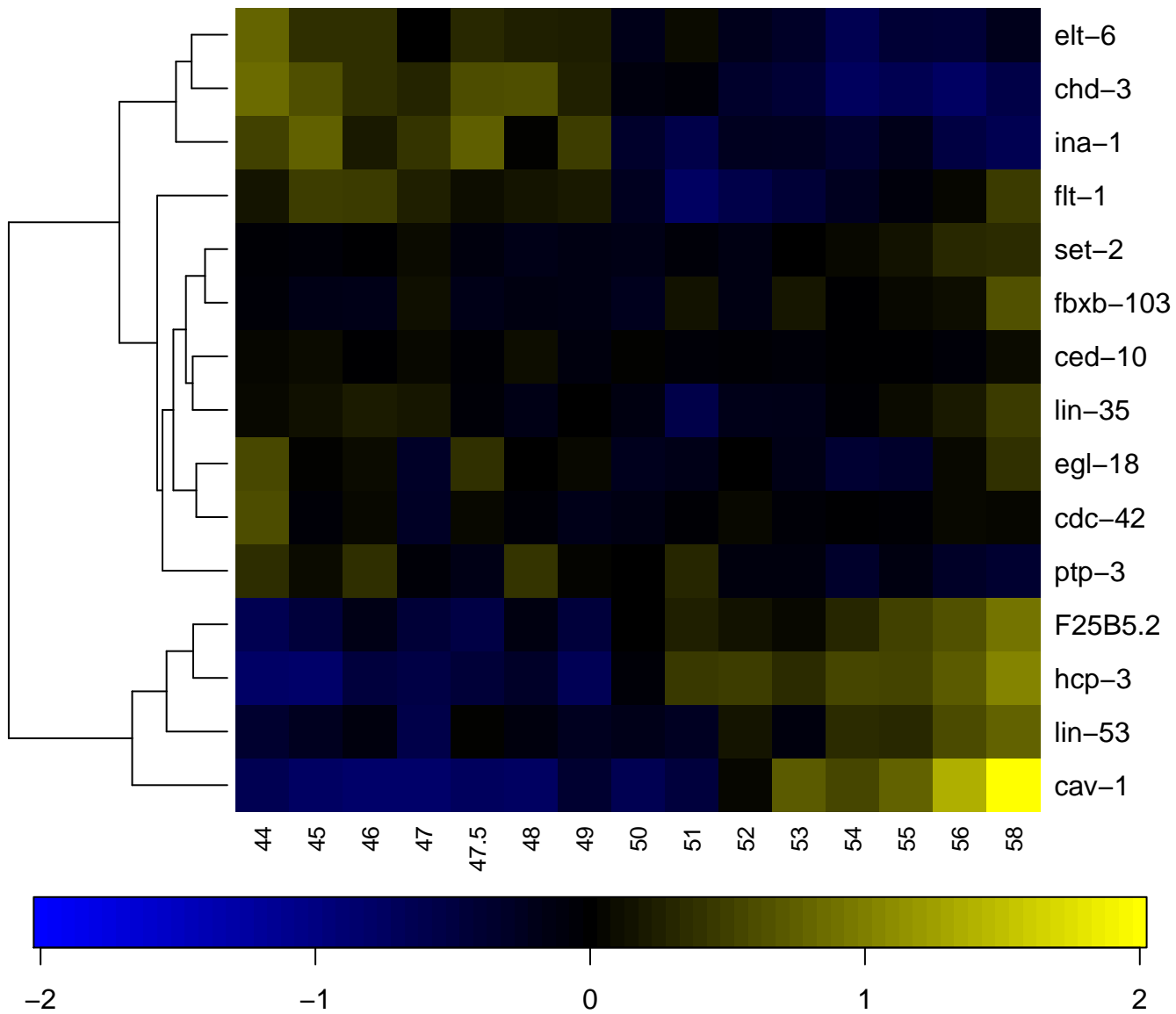
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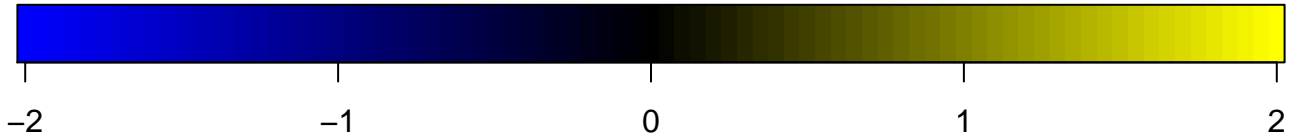
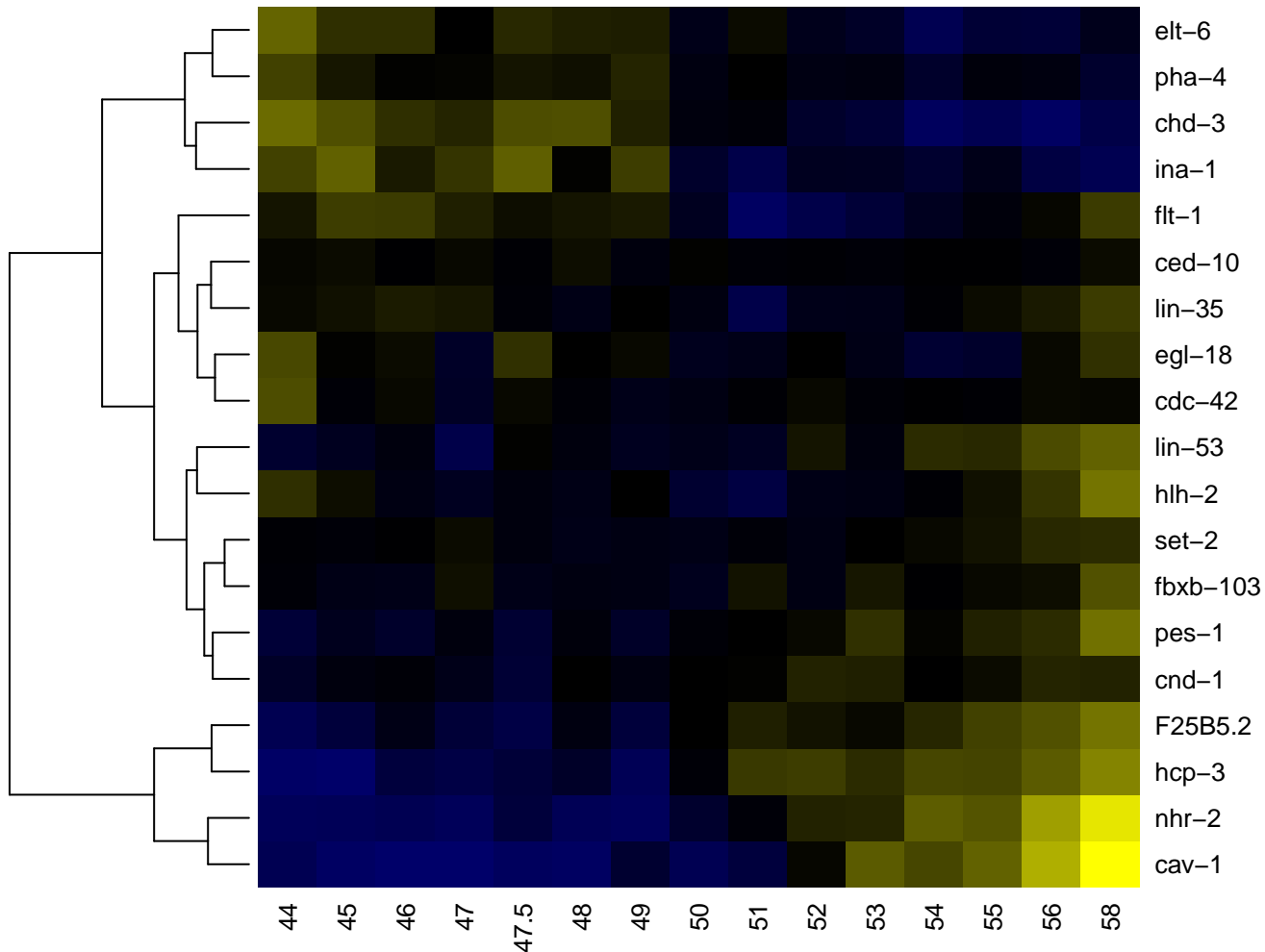
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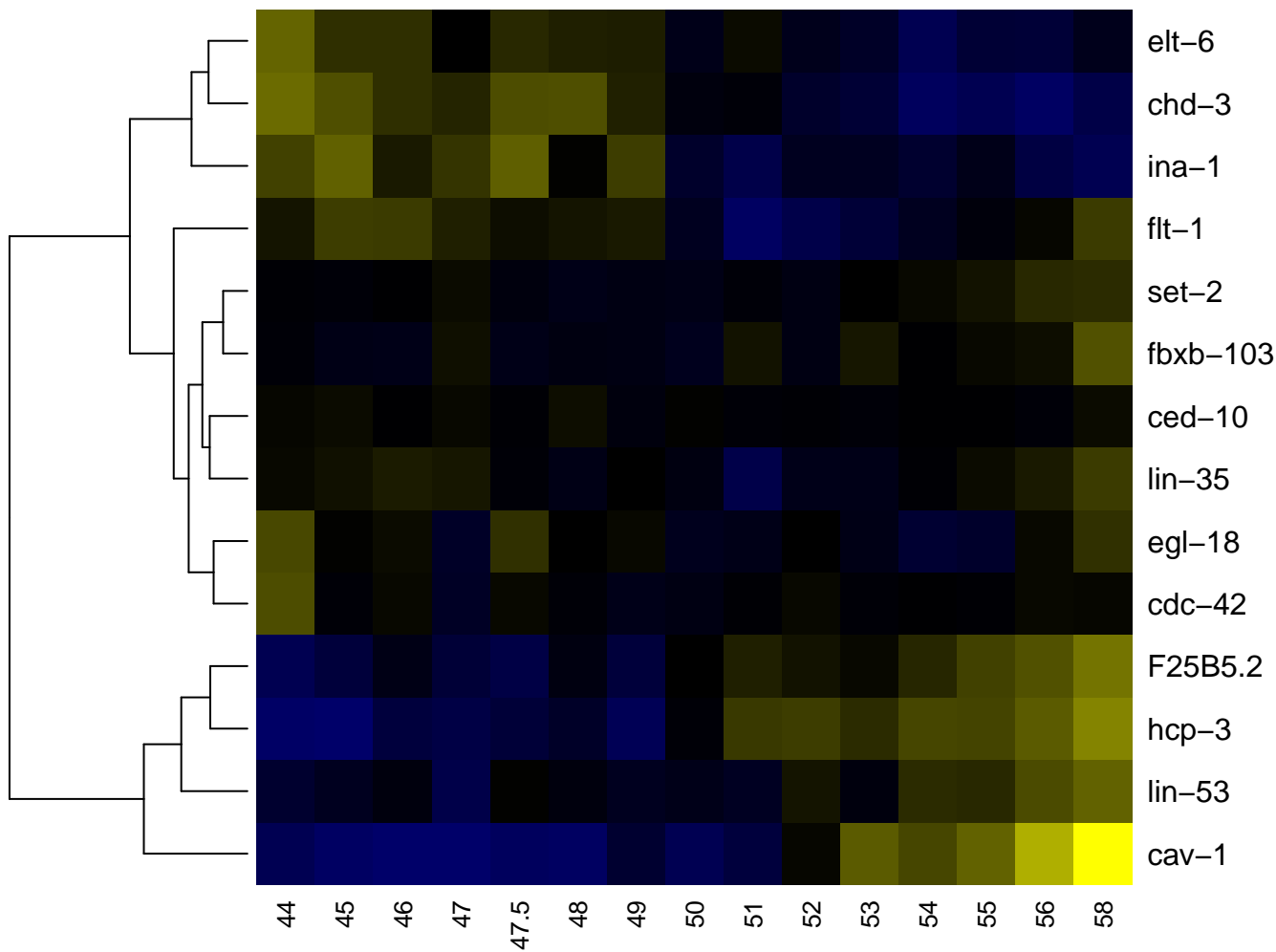
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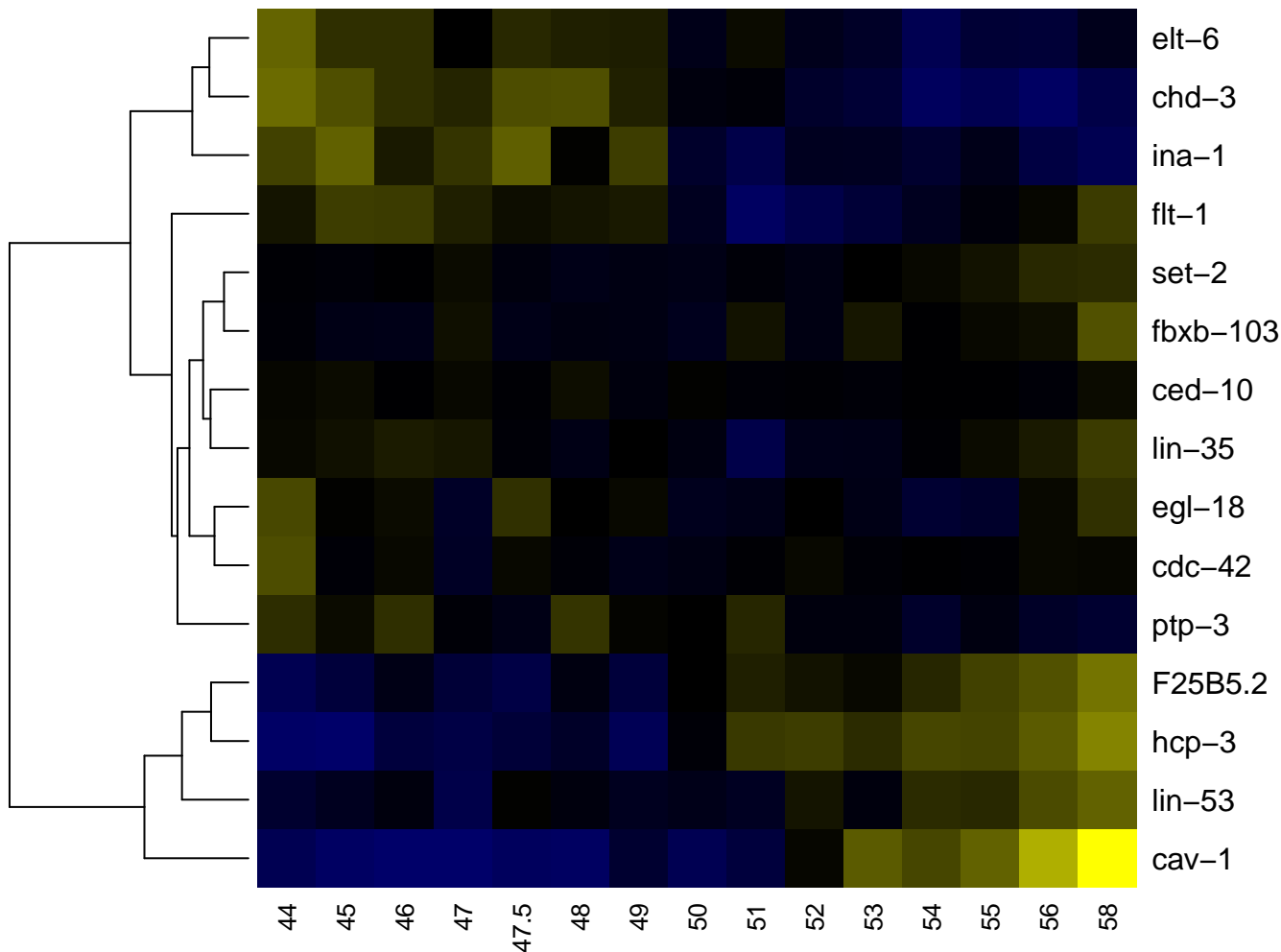
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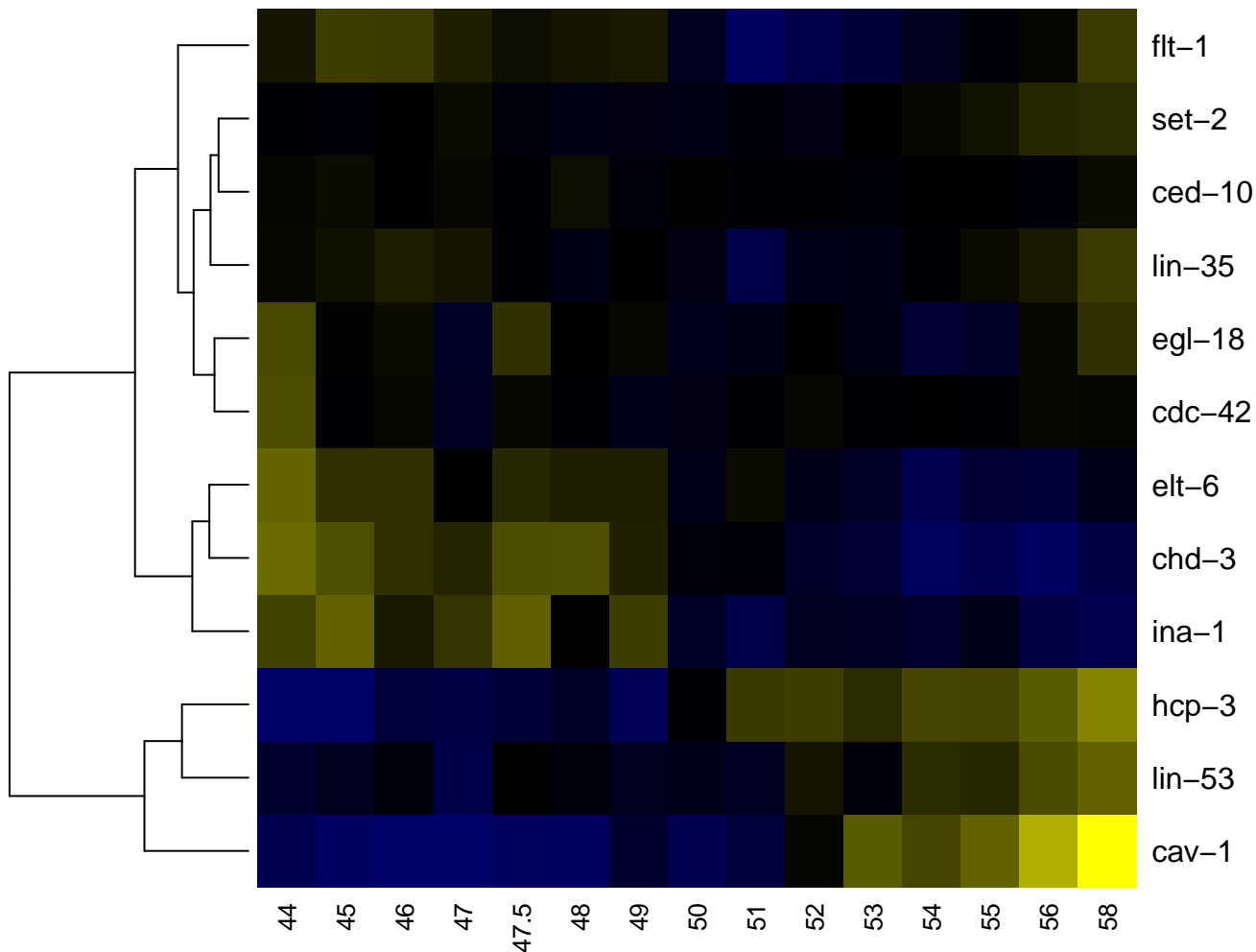
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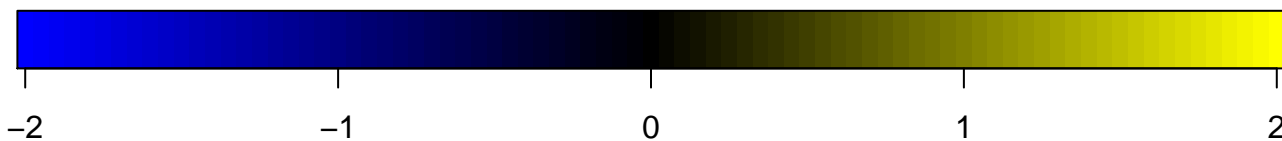
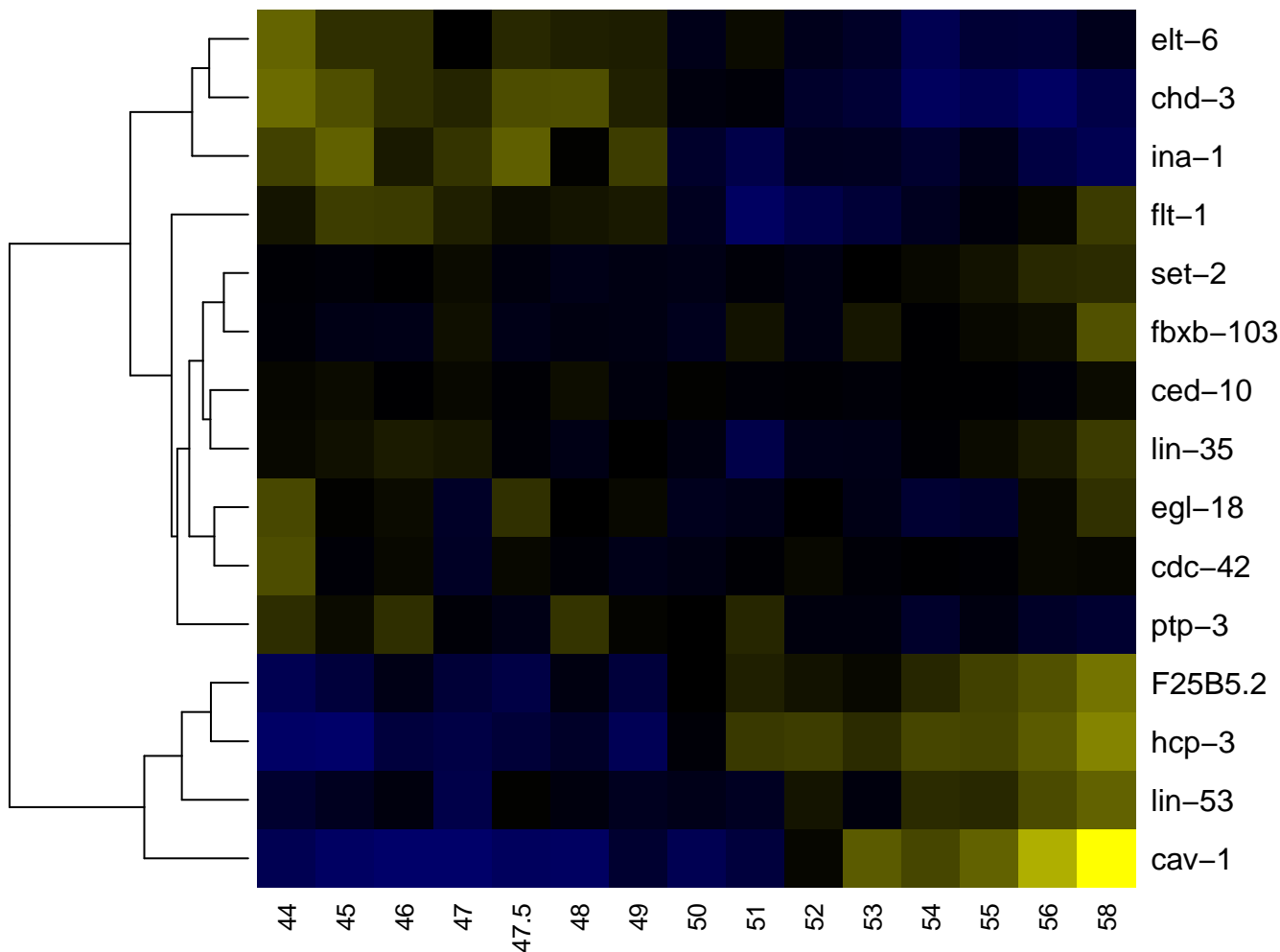
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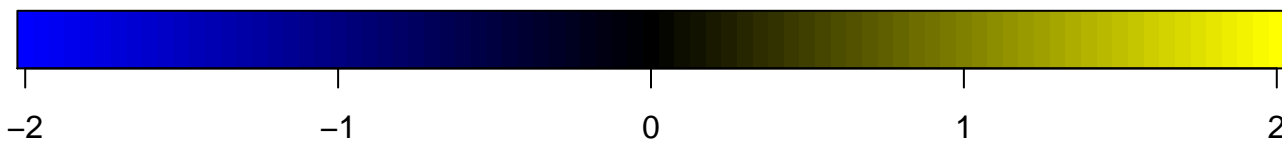
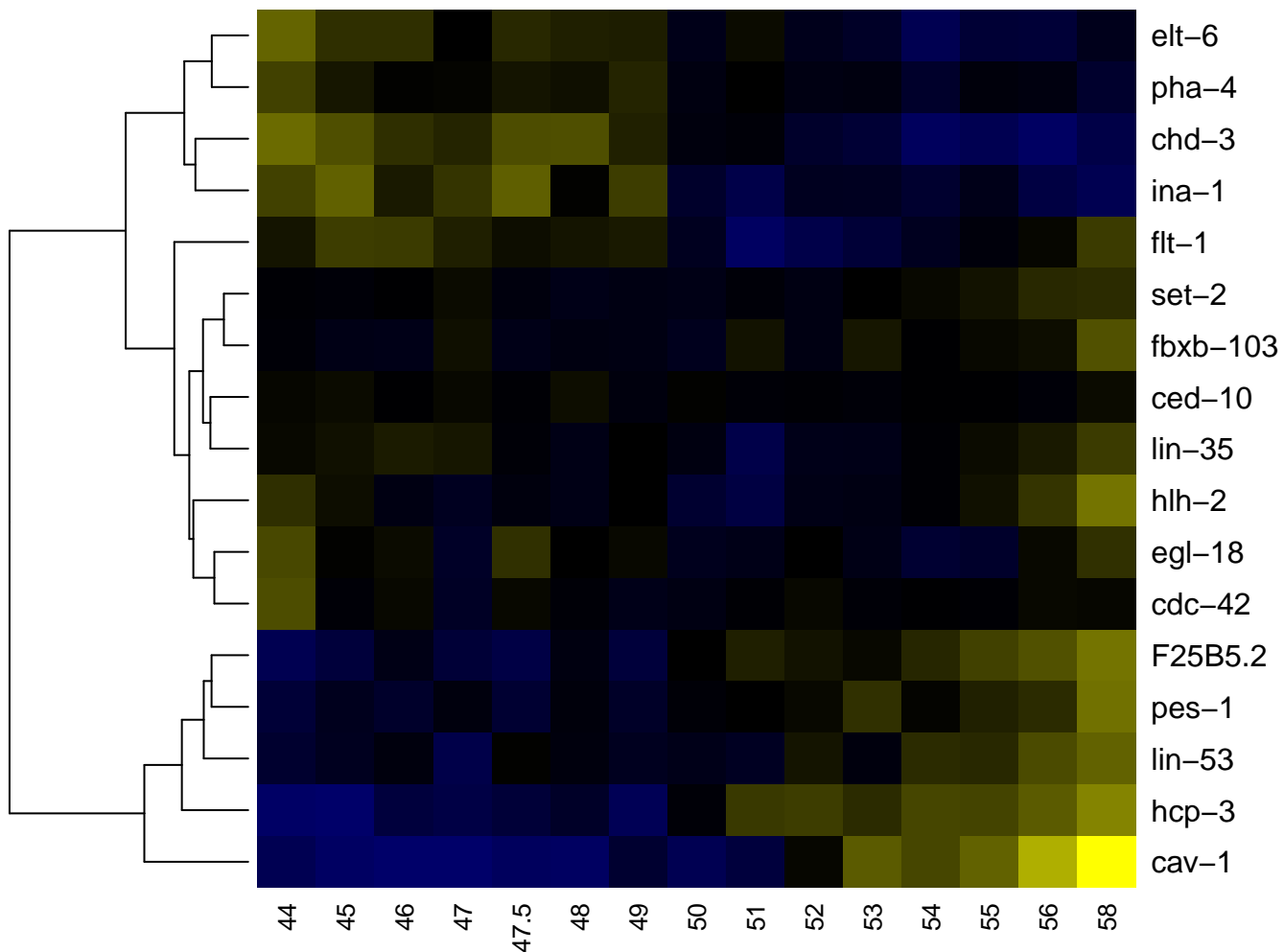
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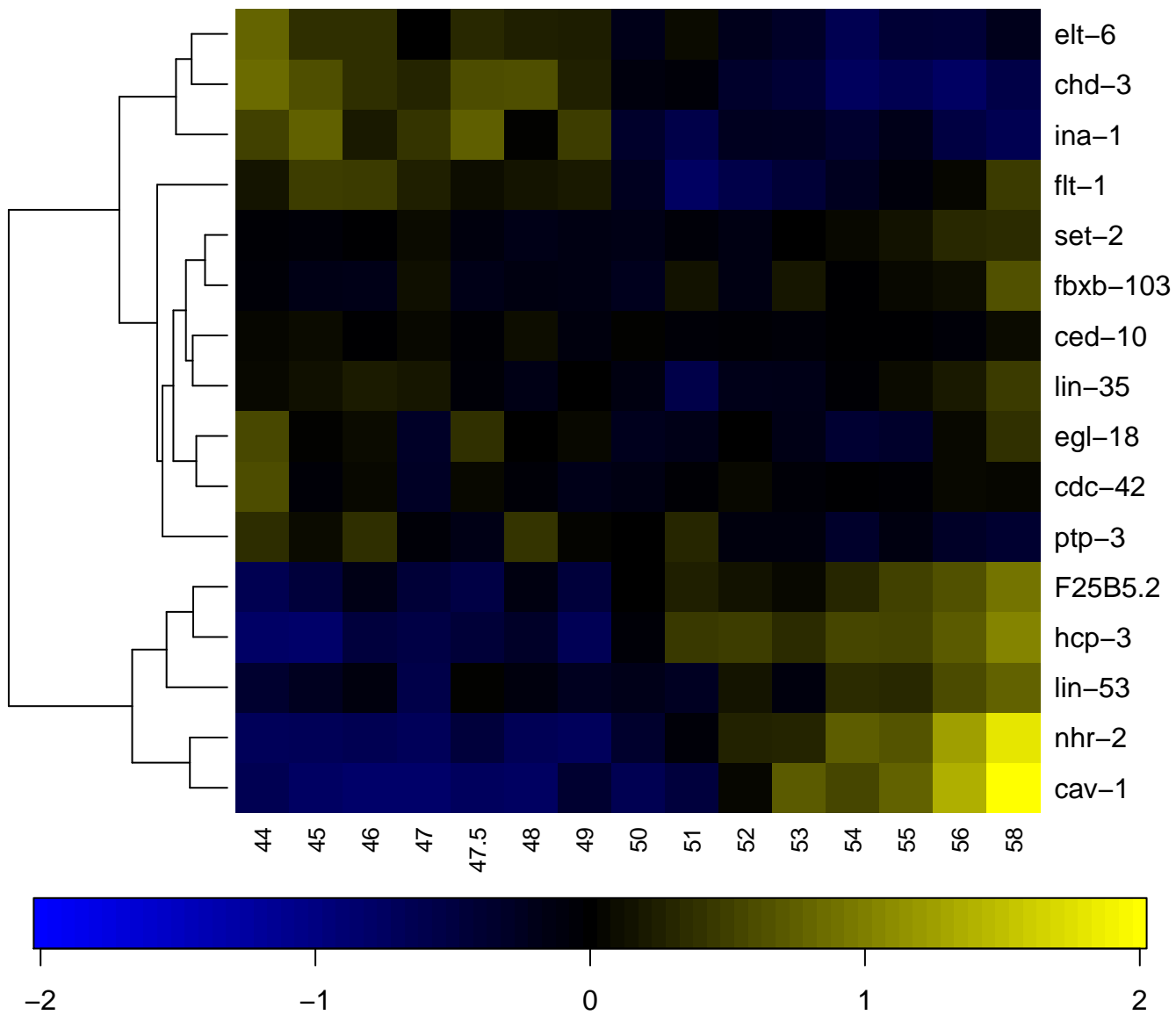
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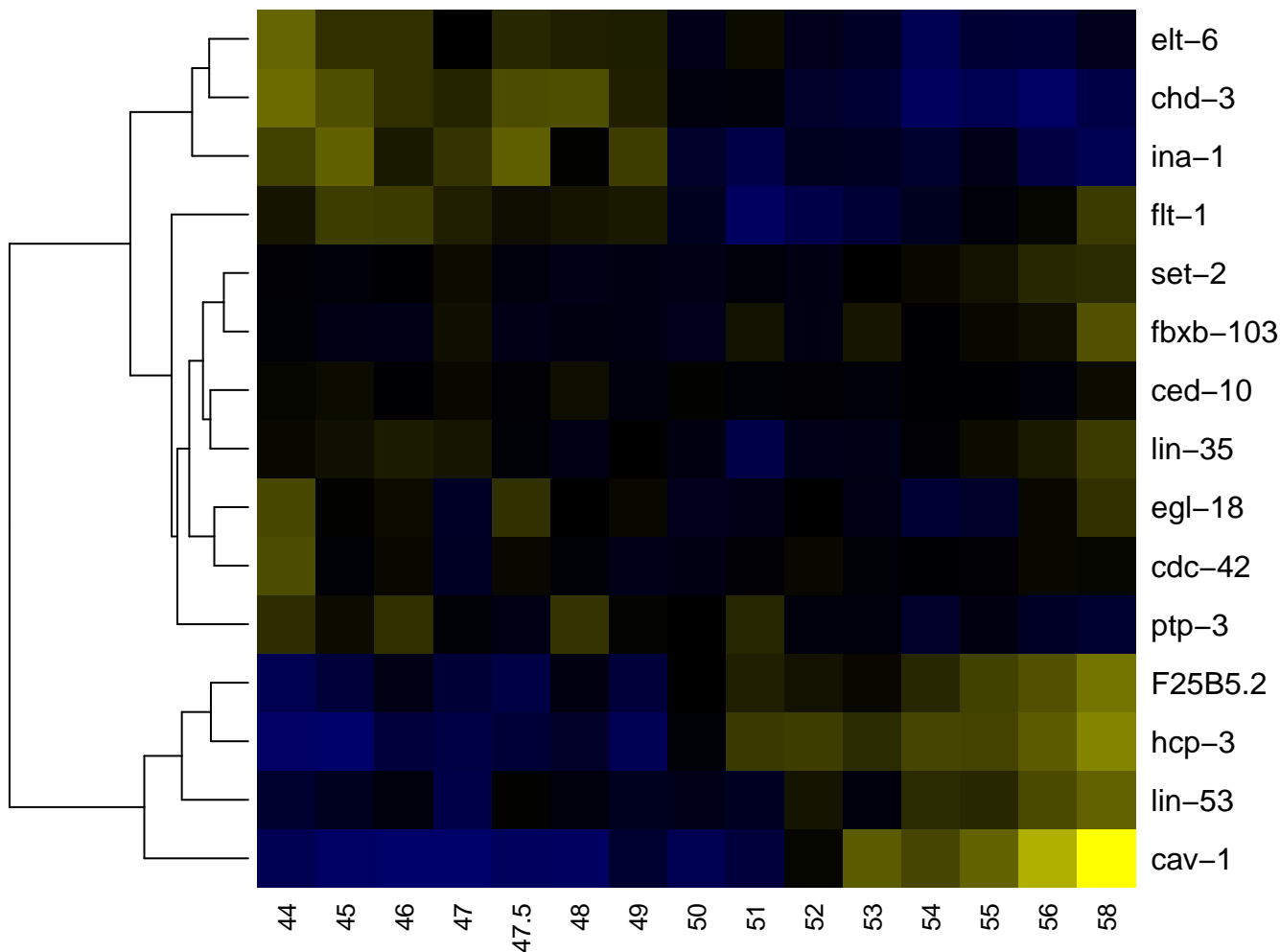
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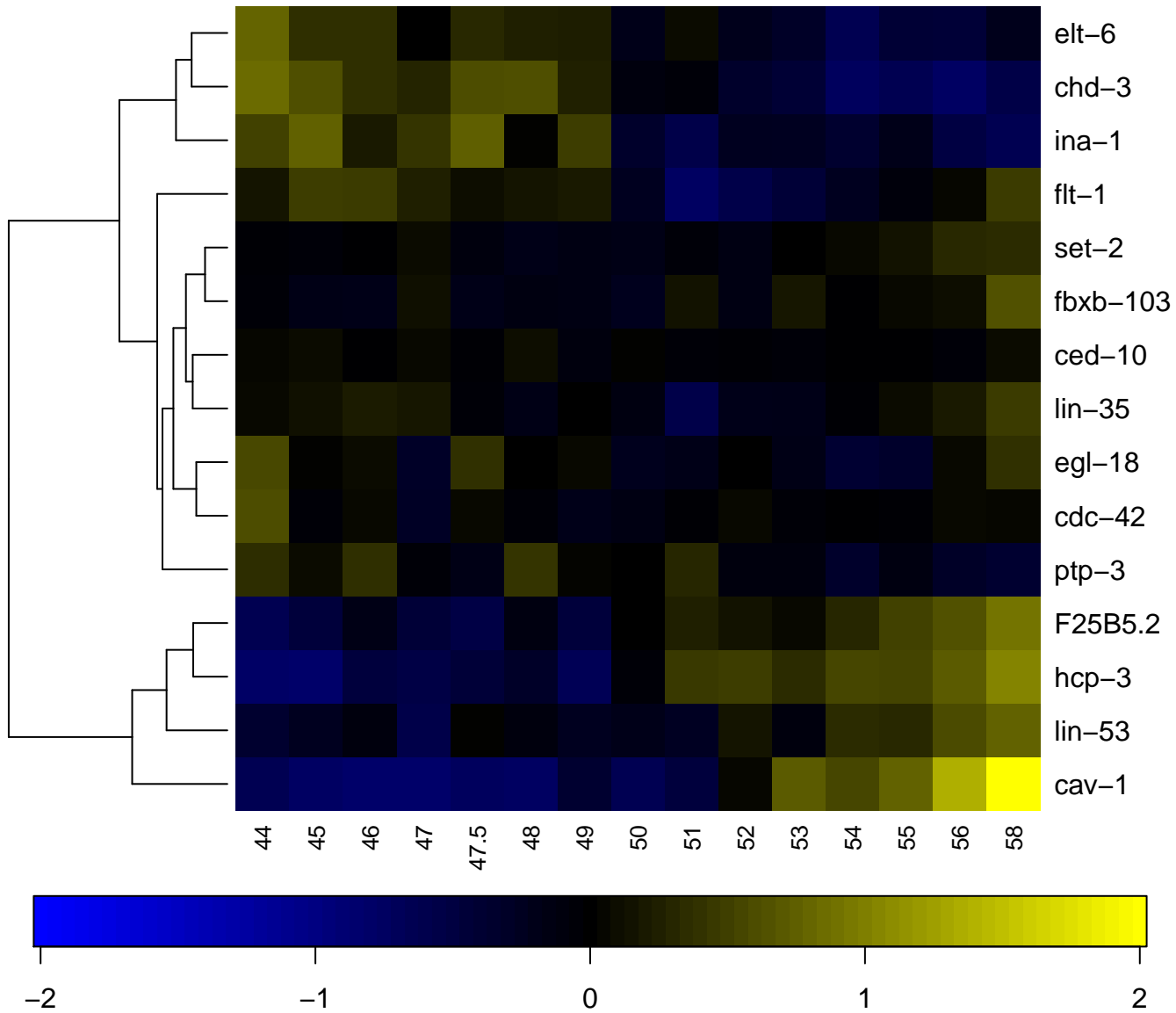
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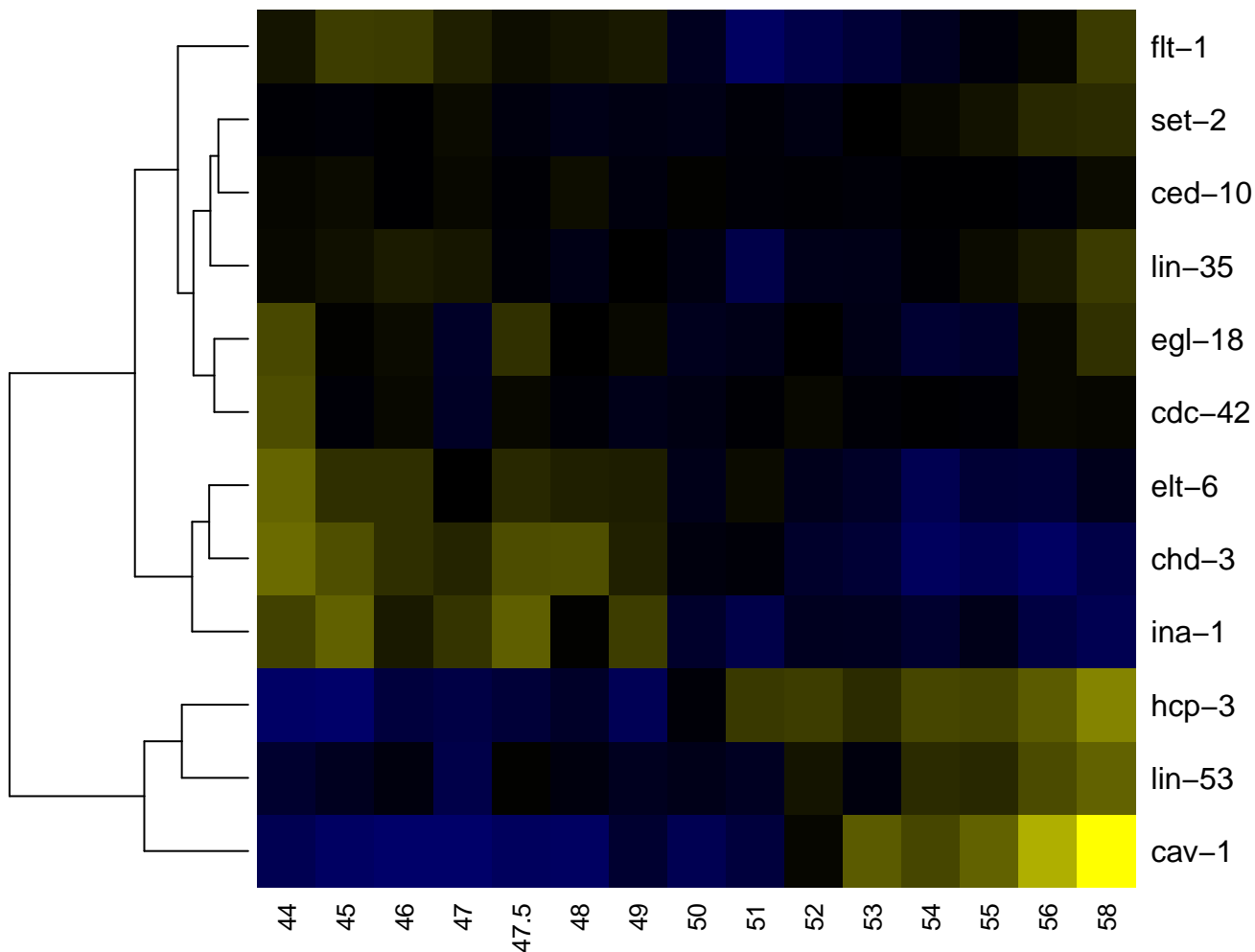
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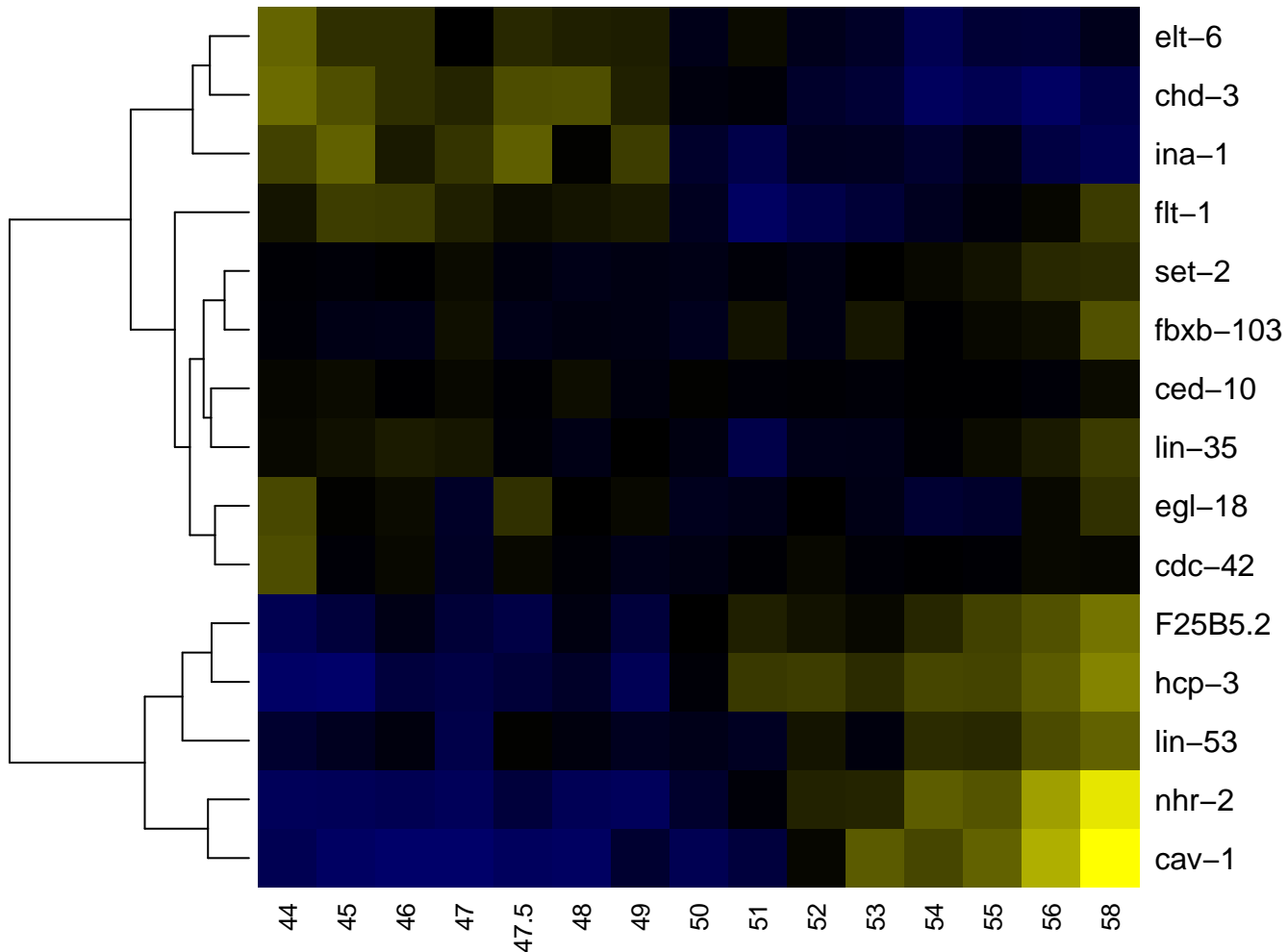
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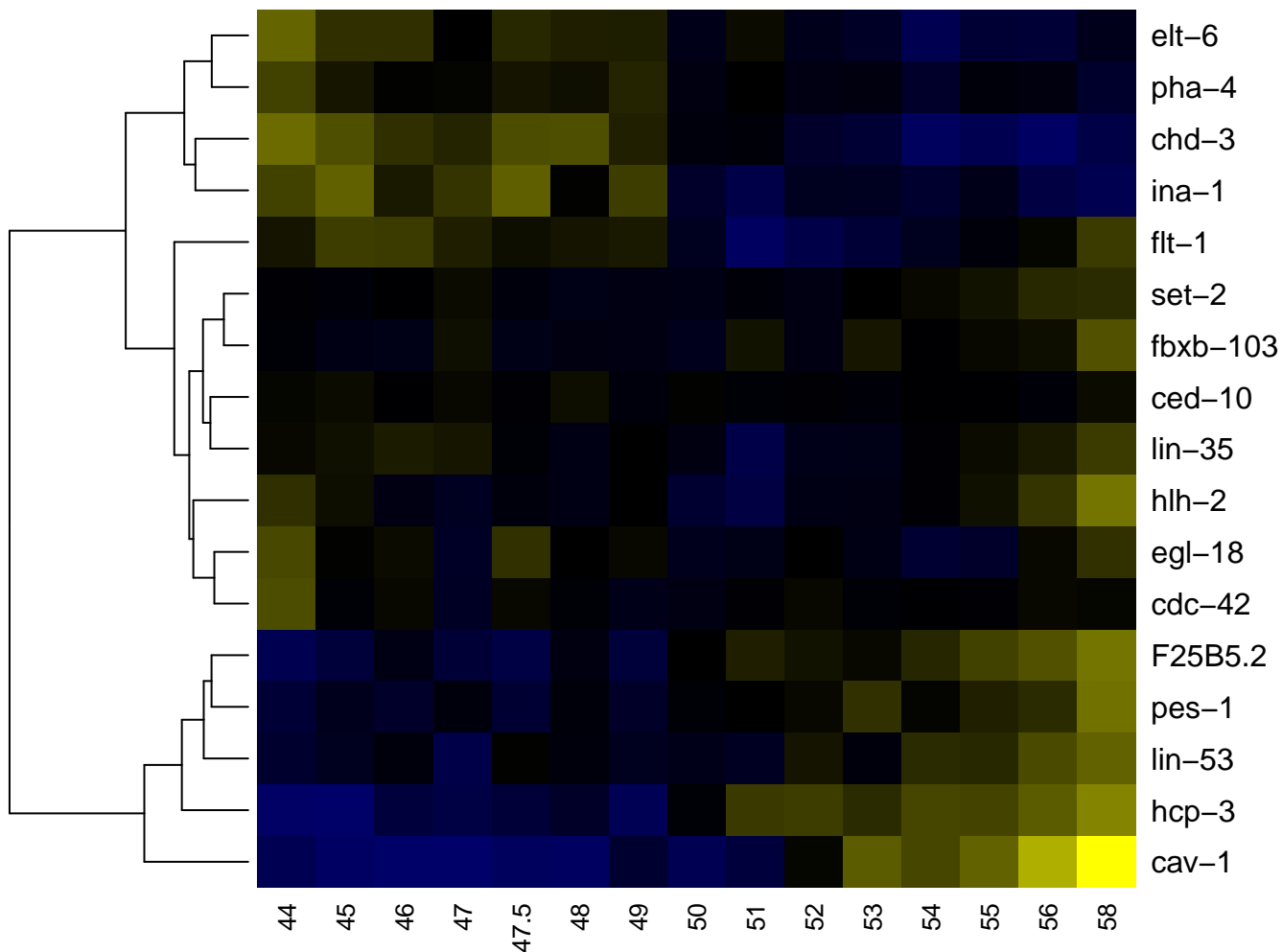
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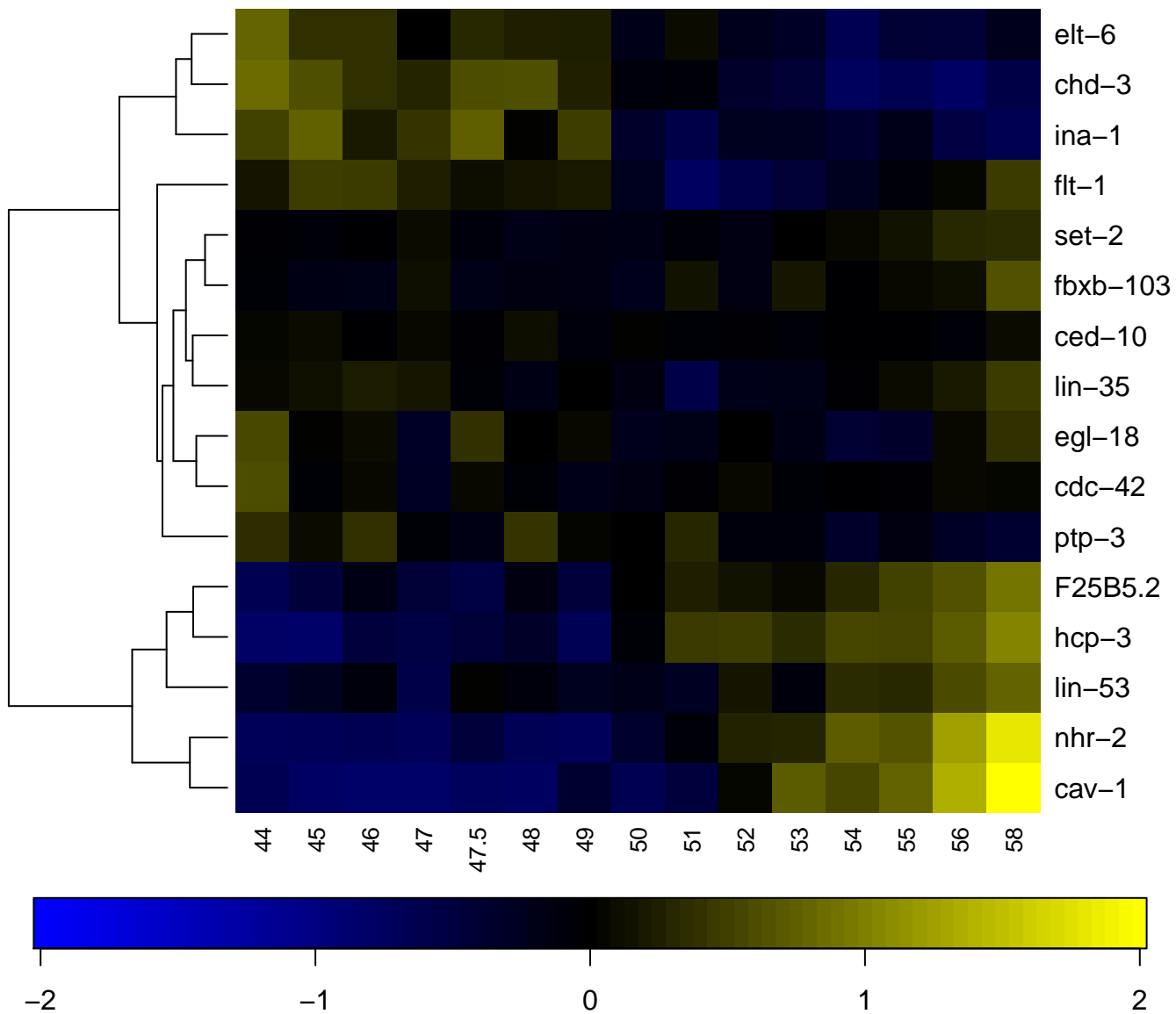
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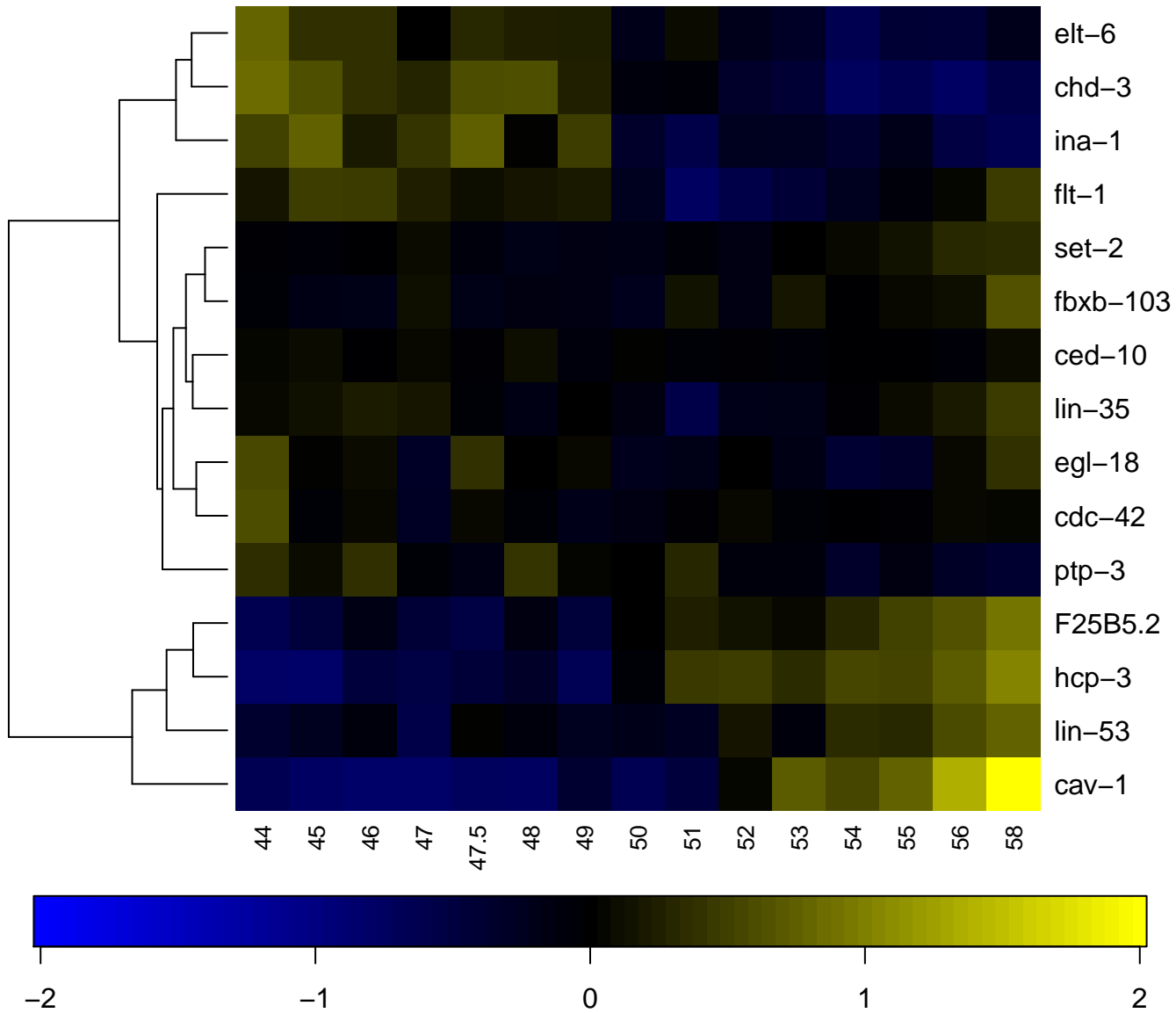
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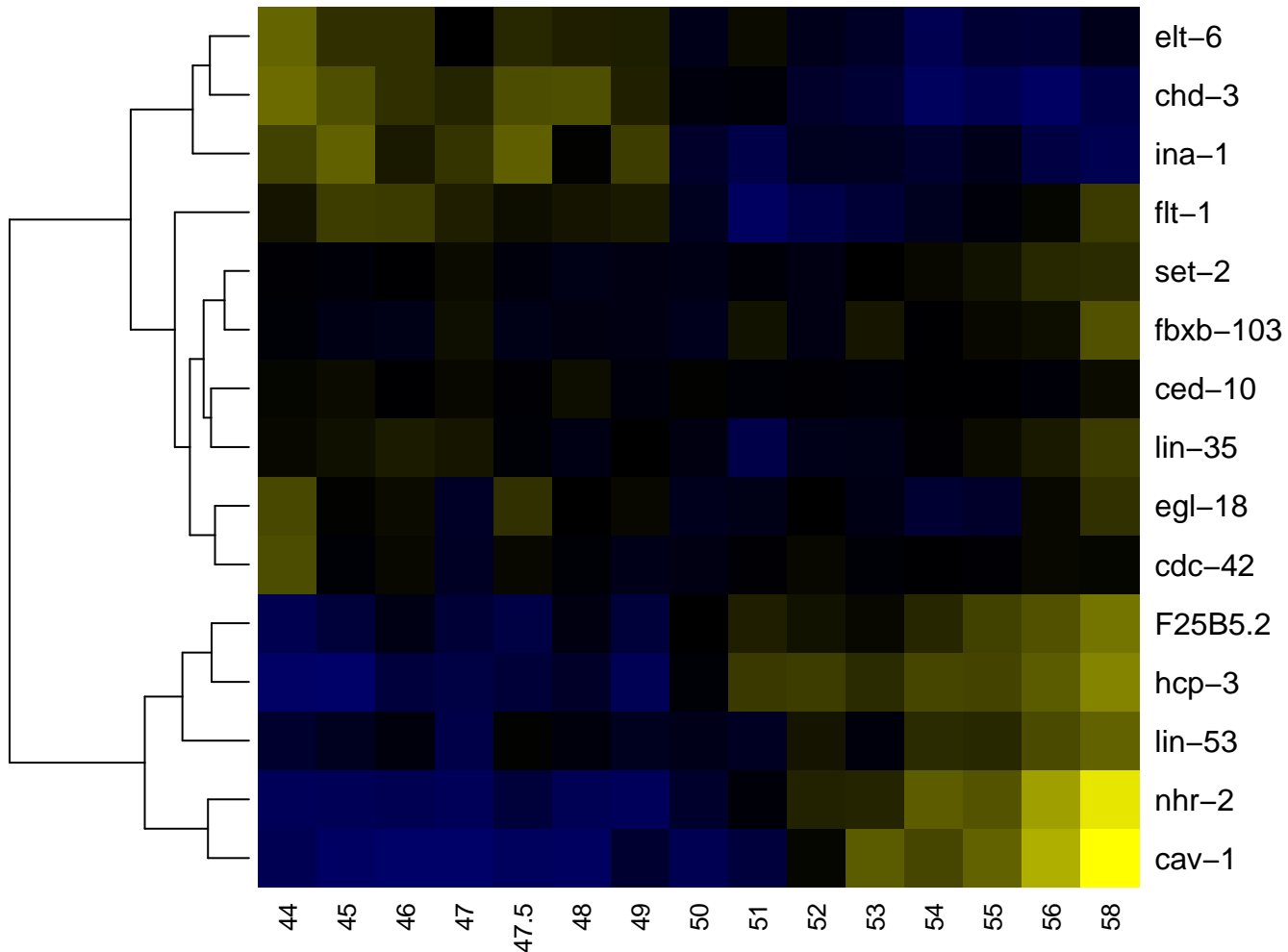
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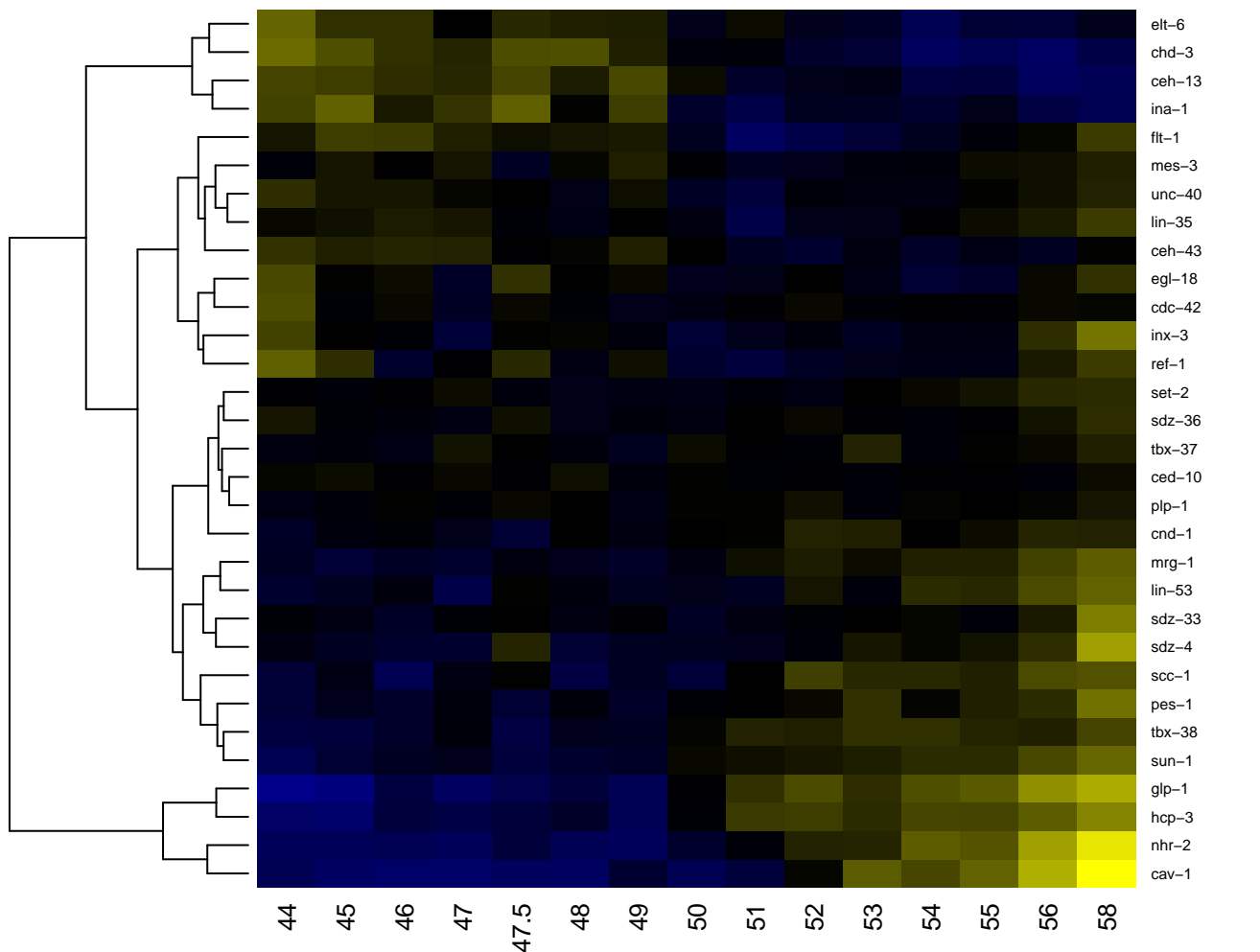
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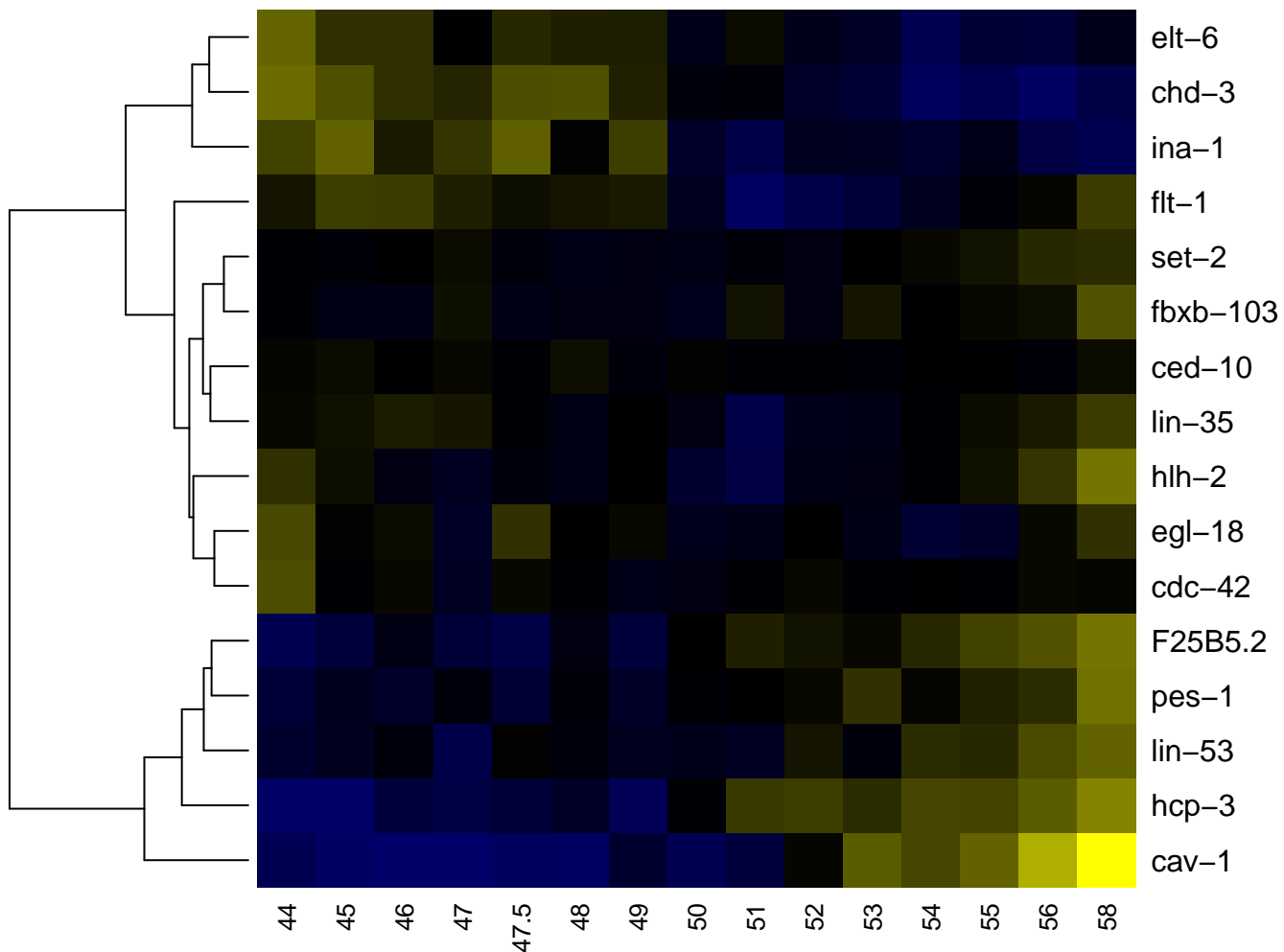
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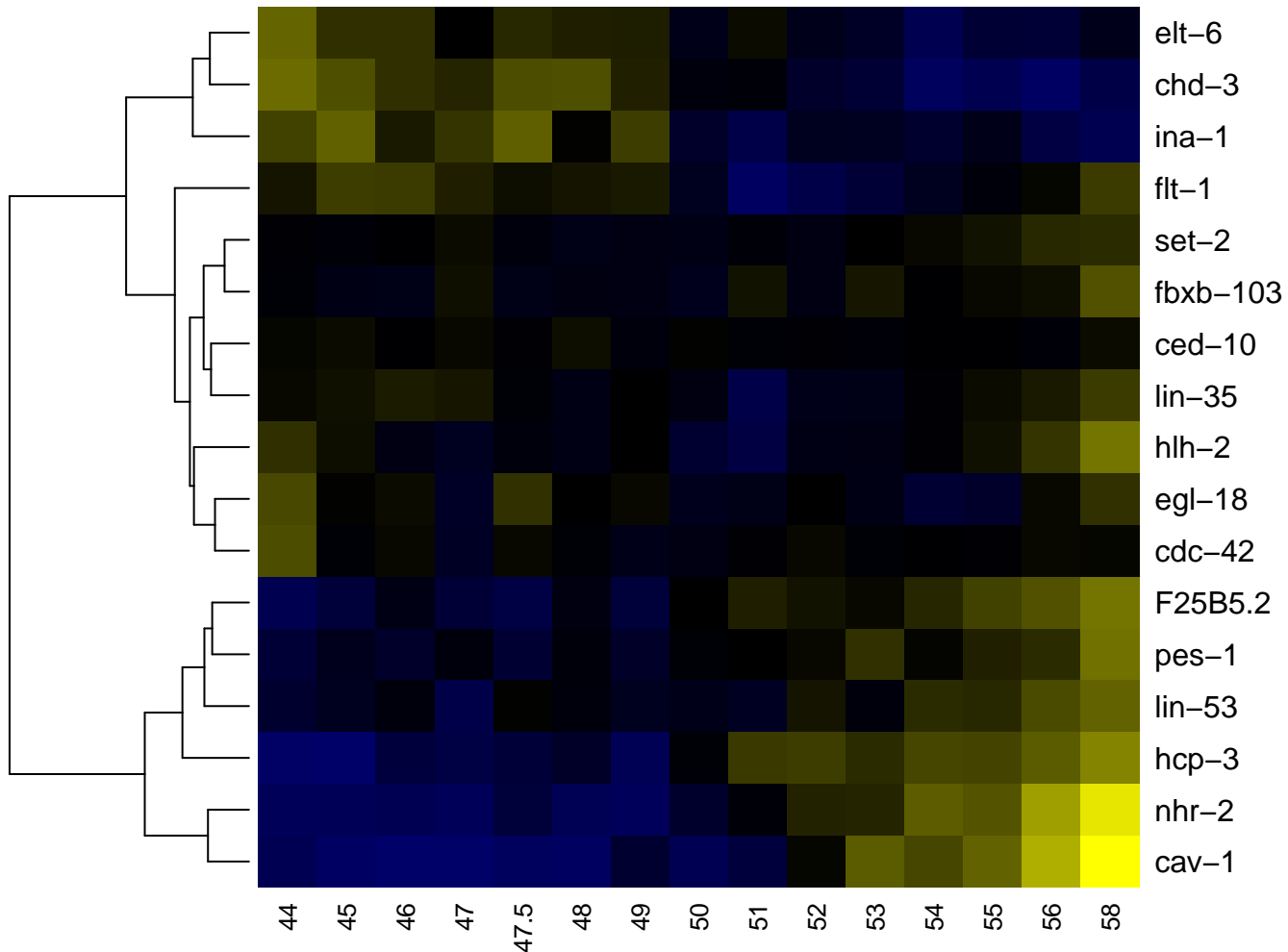
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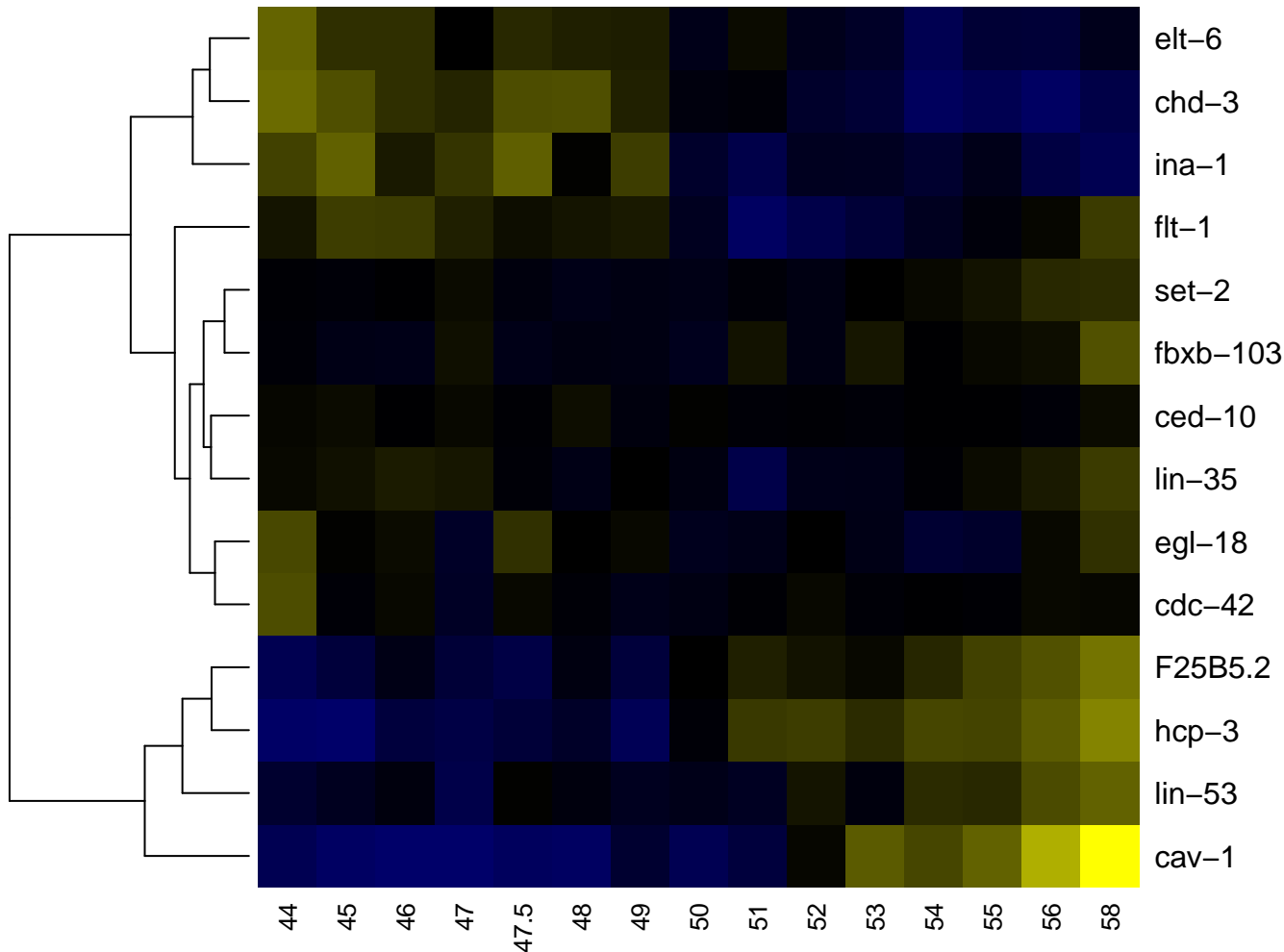
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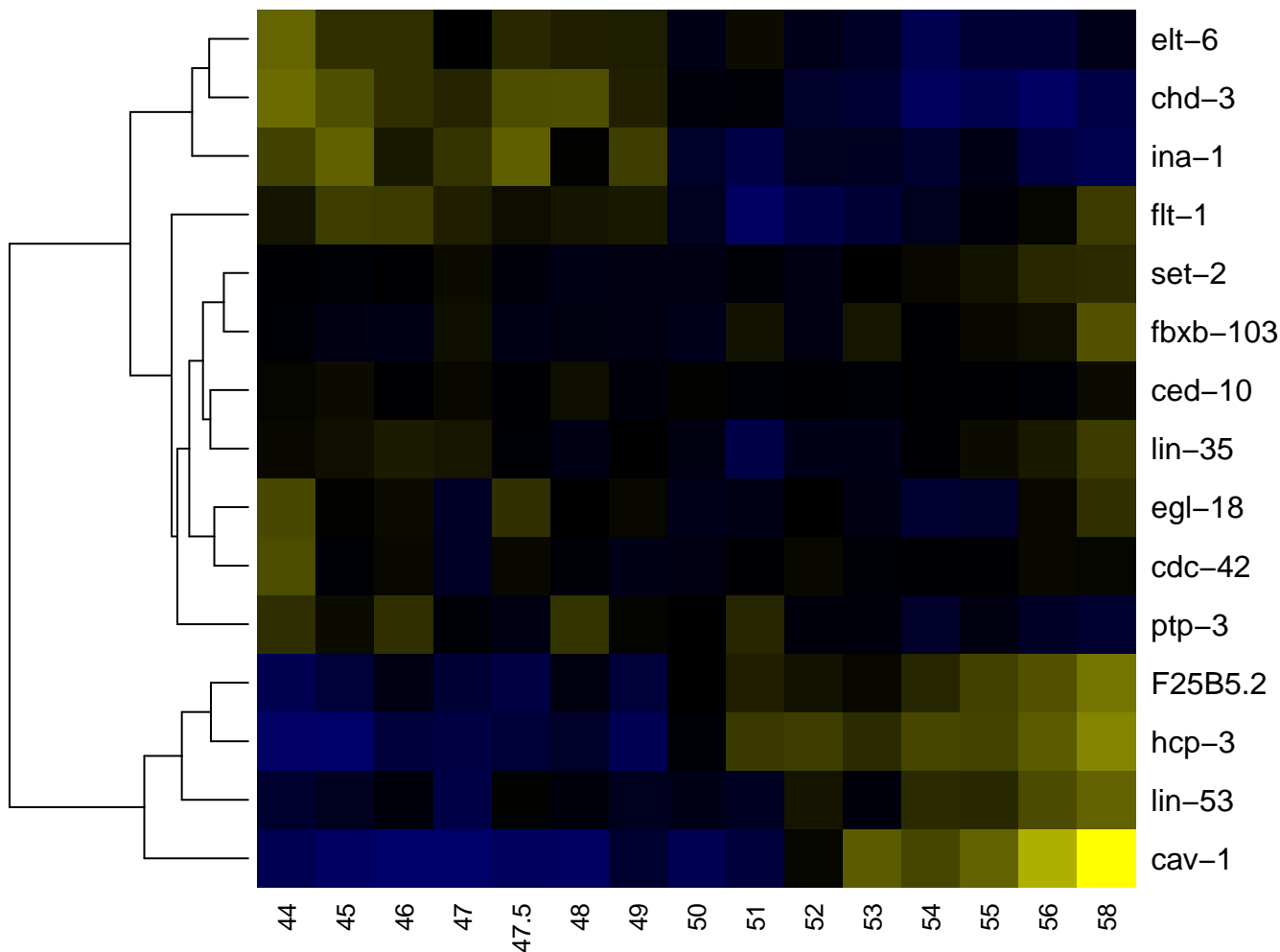
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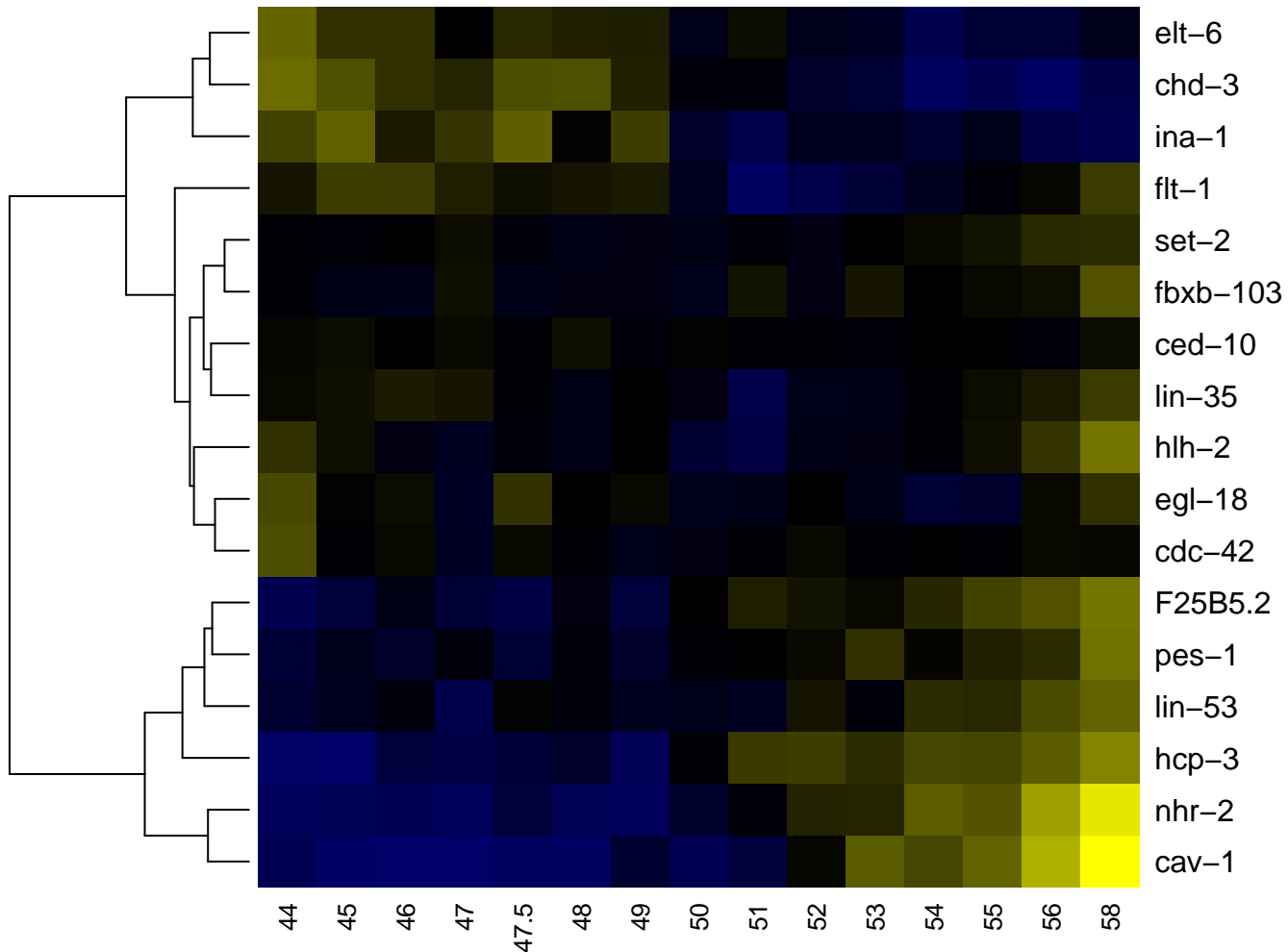
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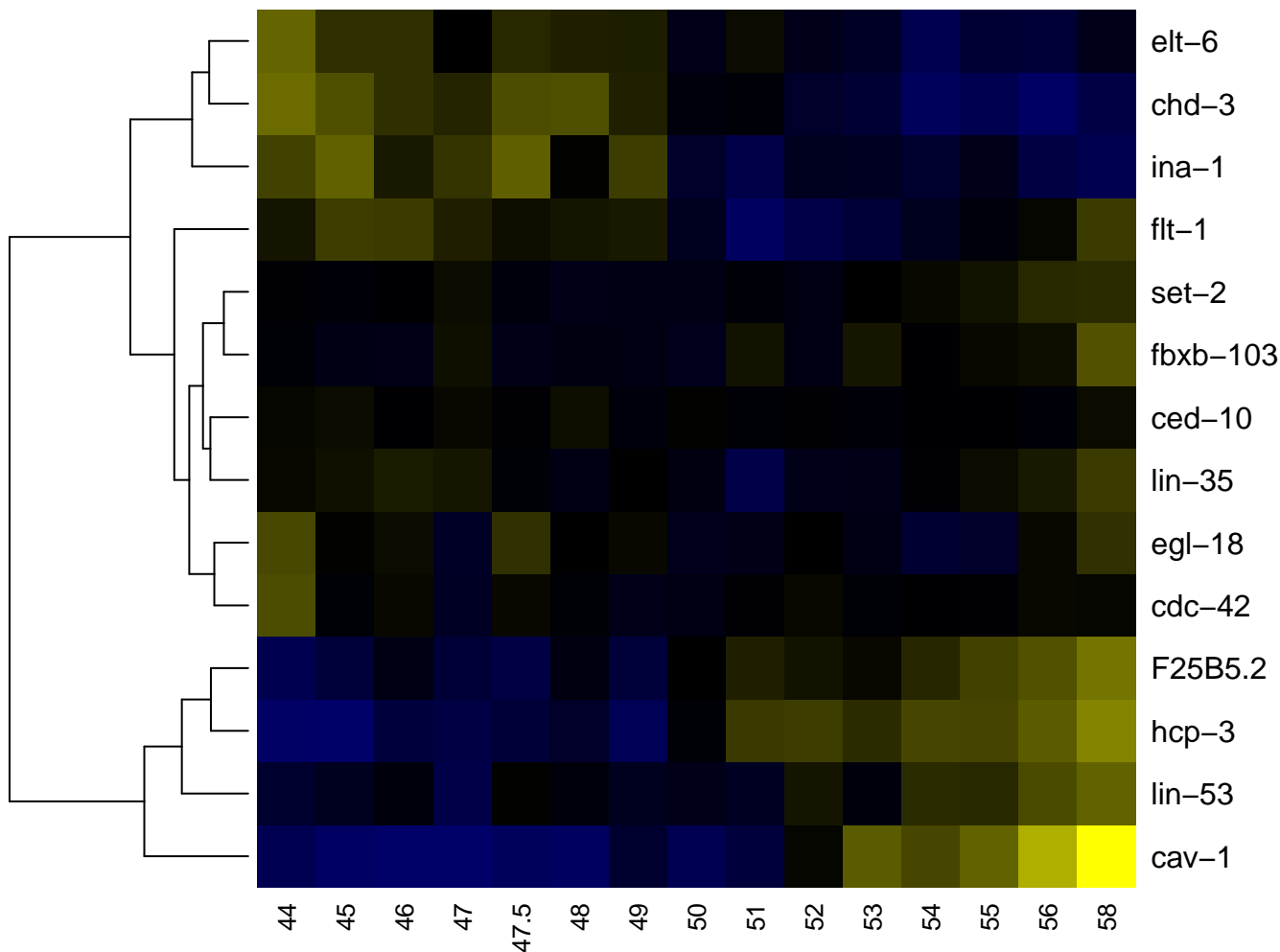
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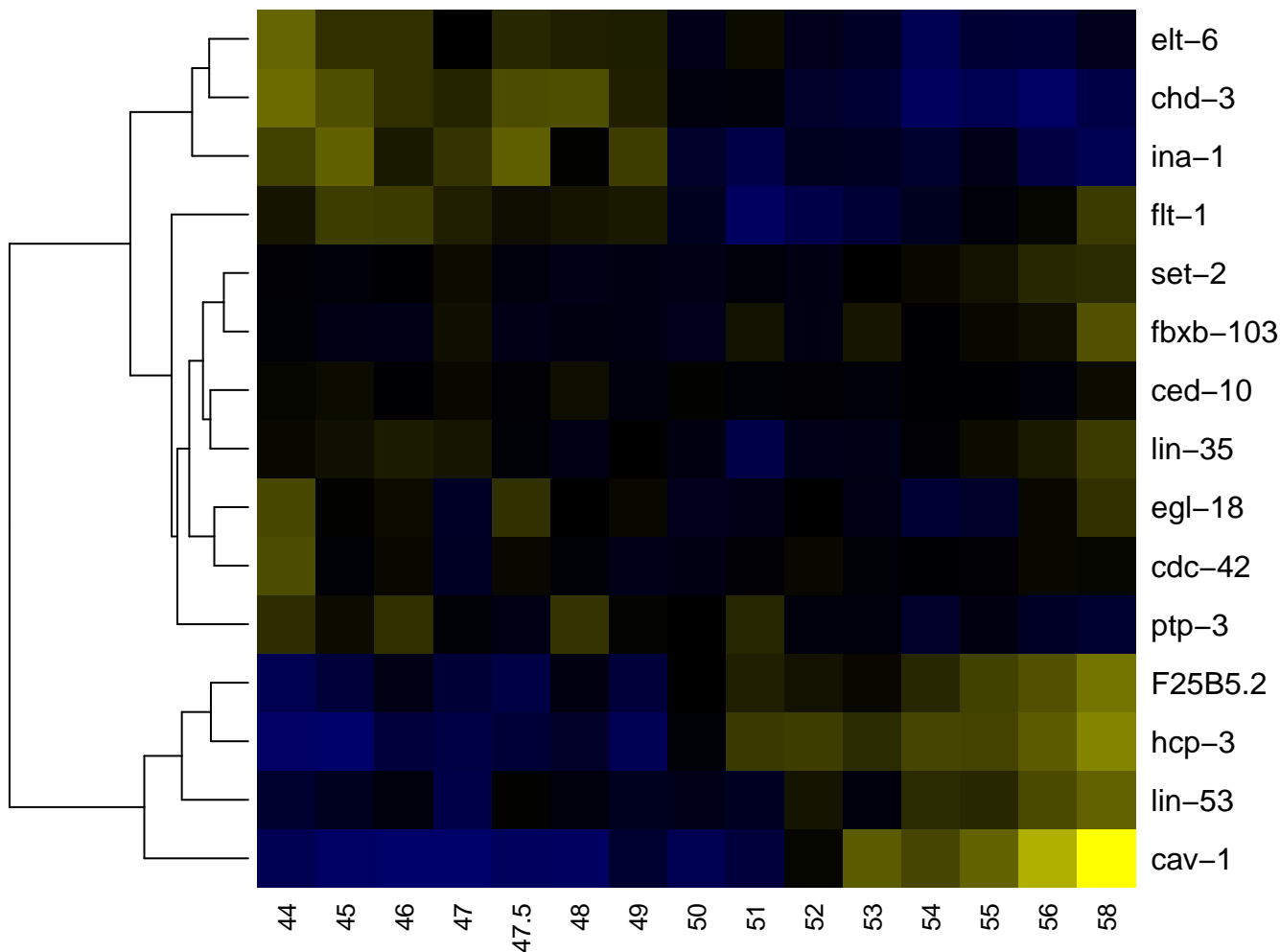
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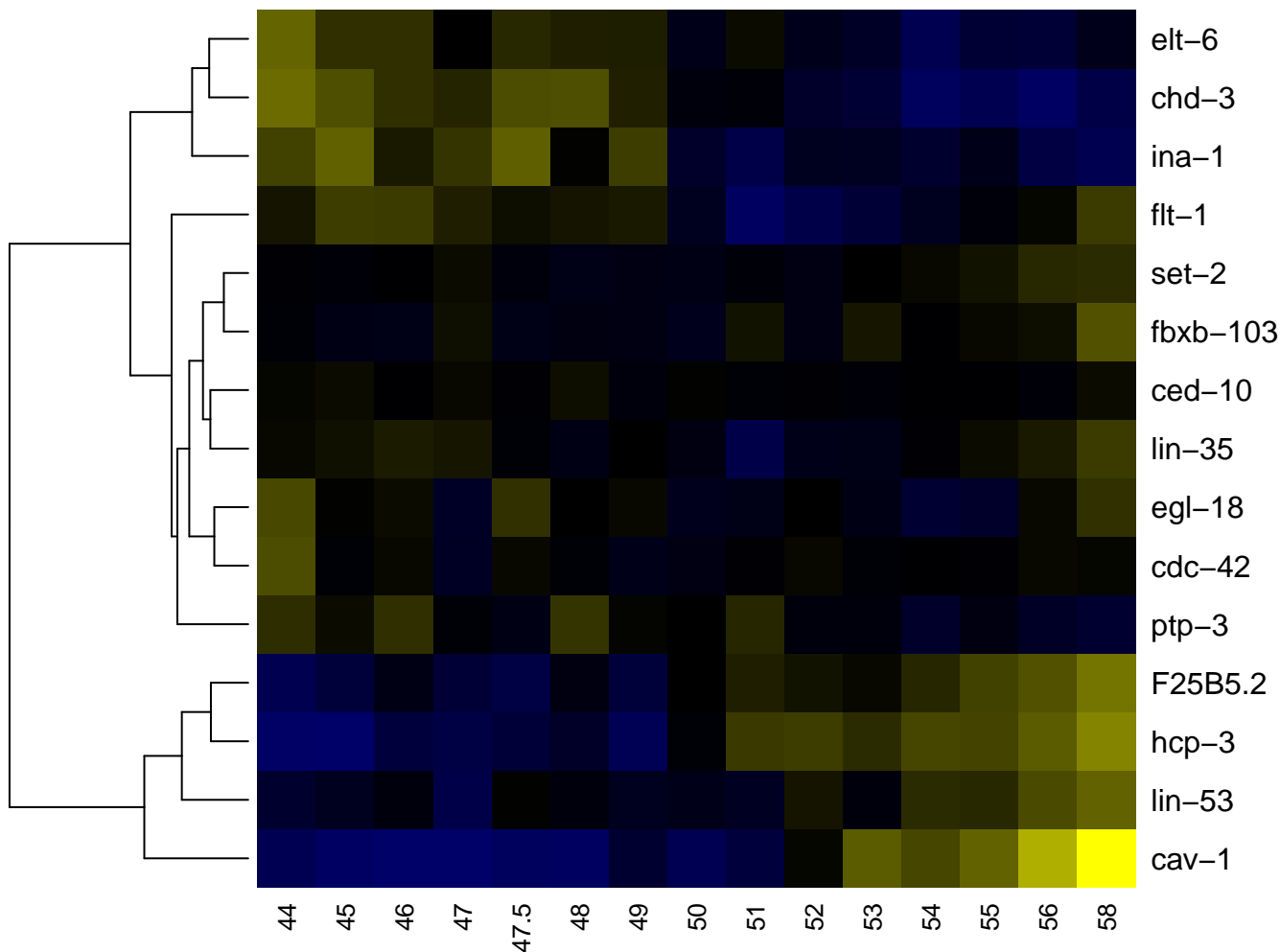
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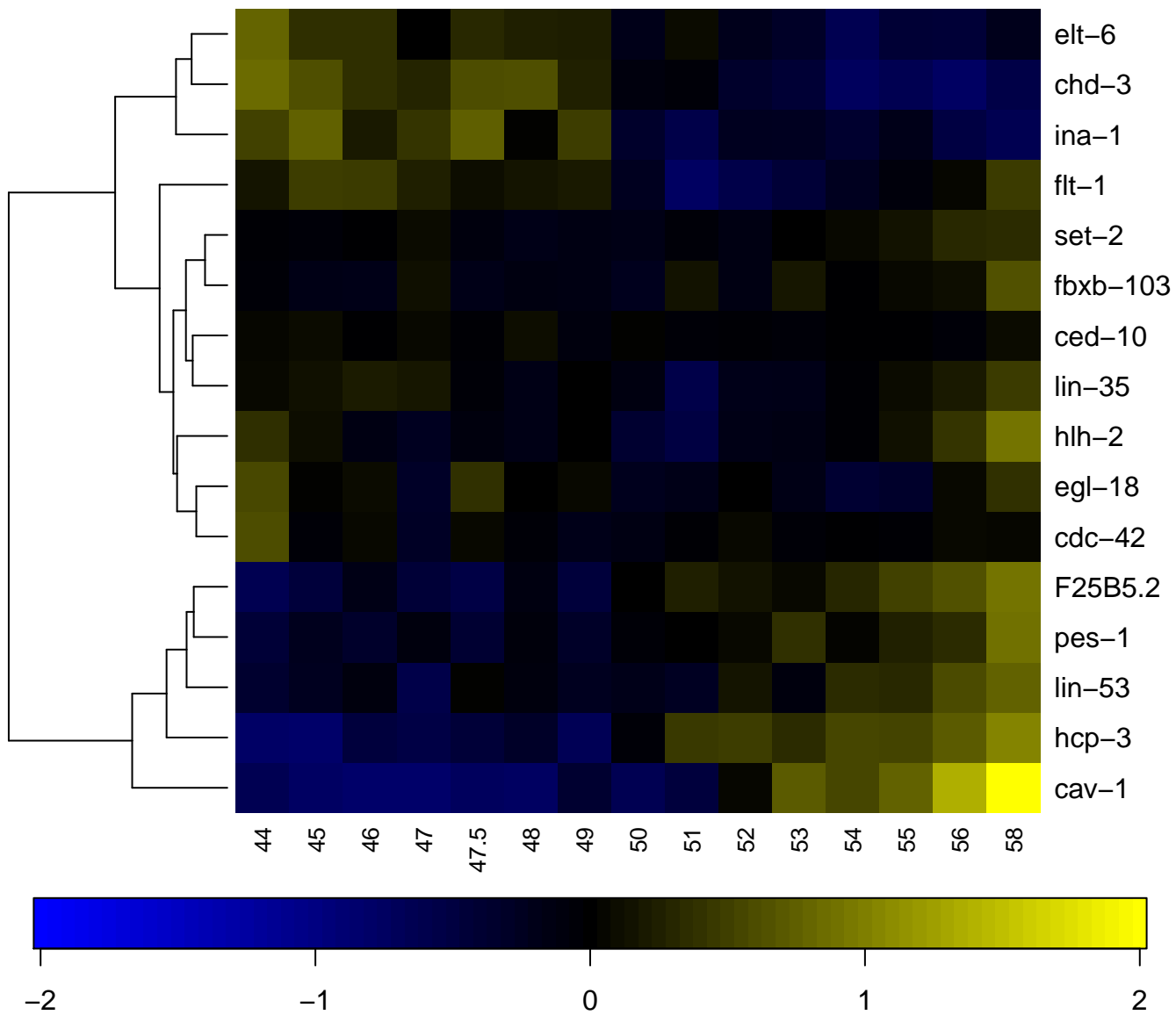
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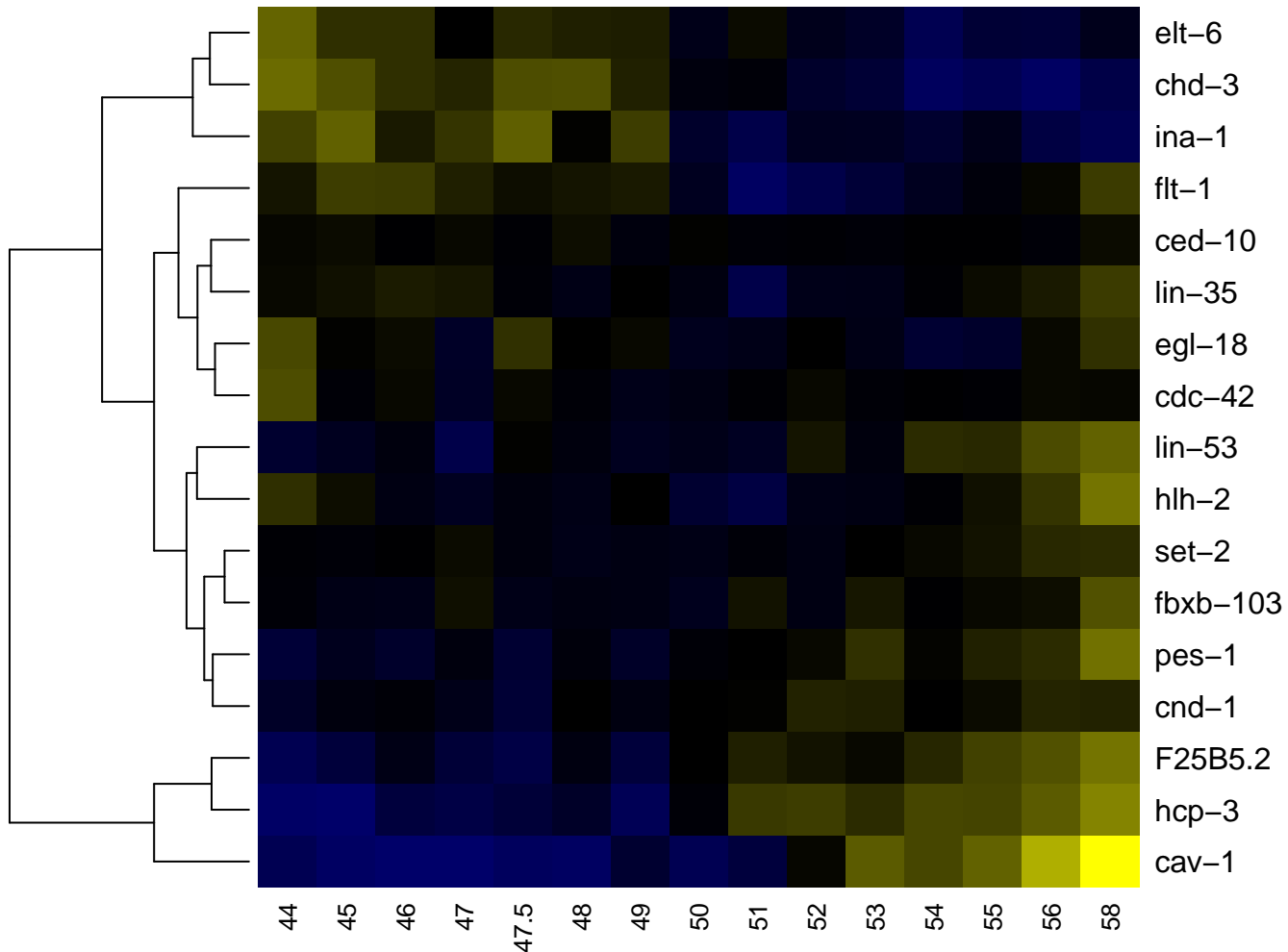
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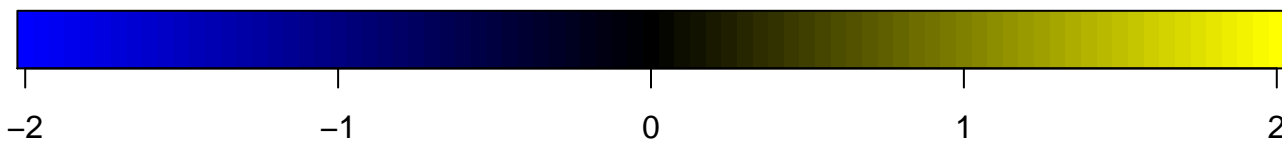
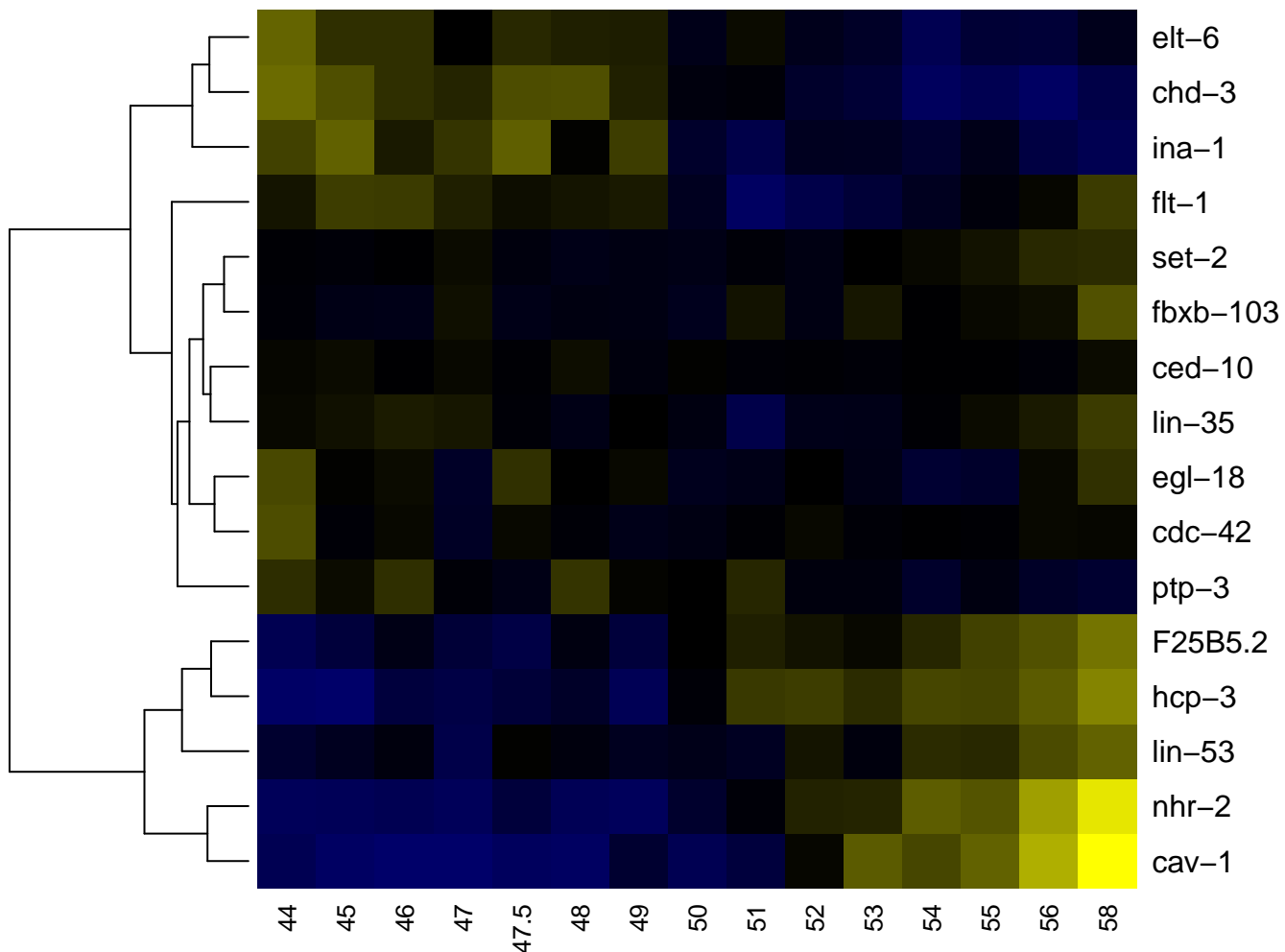
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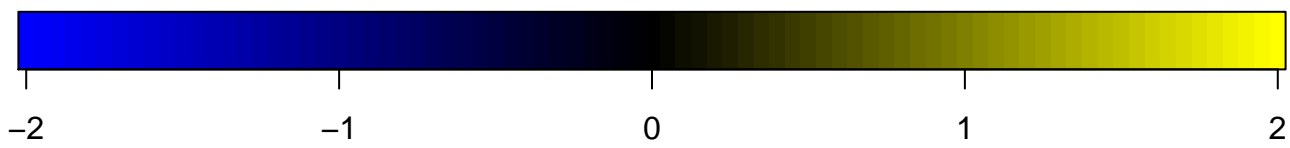
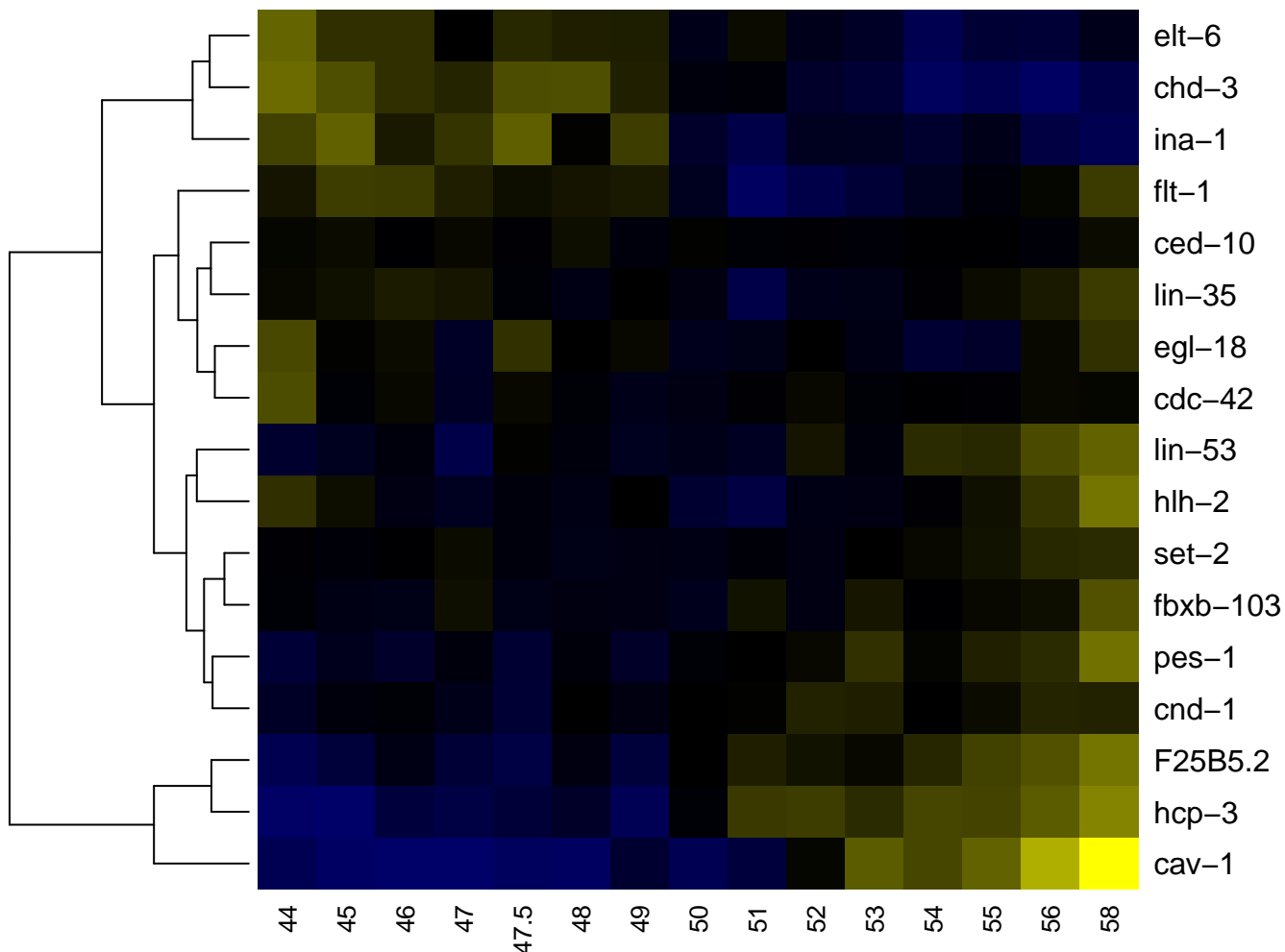
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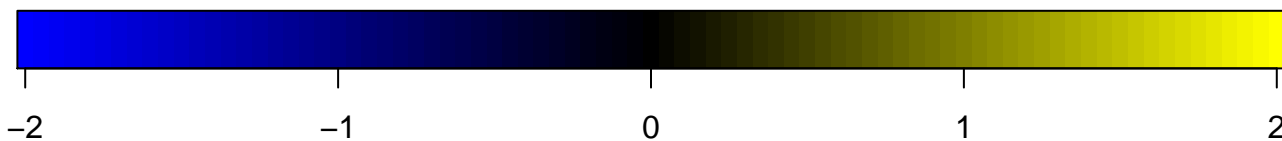
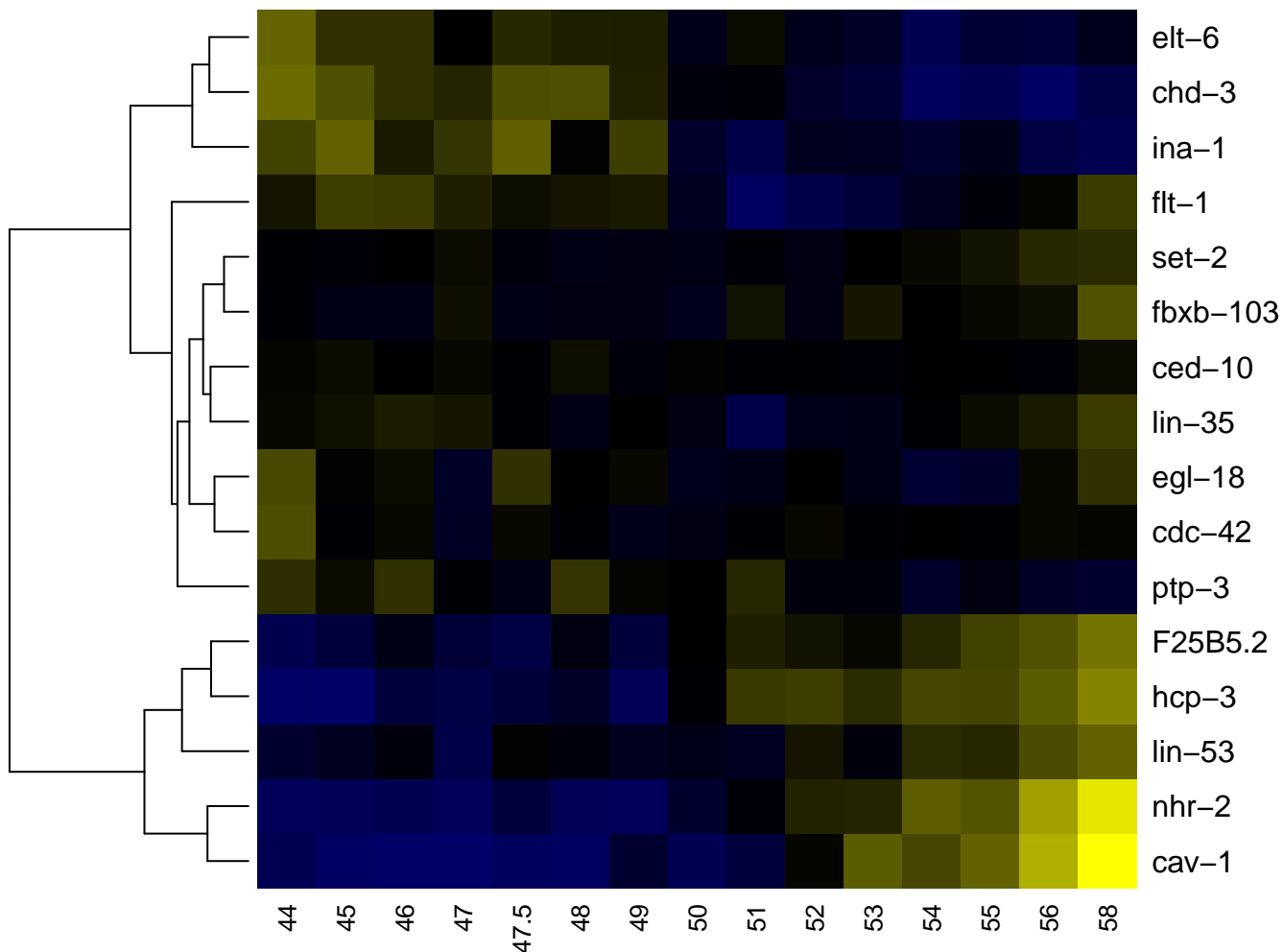
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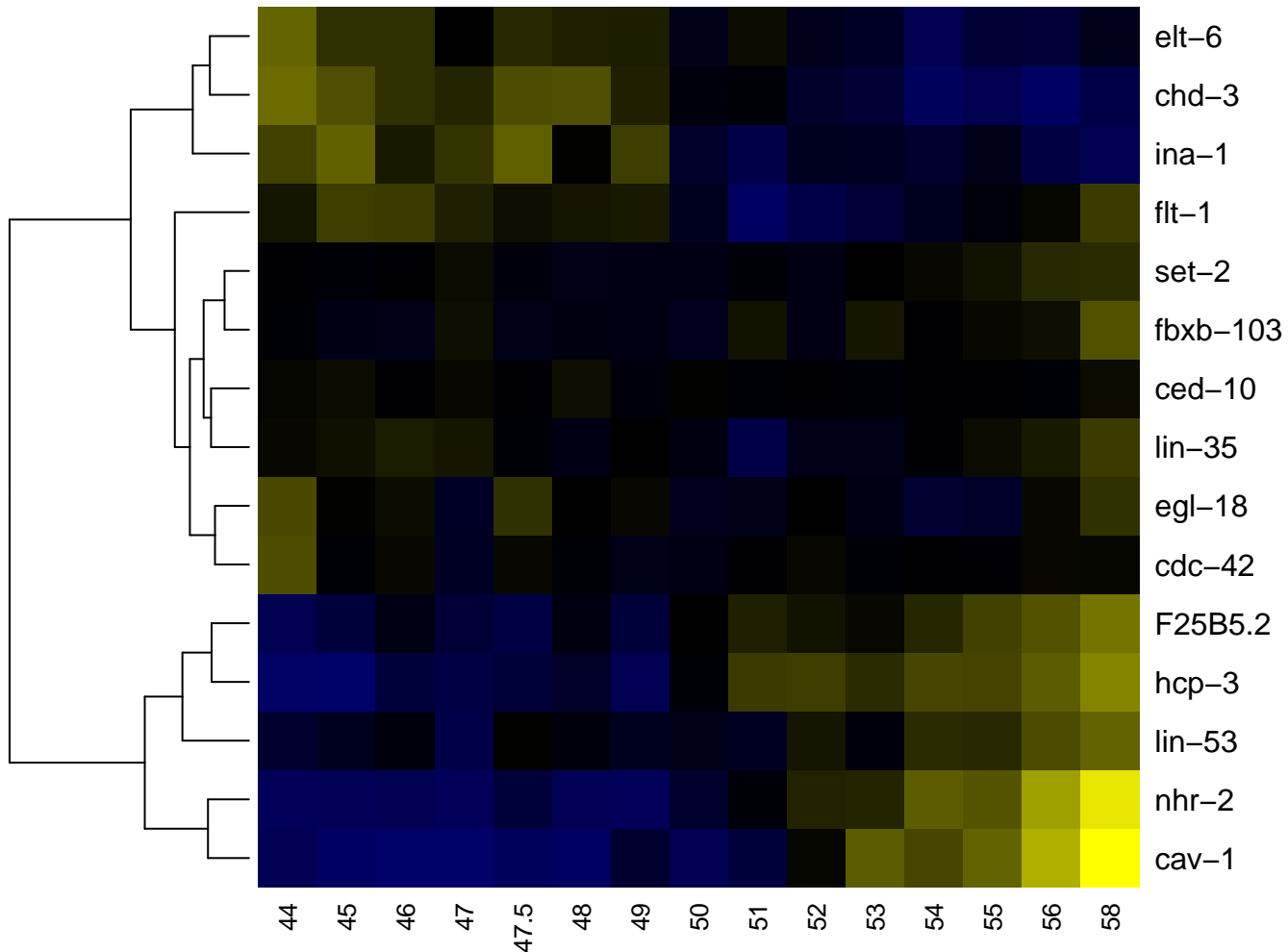
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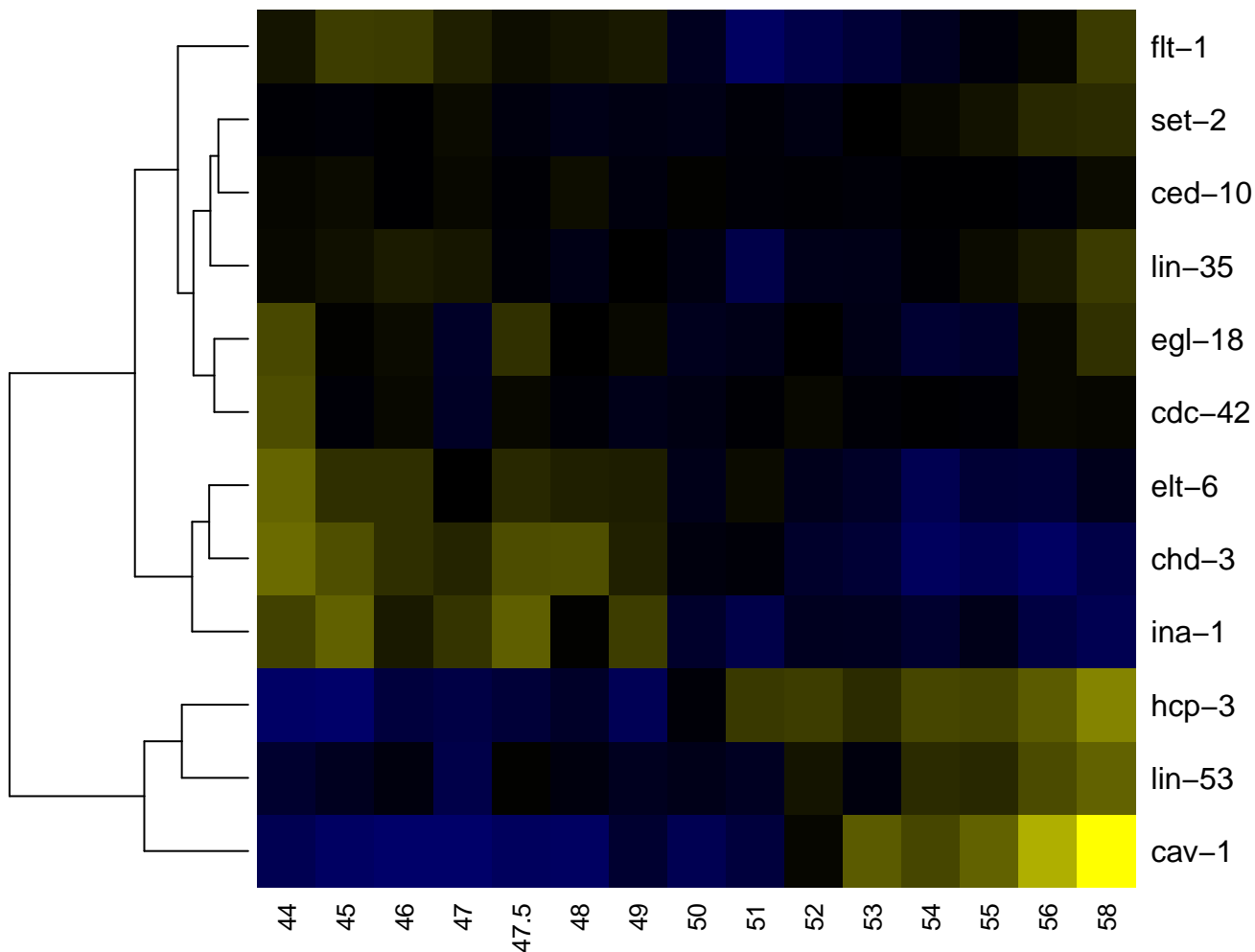
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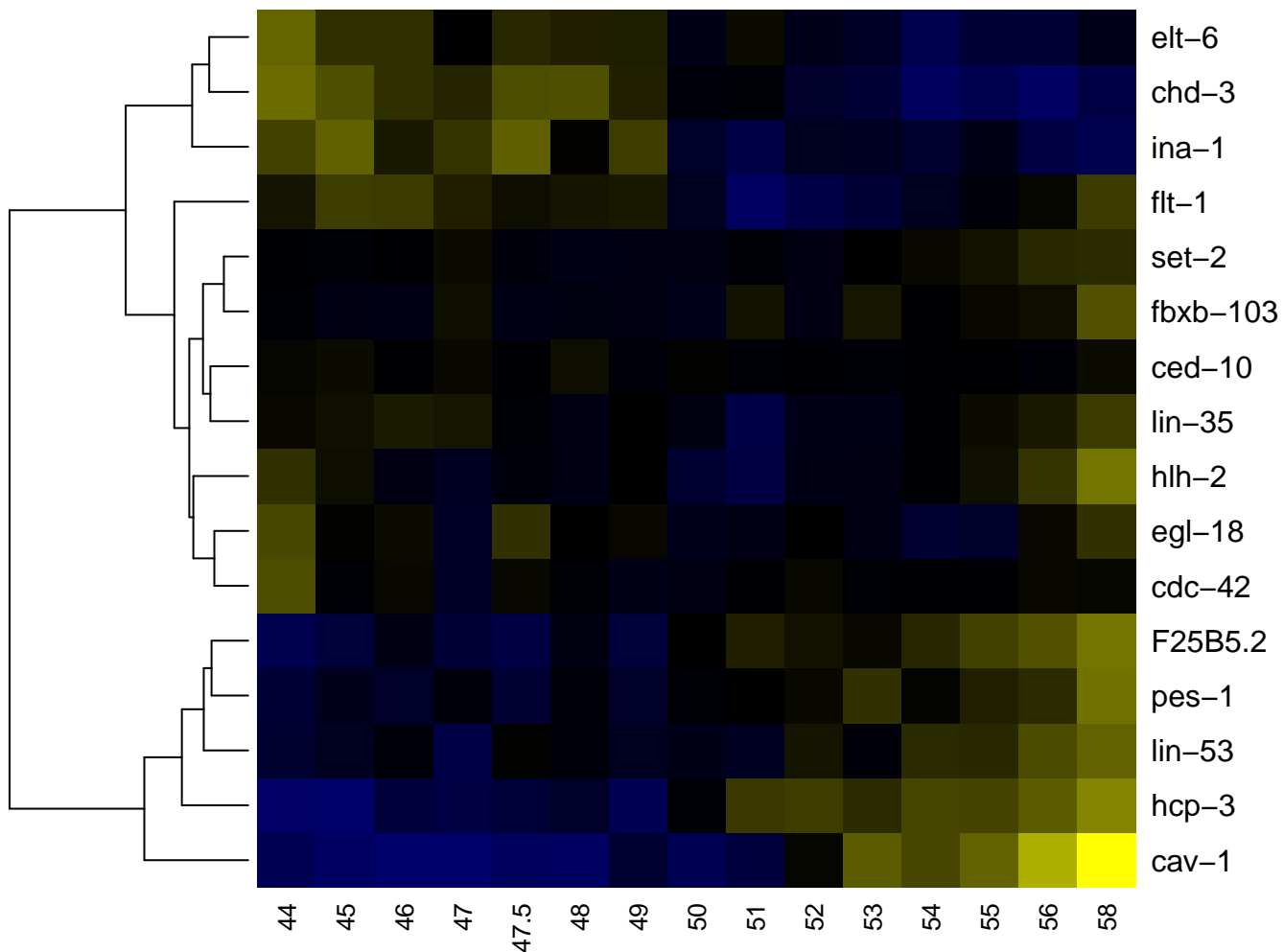
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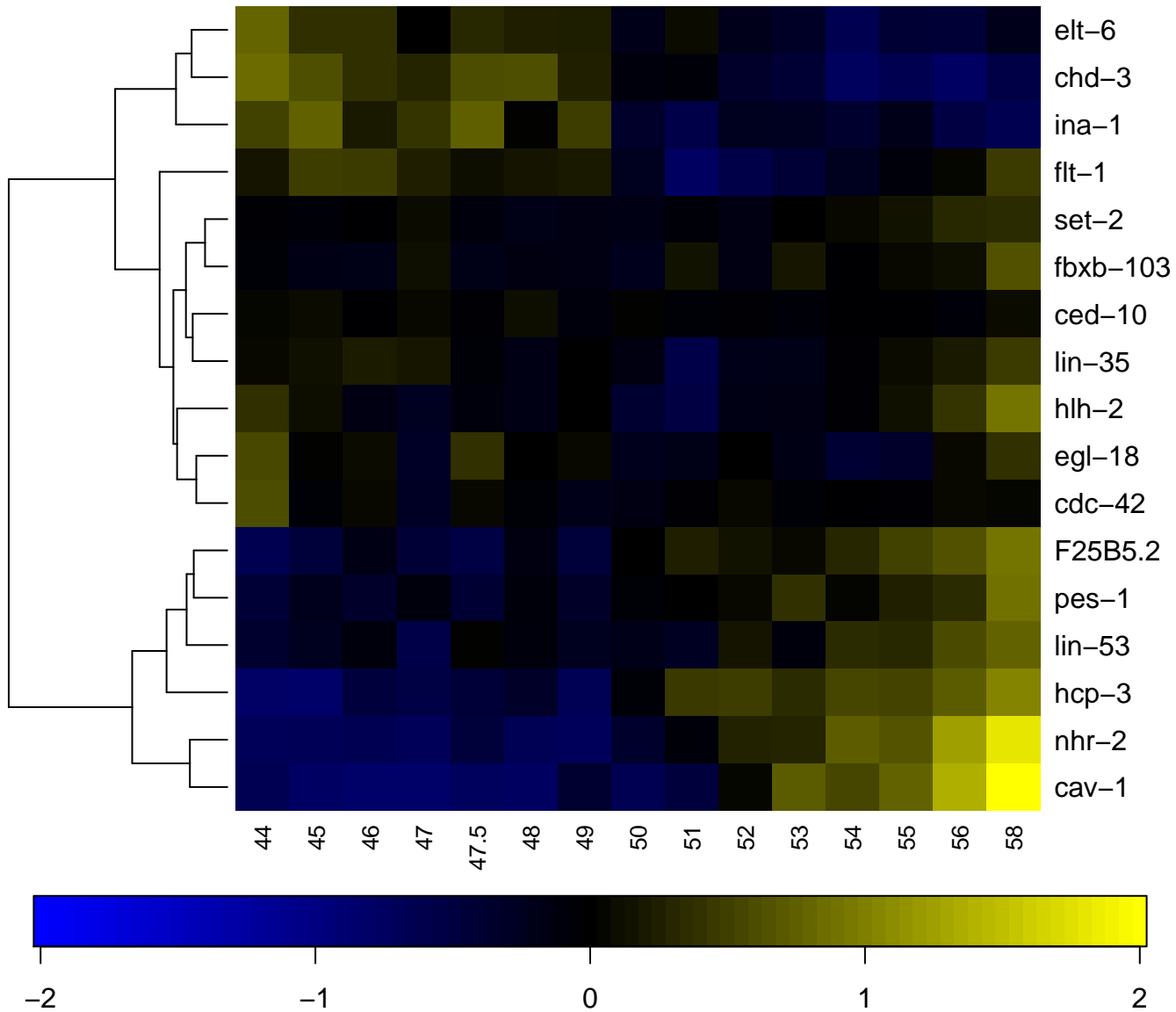
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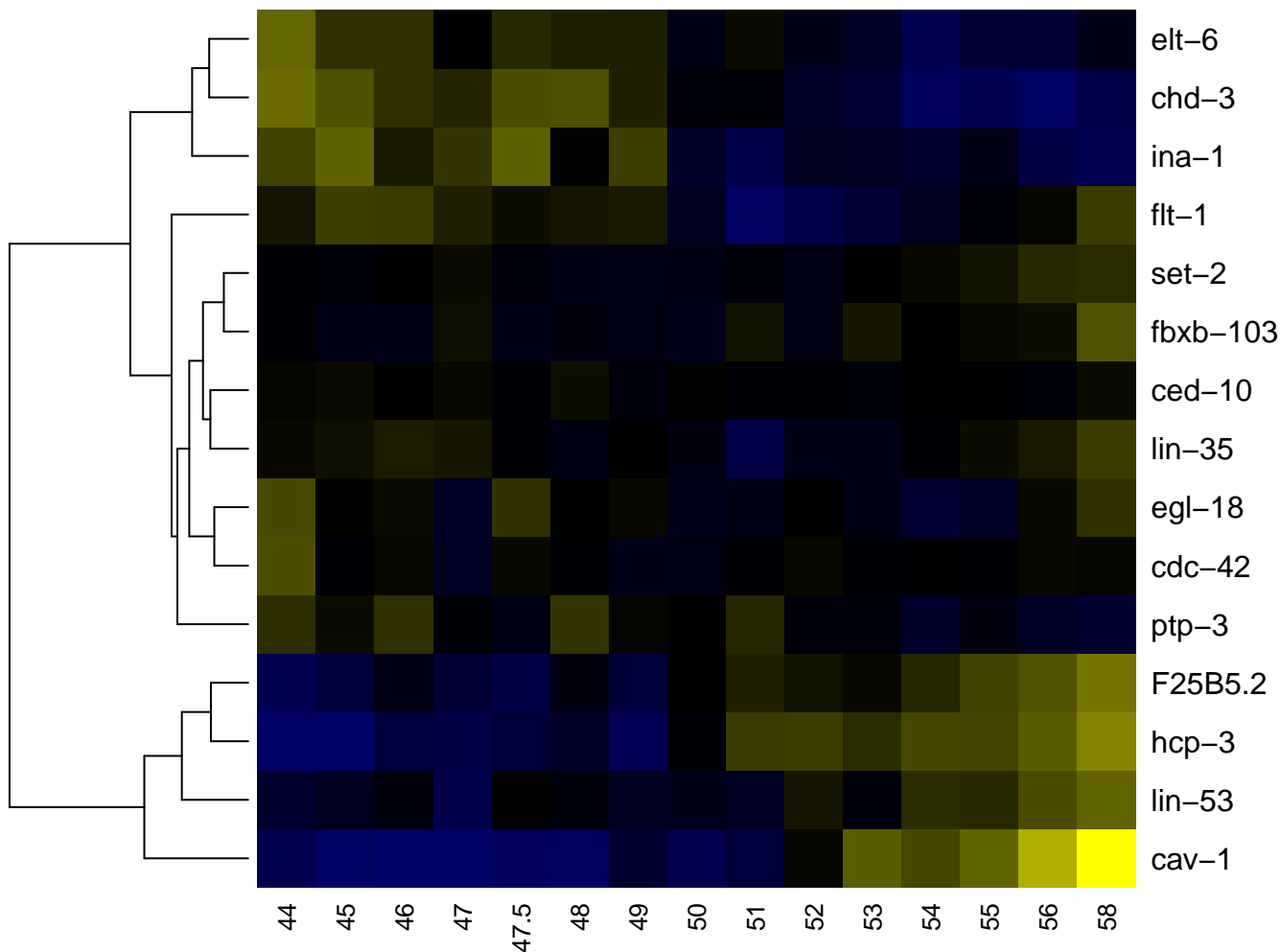
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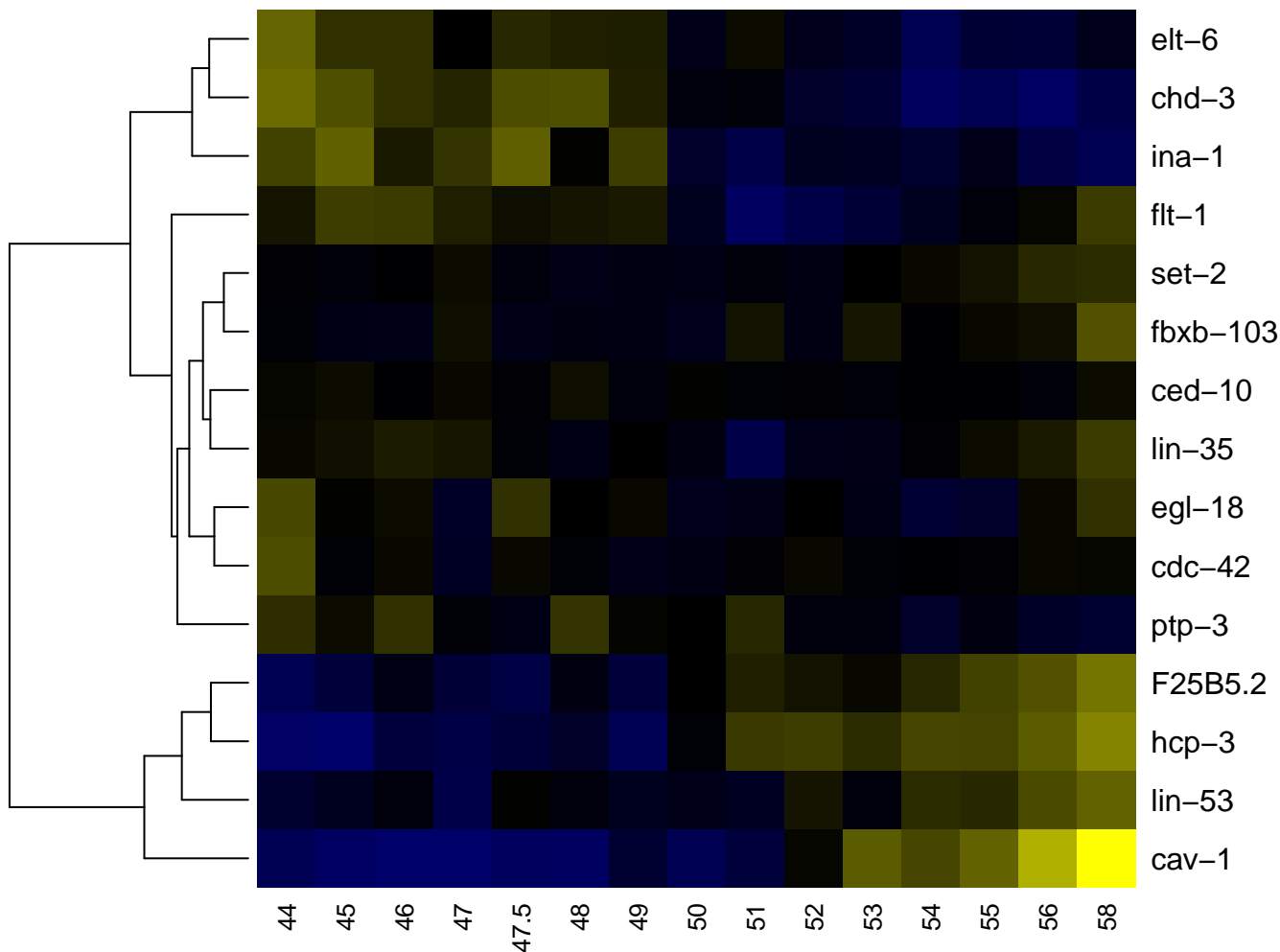
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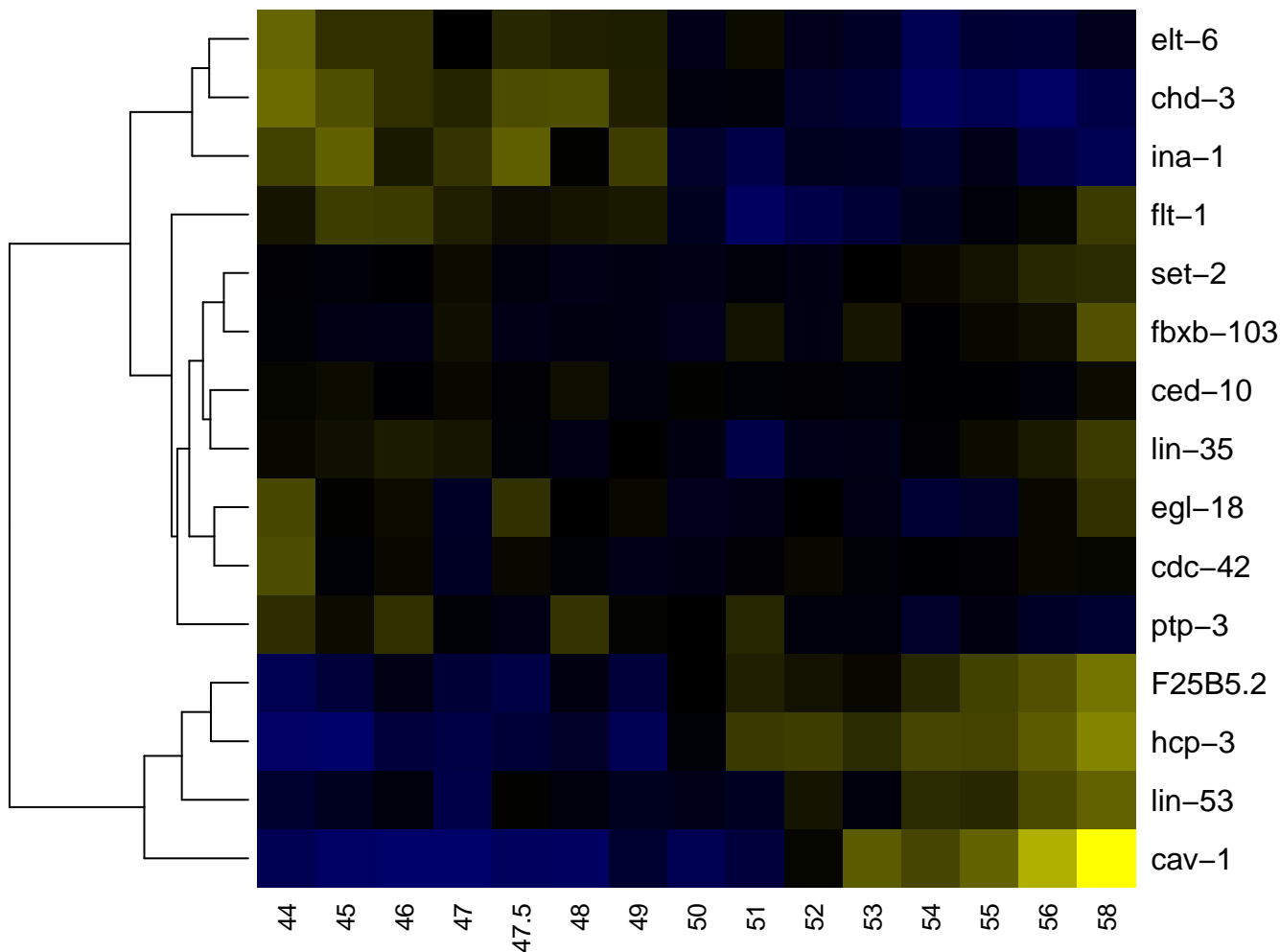
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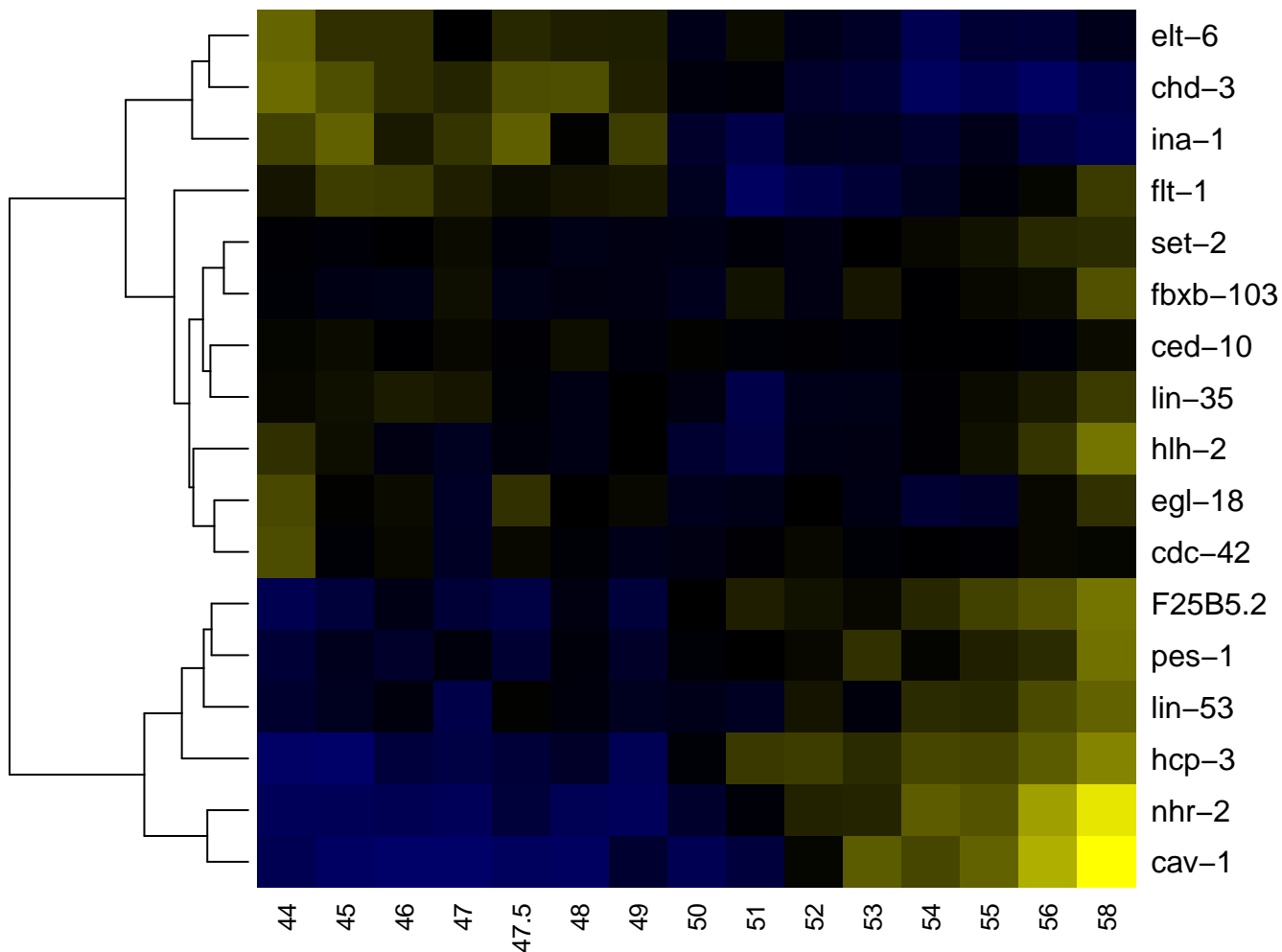
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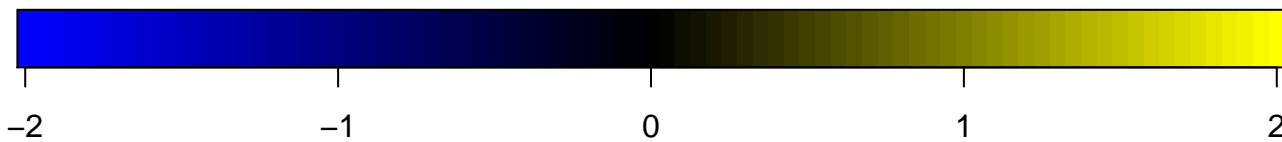
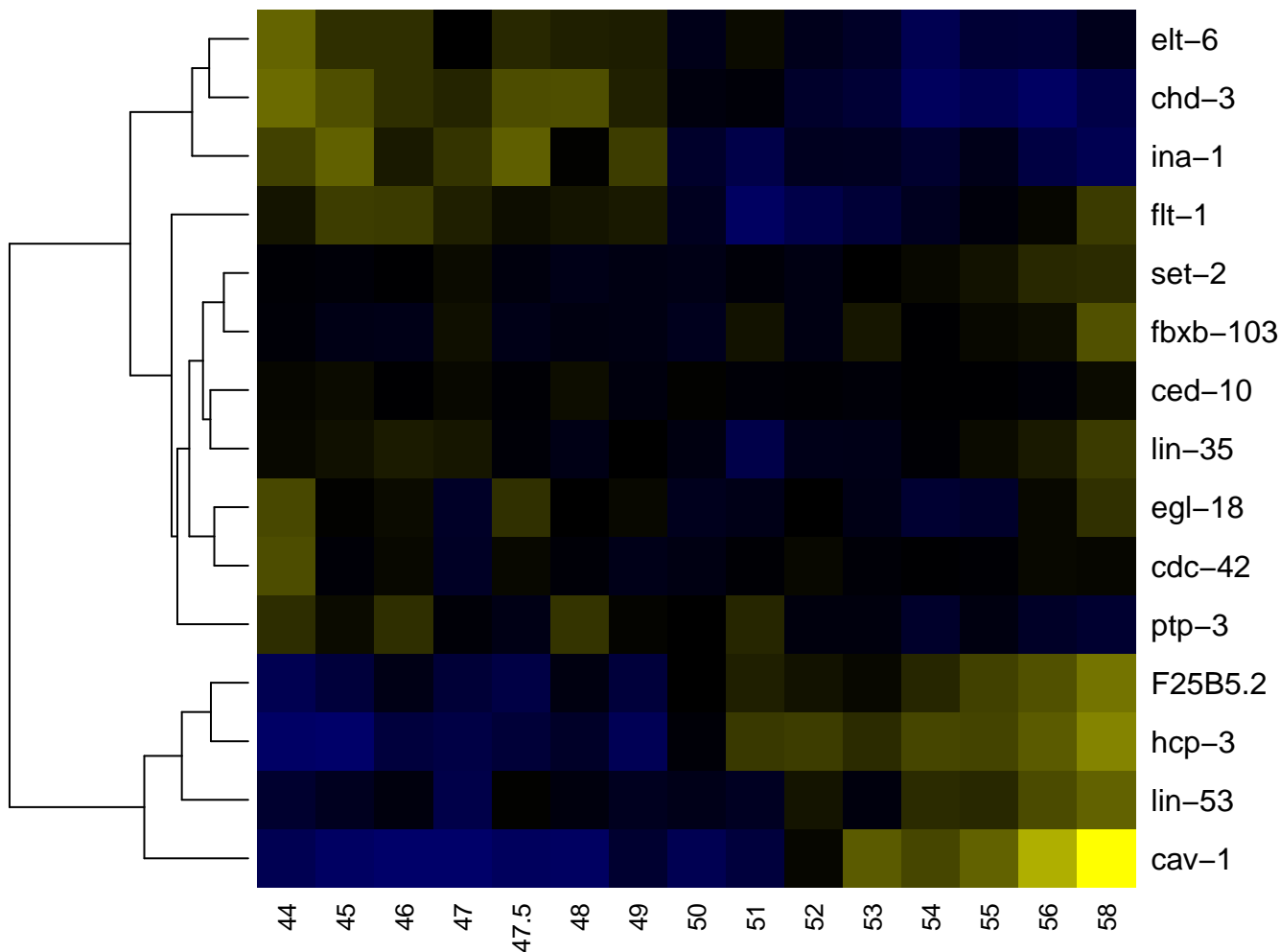
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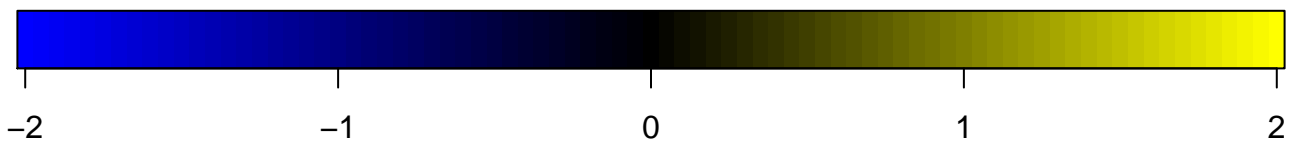
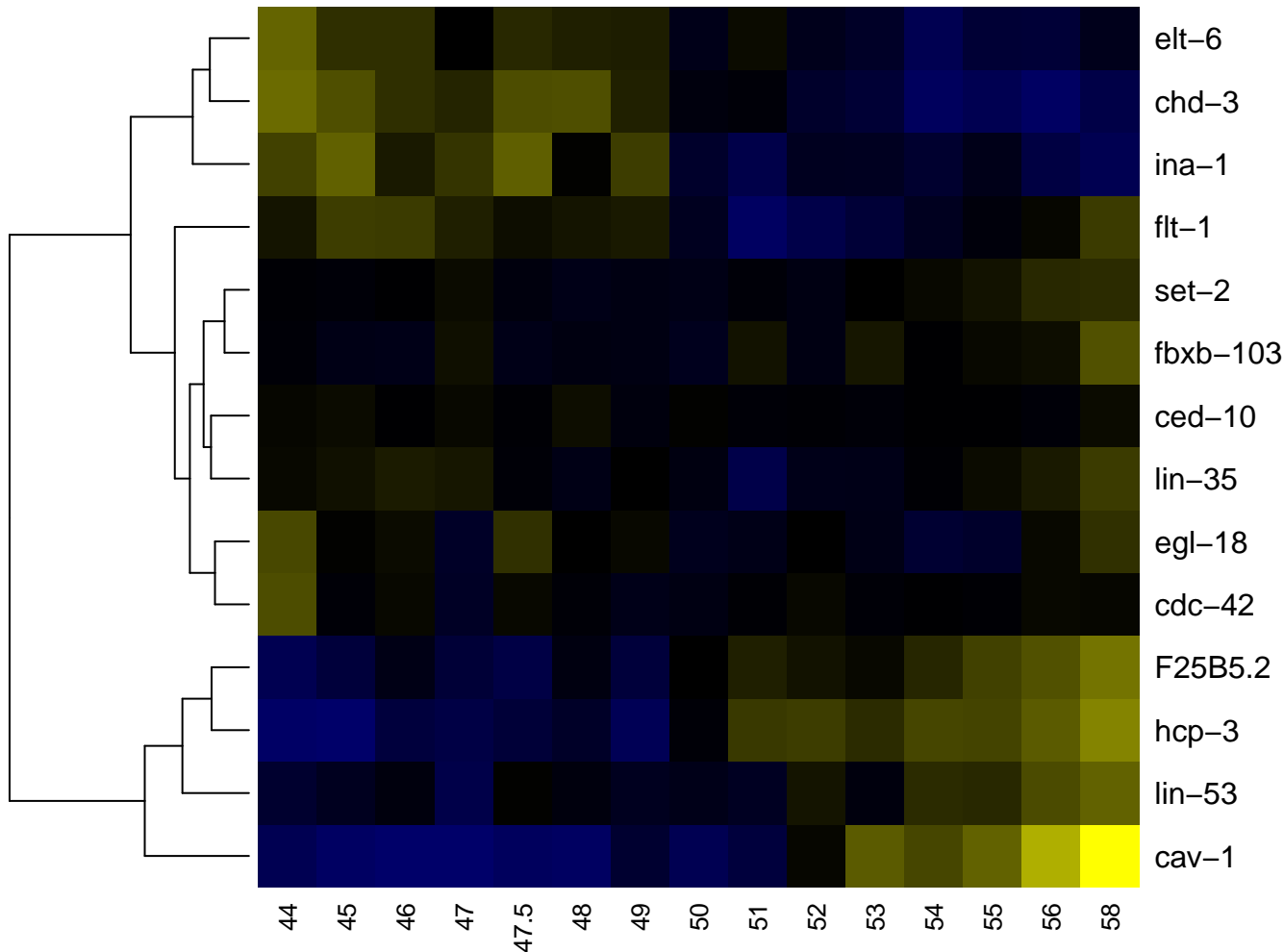
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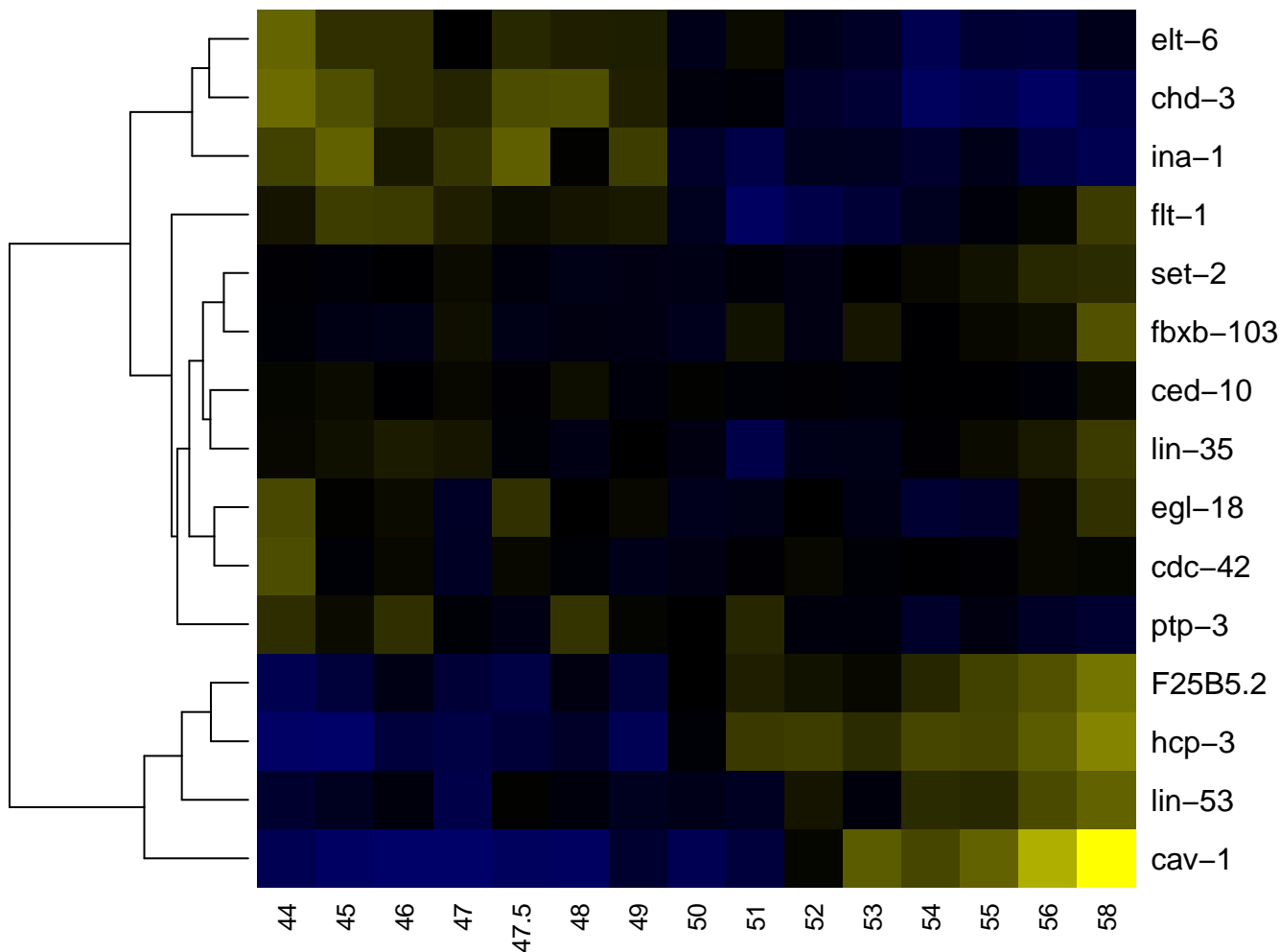
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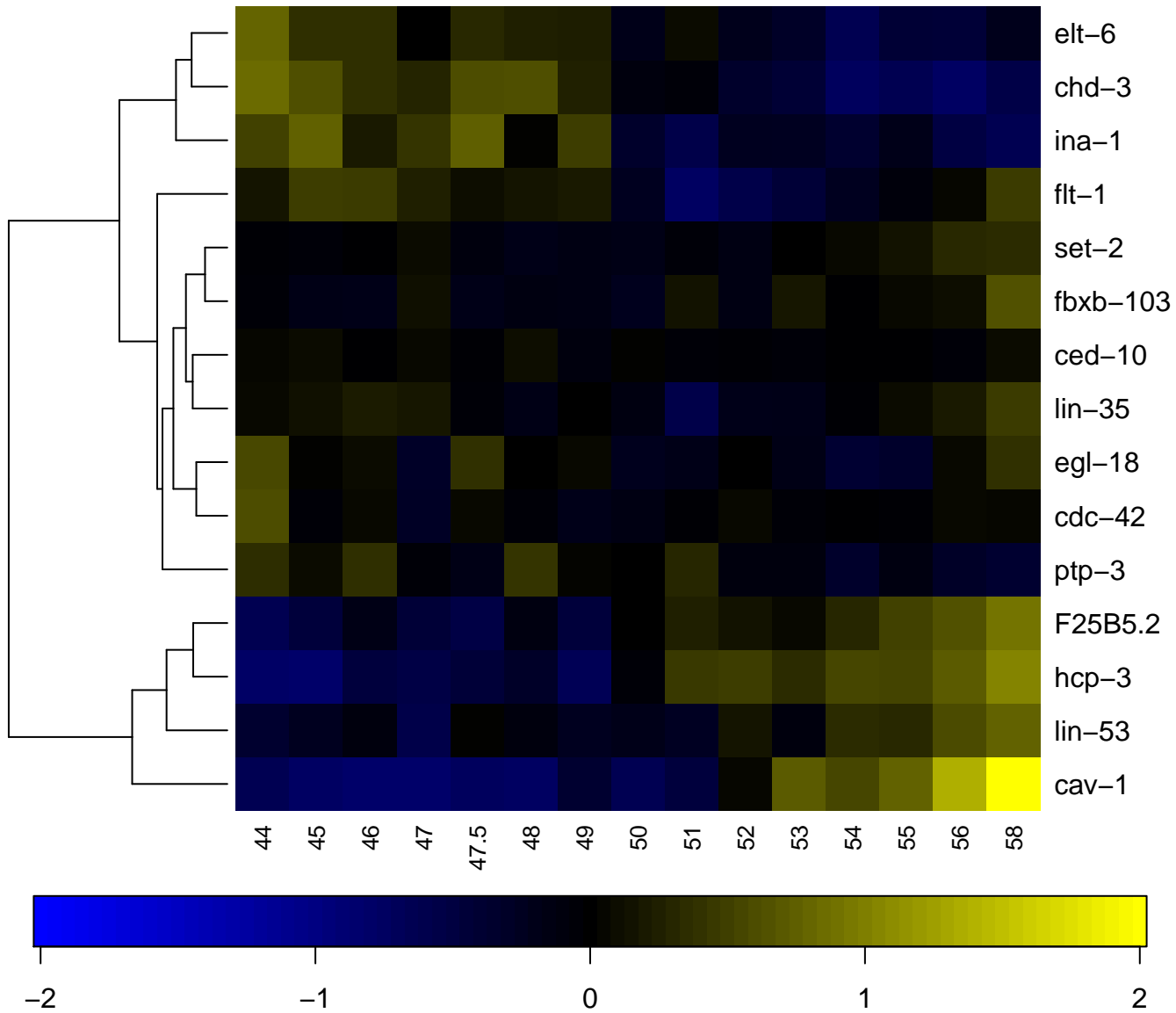
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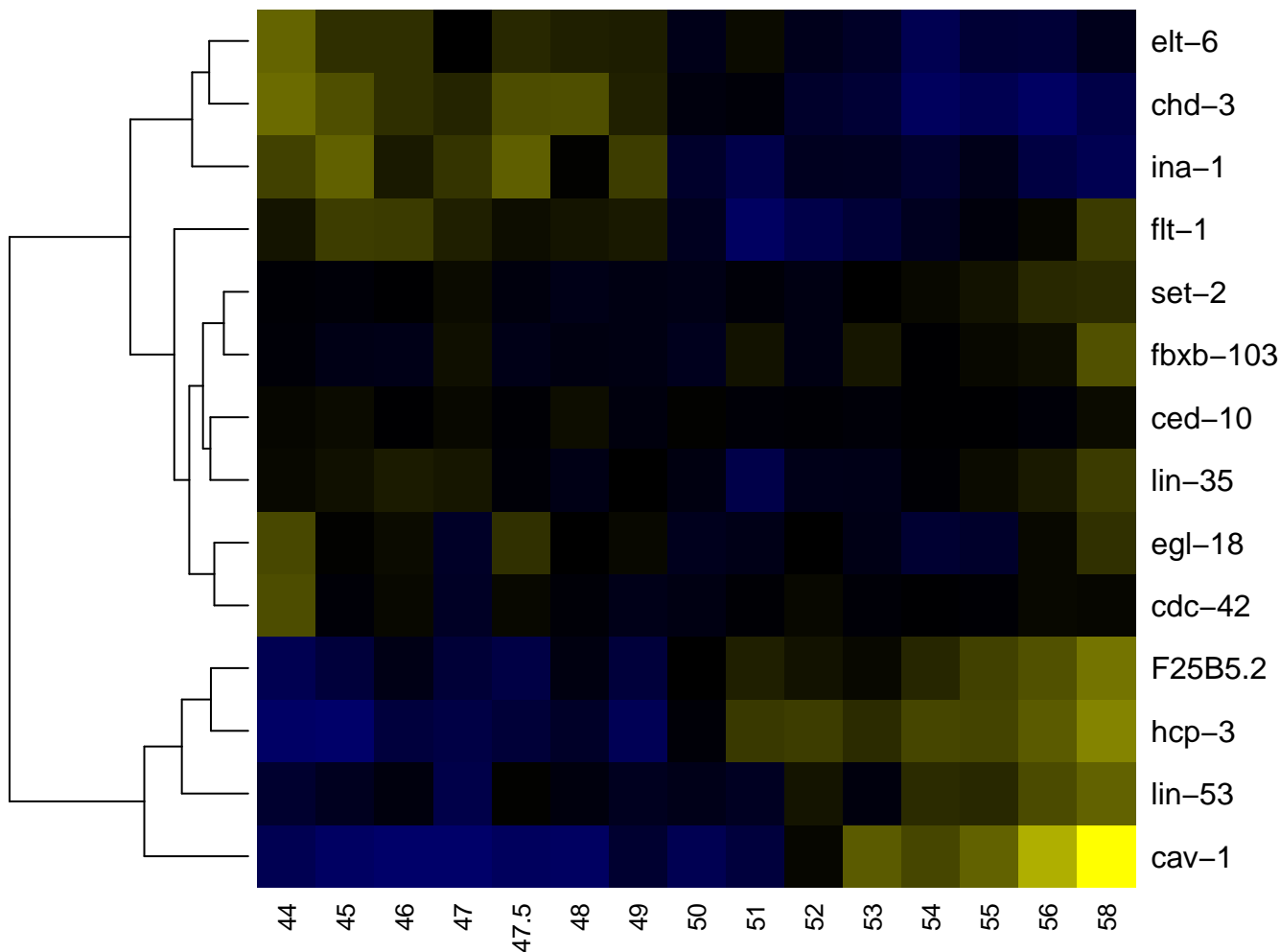
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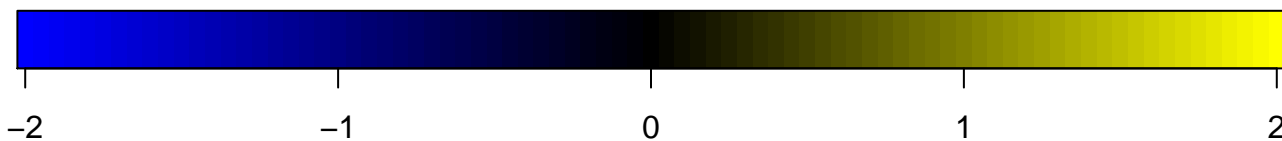
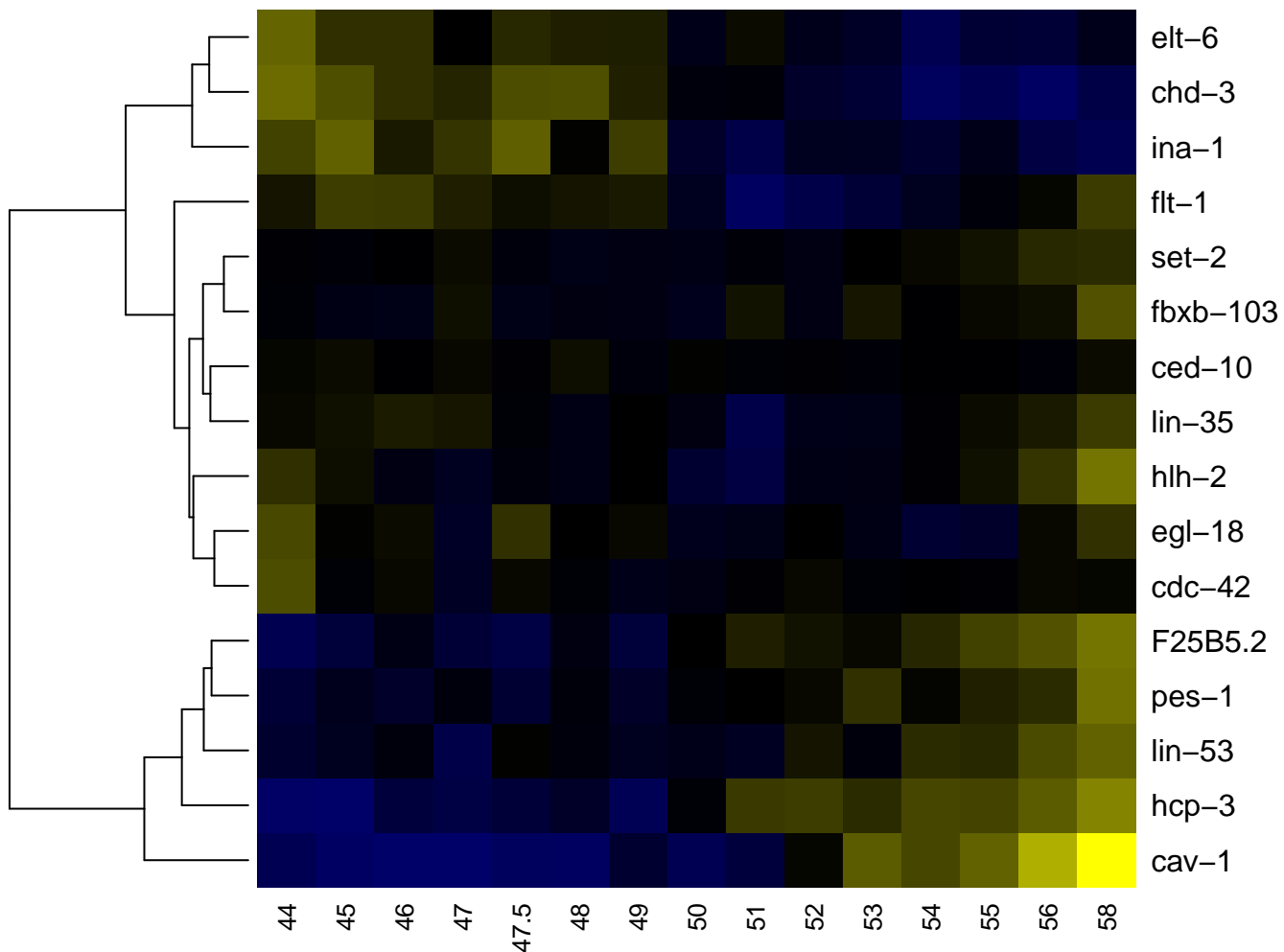
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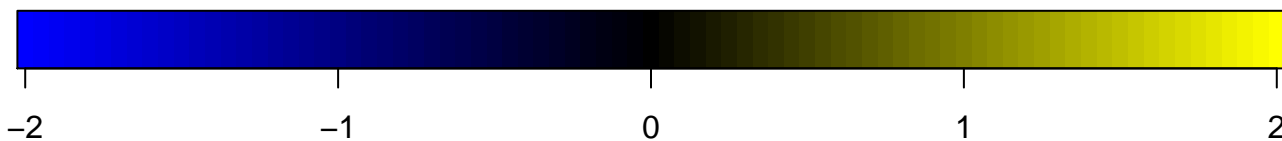
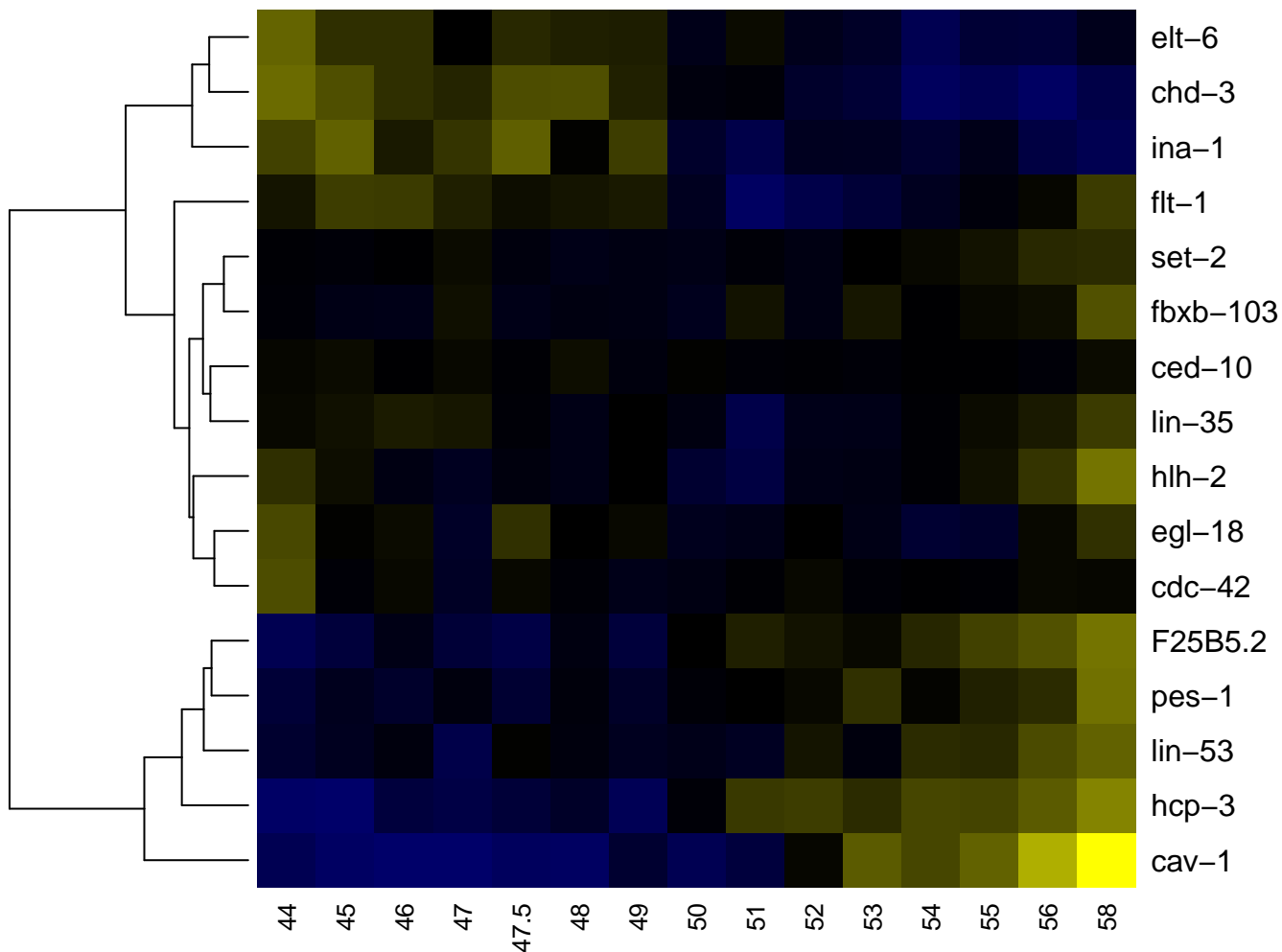
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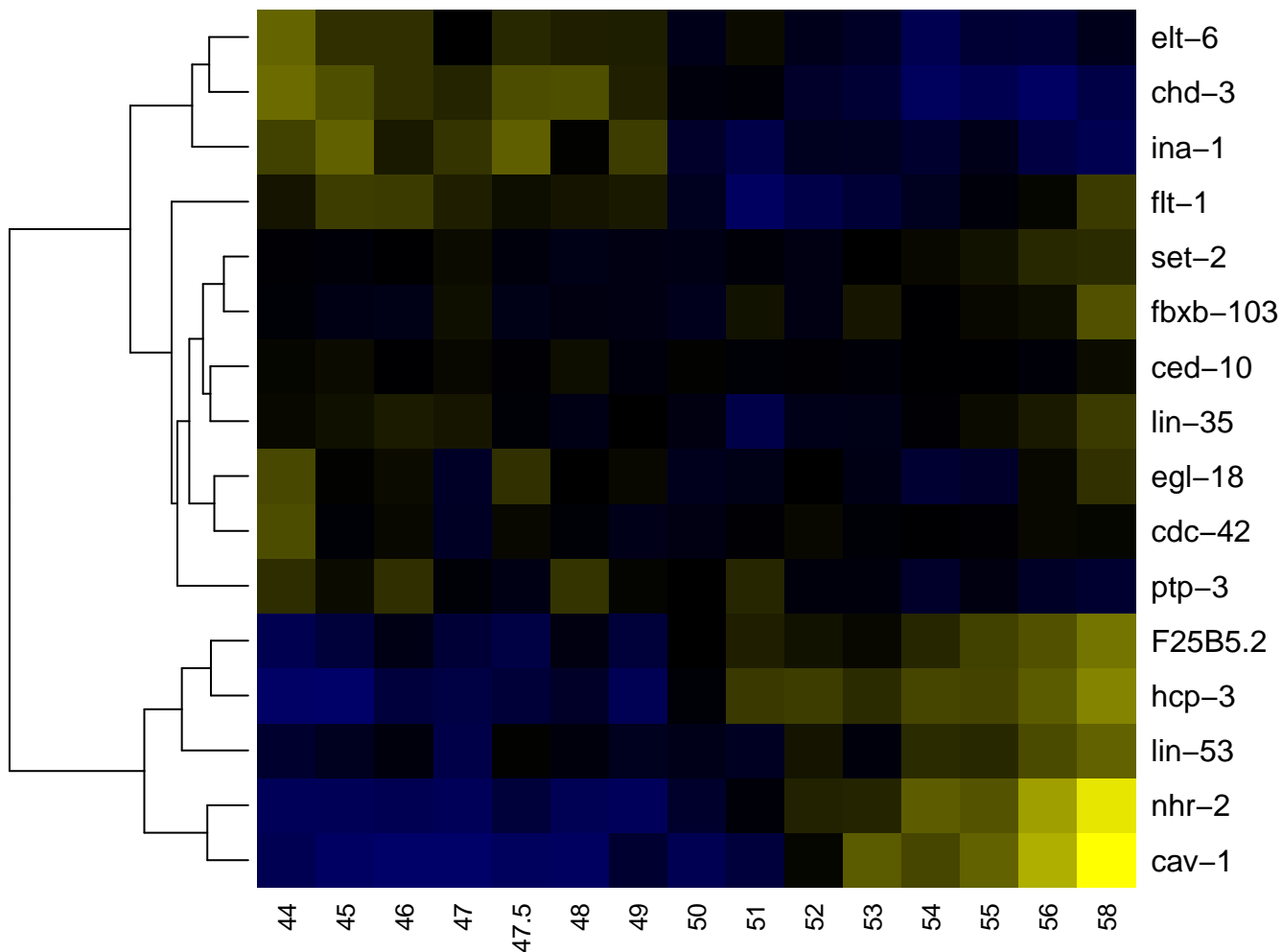
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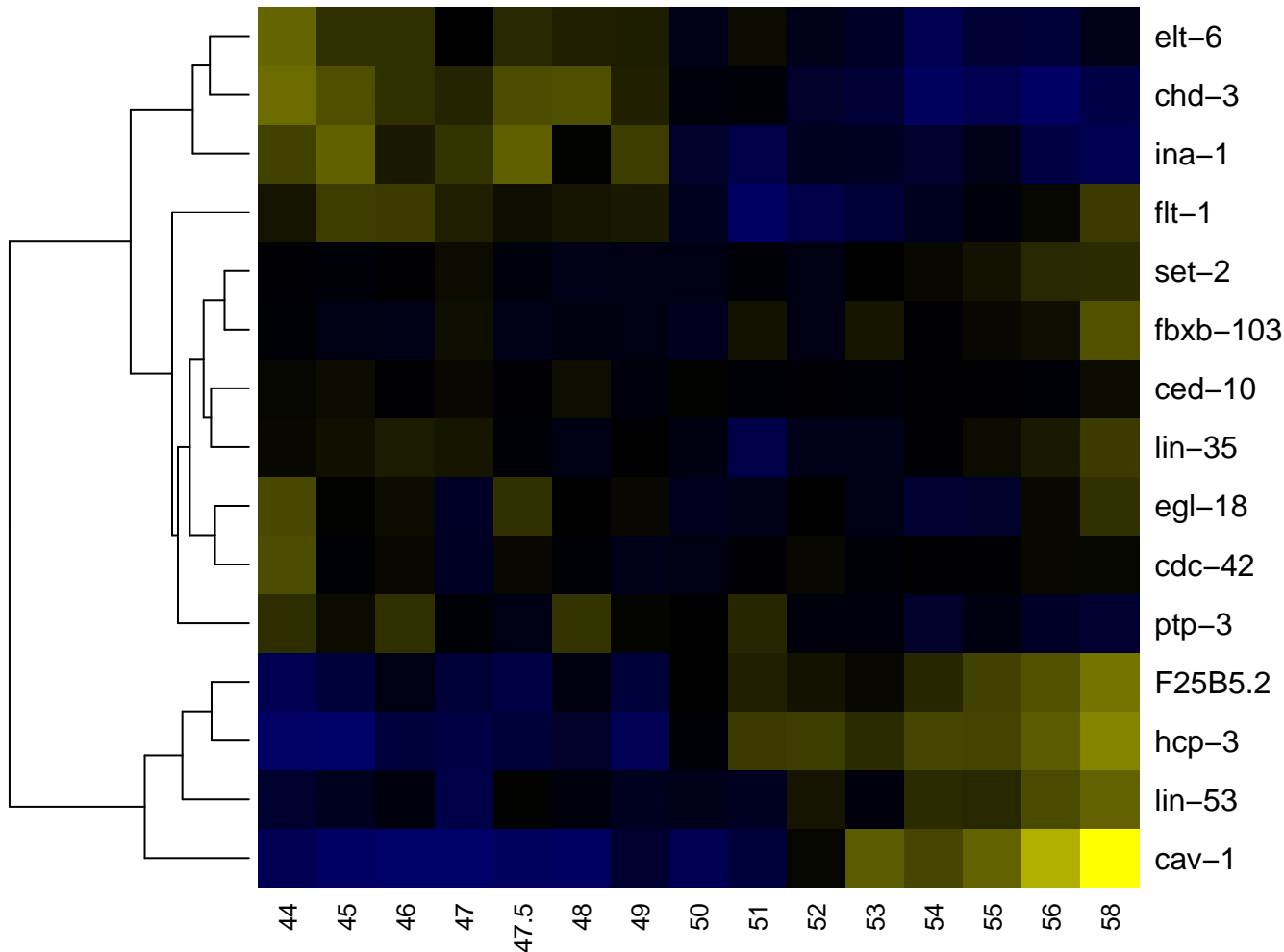
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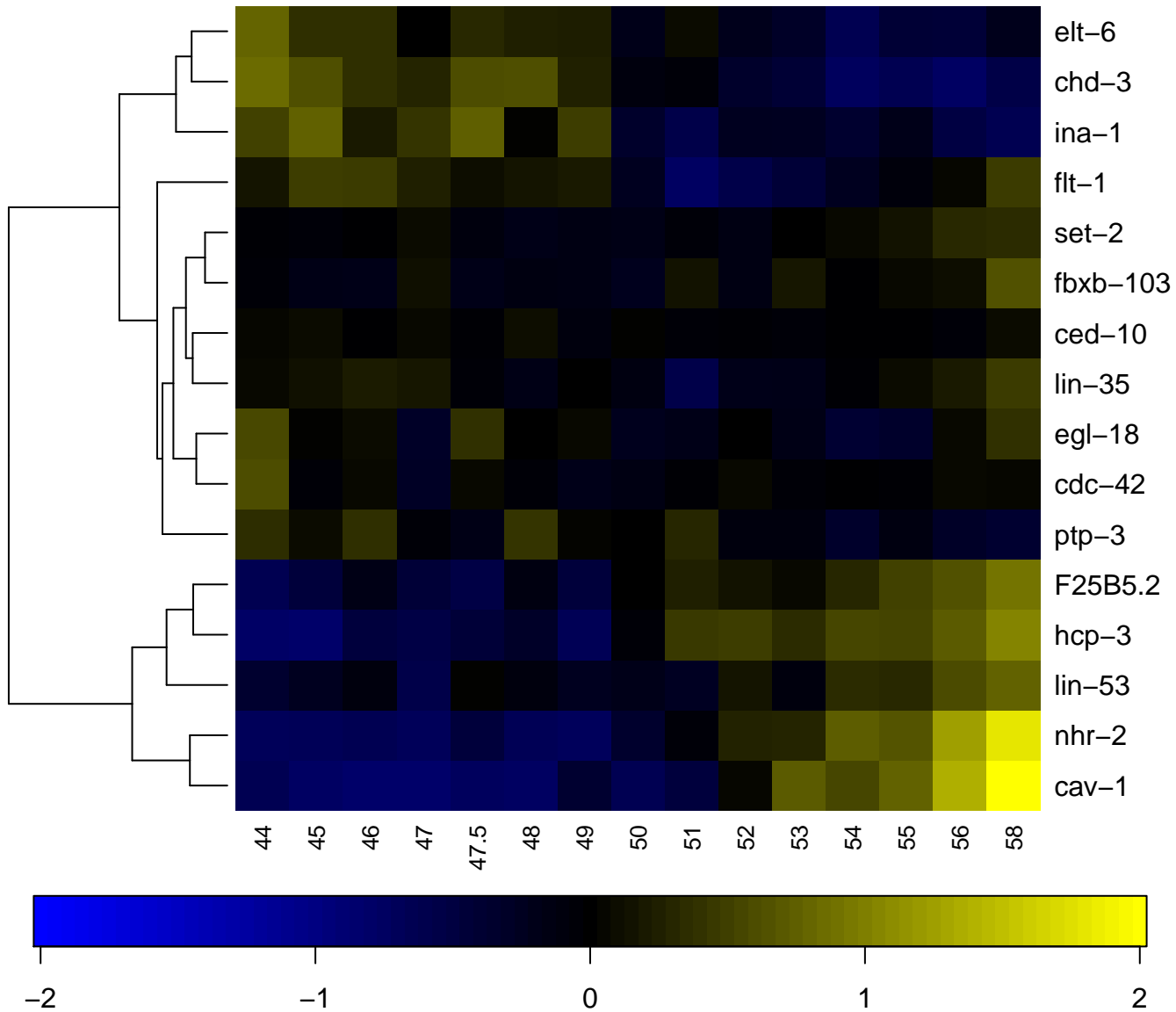
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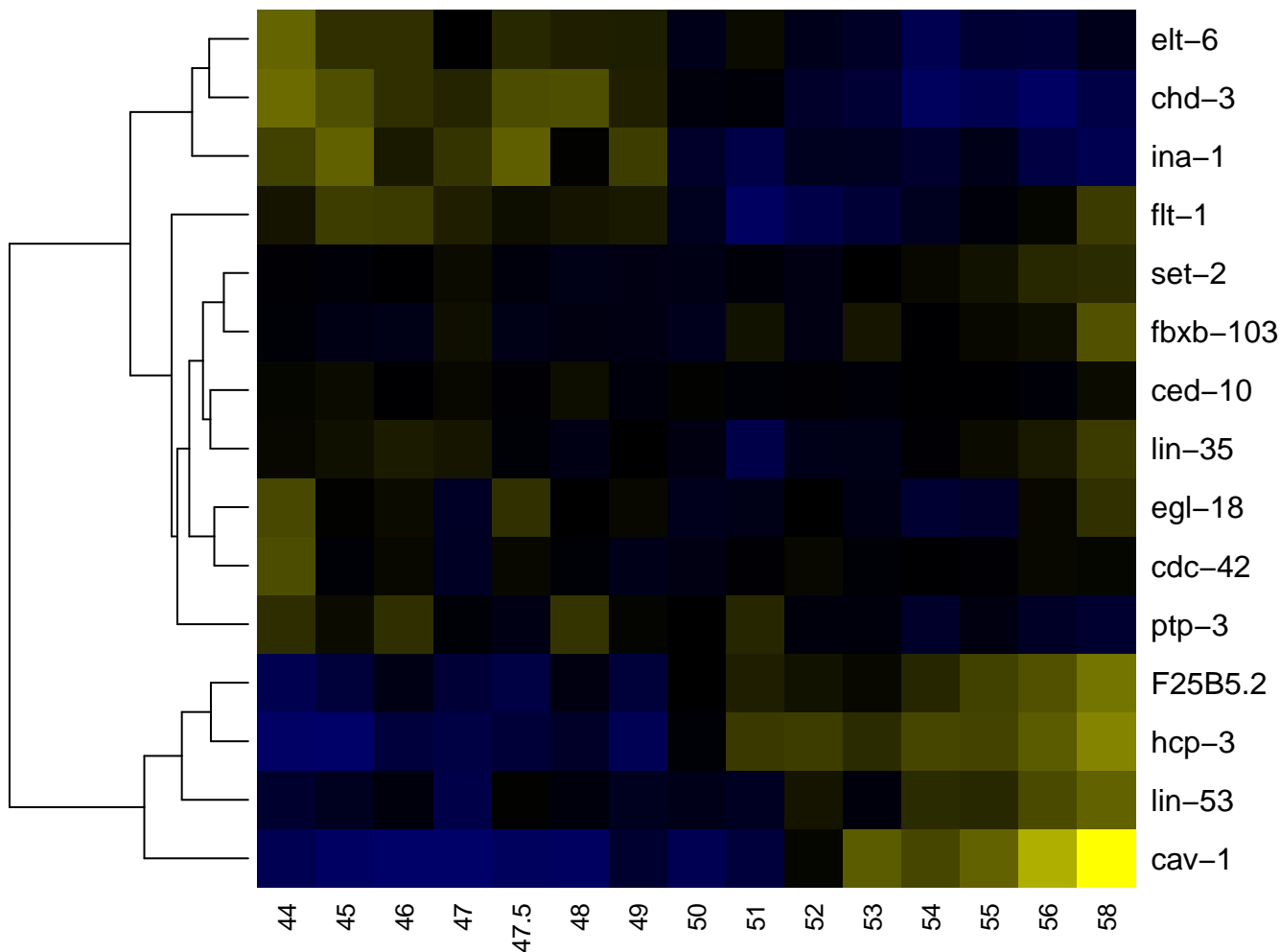
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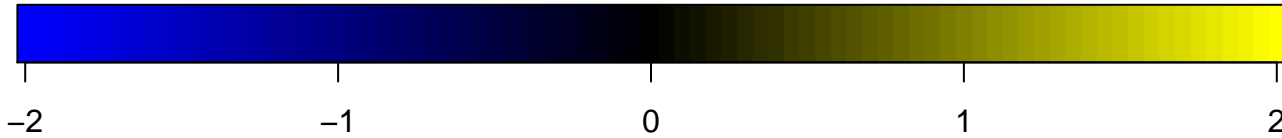
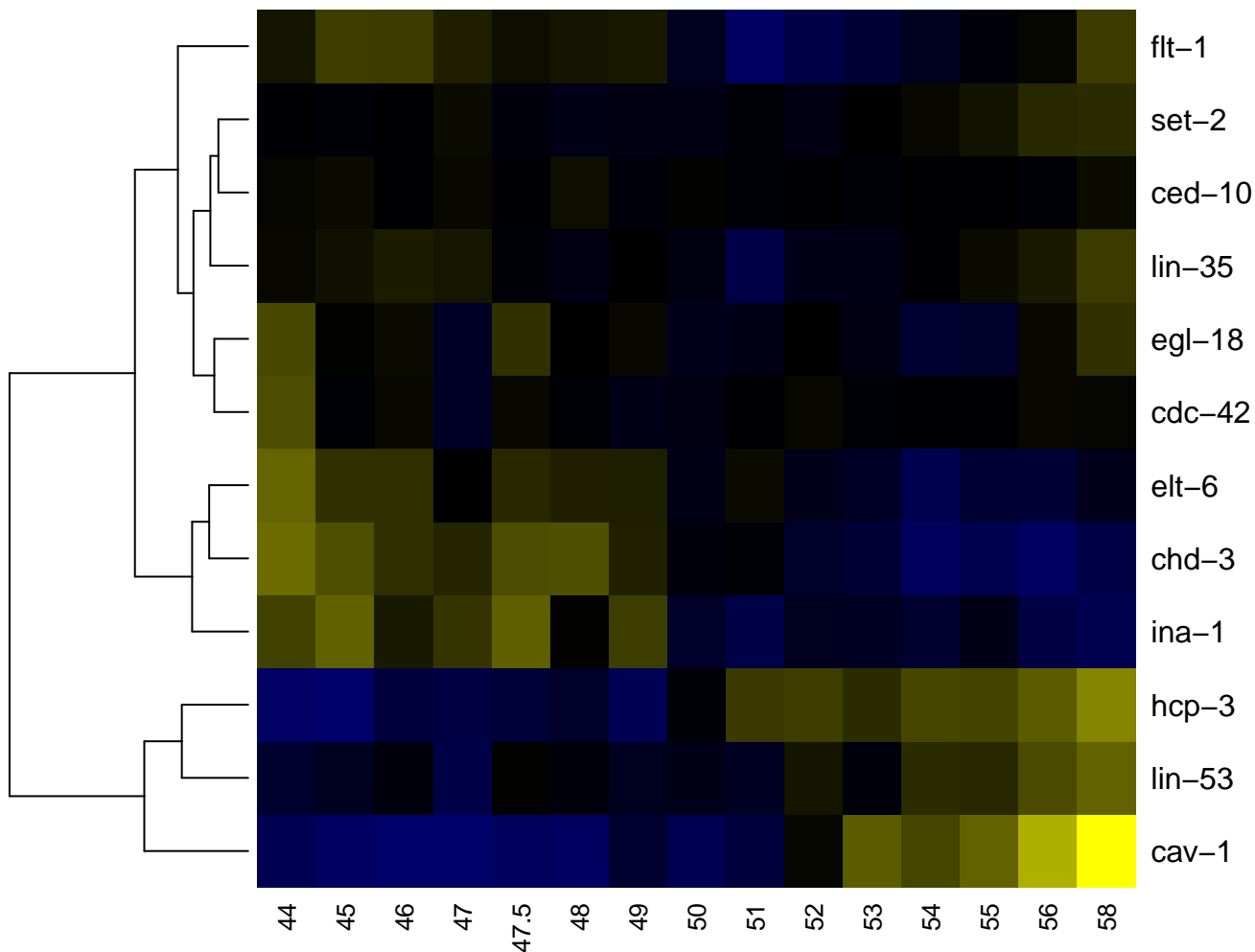
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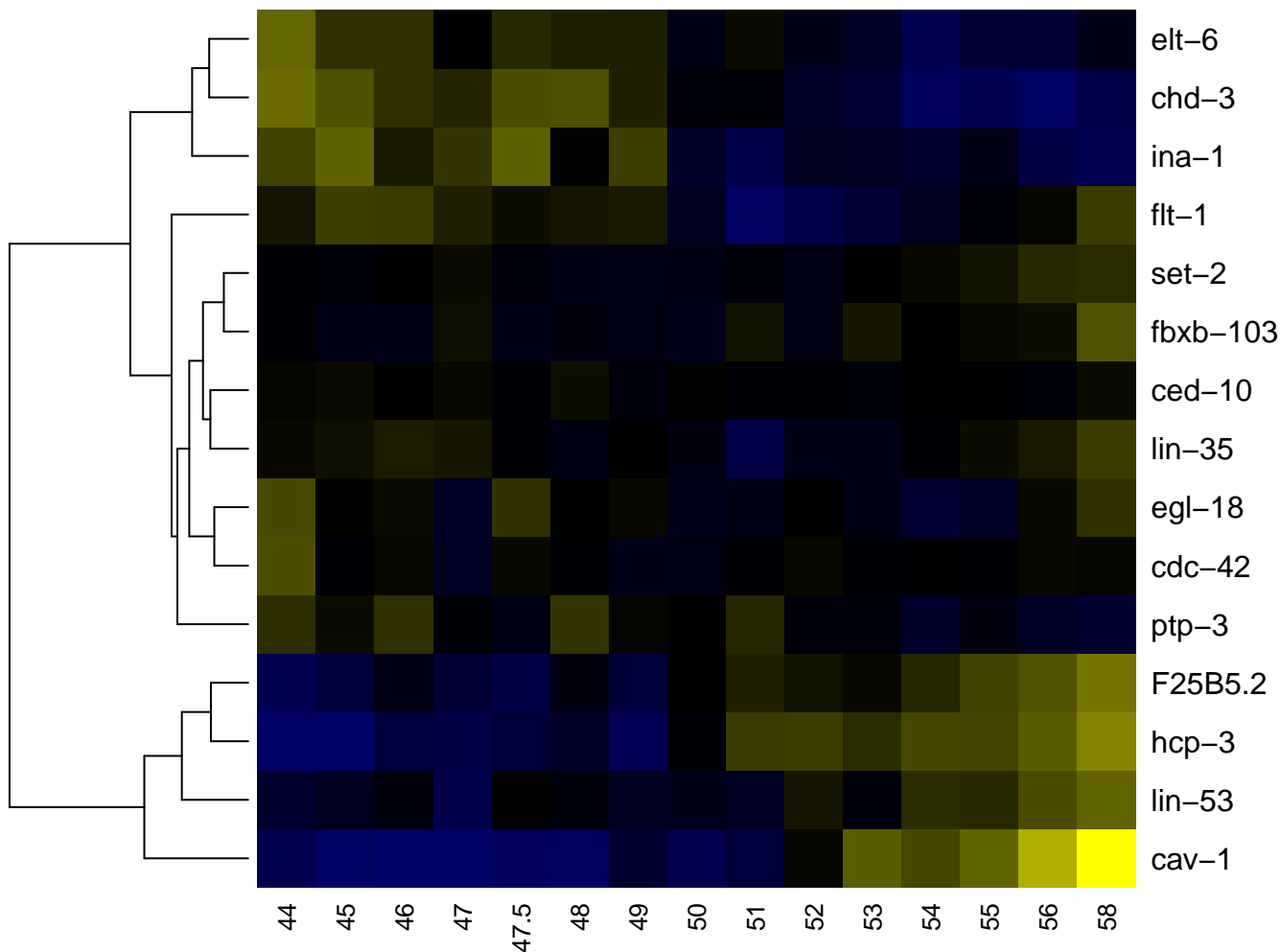
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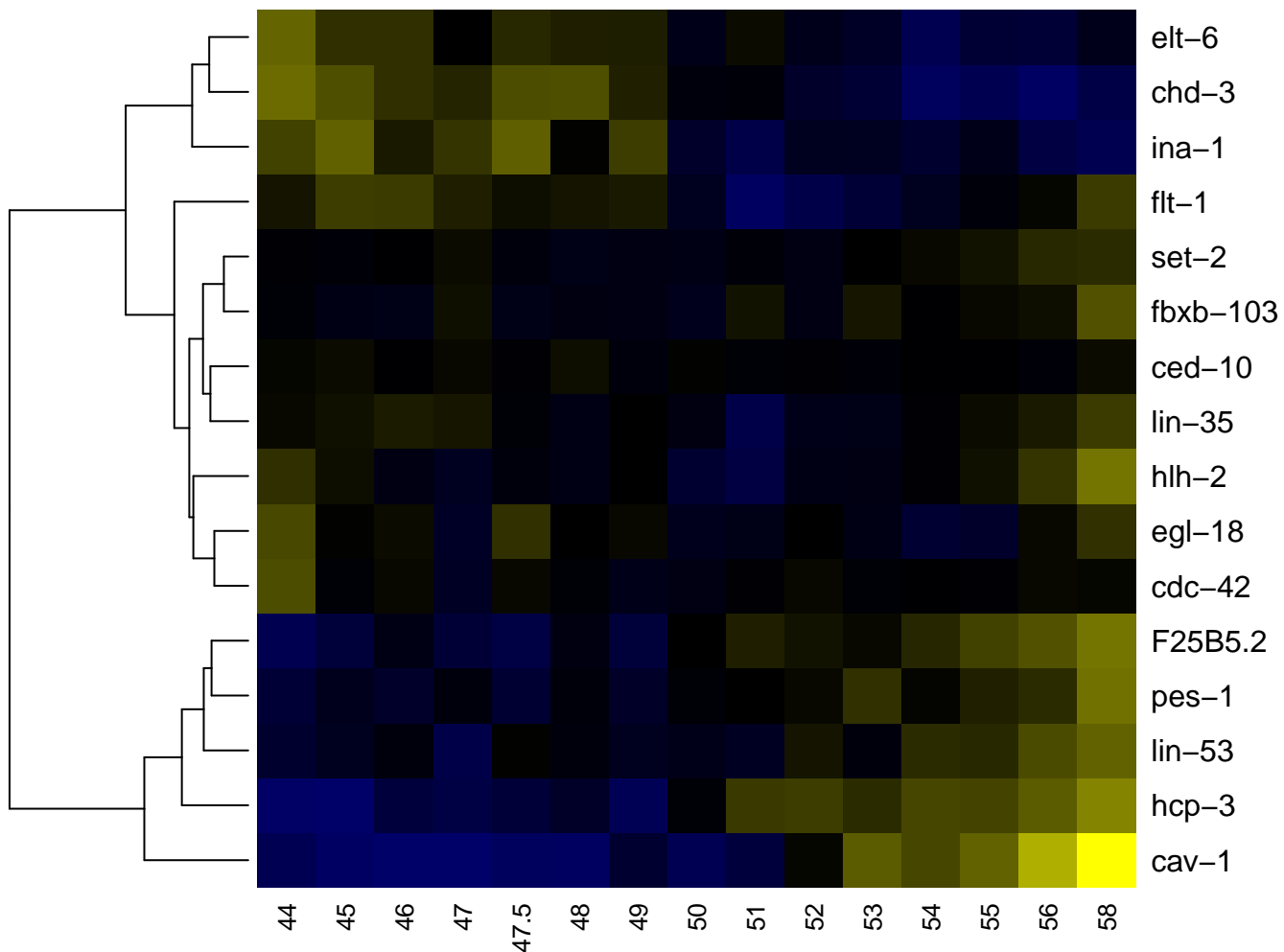
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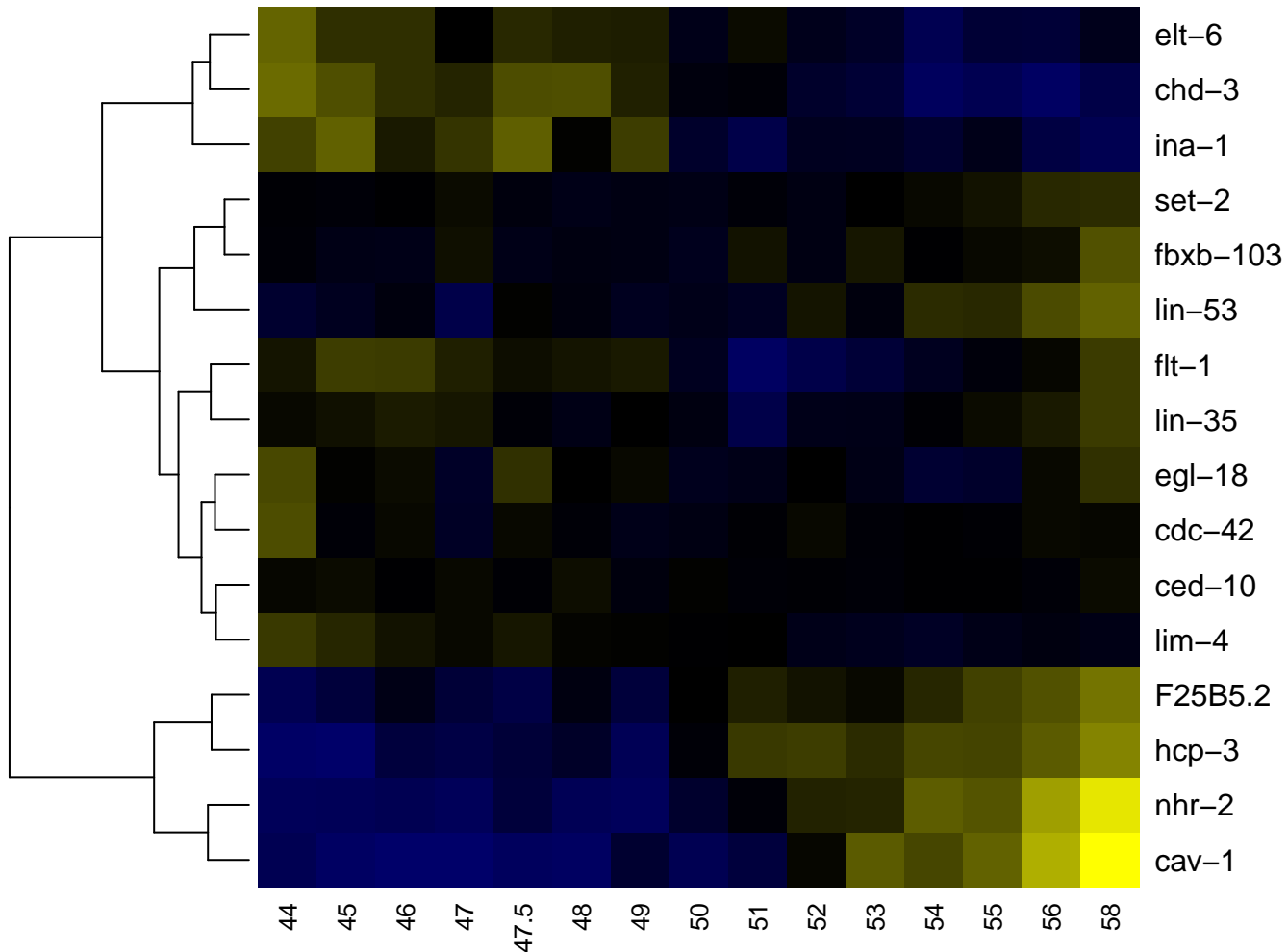
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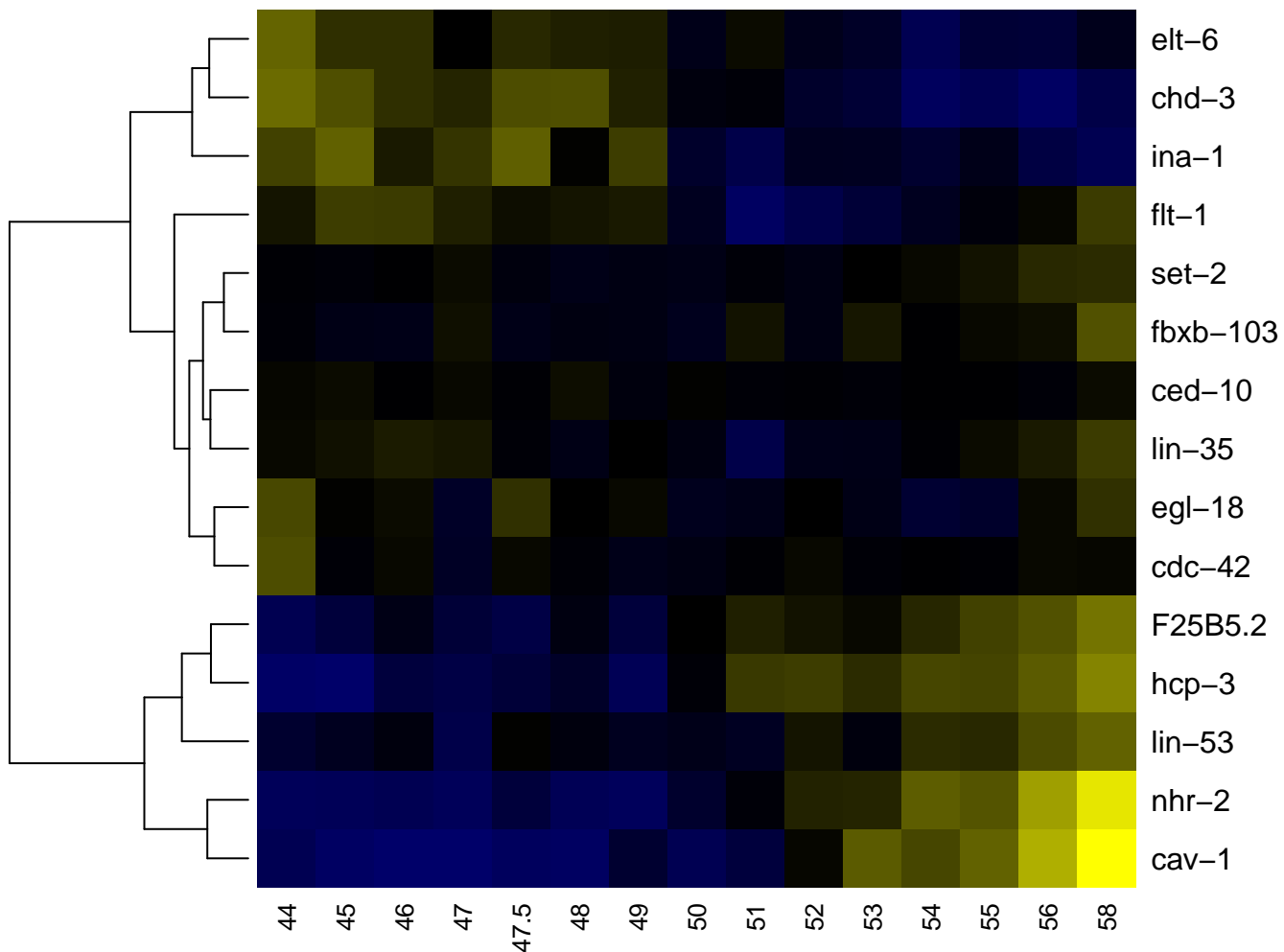
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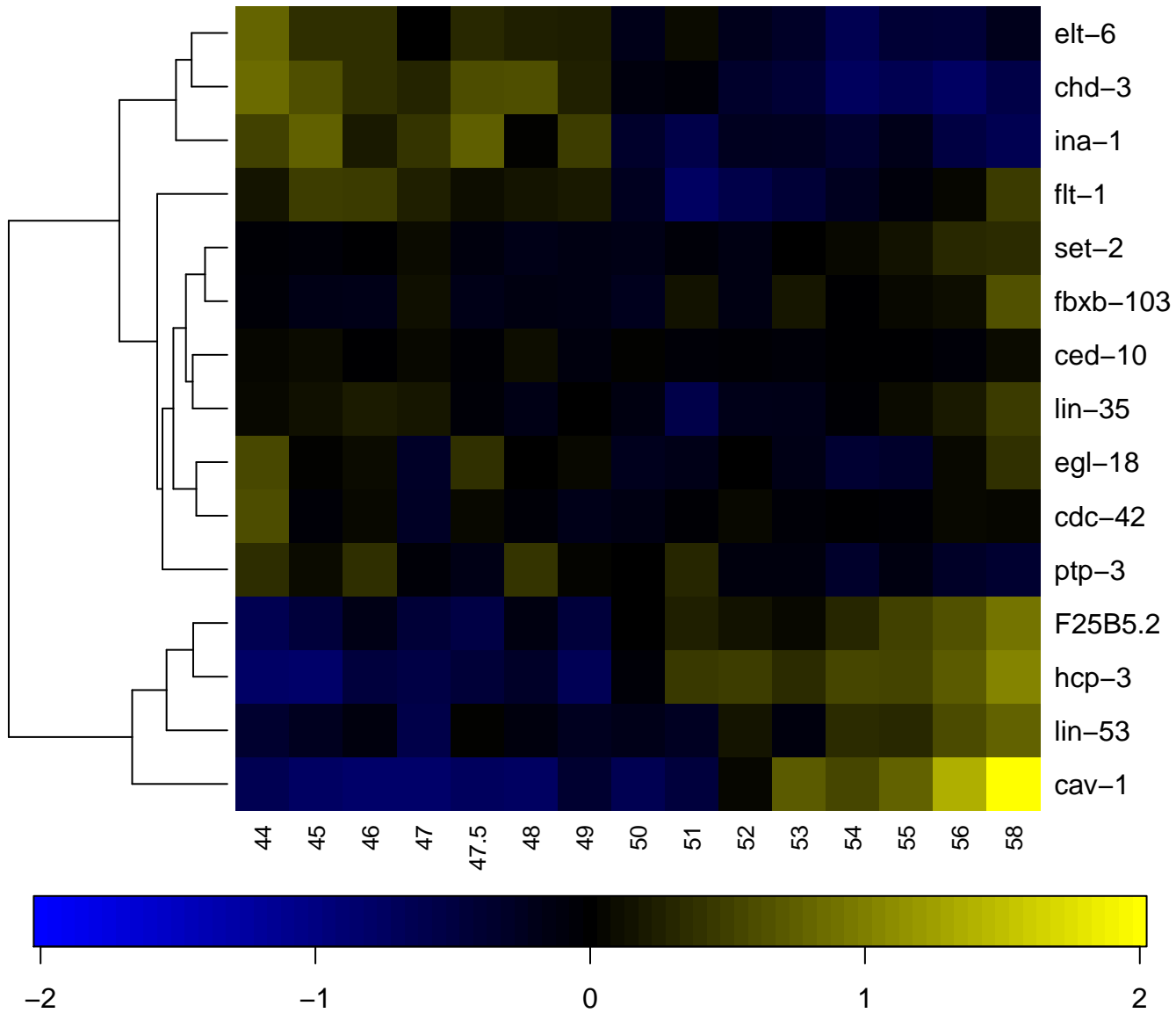
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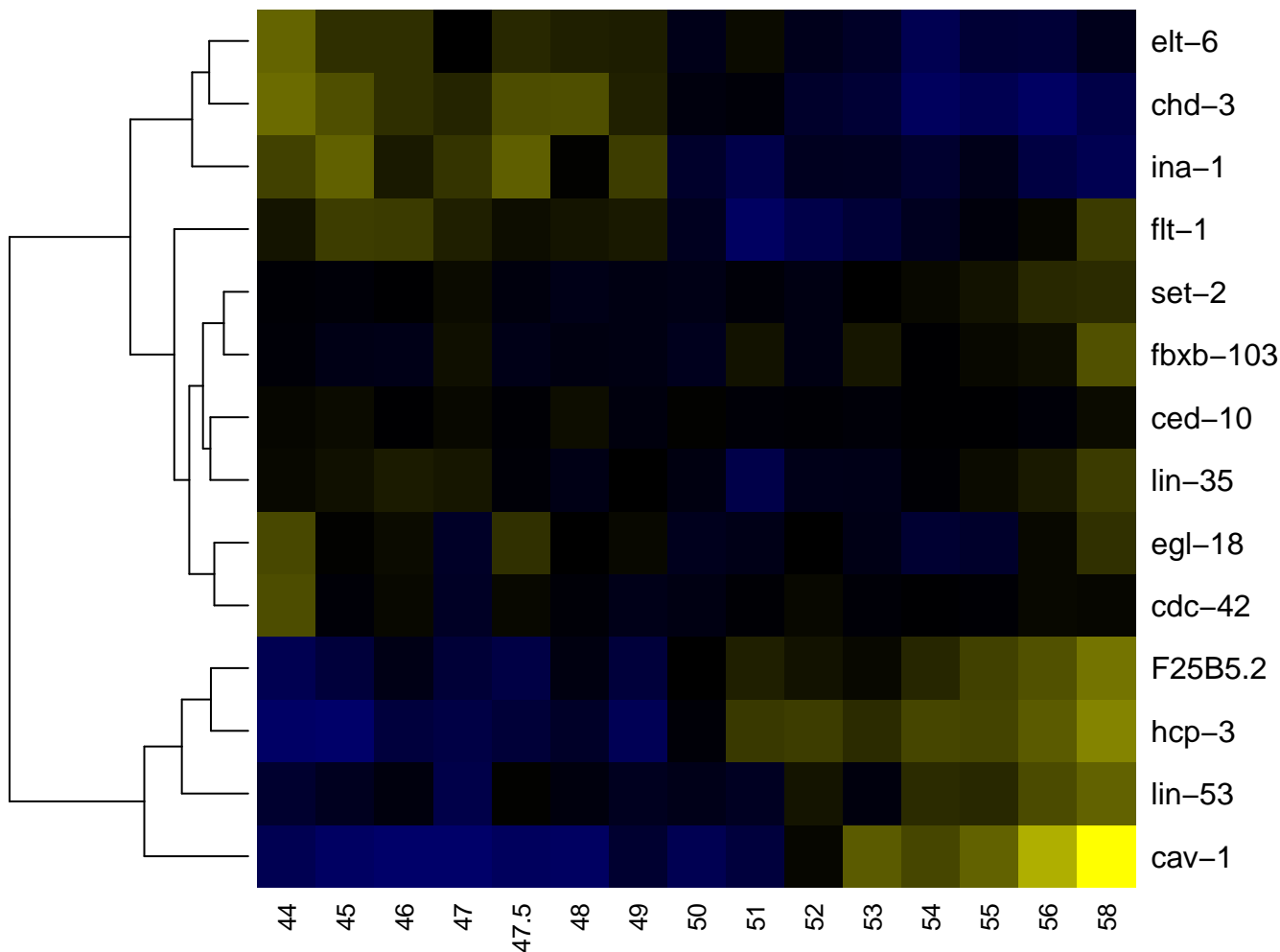
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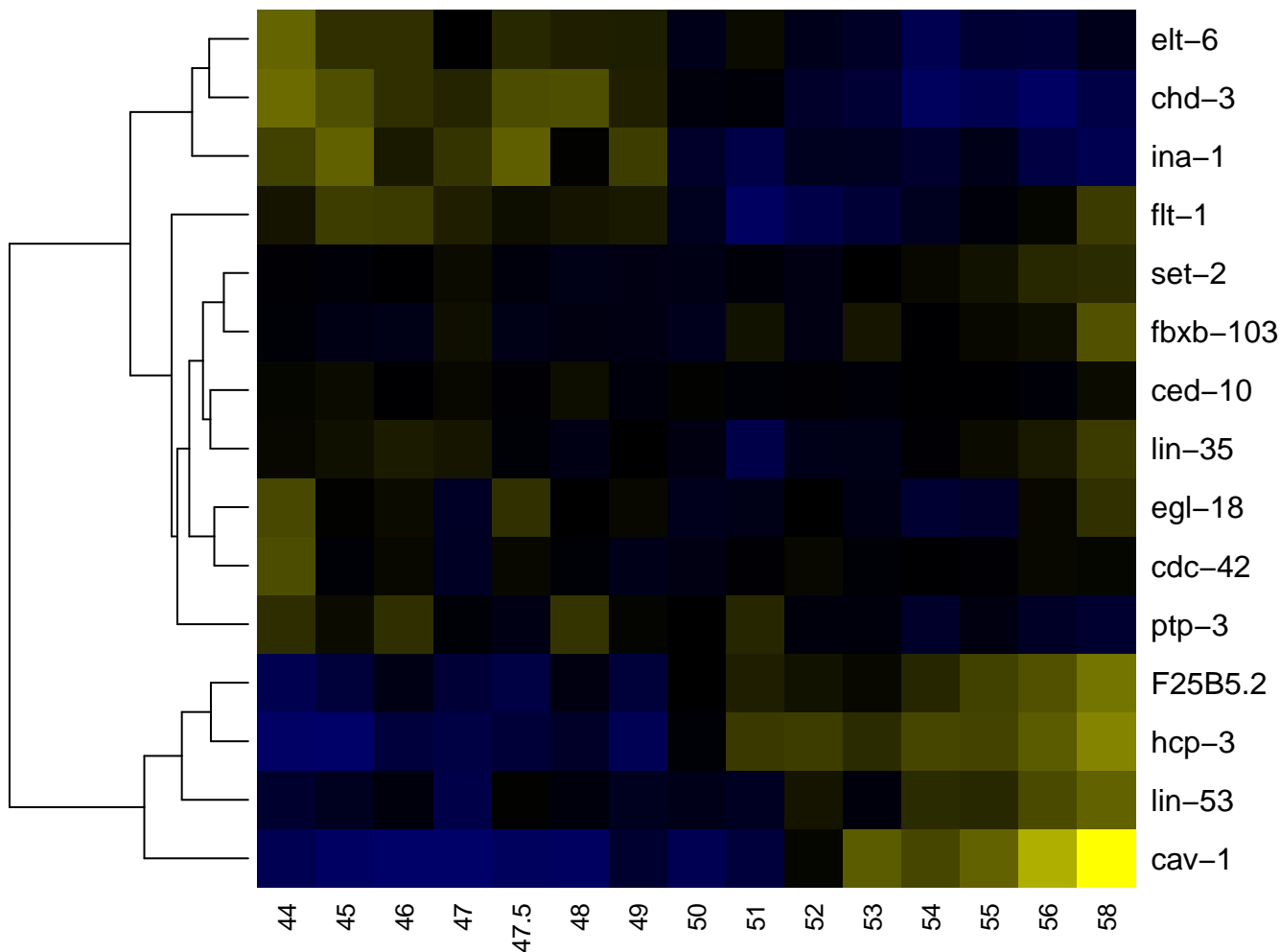
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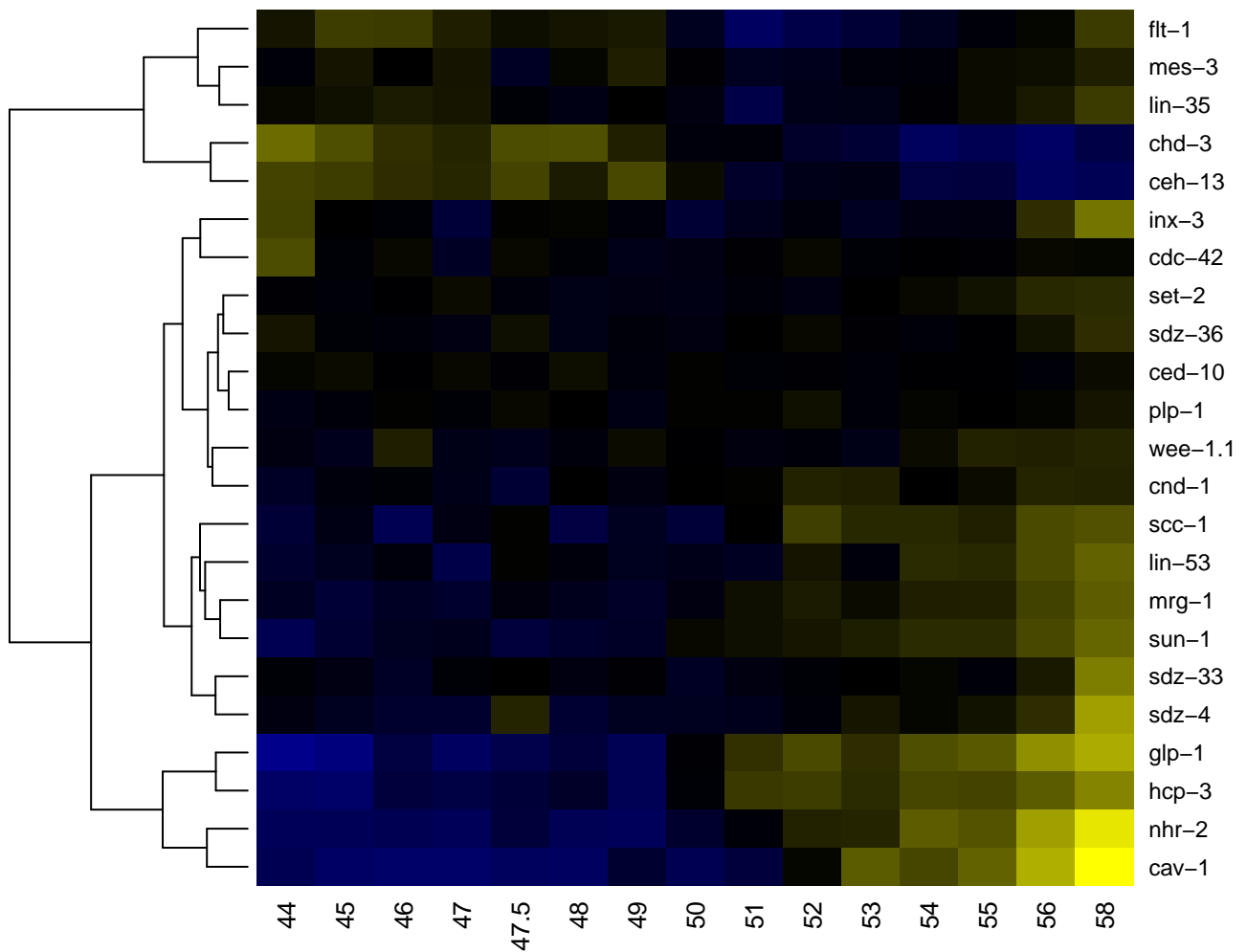
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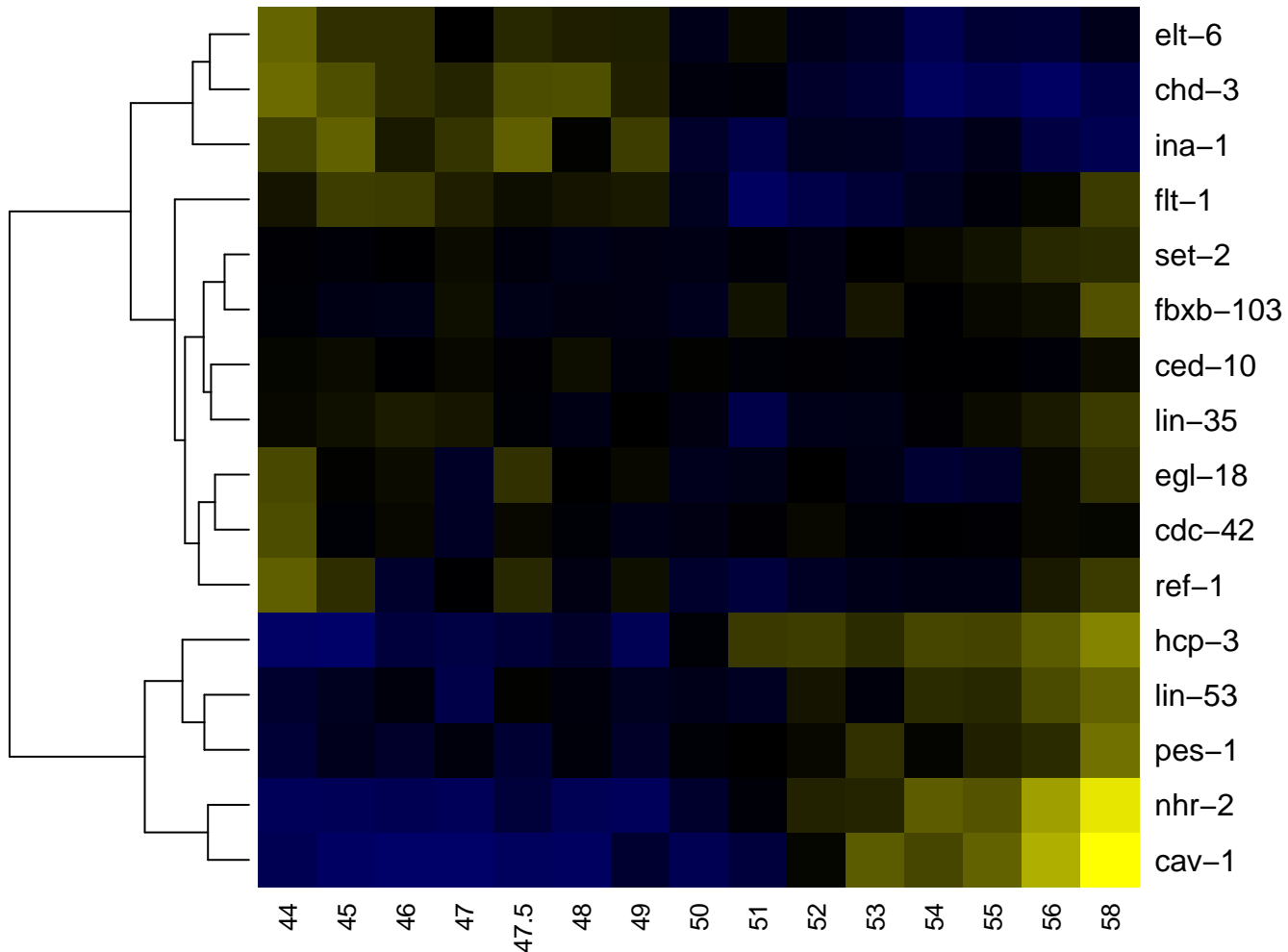
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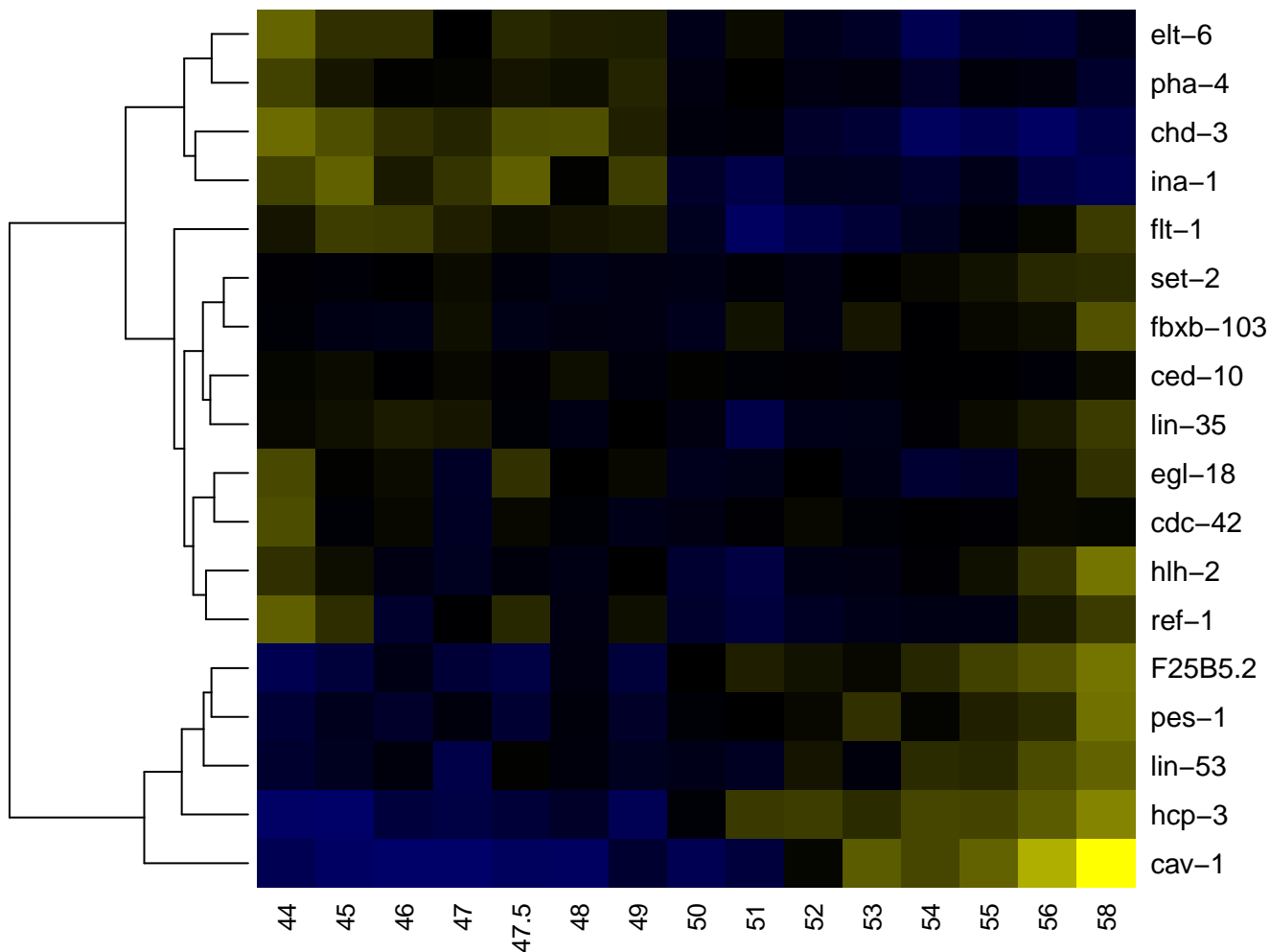
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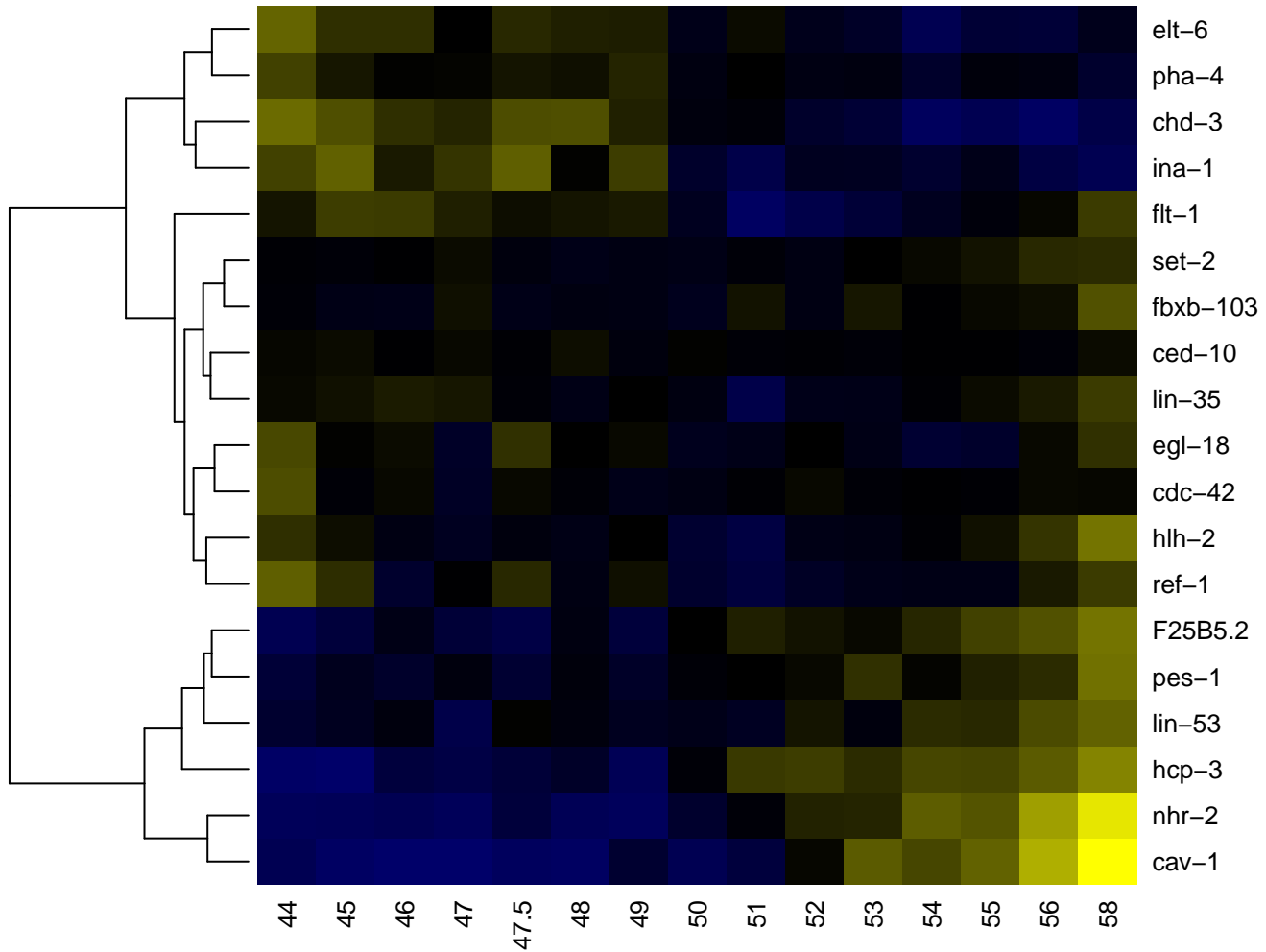
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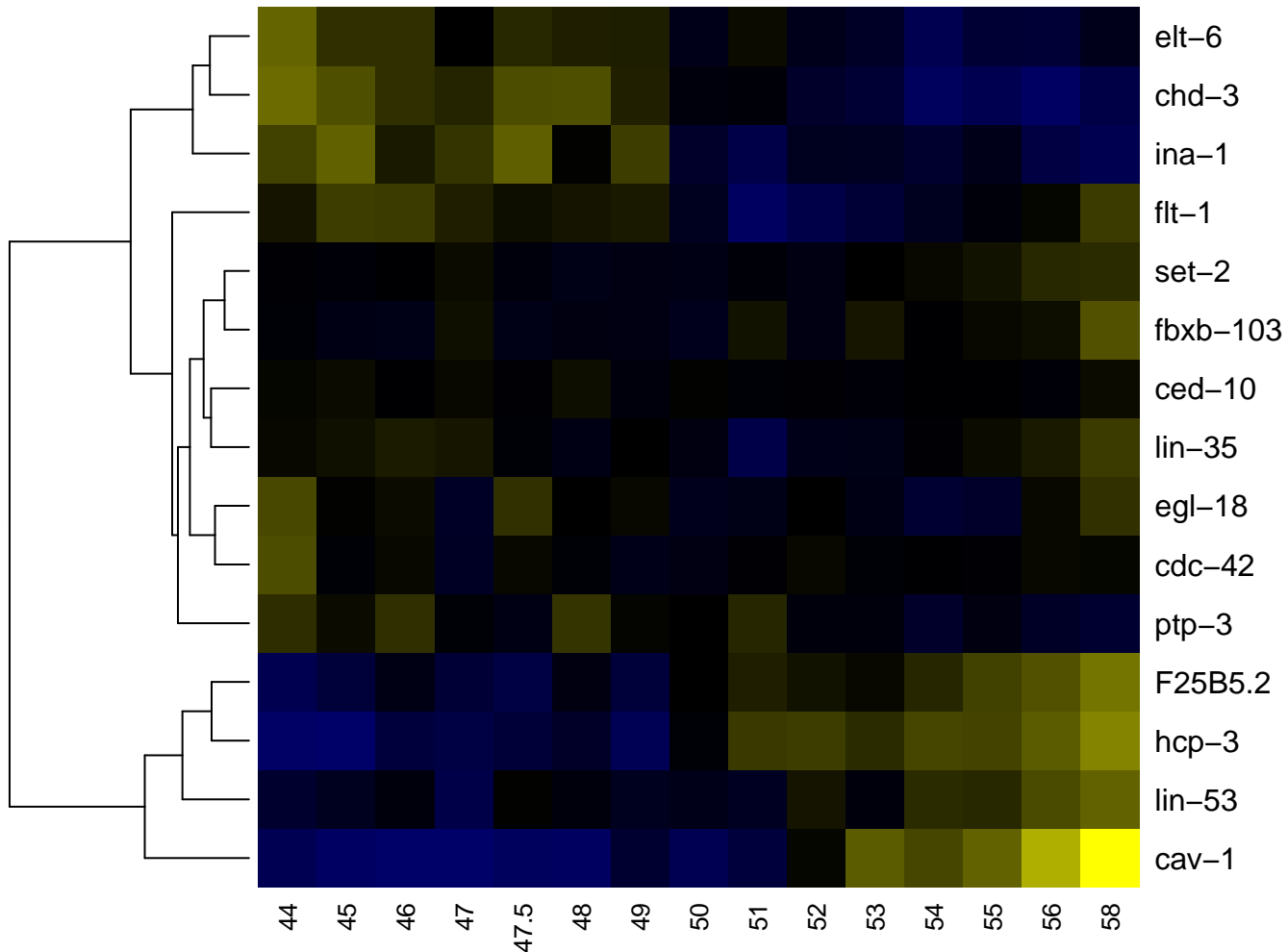
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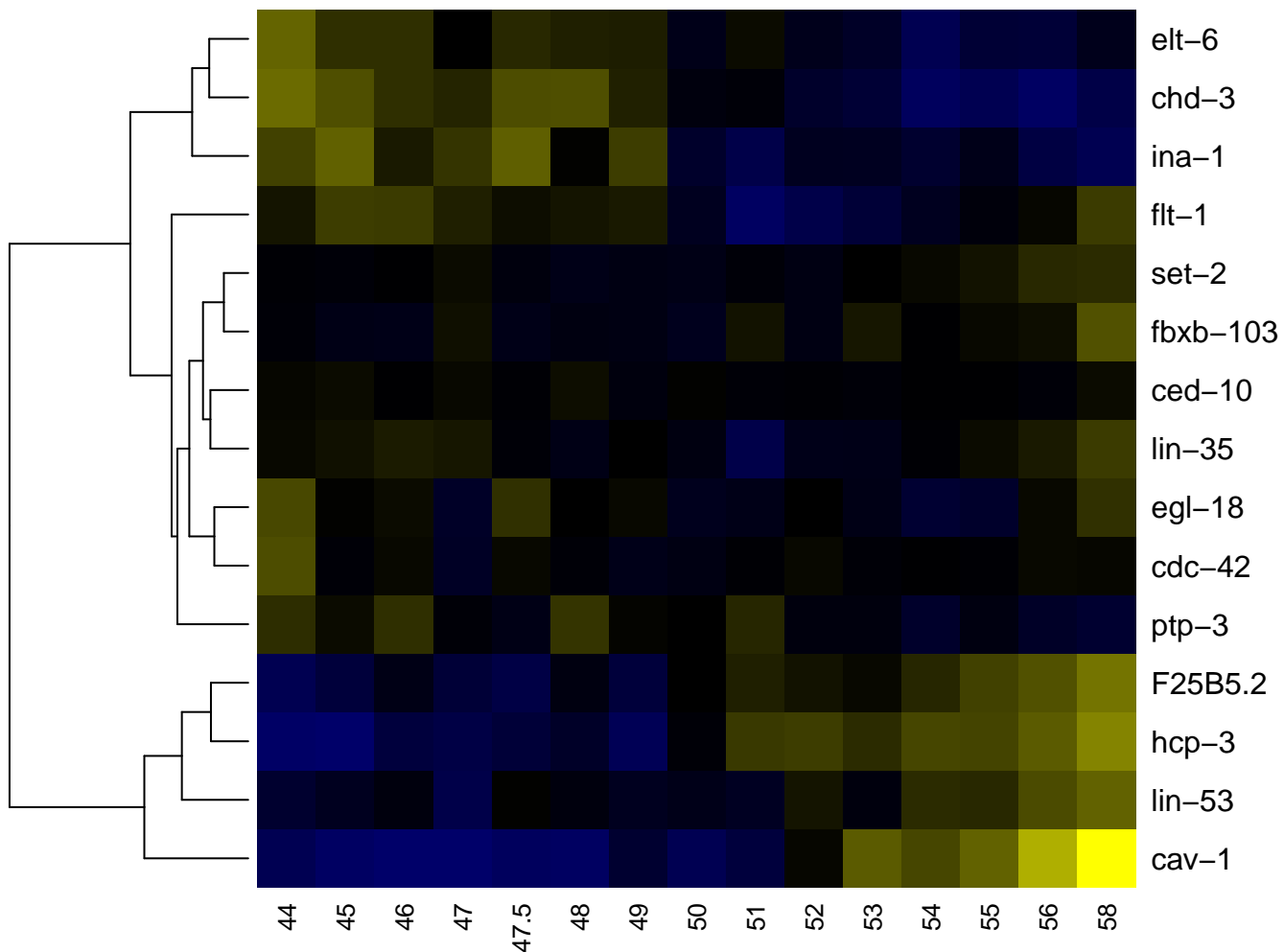
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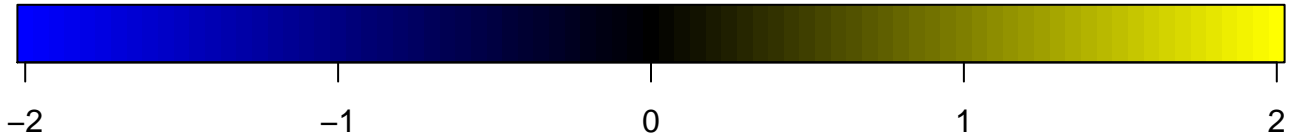
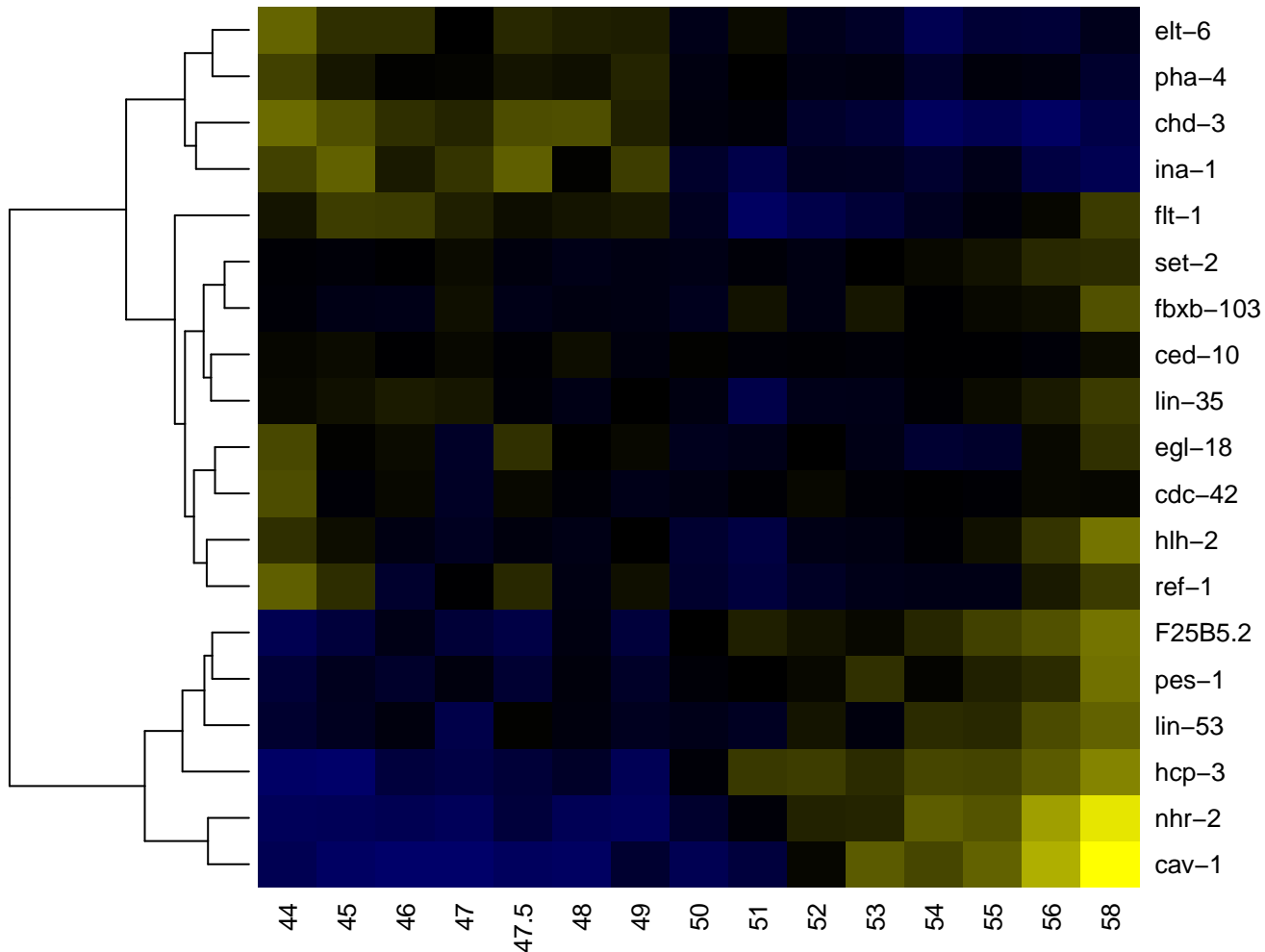
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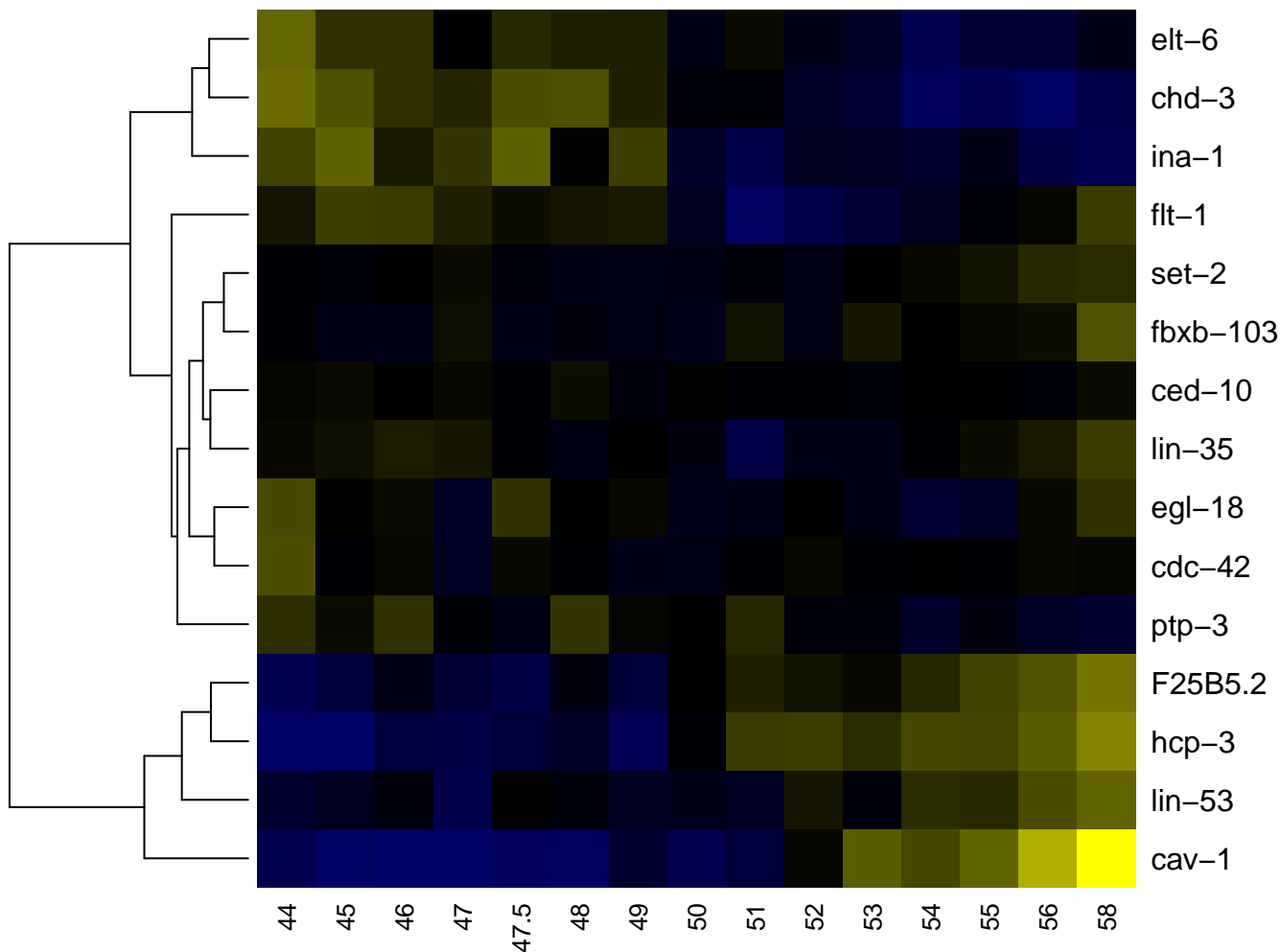
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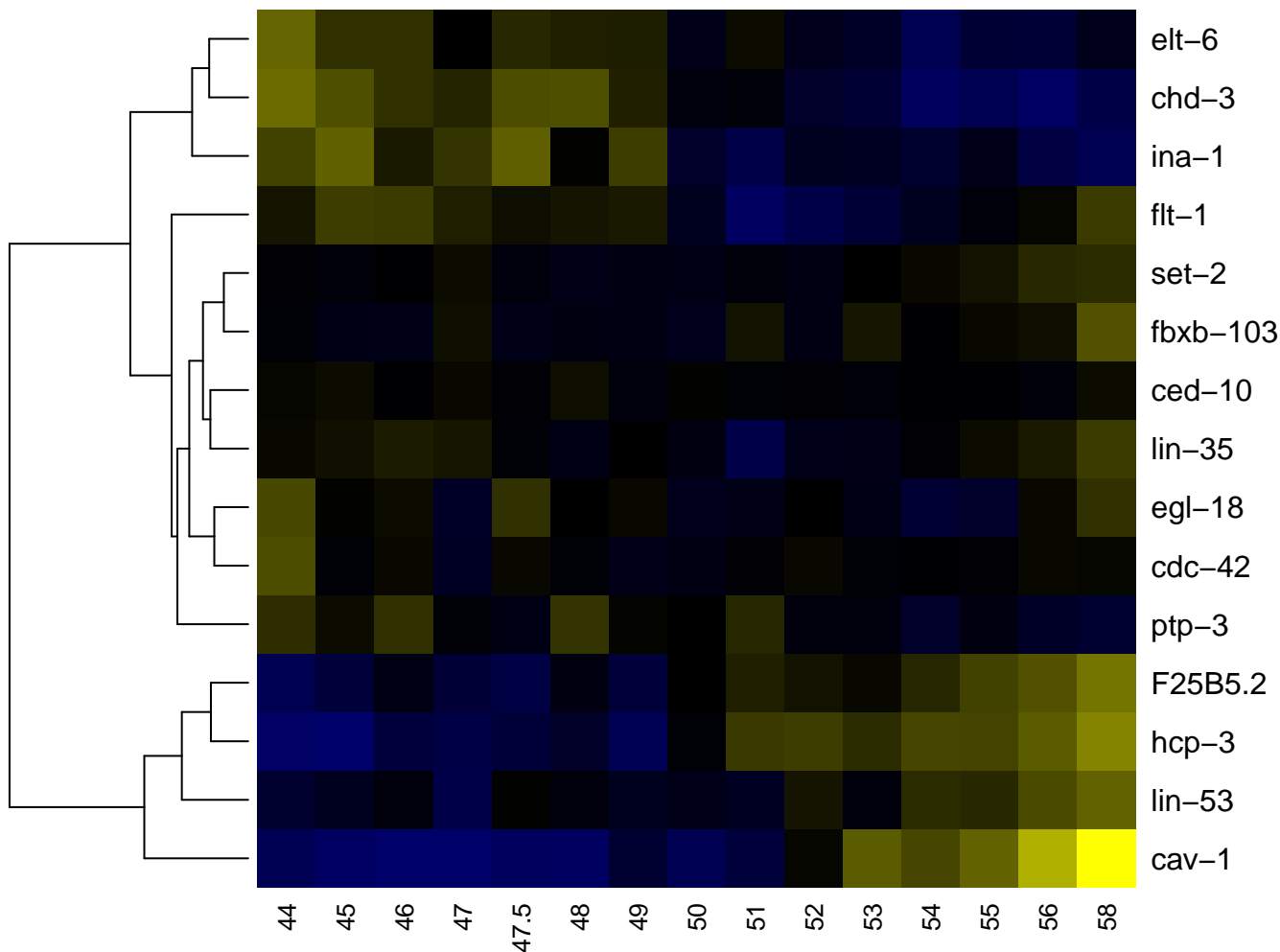
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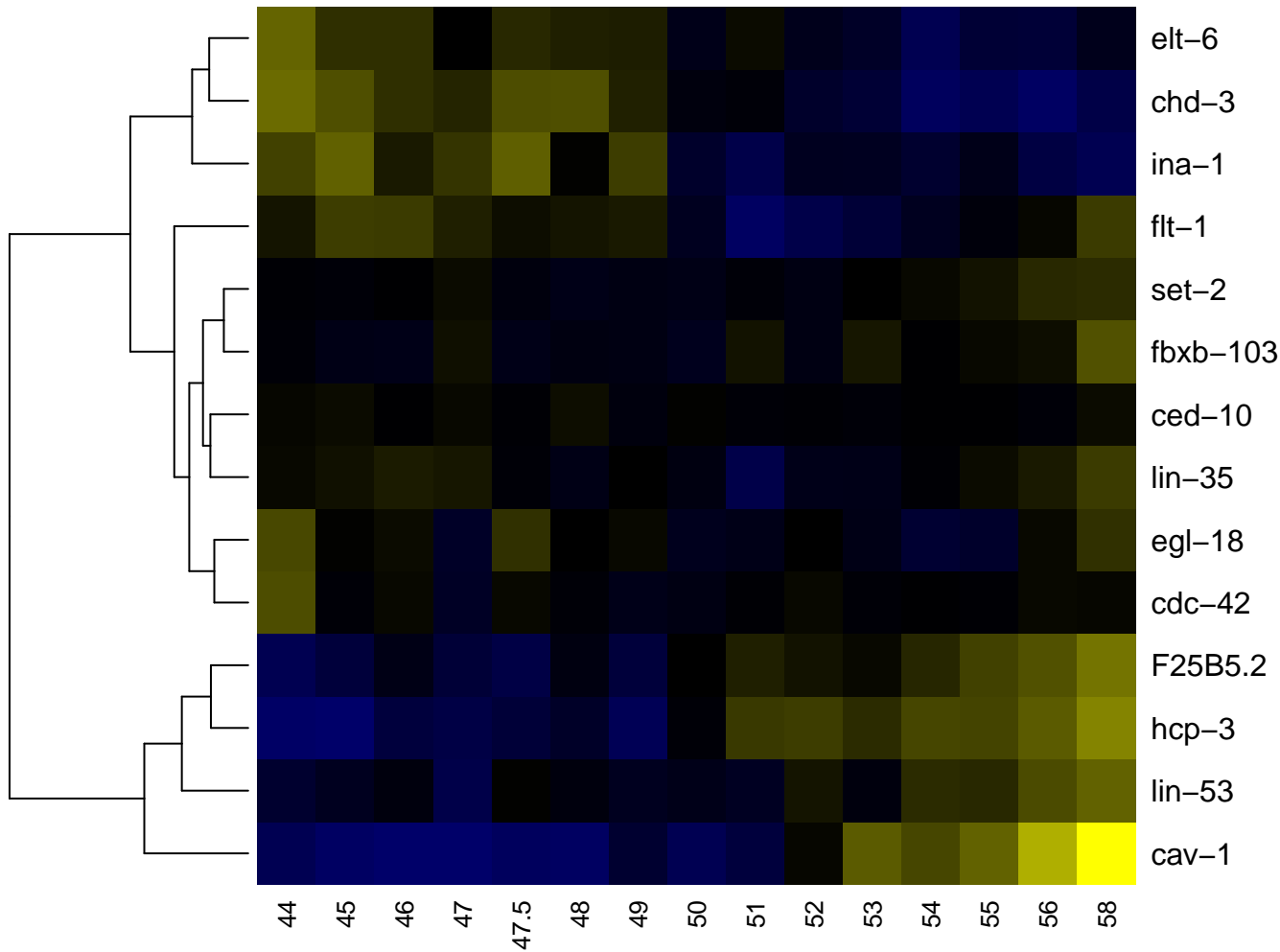
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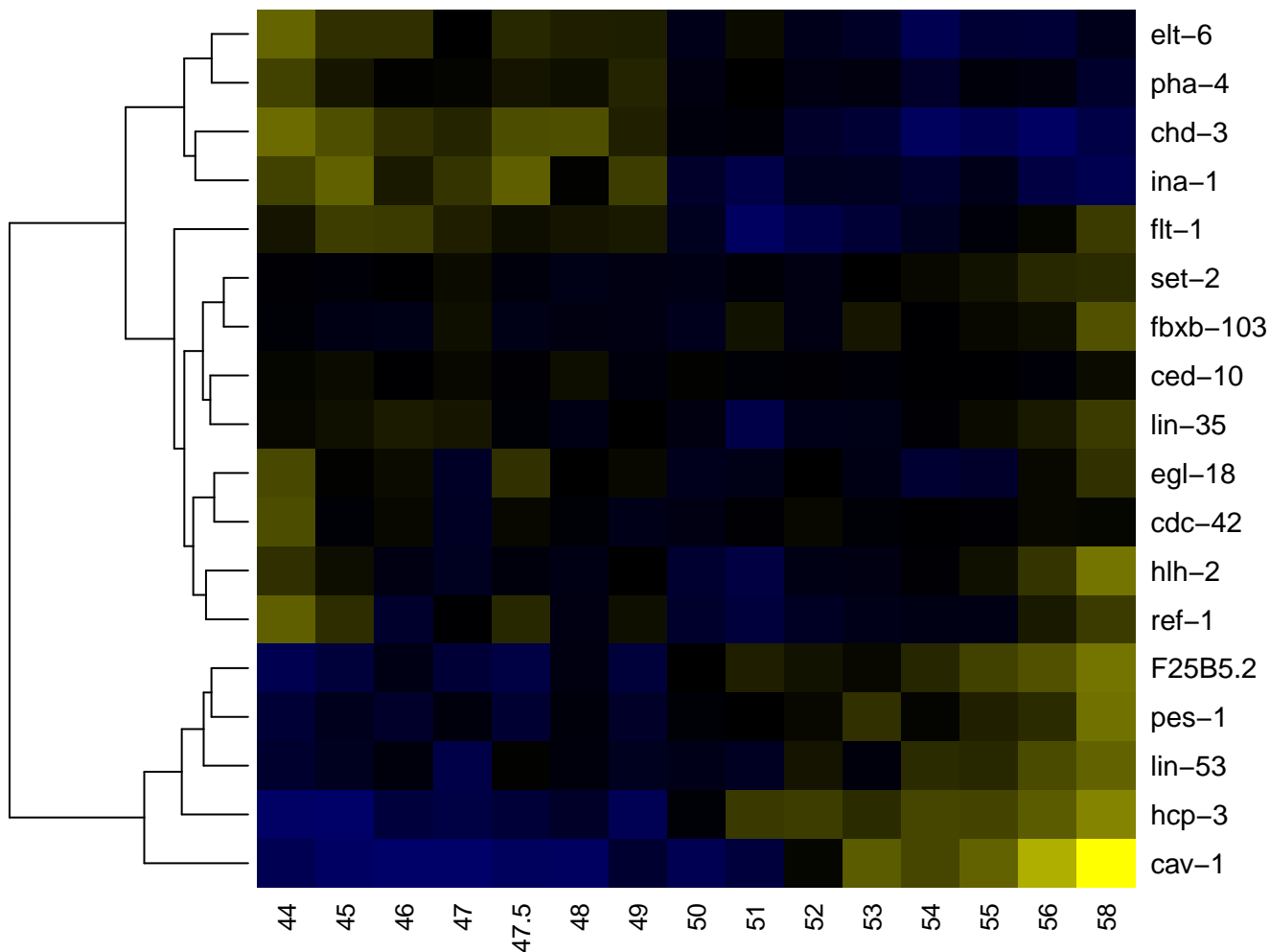
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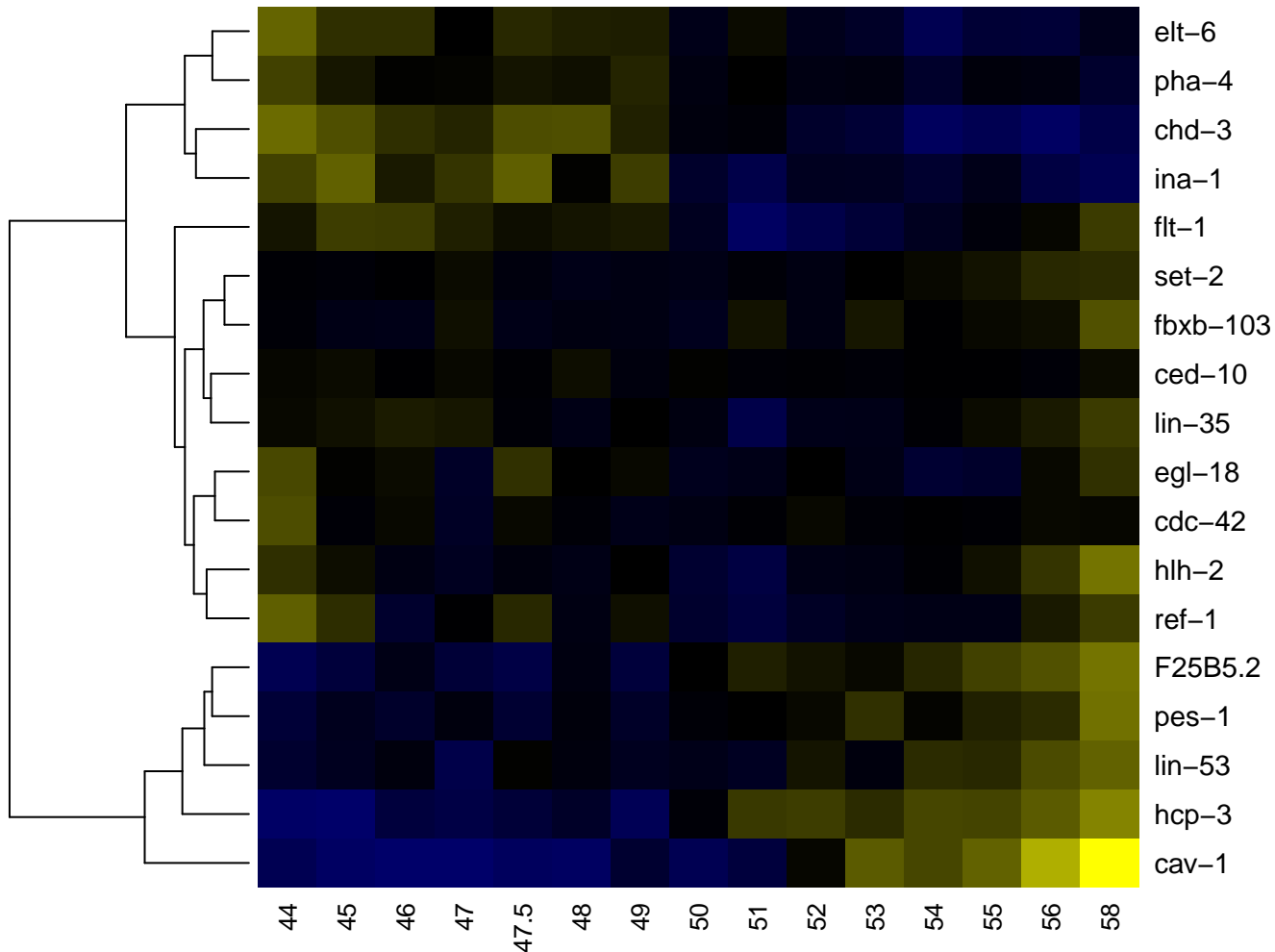
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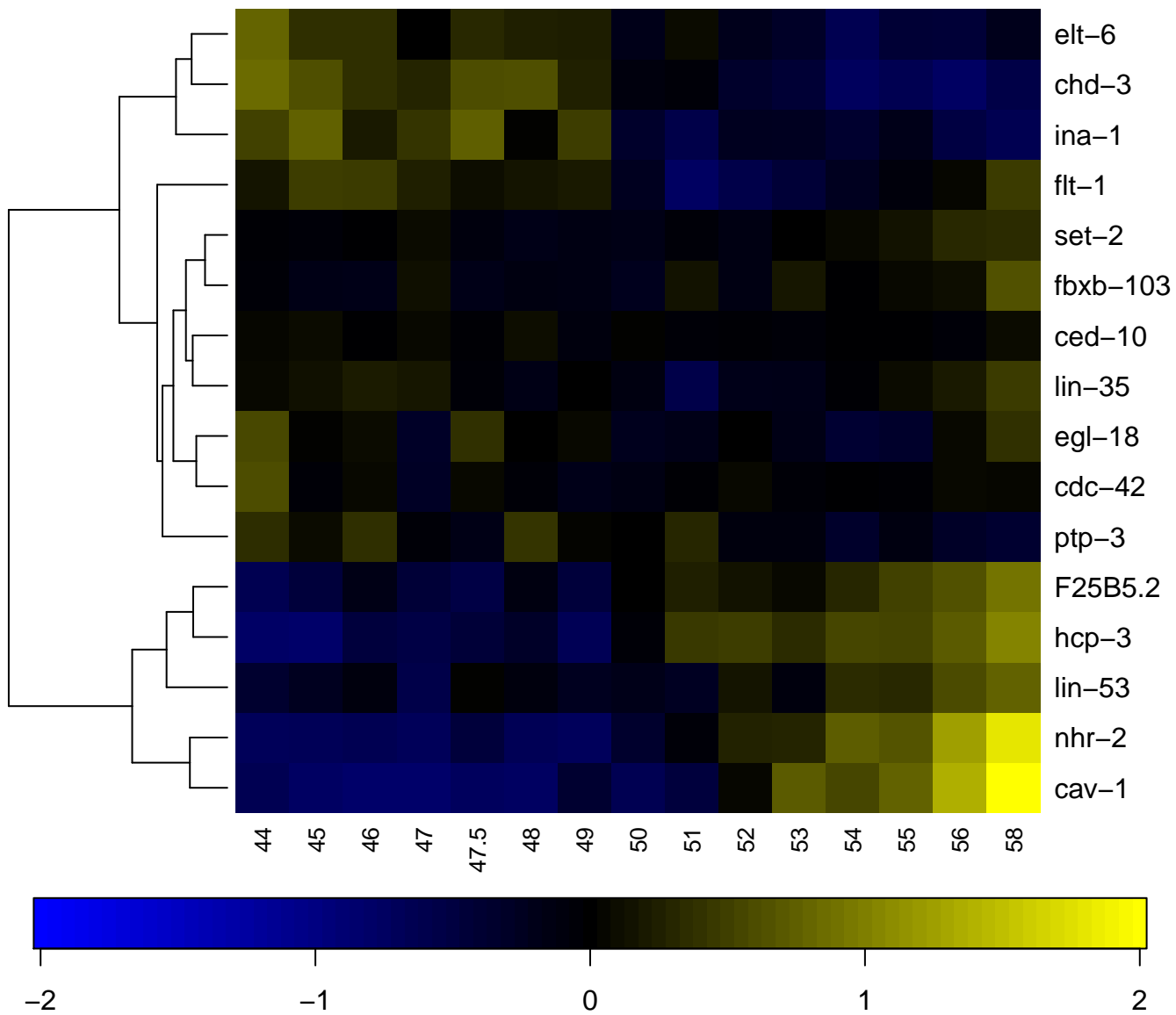
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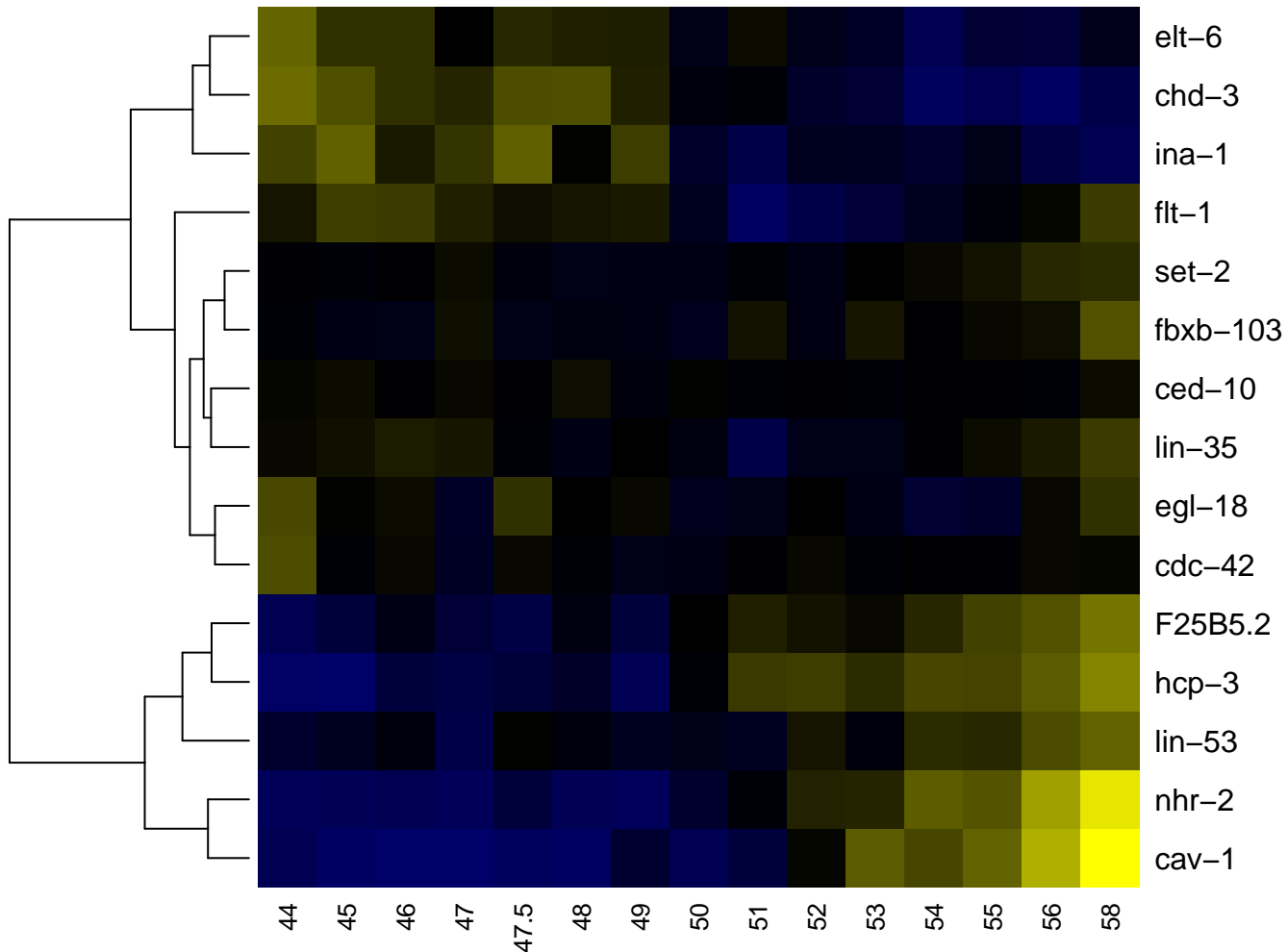
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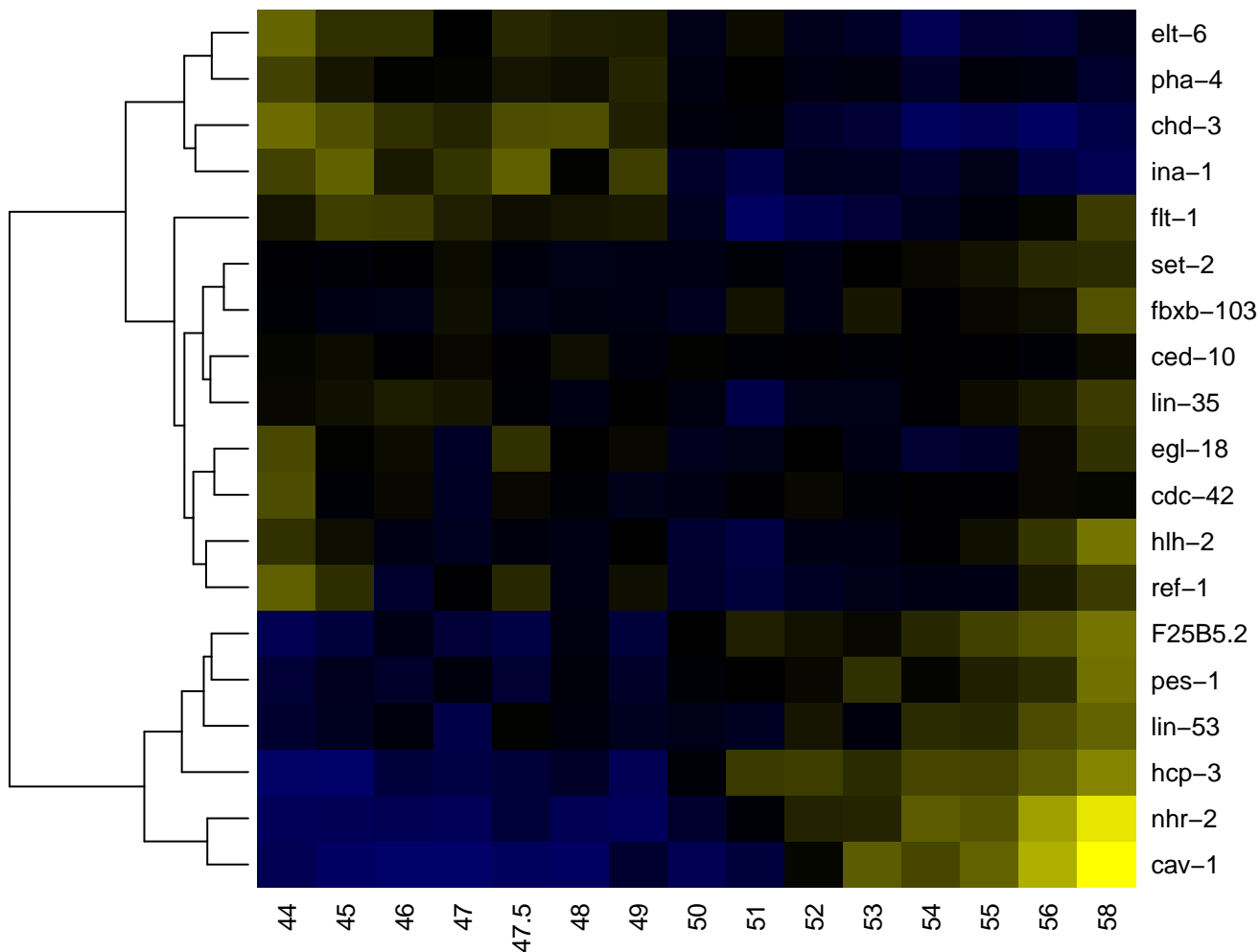
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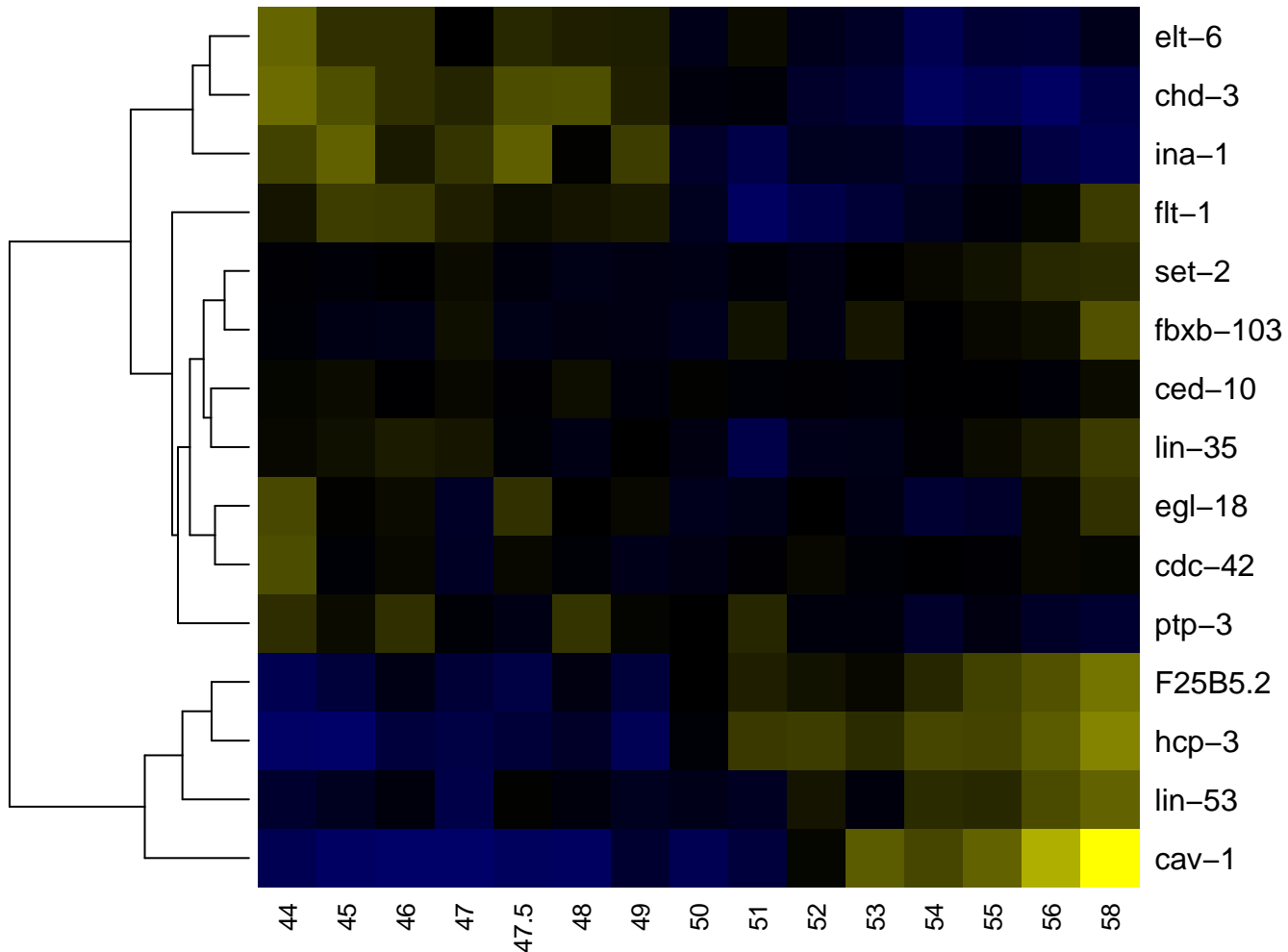
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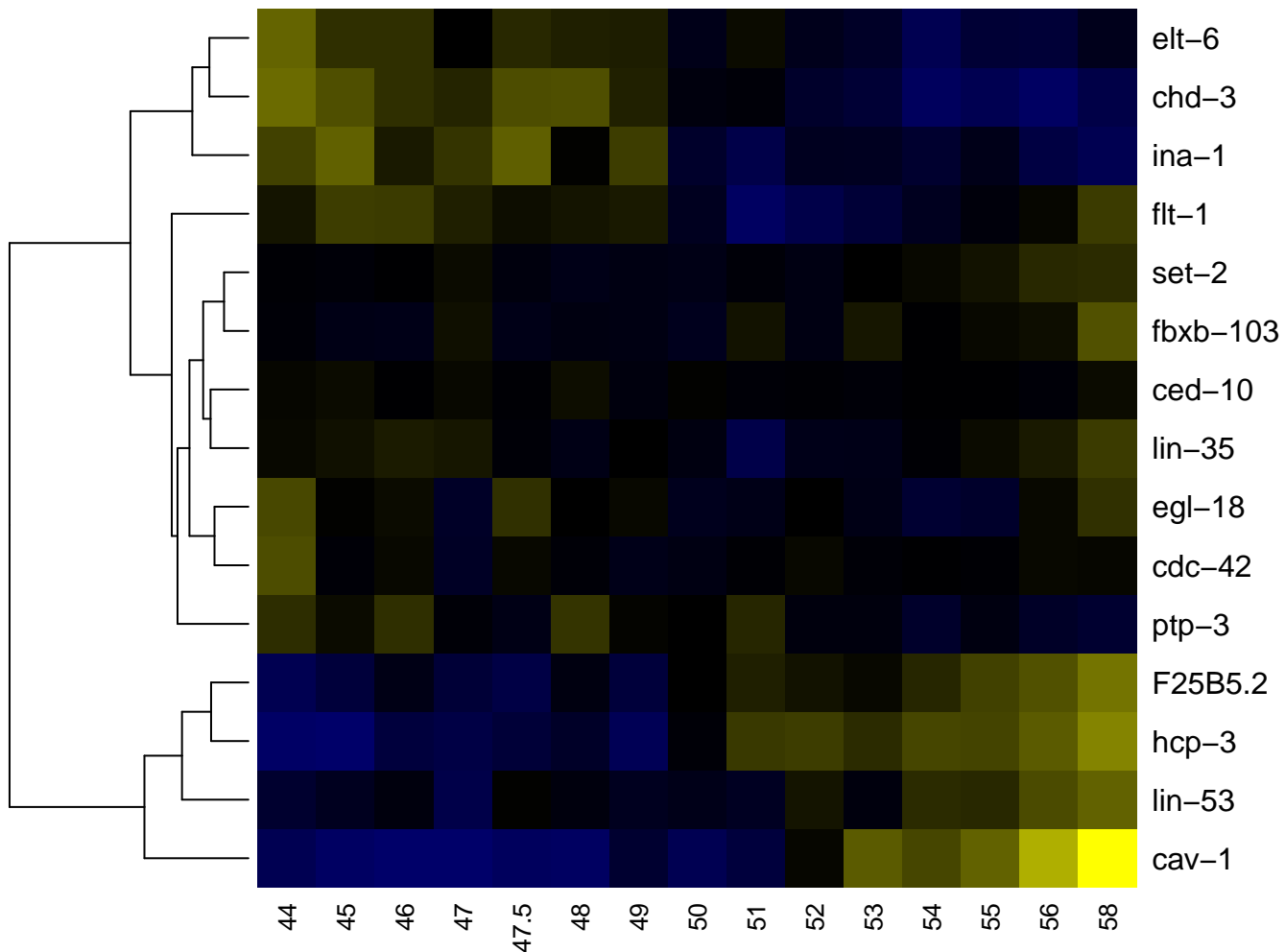
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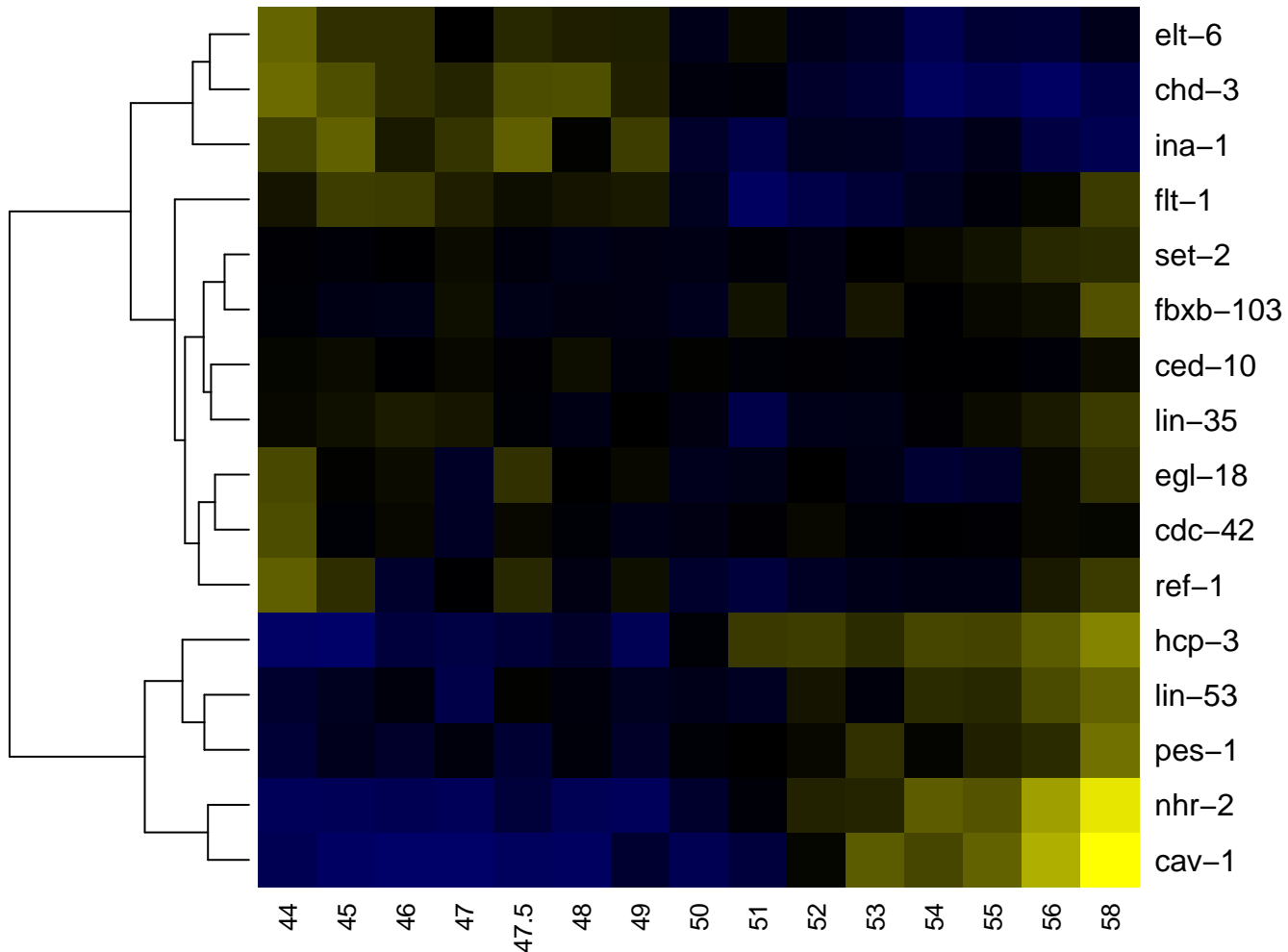
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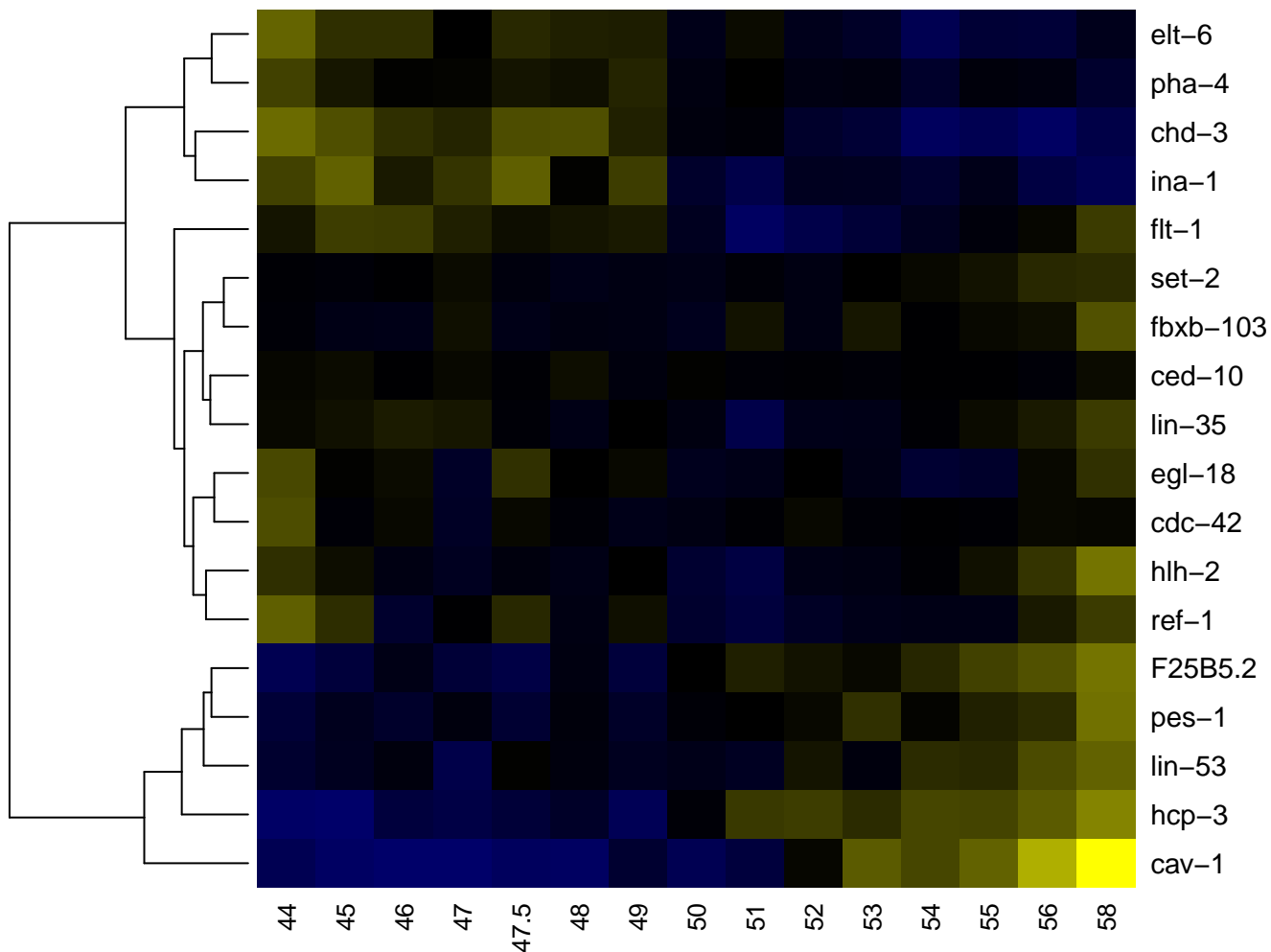
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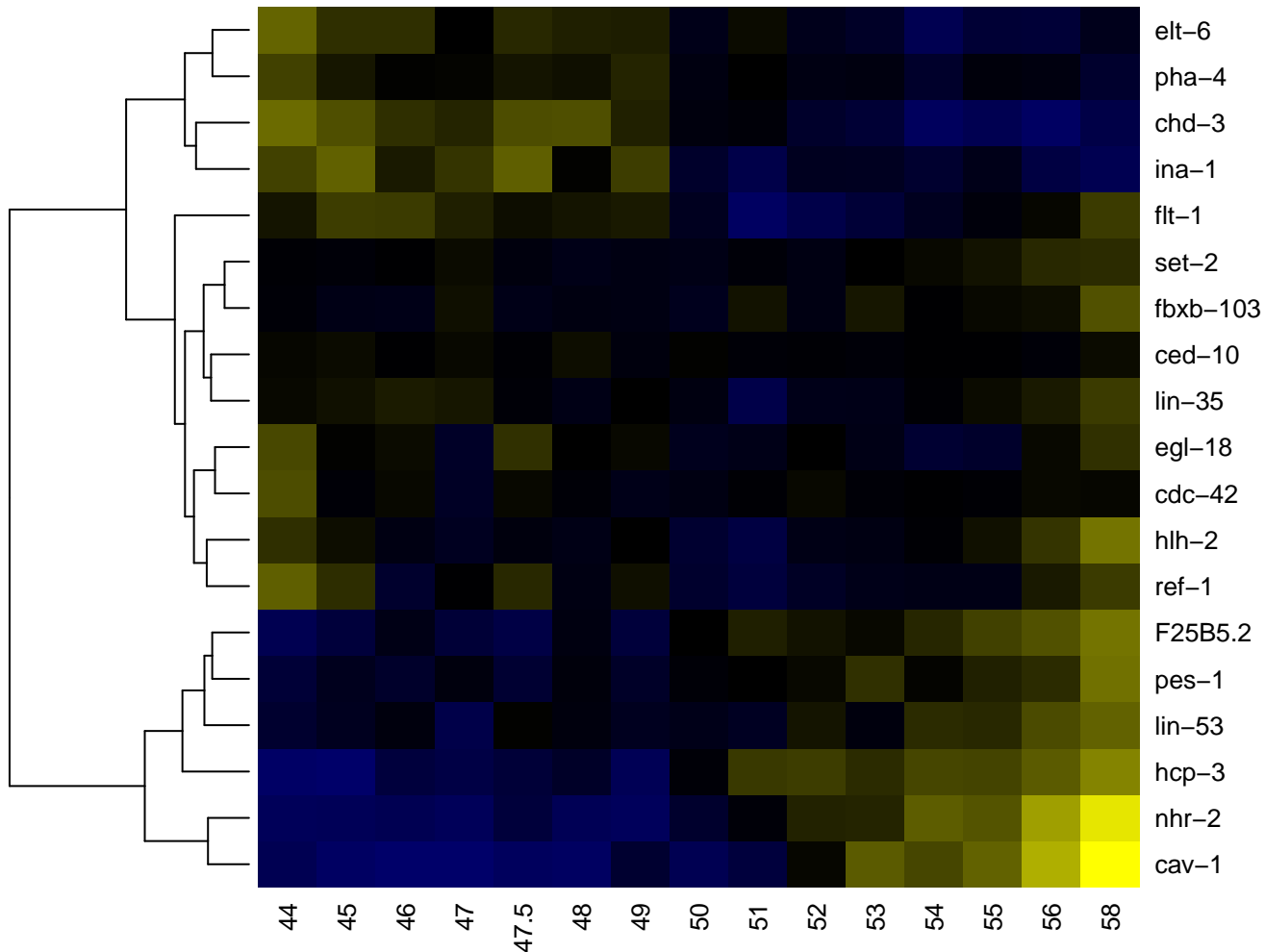
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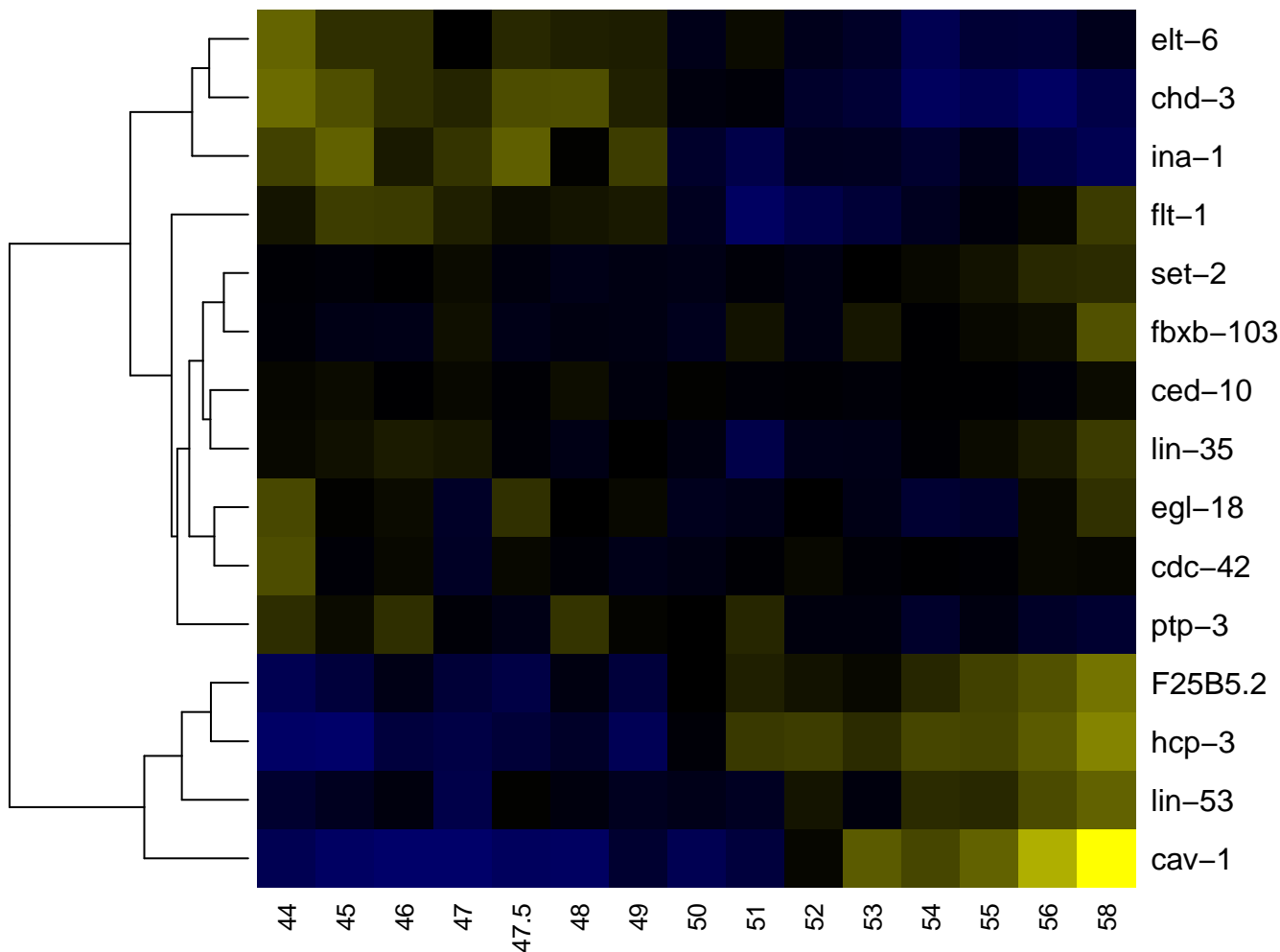
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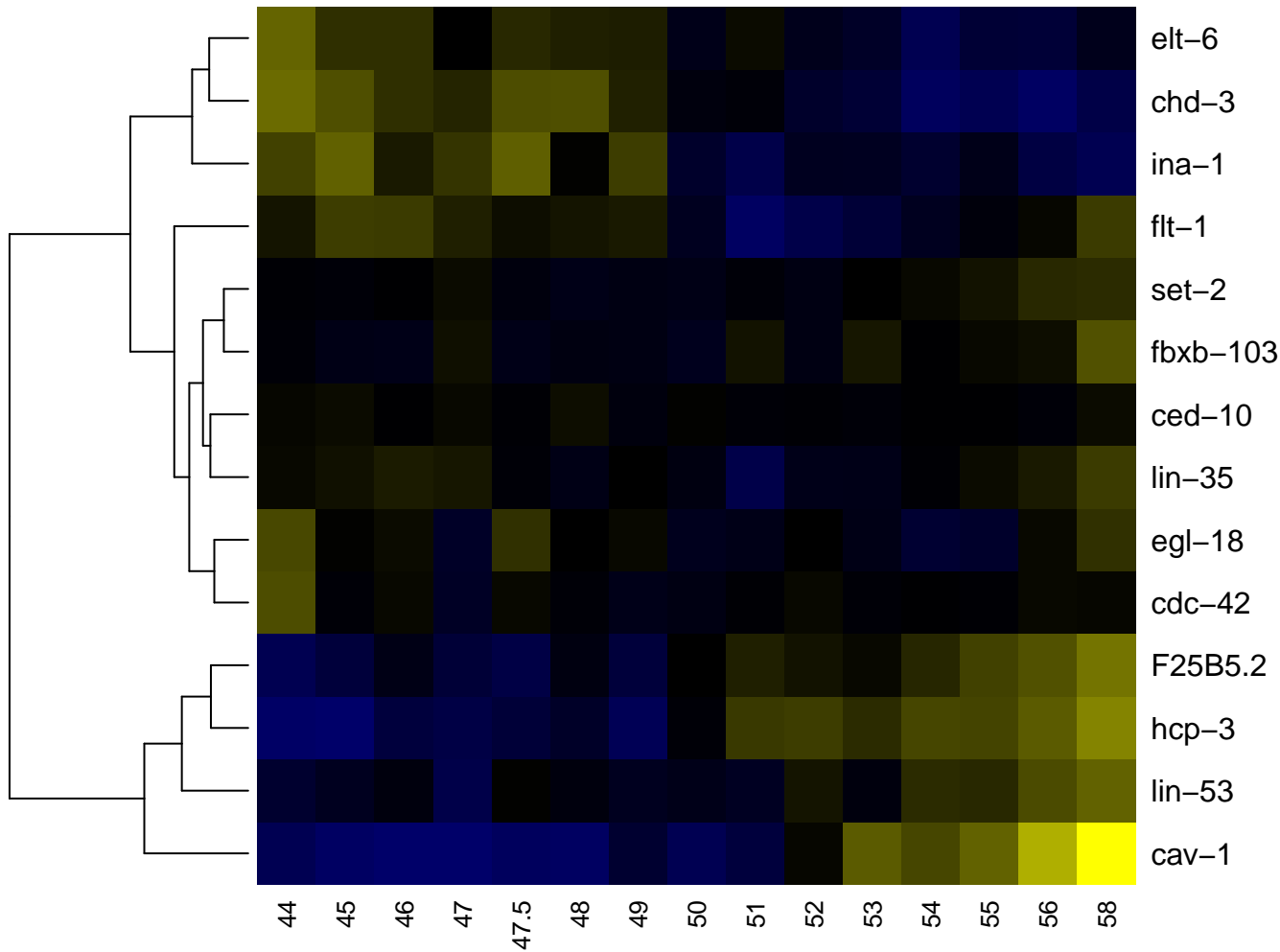
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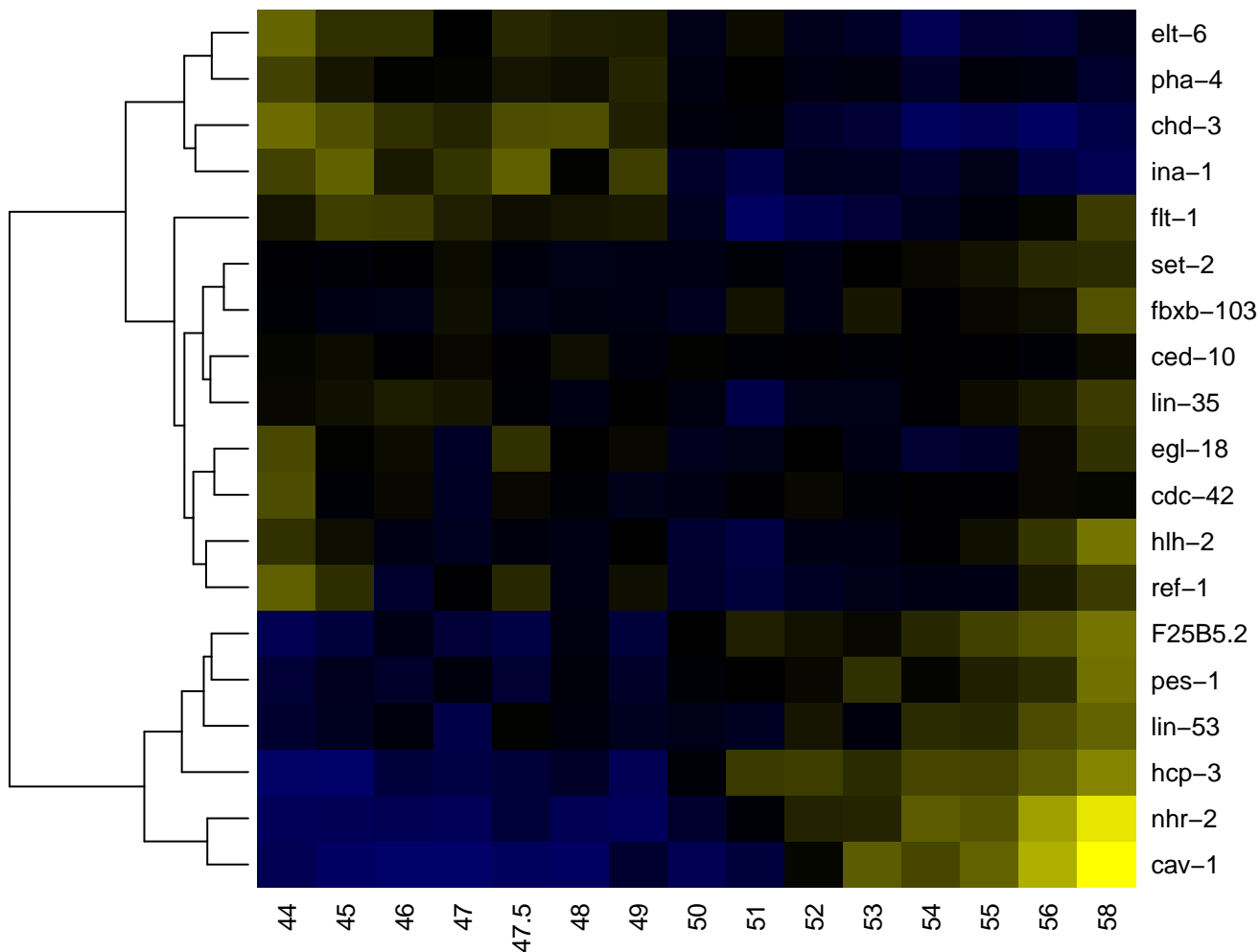
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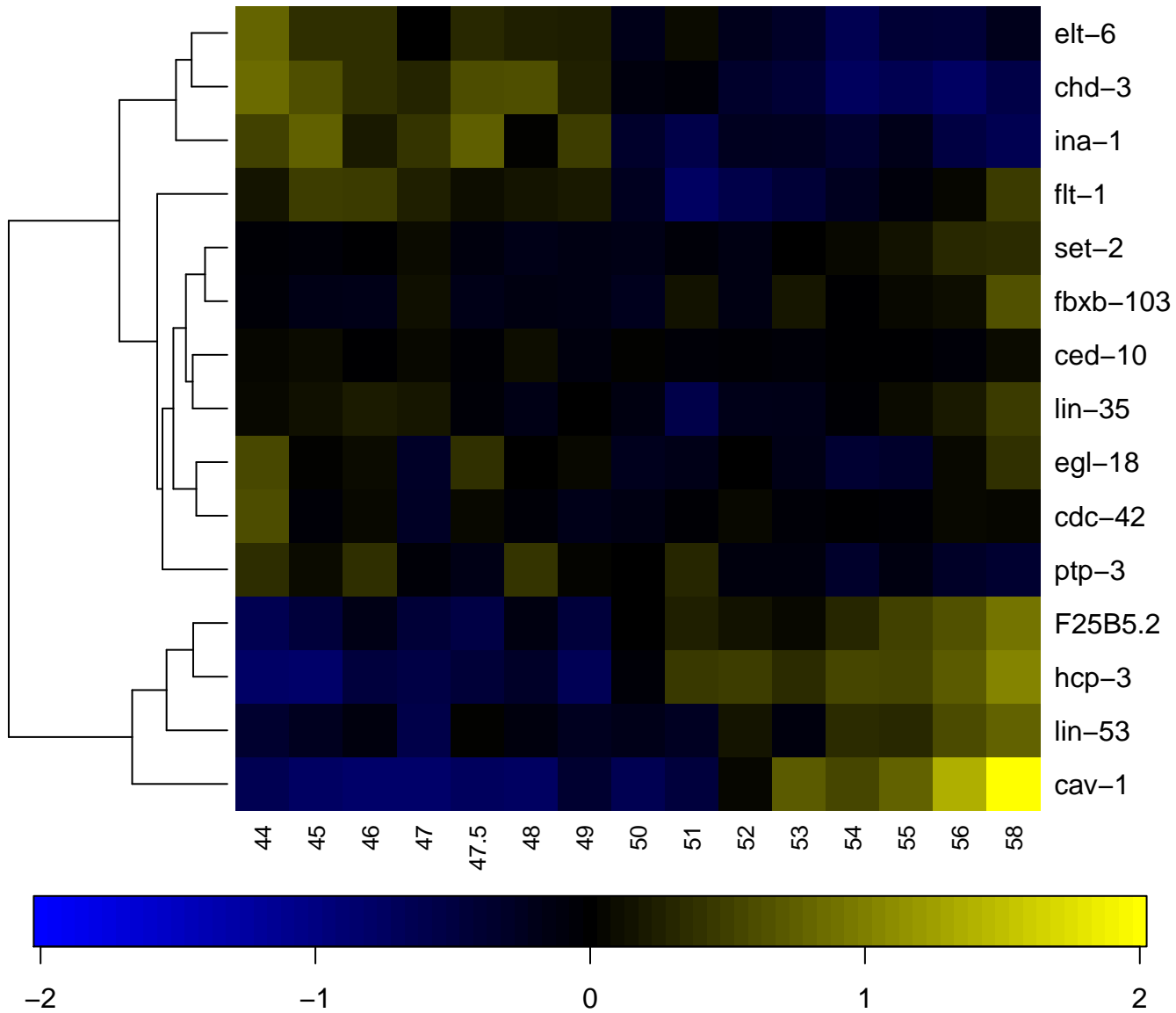
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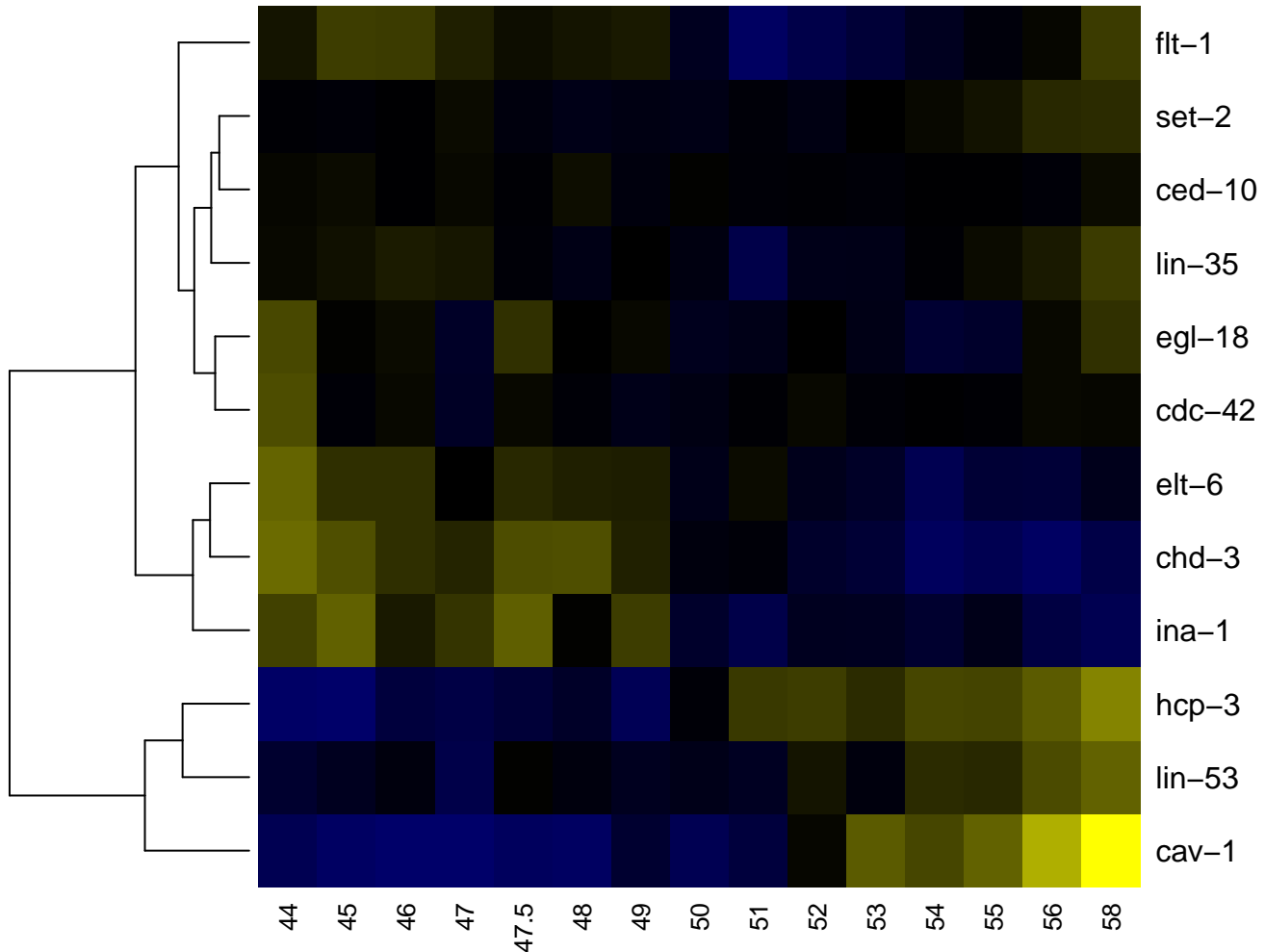
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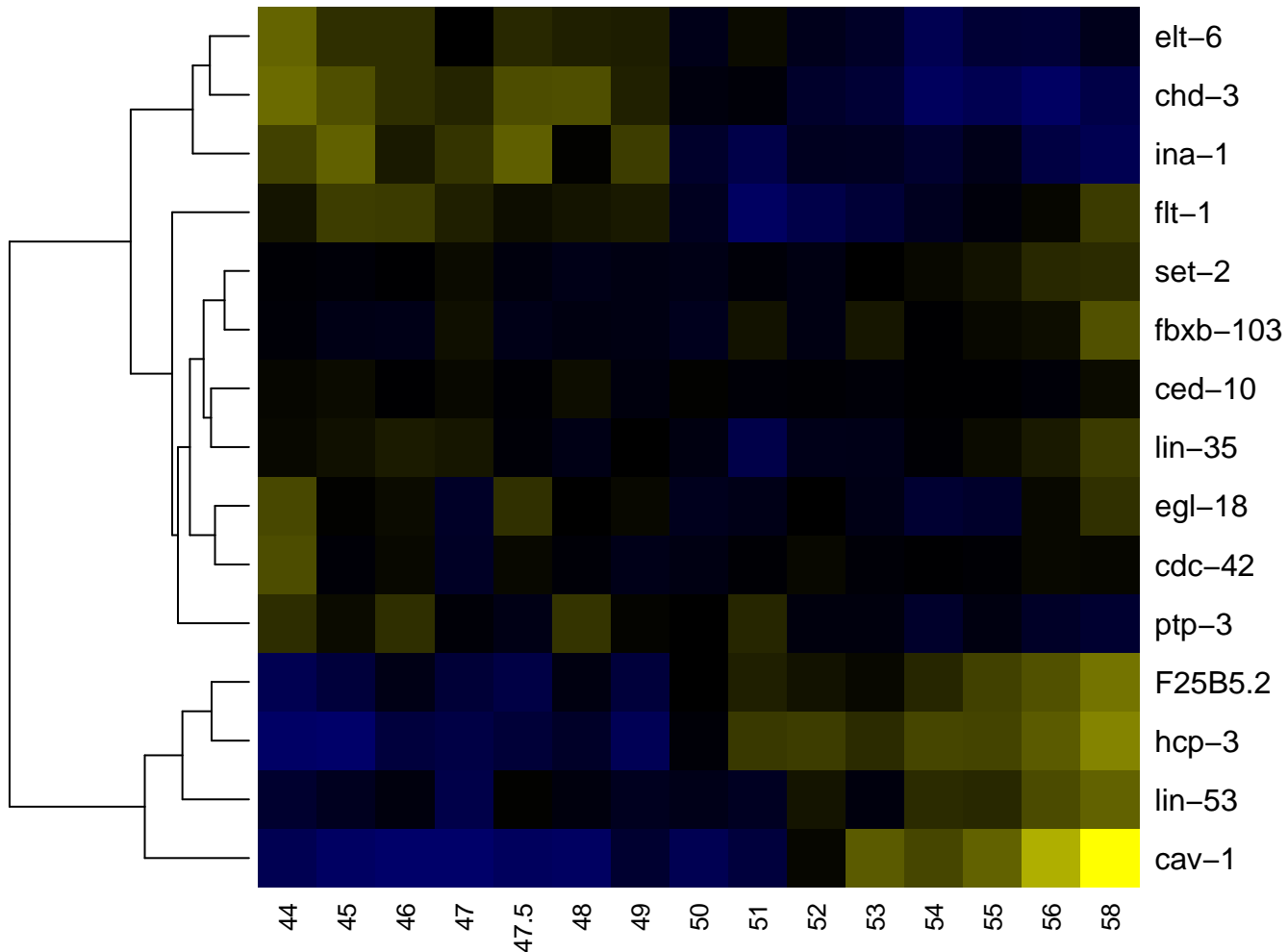
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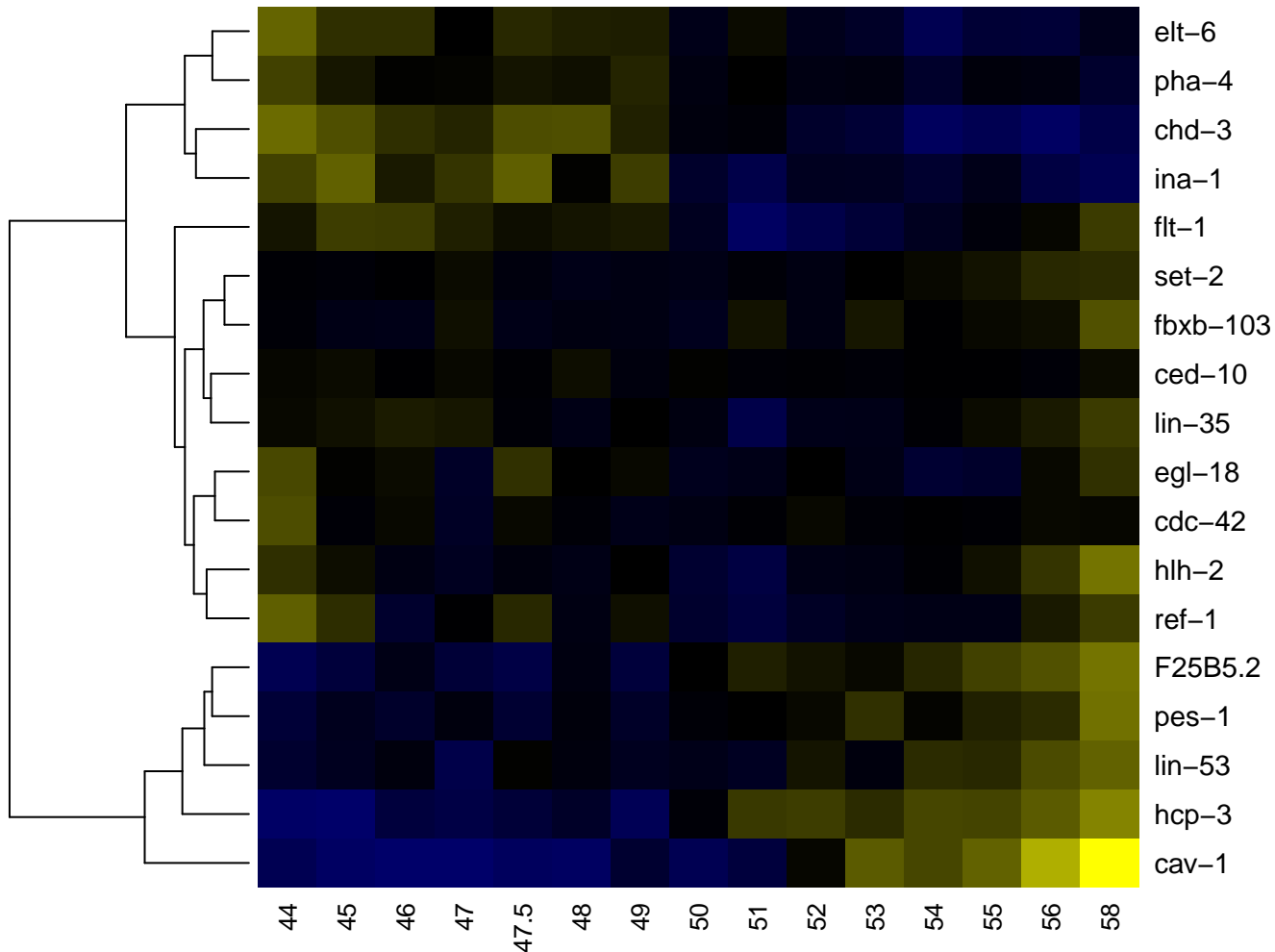
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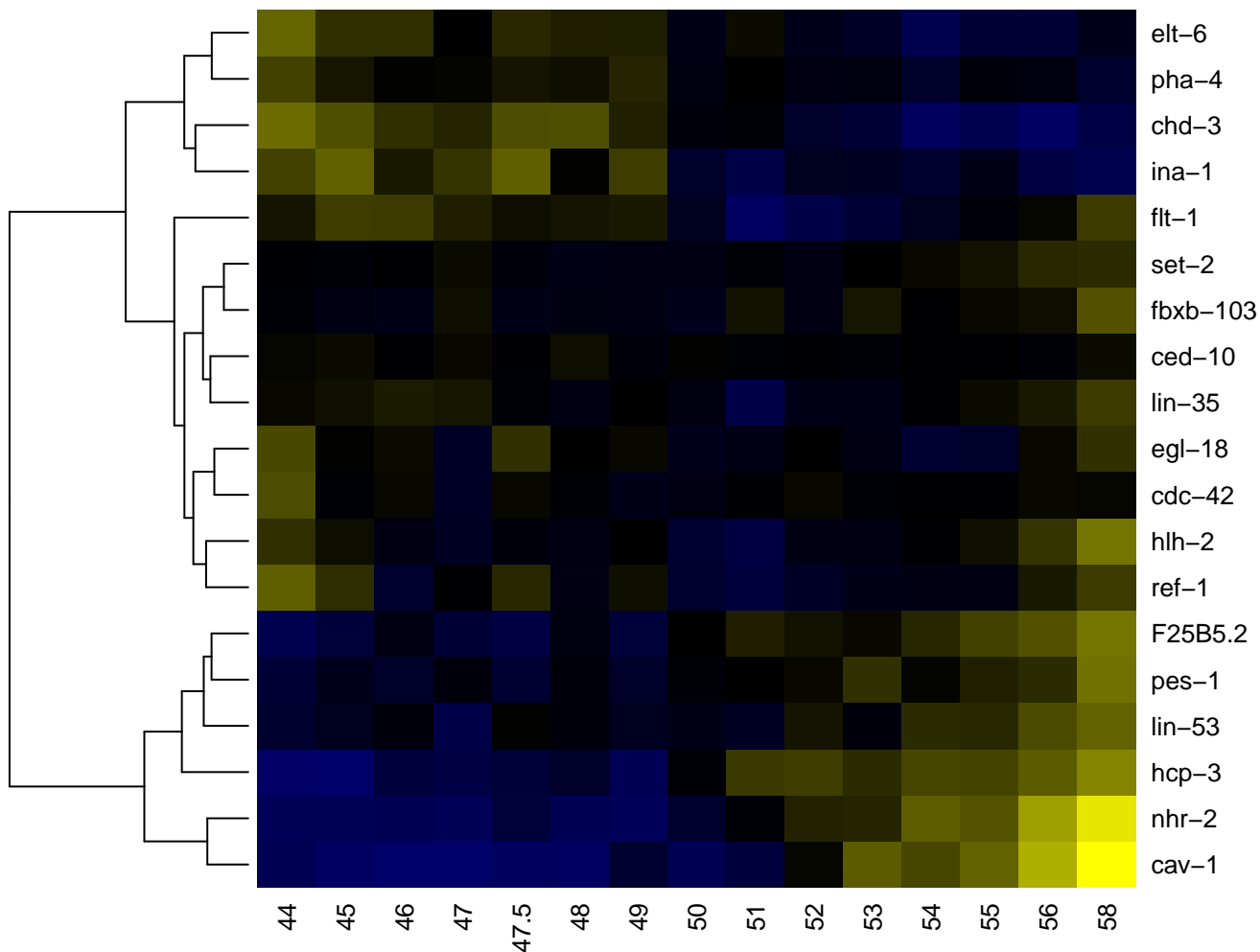
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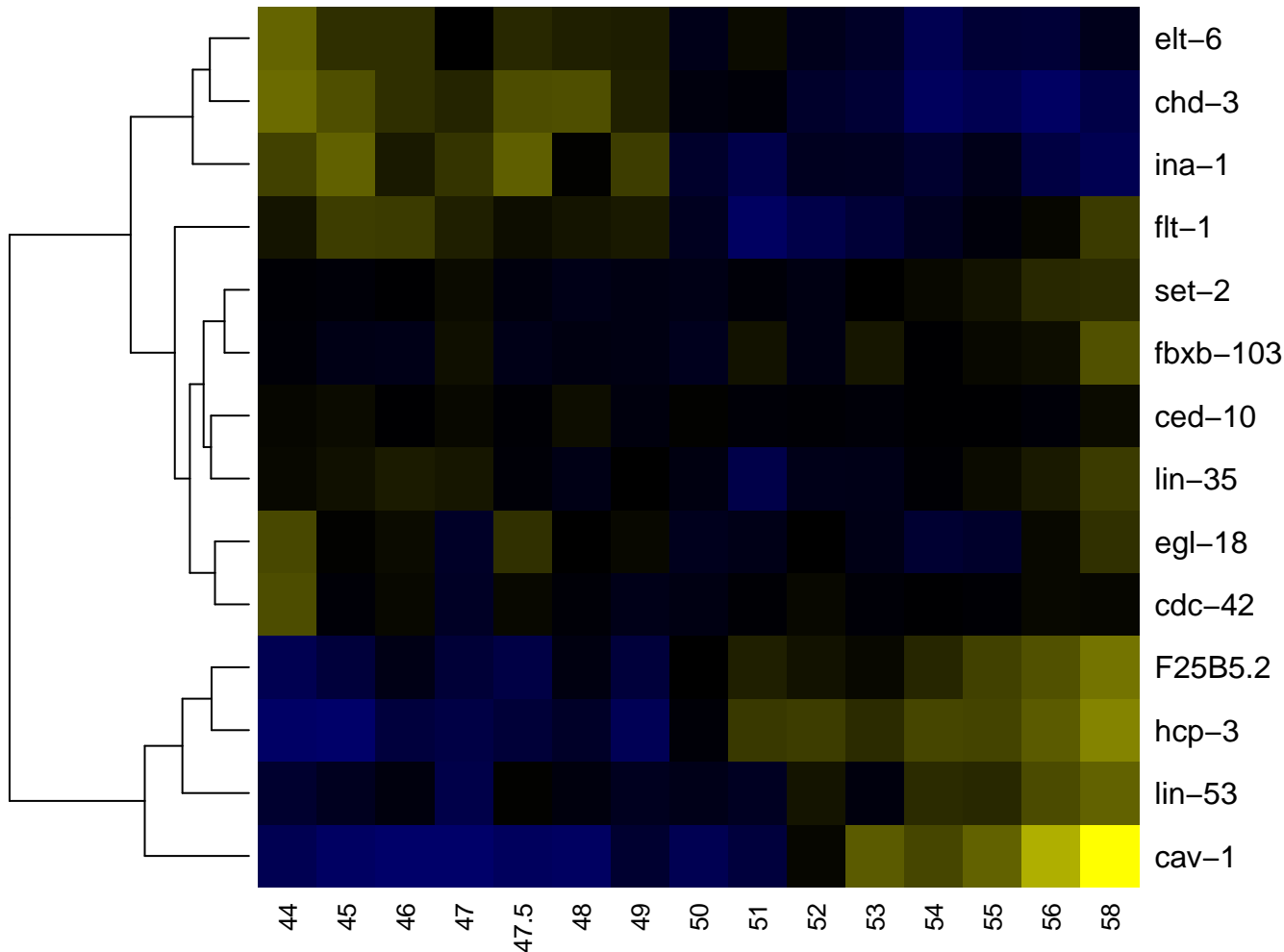
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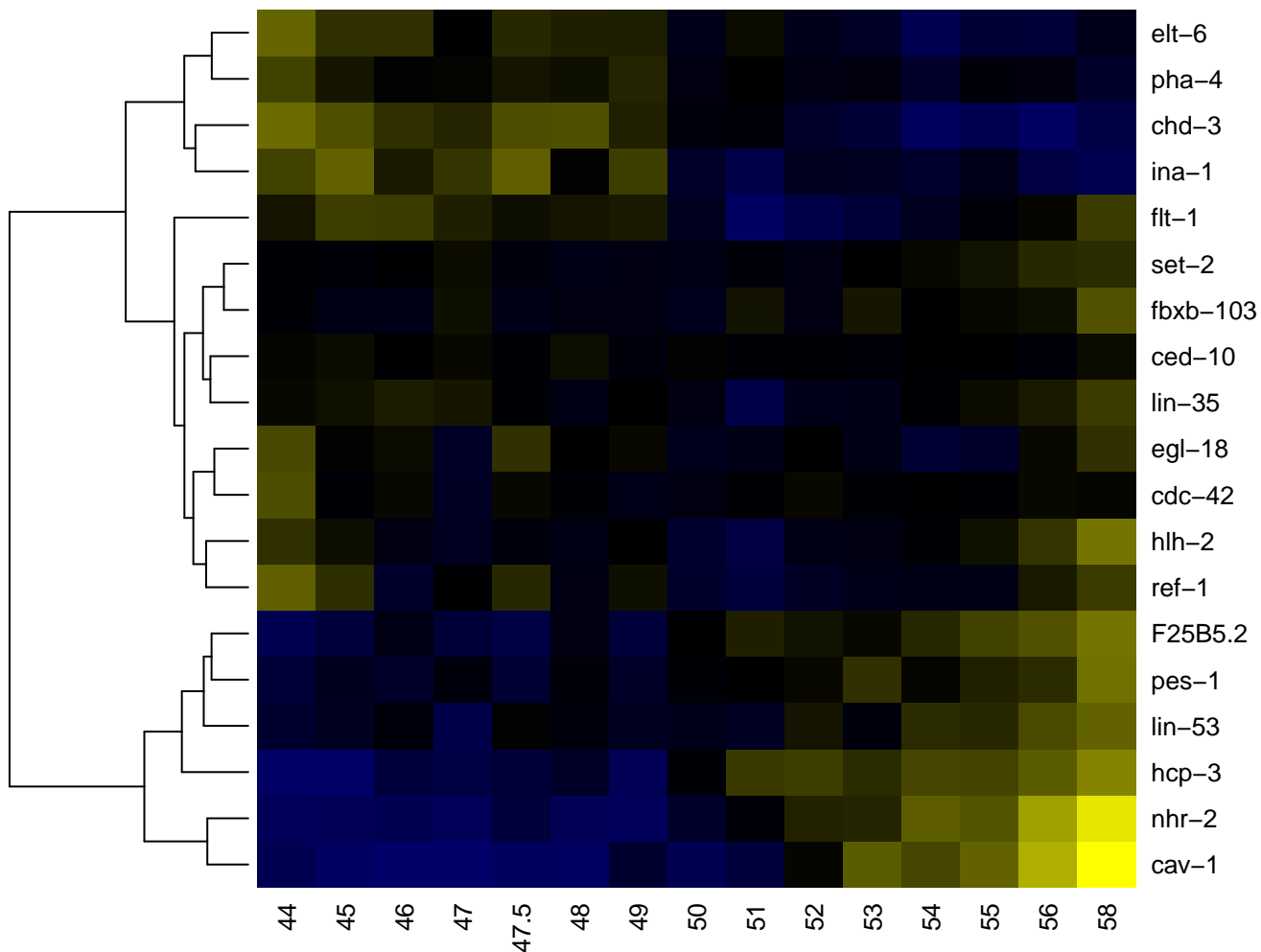
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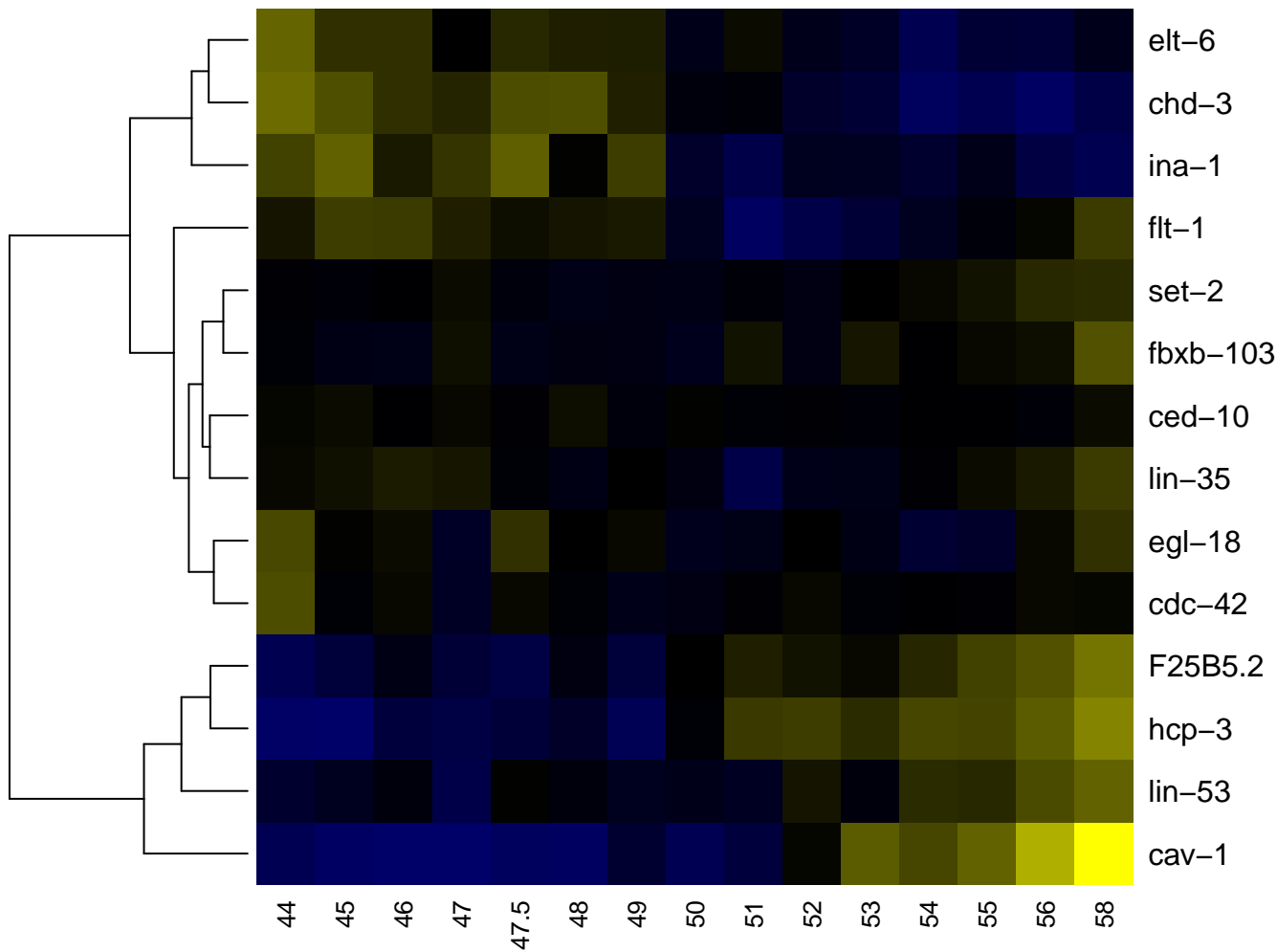
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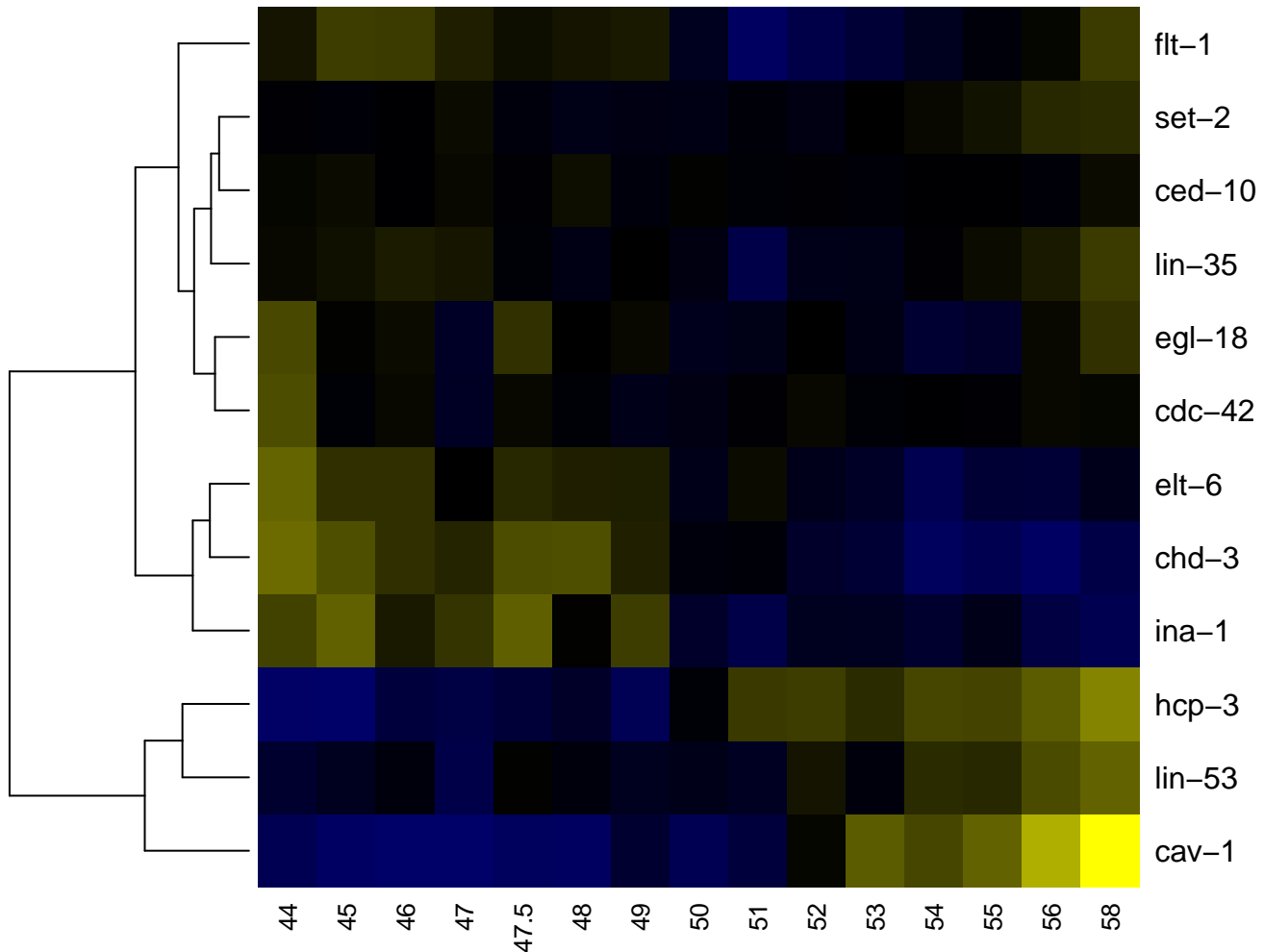
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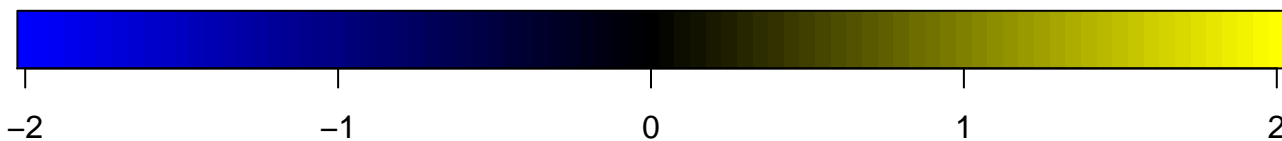
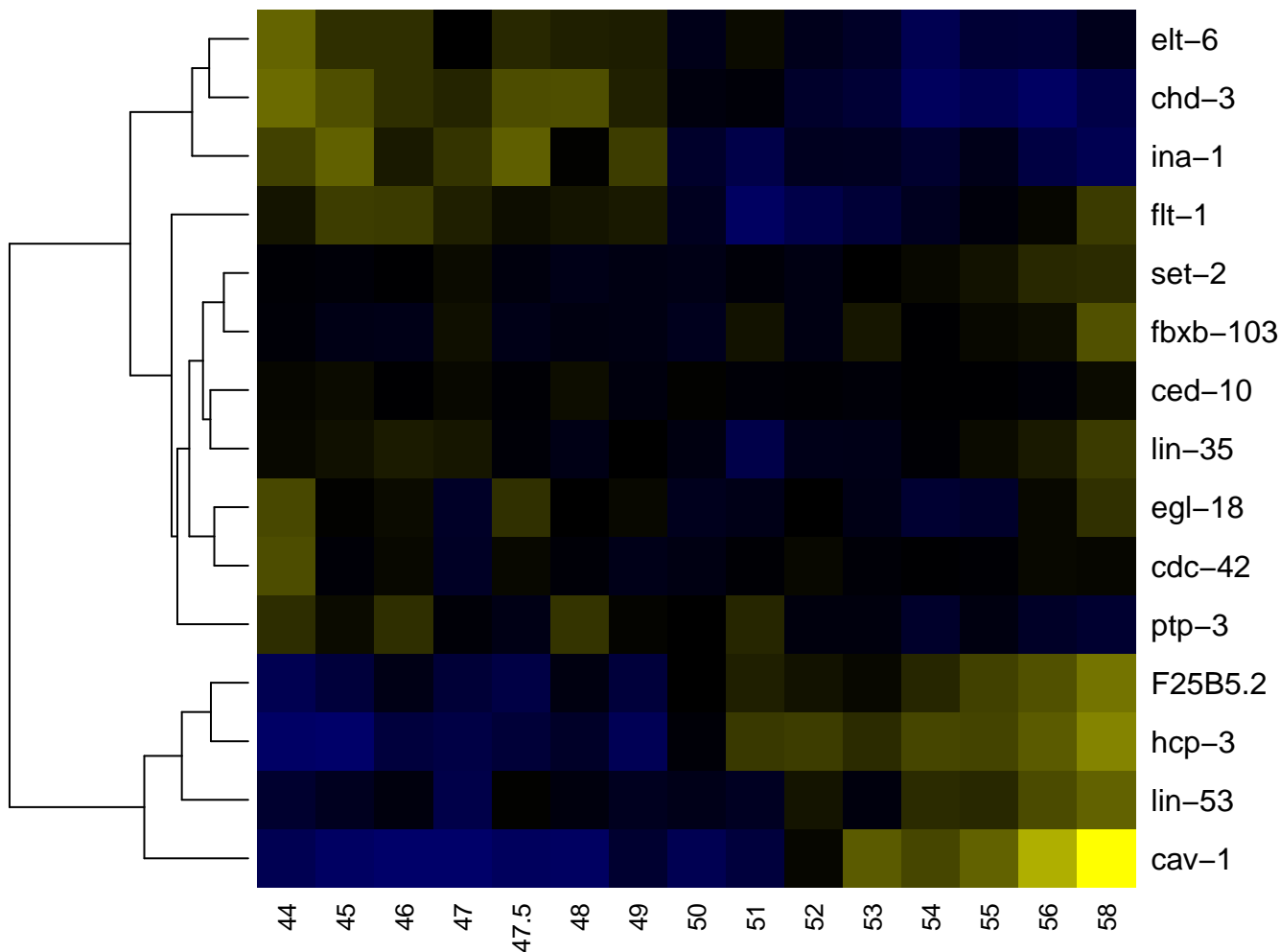
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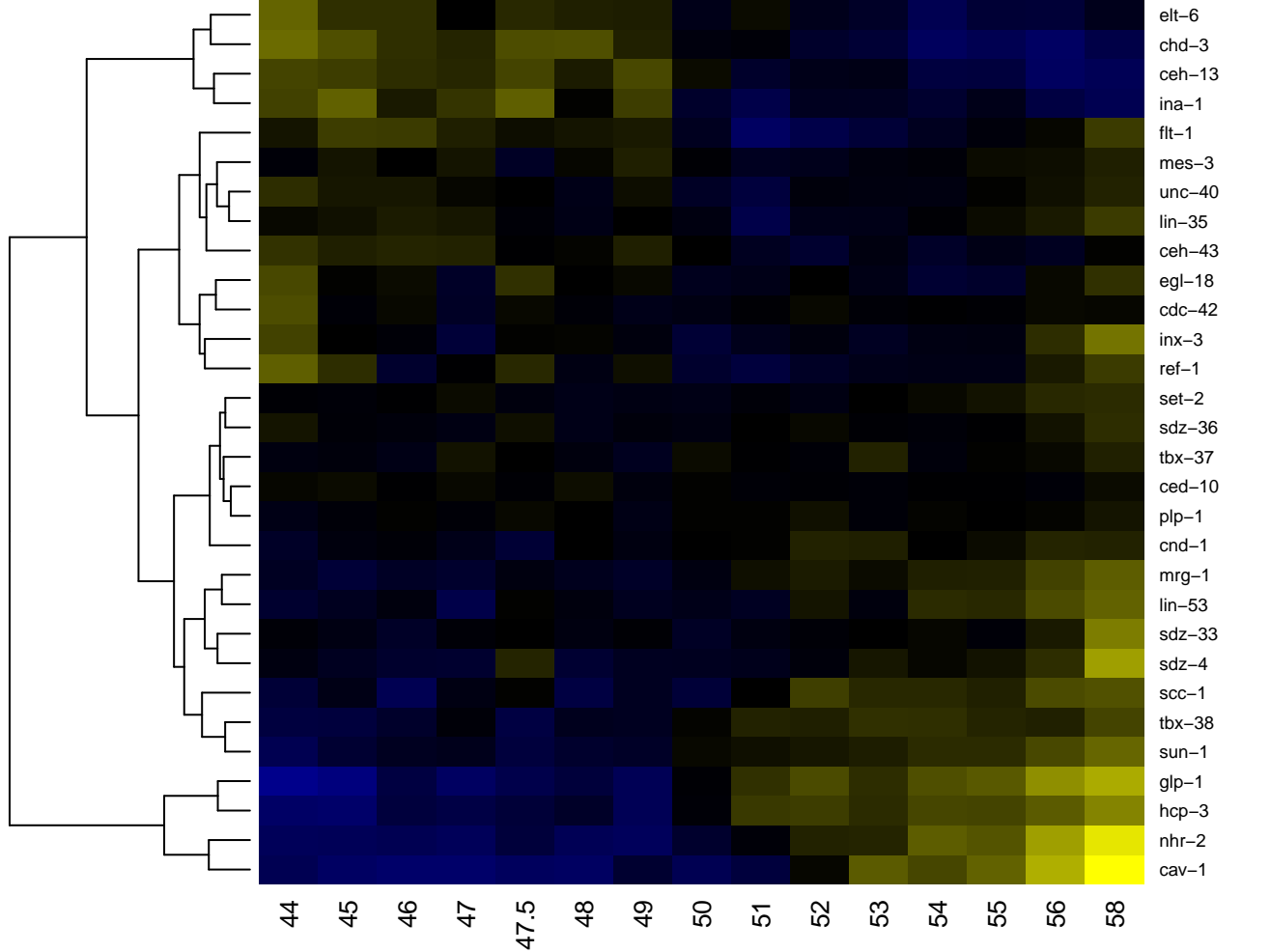
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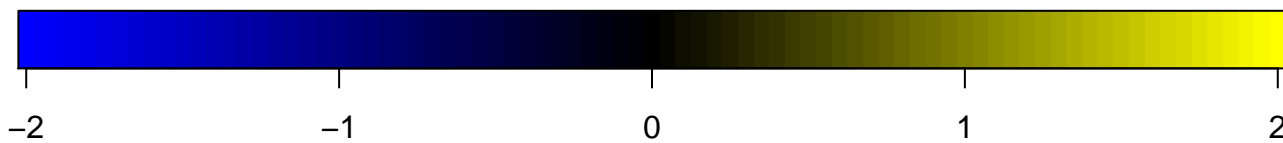
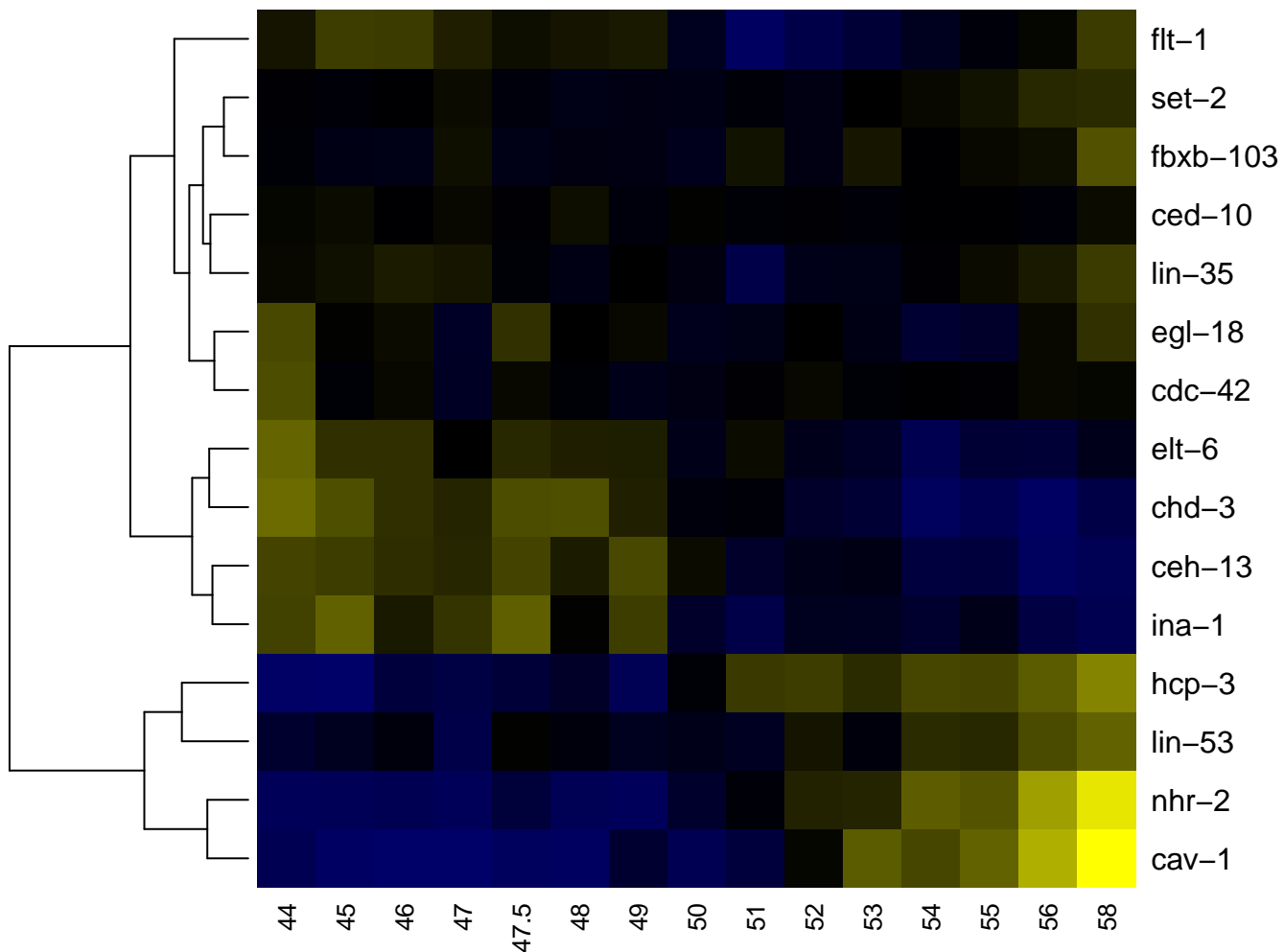
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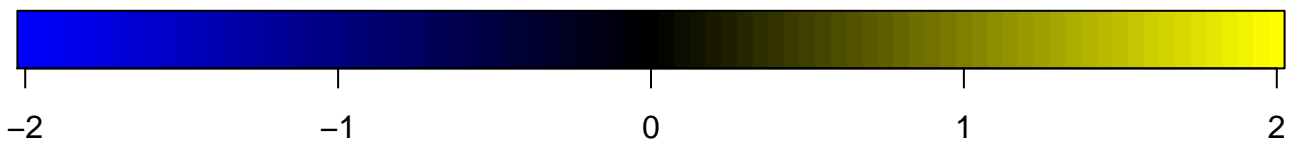
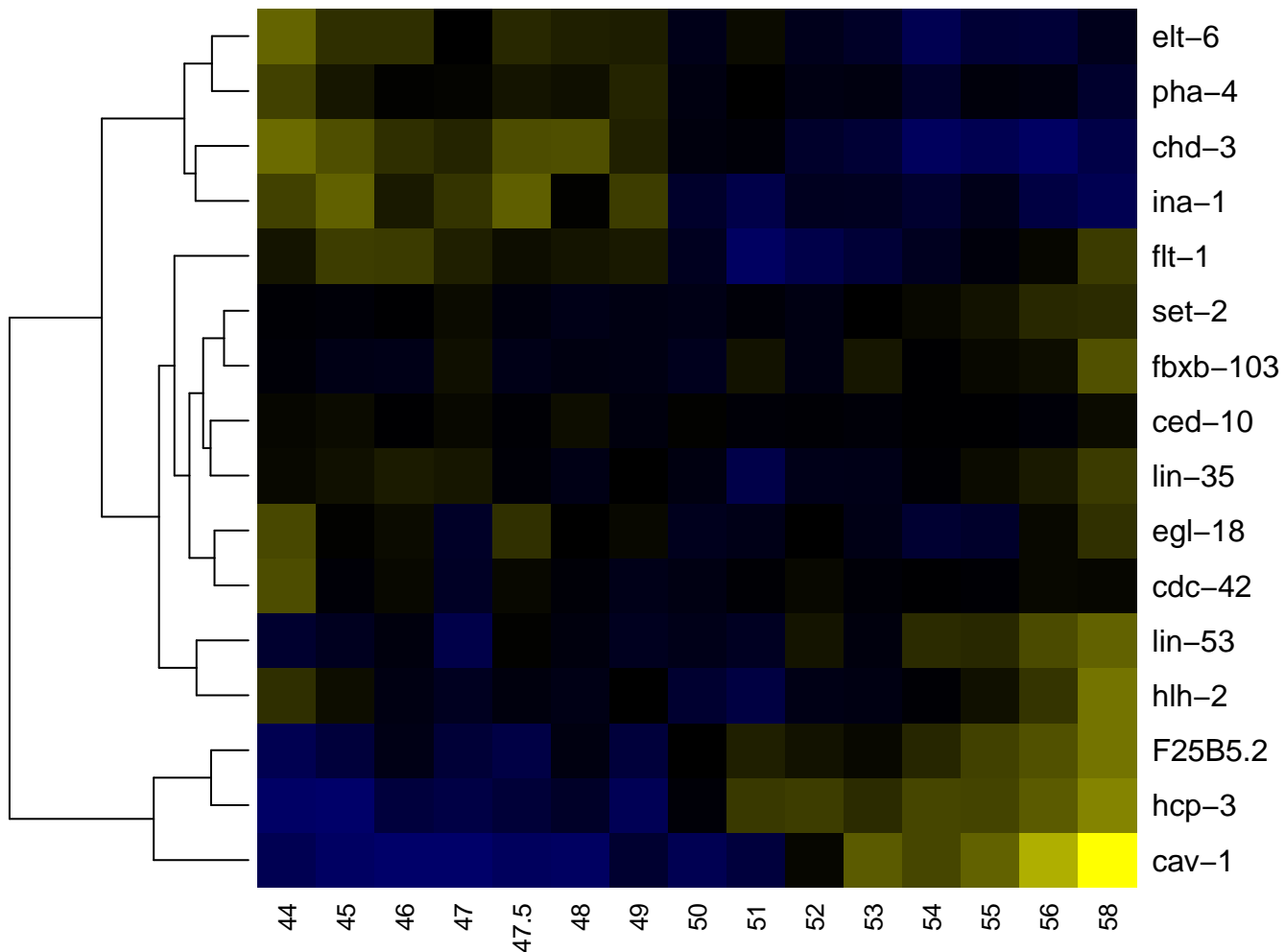
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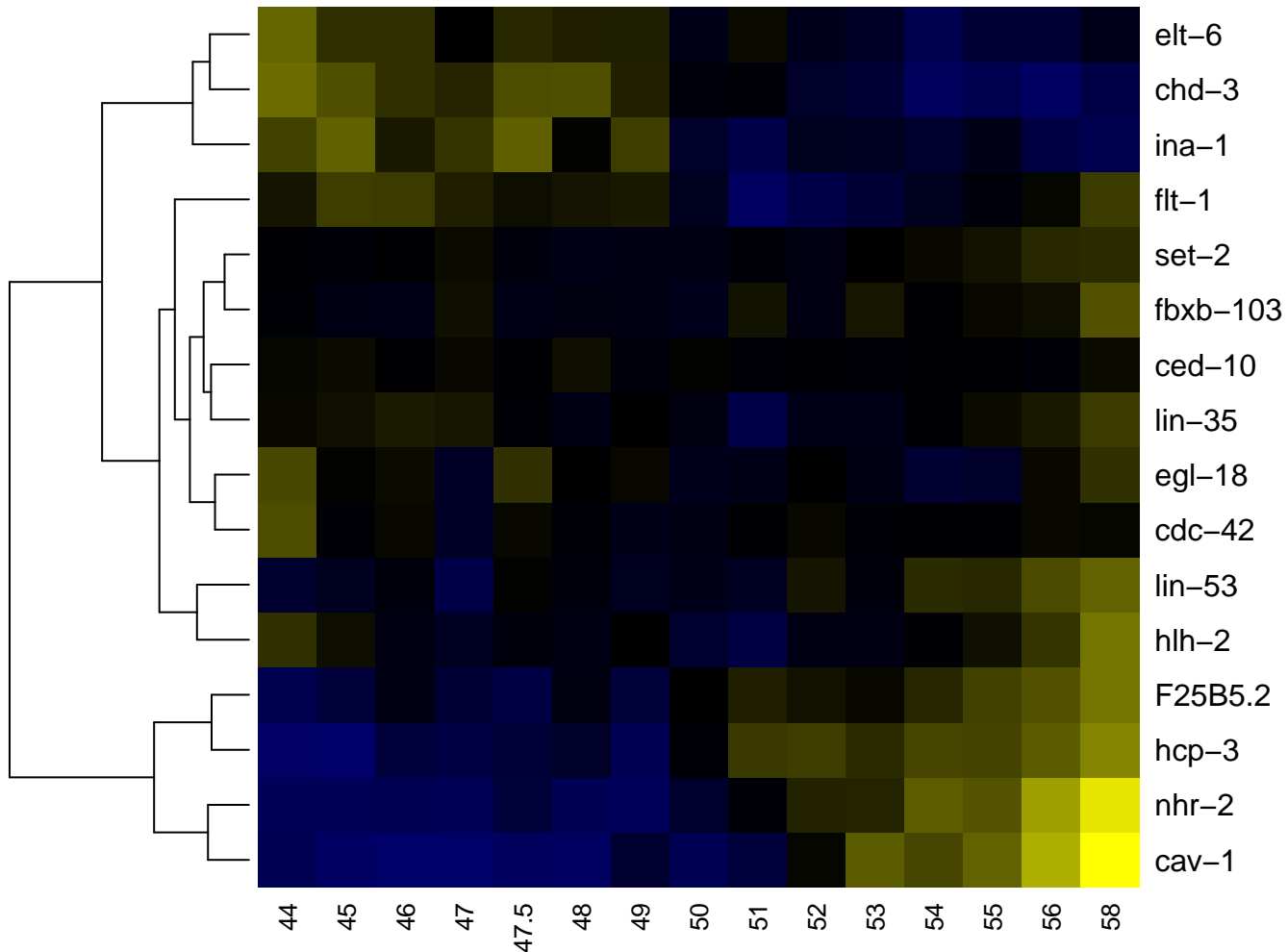
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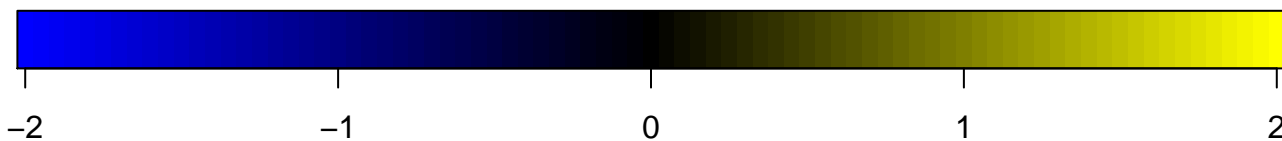
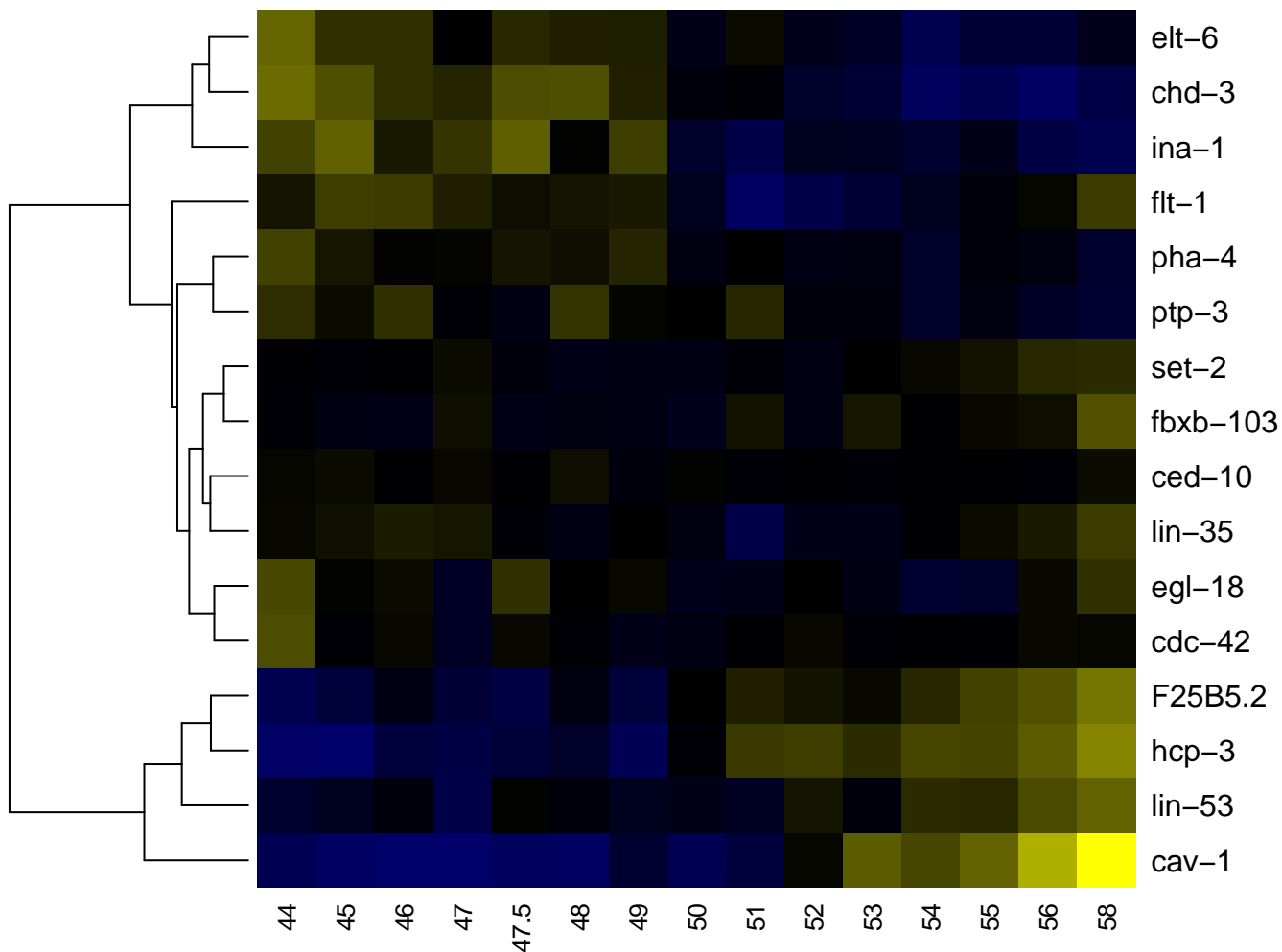
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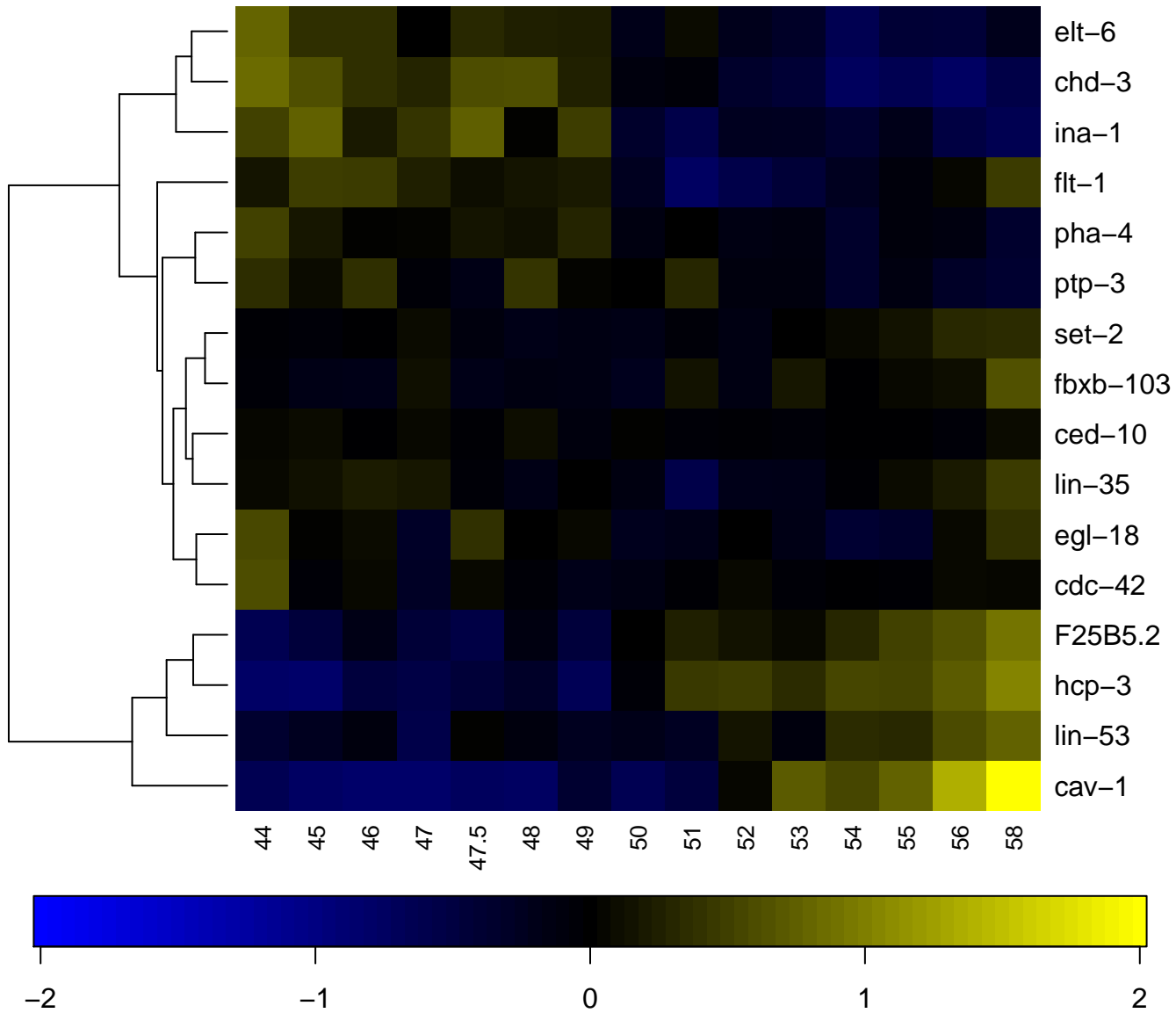
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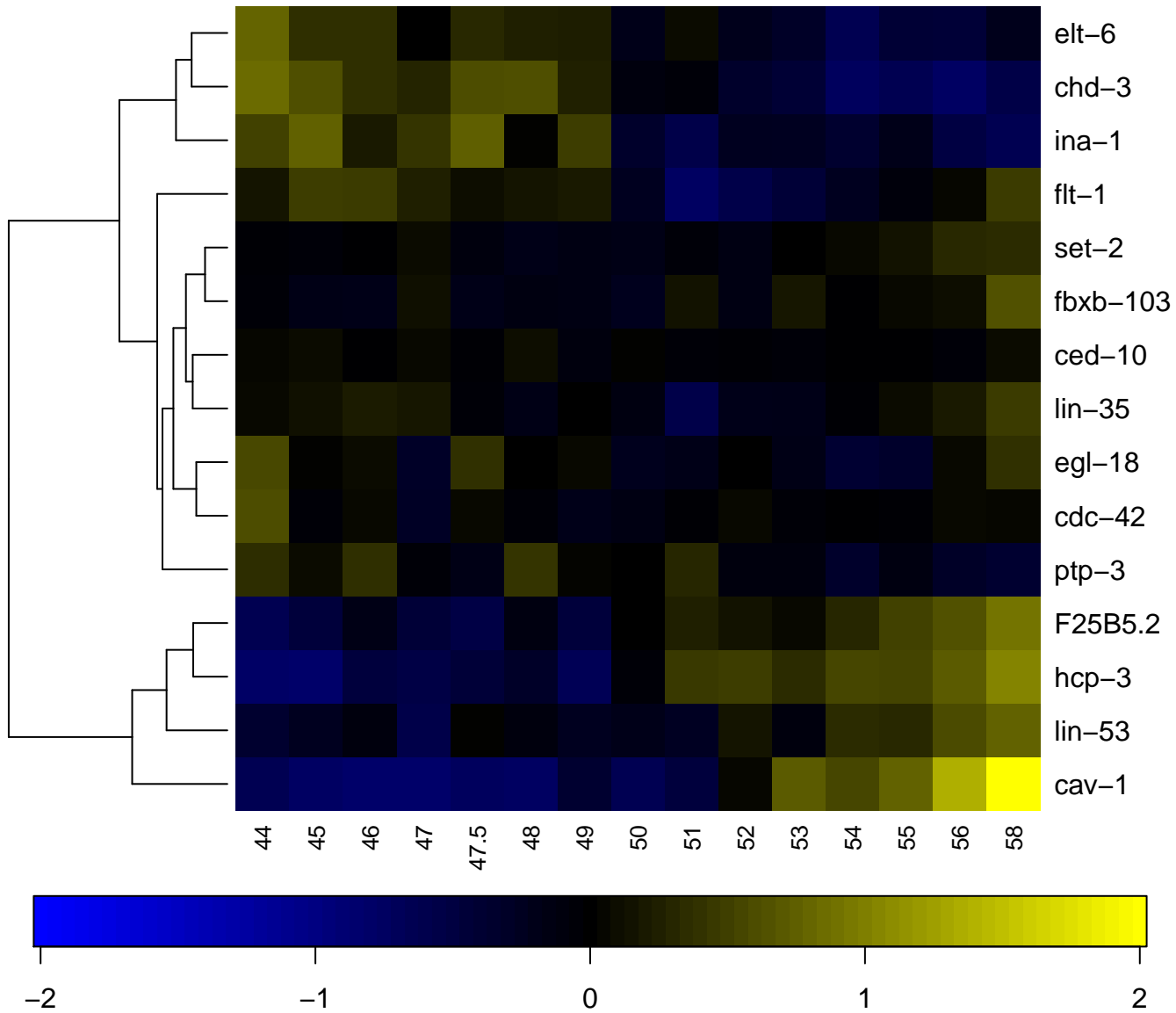
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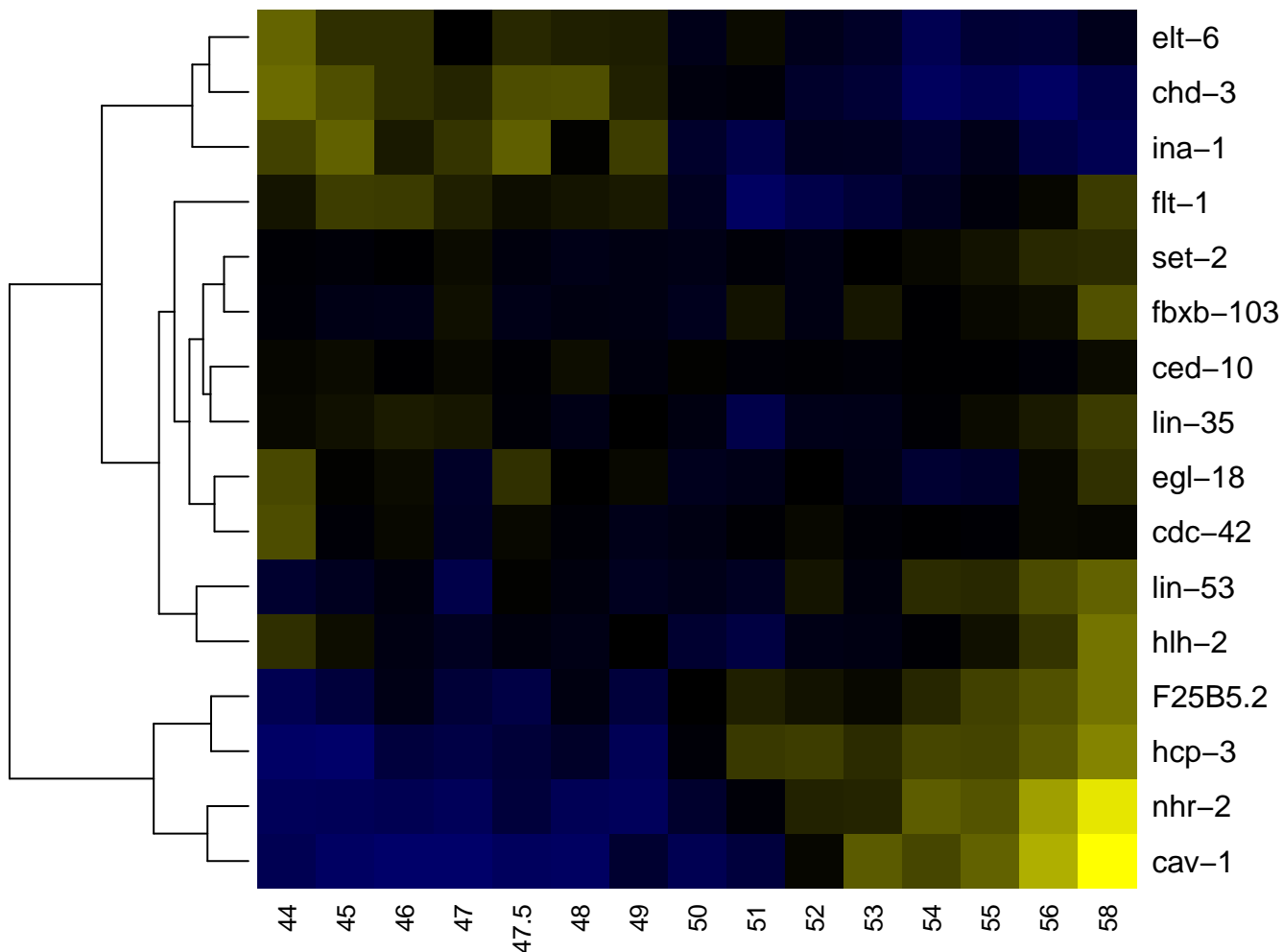
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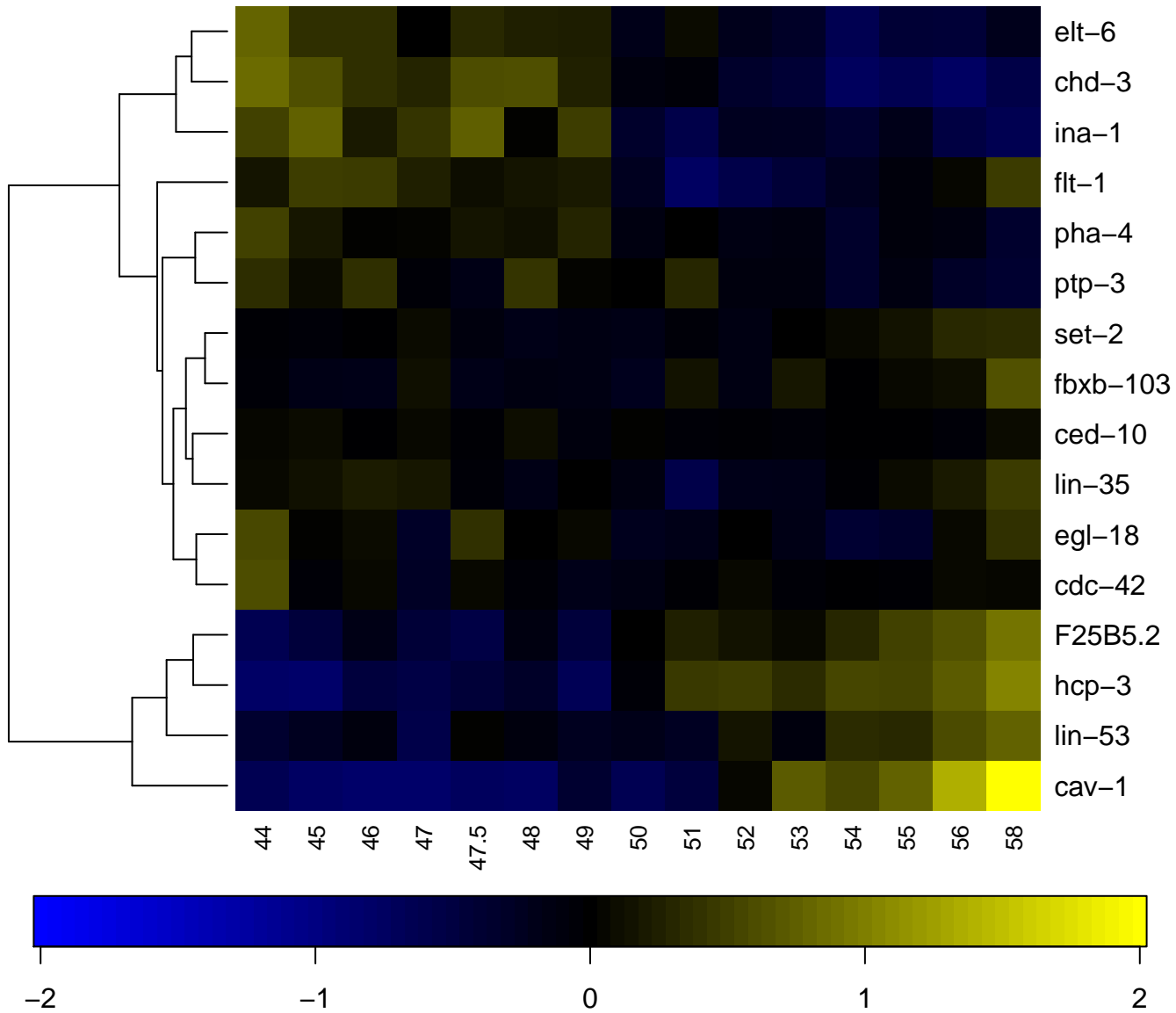
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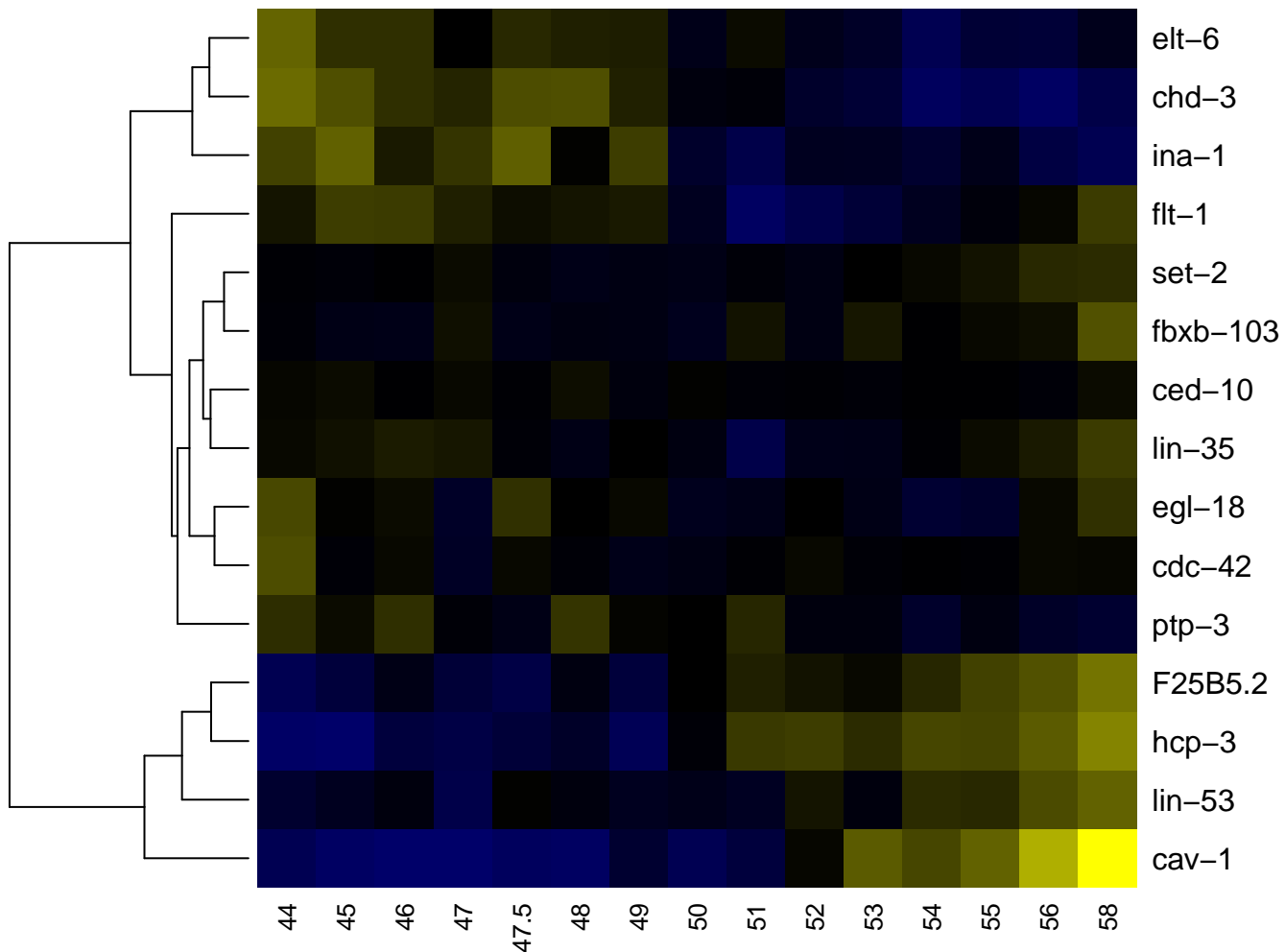
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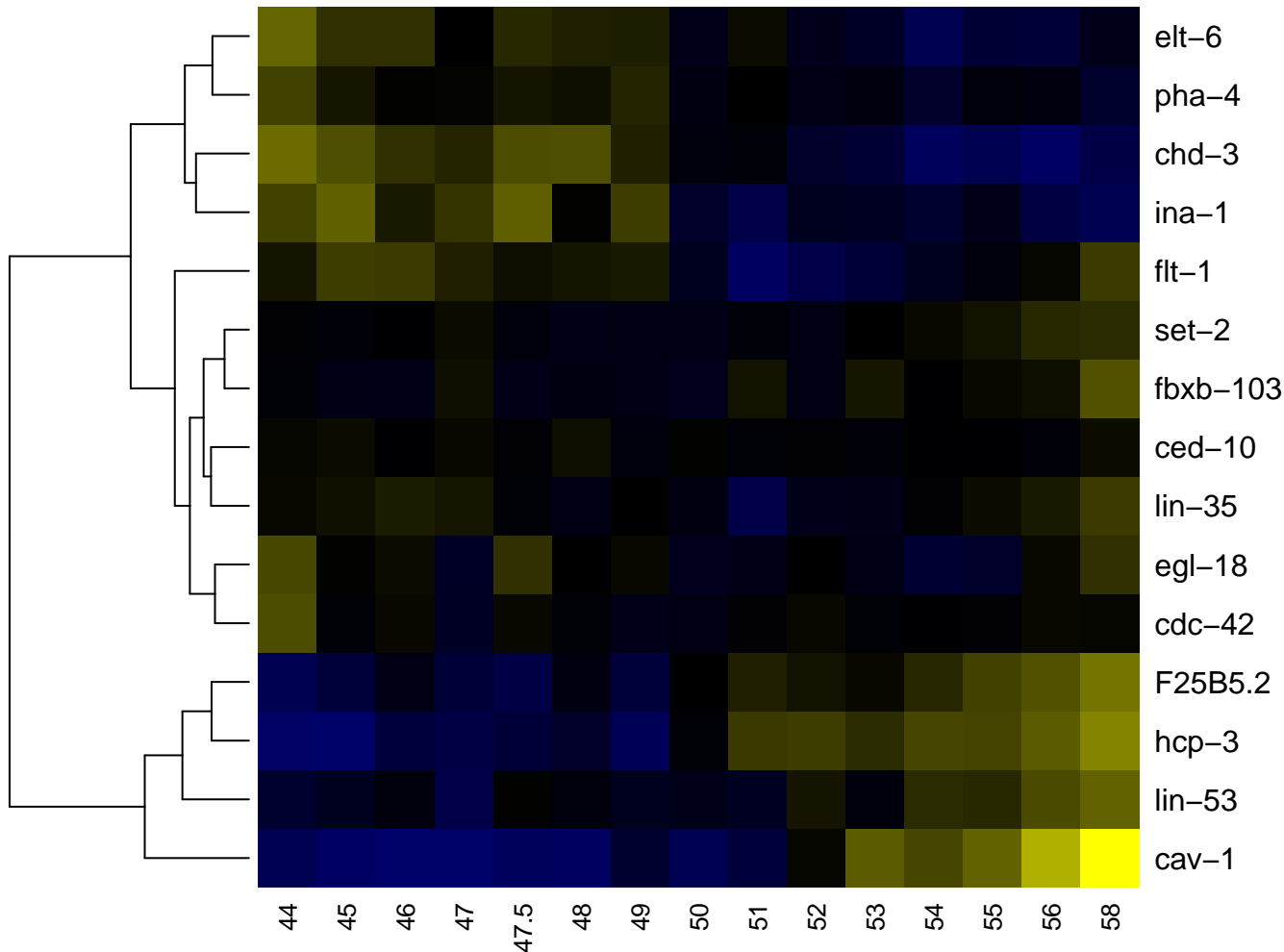
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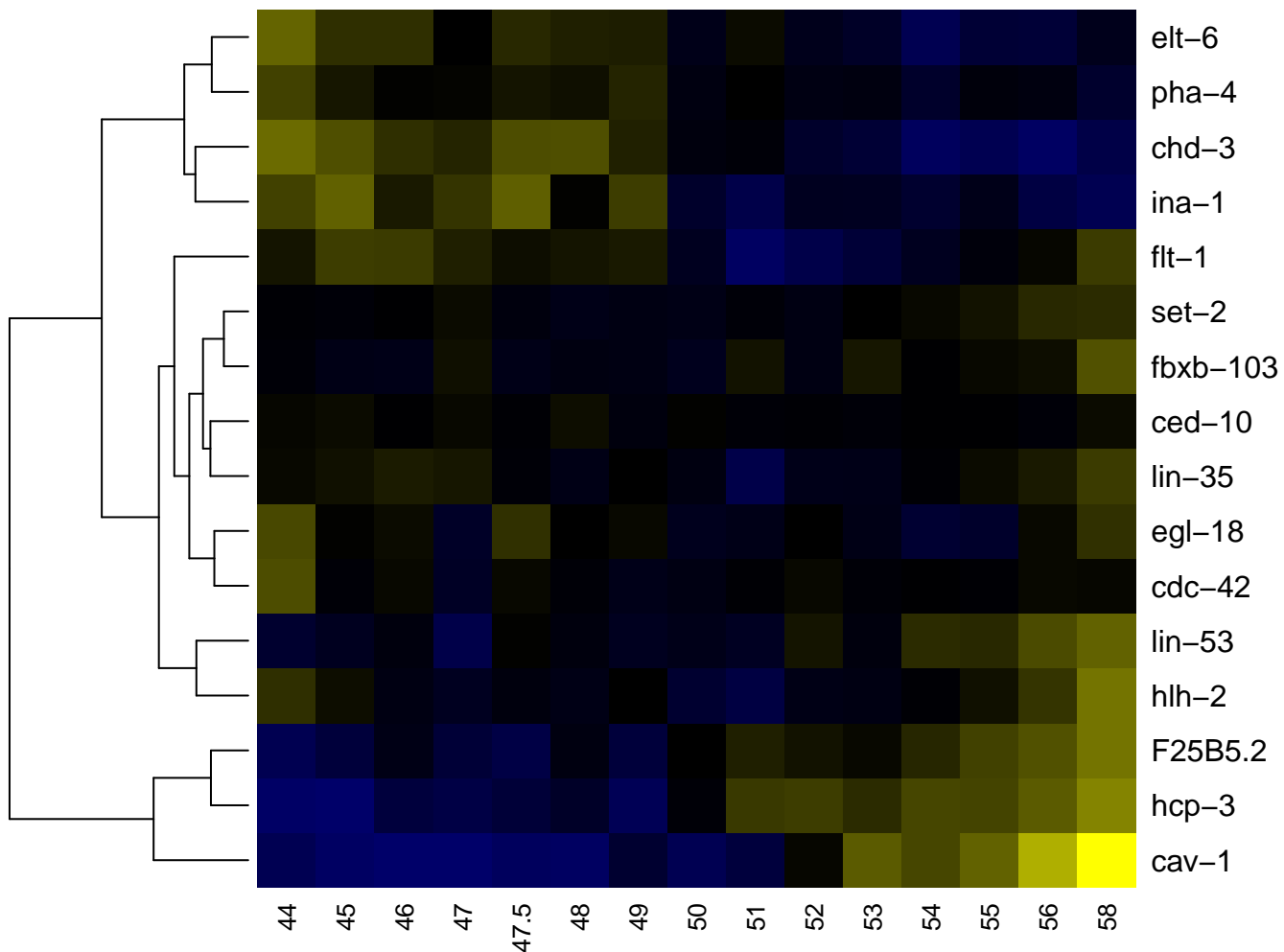
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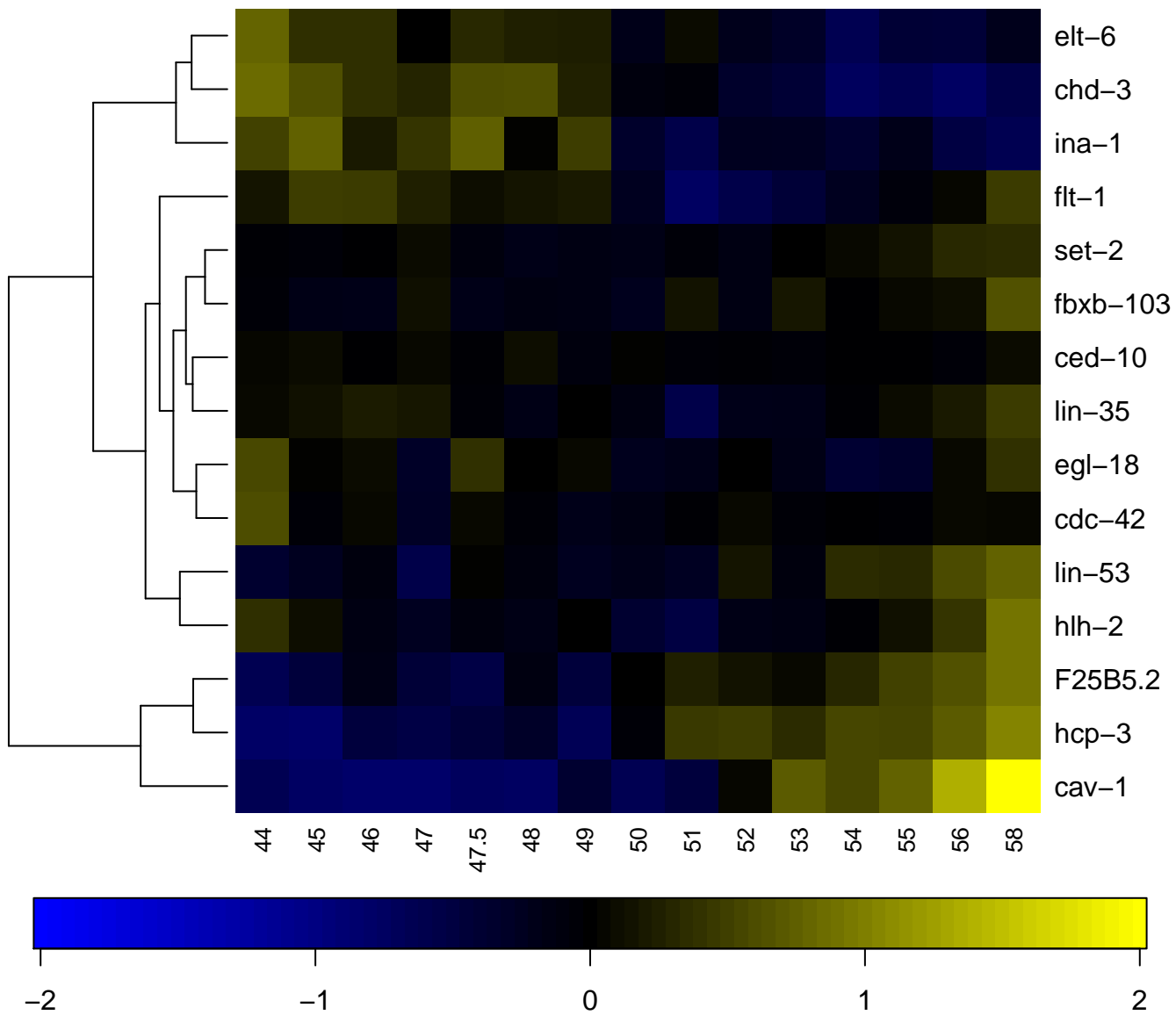
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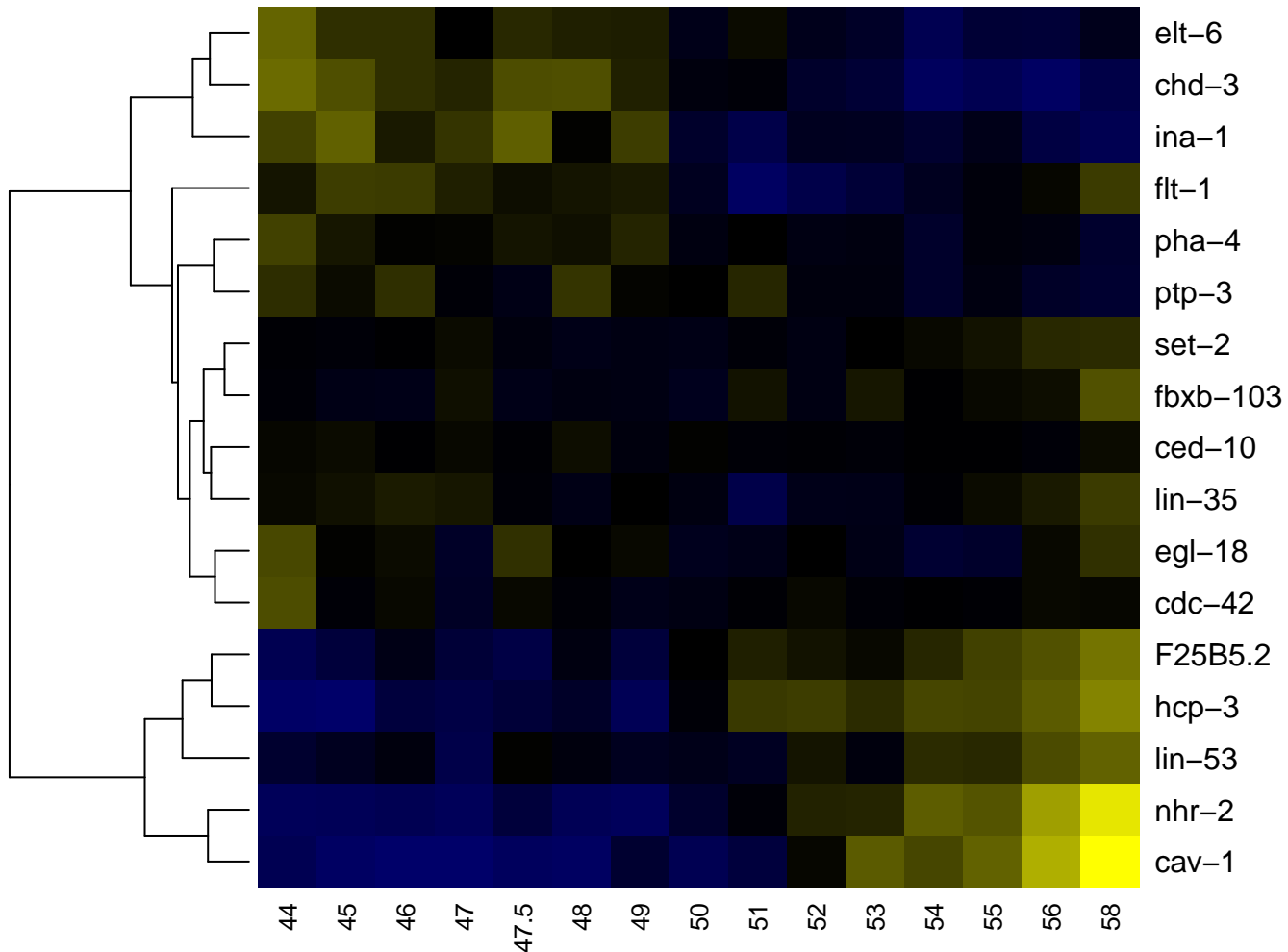
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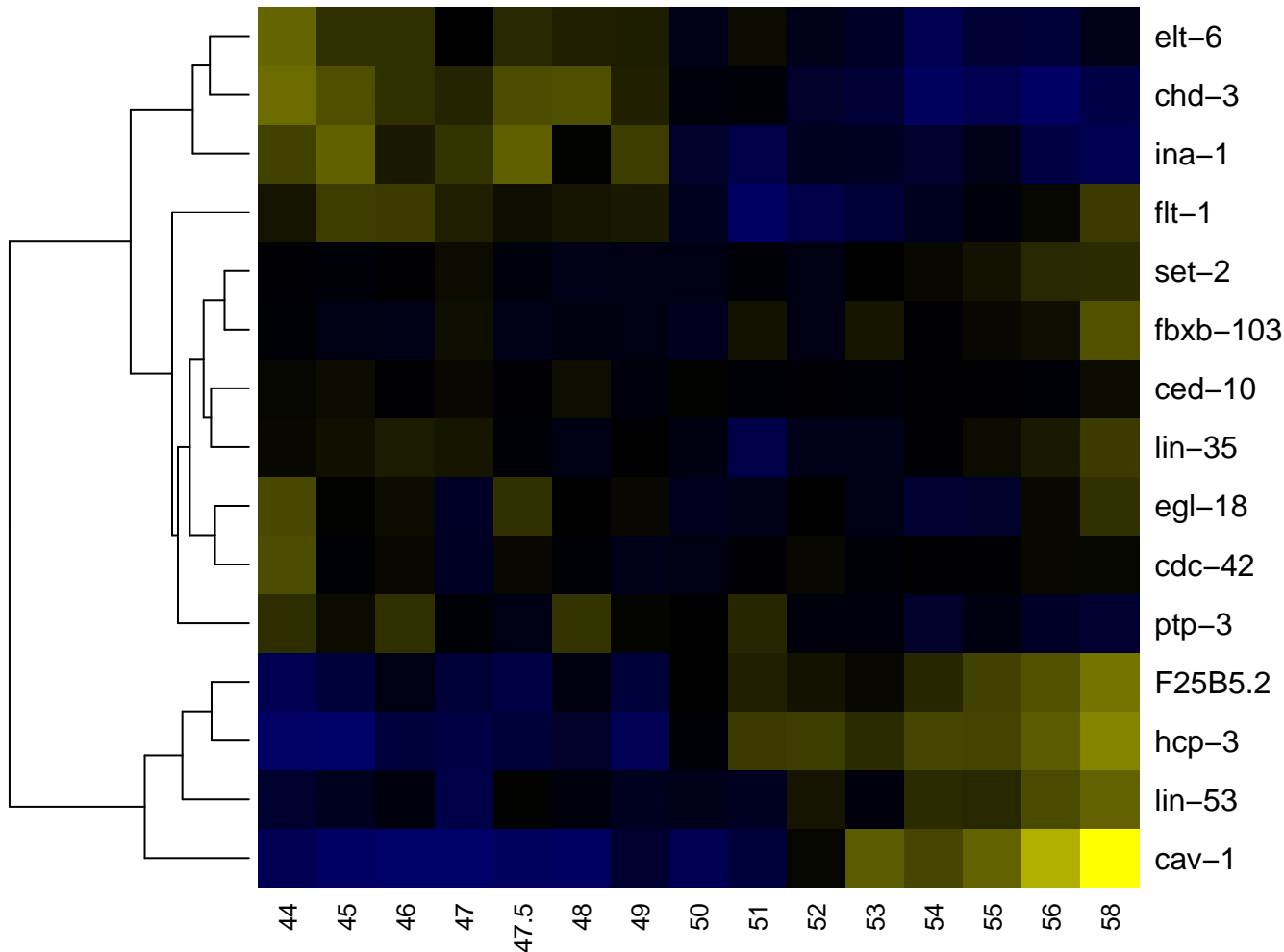
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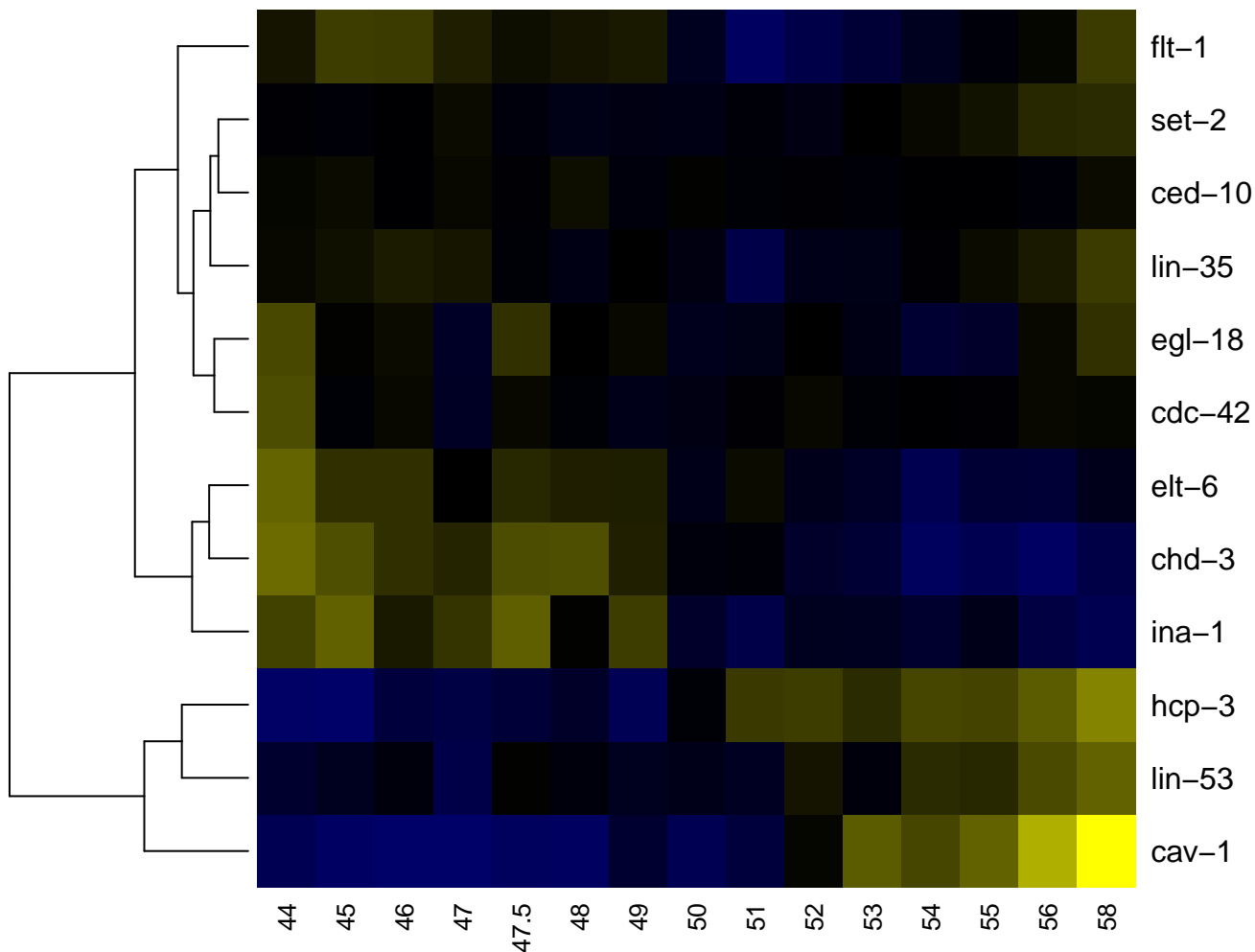
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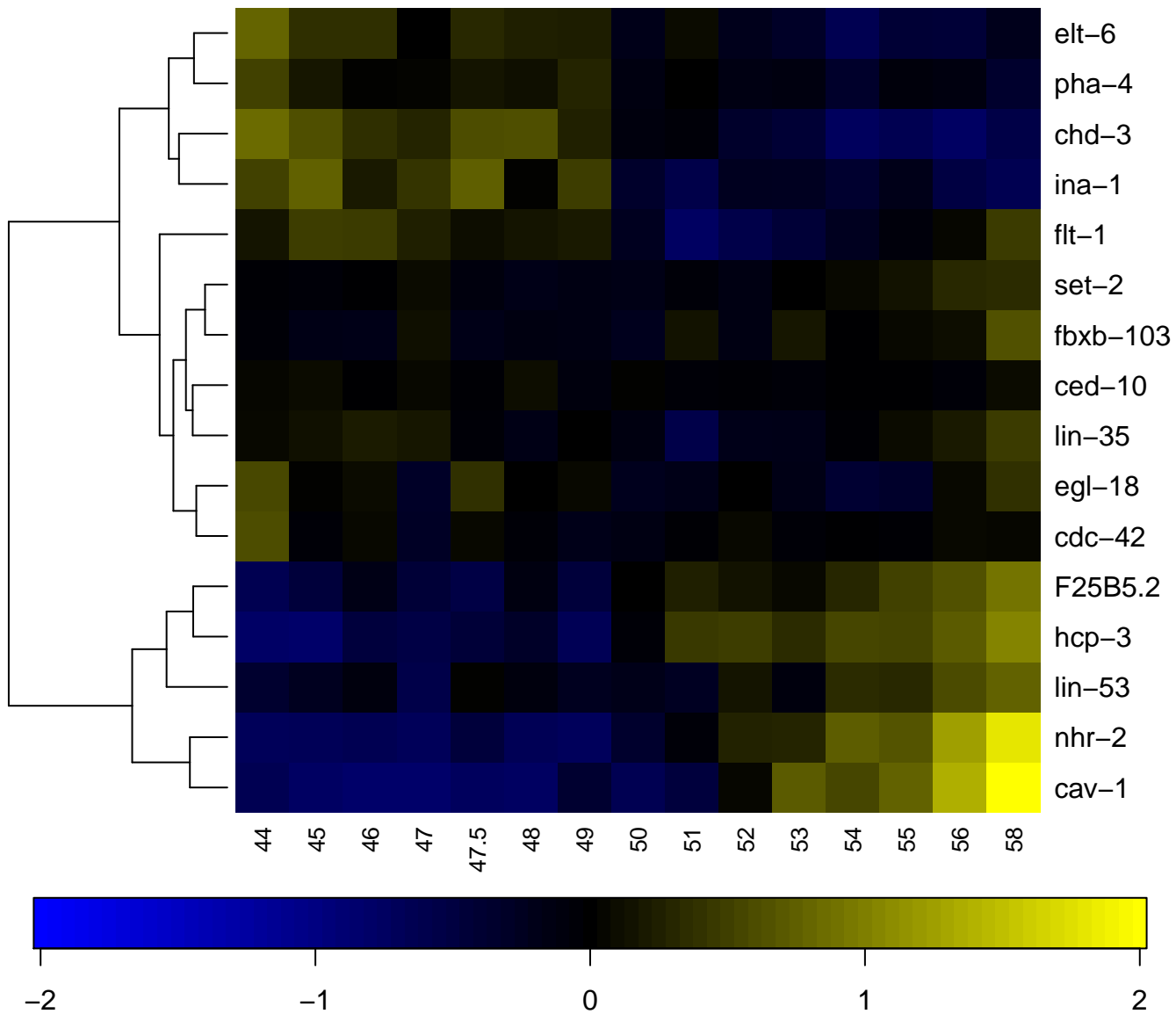
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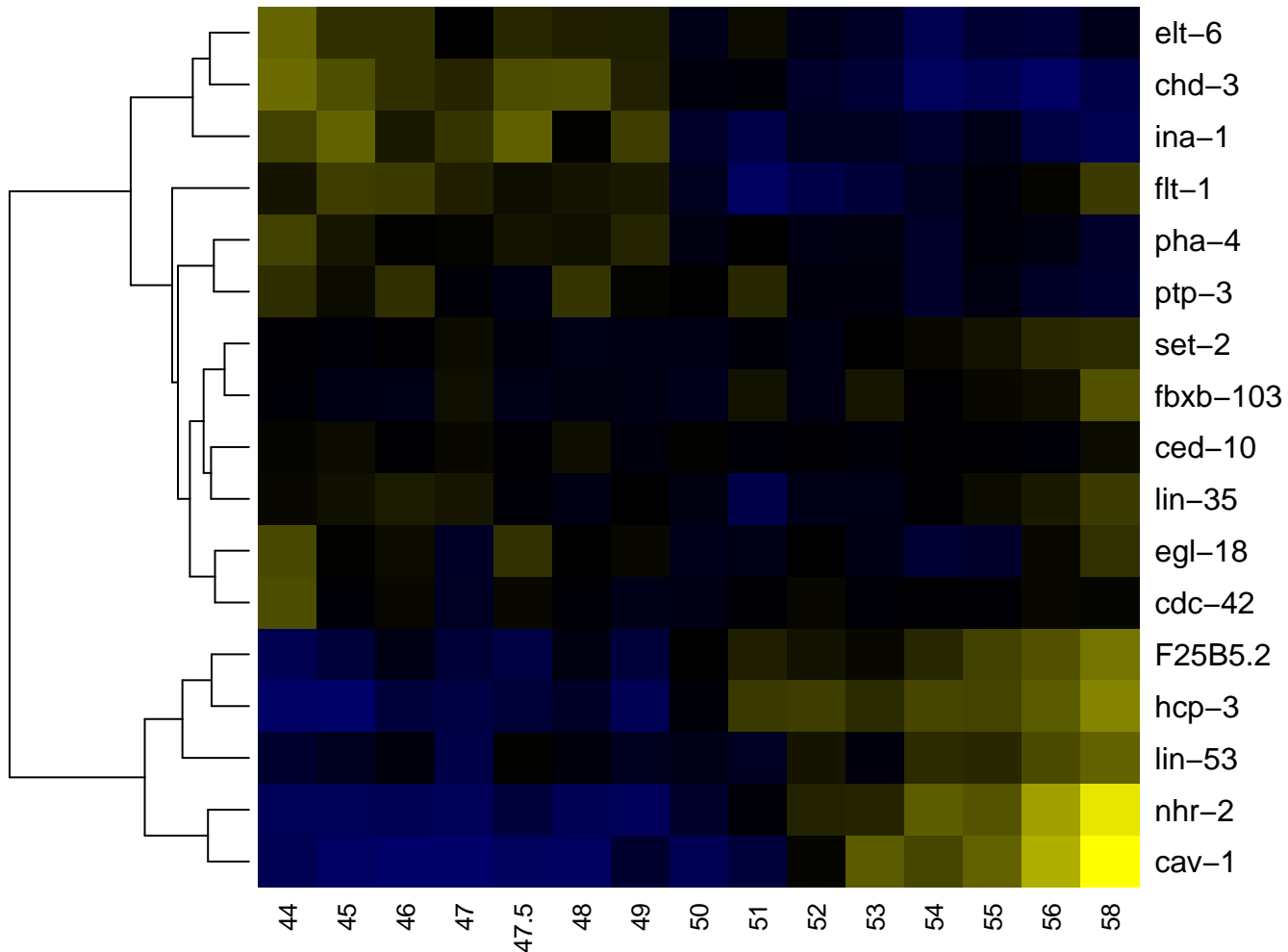
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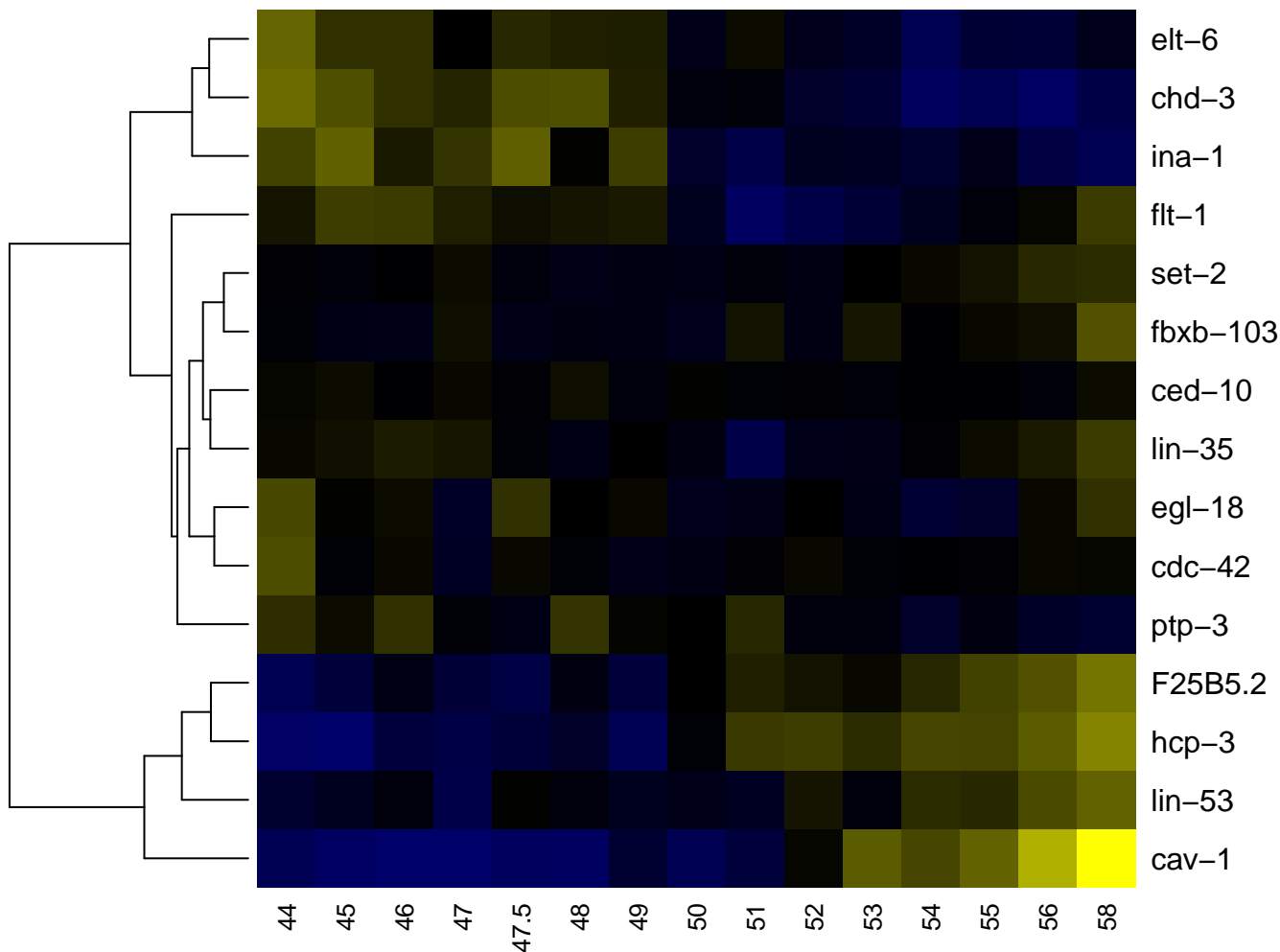
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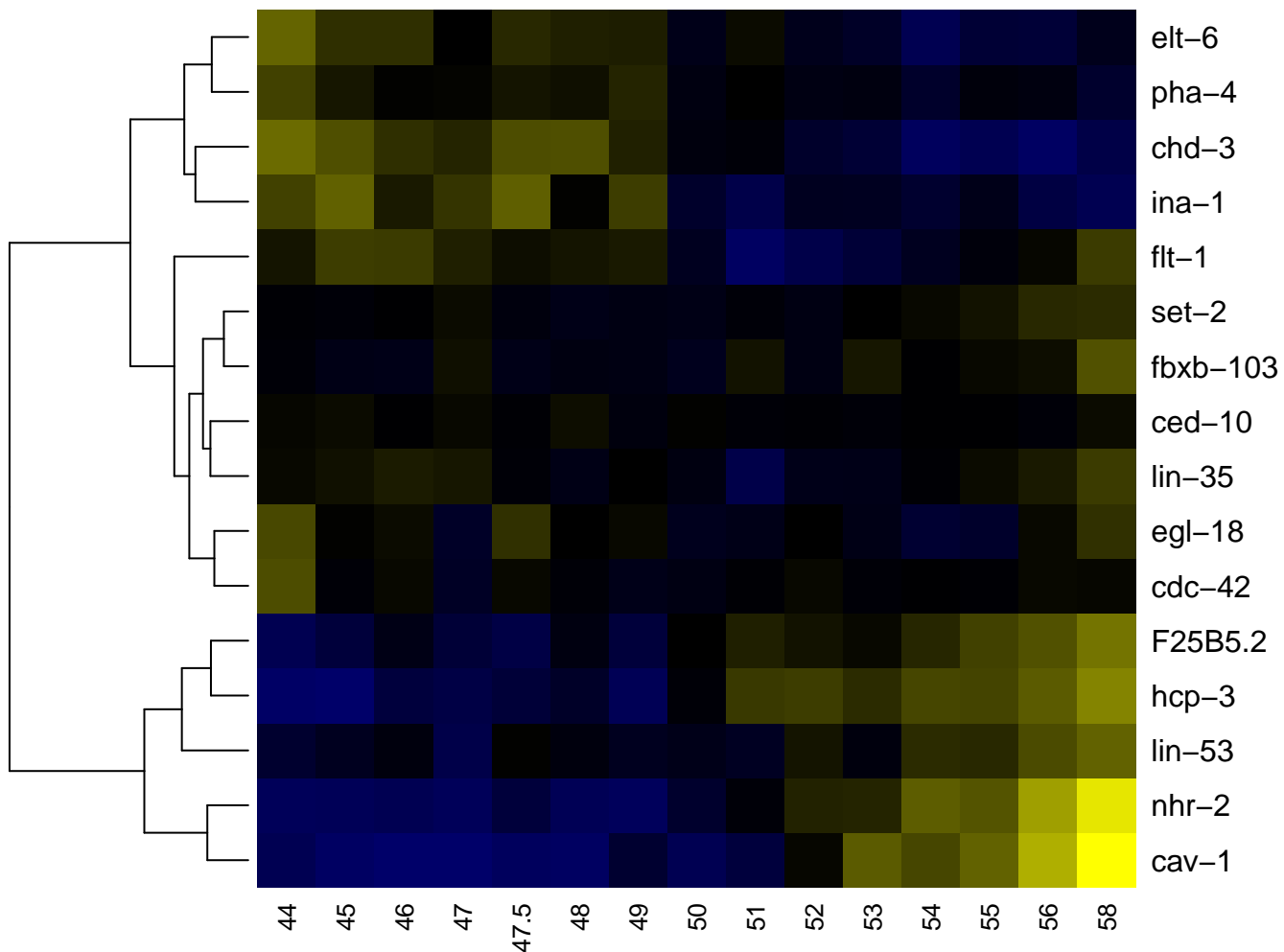
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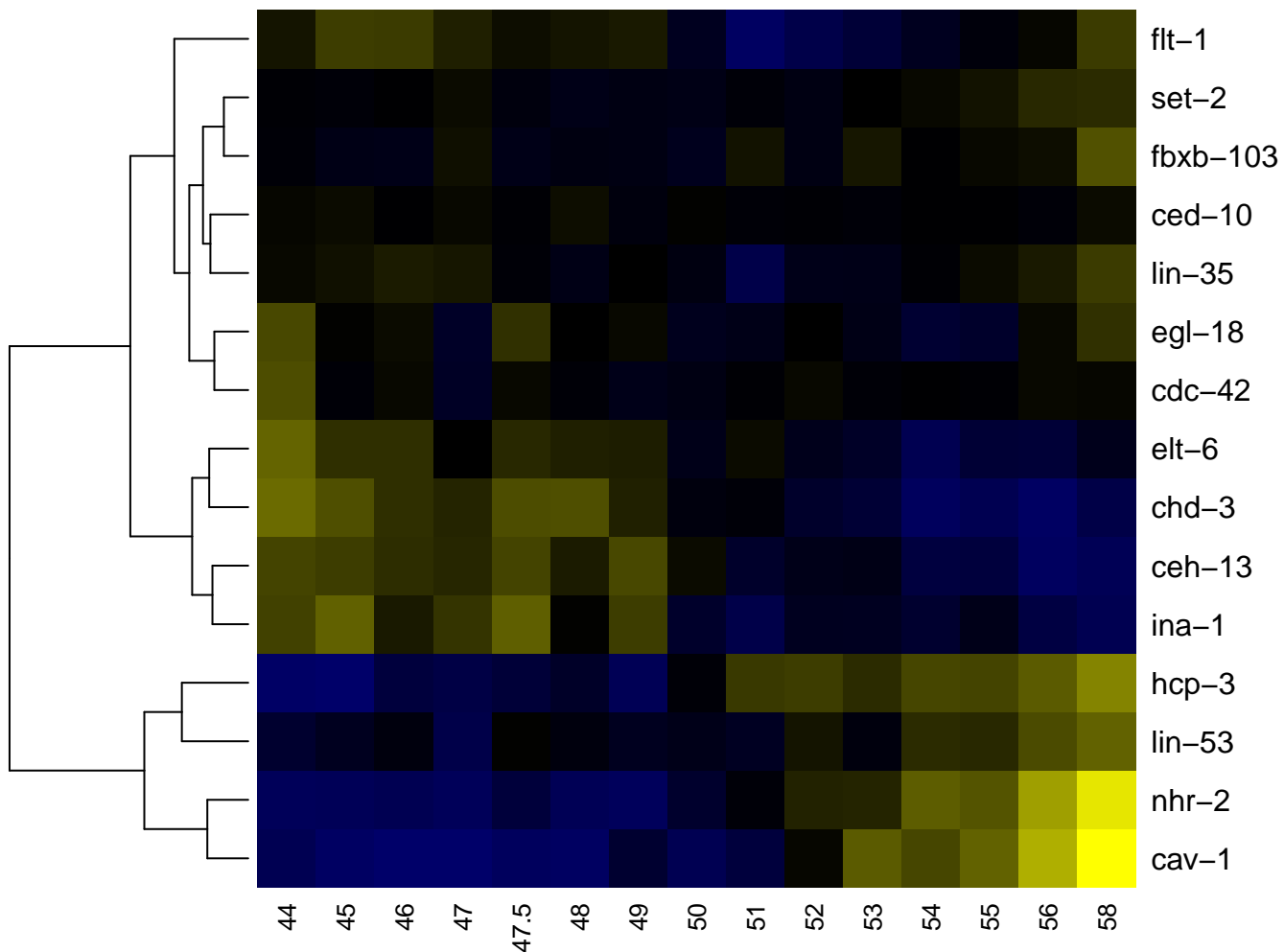
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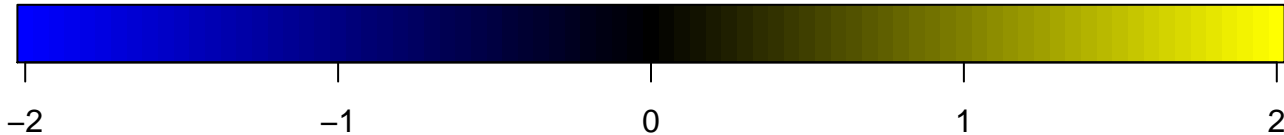
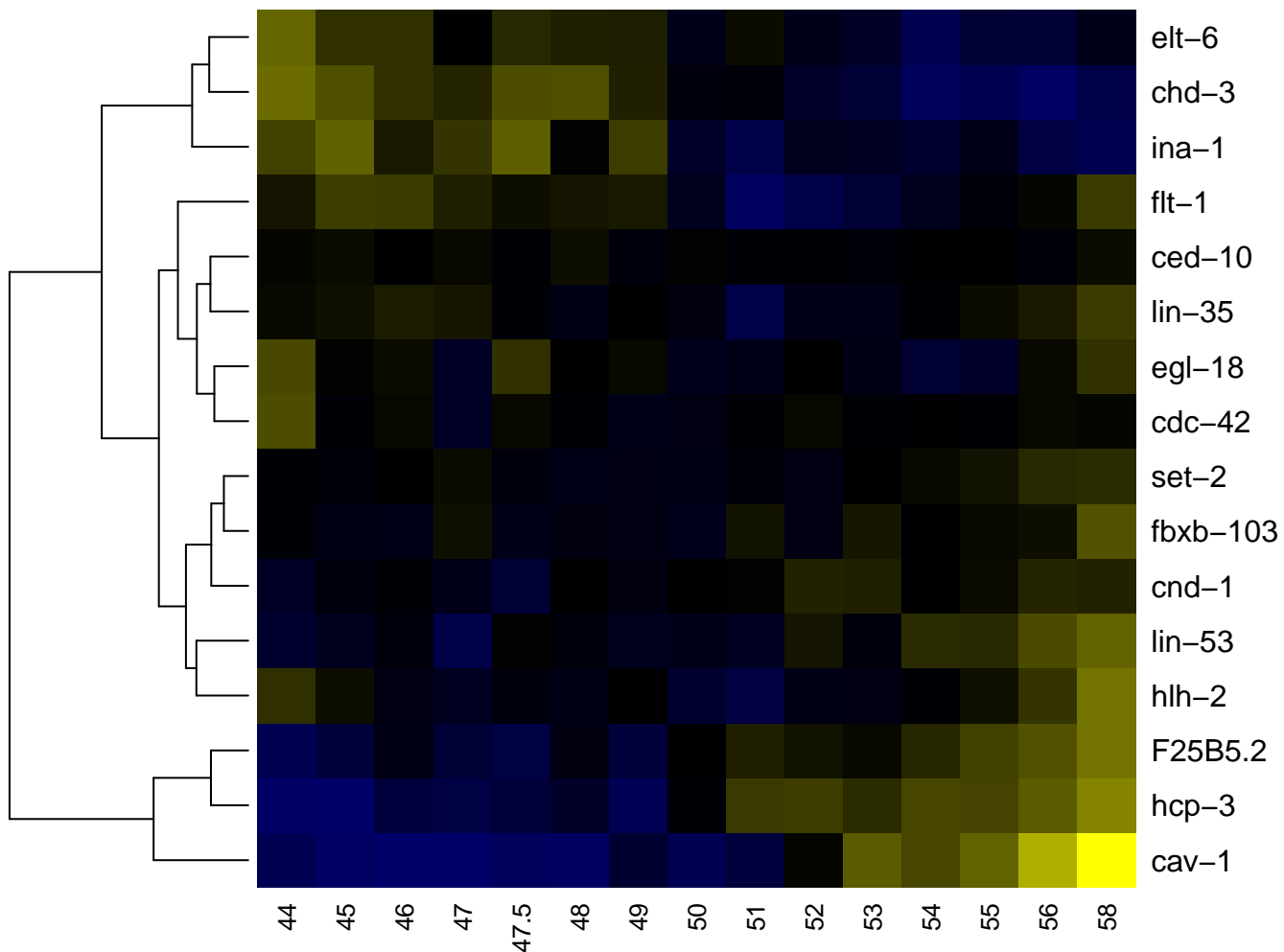
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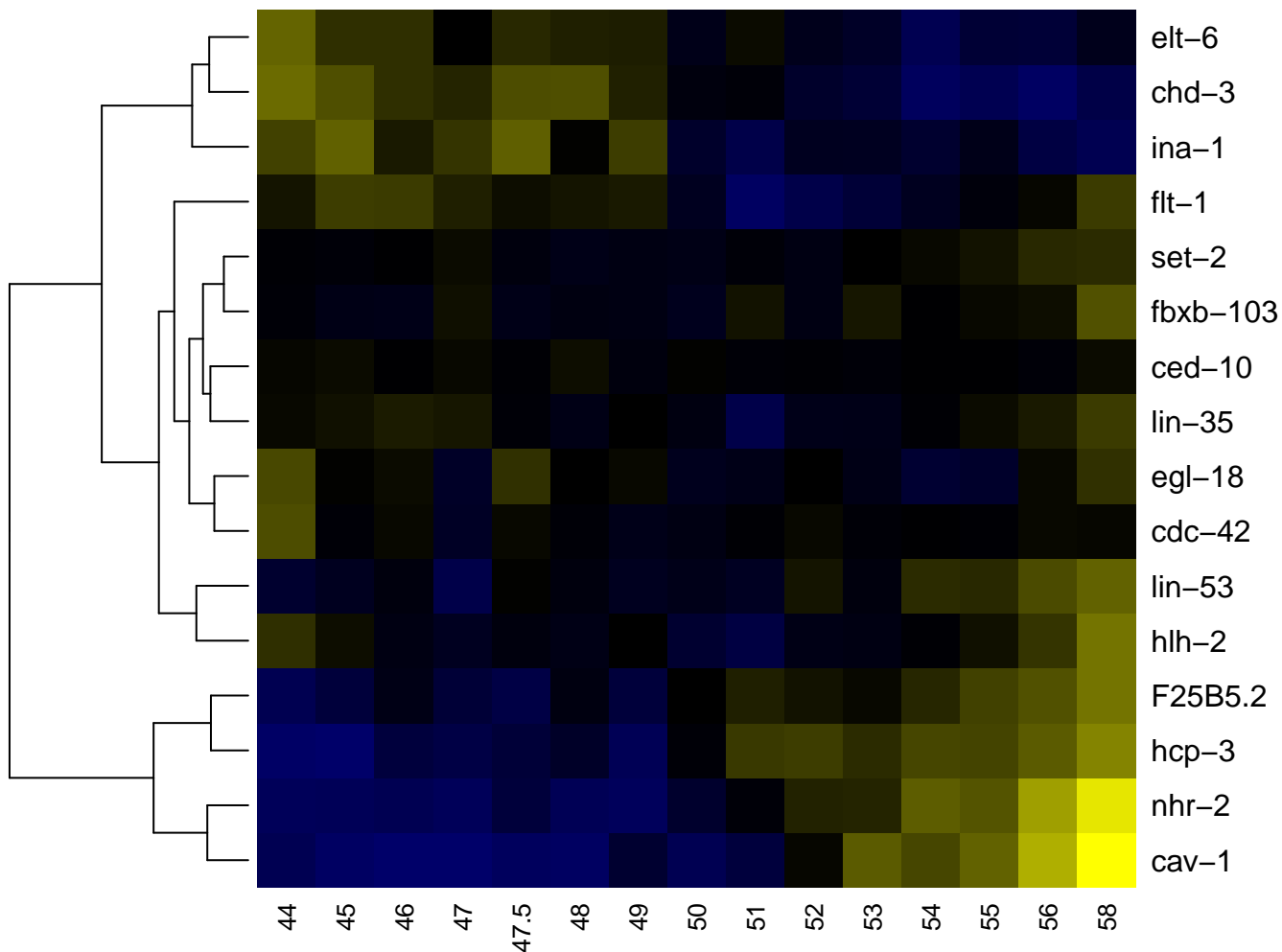
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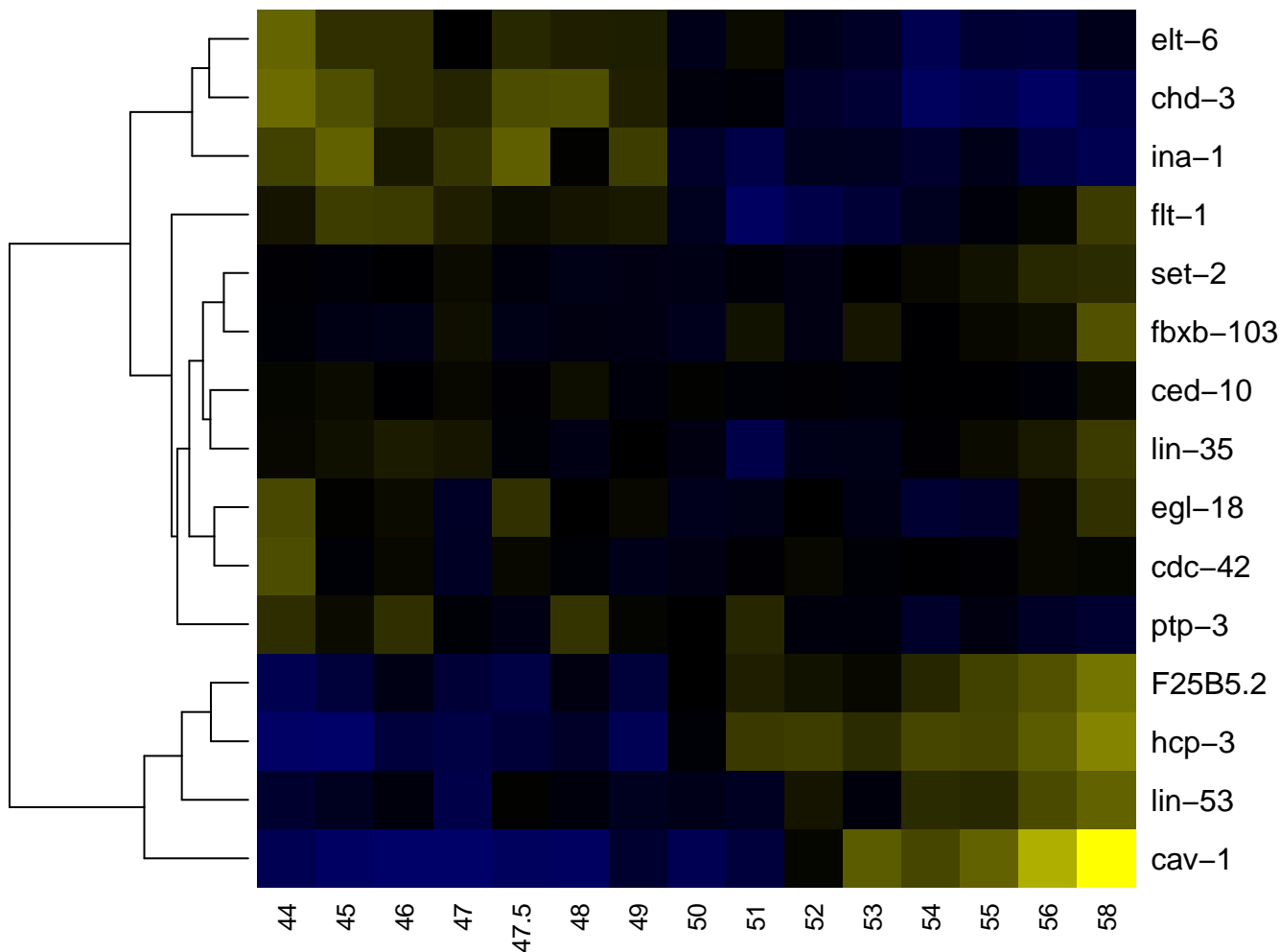
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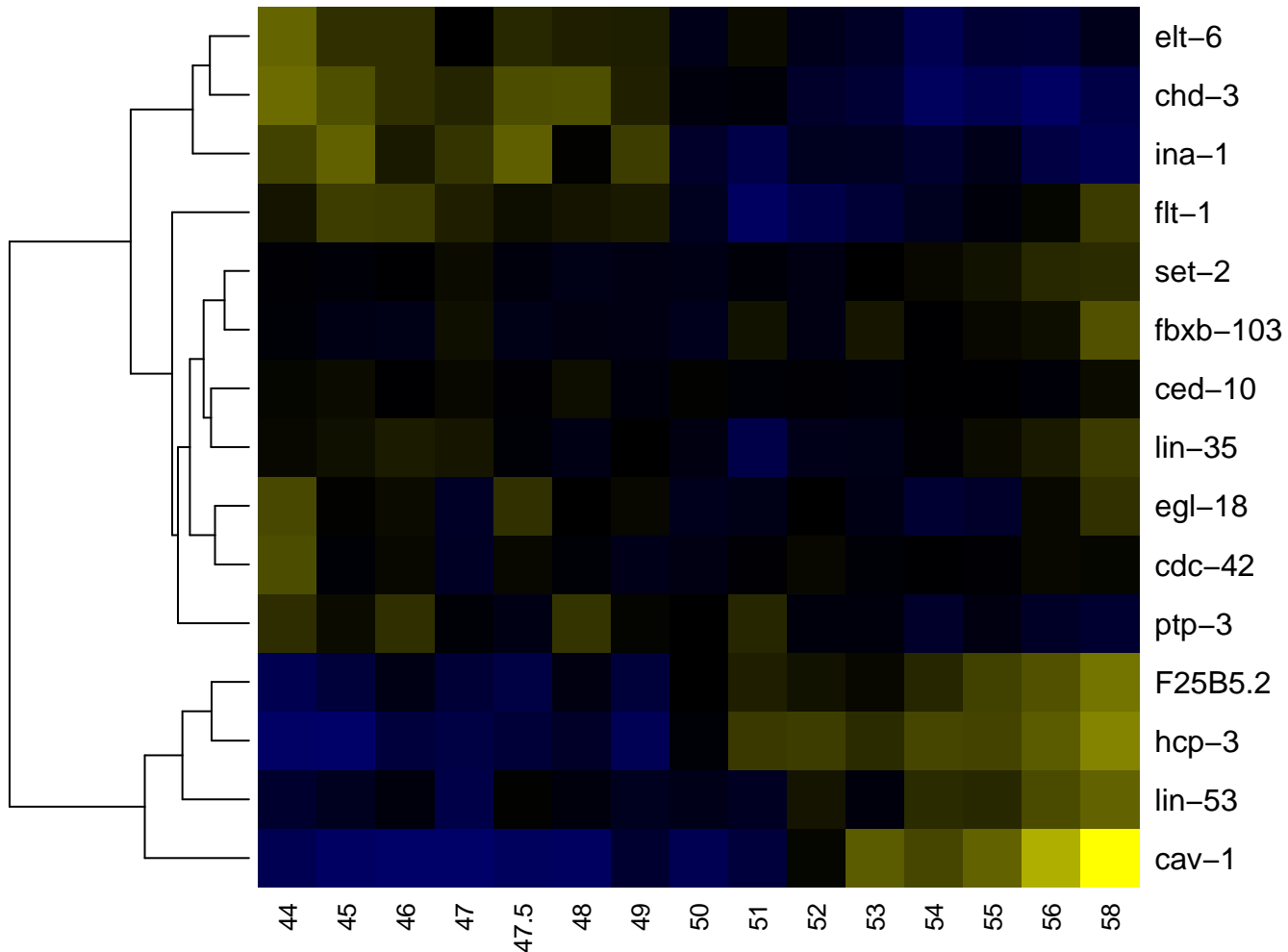
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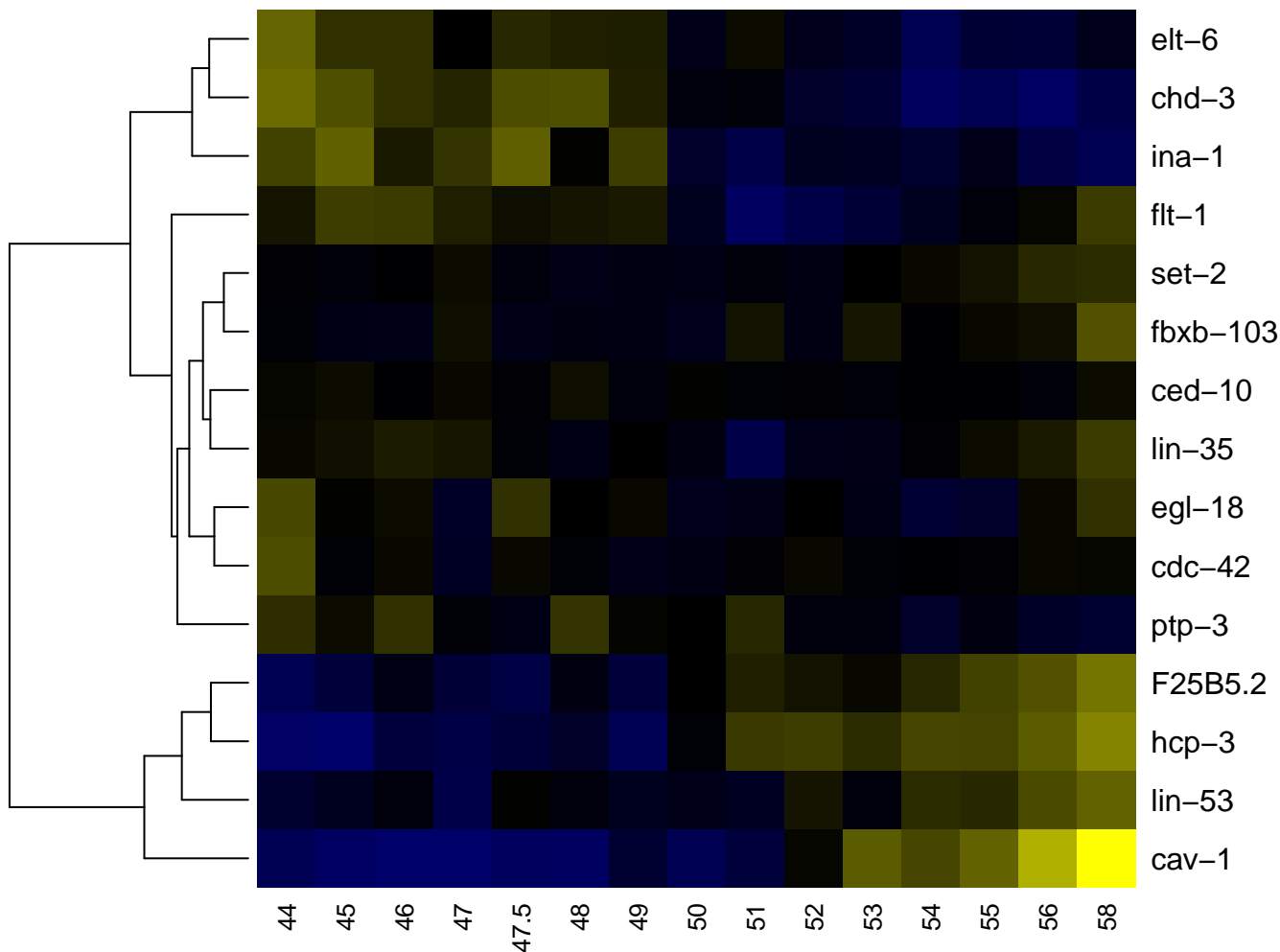
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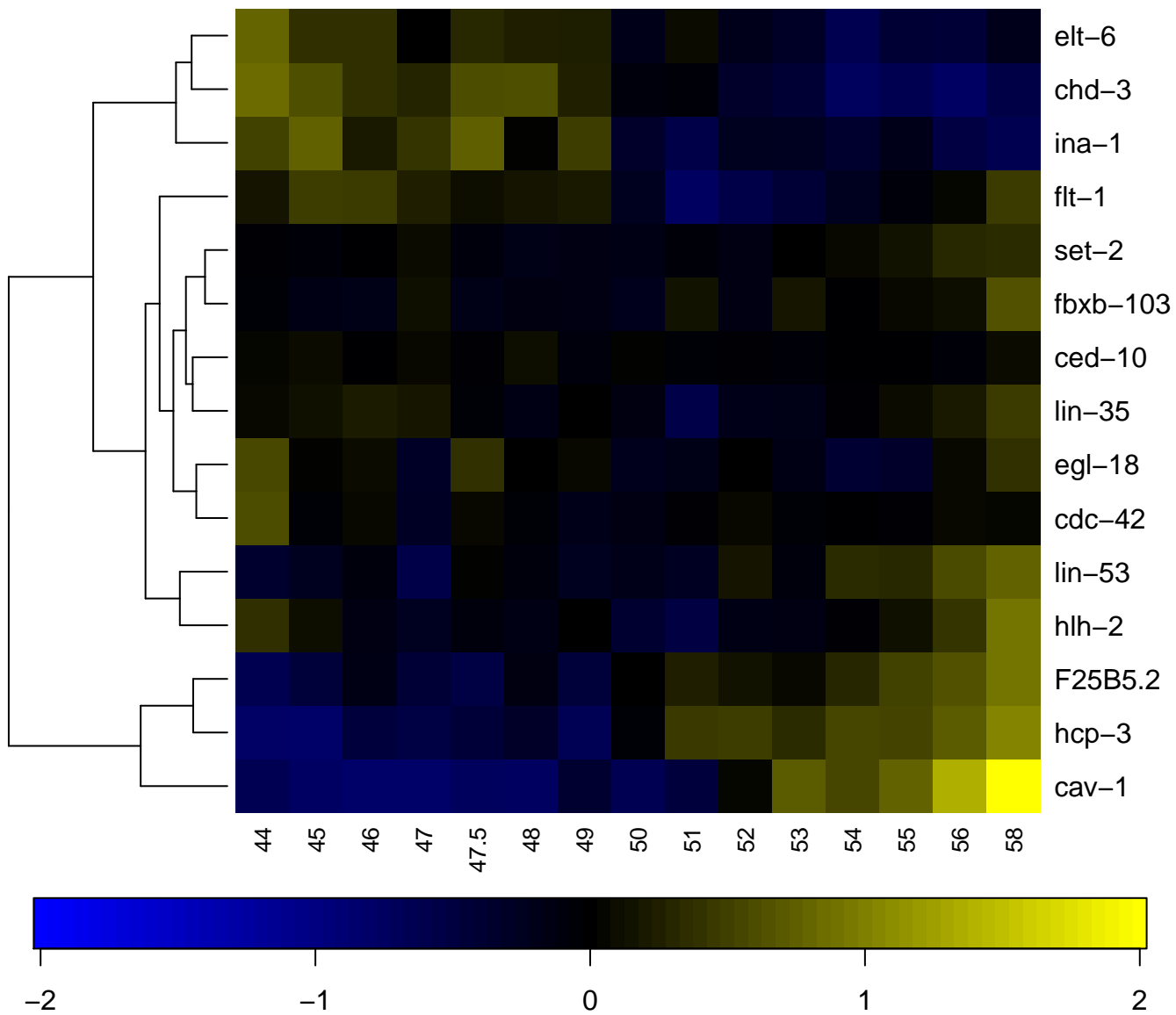
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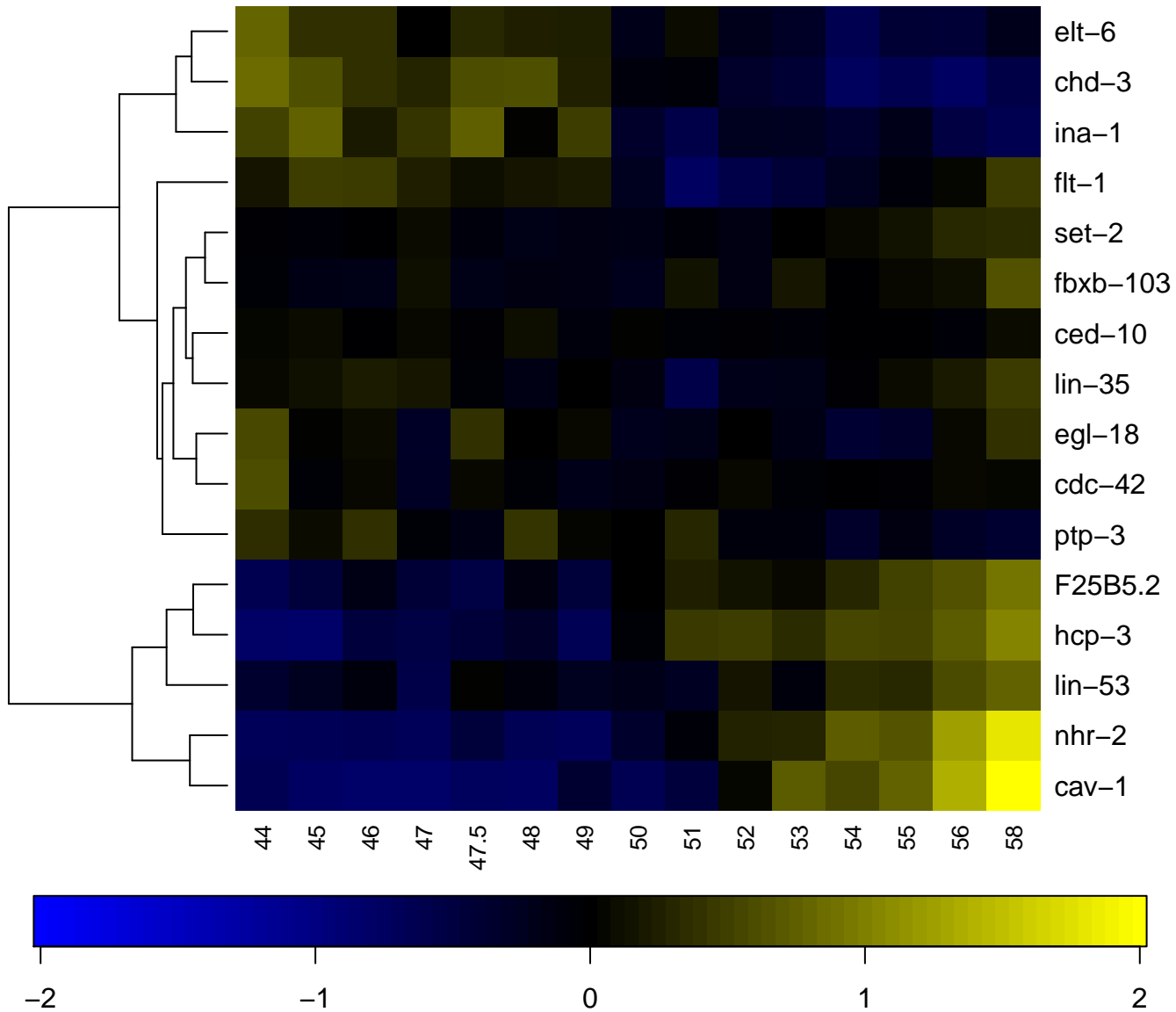
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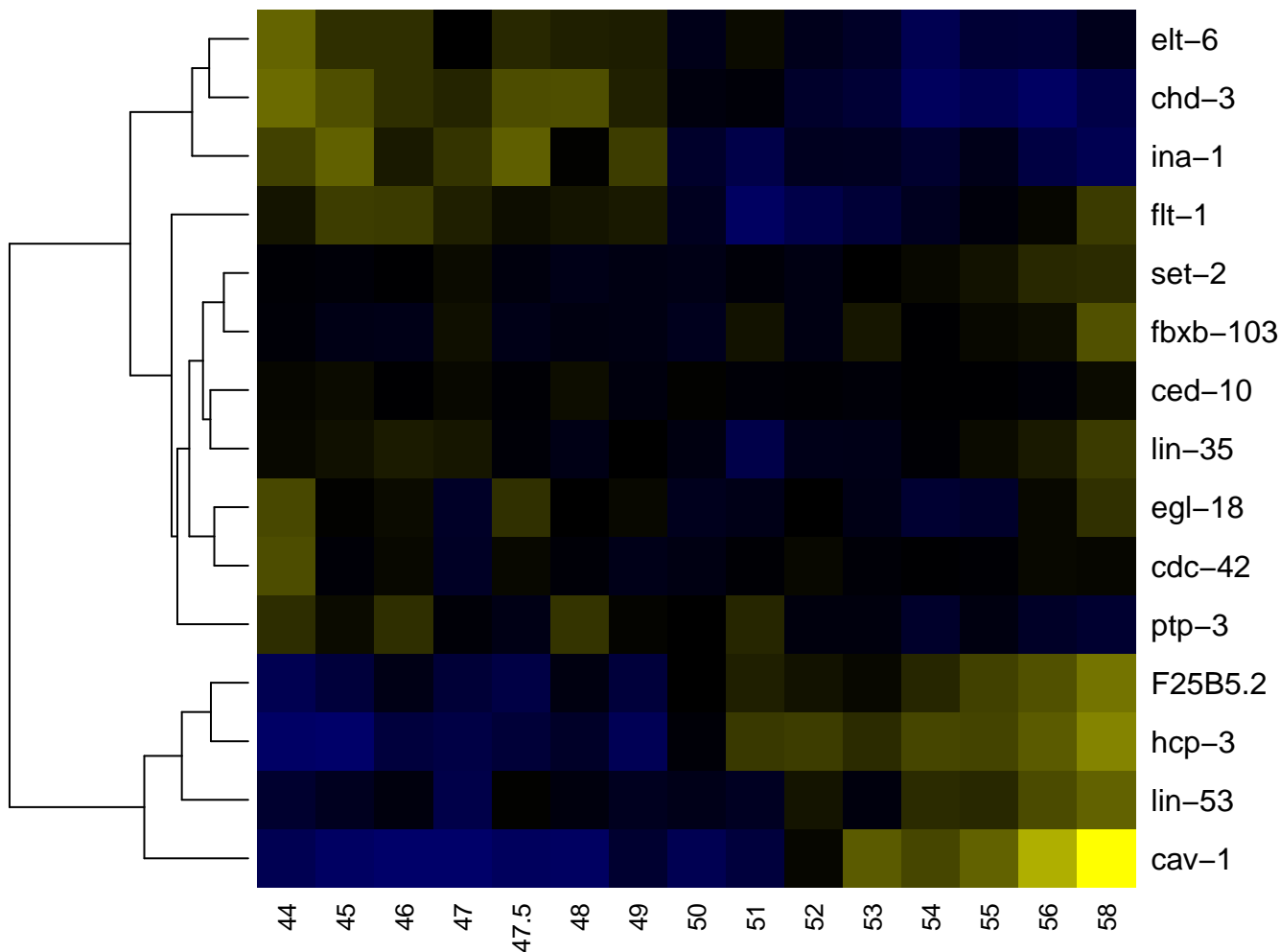
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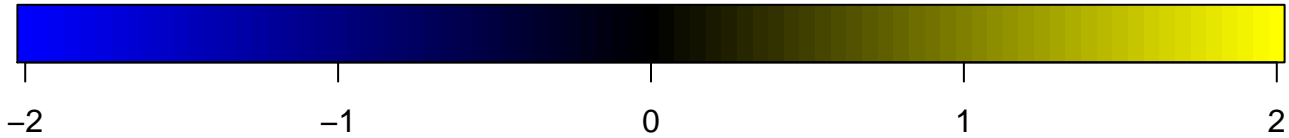
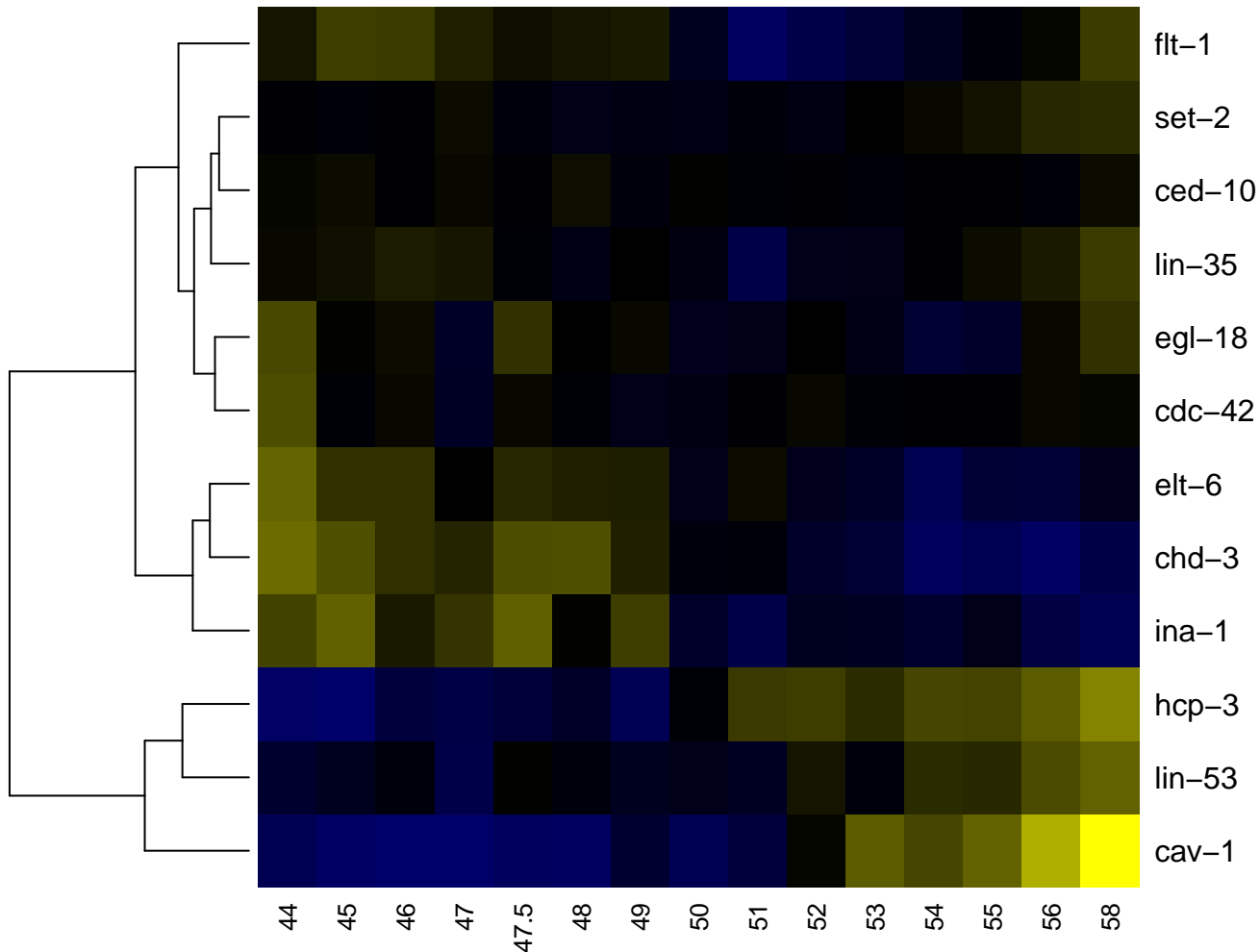
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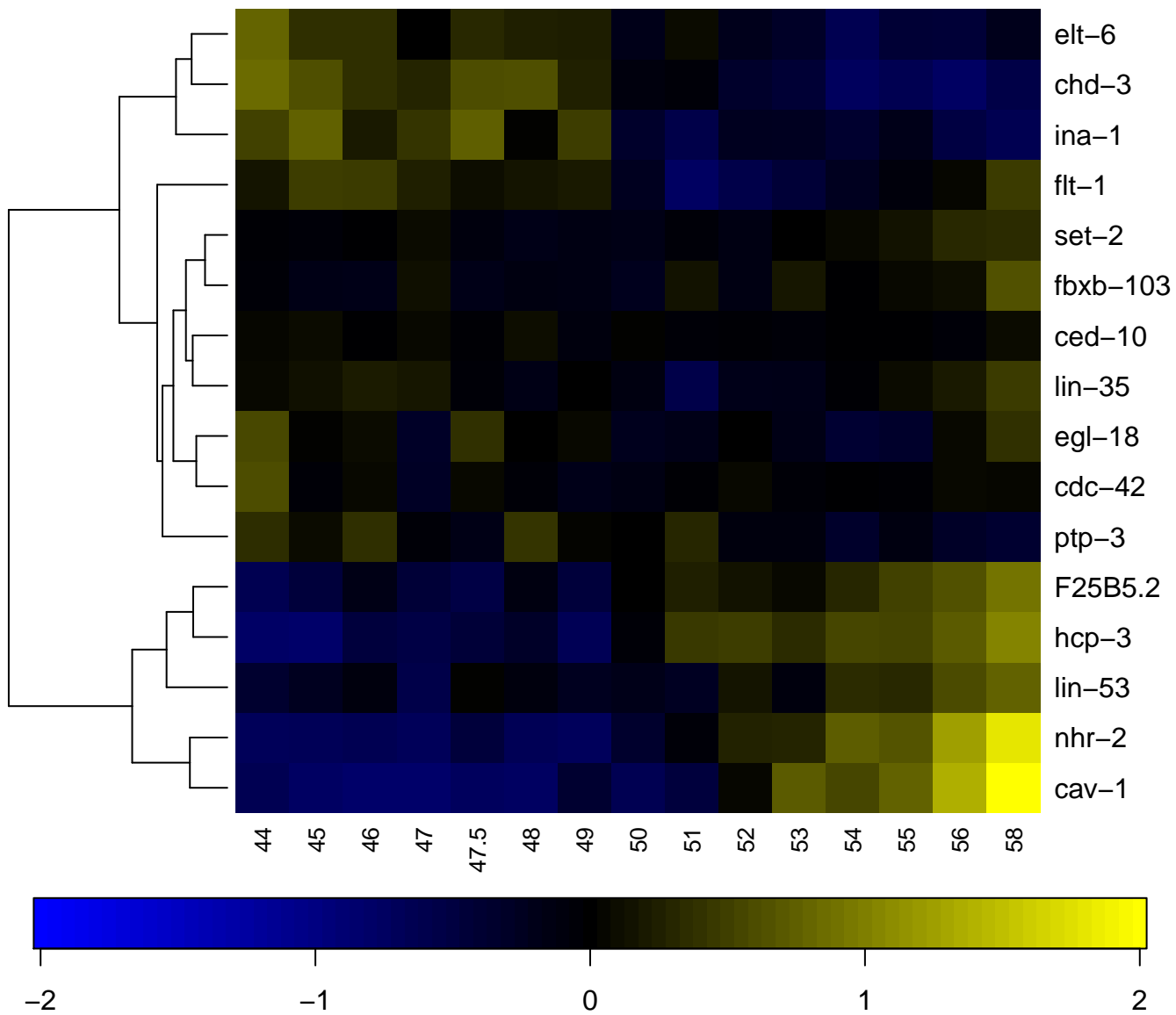
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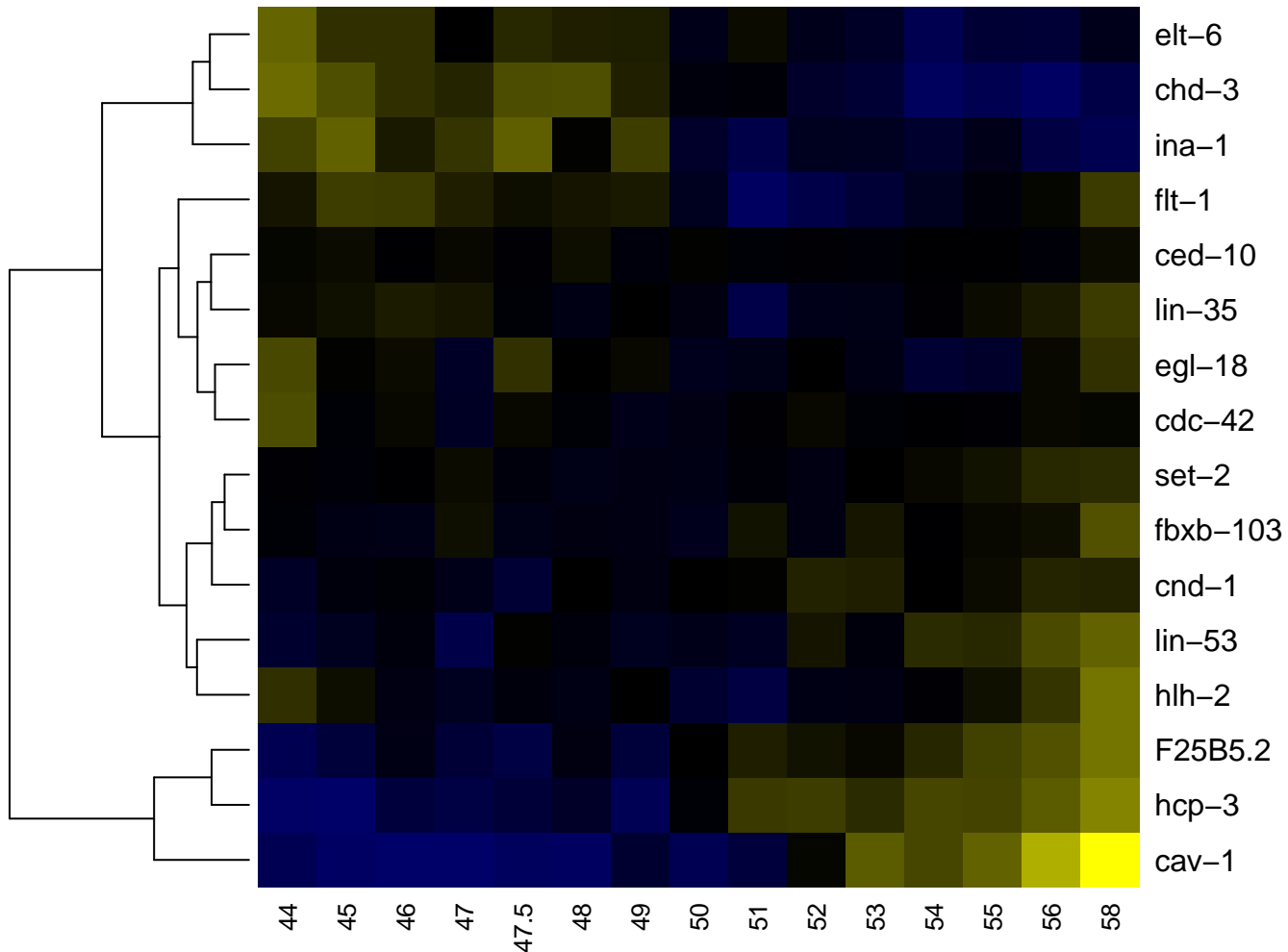
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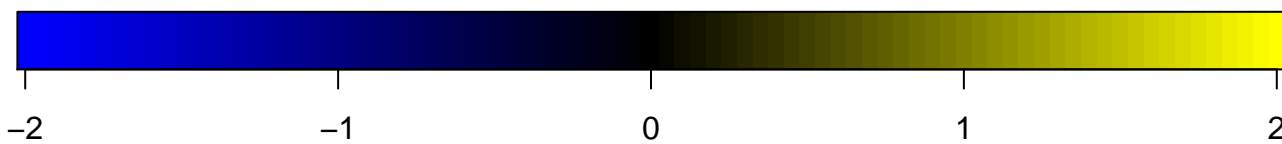
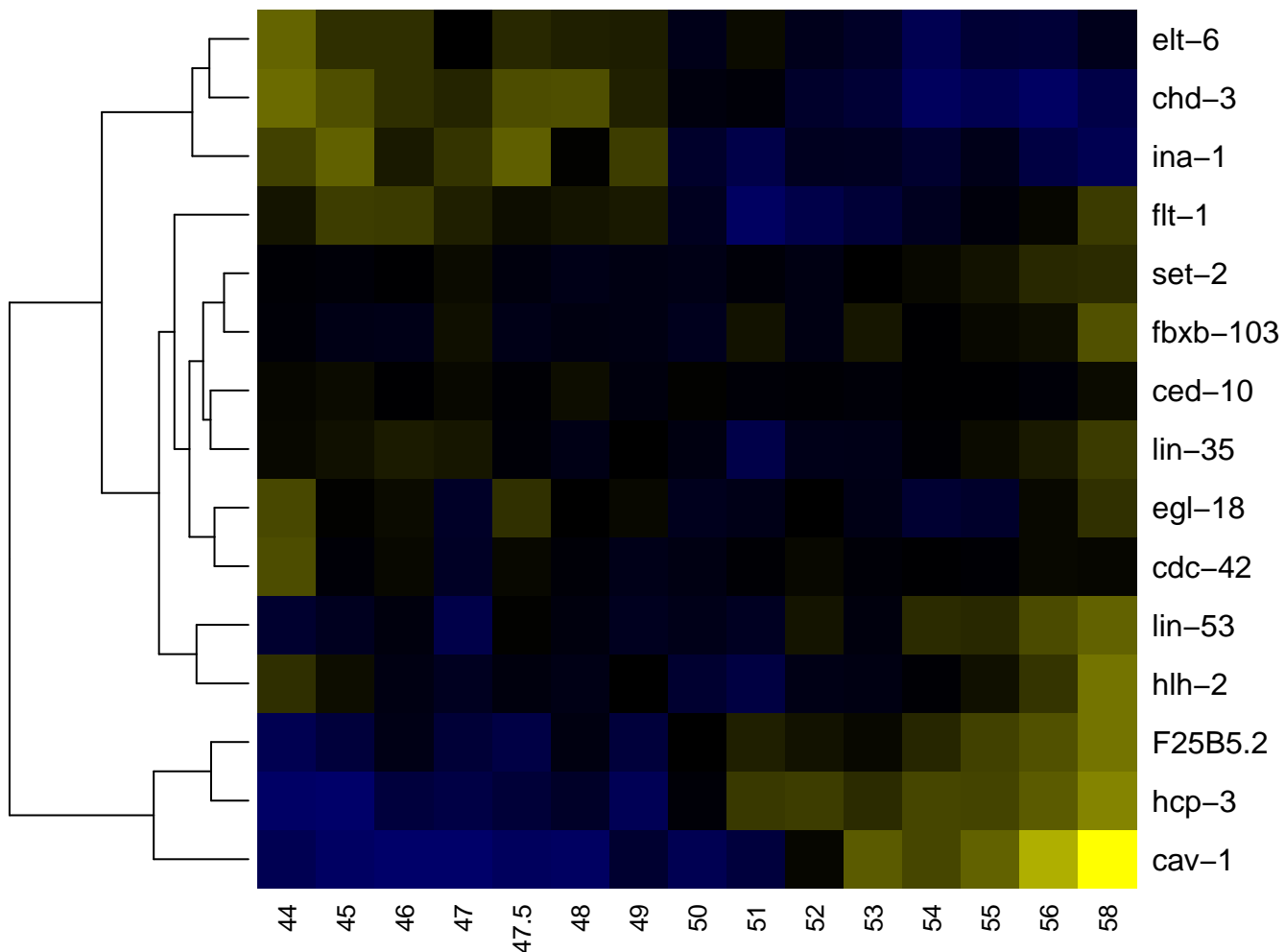
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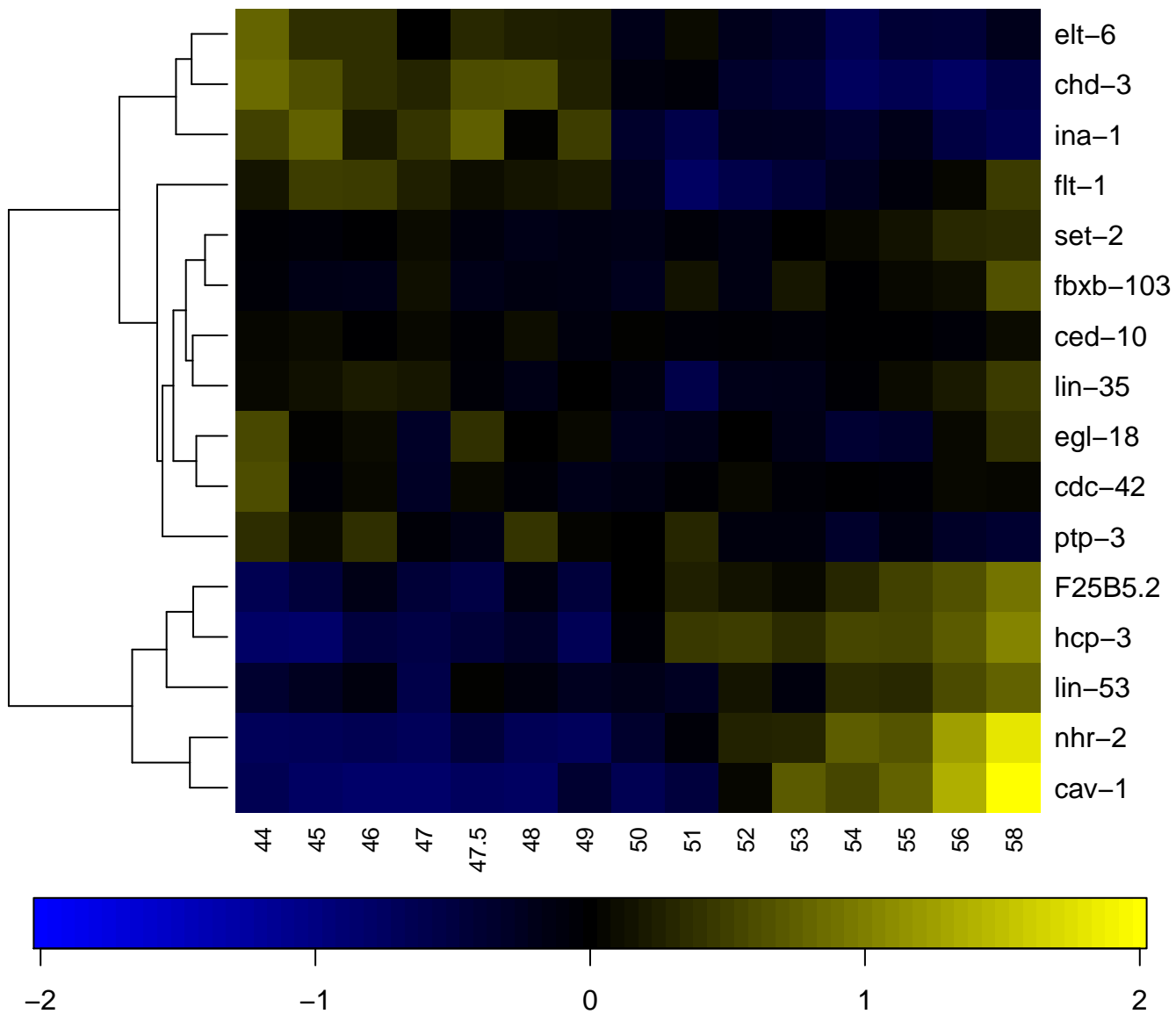
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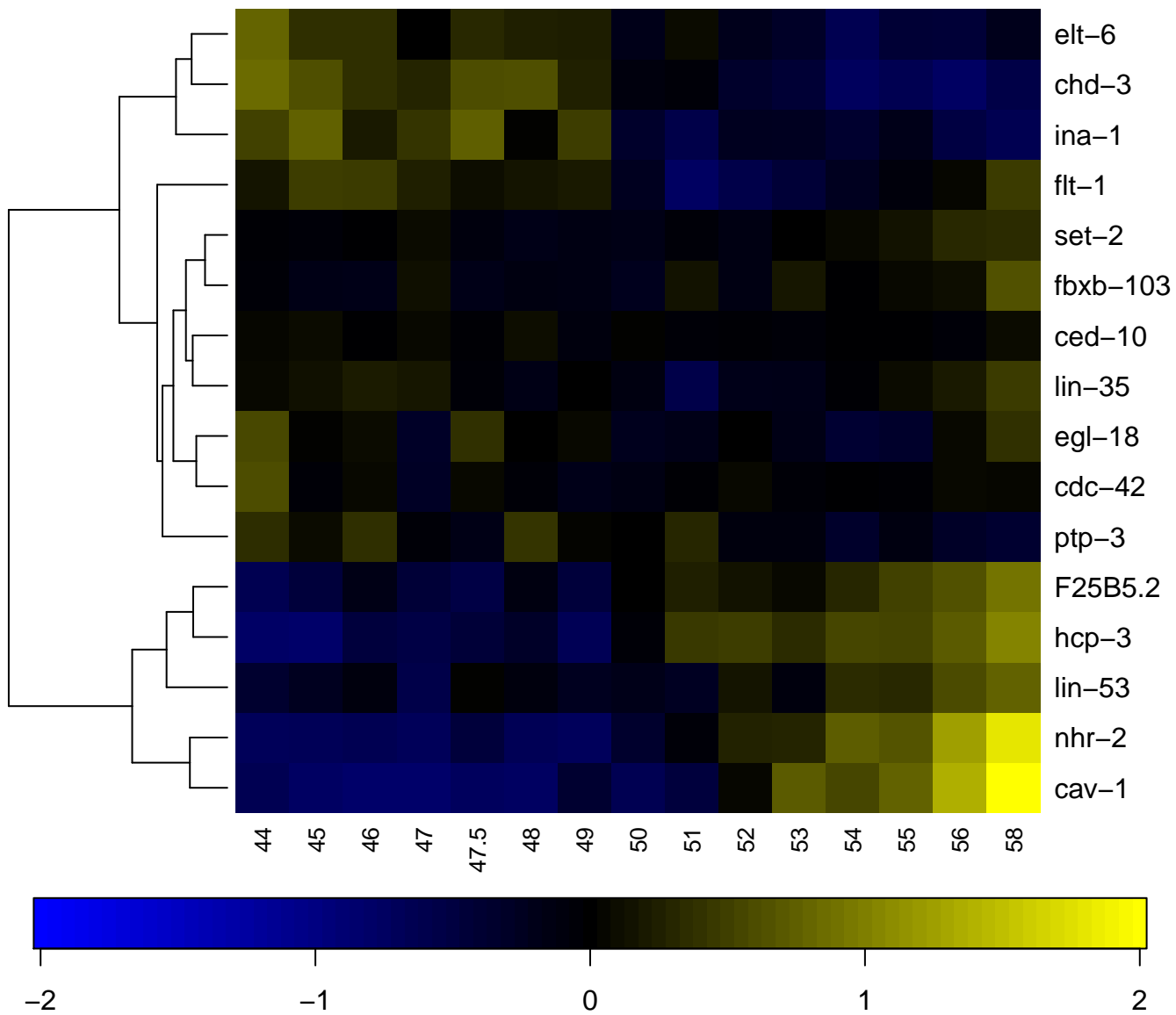
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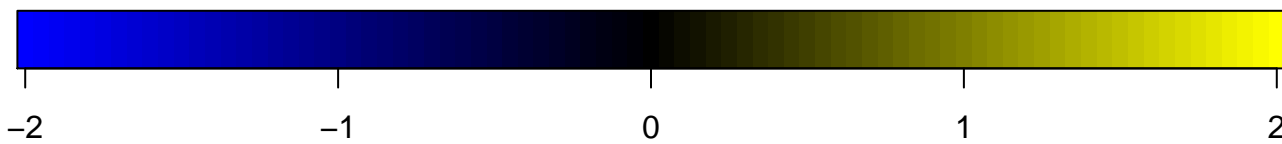
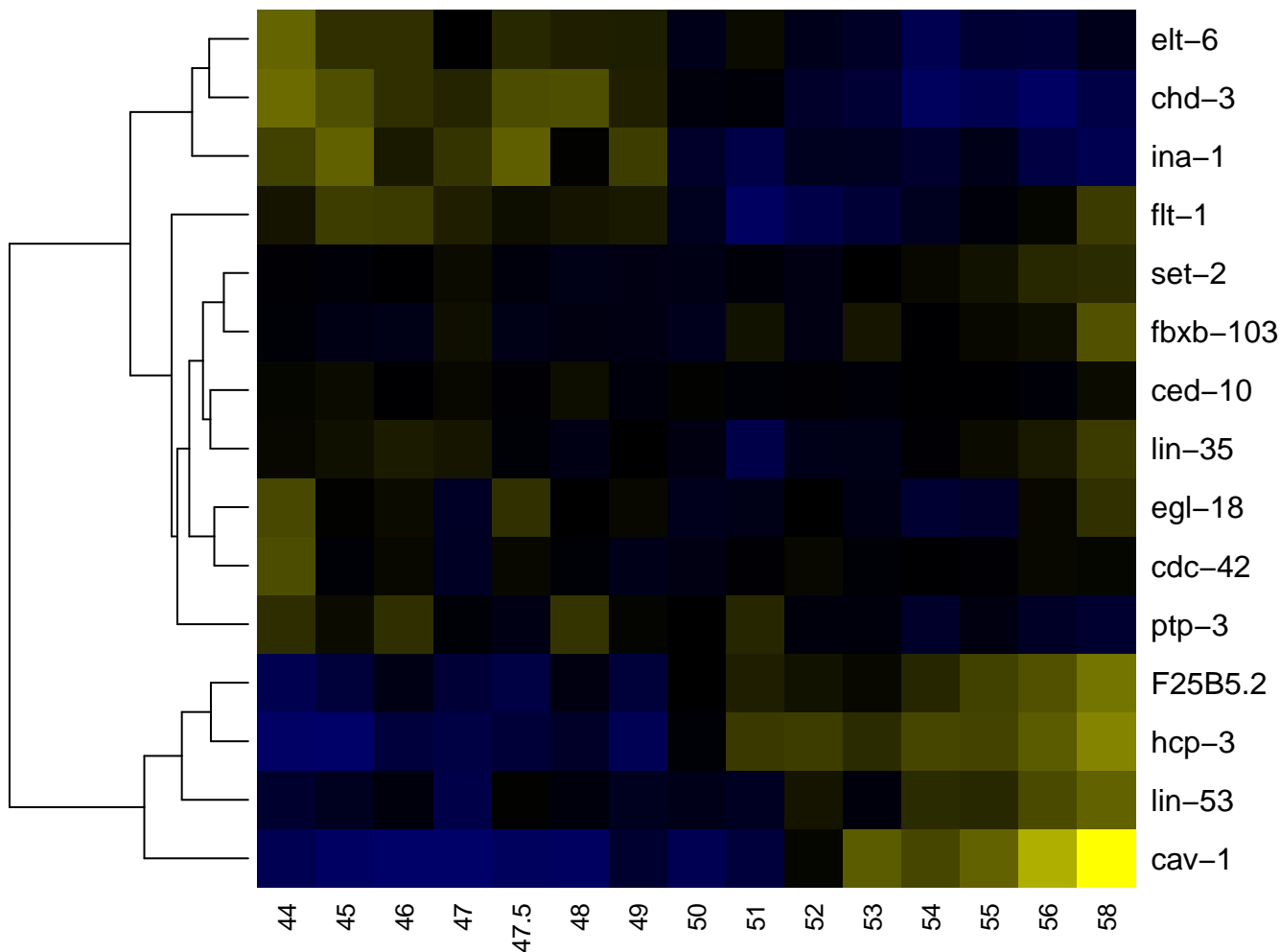
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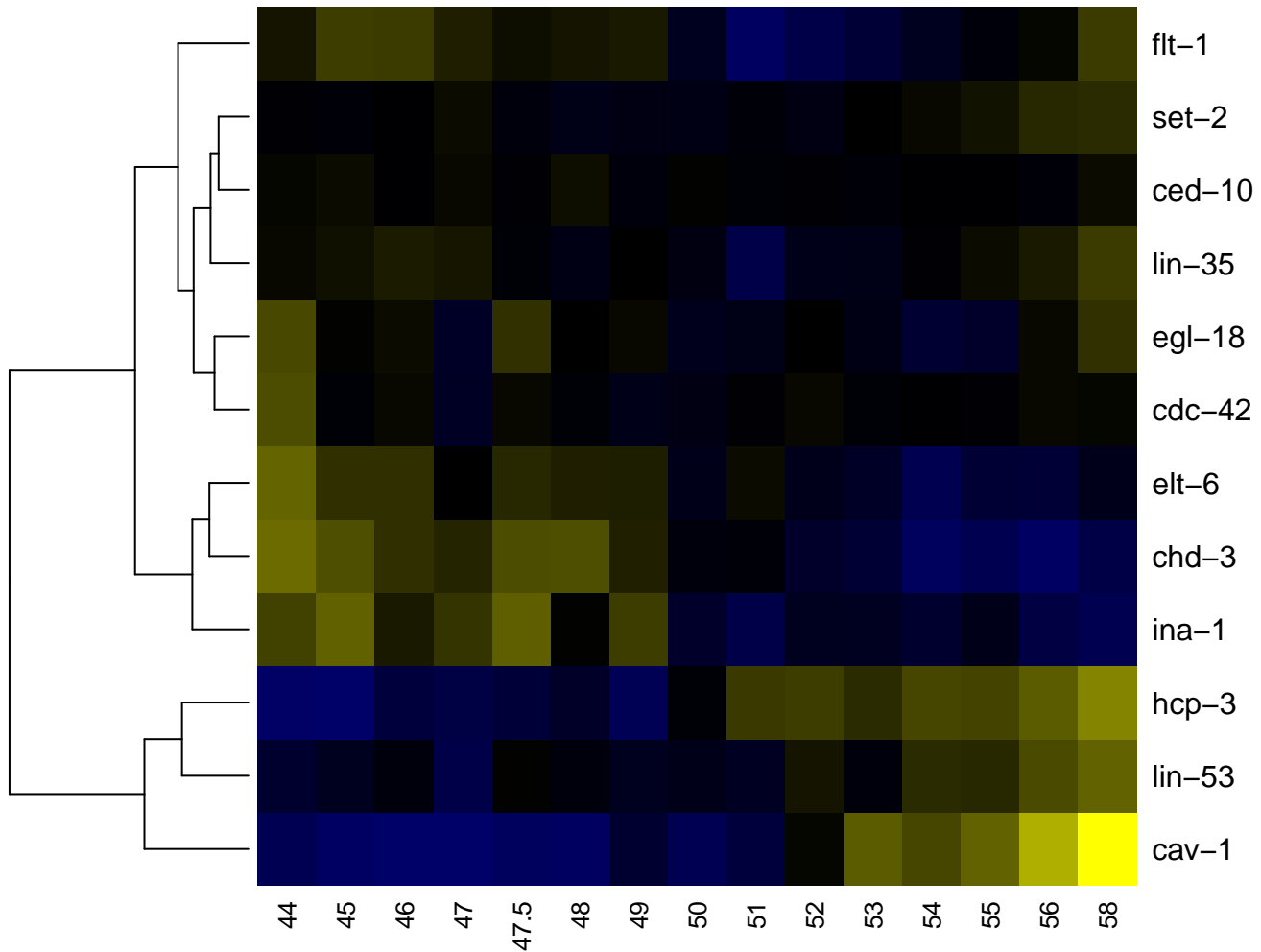
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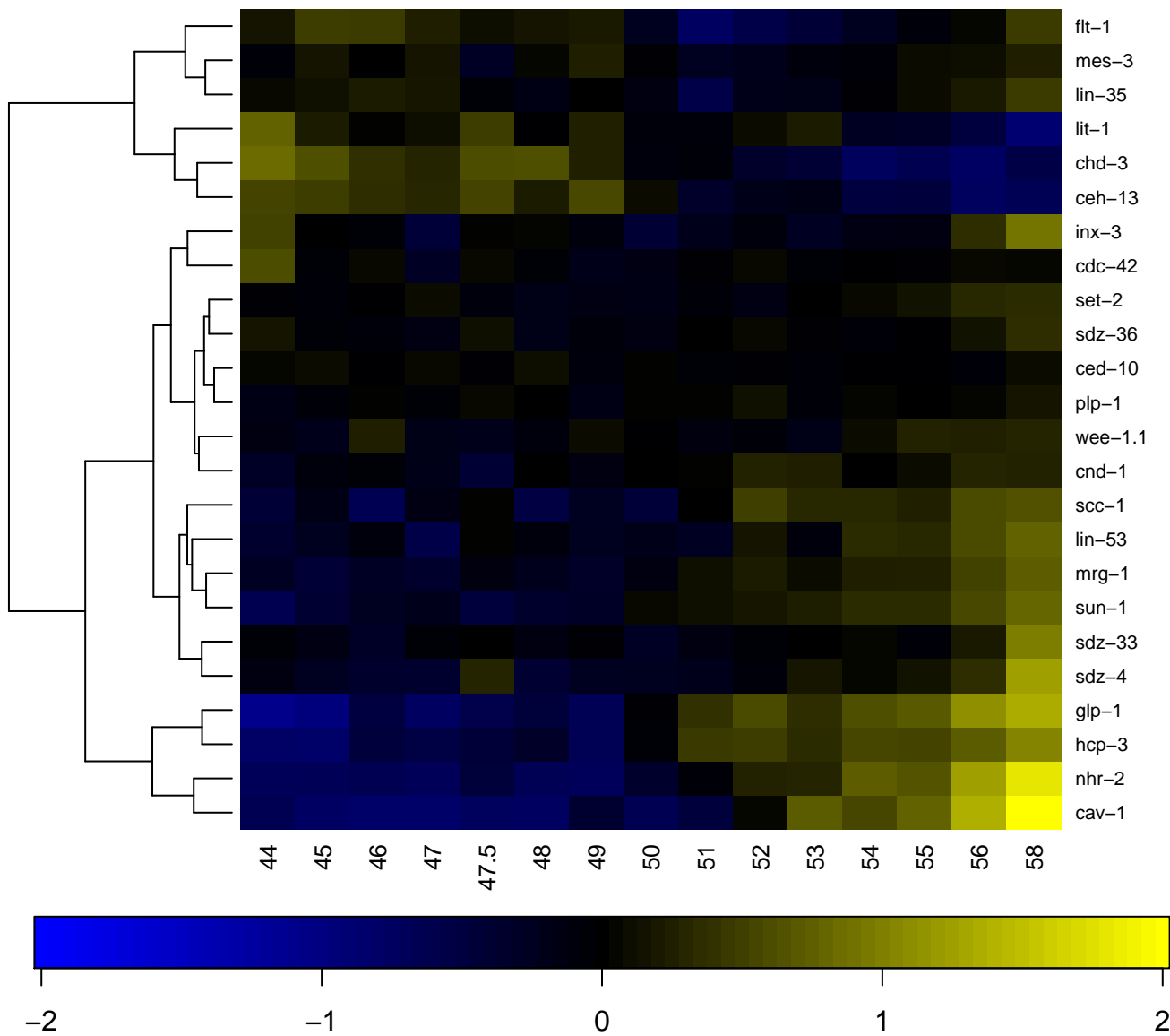
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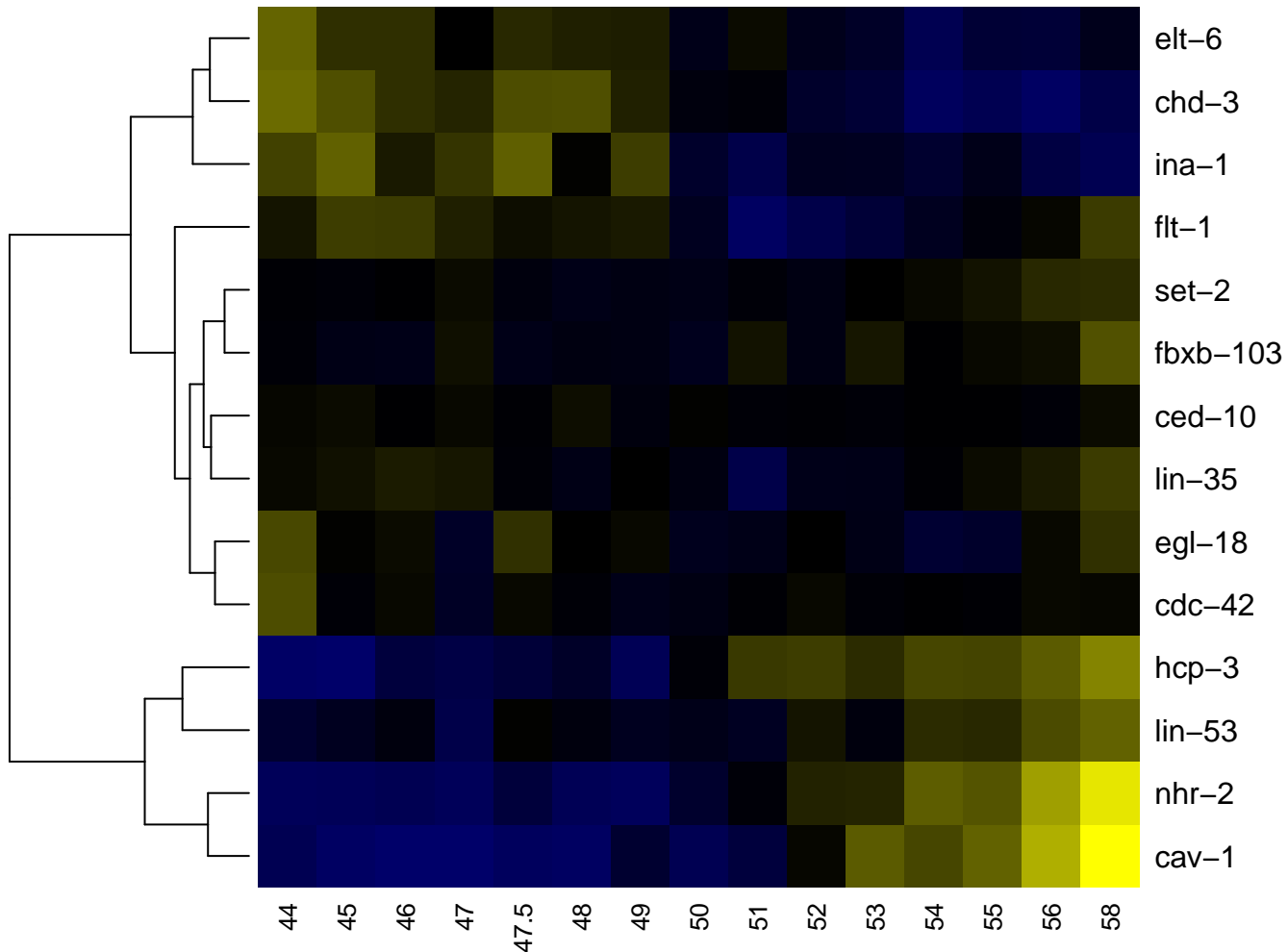
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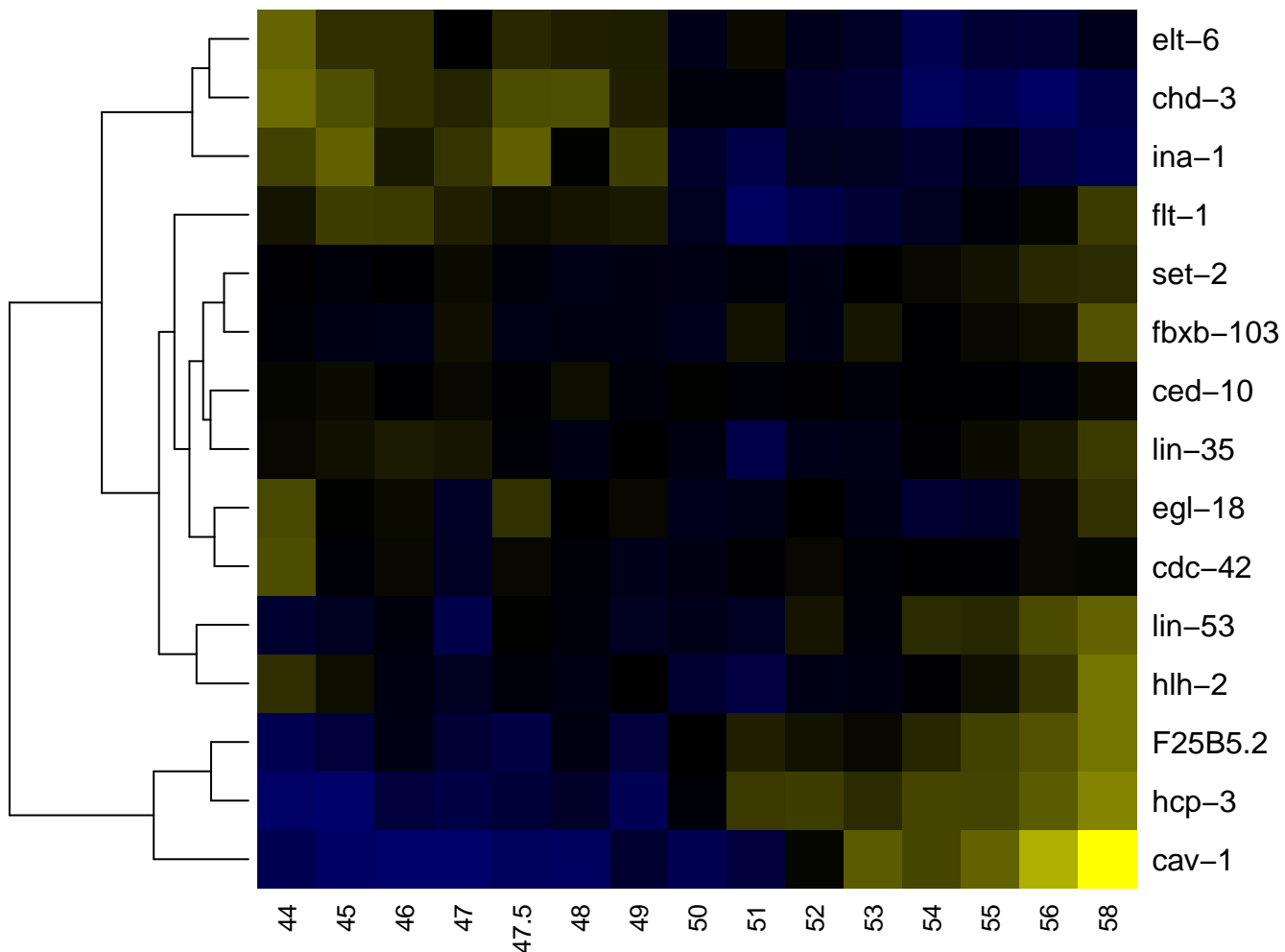
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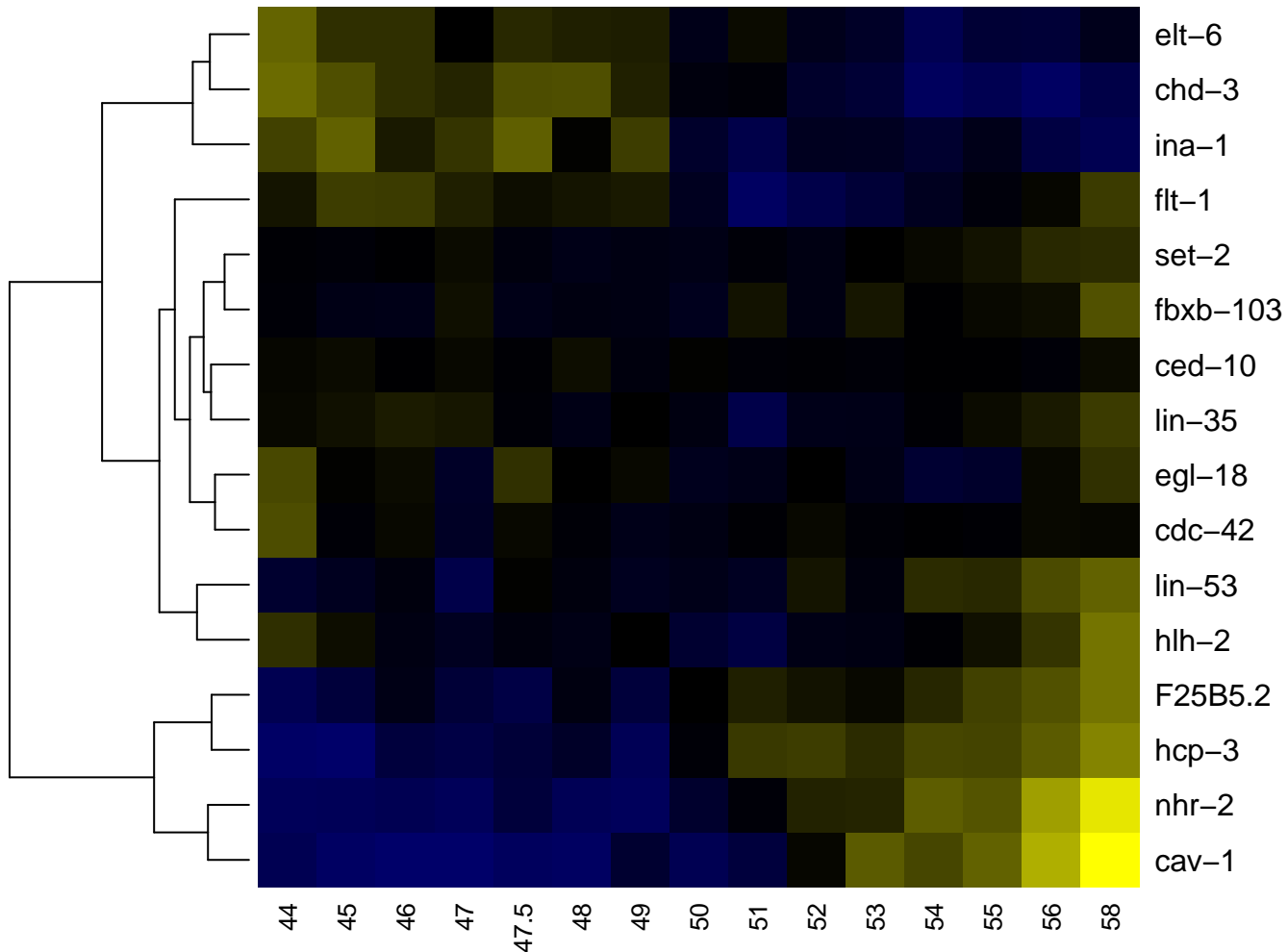
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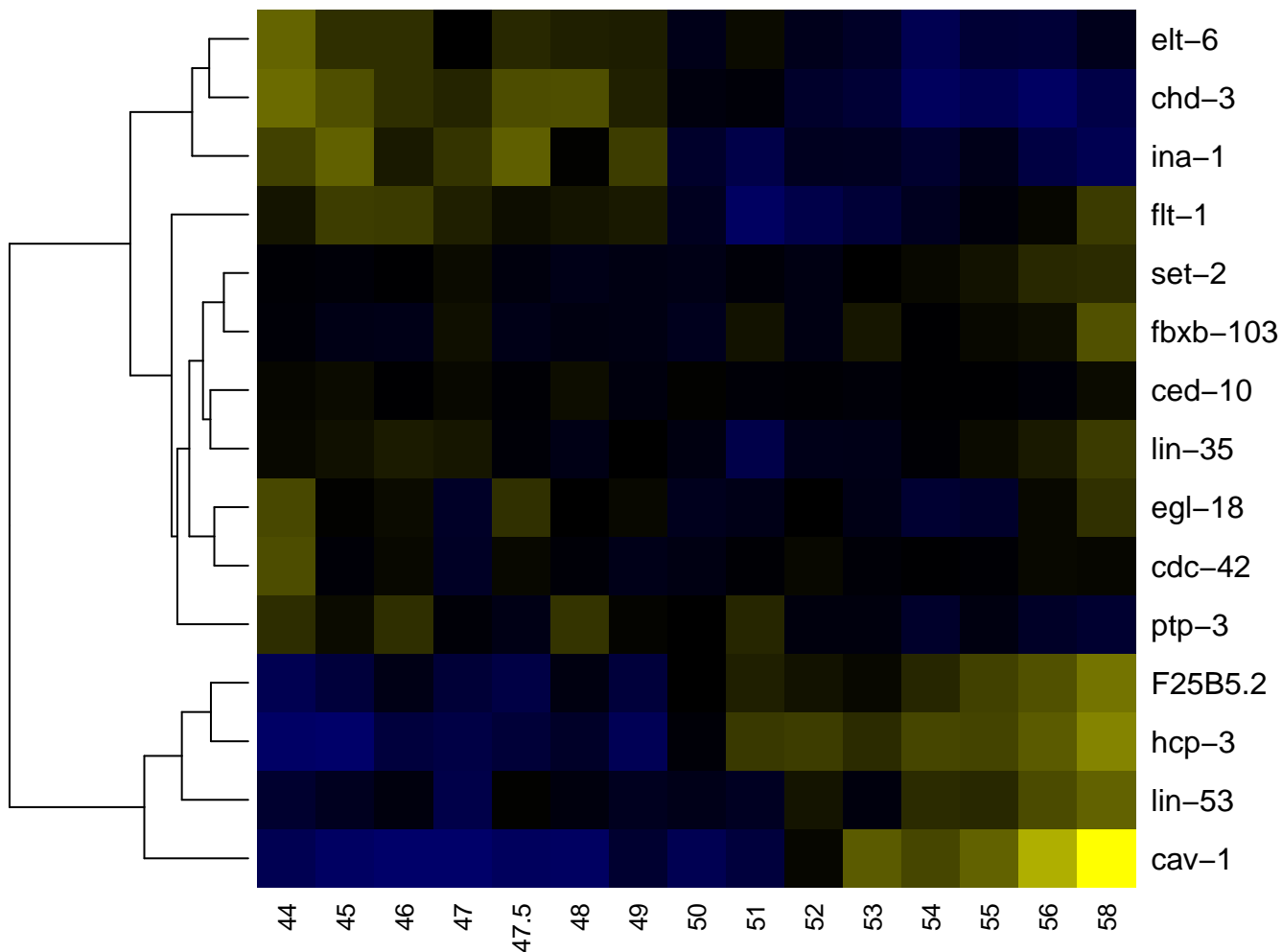
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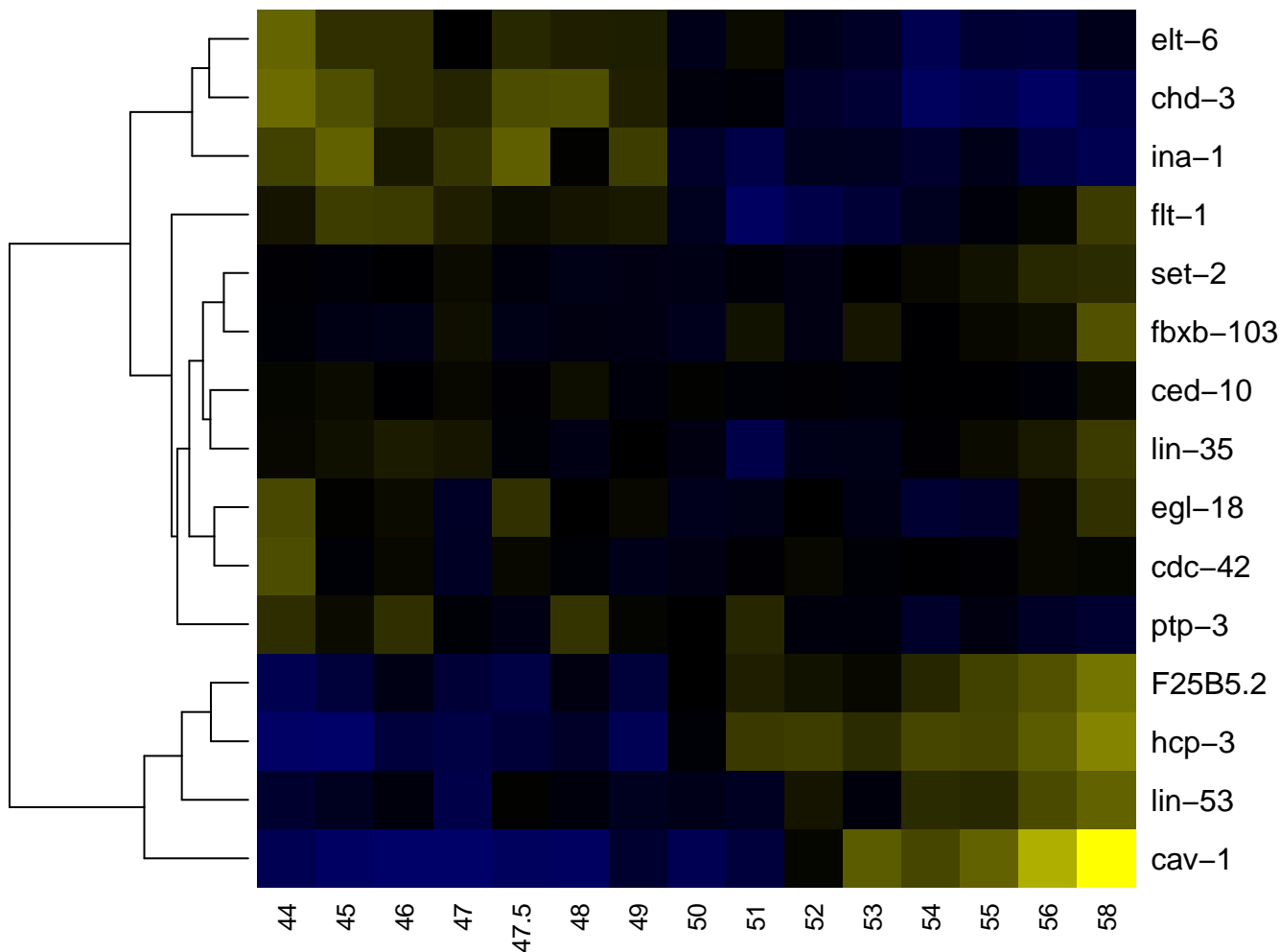
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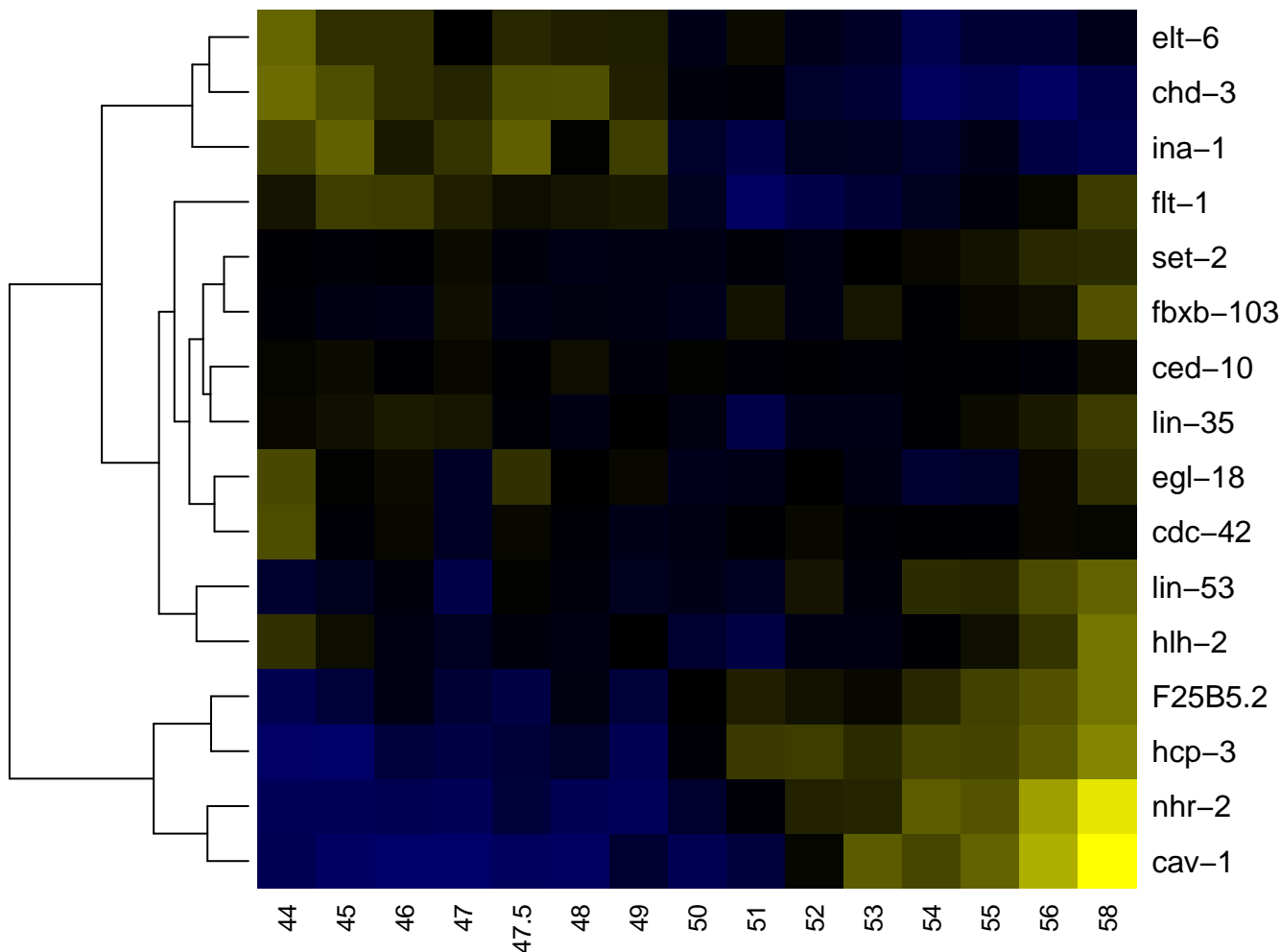
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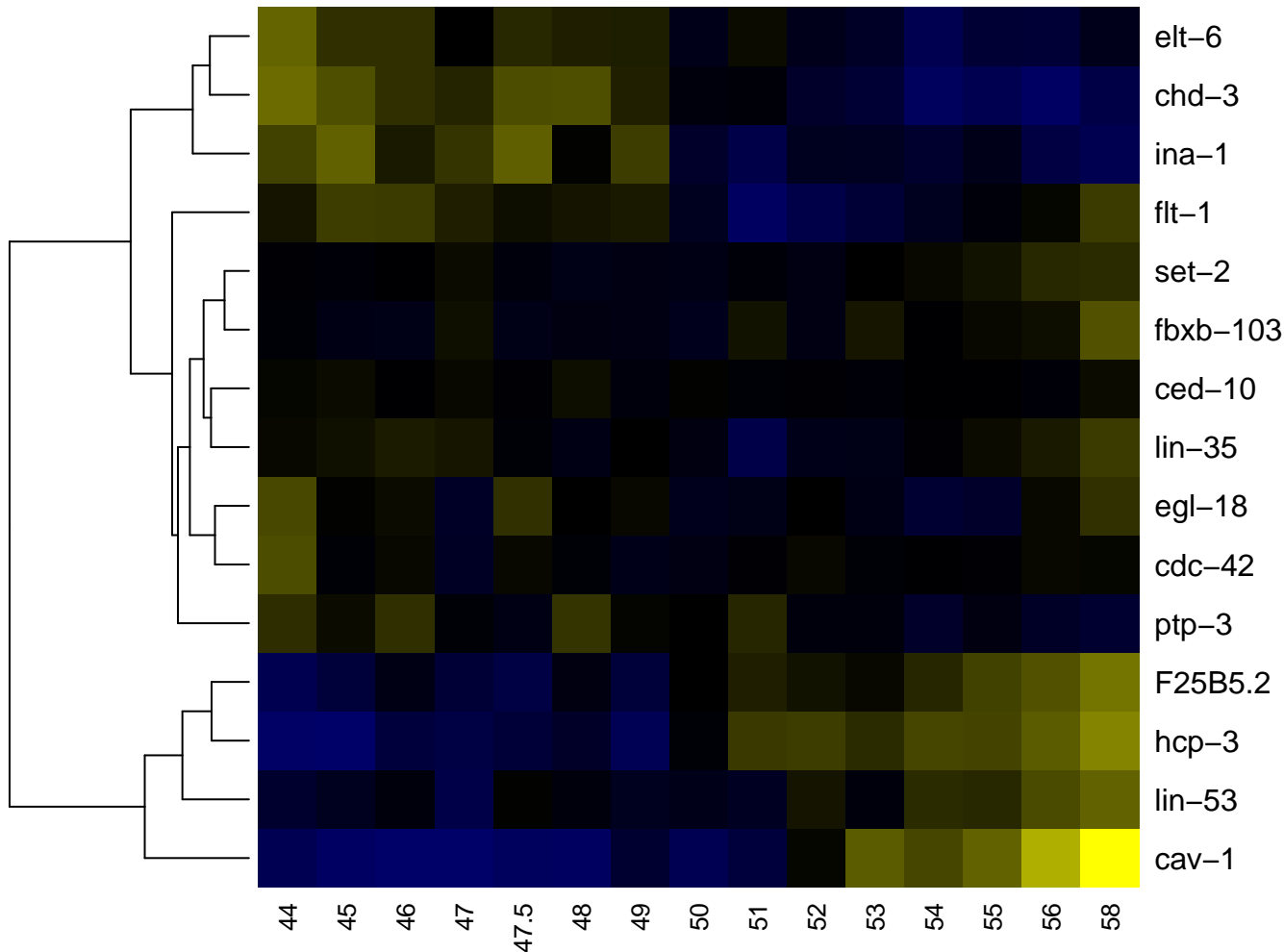
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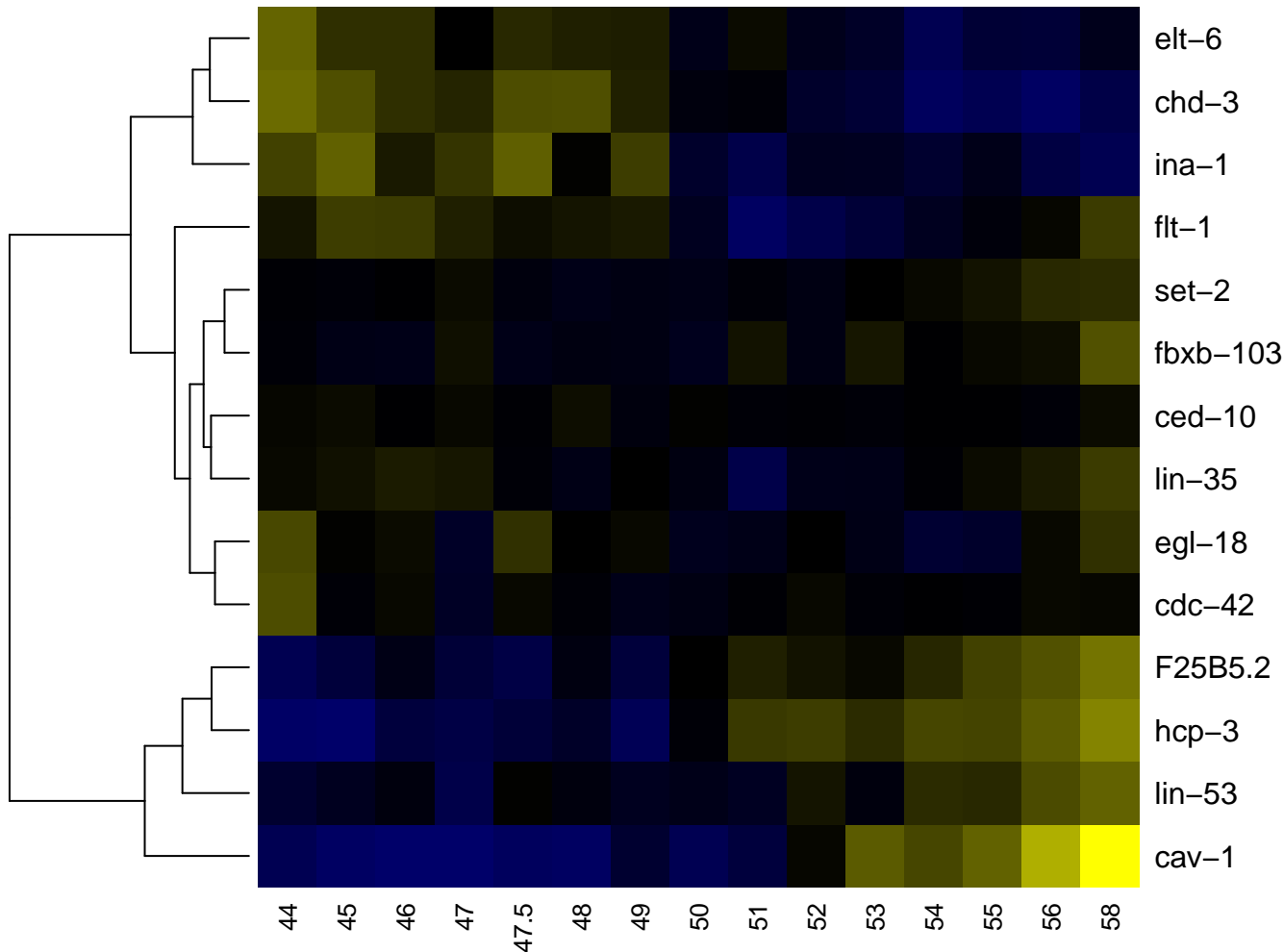
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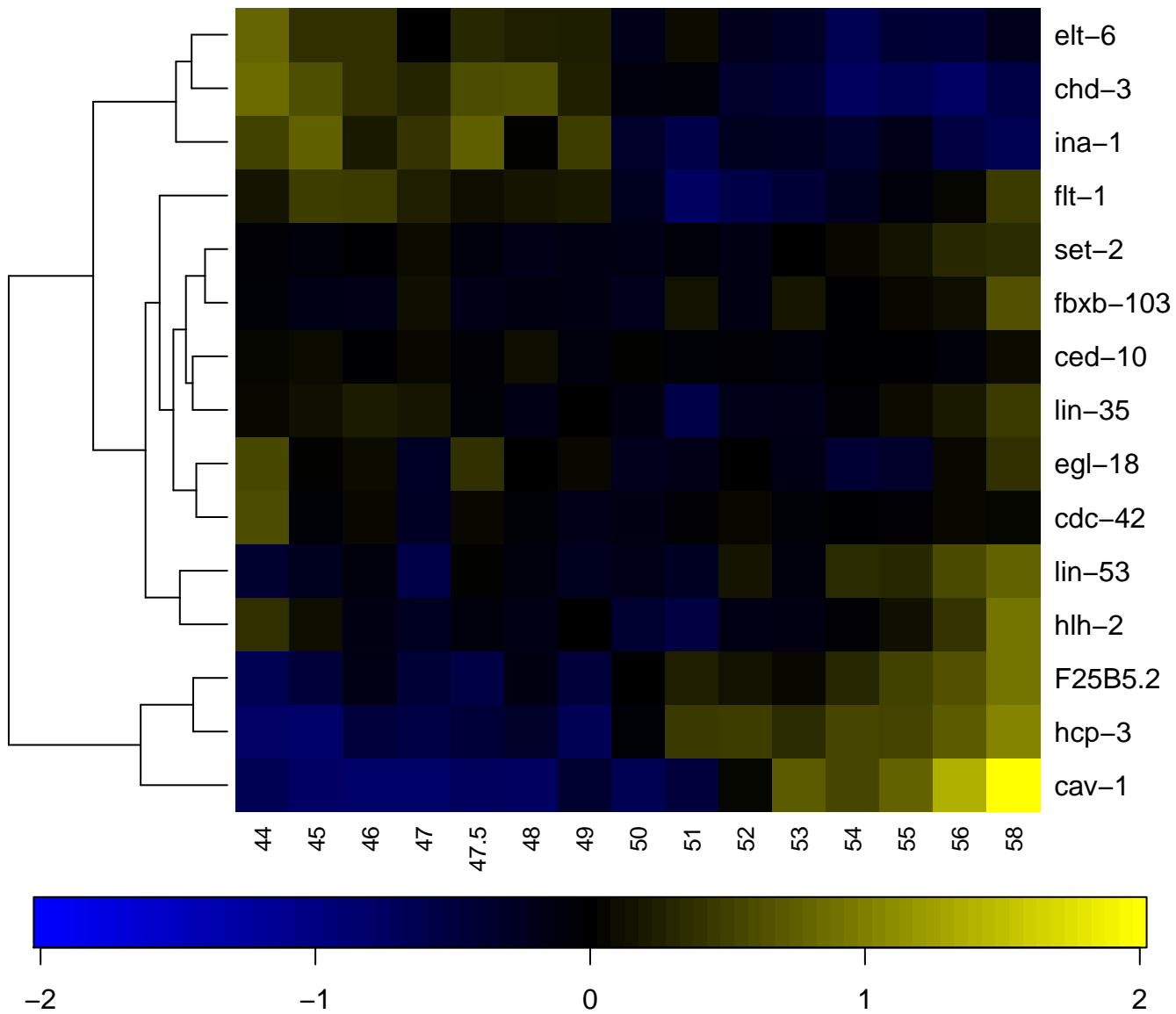
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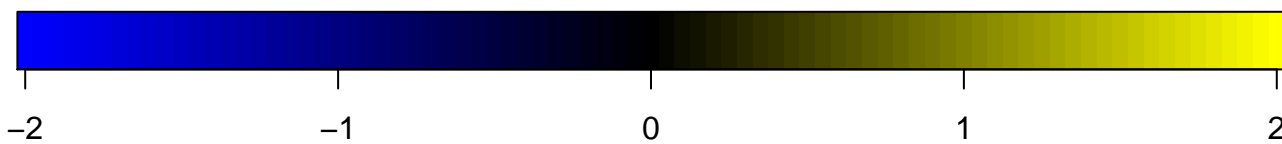
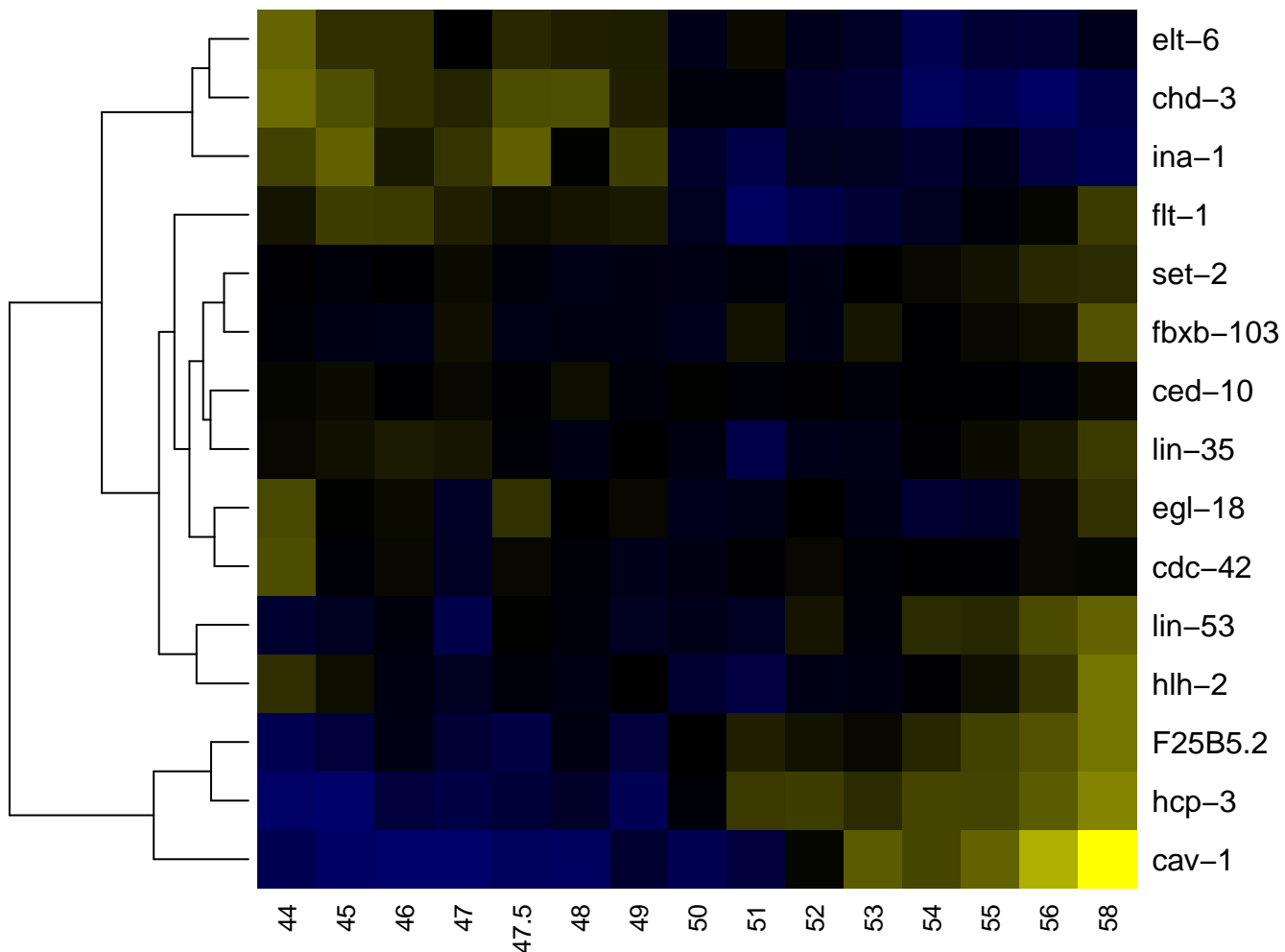
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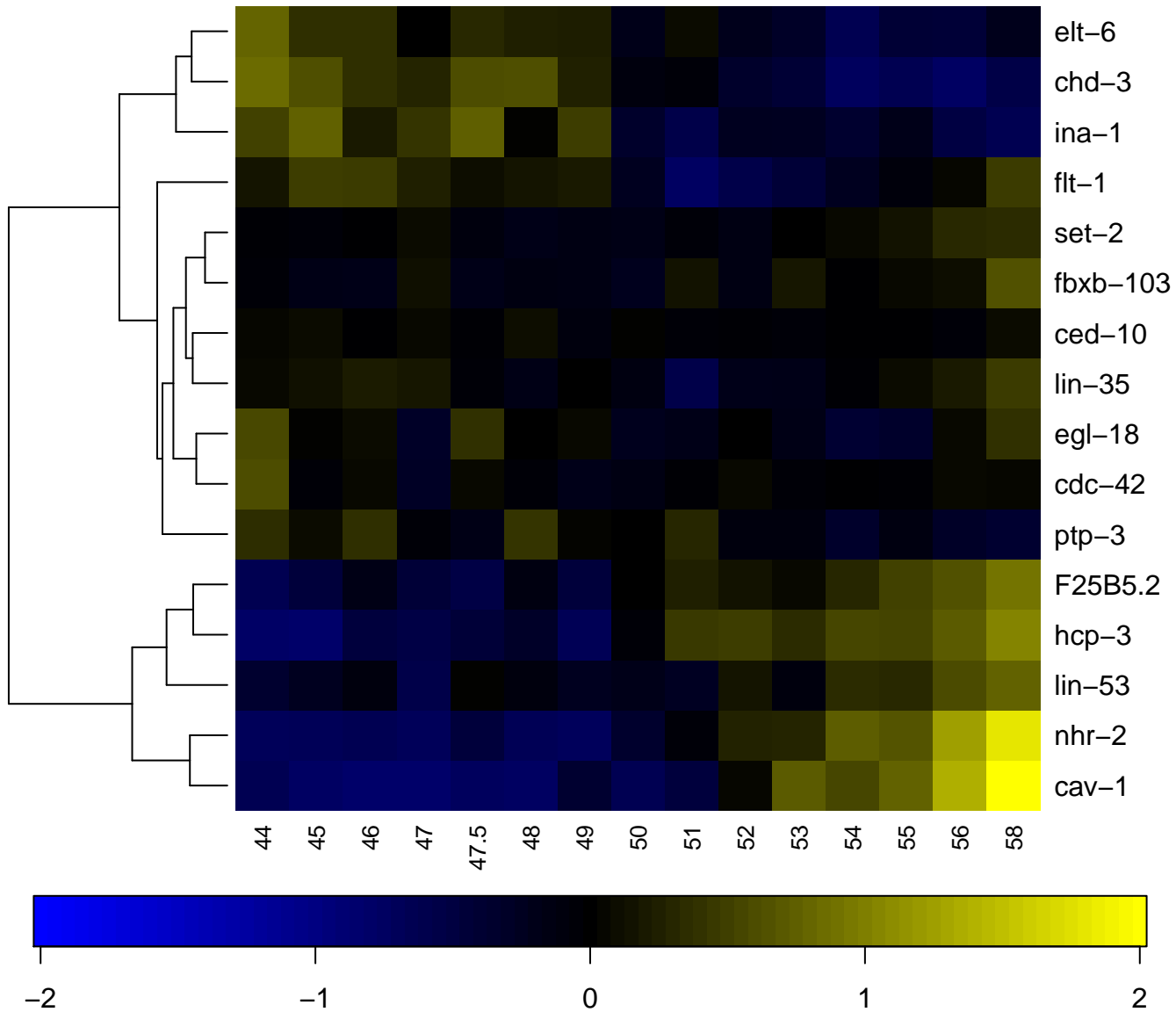
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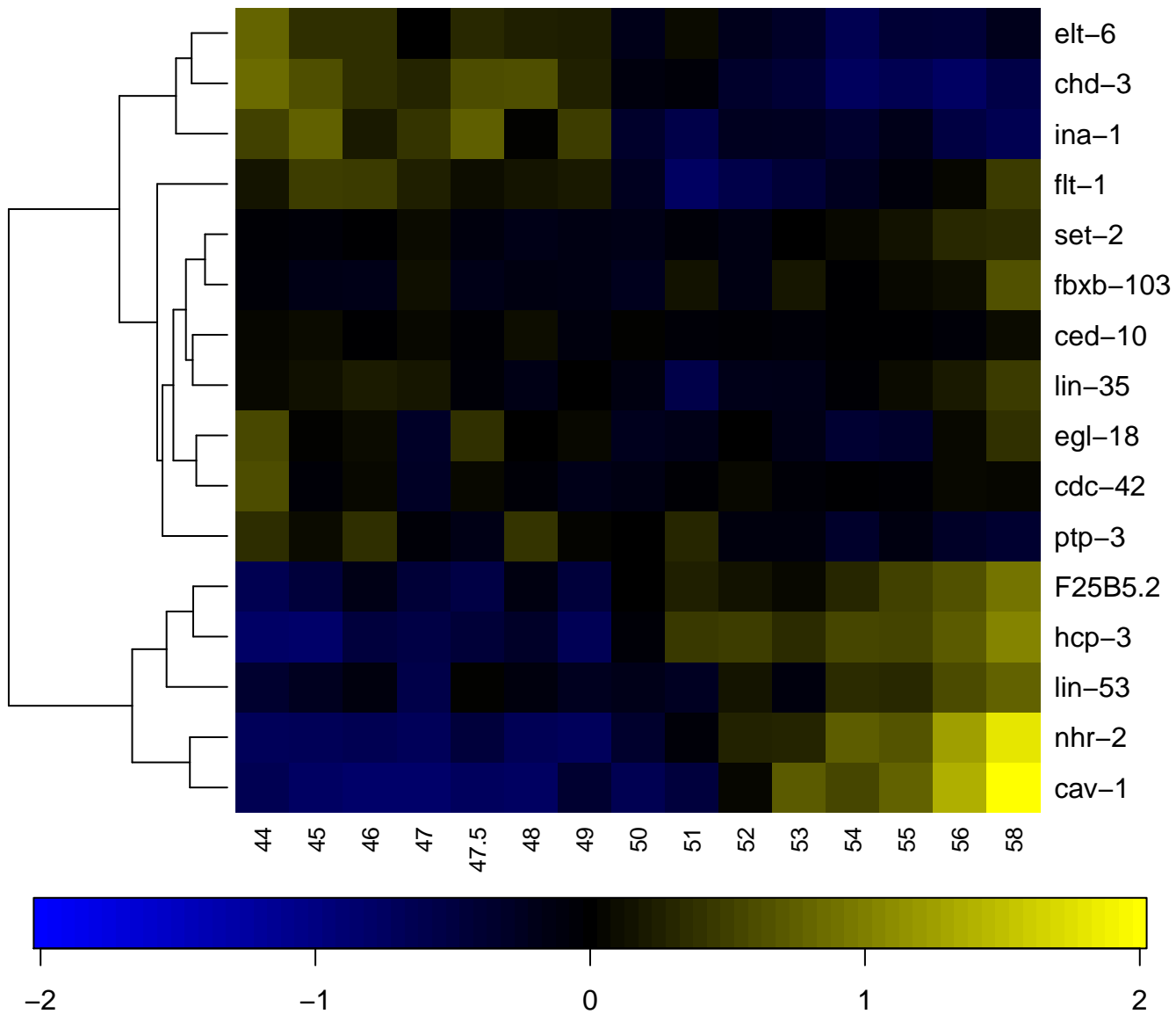
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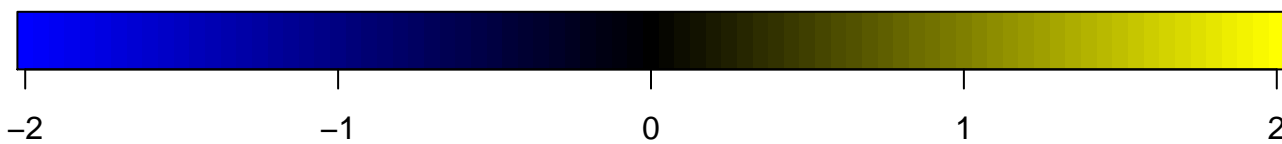
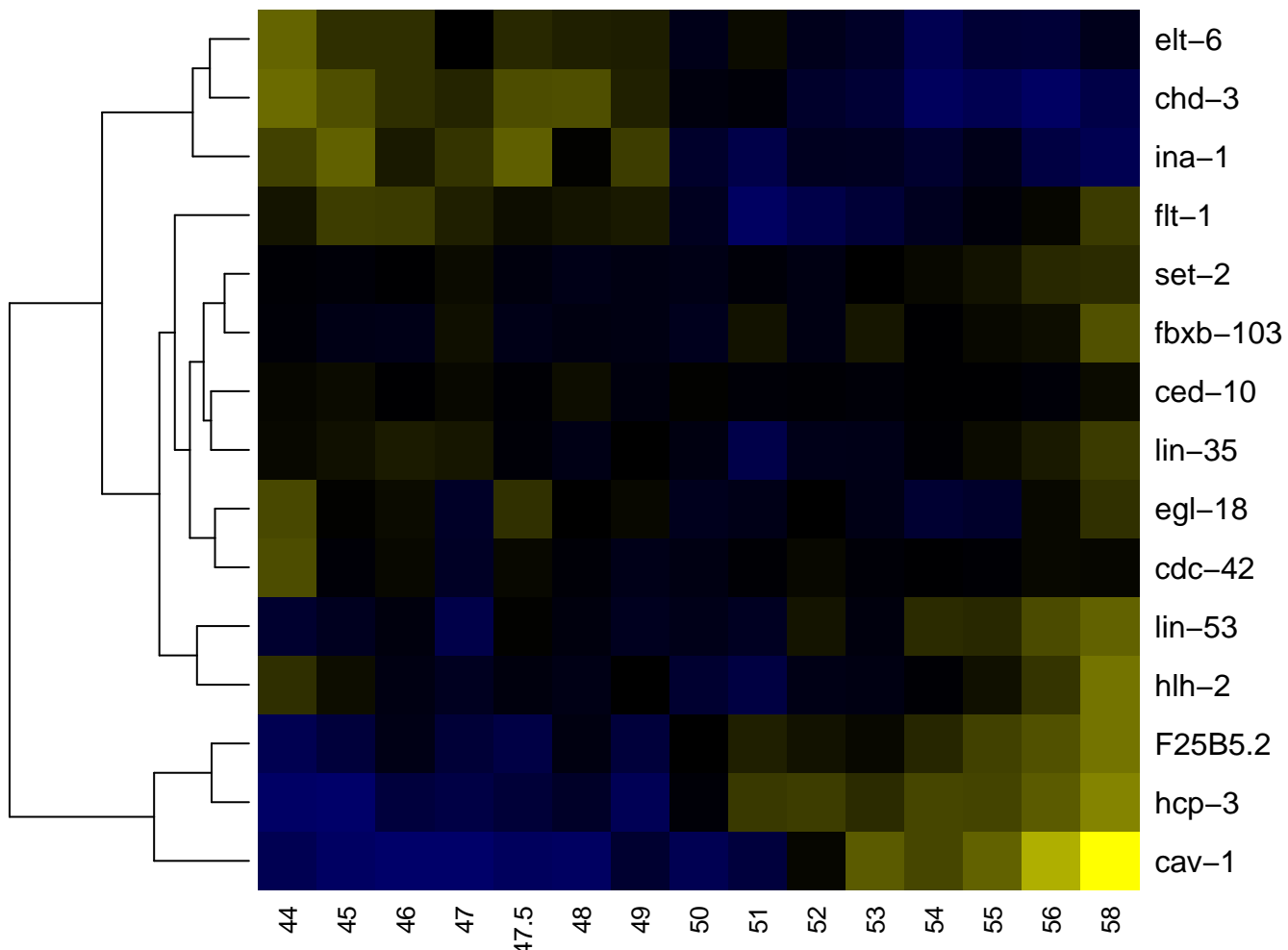
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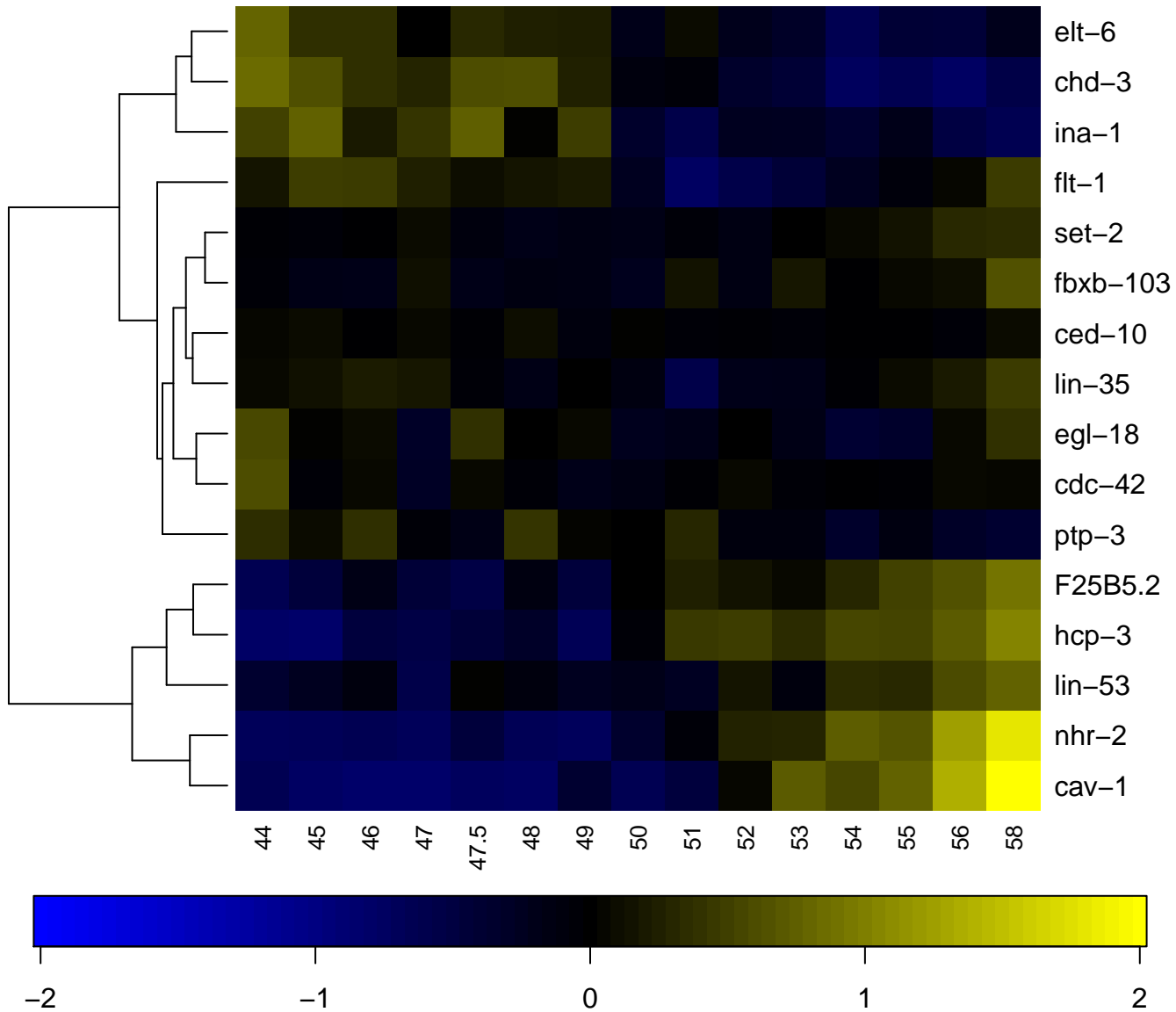
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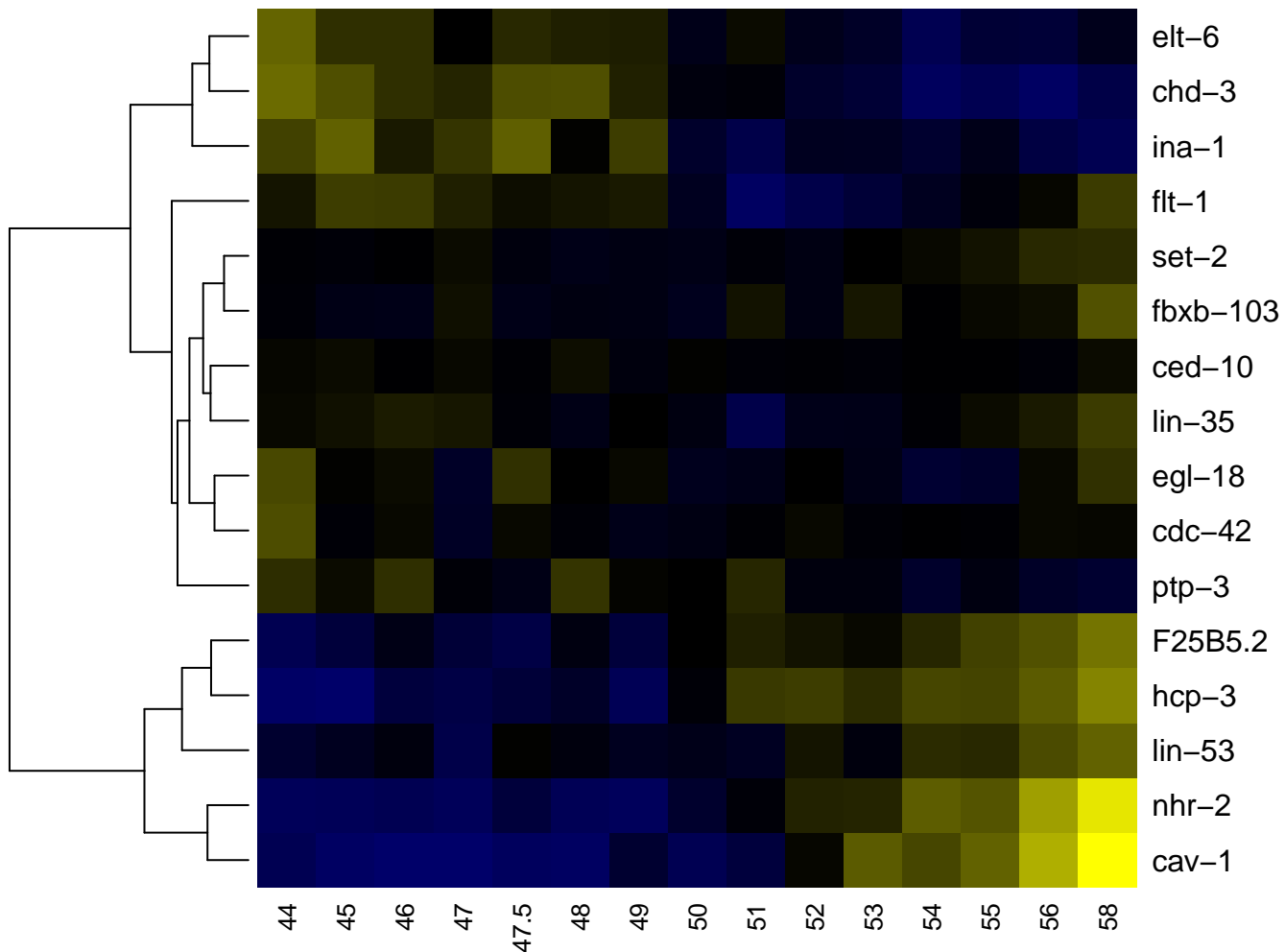
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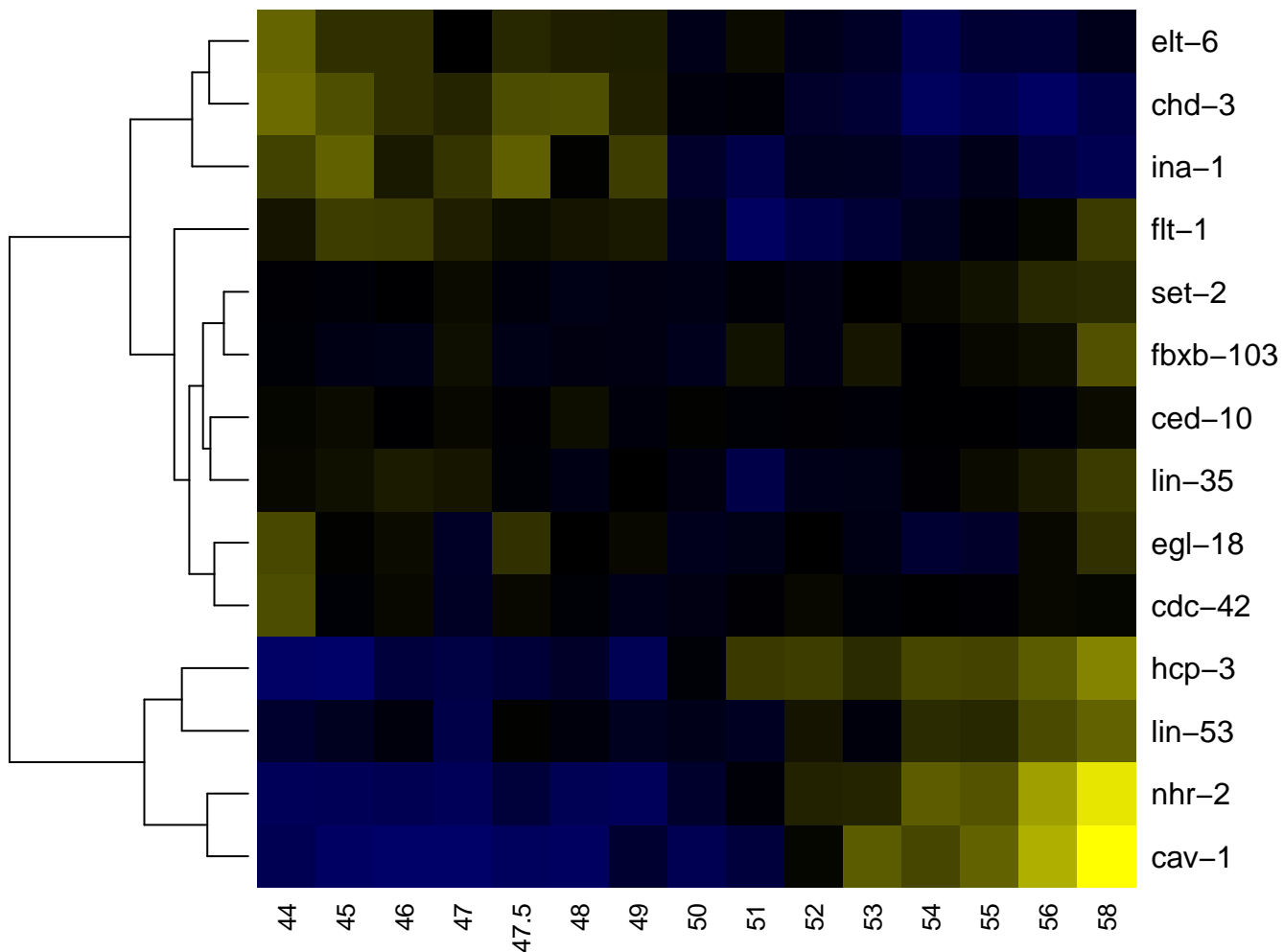
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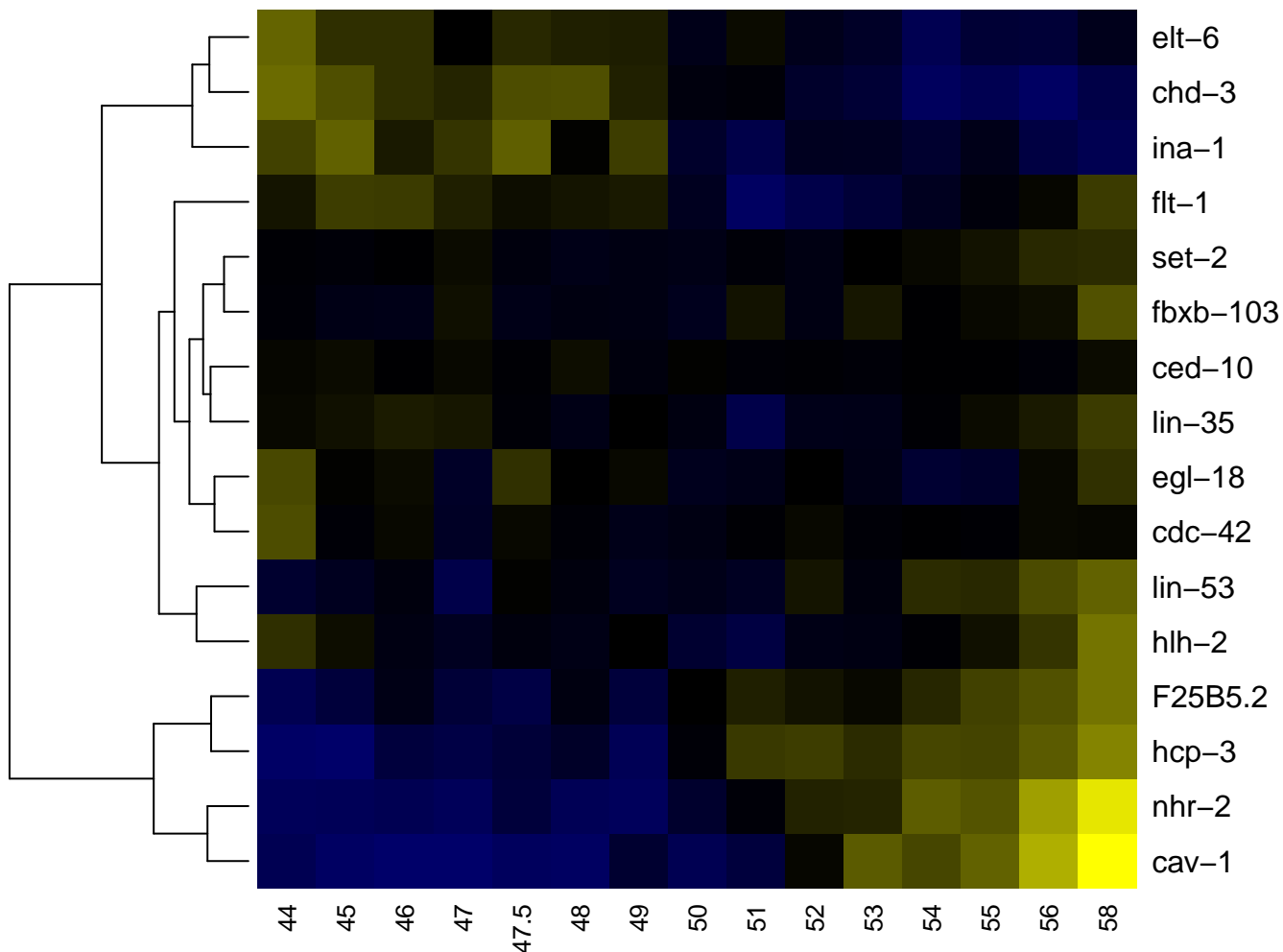
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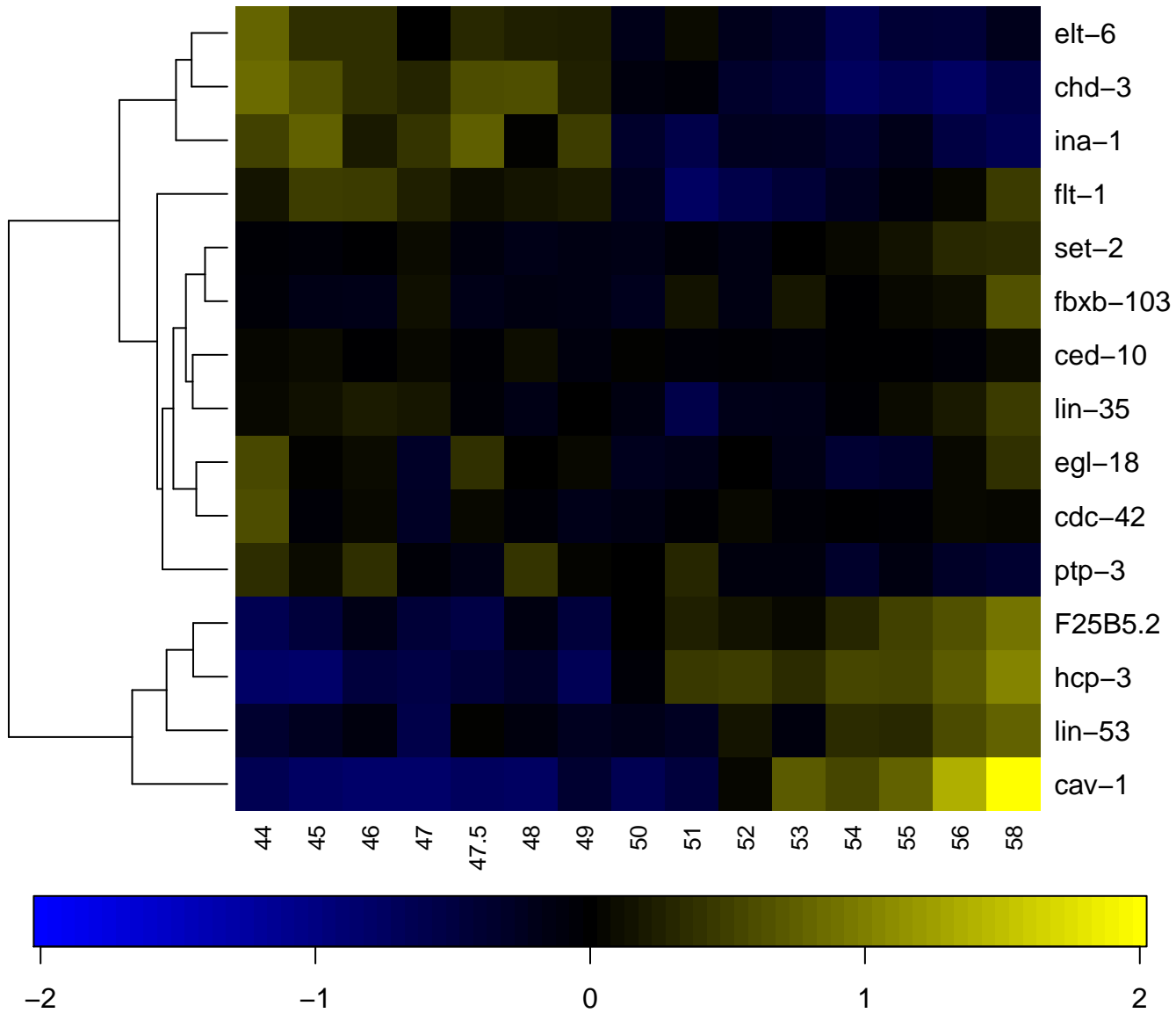
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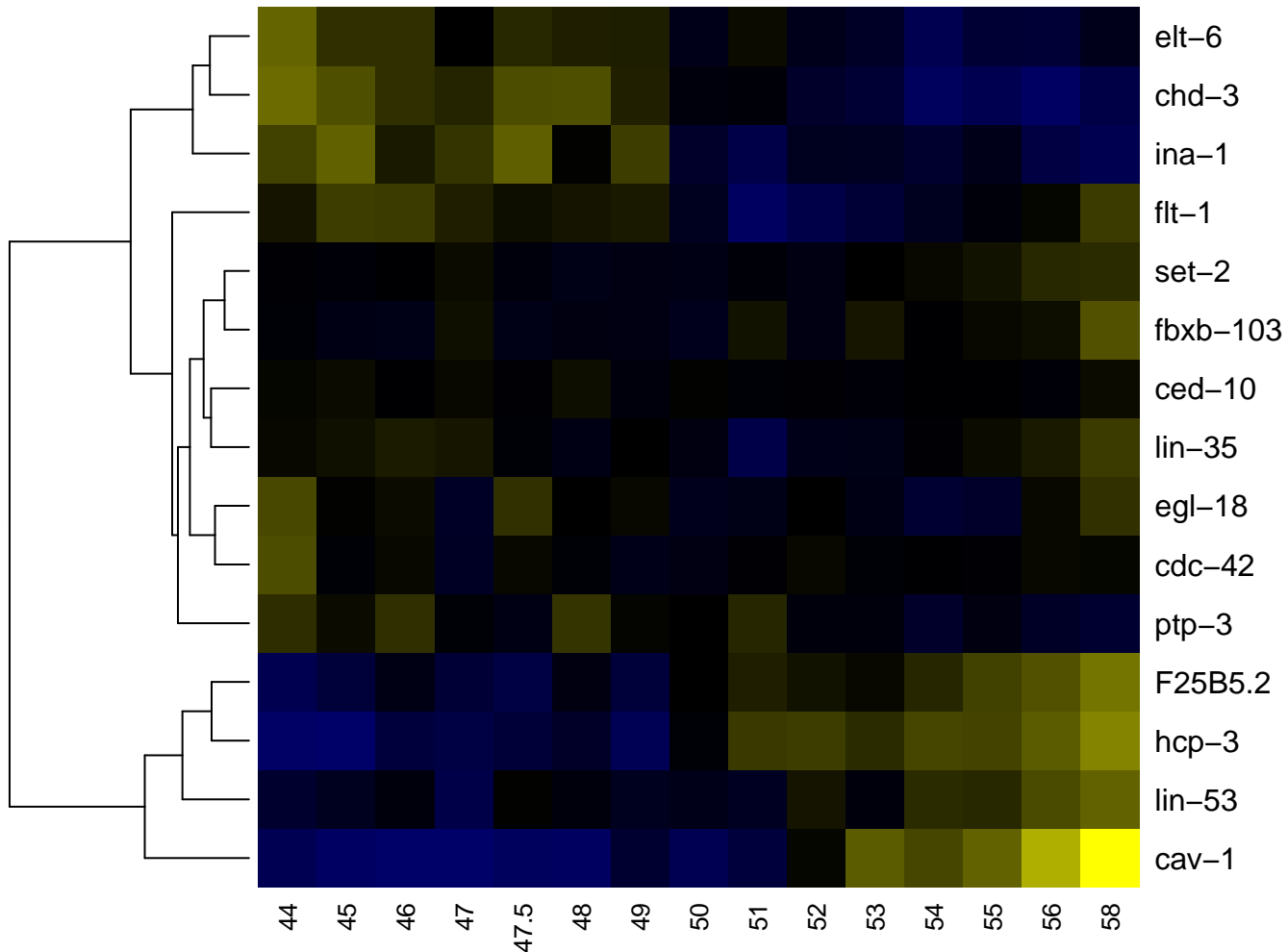
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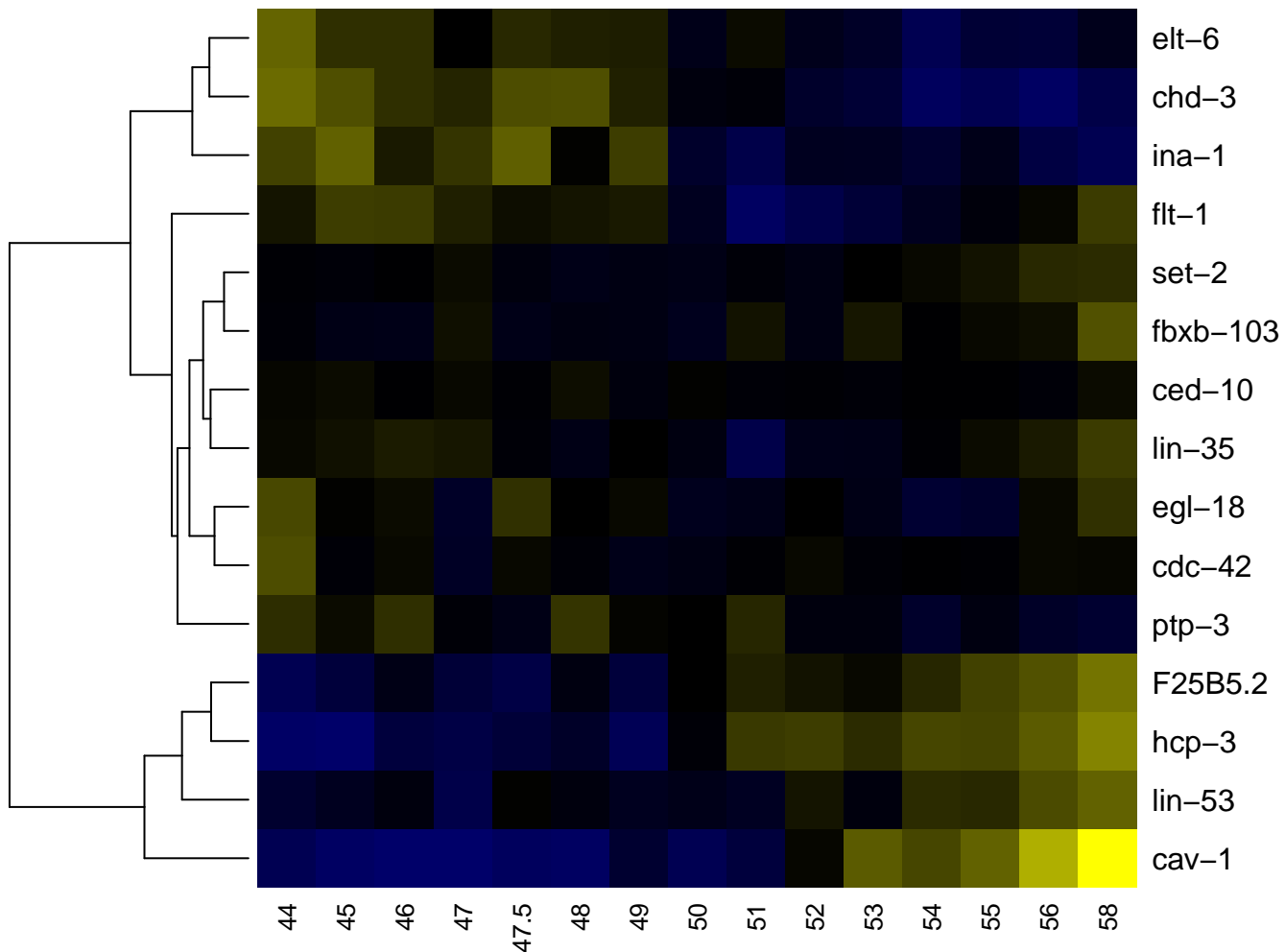
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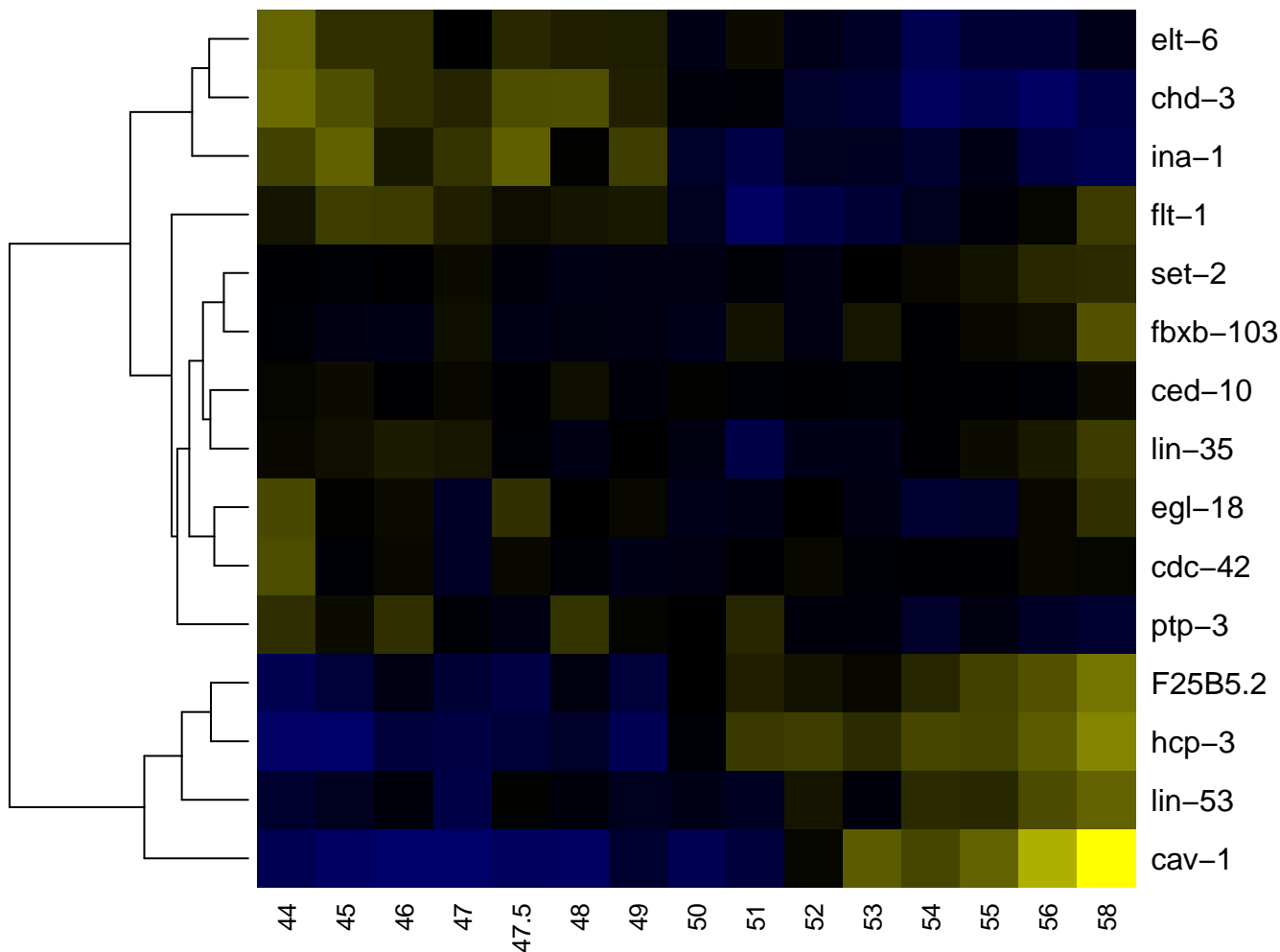
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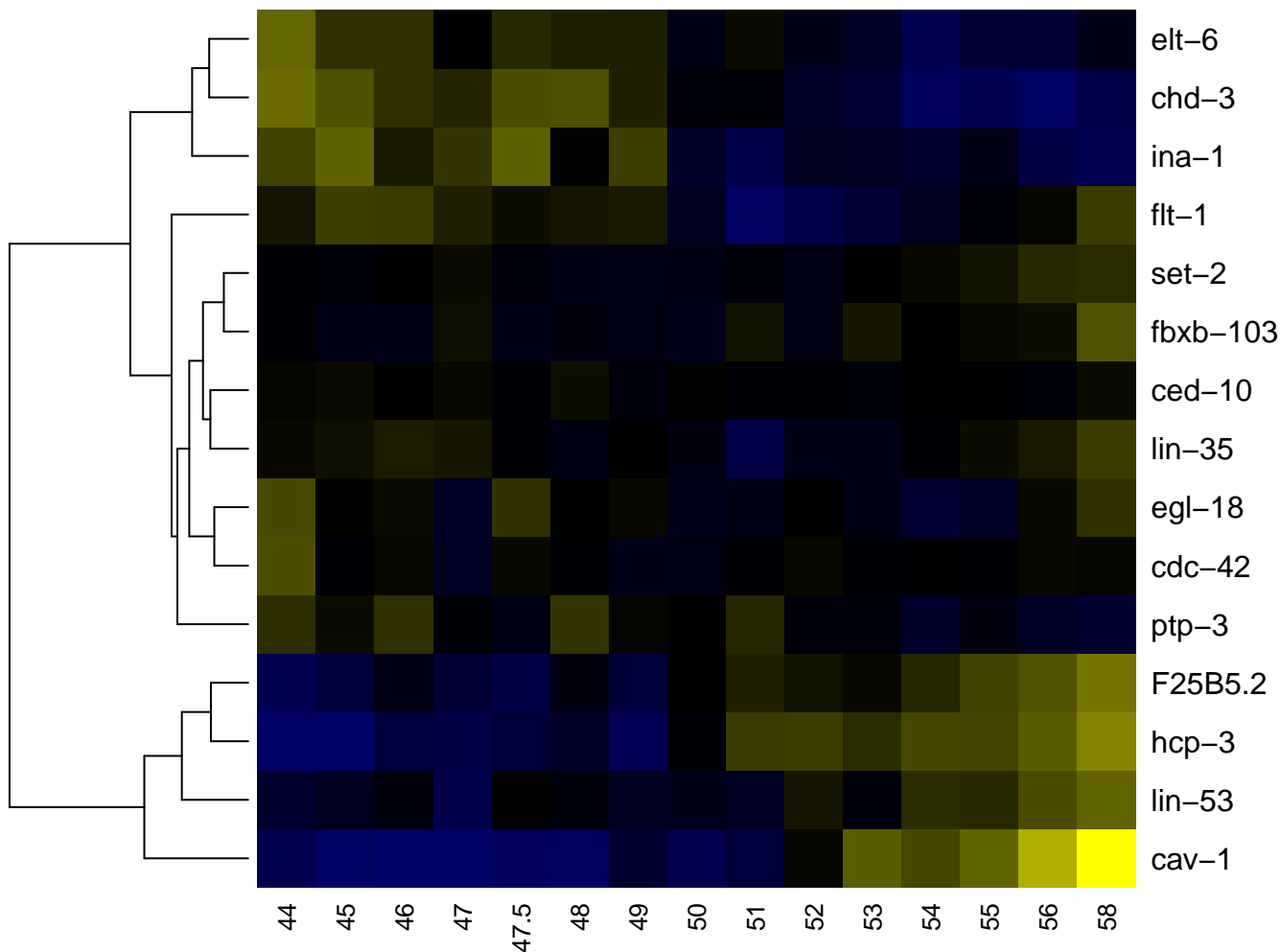
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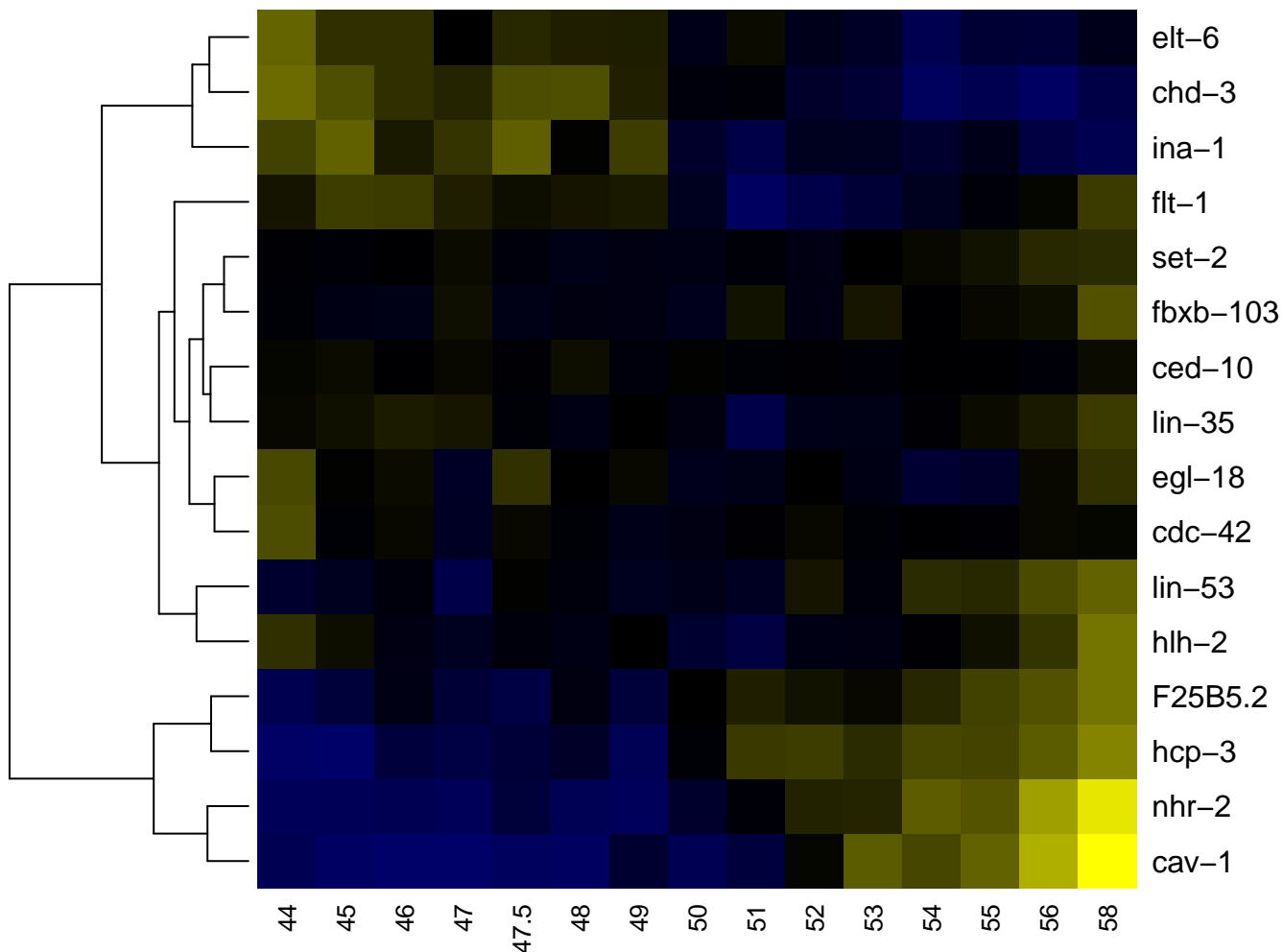
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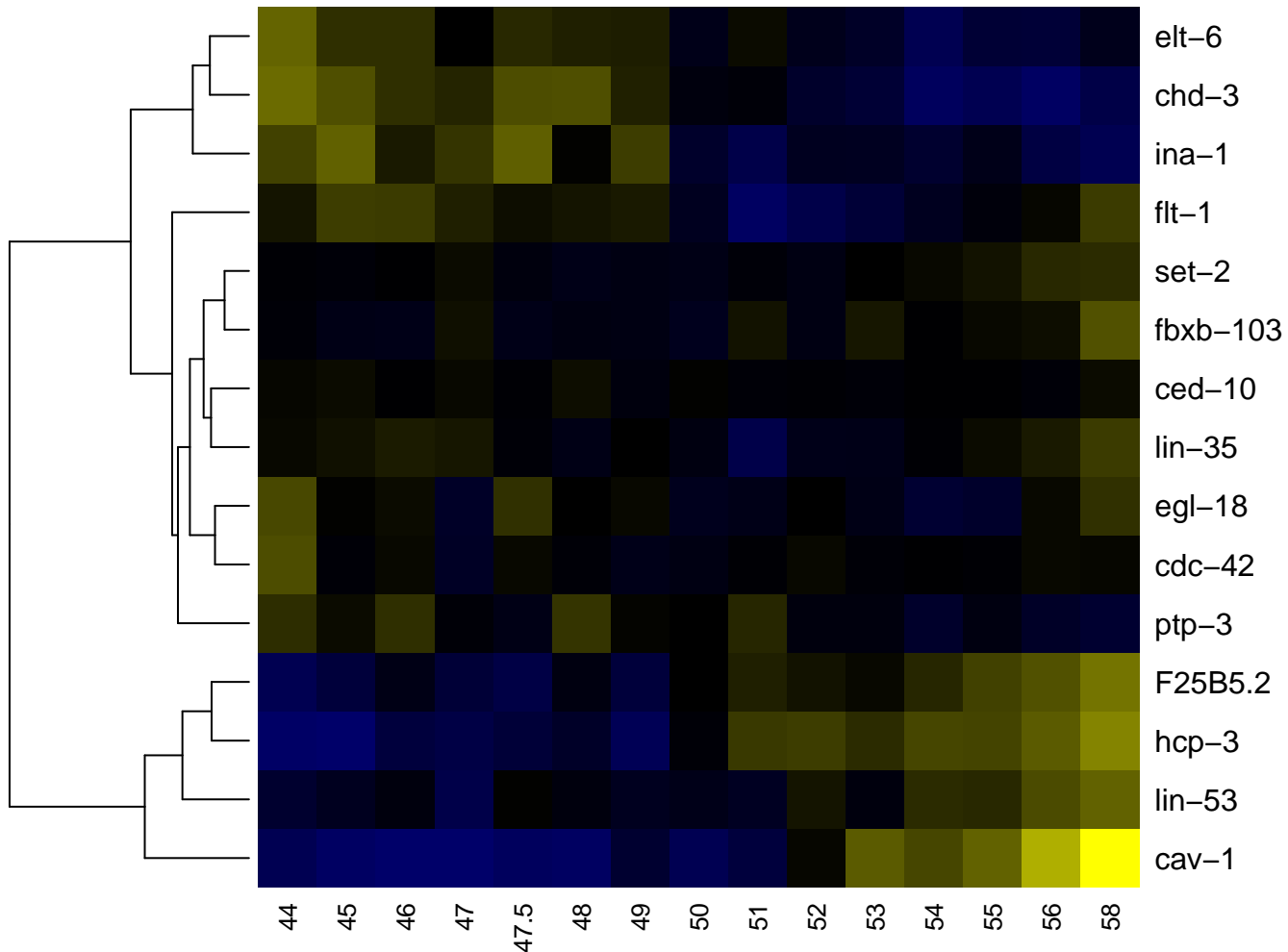
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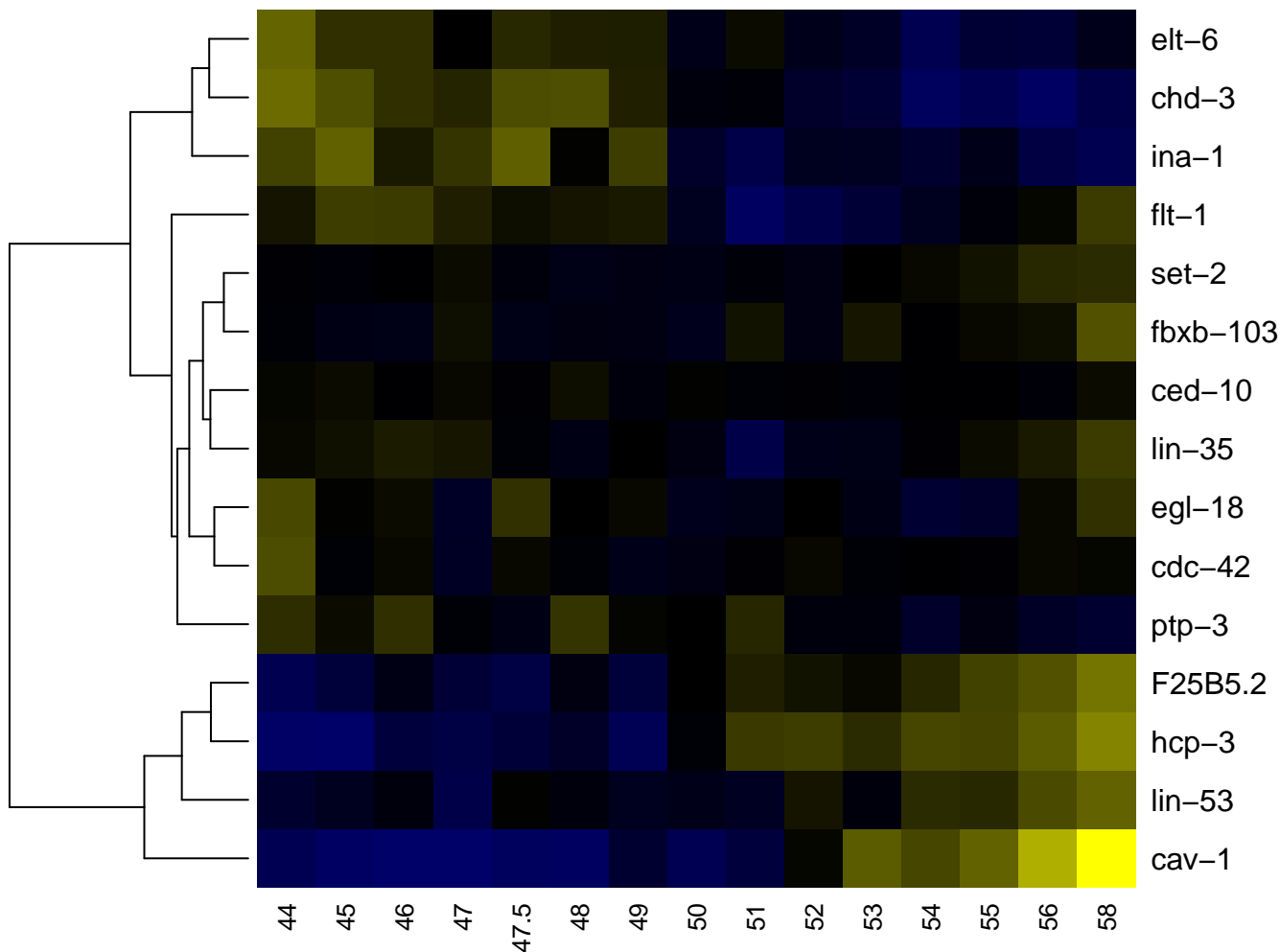
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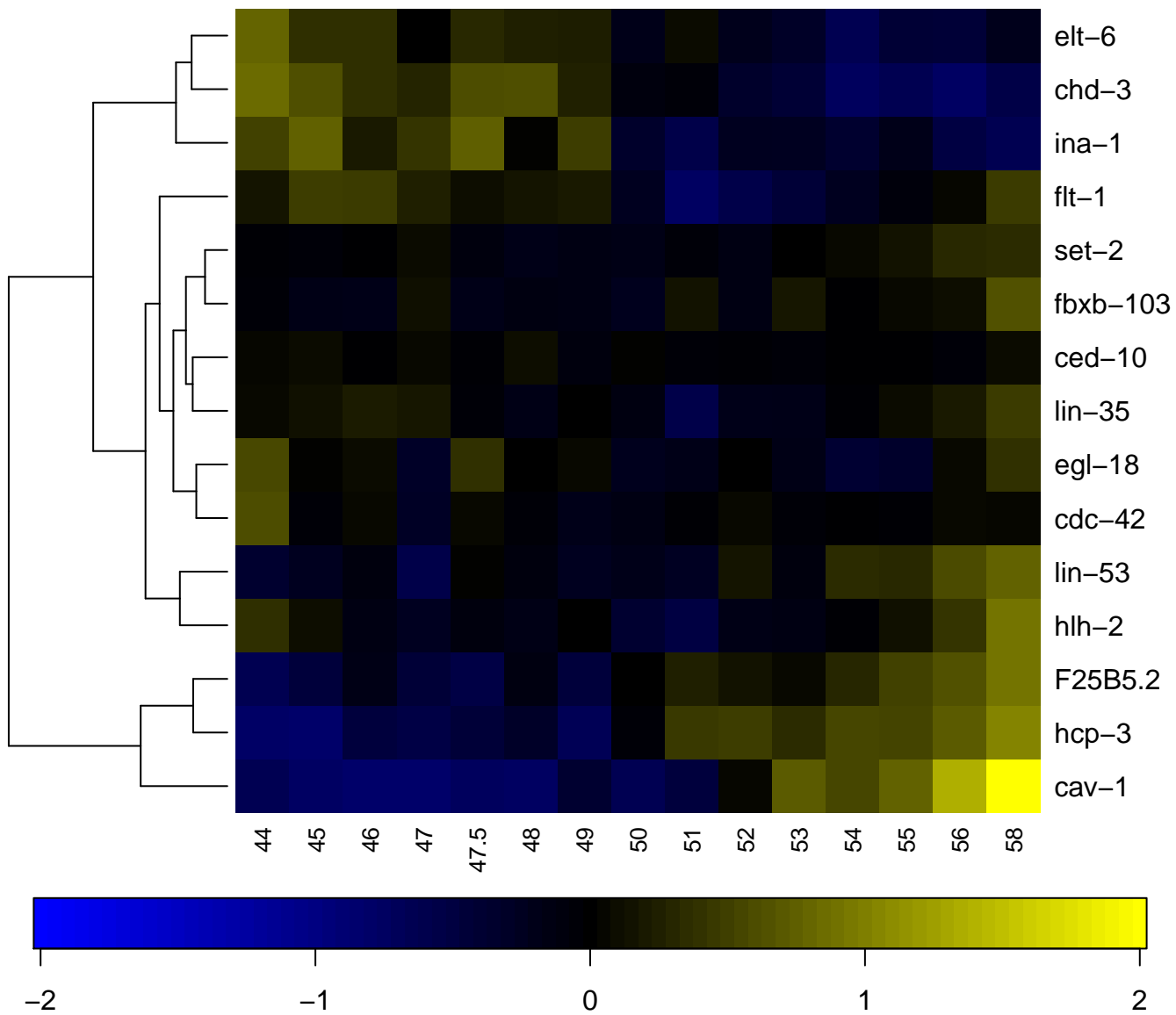
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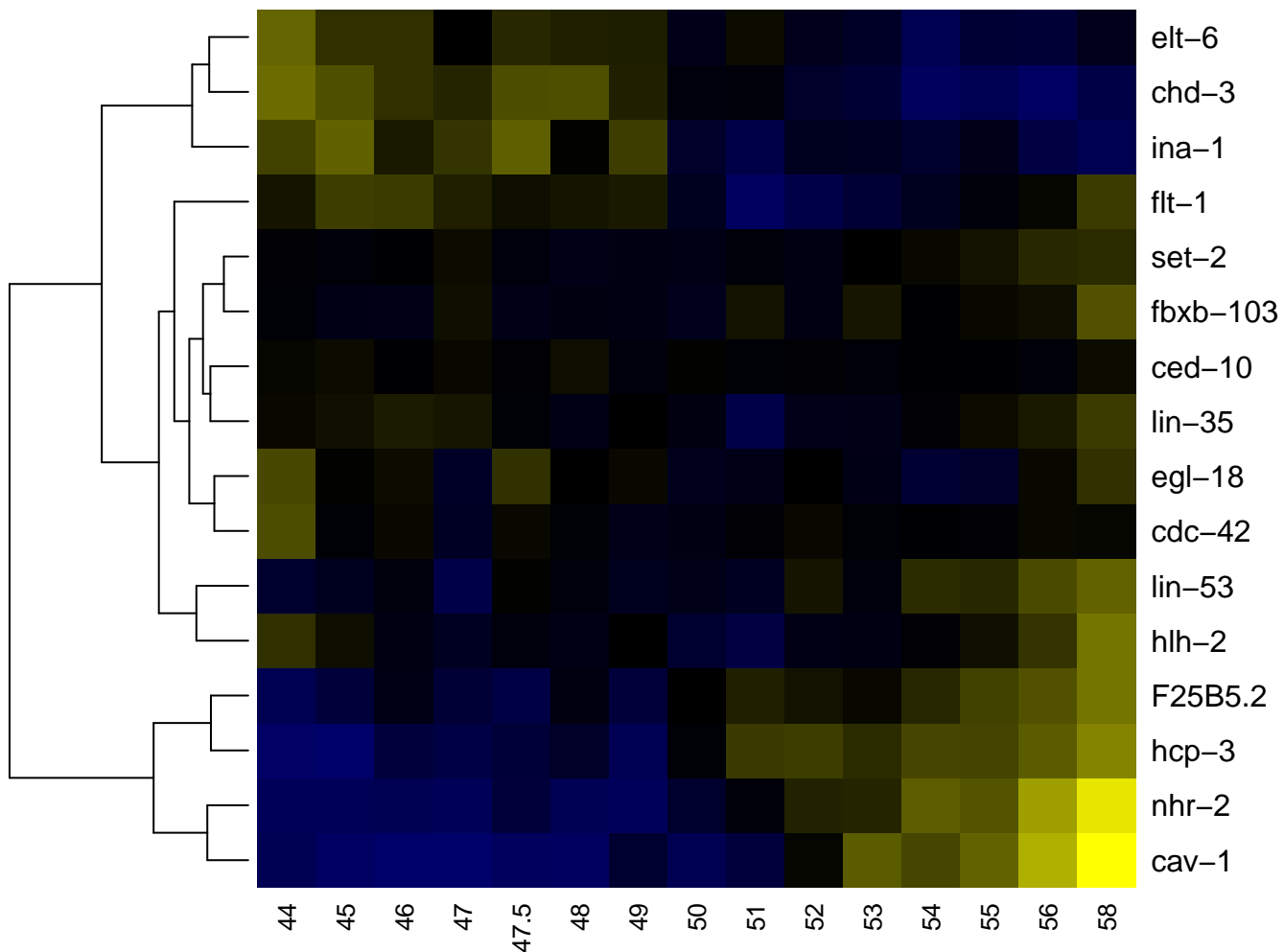
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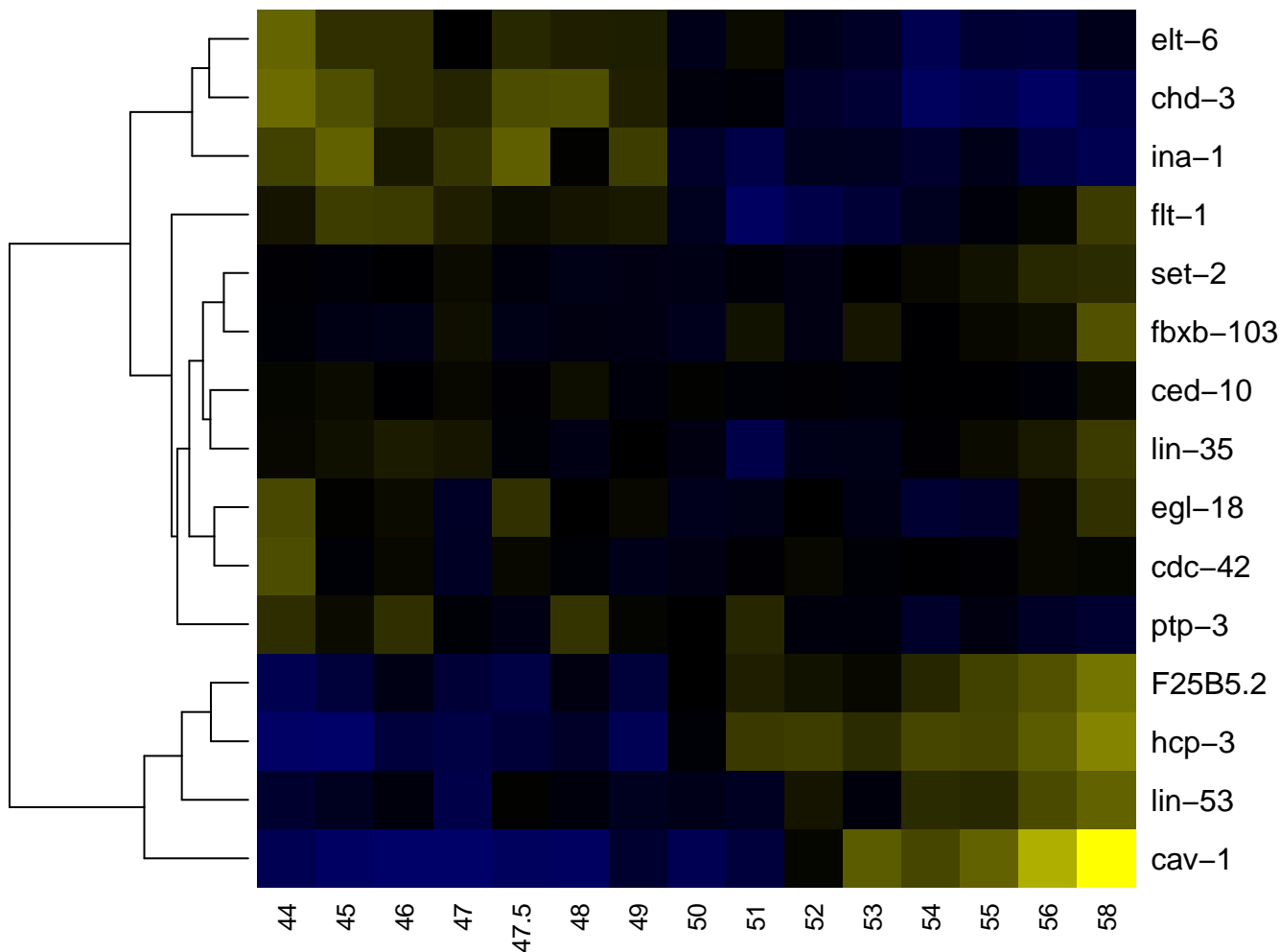
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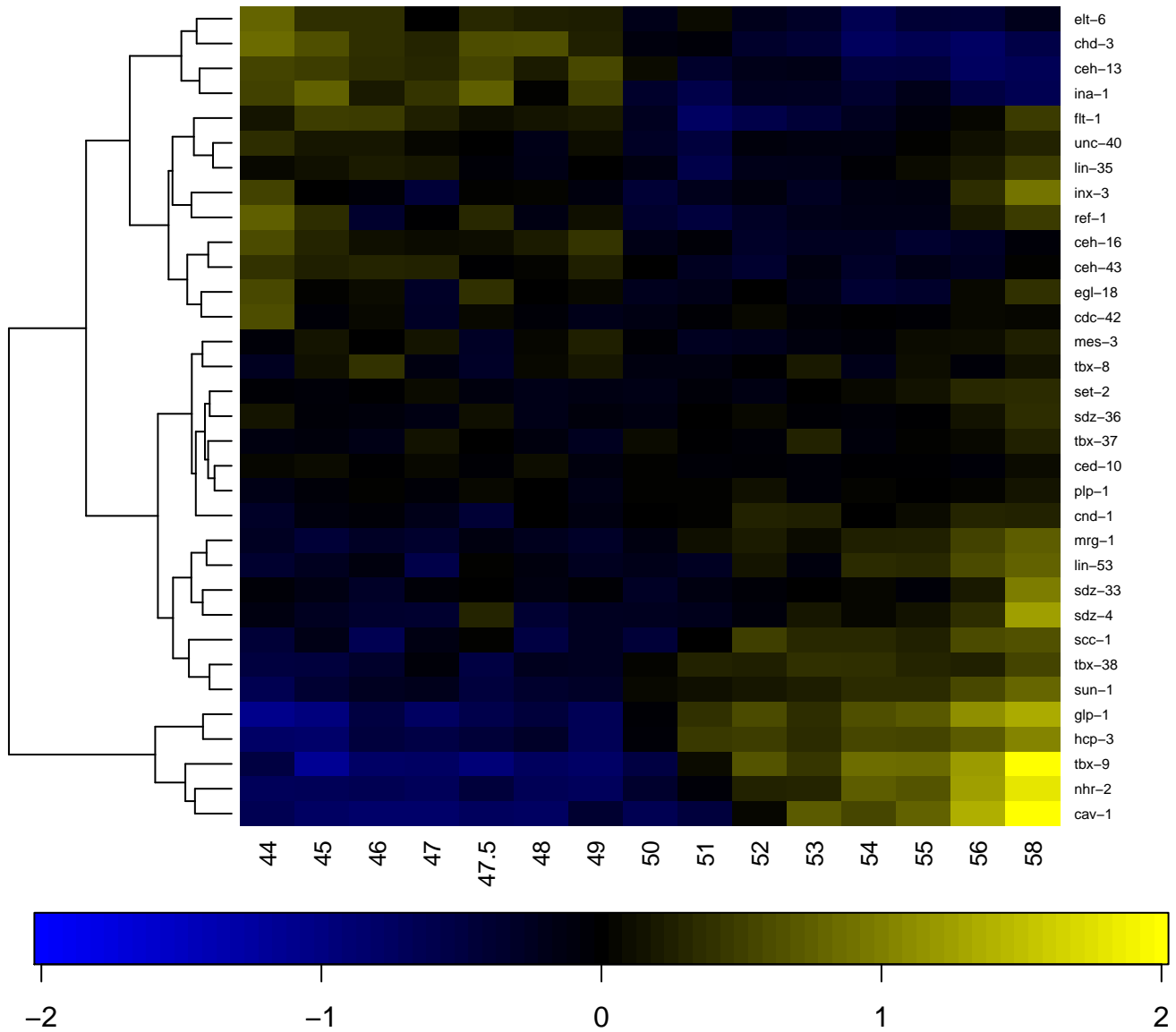
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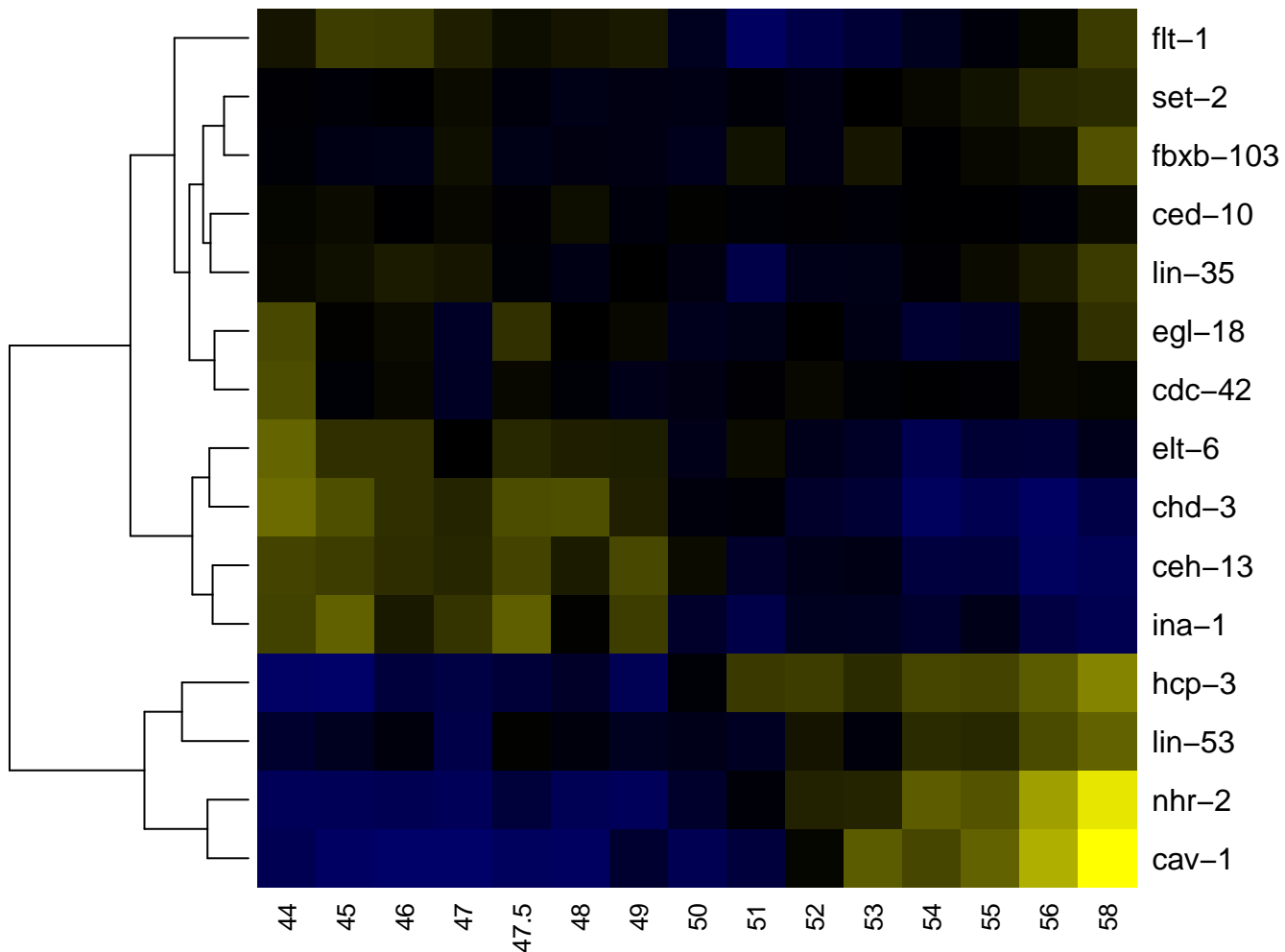
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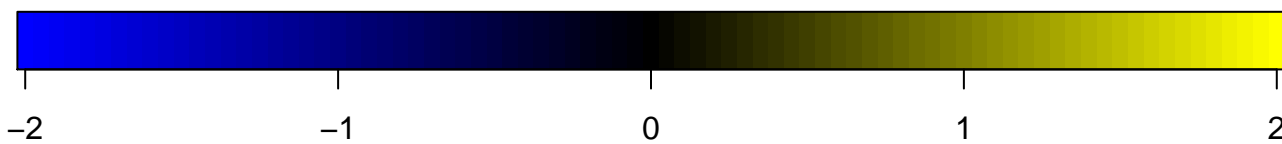
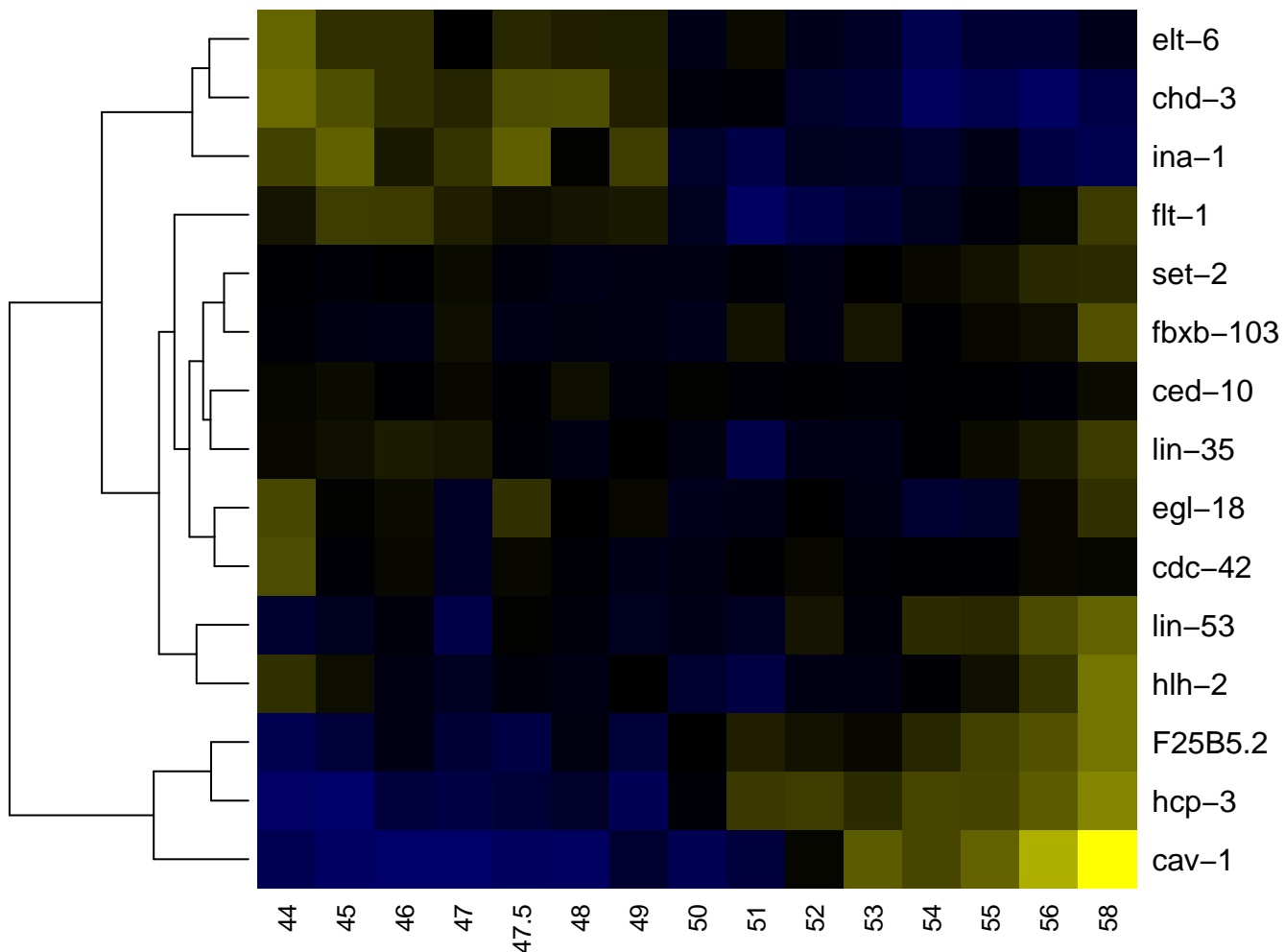
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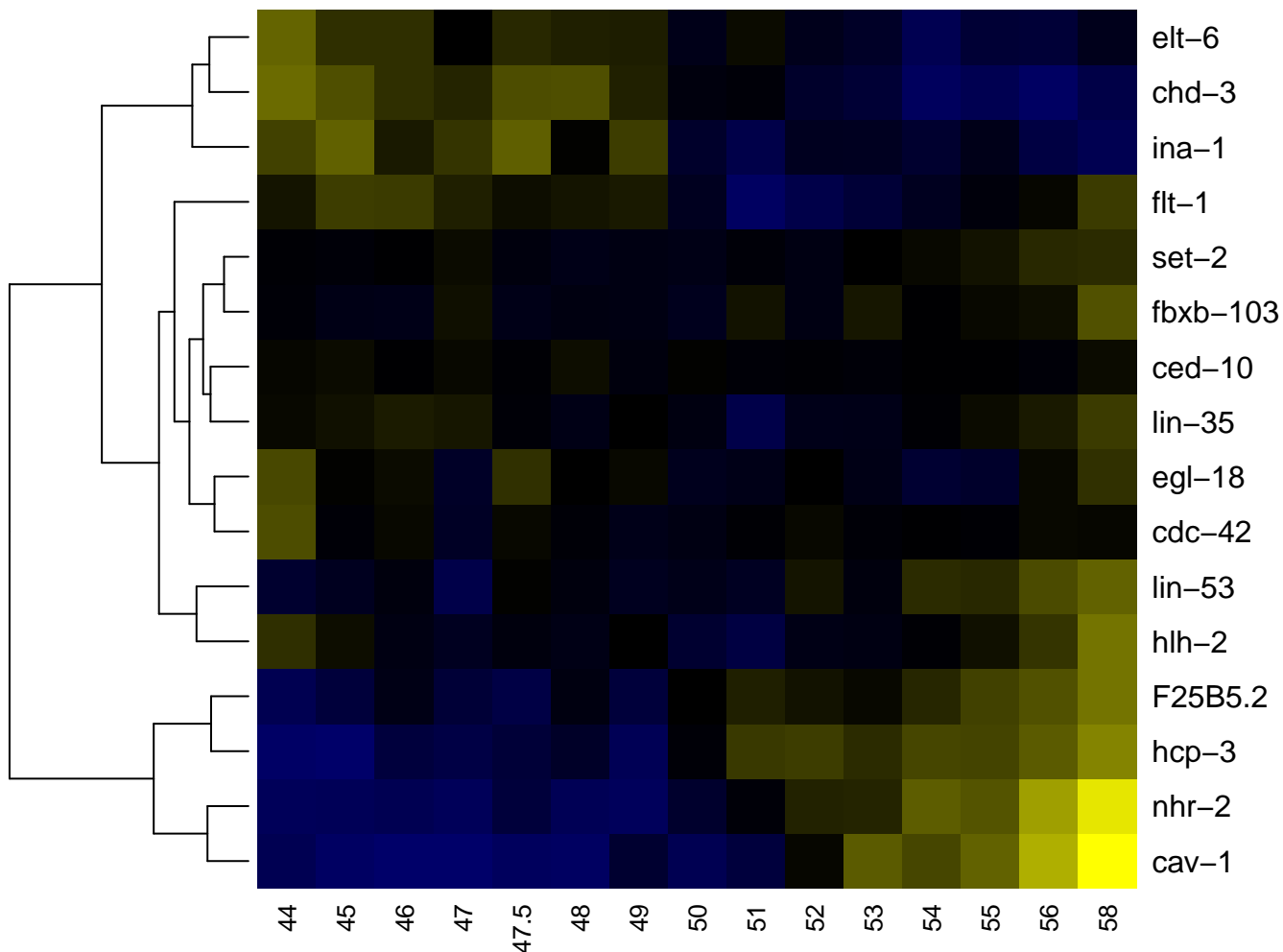
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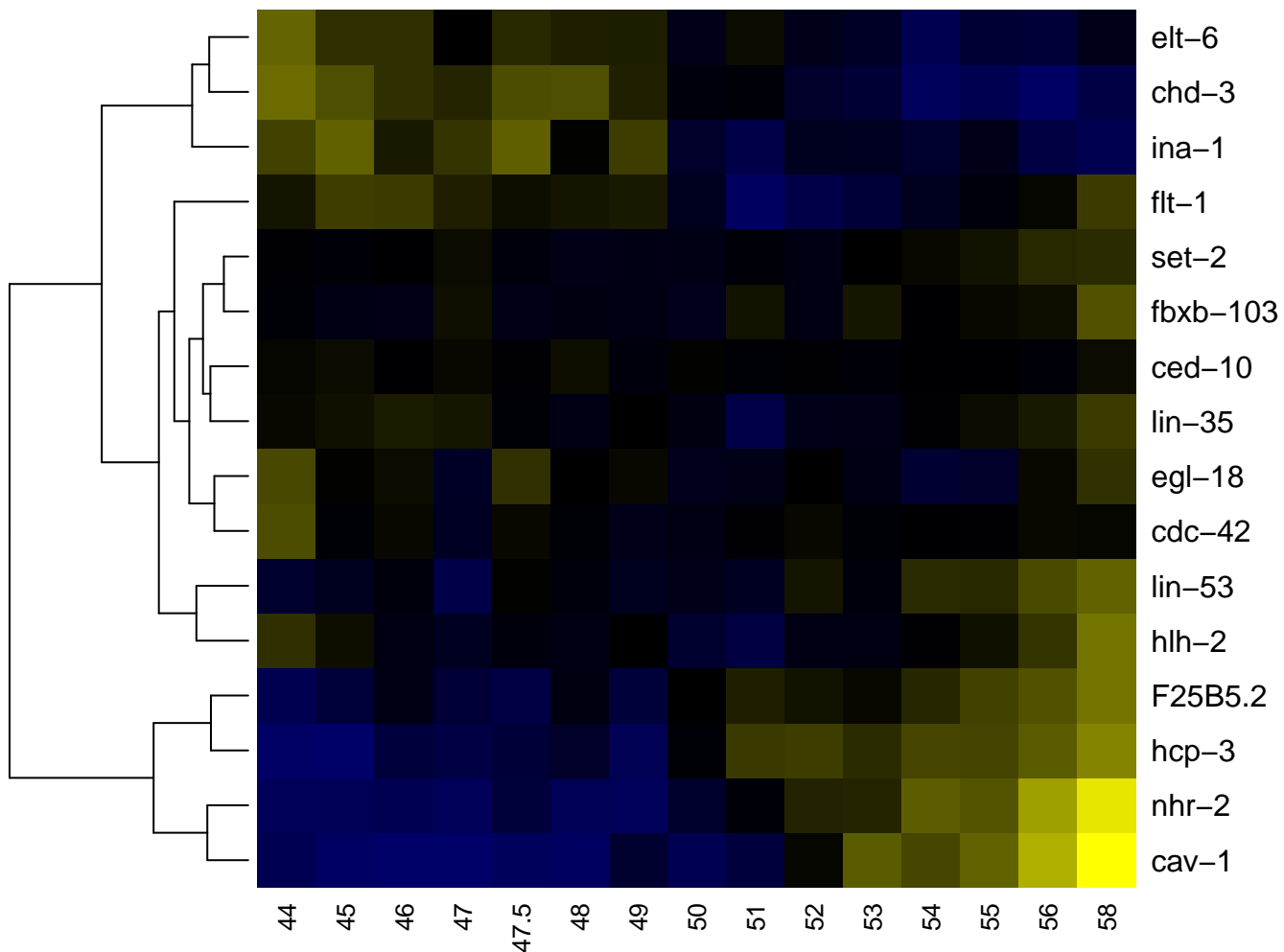
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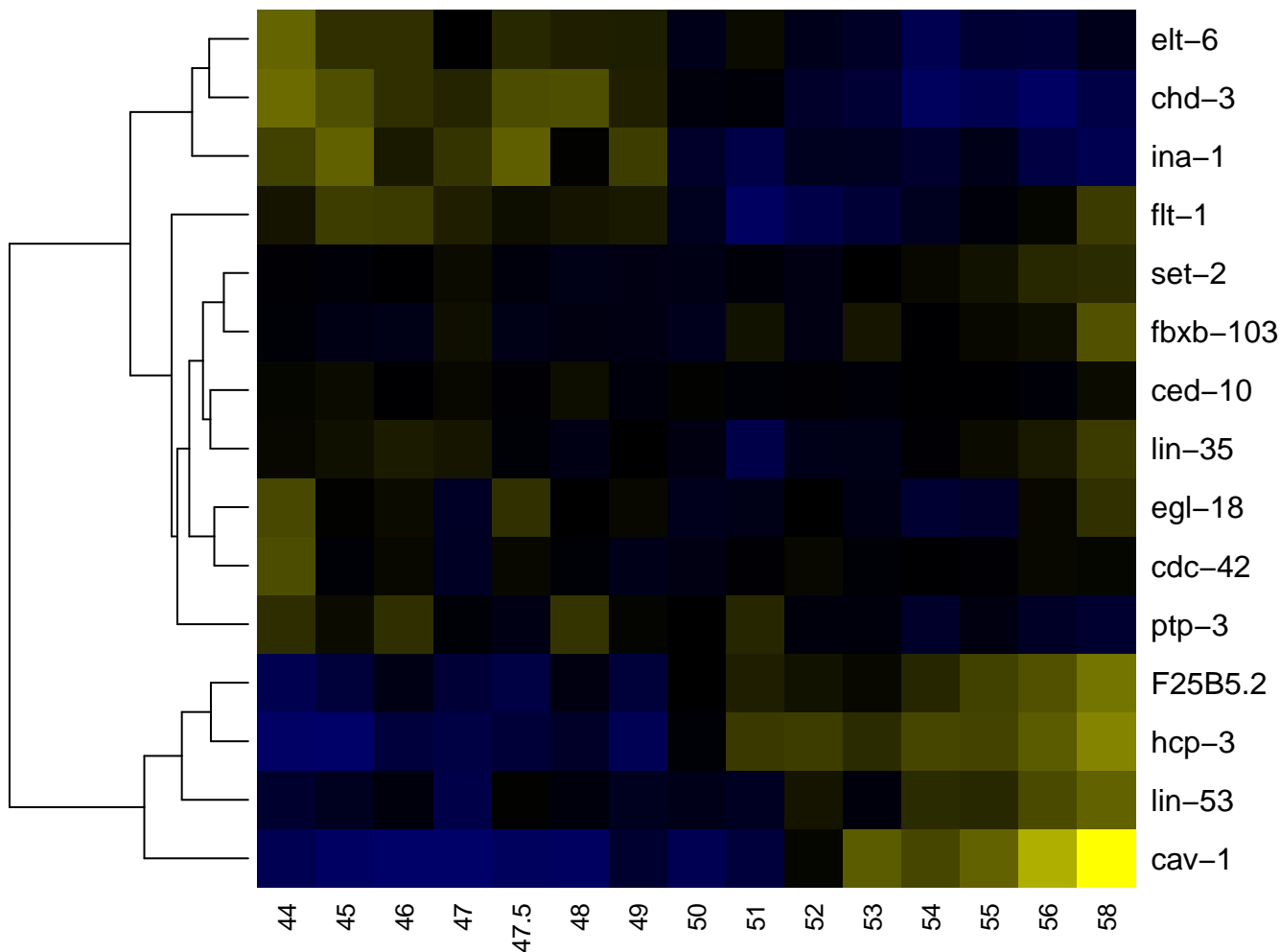
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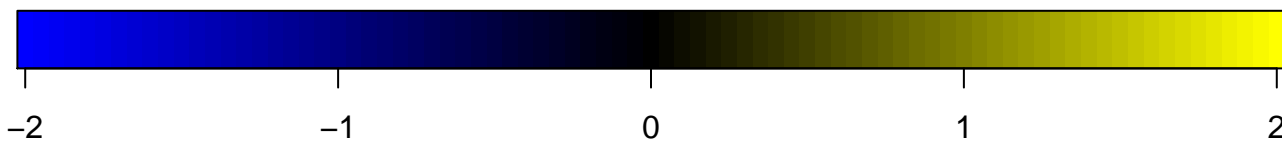
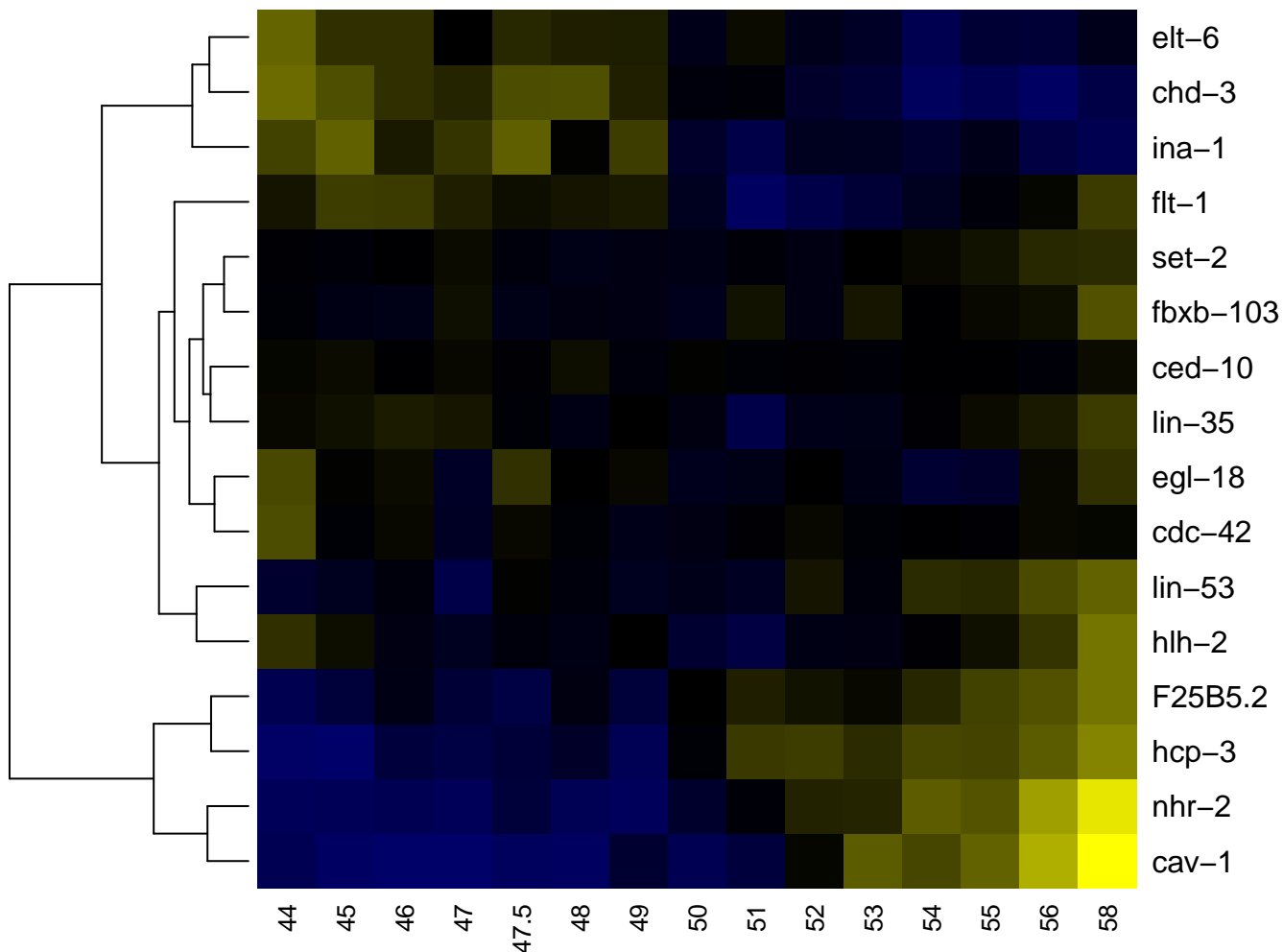
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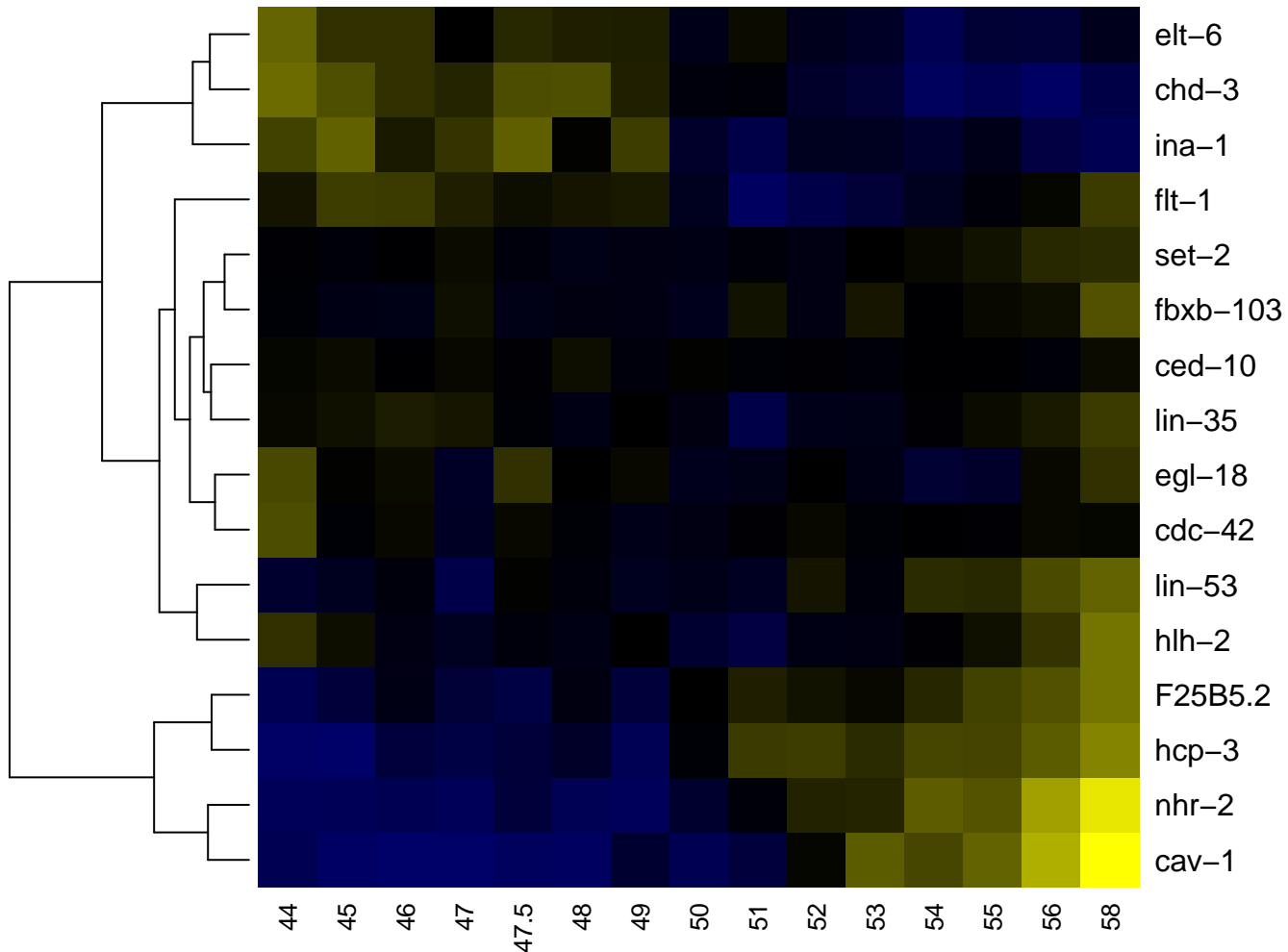
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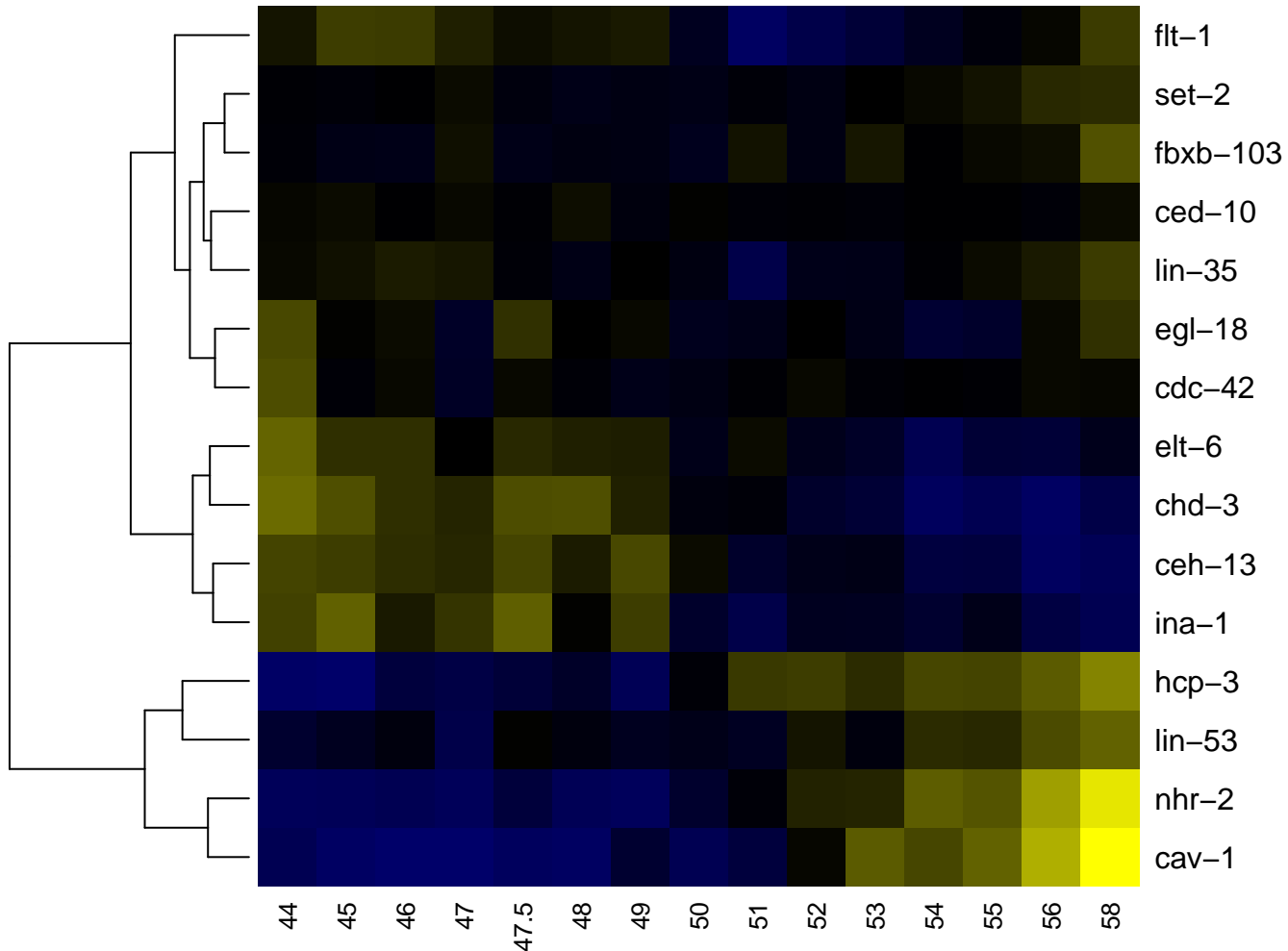
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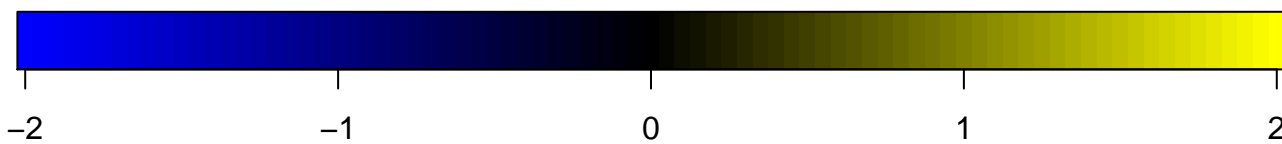
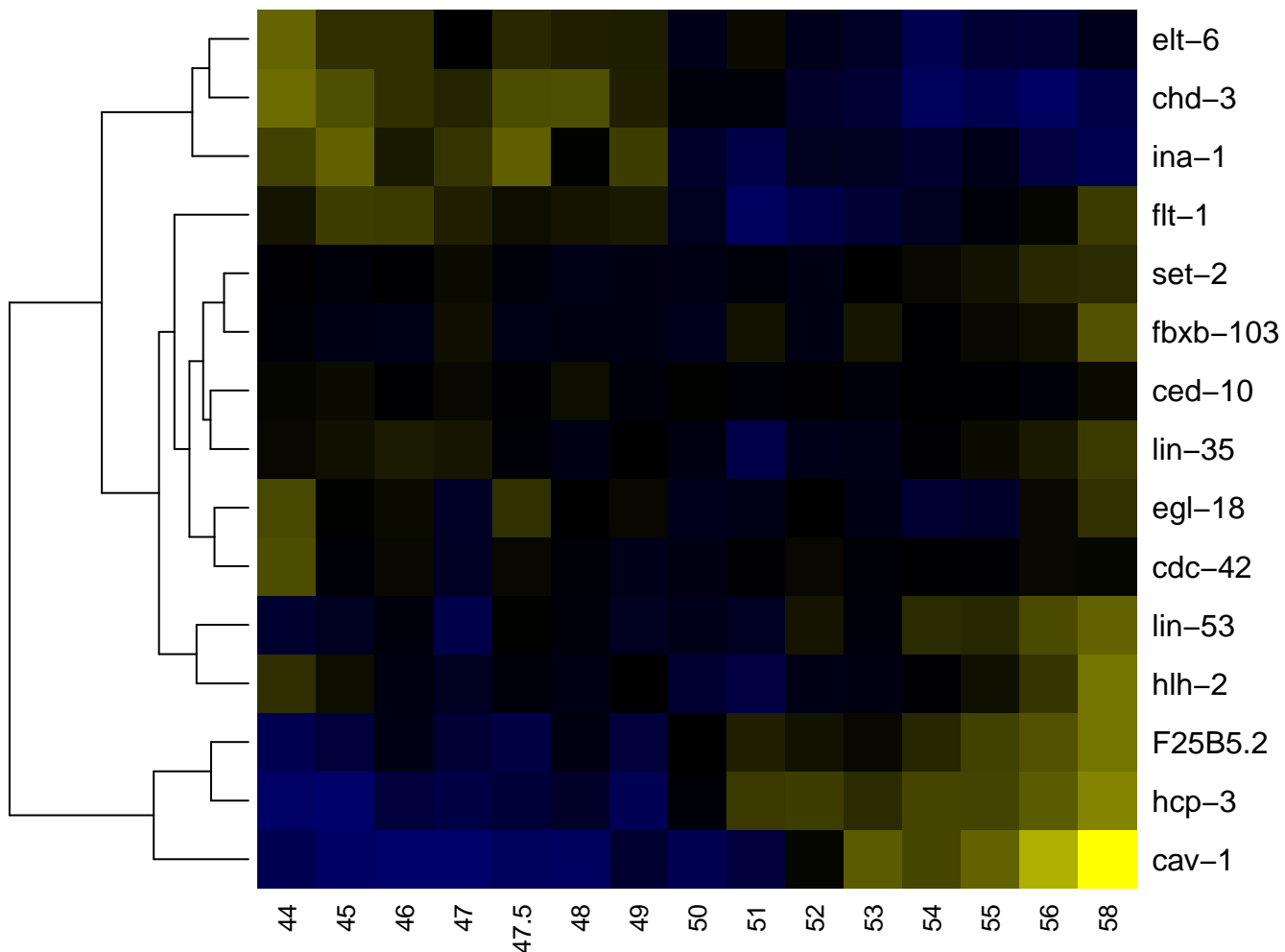
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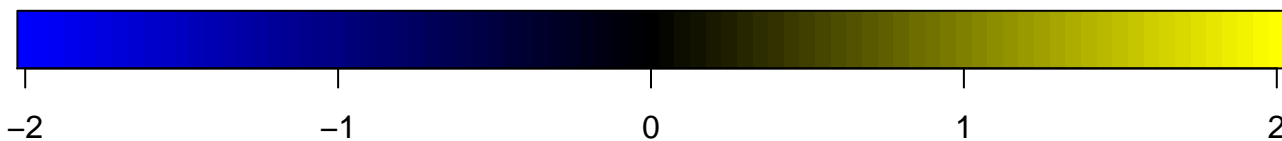
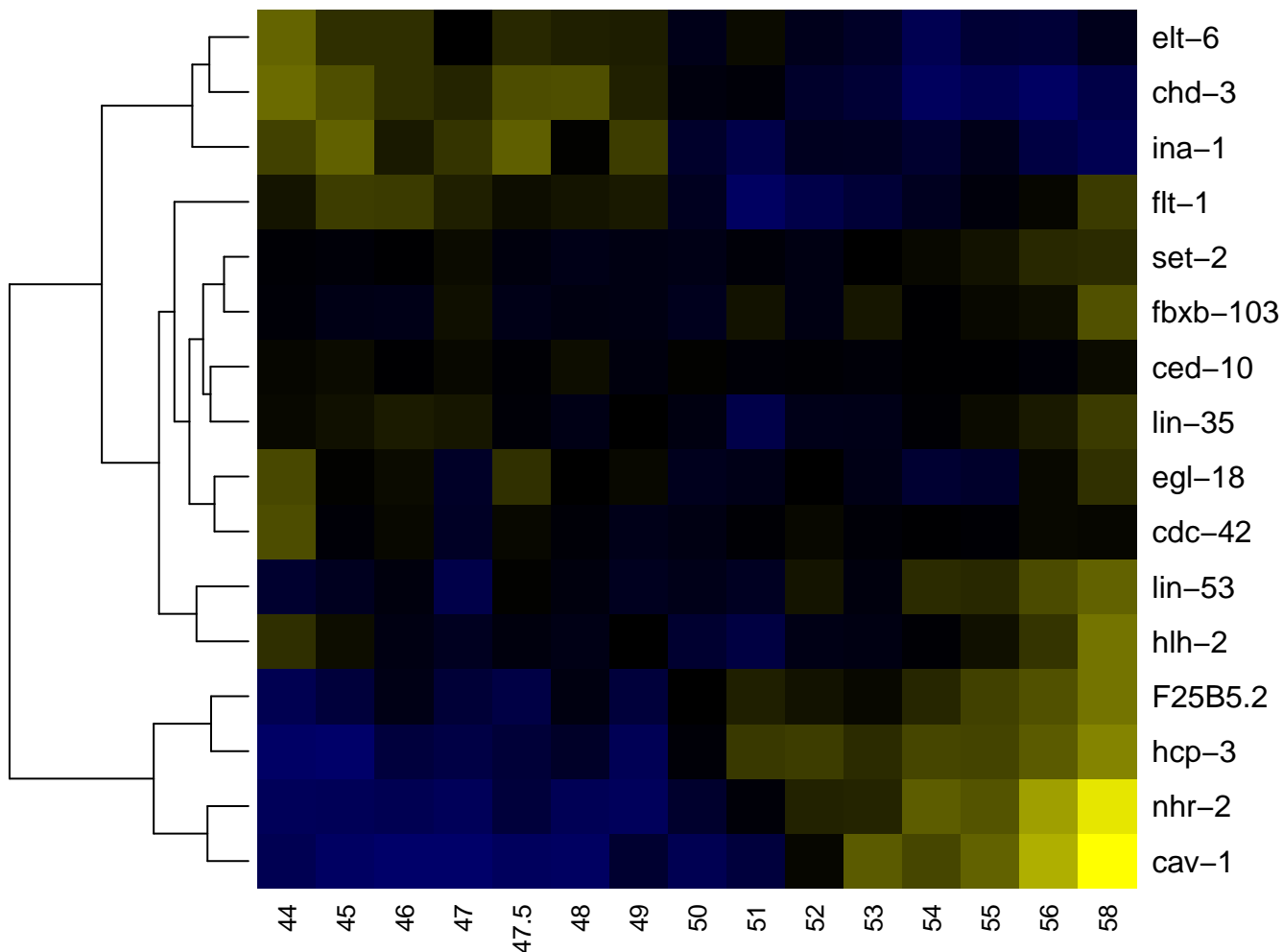
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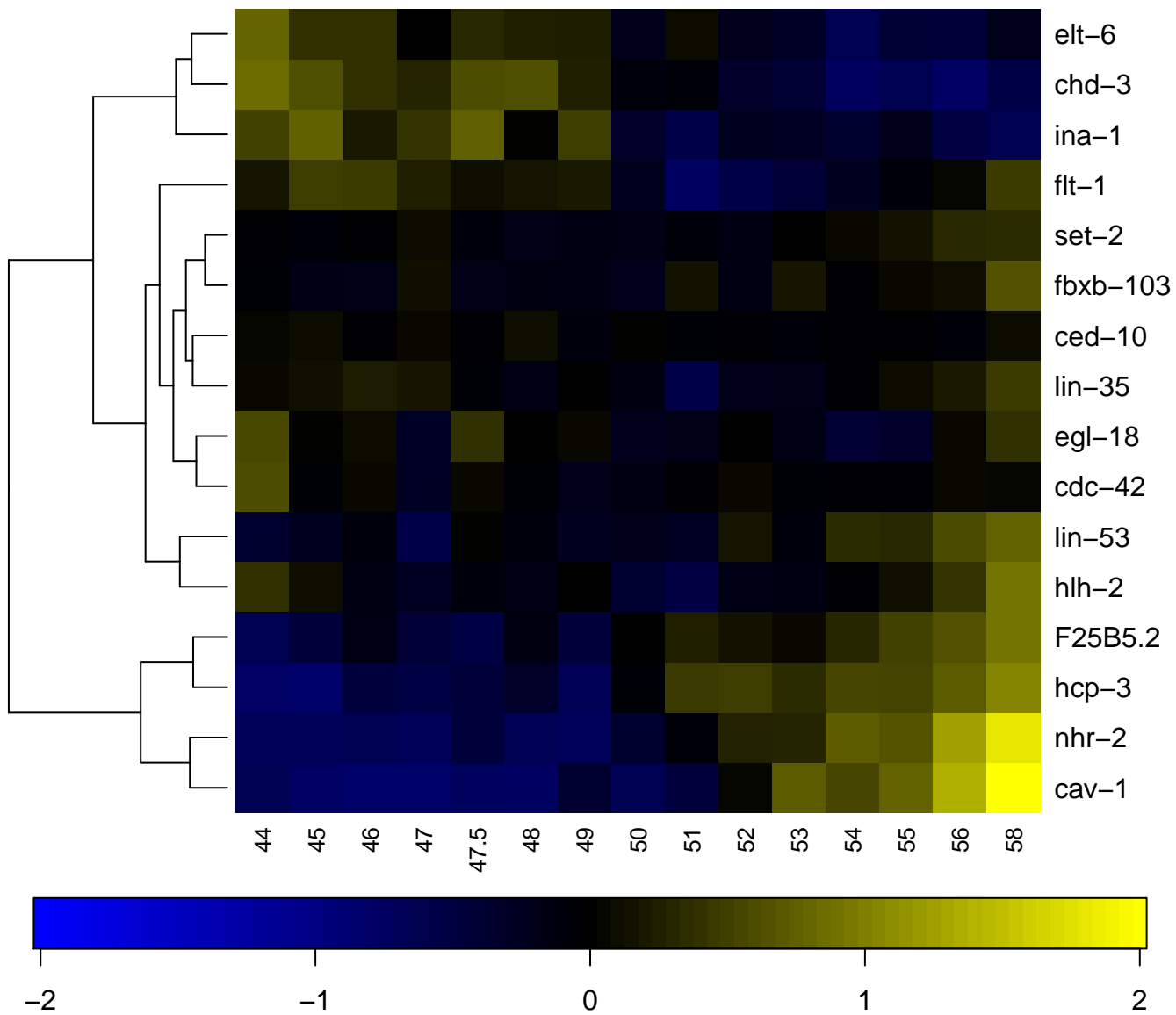
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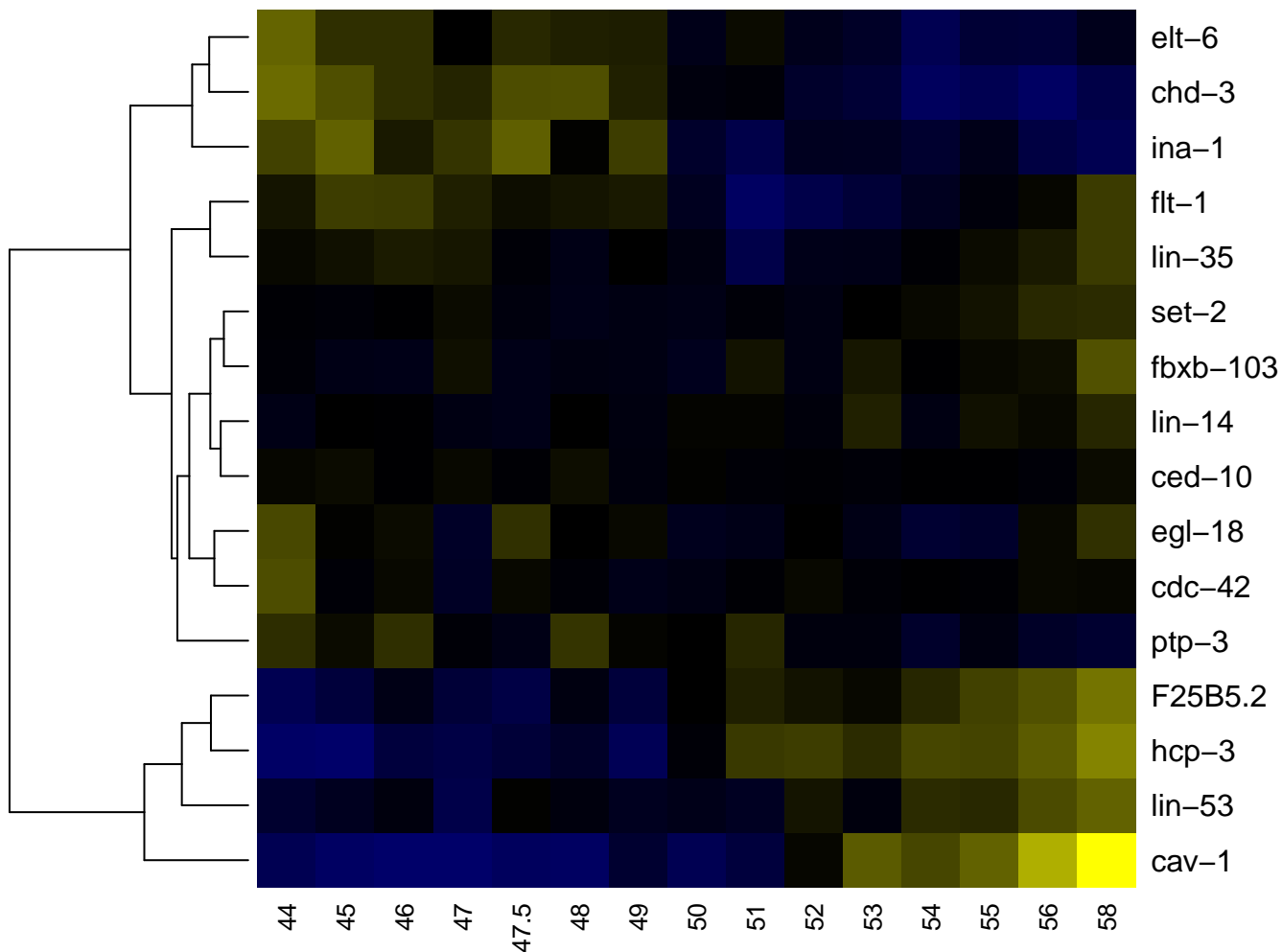
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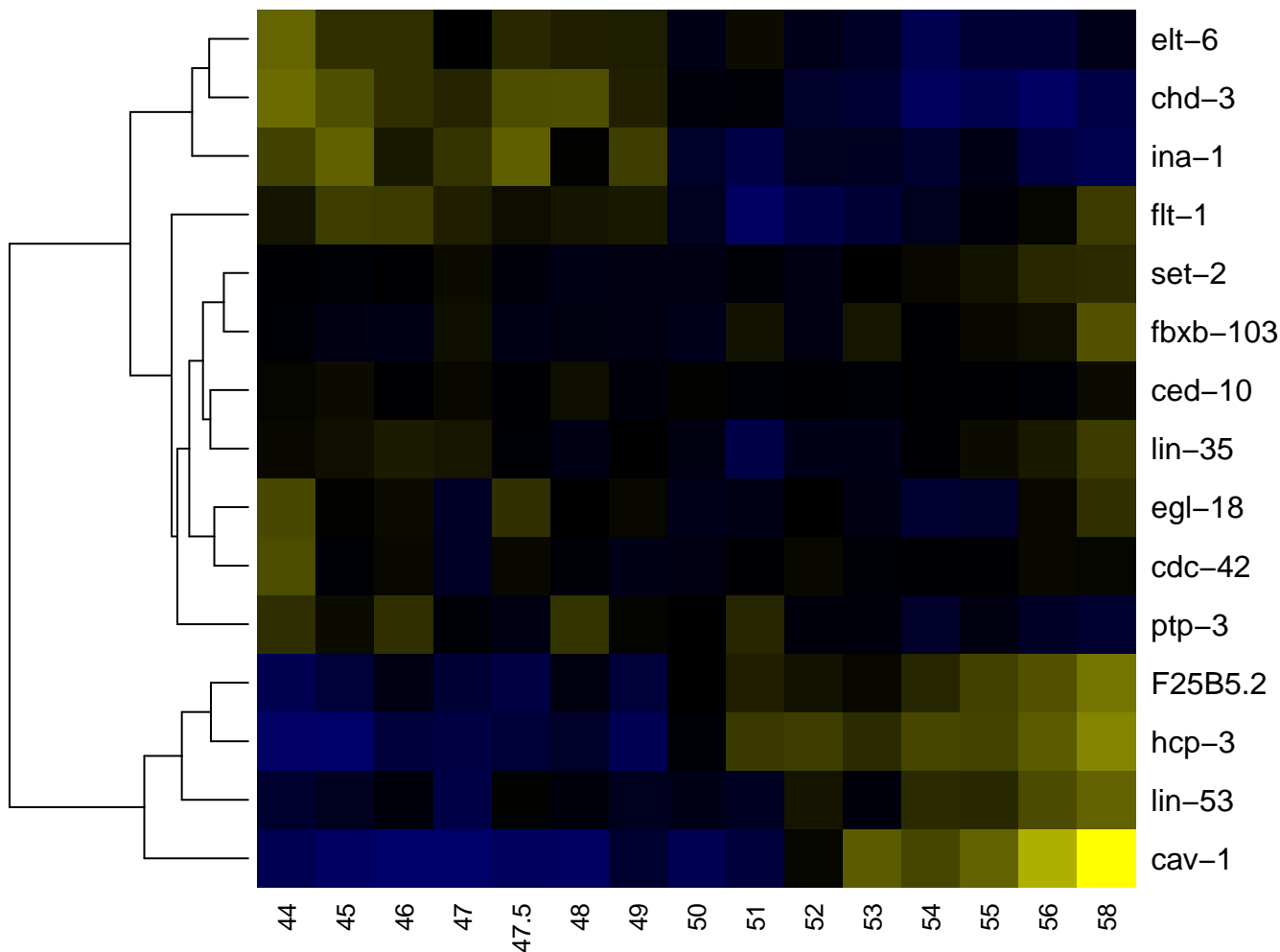
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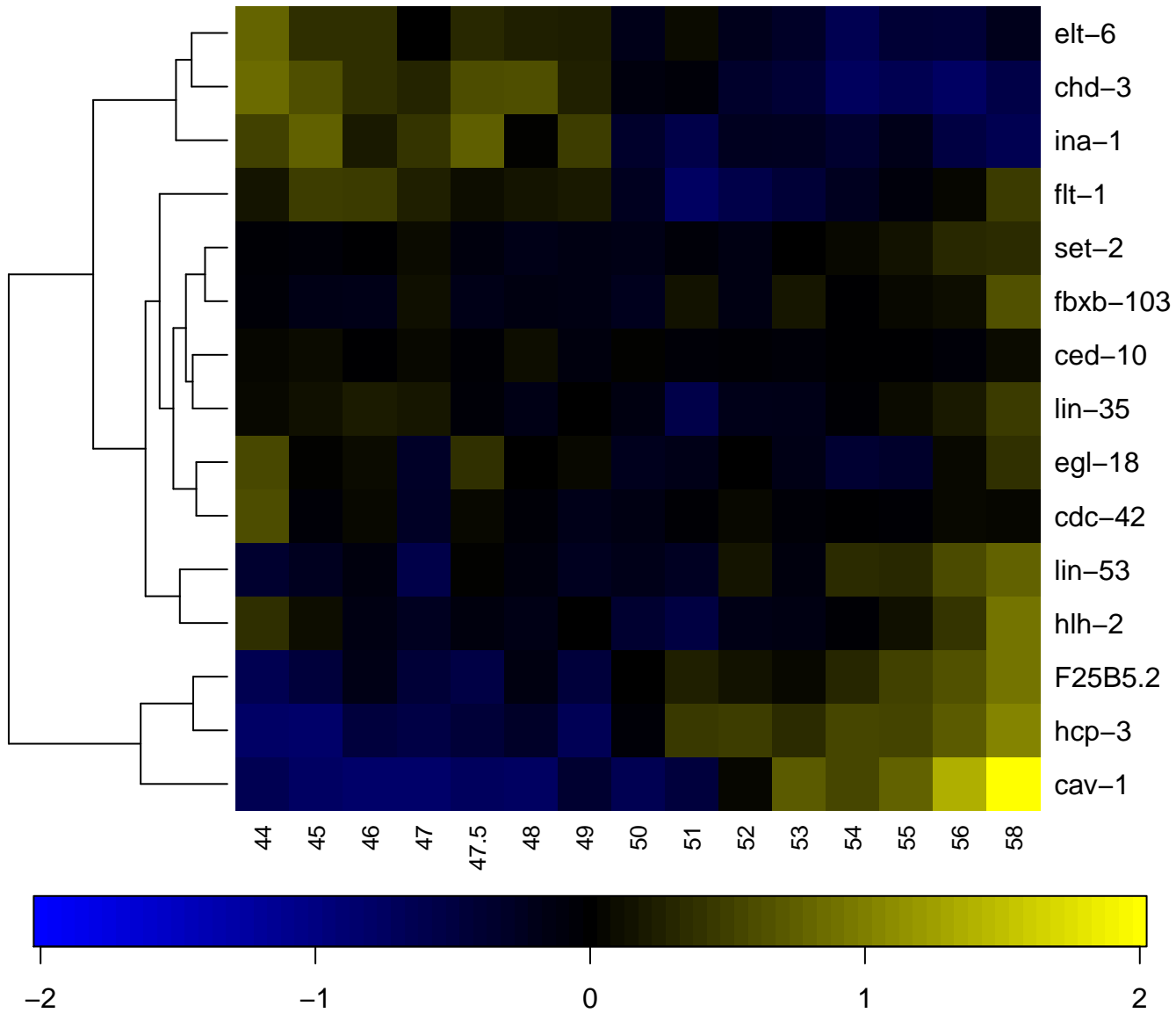
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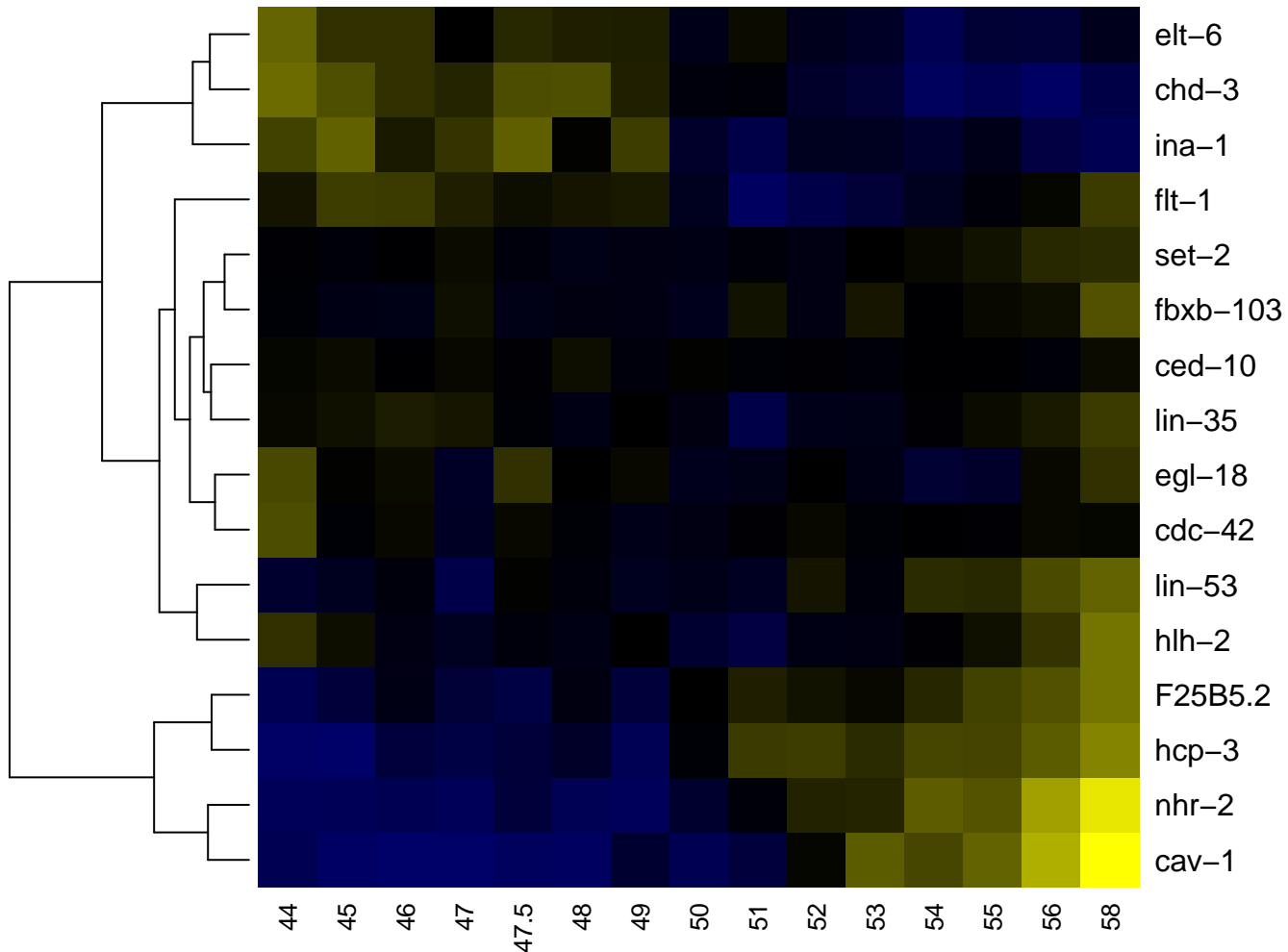
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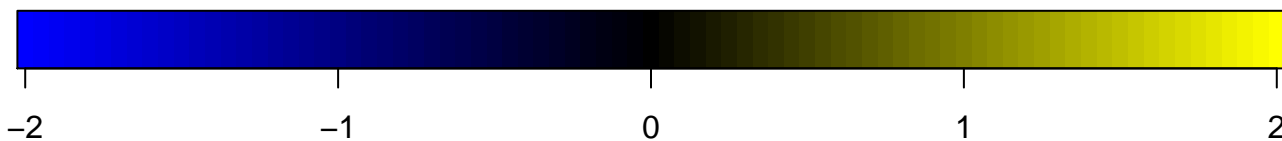
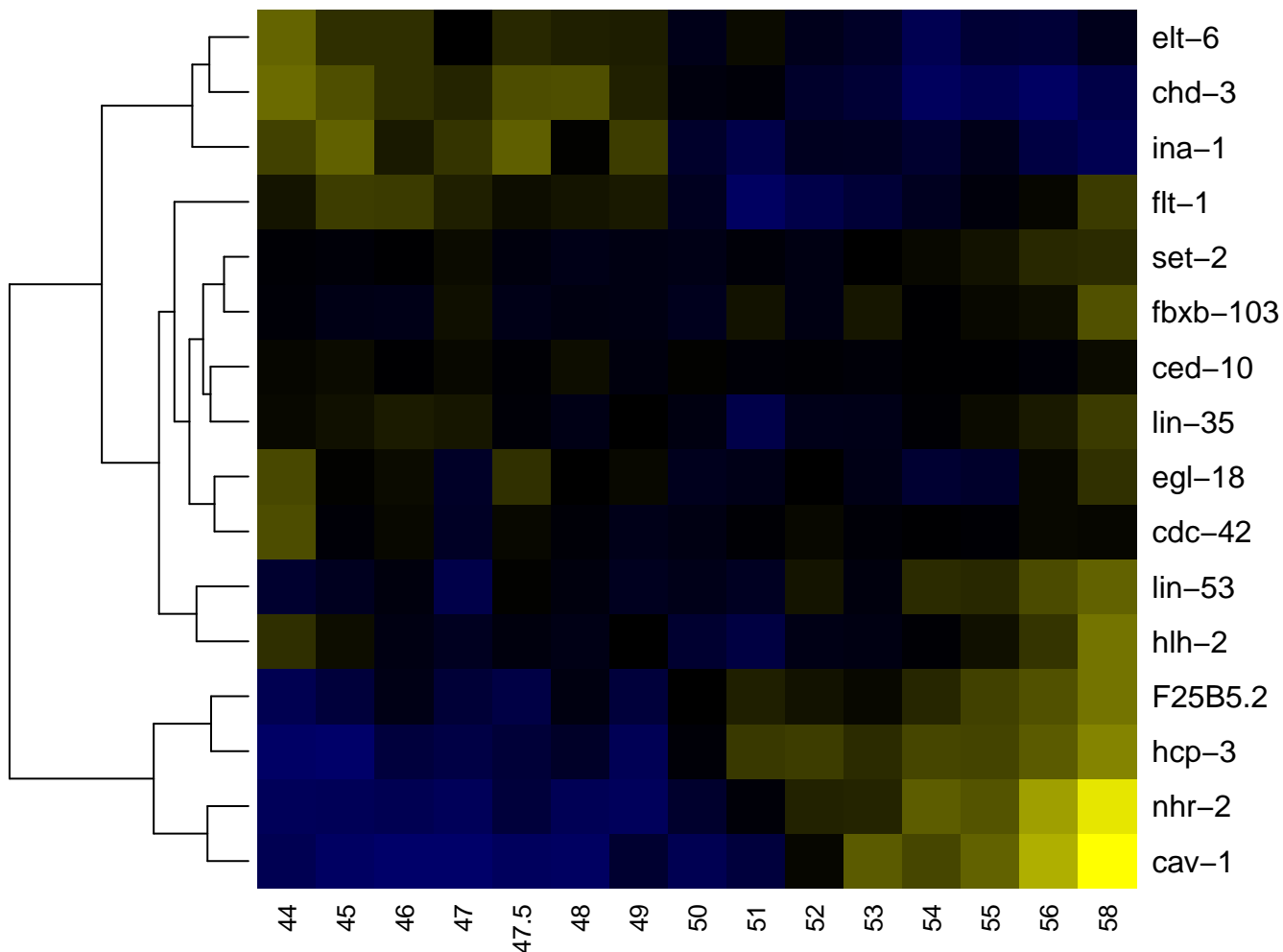
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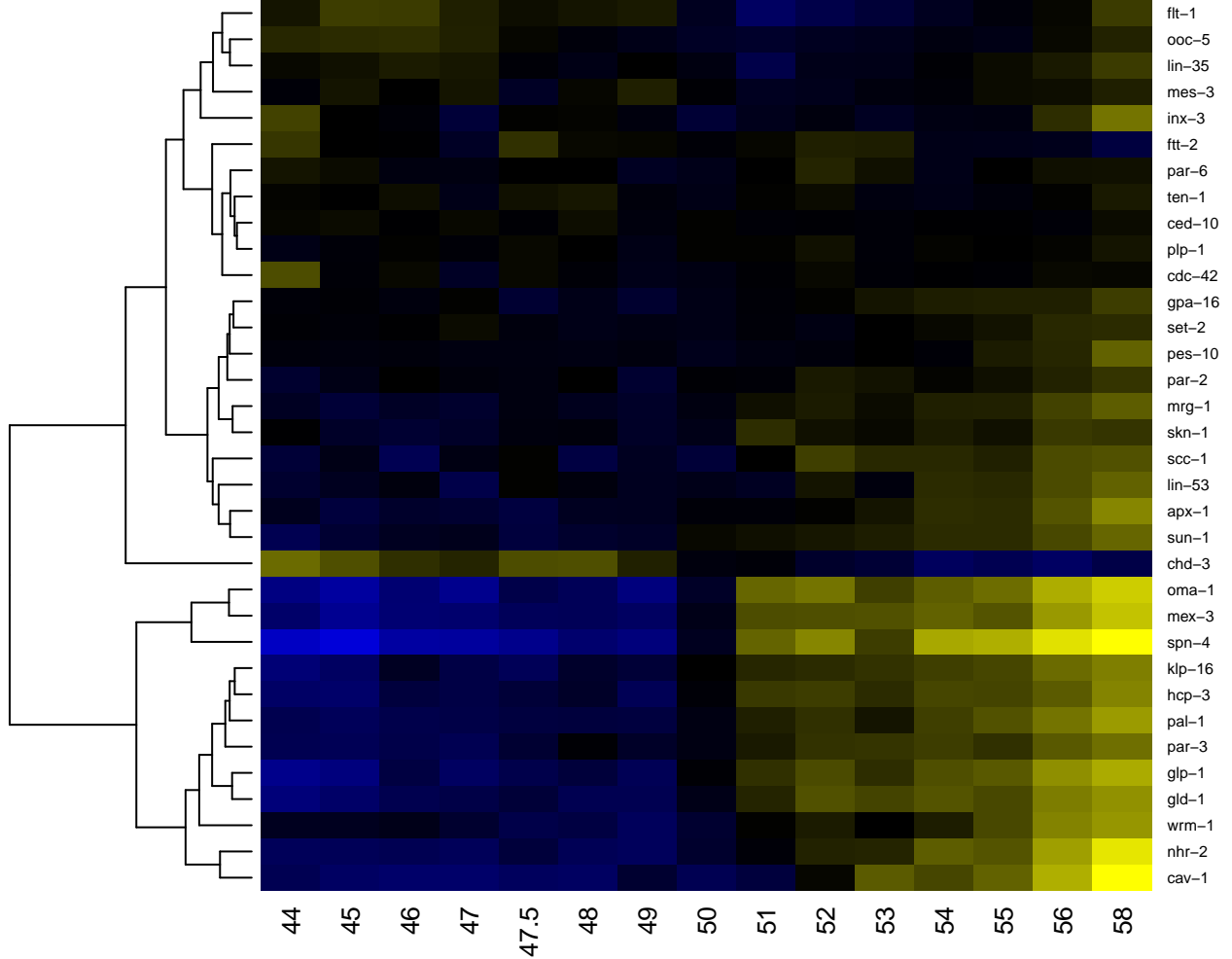
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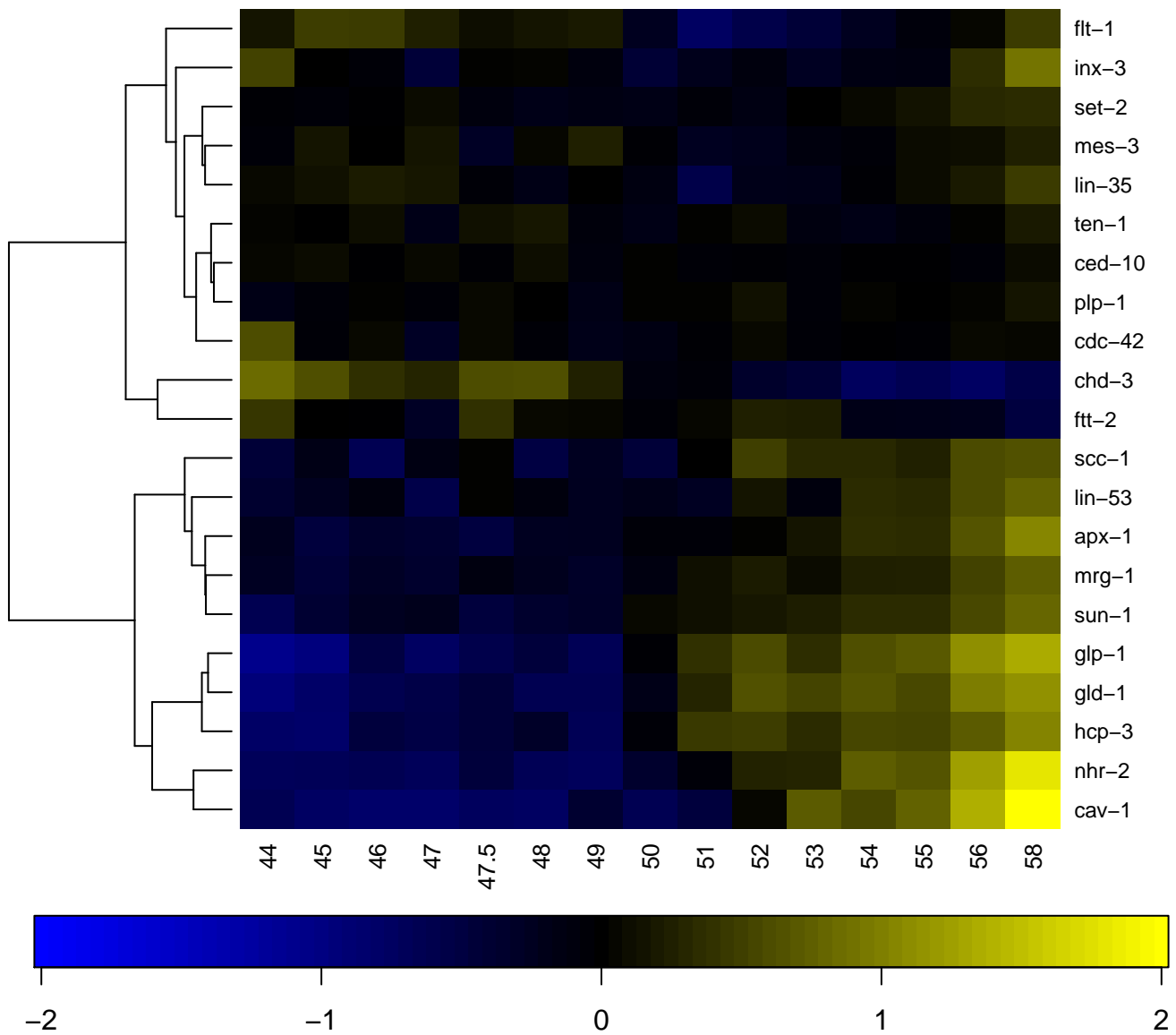
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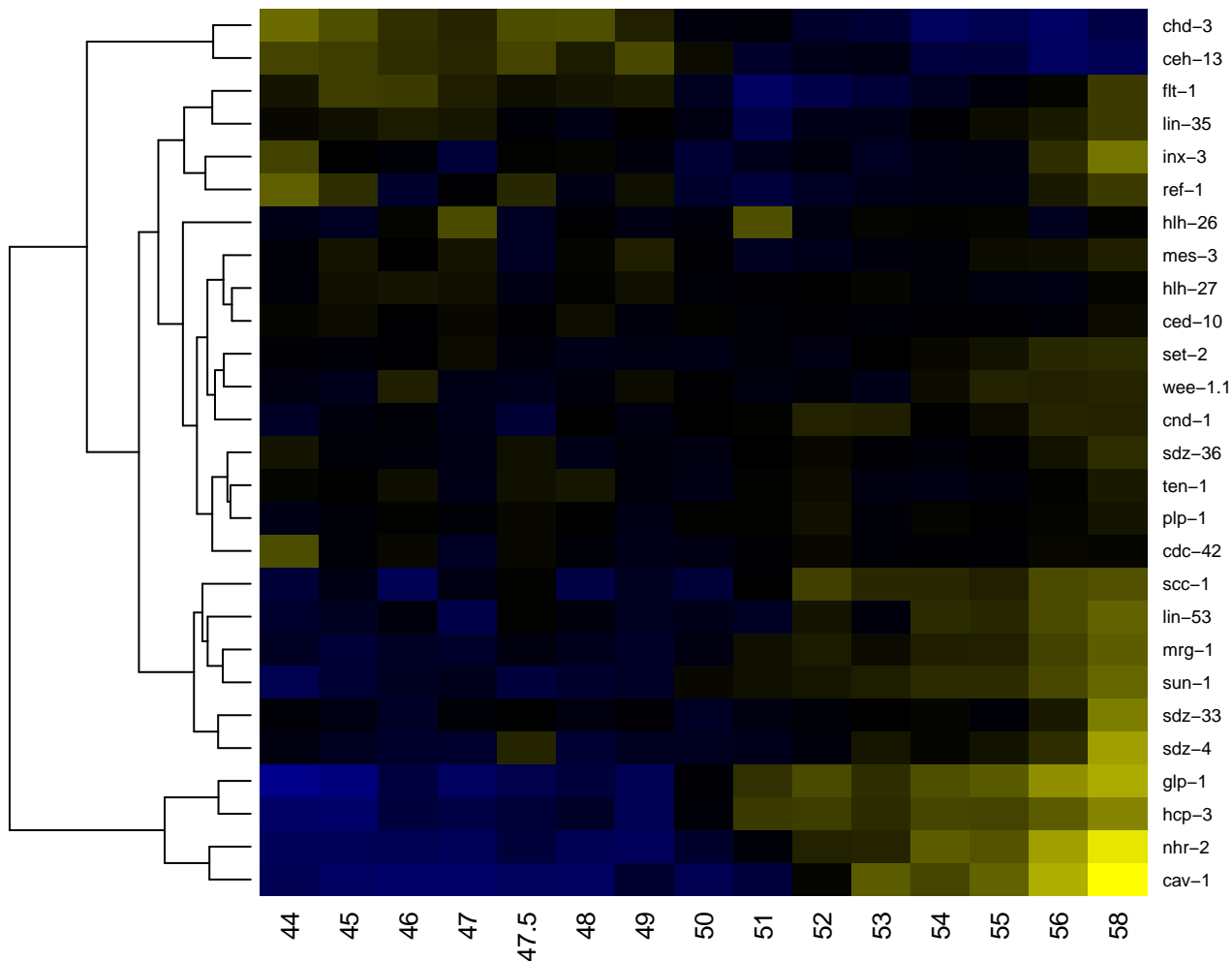
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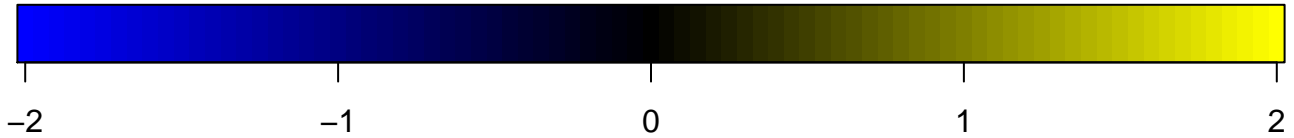
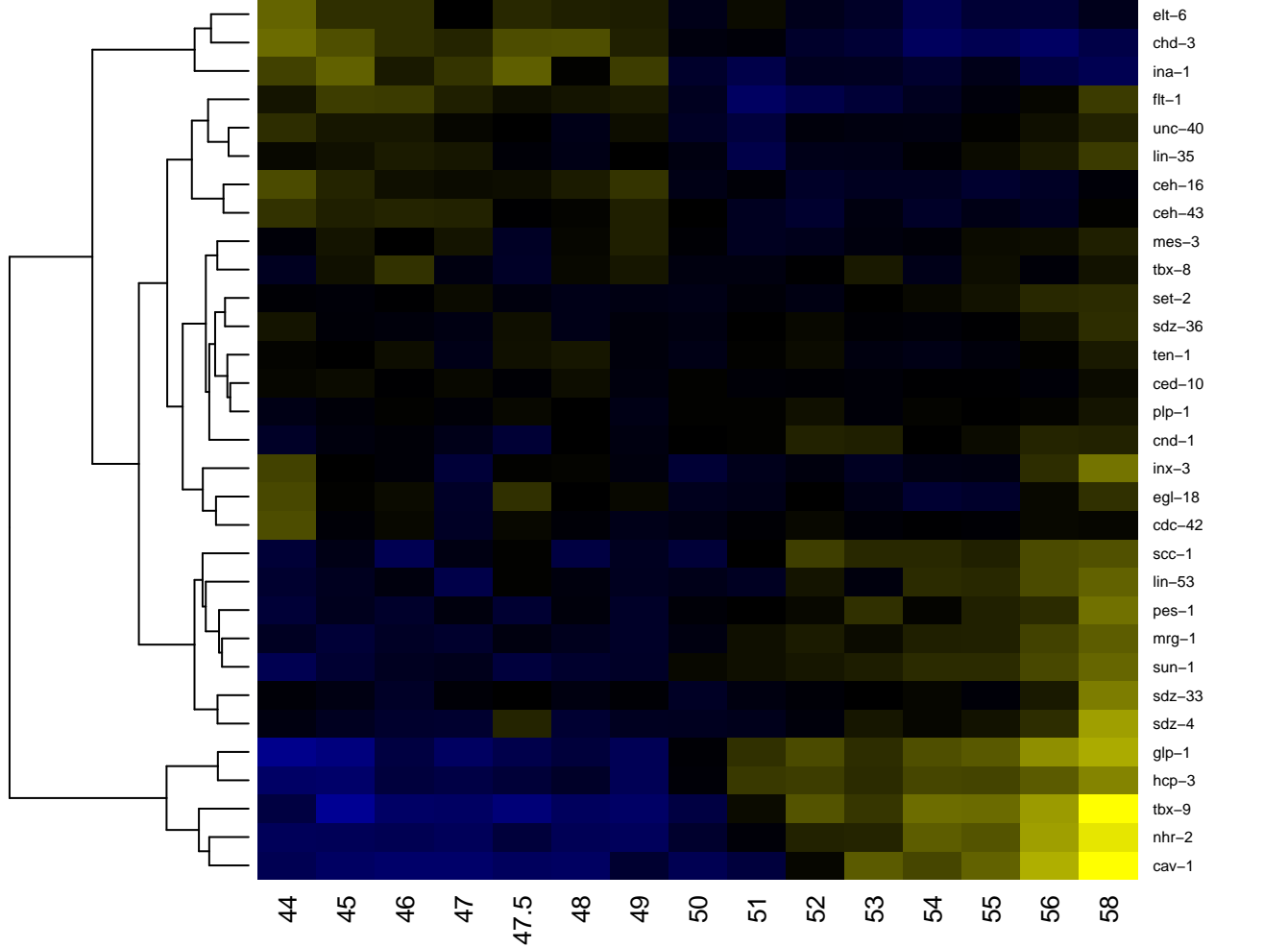
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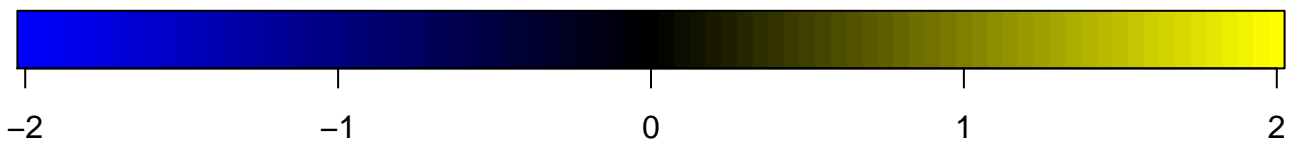
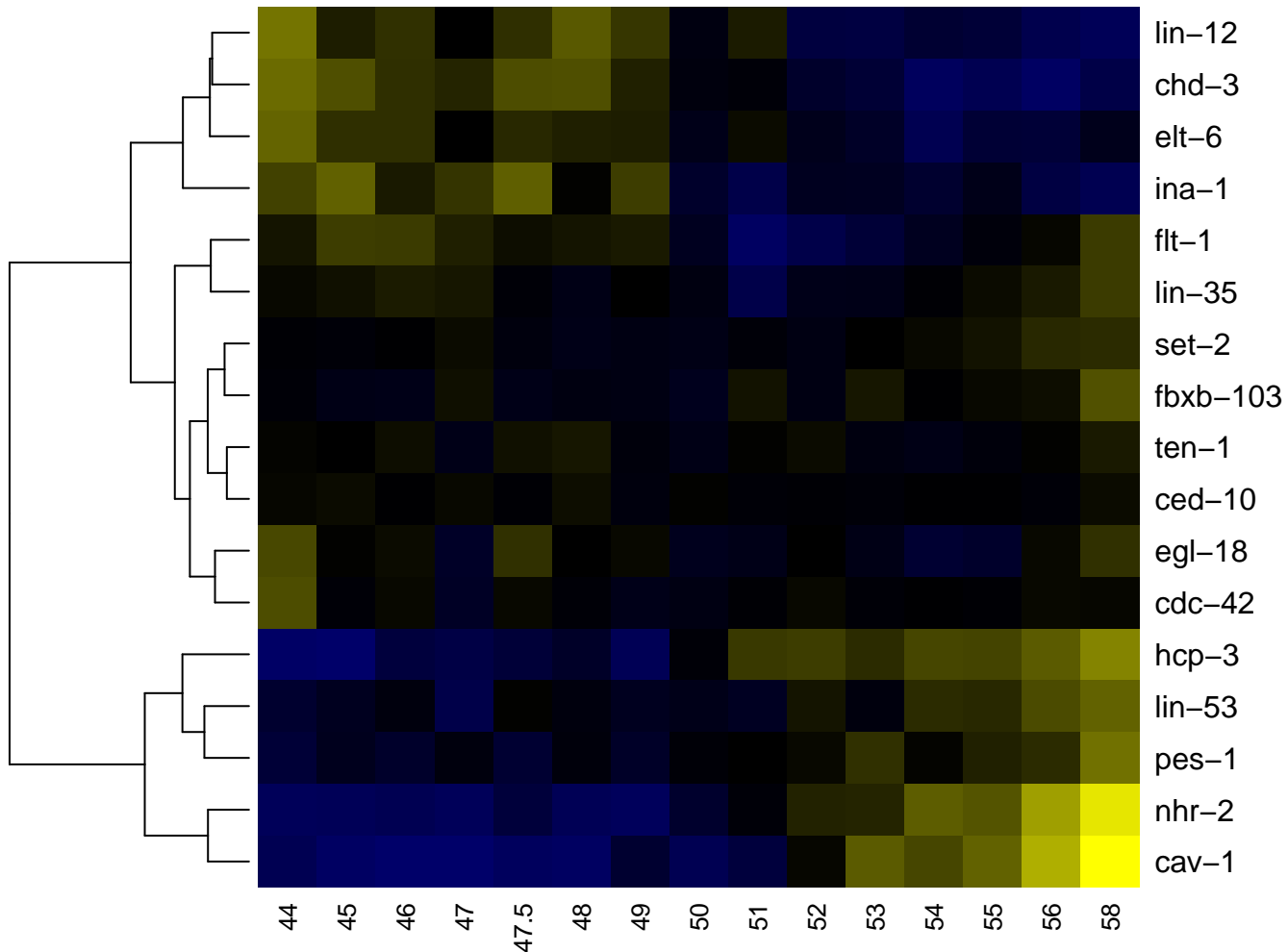
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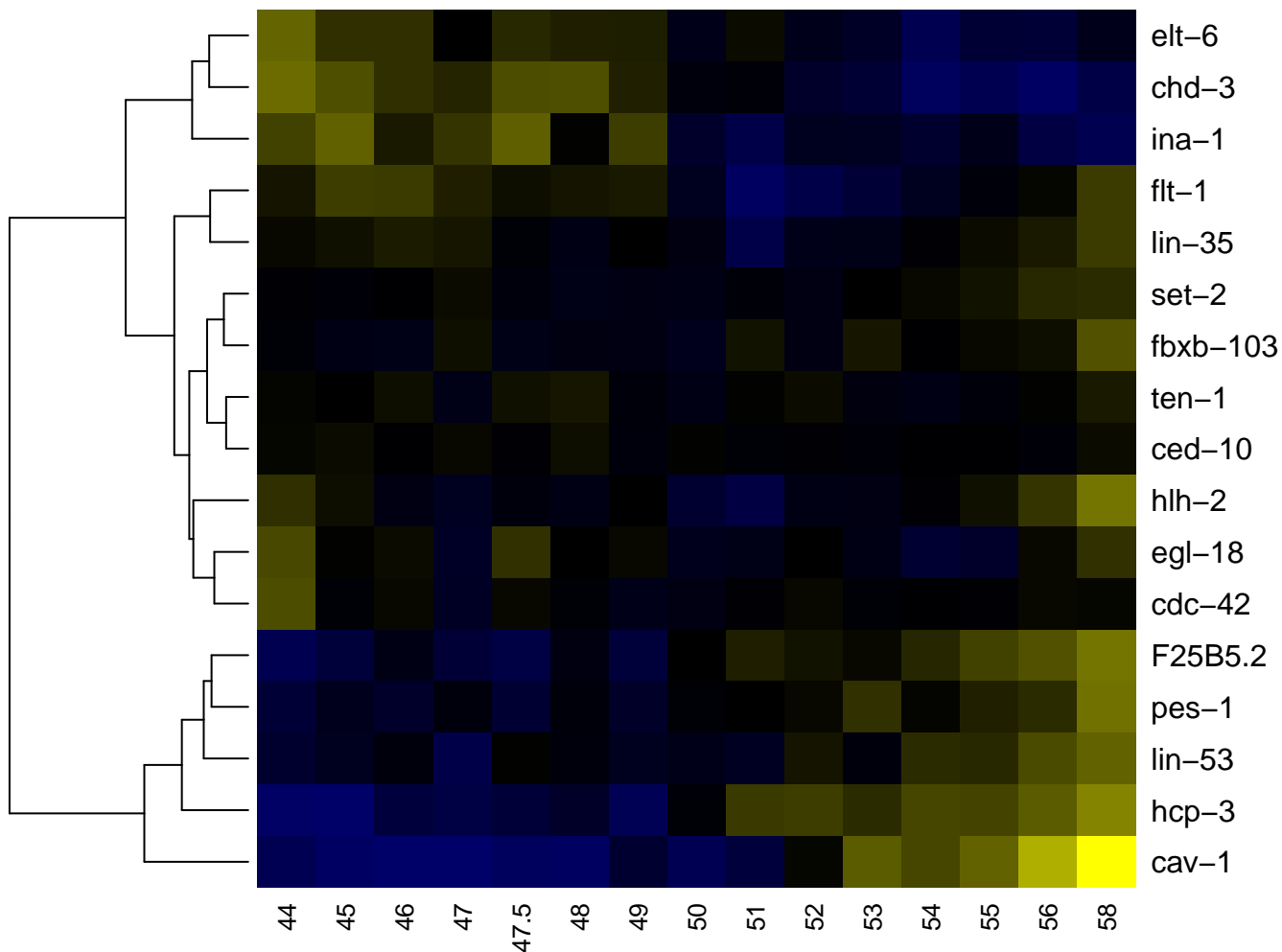
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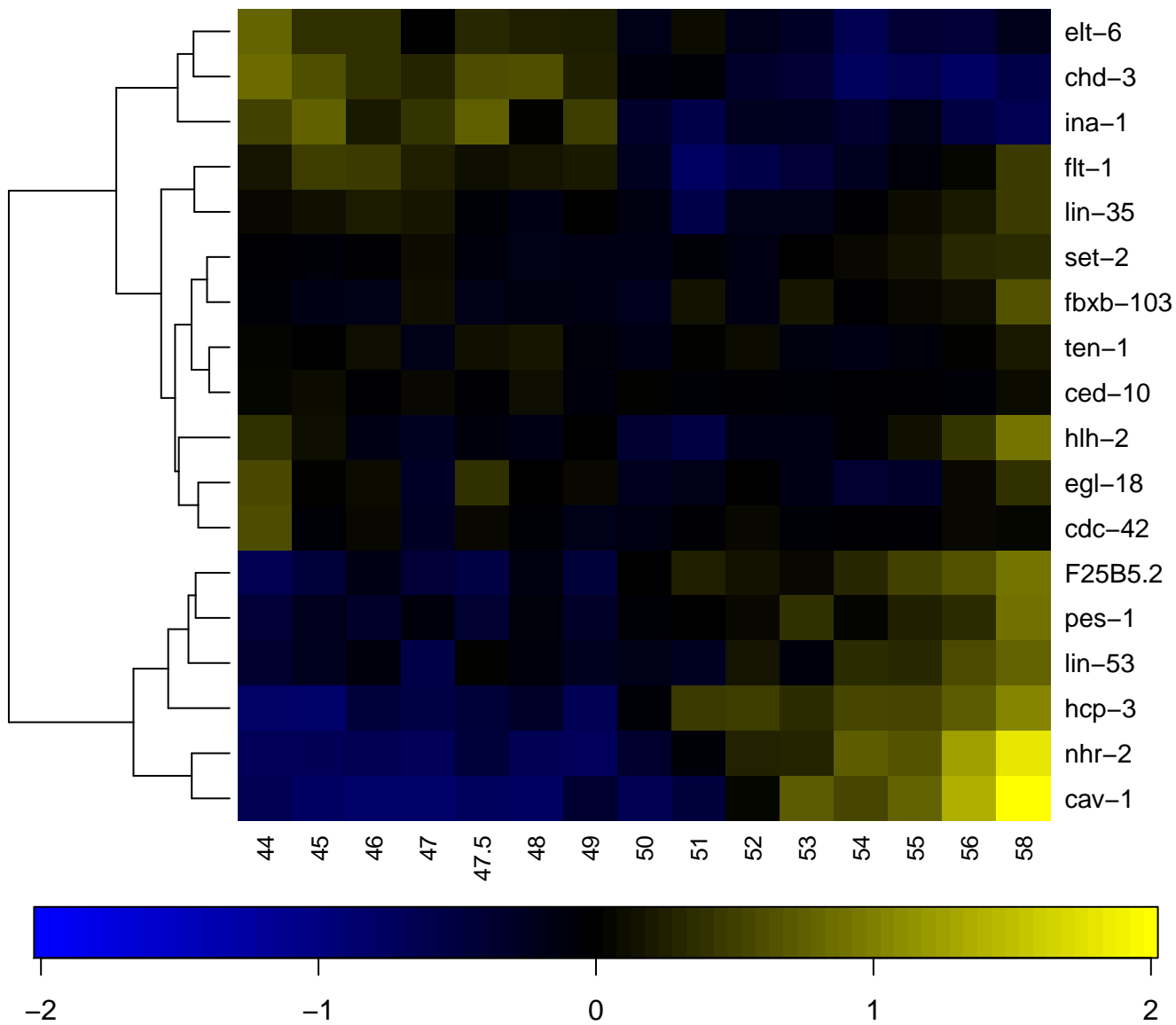
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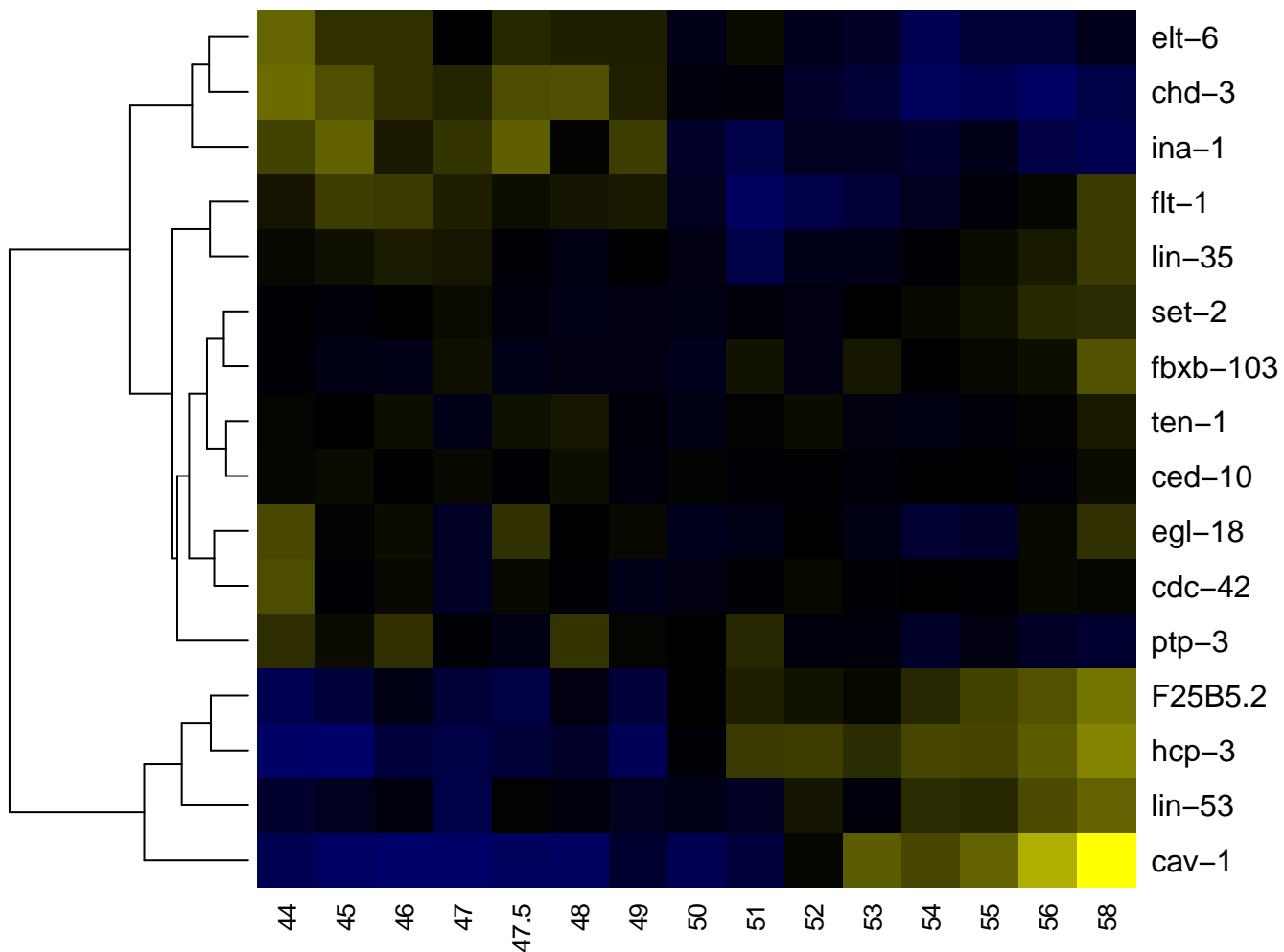
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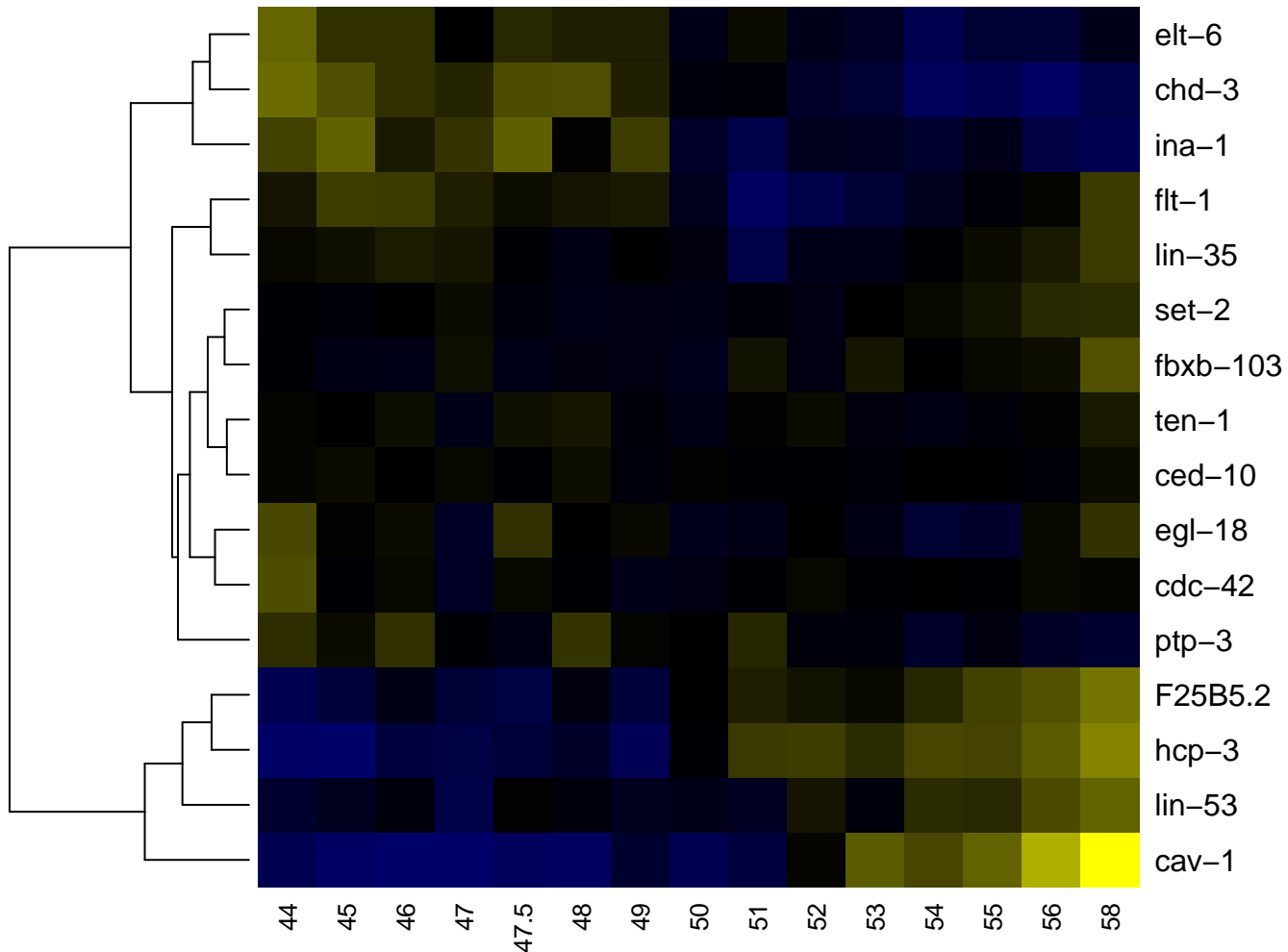
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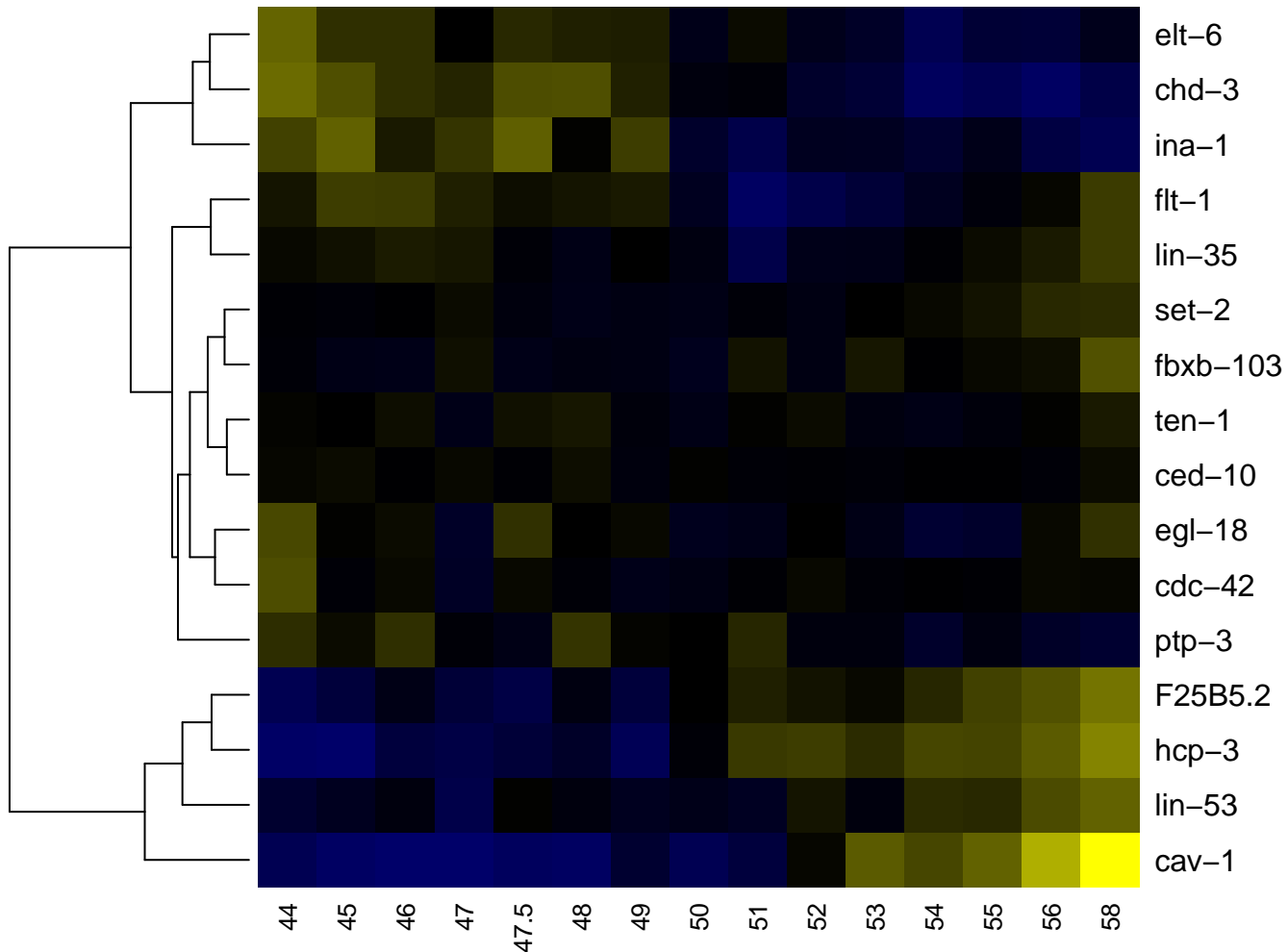
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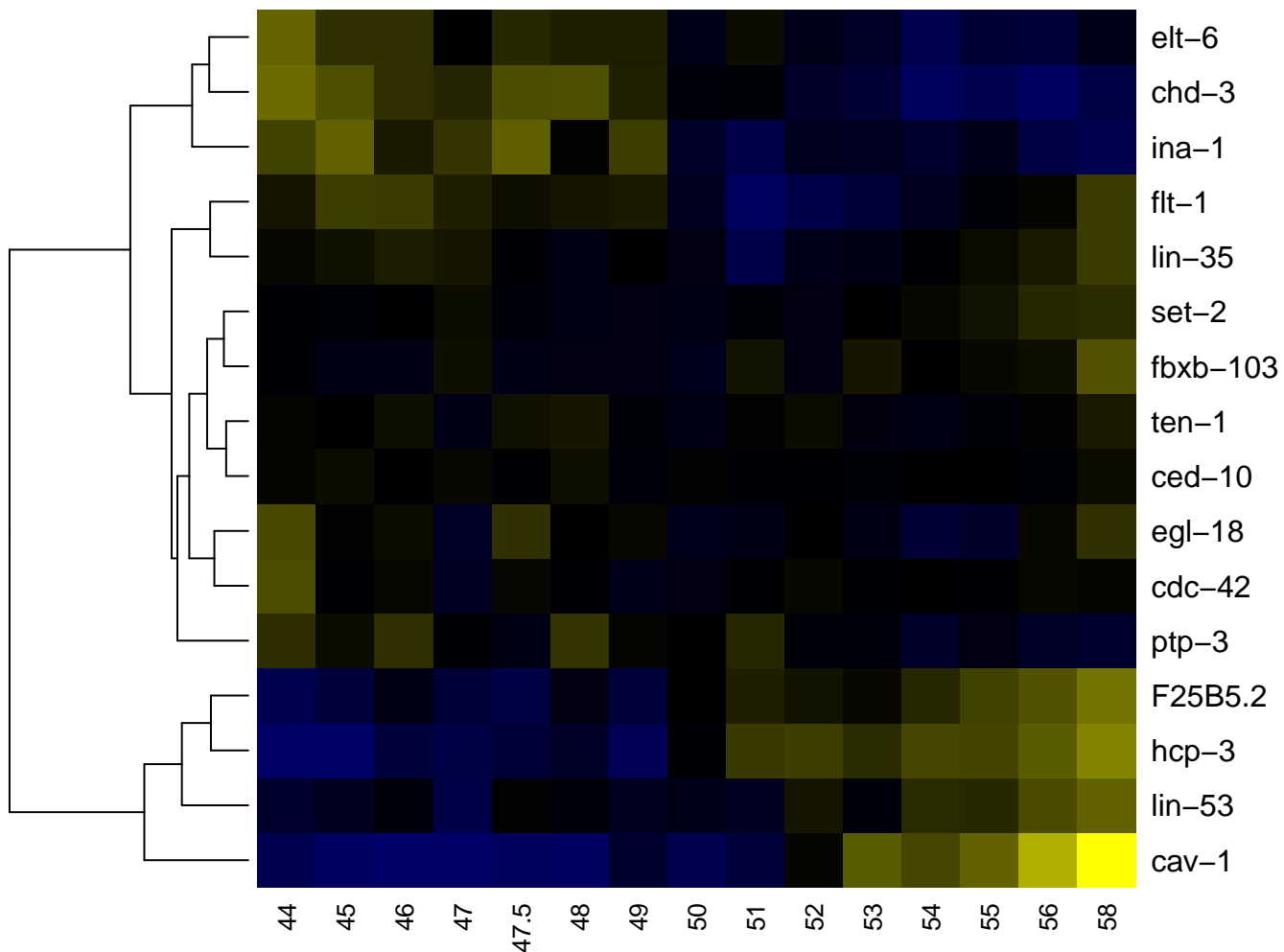
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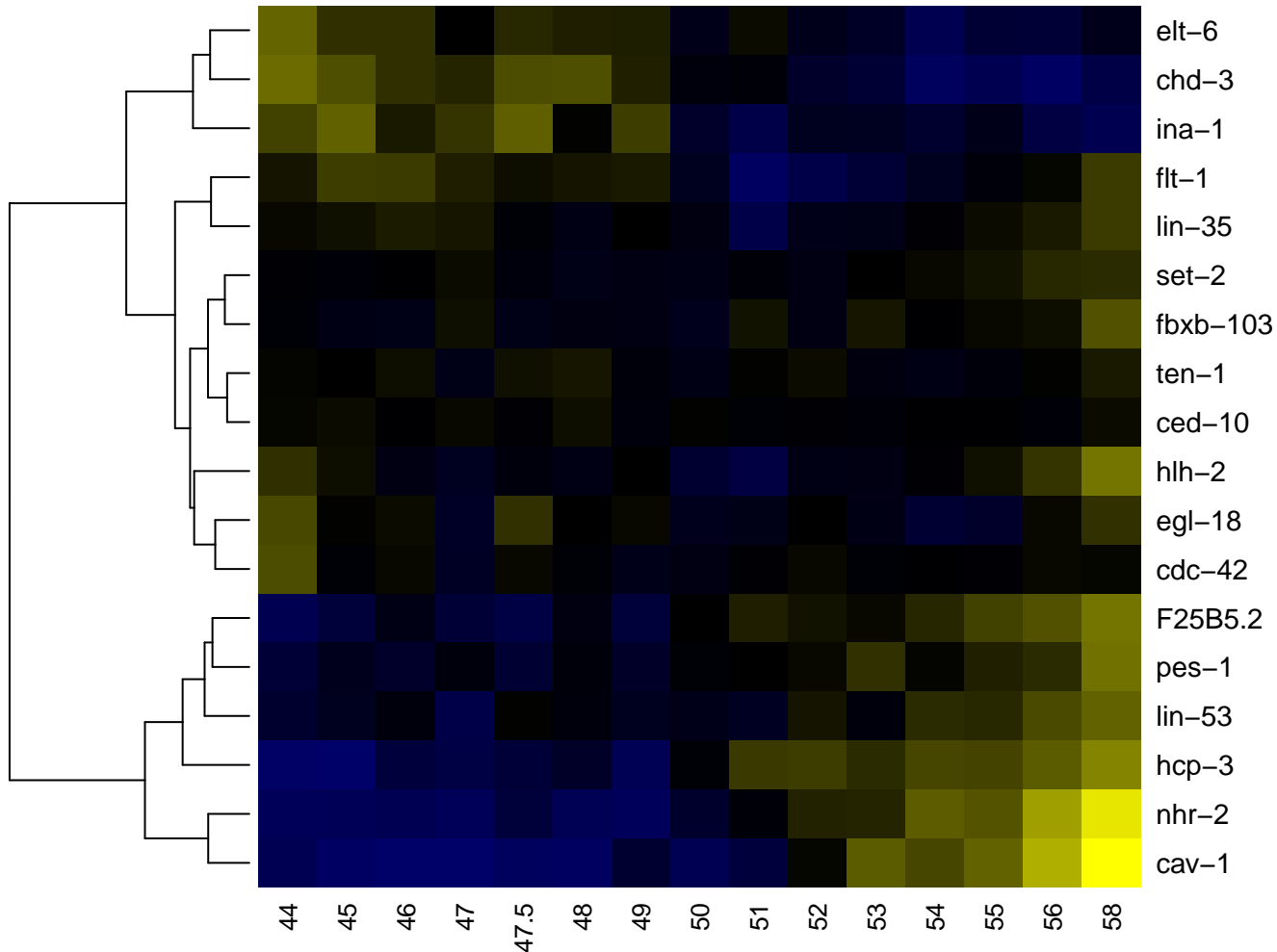
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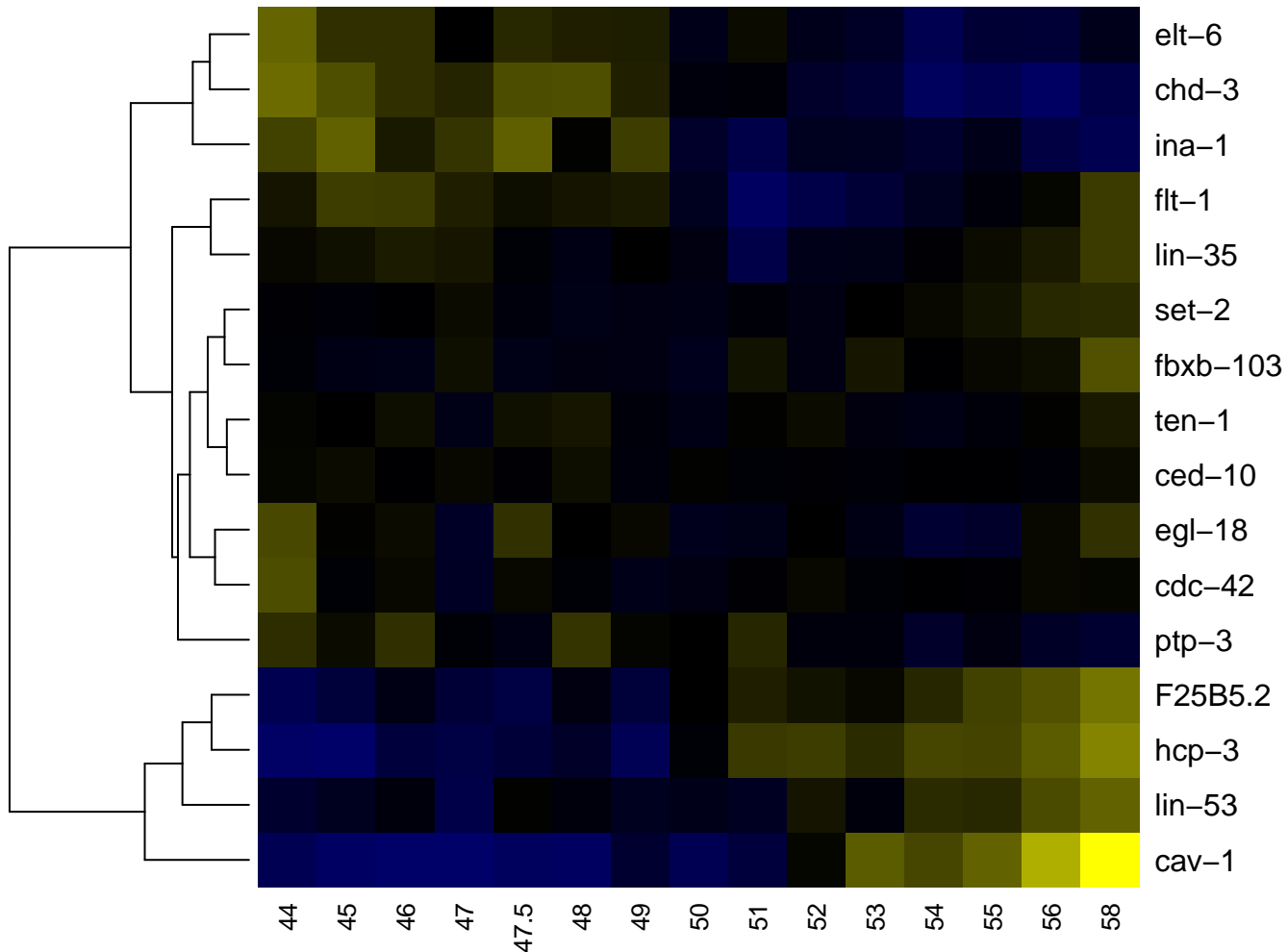
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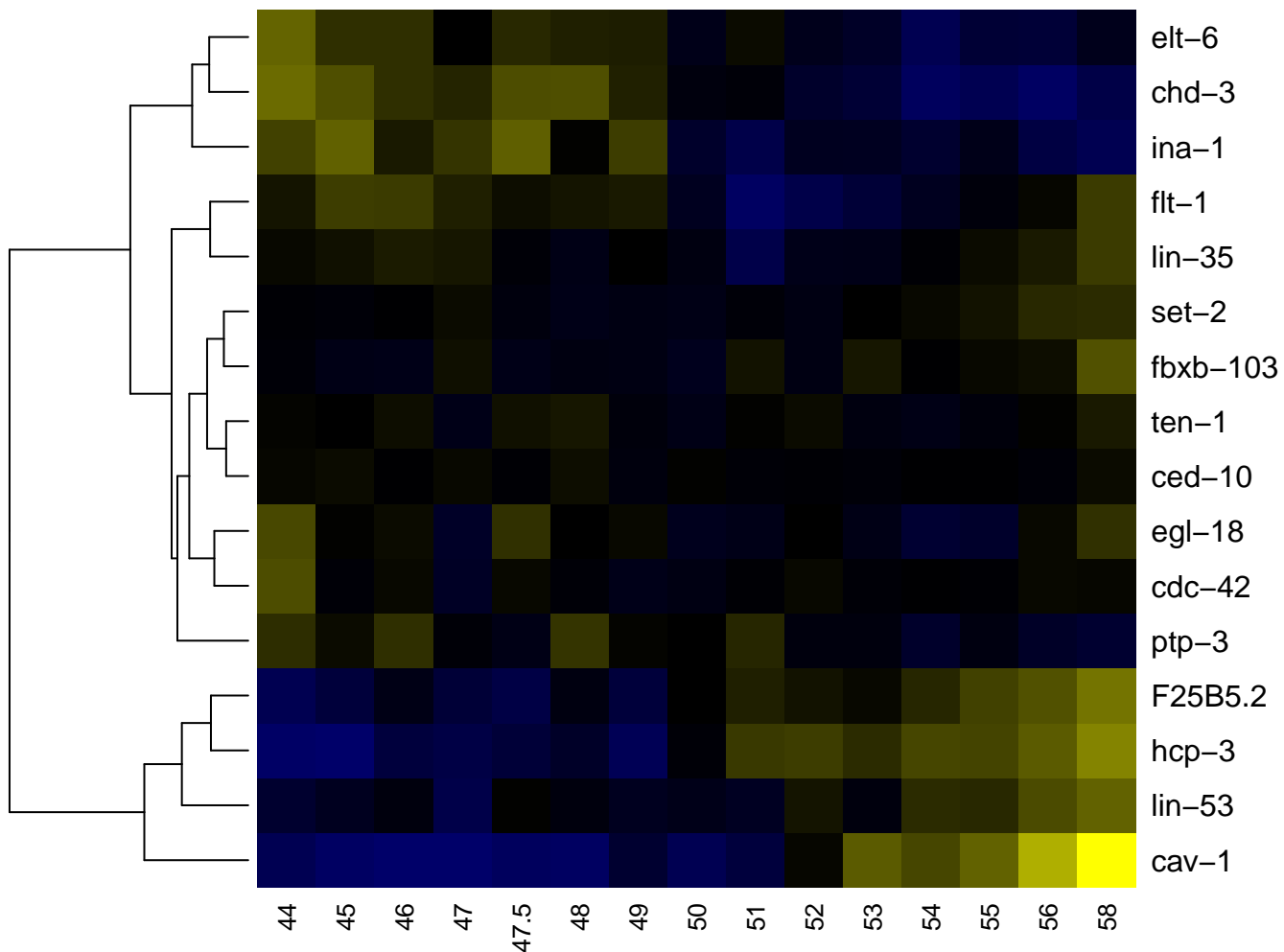
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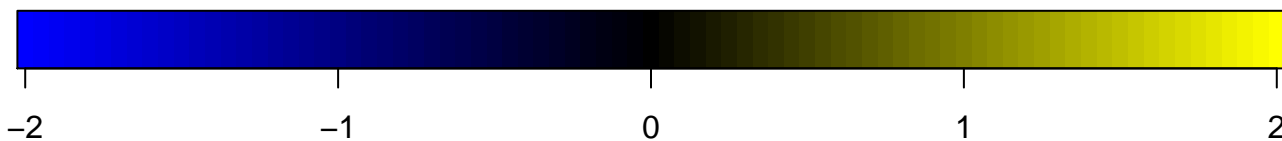
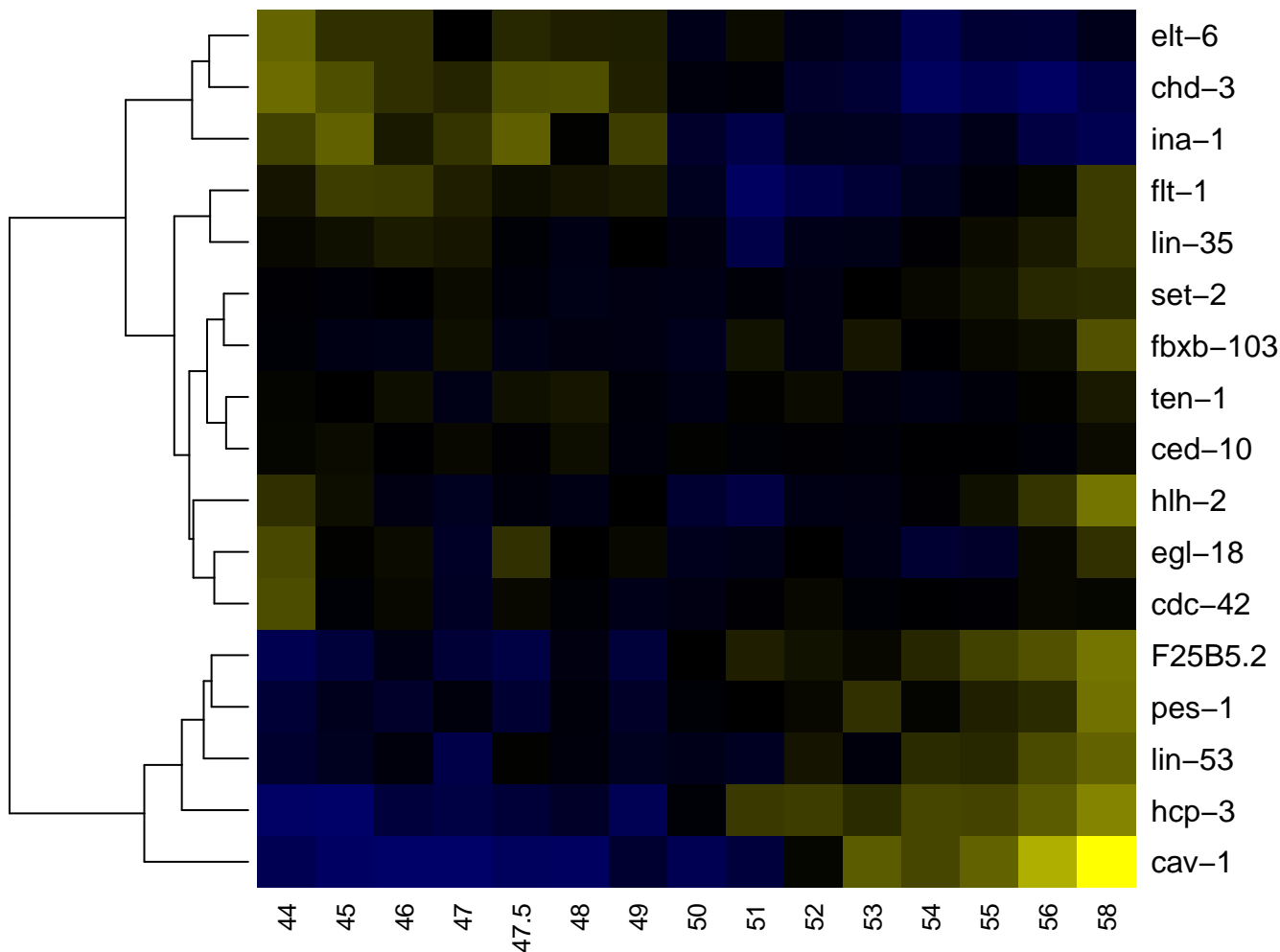
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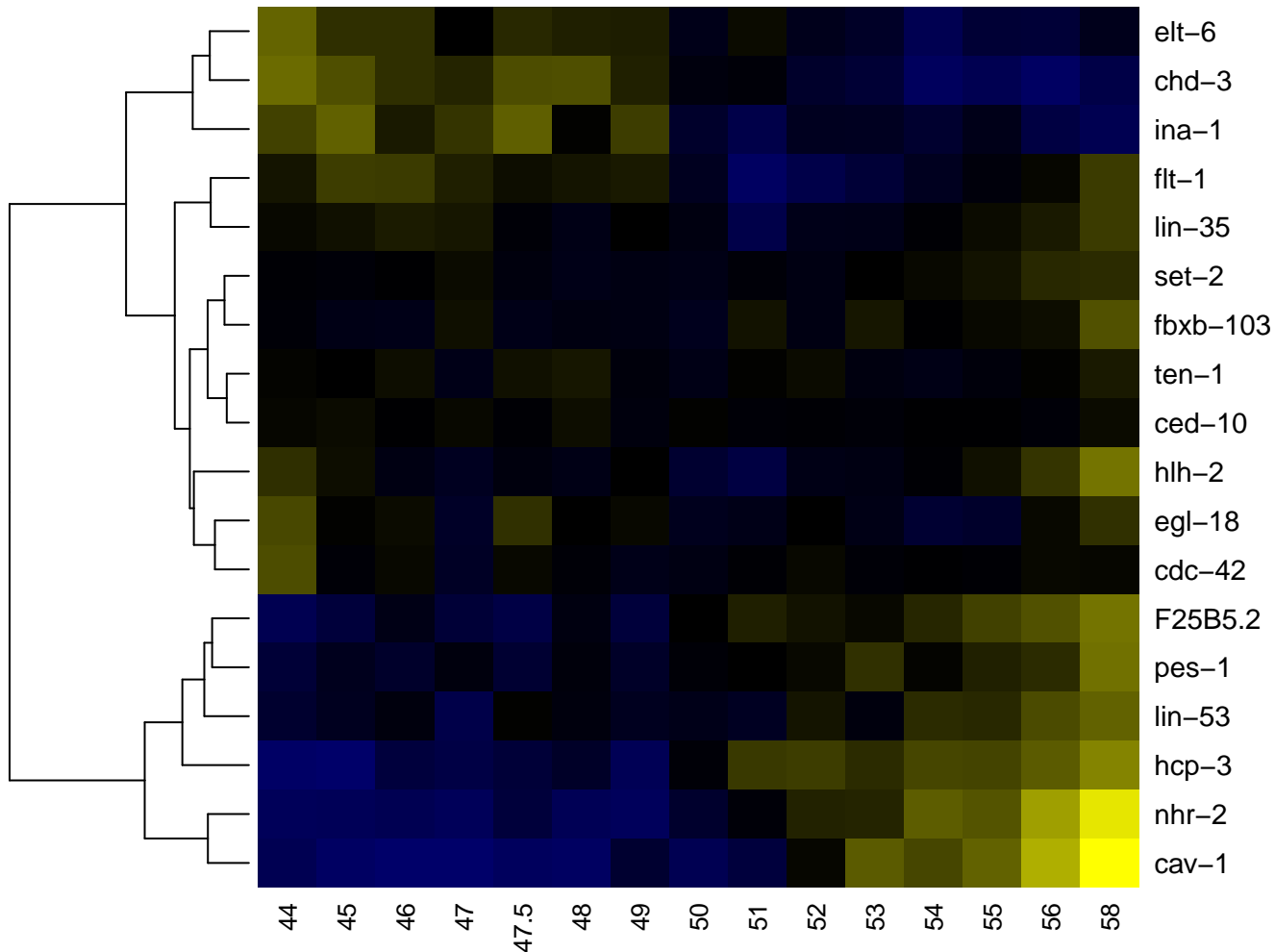
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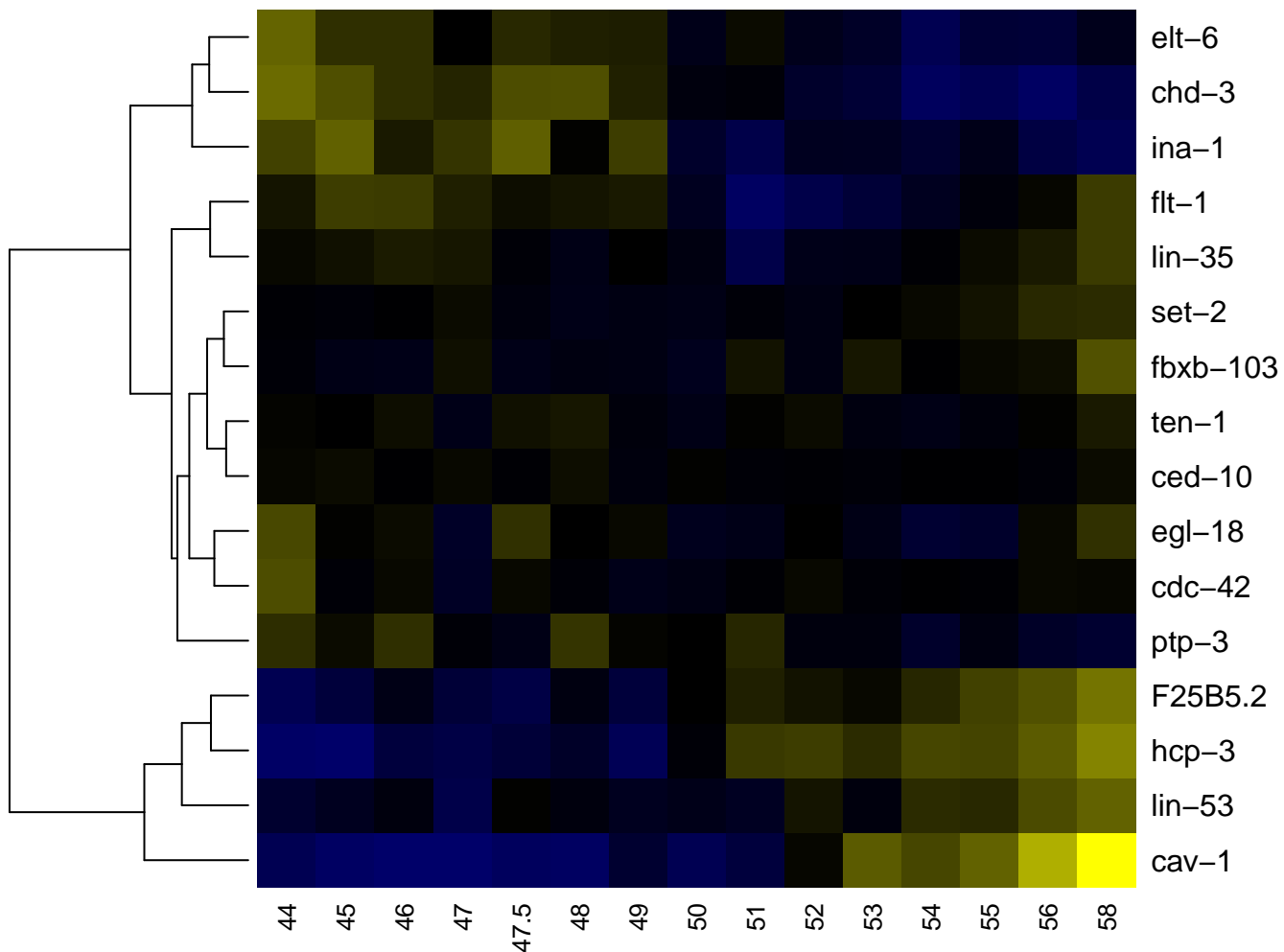
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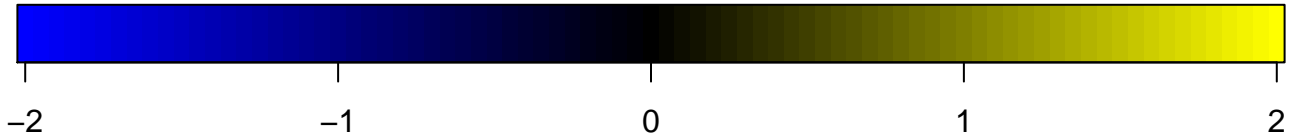
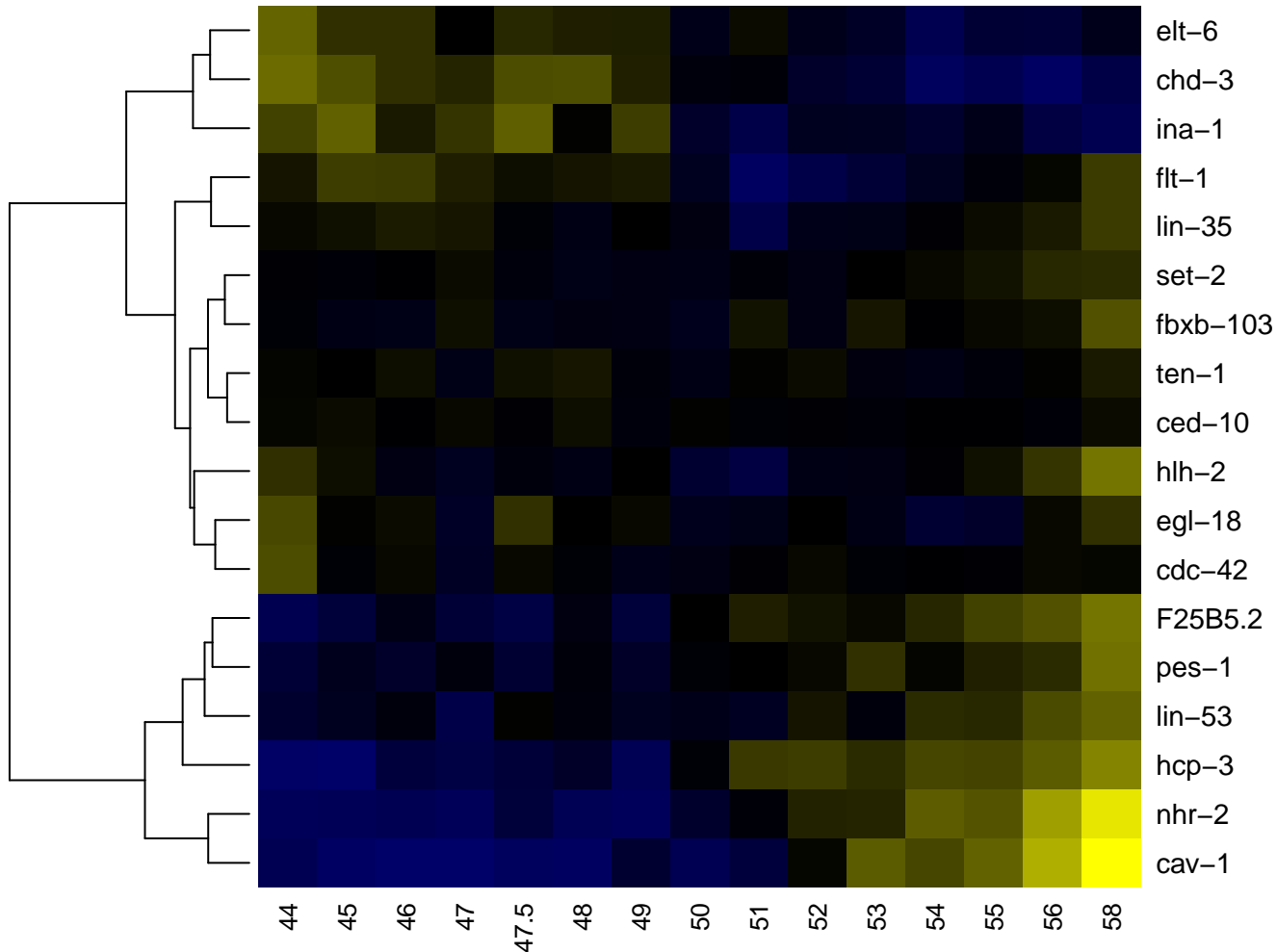
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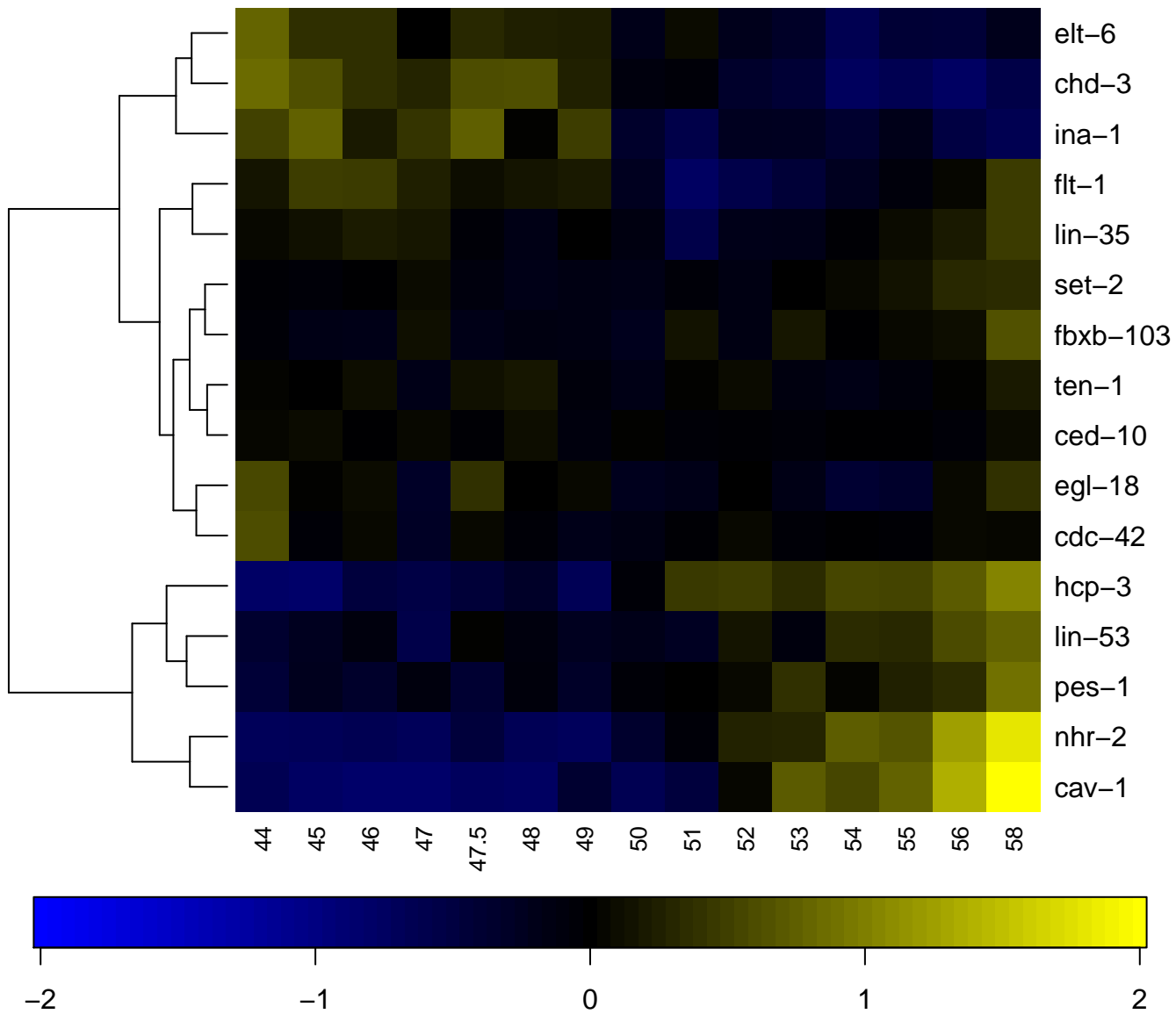
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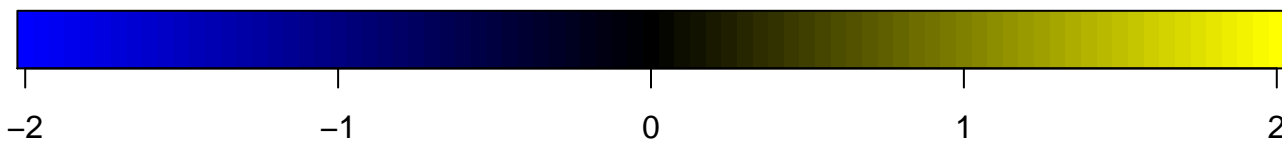
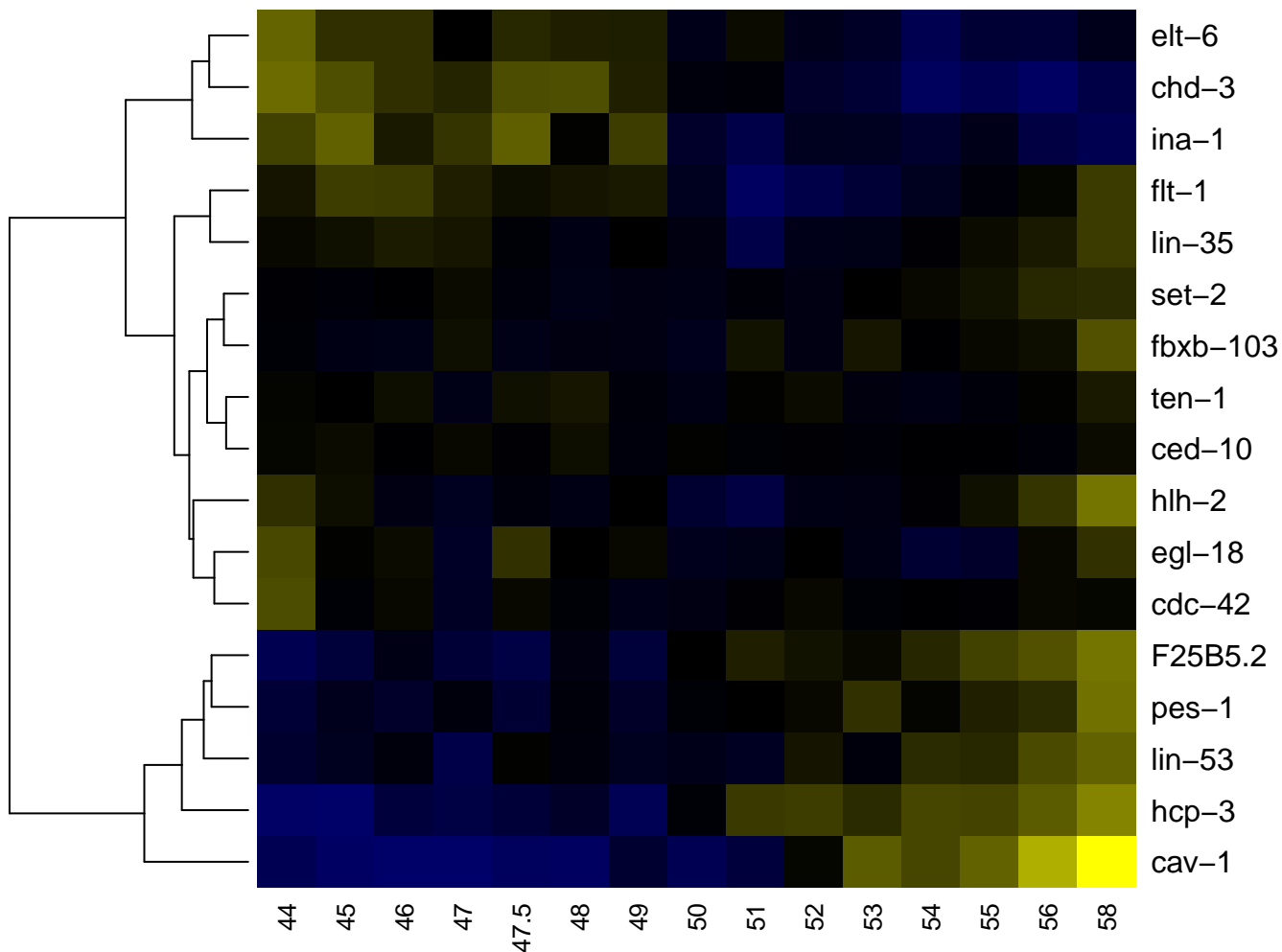
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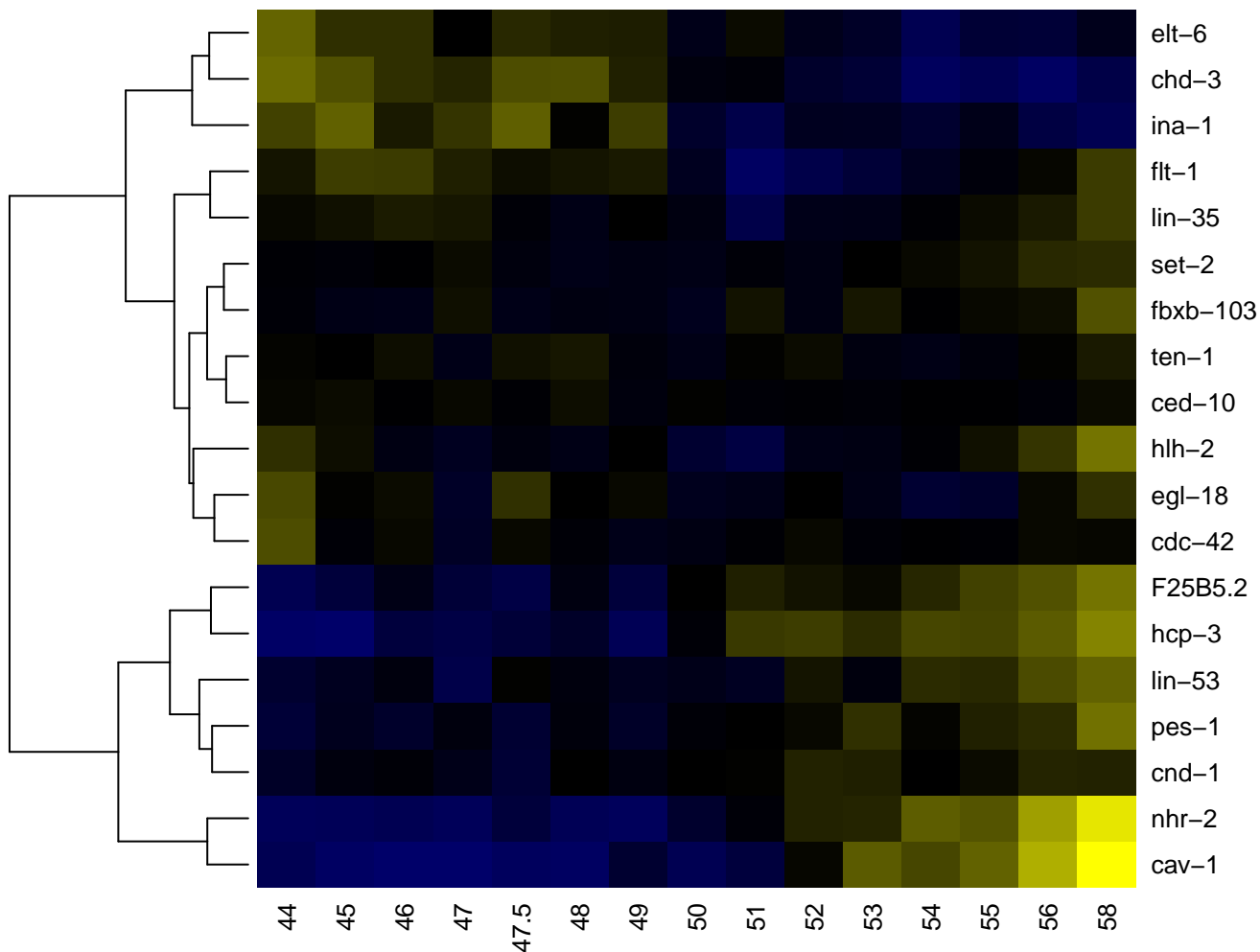
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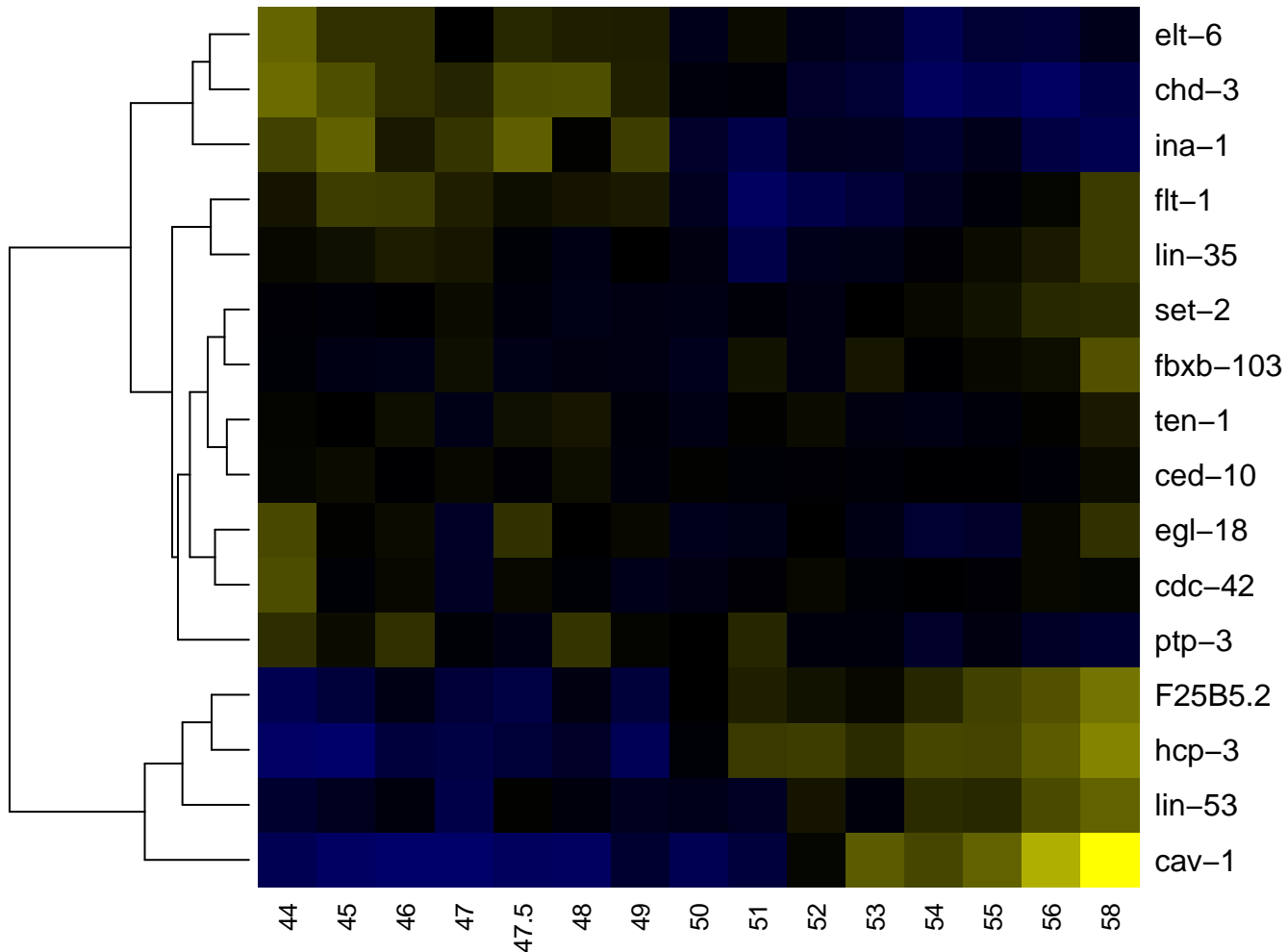
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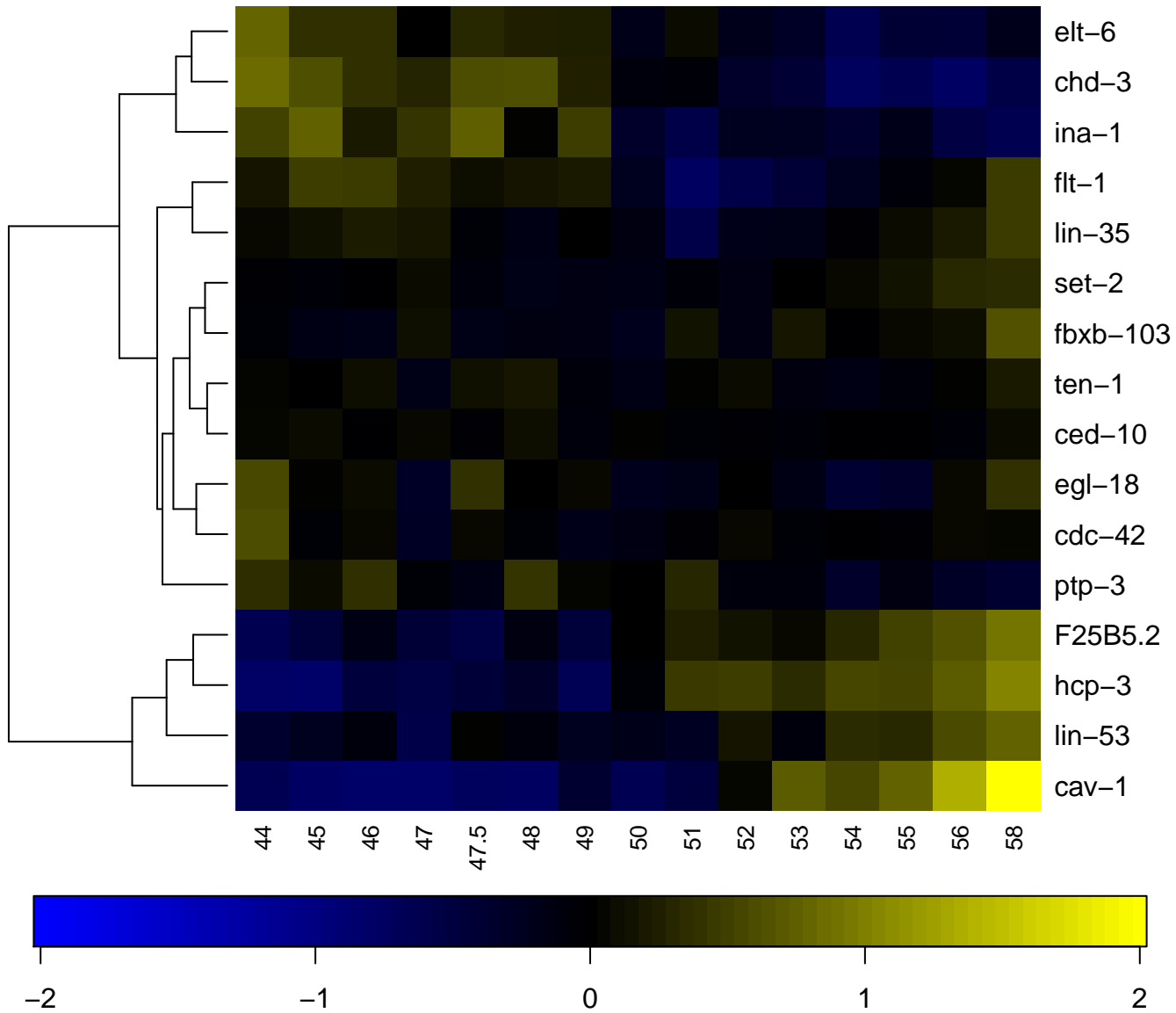
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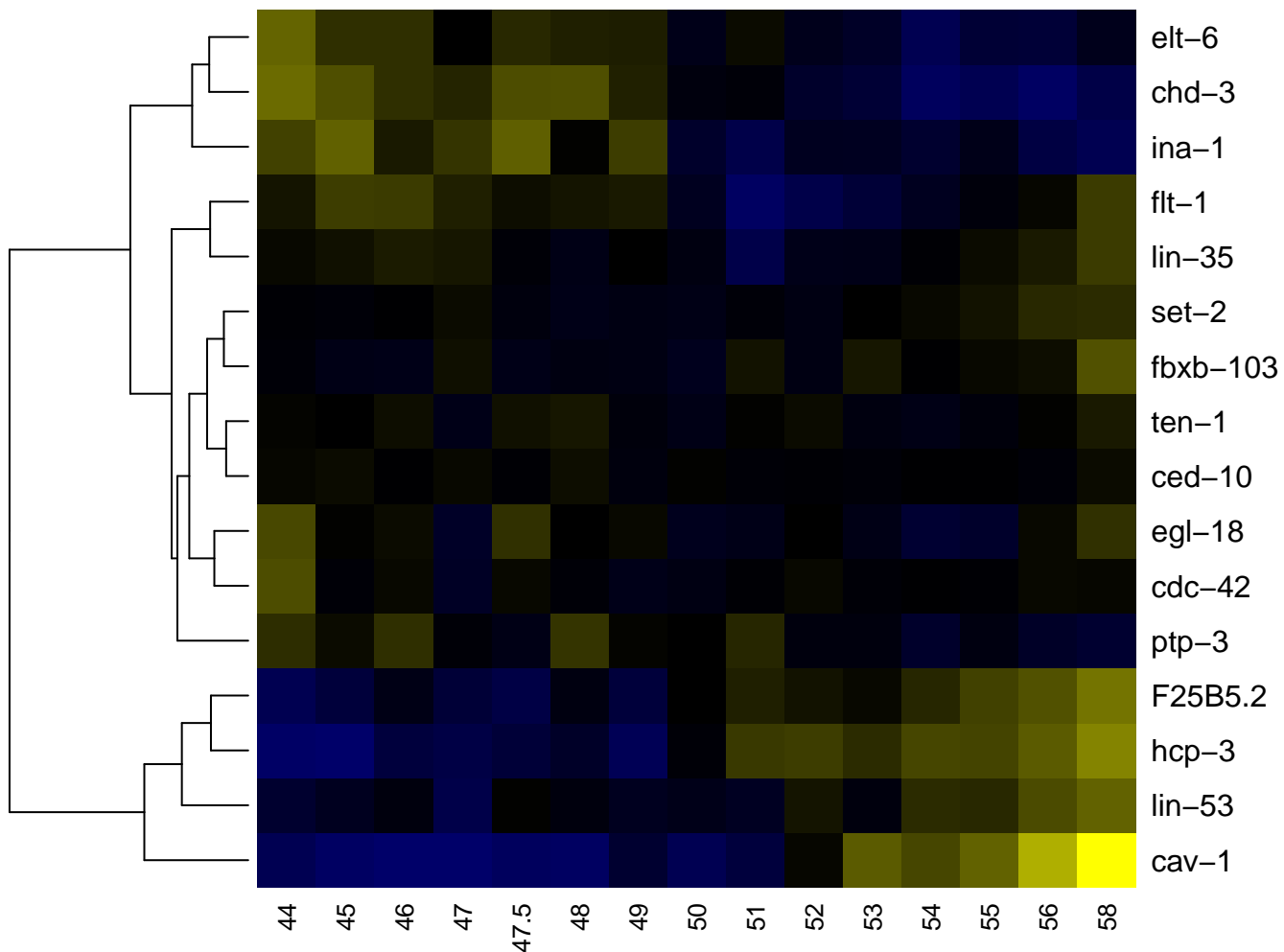
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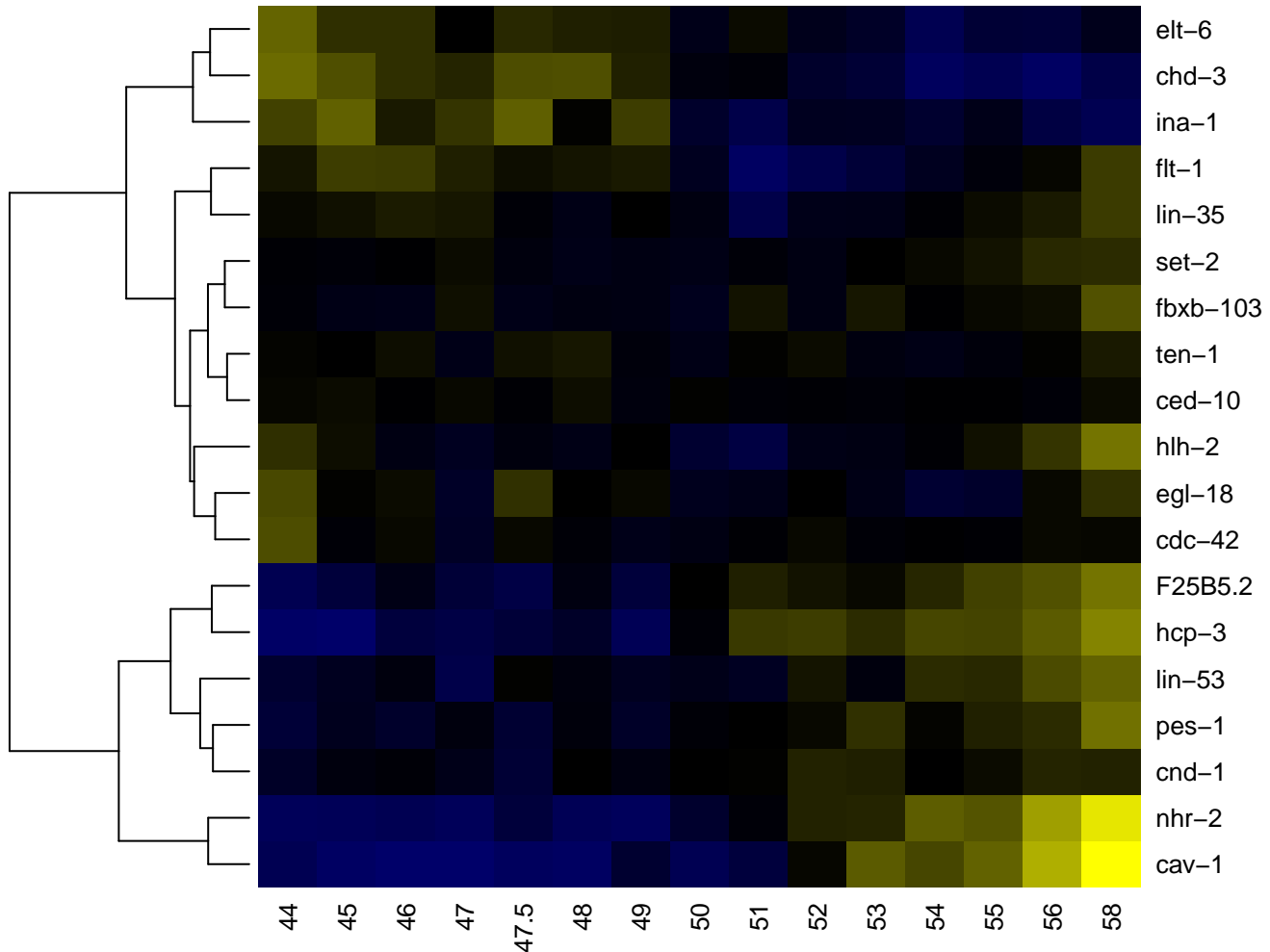
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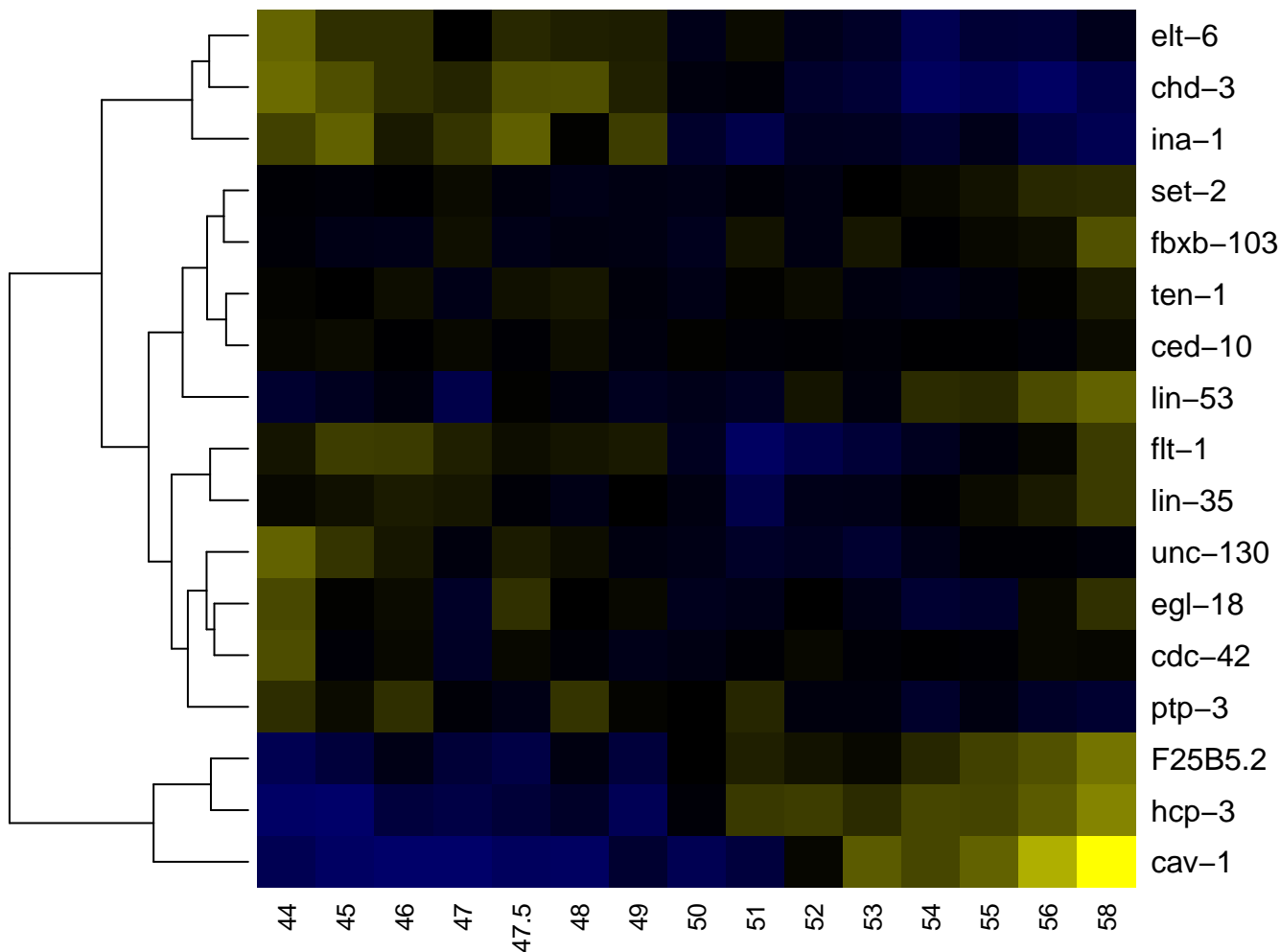
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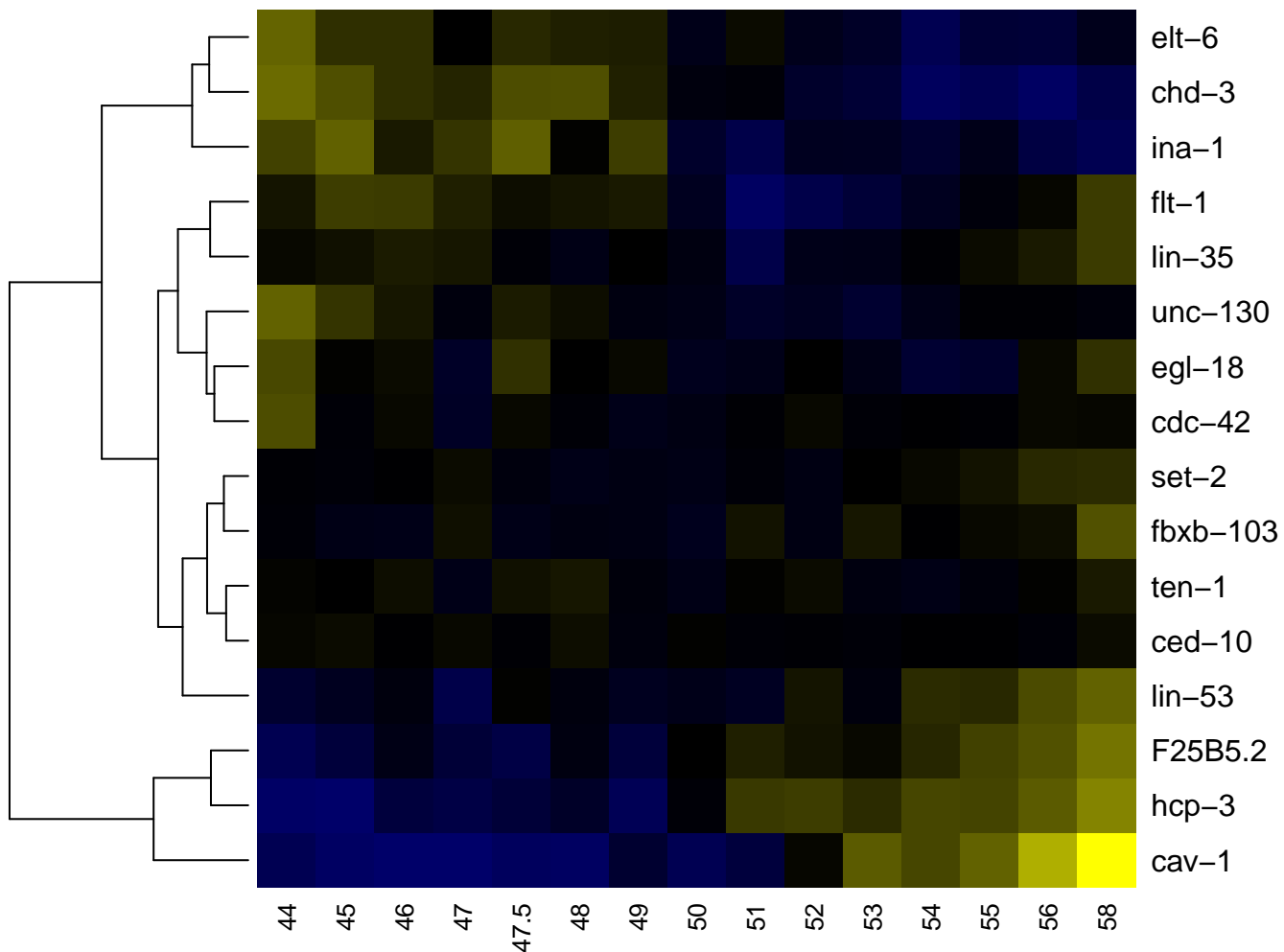
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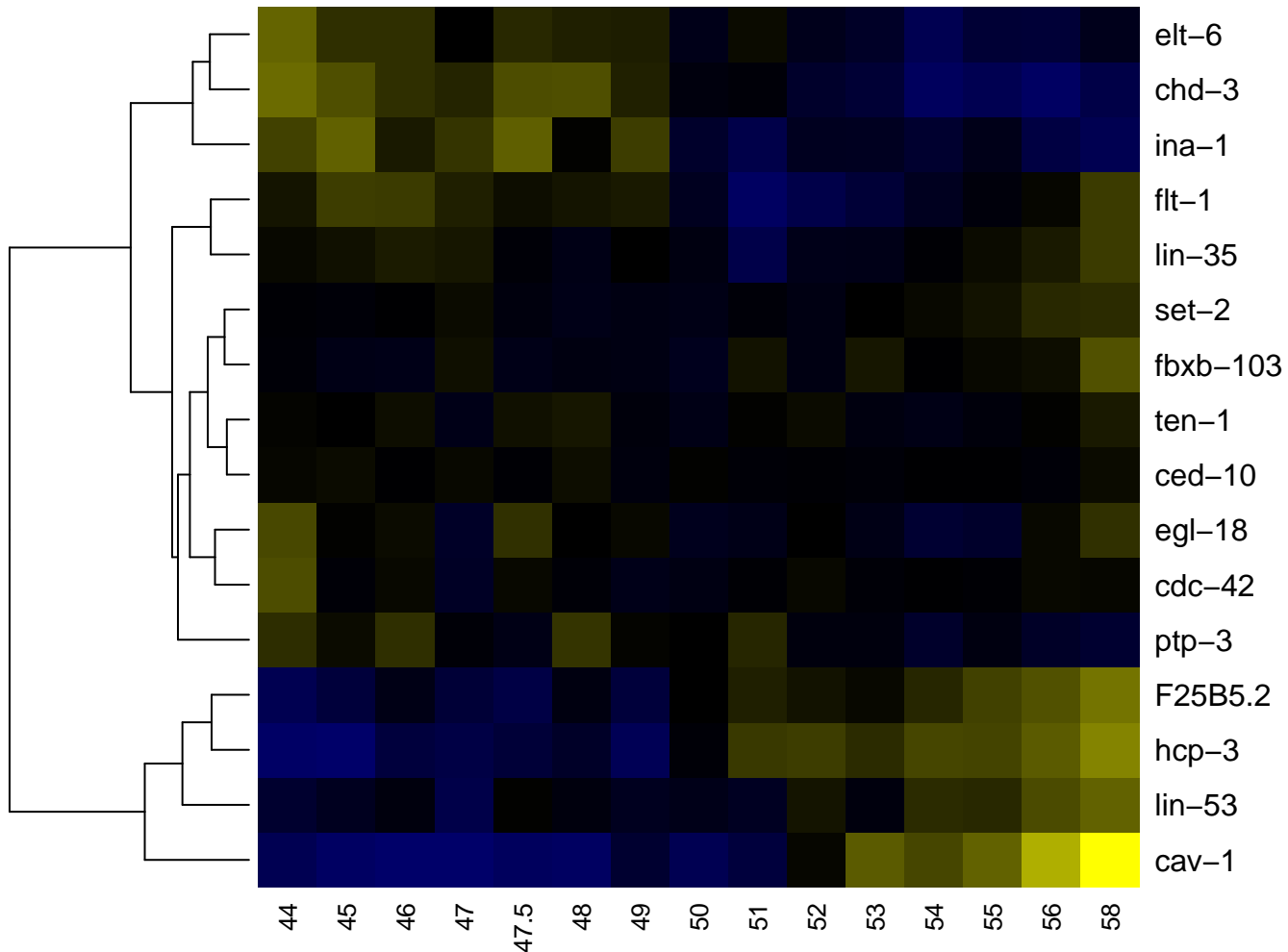
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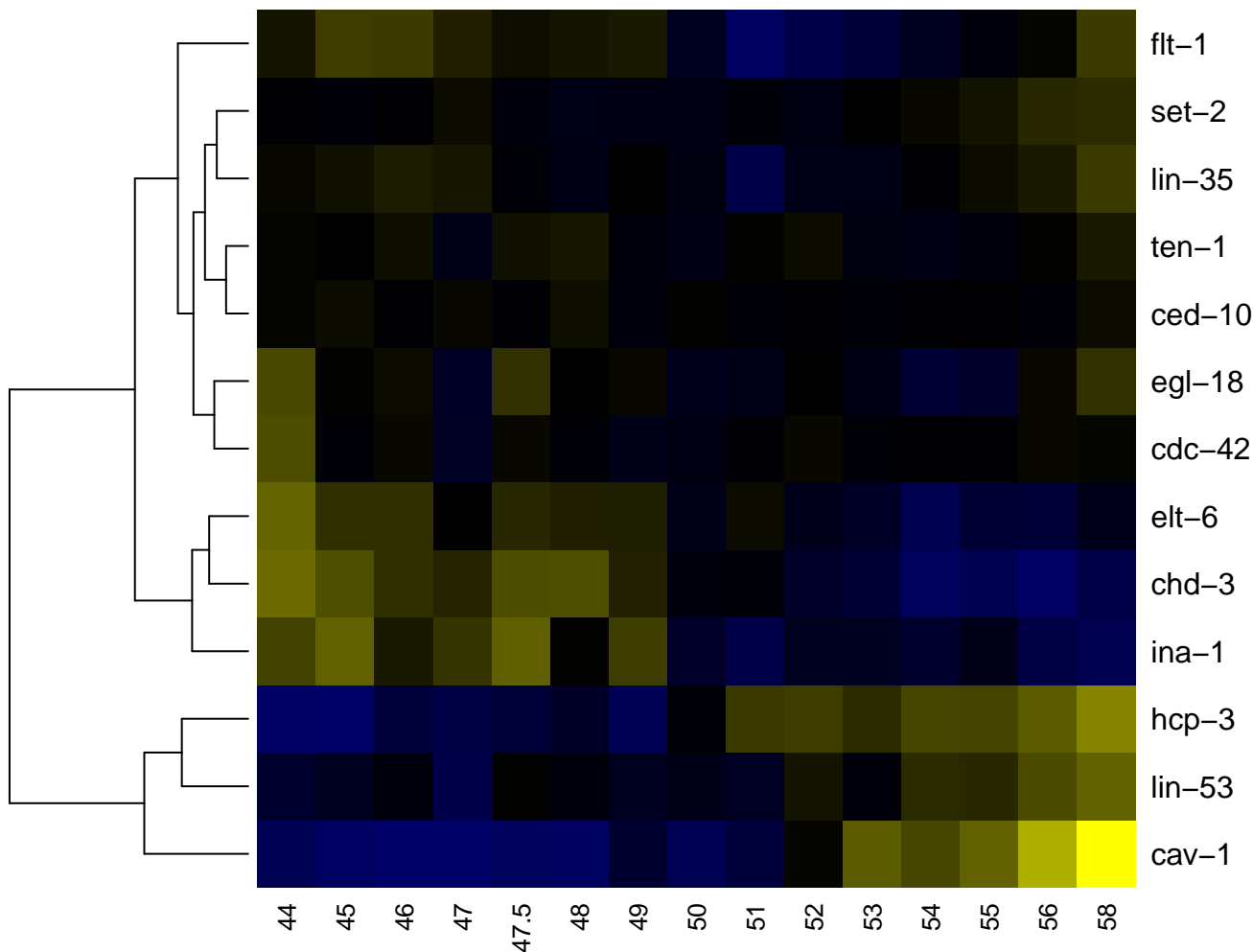
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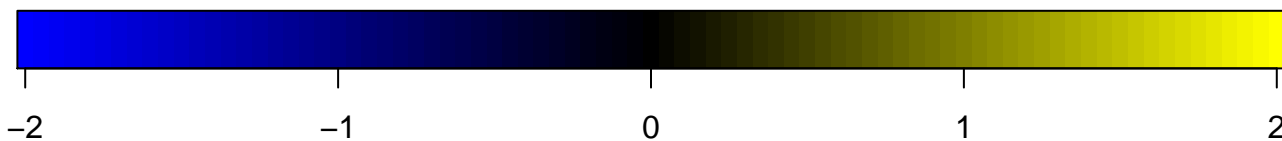
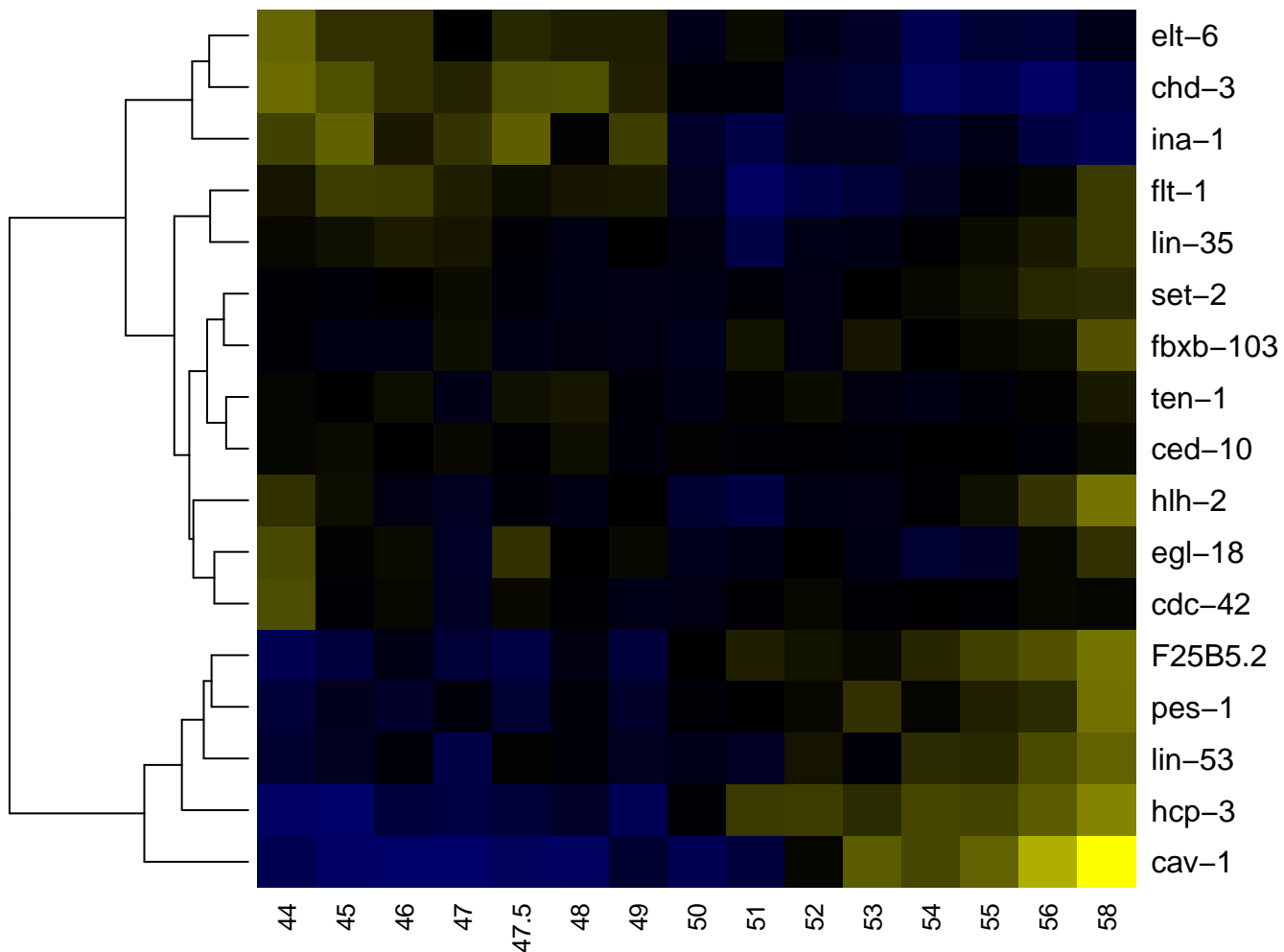
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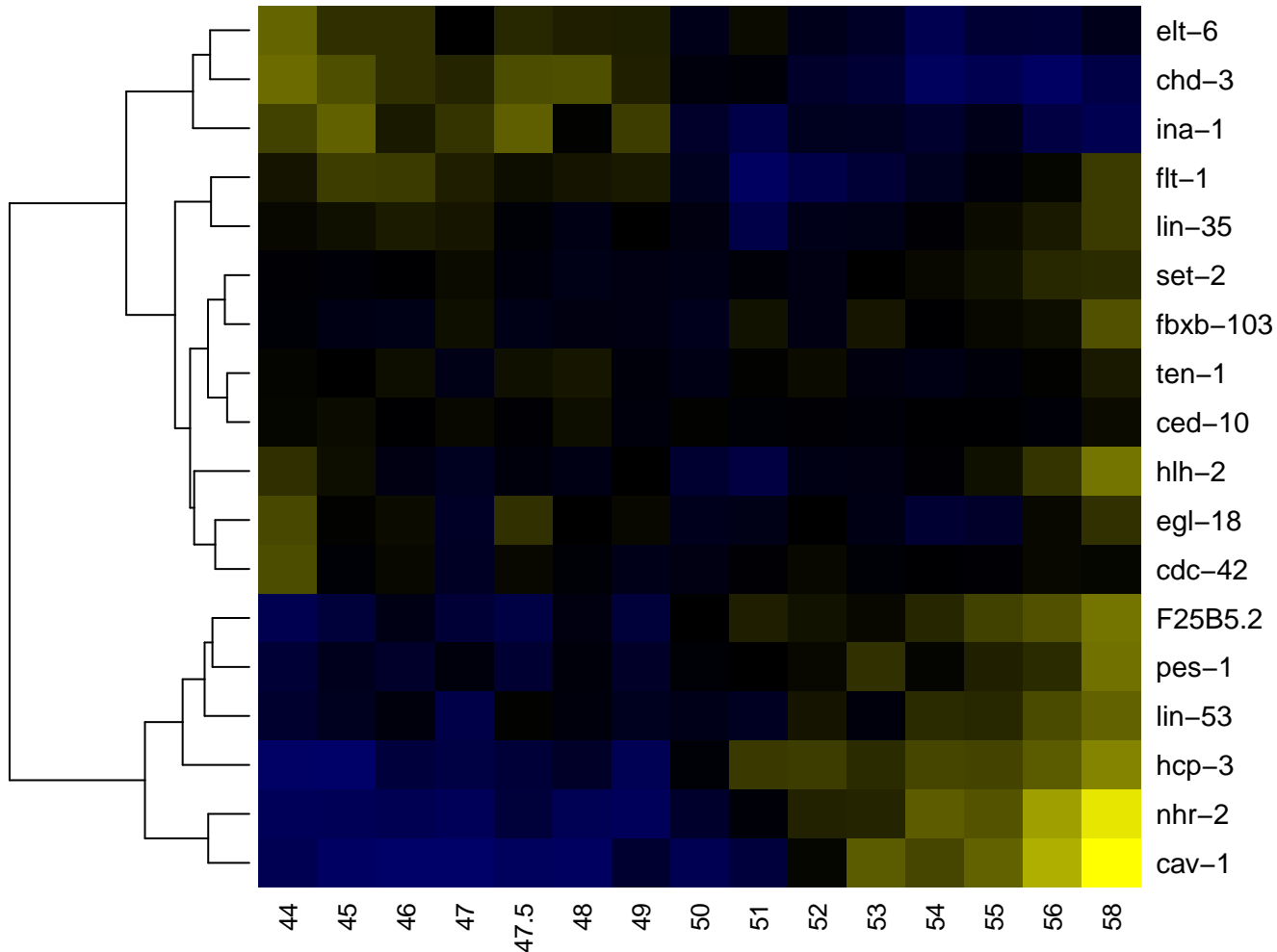
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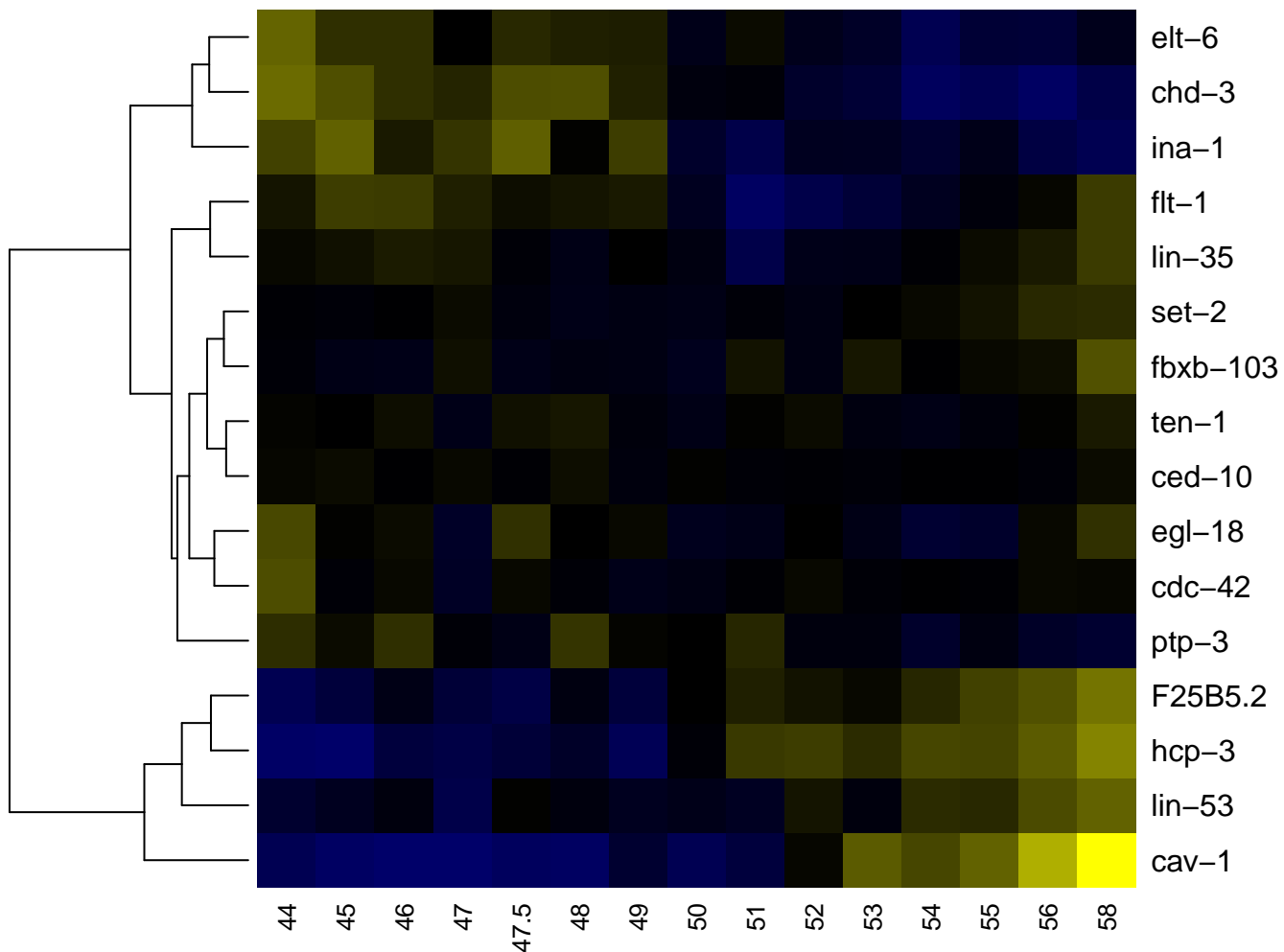
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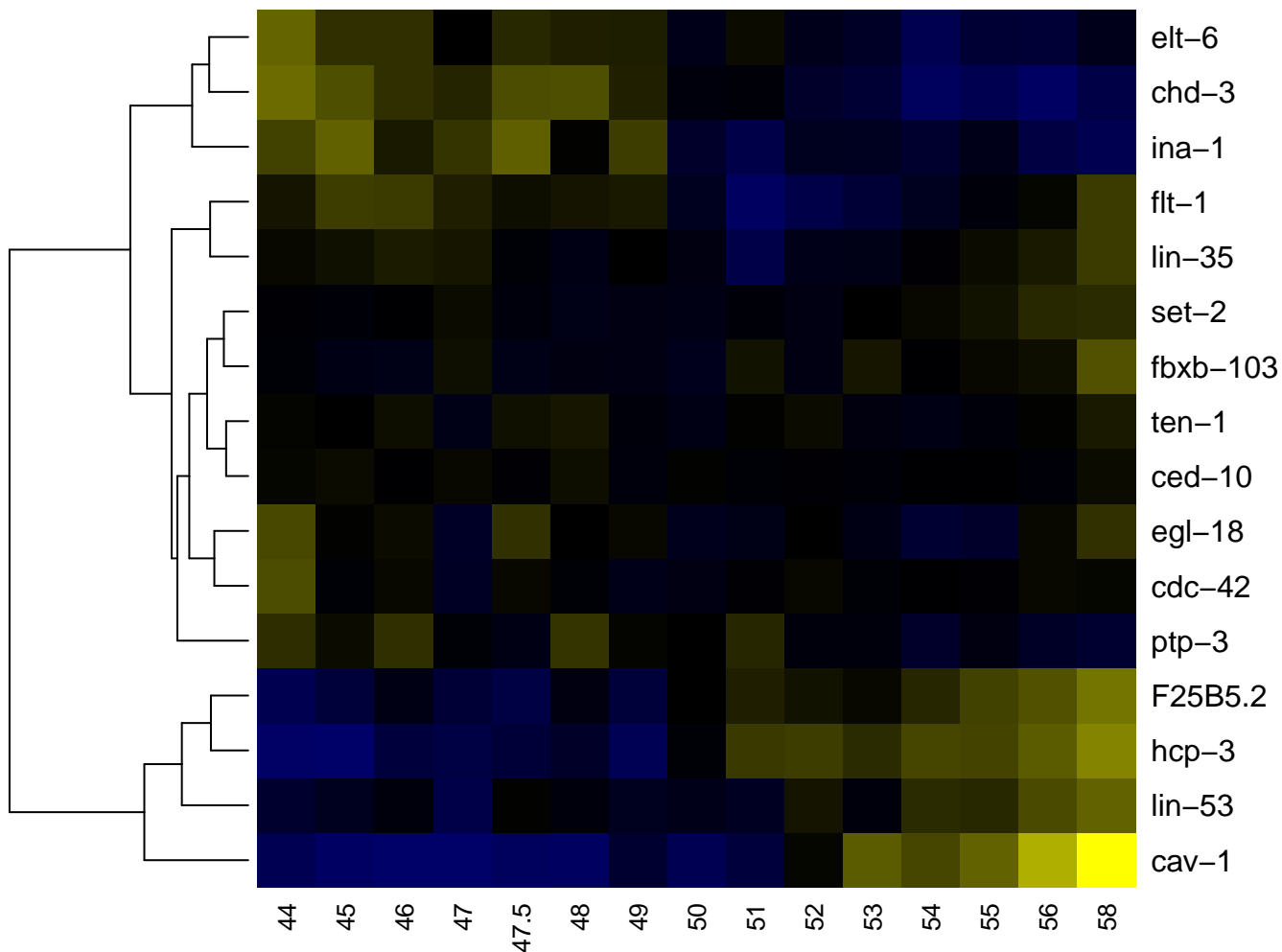
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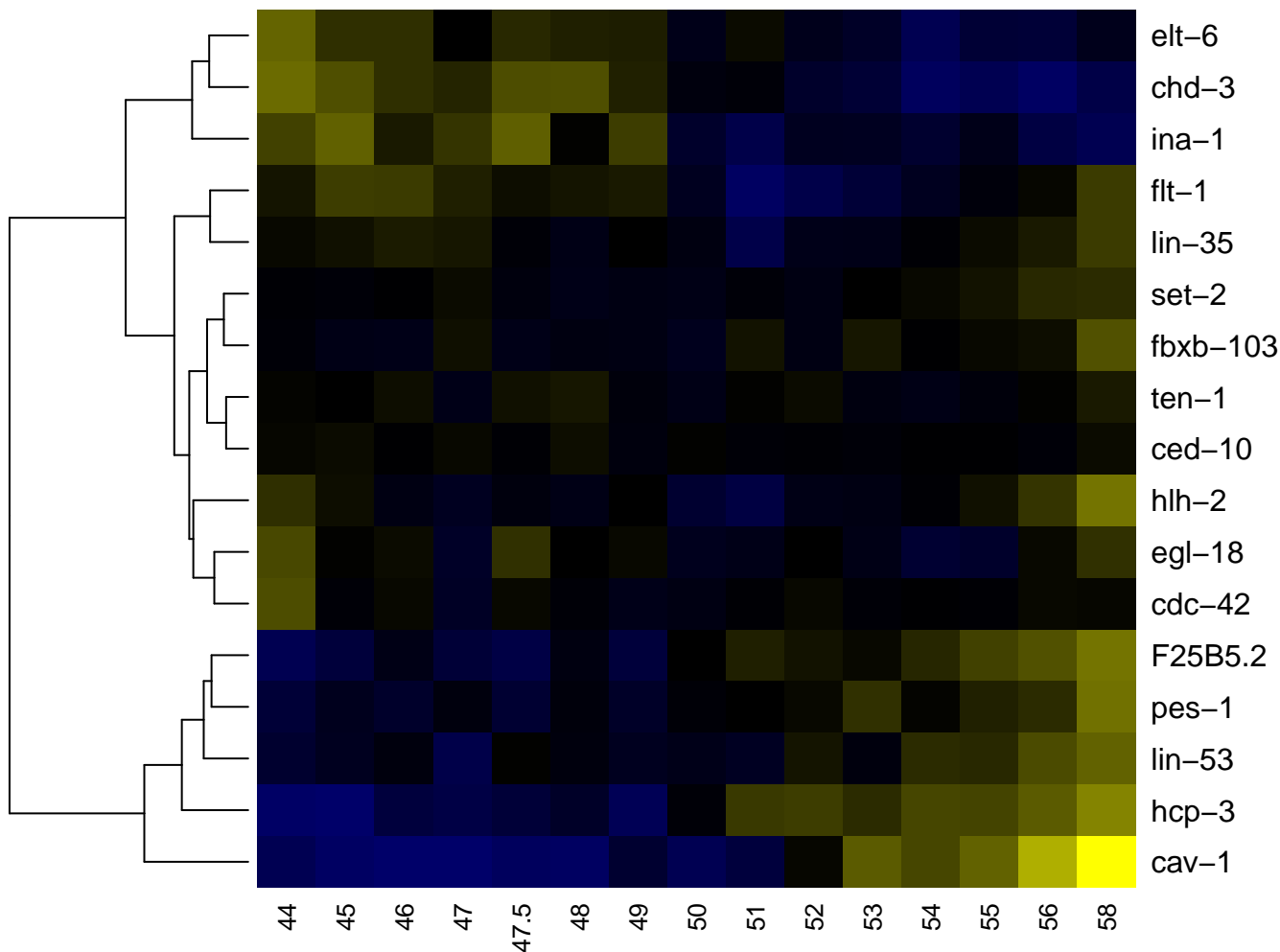
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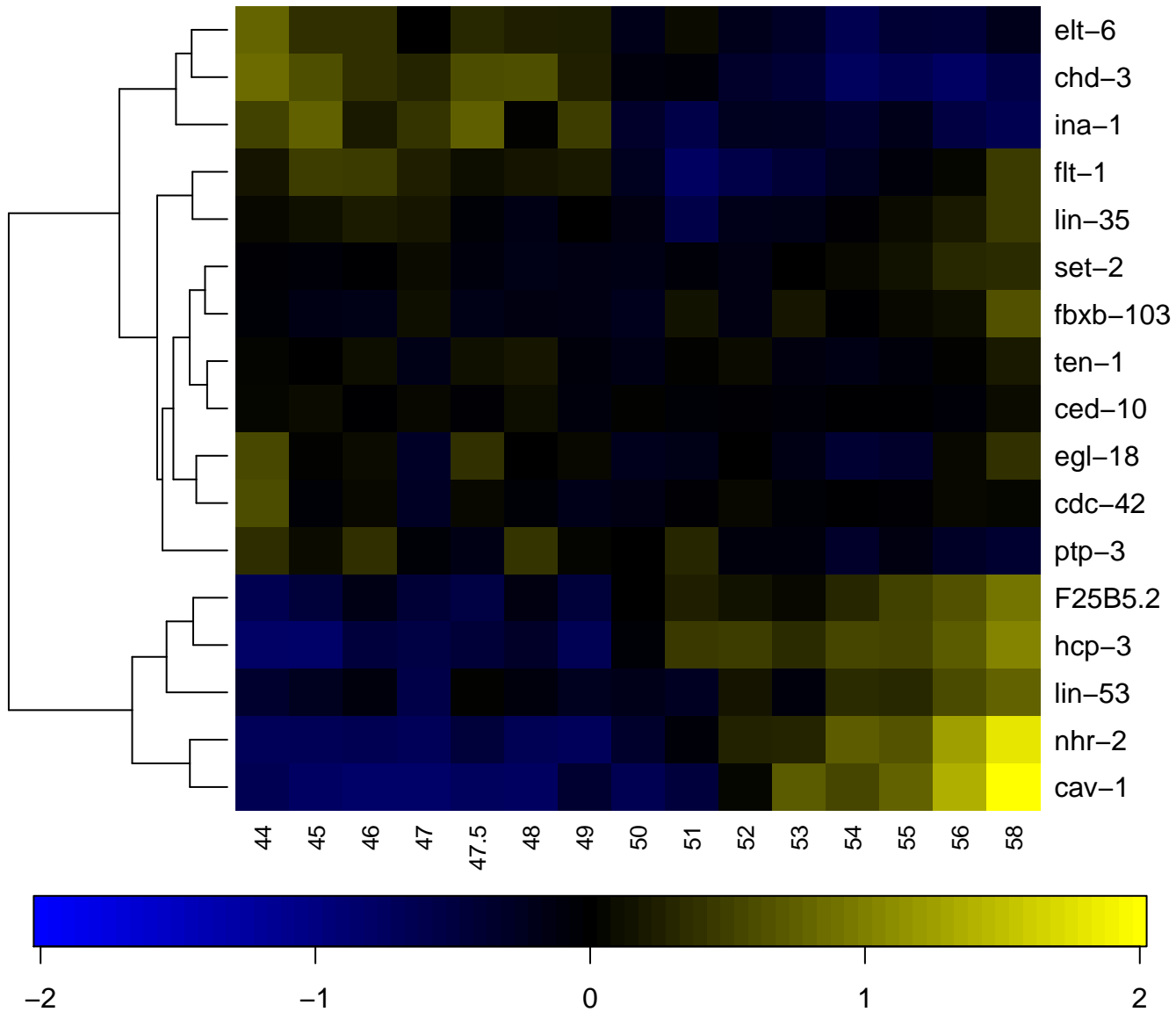
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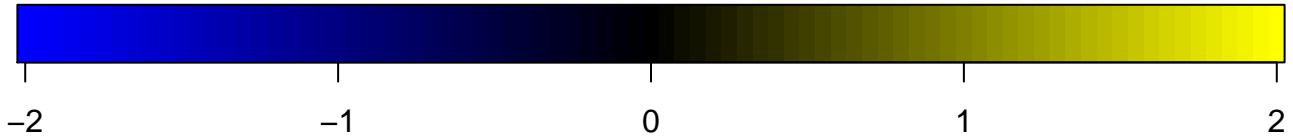
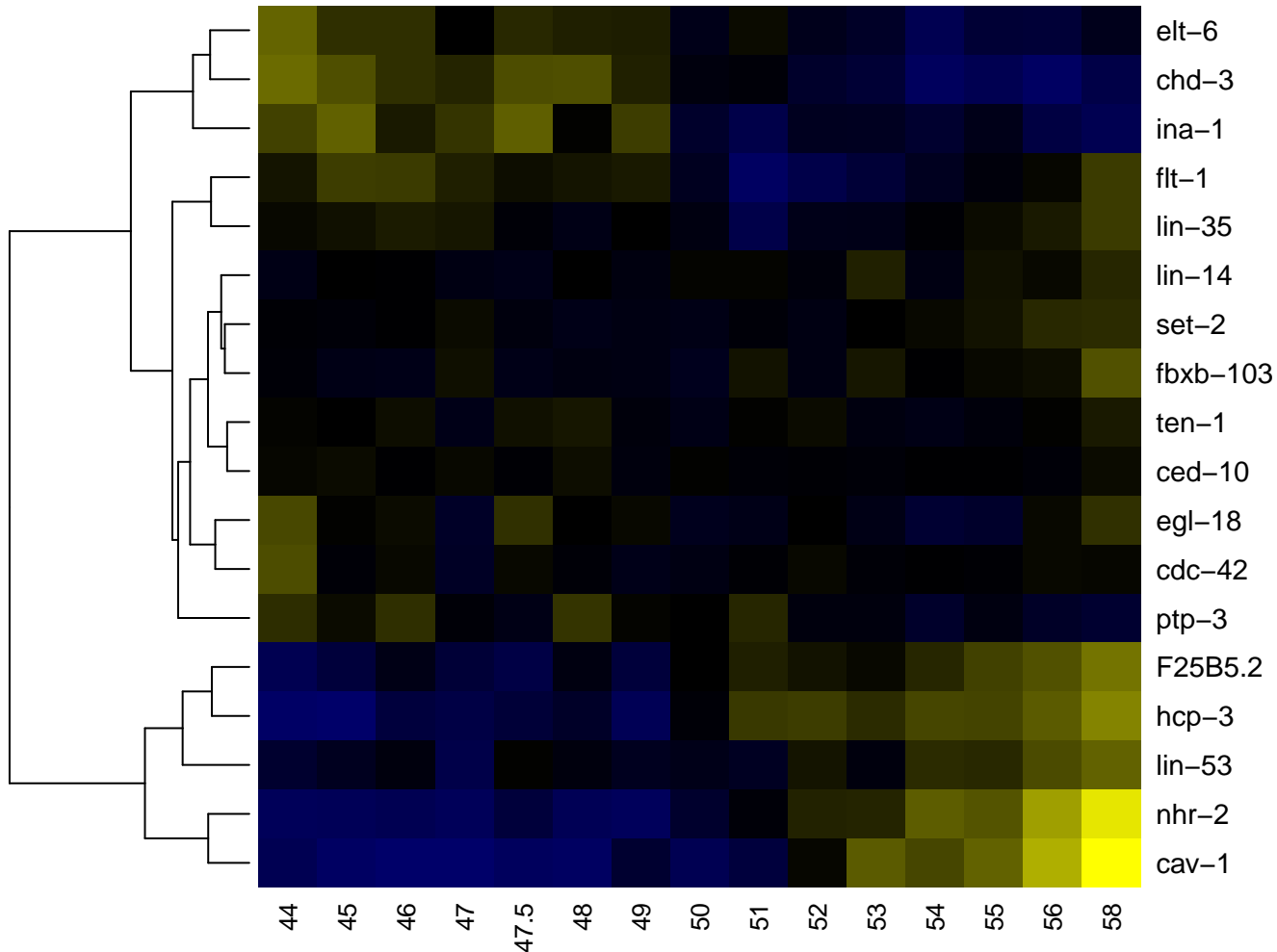
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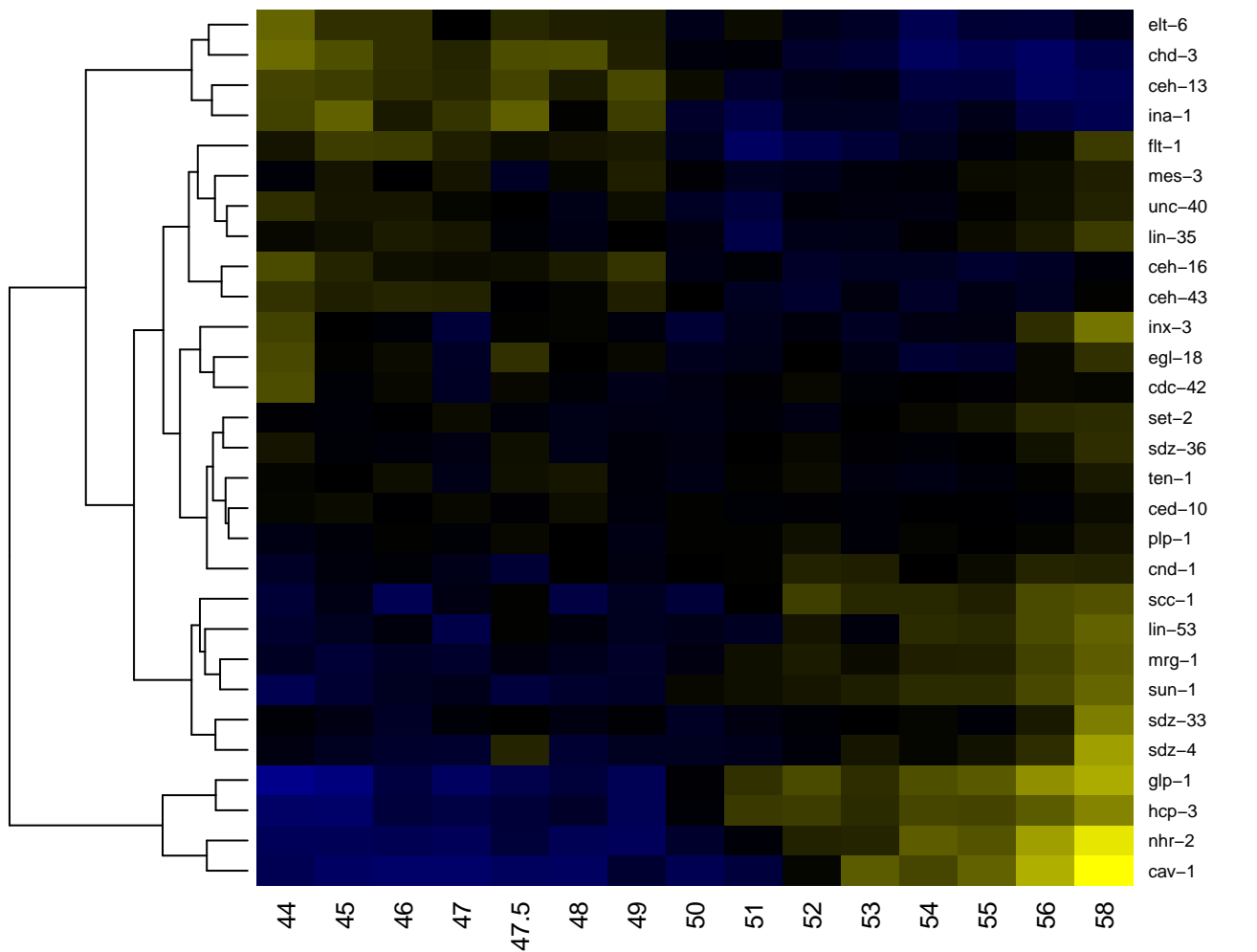
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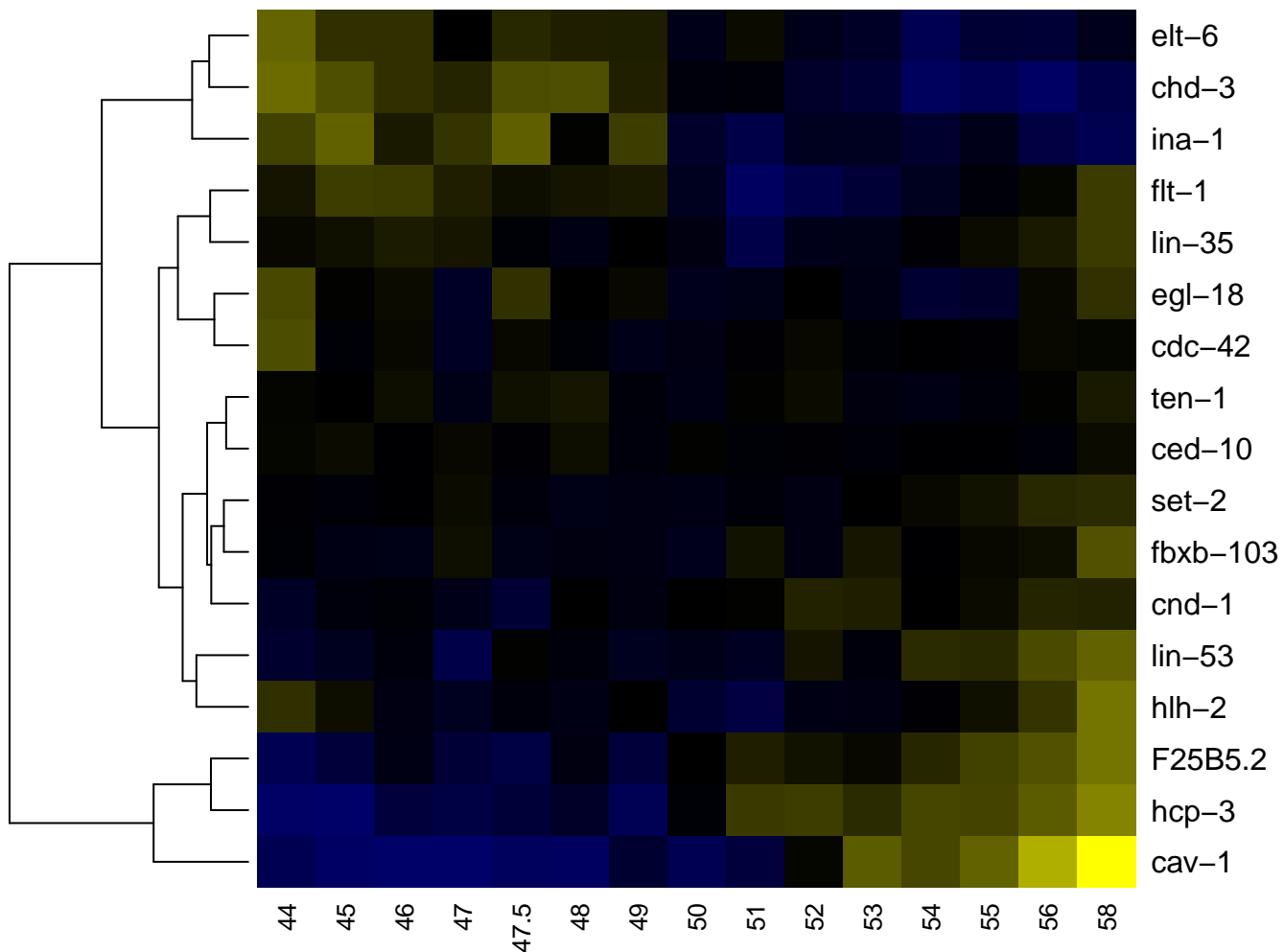
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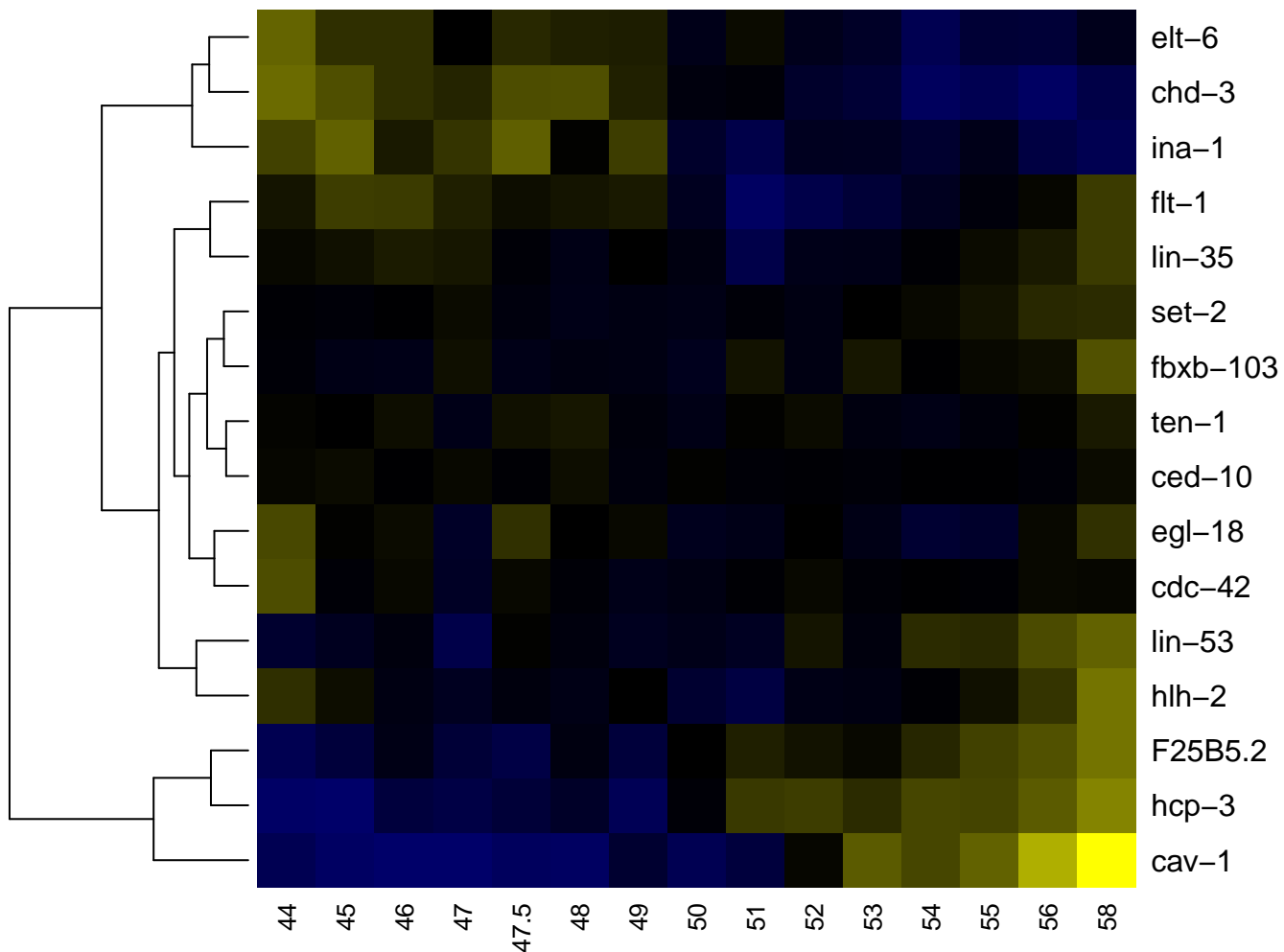
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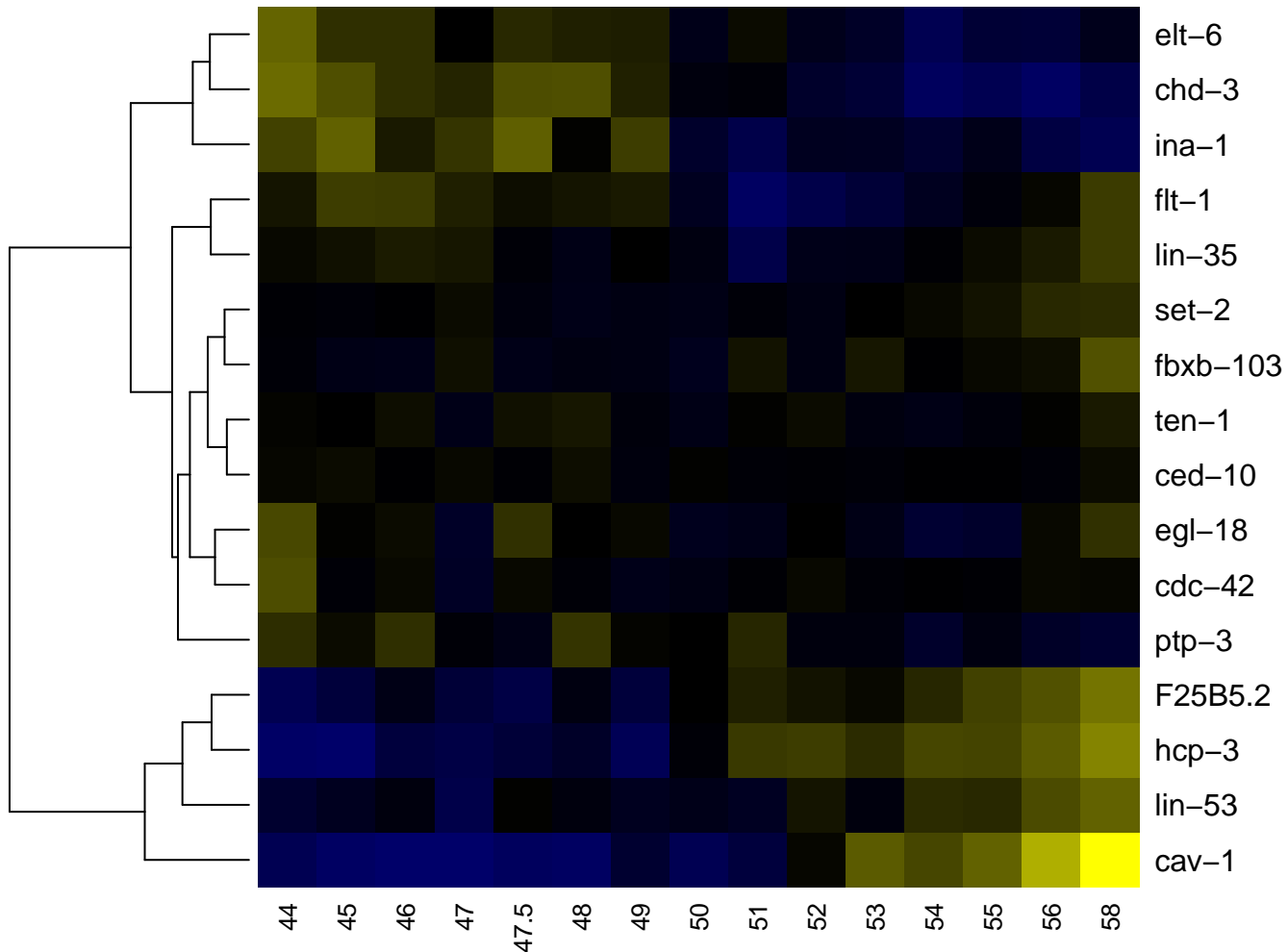
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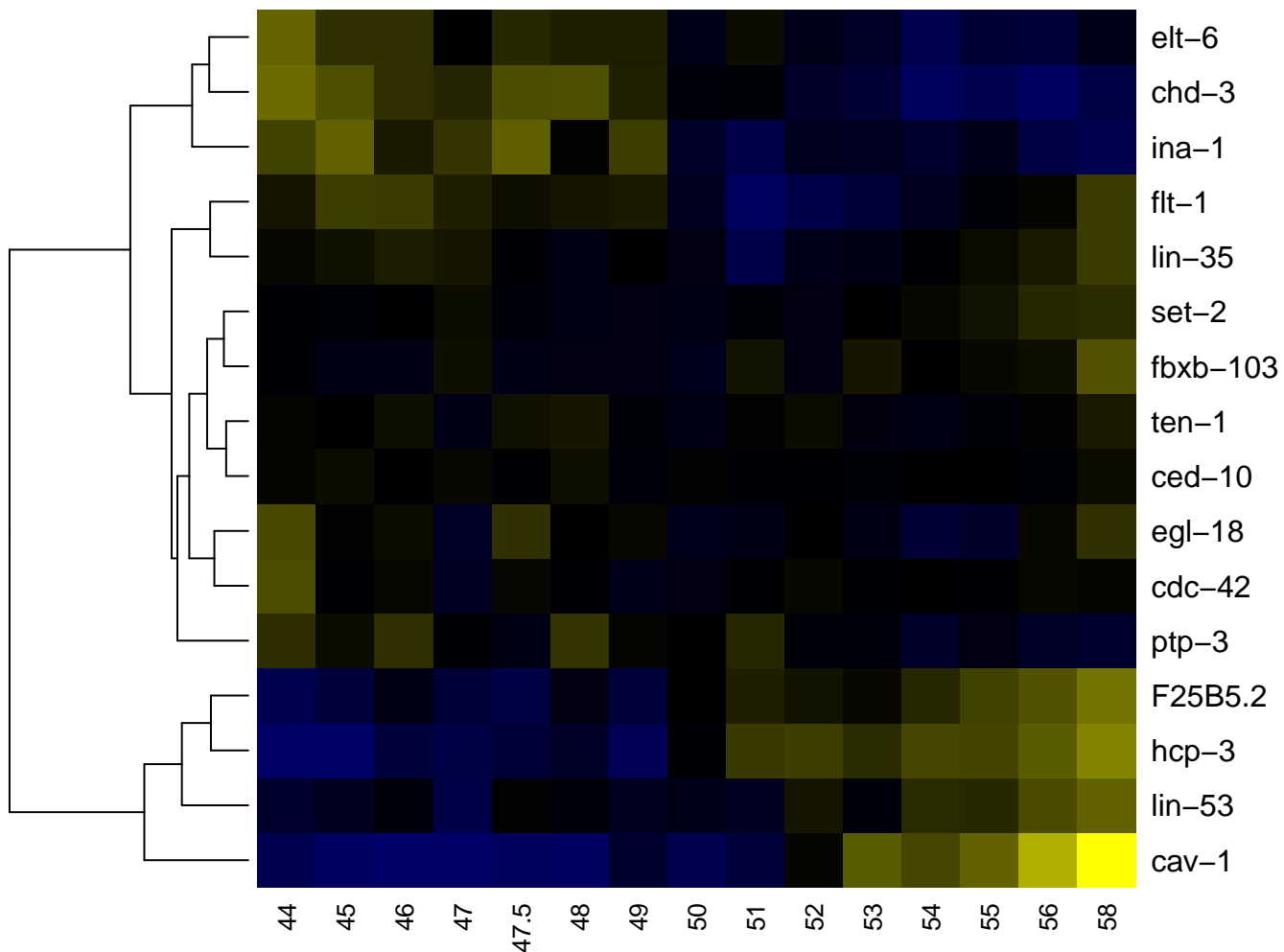
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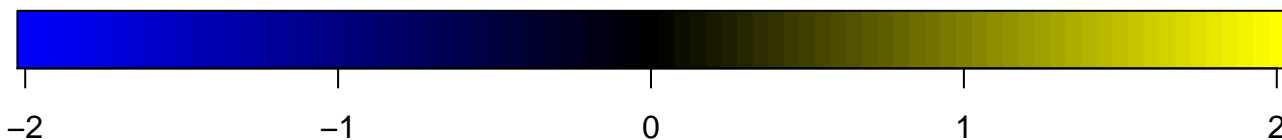
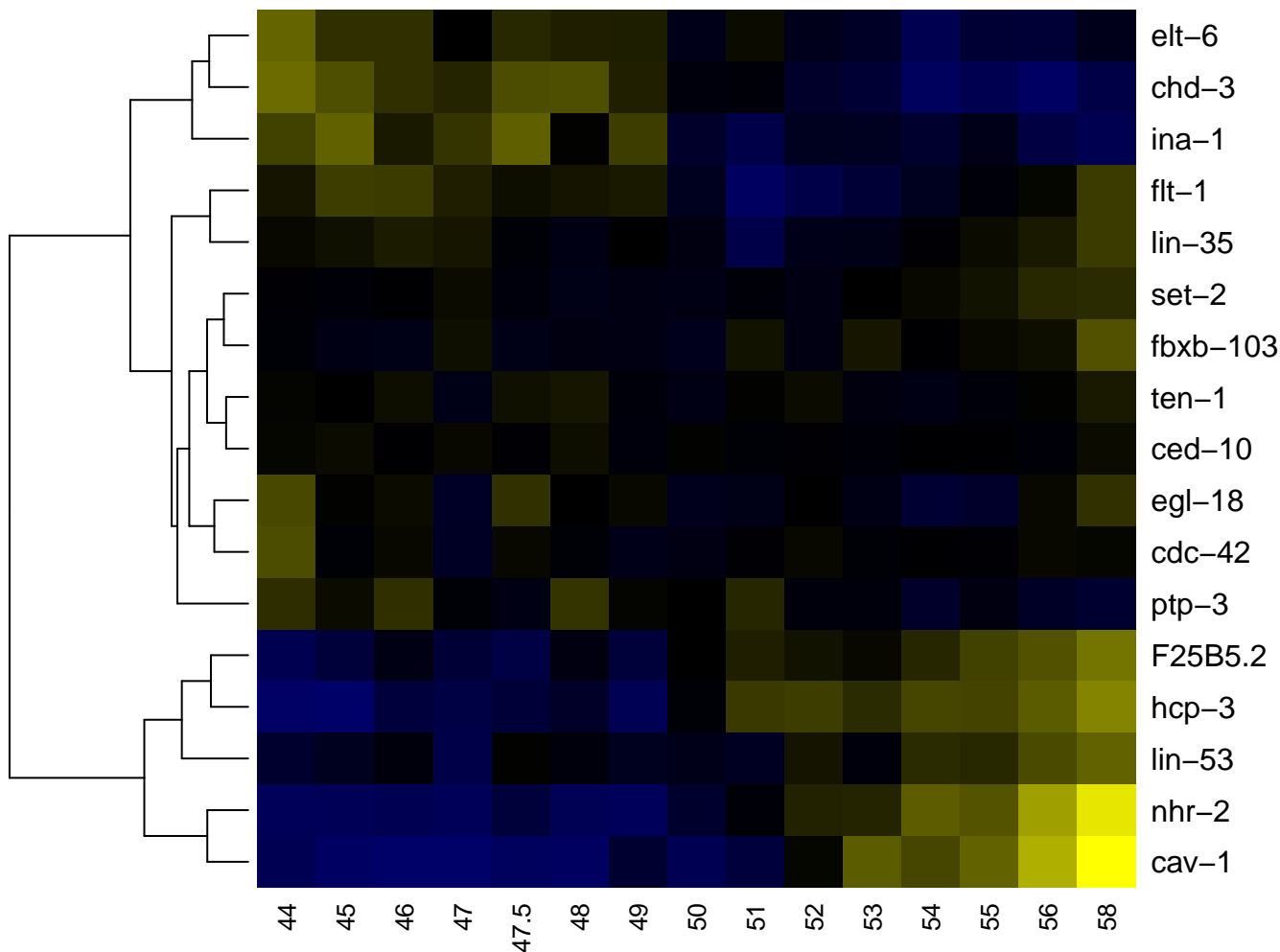
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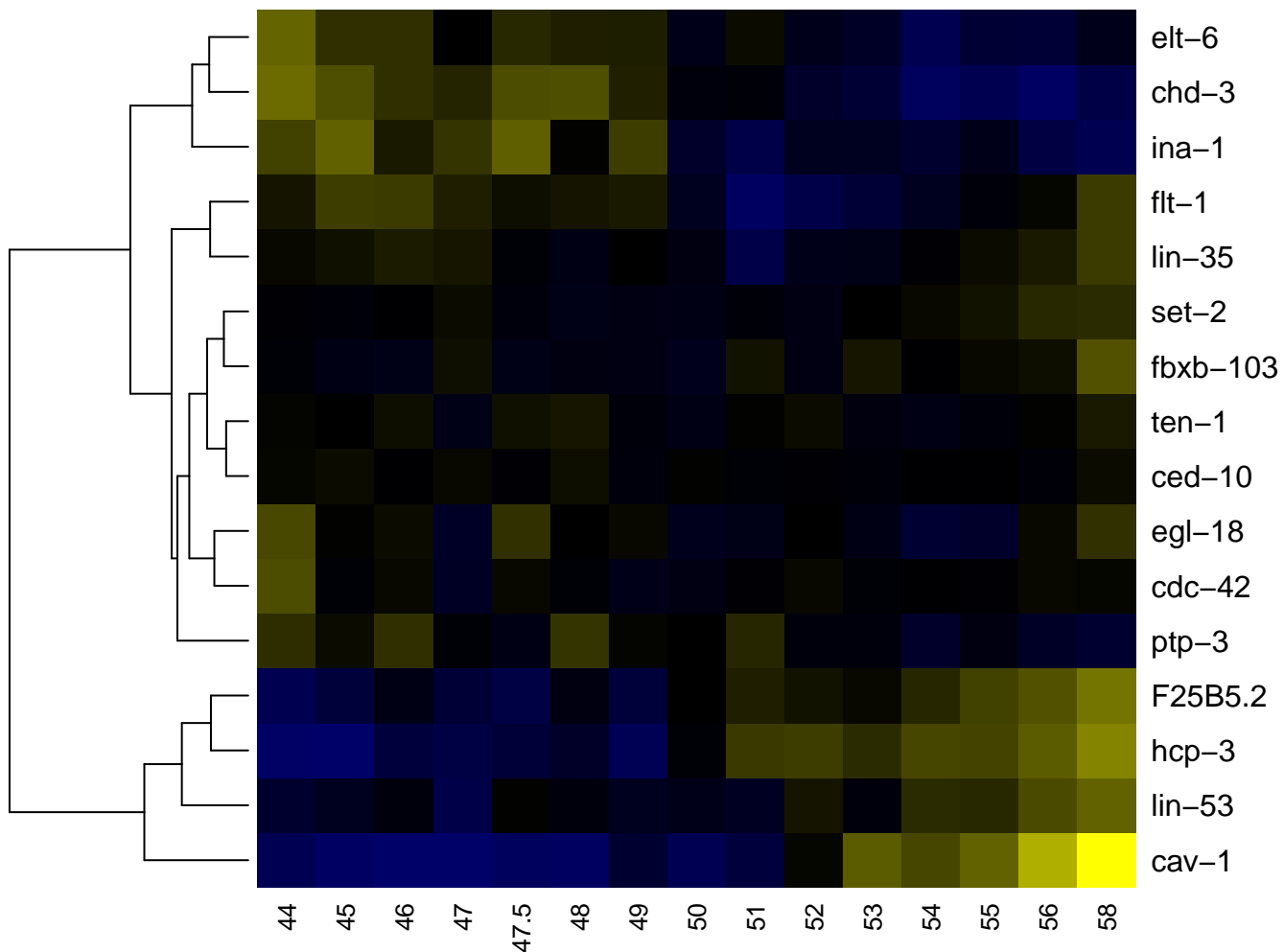
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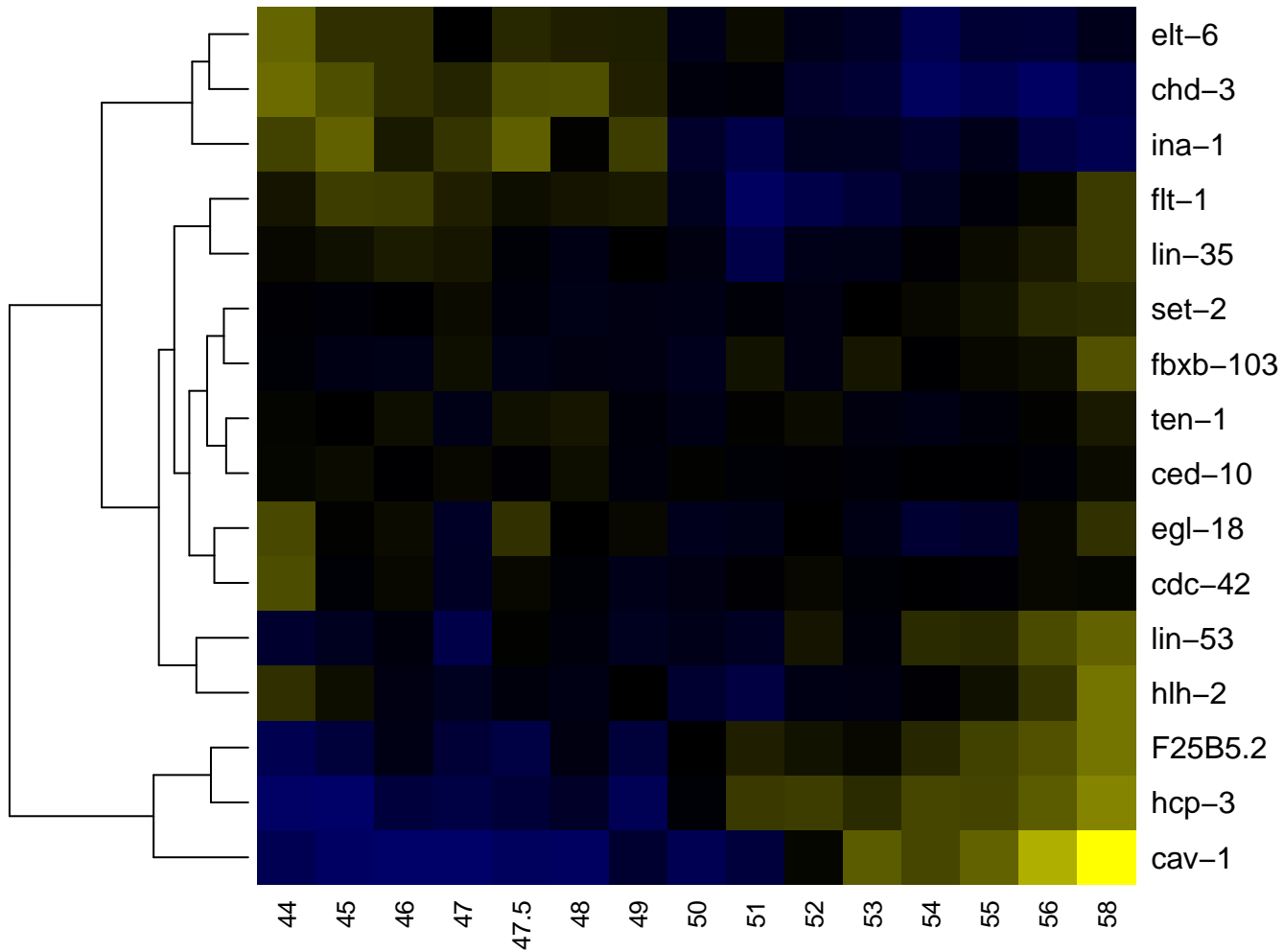
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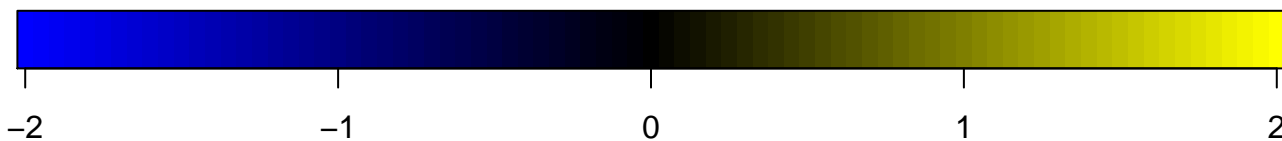
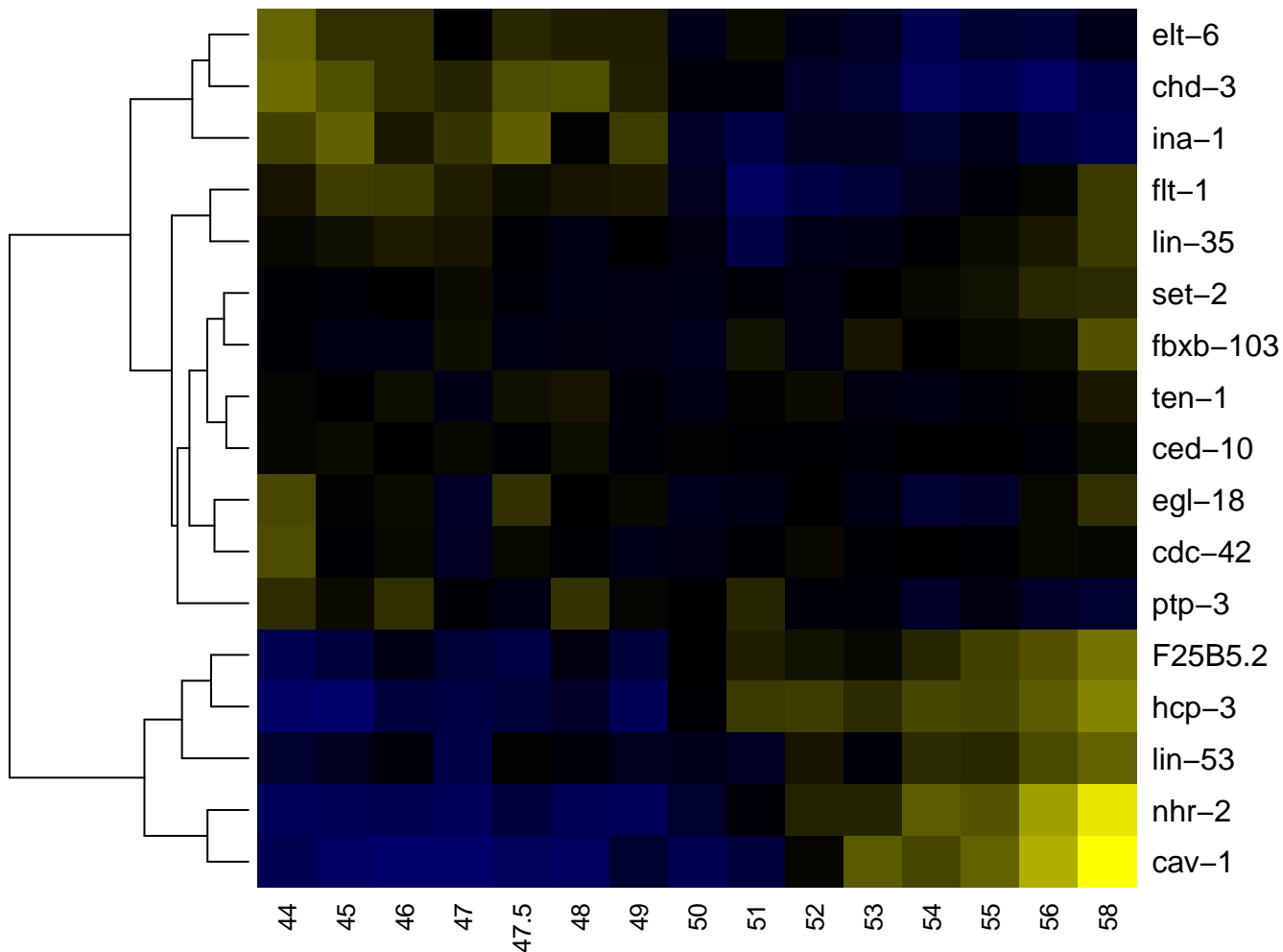
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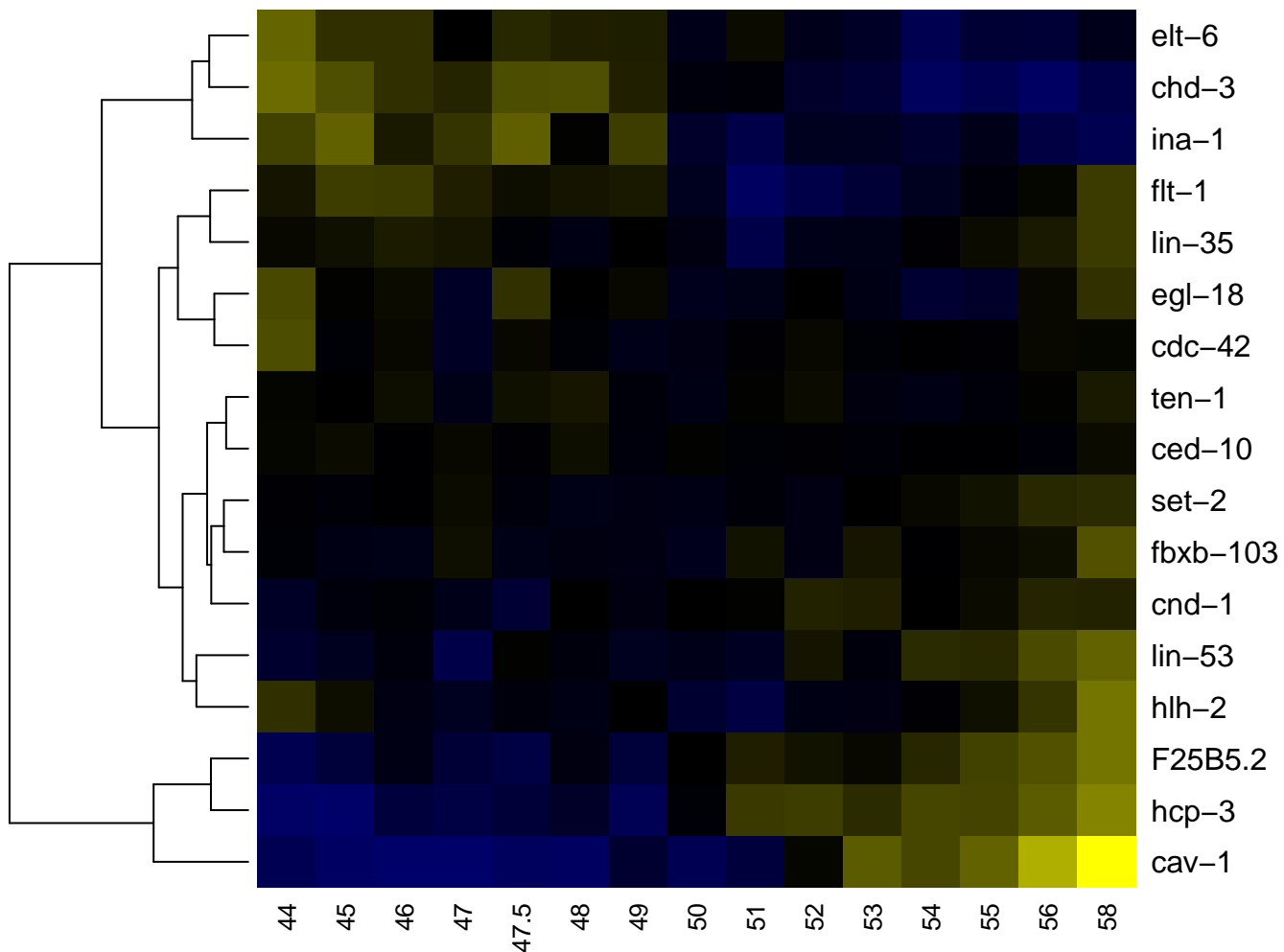
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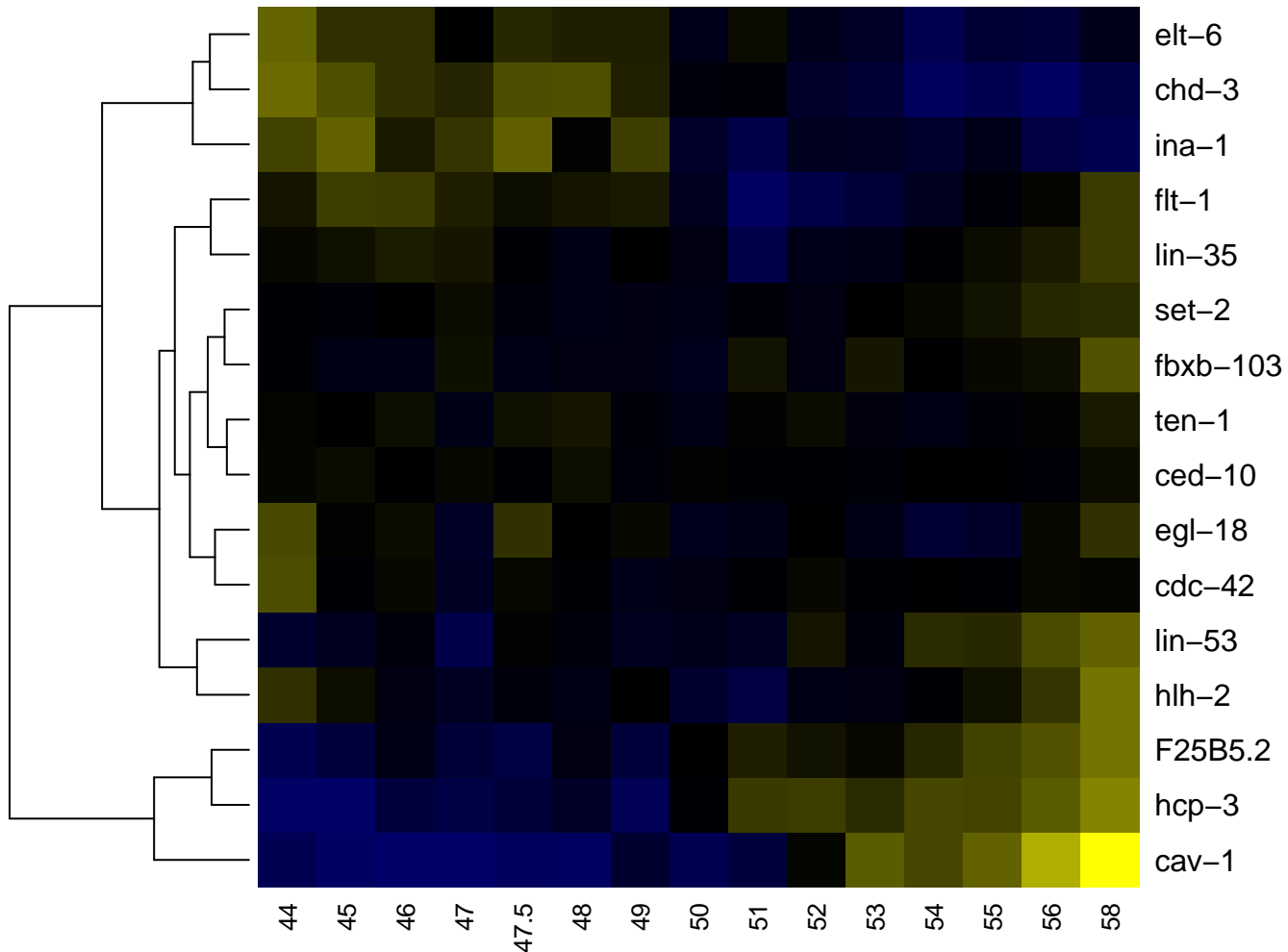
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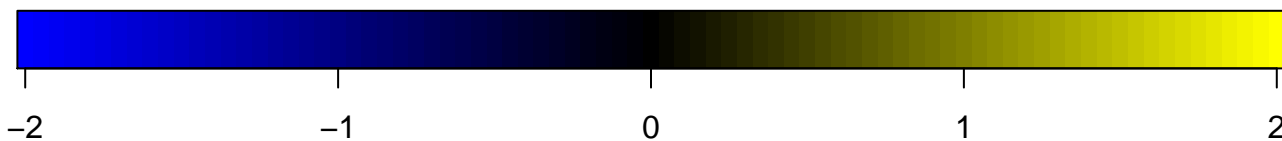
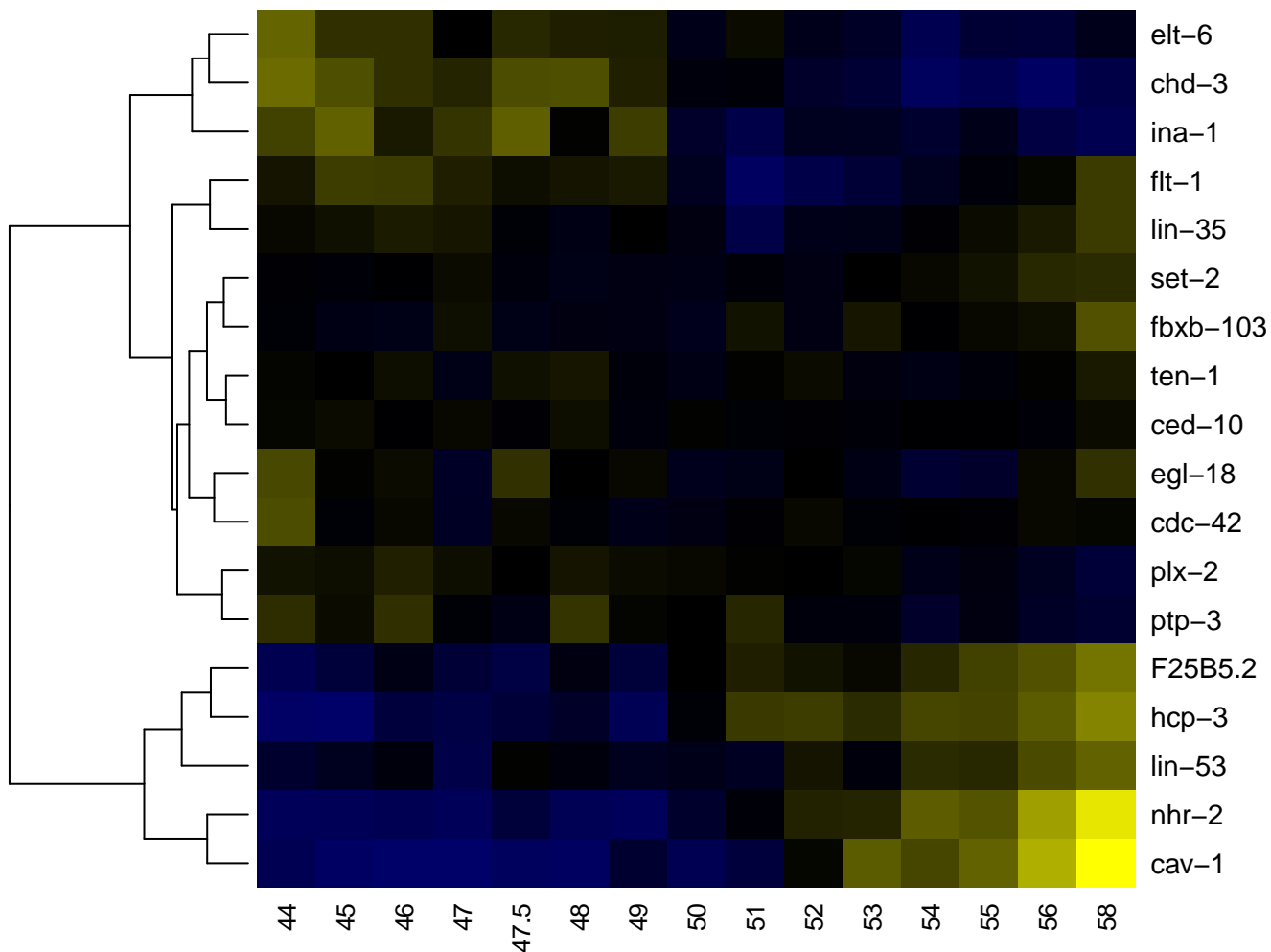
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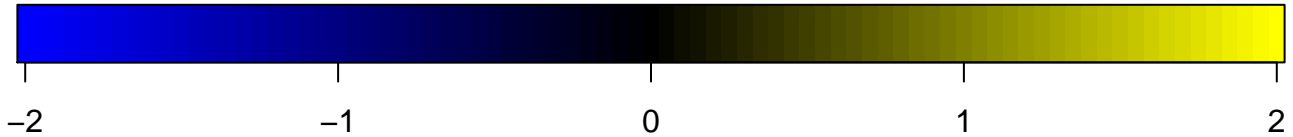
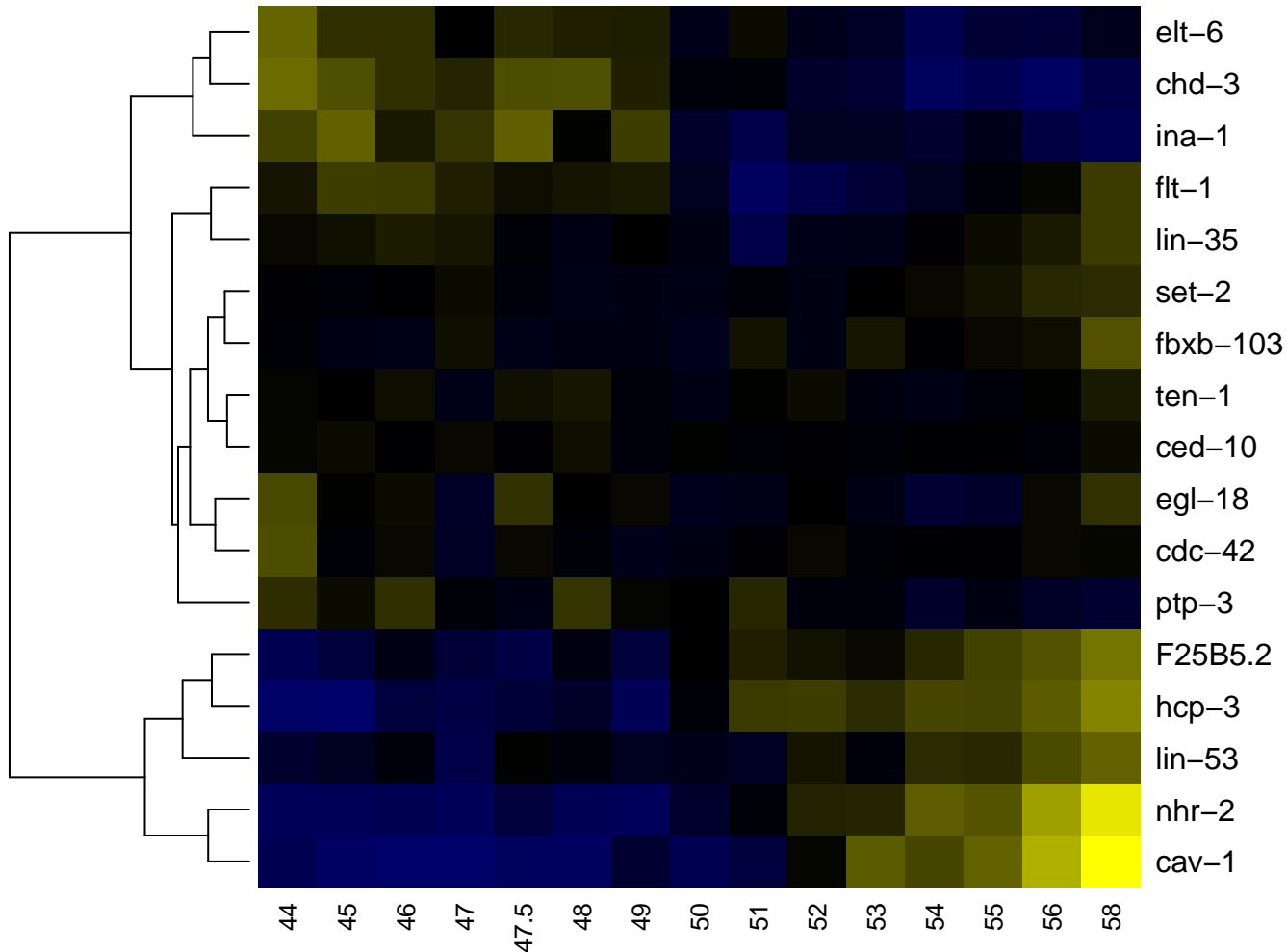
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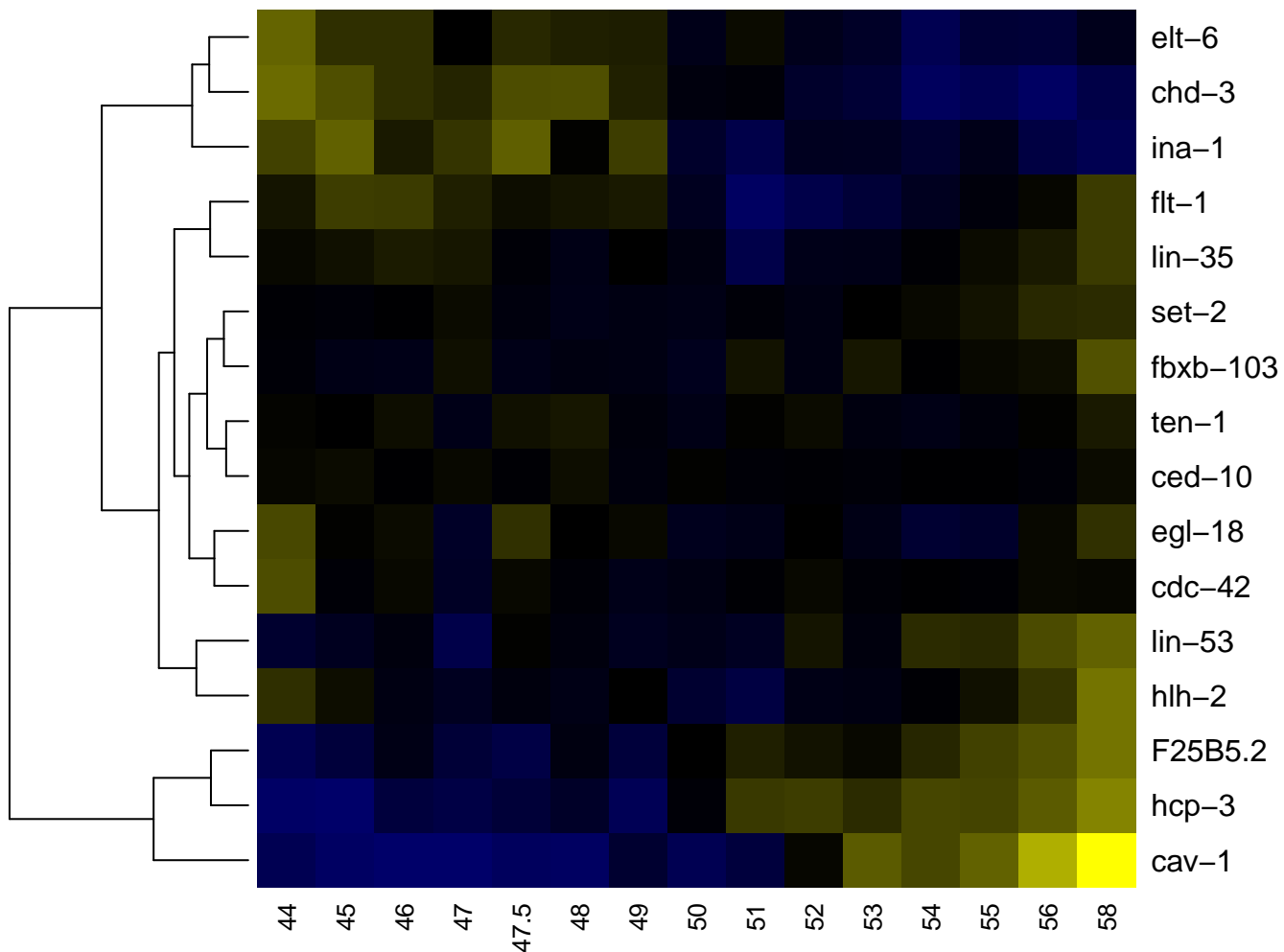
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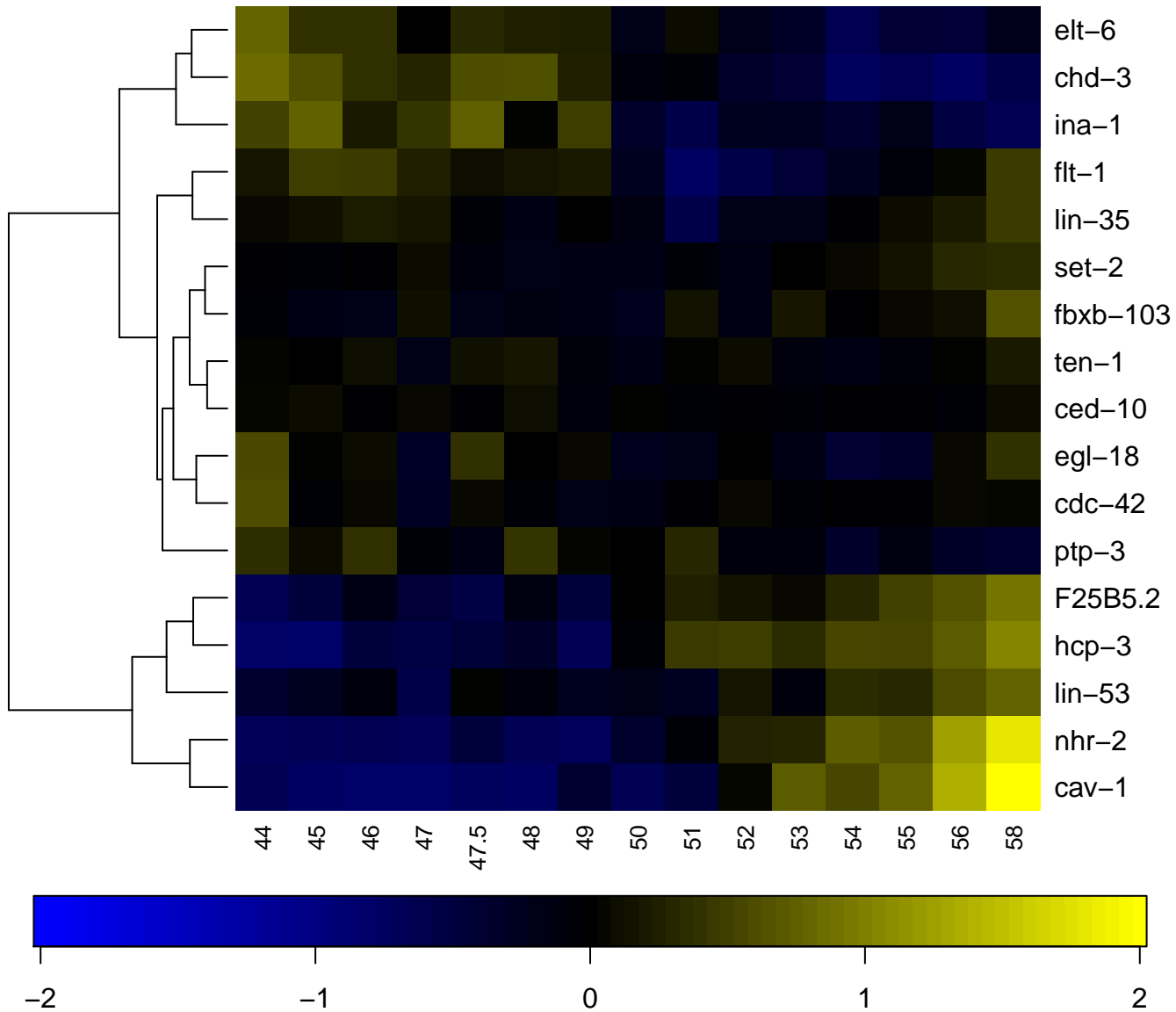
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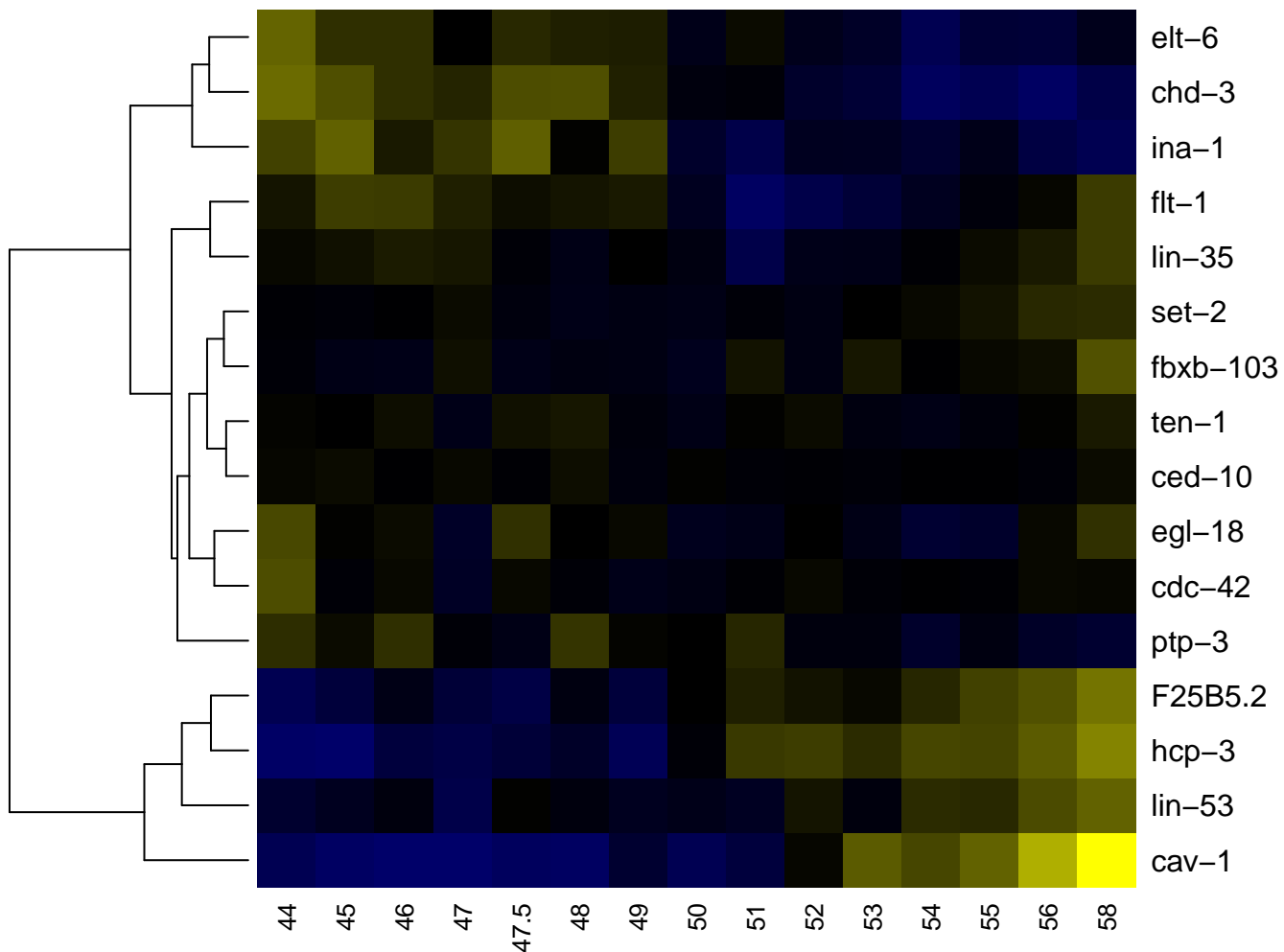
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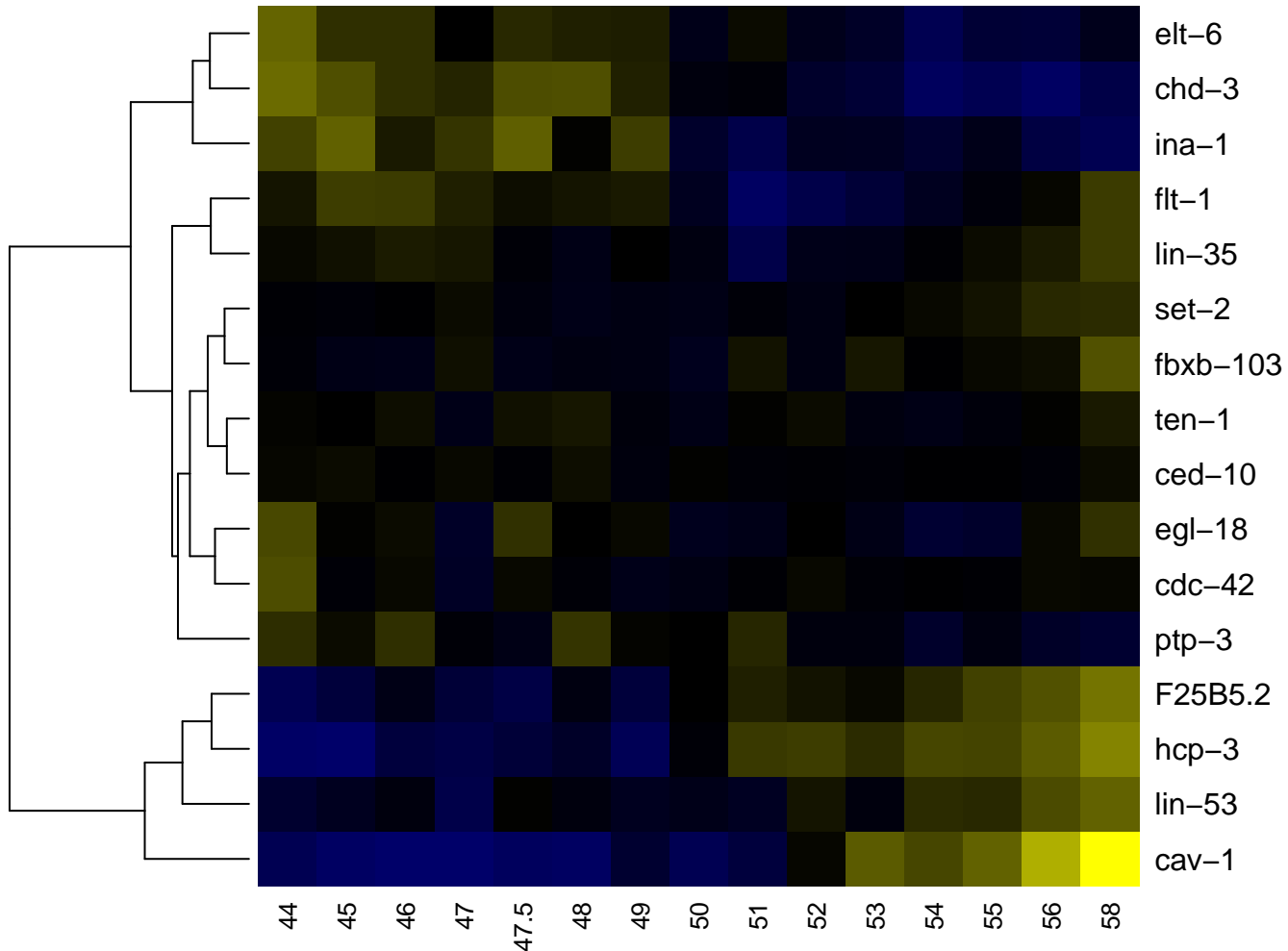
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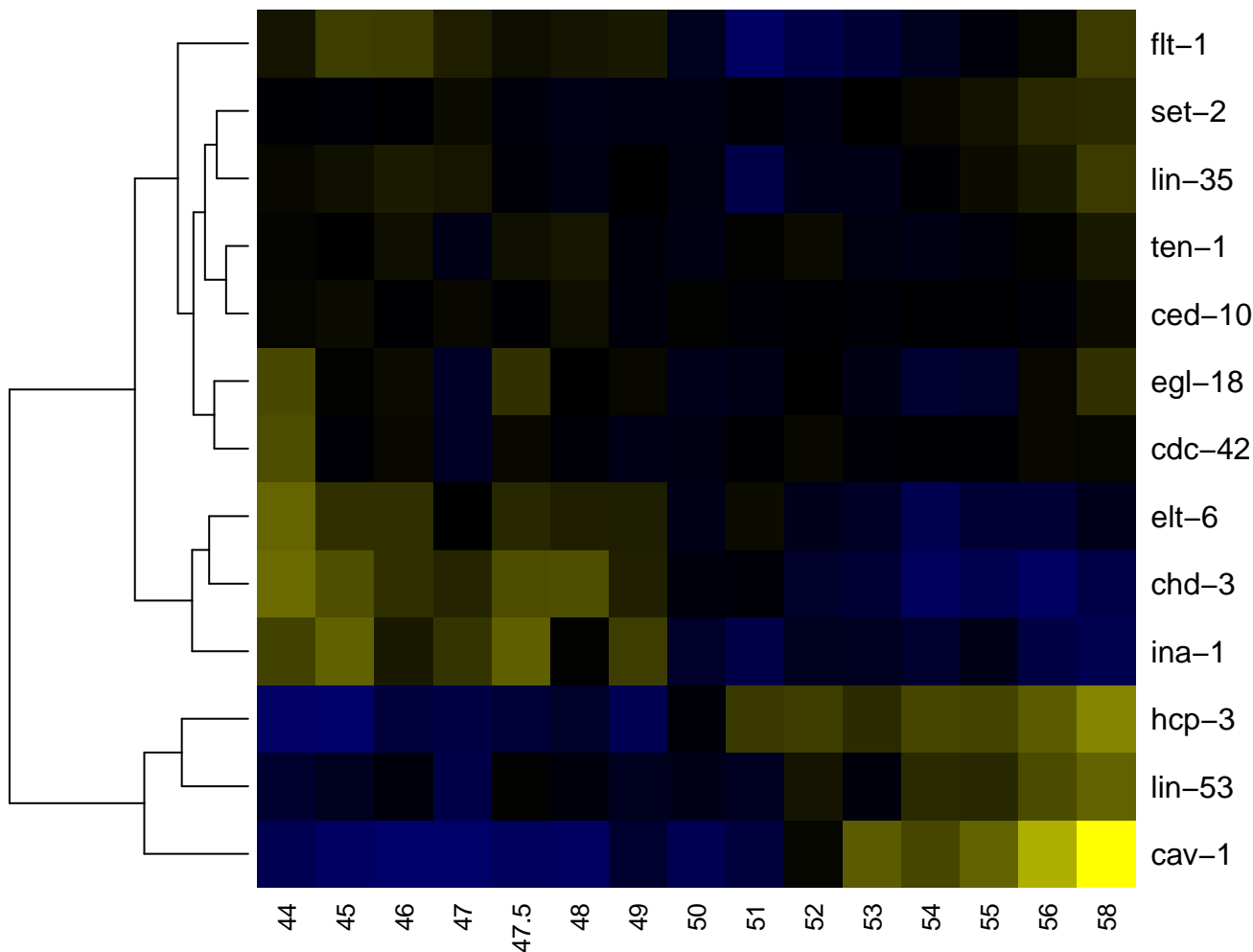
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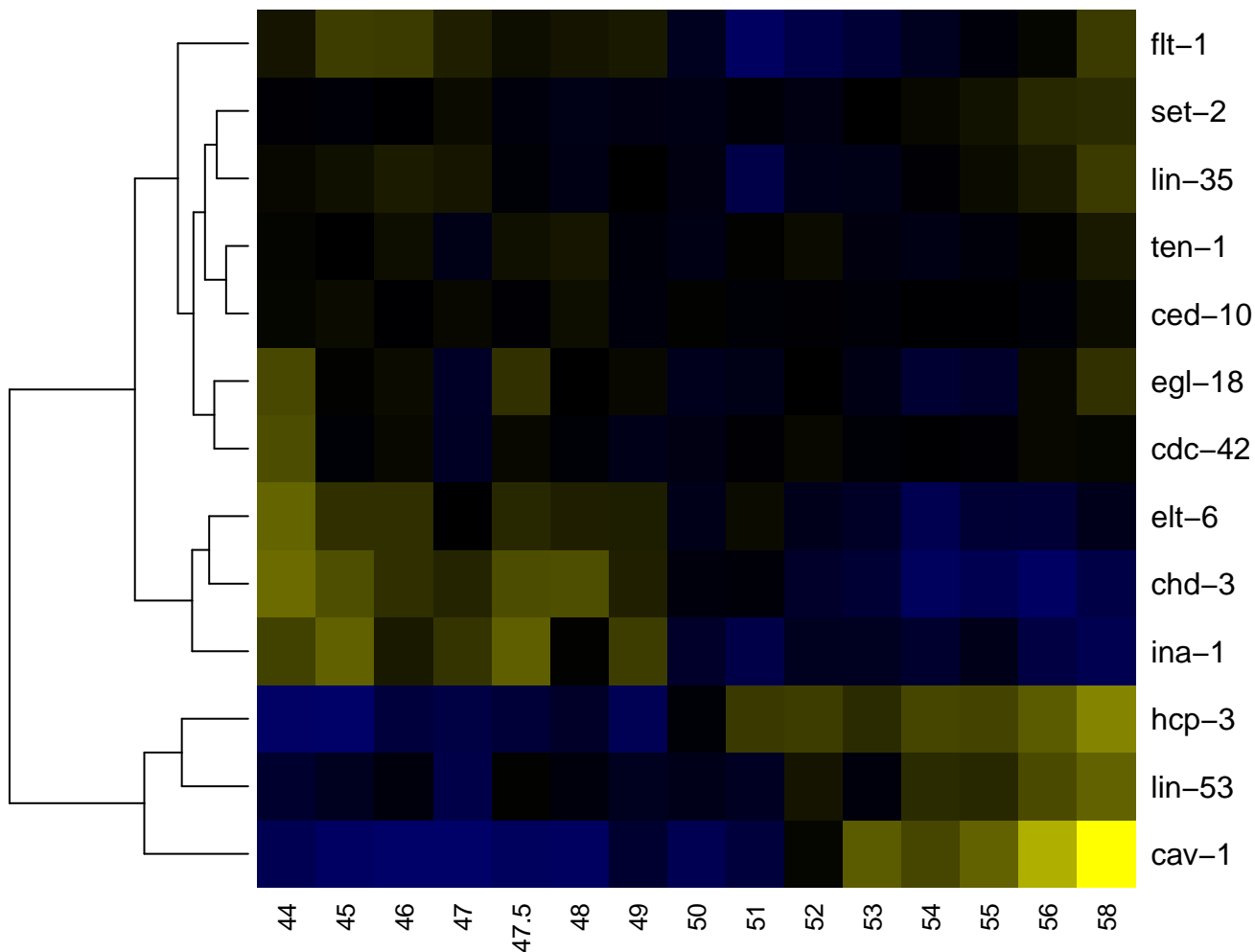
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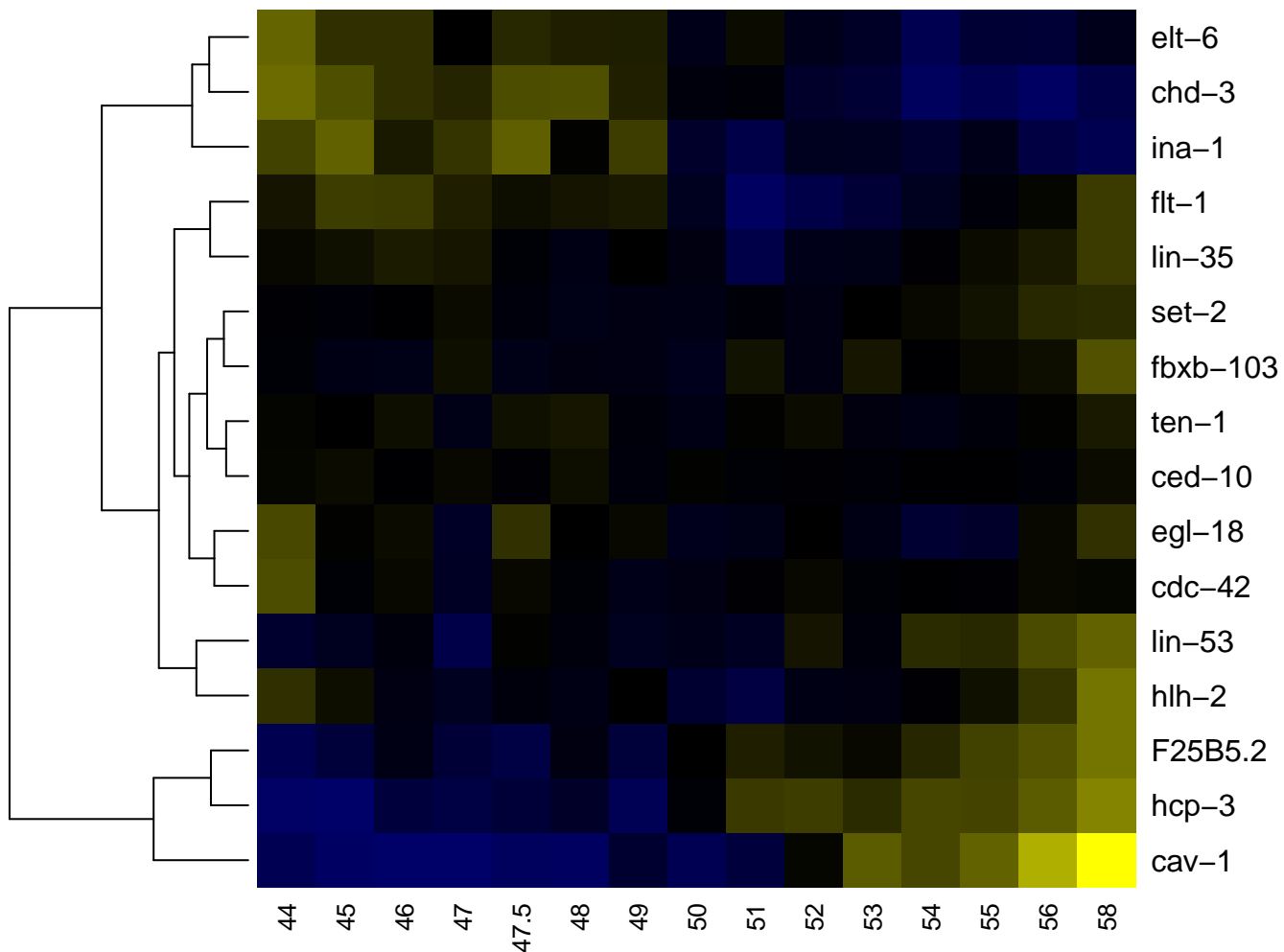
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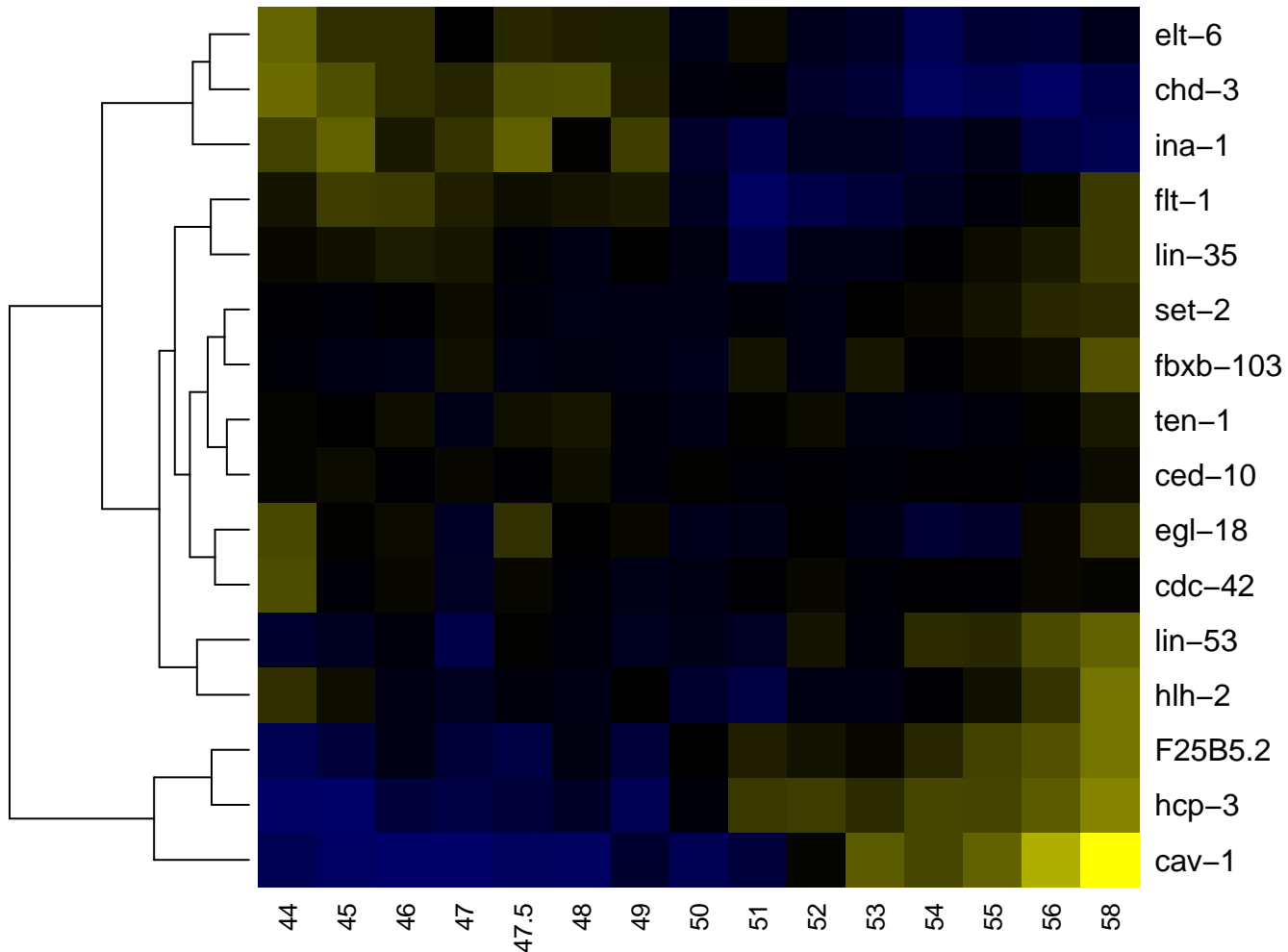
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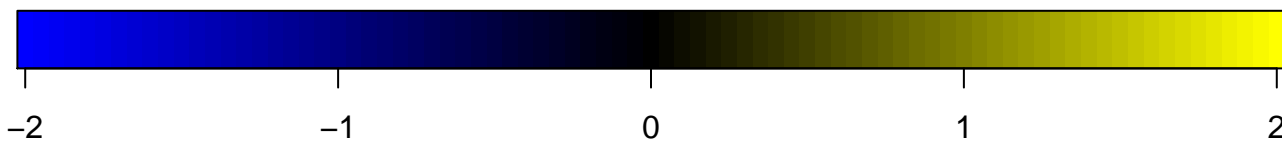
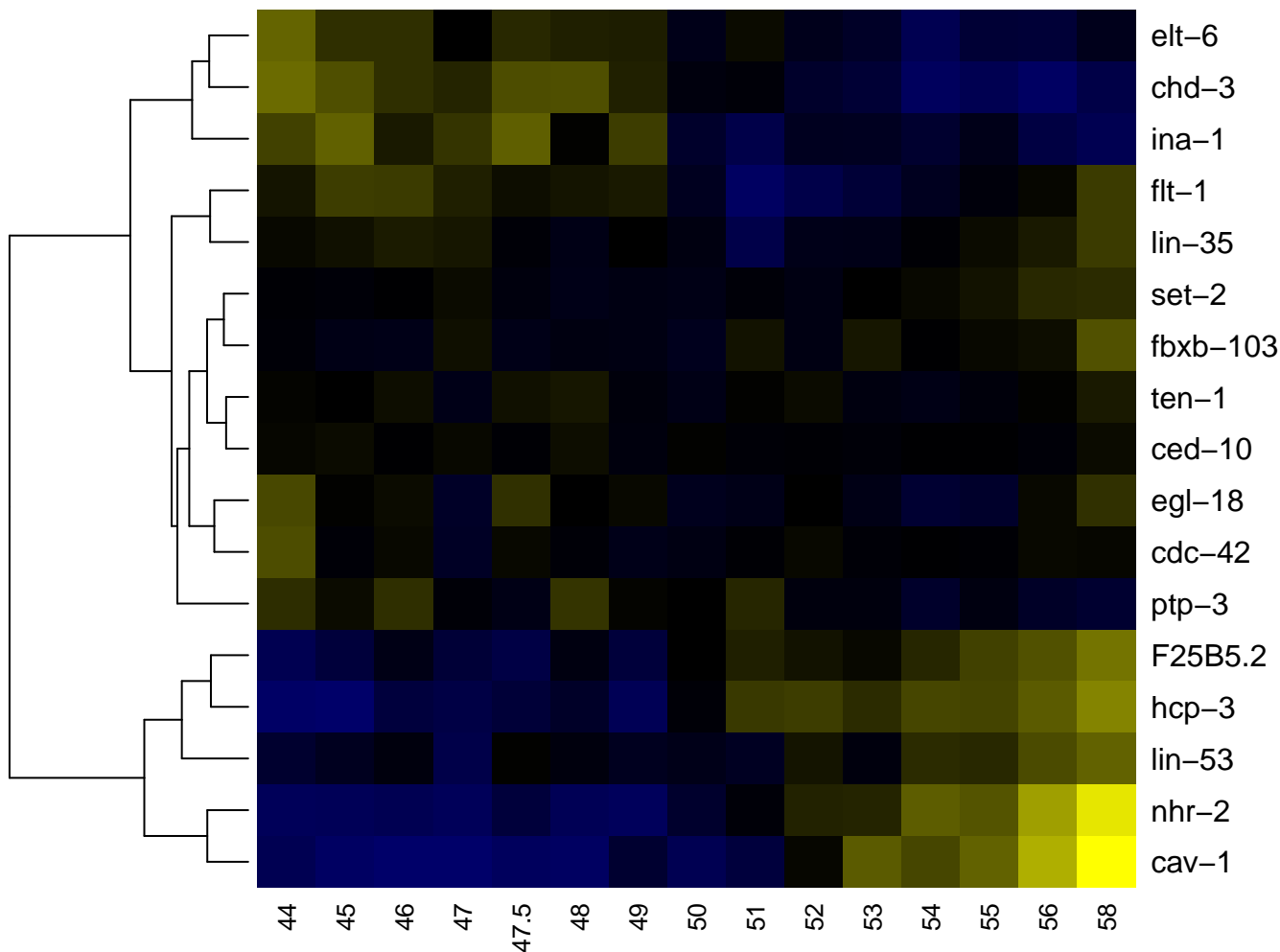
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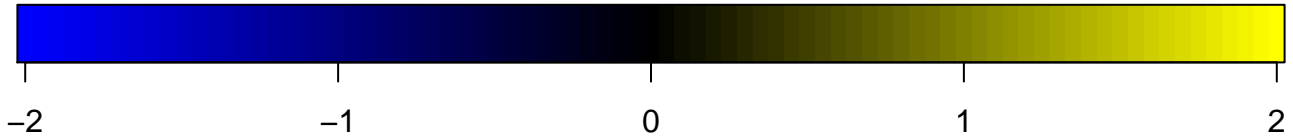
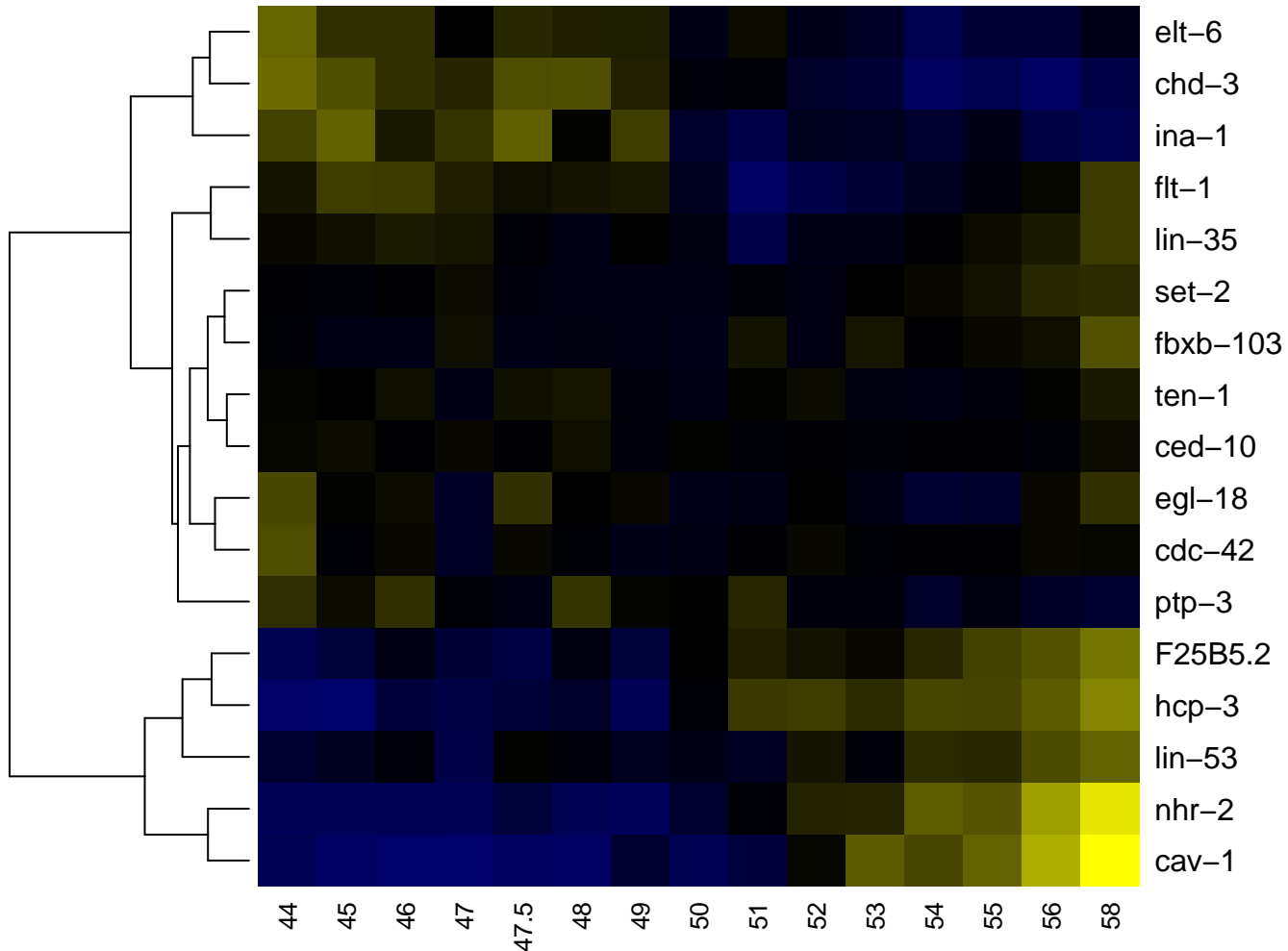
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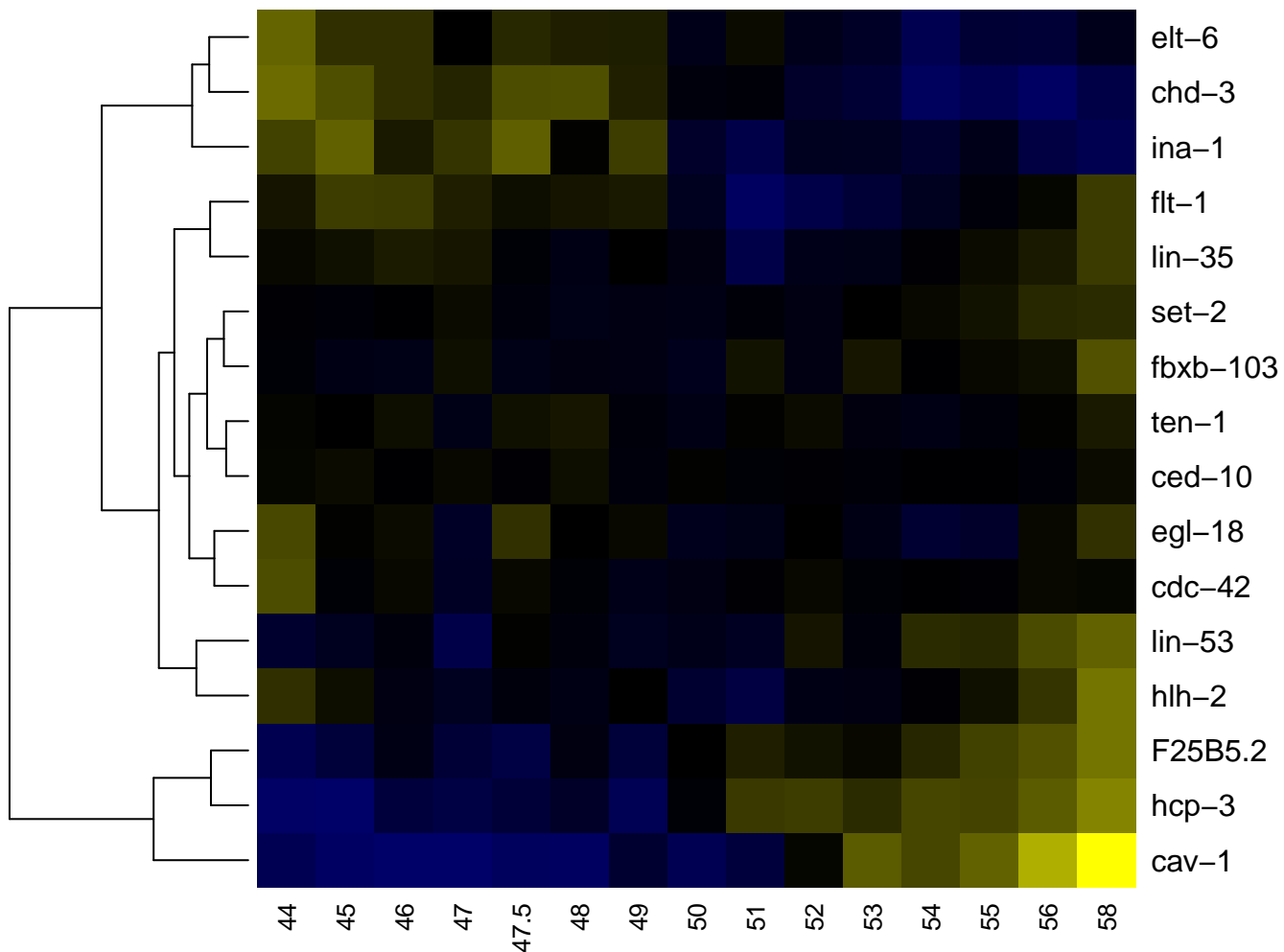
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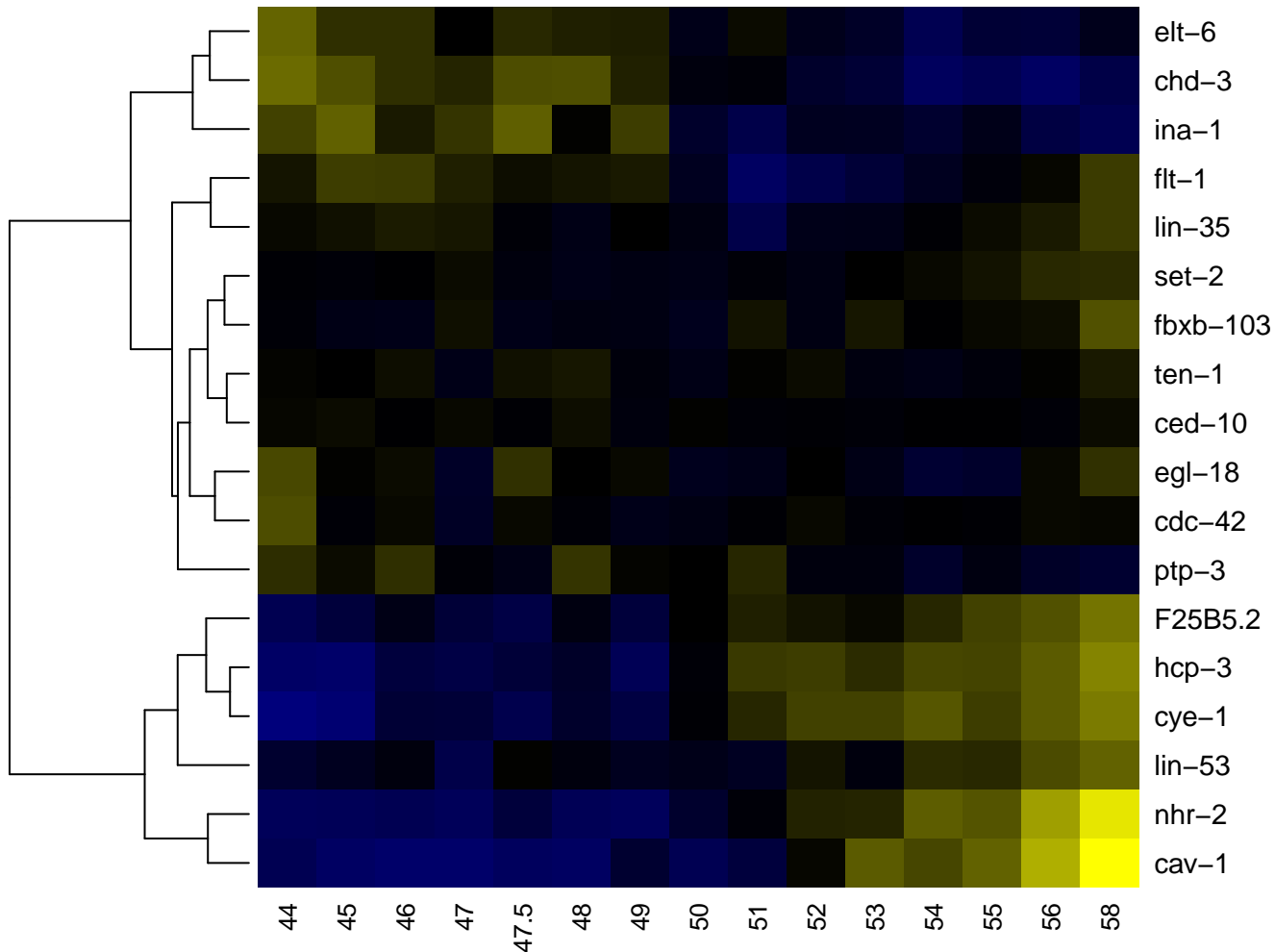
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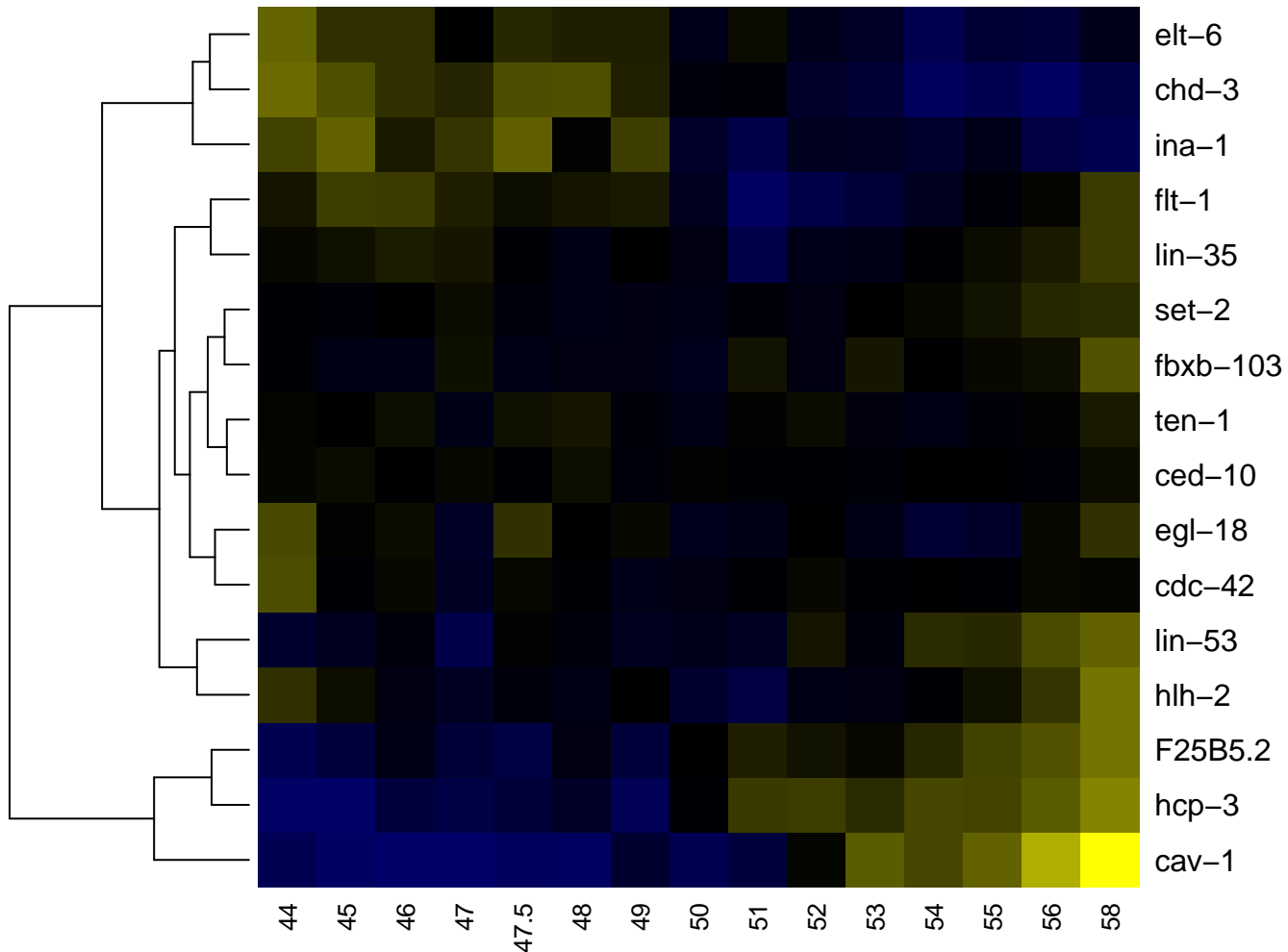
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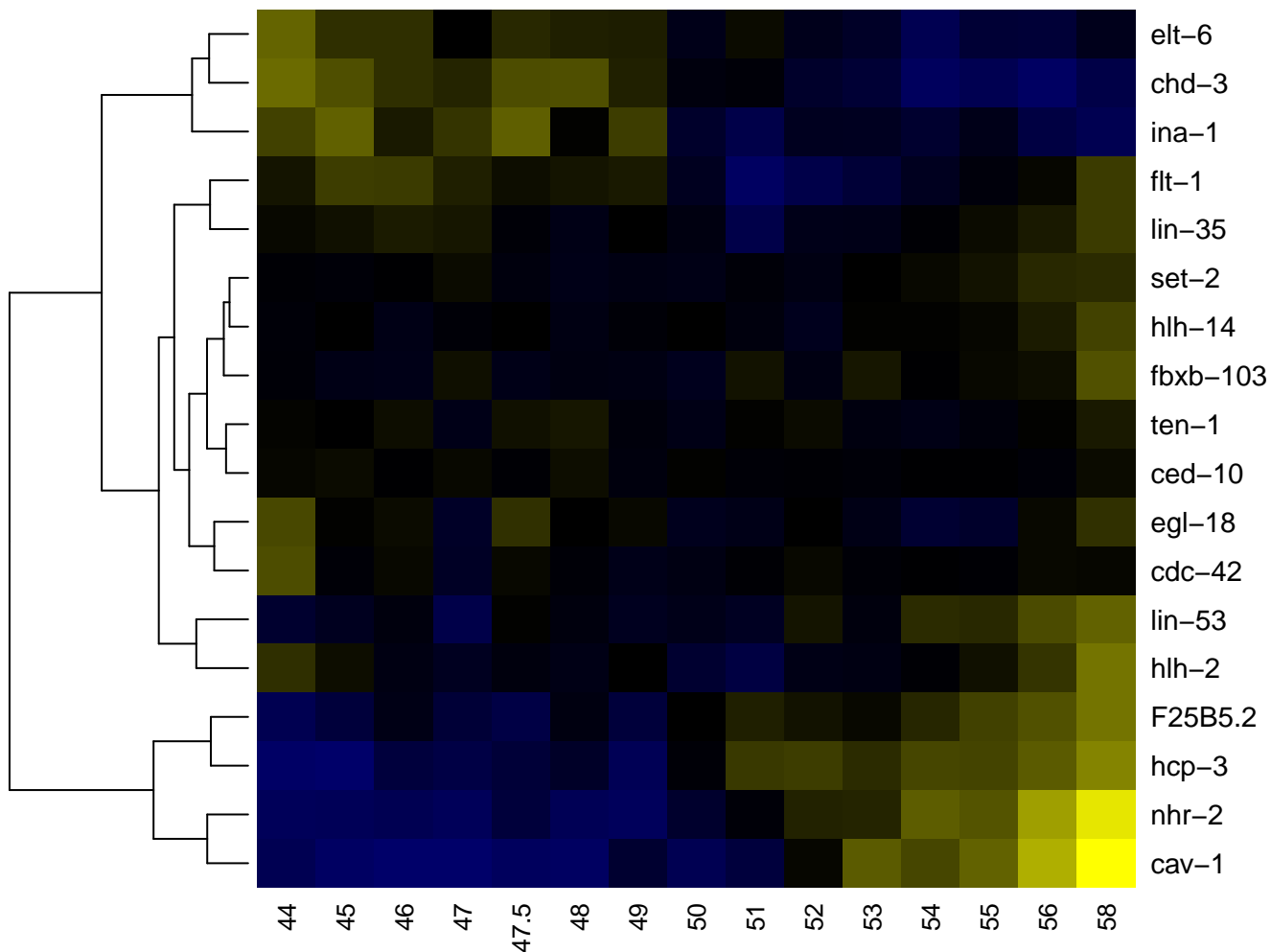
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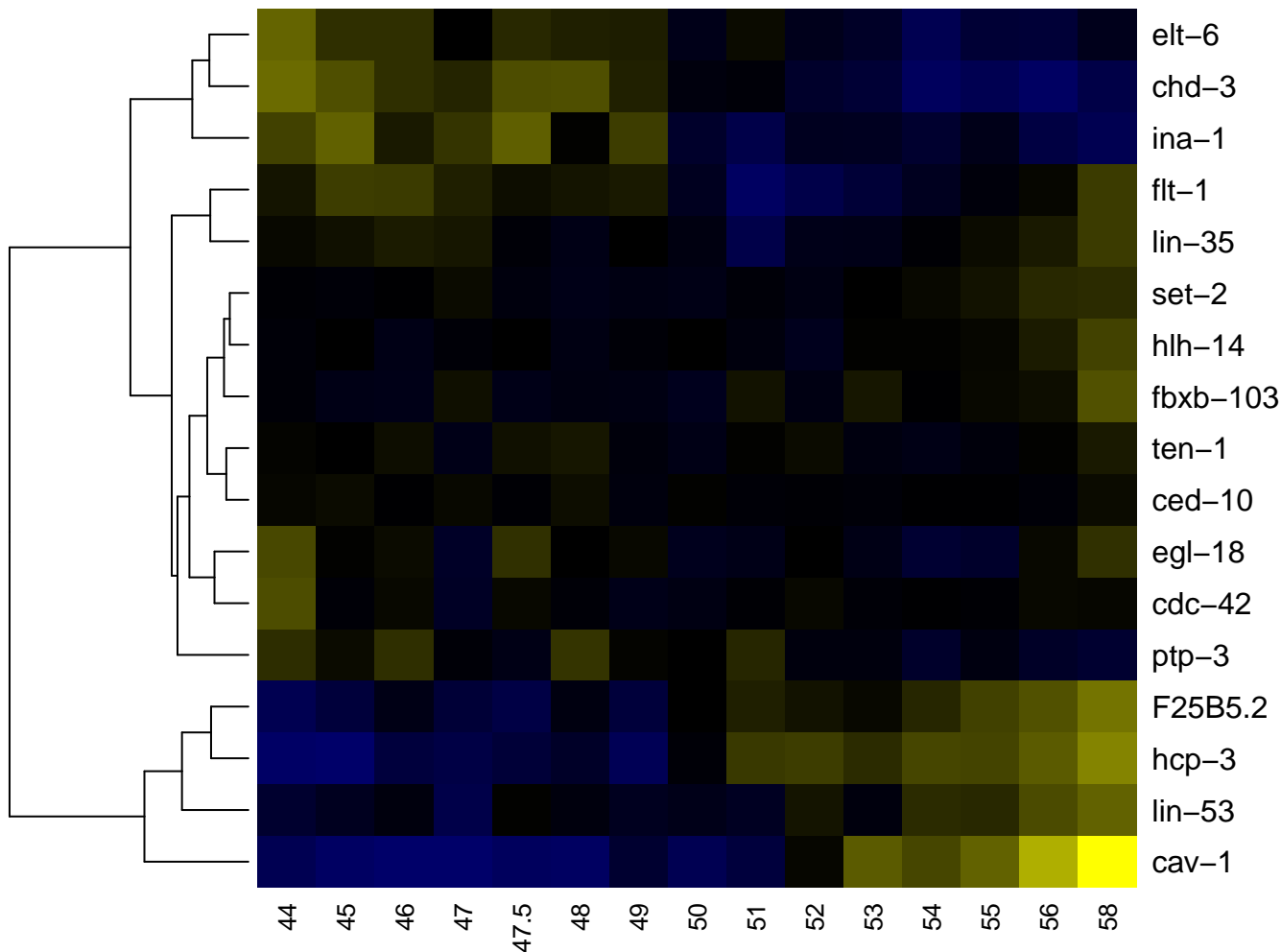
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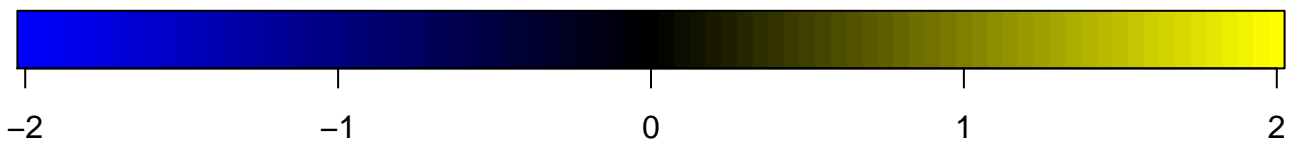
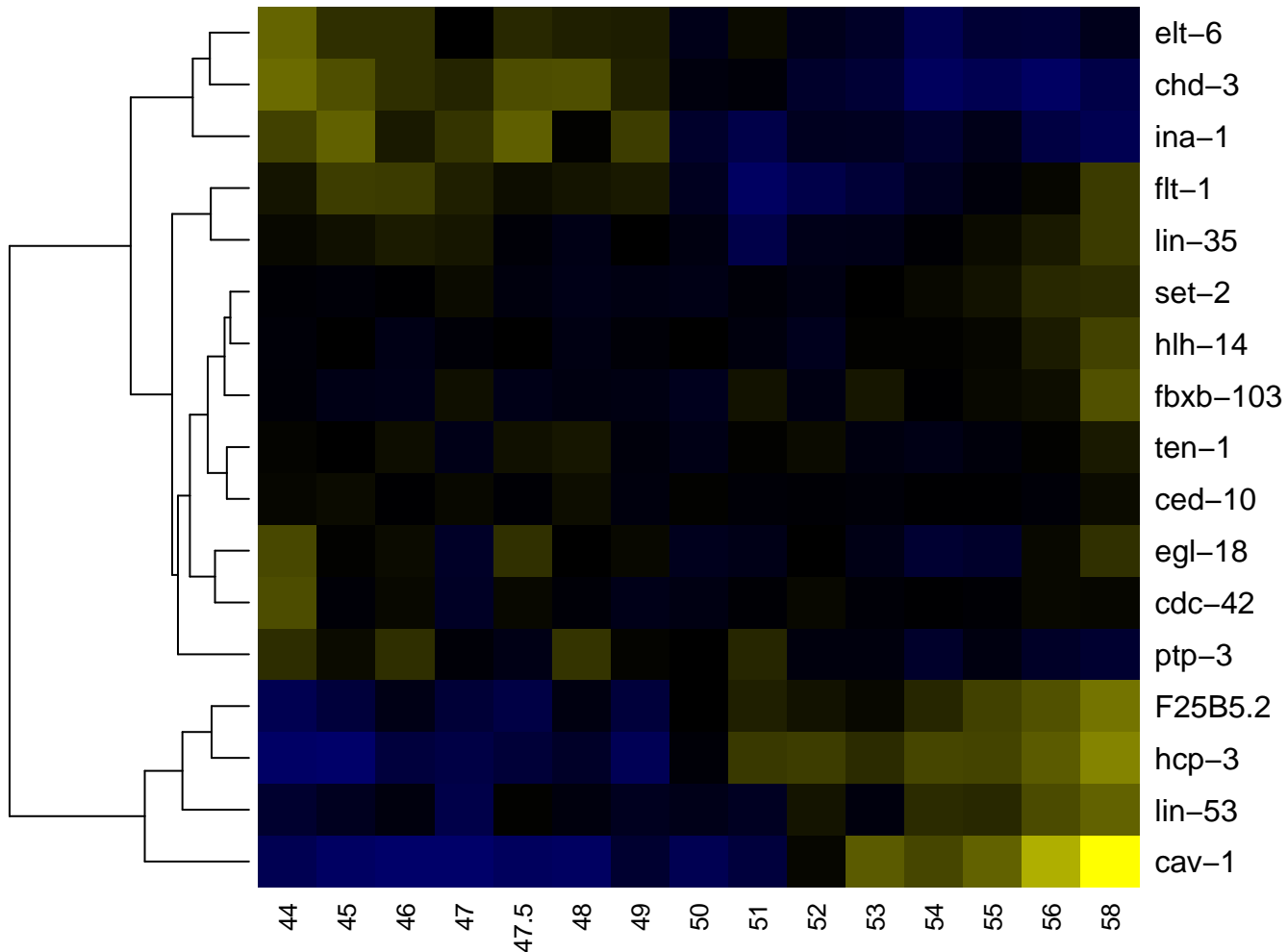
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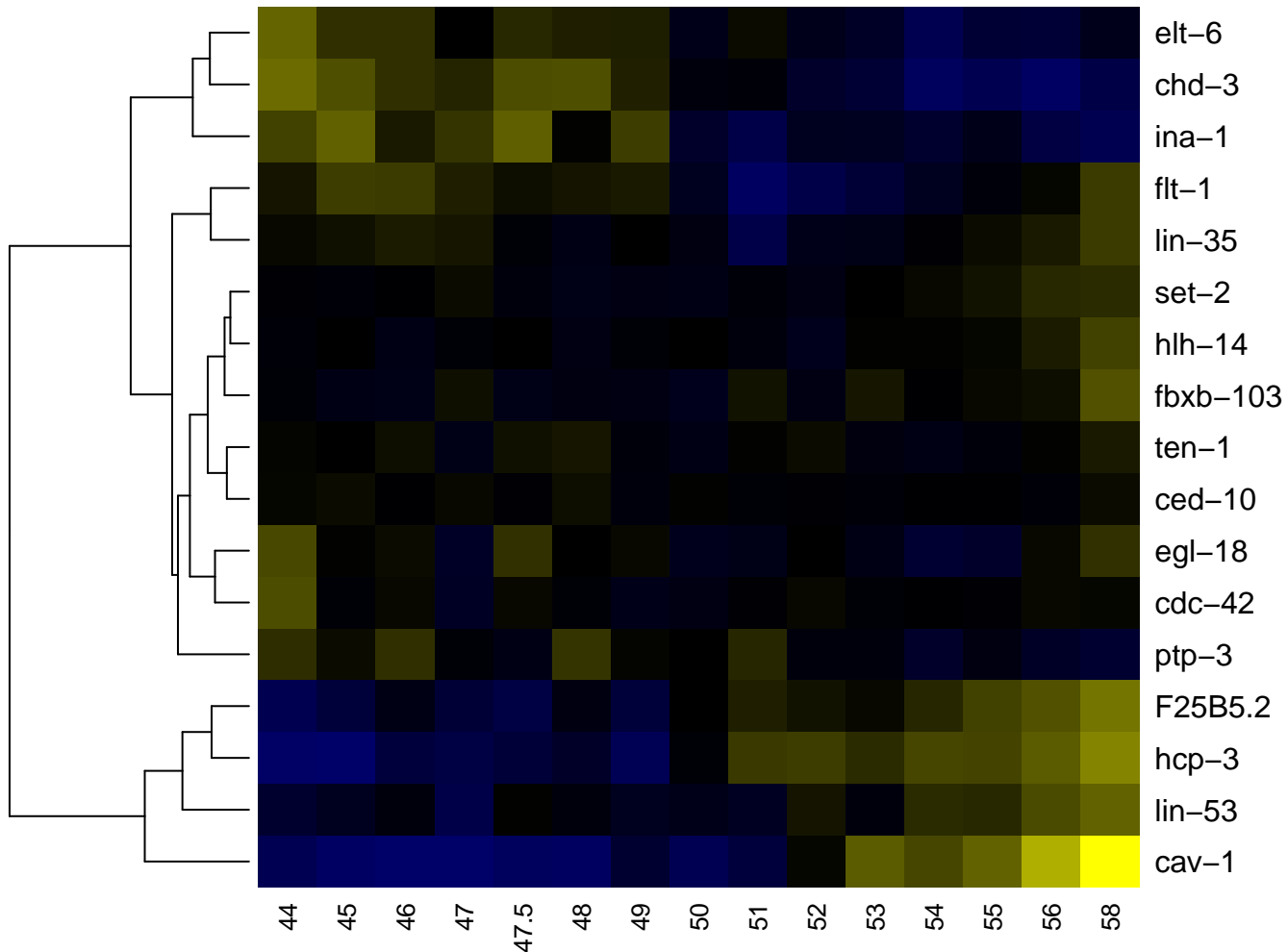
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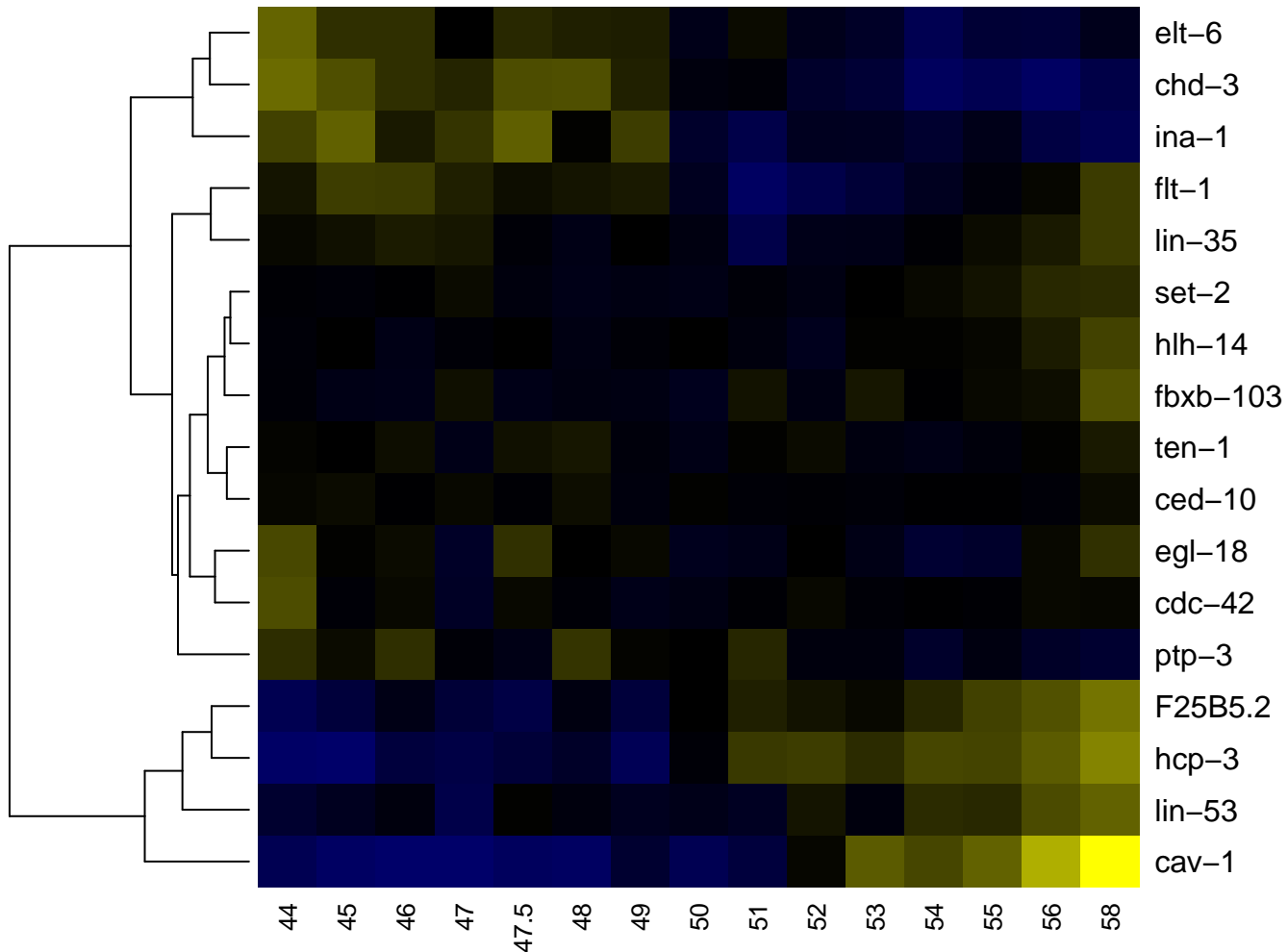
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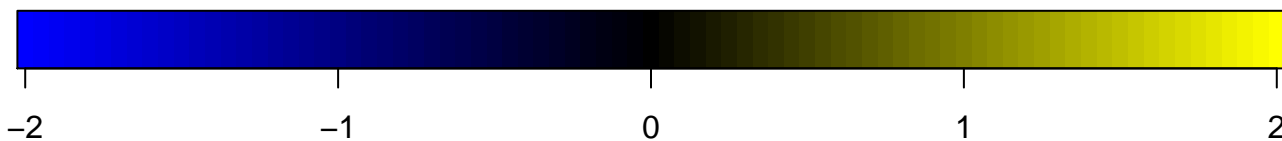
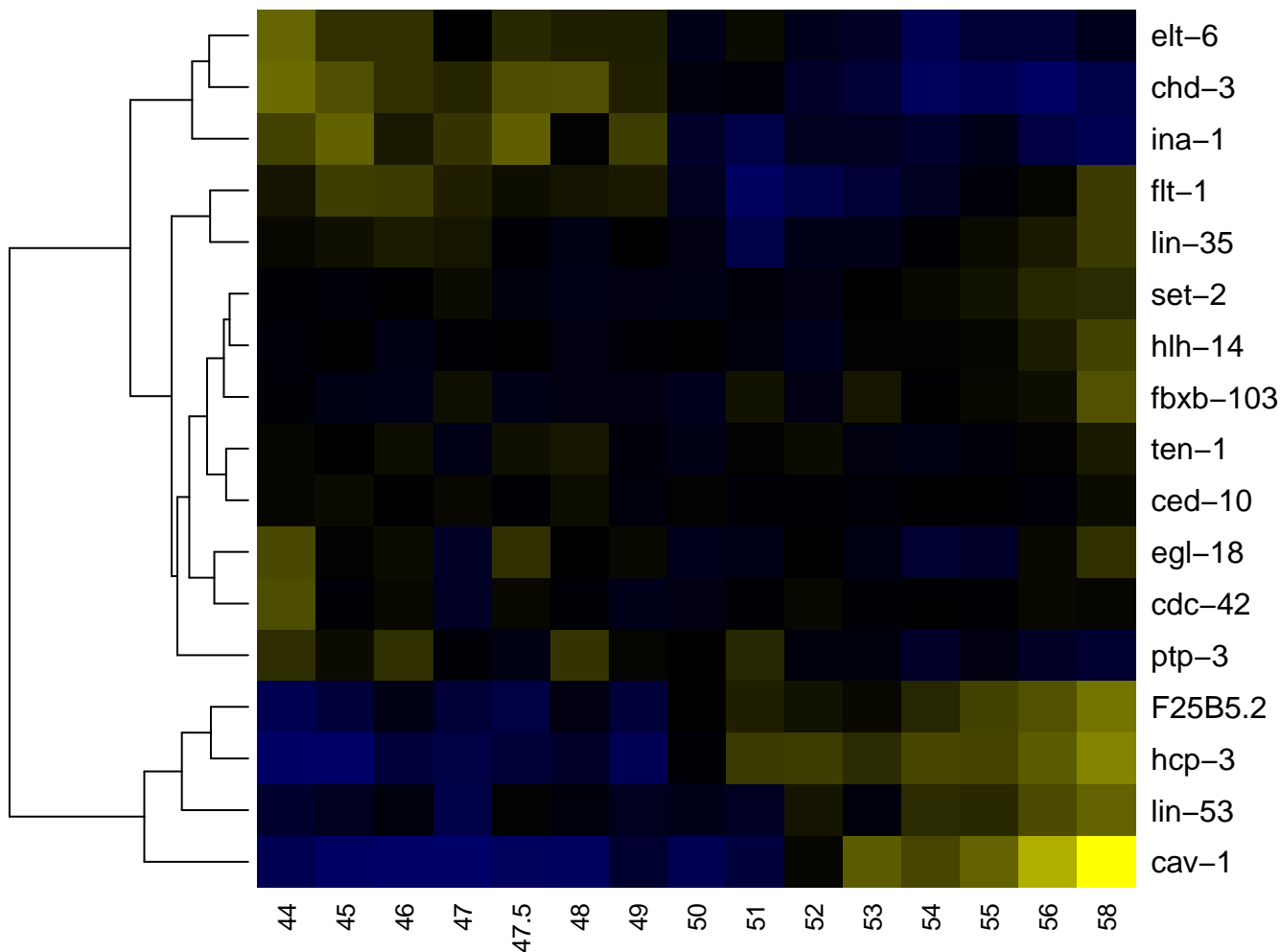
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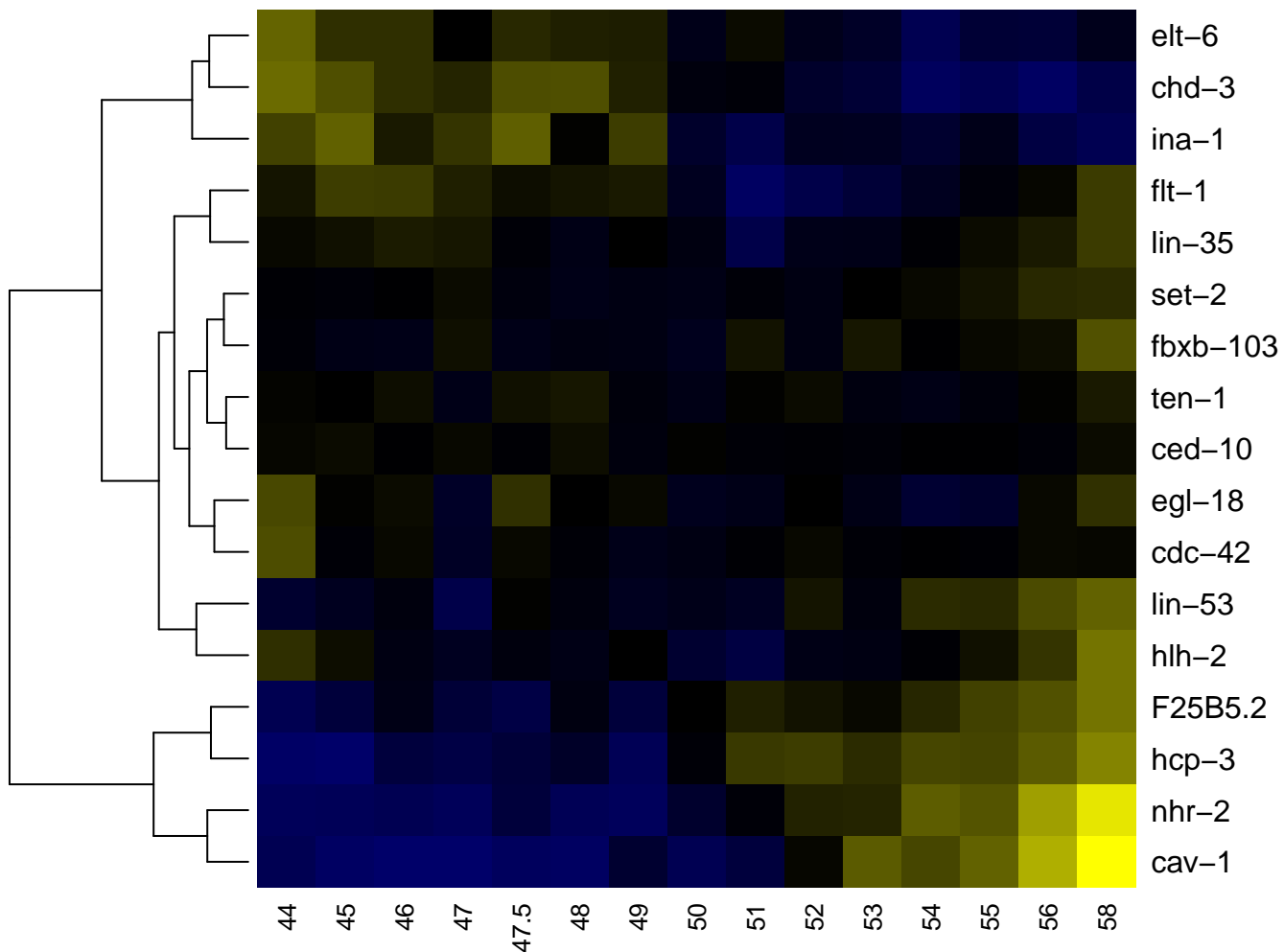
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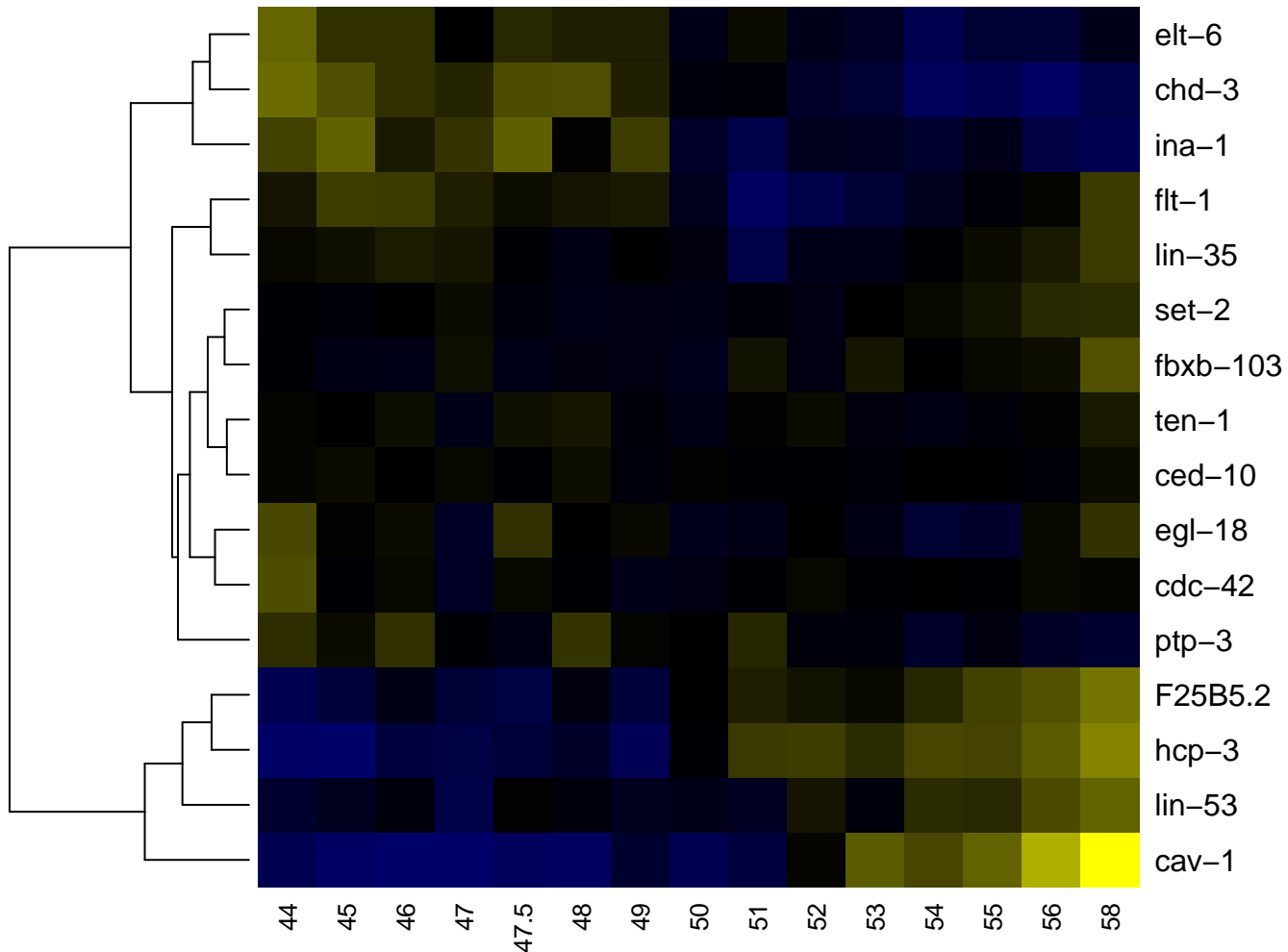
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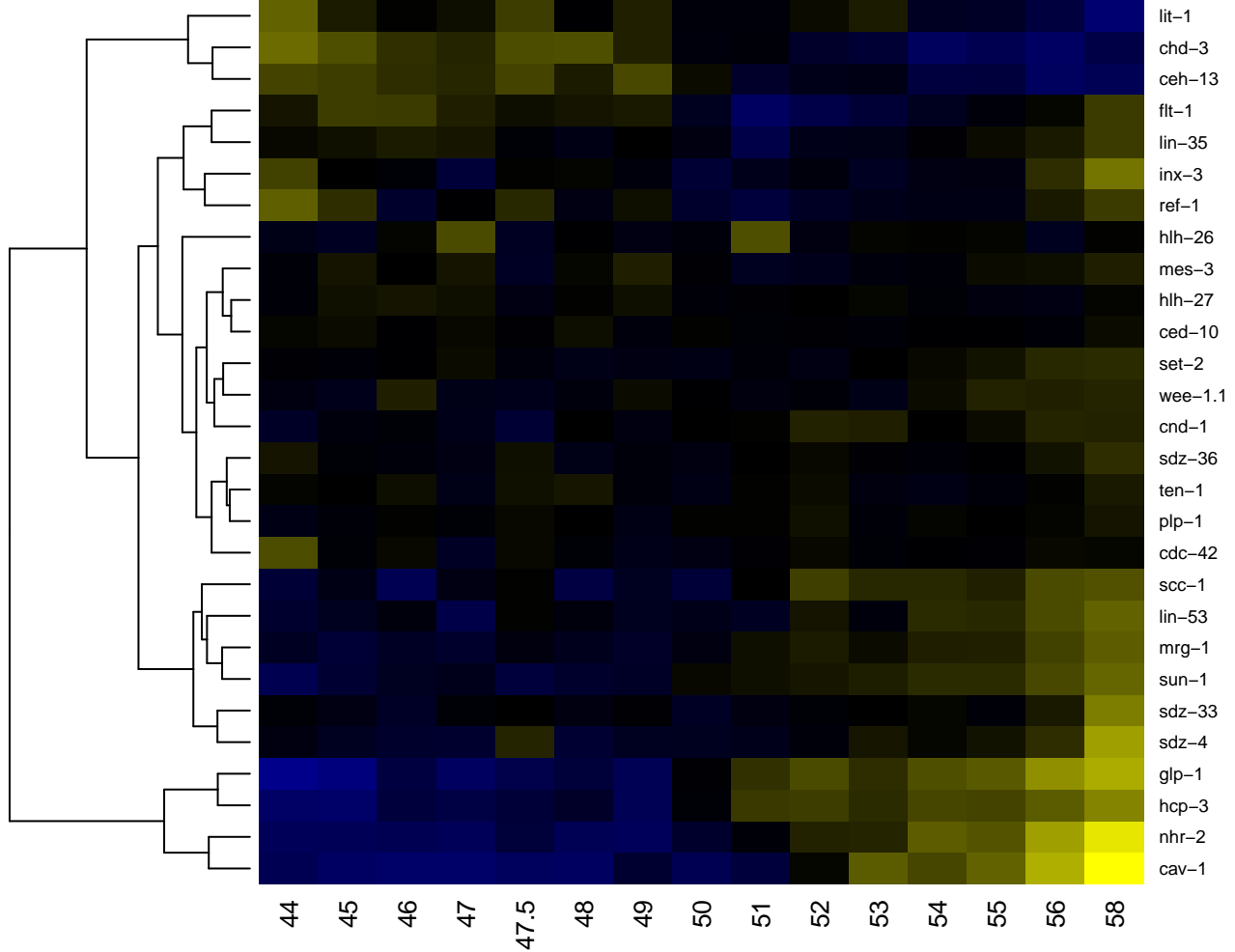
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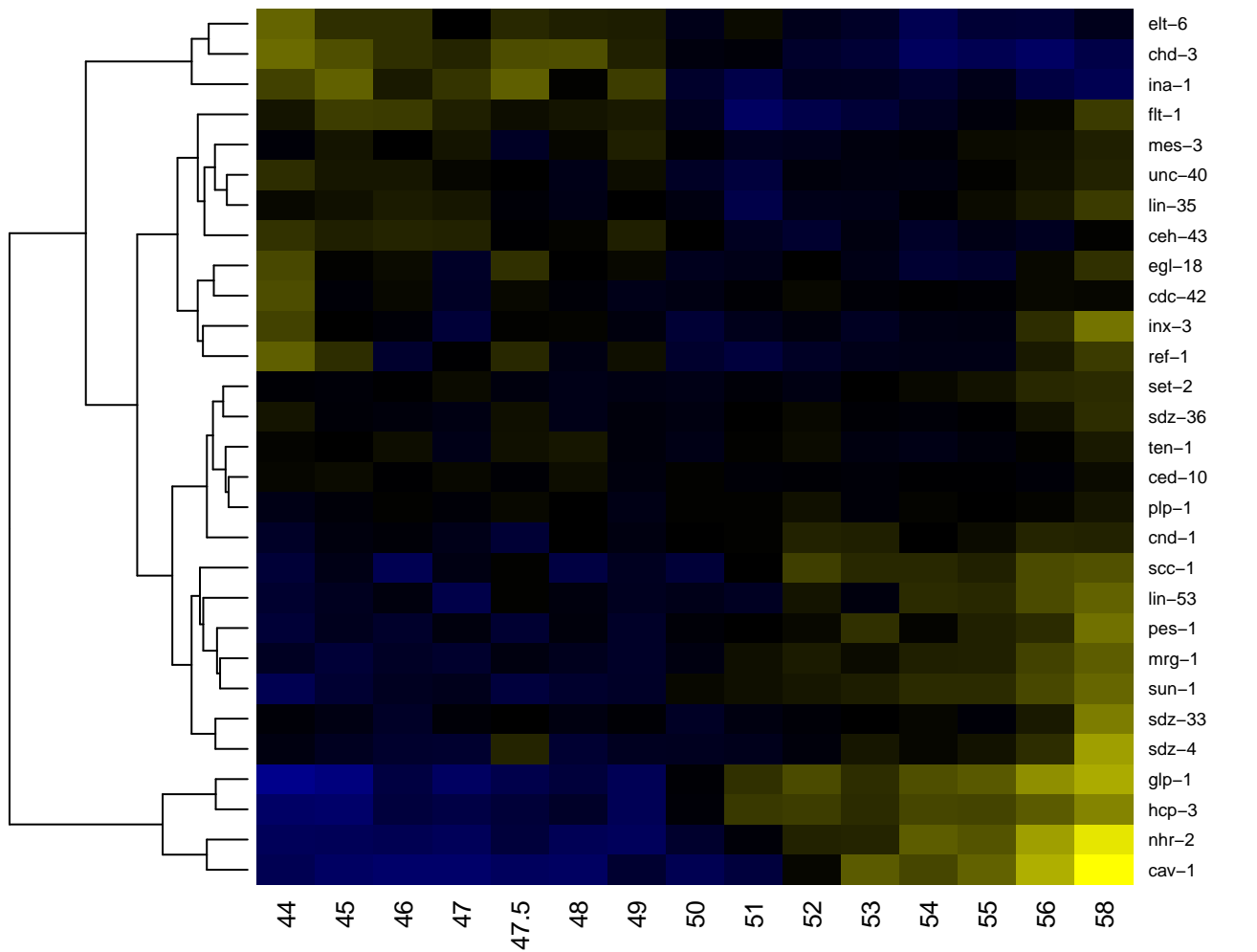
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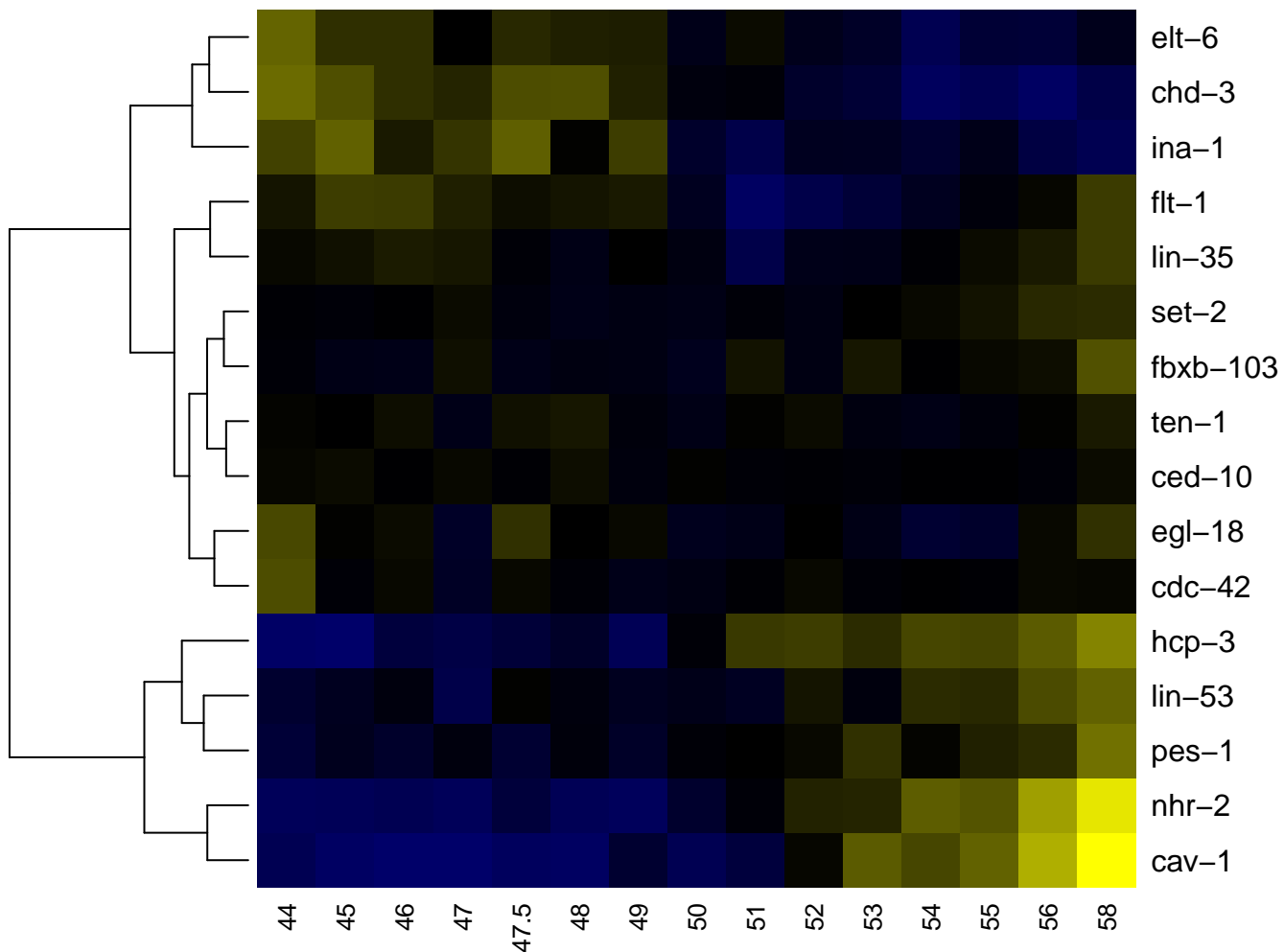
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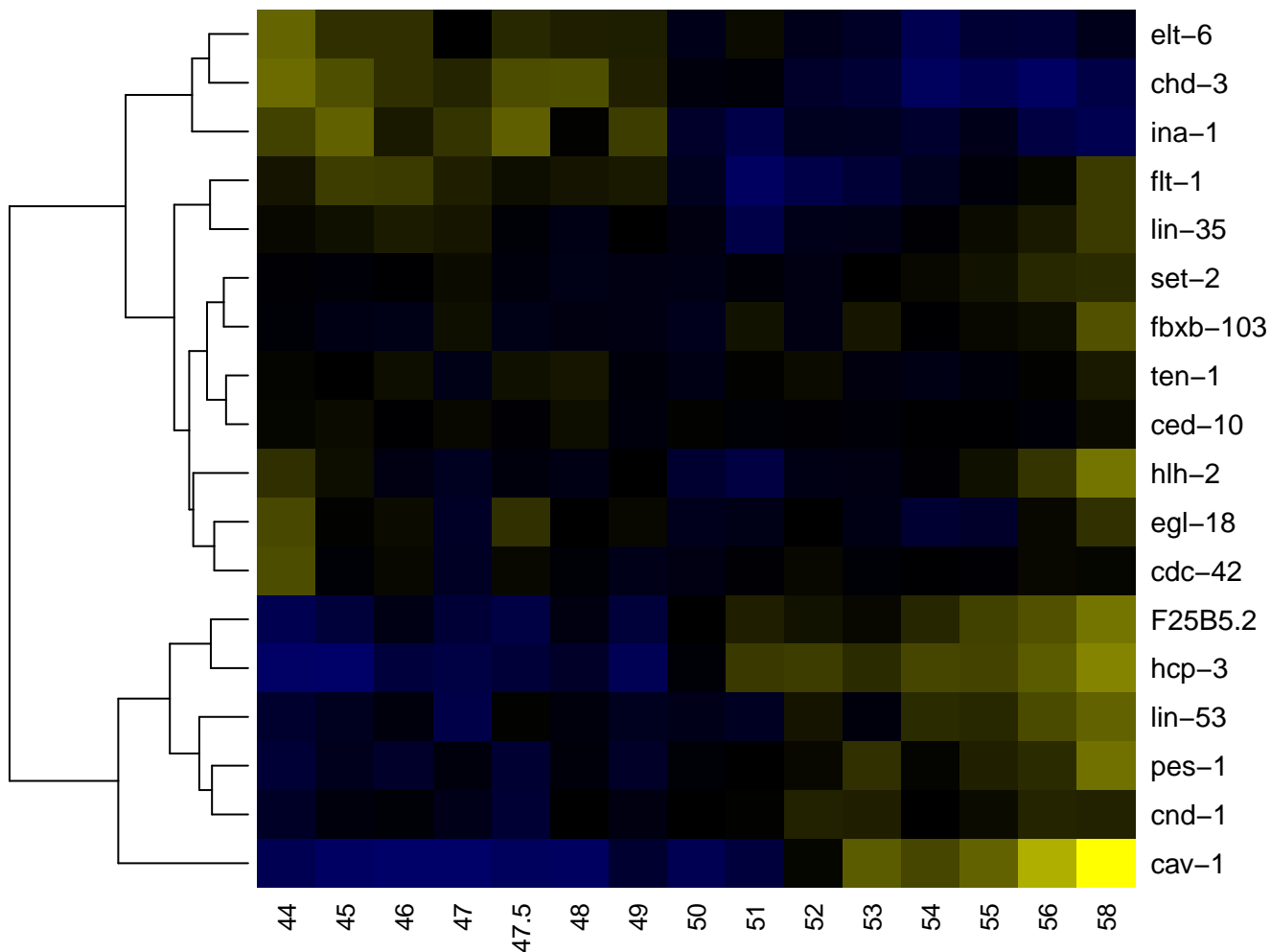
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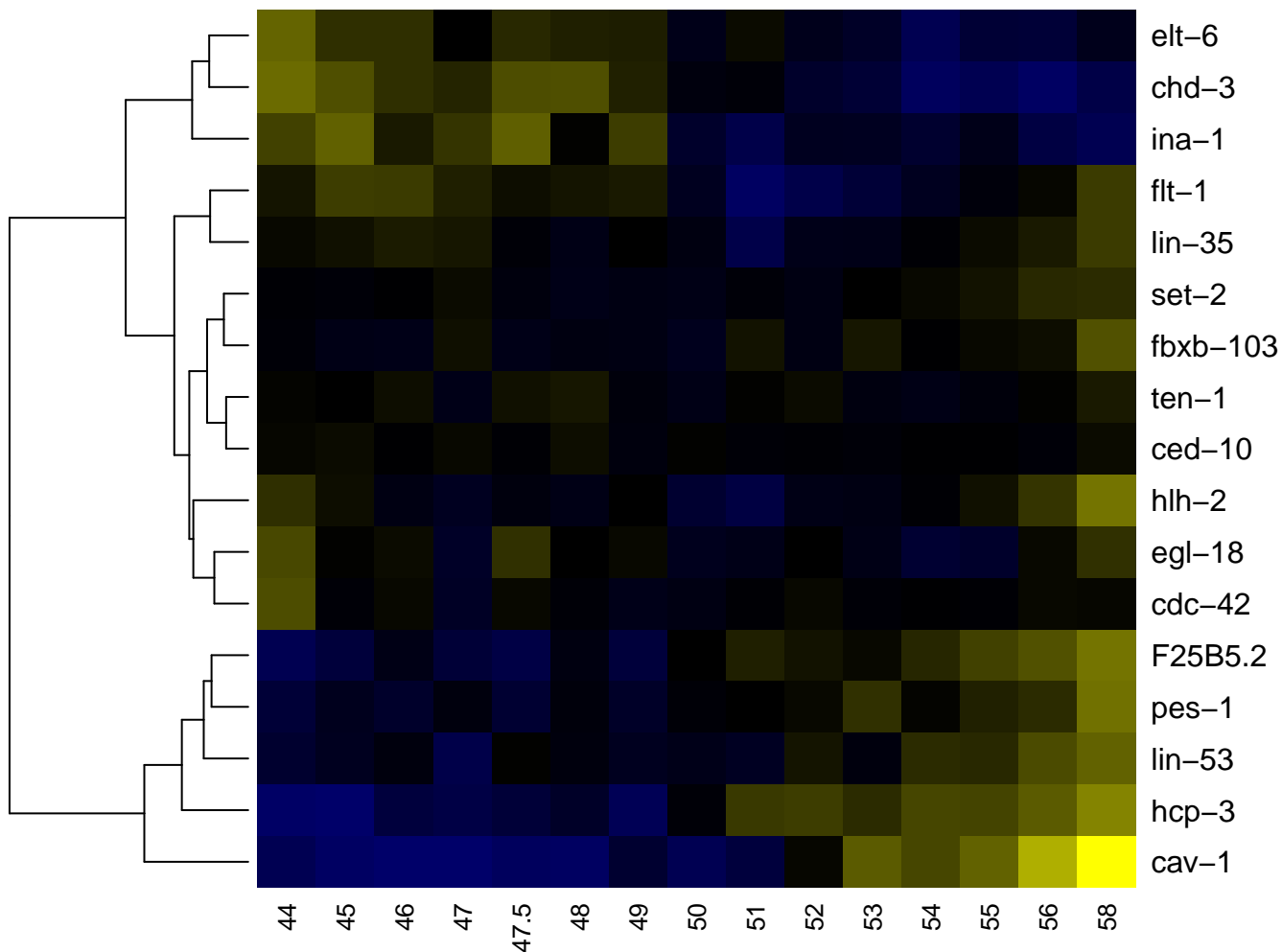
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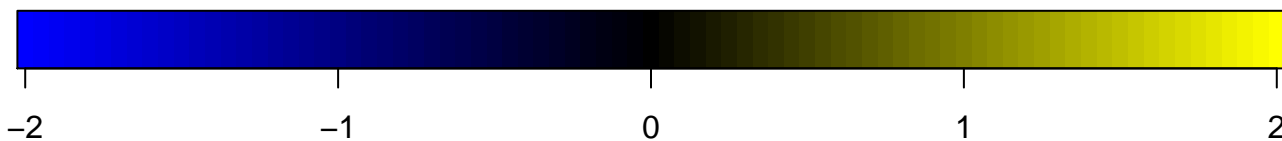
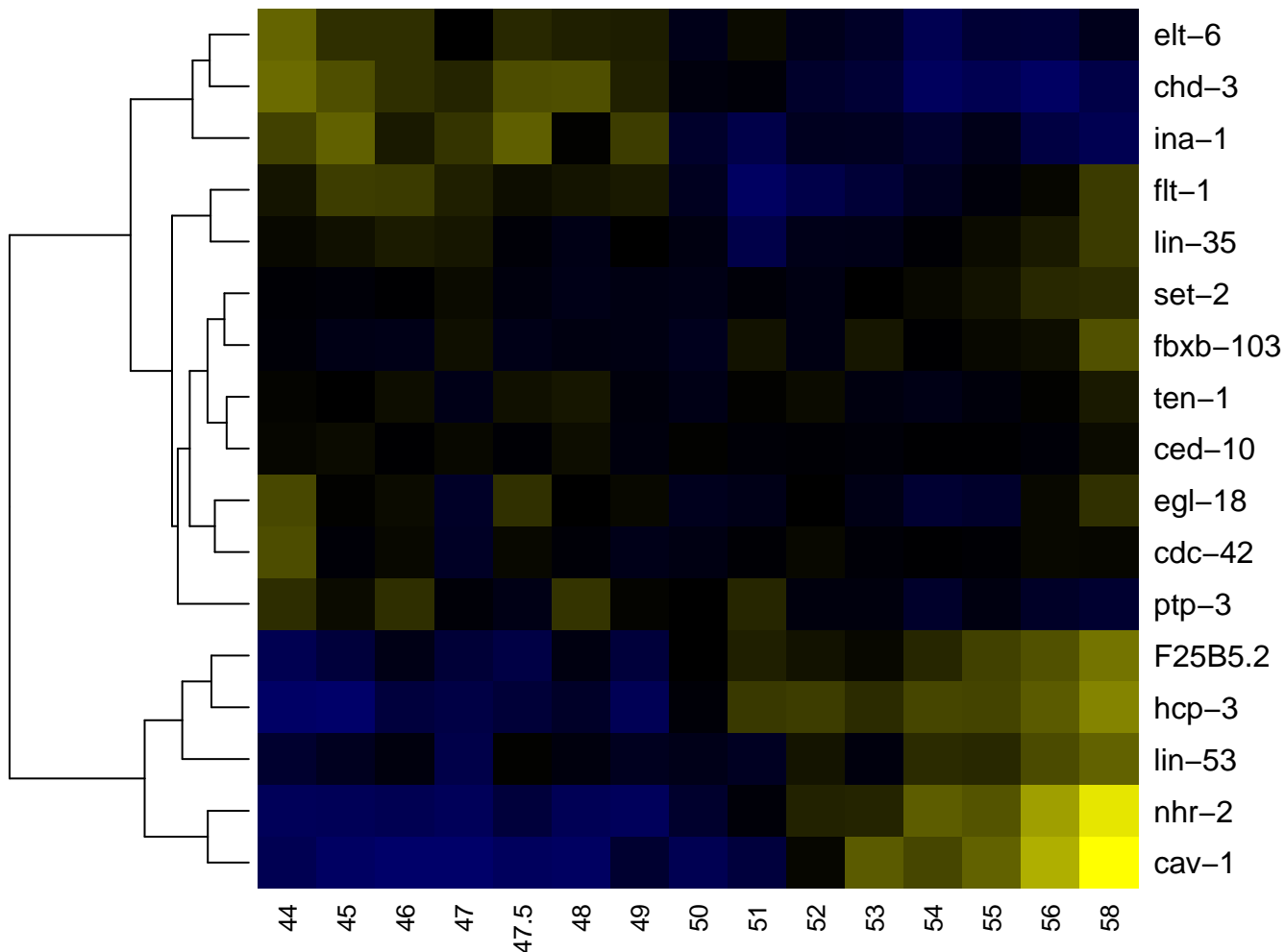
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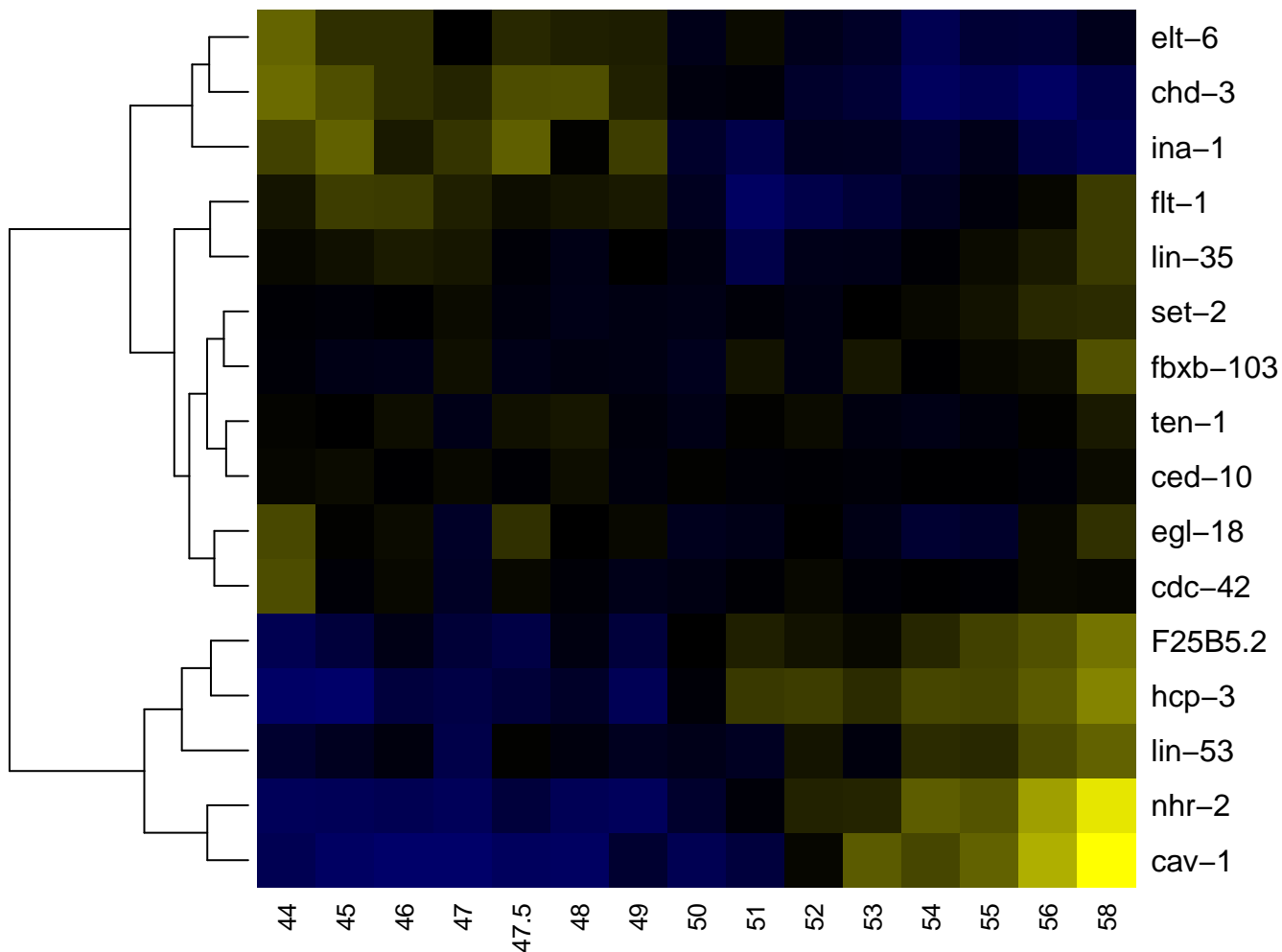
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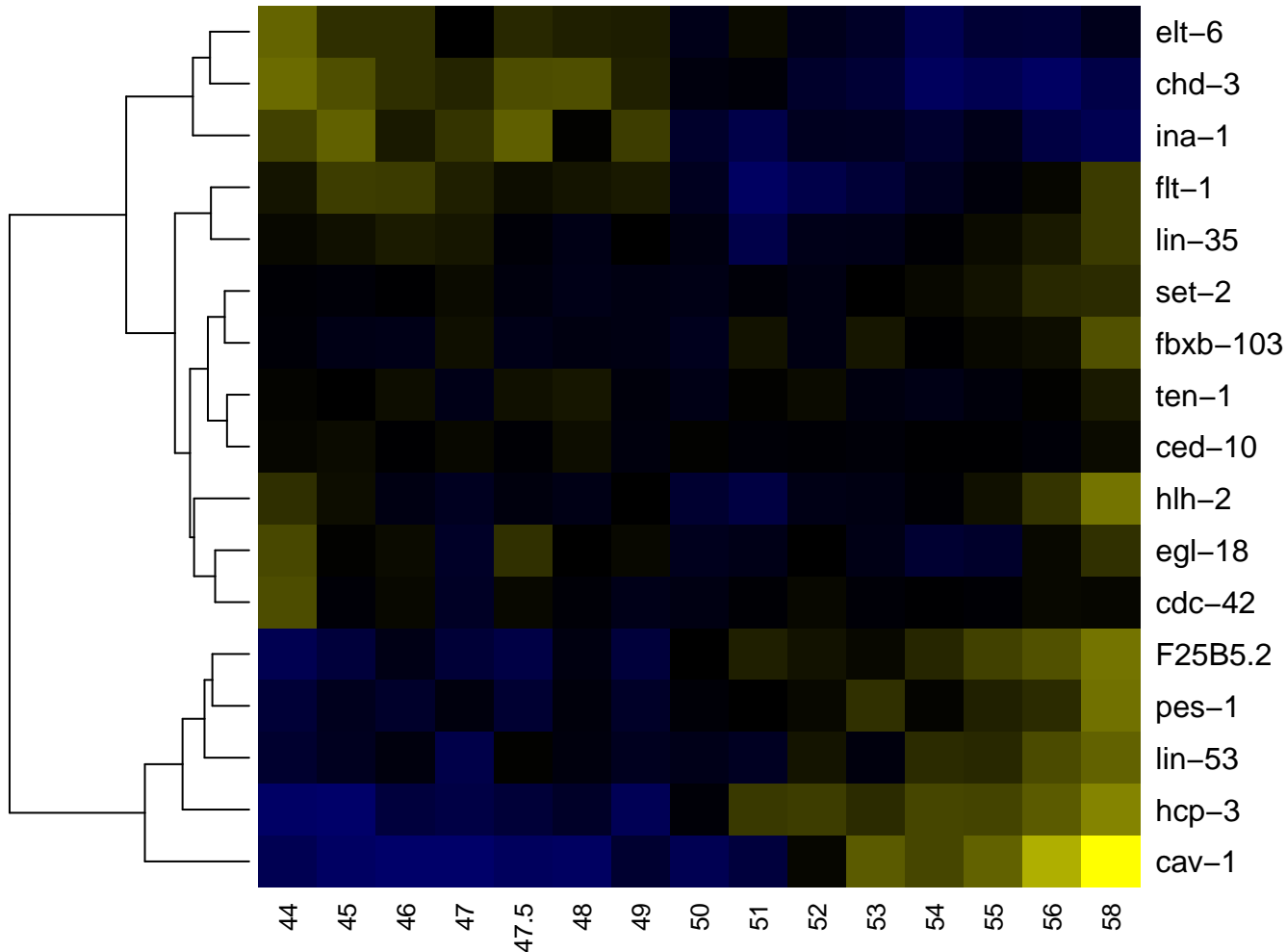
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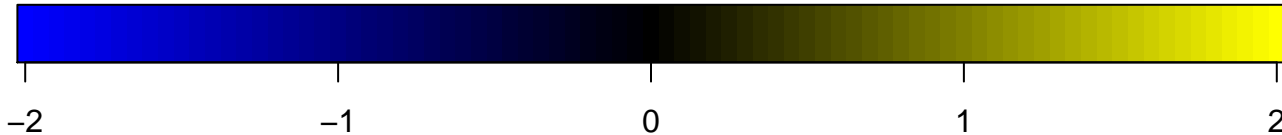
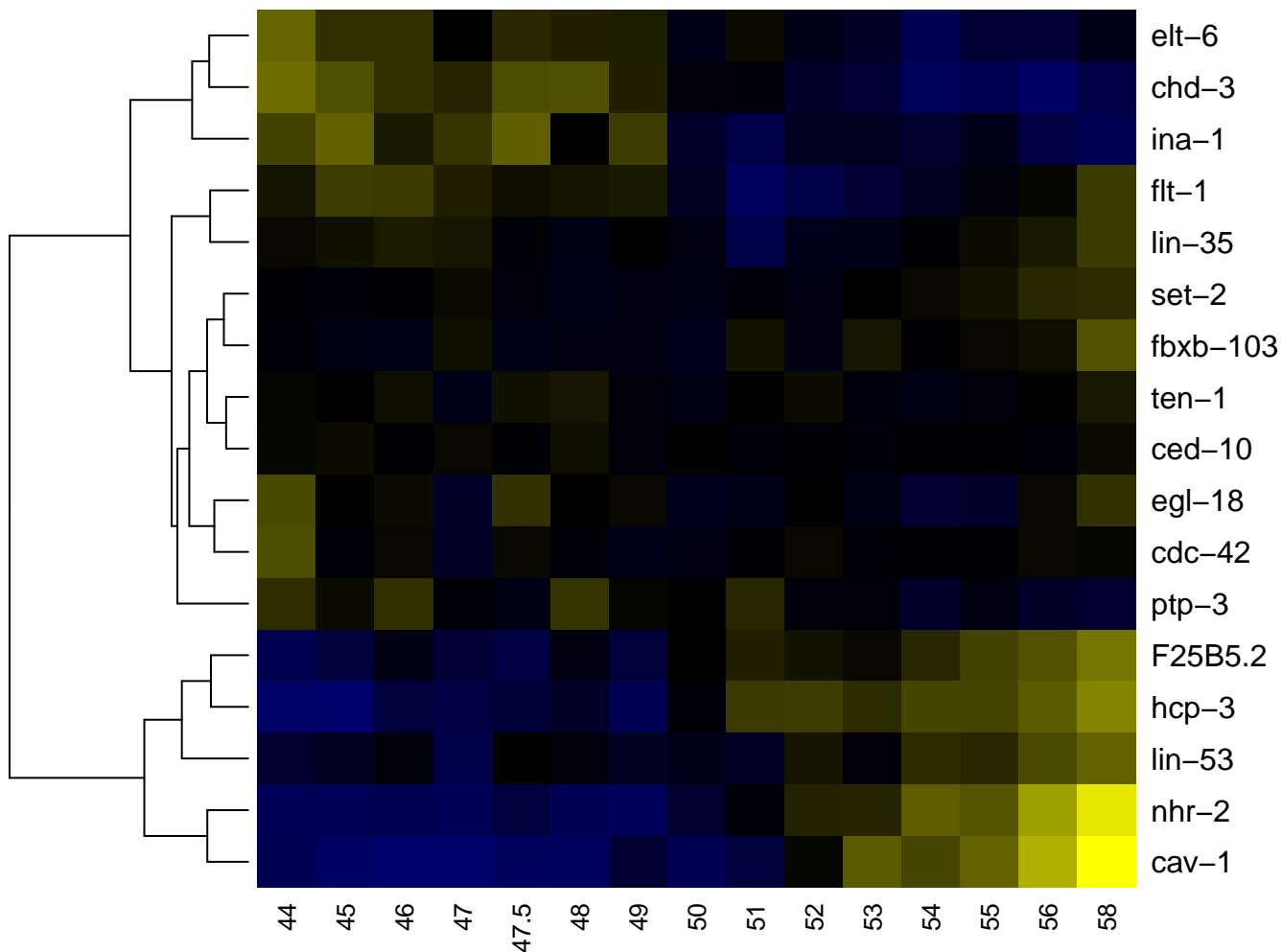
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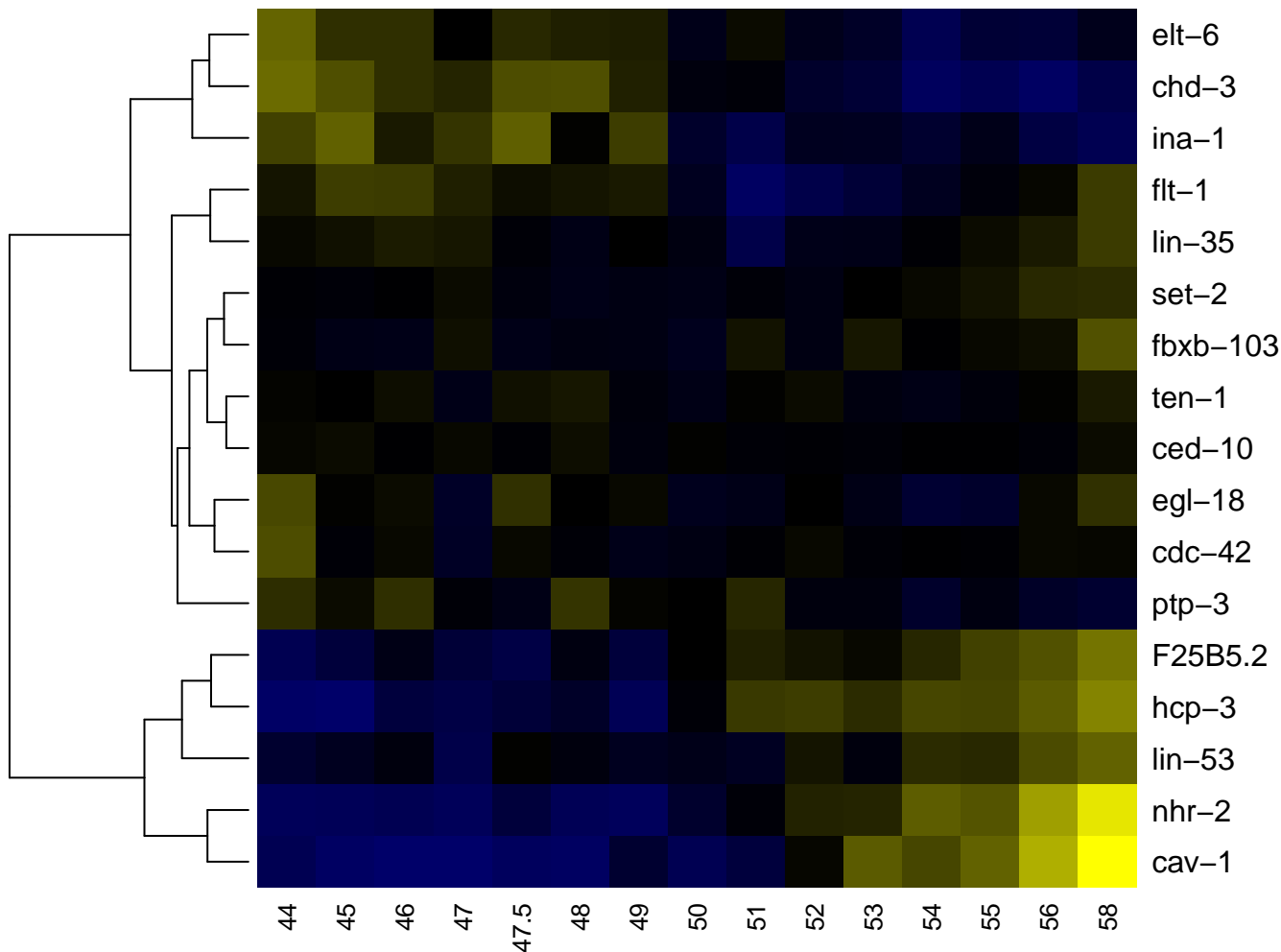
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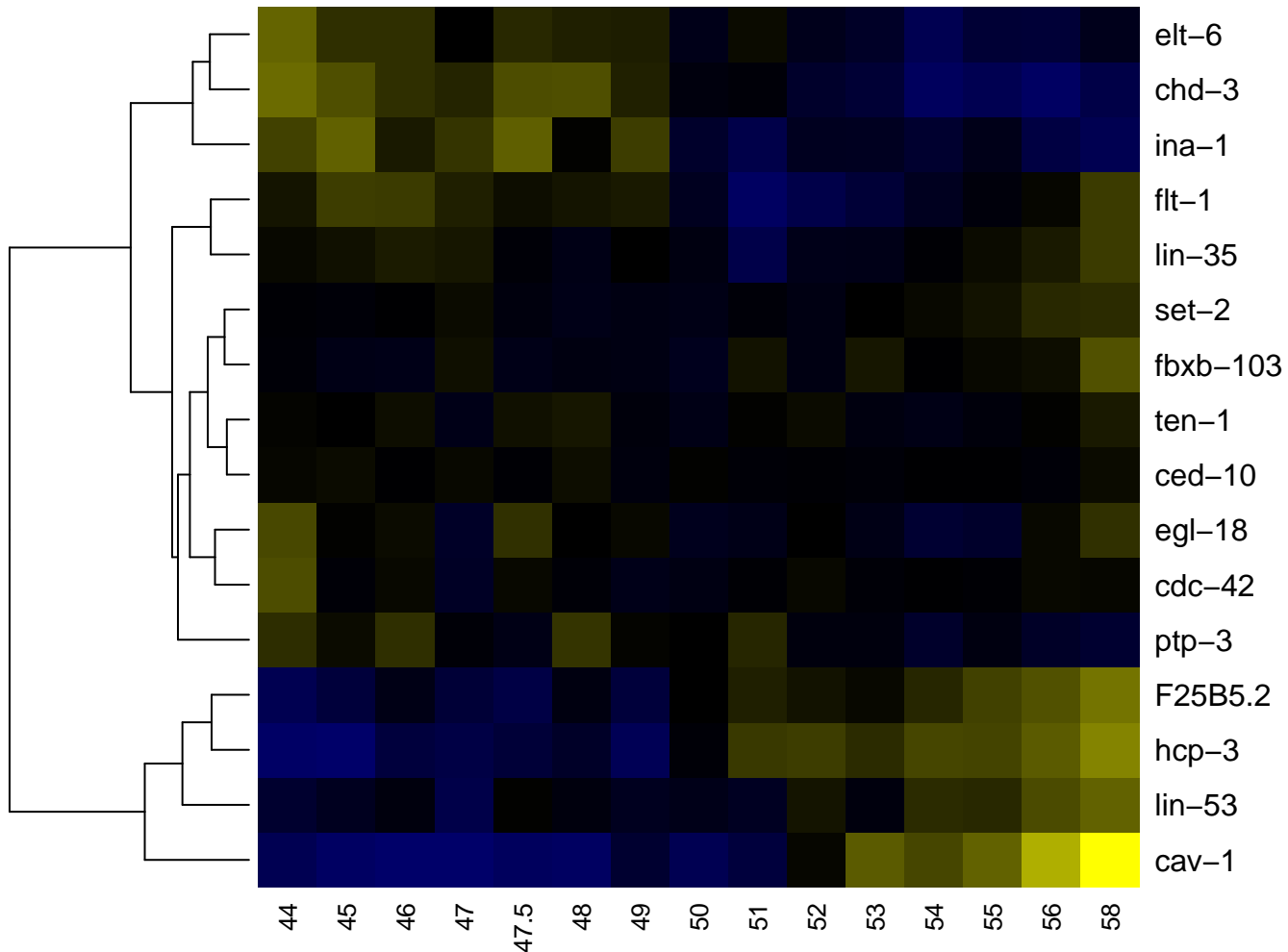
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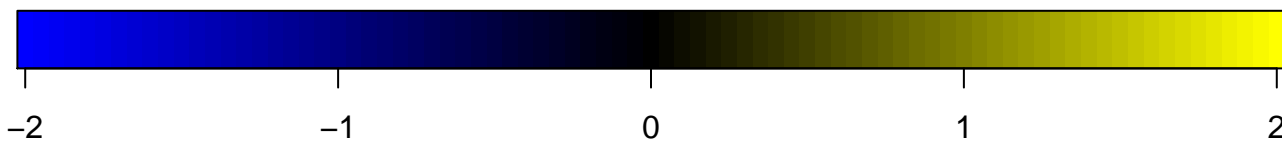
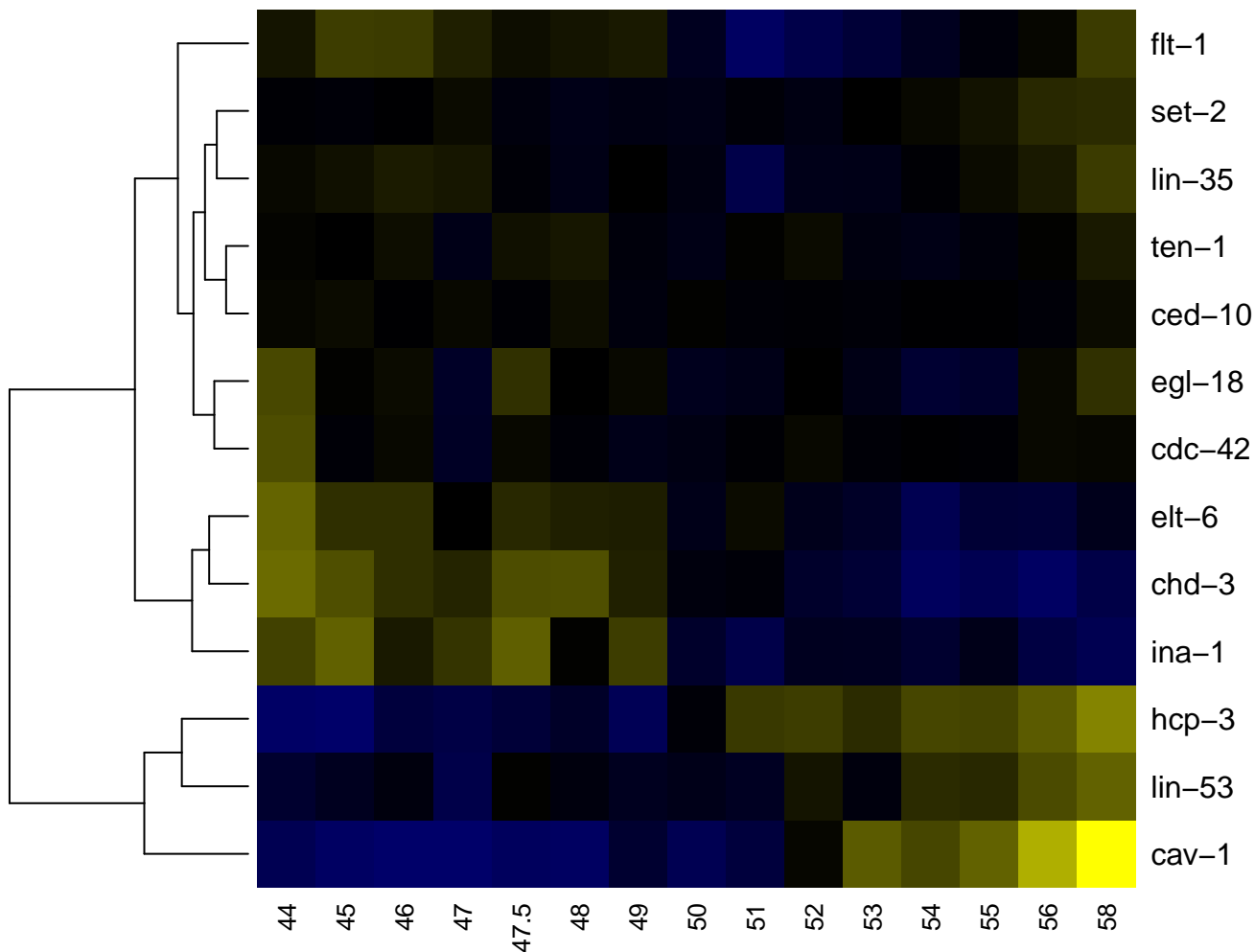
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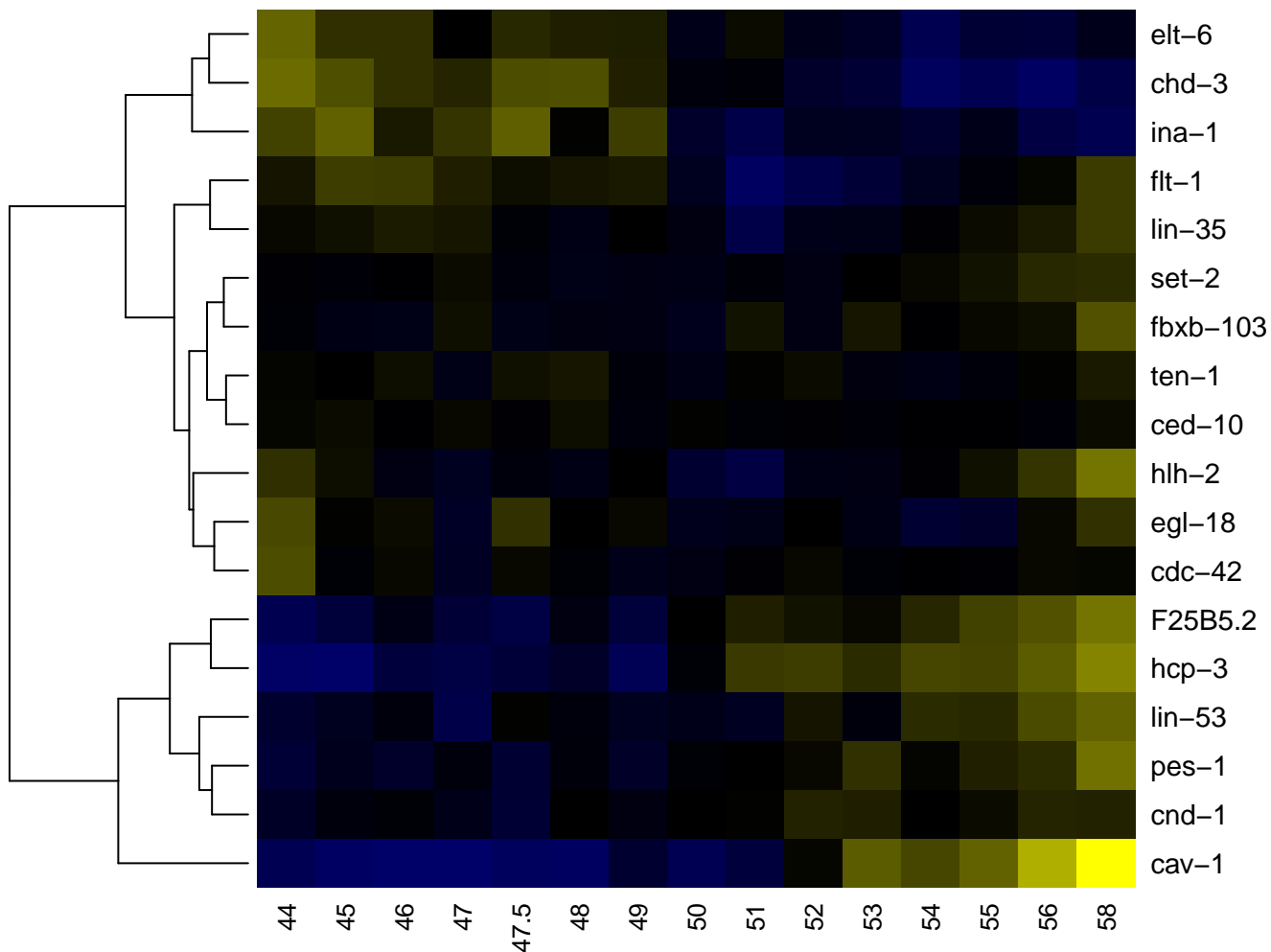
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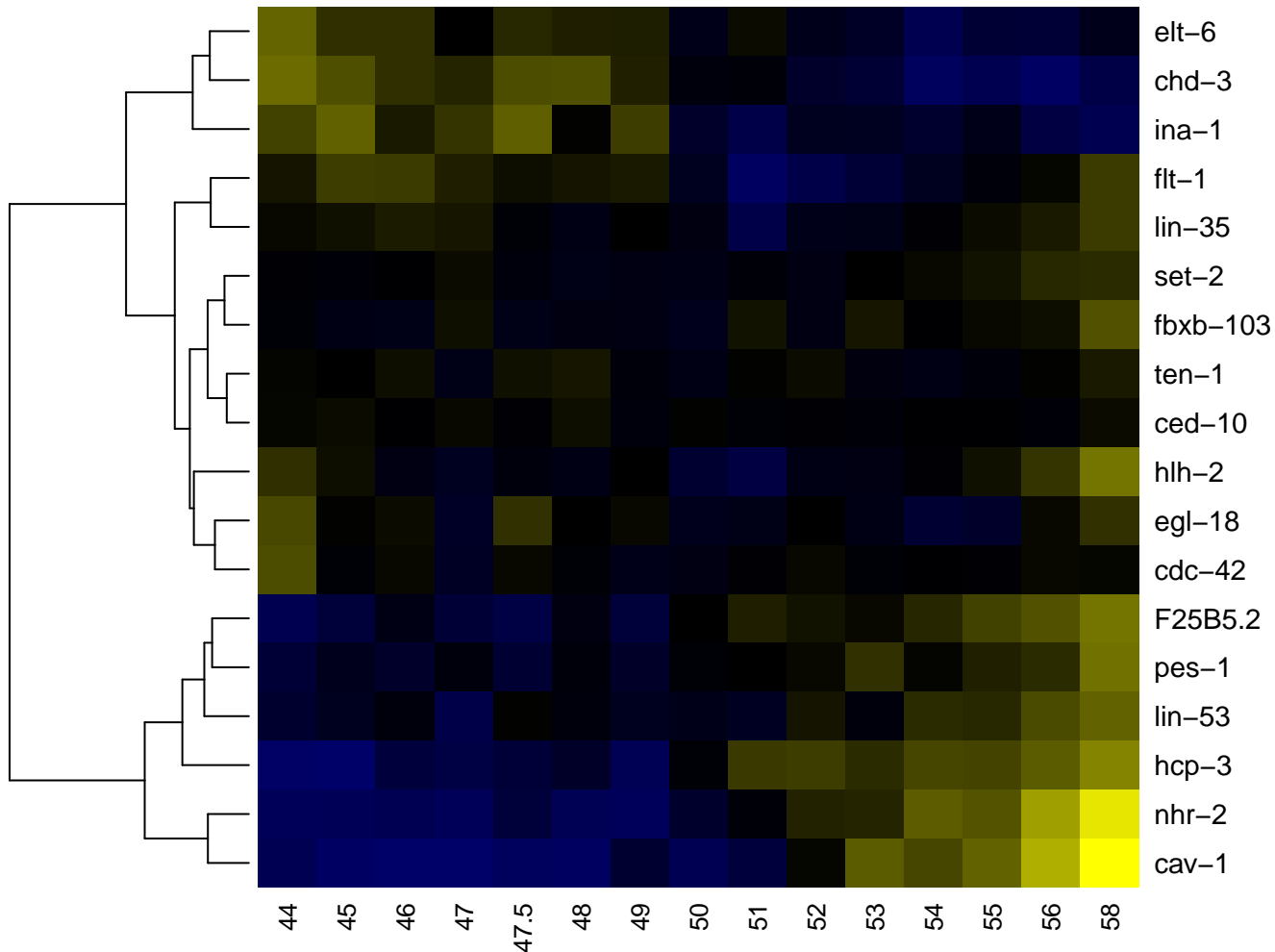
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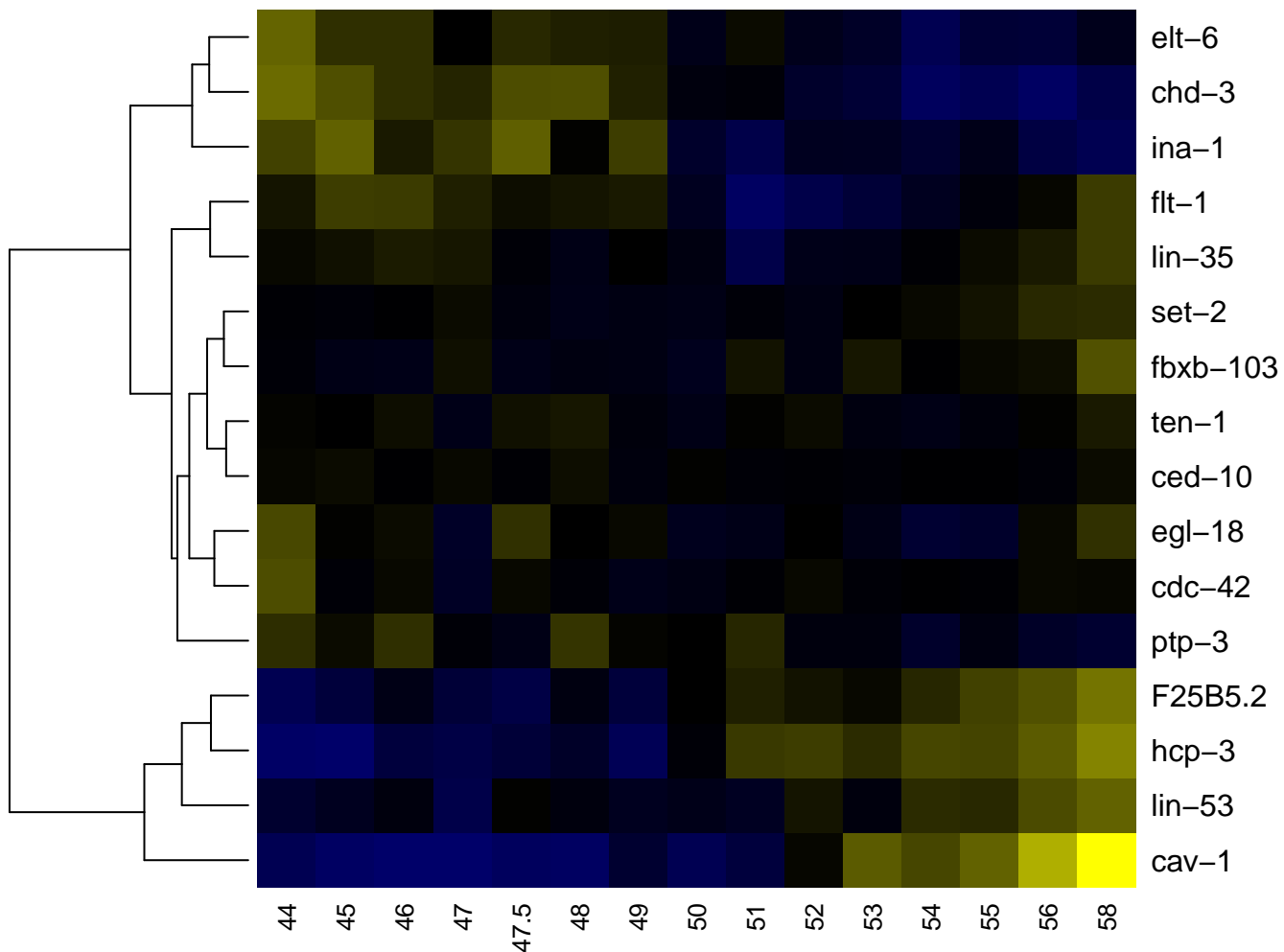
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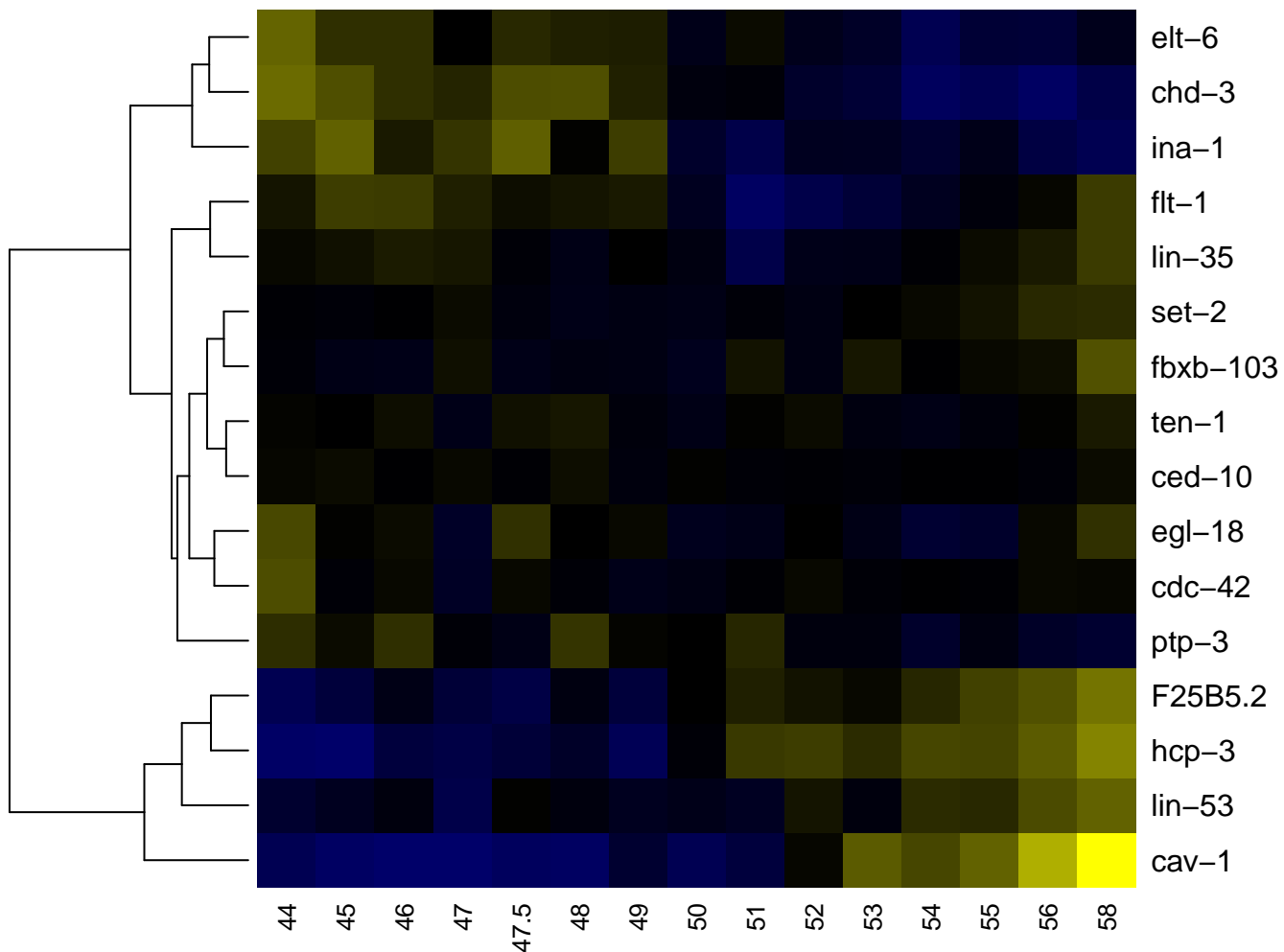
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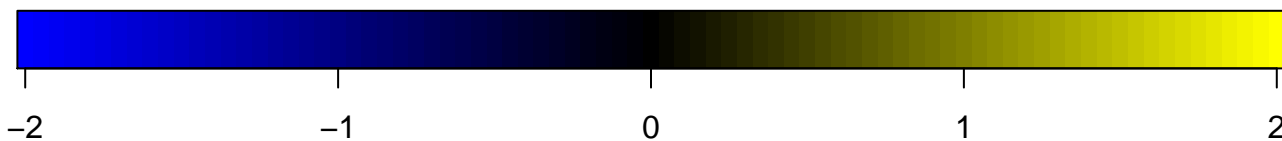
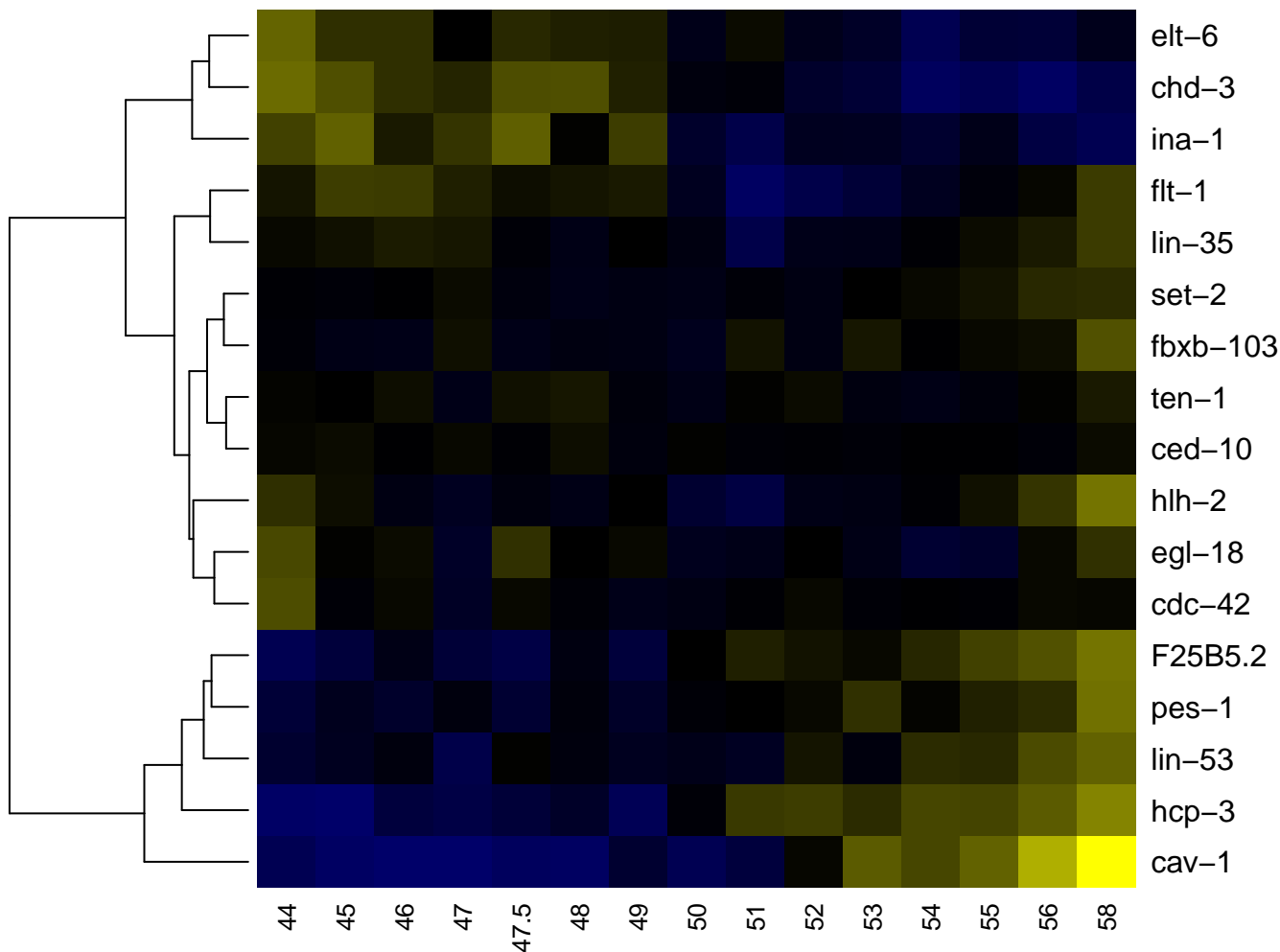
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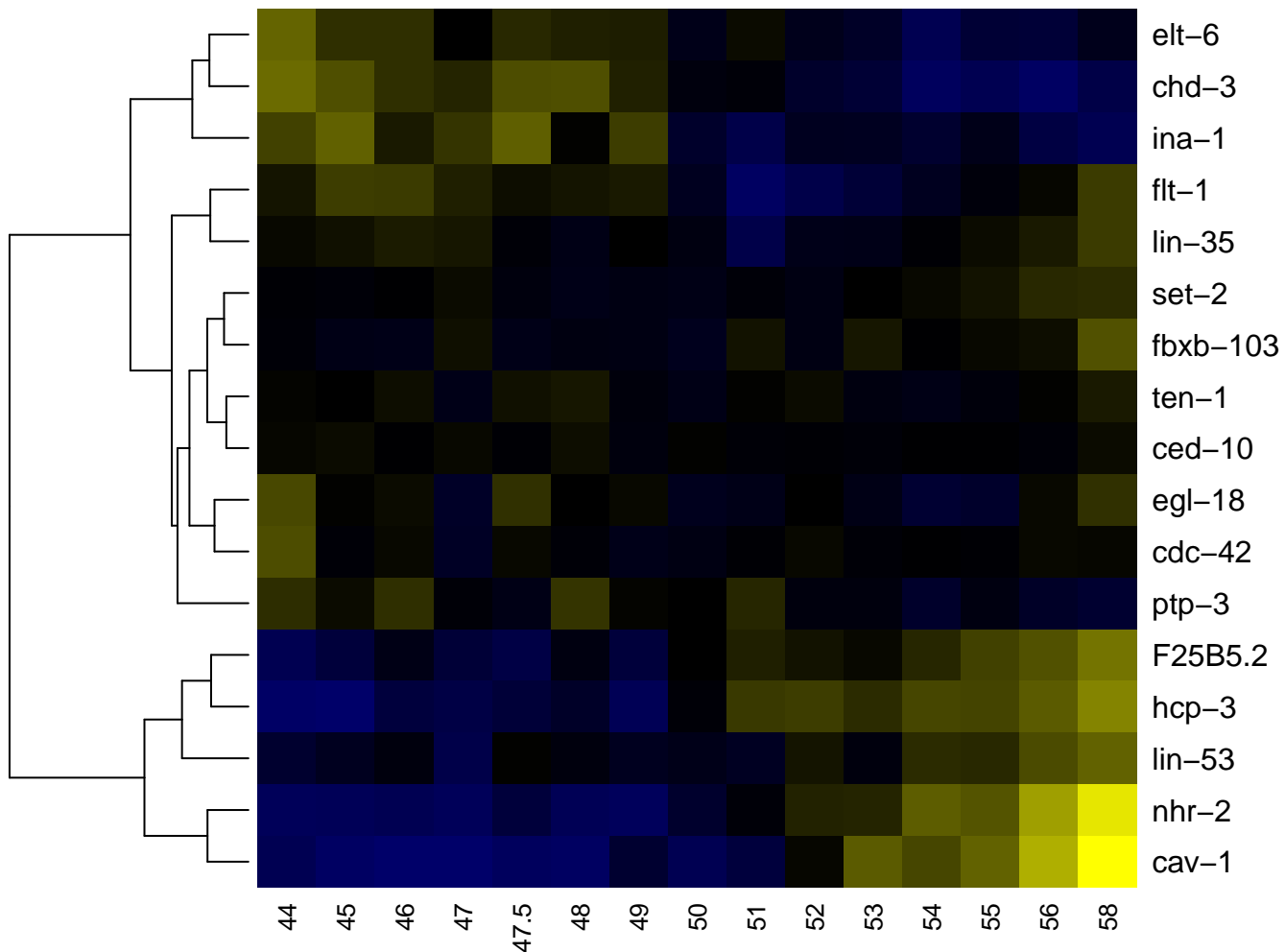
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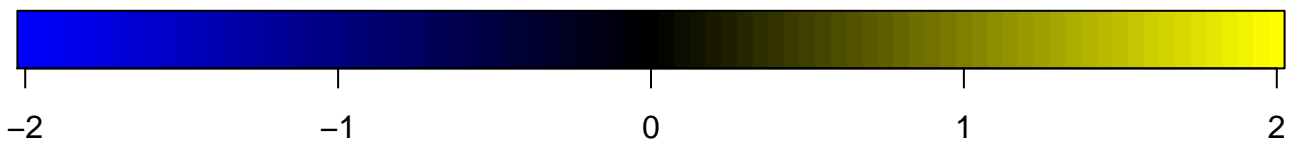
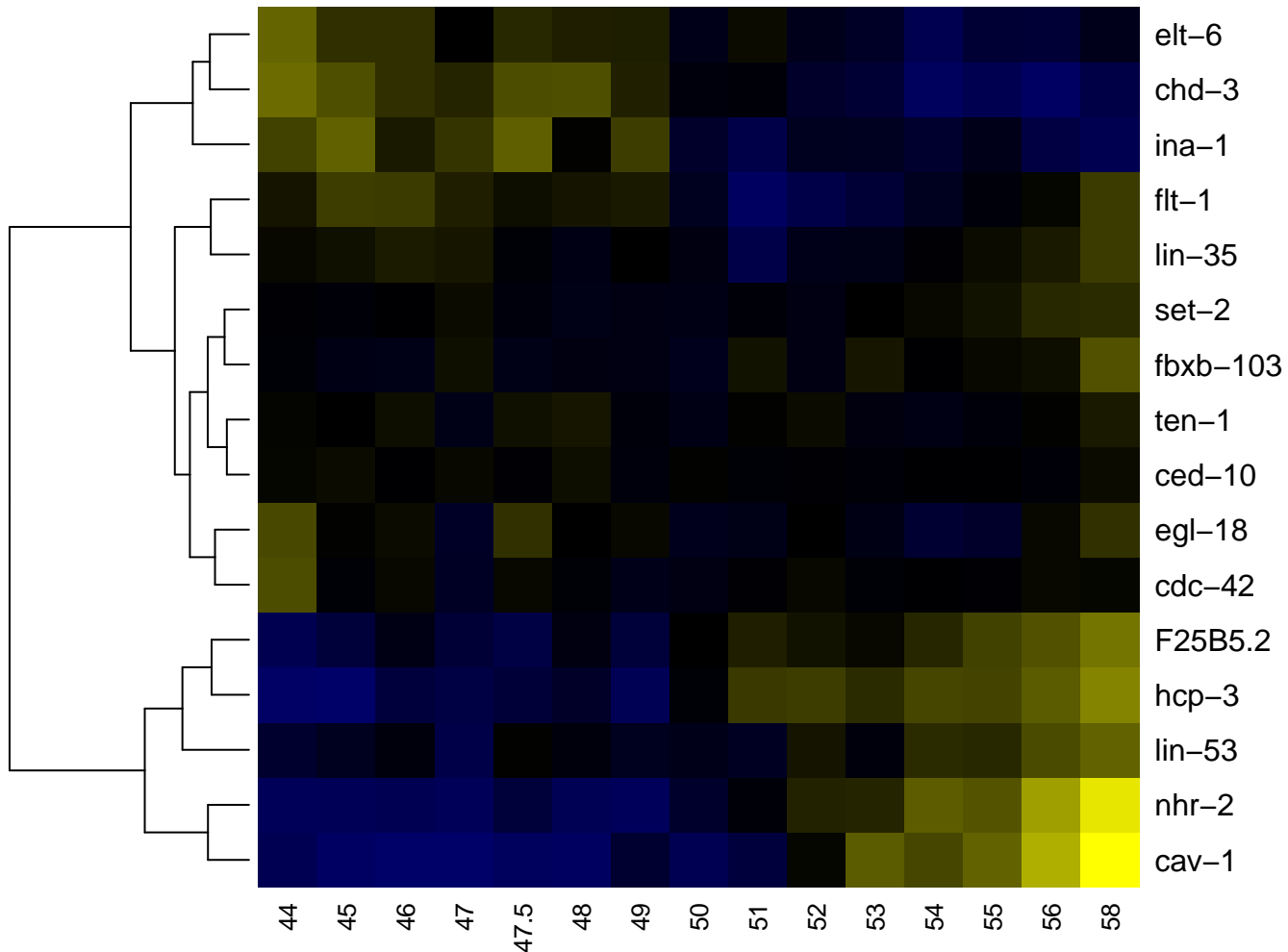
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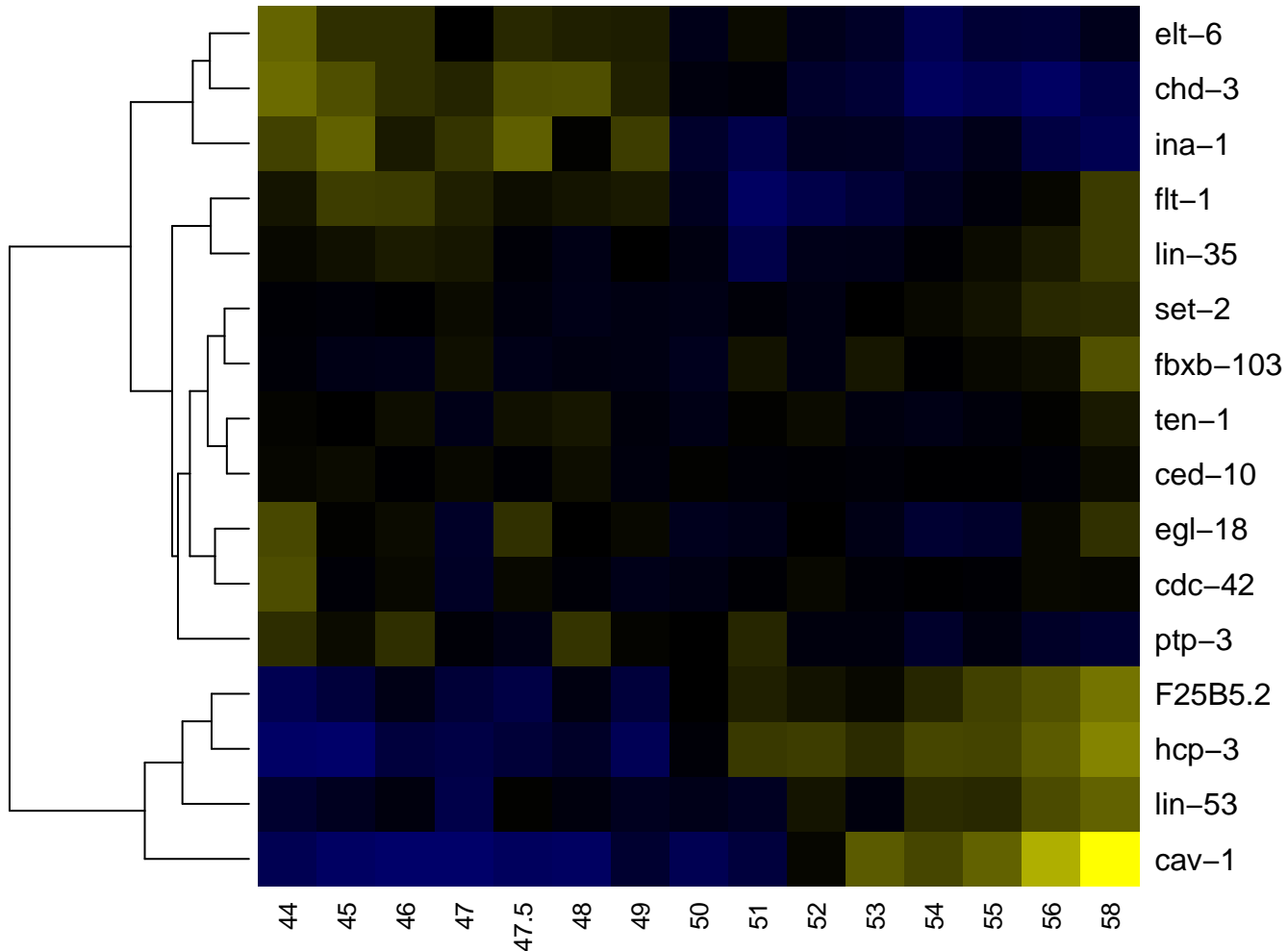
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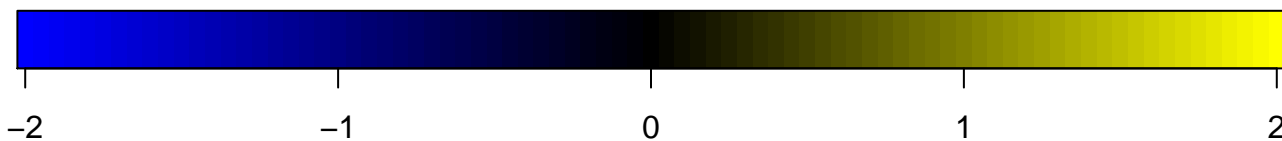
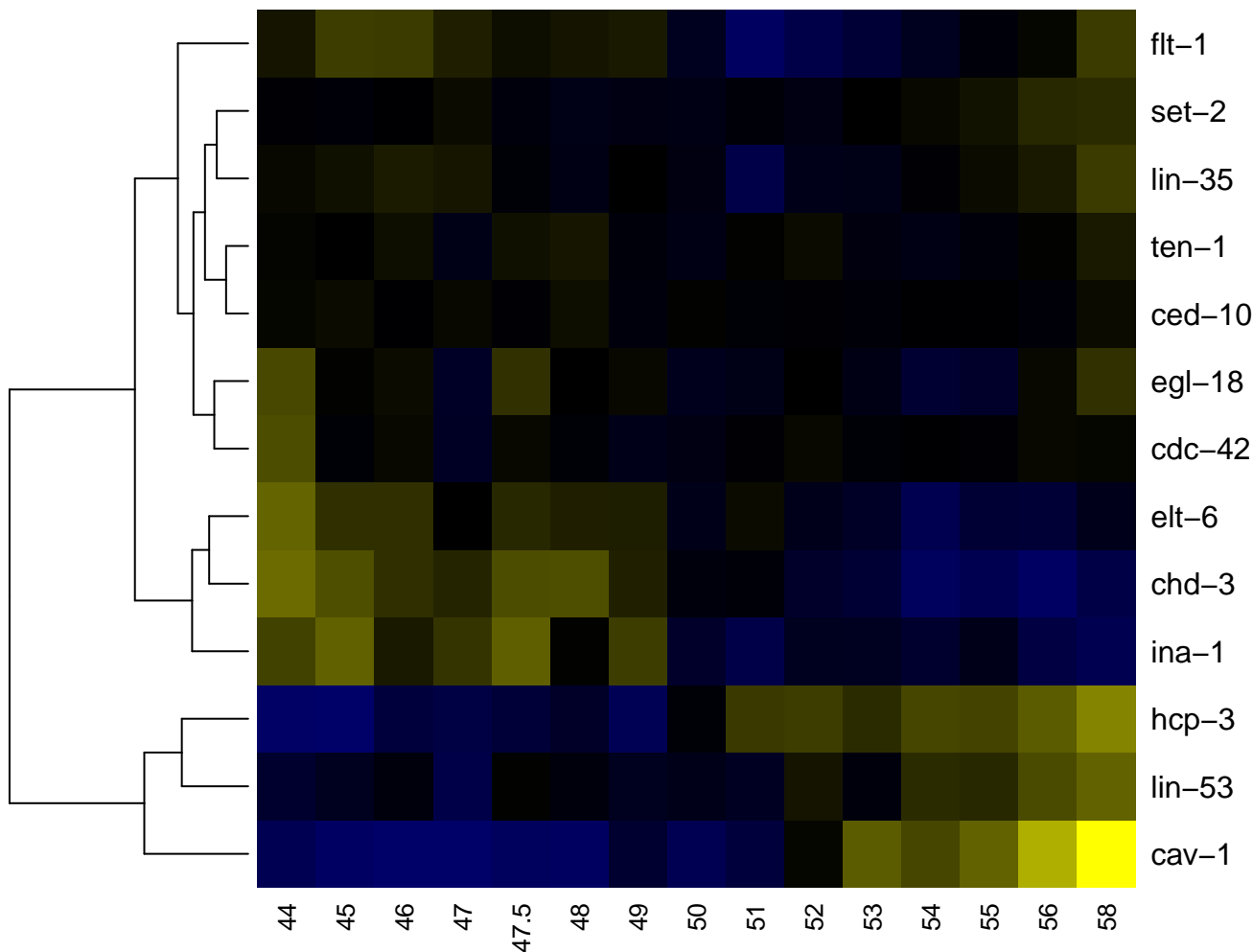
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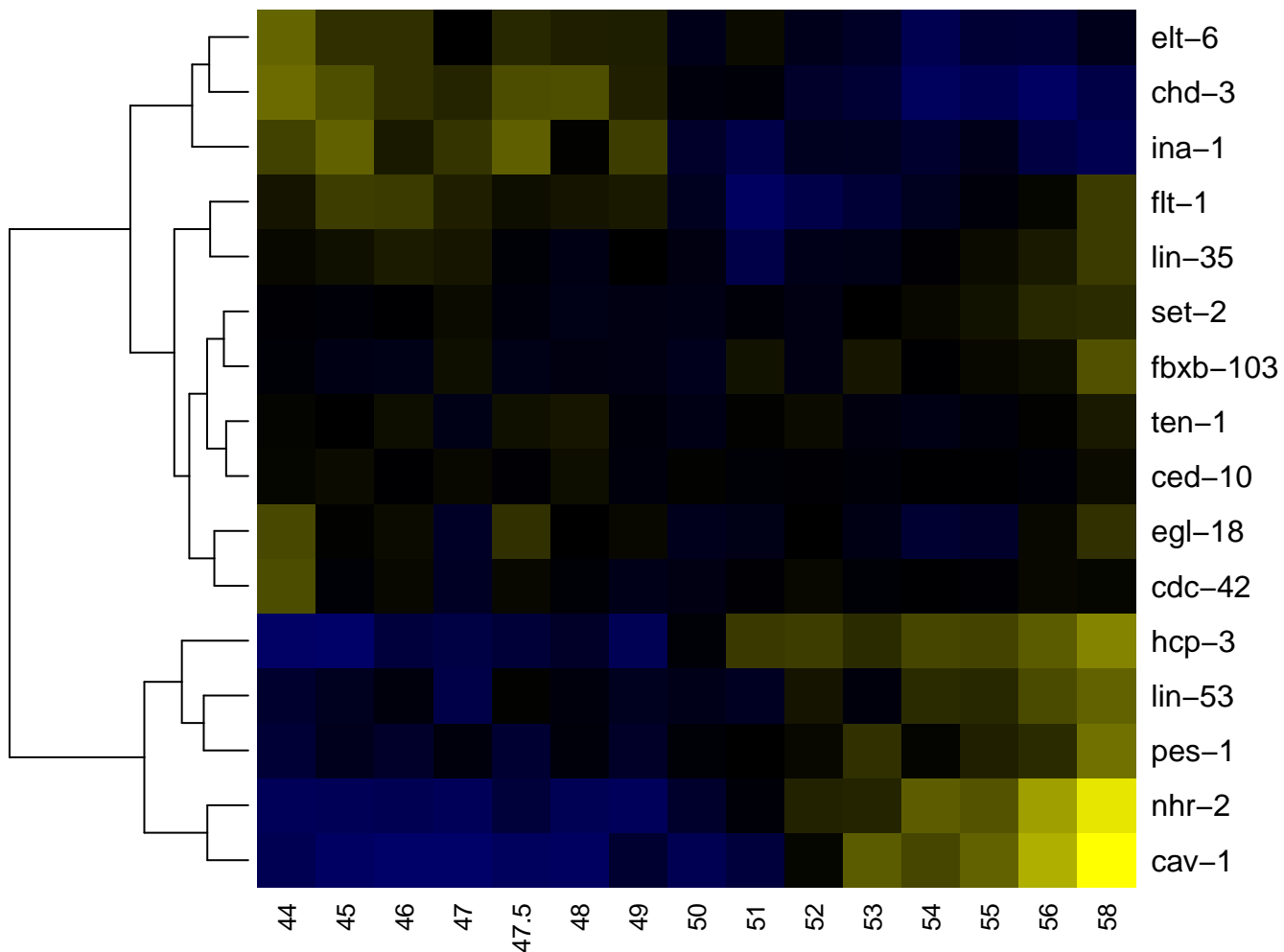
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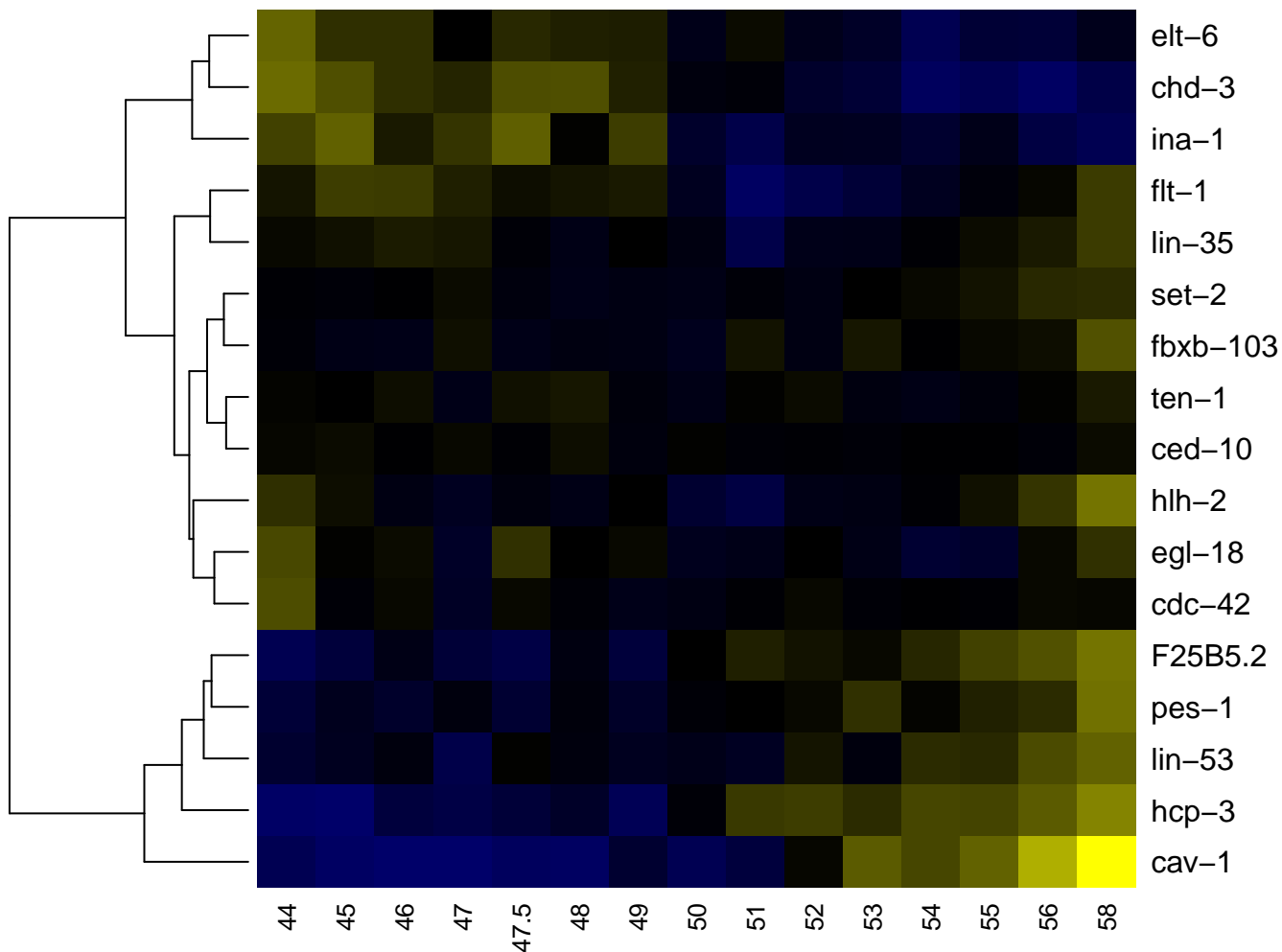
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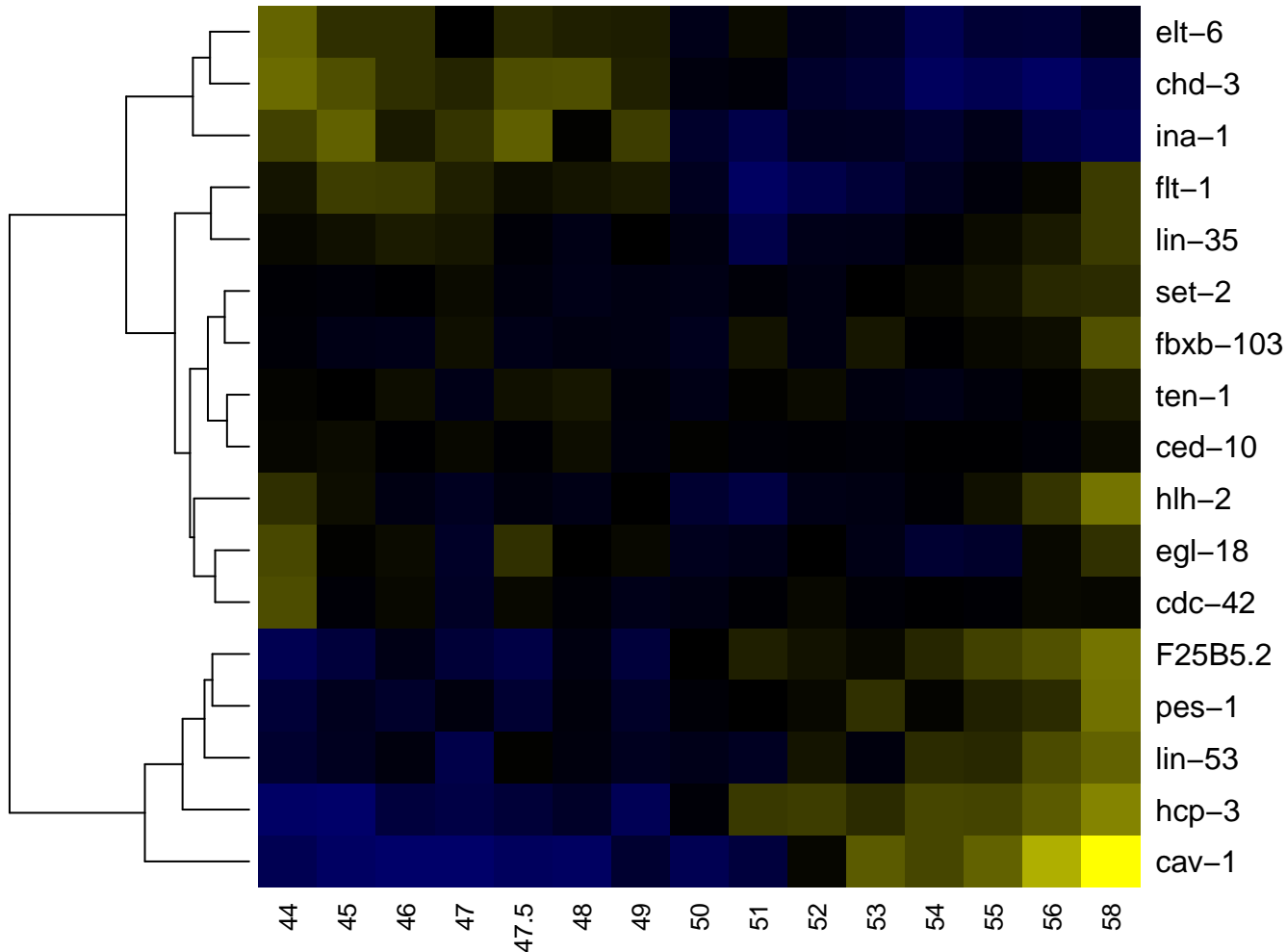
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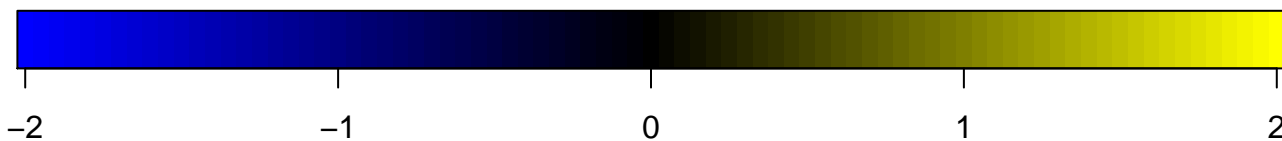
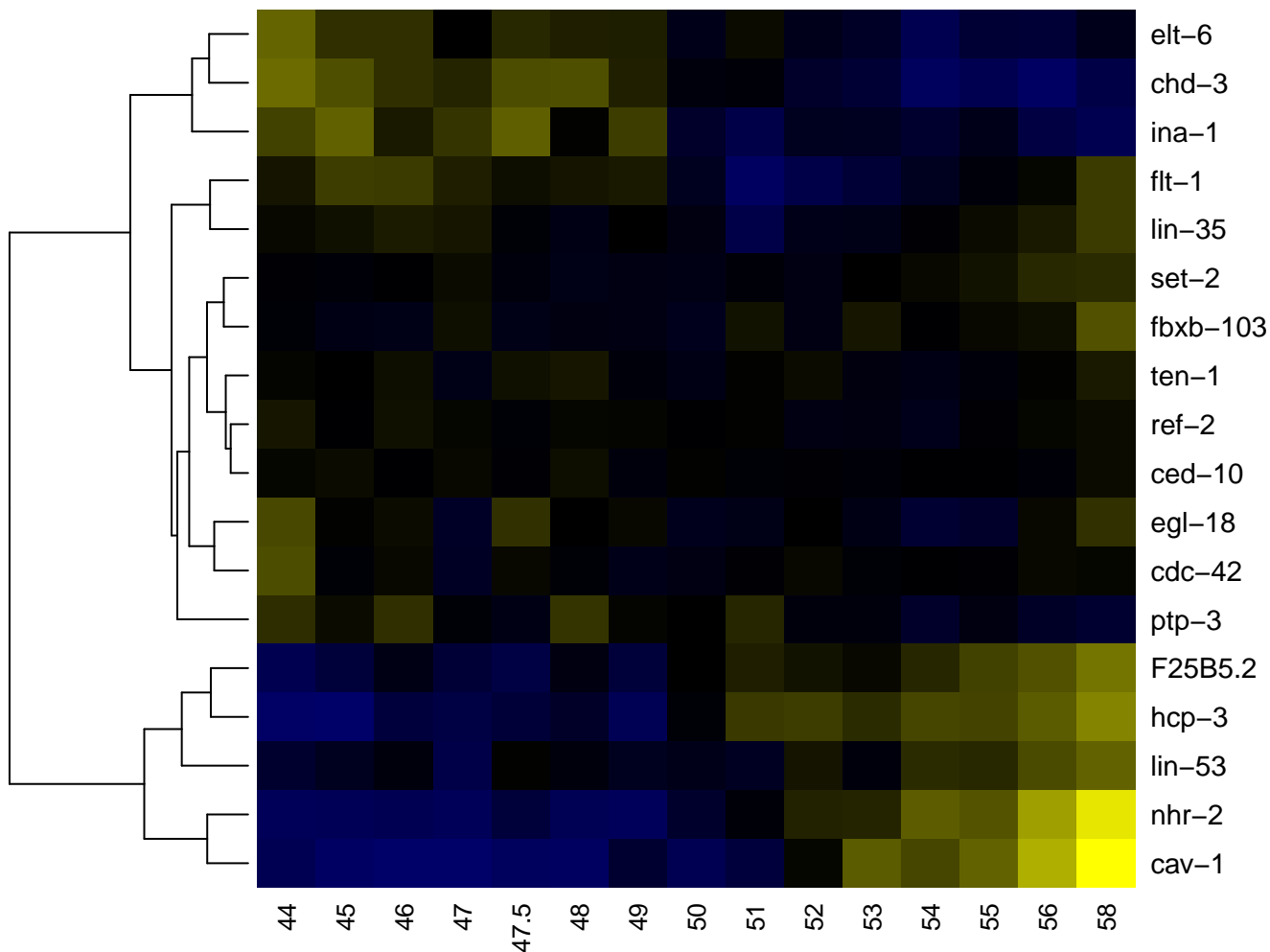
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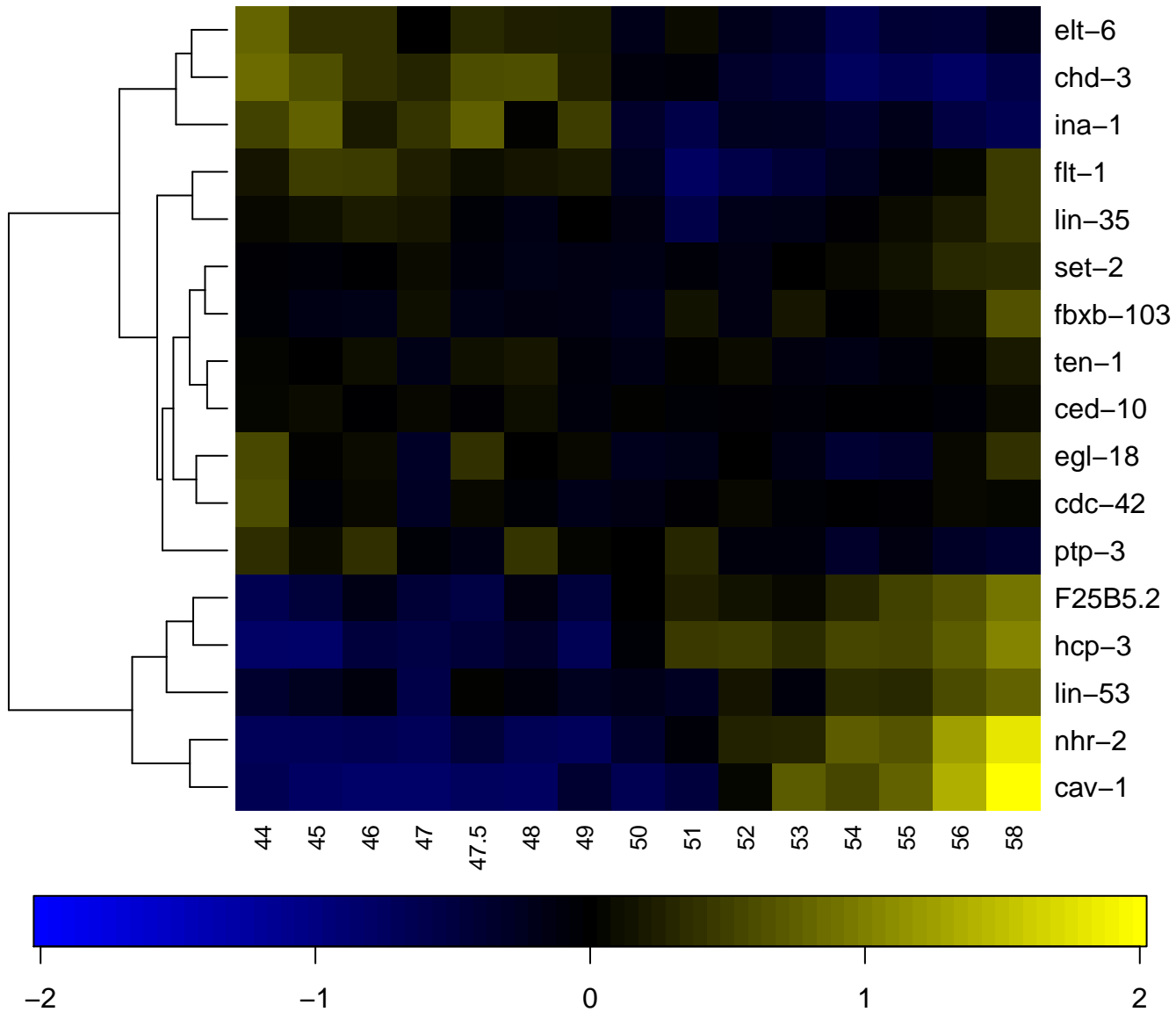
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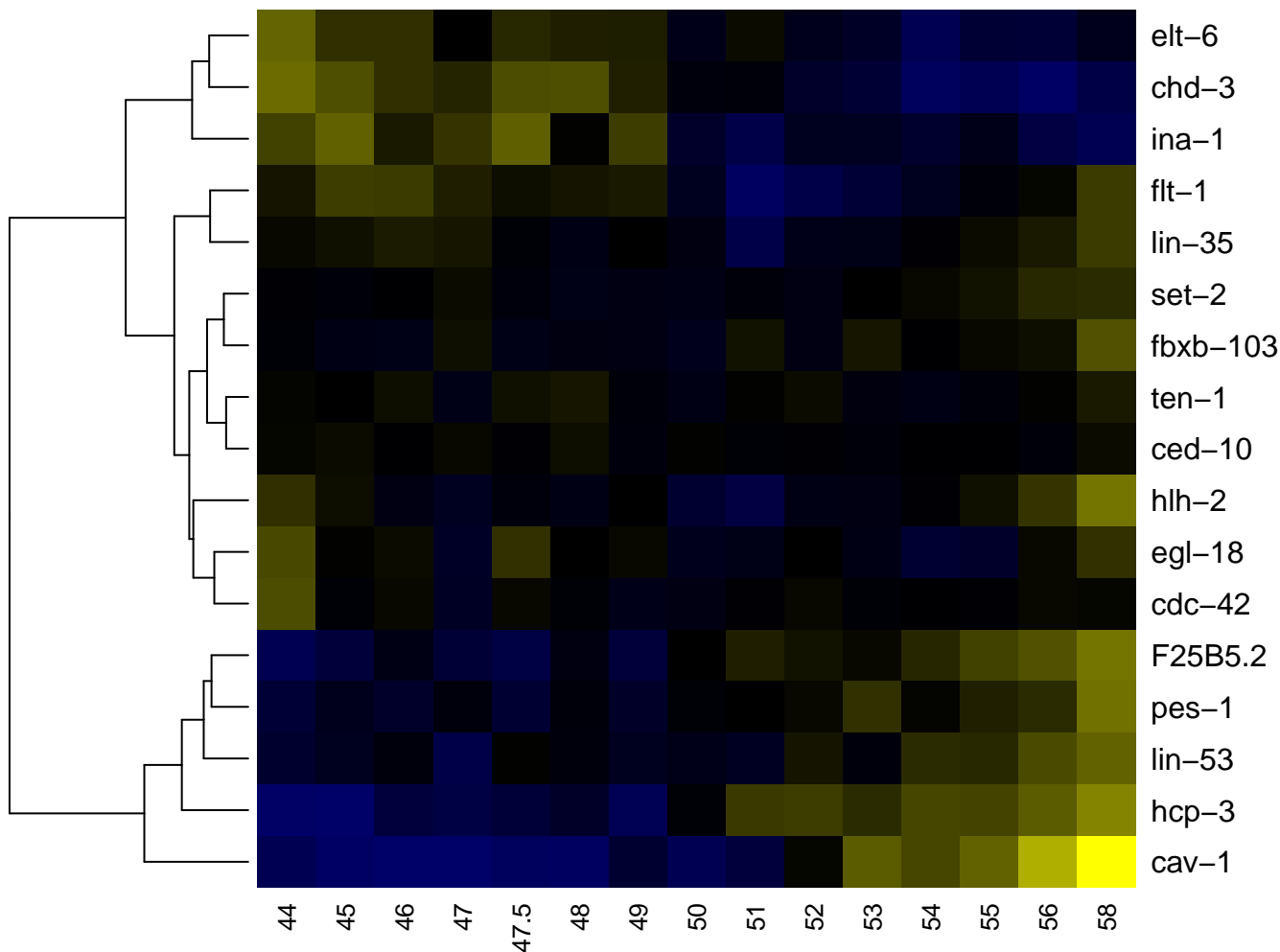
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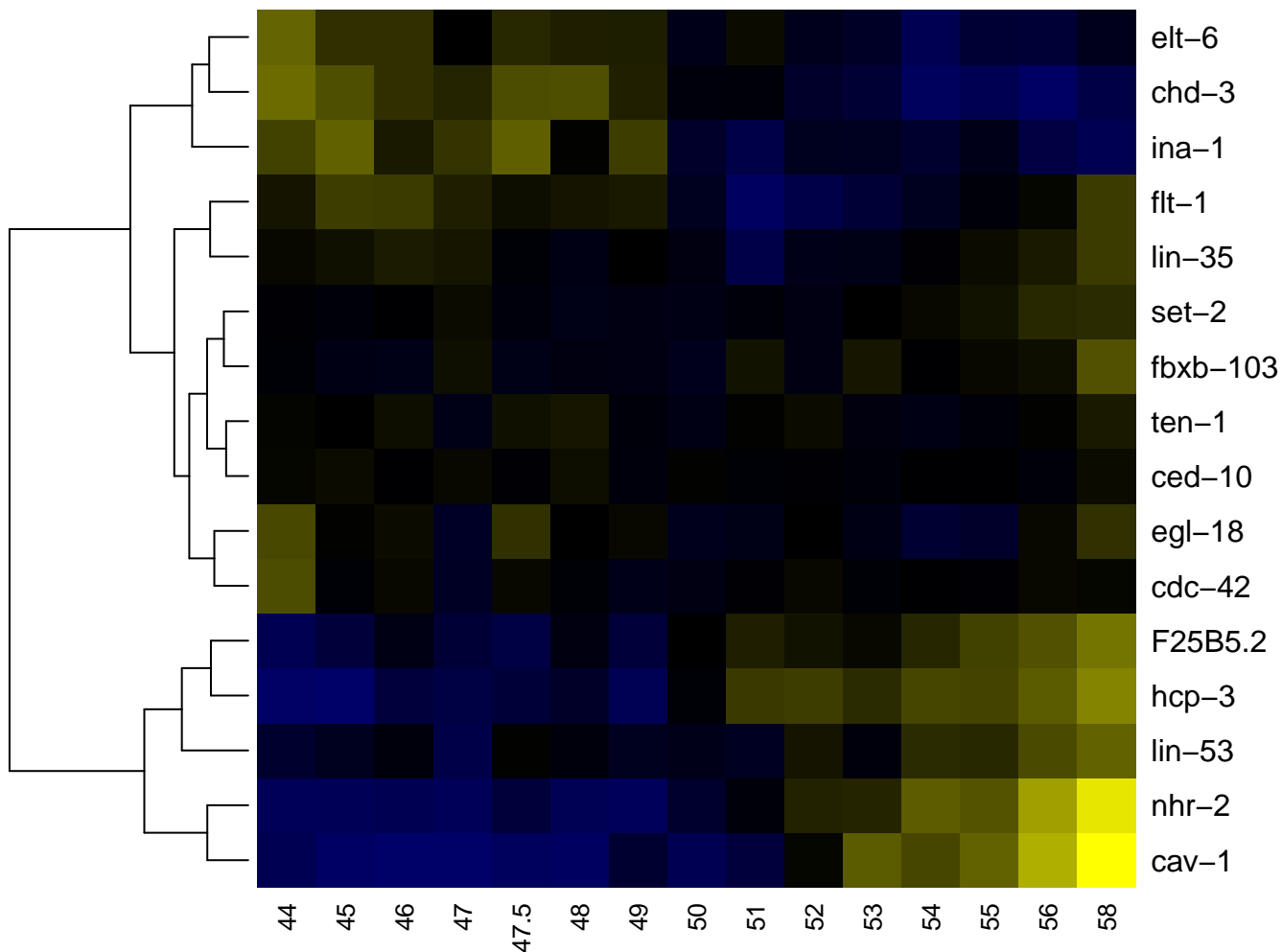
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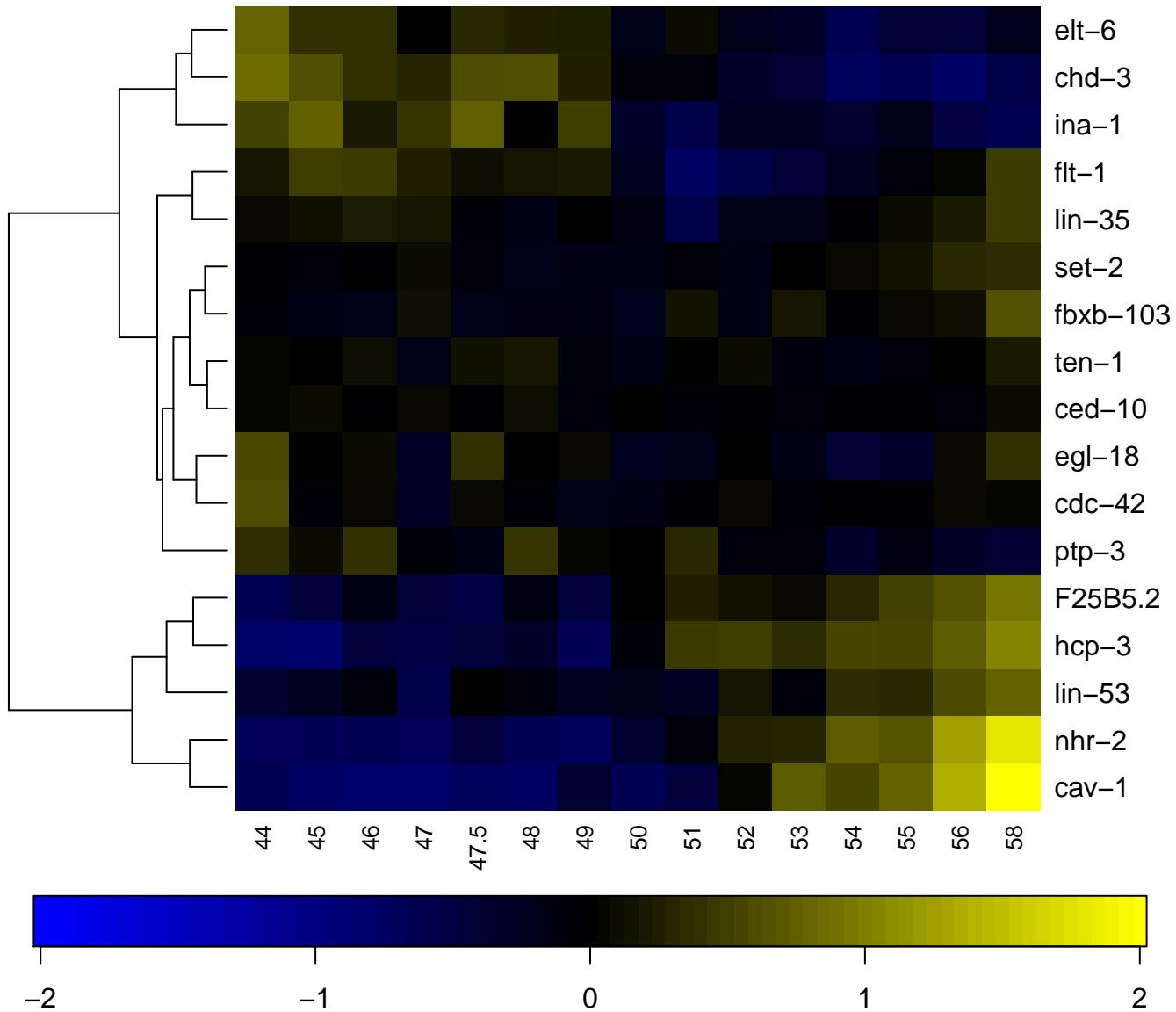
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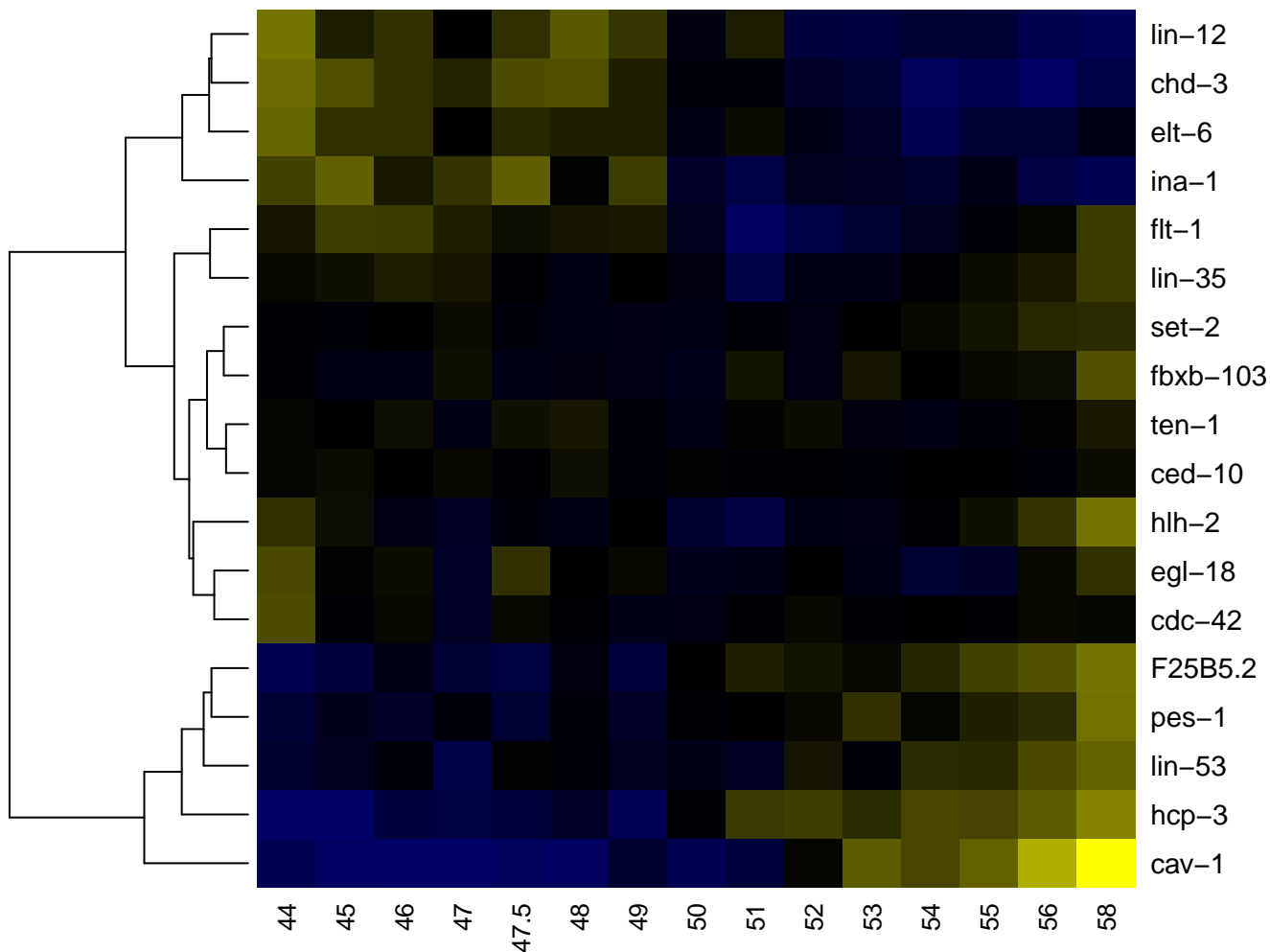
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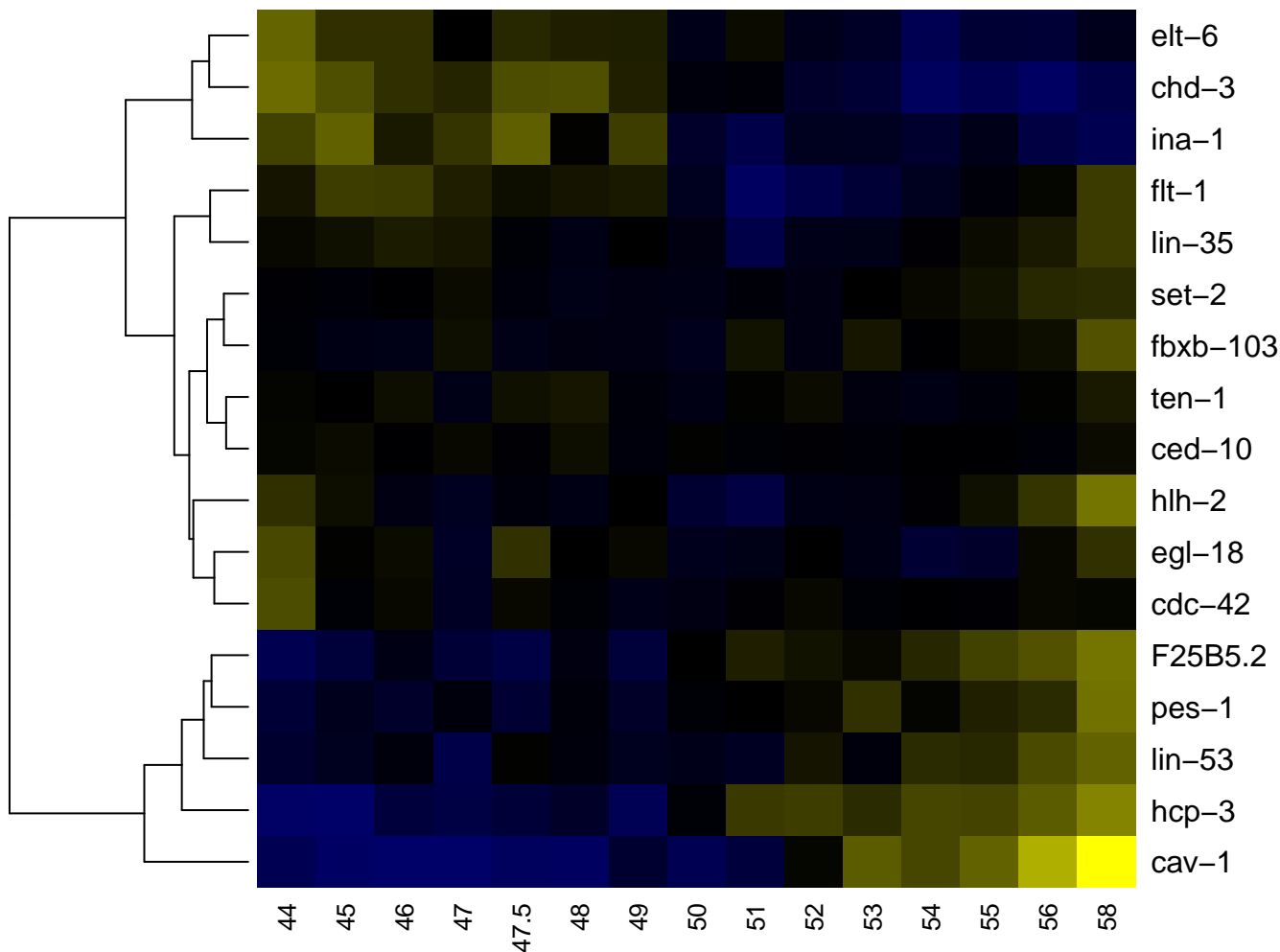
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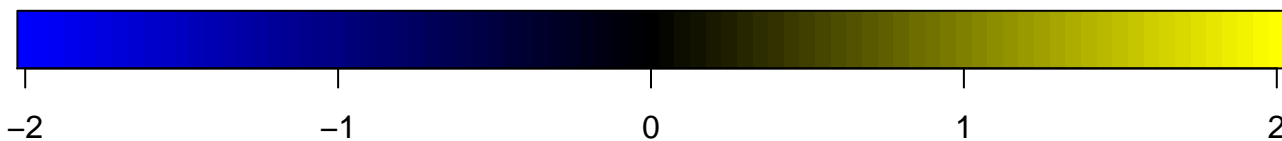
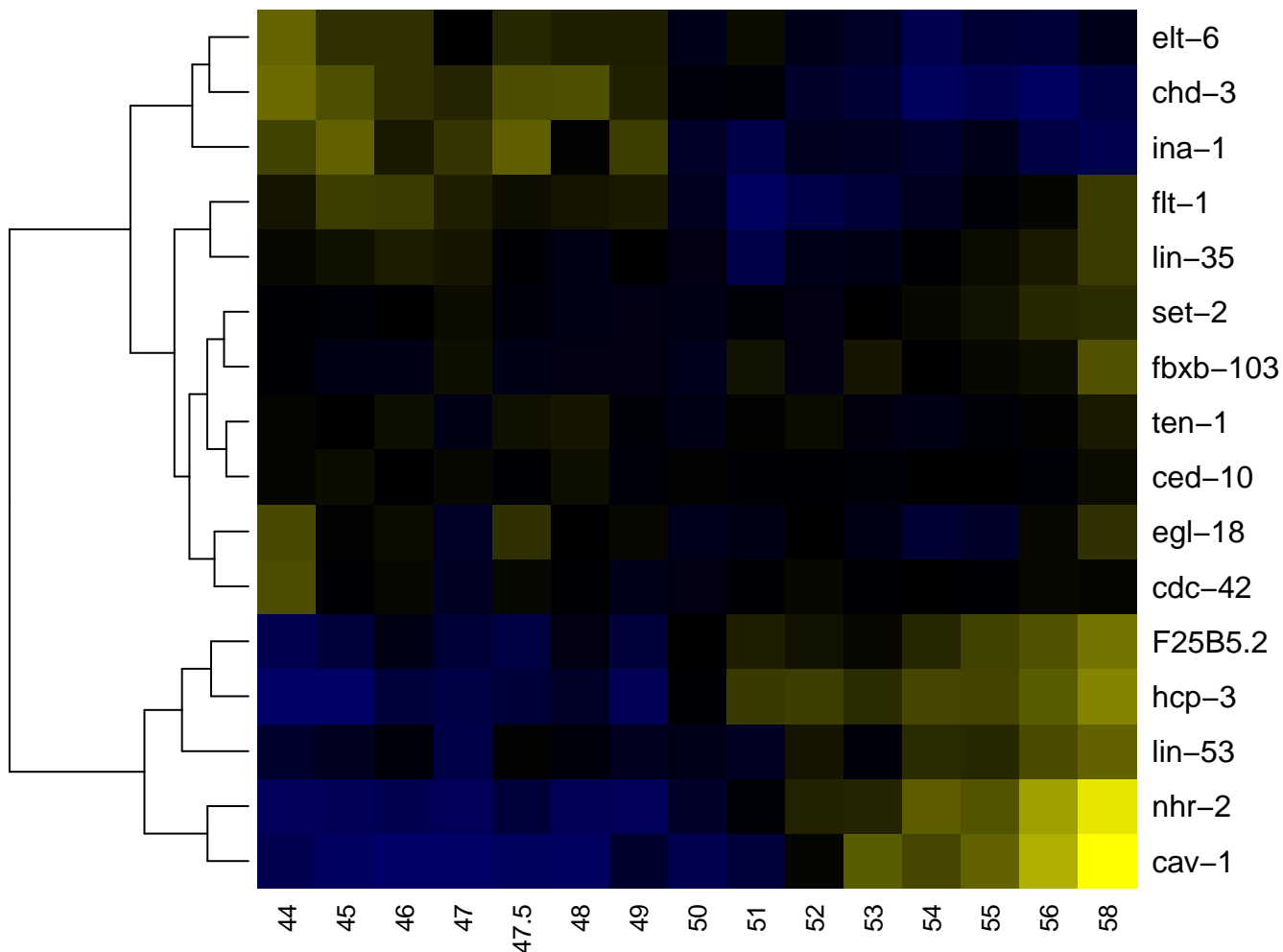
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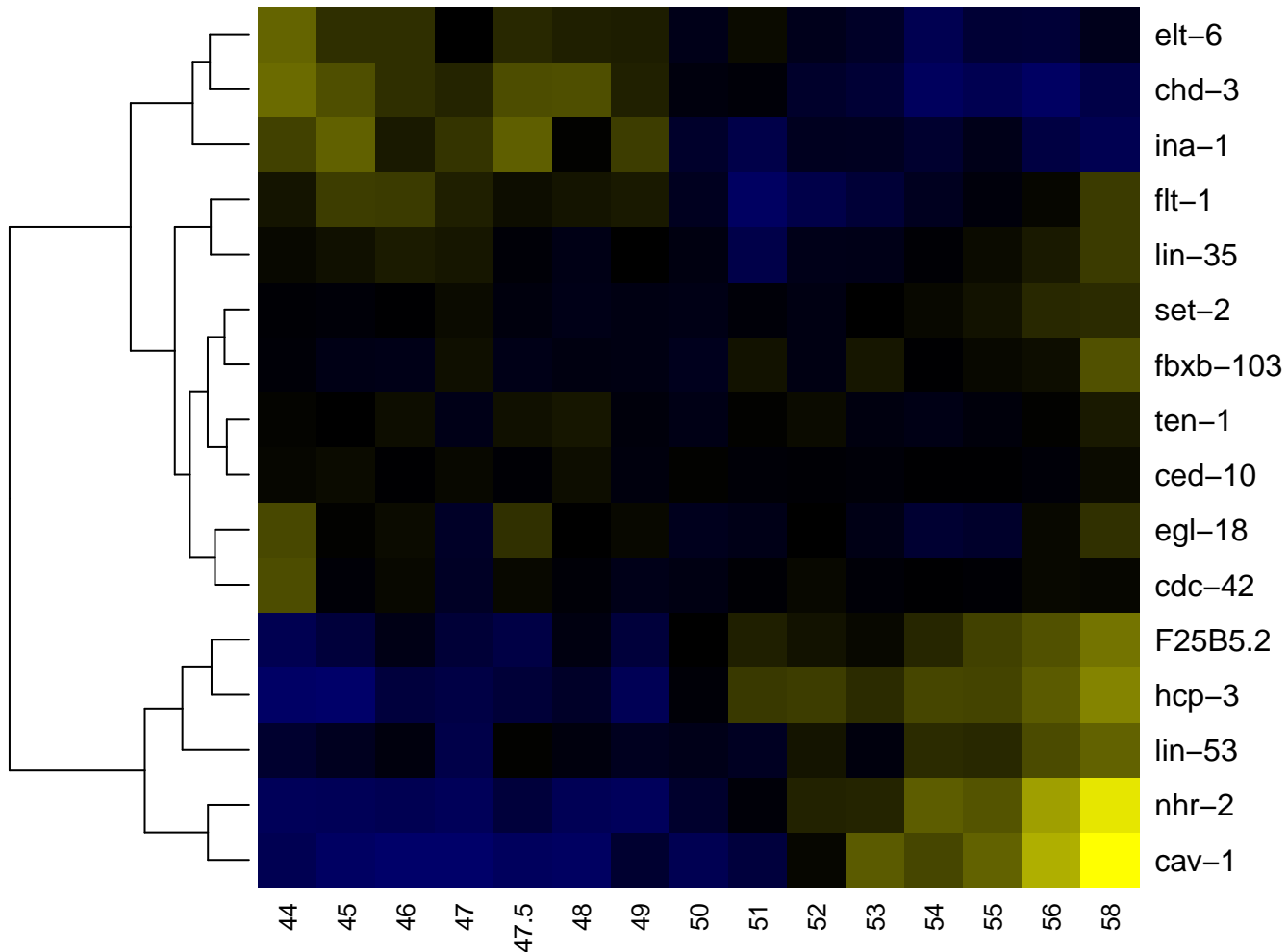
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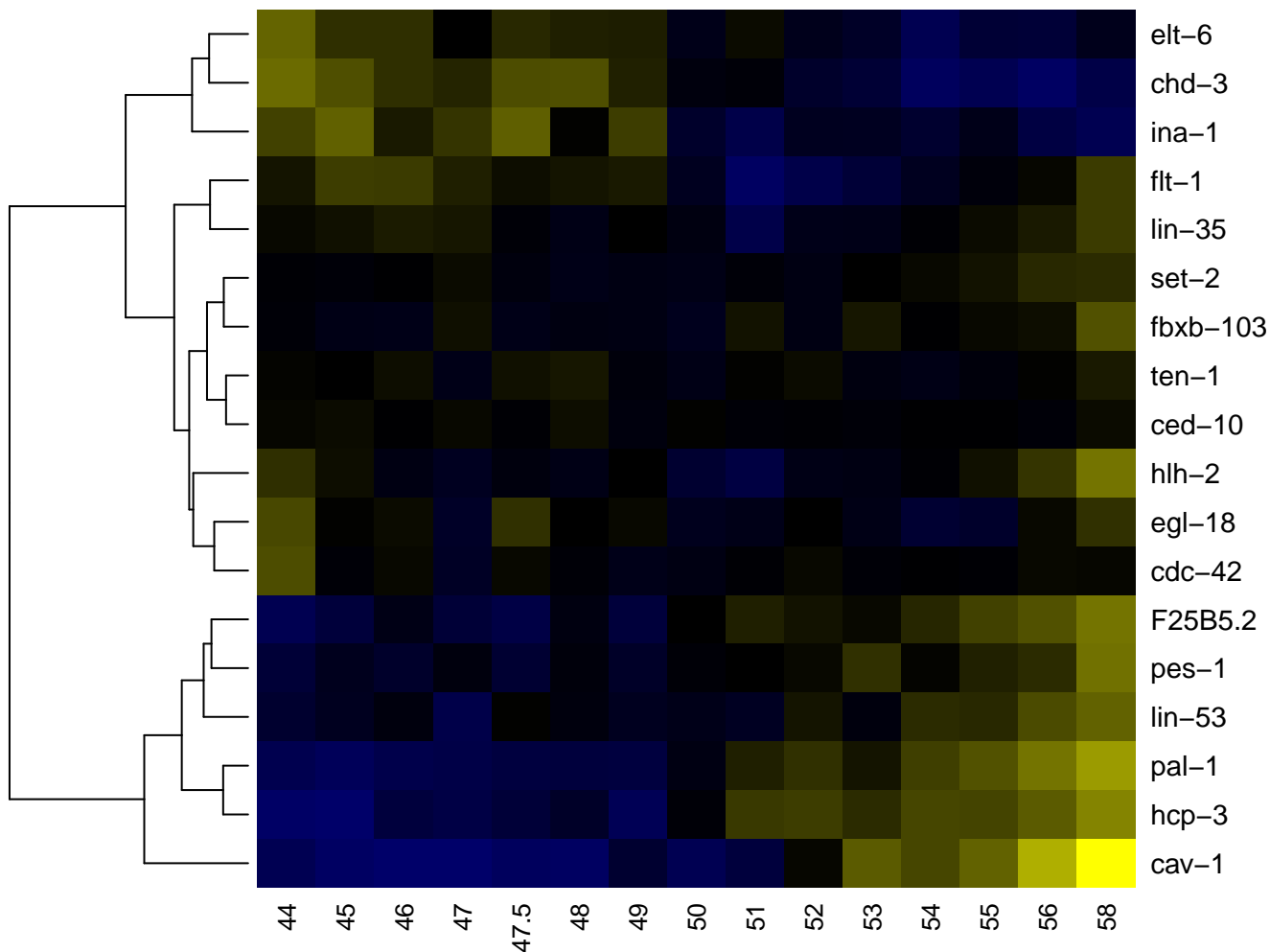
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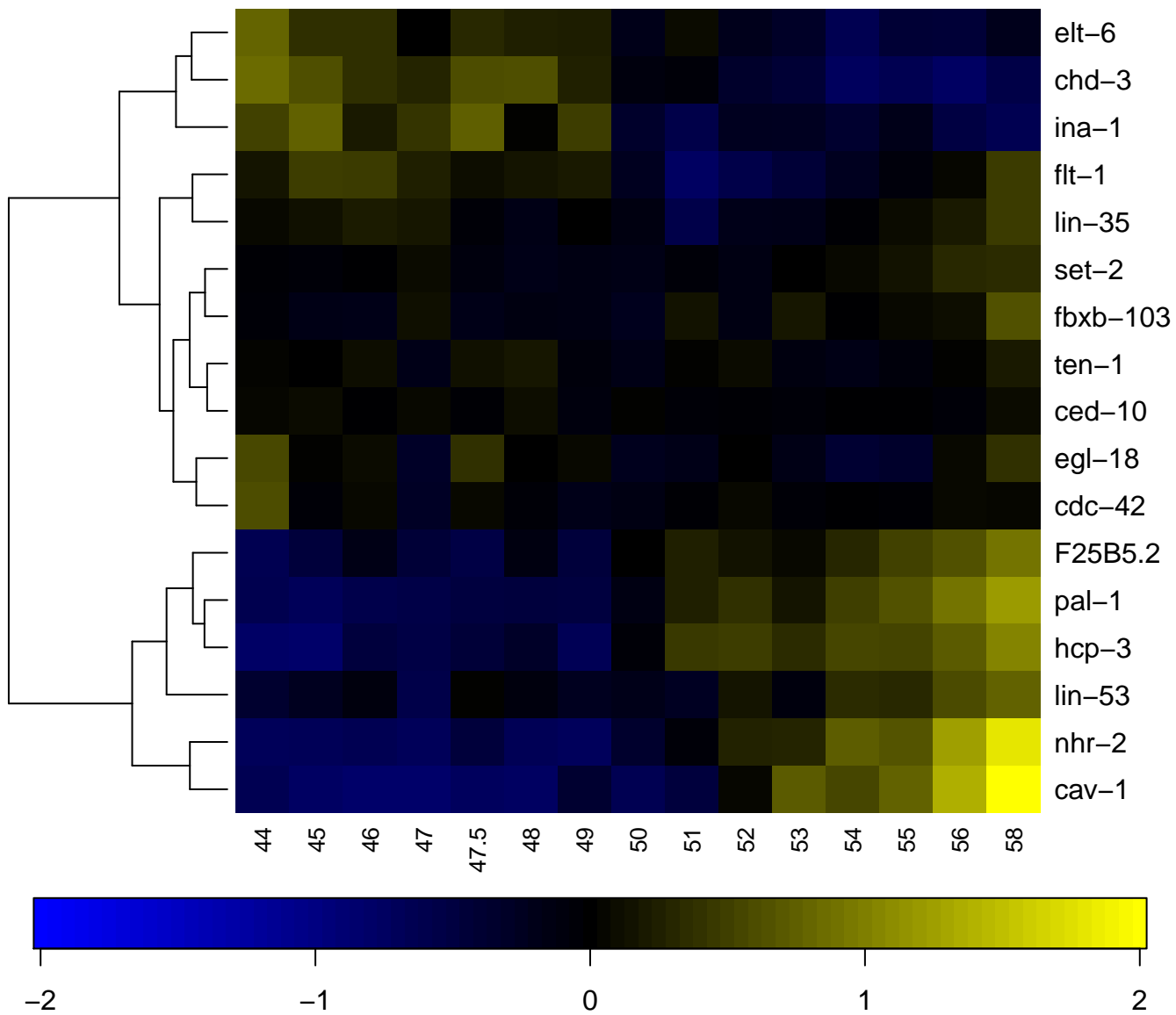
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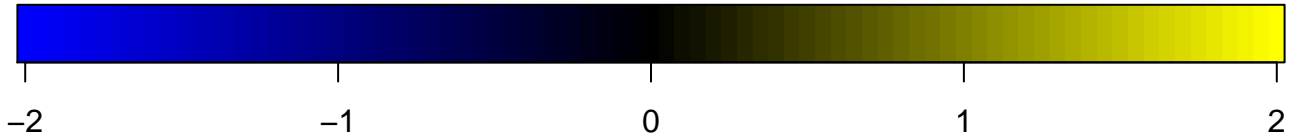
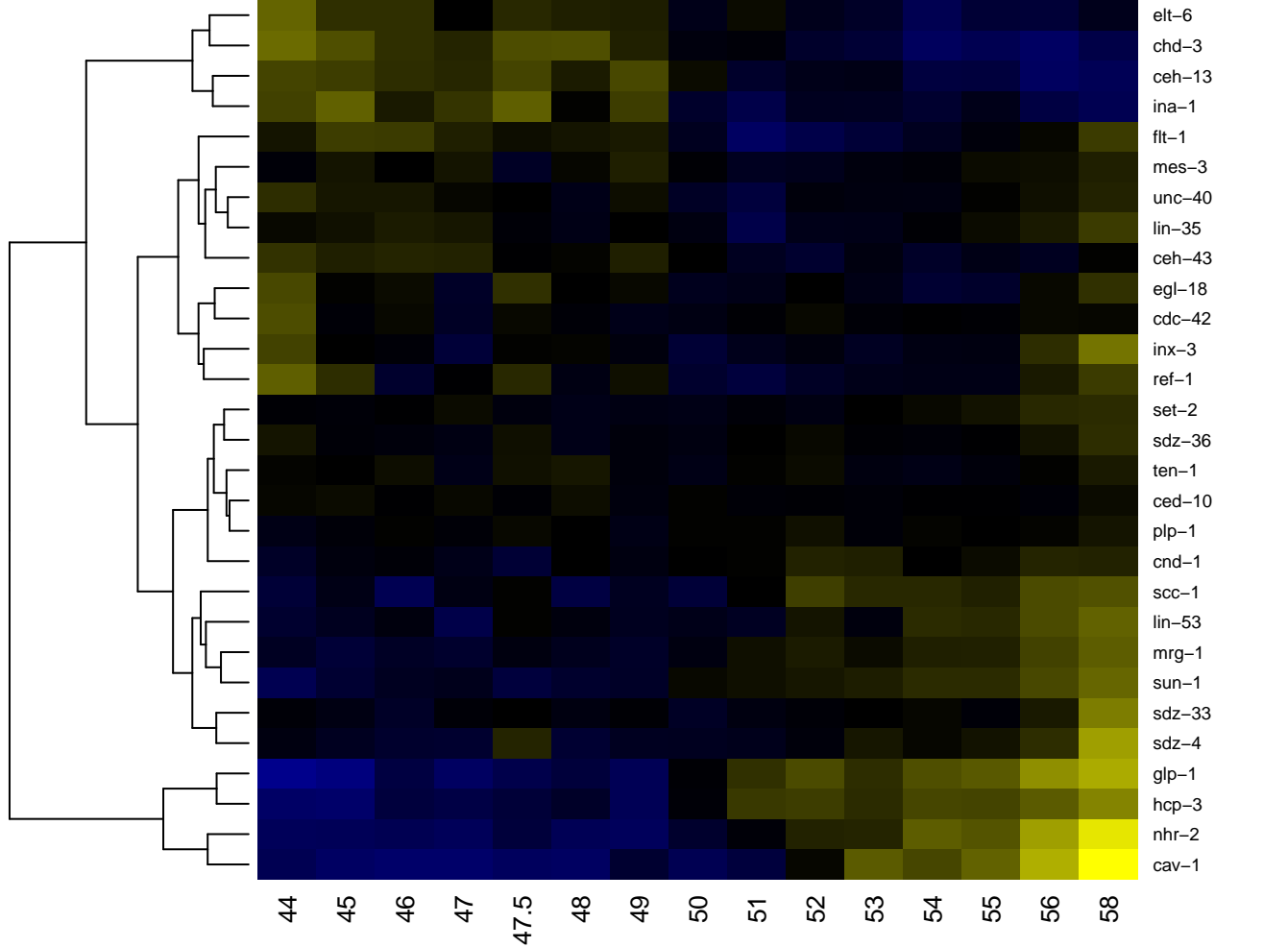
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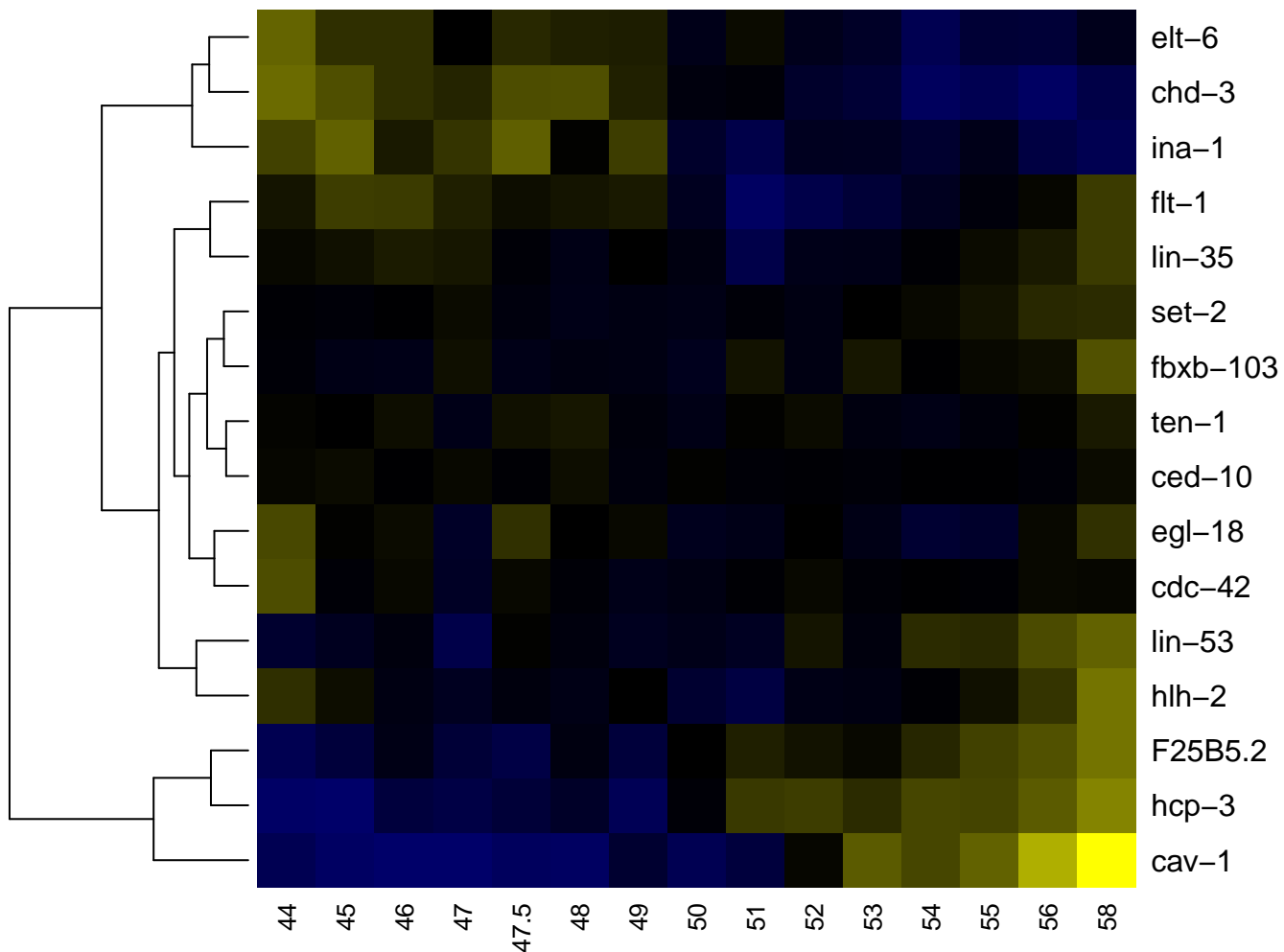
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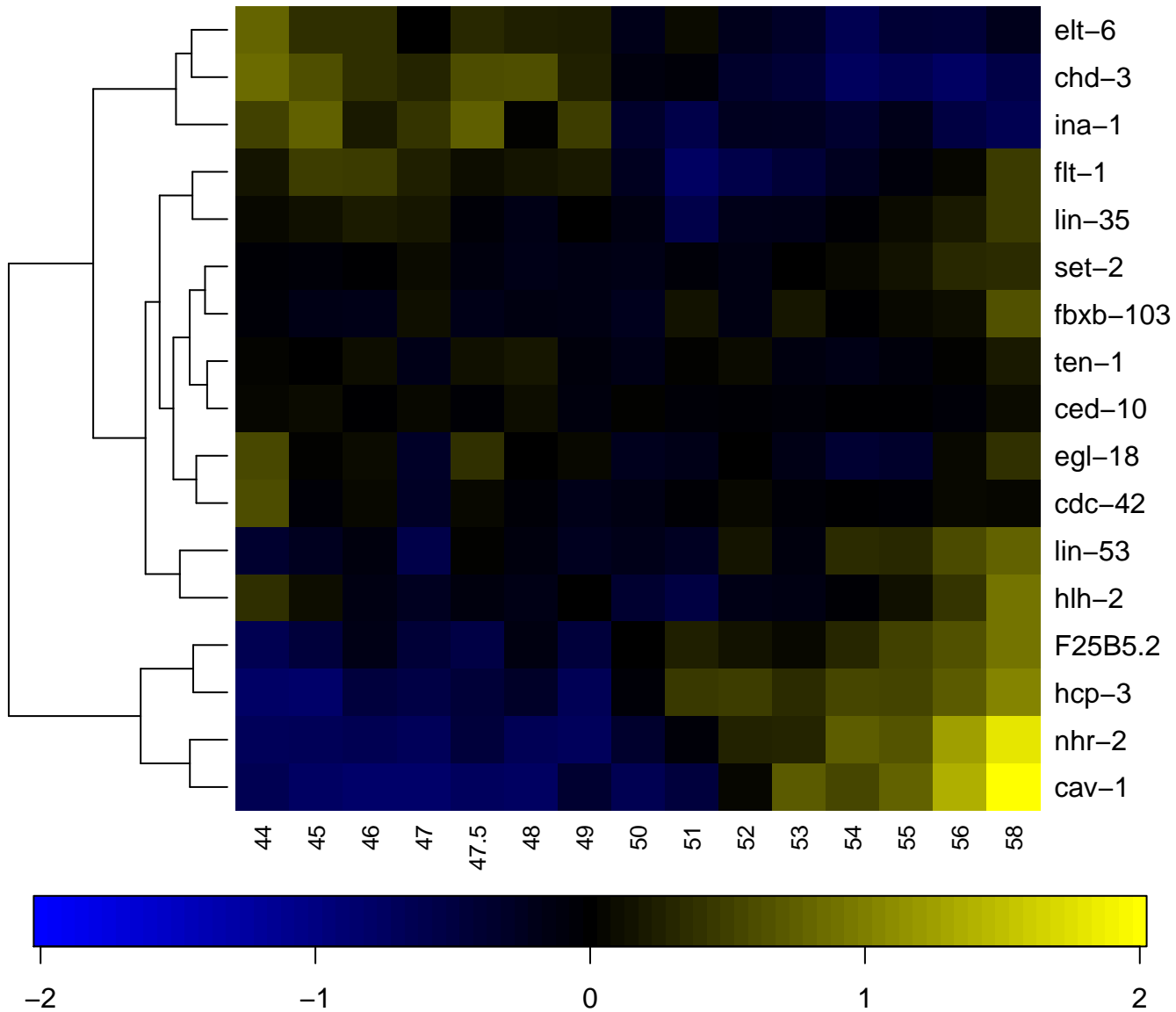
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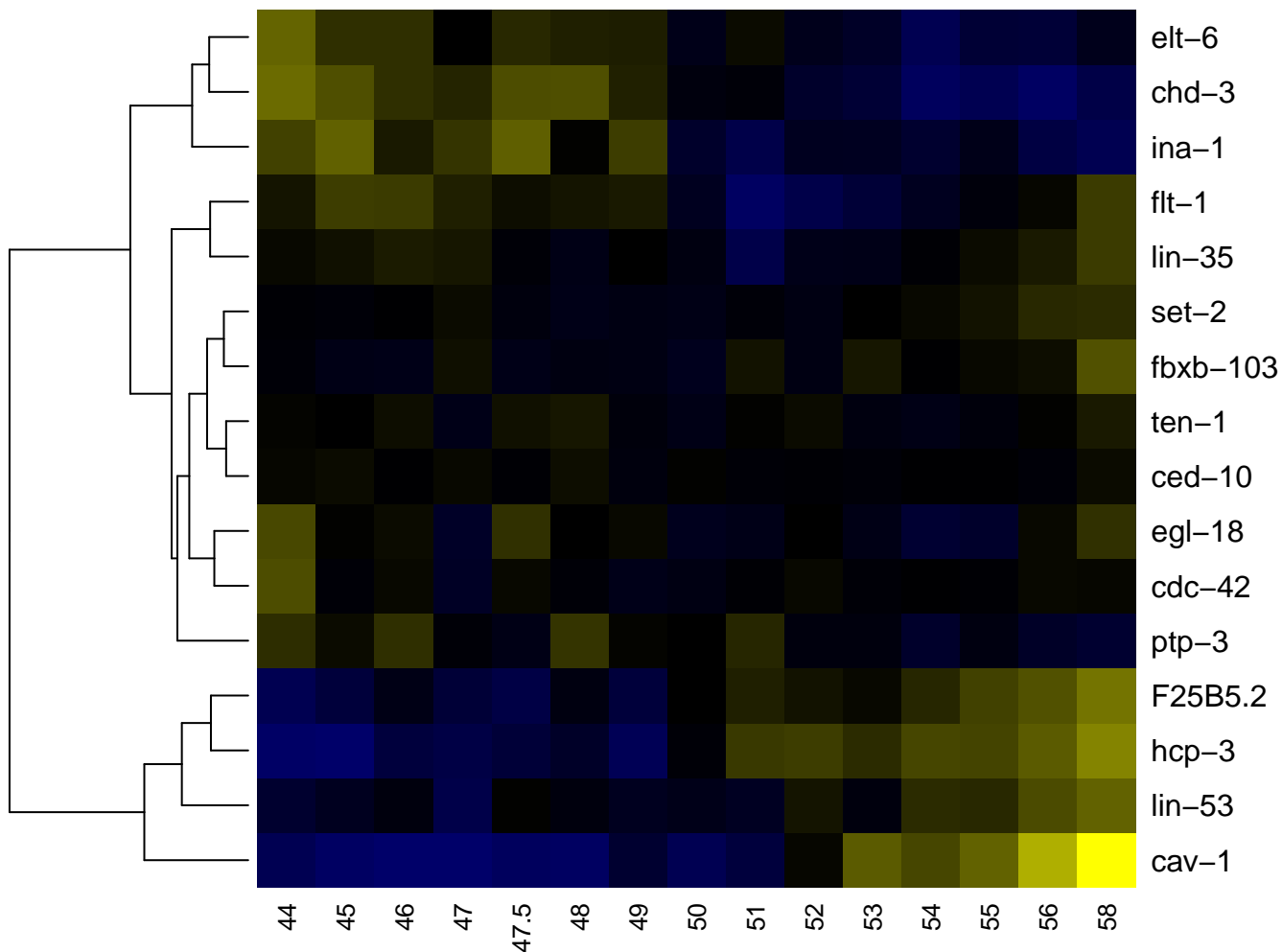
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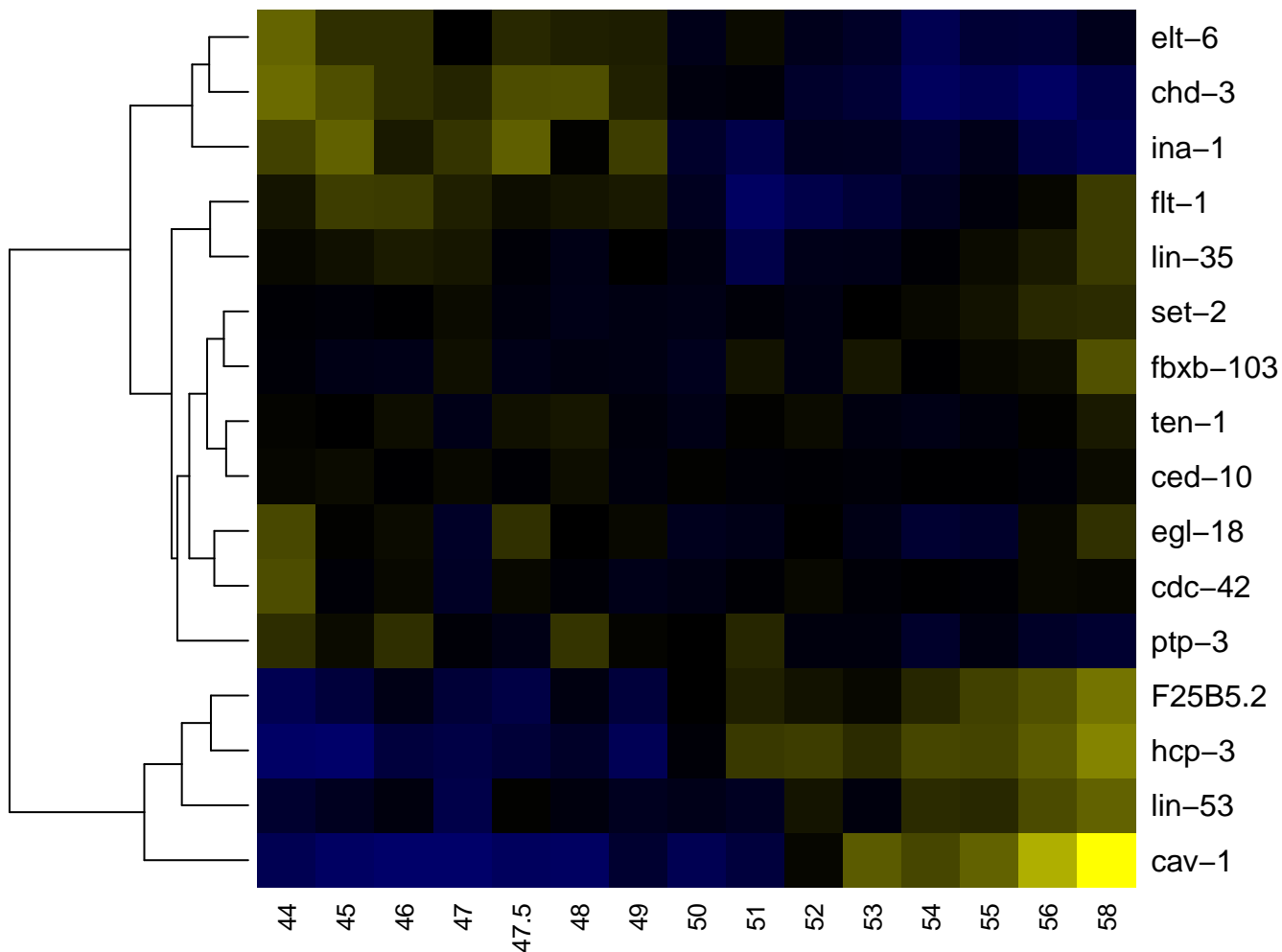
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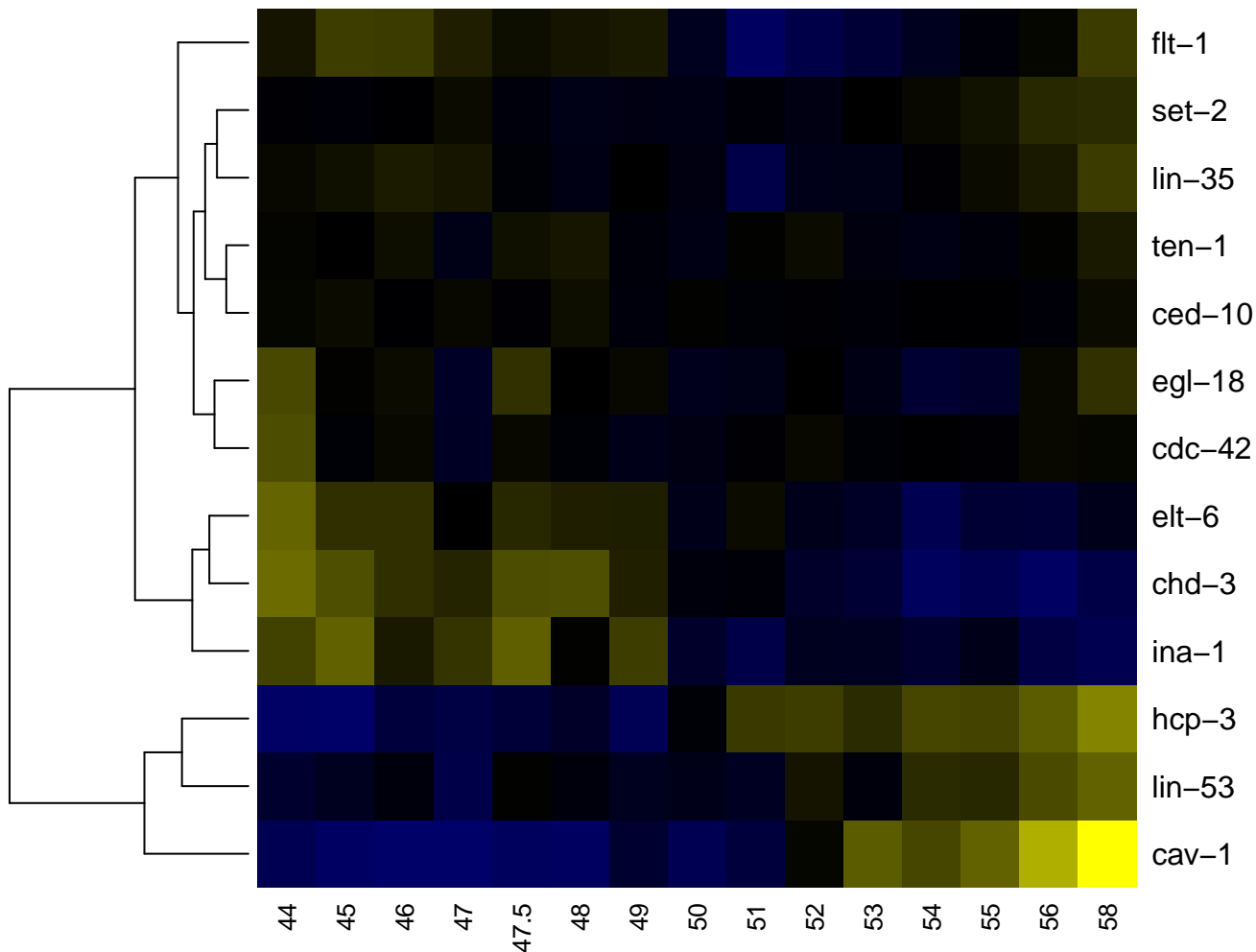
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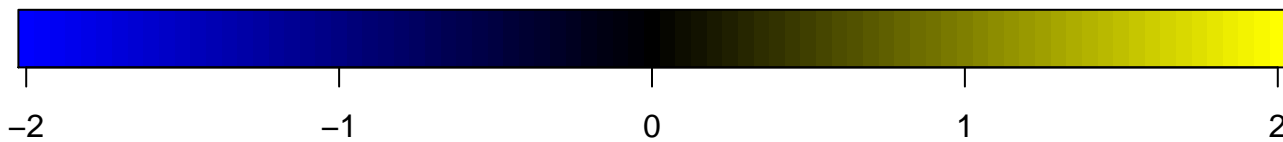
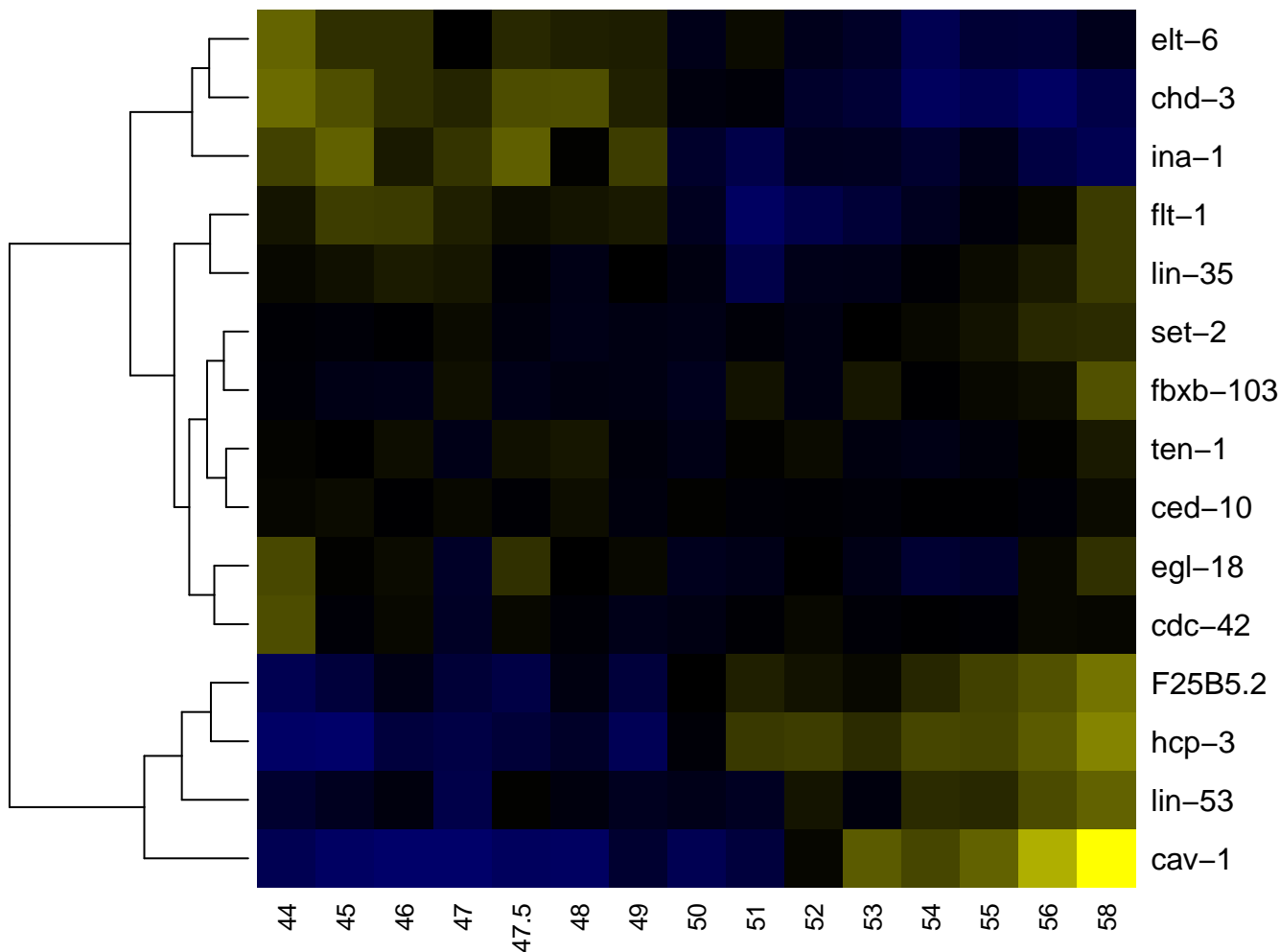
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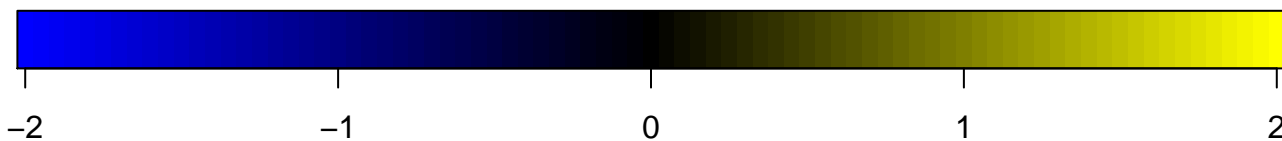
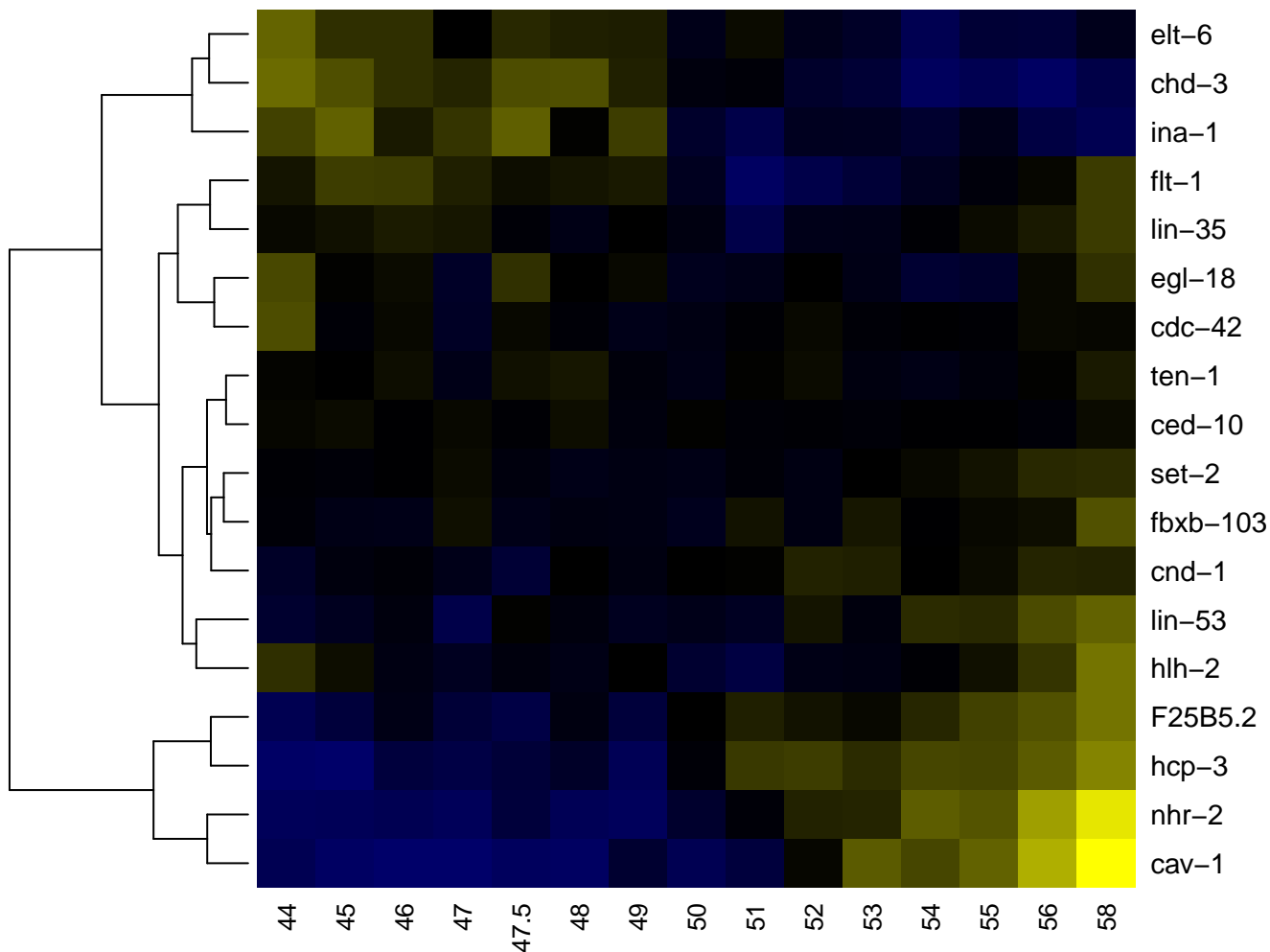
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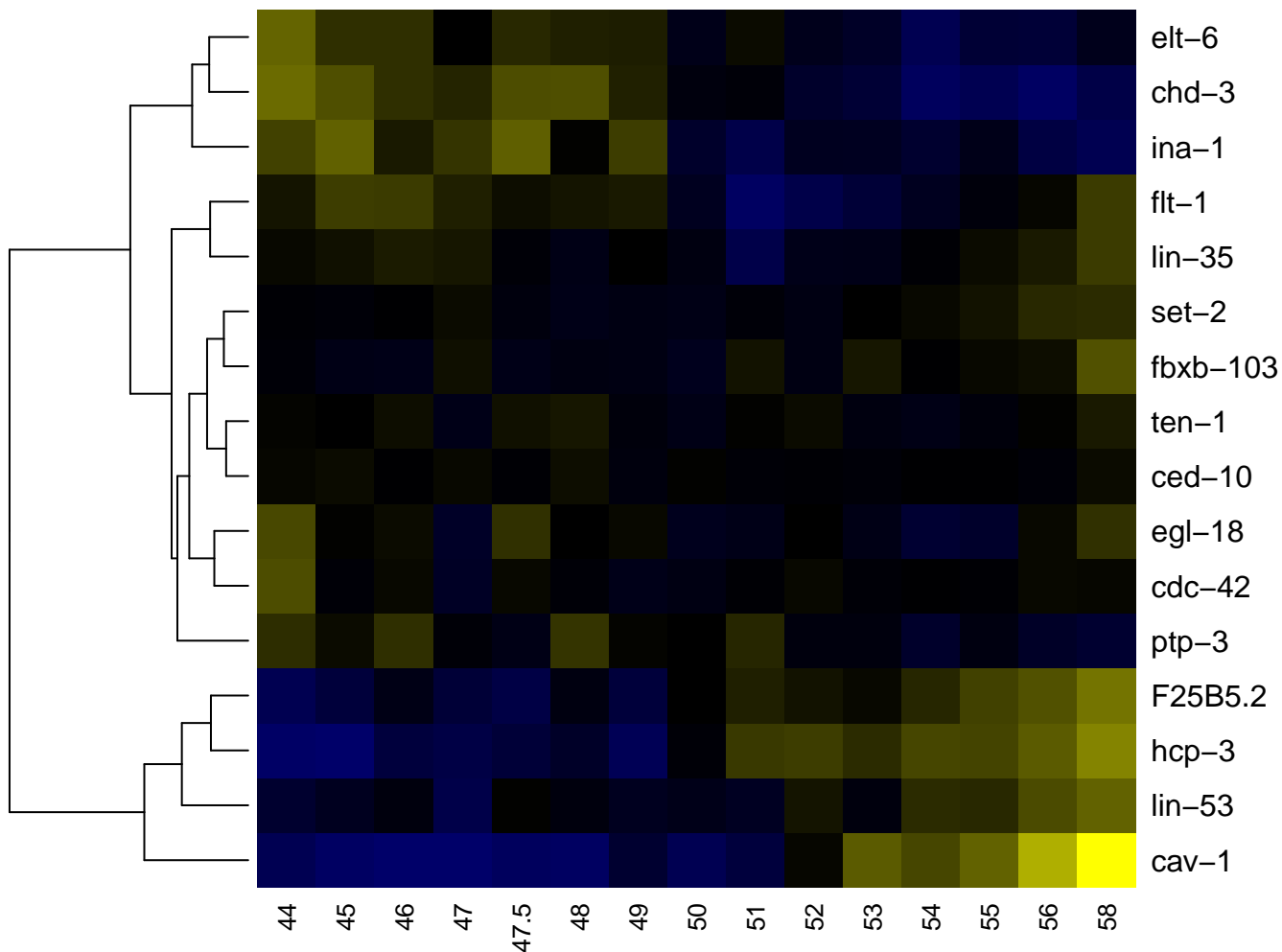
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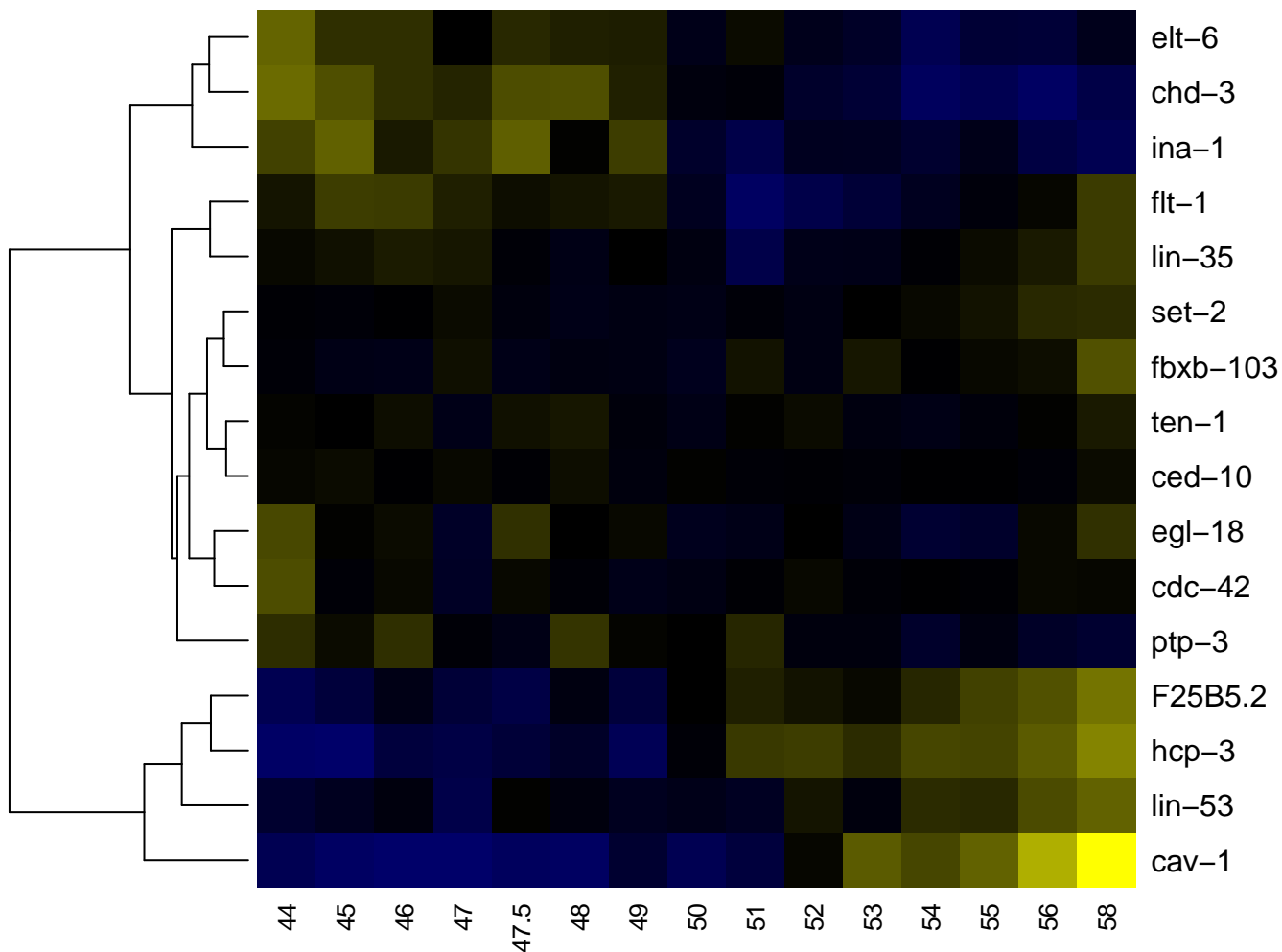
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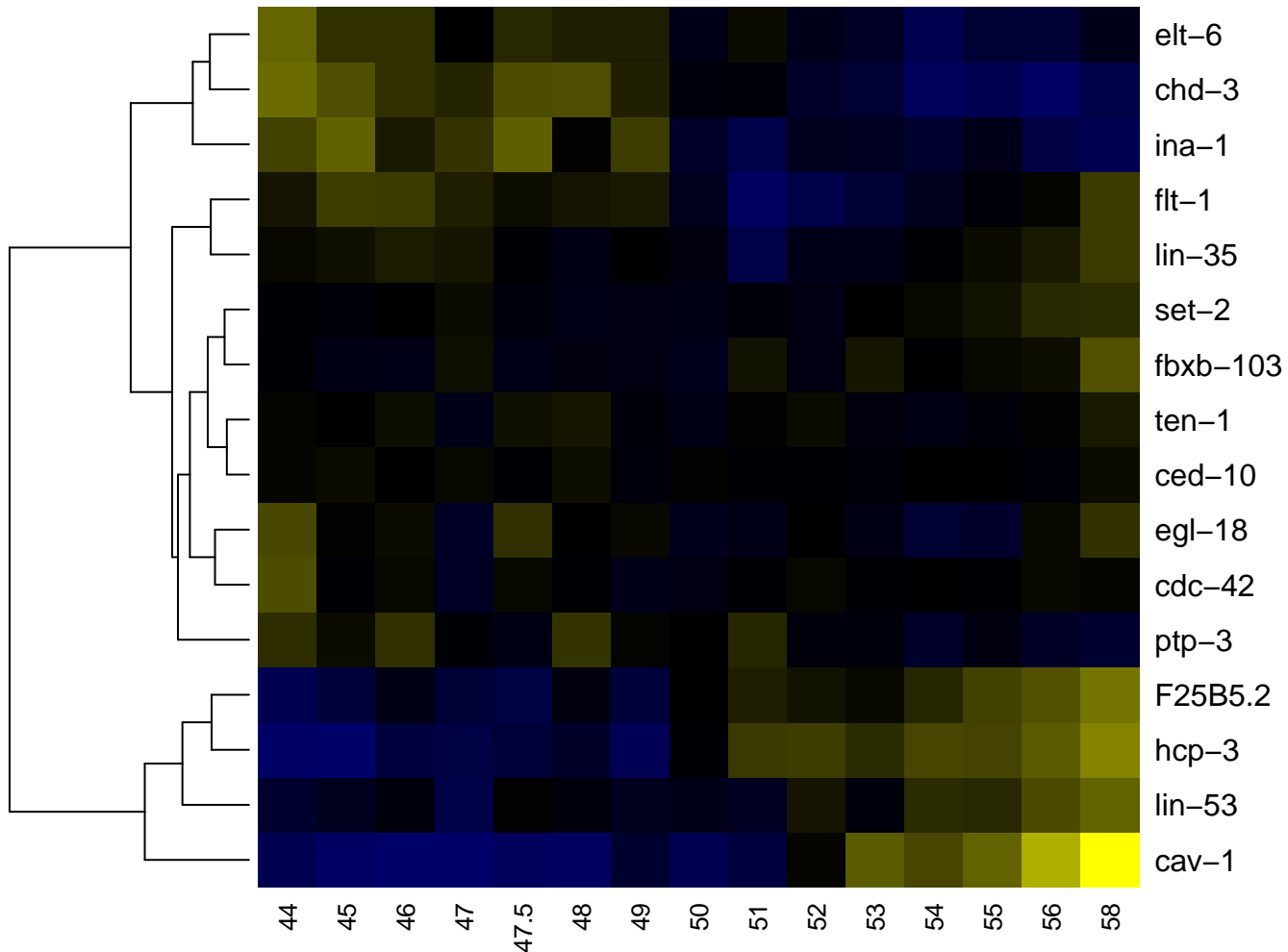
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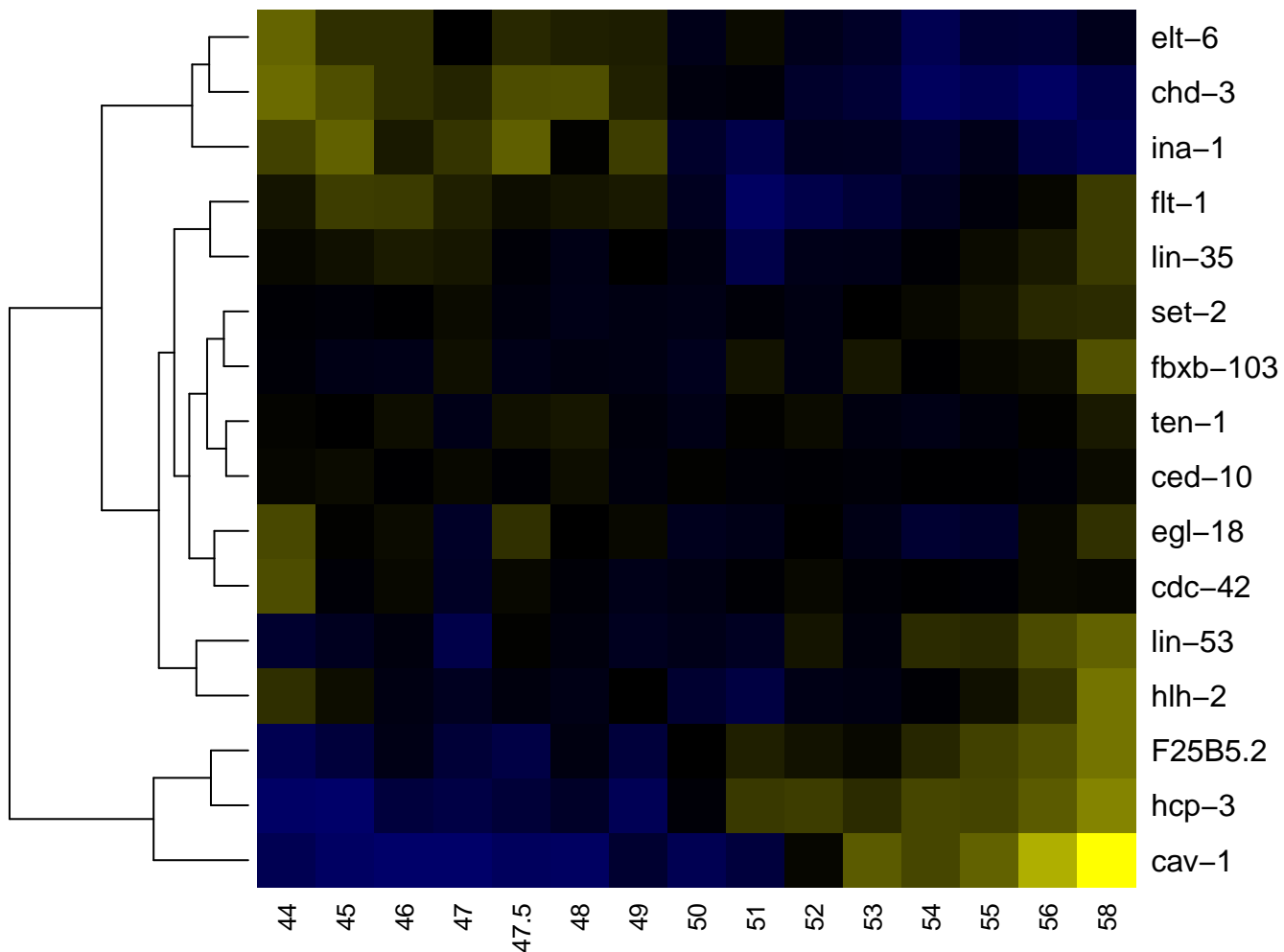
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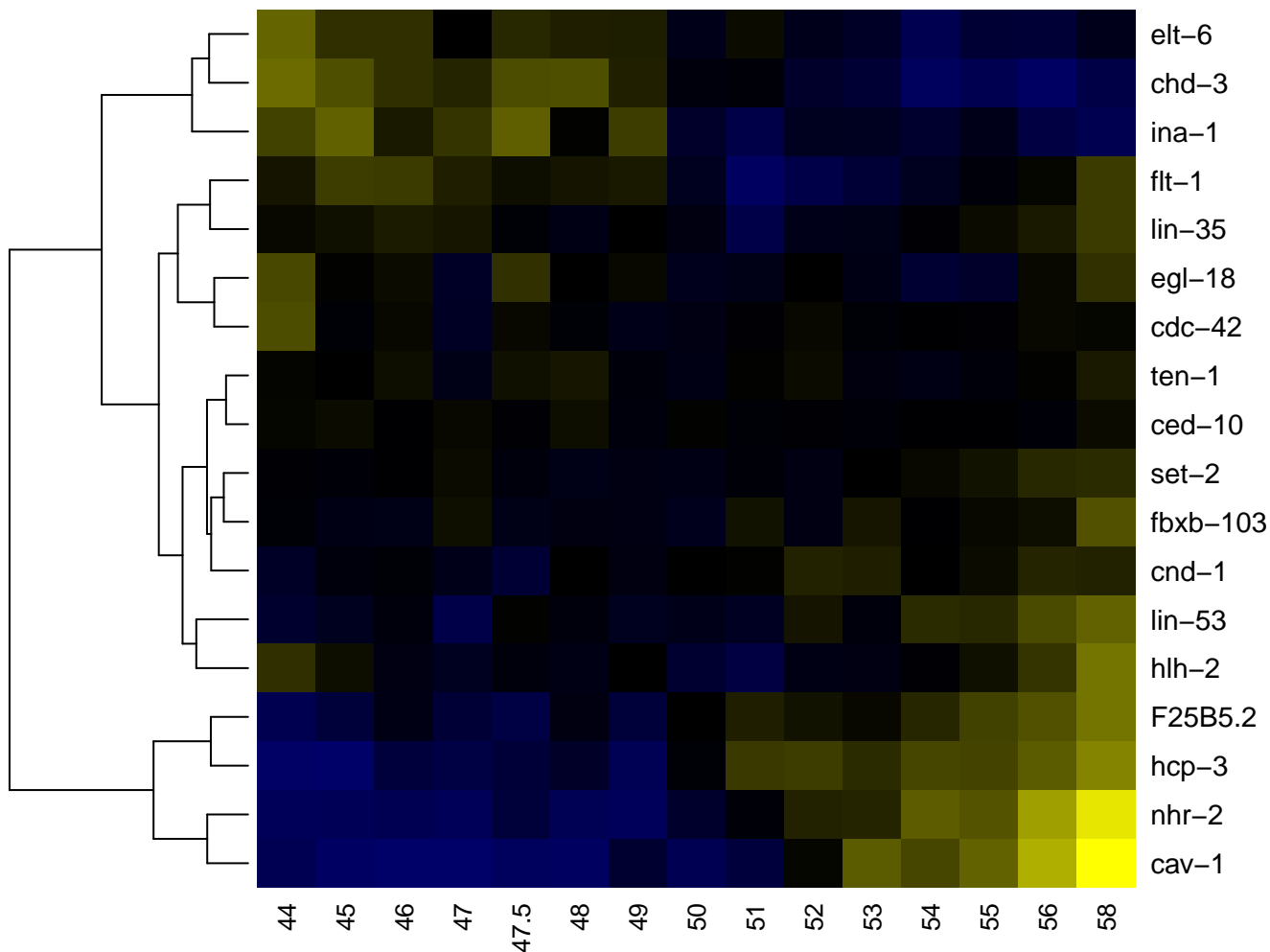
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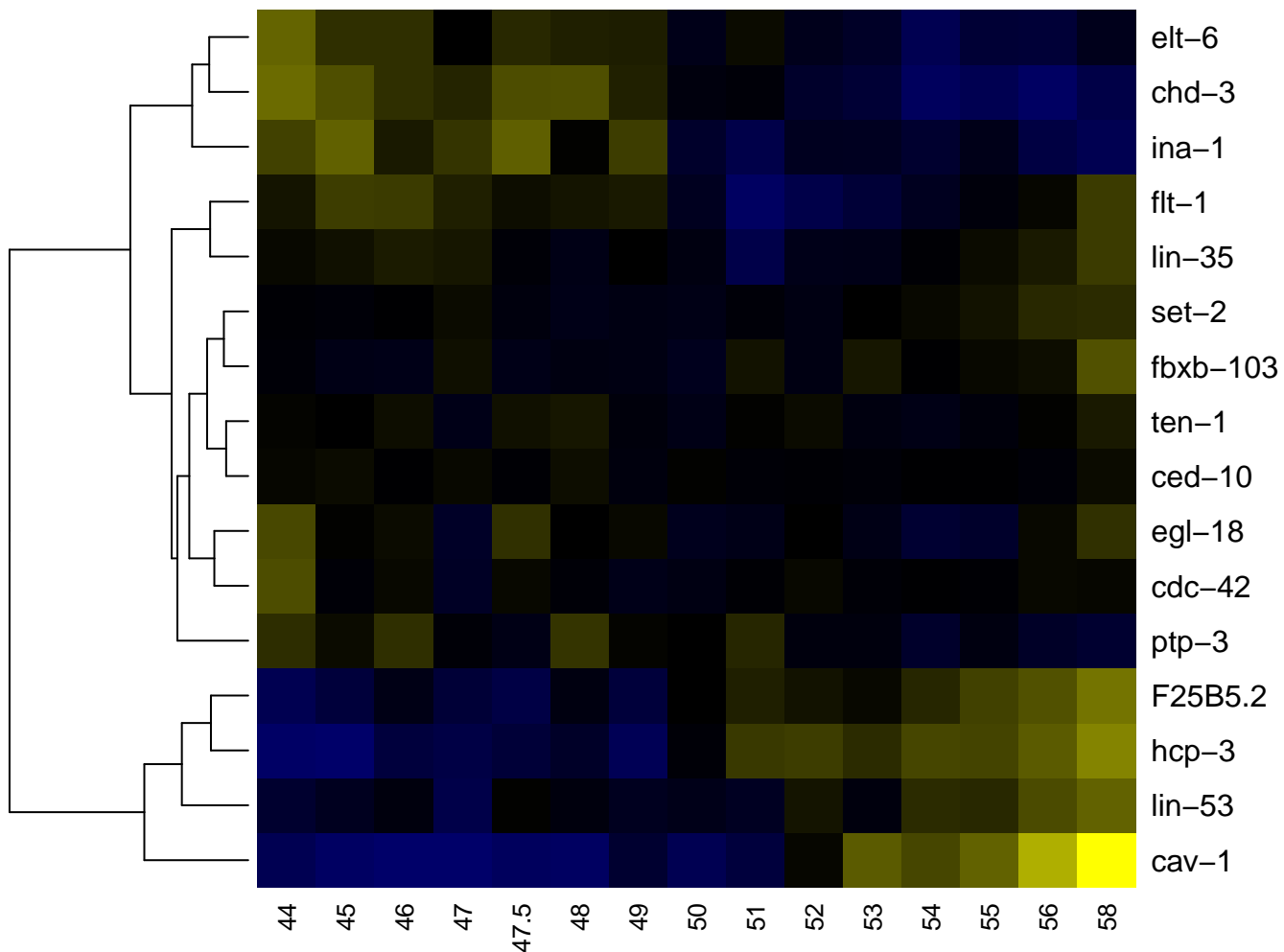
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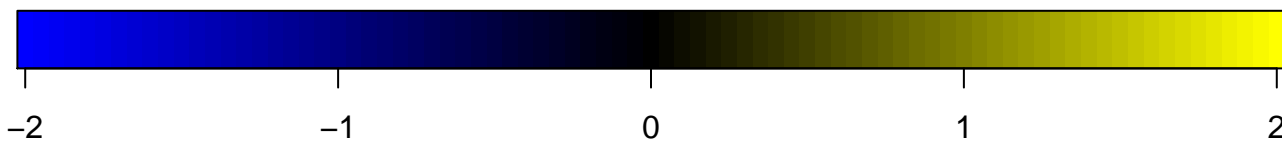
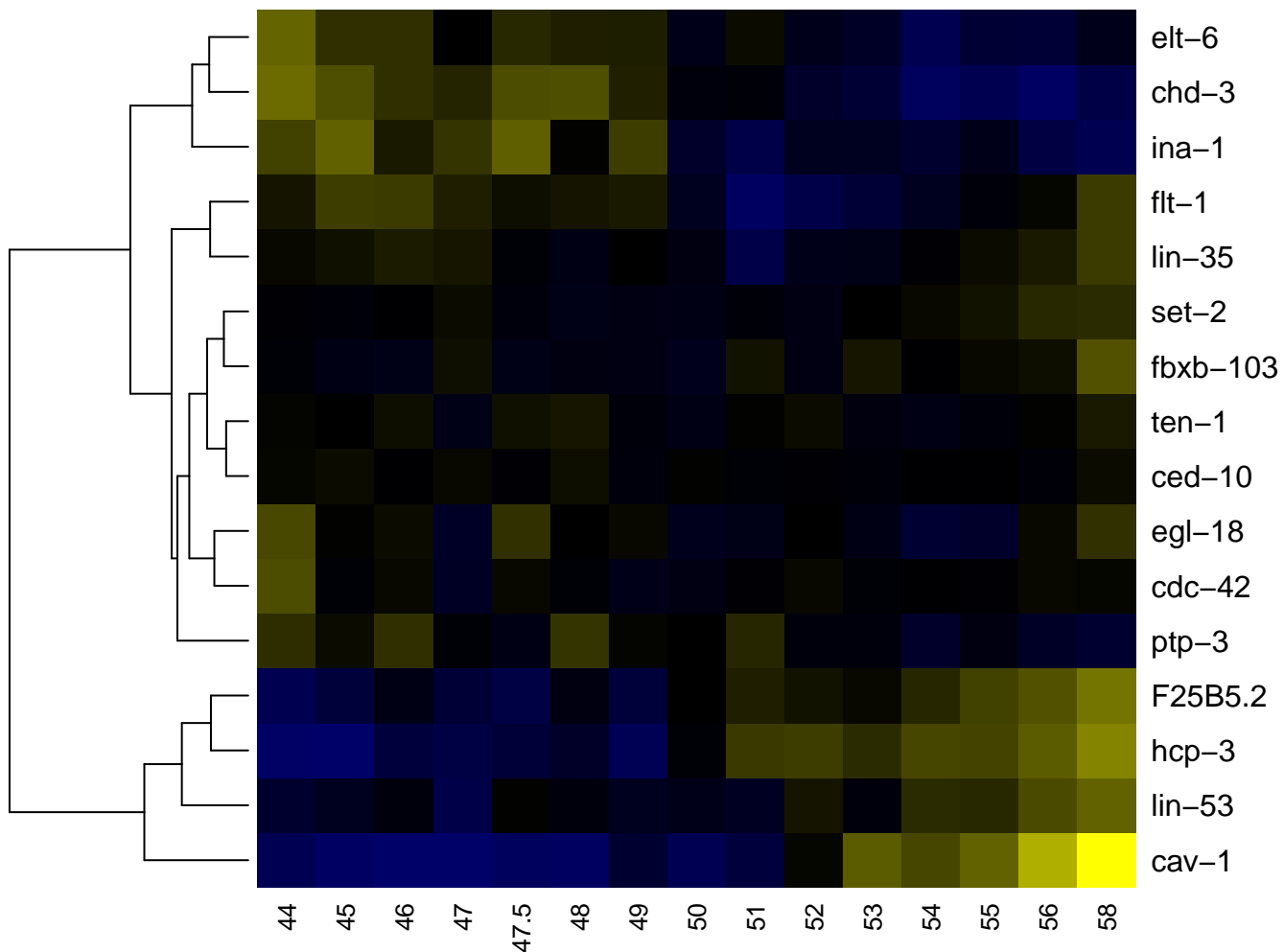
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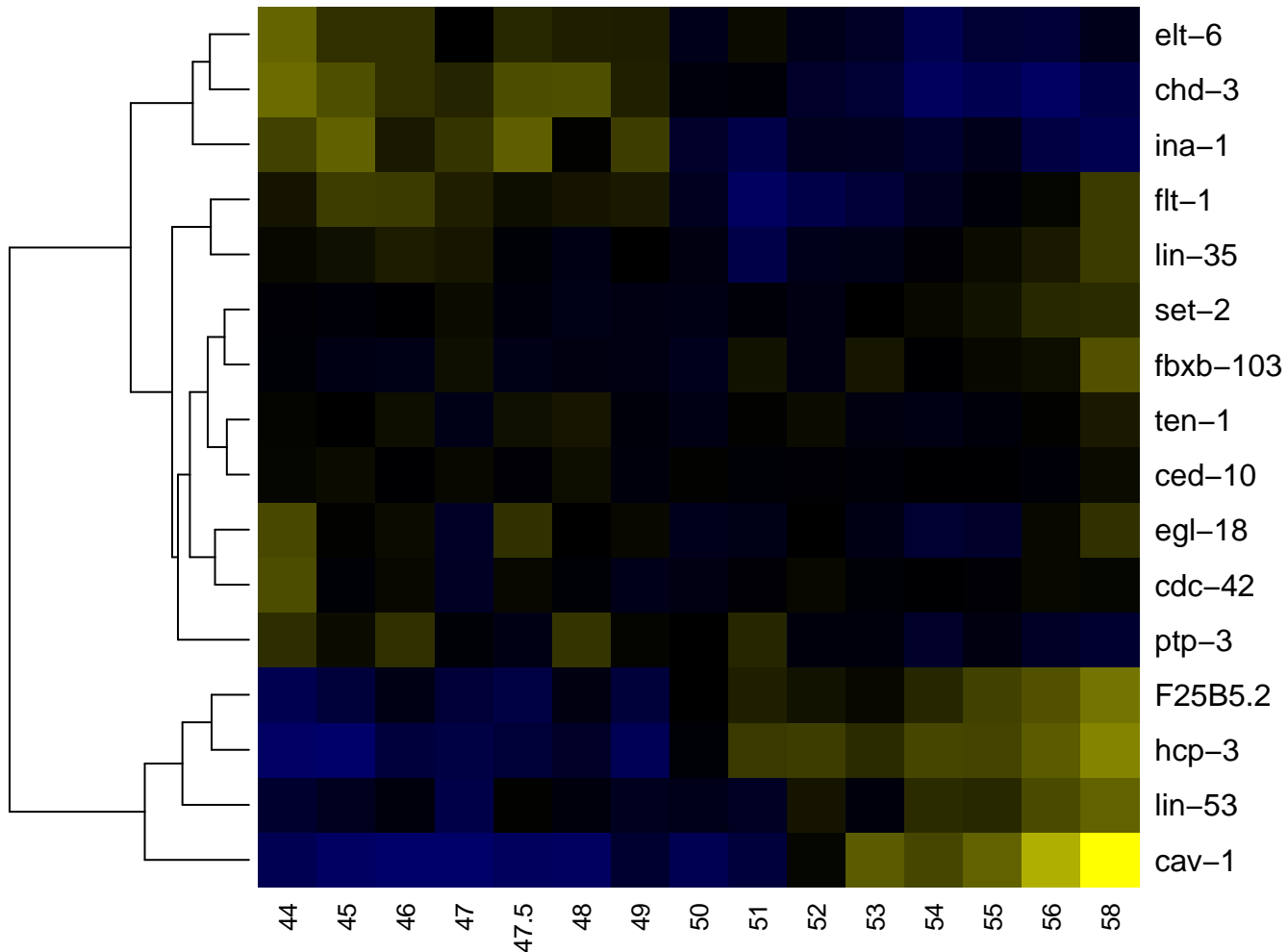
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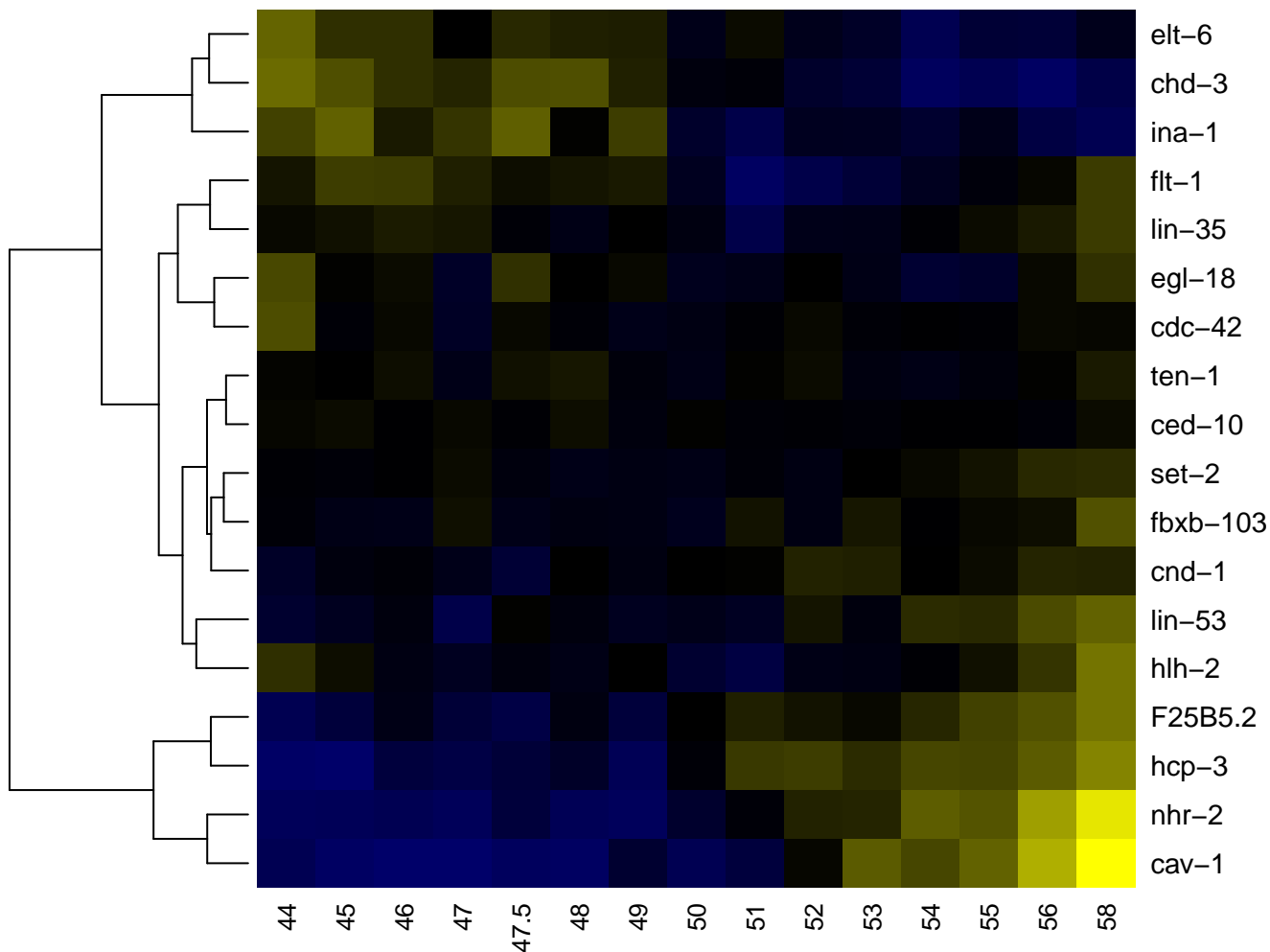
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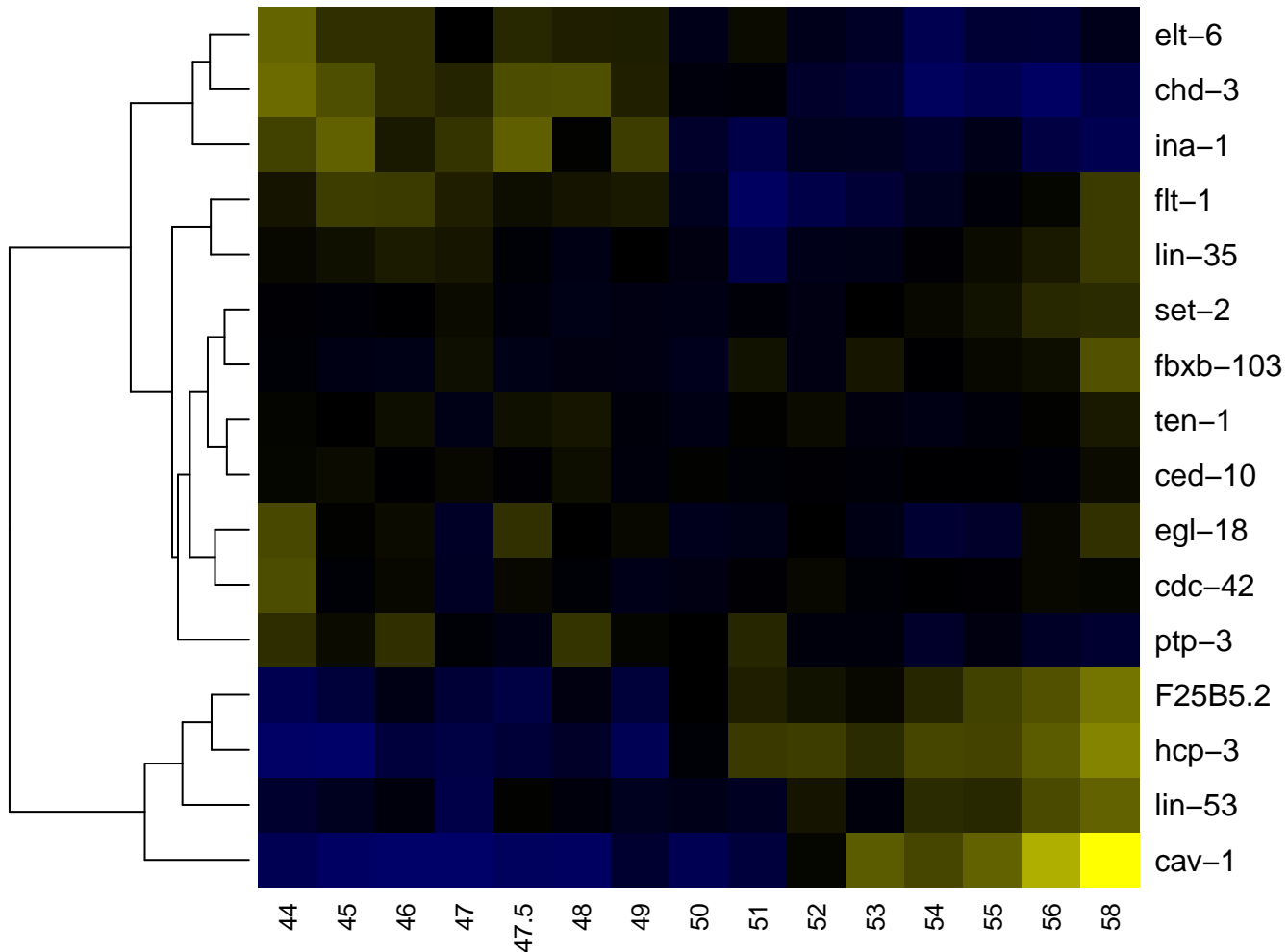
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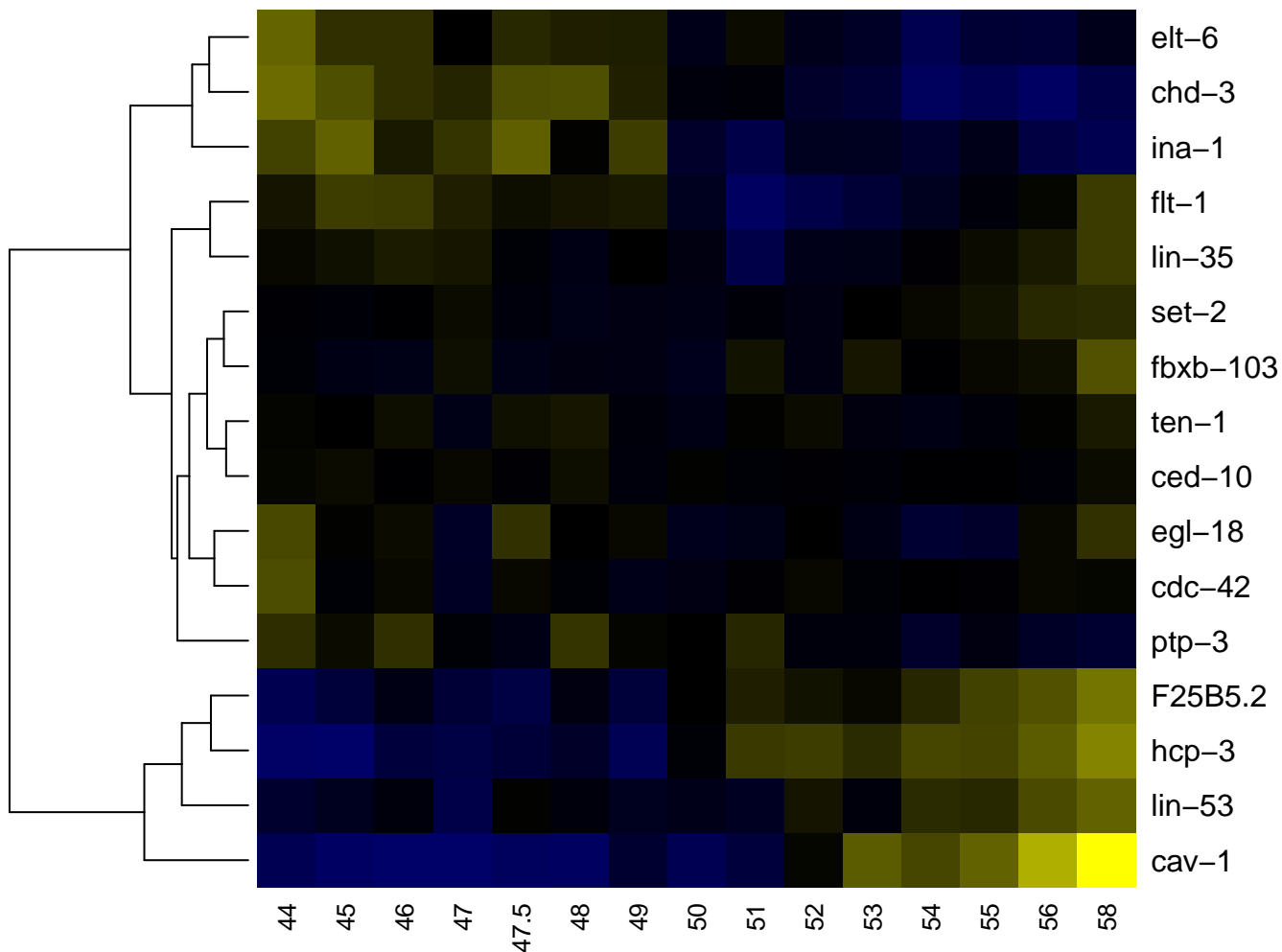
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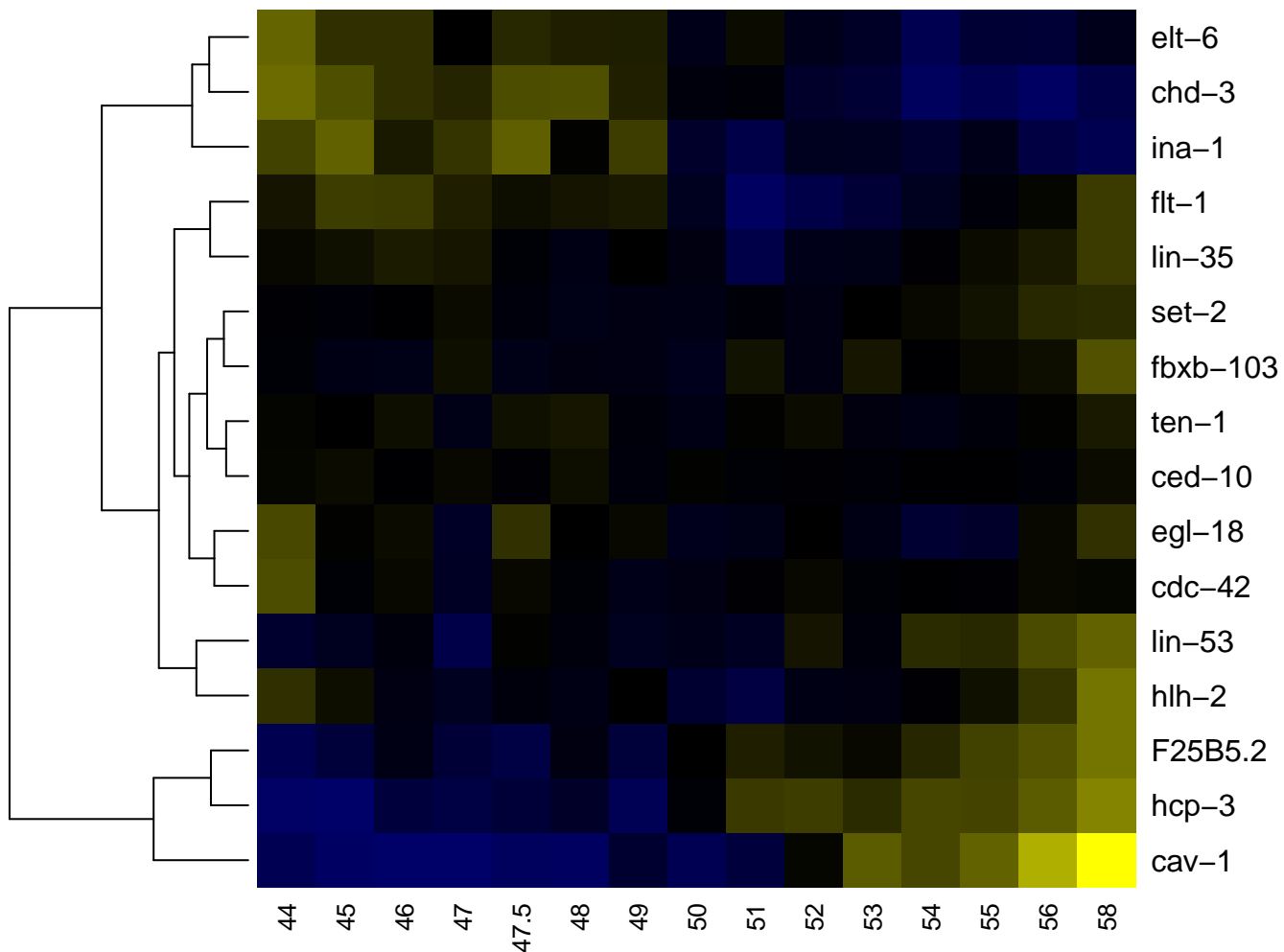
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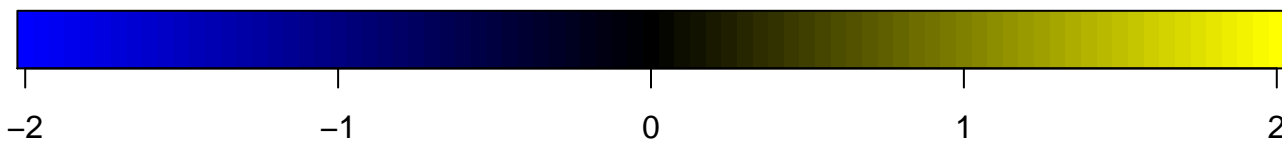
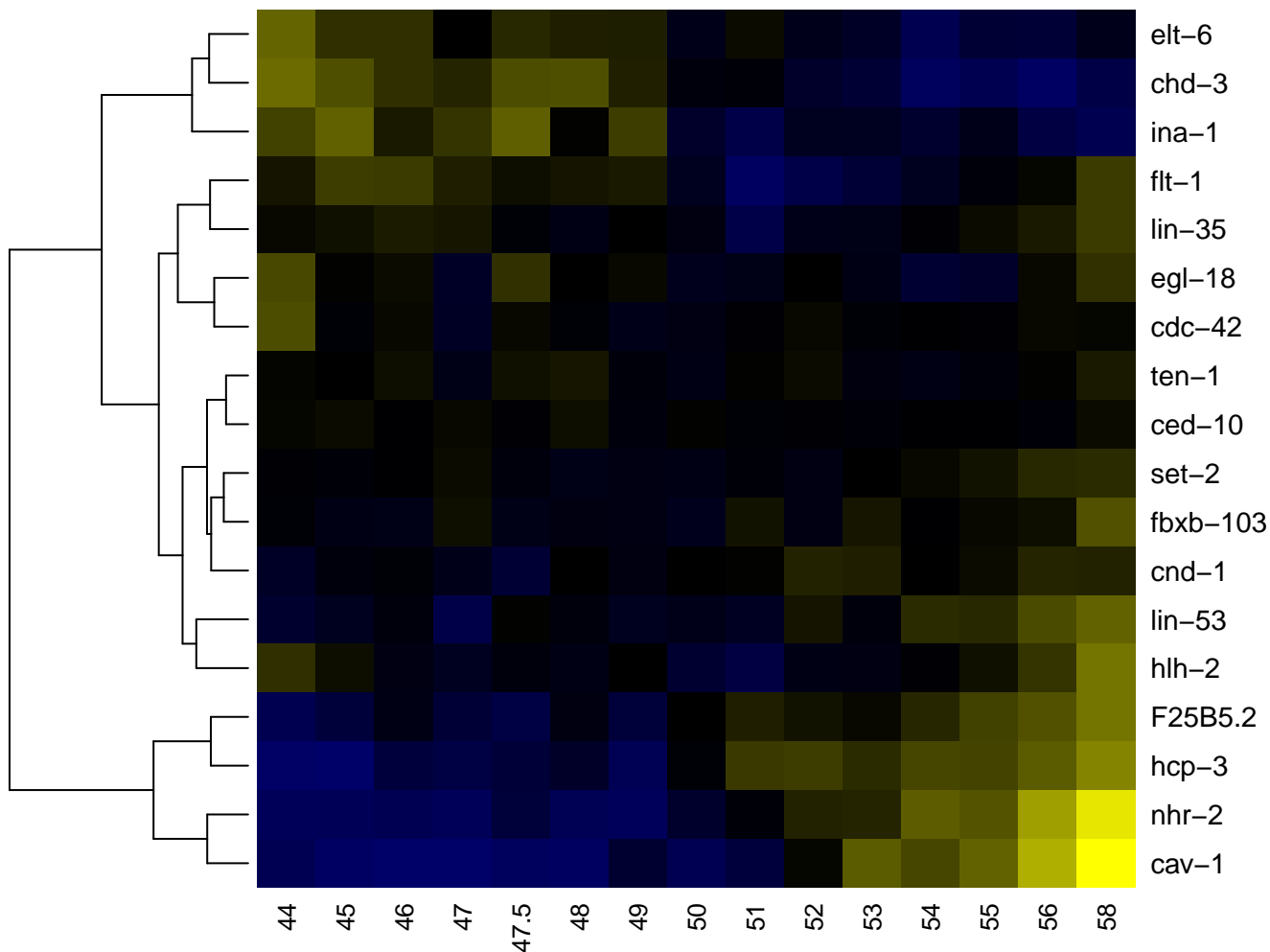
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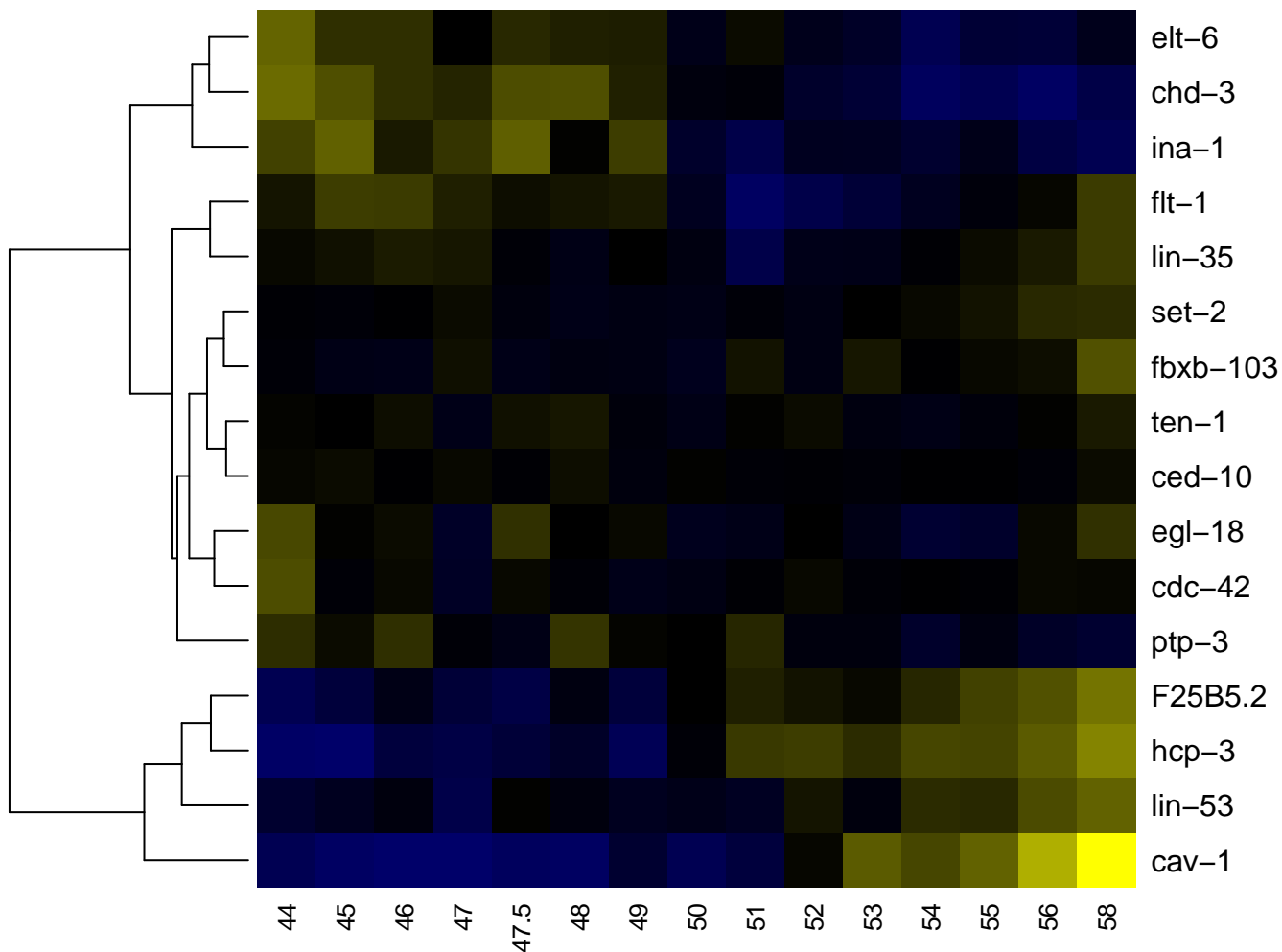
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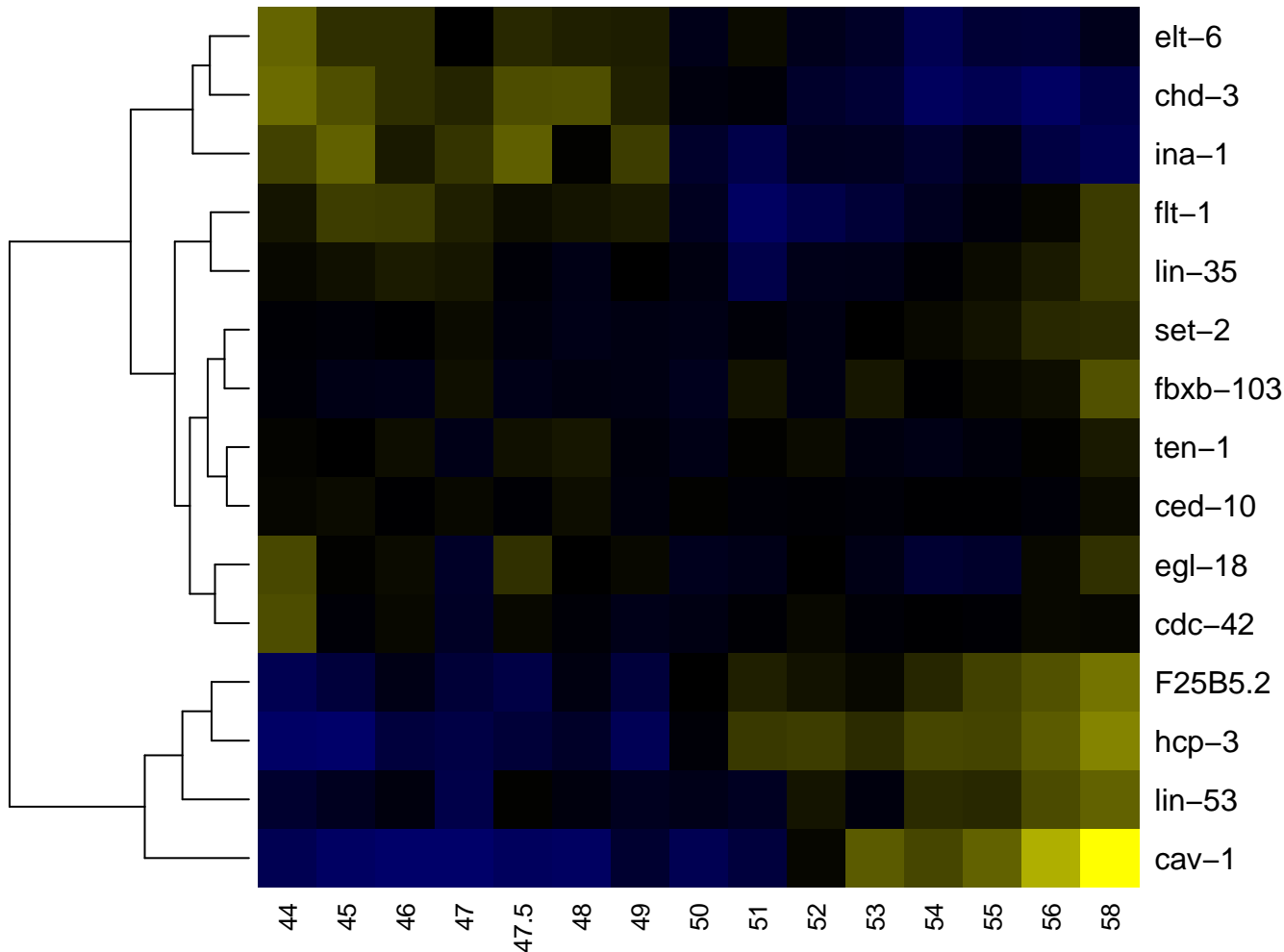
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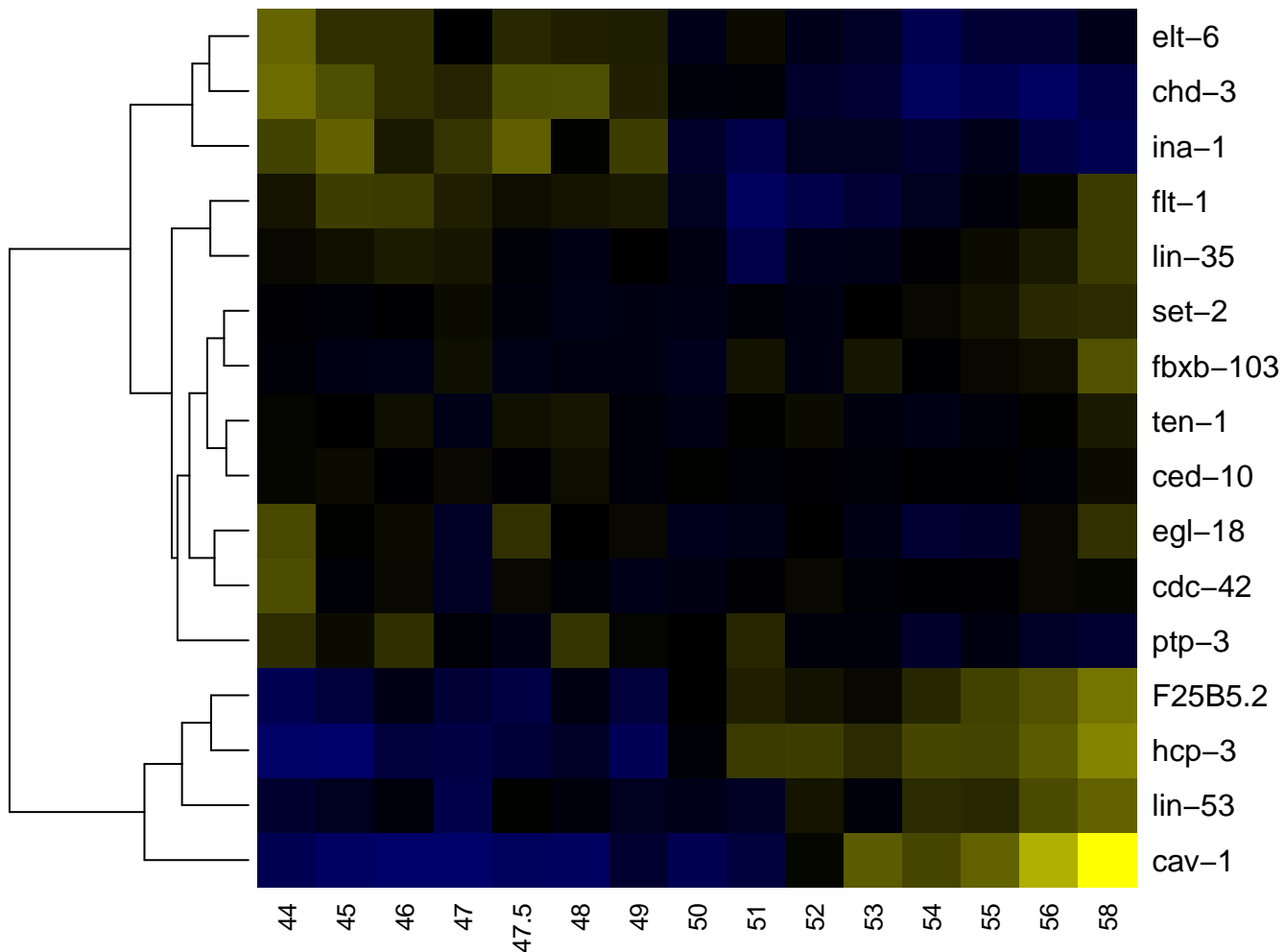
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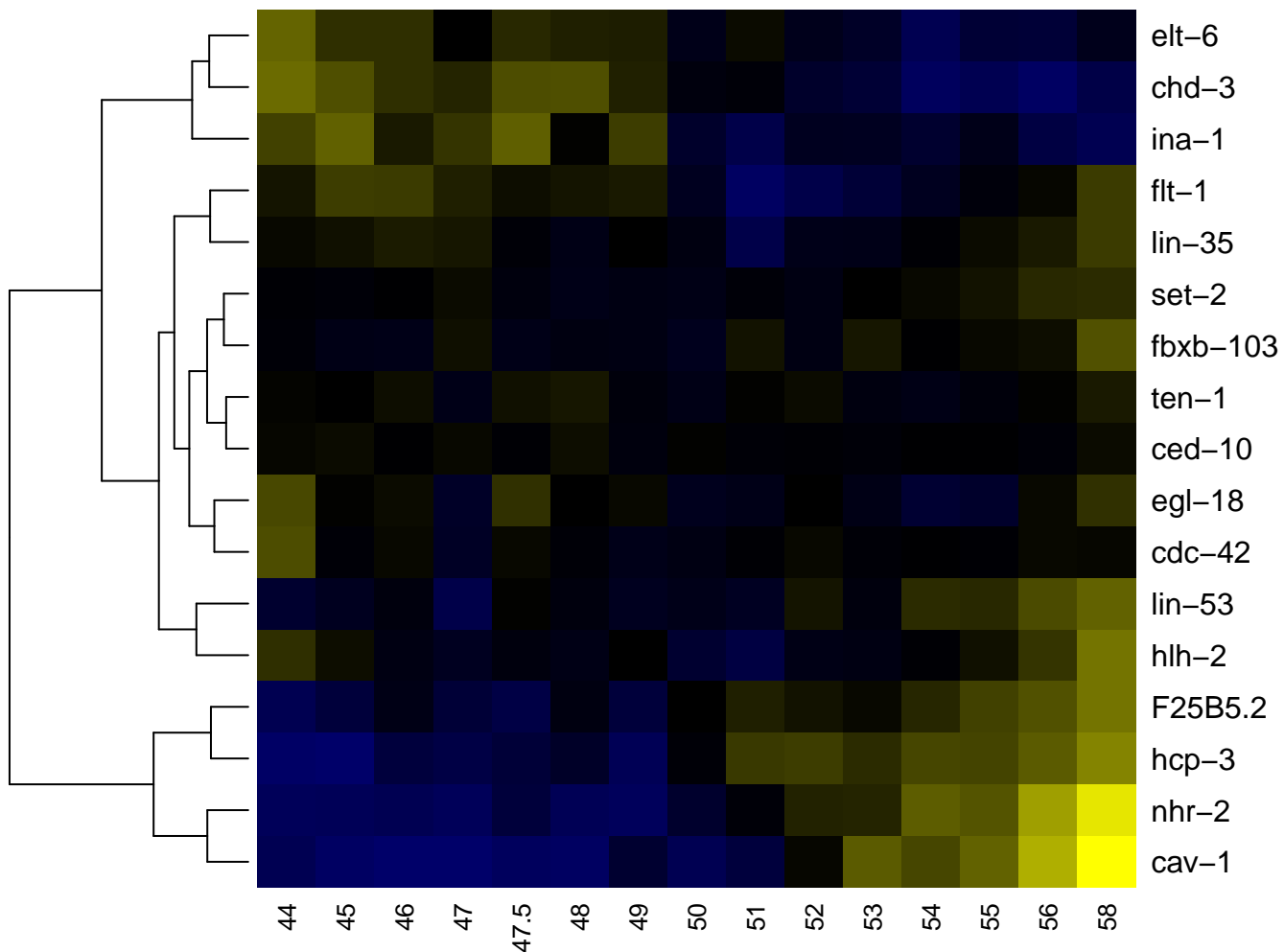
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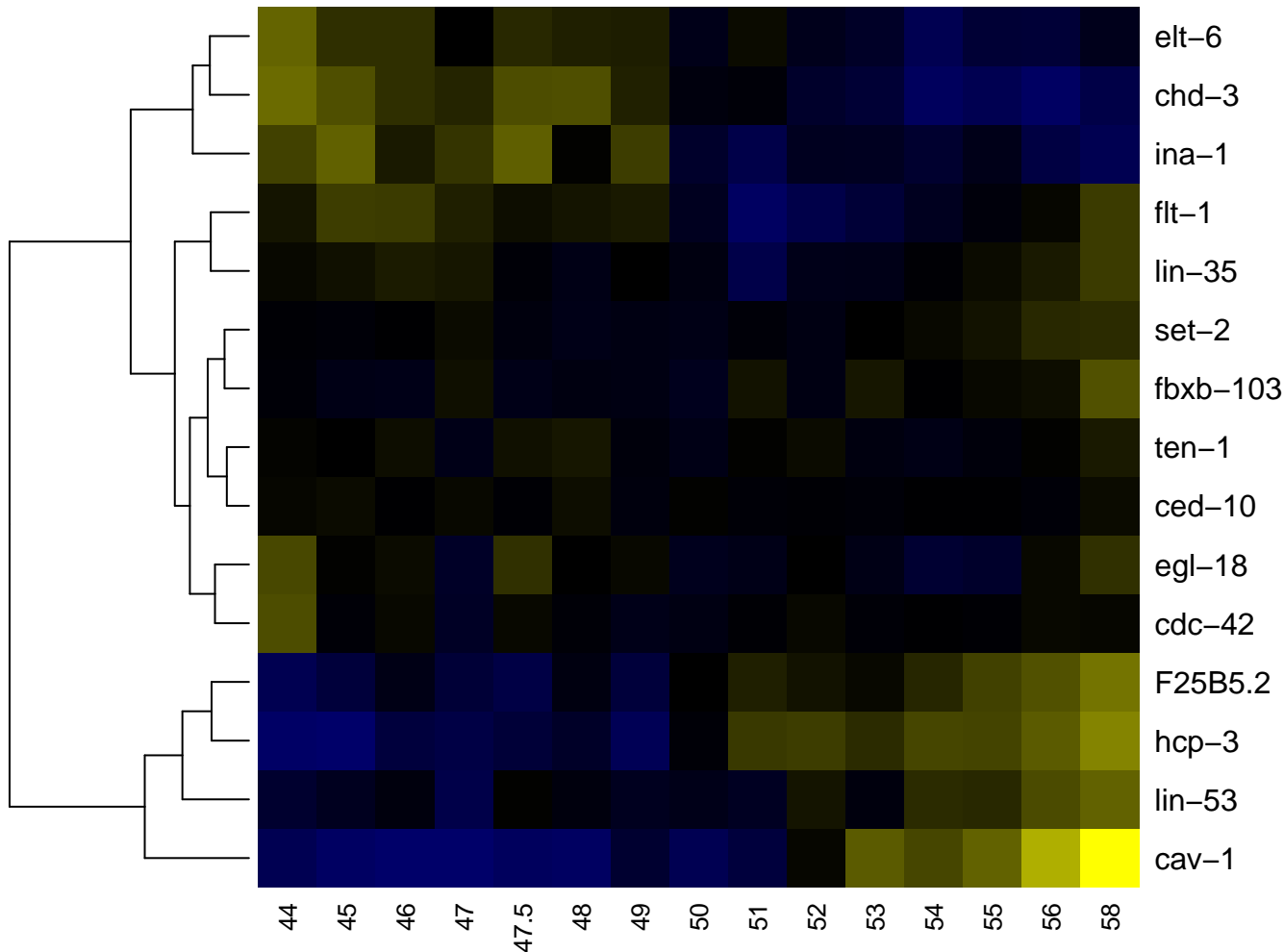
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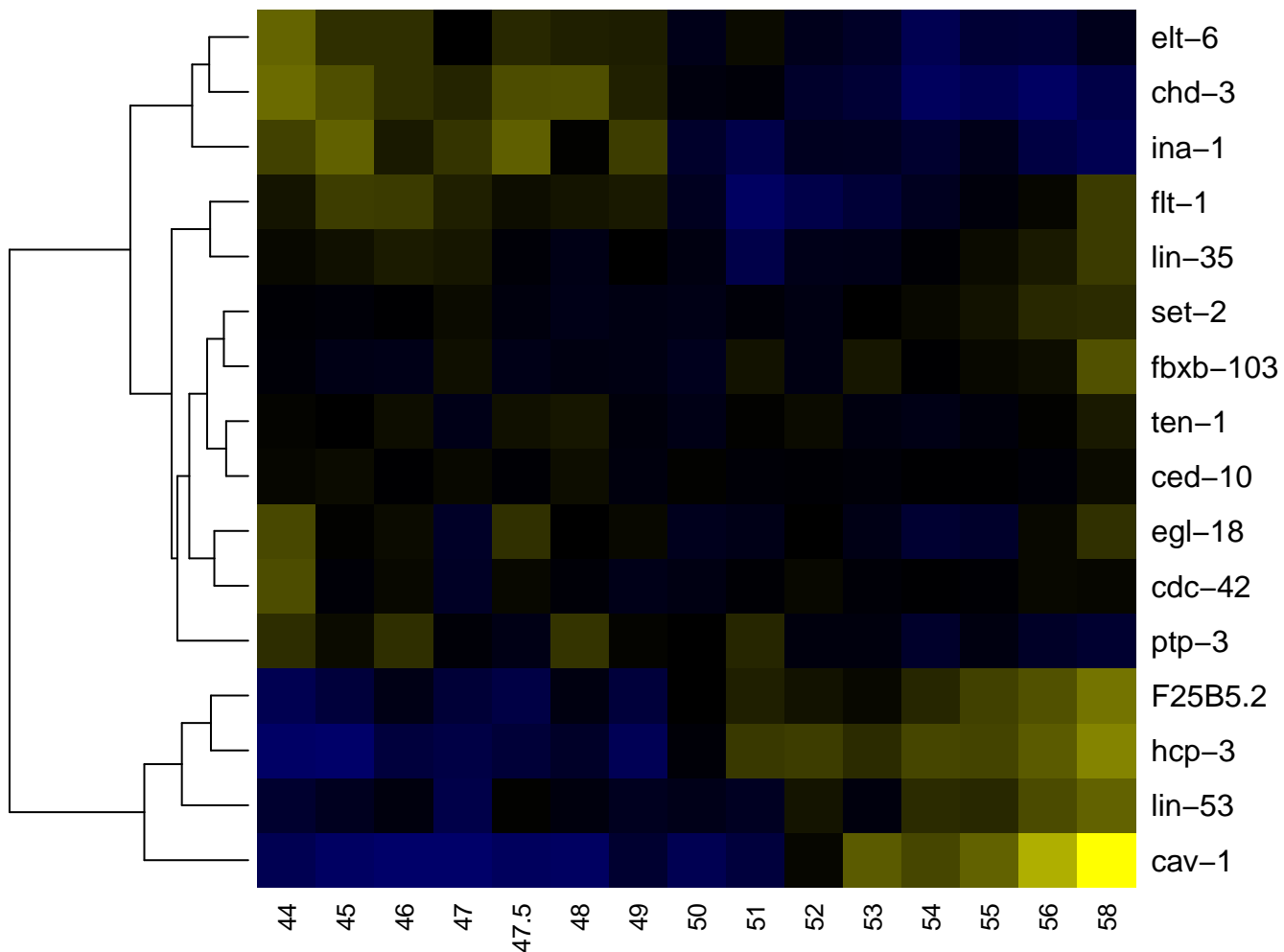
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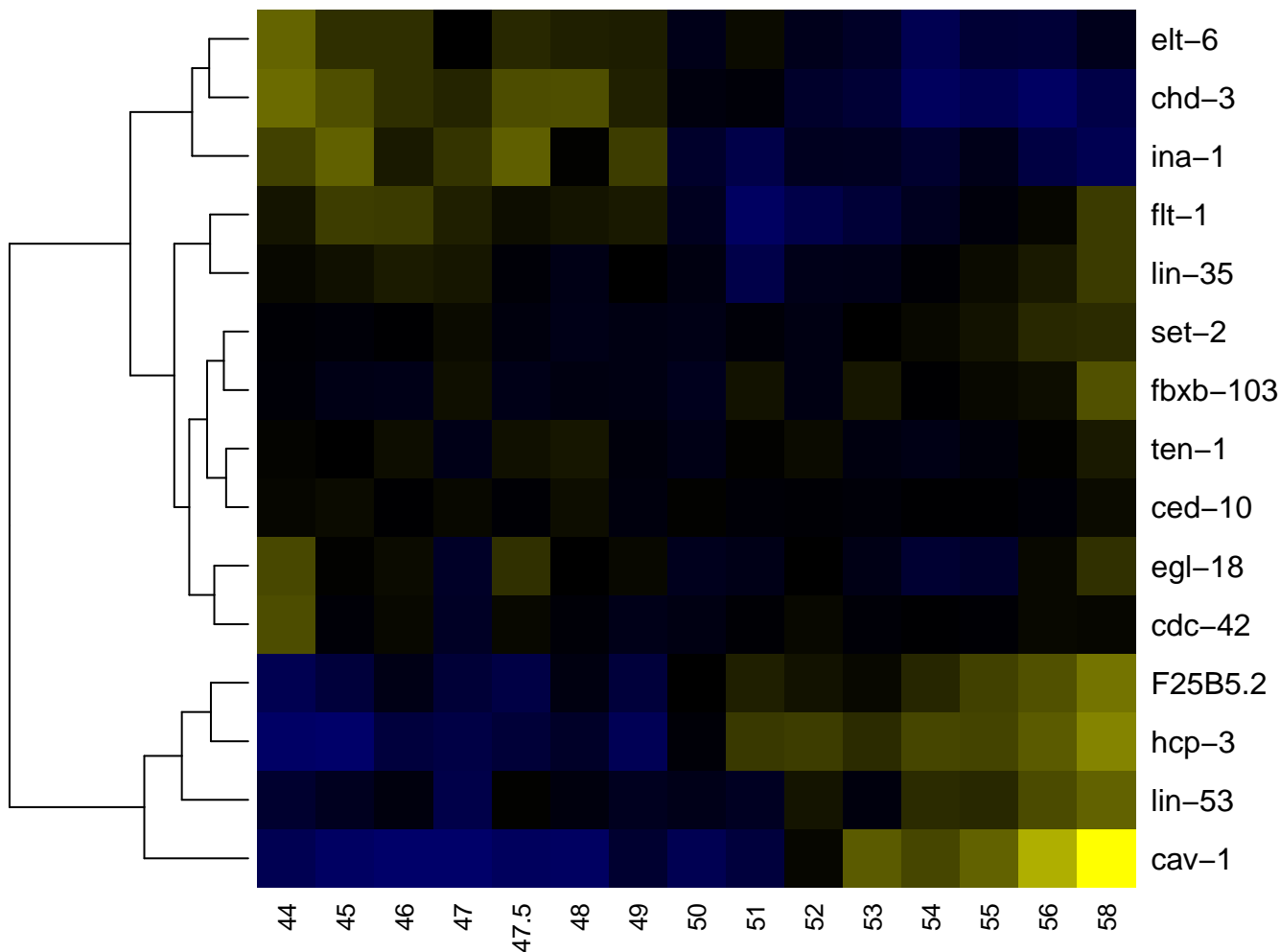
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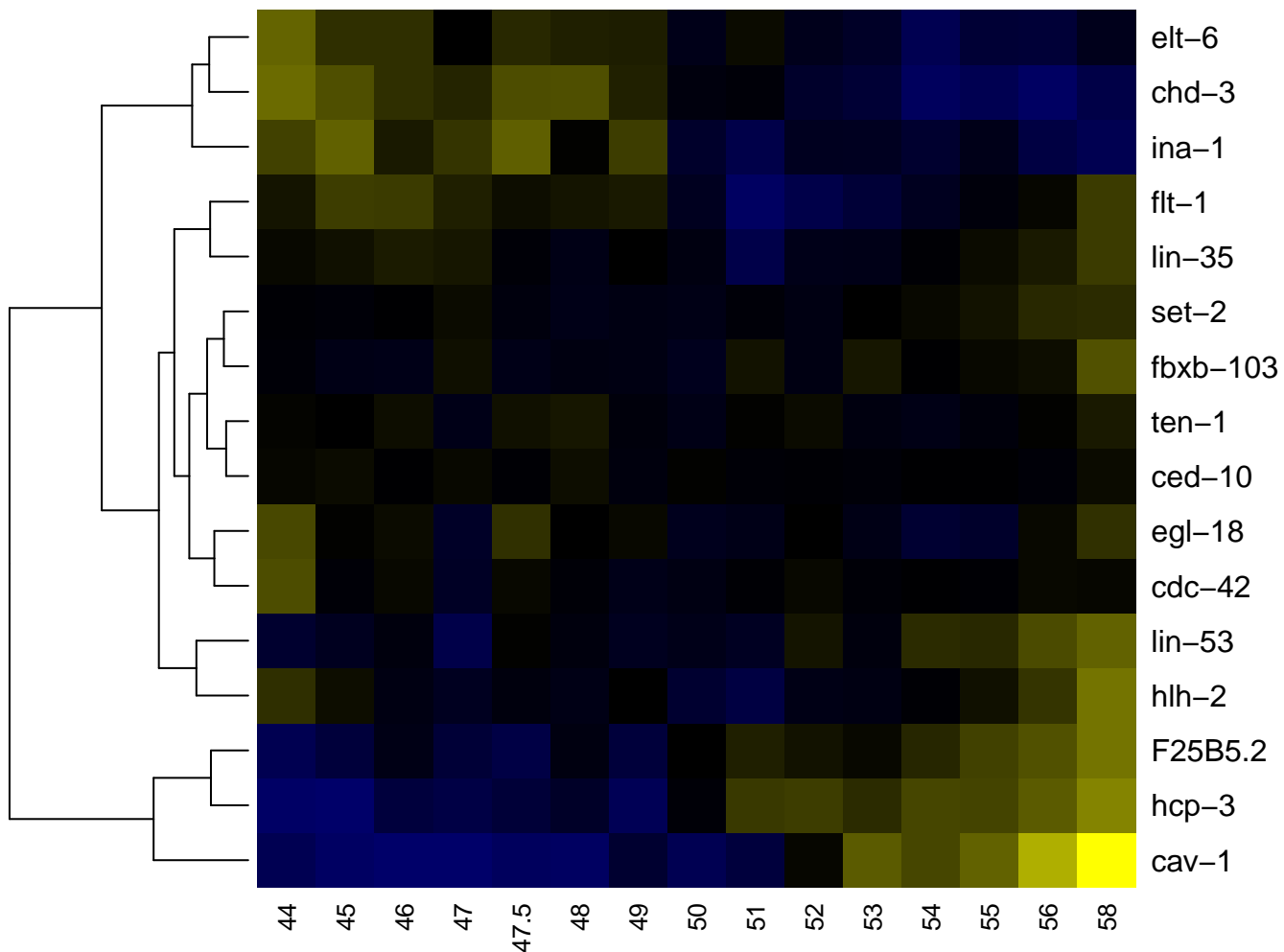
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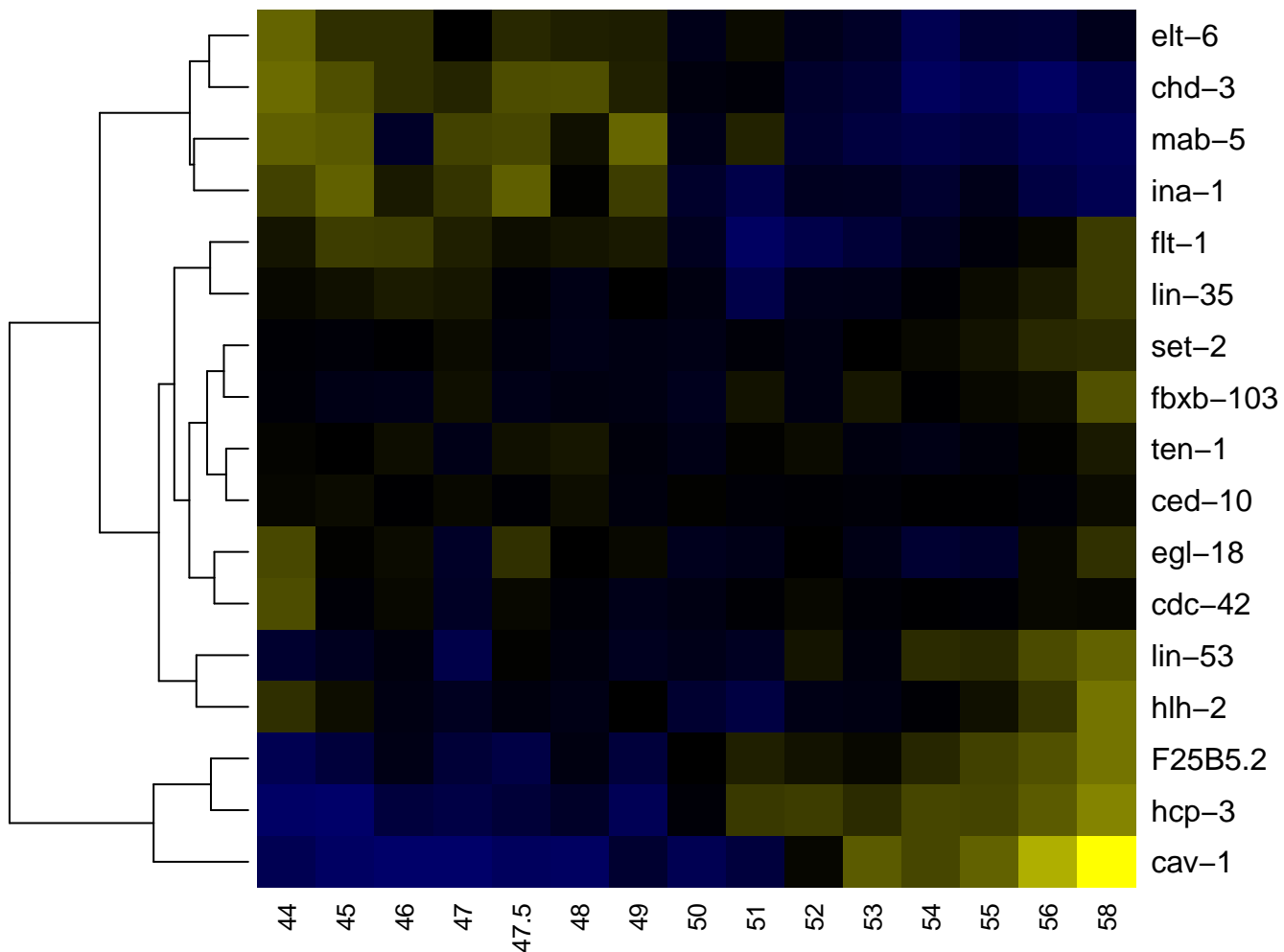
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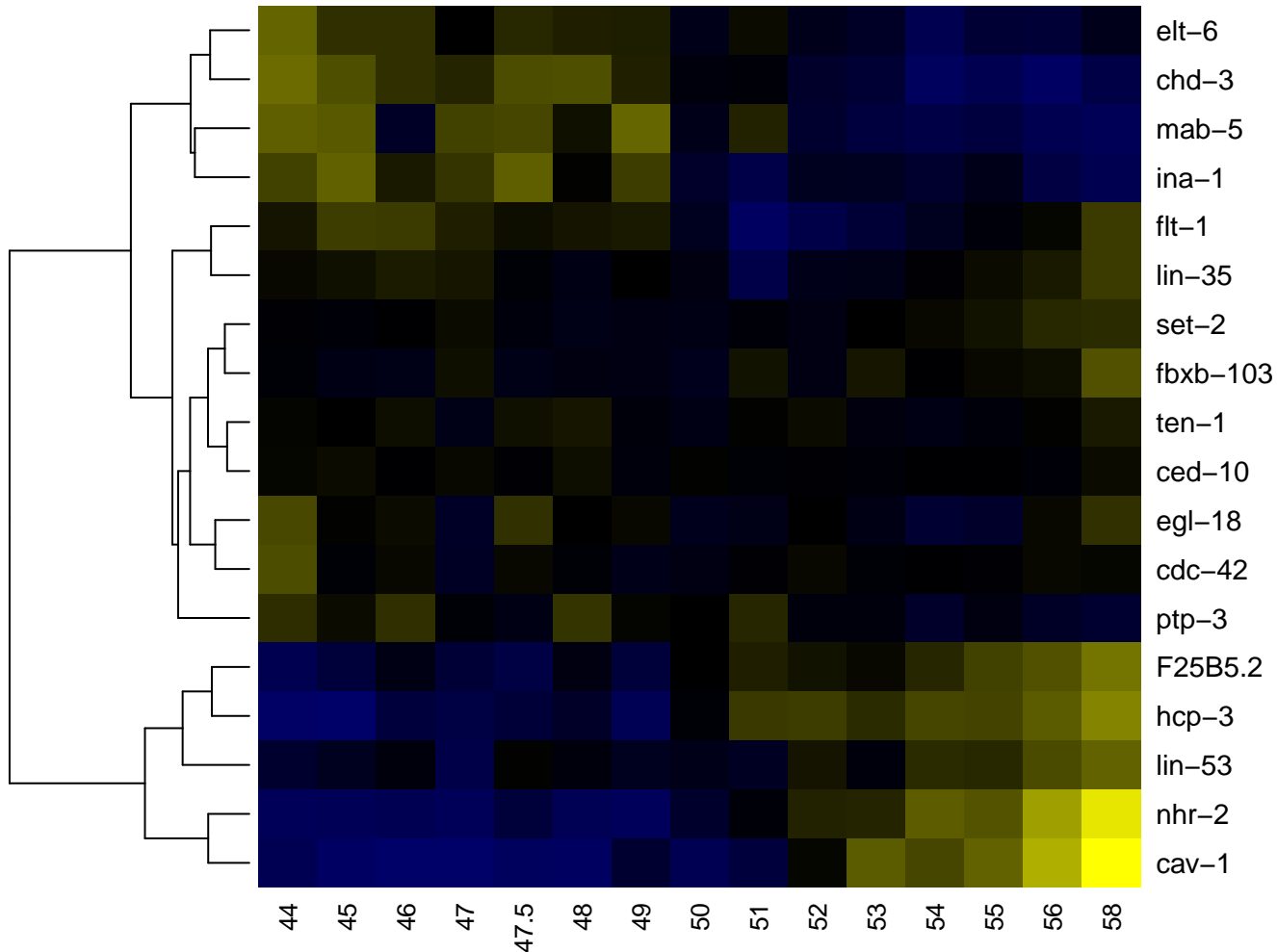
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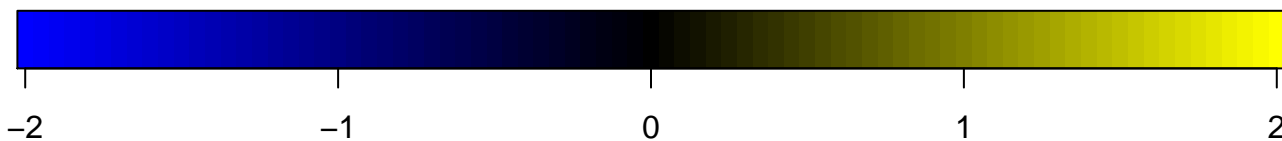
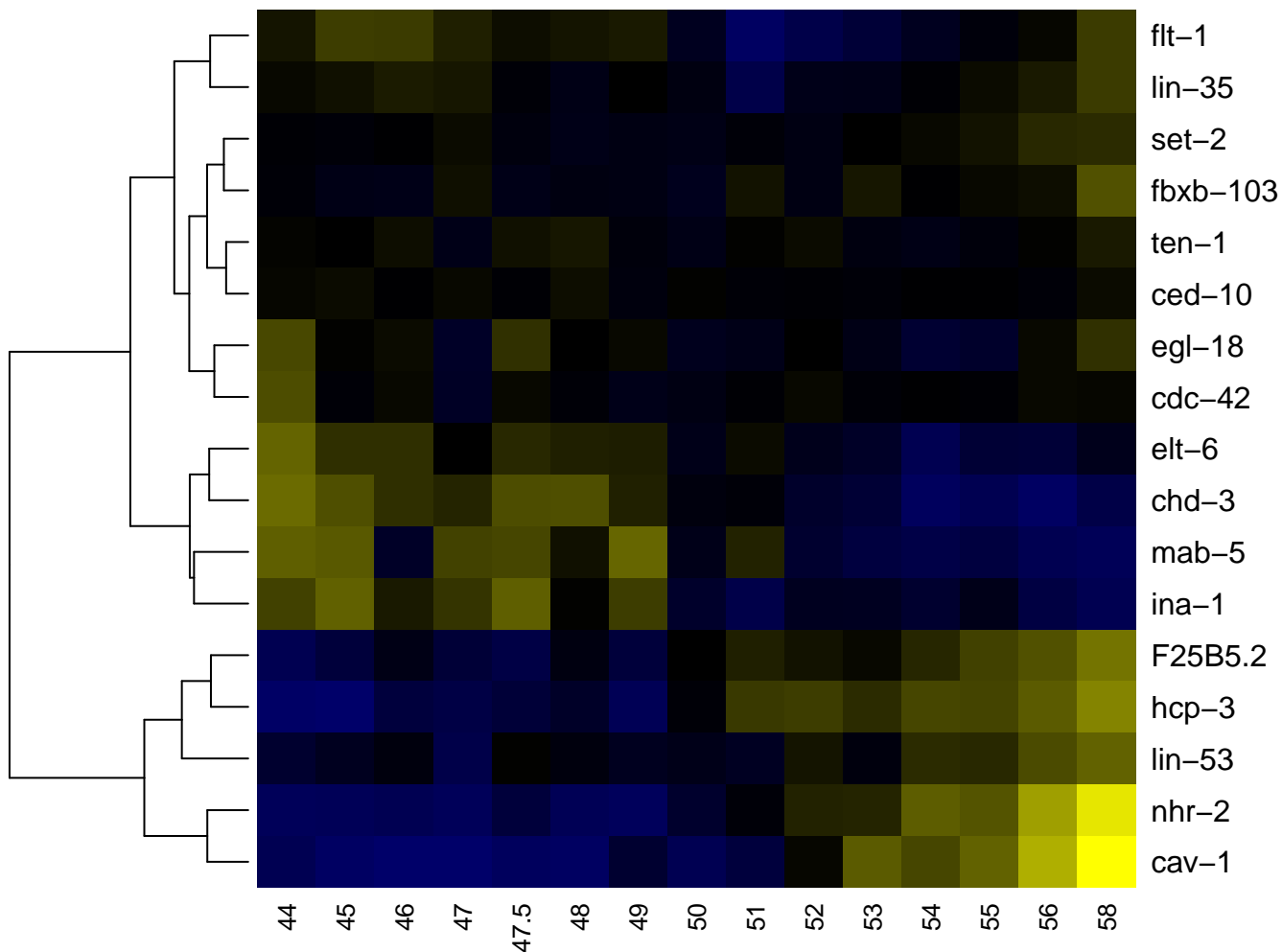
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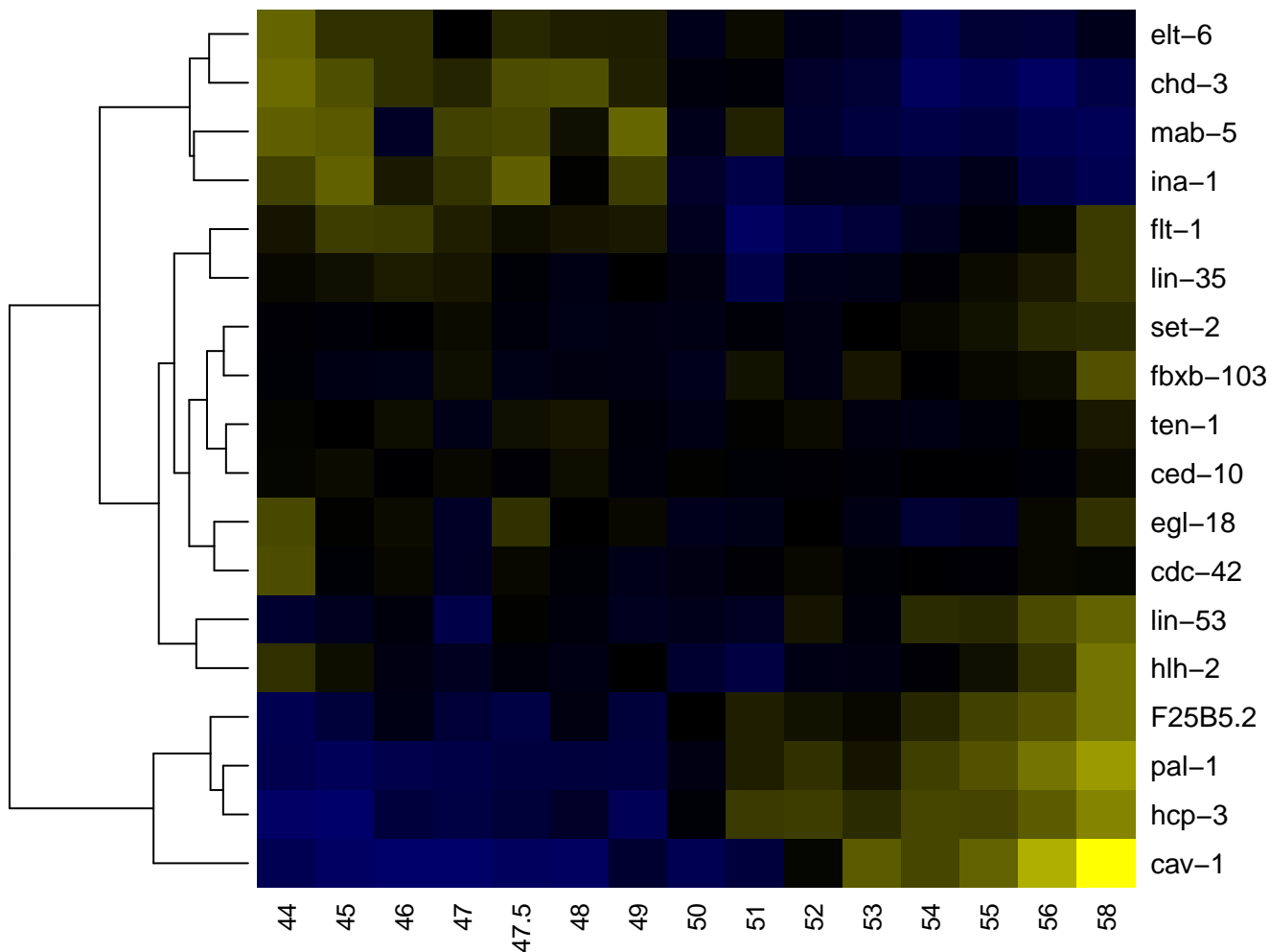
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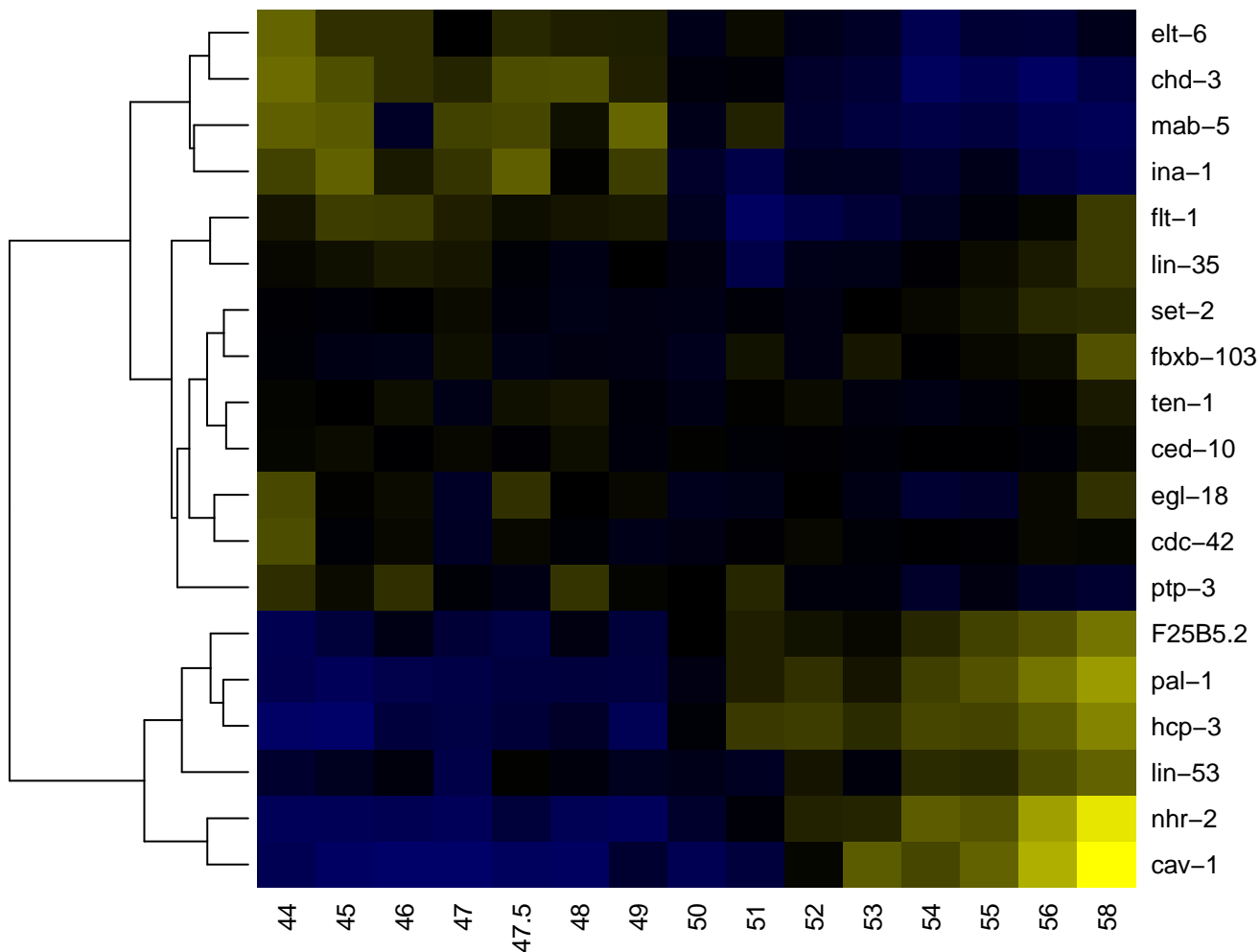
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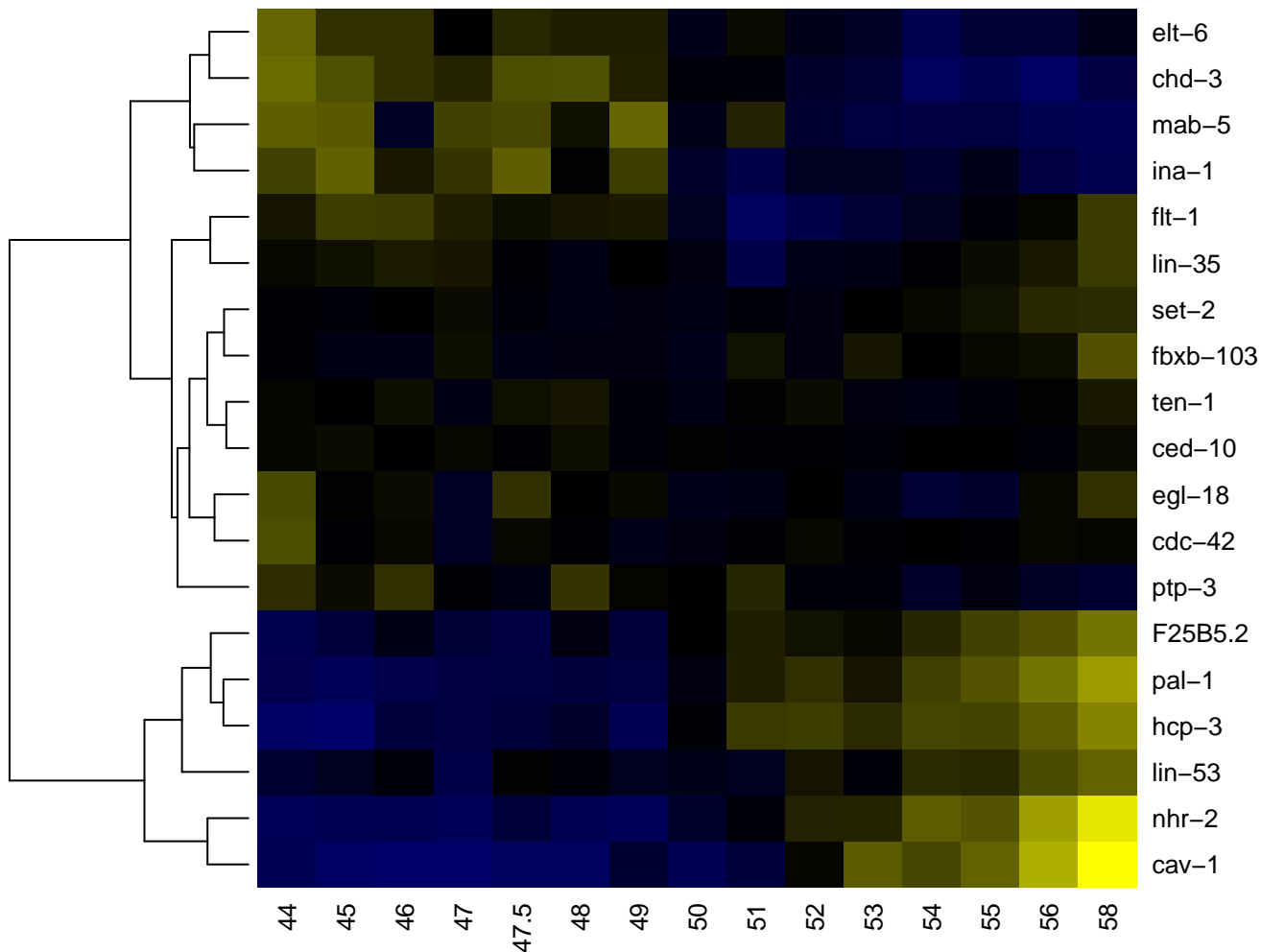
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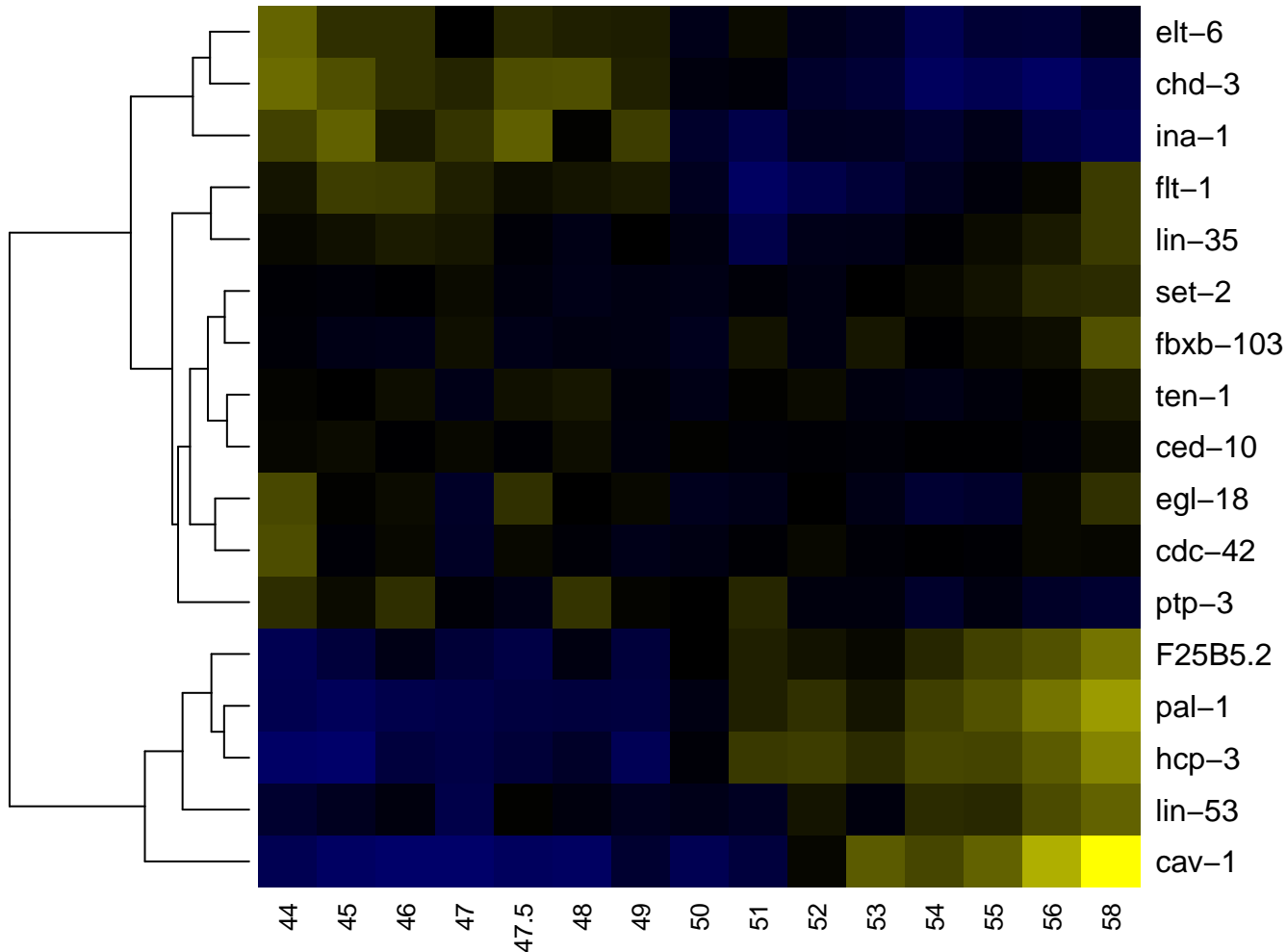
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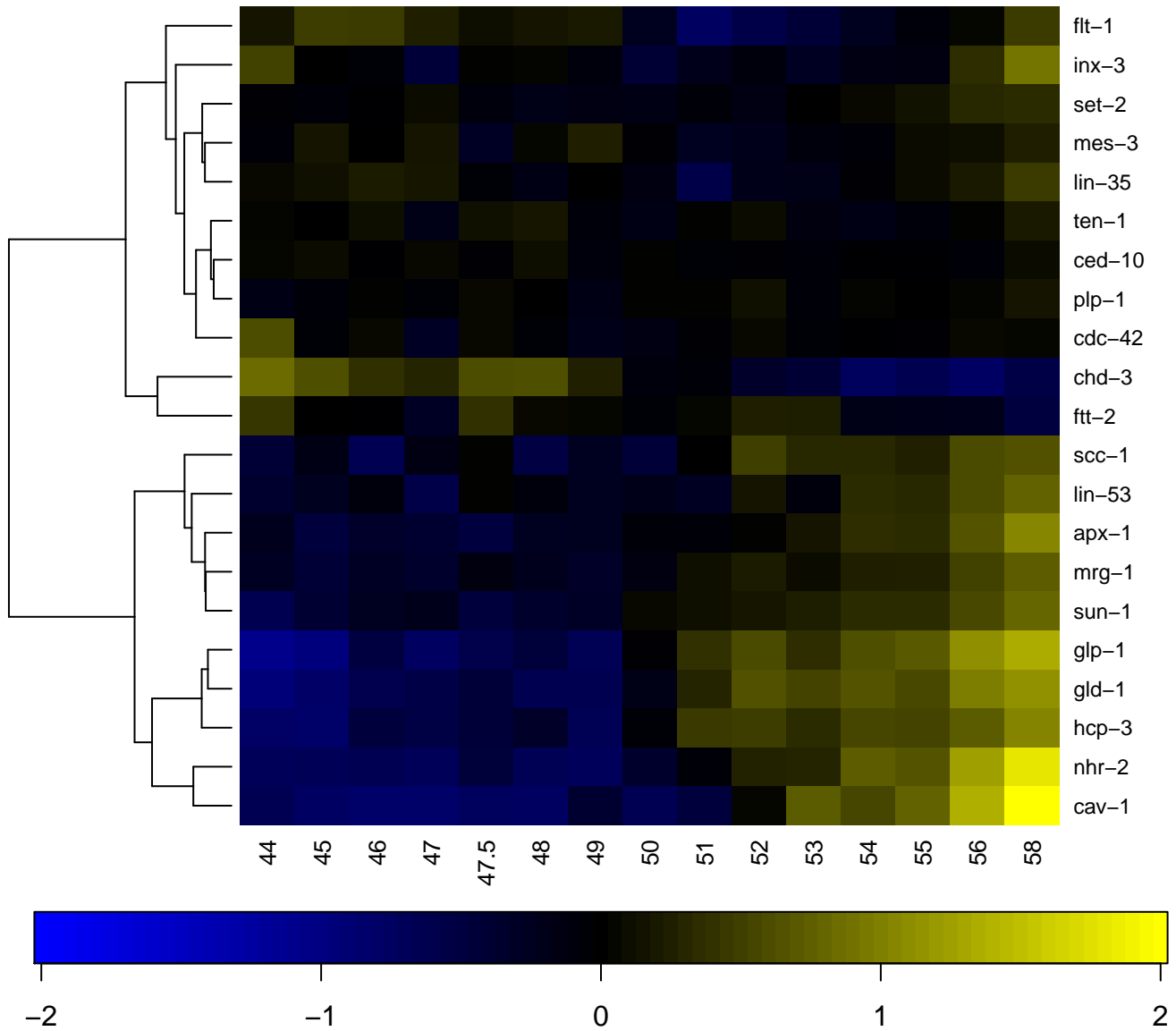
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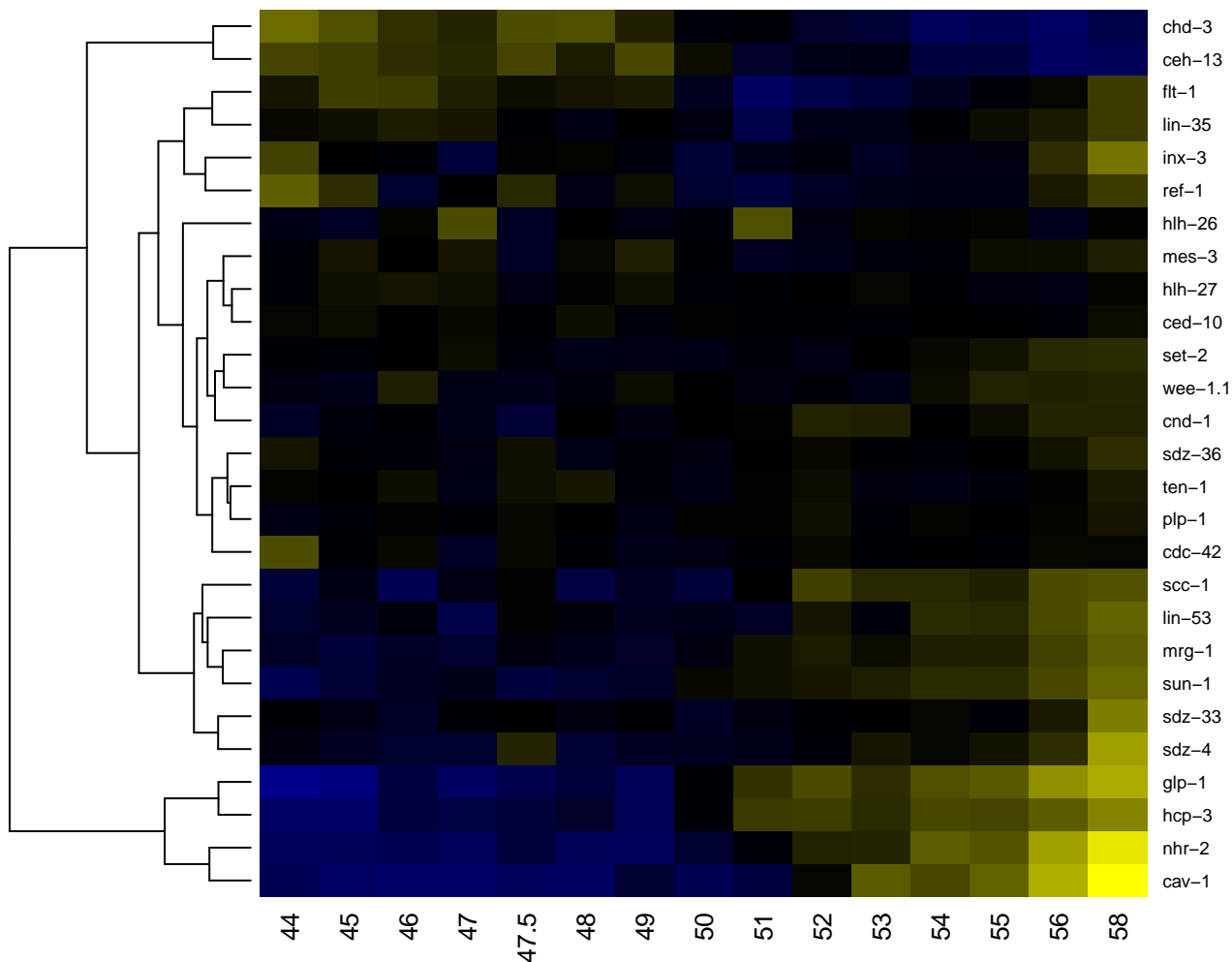
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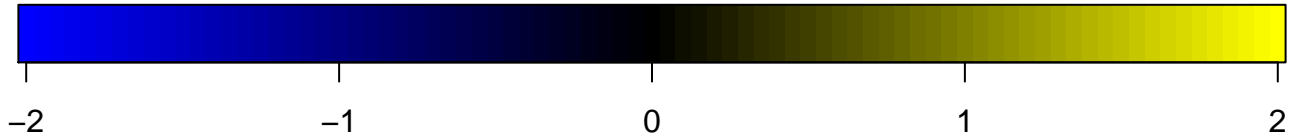
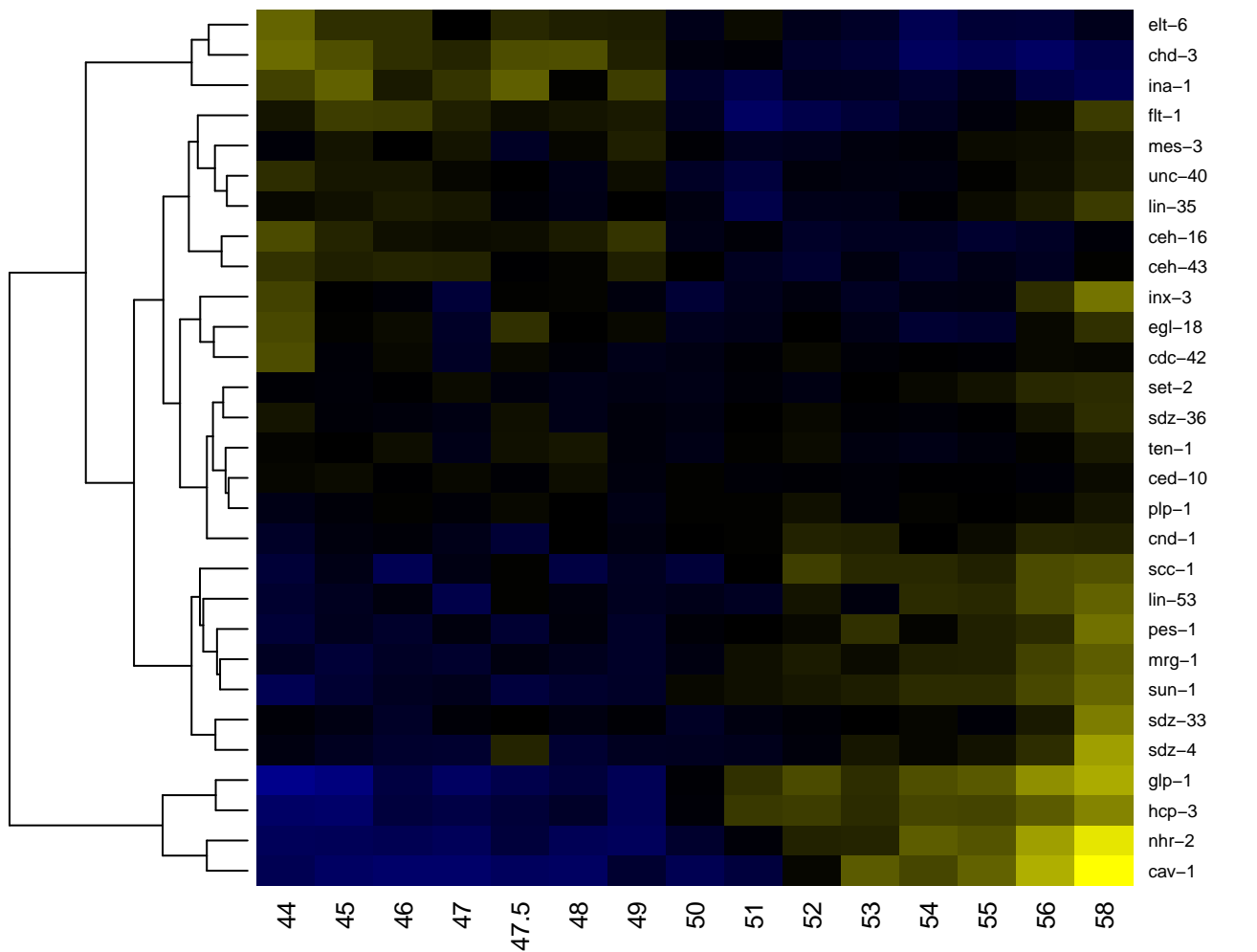
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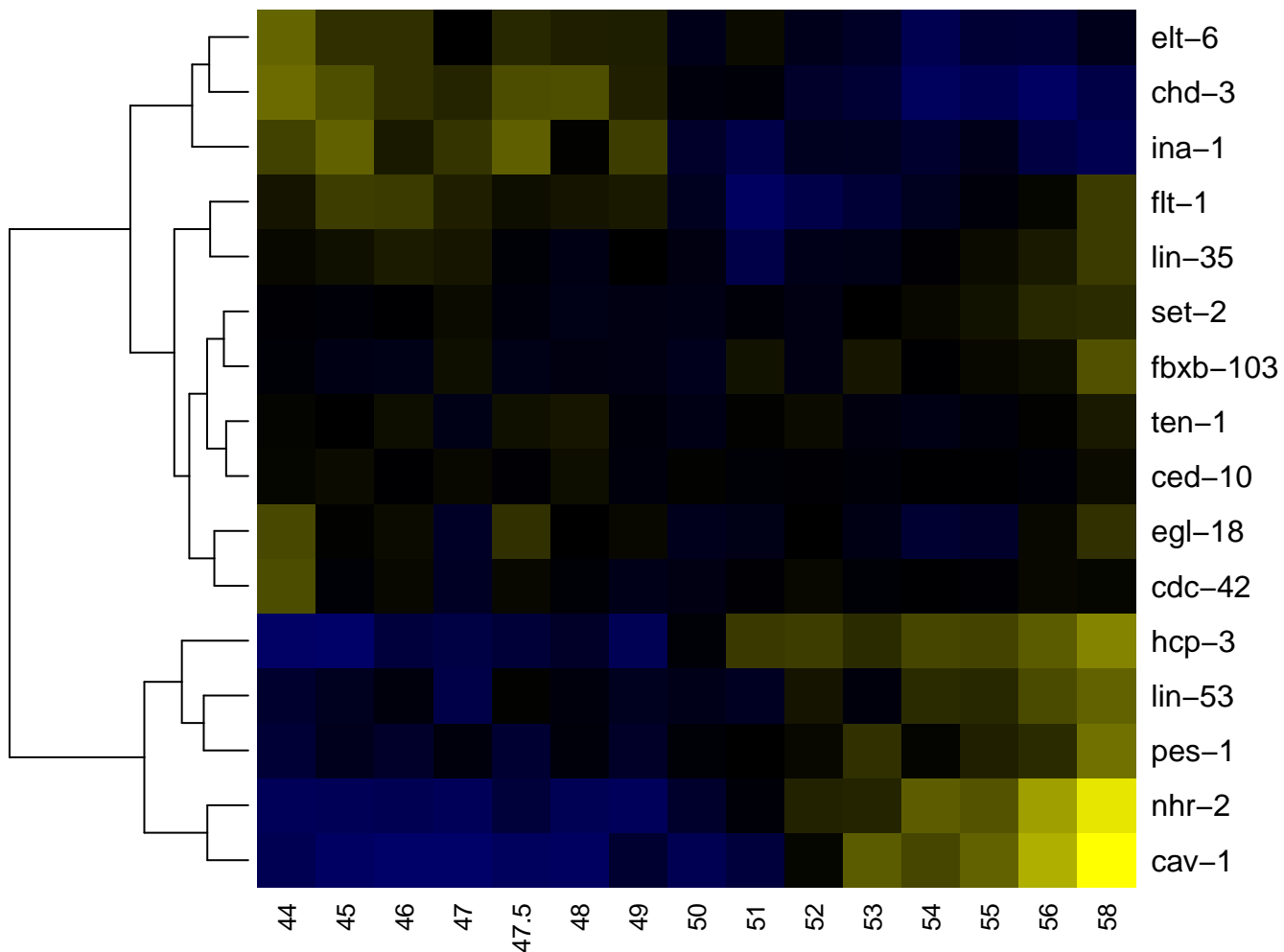
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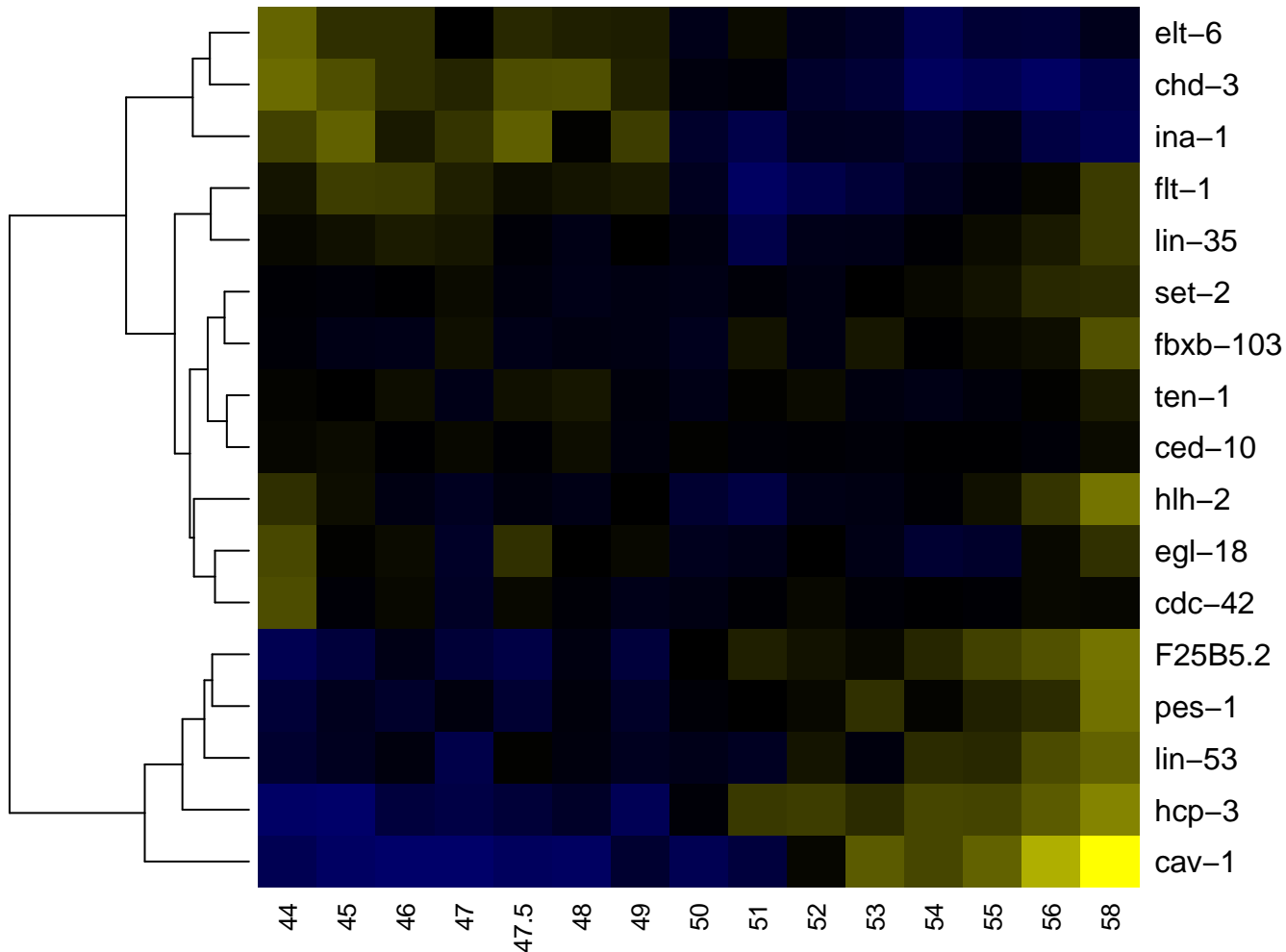
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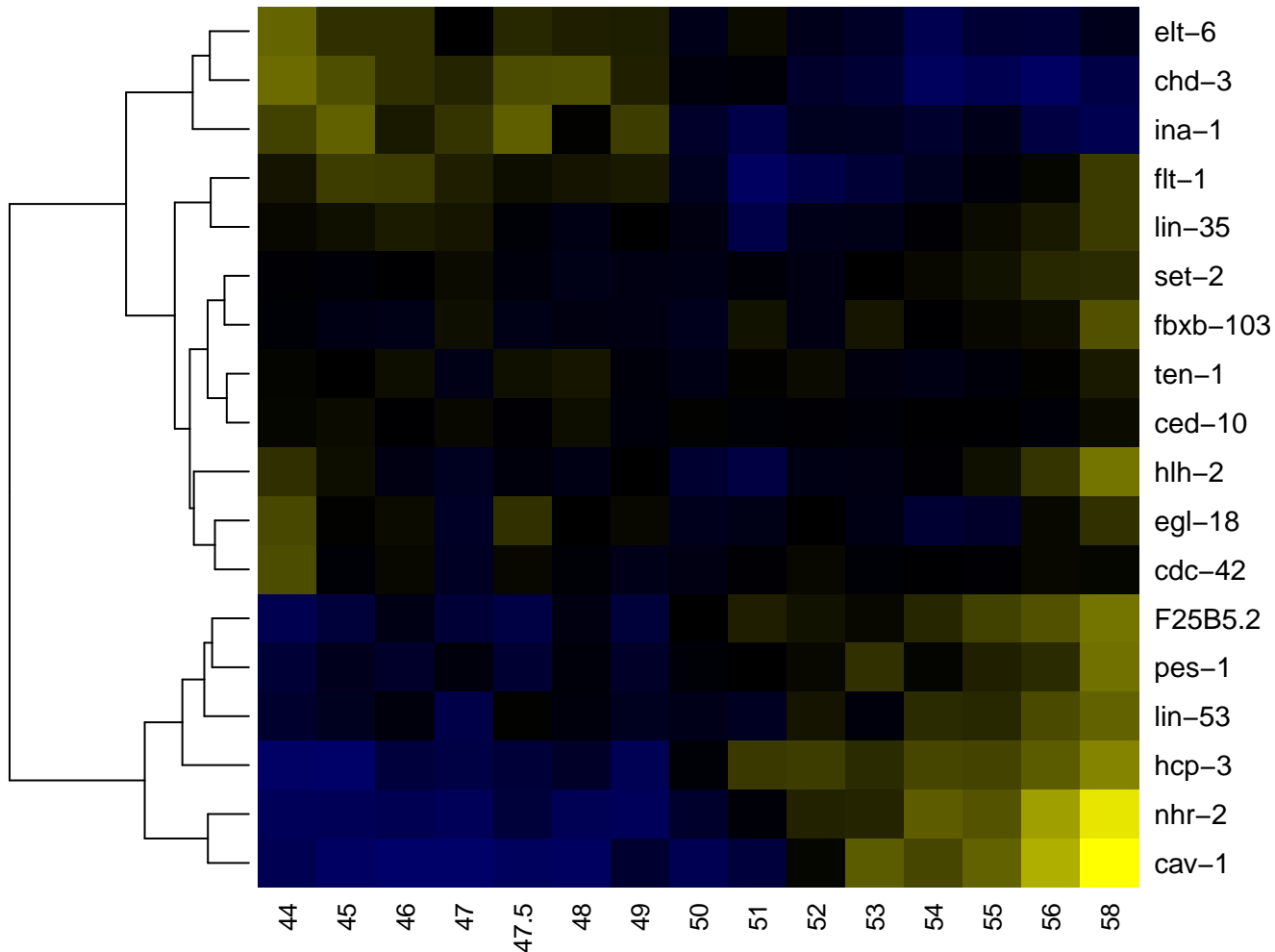
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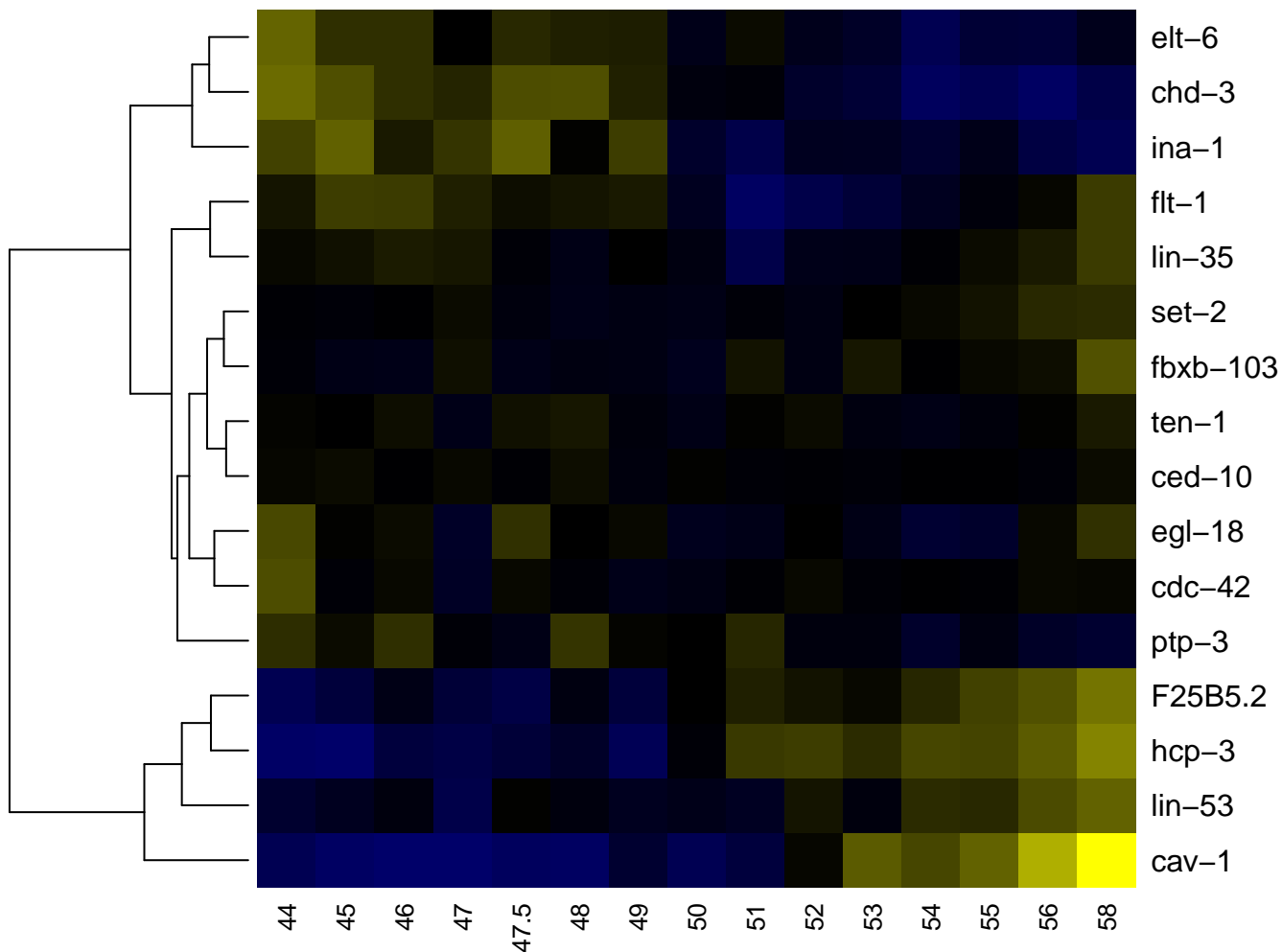
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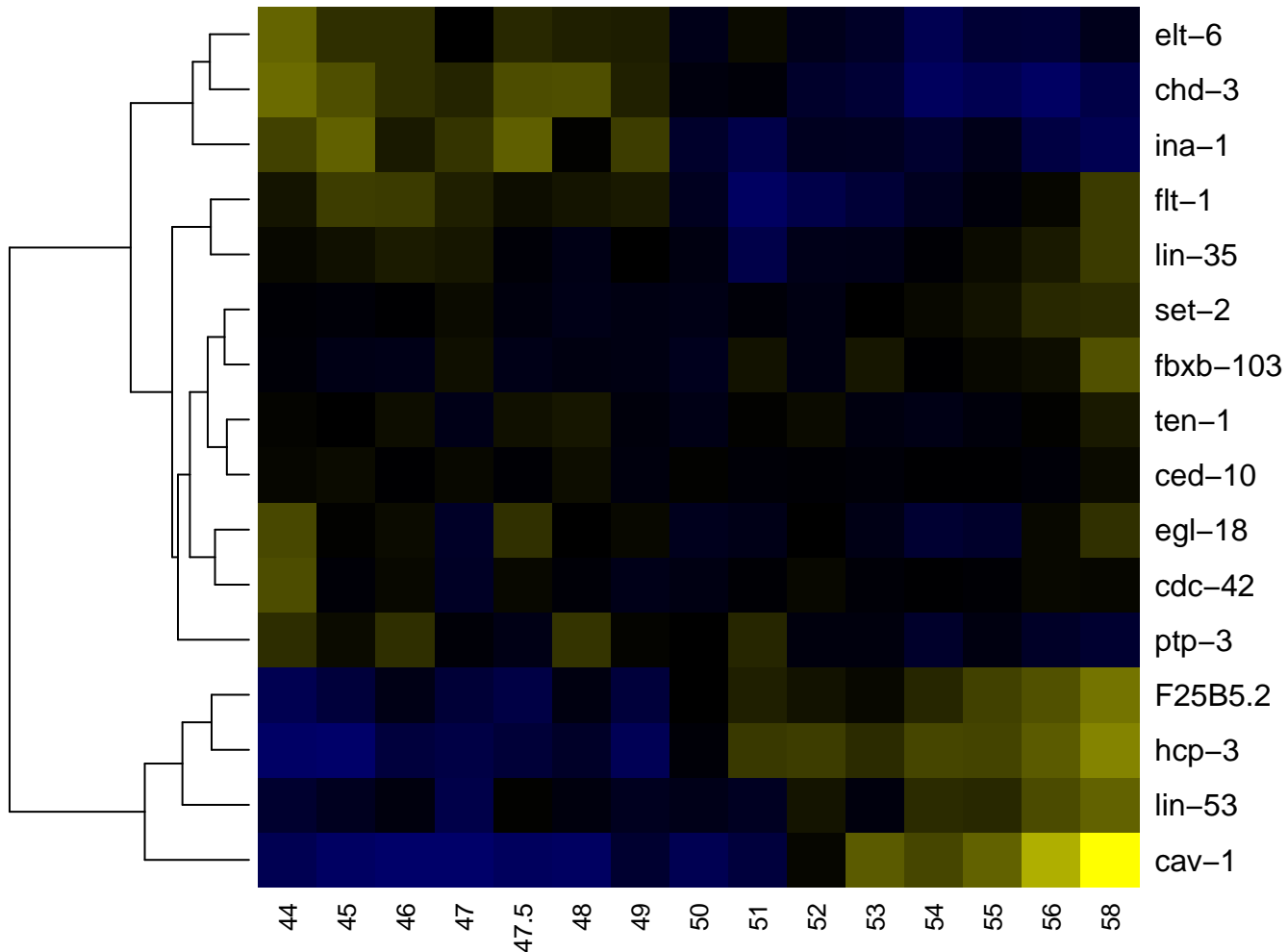
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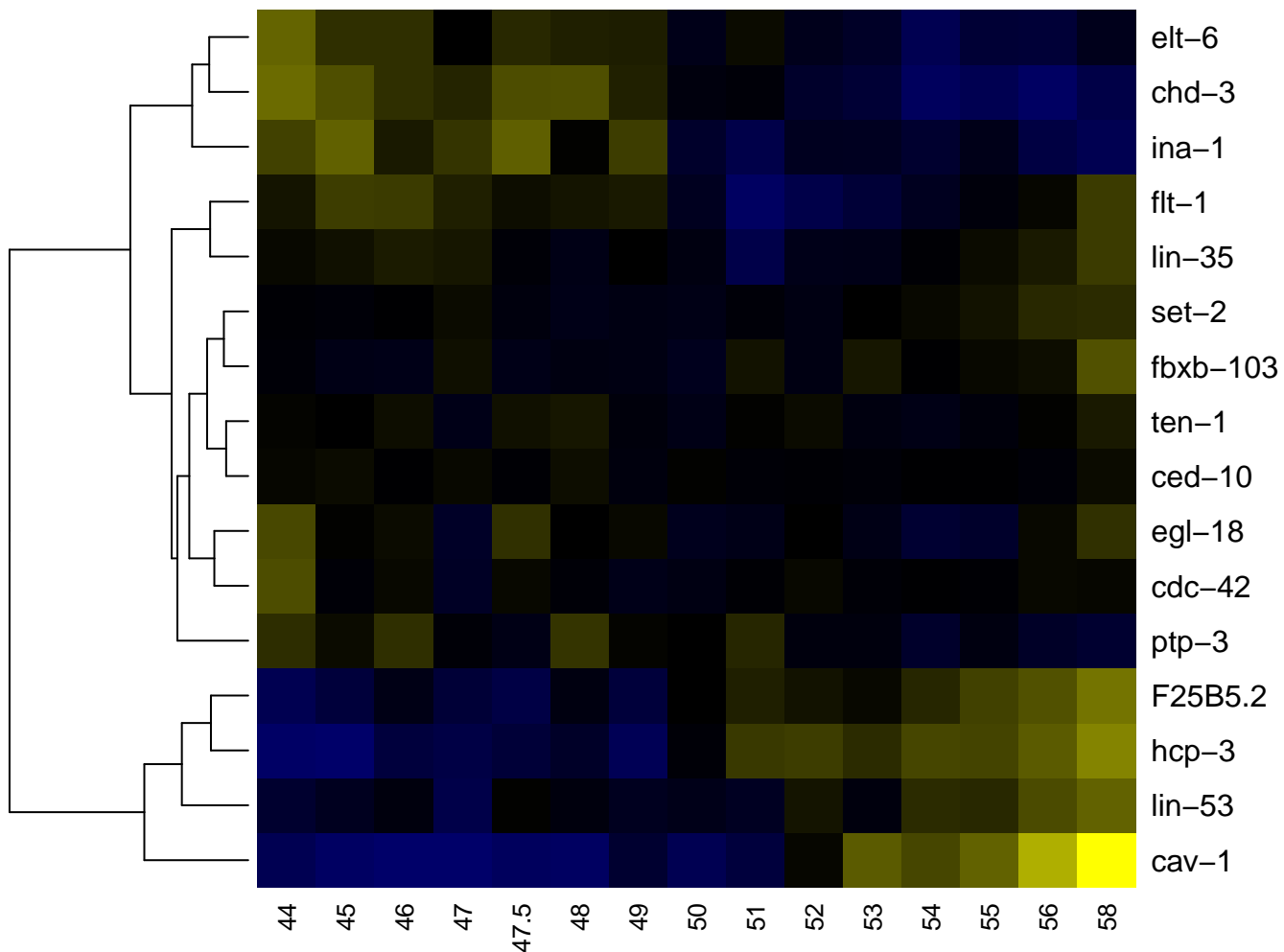
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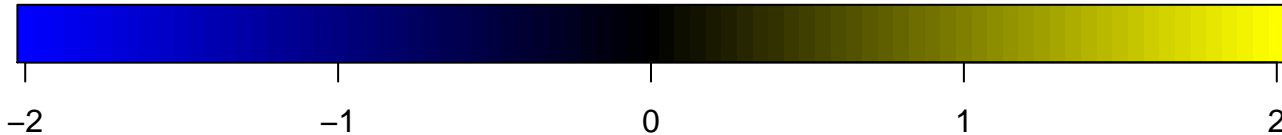
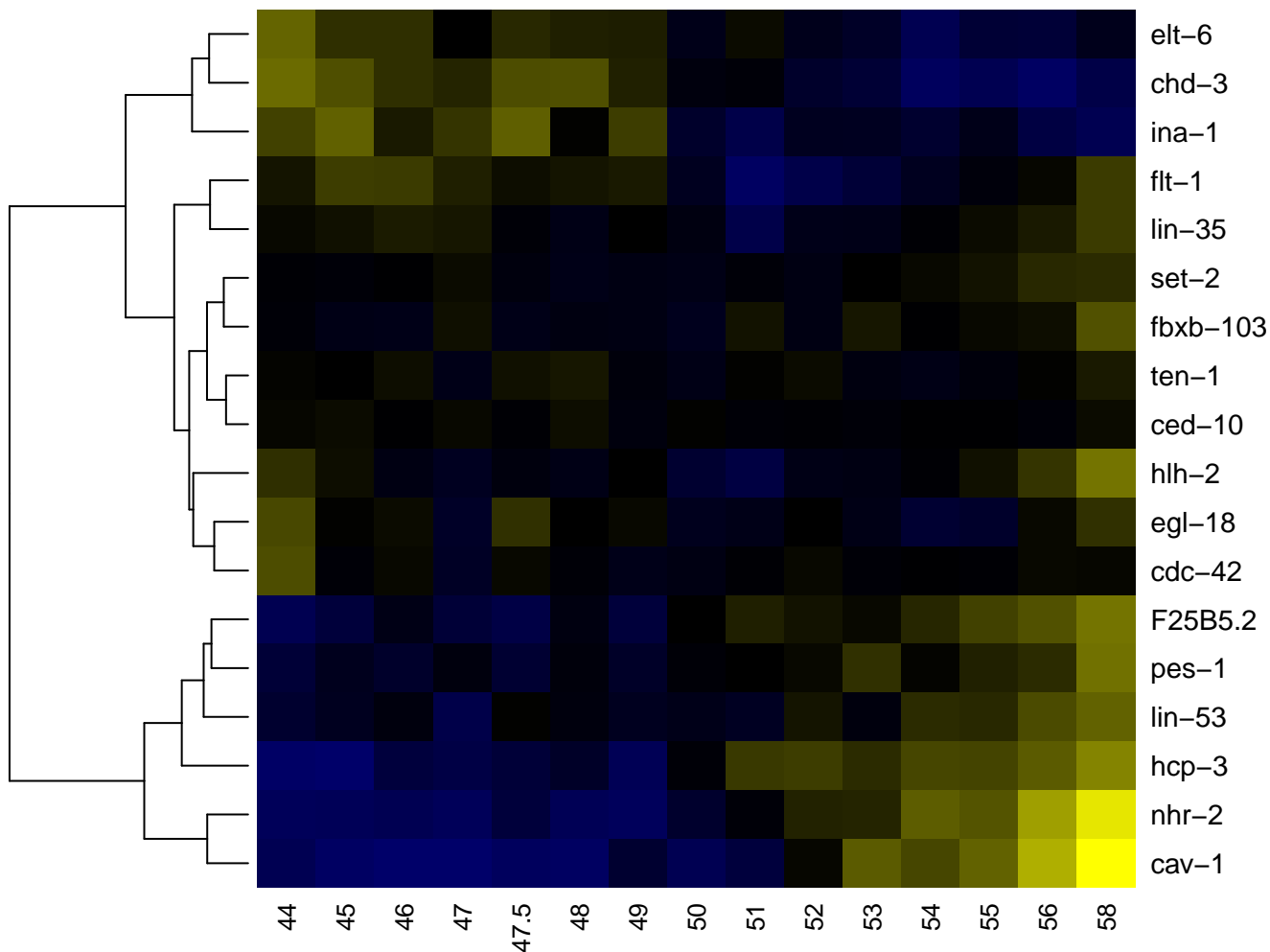
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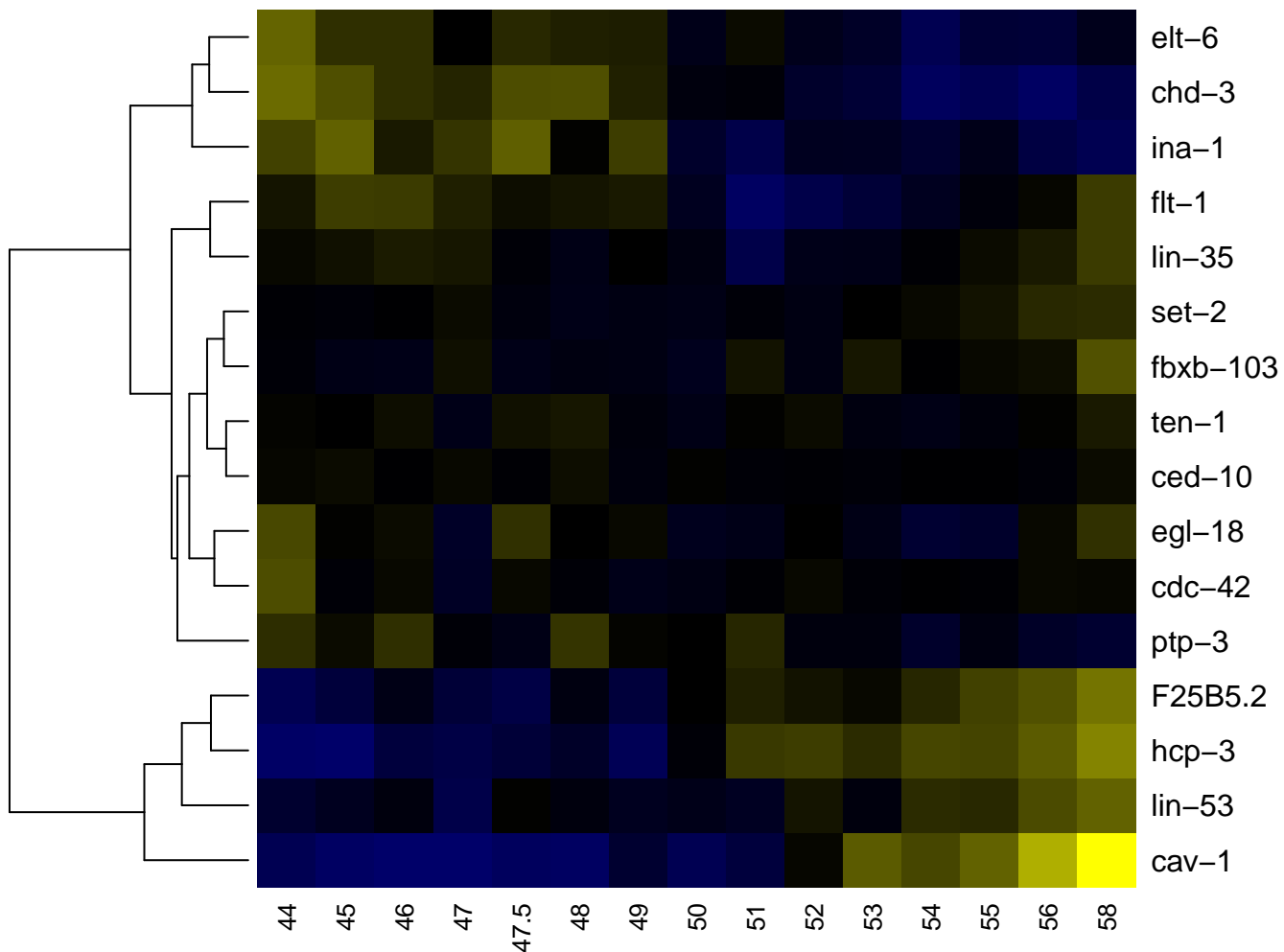
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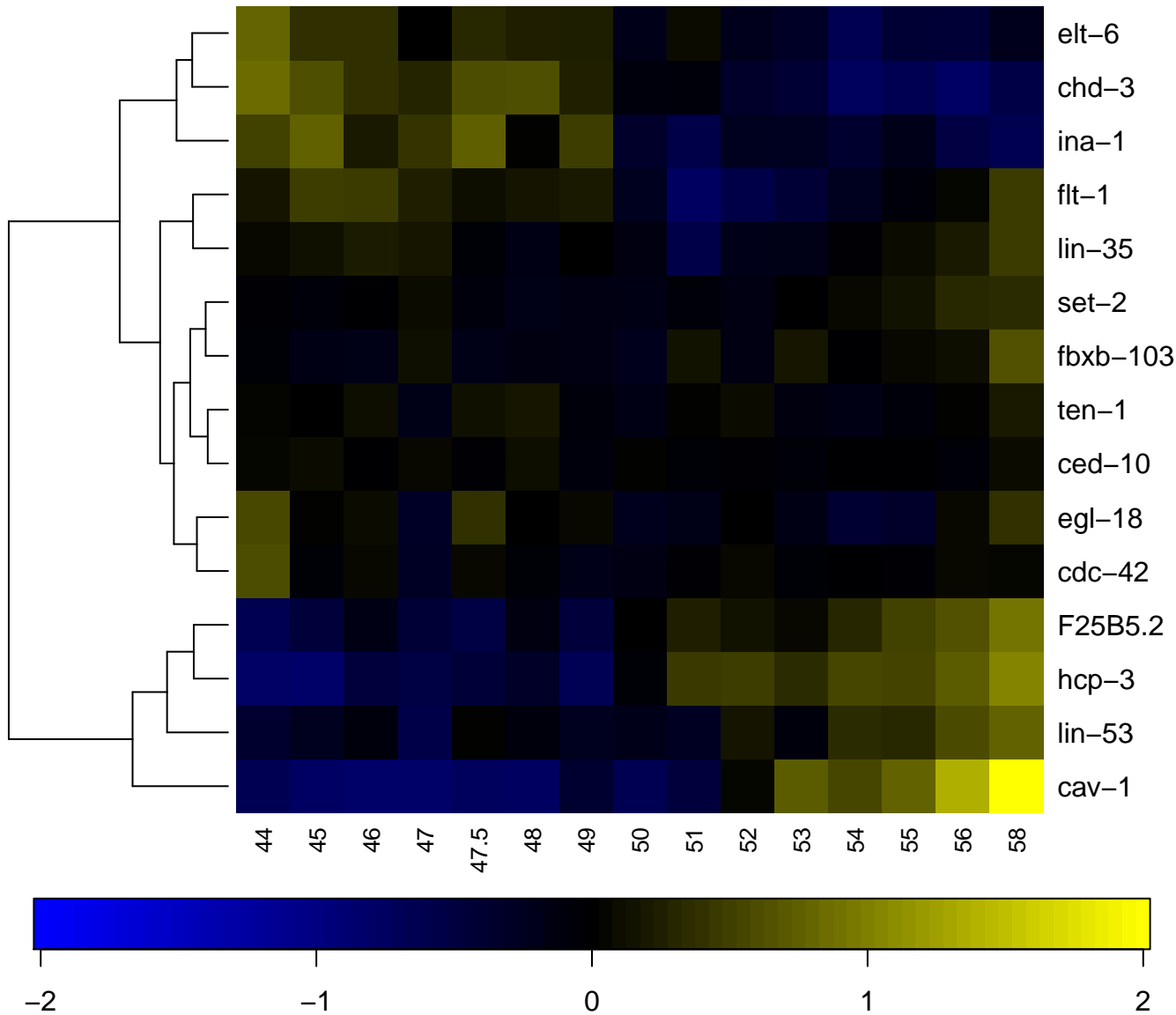
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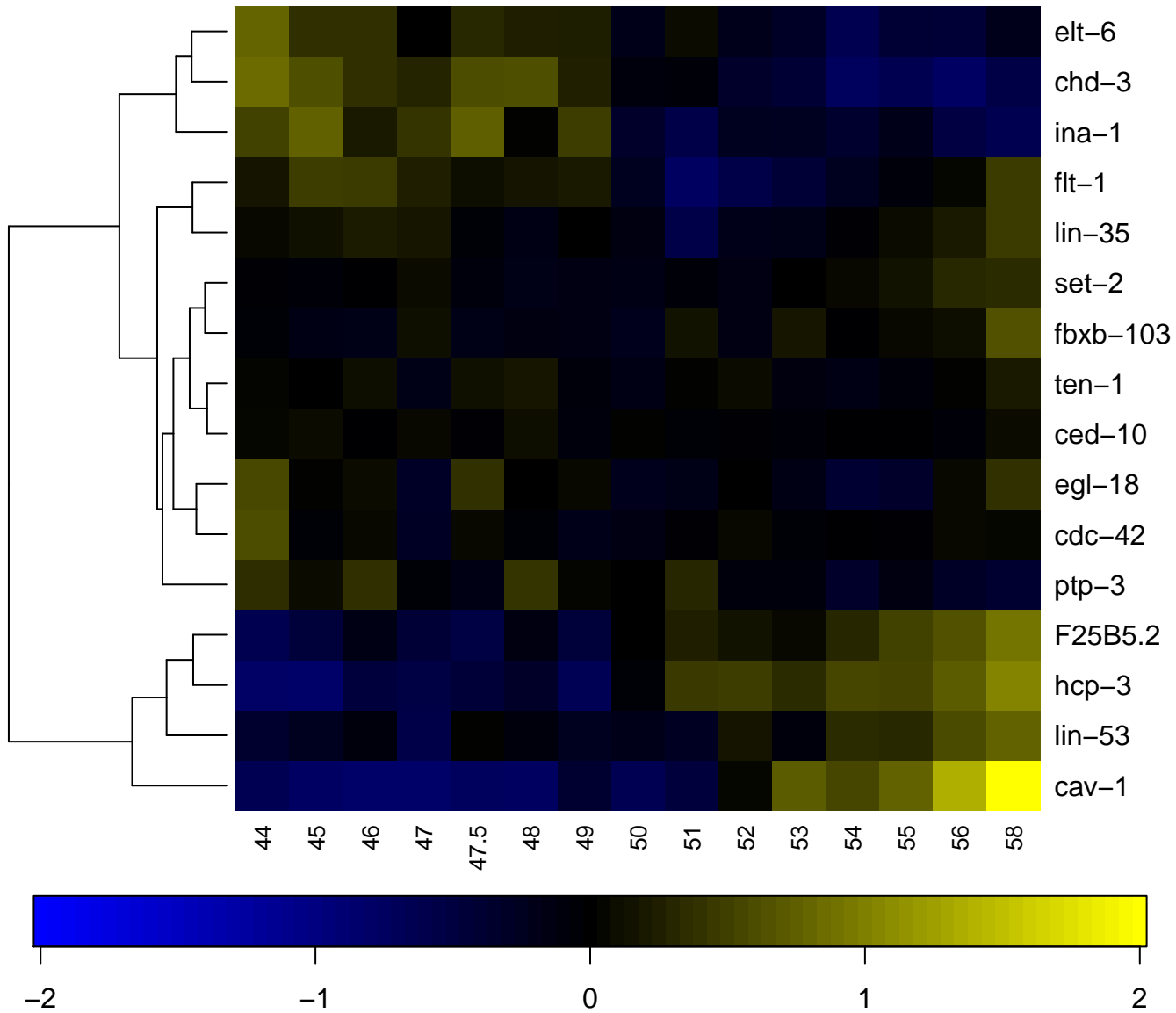
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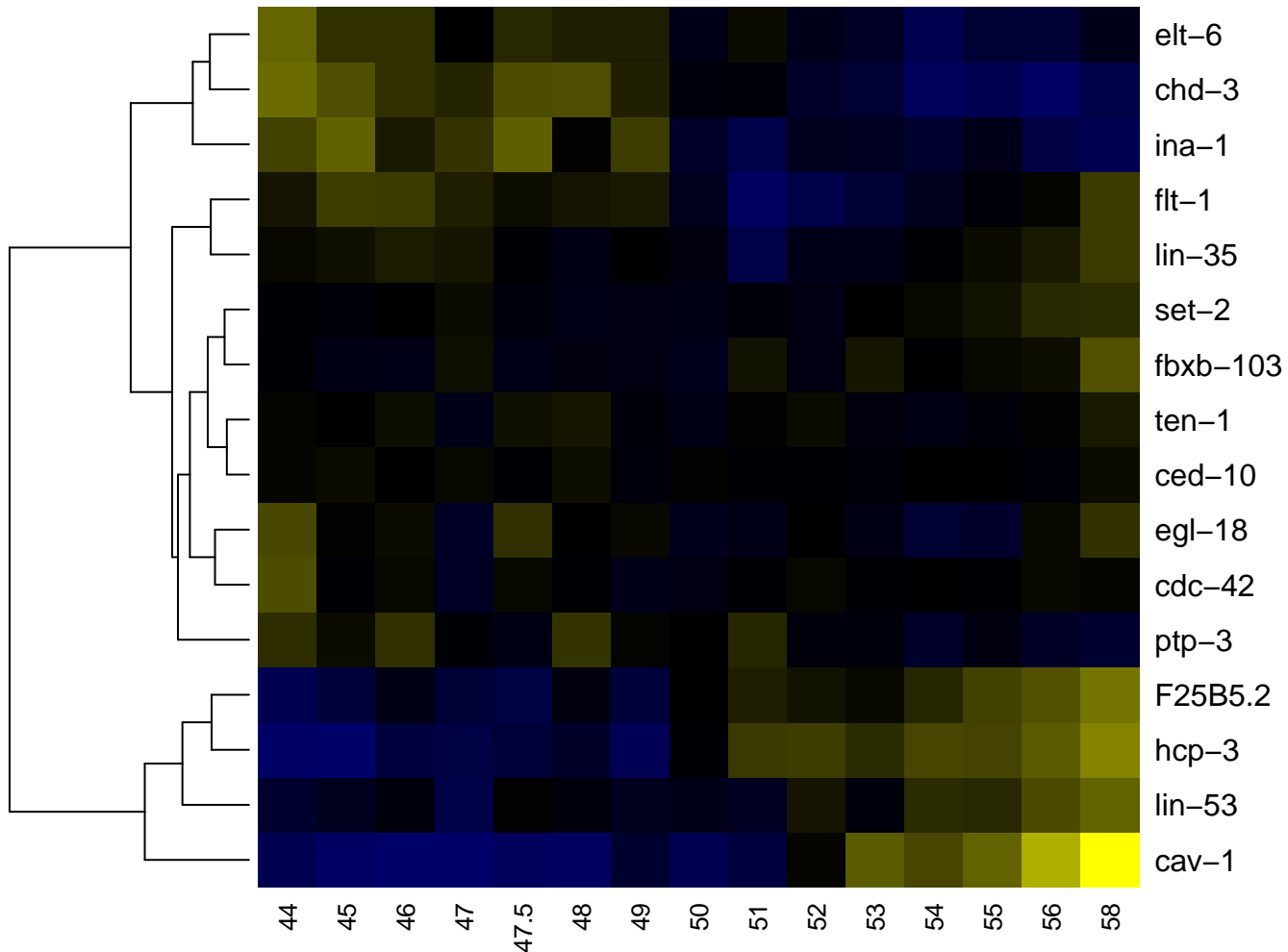
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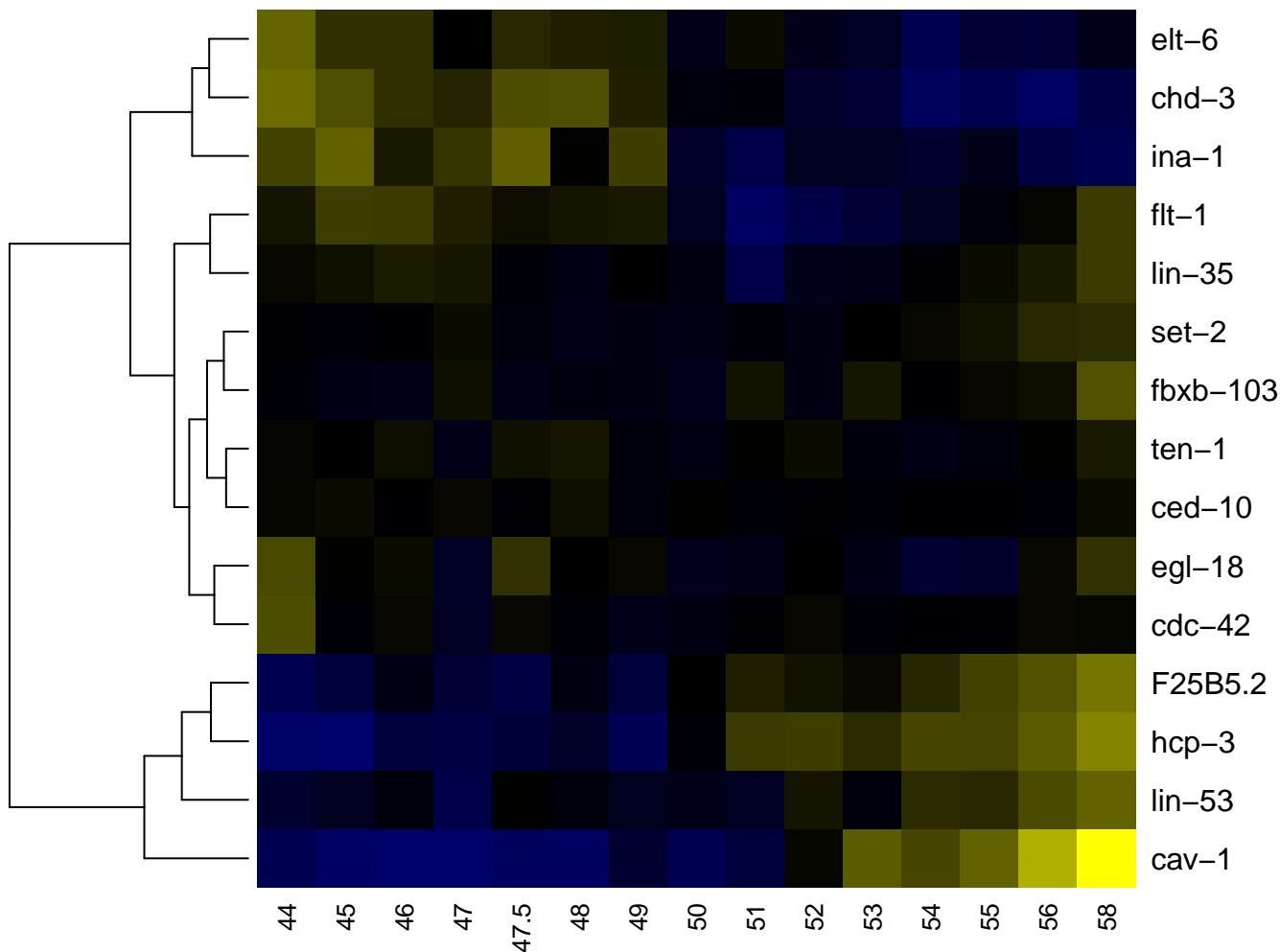
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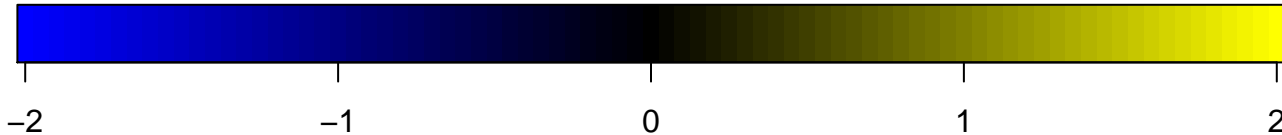
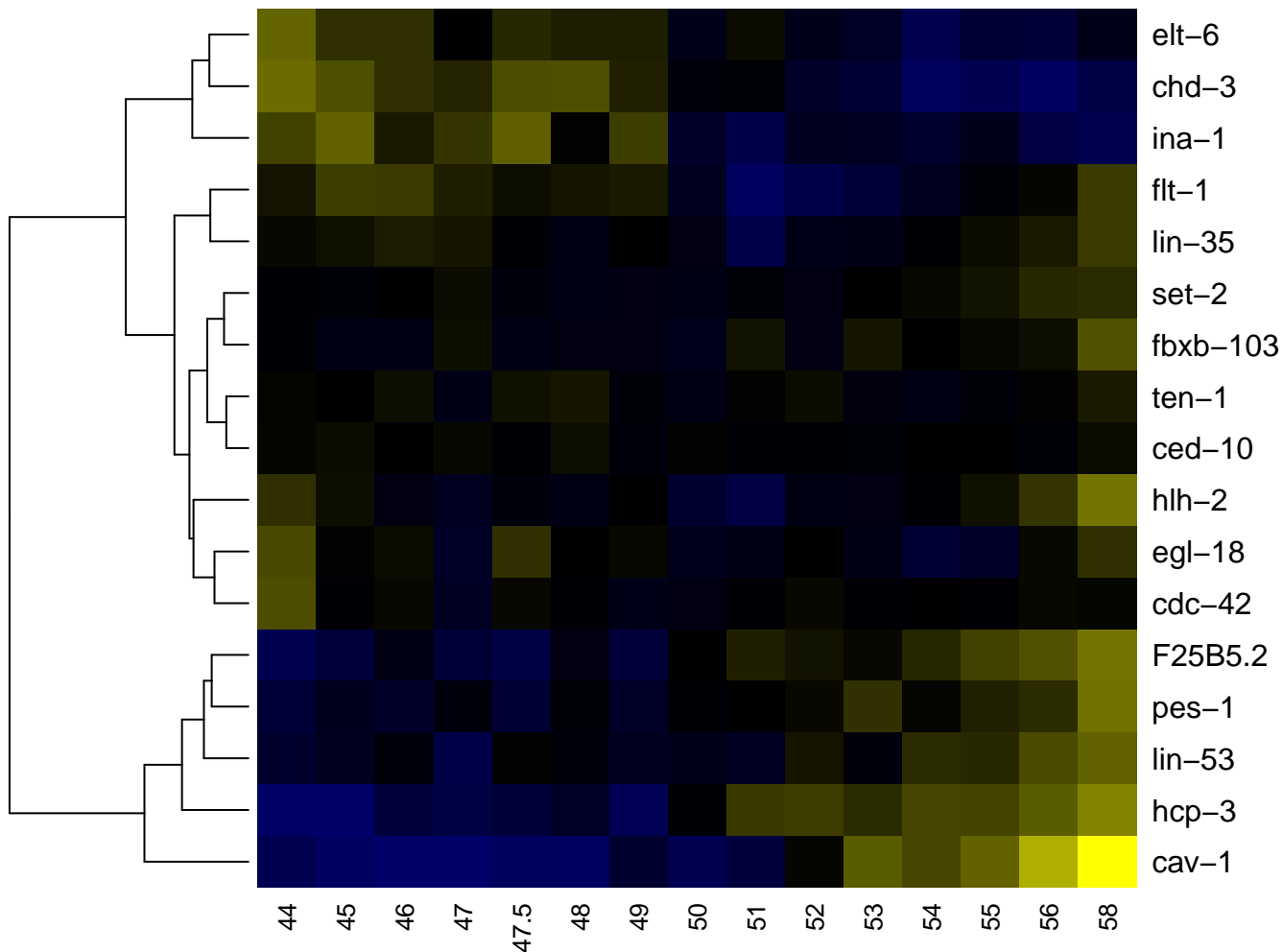
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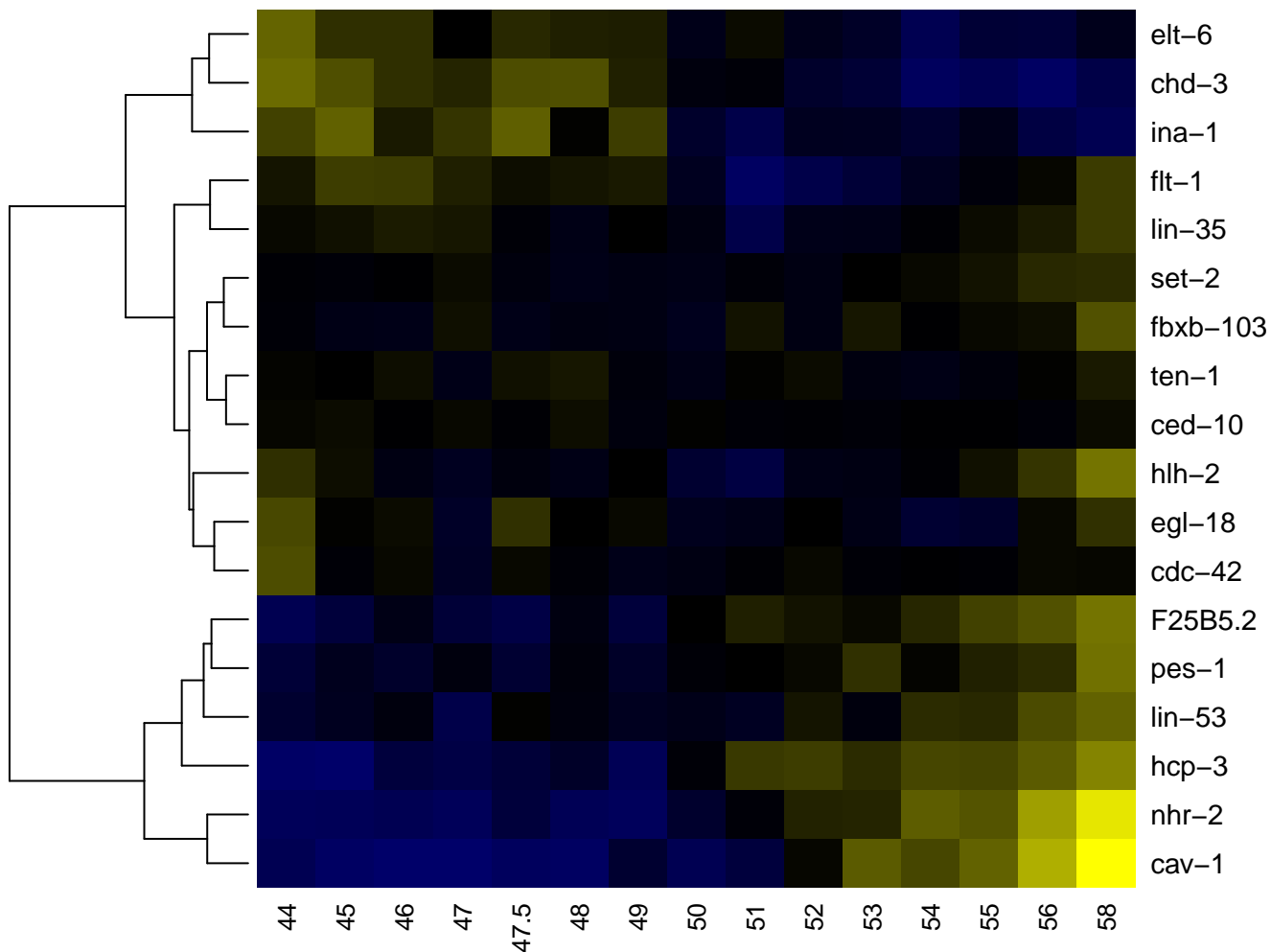
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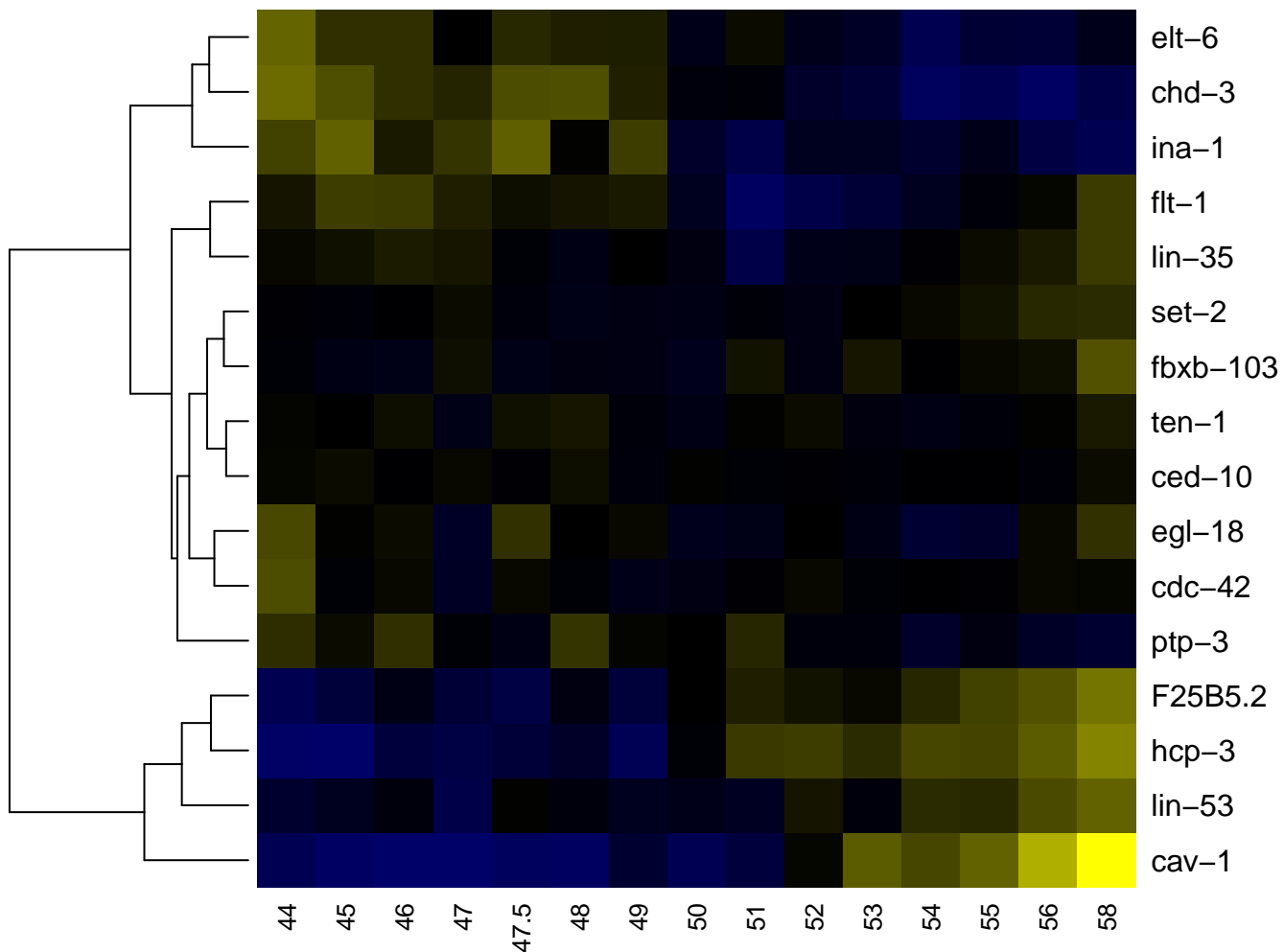
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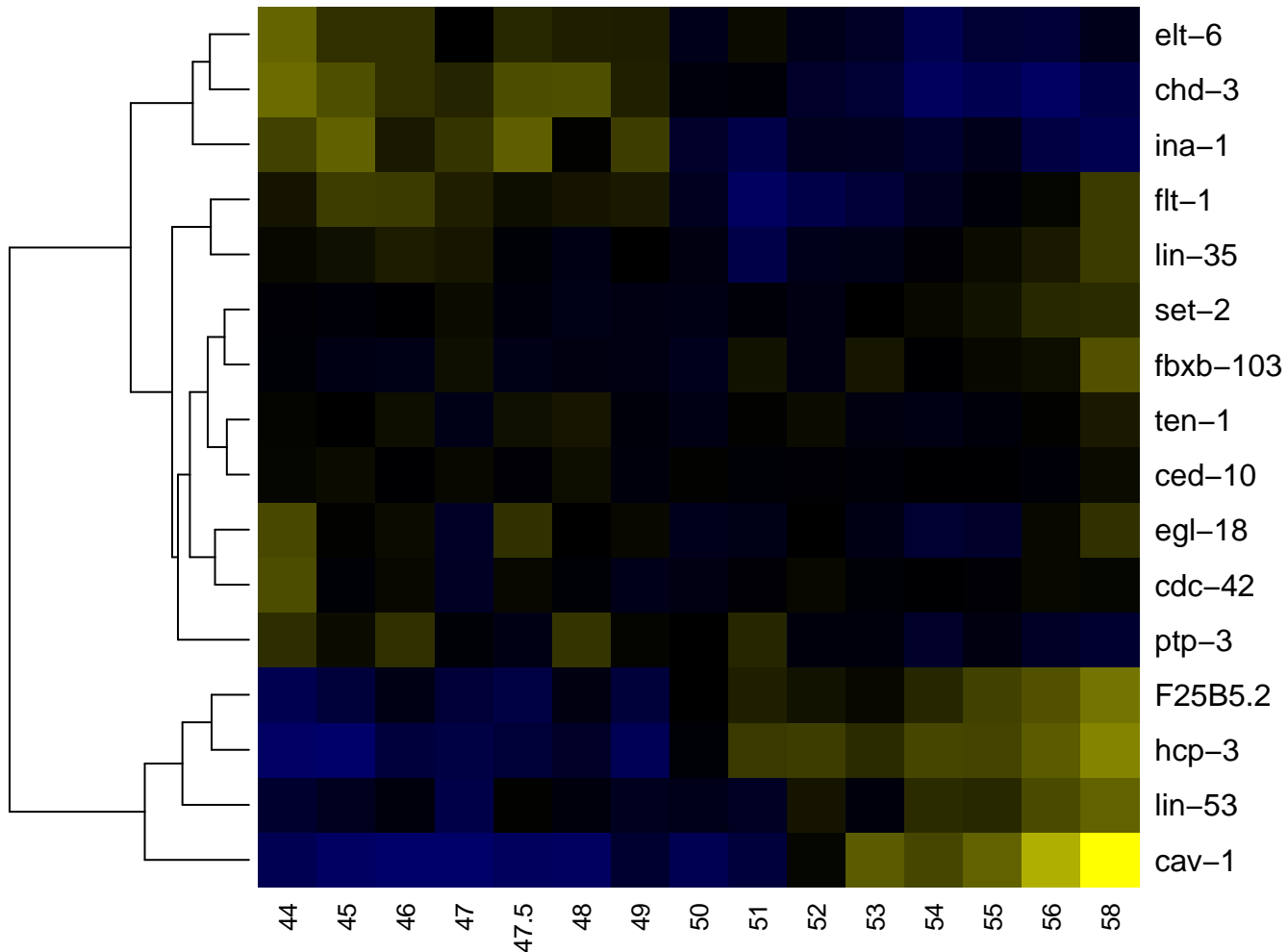
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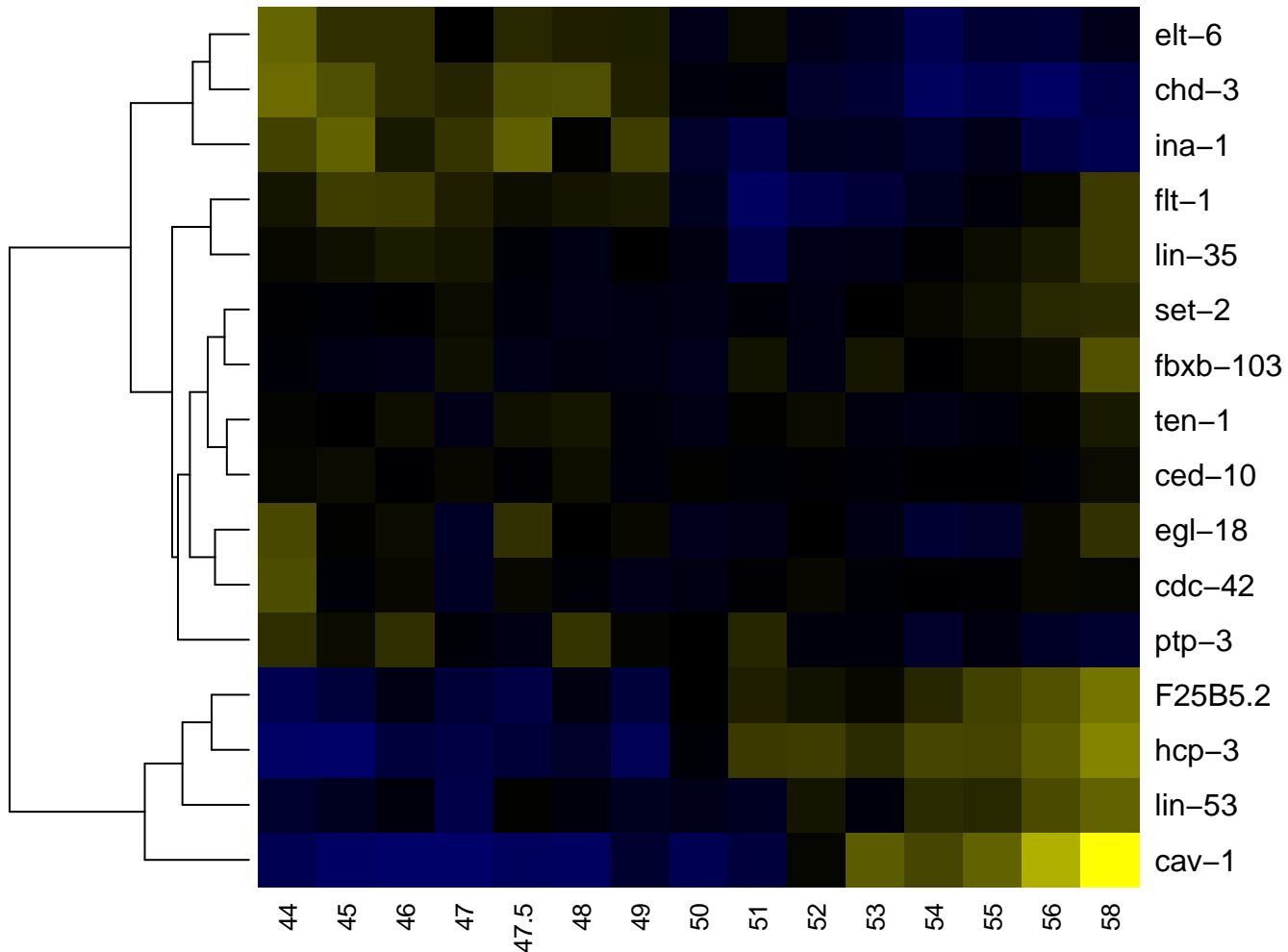
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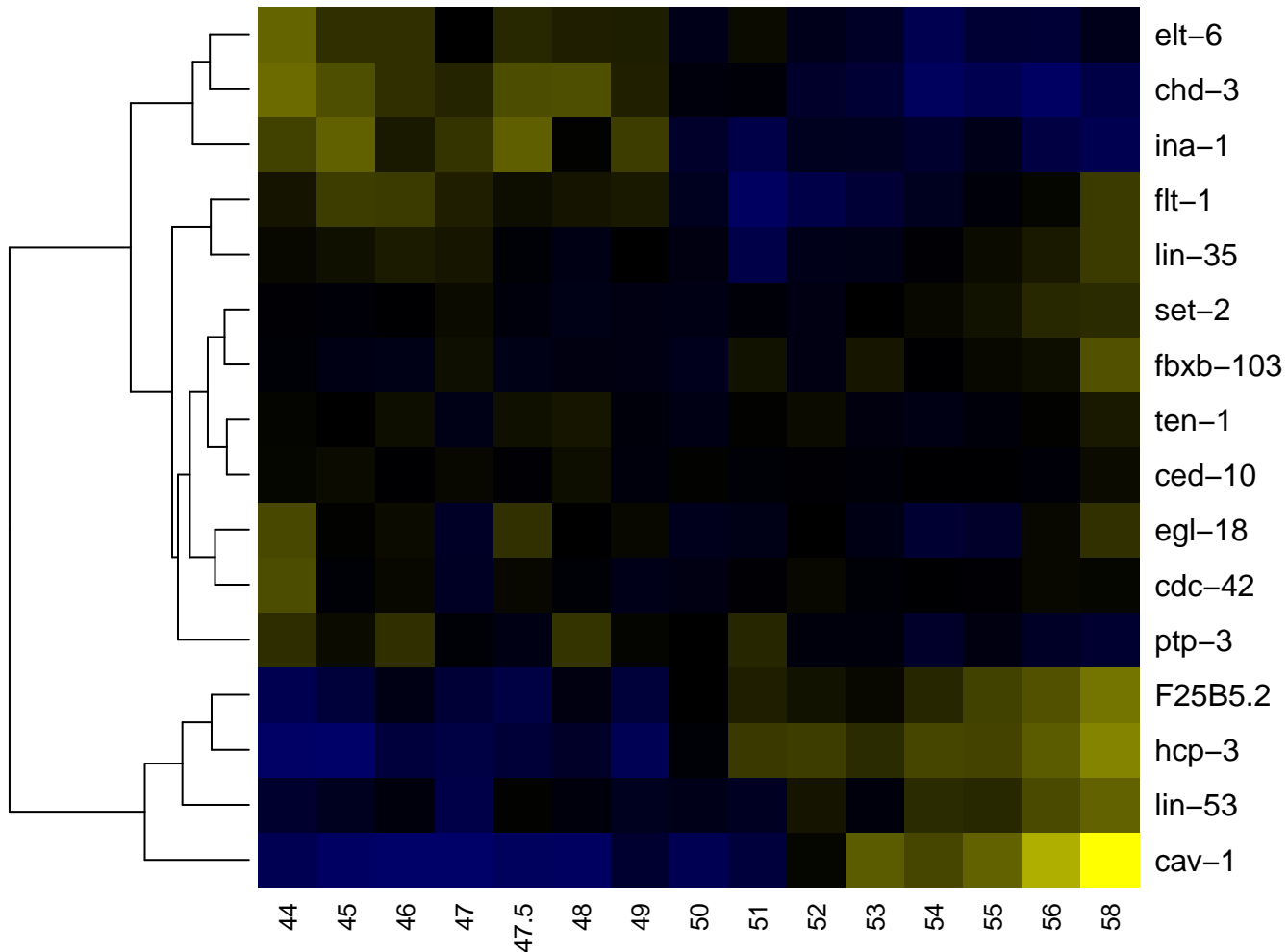
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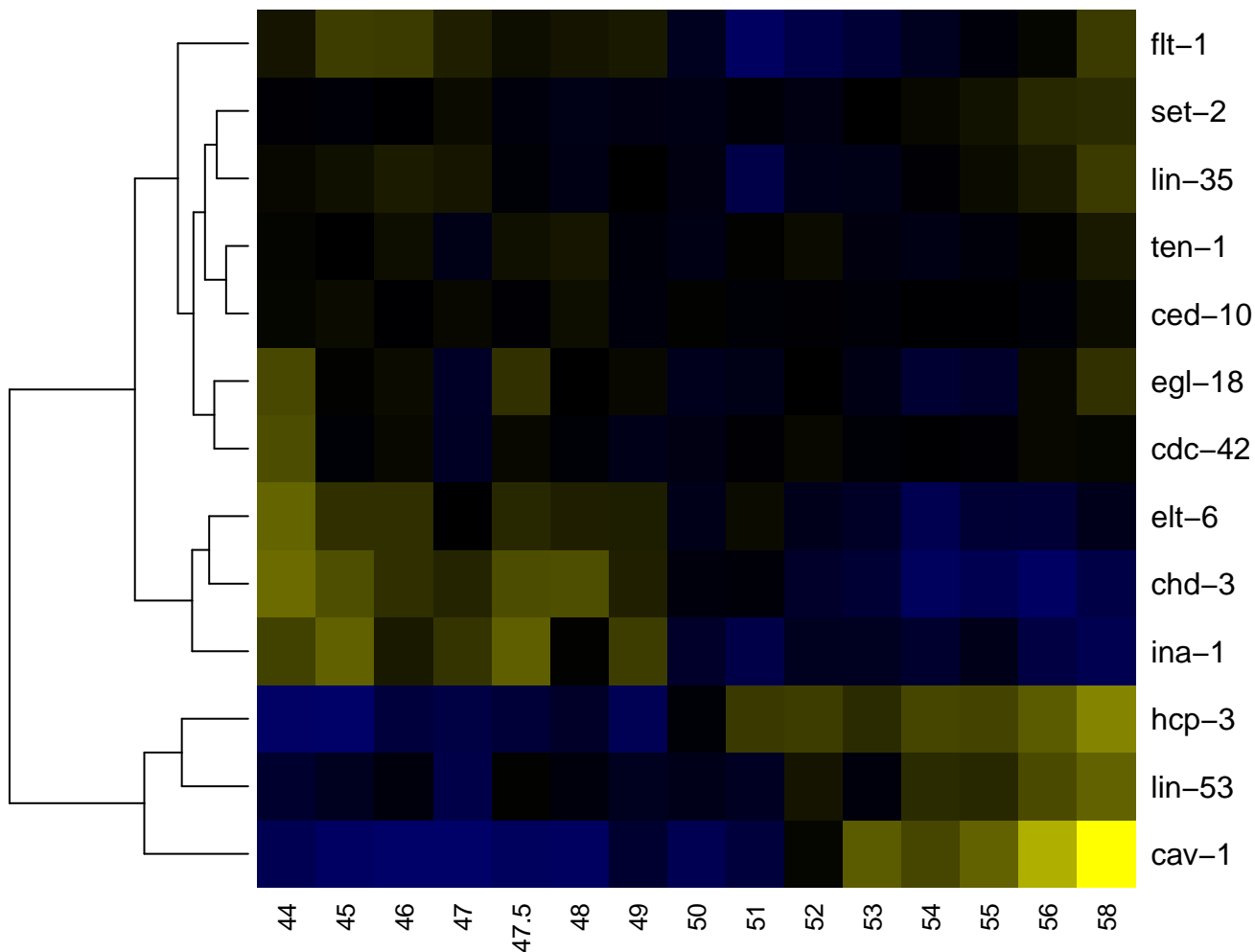
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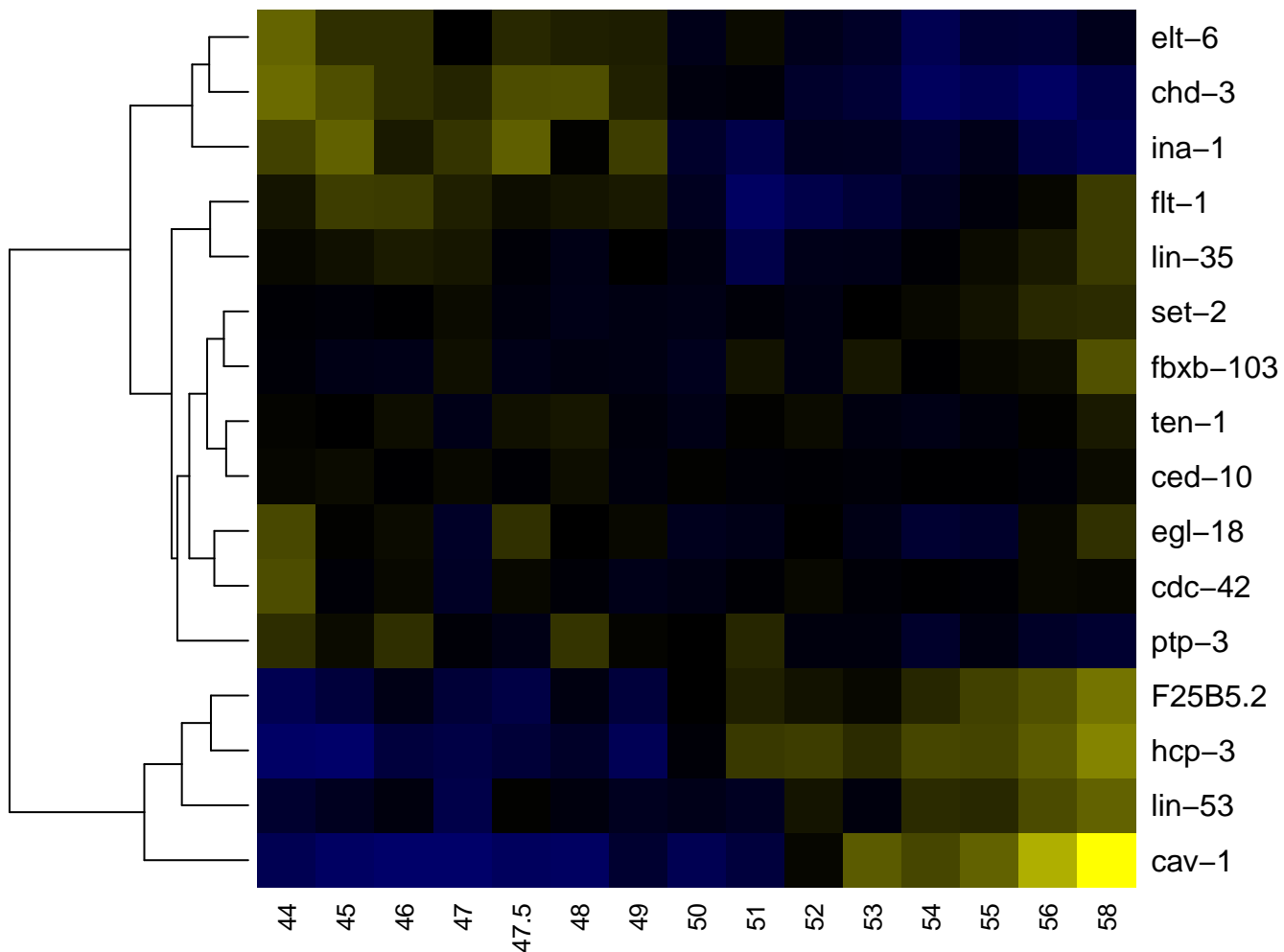
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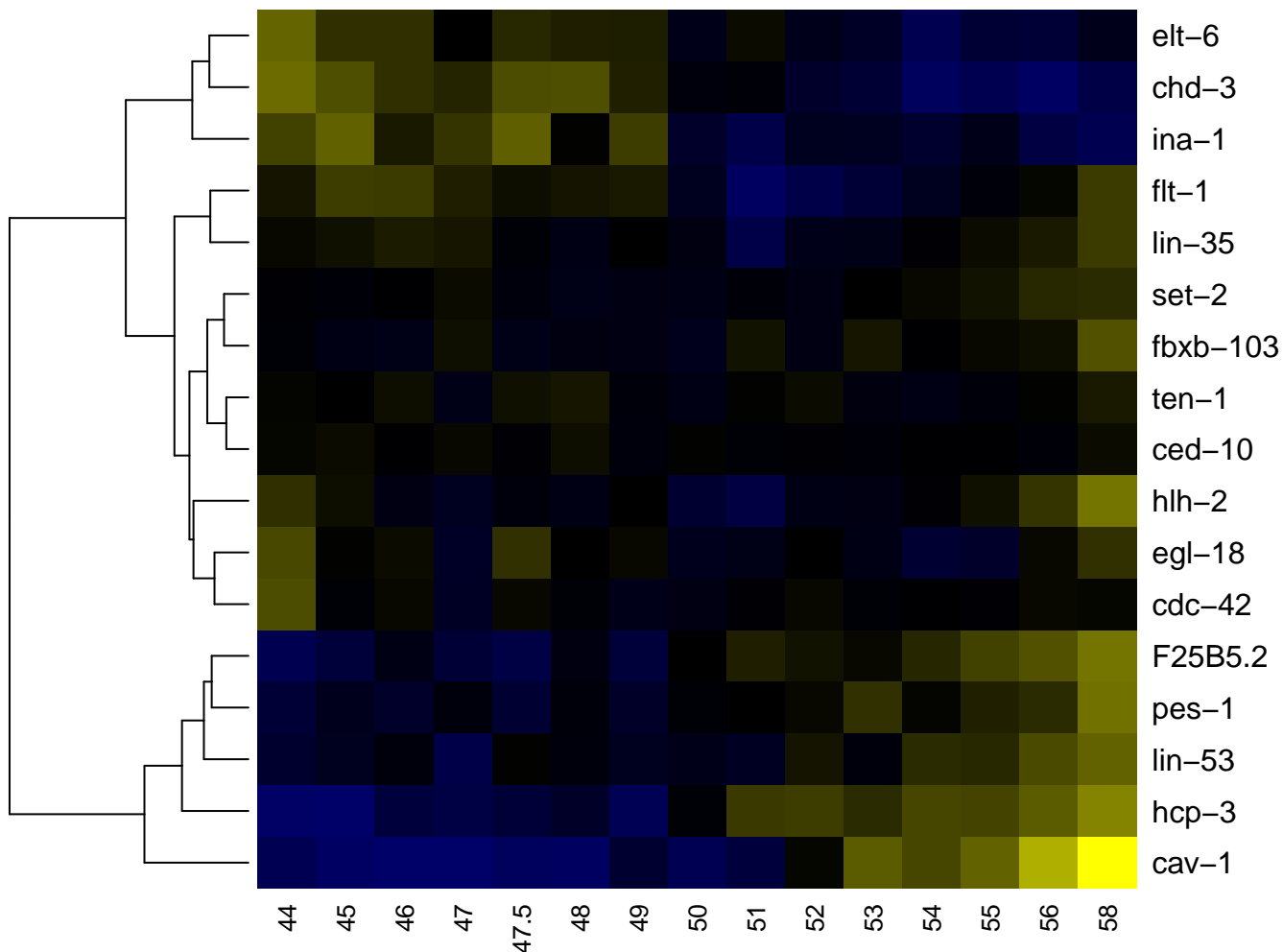
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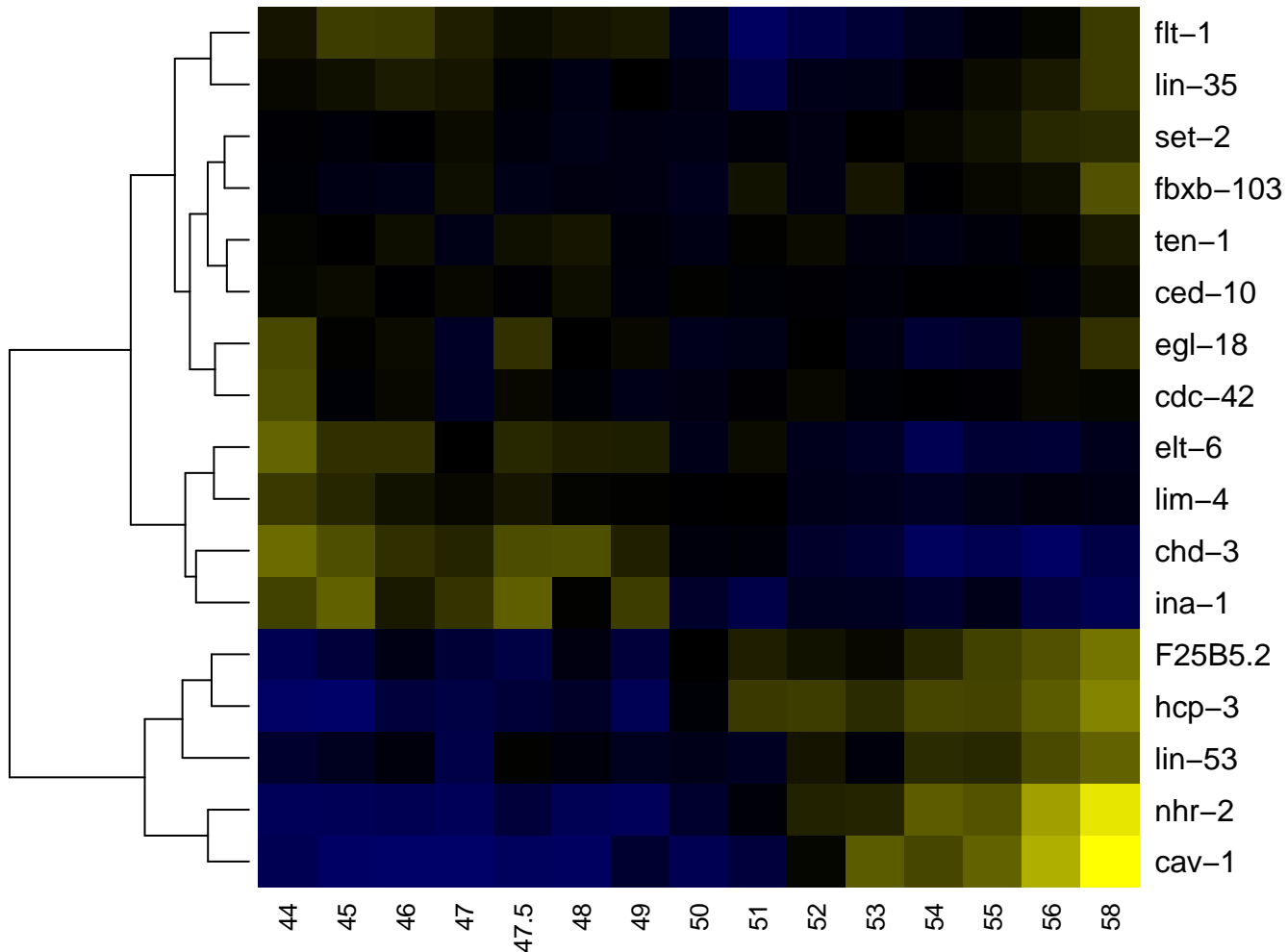
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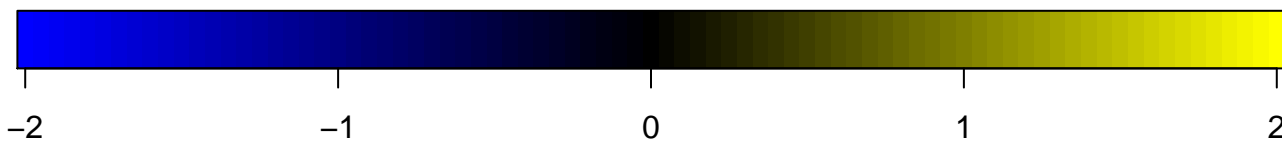
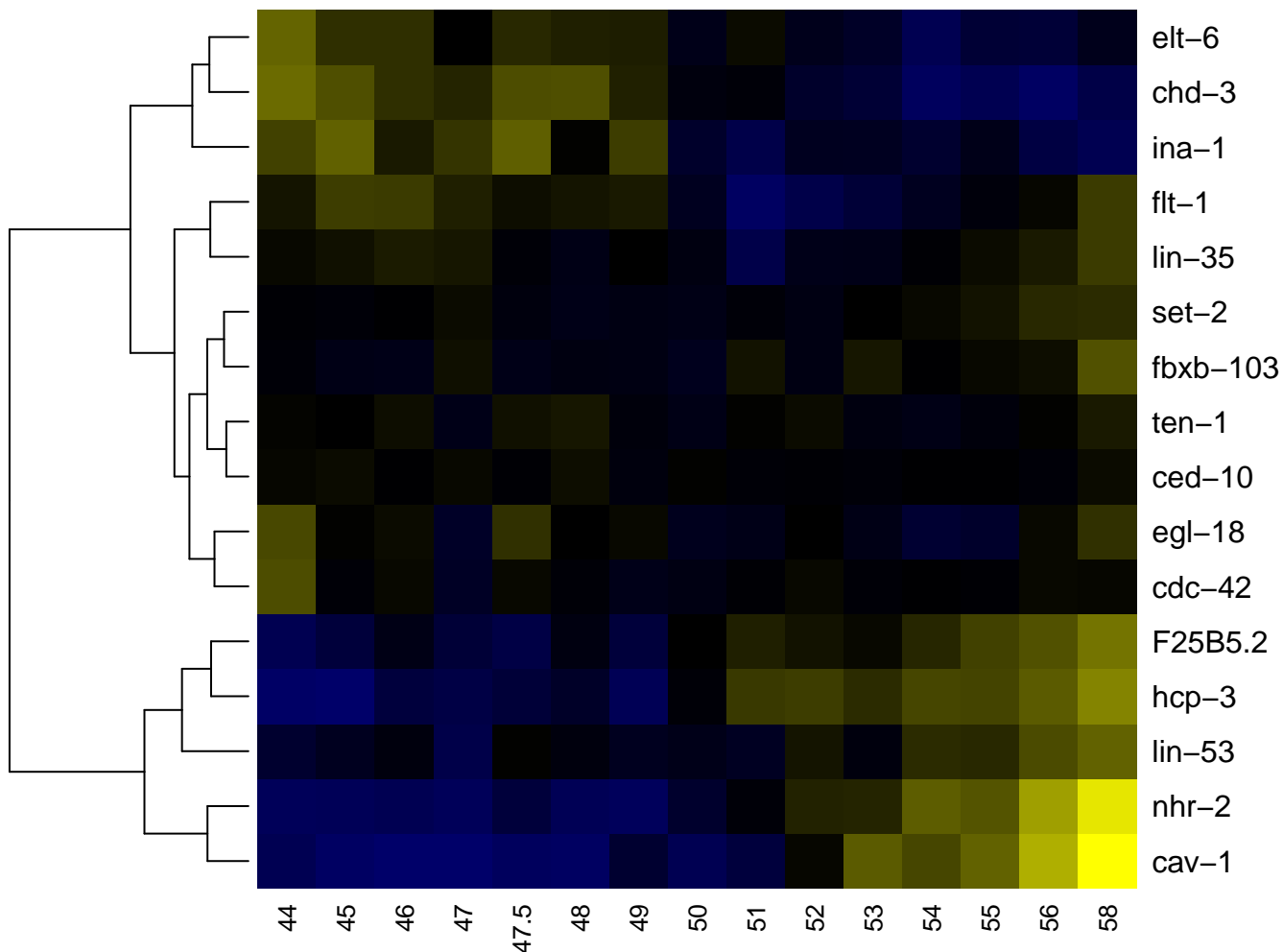
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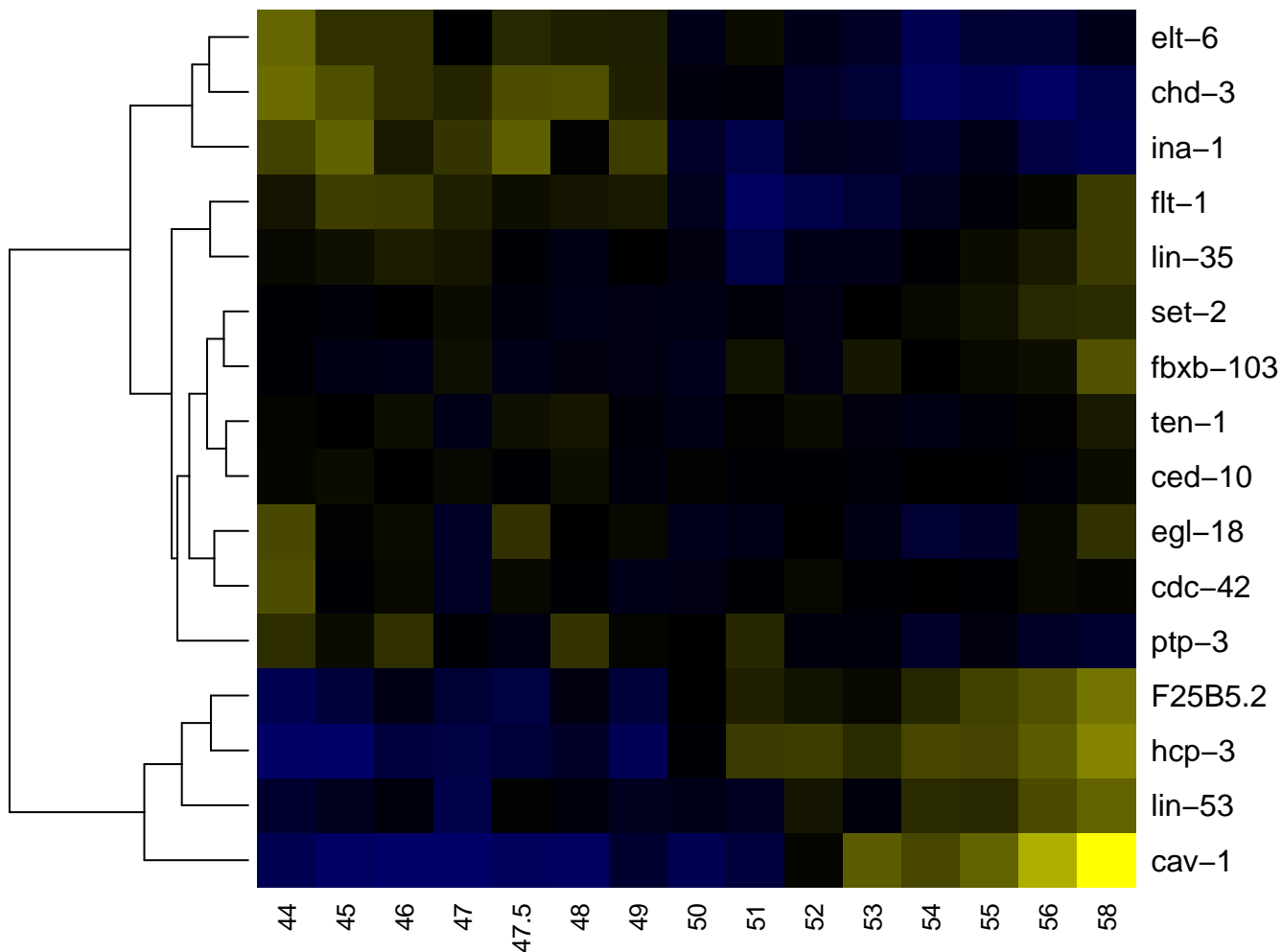
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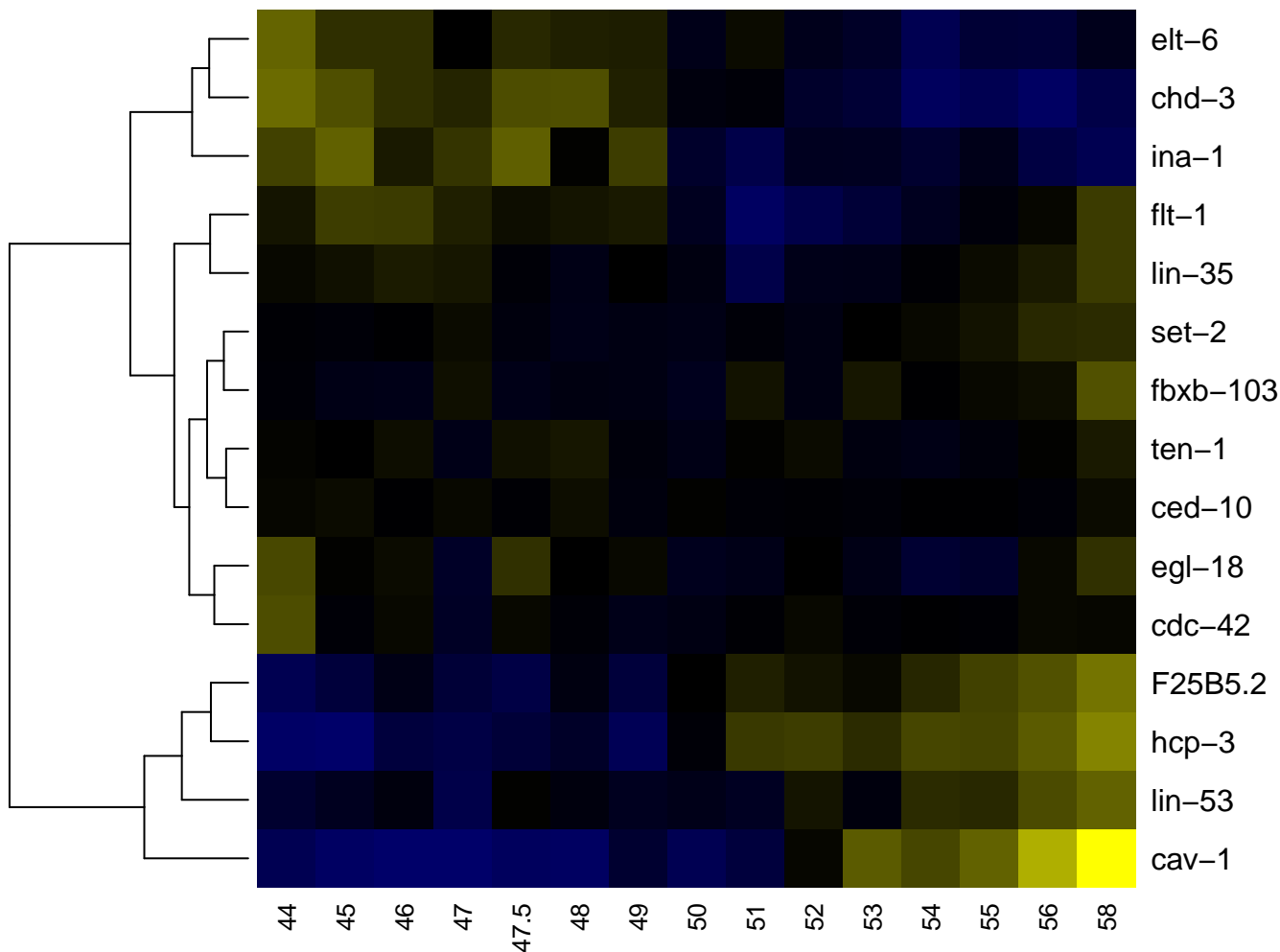
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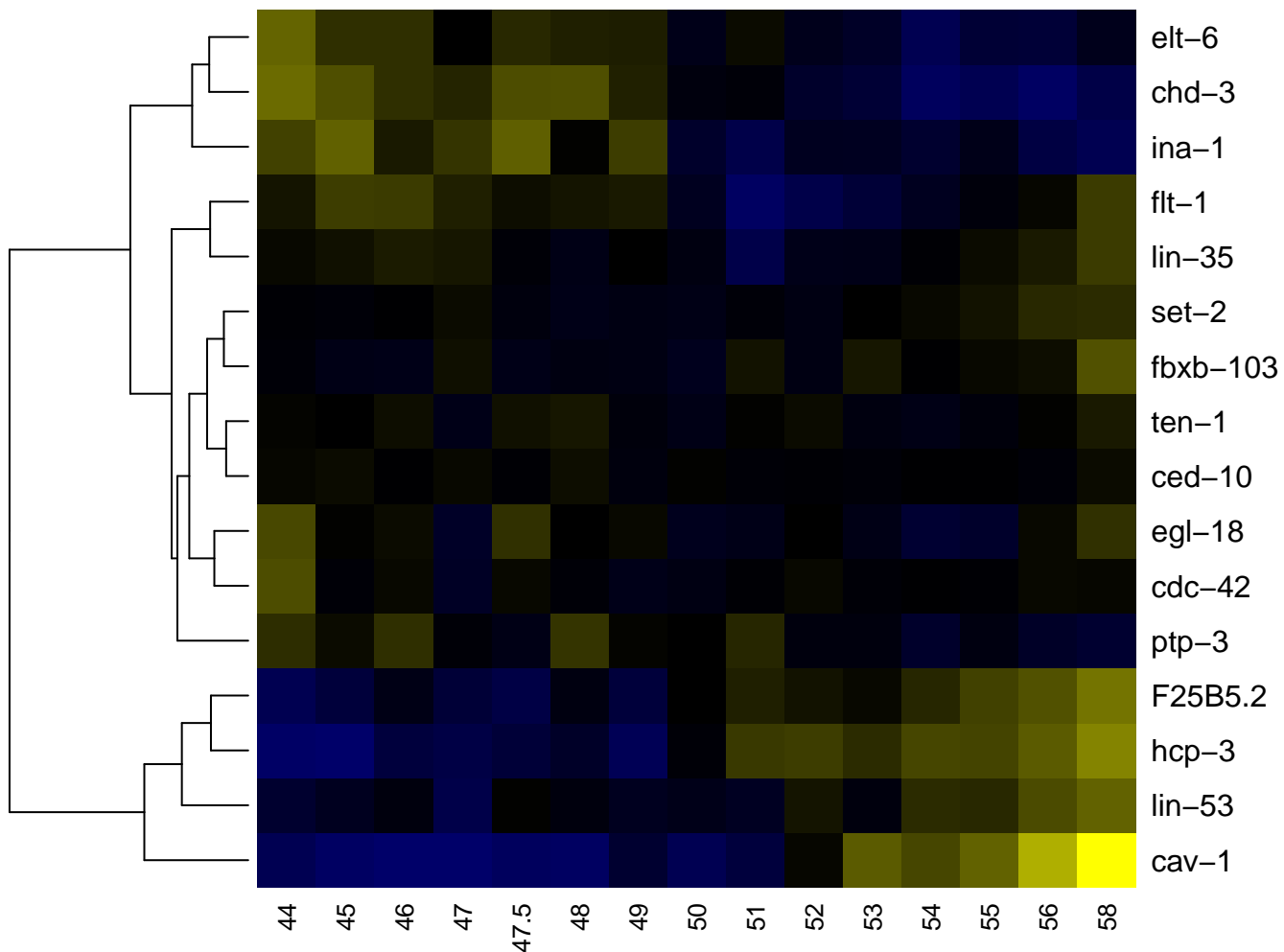
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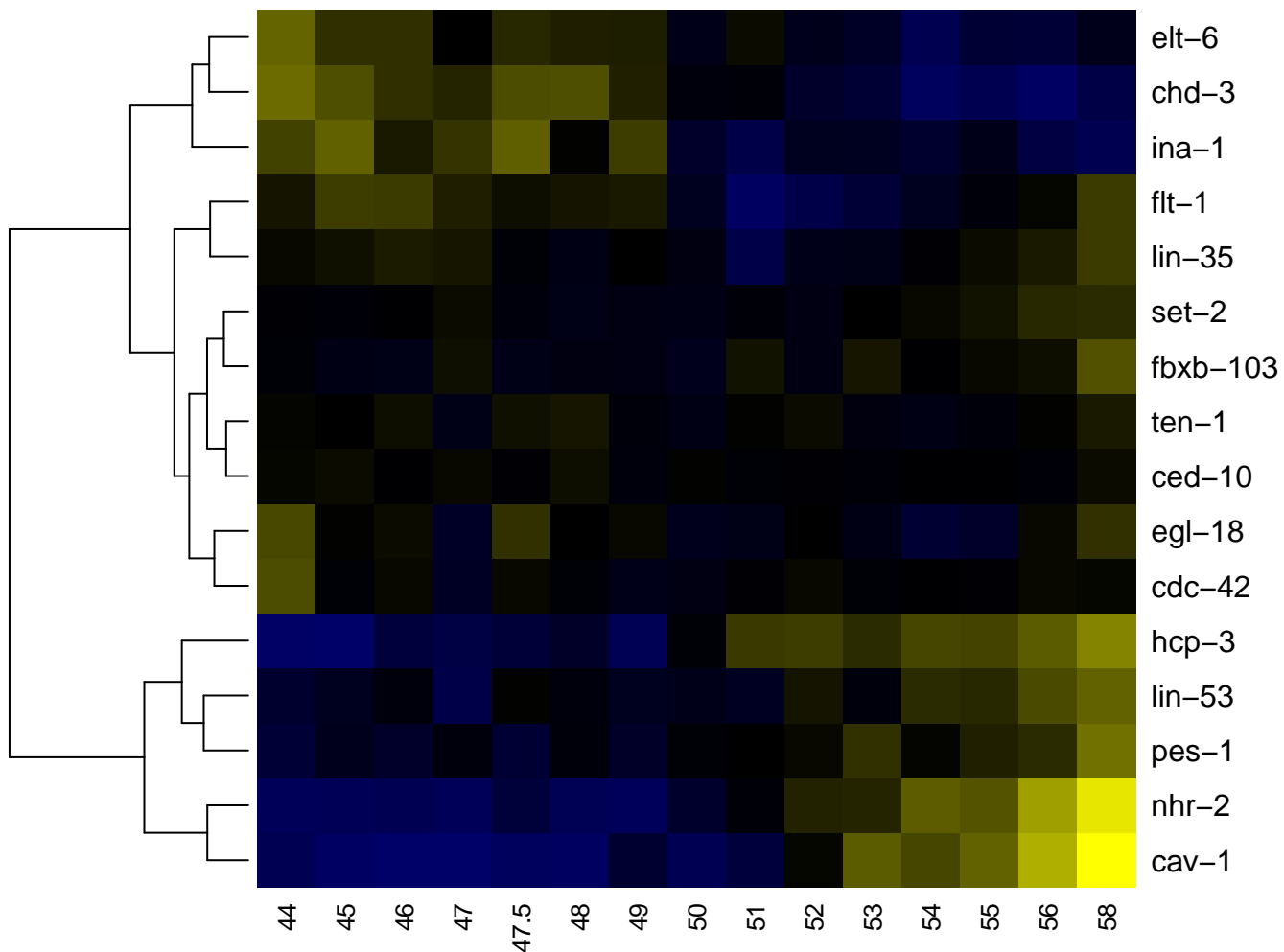
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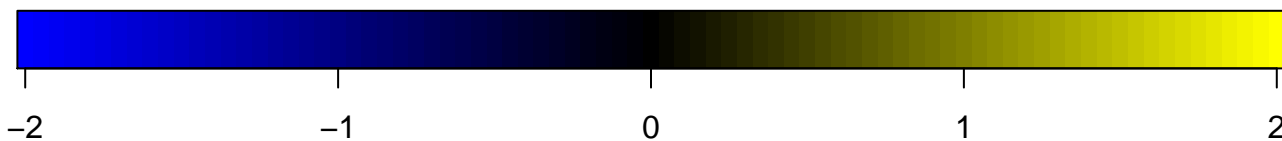
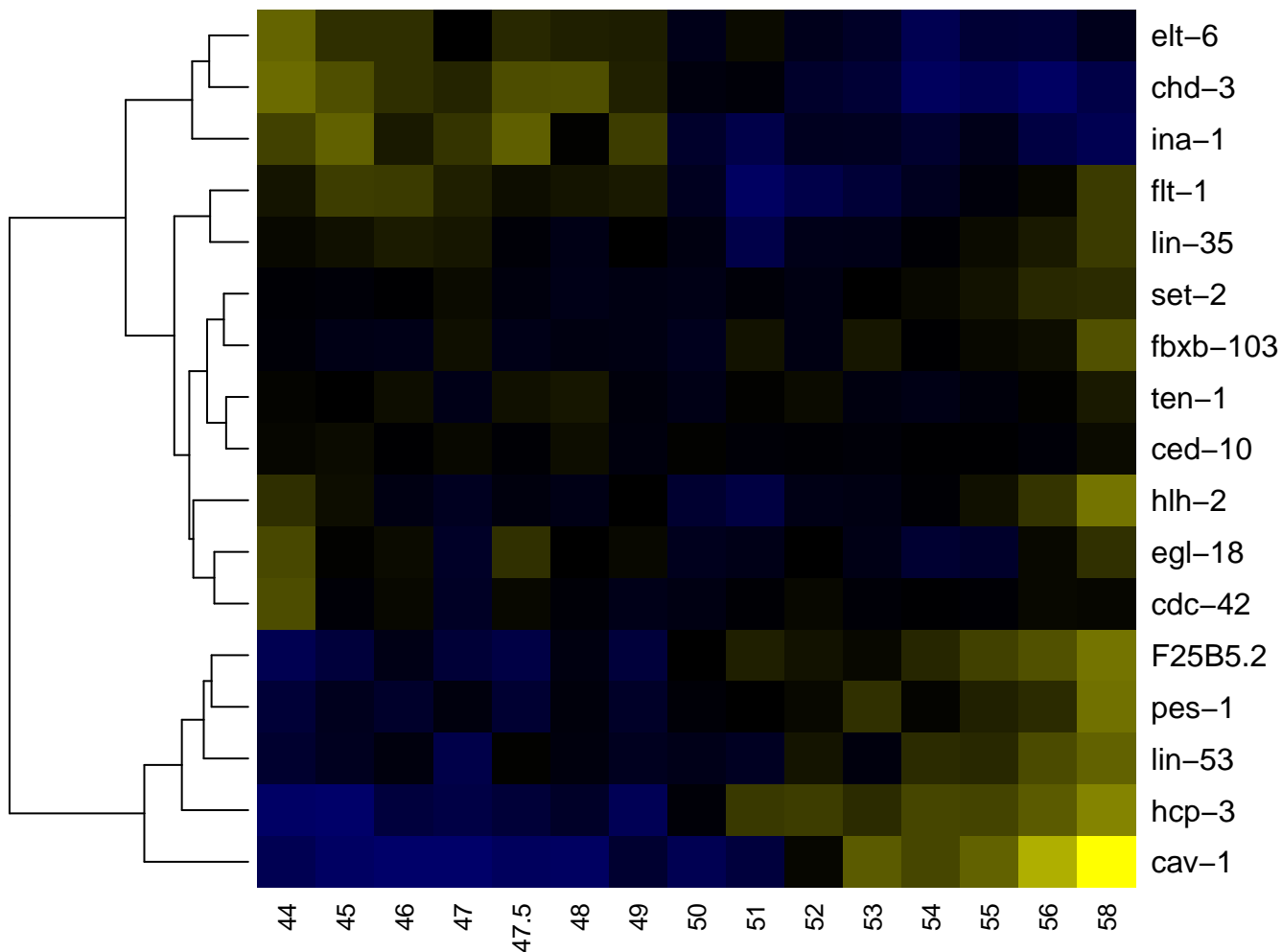
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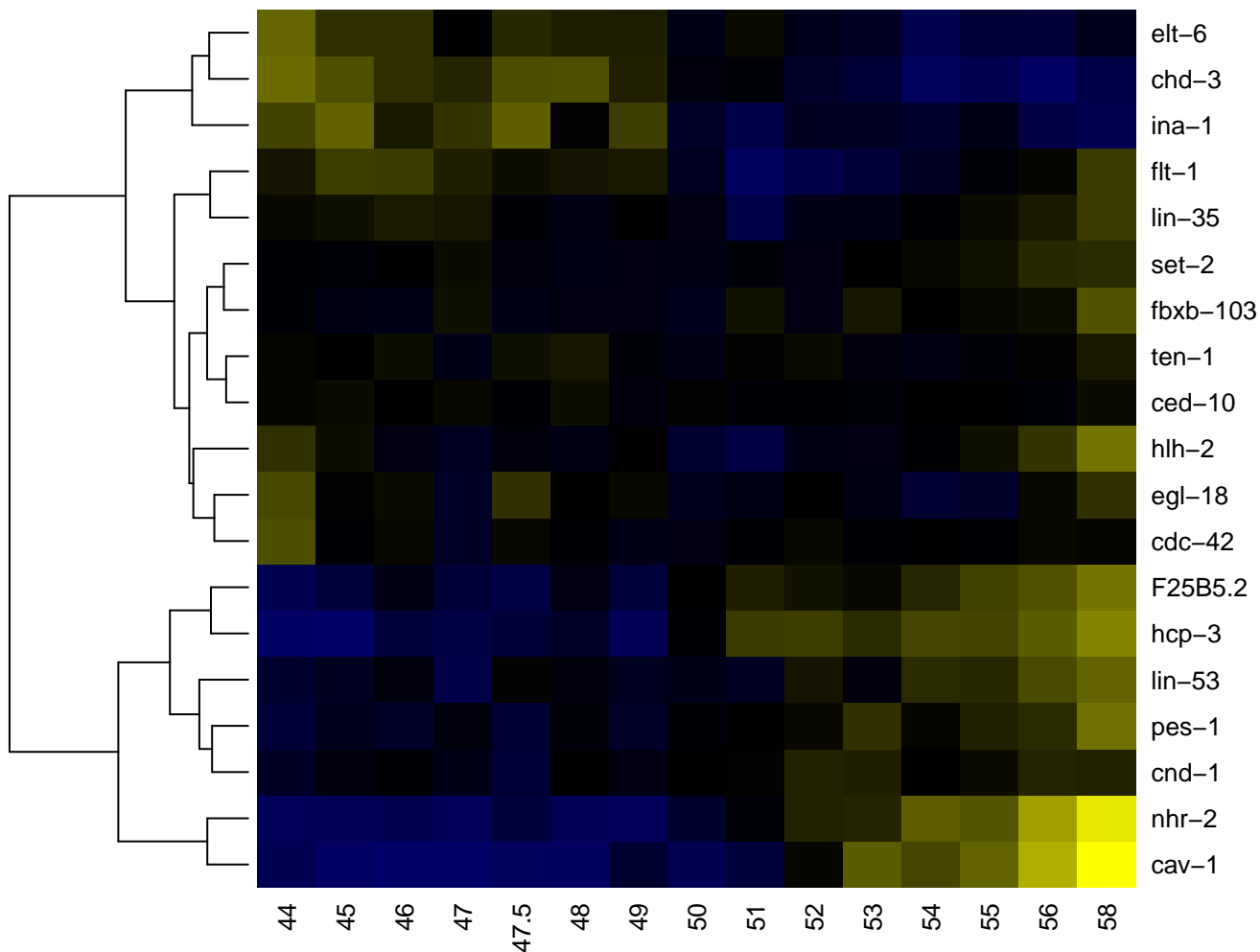
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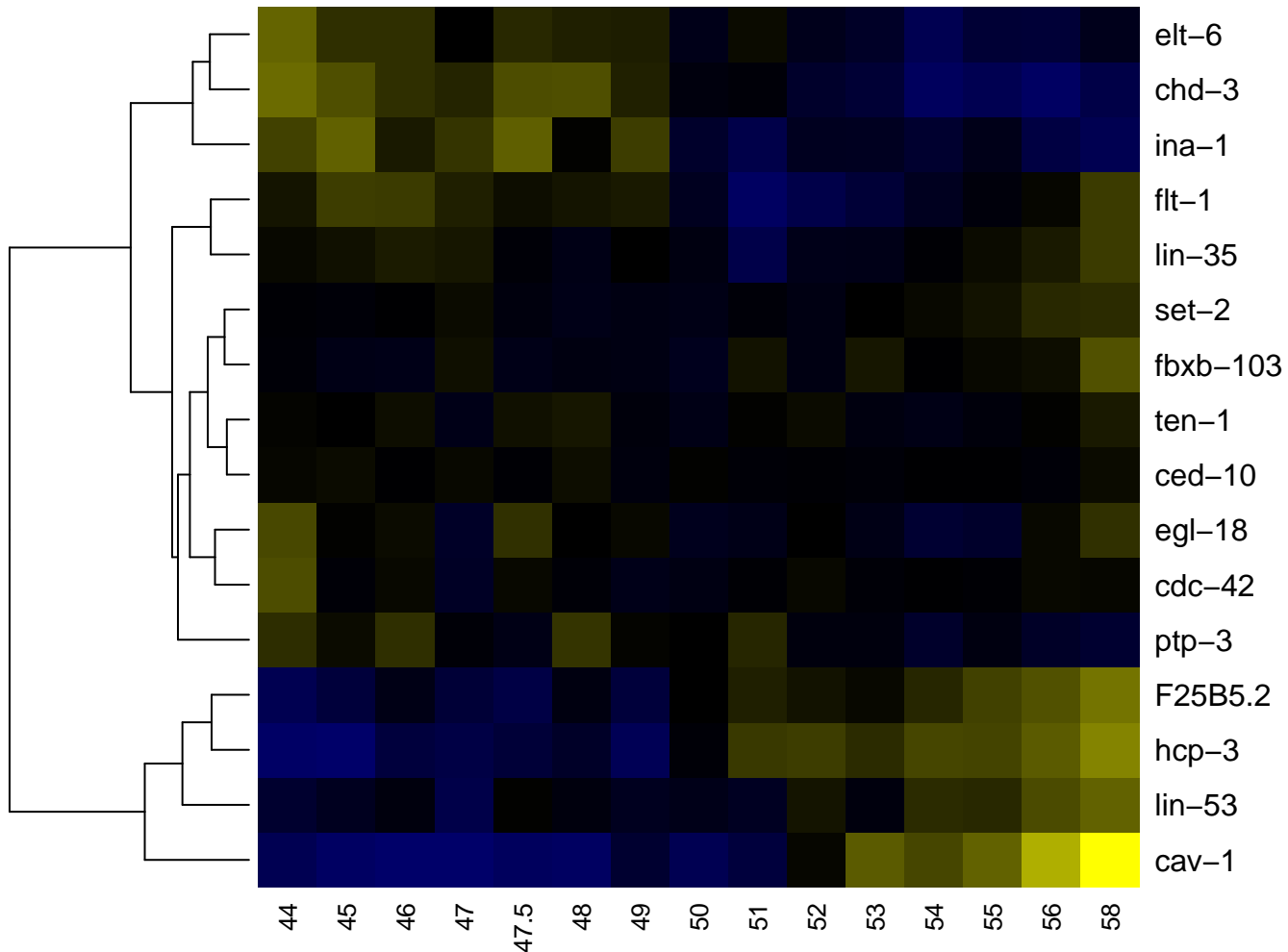
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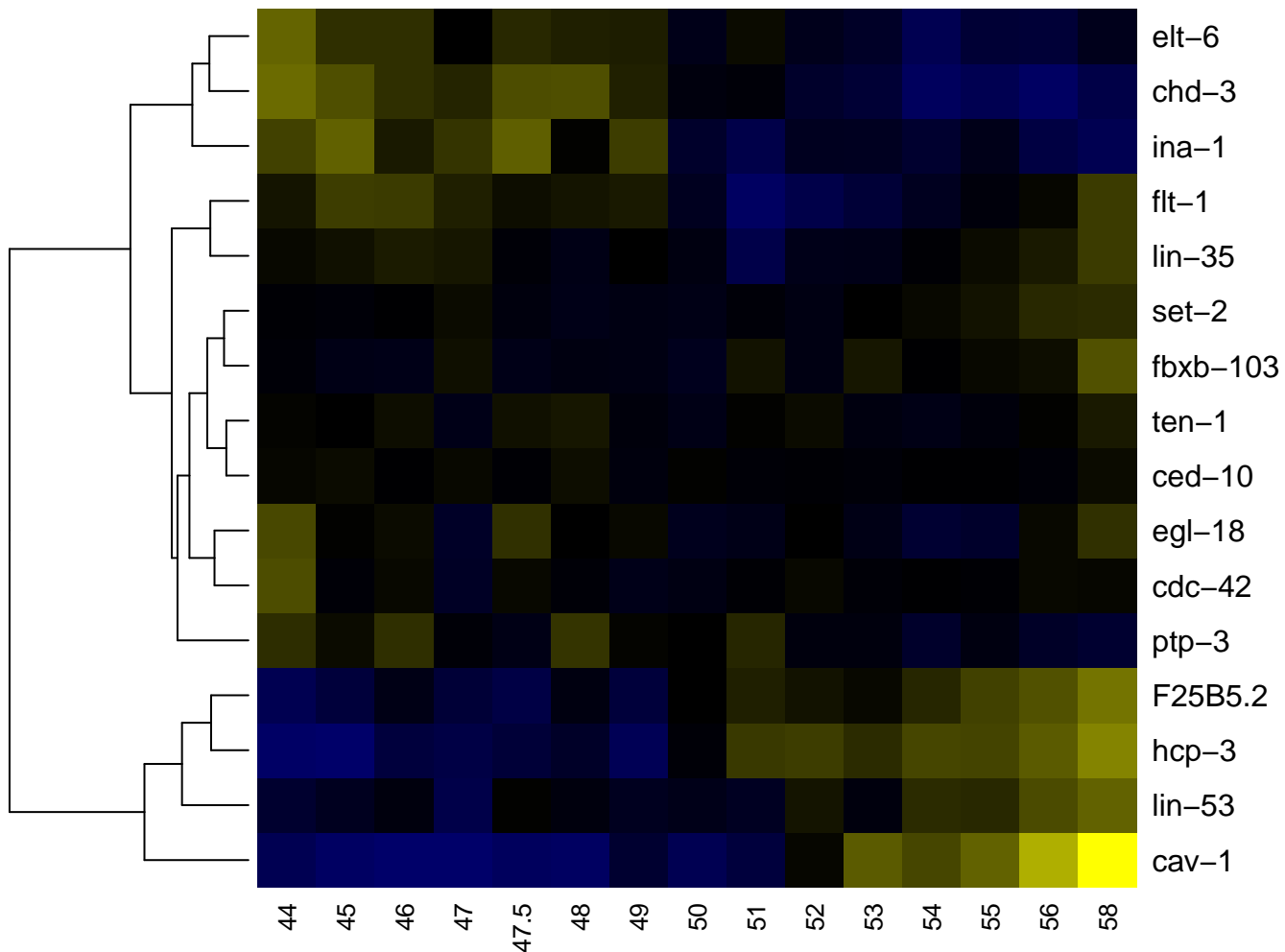
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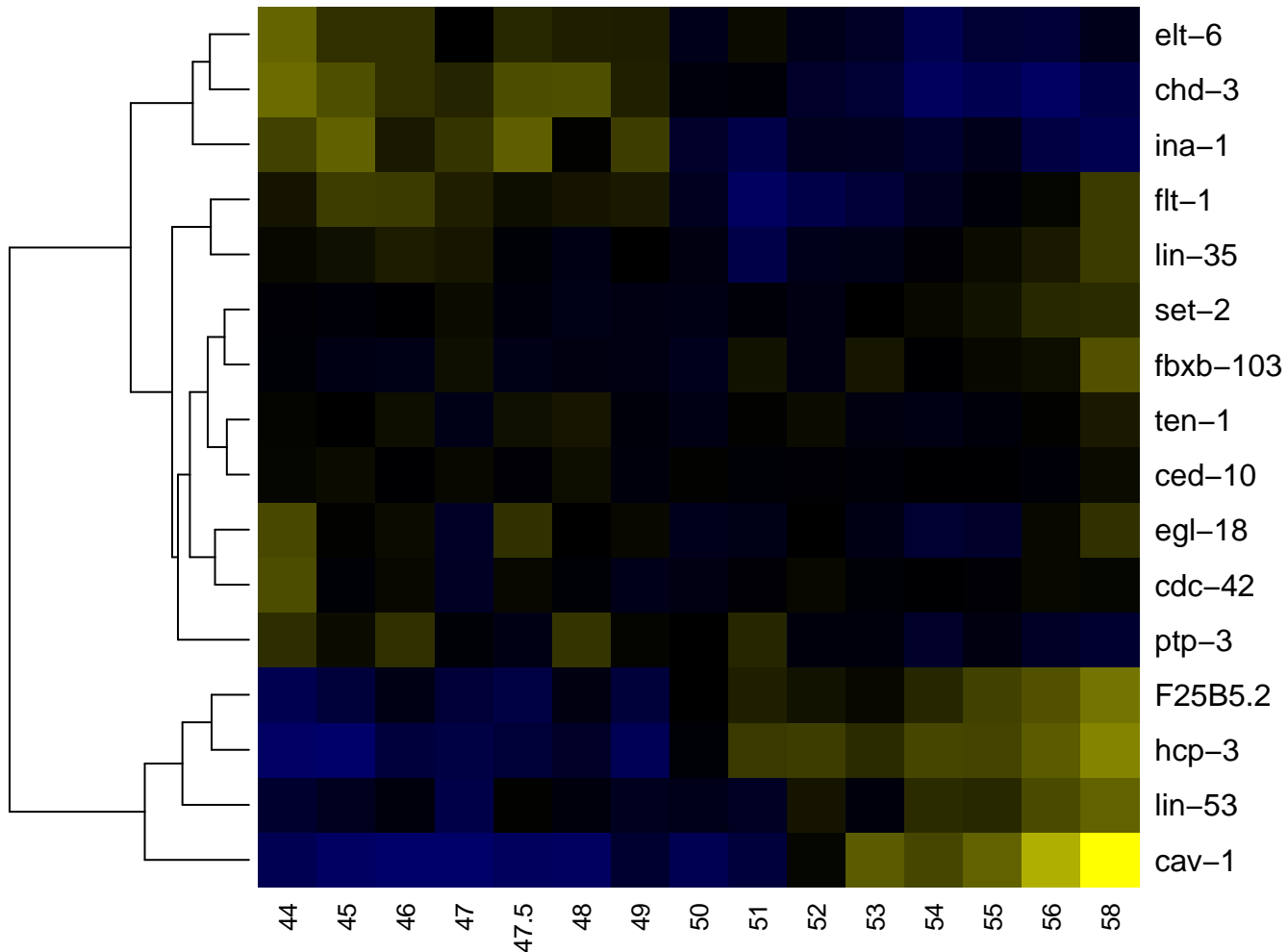
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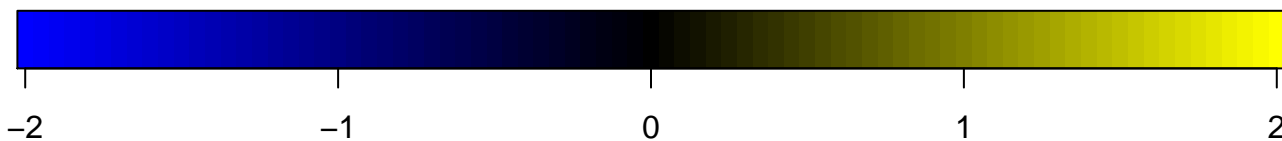
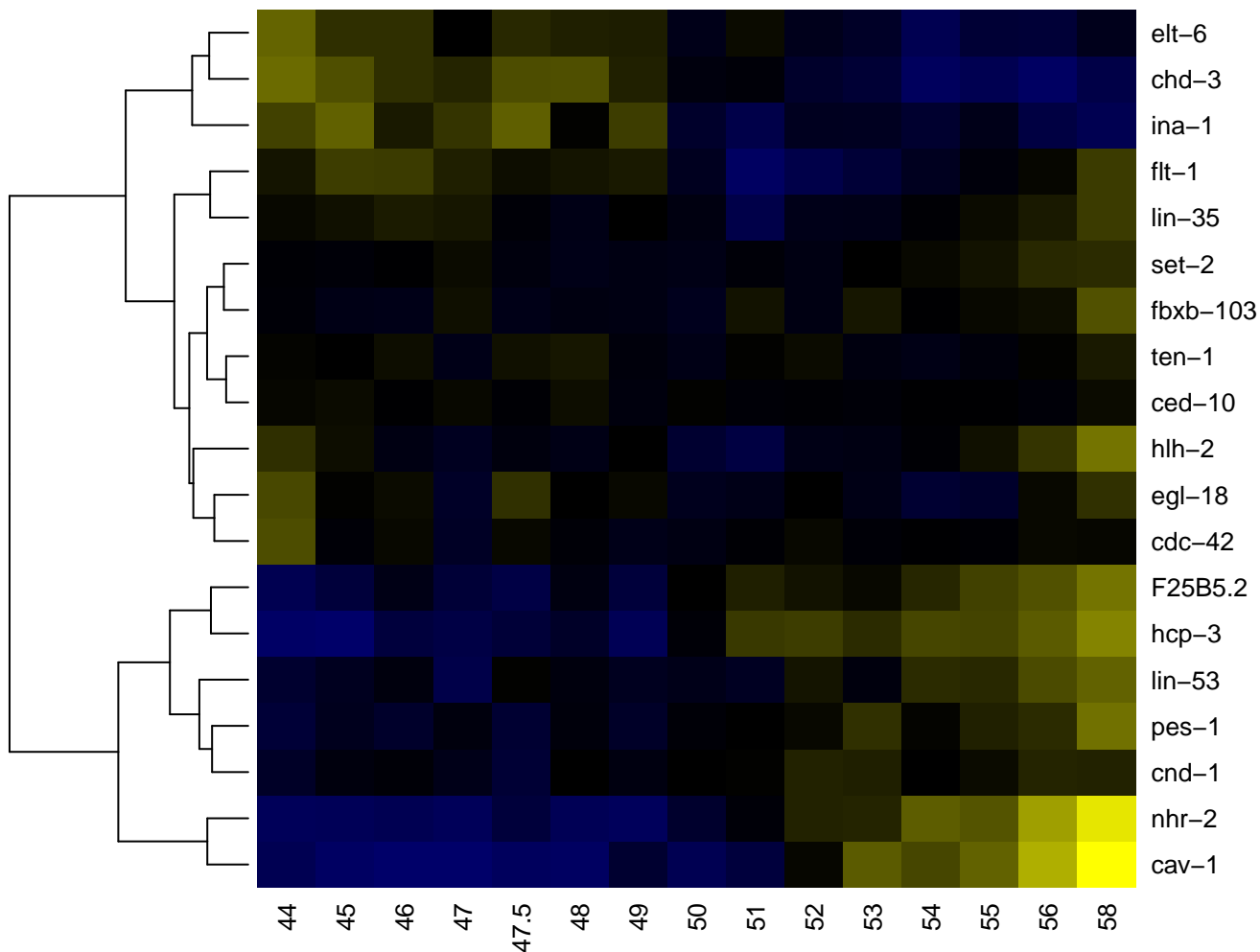
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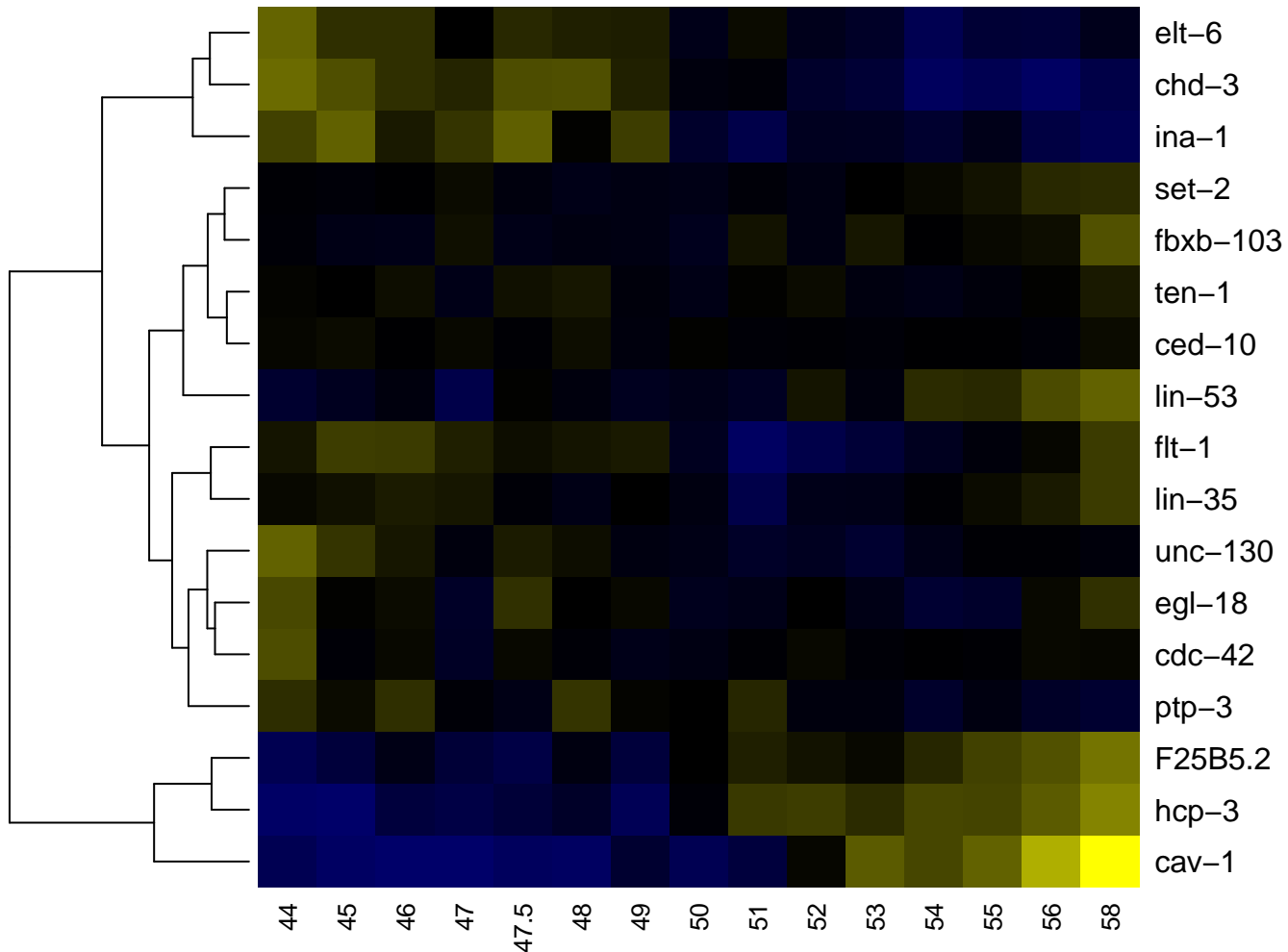
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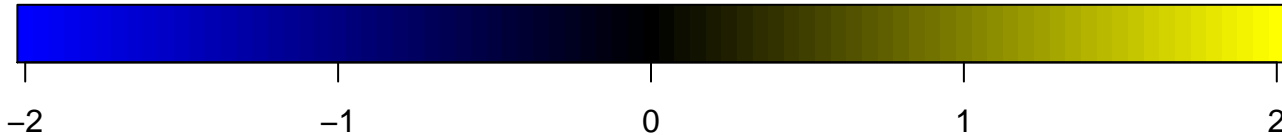
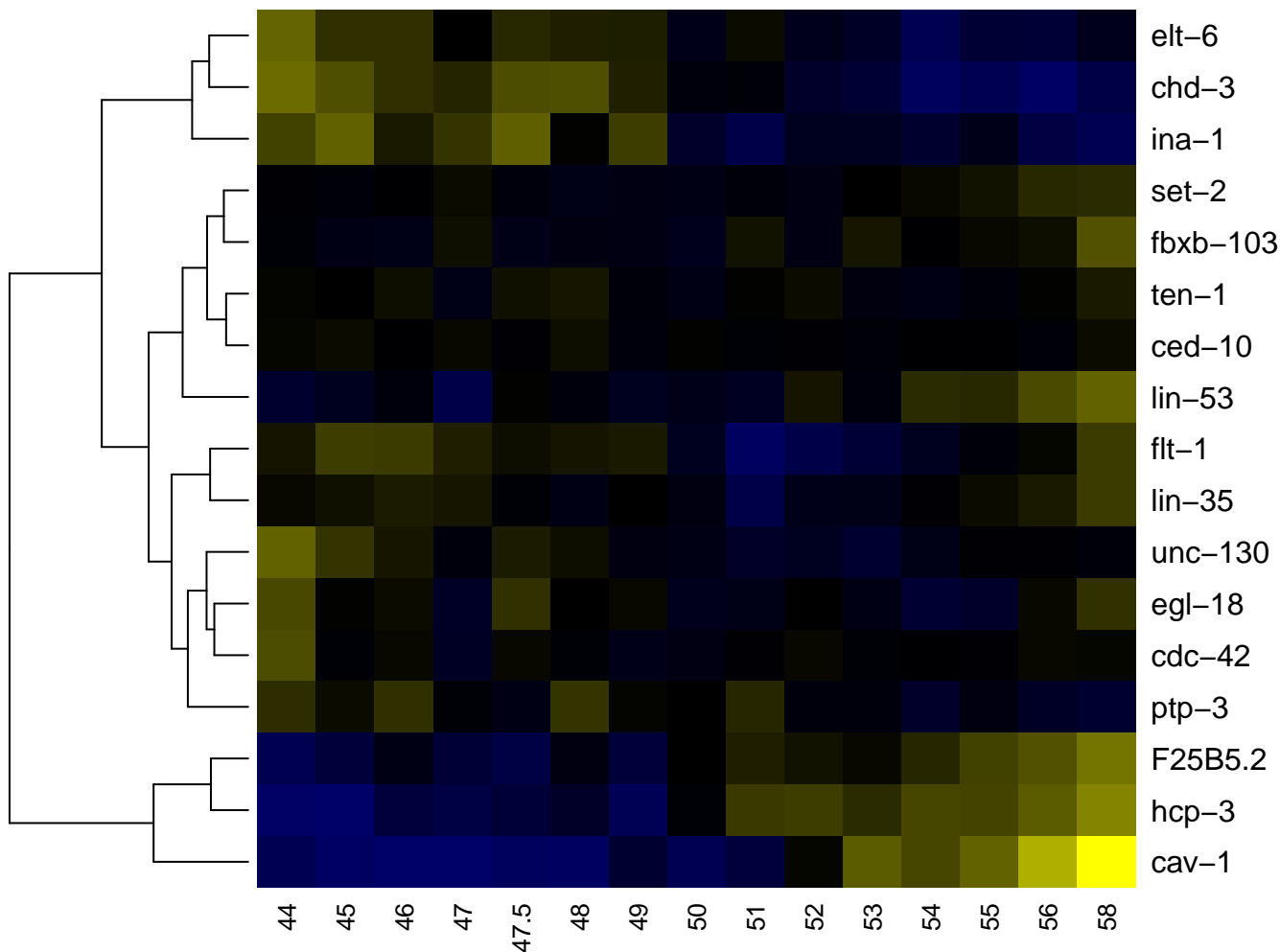
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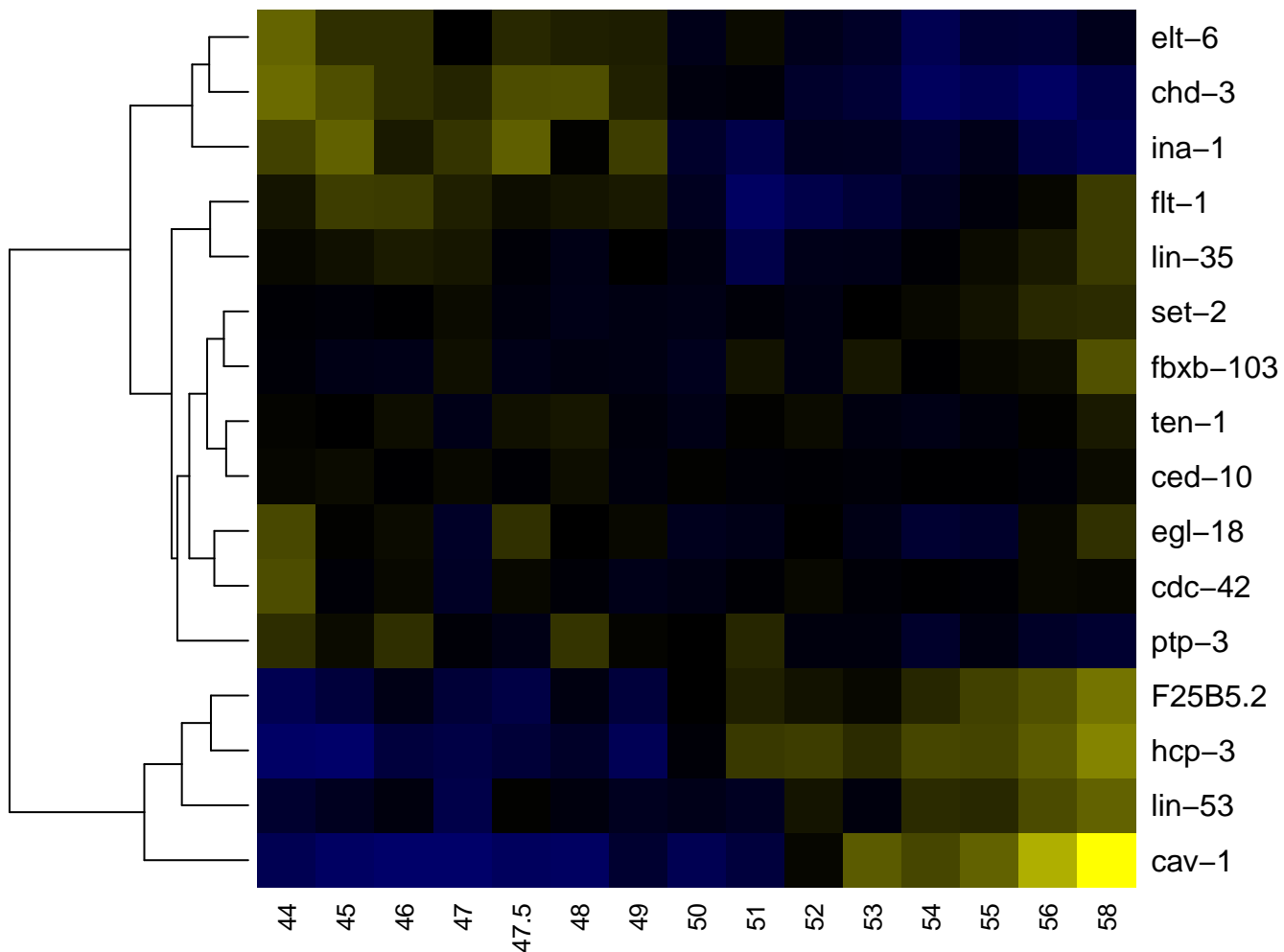
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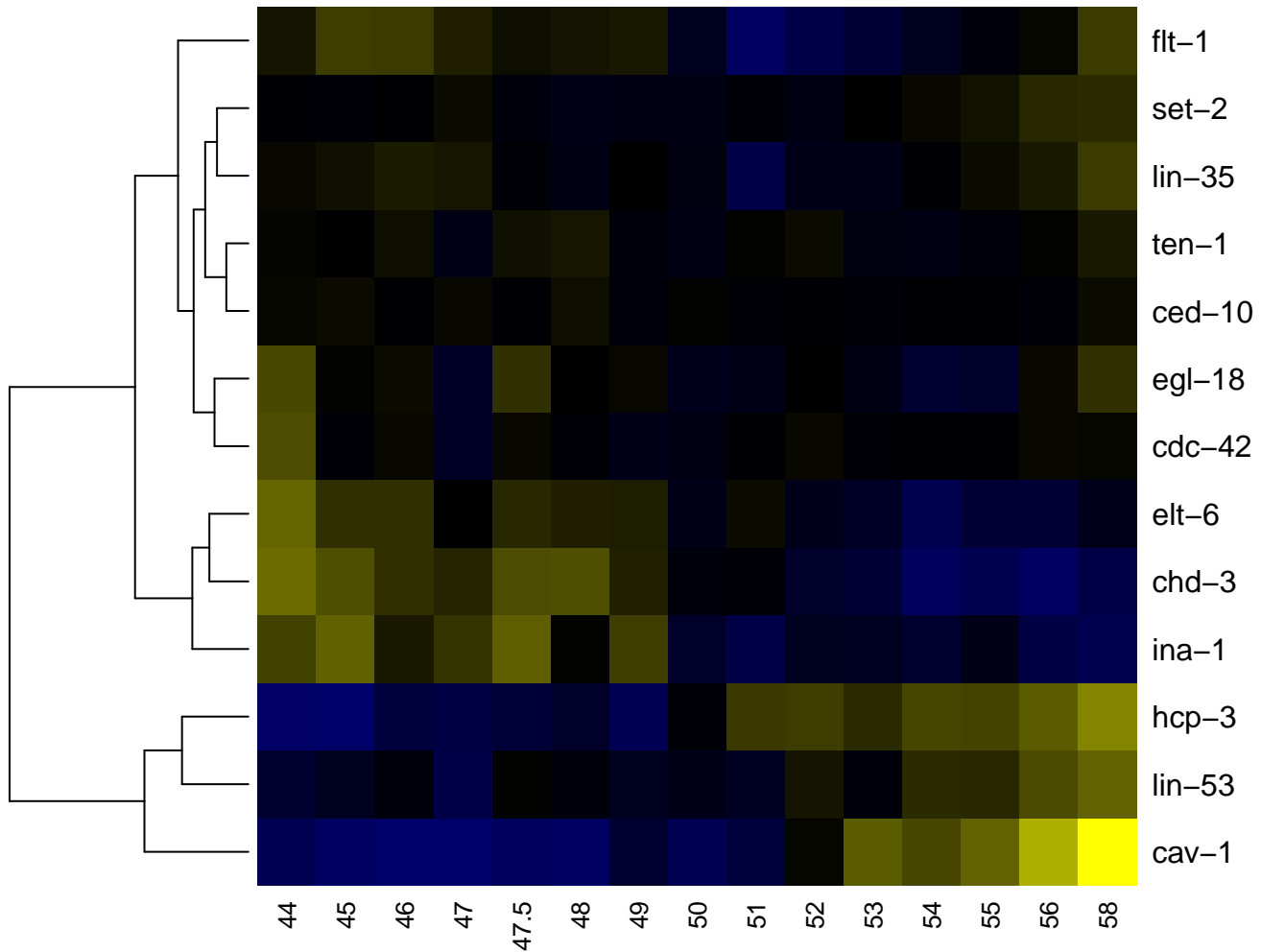
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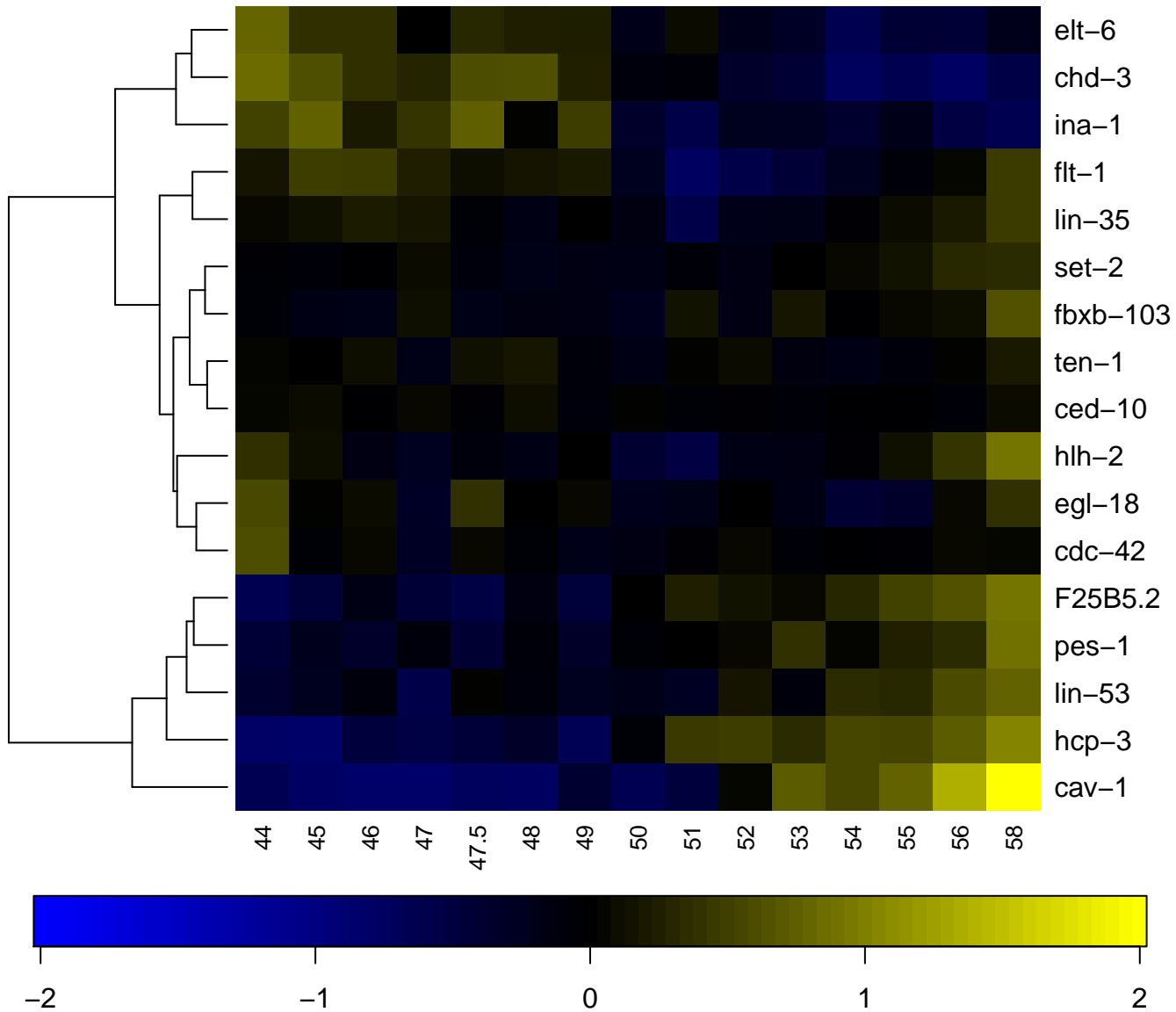
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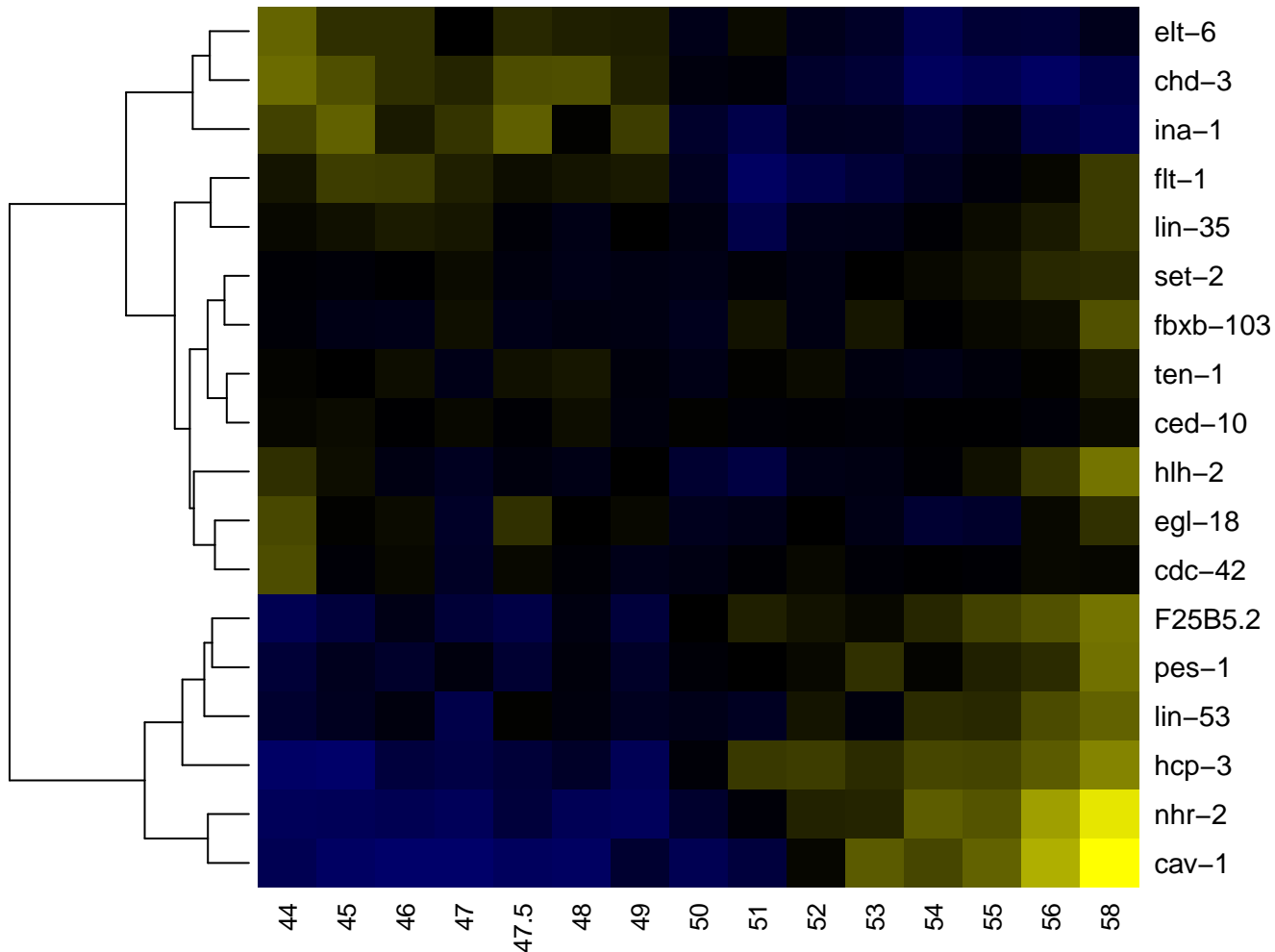
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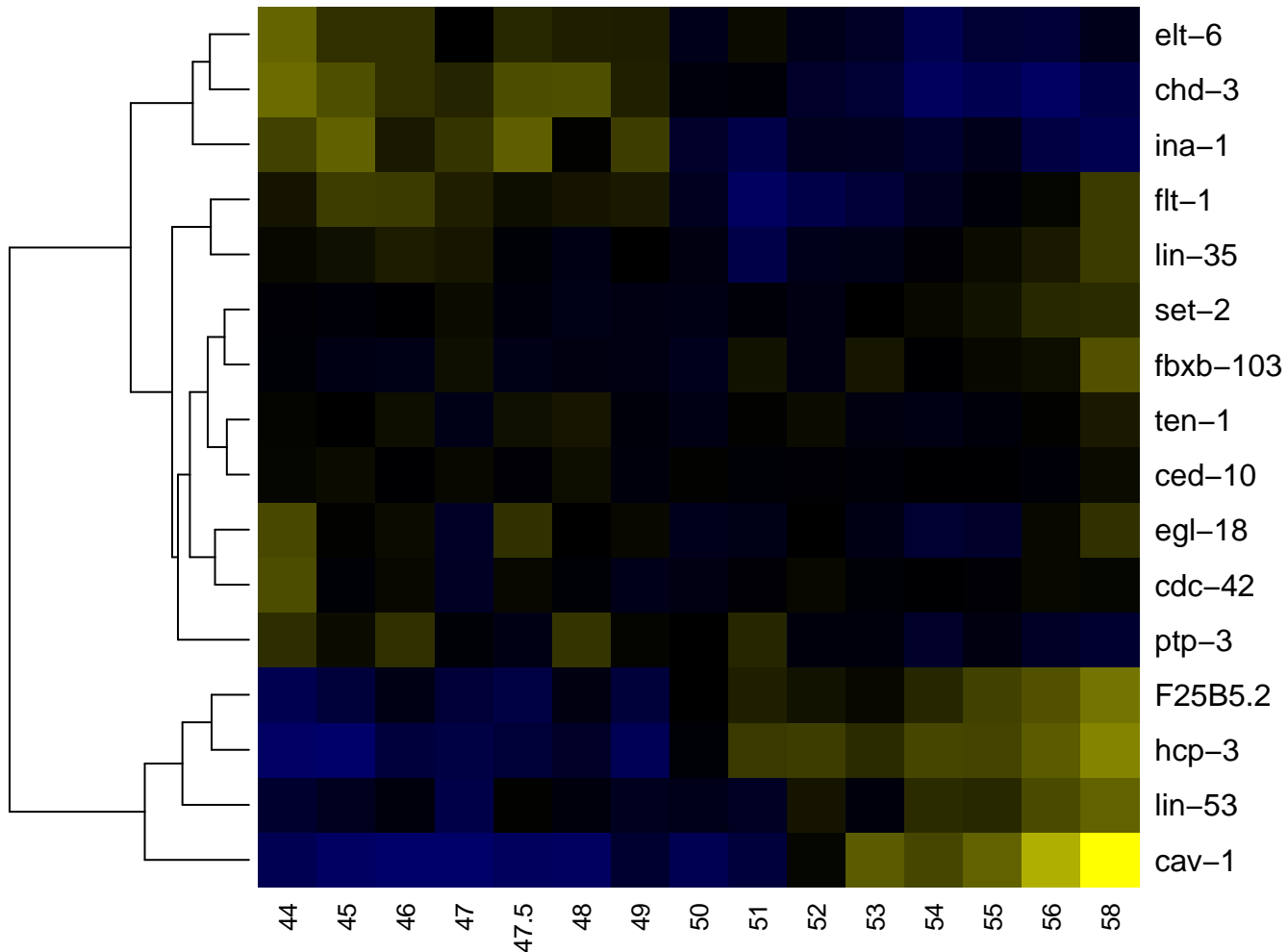
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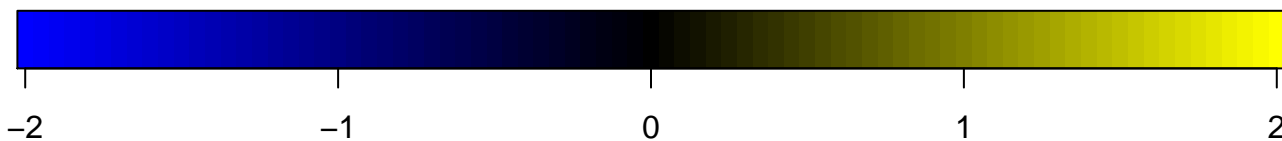
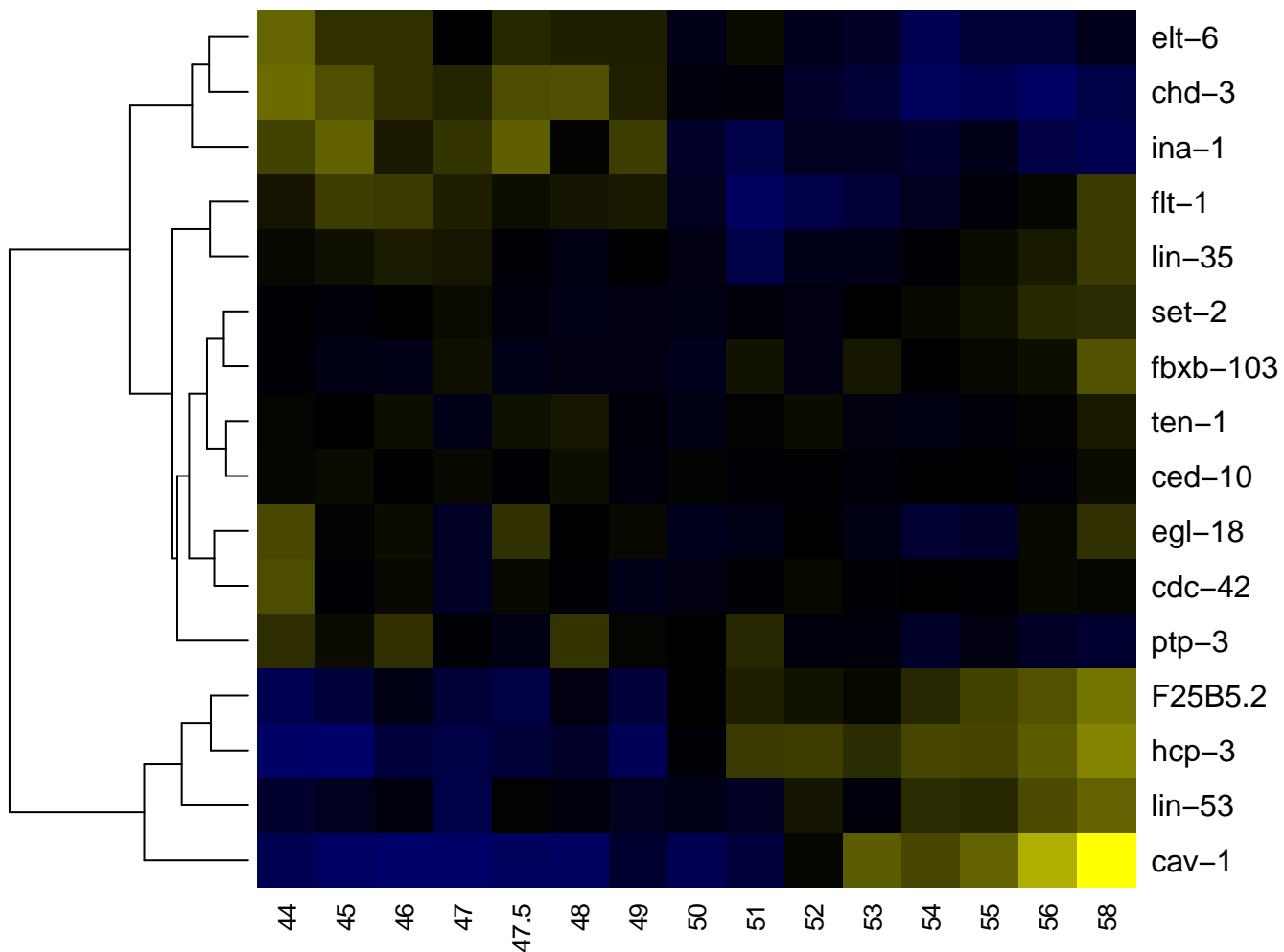
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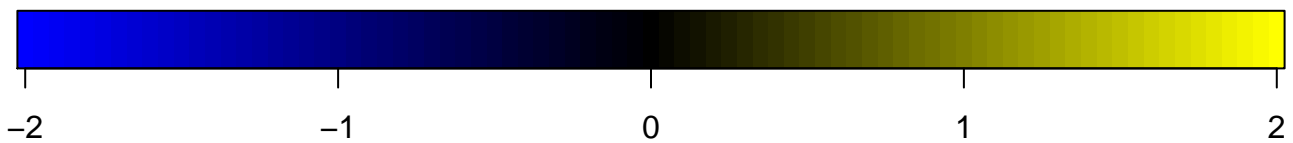
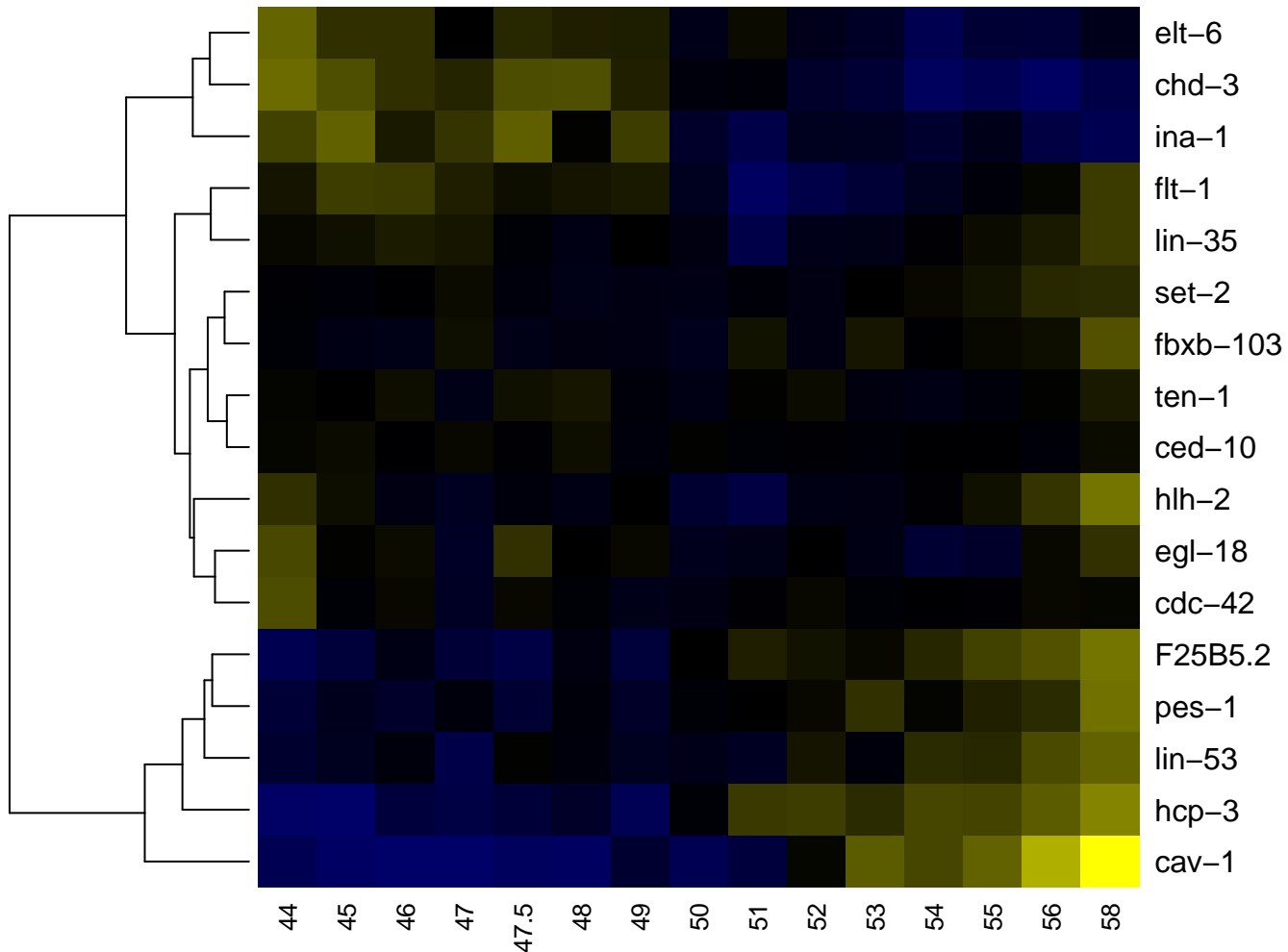
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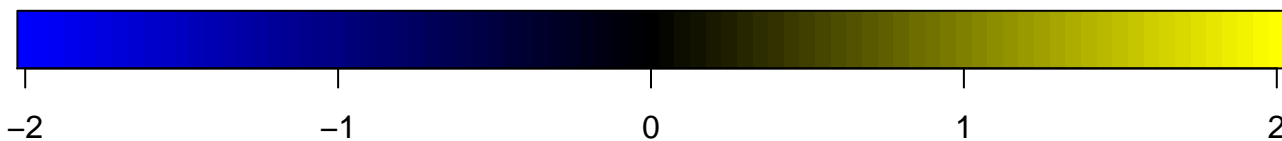
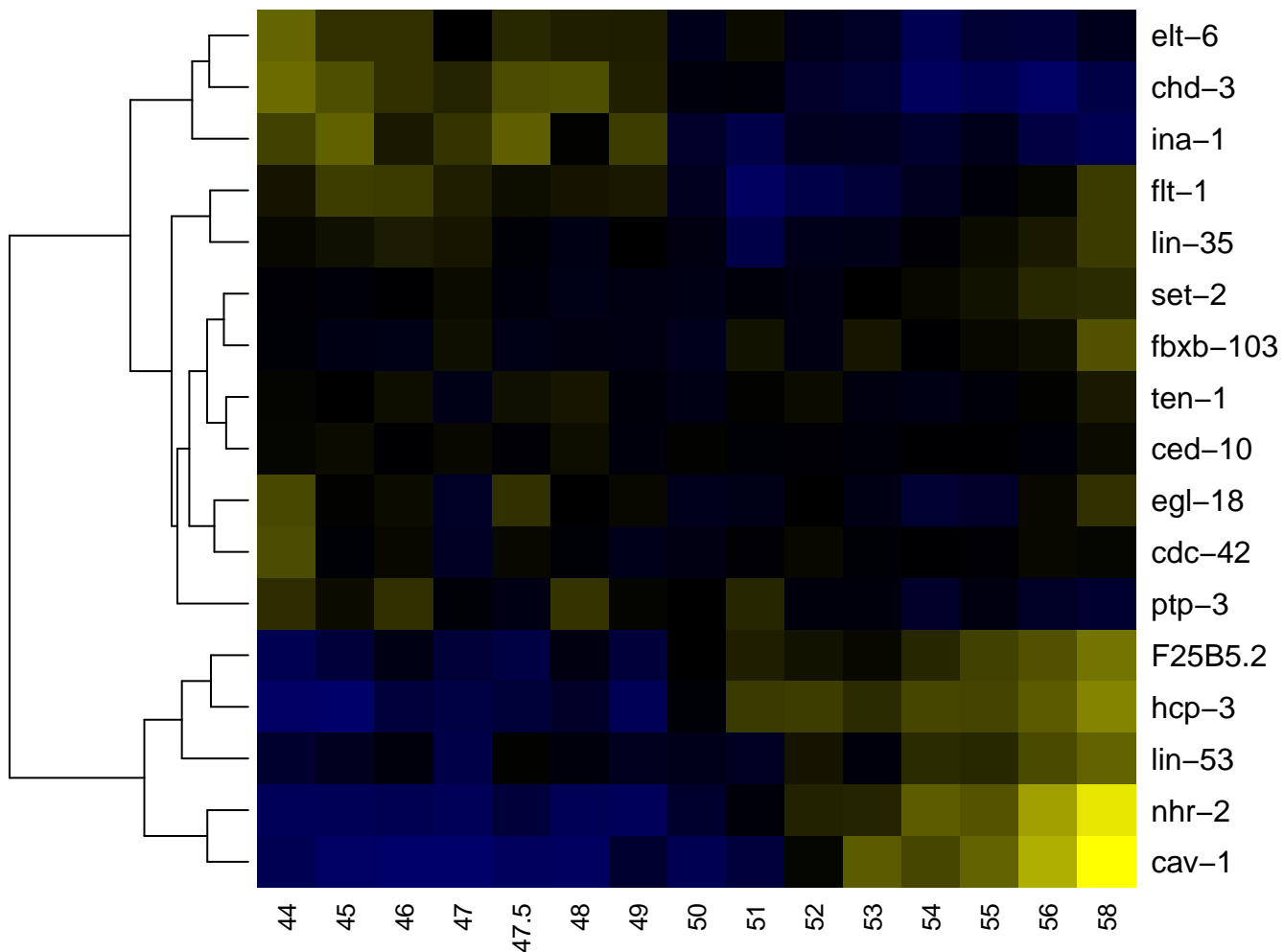
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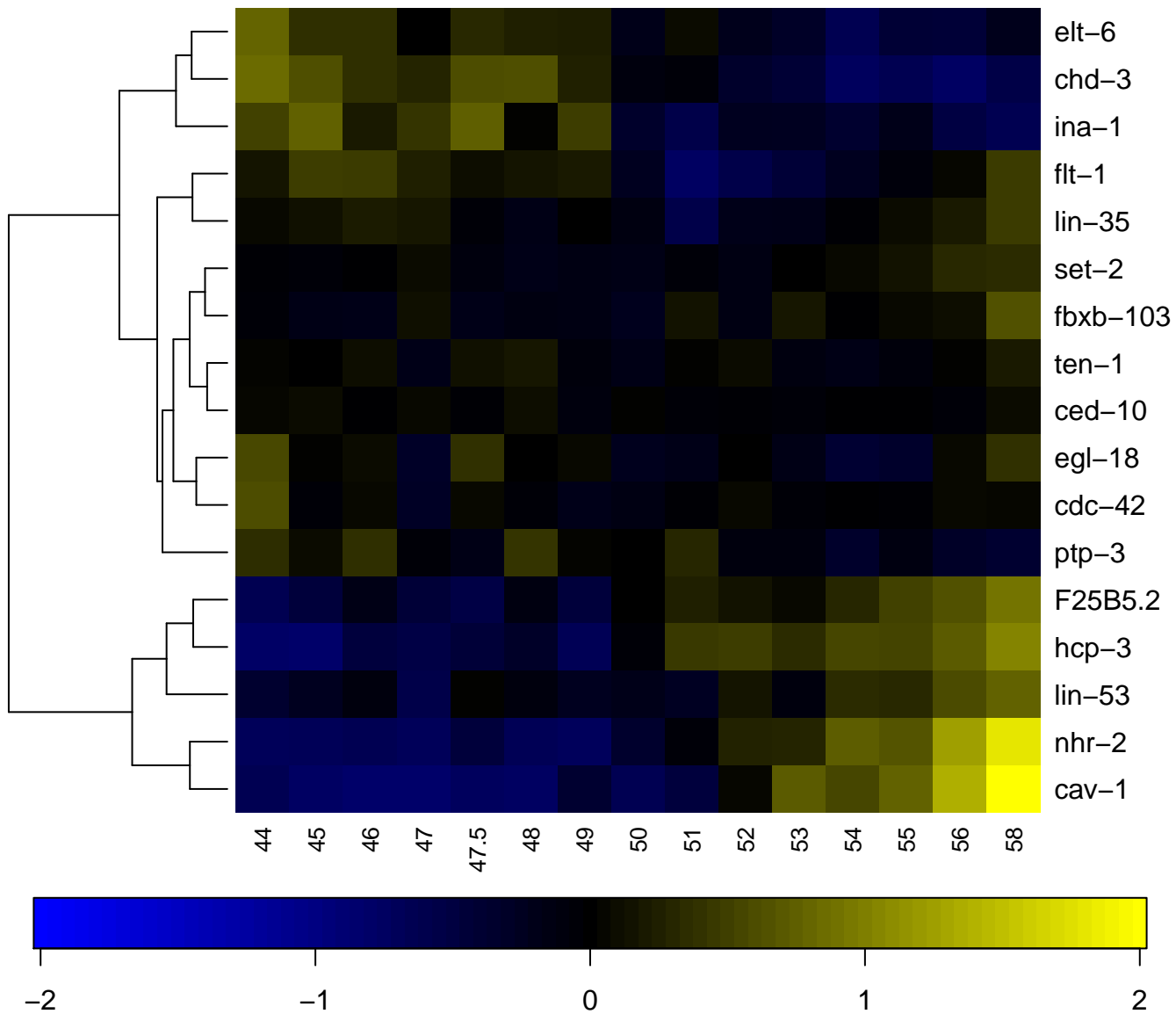
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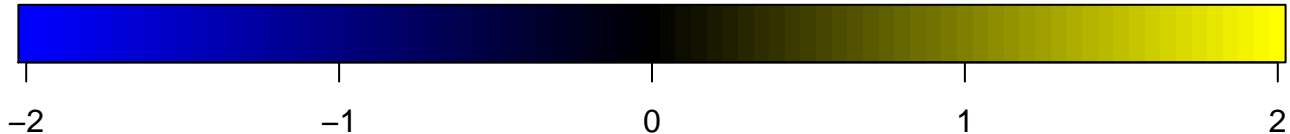
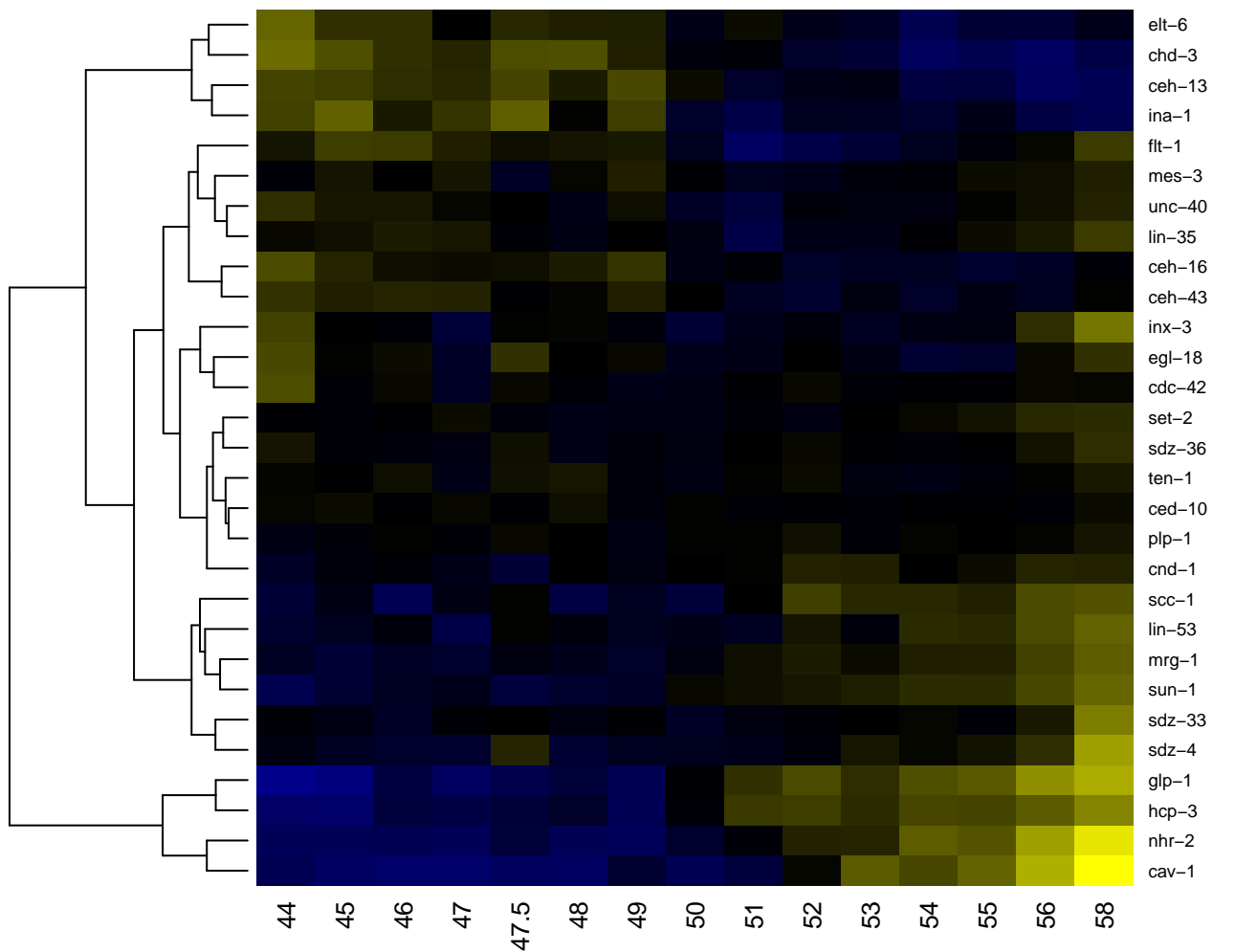
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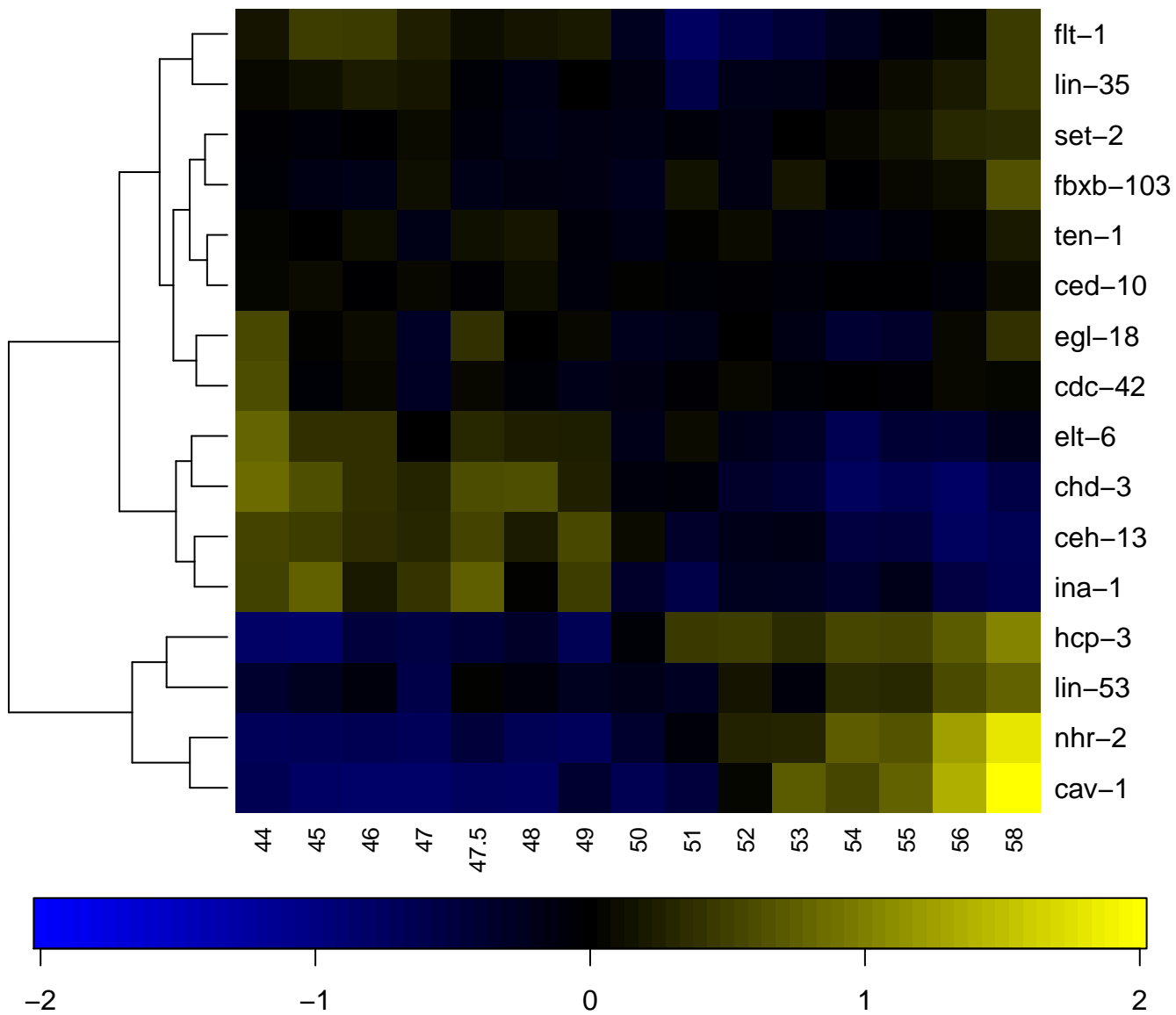
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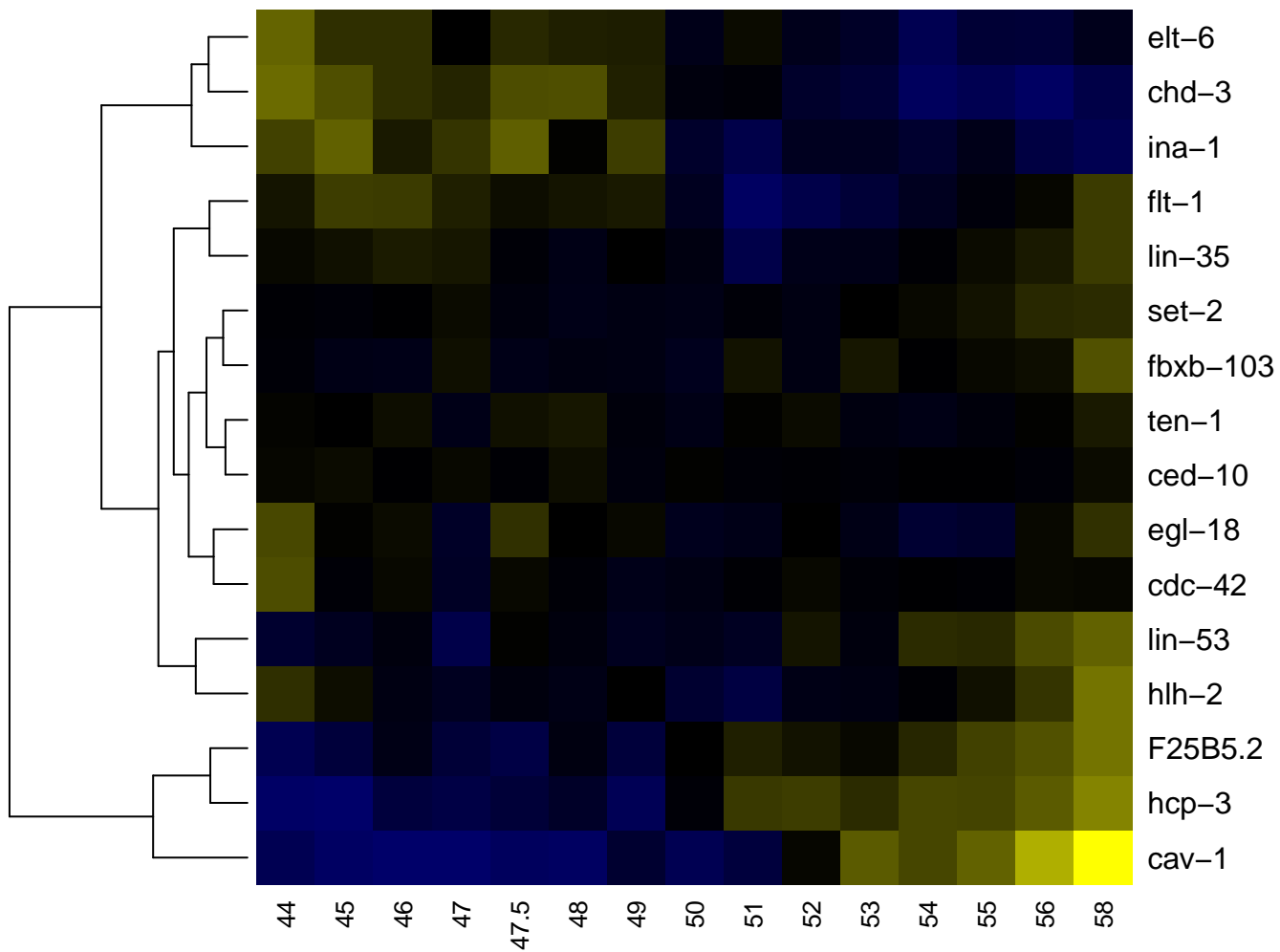
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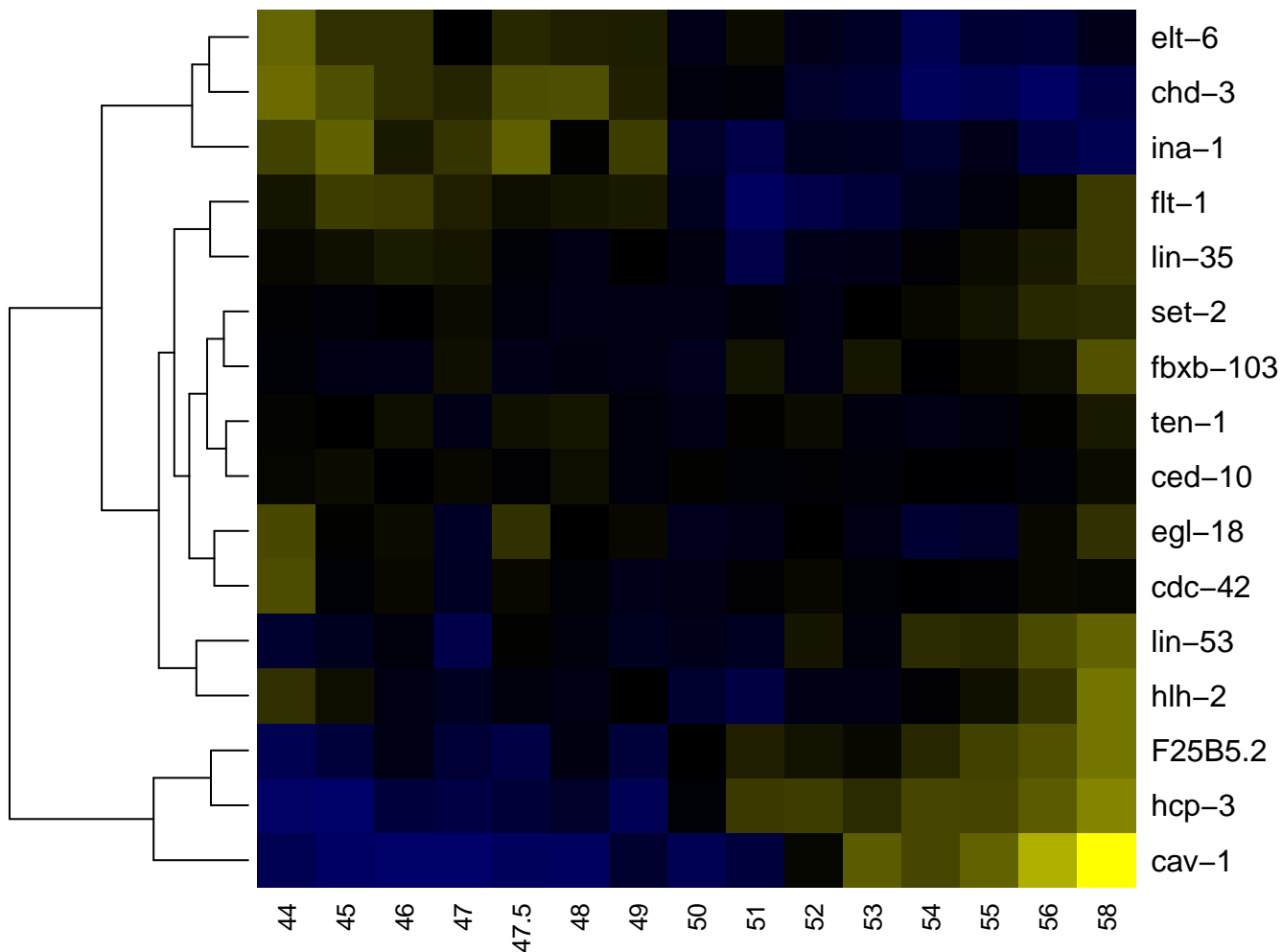
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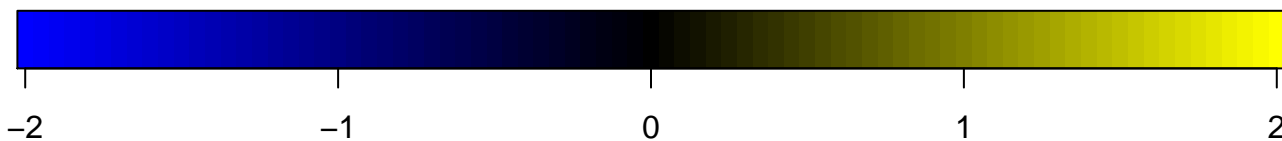
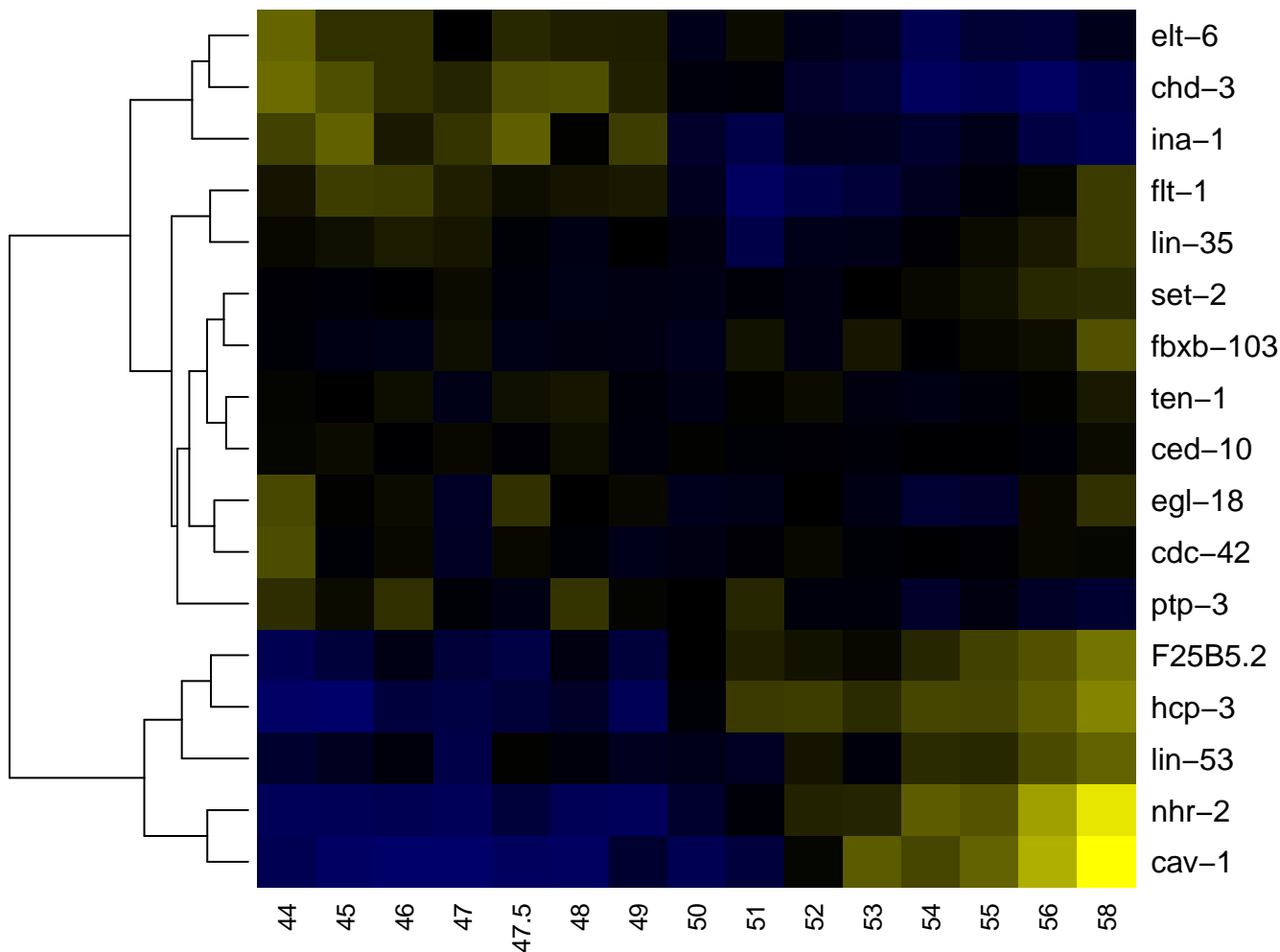
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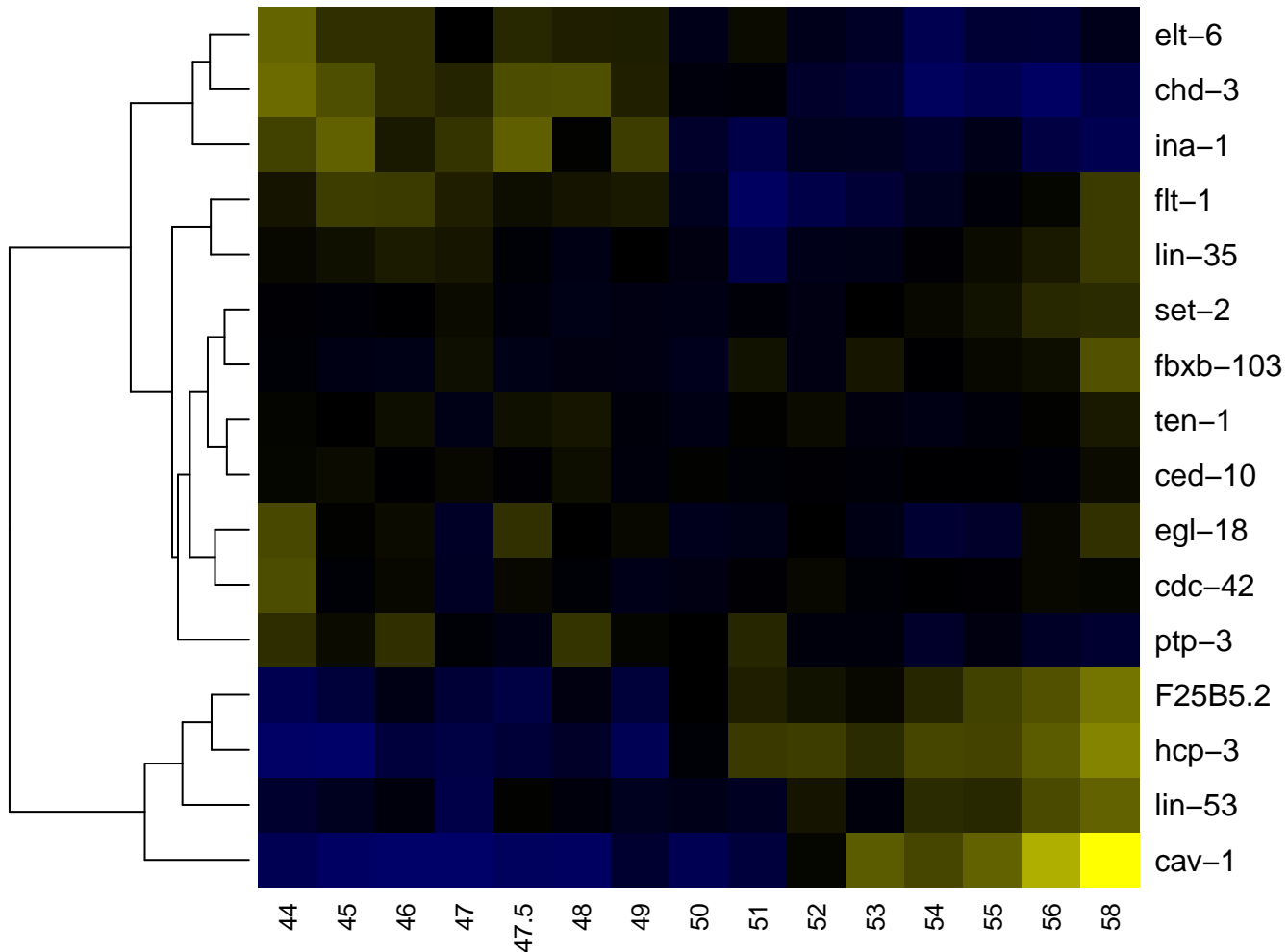
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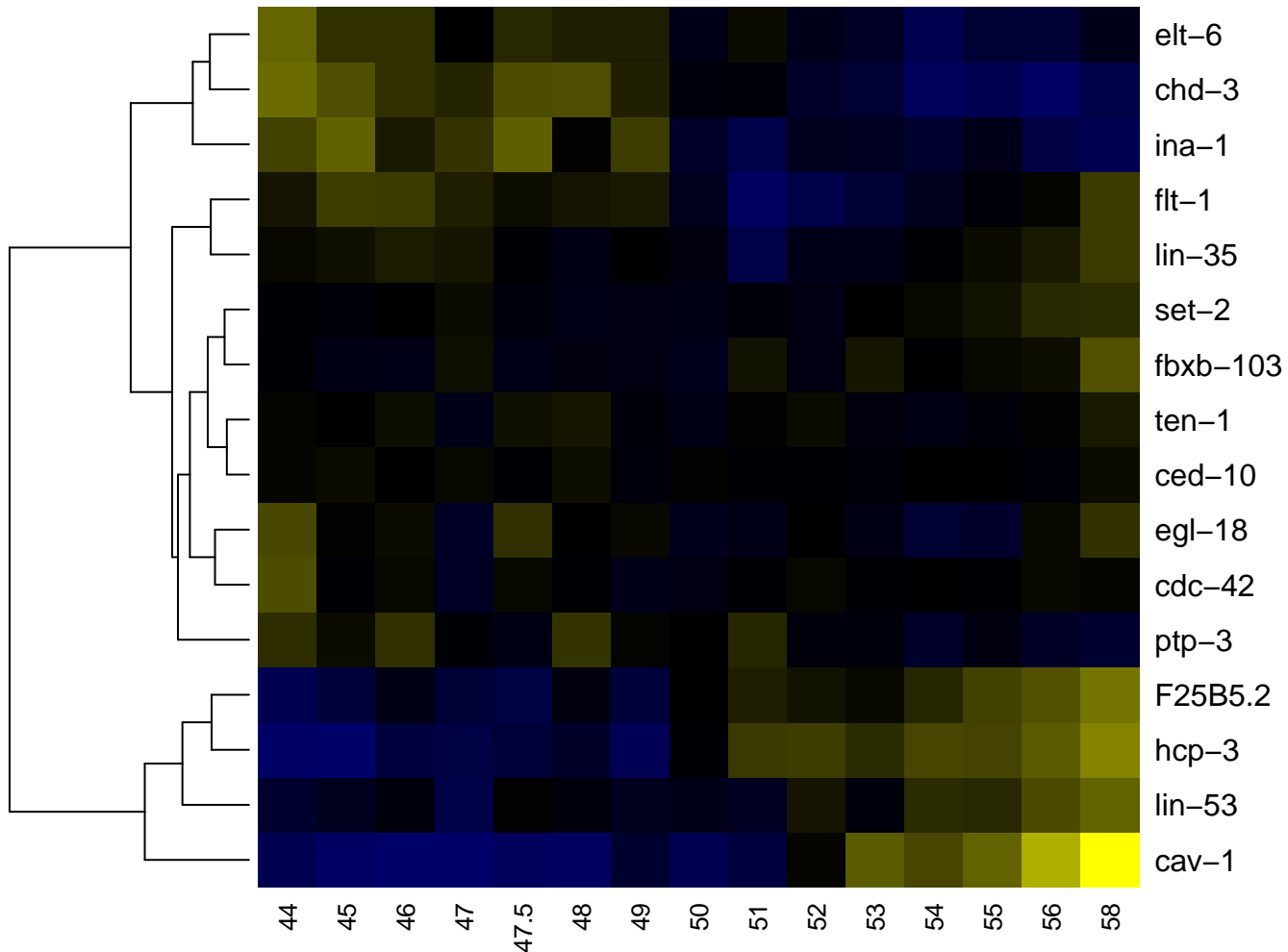
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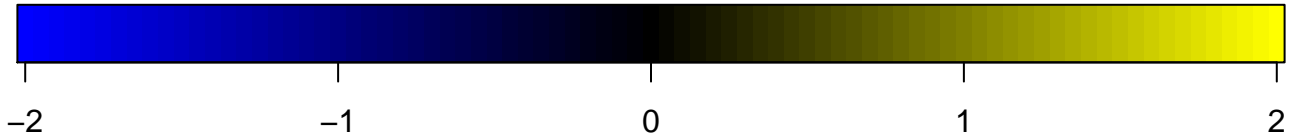
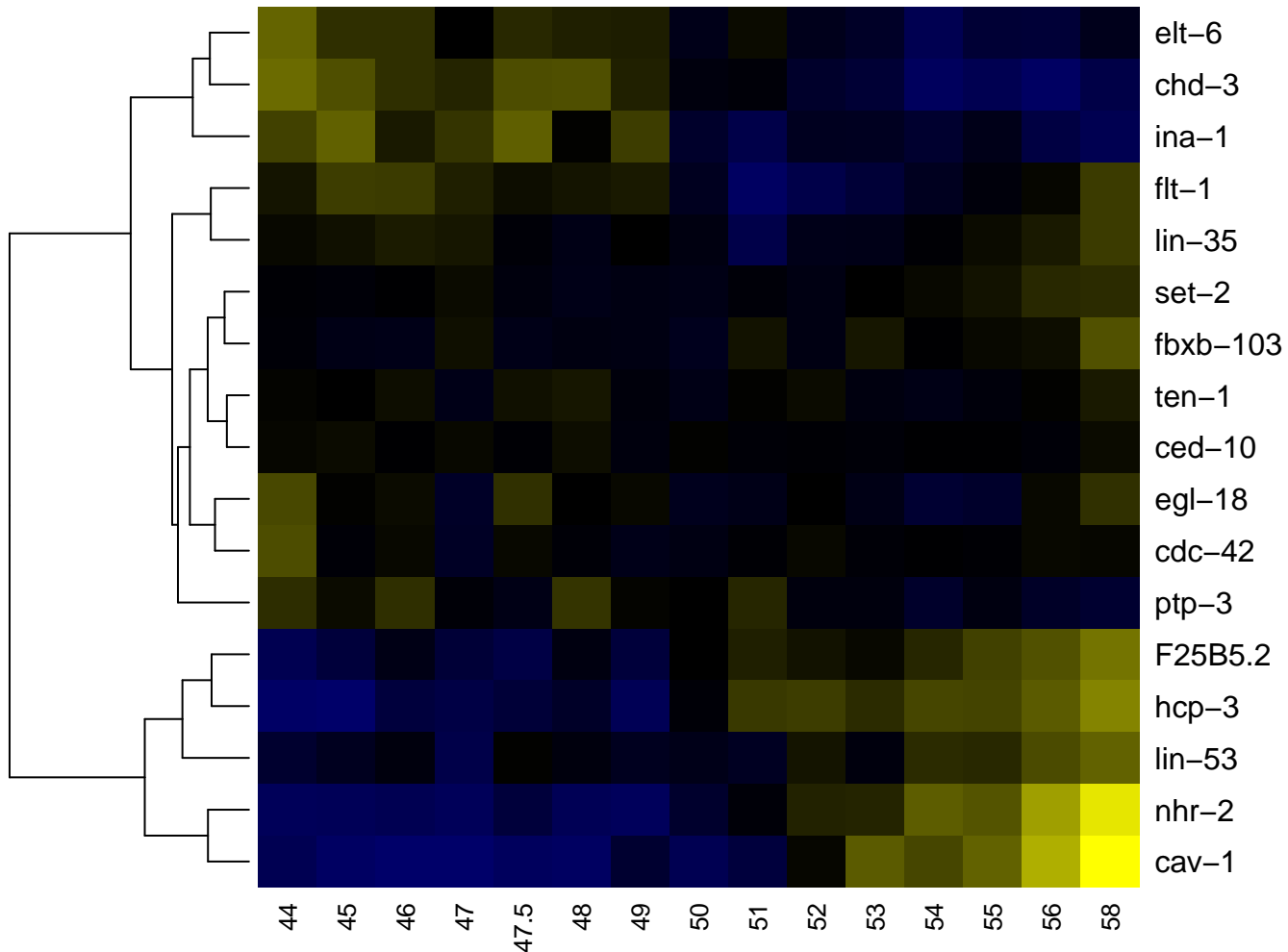
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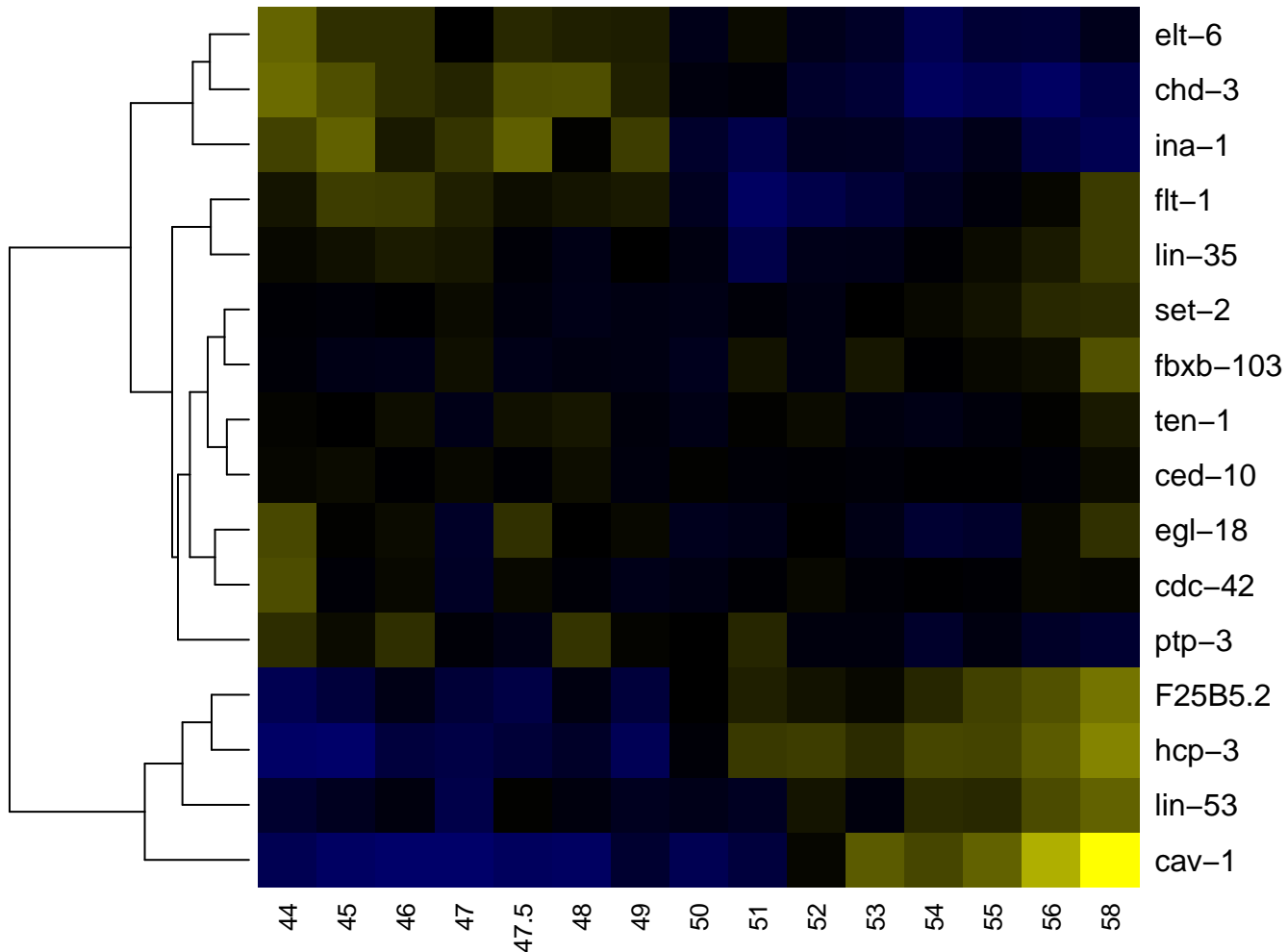
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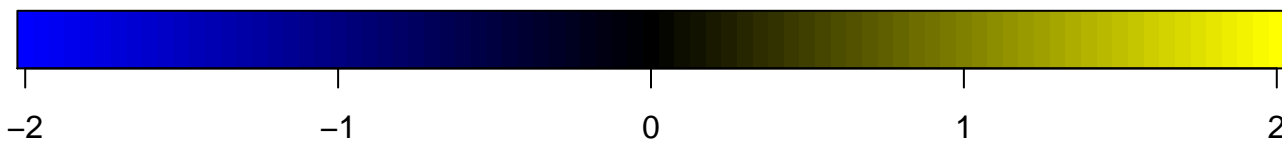
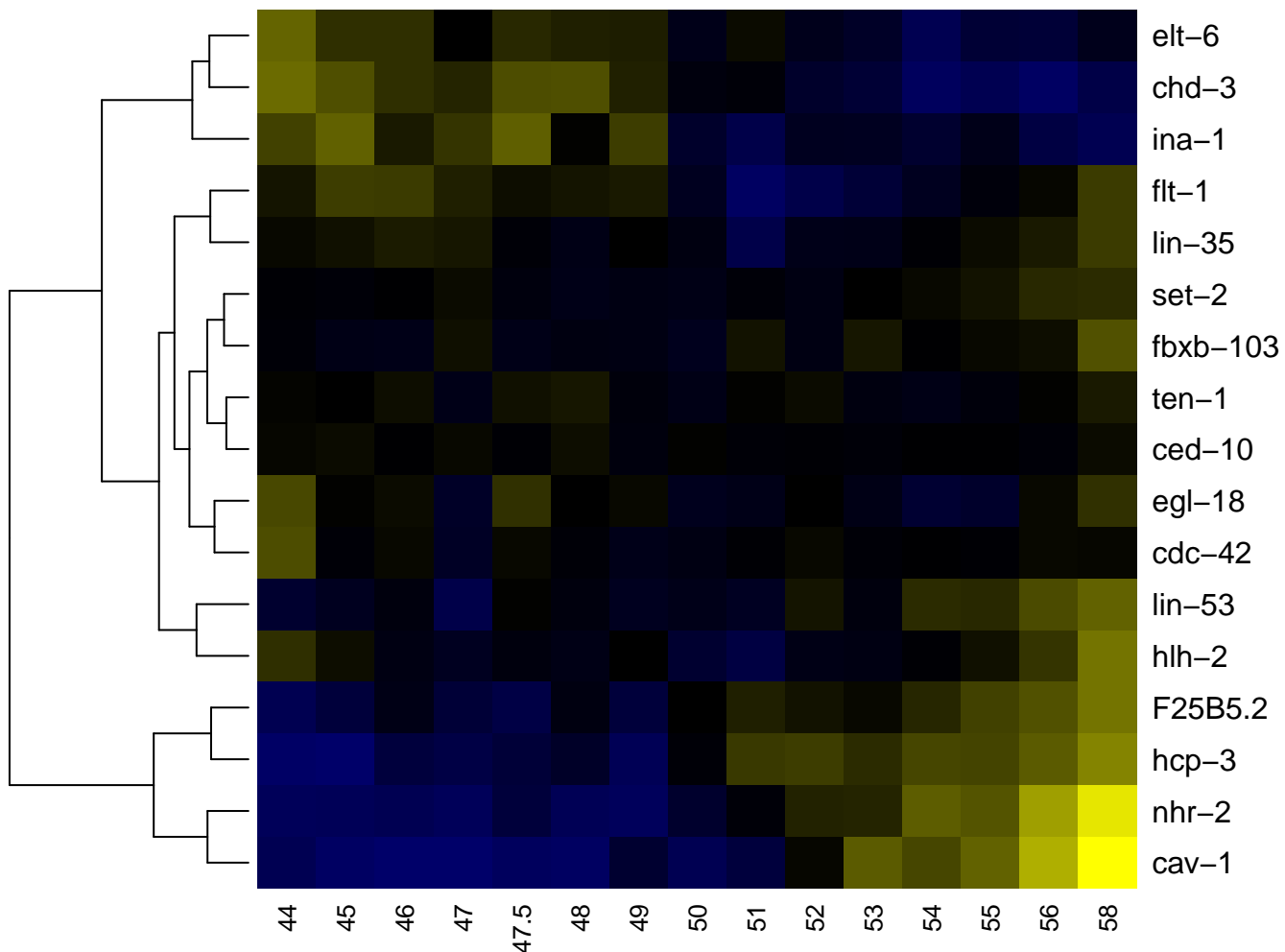
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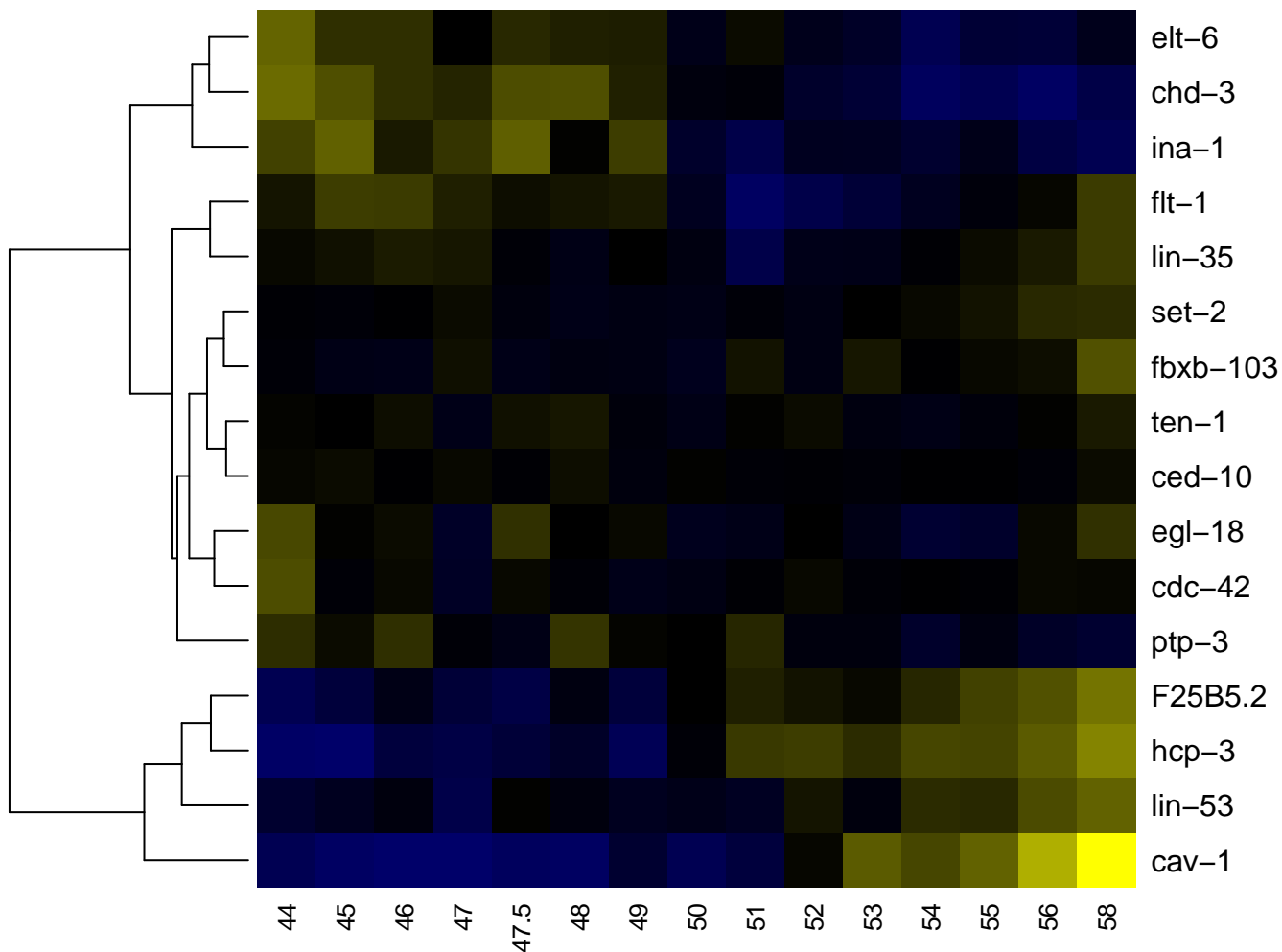
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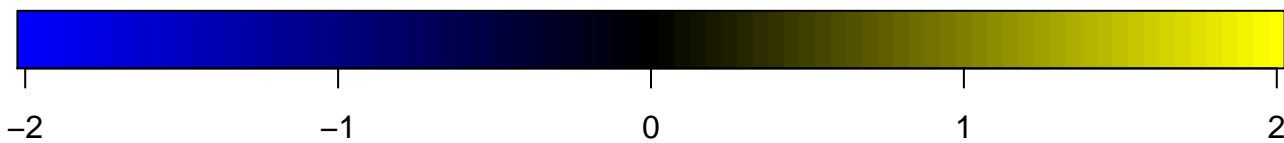
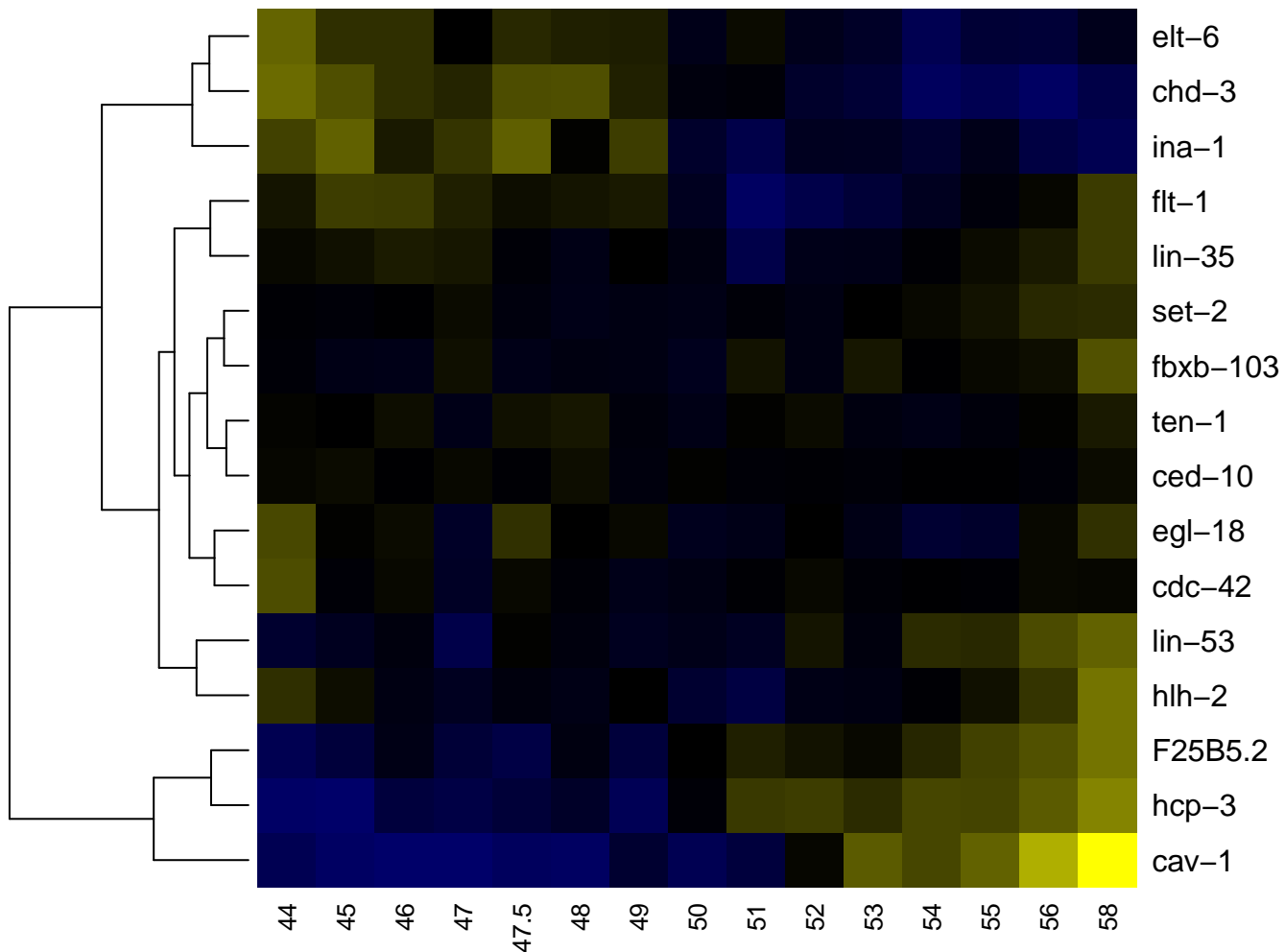
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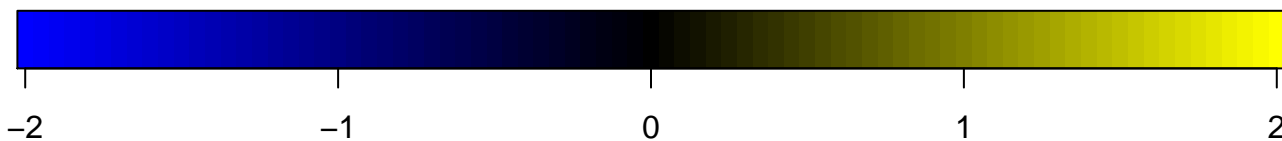
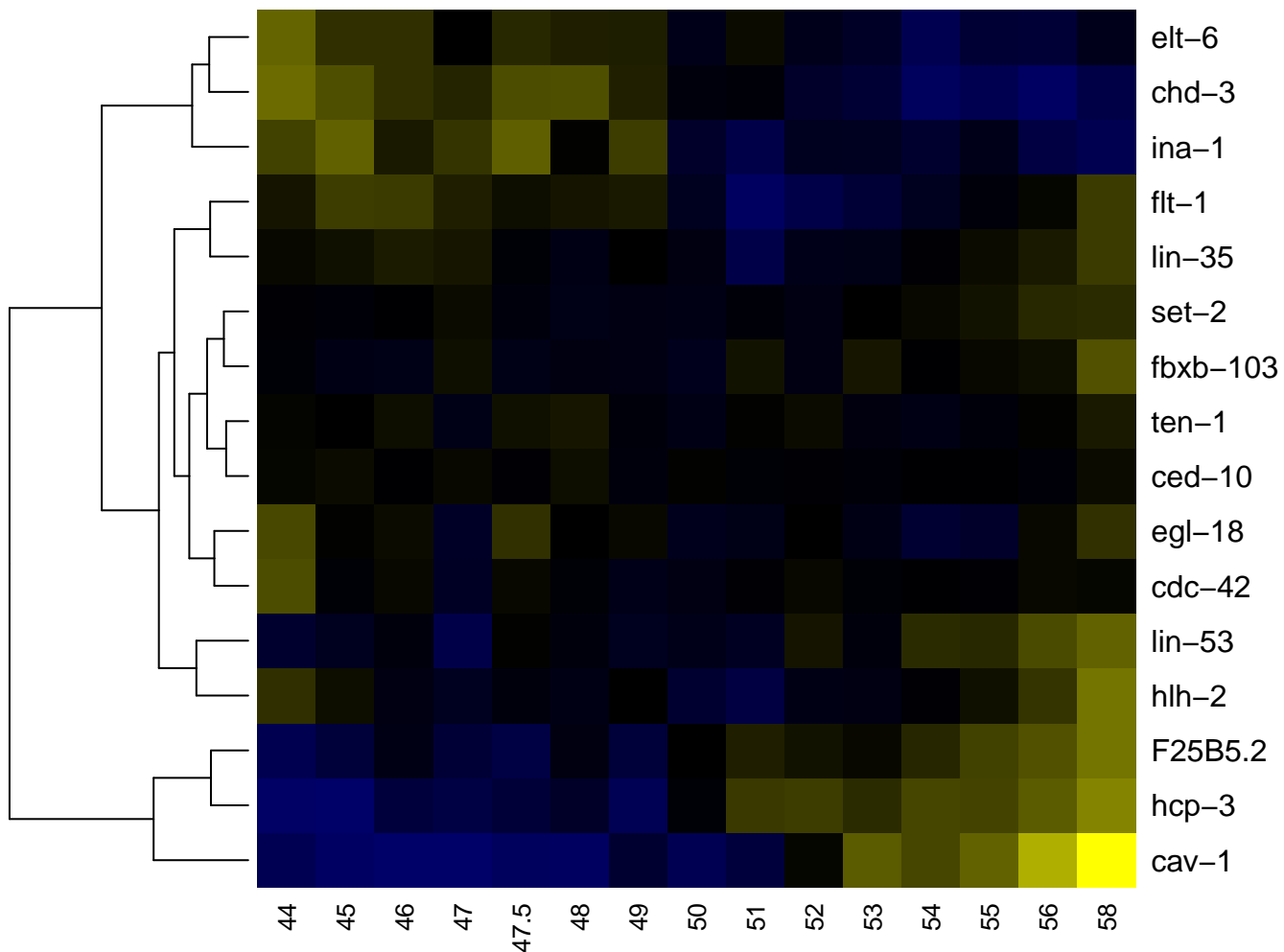
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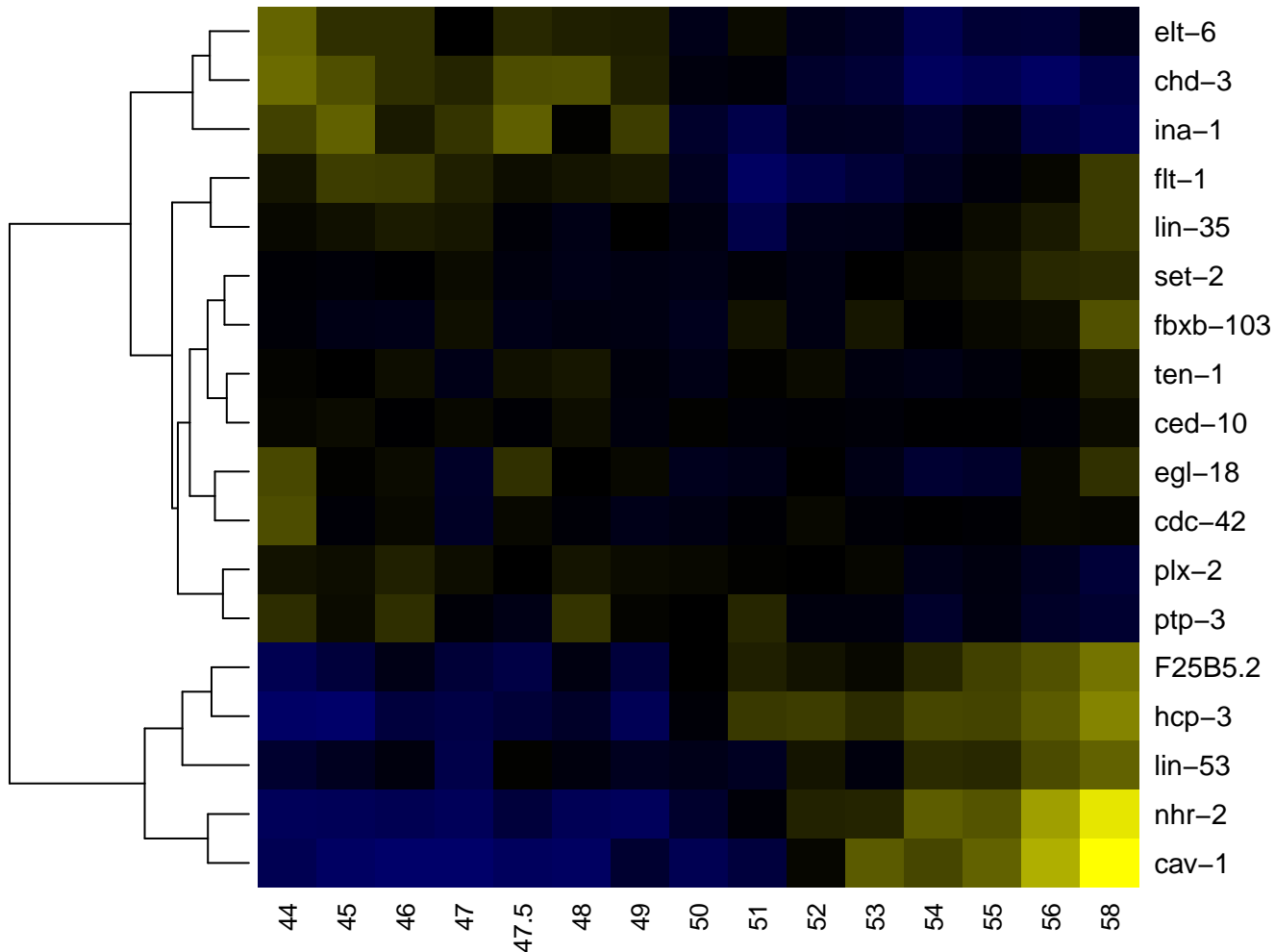
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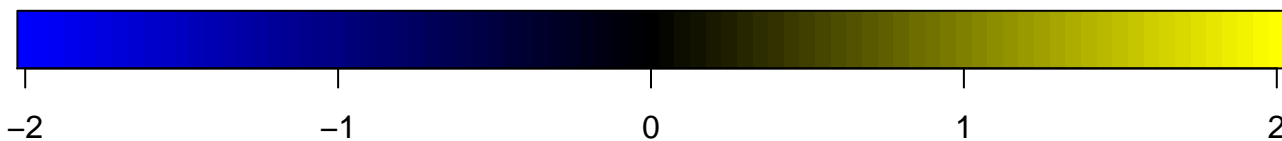
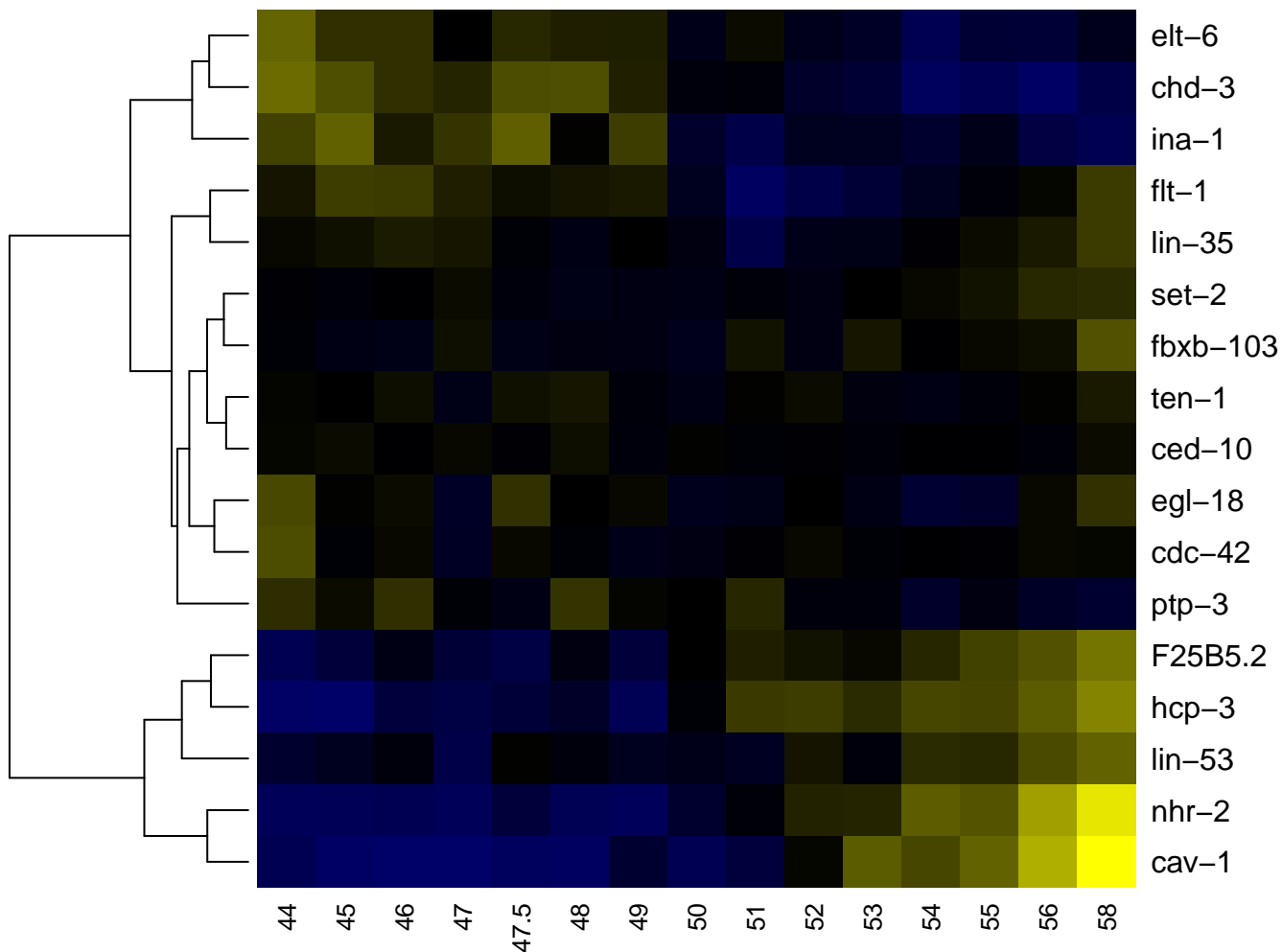
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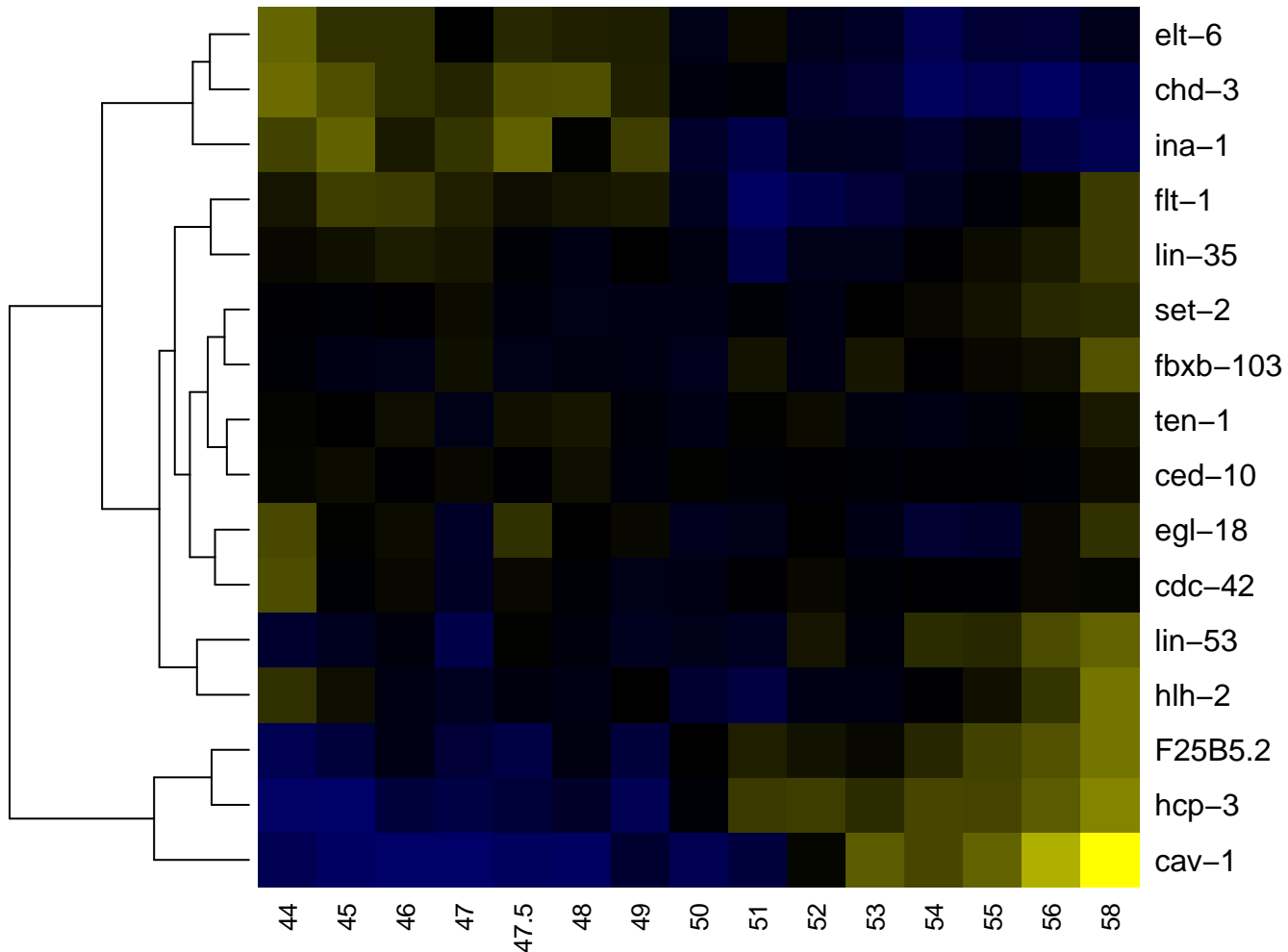
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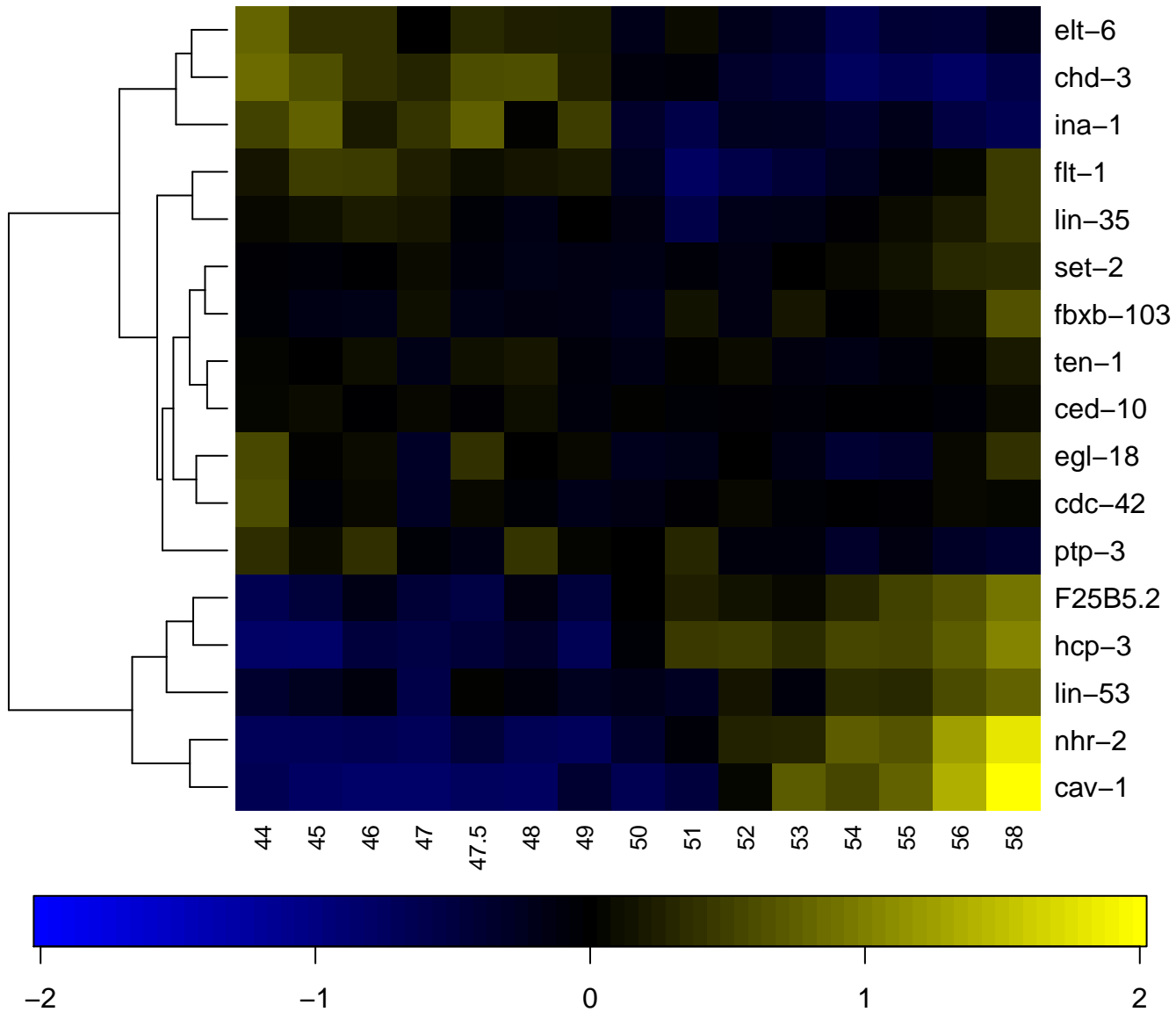
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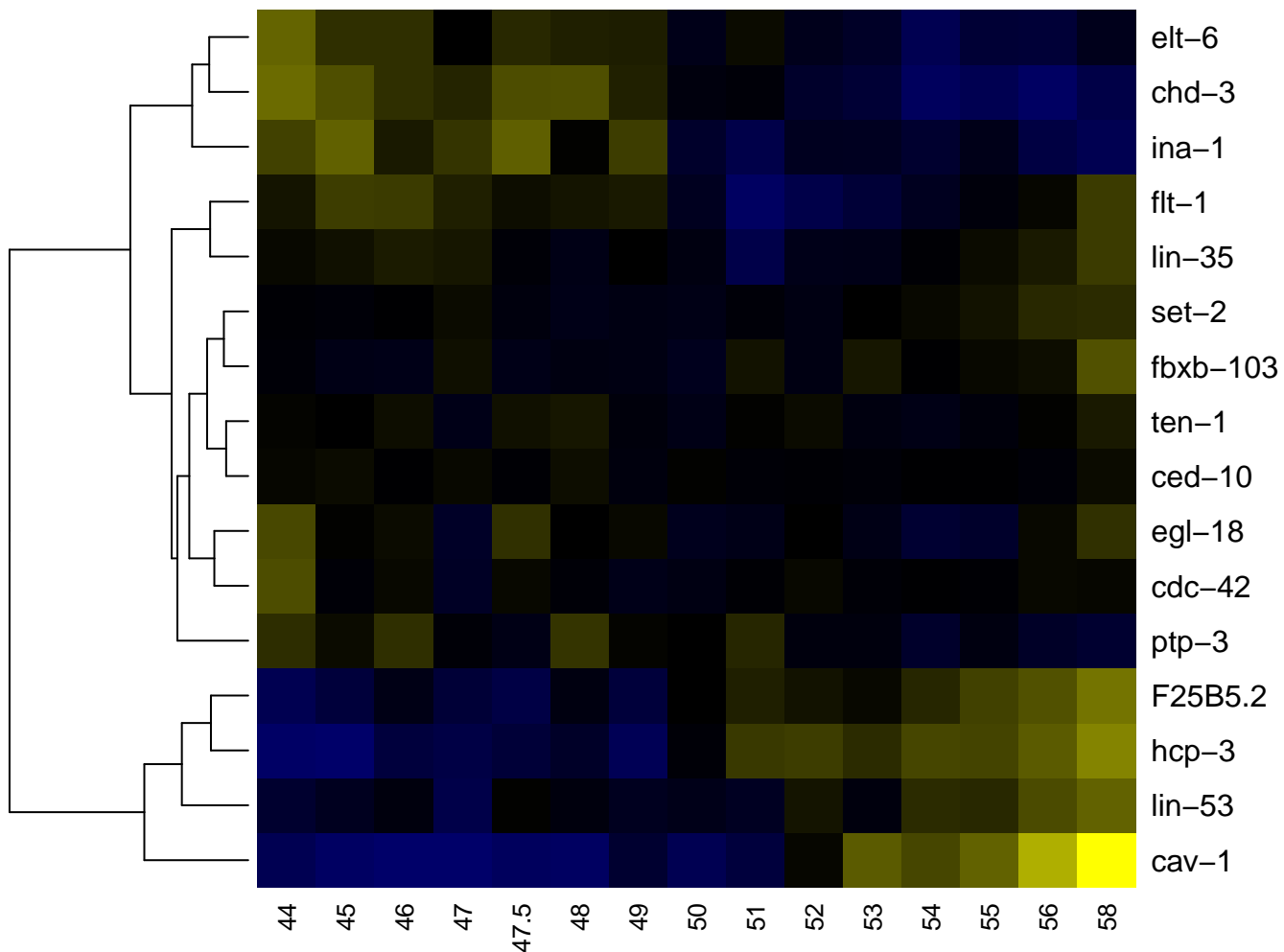
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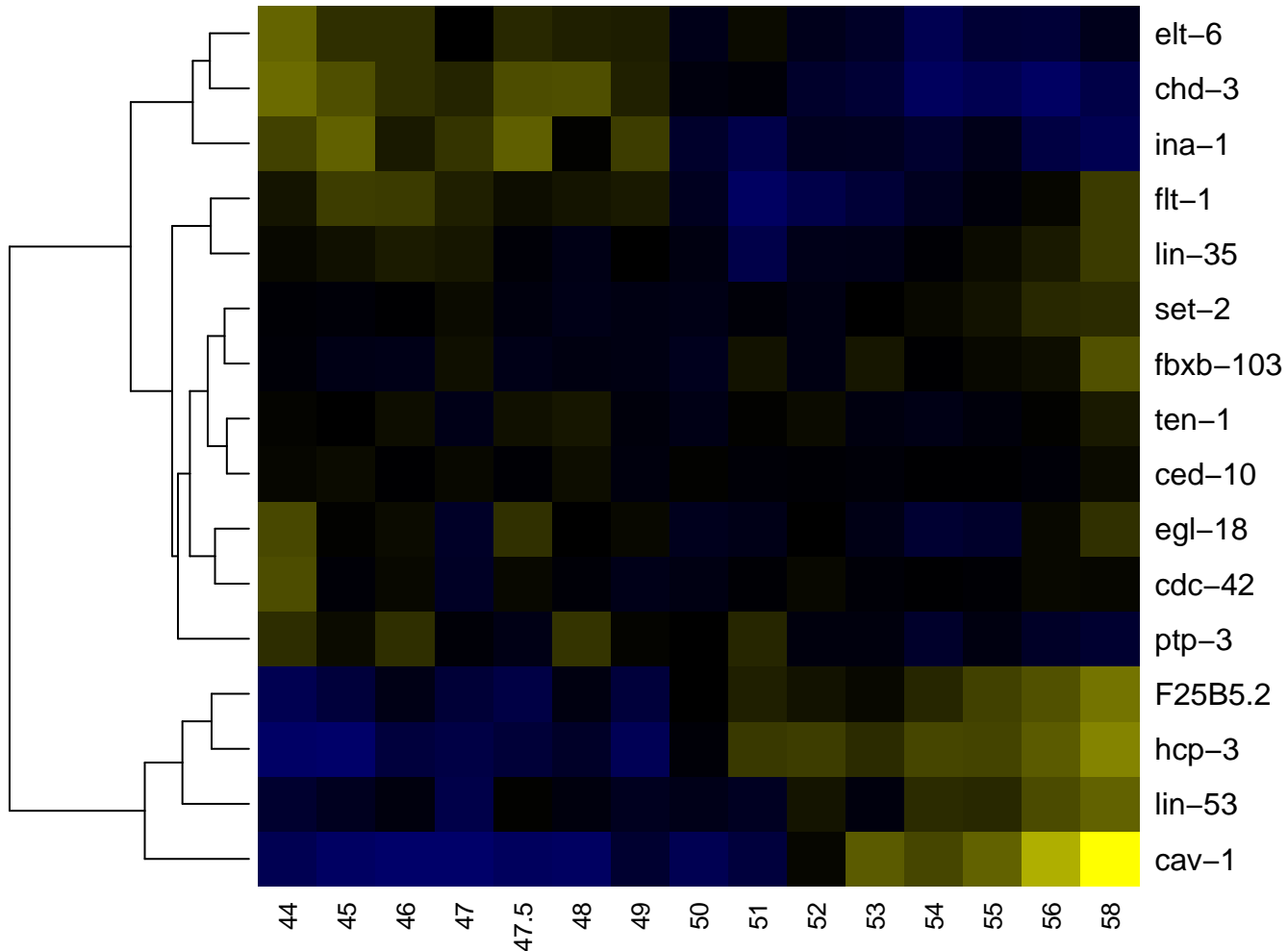
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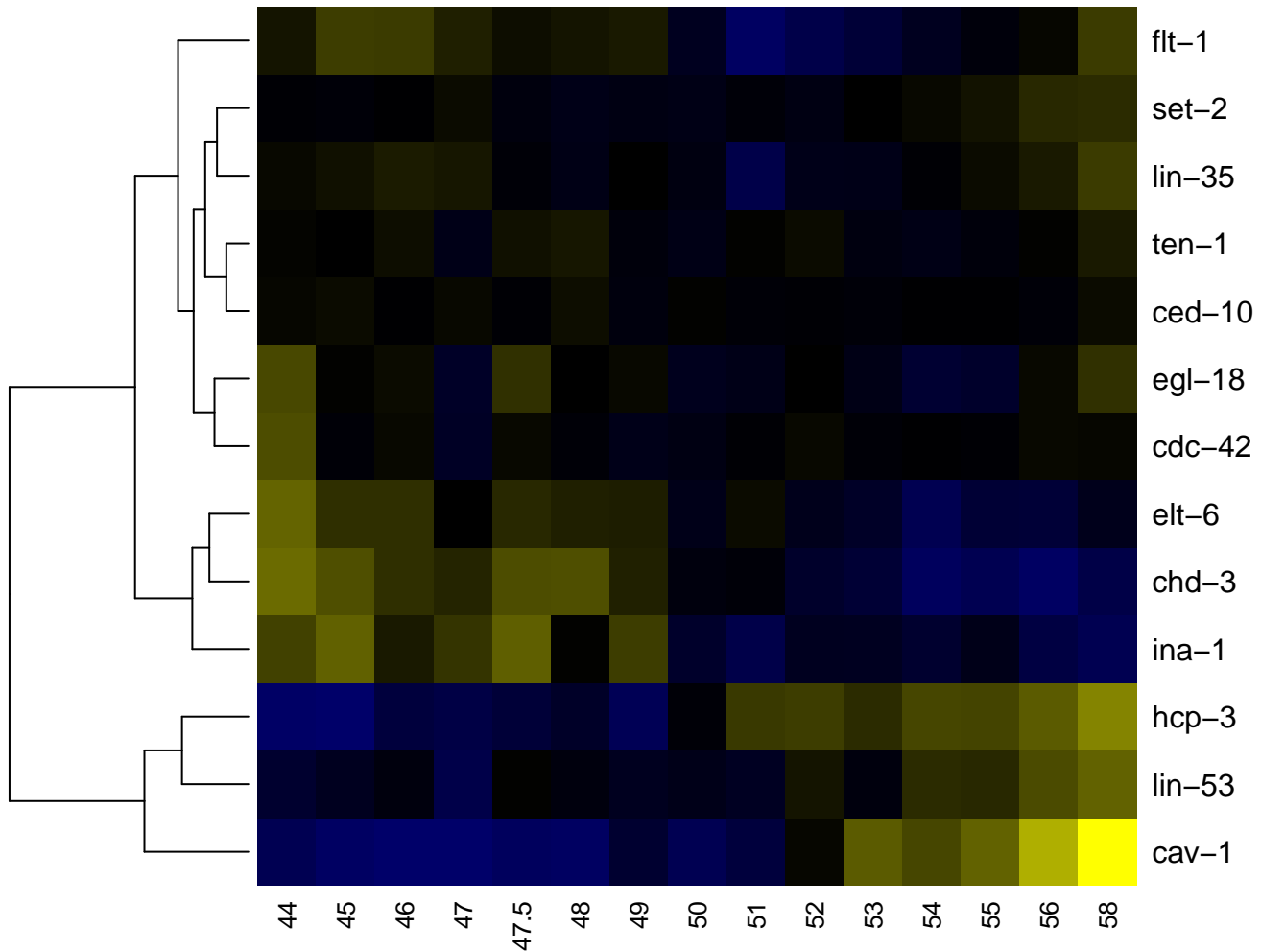
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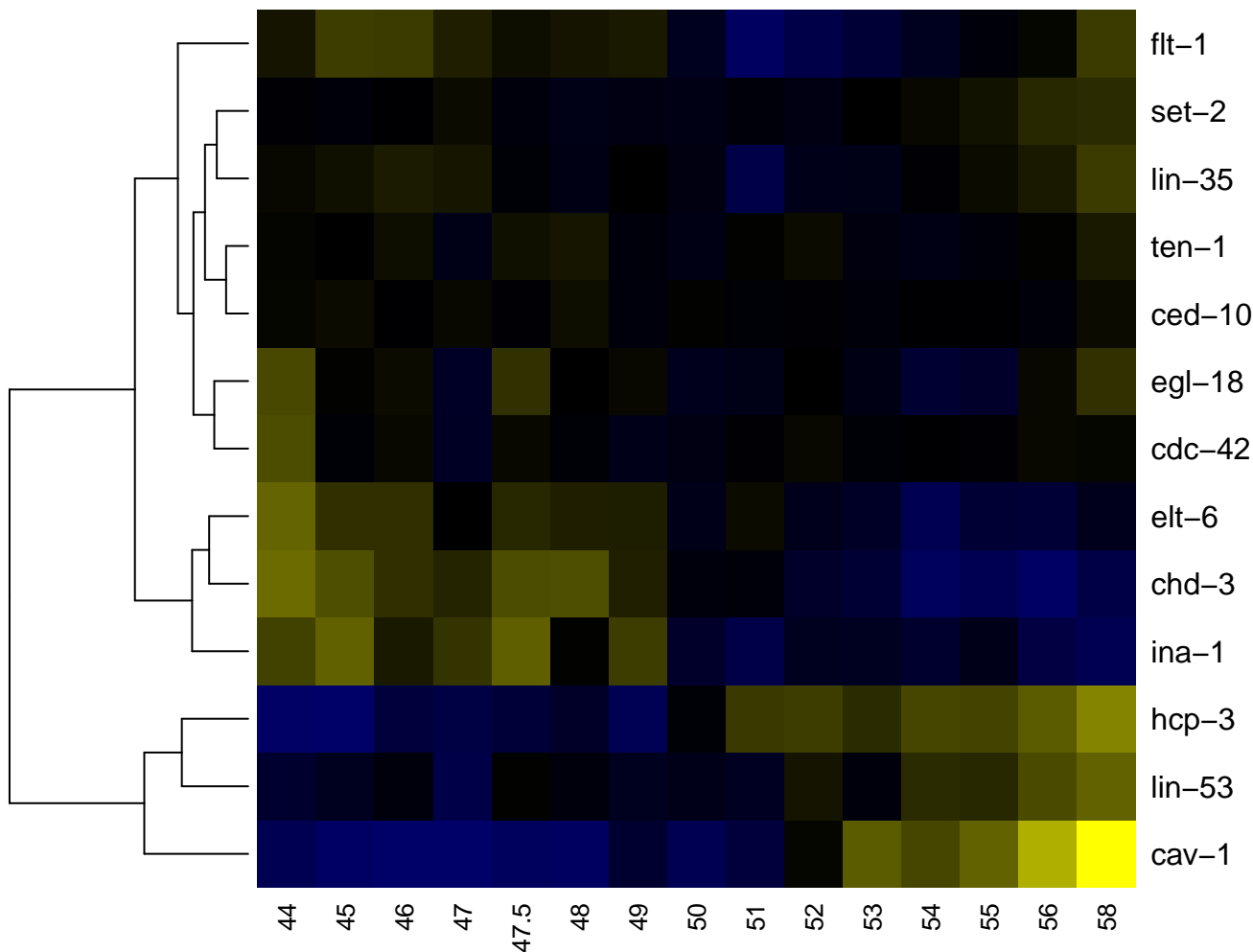
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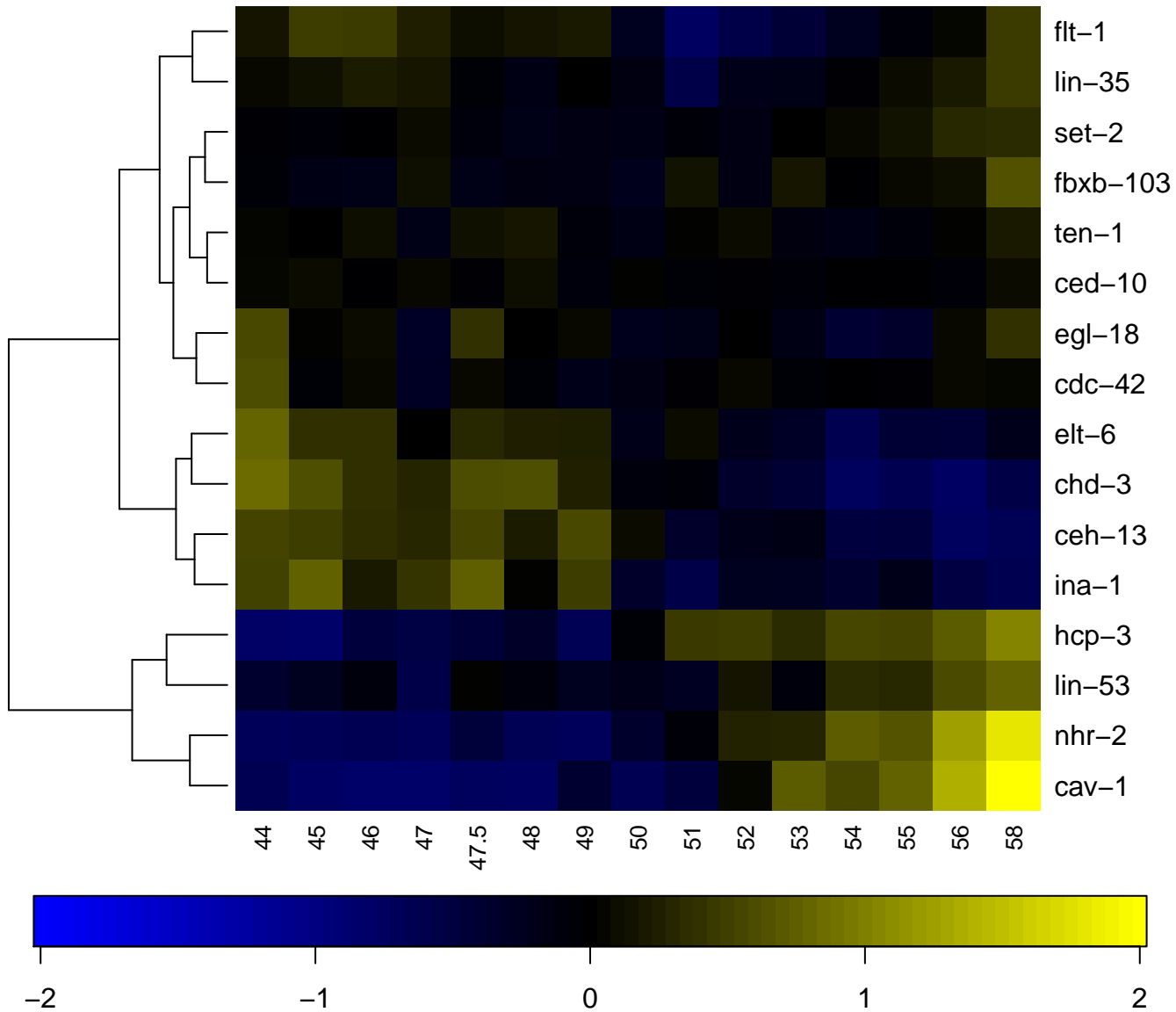
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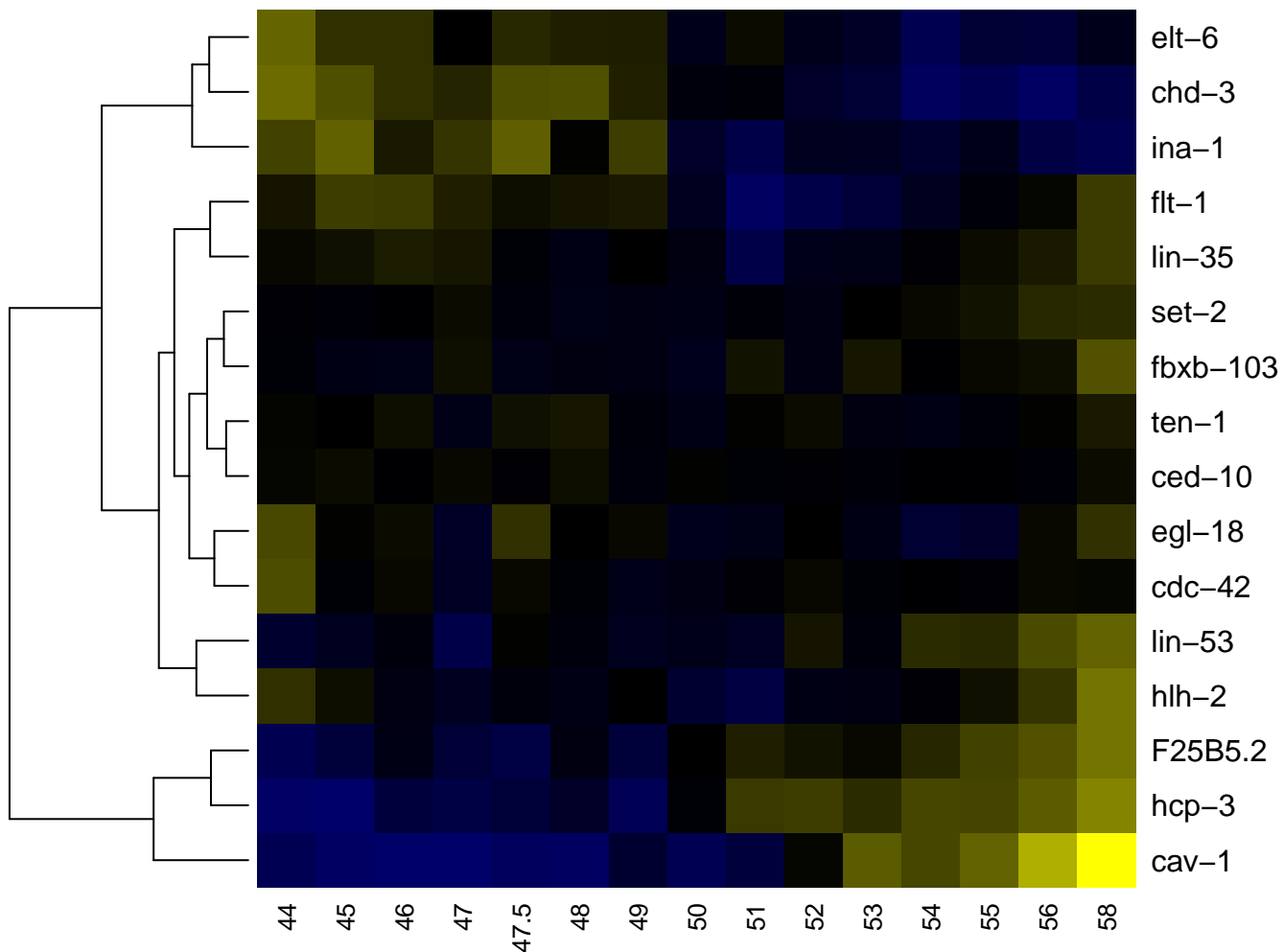
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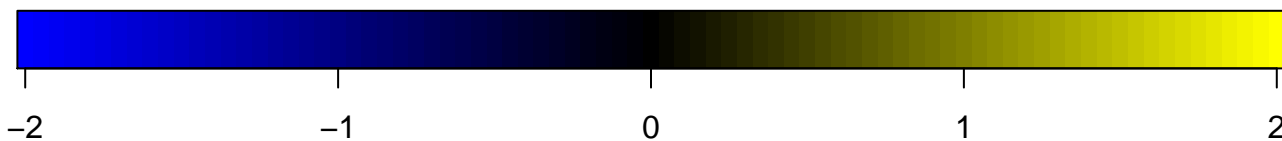
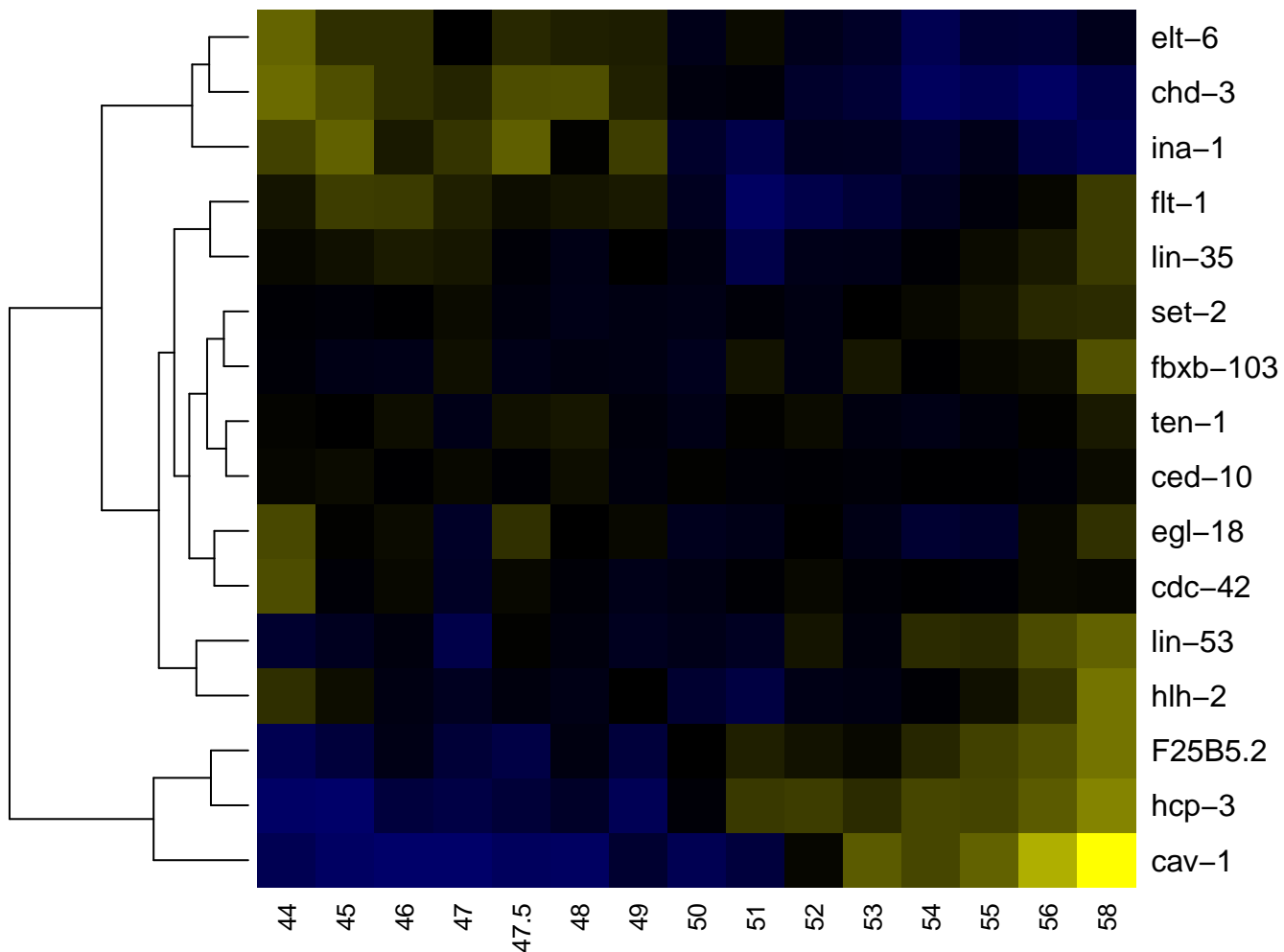
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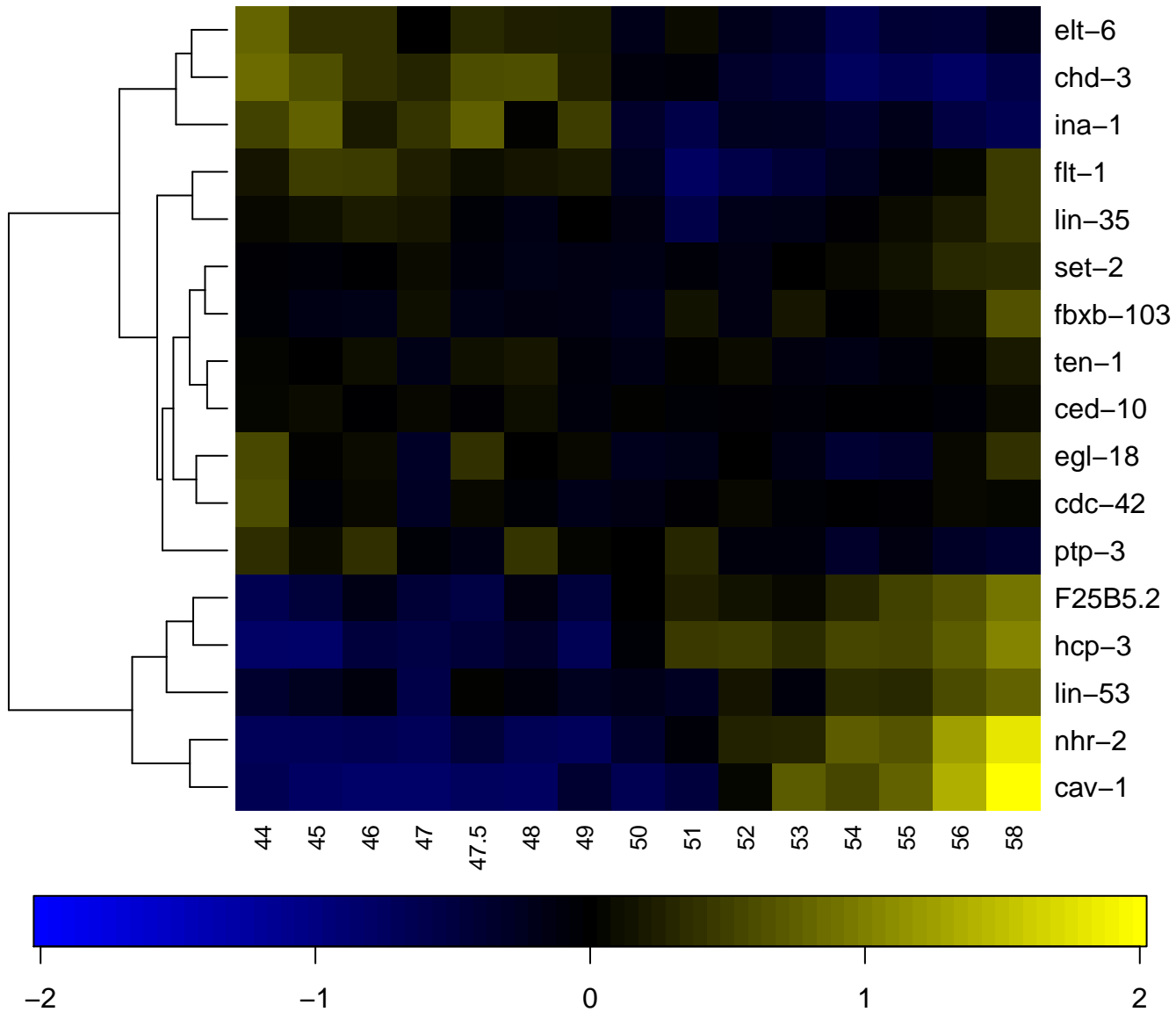
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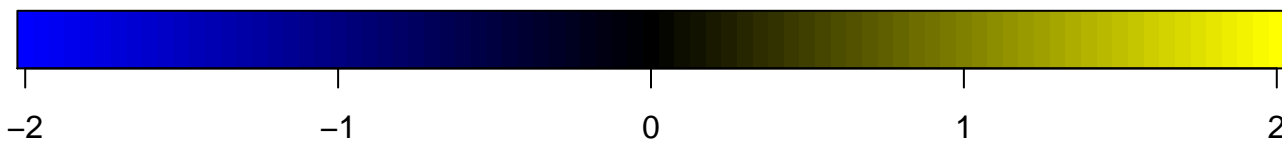
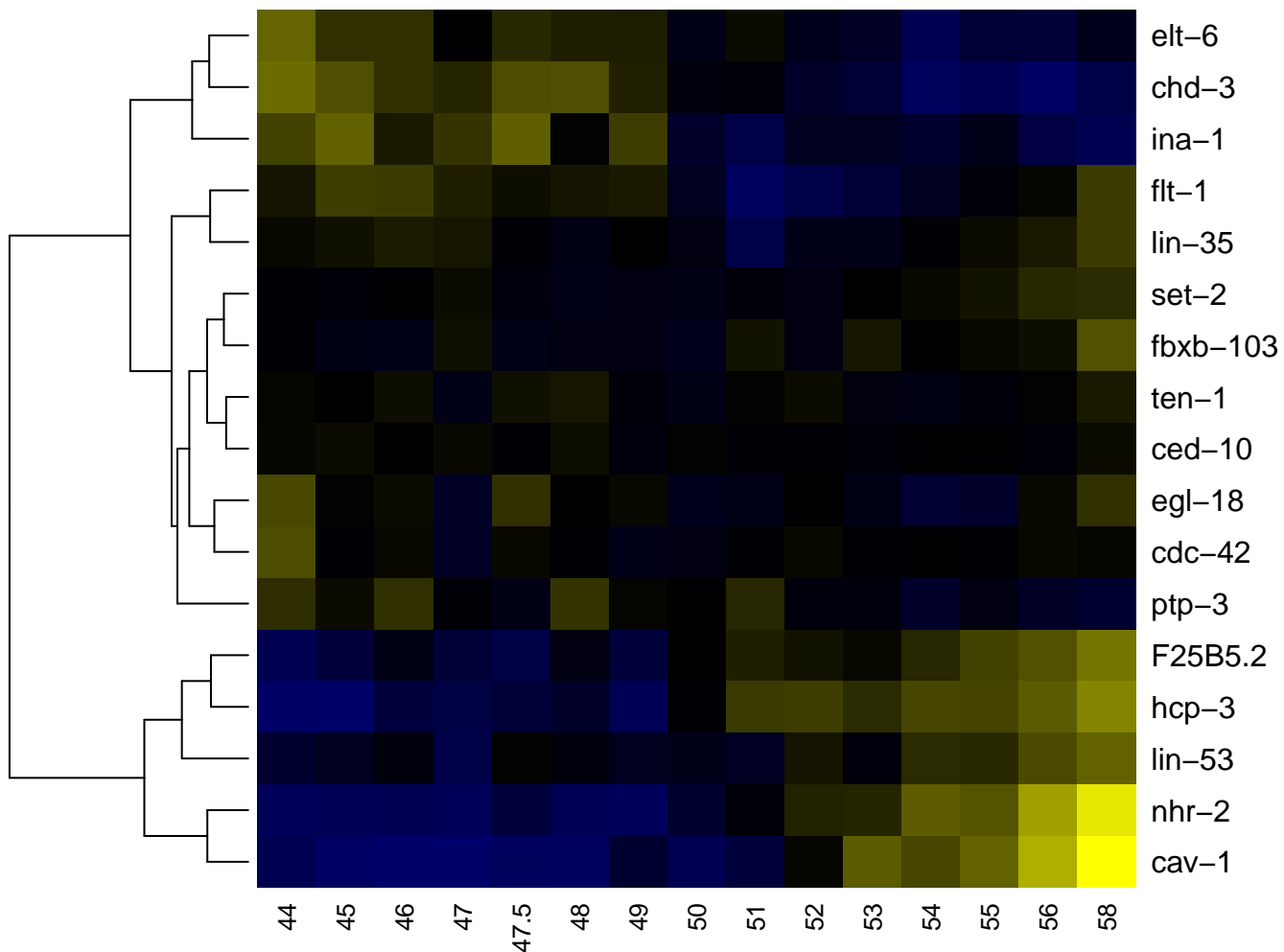
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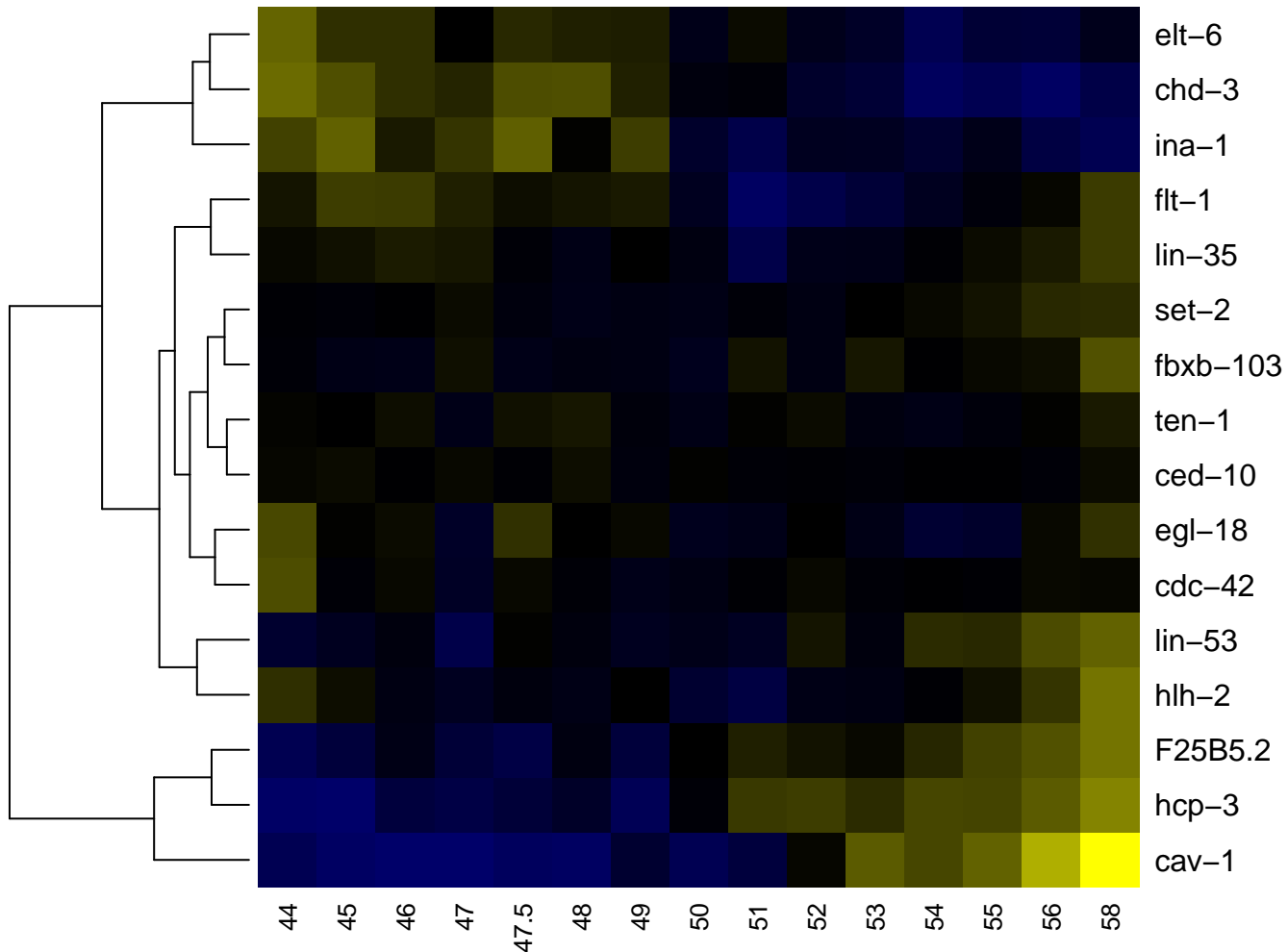
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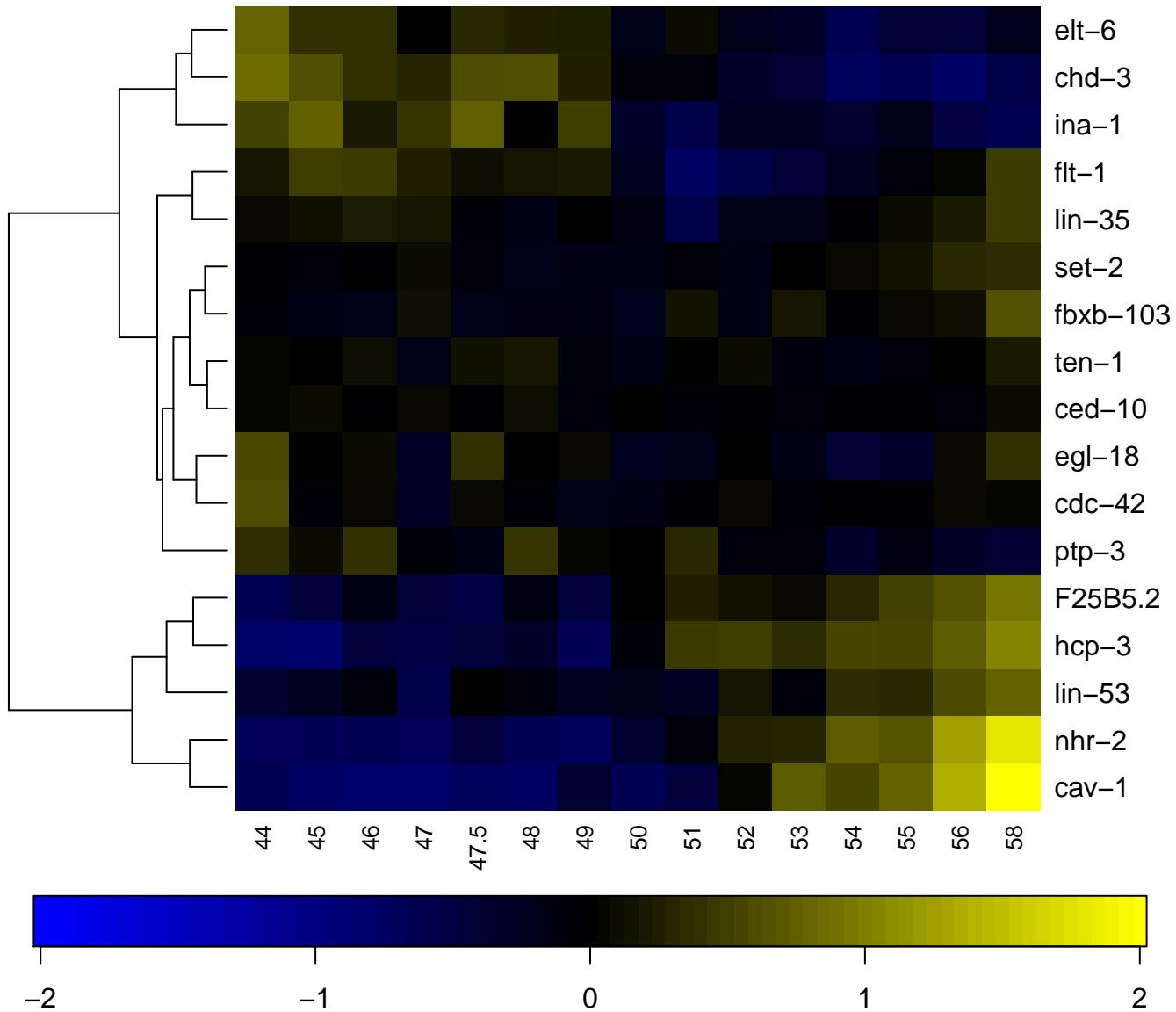
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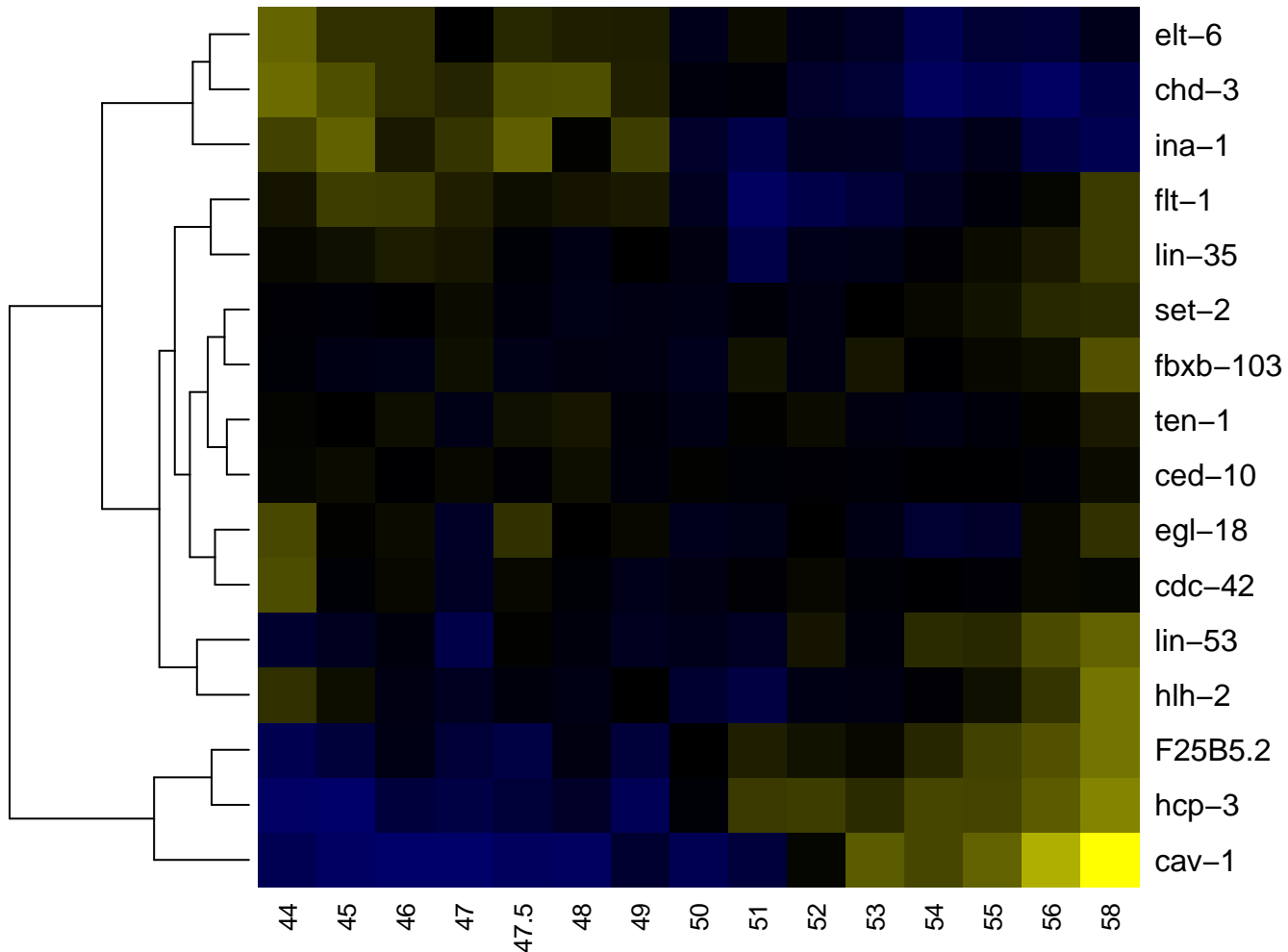
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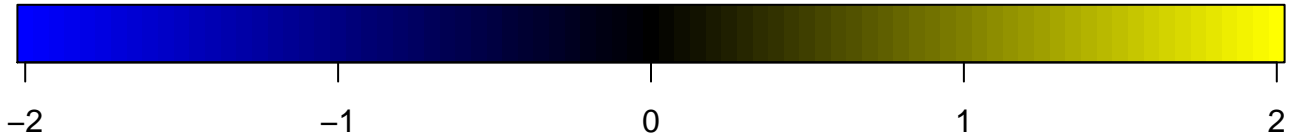
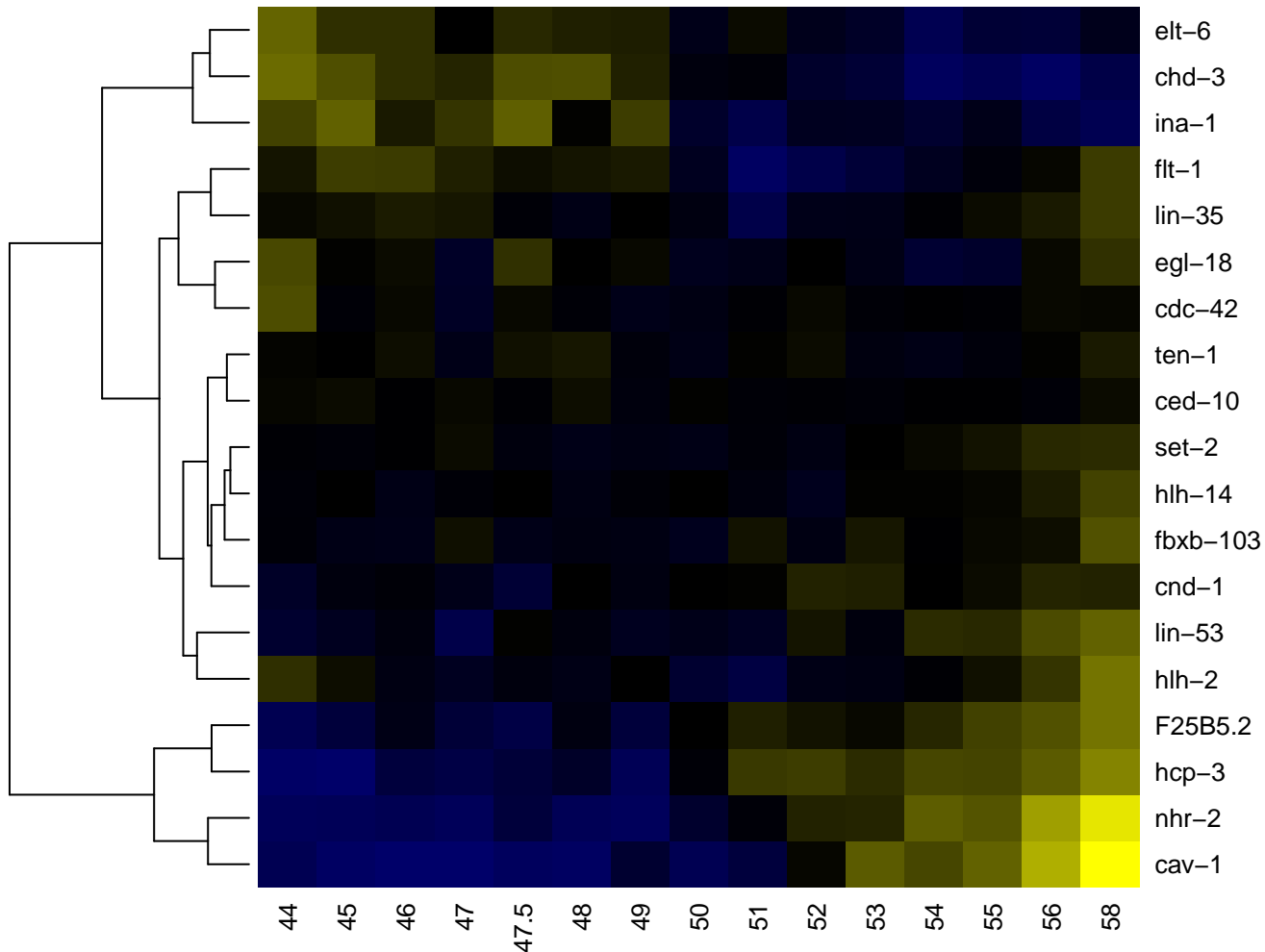
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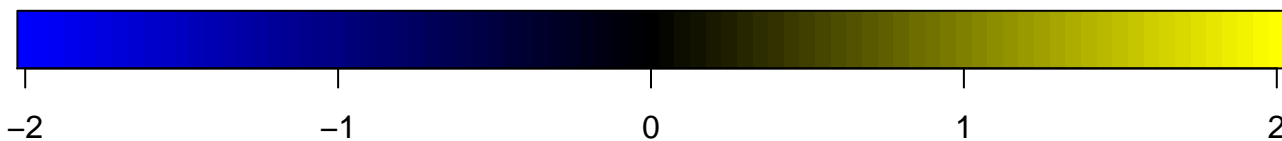
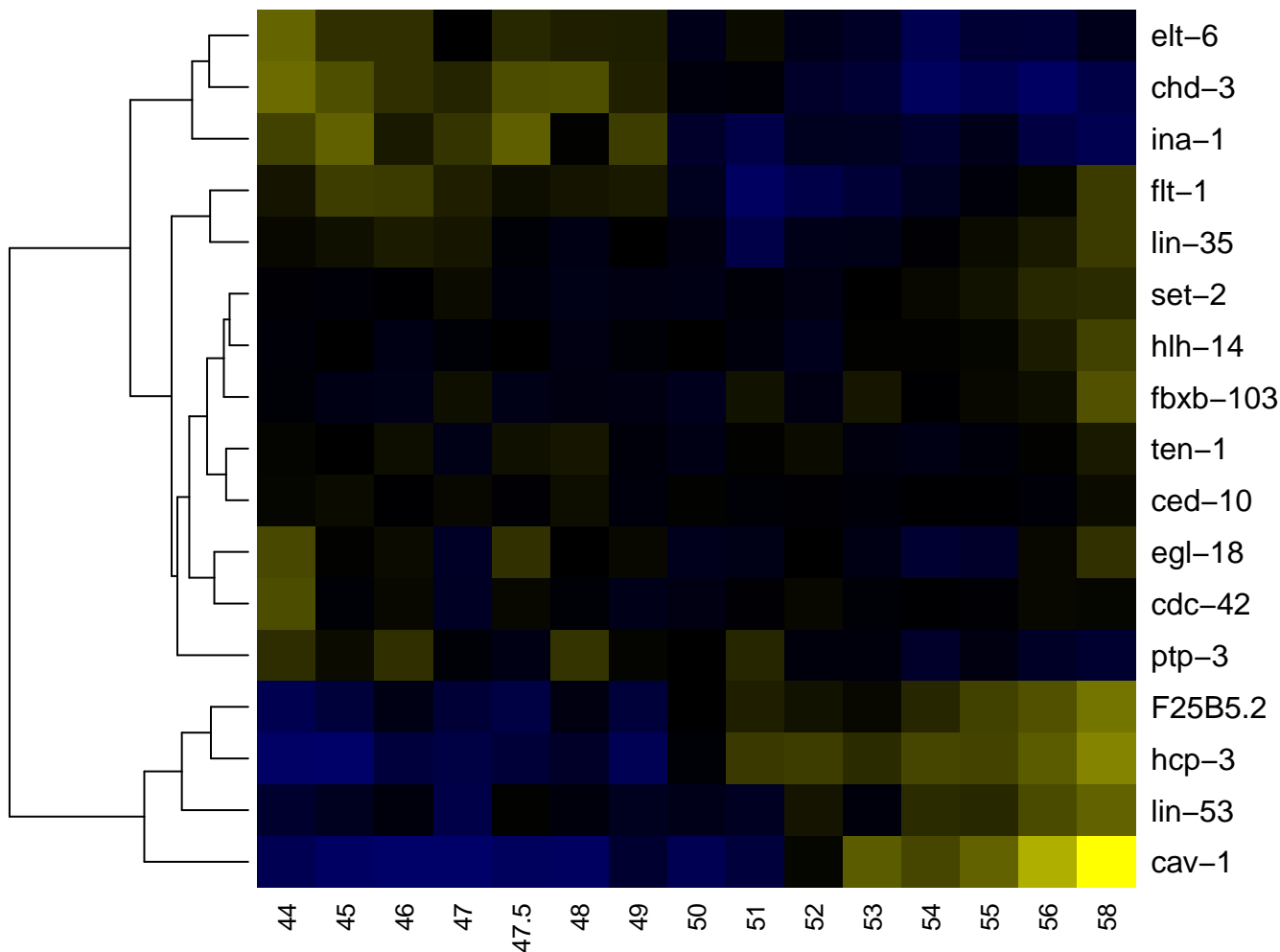
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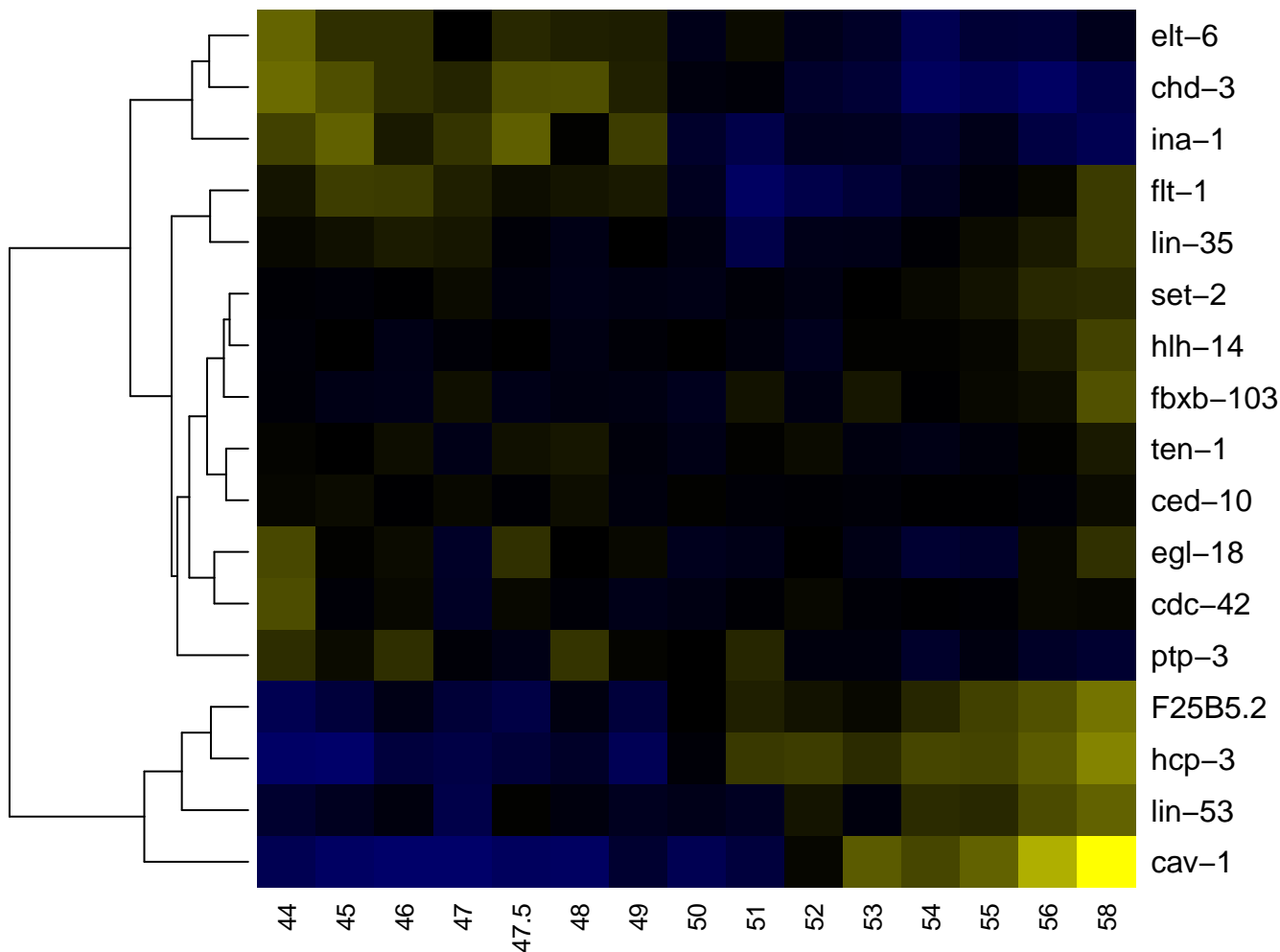
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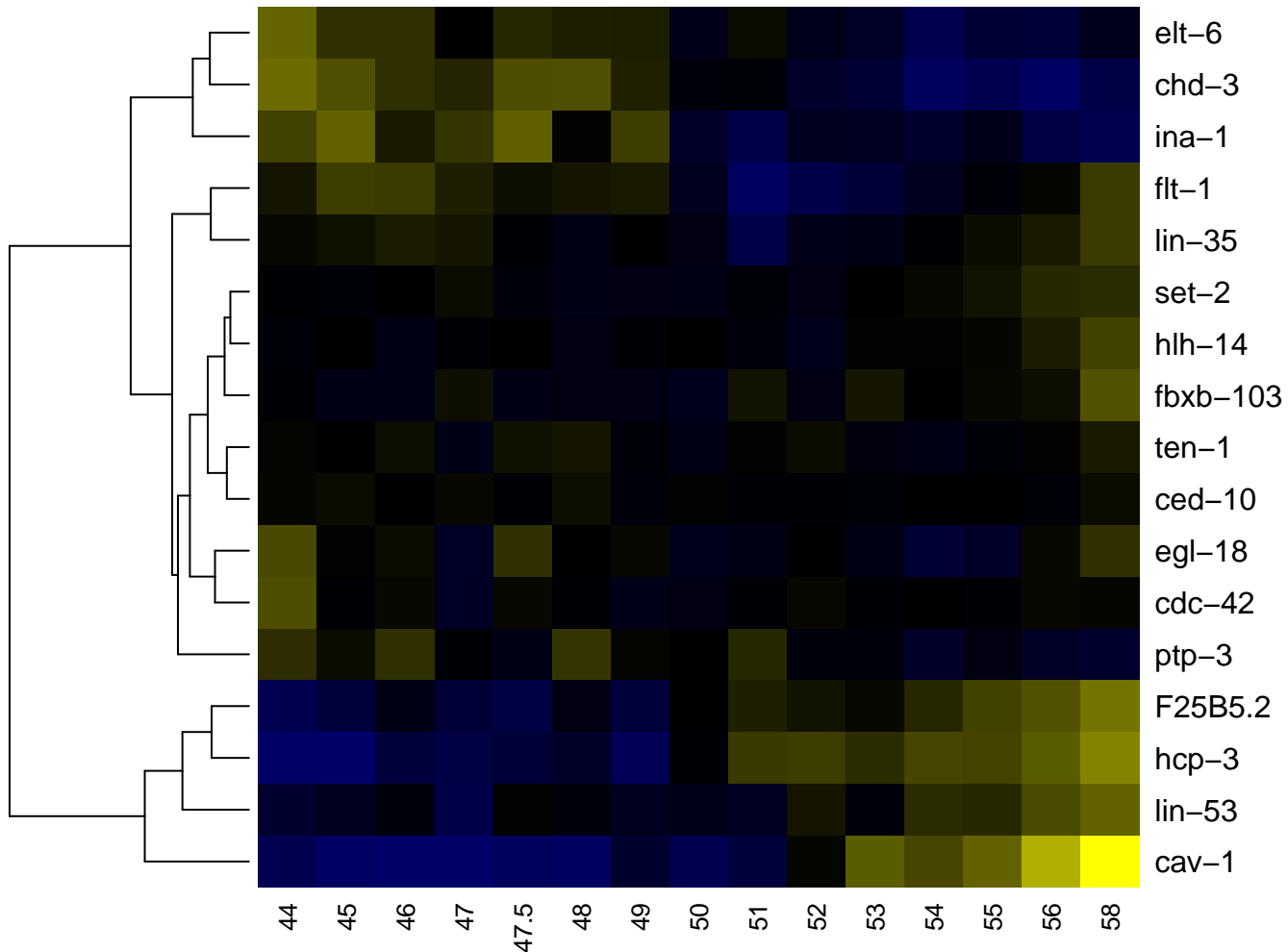
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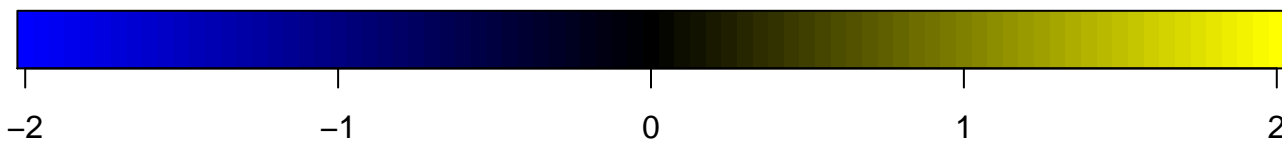
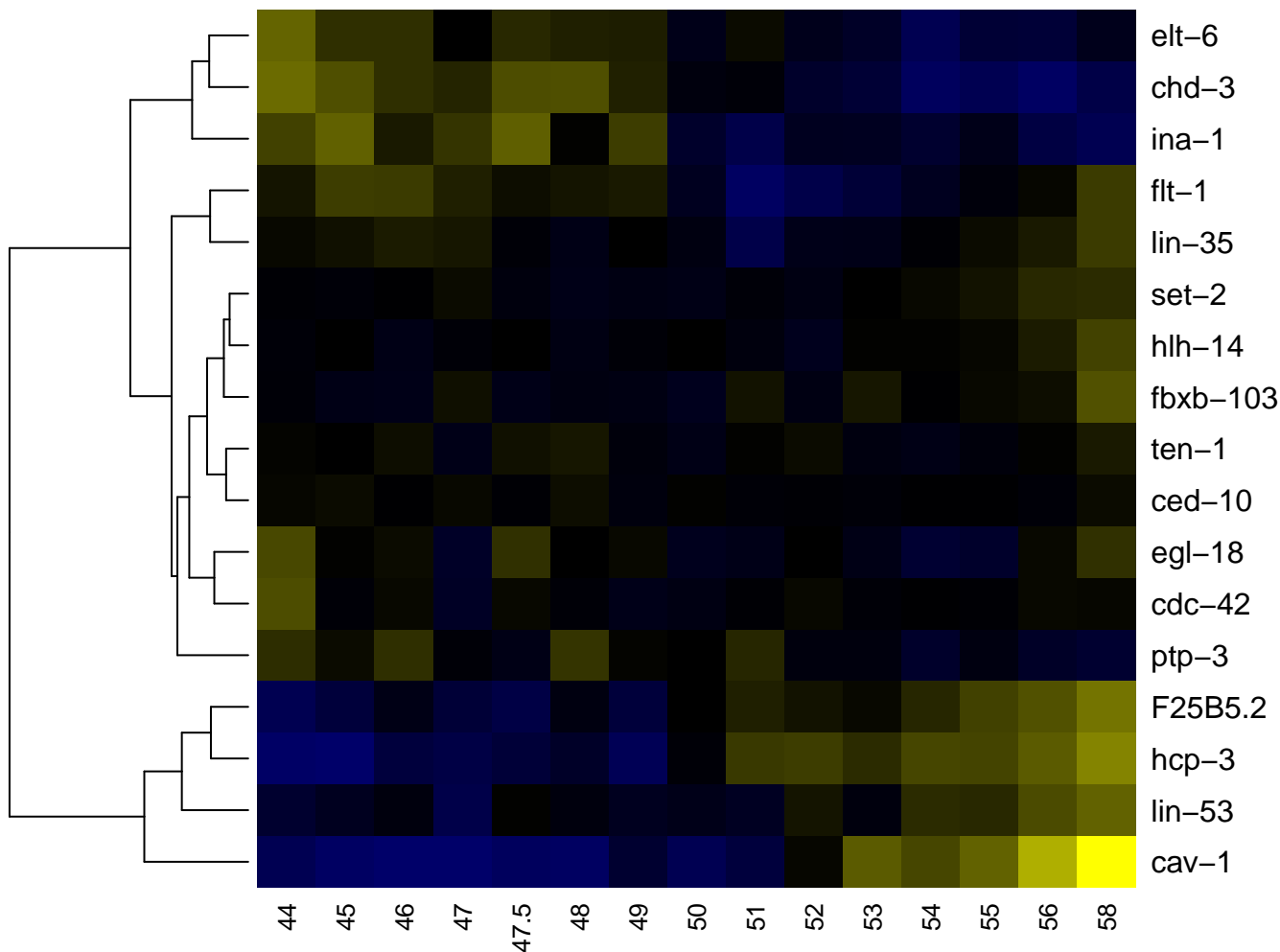
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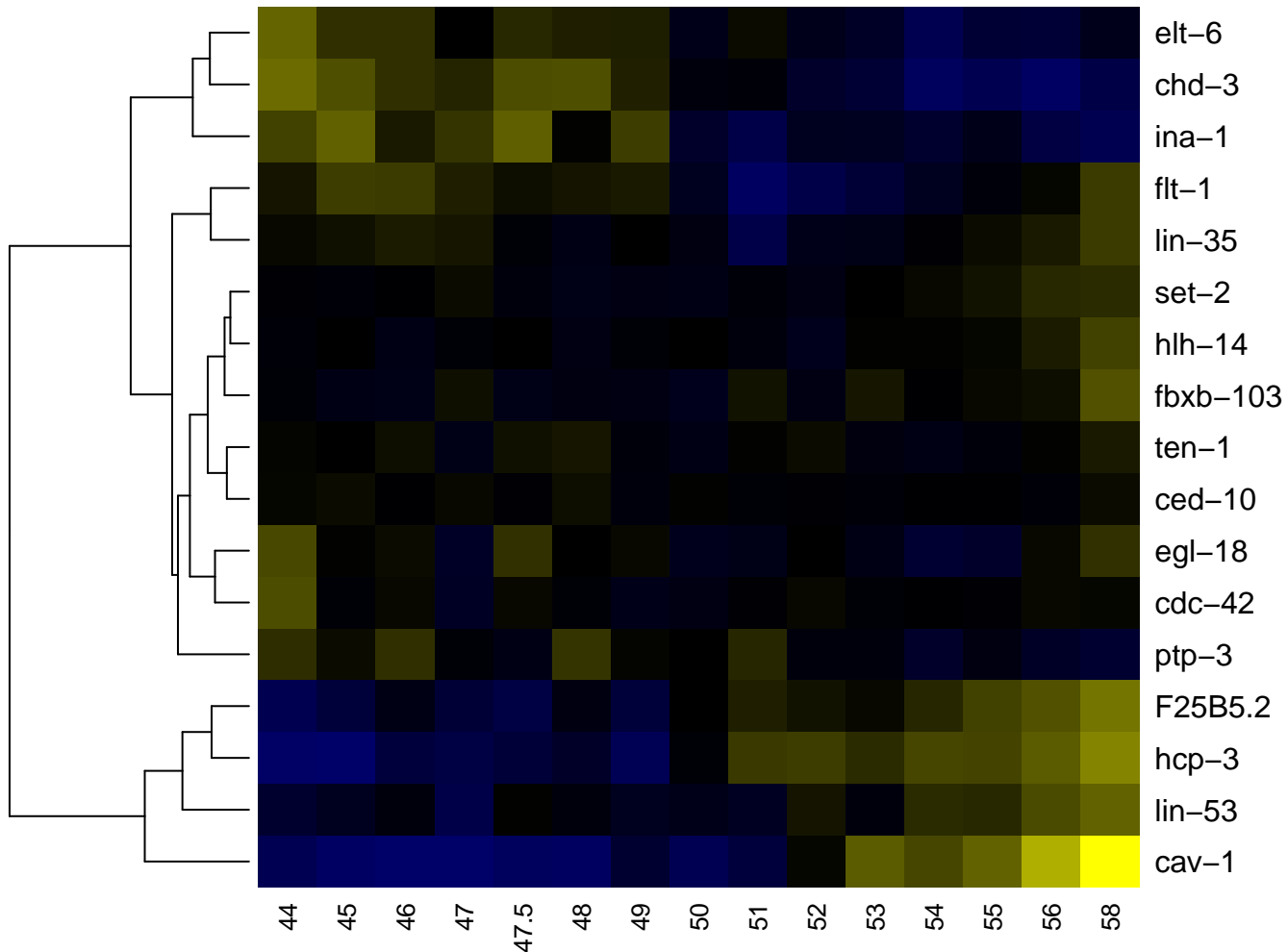
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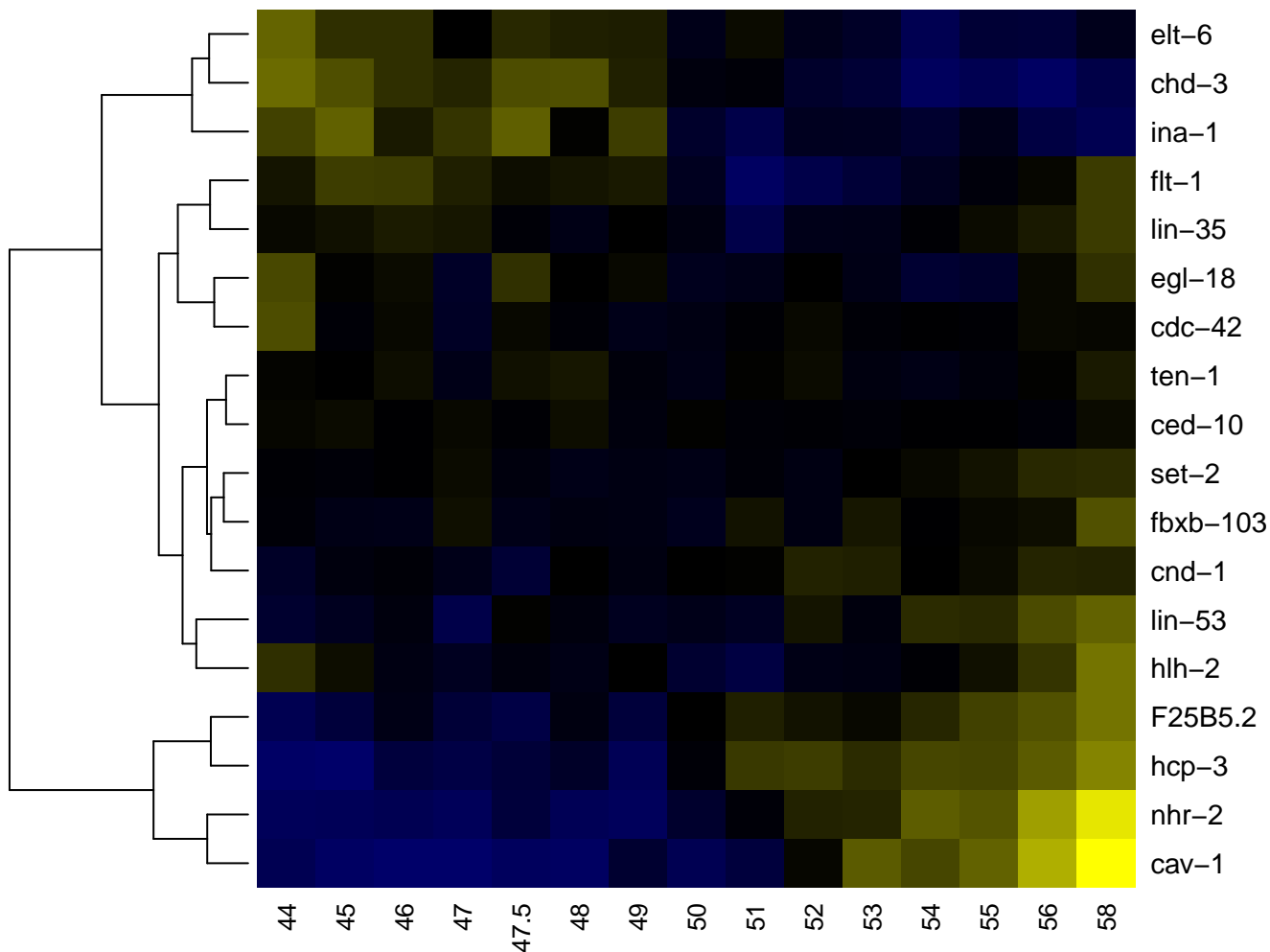
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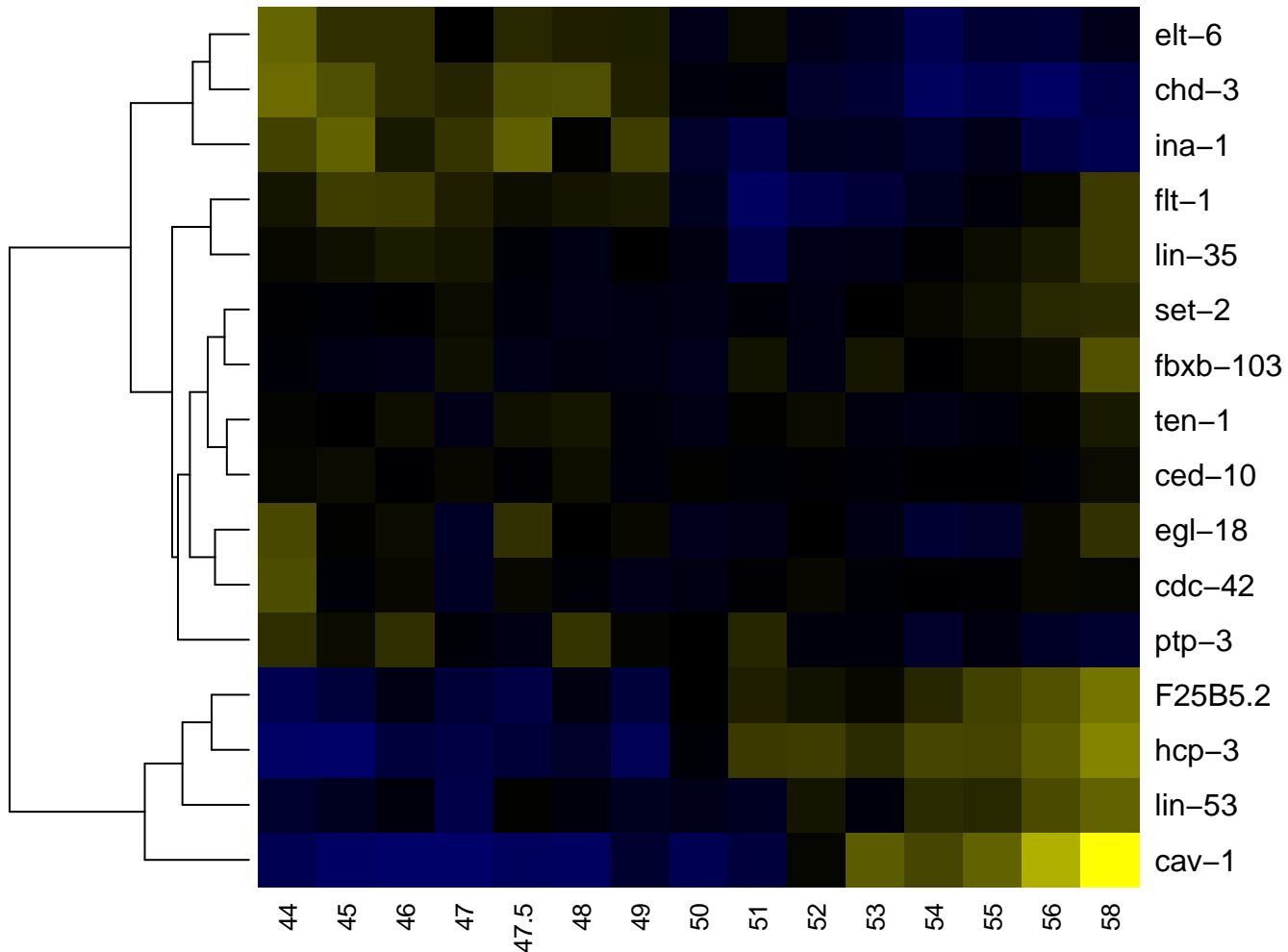
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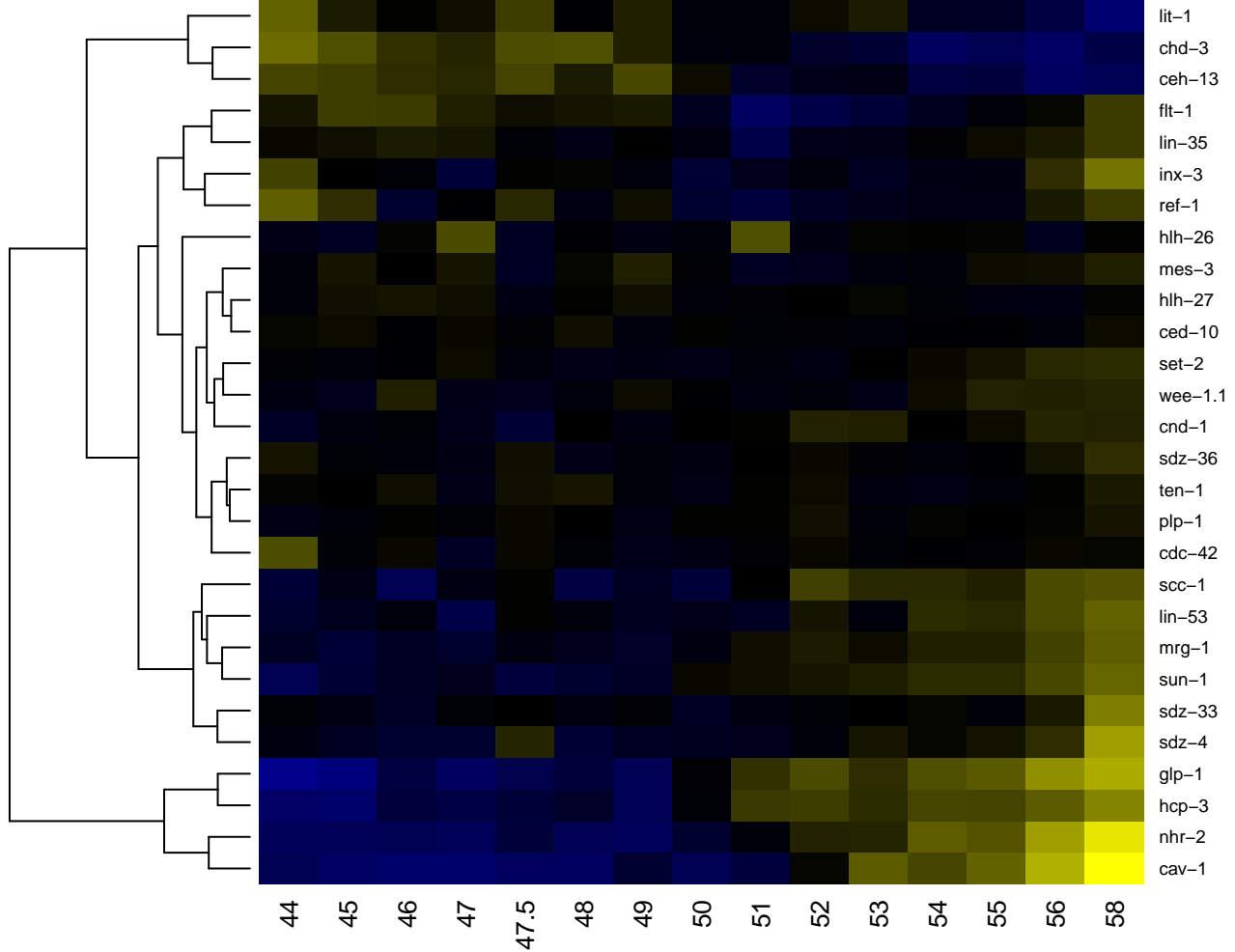
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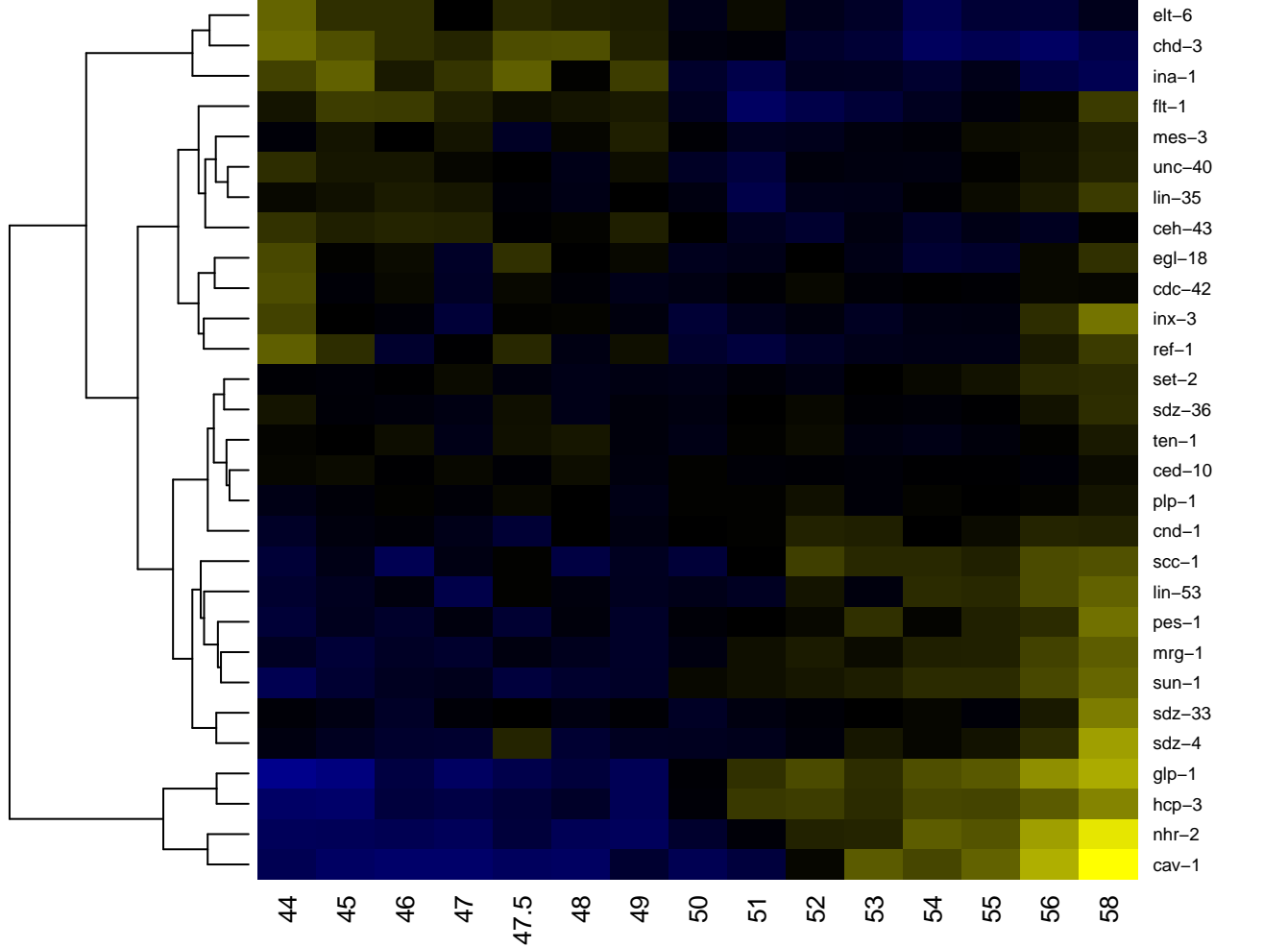
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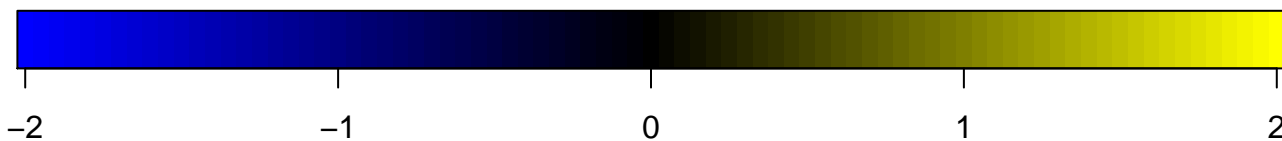
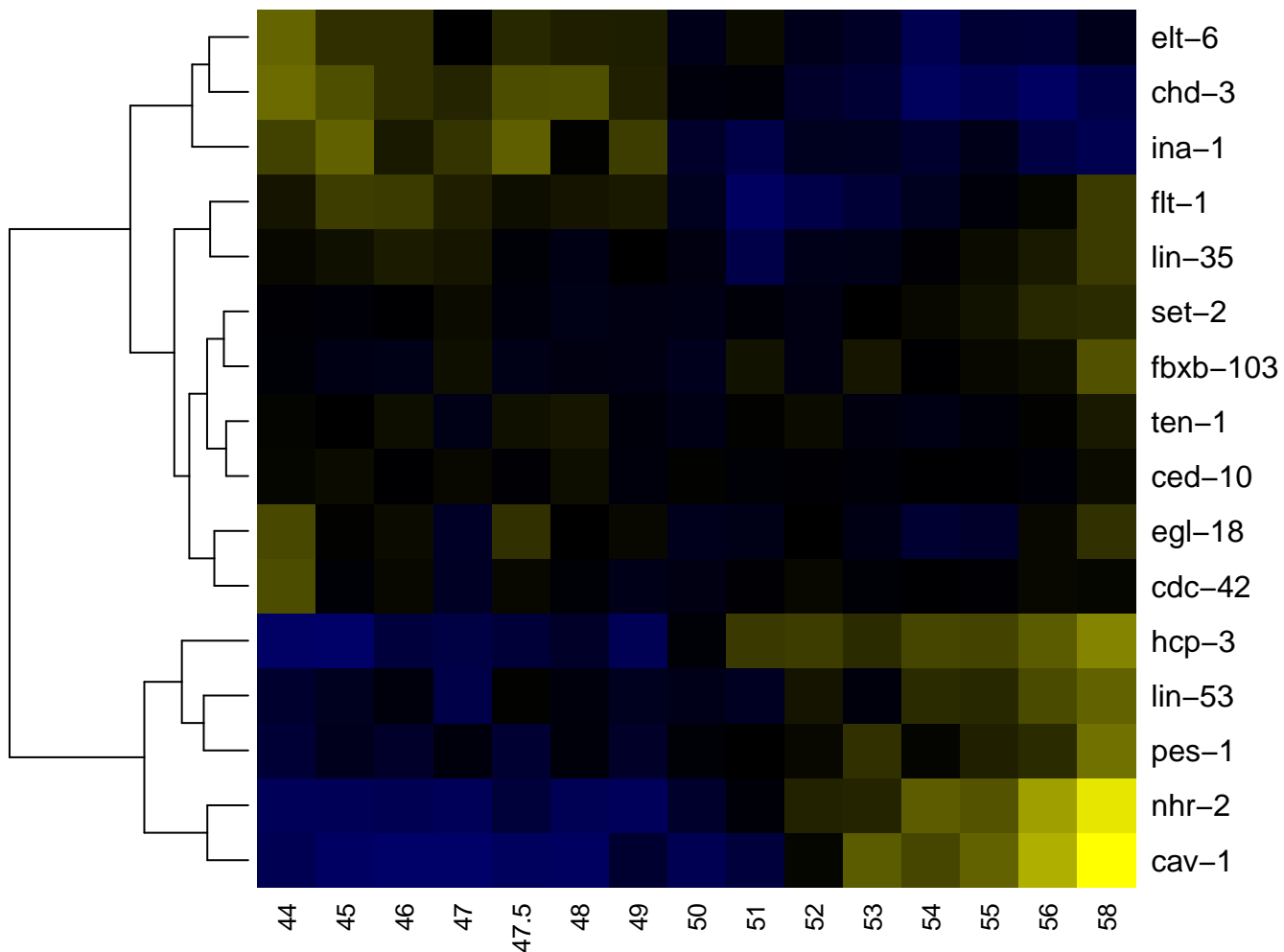
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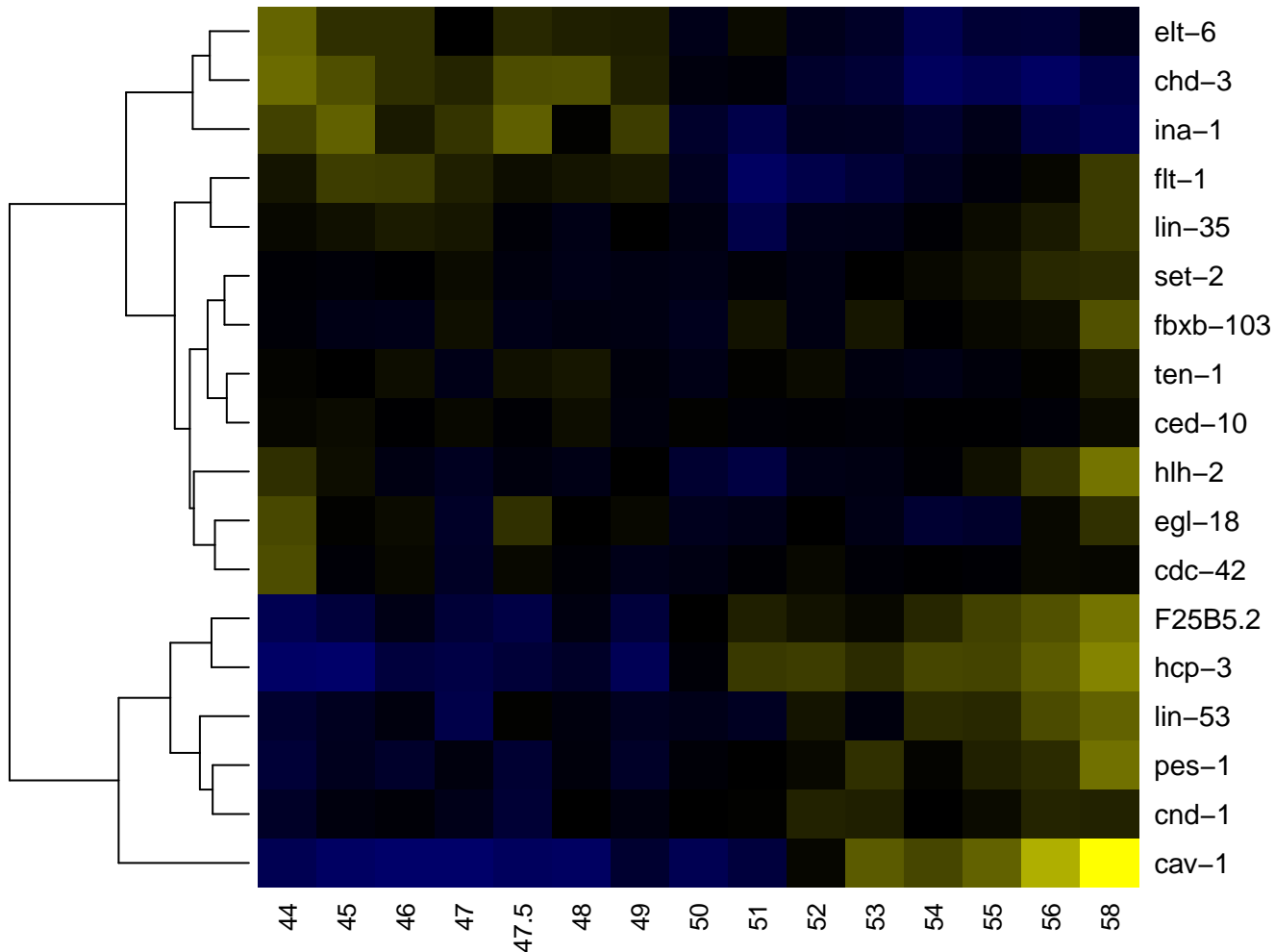
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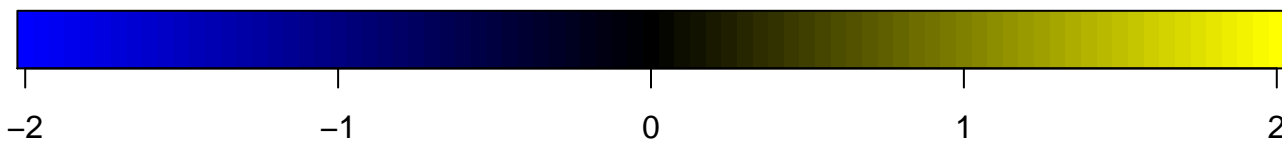
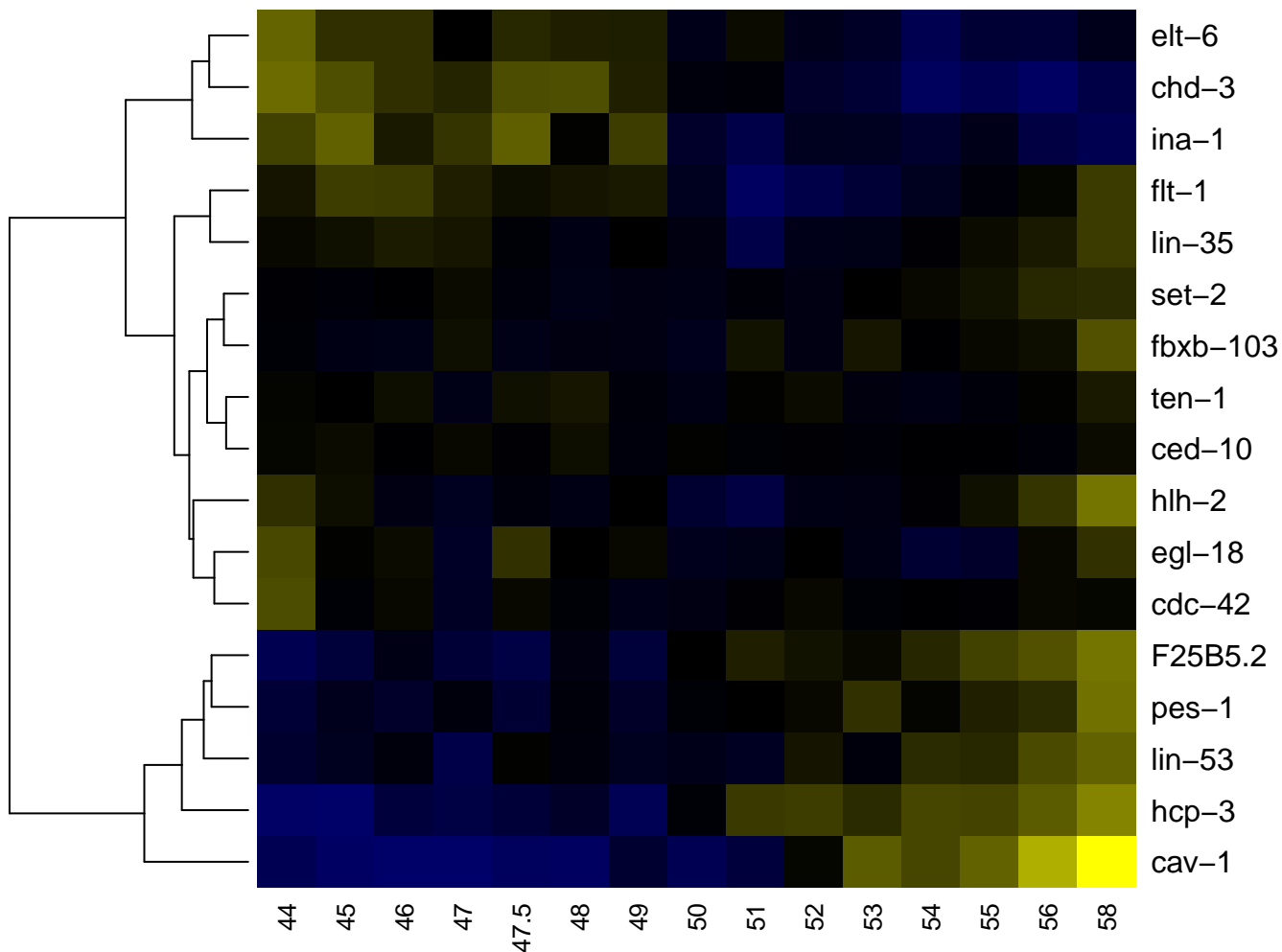
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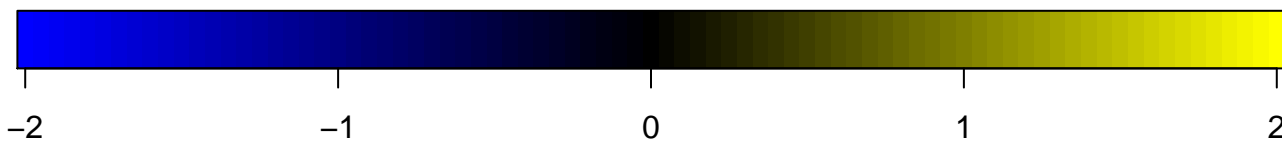
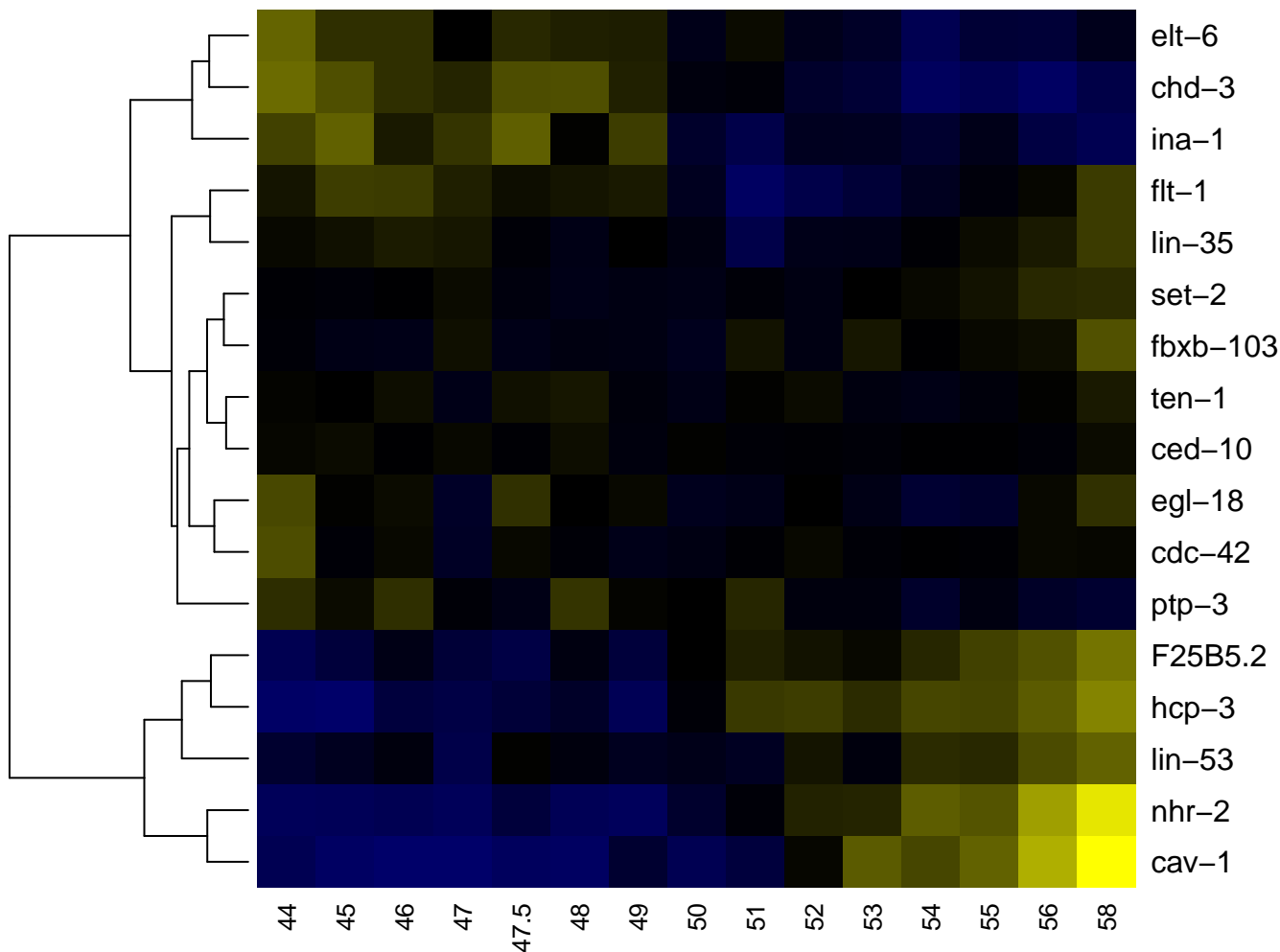
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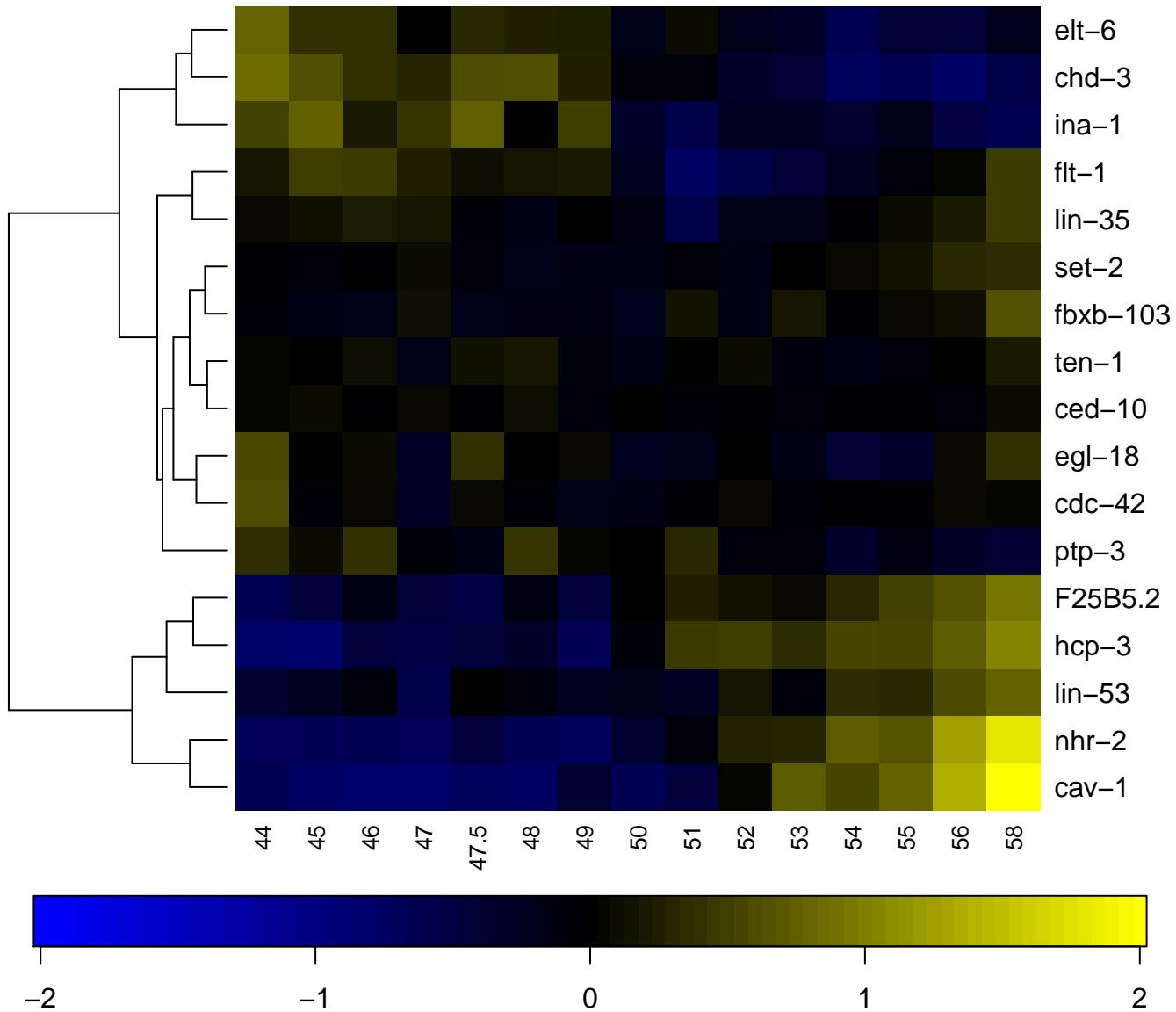
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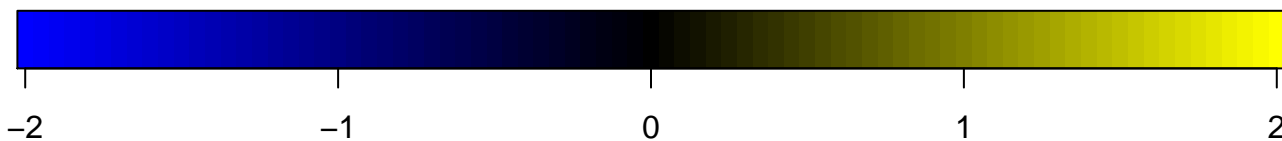
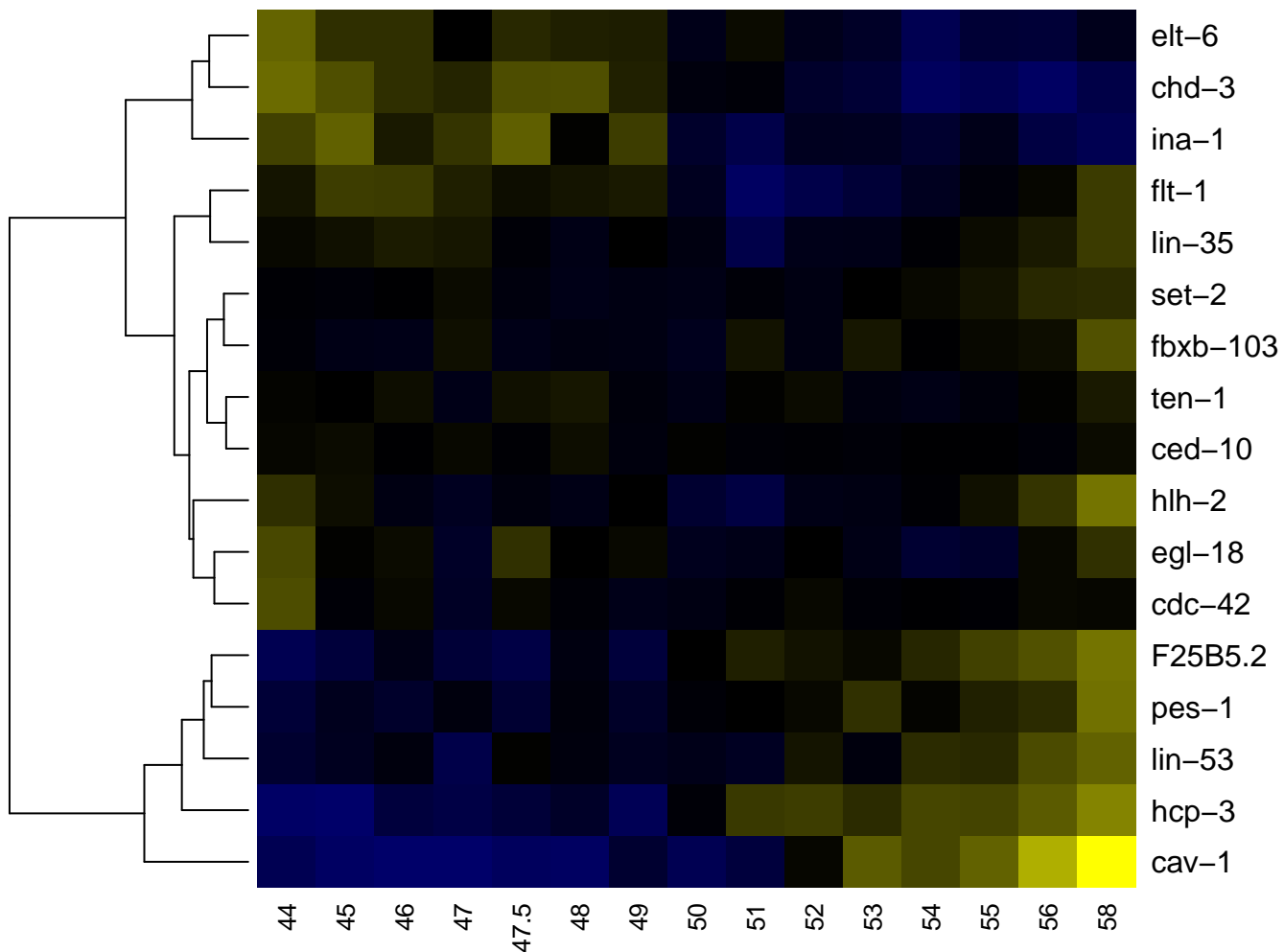
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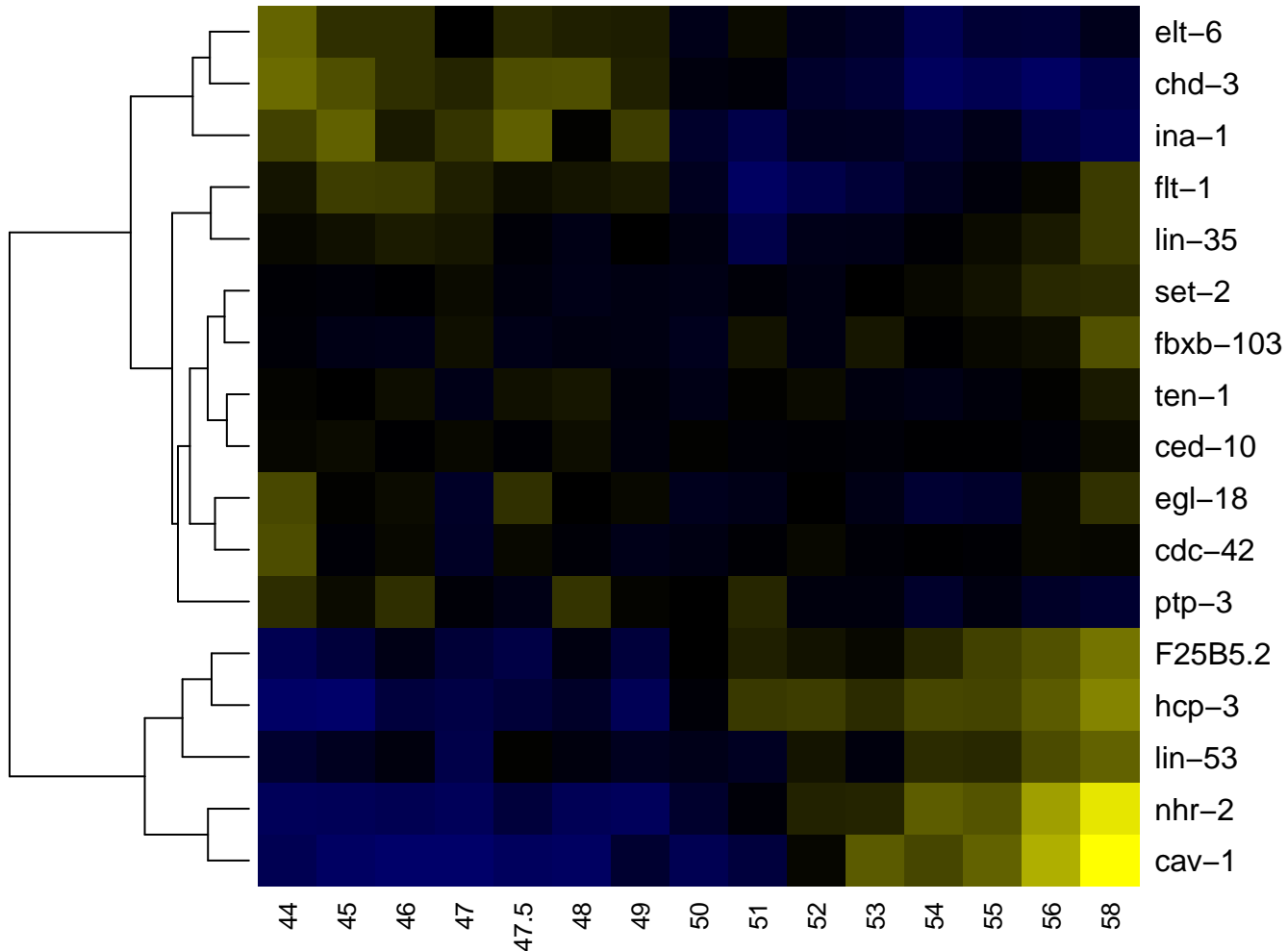
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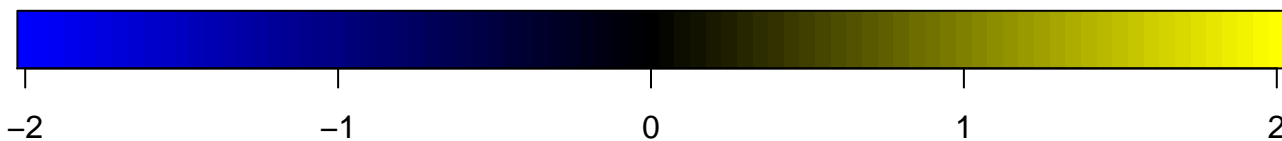
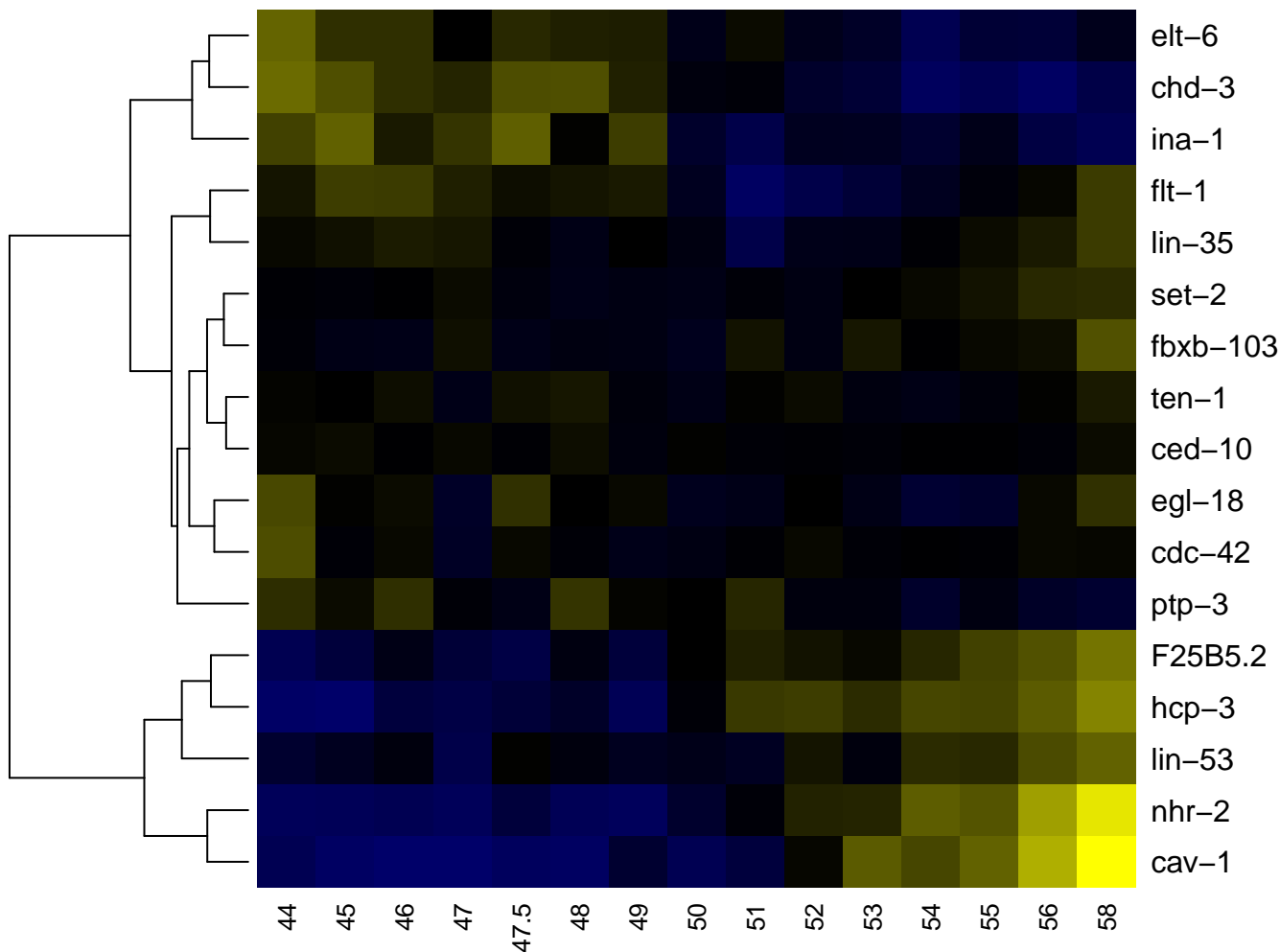
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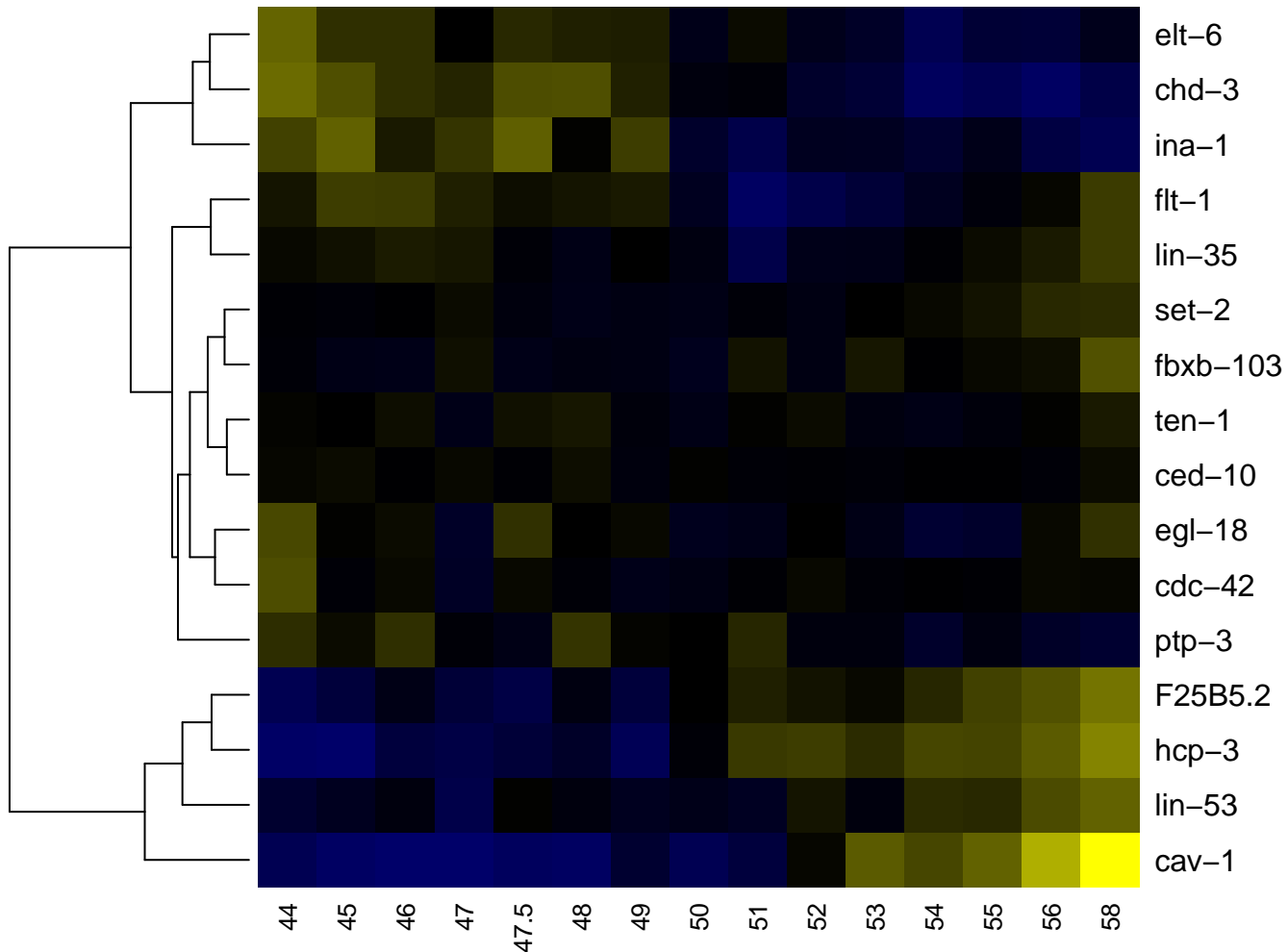
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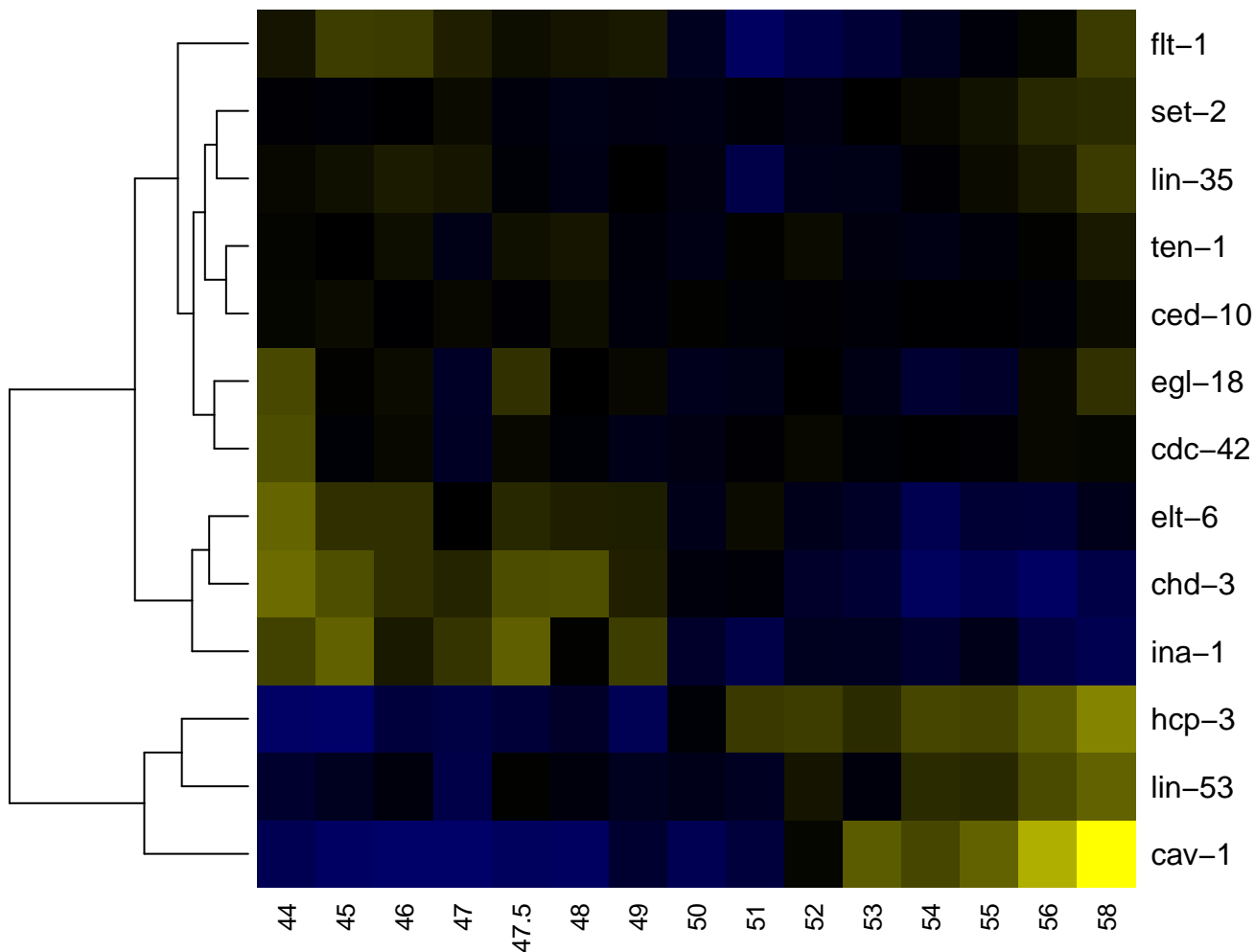
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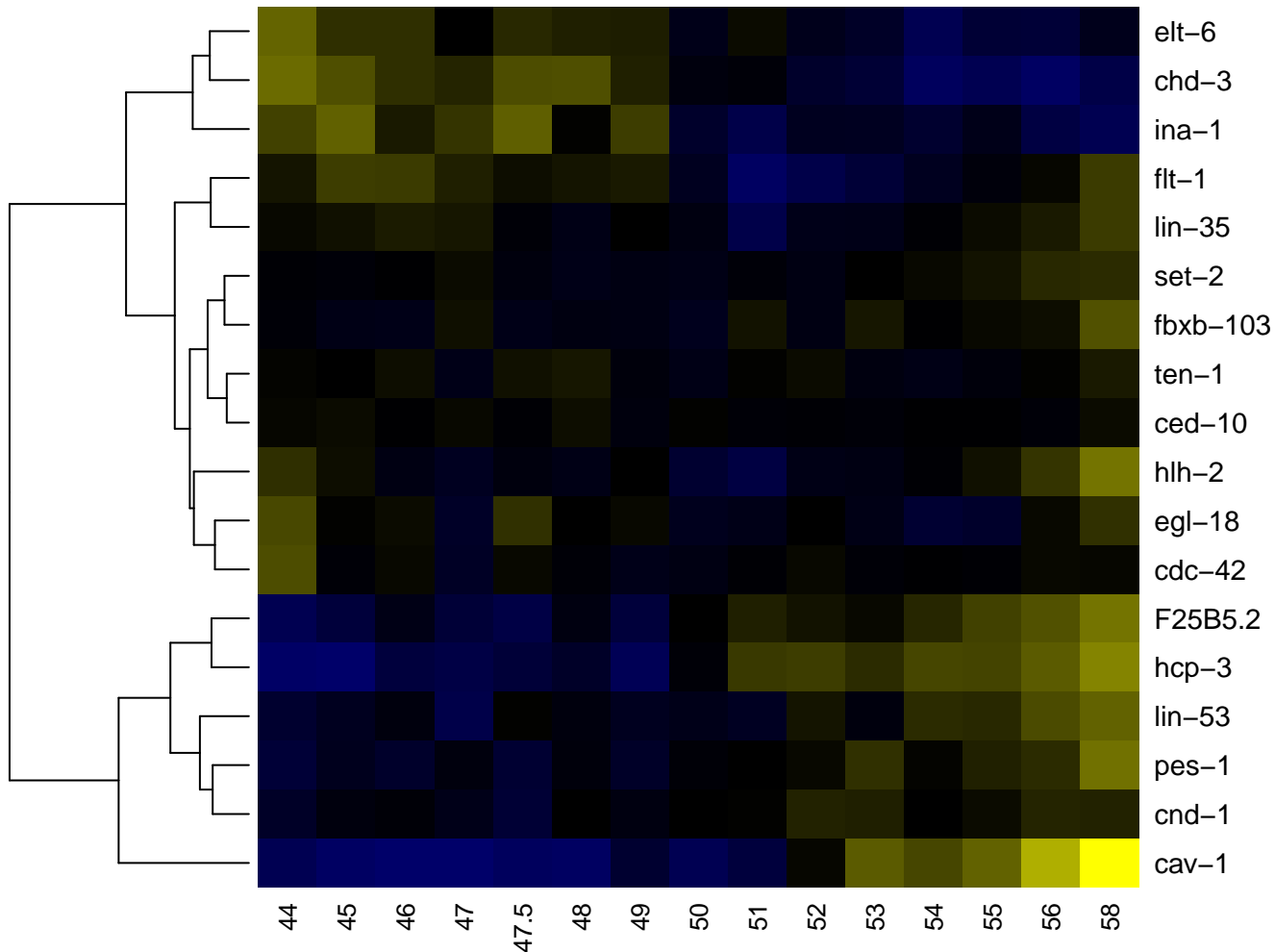
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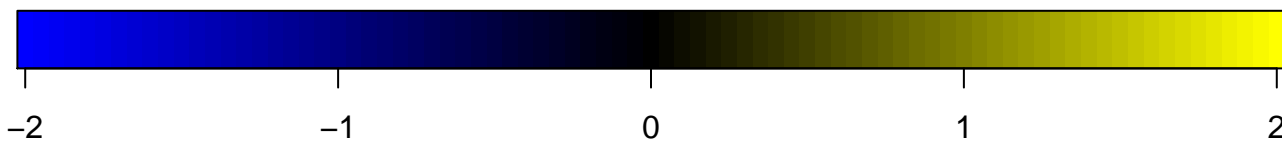
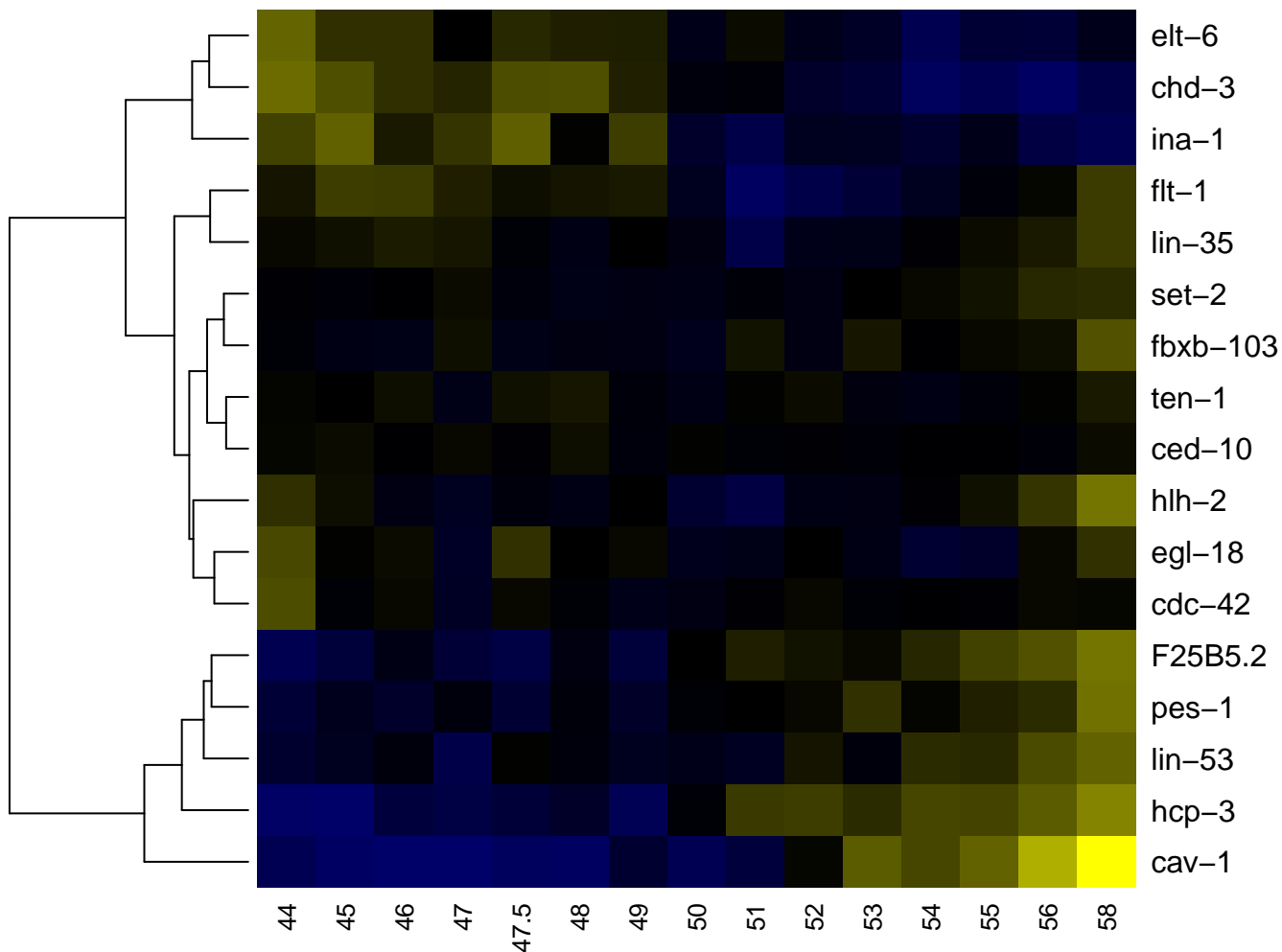
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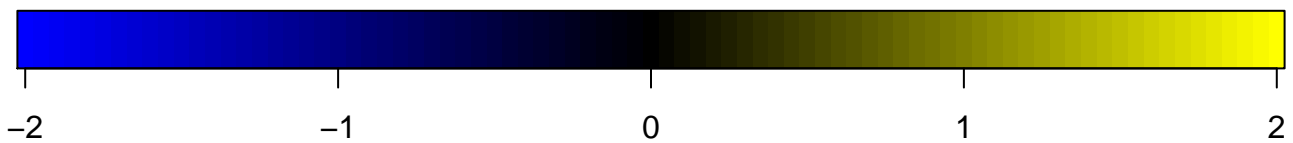
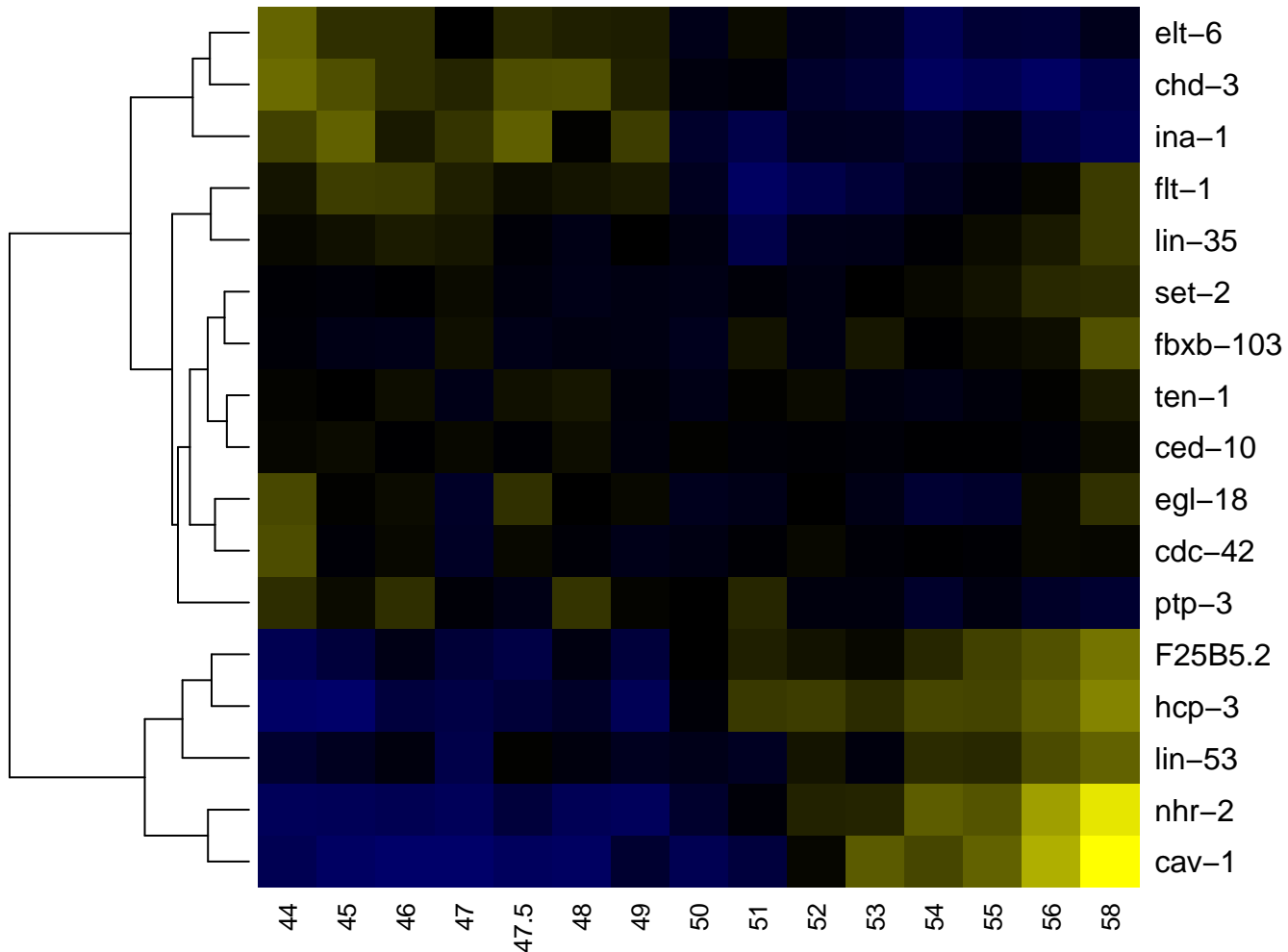
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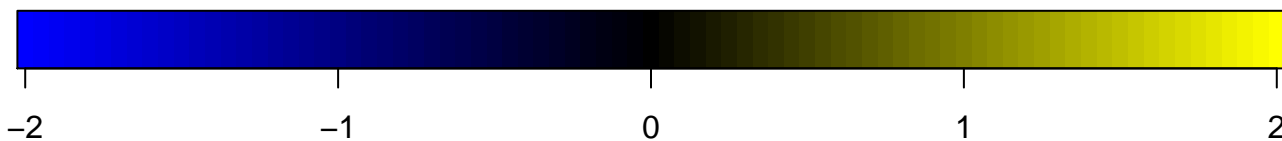
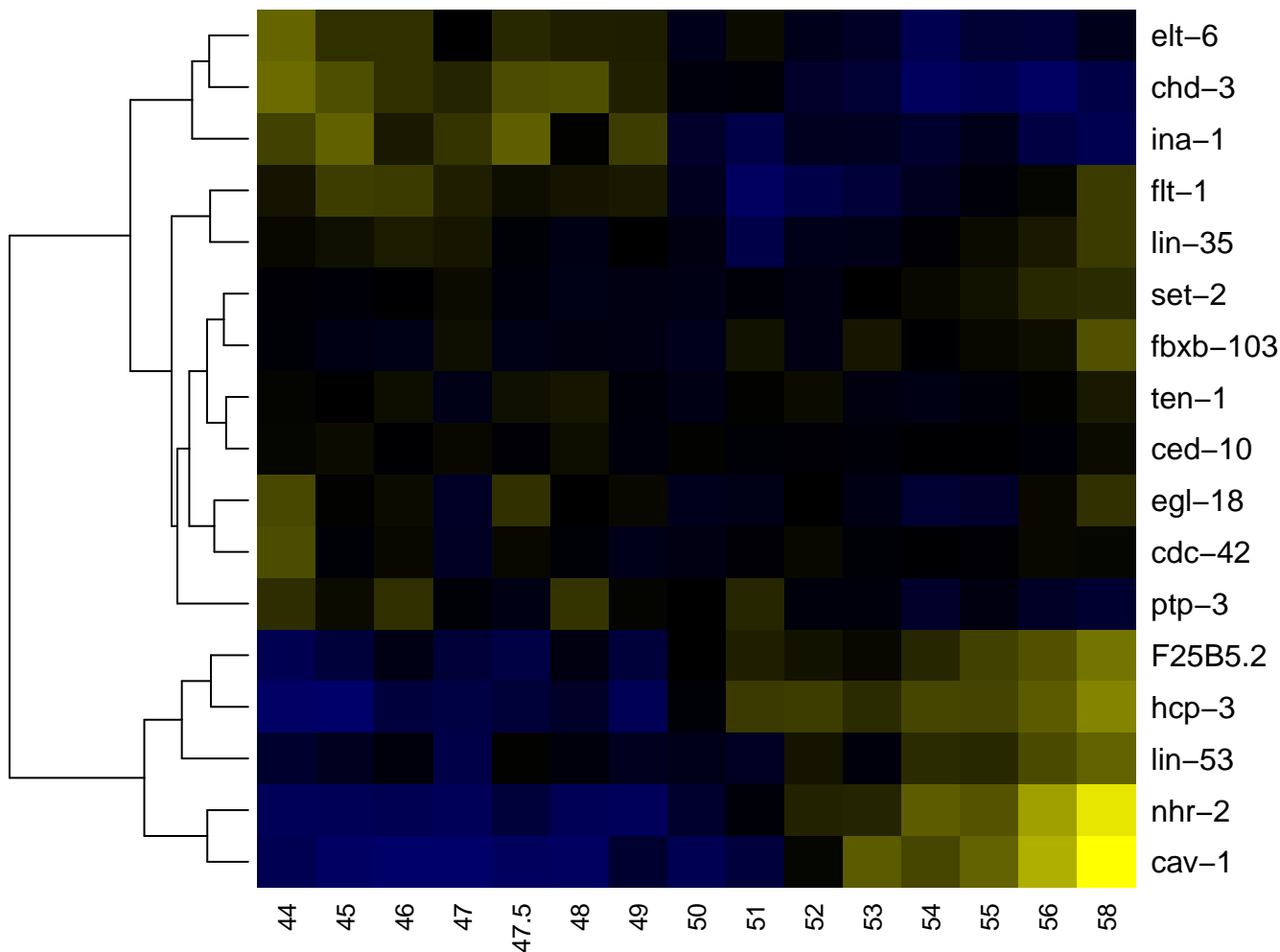
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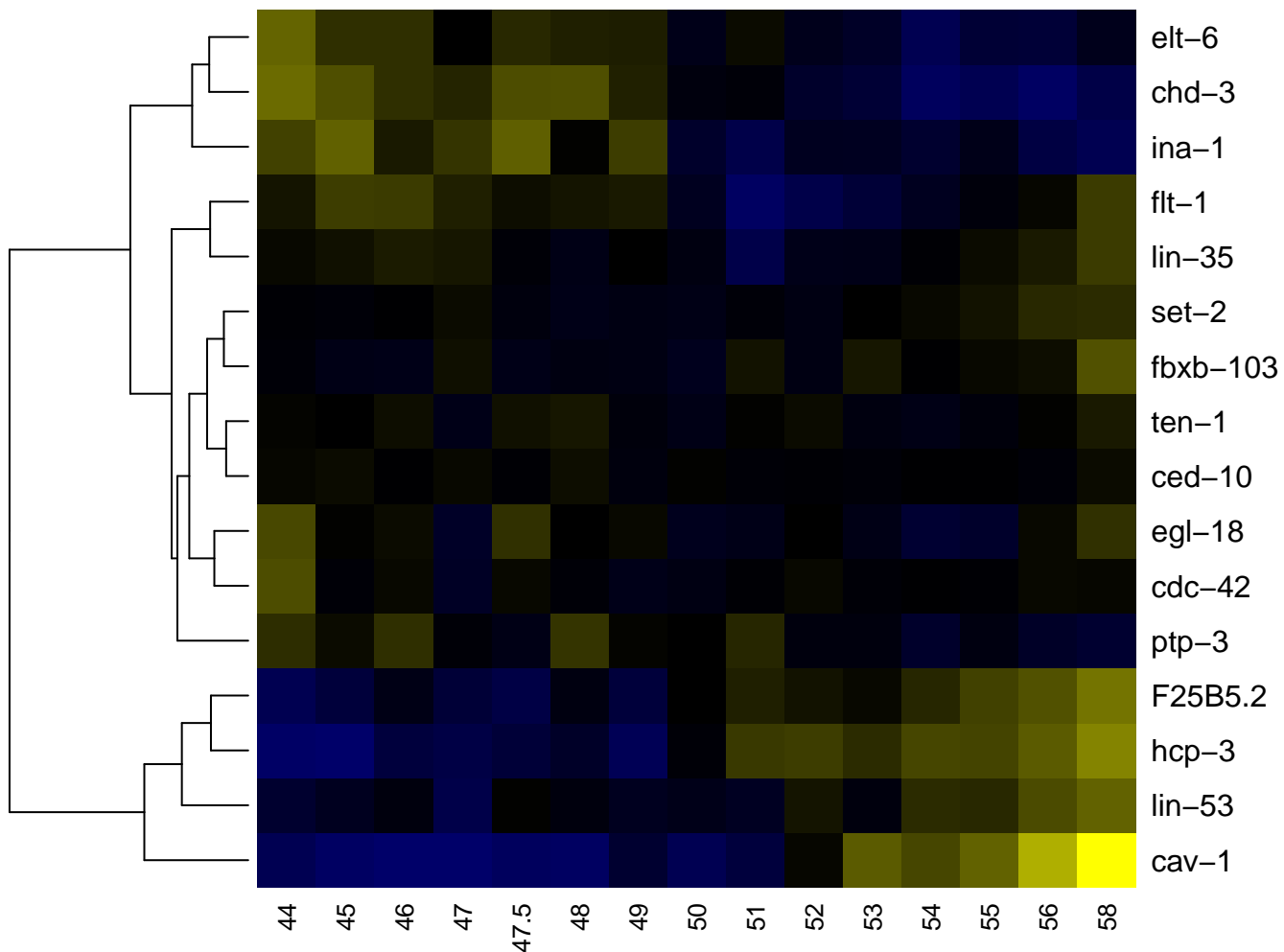
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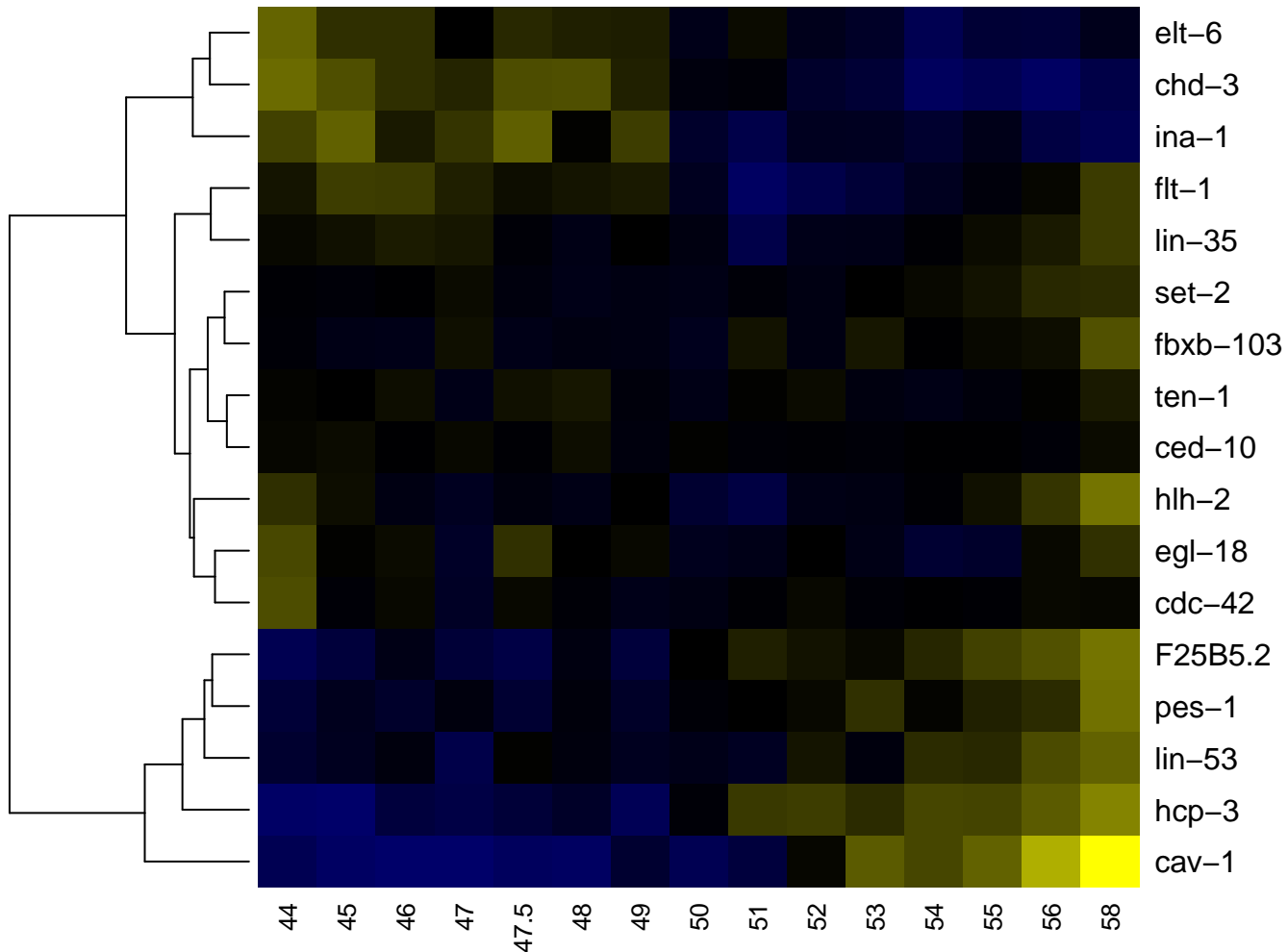
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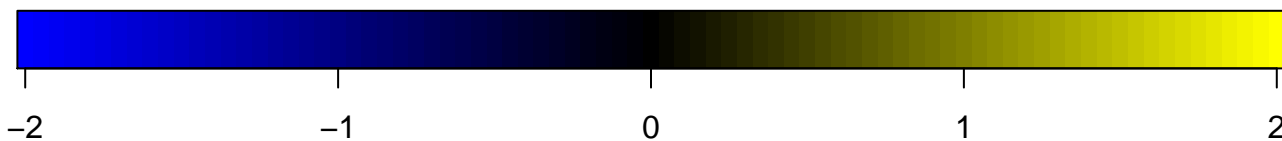
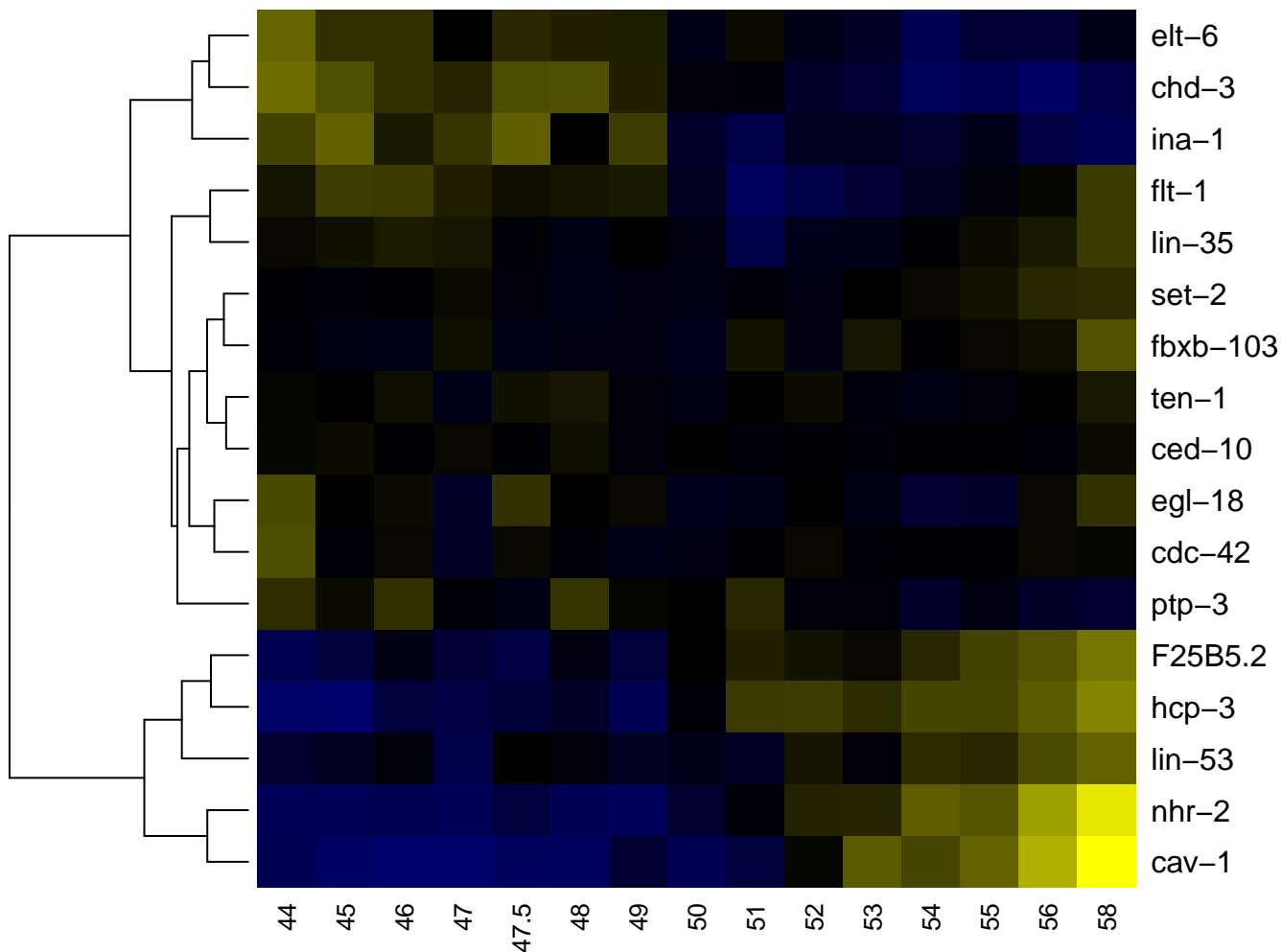
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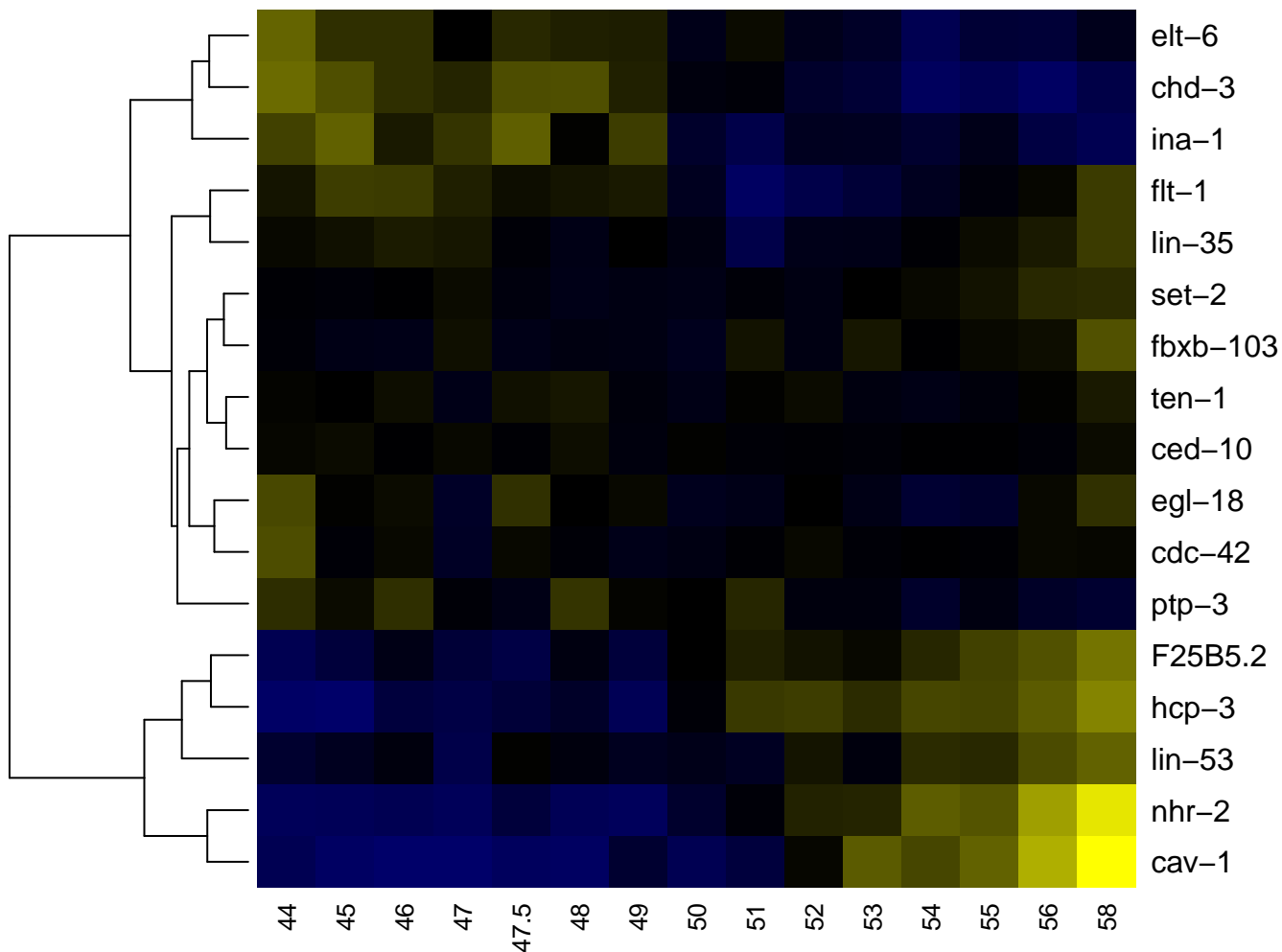
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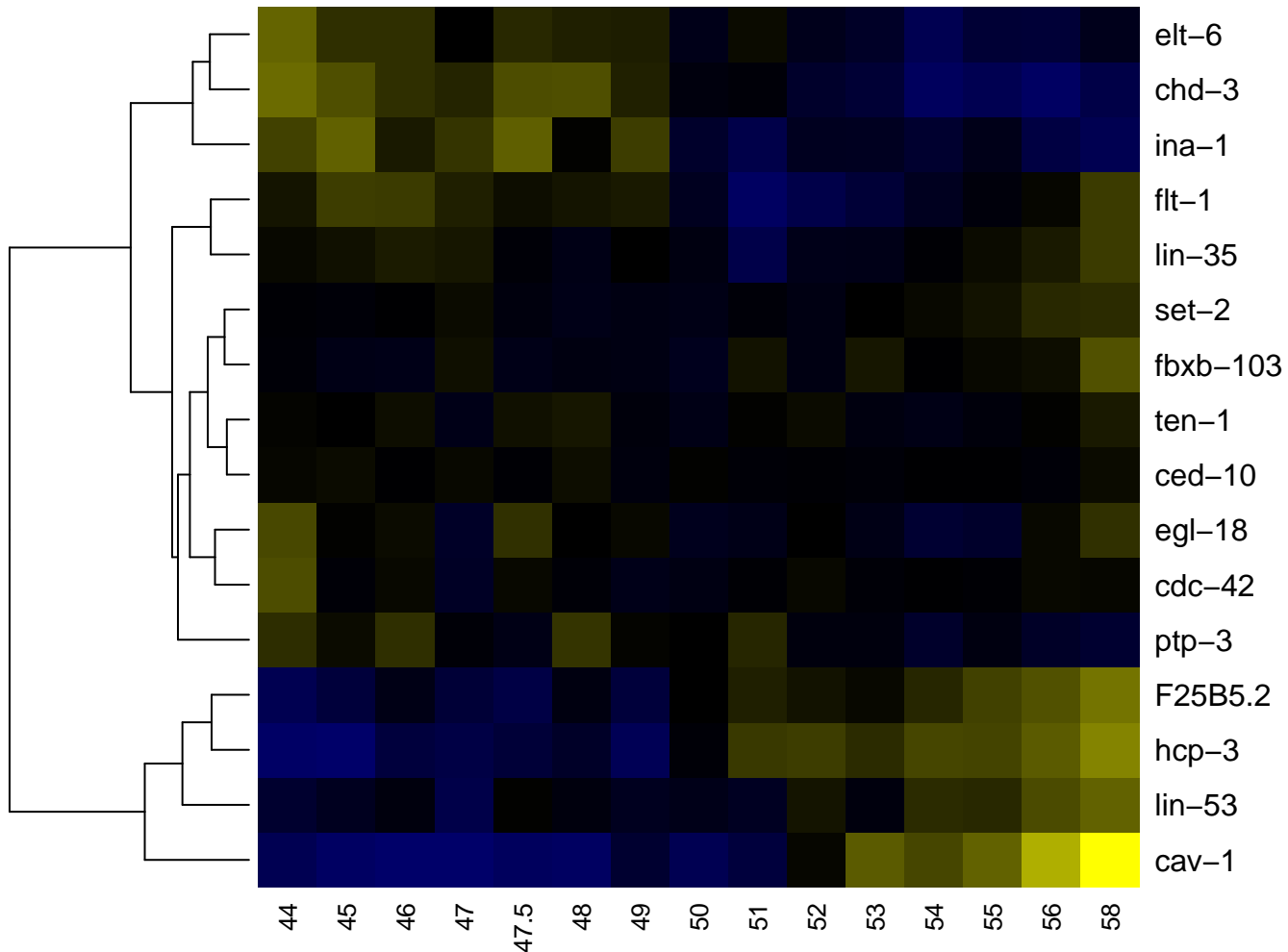
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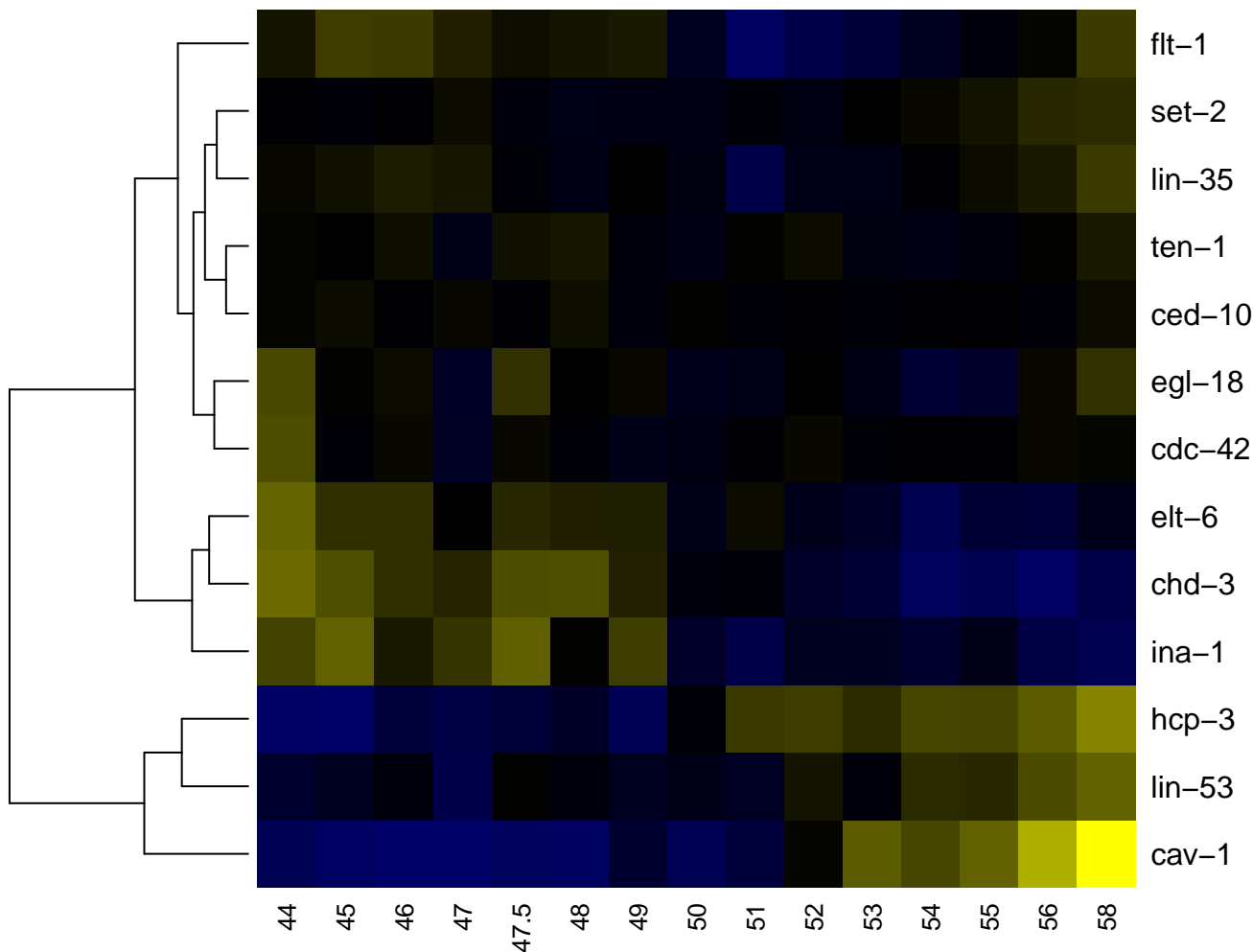
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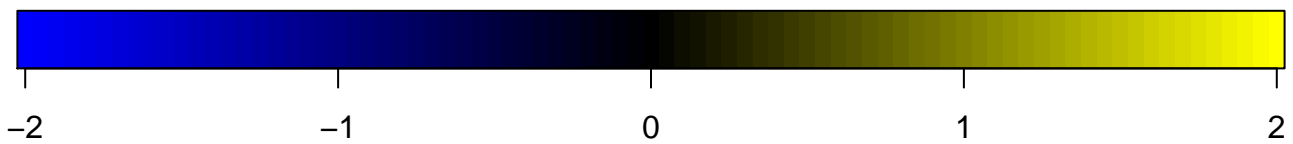
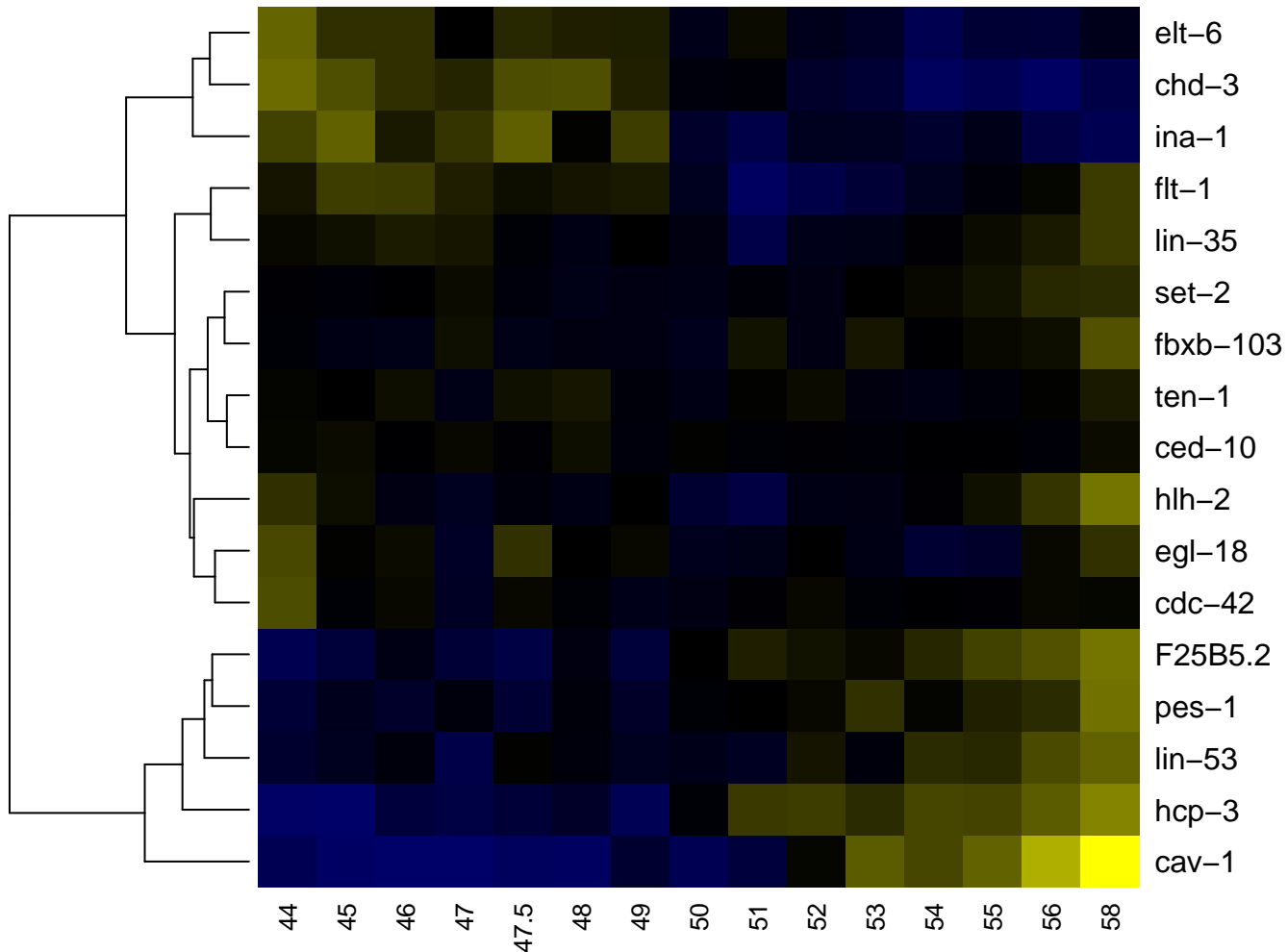
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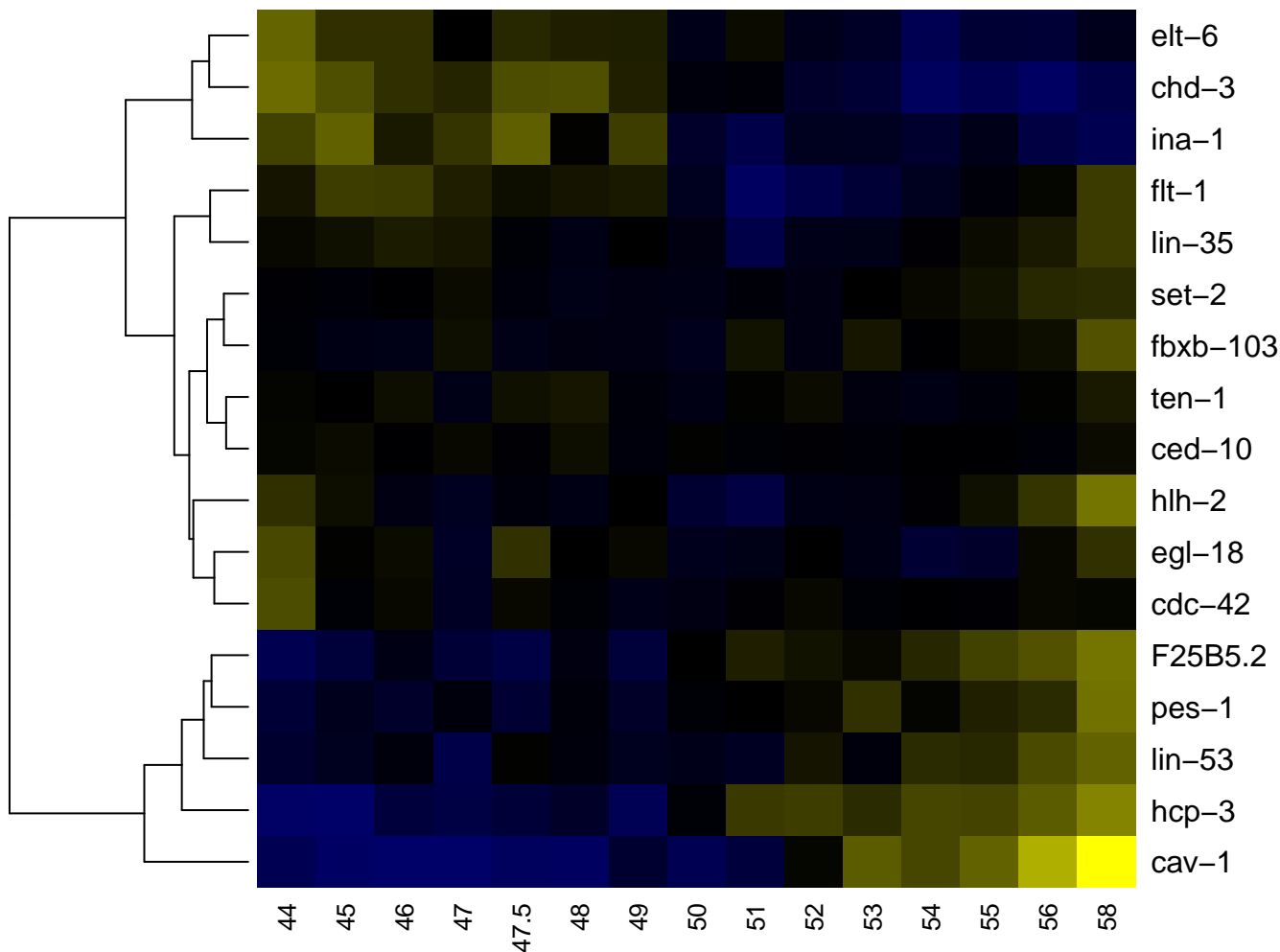
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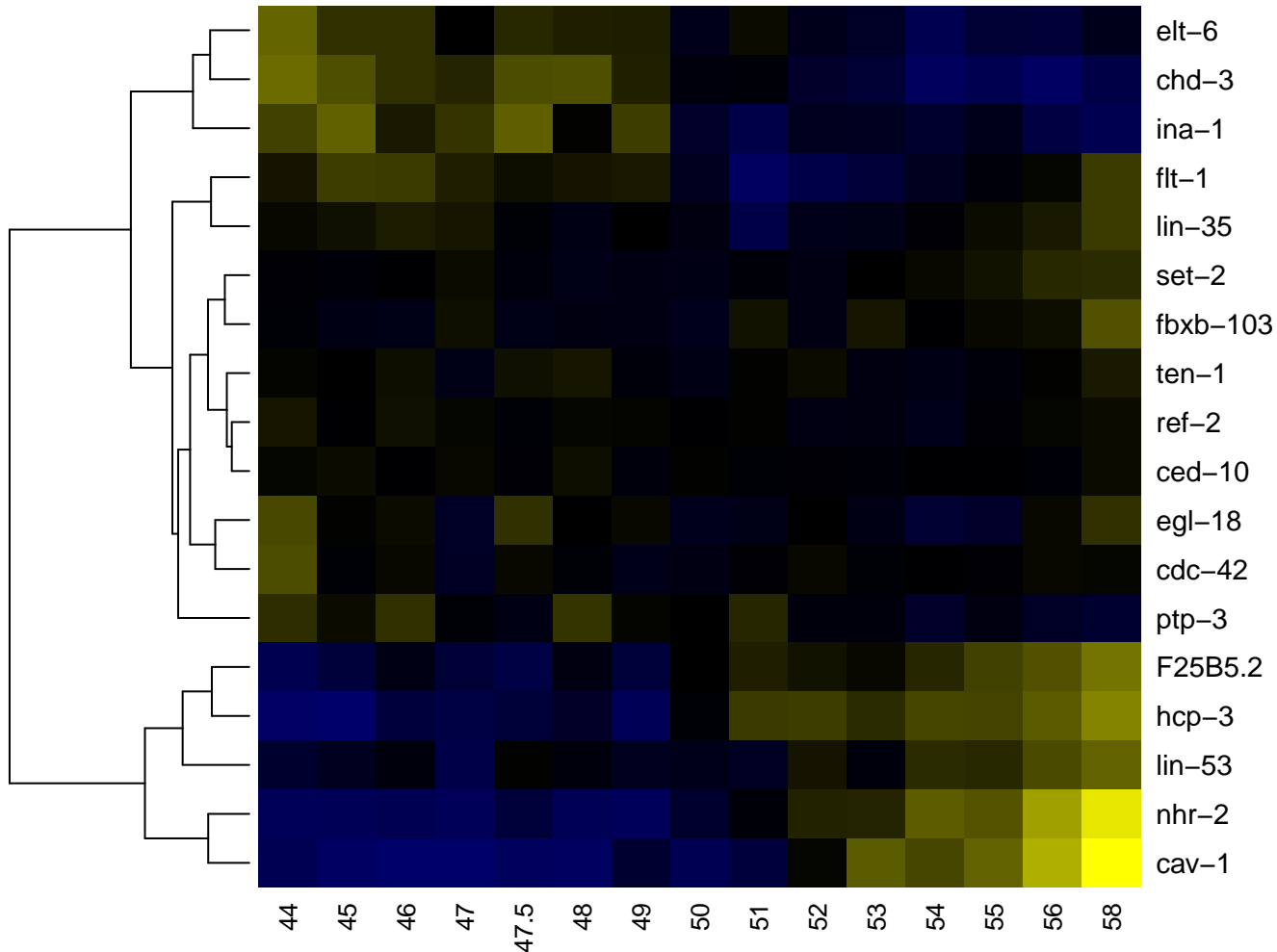
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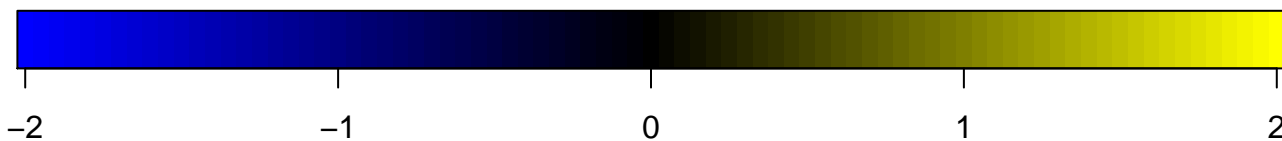
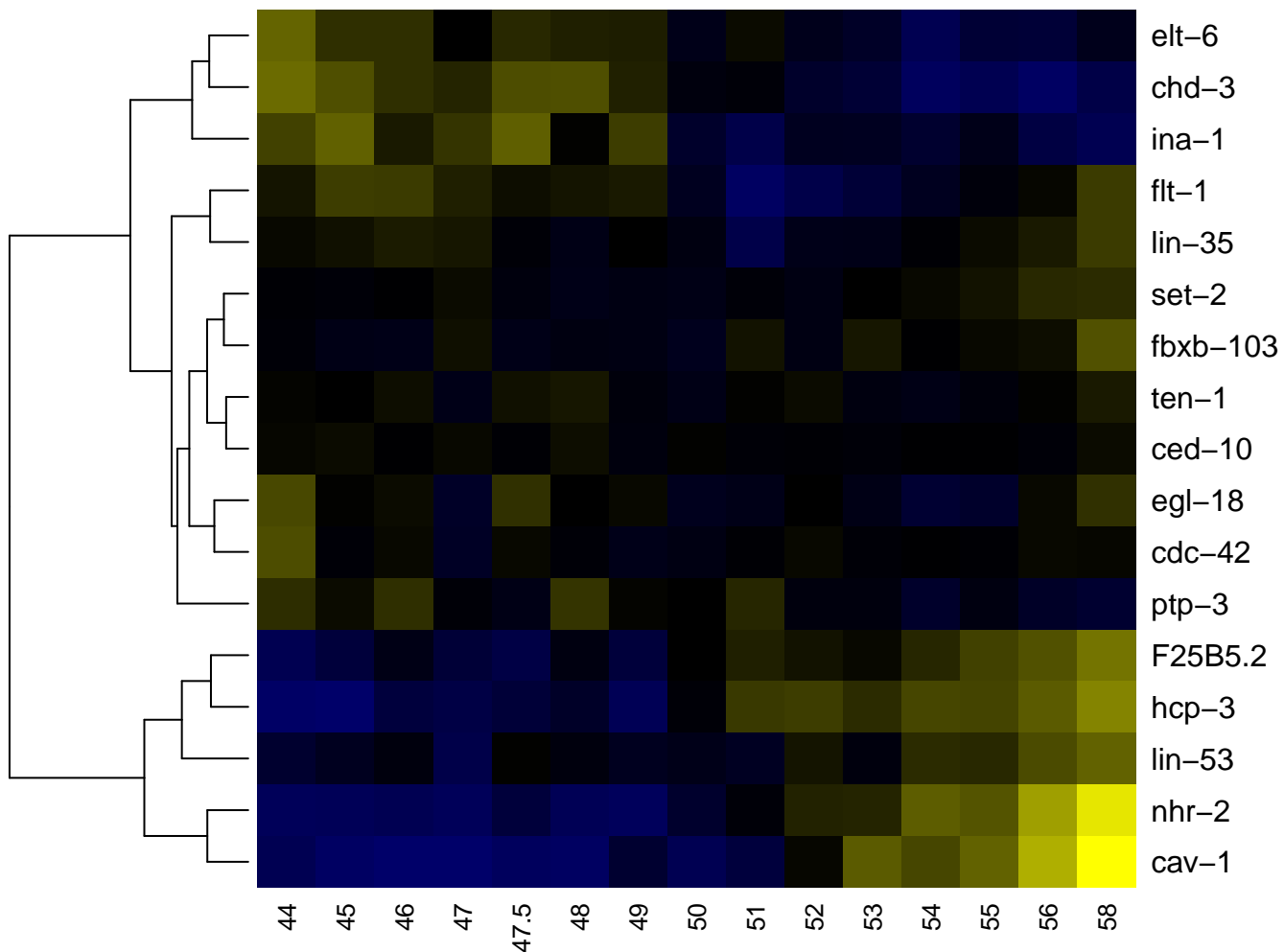
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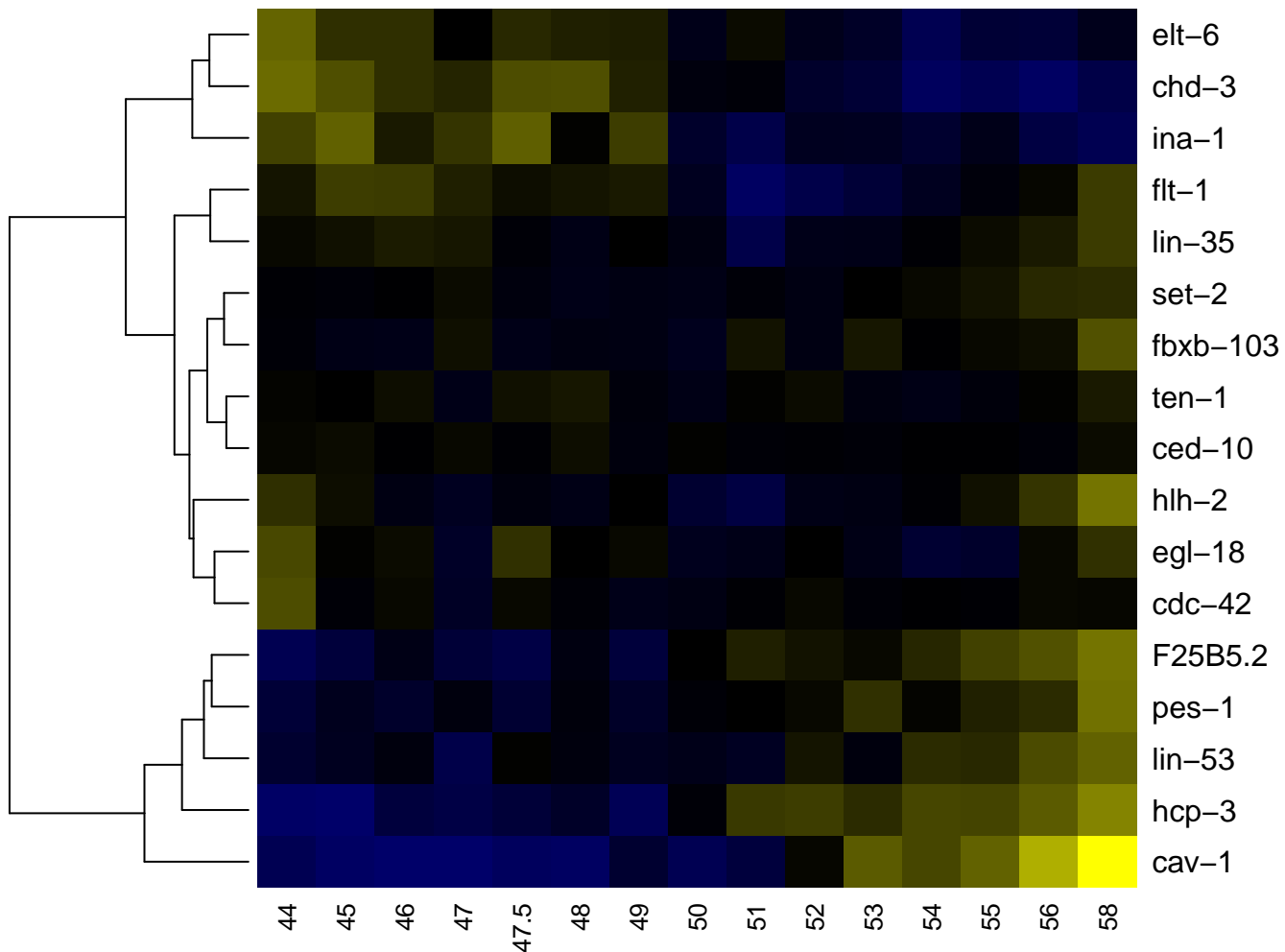
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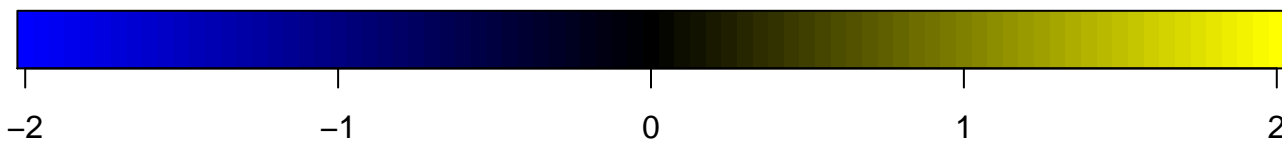
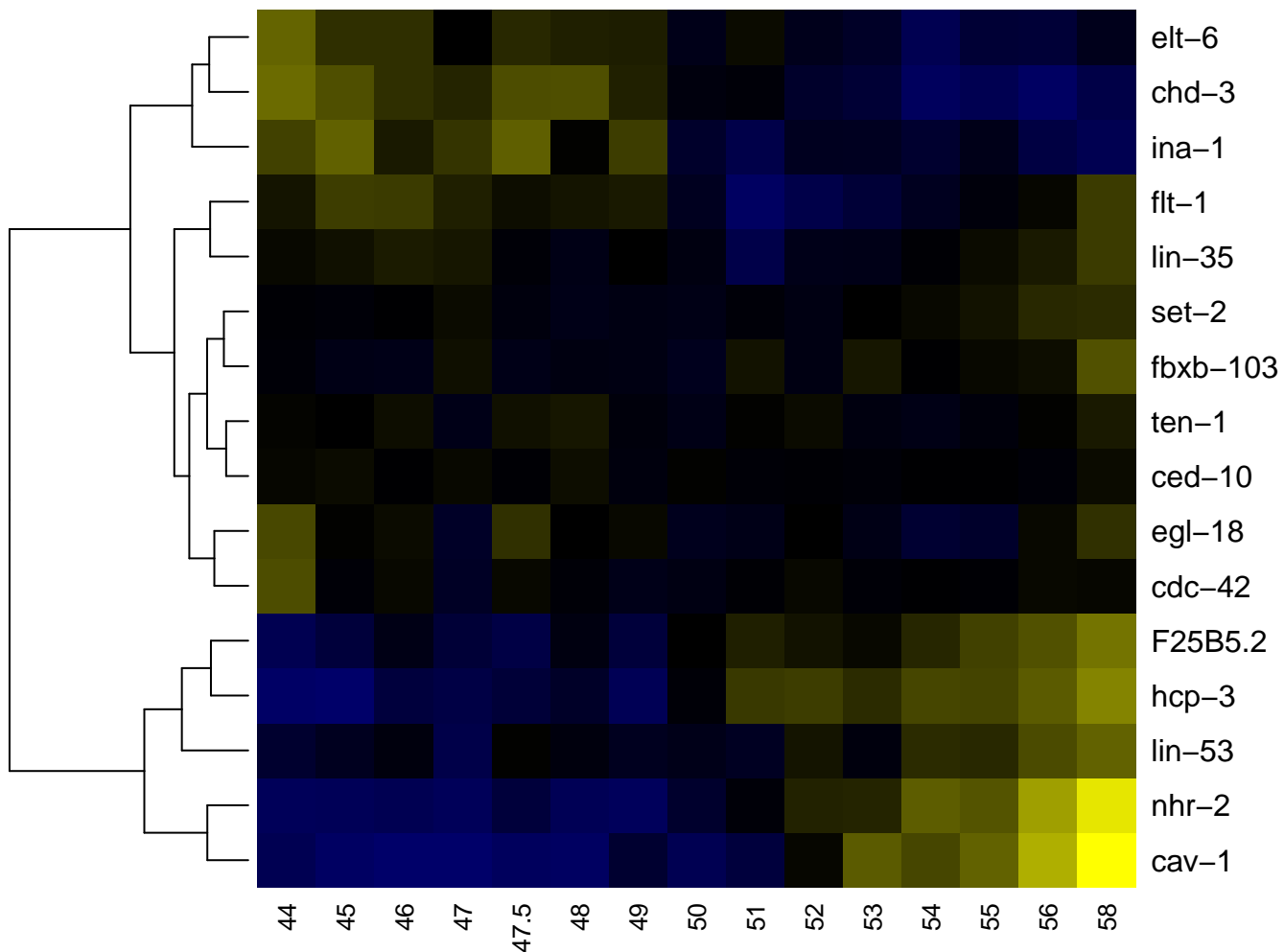
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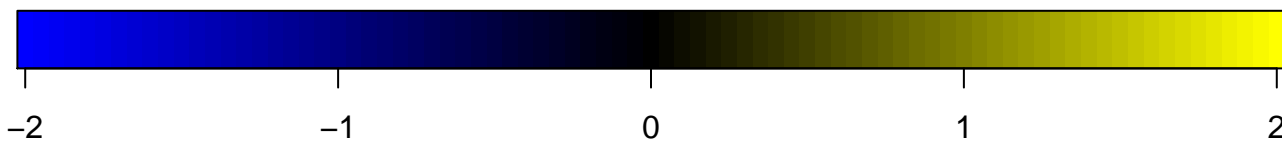
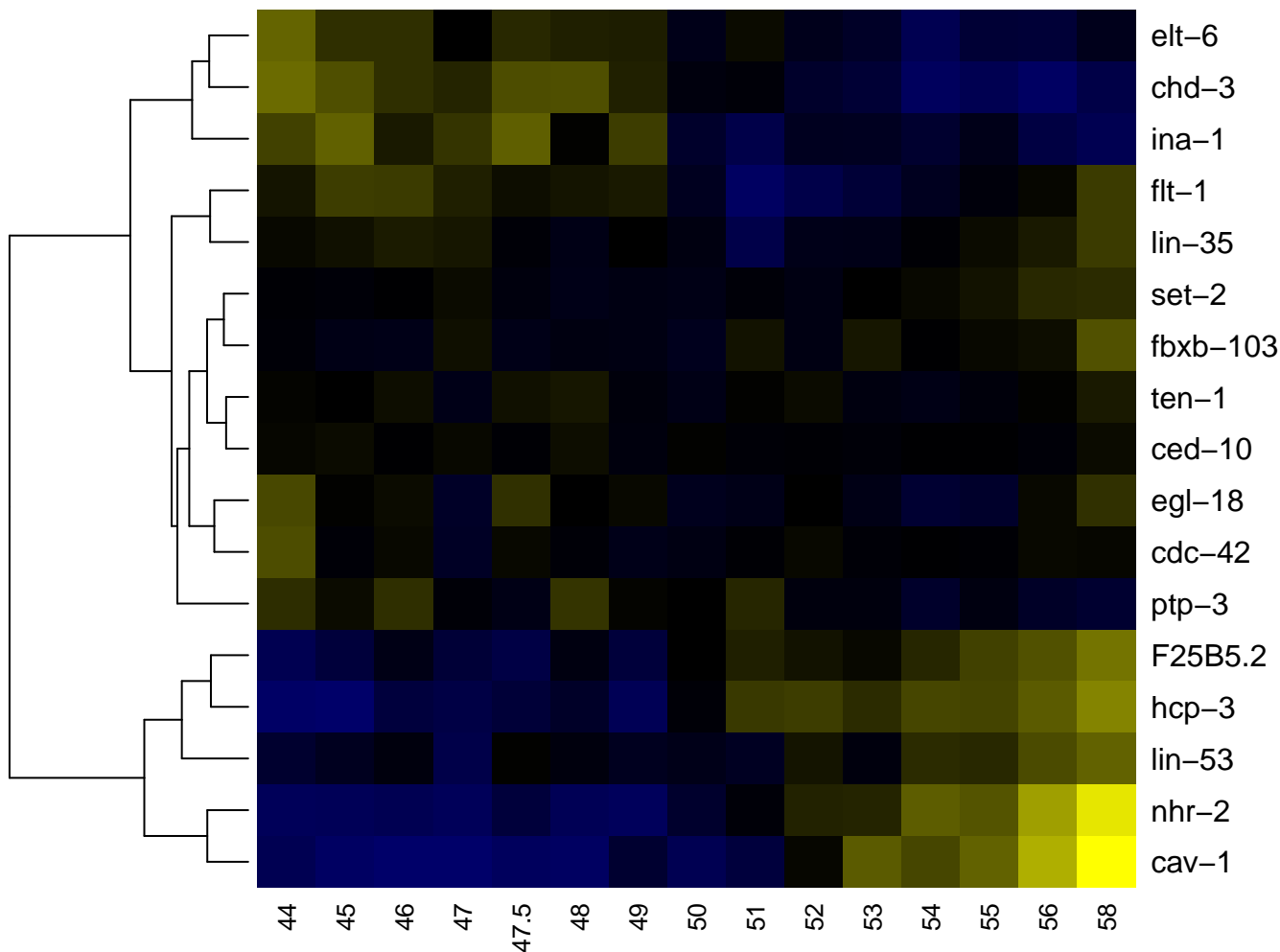
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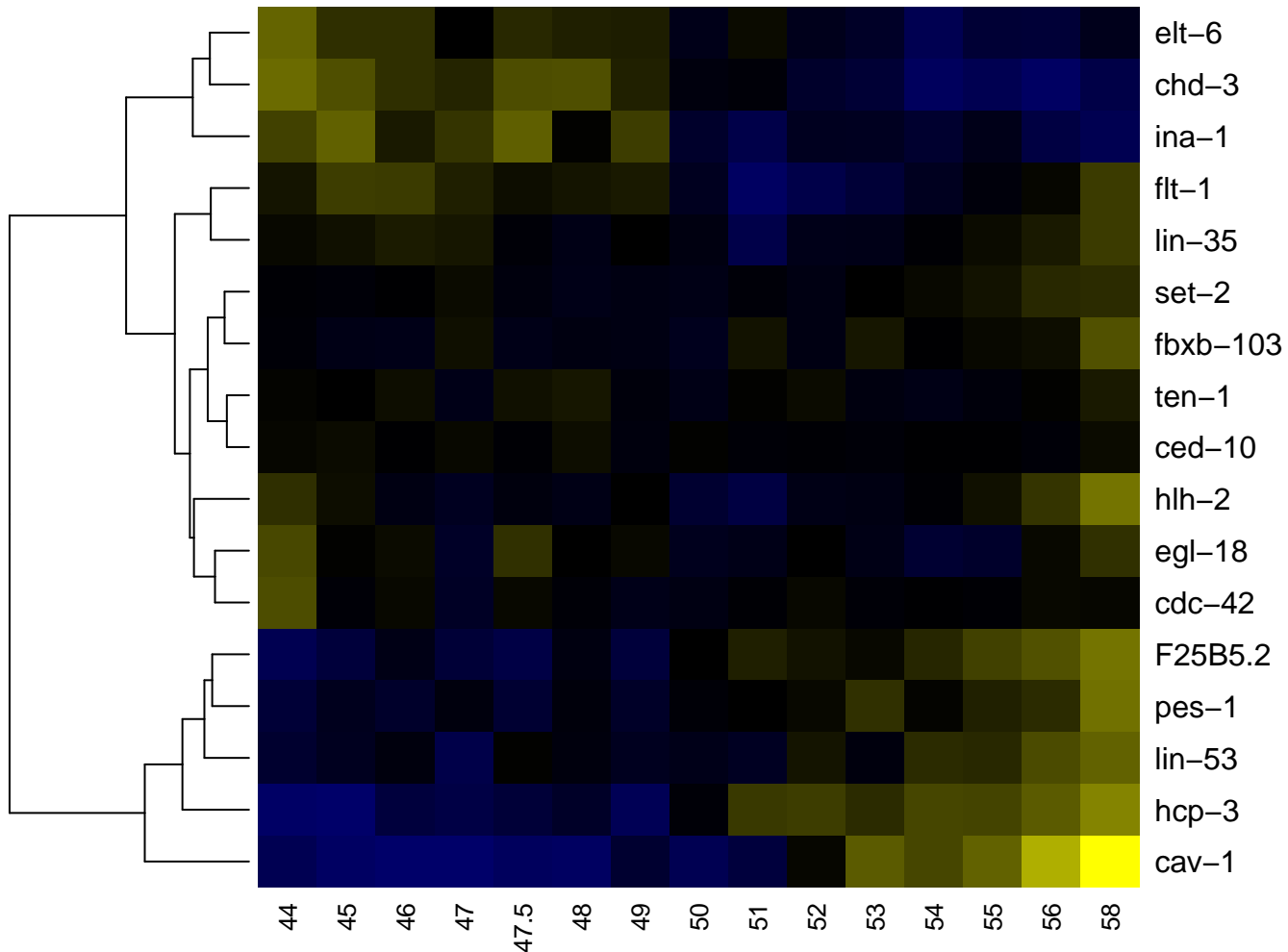
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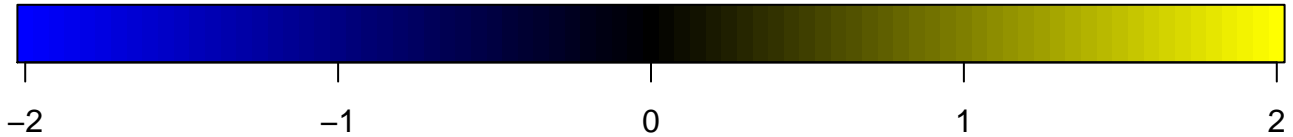
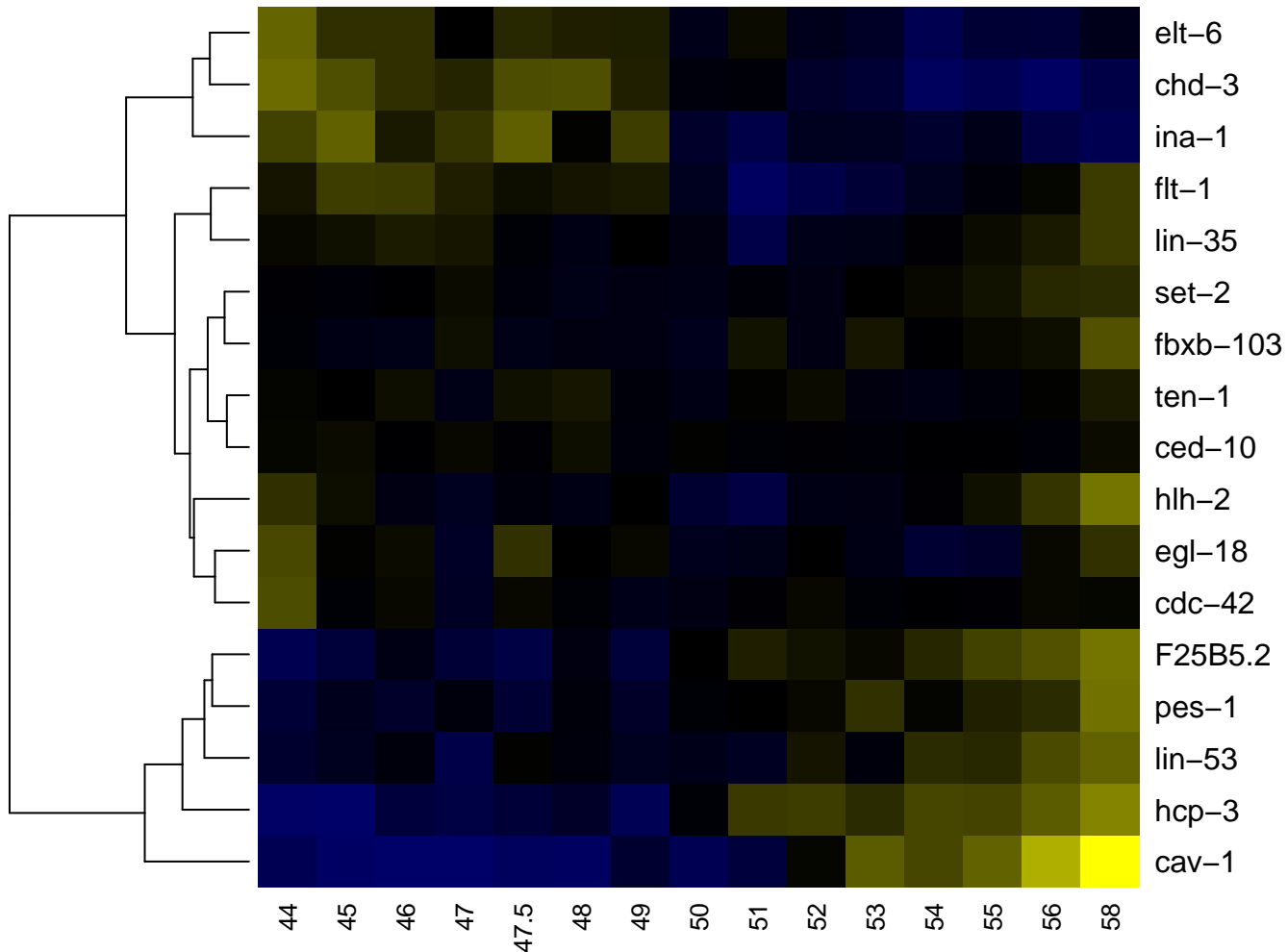
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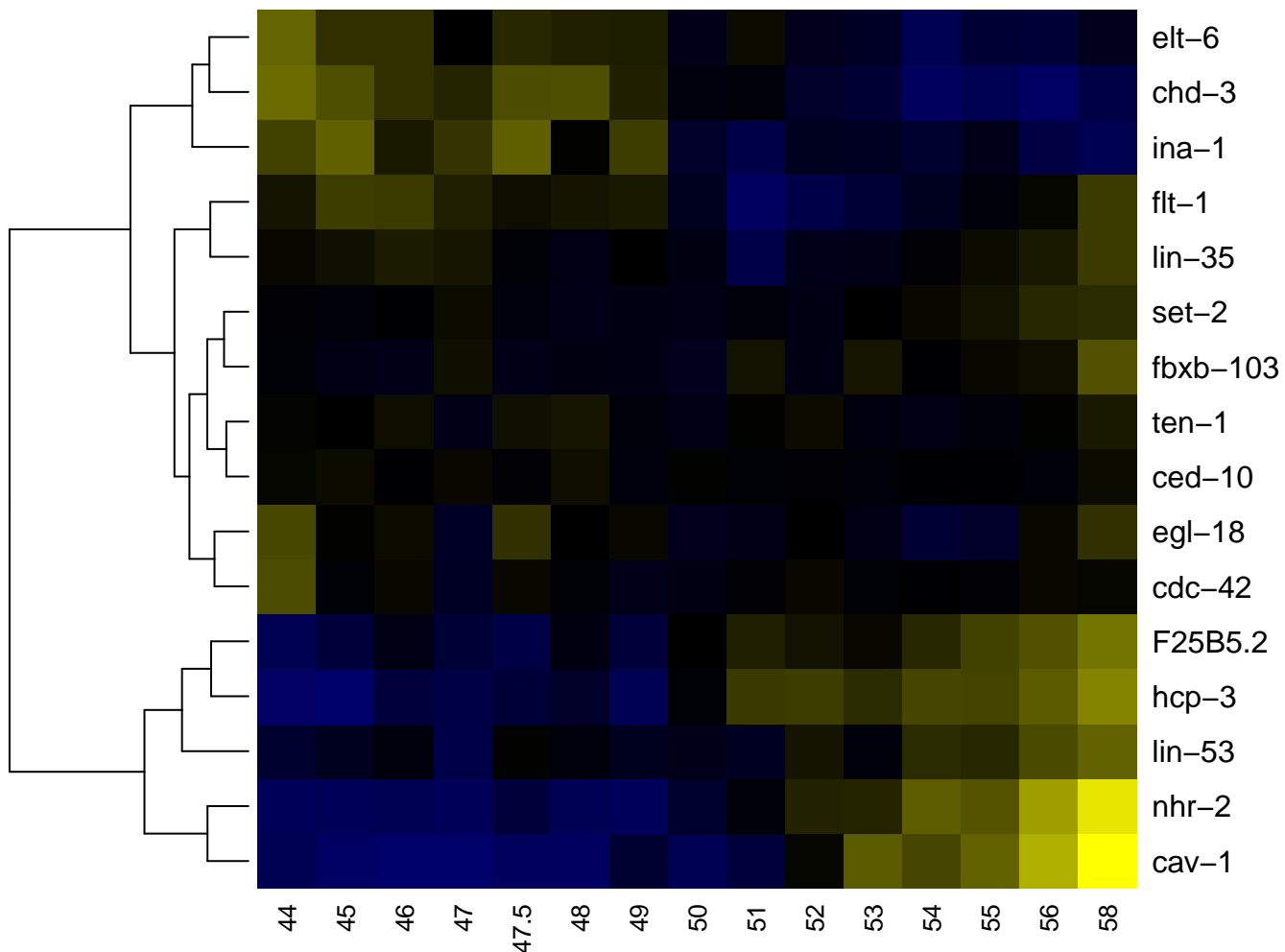
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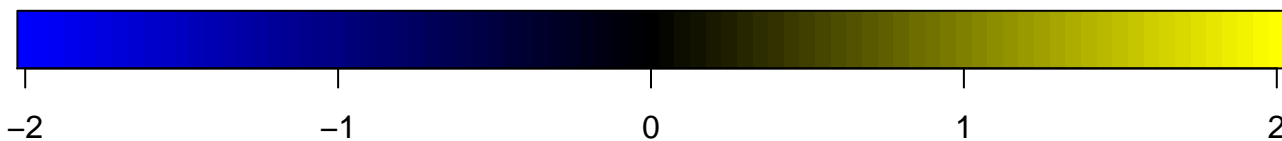
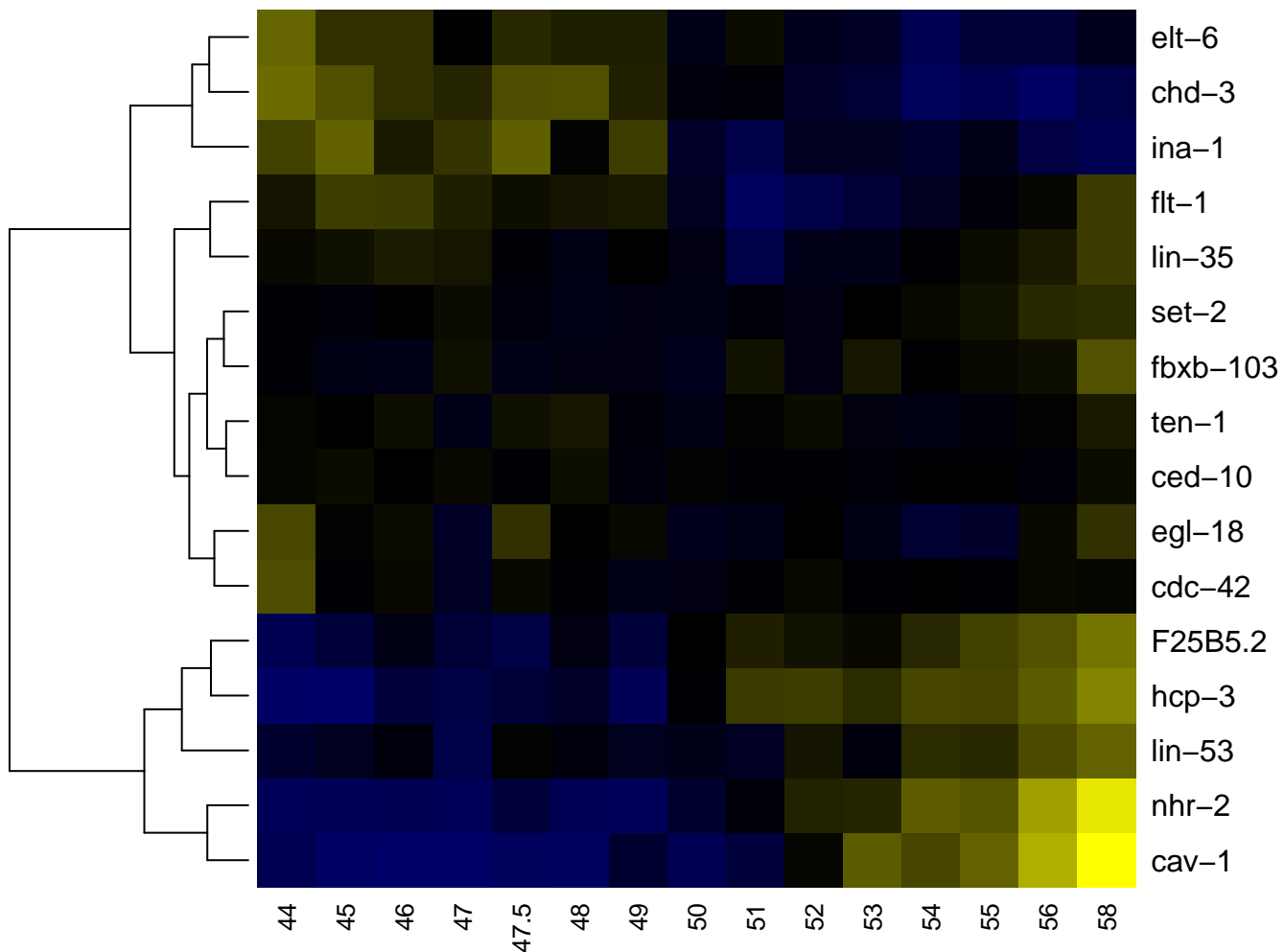
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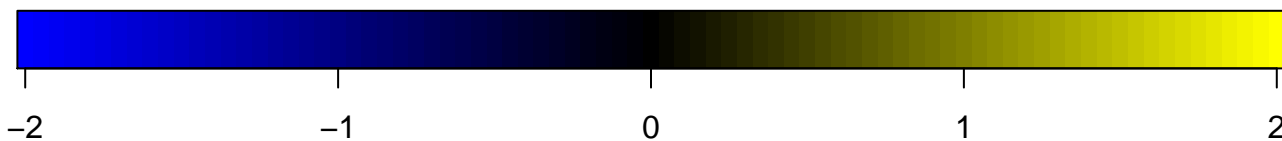
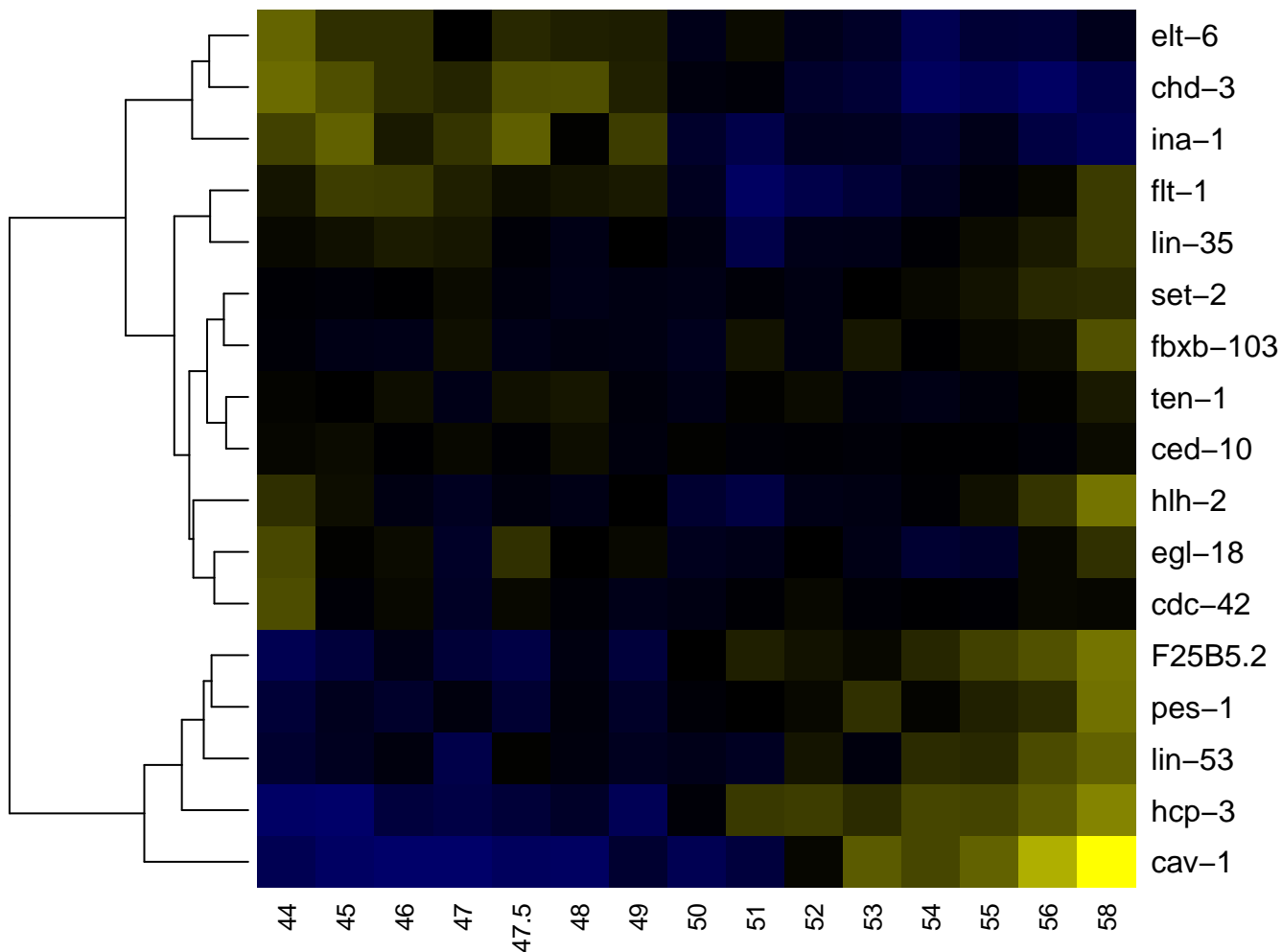
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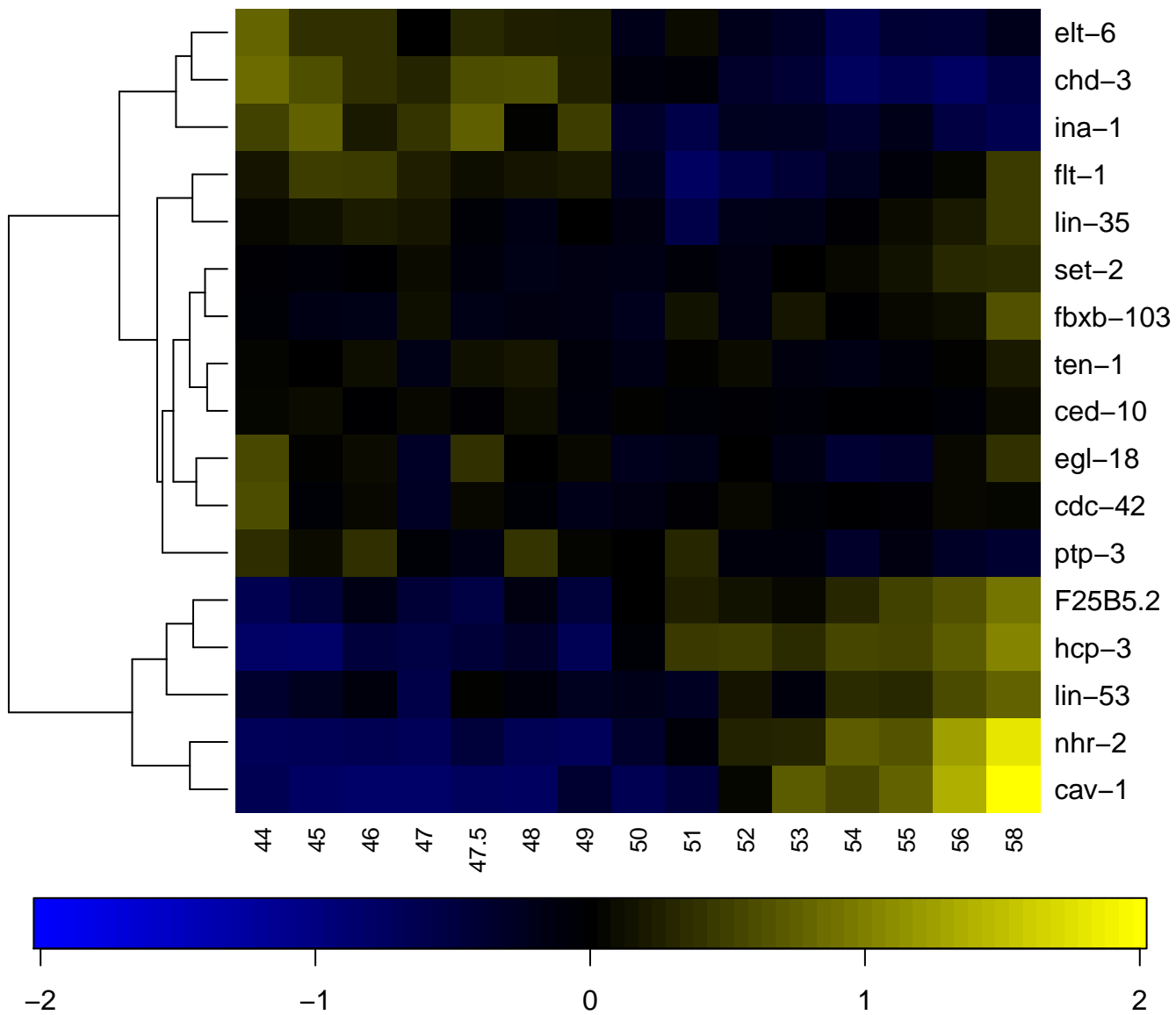
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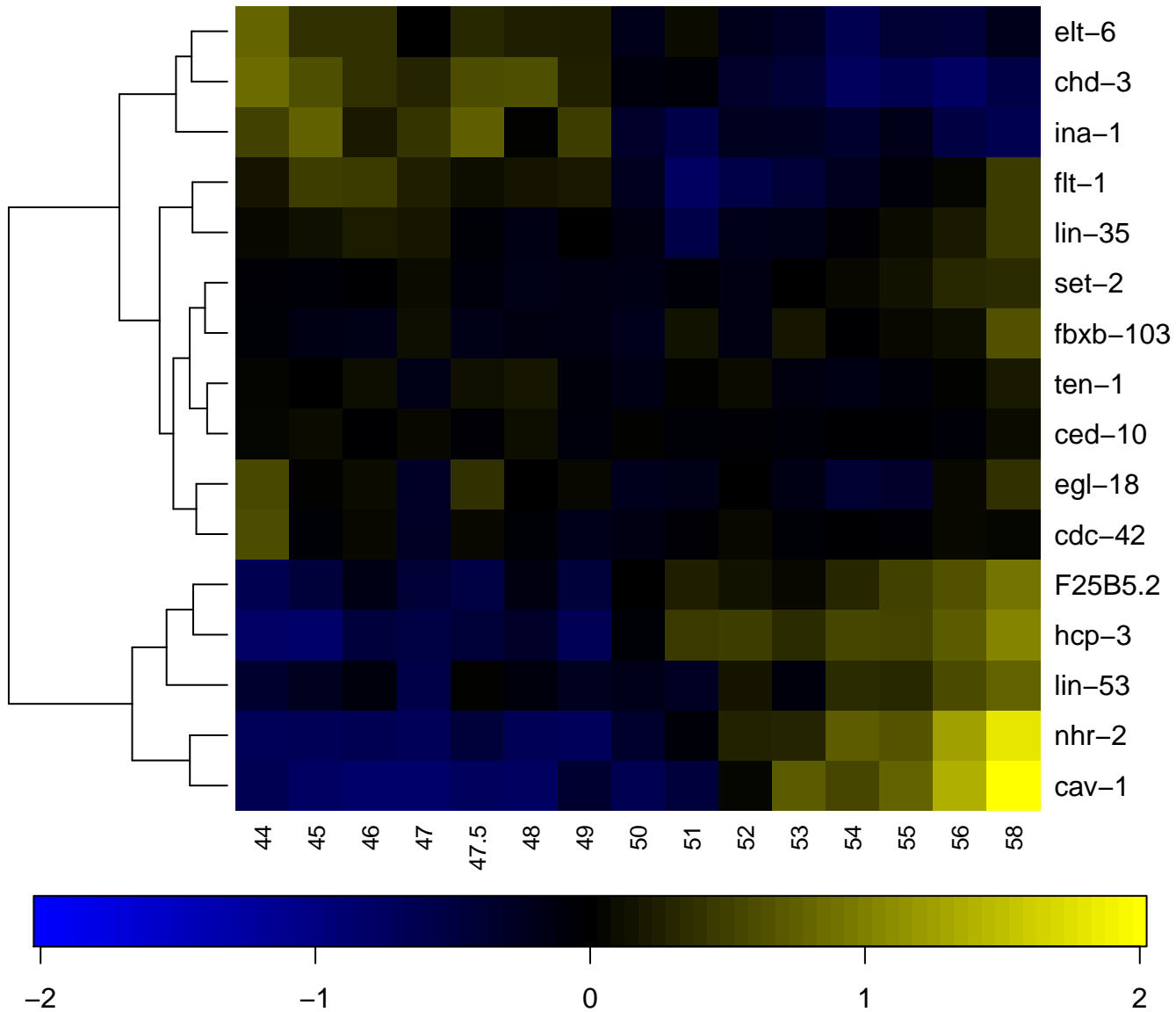
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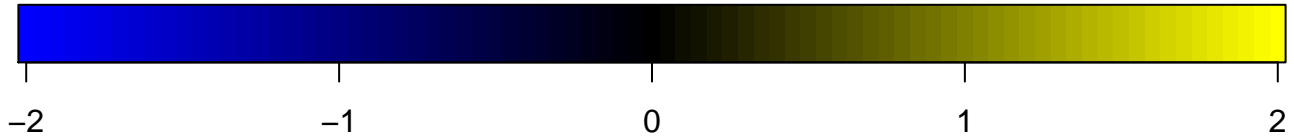
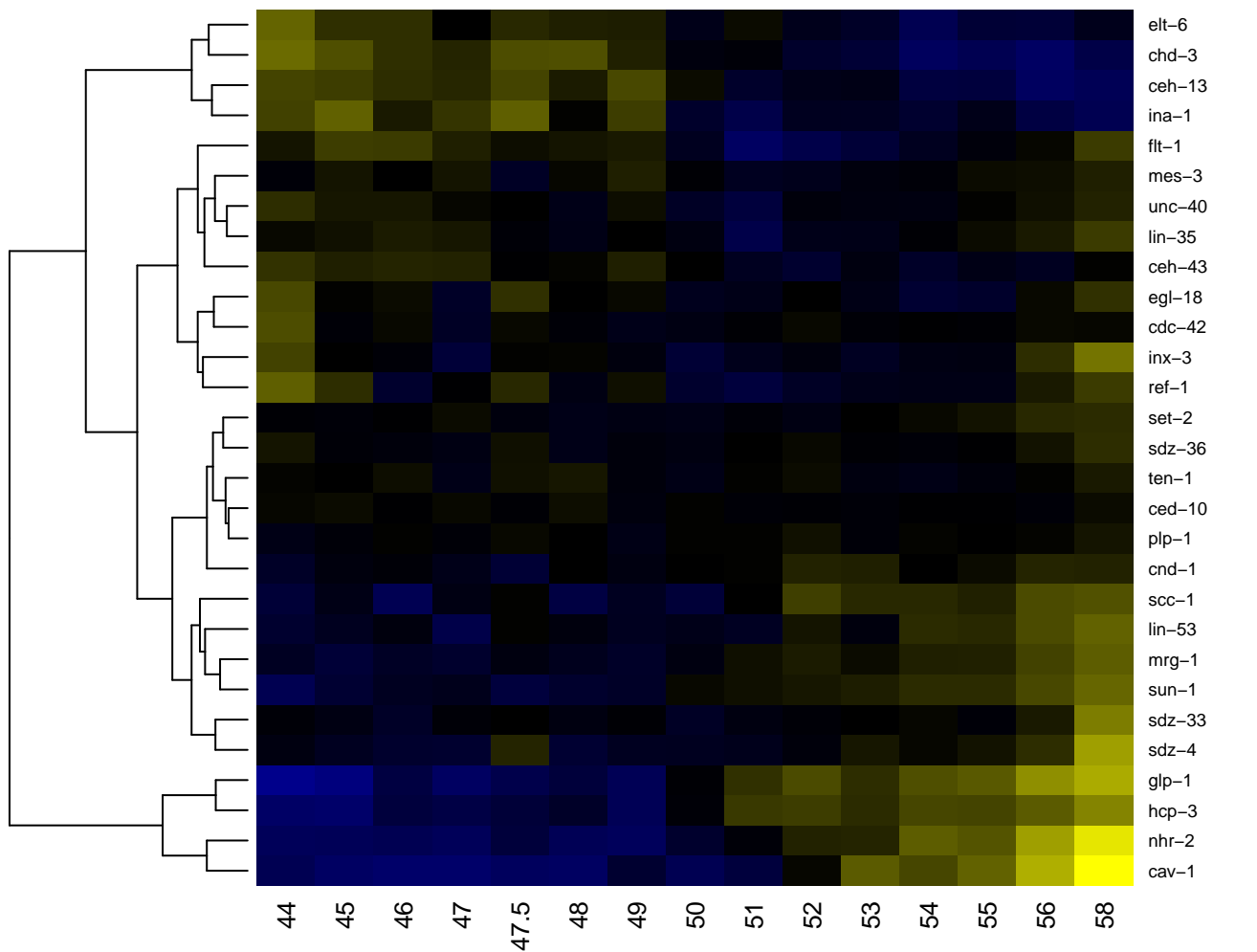
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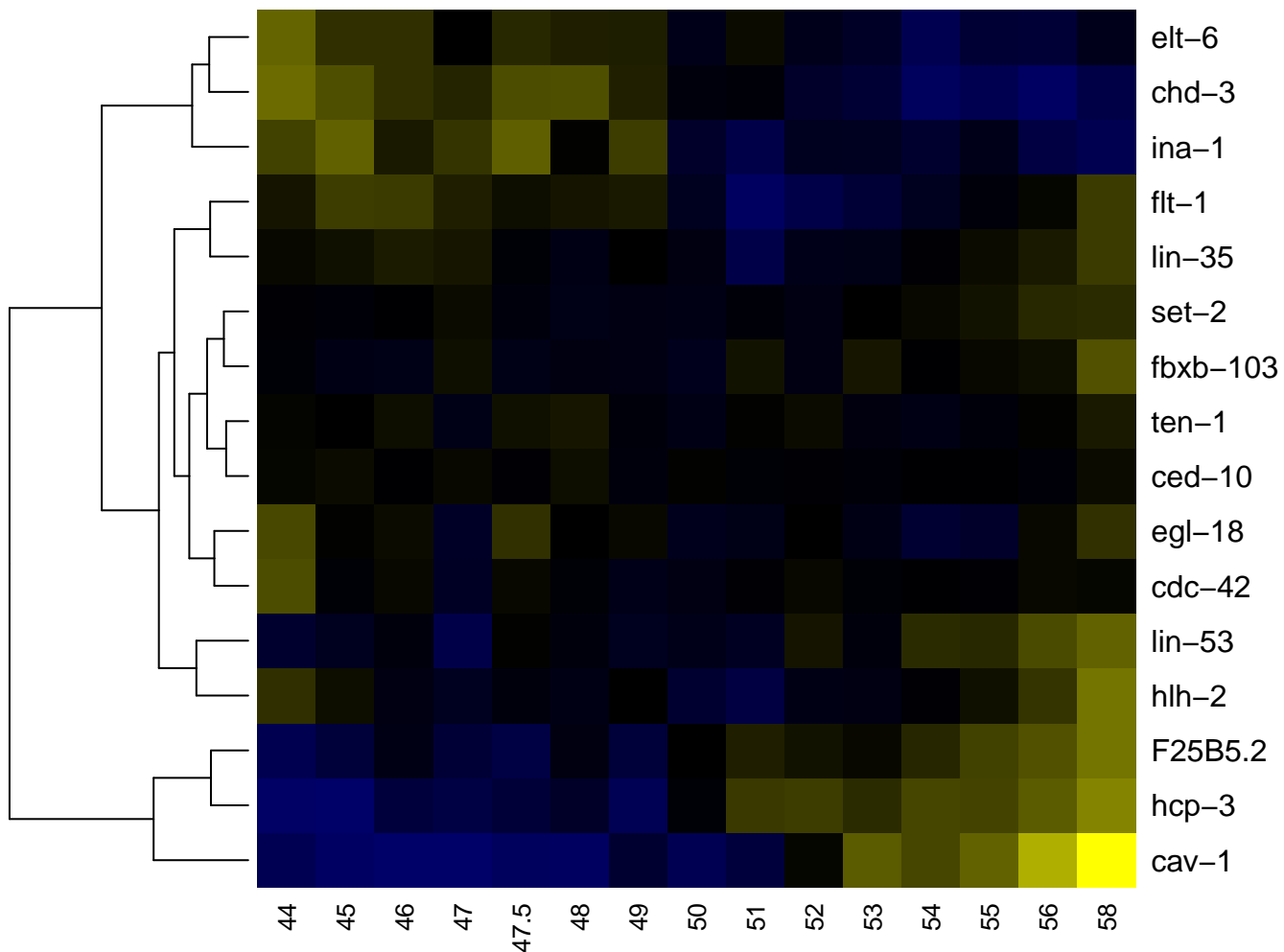
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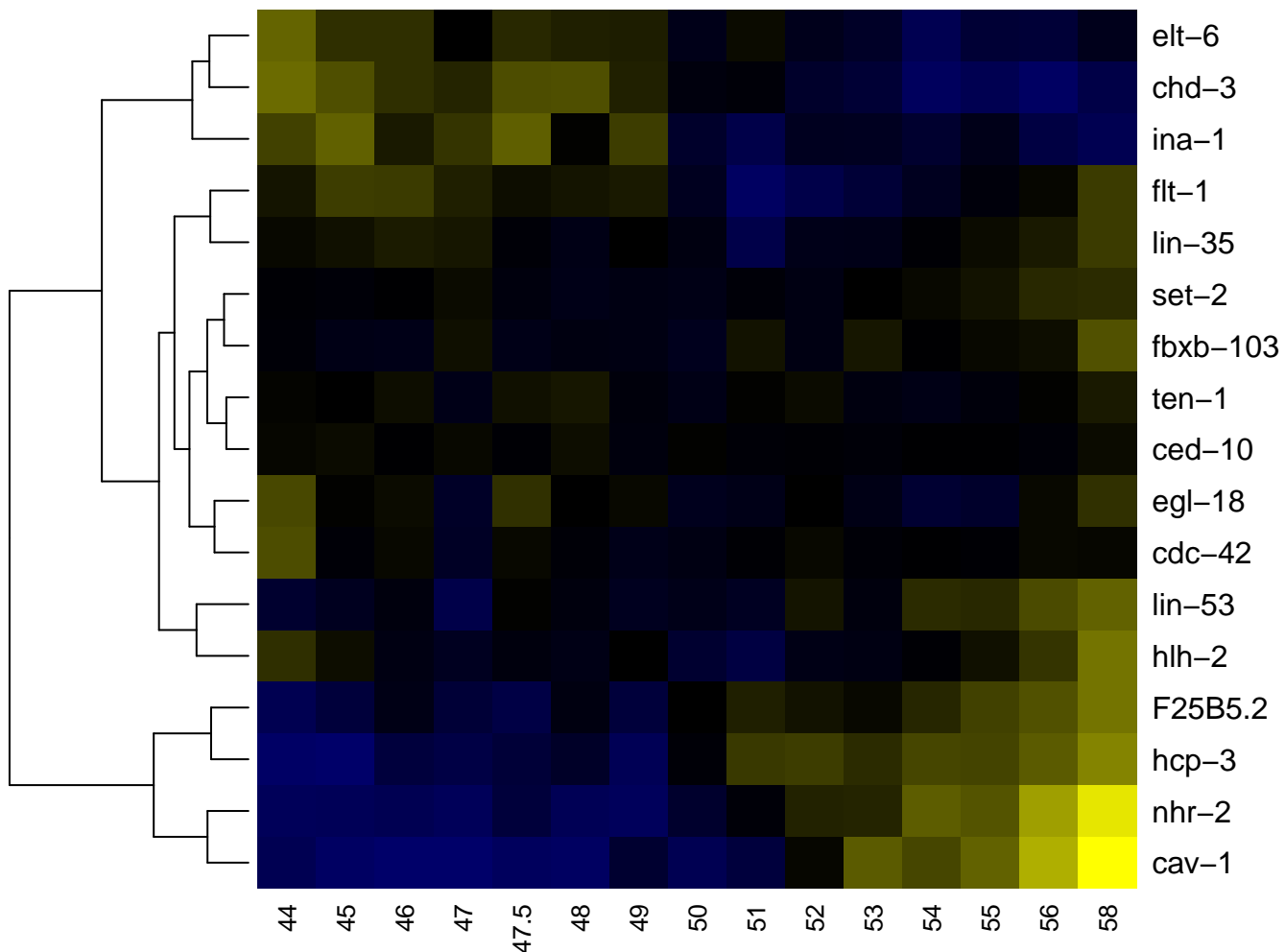
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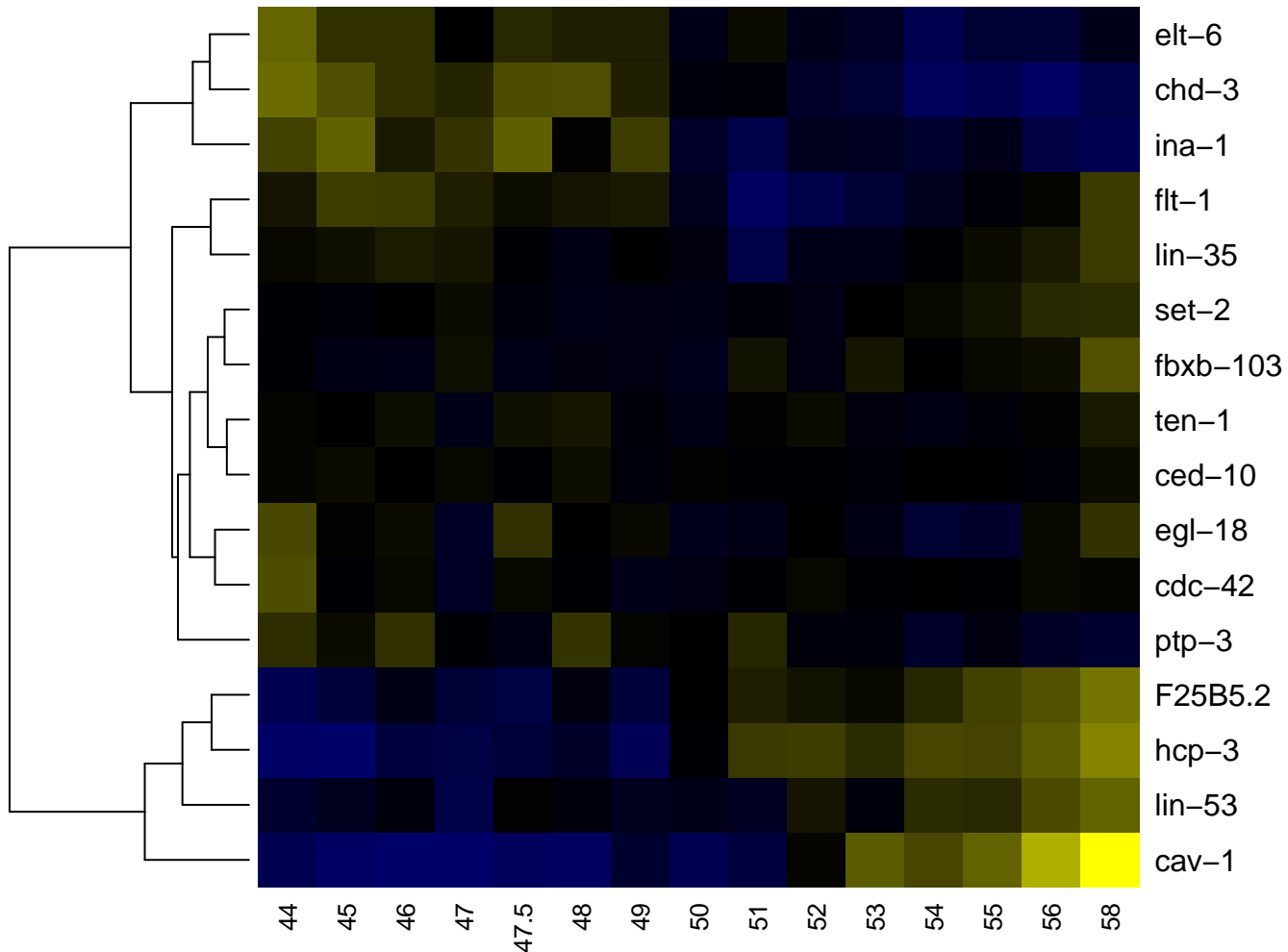
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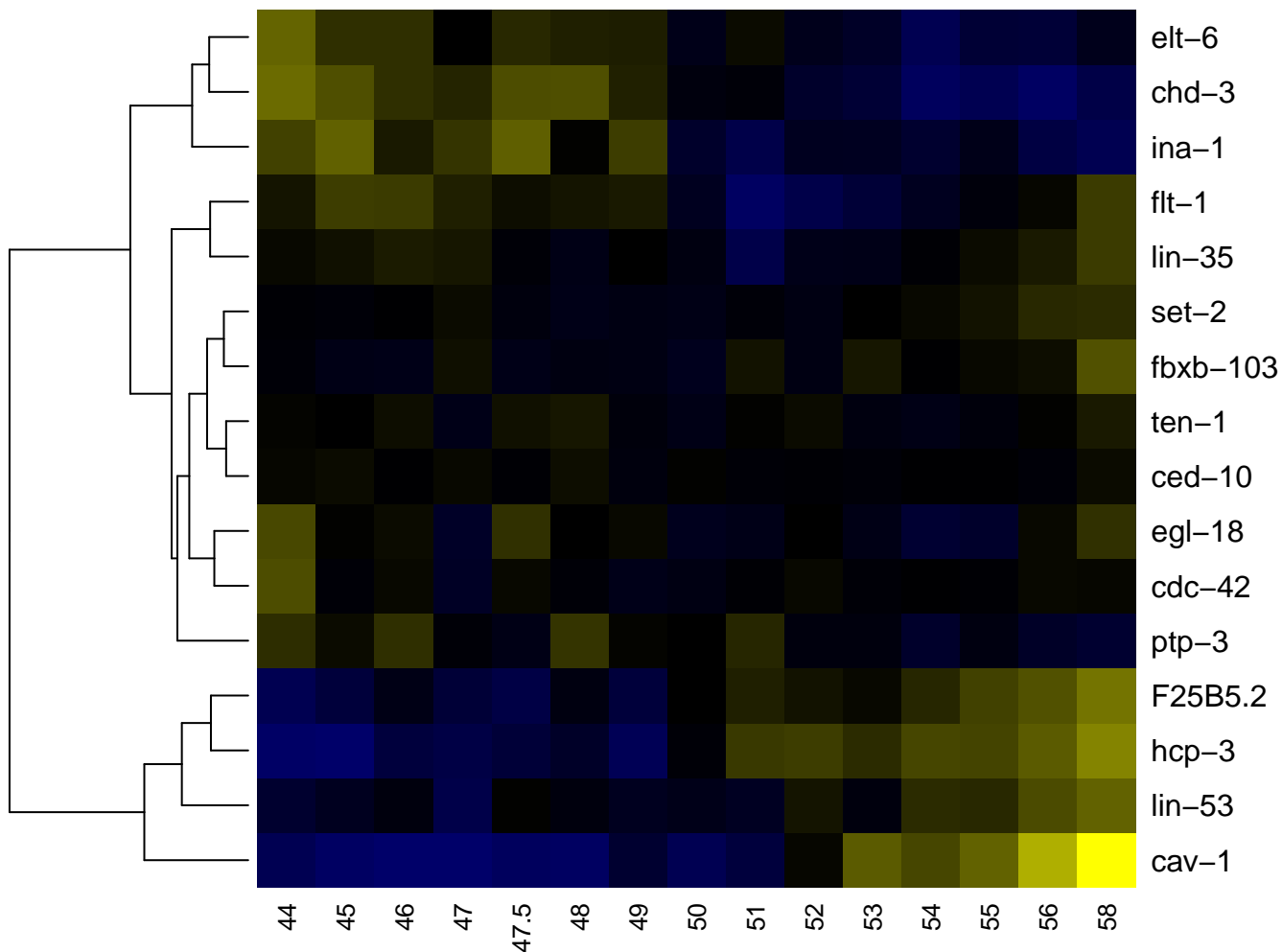
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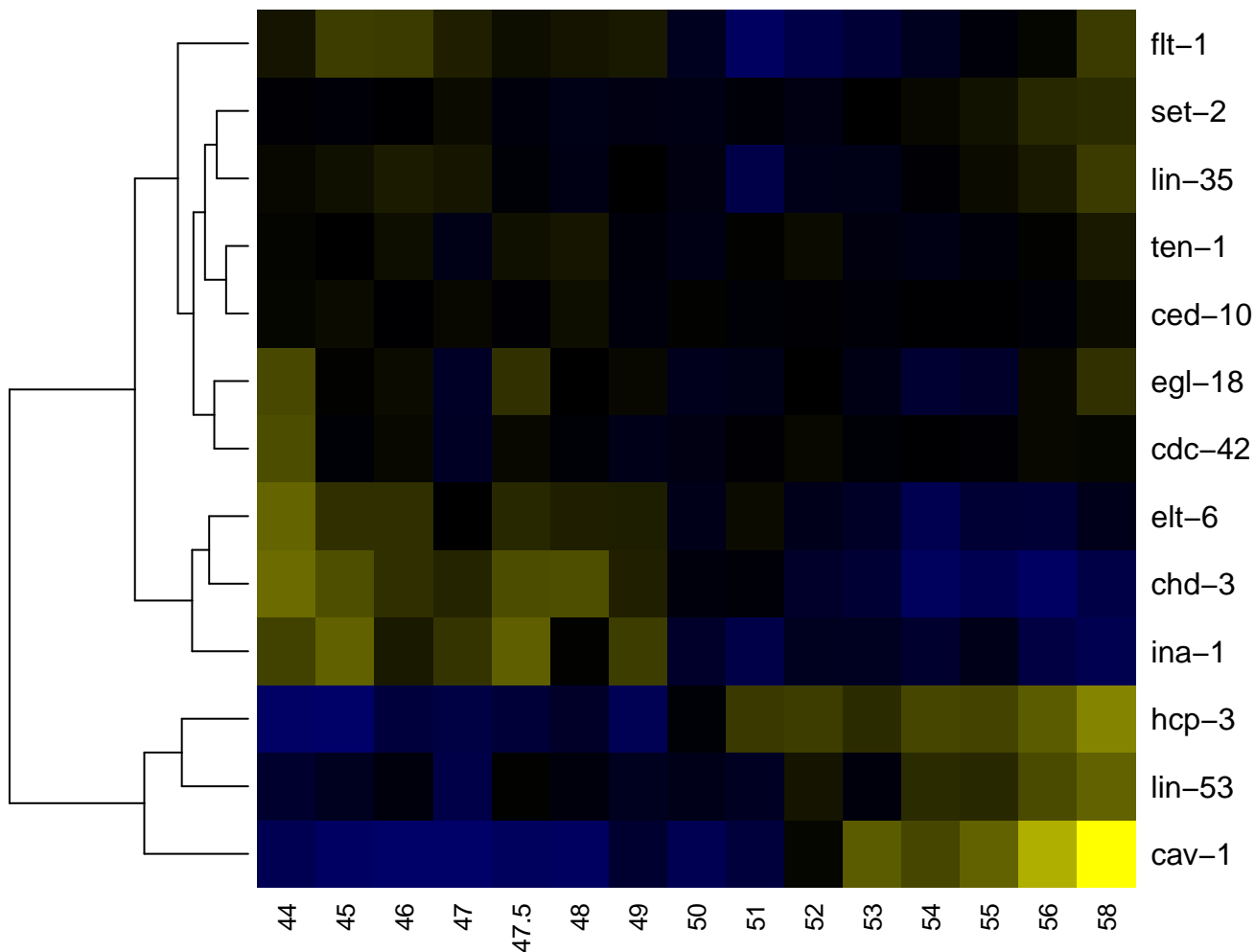
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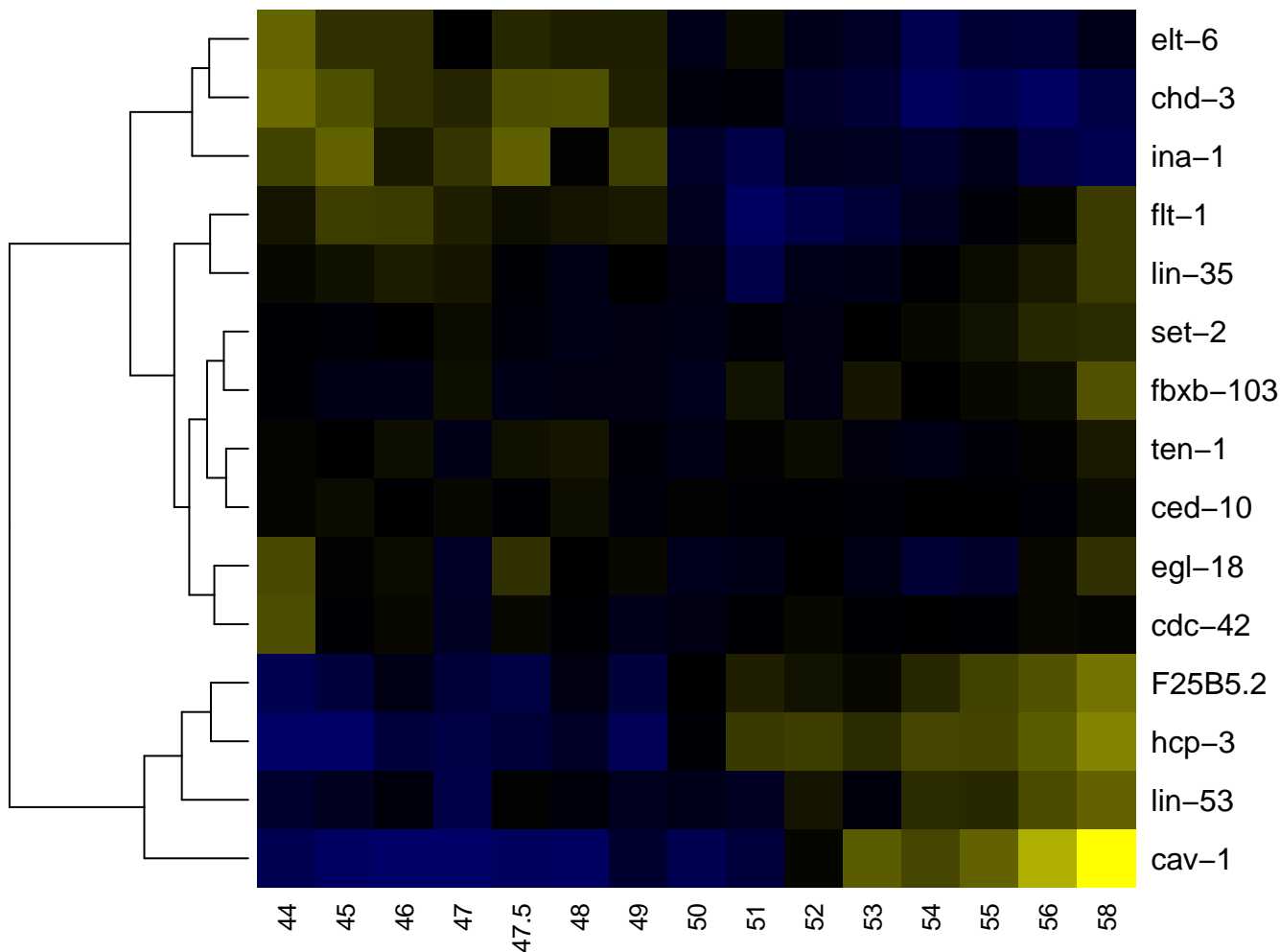
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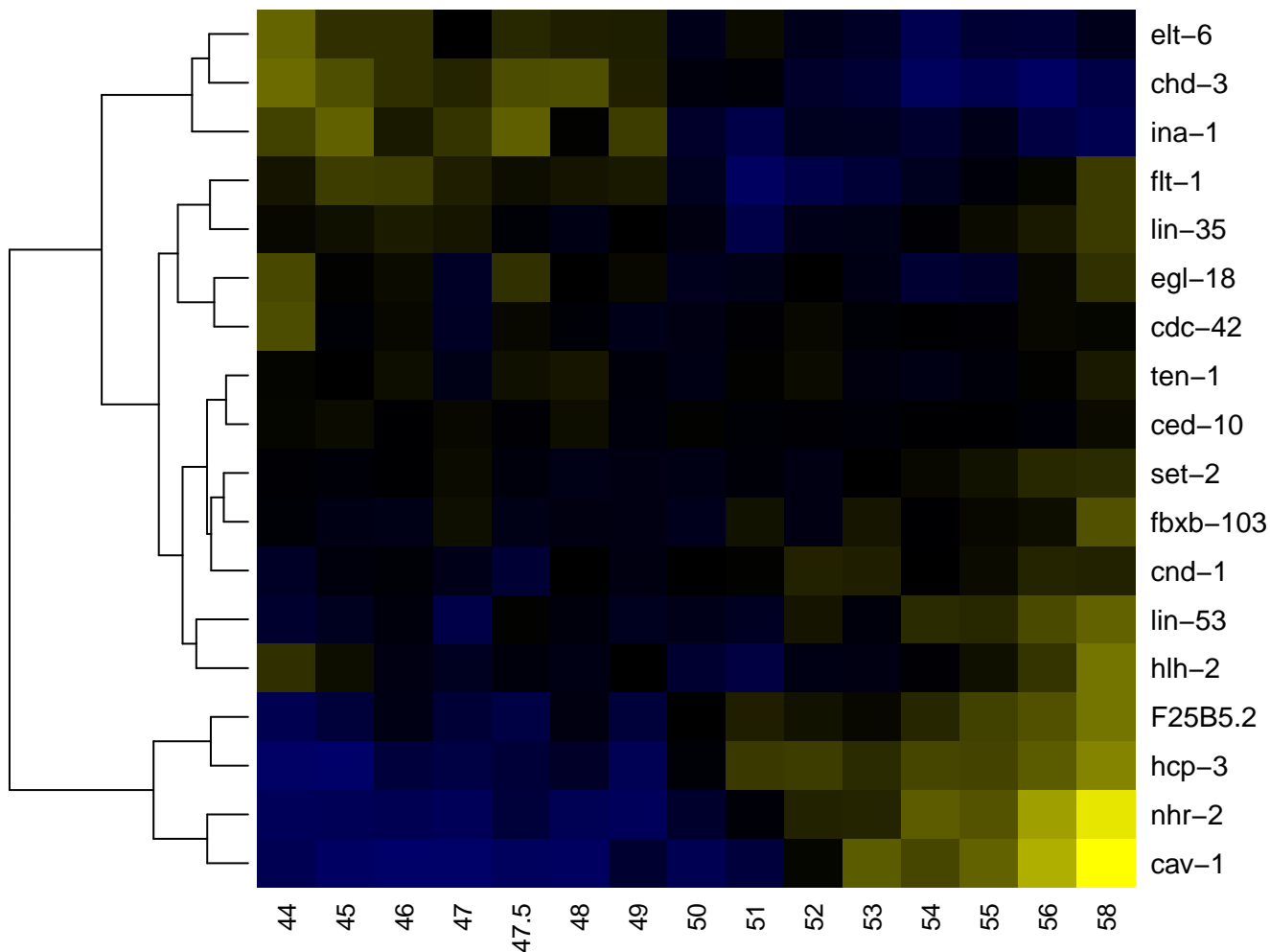
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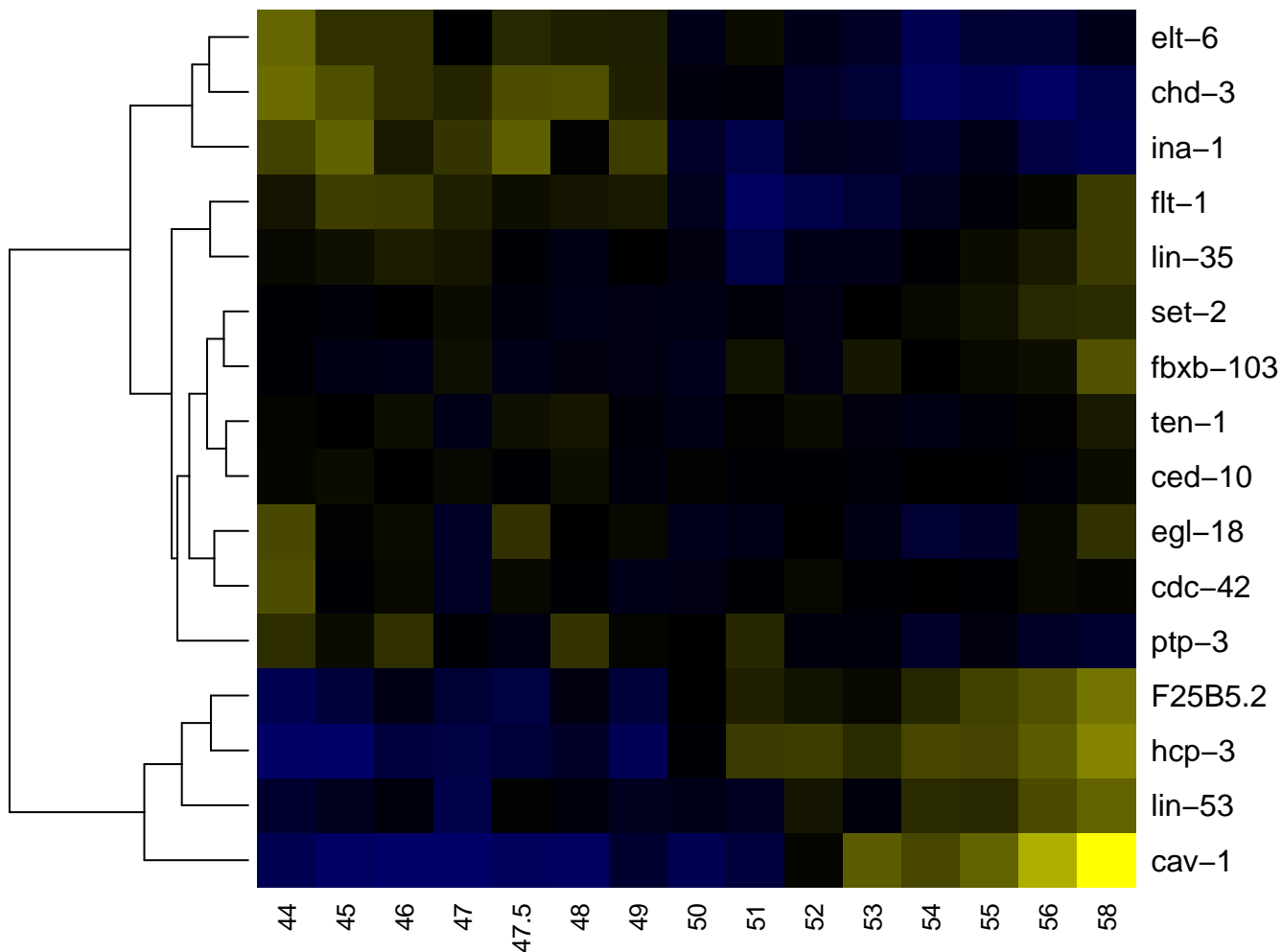
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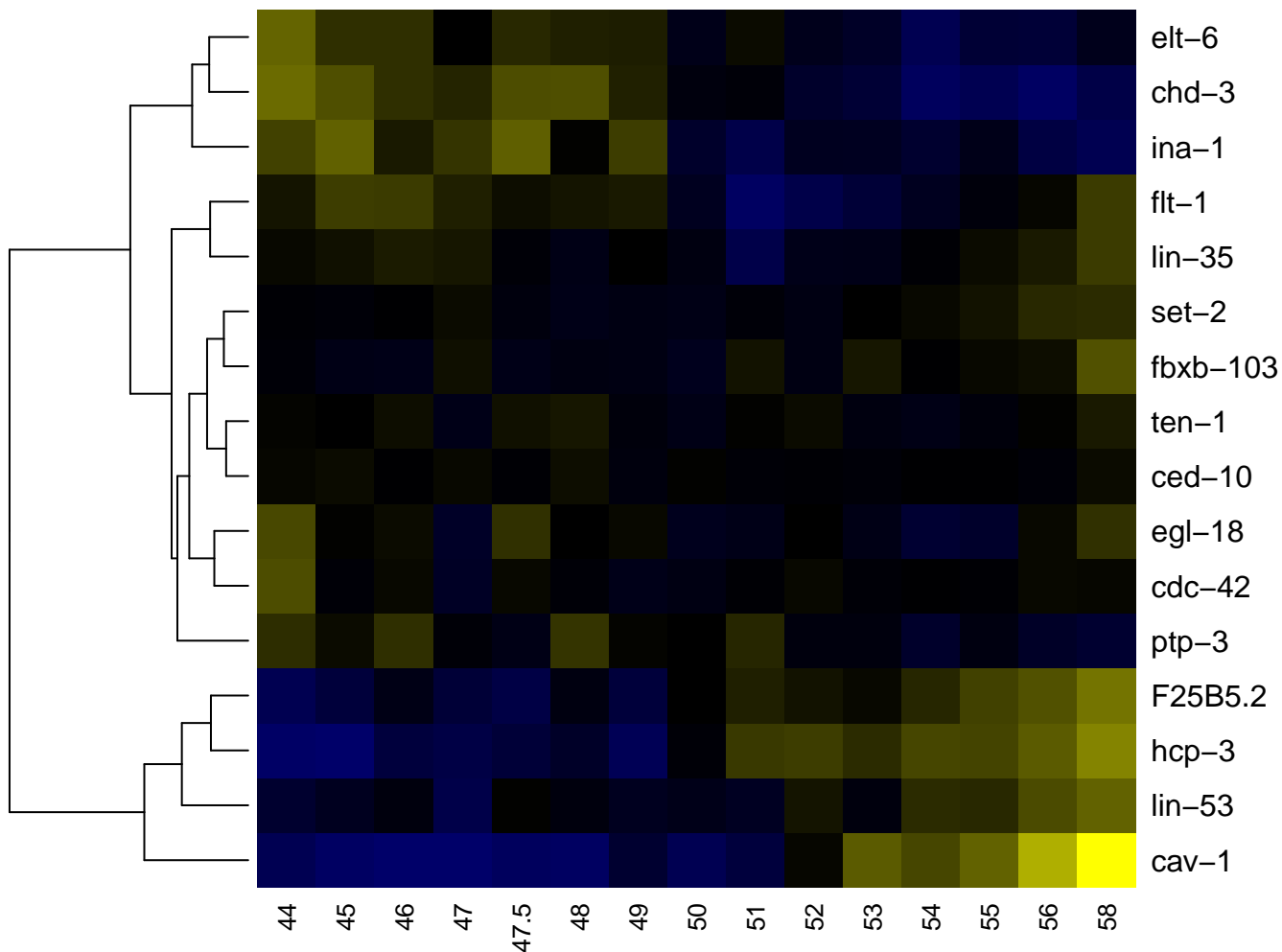
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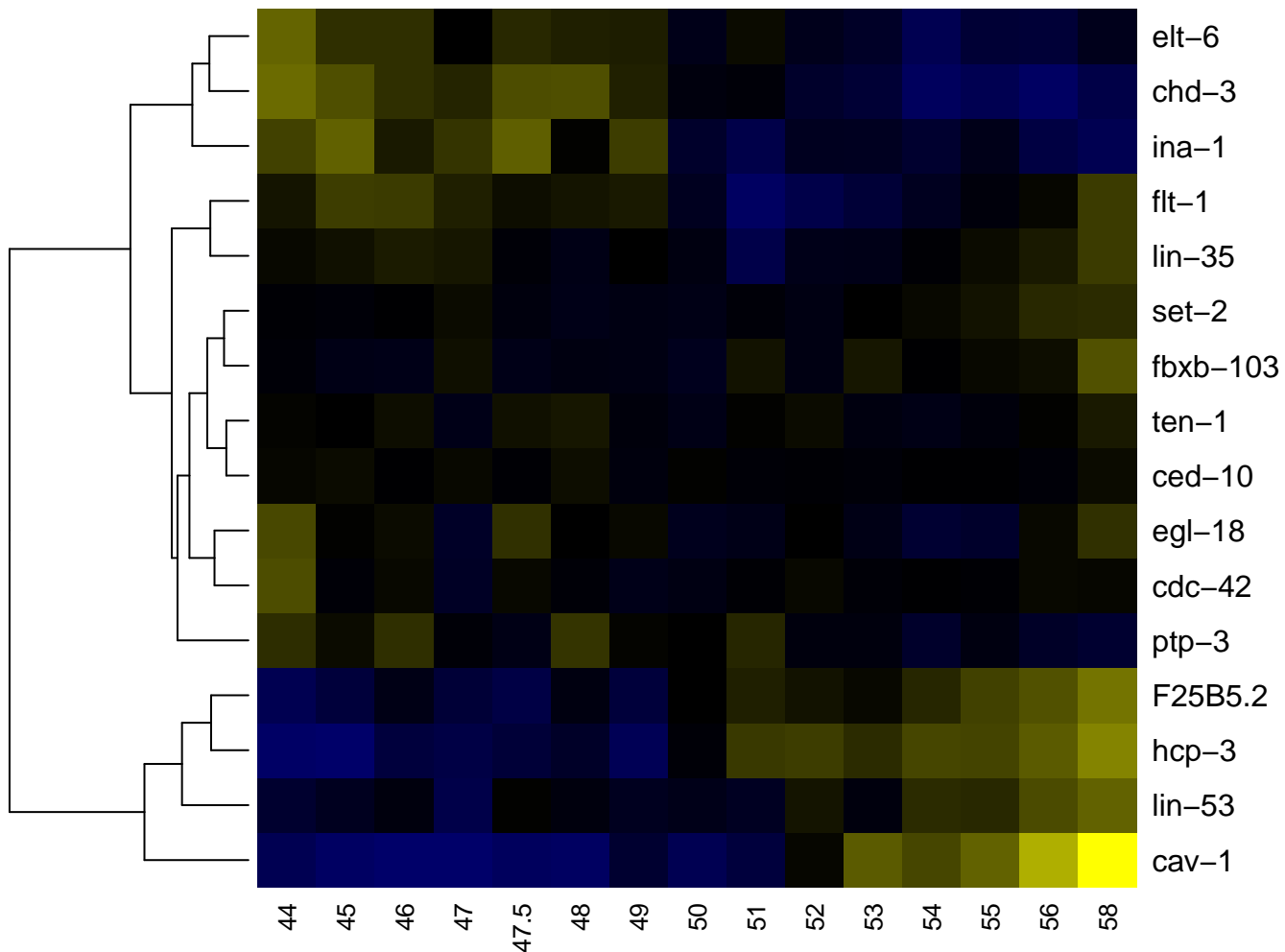
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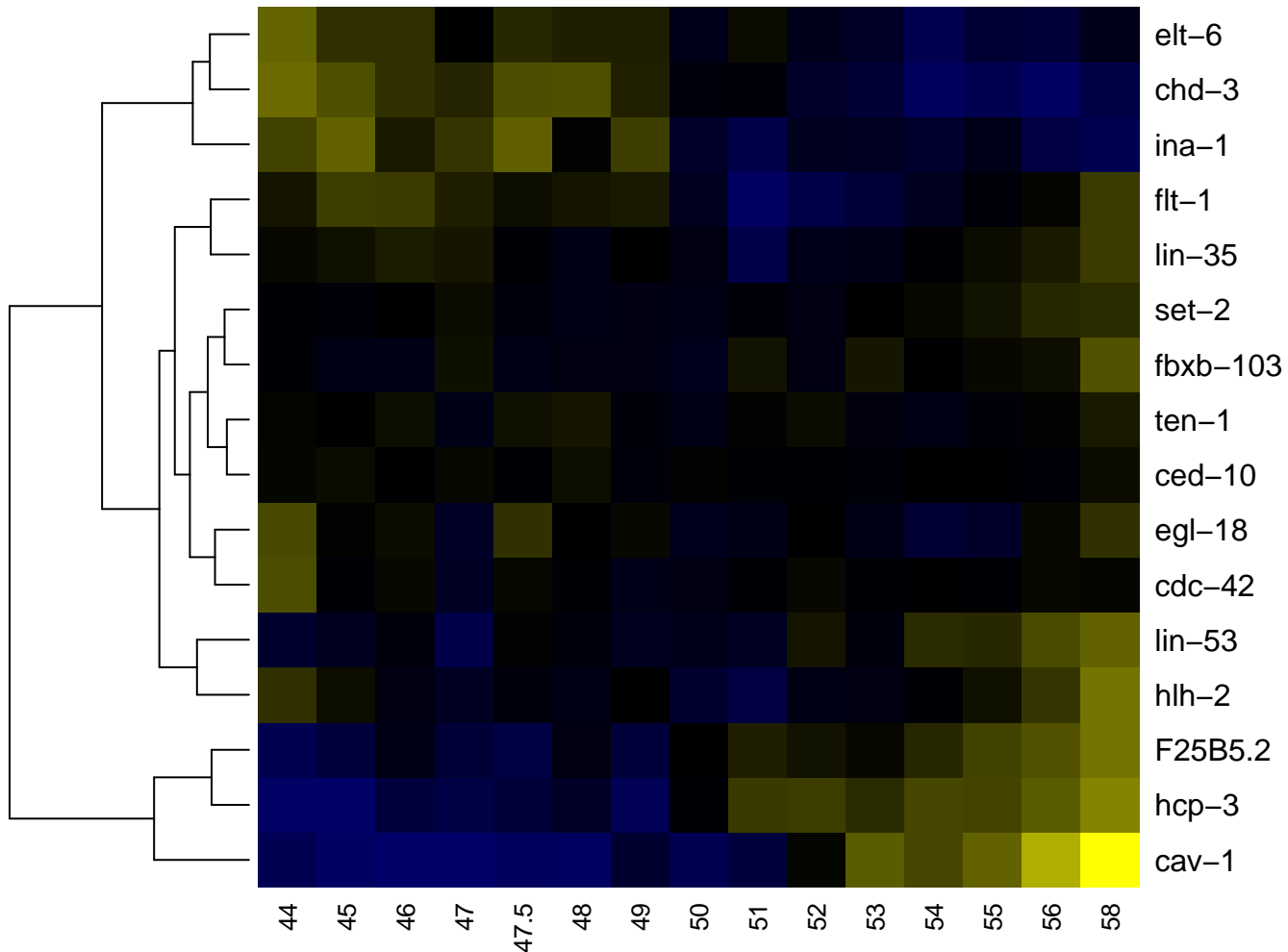
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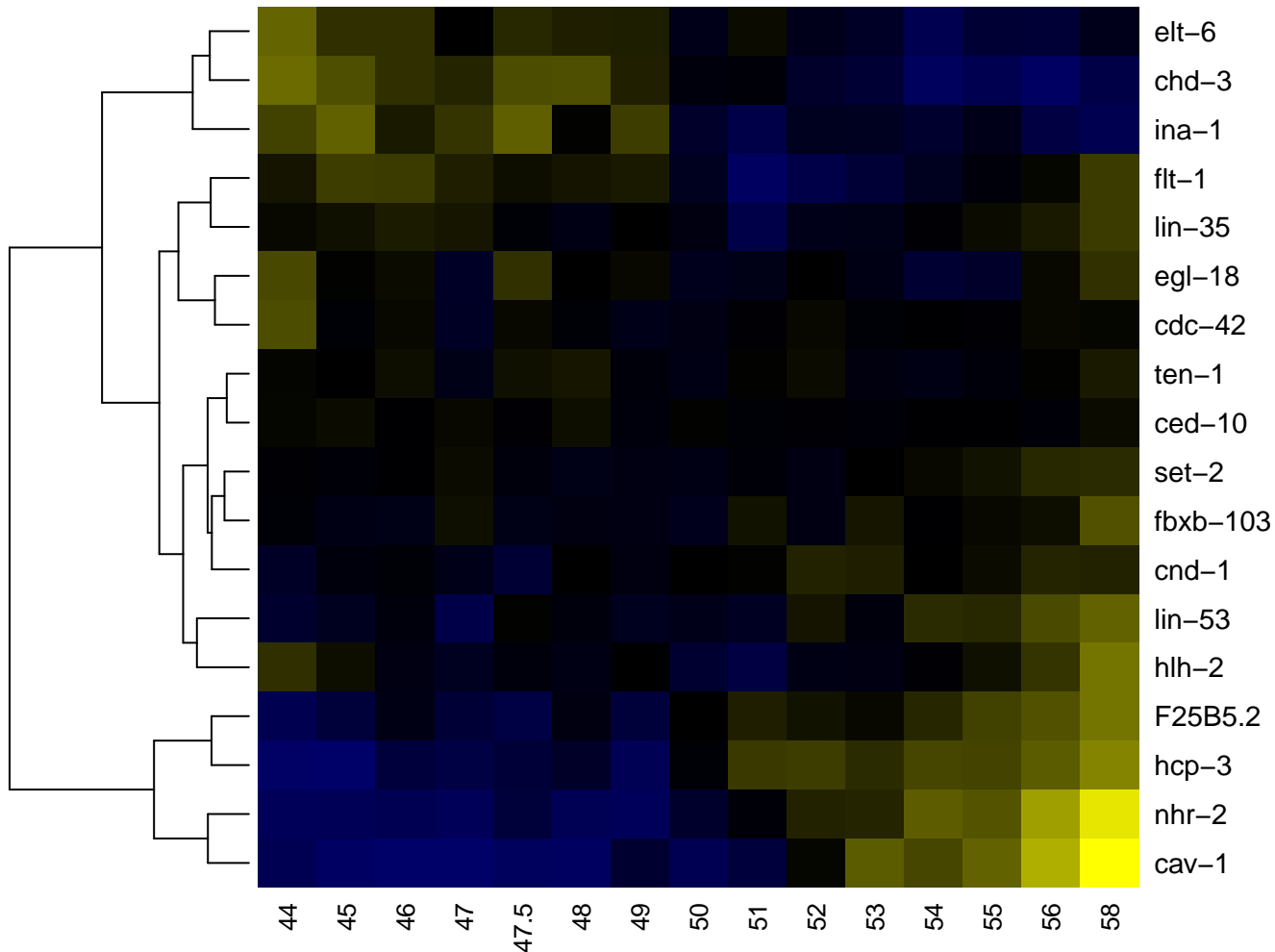
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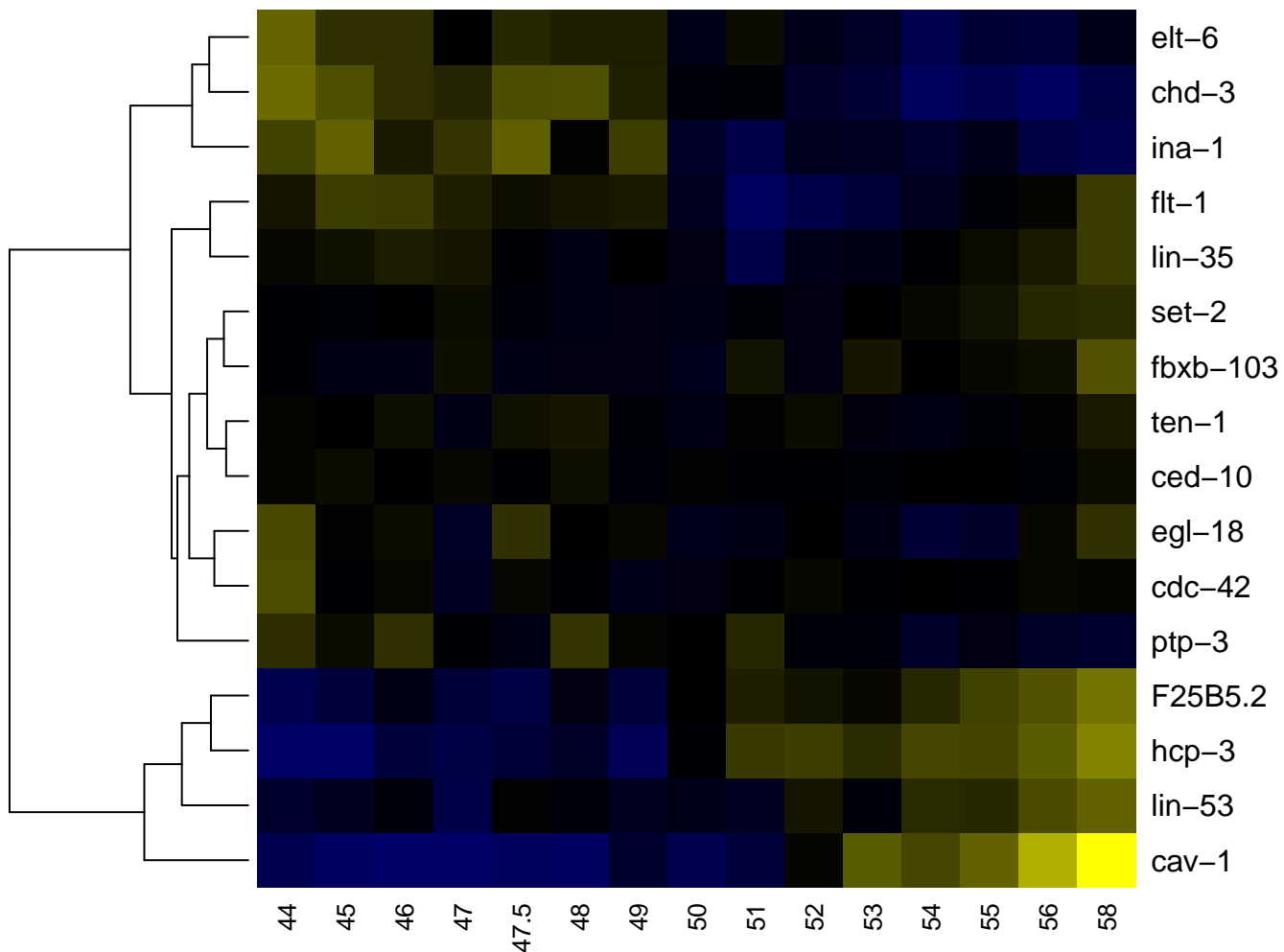
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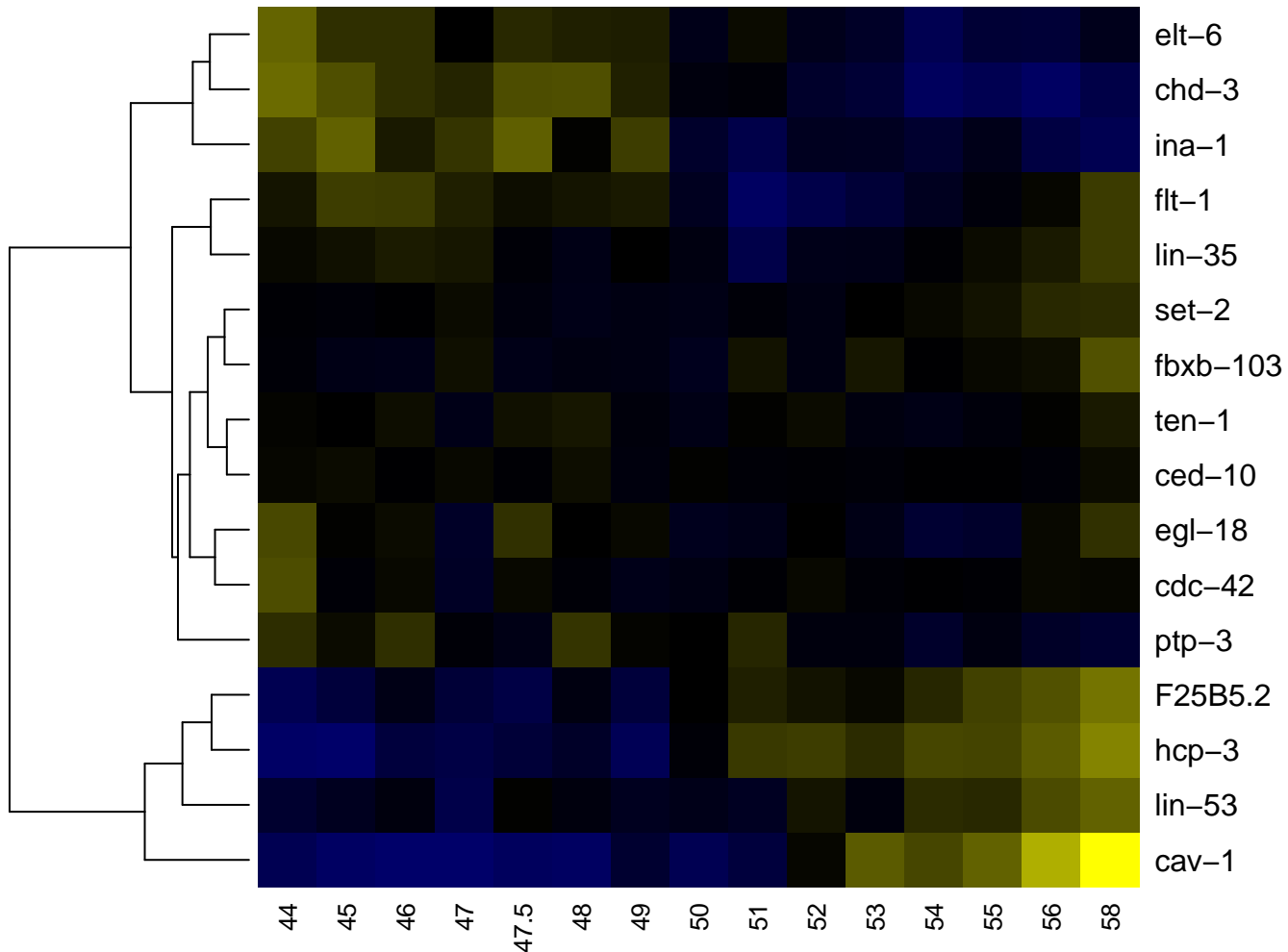
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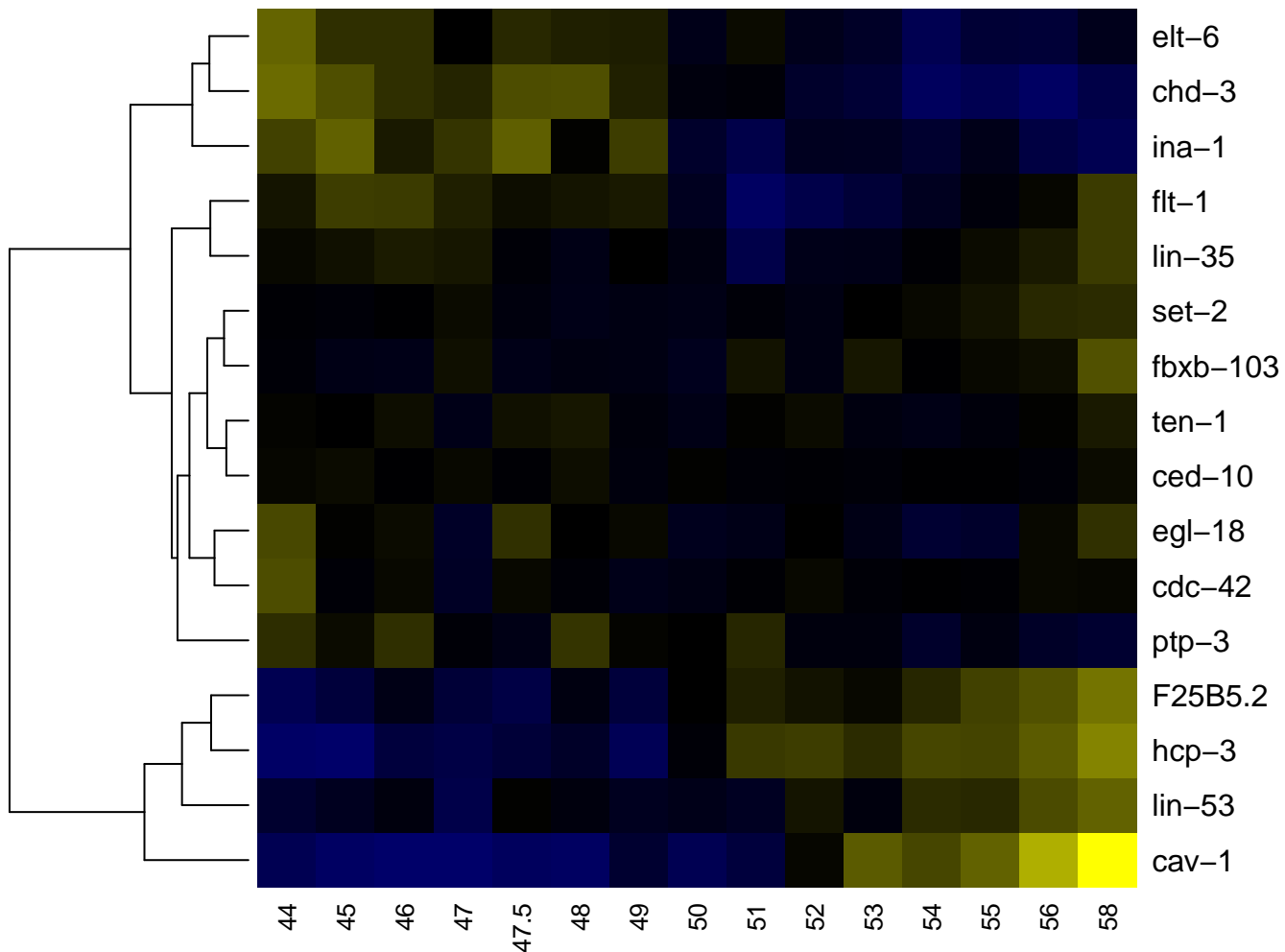
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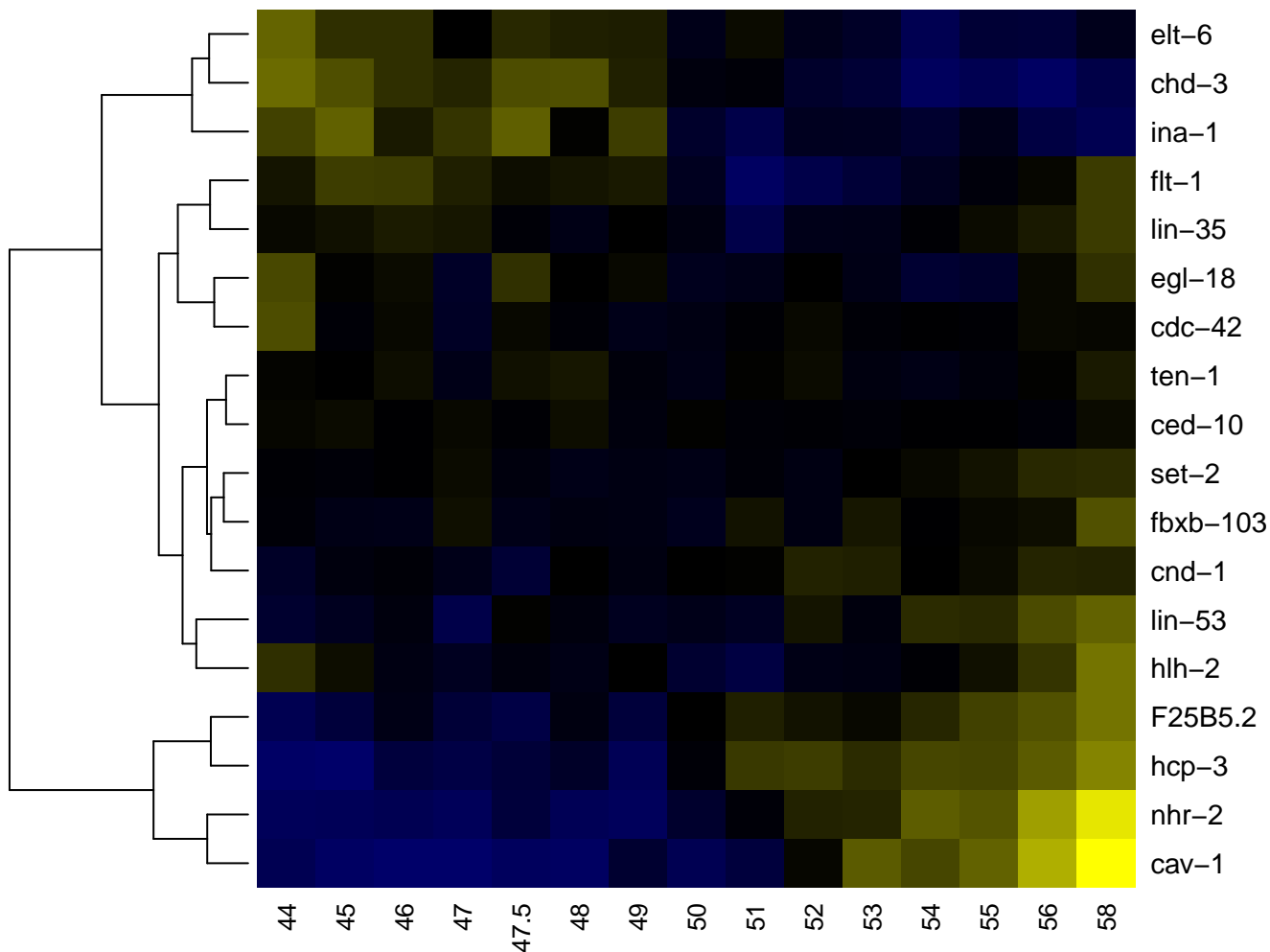
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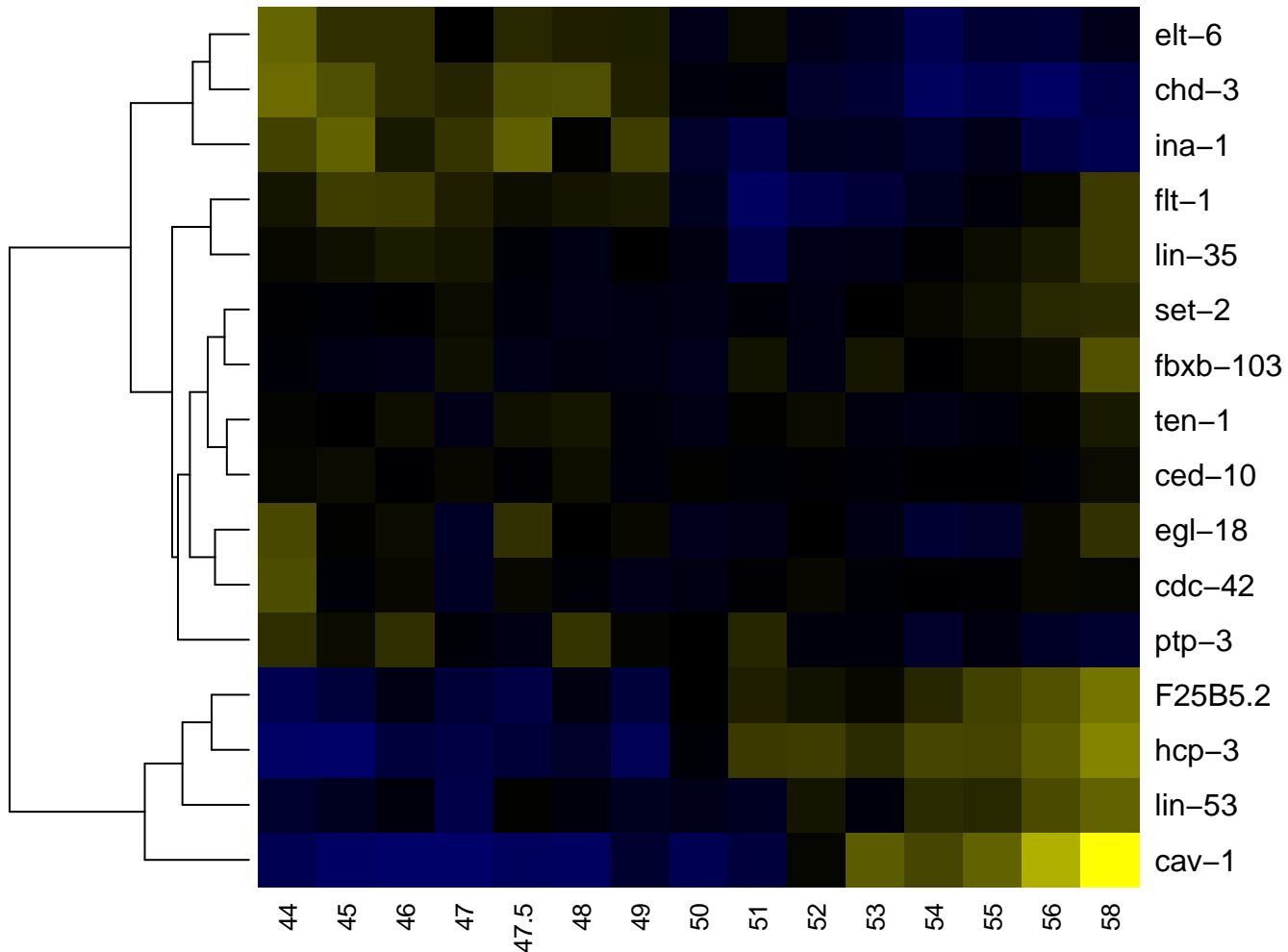
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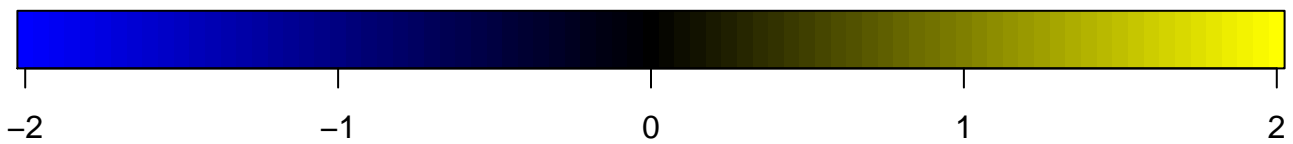
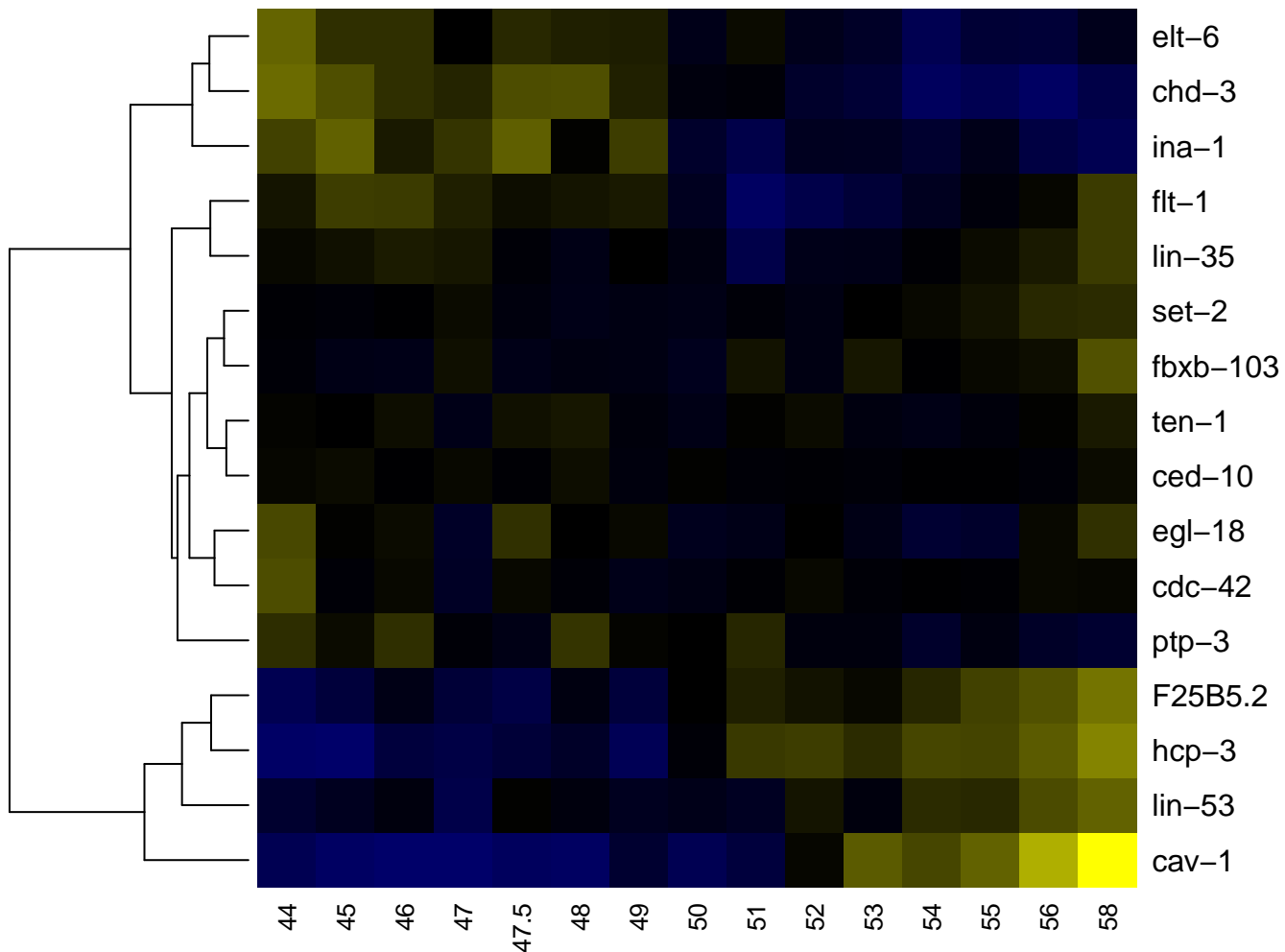
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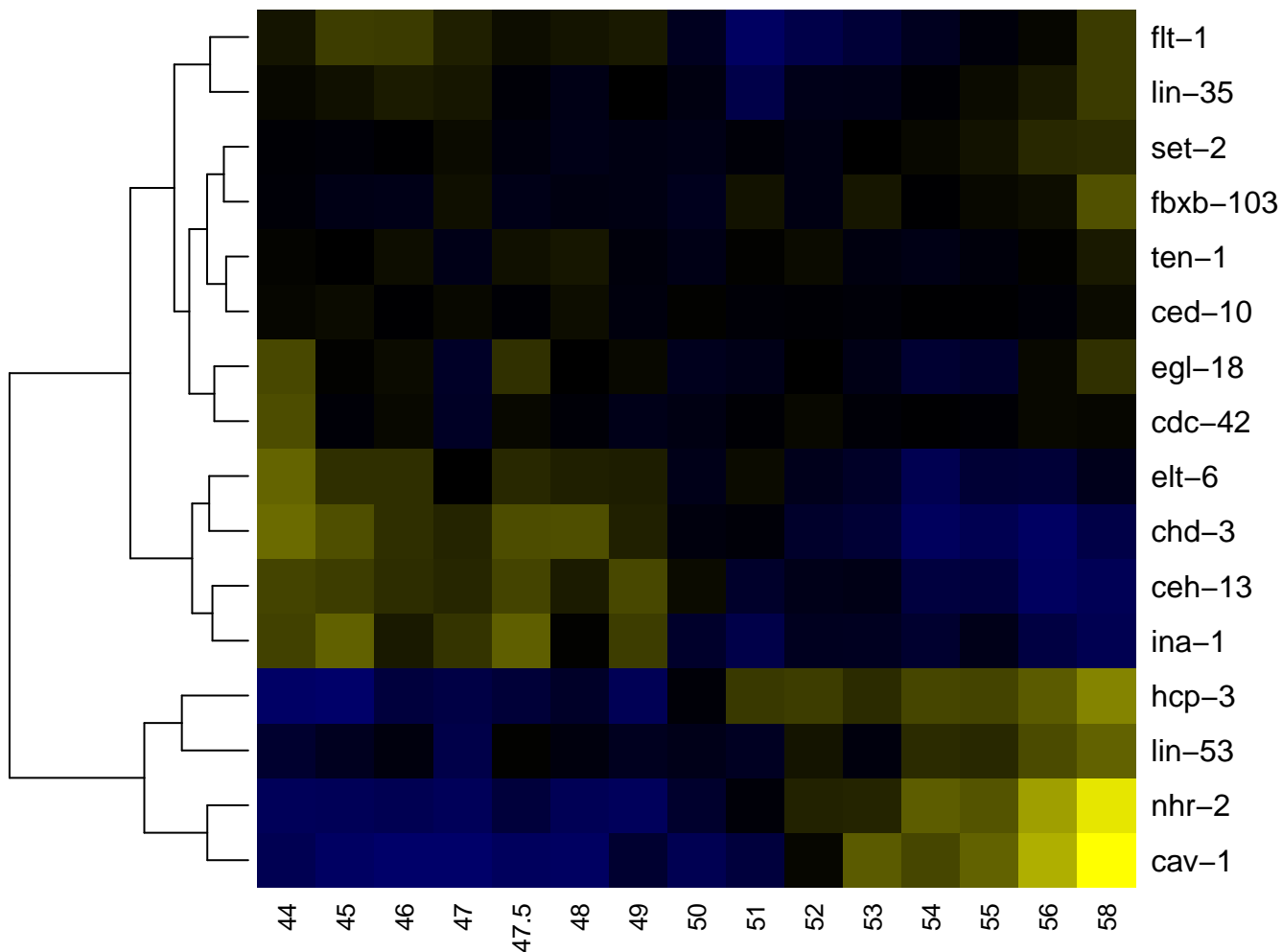
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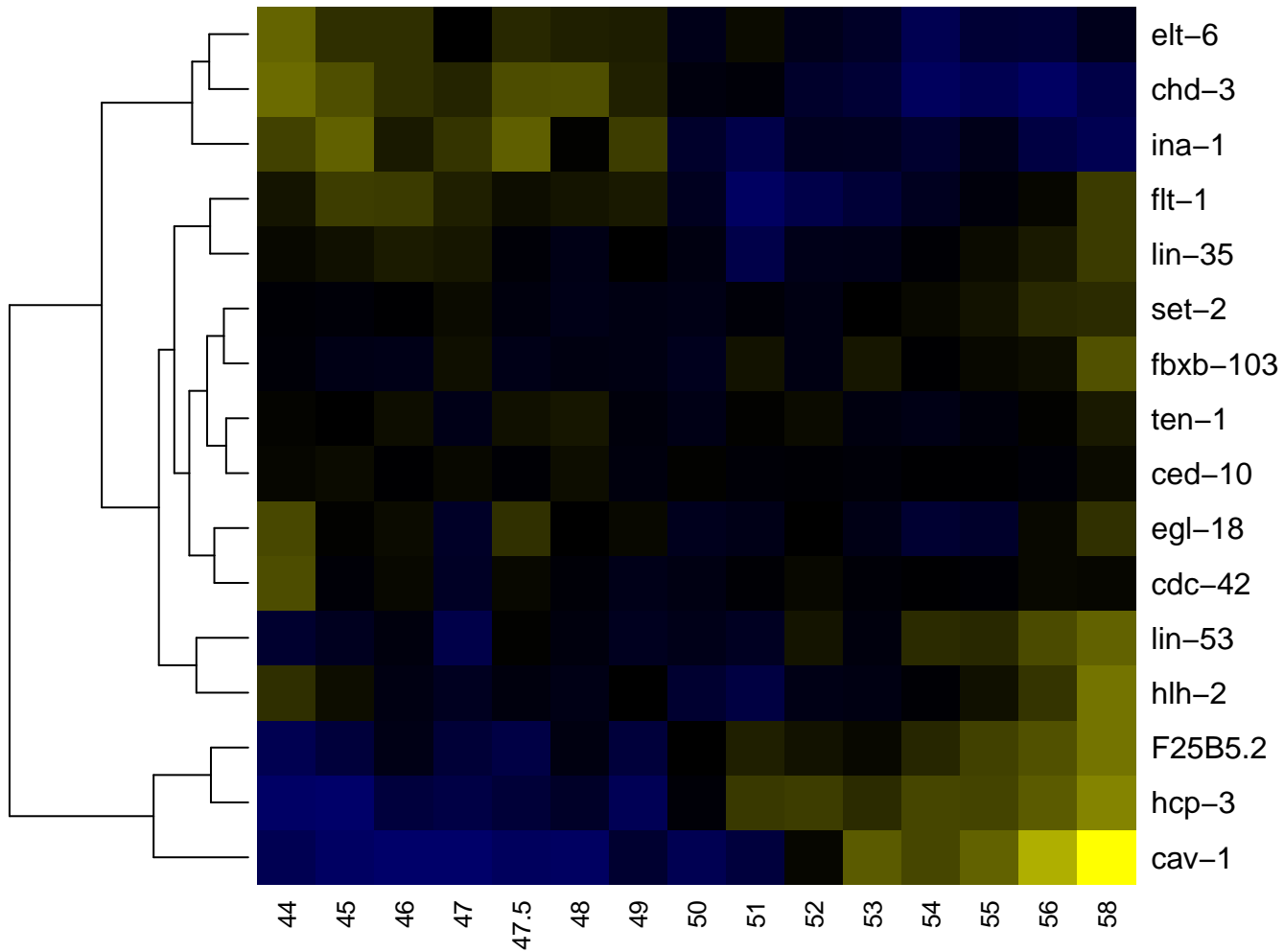
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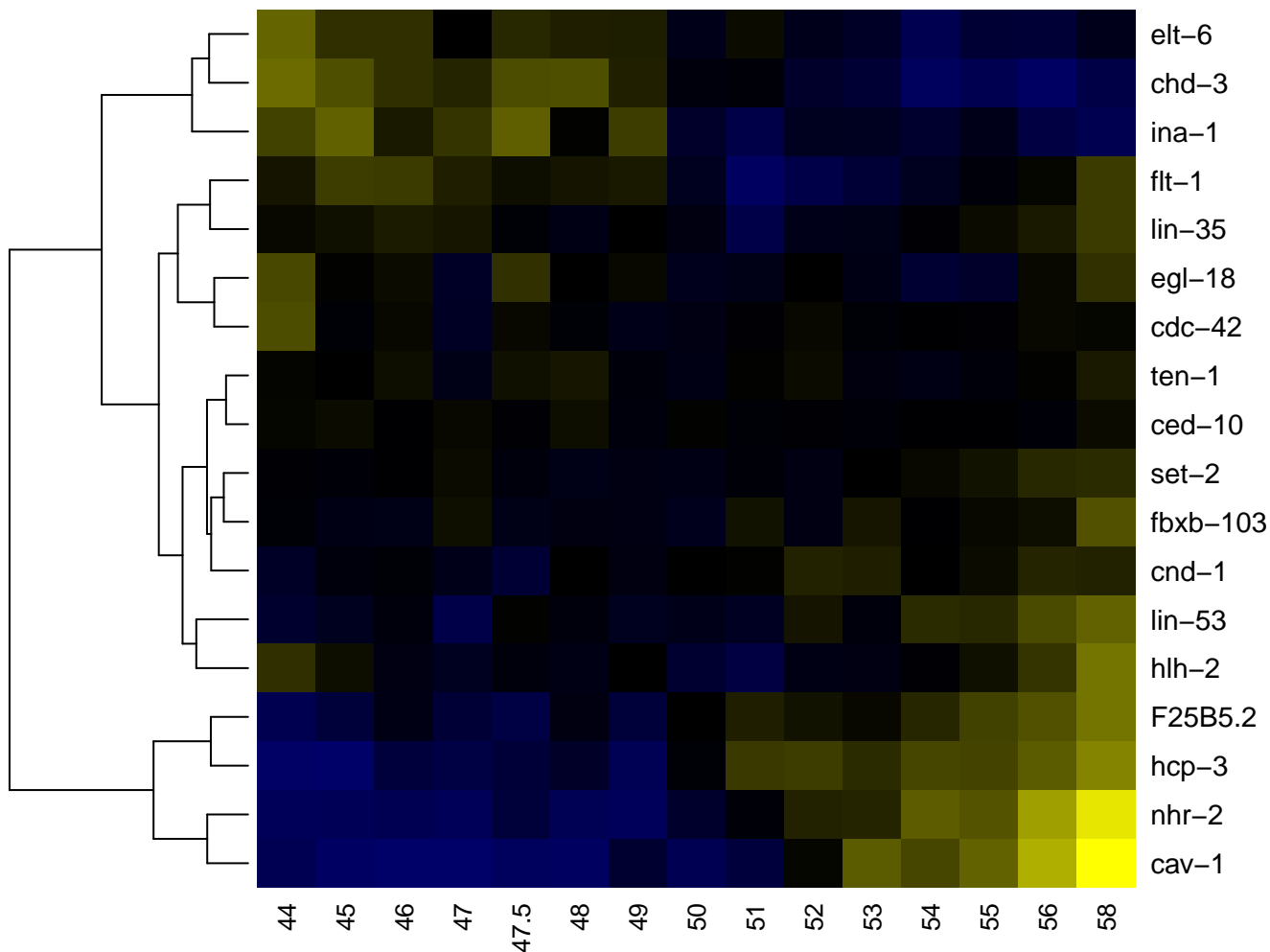
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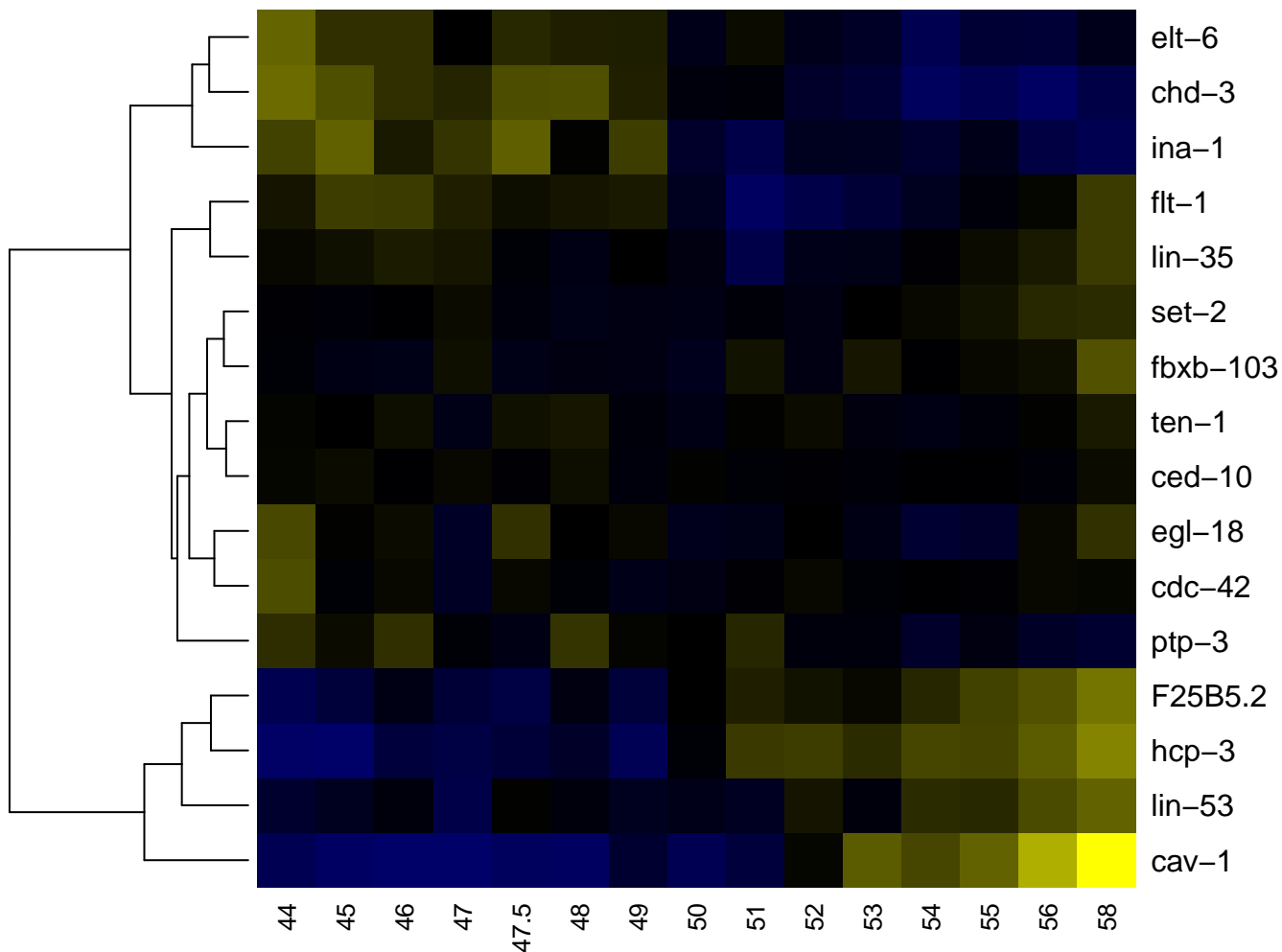
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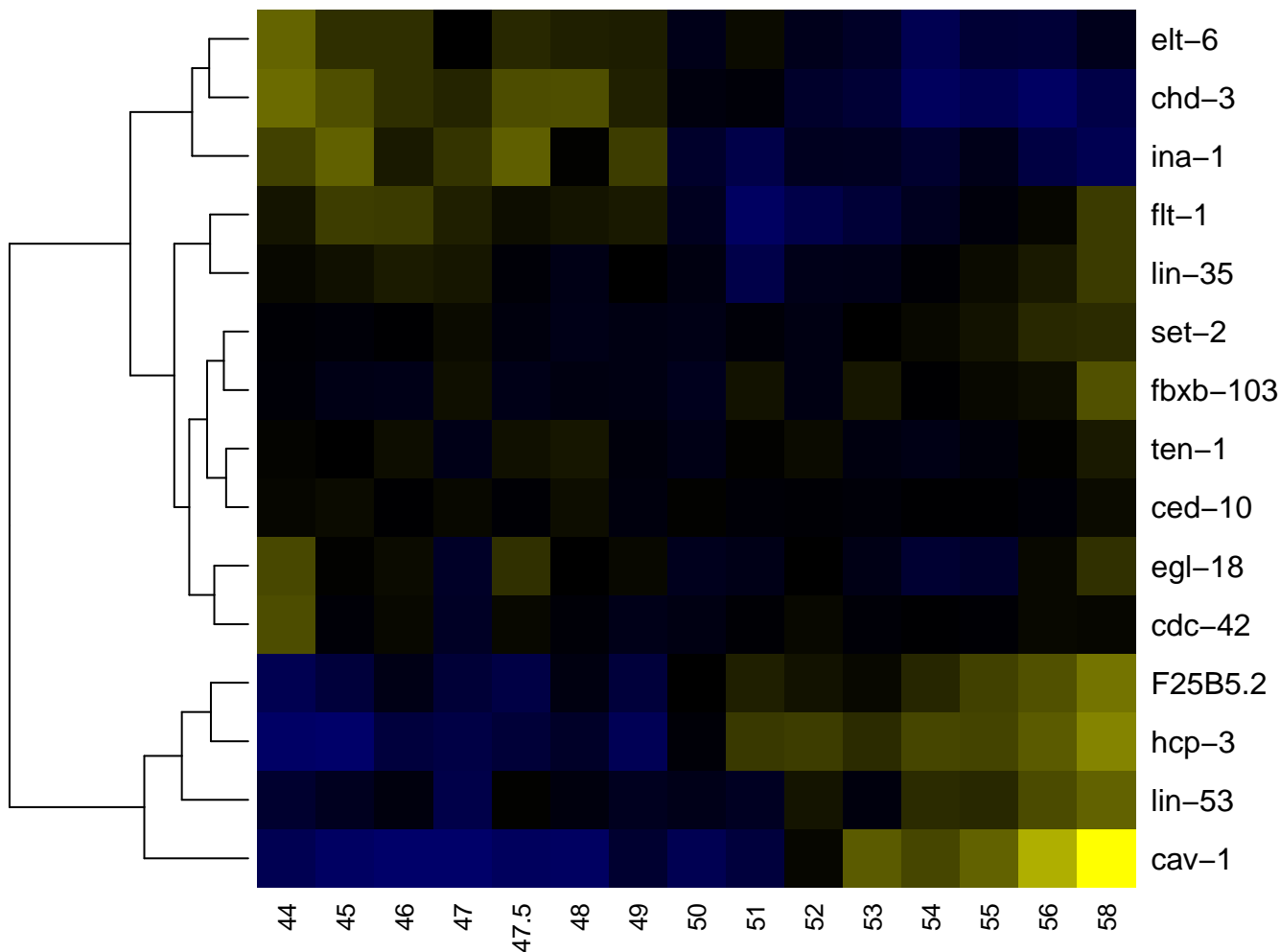
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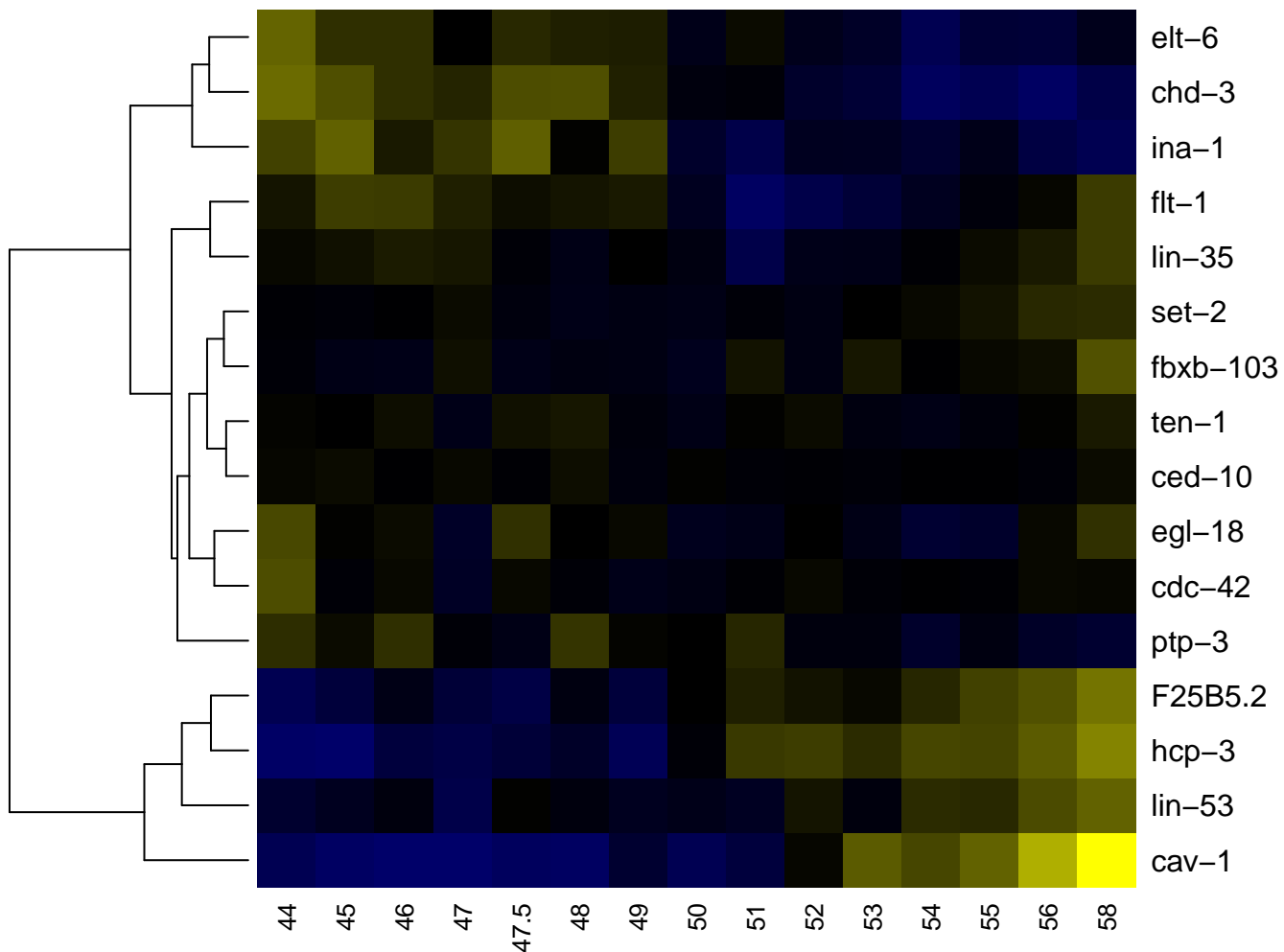
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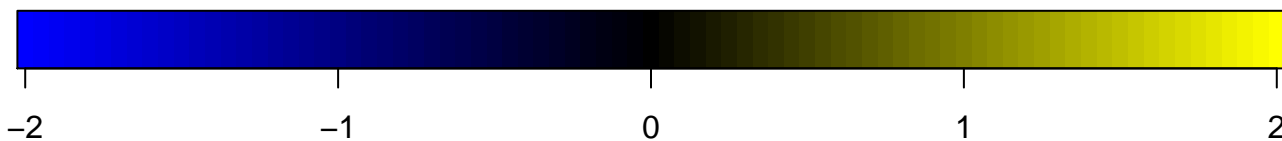
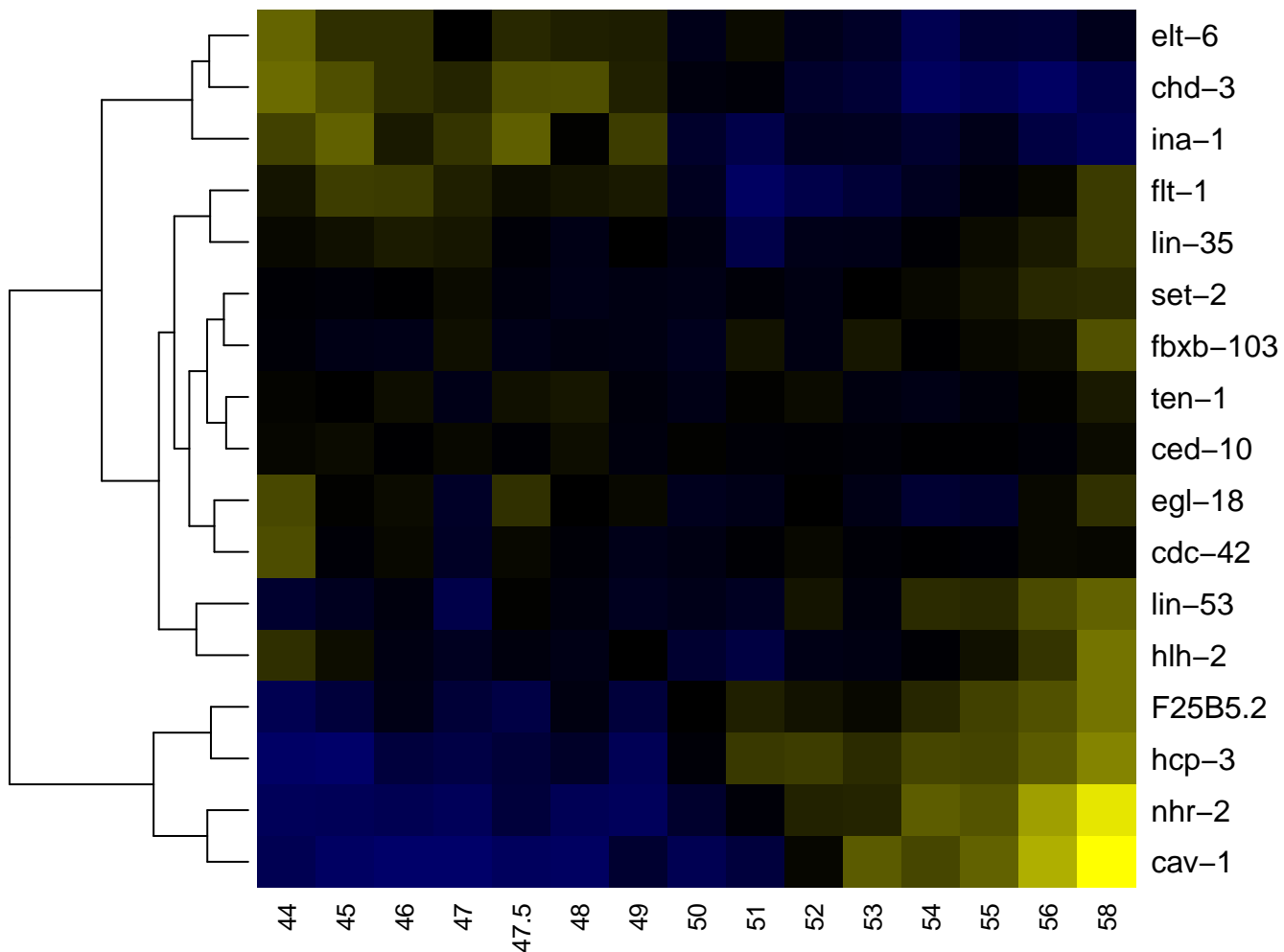
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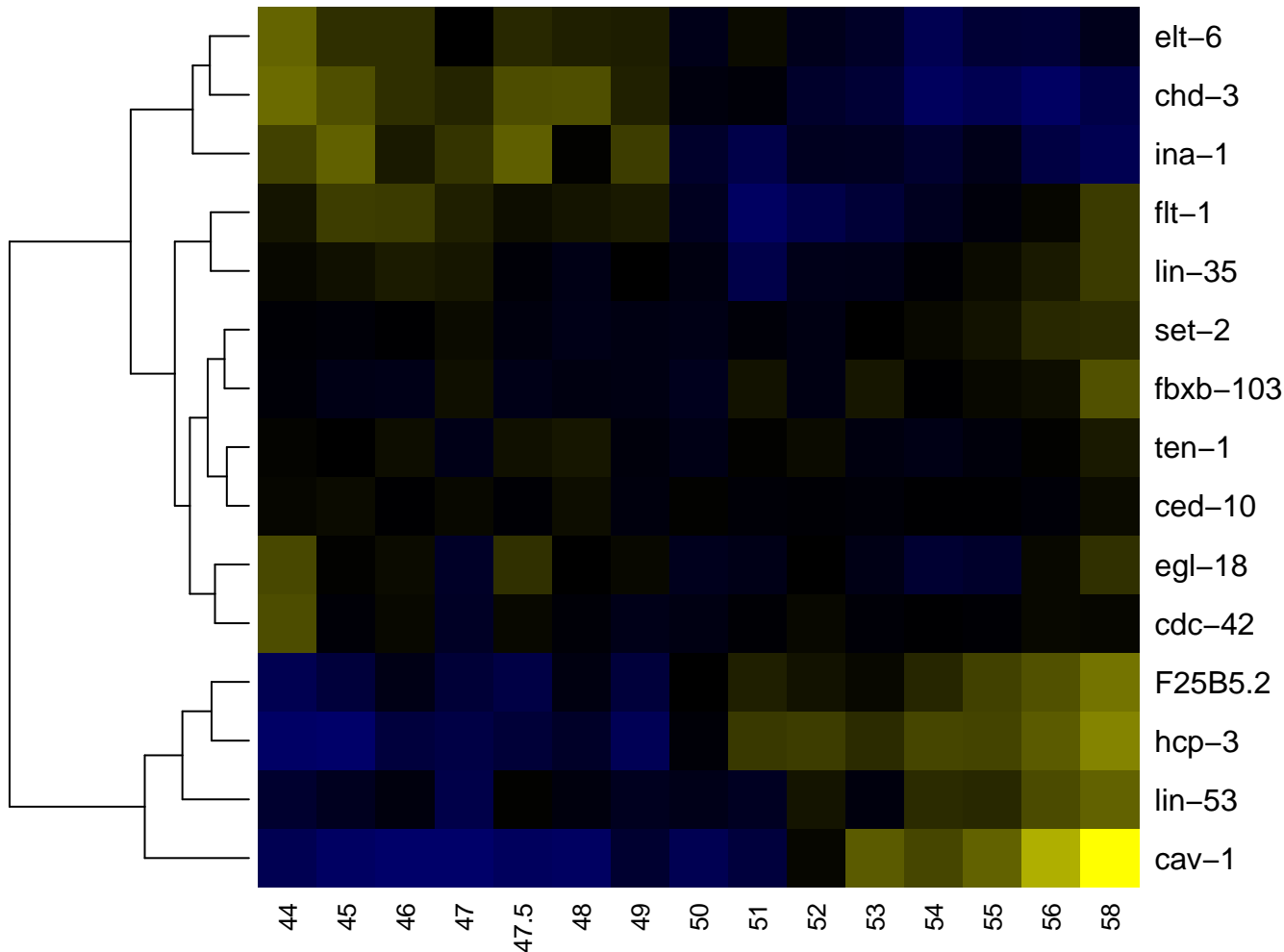
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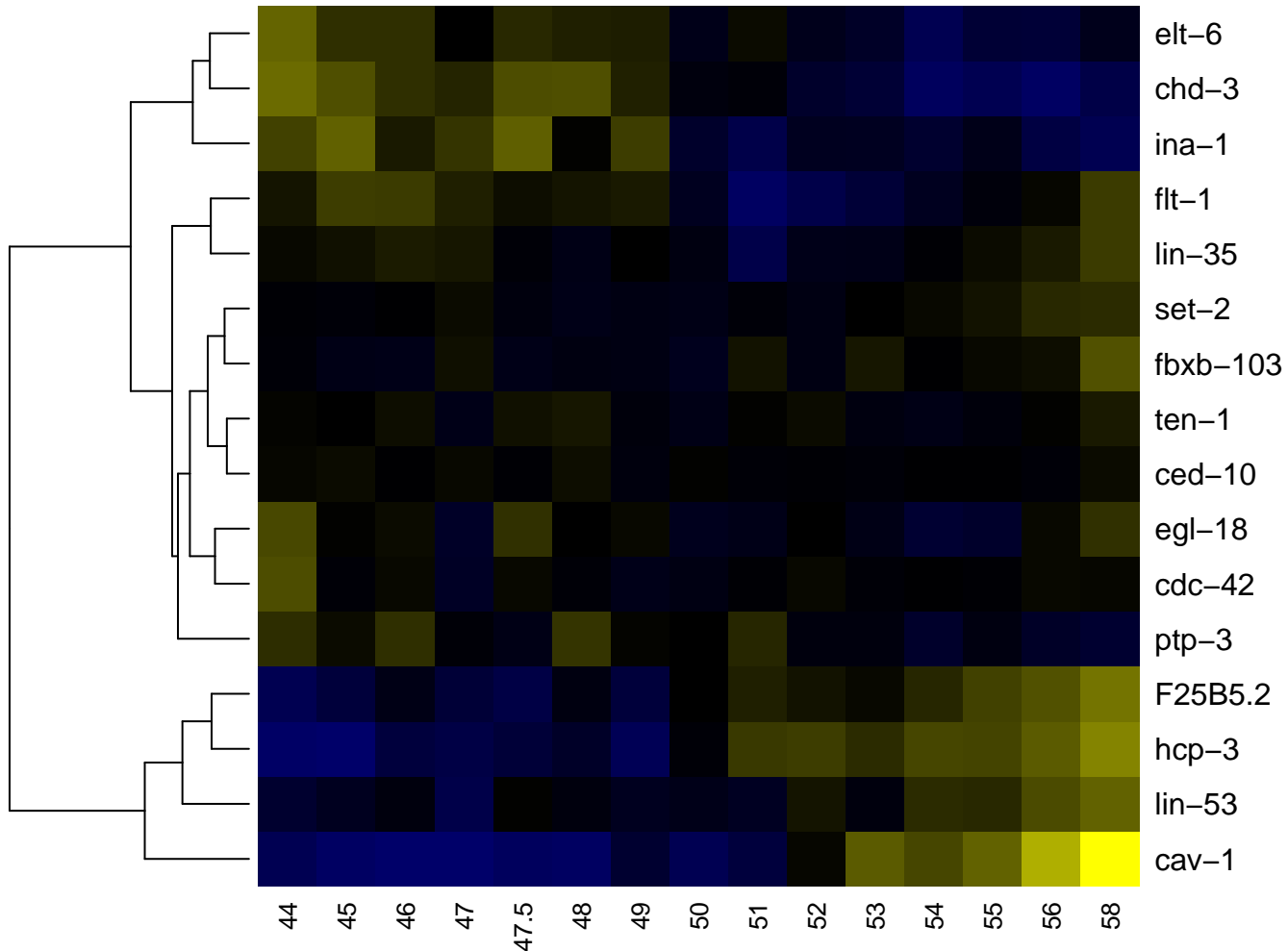
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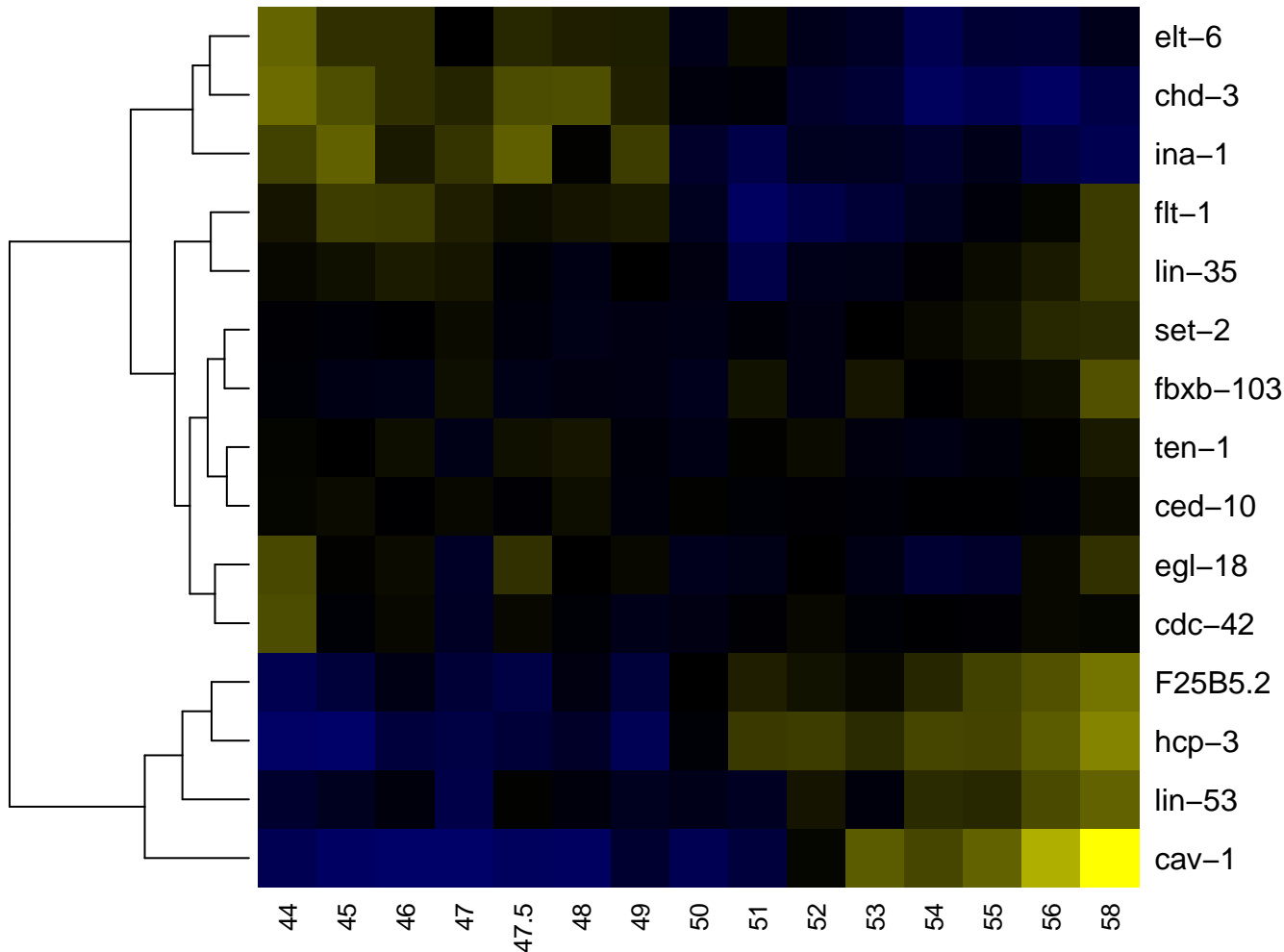
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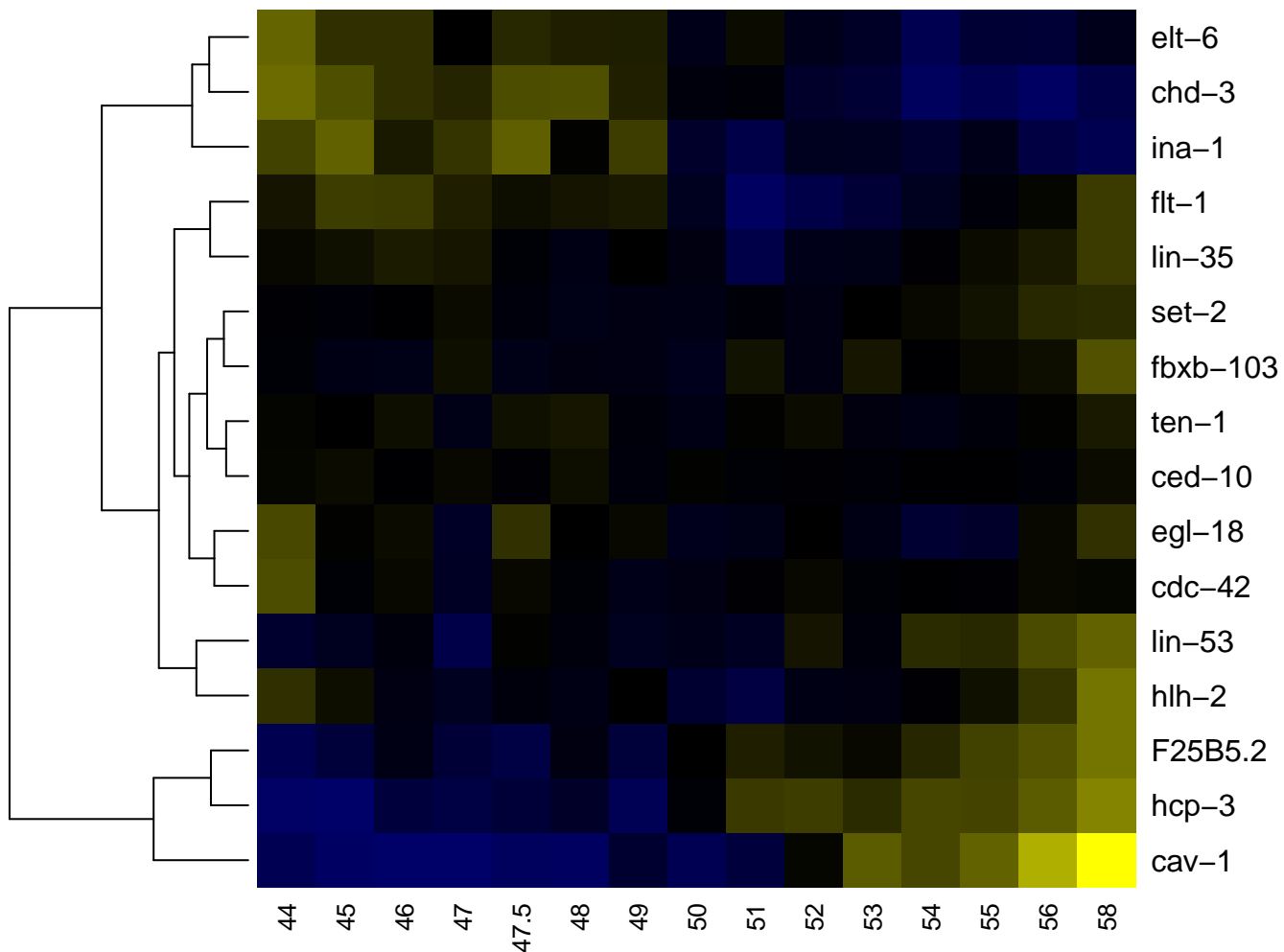
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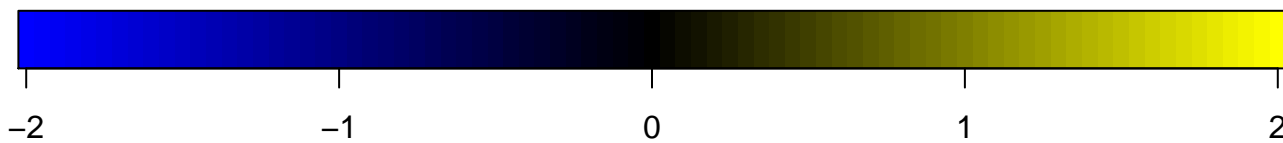
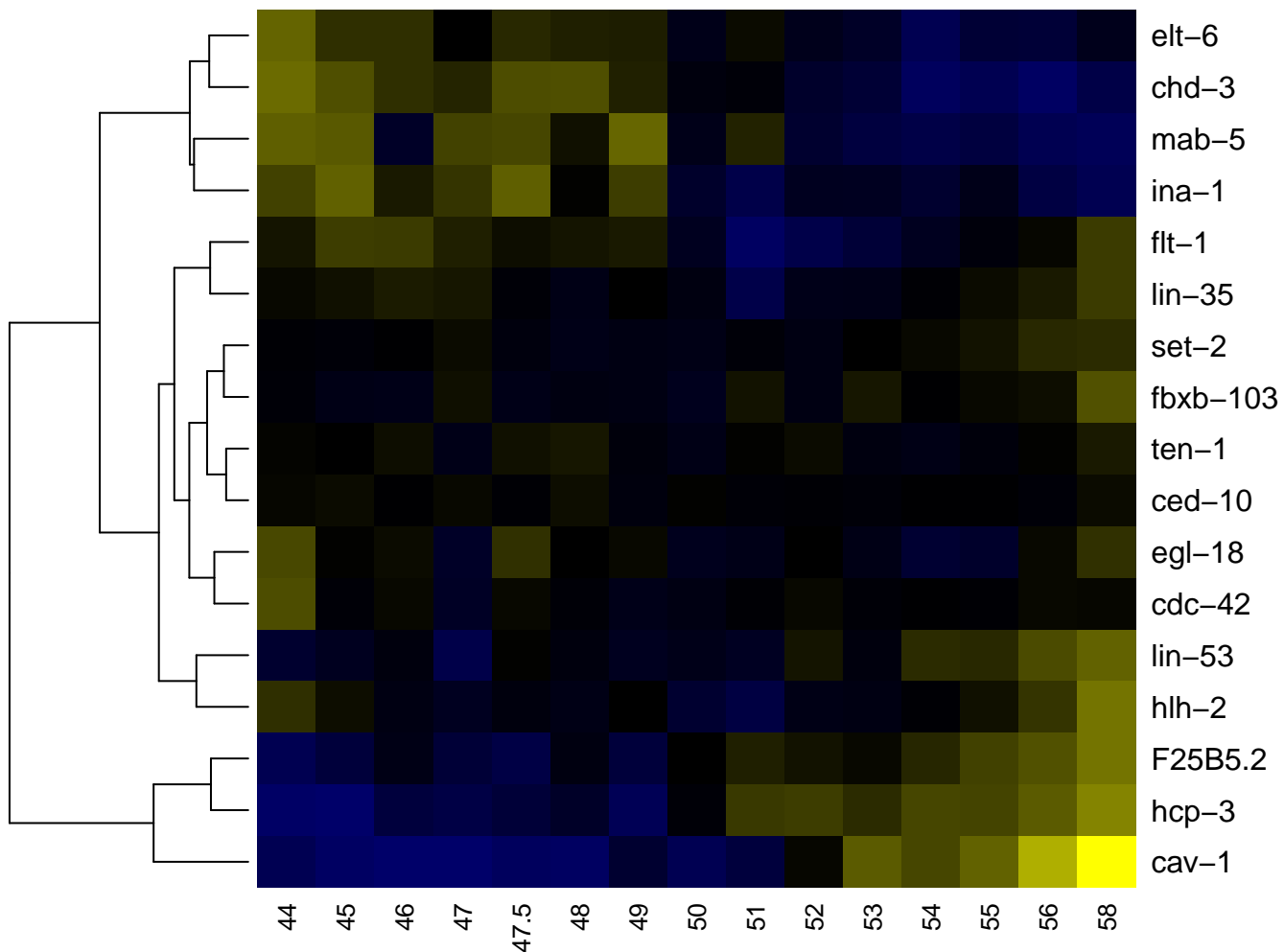
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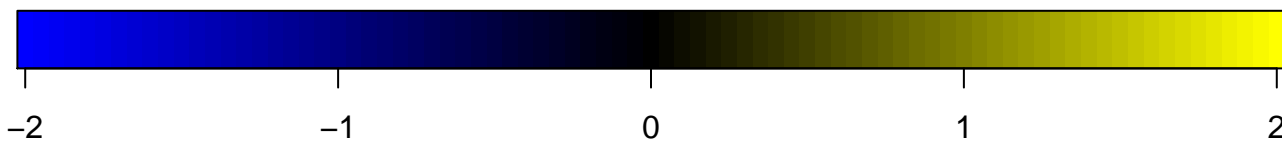
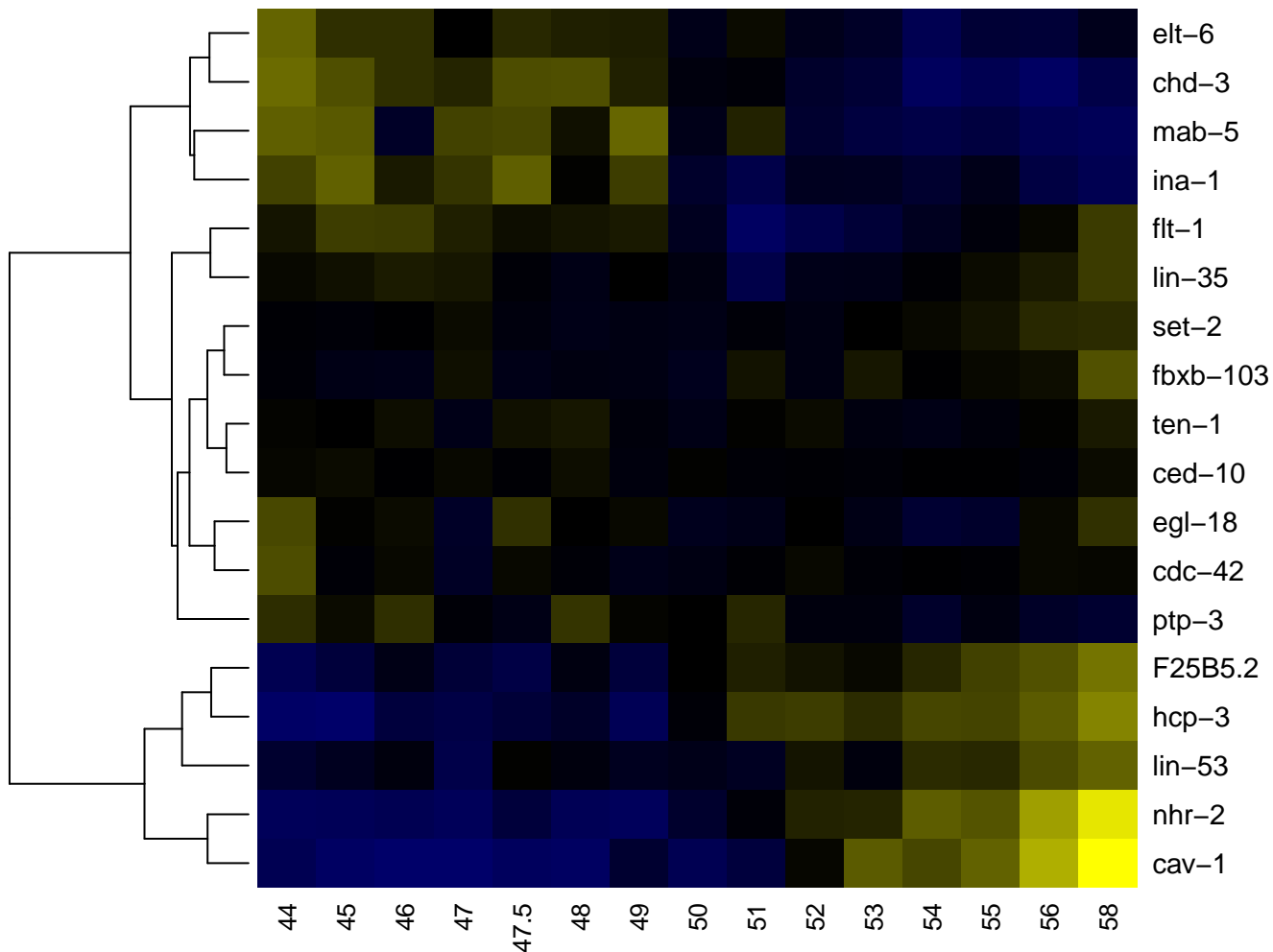
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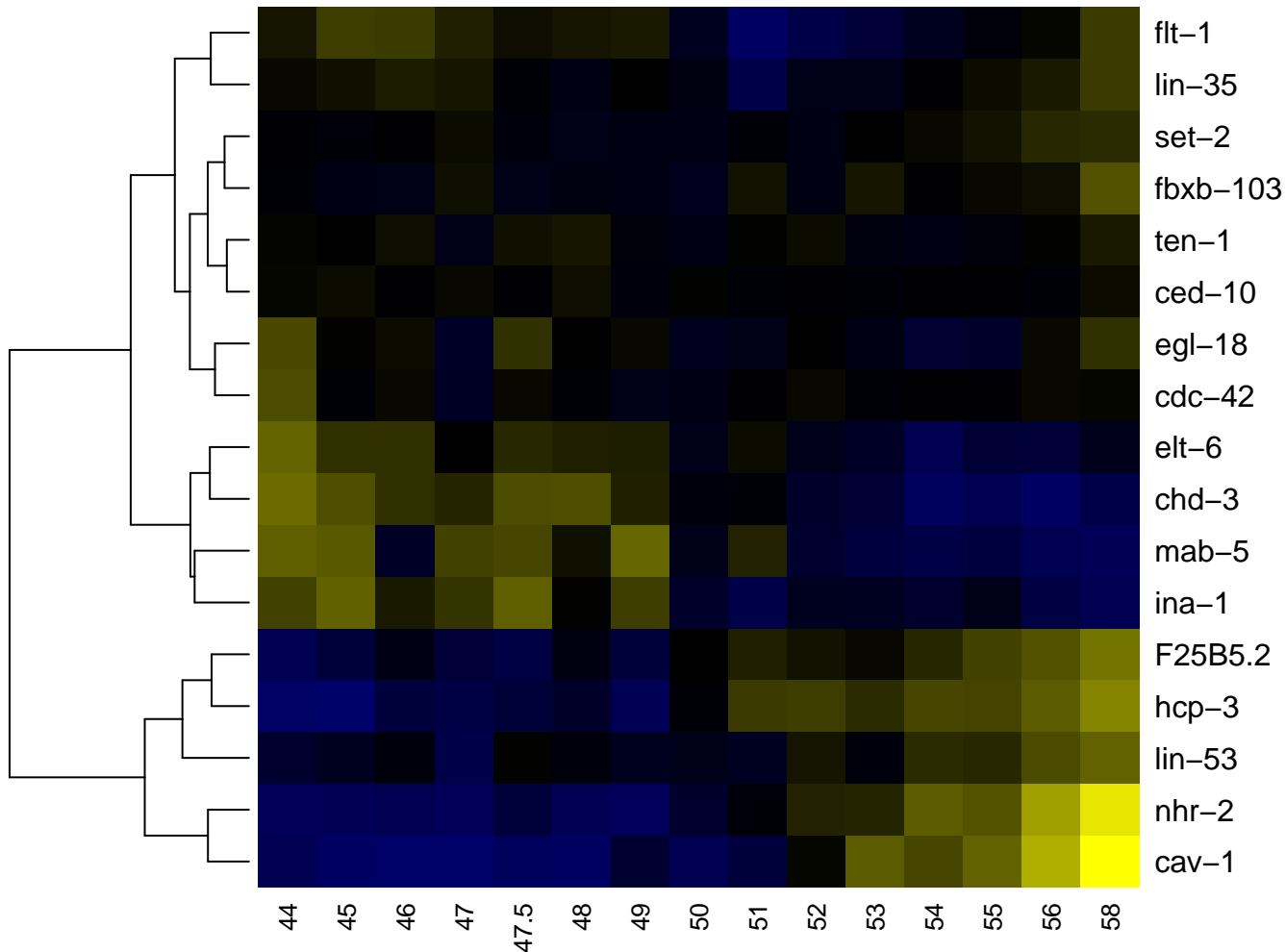
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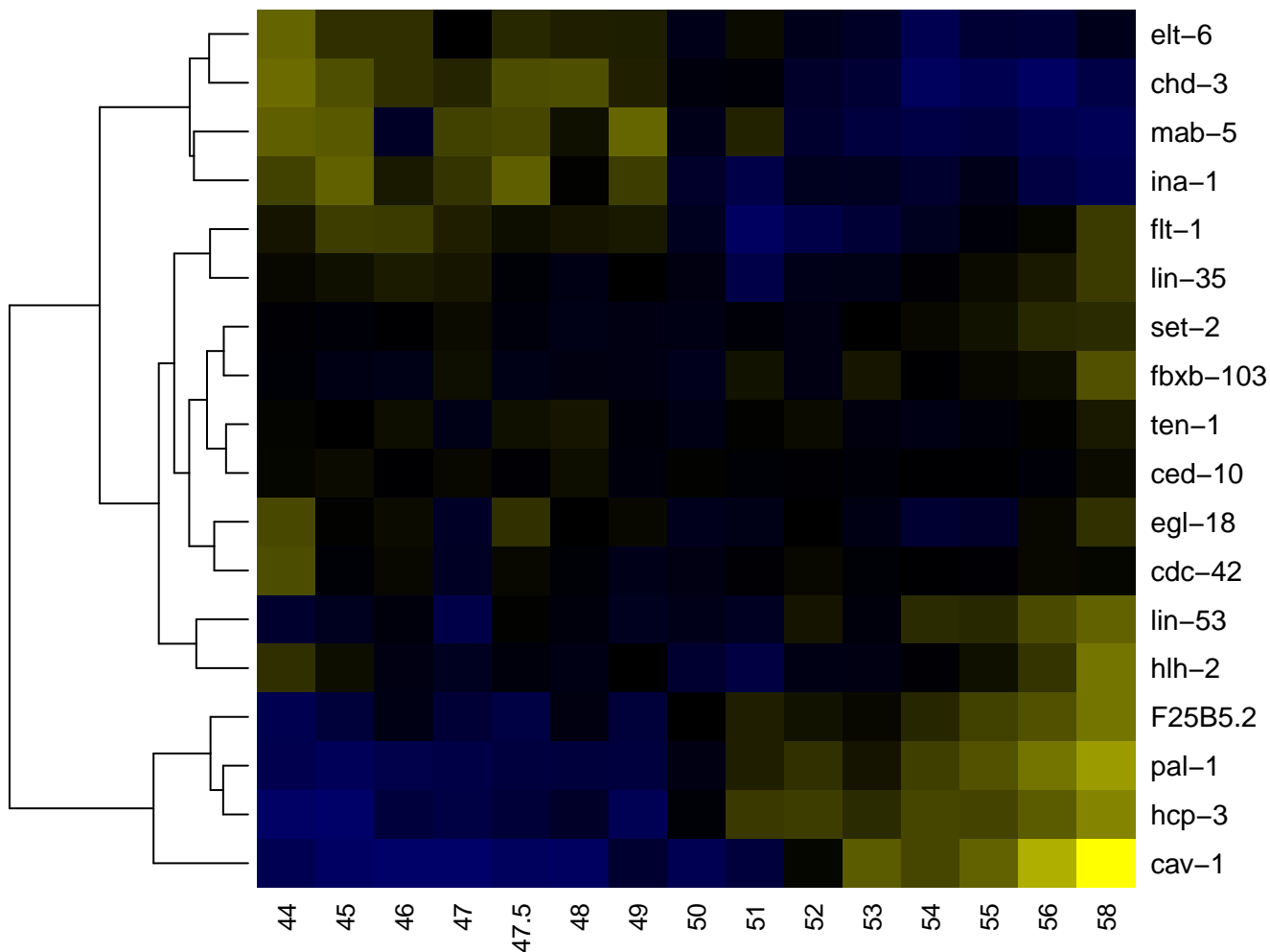
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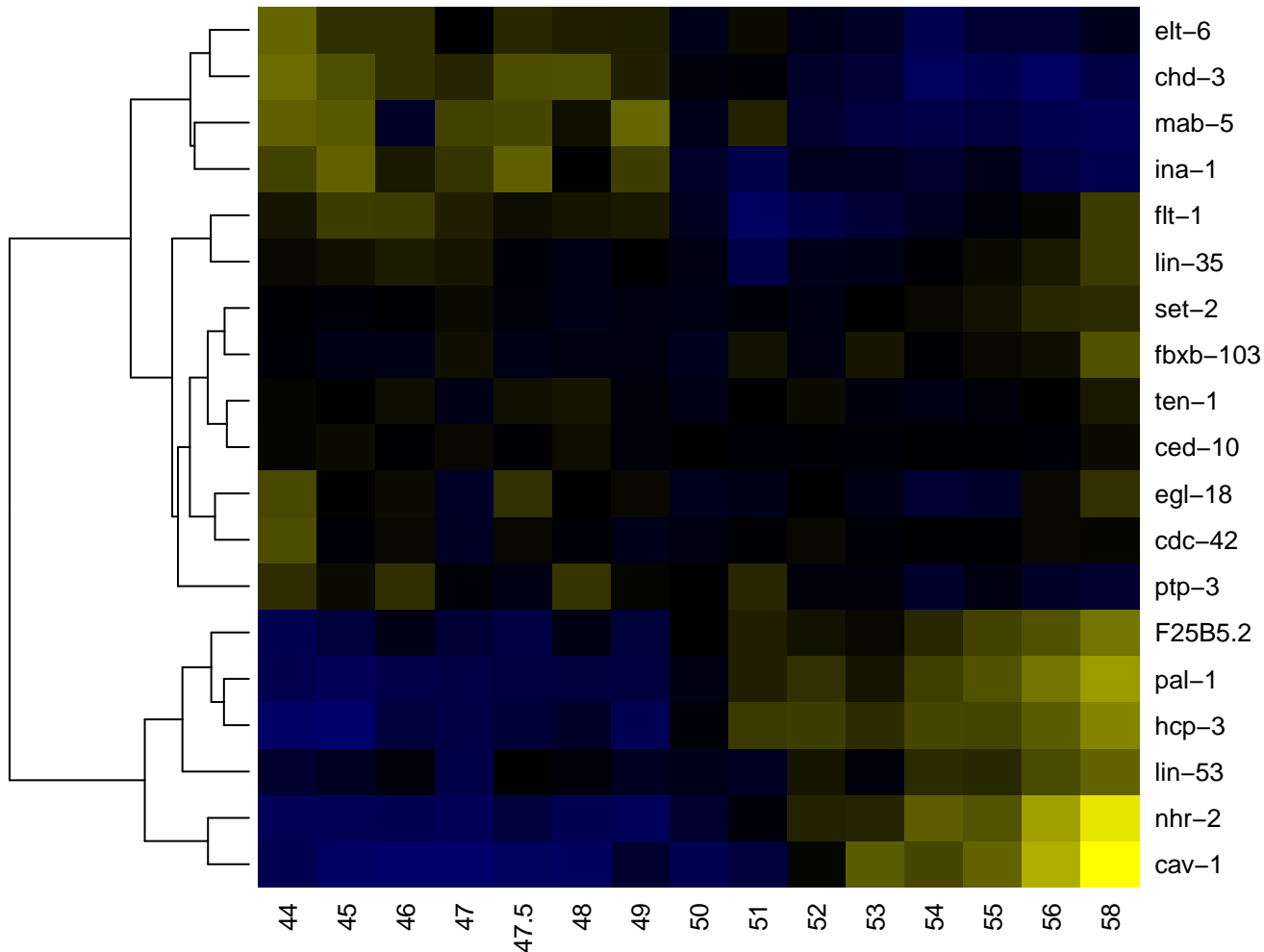
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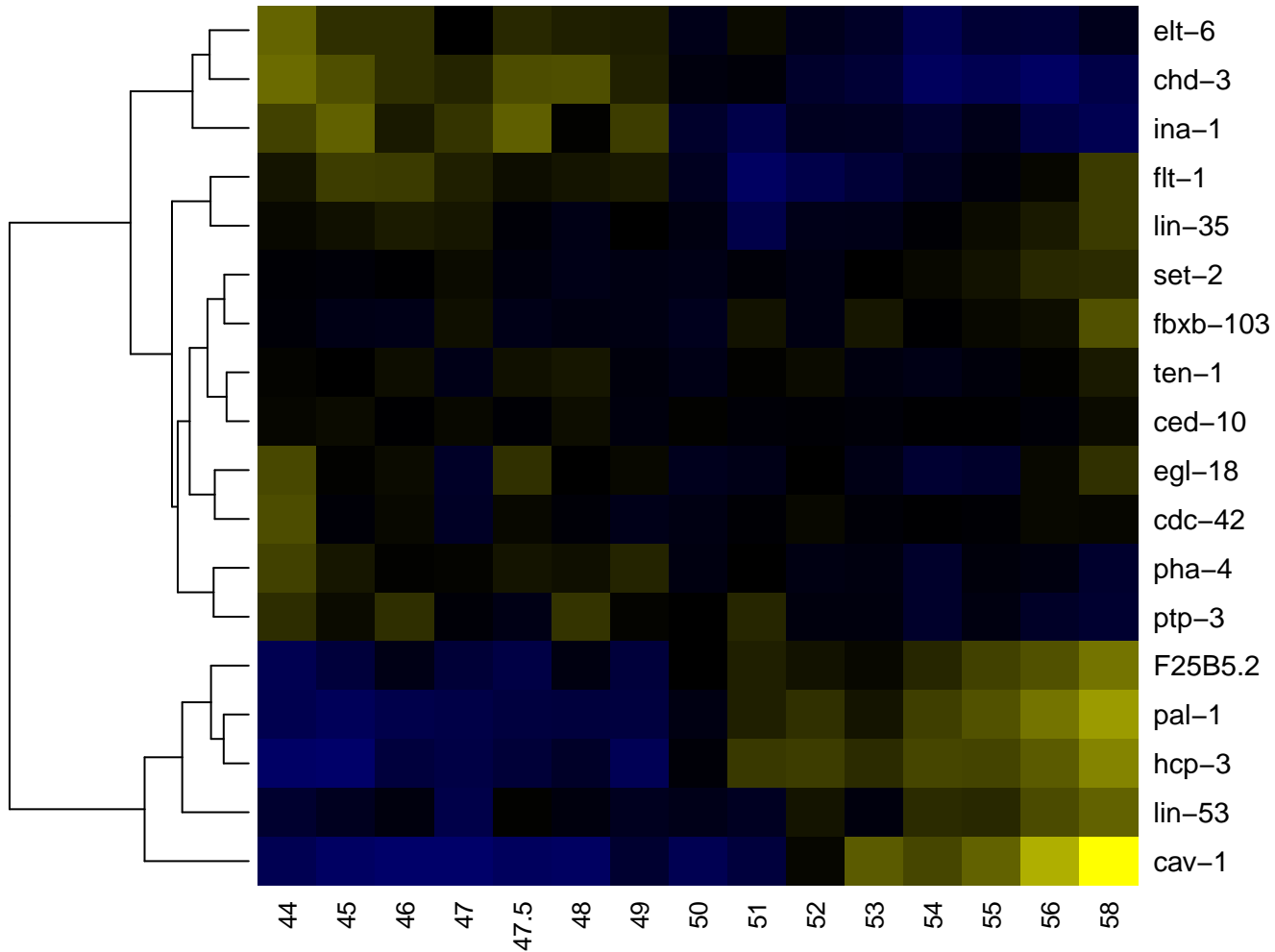
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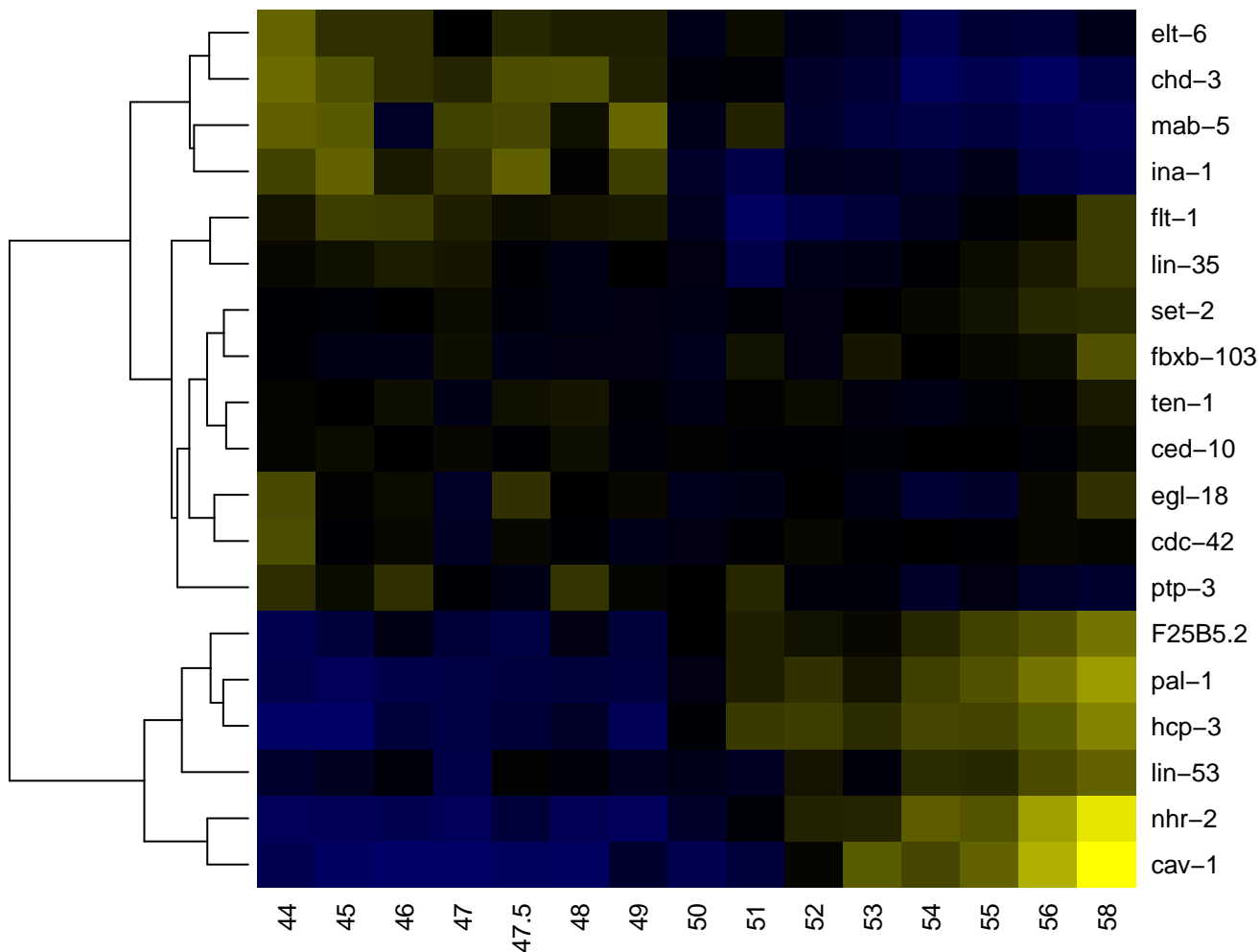
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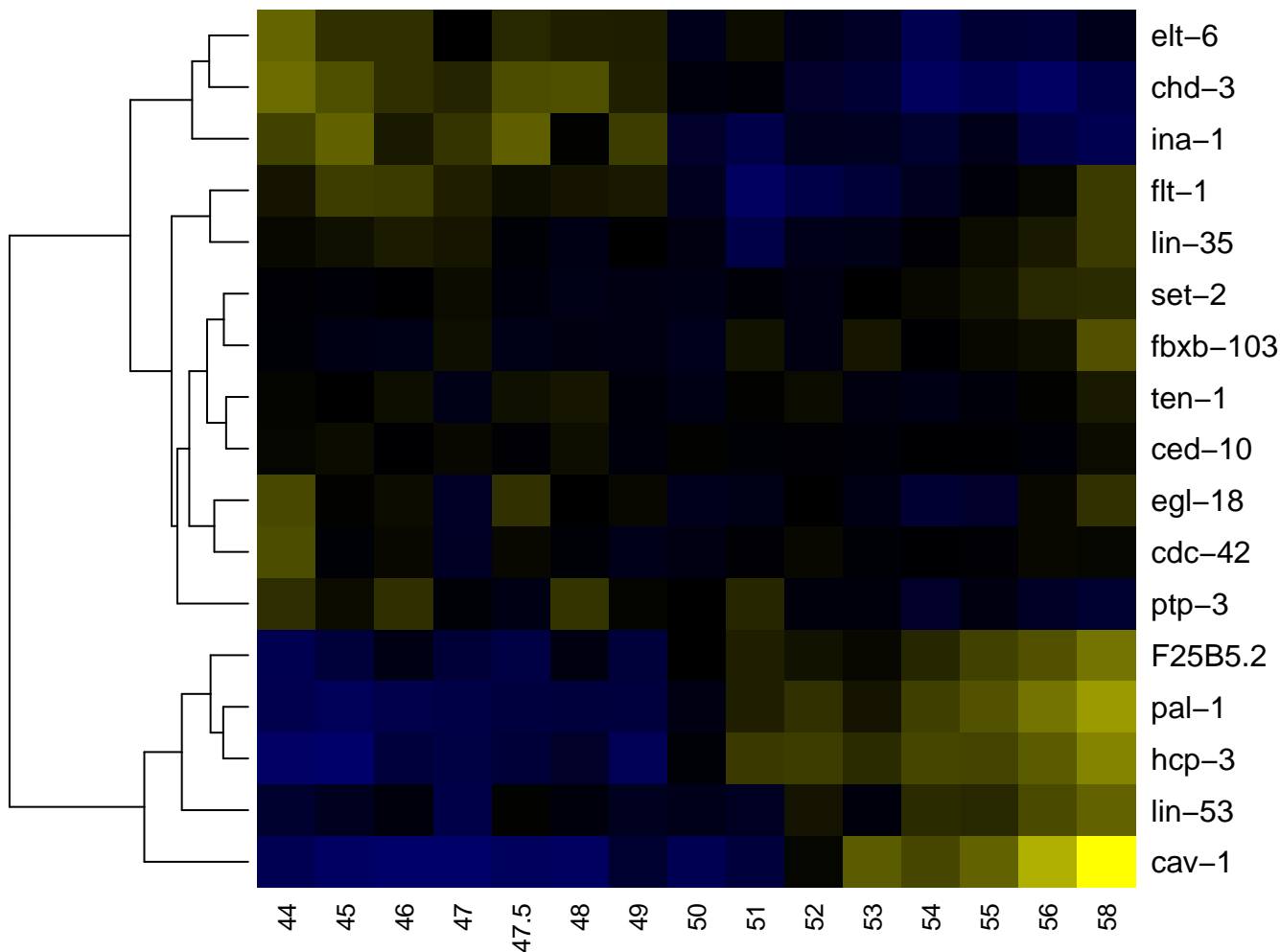
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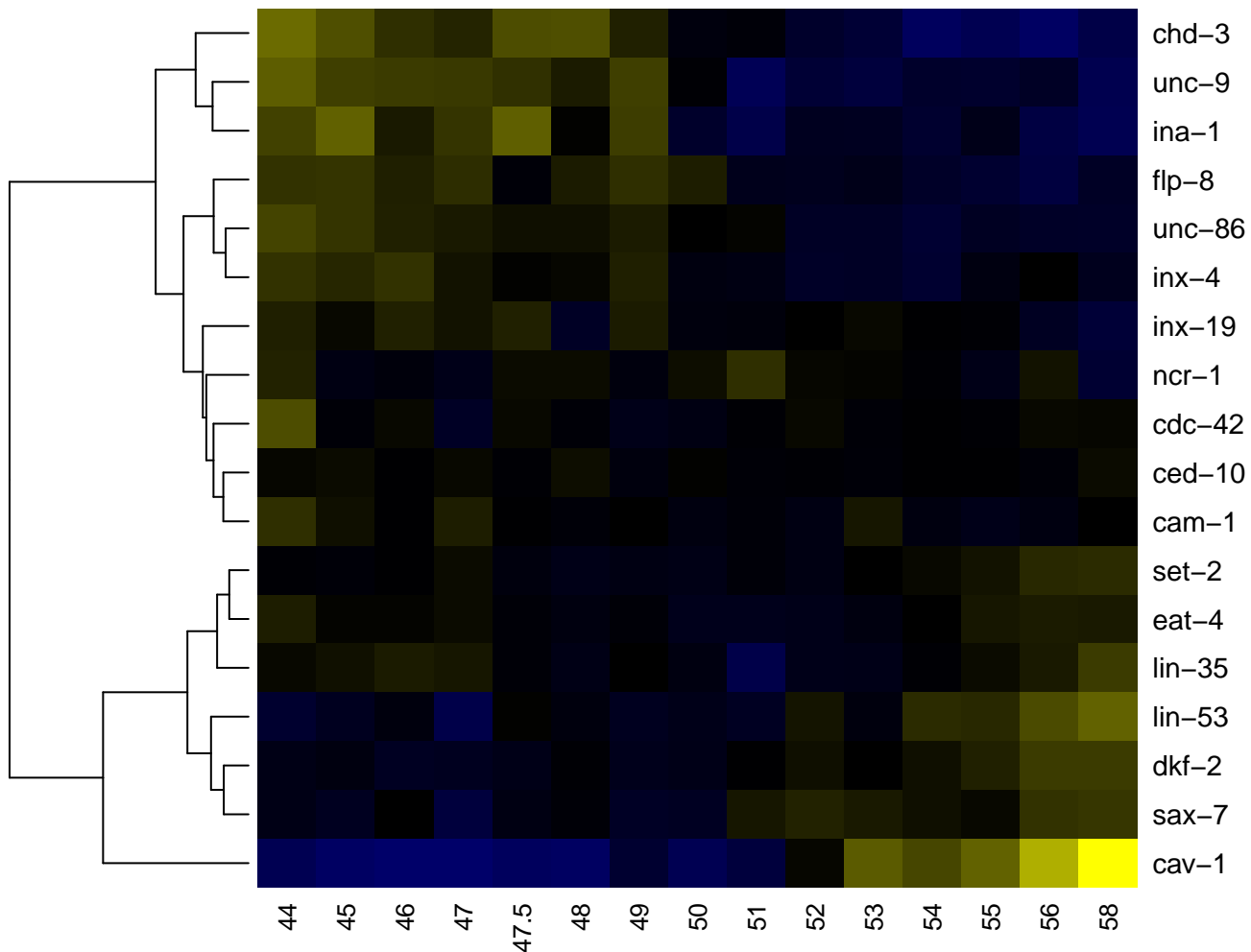
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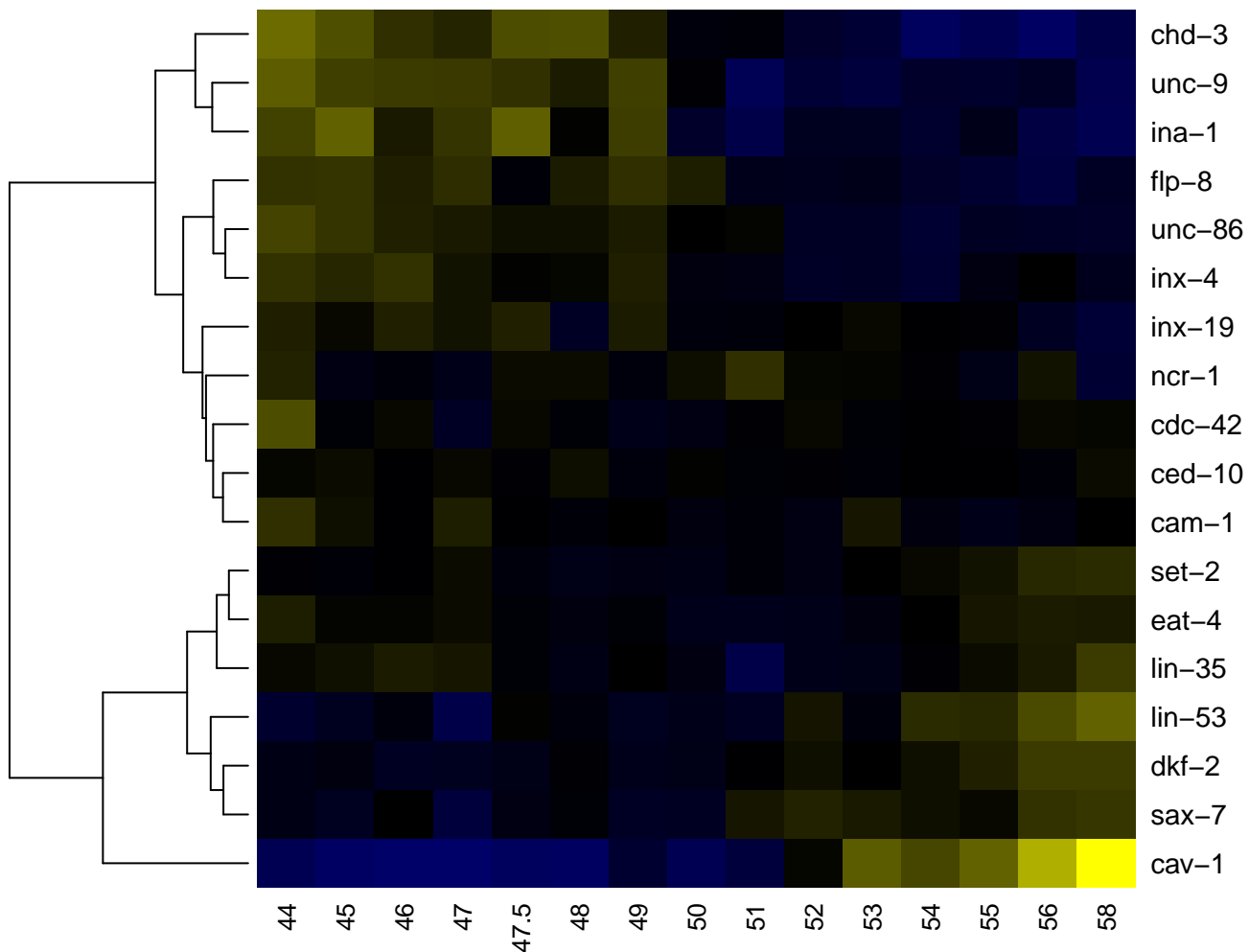
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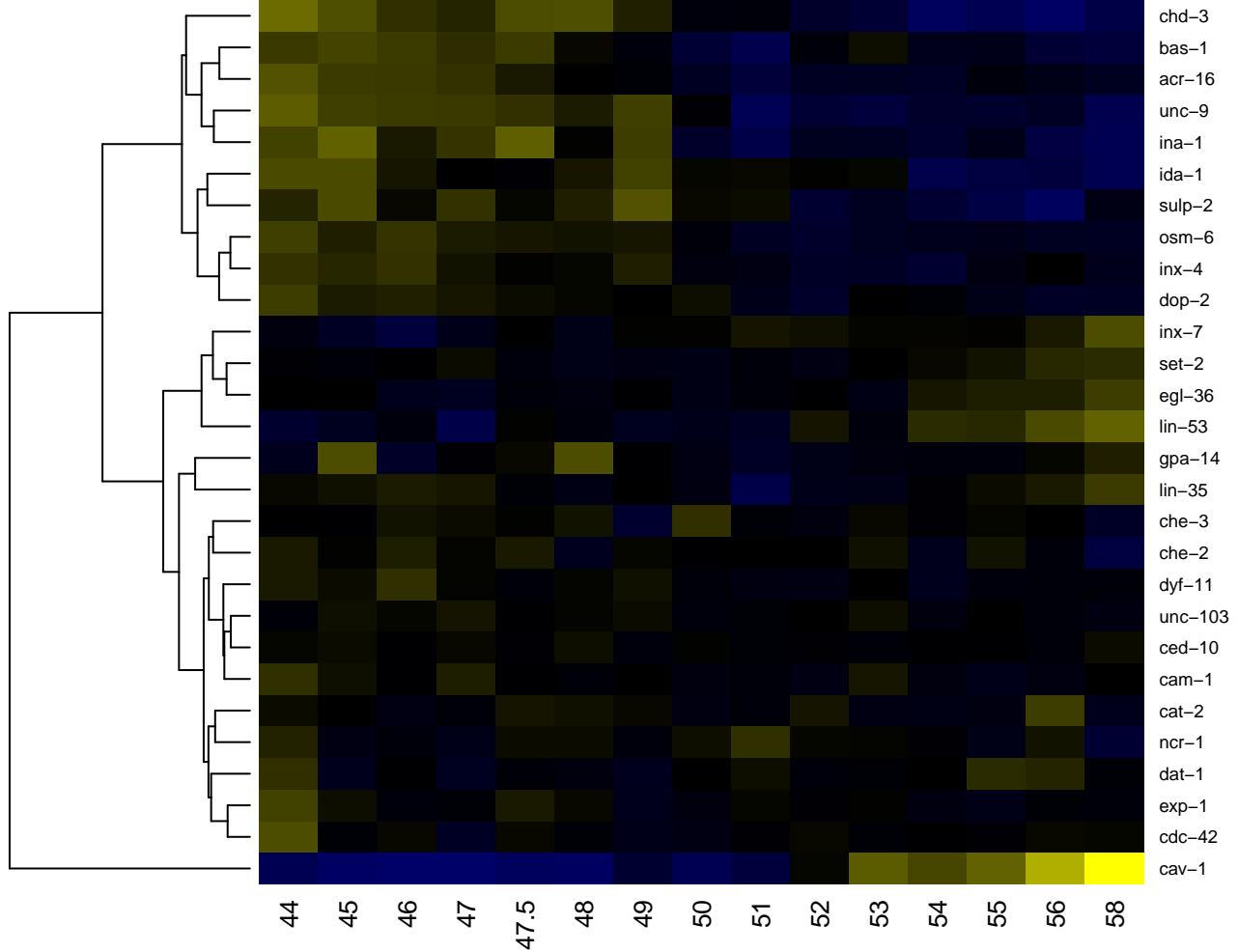
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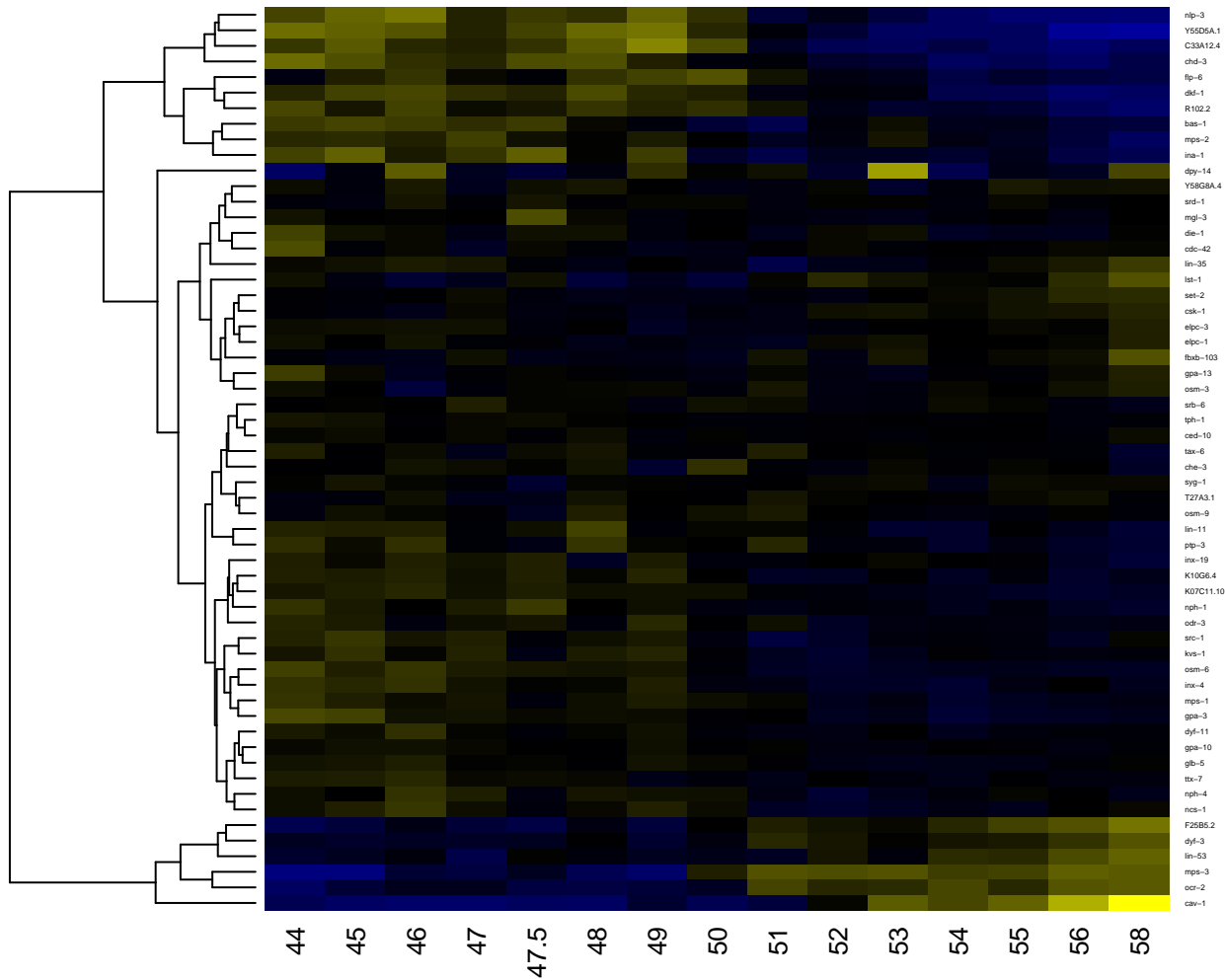
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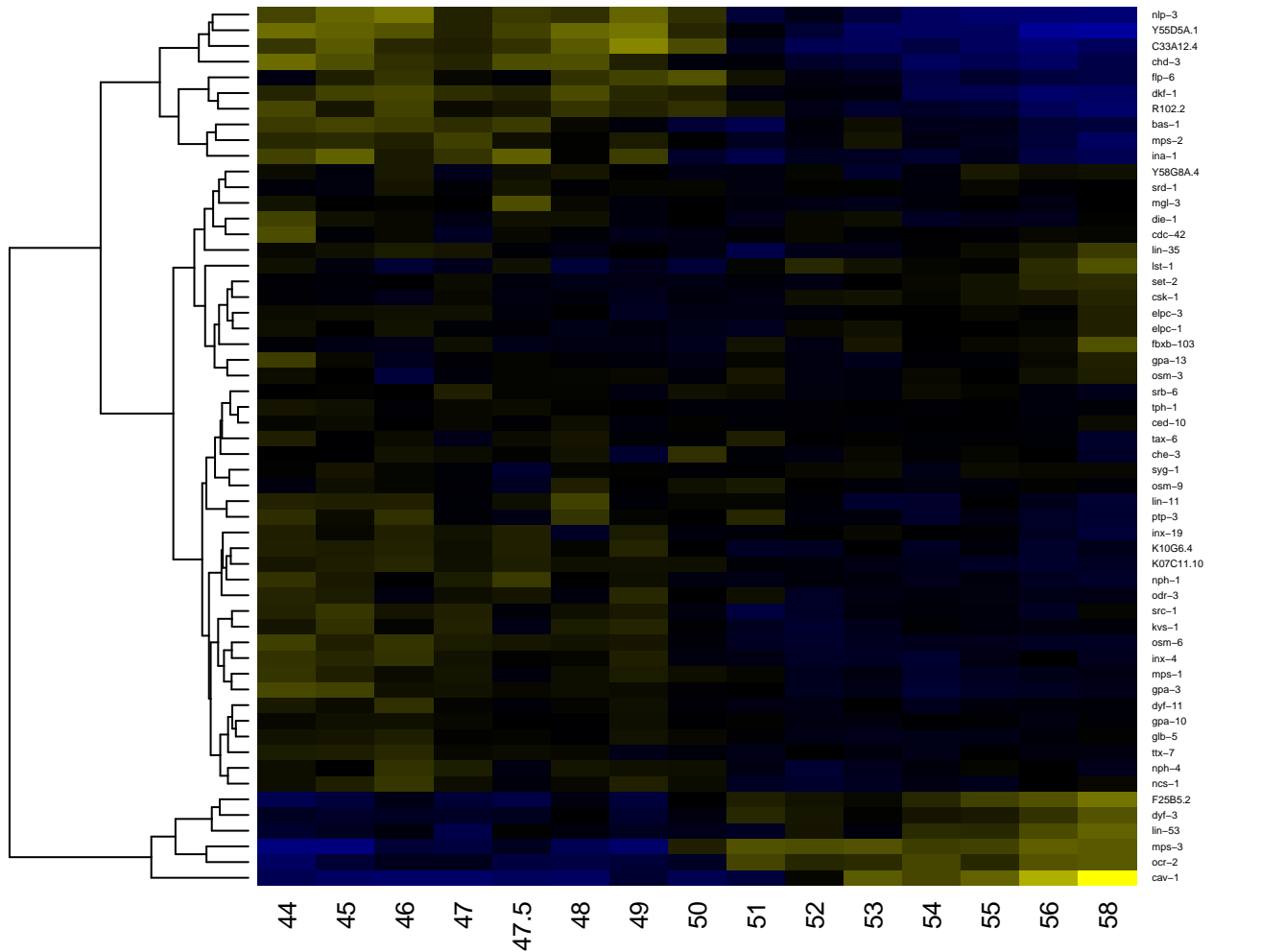
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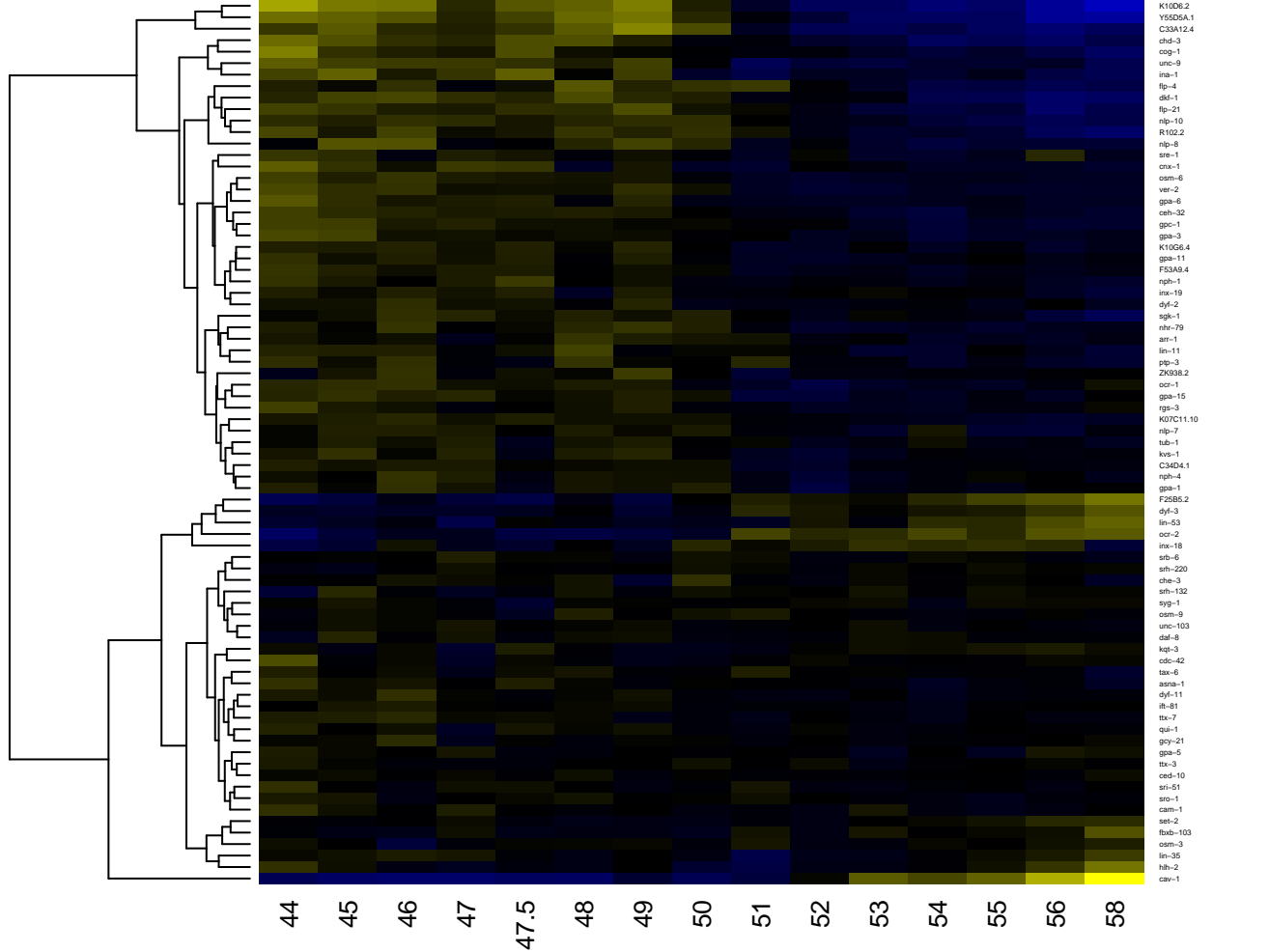
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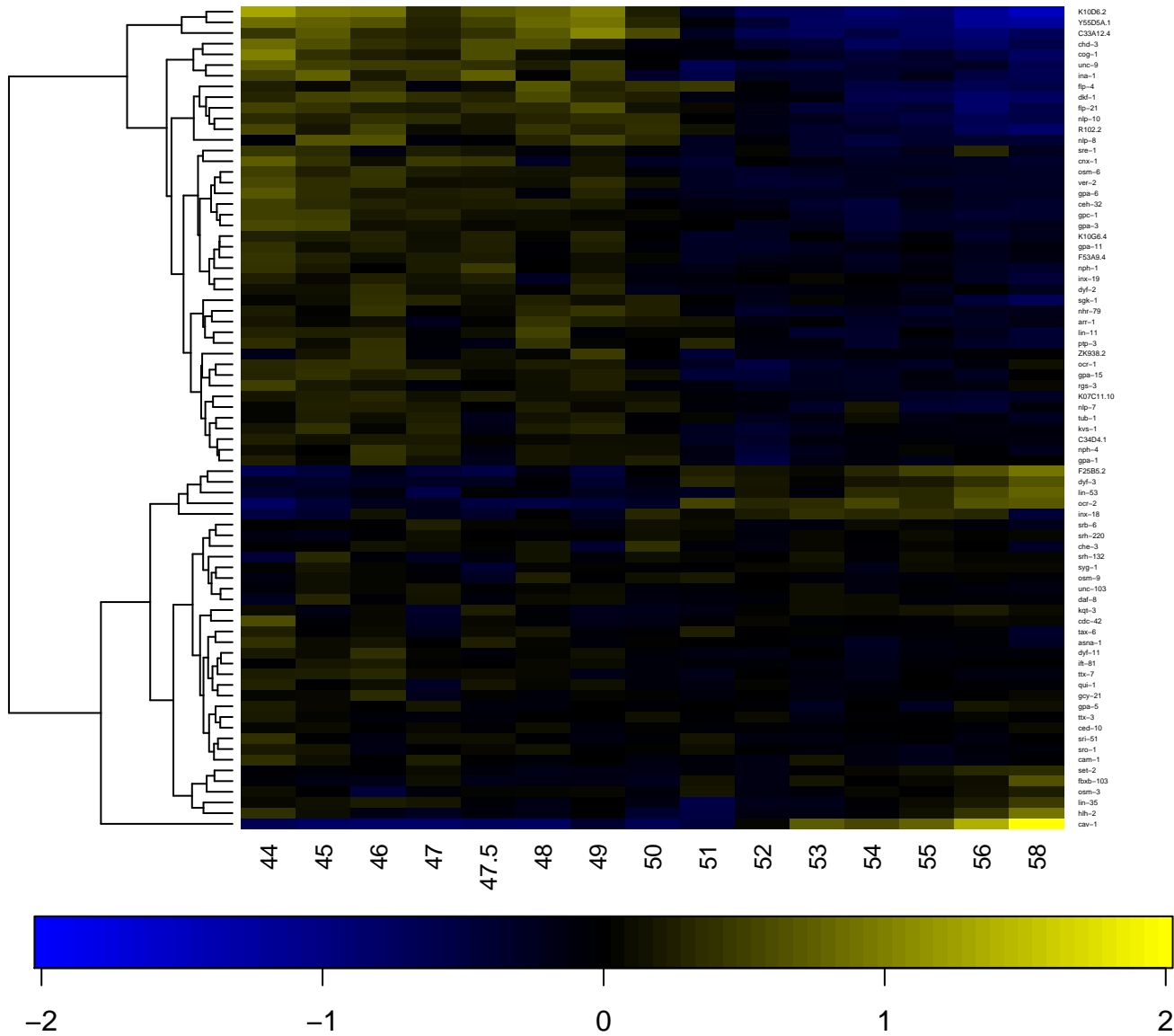
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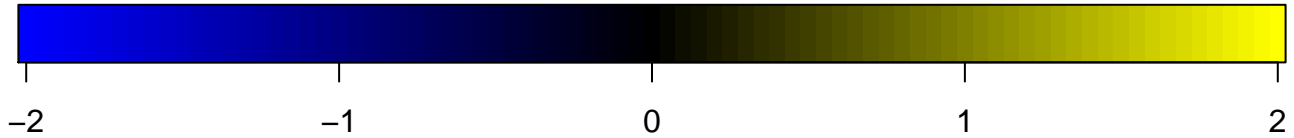
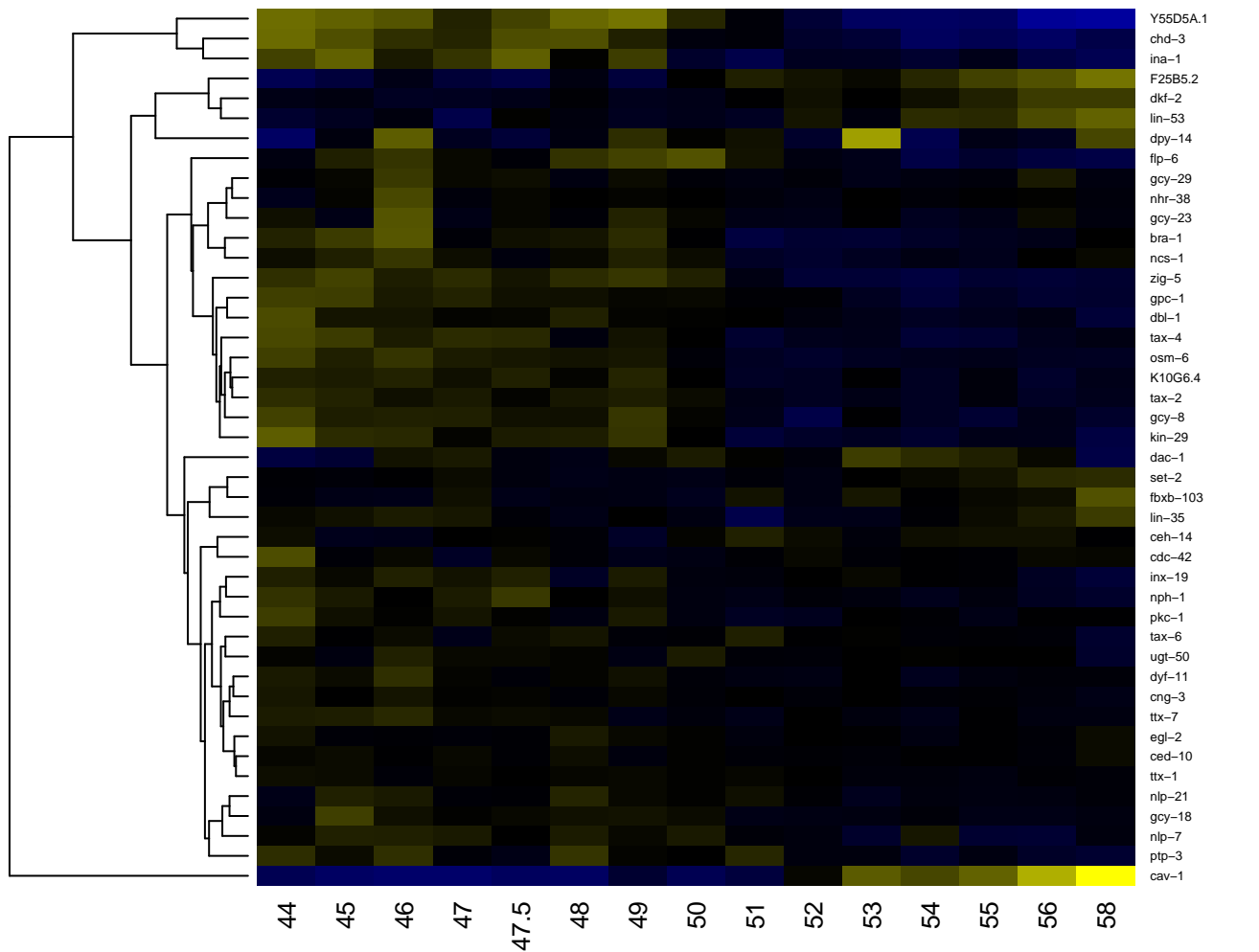
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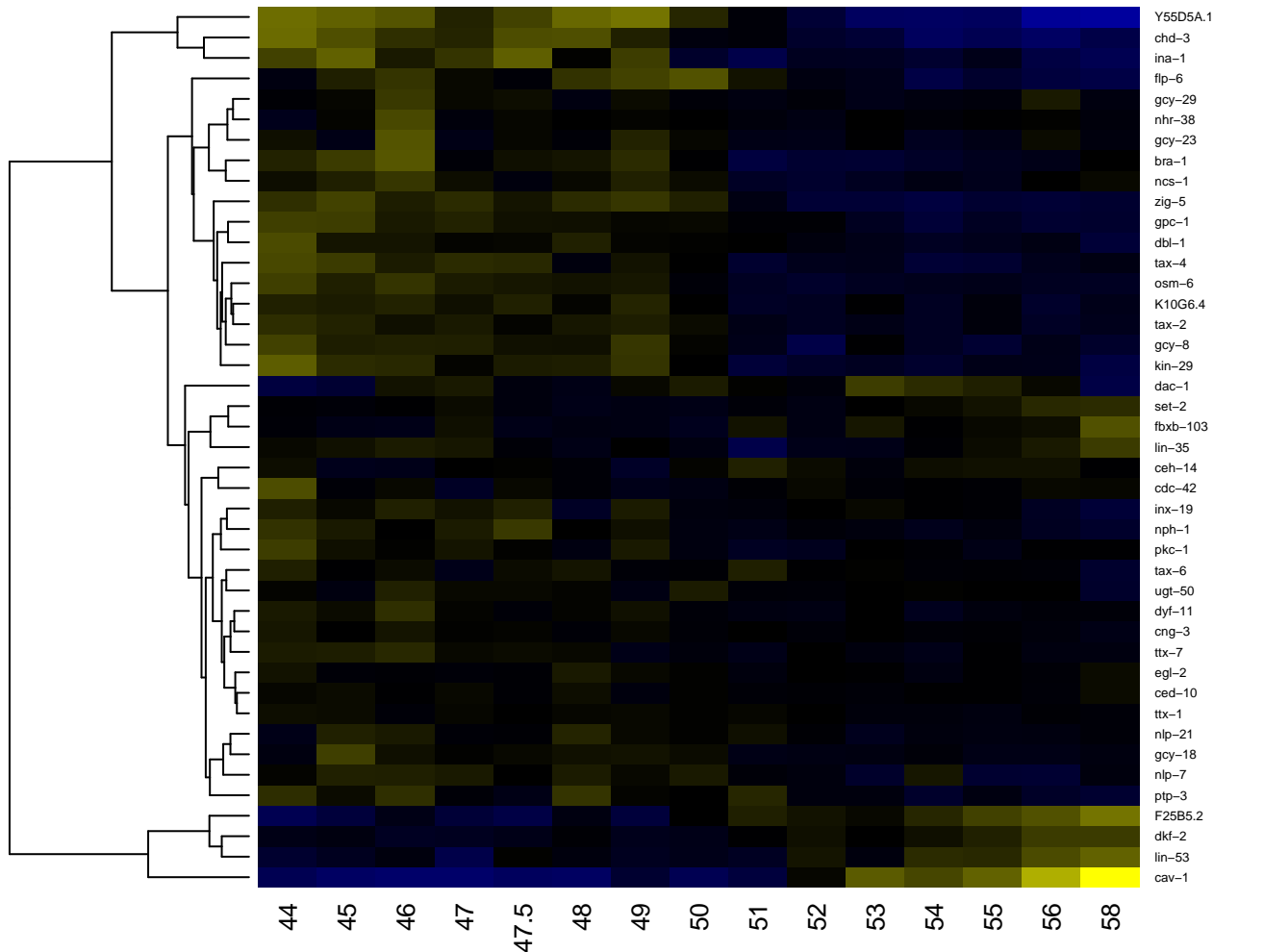
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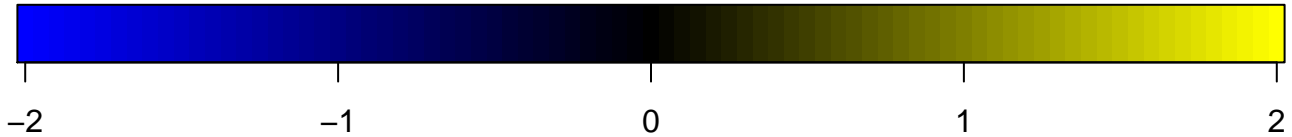
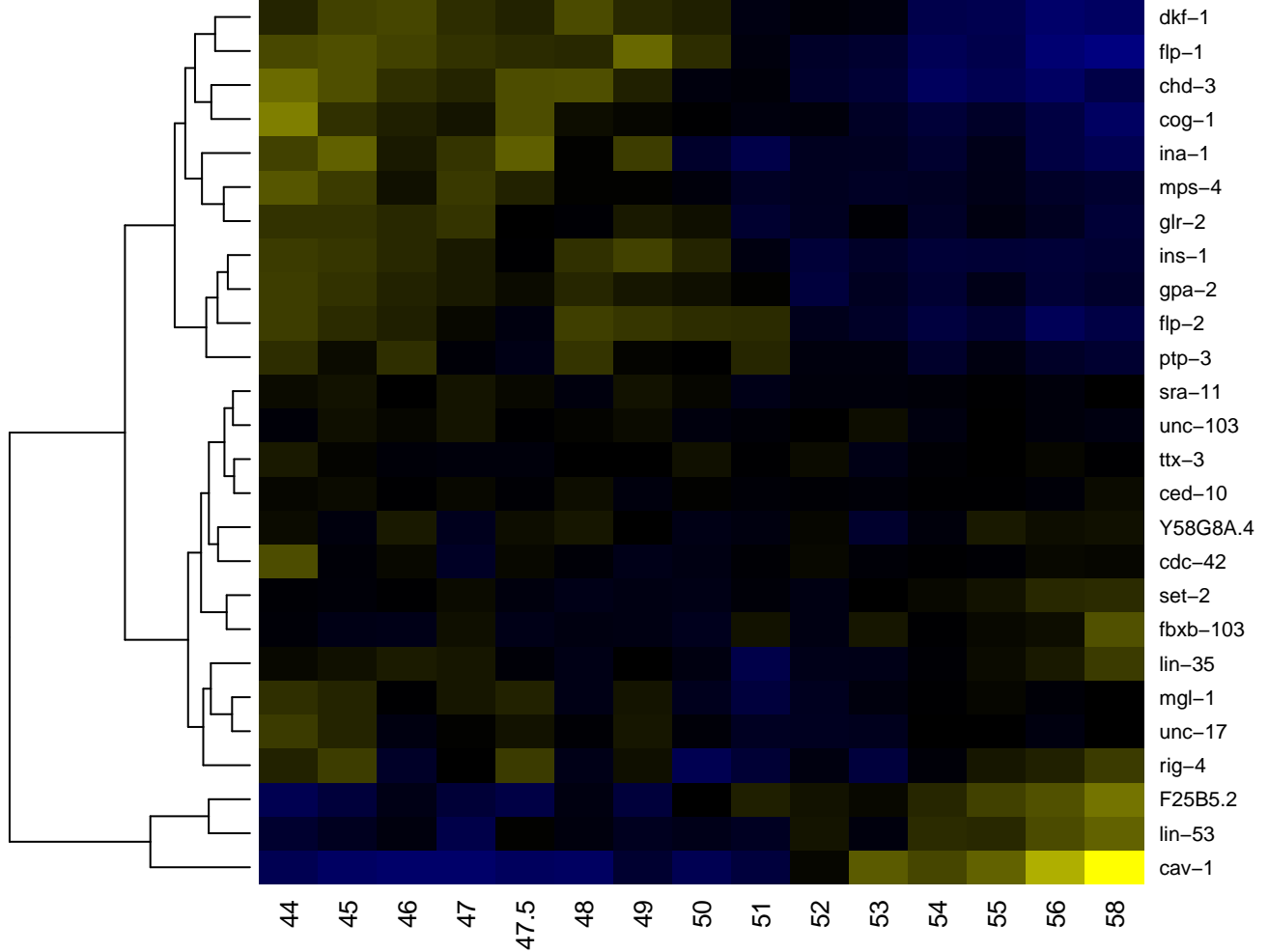
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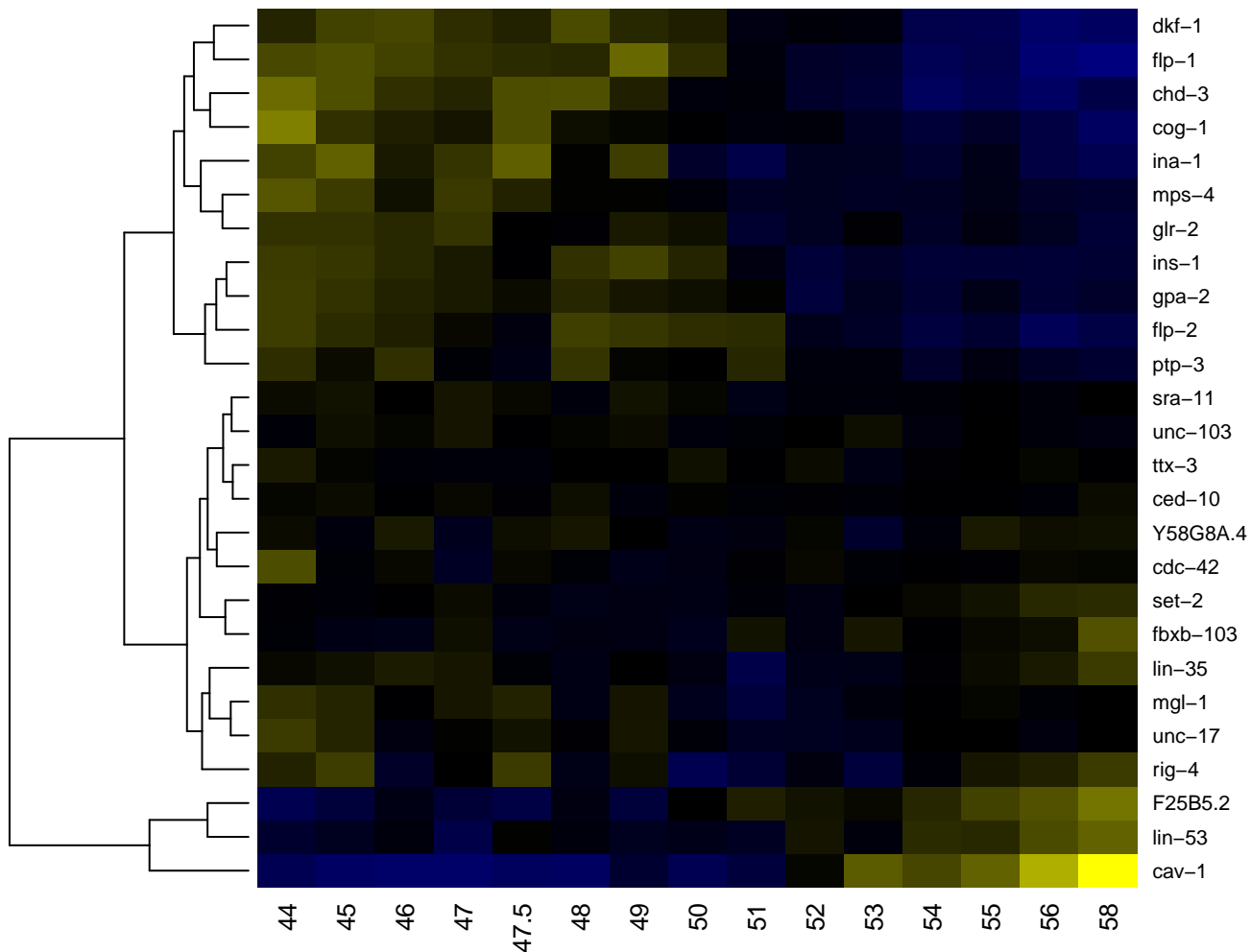
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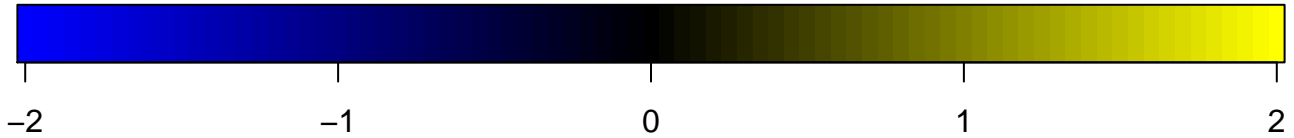
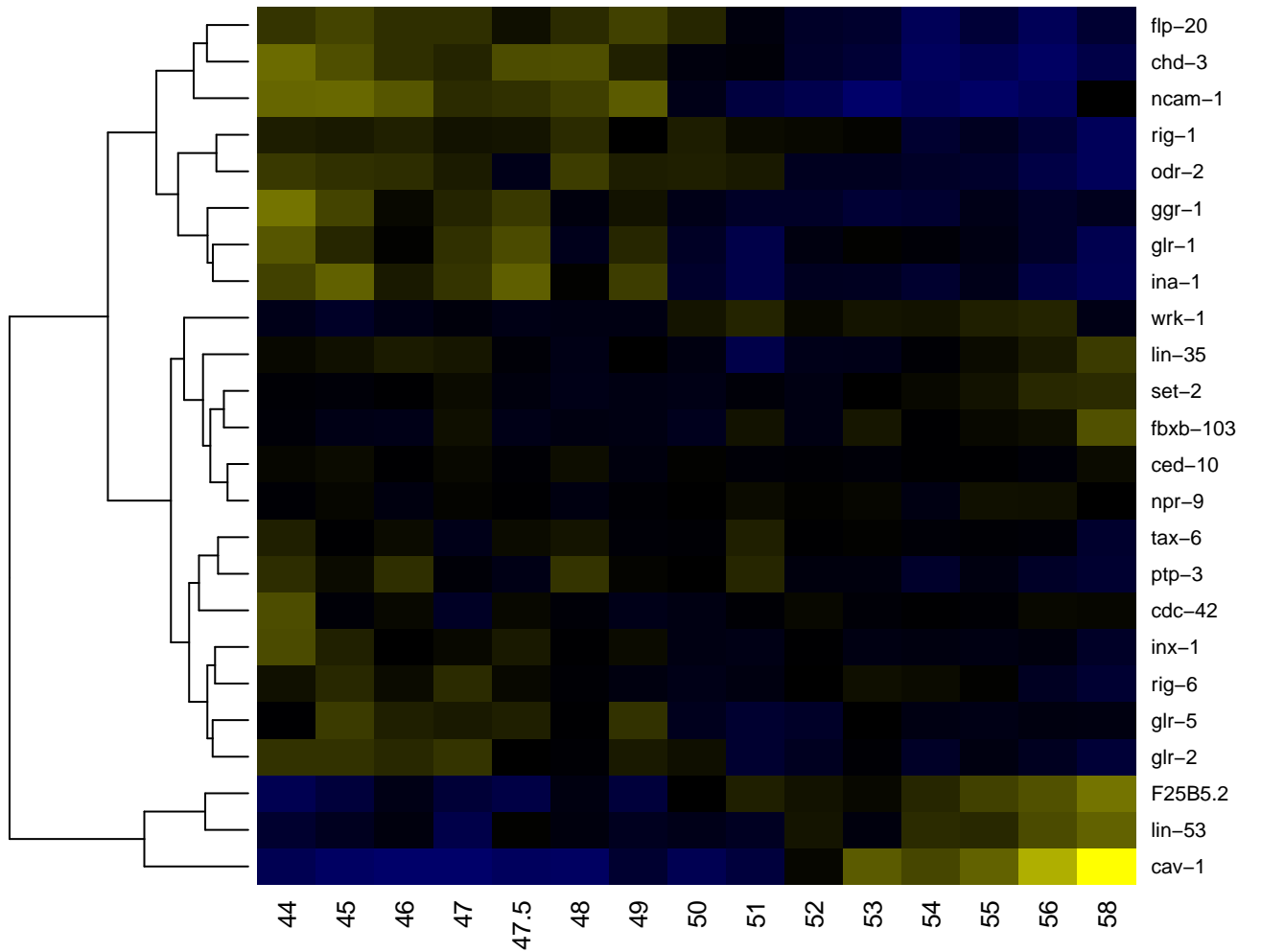
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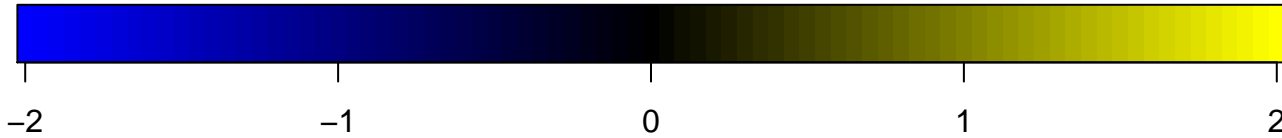
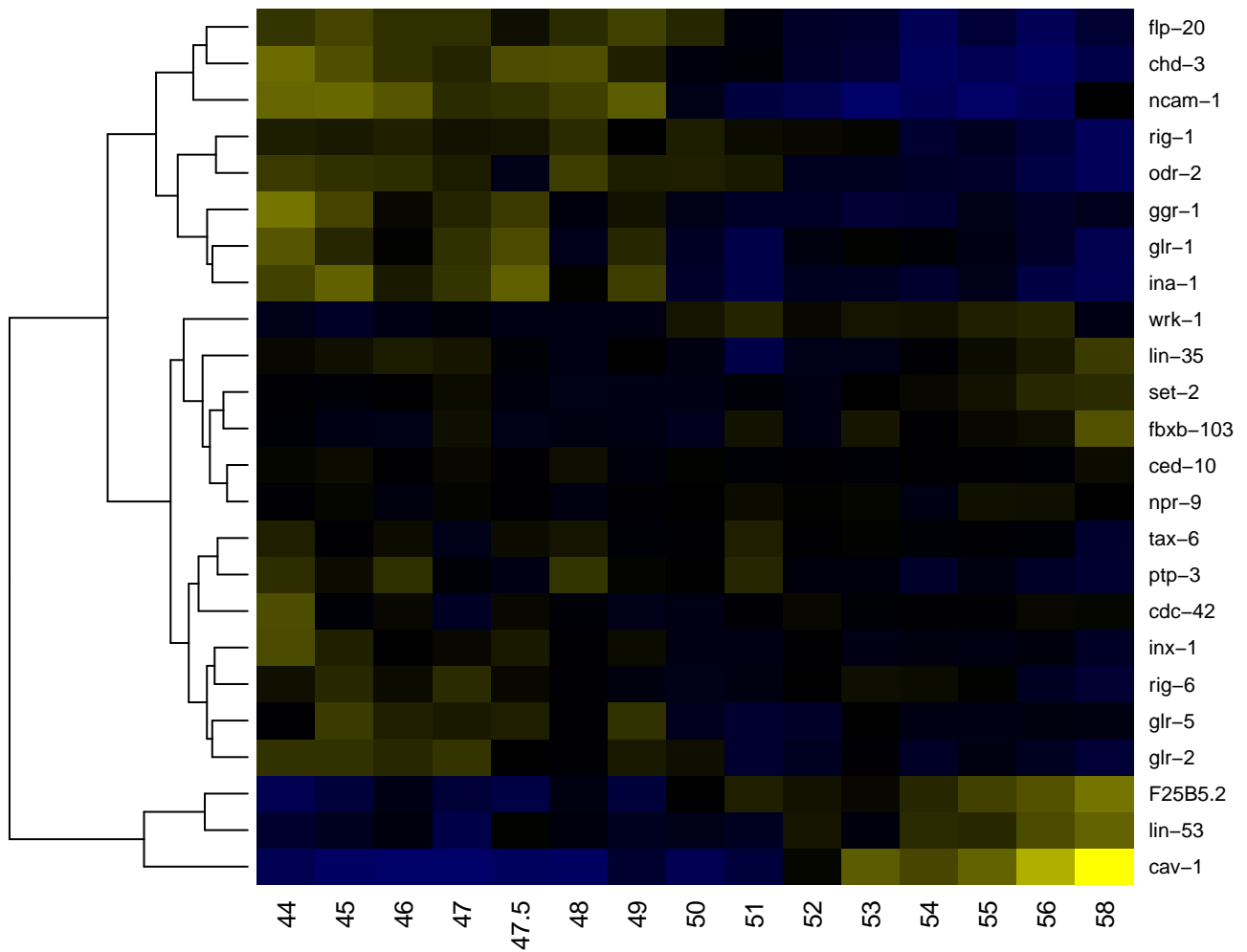
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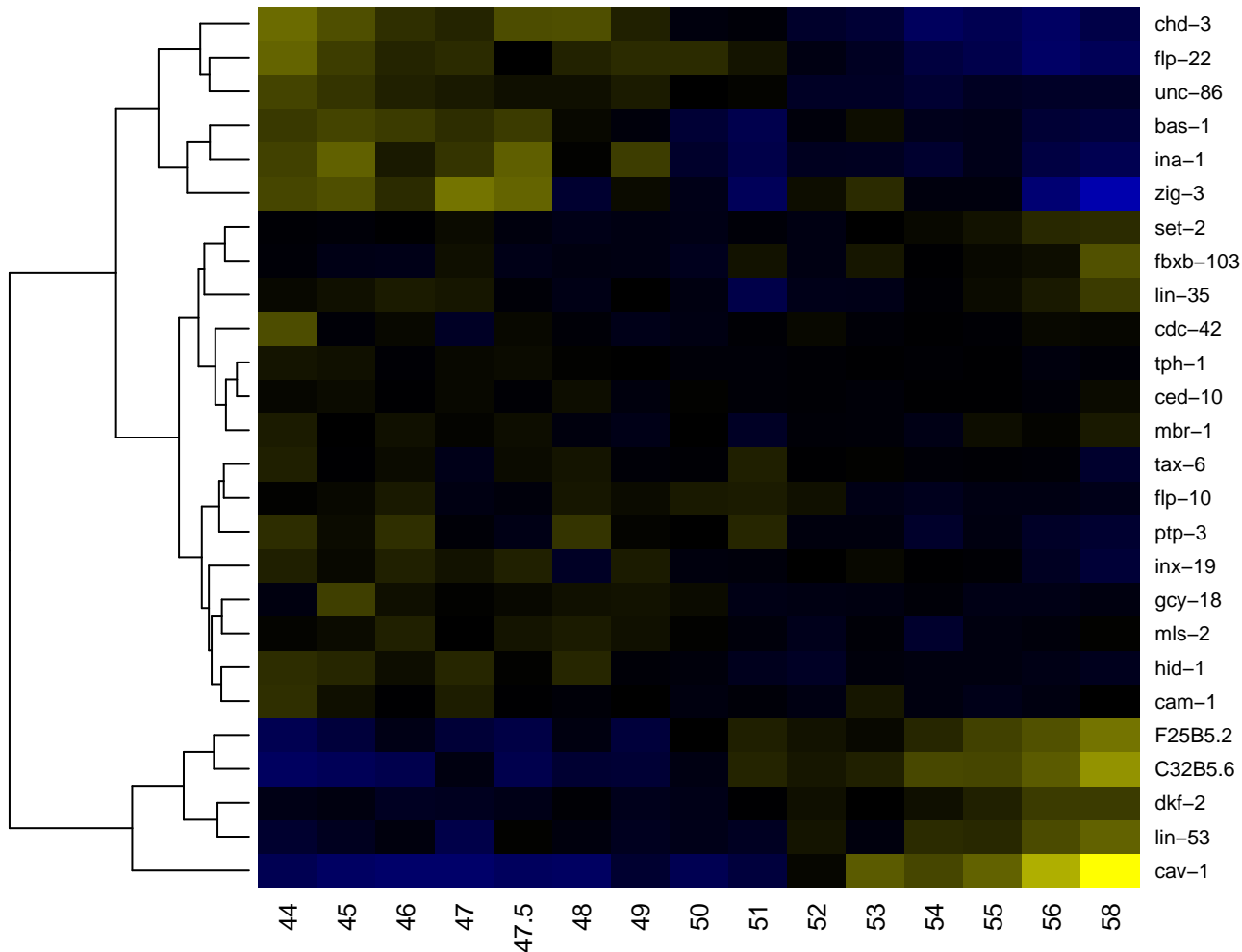
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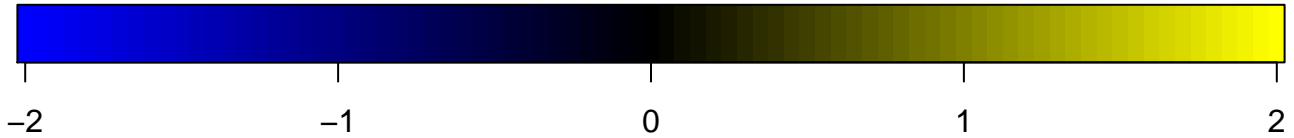
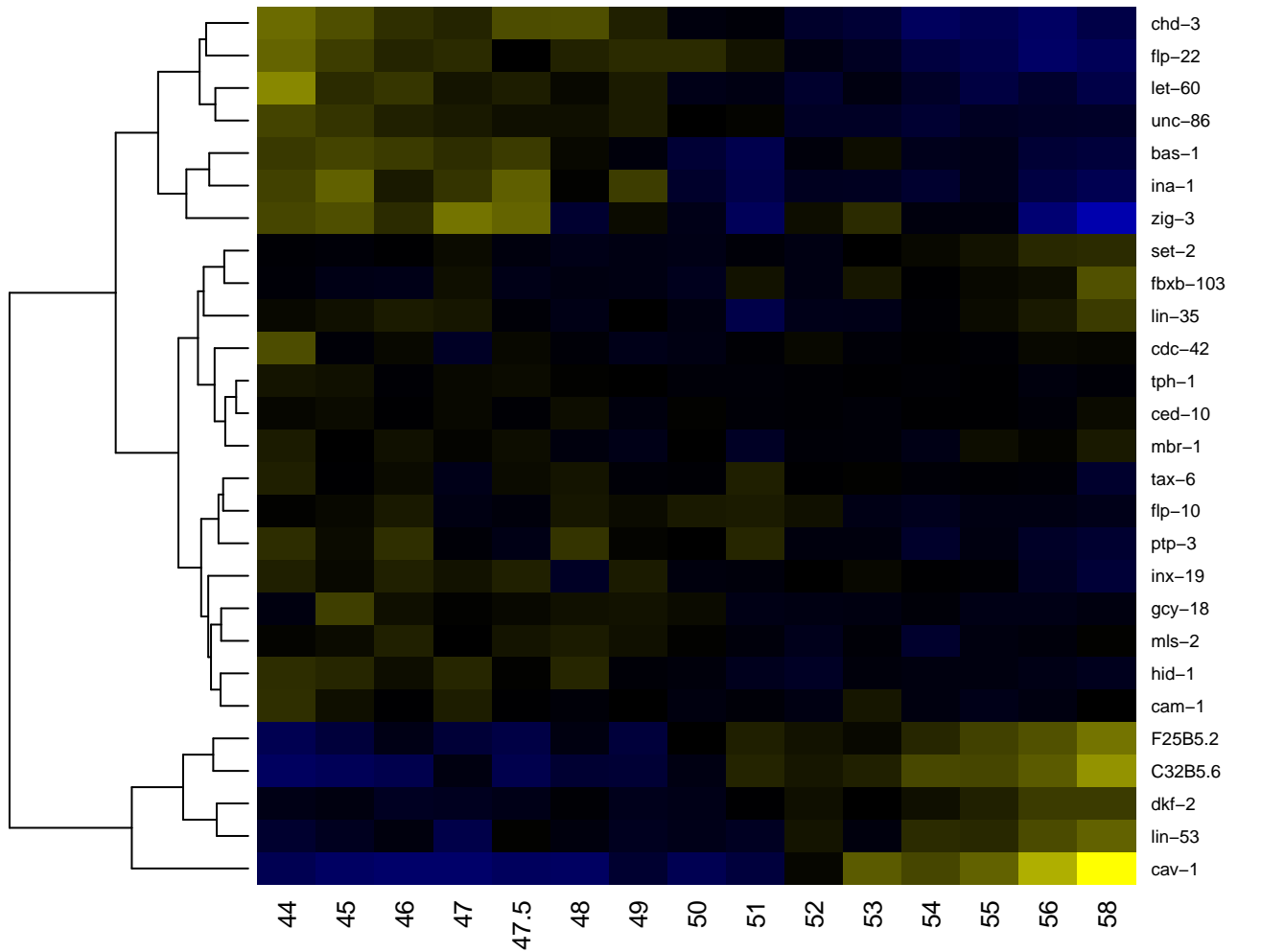
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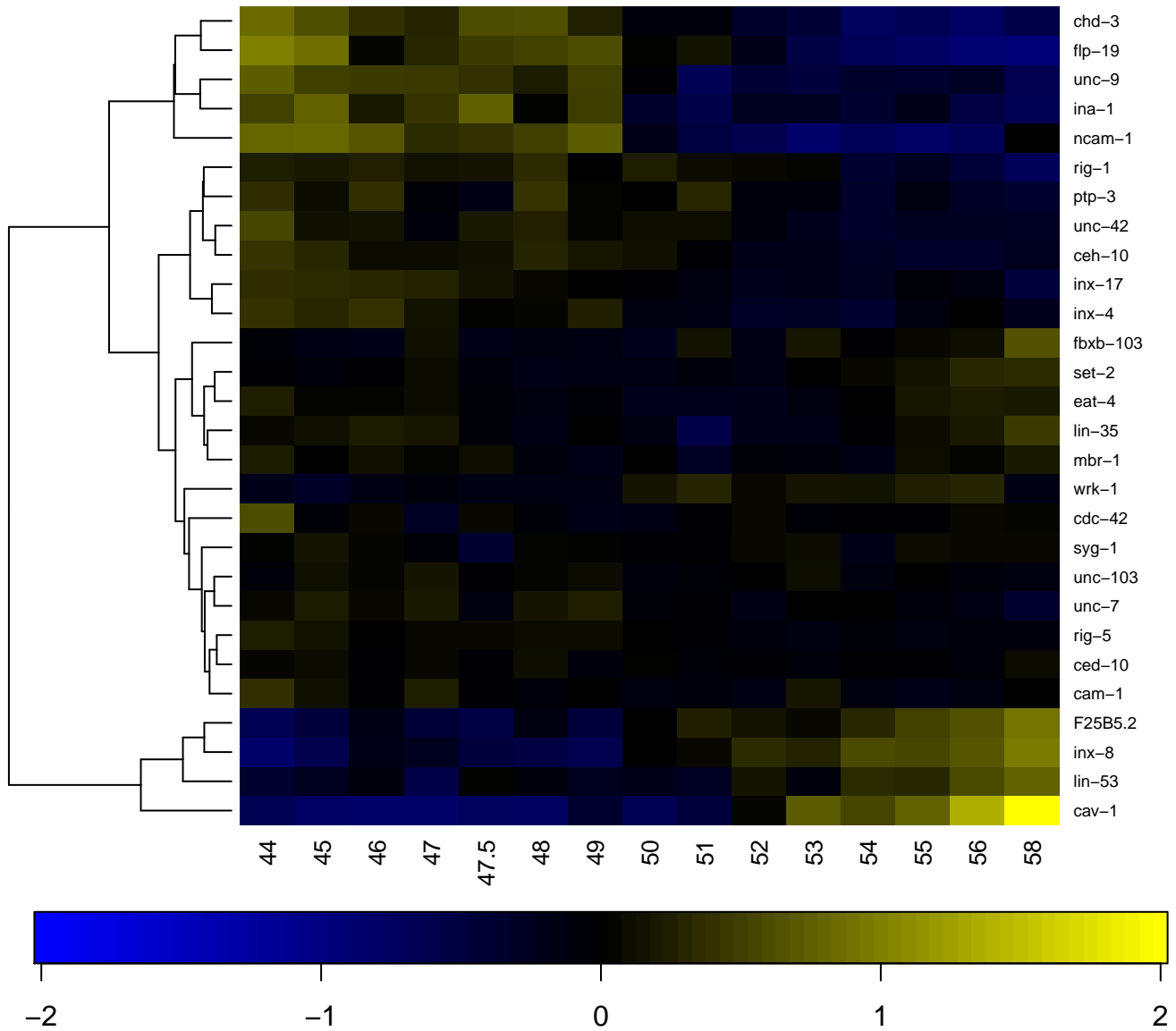
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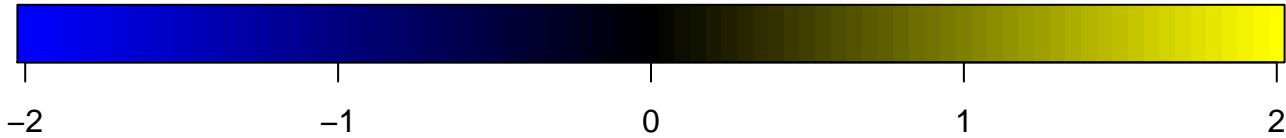
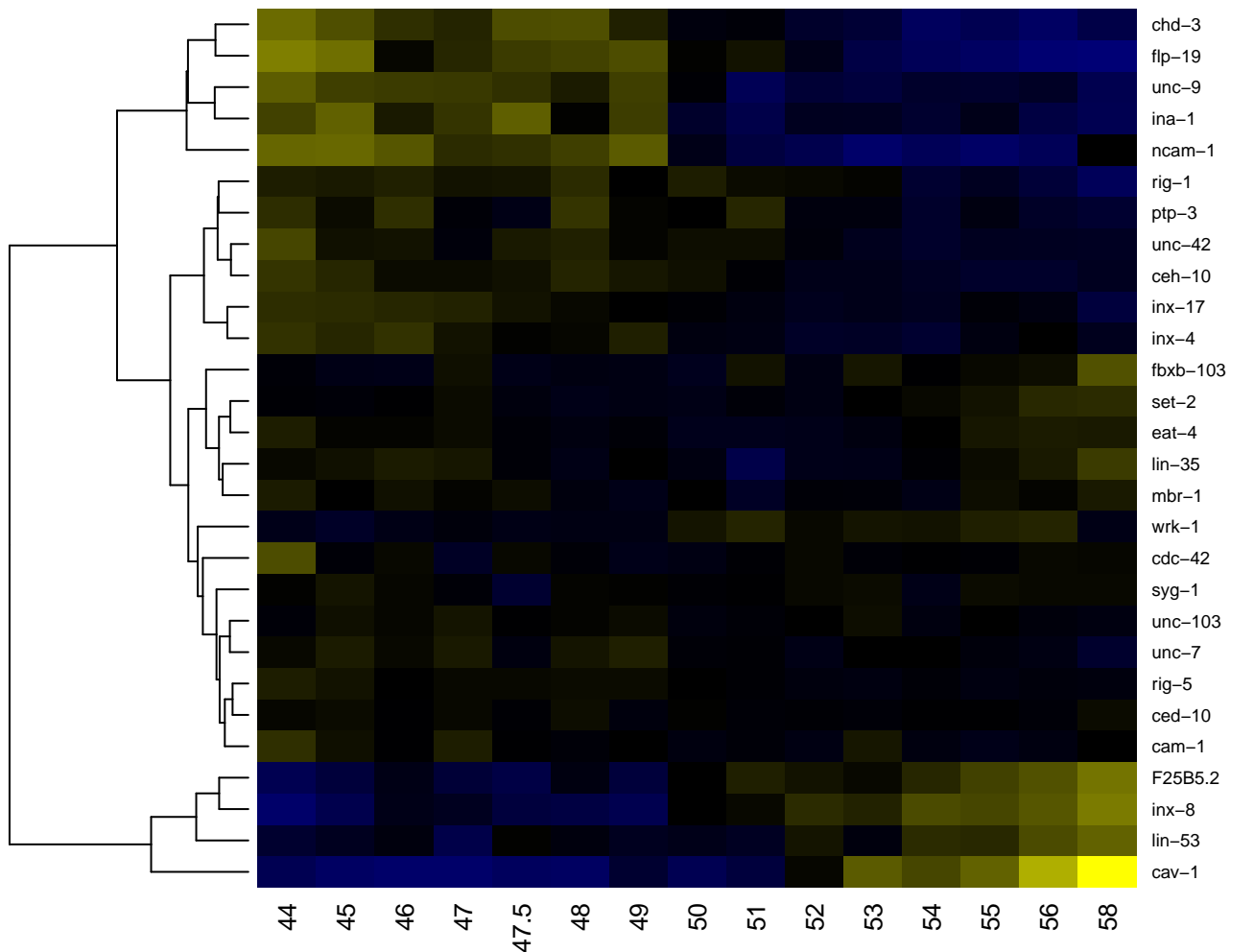
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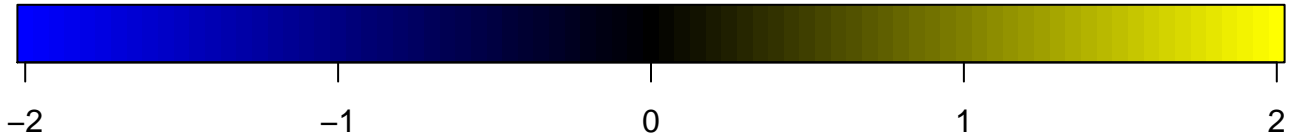
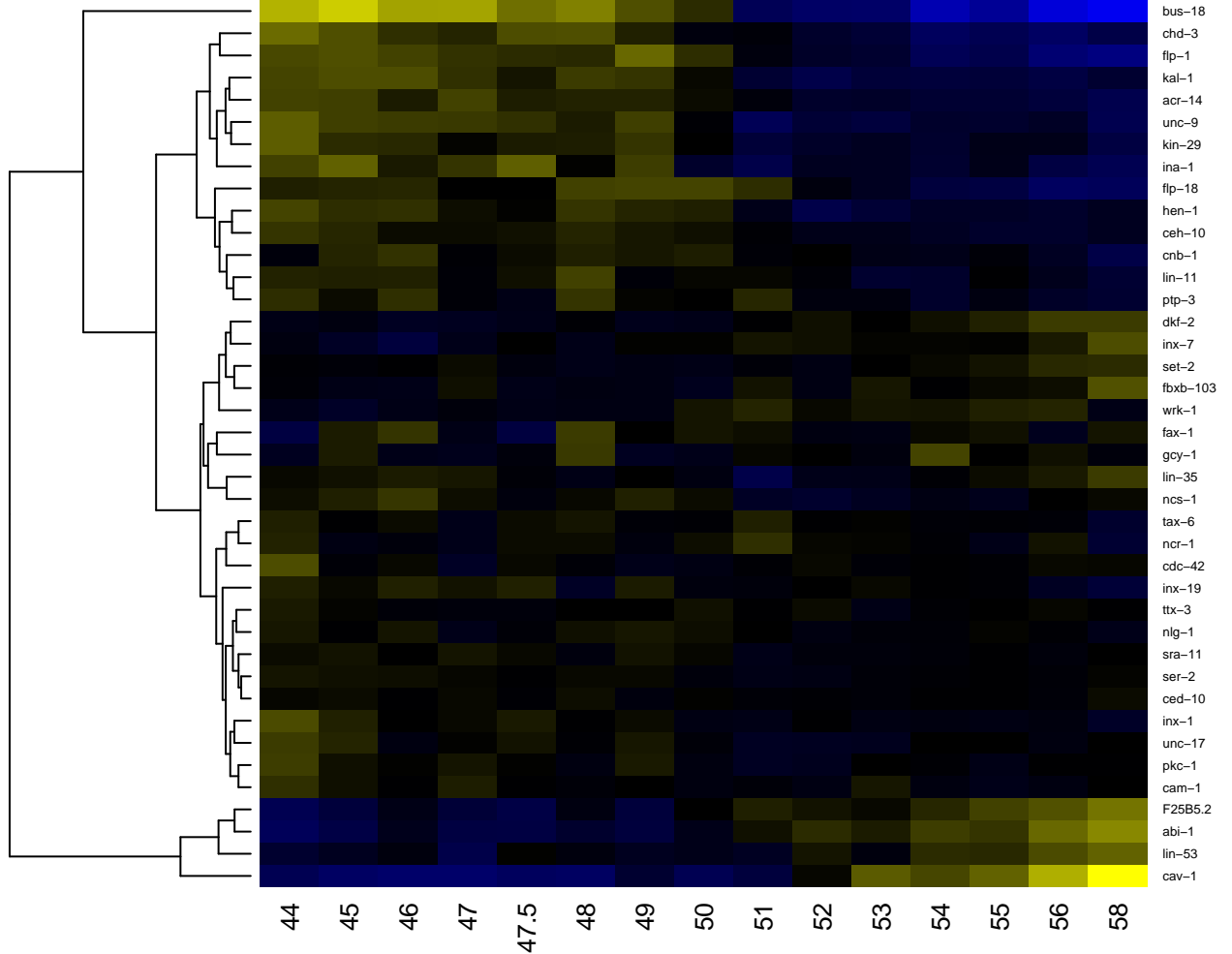
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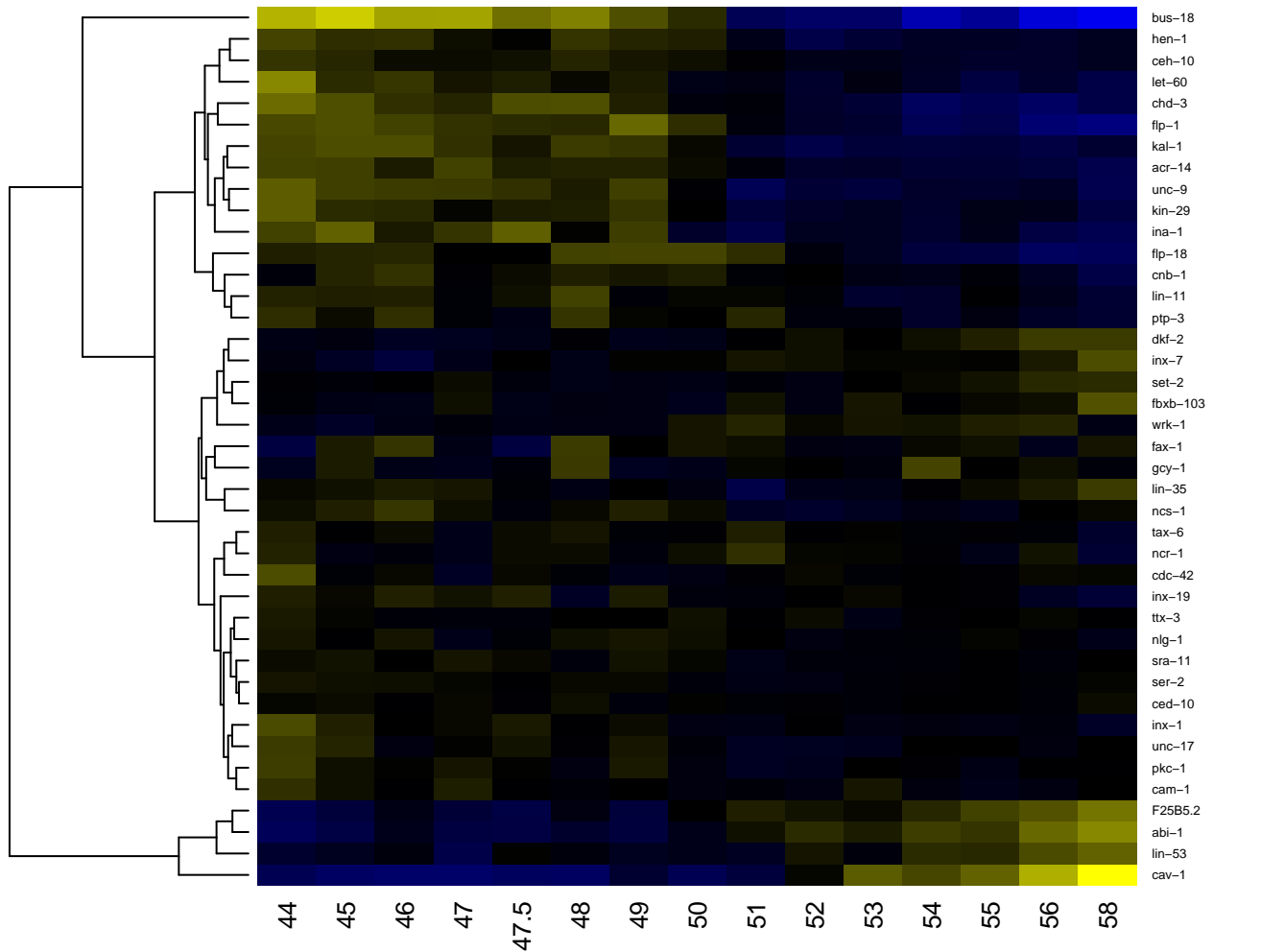
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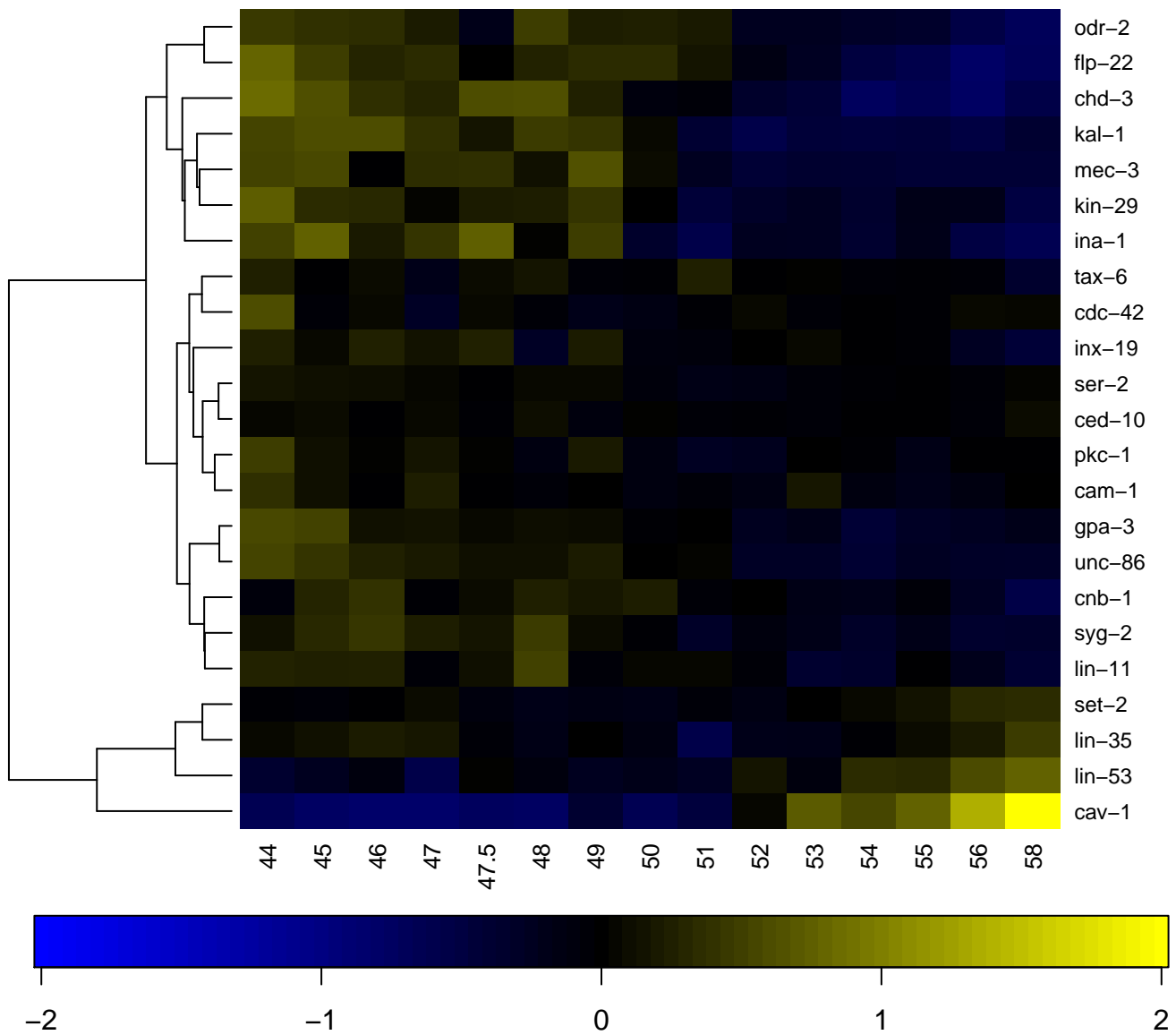
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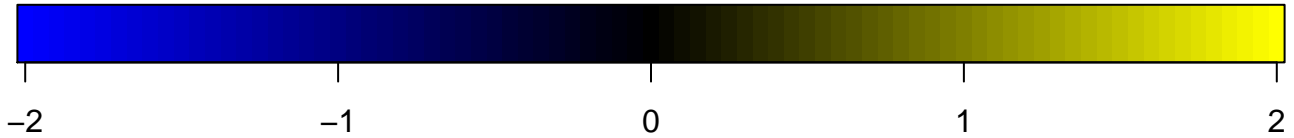
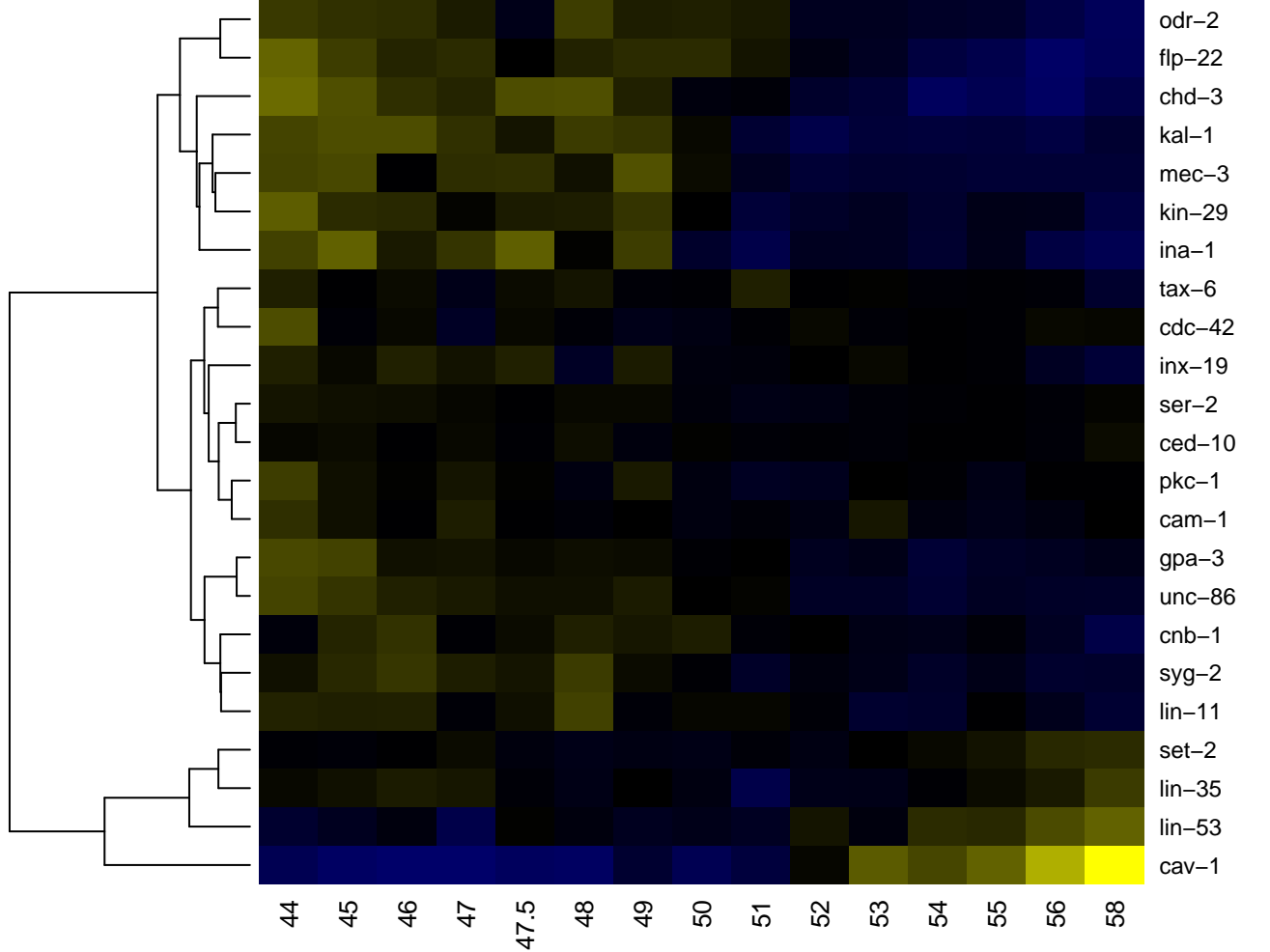
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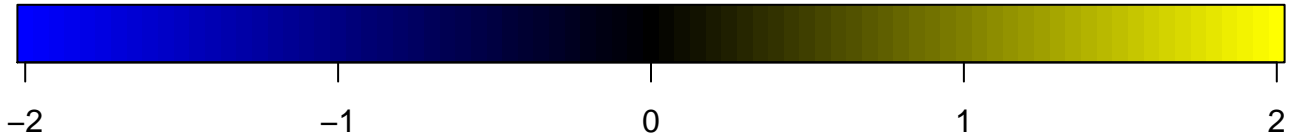
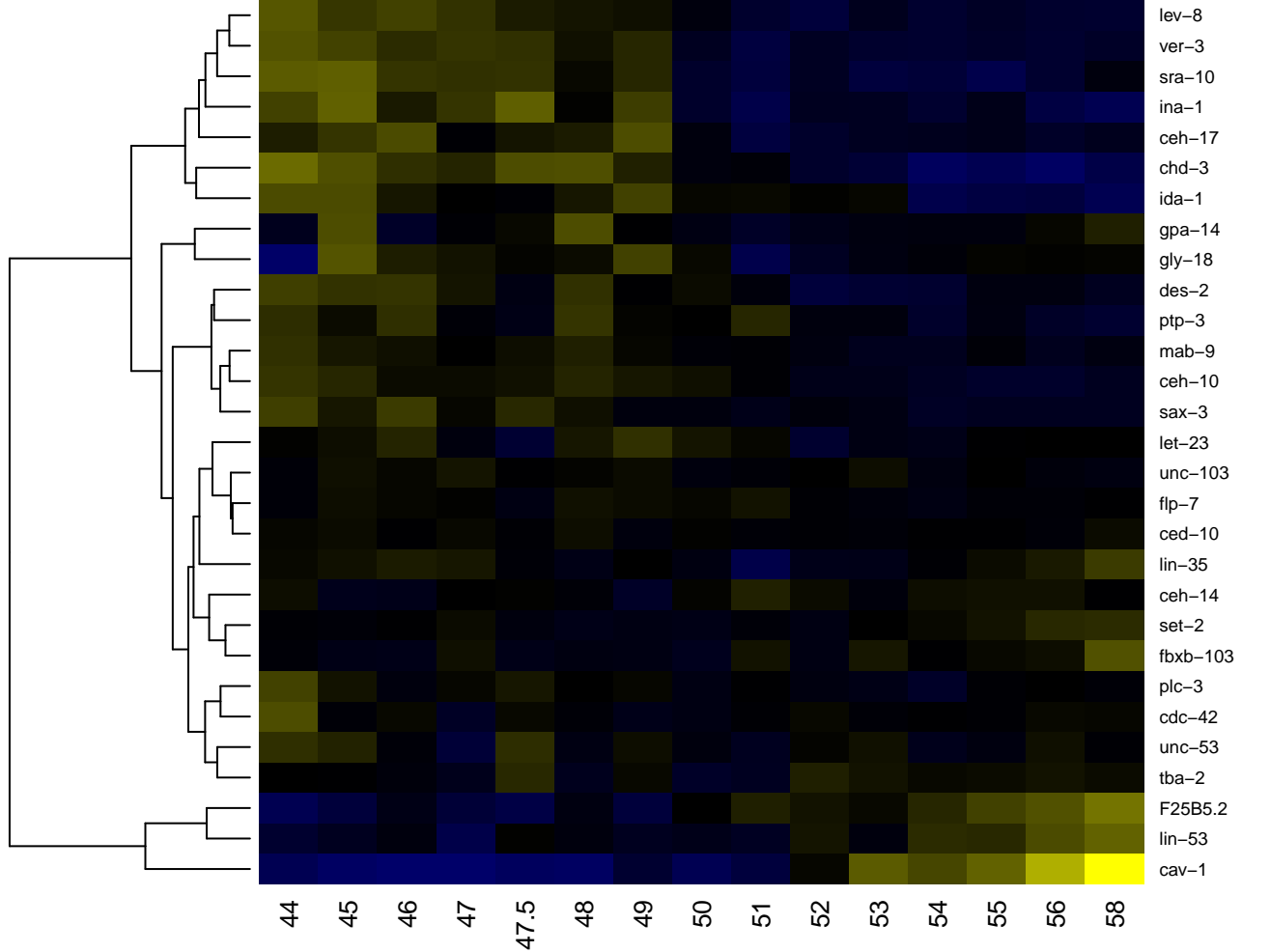
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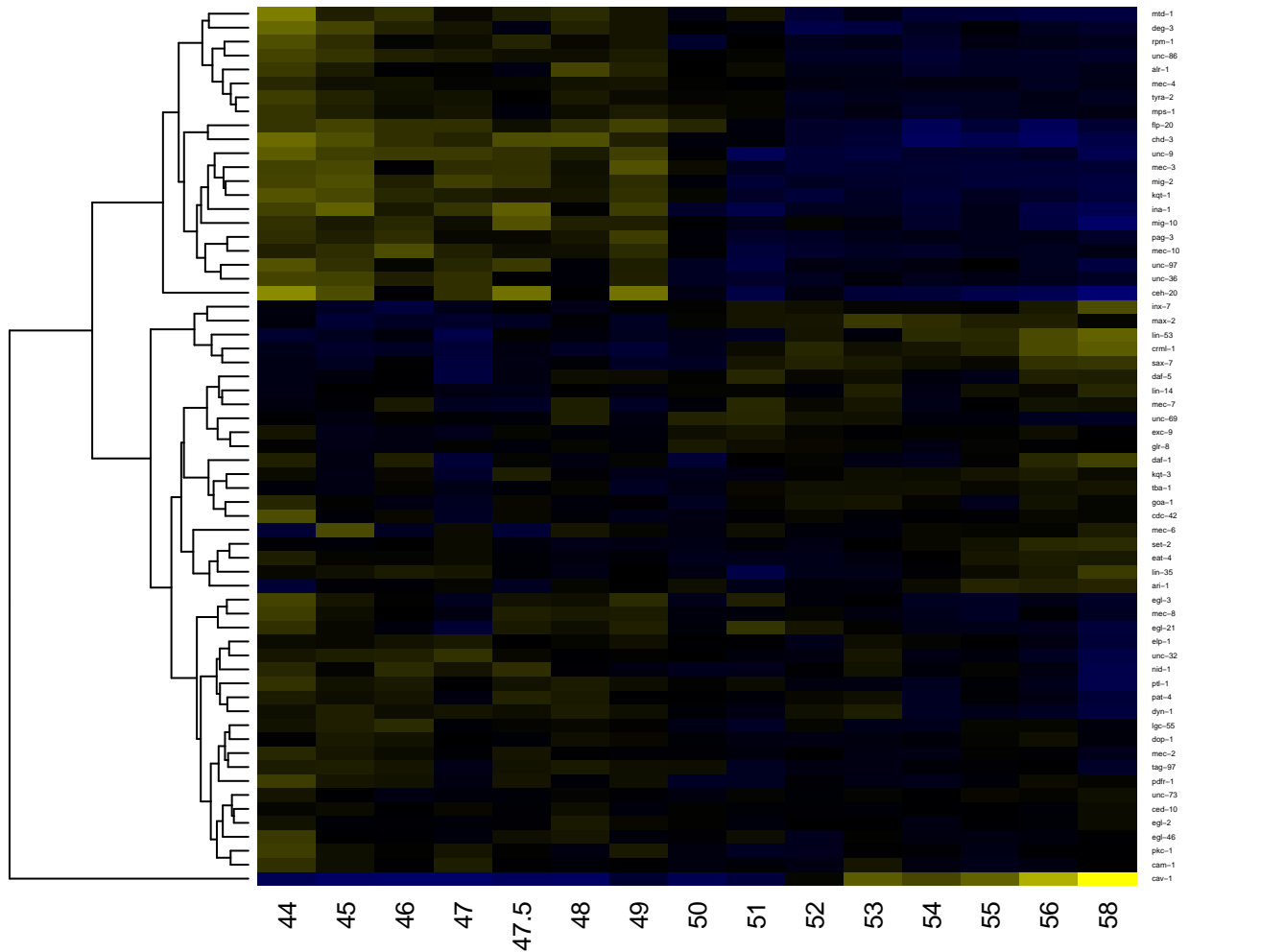
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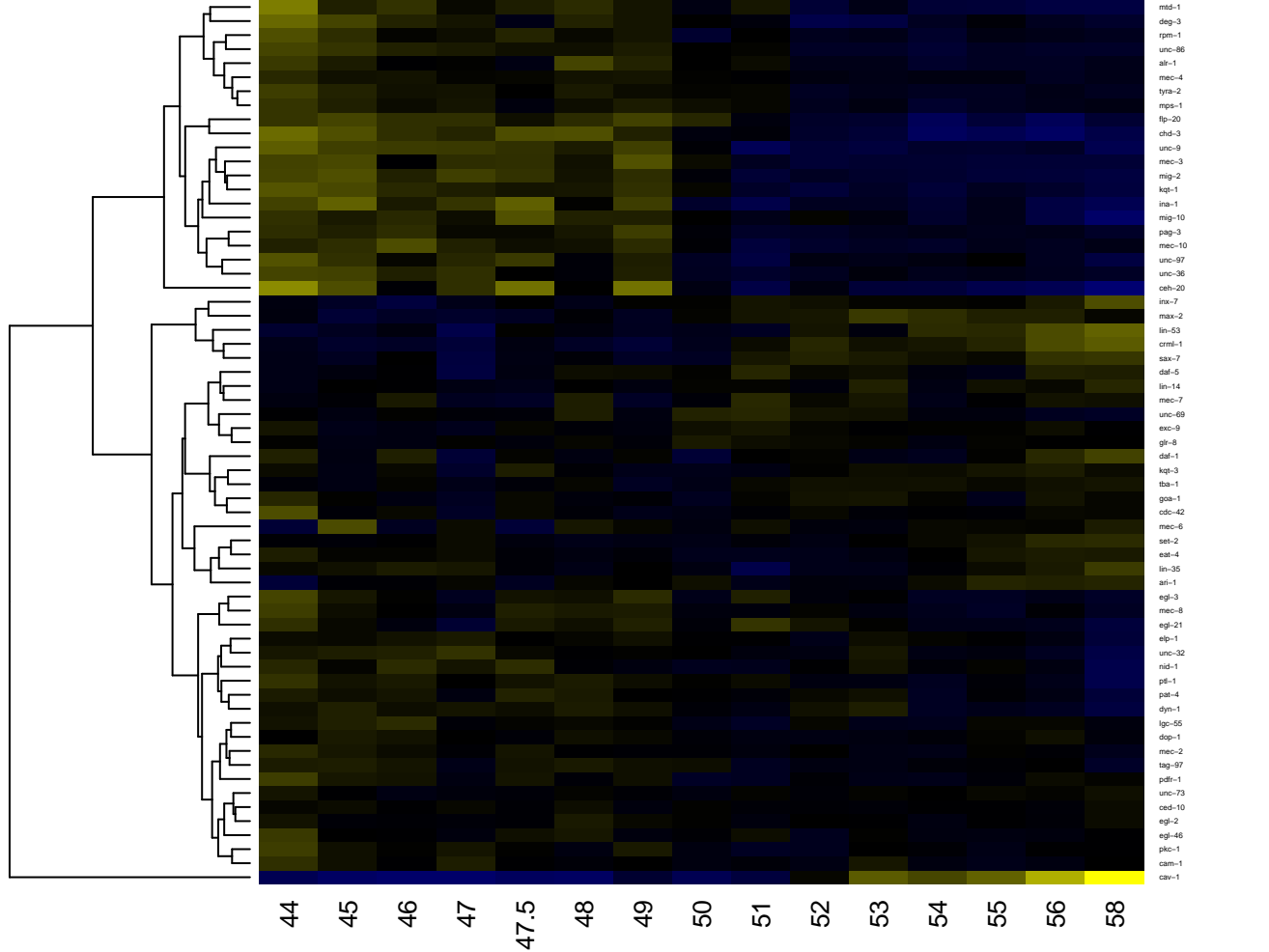
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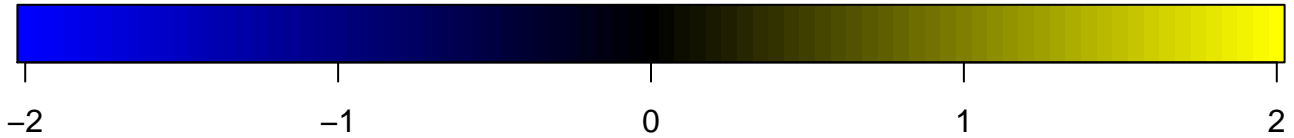
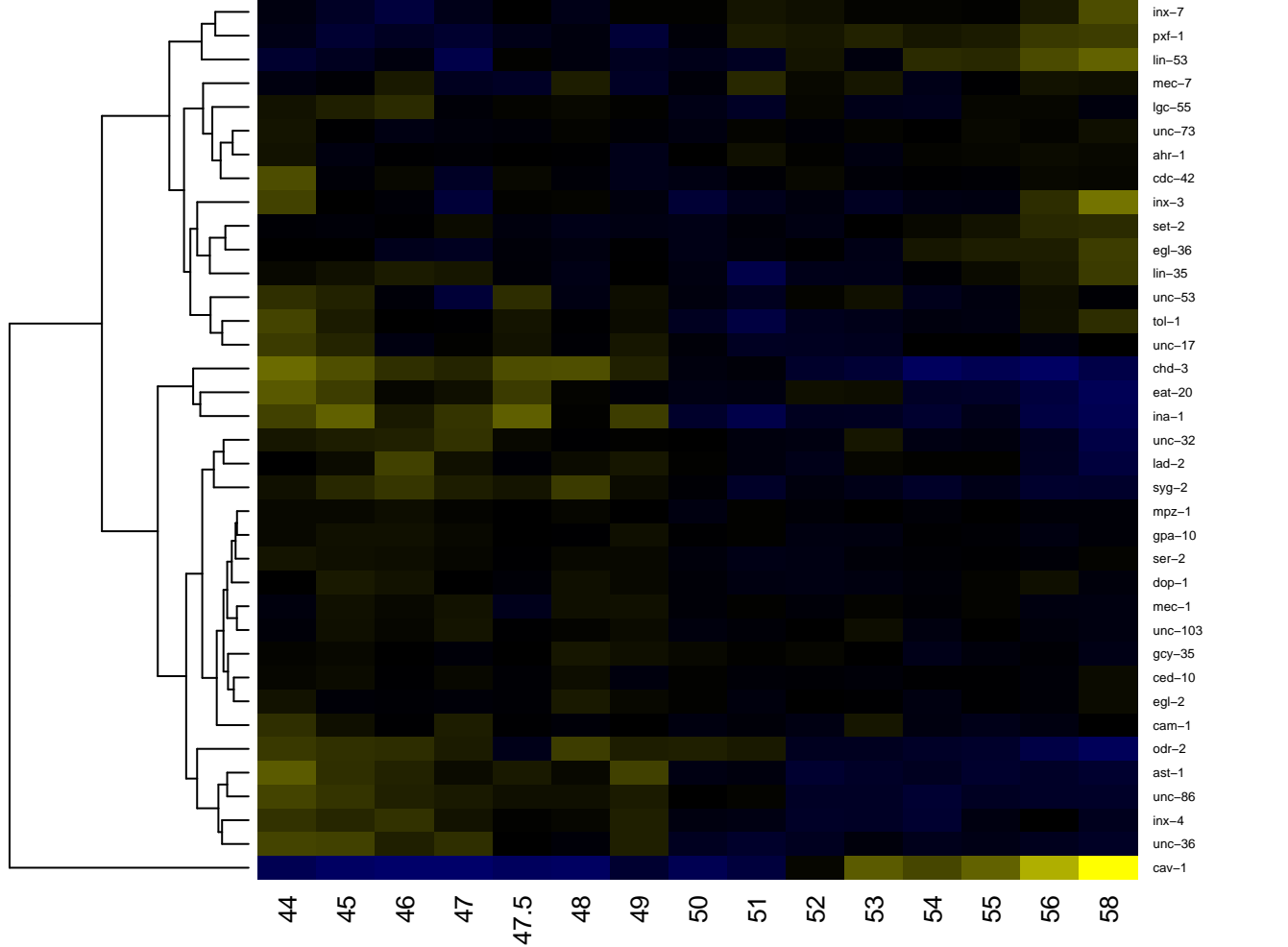
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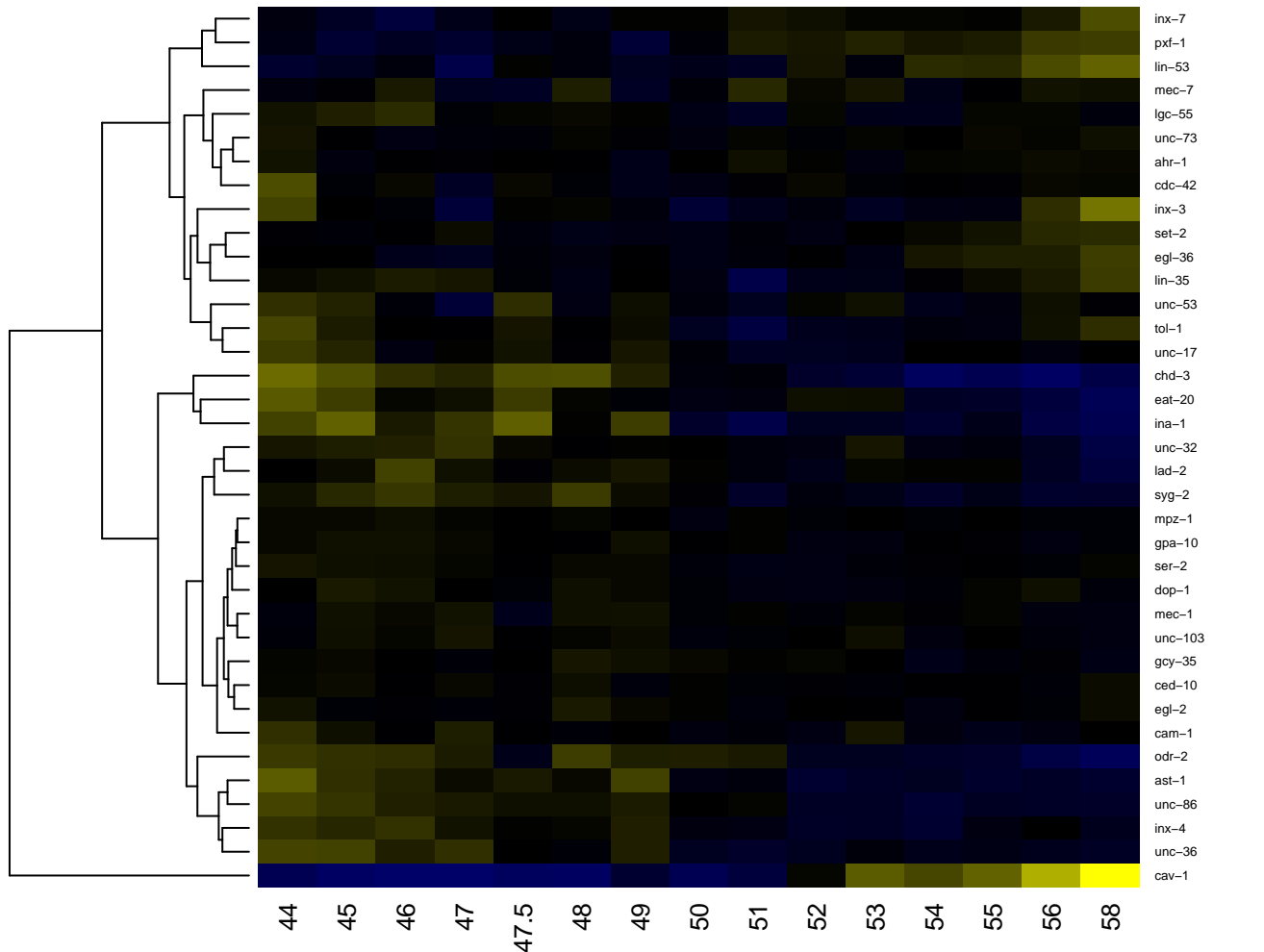
ALMR



ALNL



ALNR



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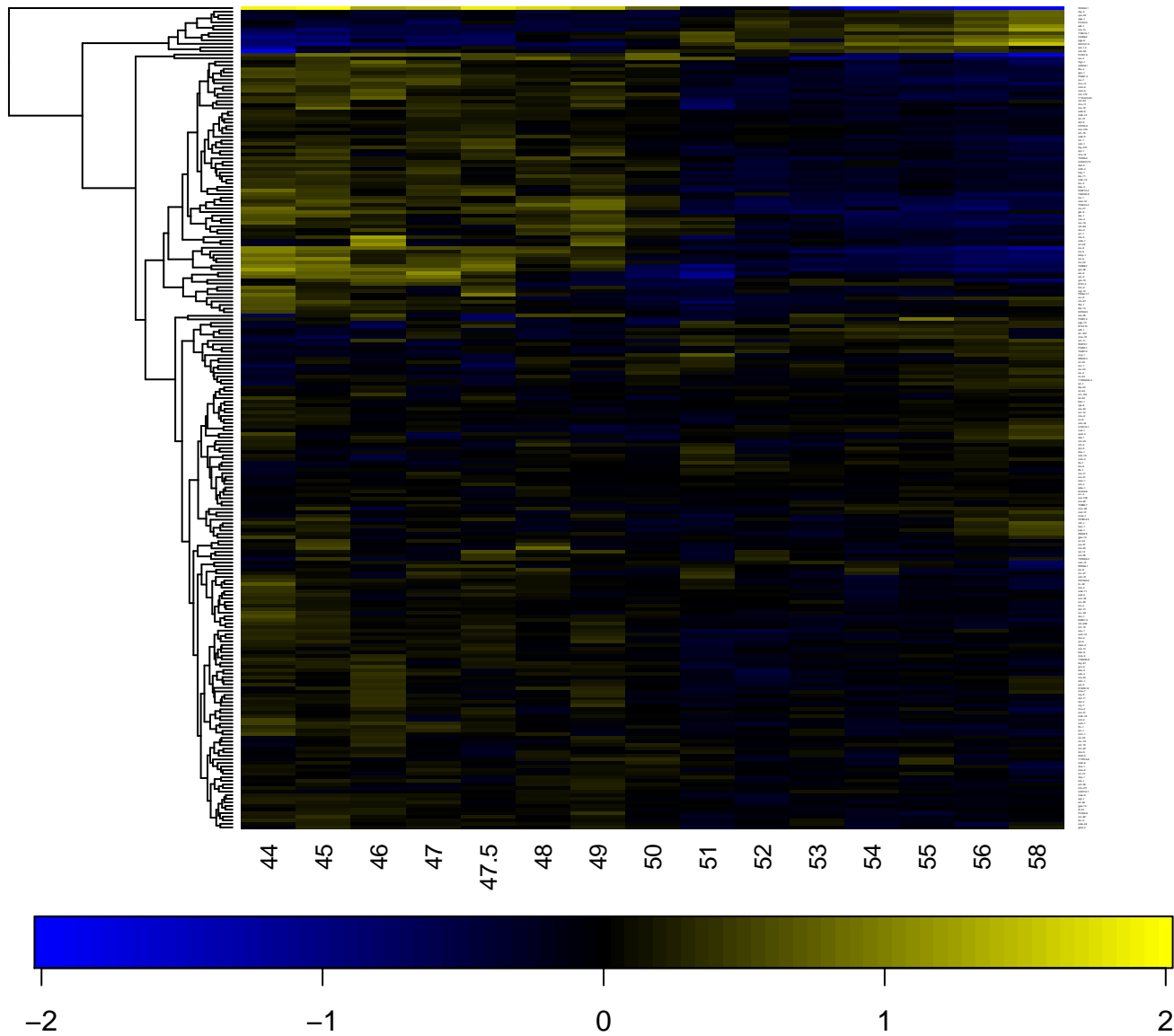
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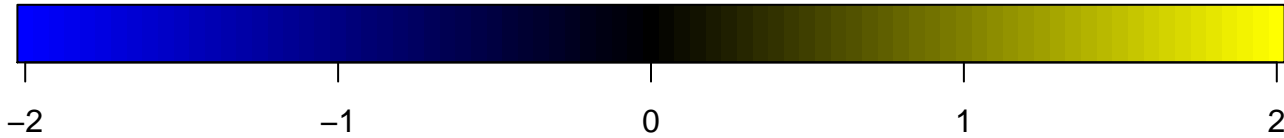
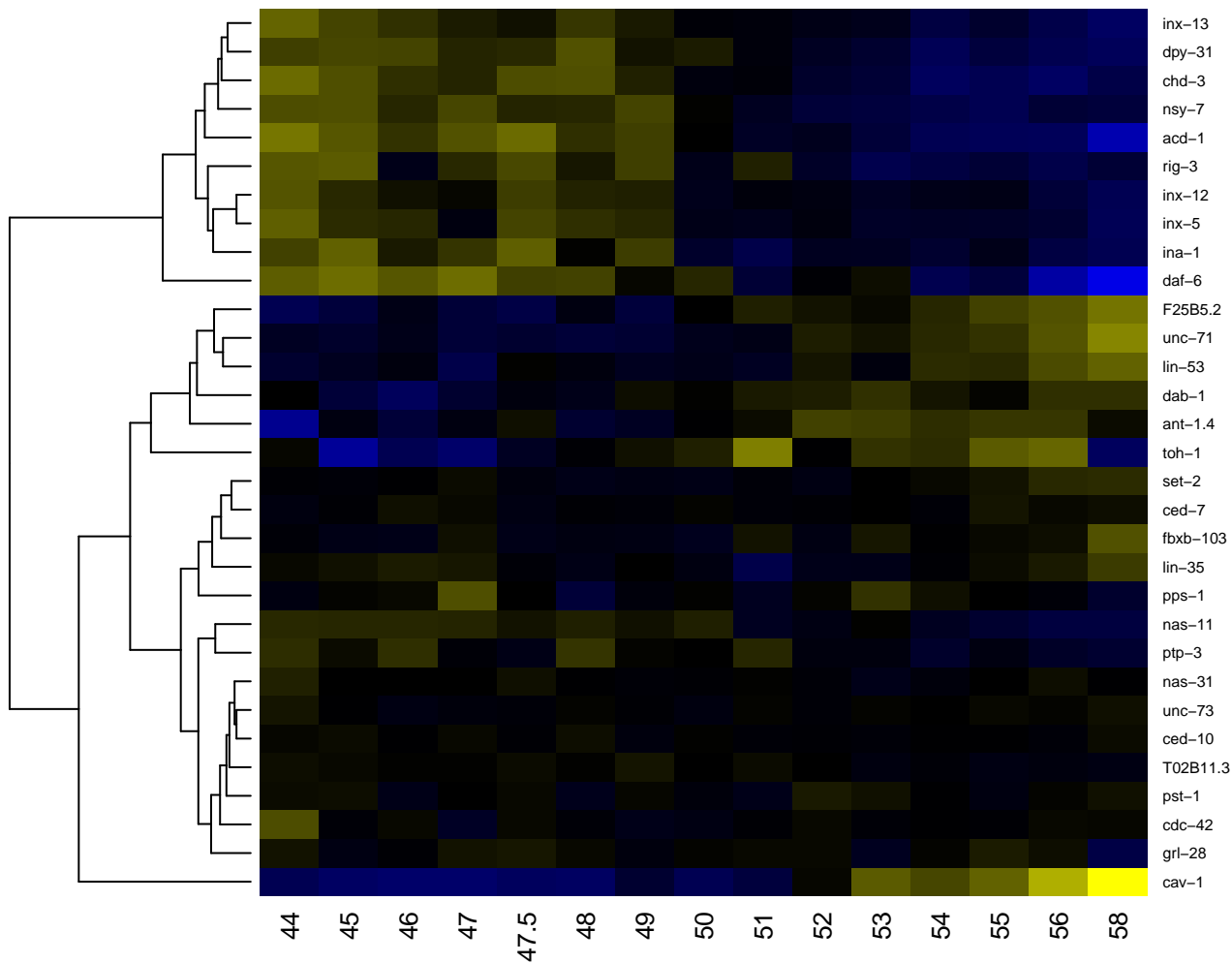
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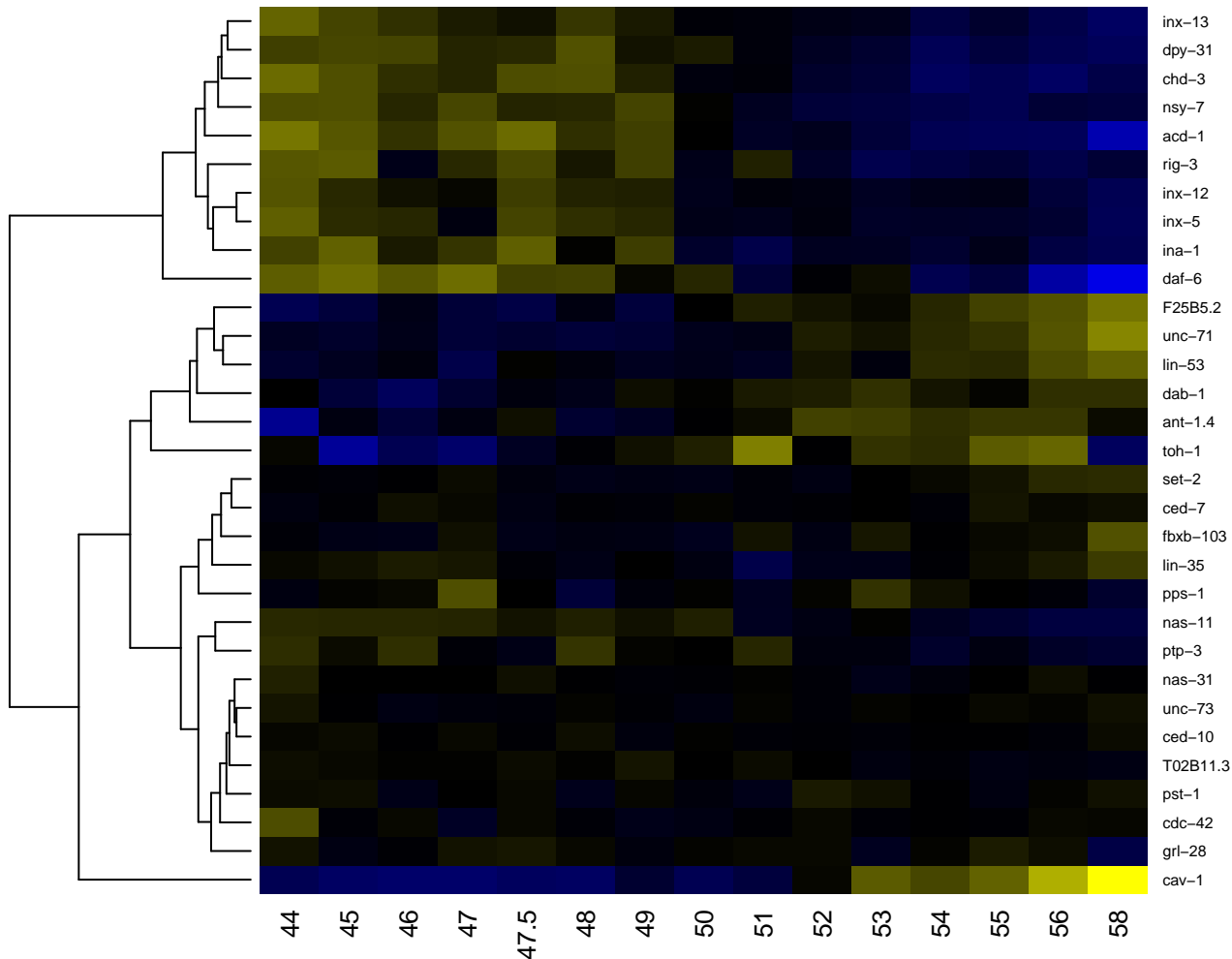
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AMshL



AMshR



-2

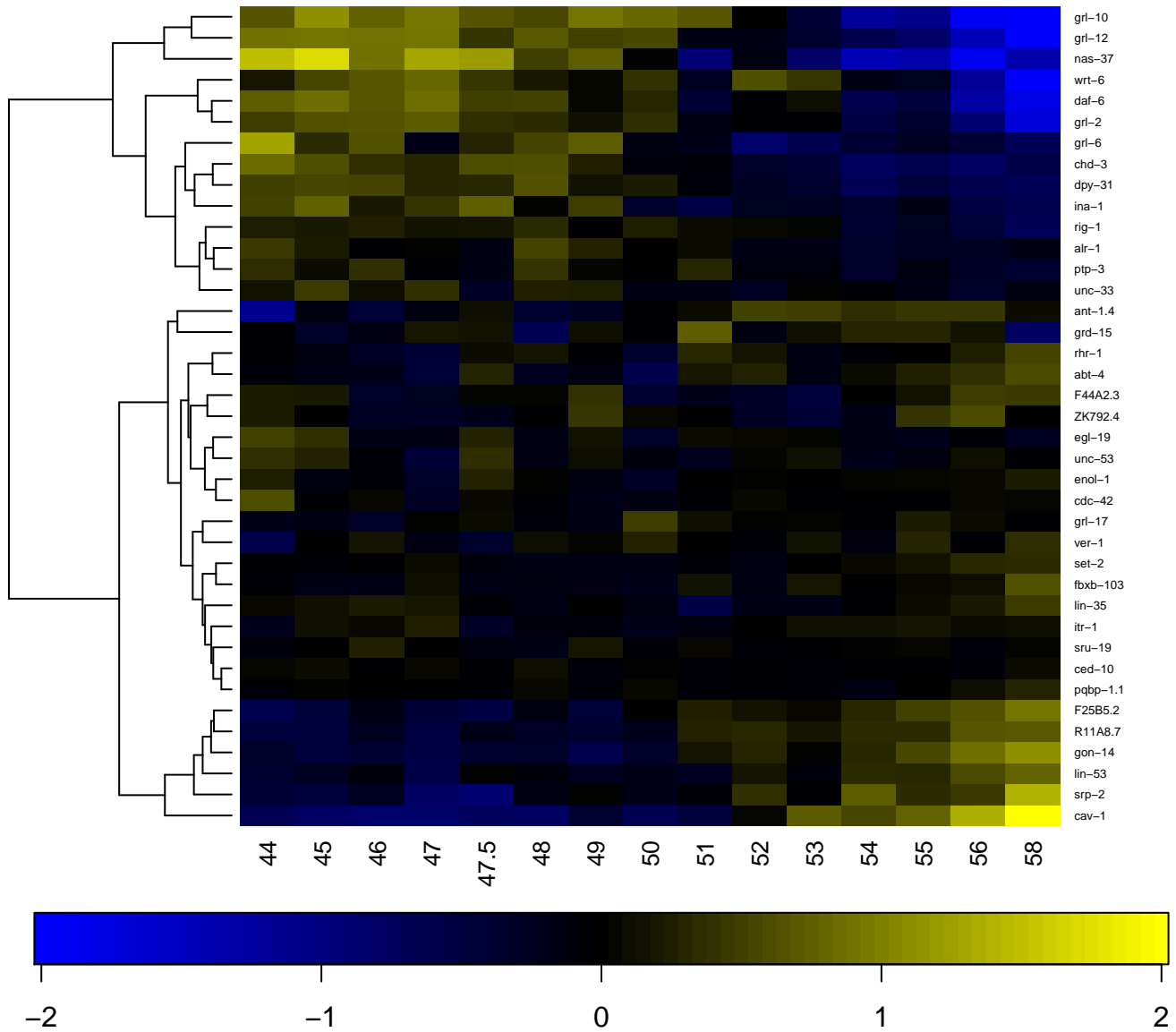
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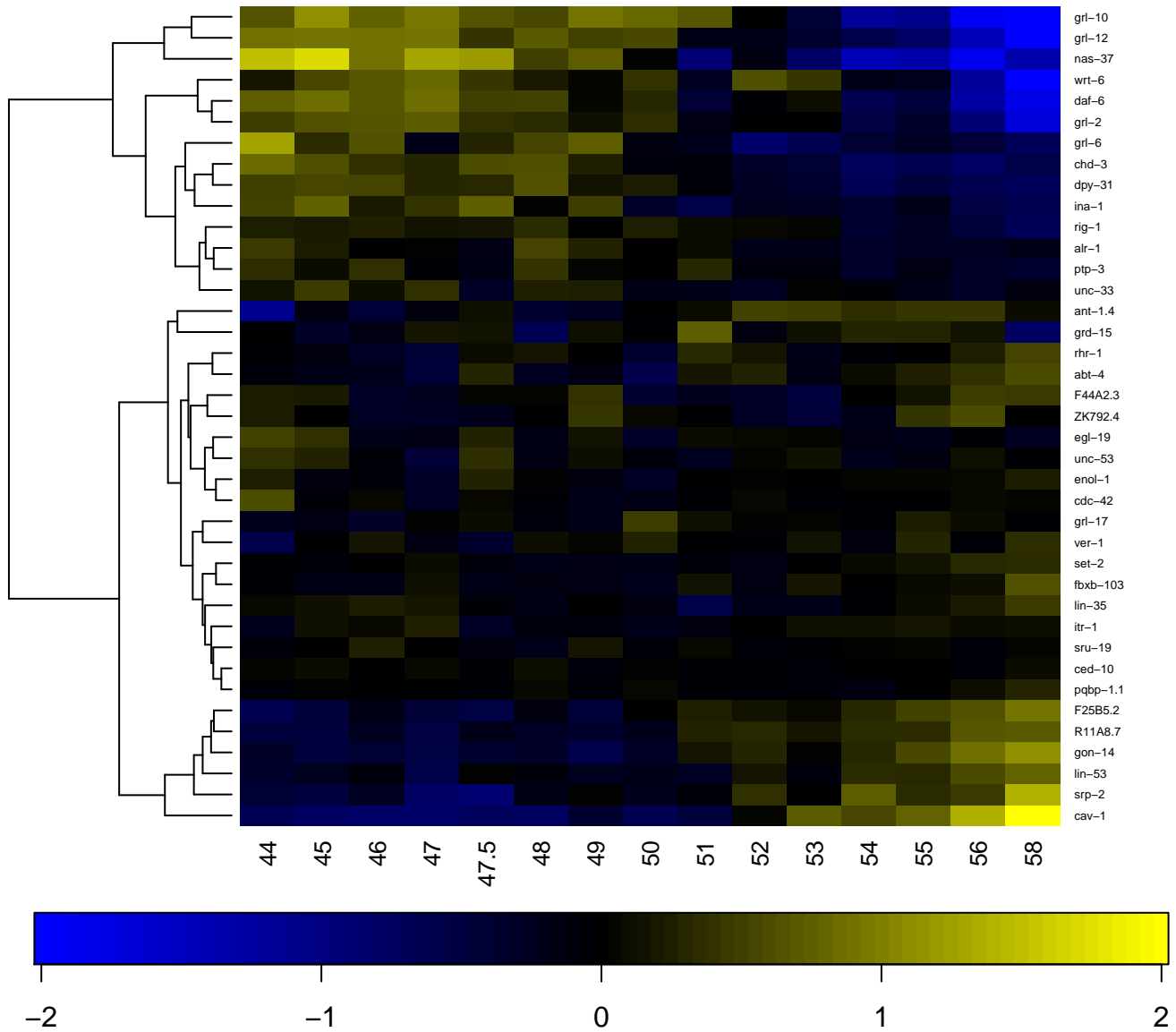
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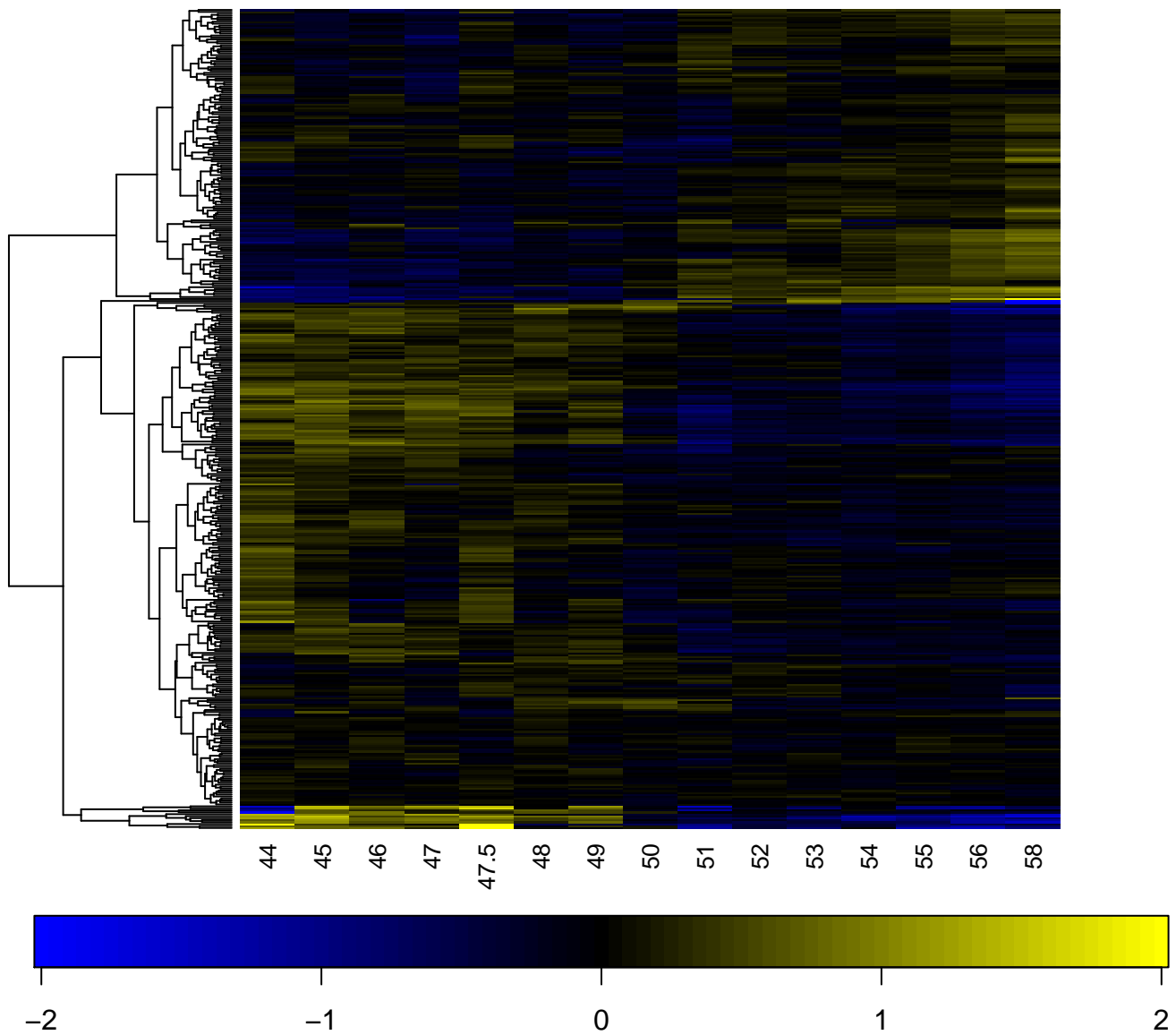
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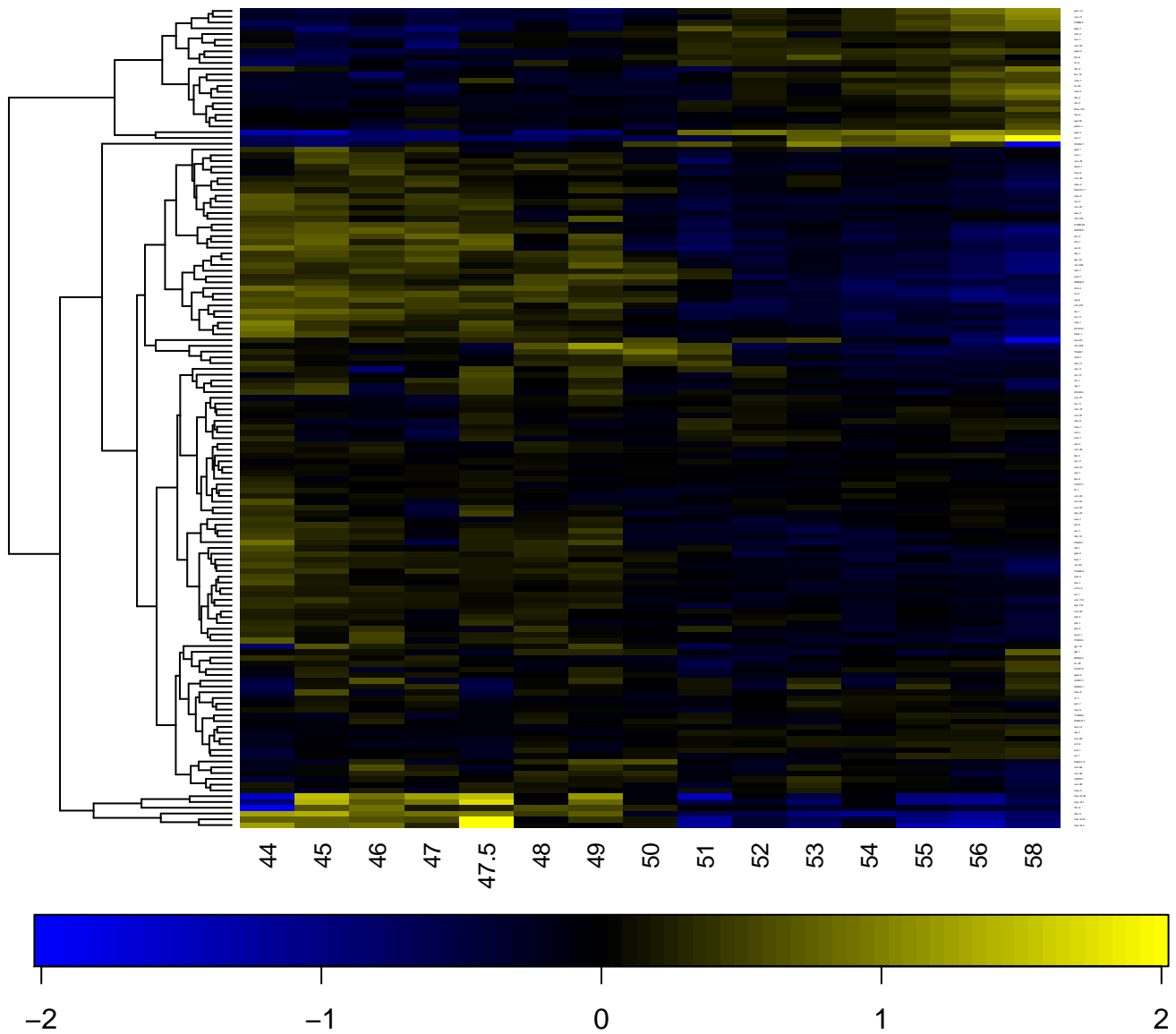
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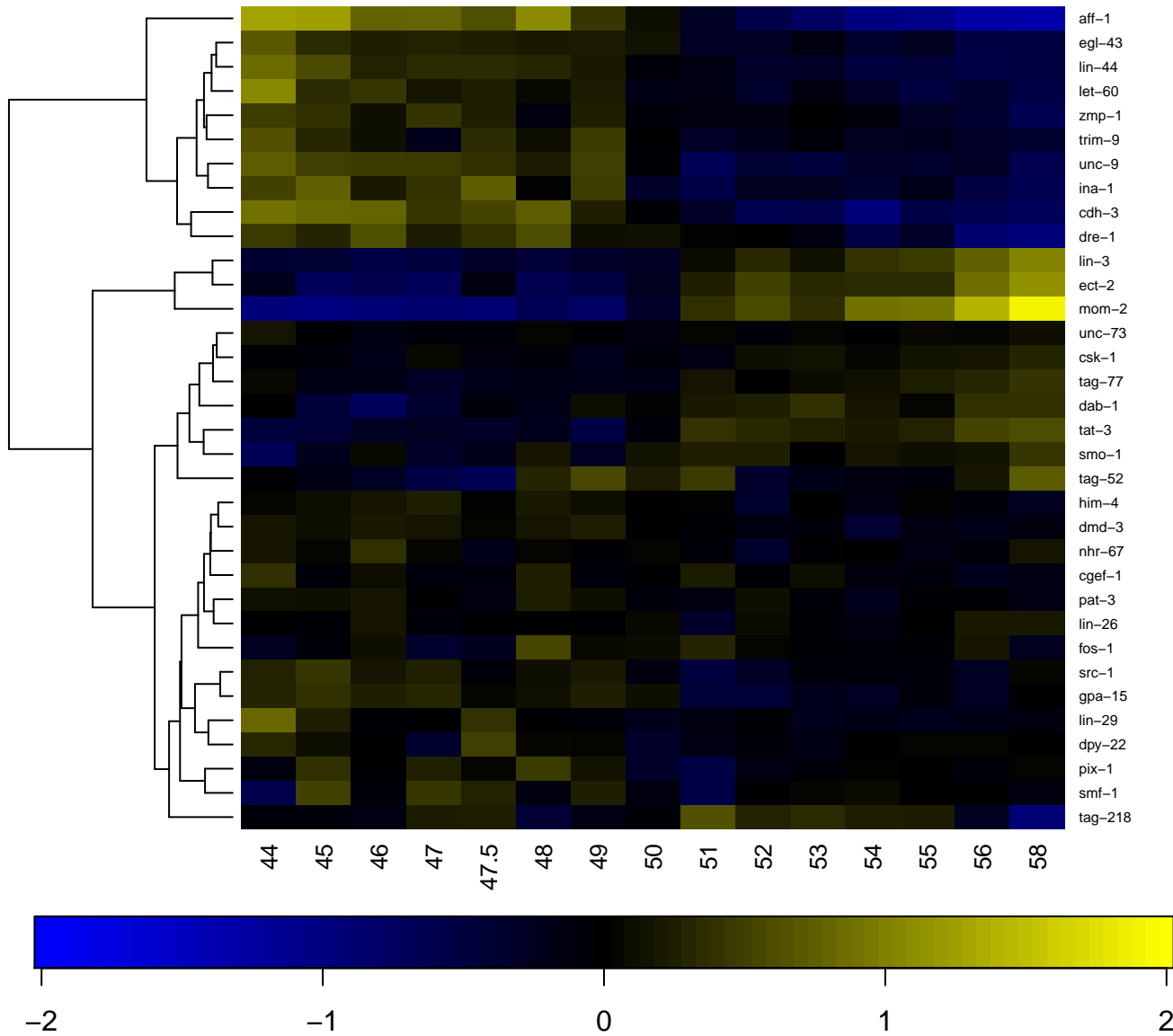
anal depressor muscle



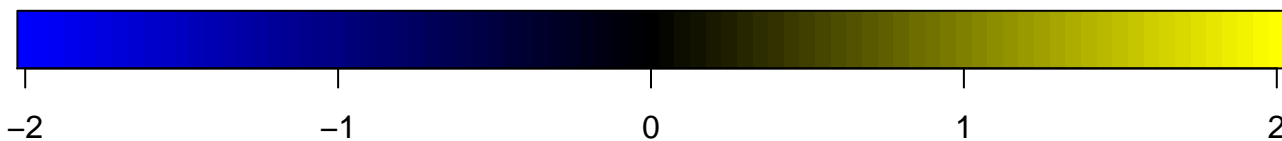
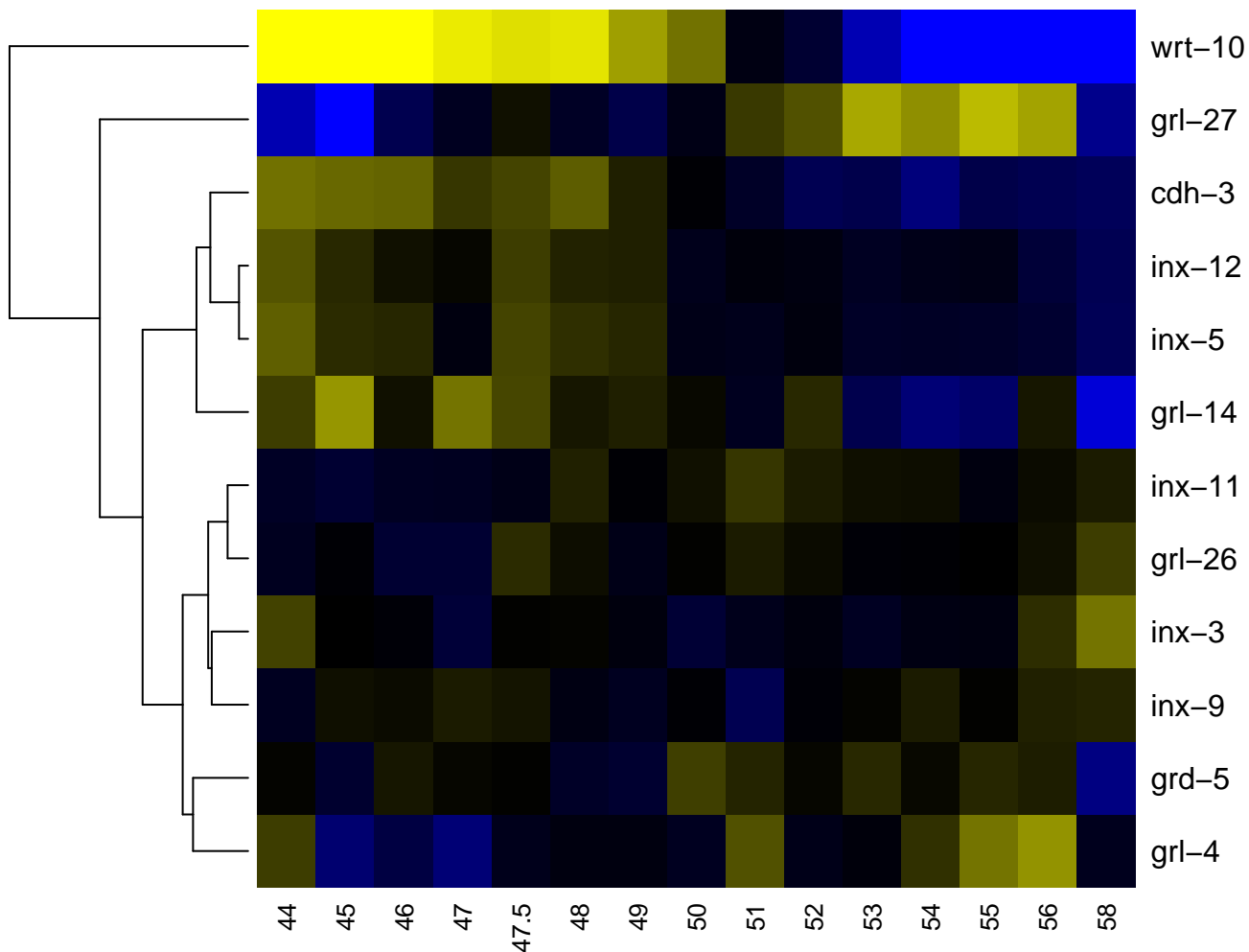
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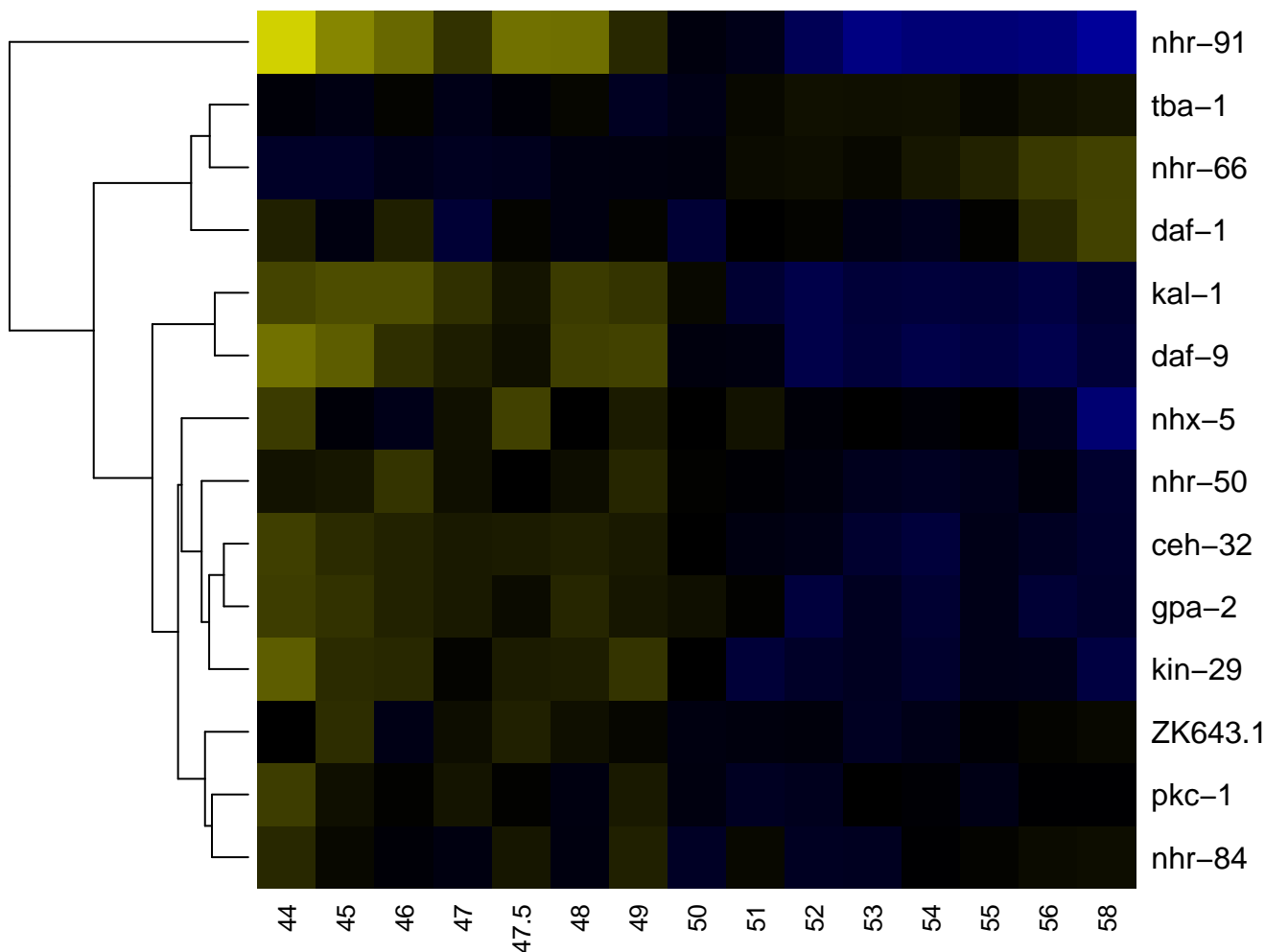
Anchor cell



anterior arcade cell



anterior ganglion



-2

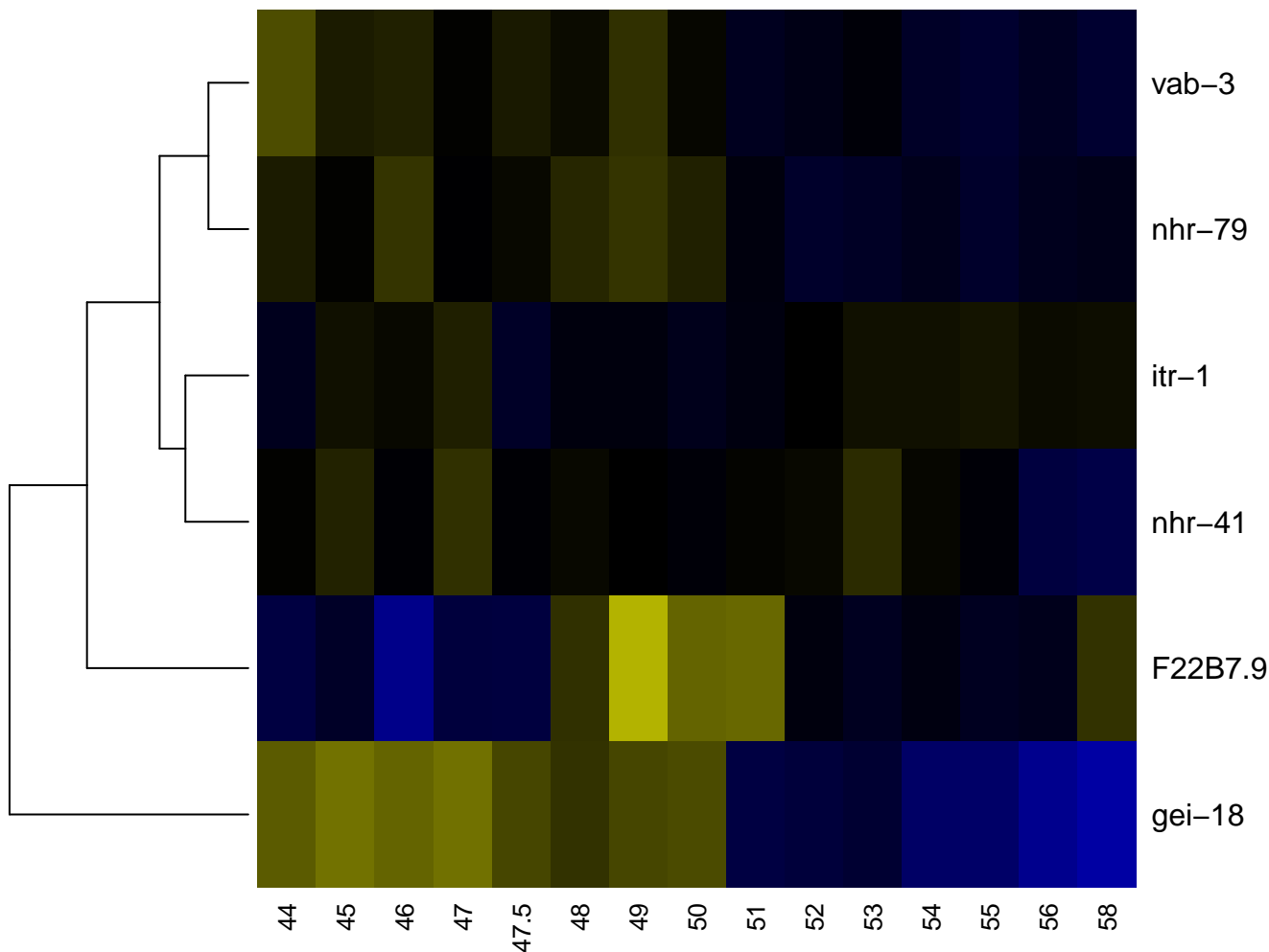
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anterior hypodermis



-2

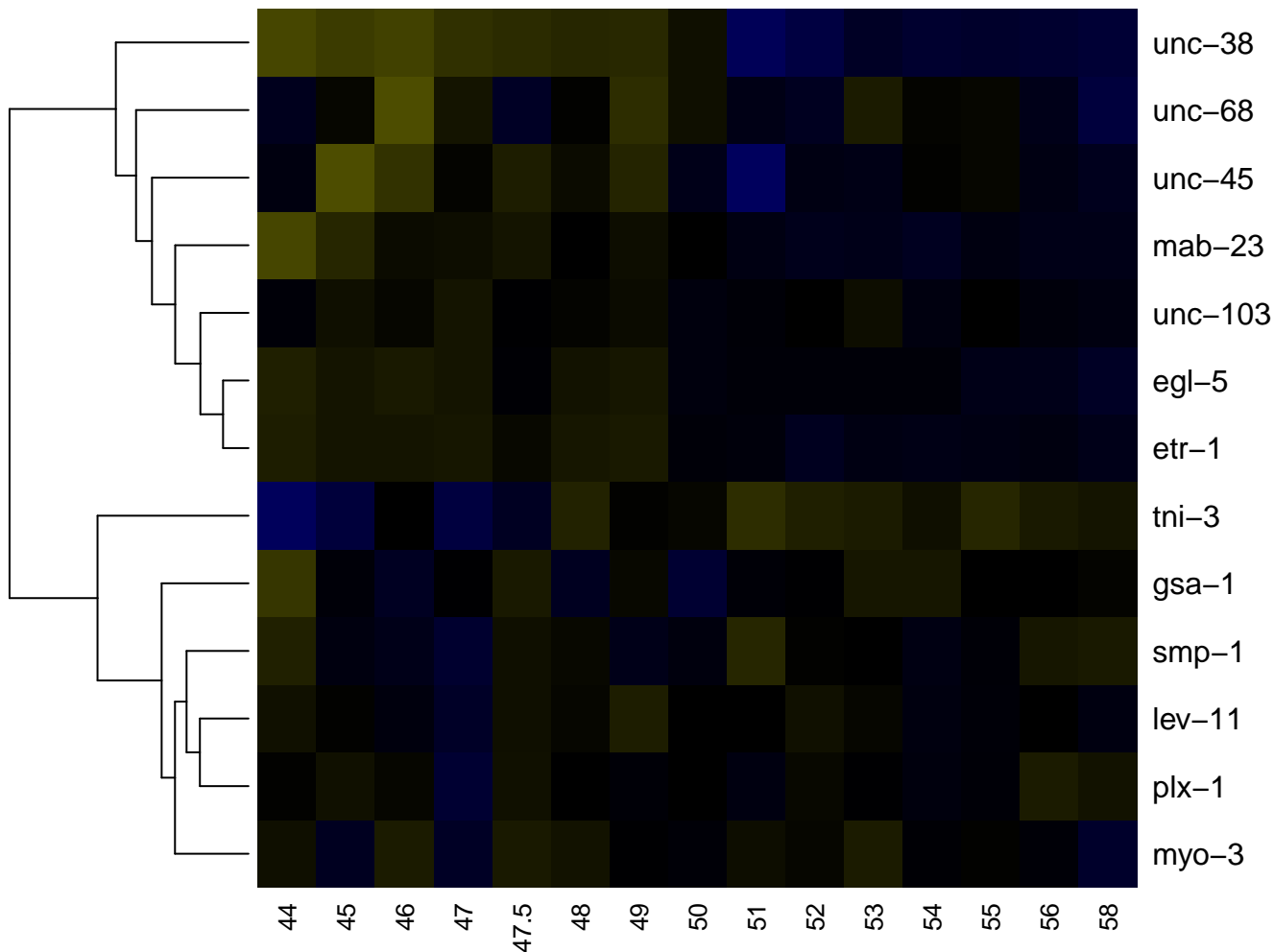
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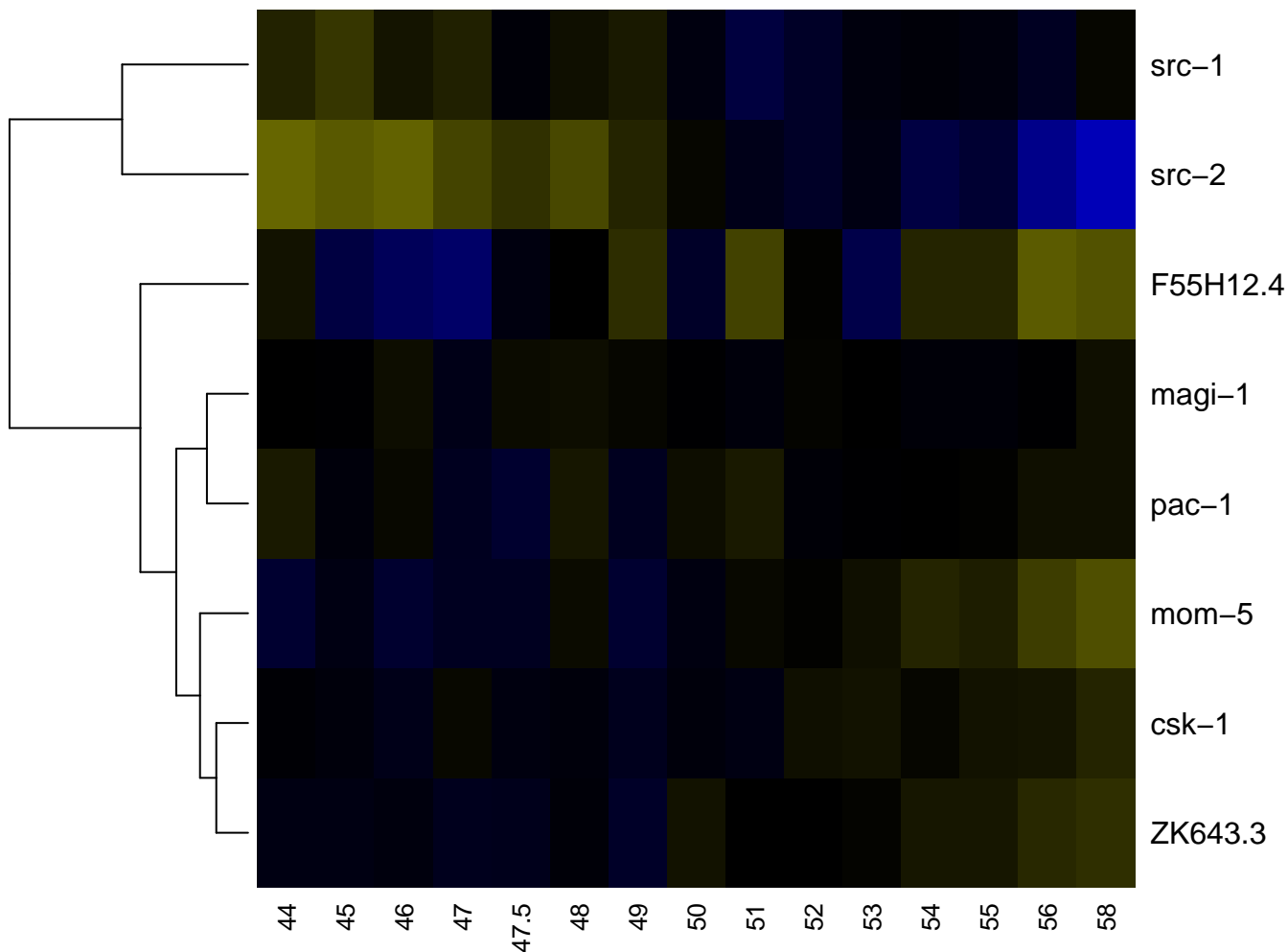
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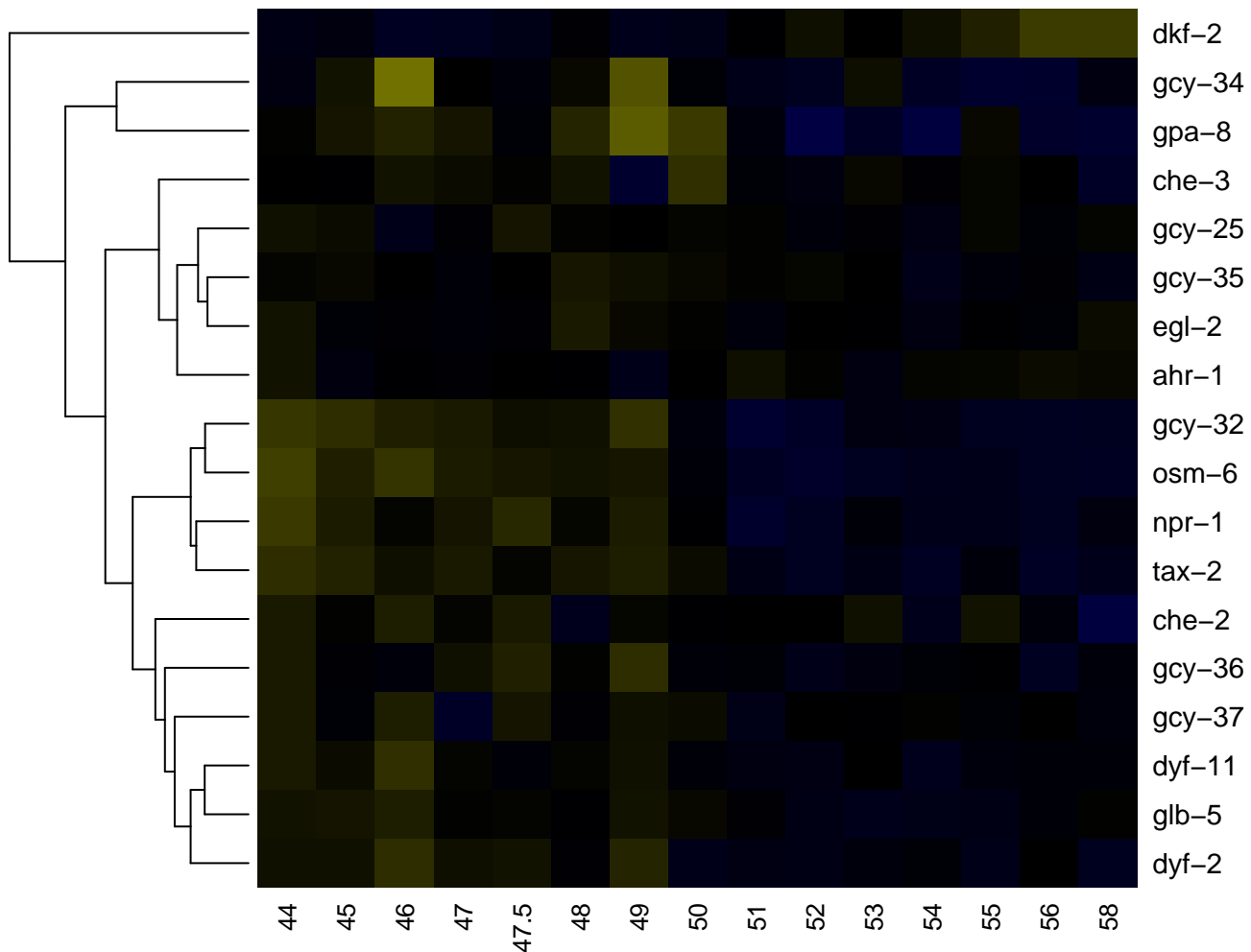
anterior oblique muscle



anus



AQR



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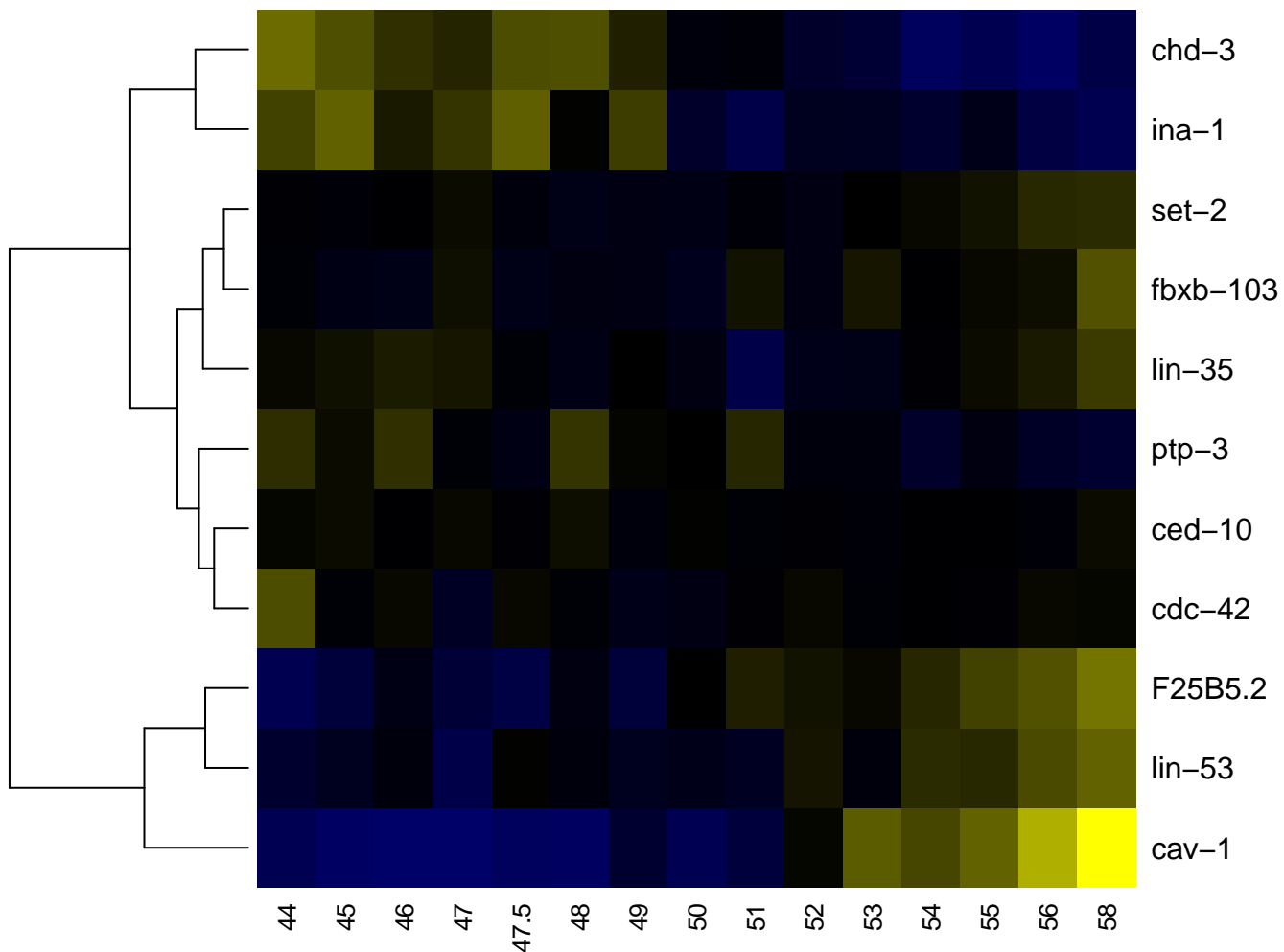
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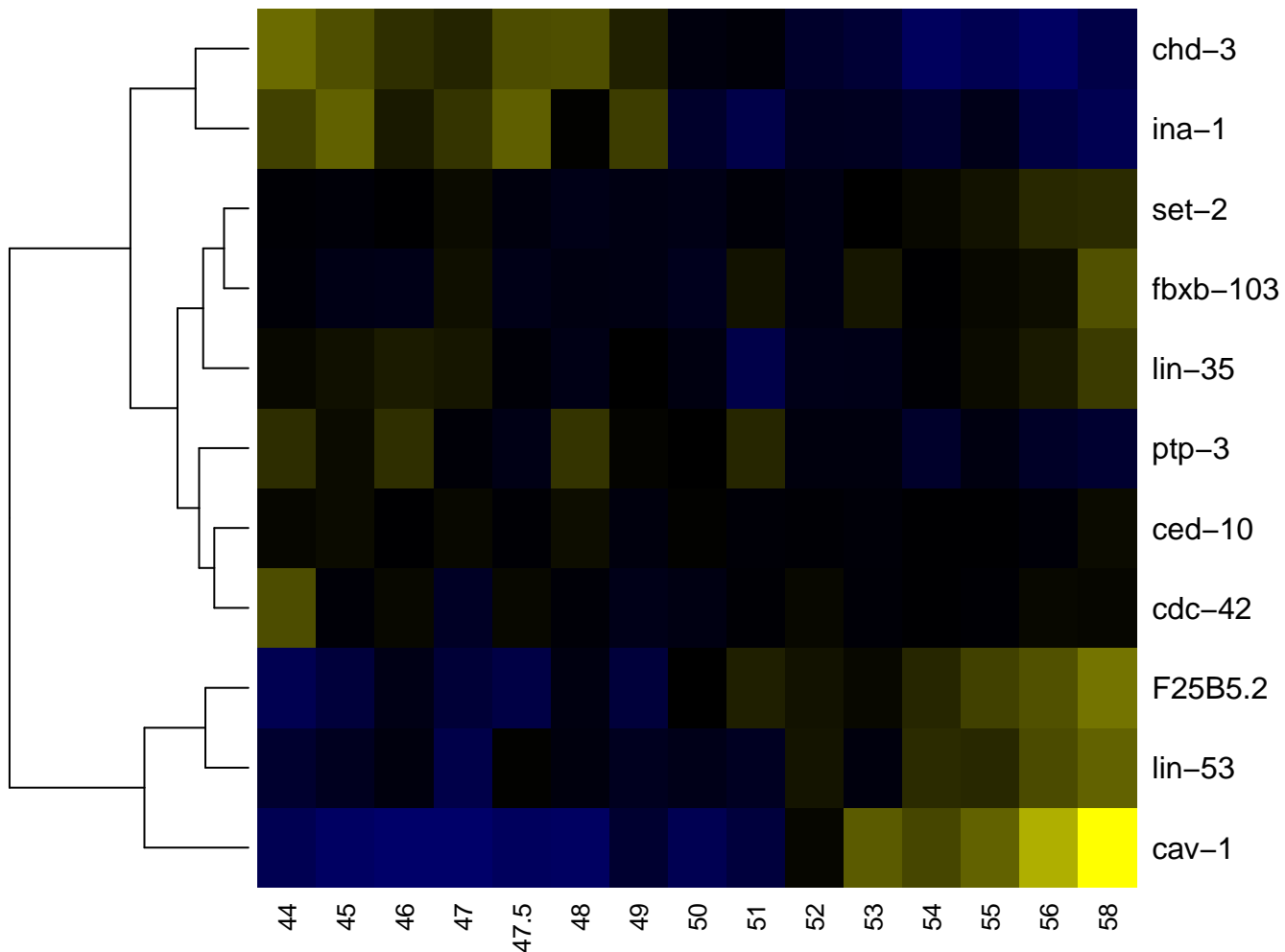
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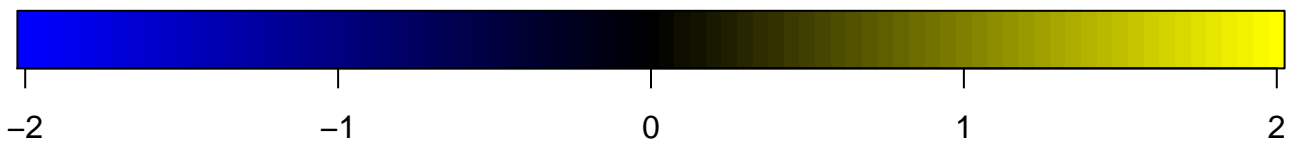
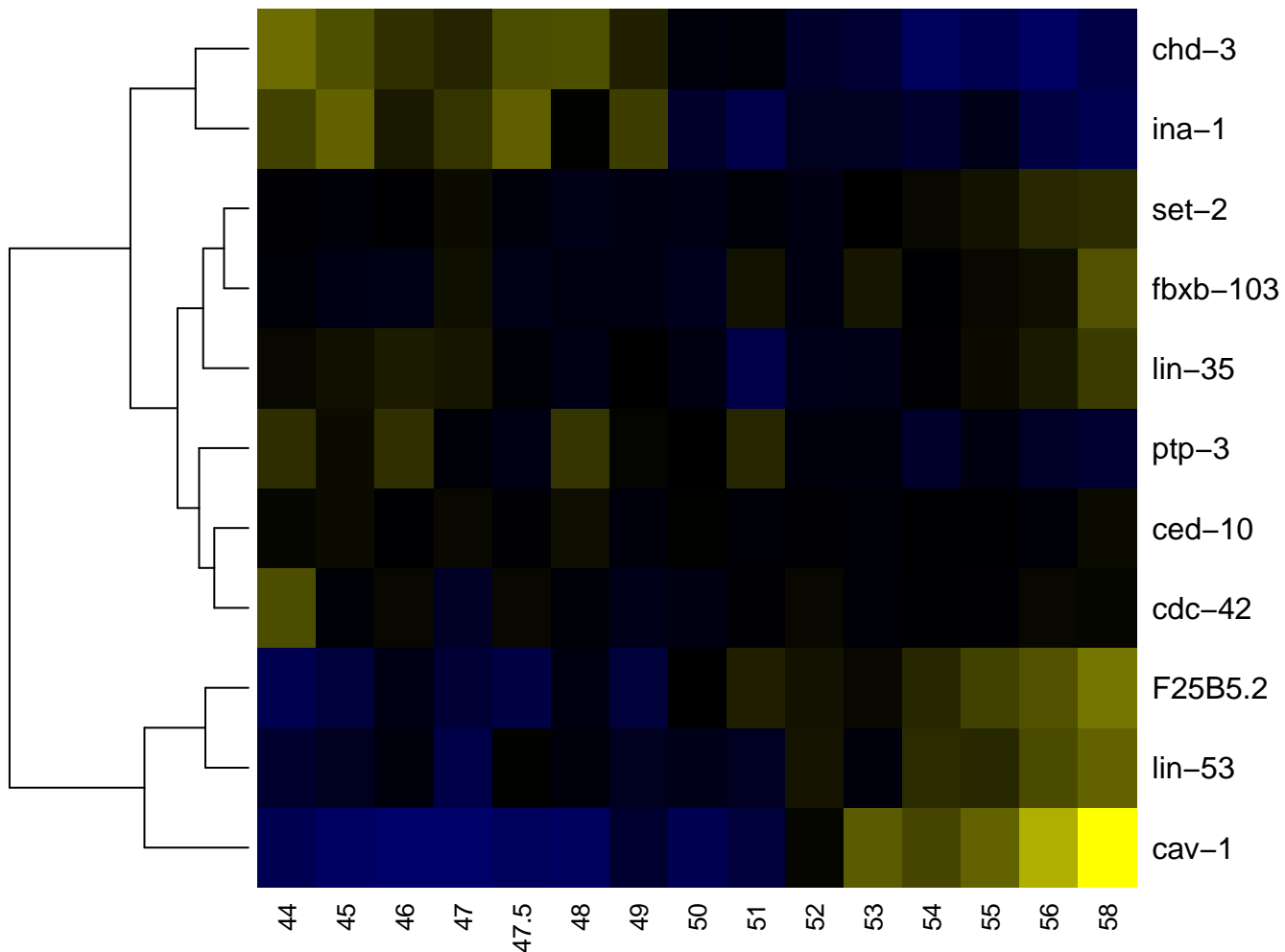
arc ant DL



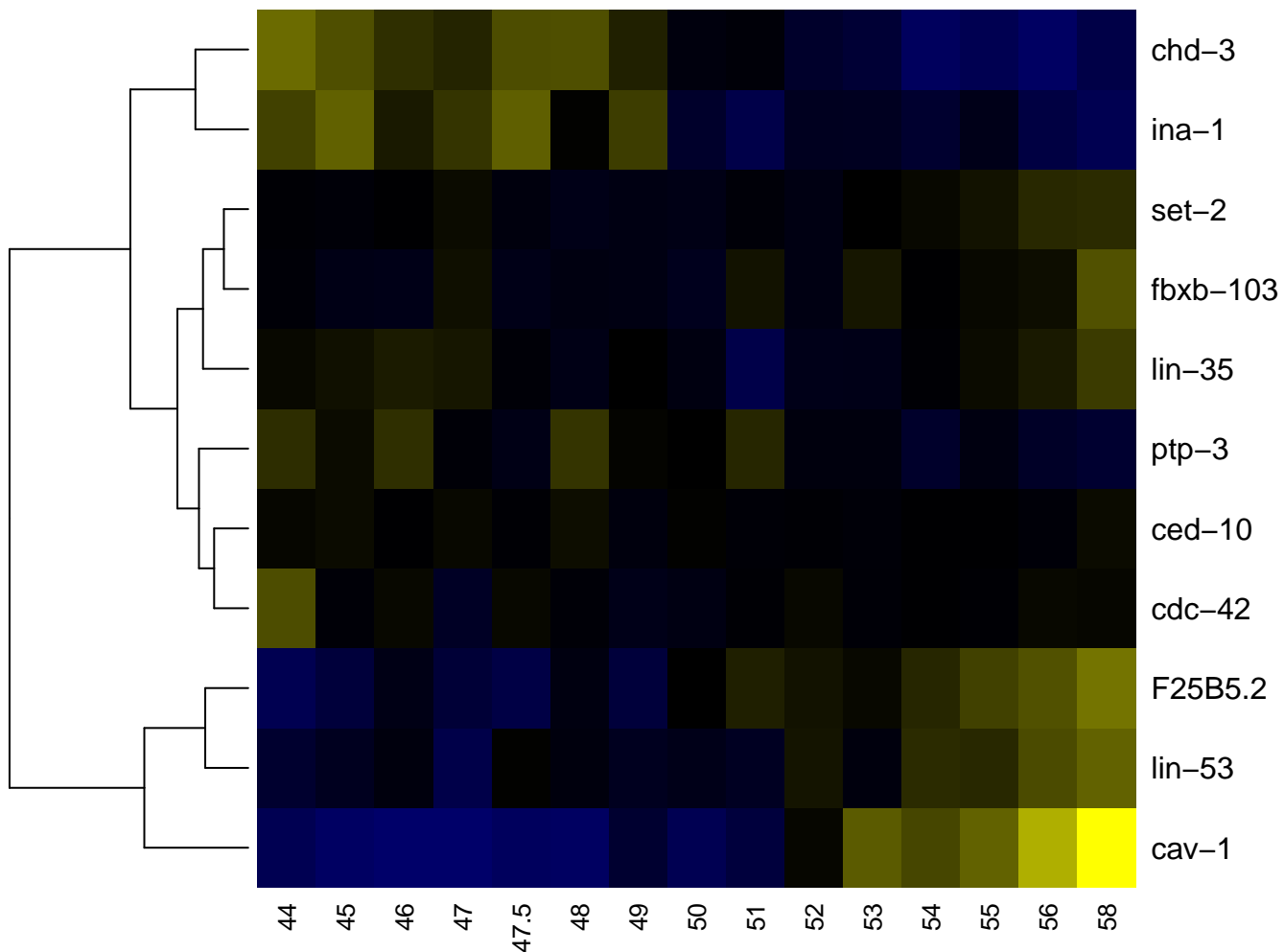
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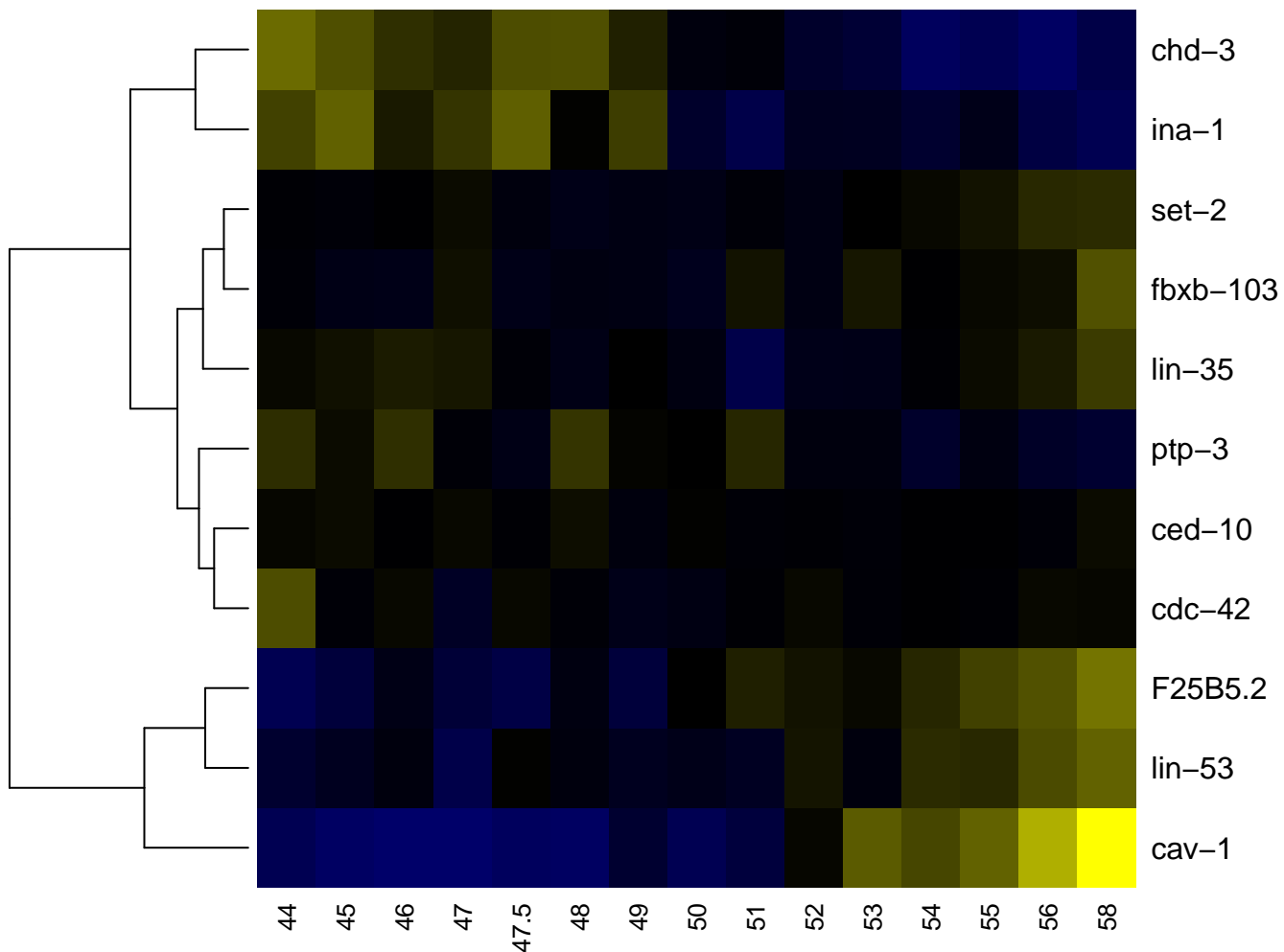
arc ant V



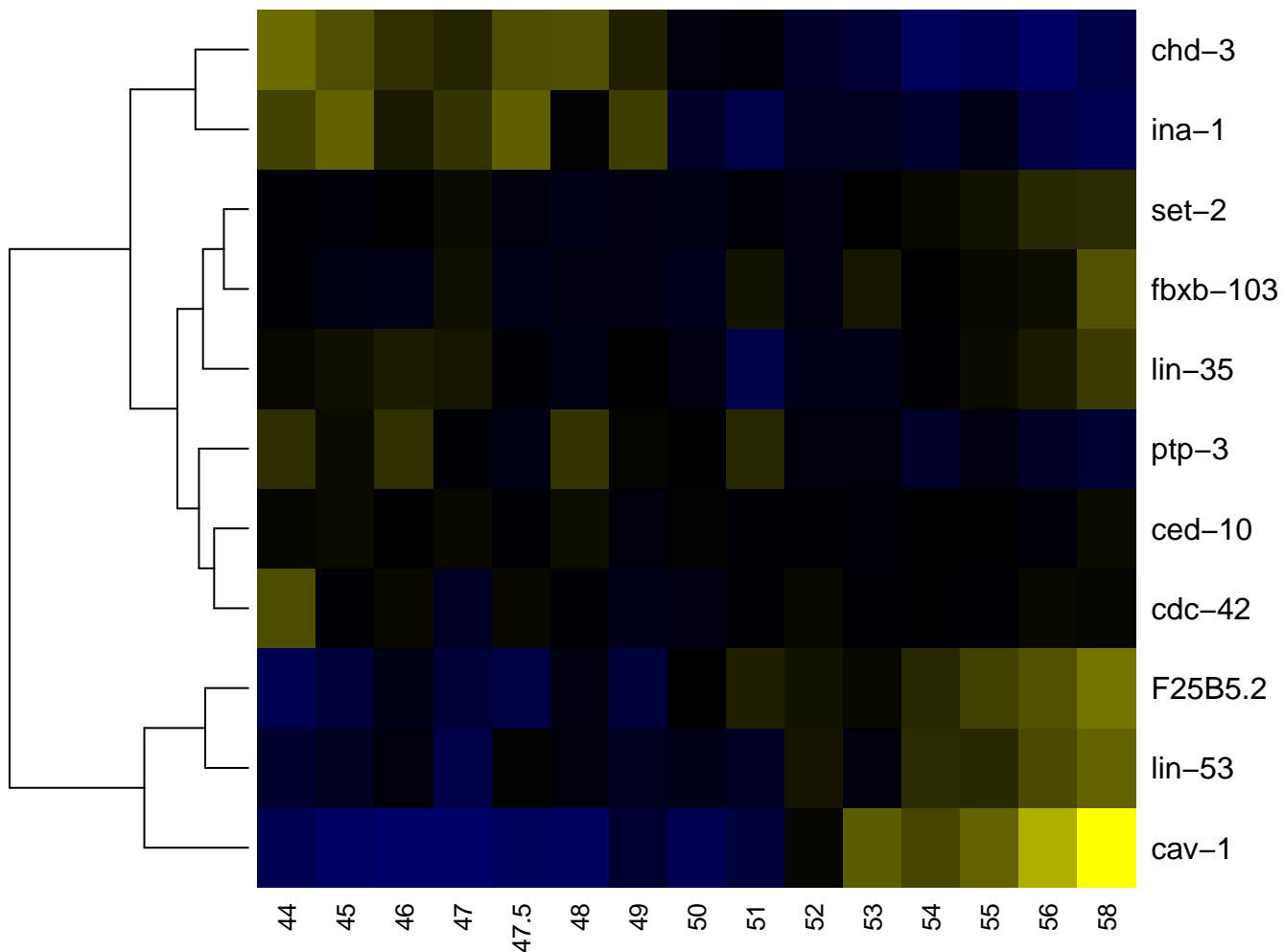
arc post D



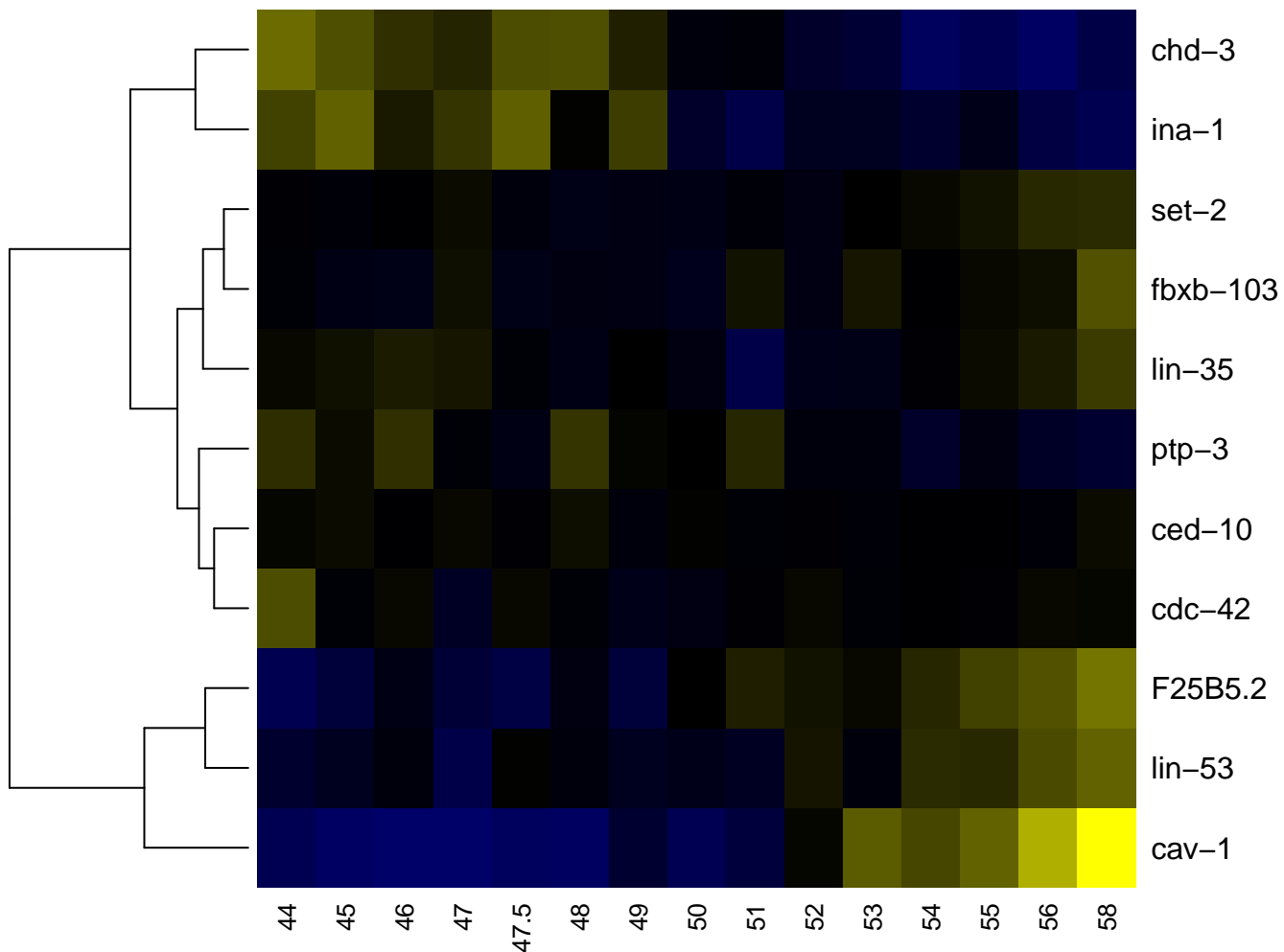
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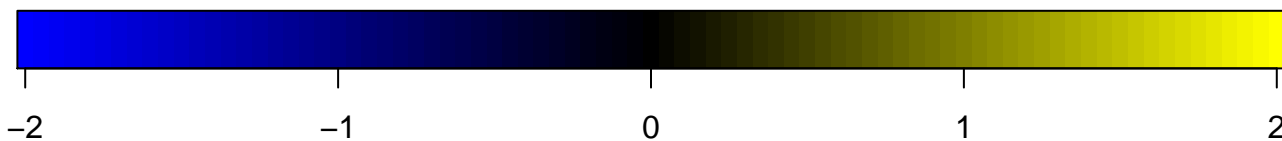
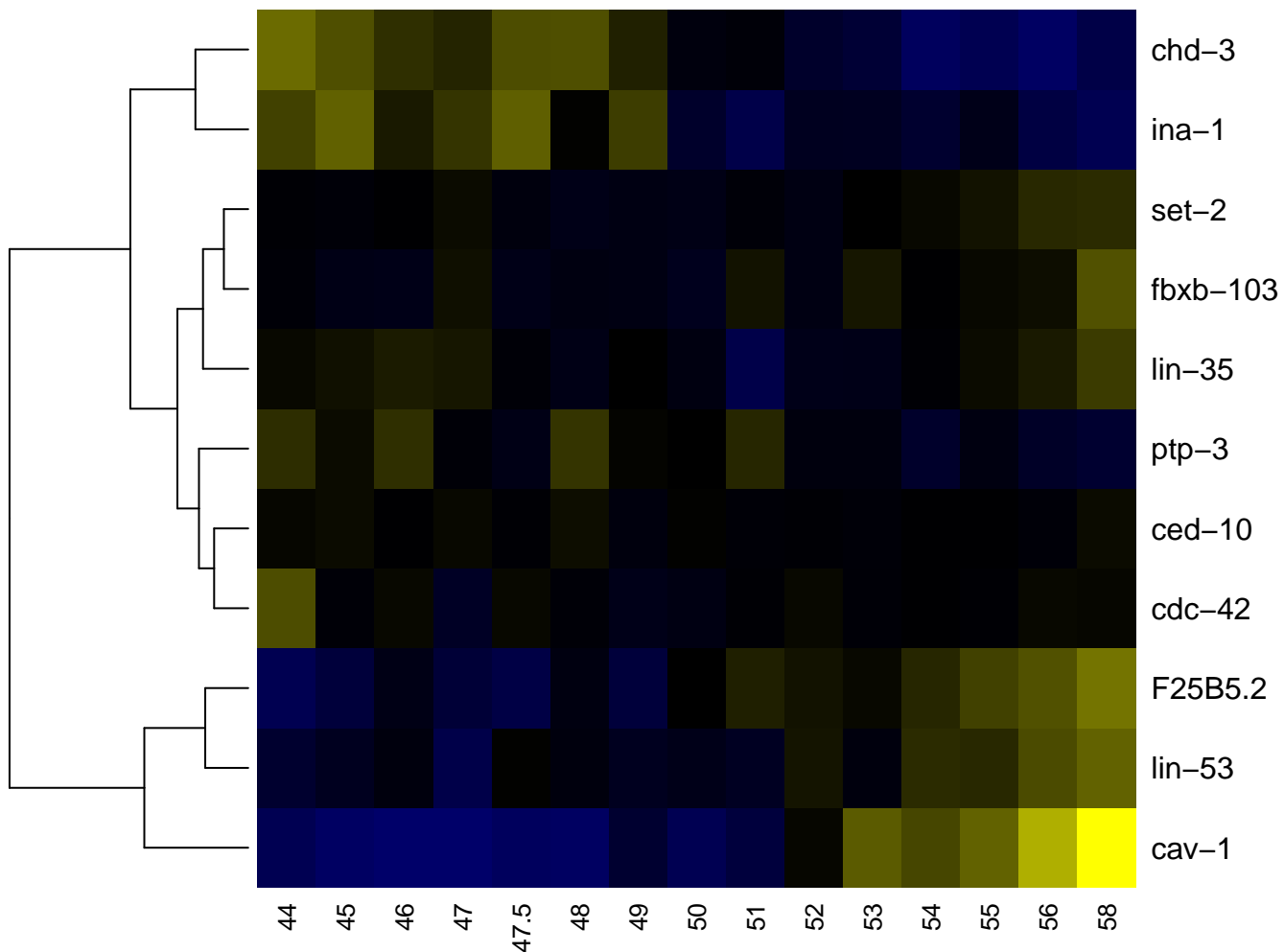
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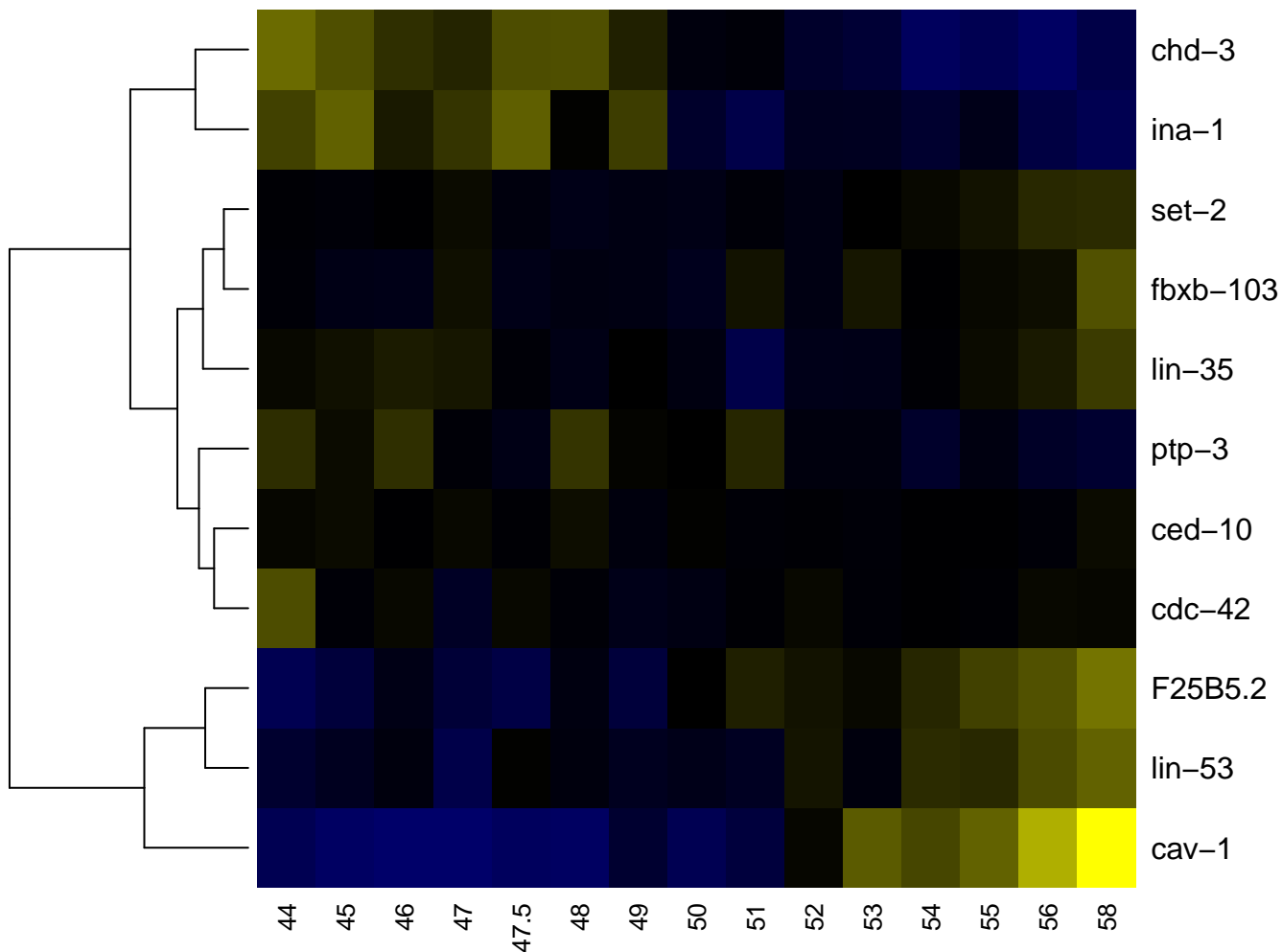
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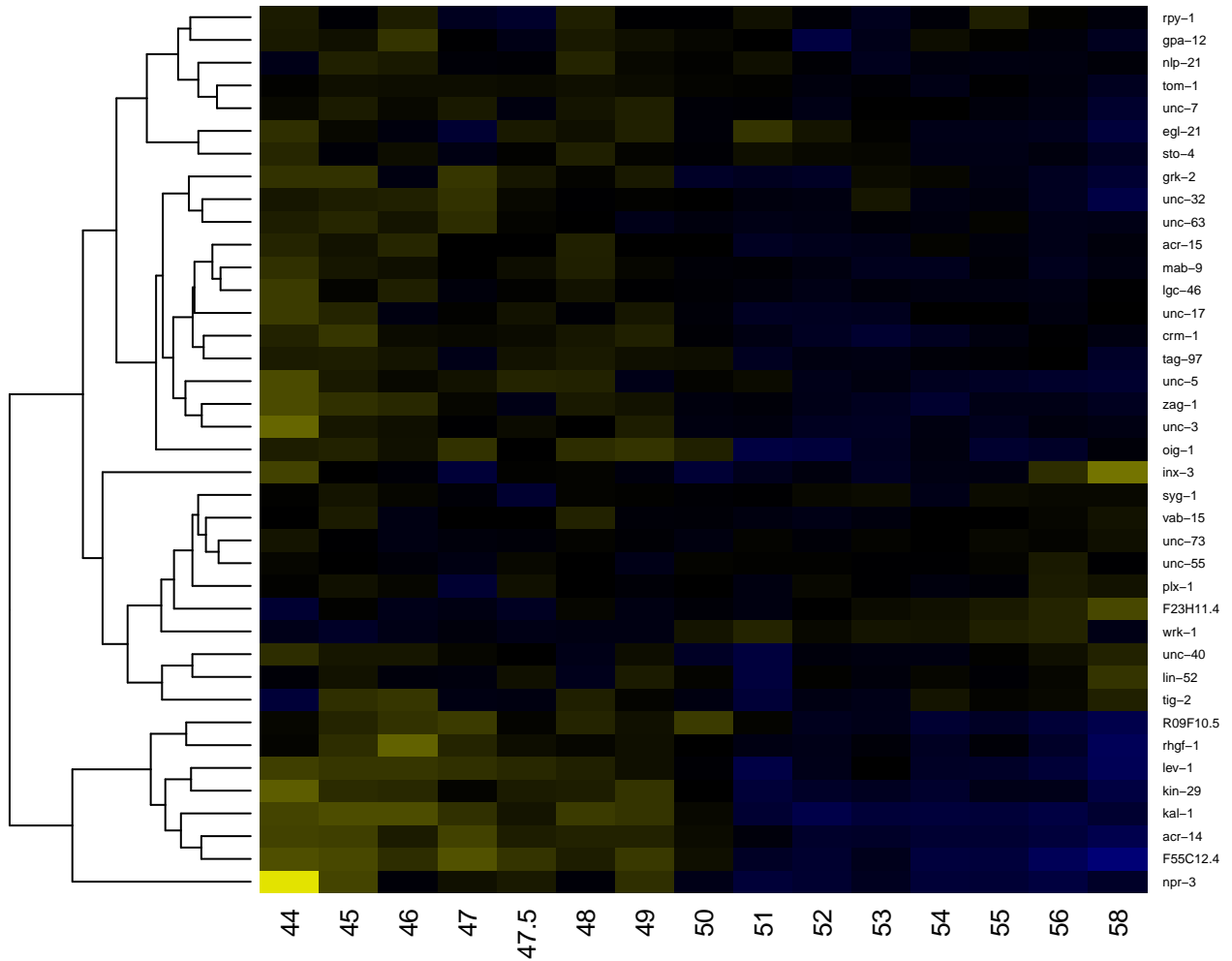
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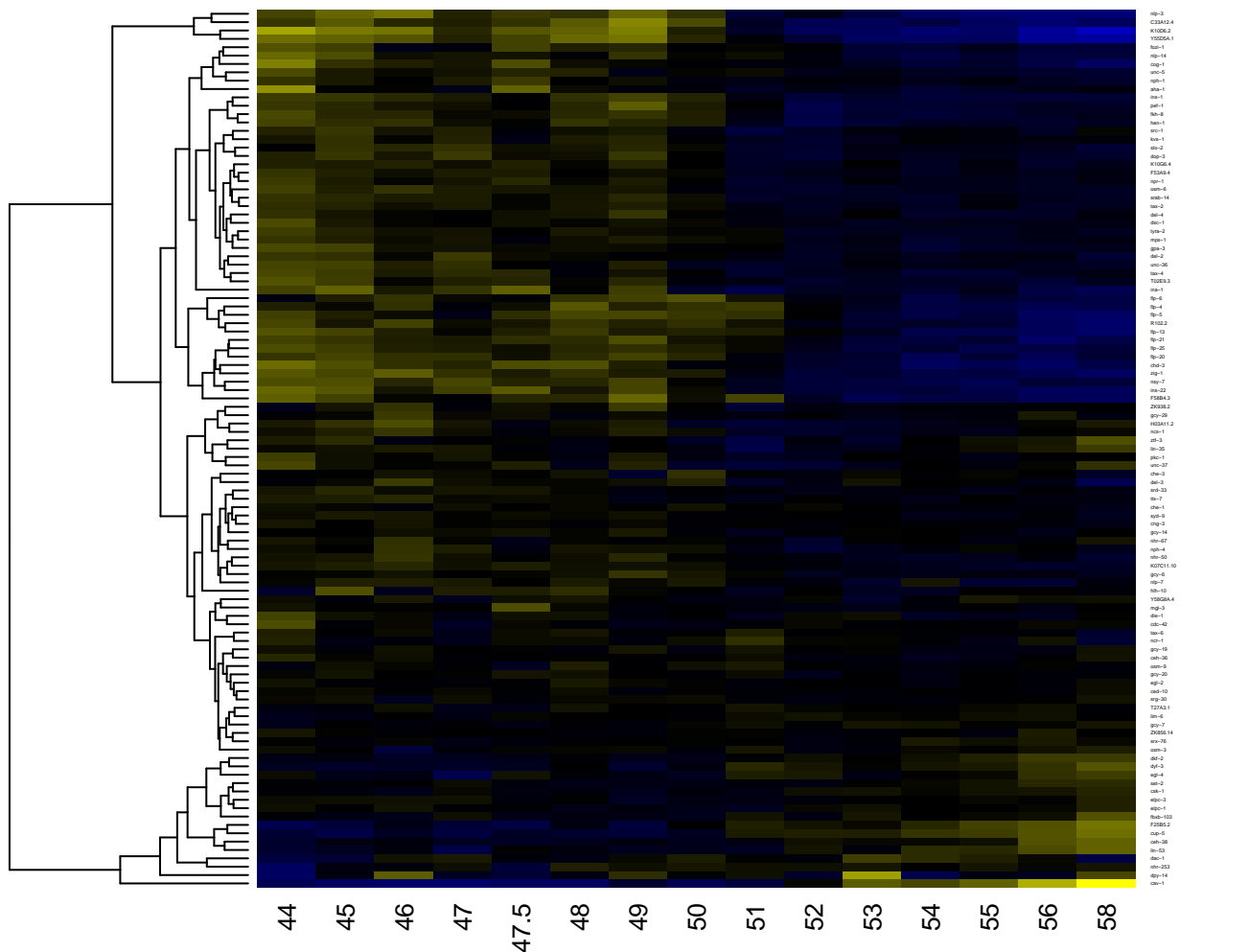
arc post VR



AS neuron



ASEL



-2

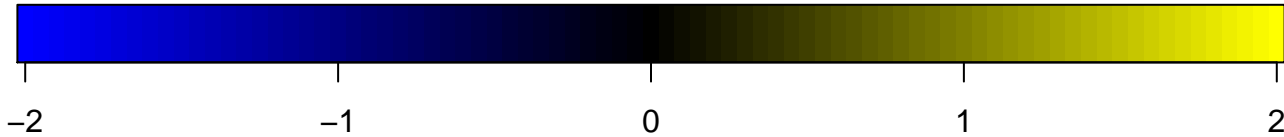
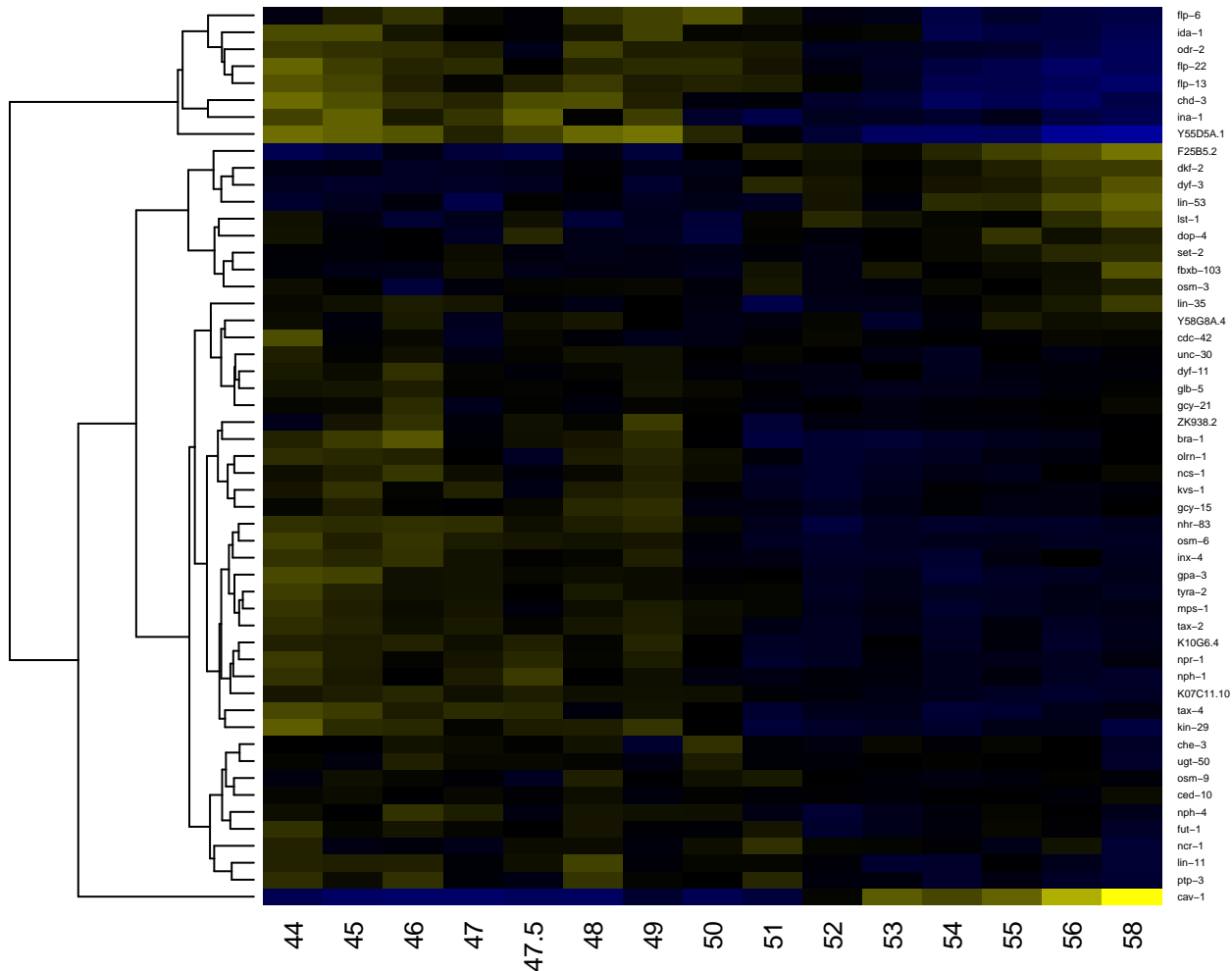
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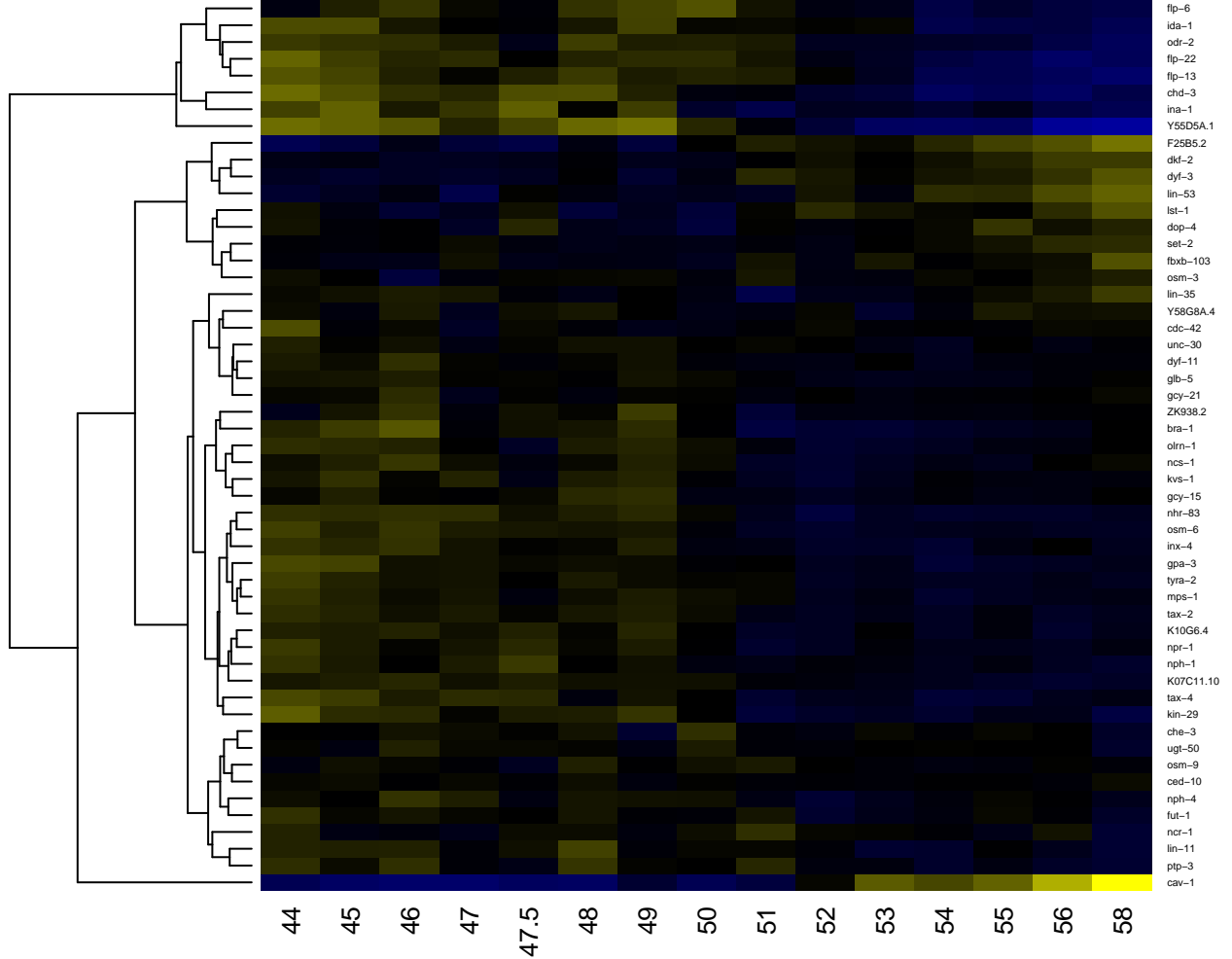
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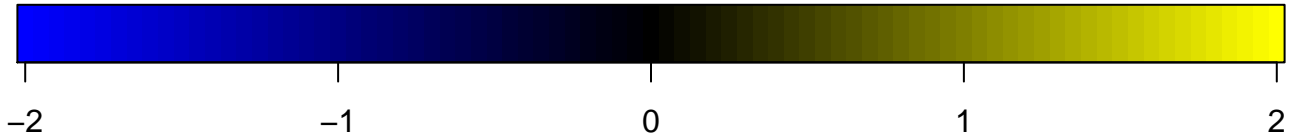
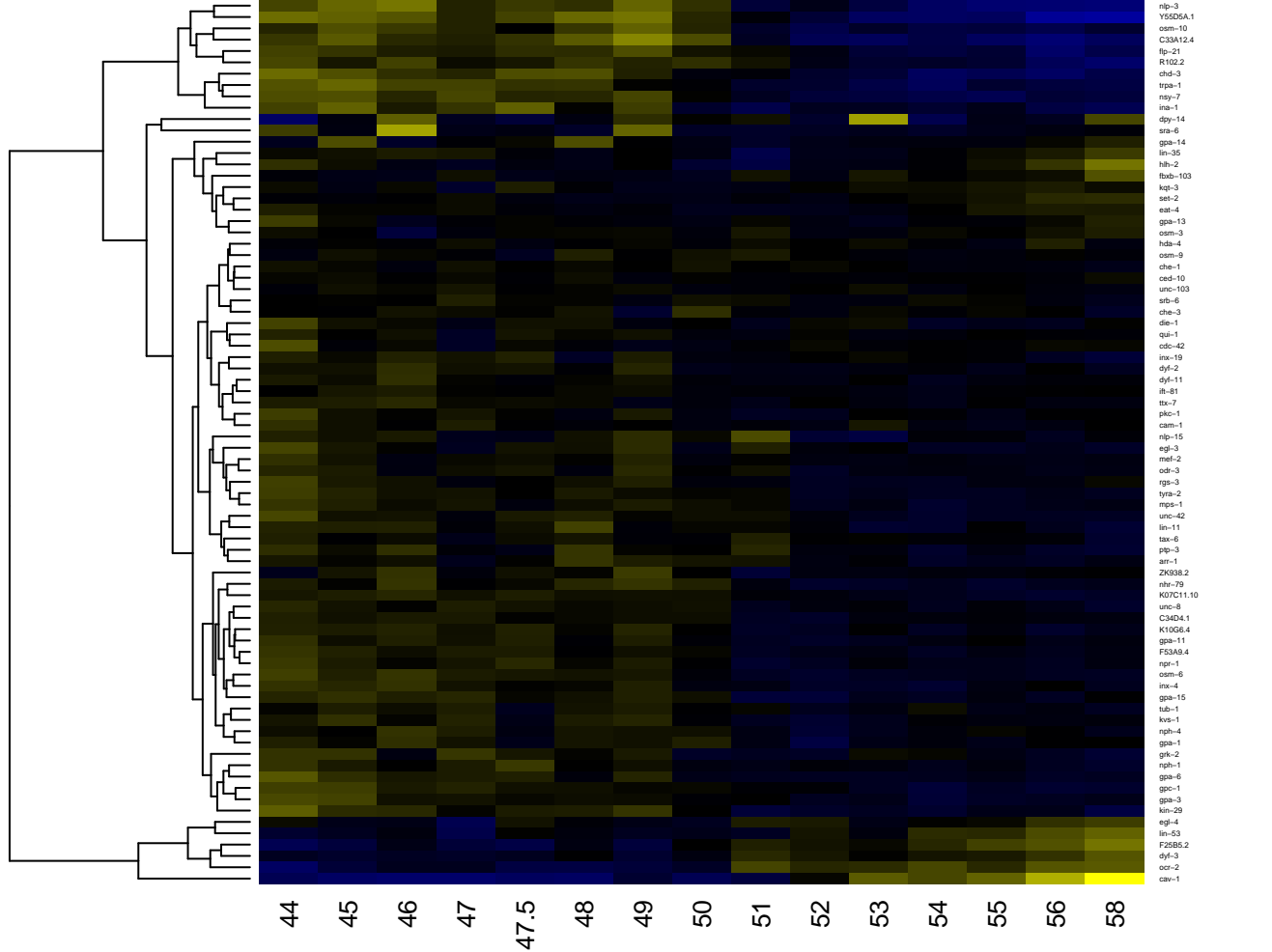
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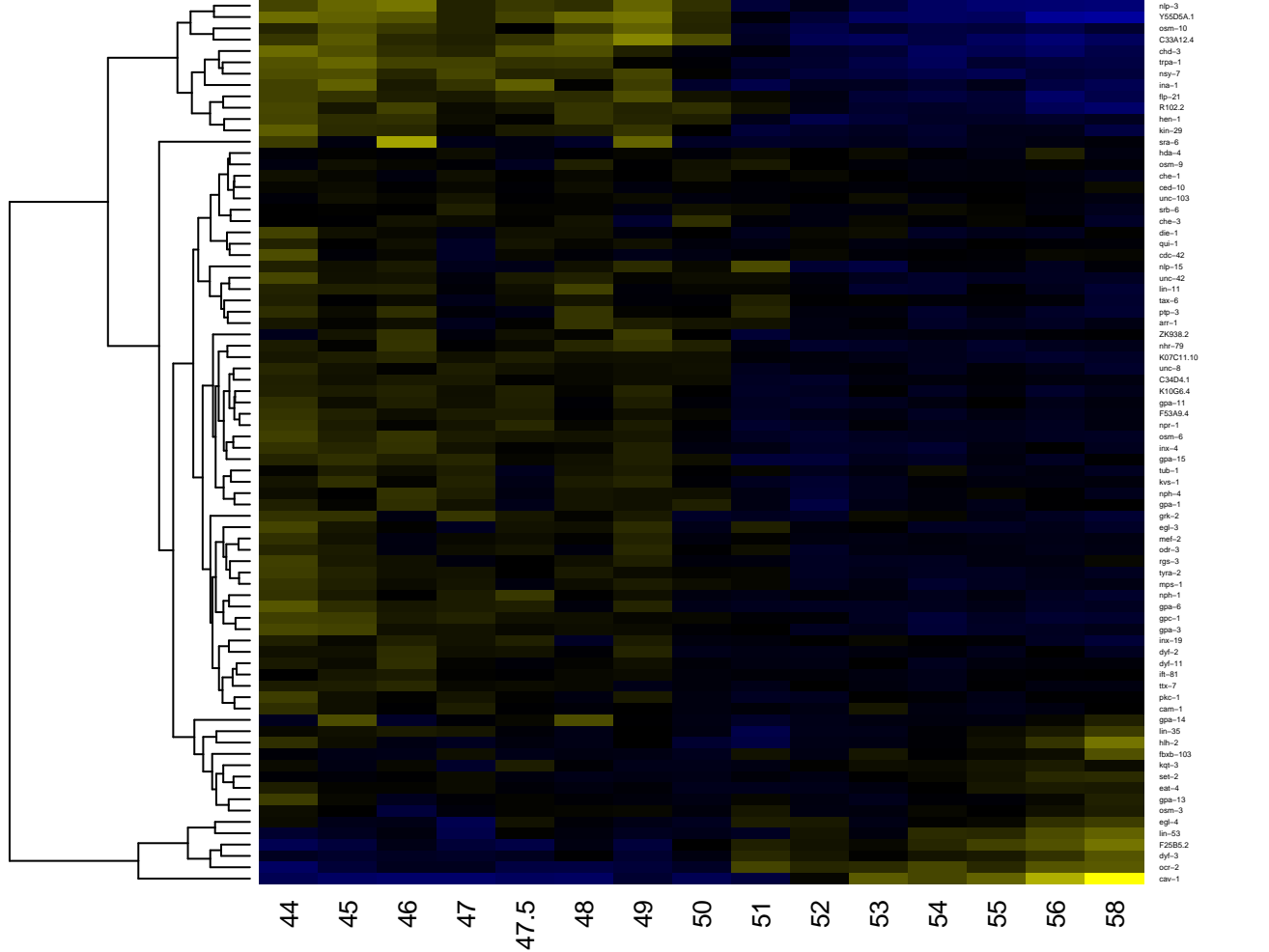
ASGR



ASHL



ASHR



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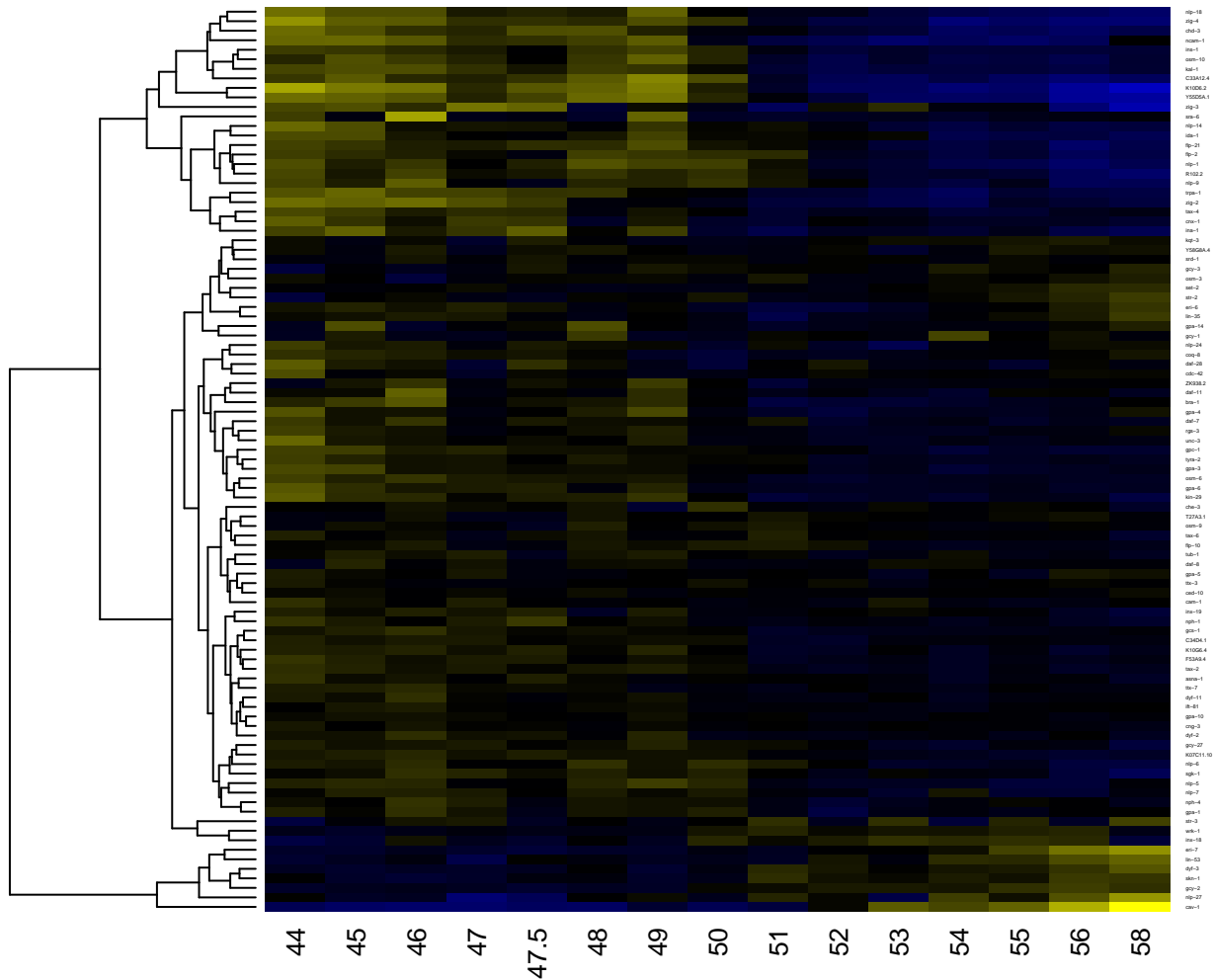
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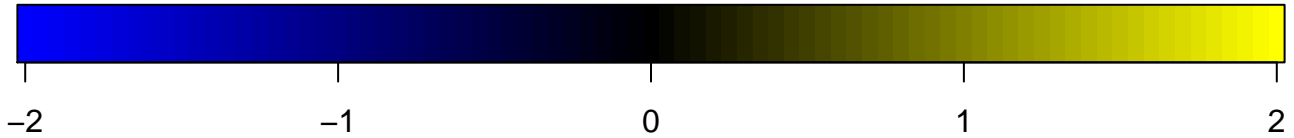
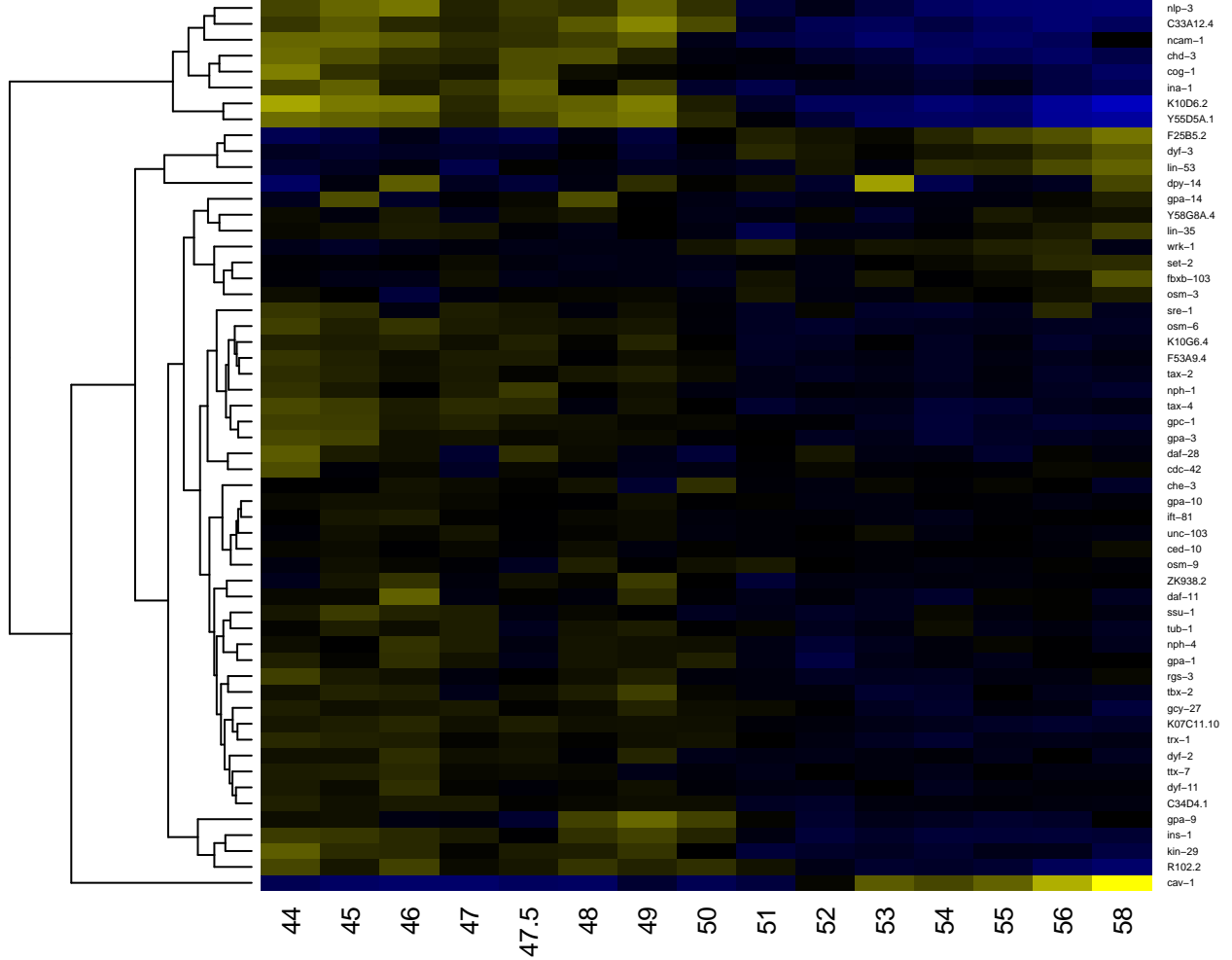
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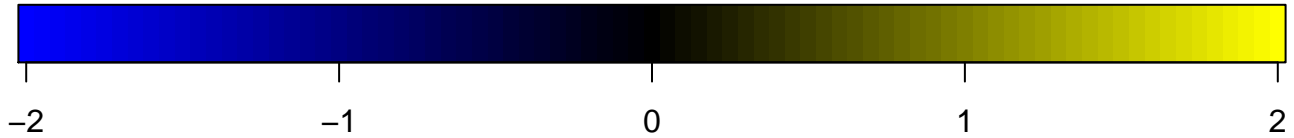
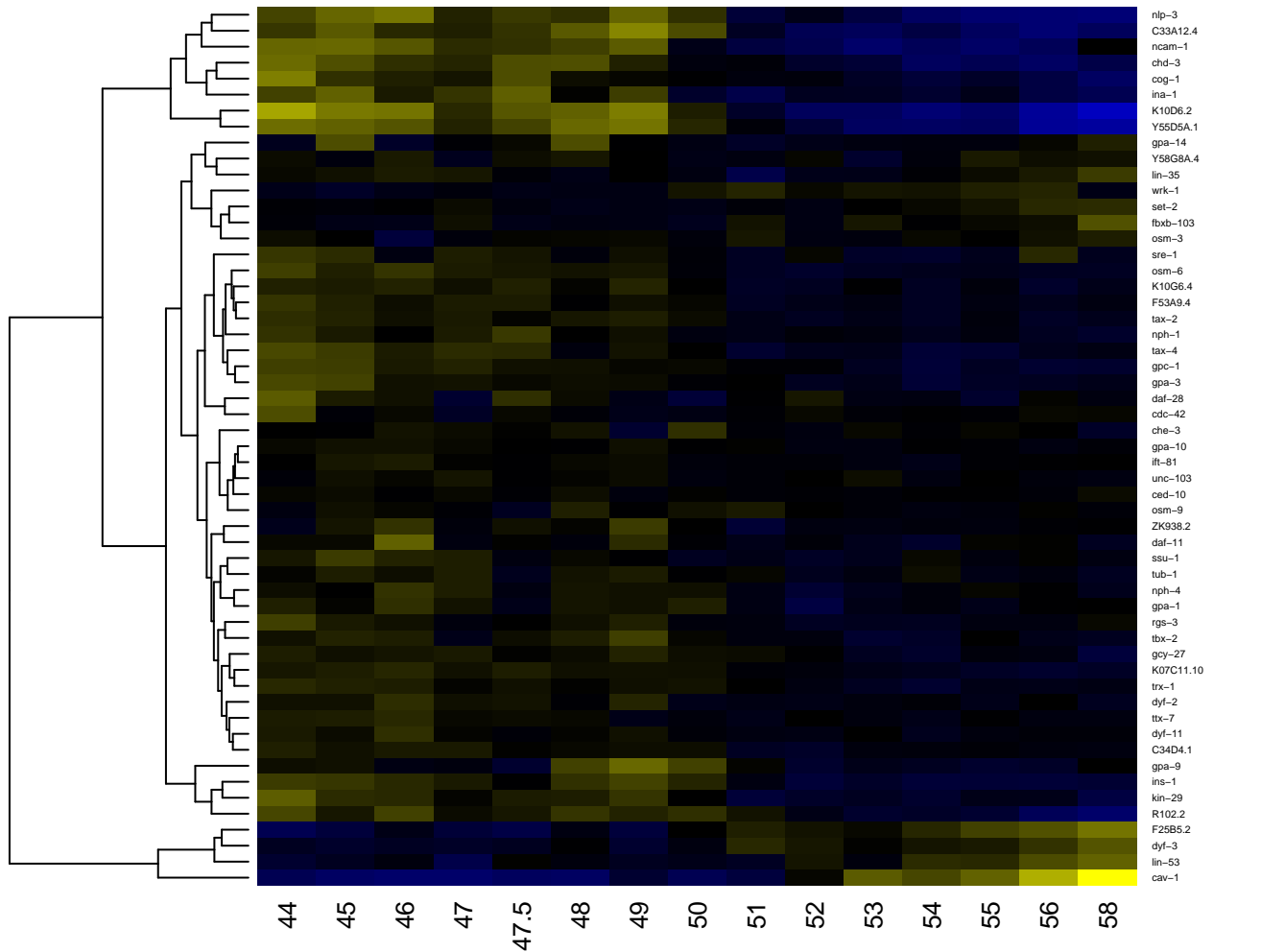
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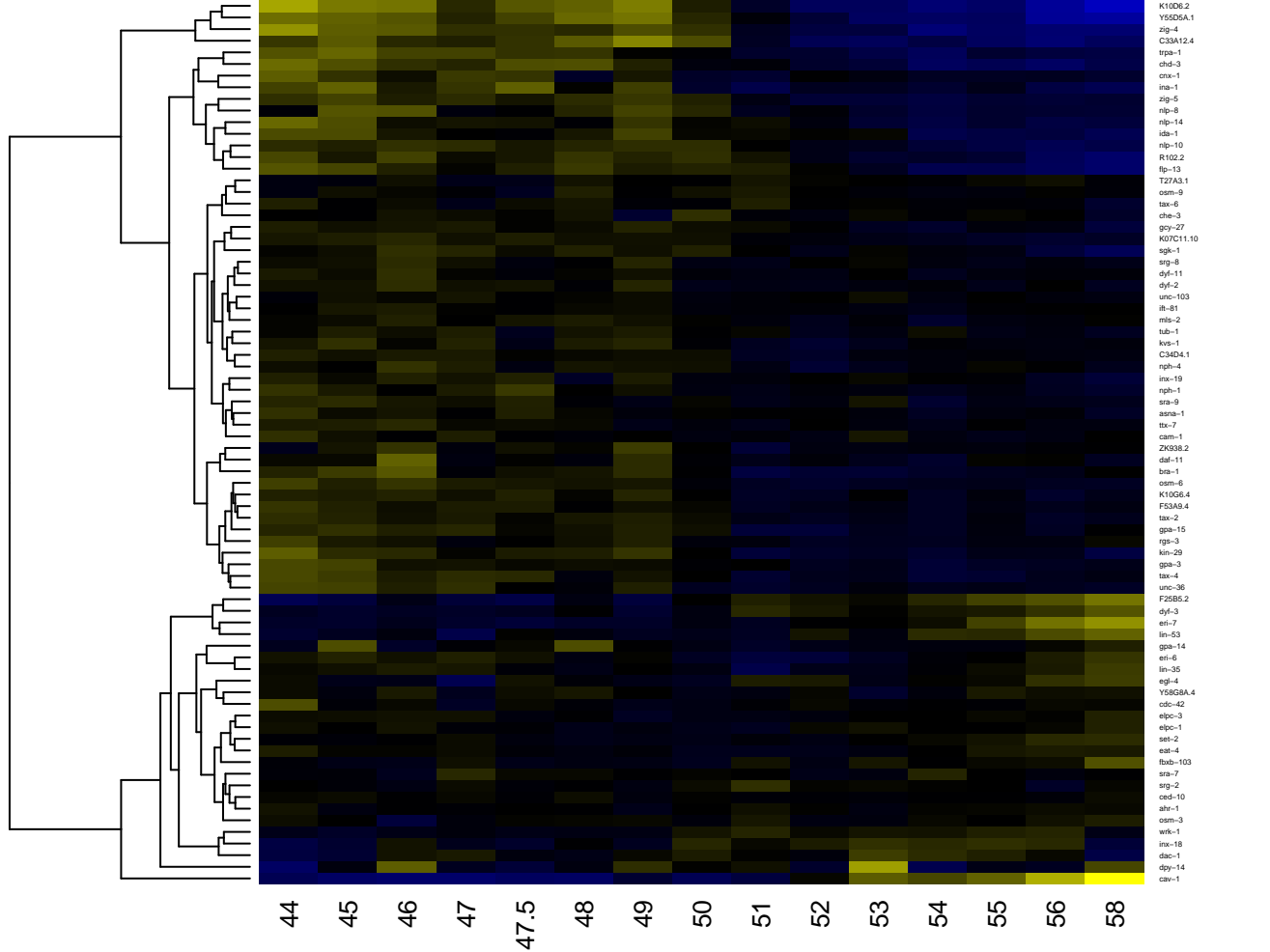
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ASJR



ASKL



-2

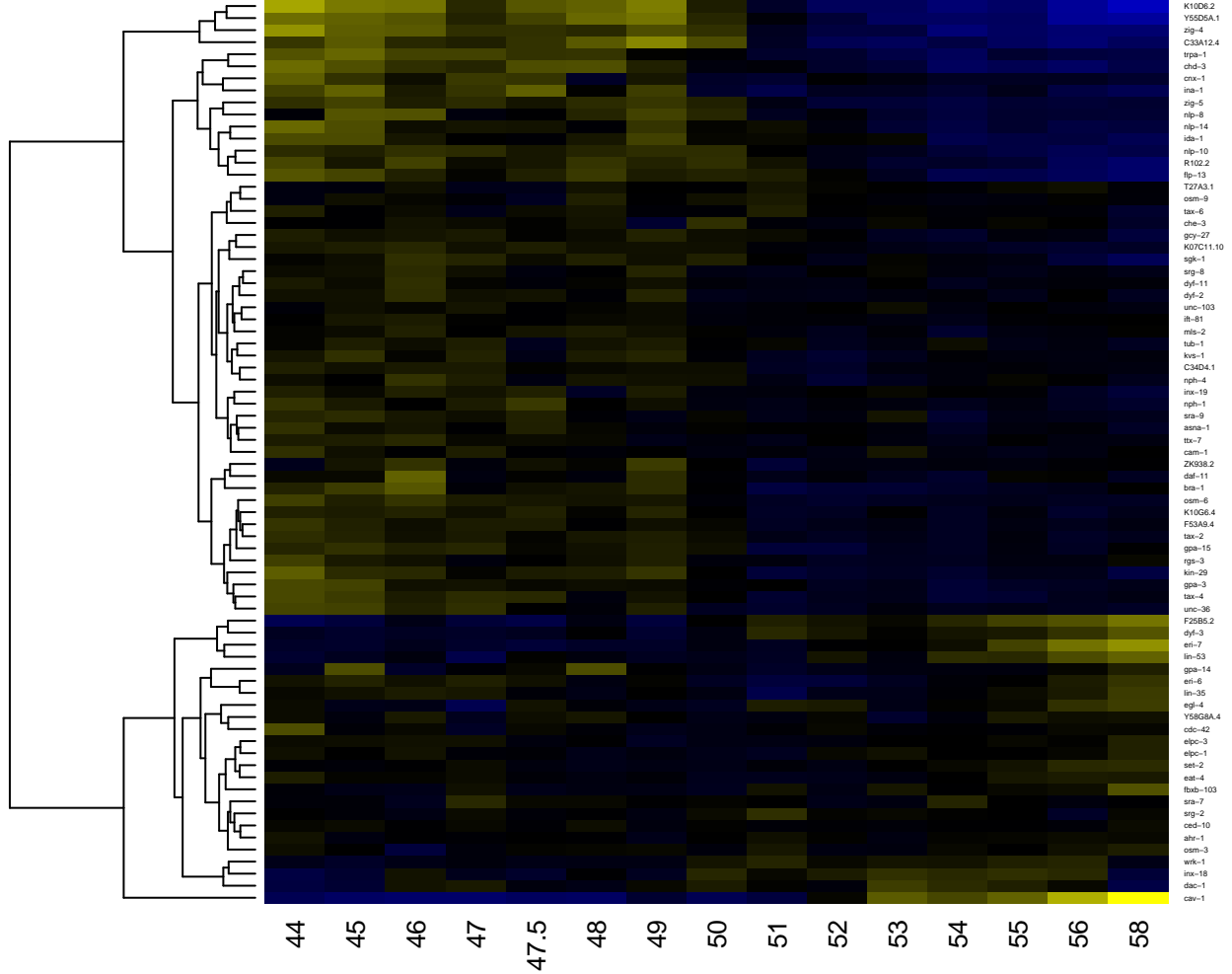
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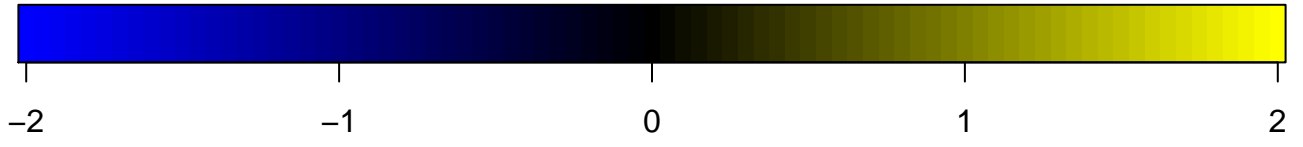
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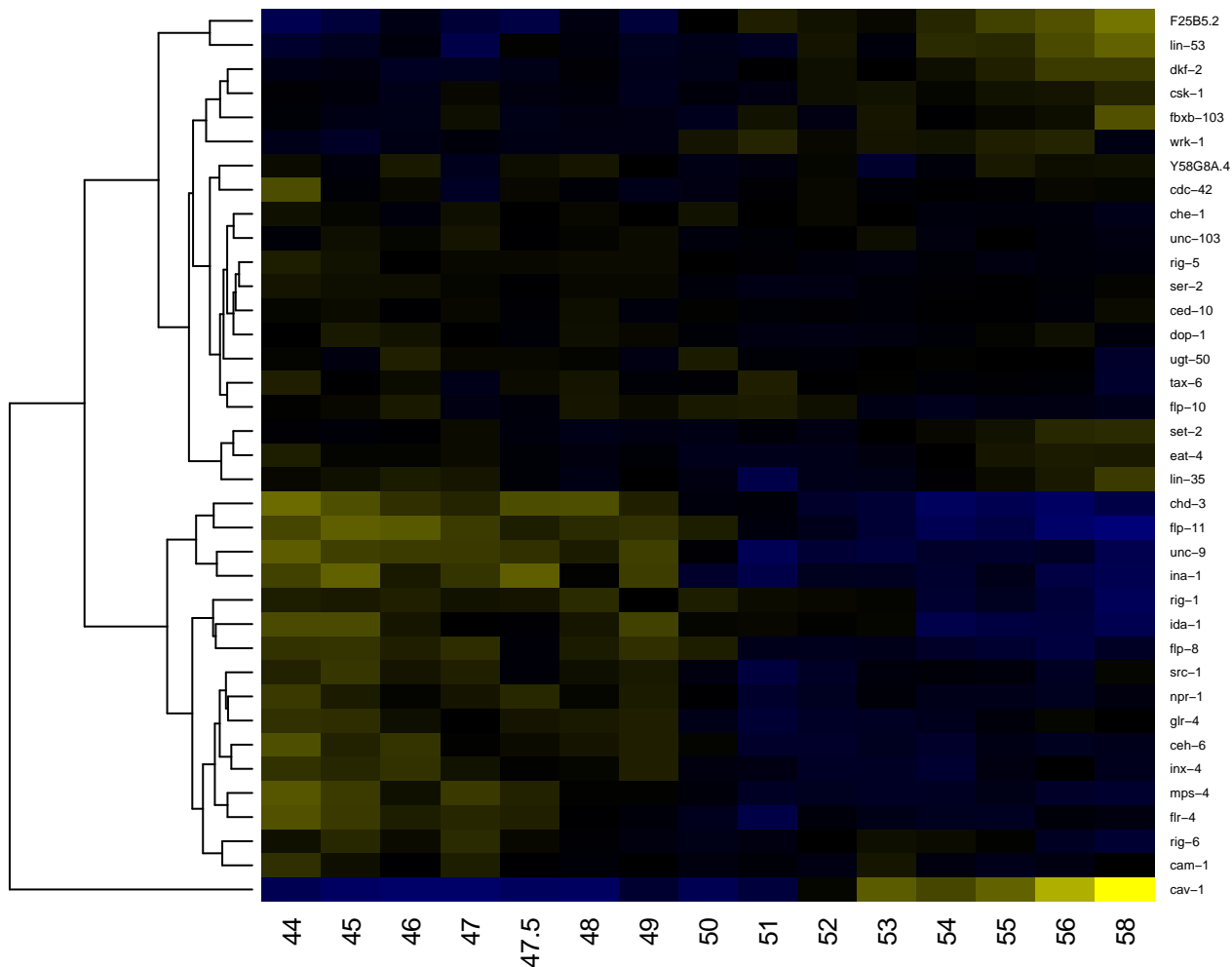
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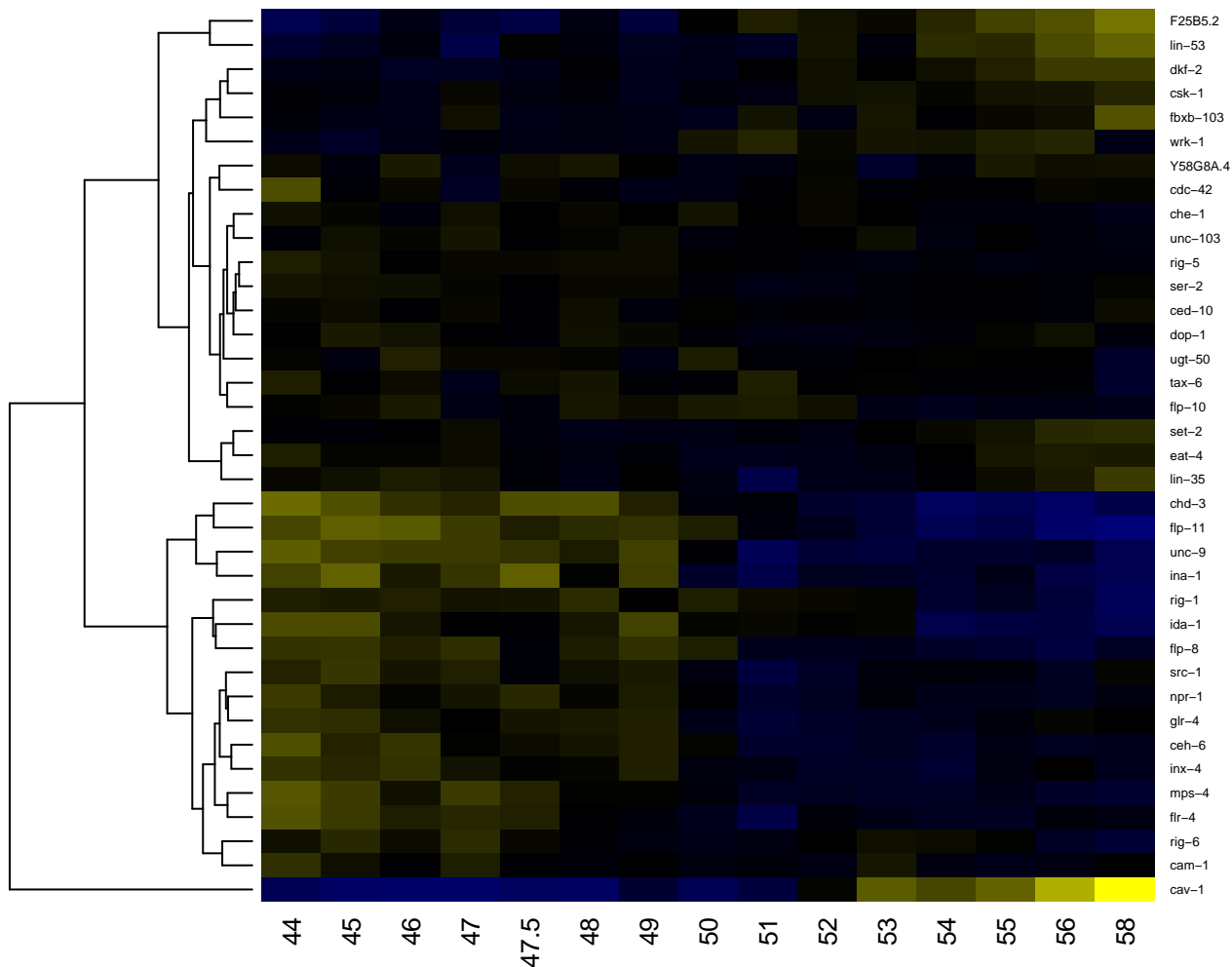
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tax-6
che-3
gcy-27
K07C11.10
sgs-1
srg-8
dyf-11
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il-81
mfs-2
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gpa-3
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elpc-3
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eat-2
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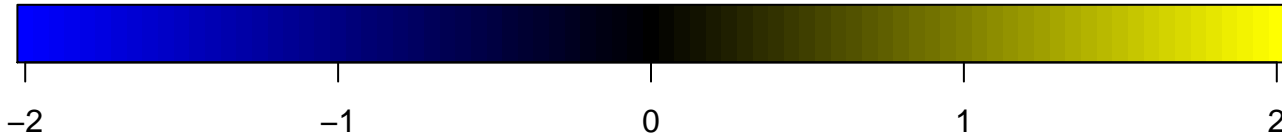
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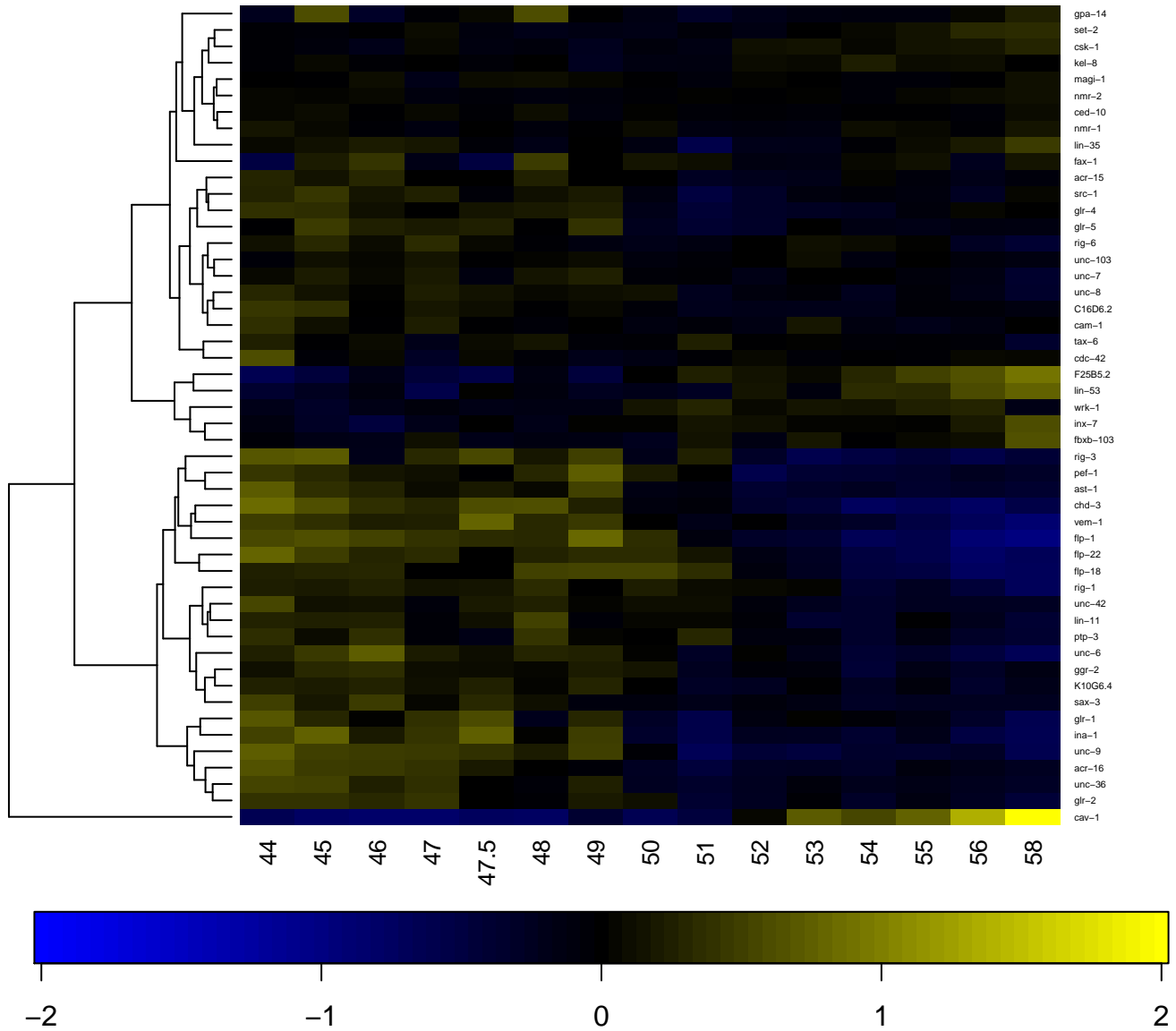
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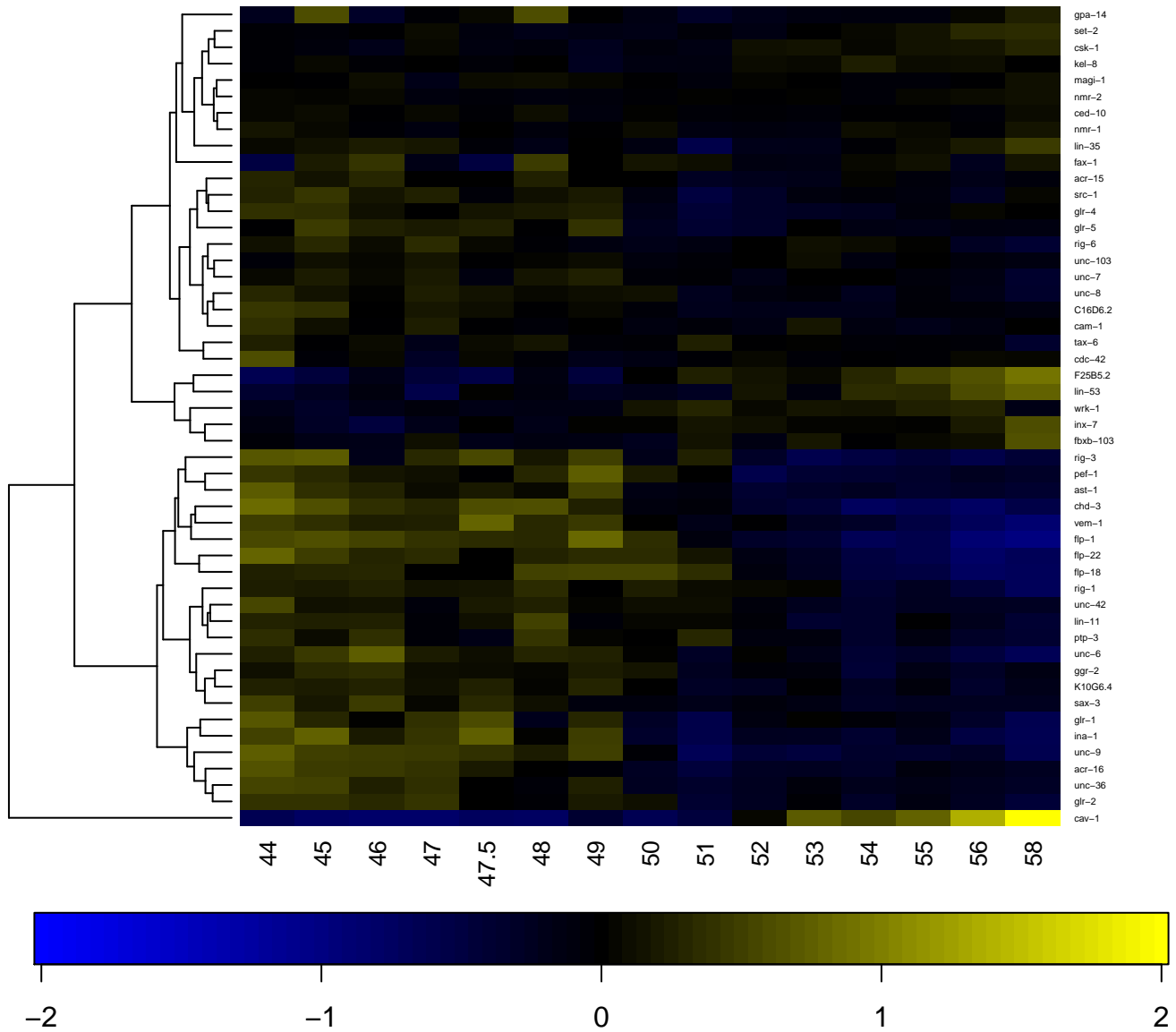
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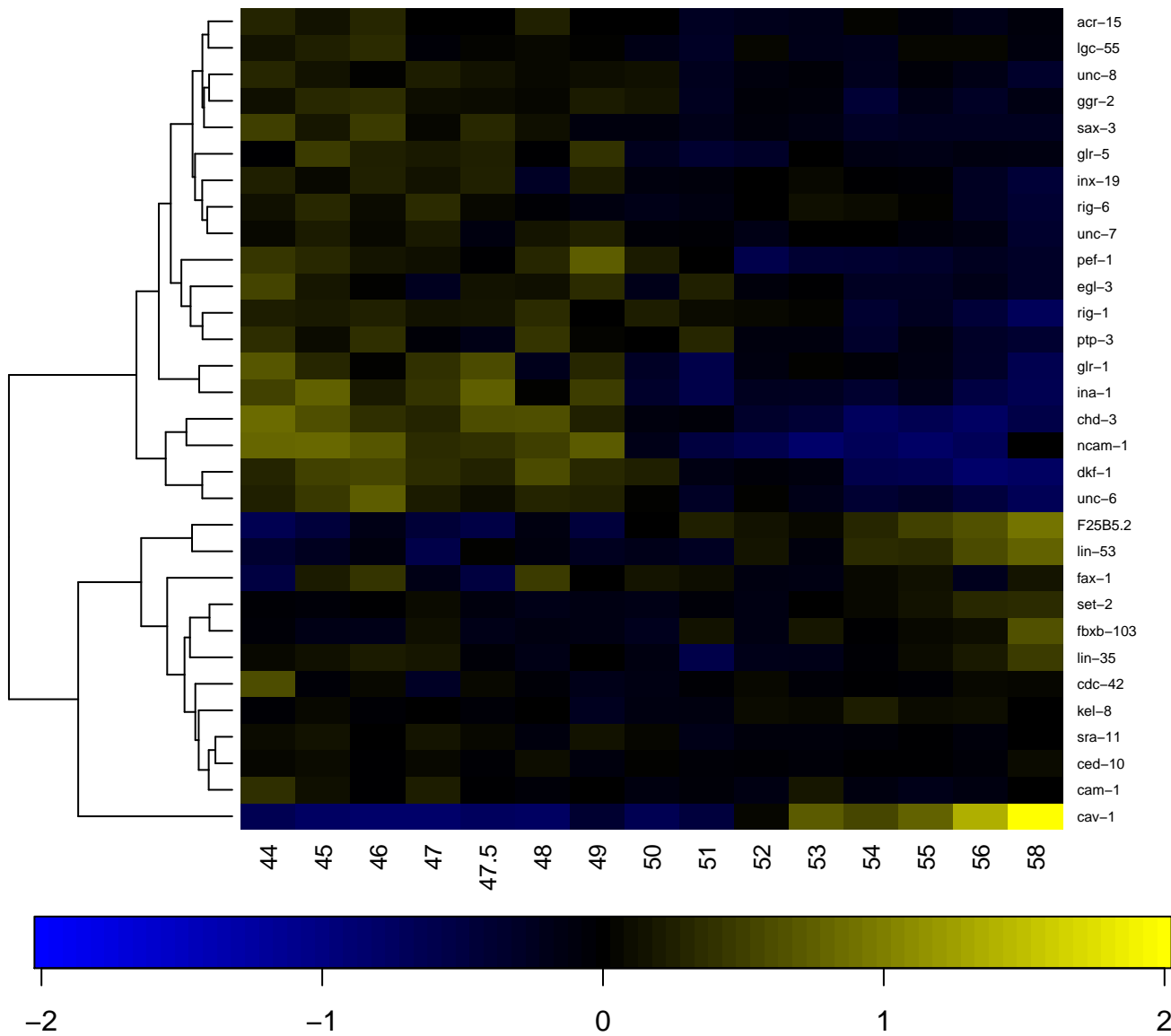
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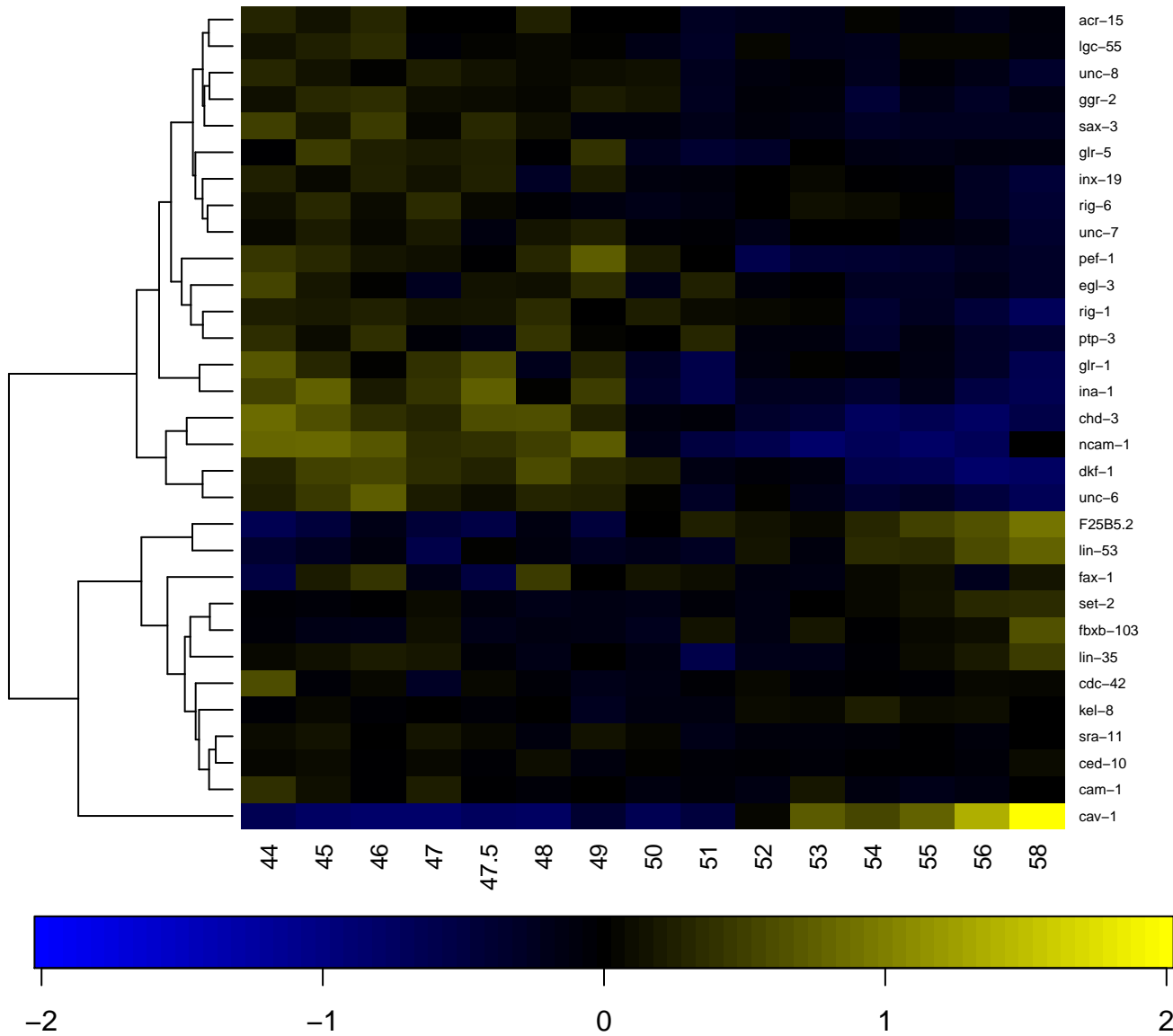
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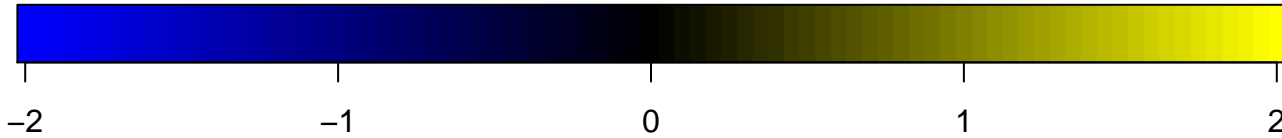
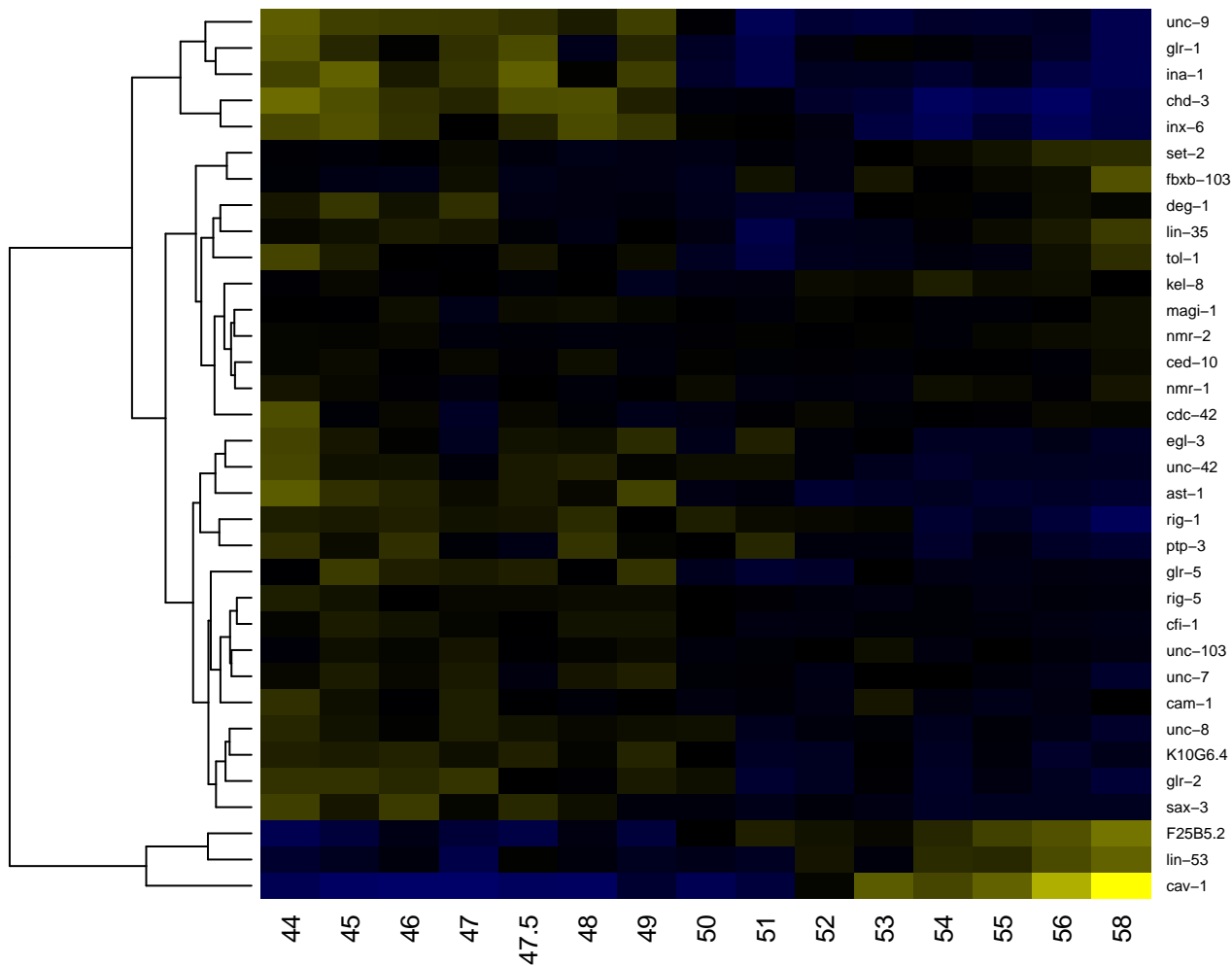
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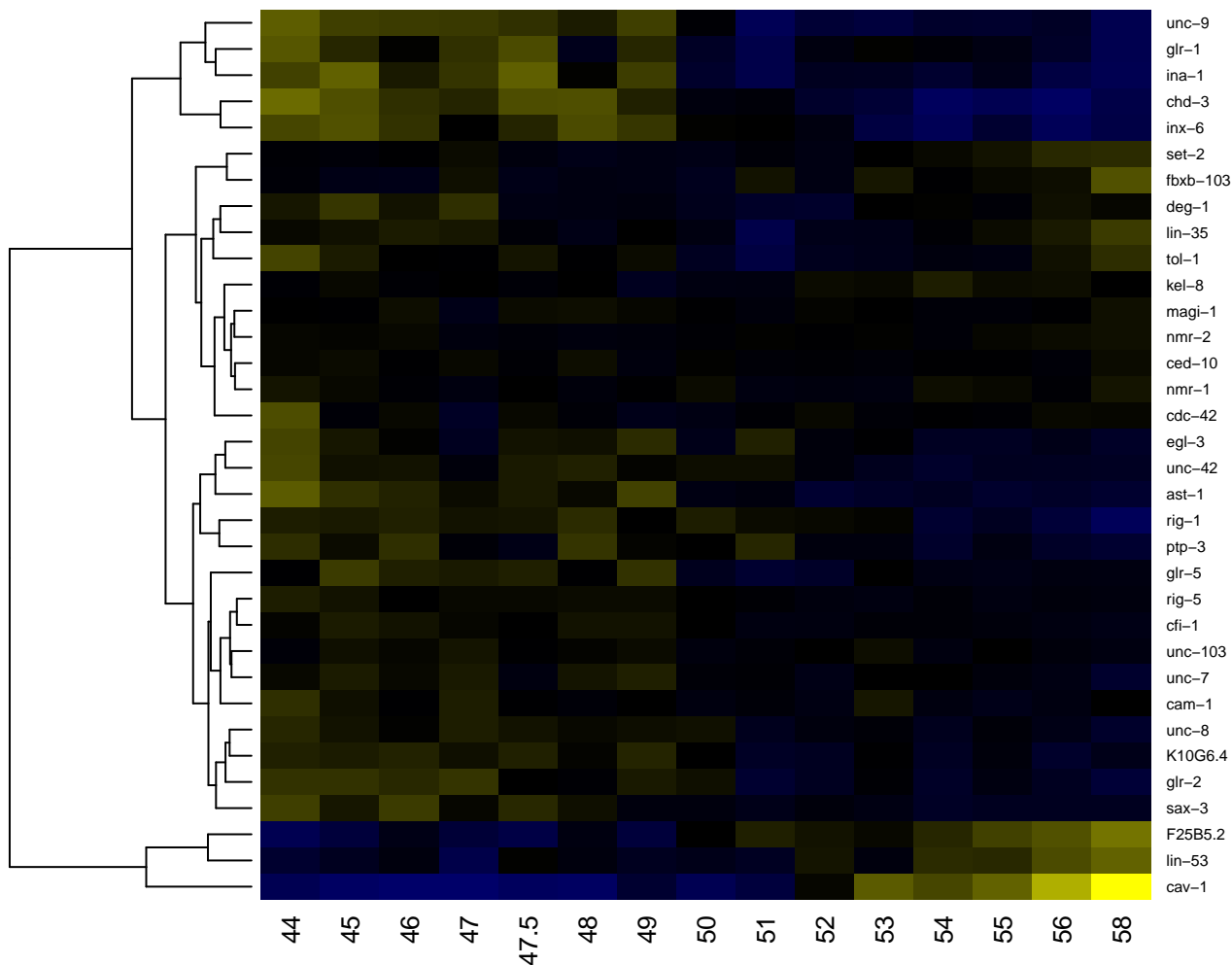
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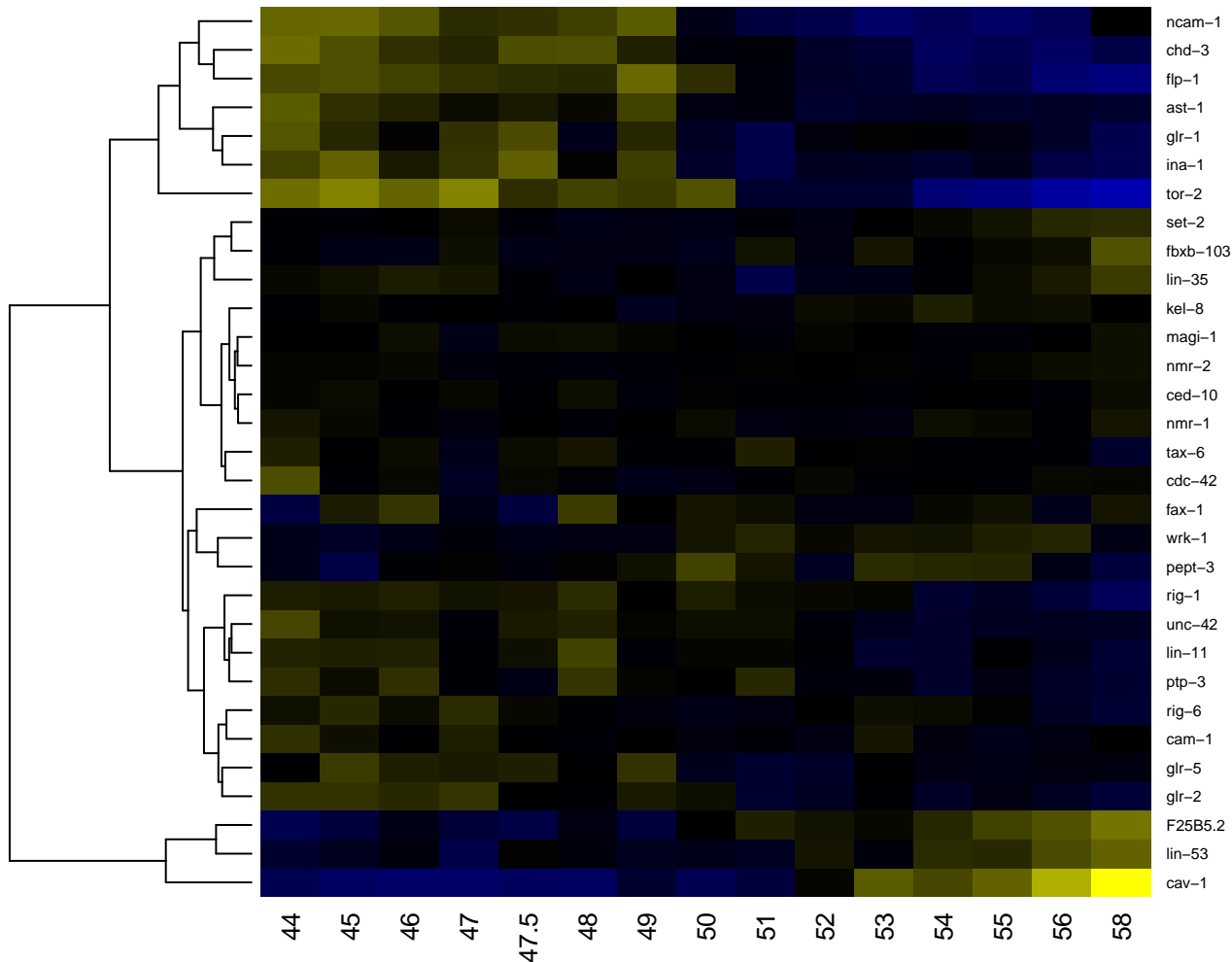
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AVDR



AVEL



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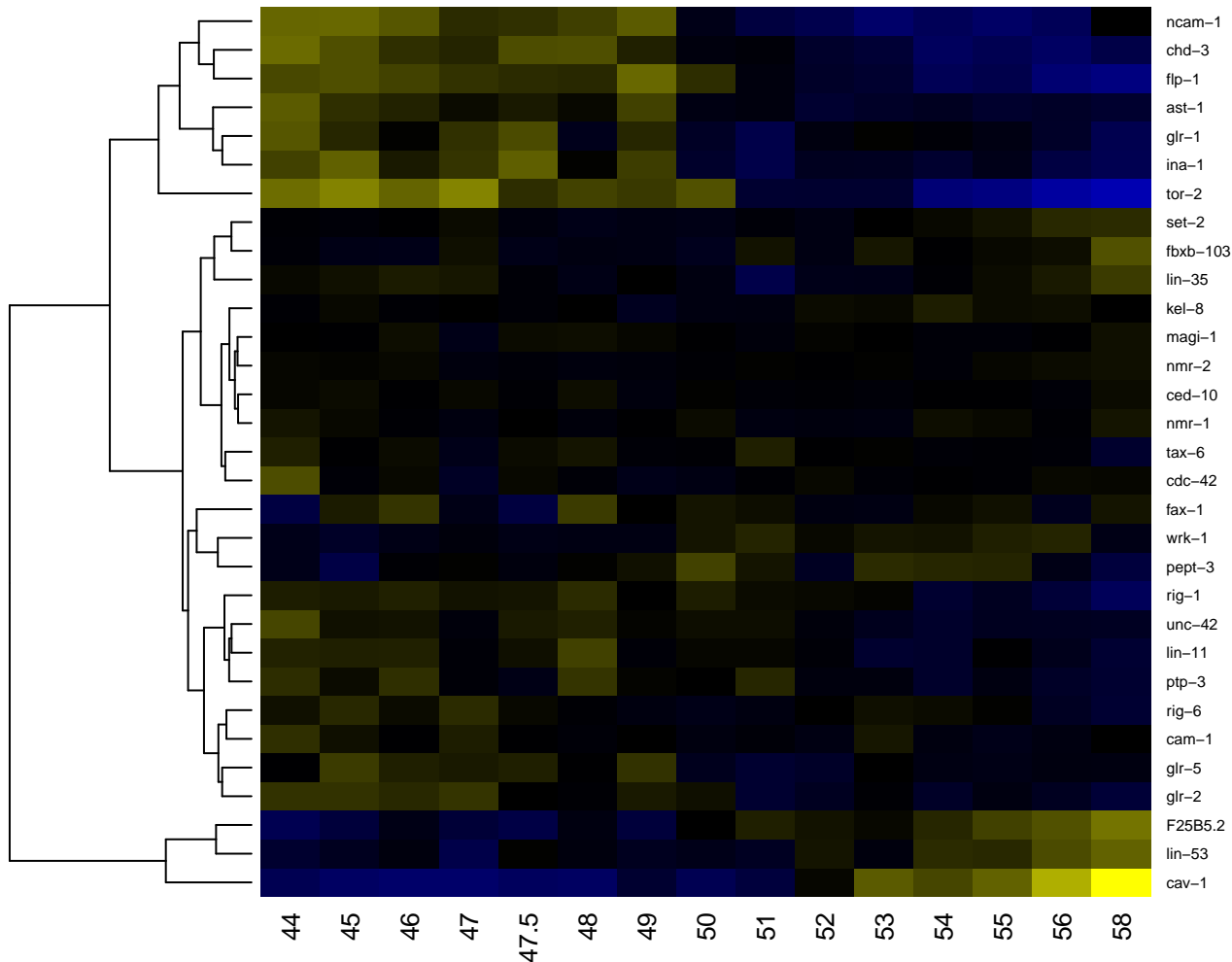
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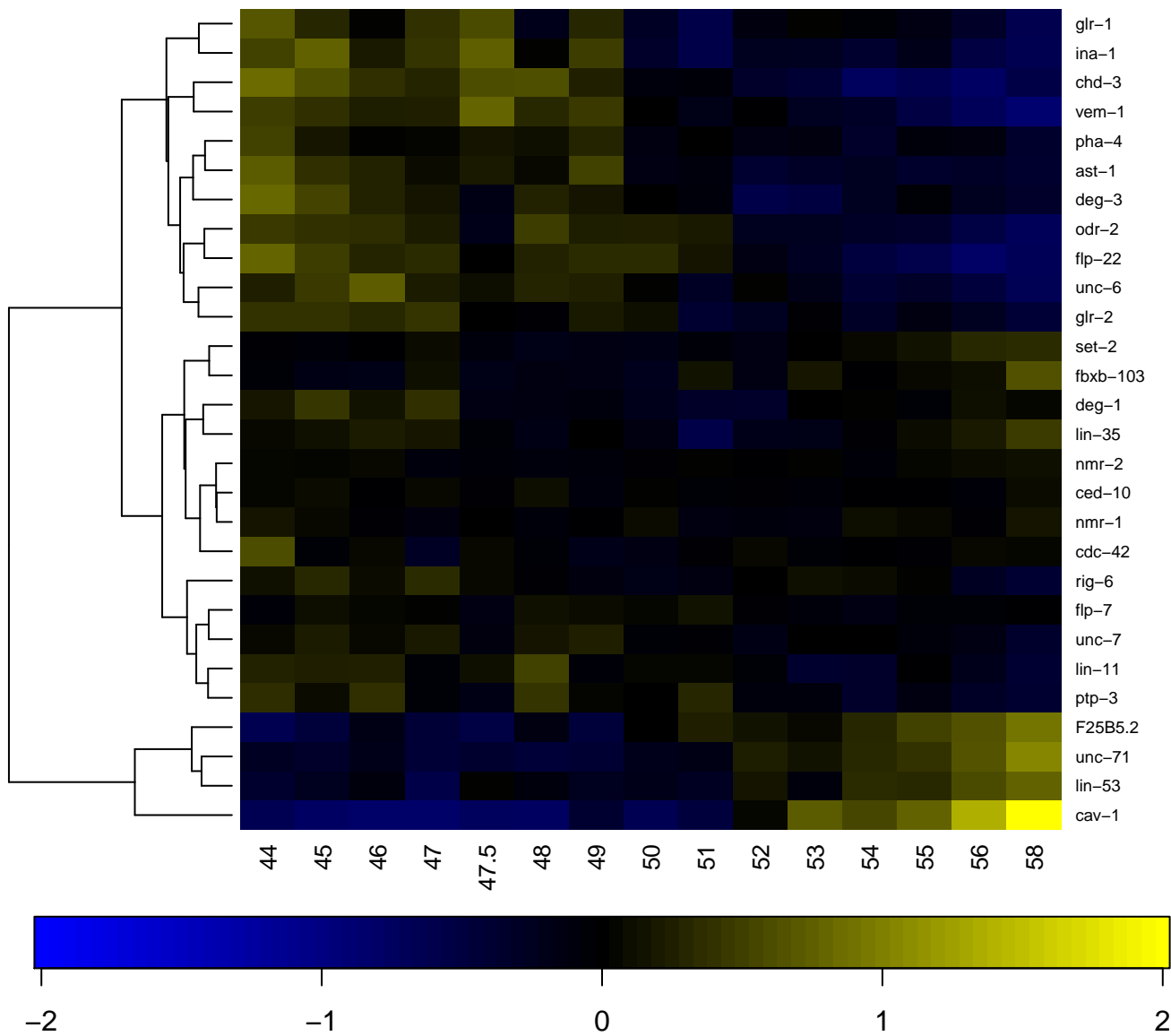
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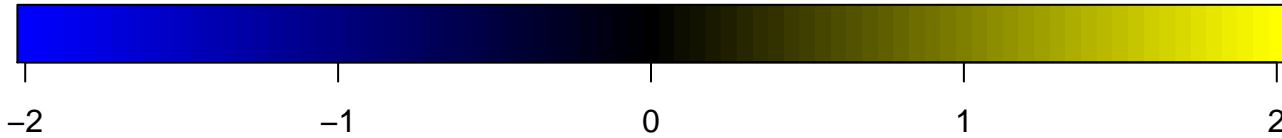
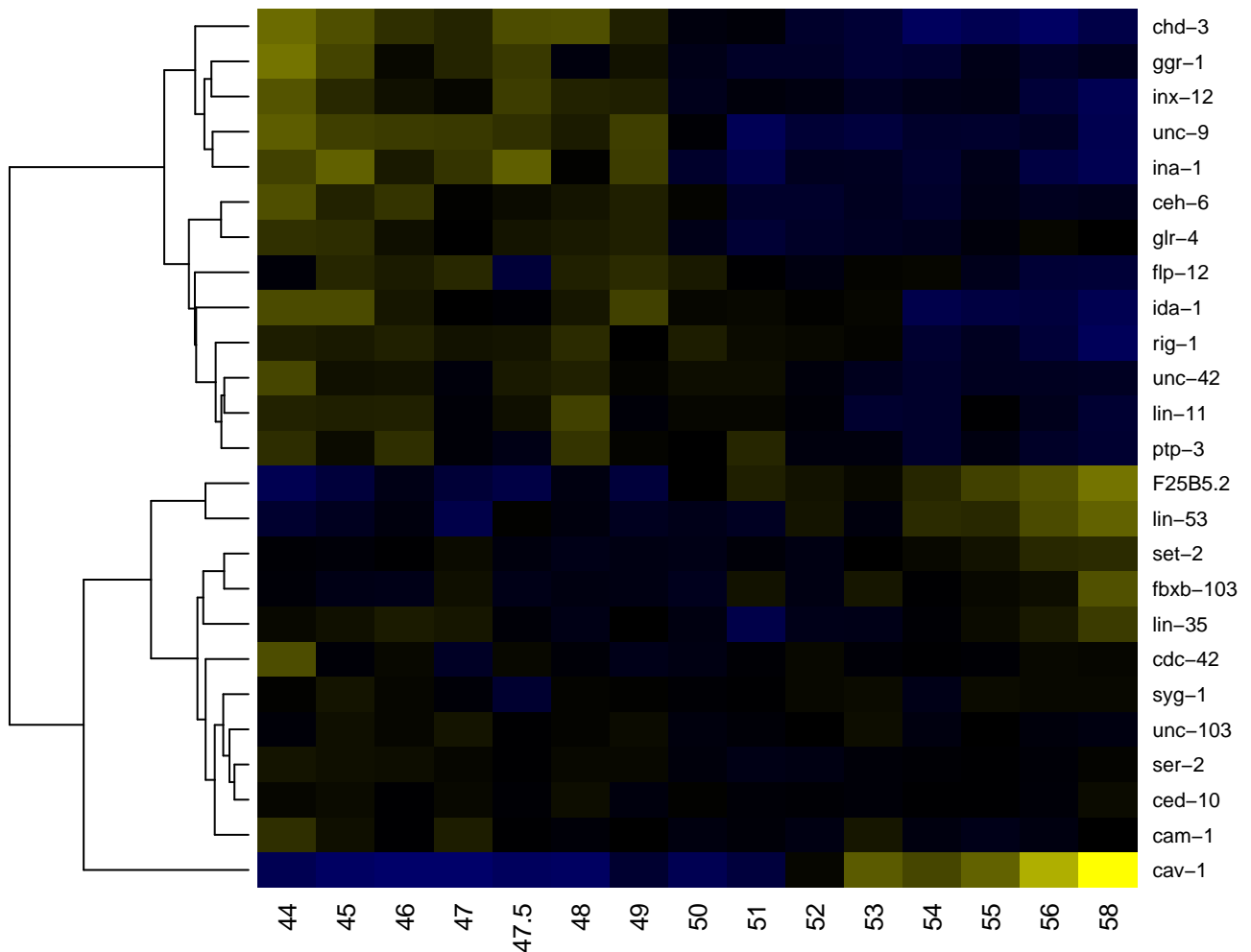
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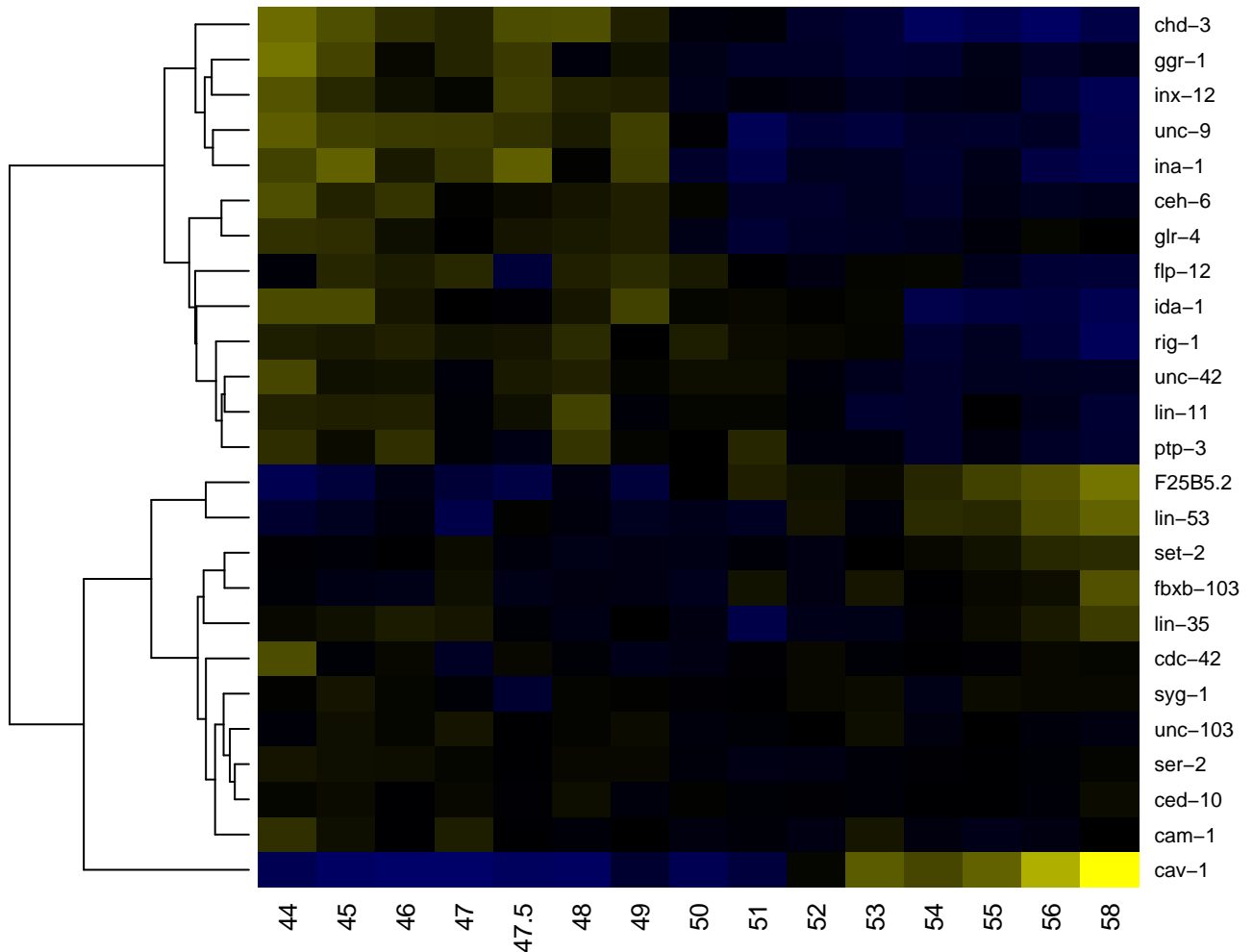
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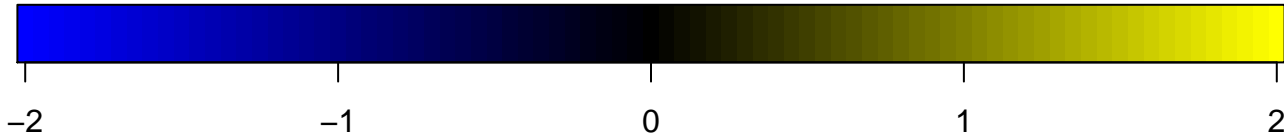
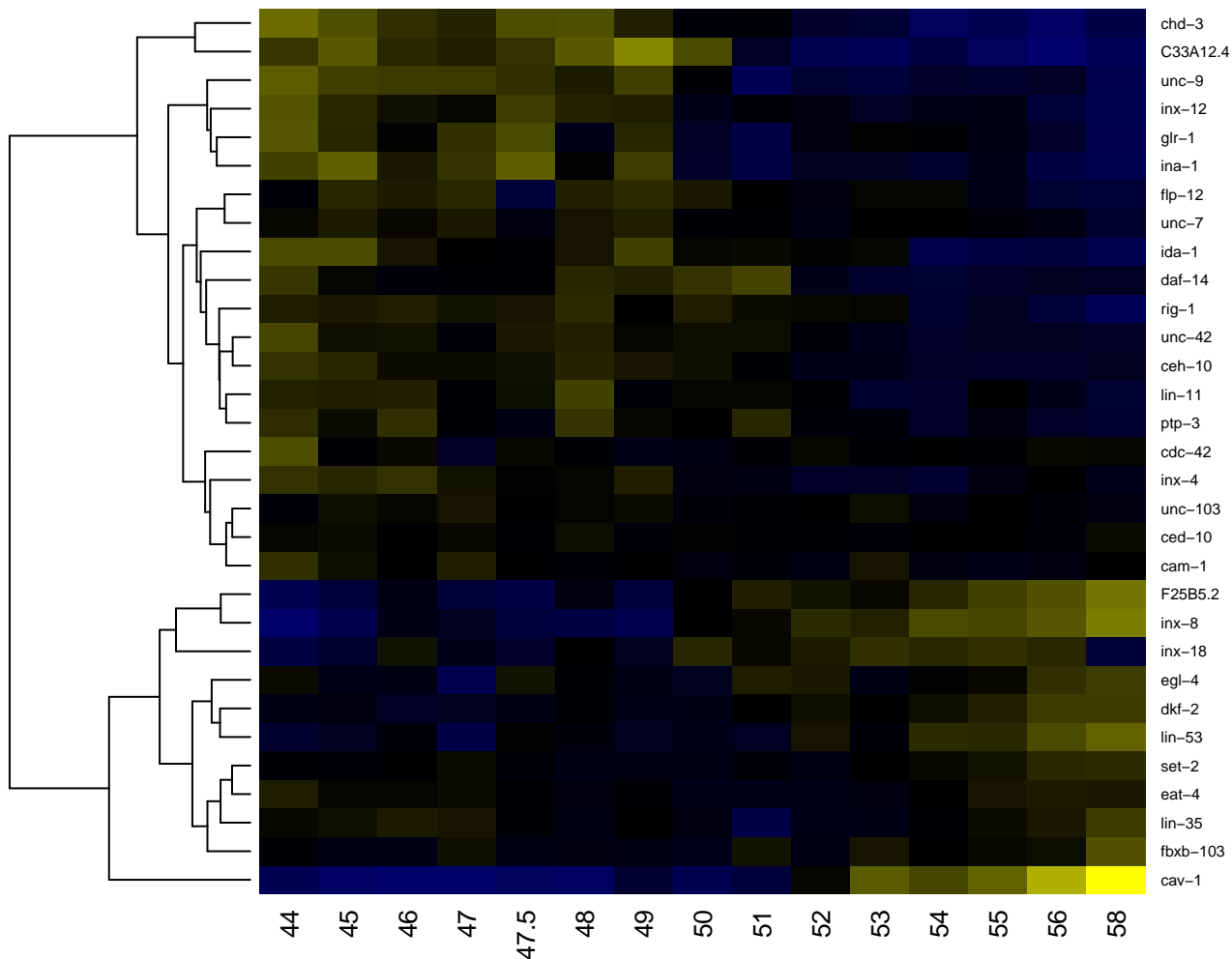
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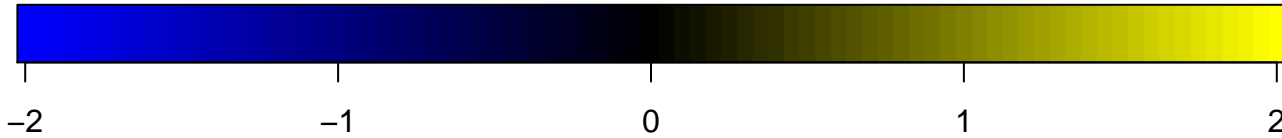
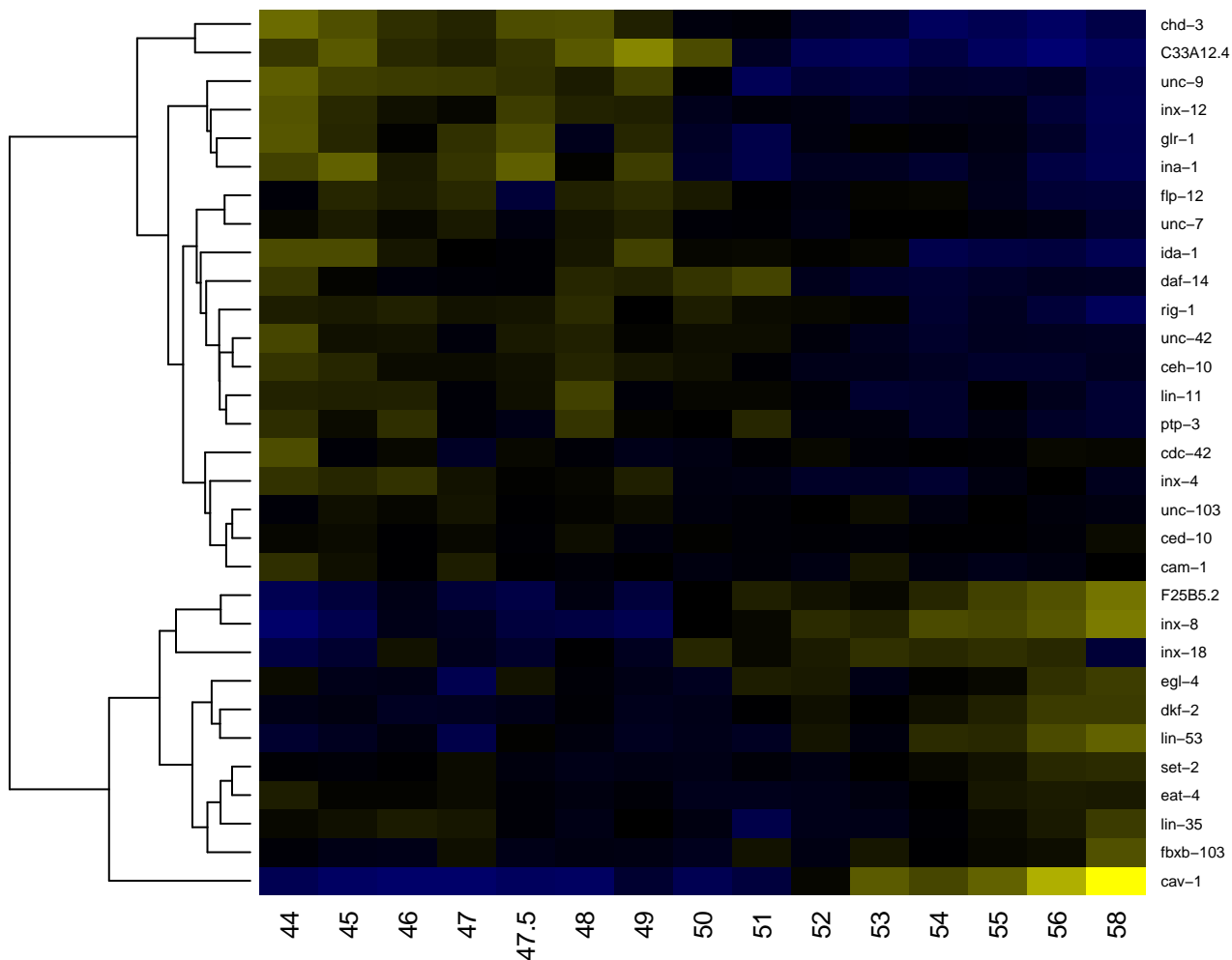
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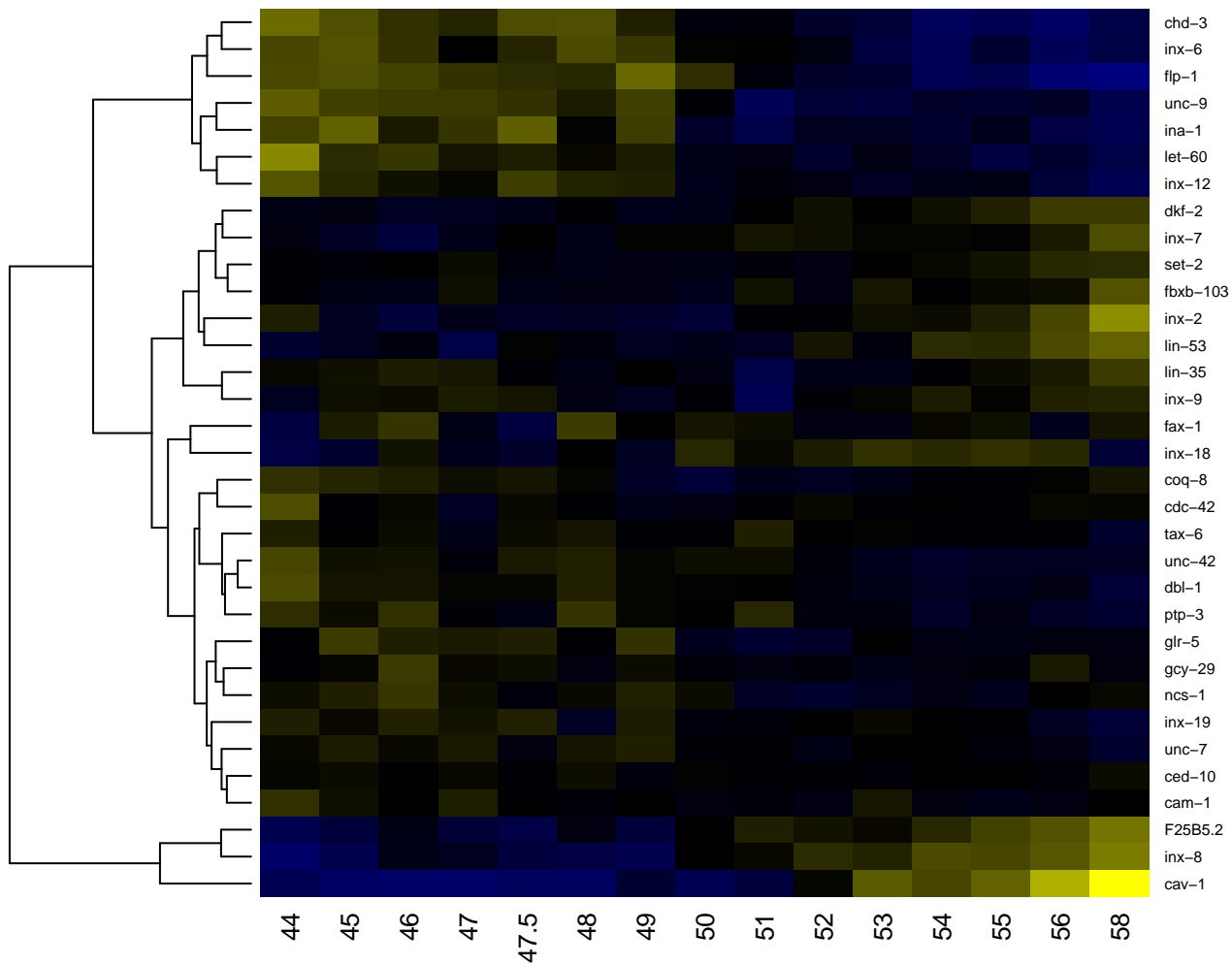
AVJL



AVJR



AVKL



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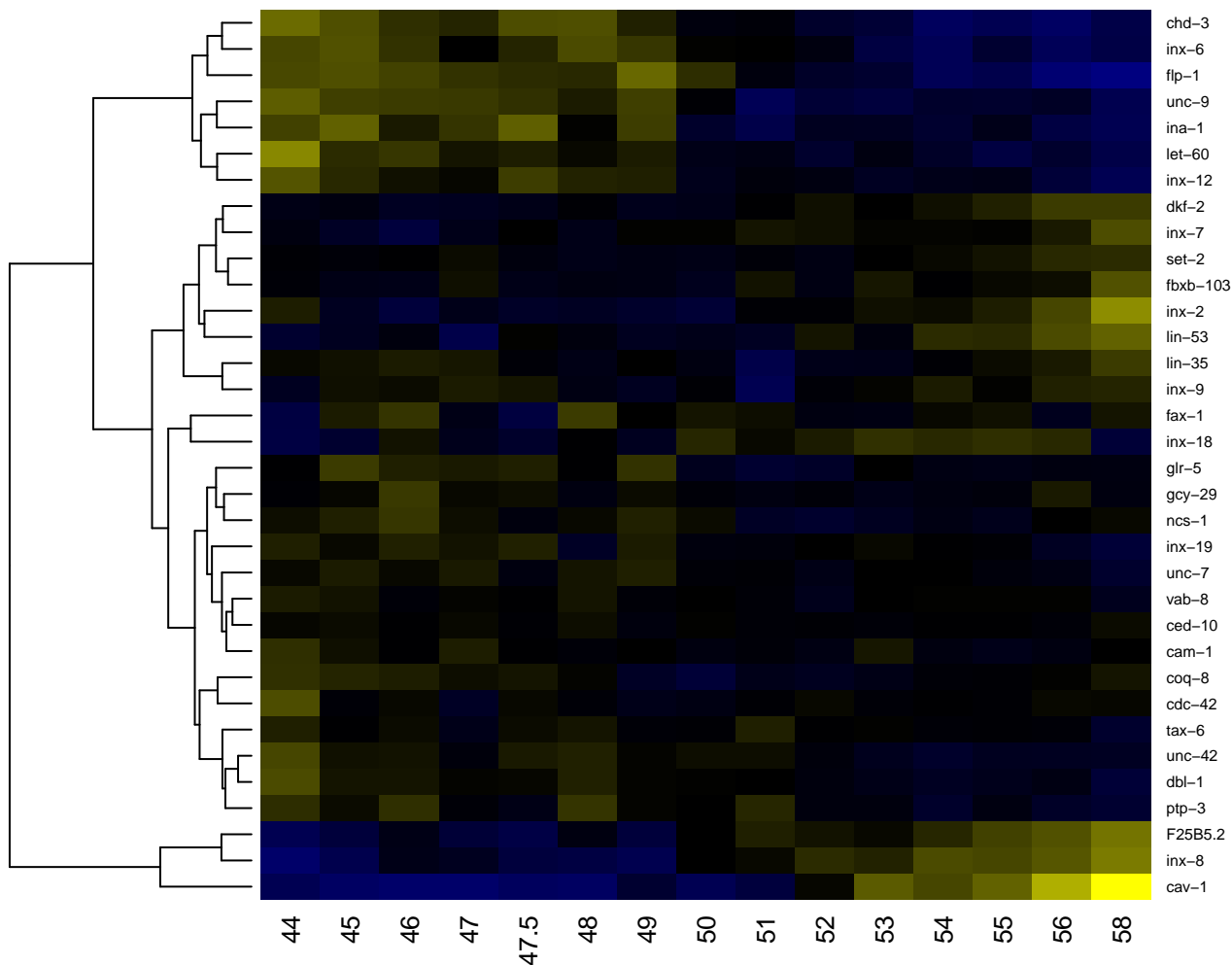
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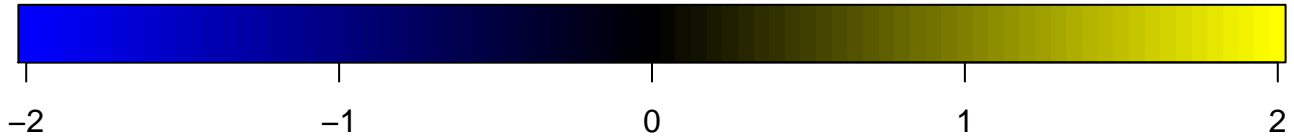
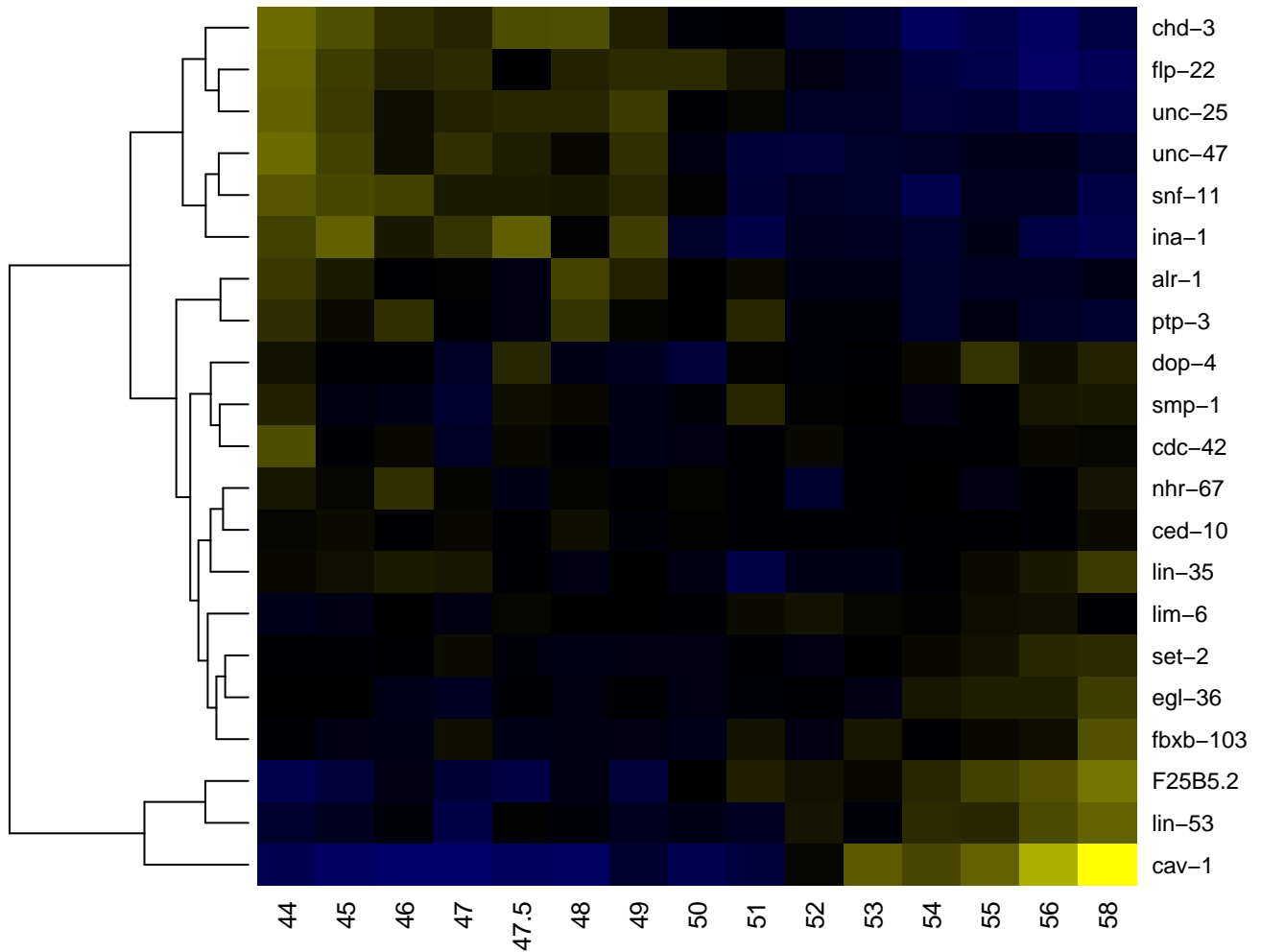
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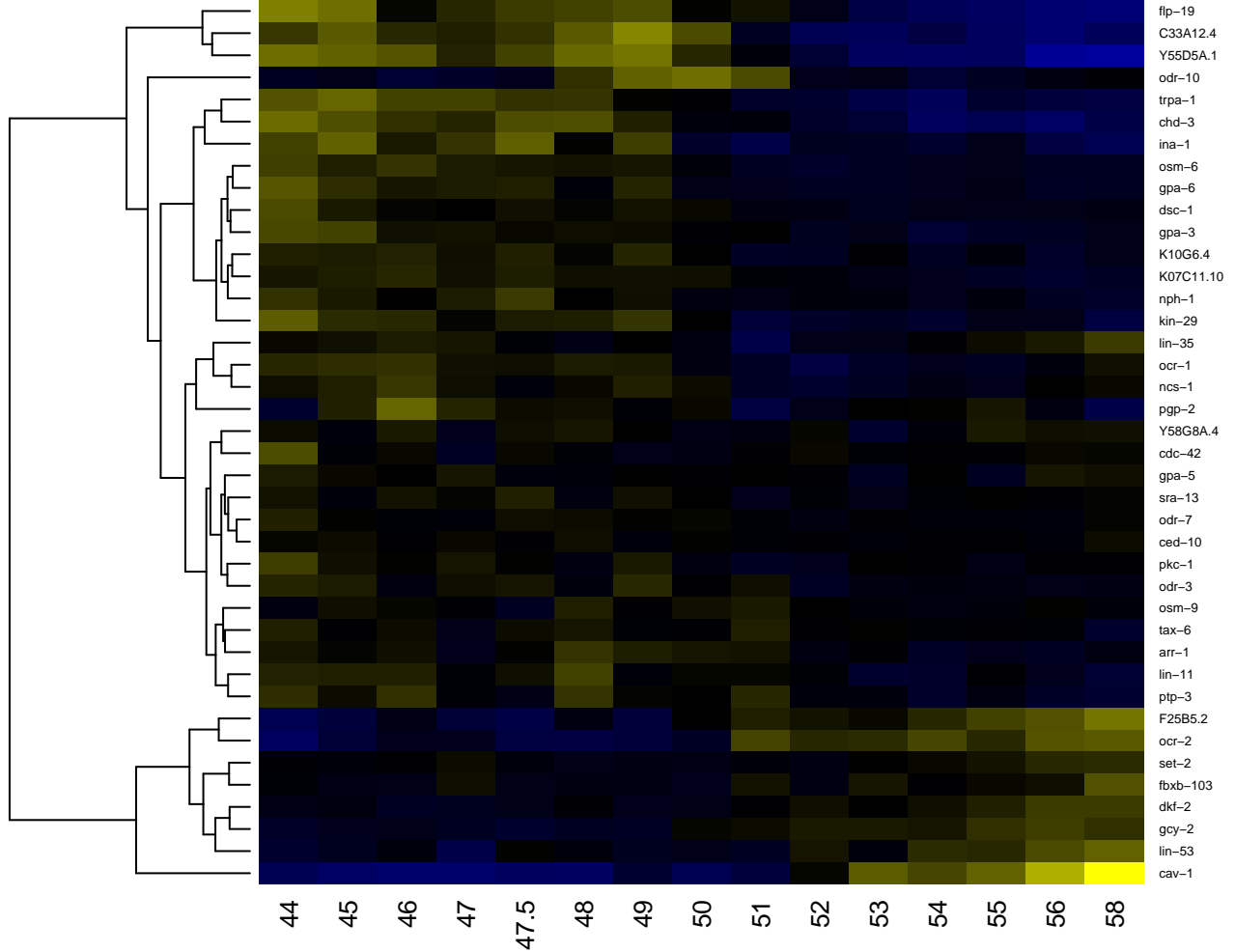
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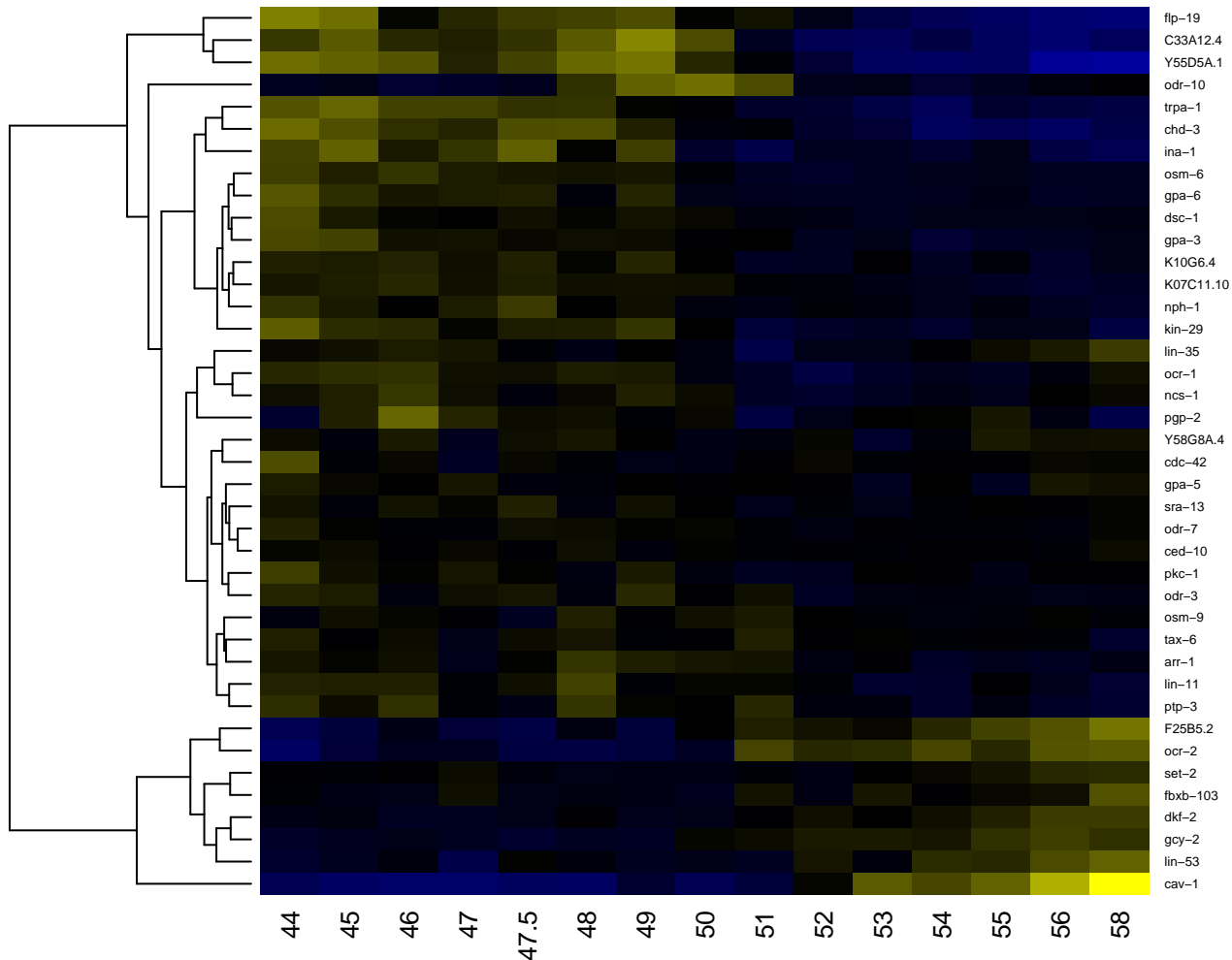
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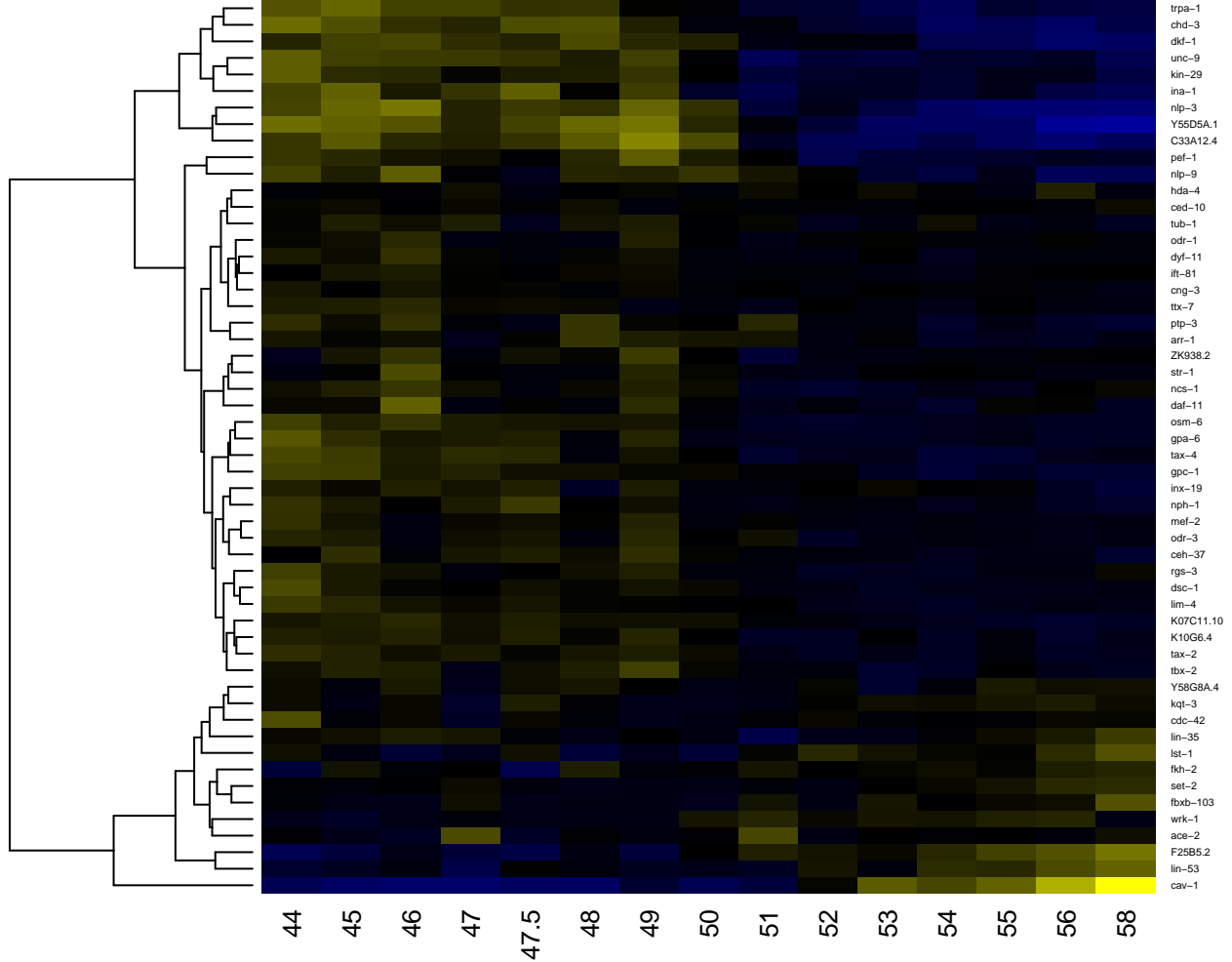
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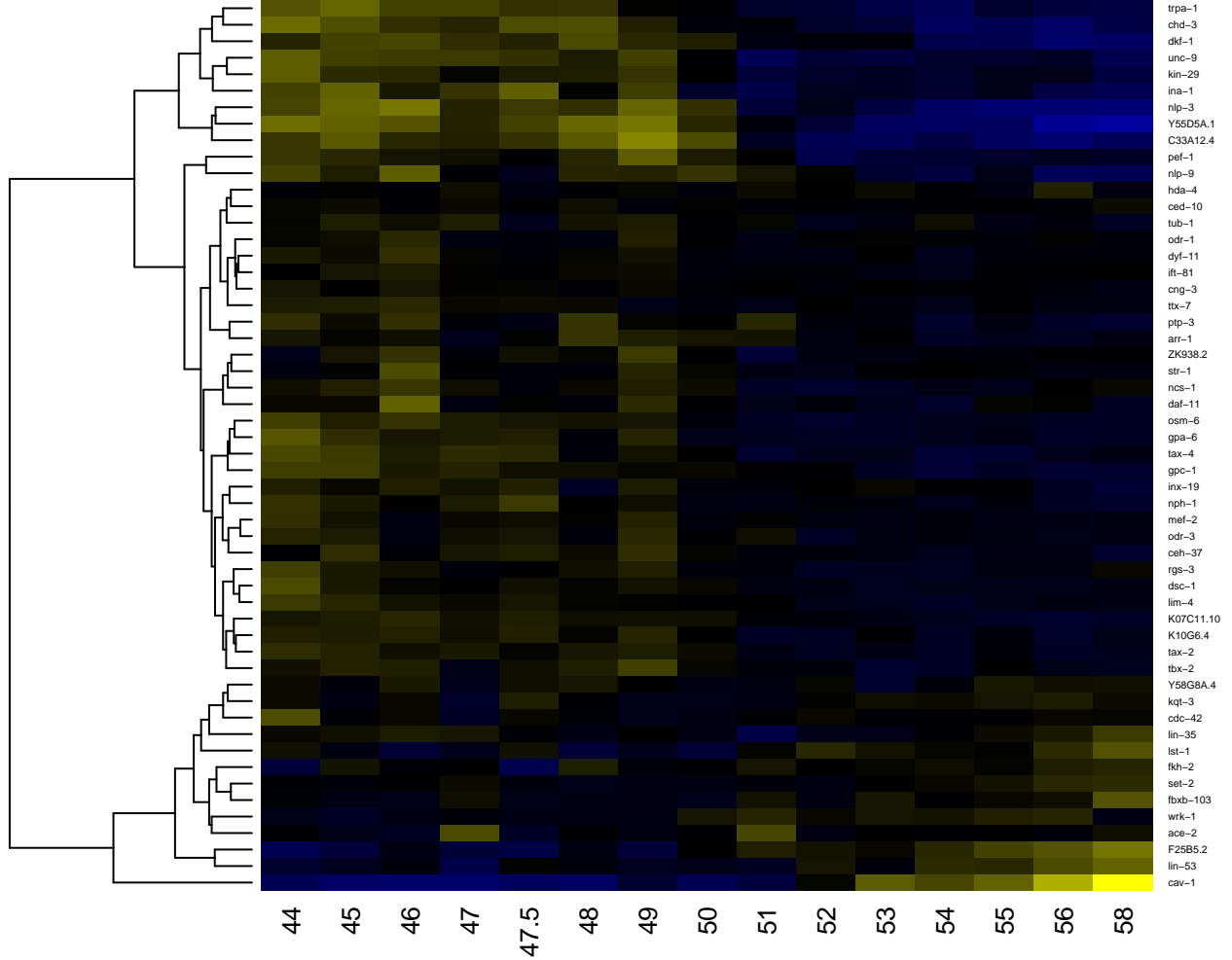
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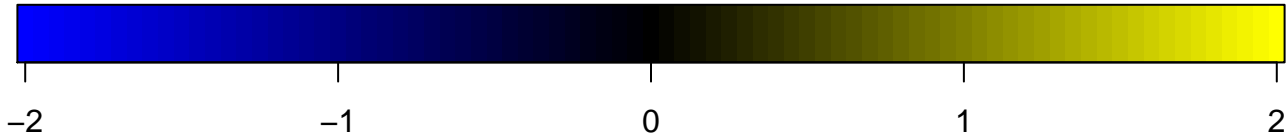
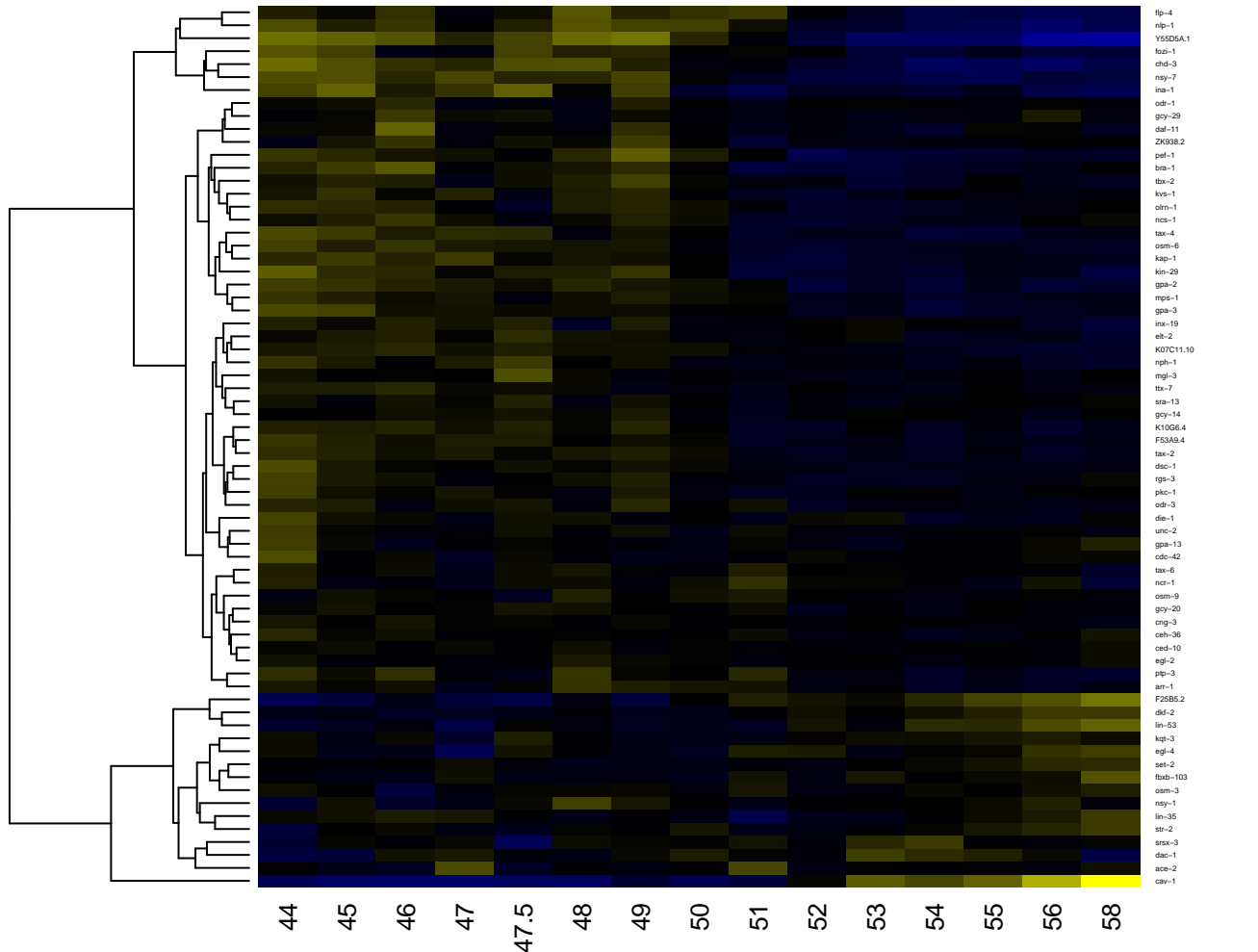
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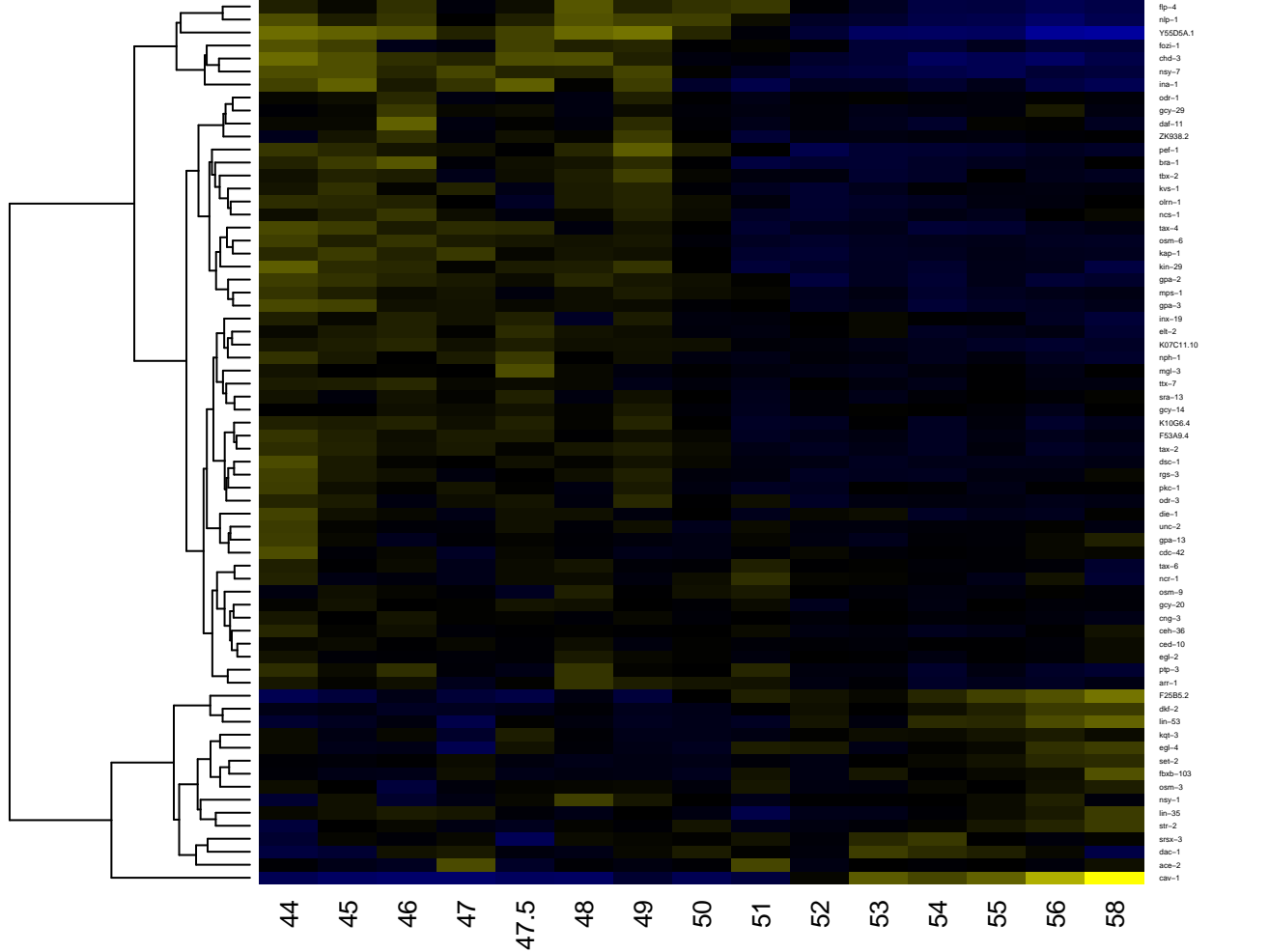
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AWCL



AWCR



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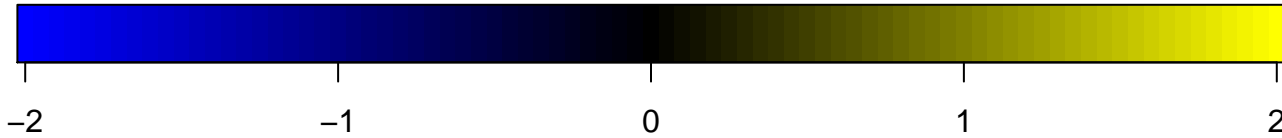
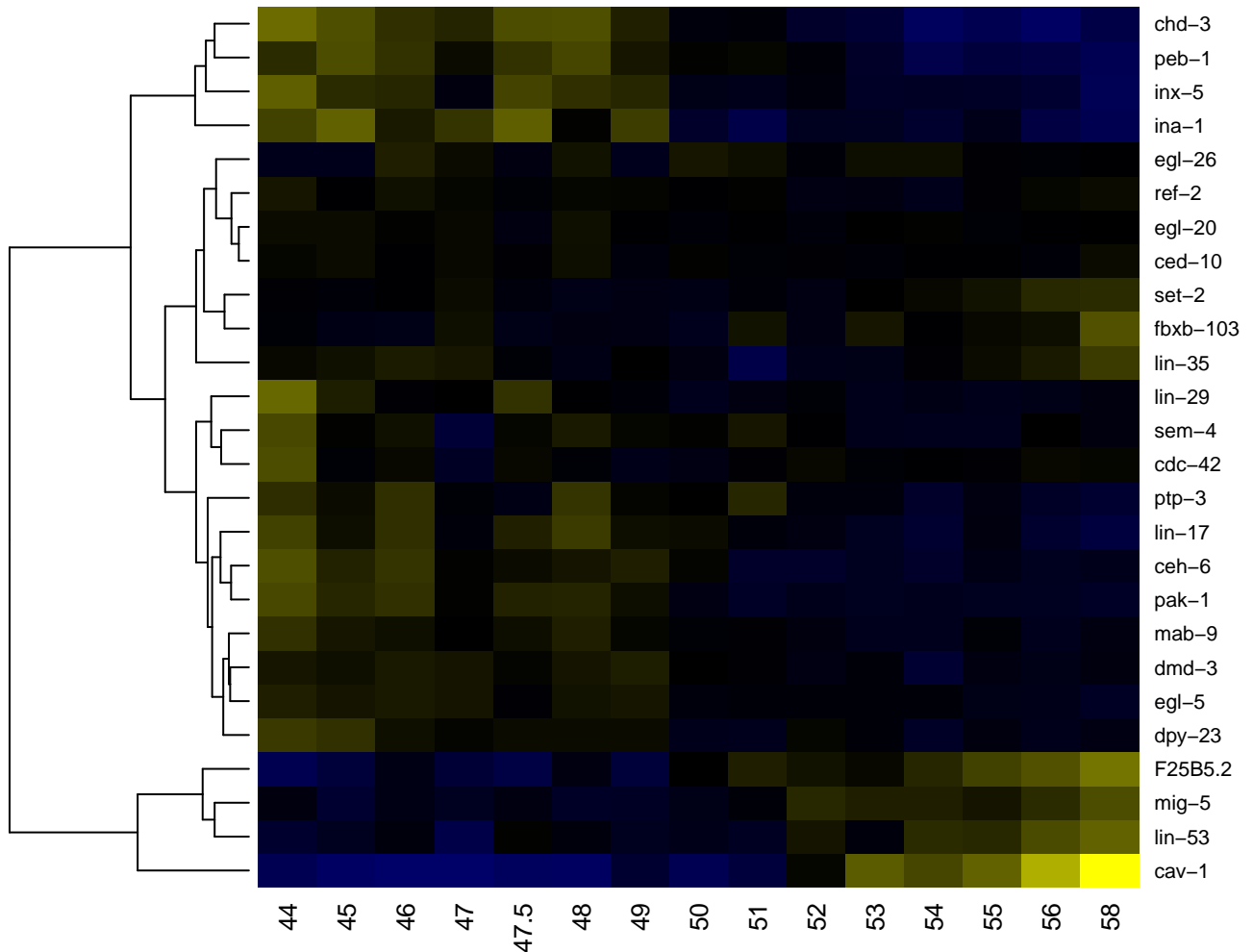
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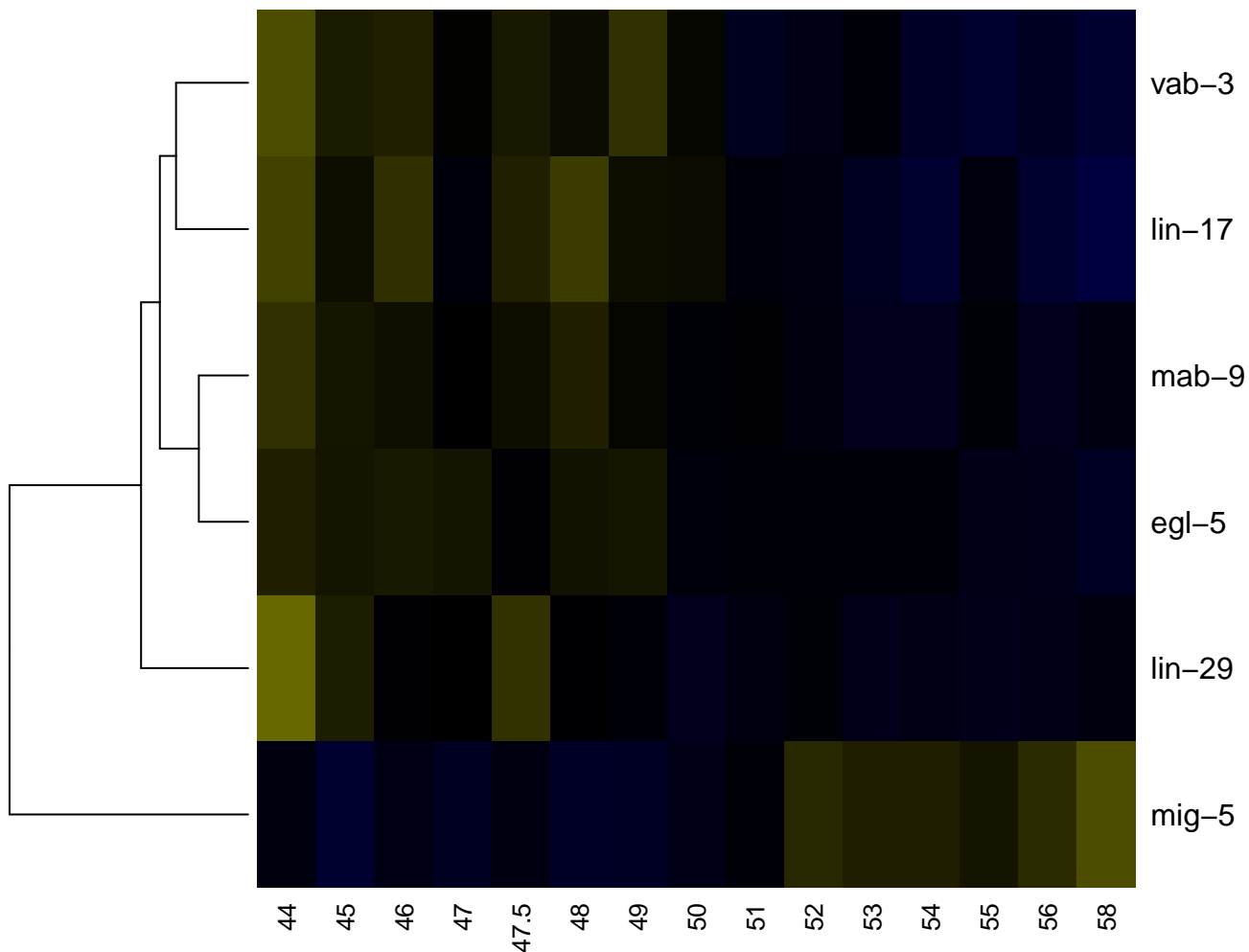
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B cell



B.a



-2

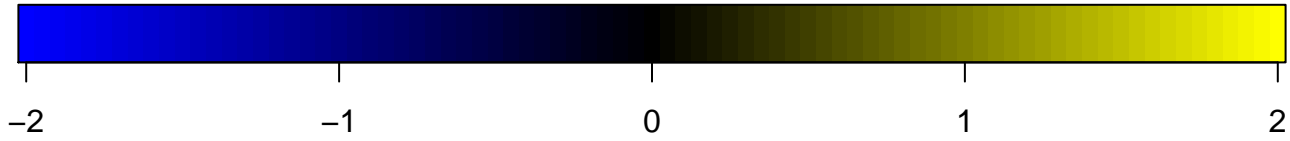
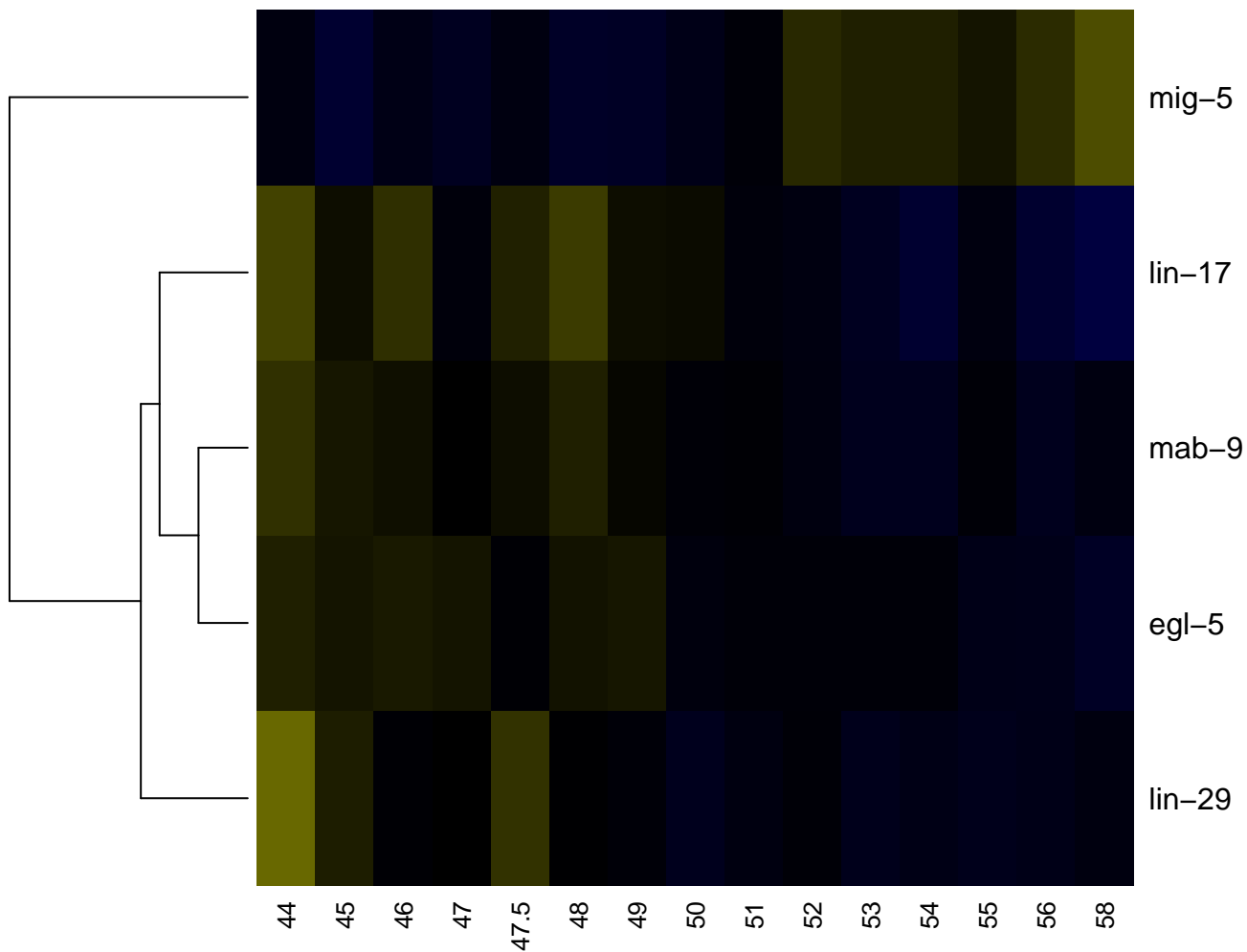
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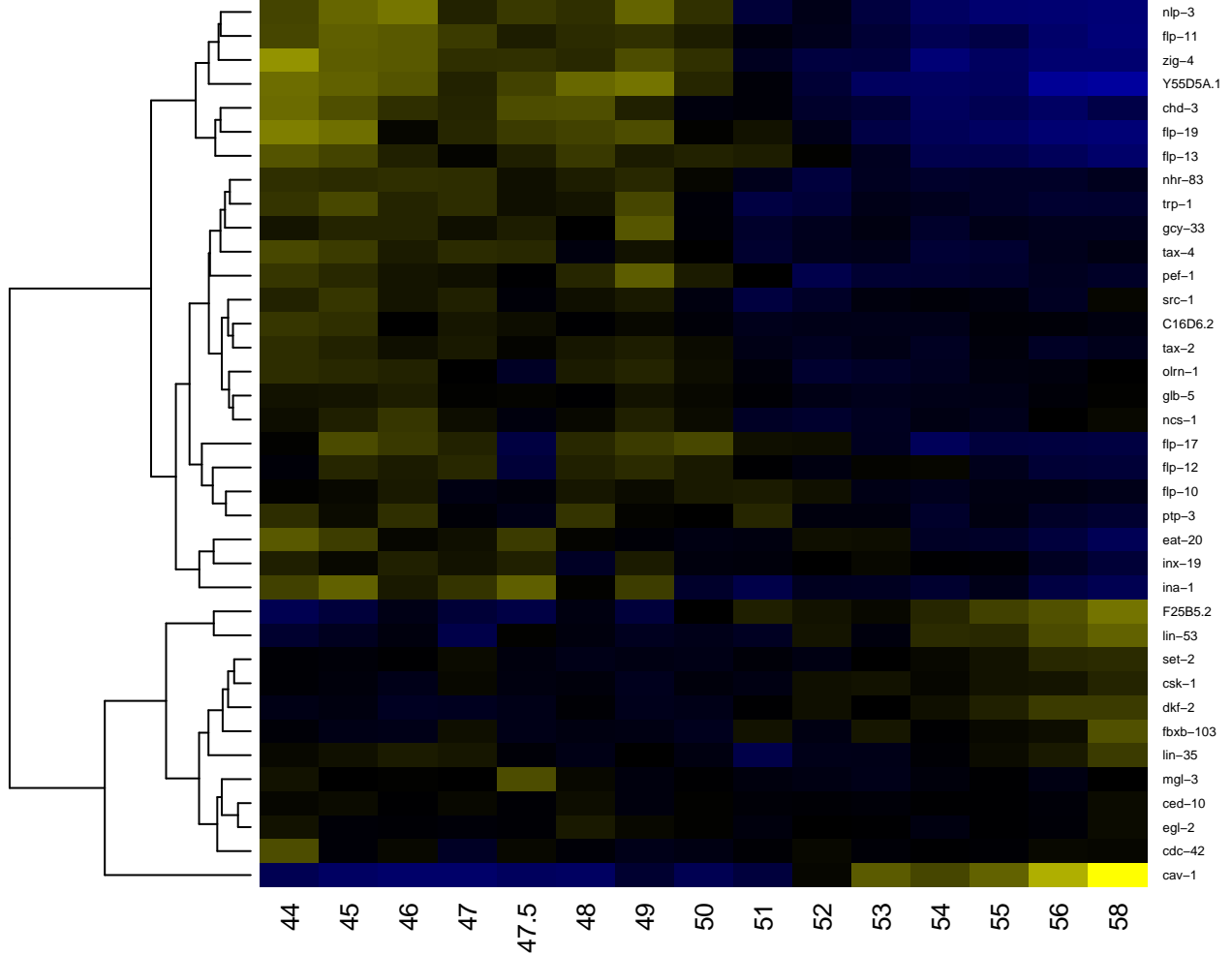
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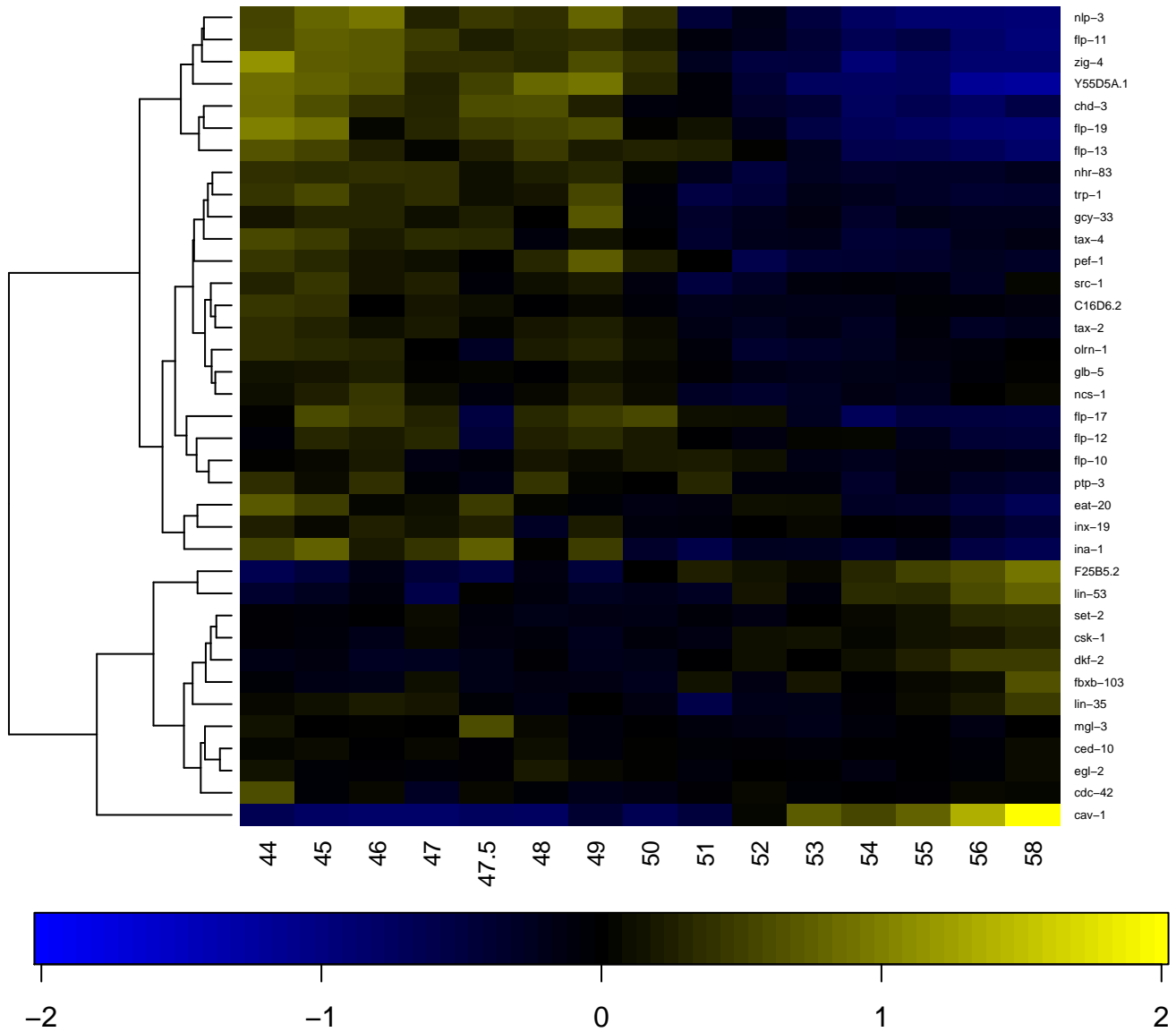
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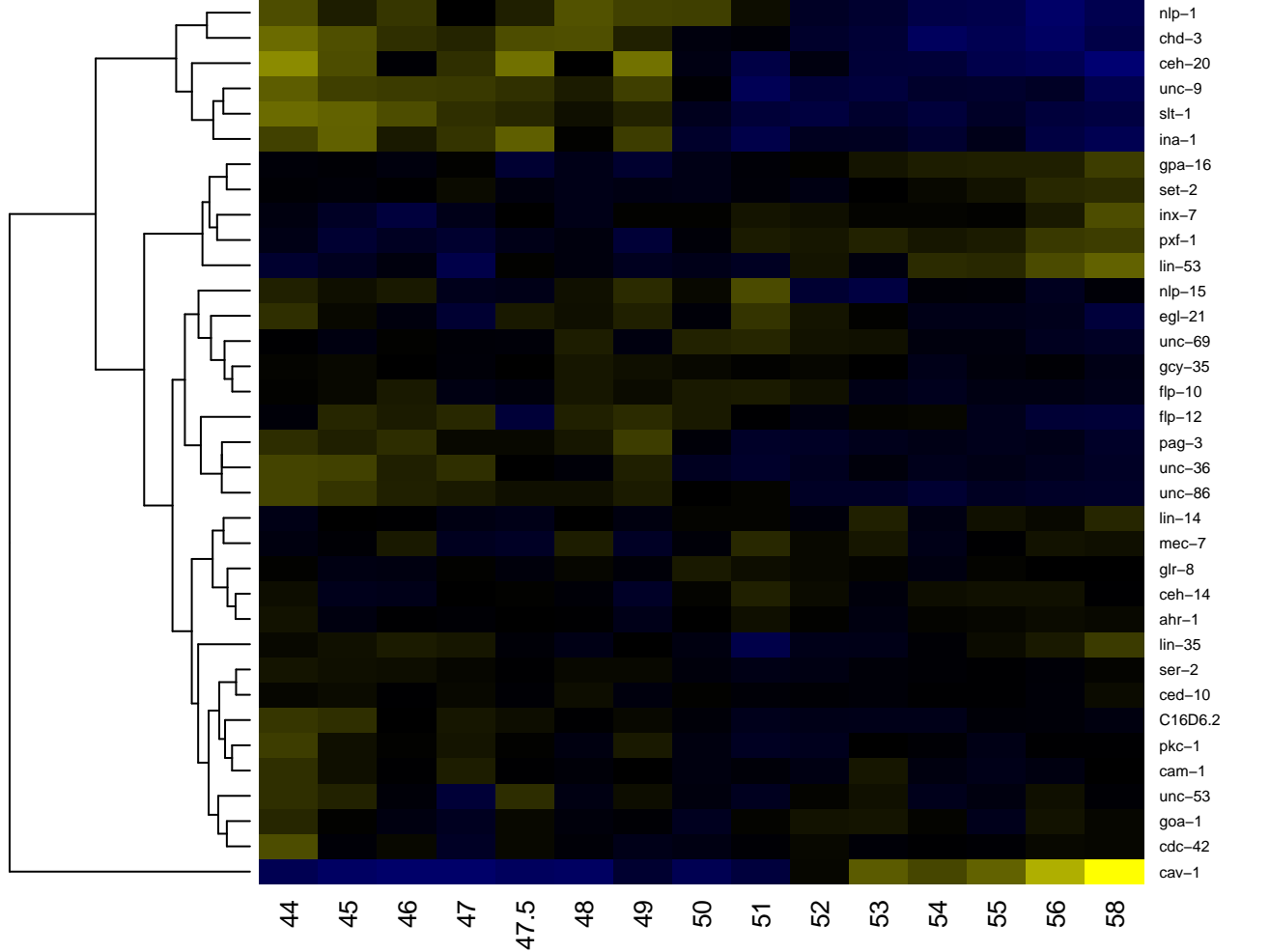
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BAGR



BDUL



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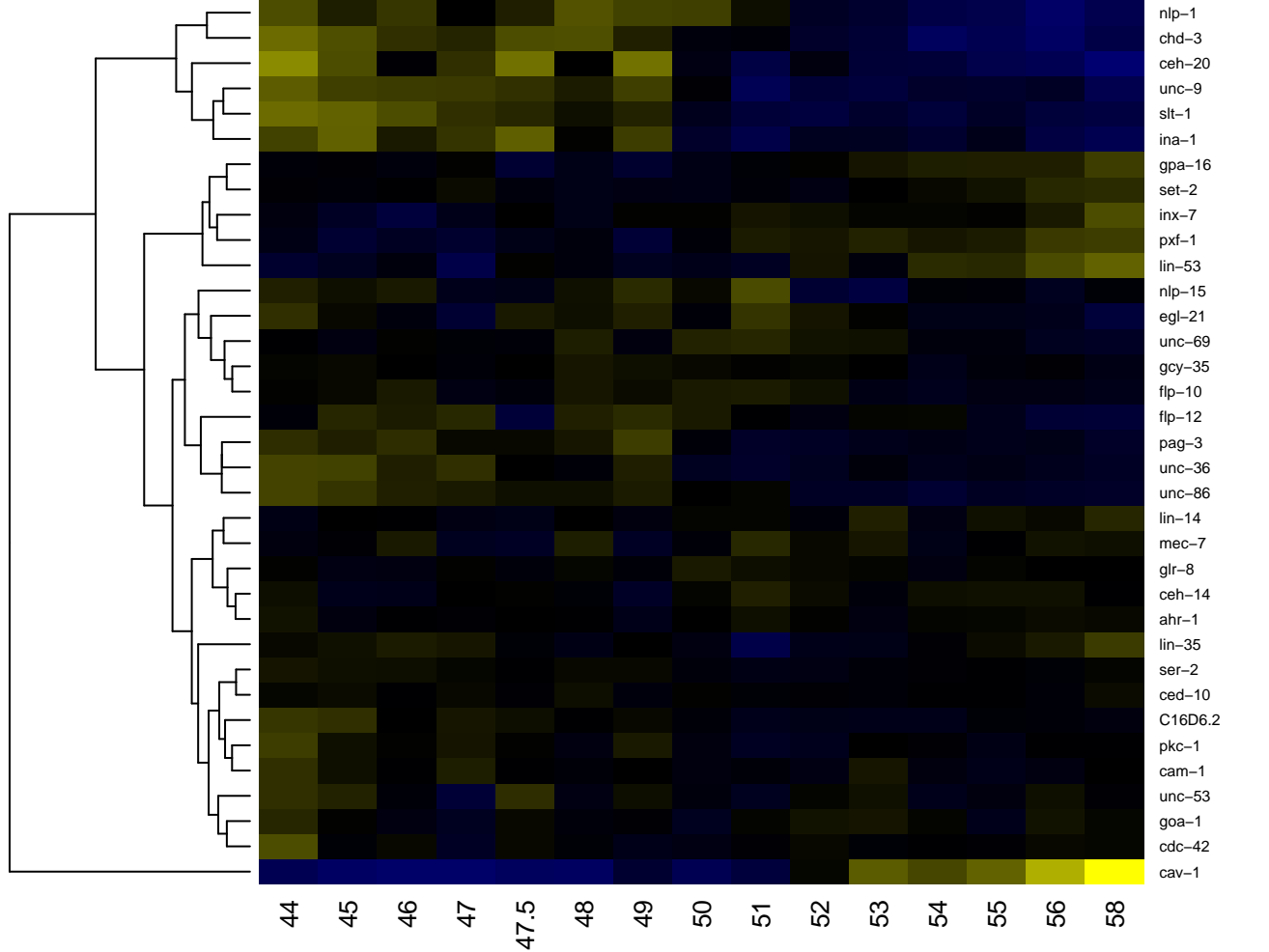
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BDUR



-2

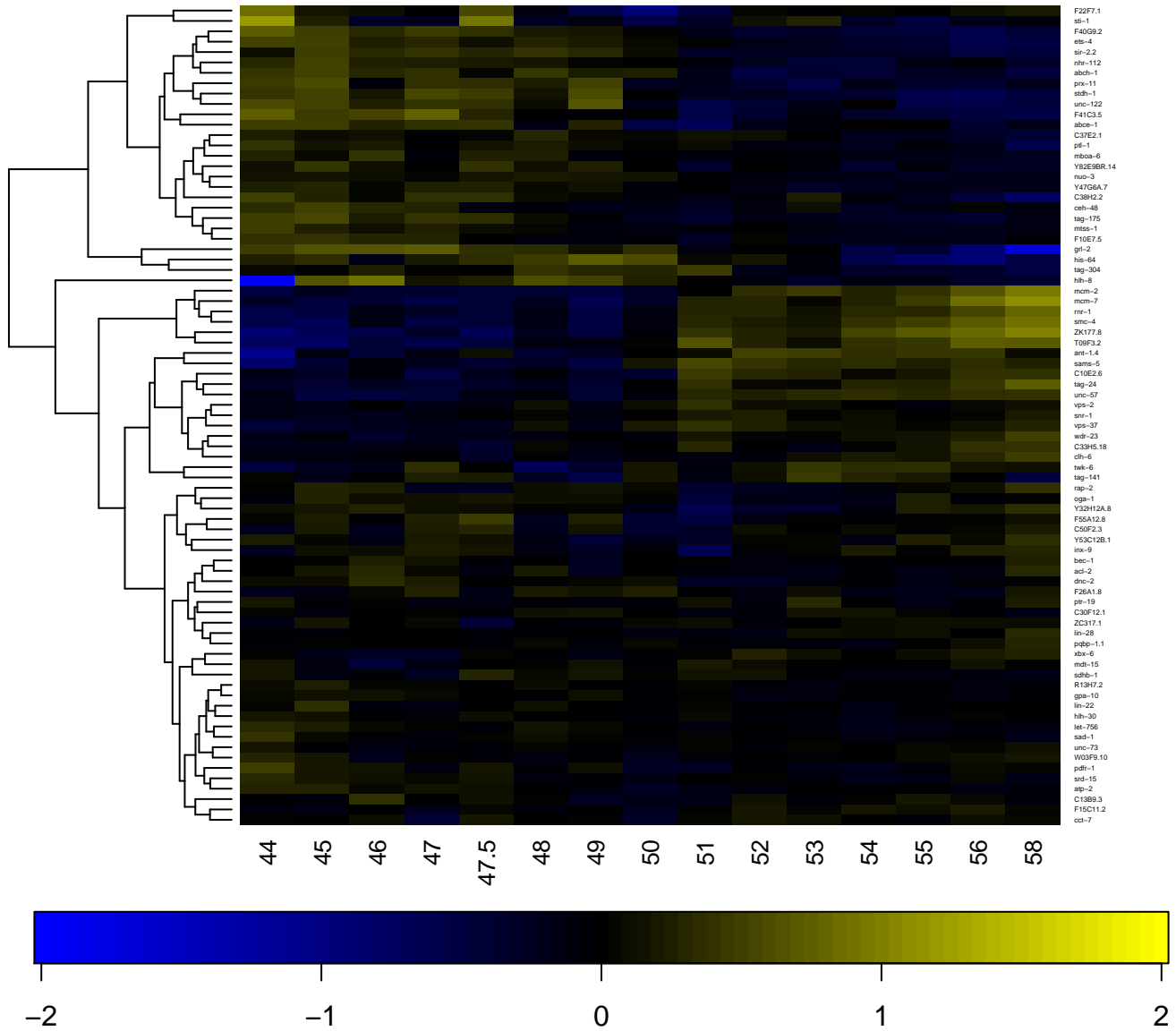
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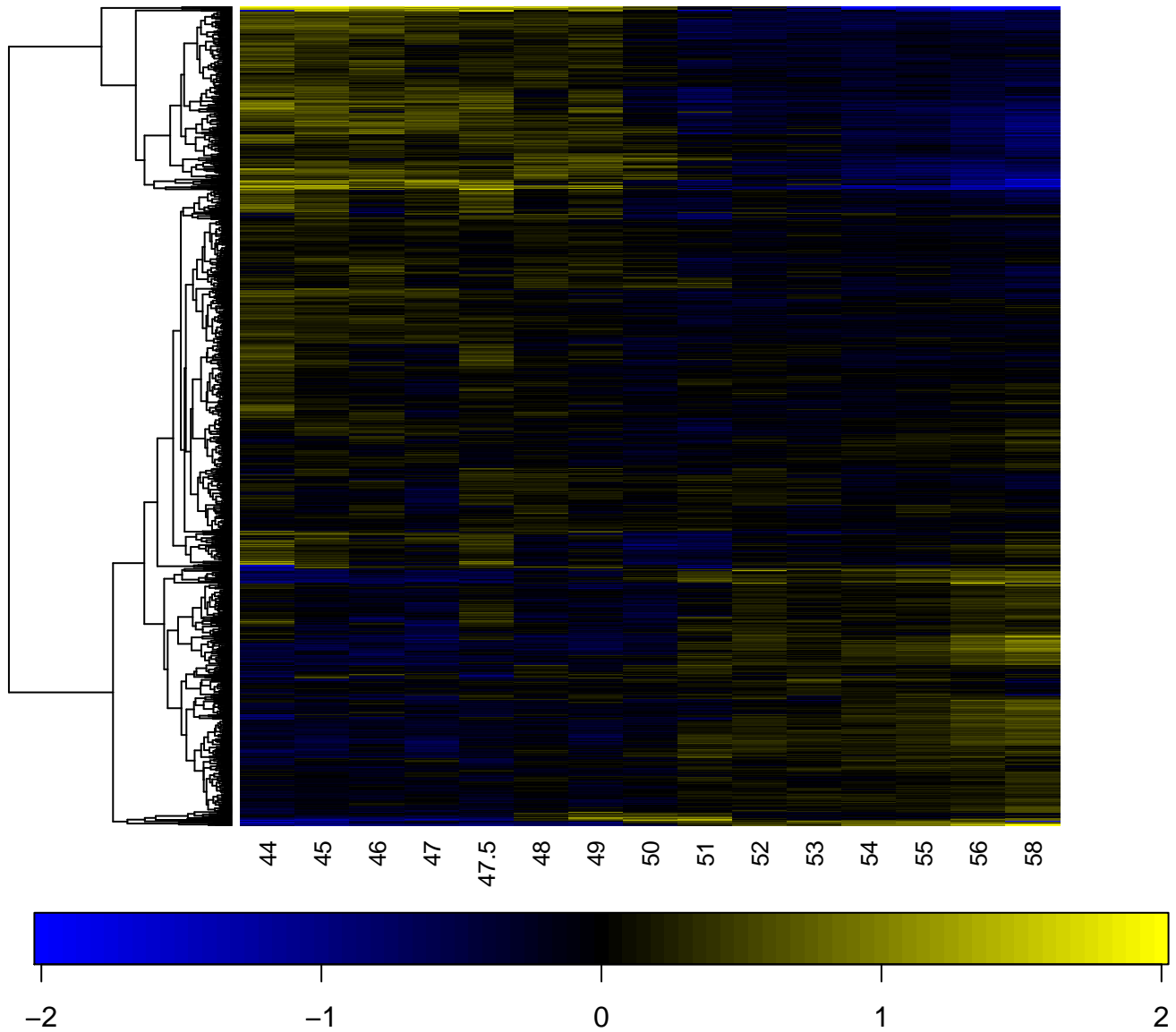
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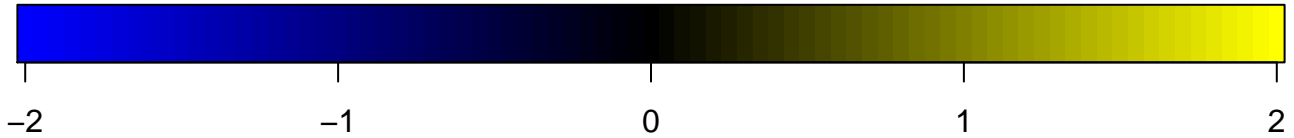
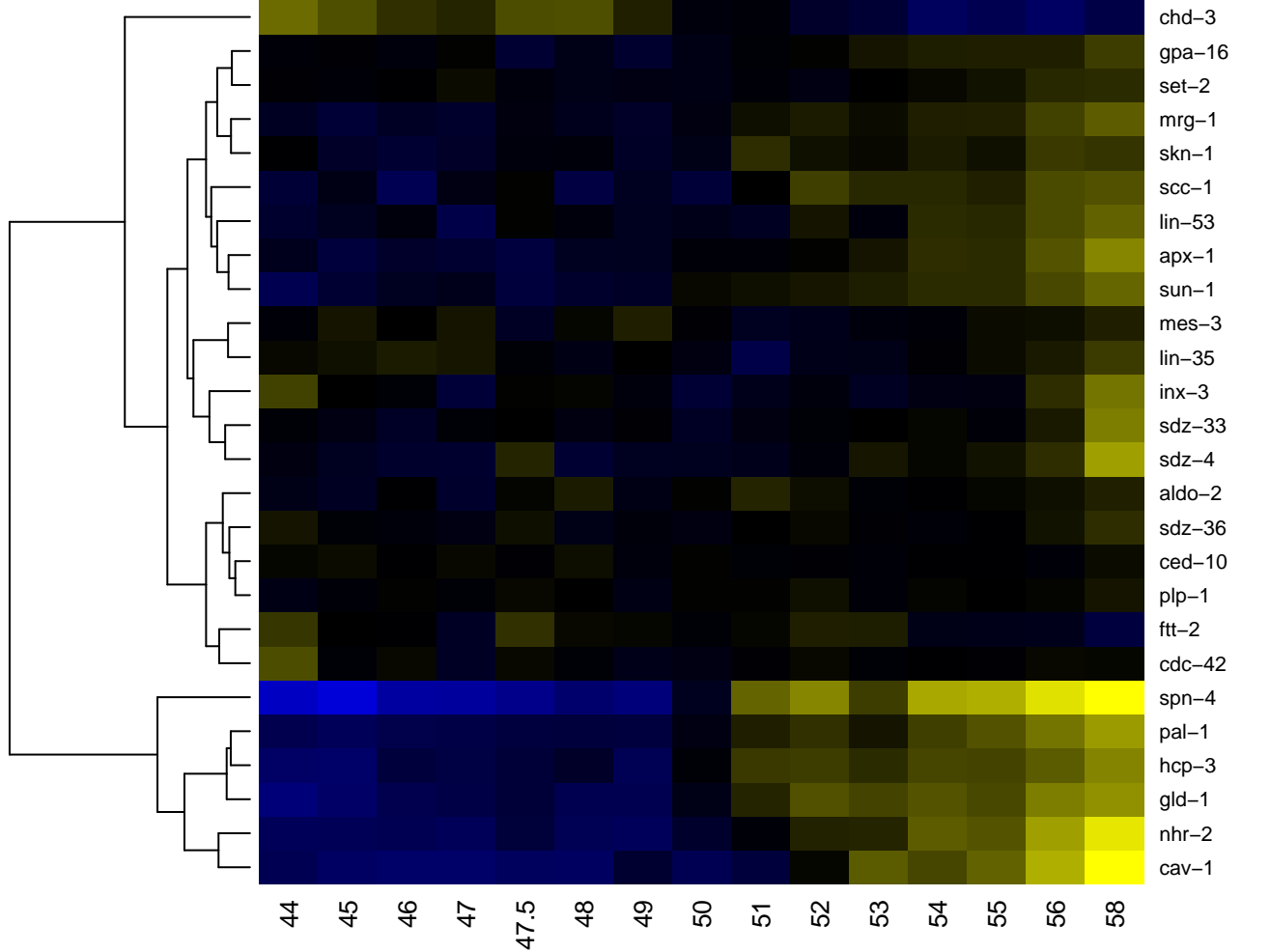
body region



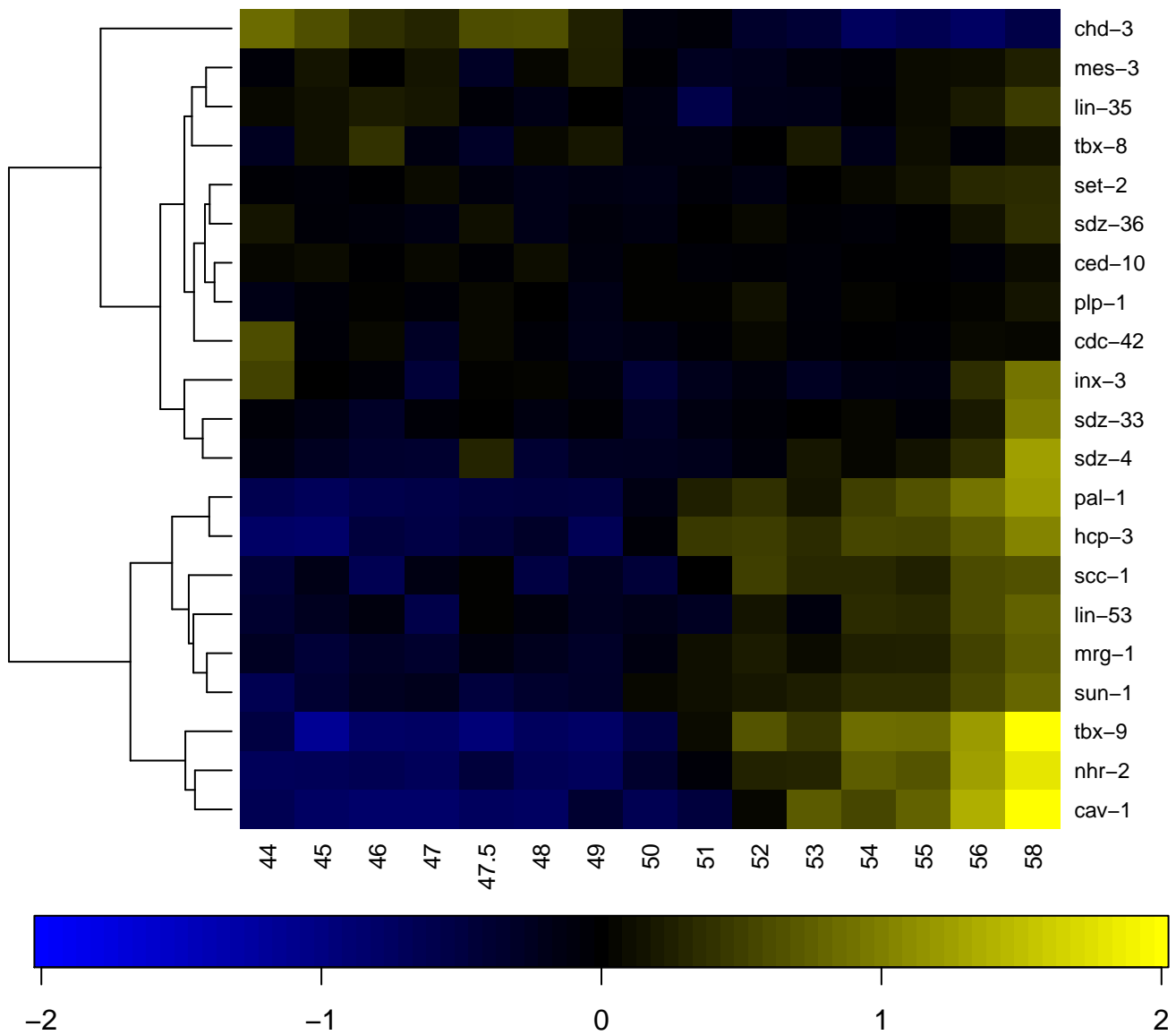
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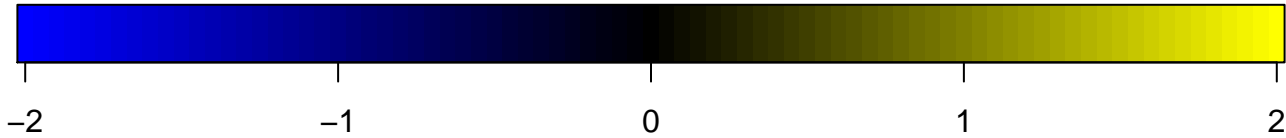
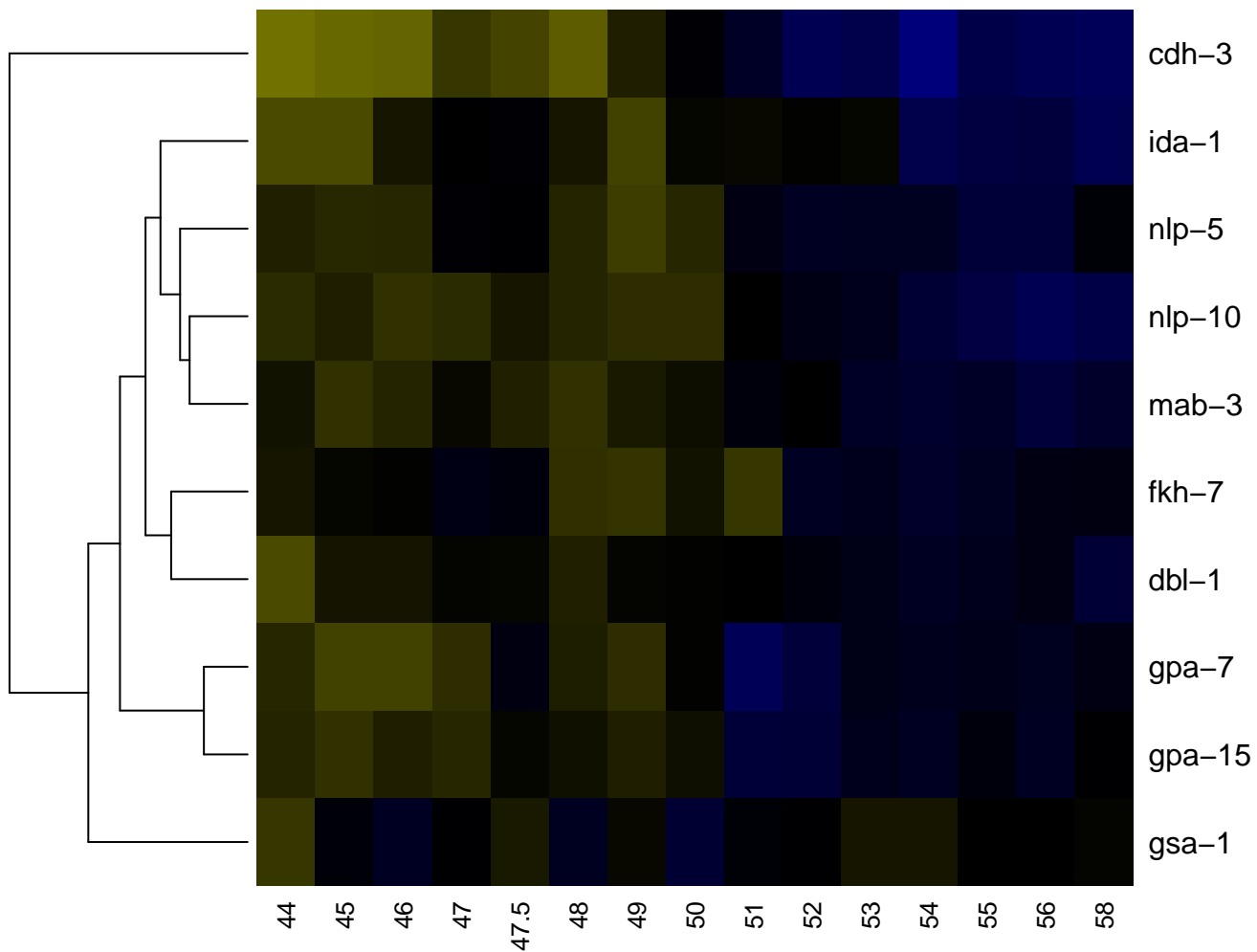
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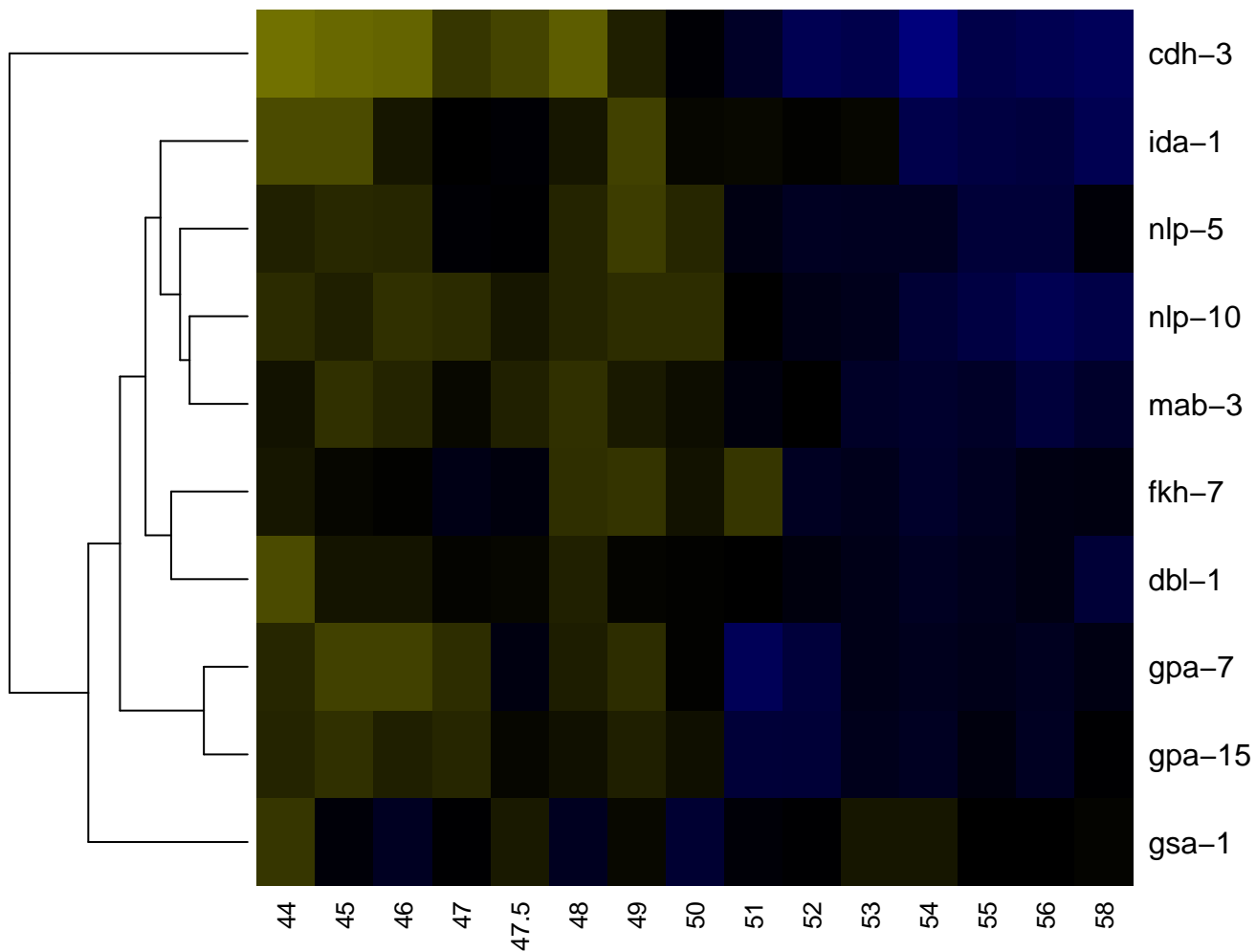
Ca



CA1



CA2



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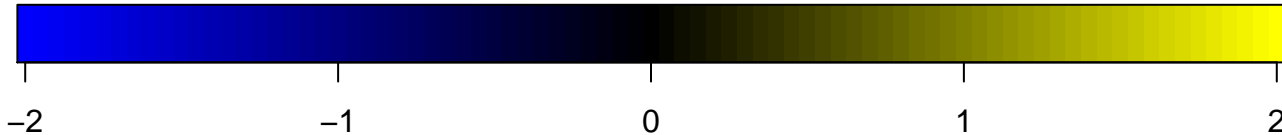
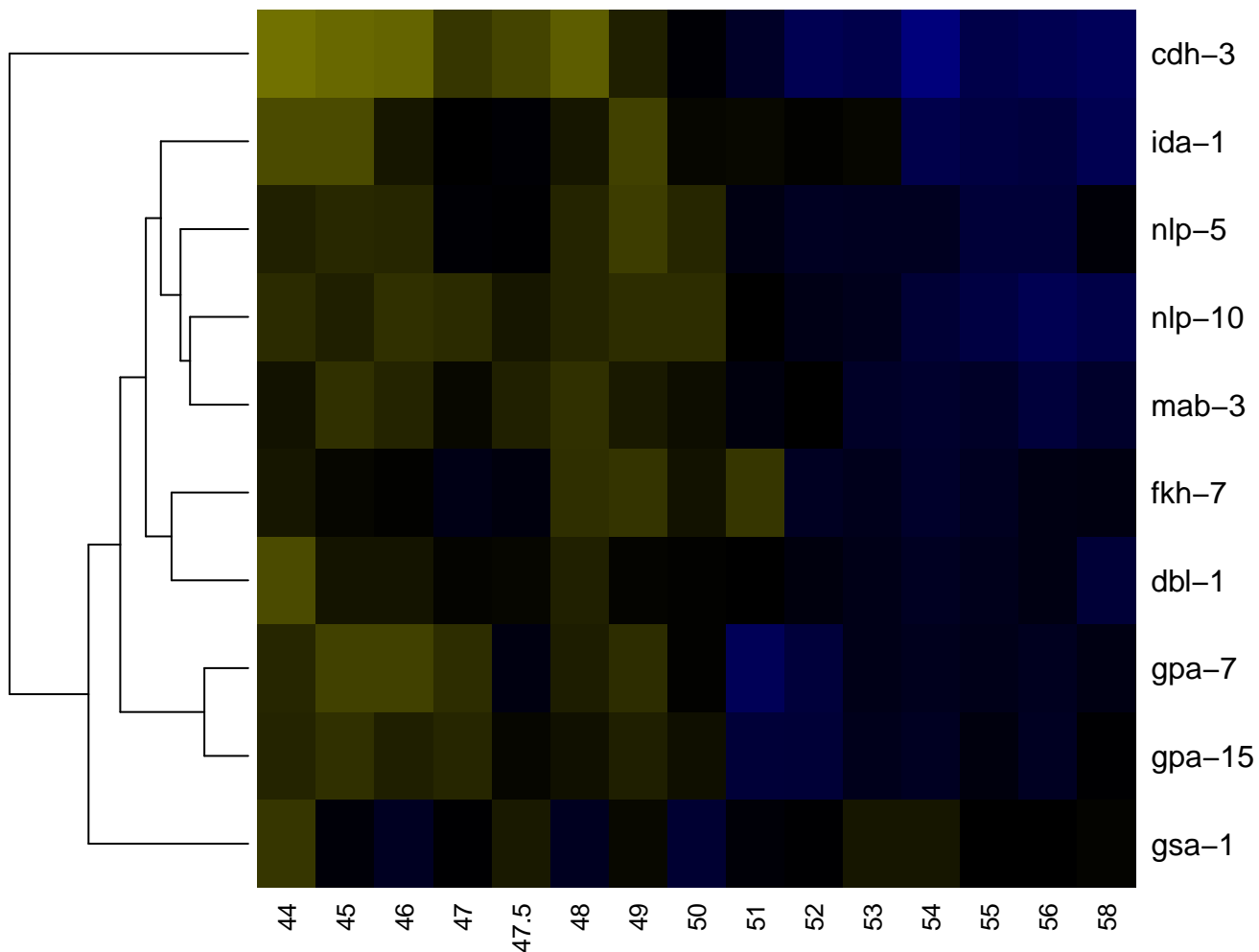
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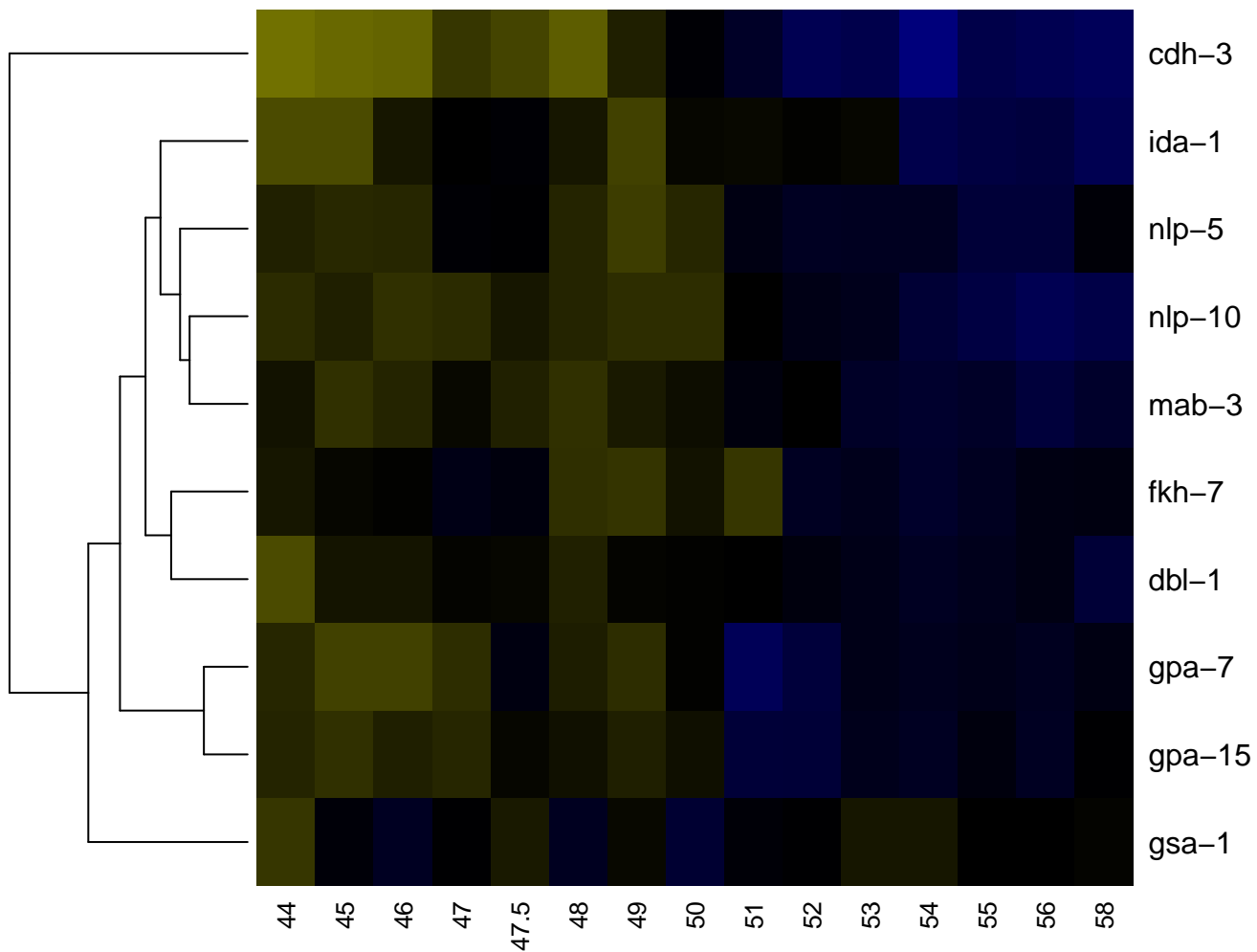
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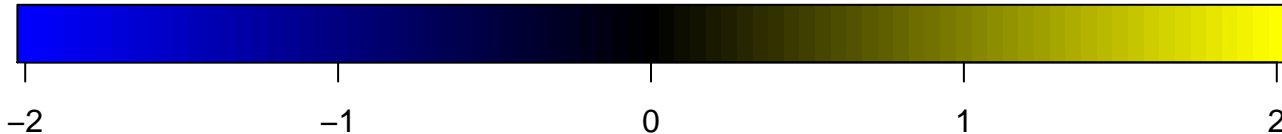
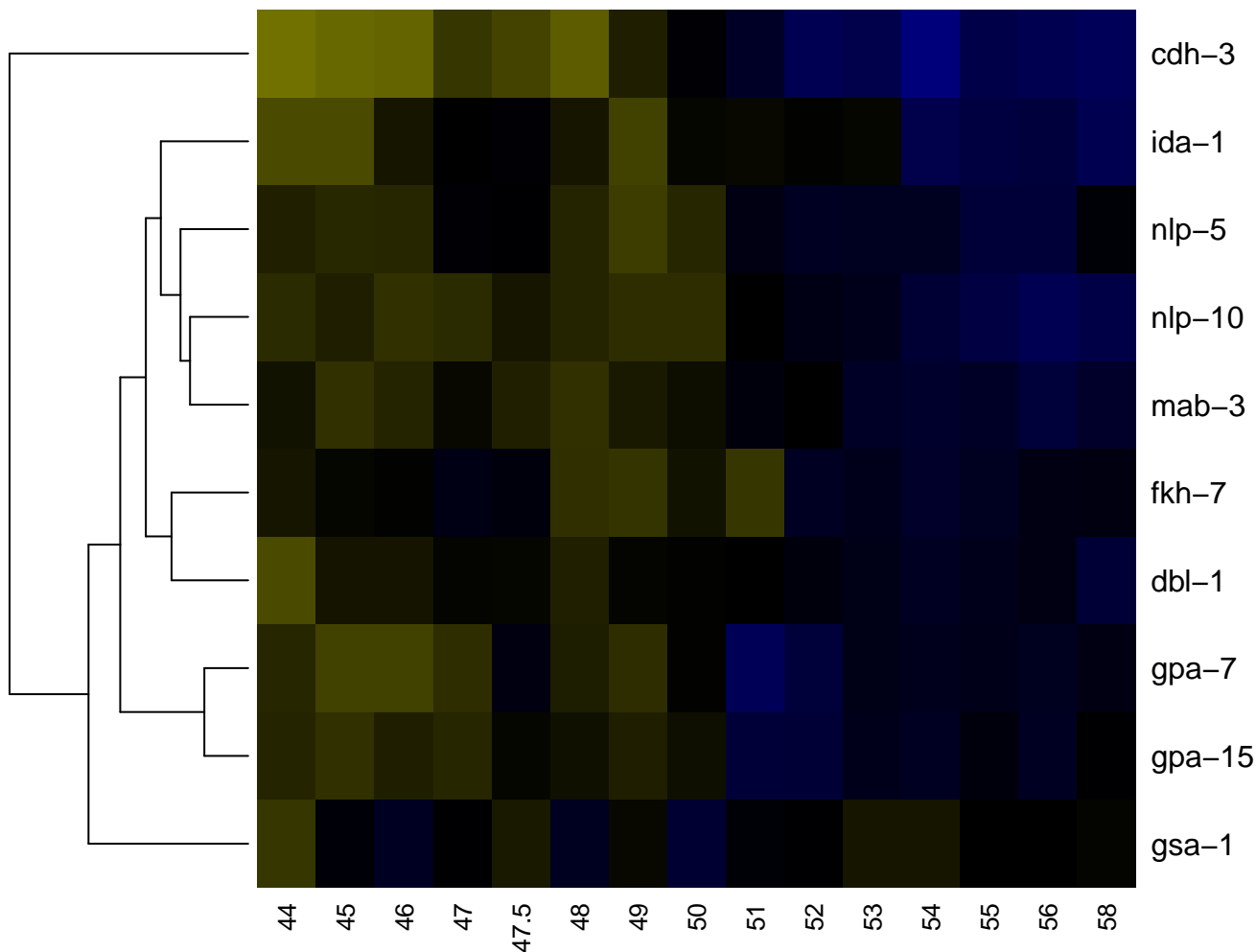
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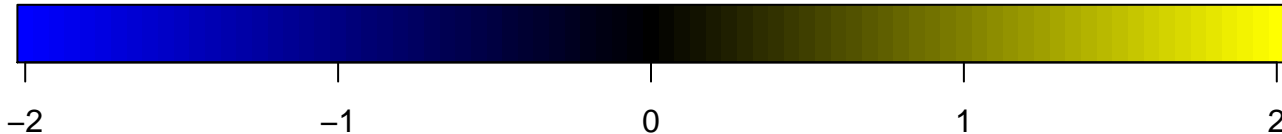
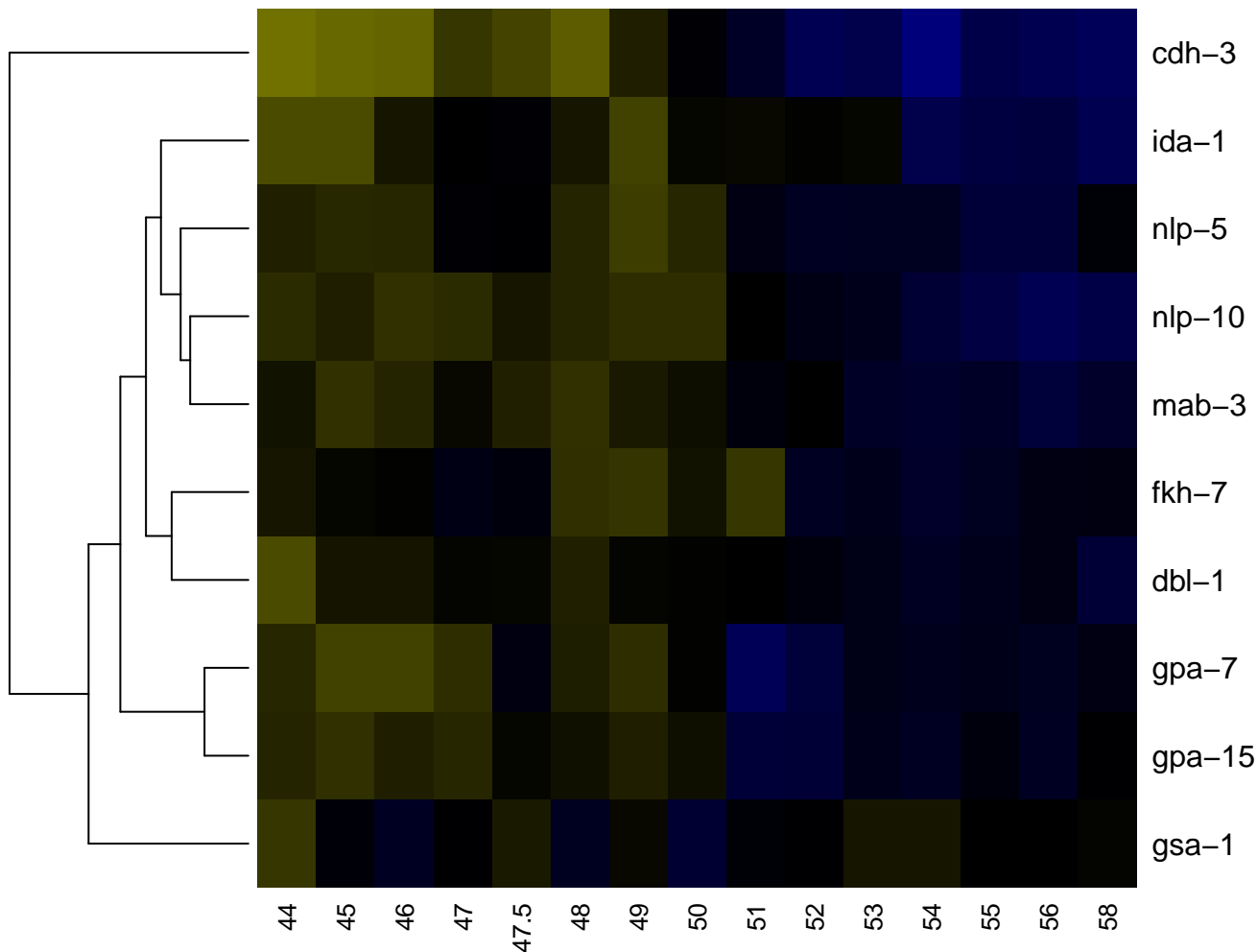
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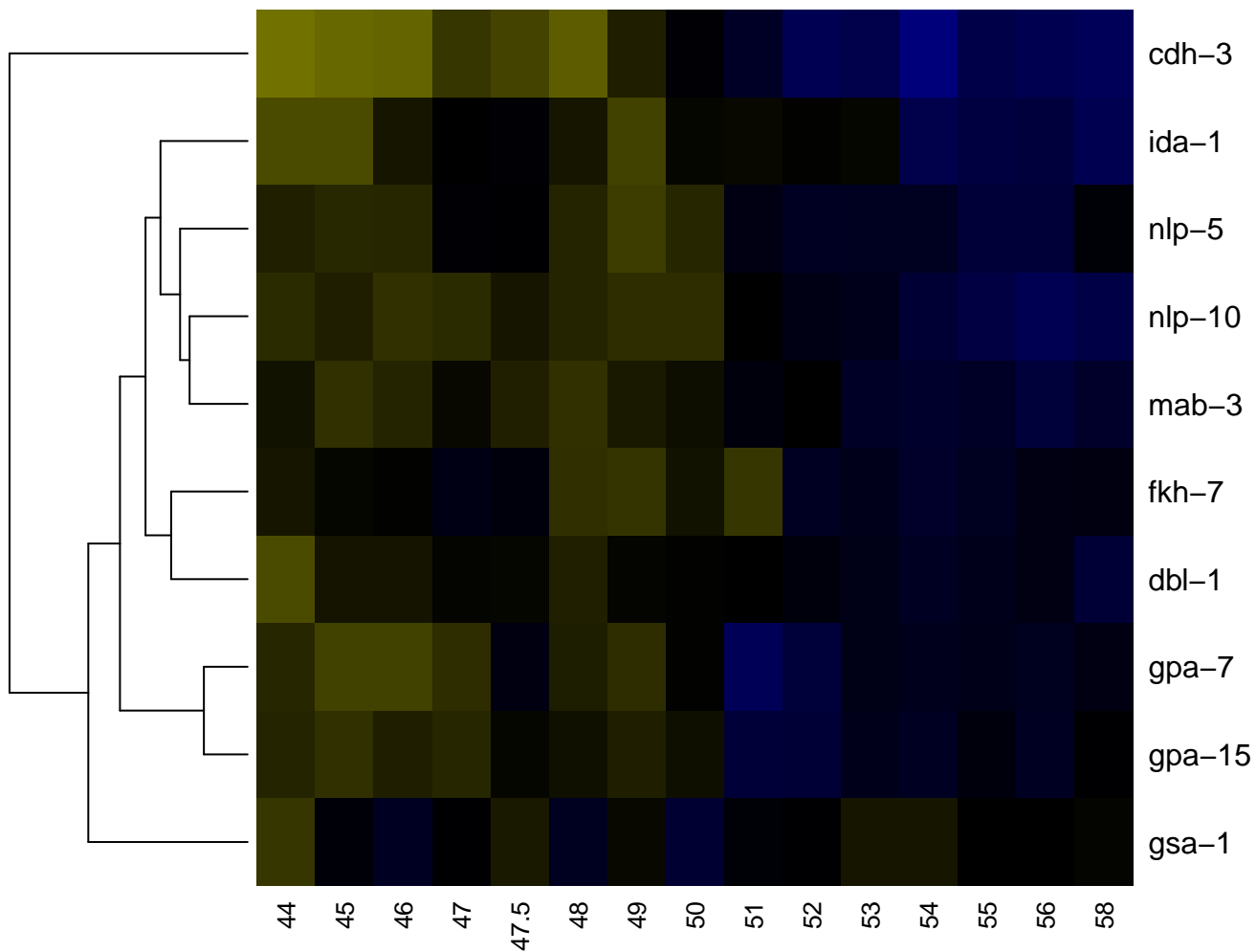
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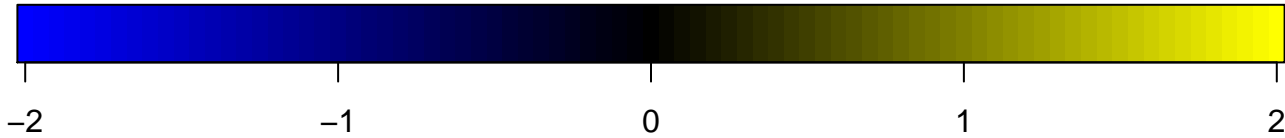
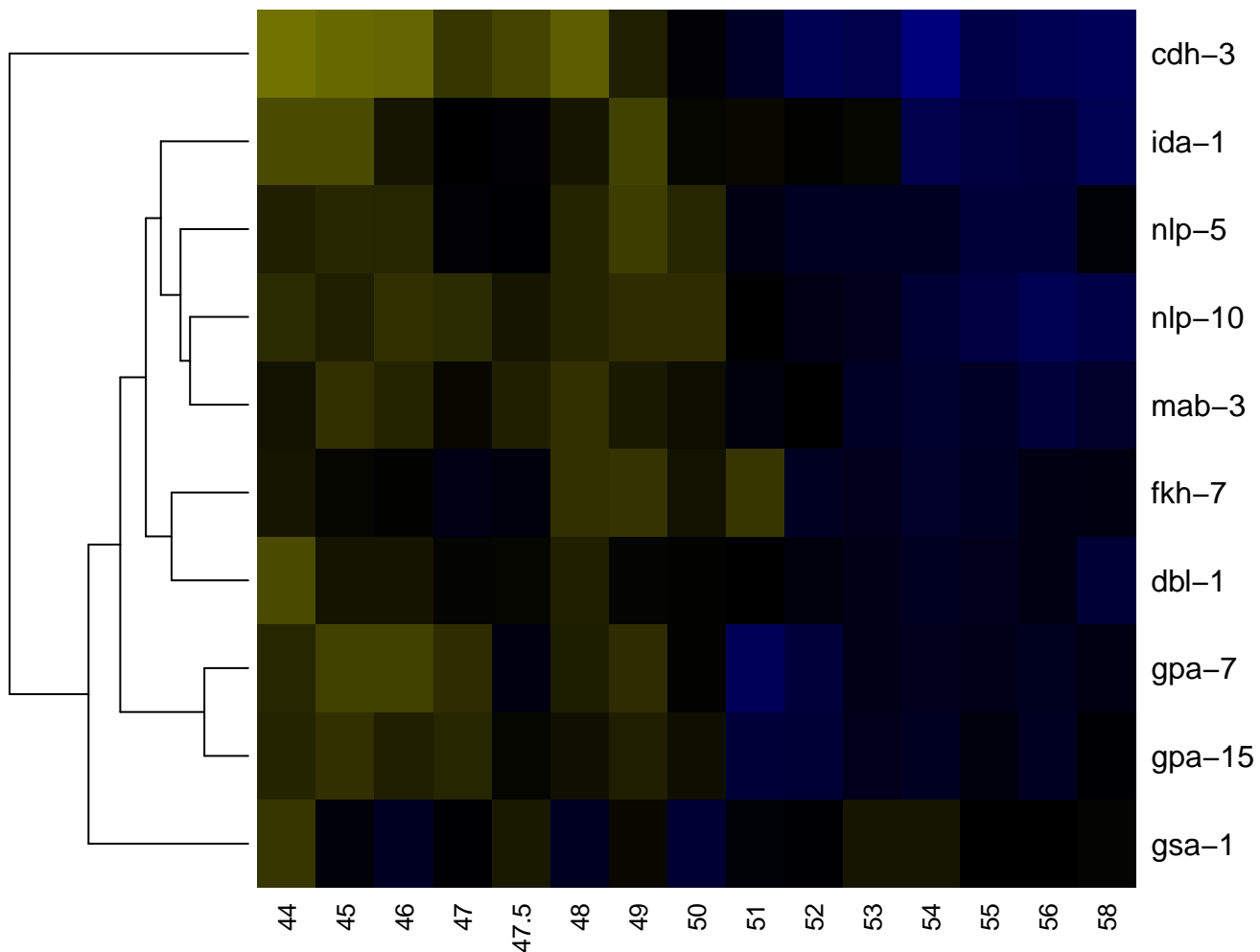
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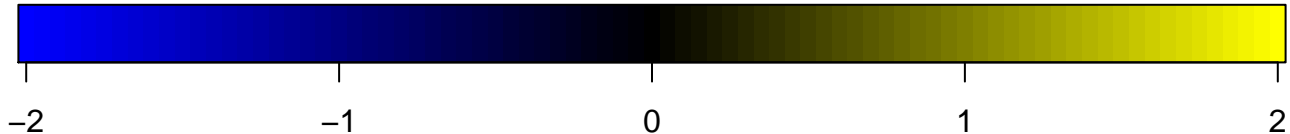
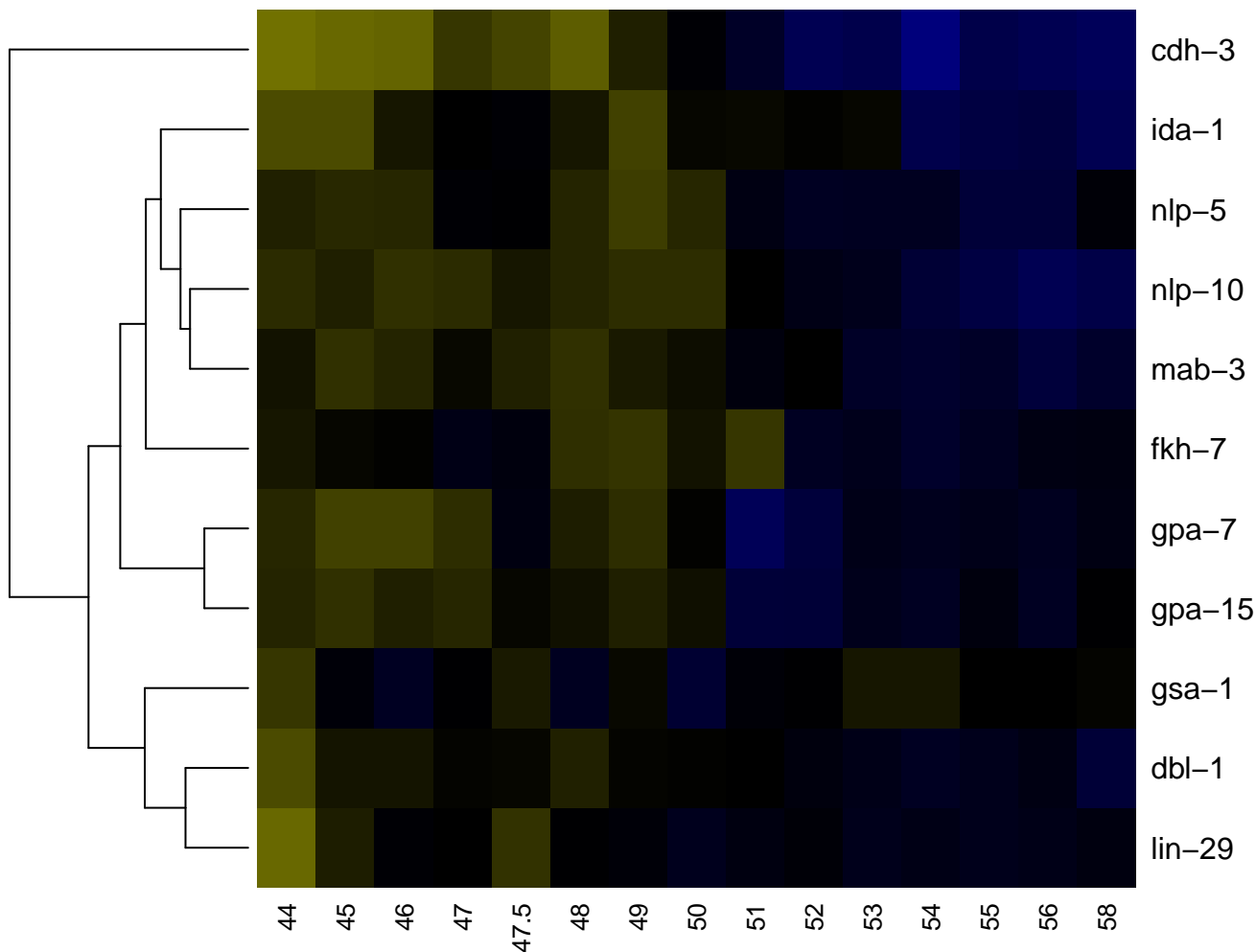
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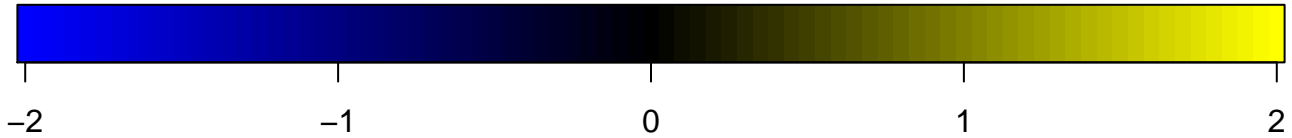
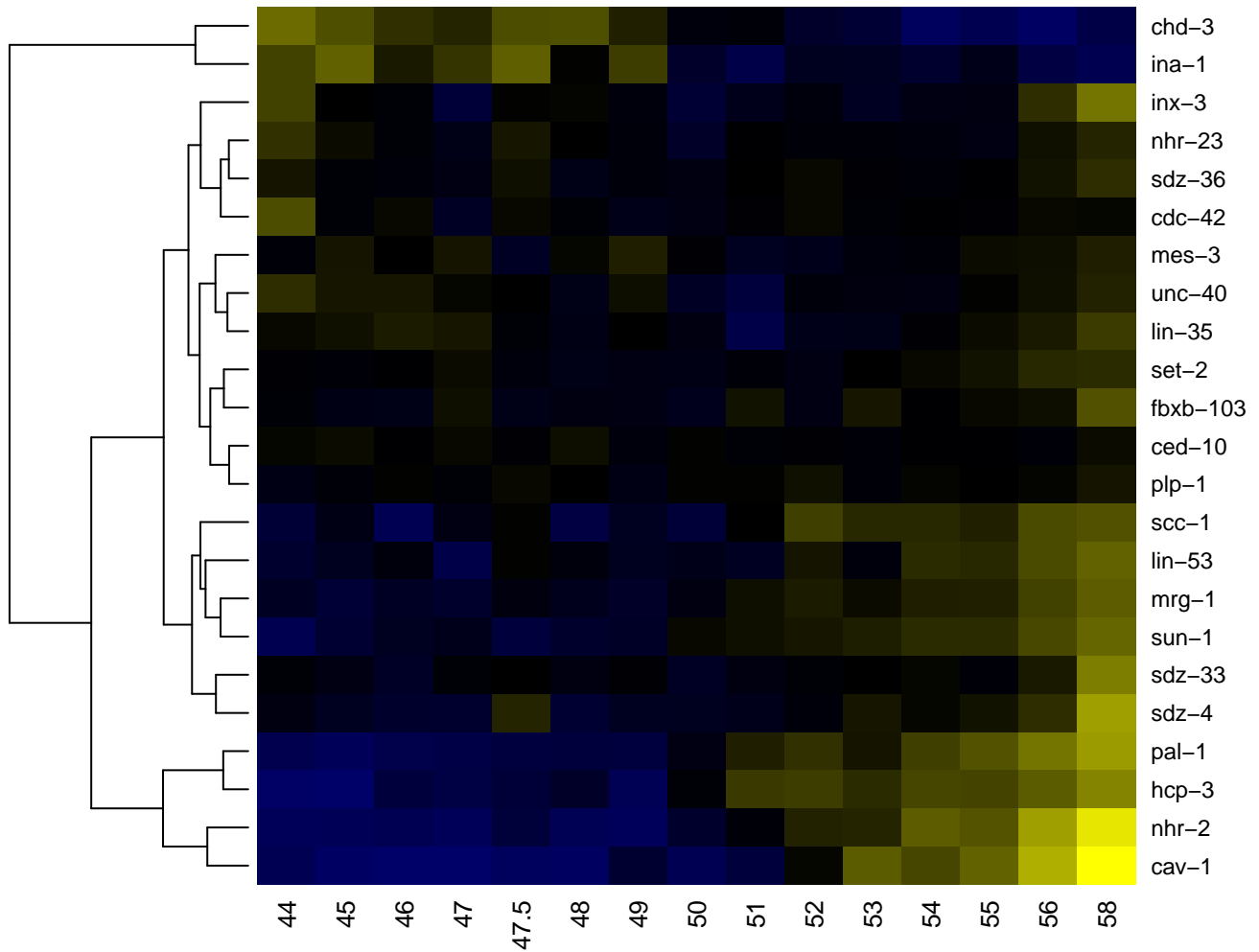
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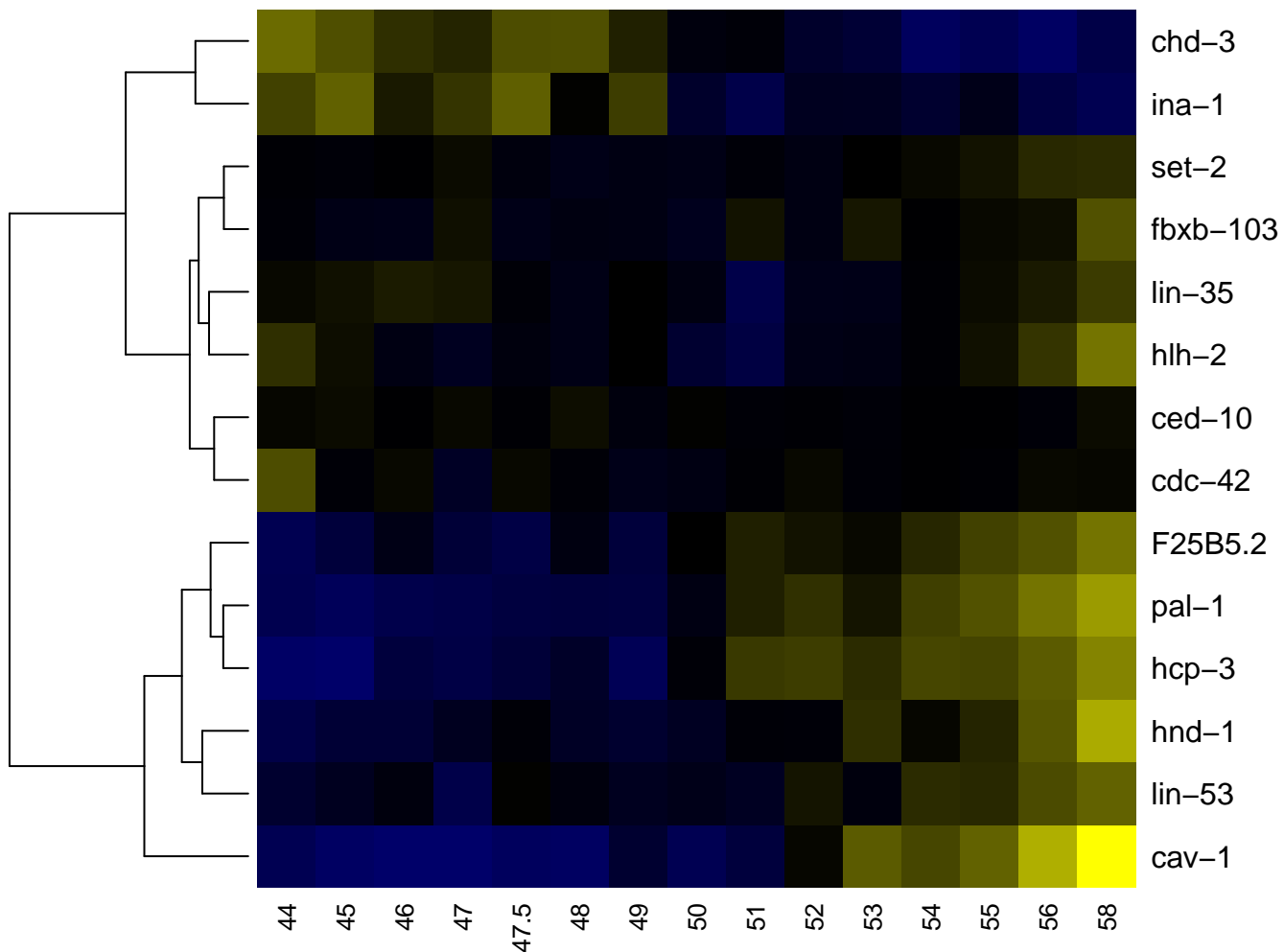
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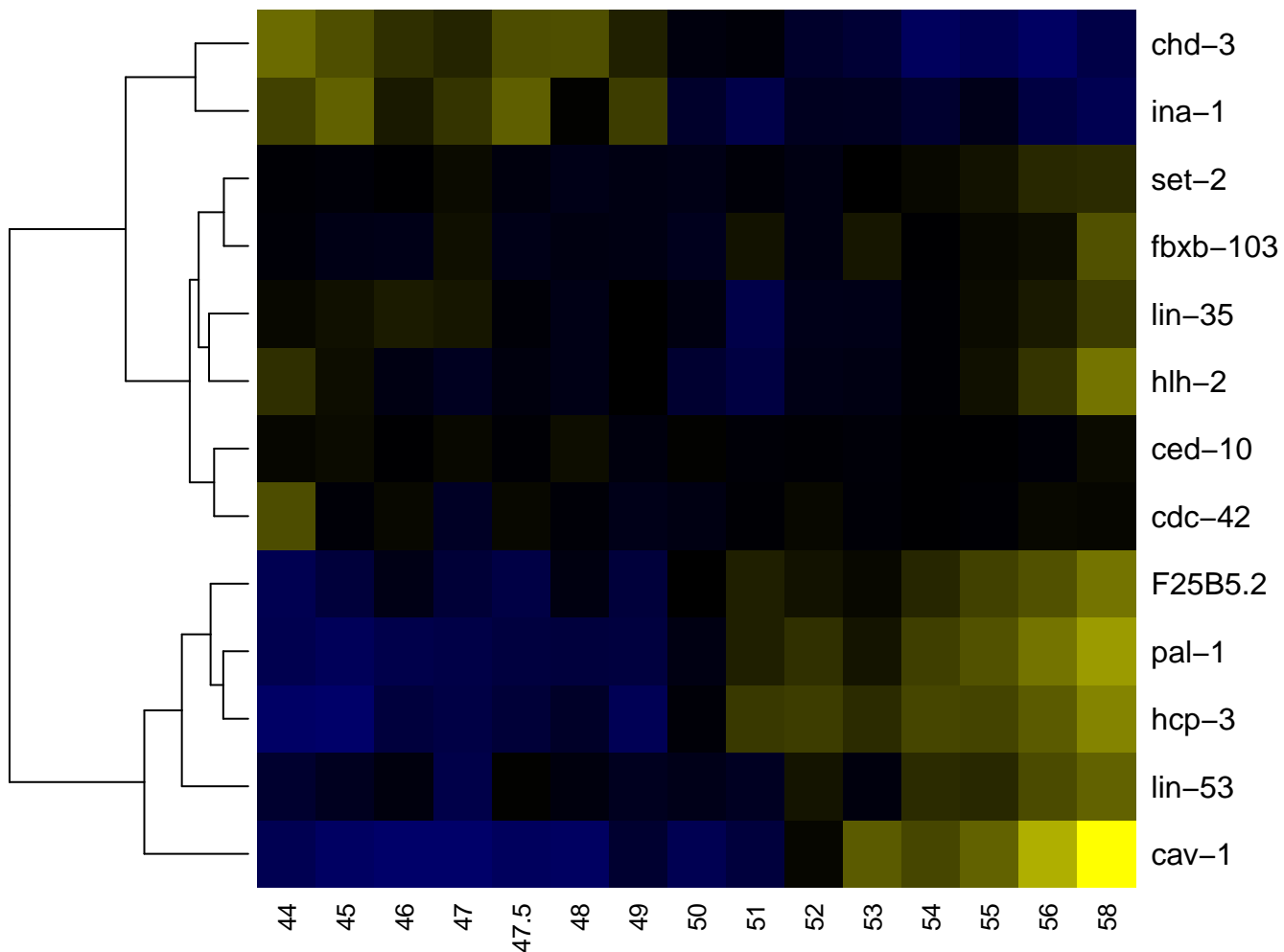
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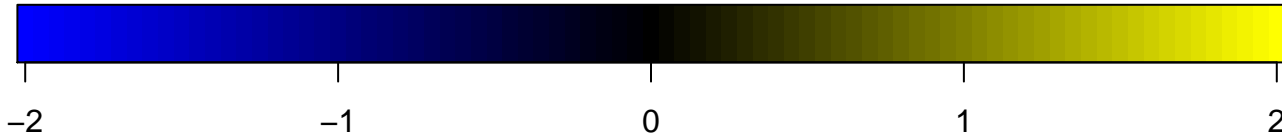
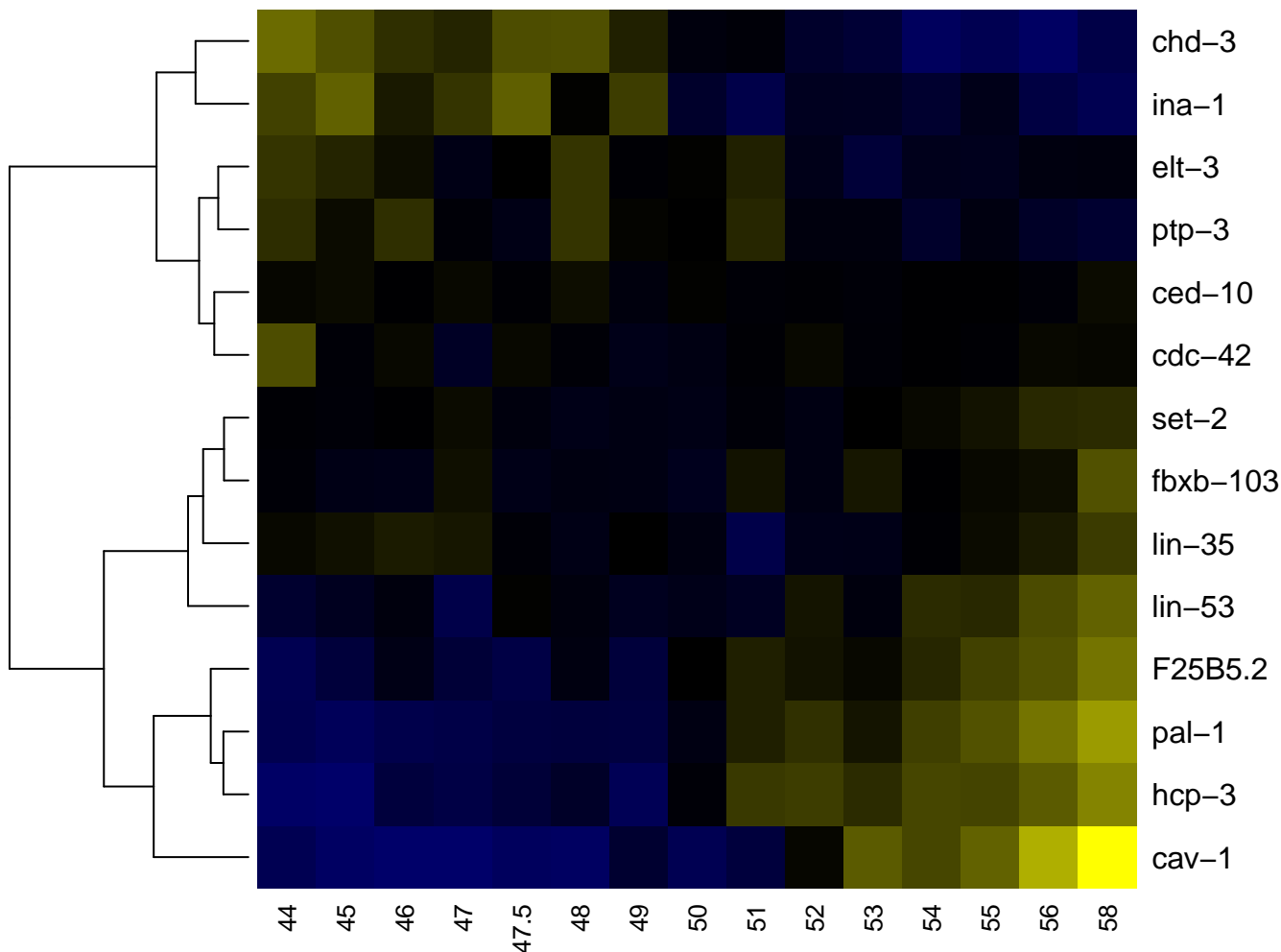
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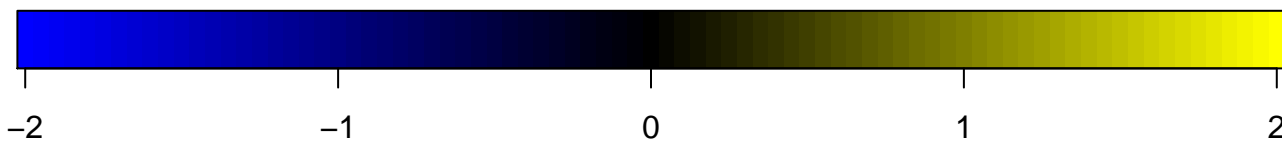
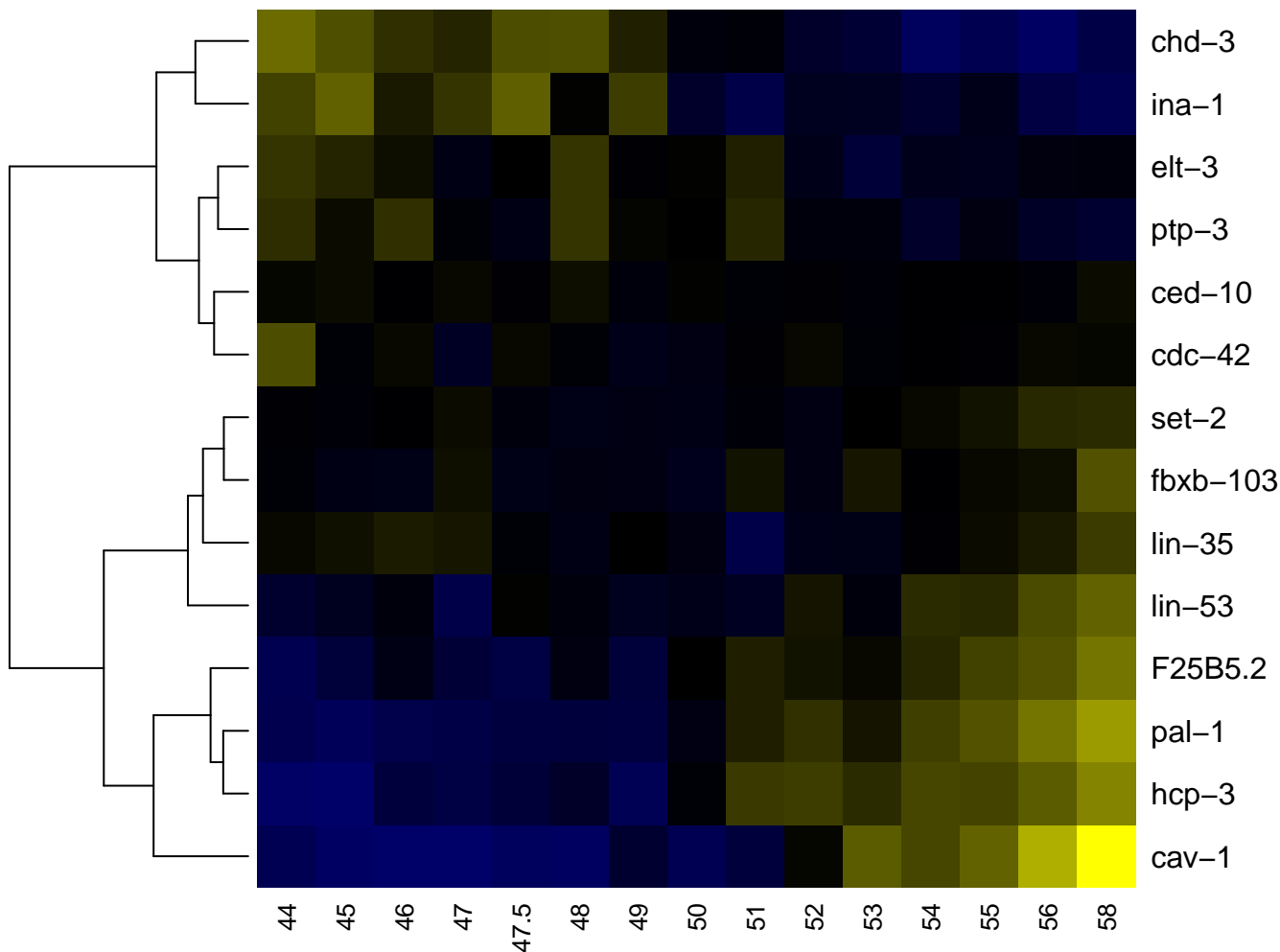
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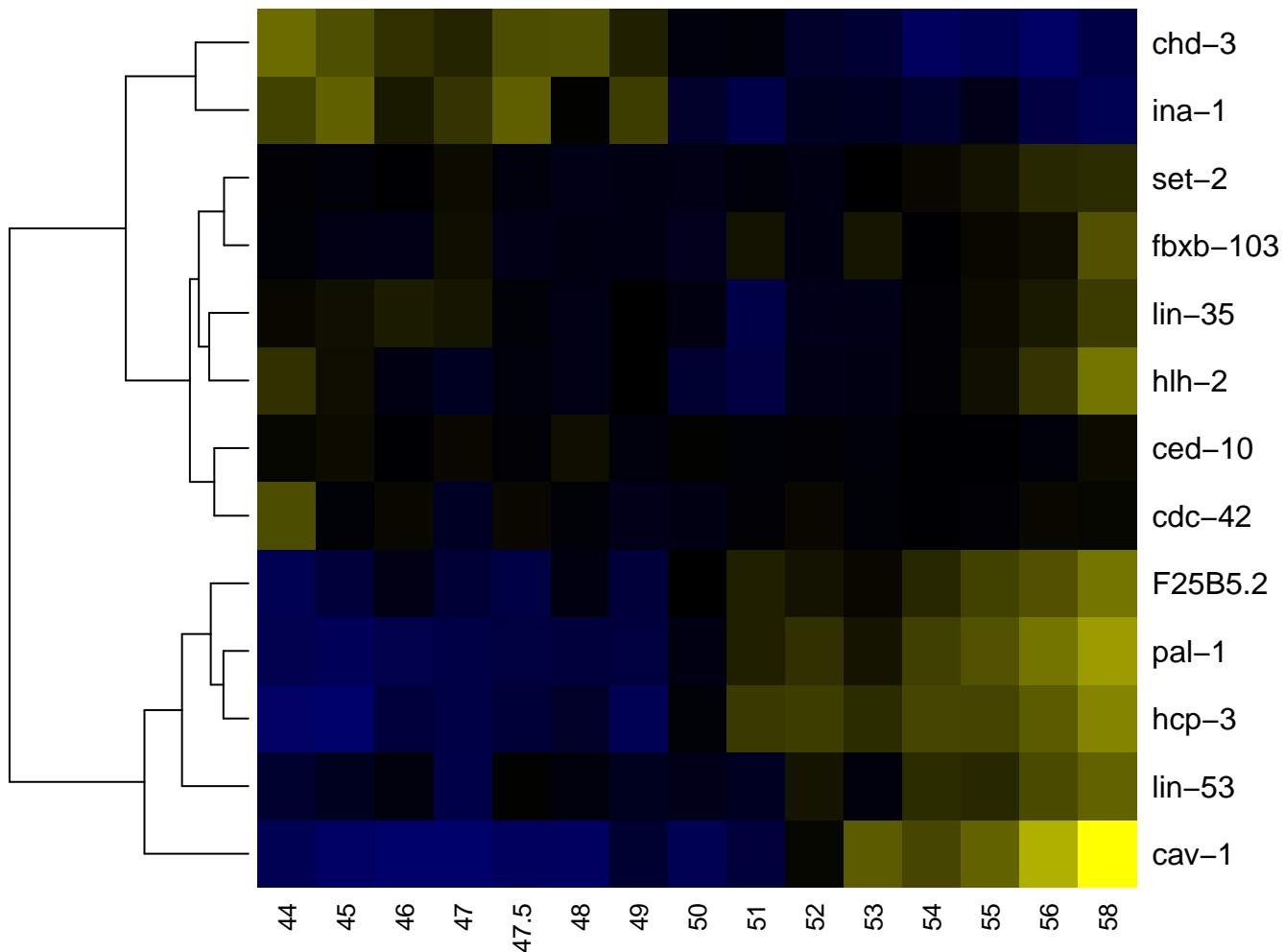
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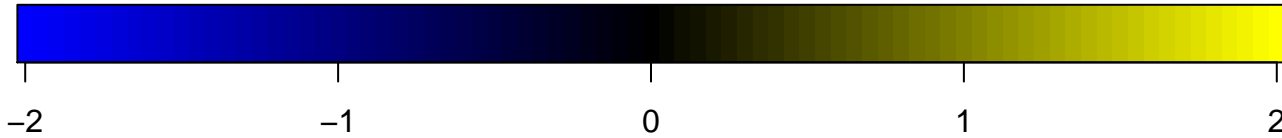
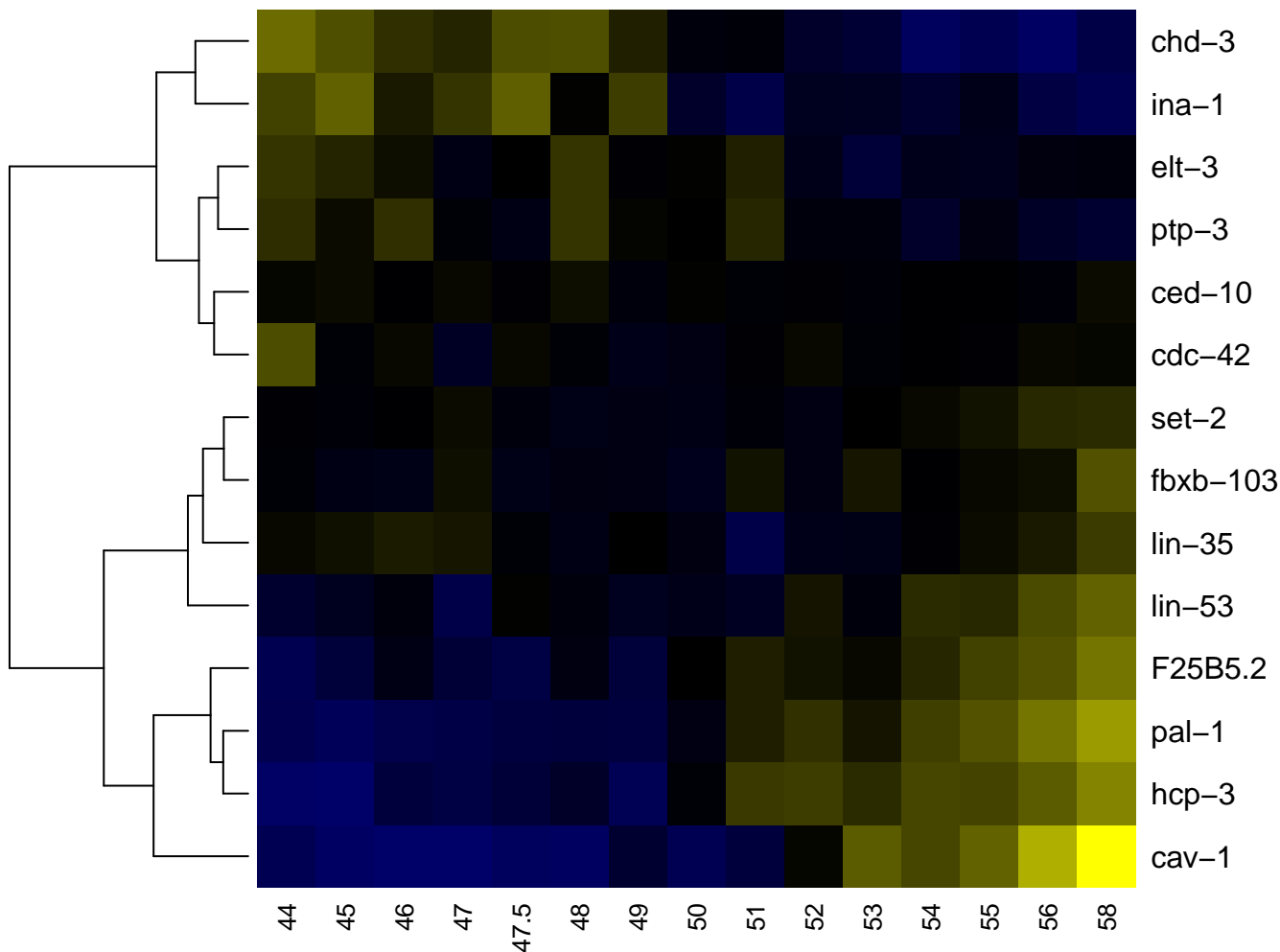
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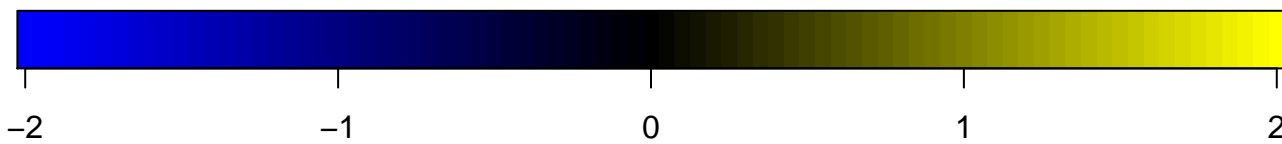
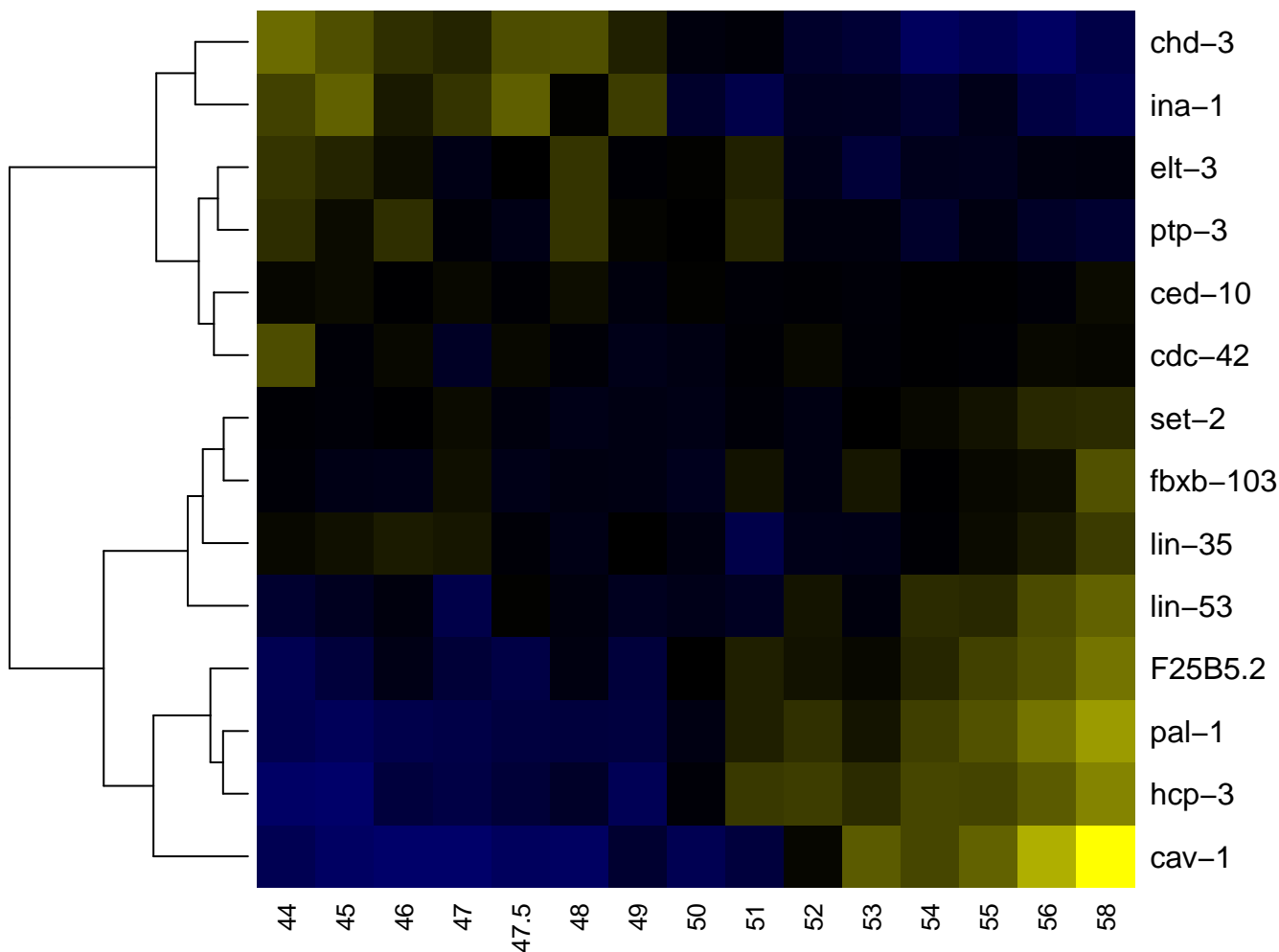
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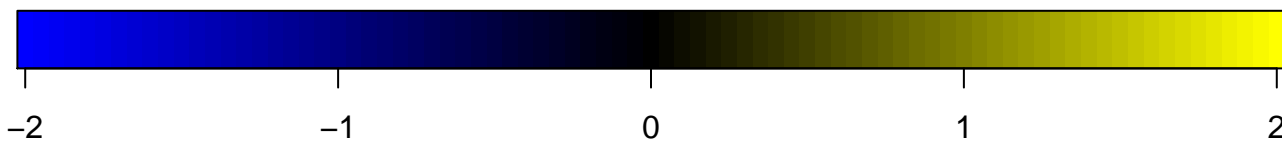
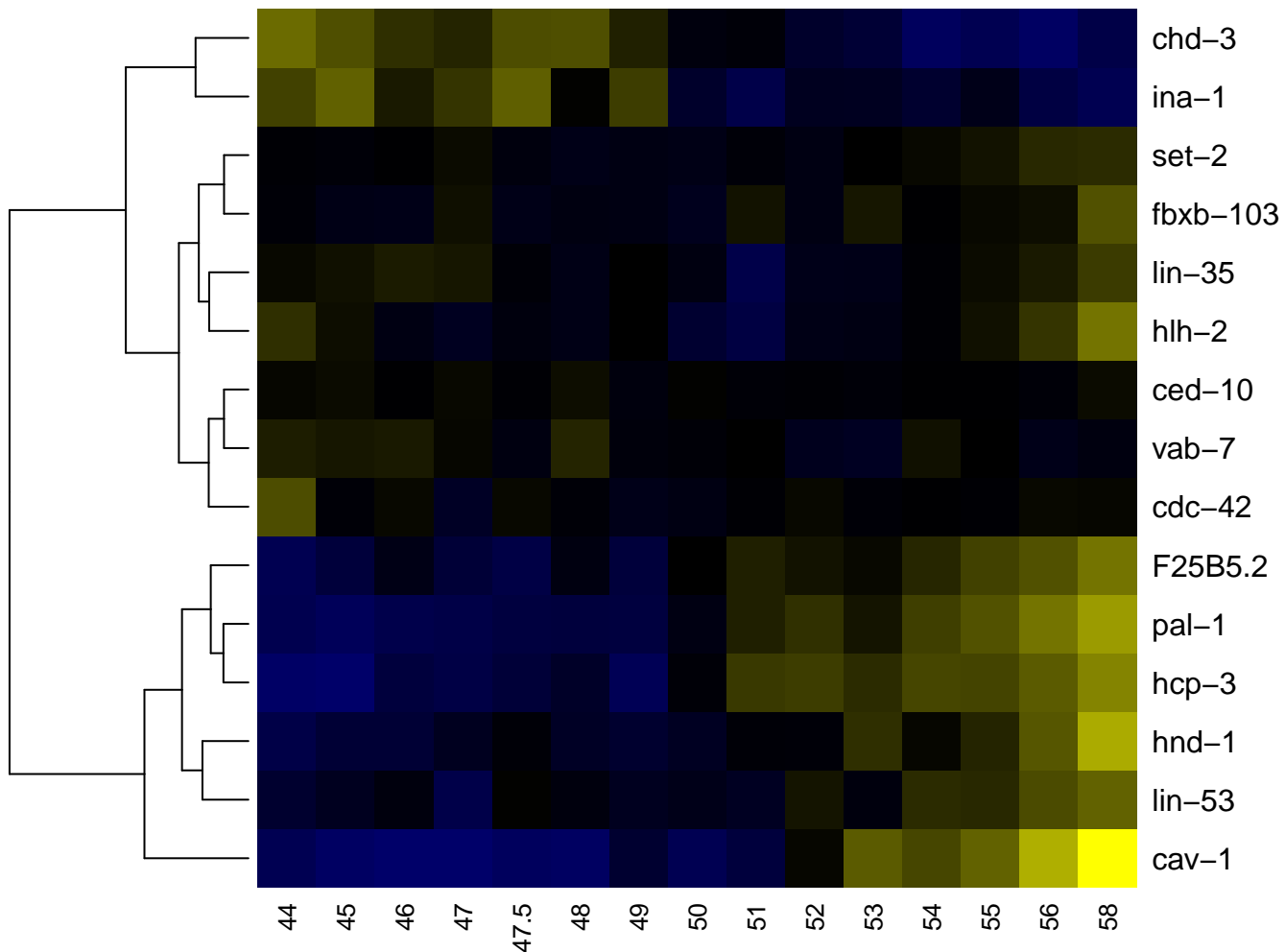
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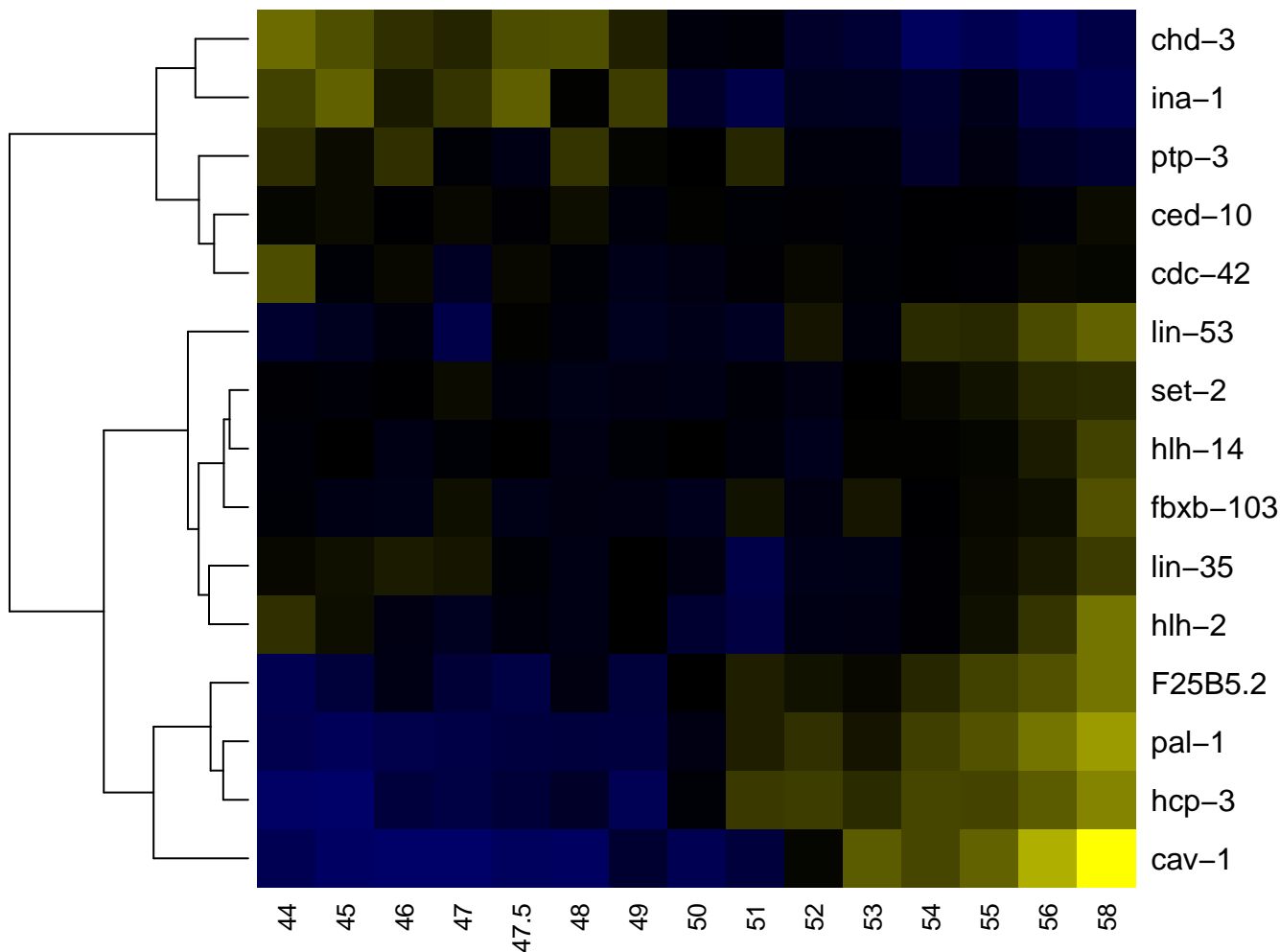
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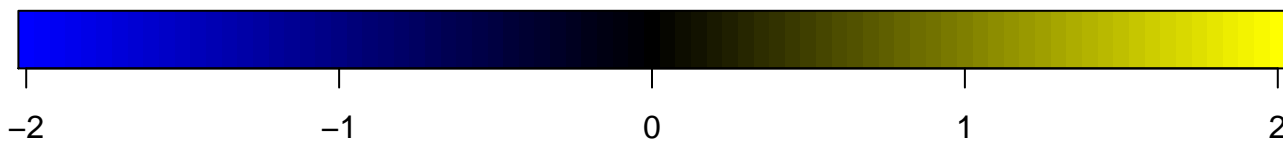
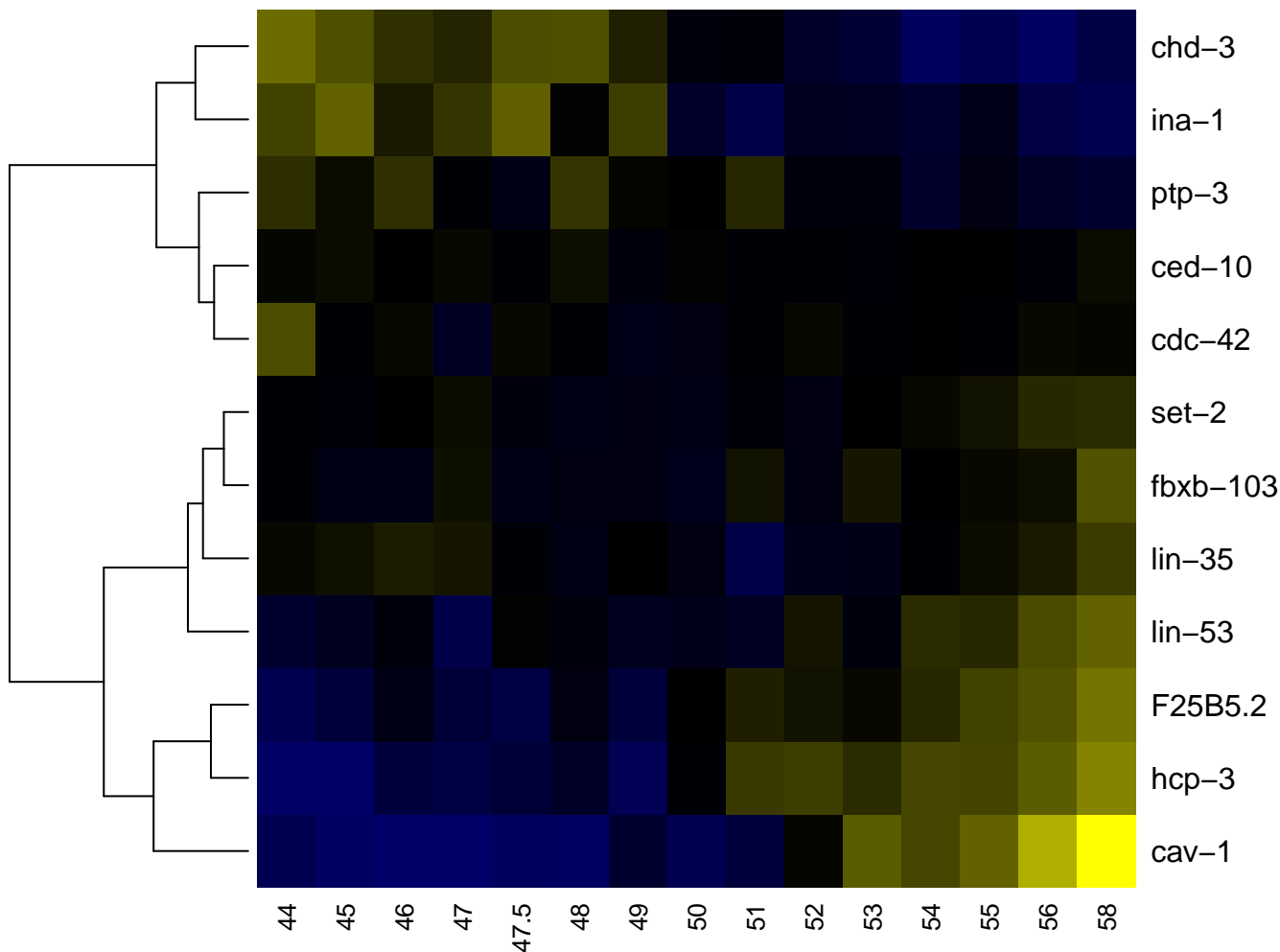
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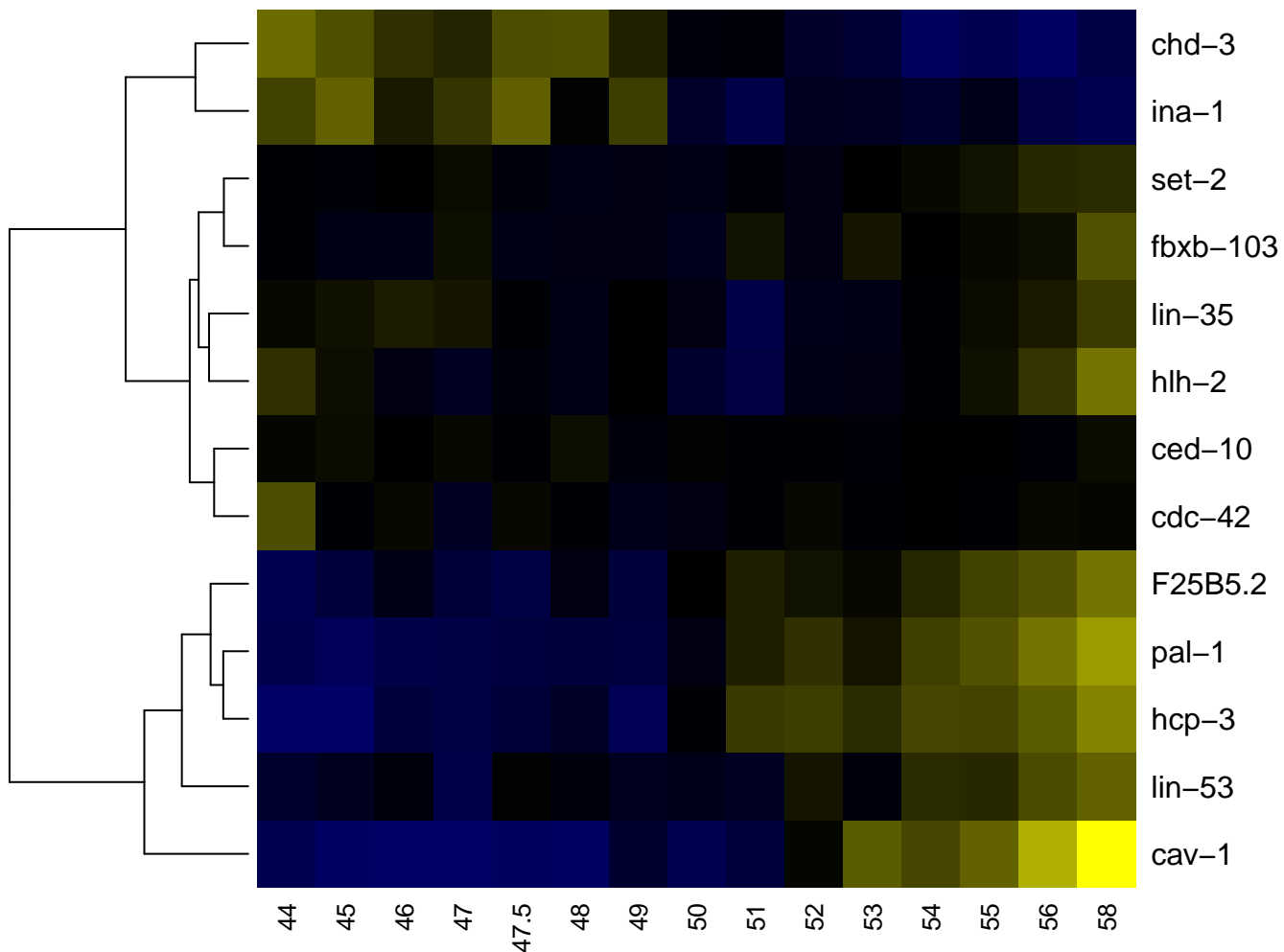
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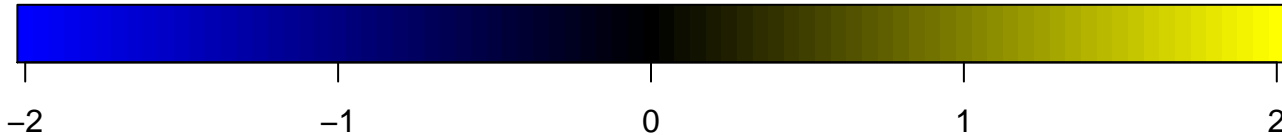
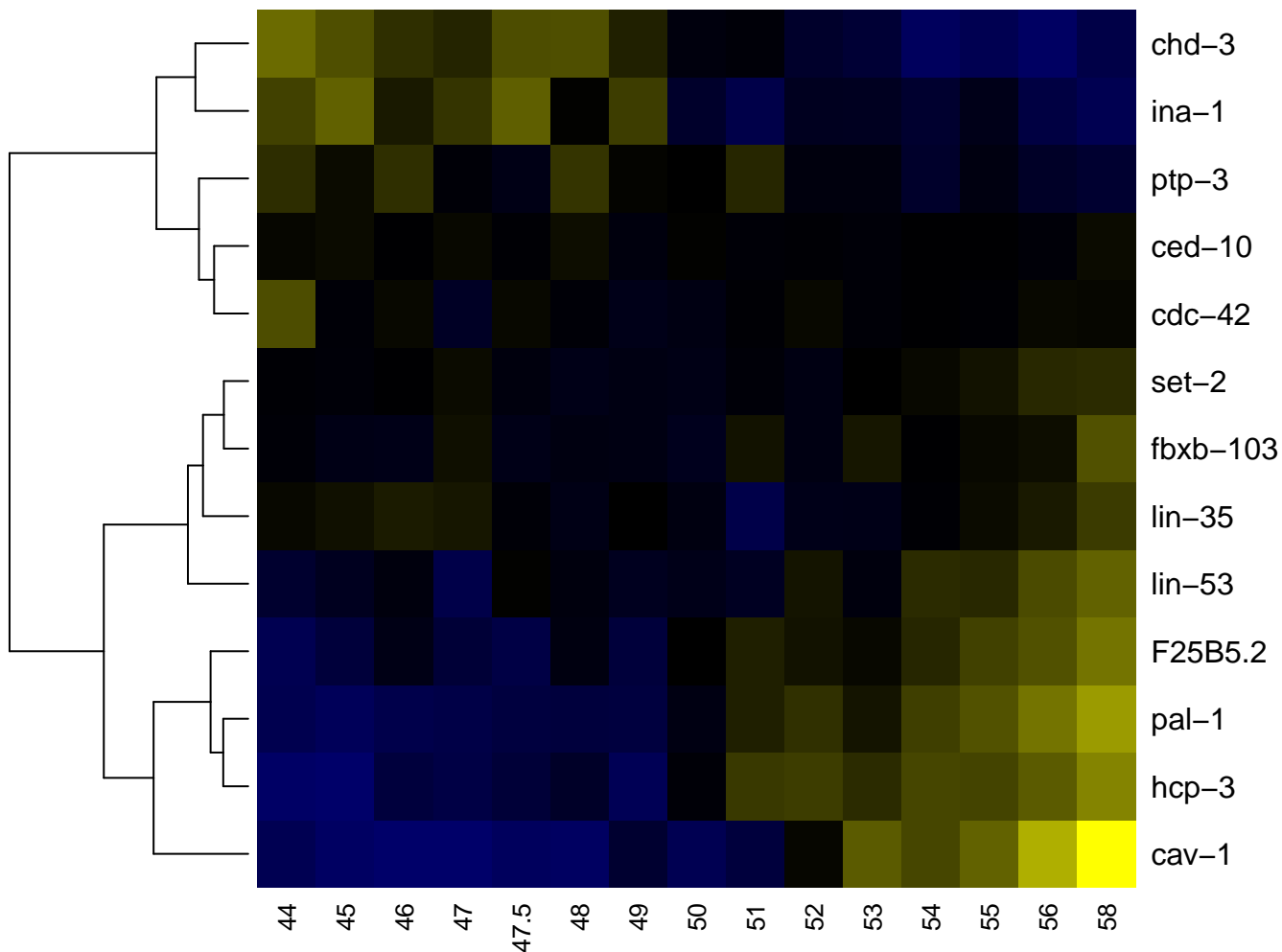
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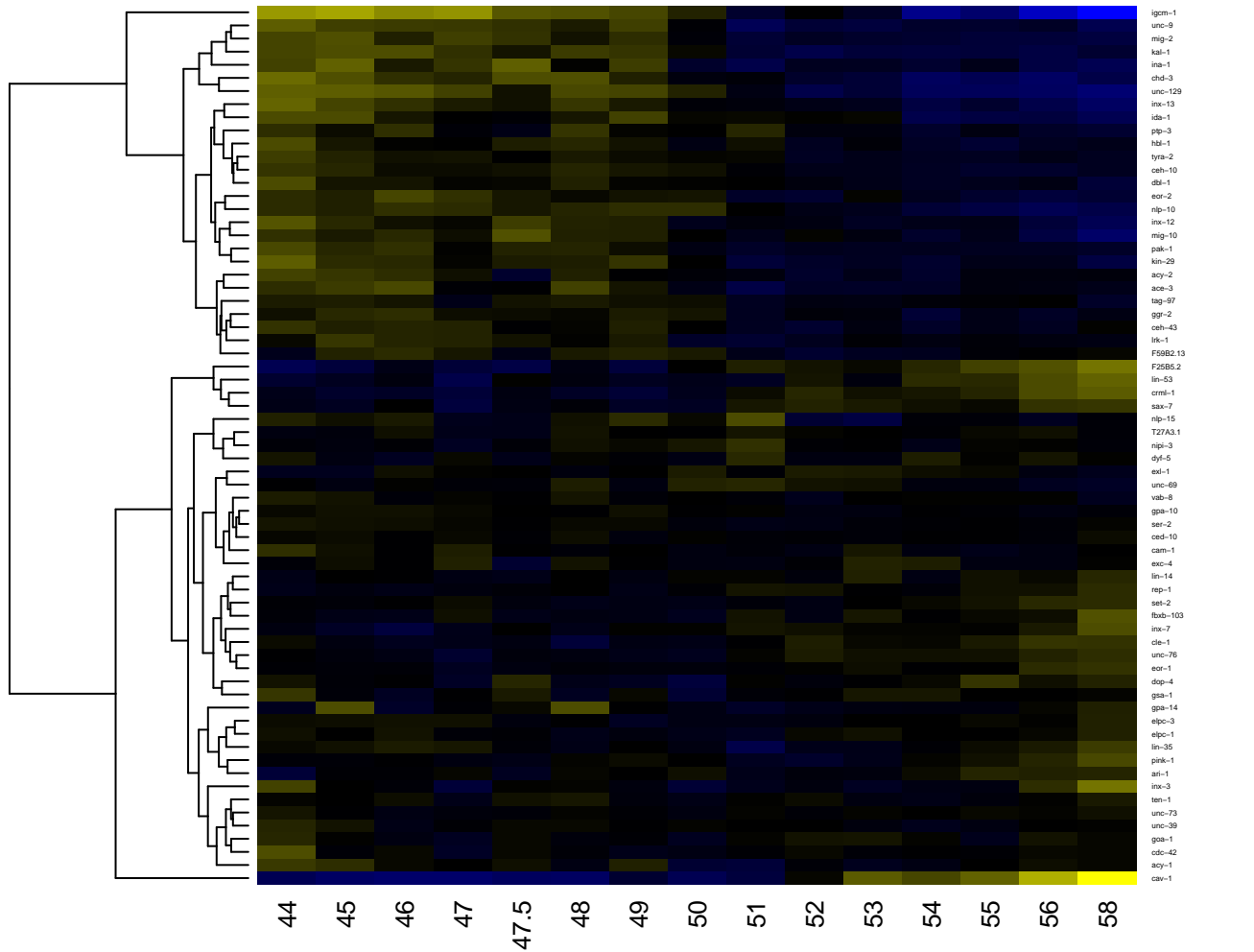
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Caappd



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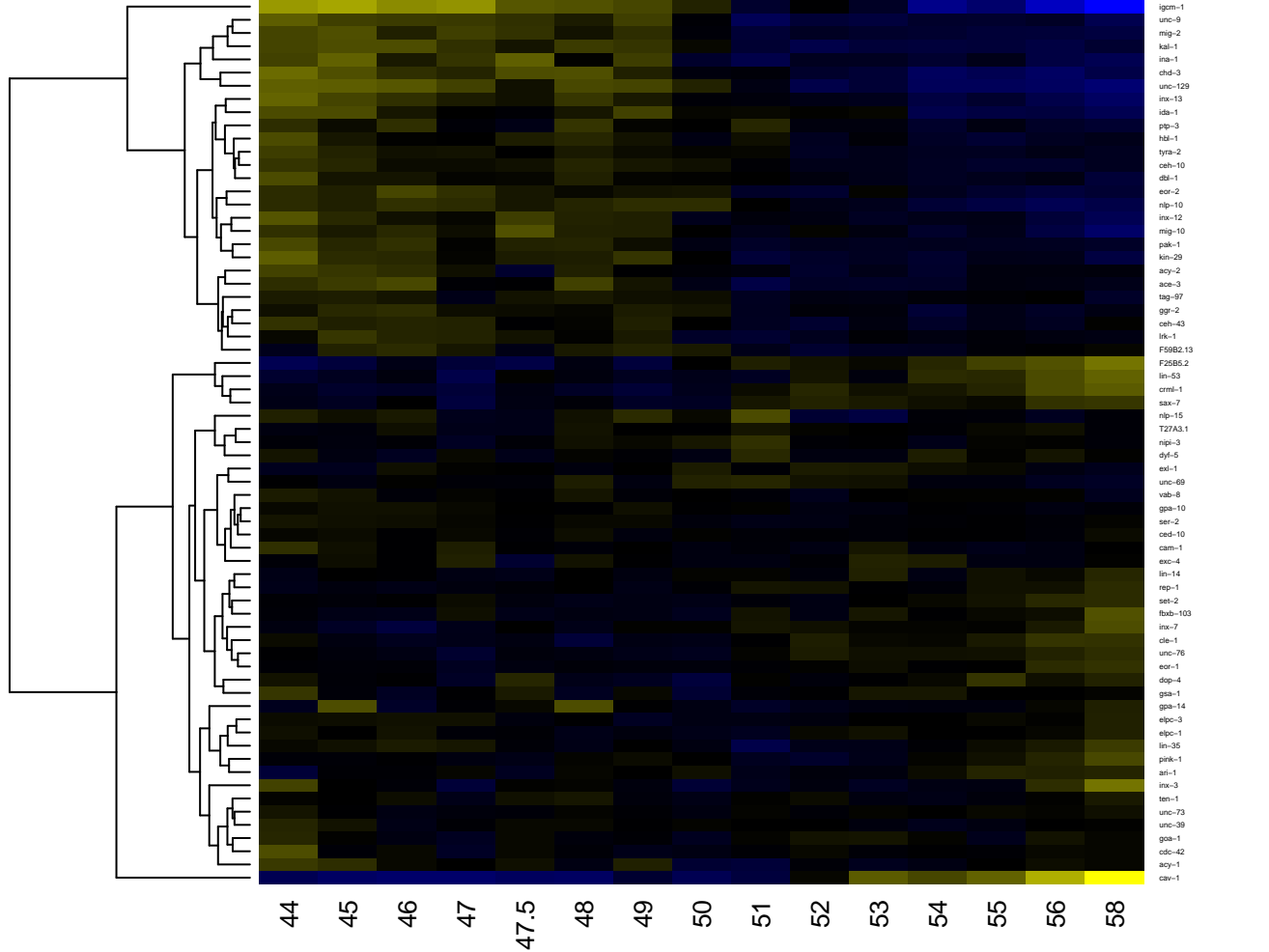
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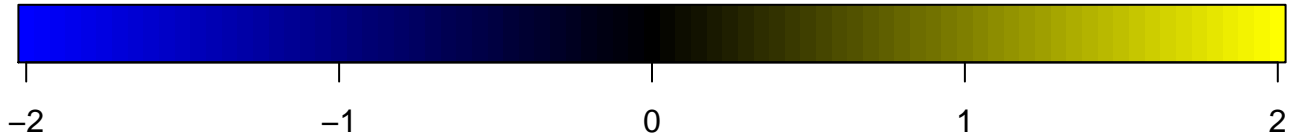
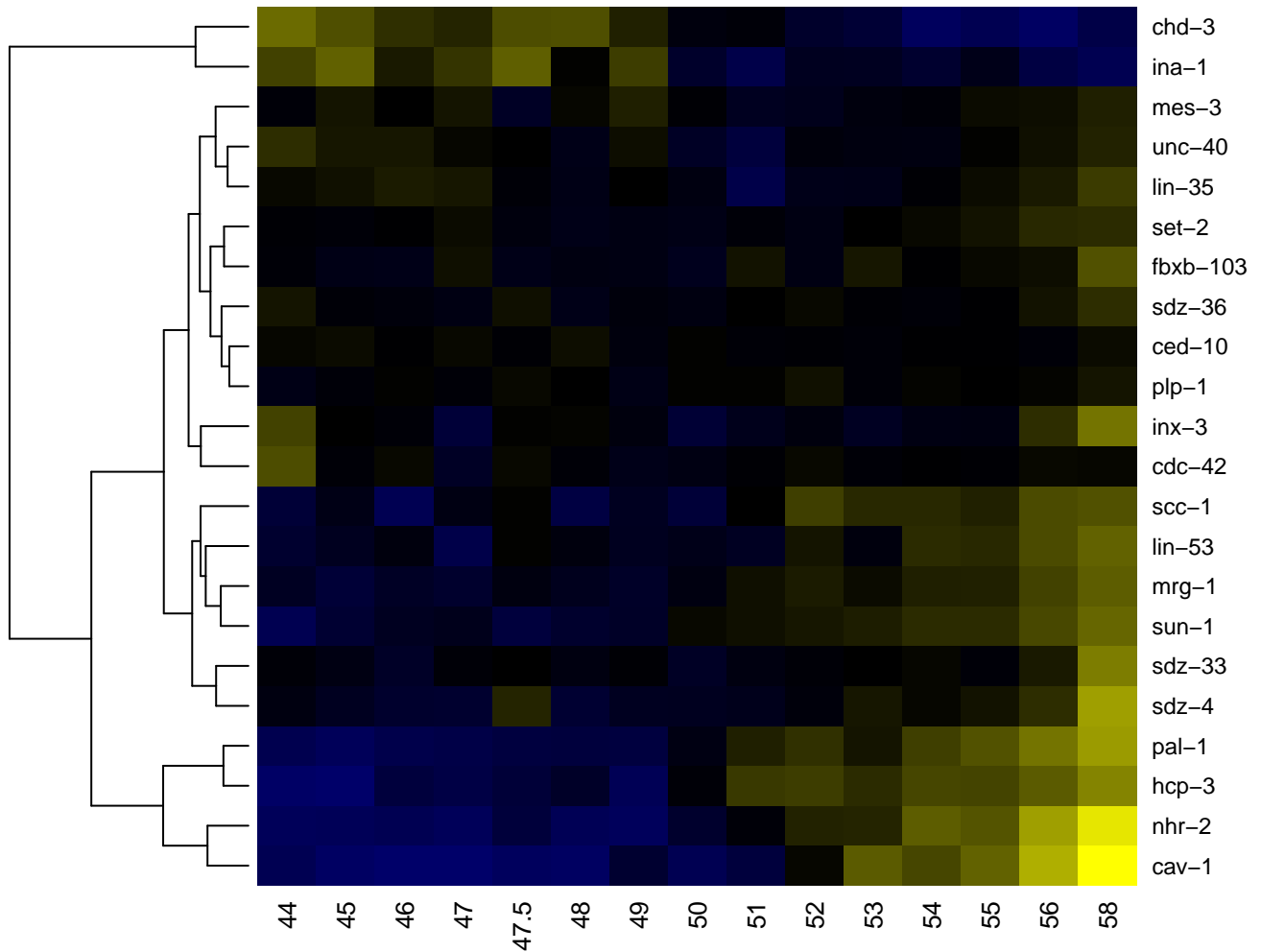
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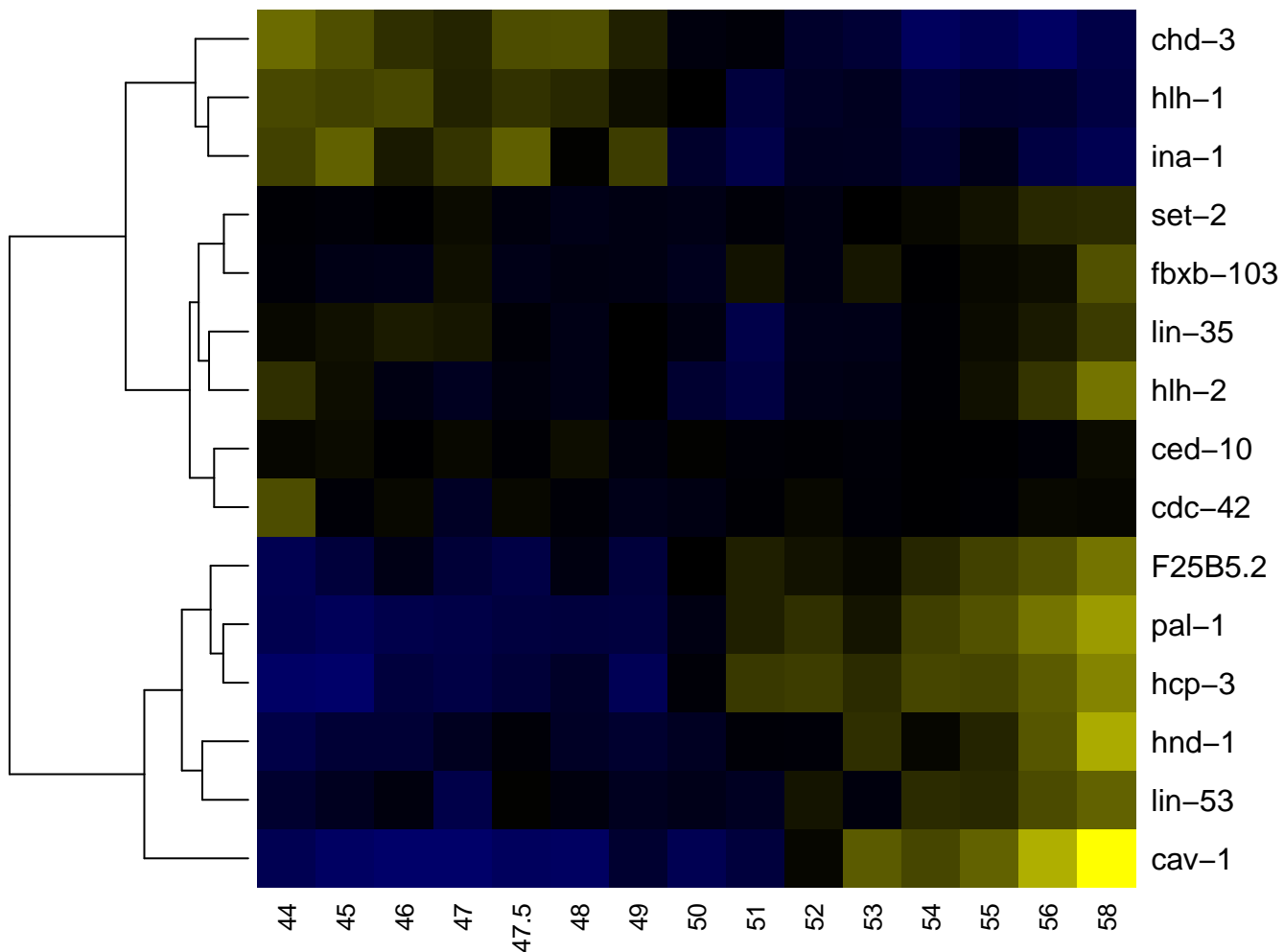
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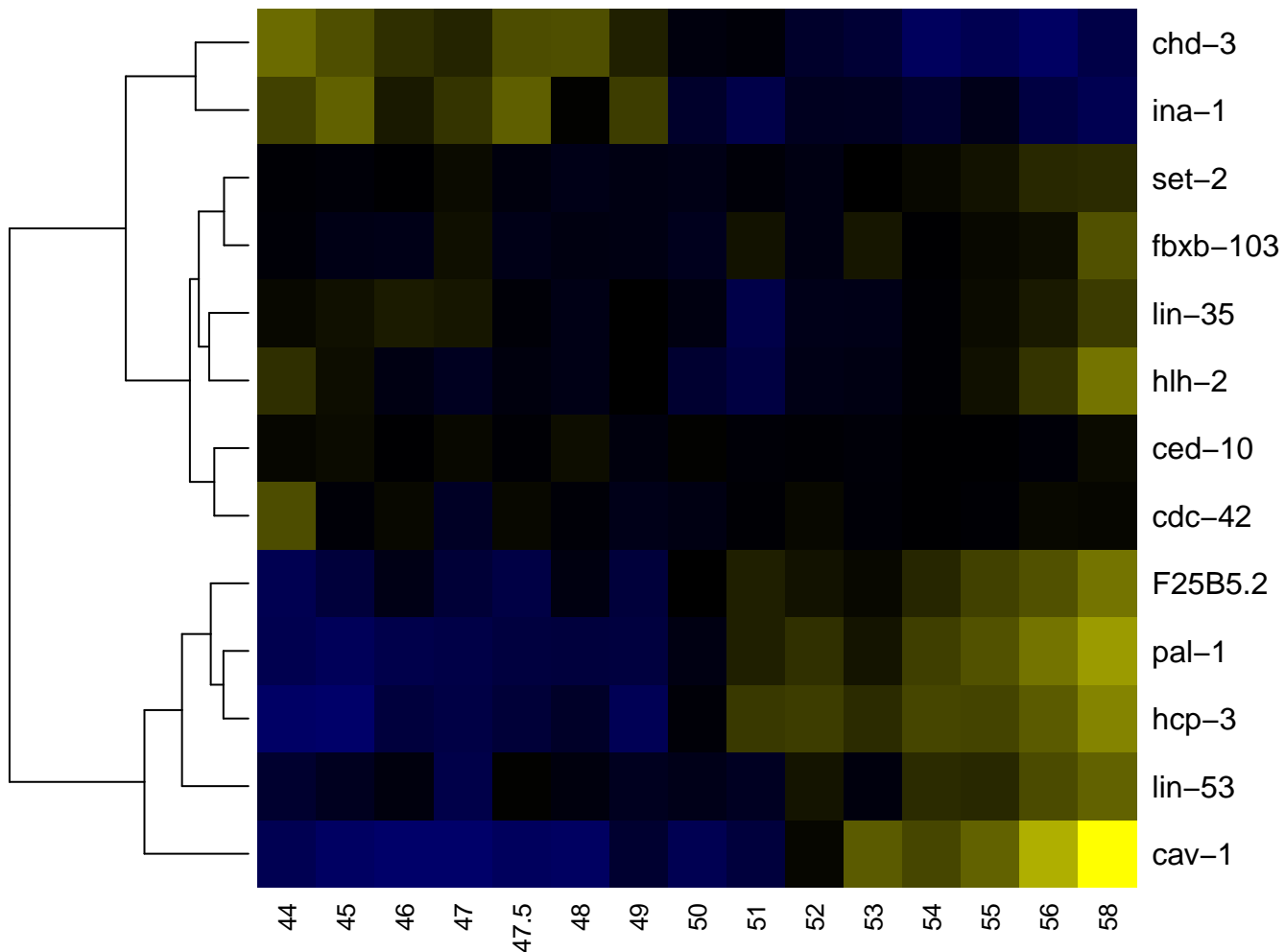
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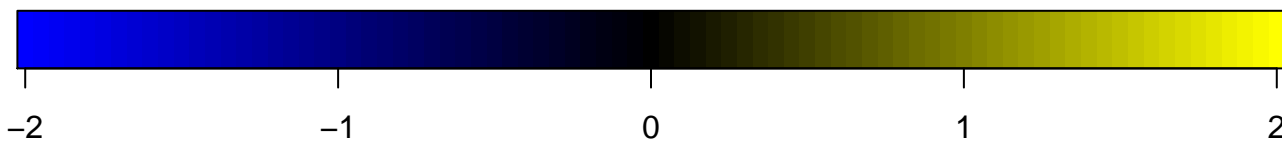
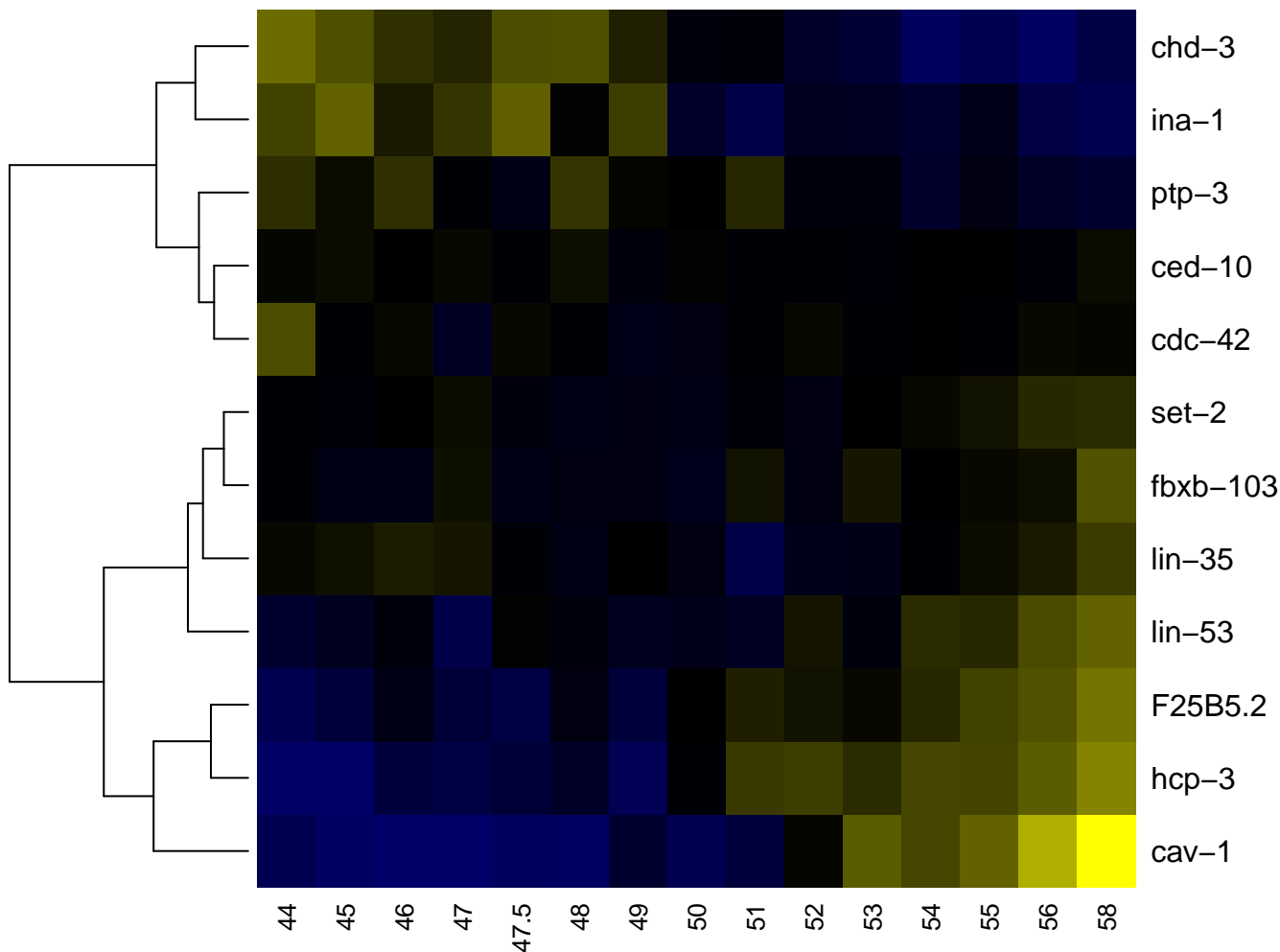
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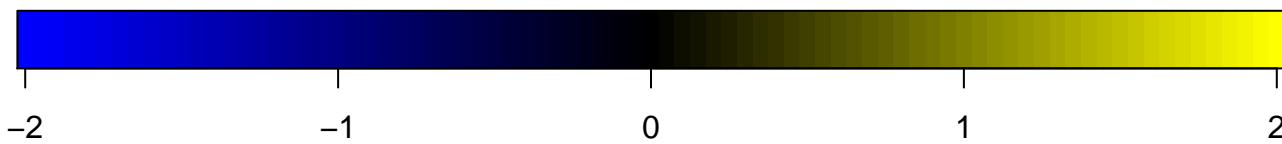
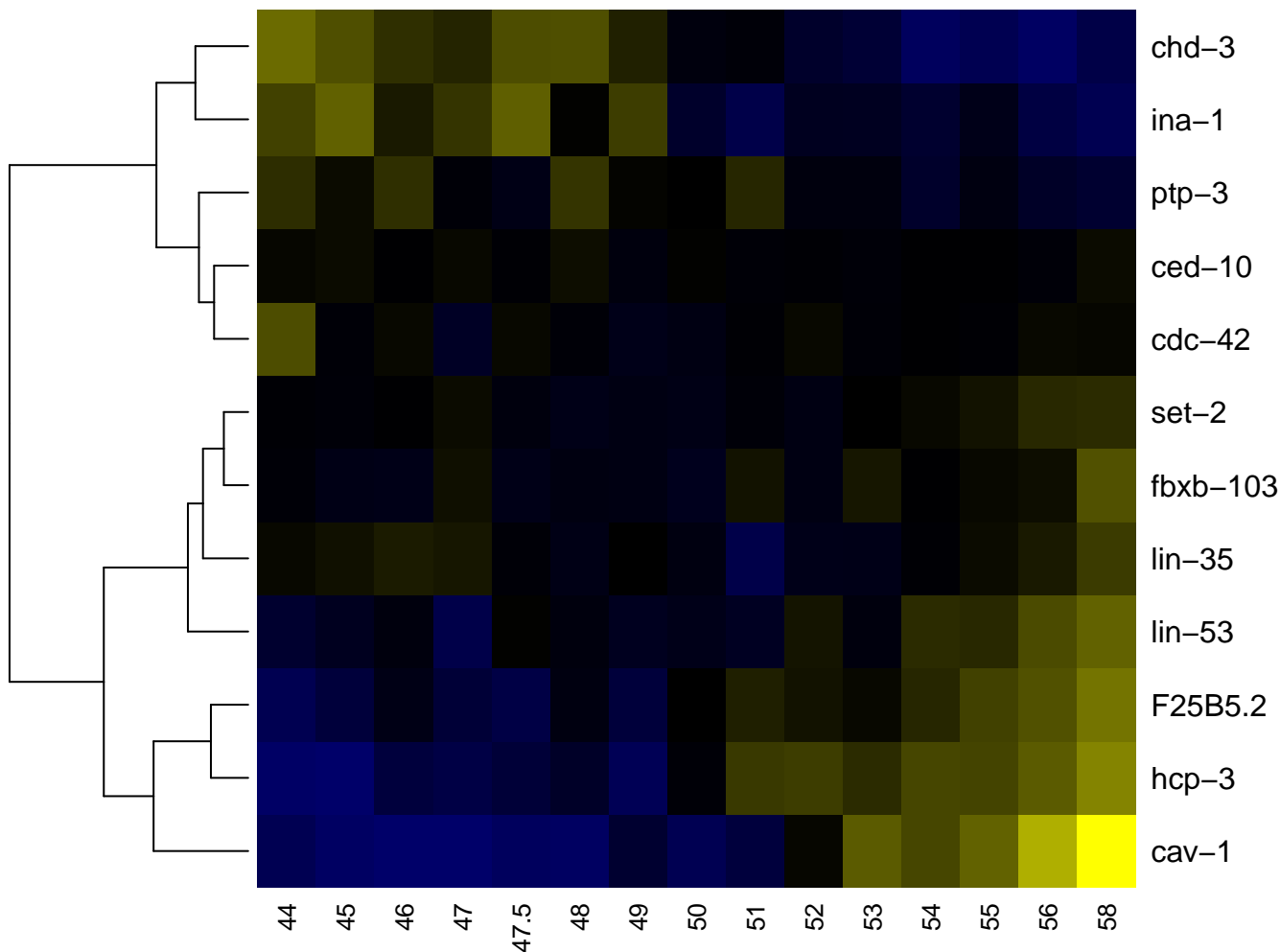
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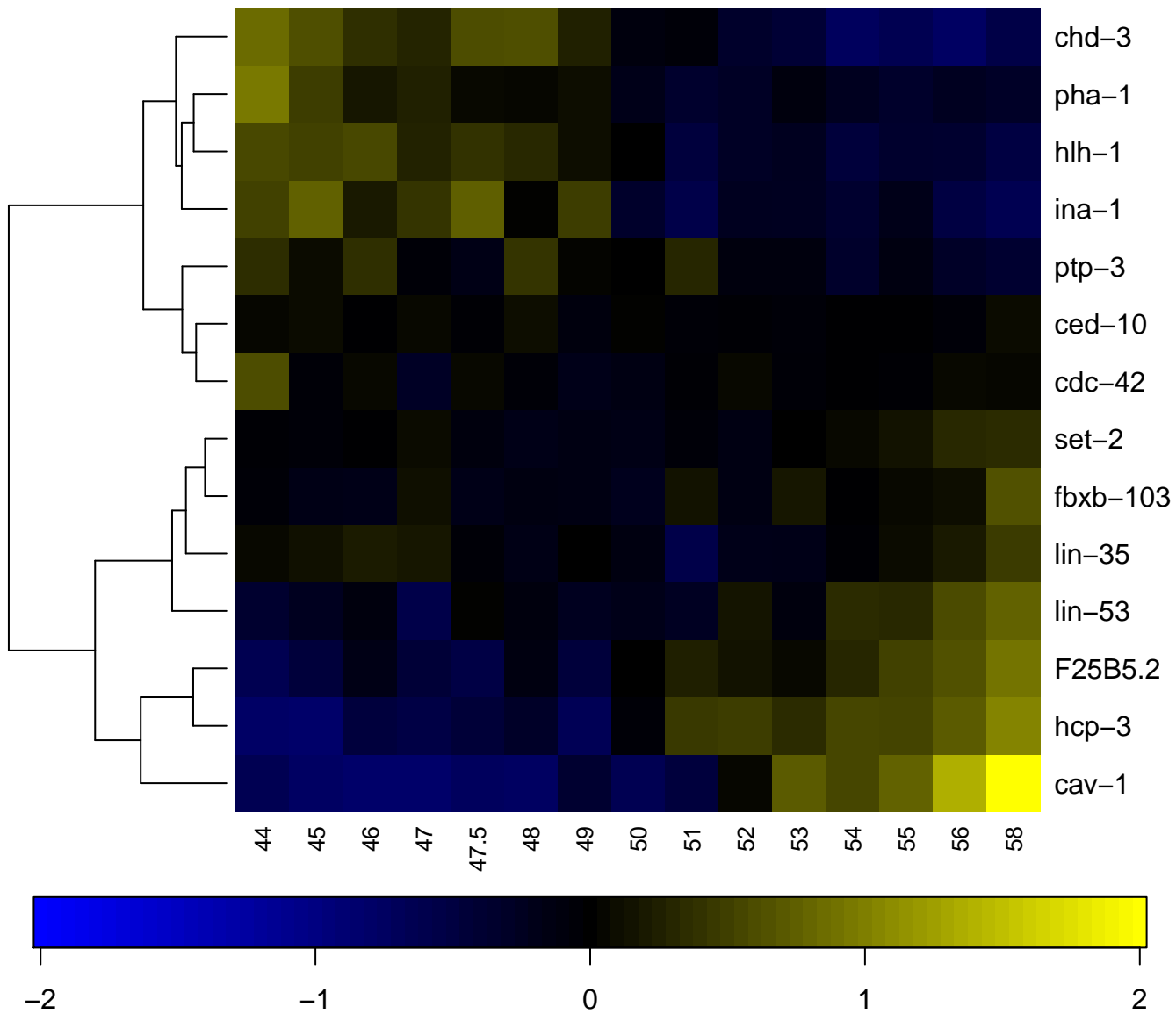
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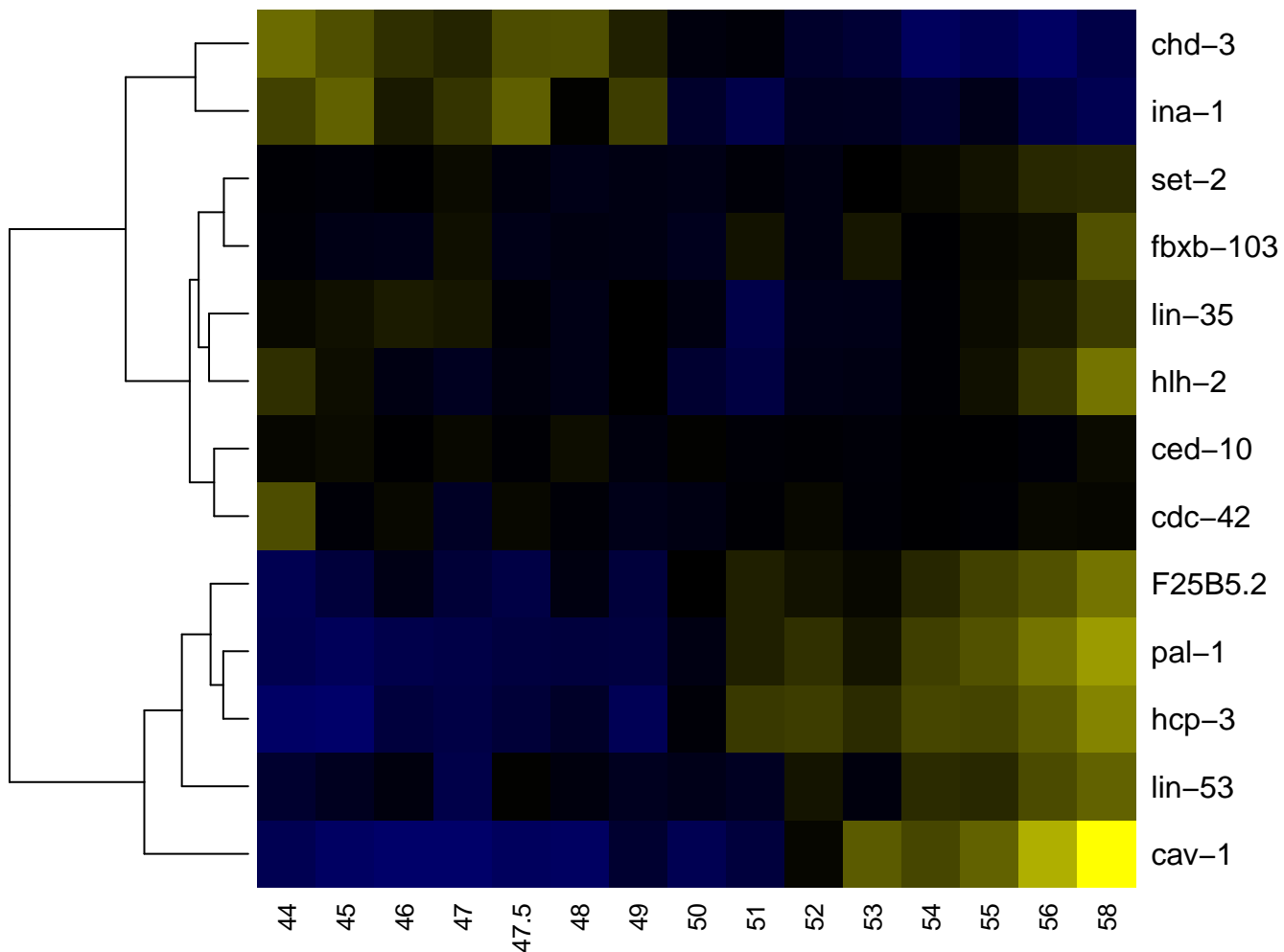
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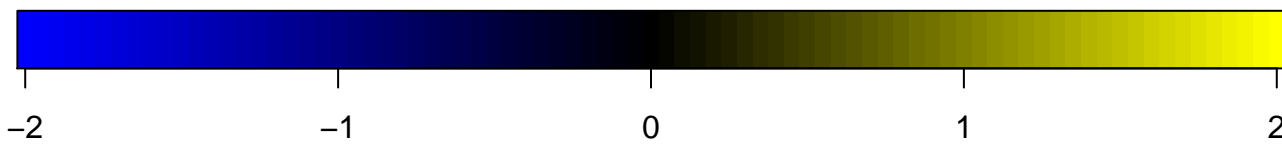
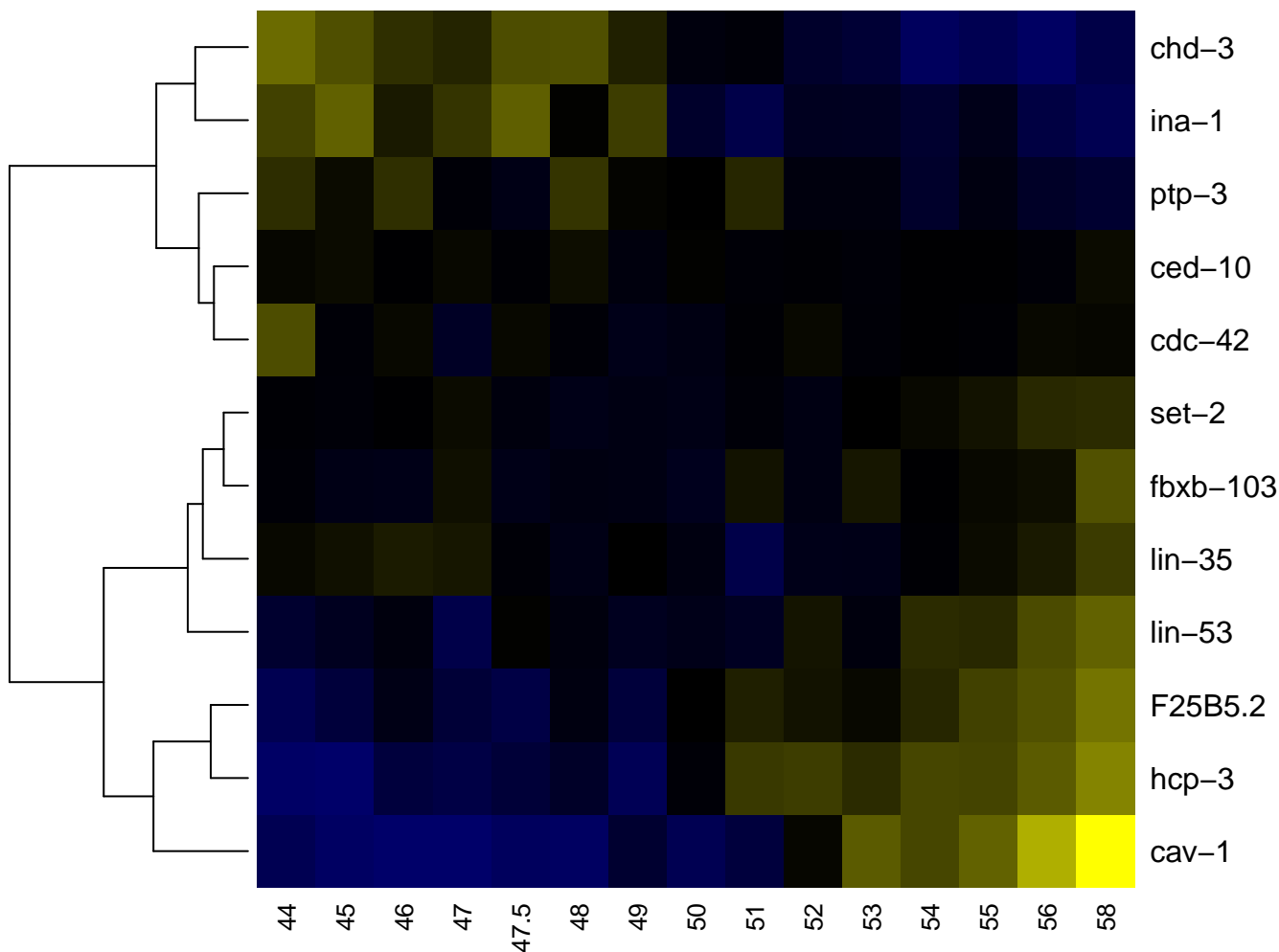
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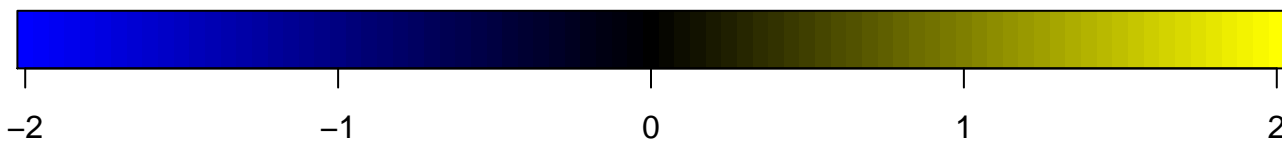
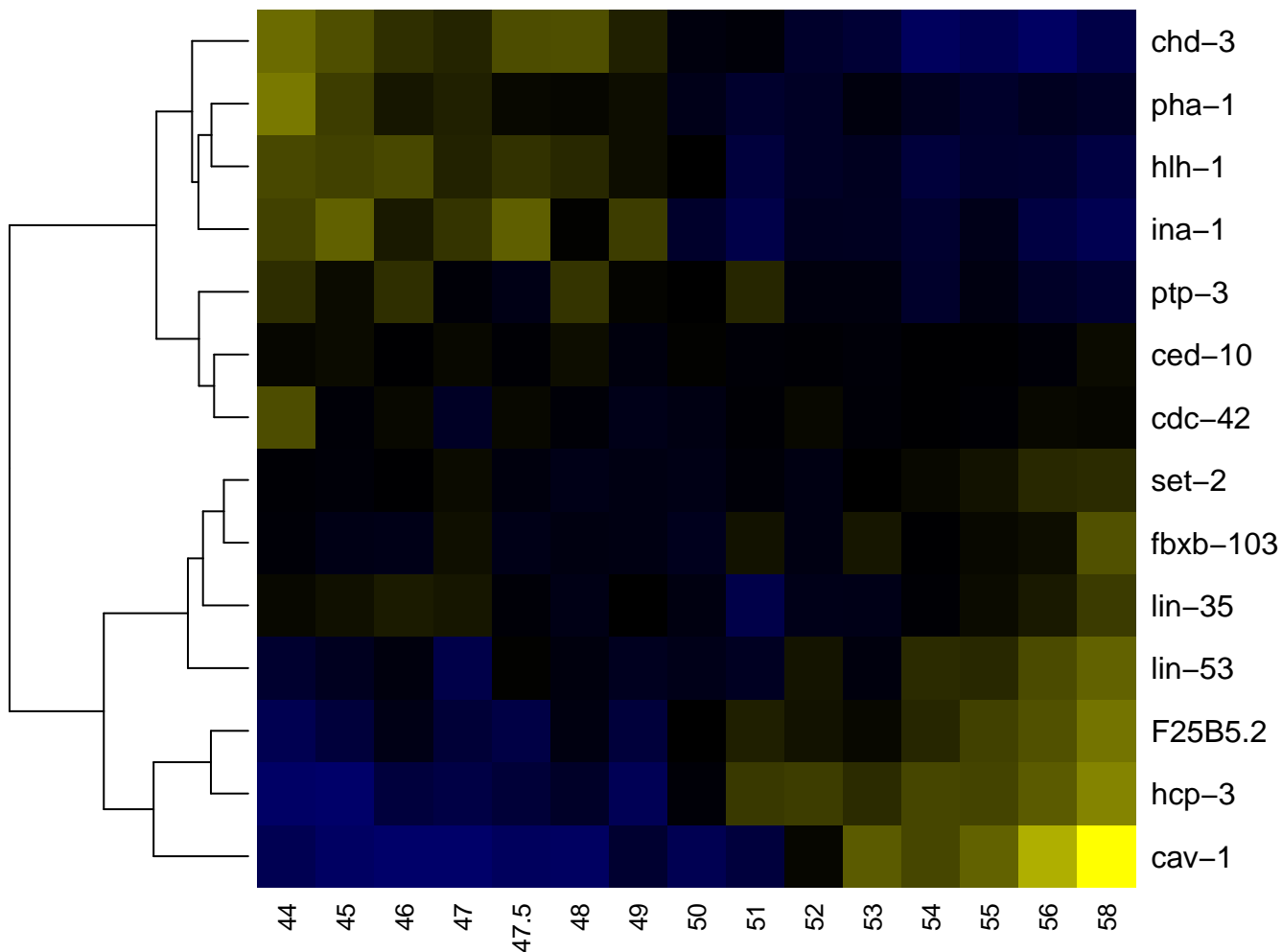
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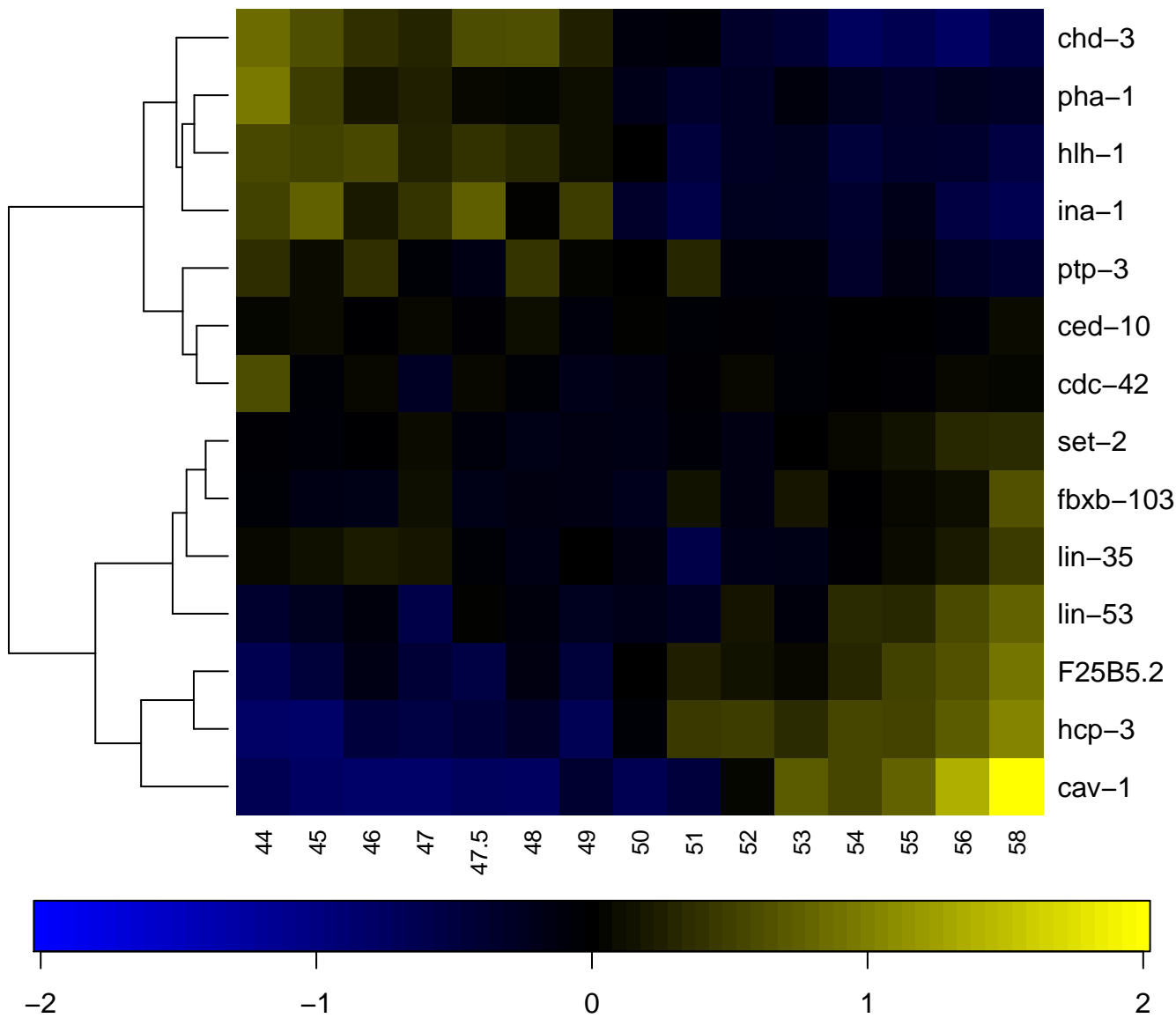
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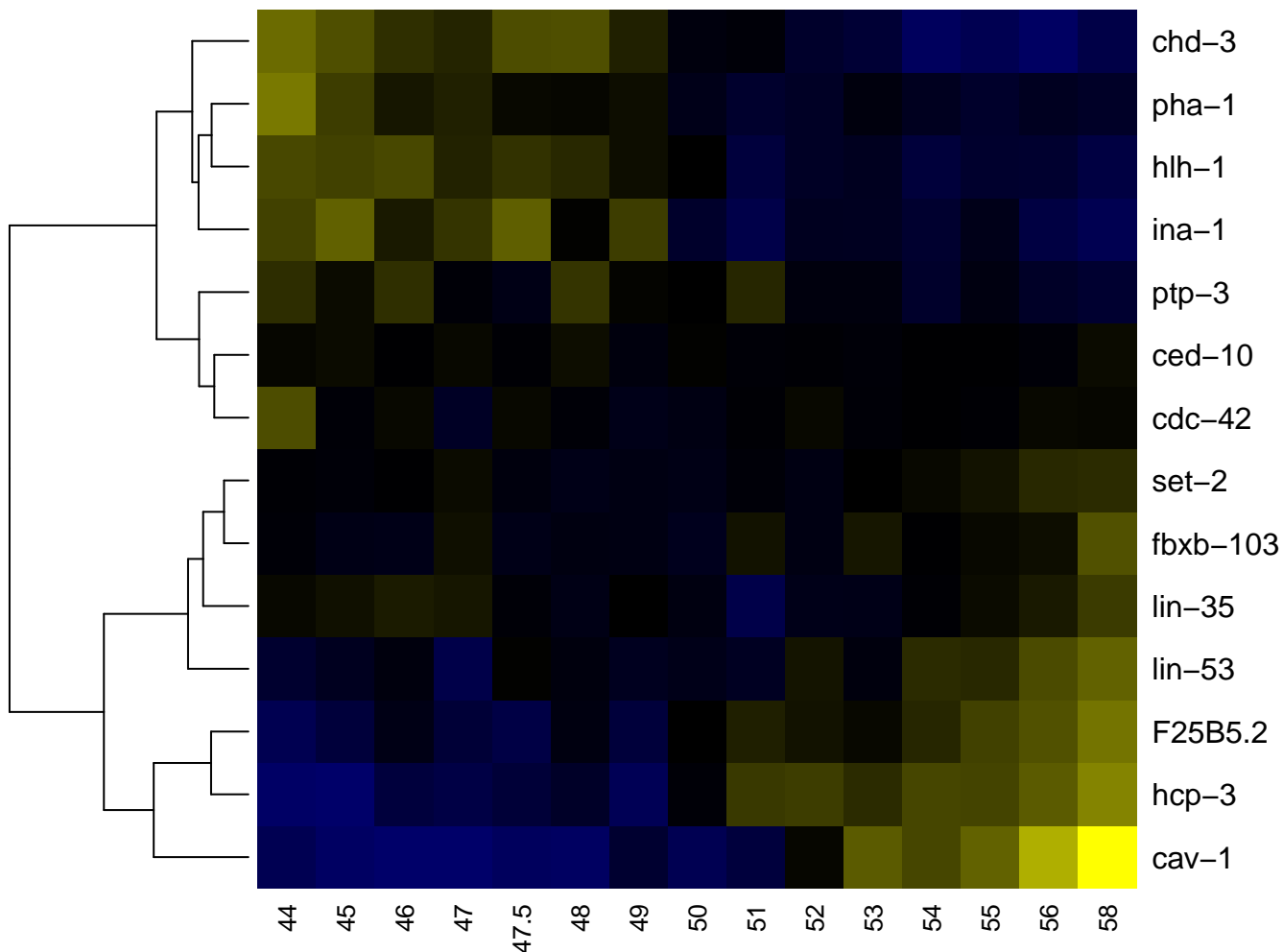
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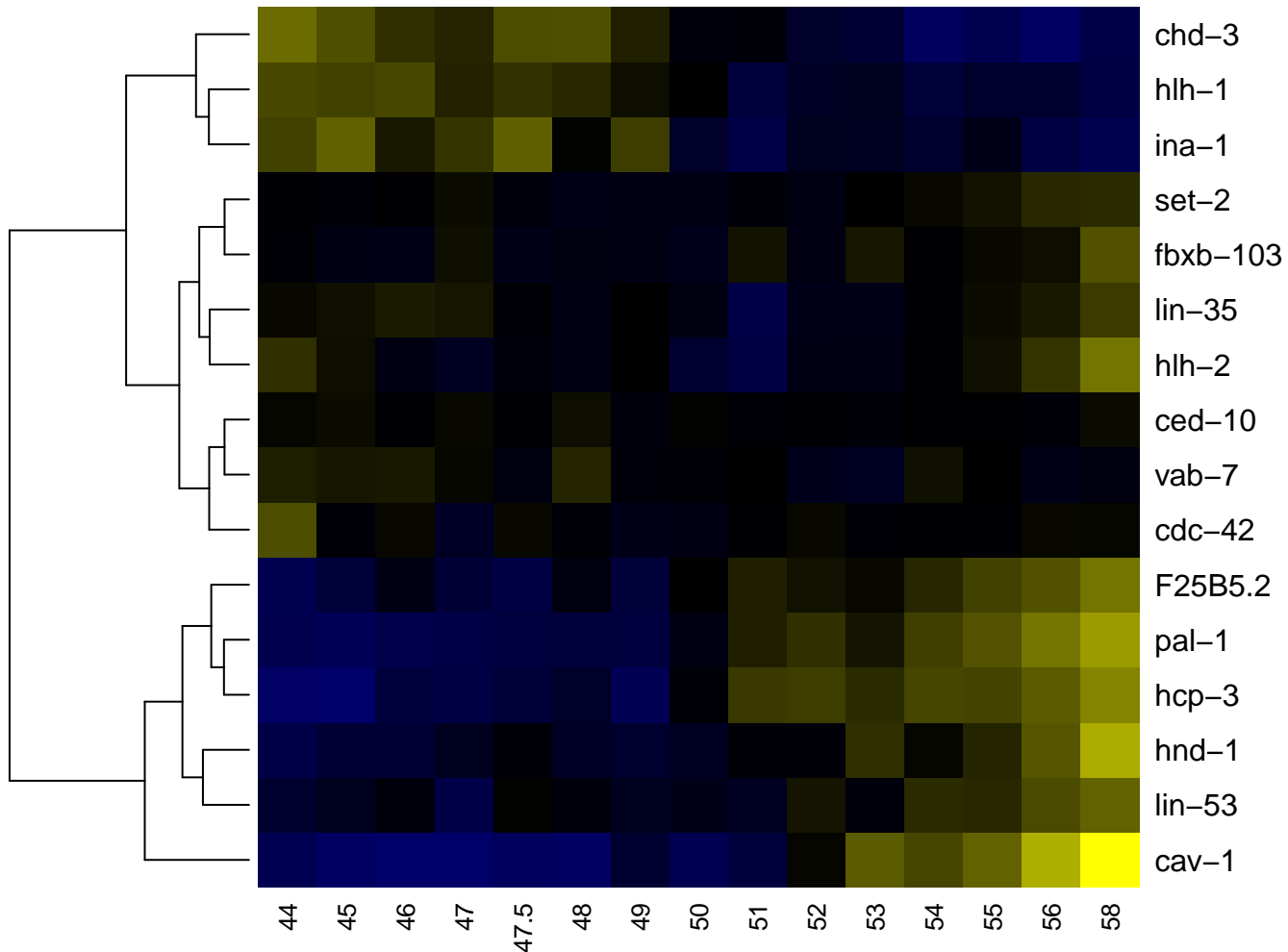
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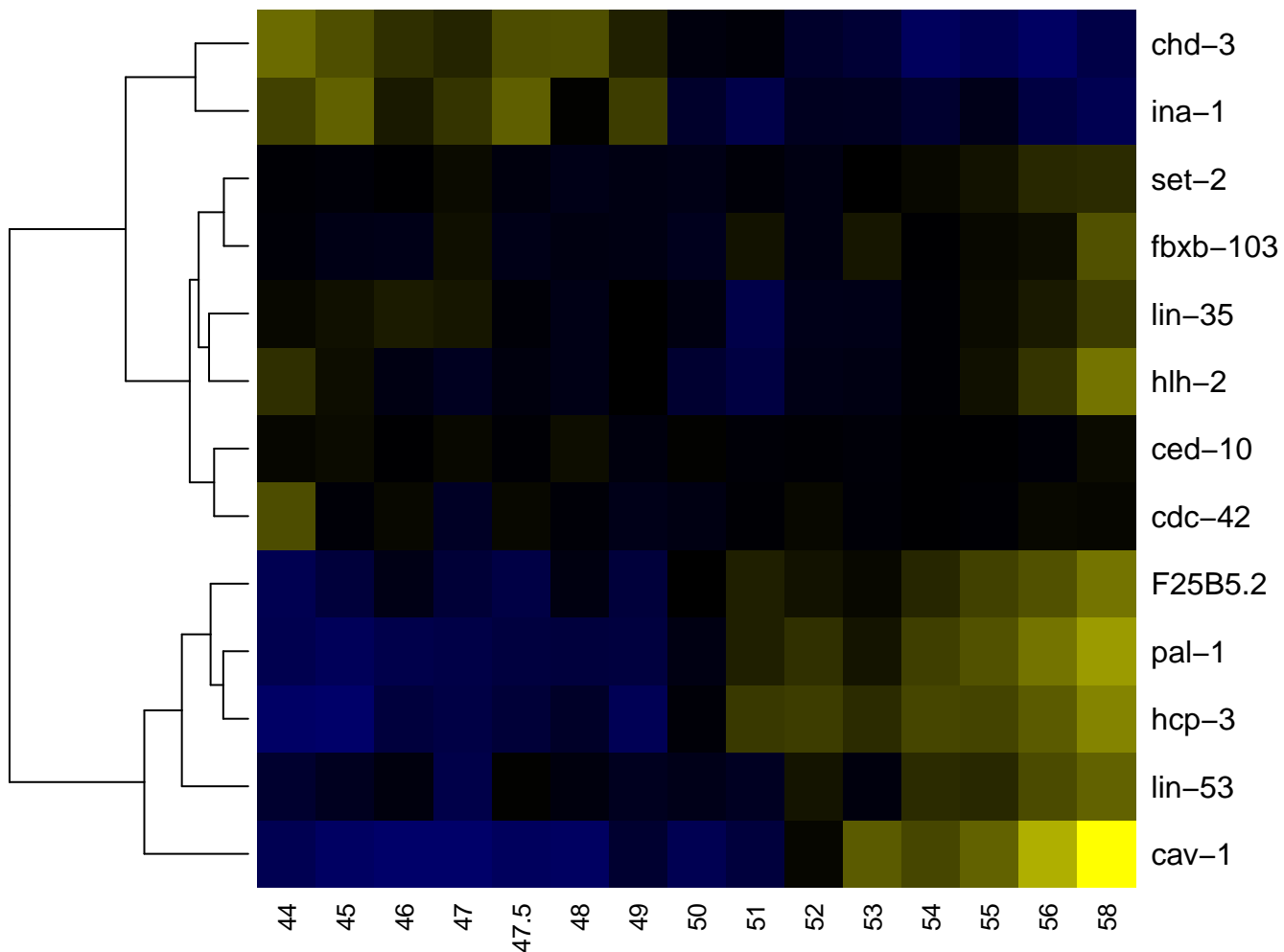
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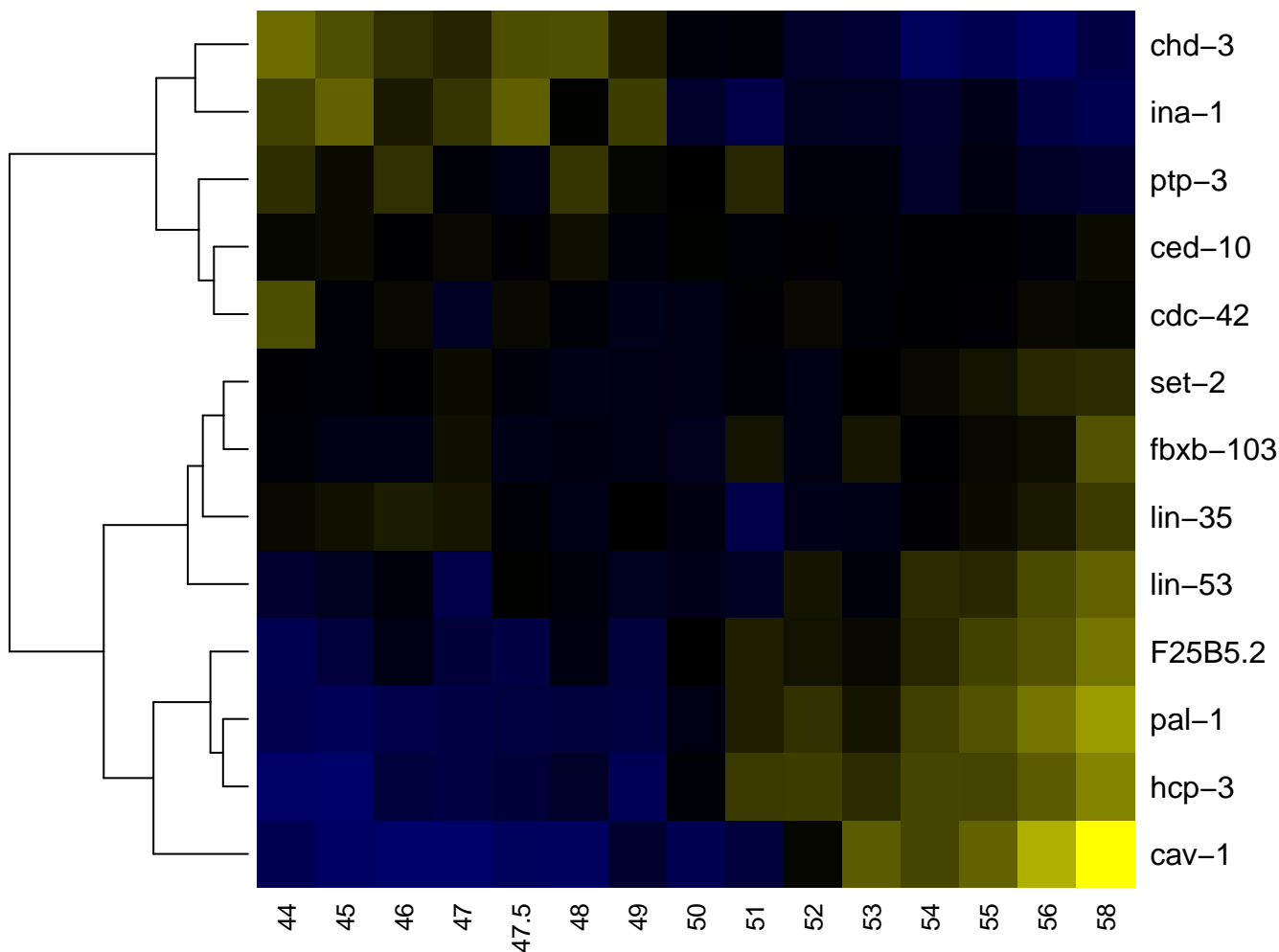
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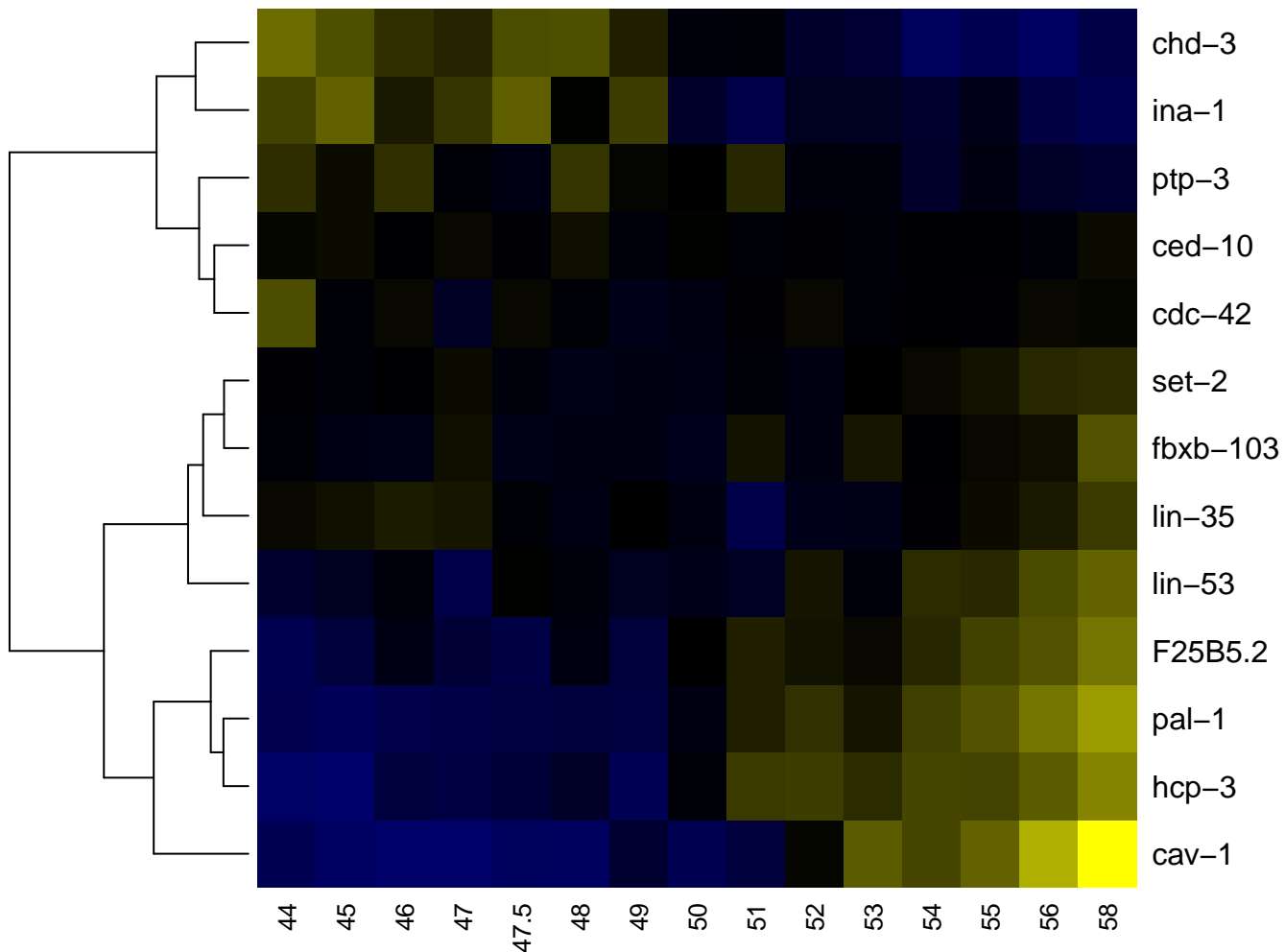
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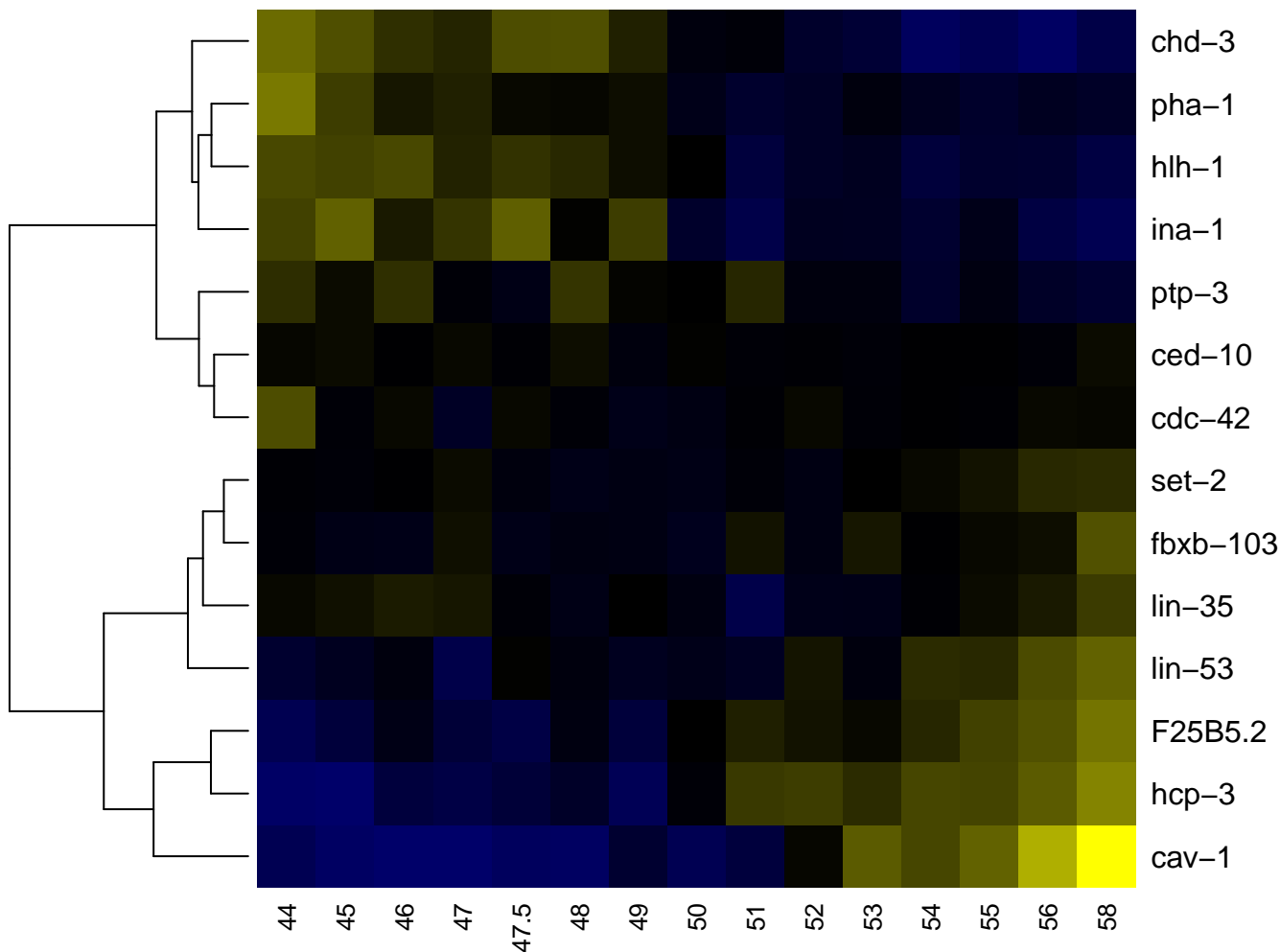
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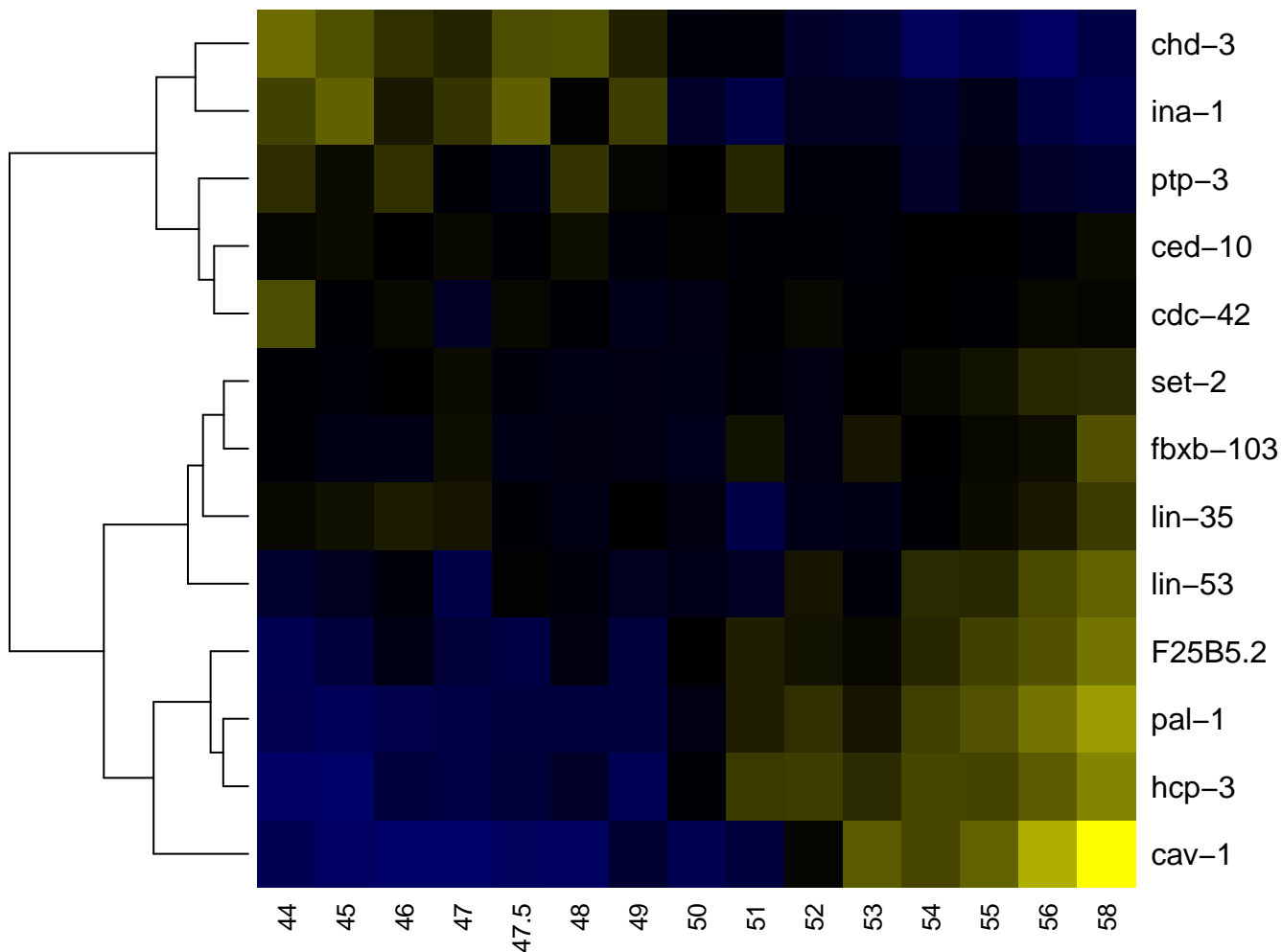
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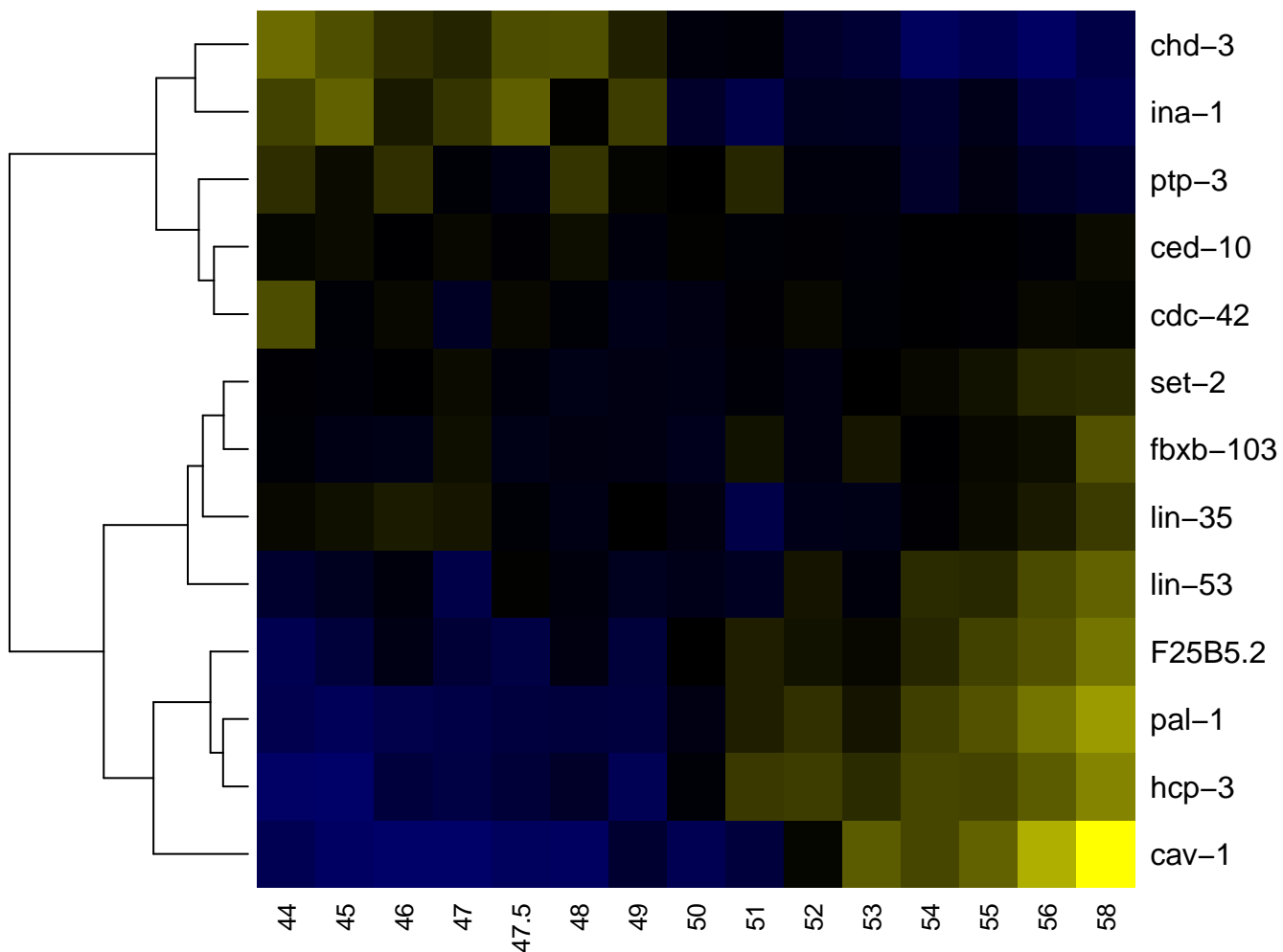
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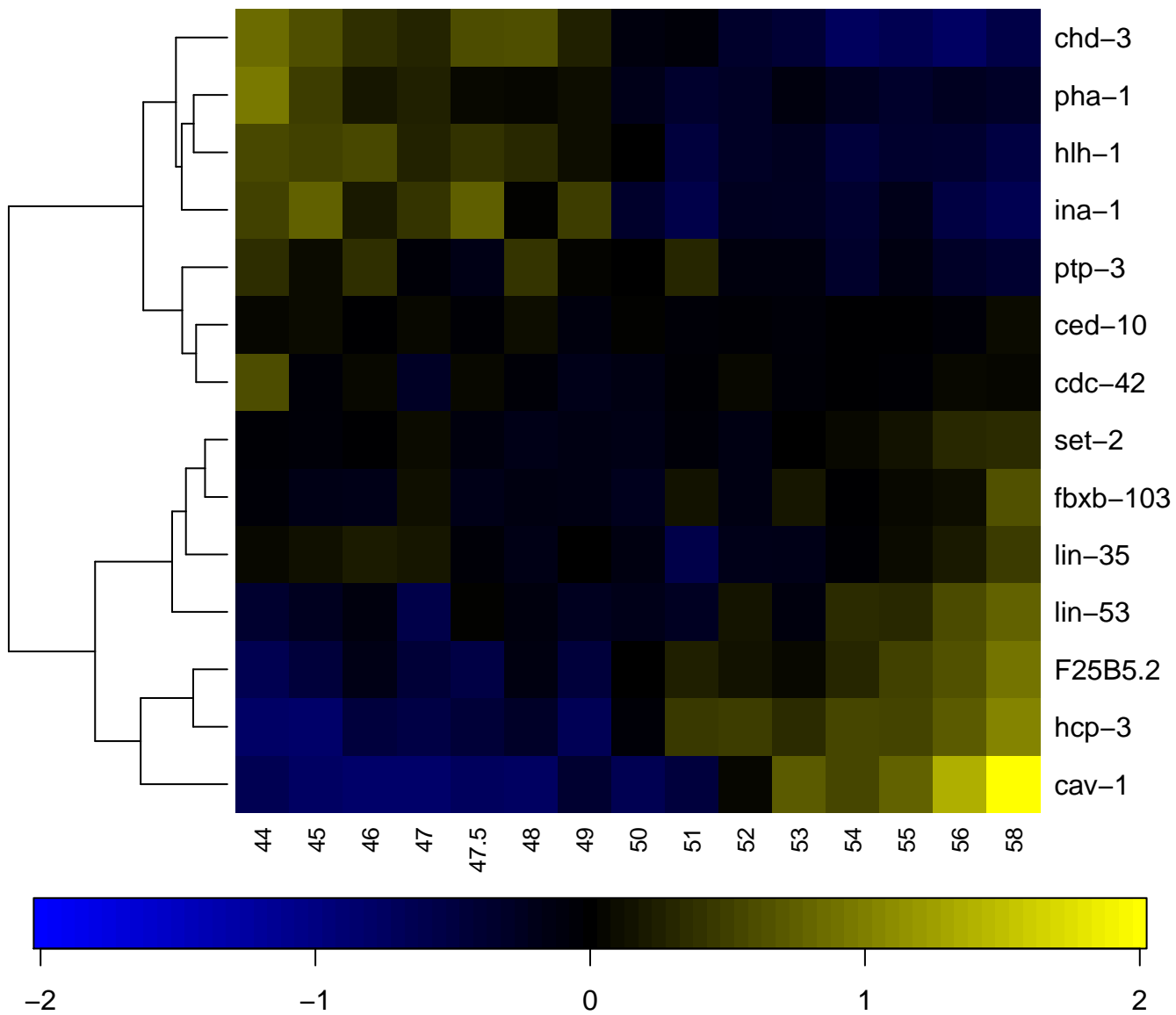
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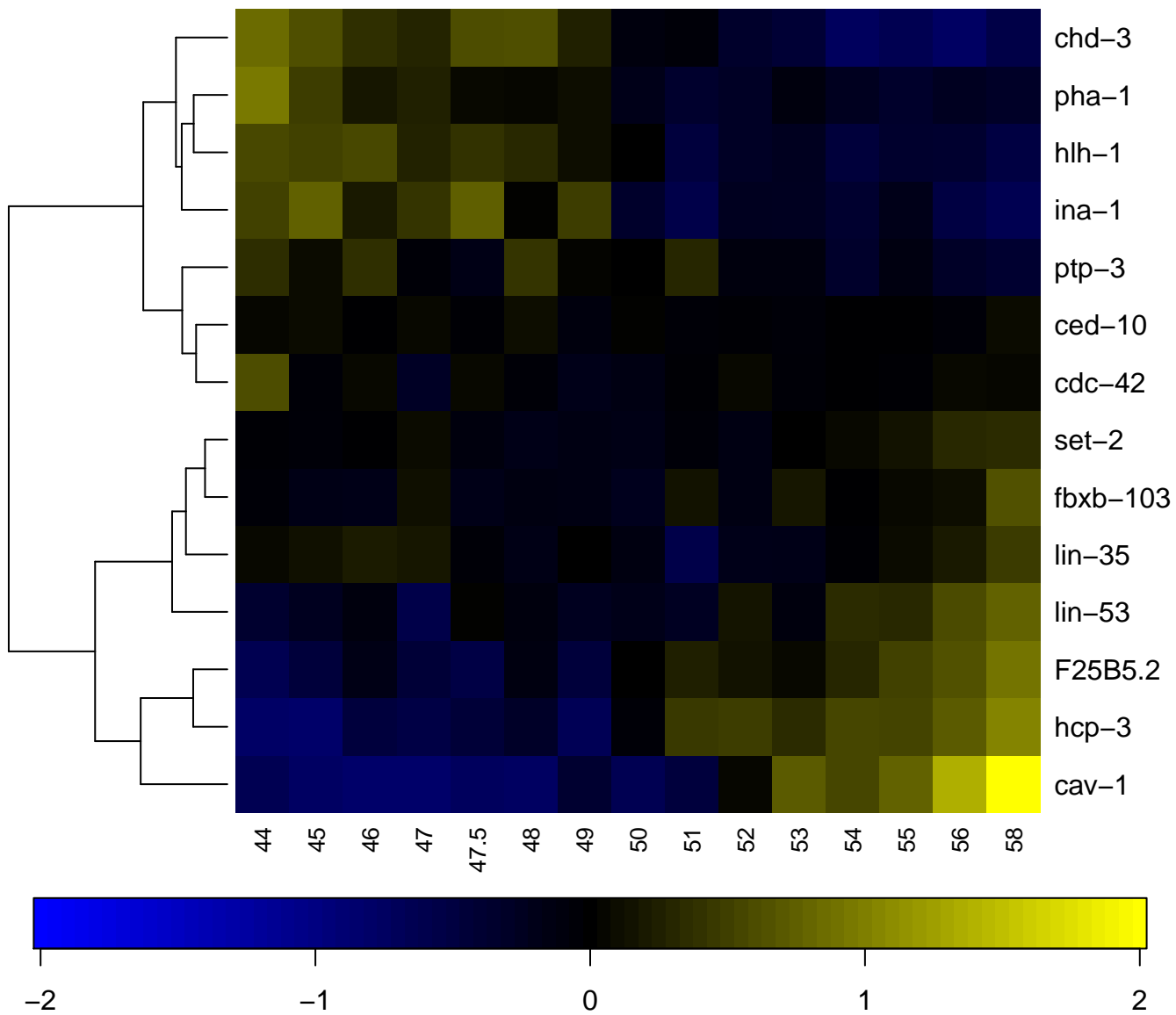
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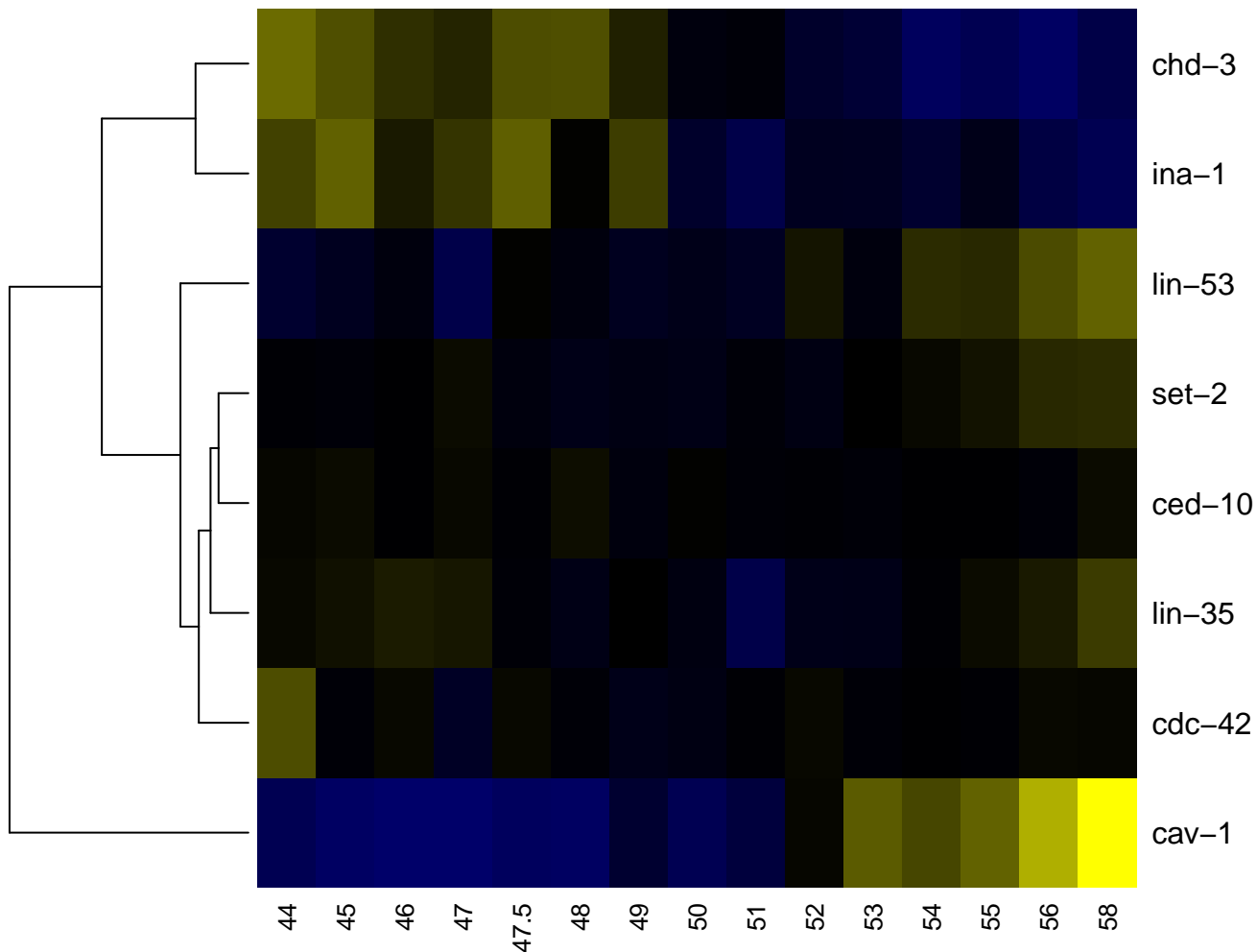
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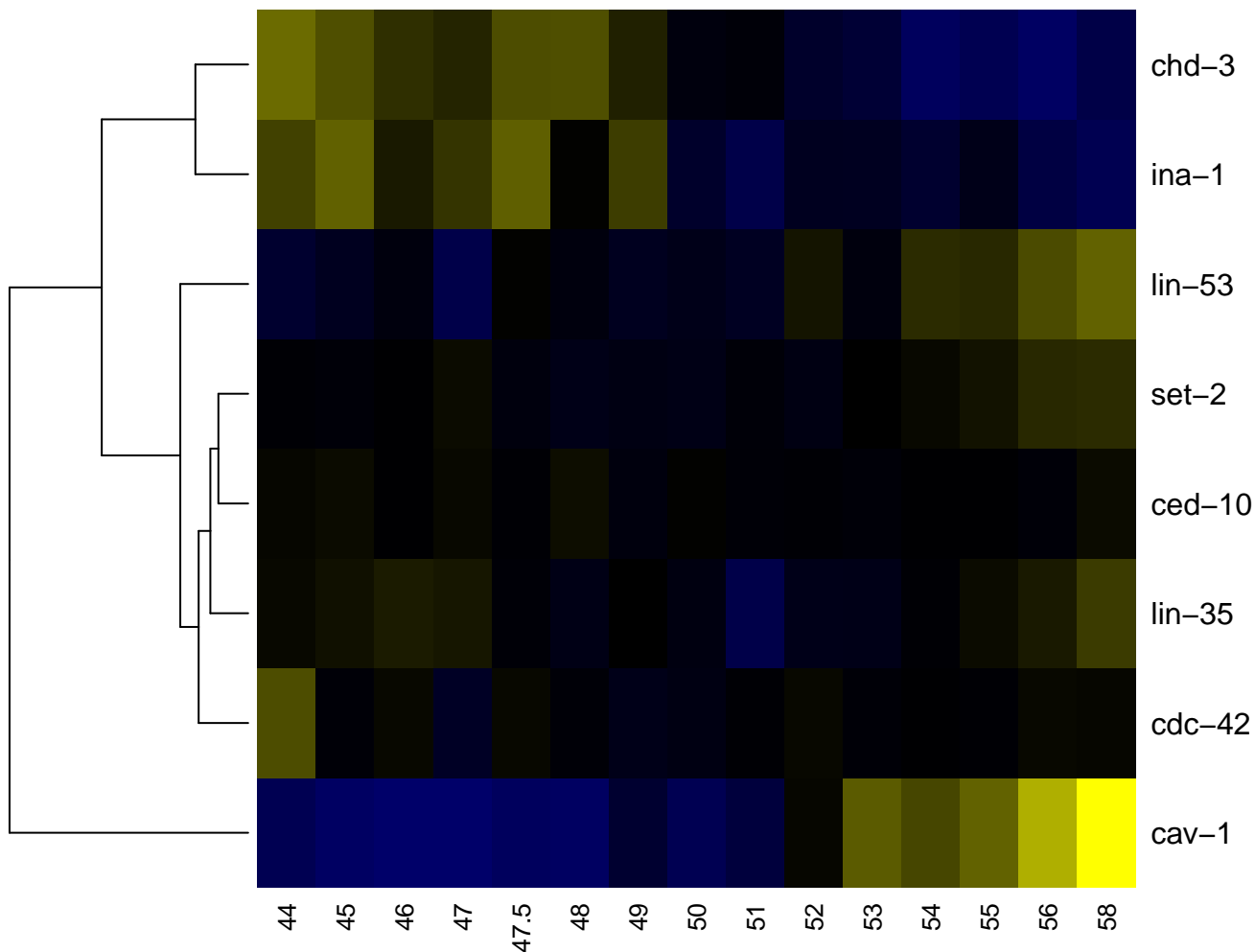
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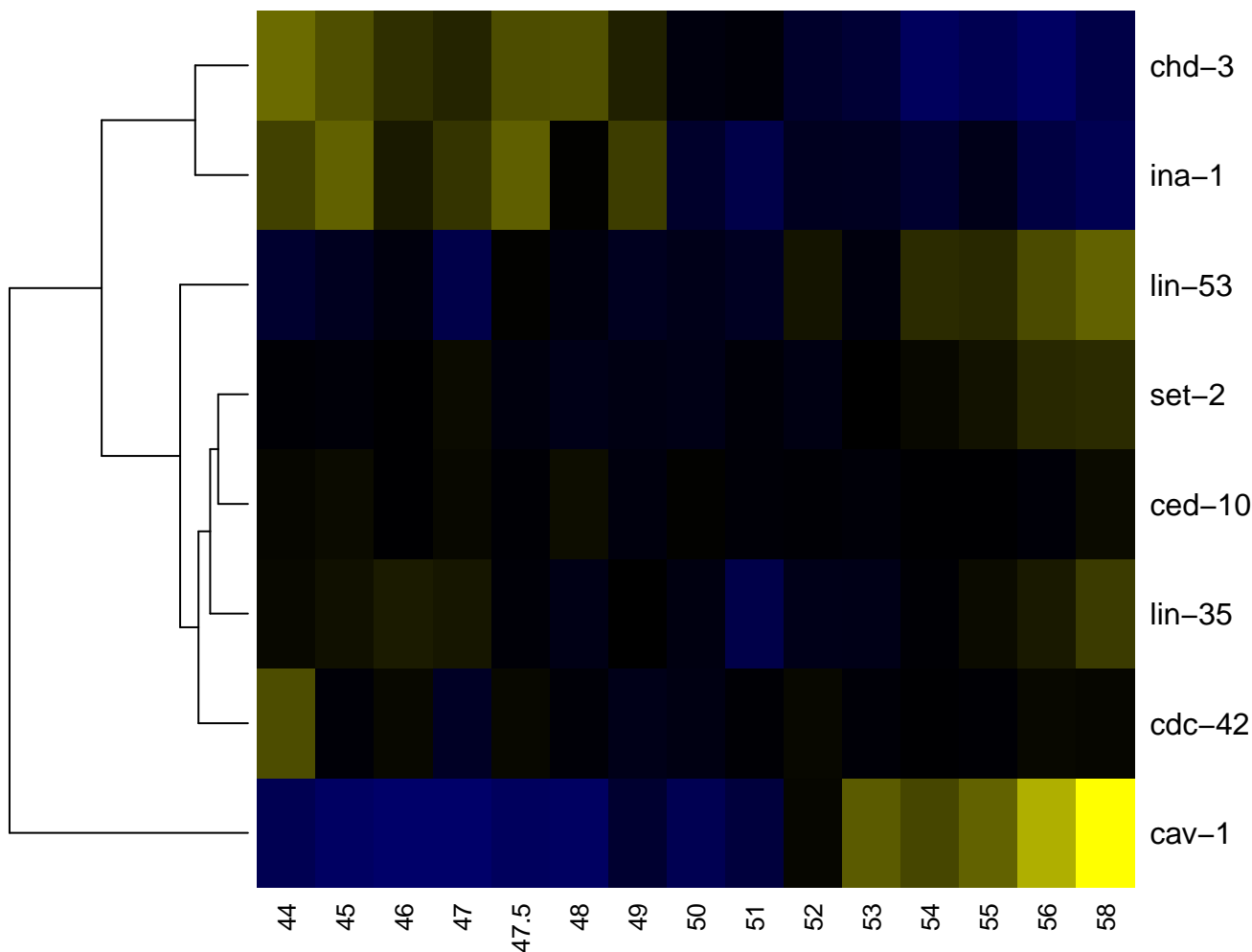
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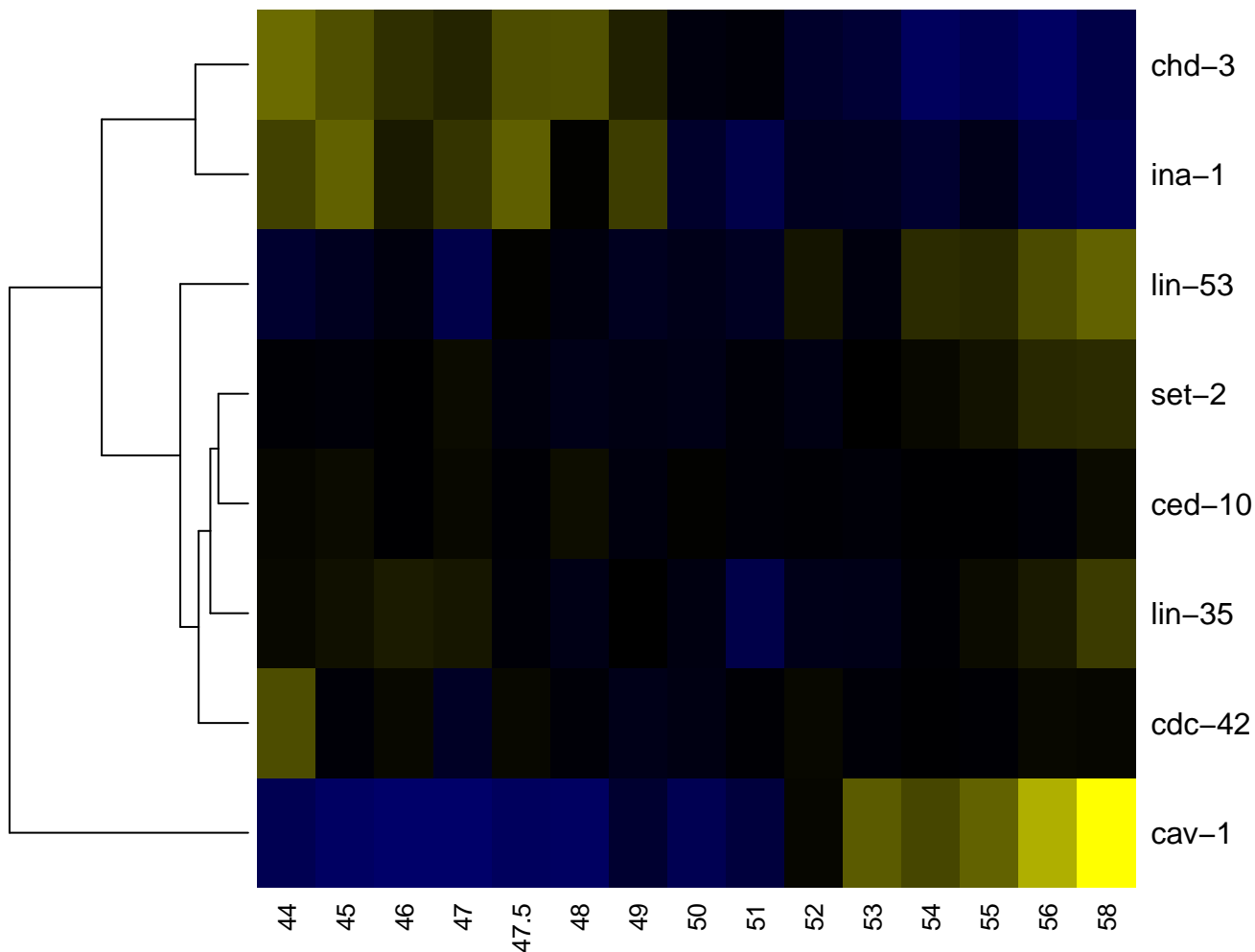
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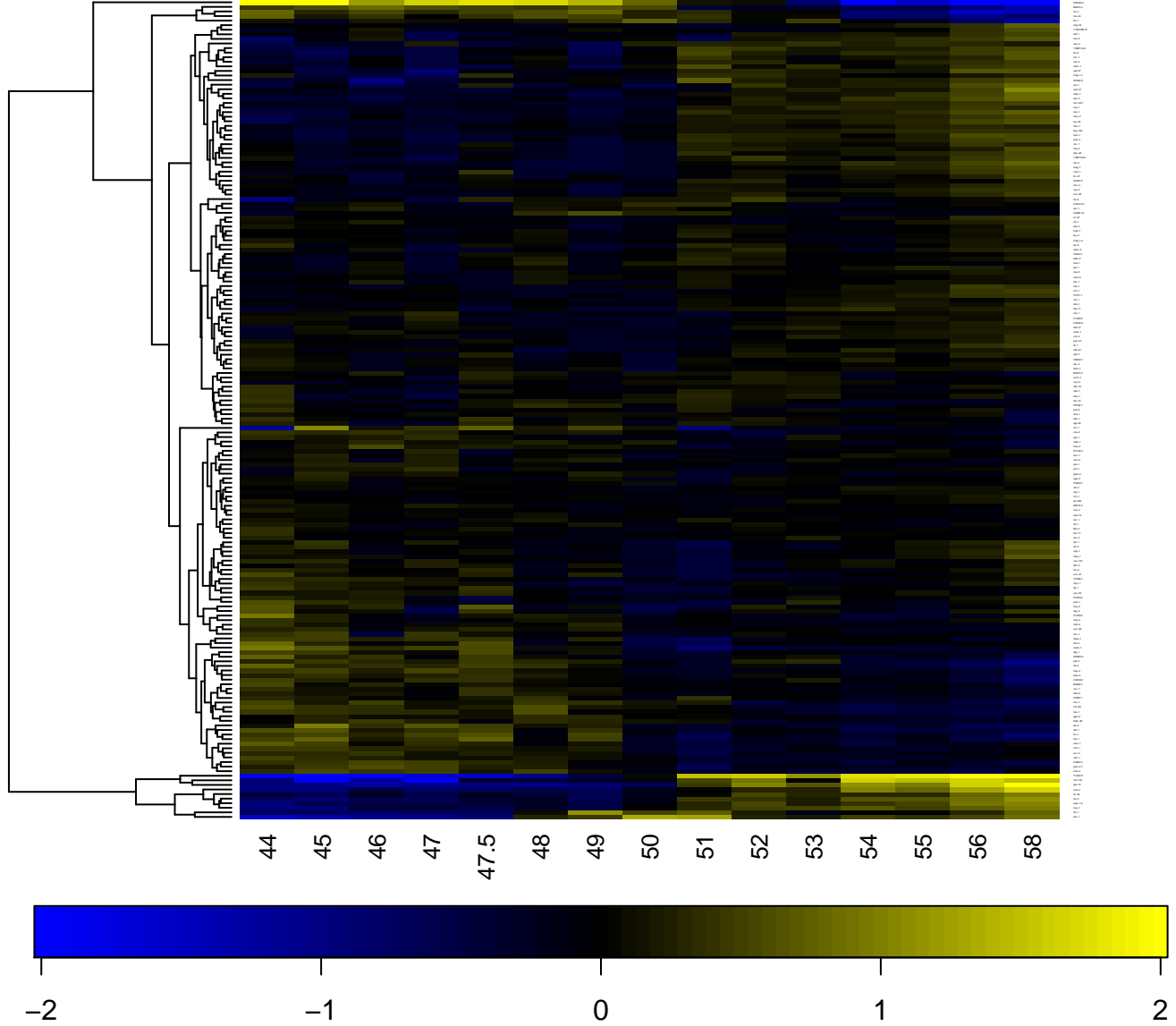
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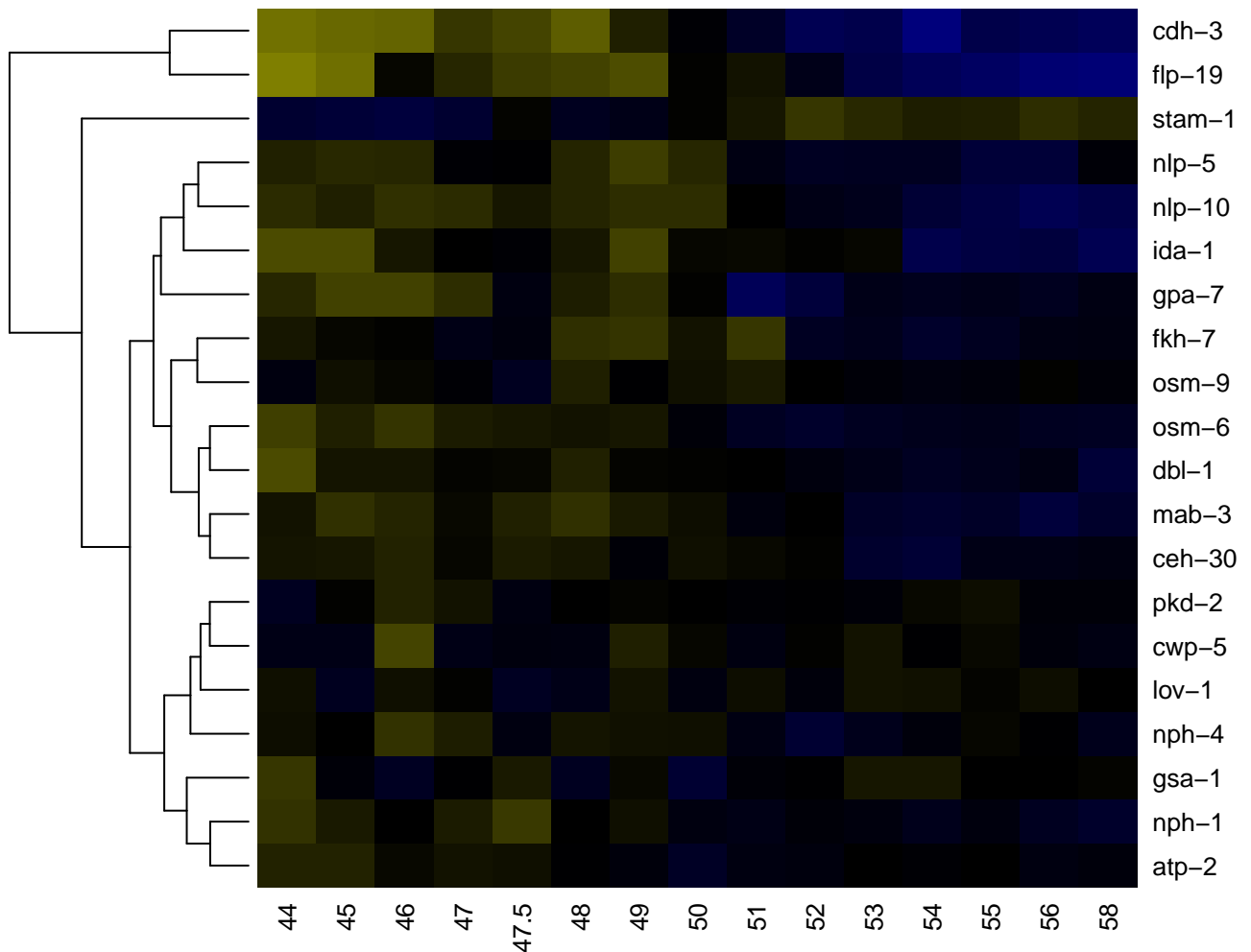
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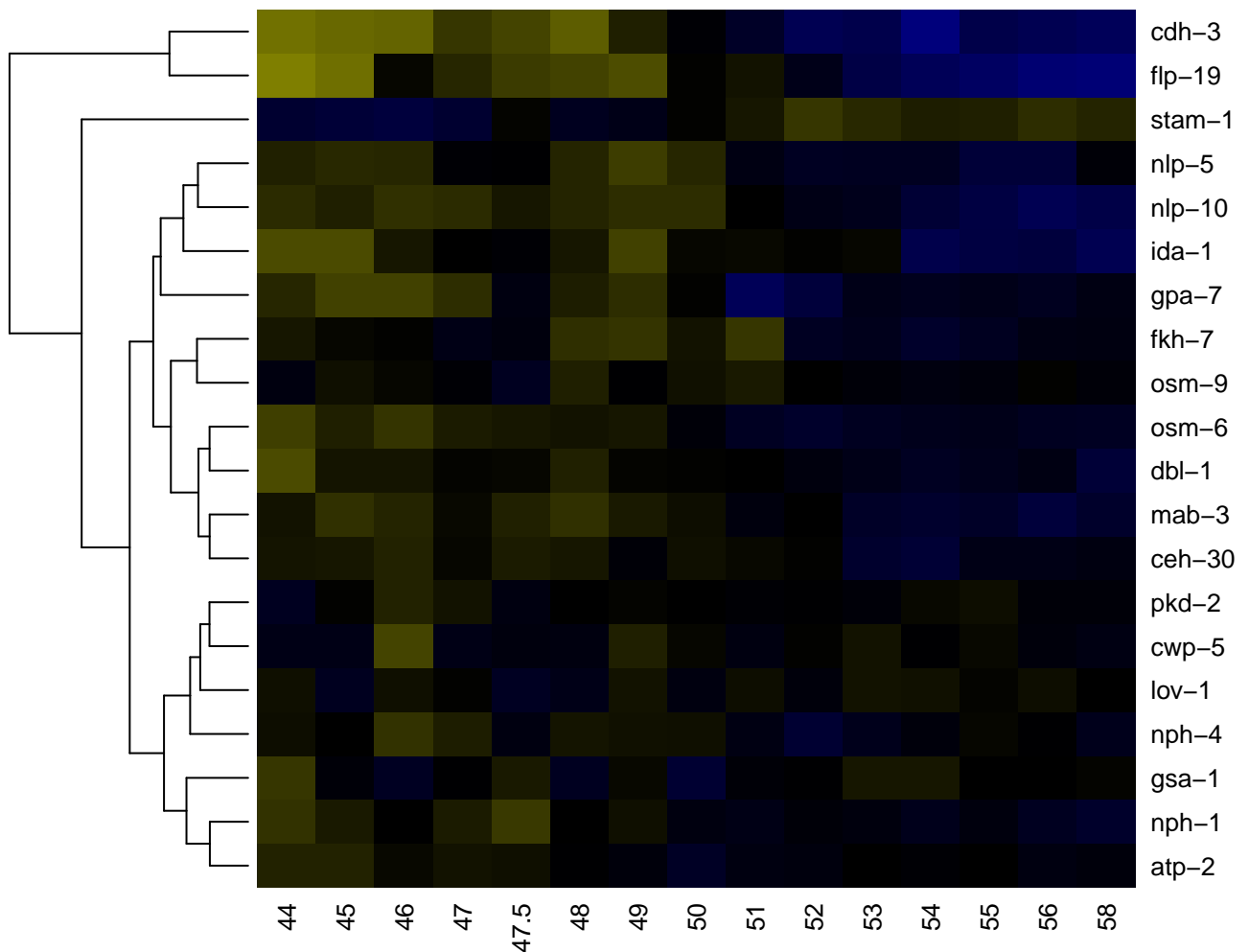
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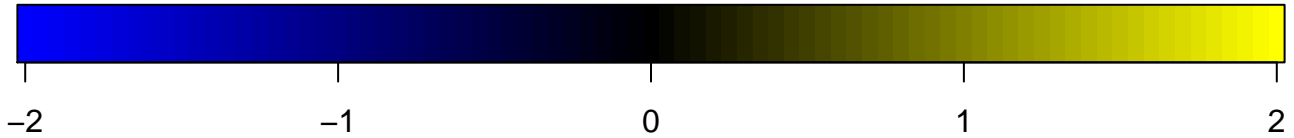
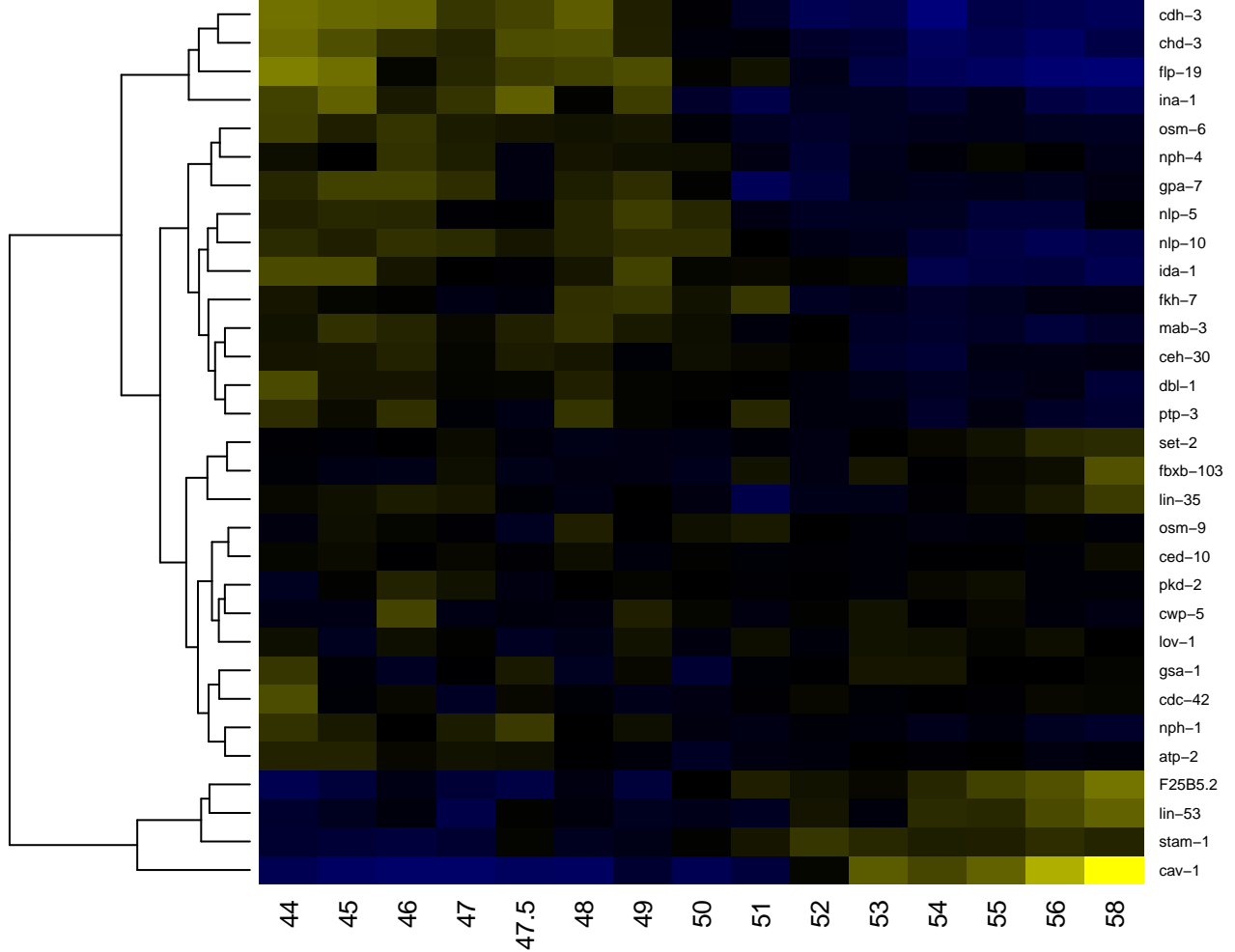
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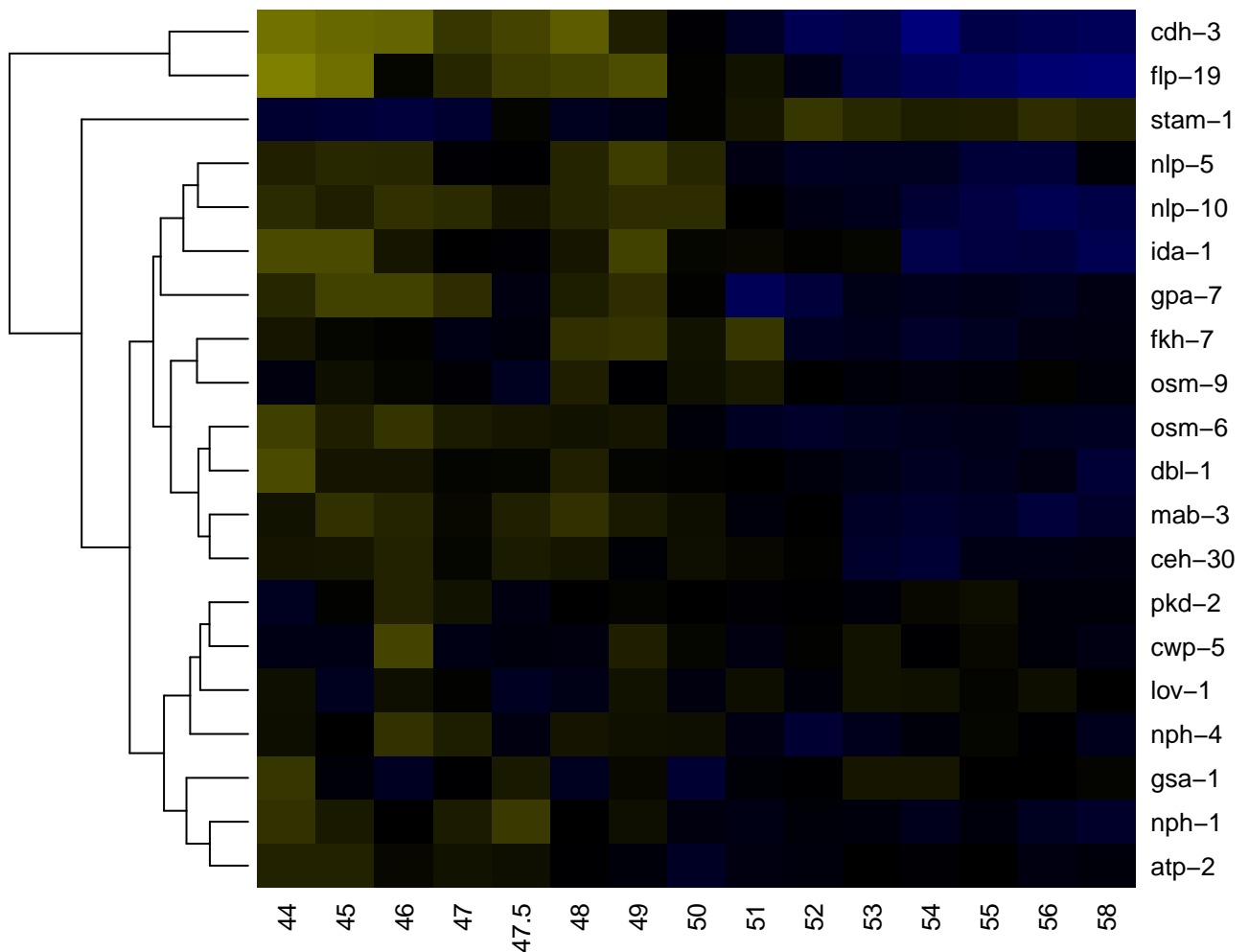
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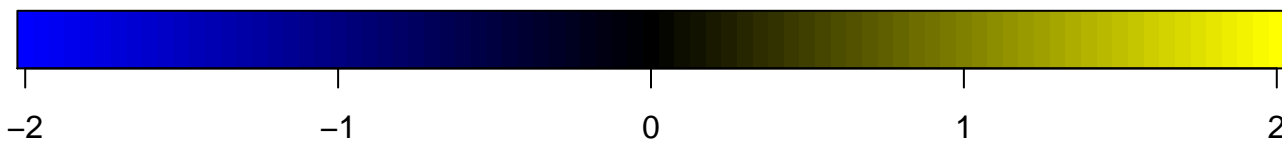
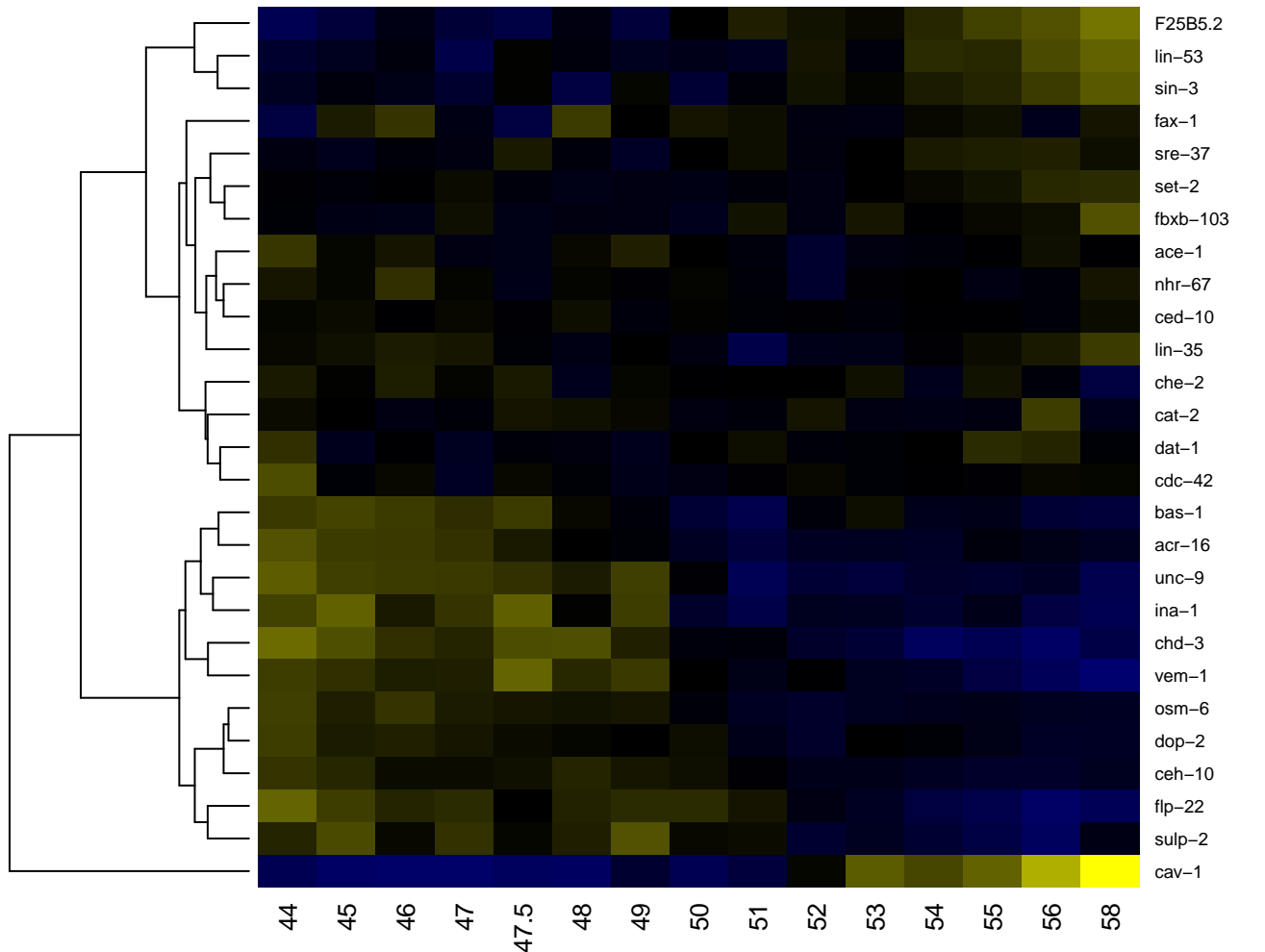
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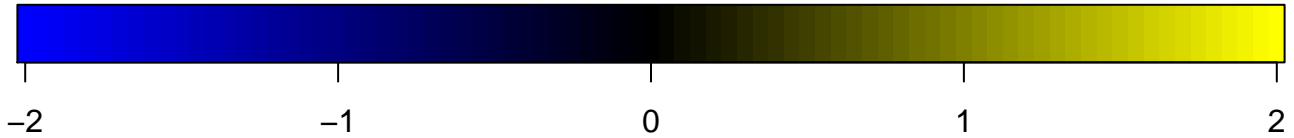
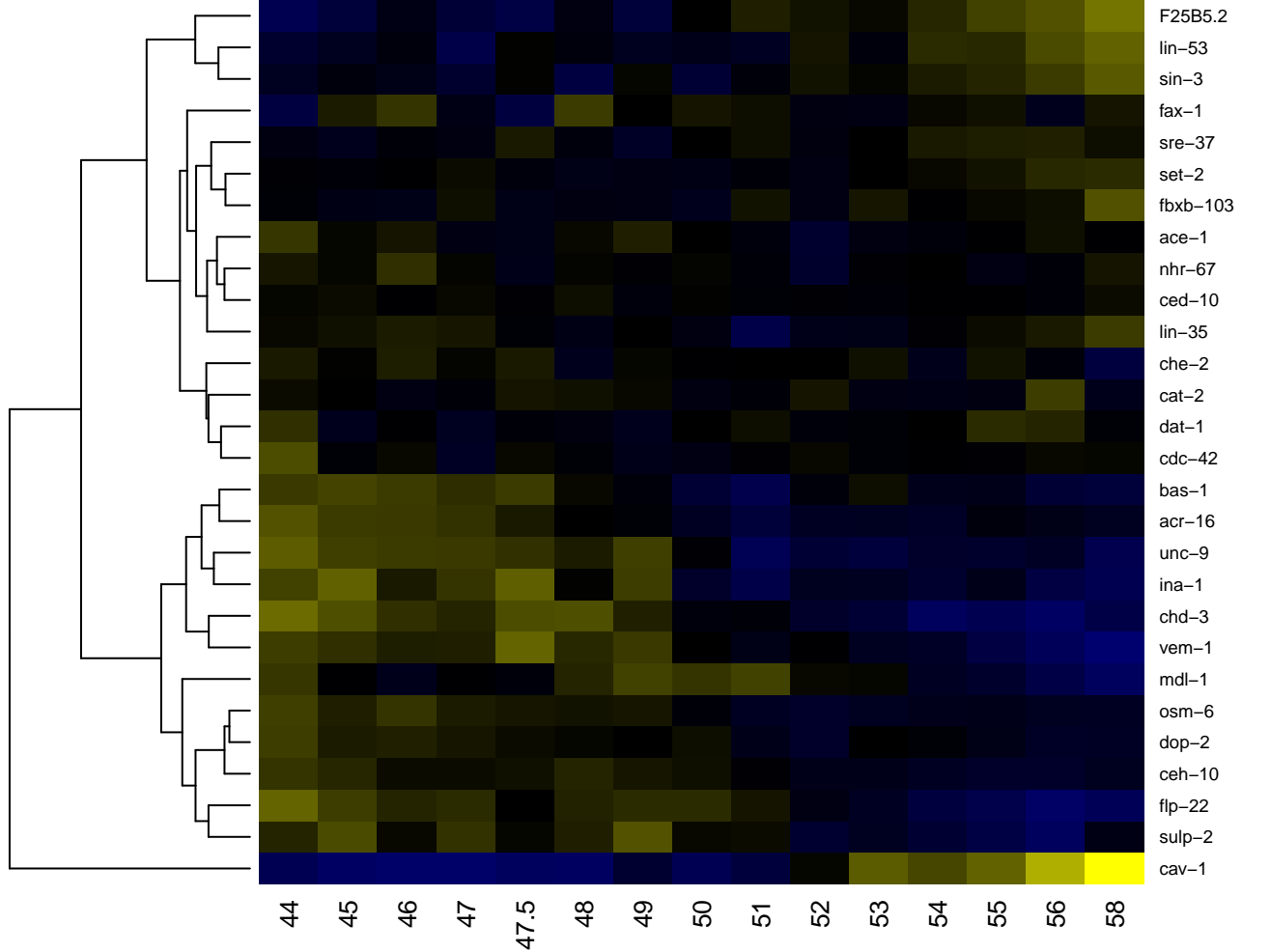
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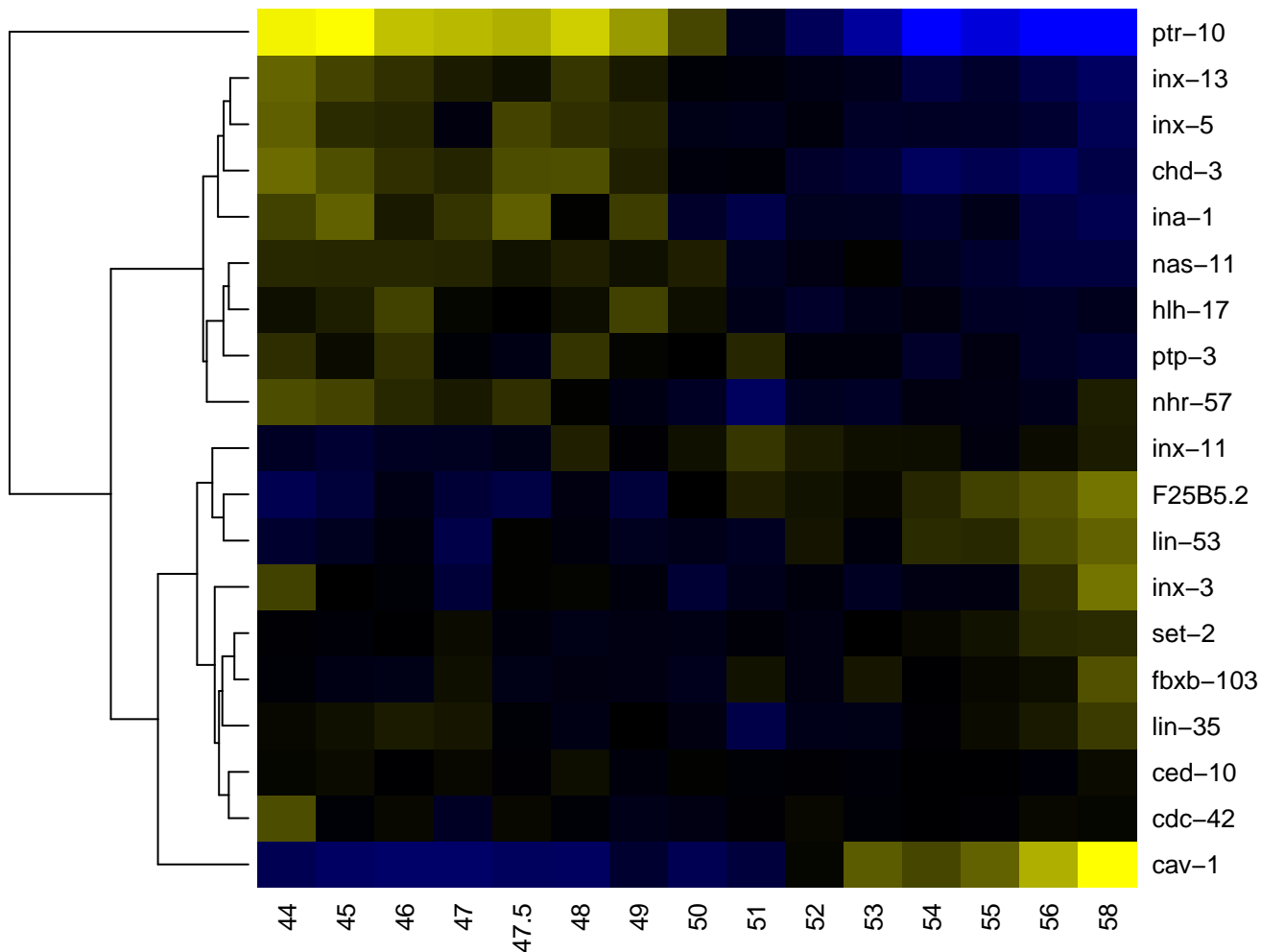
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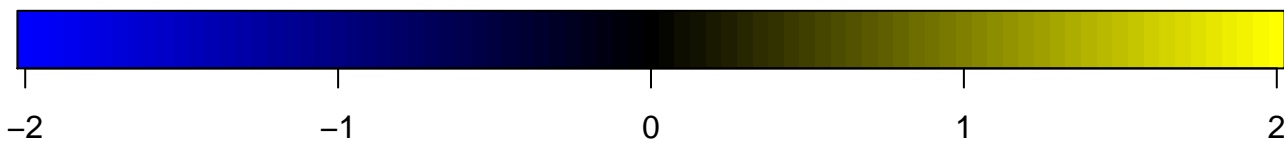
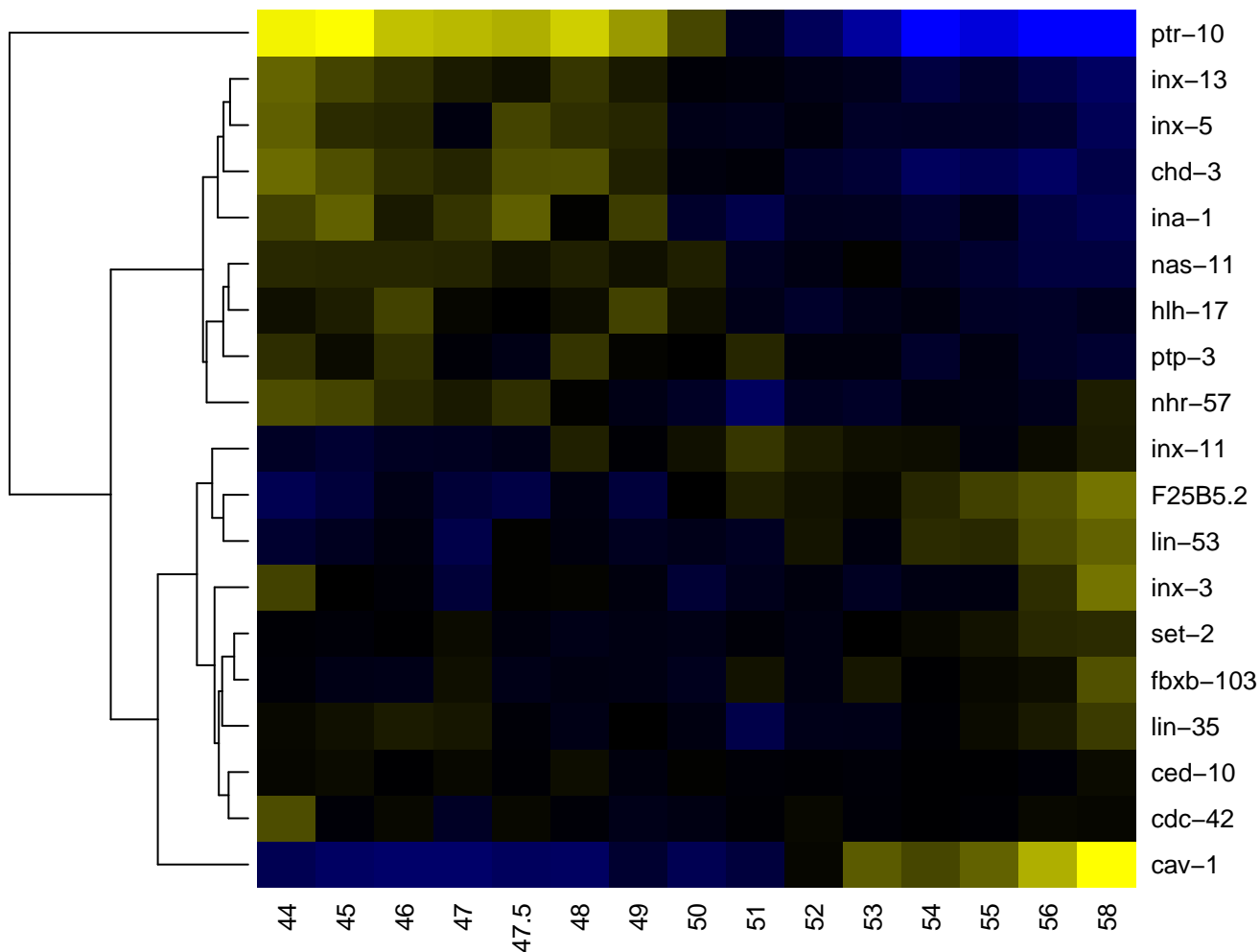
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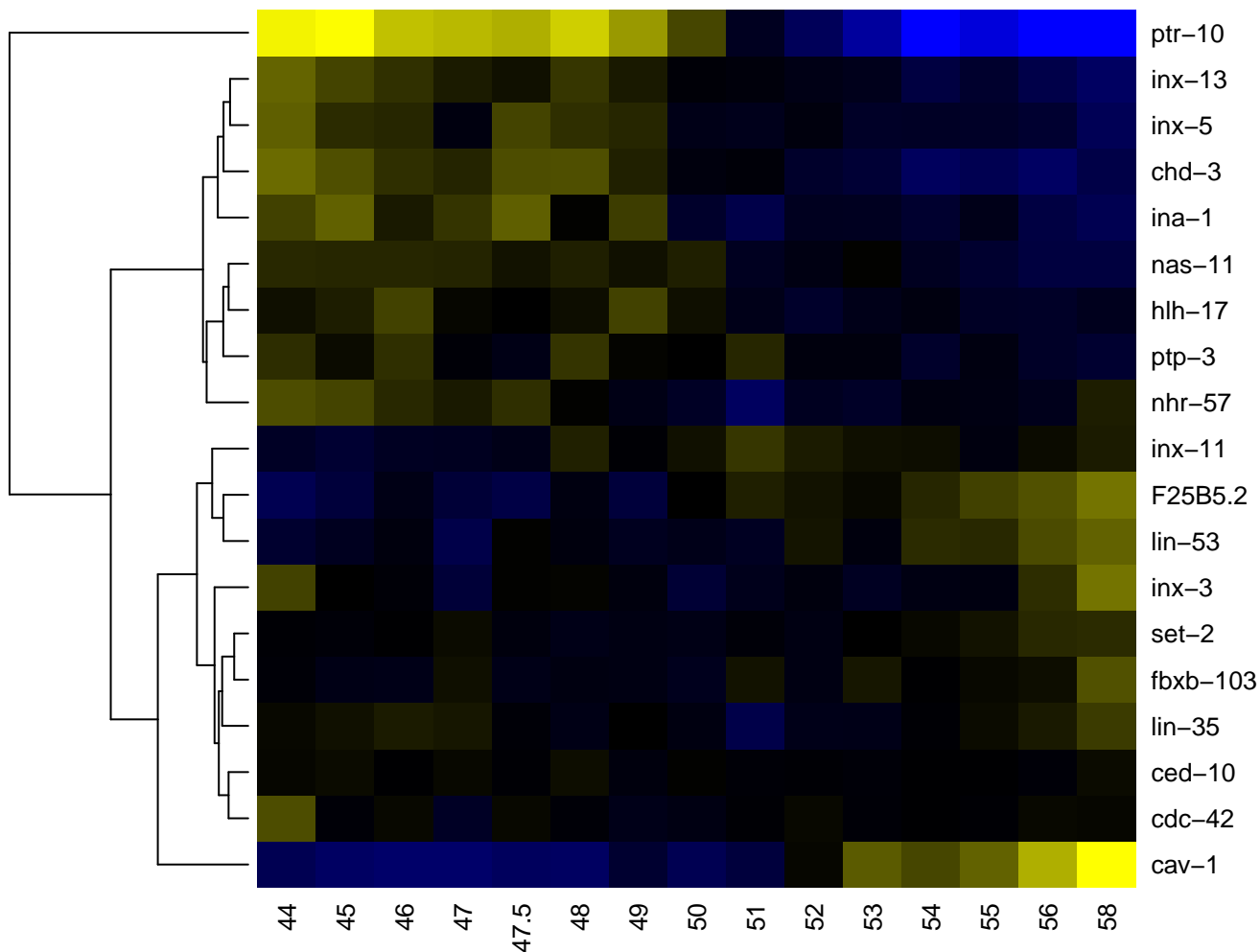
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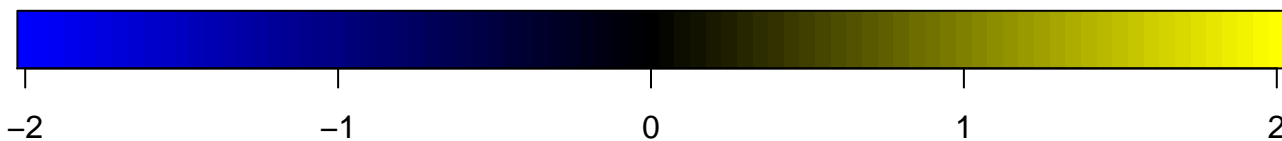
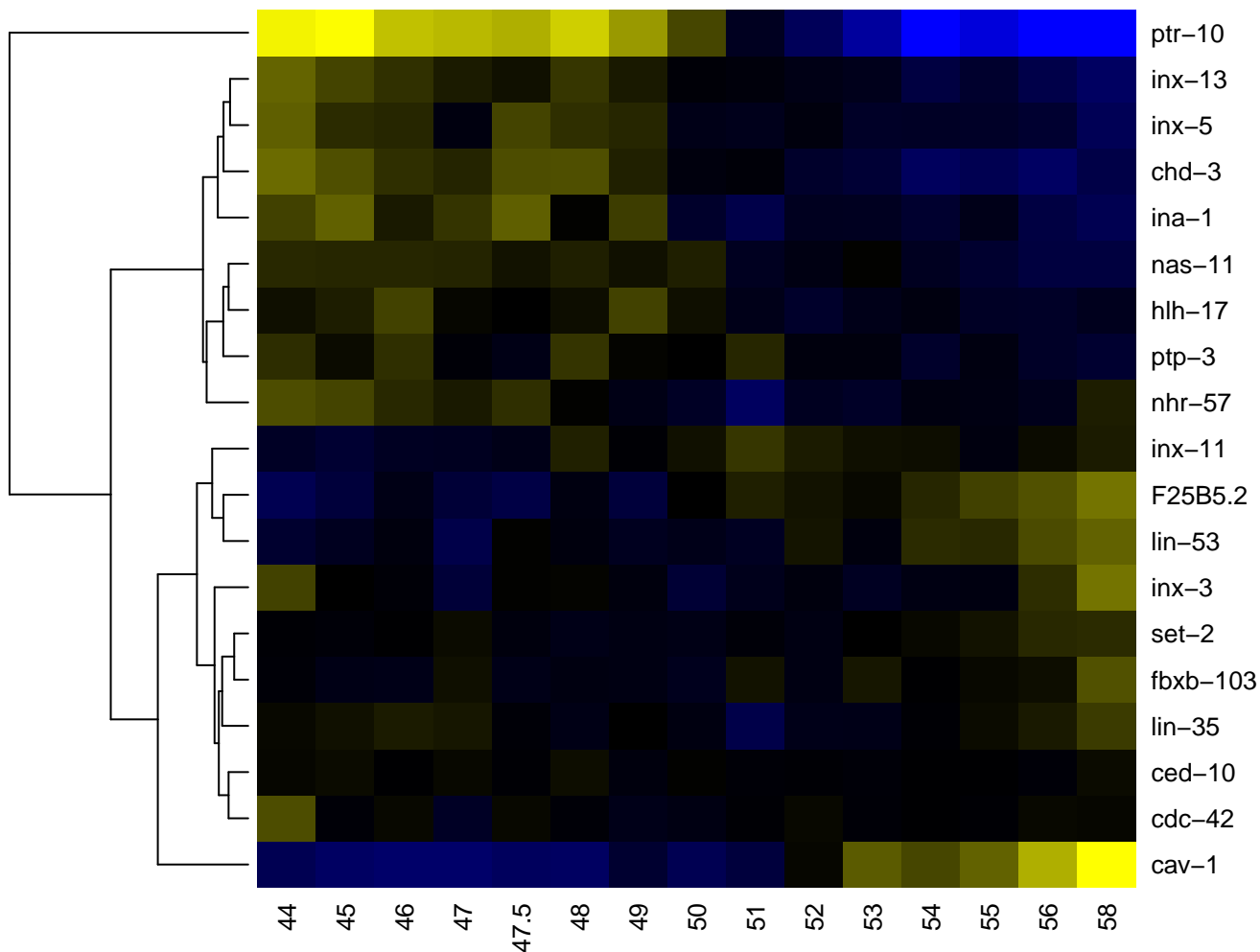
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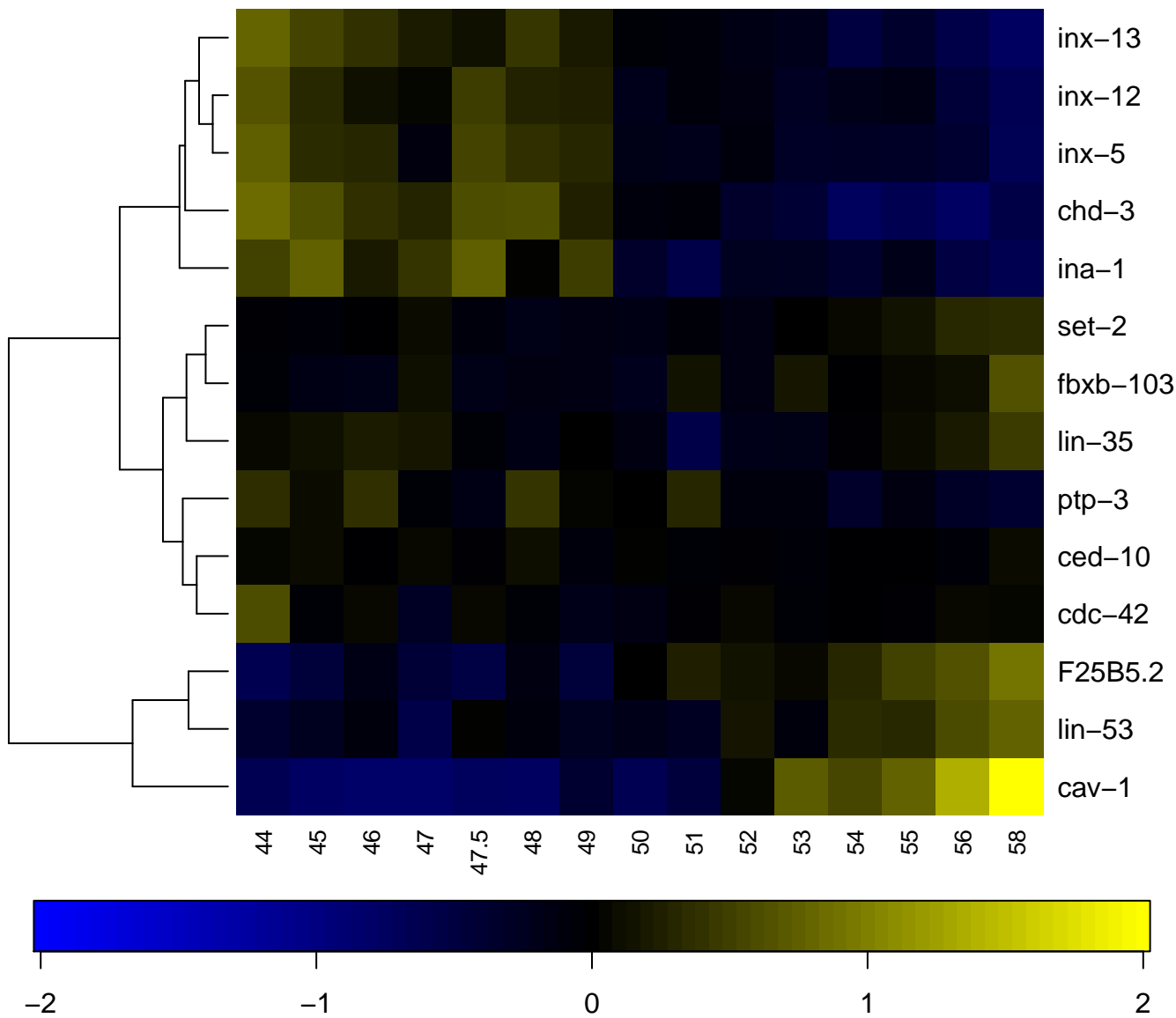
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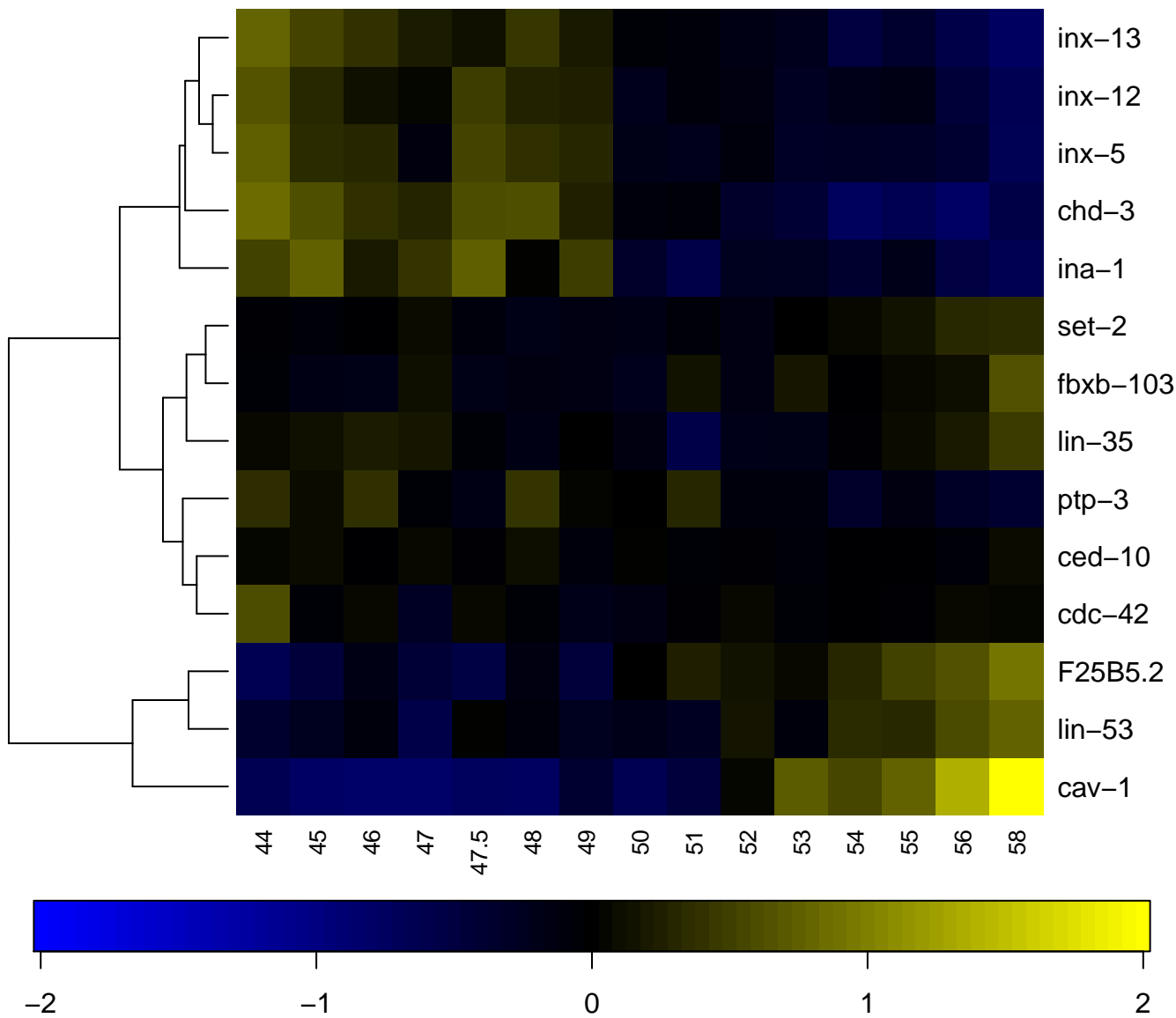
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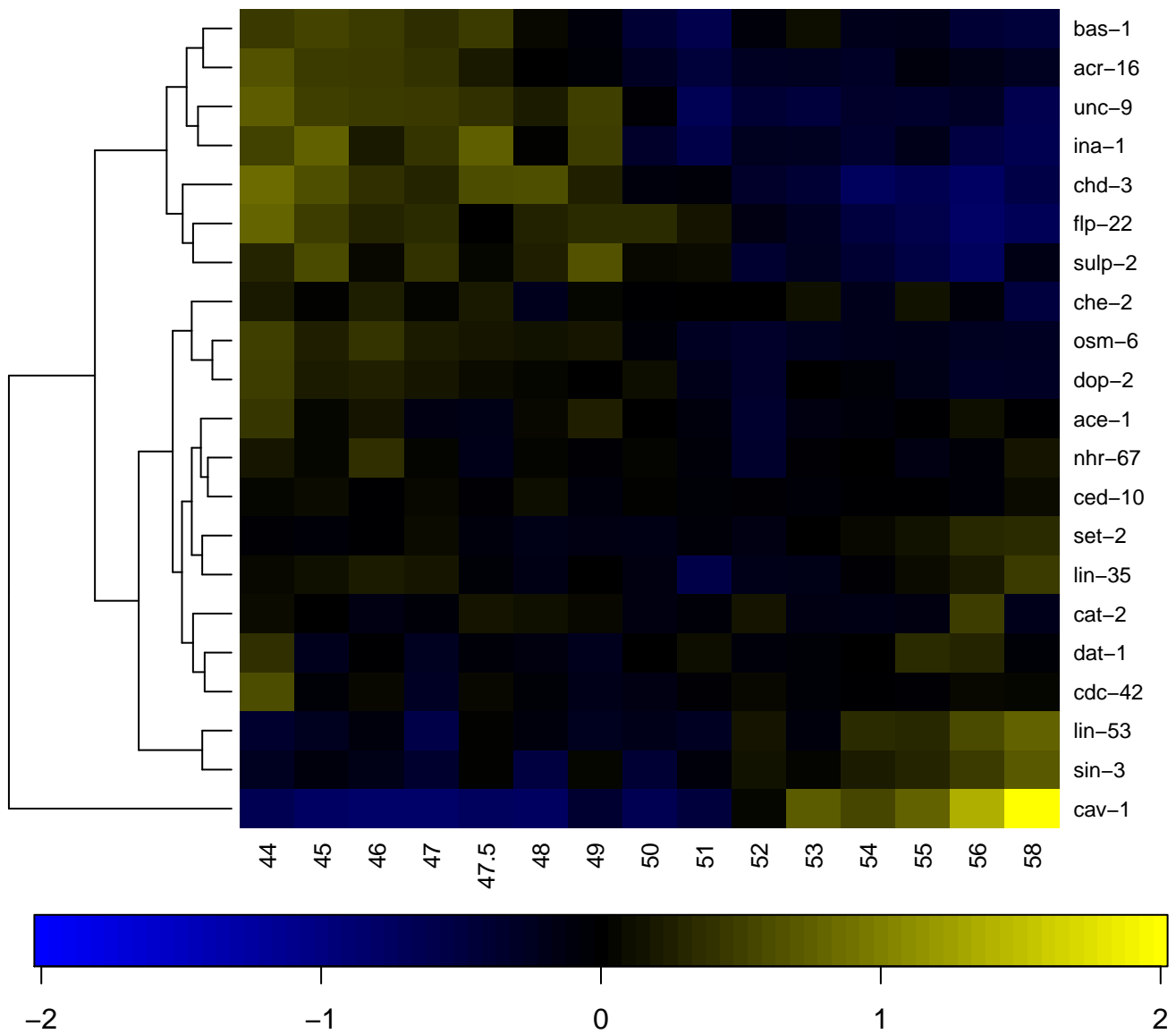
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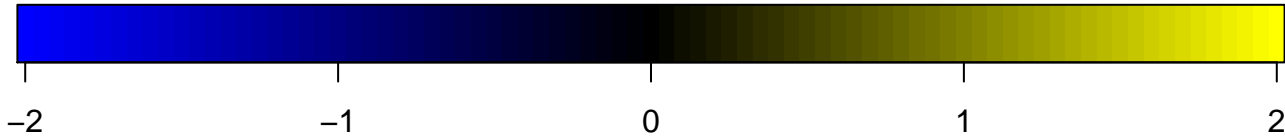
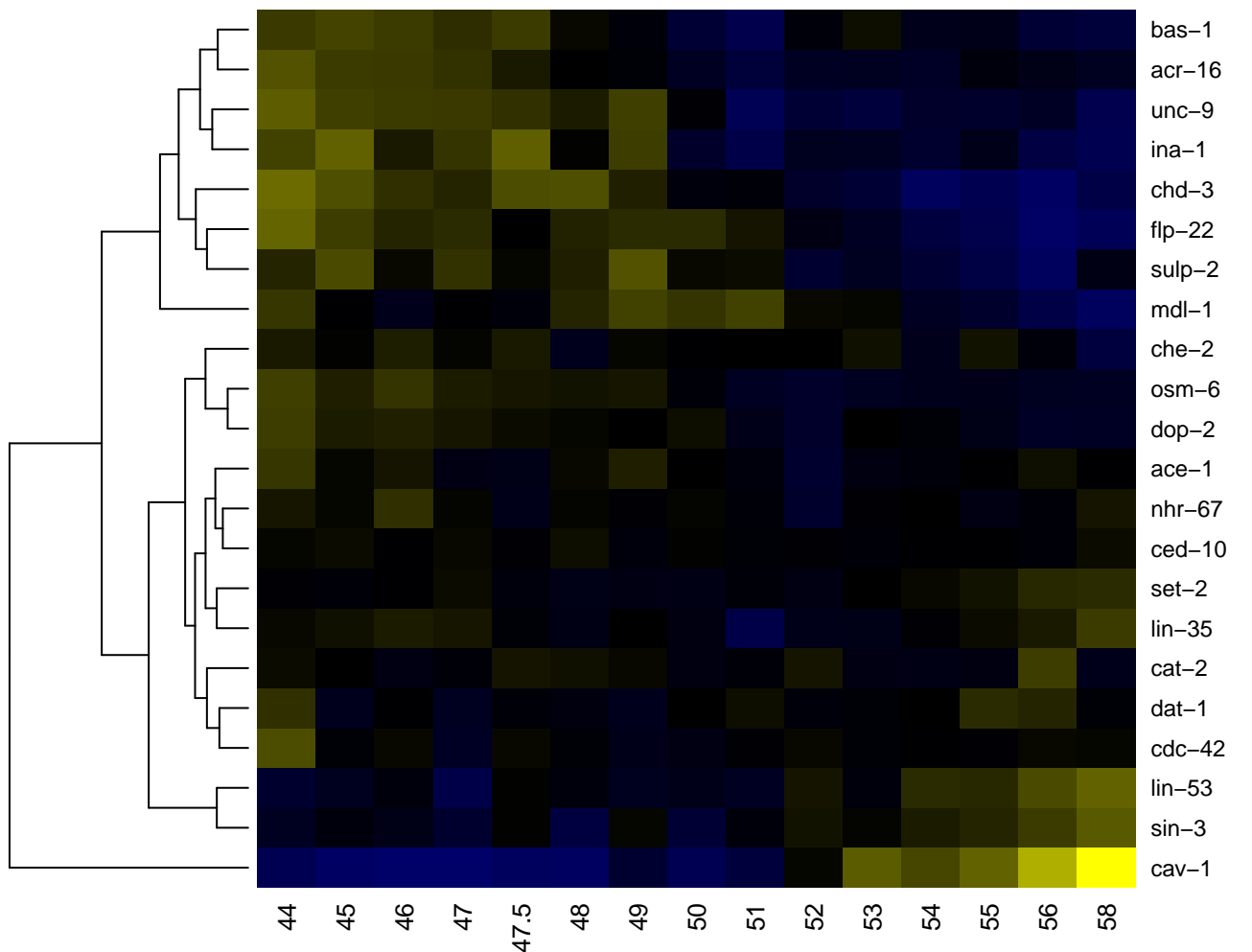
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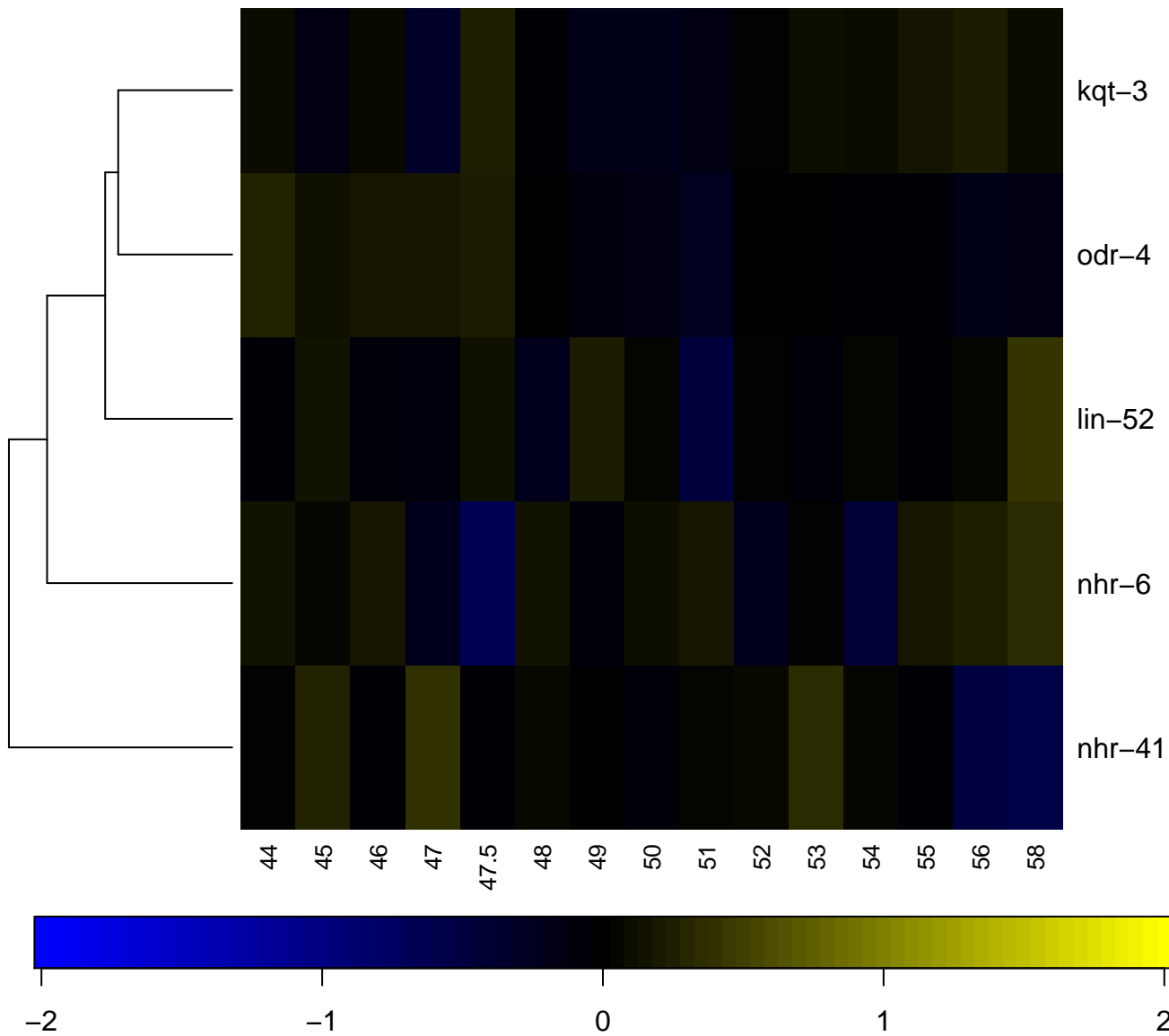
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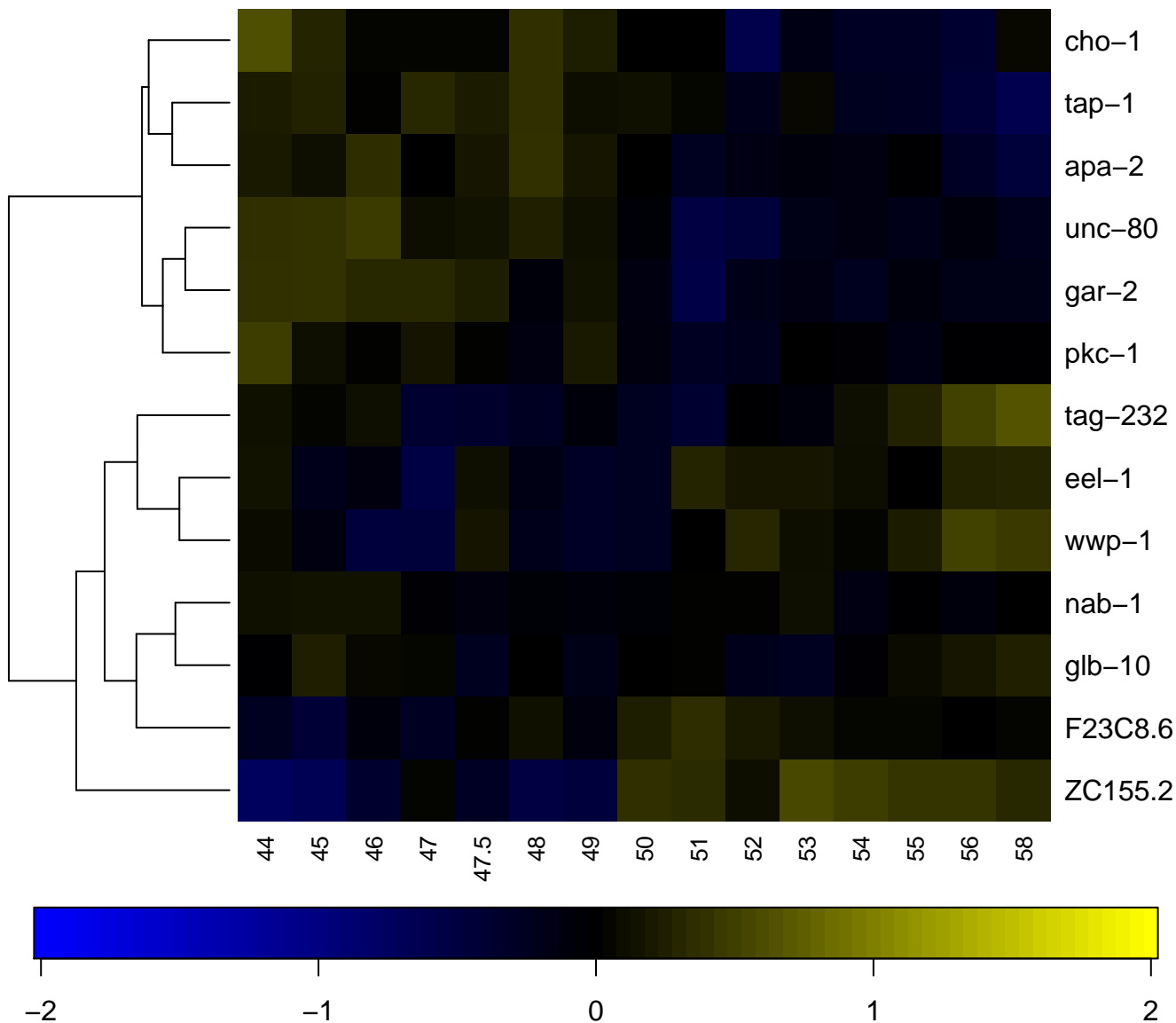
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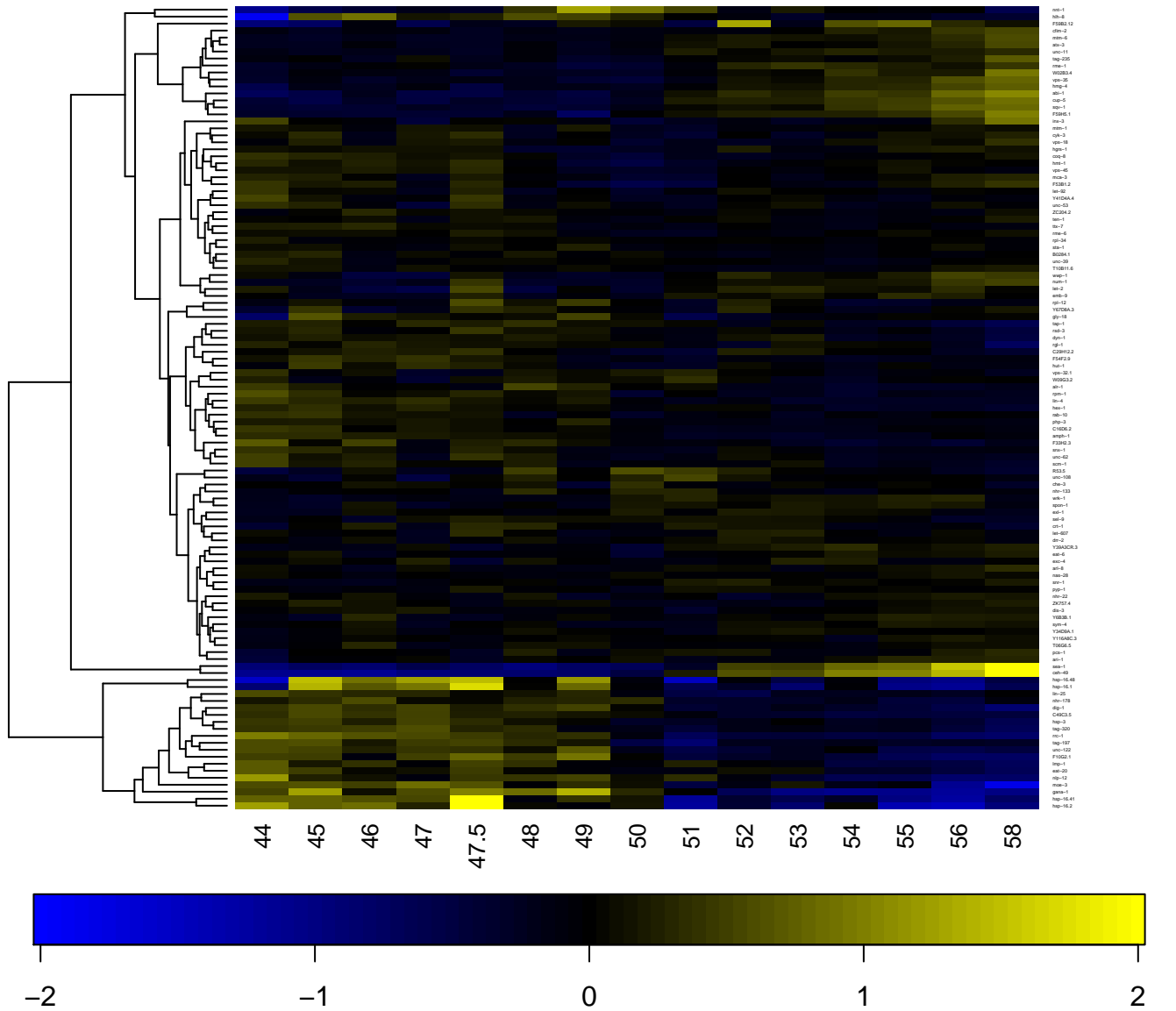
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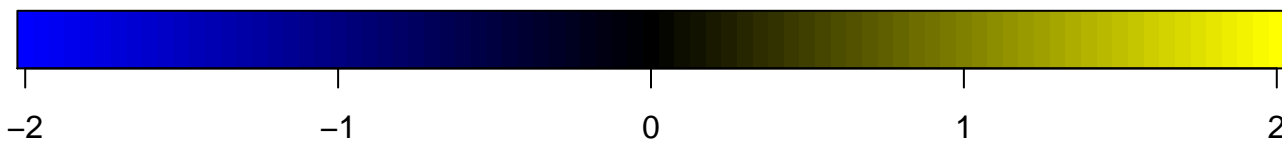
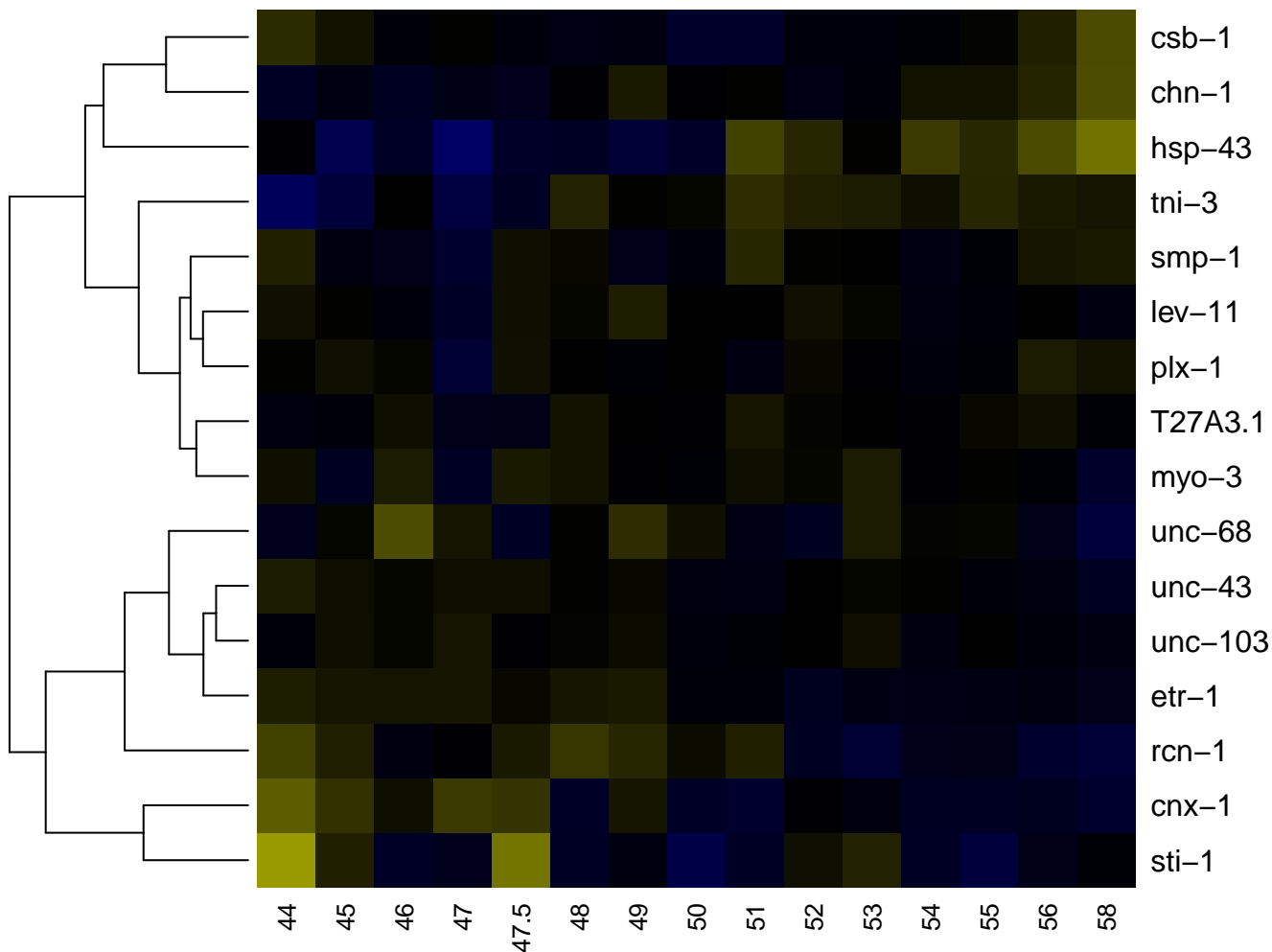
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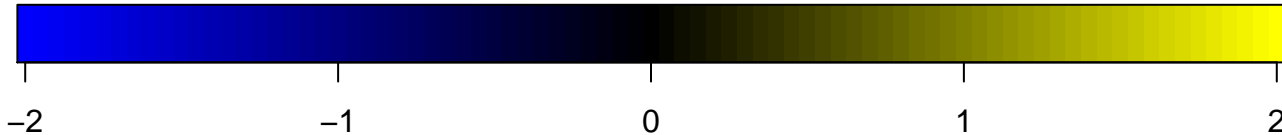
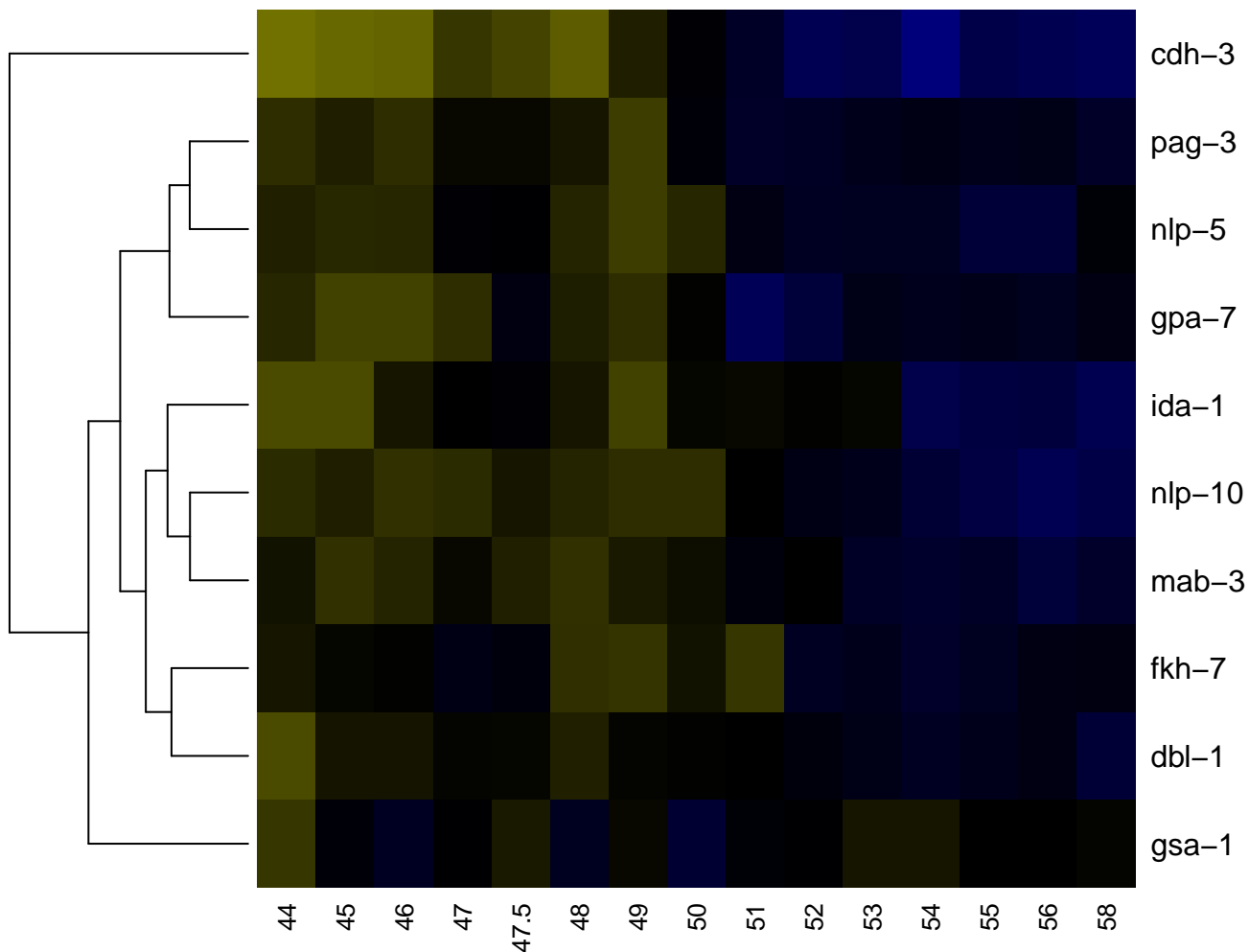
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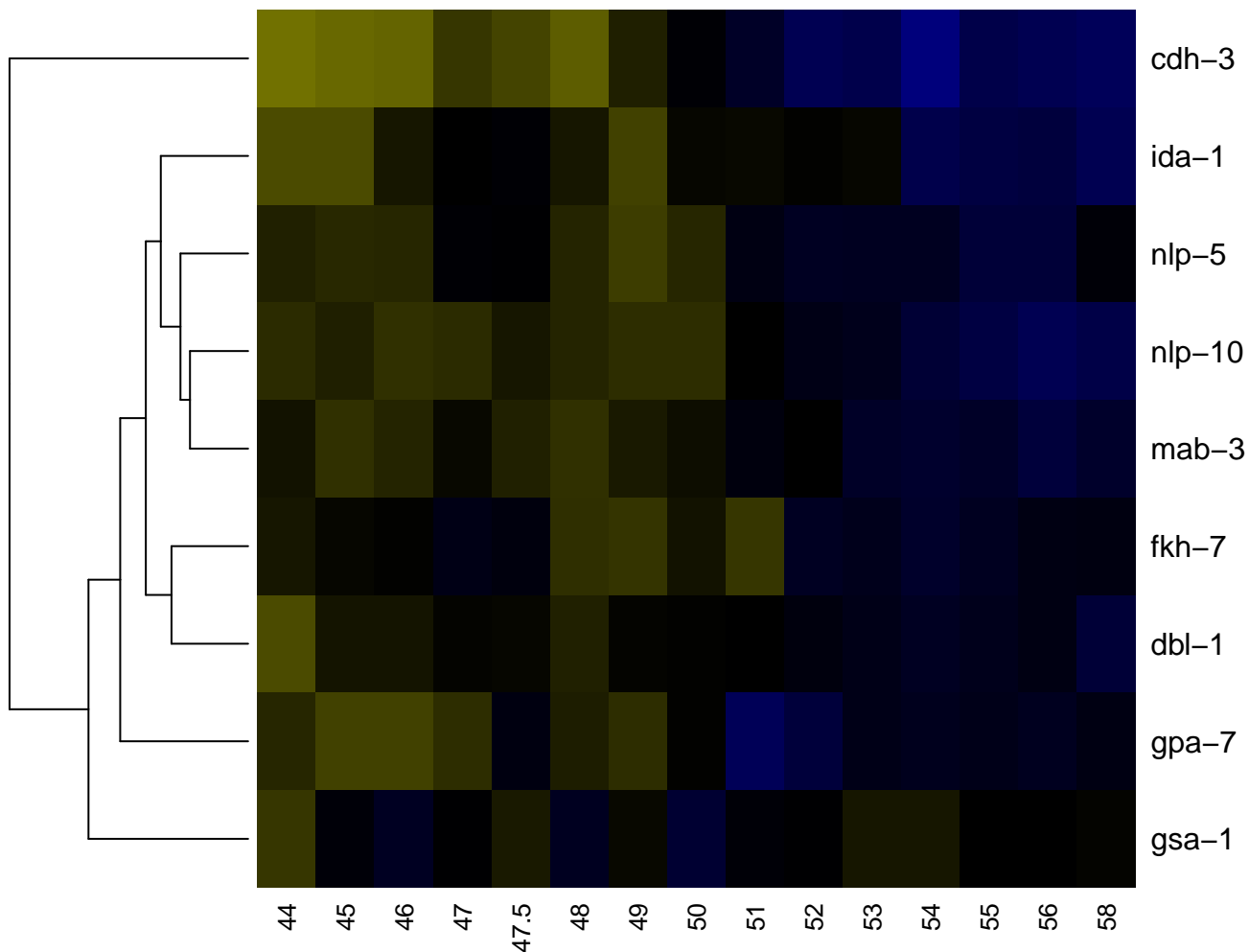
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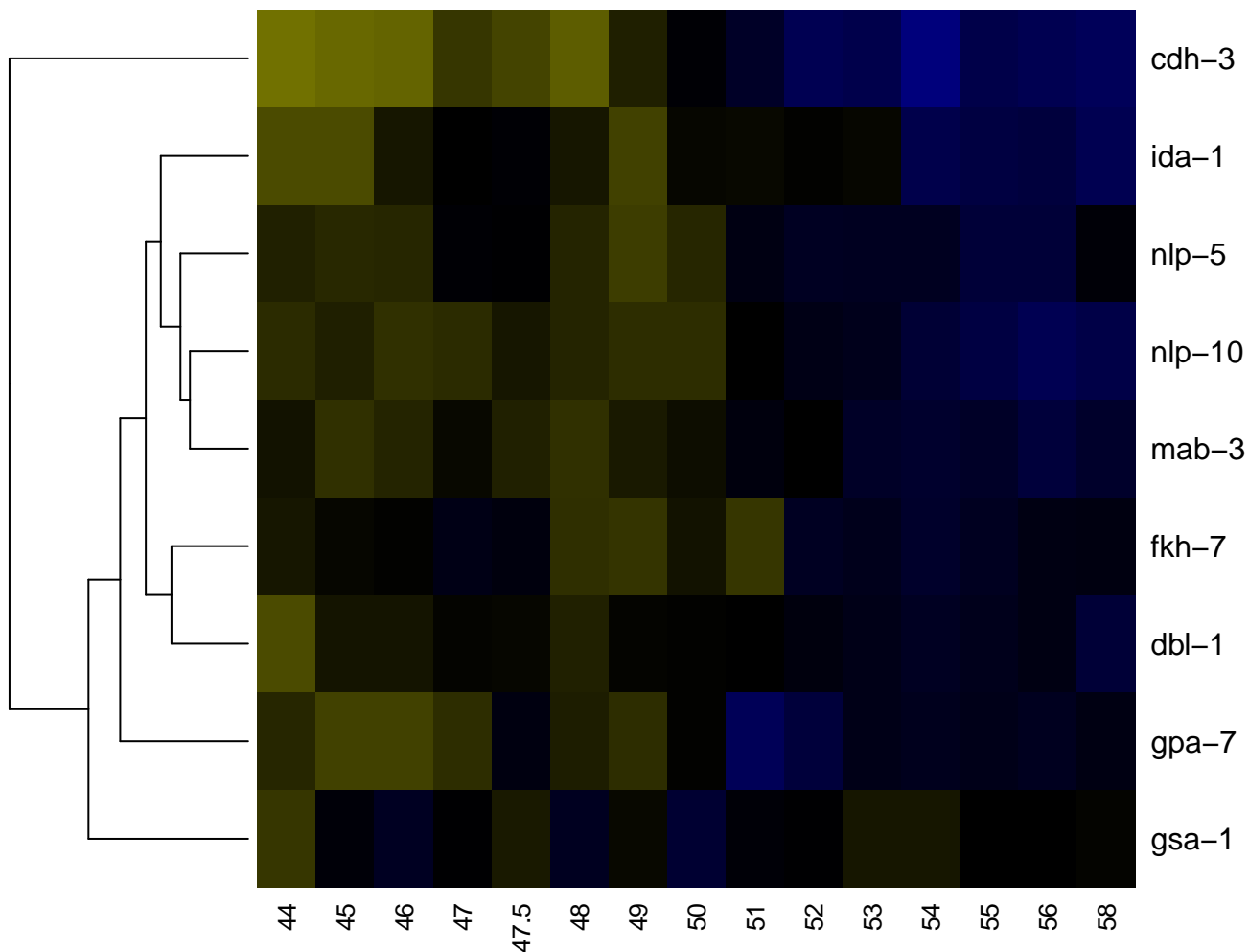
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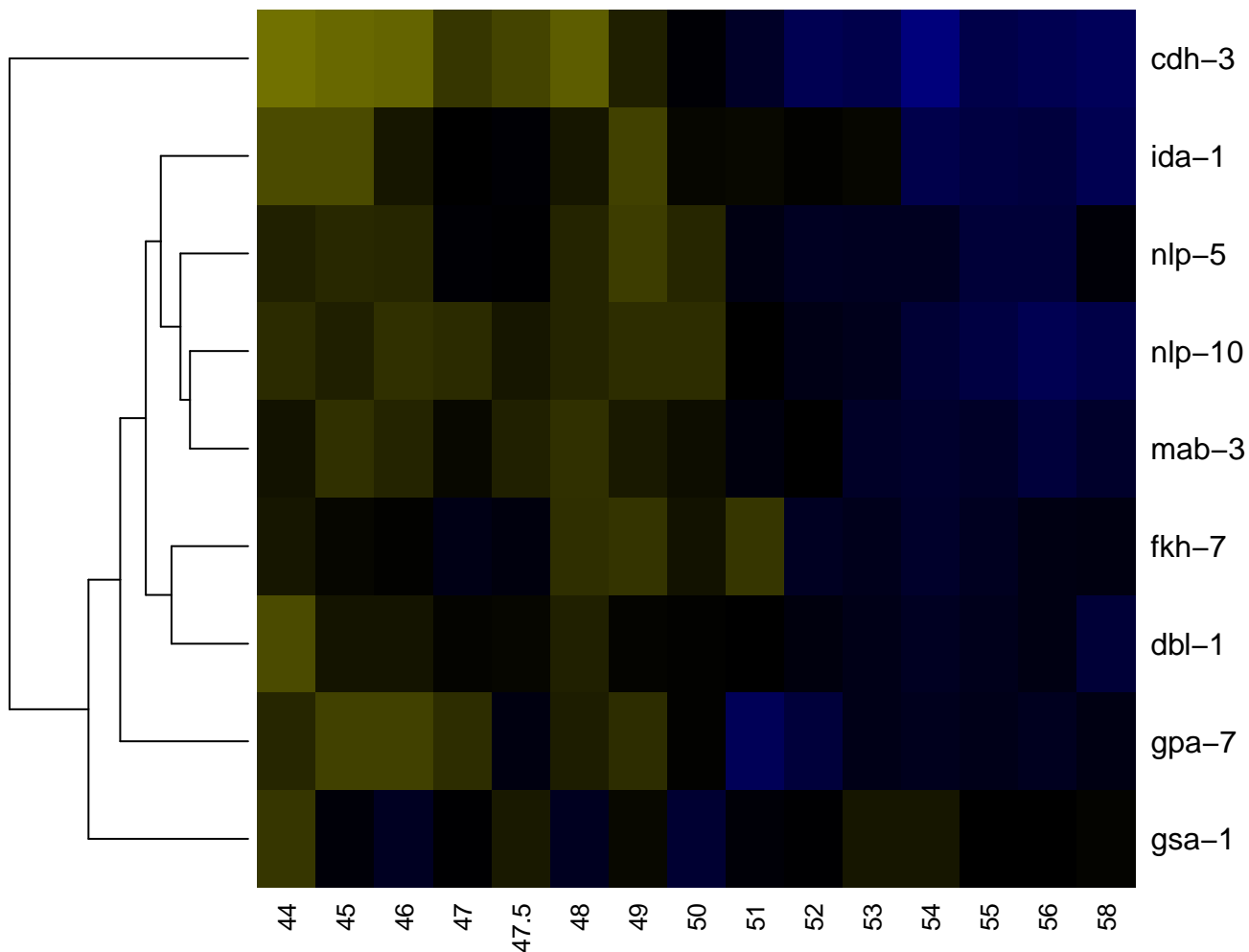
CP1



CP2



CP3



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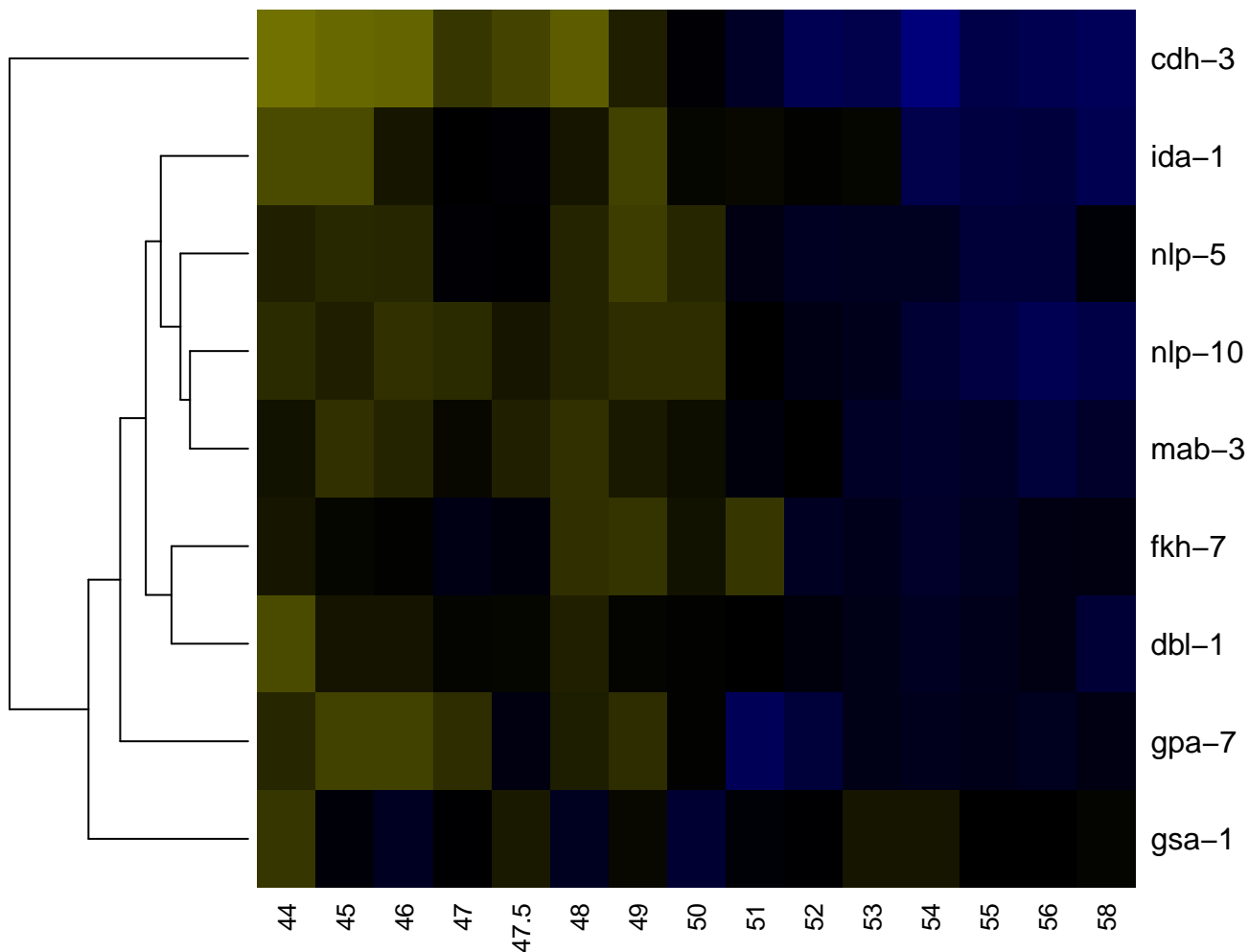
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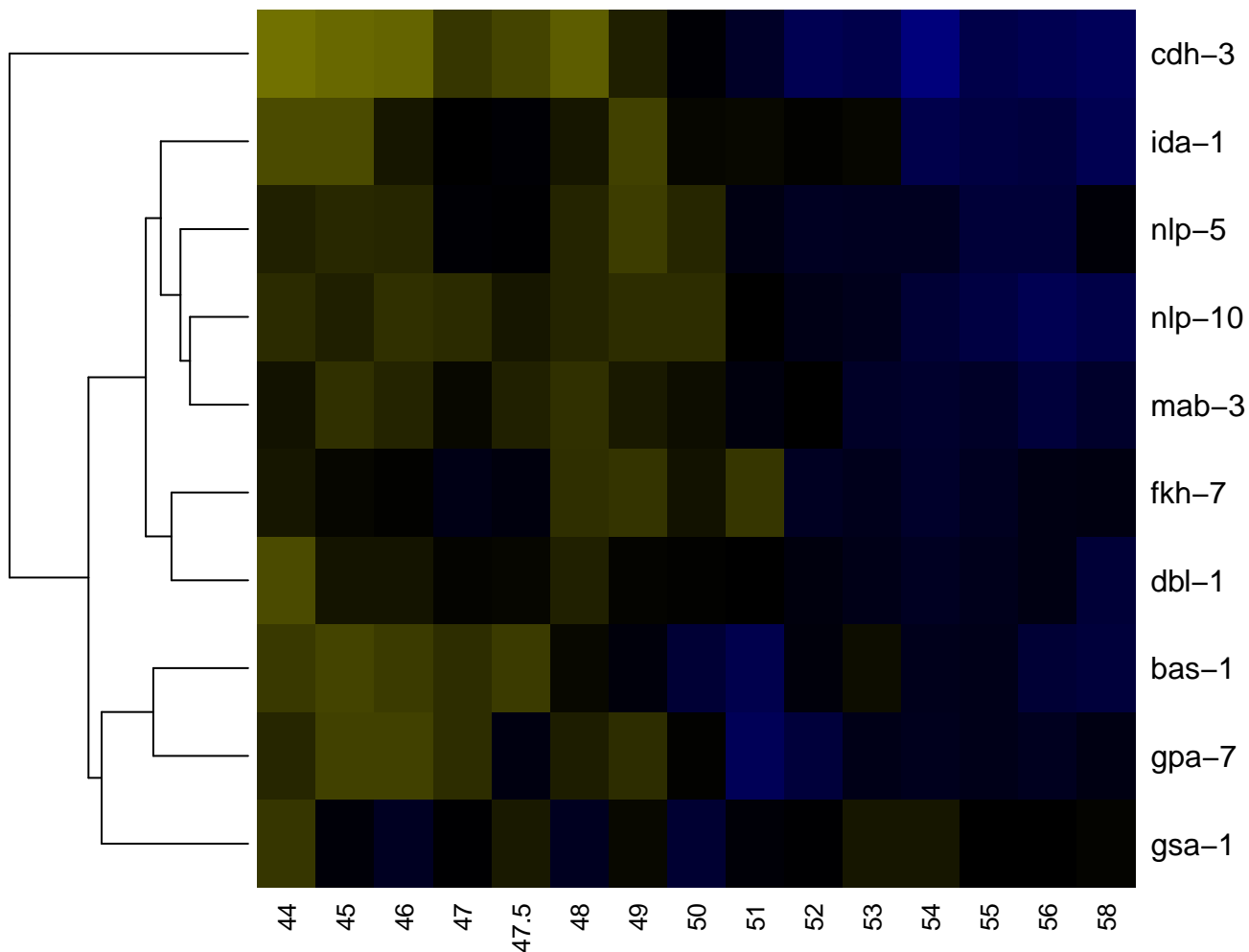
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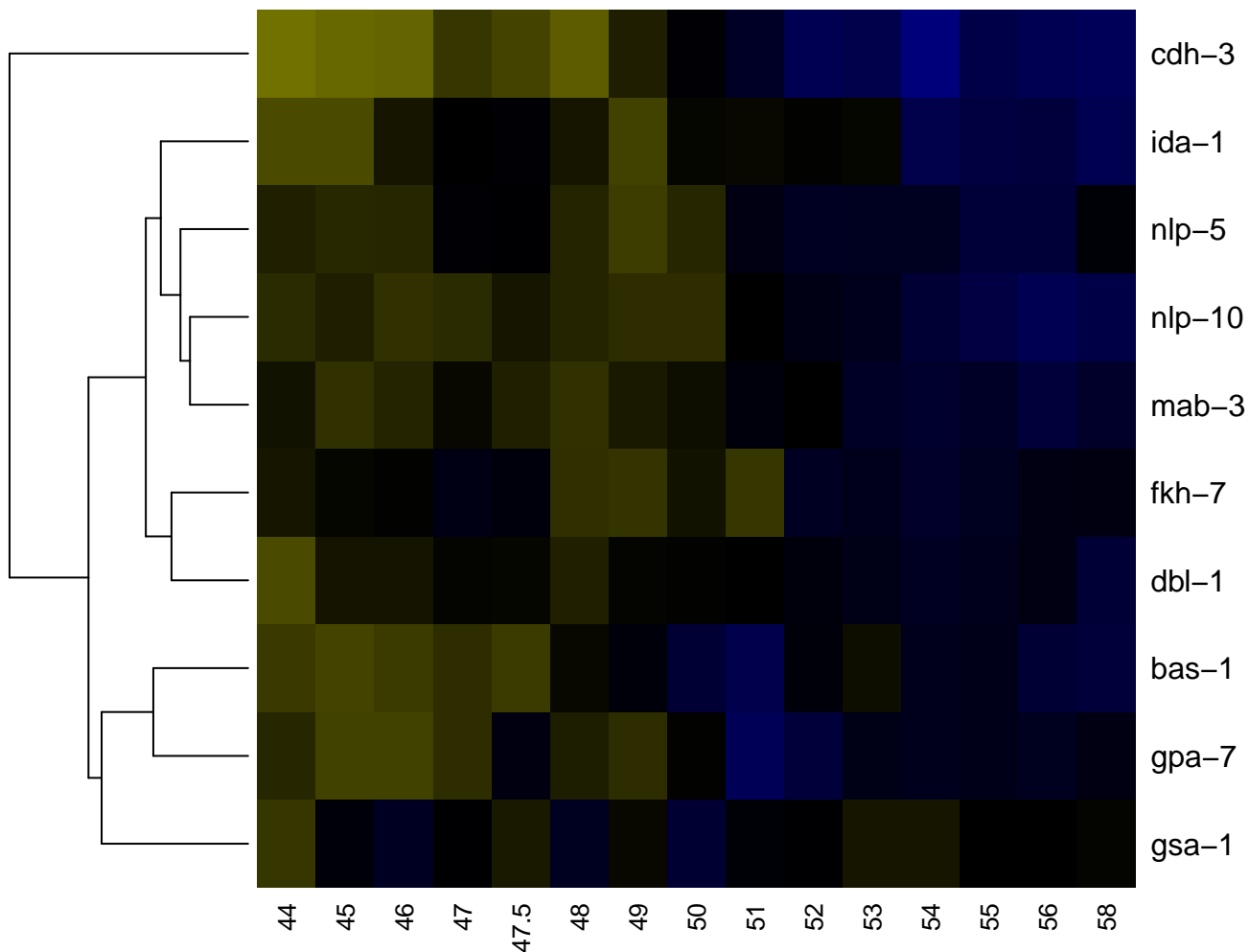
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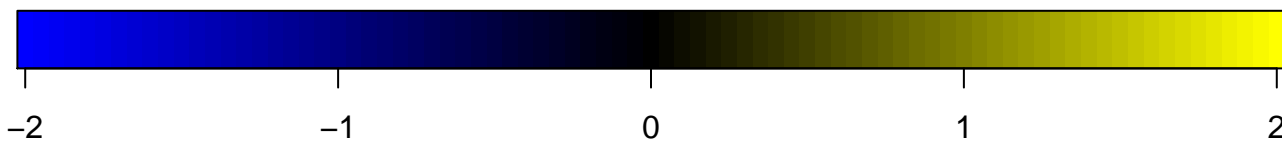
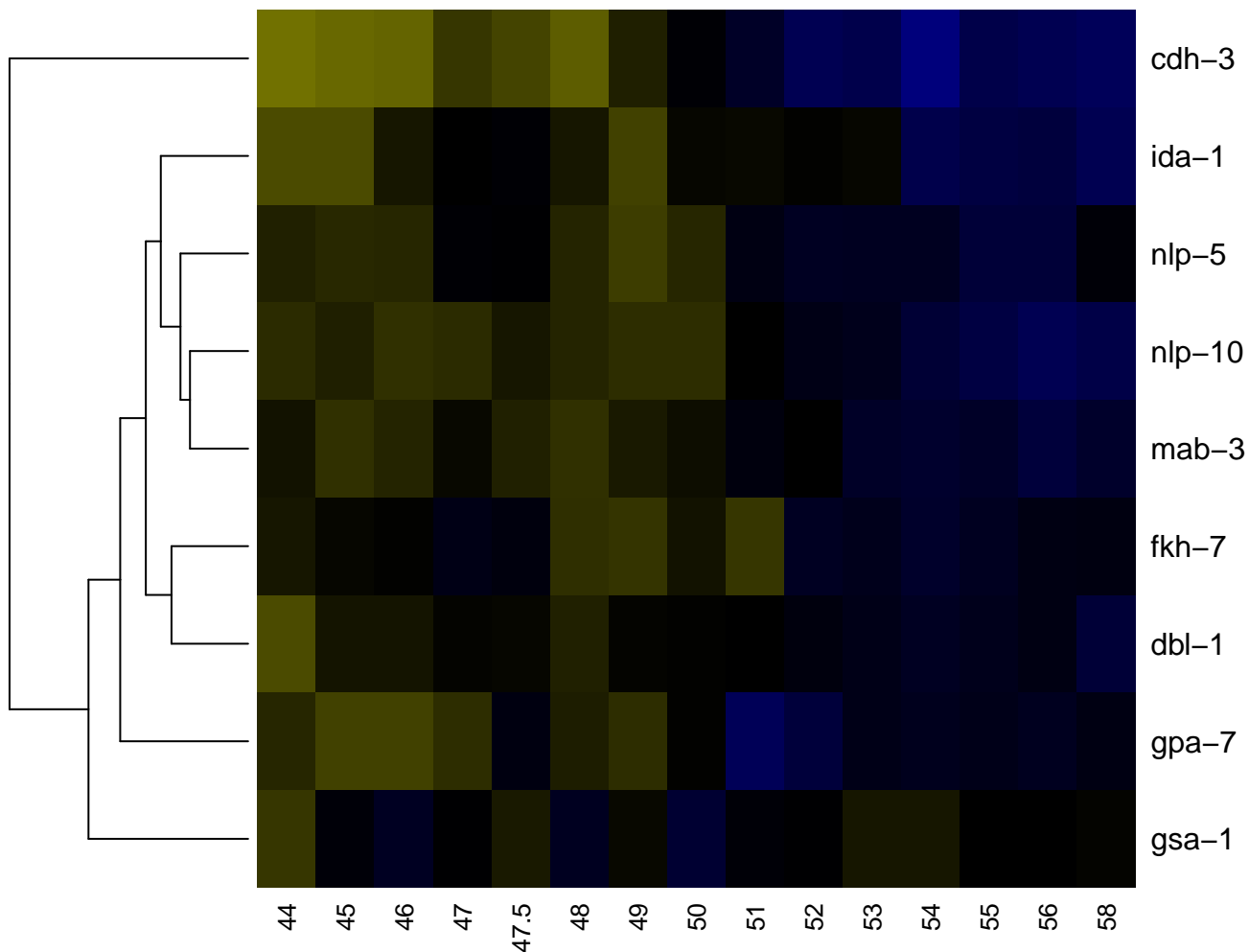
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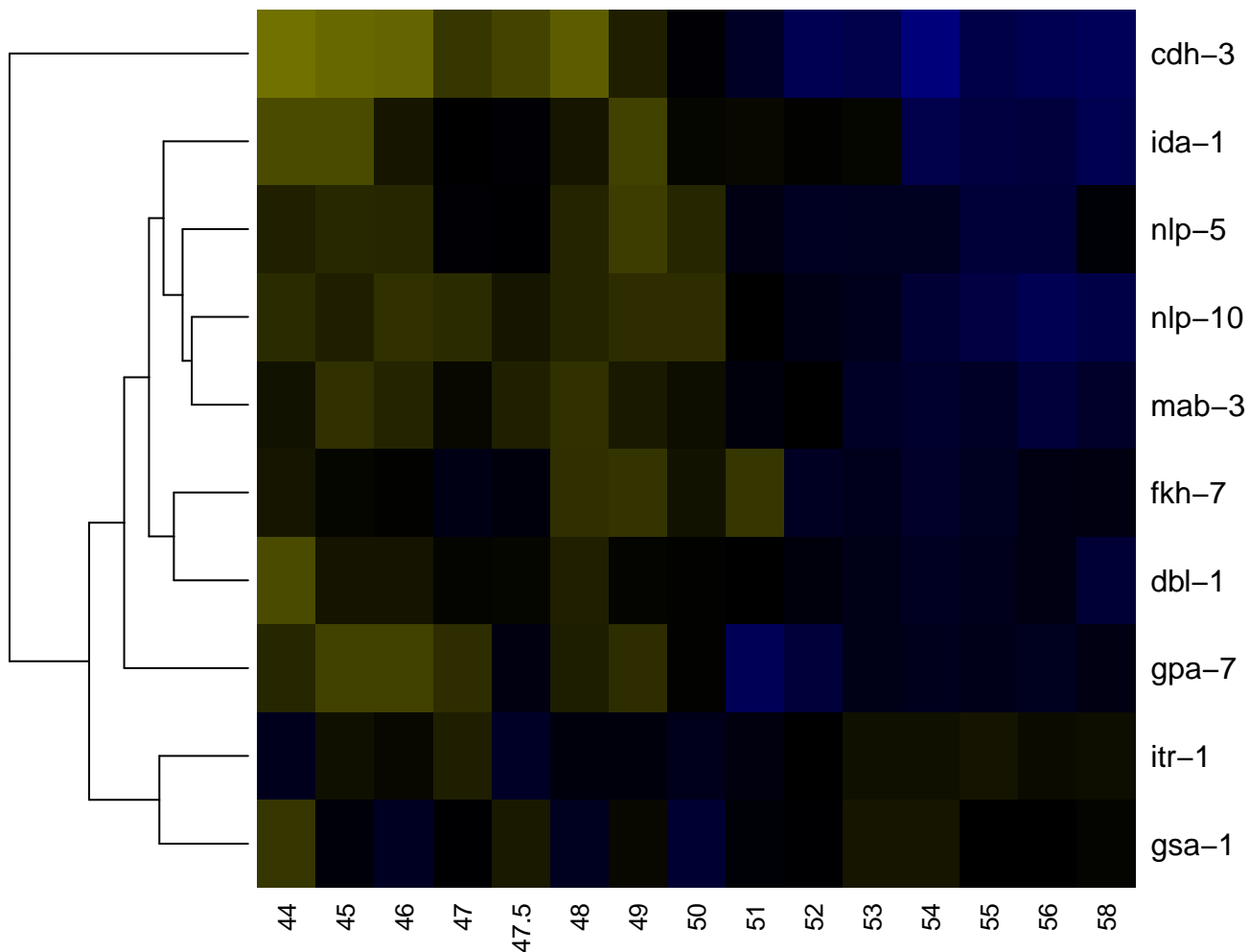
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CP7



CP8



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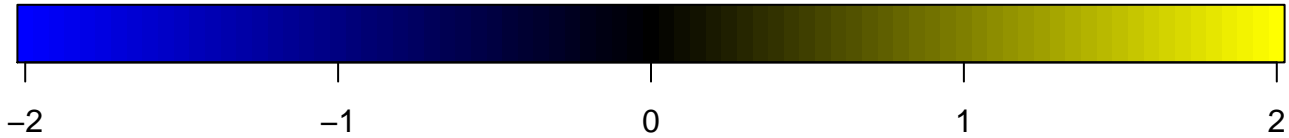
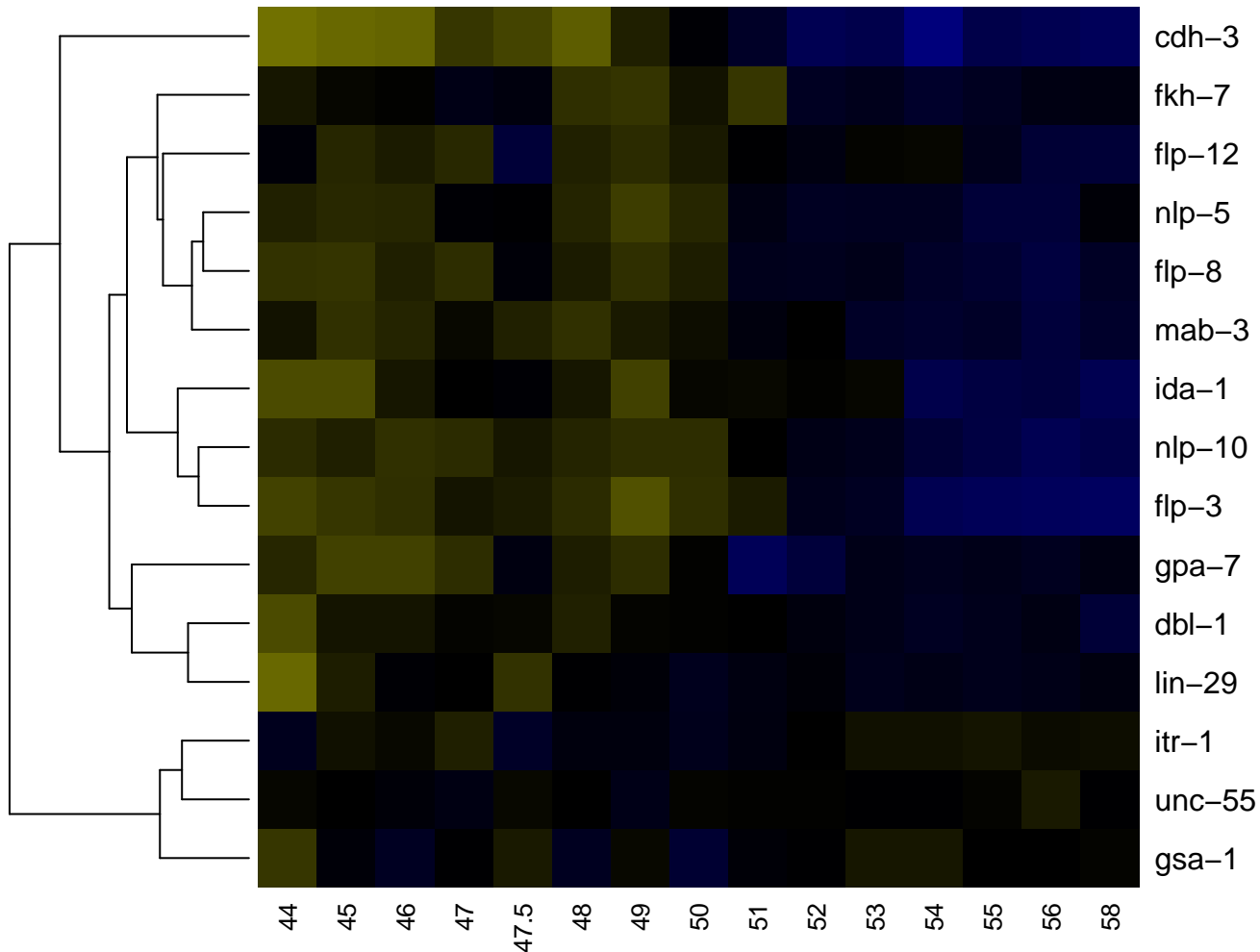
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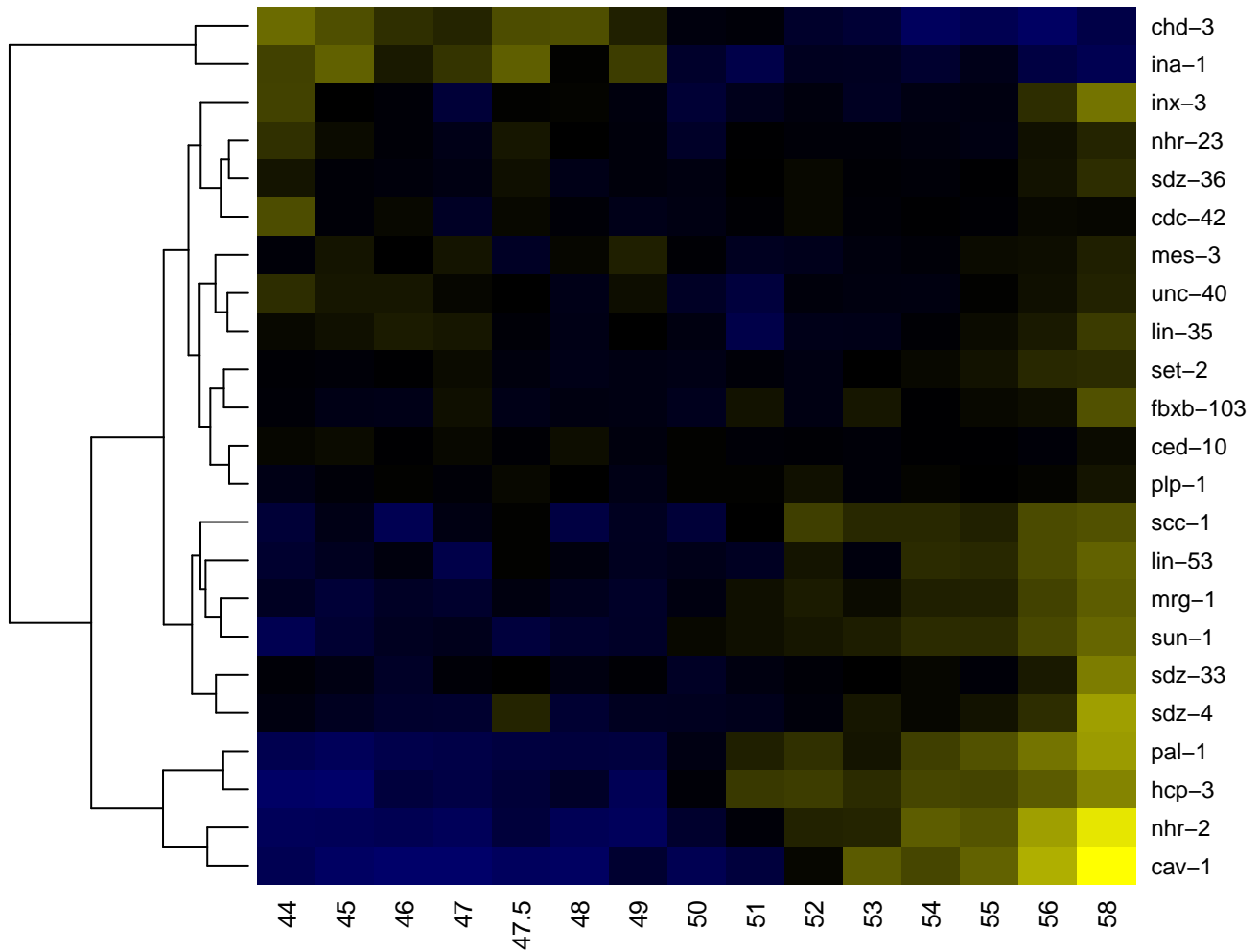
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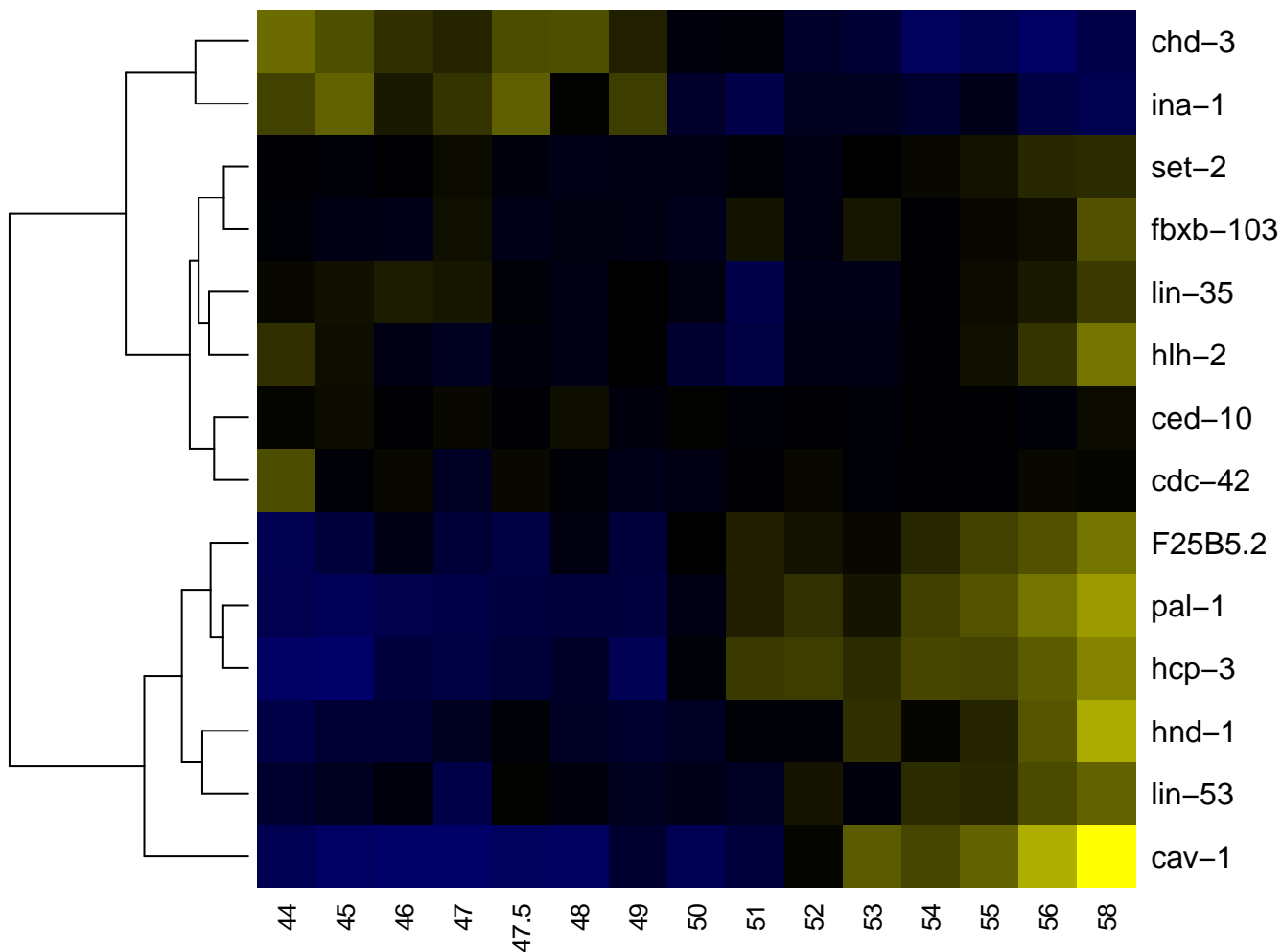
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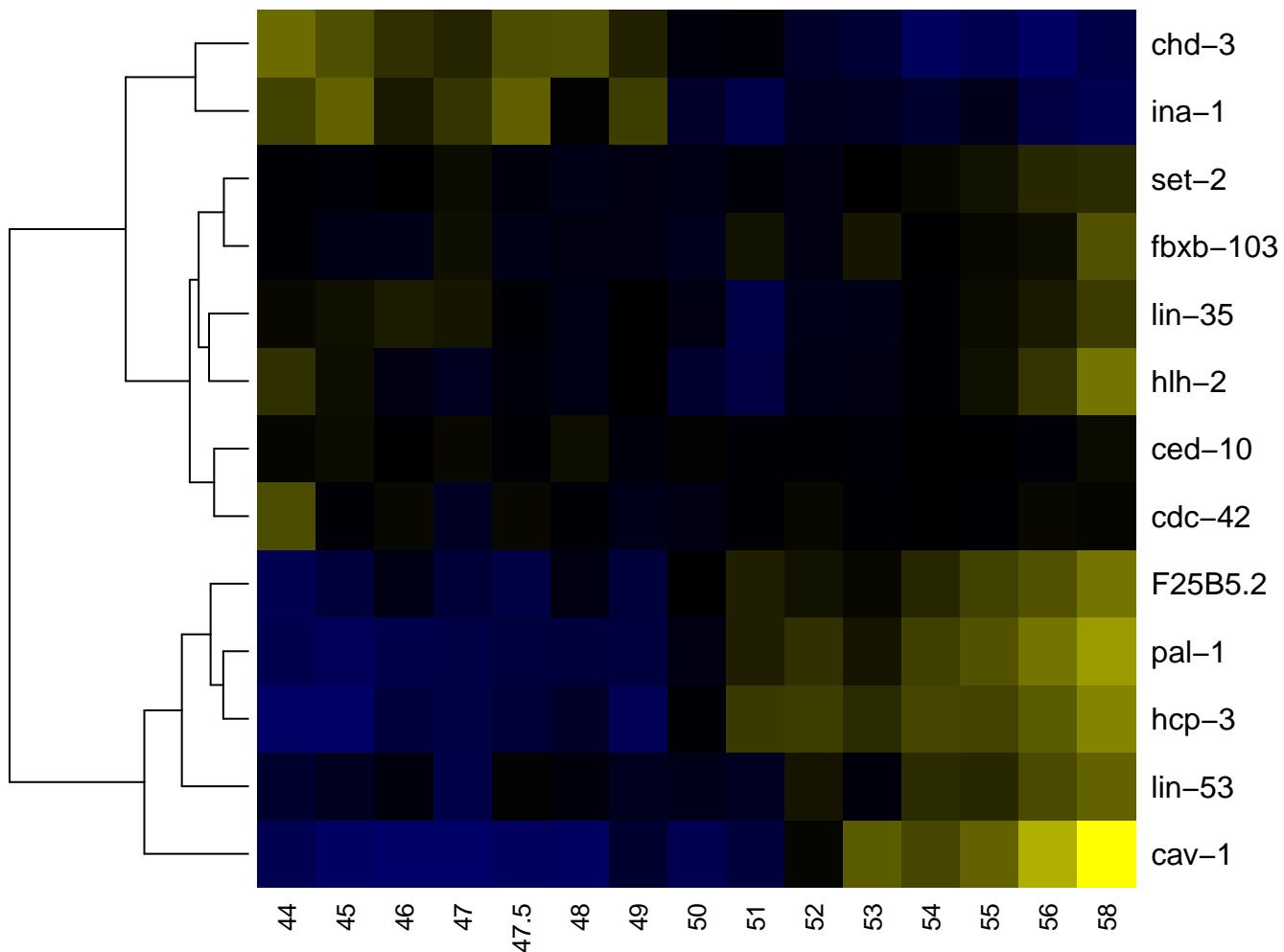
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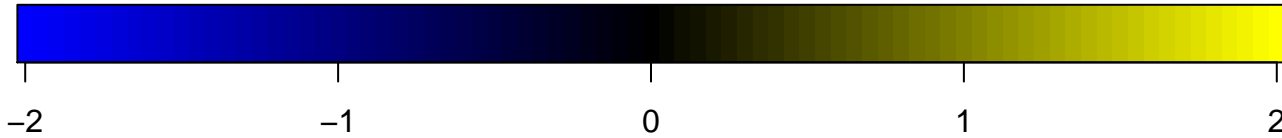
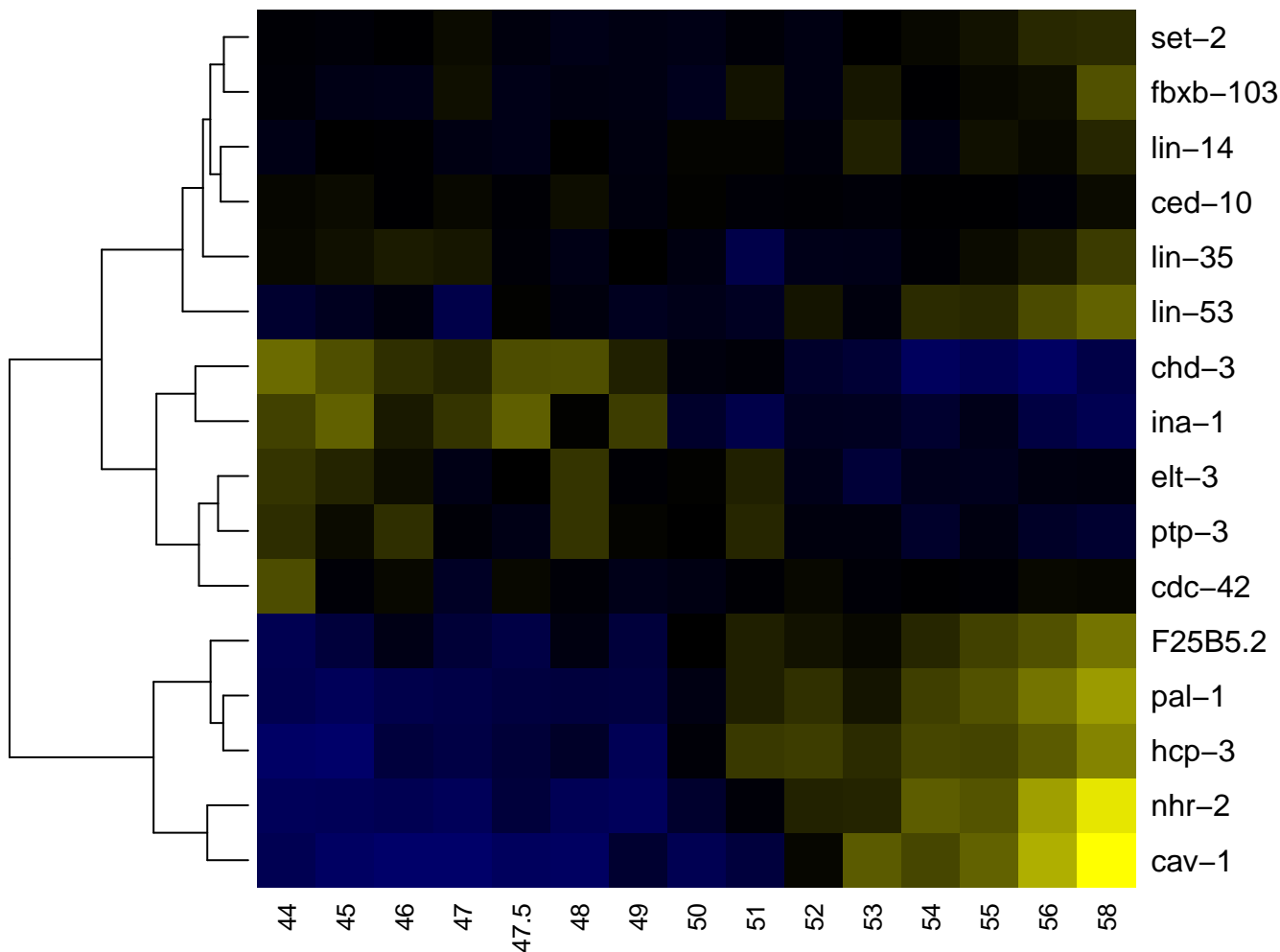
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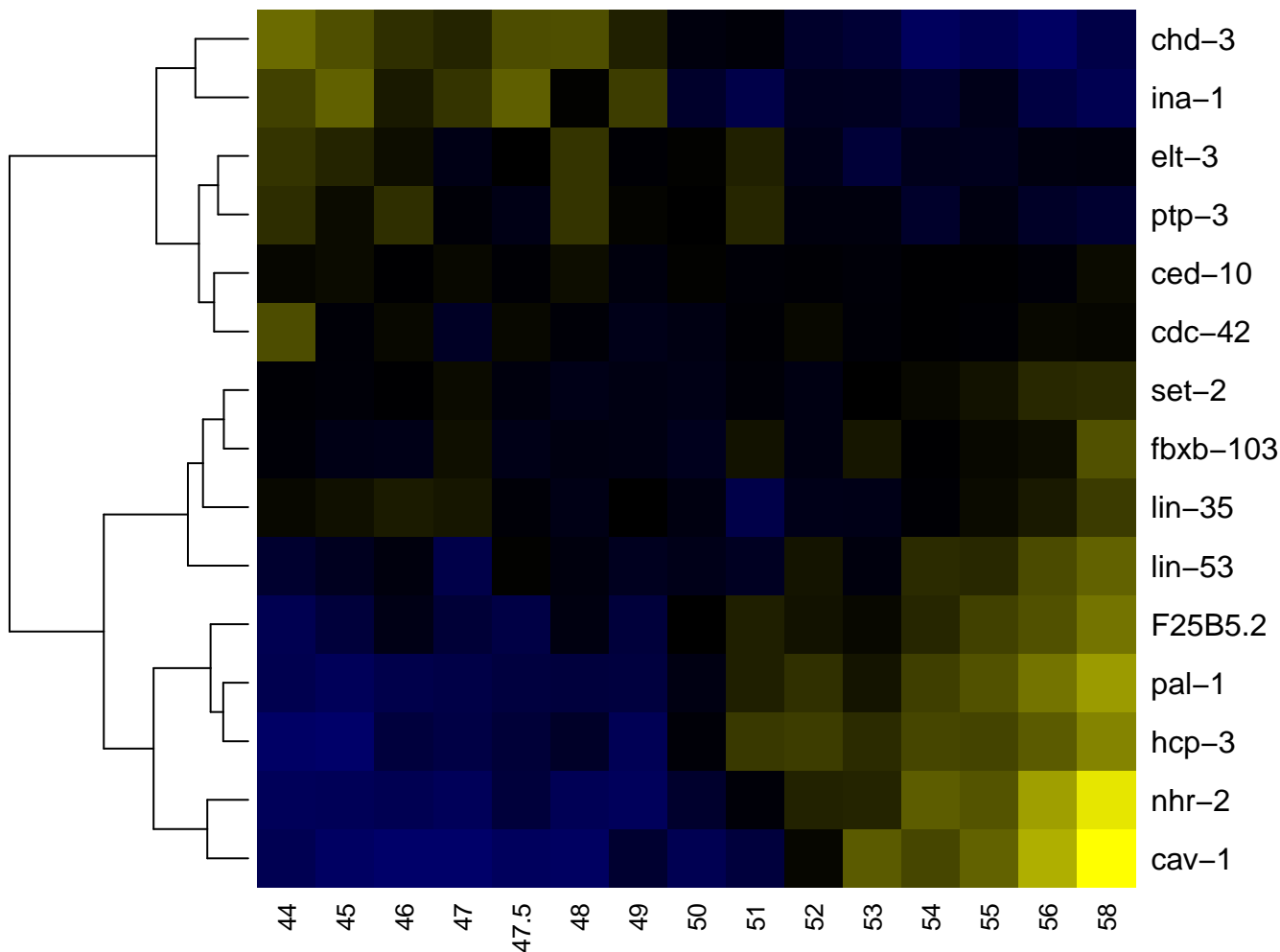
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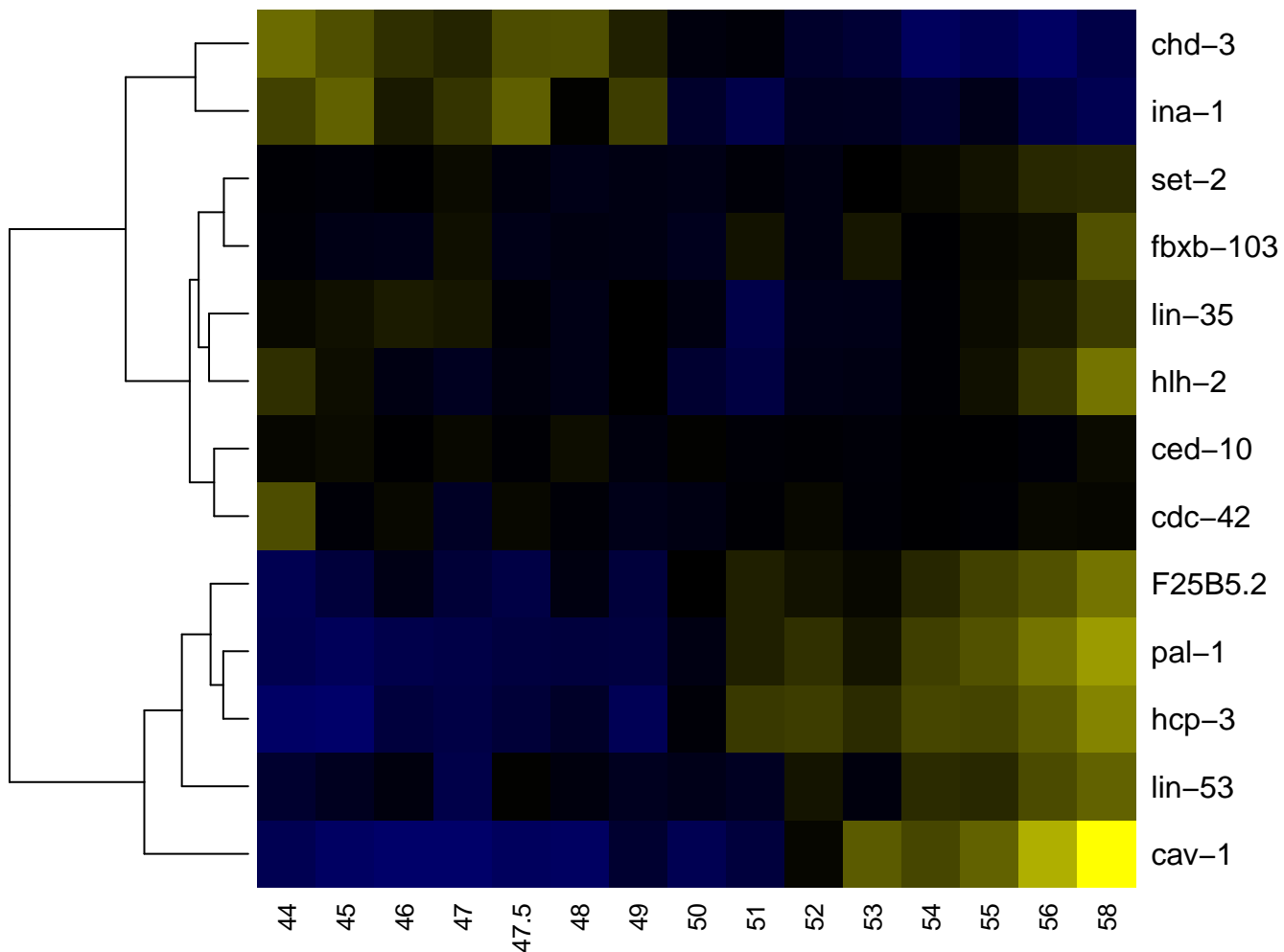
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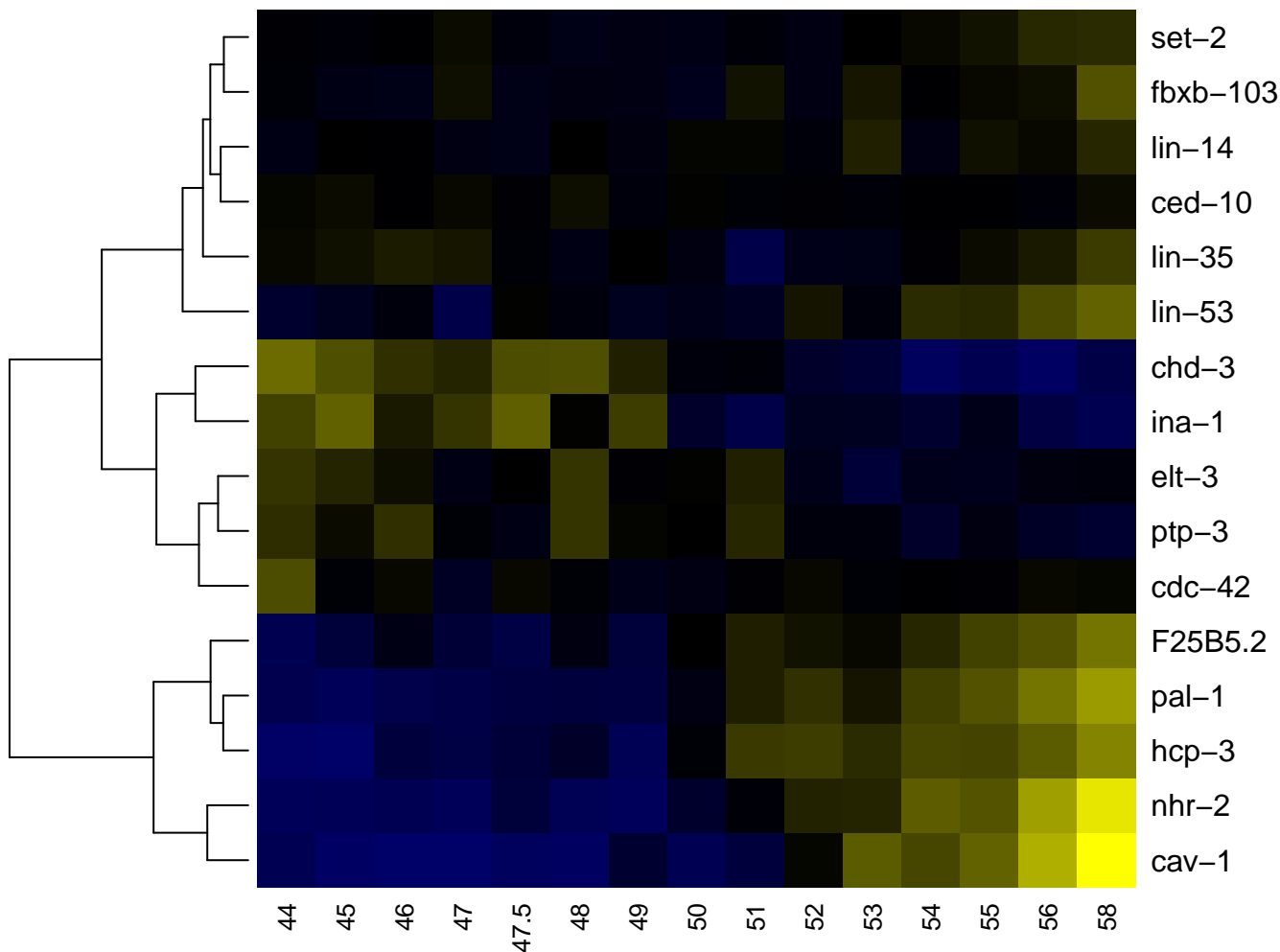
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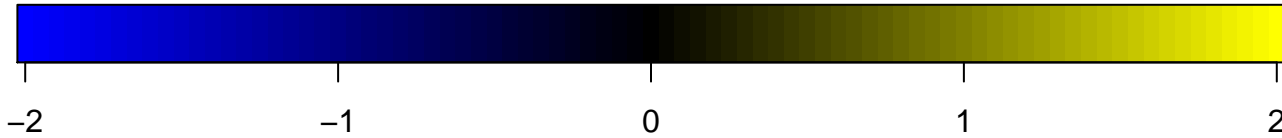
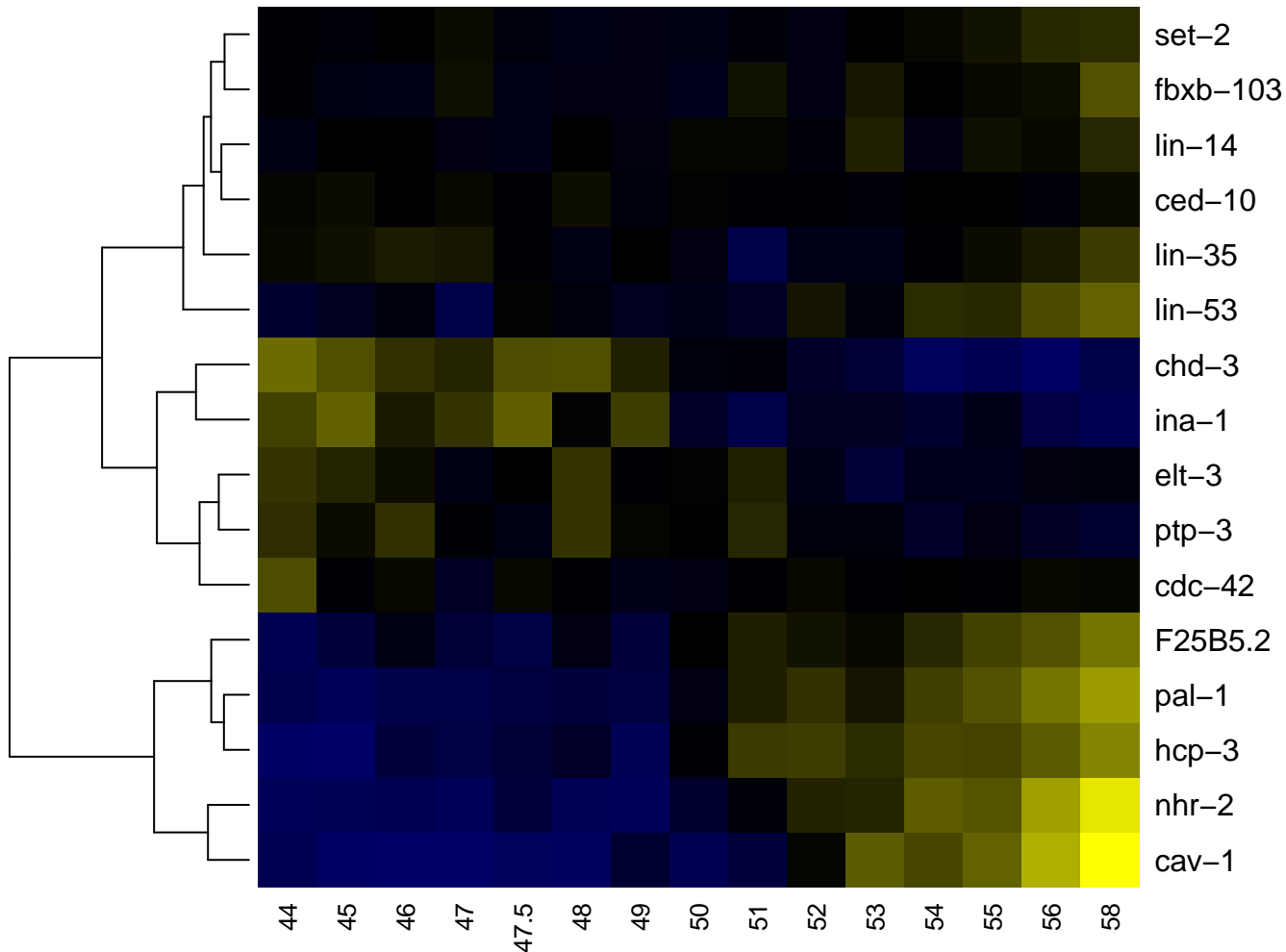
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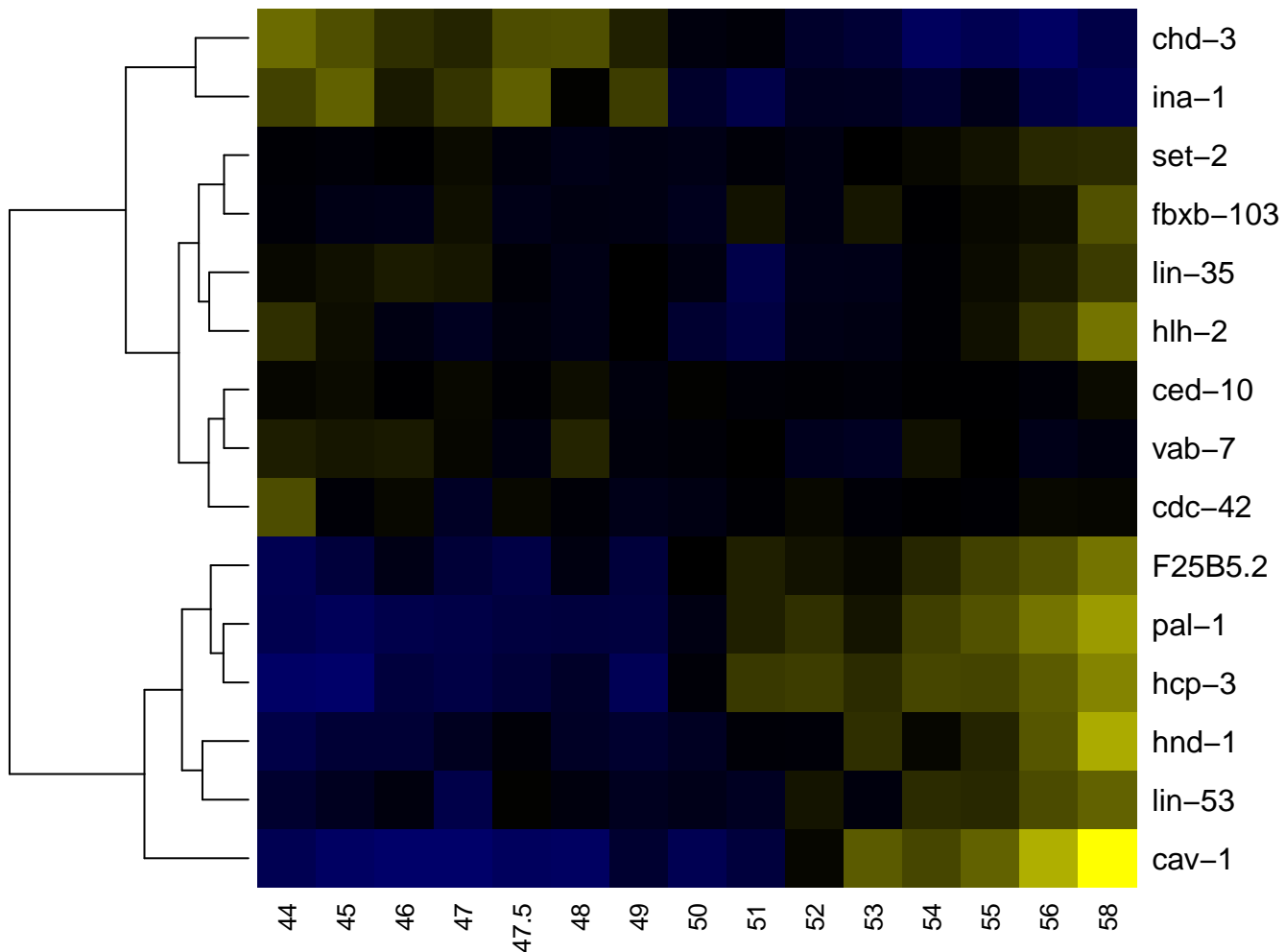
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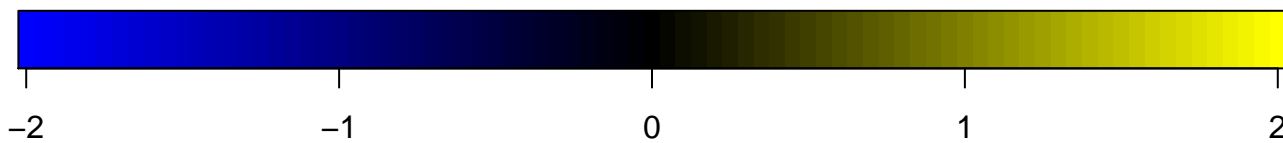
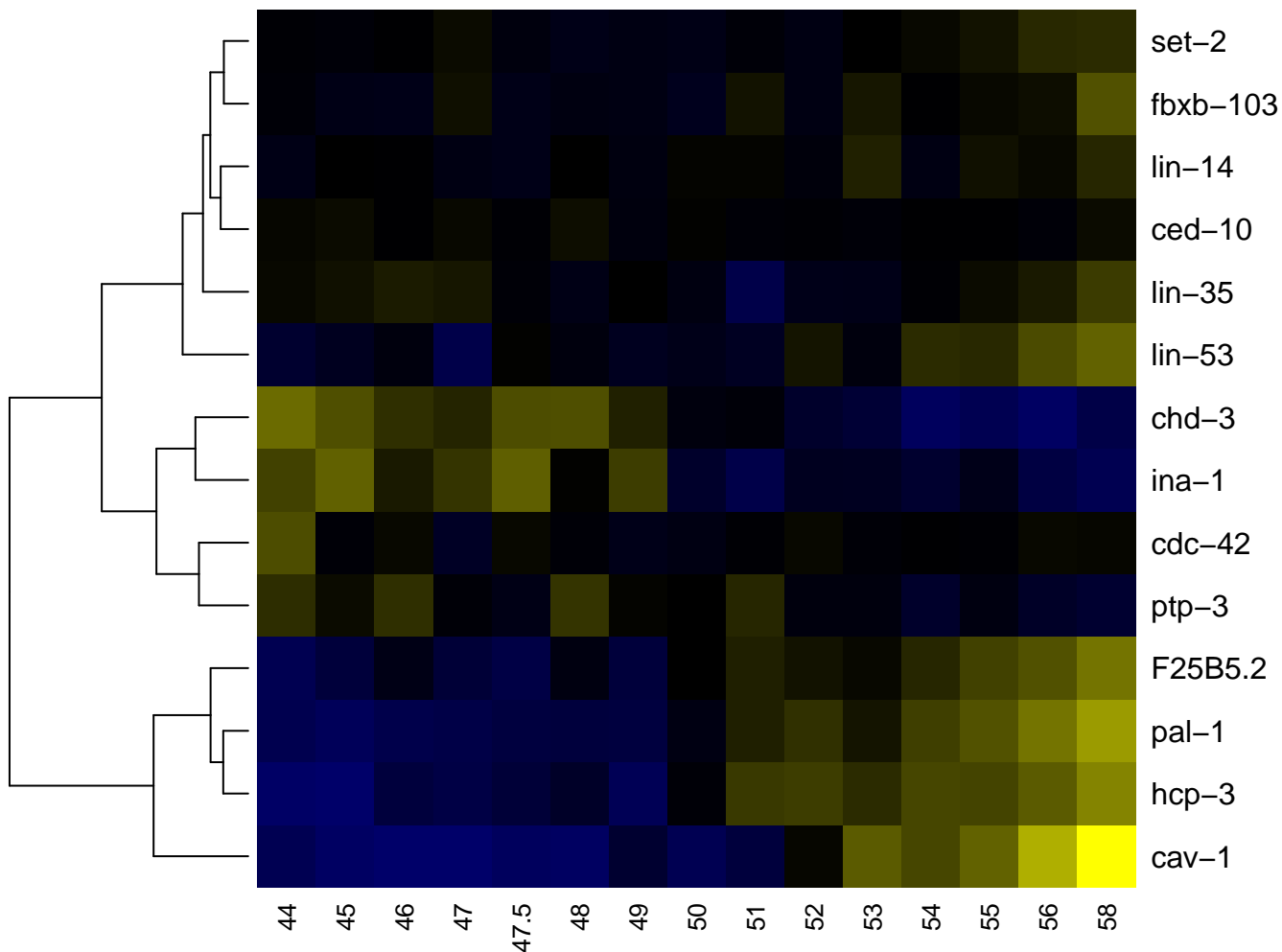
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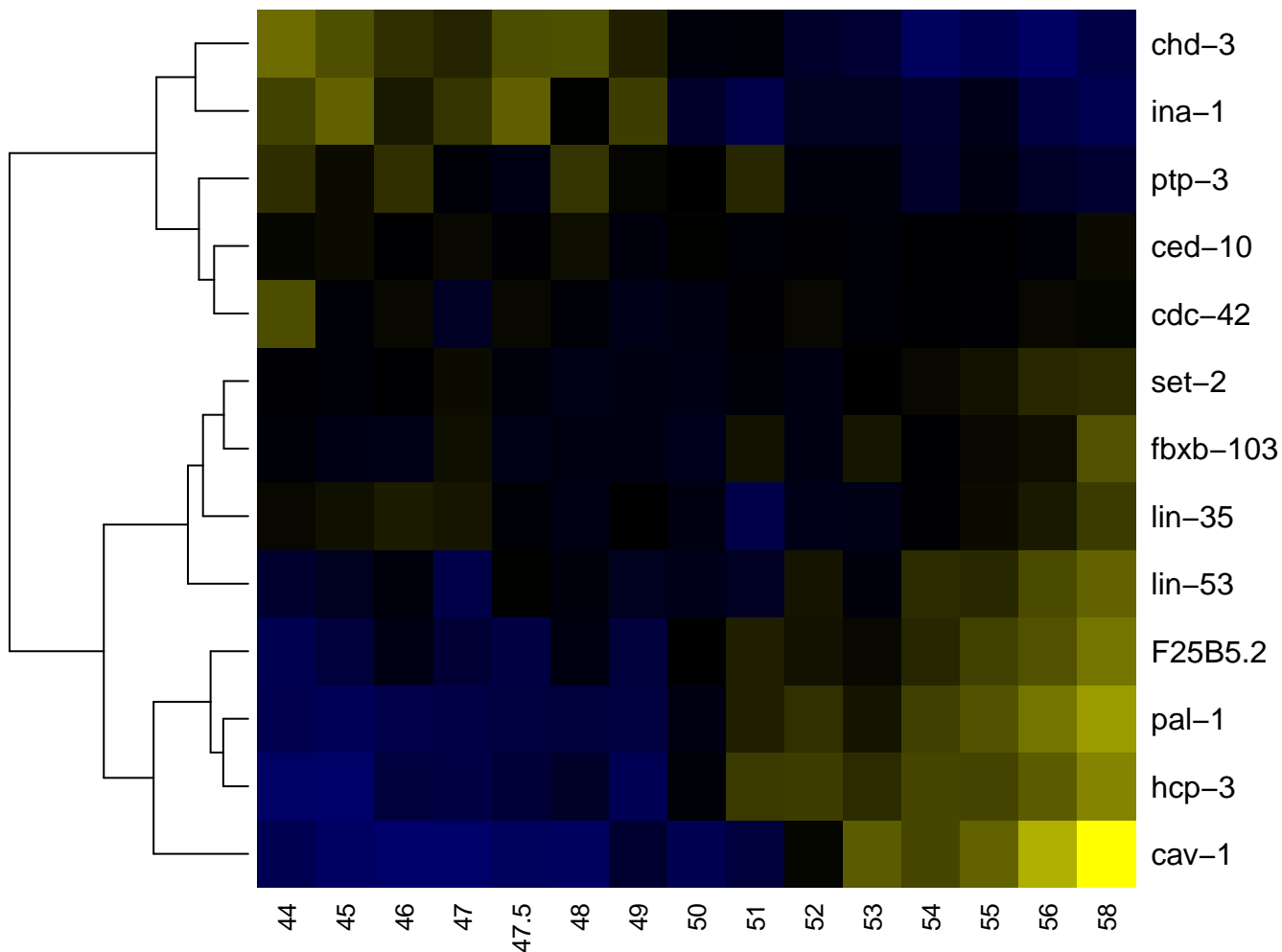
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Сррррр



Cpapap



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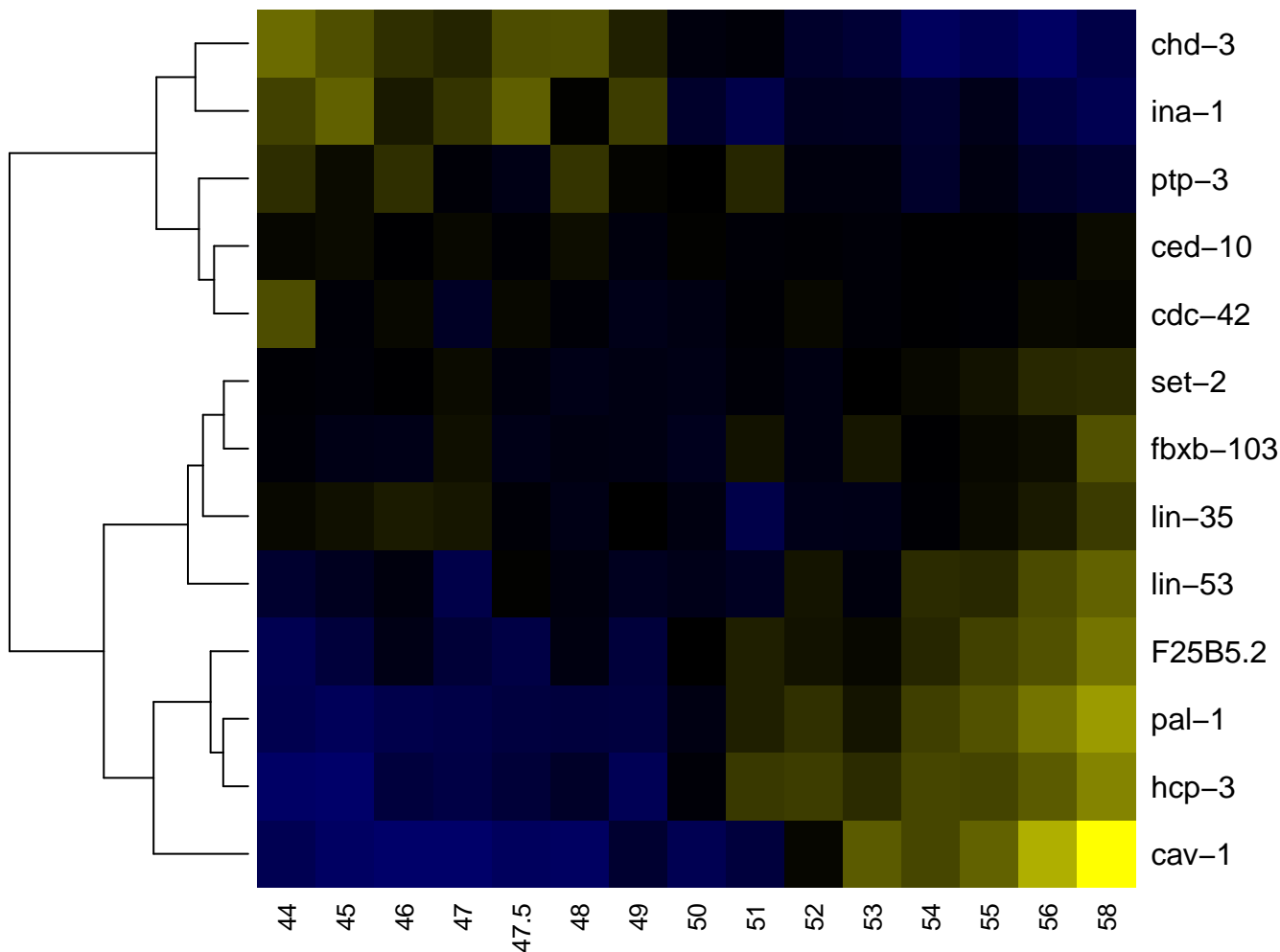
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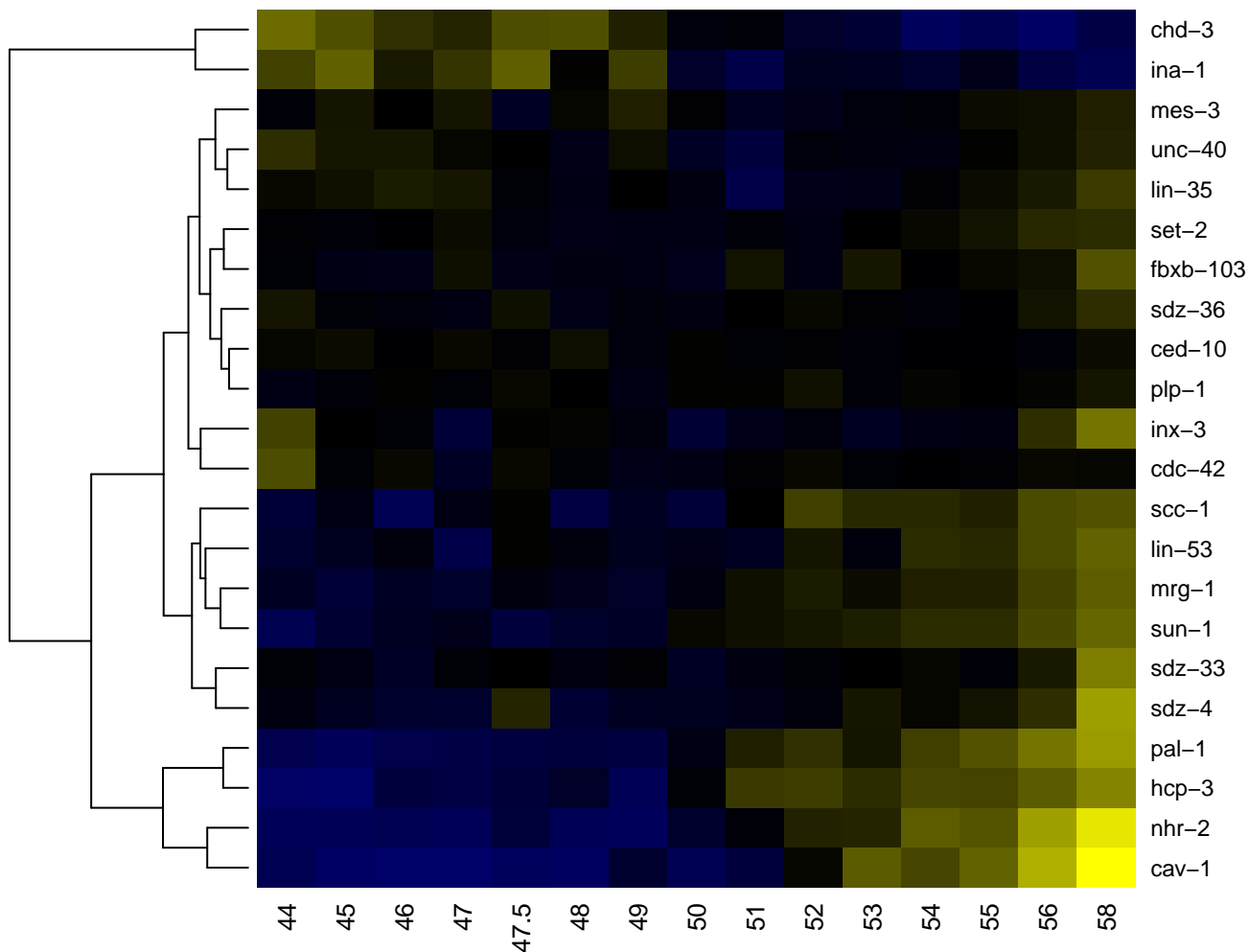
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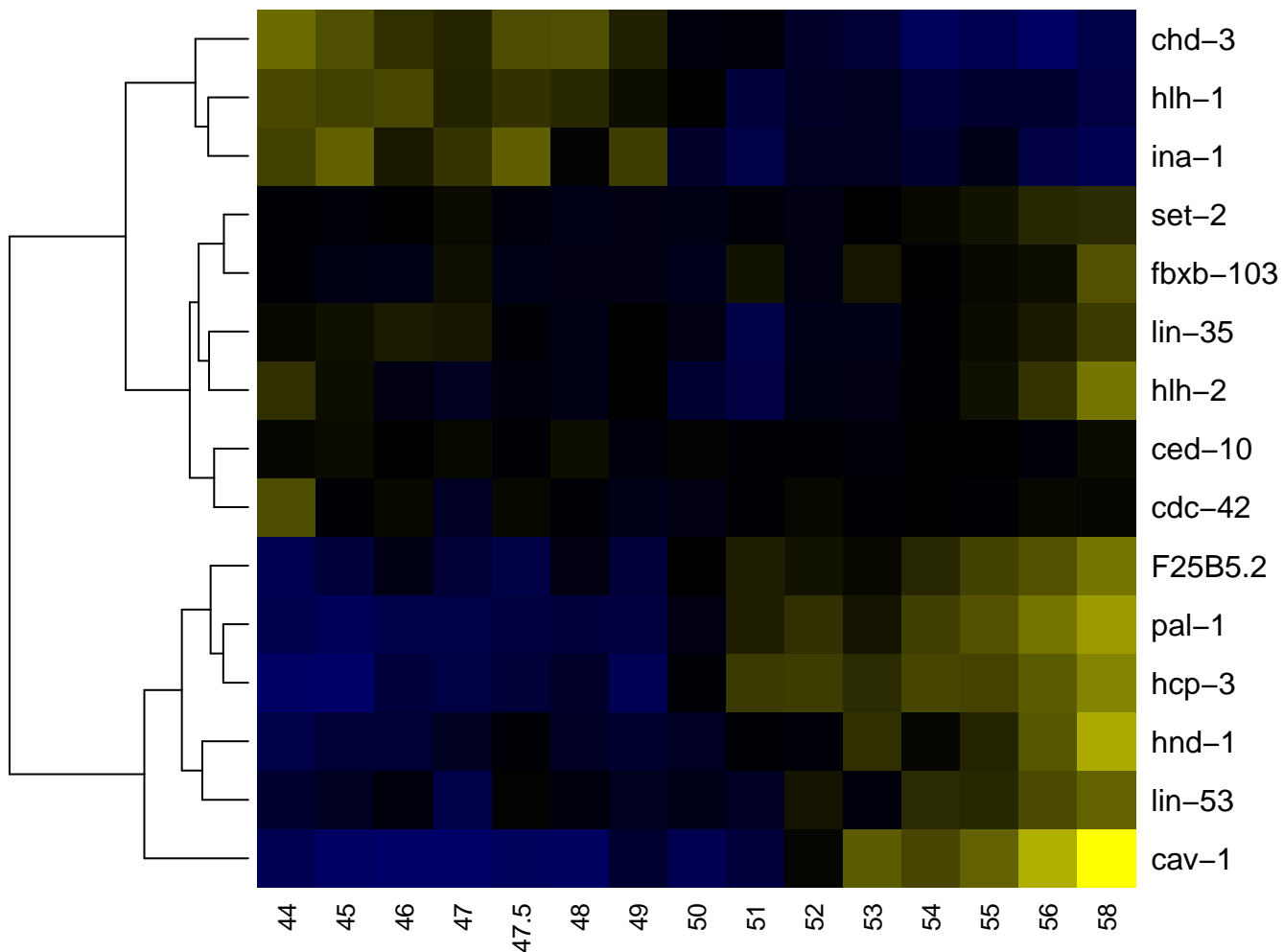
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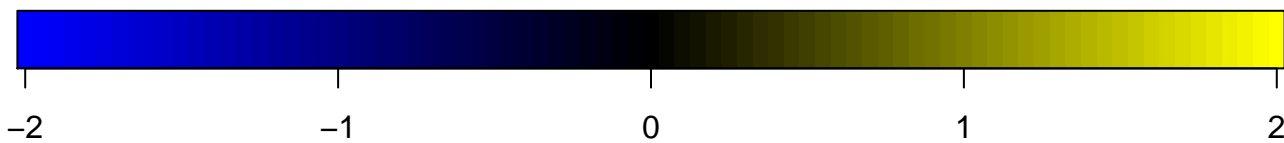
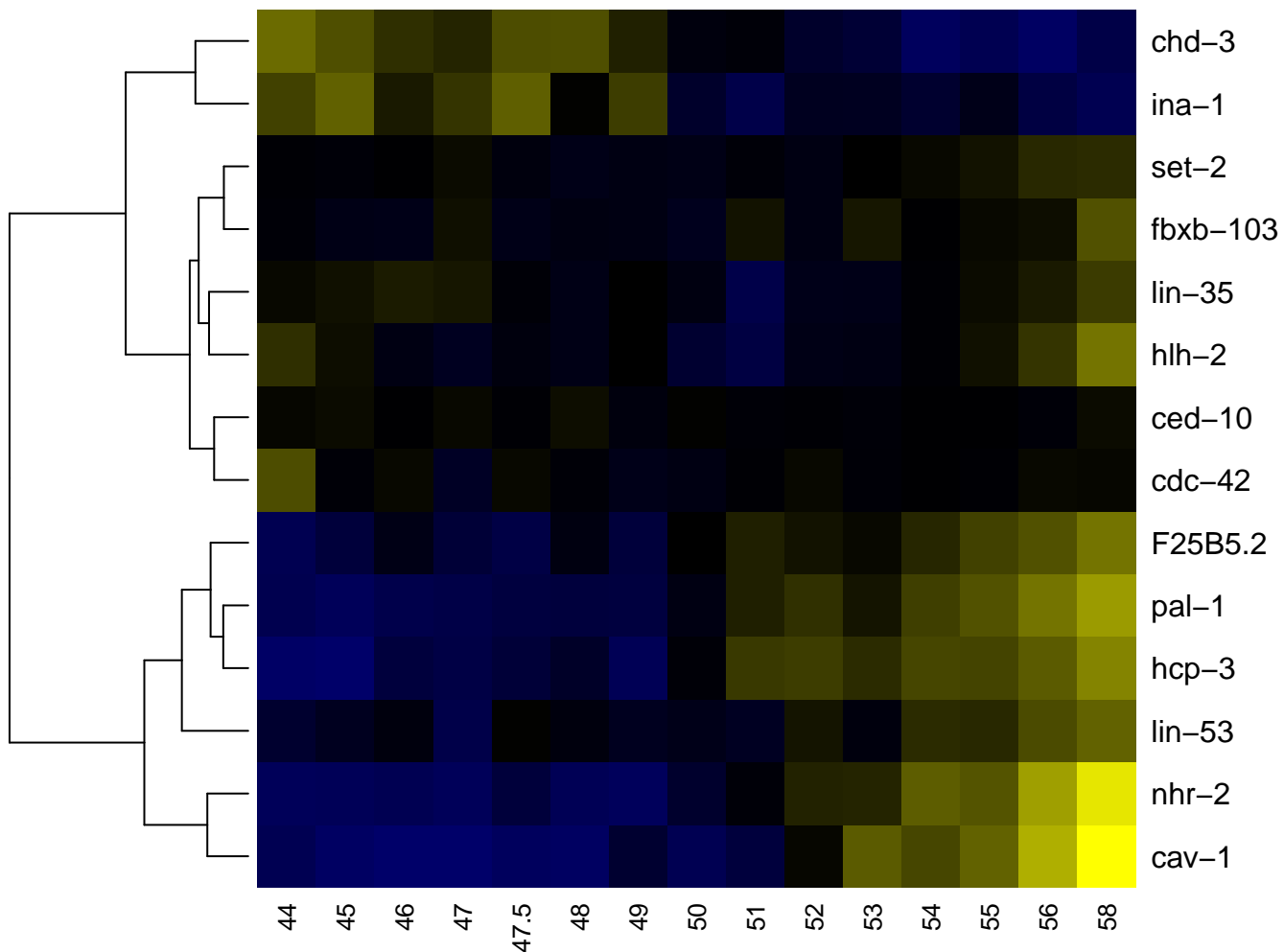
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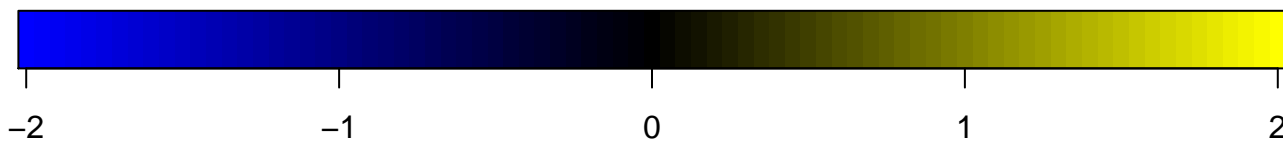
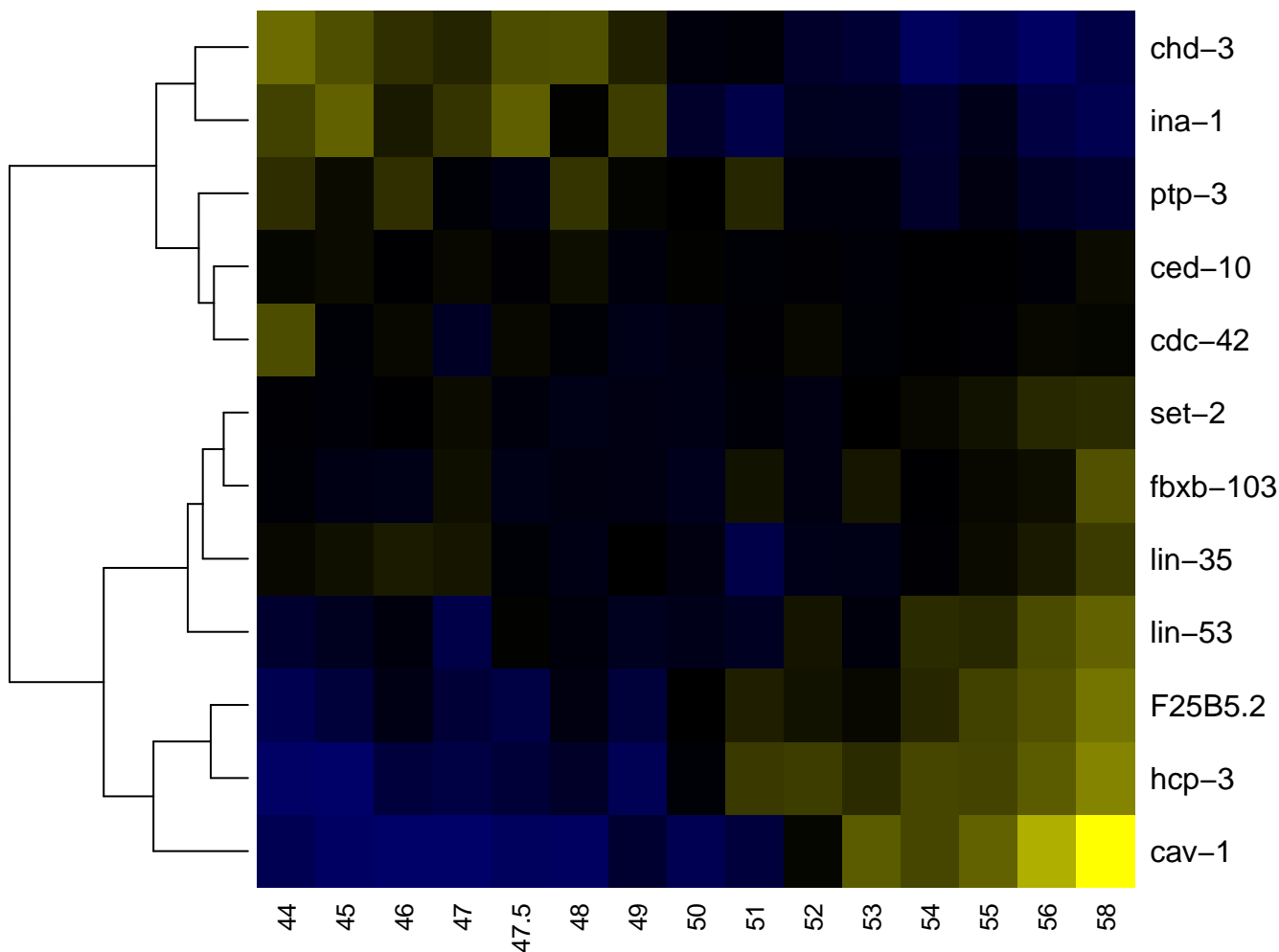
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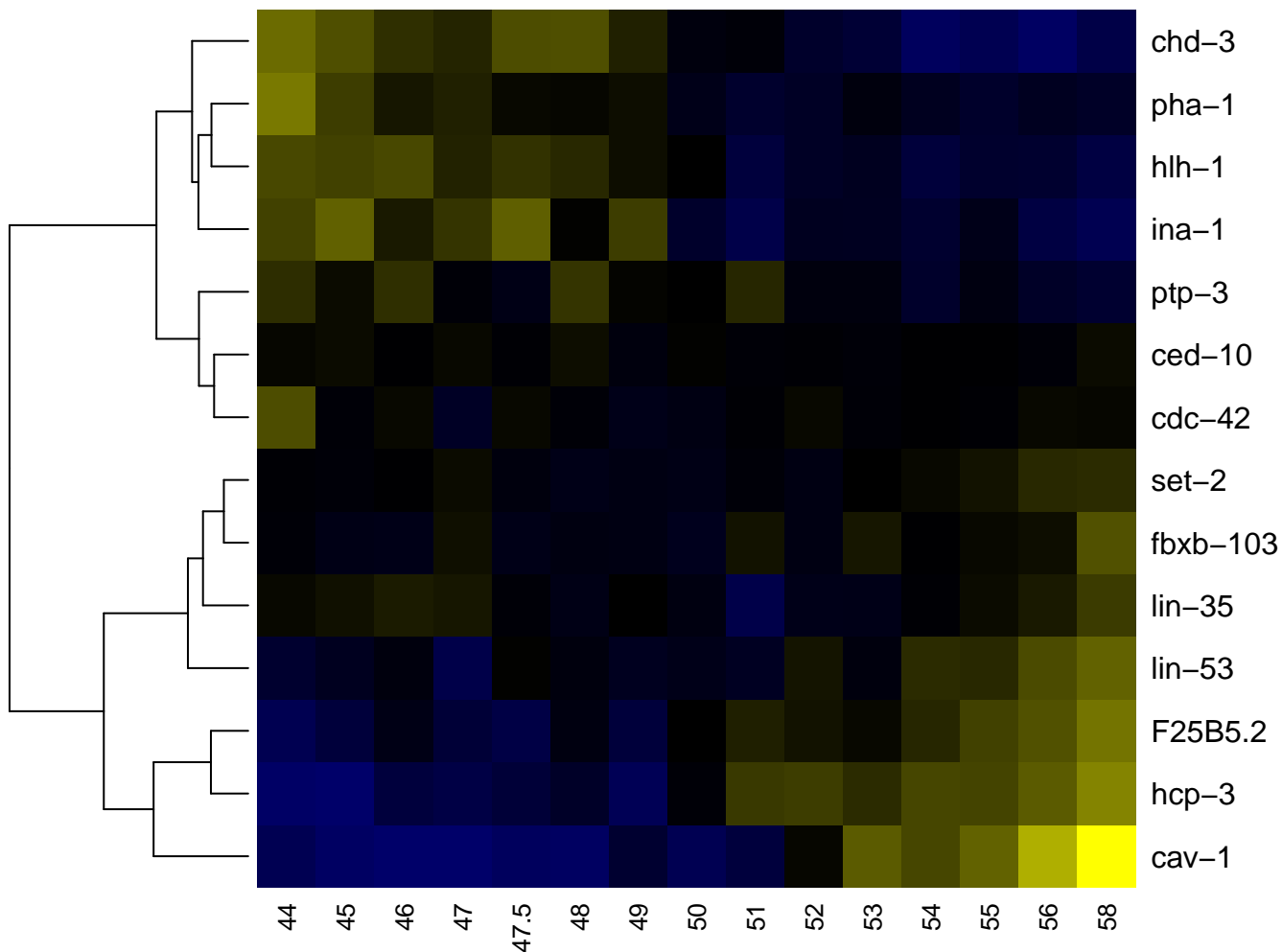
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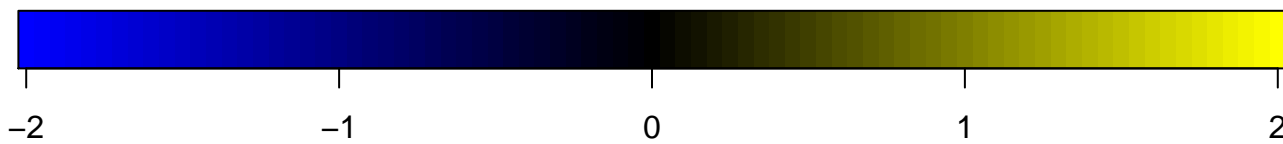
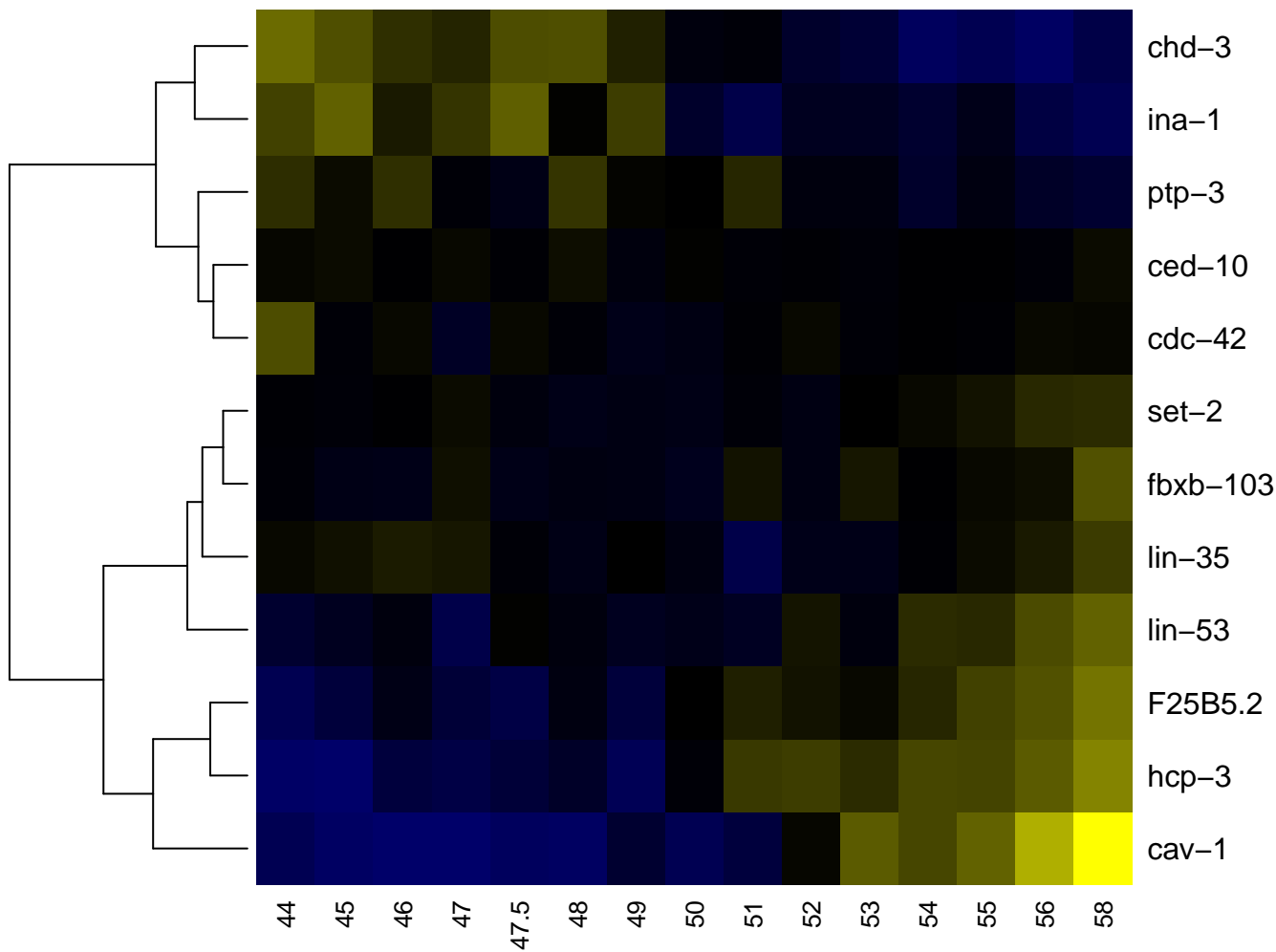
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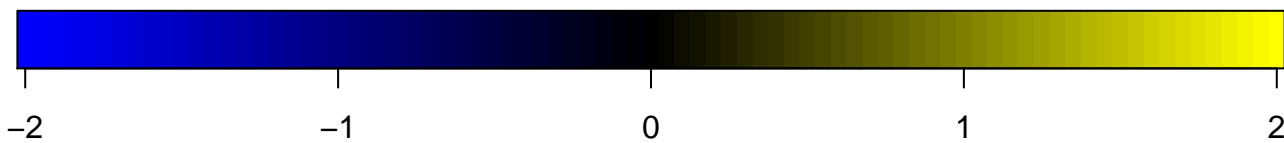
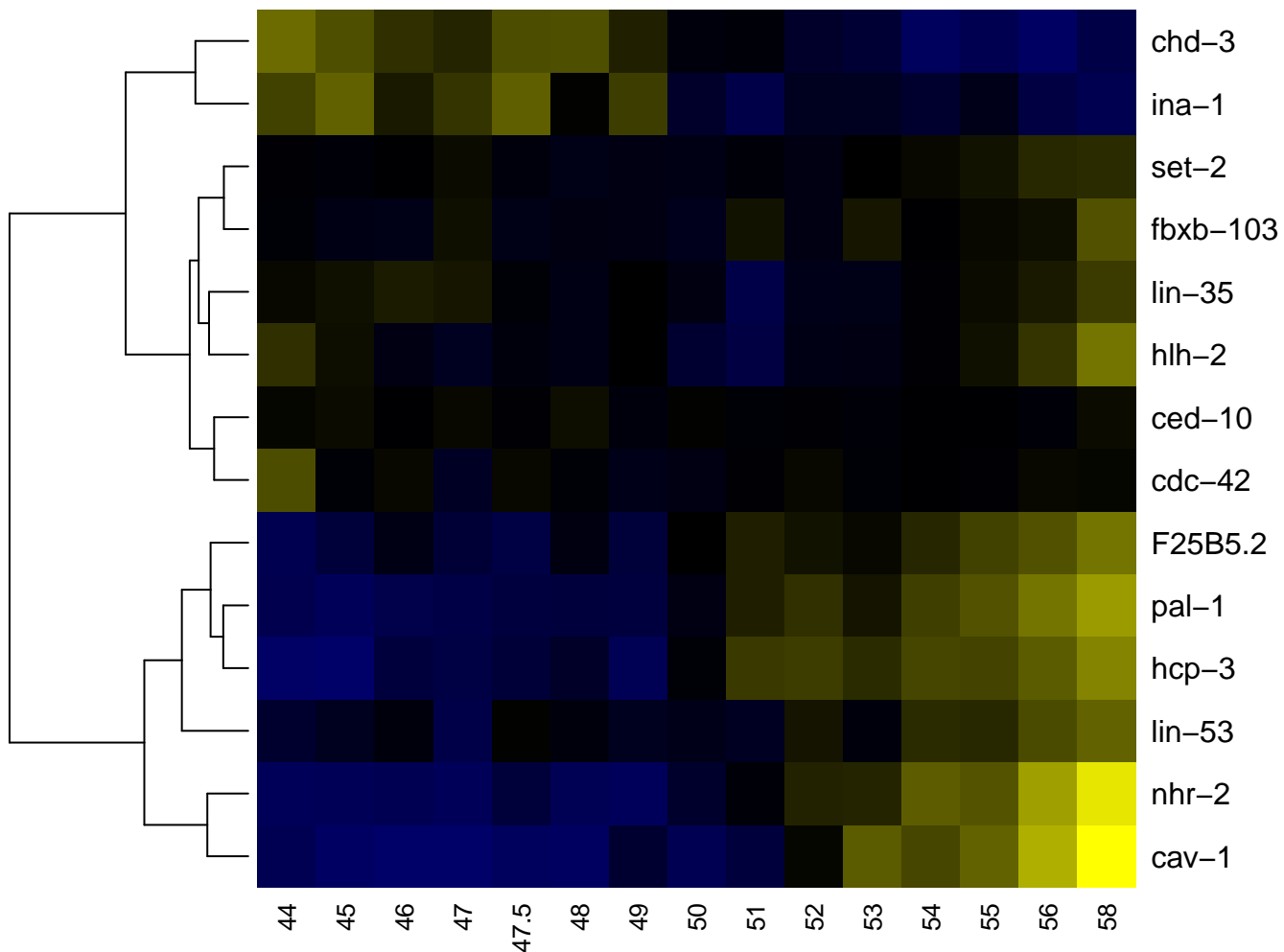
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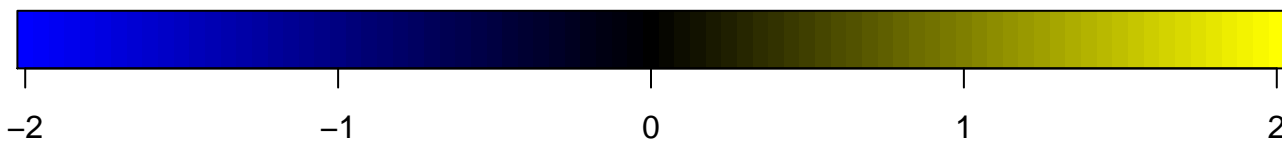
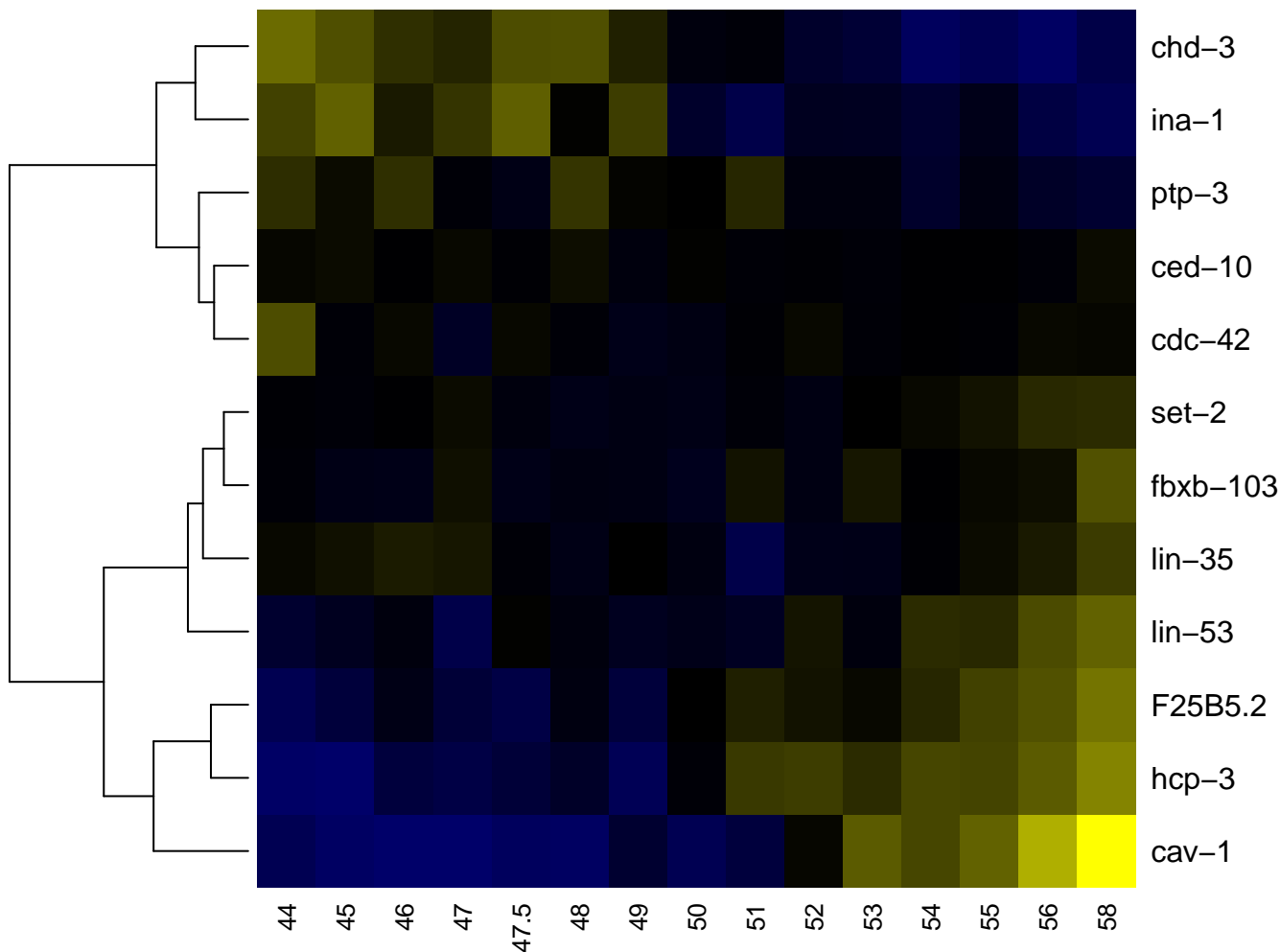
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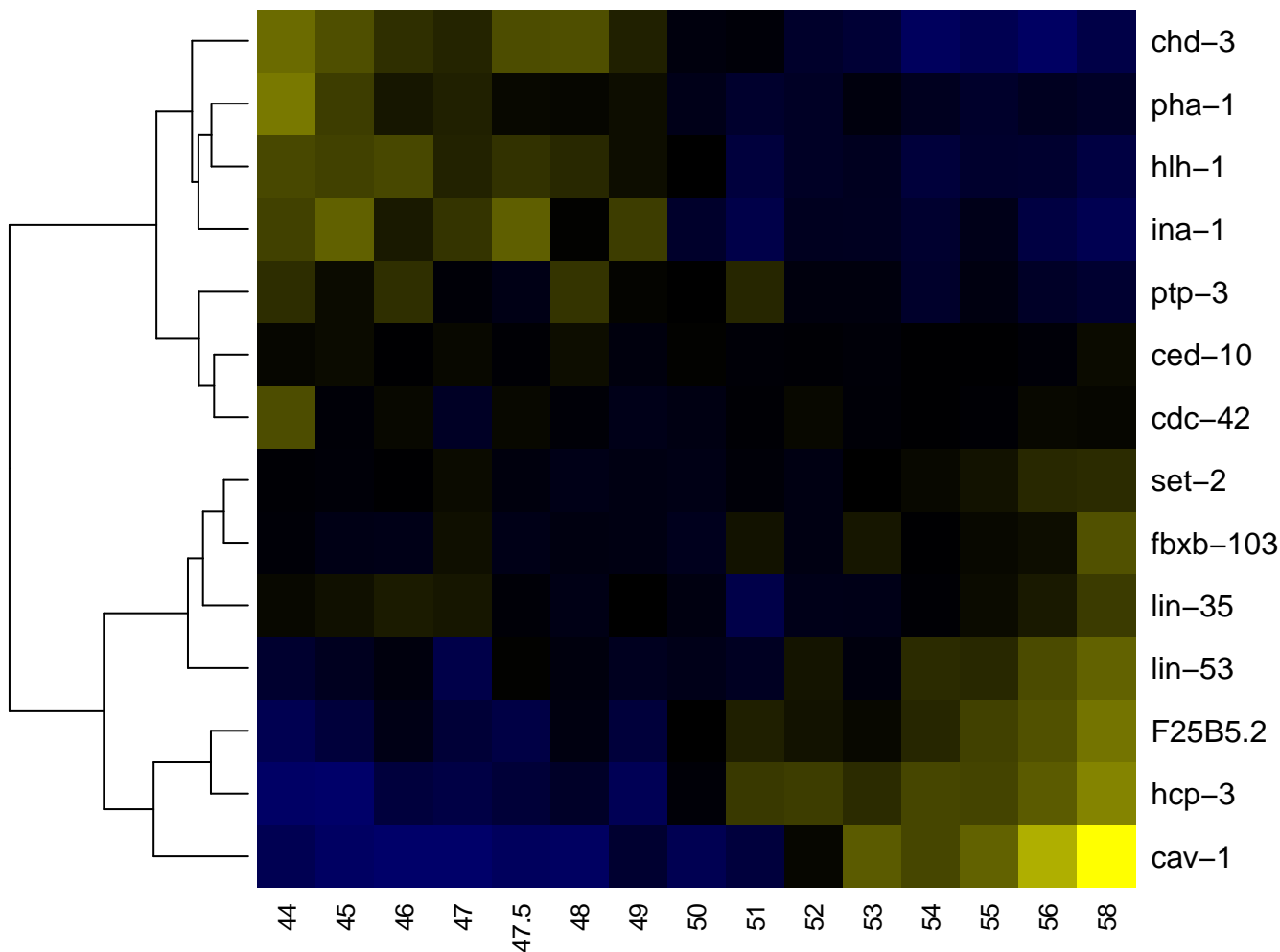
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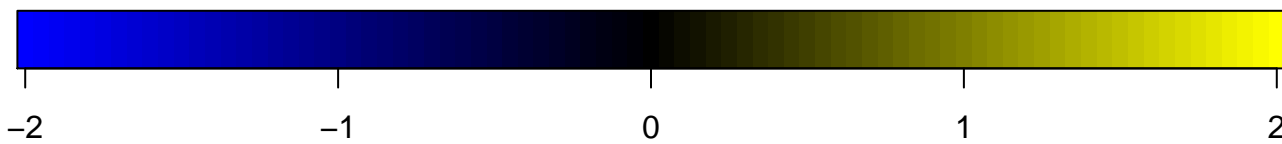
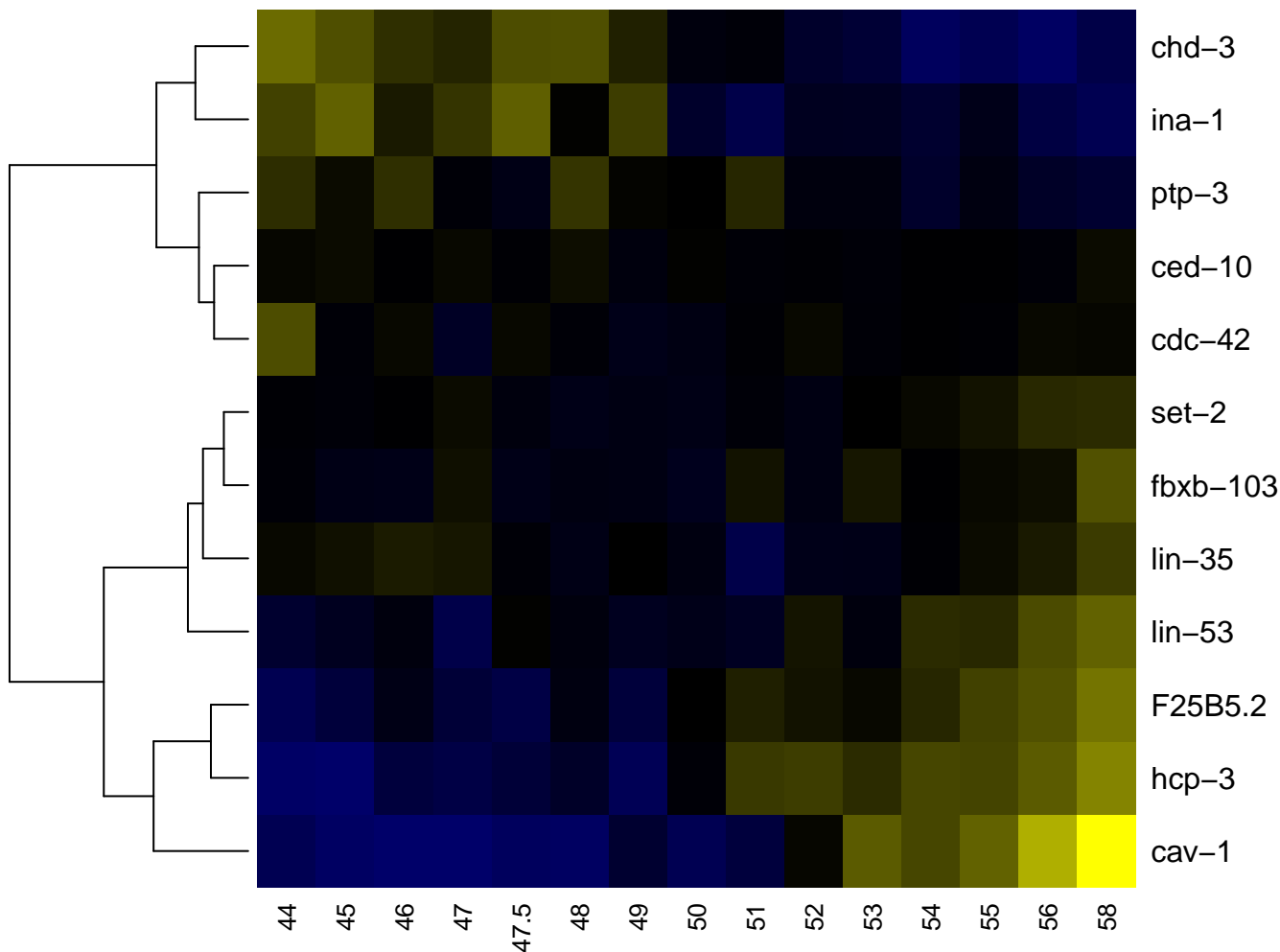
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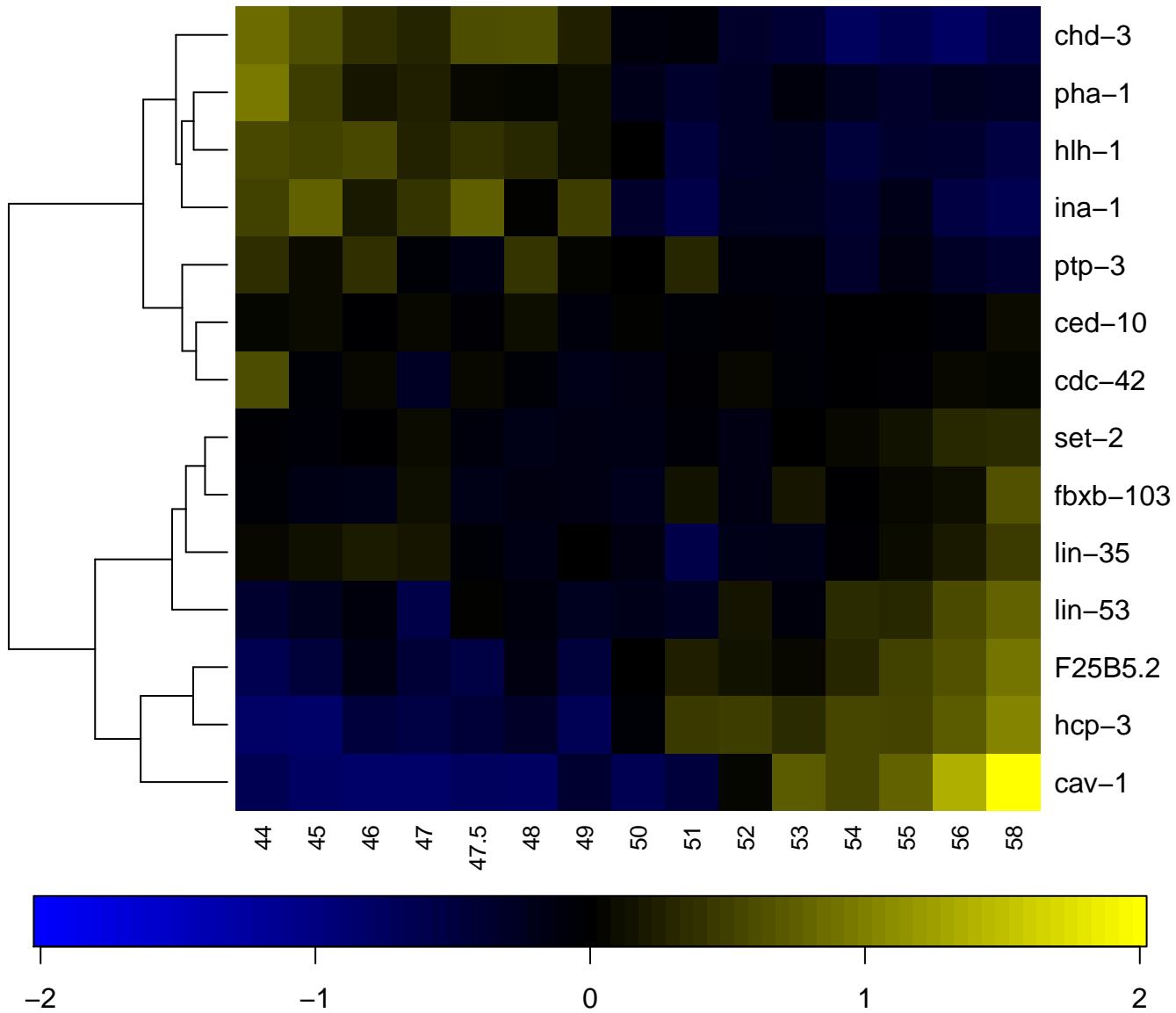
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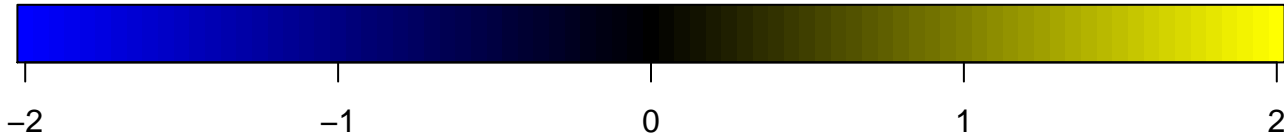
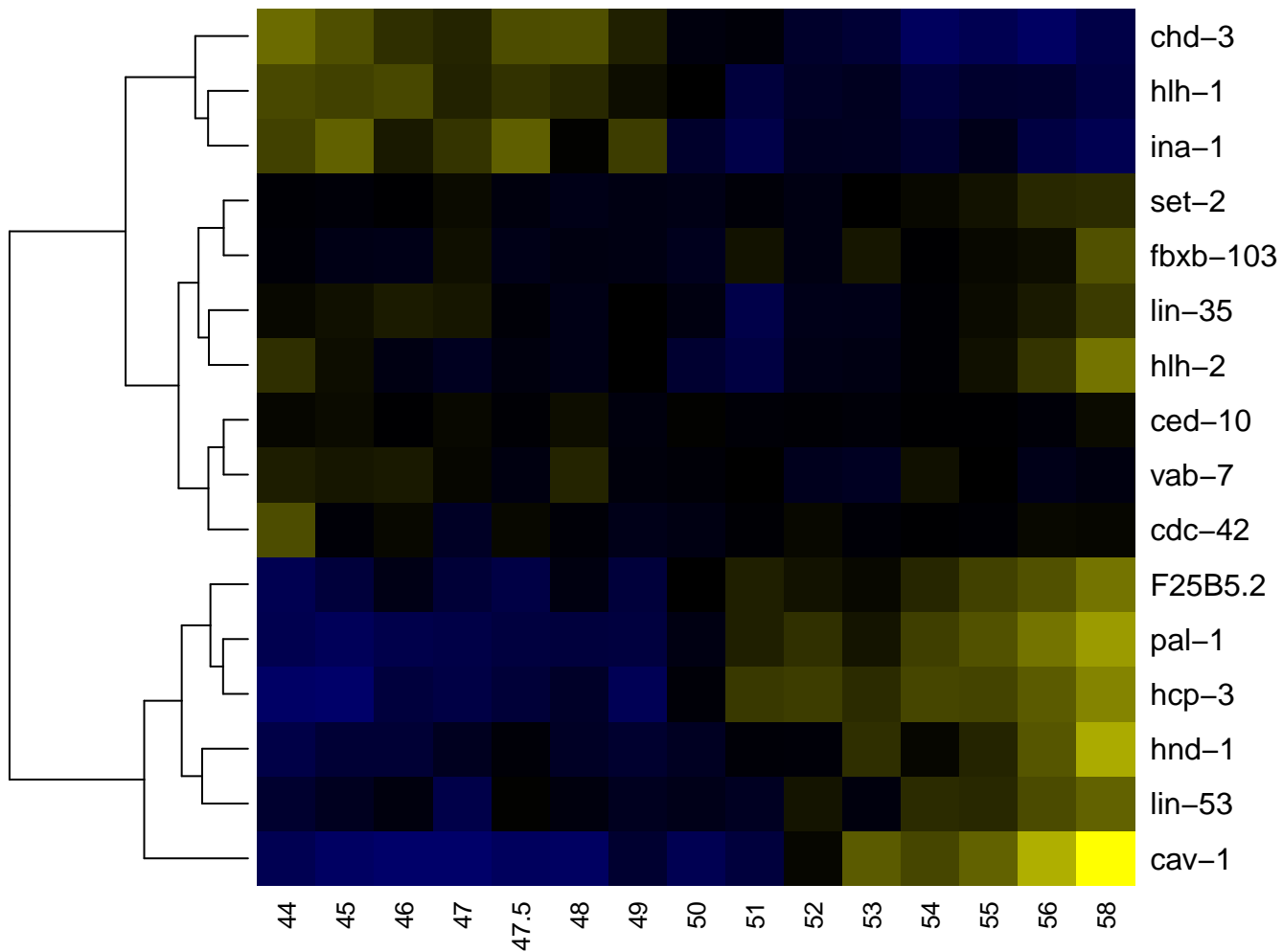
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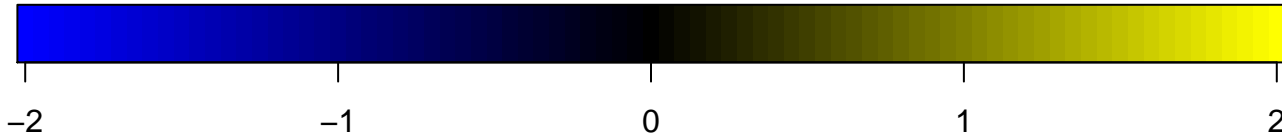
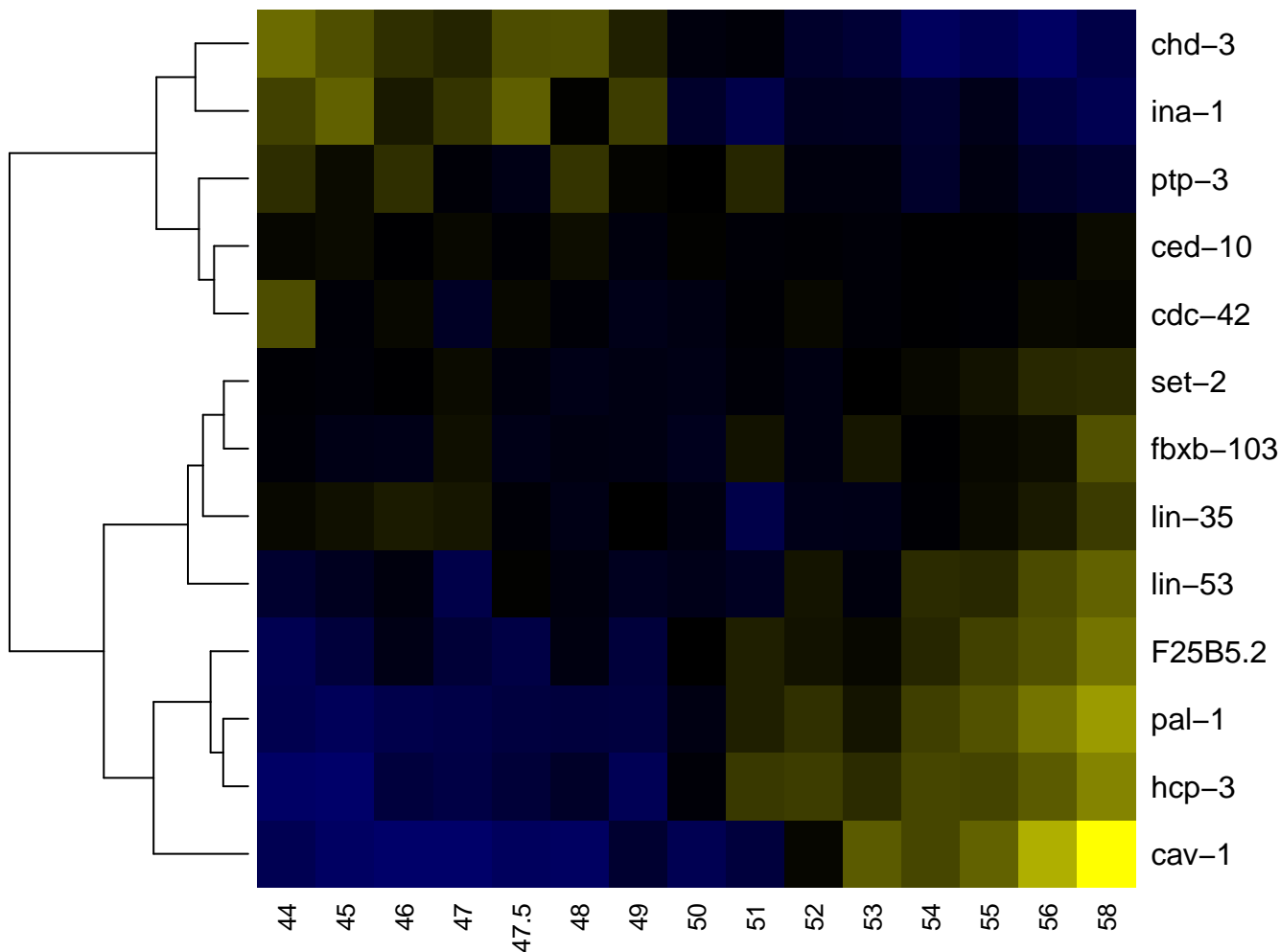
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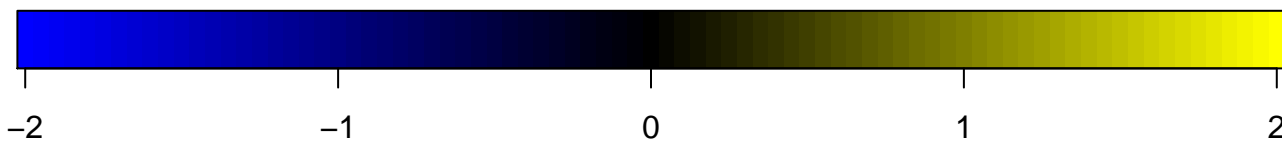
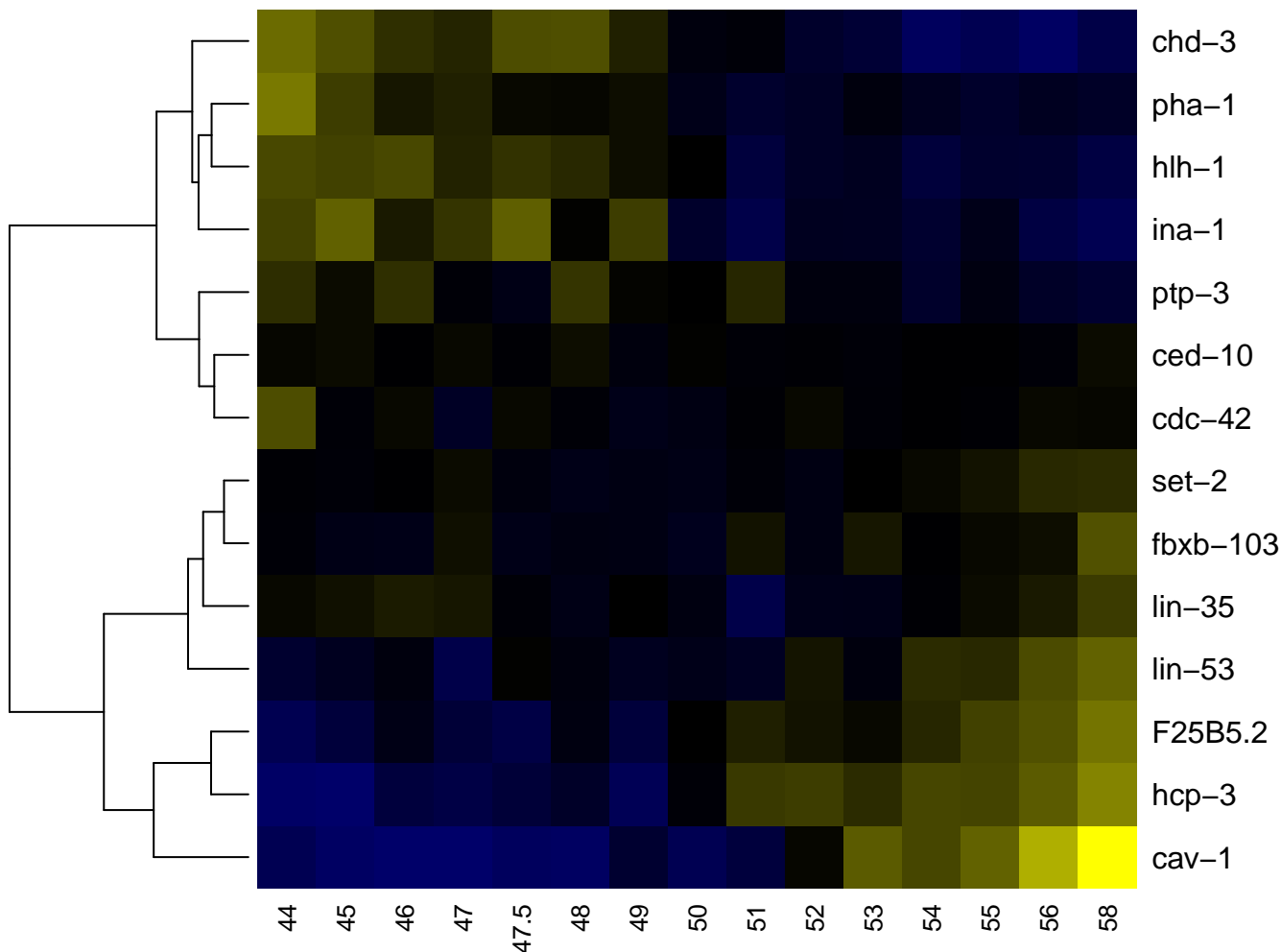
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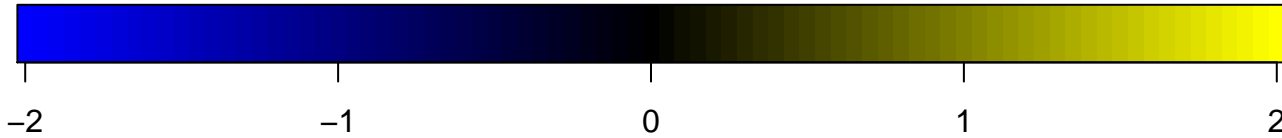
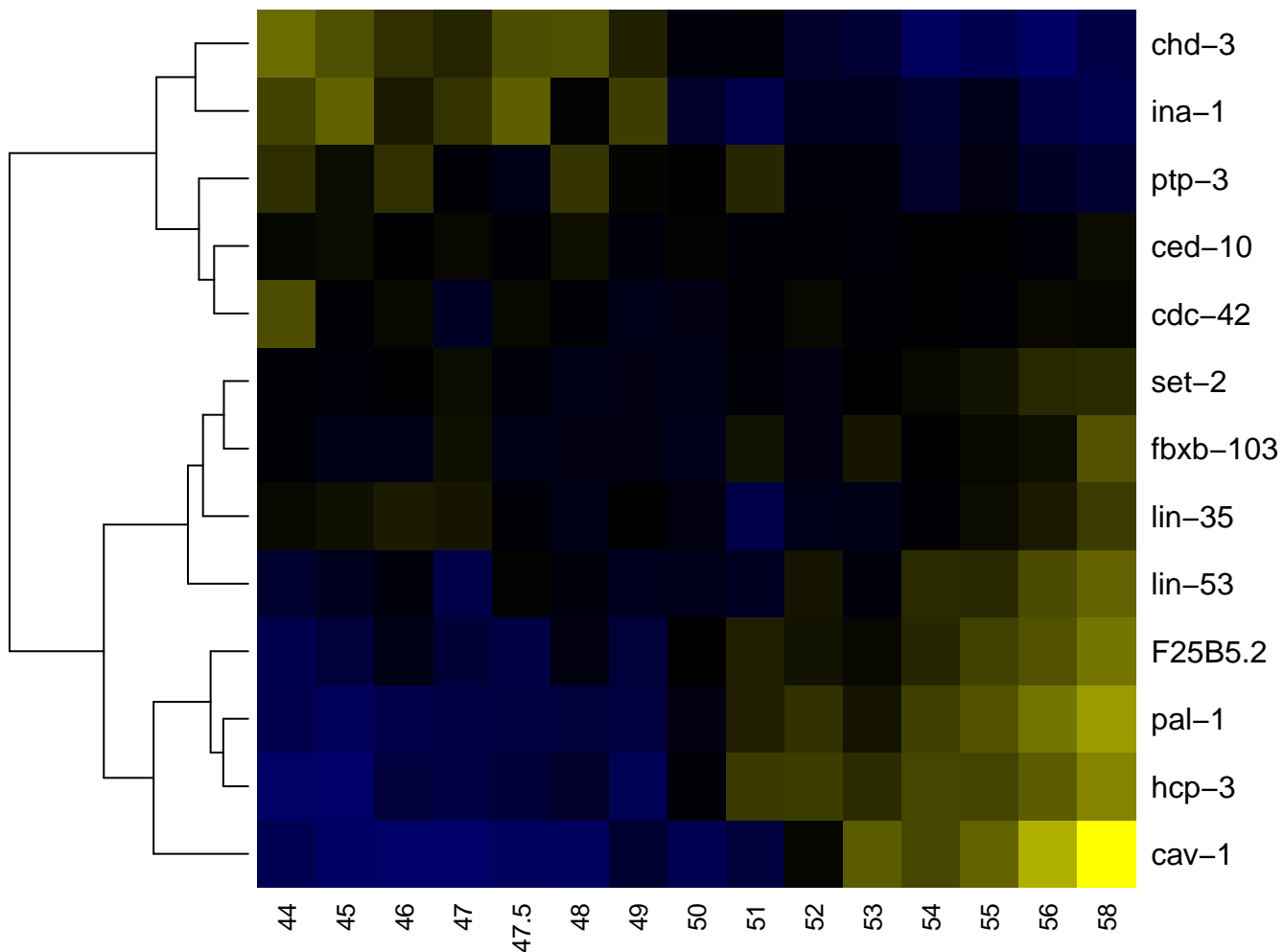
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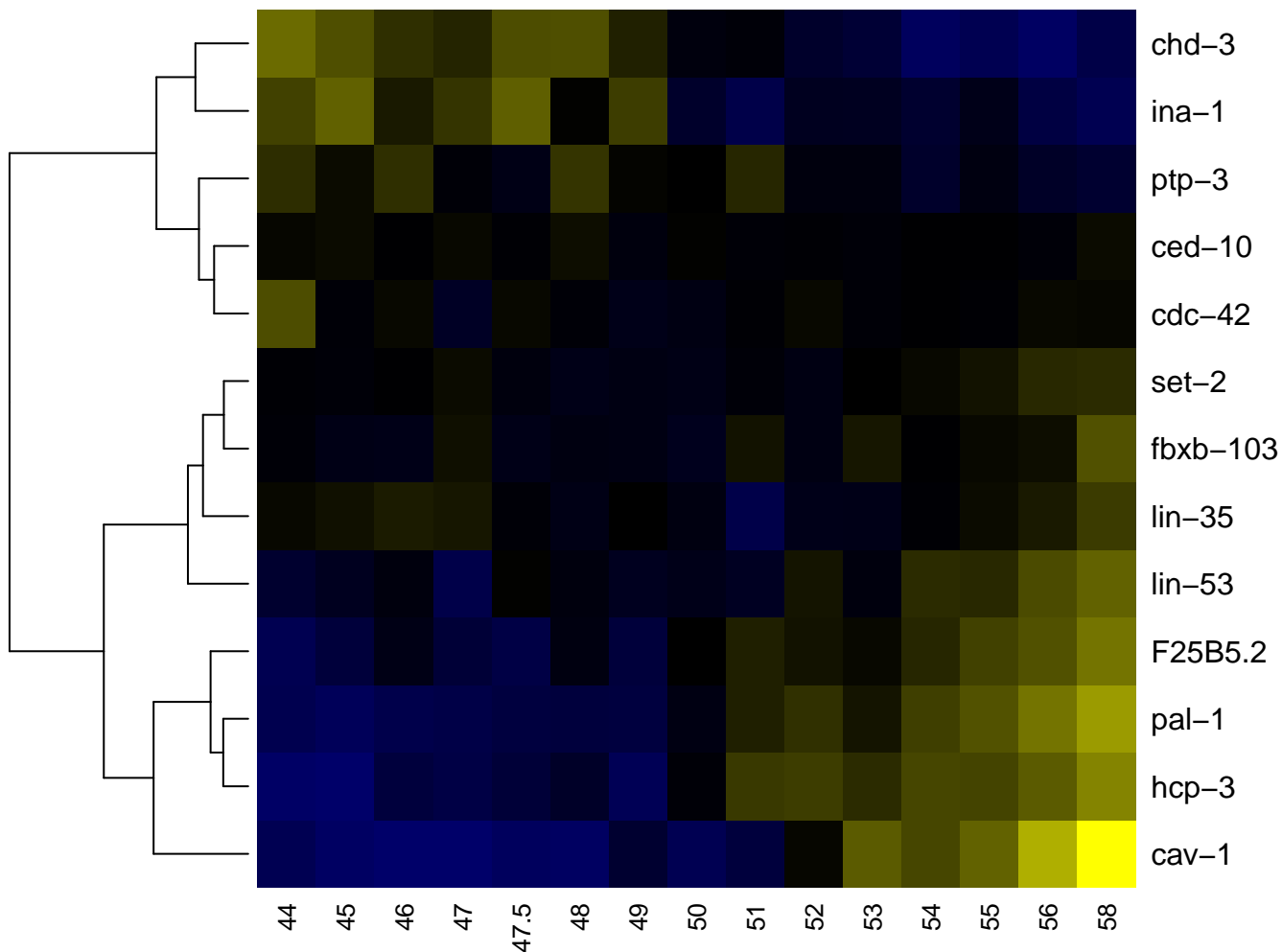
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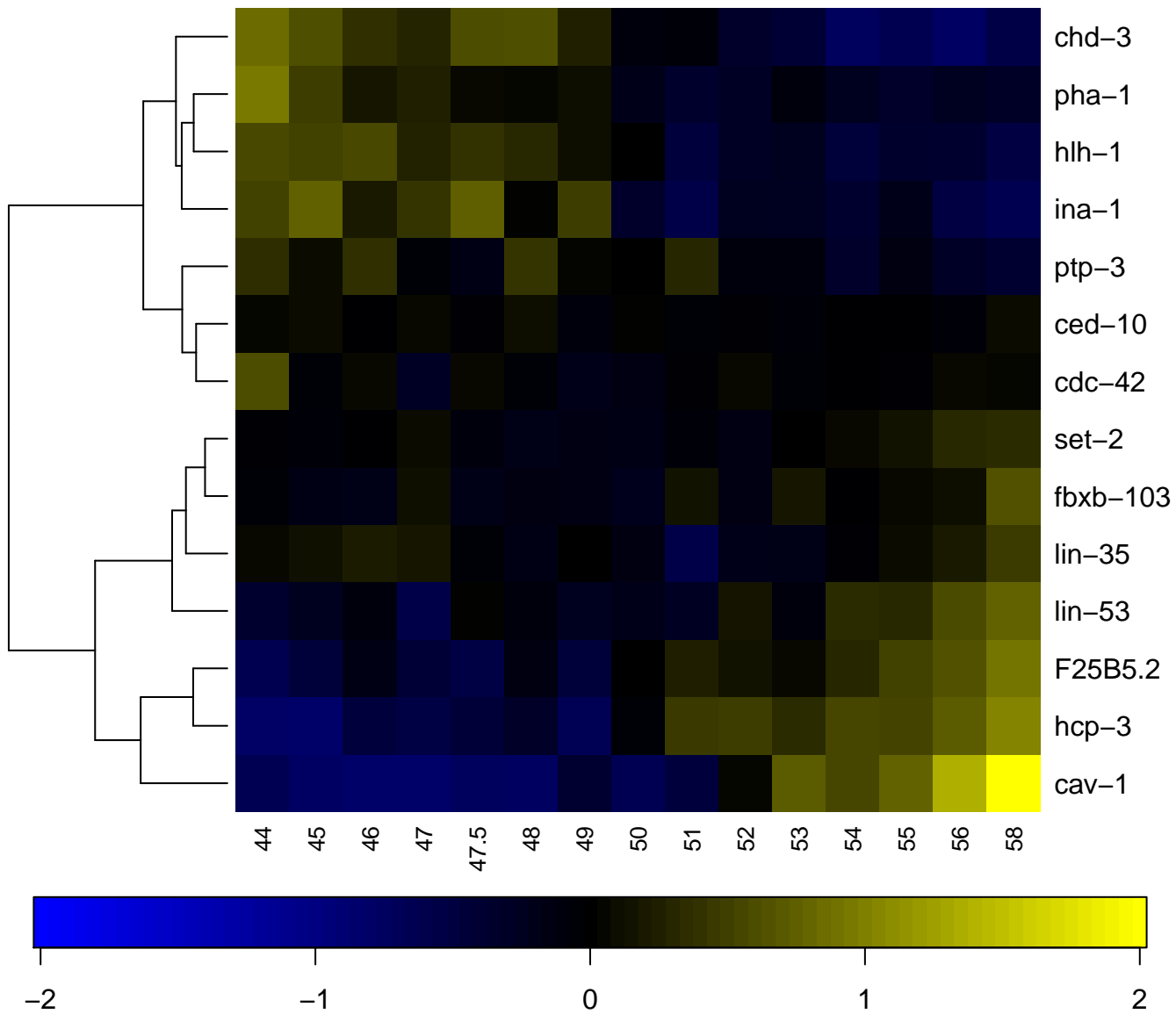
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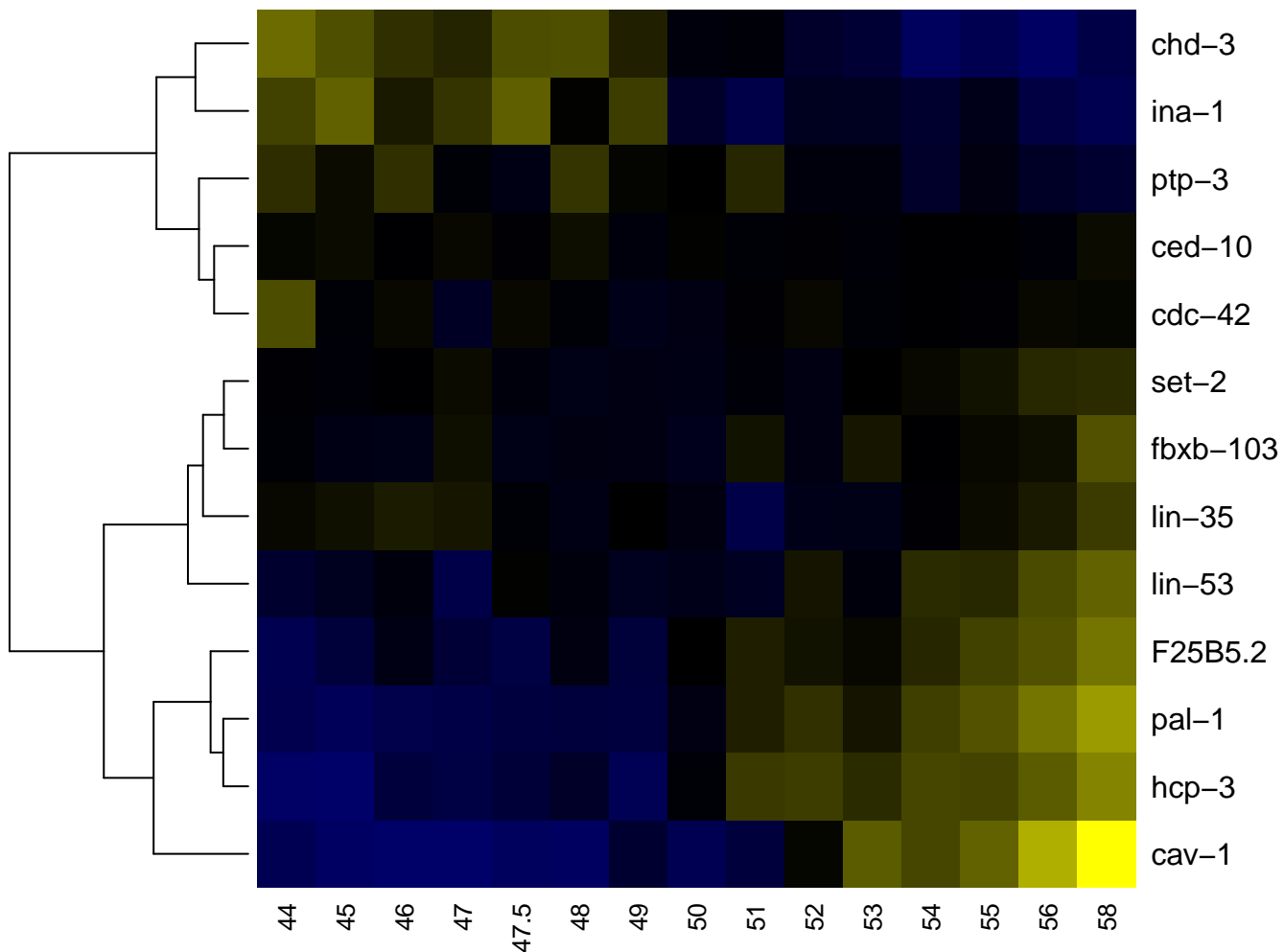
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Cppppap



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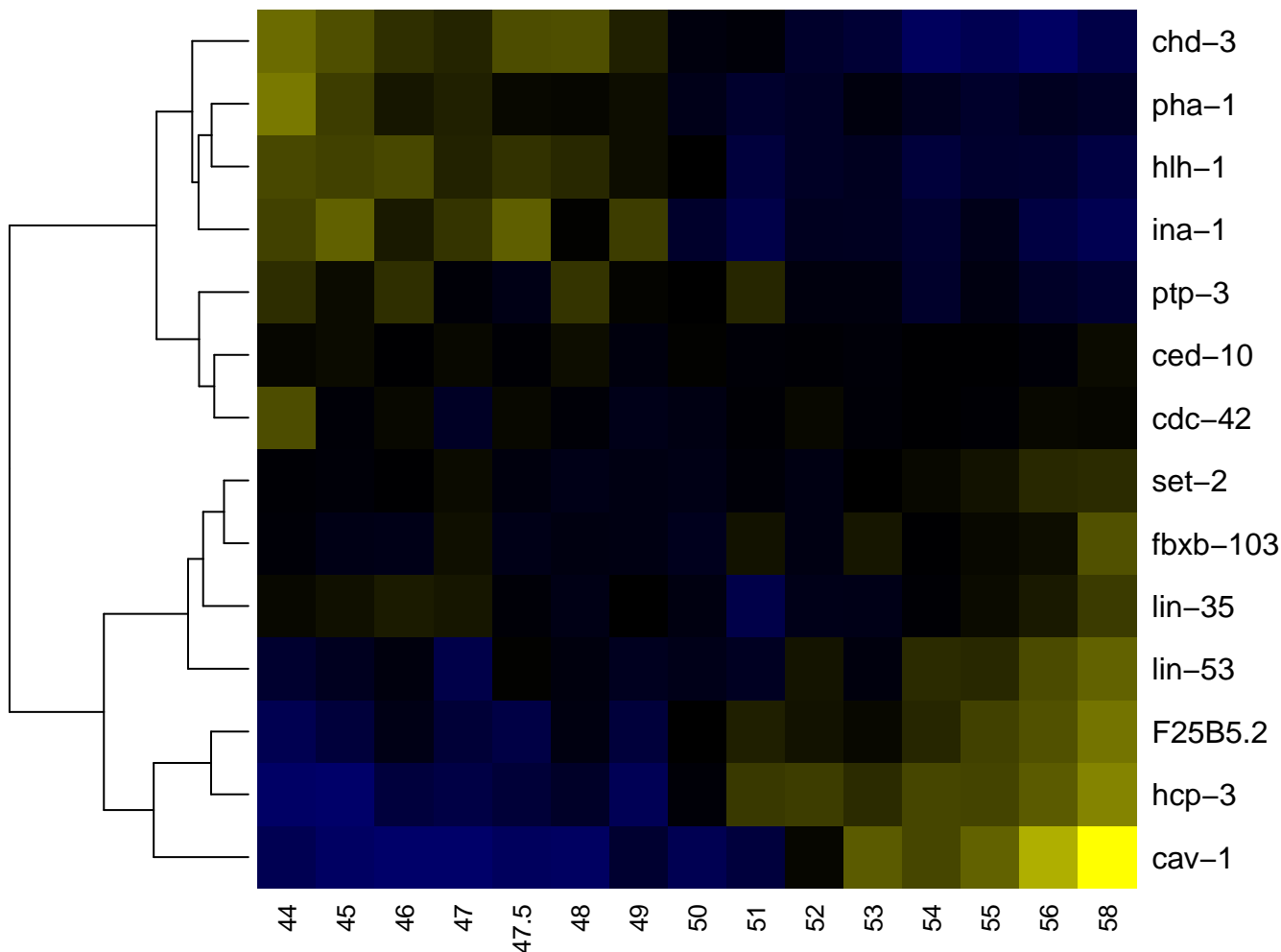
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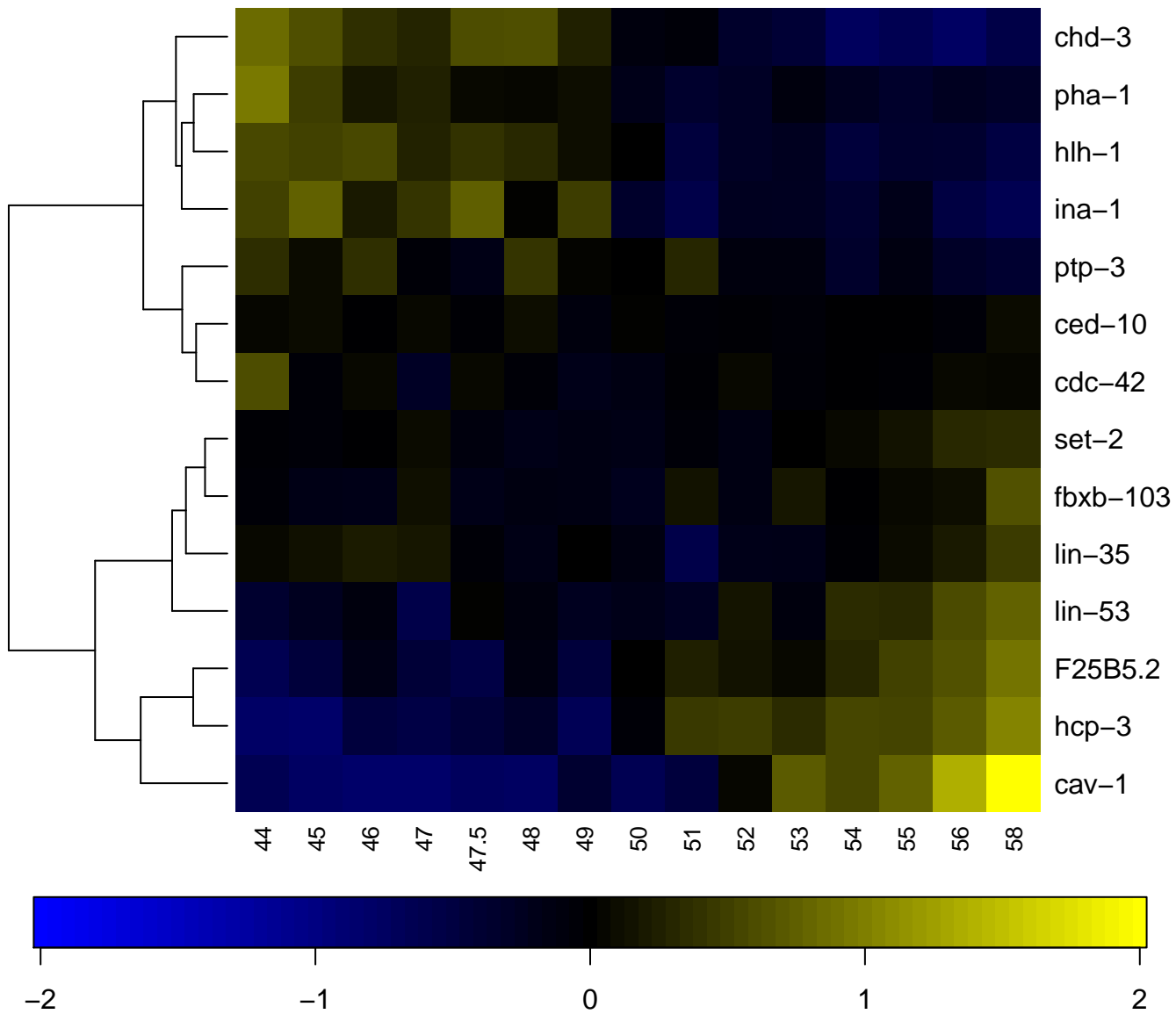
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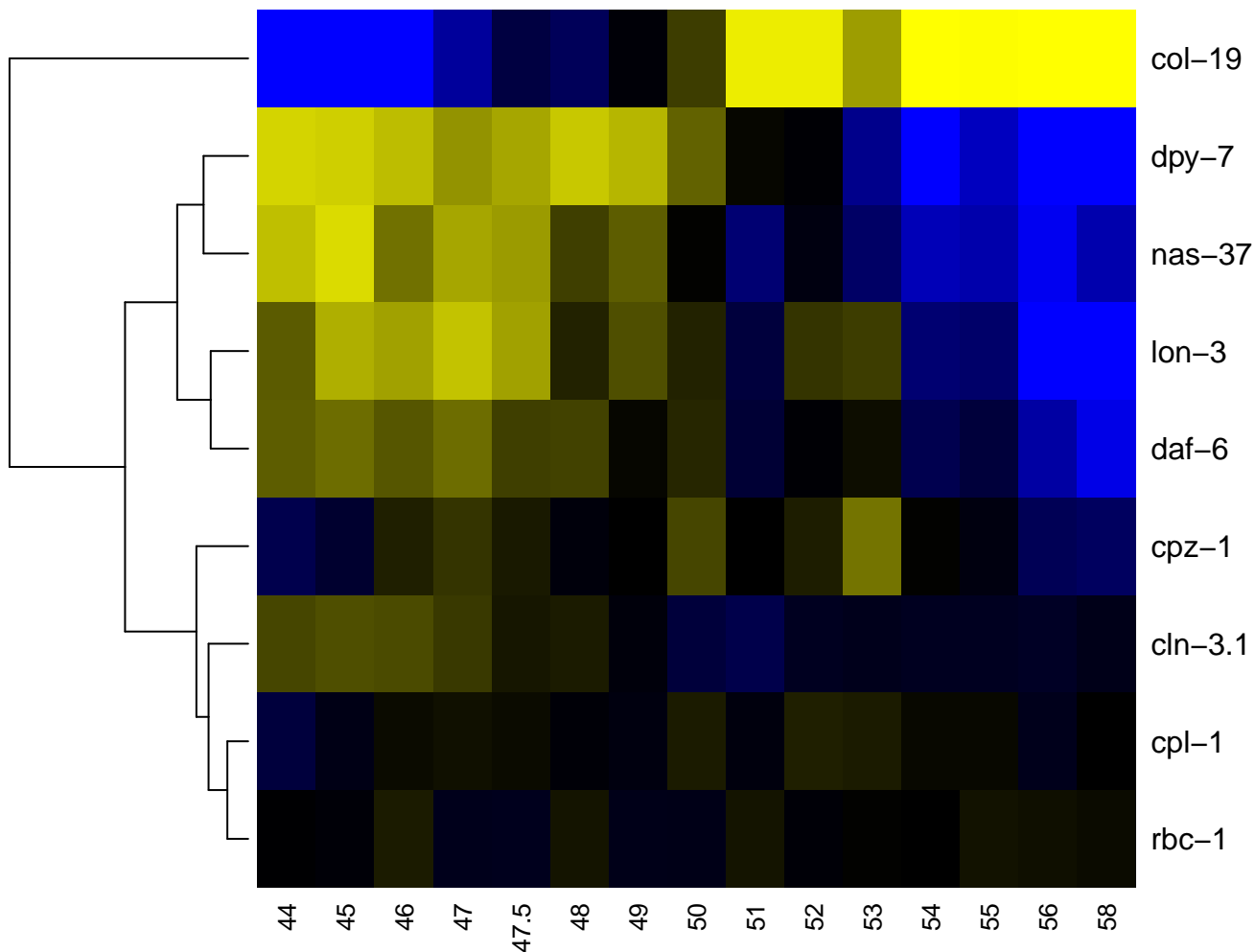
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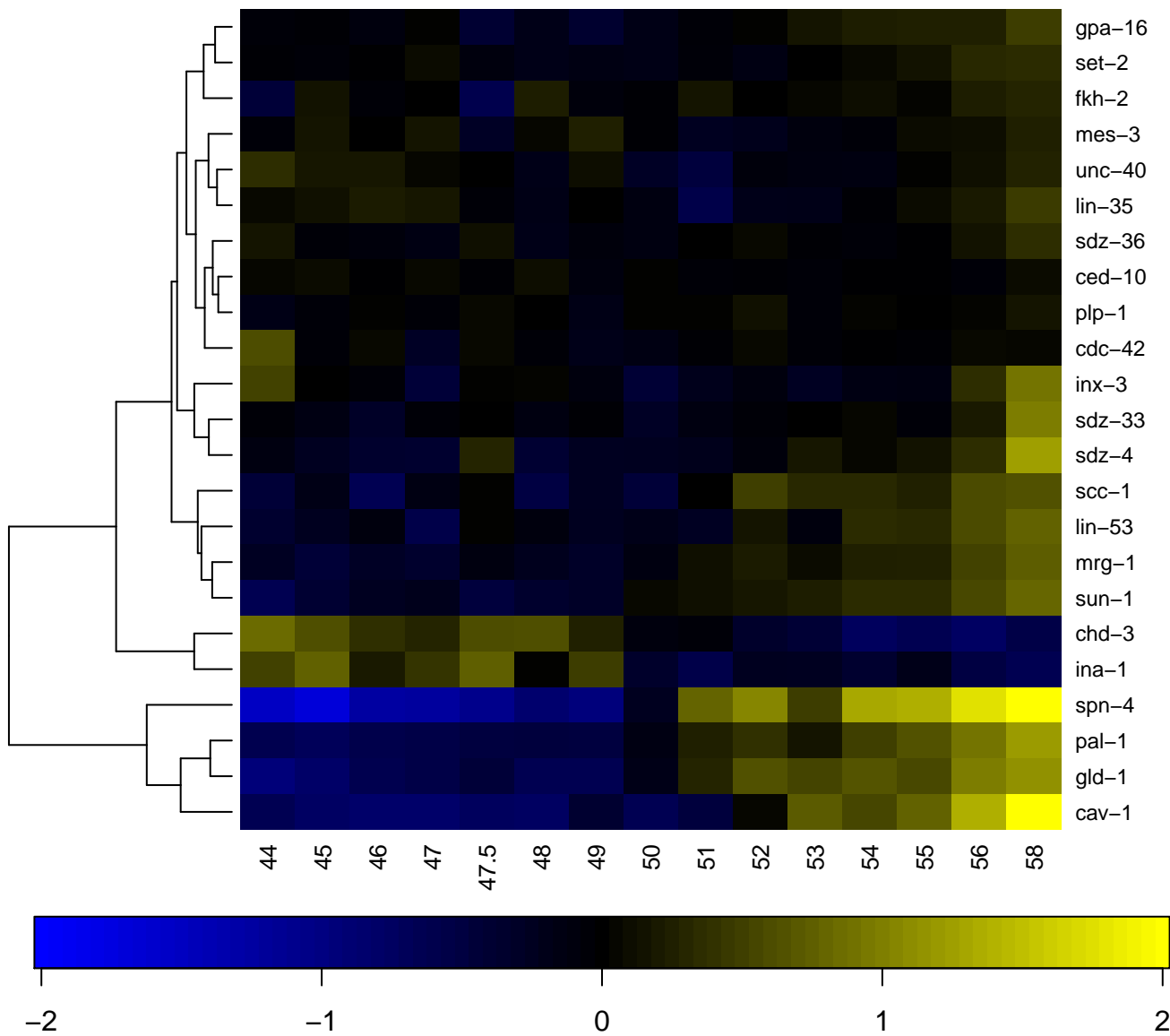
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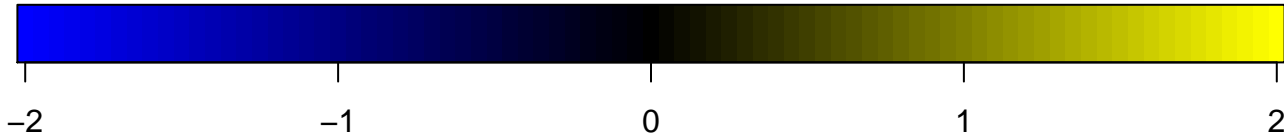
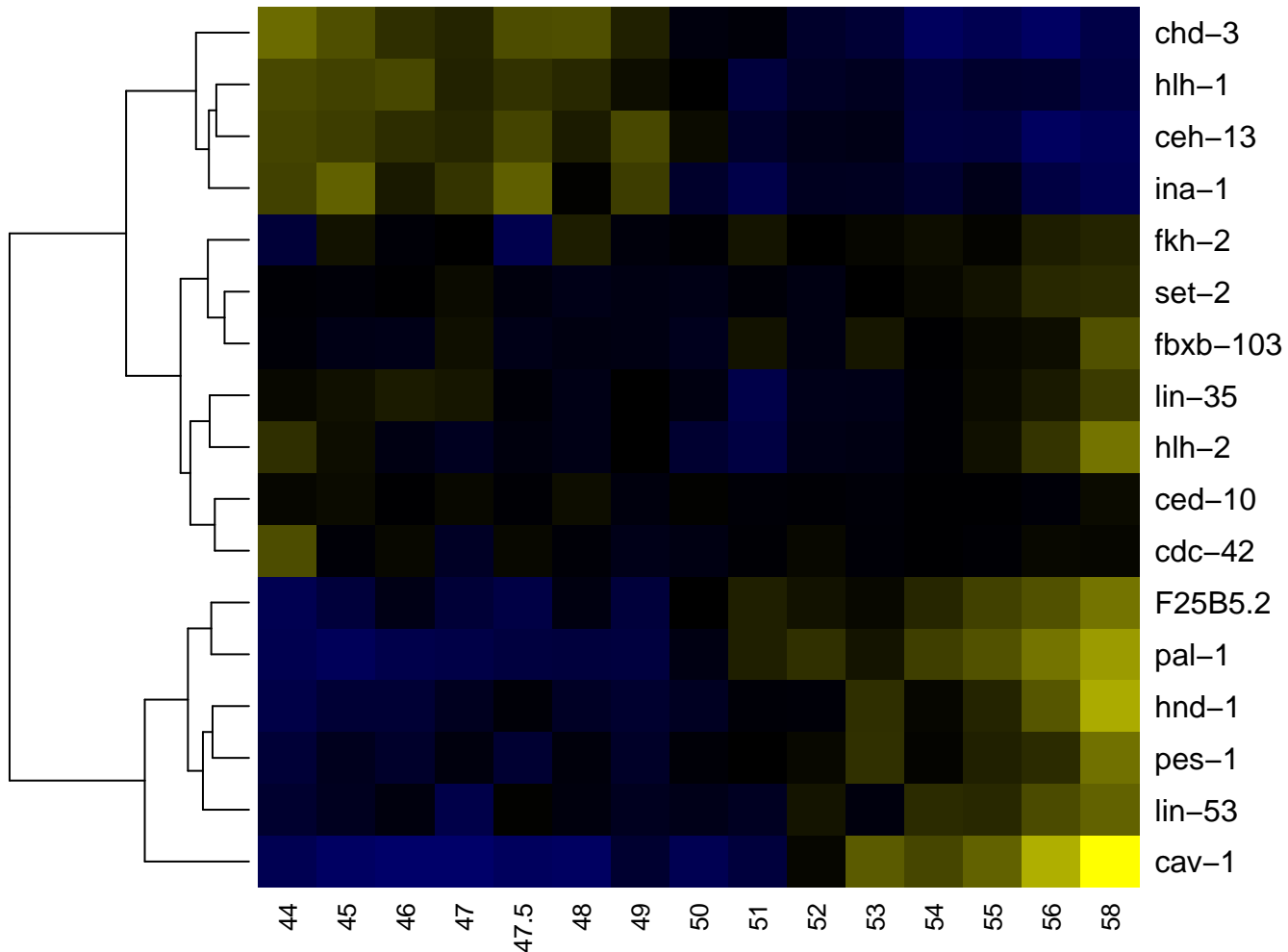
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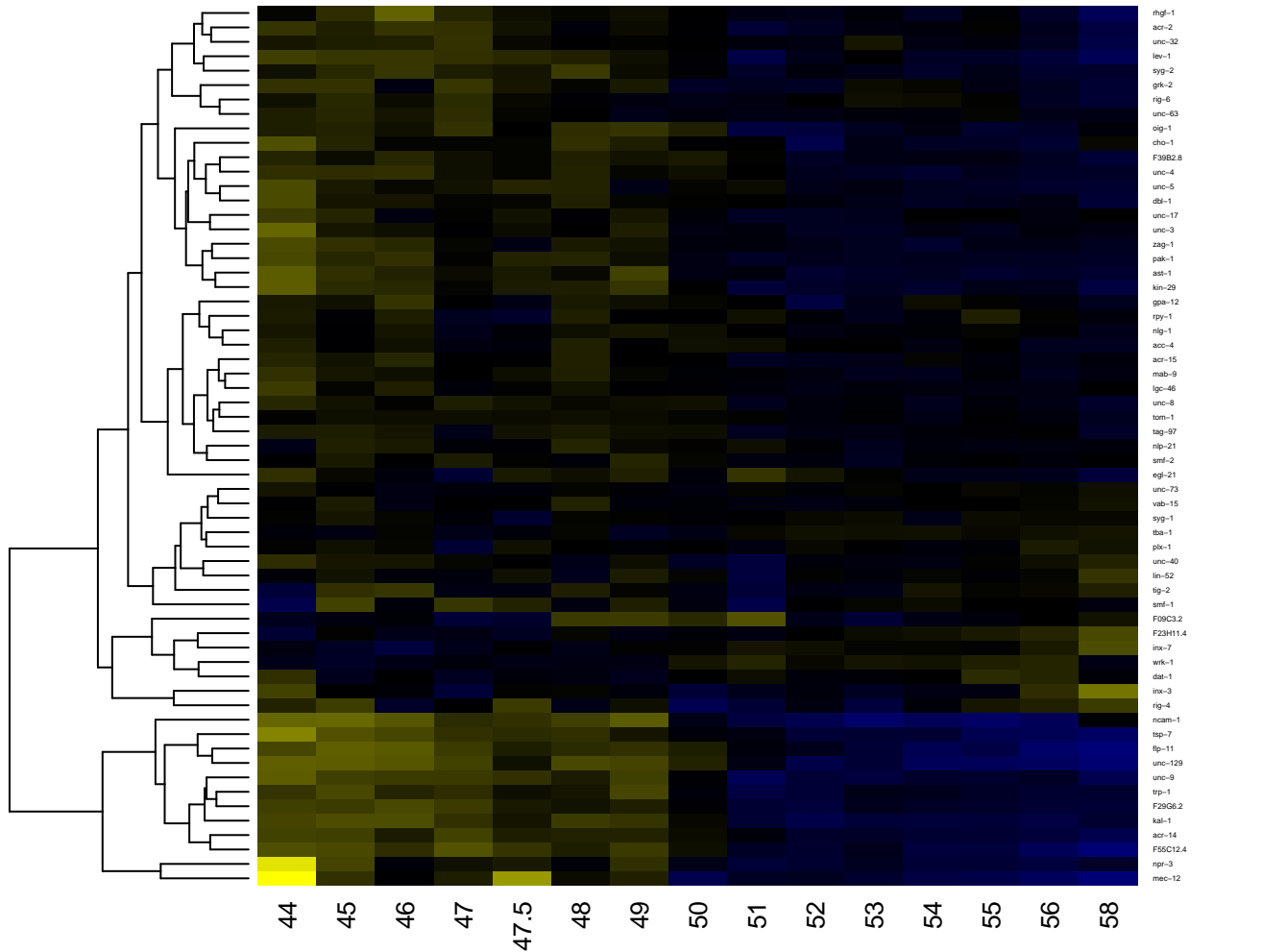
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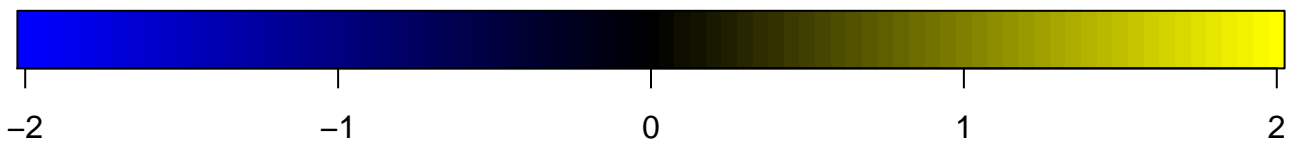
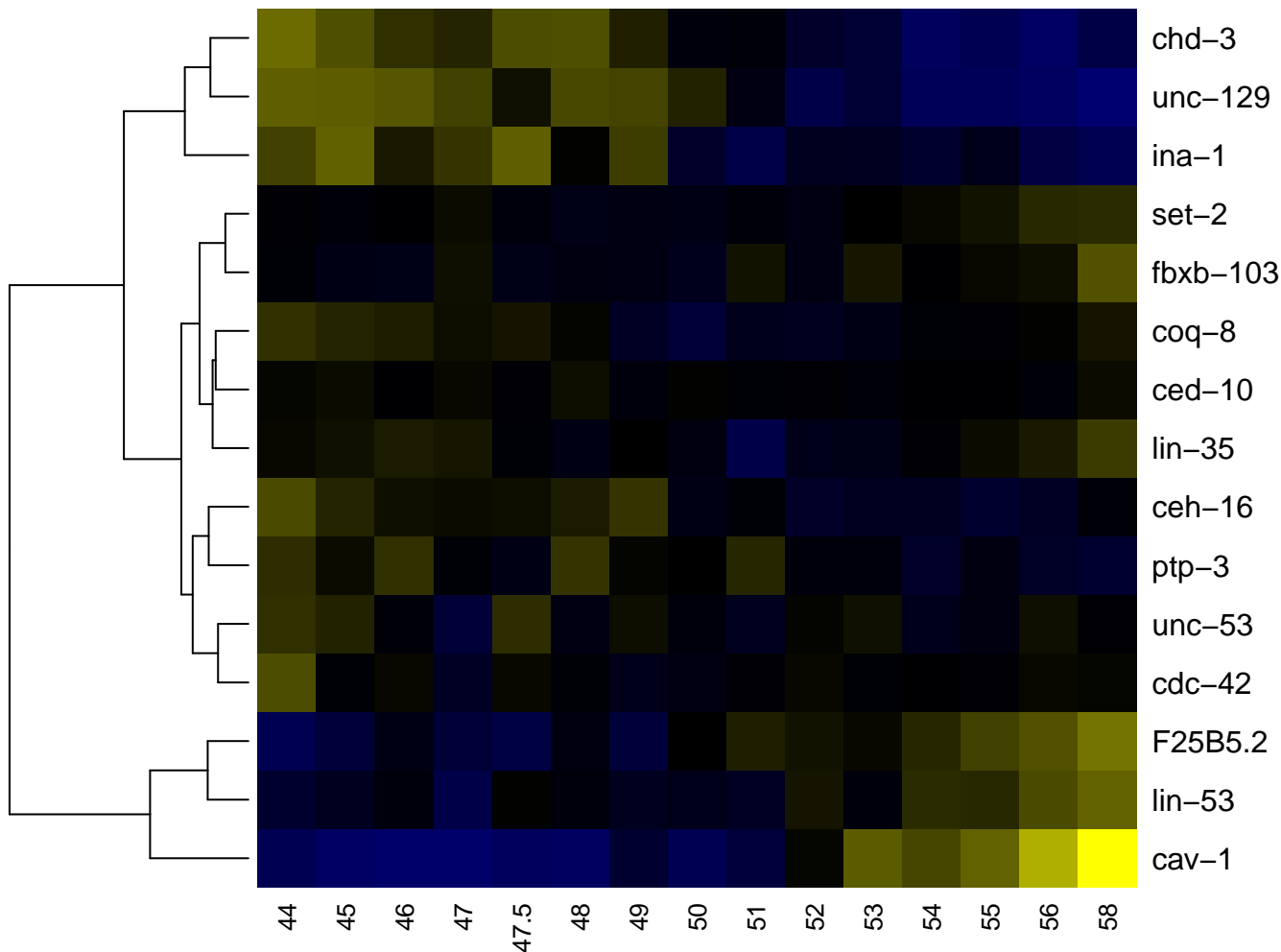
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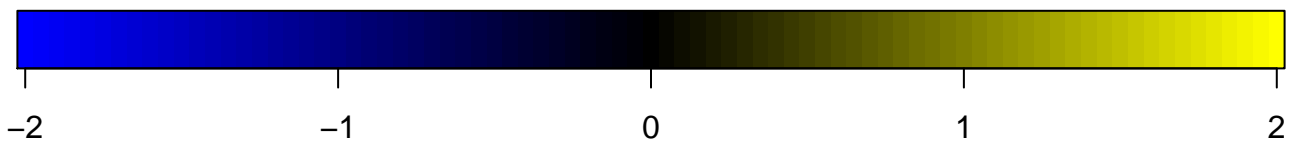
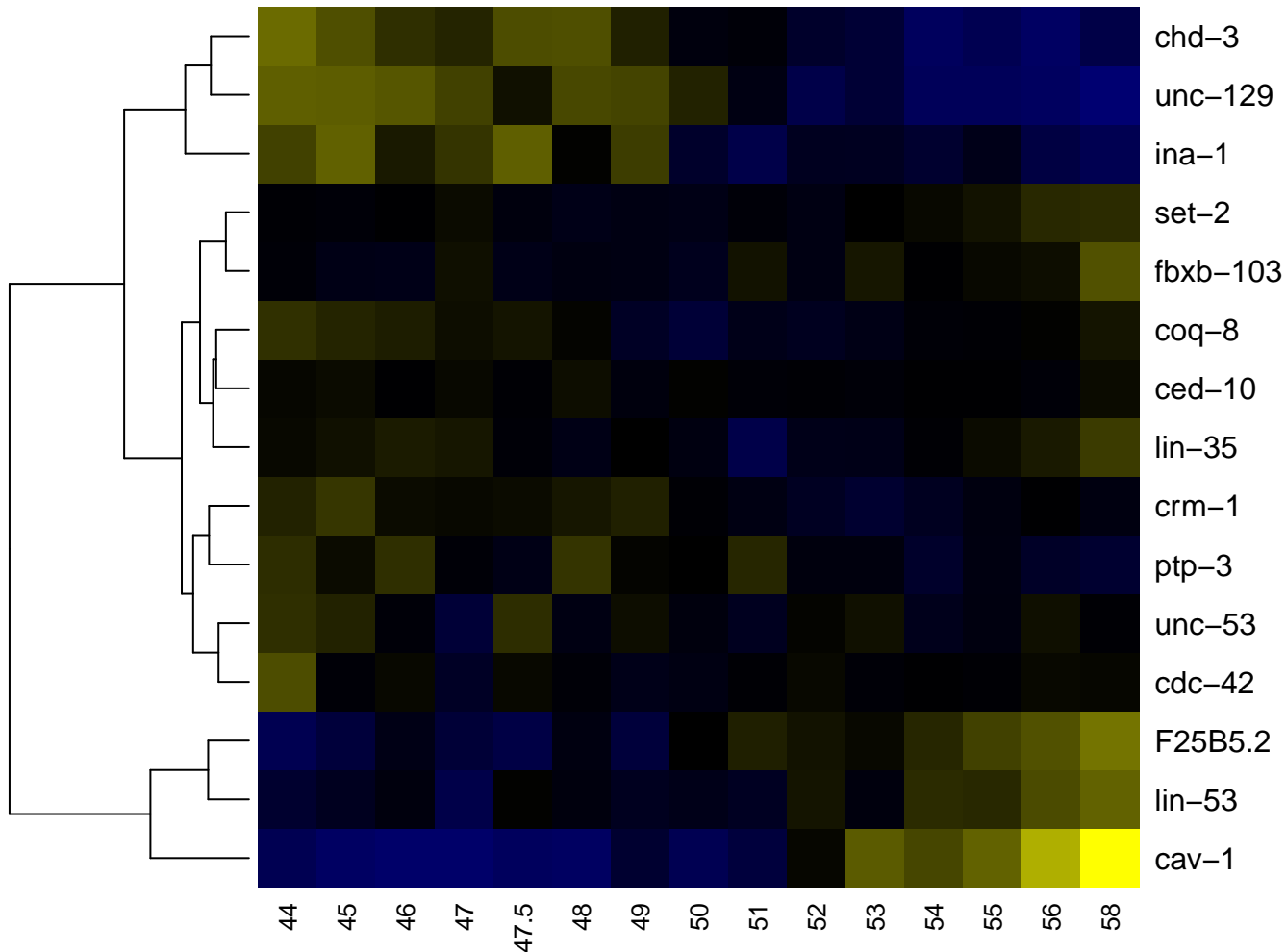
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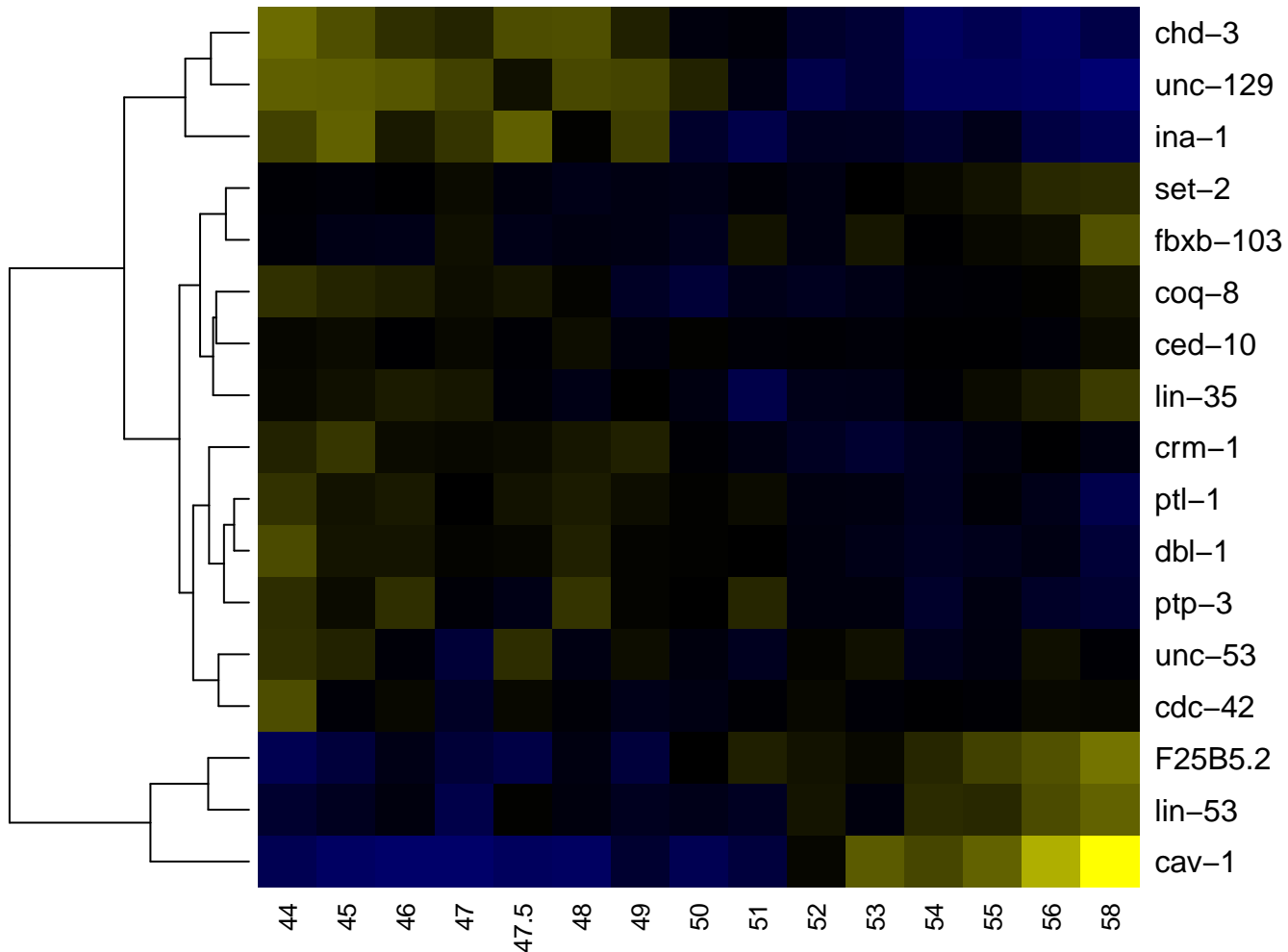
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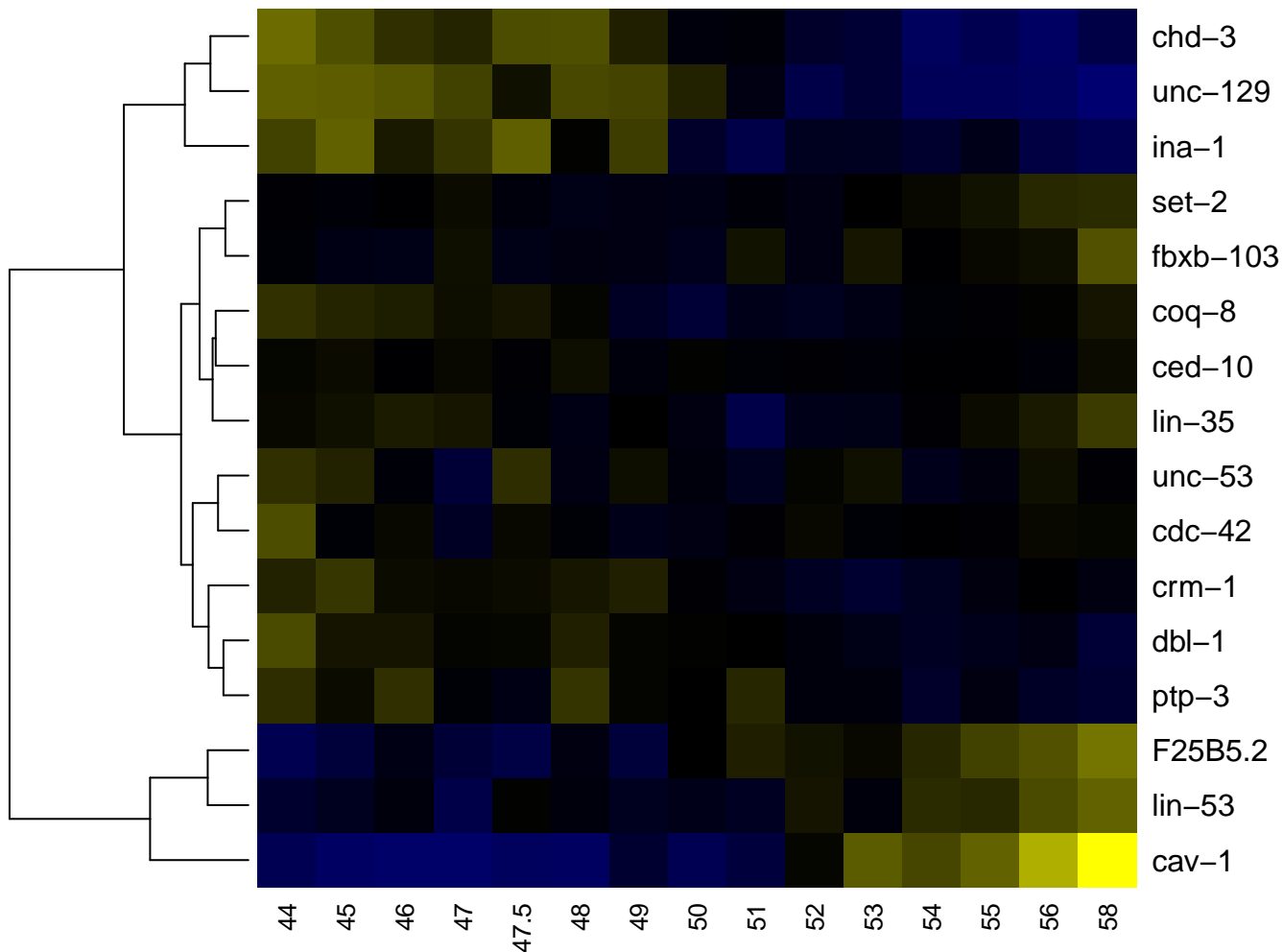
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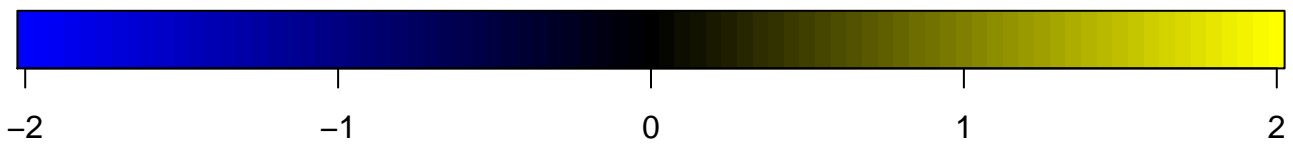
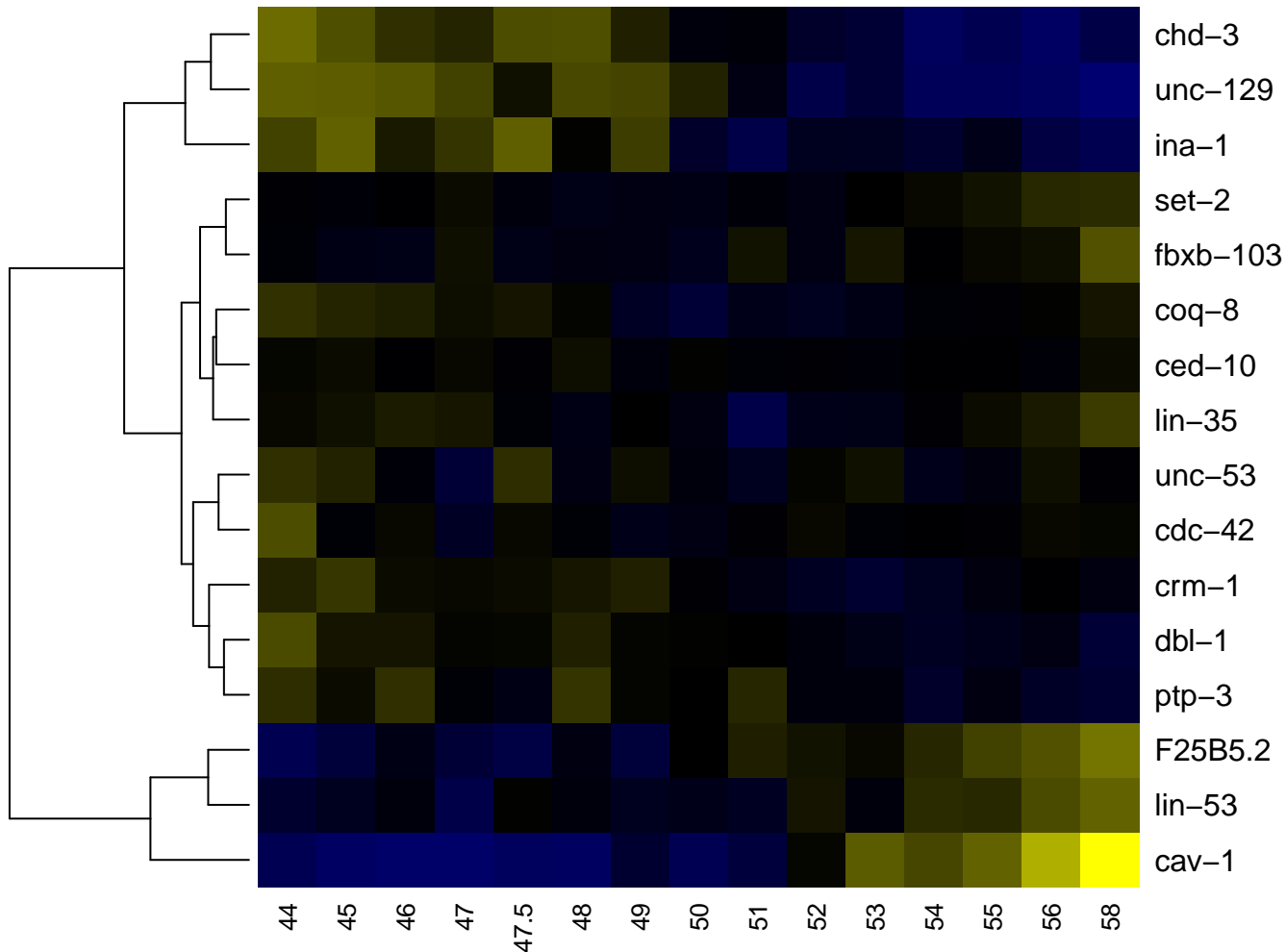
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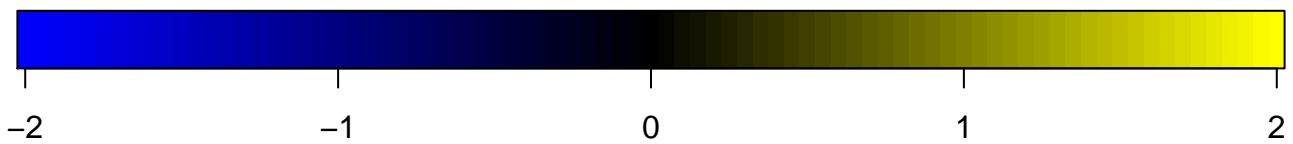
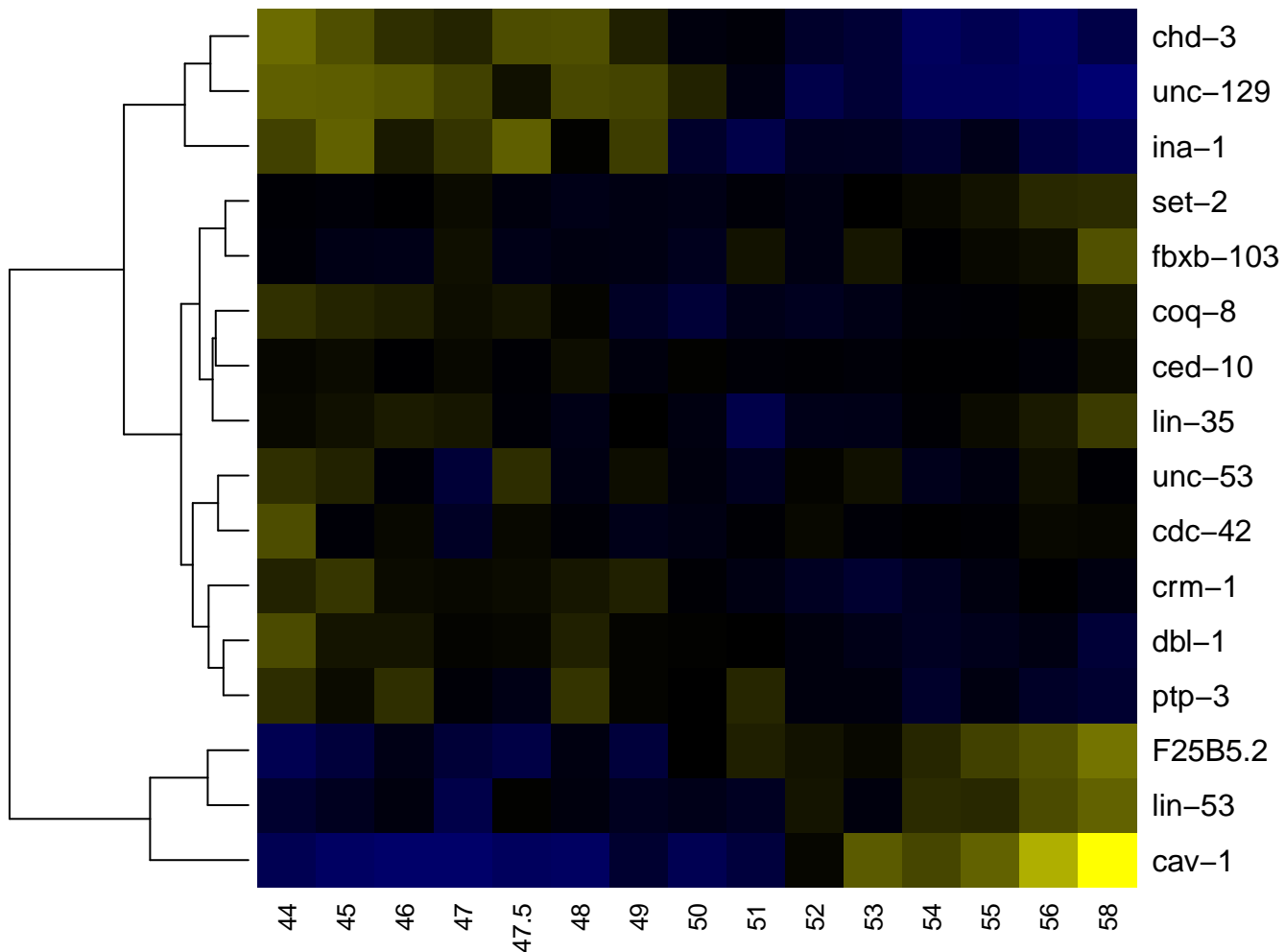
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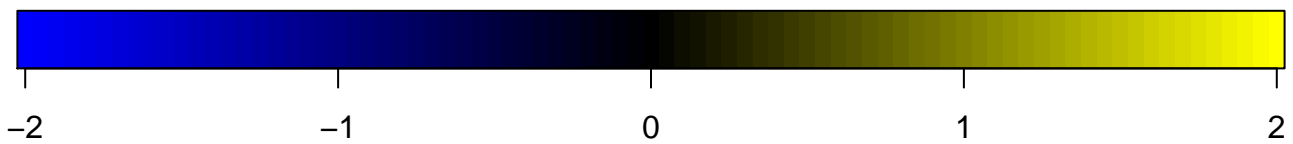
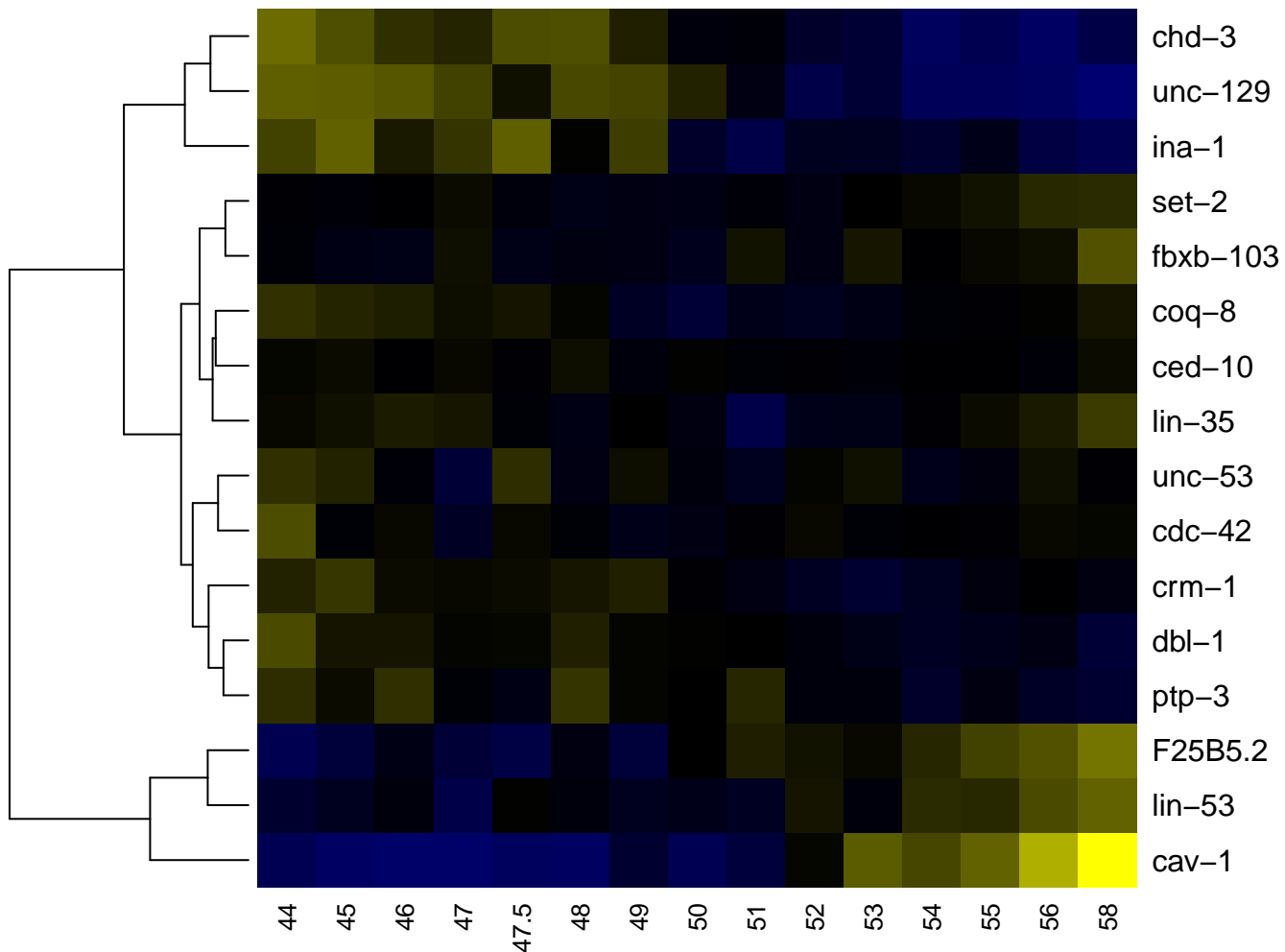
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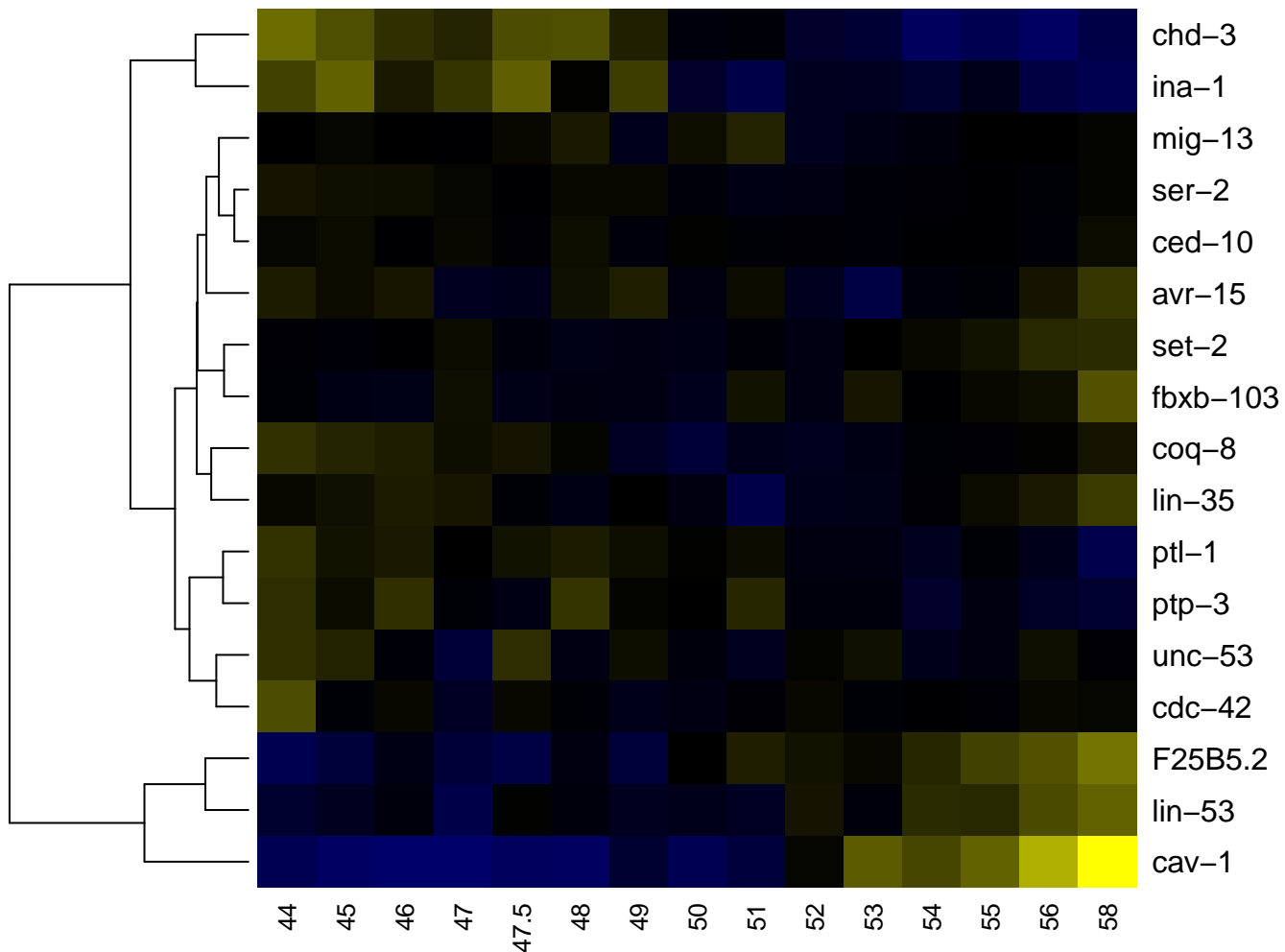
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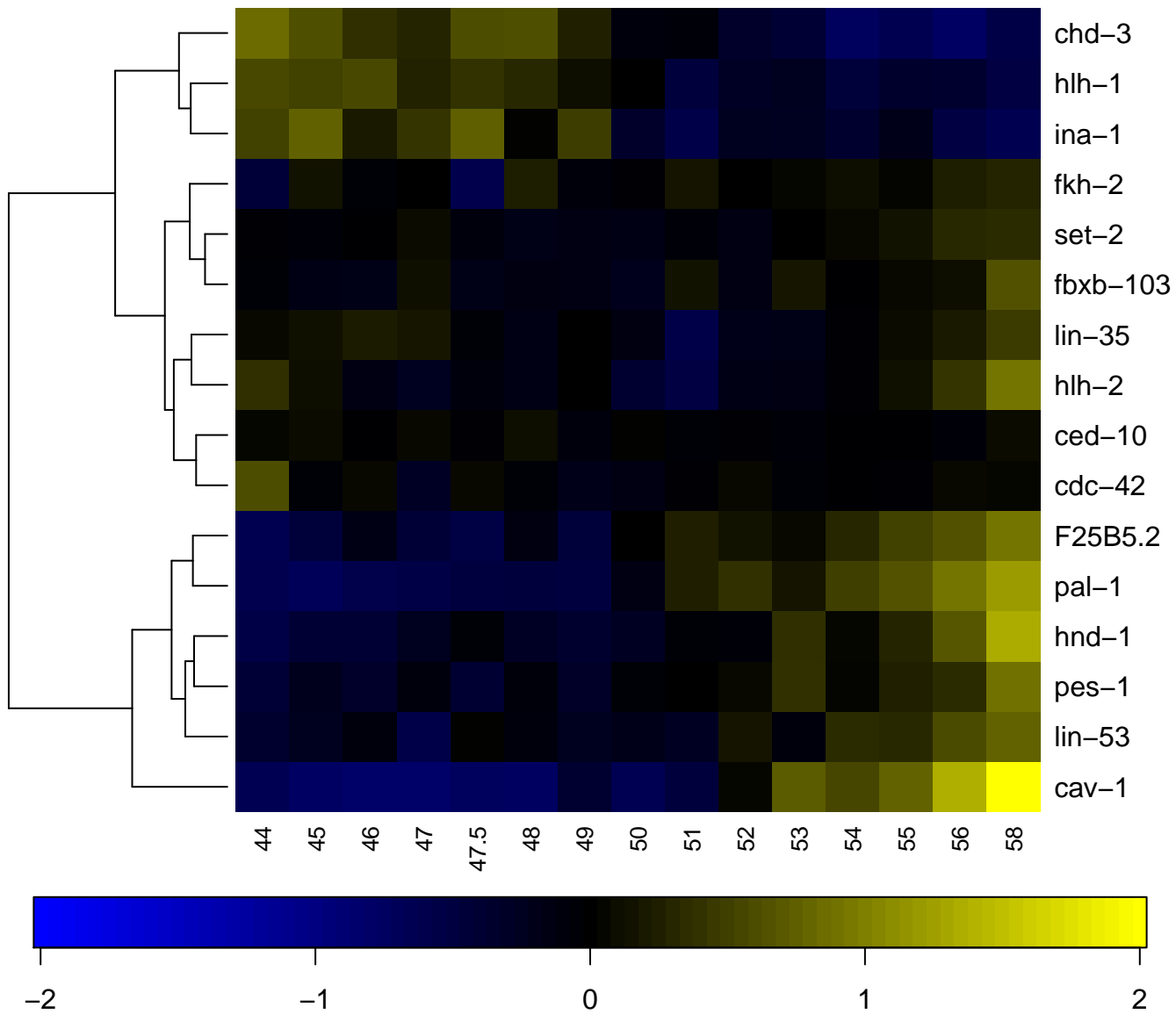
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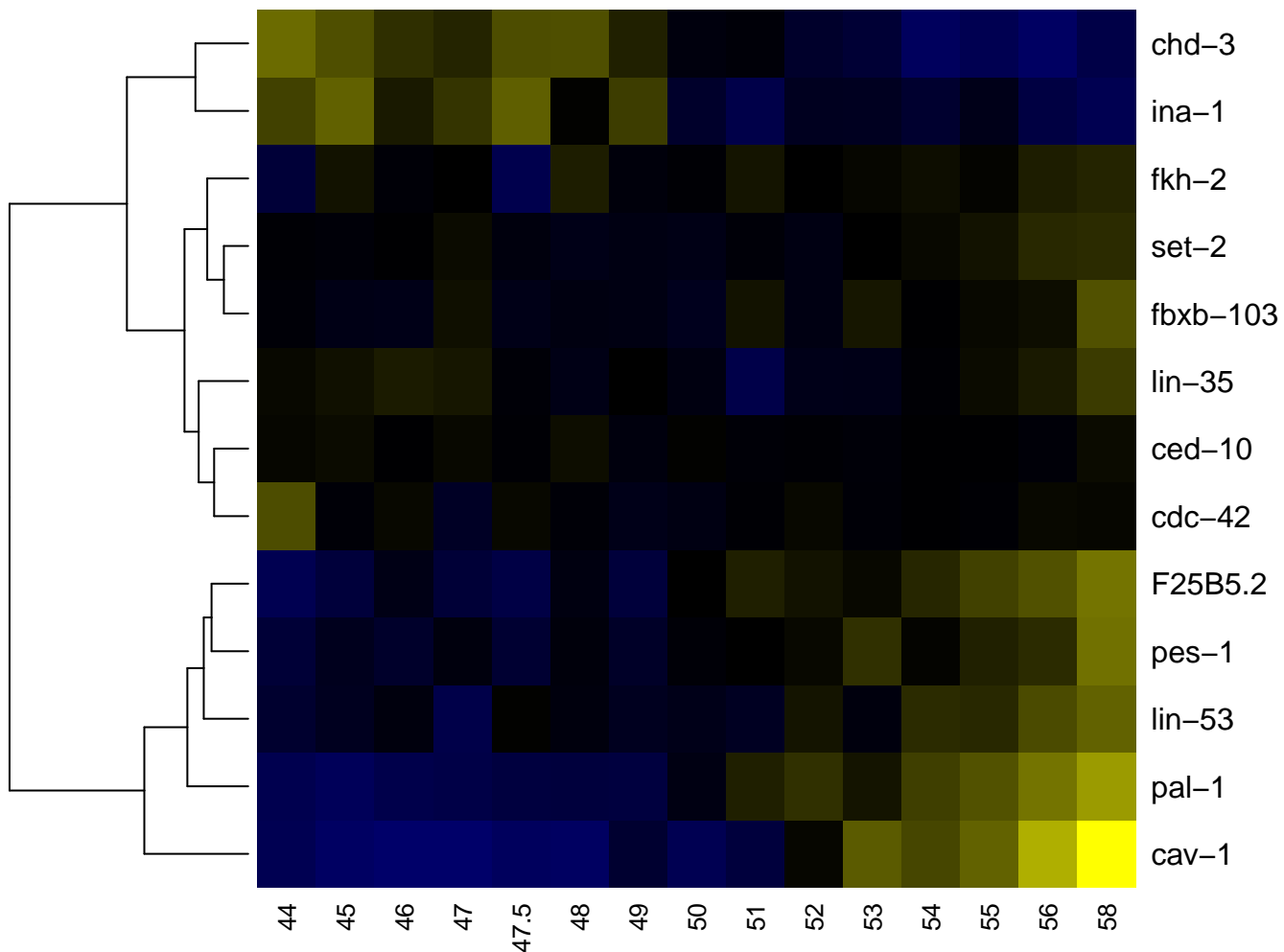
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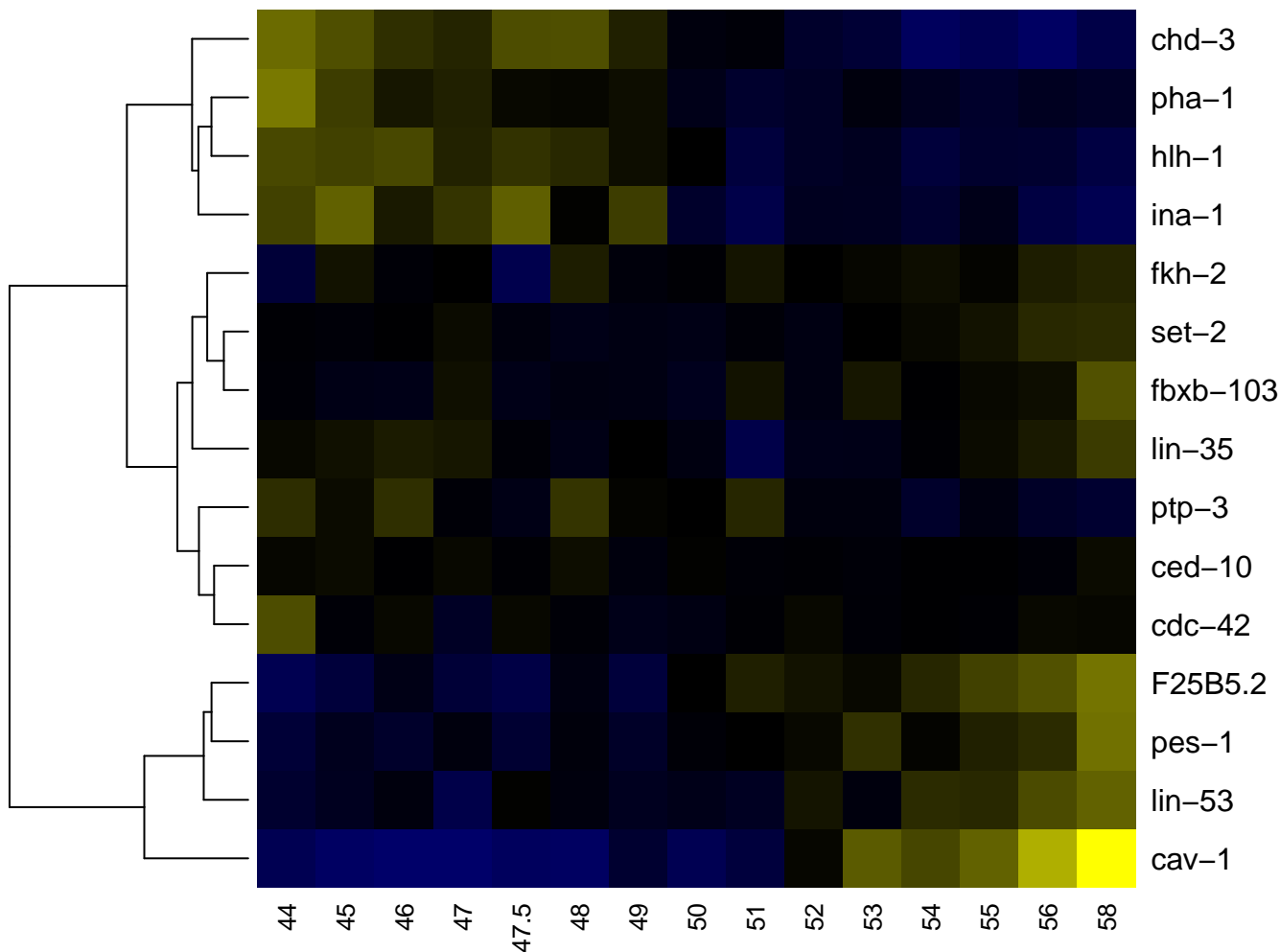
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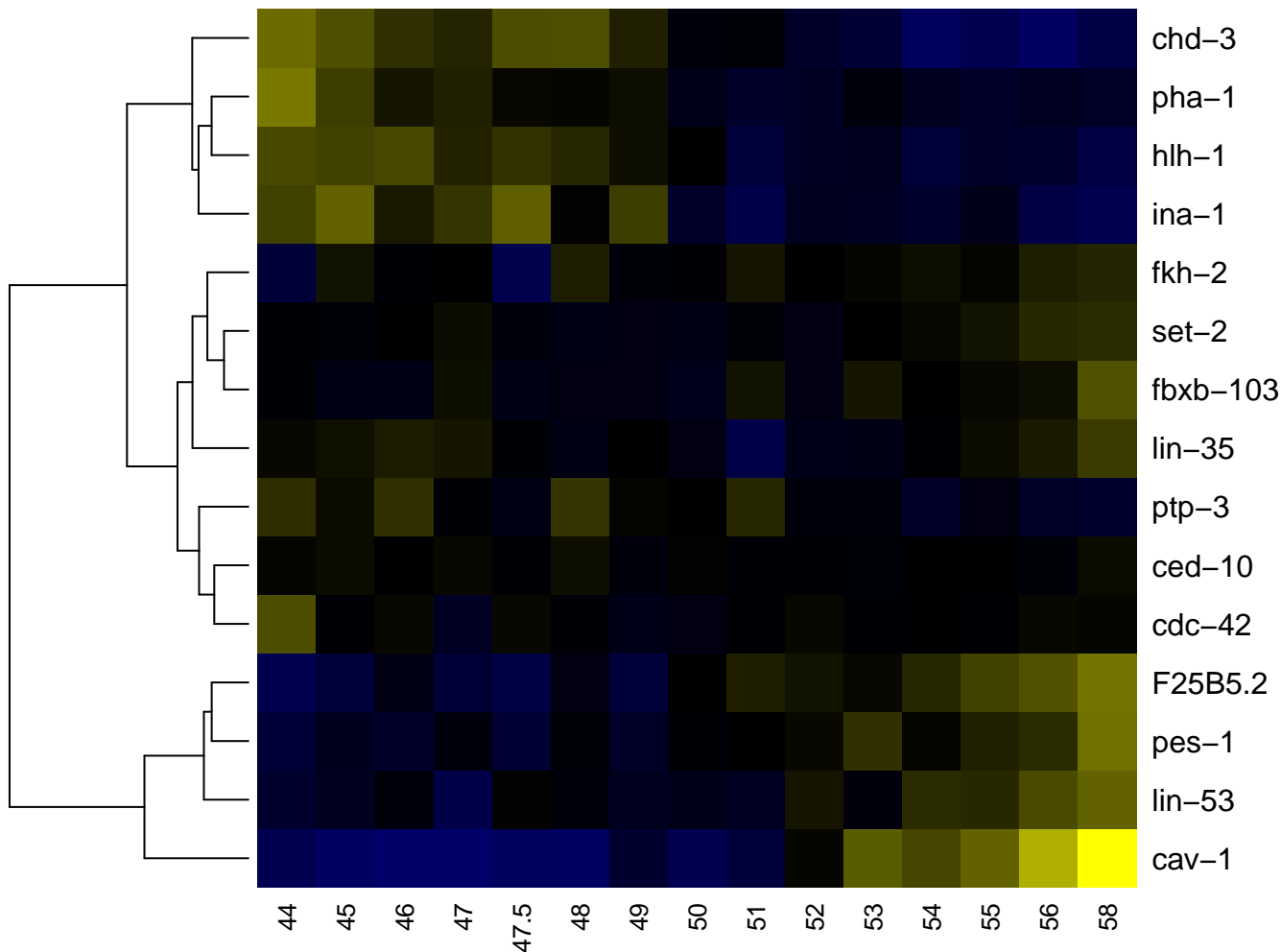
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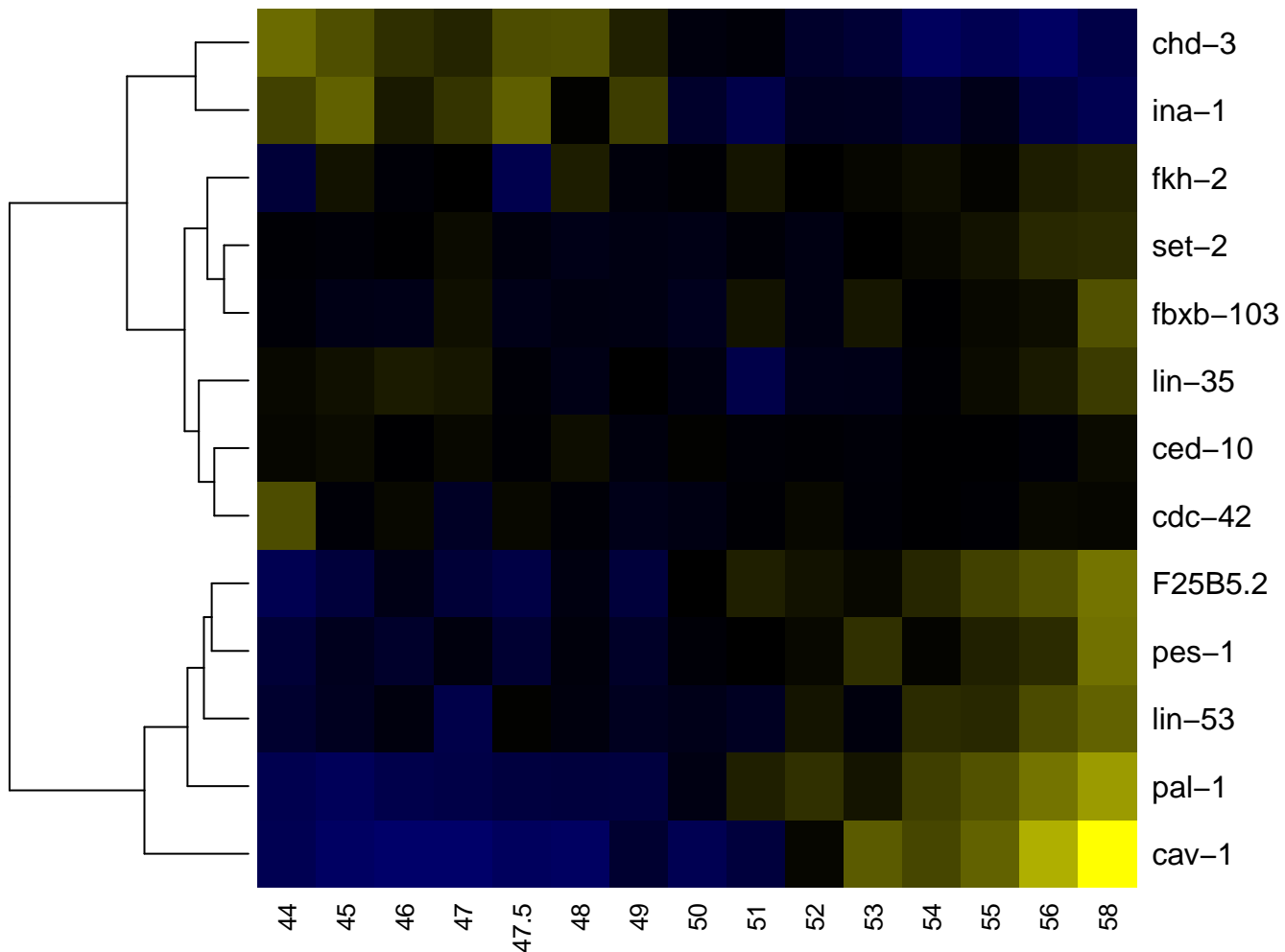
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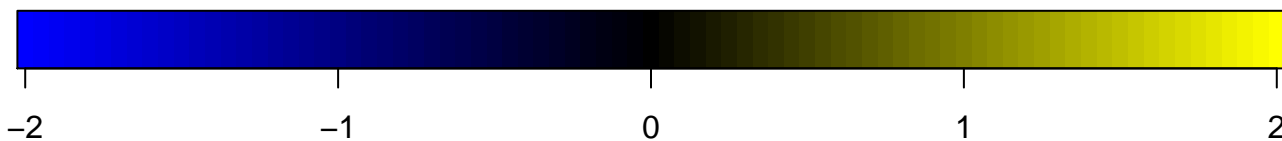
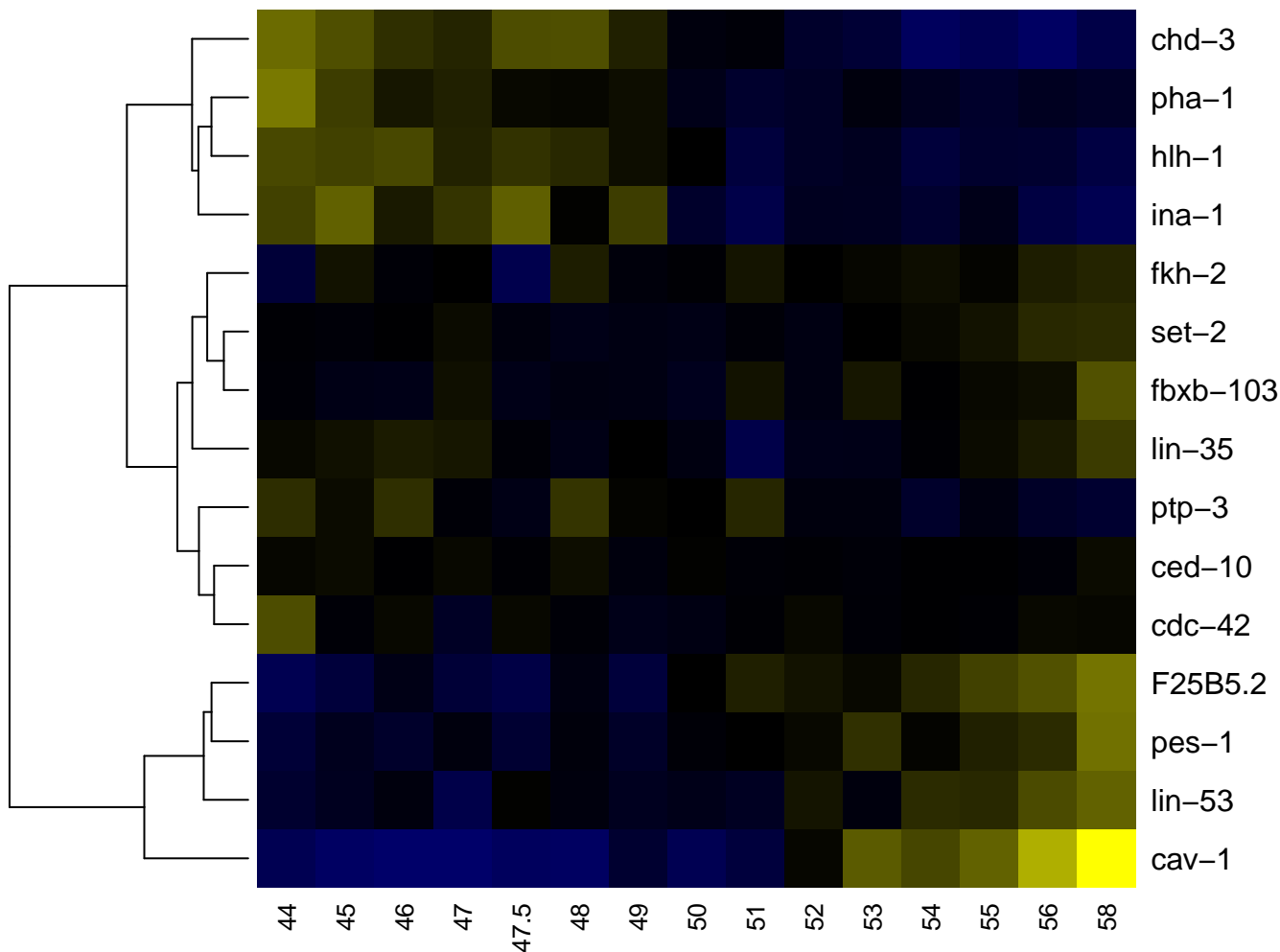
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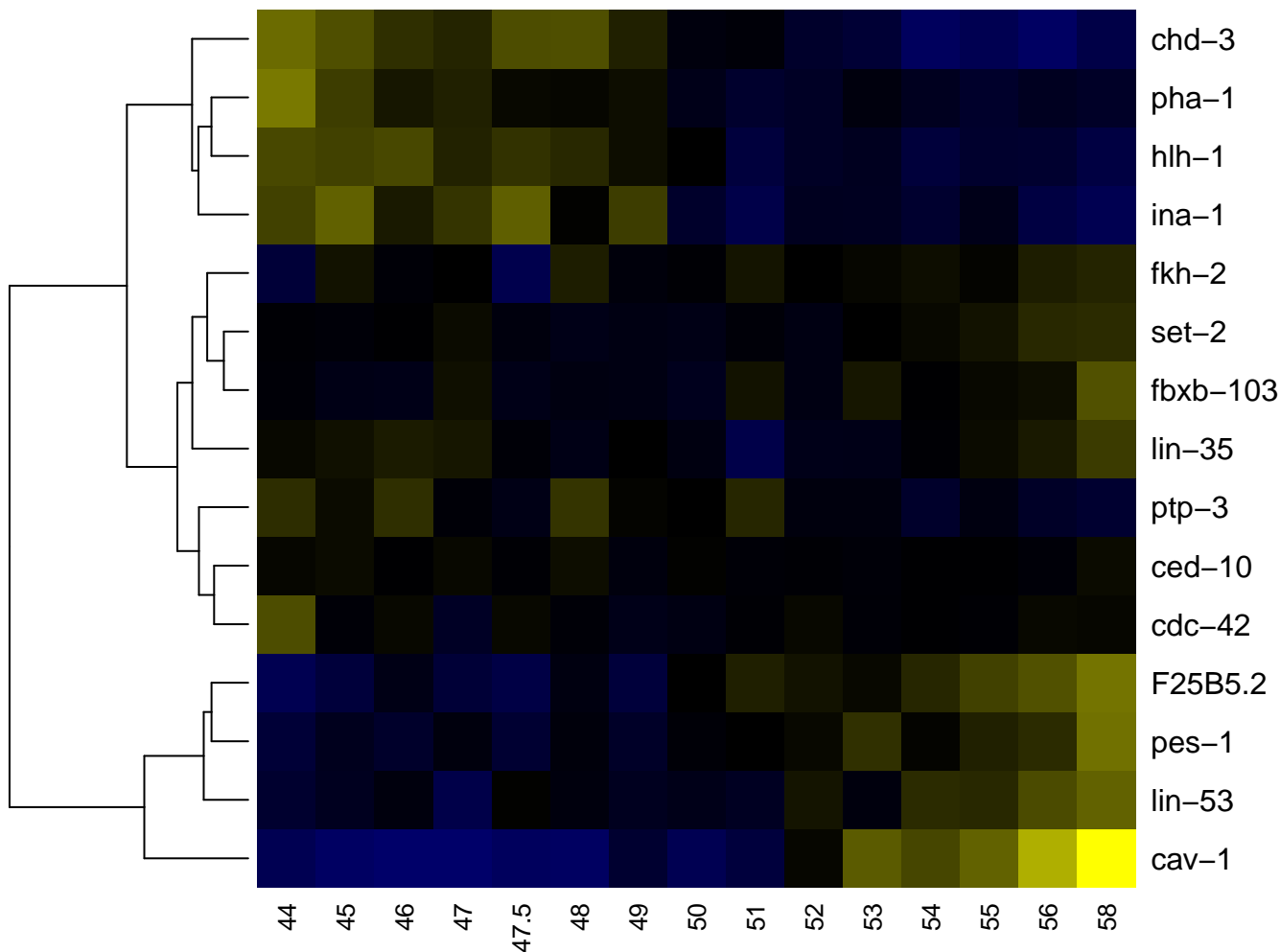
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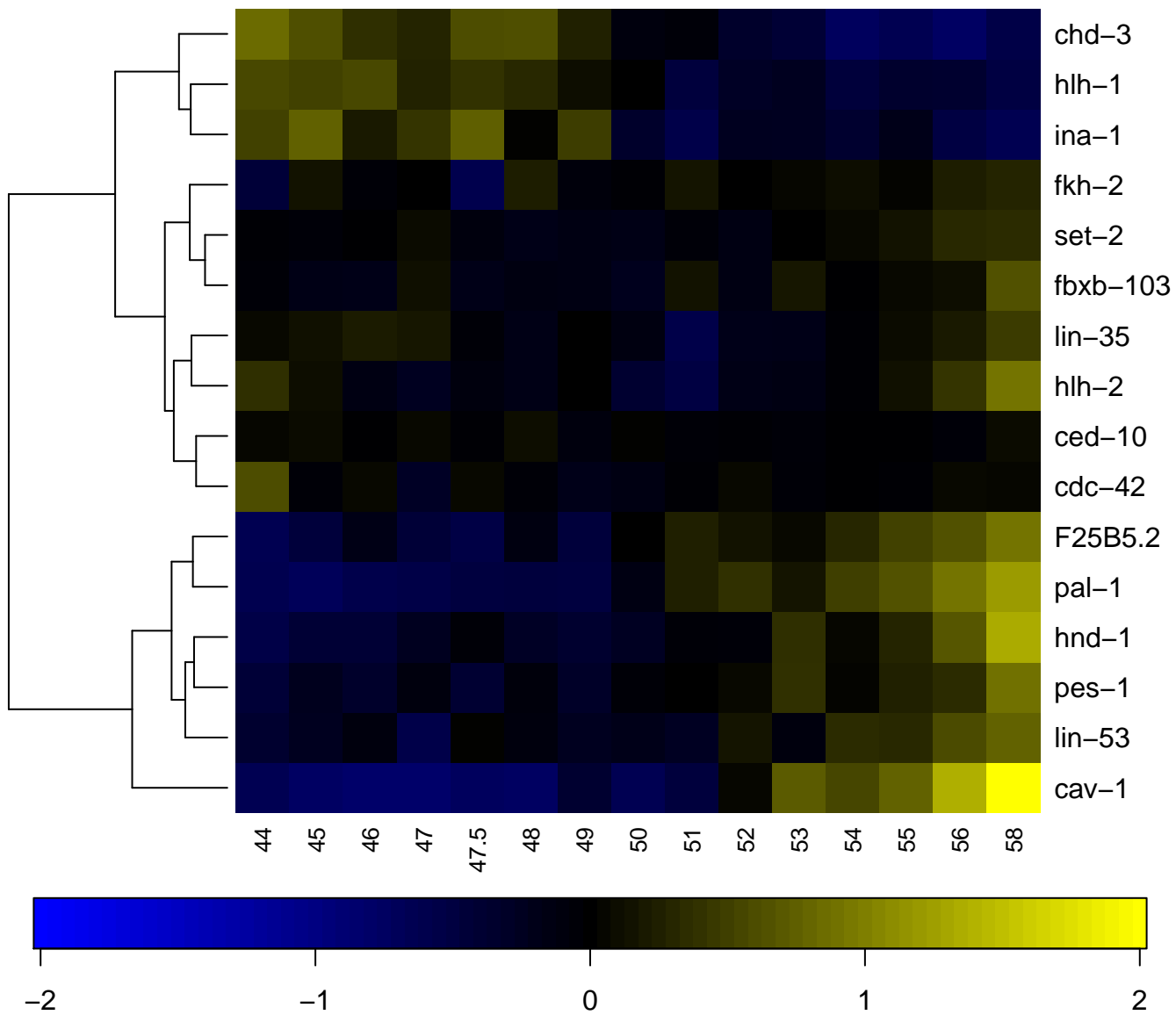
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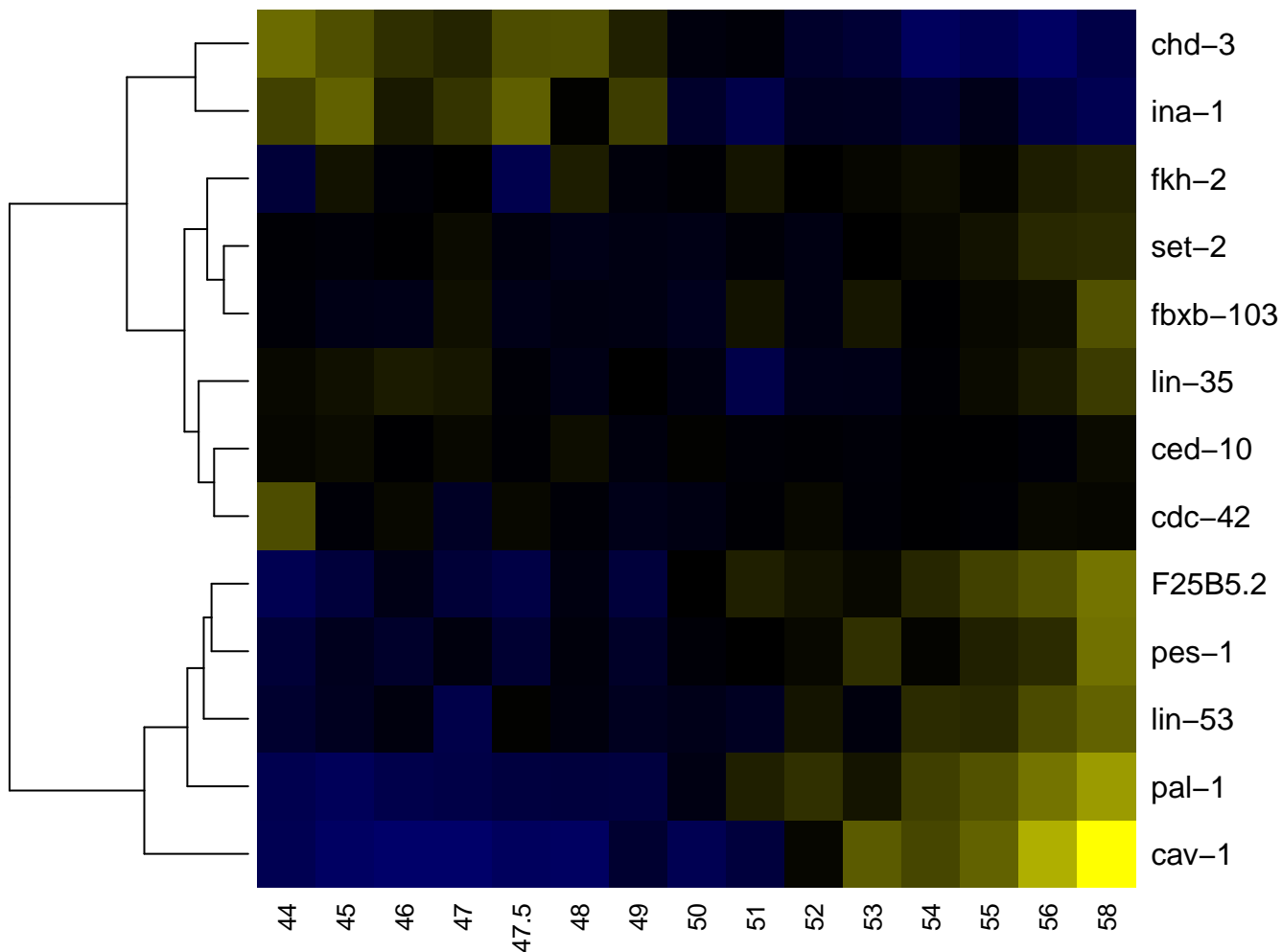
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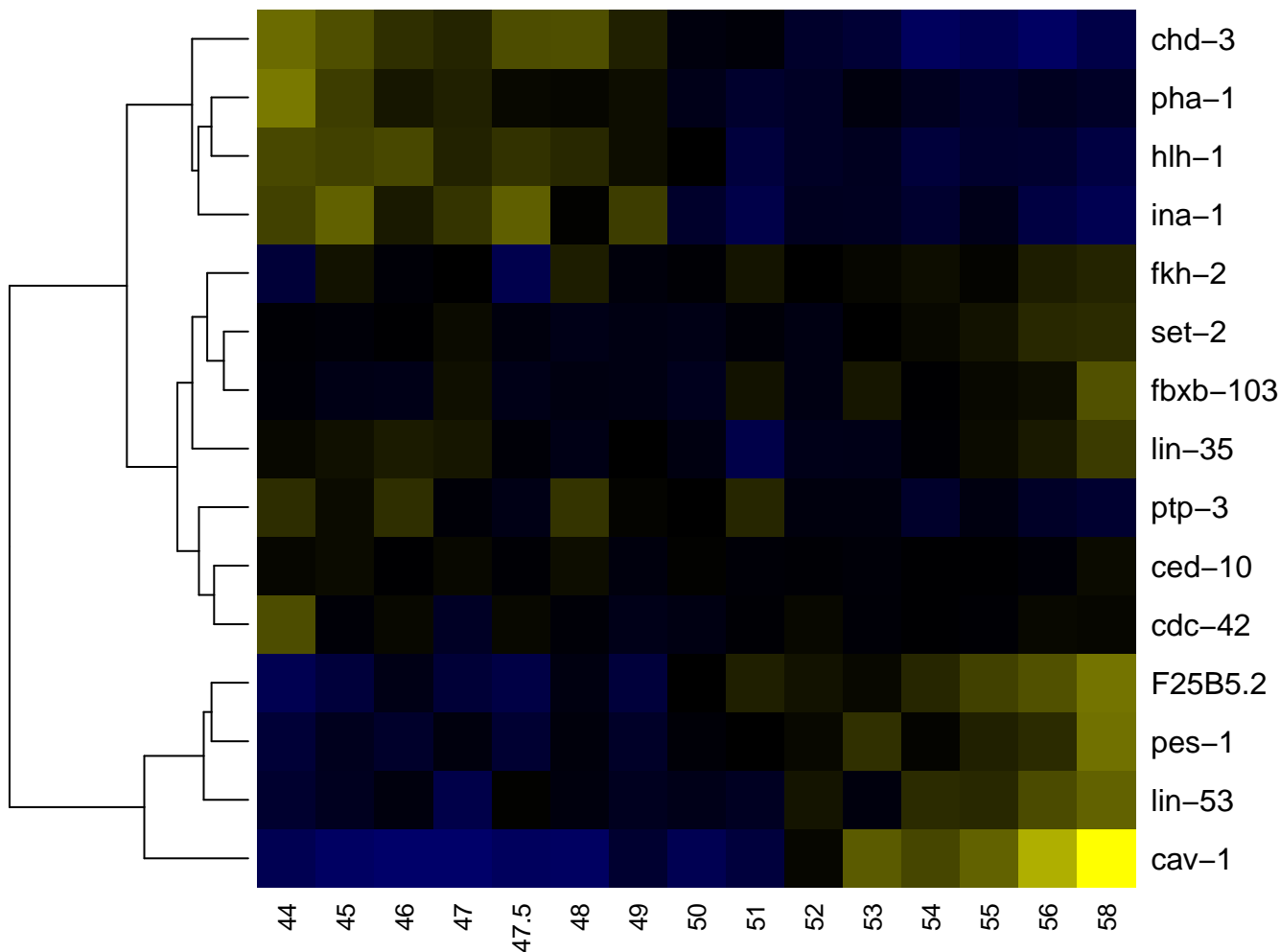
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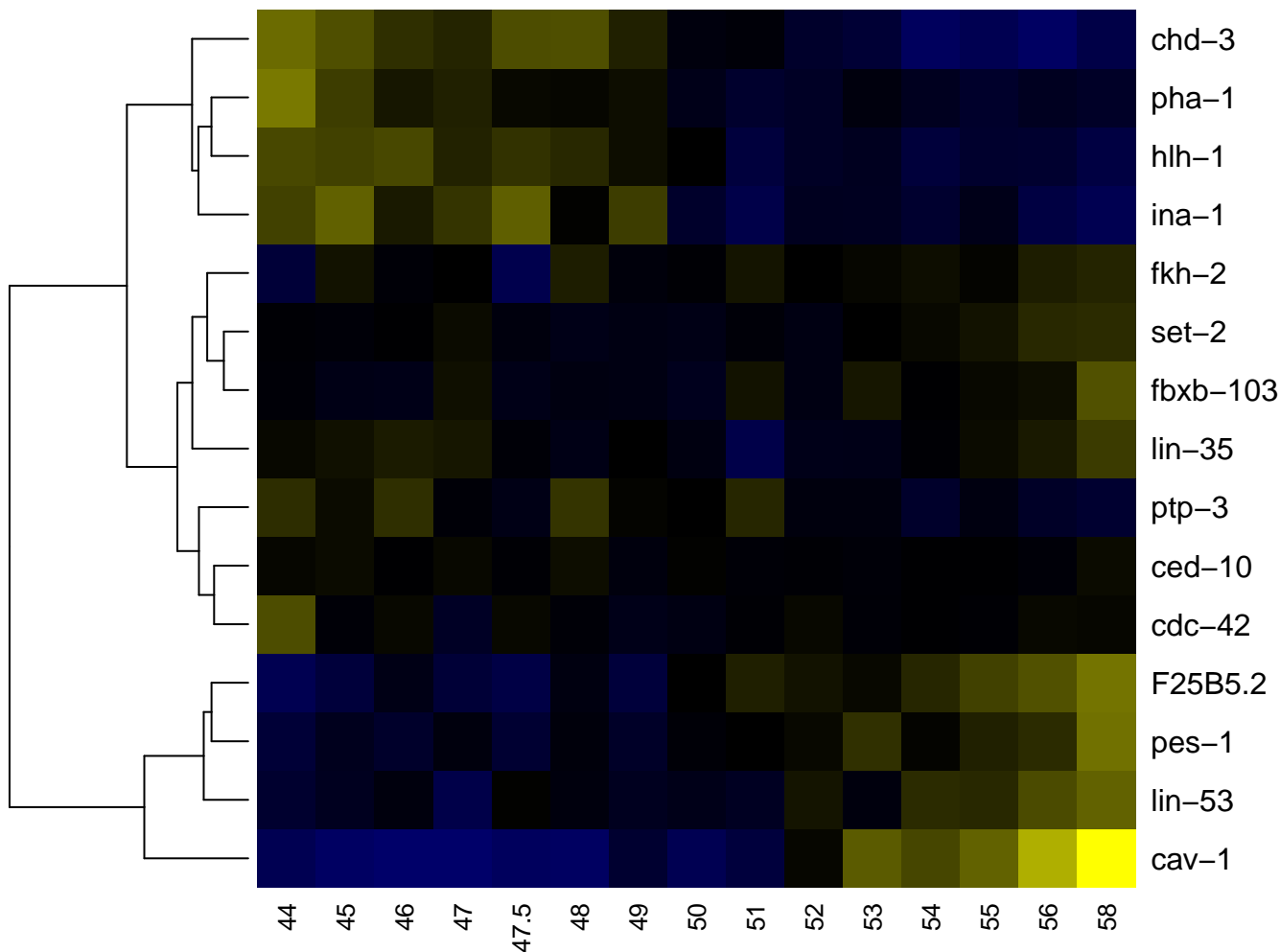
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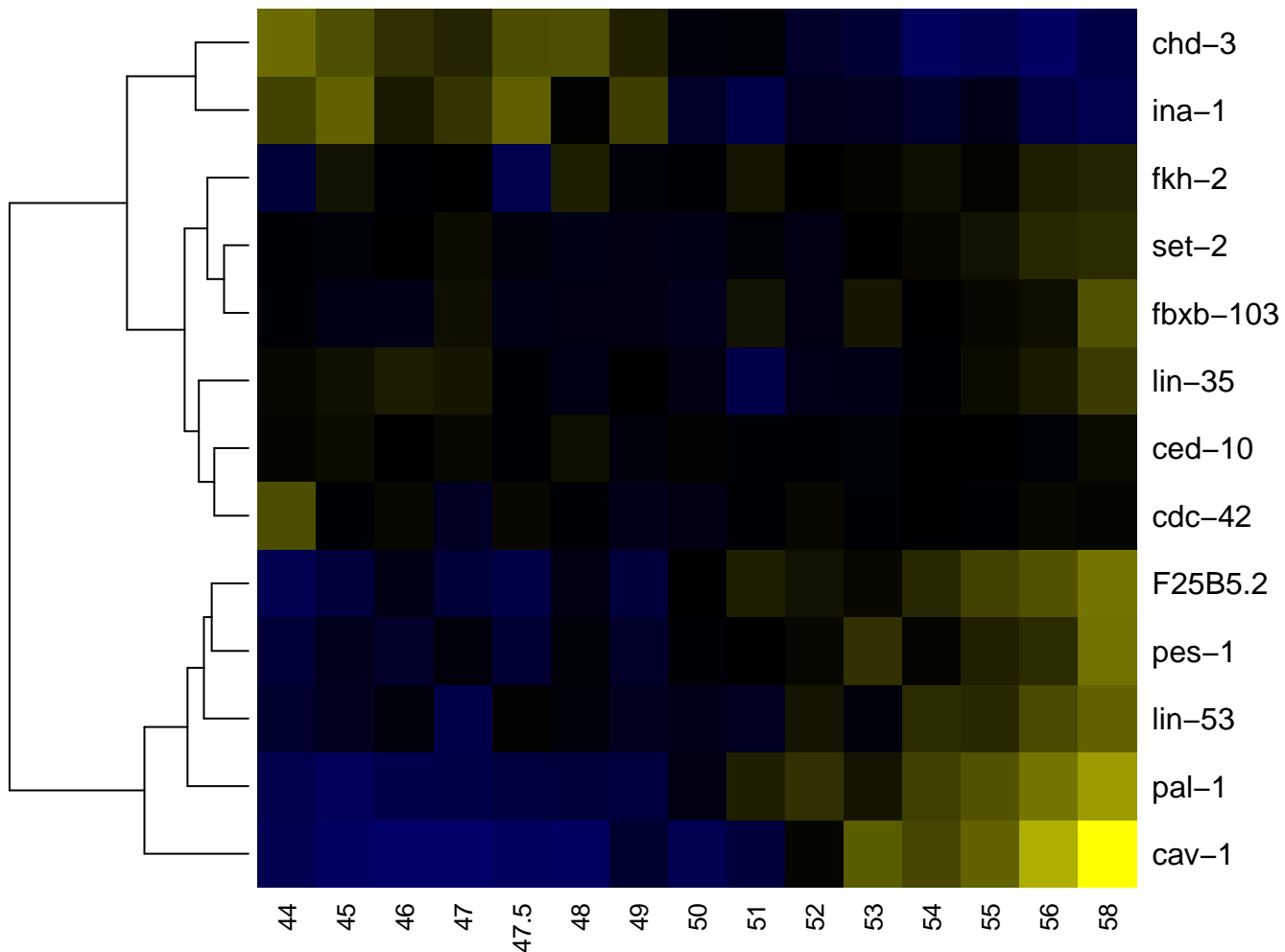
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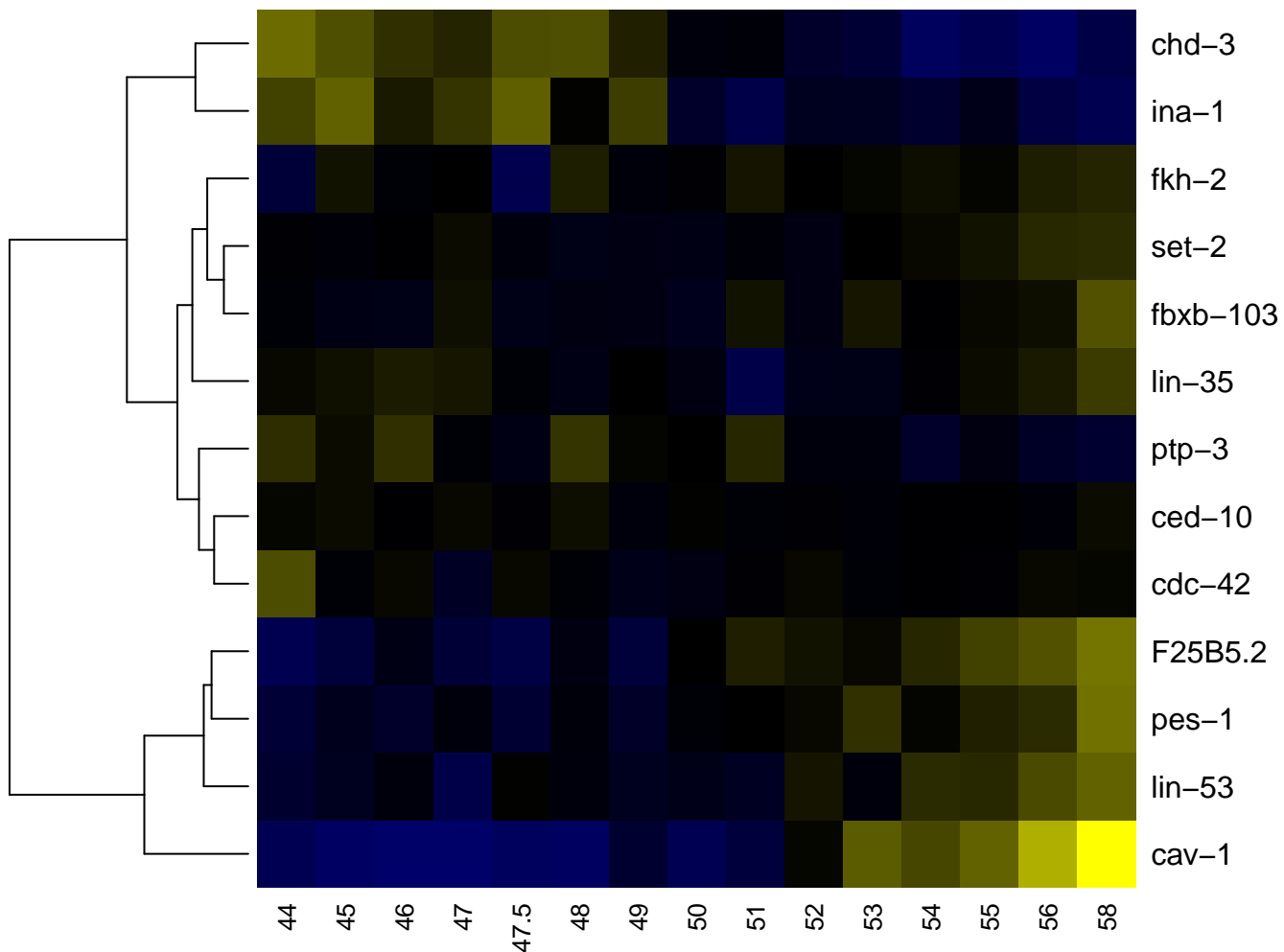
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Dapp



Dappa



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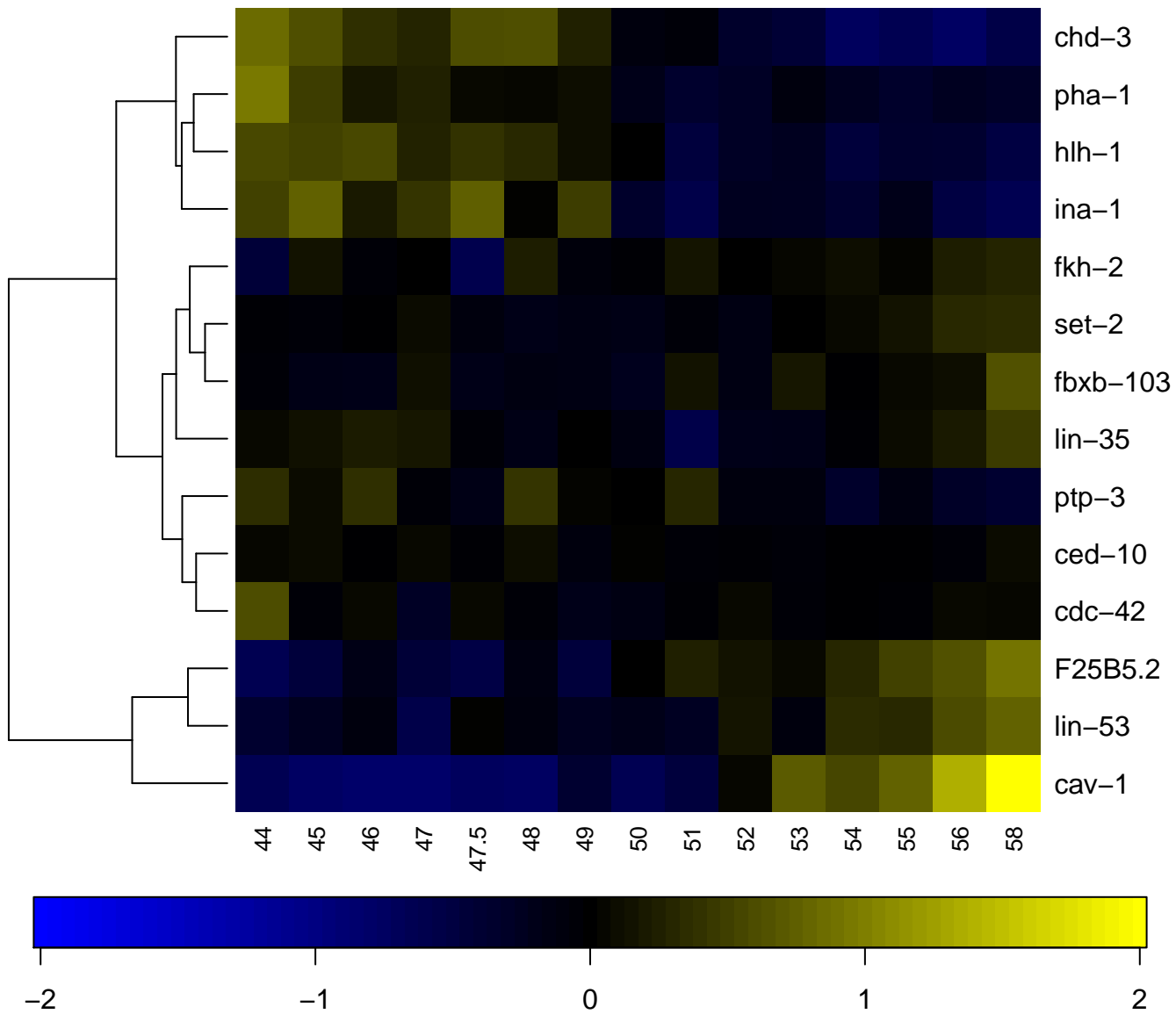
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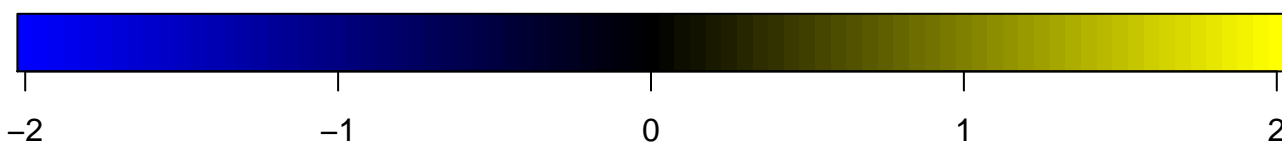
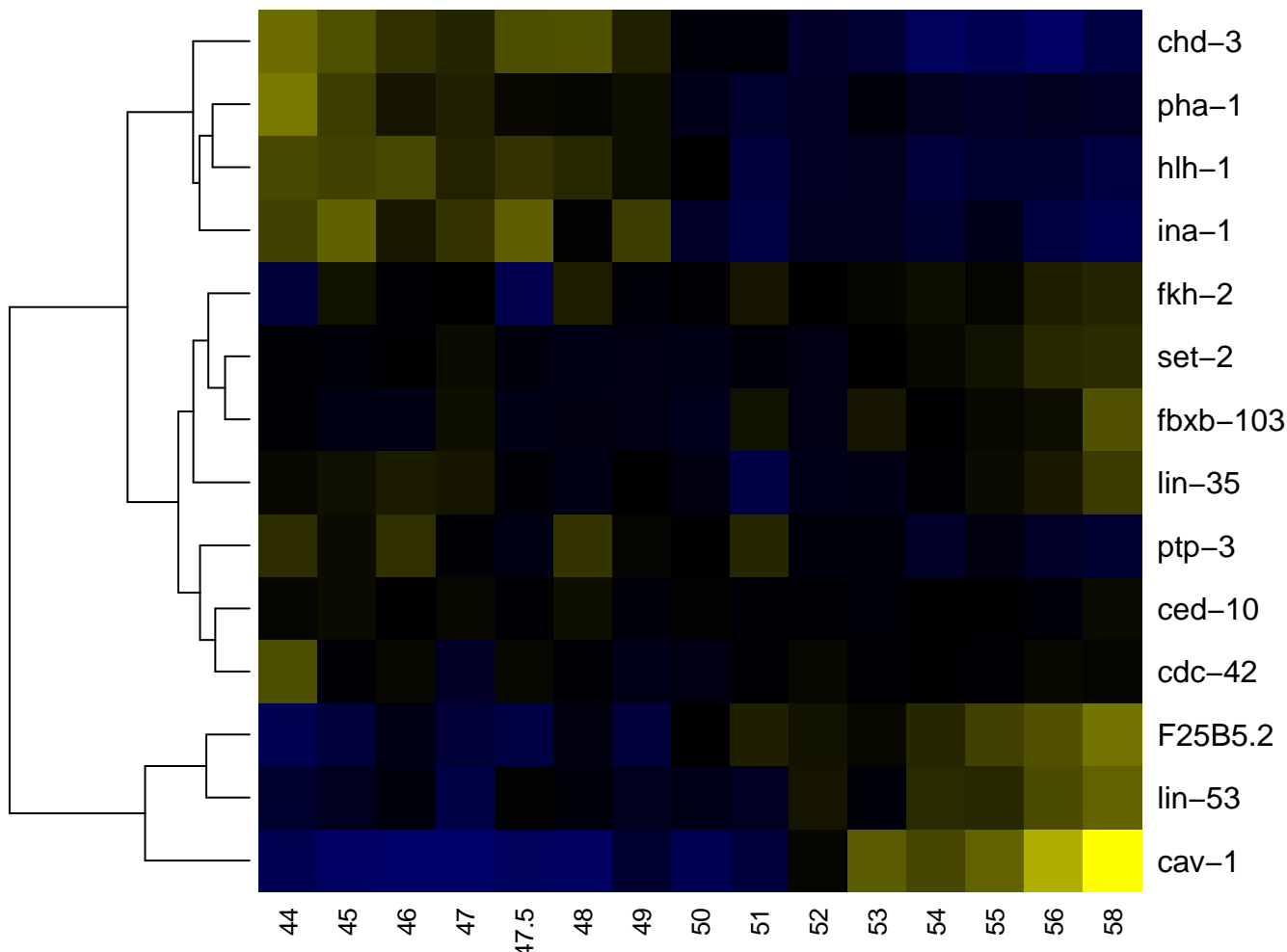
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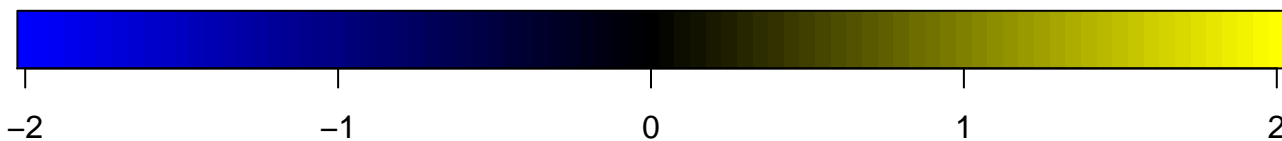
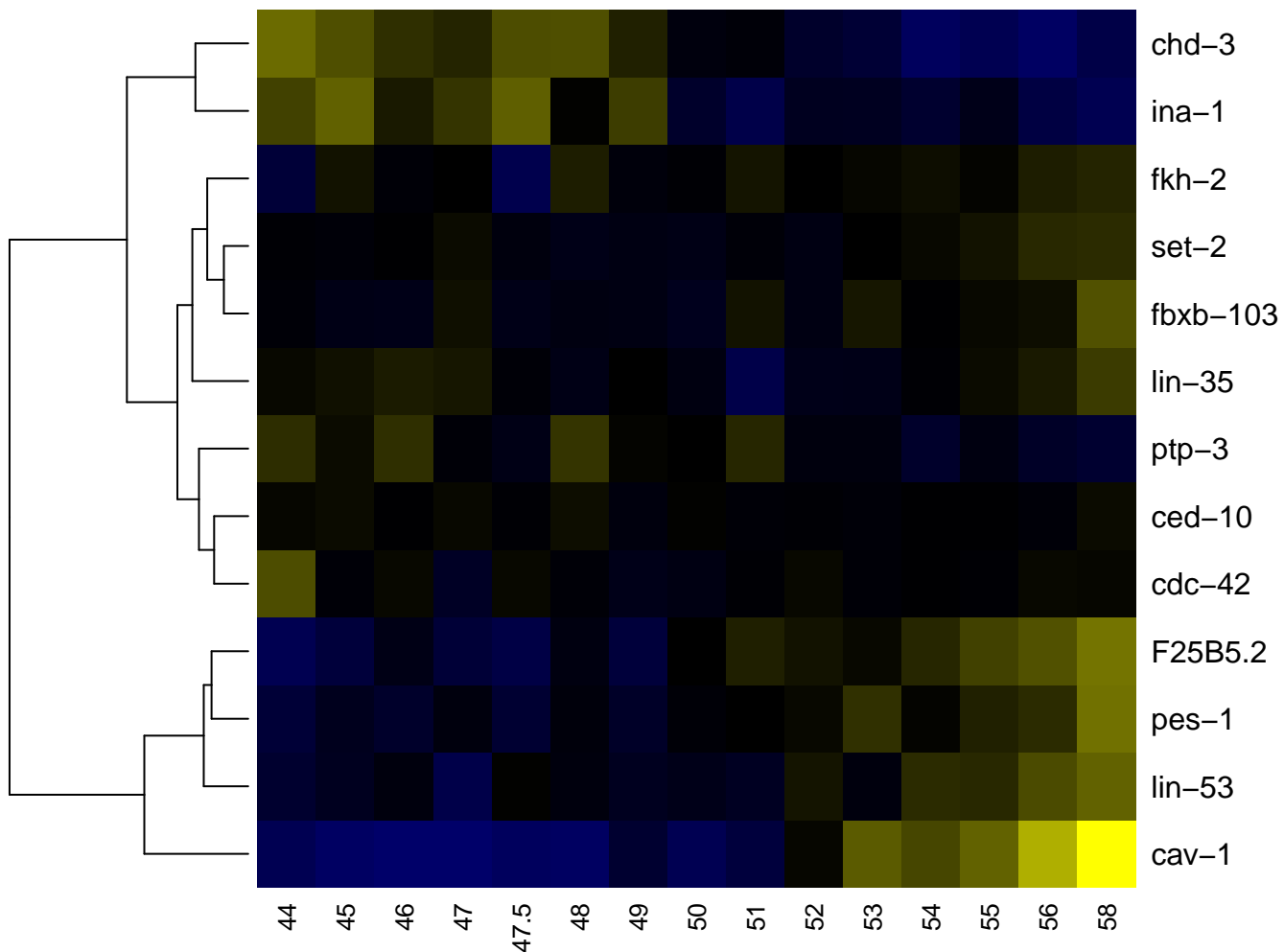
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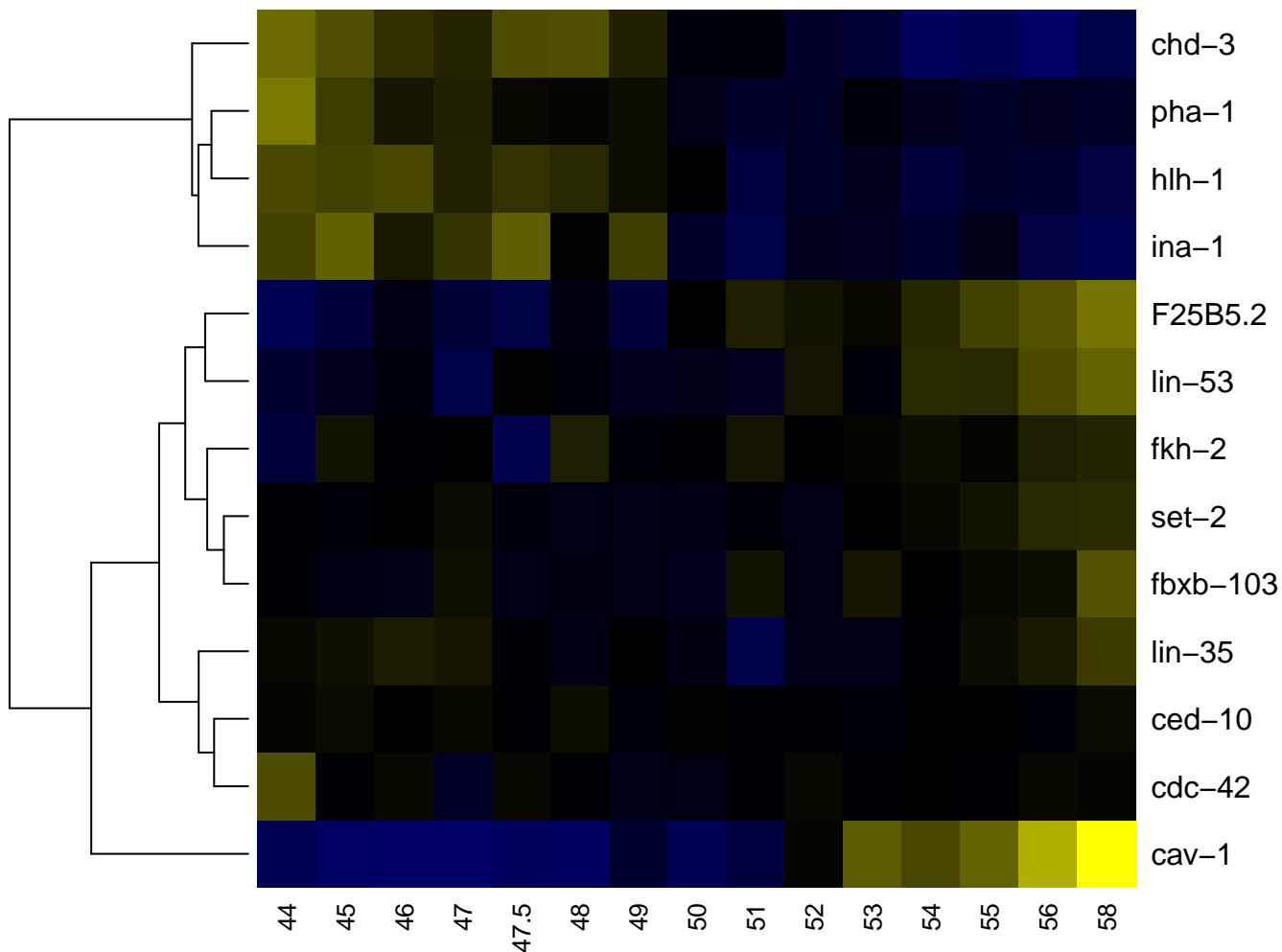
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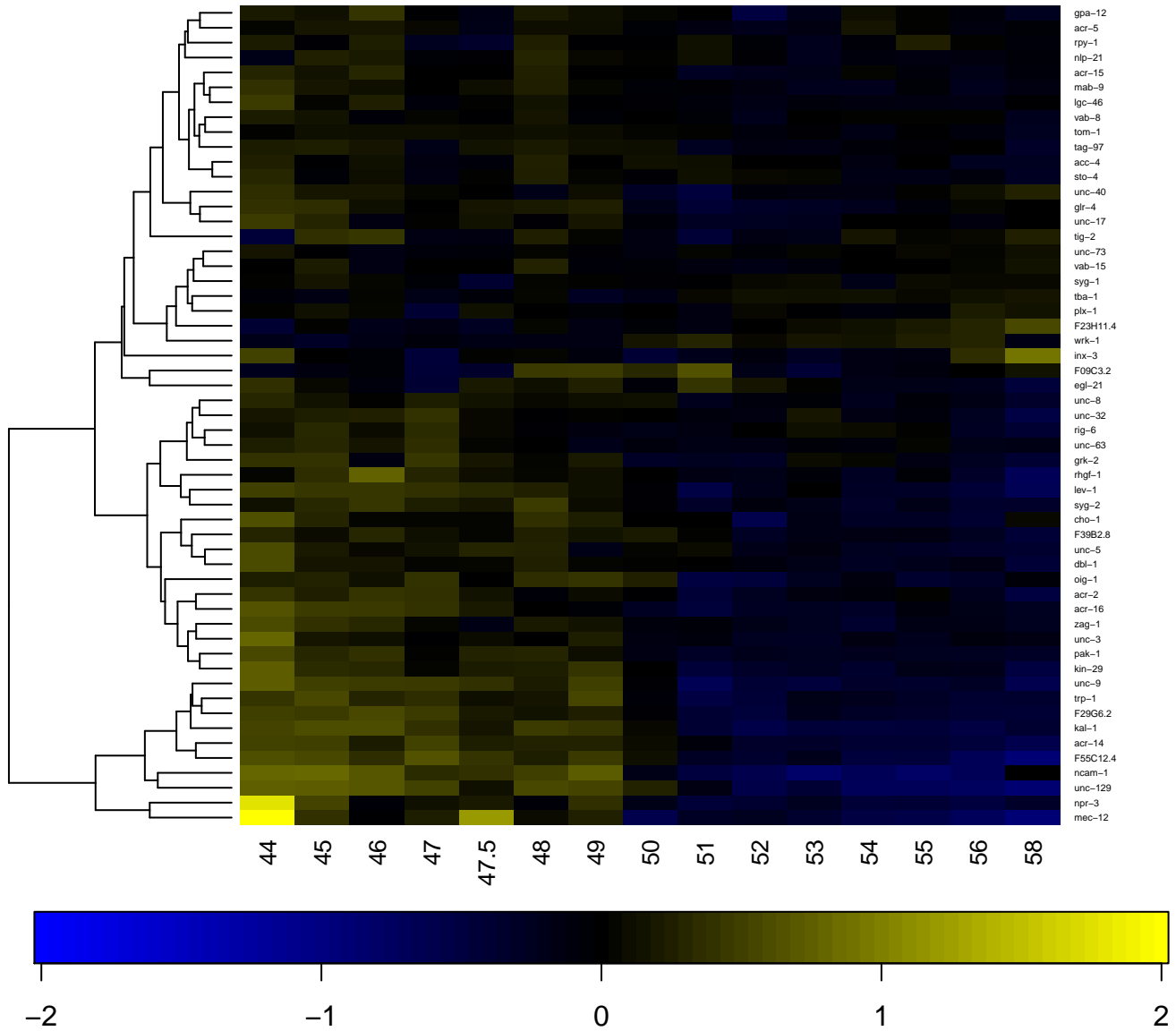
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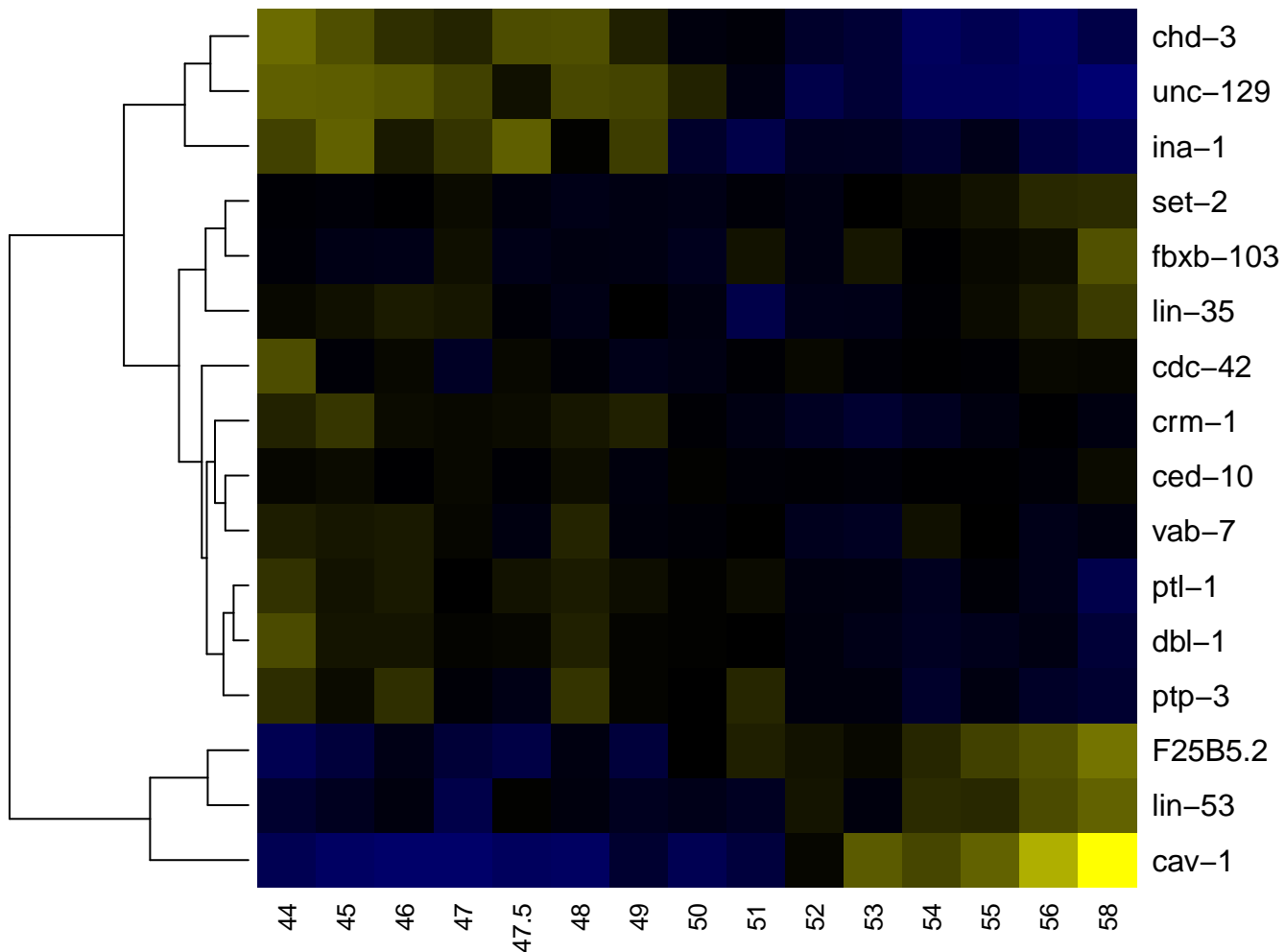
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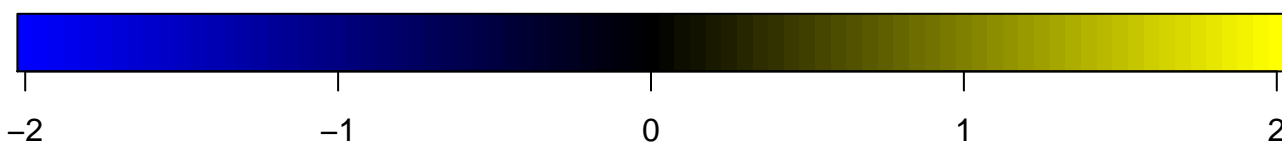
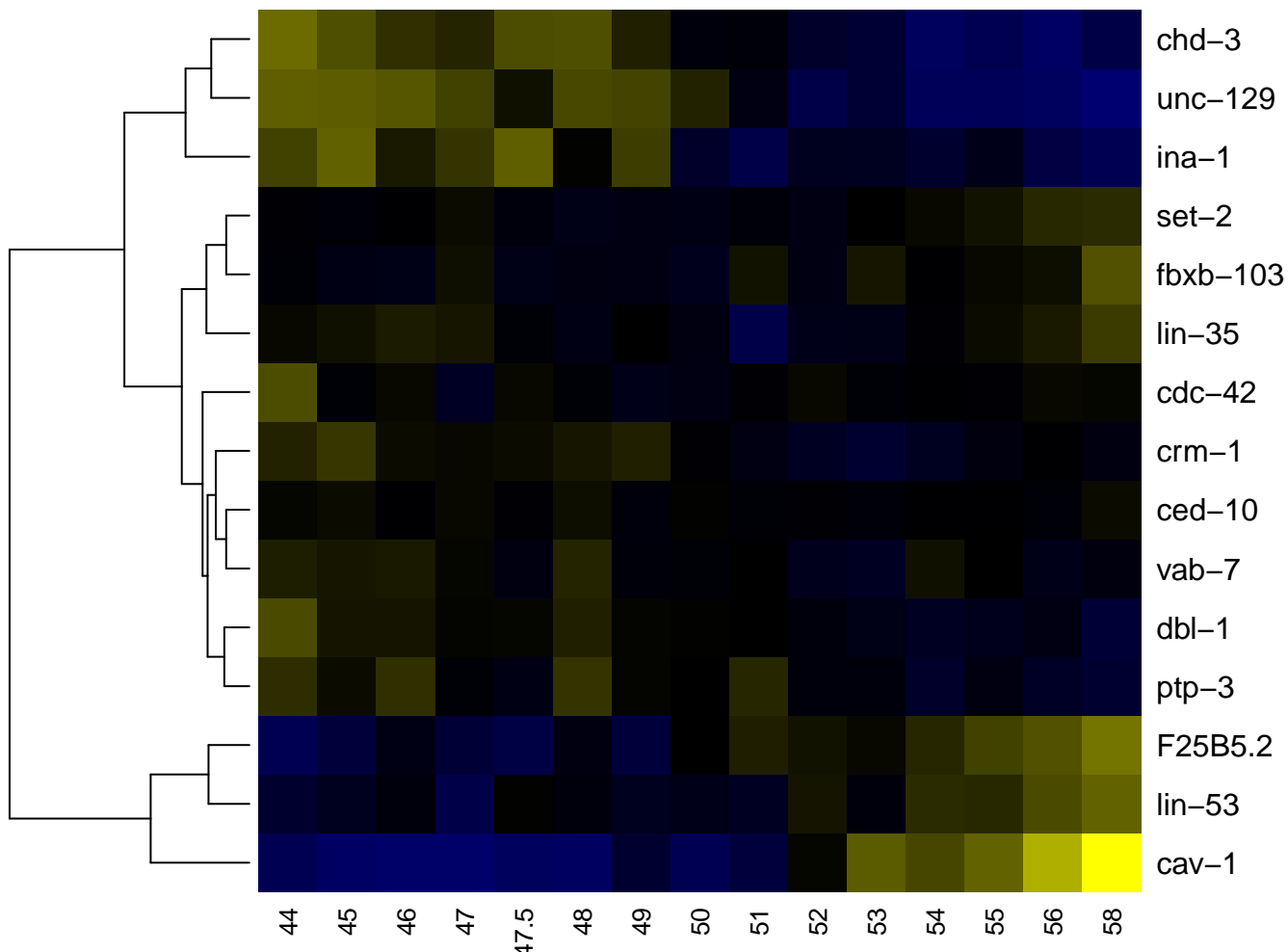
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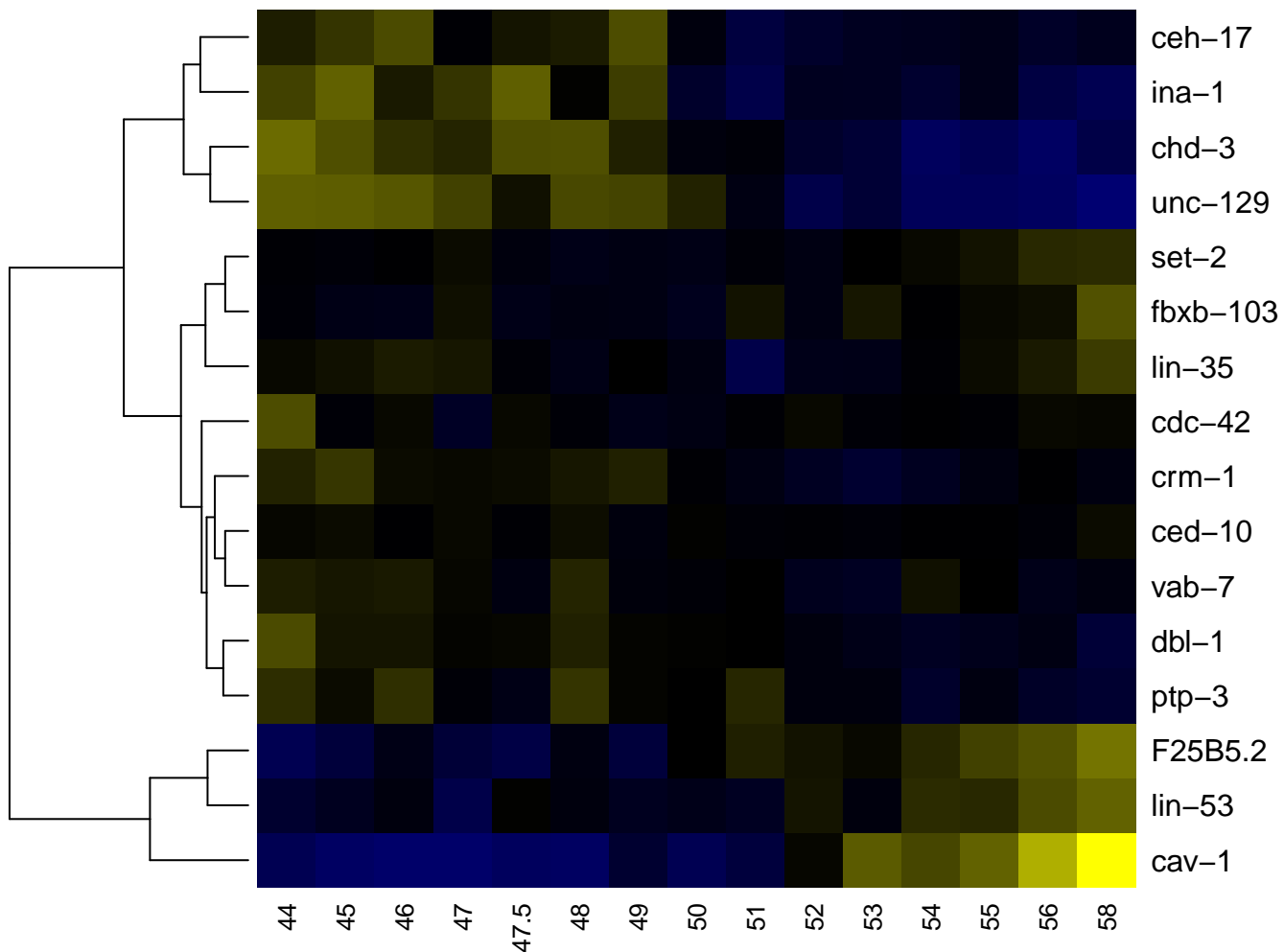
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DB5



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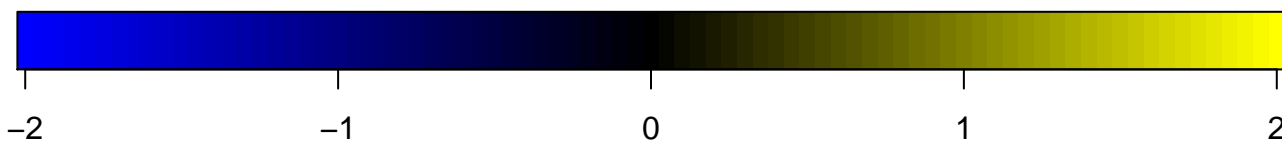
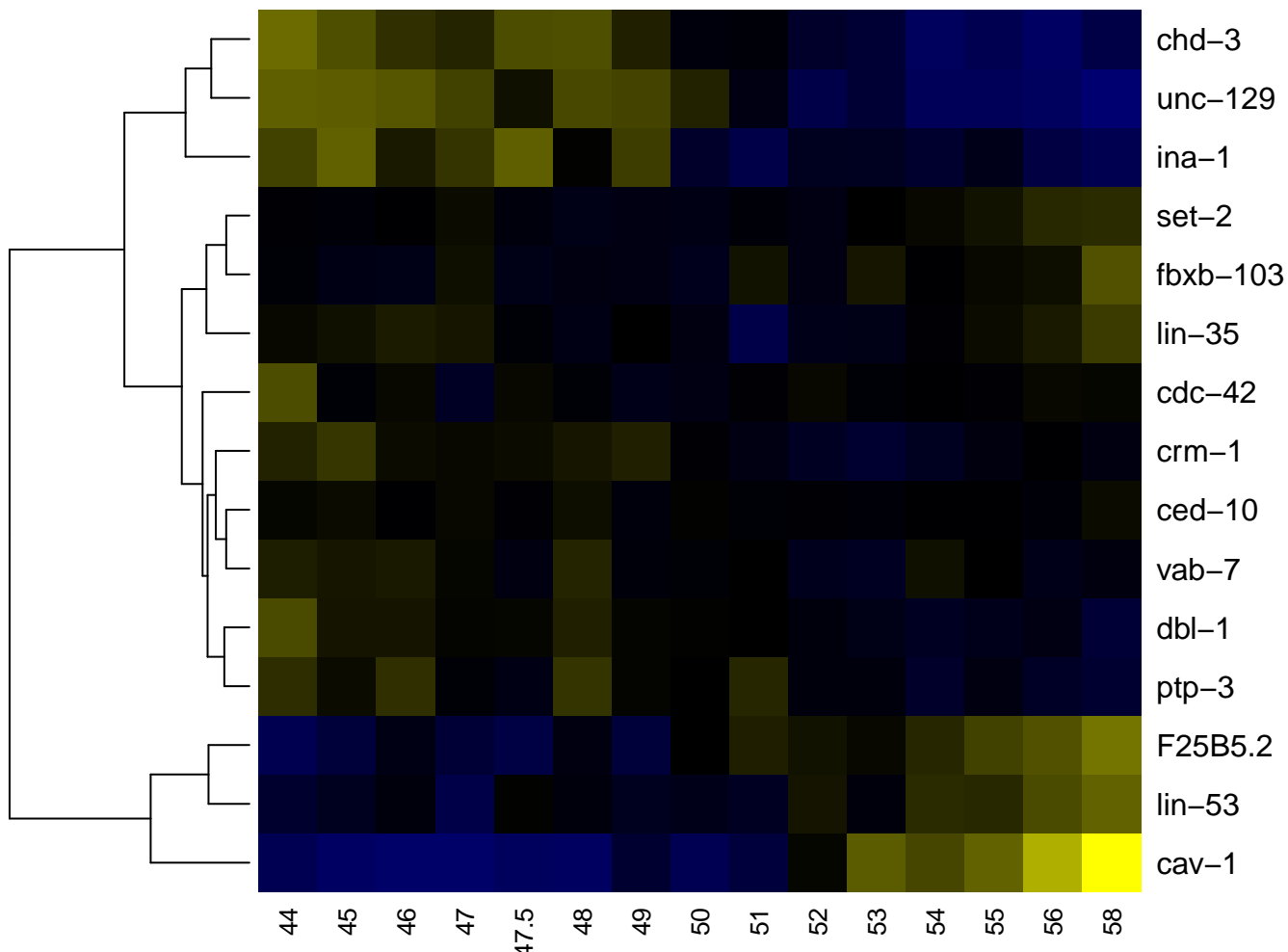
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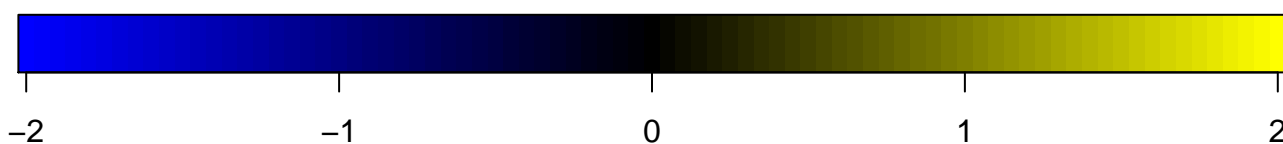
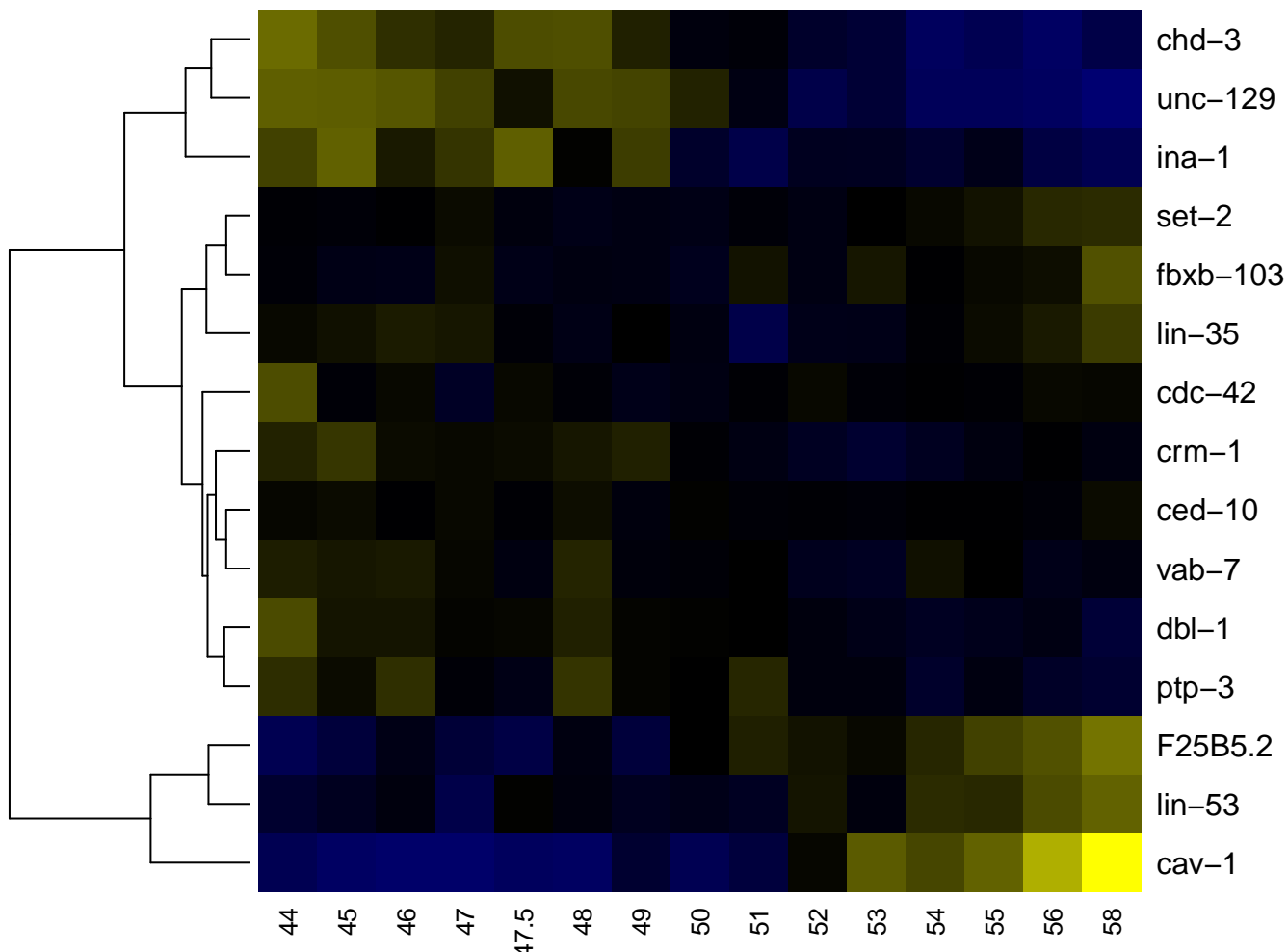
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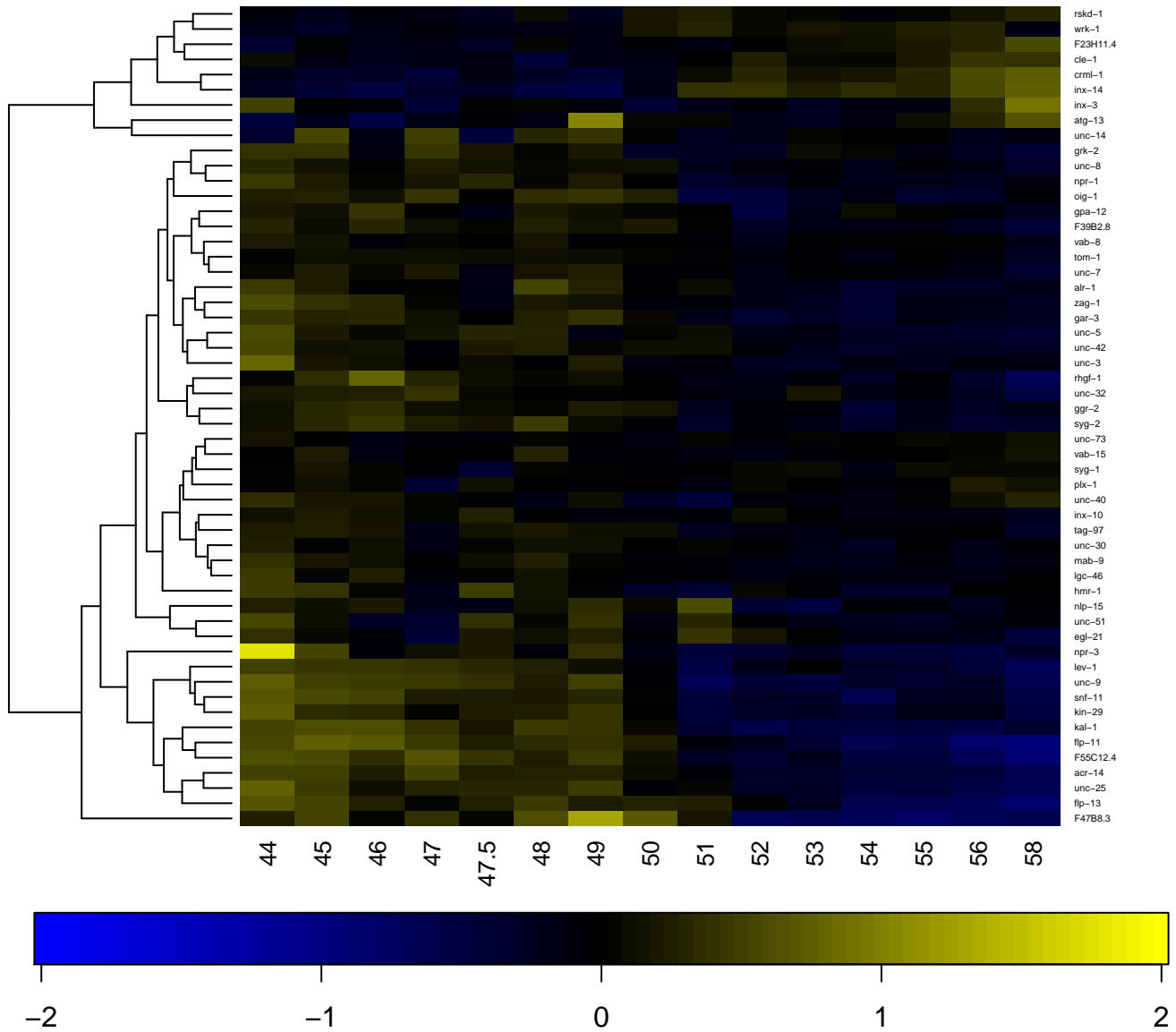
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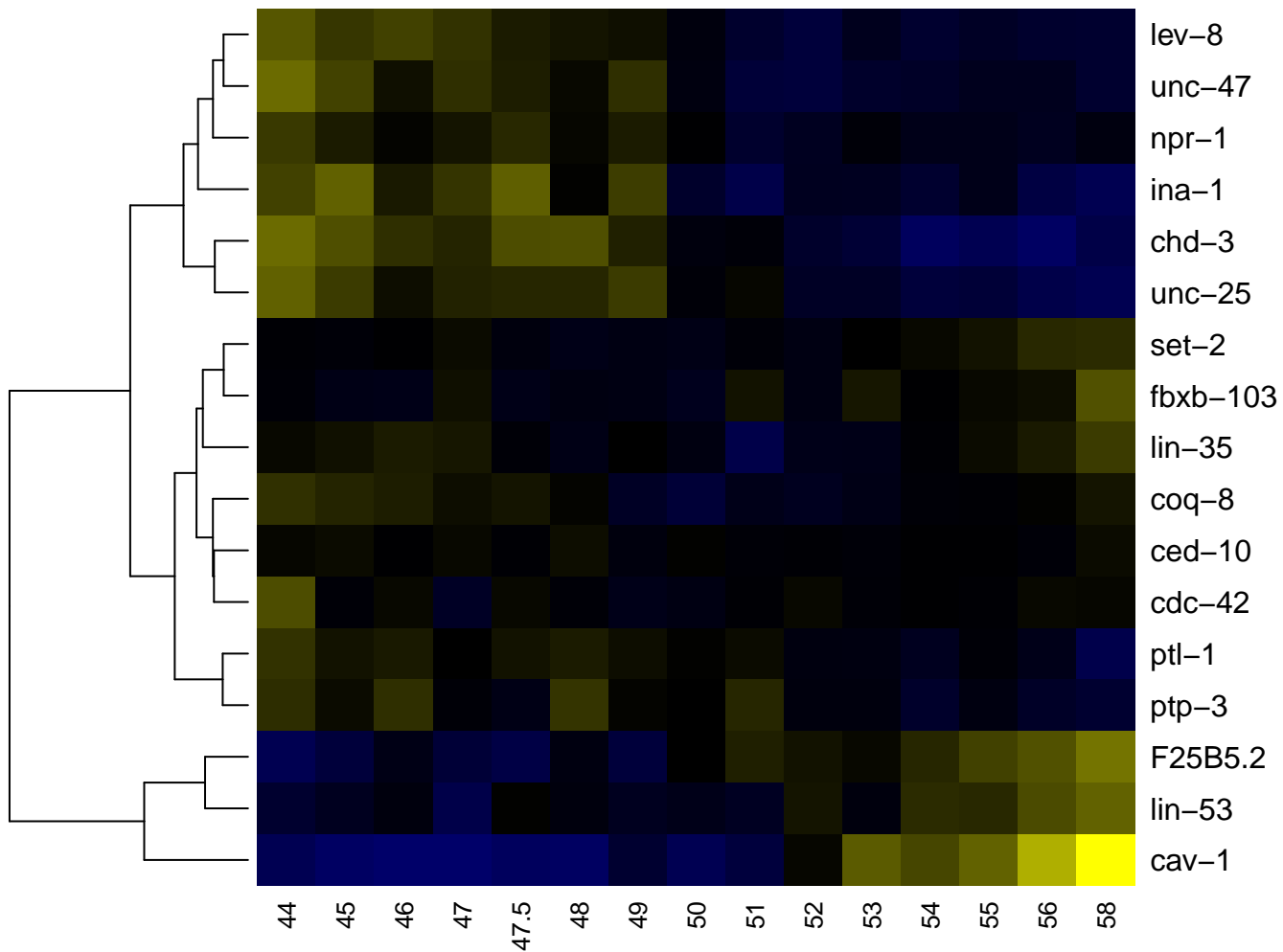
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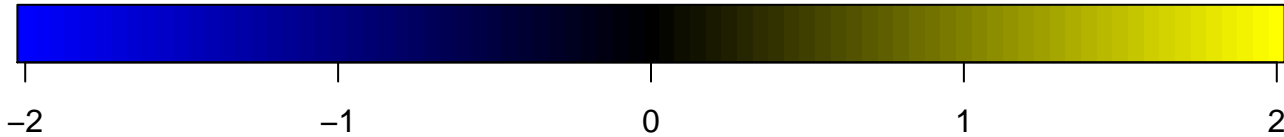
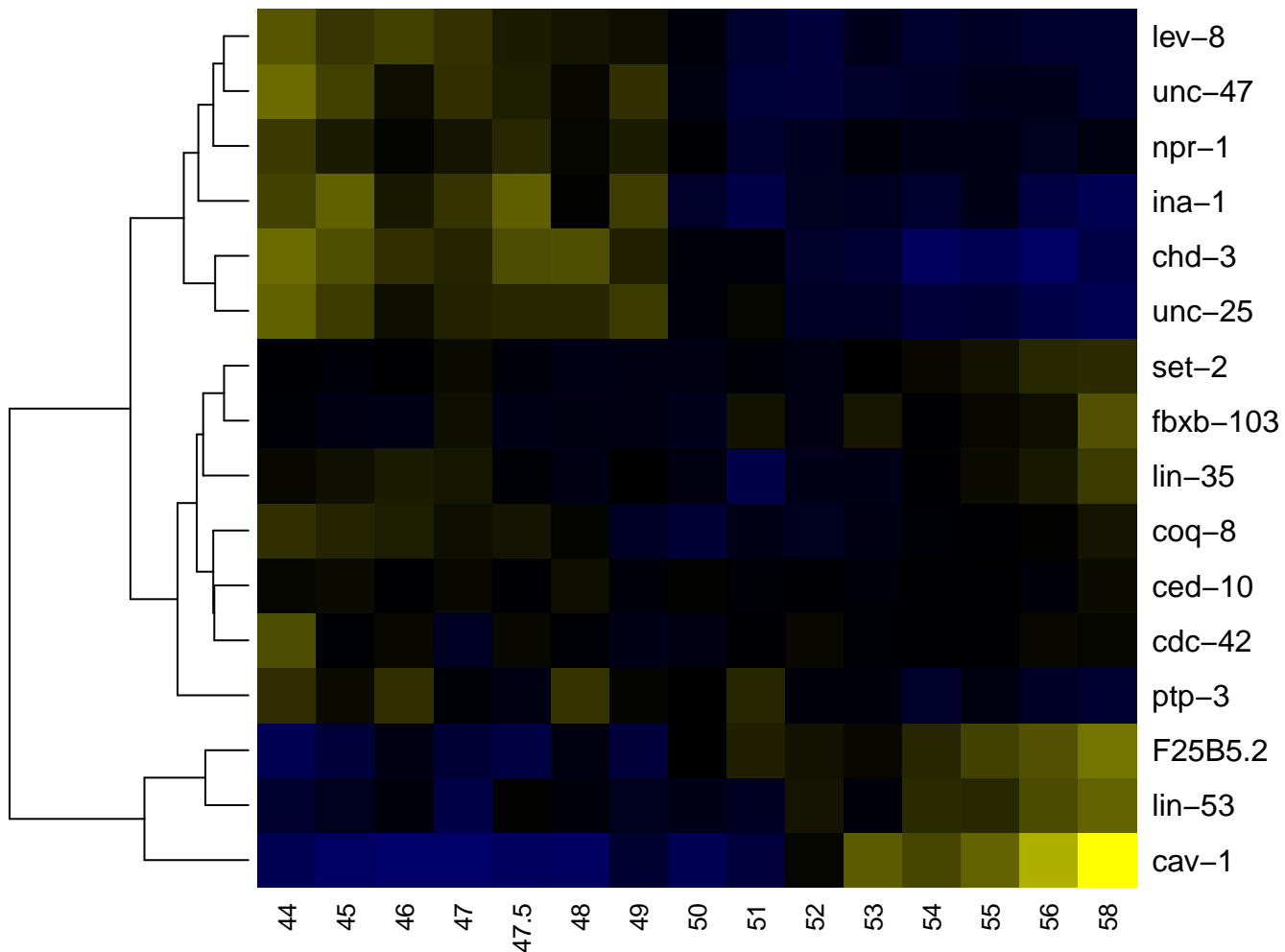
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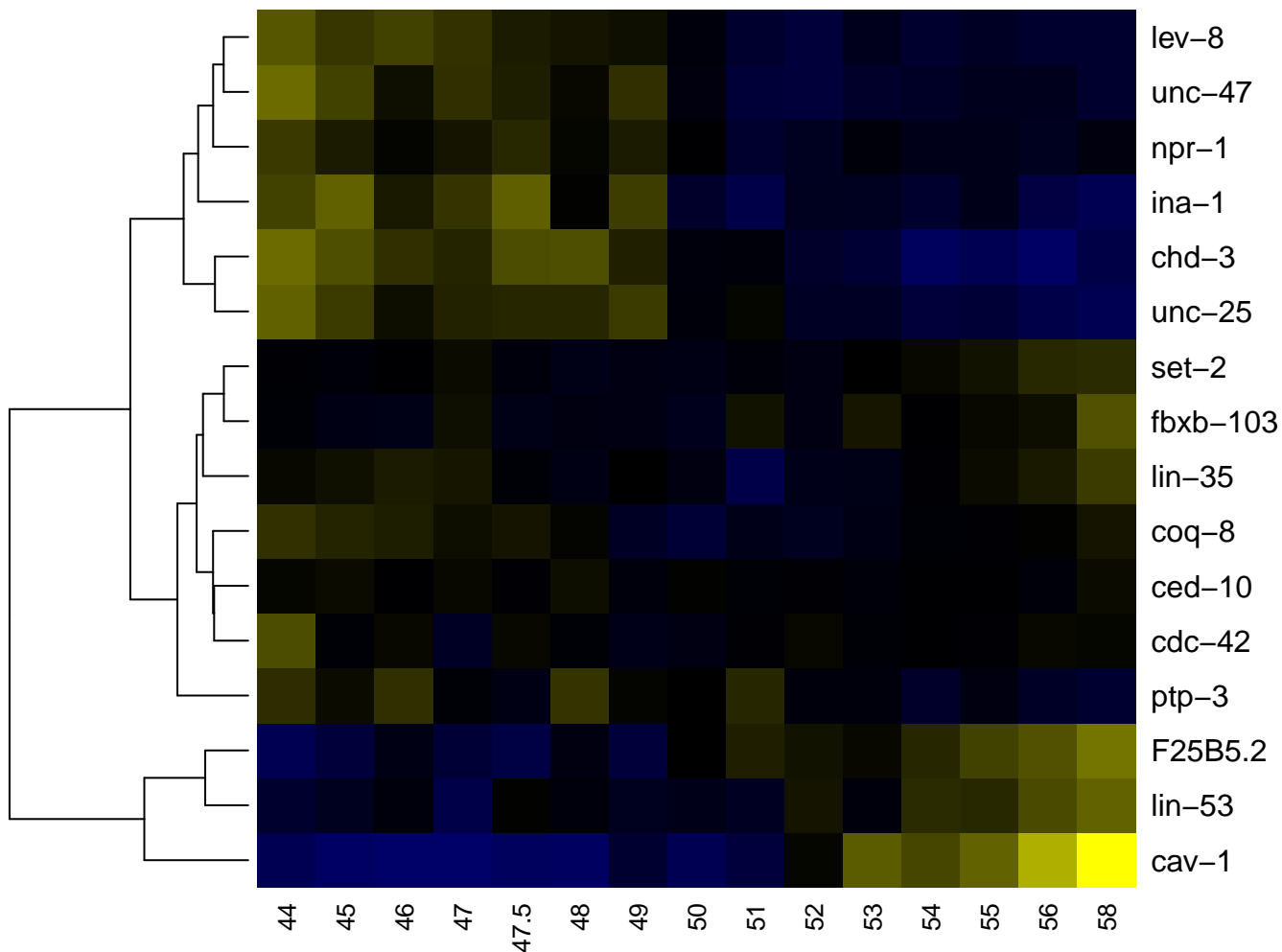
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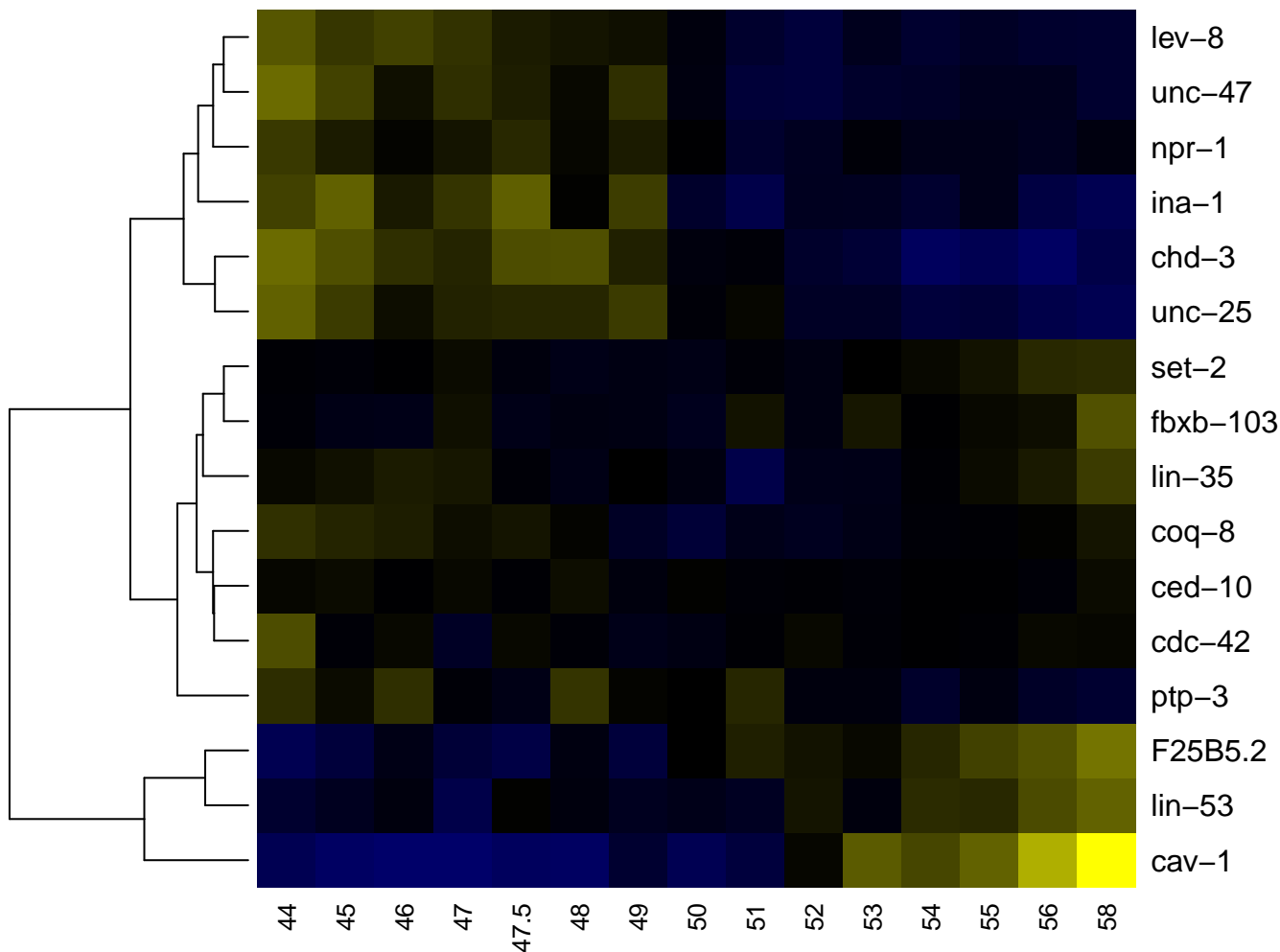
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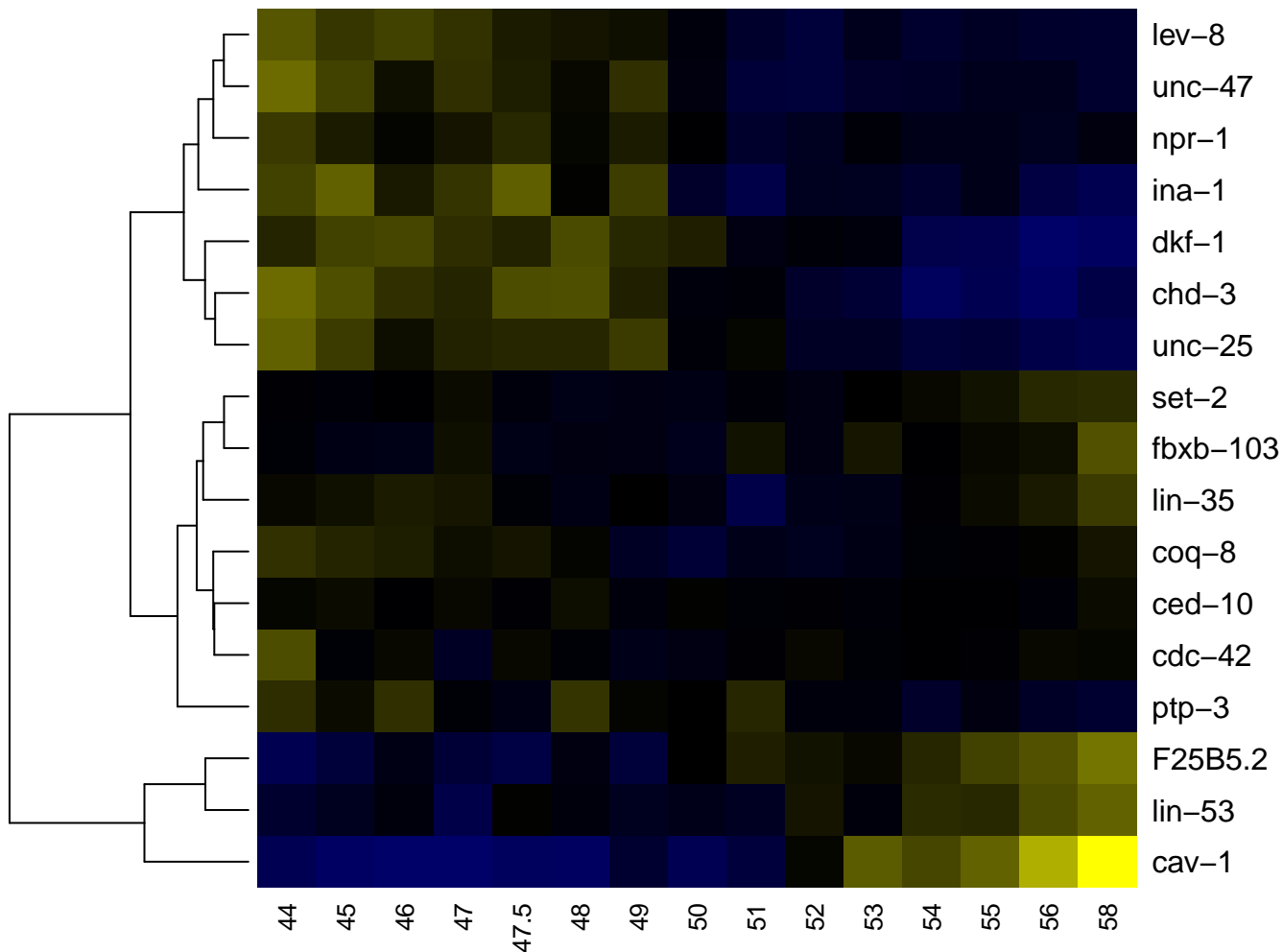
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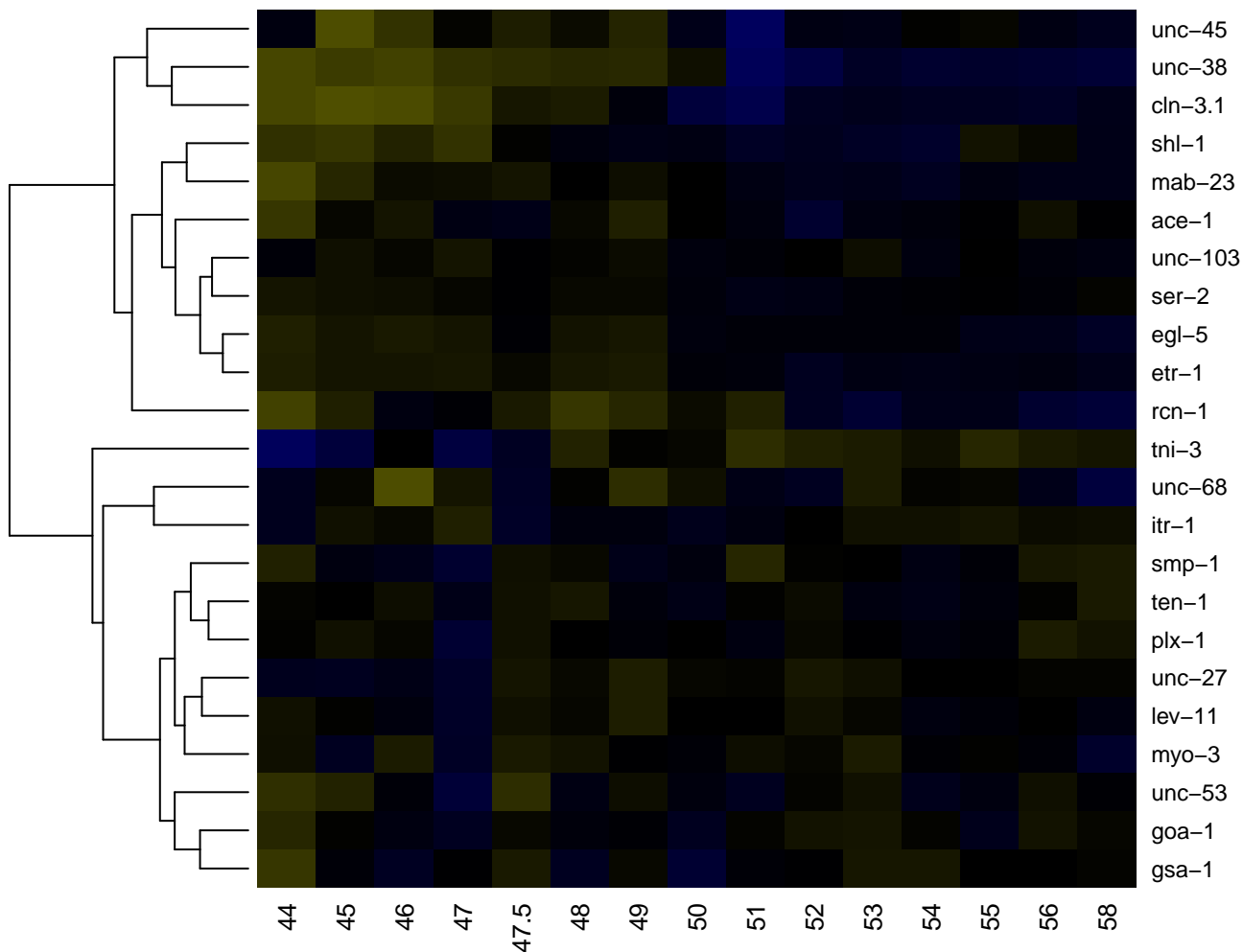
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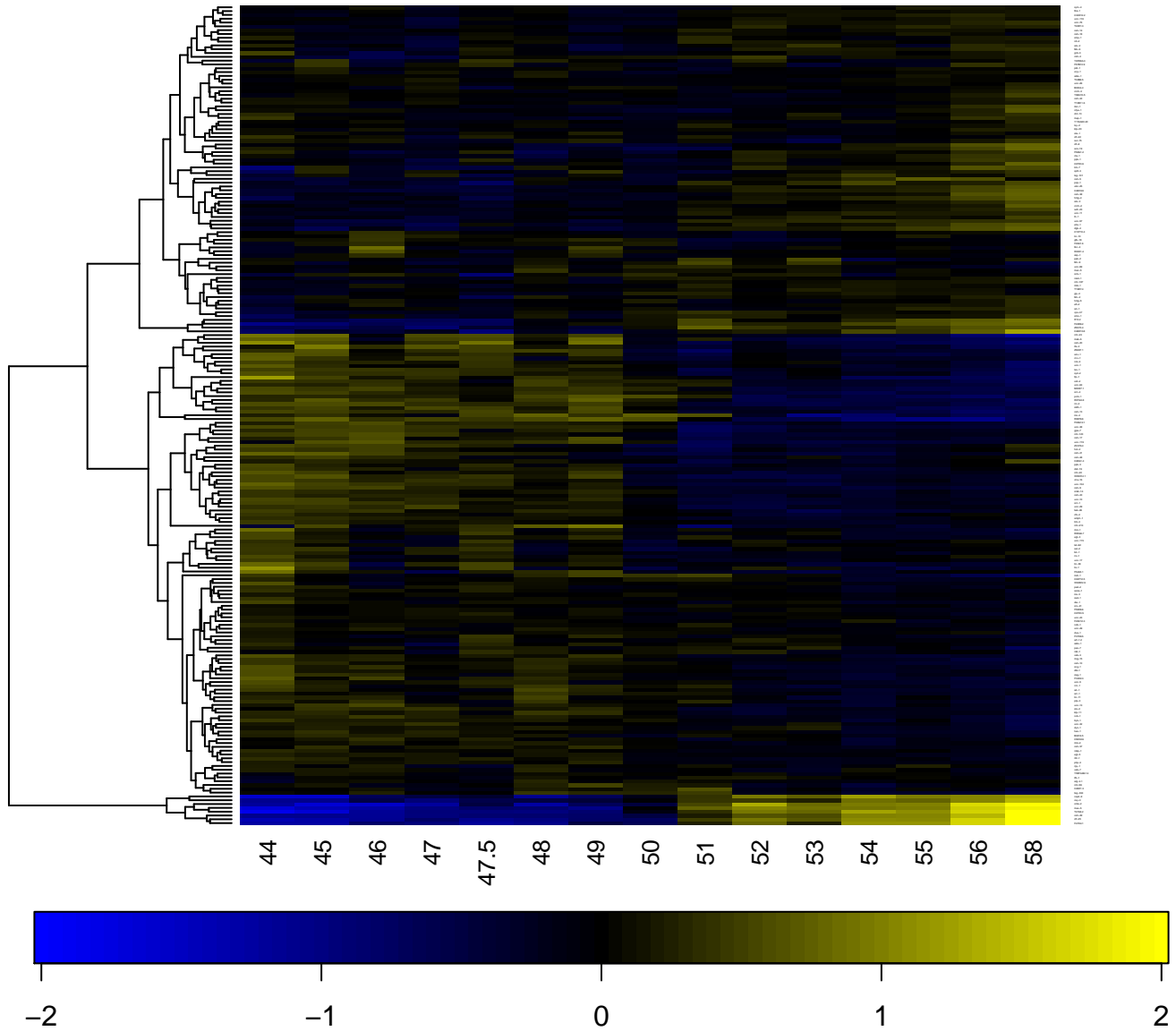
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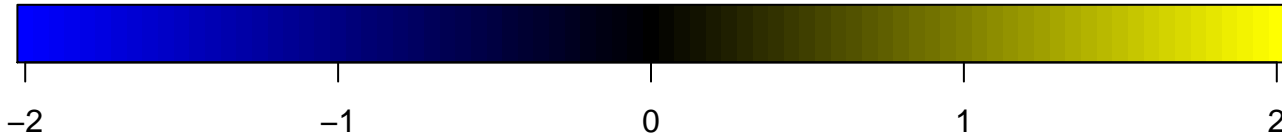
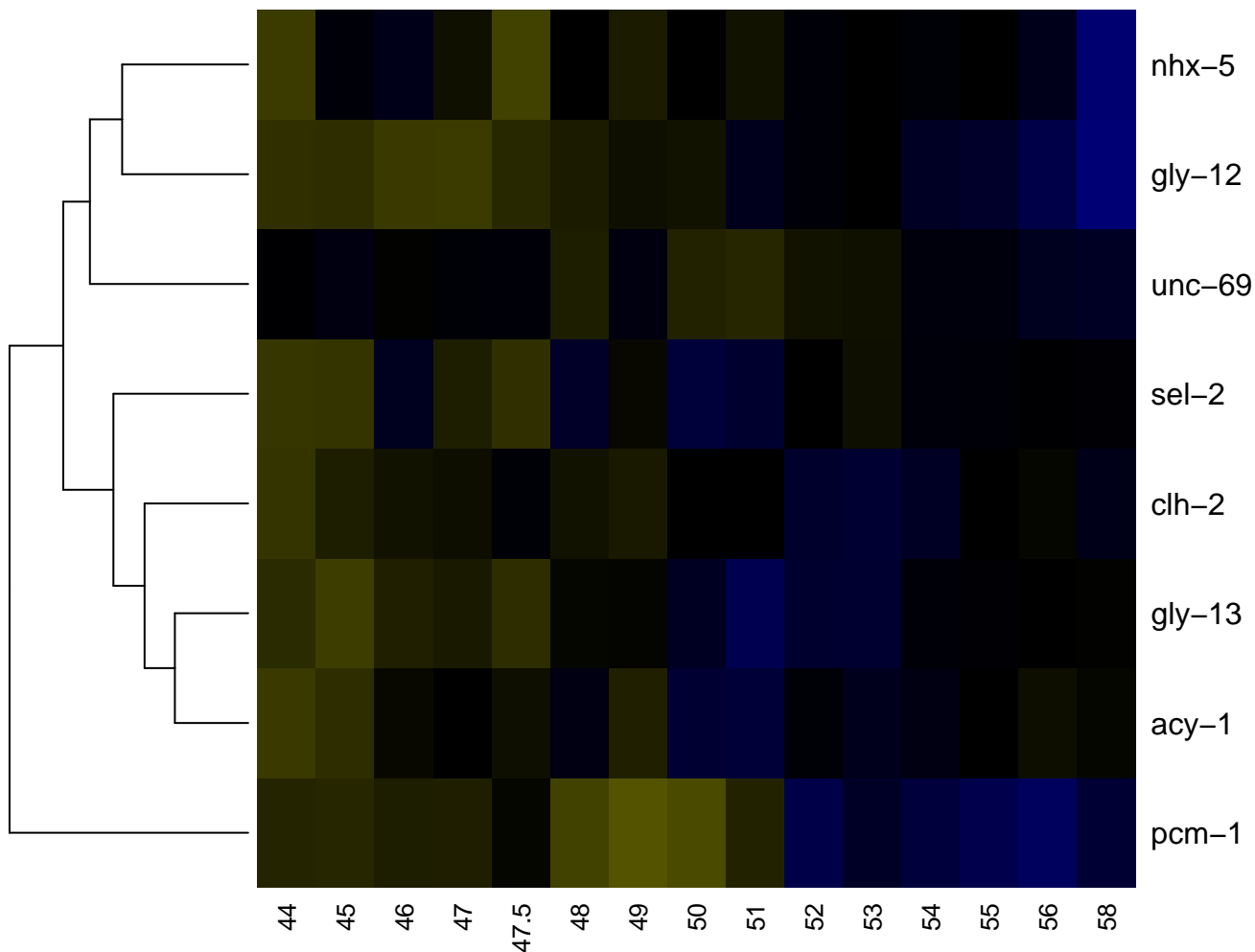
diagonal muscle



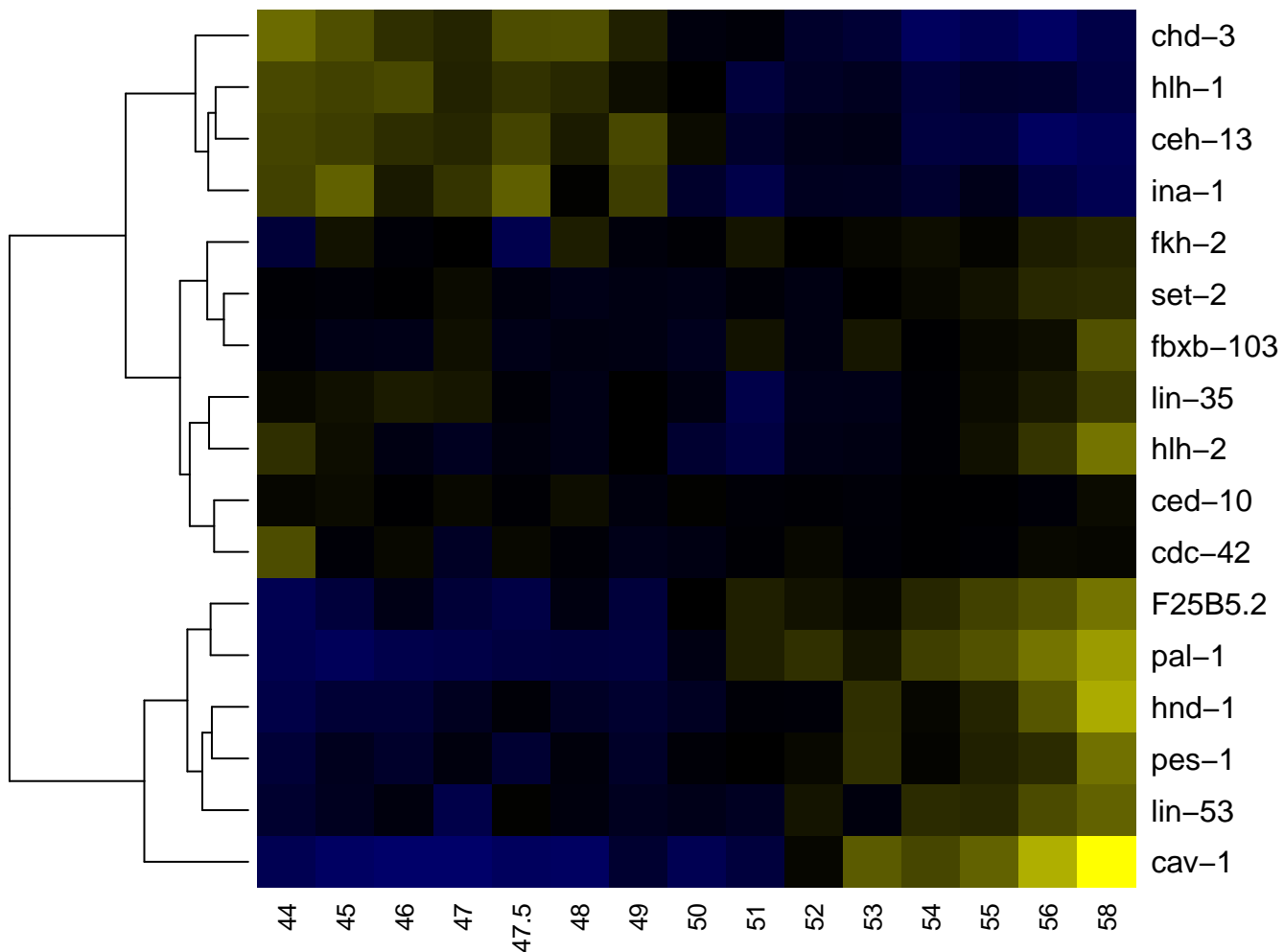
dorsal nerve cord



dorso-rectal ganglion



Dp



-2

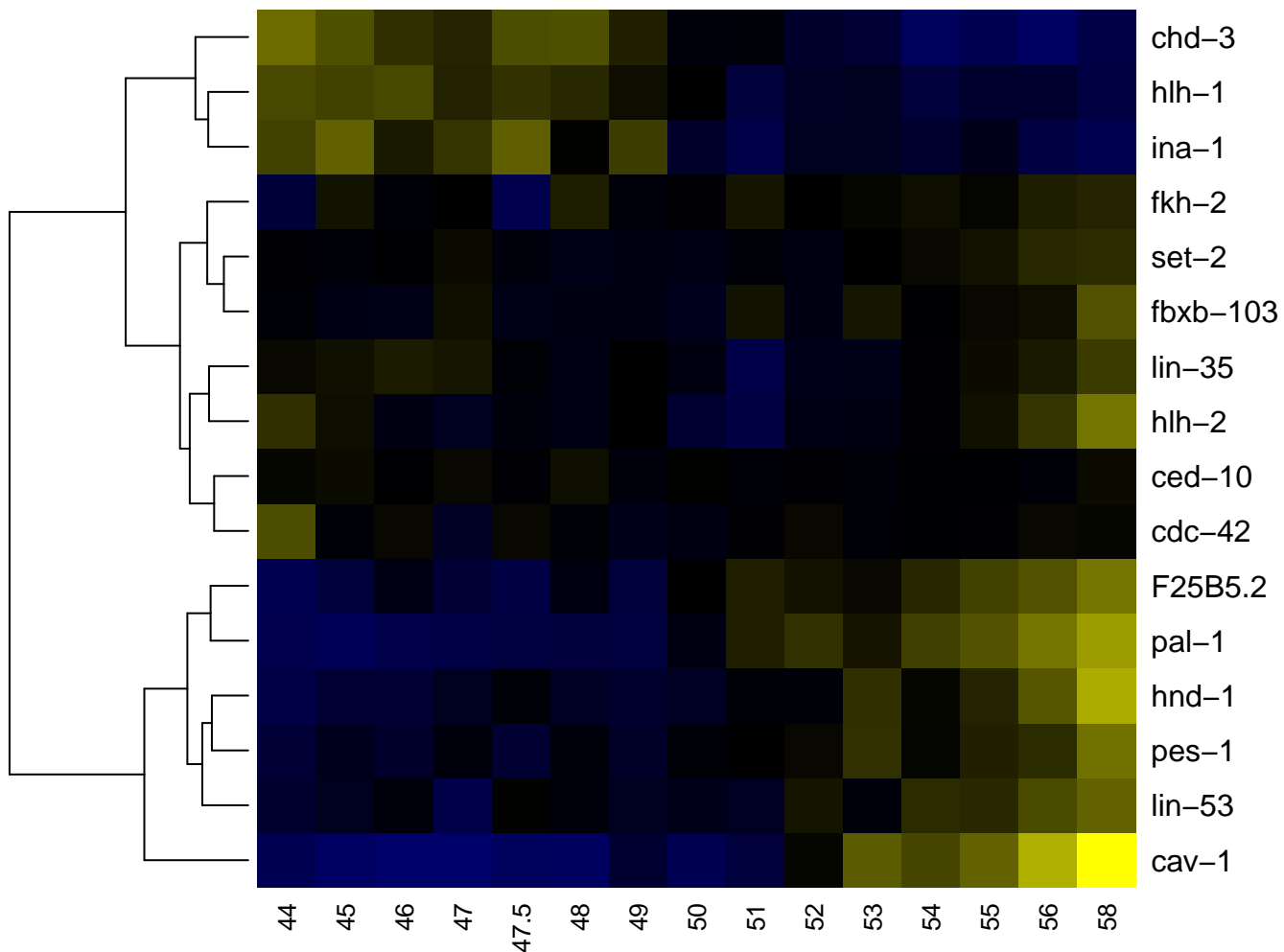
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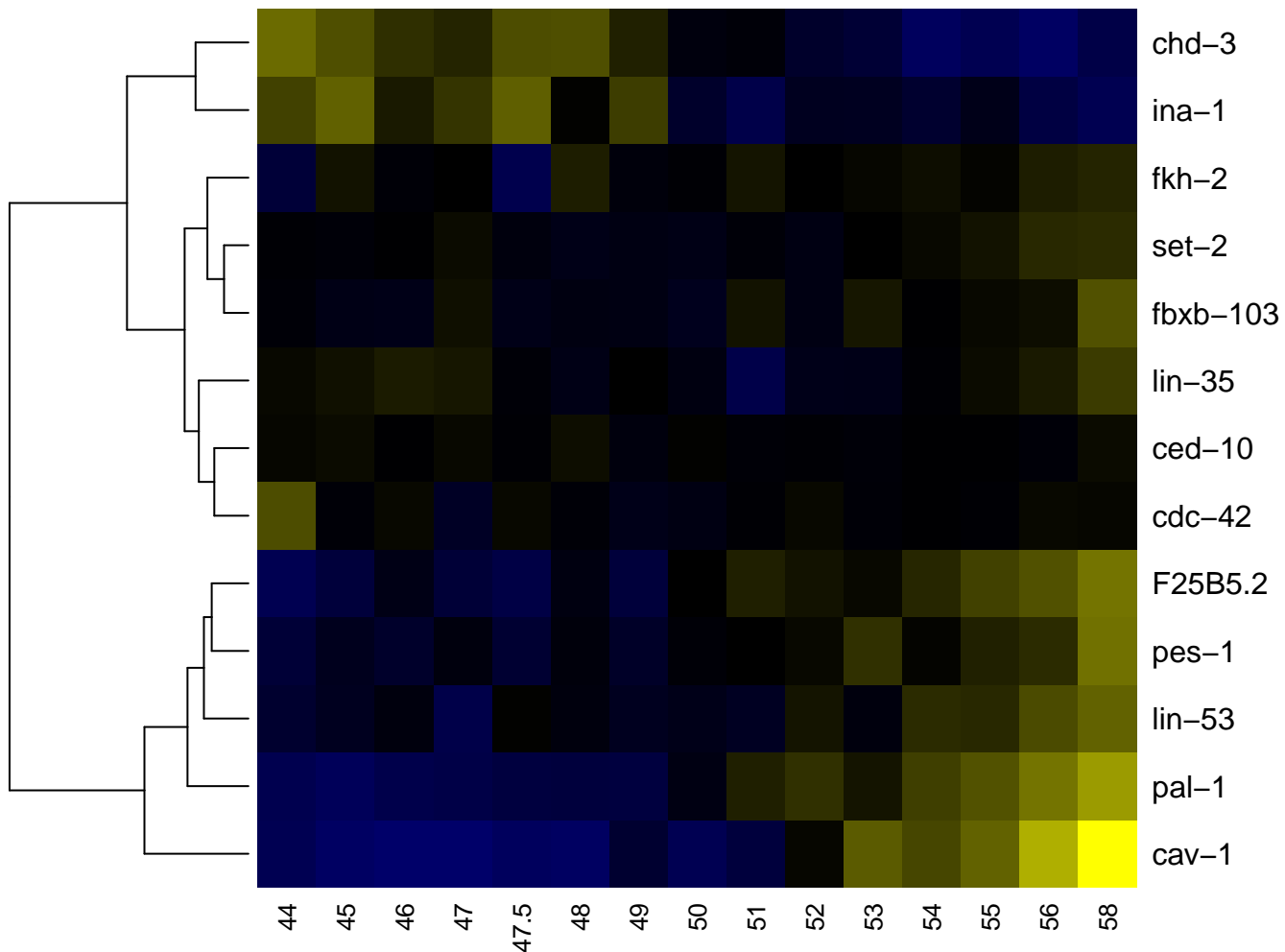
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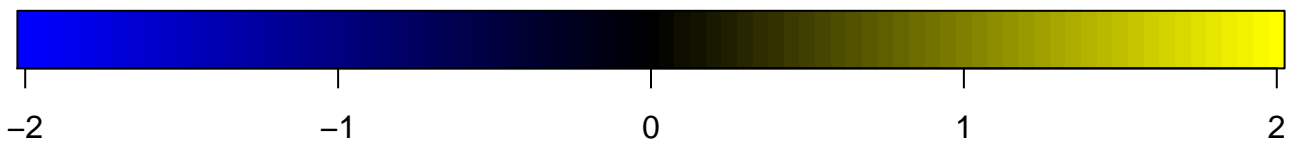
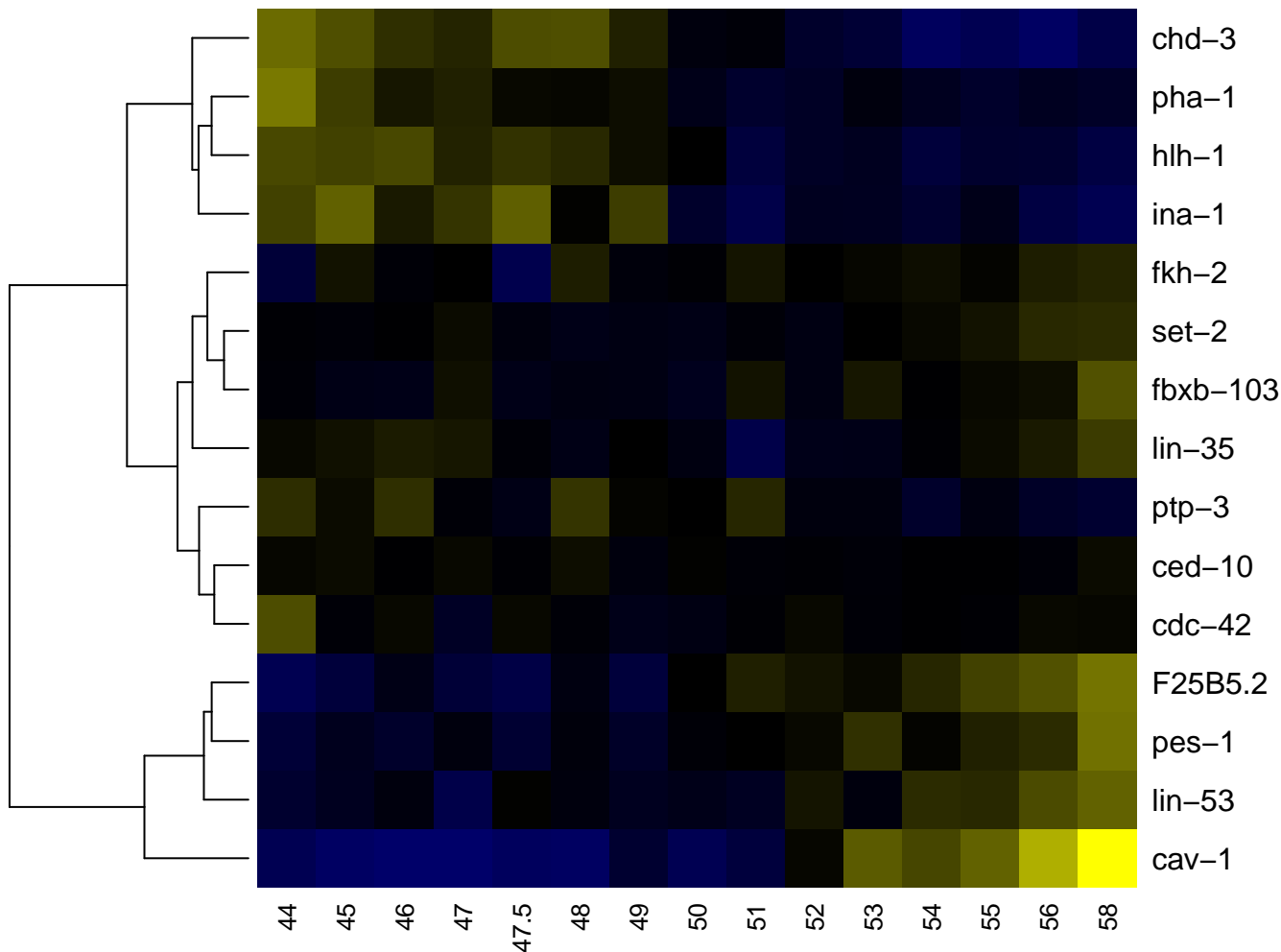
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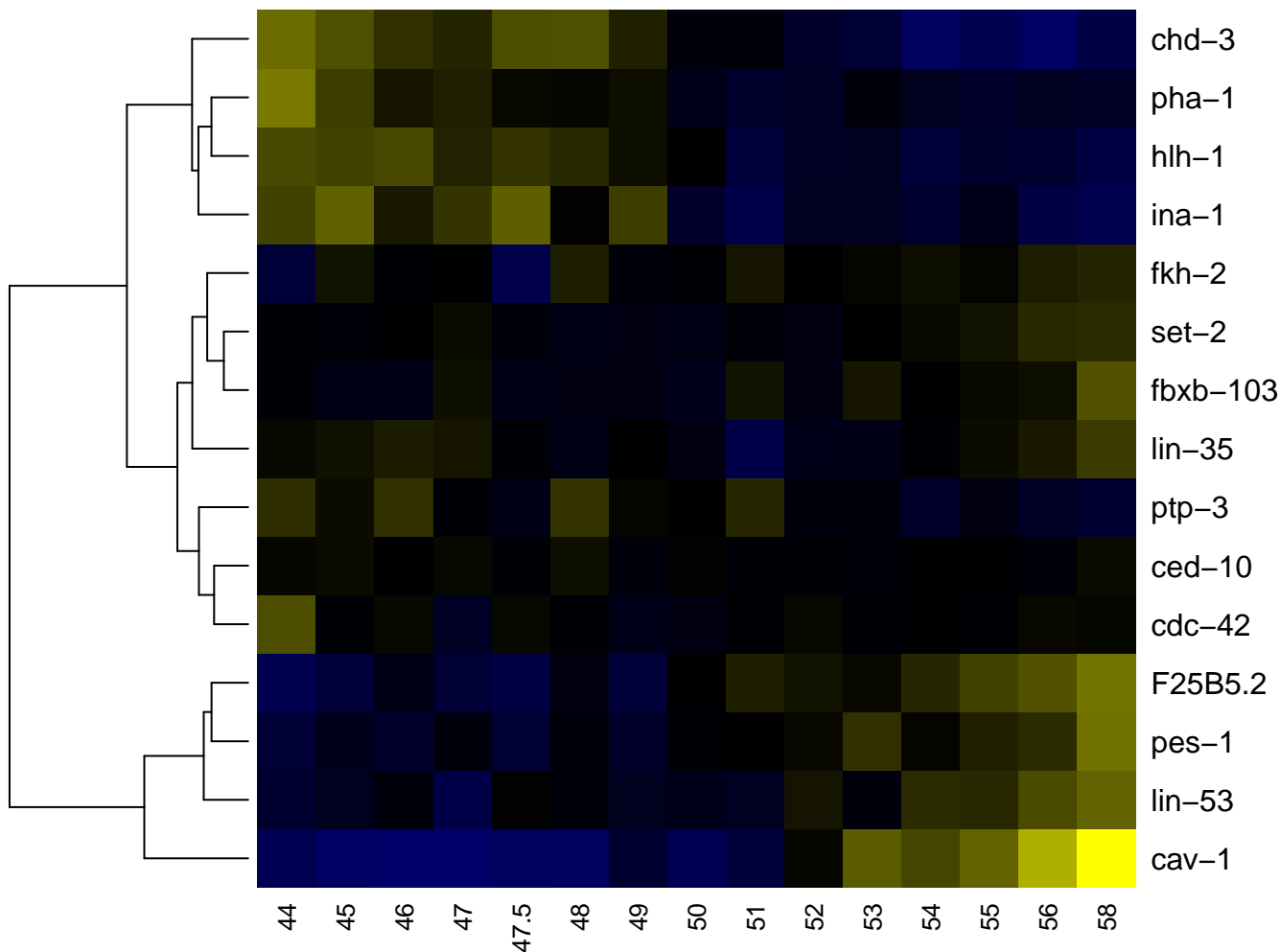
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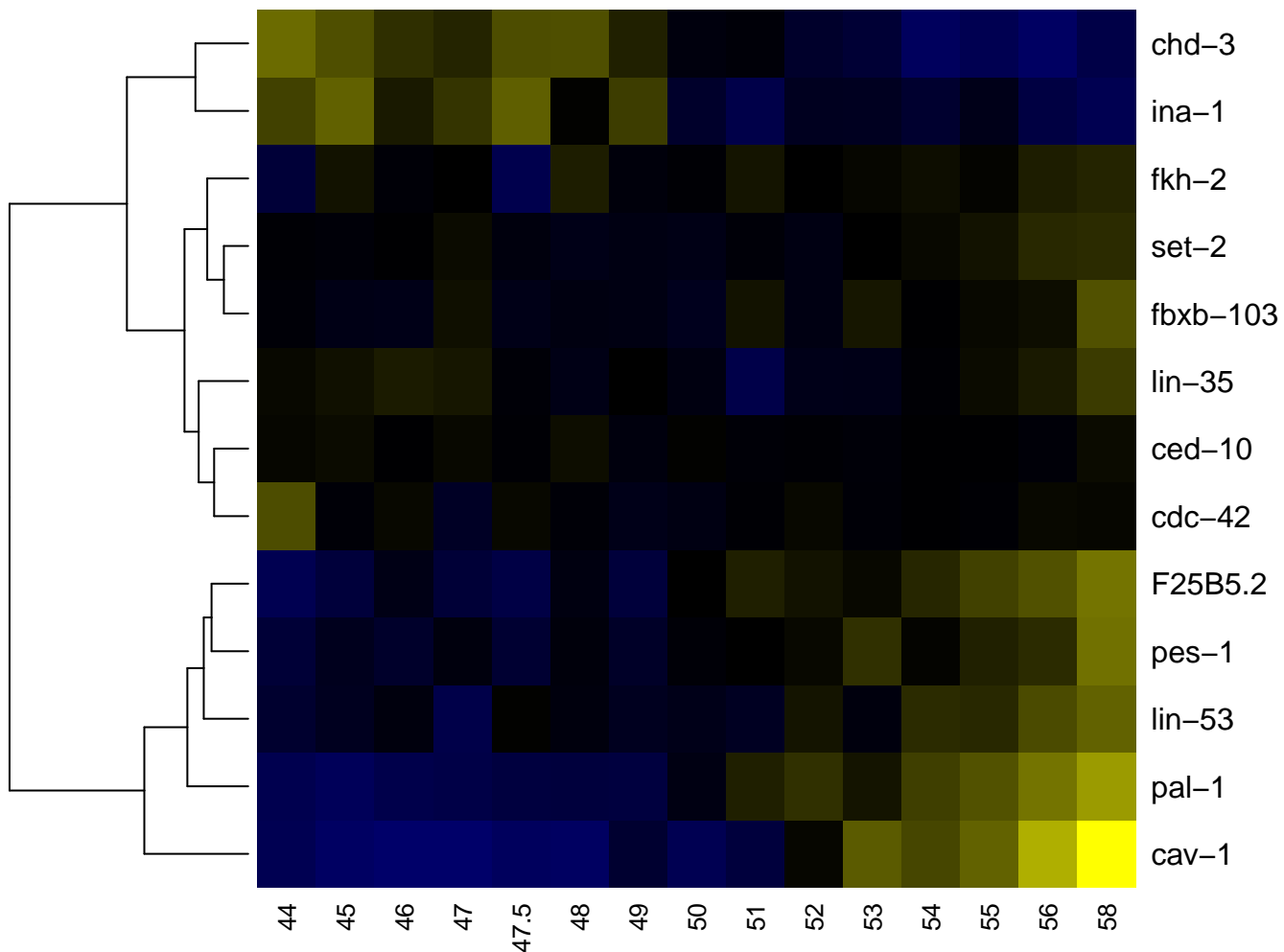
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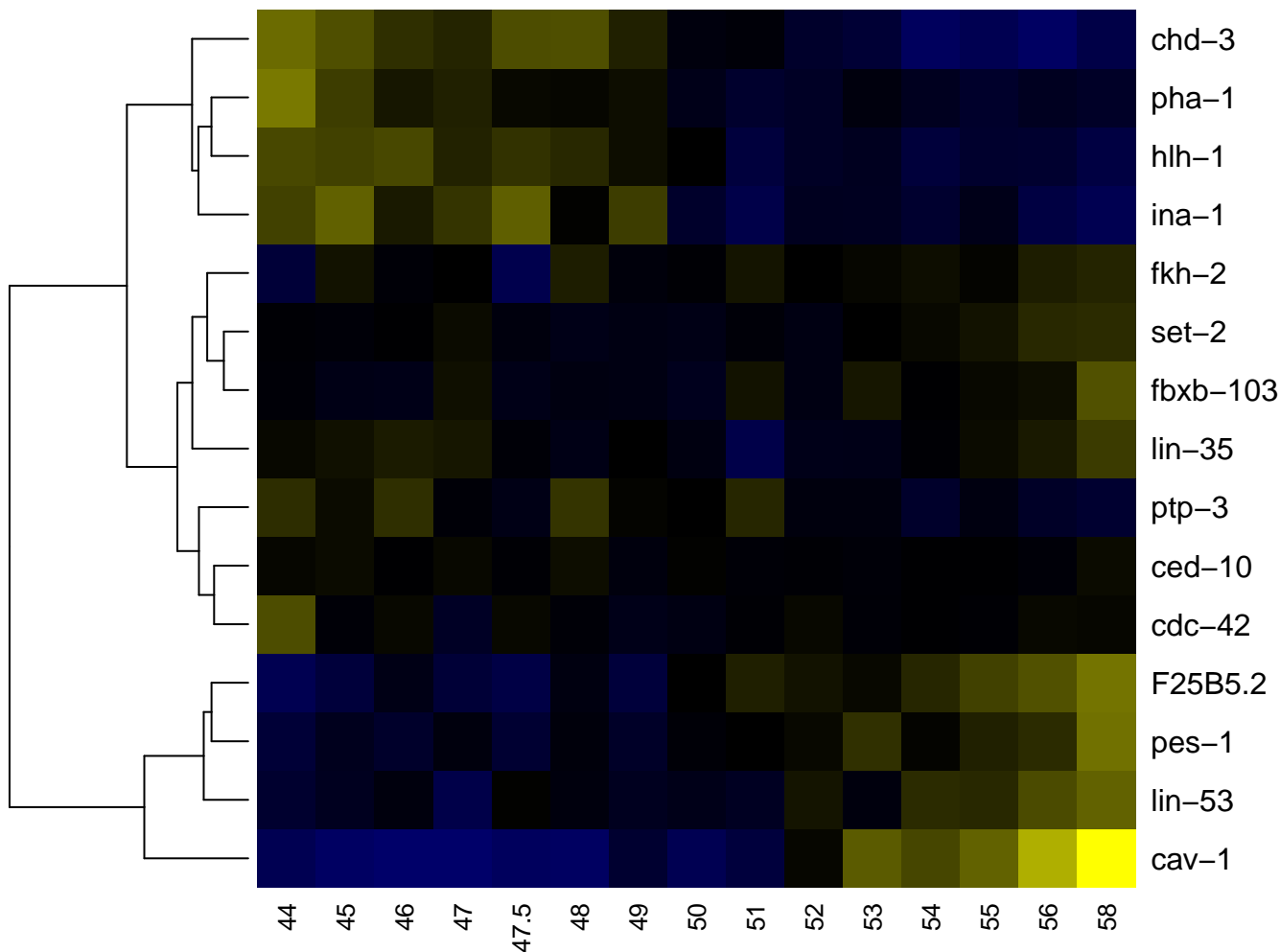
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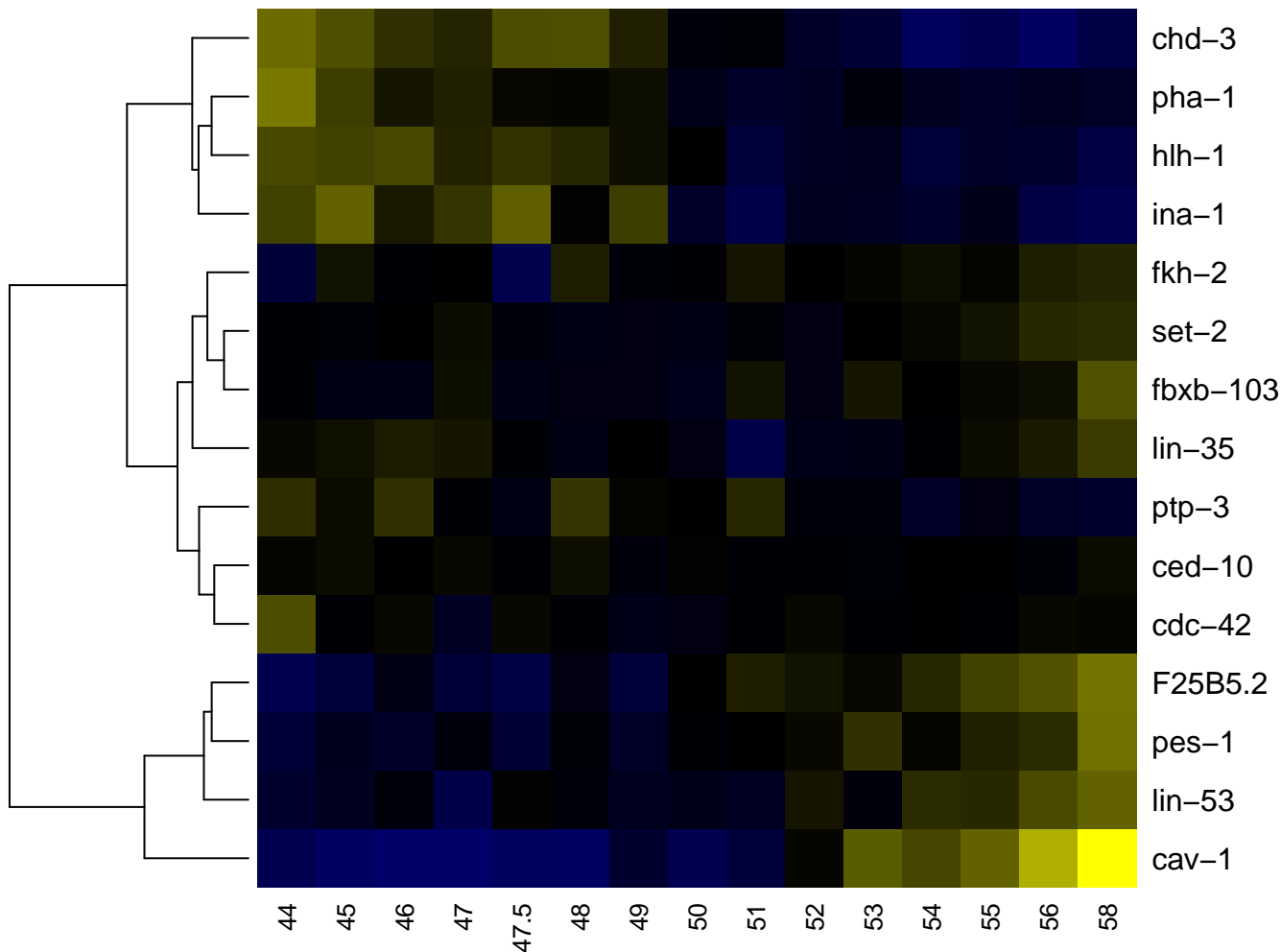
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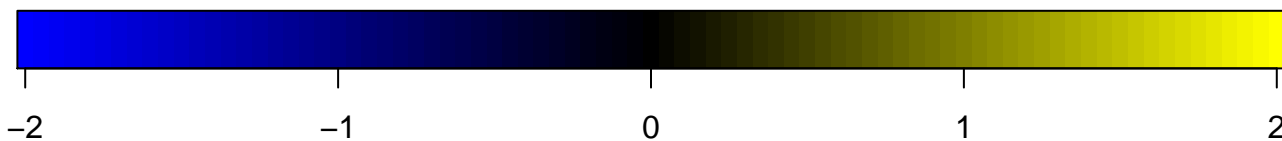
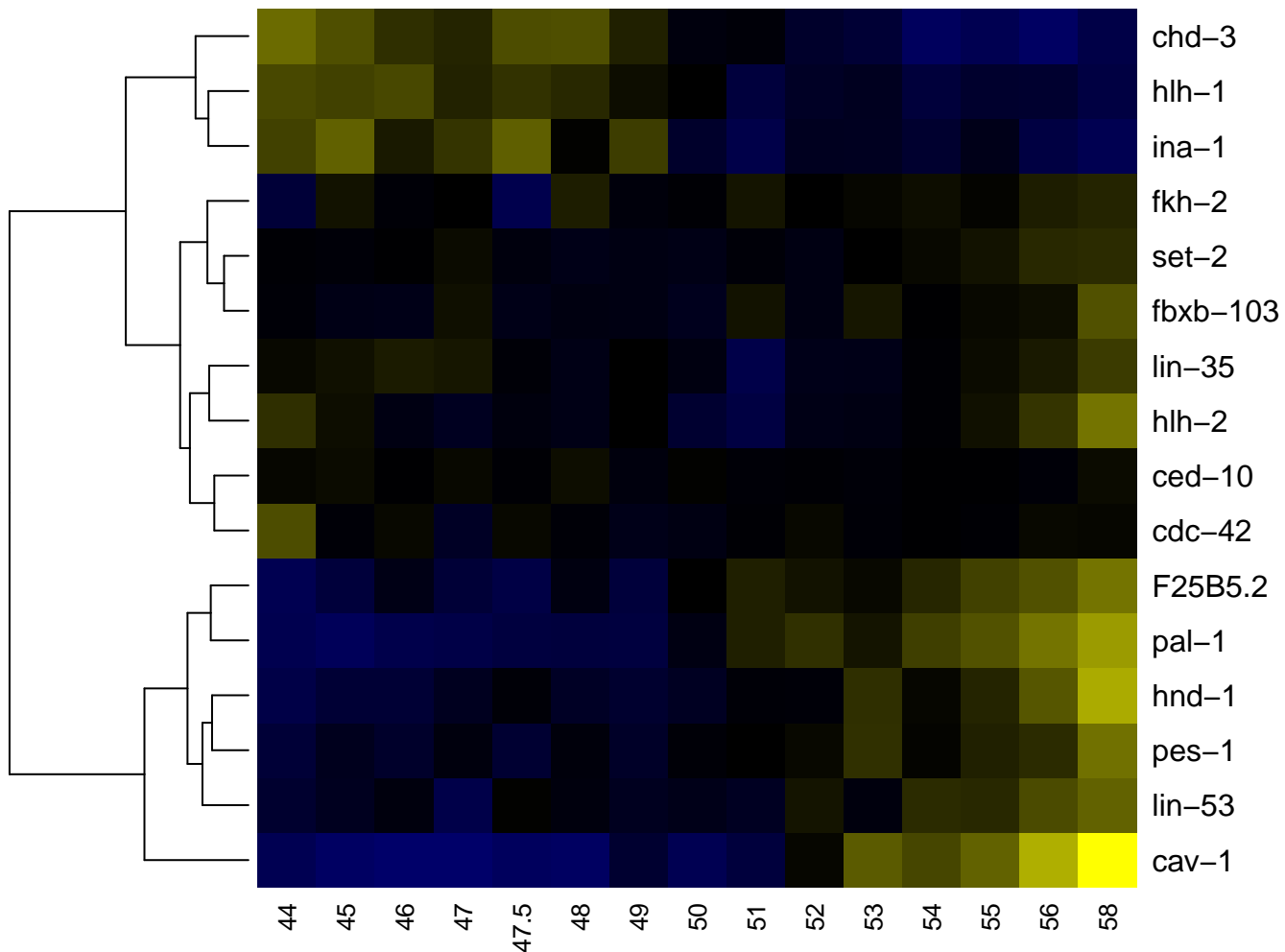
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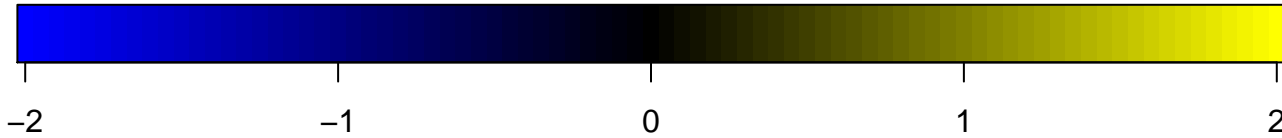
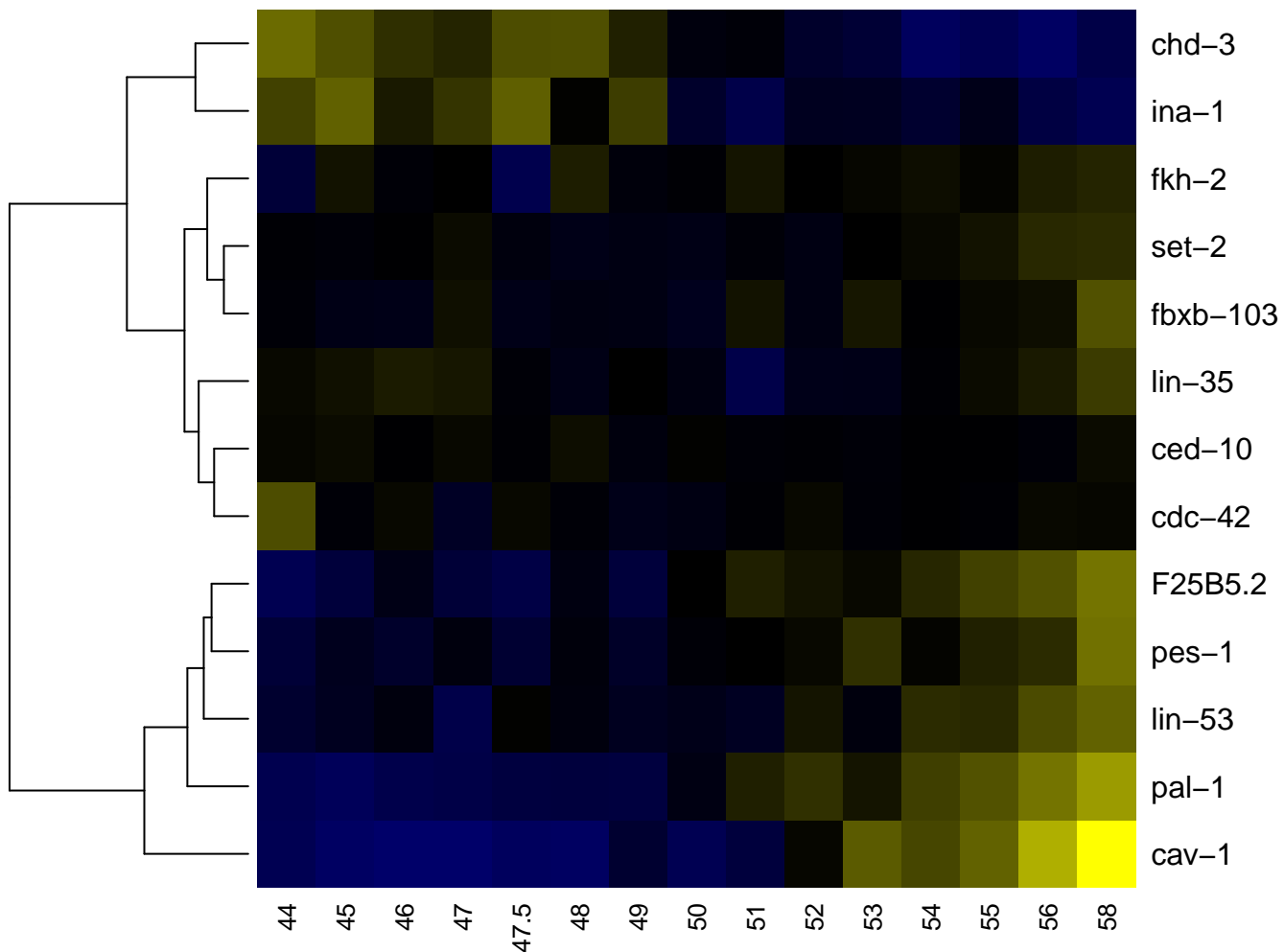
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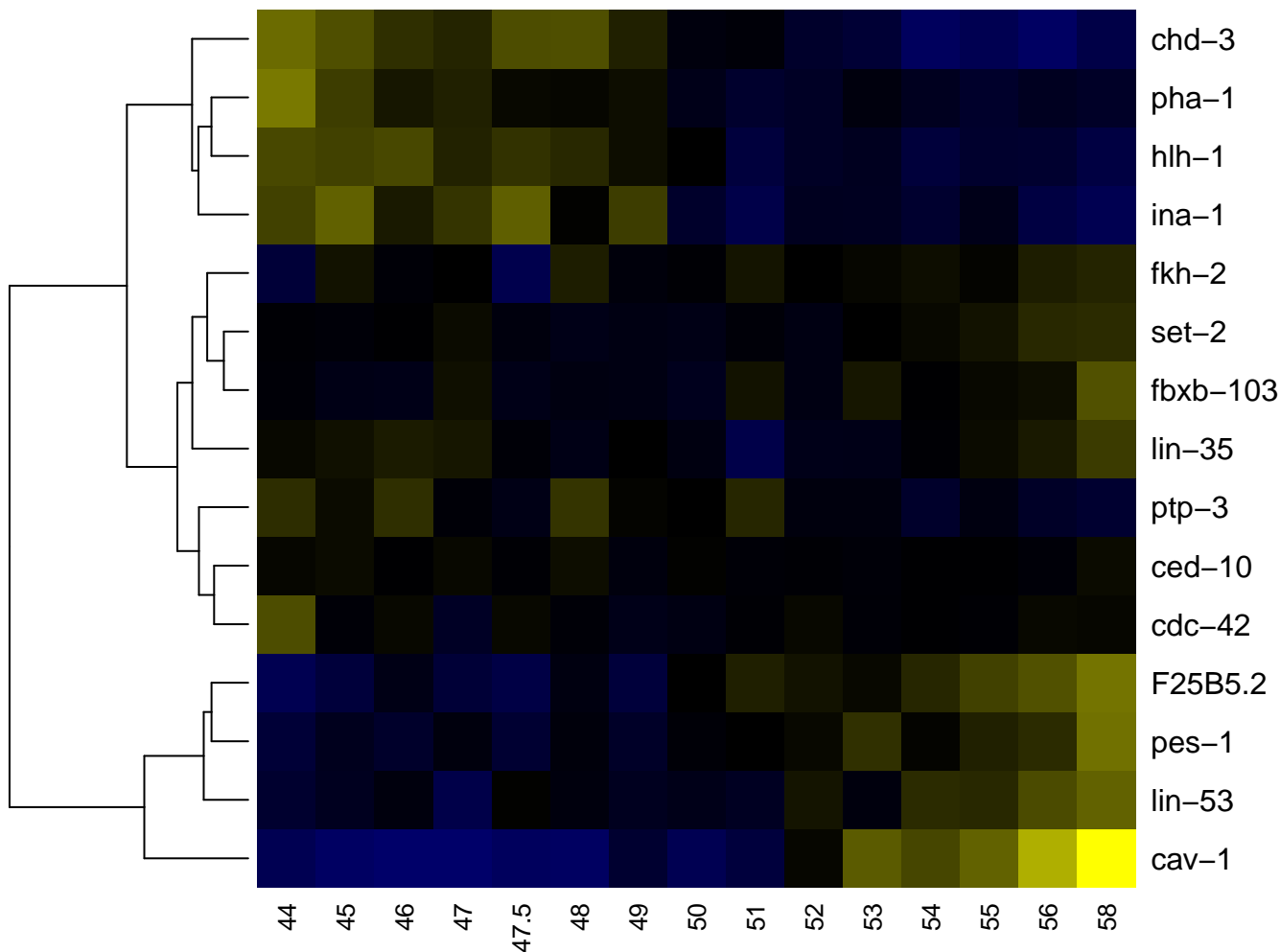
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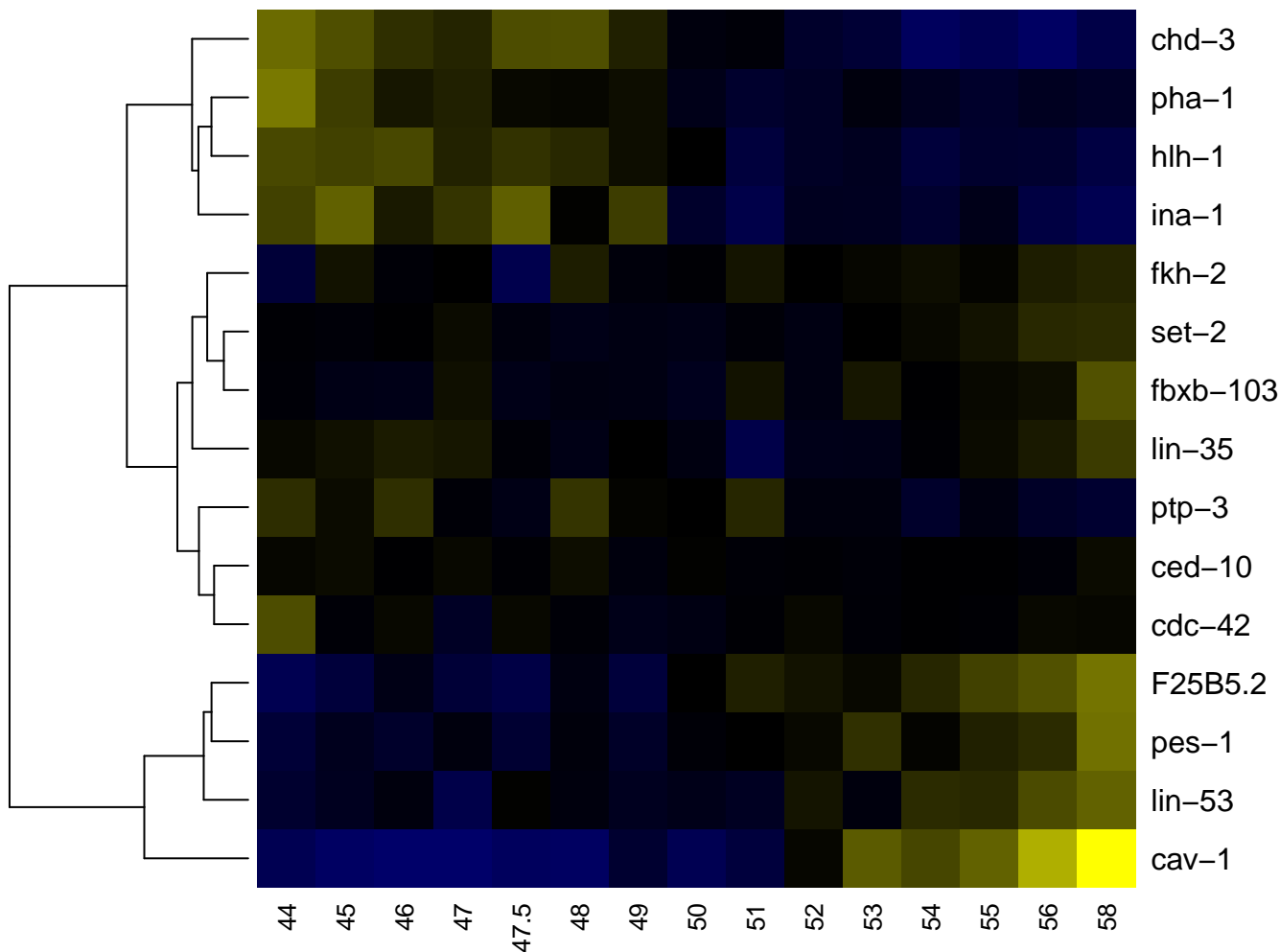
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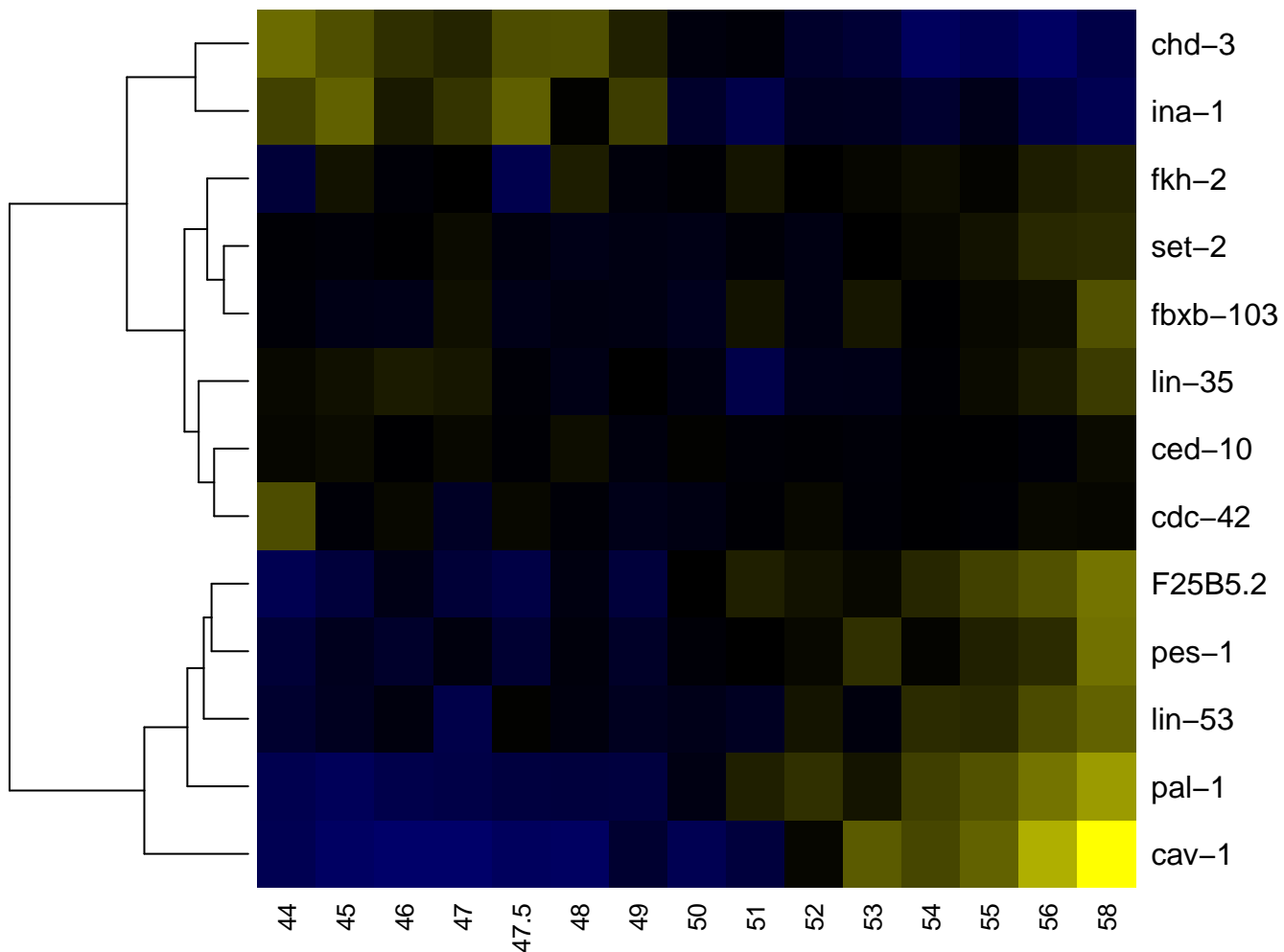
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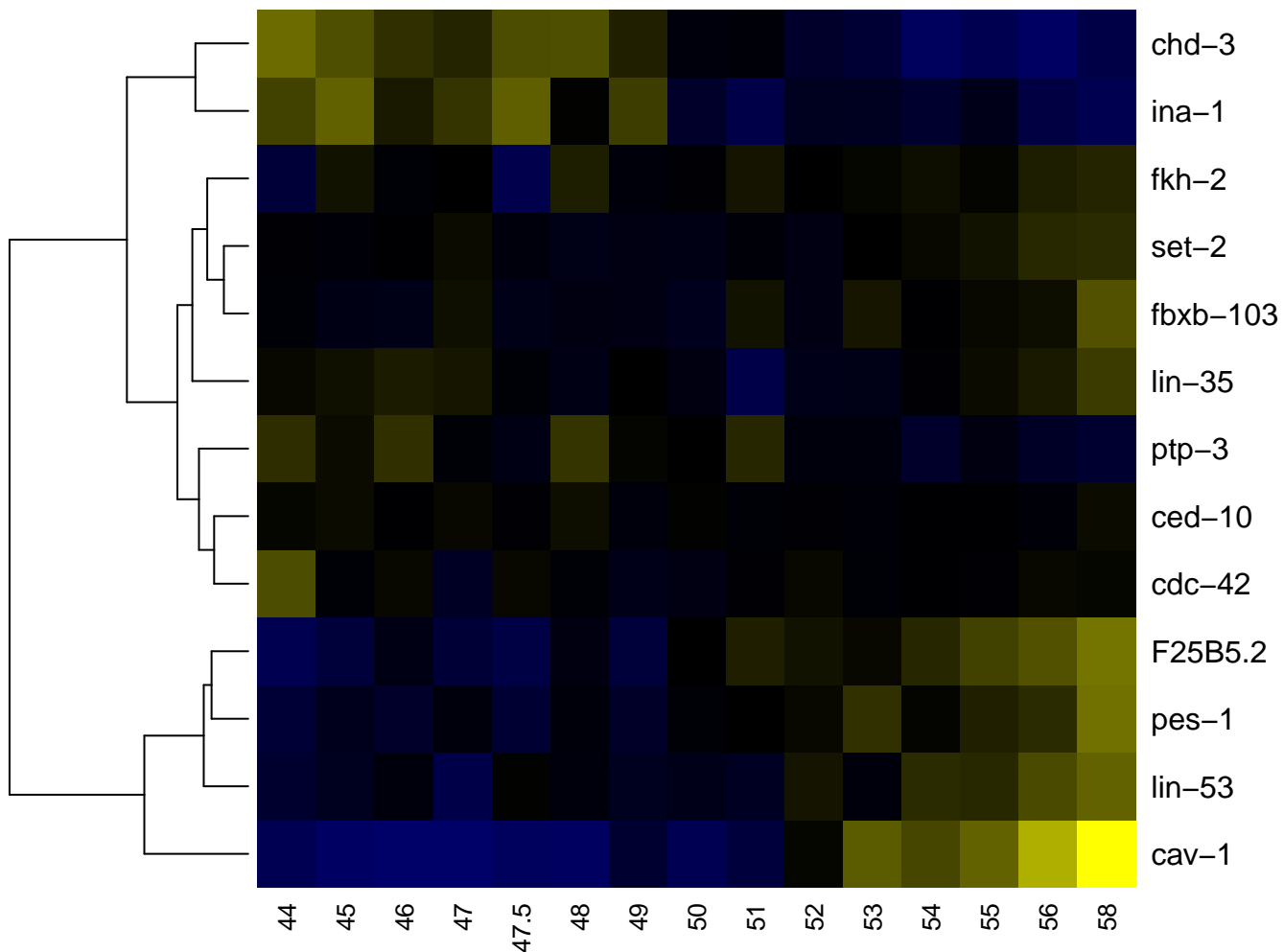
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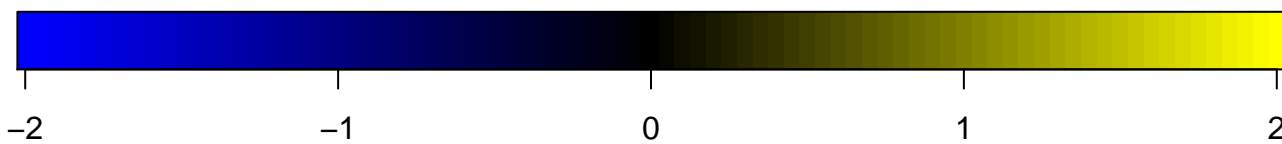
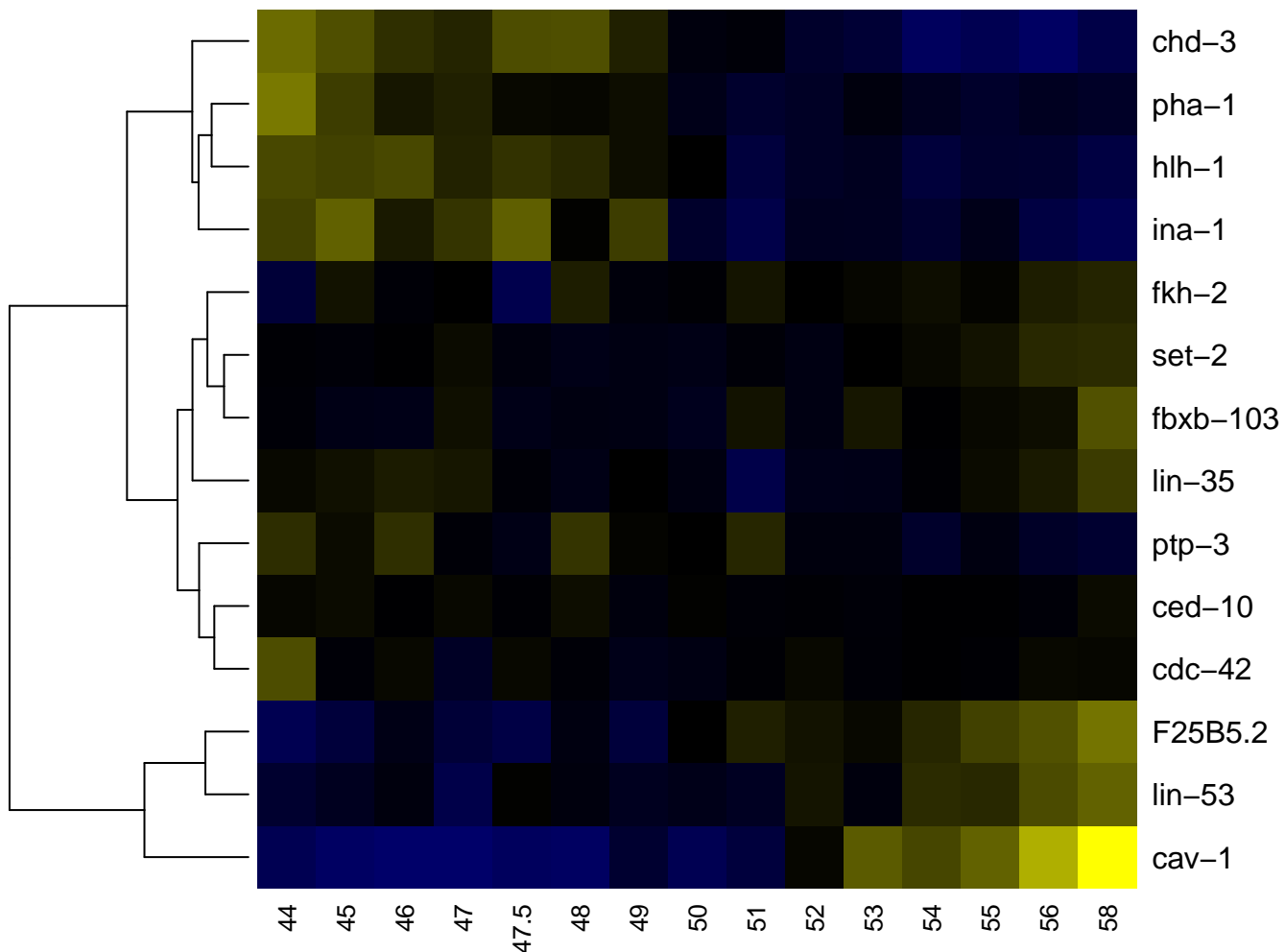
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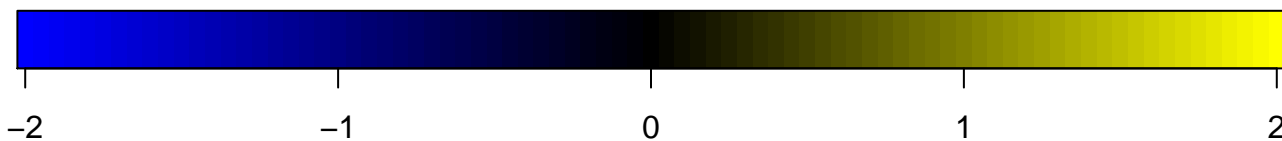
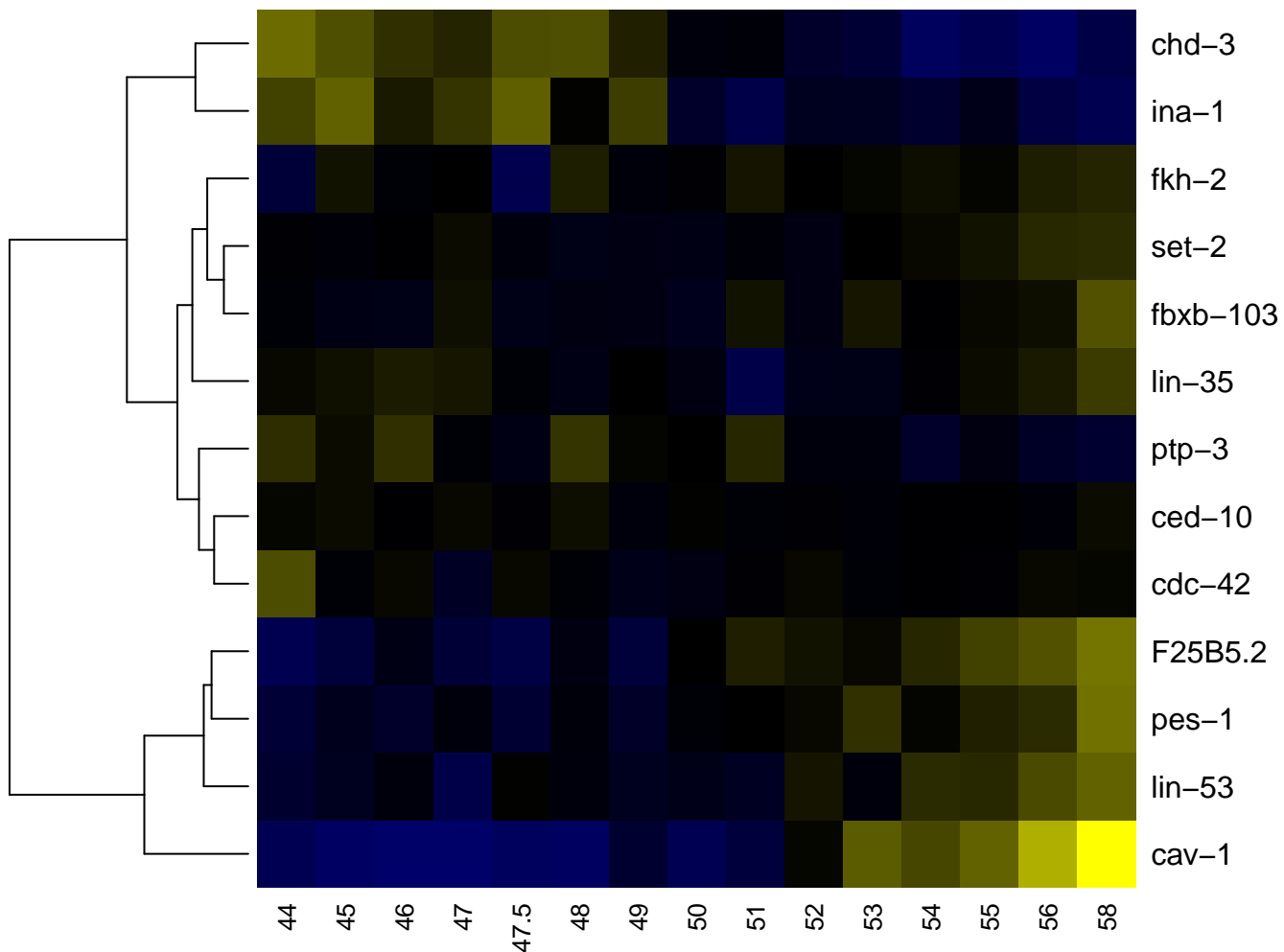
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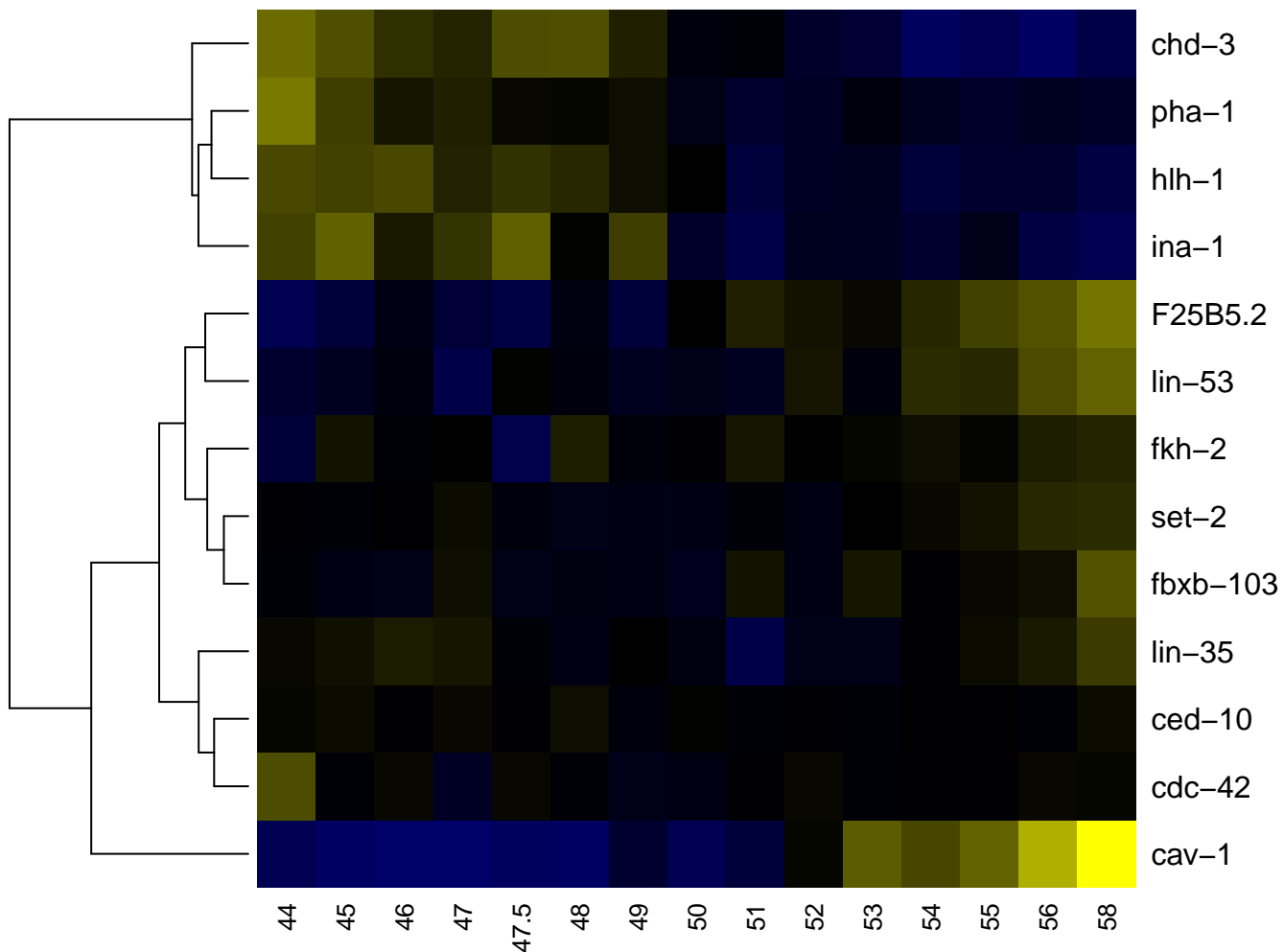
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Dppppp



Dppppp



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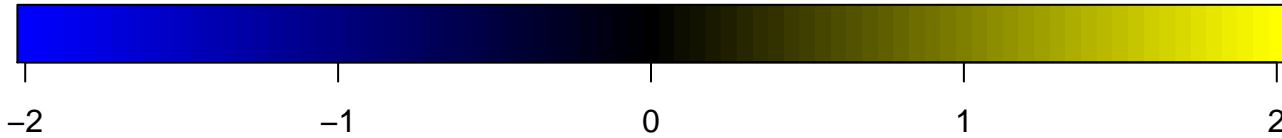
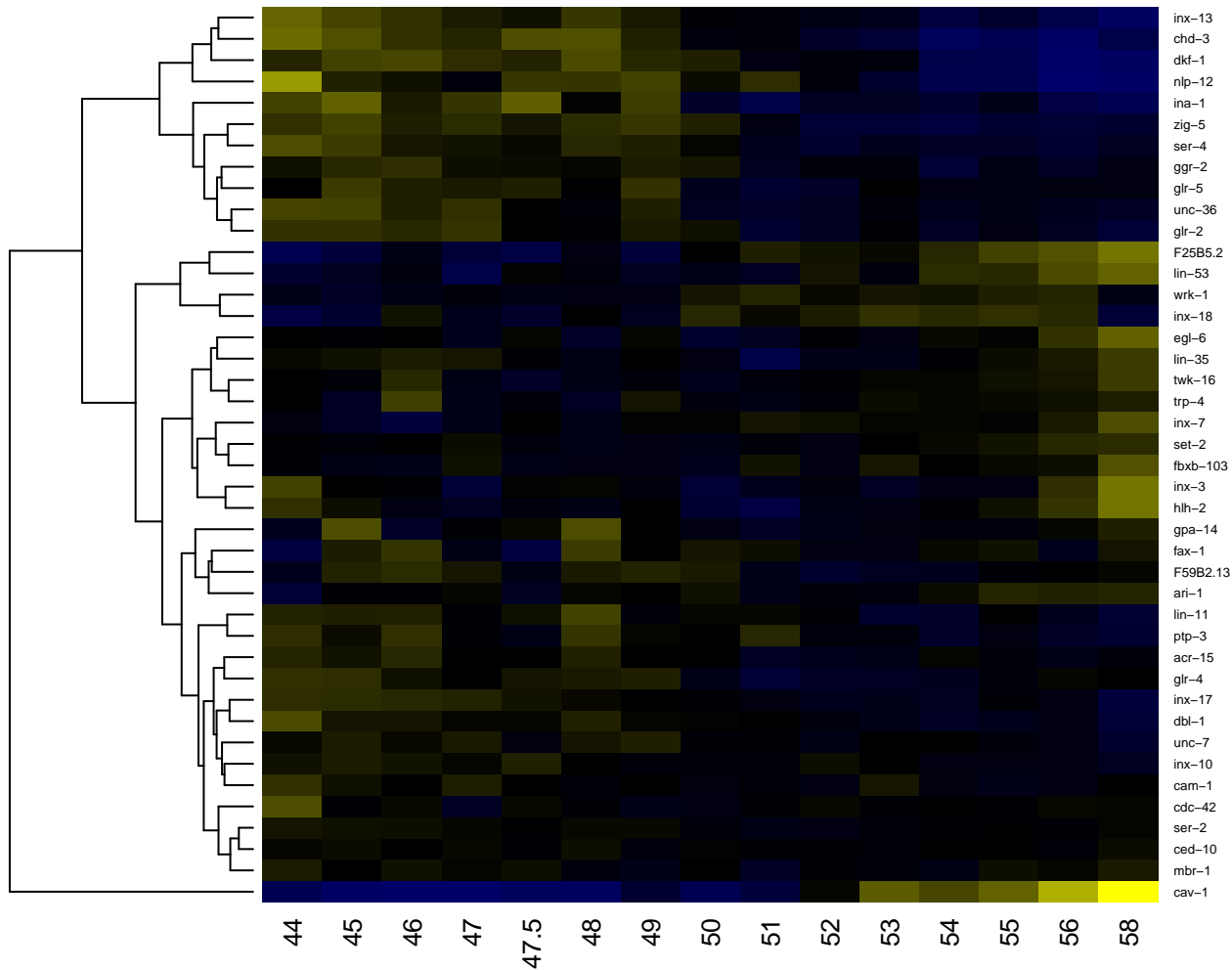
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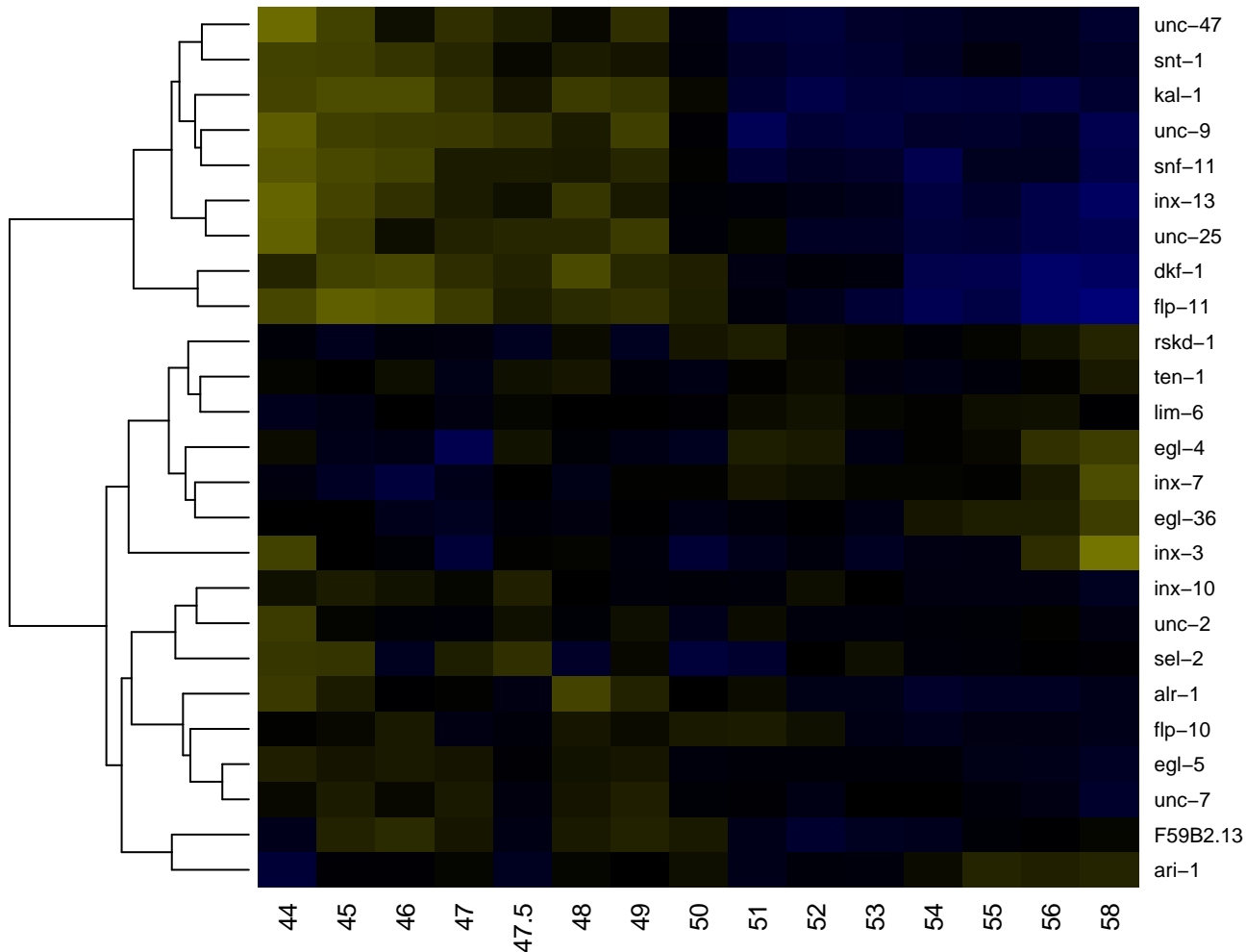
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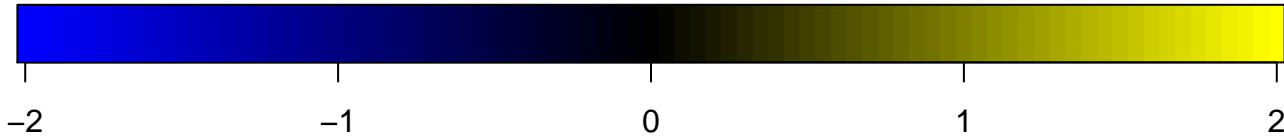
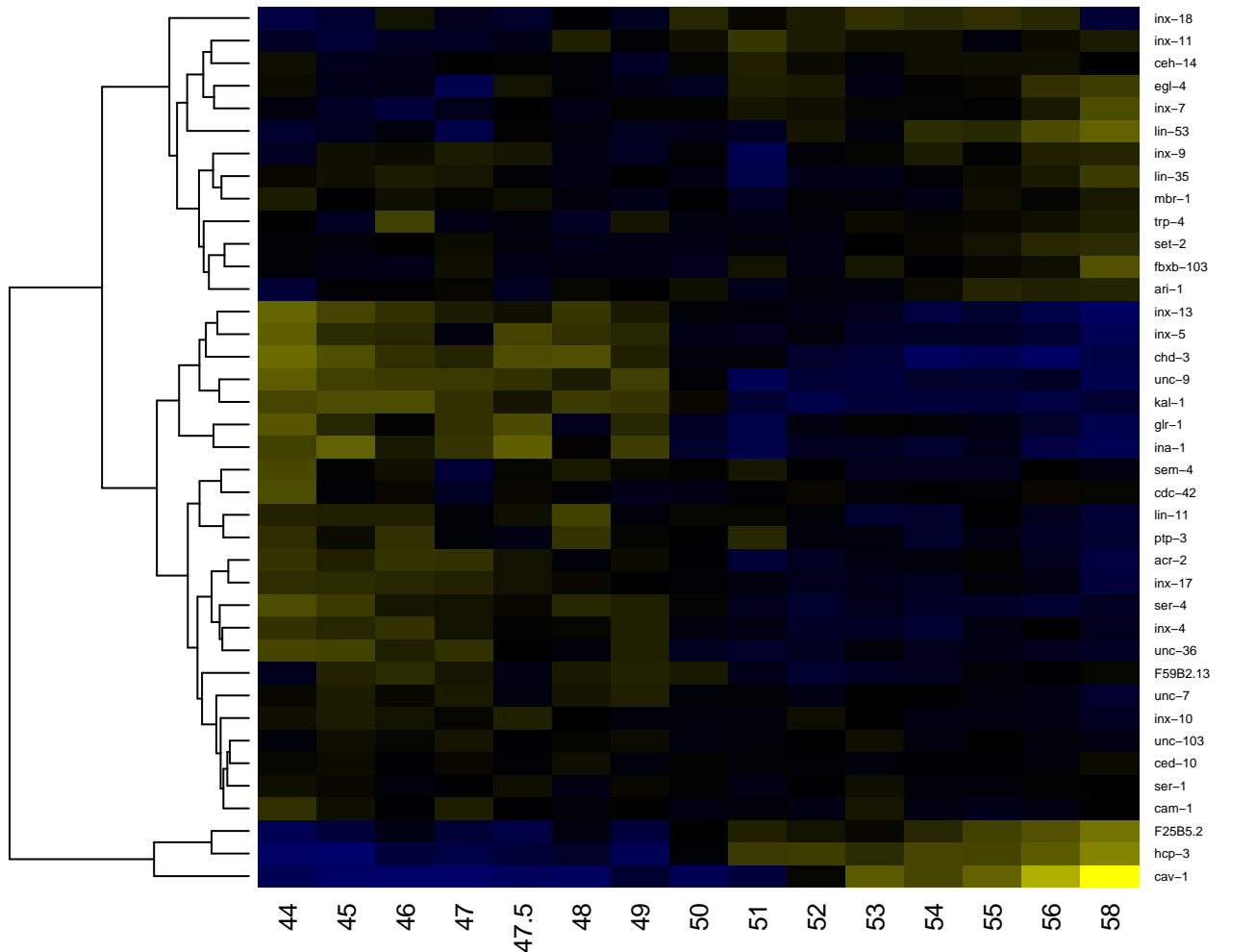
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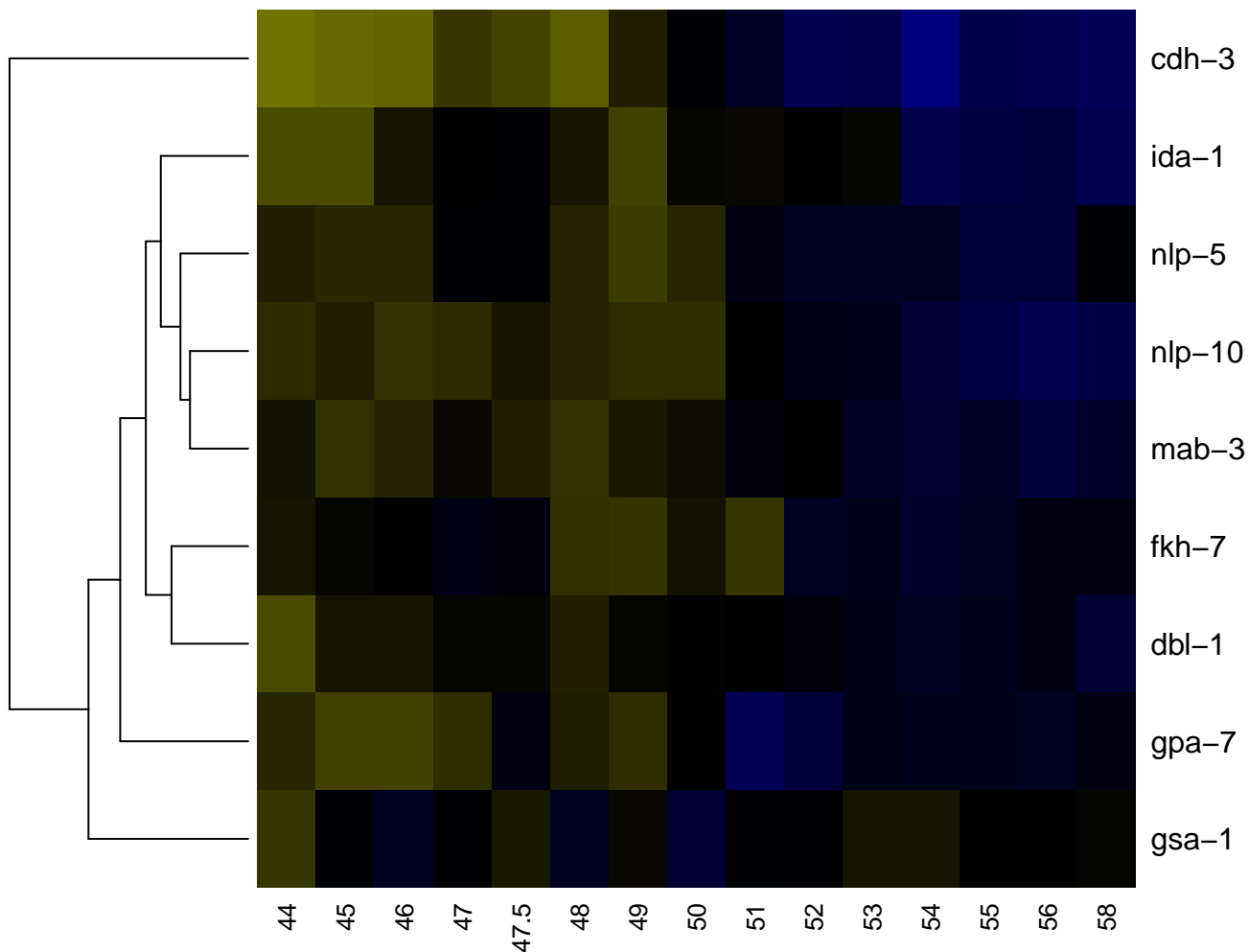
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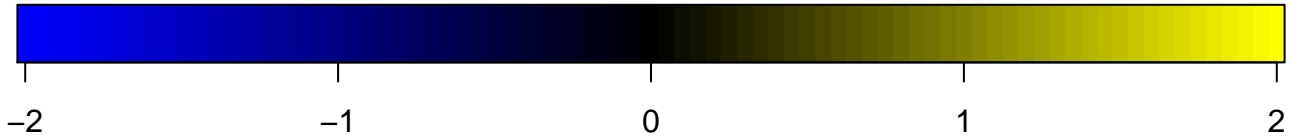
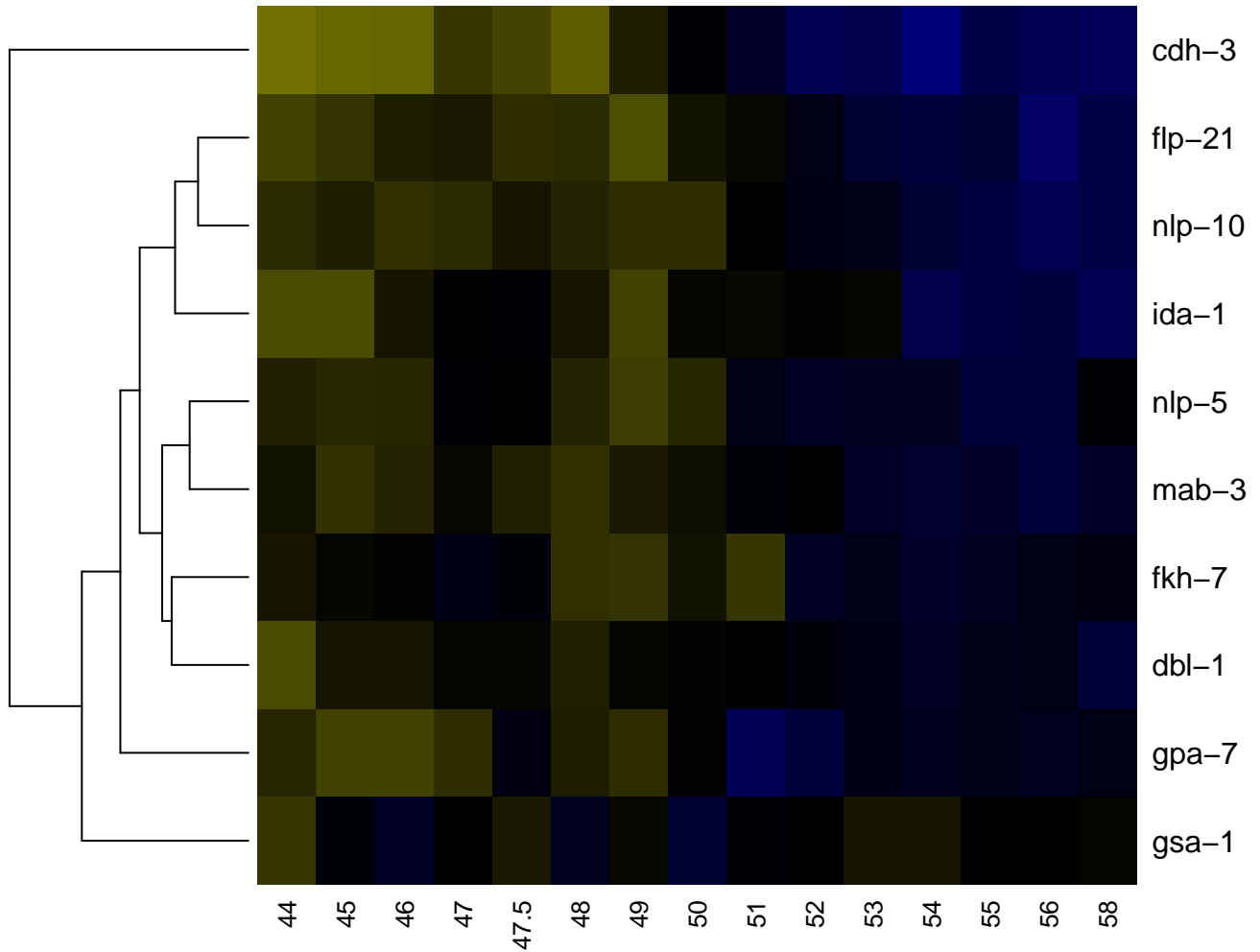
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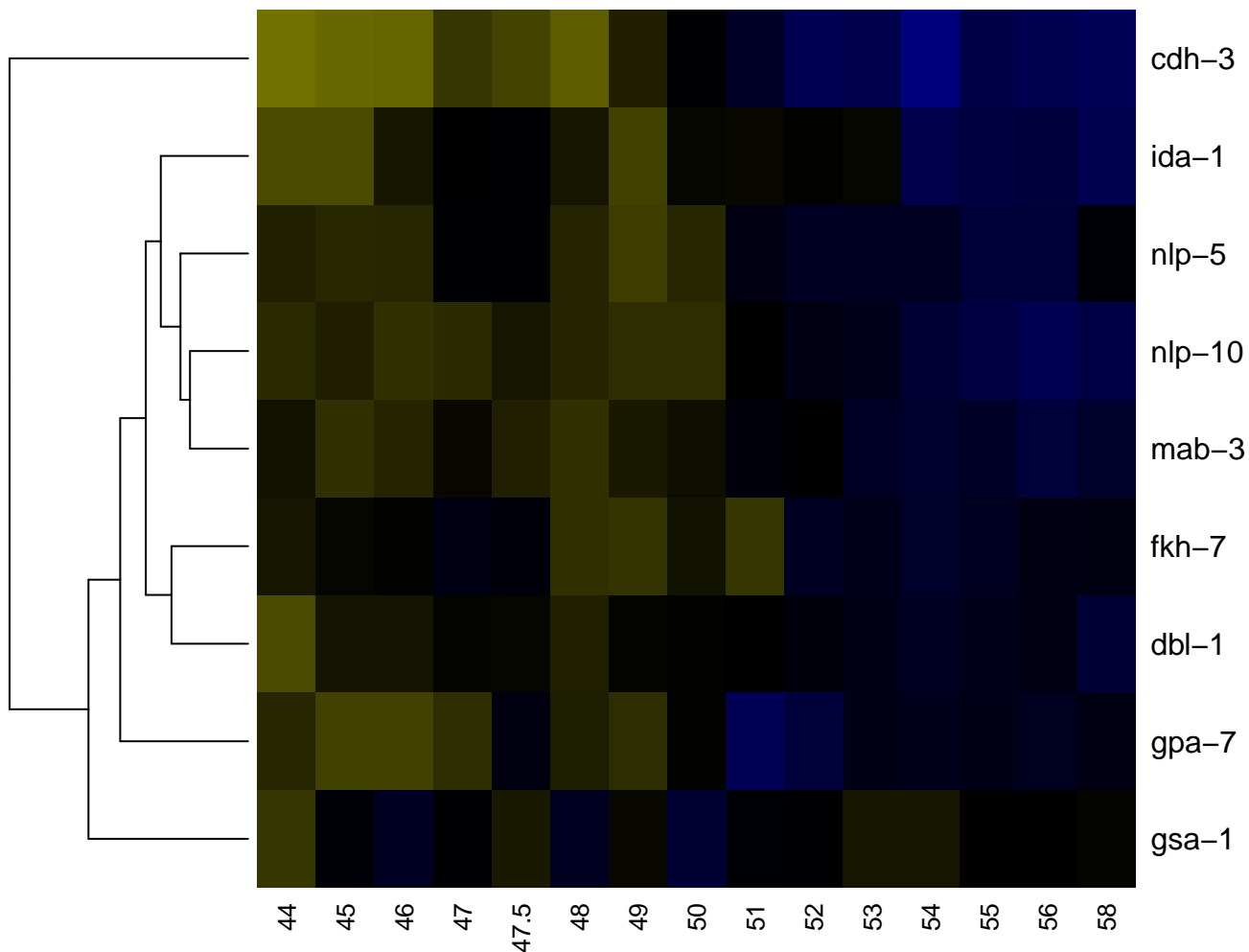
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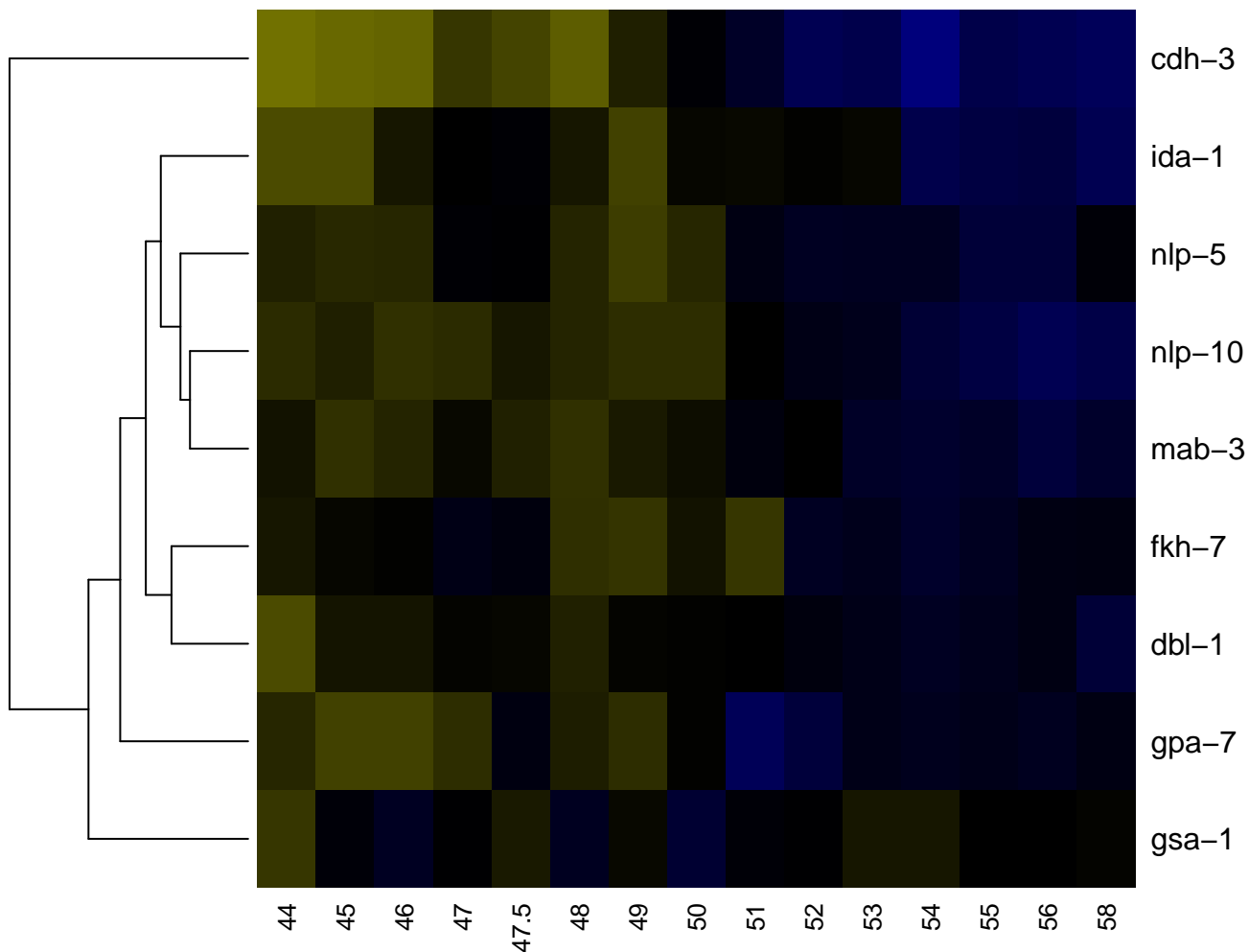
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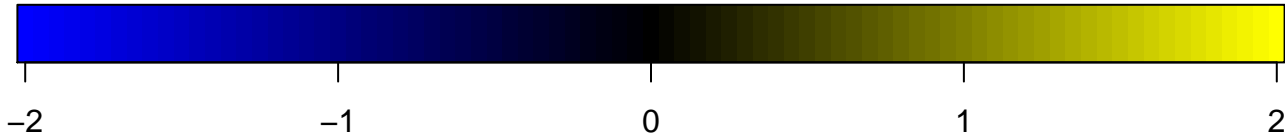
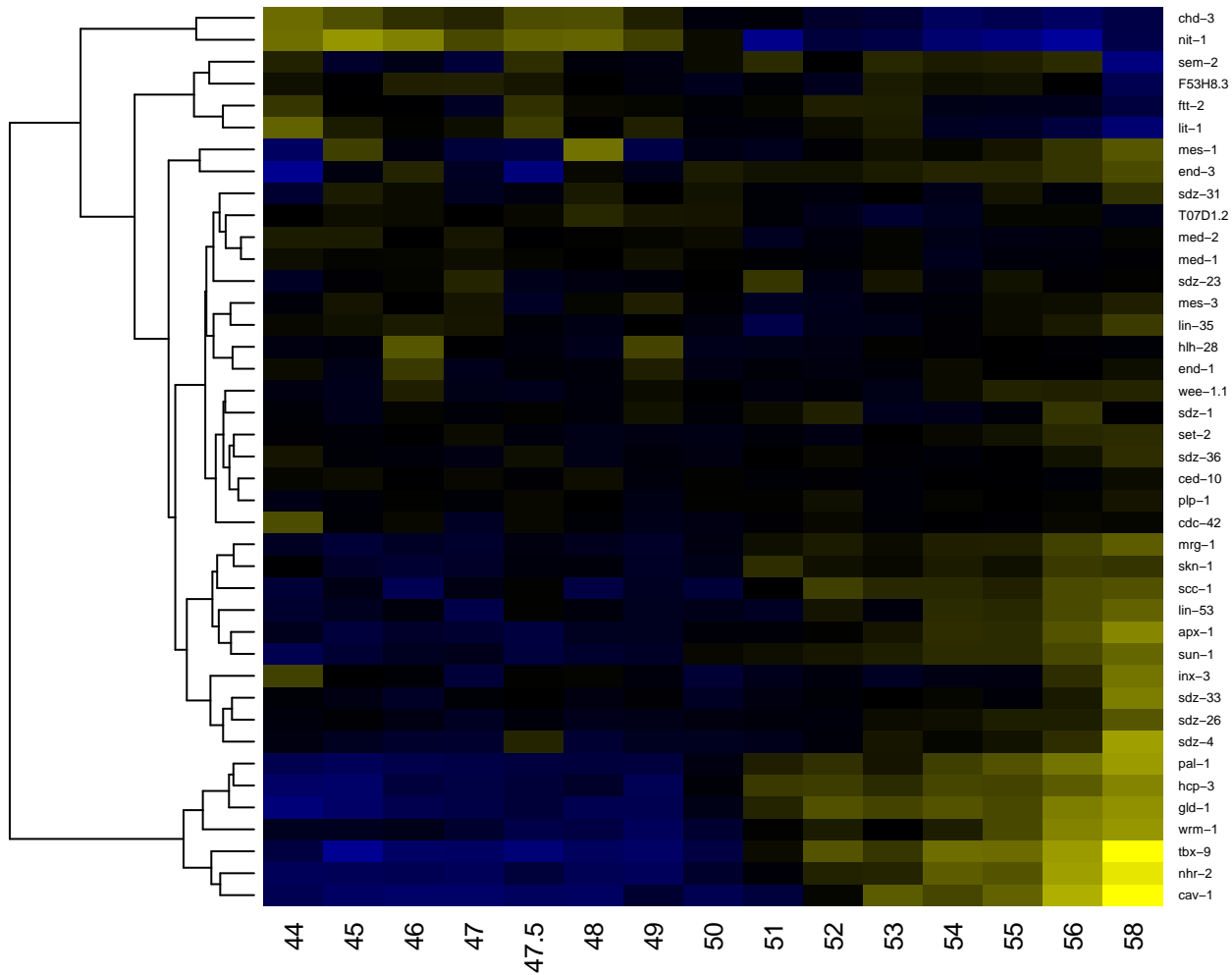
DX1/2



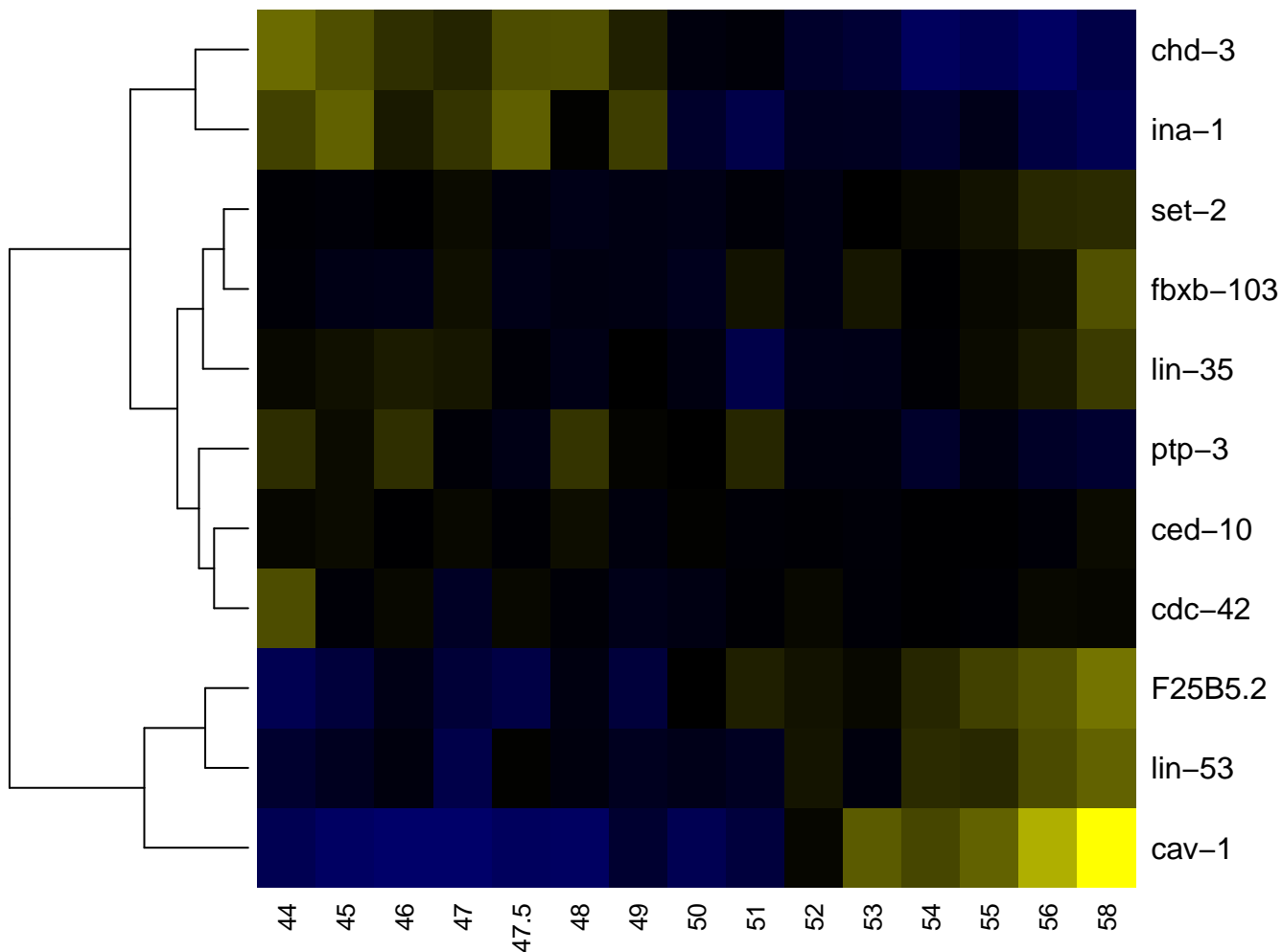
DX3/4



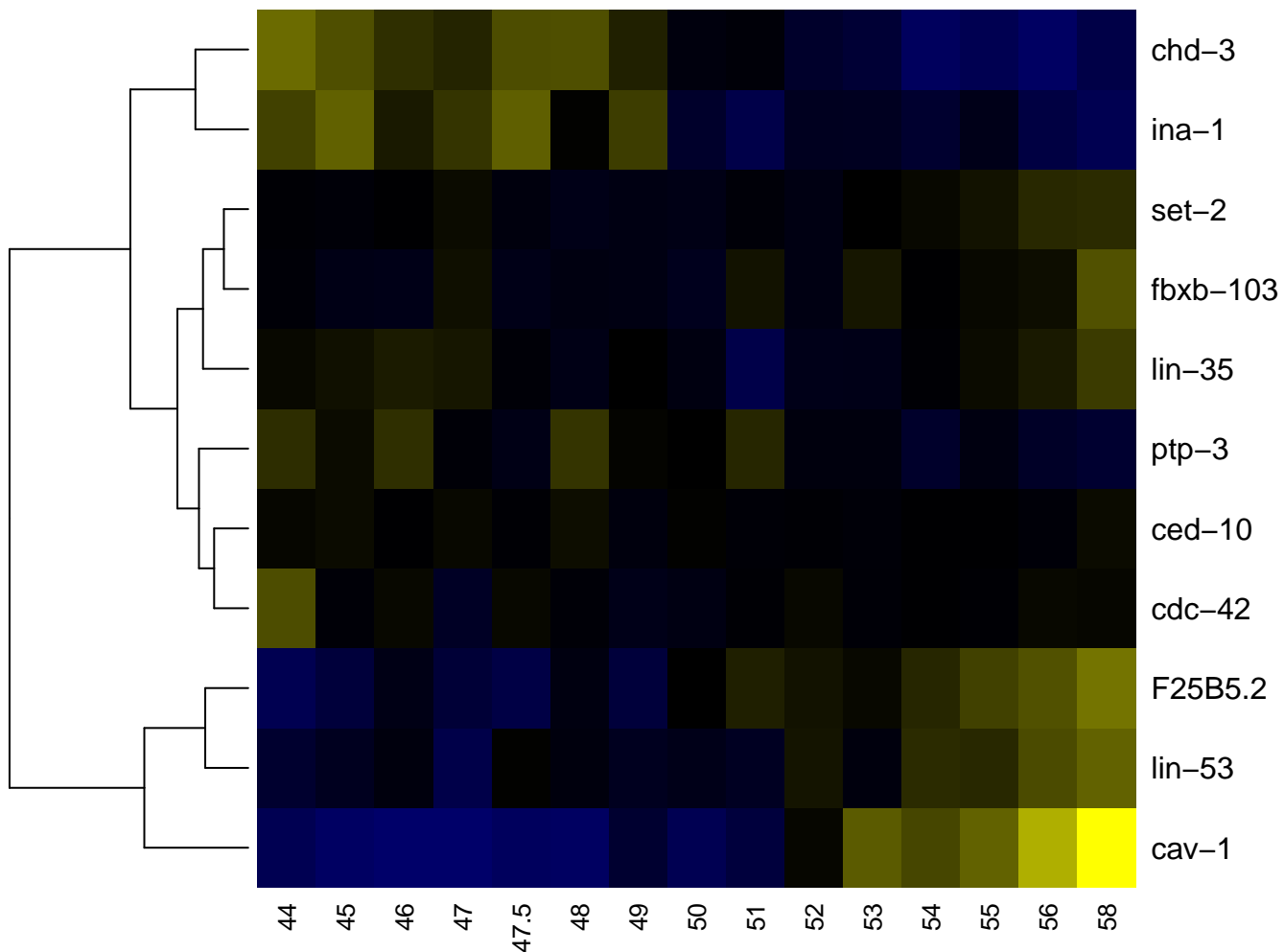
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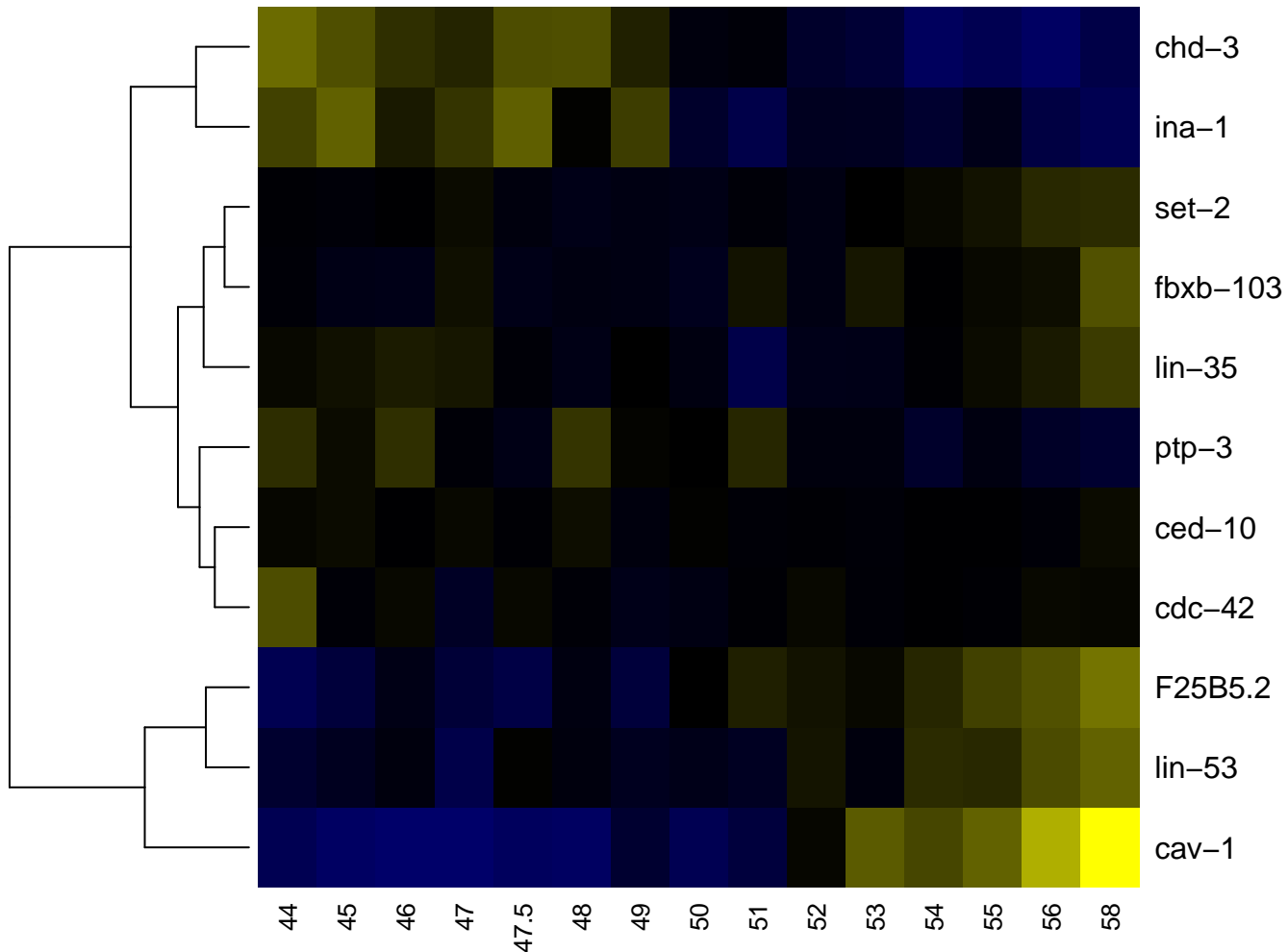
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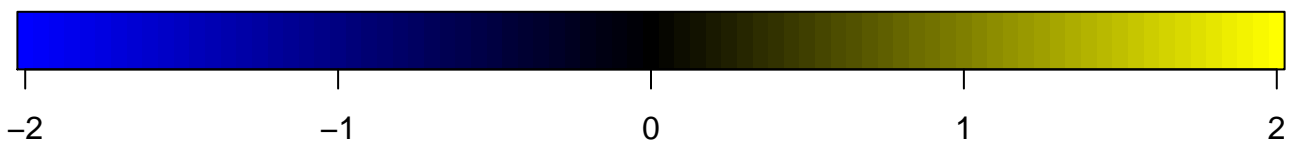
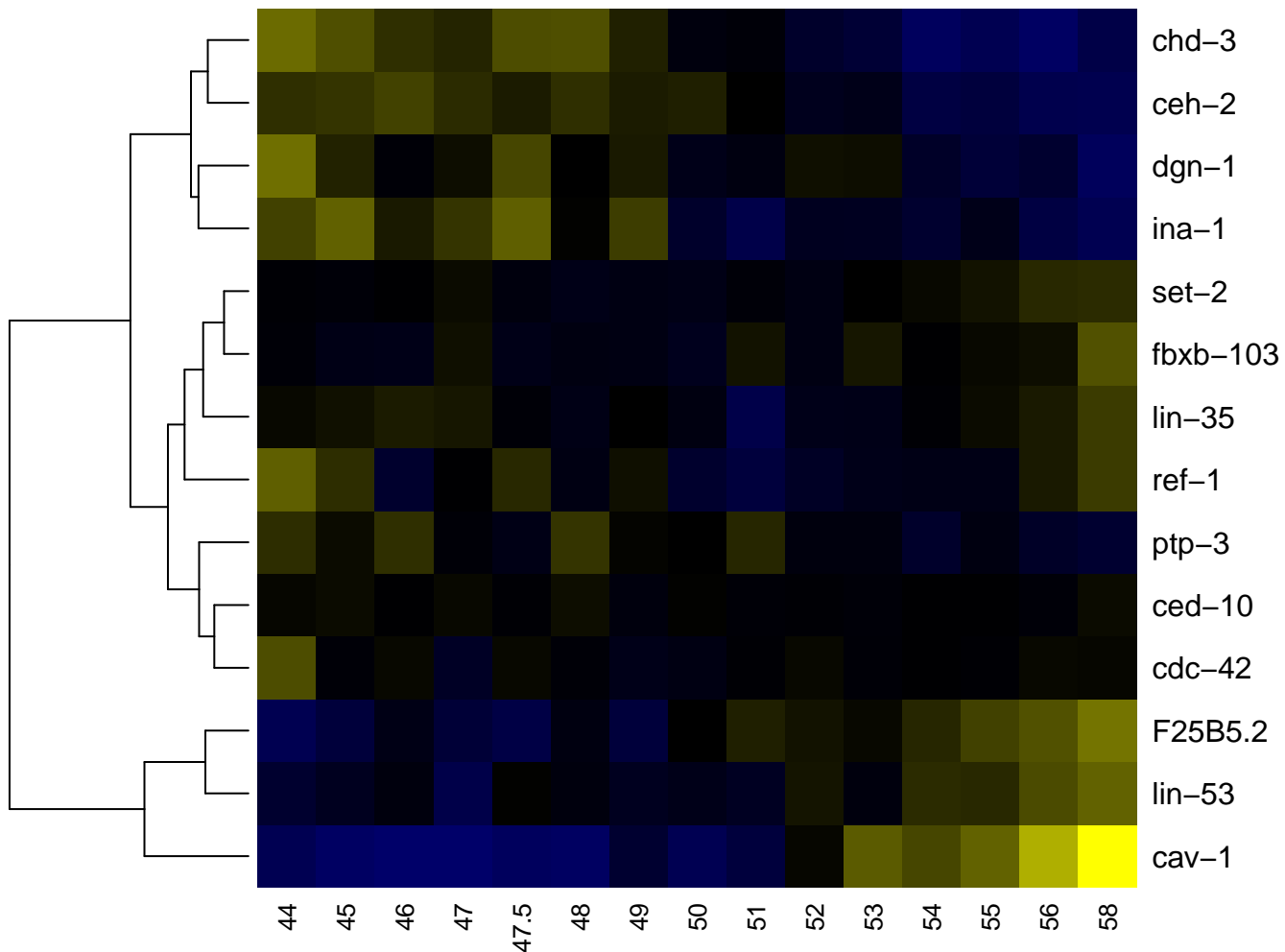
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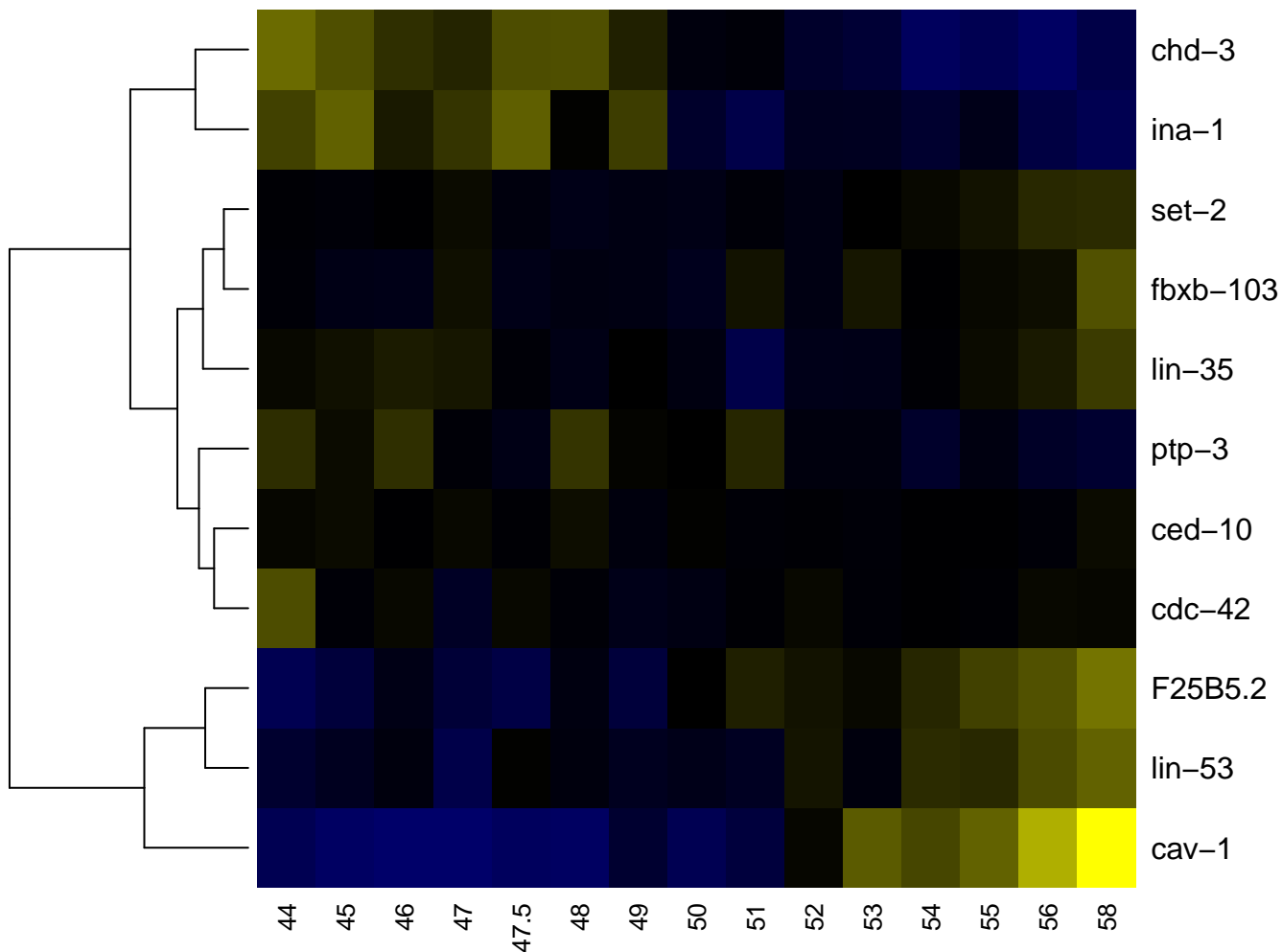
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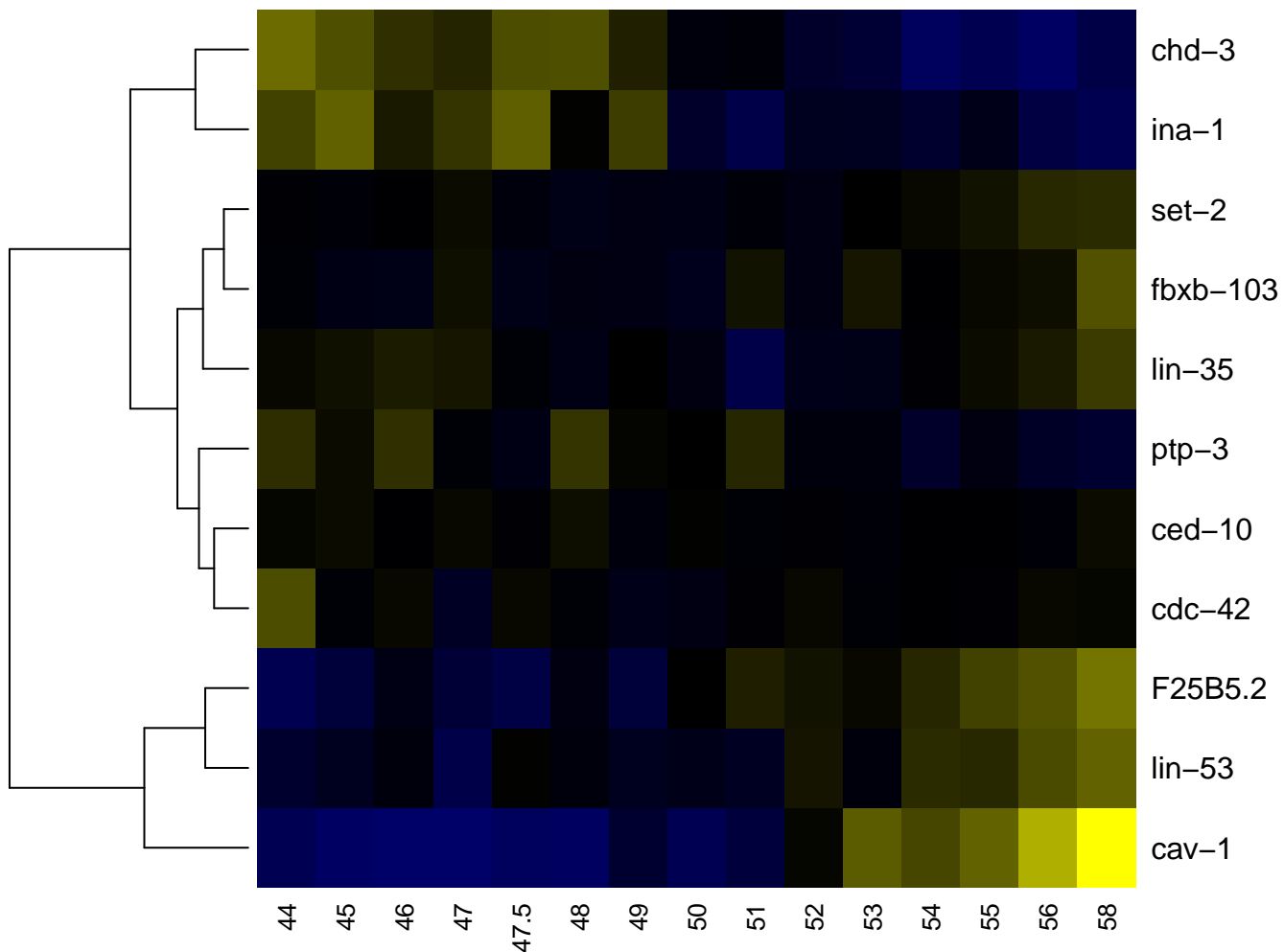
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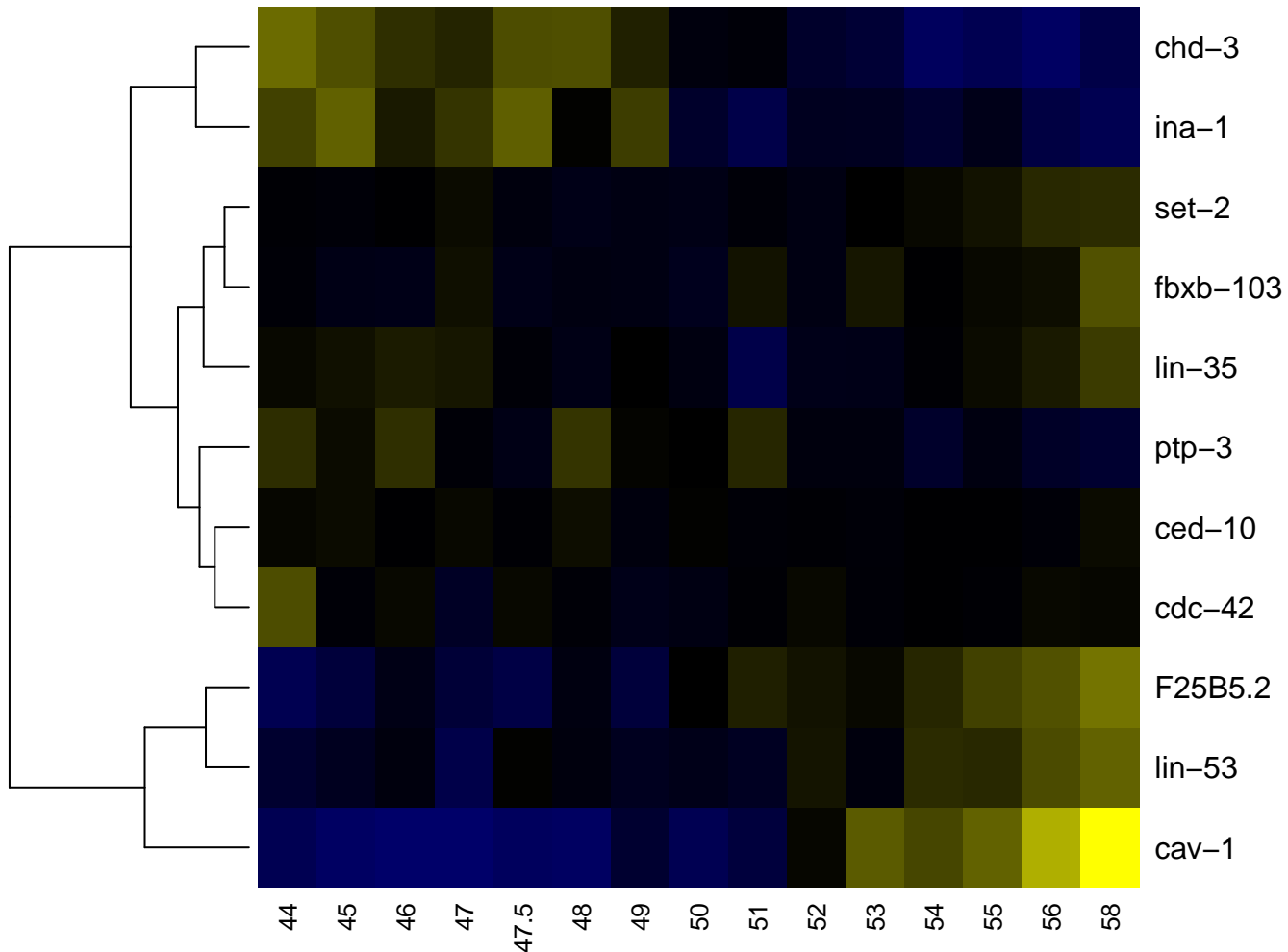
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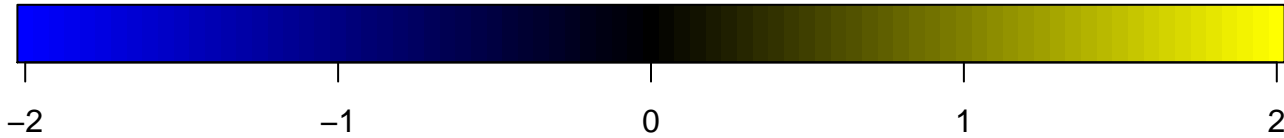
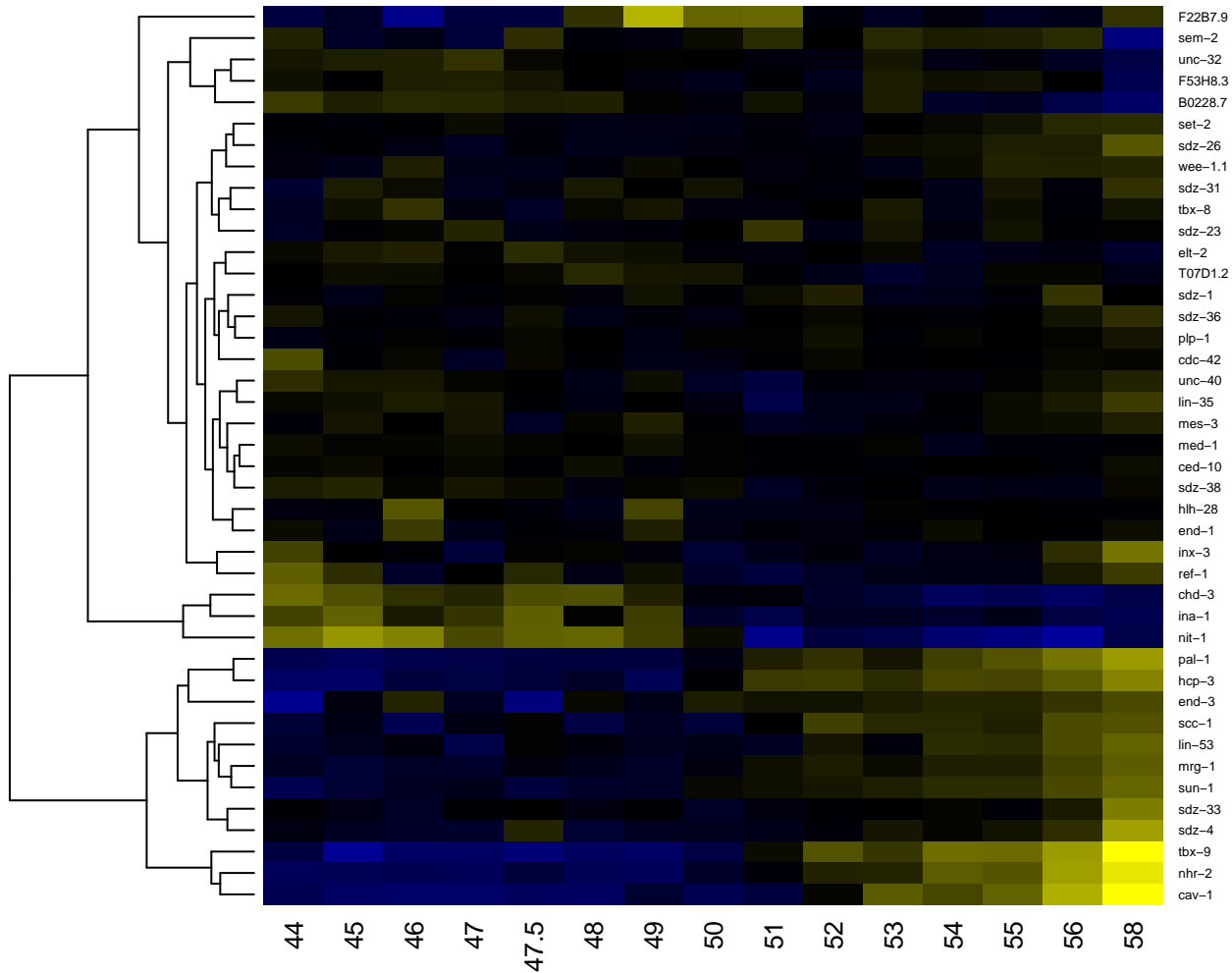
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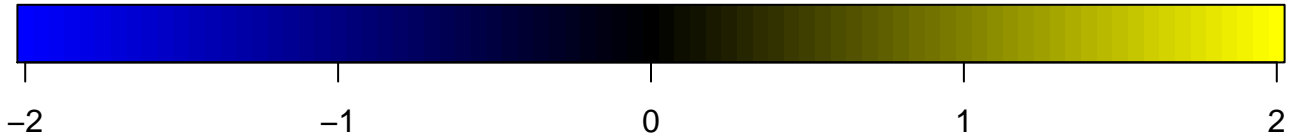
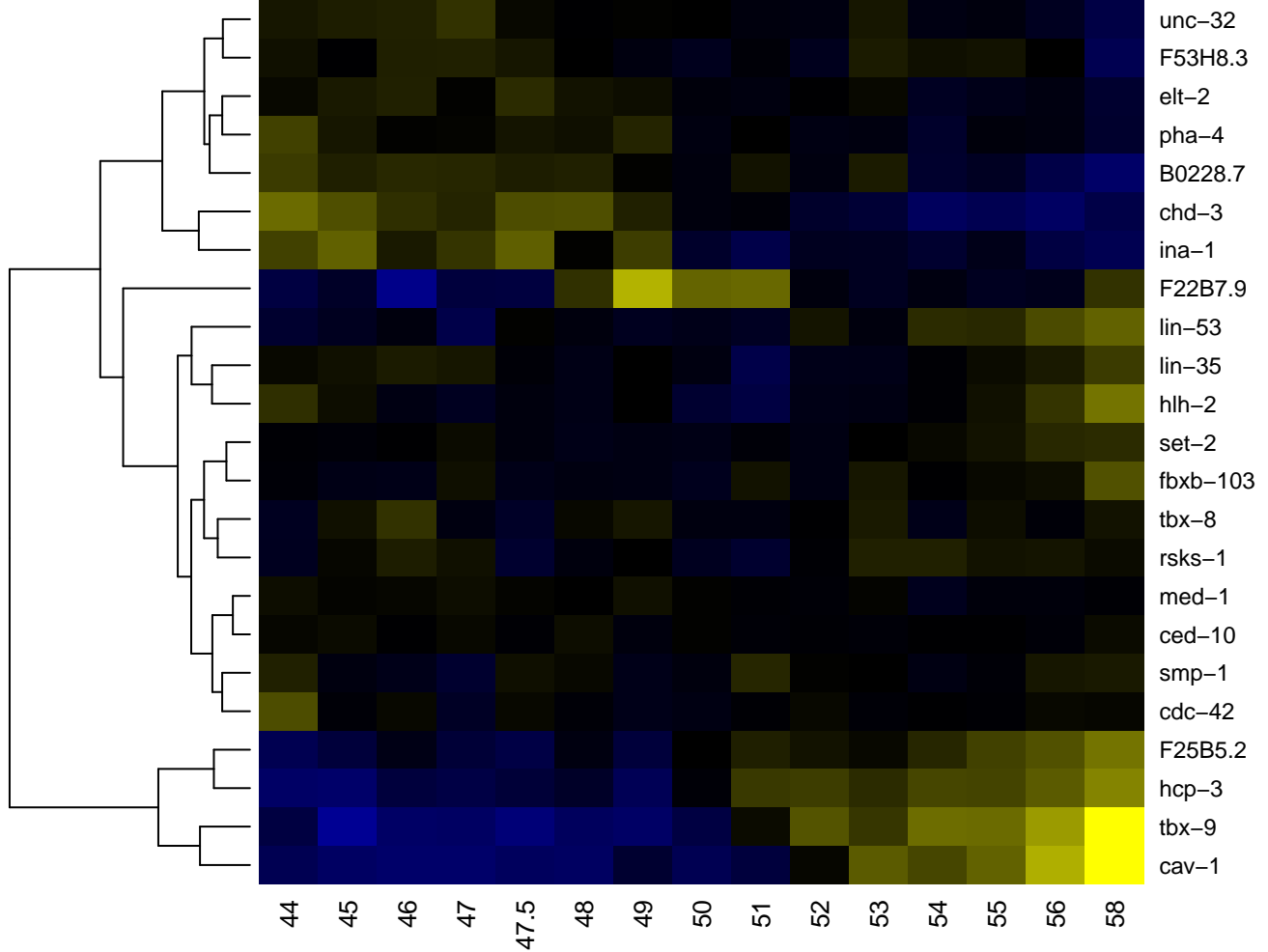
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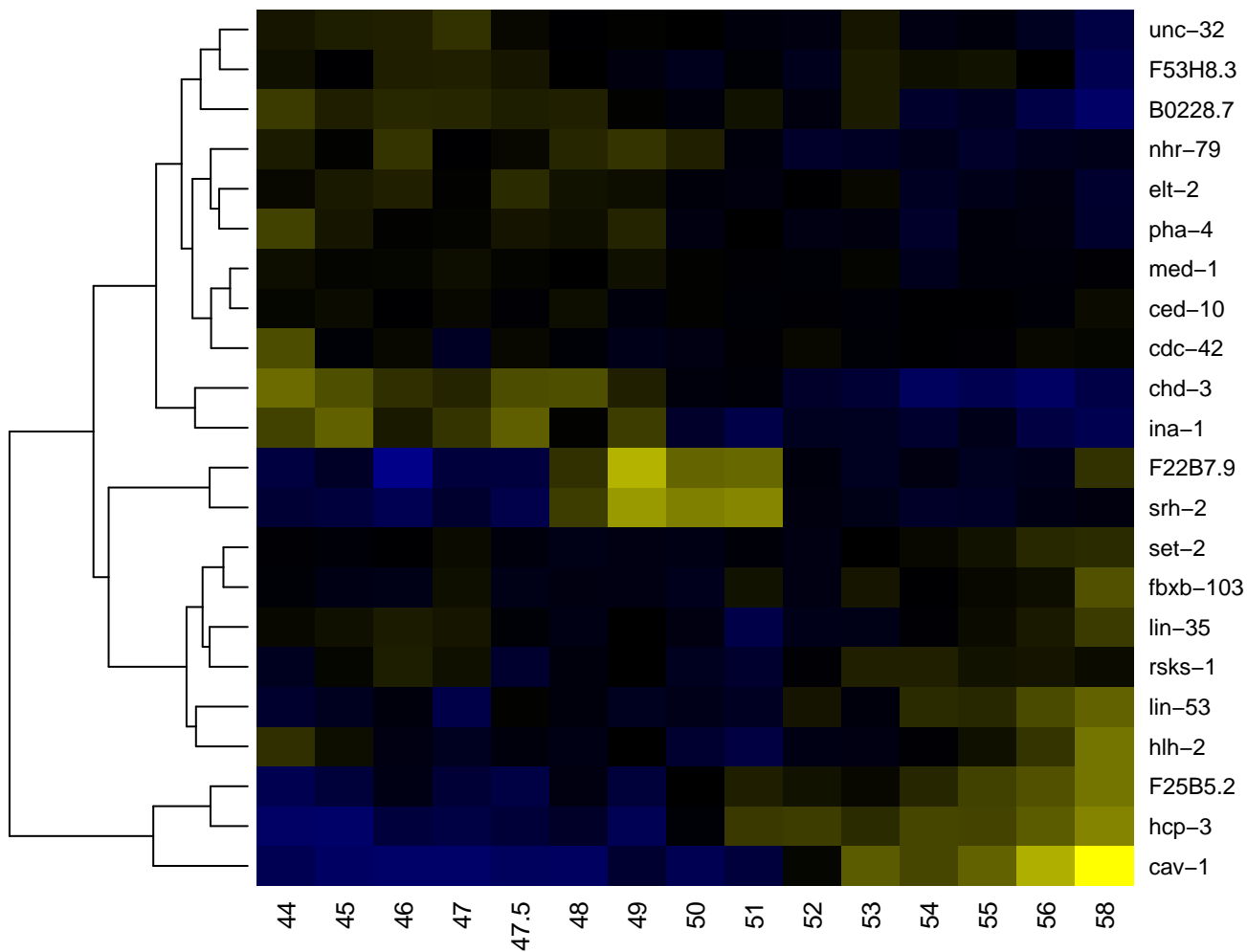
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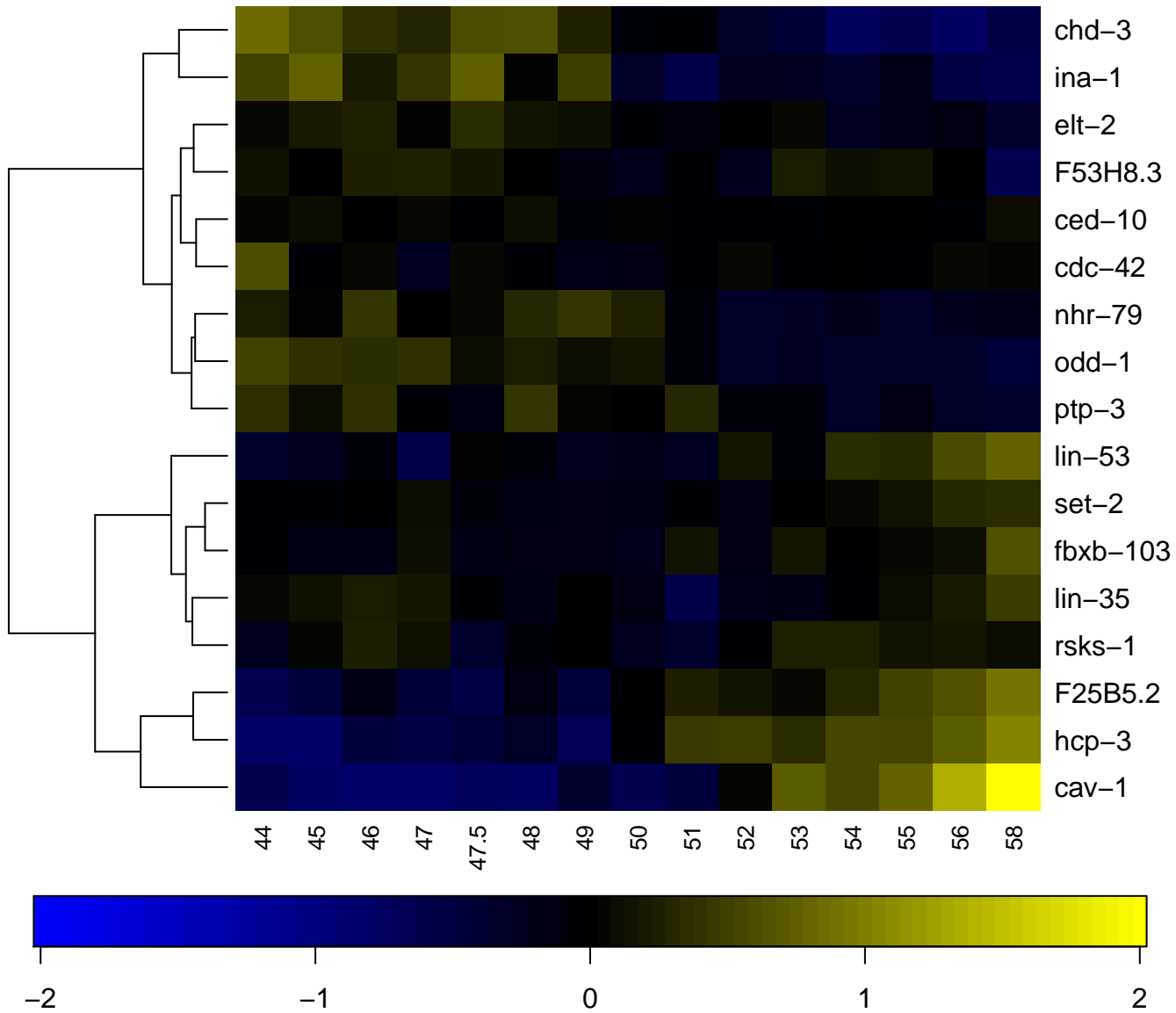
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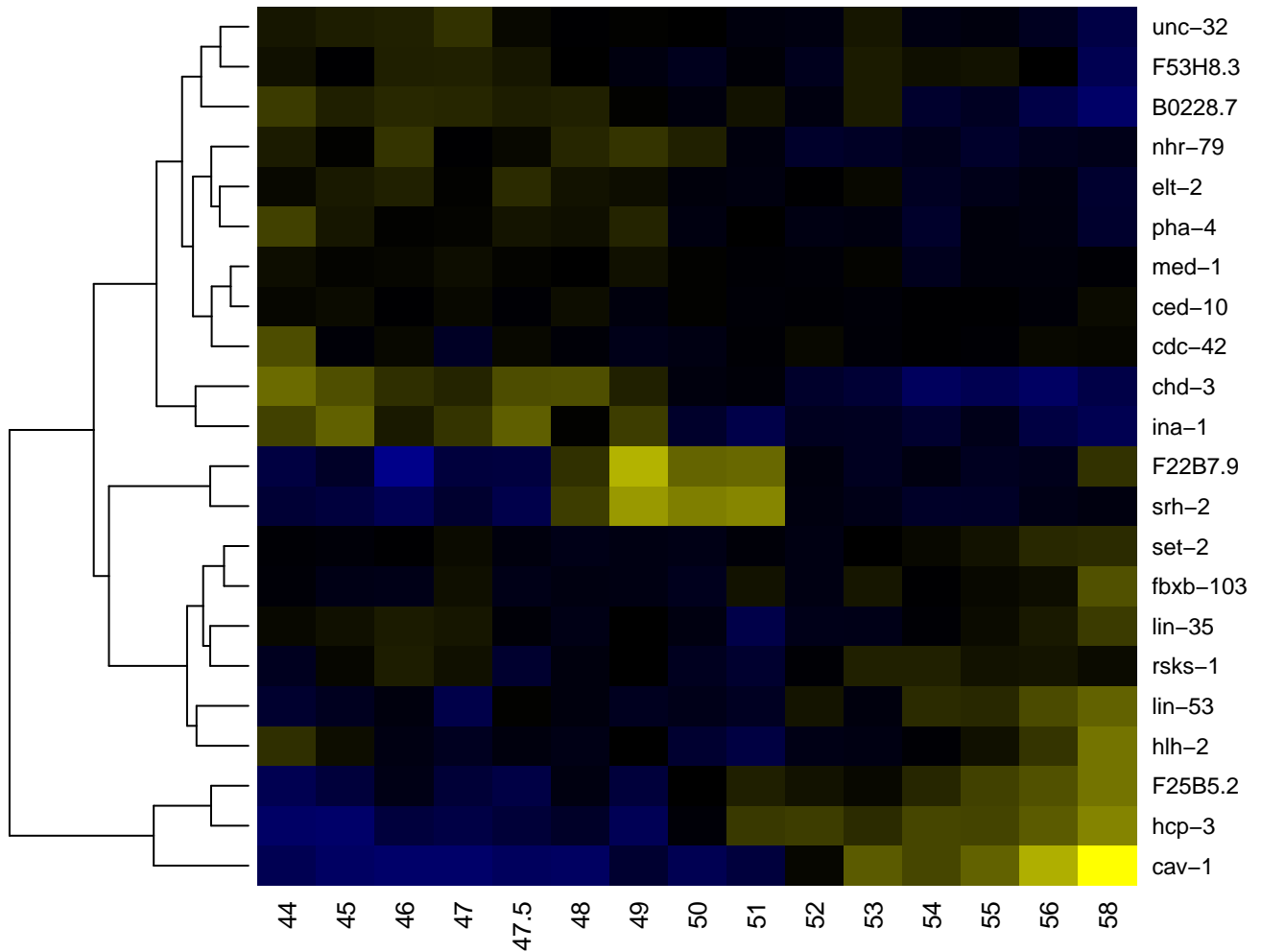
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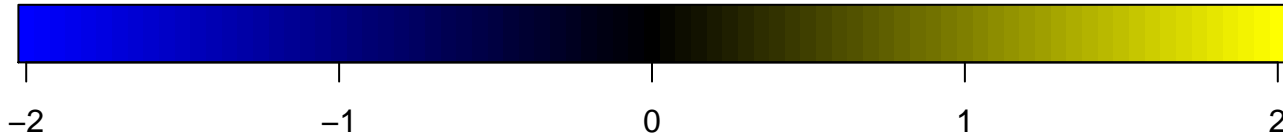
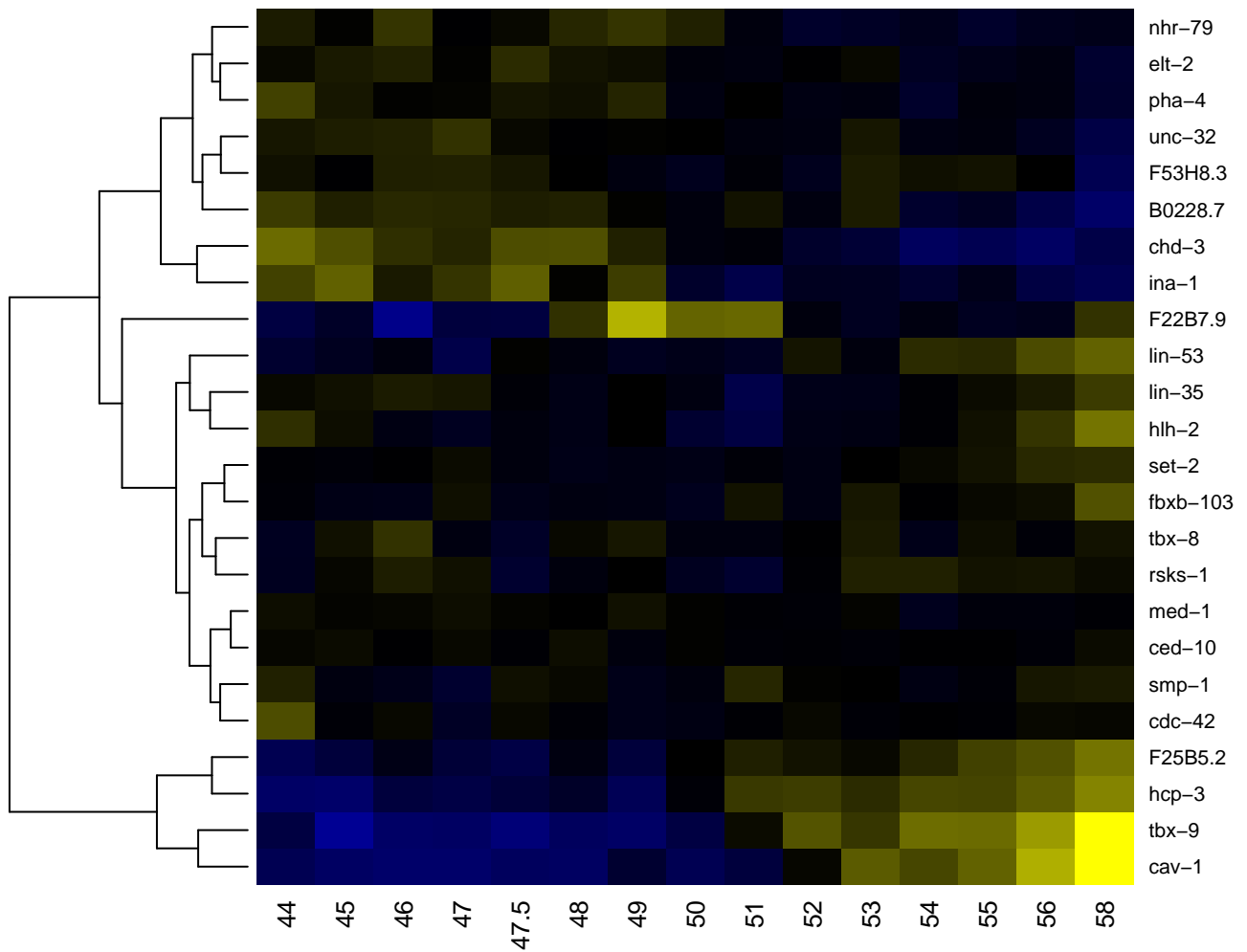
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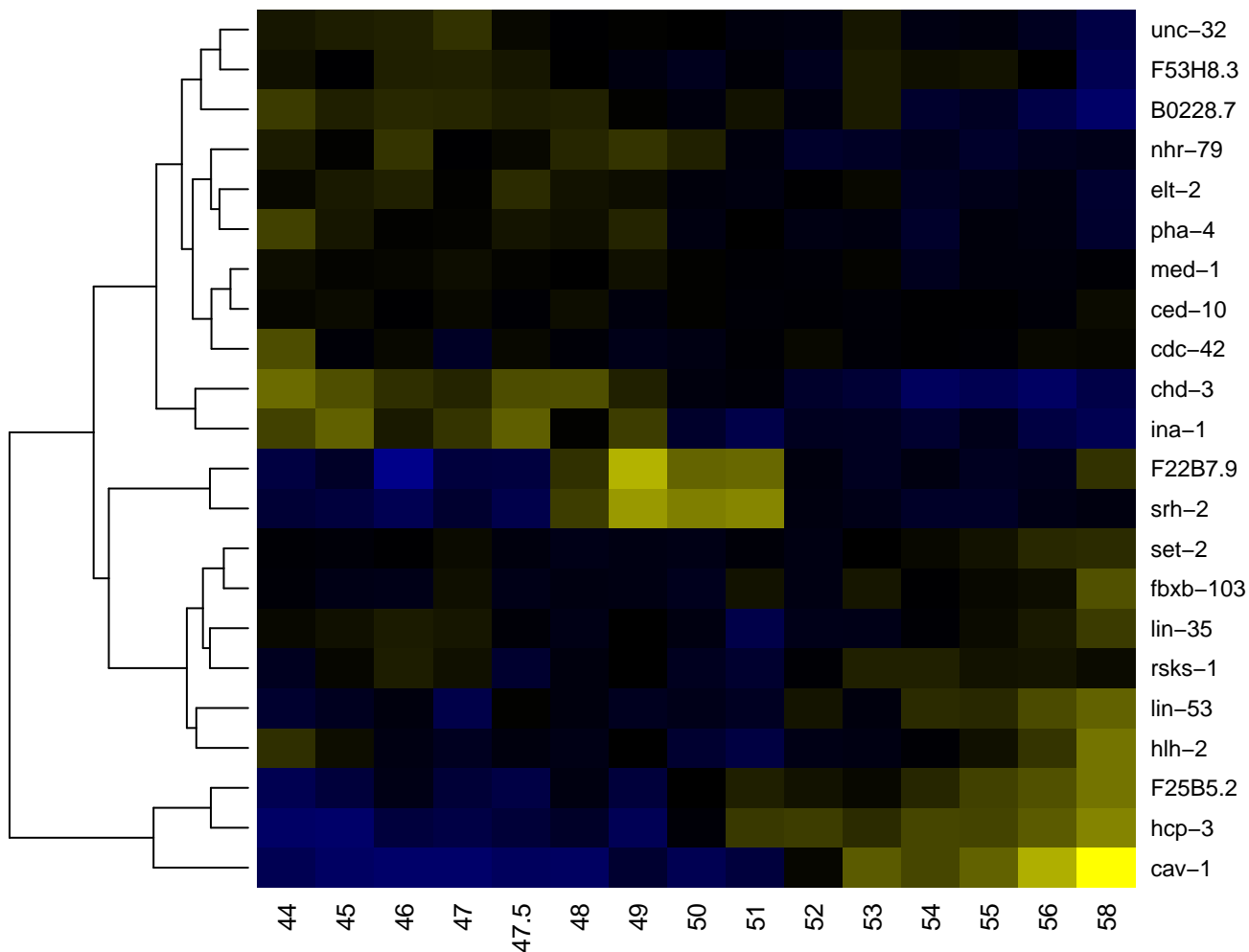
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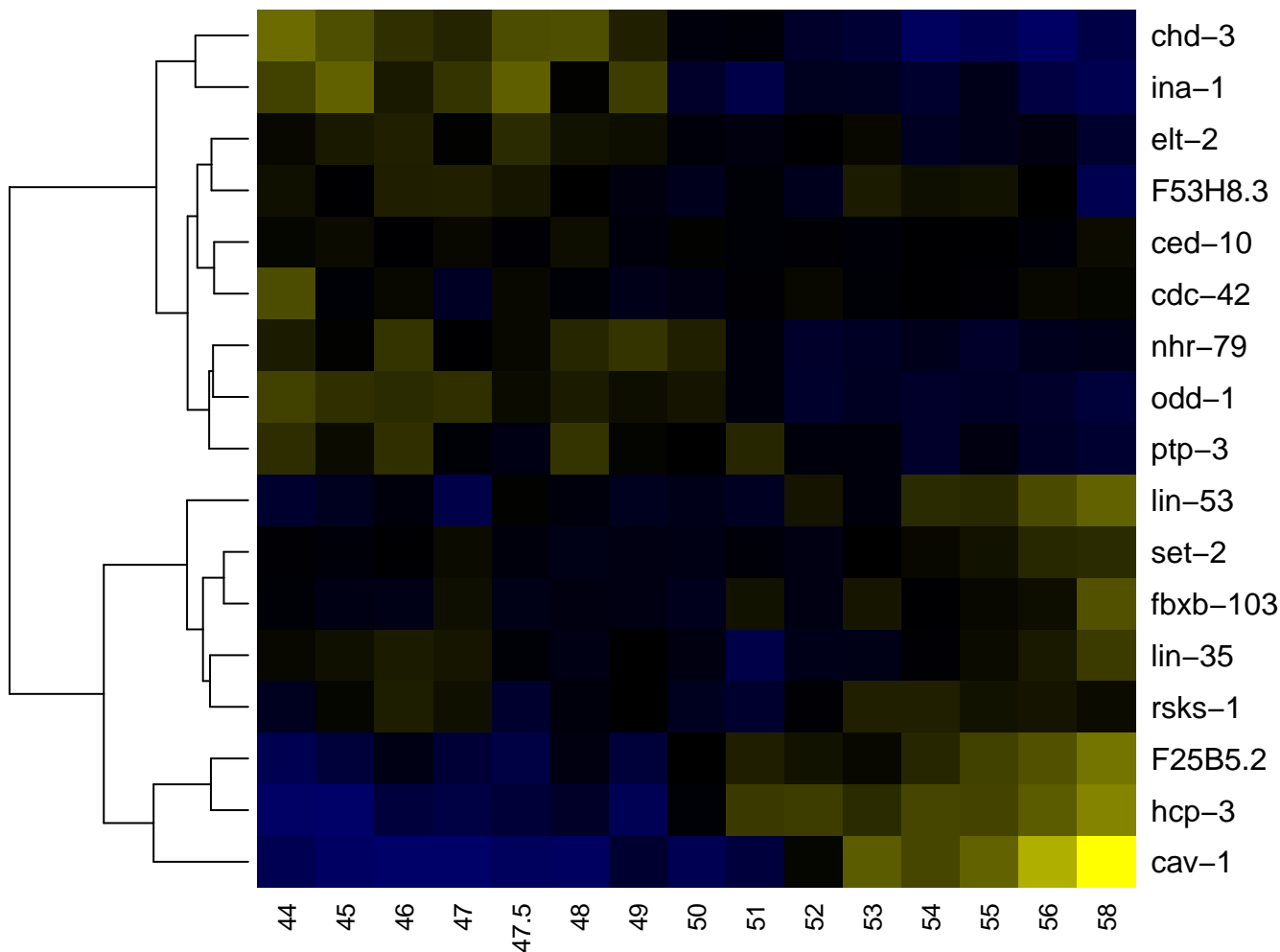
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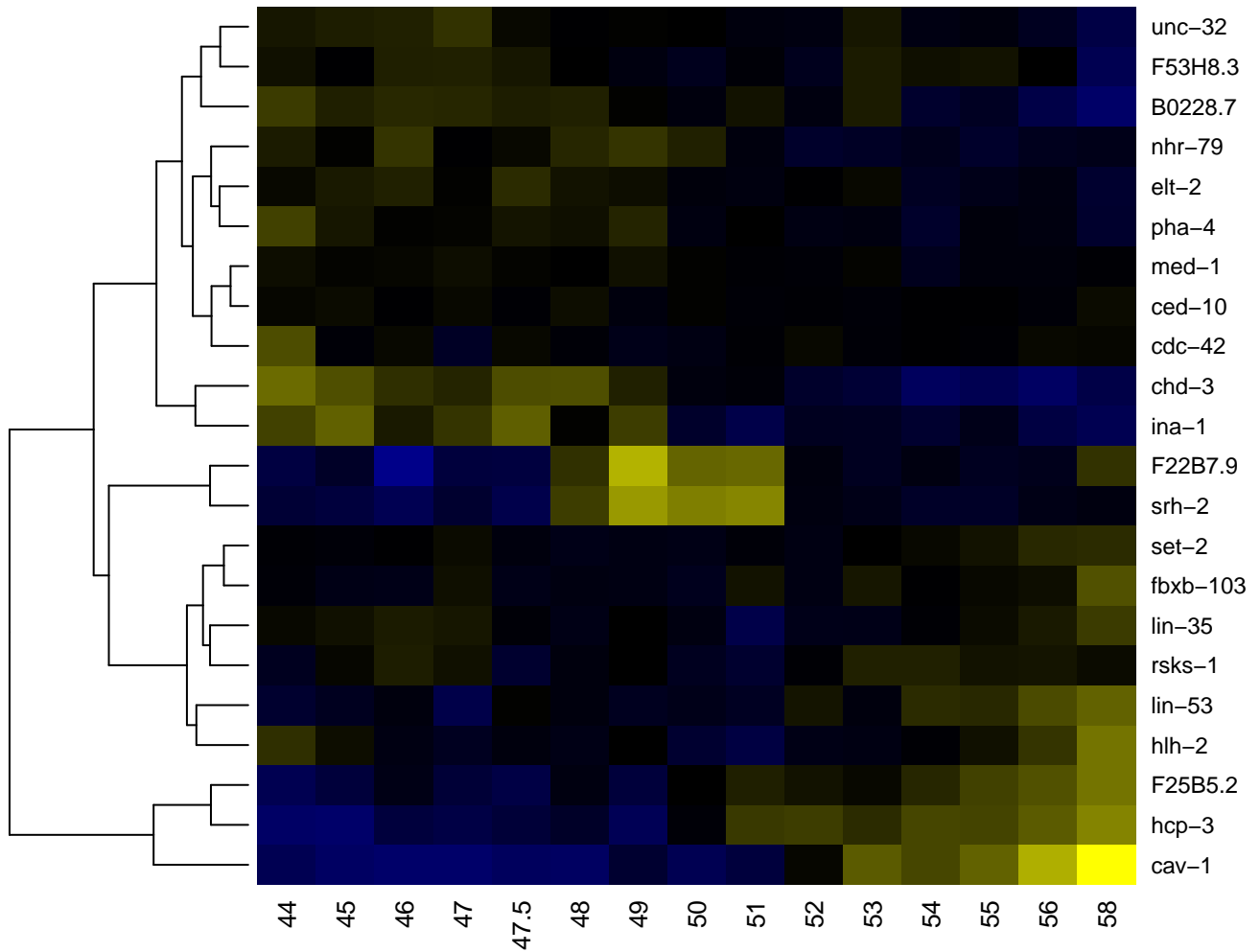
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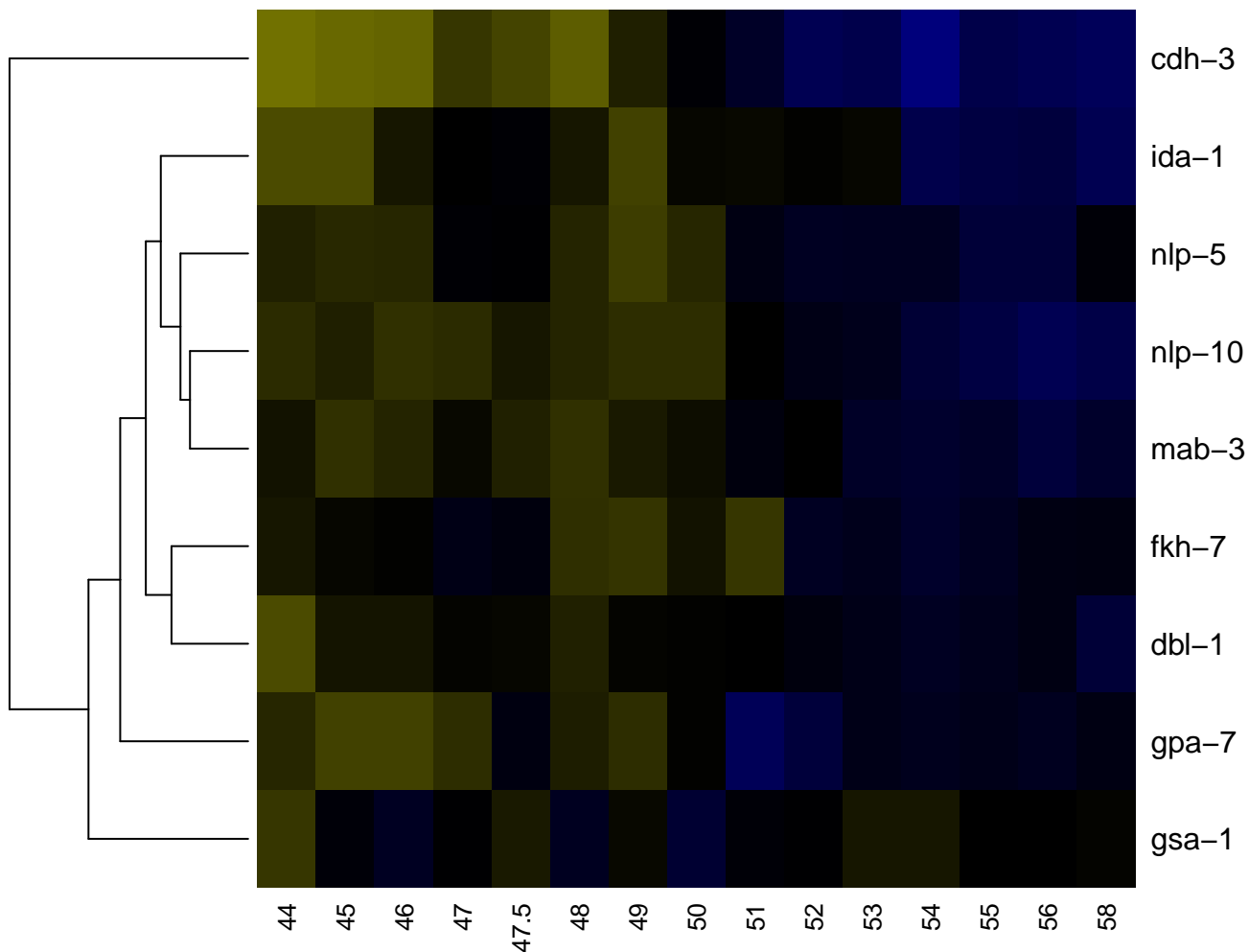
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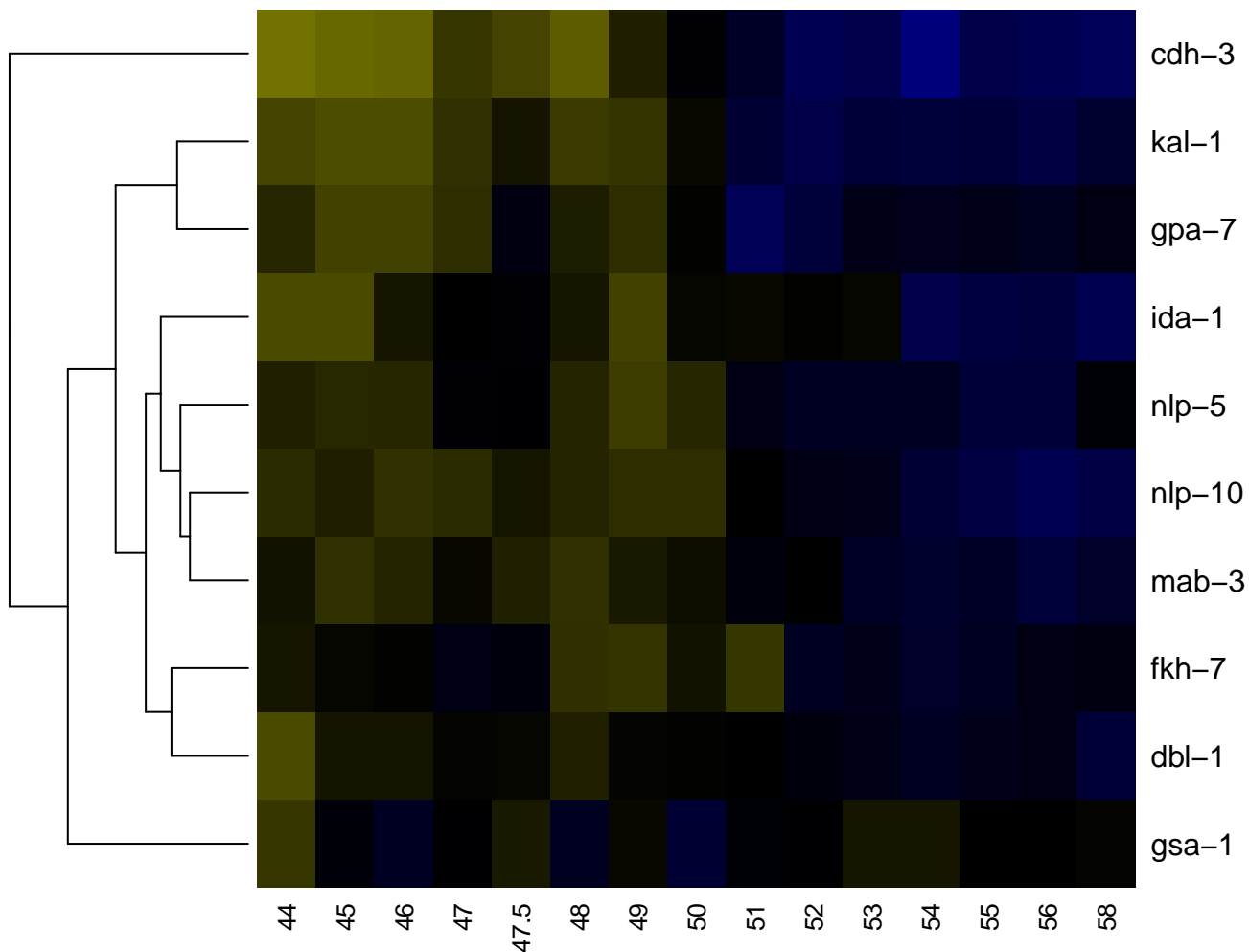
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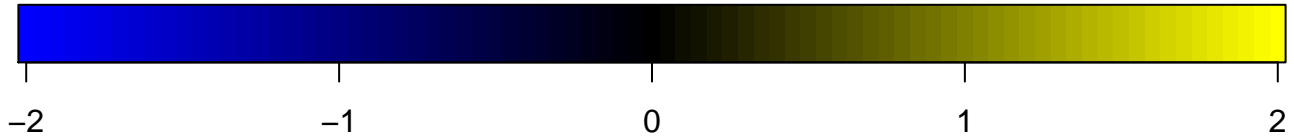
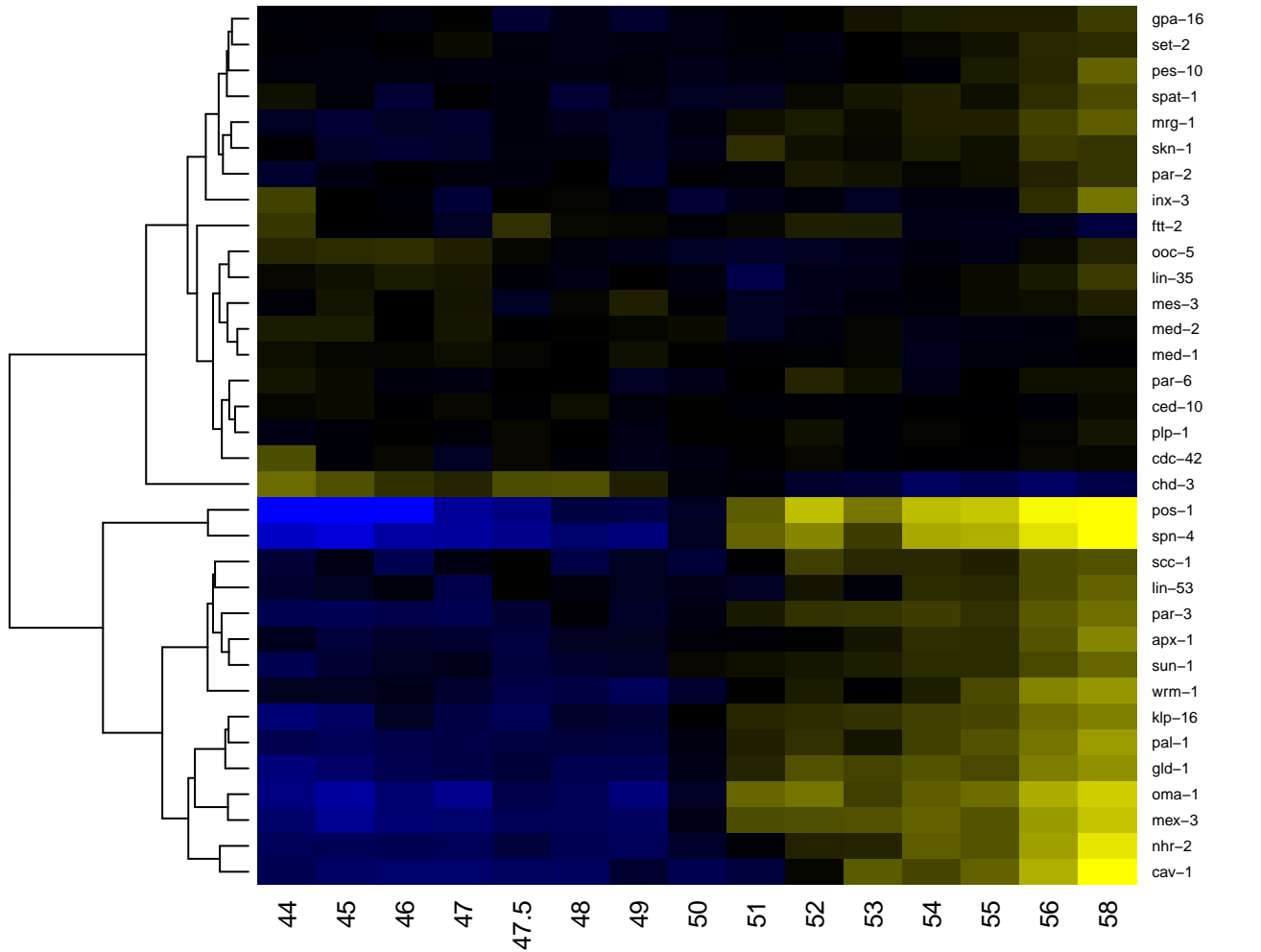
EF1/2



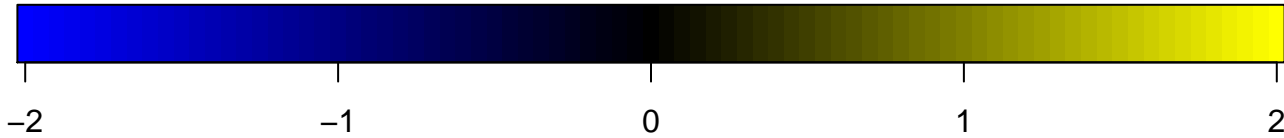
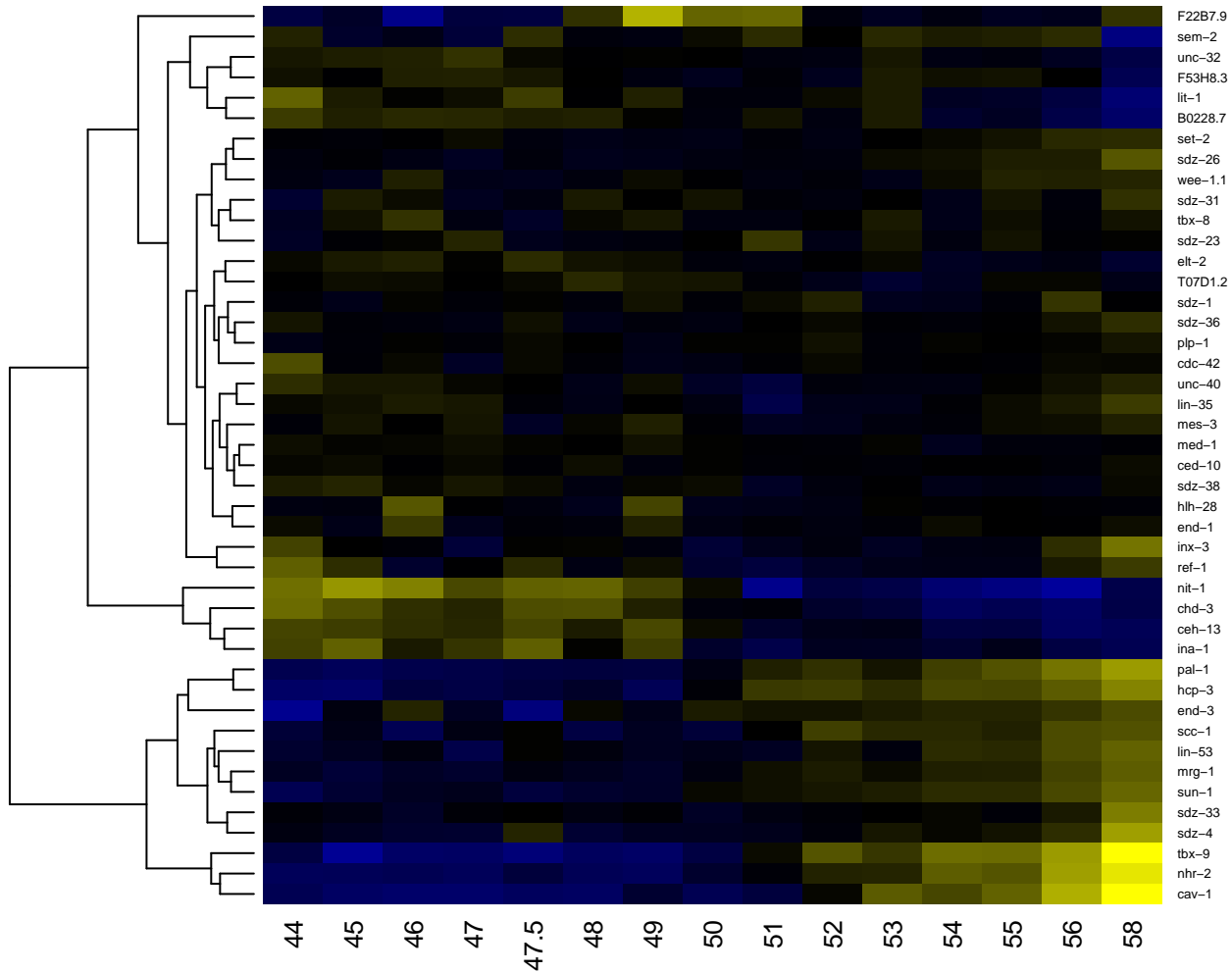
EF3/4



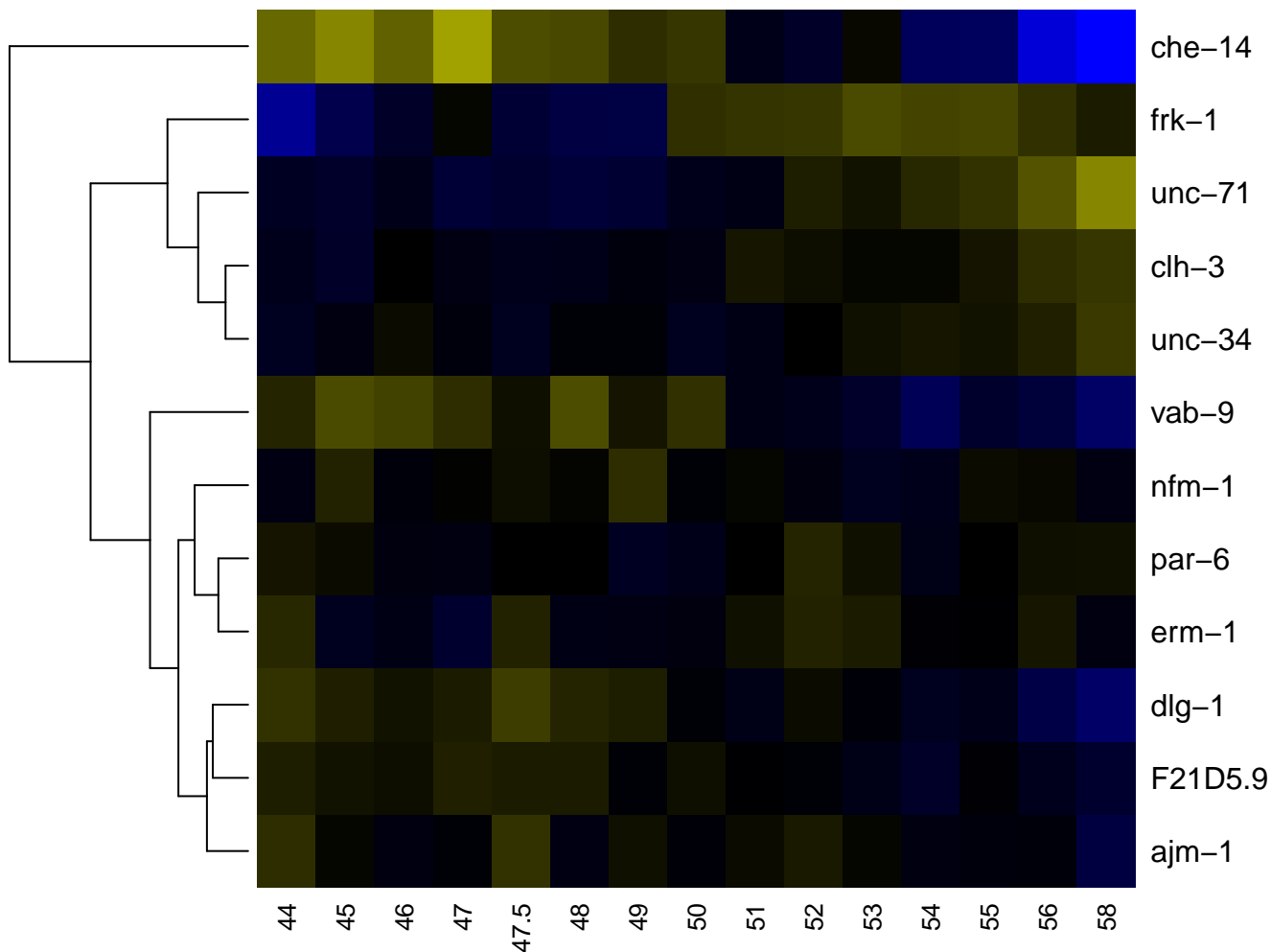
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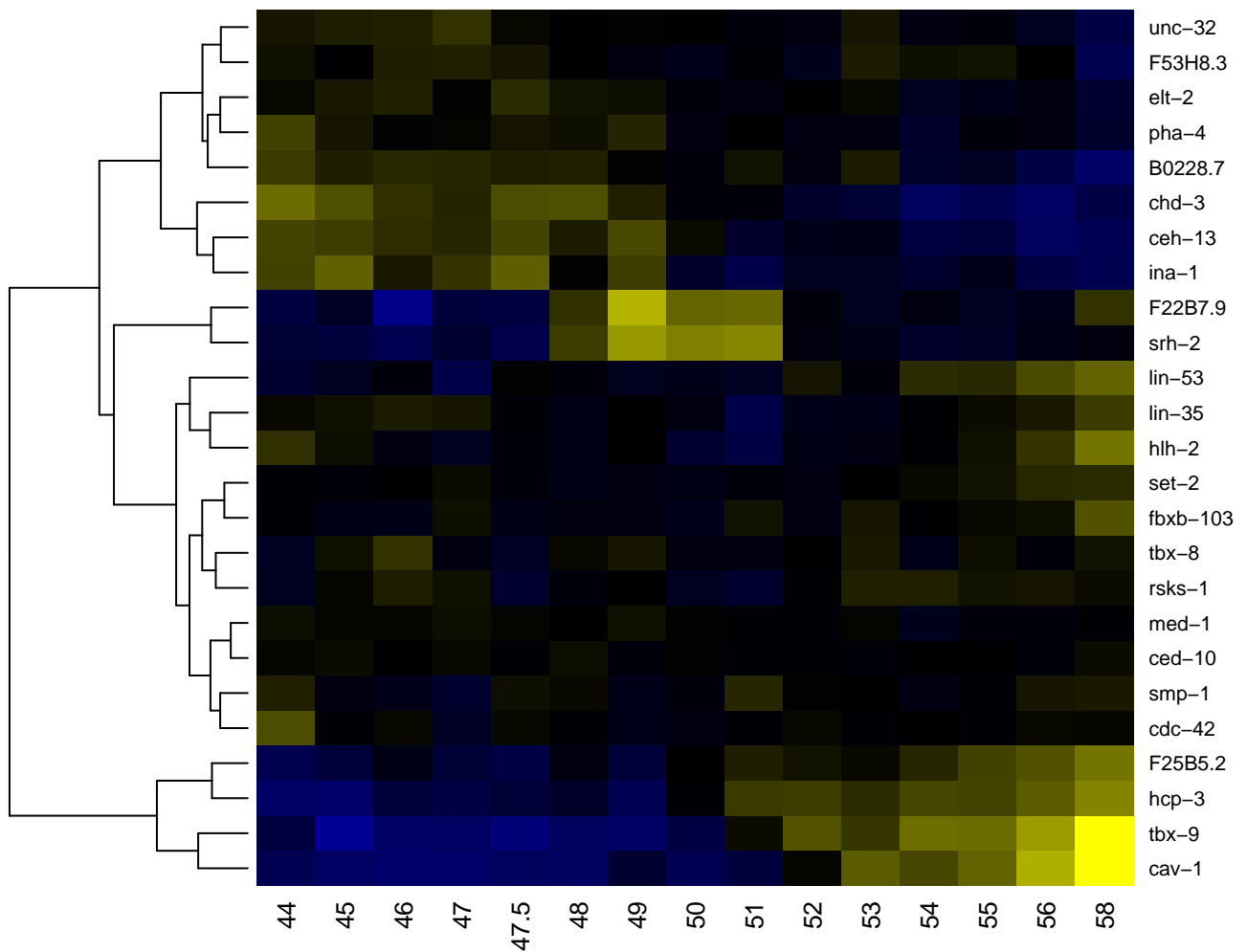
Ep



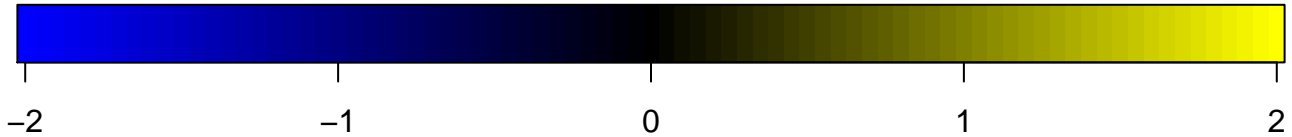
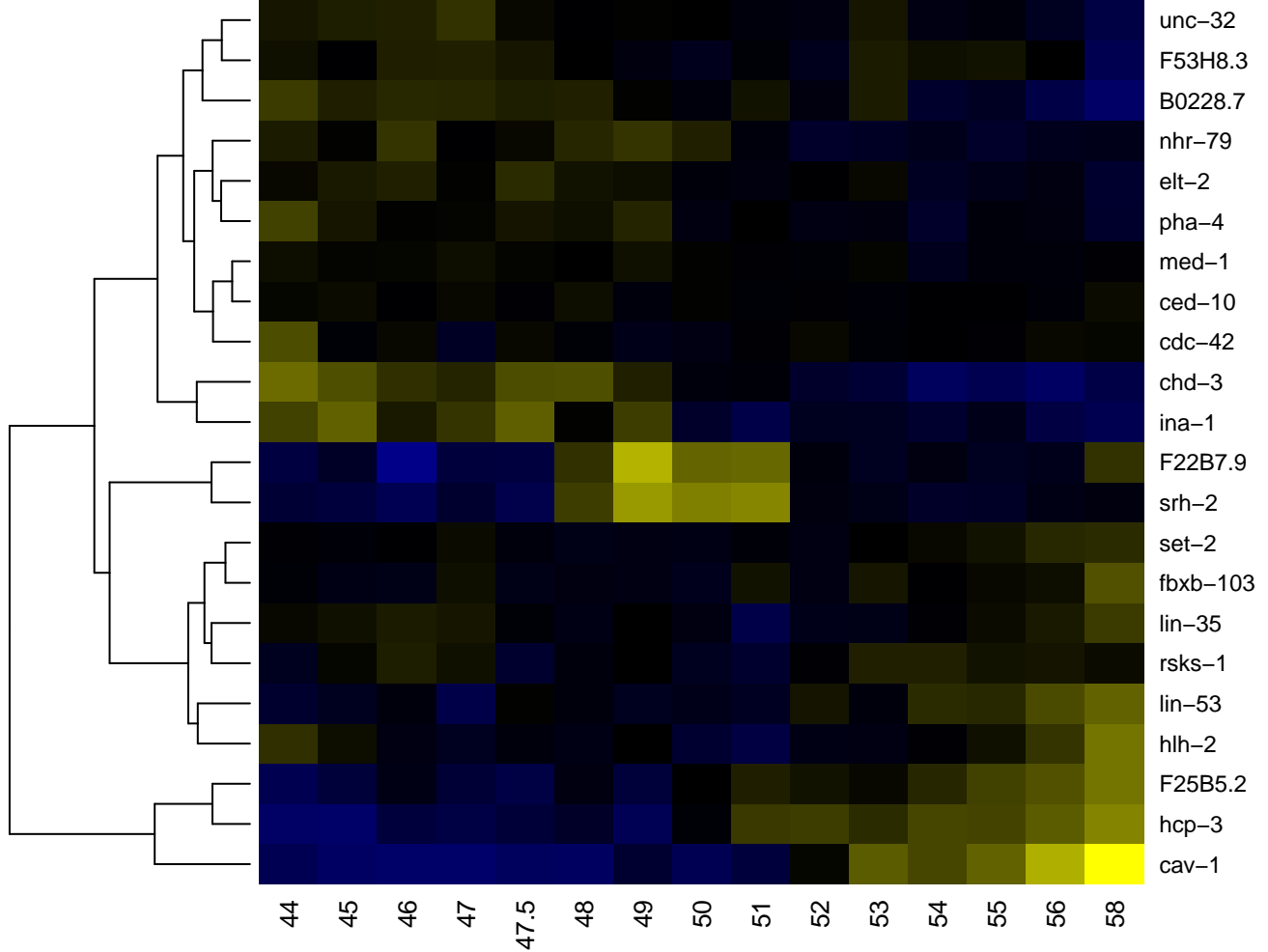
epithelial cell



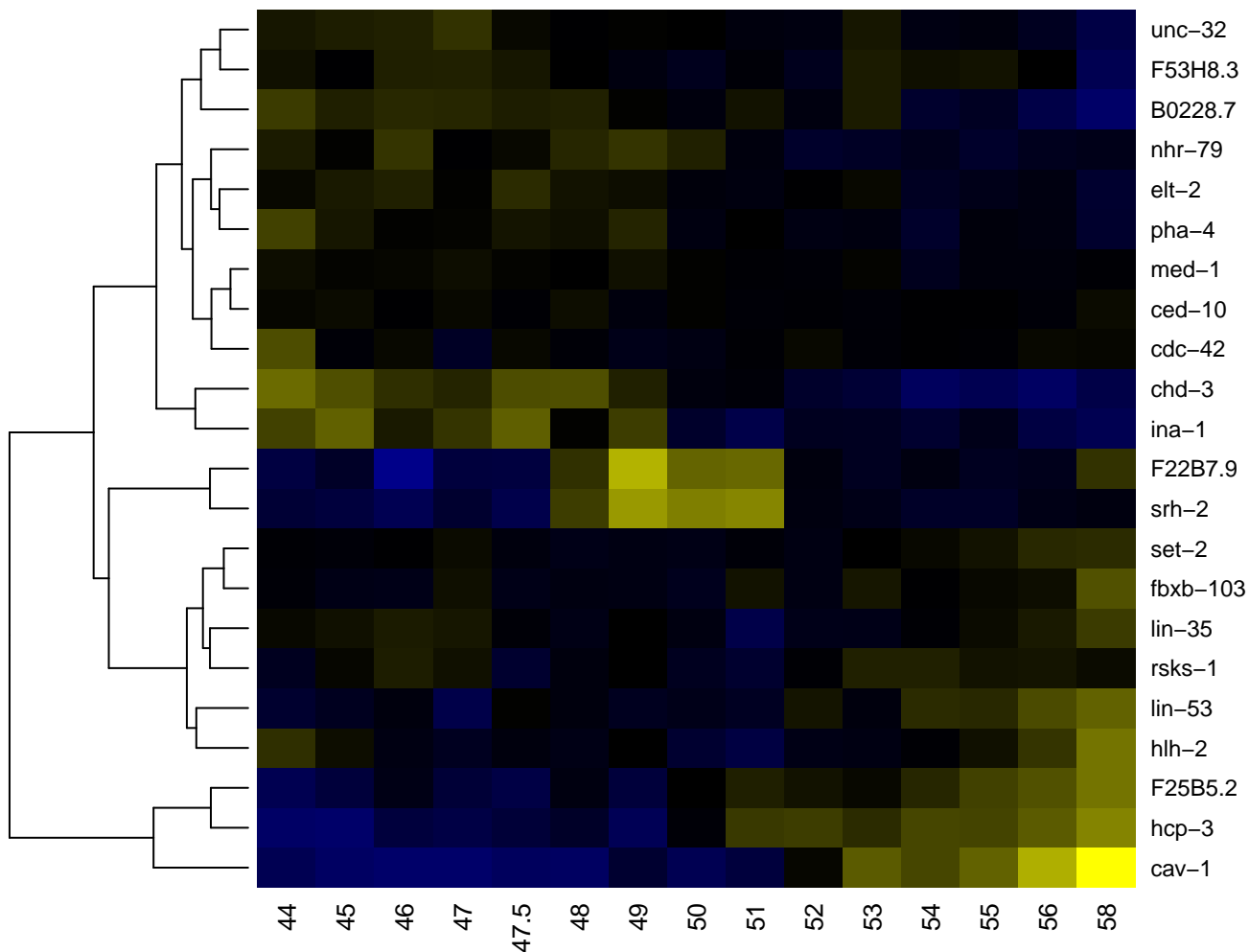
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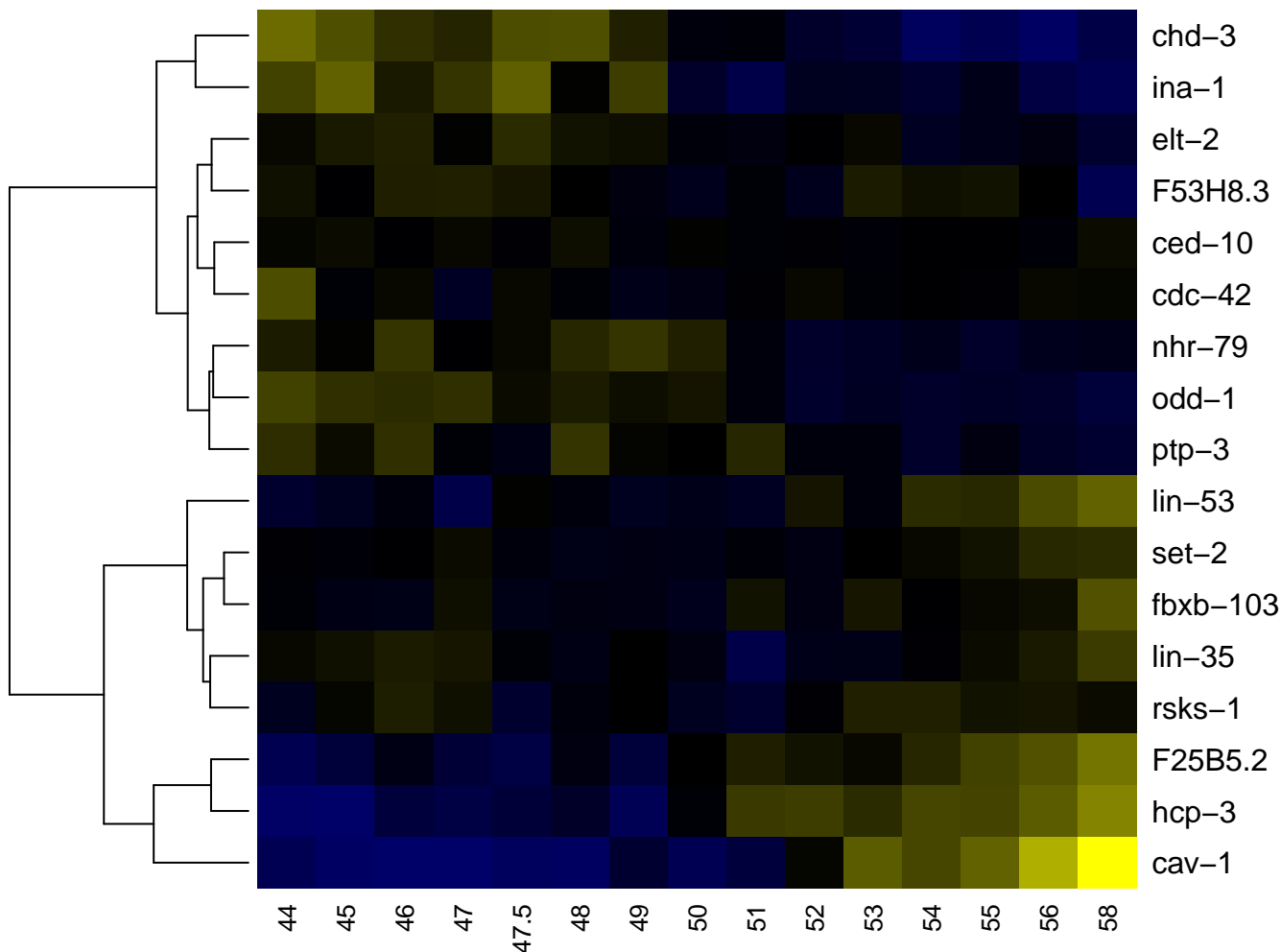
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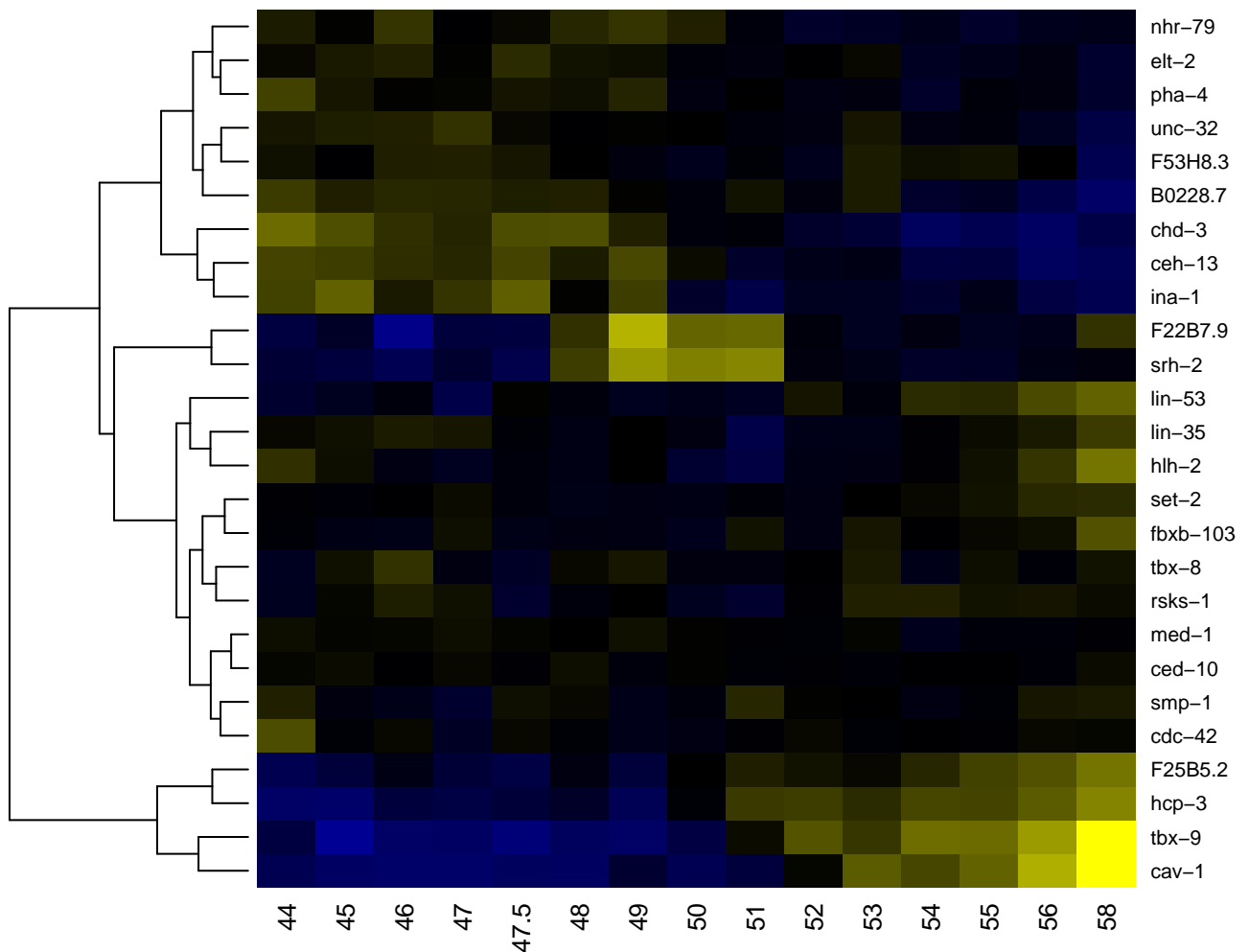
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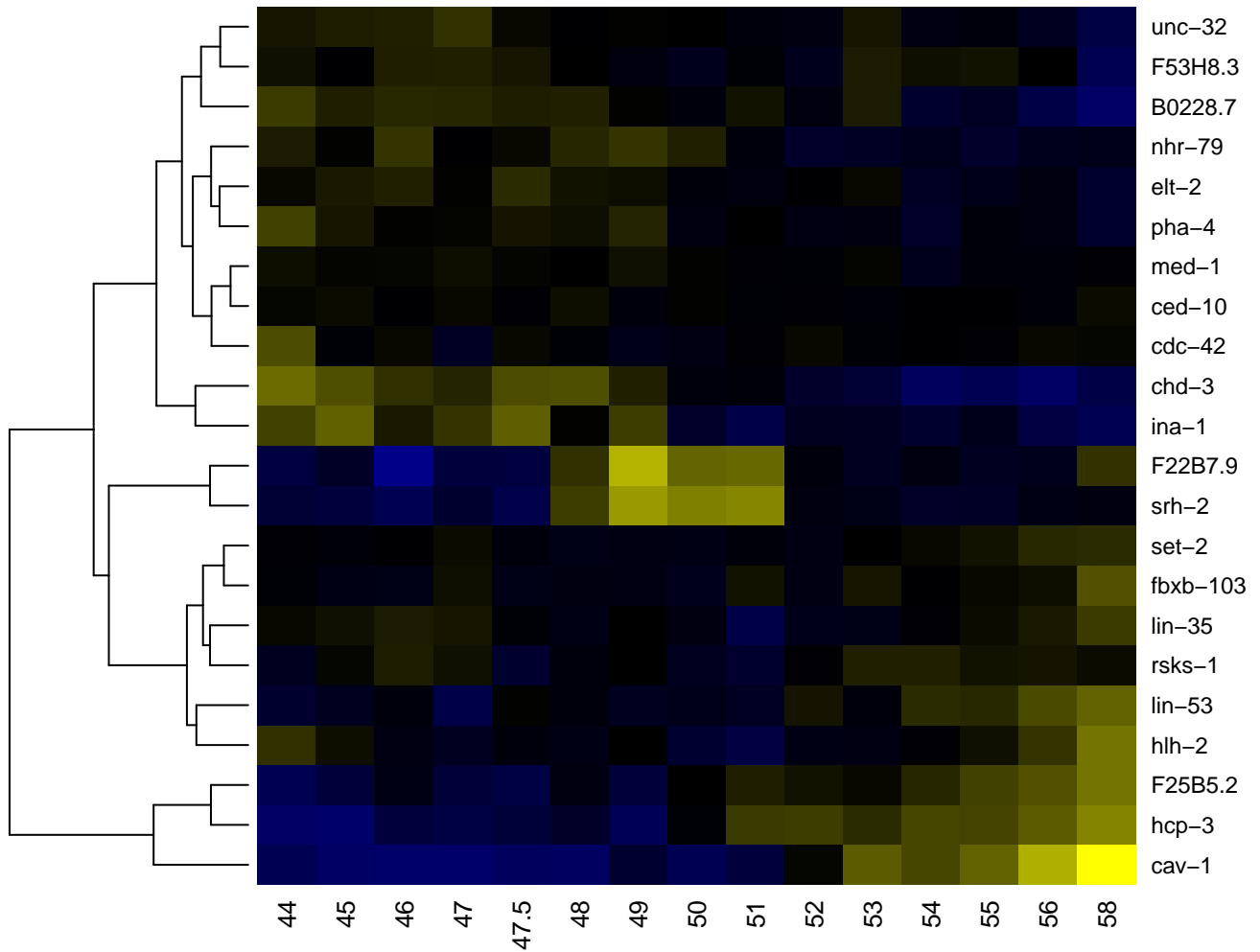
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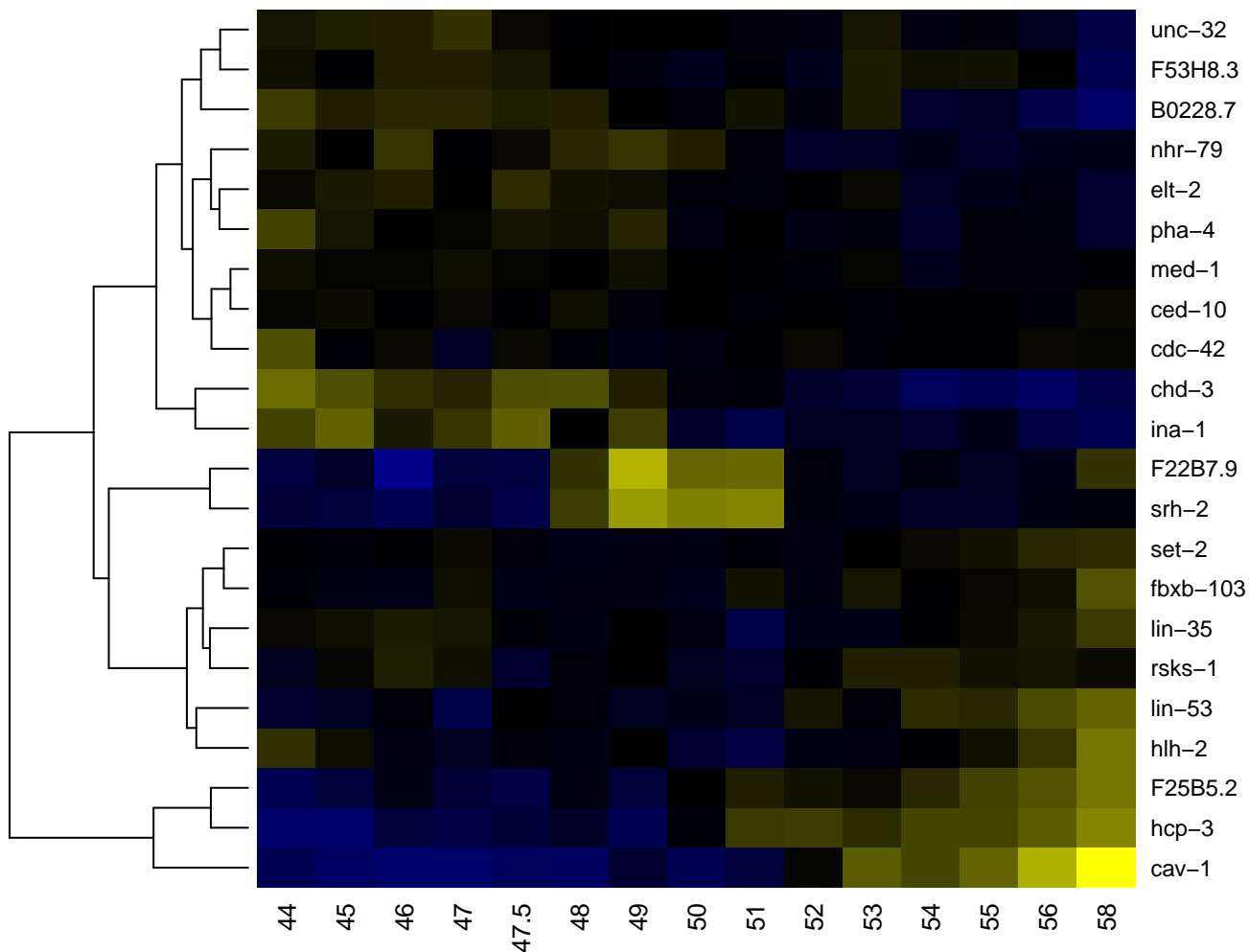
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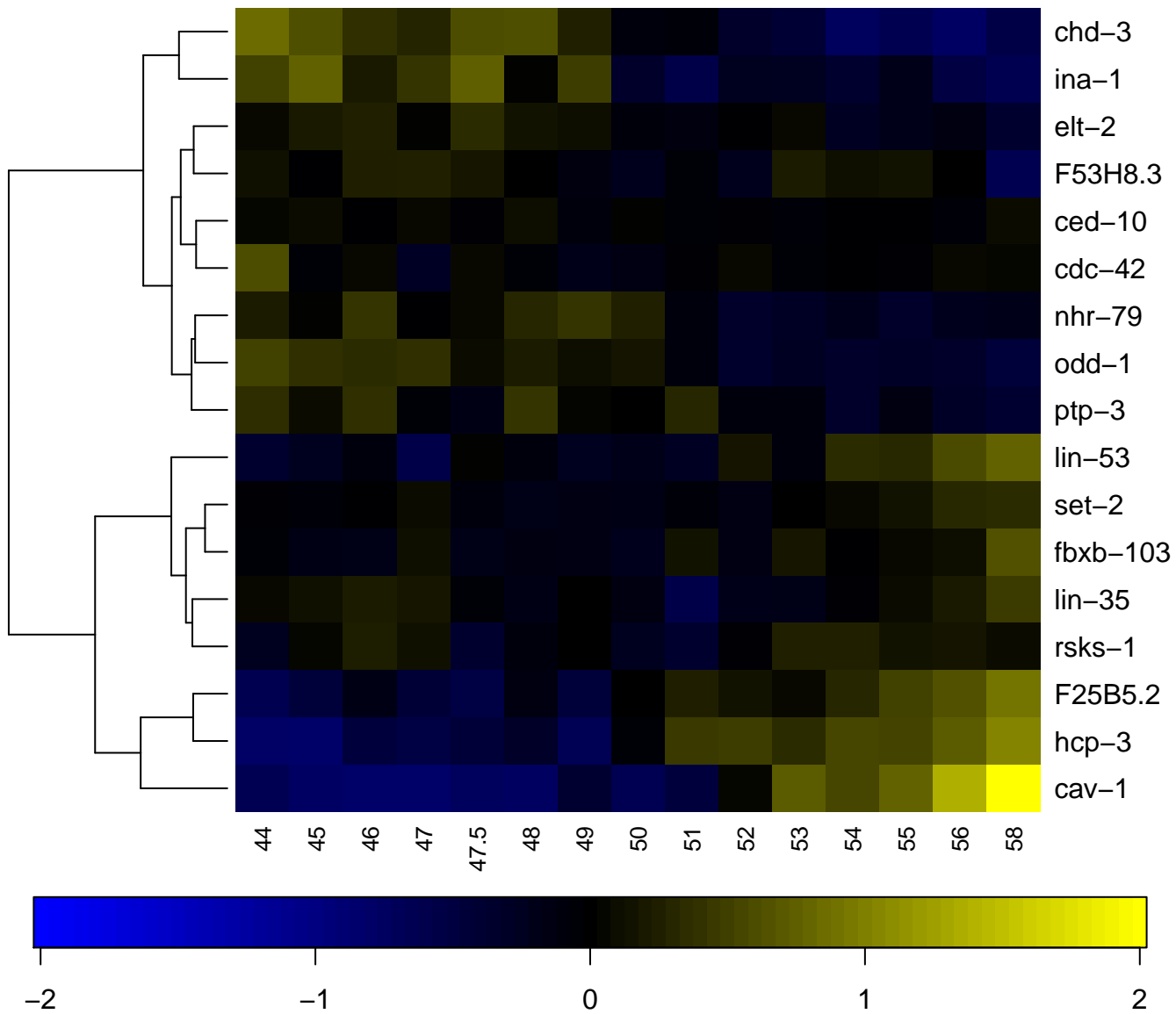
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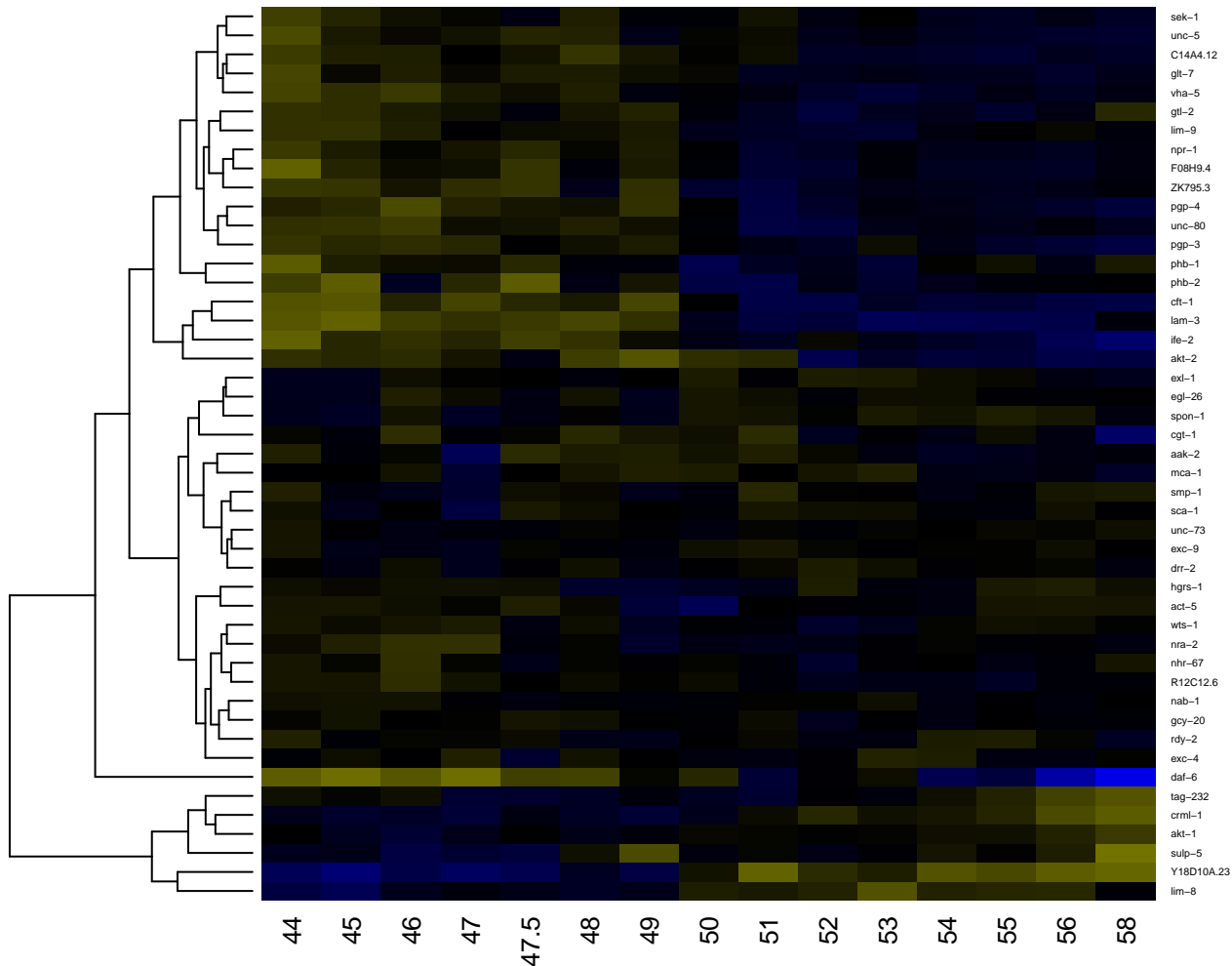
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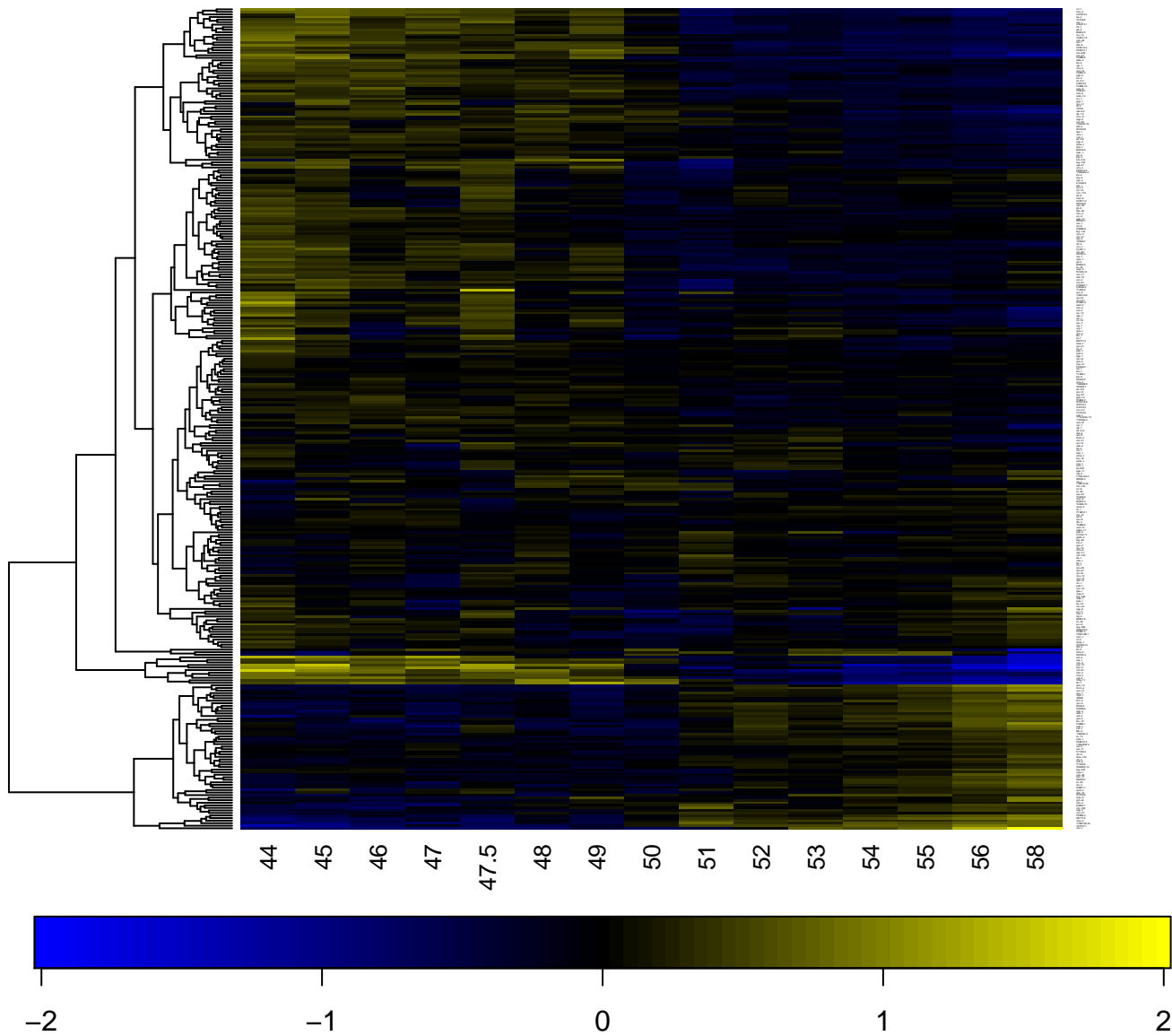
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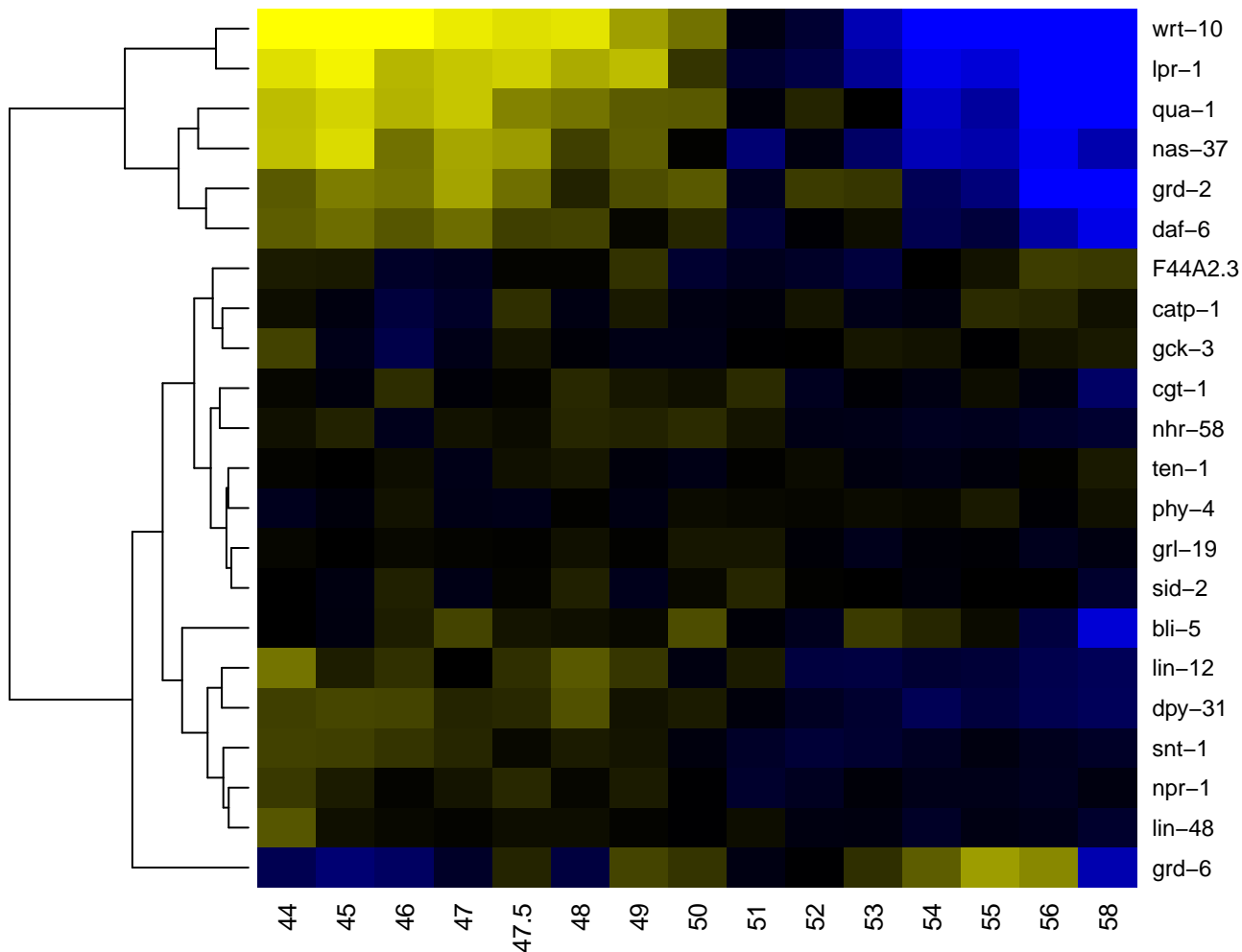
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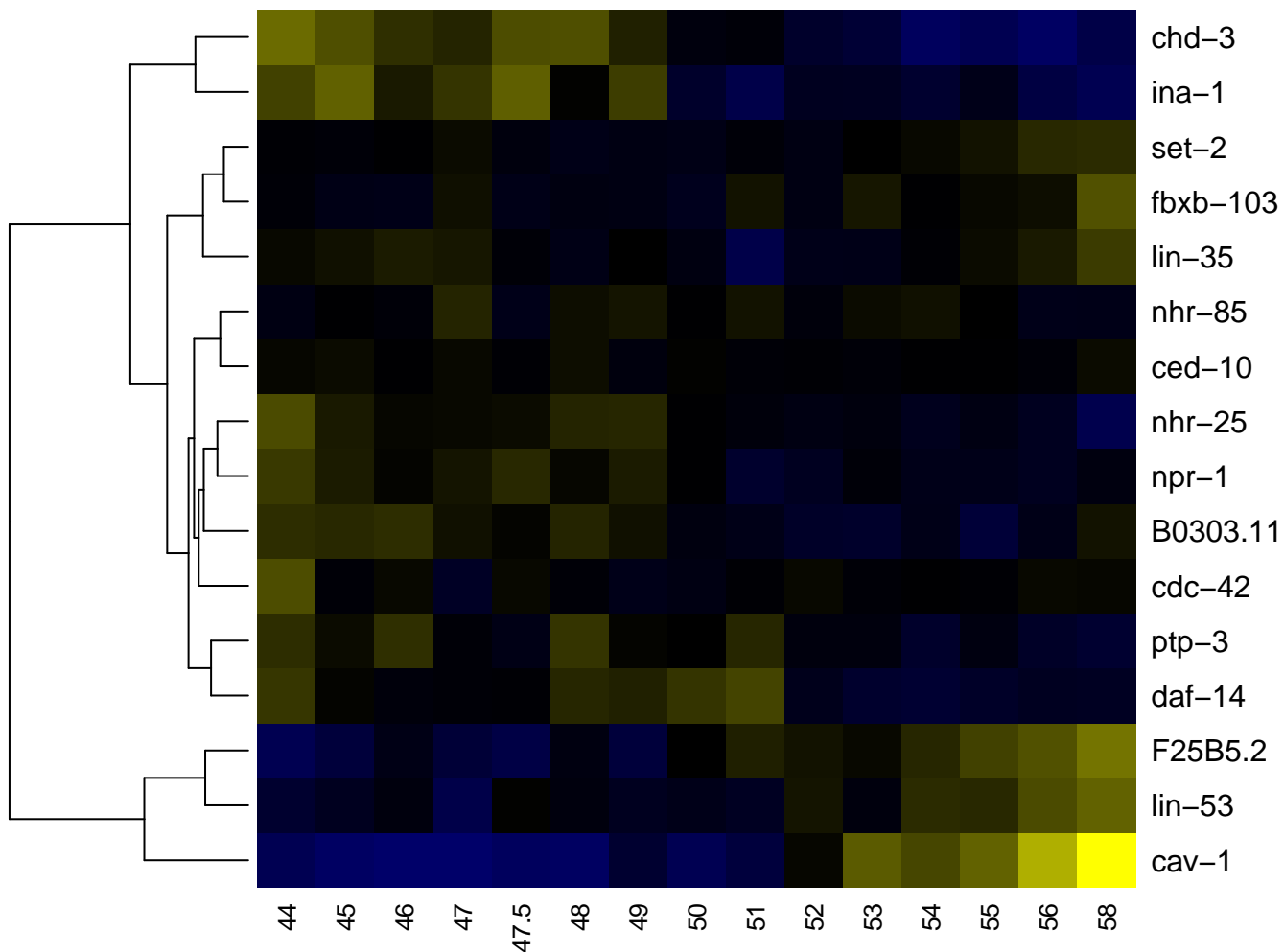
excretory cell



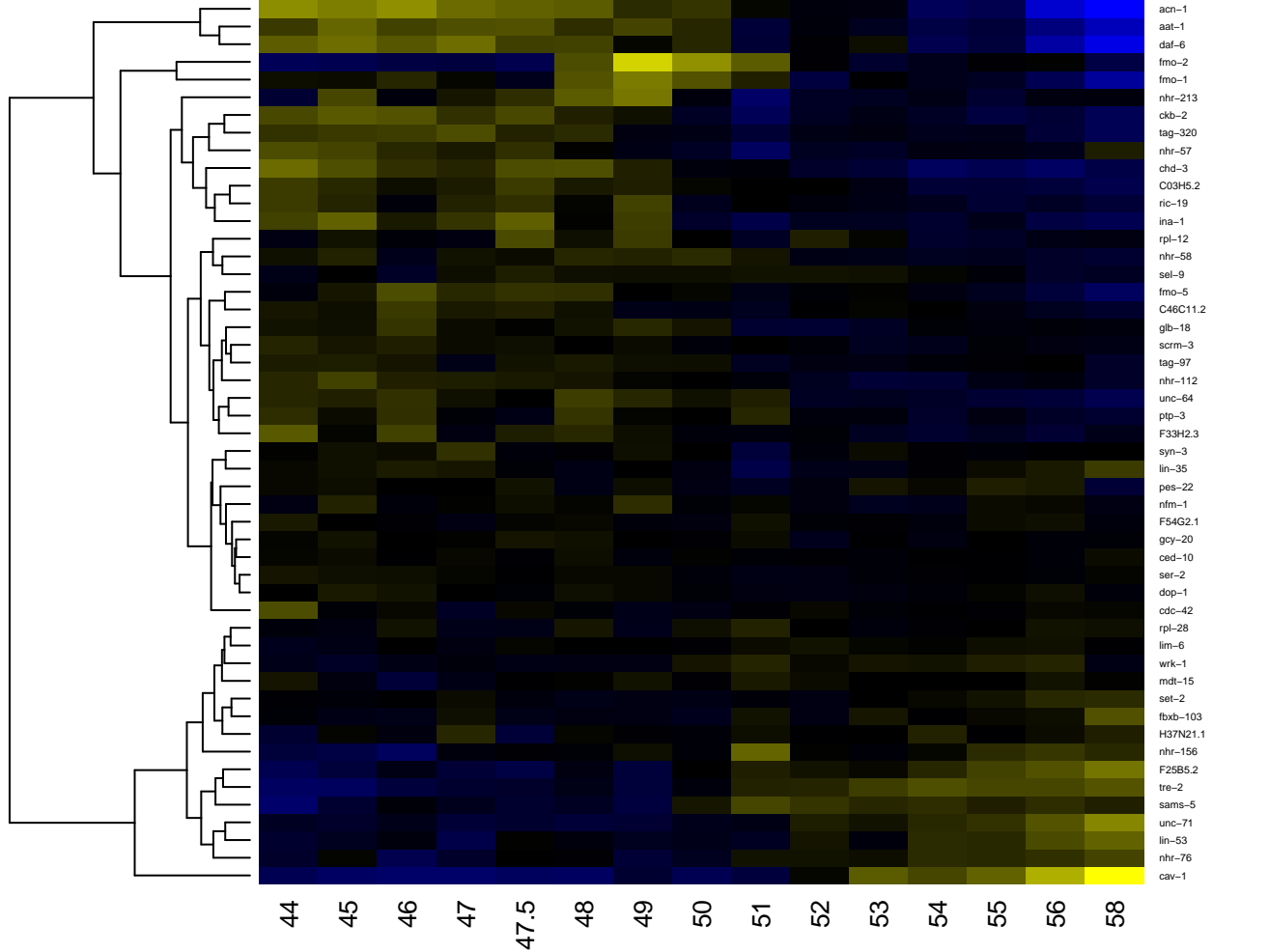
Excretory duct



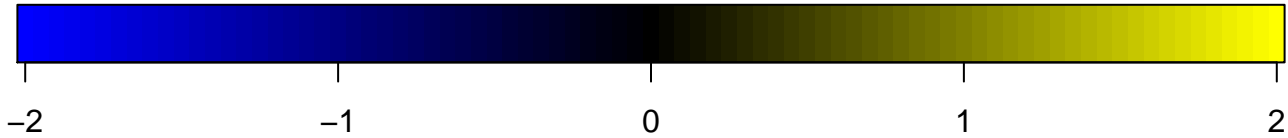
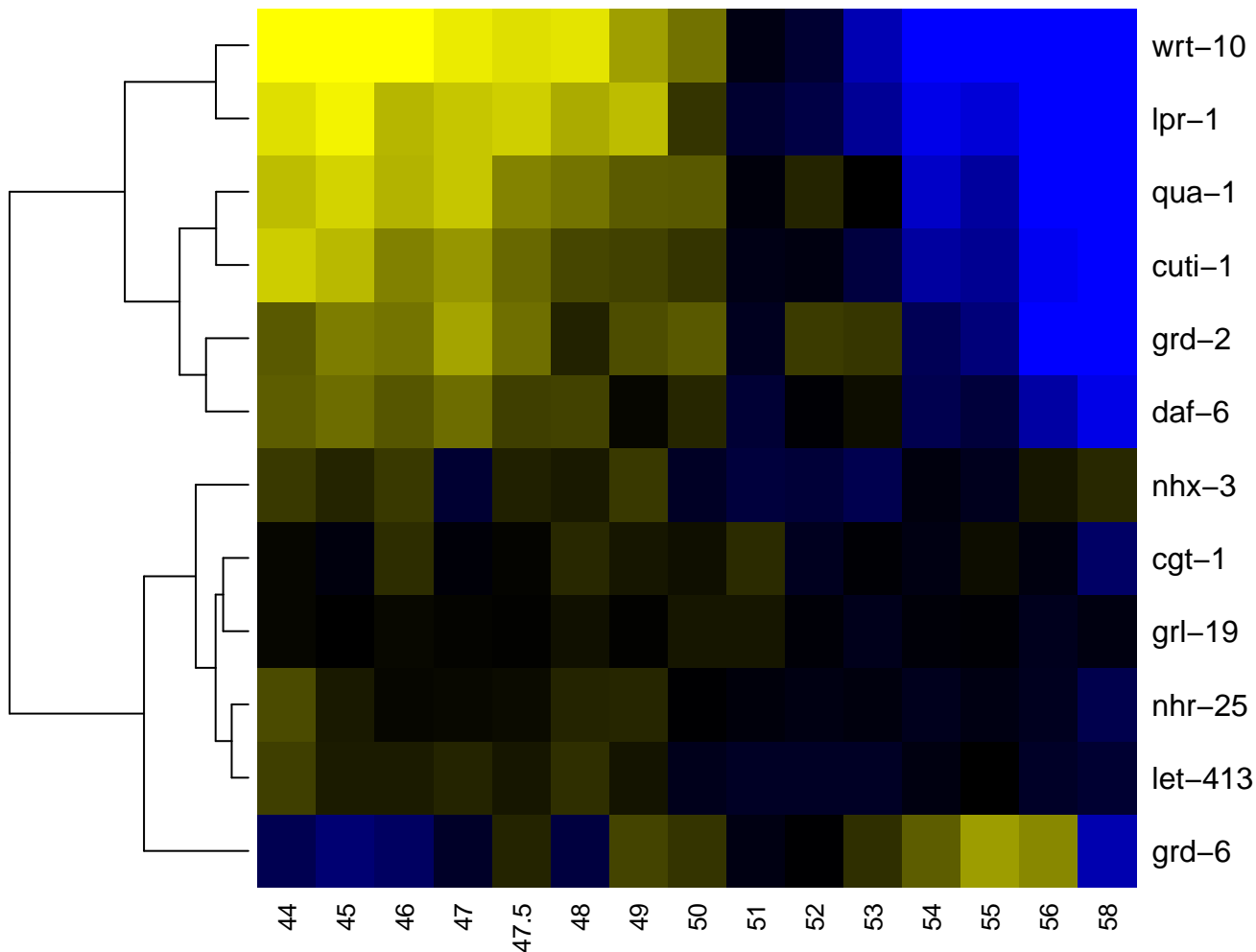
excretory duct cell



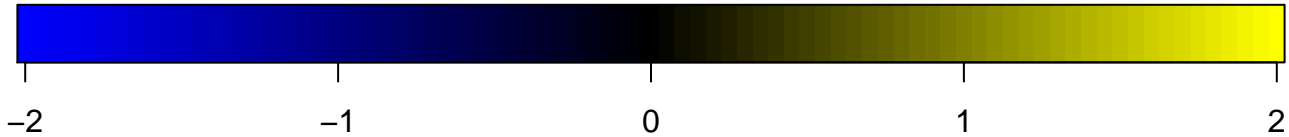
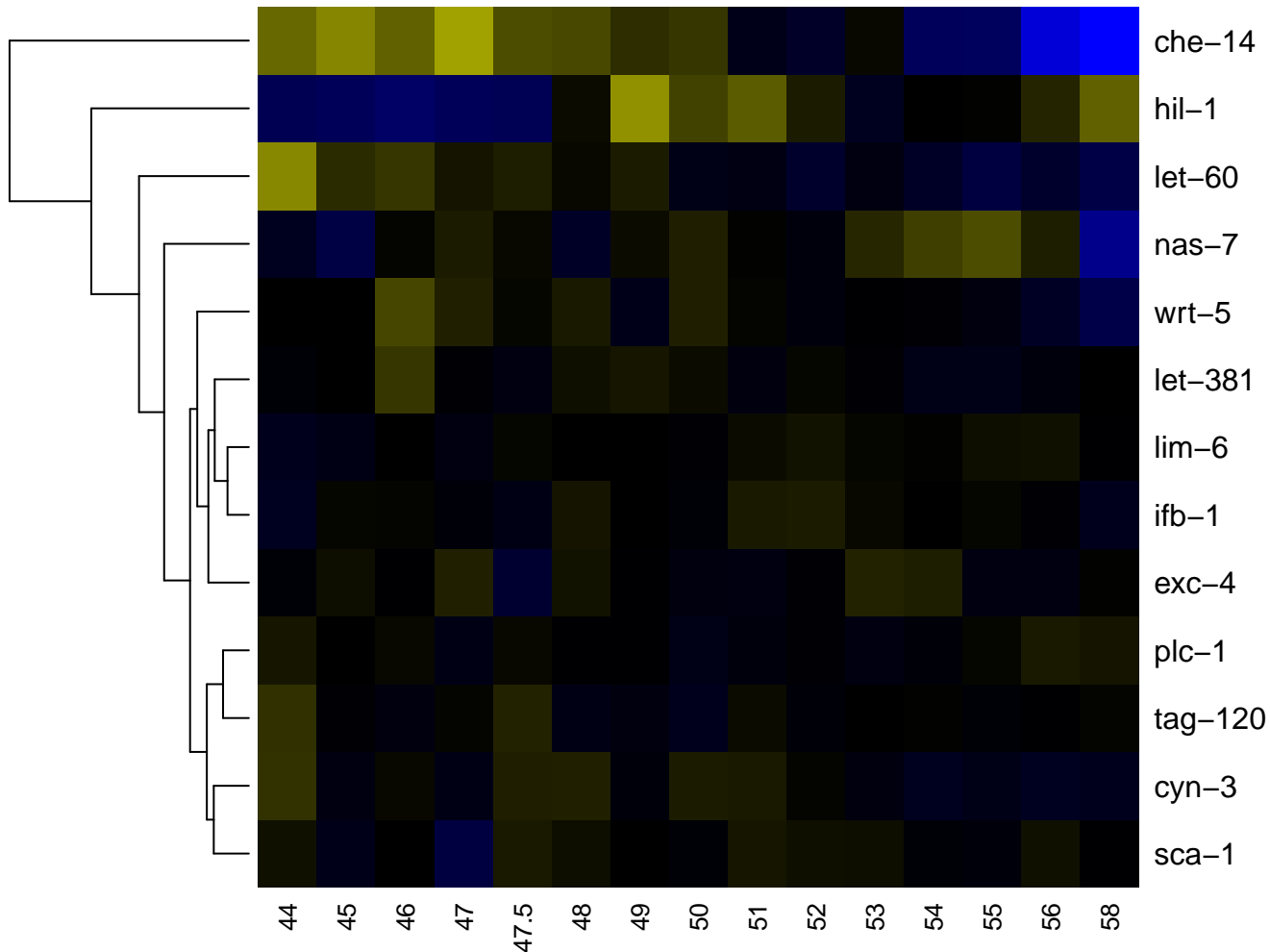
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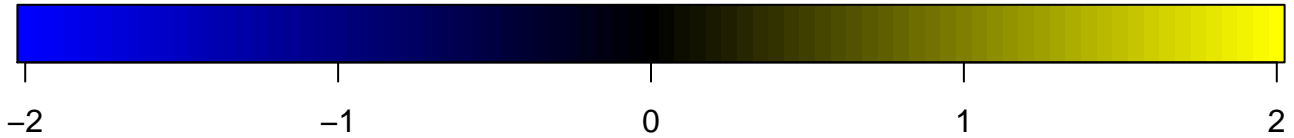
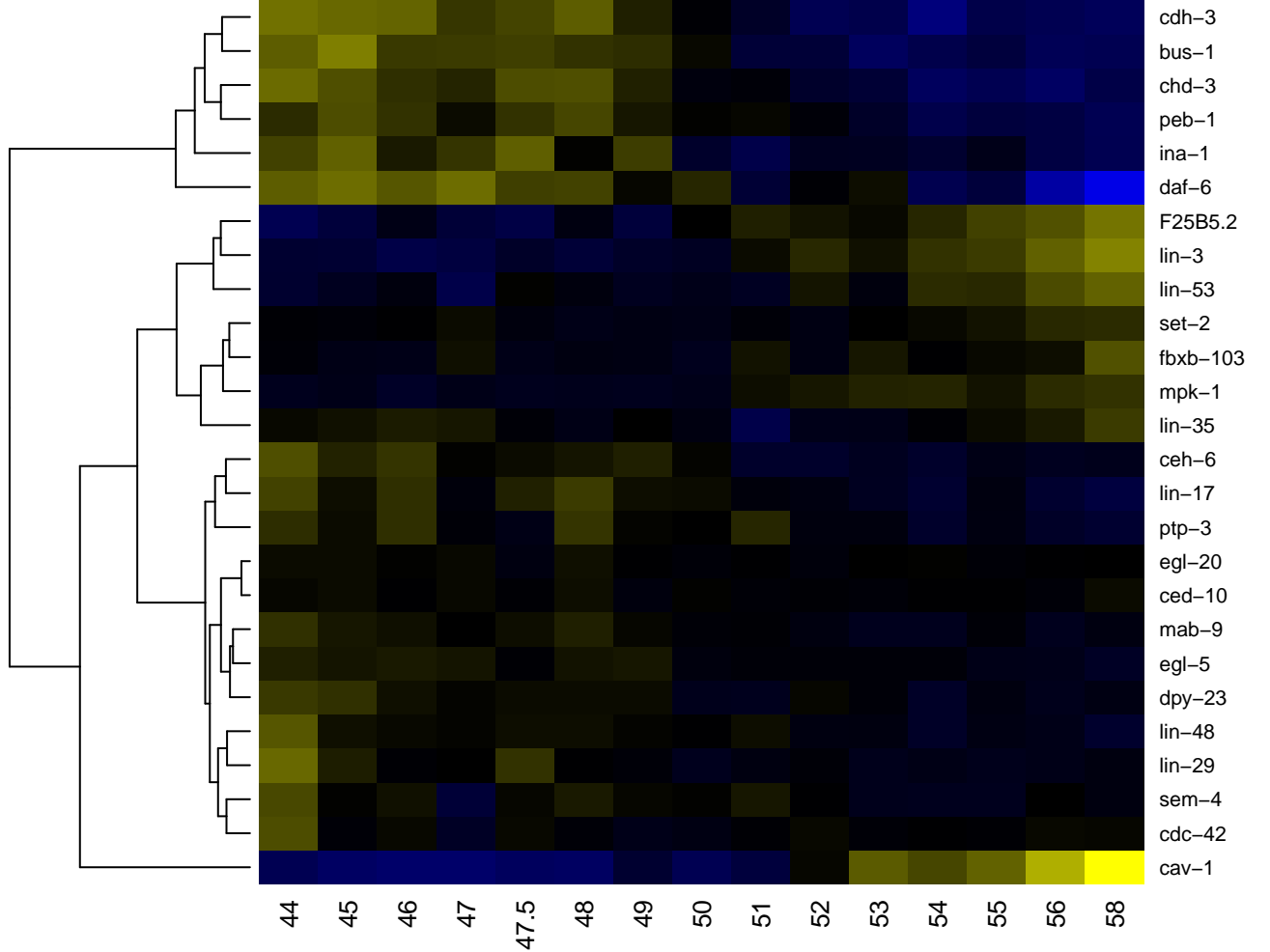
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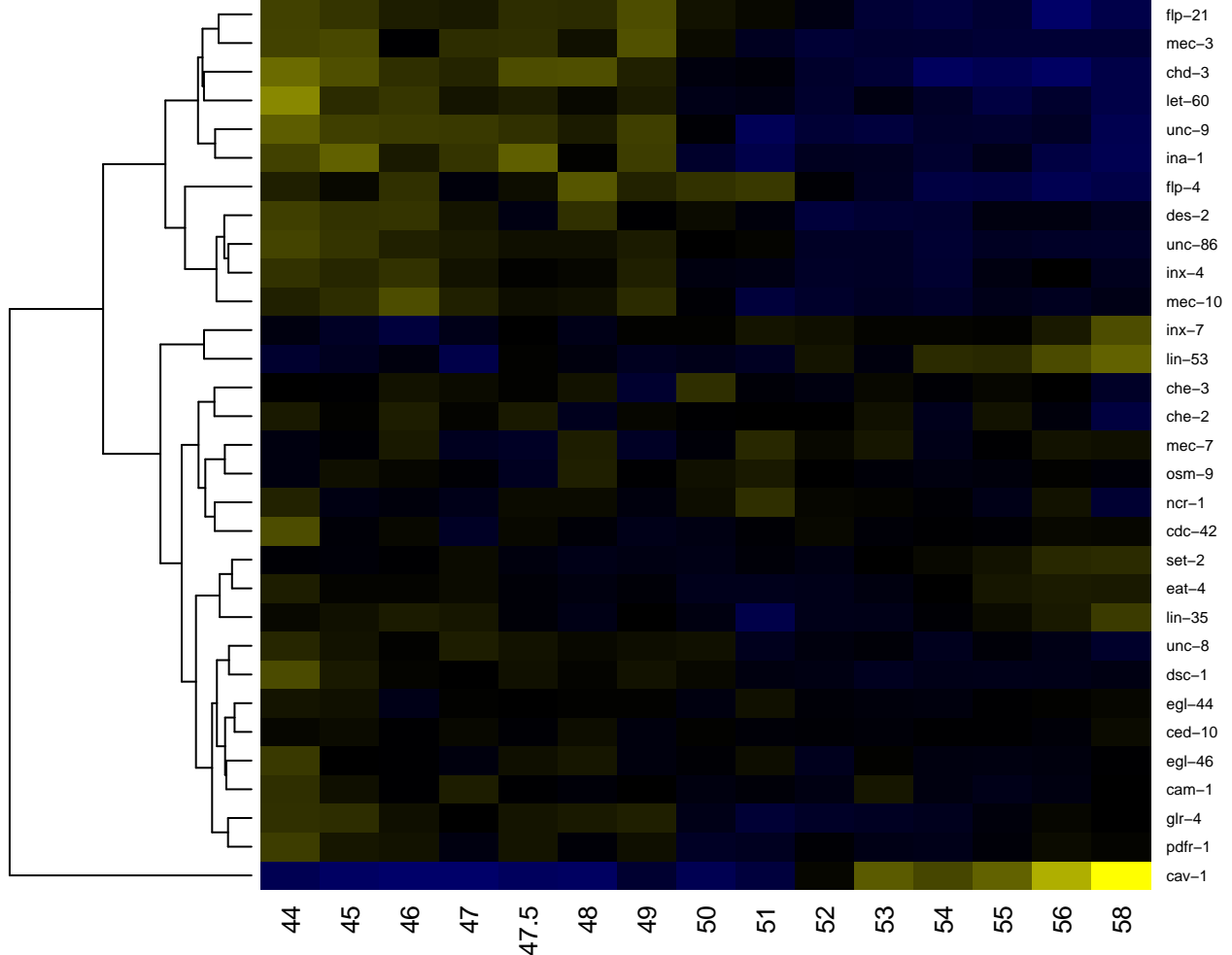
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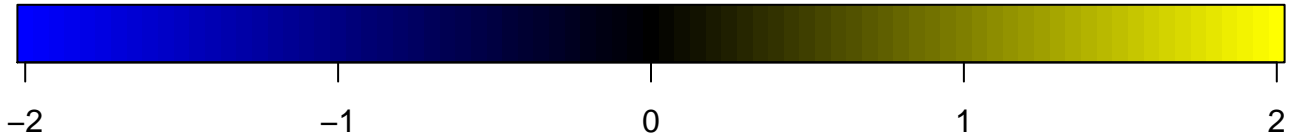
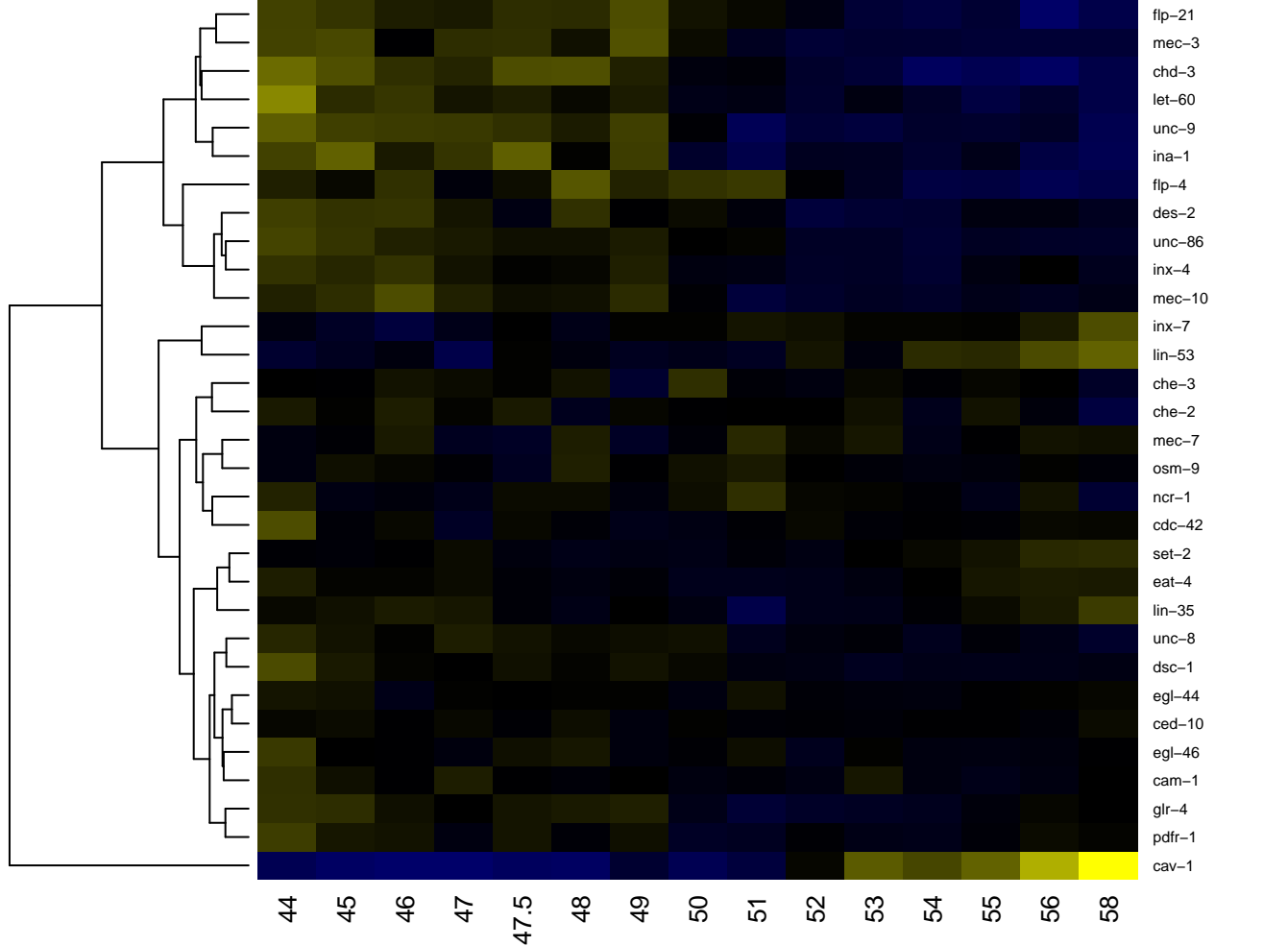
F cell



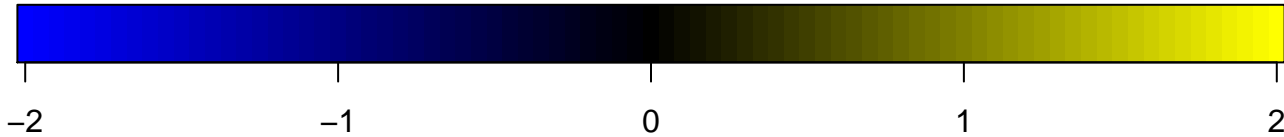
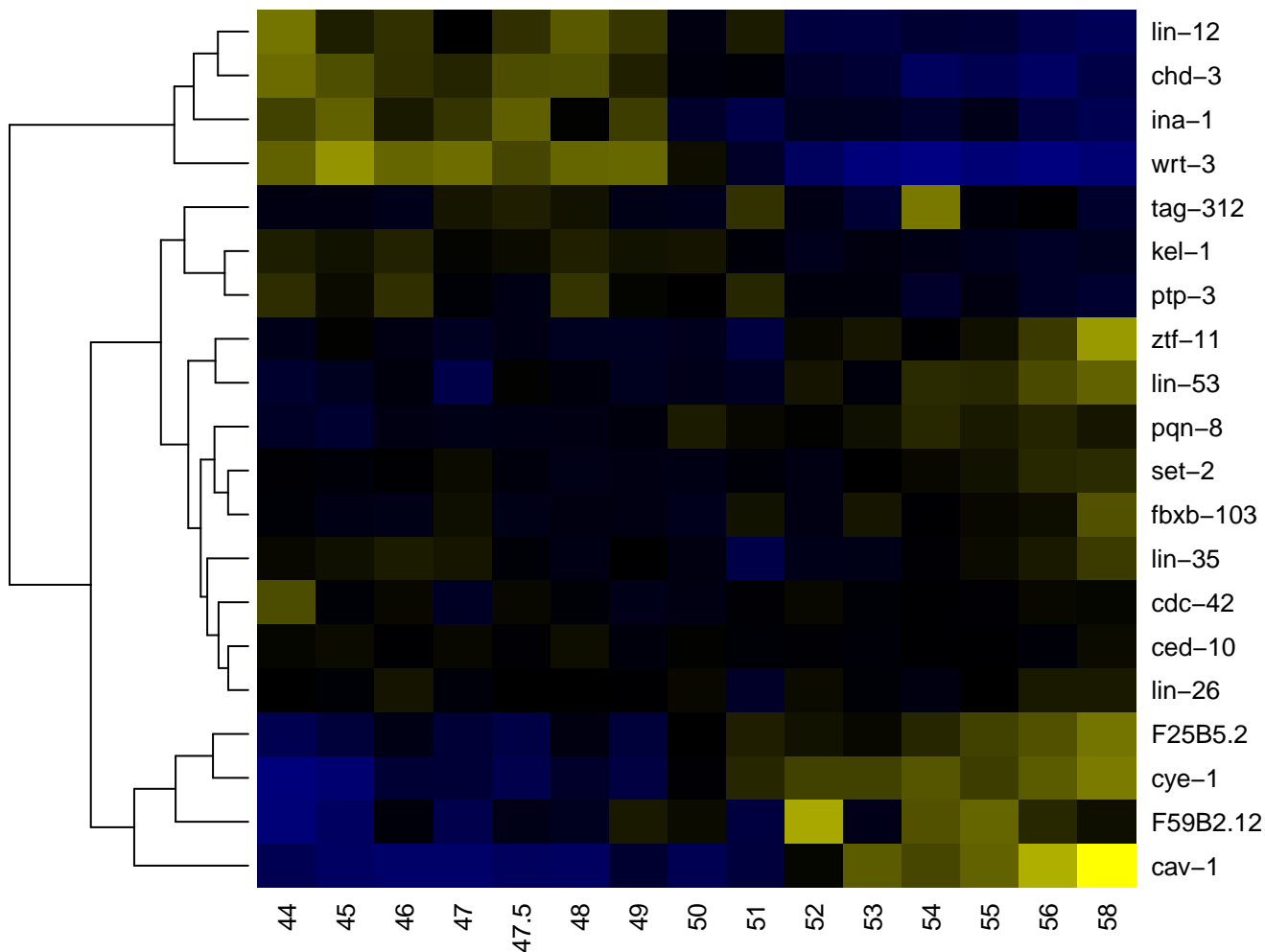
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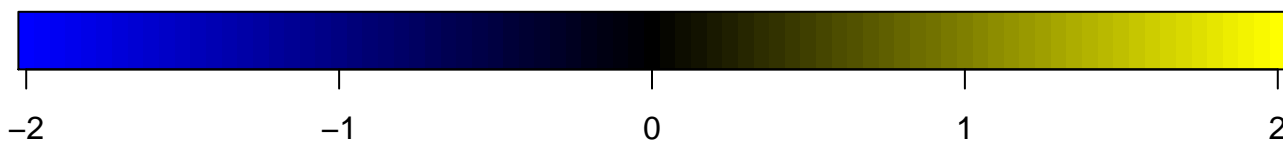
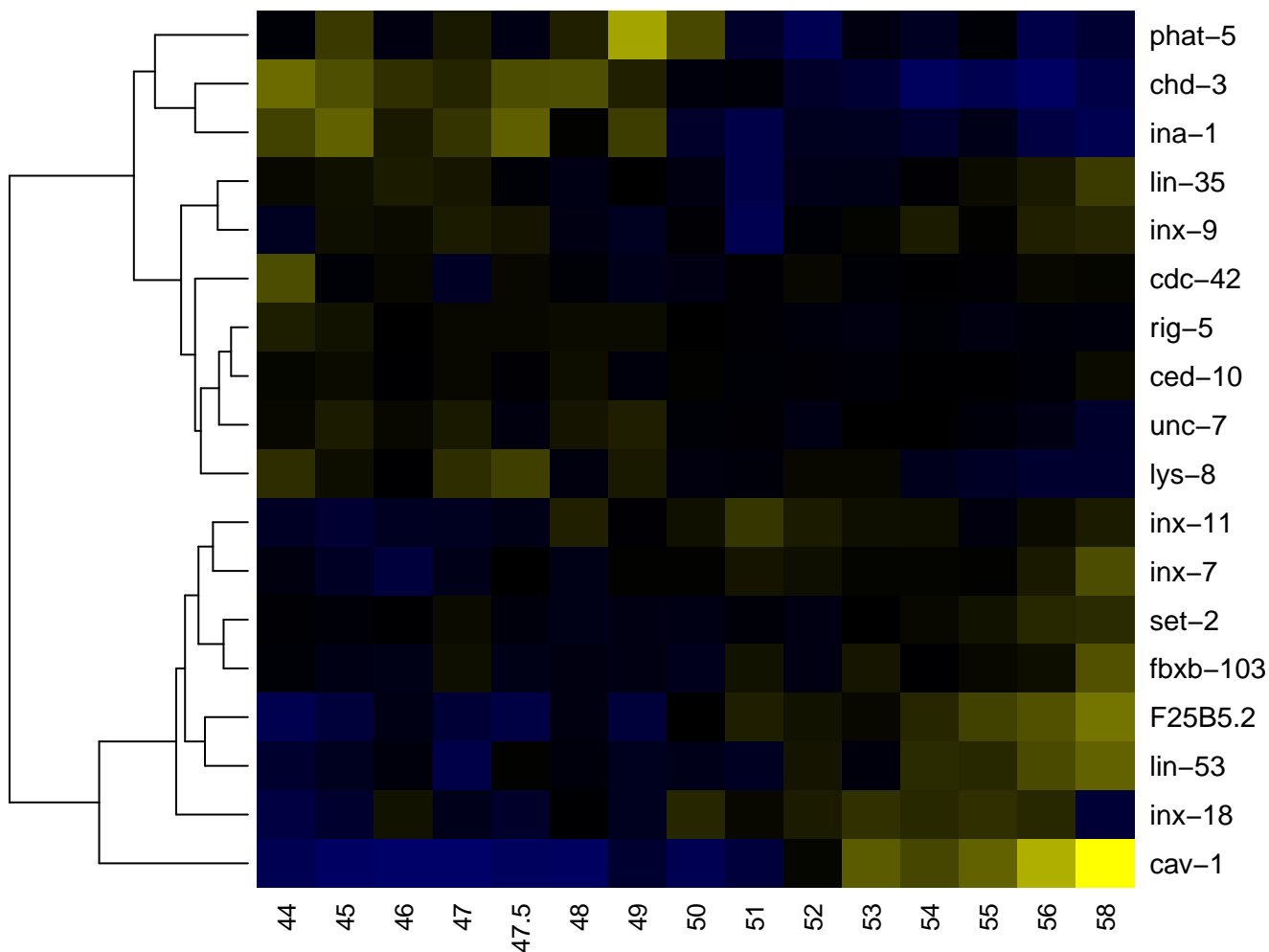
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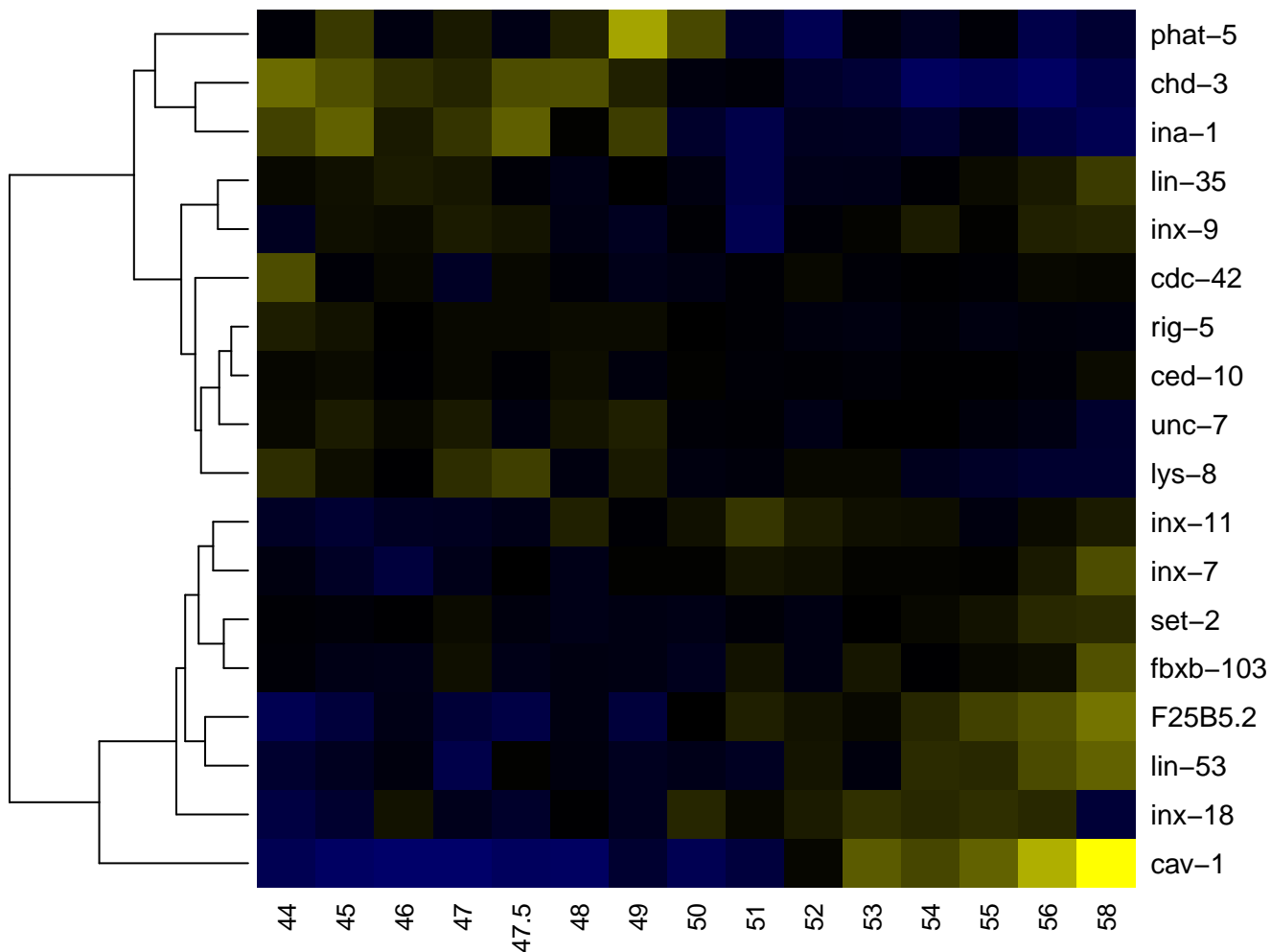
G1



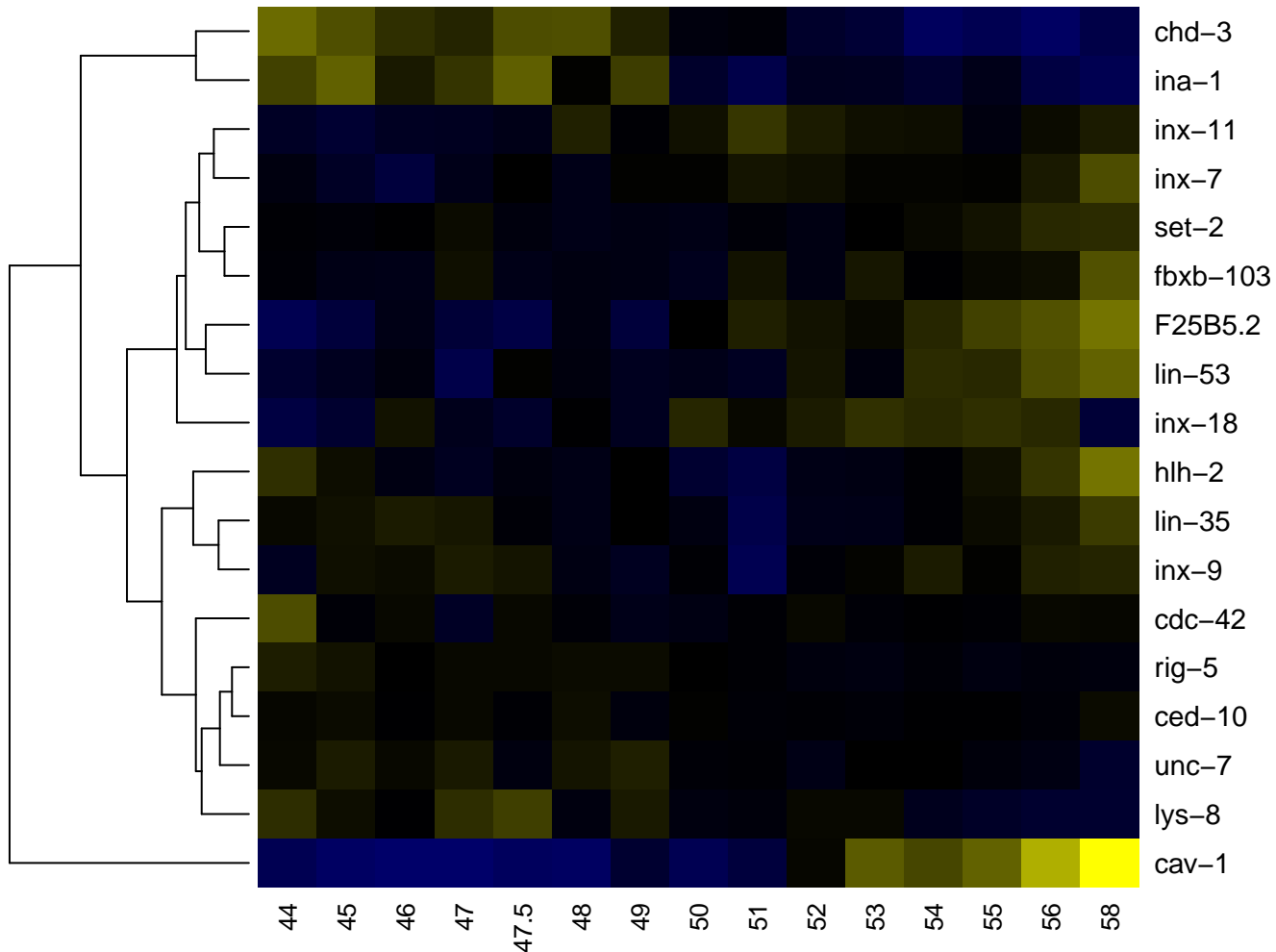
g1AL



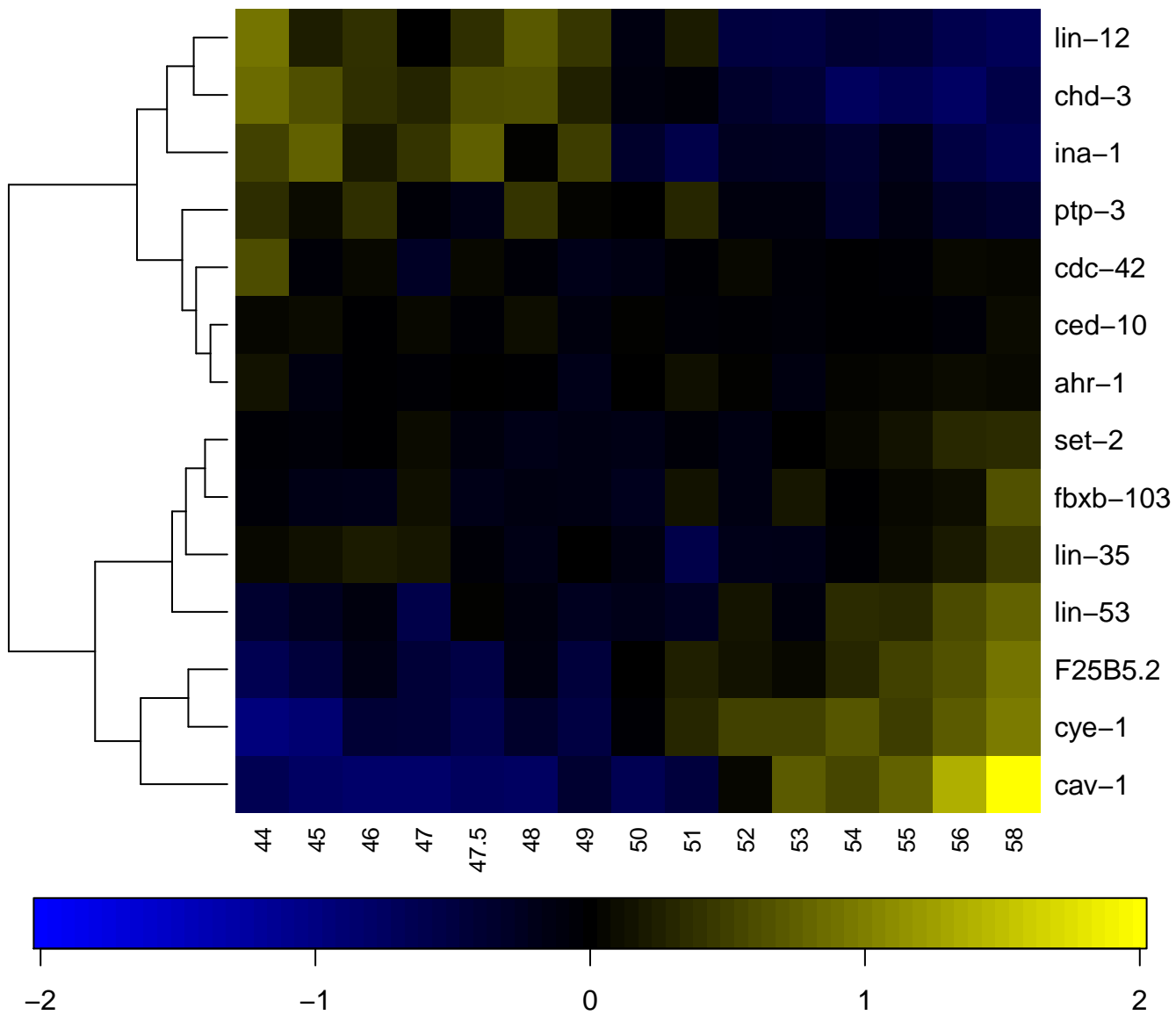
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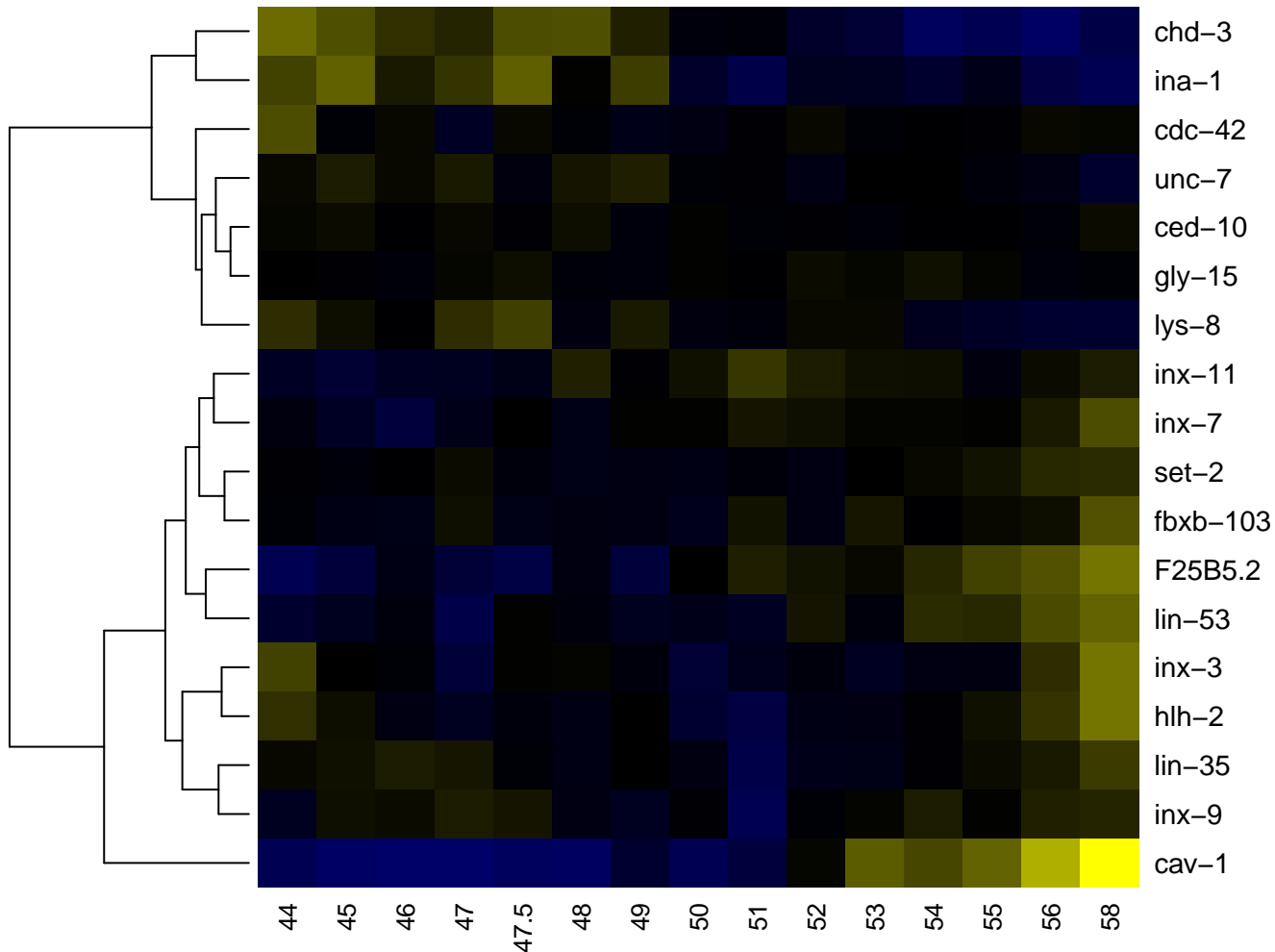
g1P



G2



g2L



-2

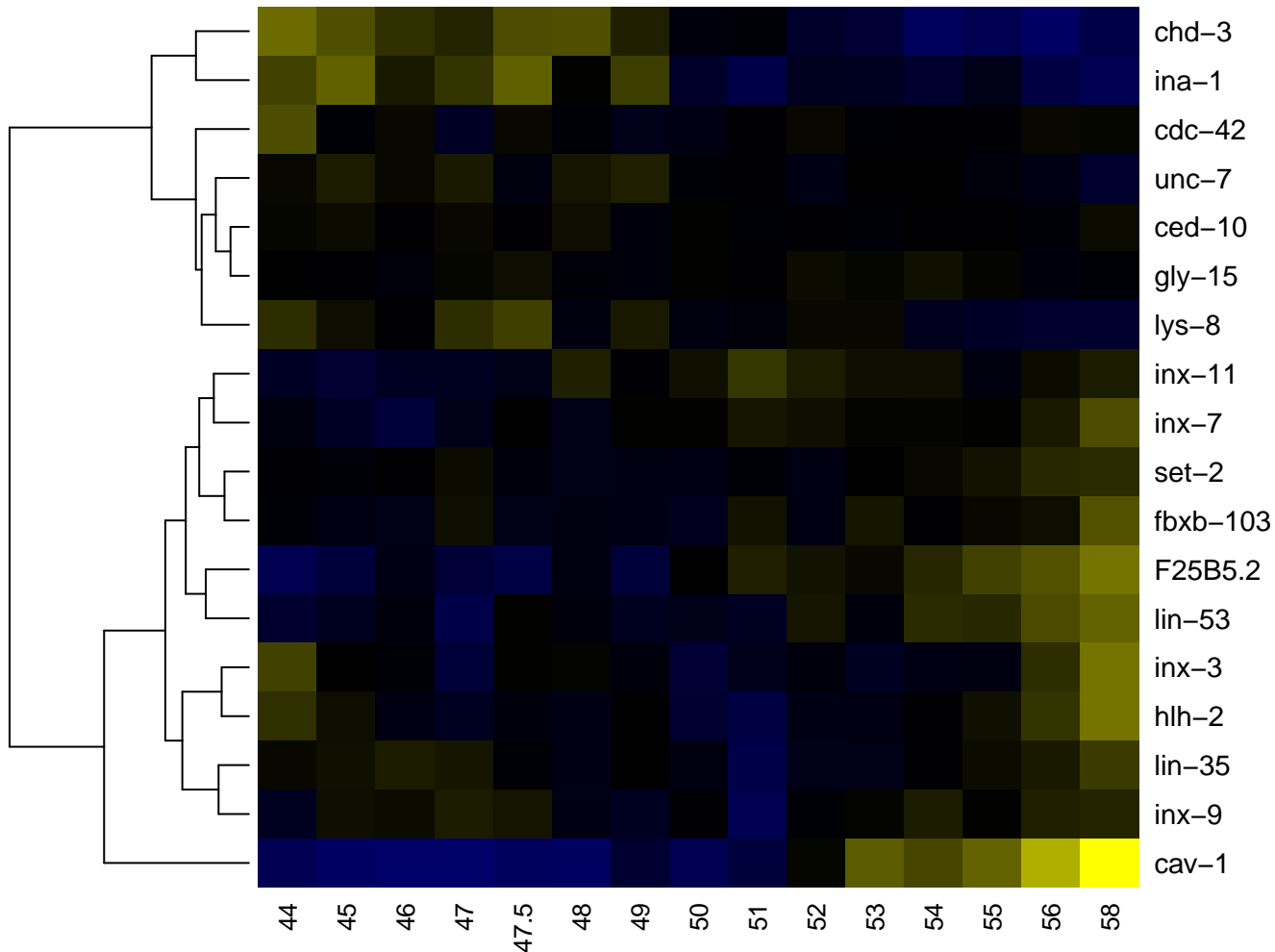
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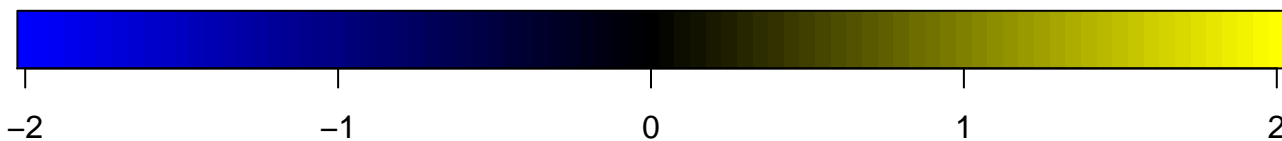
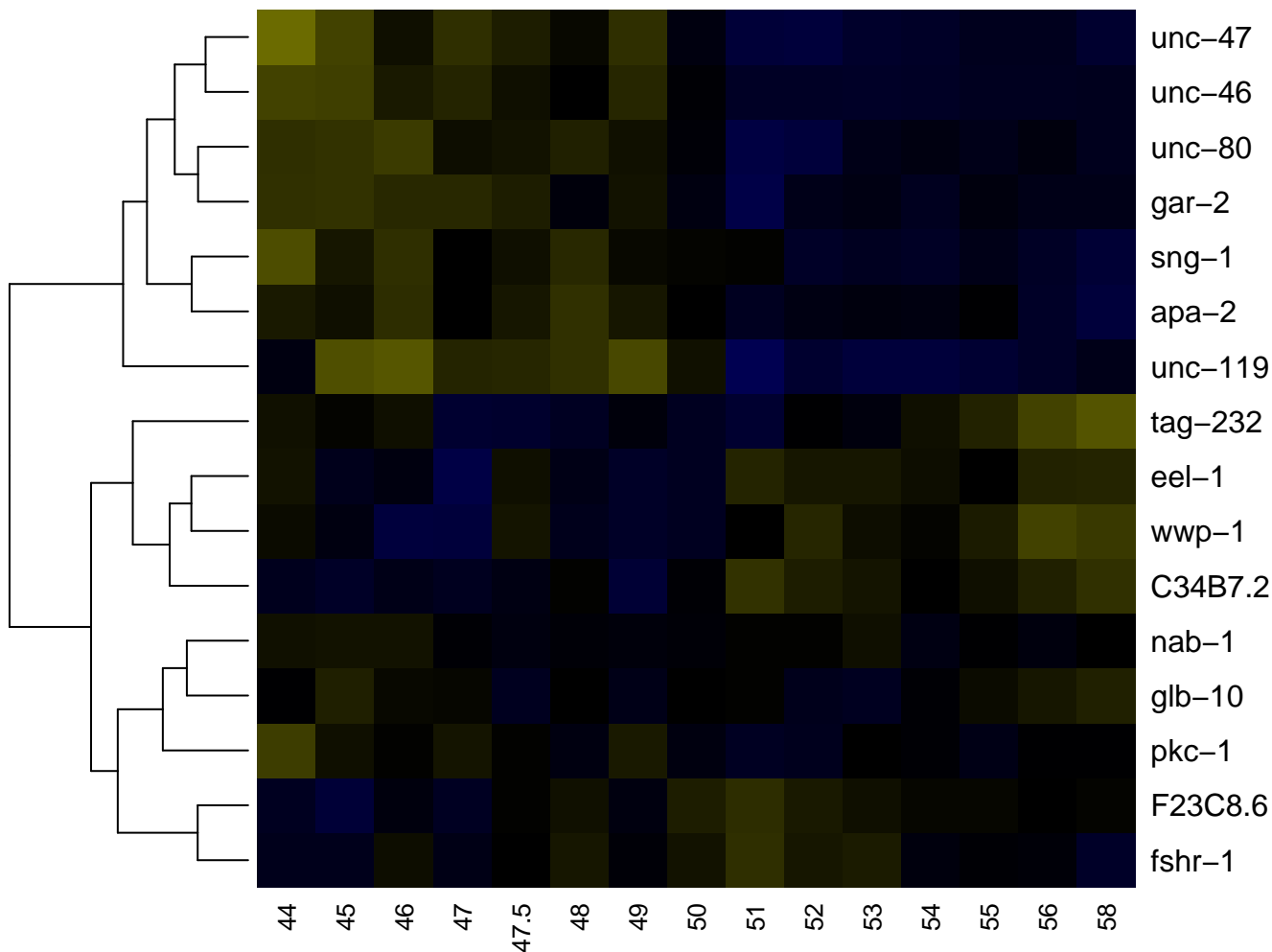
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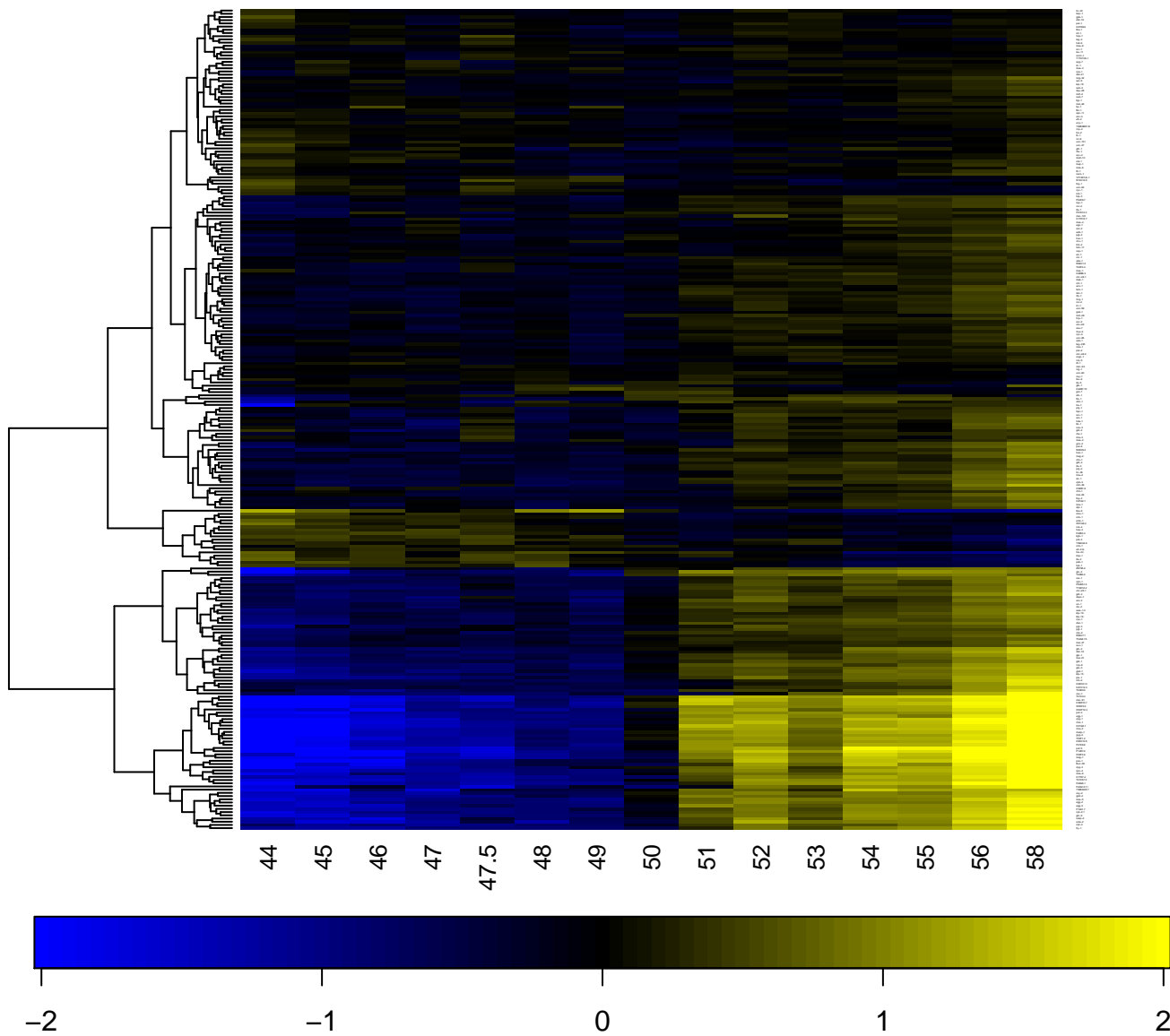
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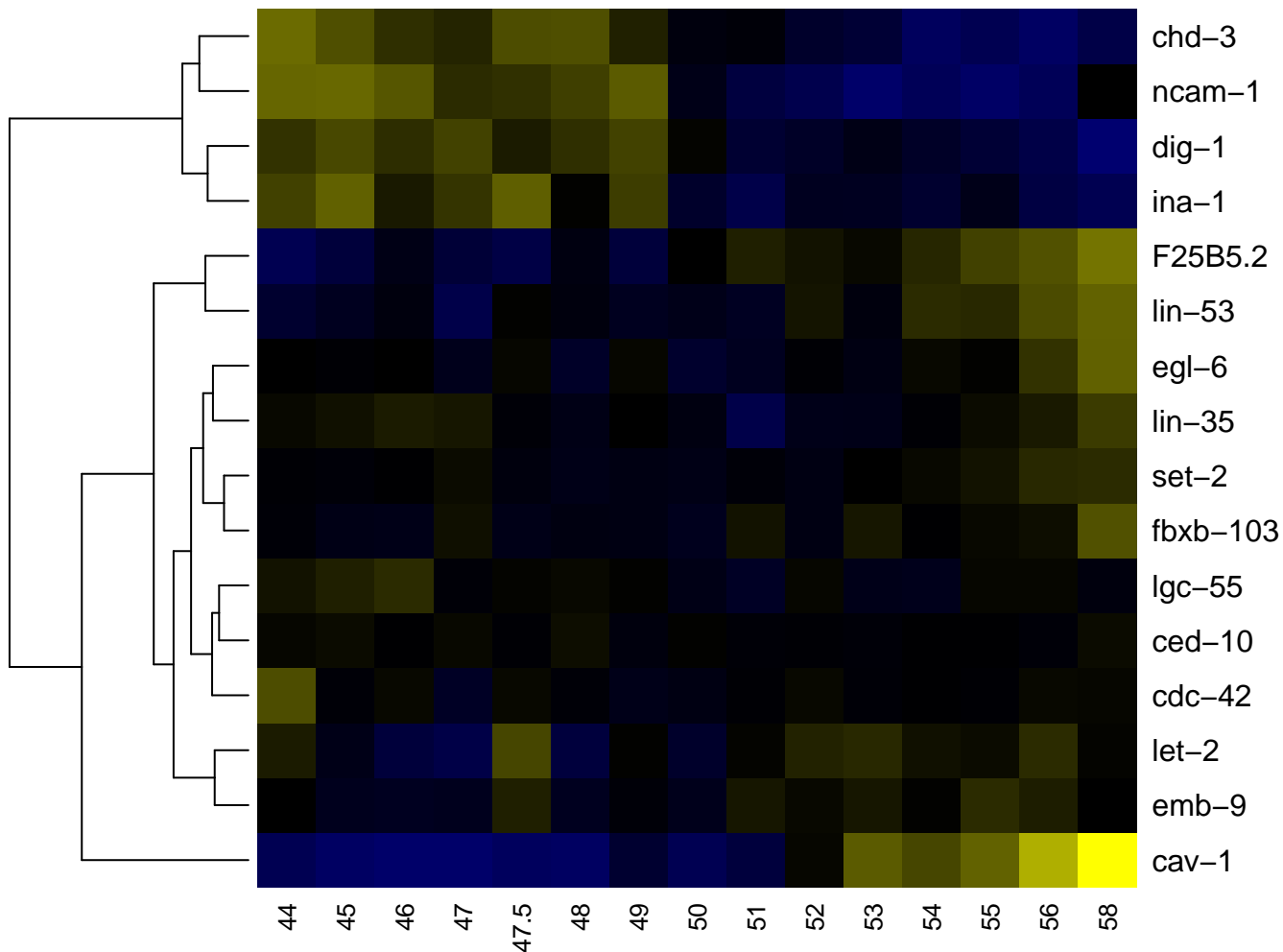
GABAergic neuron



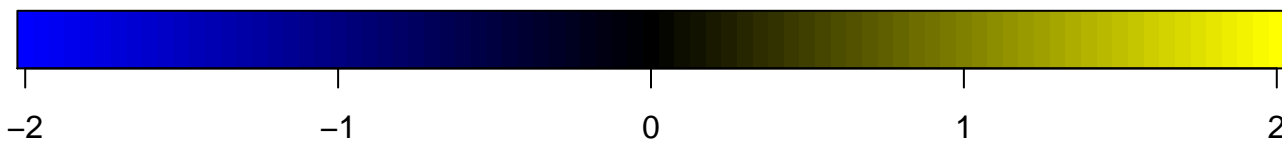
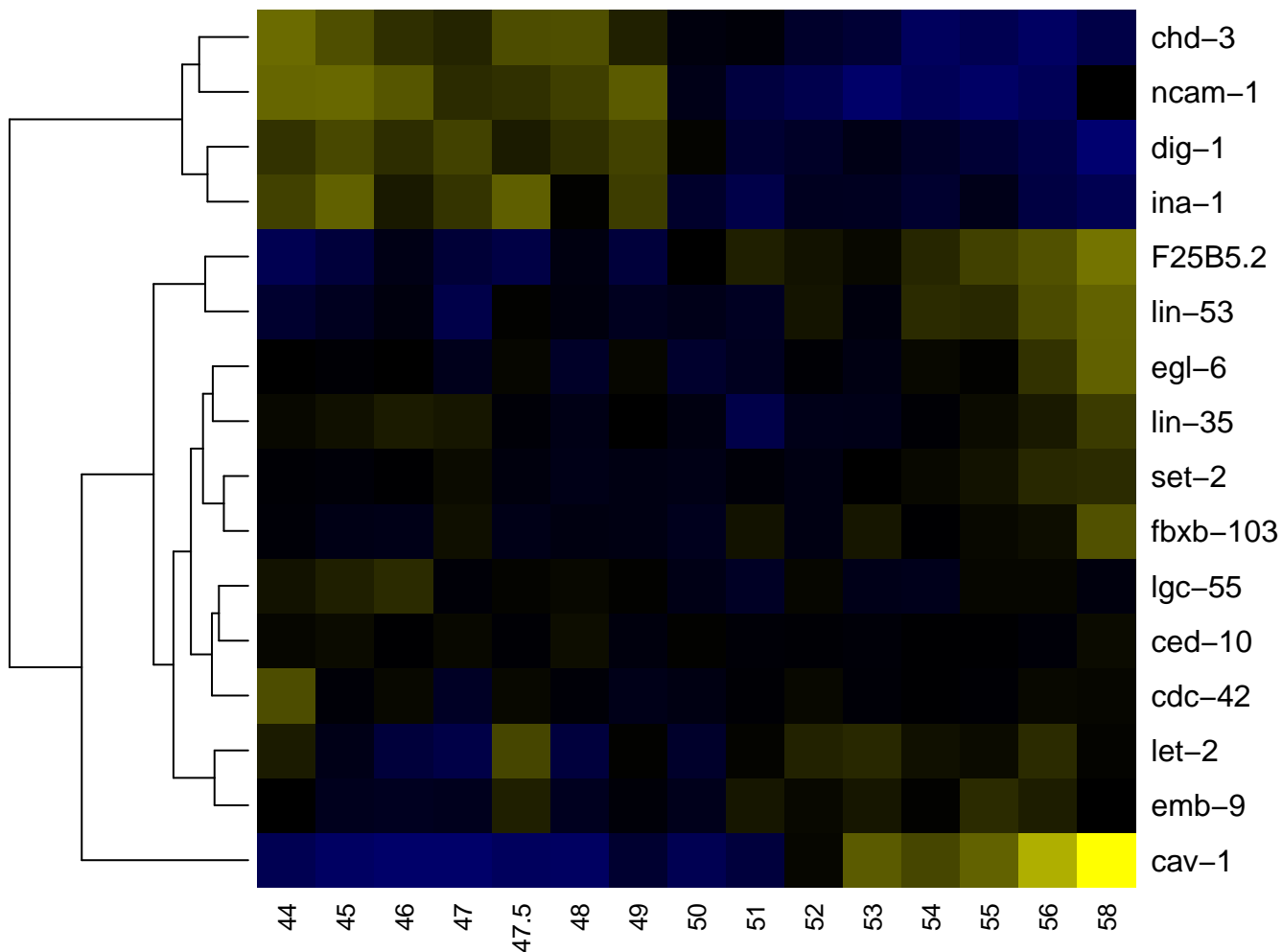
germ line



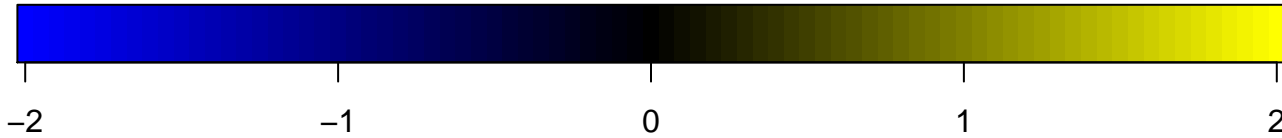
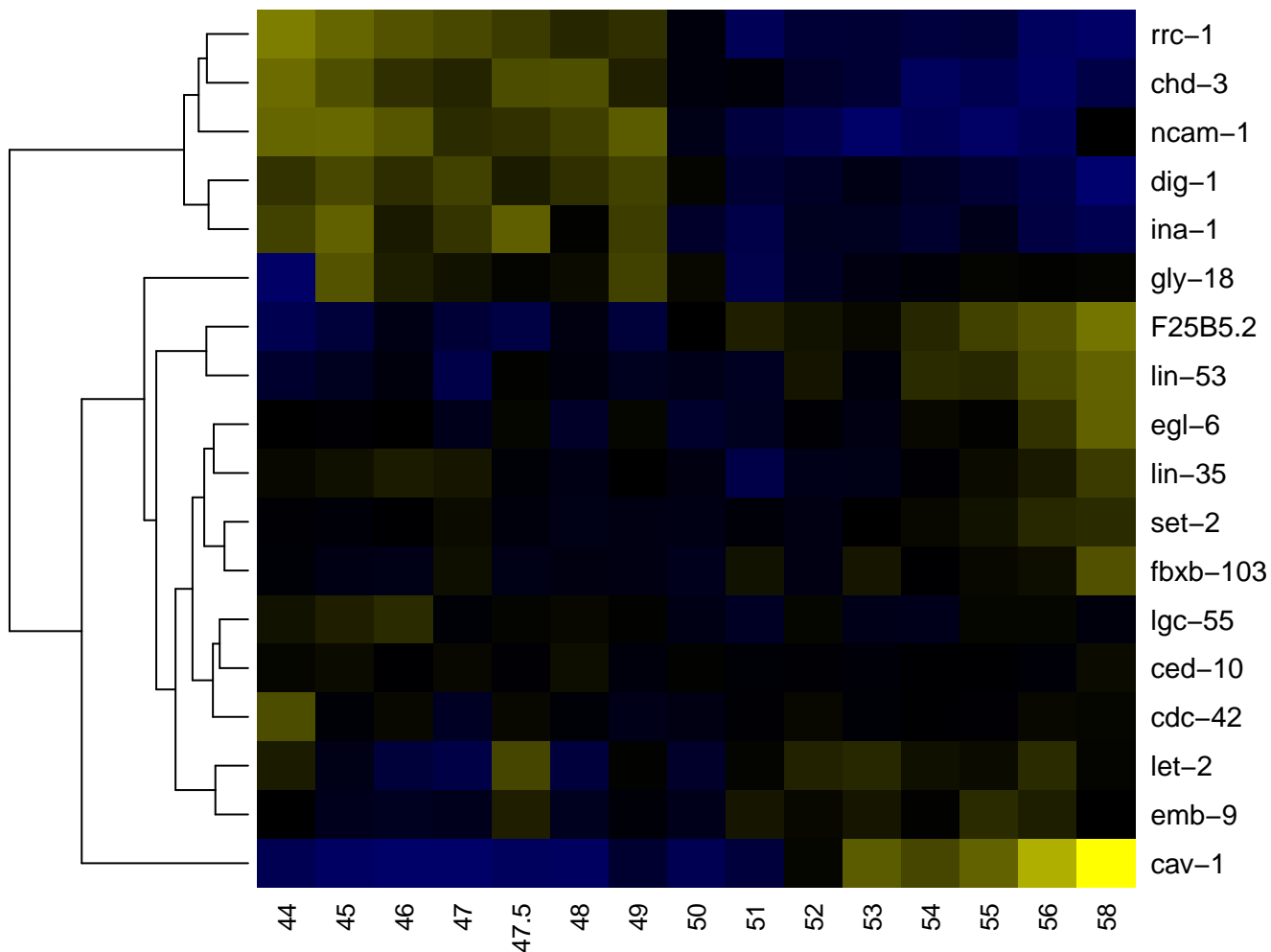
GLRD



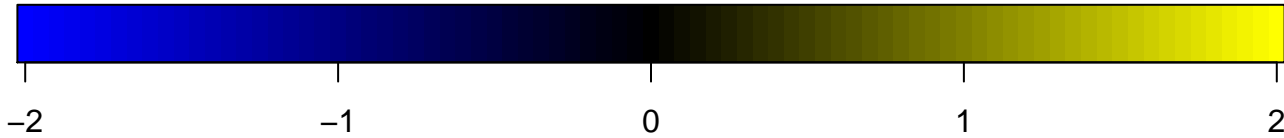
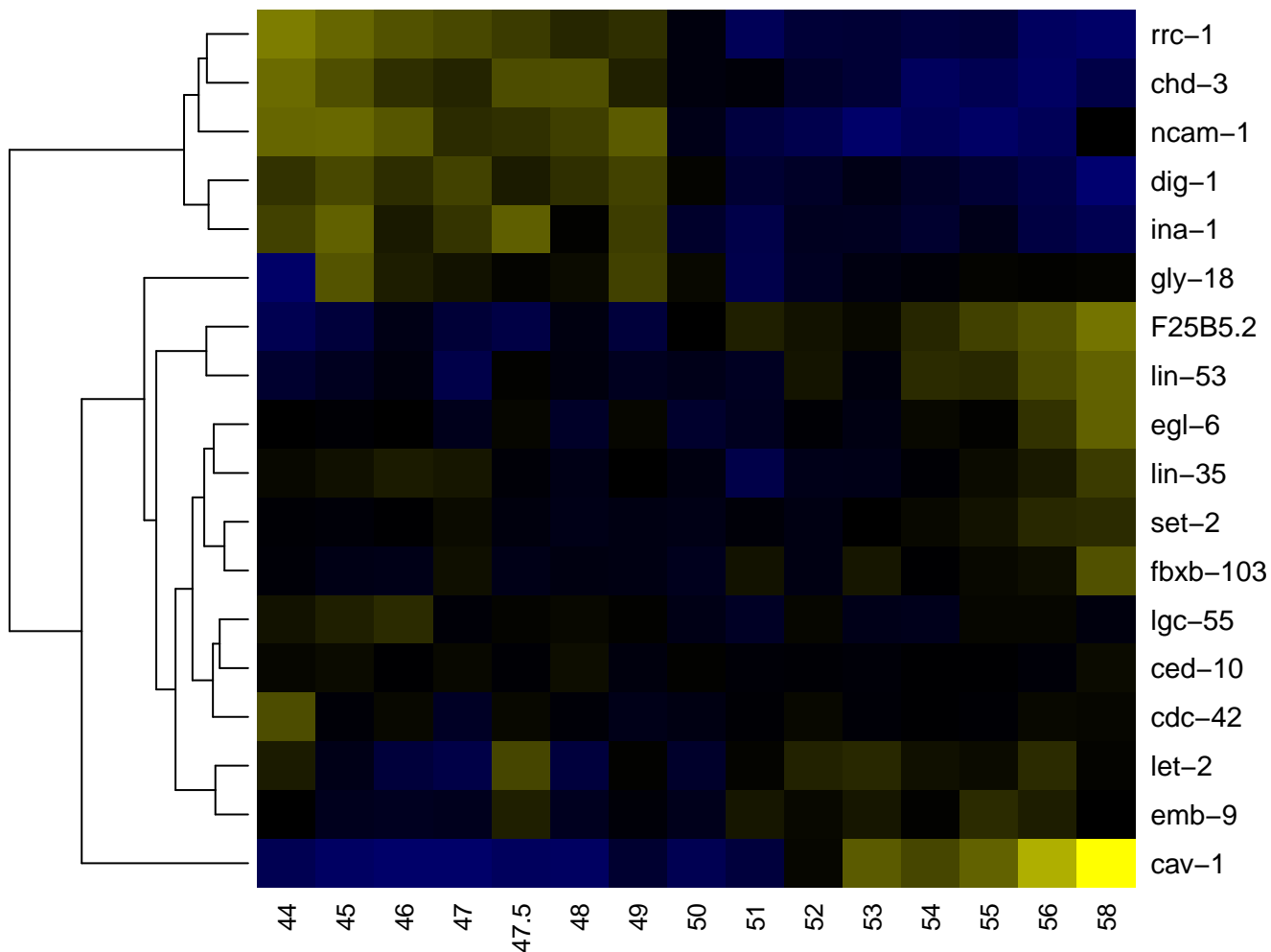
GLRDR



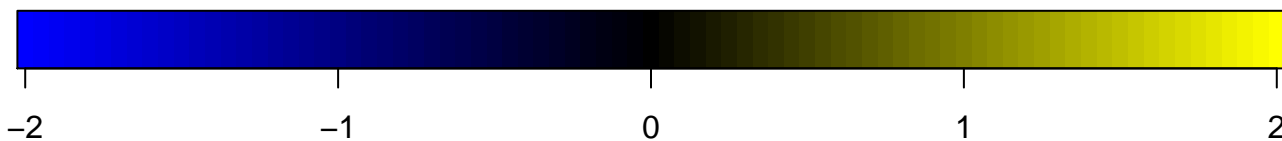
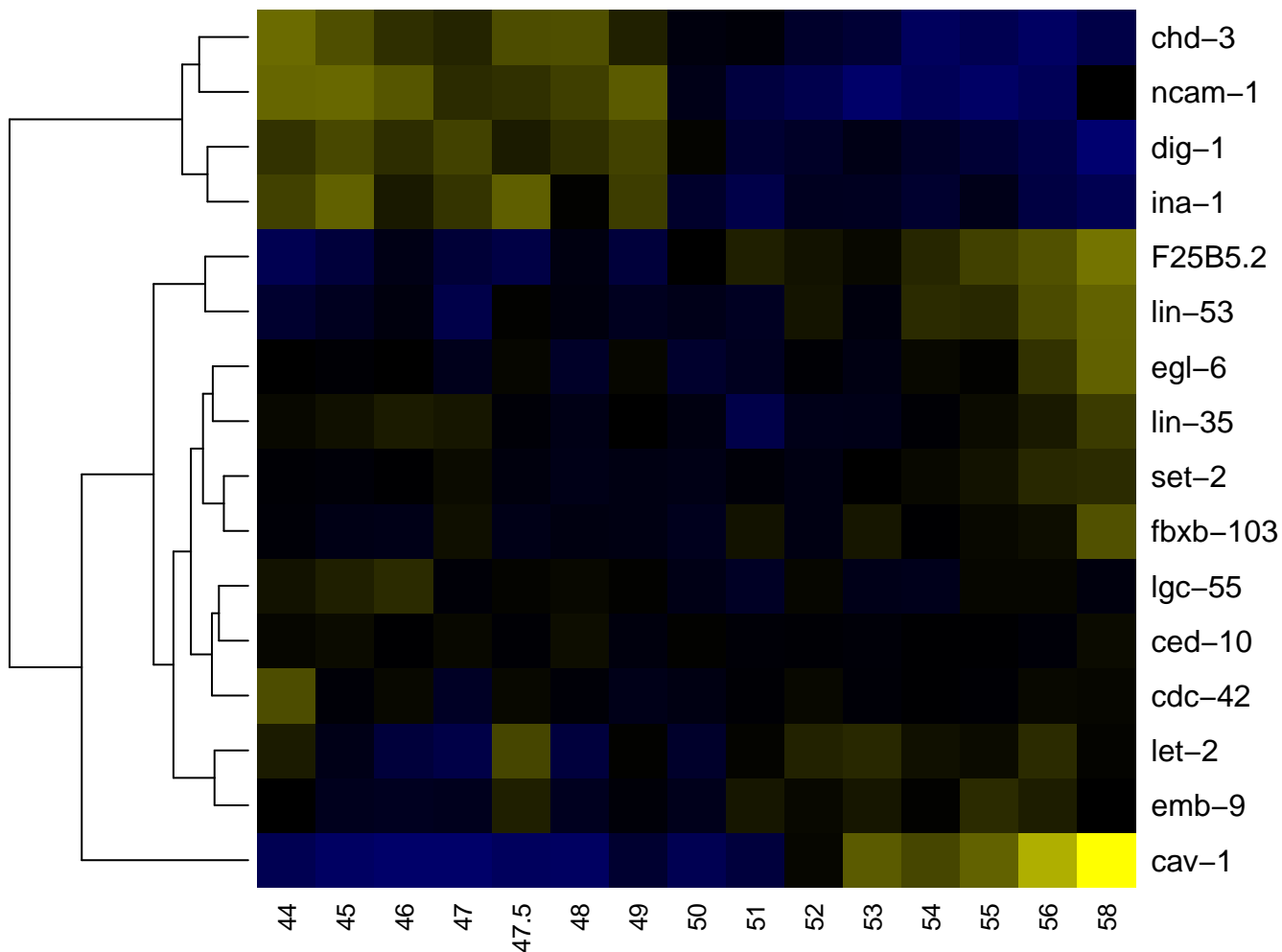
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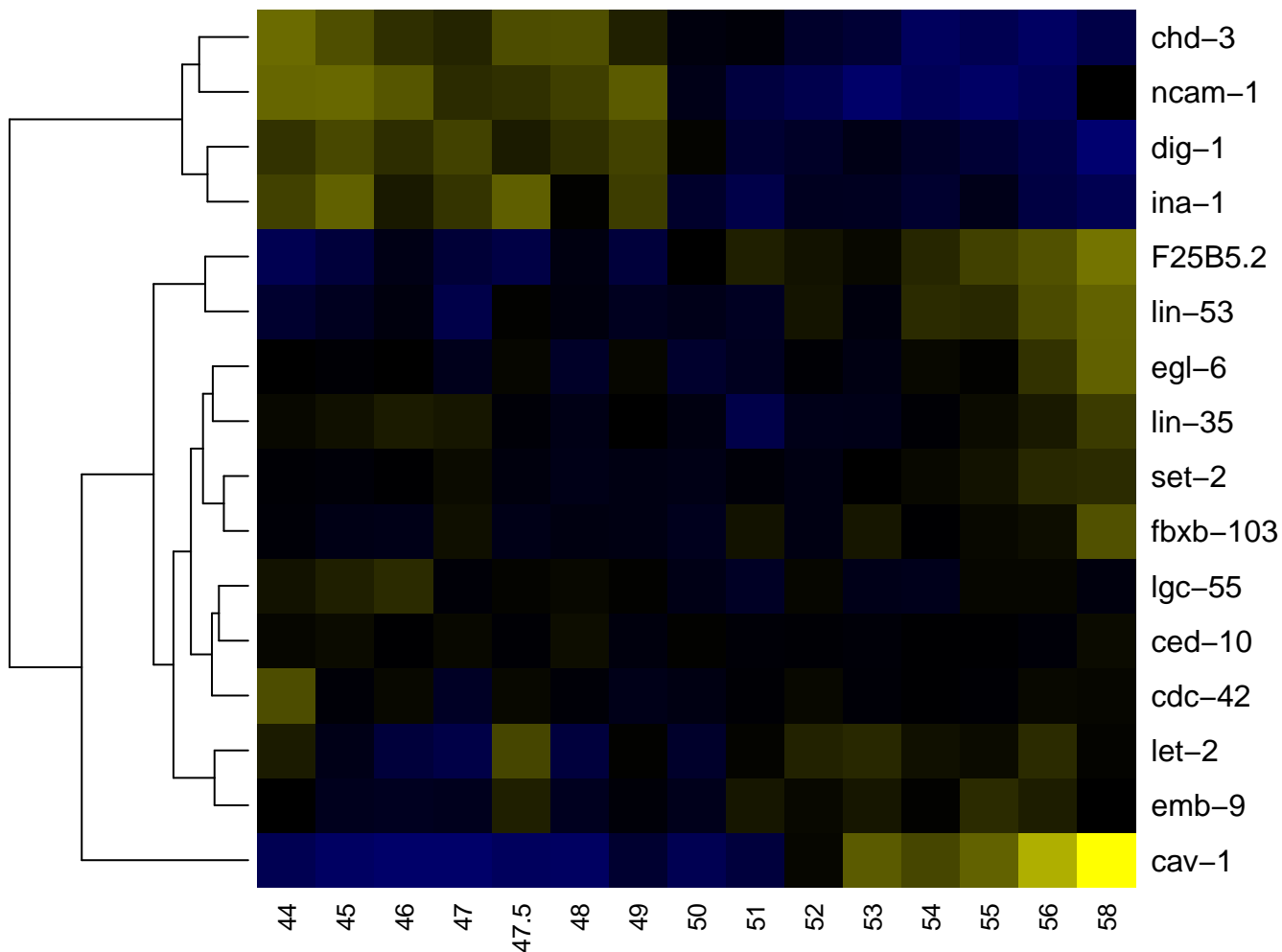
GLRR



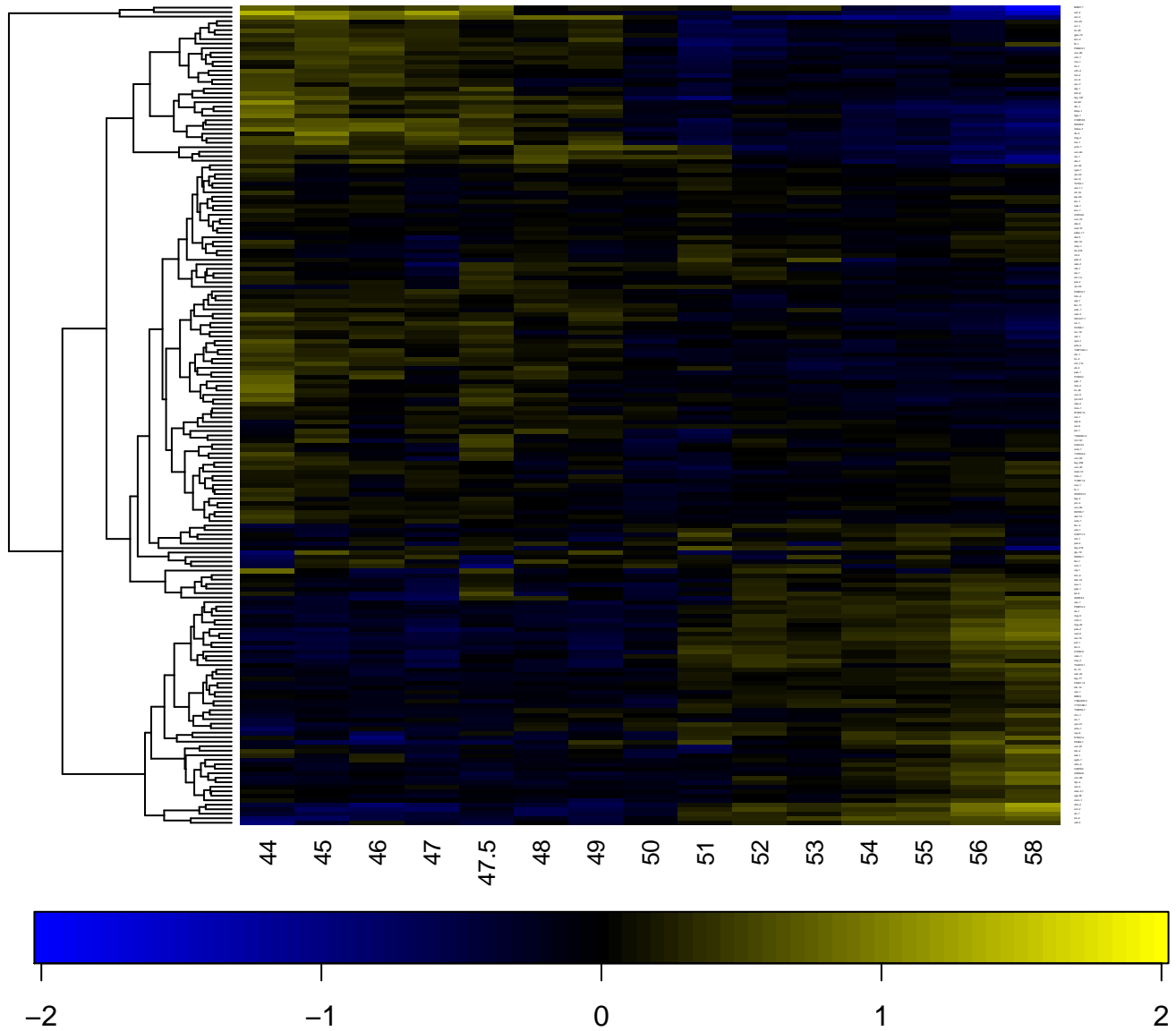
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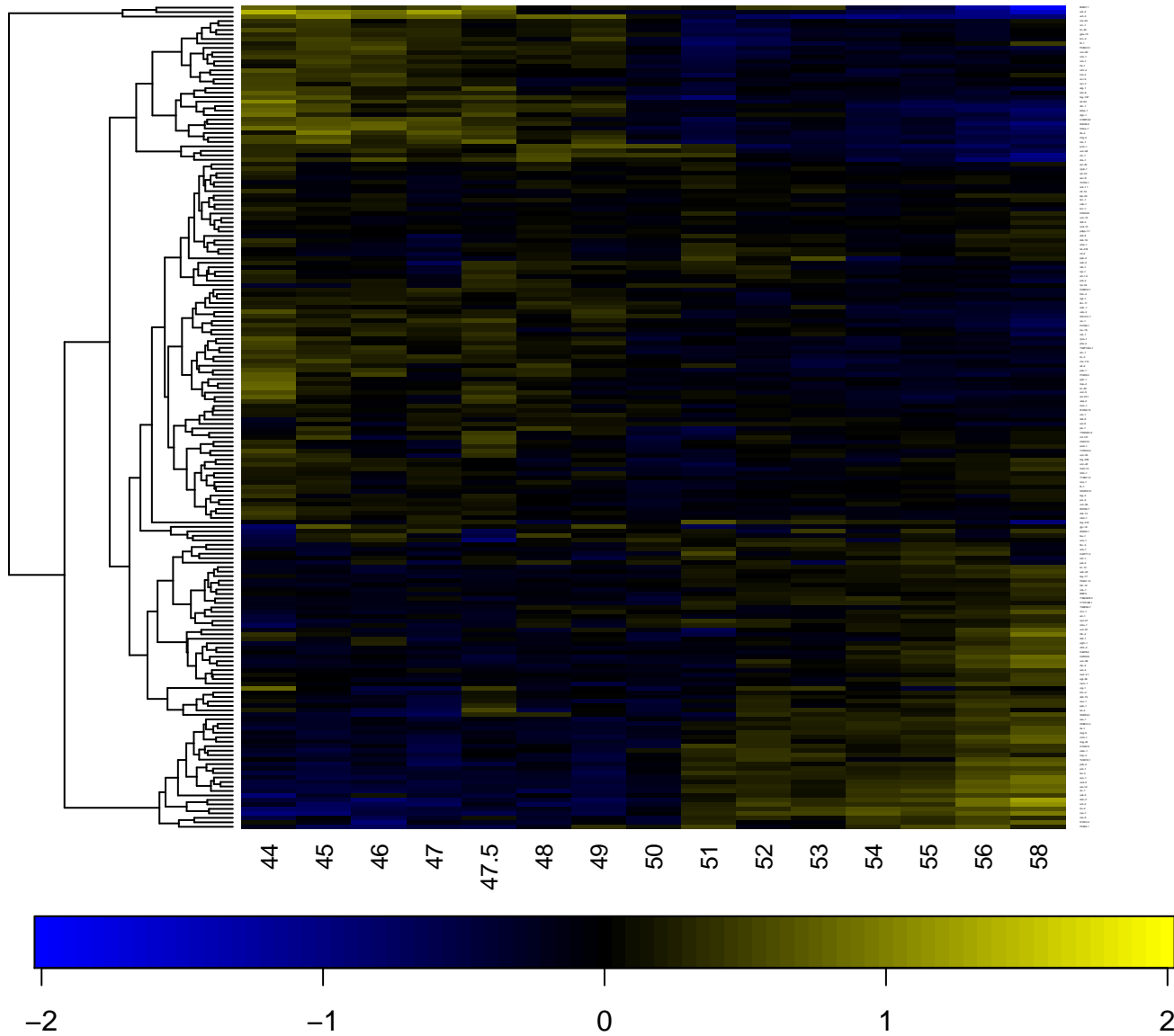
GLRVR



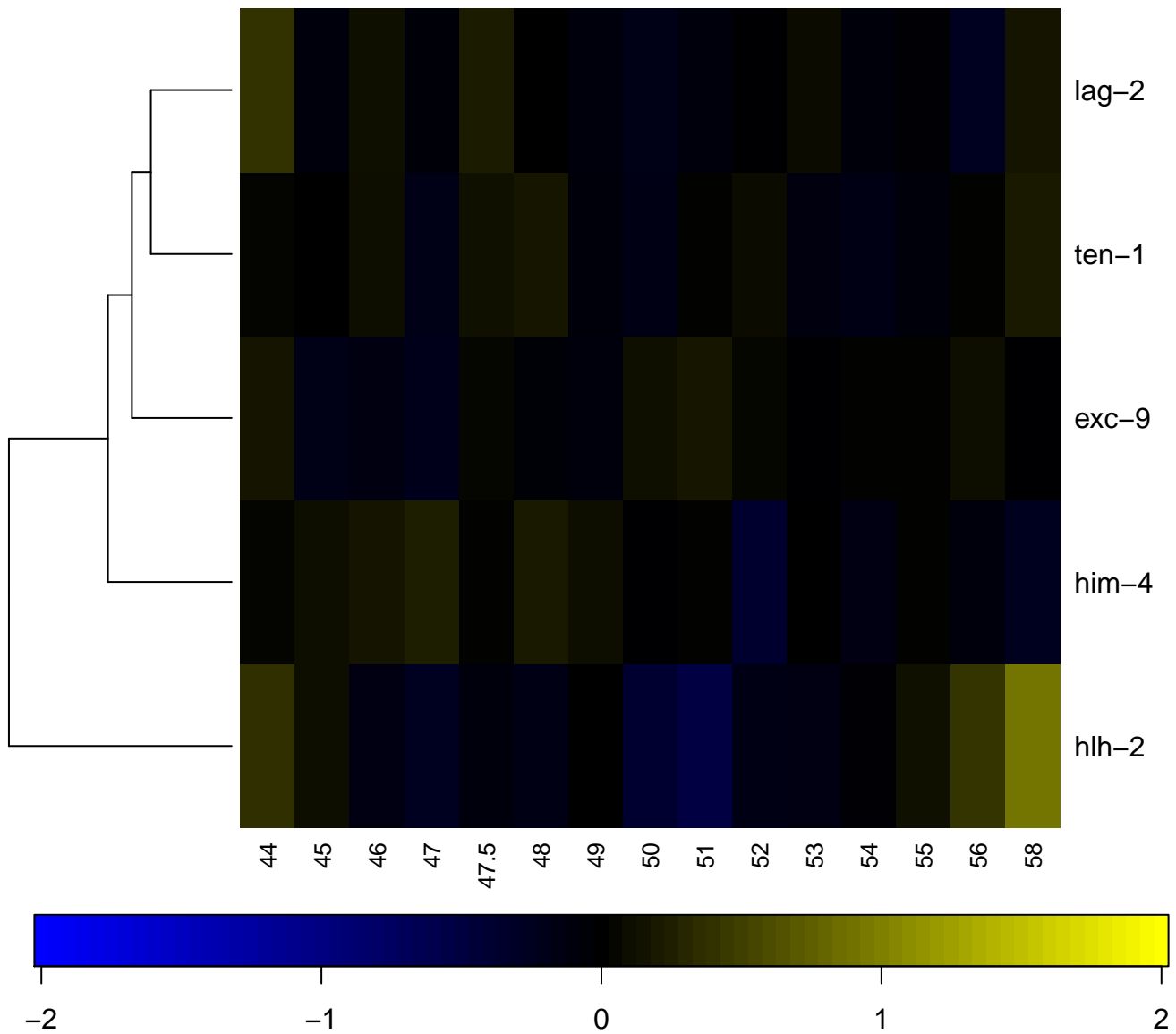
gon_herm_dtc_A



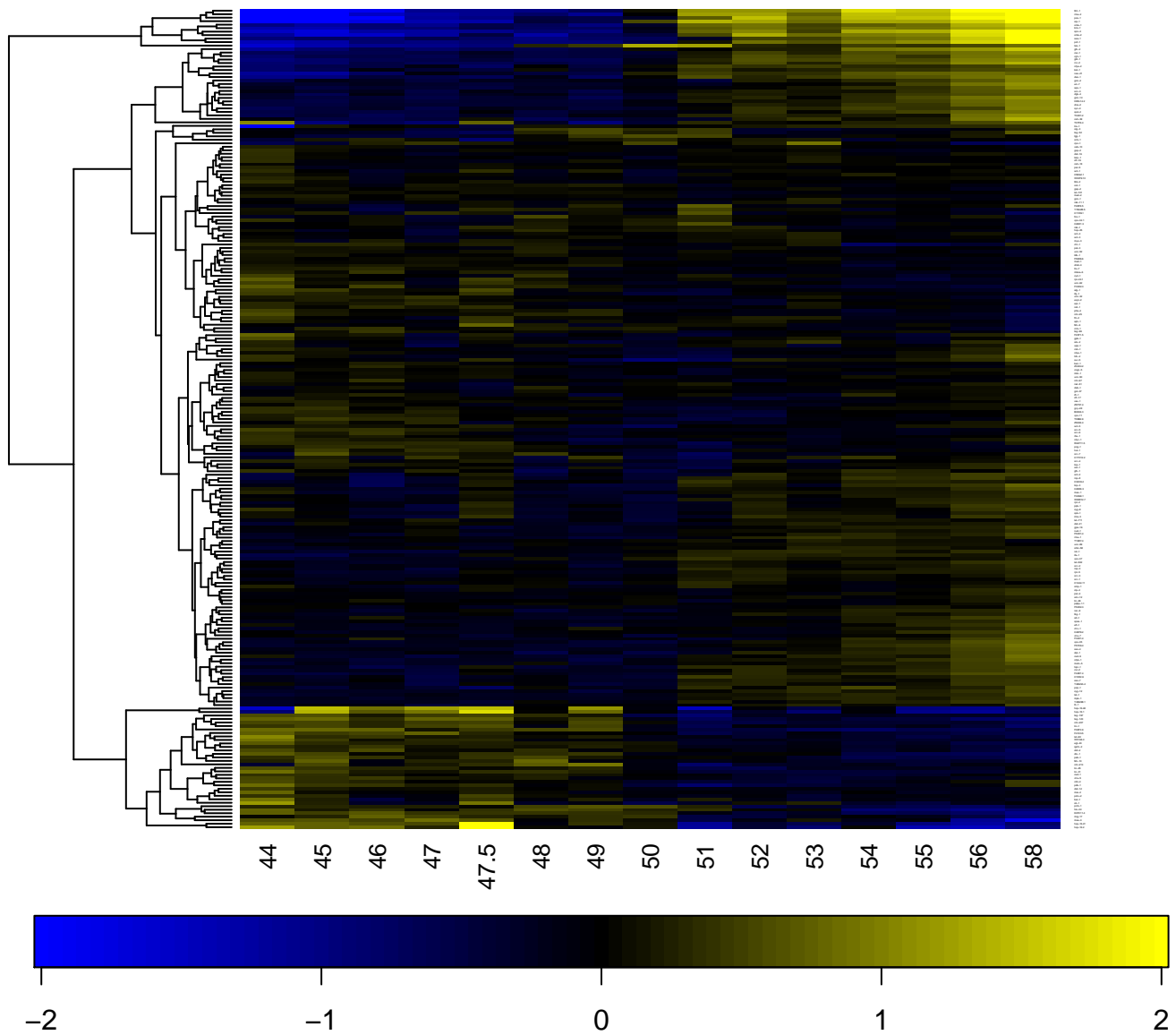
gon_herm_dtc_P



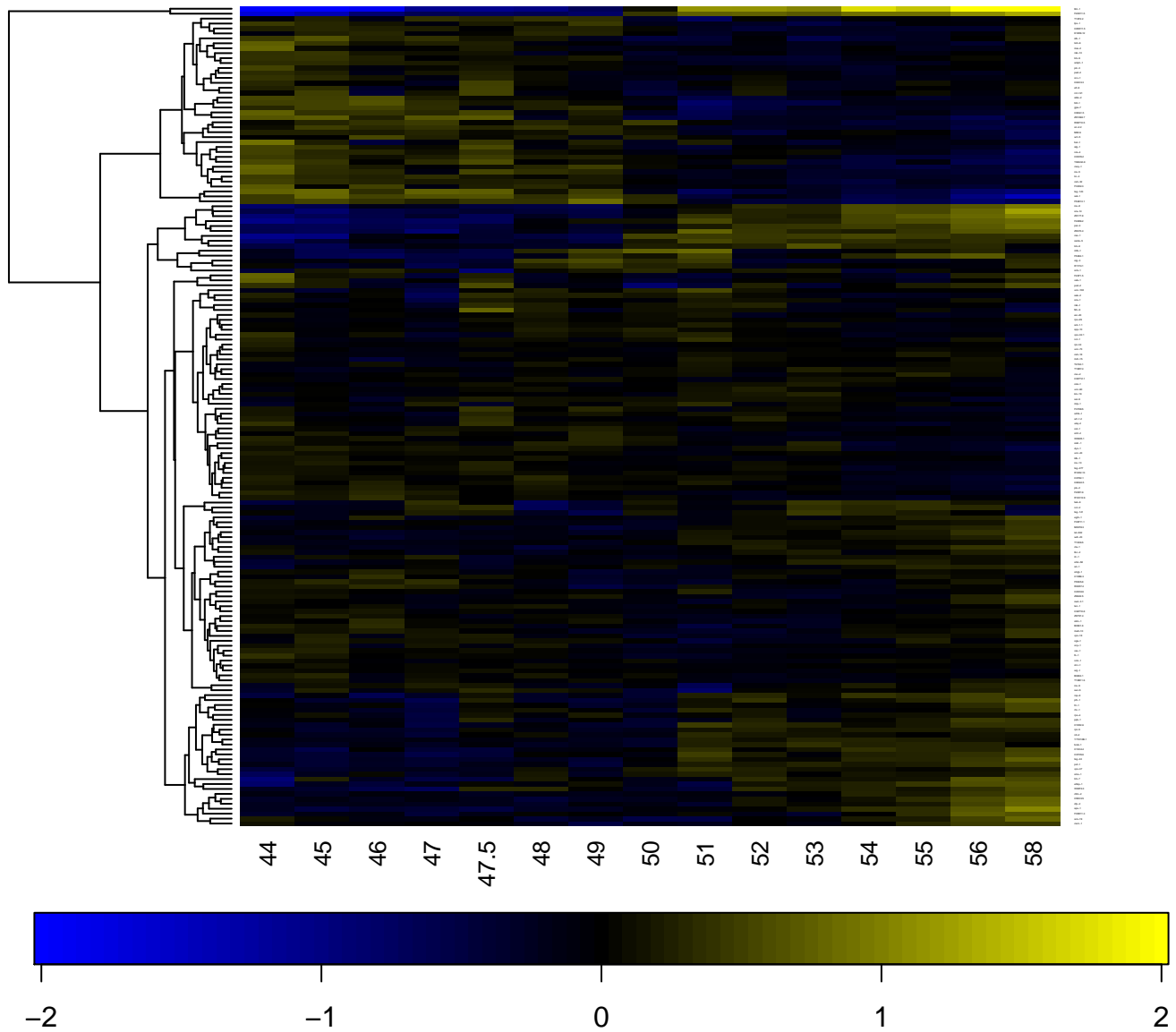
gon_male_dtc posterior



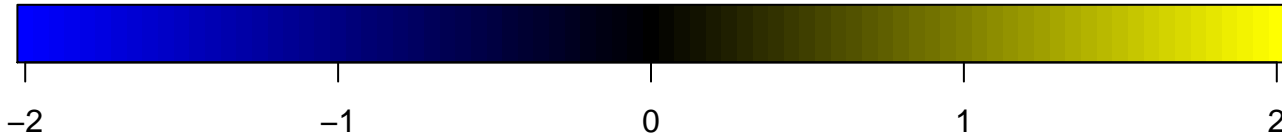
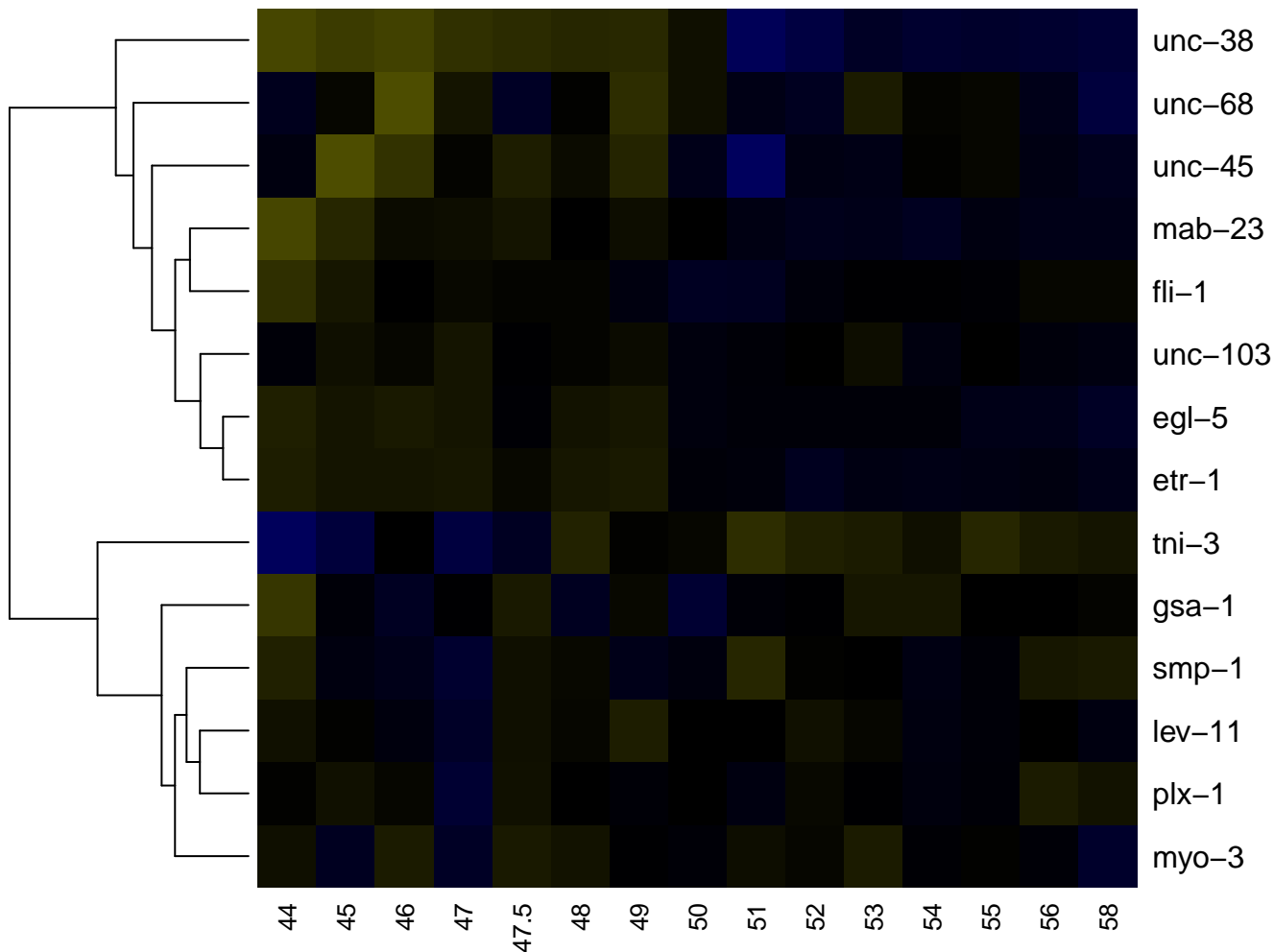
gonad



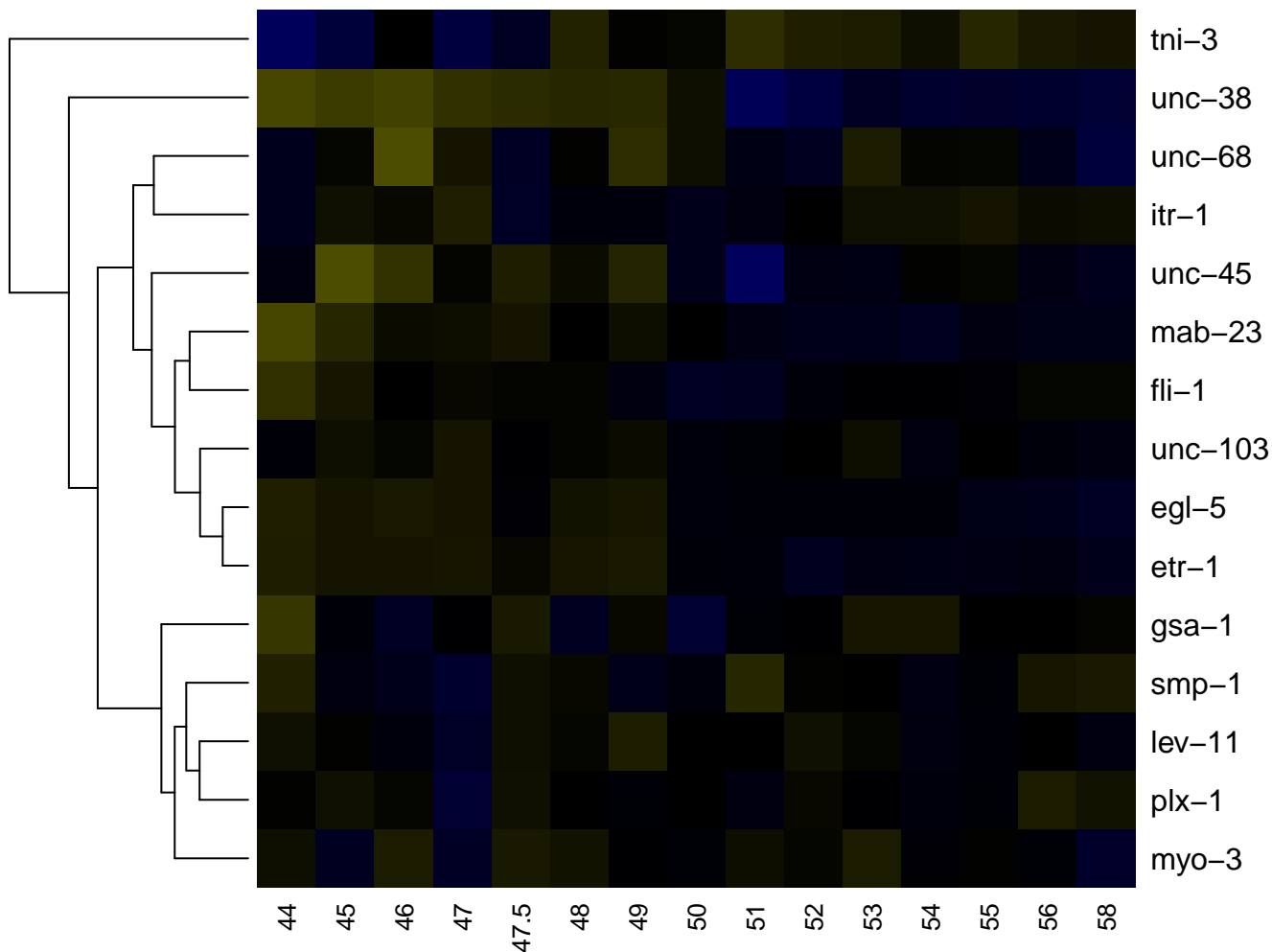
gonadal sheath cell



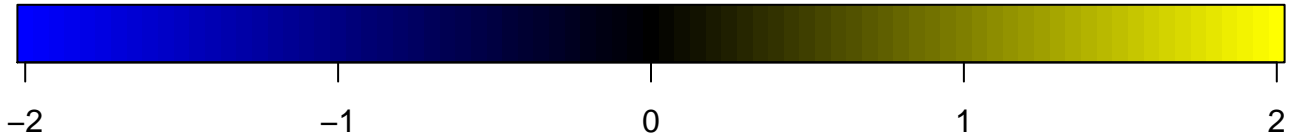
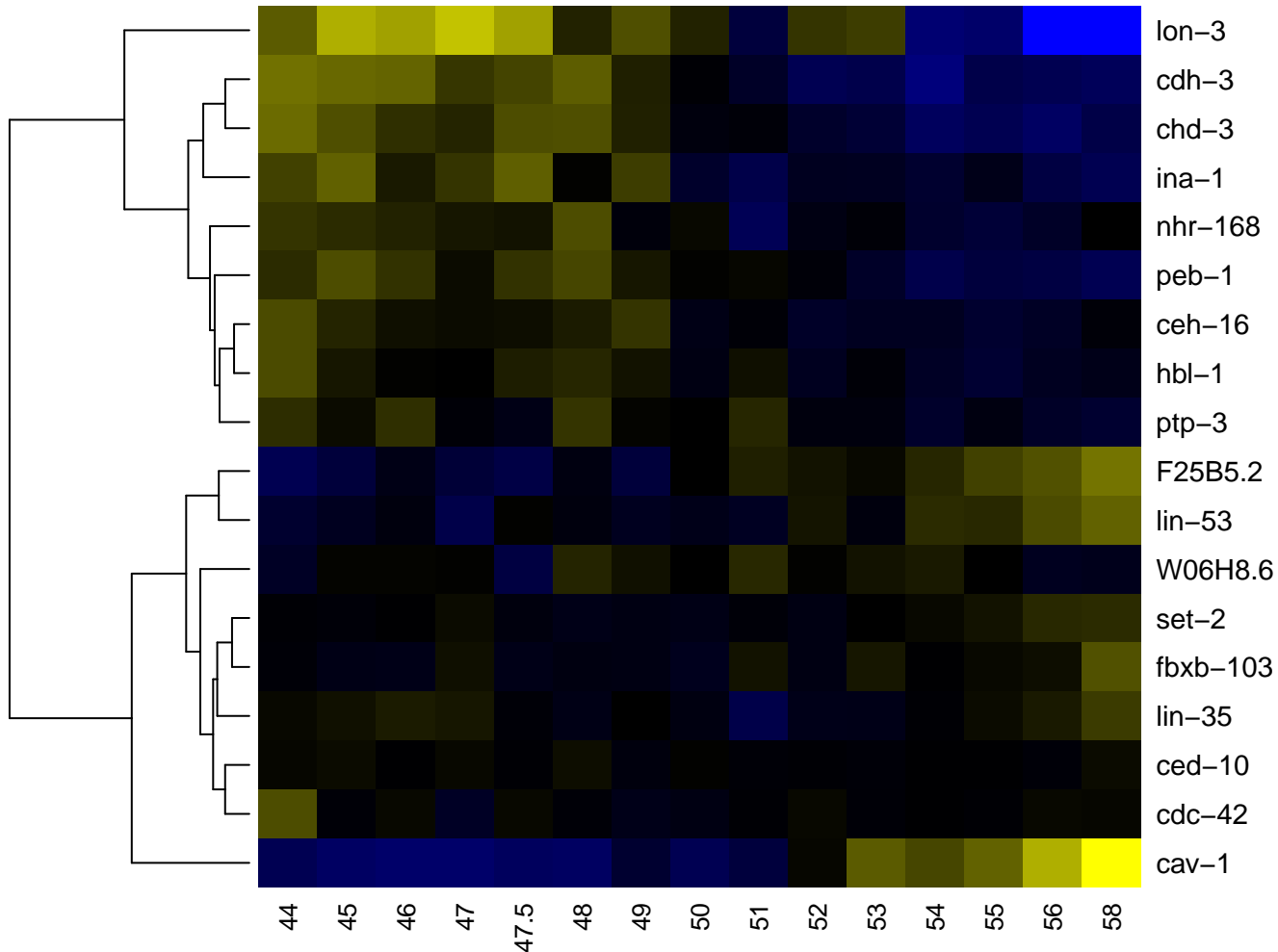
gubernacular erector muscle



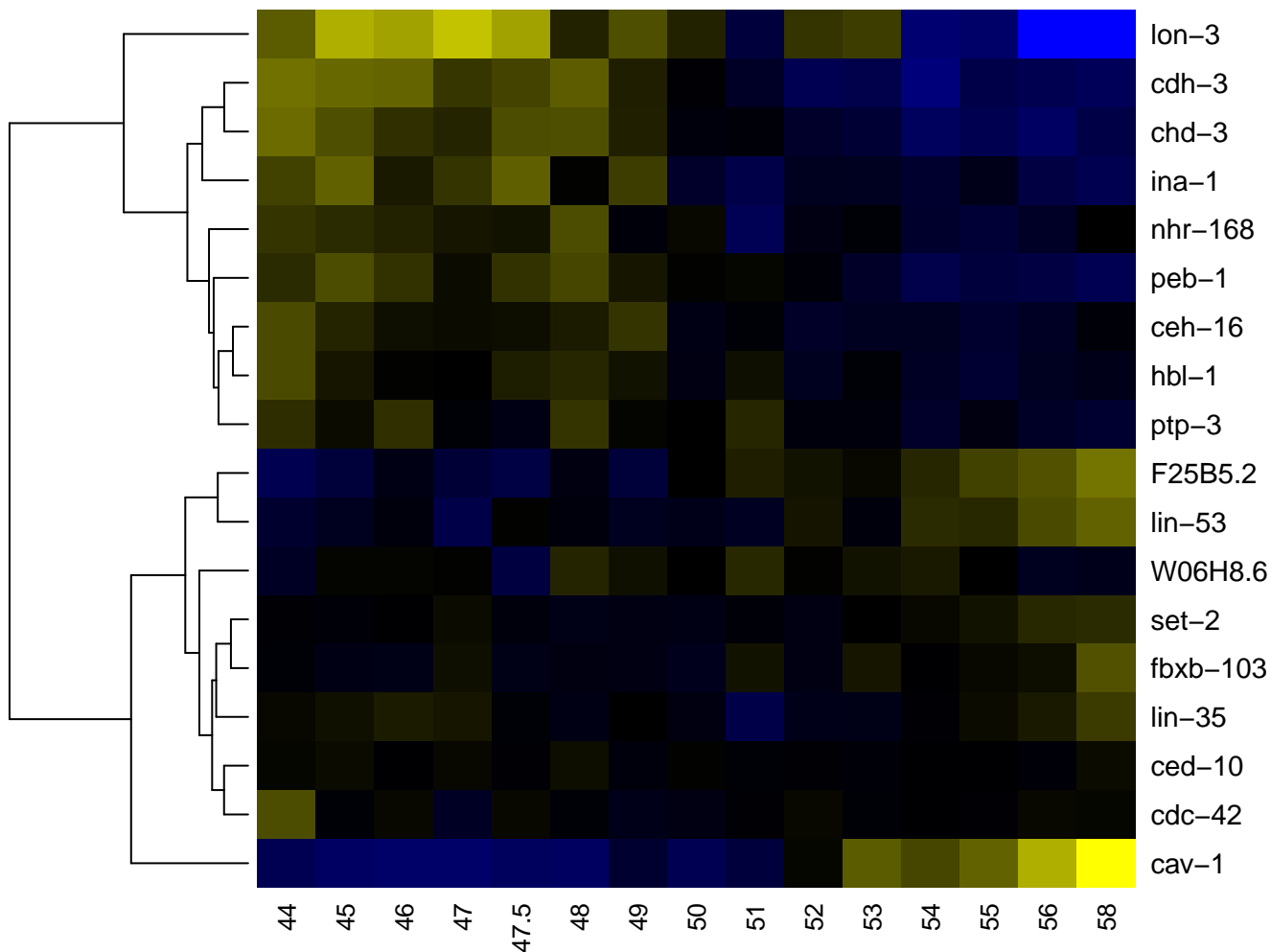
gubernacular retractor muscle



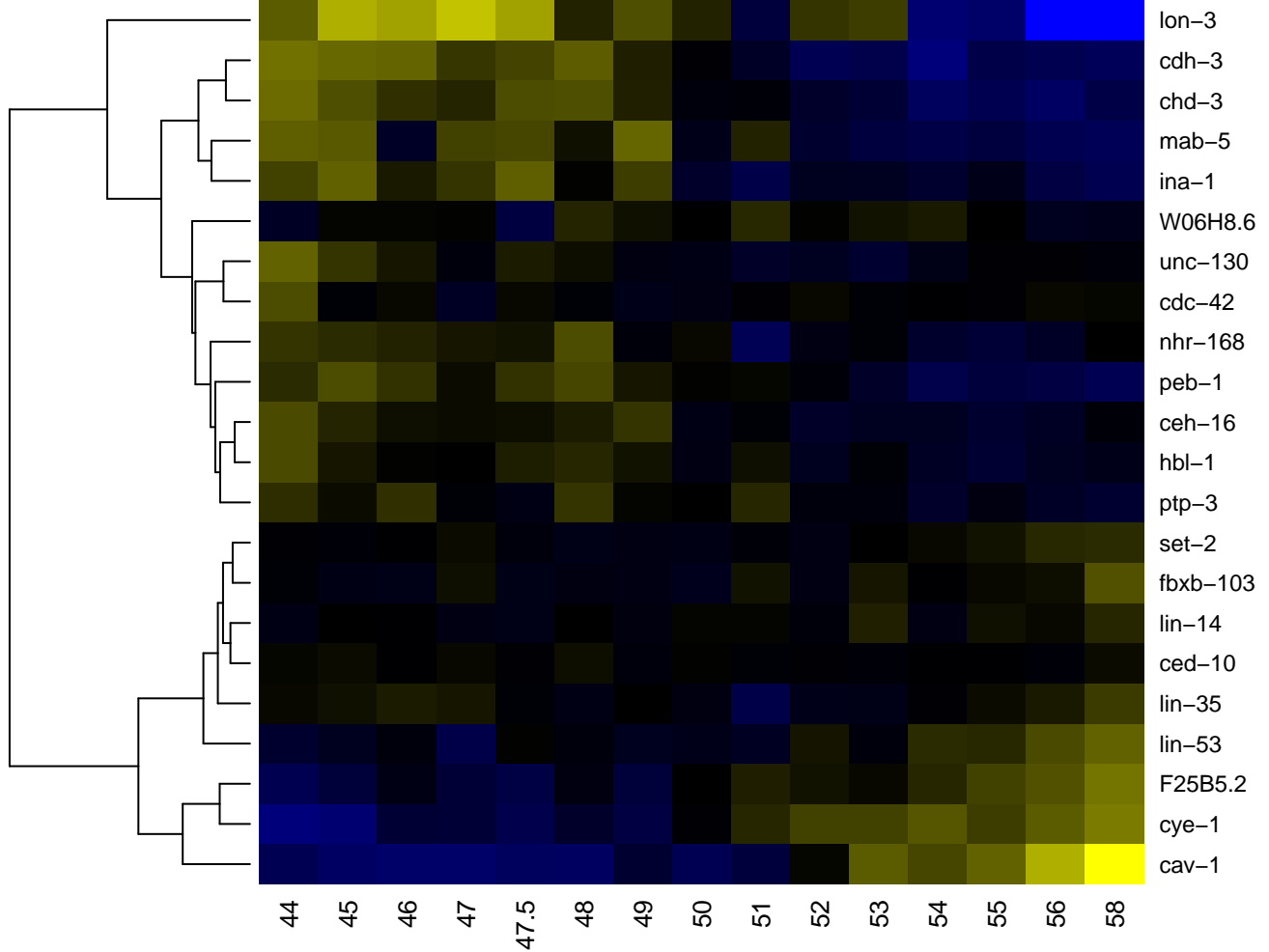
HOL



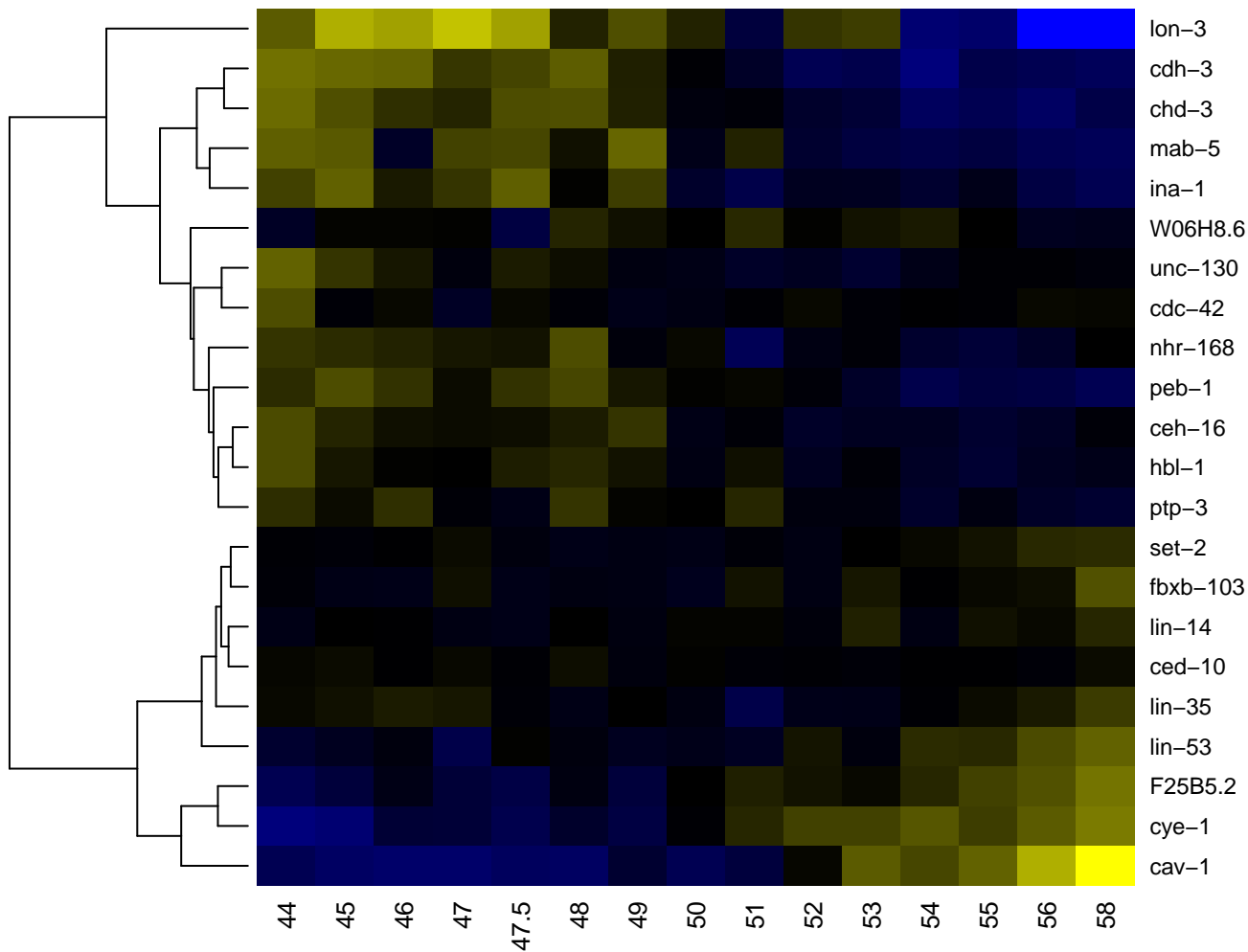
H0R



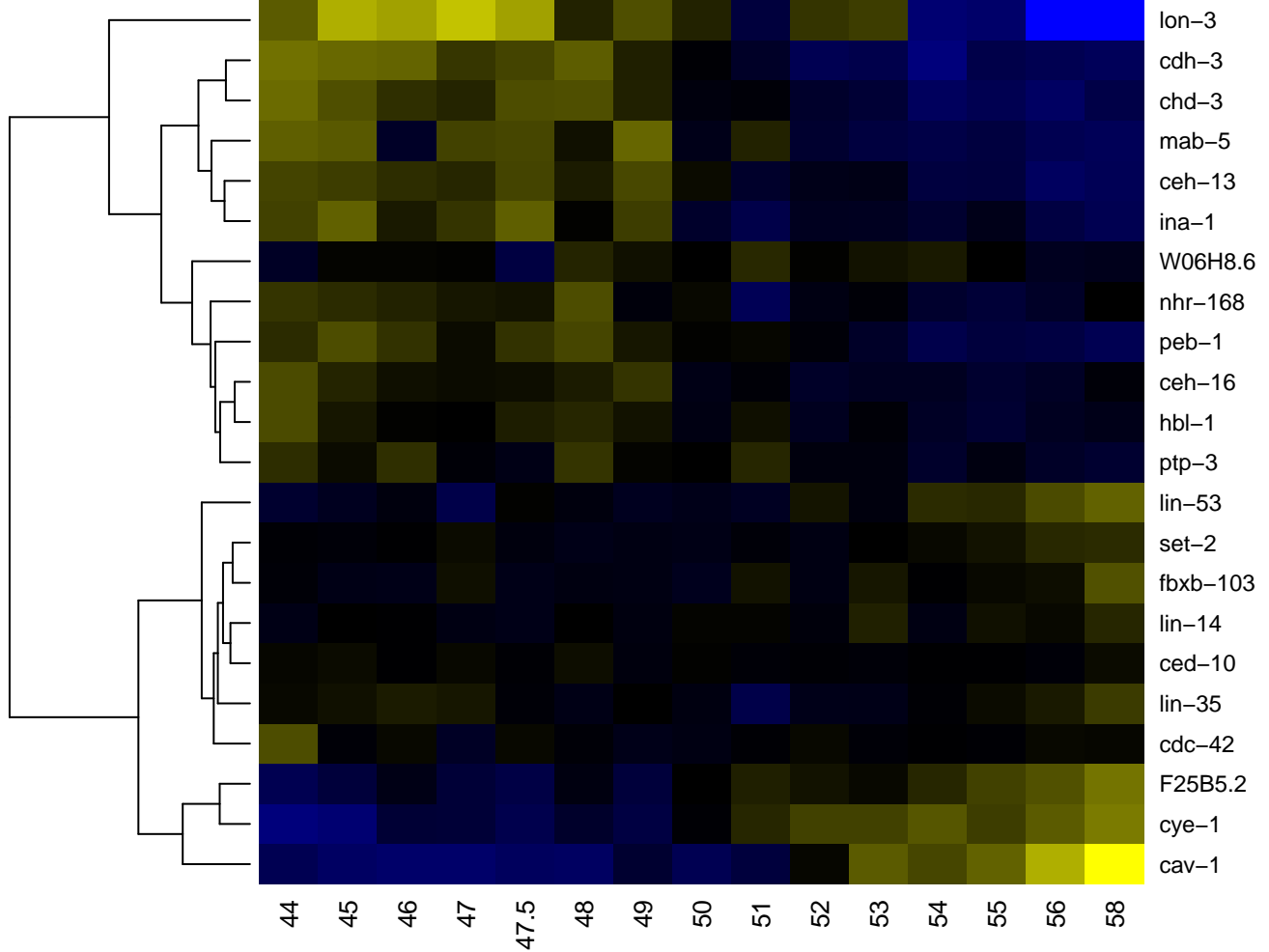
H1L



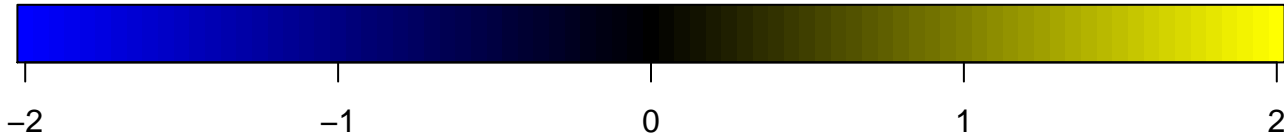
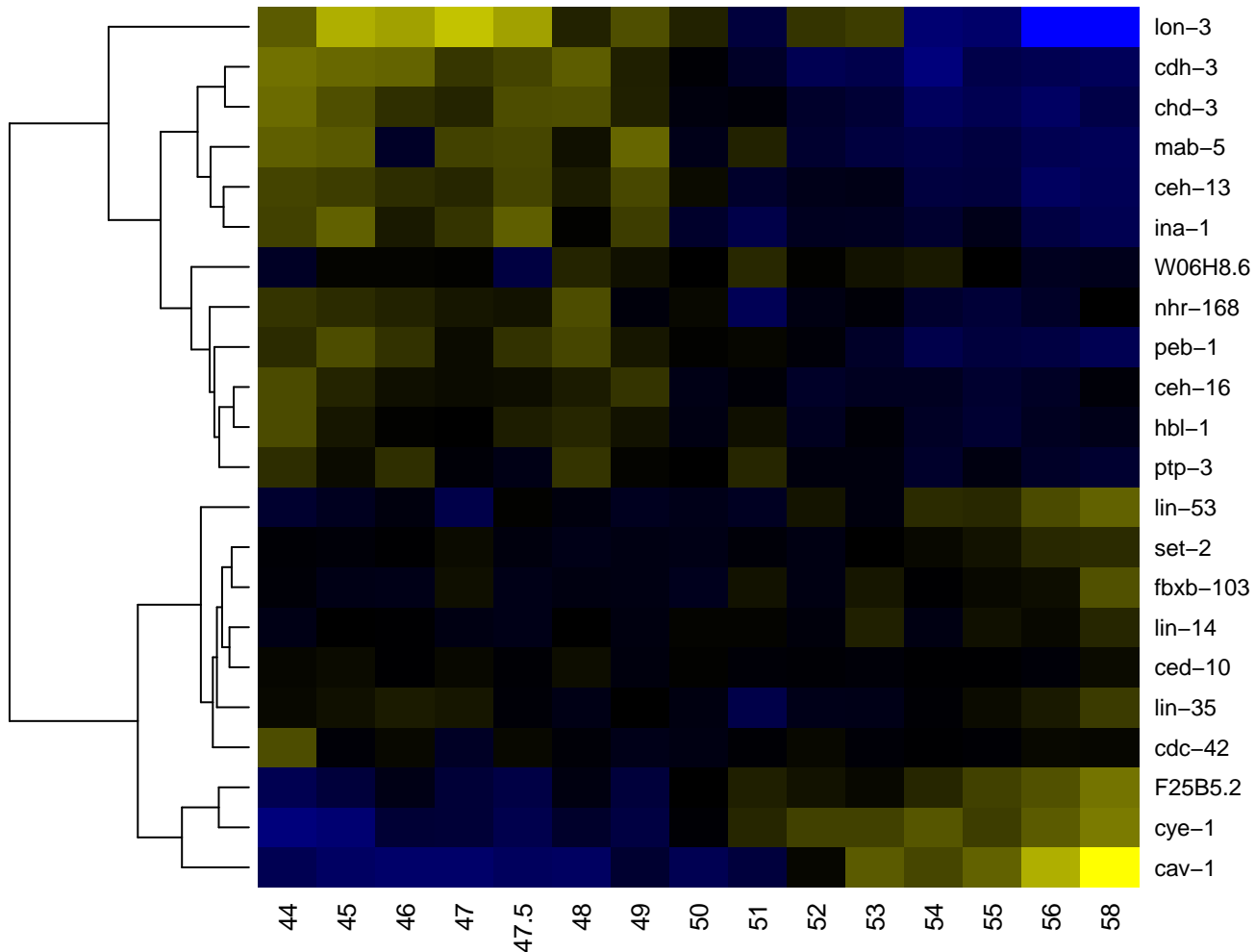
H1R



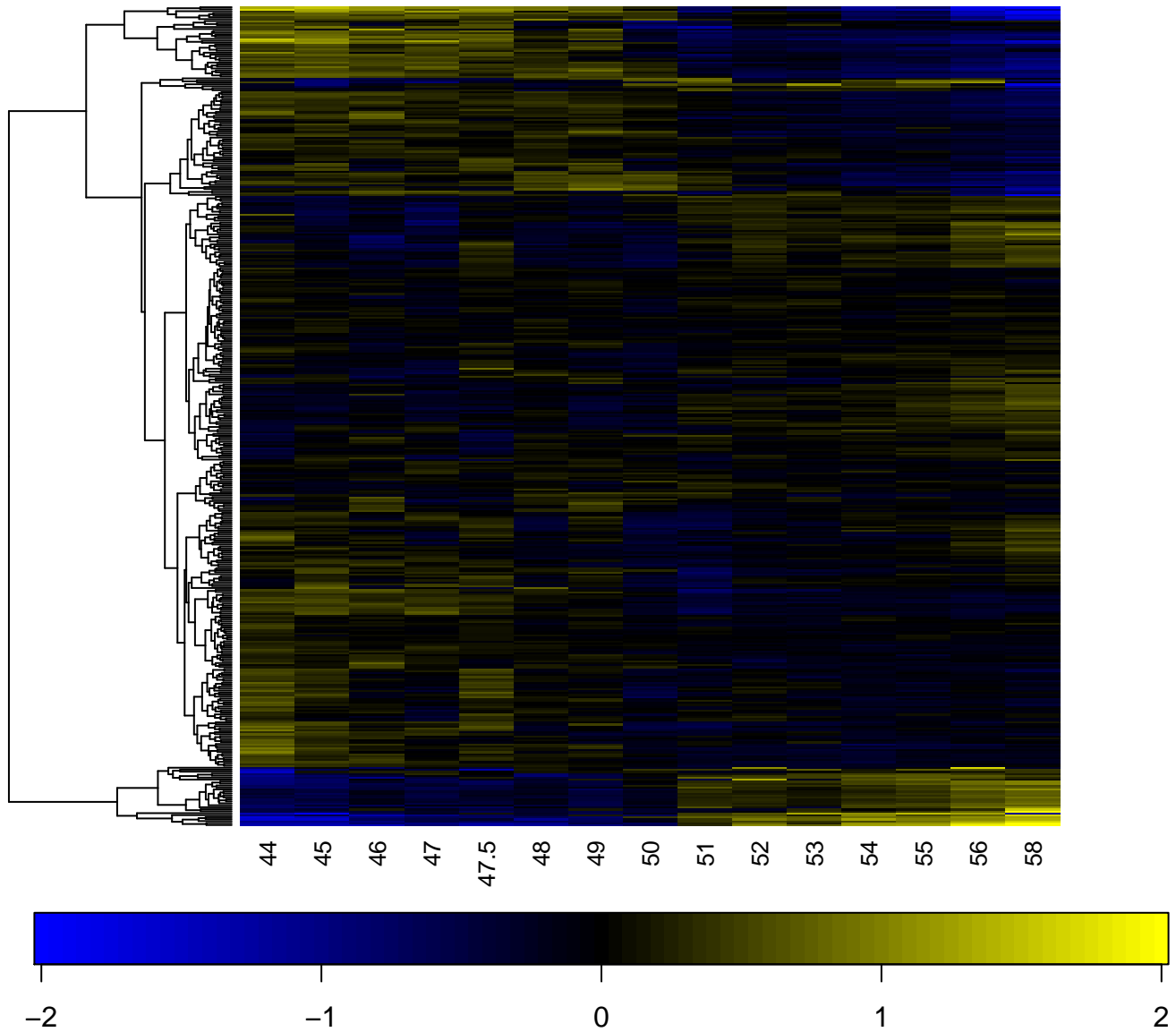
H2L



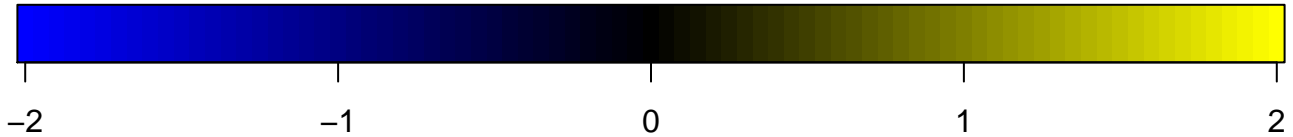
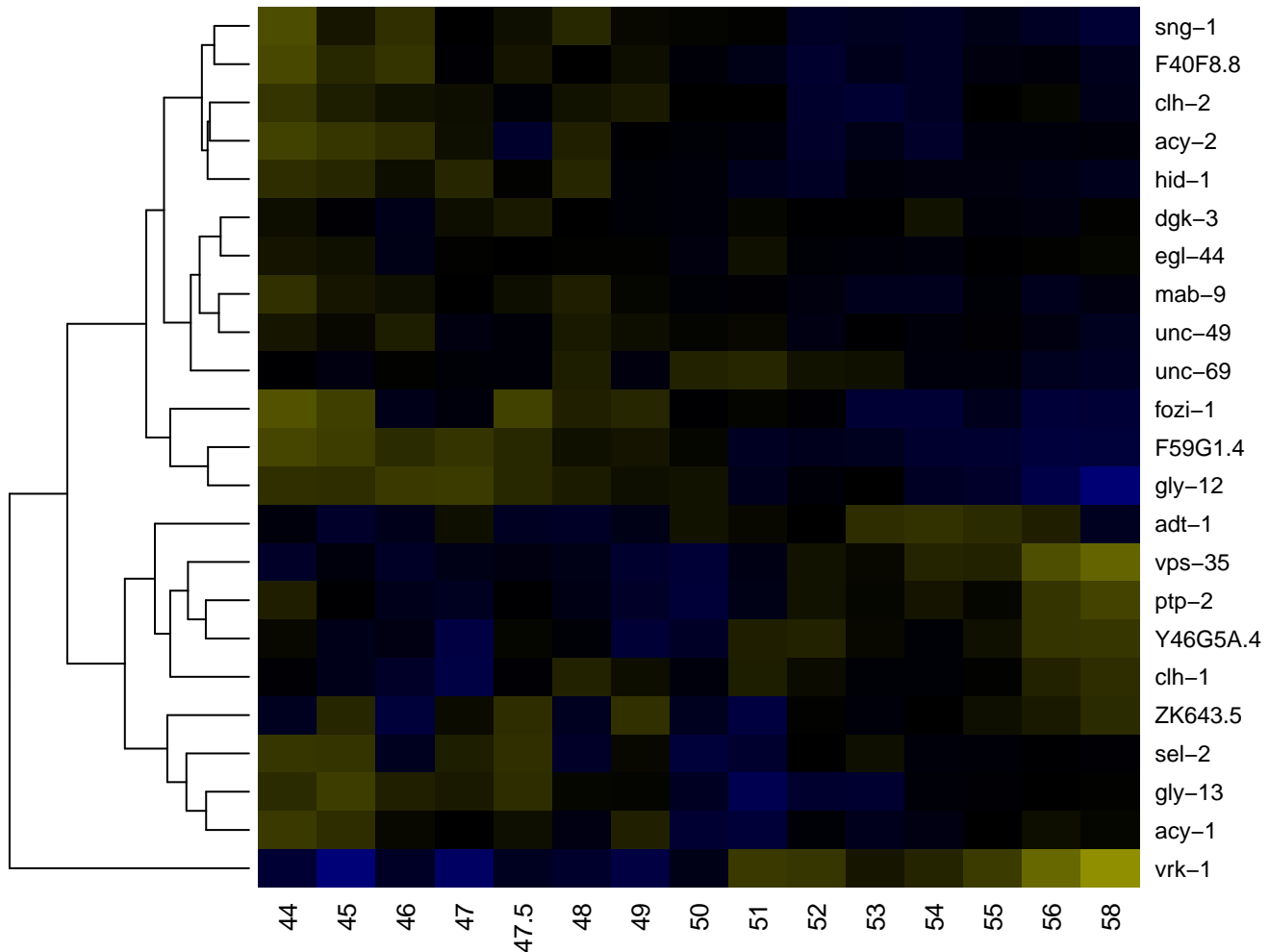
H2R



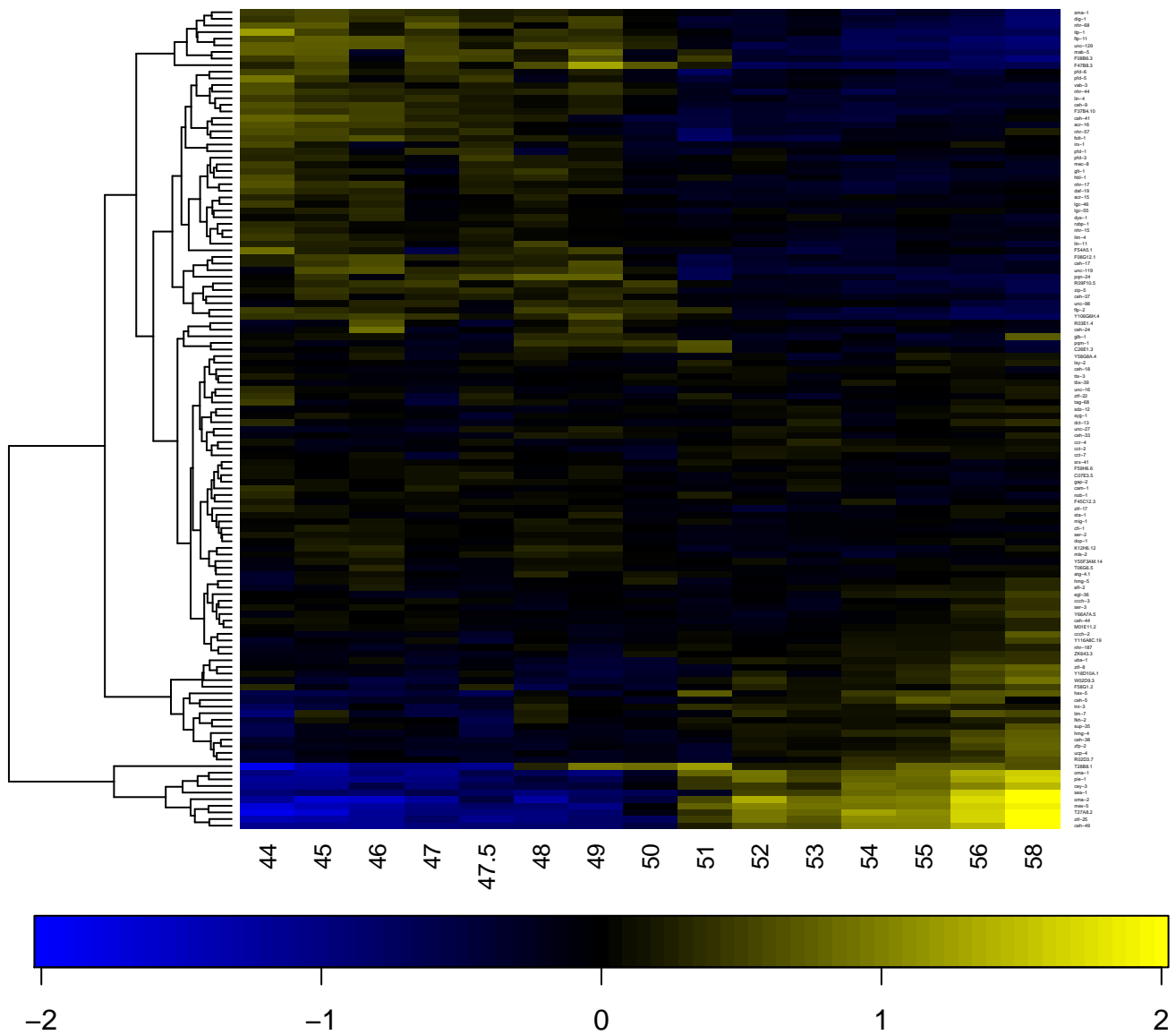
head



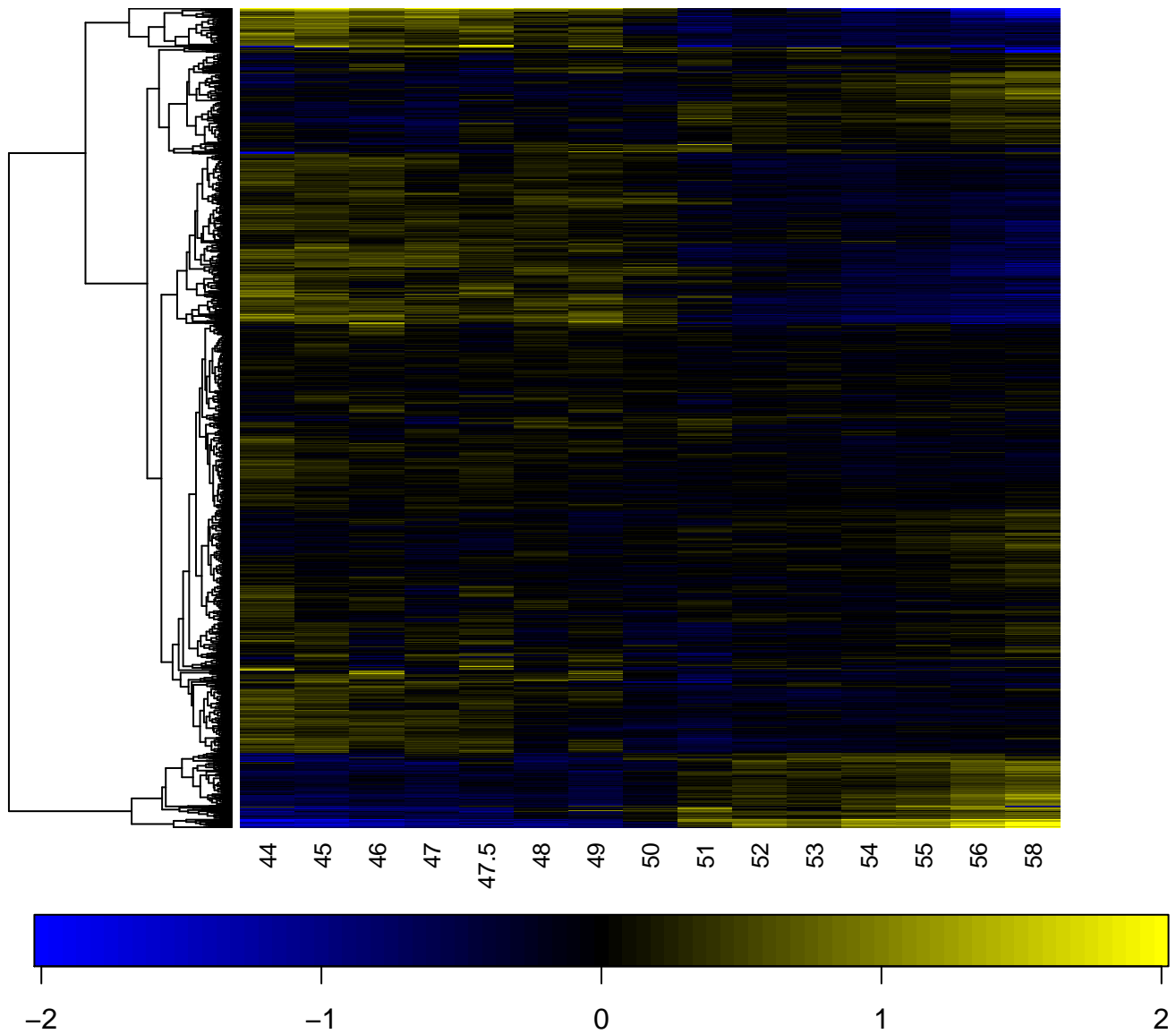
head ganglion



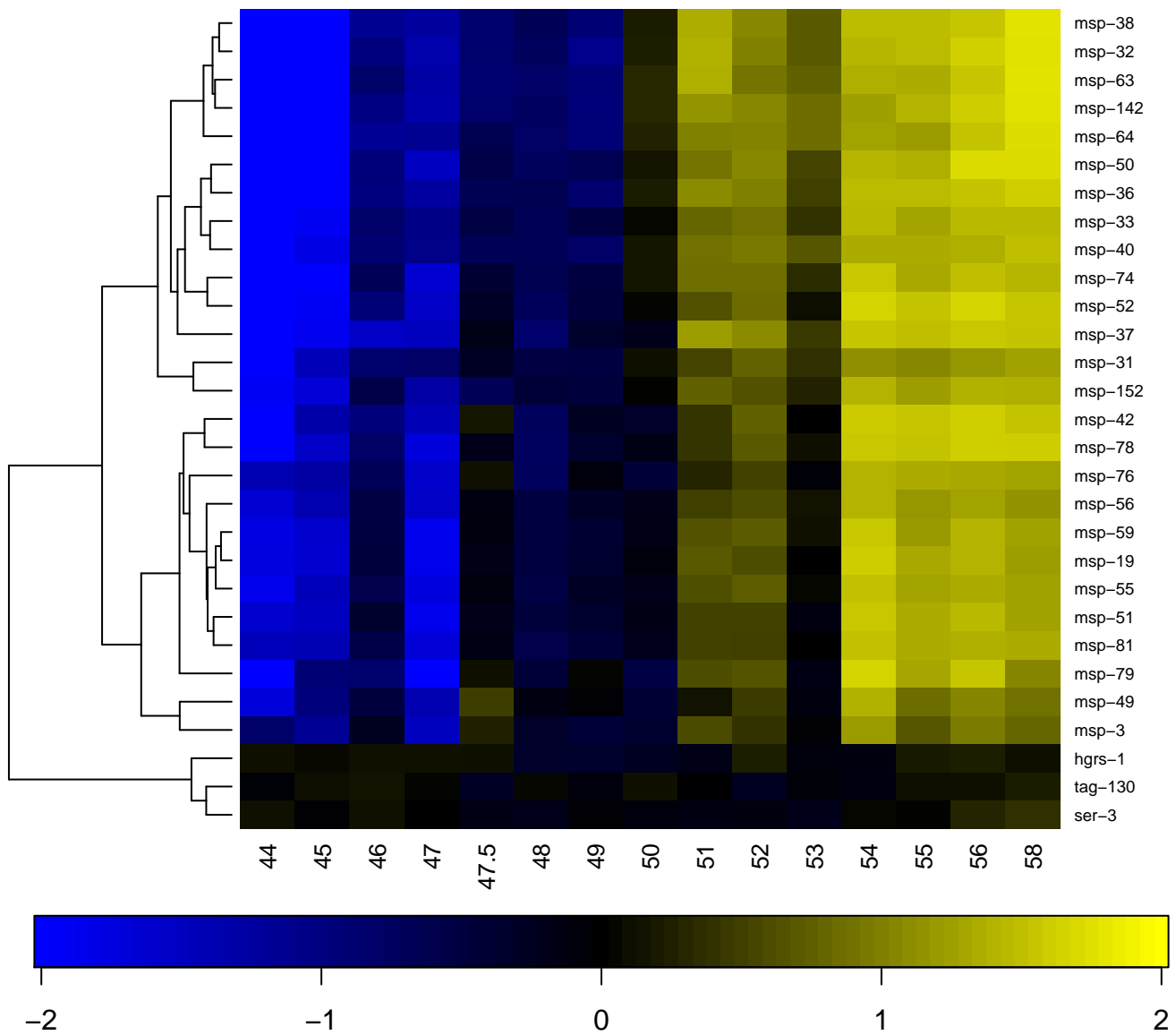
head muscle



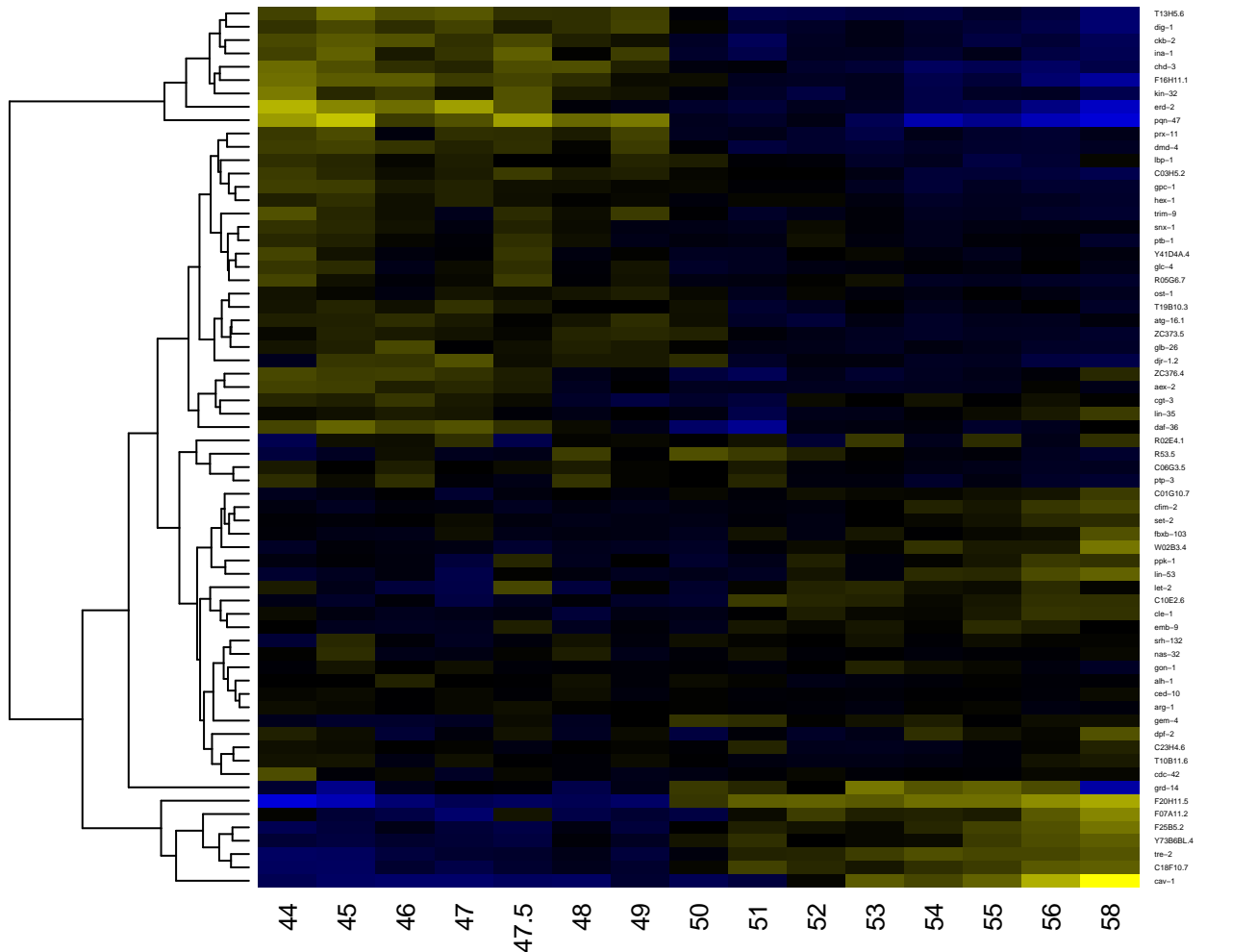
head neuron



hermaphrodite gonad



hmc



-2

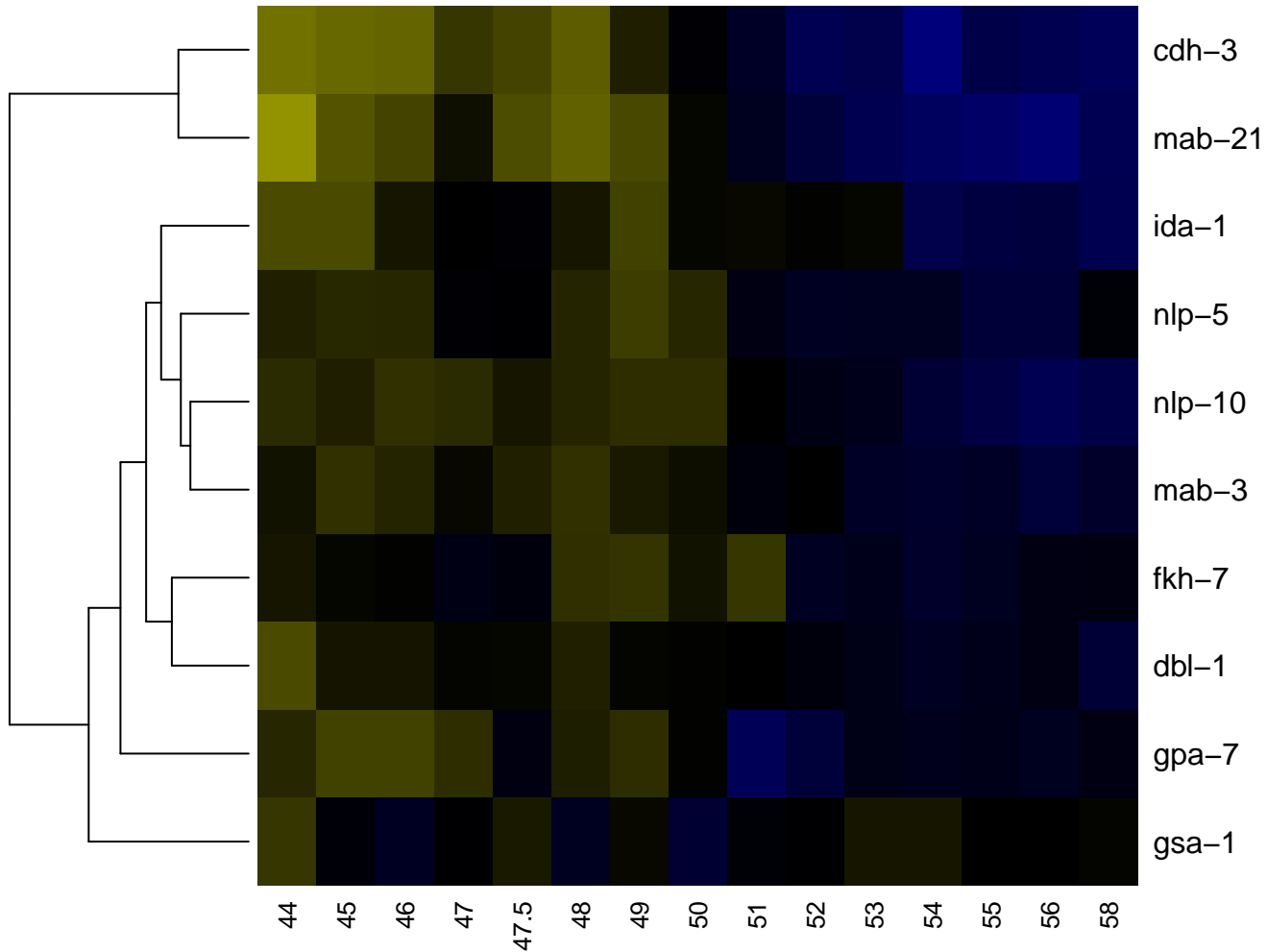
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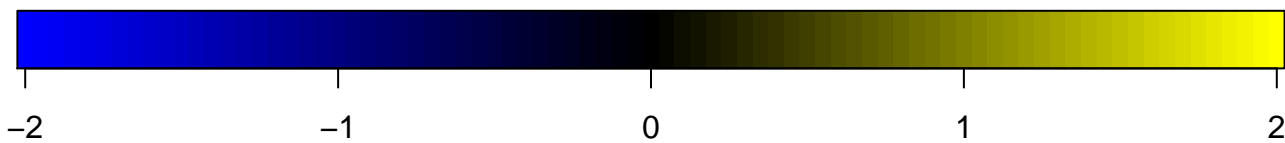
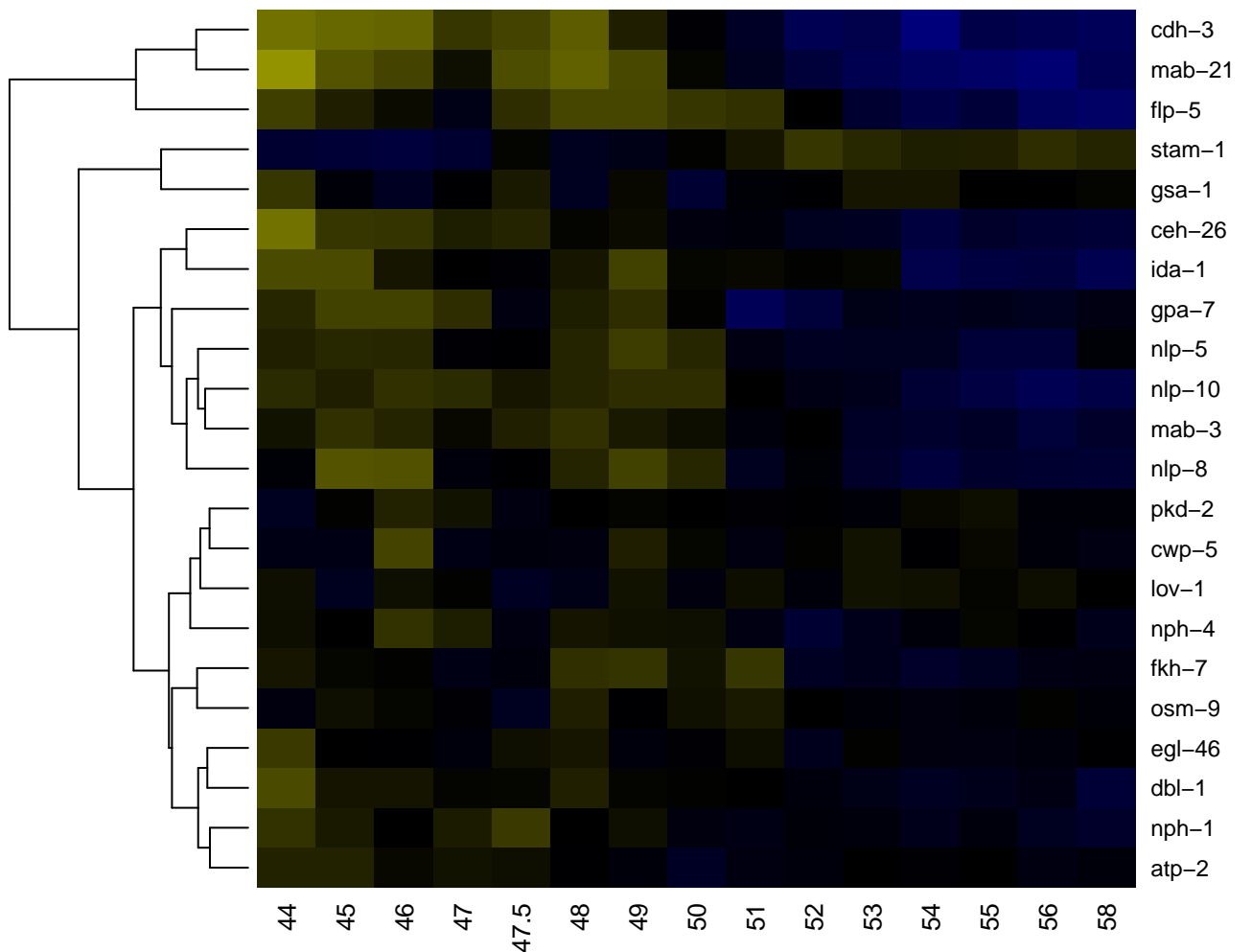
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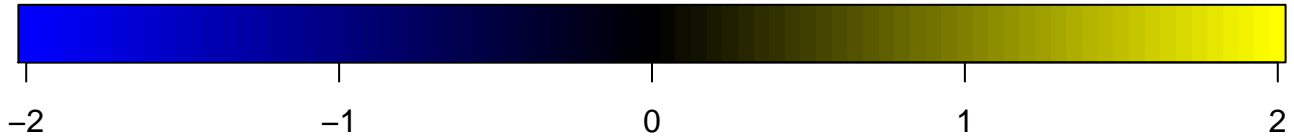
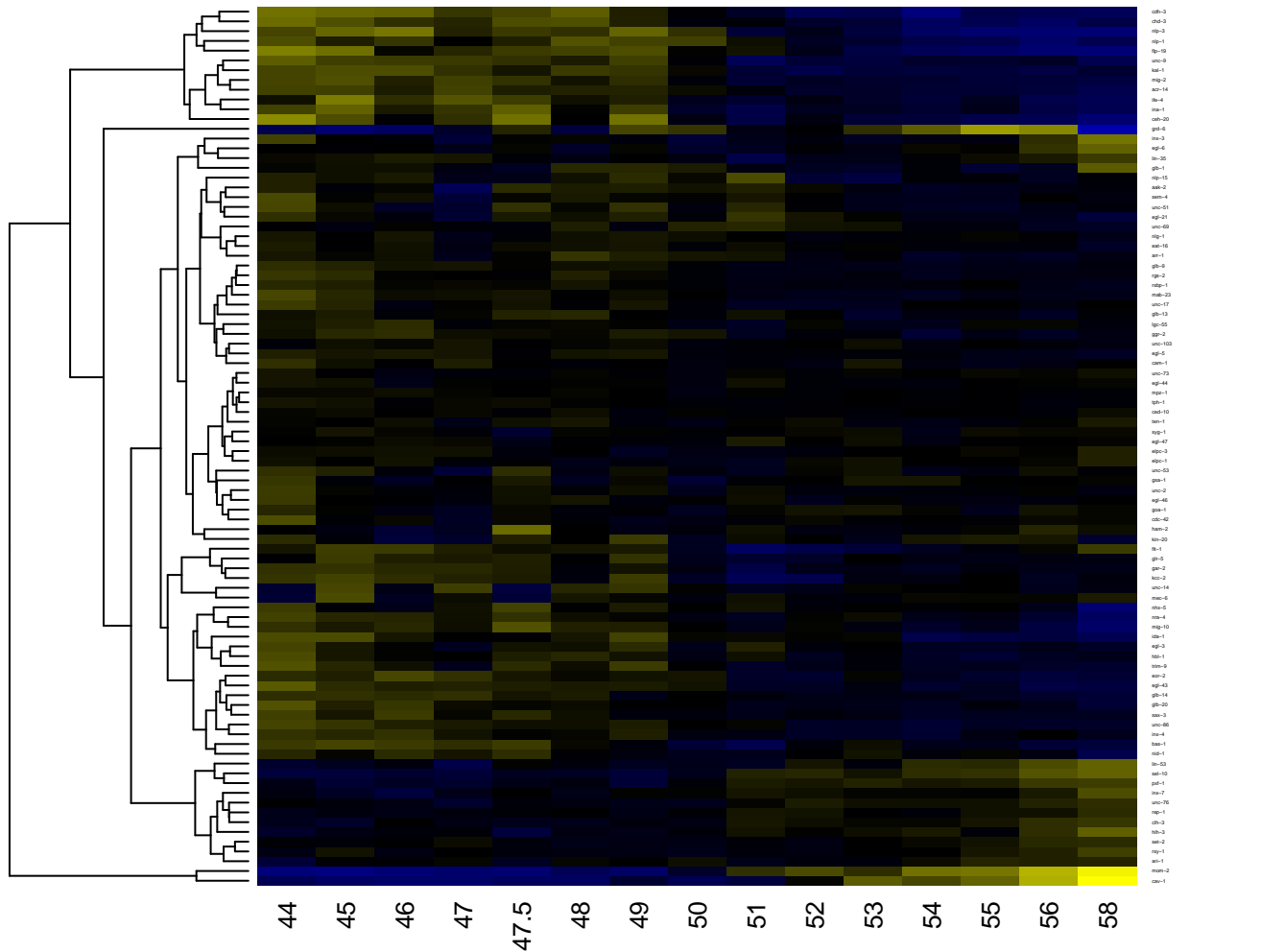
HOA



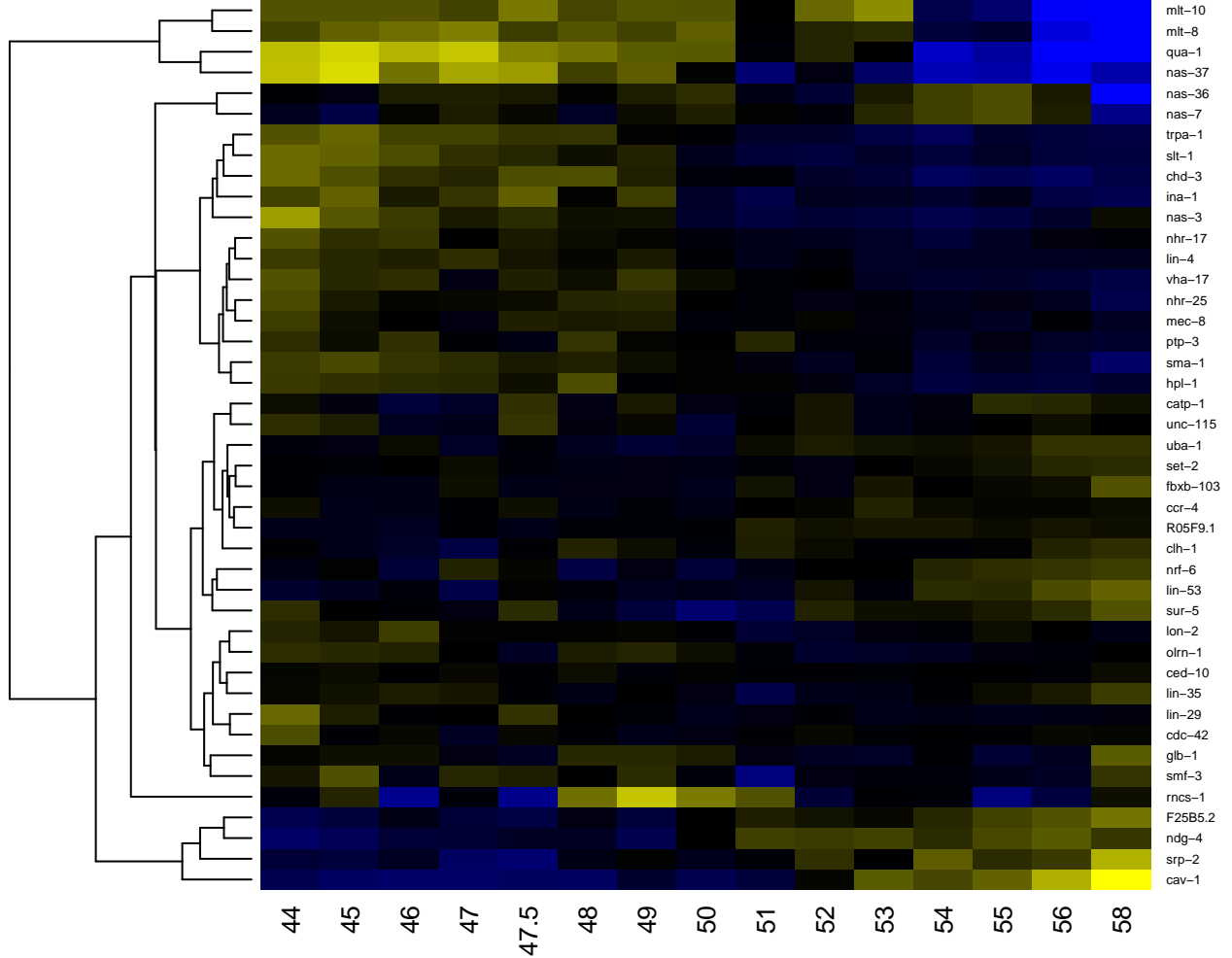
HOB



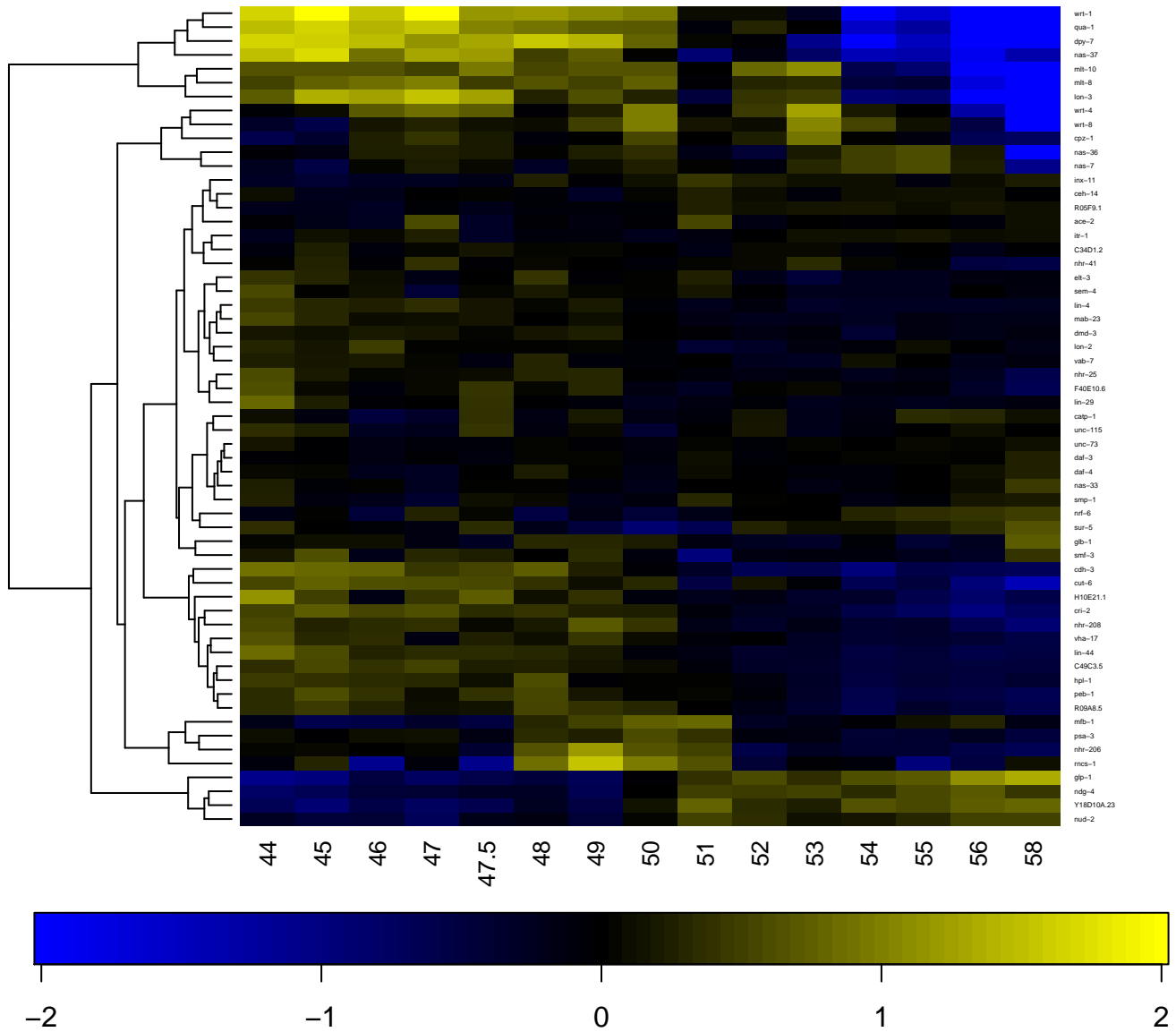
HSNL



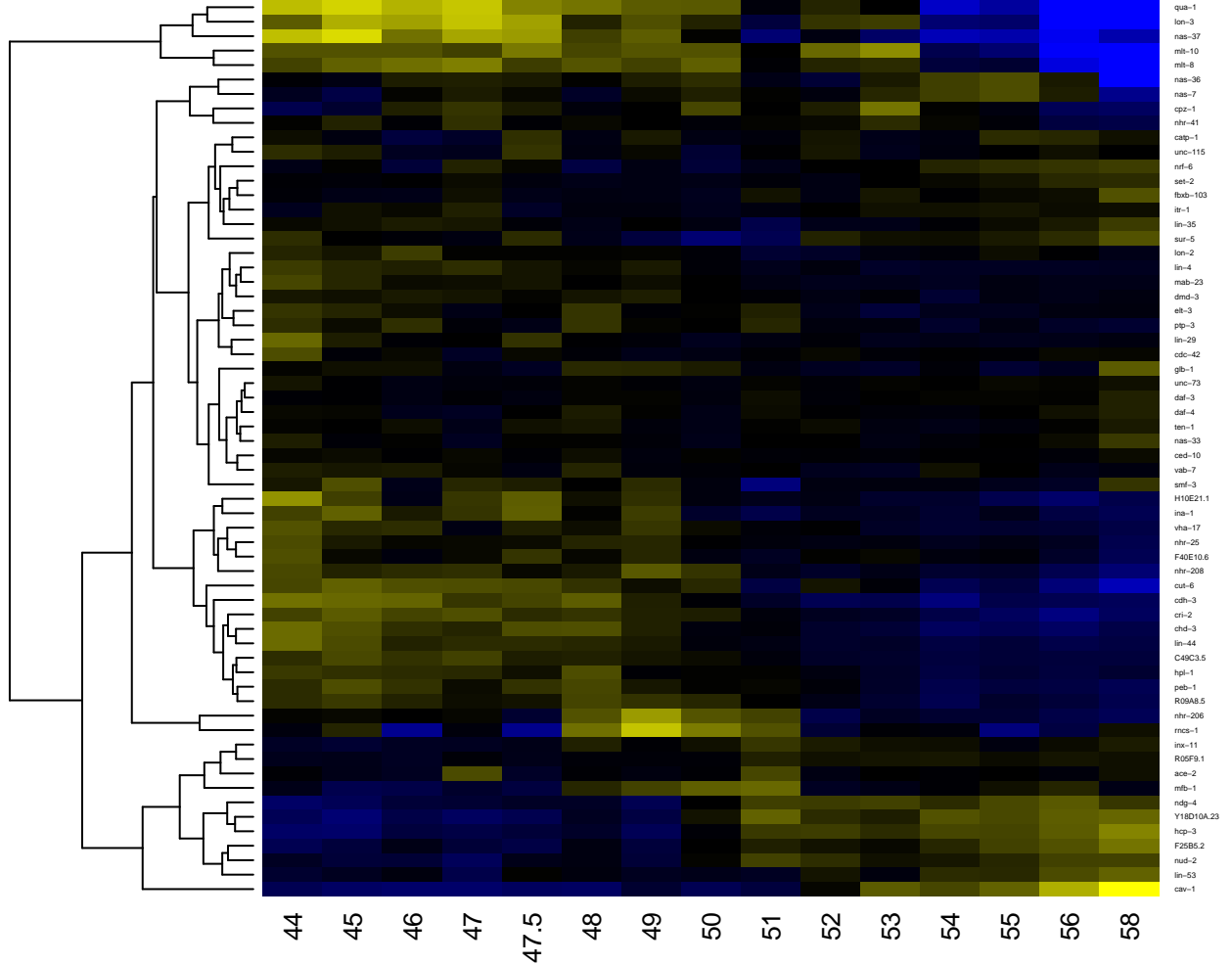
hyp1



hyp10



hyp11



-2

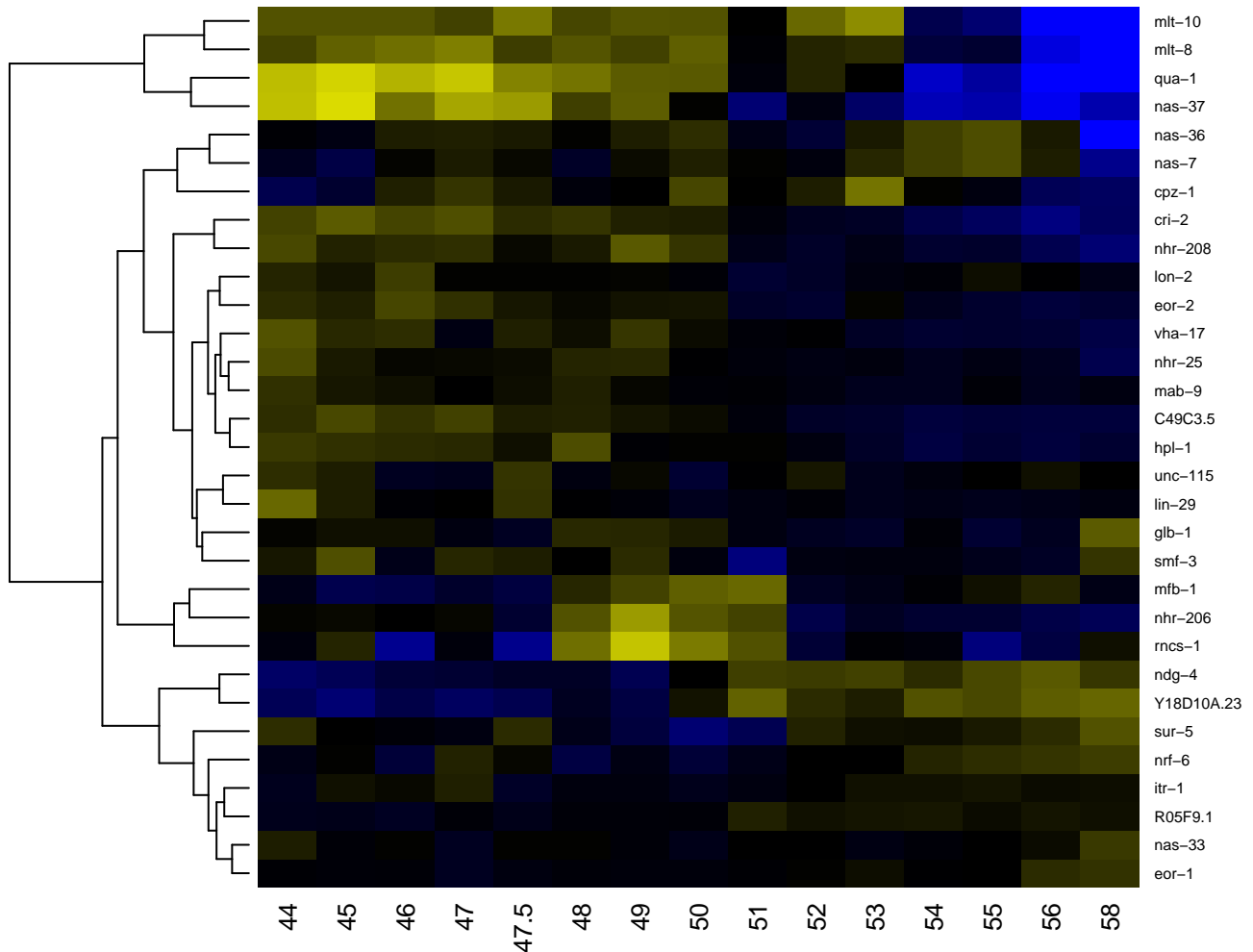
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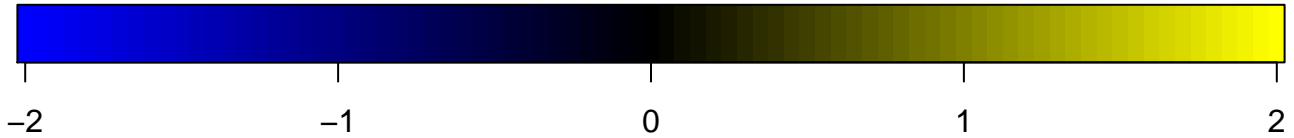
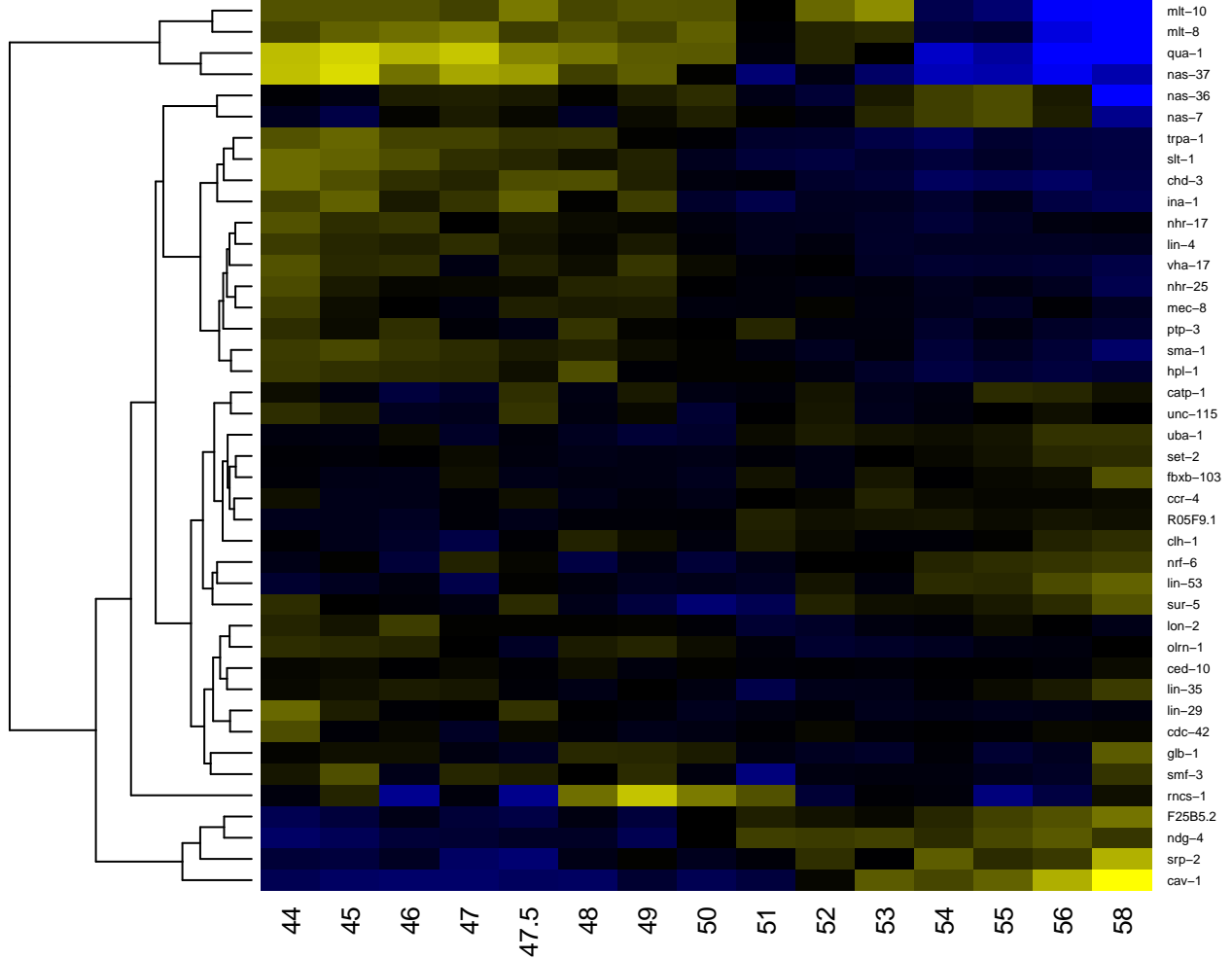
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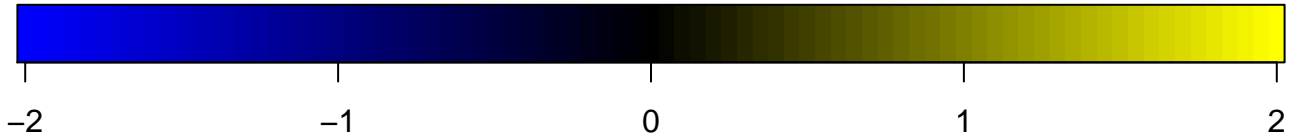
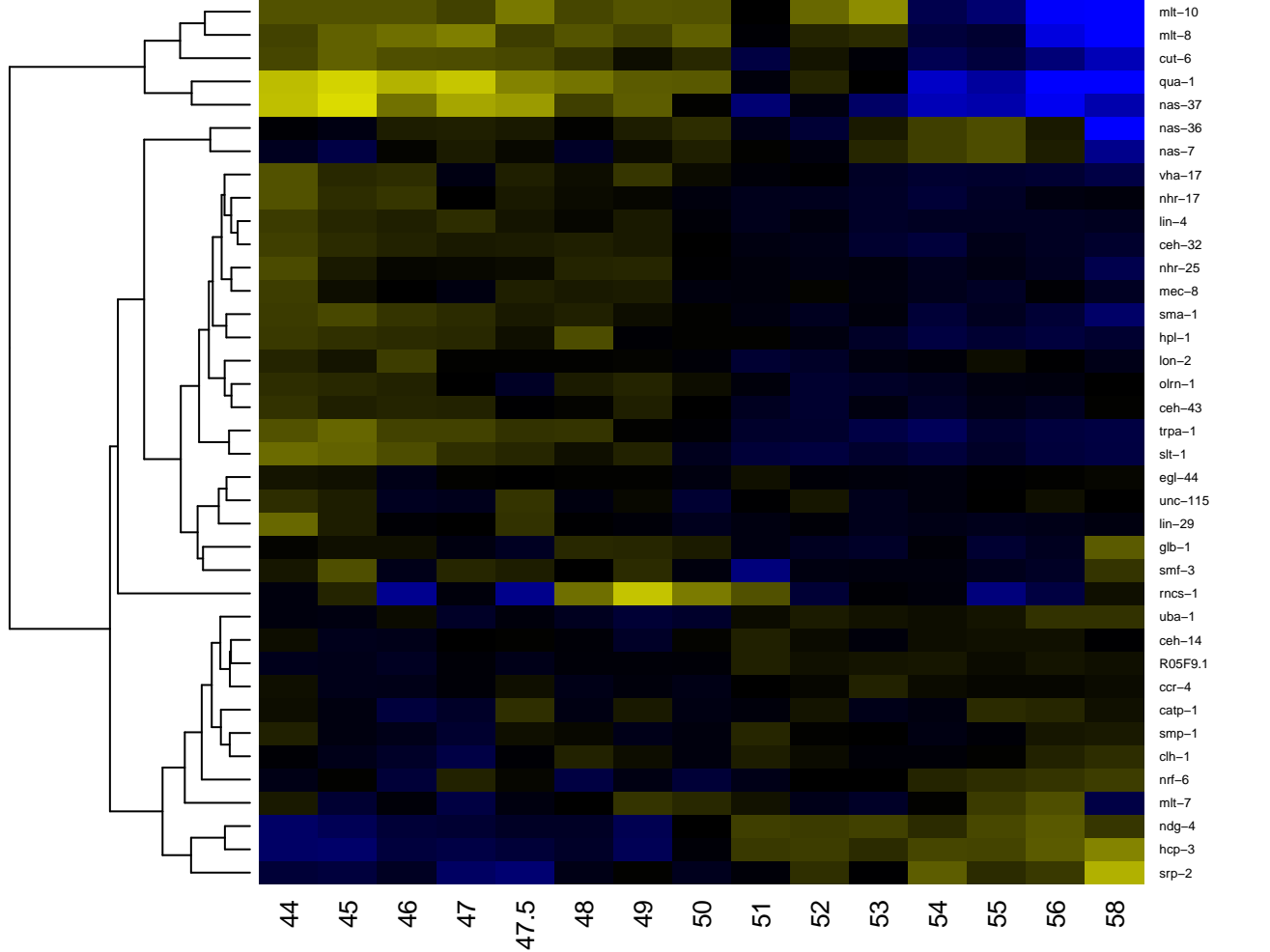
hyp12



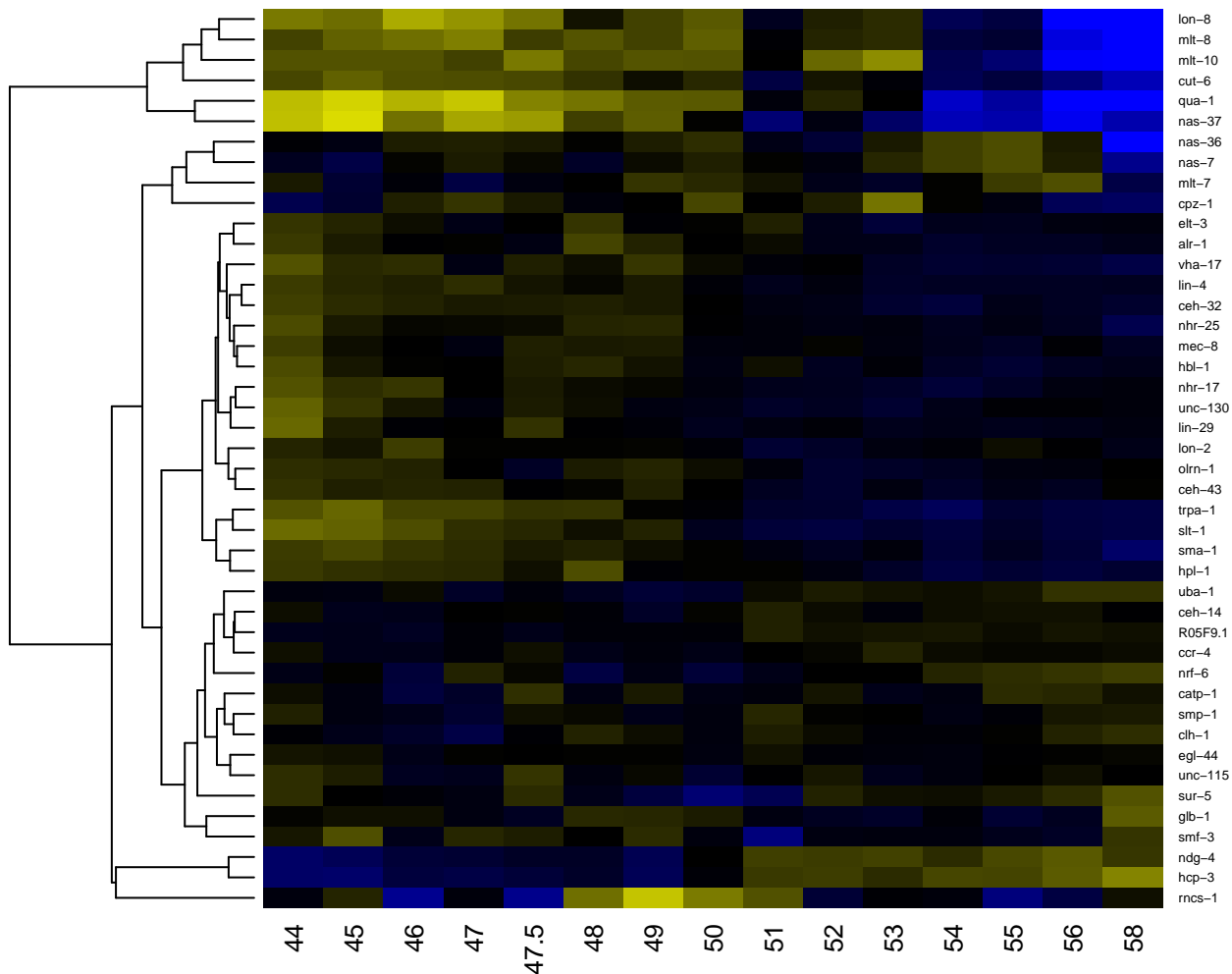
hyp2



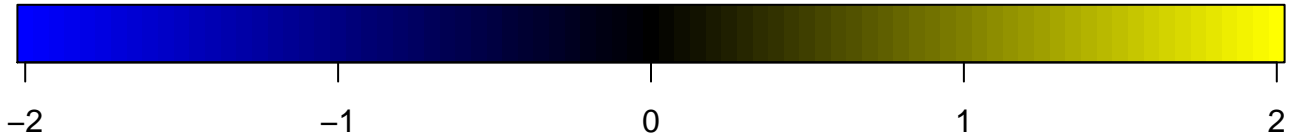
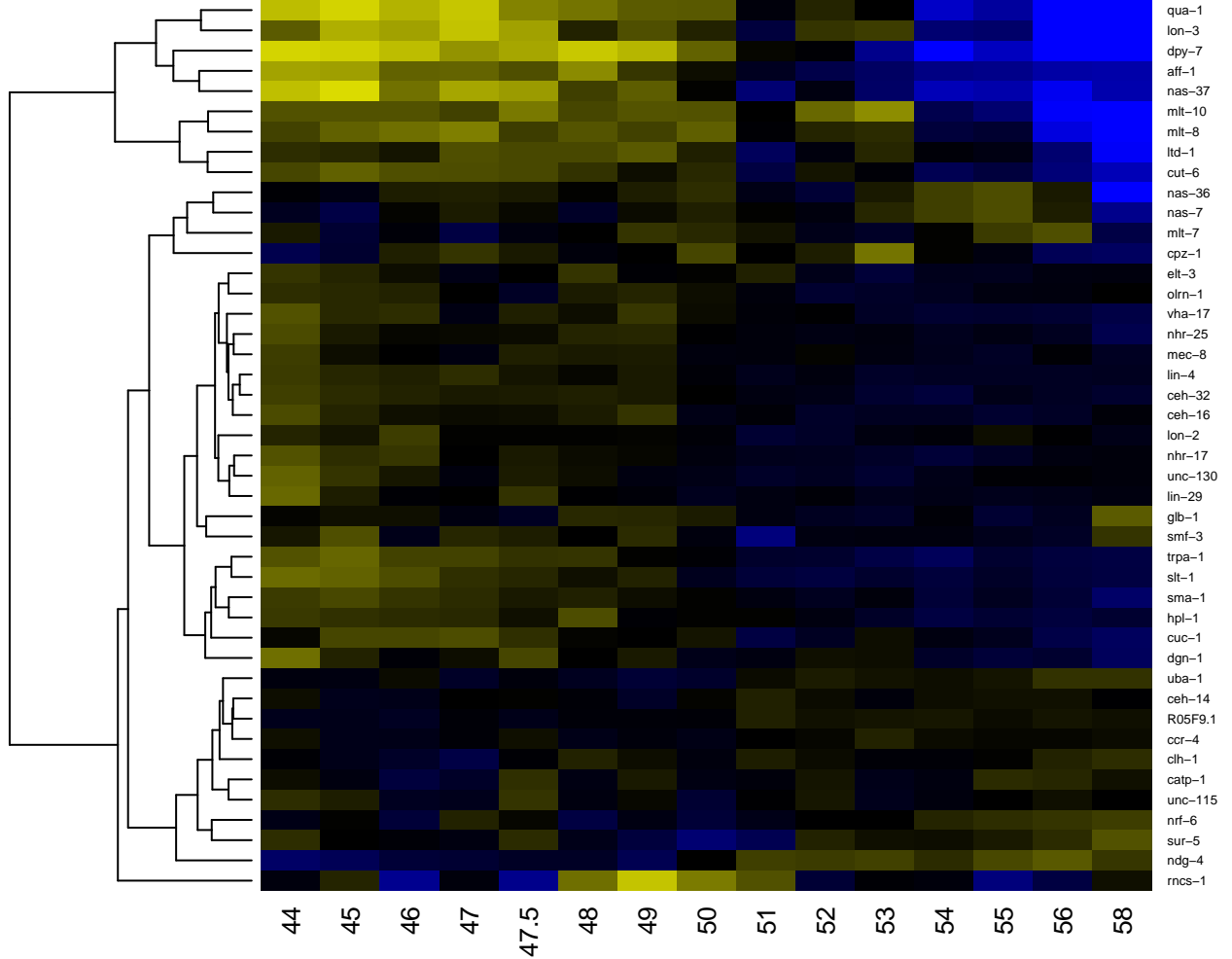
hyp3



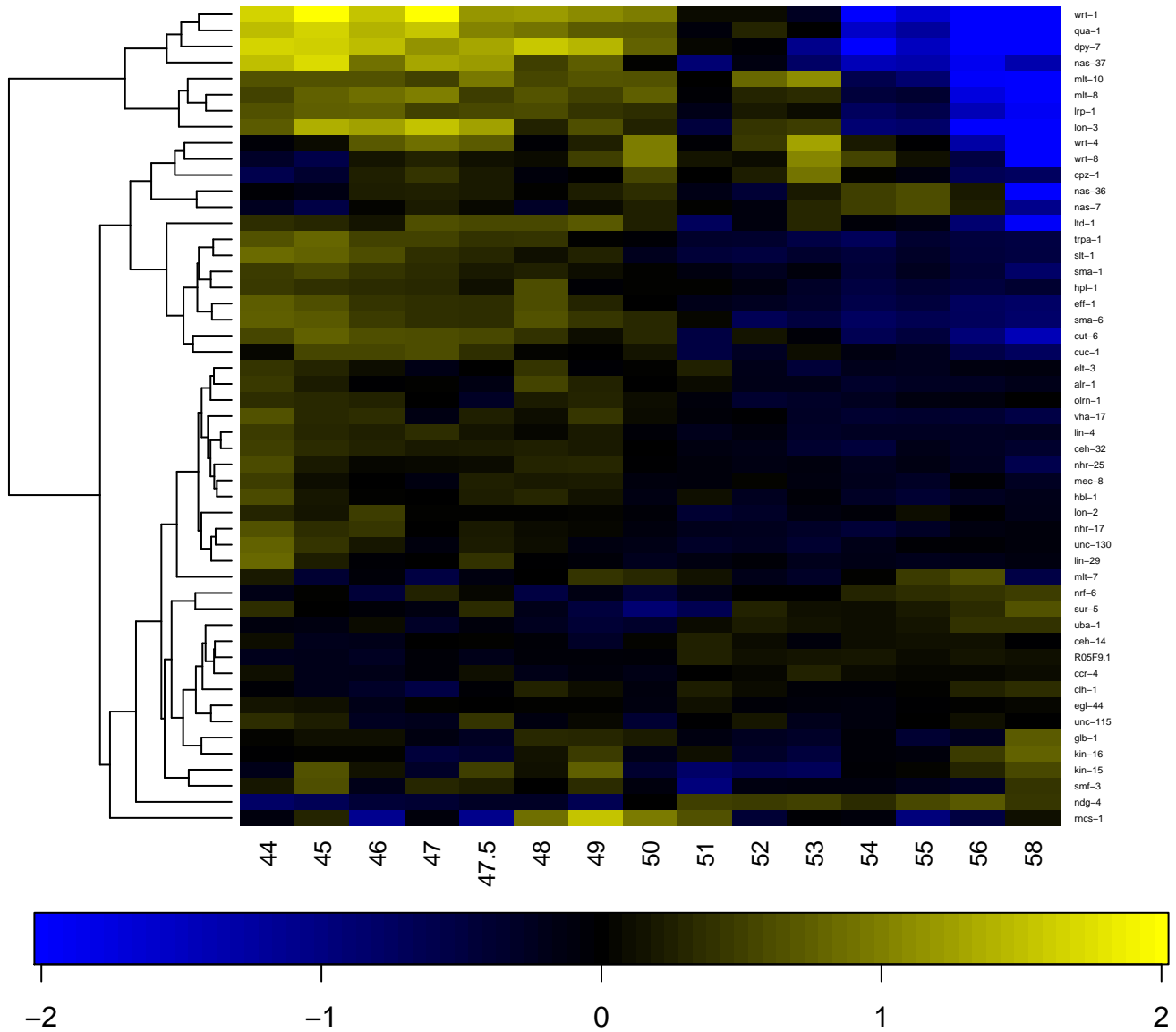
hyp4



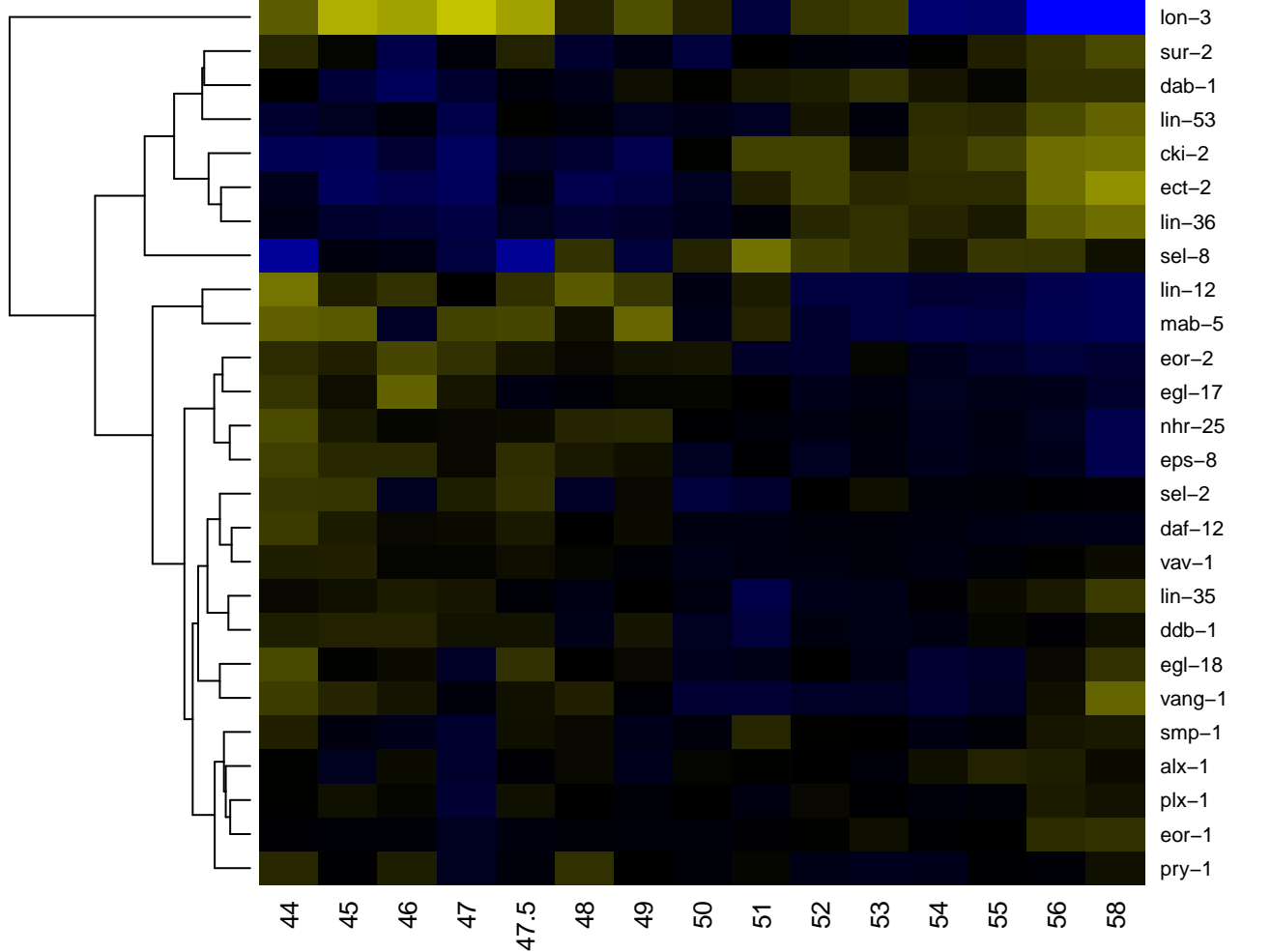
hyp5



hyp6



hyp7



-2

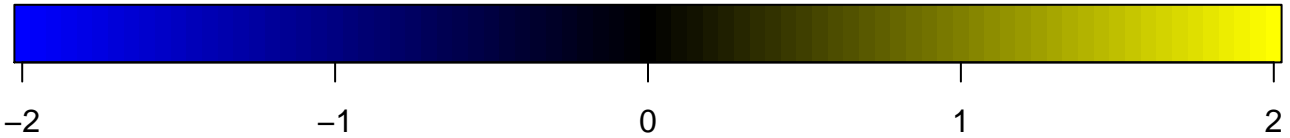
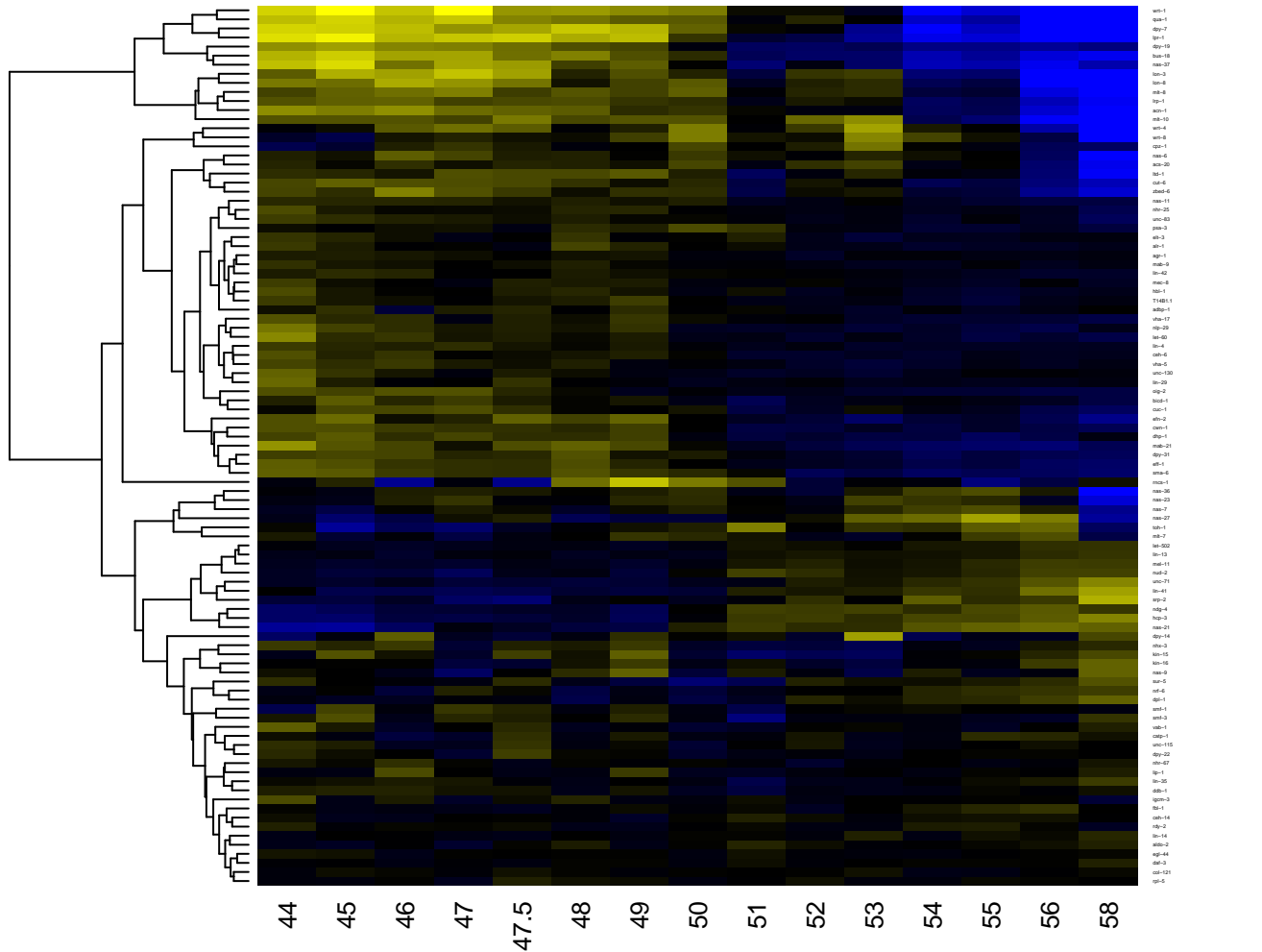
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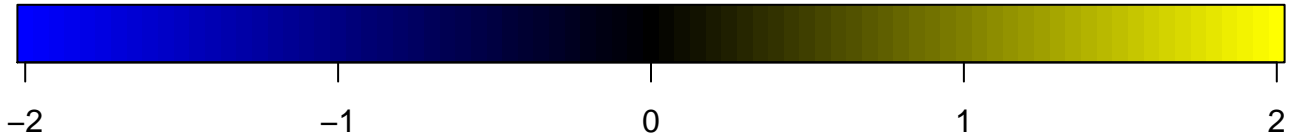
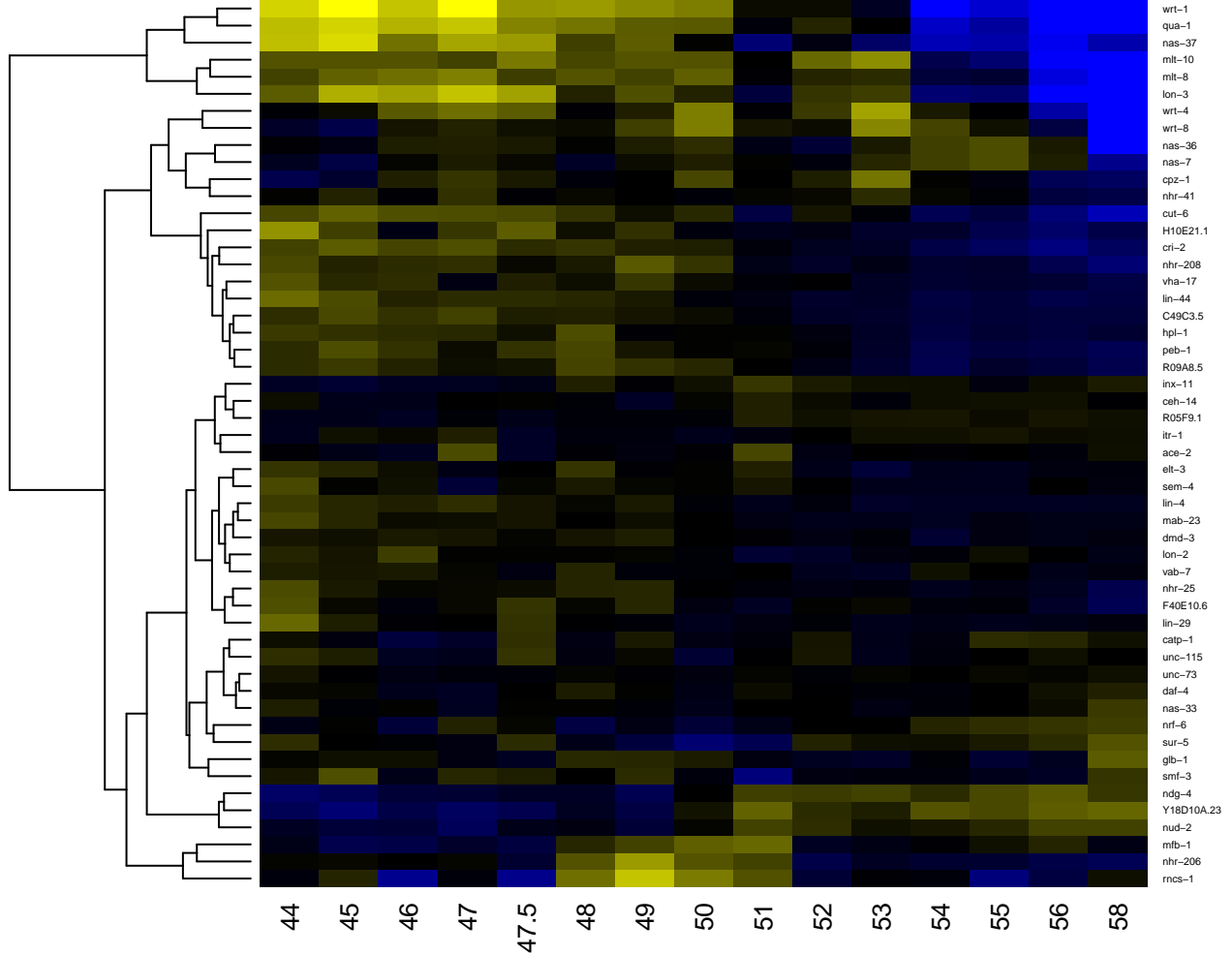
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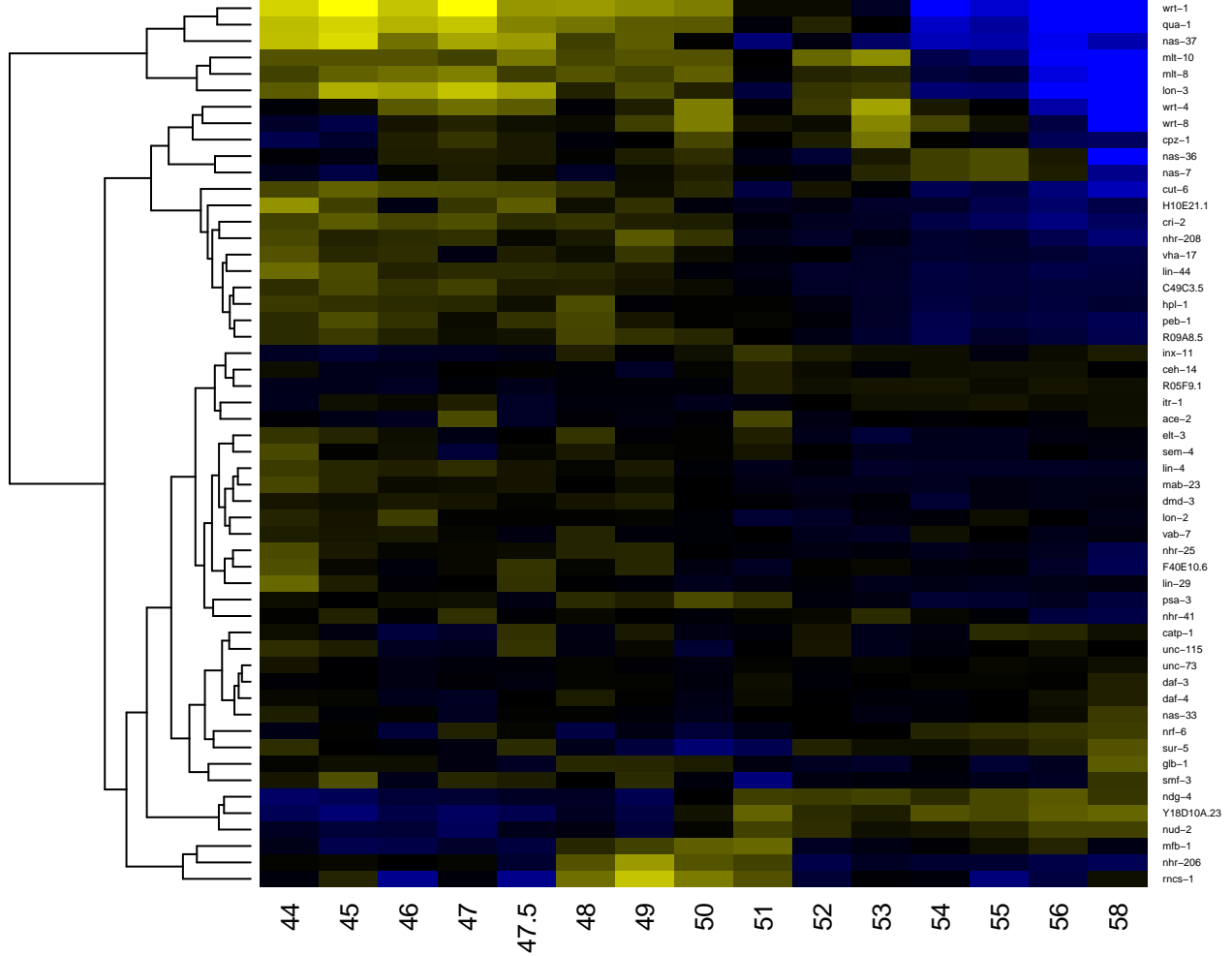
hyp7 syncytium



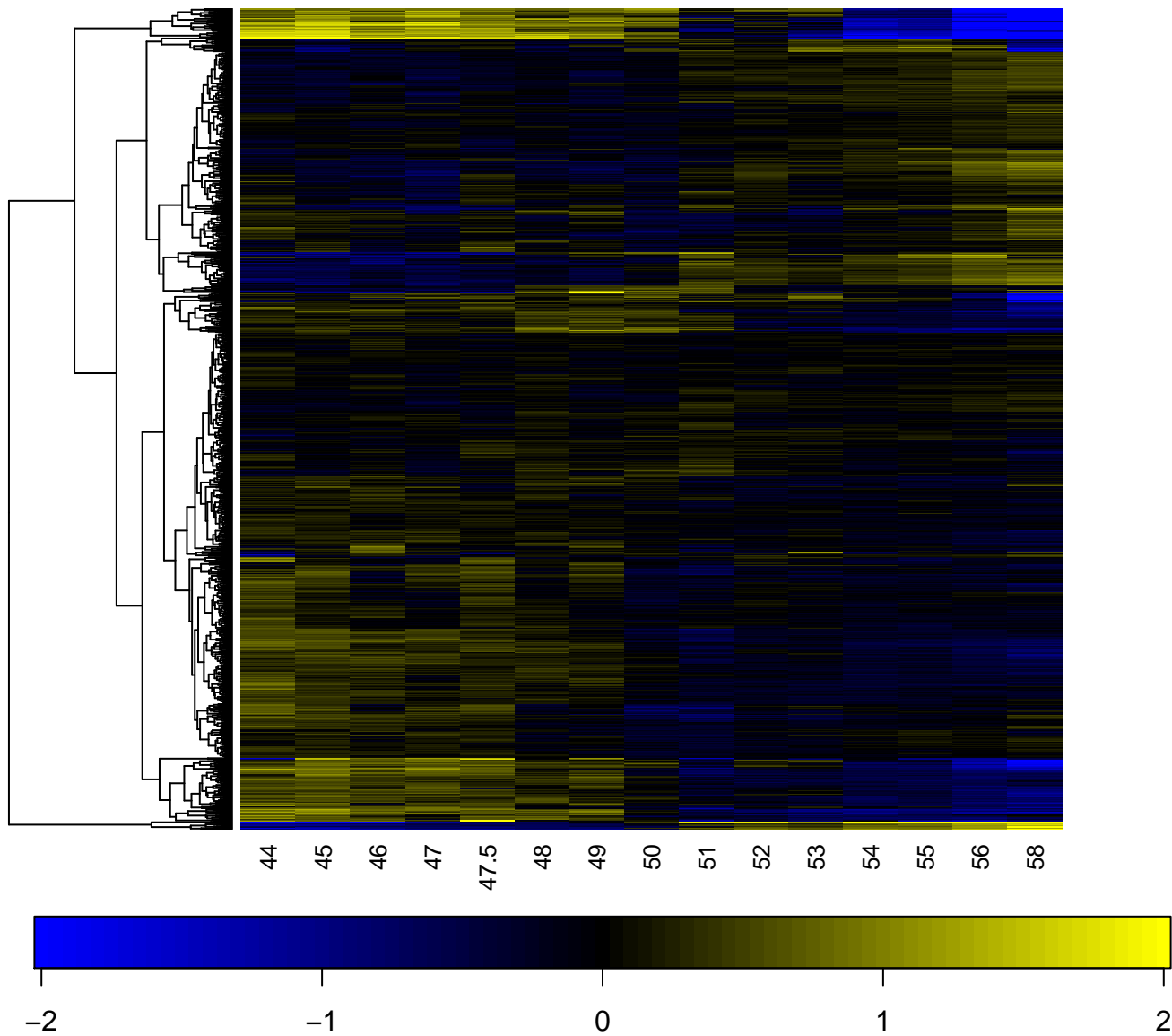
hyp8



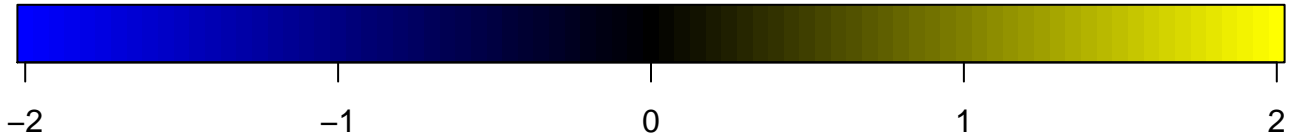
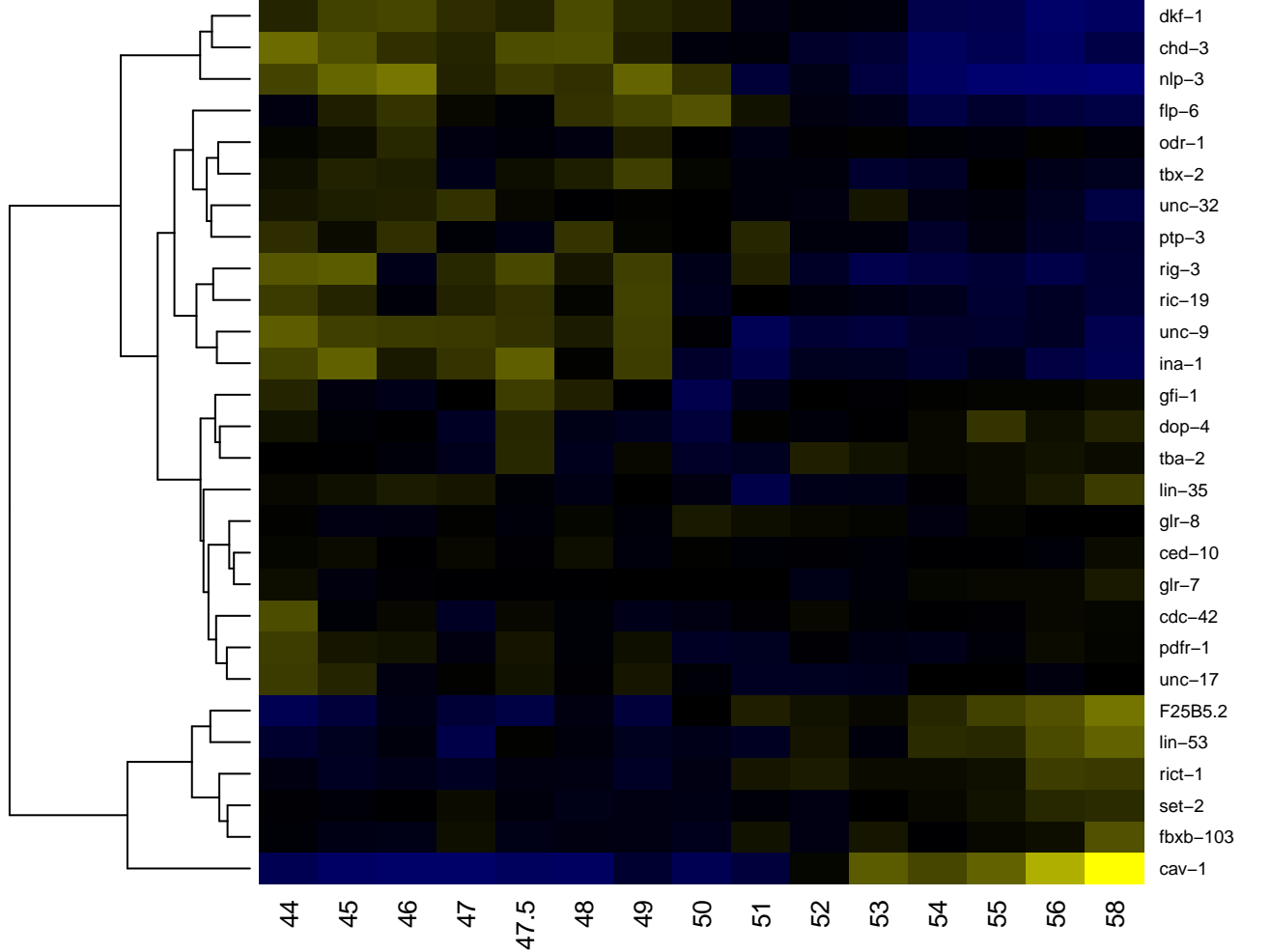
hyp9



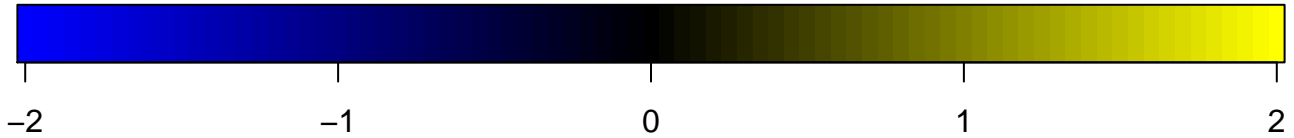
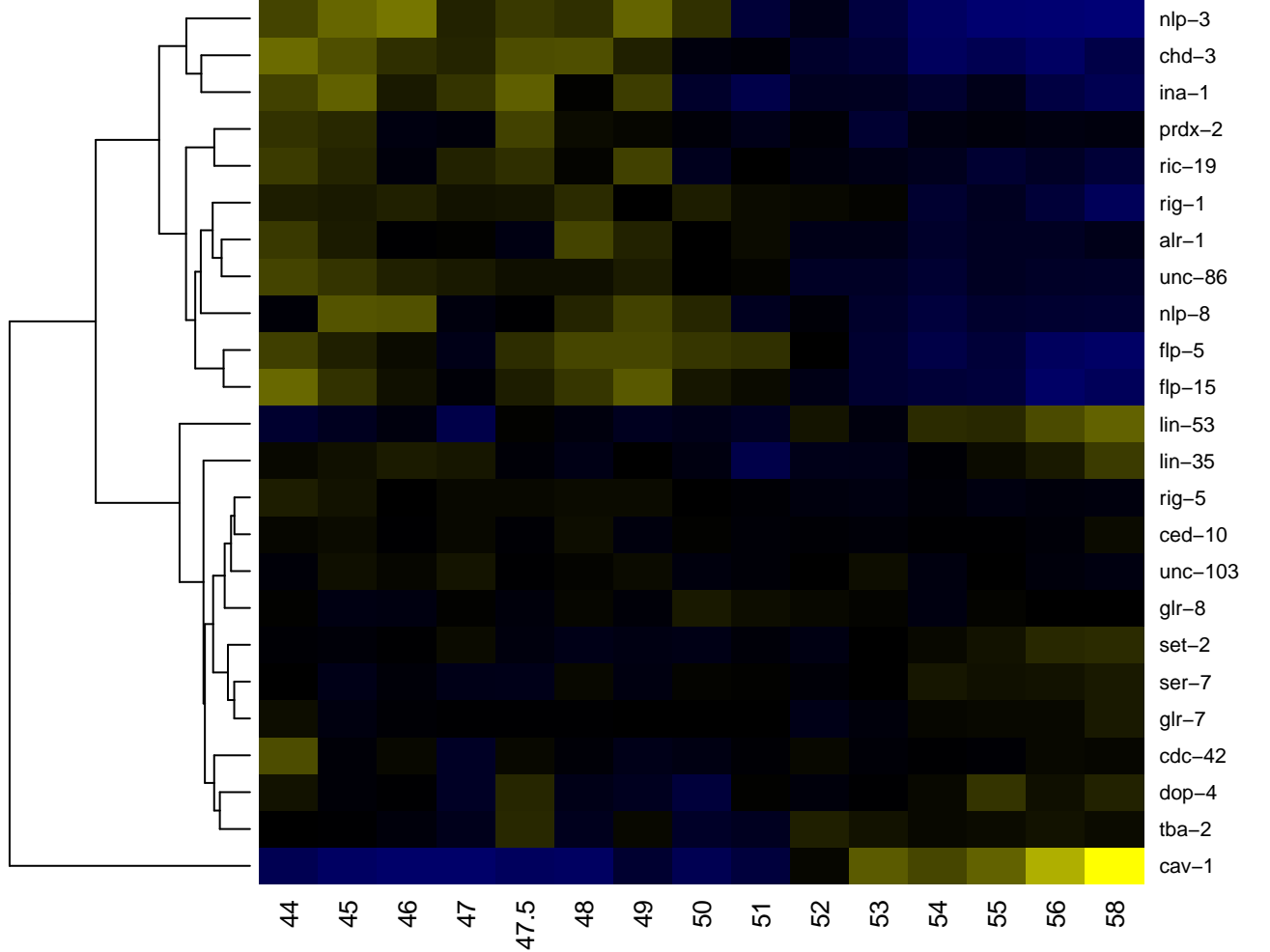
hypodermis



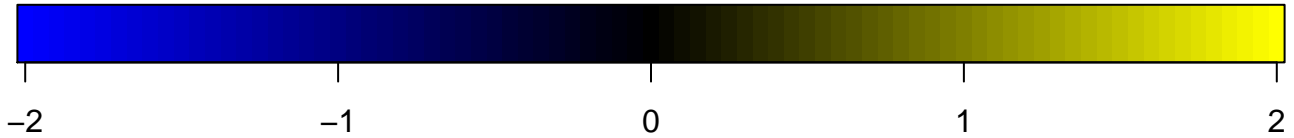
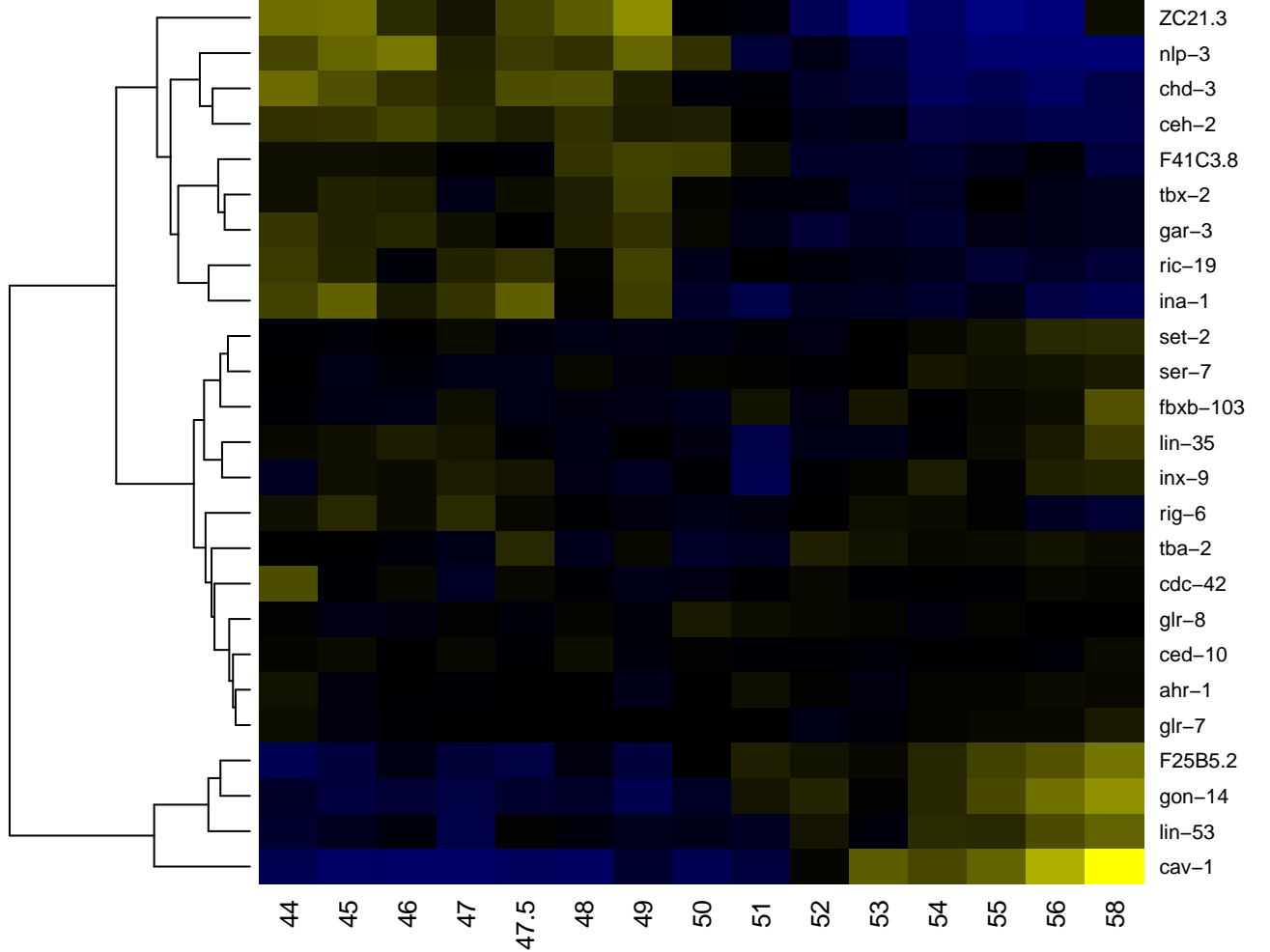
I1R



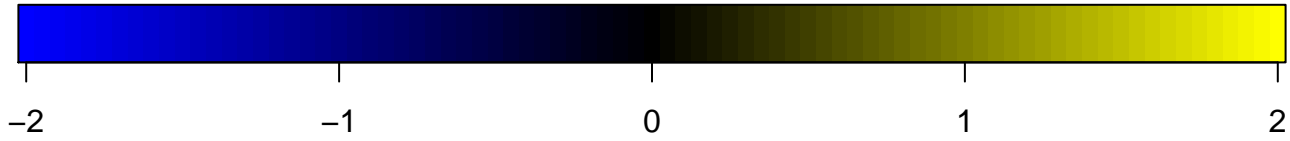
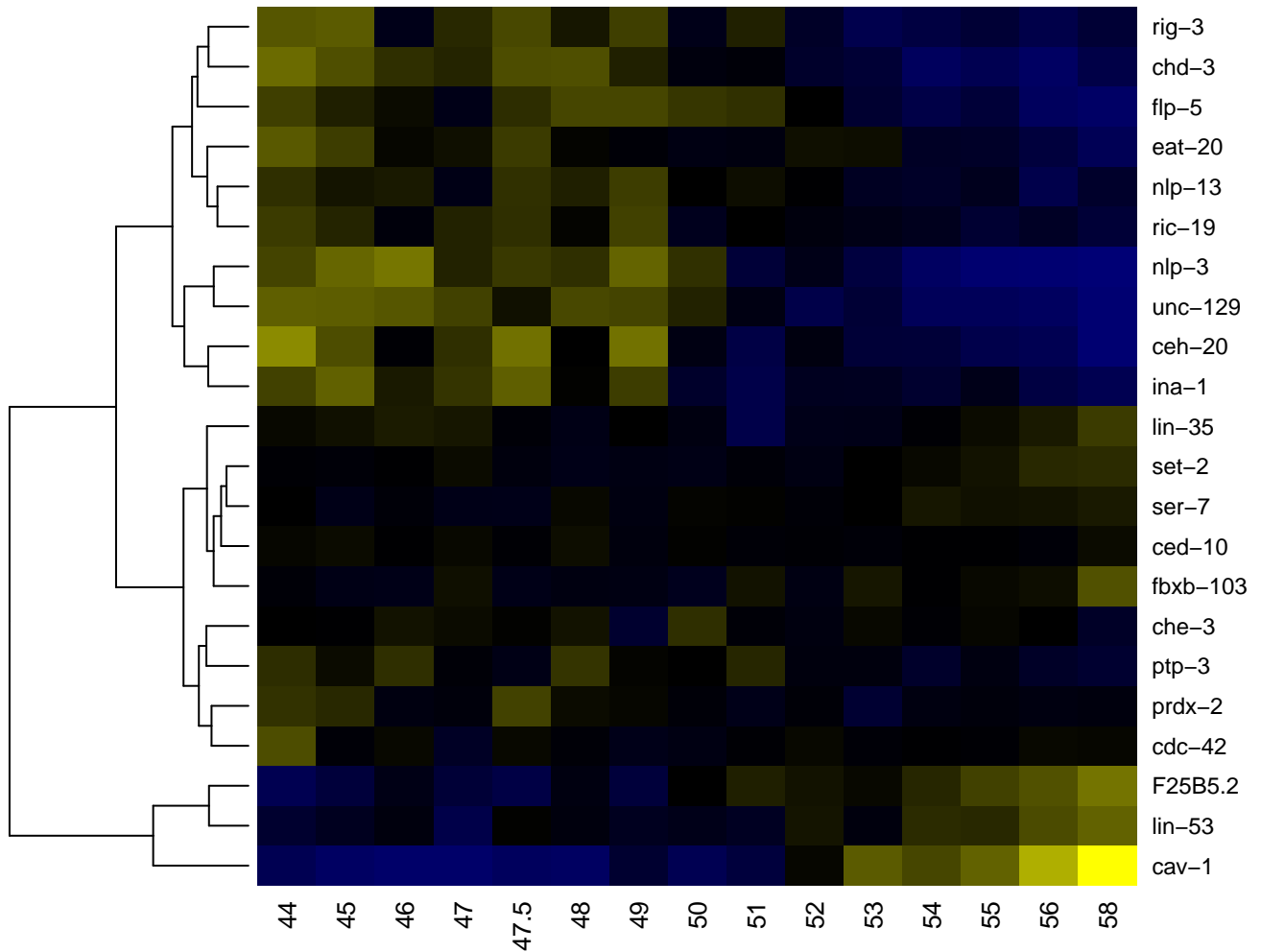
I2R



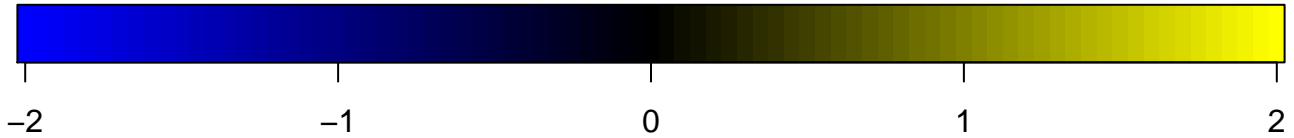
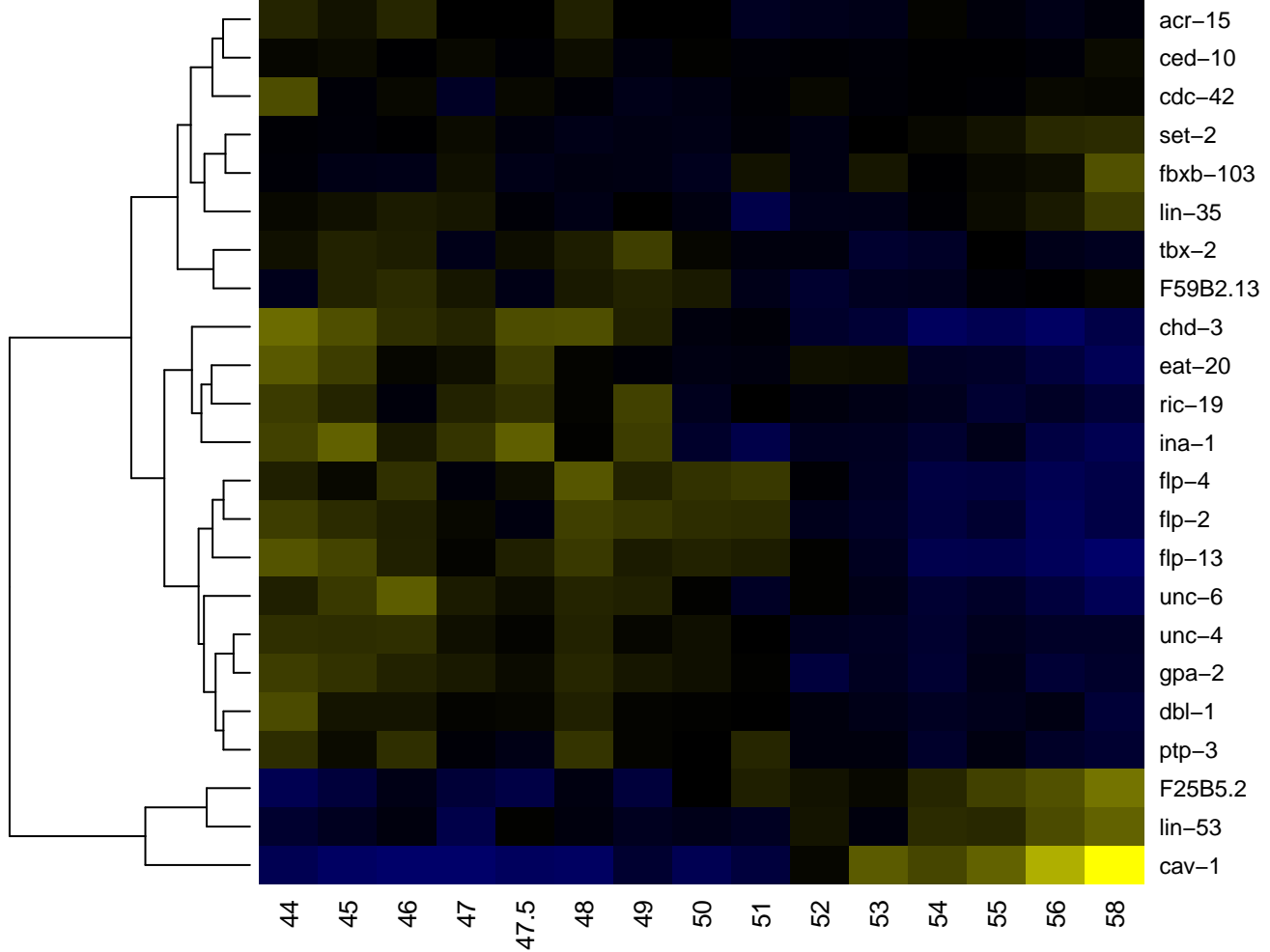
I3



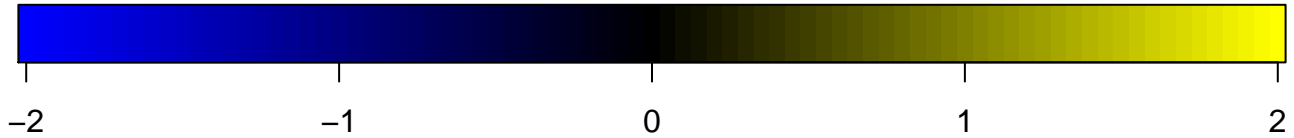
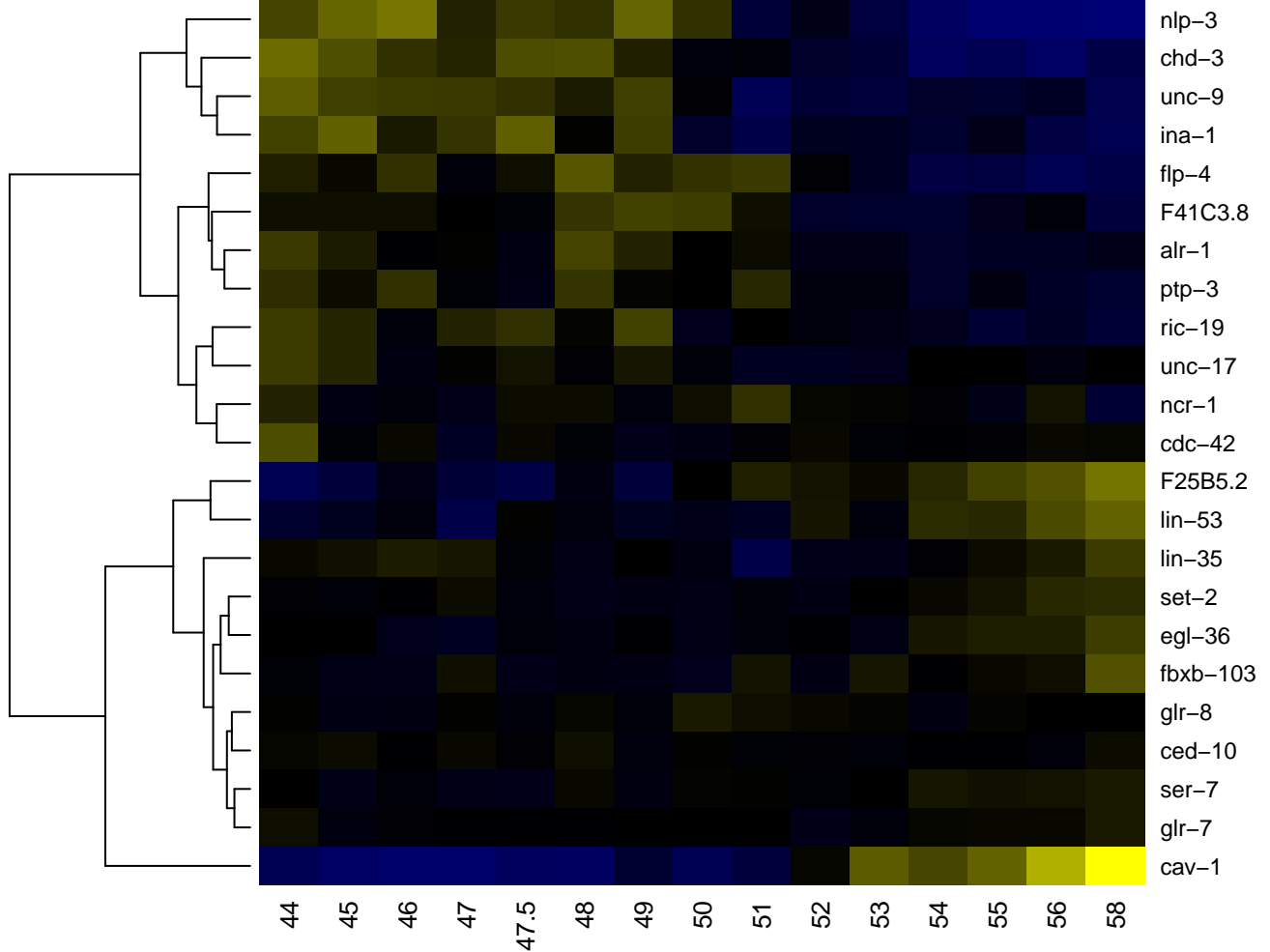
I4



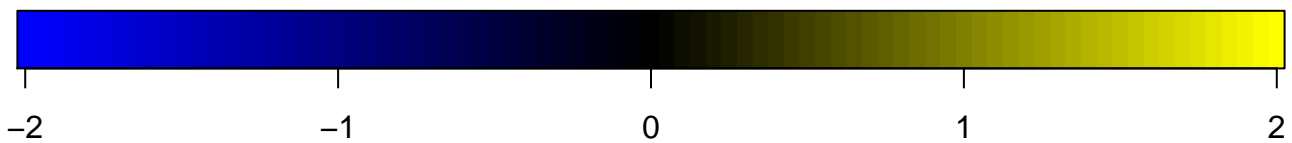
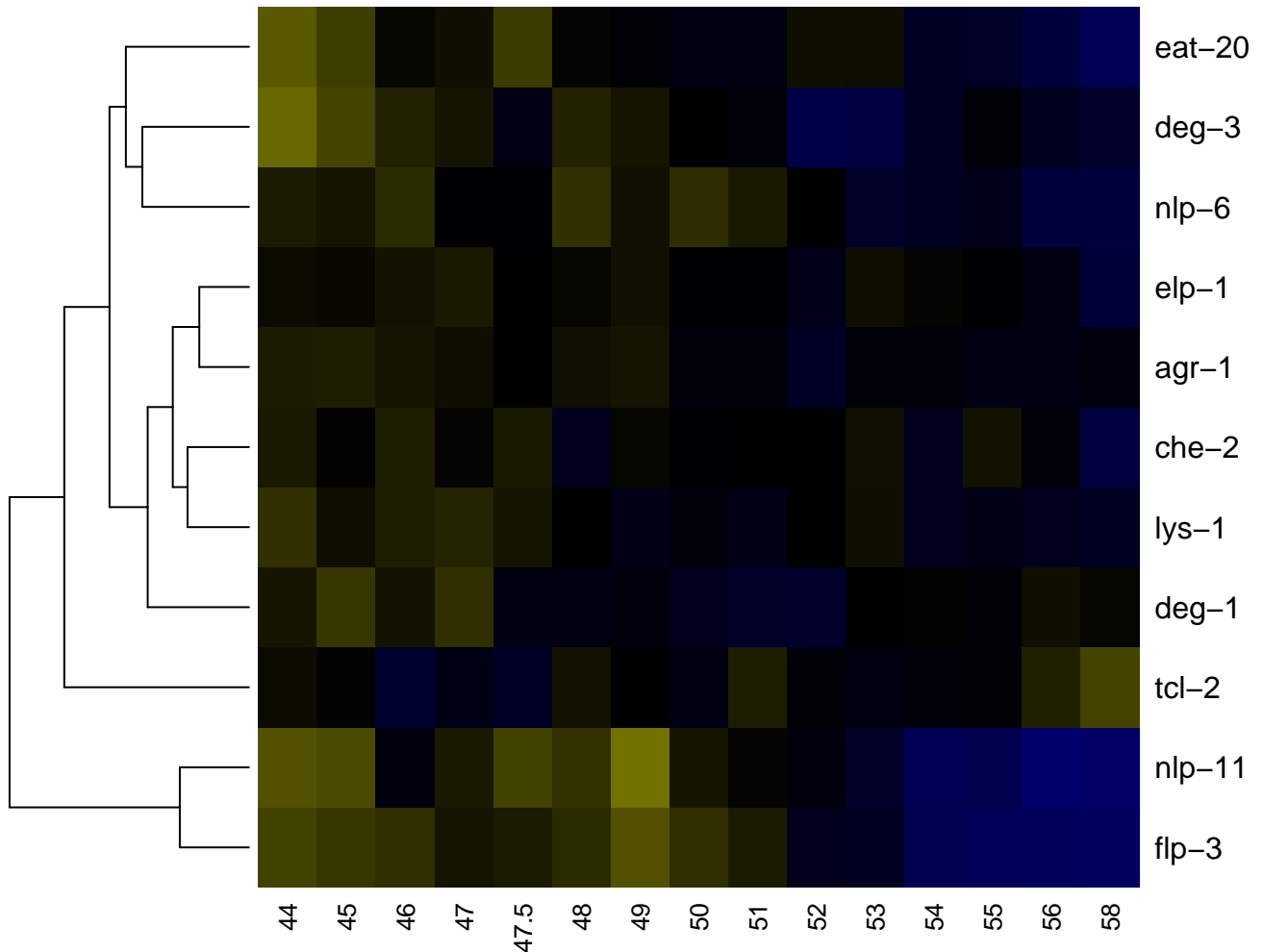
15



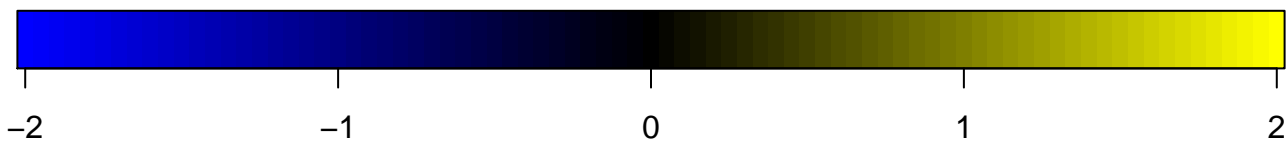
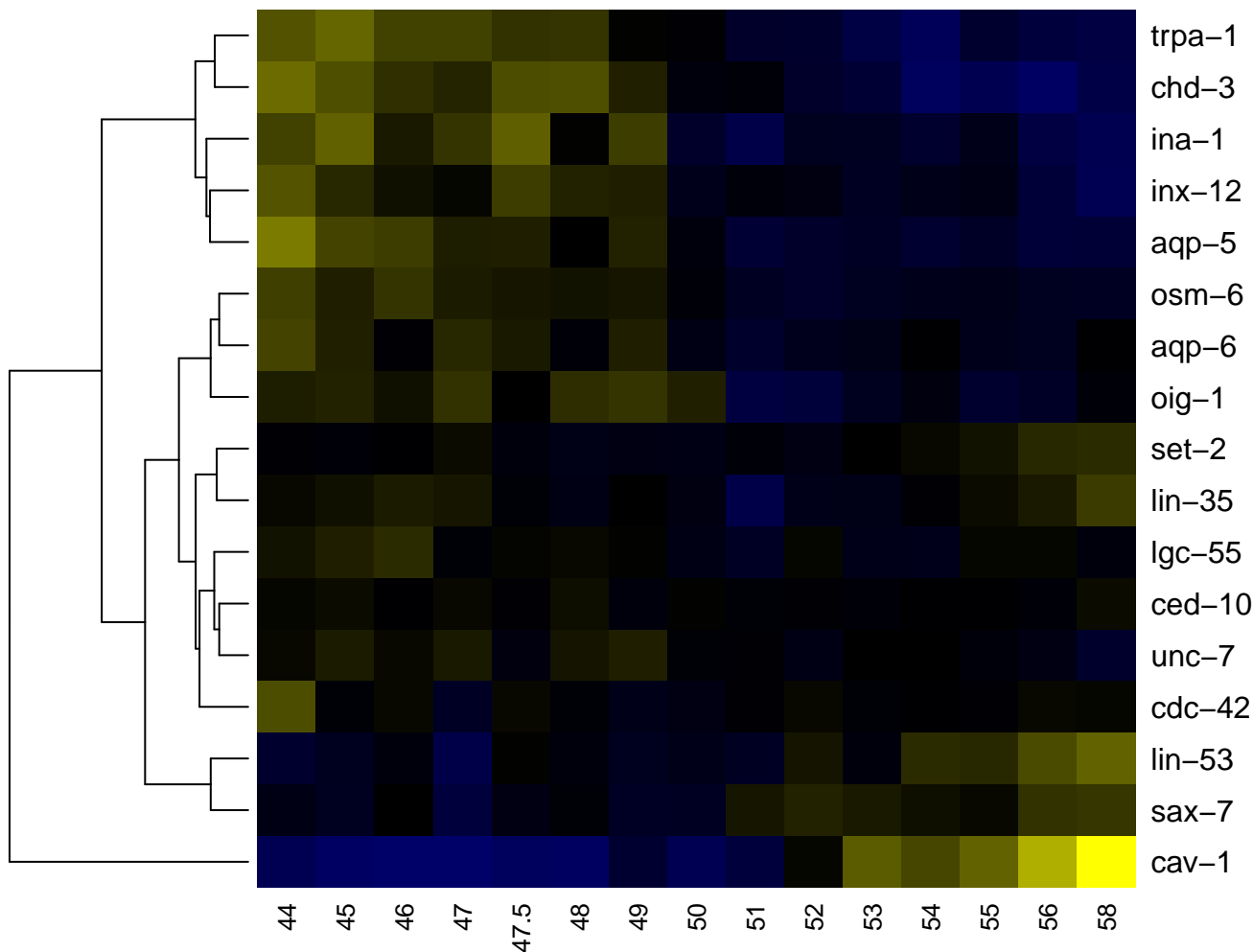
I6



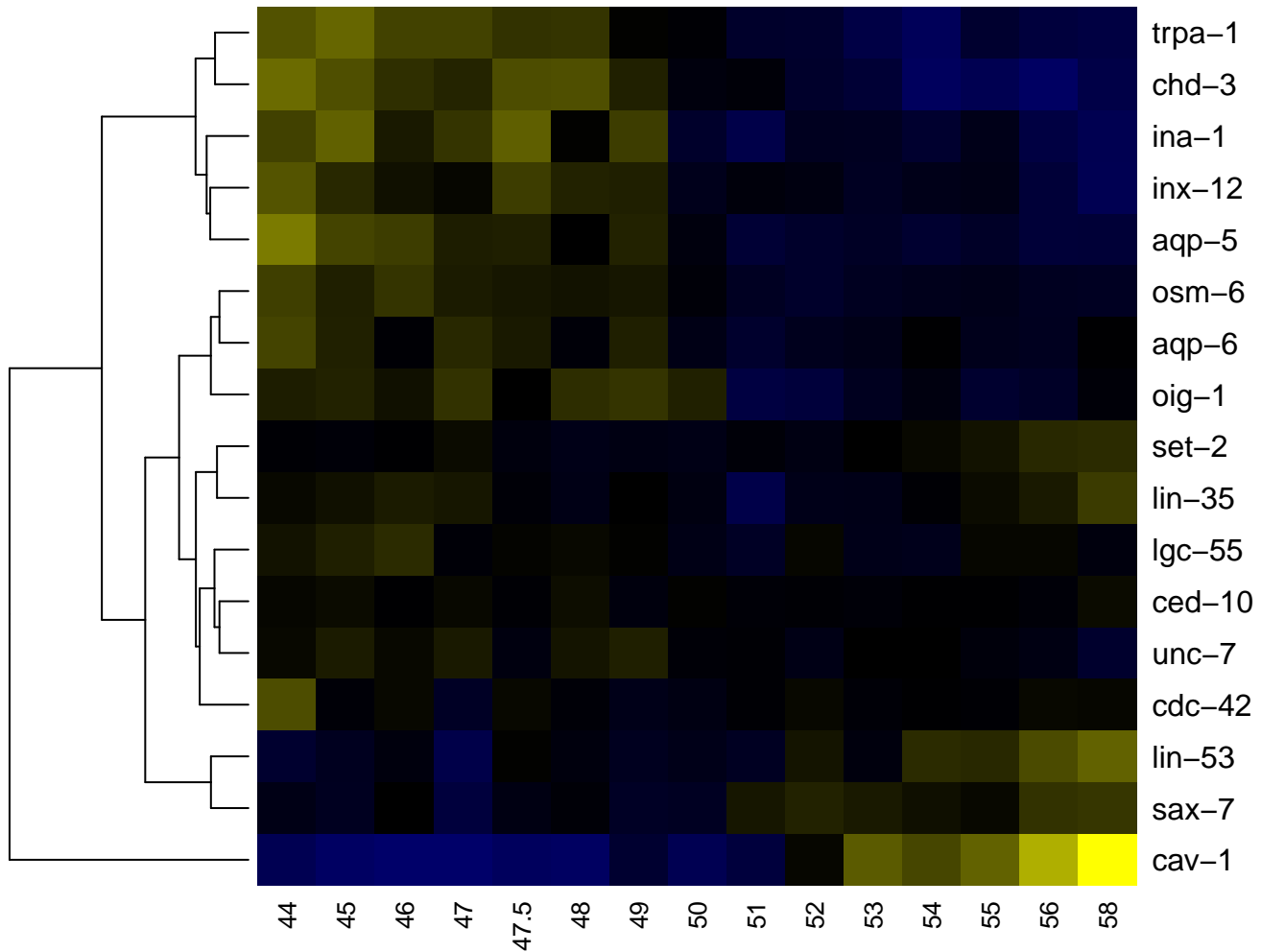
IL1 neuron



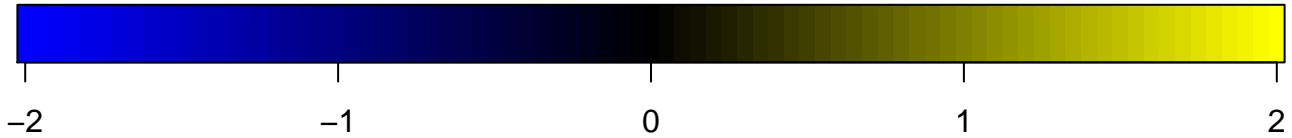
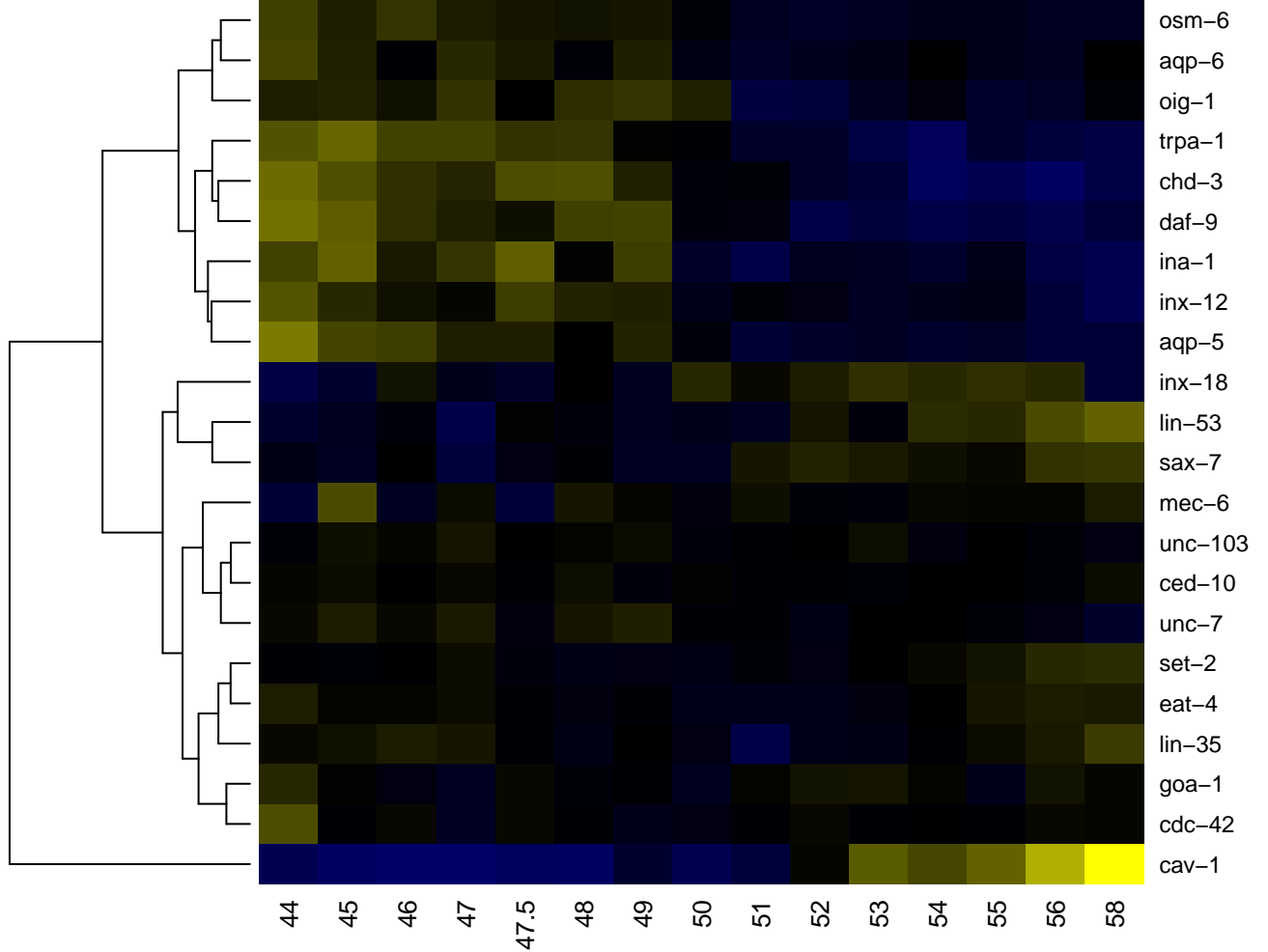
IL1DL



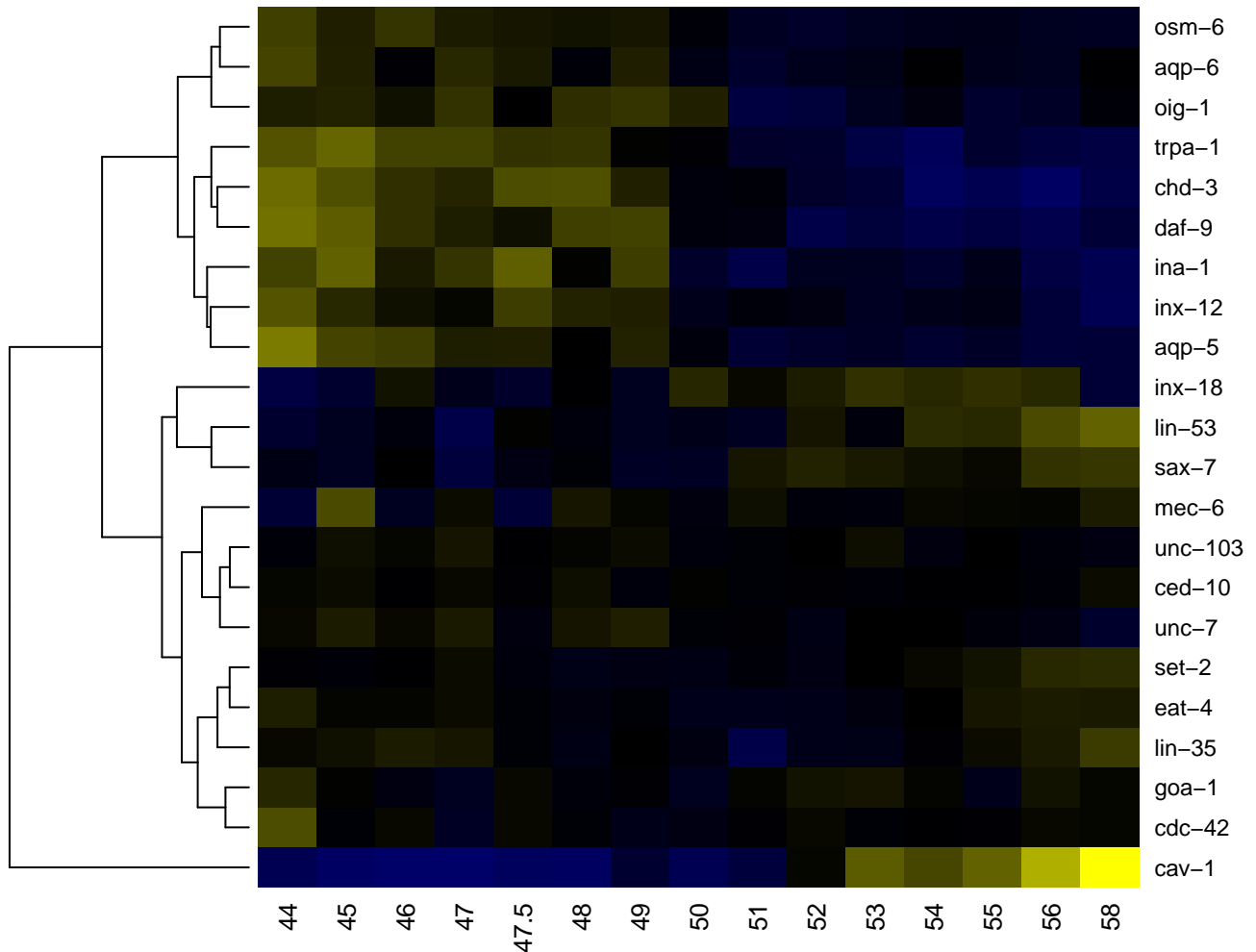
IL1DR



IL1L



IL1R



-2

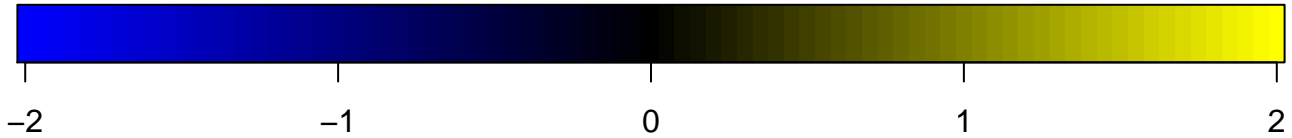
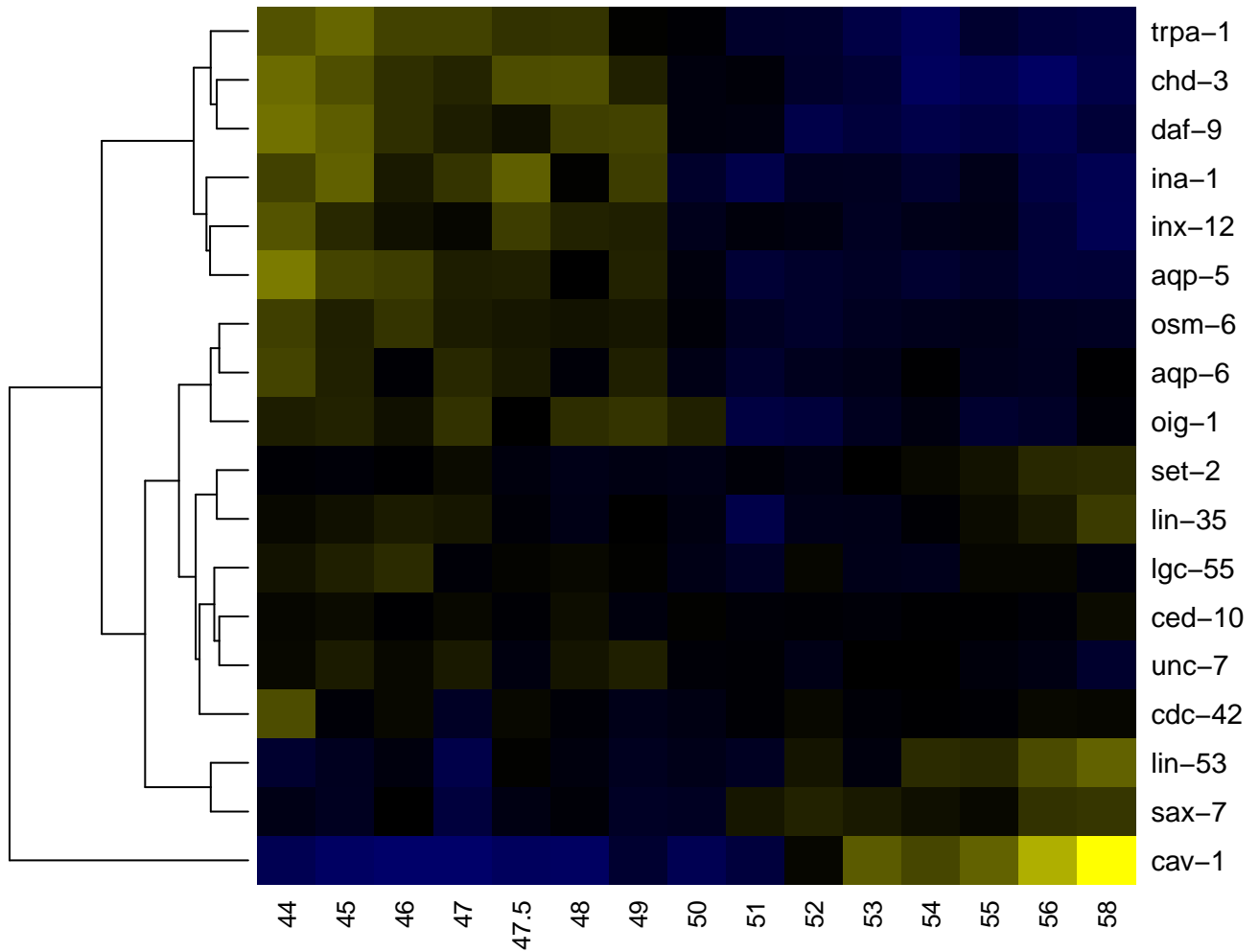
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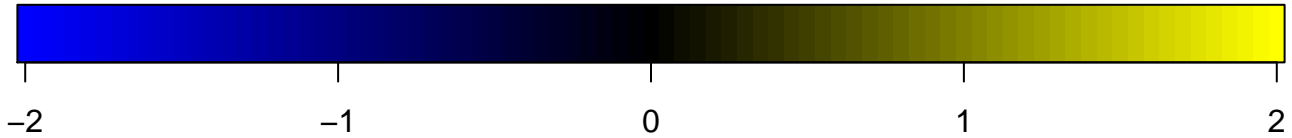
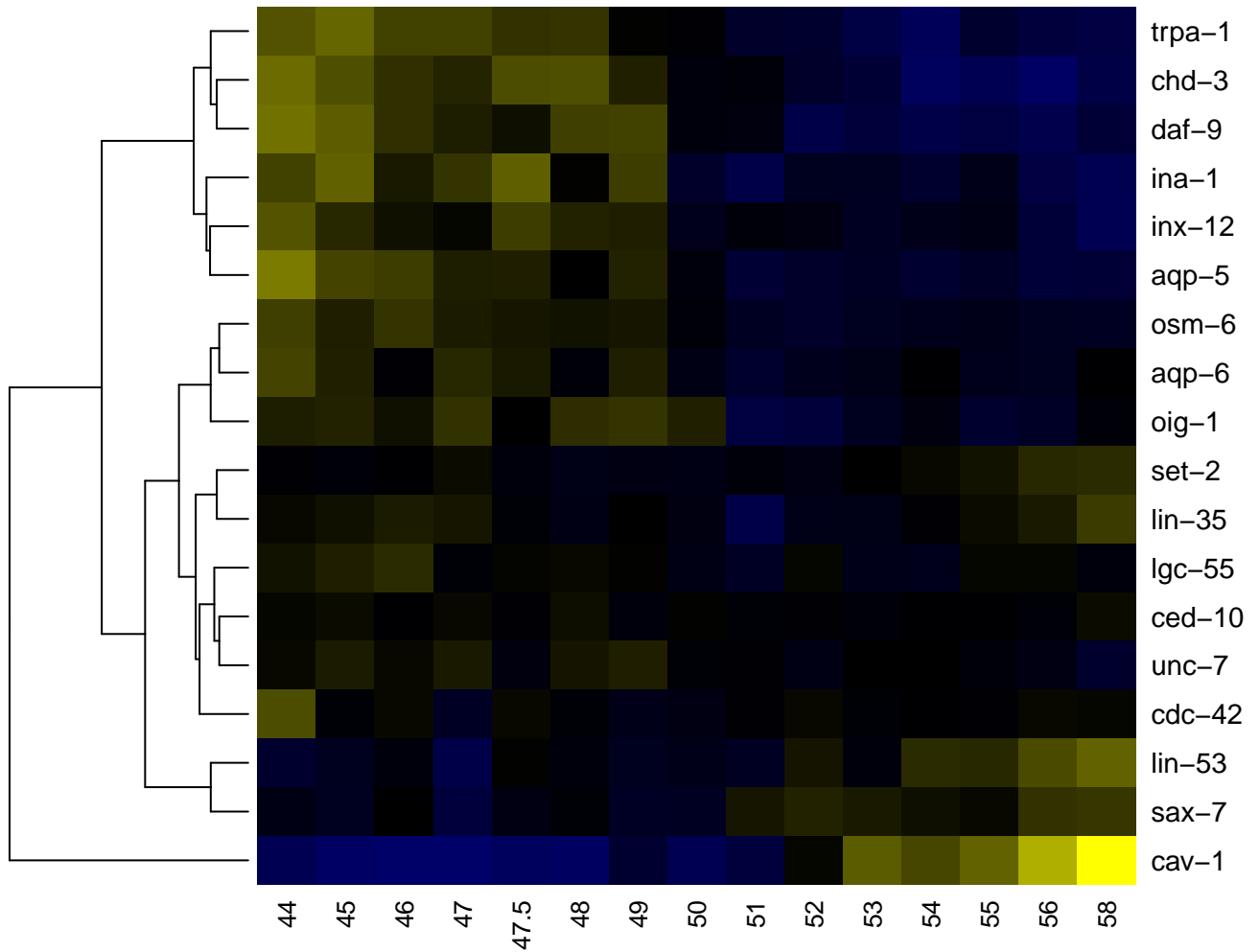
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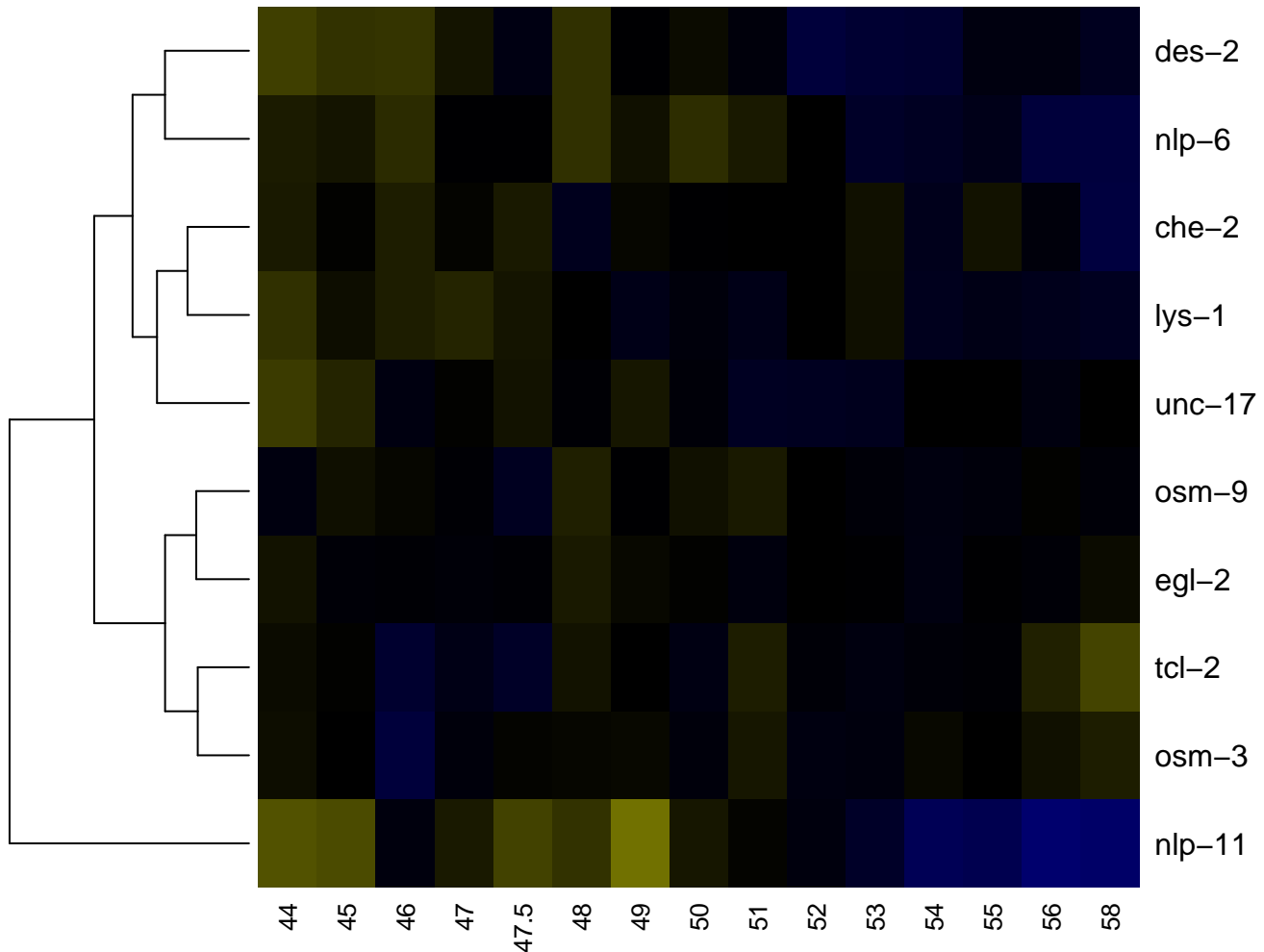
IL1VL



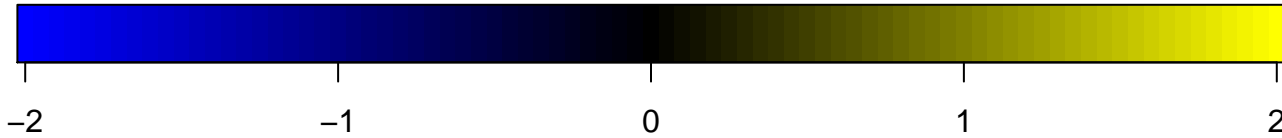
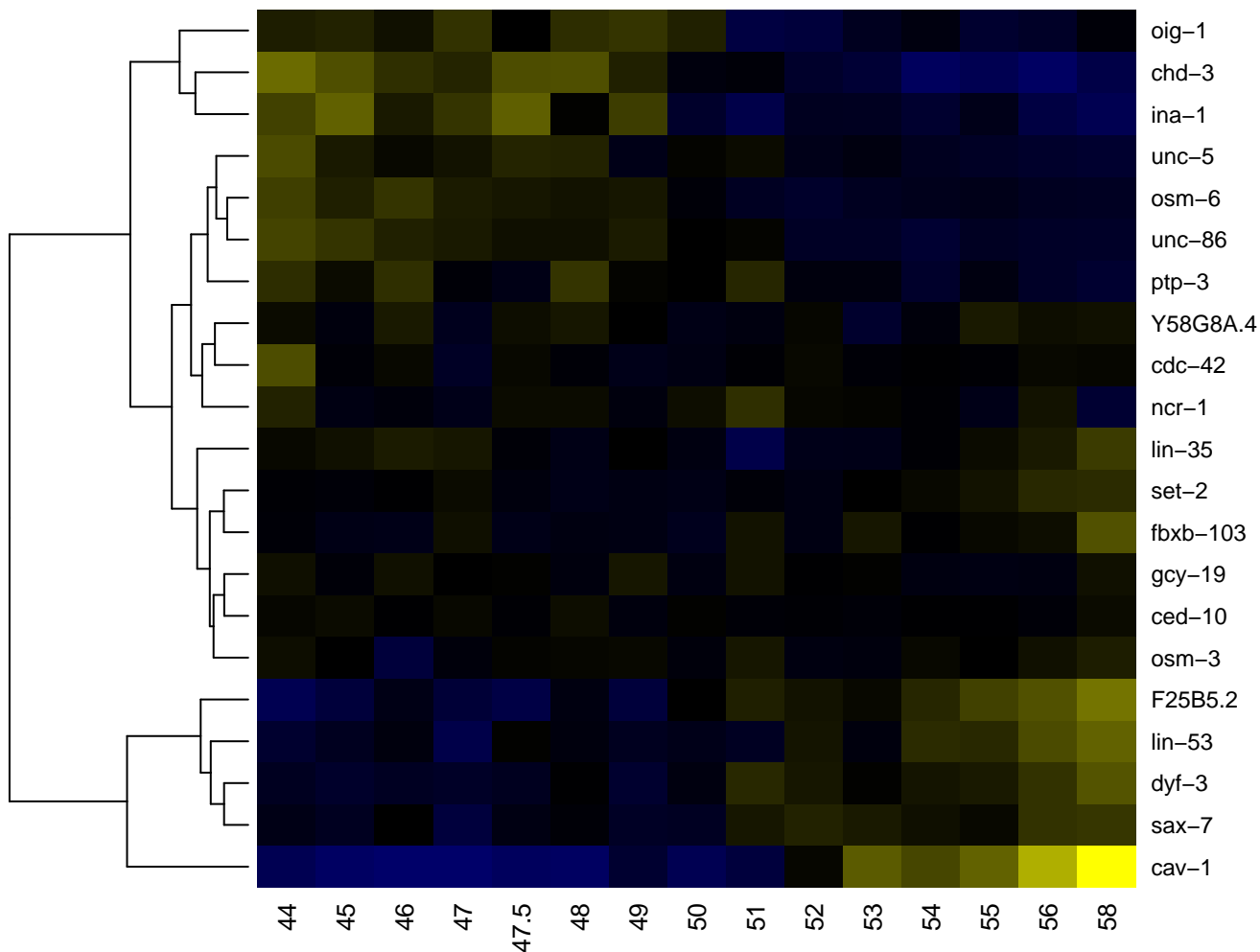
IL1VR



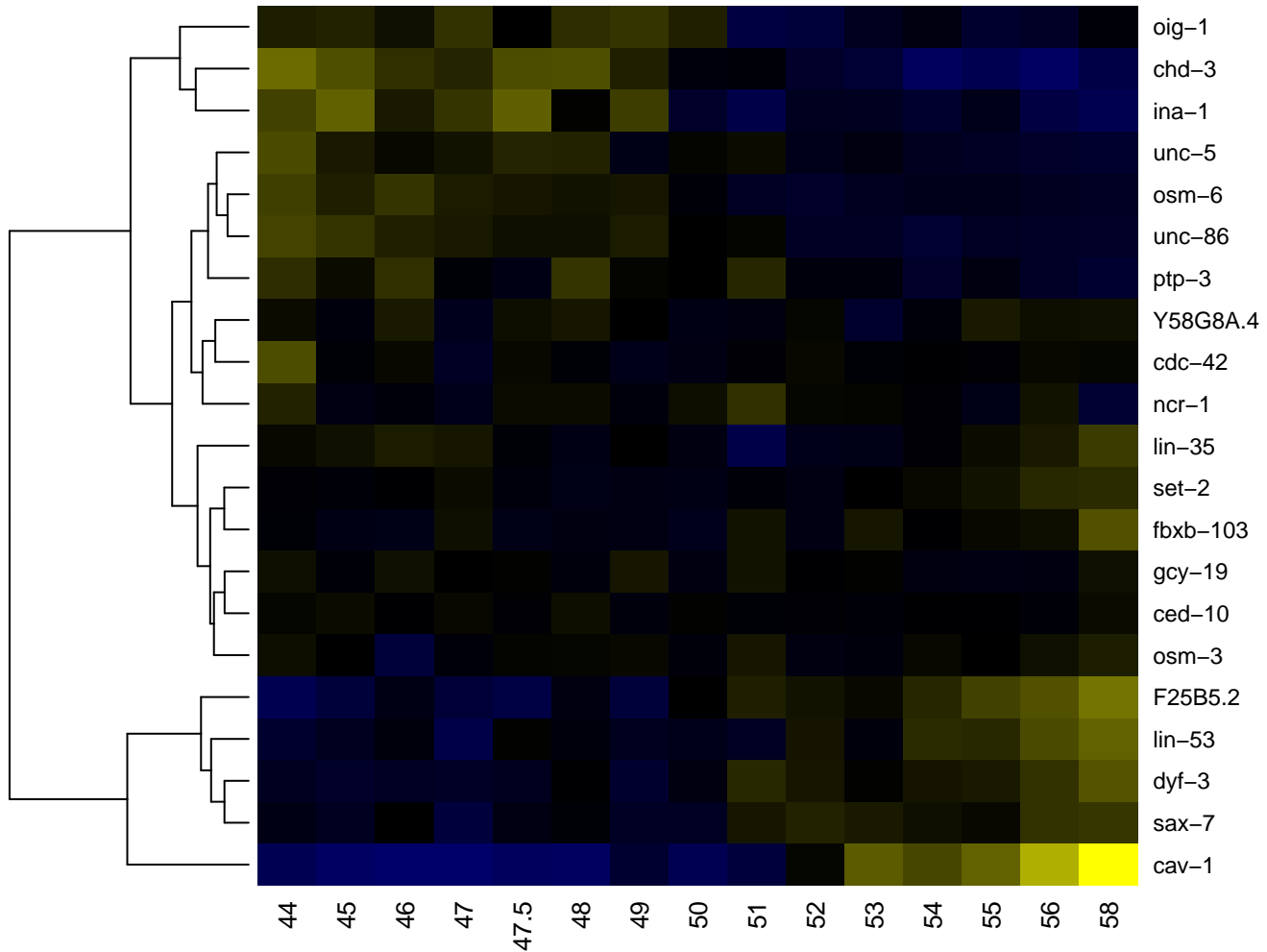
IL2 neuron



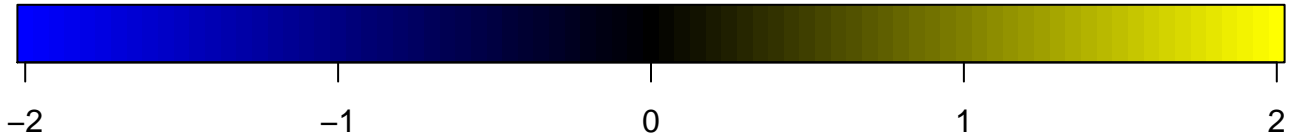
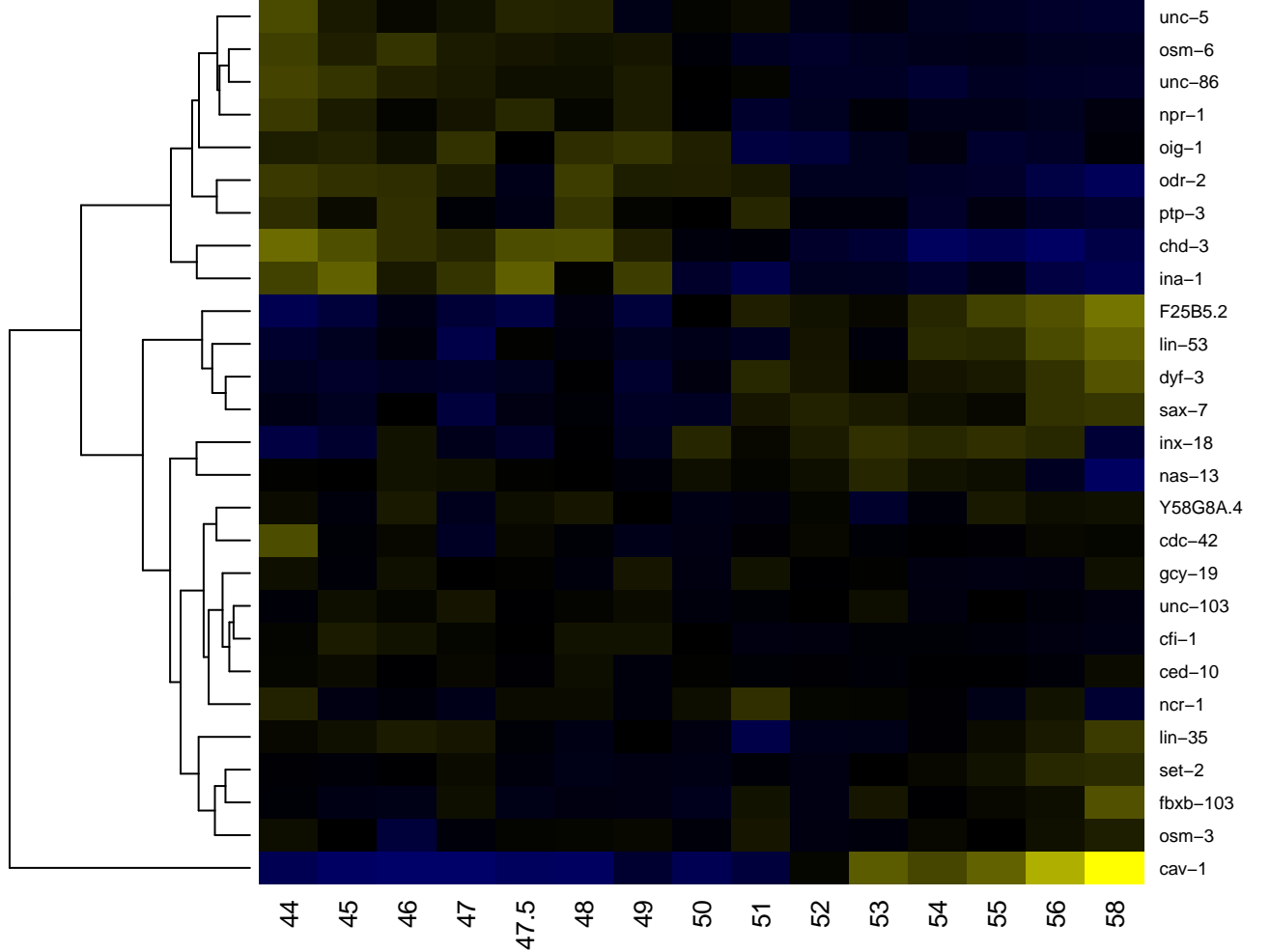
IL2DL



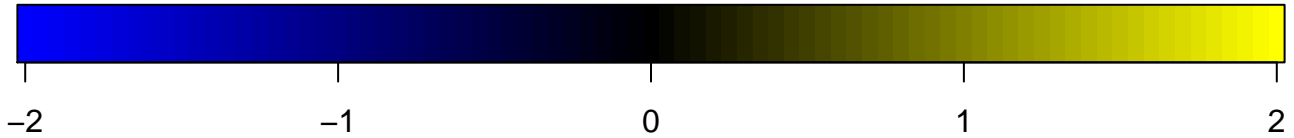
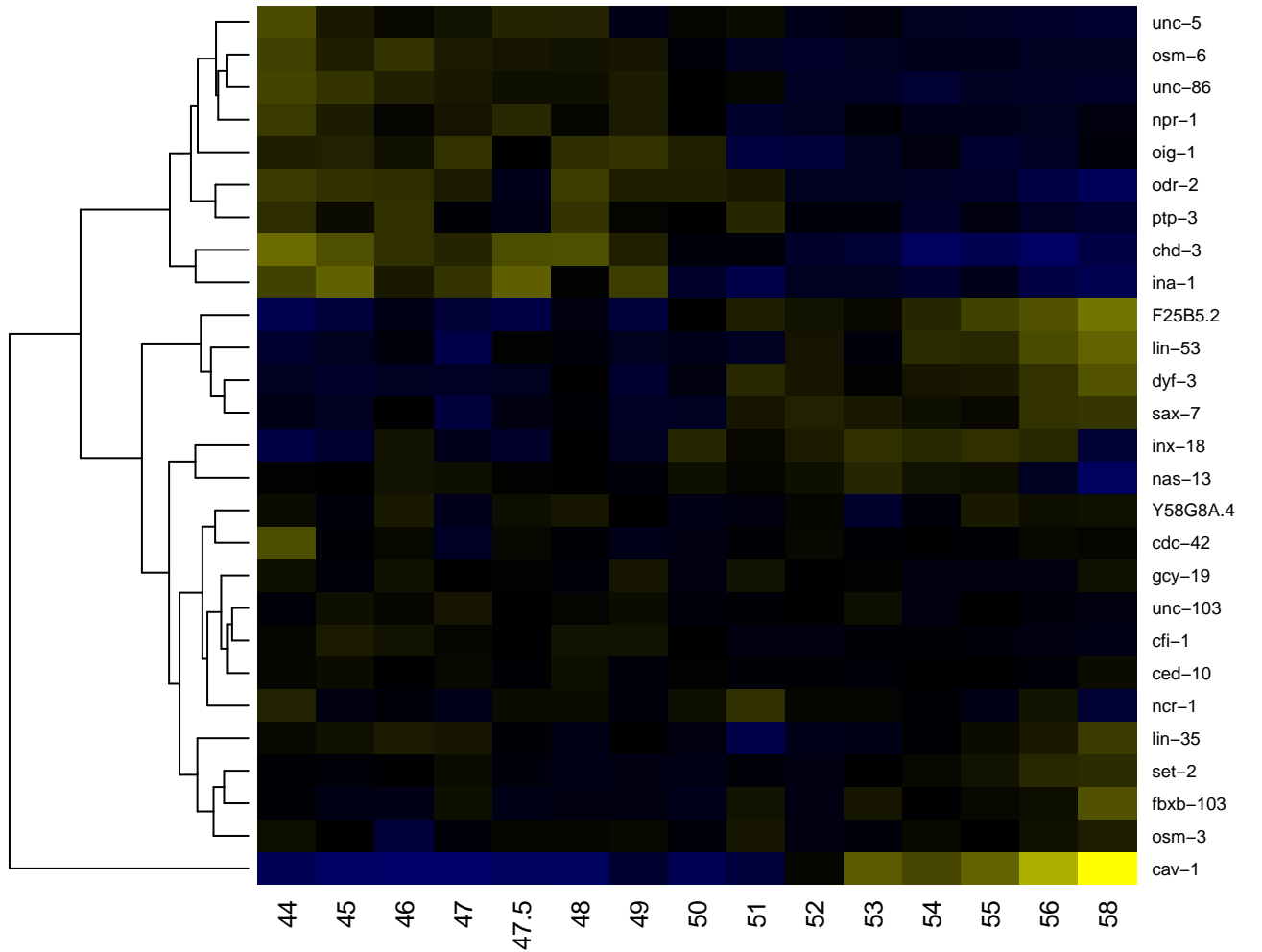
IL2DR



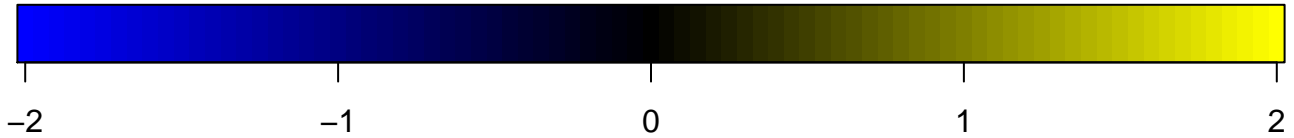
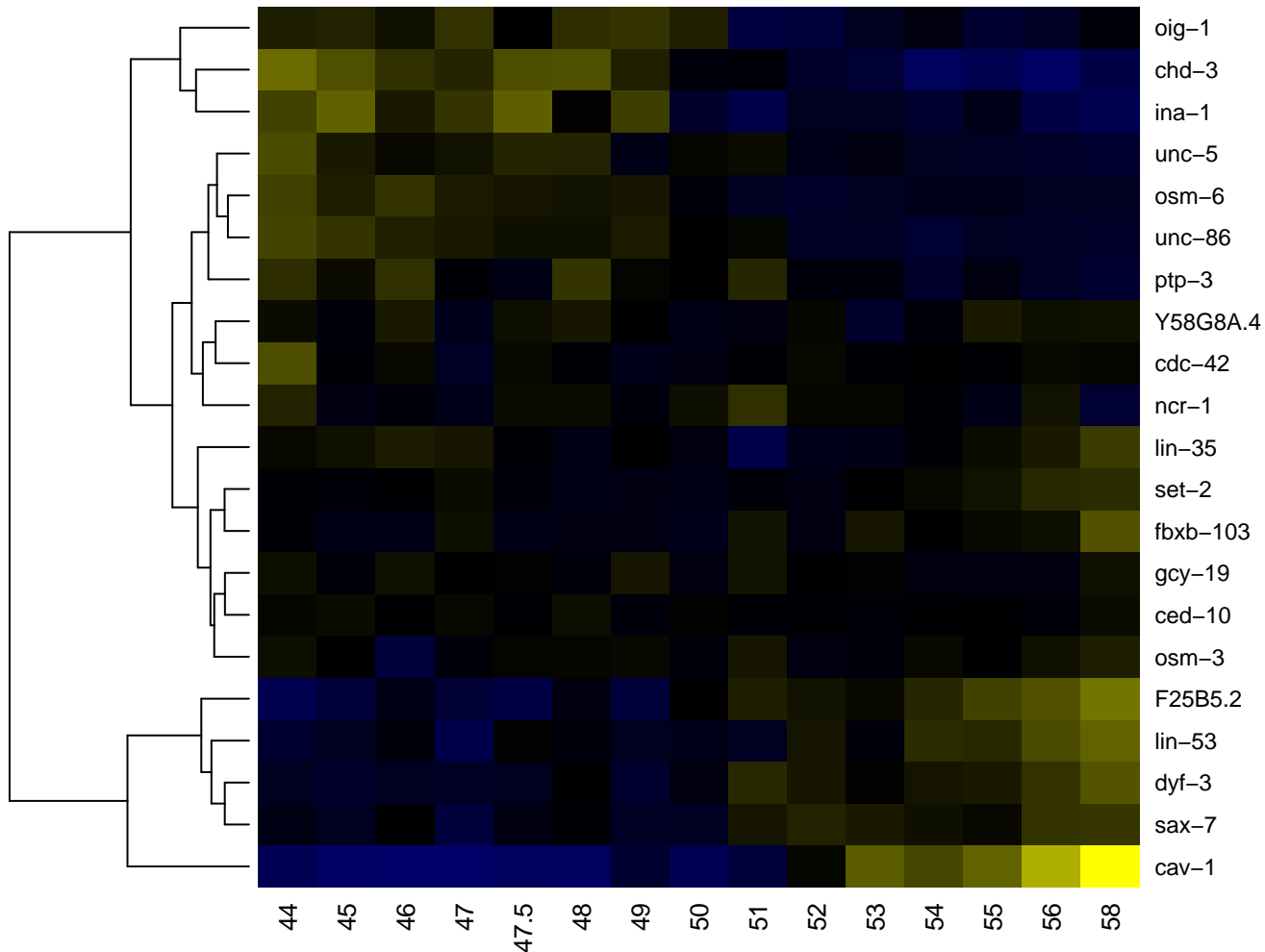
IL2L



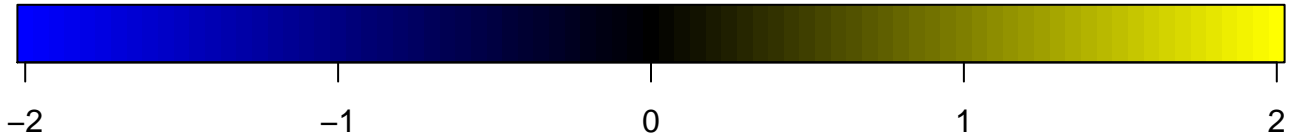
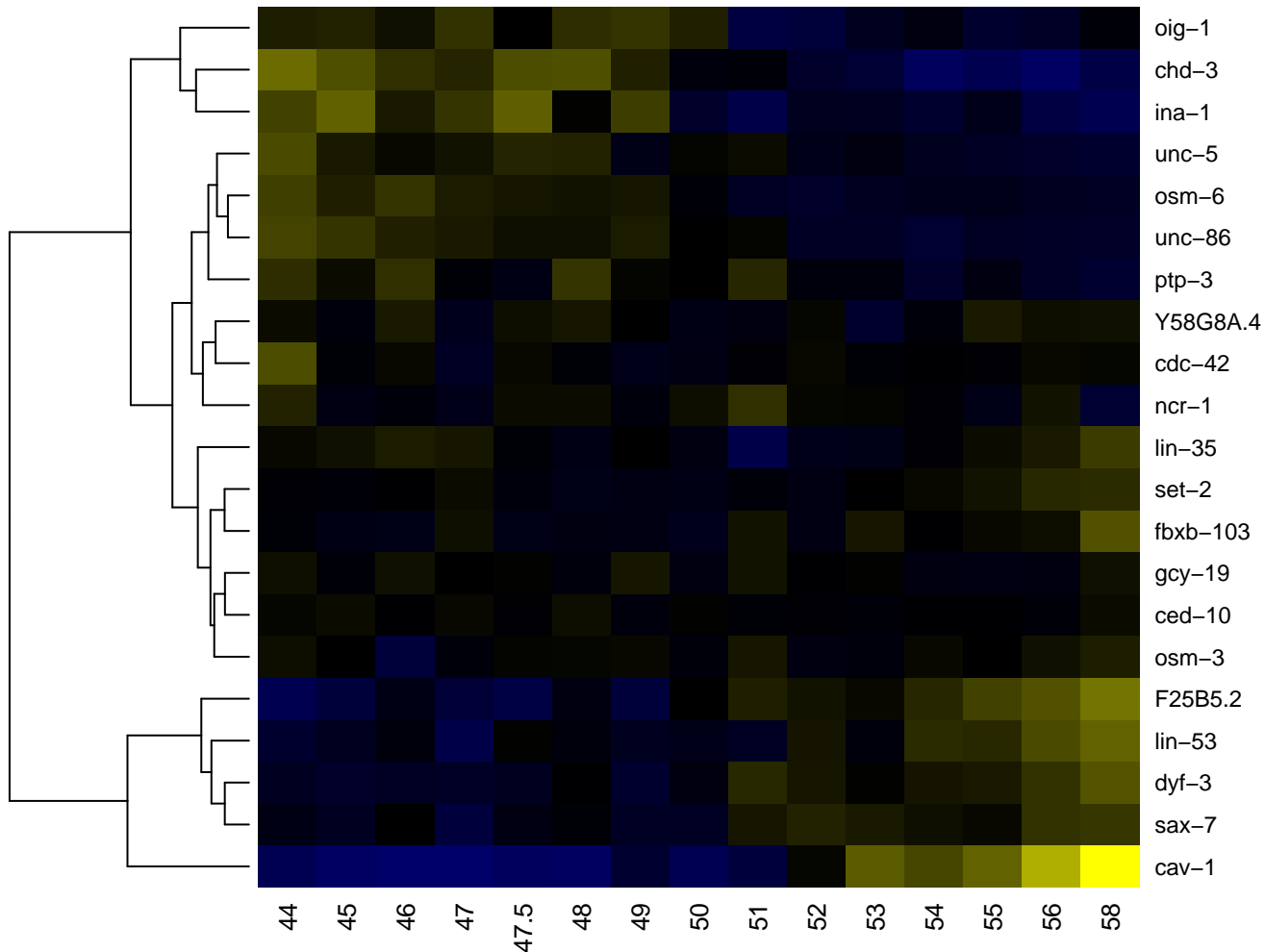
IL2R



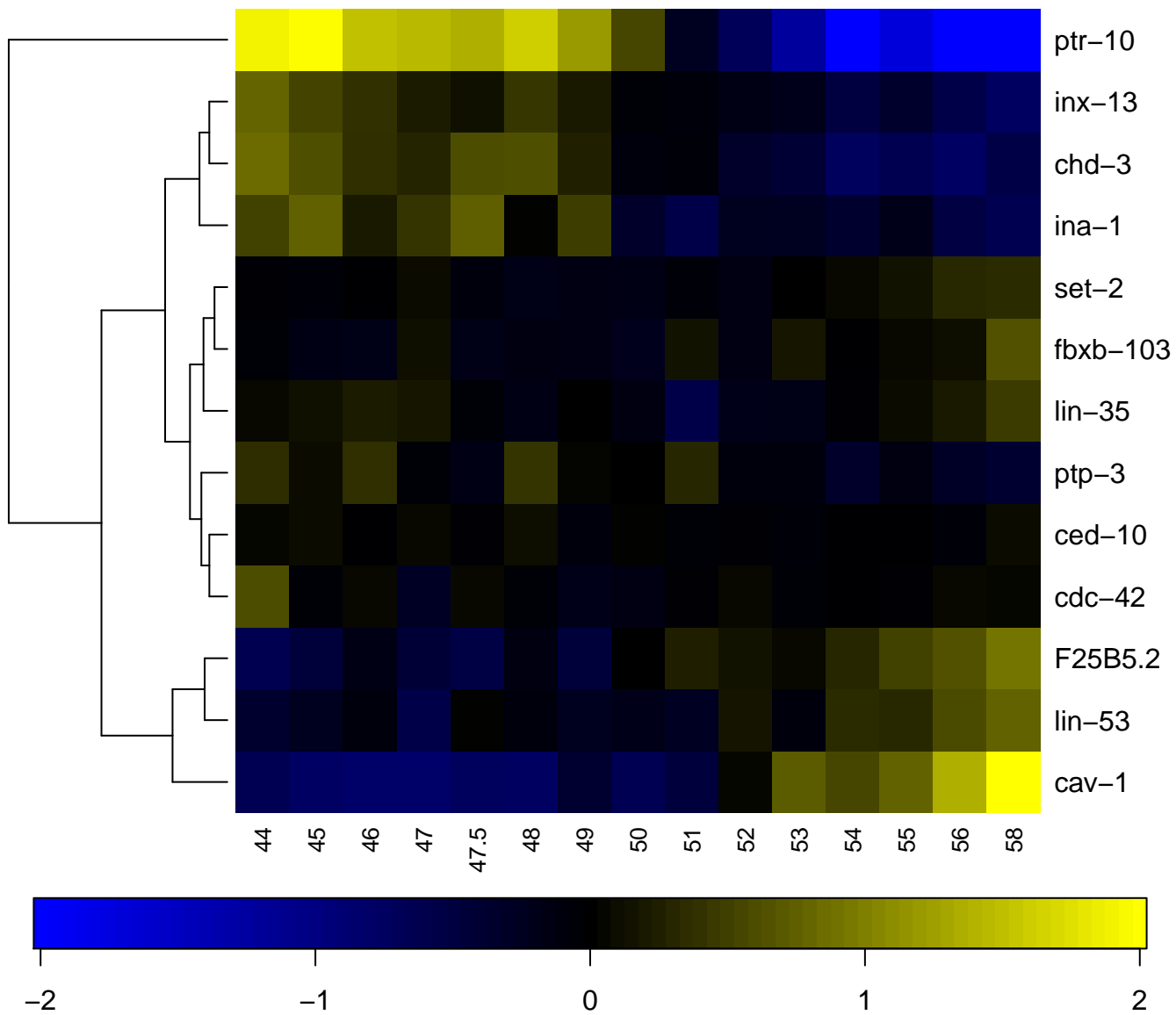
IL2VL



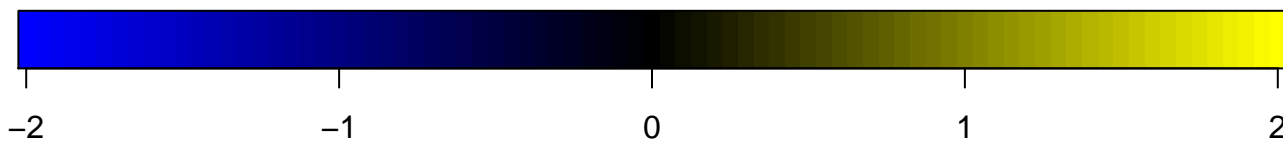
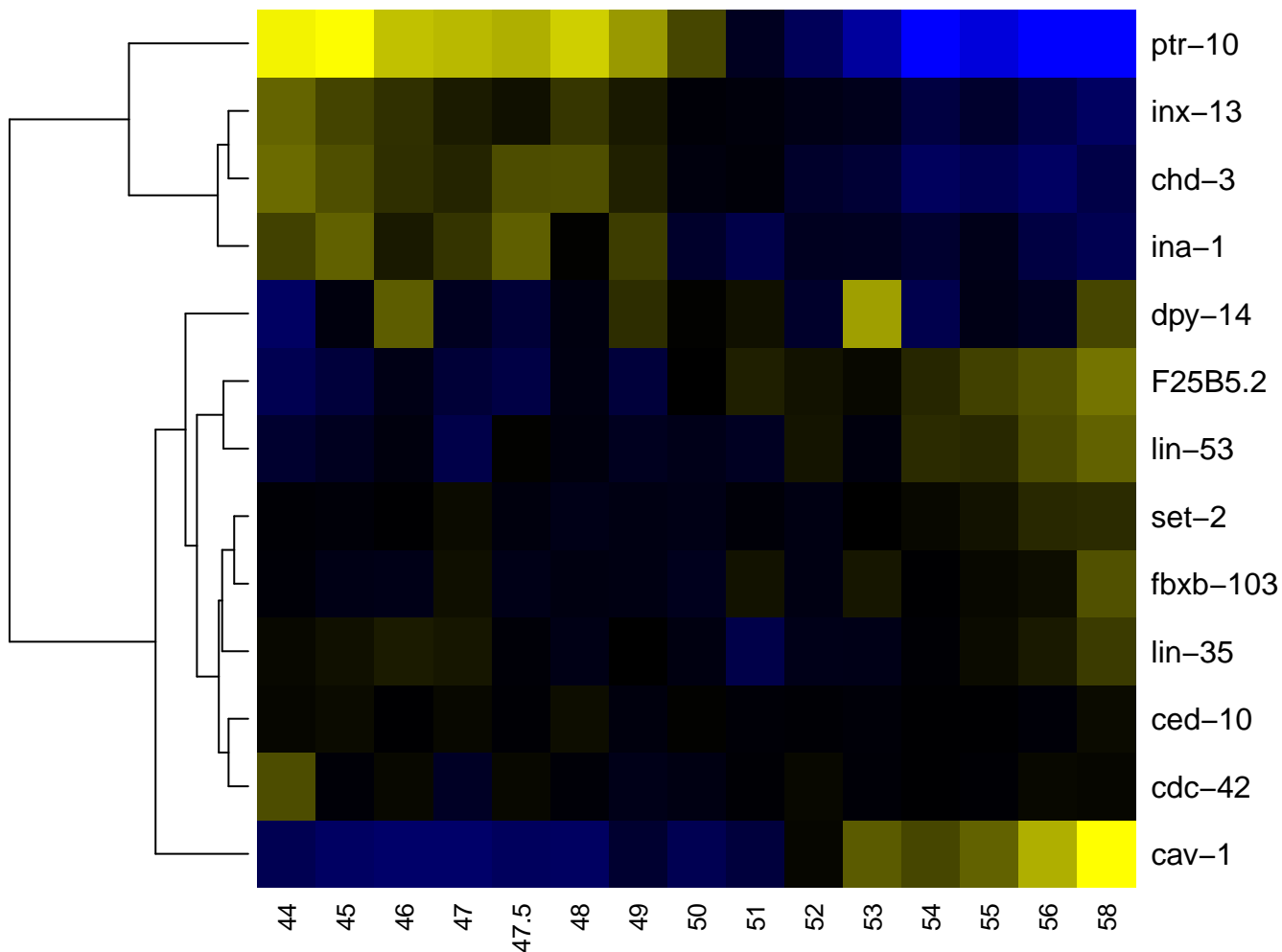
IL2VR



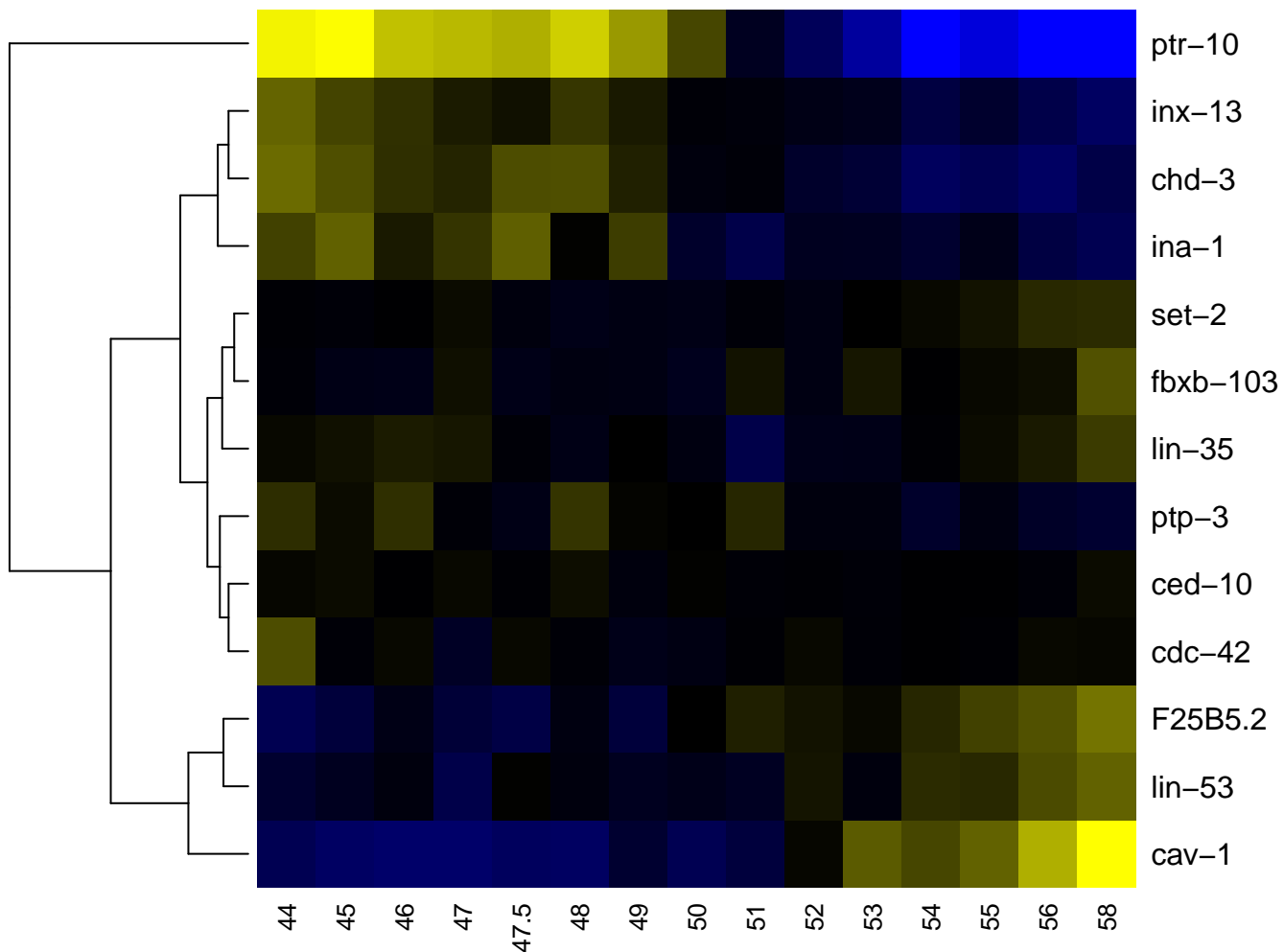
ILshDL



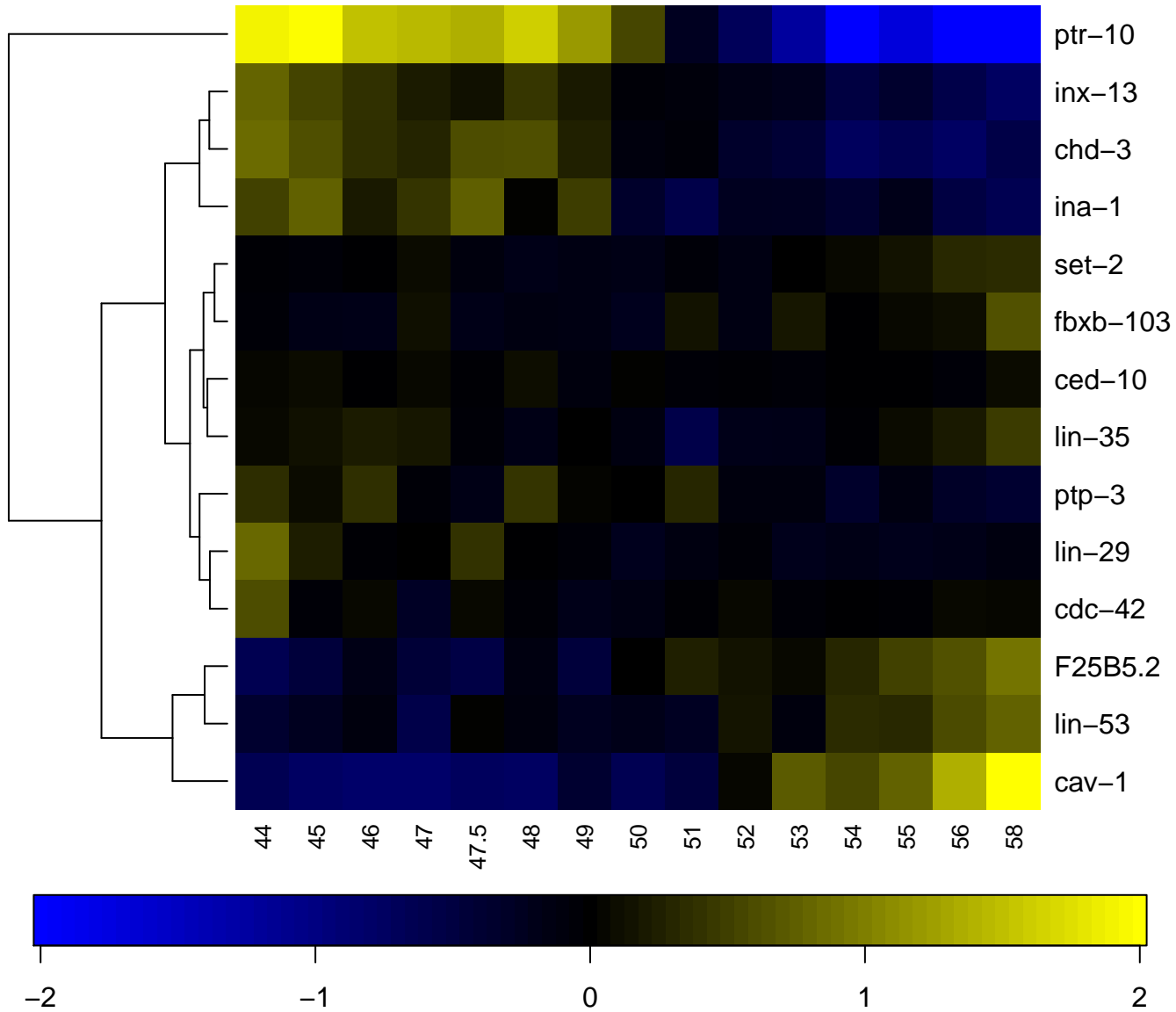
ILshL



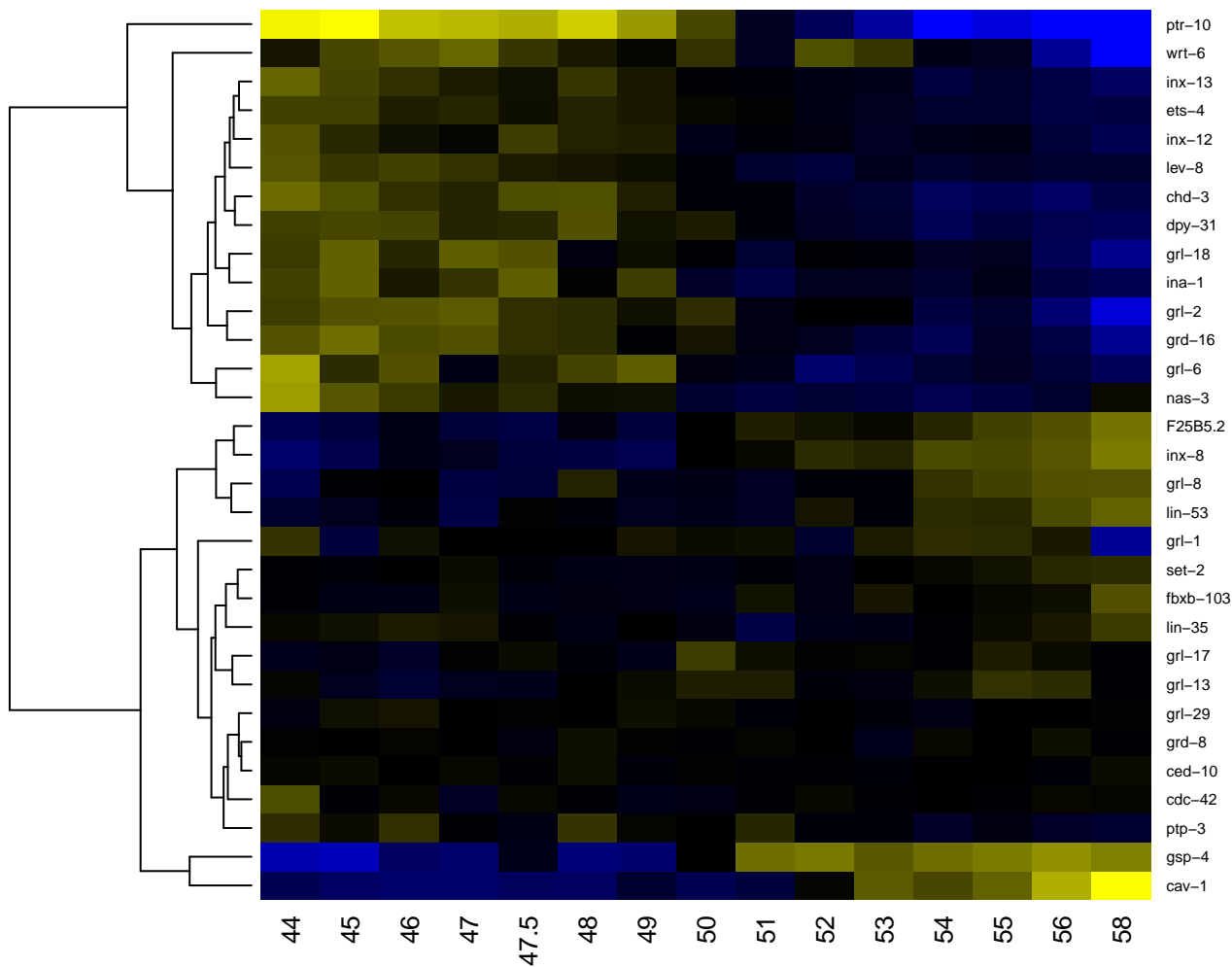
ILshR



ILshVR



ILsoDL



-2

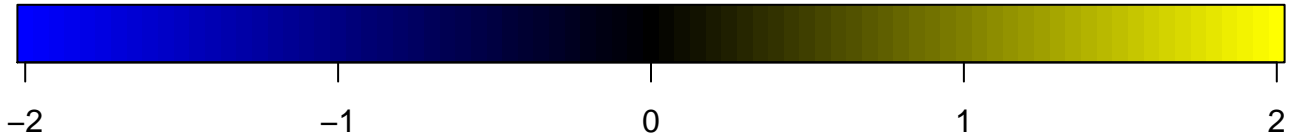
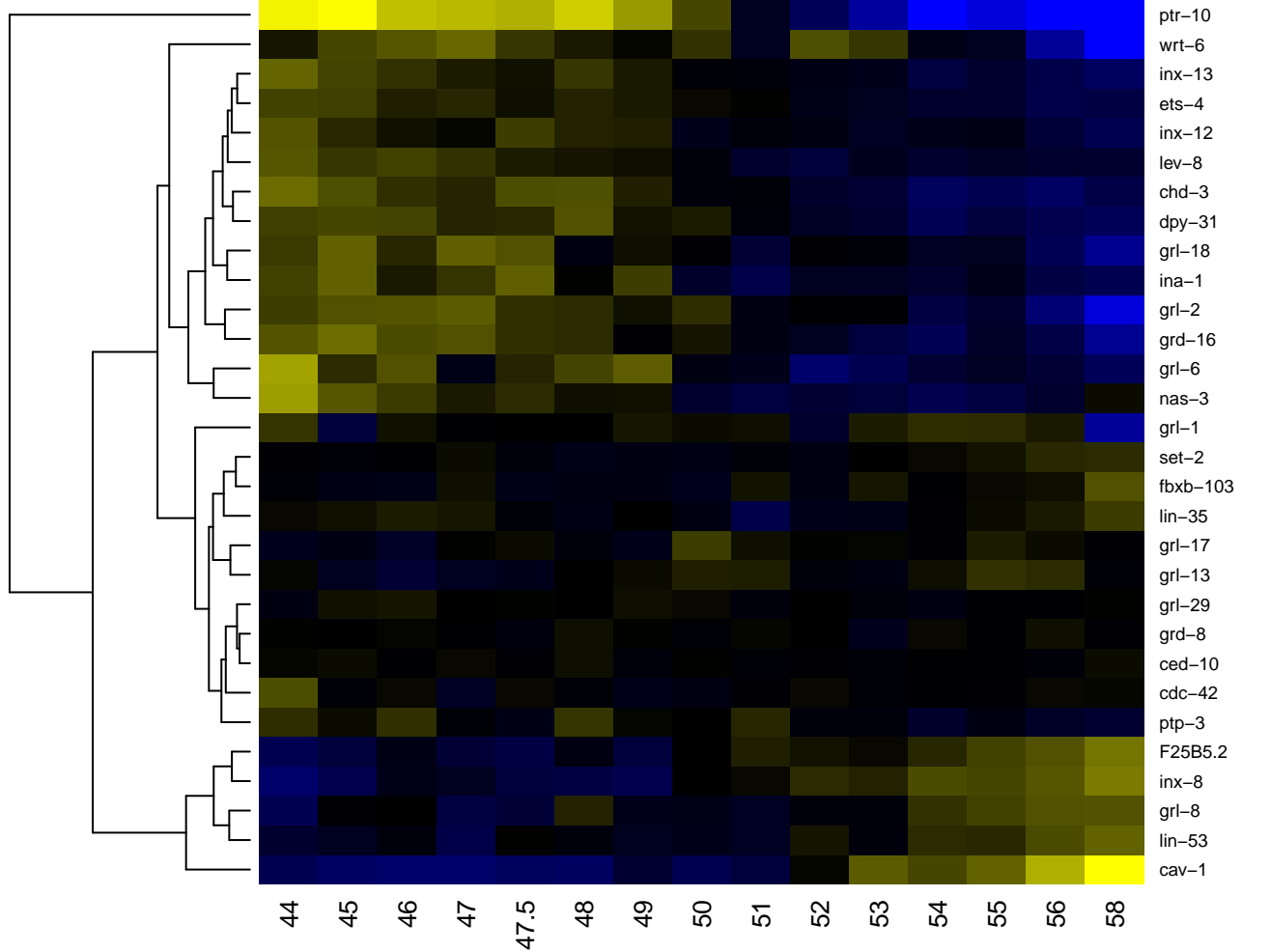
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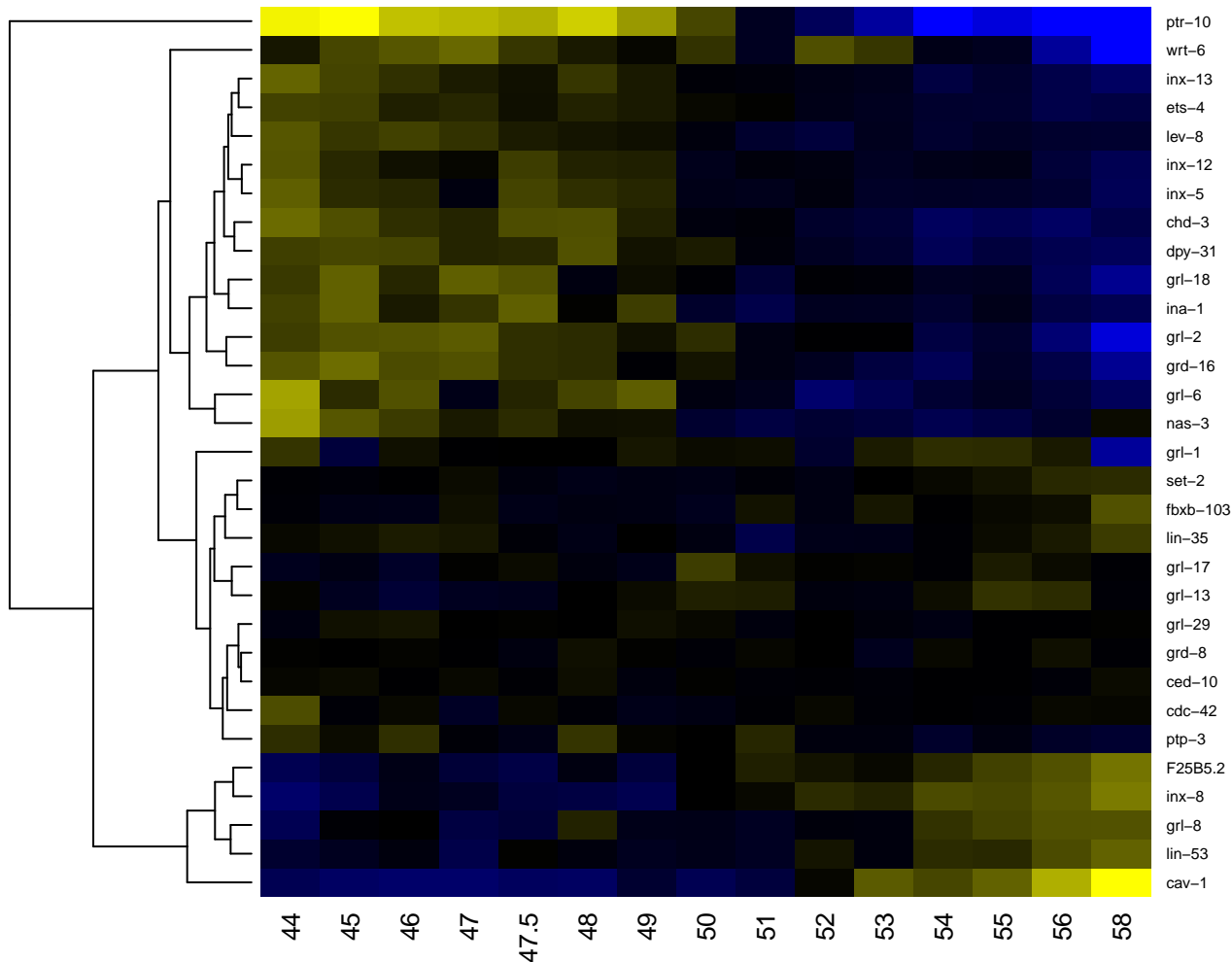
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2

ILsoDR



ILsOL



-2

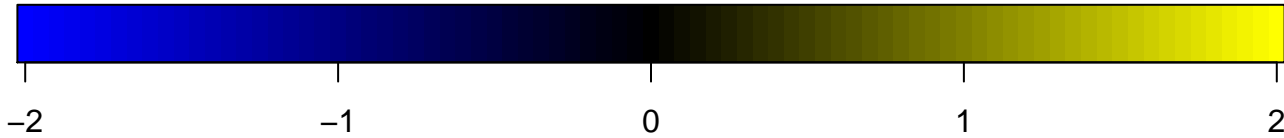
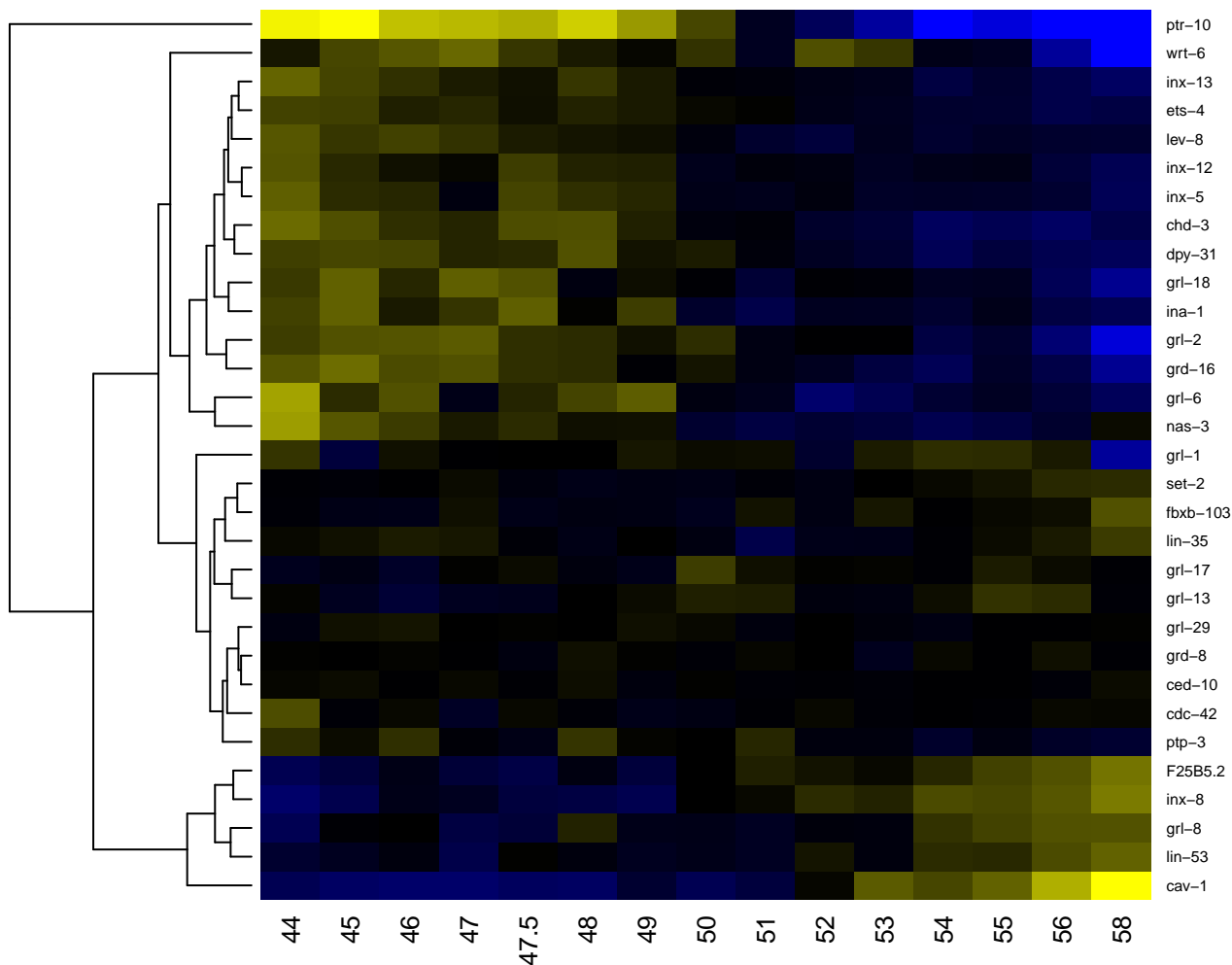
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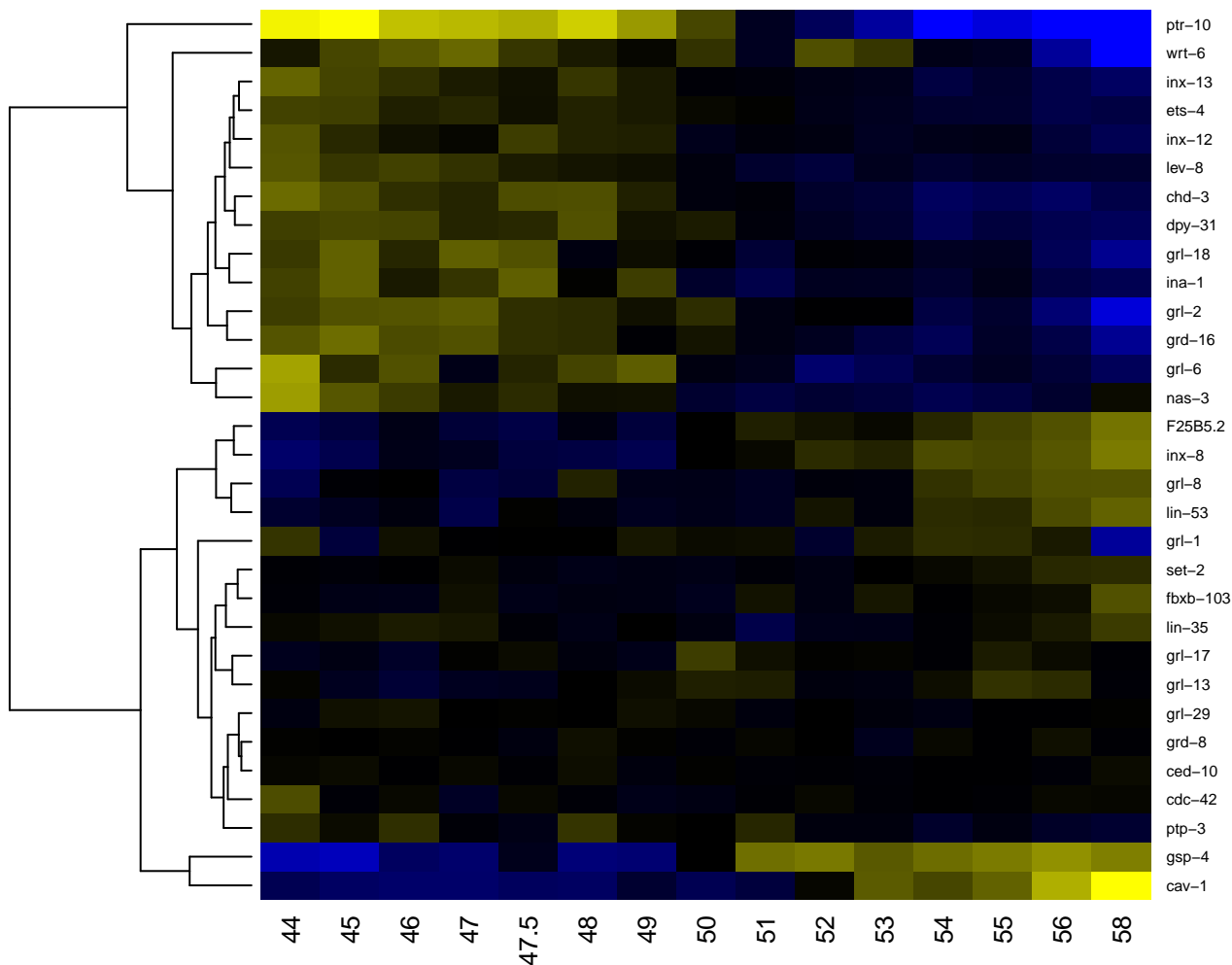
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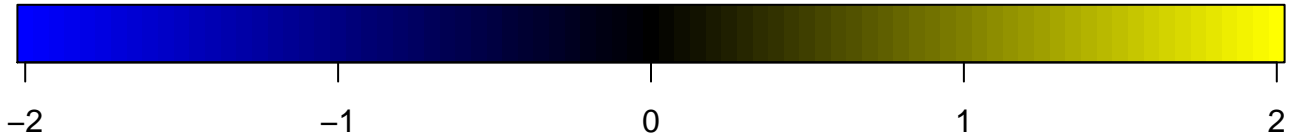
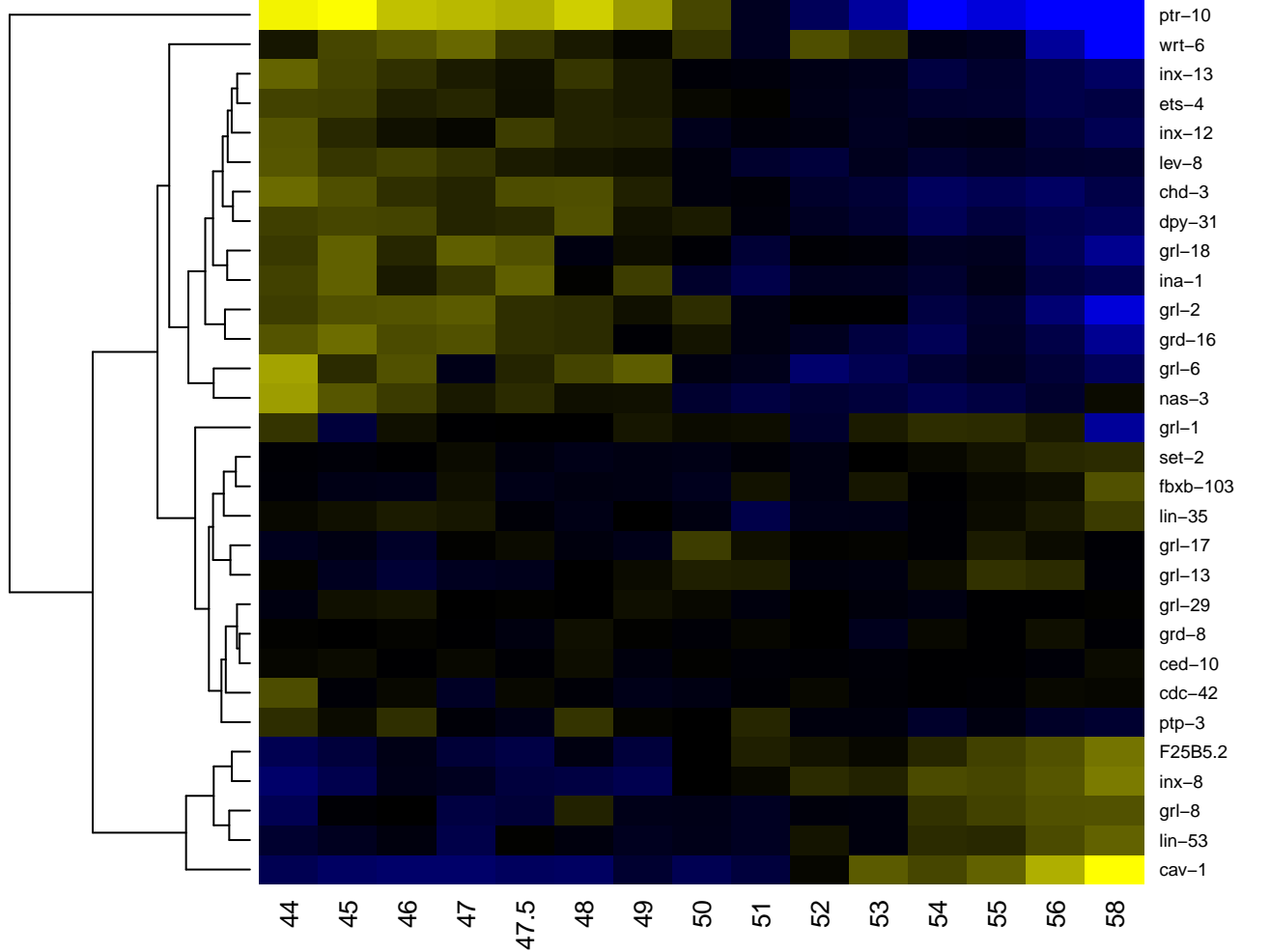
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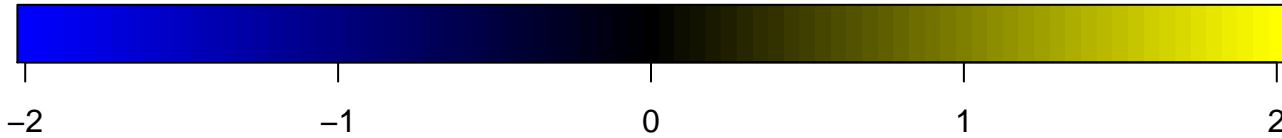
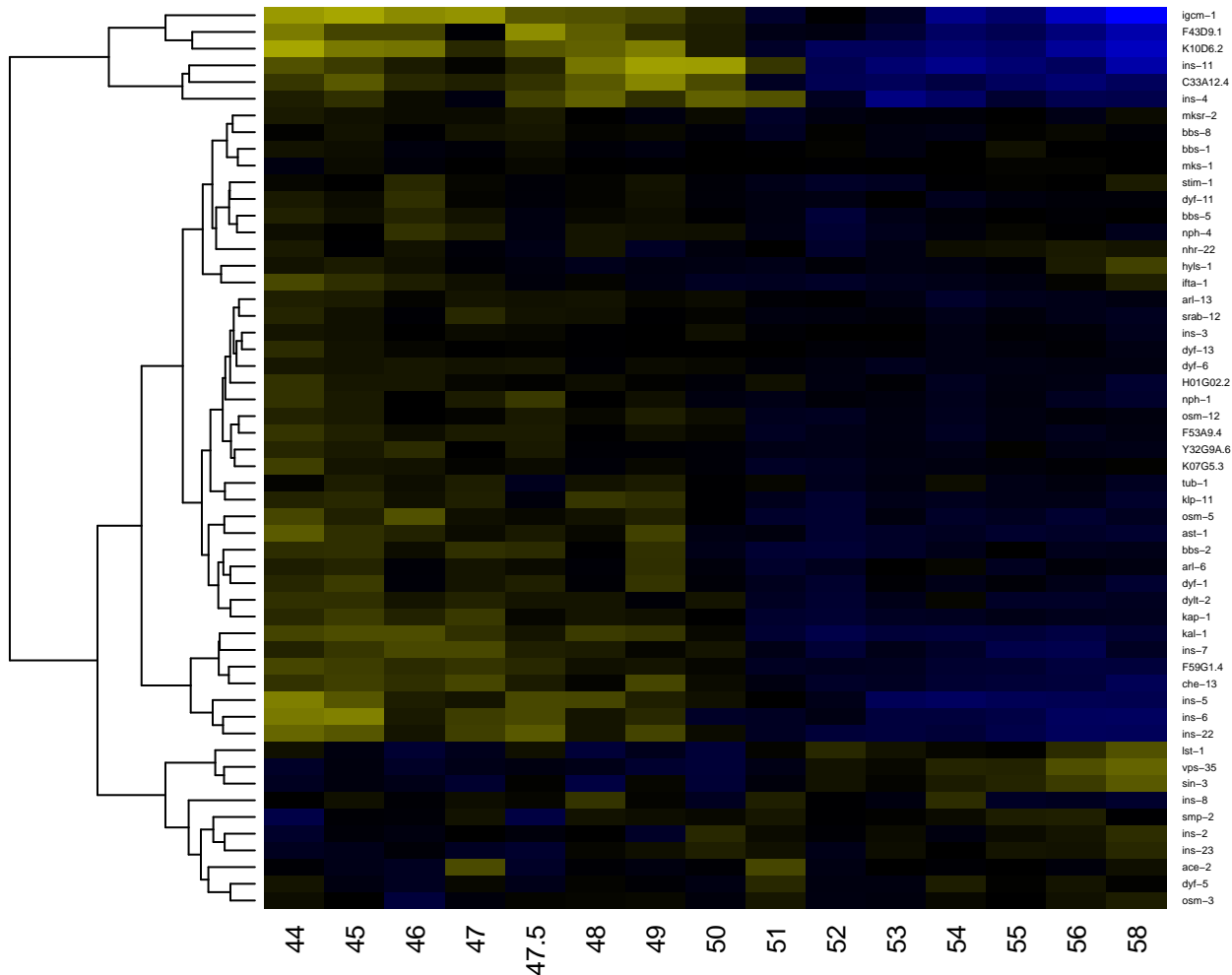
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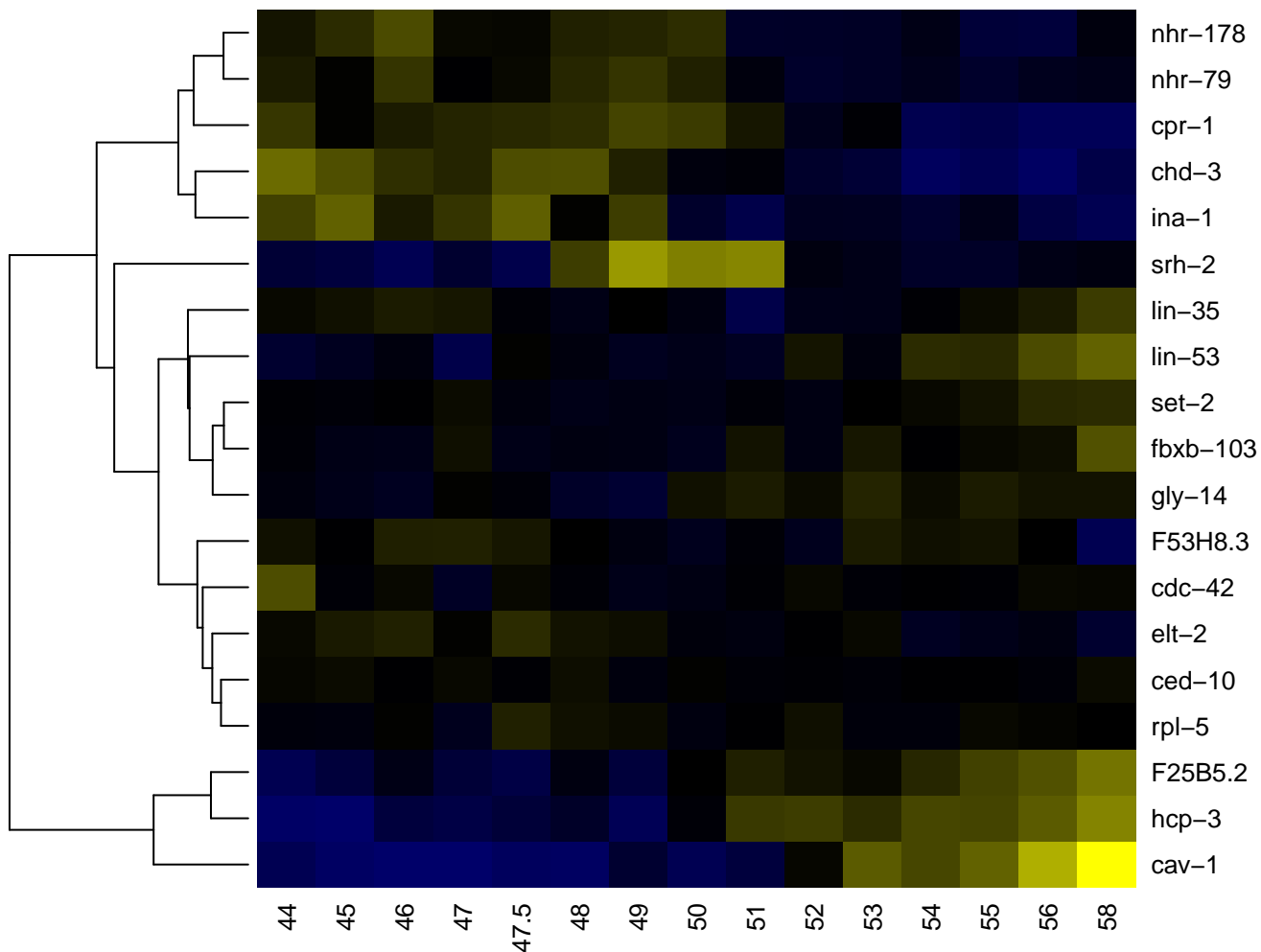
ILsoVR



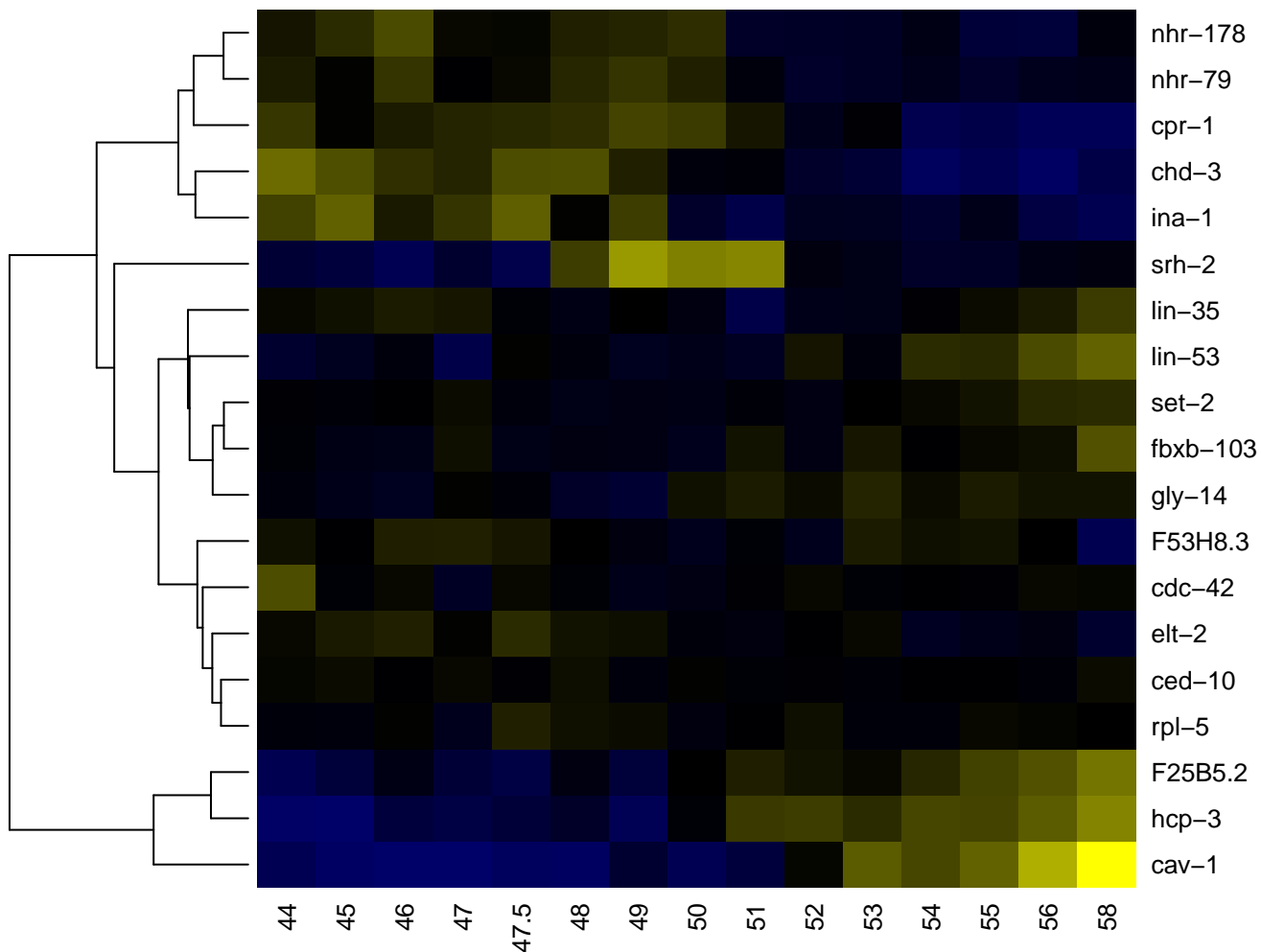
inner labial neuron



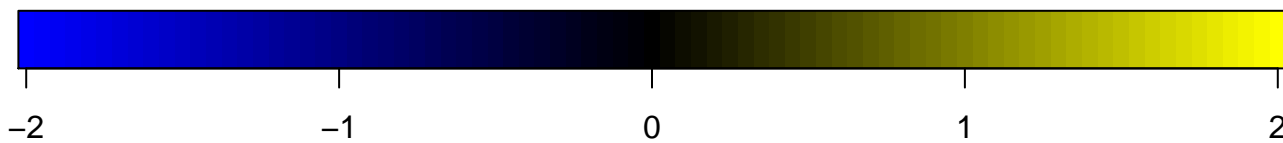
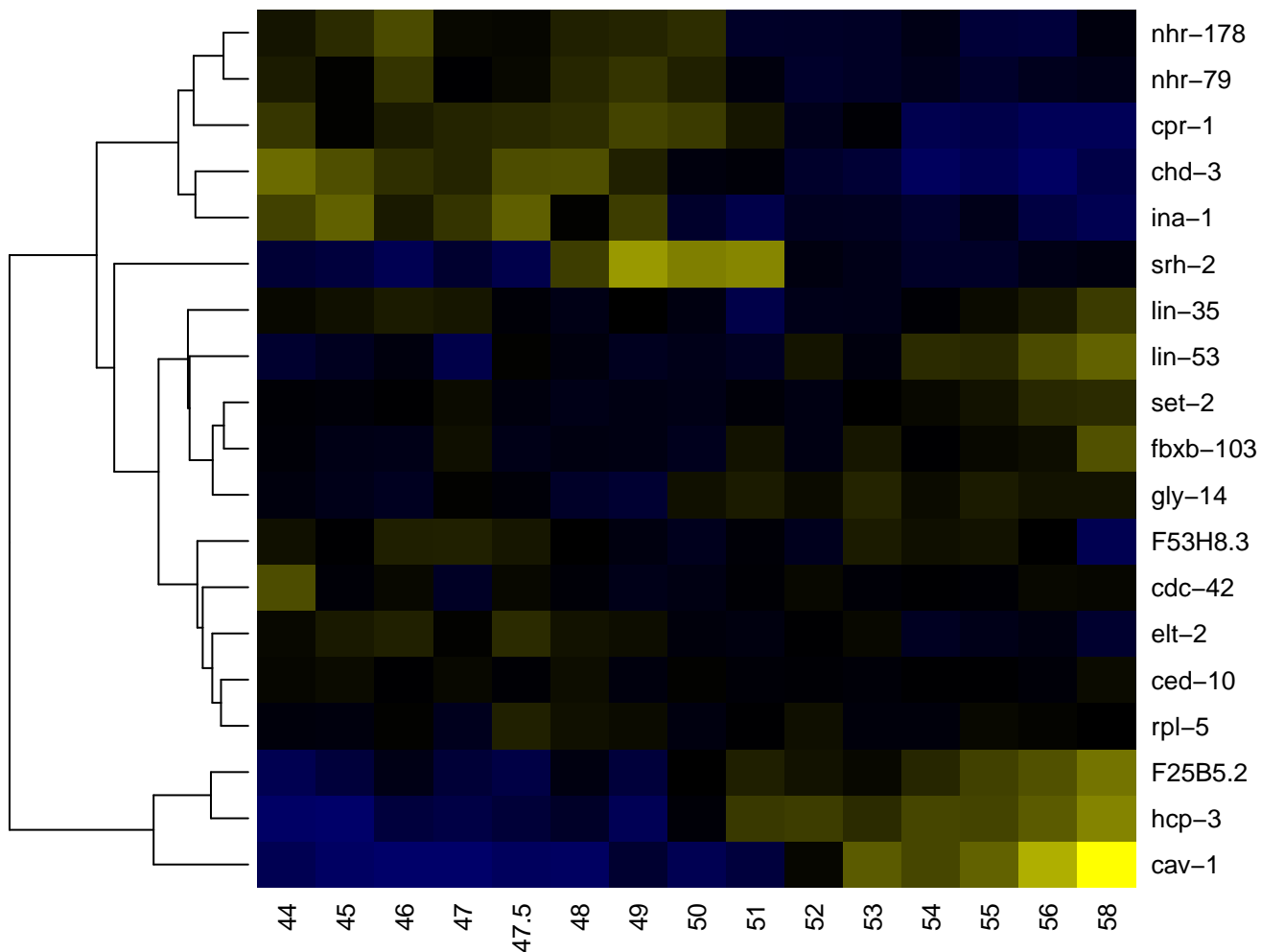
int1DL



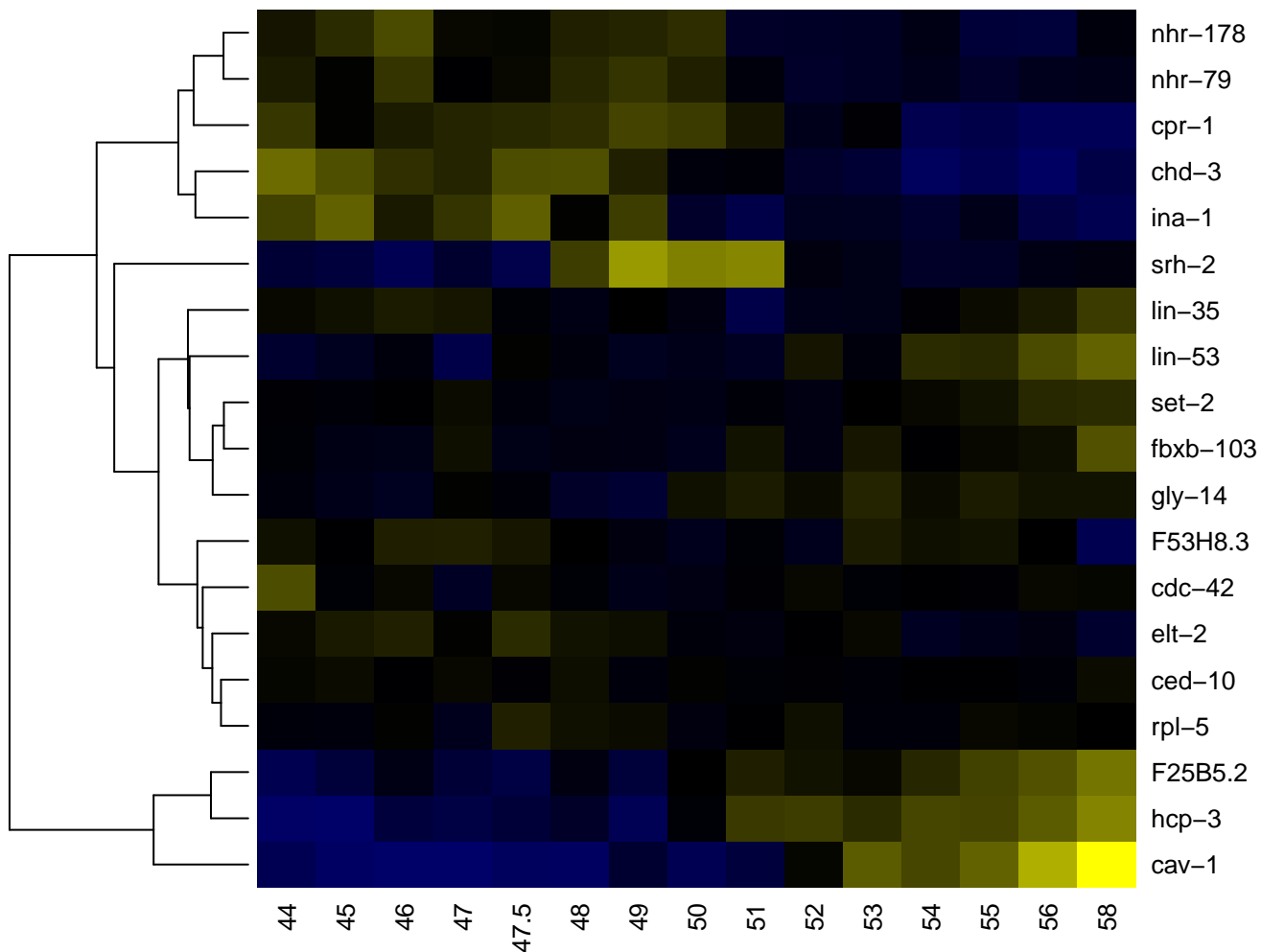
int1DR



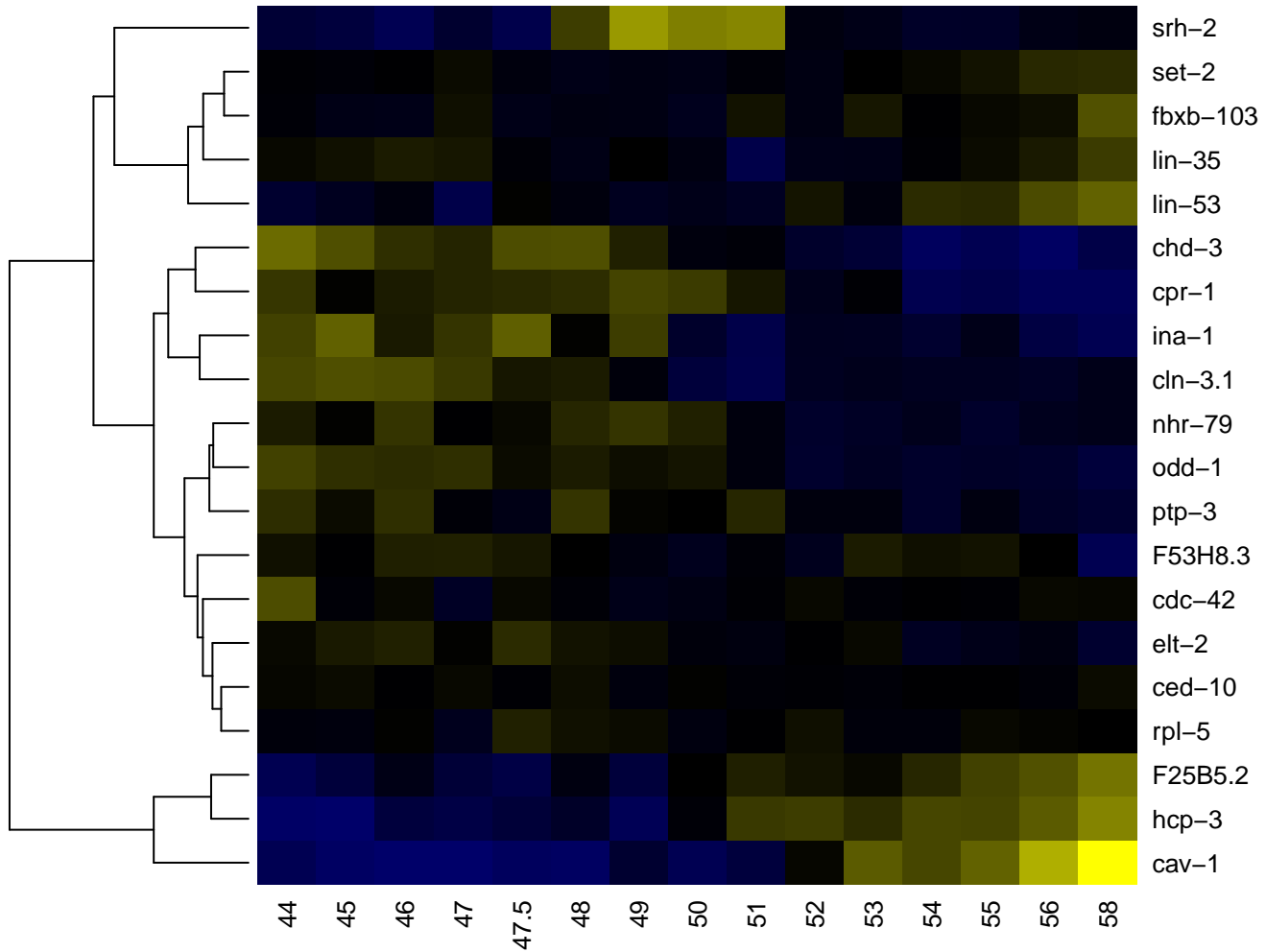
int1VL



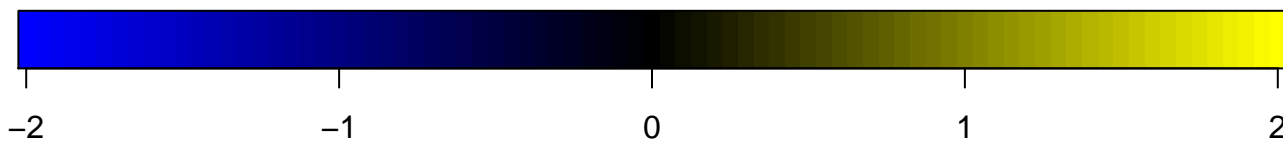
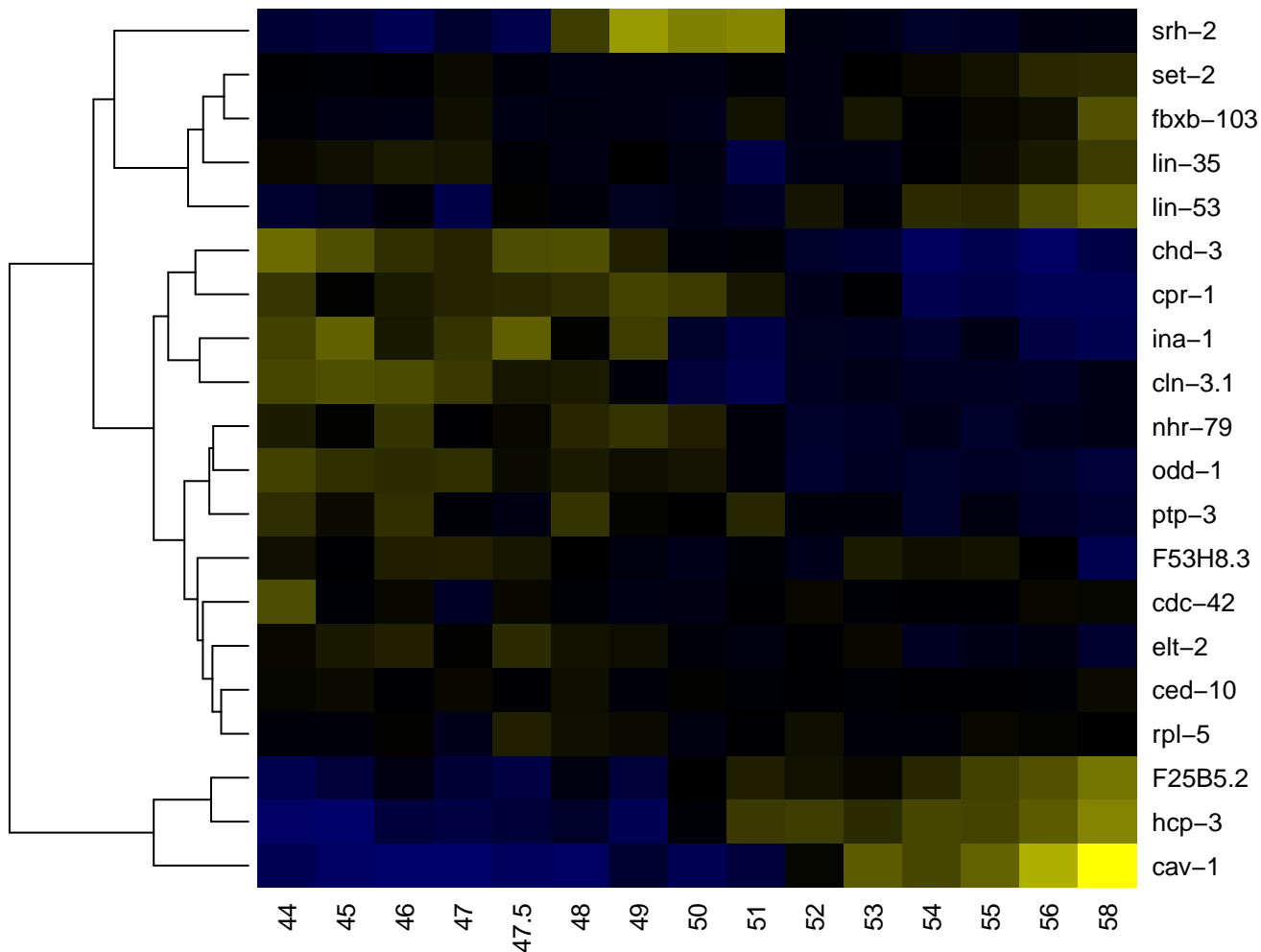
int1VR



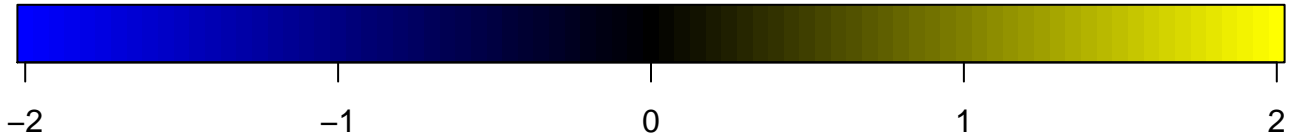
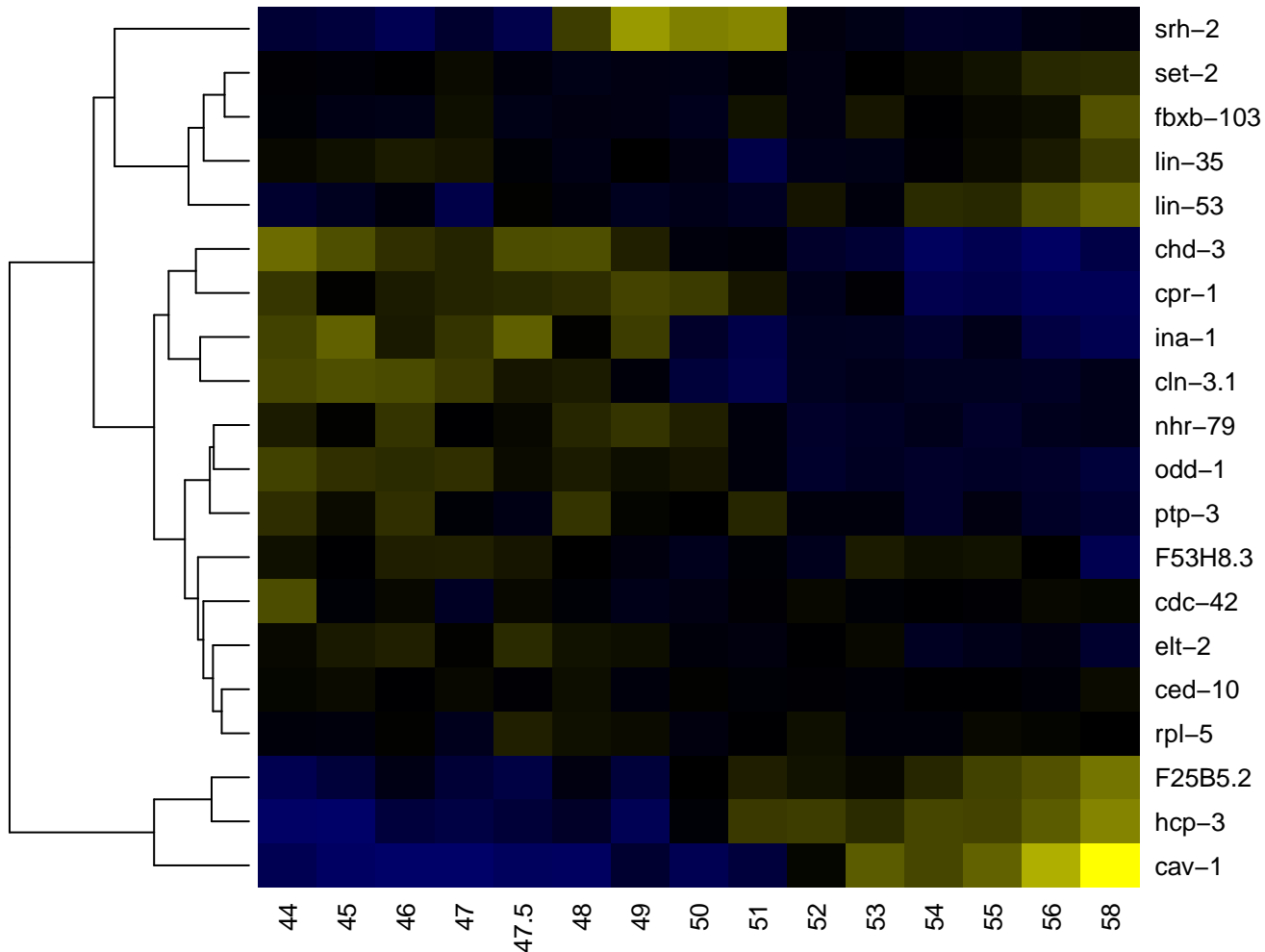
int2D



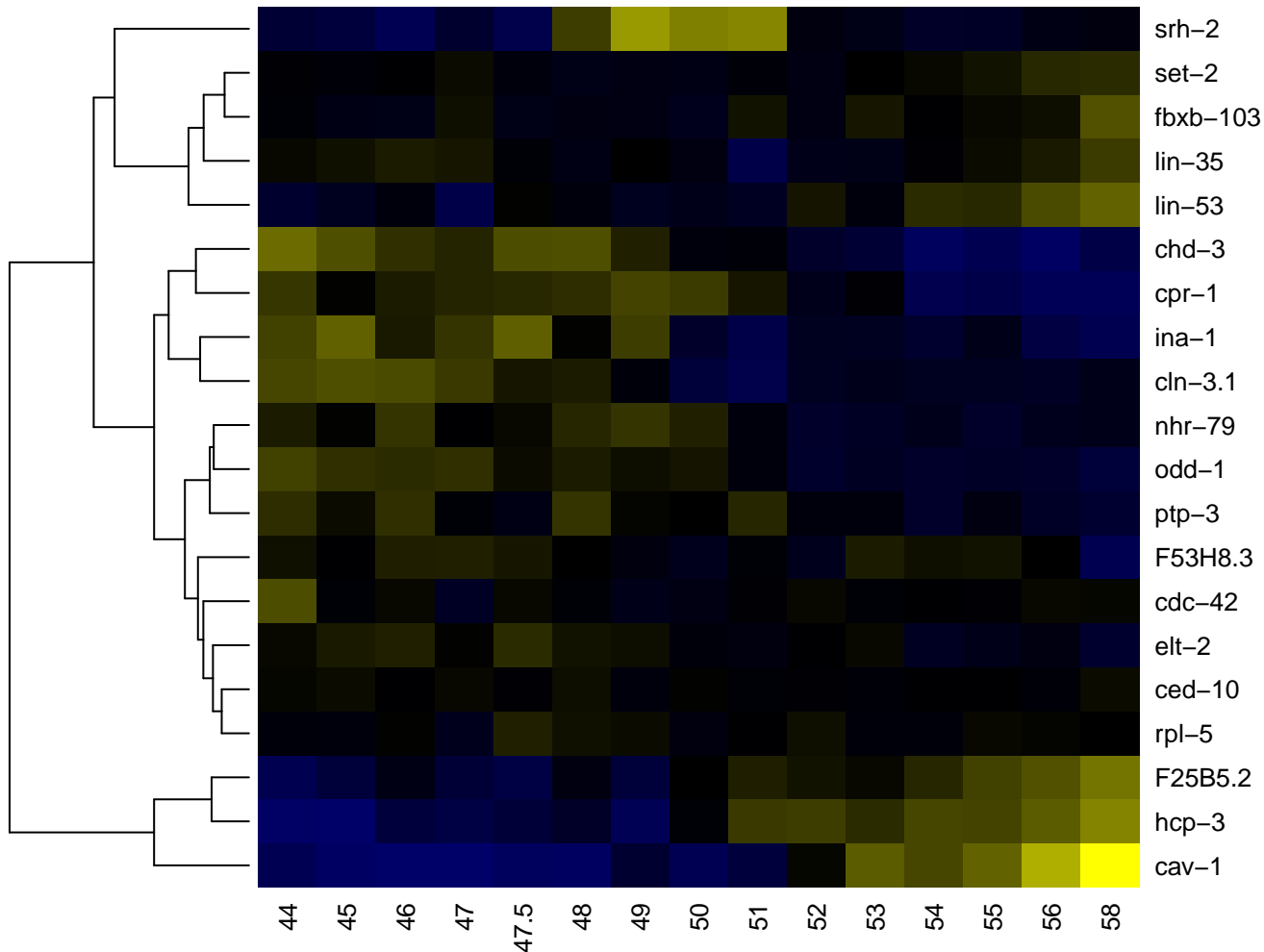
int2V



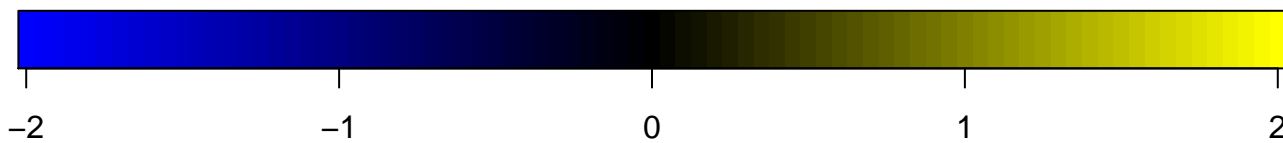
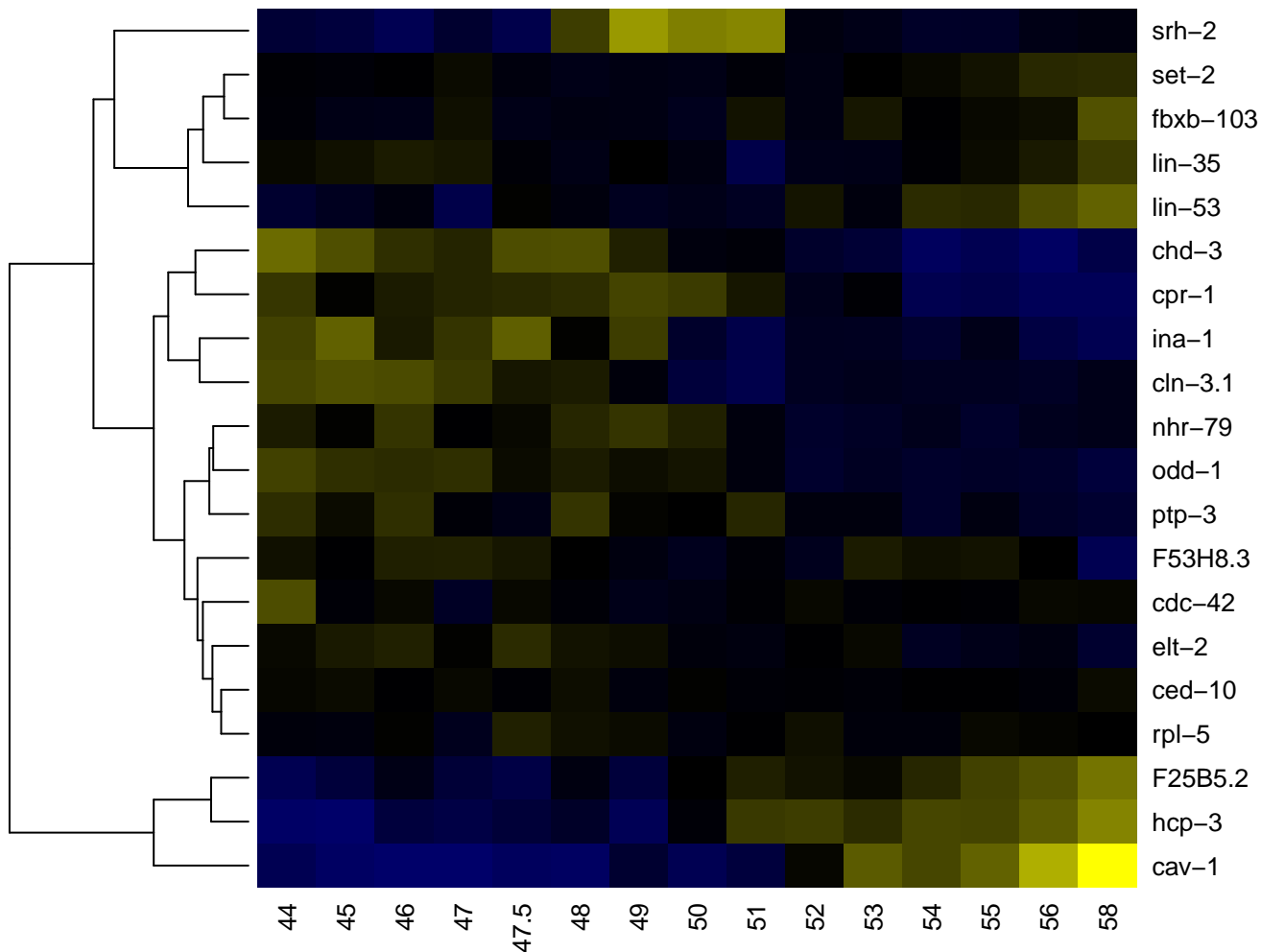
int3D



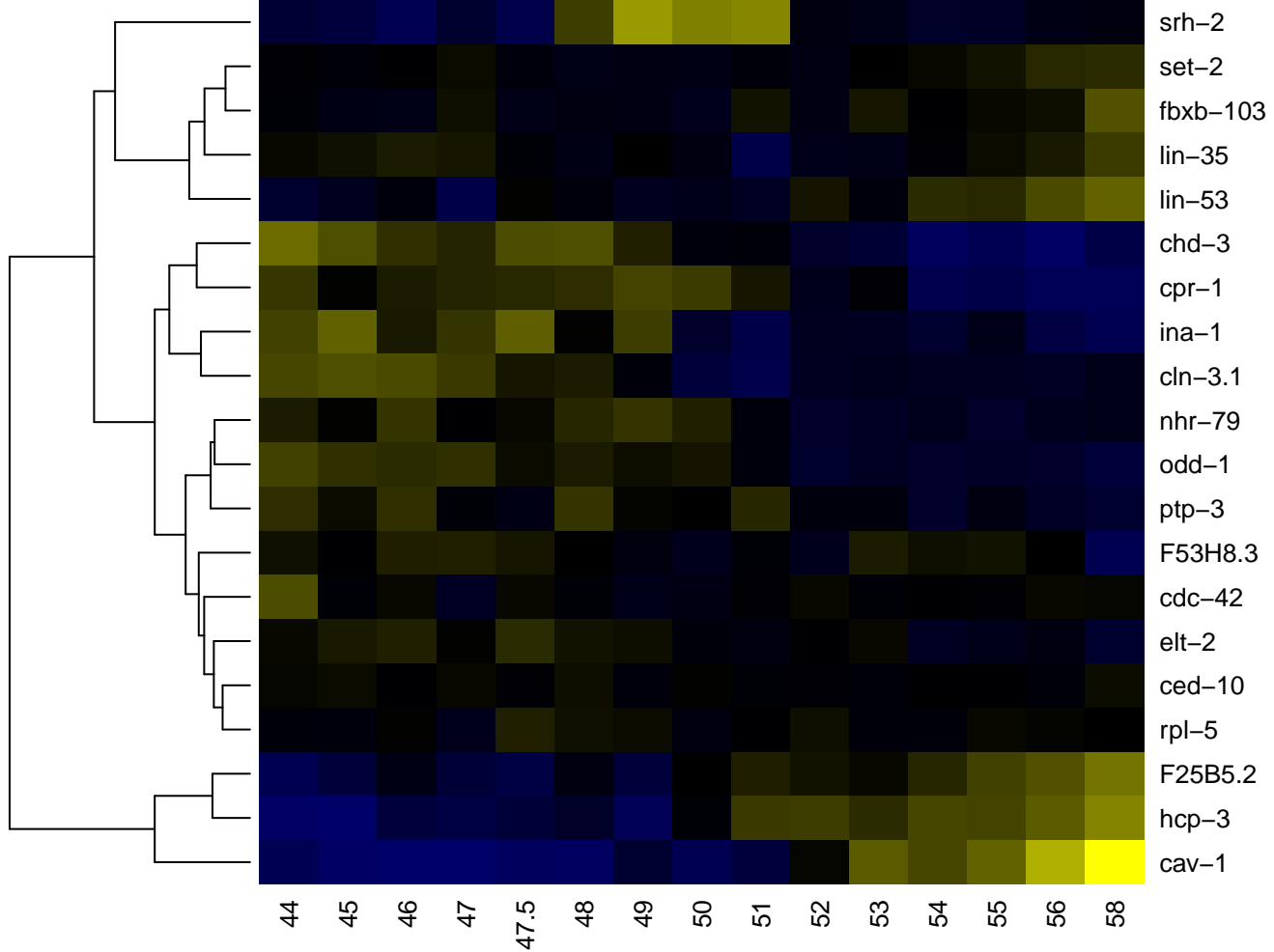
int3V



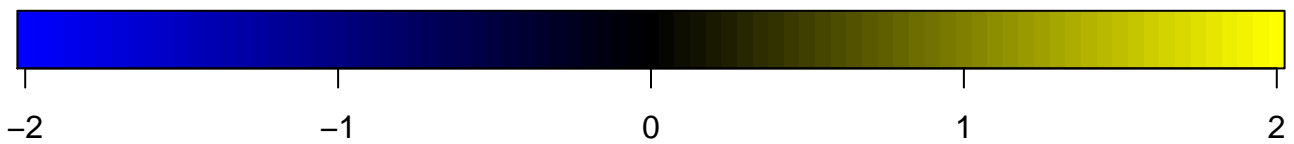
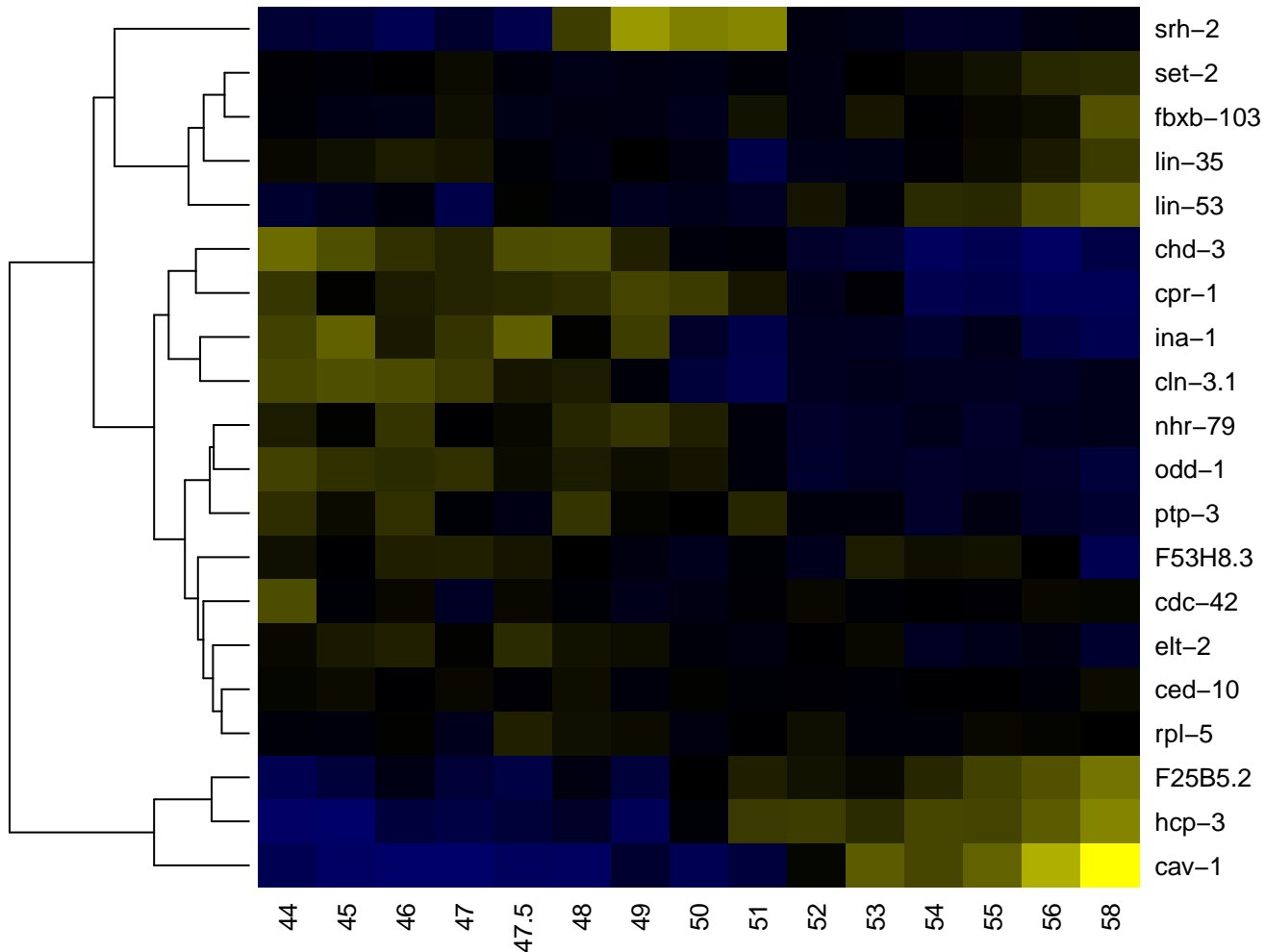
int4D



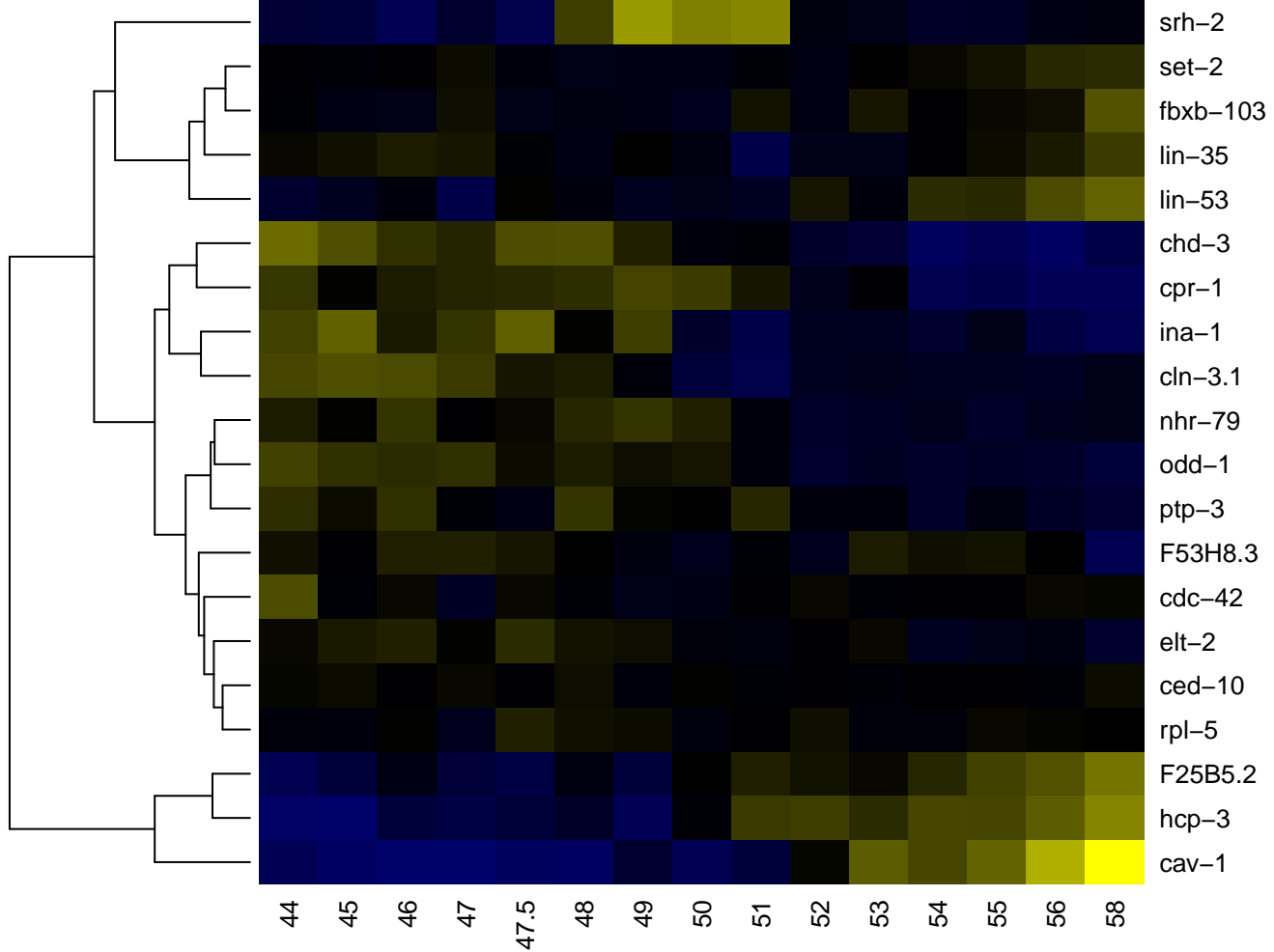
int4V



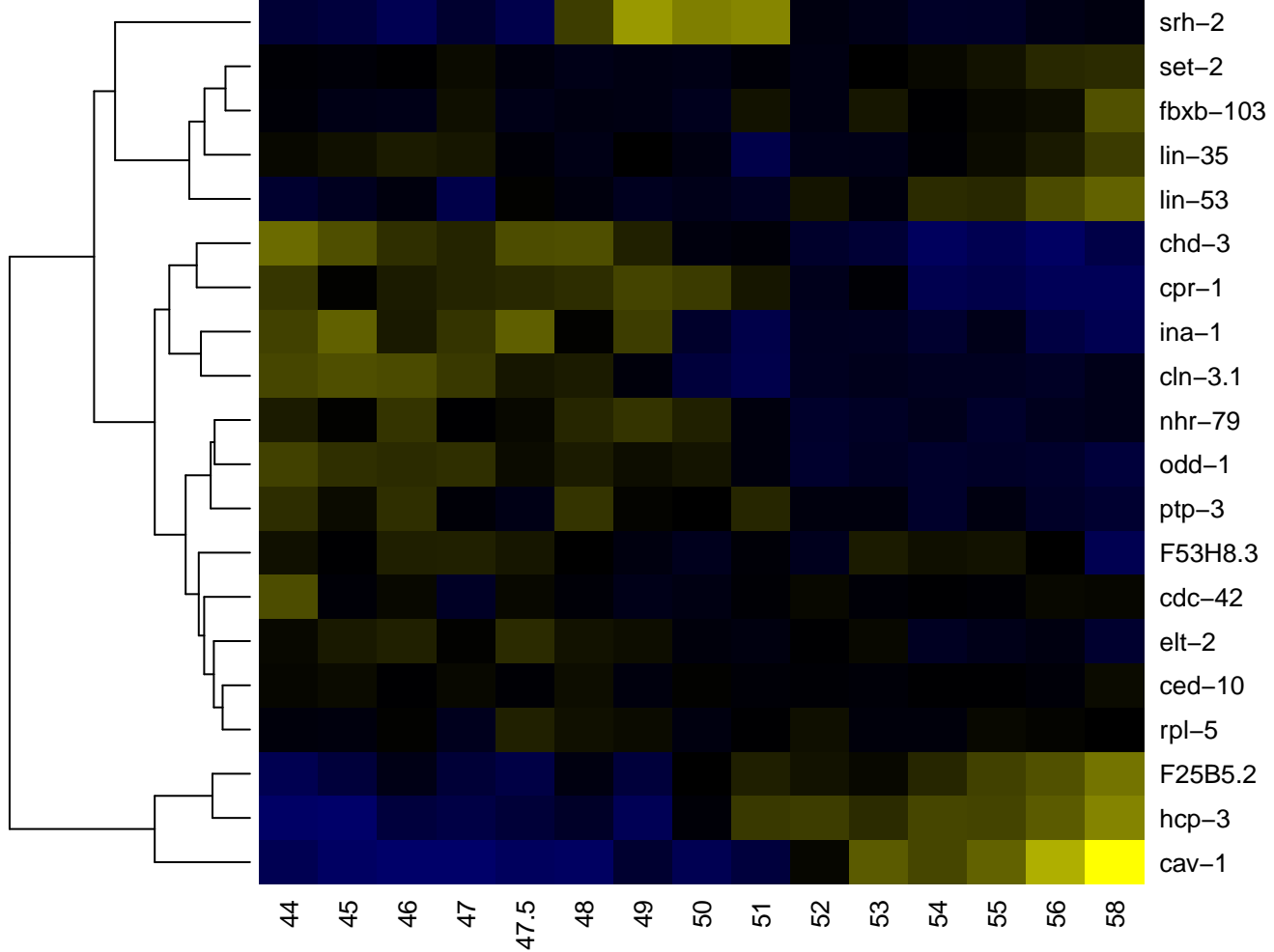
int5L



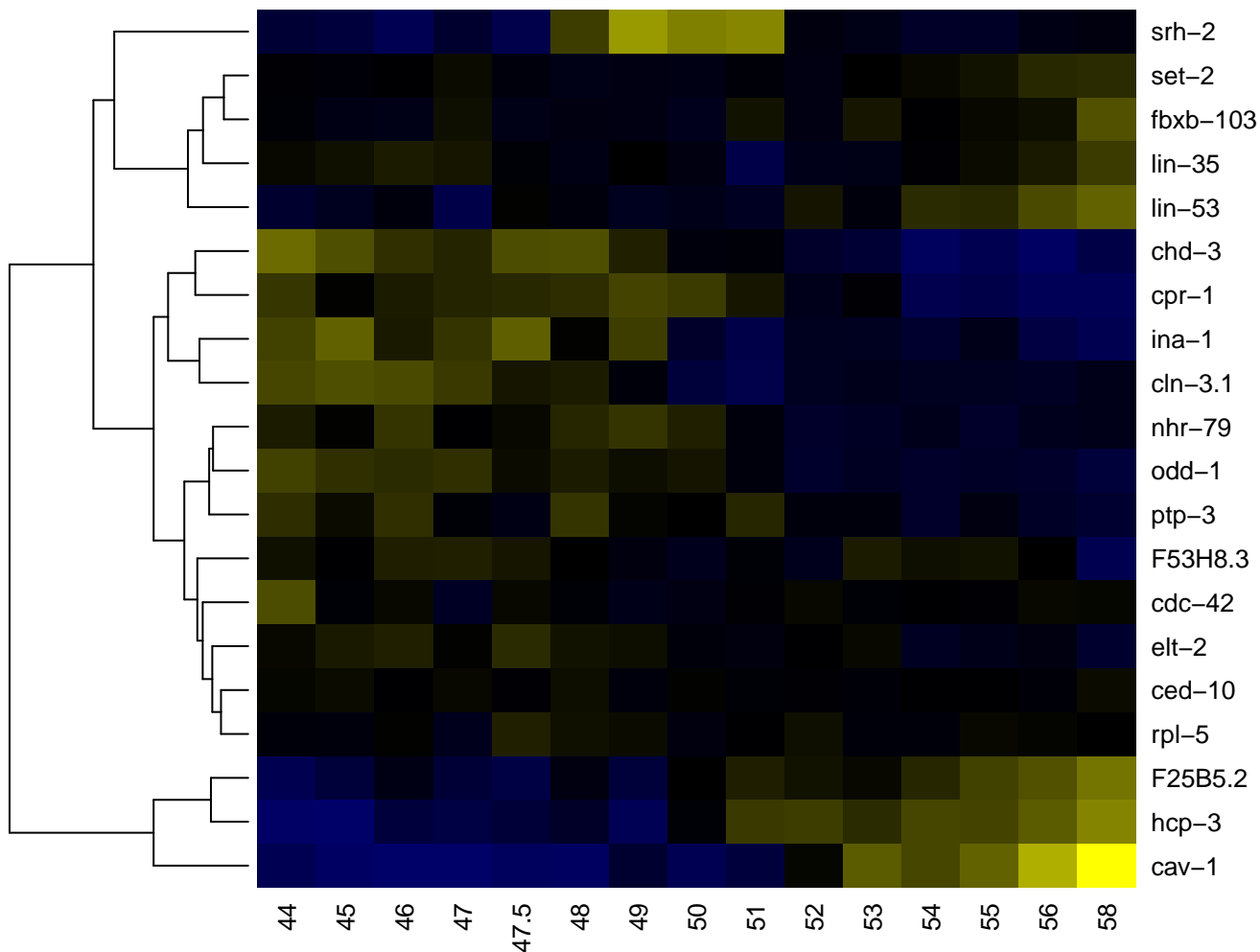
int5R



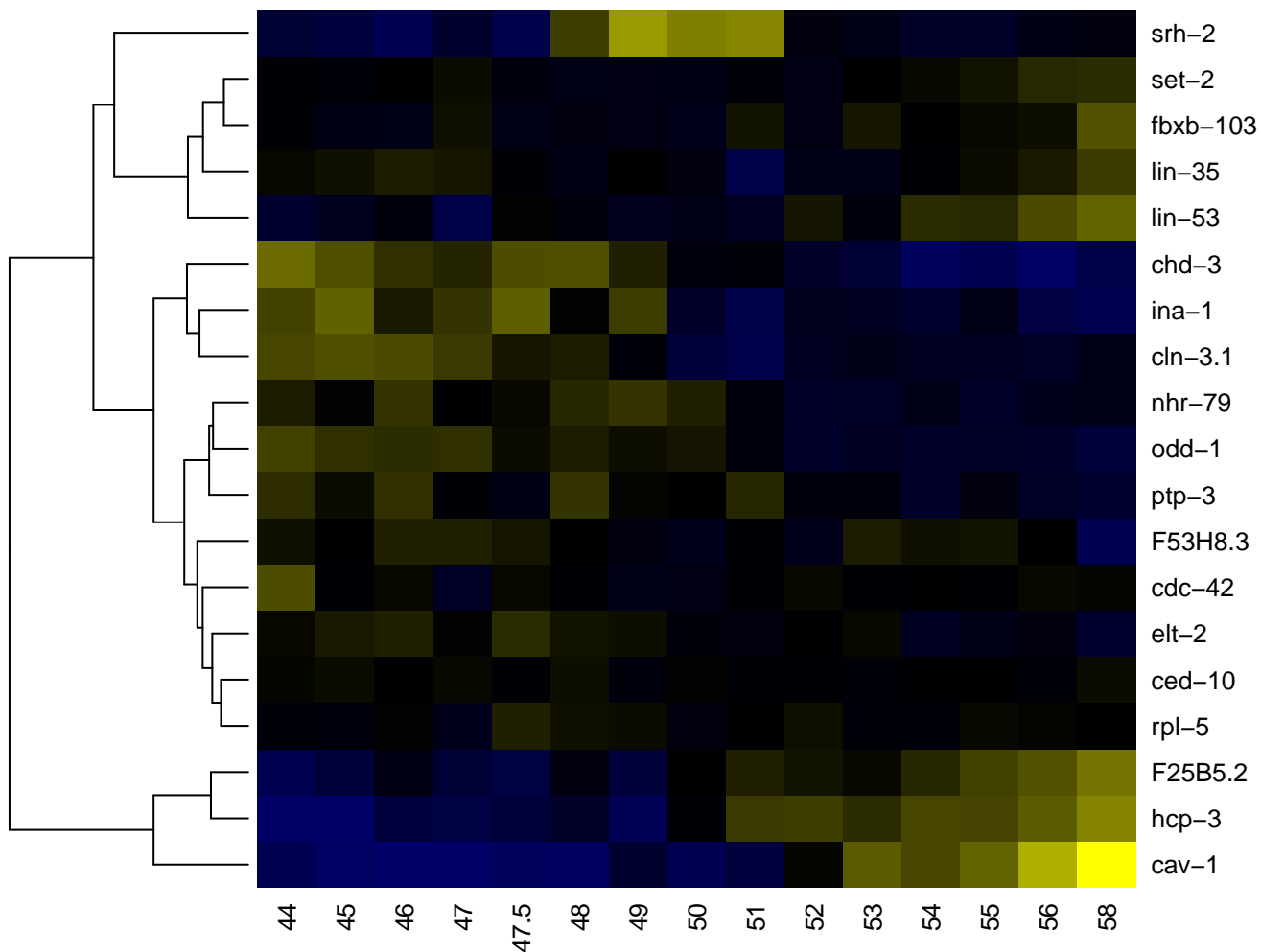
int6L



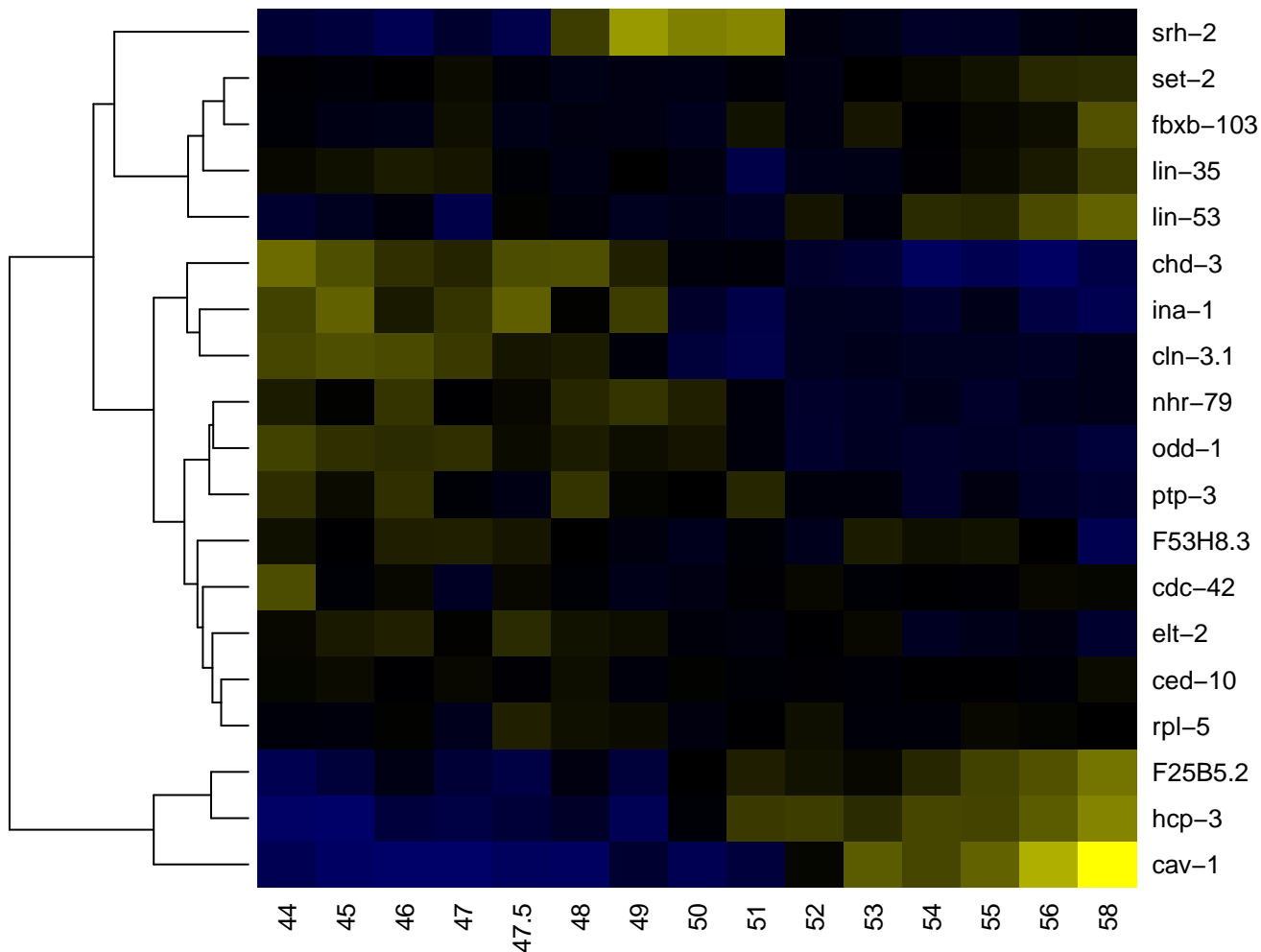
int6R



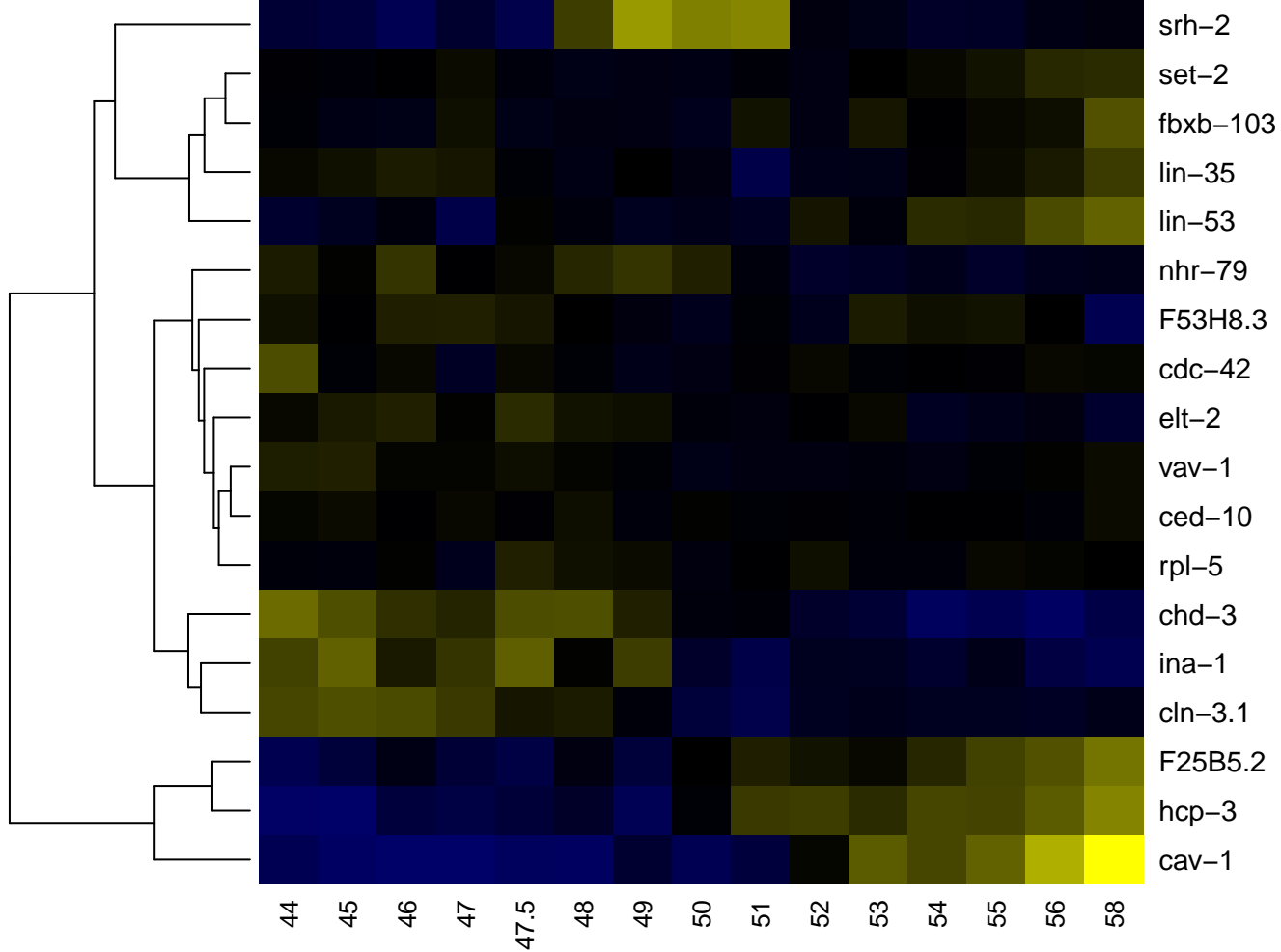
int7L



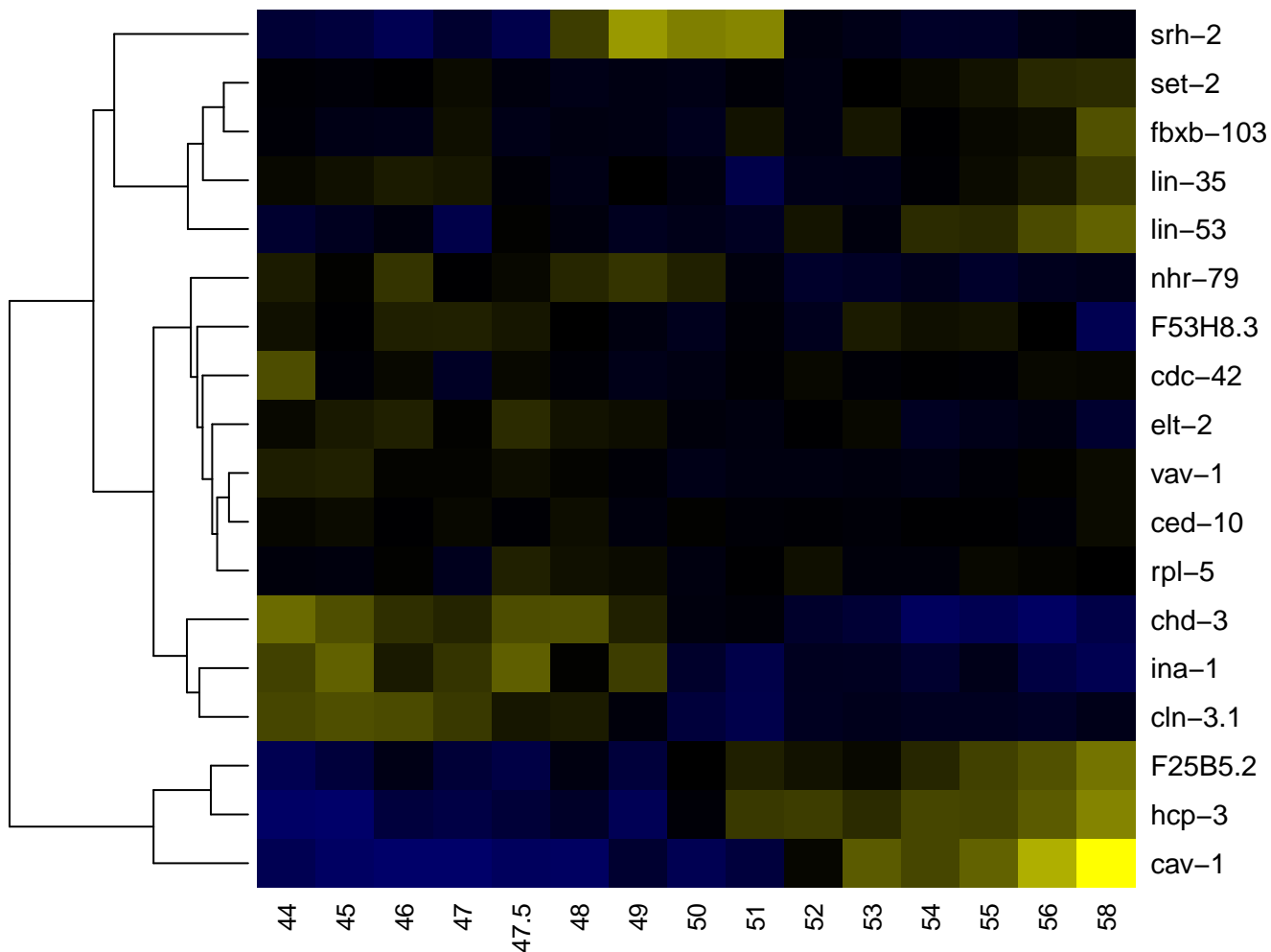
int7R



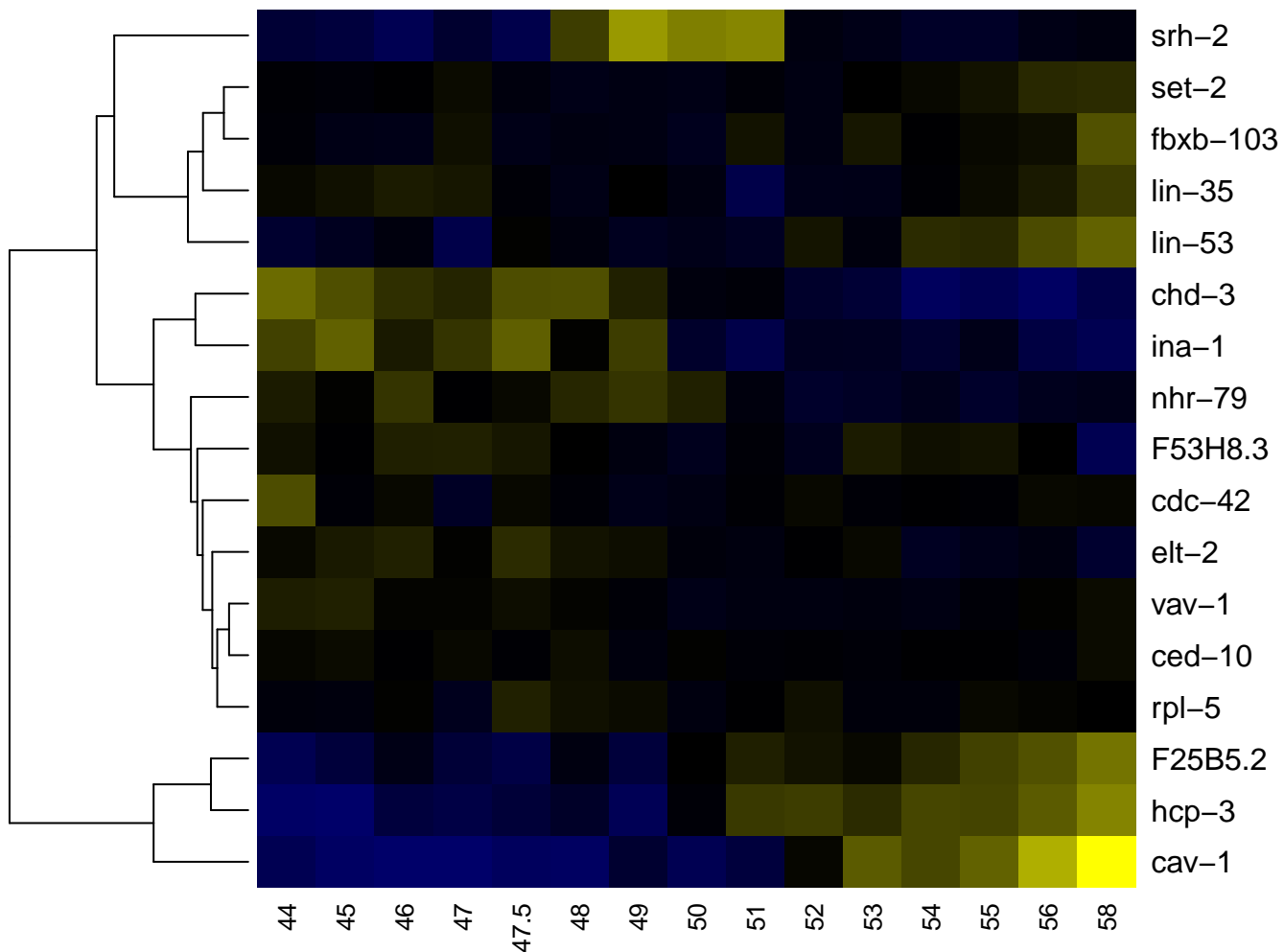
int8L



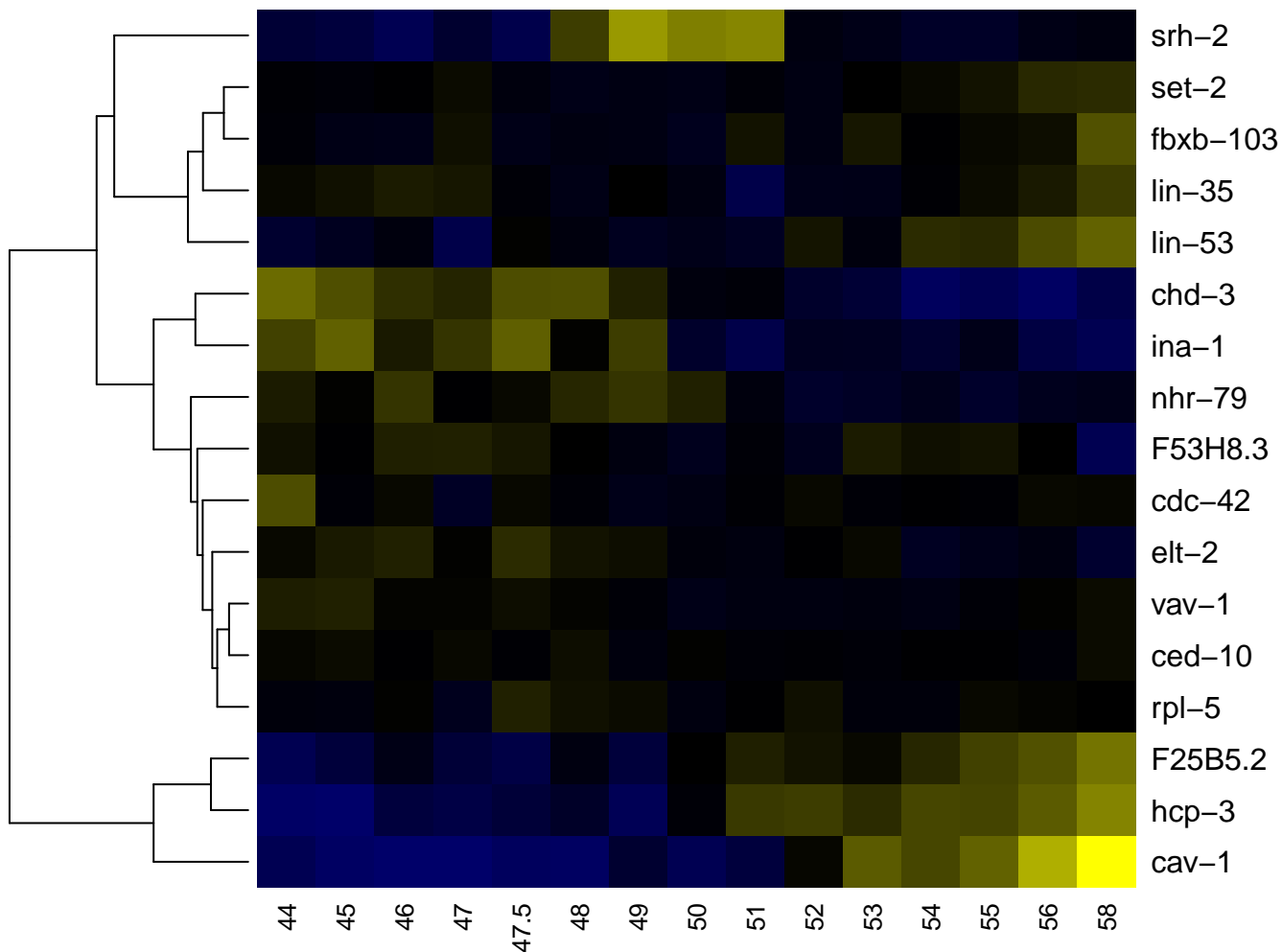
int8R



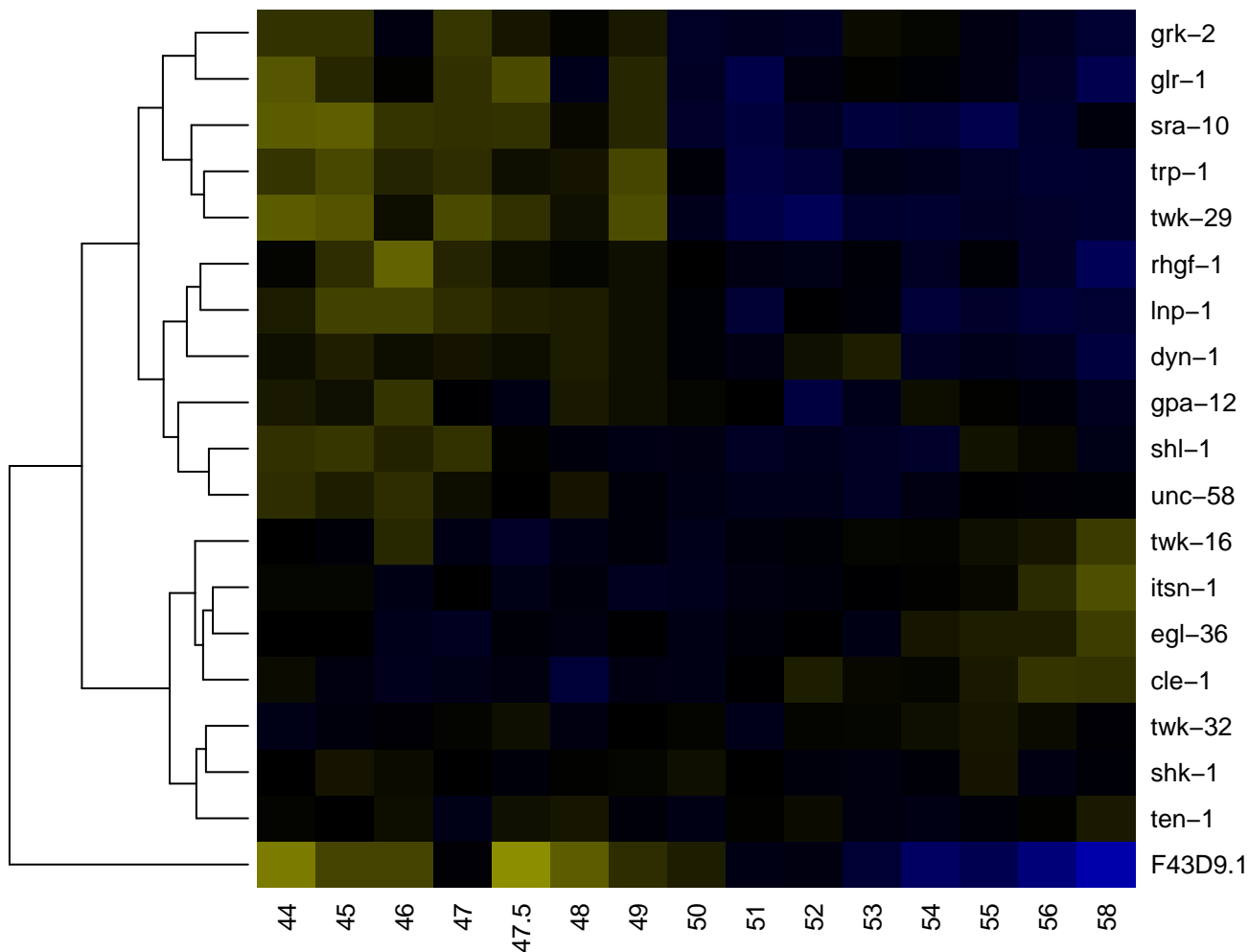
int9L



int9R



interneuron



-2

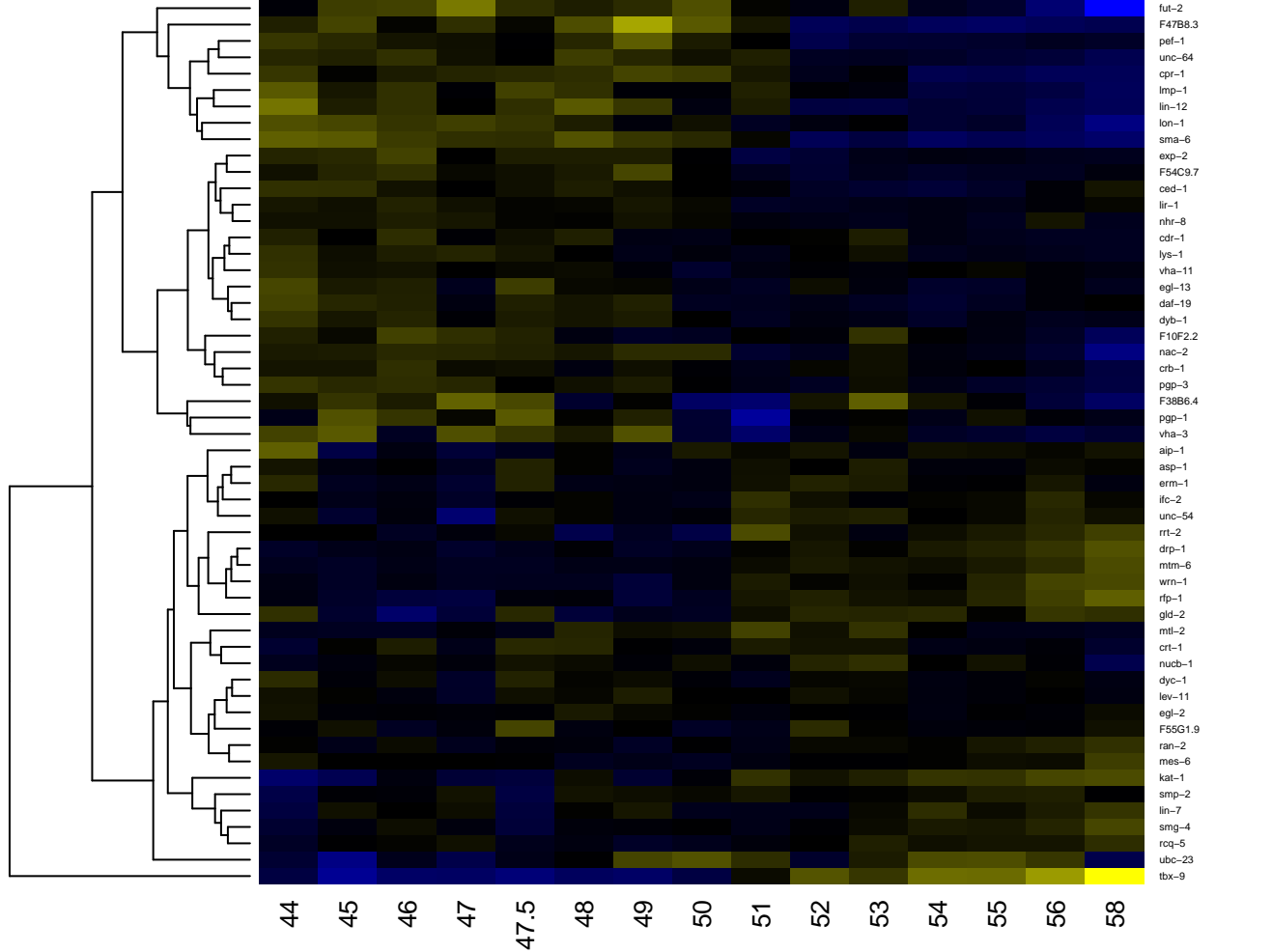
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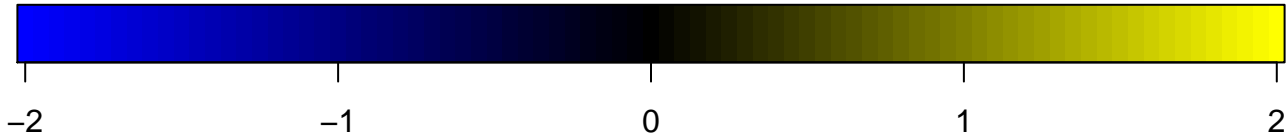
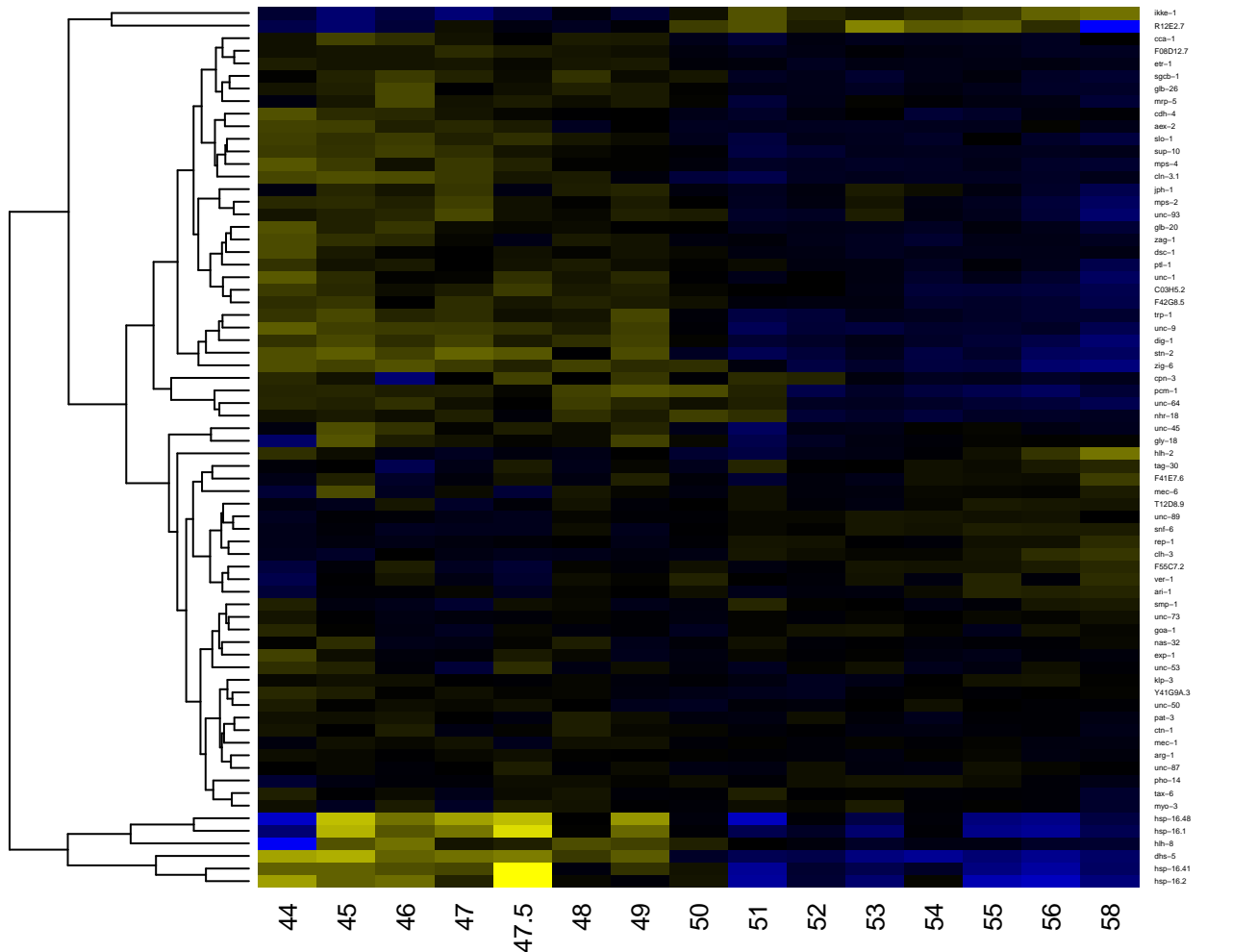
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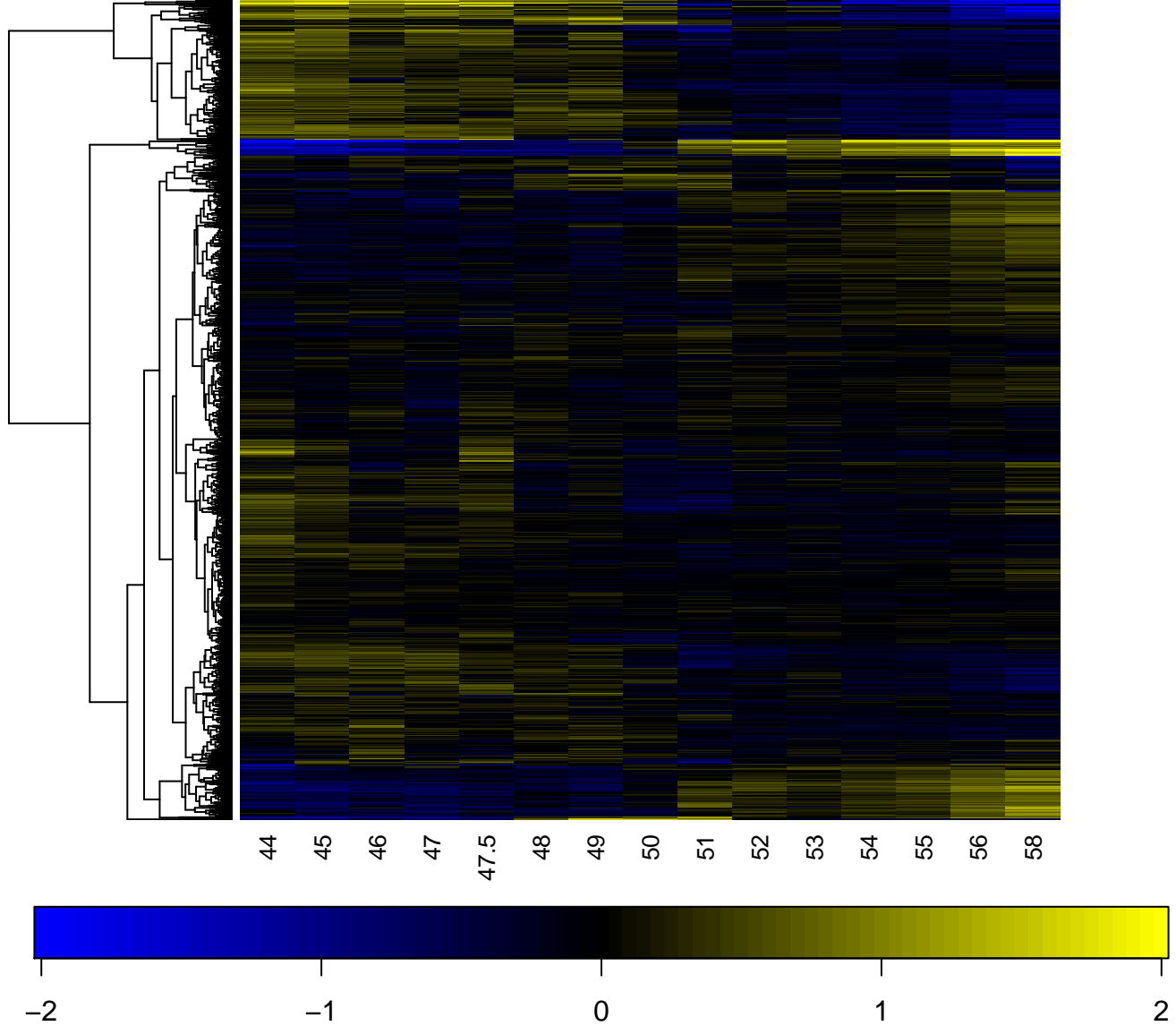
intestinal cell



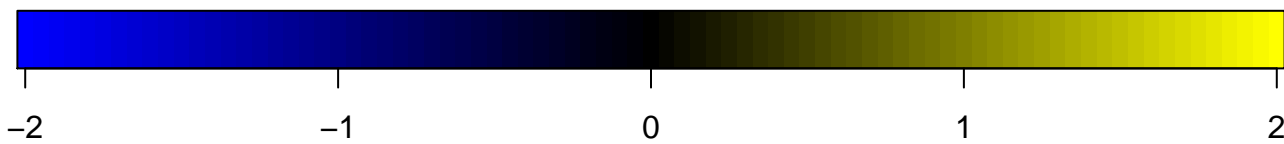
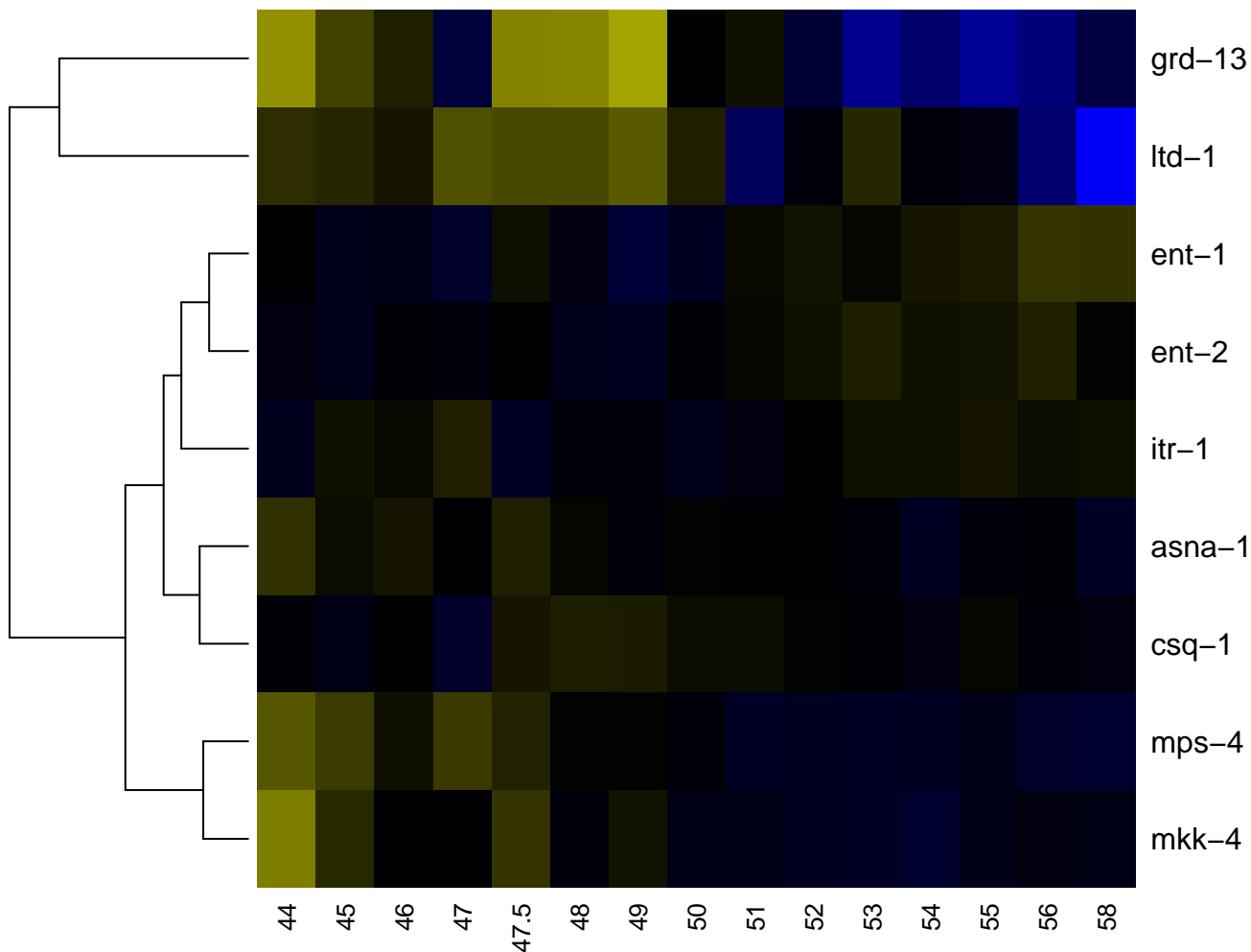
intestinal muscle



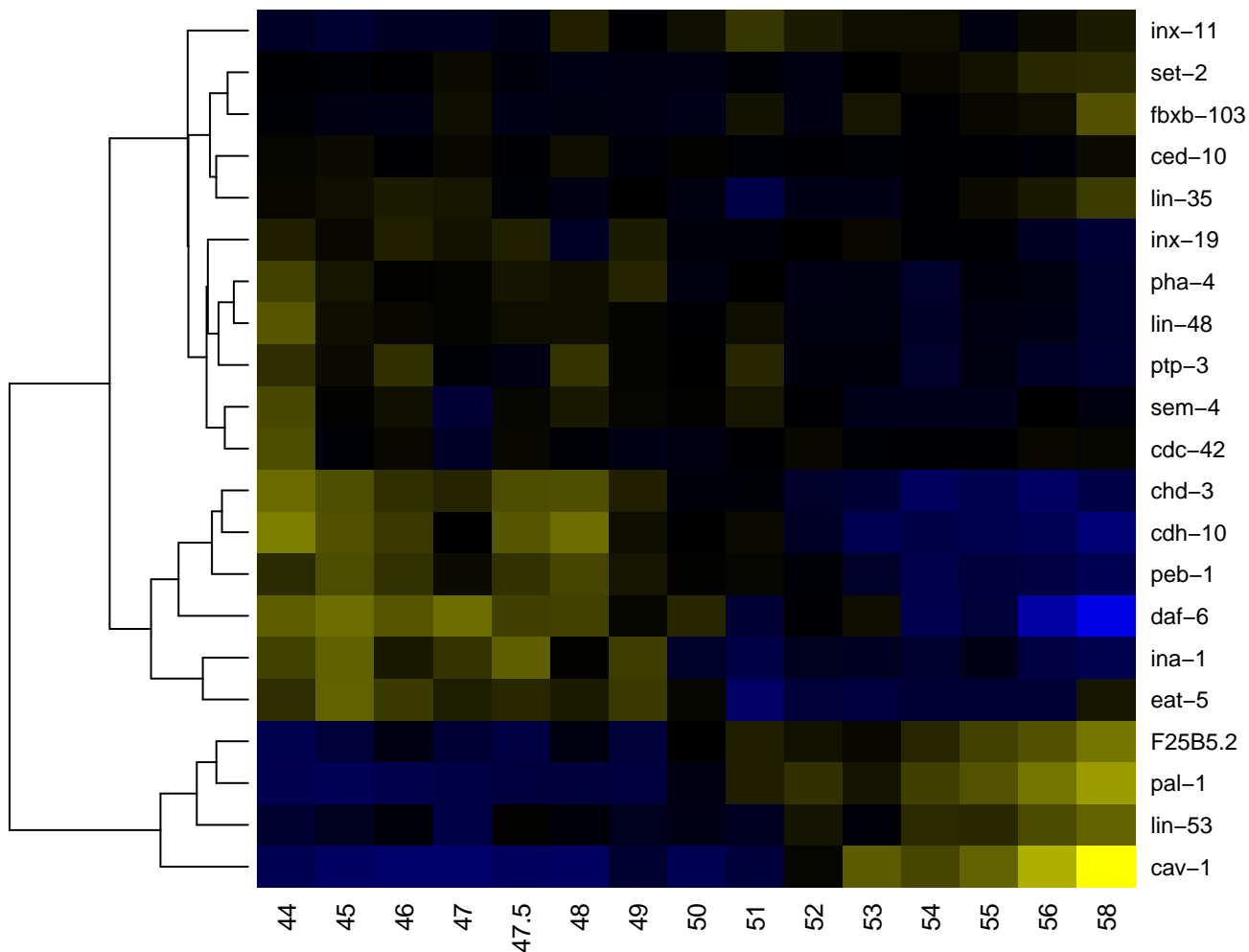
intestine



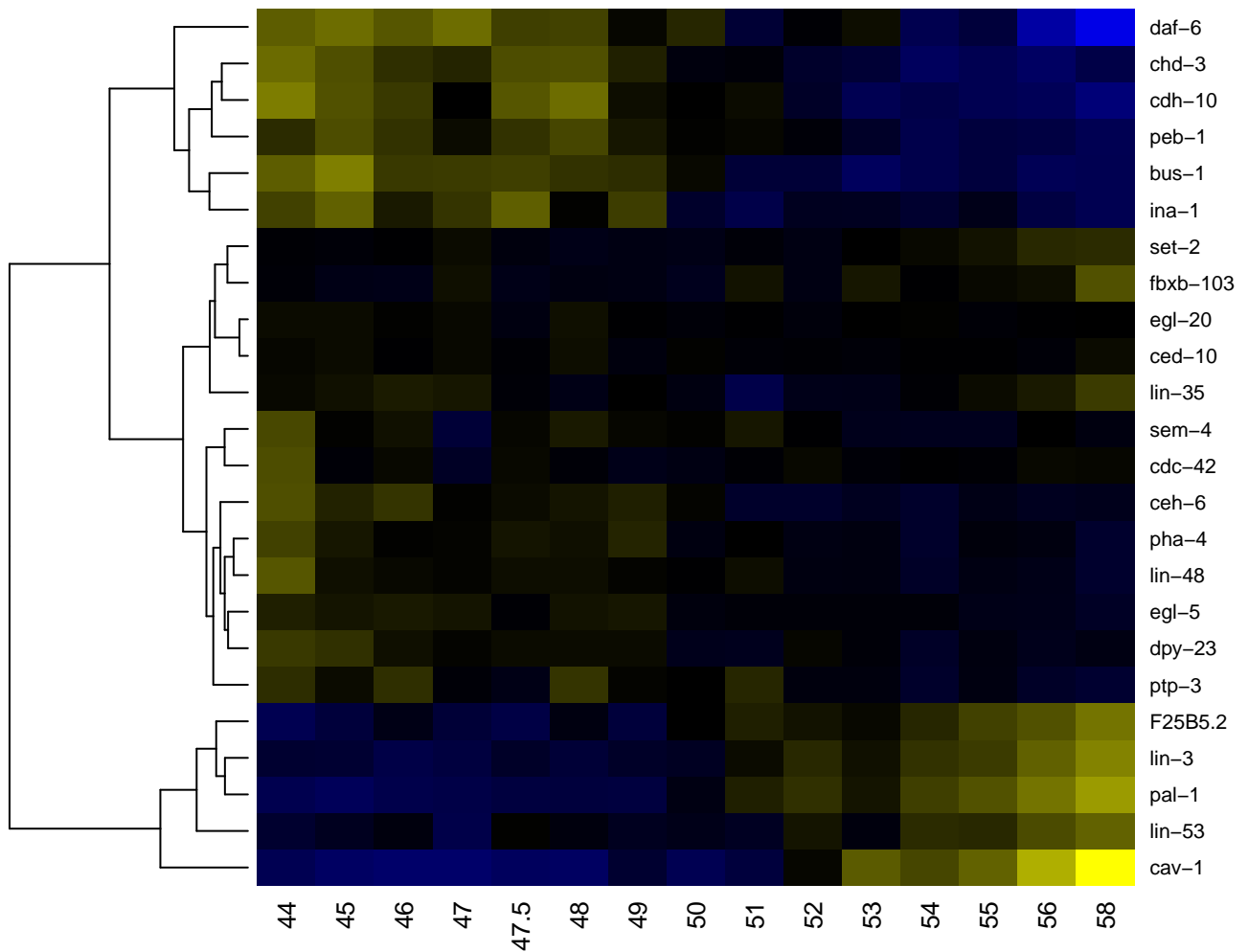
isthmus



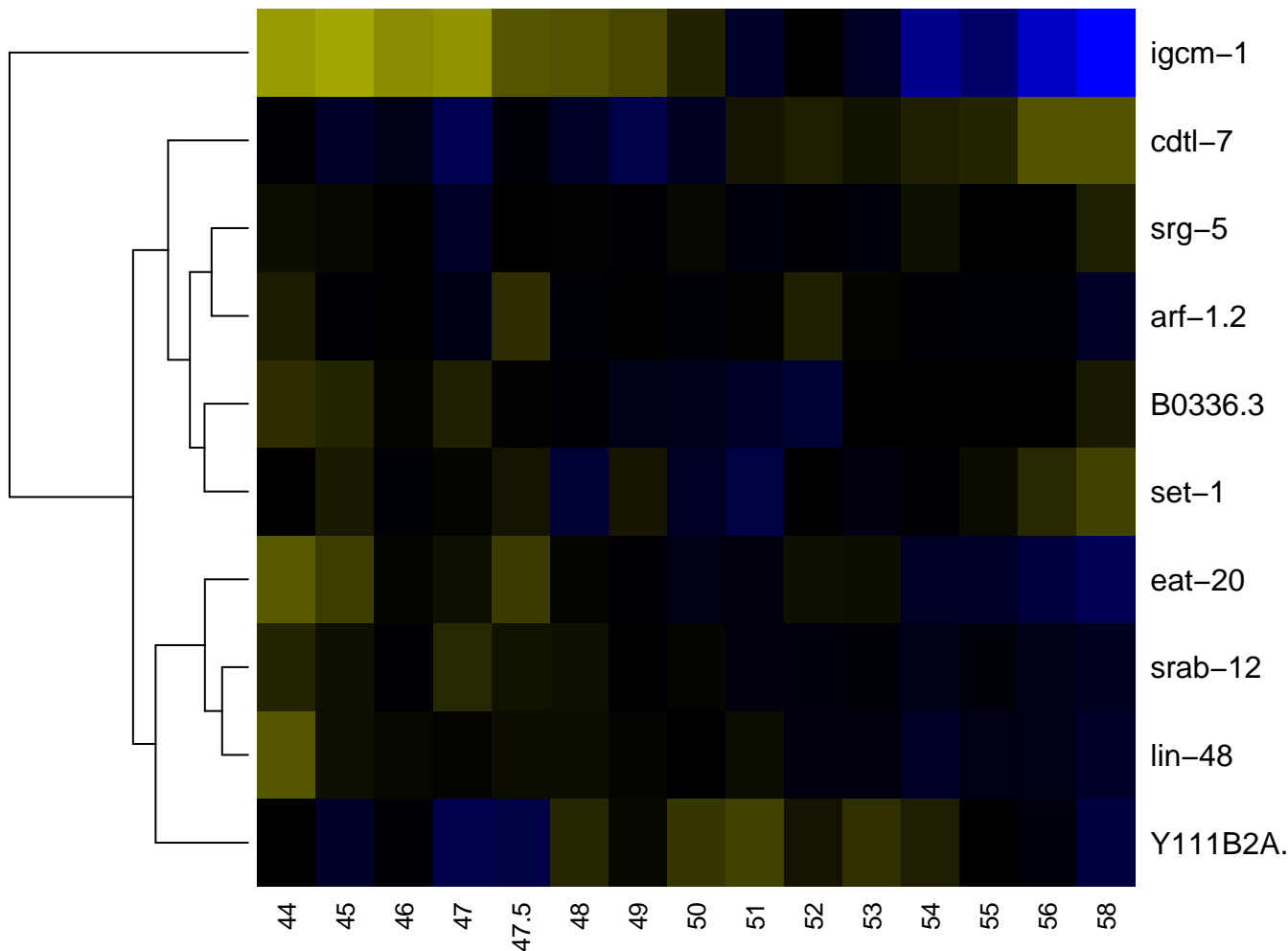
K' cell



K cell



labial sensillum



-2

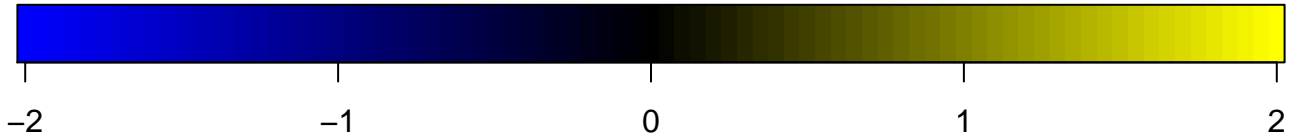
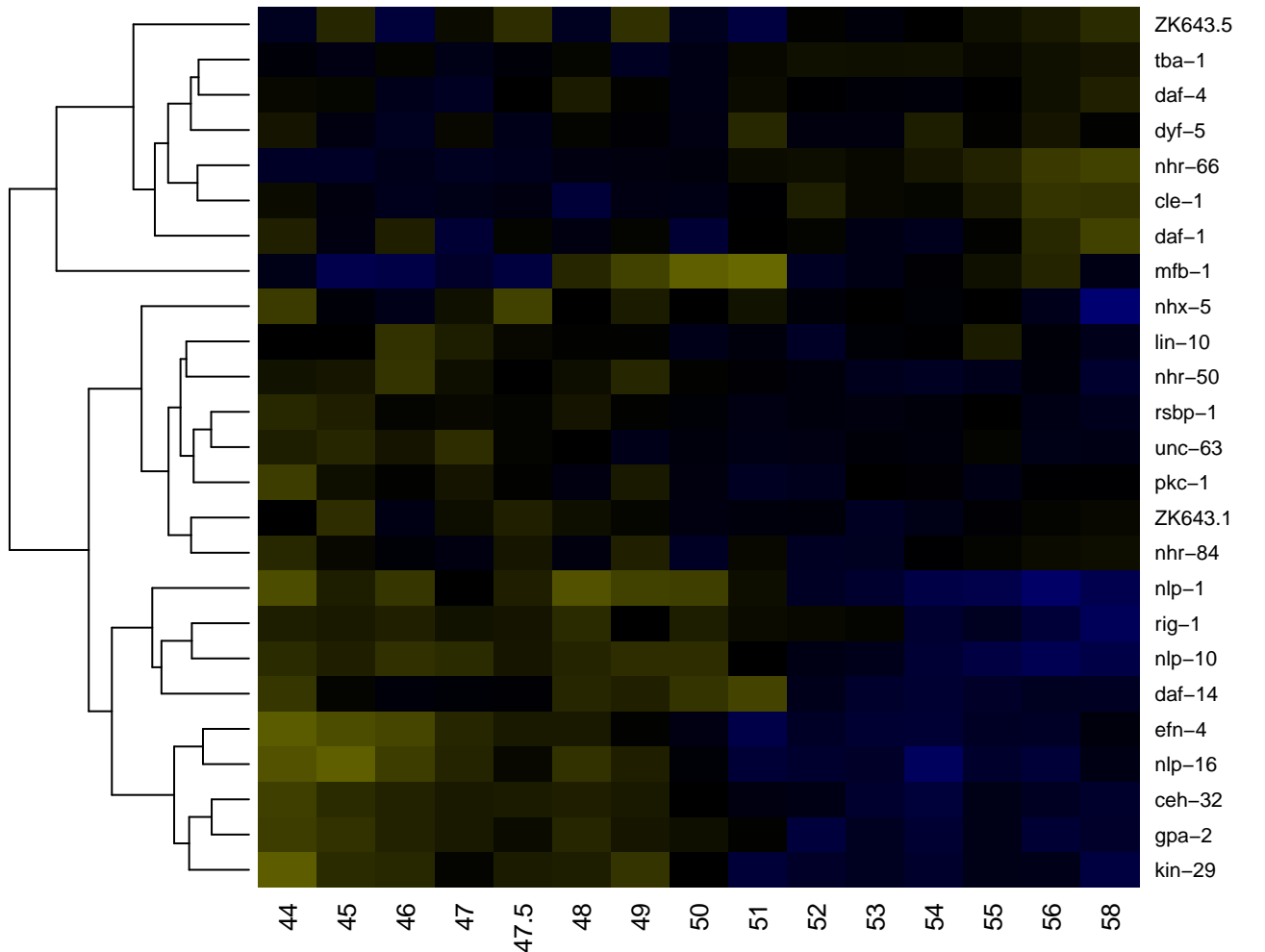
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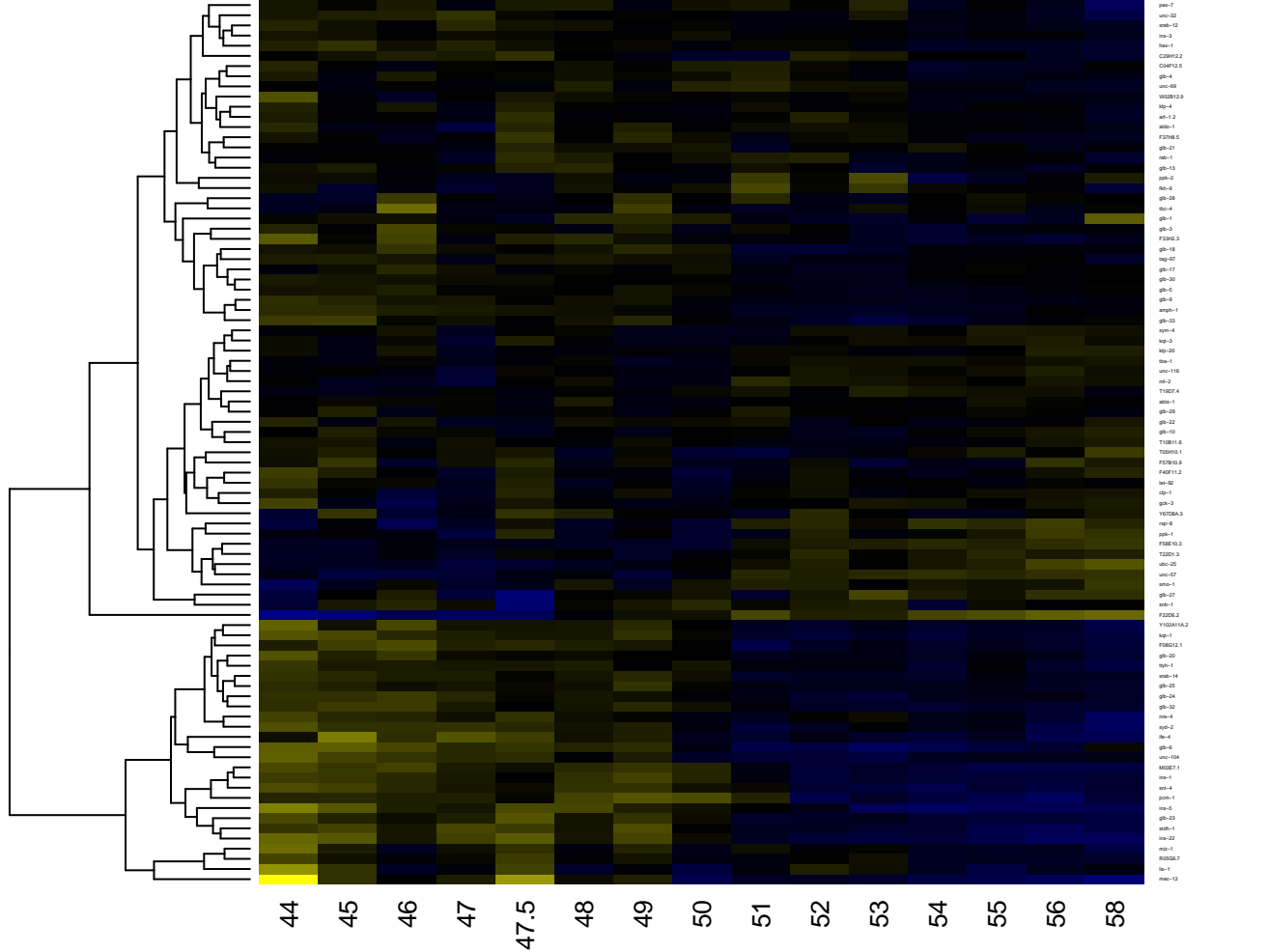
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2

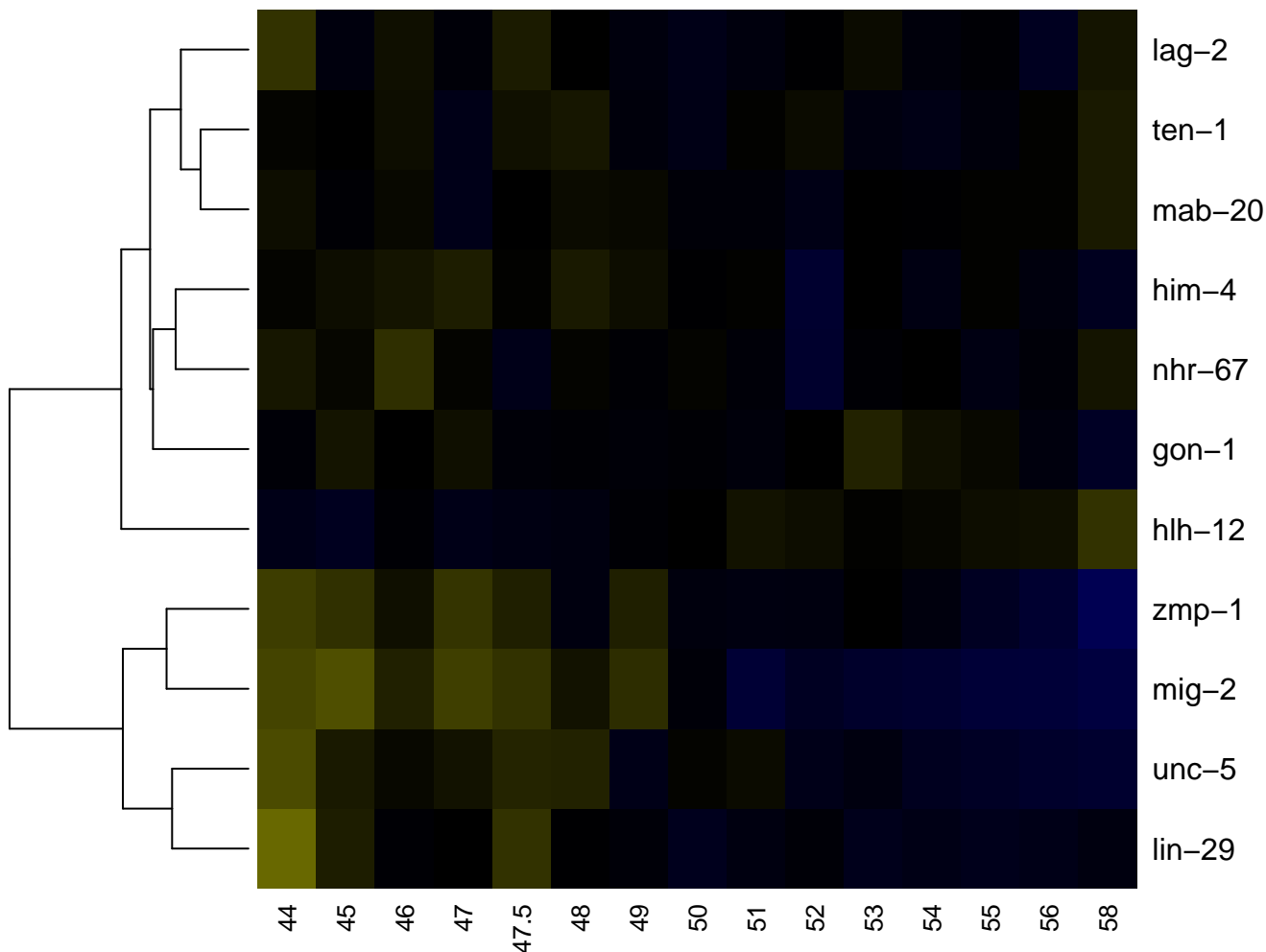
lateral ganglion



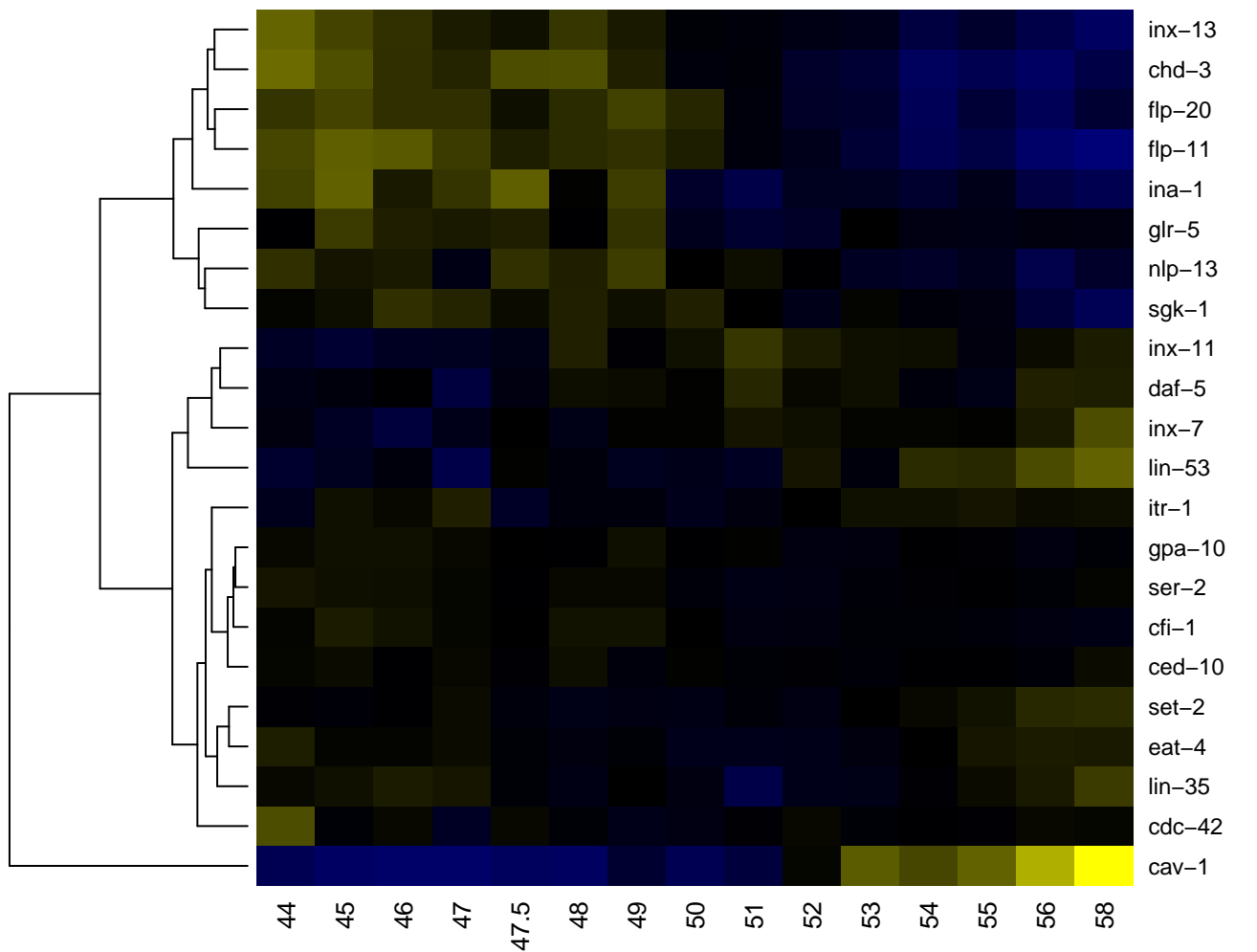
lateral nerve cord



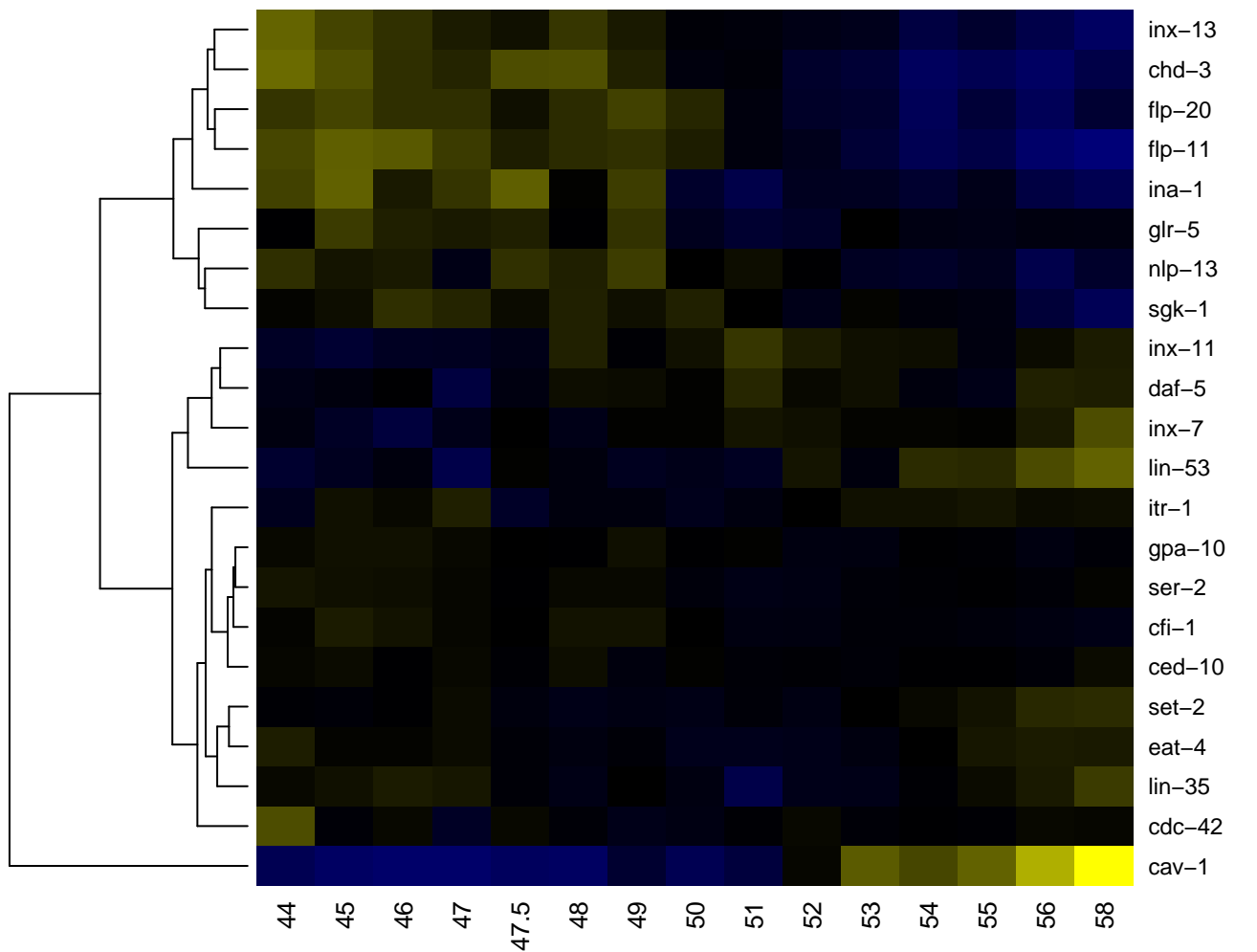
linker cell



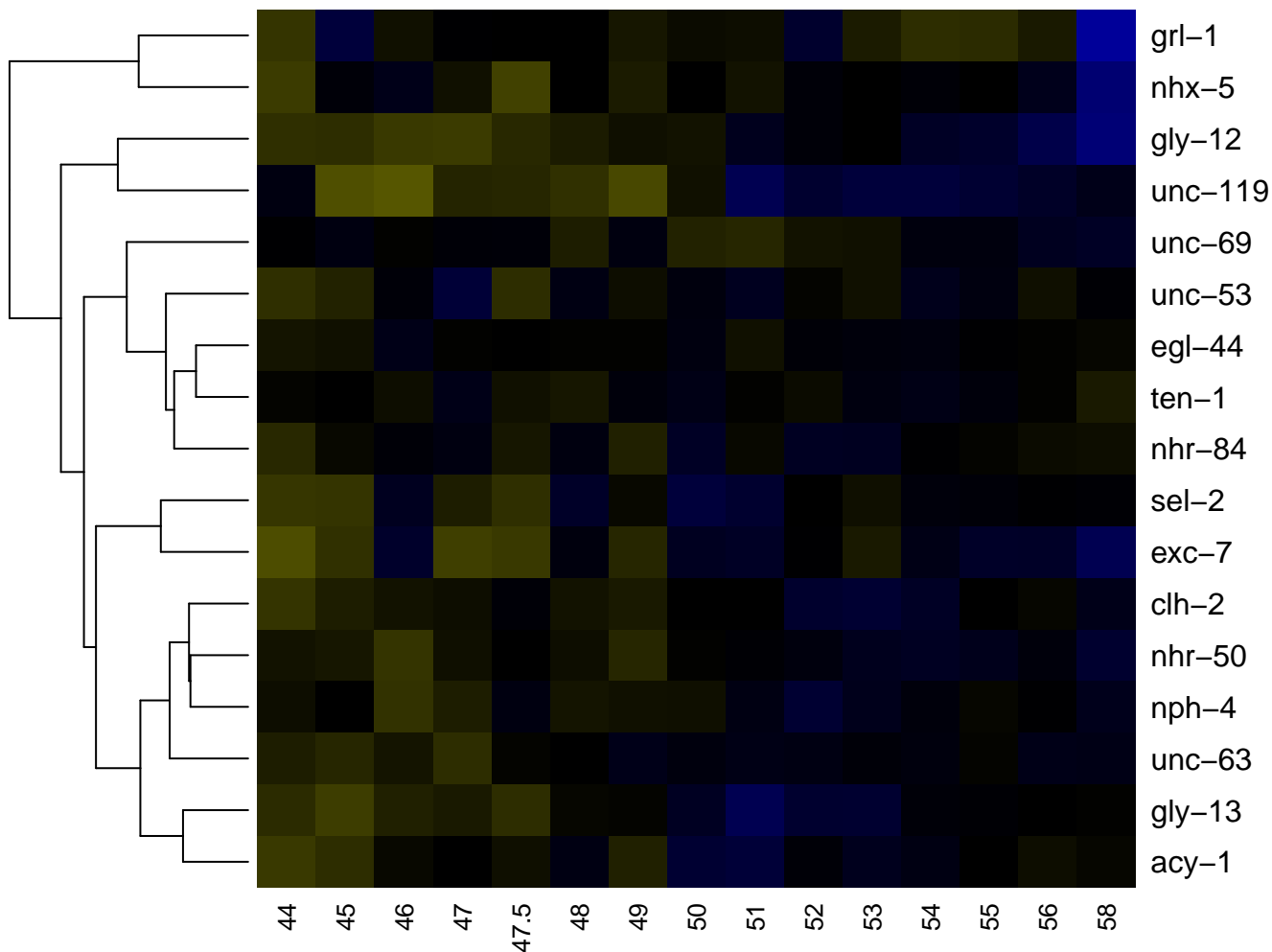
LUAL



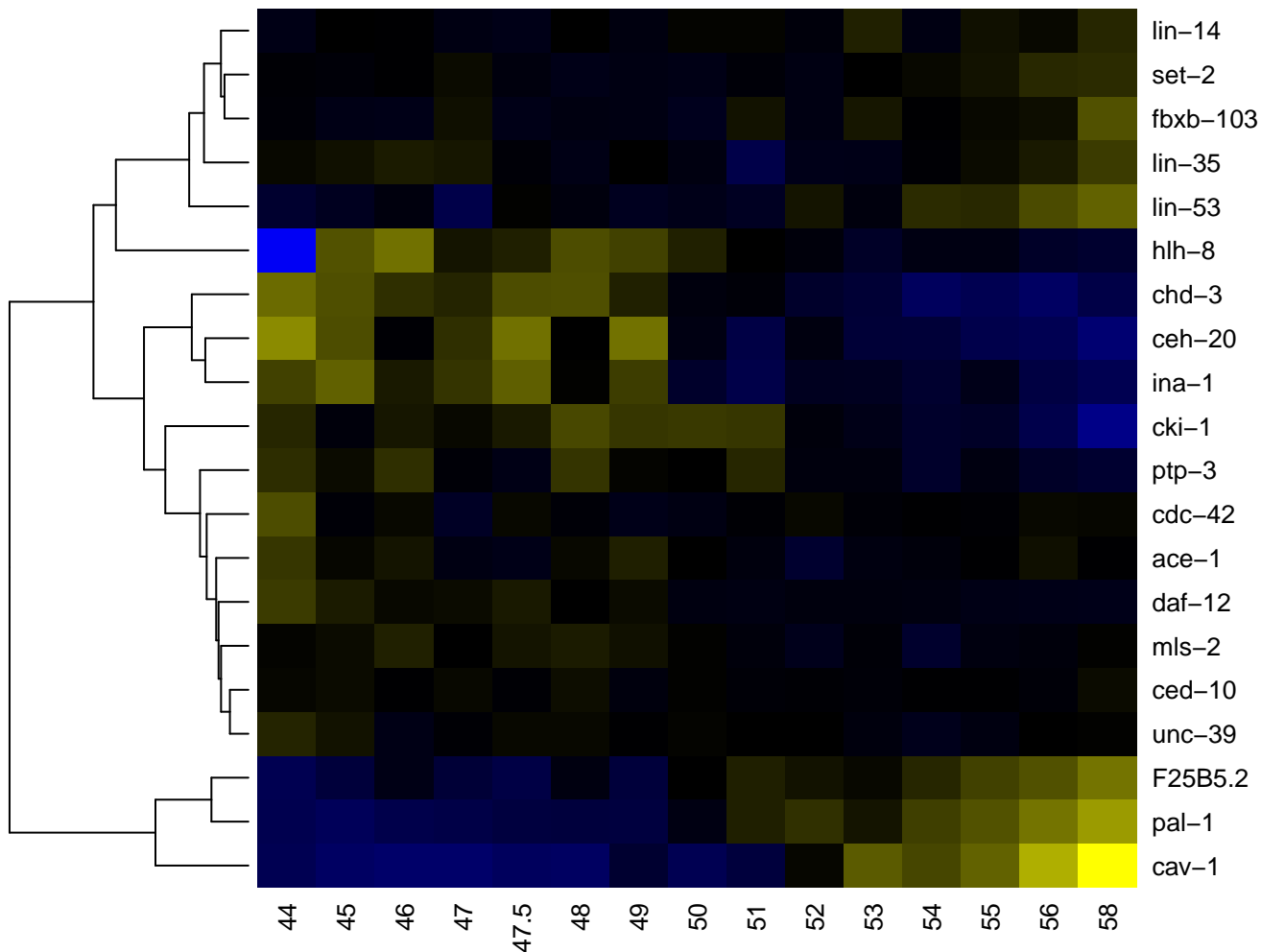
LUAR



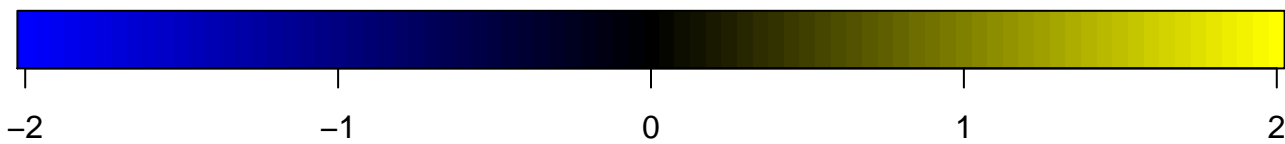
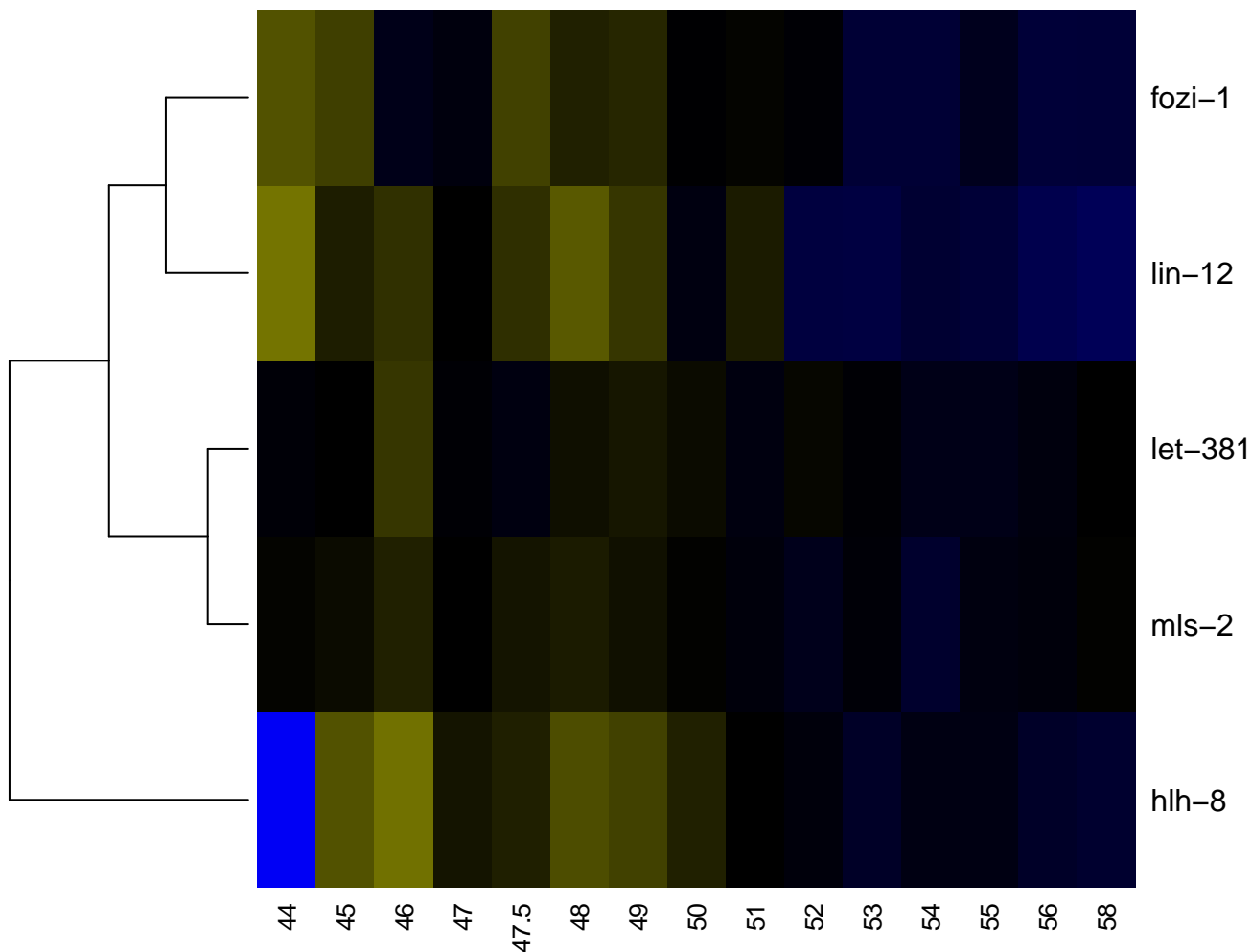
lumbar ganglion



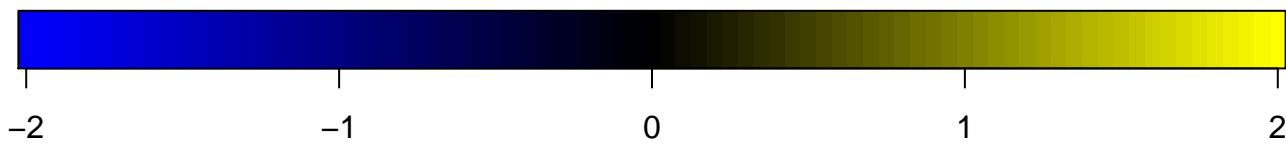
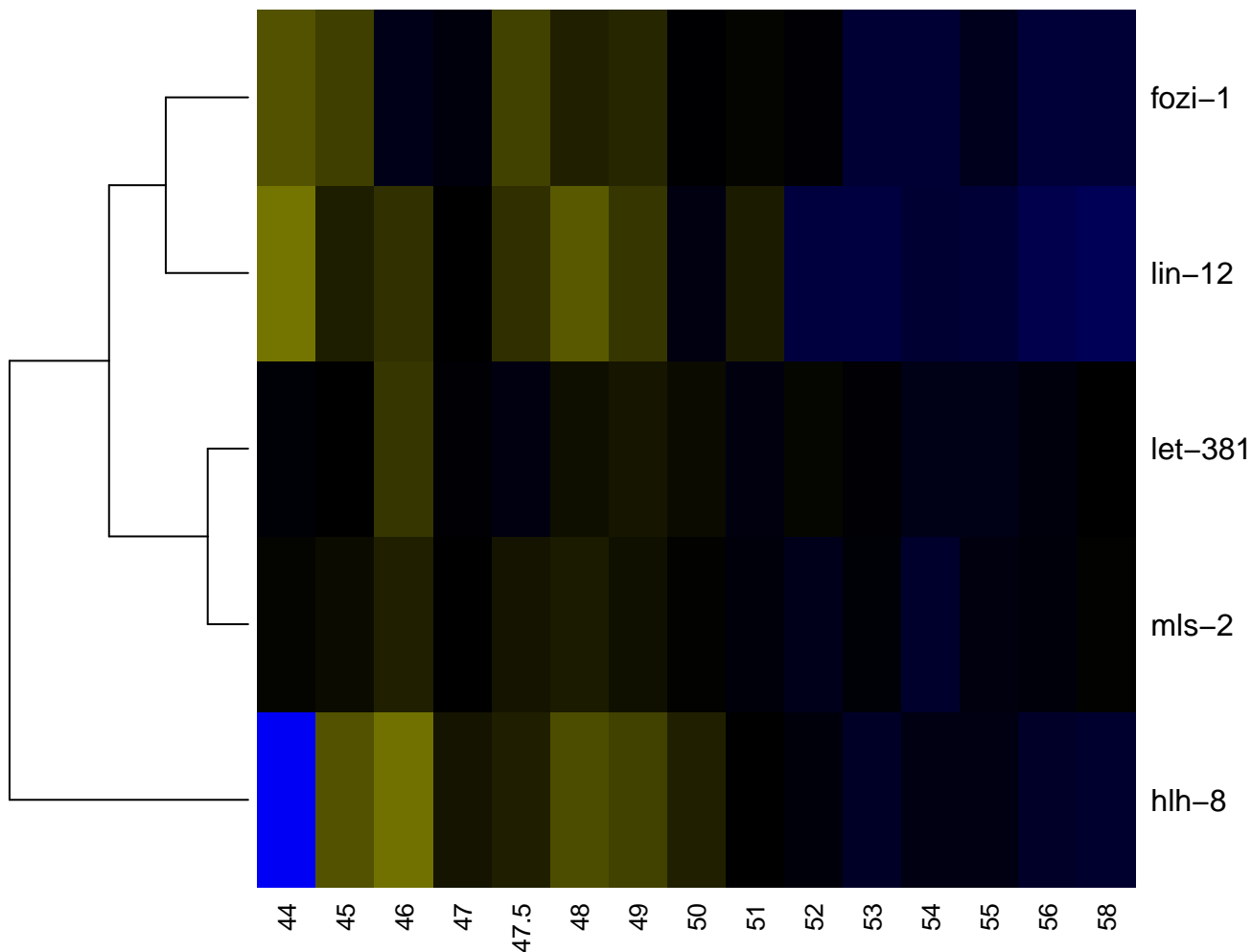
M cell



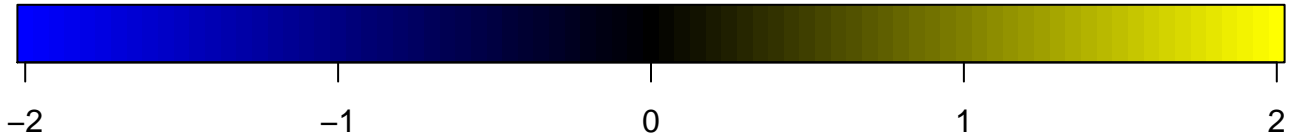
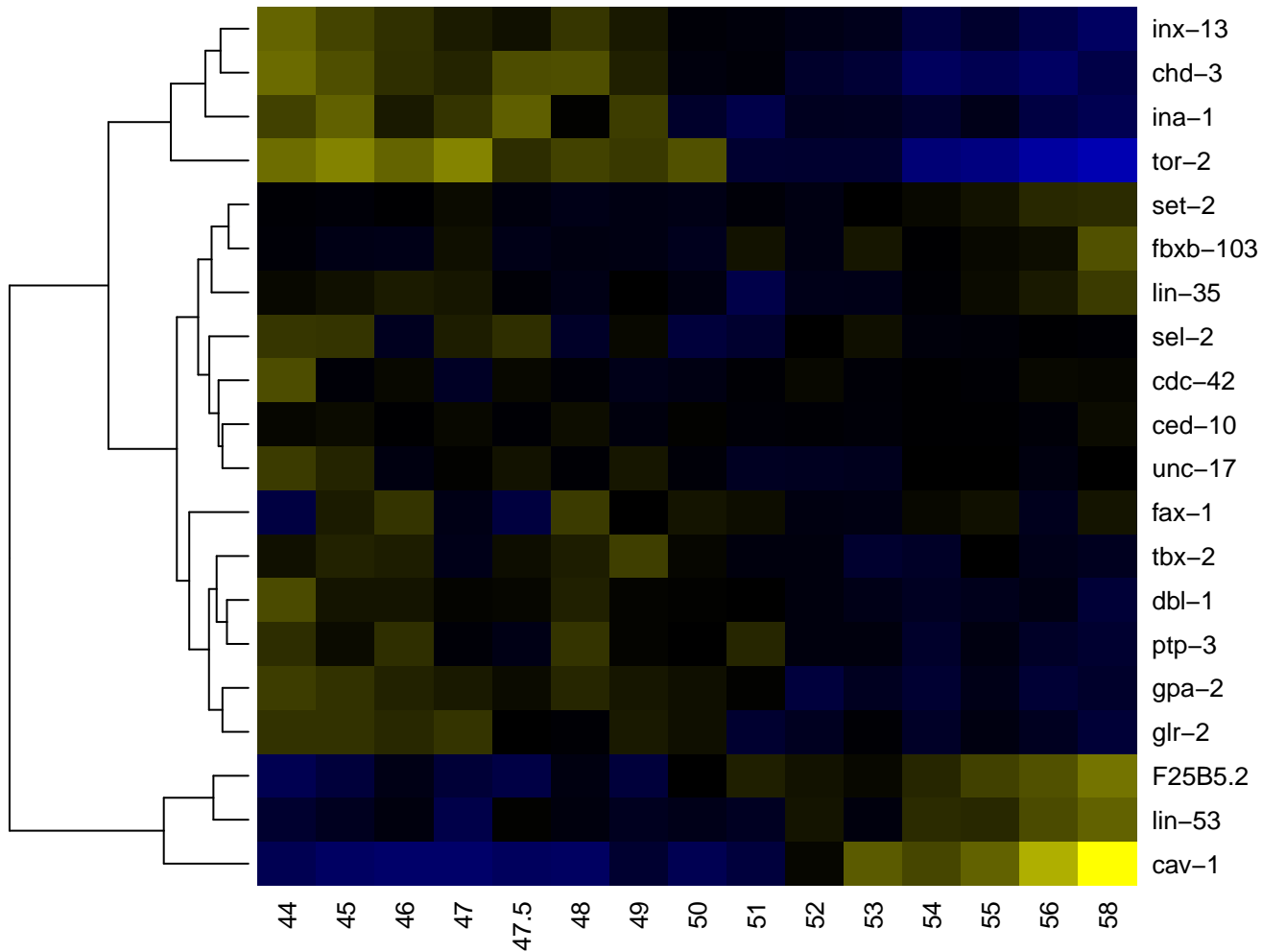
M.dlp



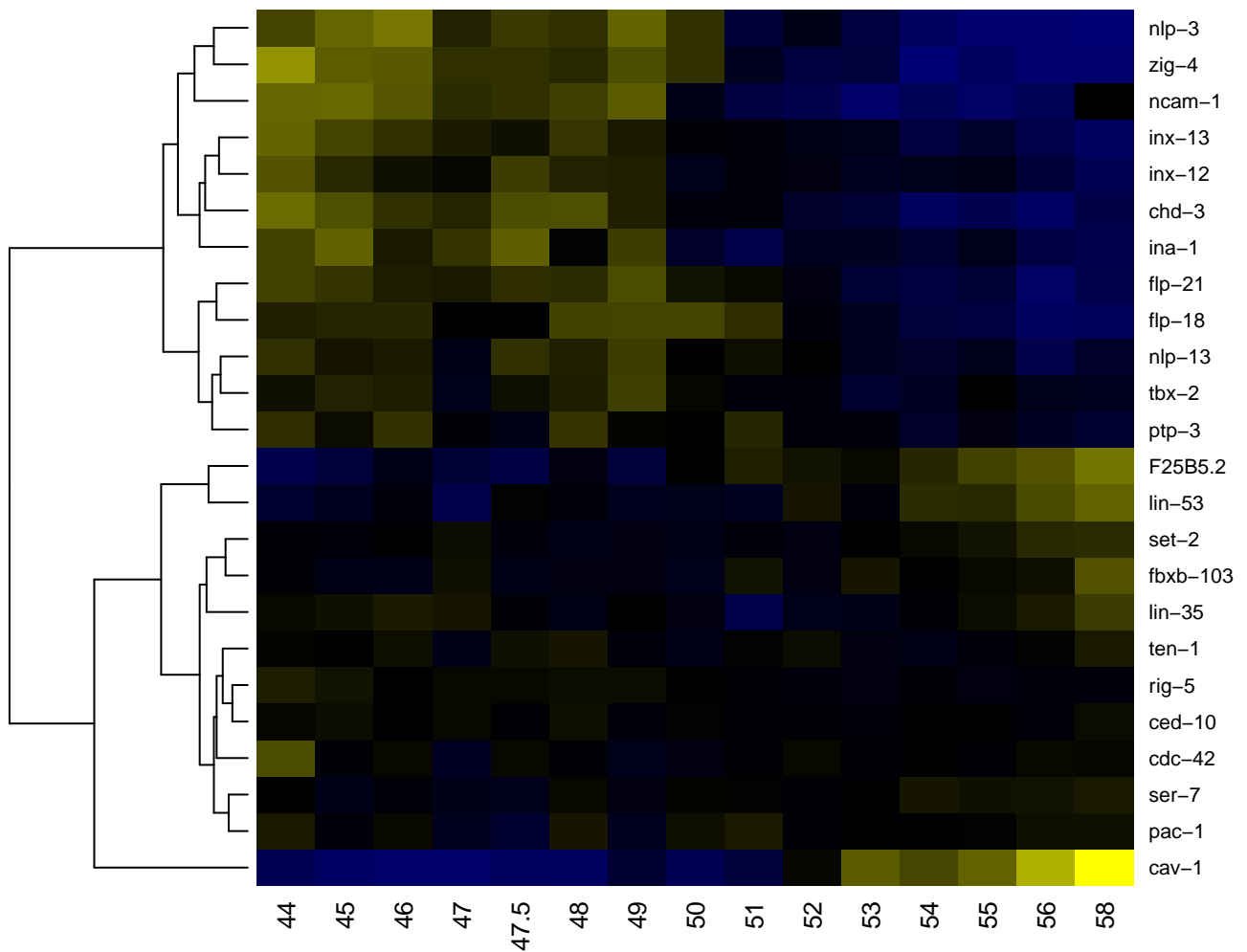
M.drp



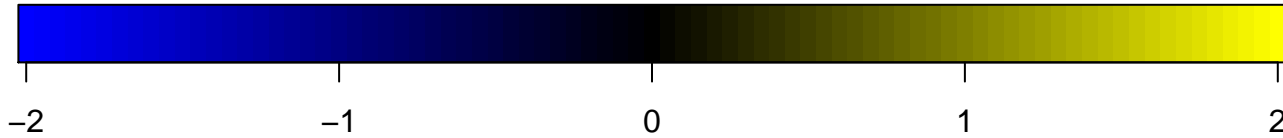
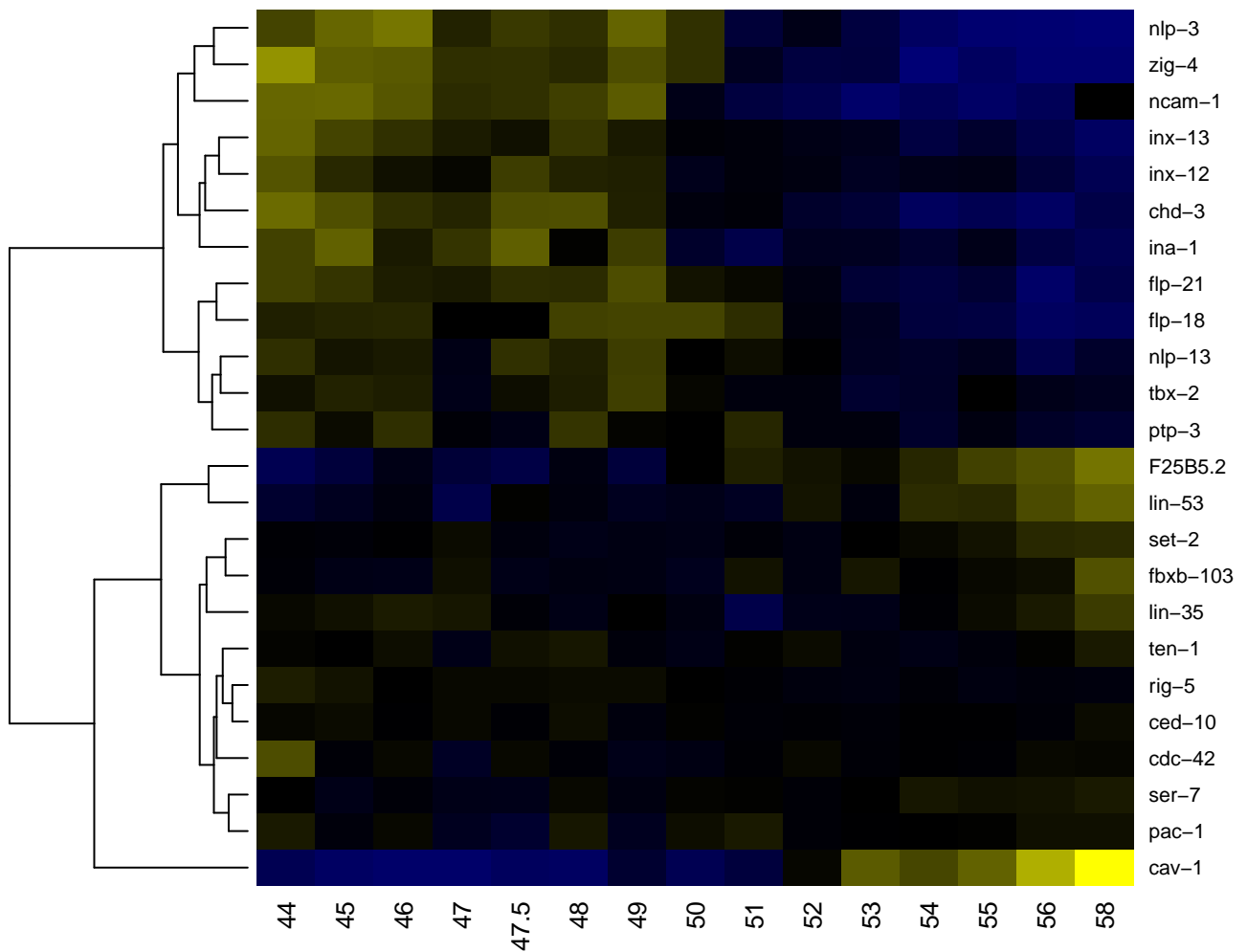
M1



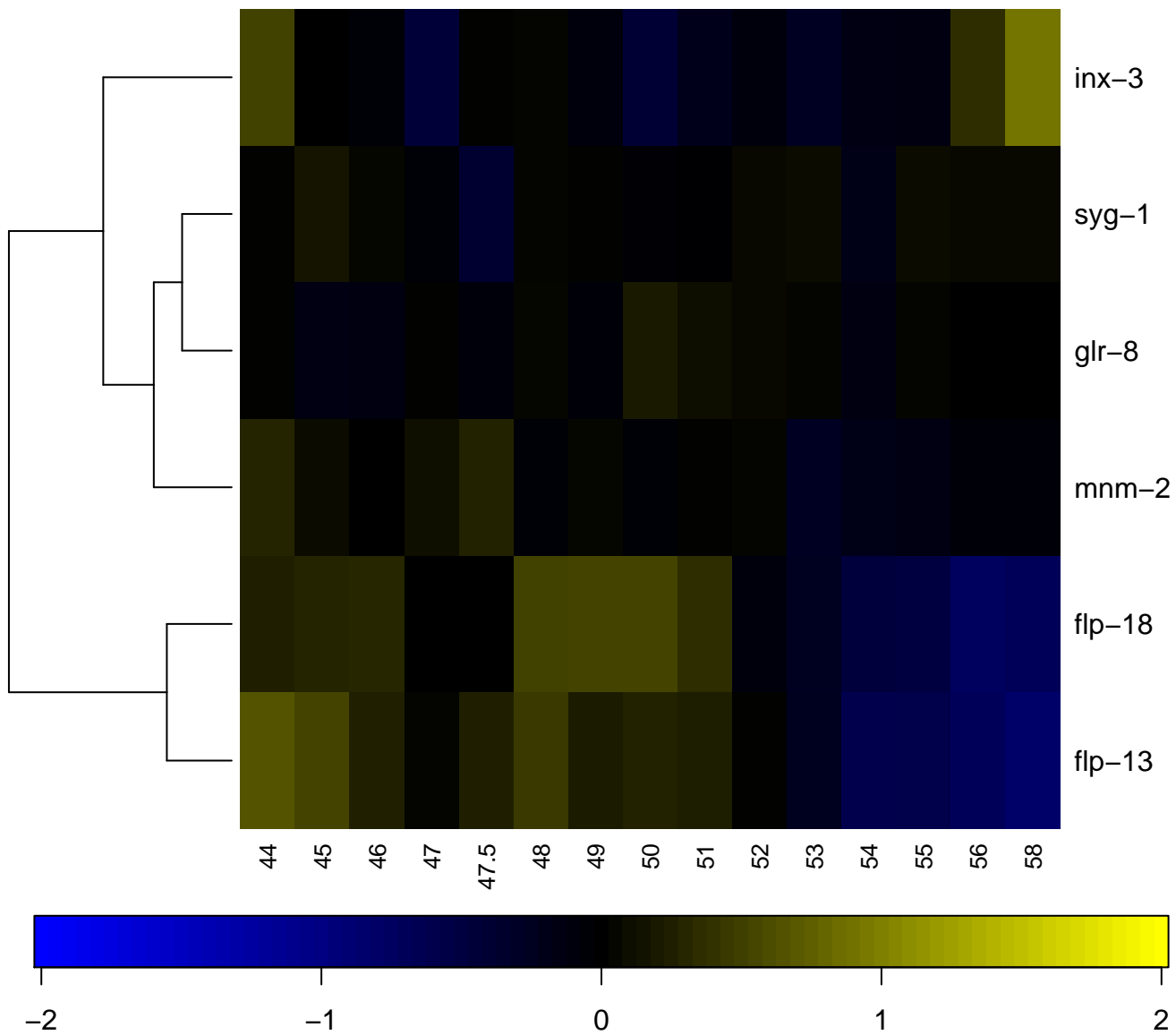
m2L



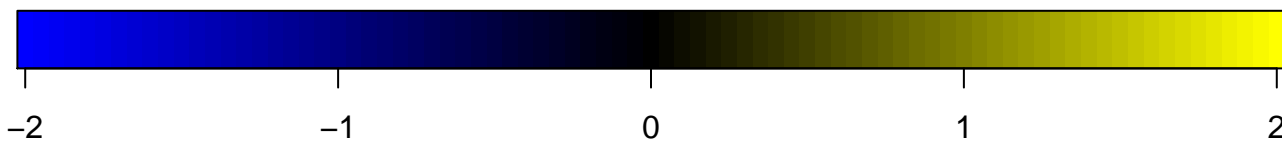
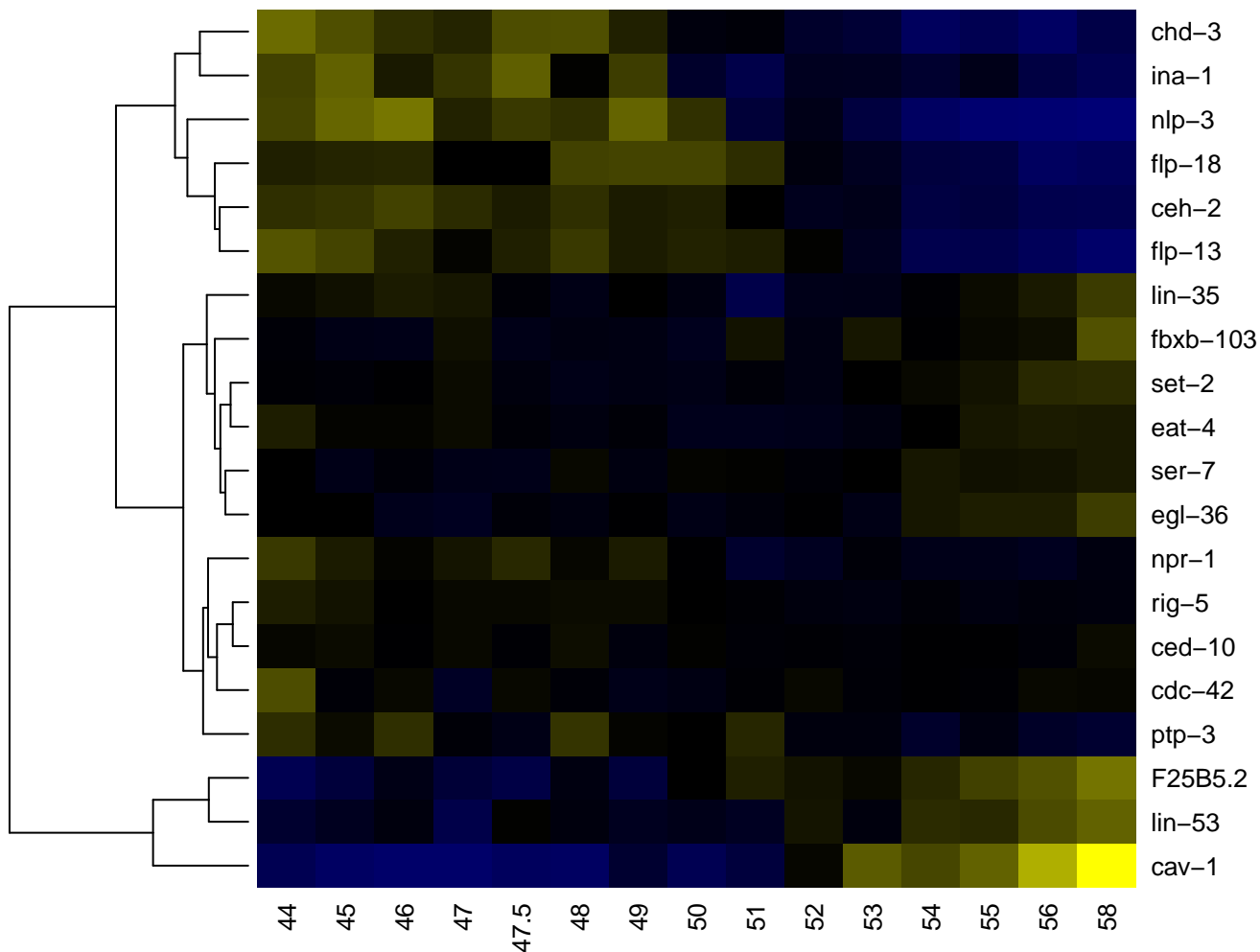
m2R



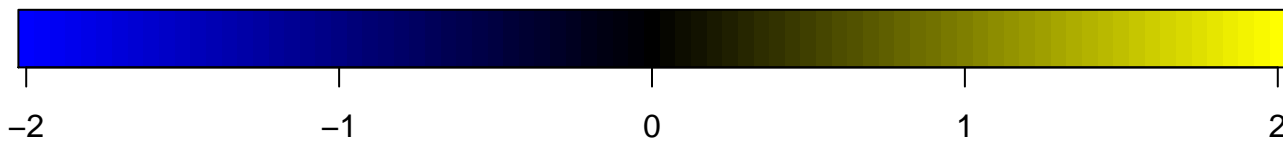
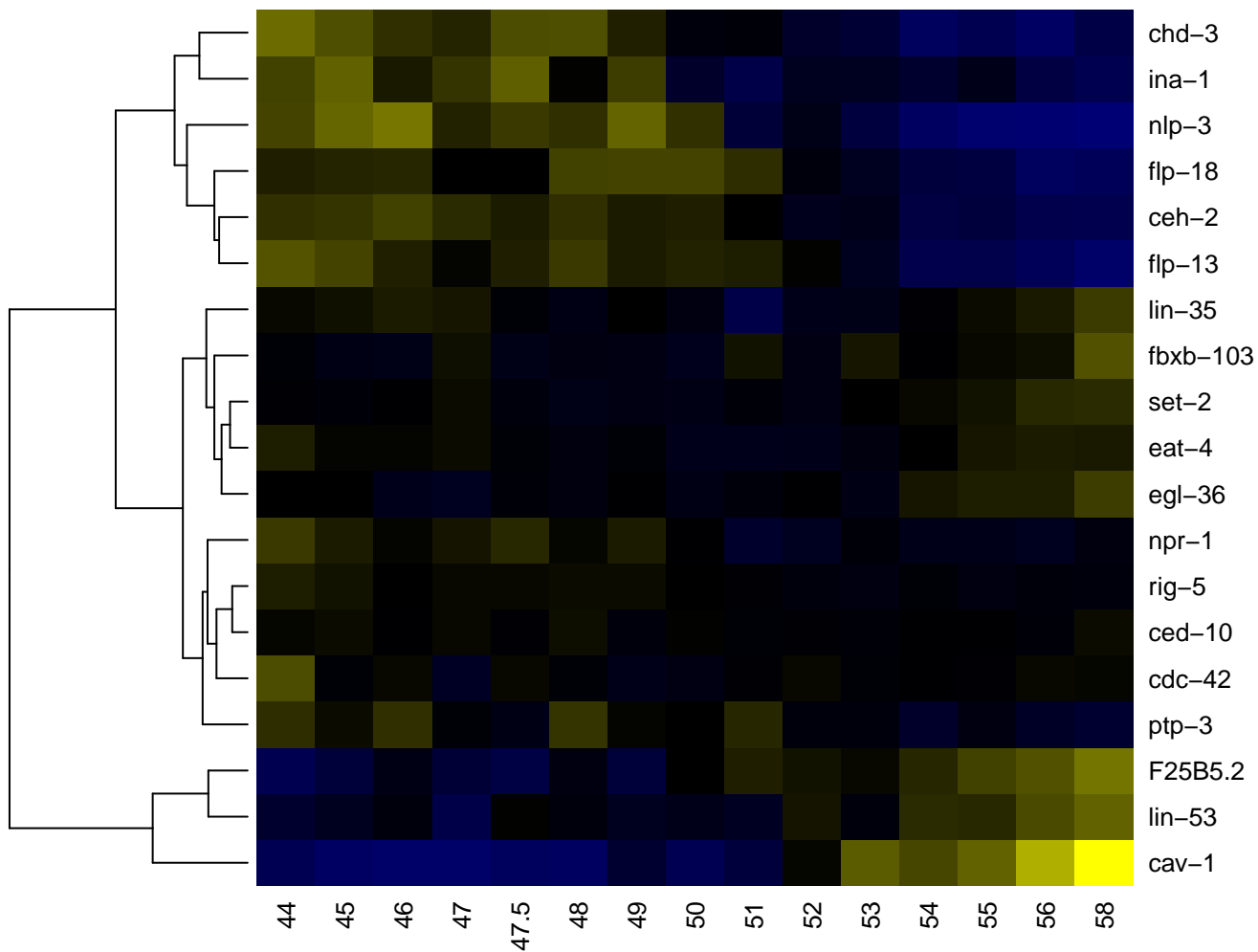
M3 neuron



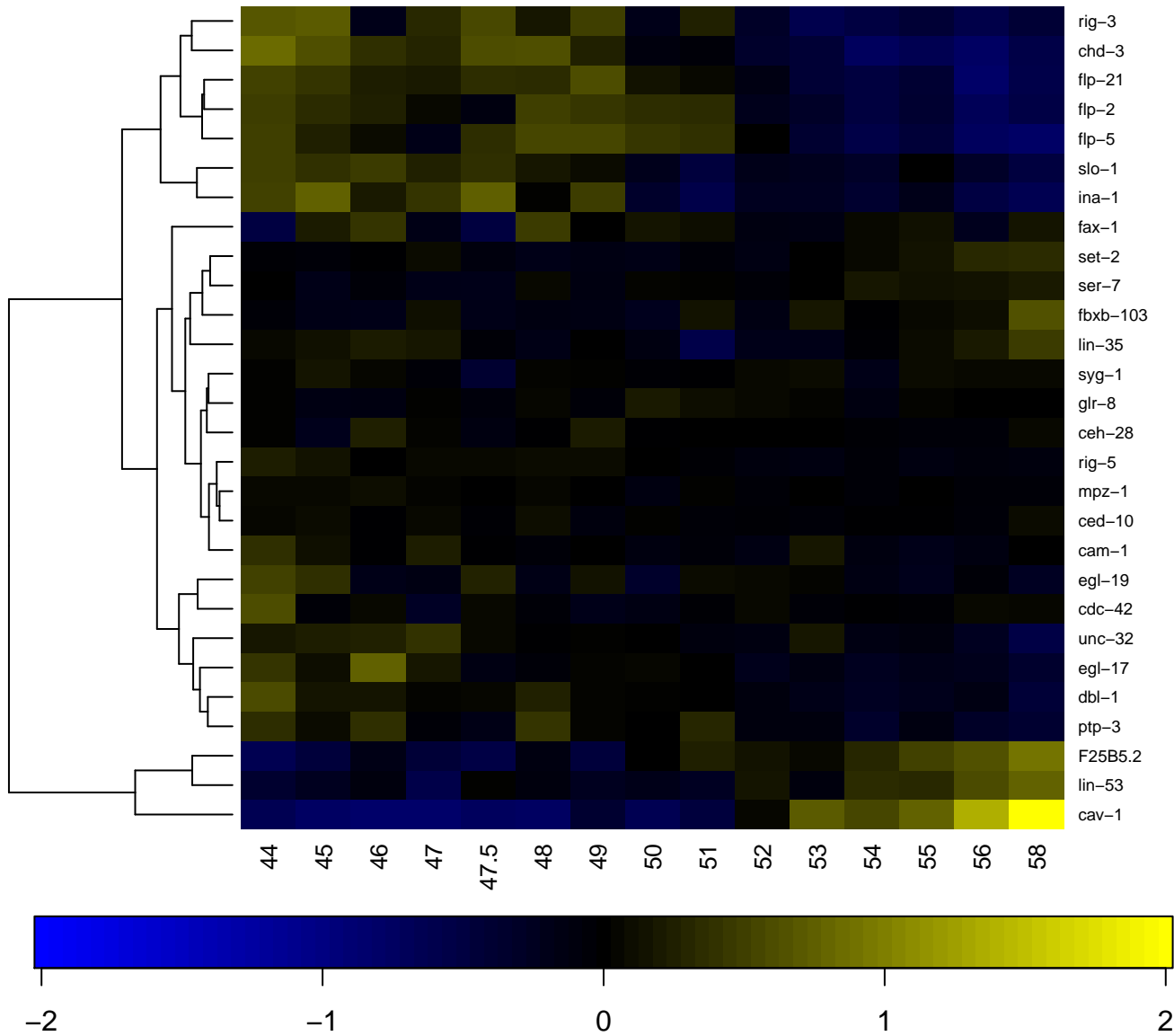
m3L



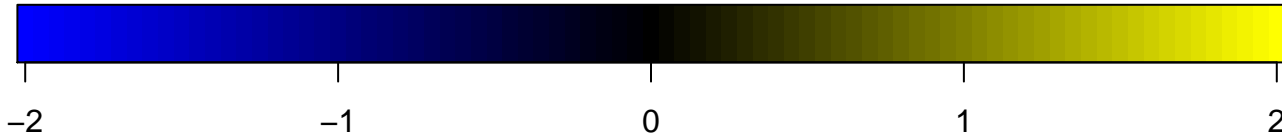
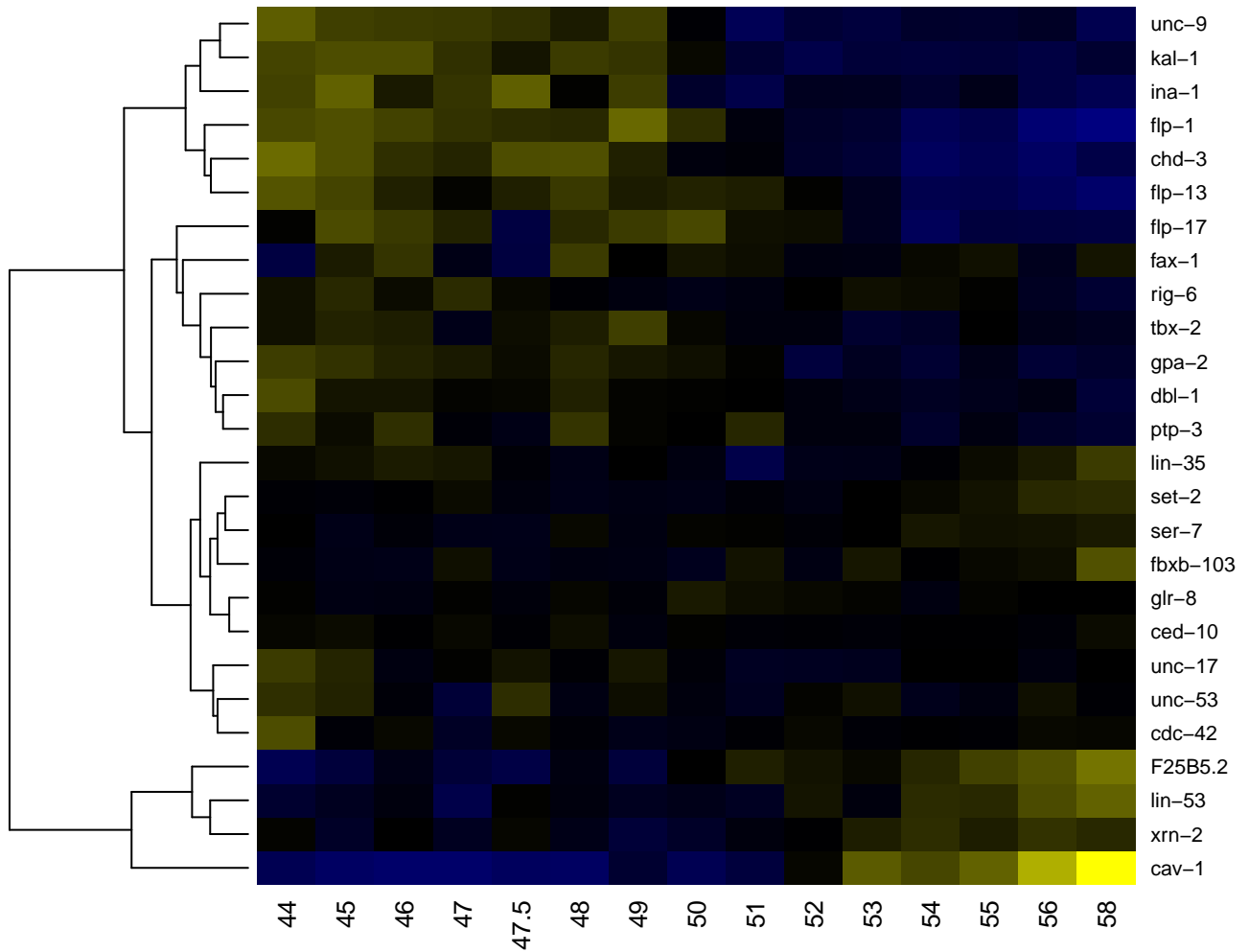
m3R



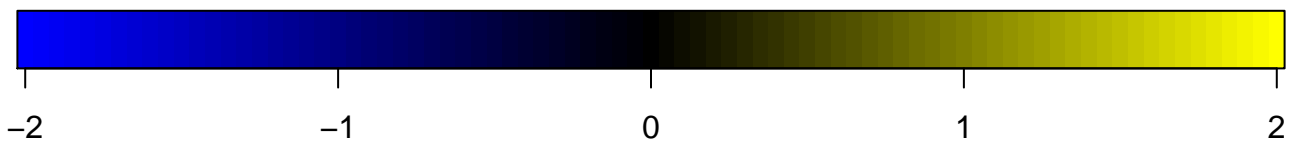
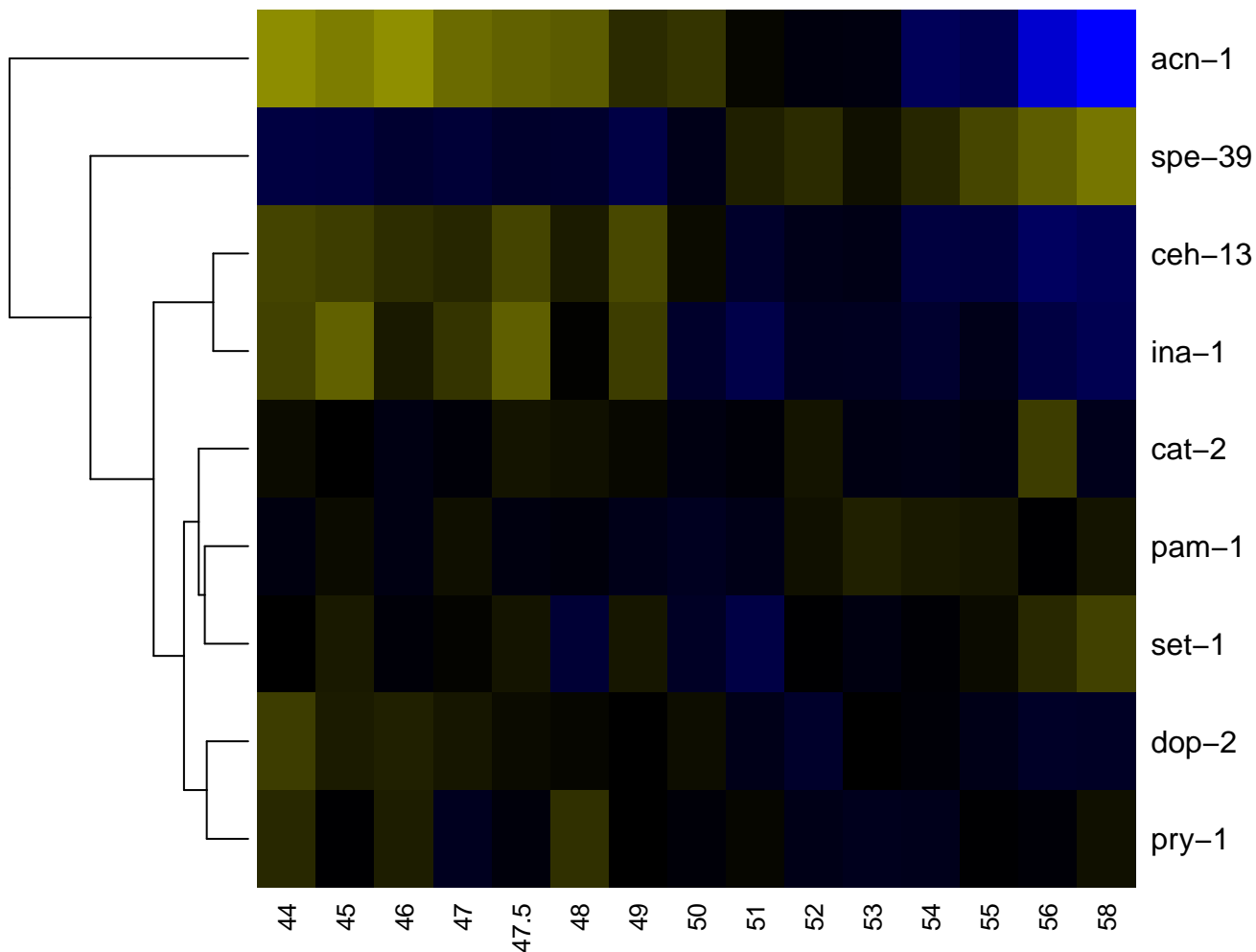
M4



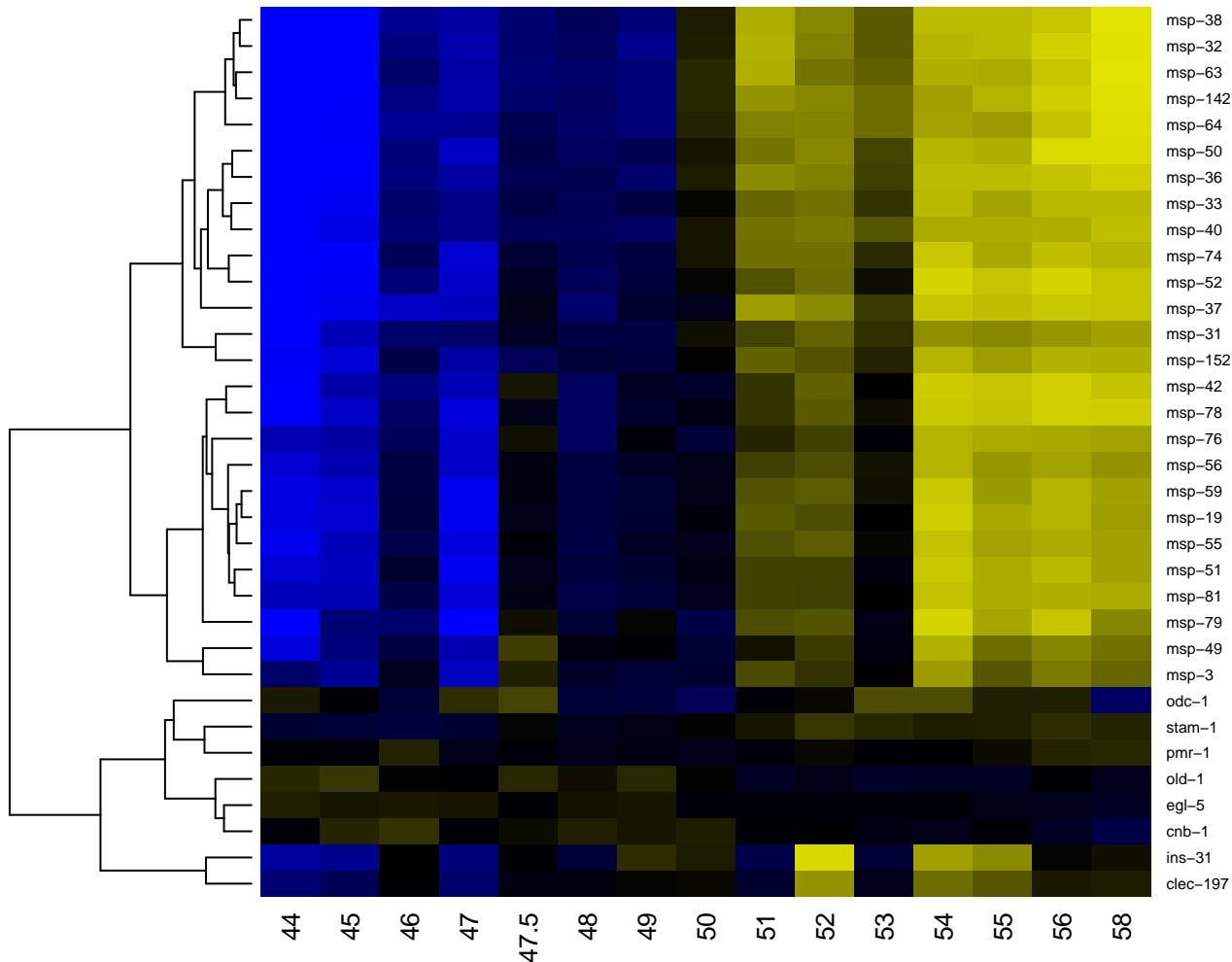
M5



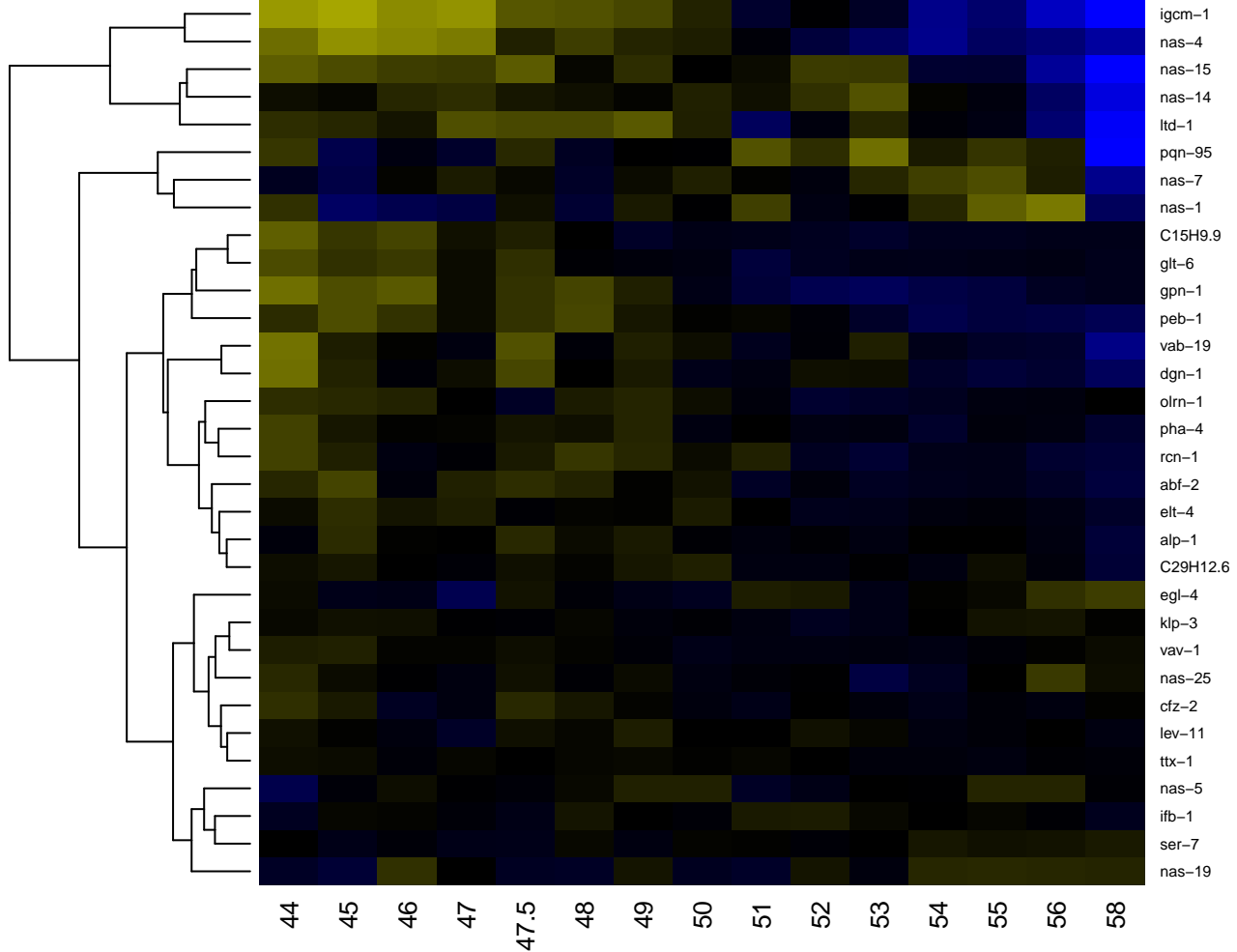
male-specific



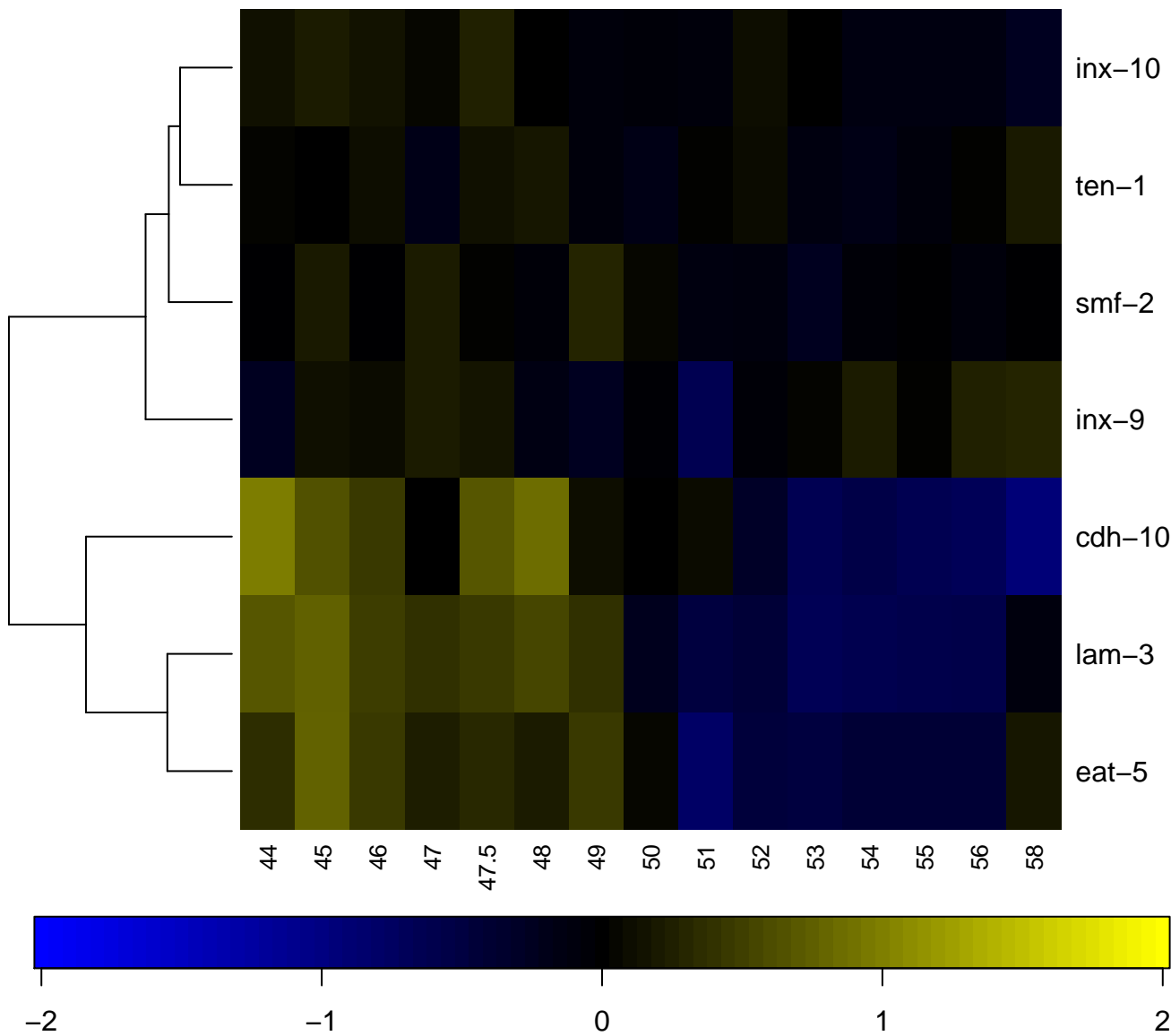
male gonad



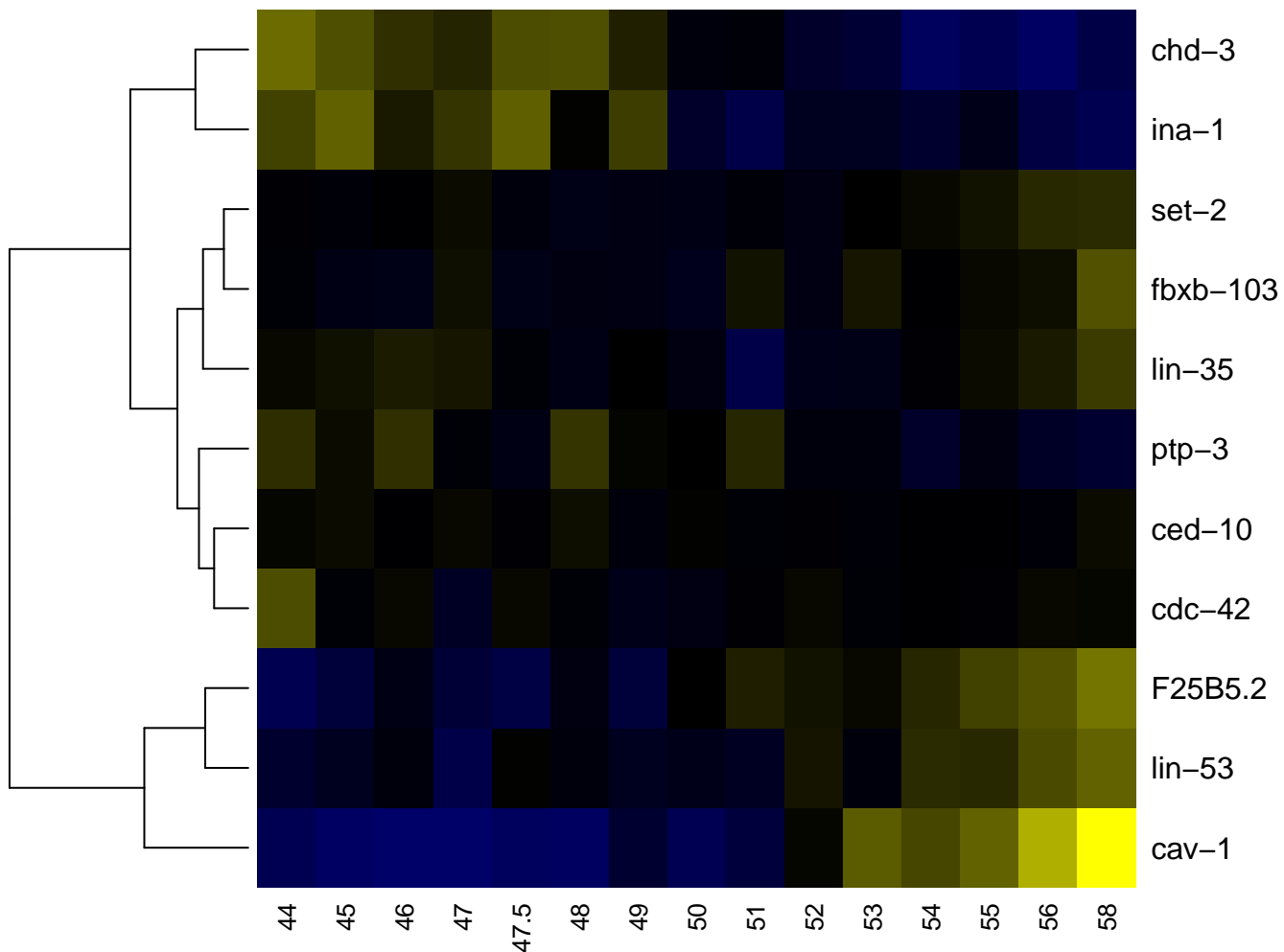
marginal cell



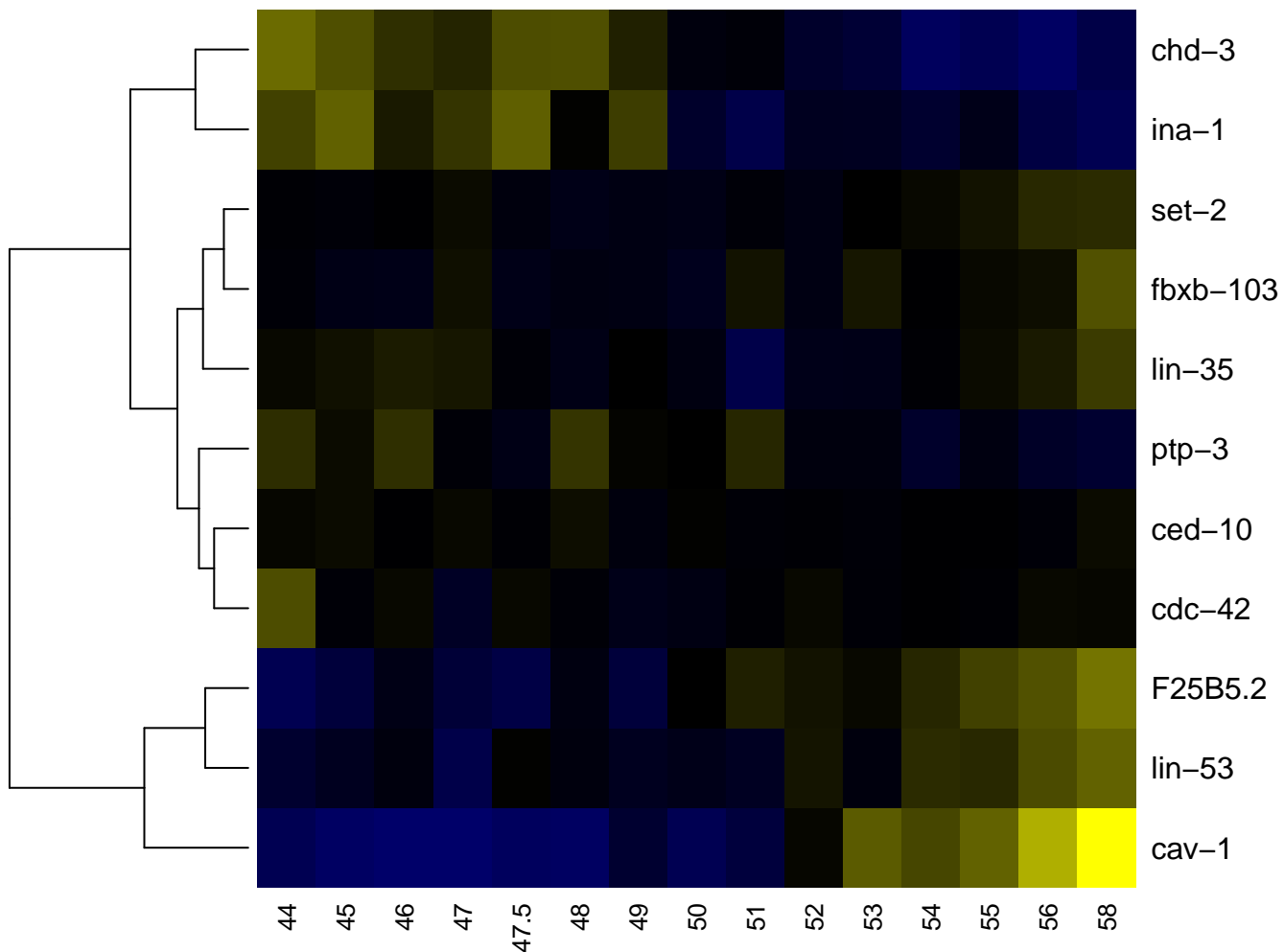
mc1



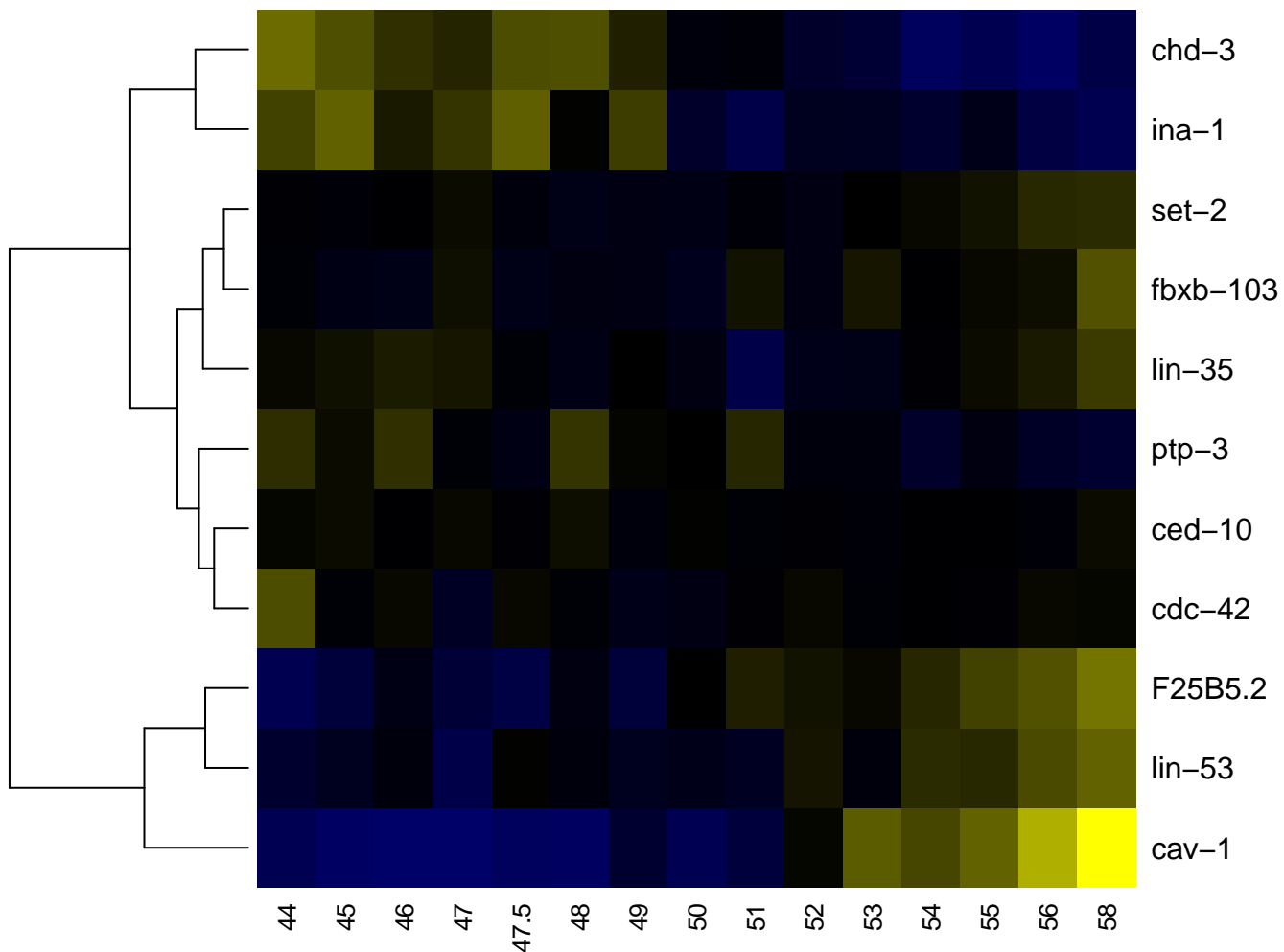
mc1DL



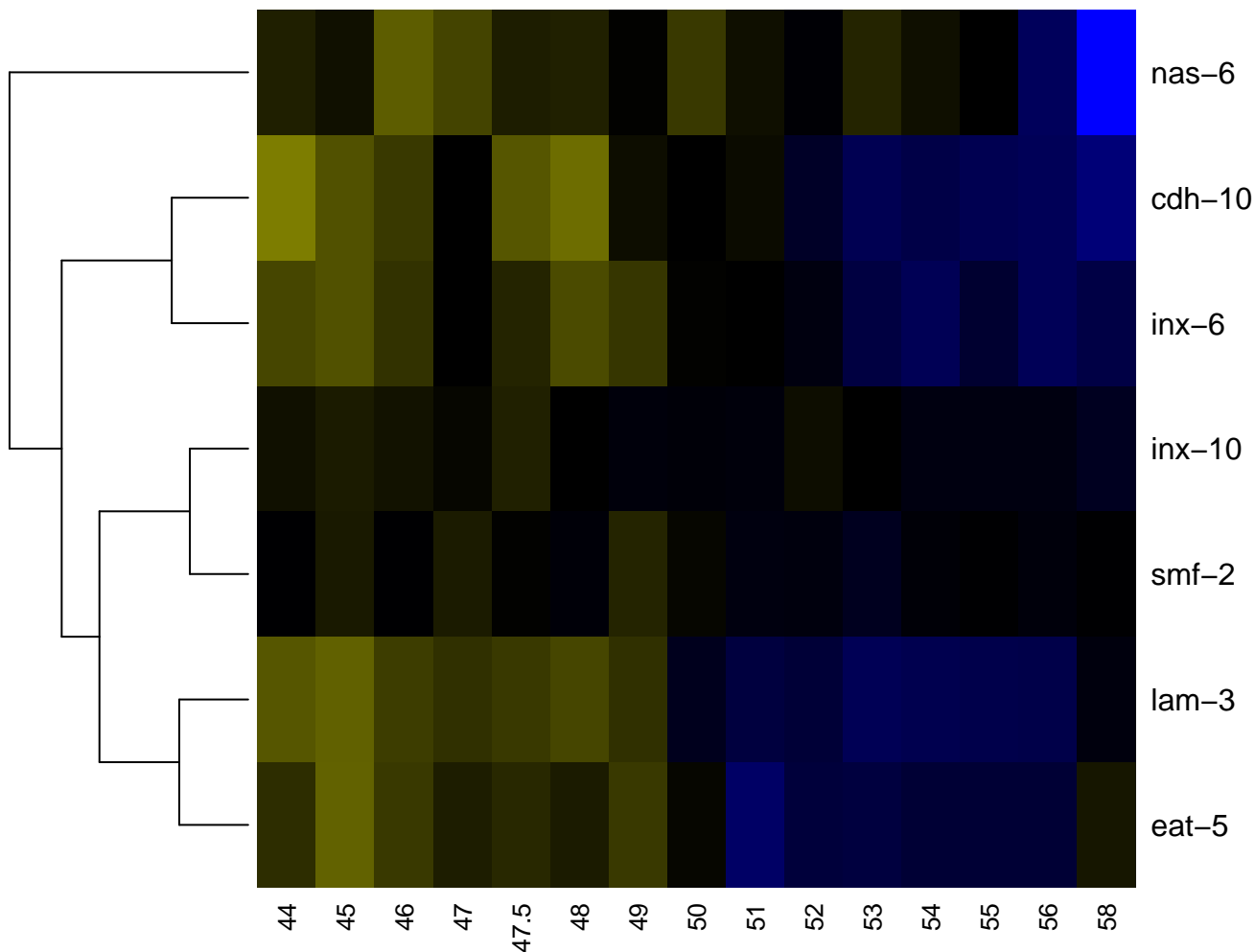
mc1DR



mc1V



mc2



-2

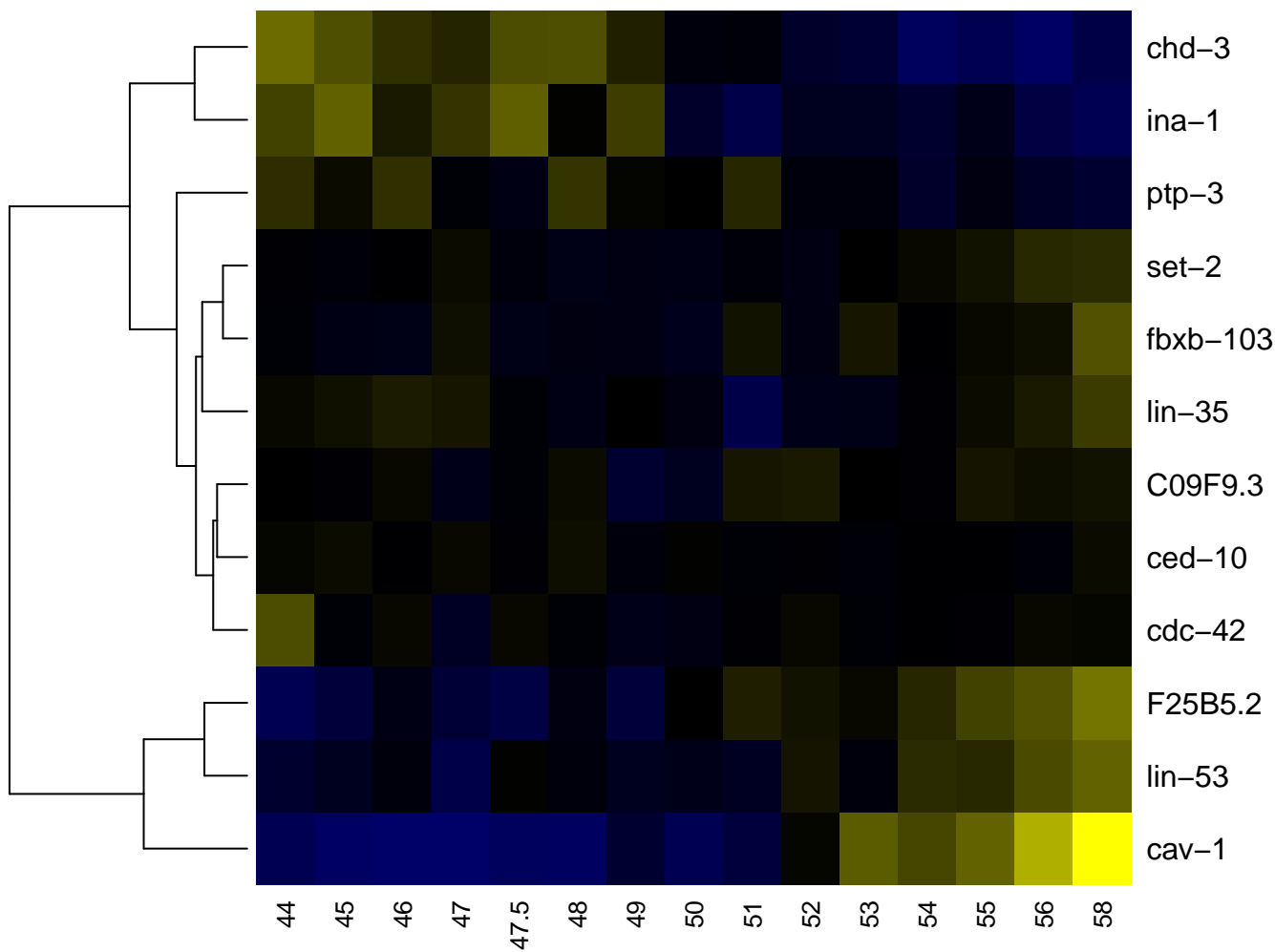
-1

0

1

2

mc2DL



-2

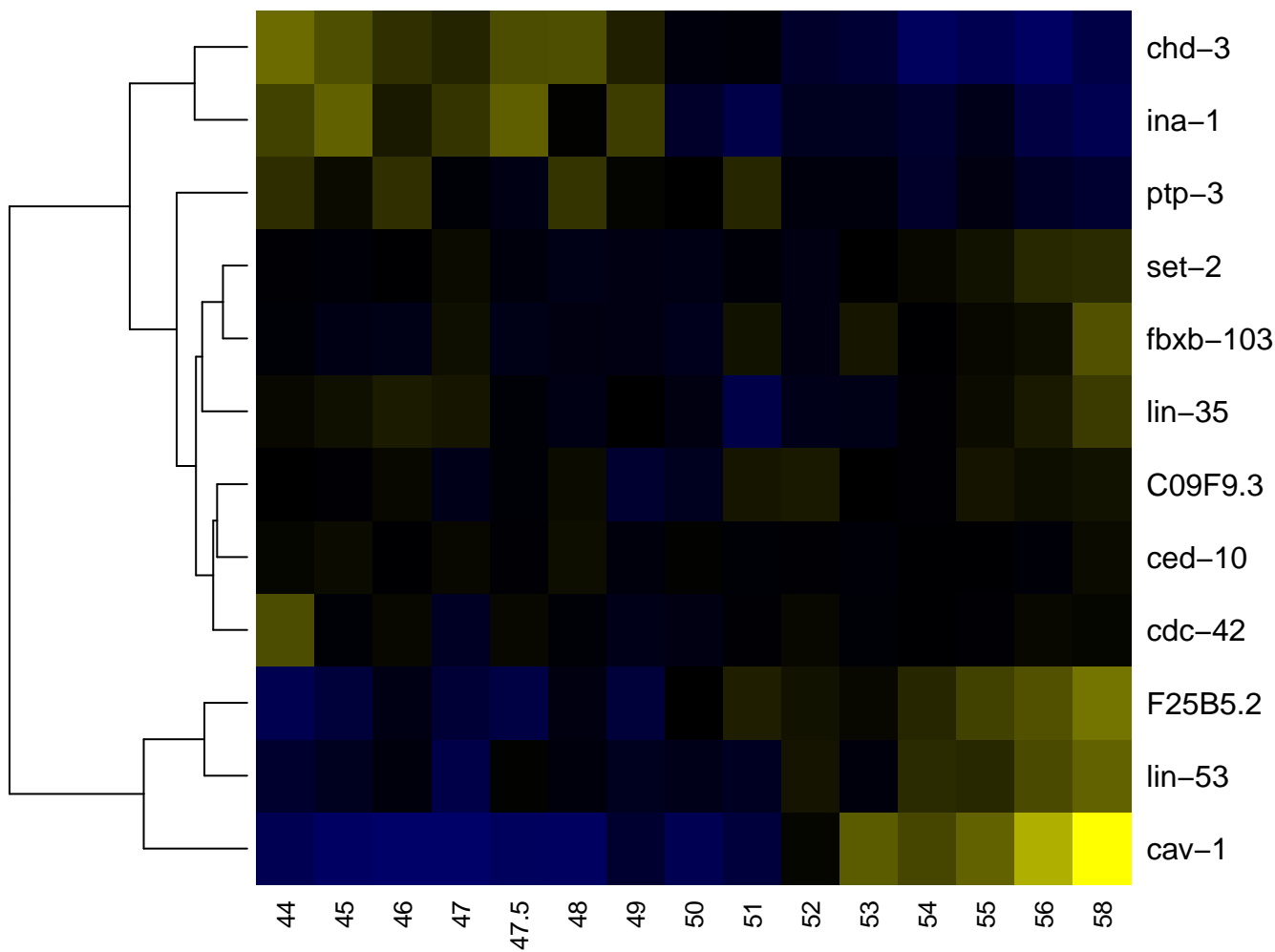
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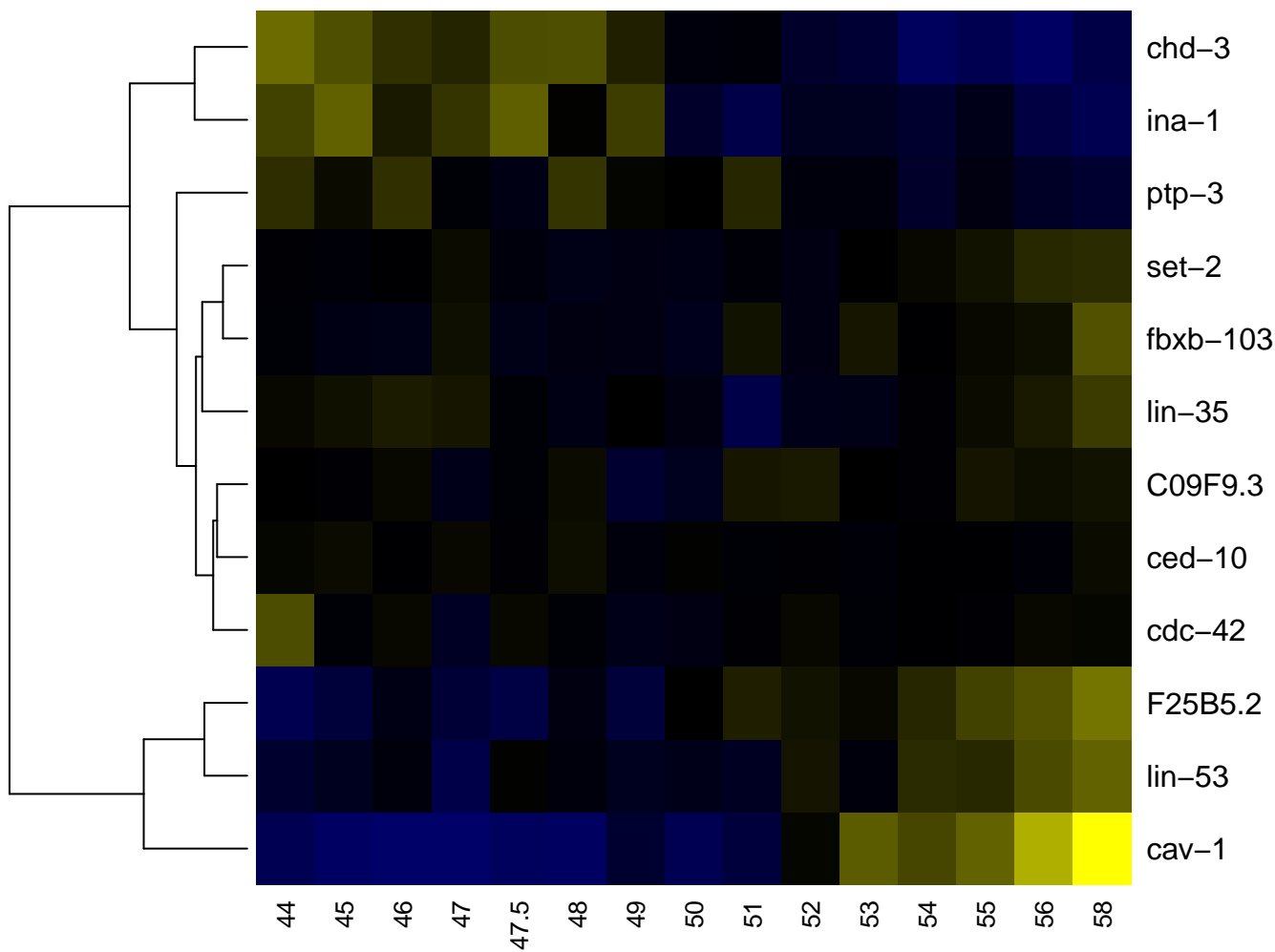
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mc2V



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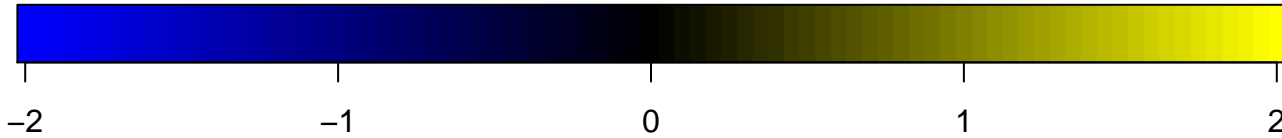
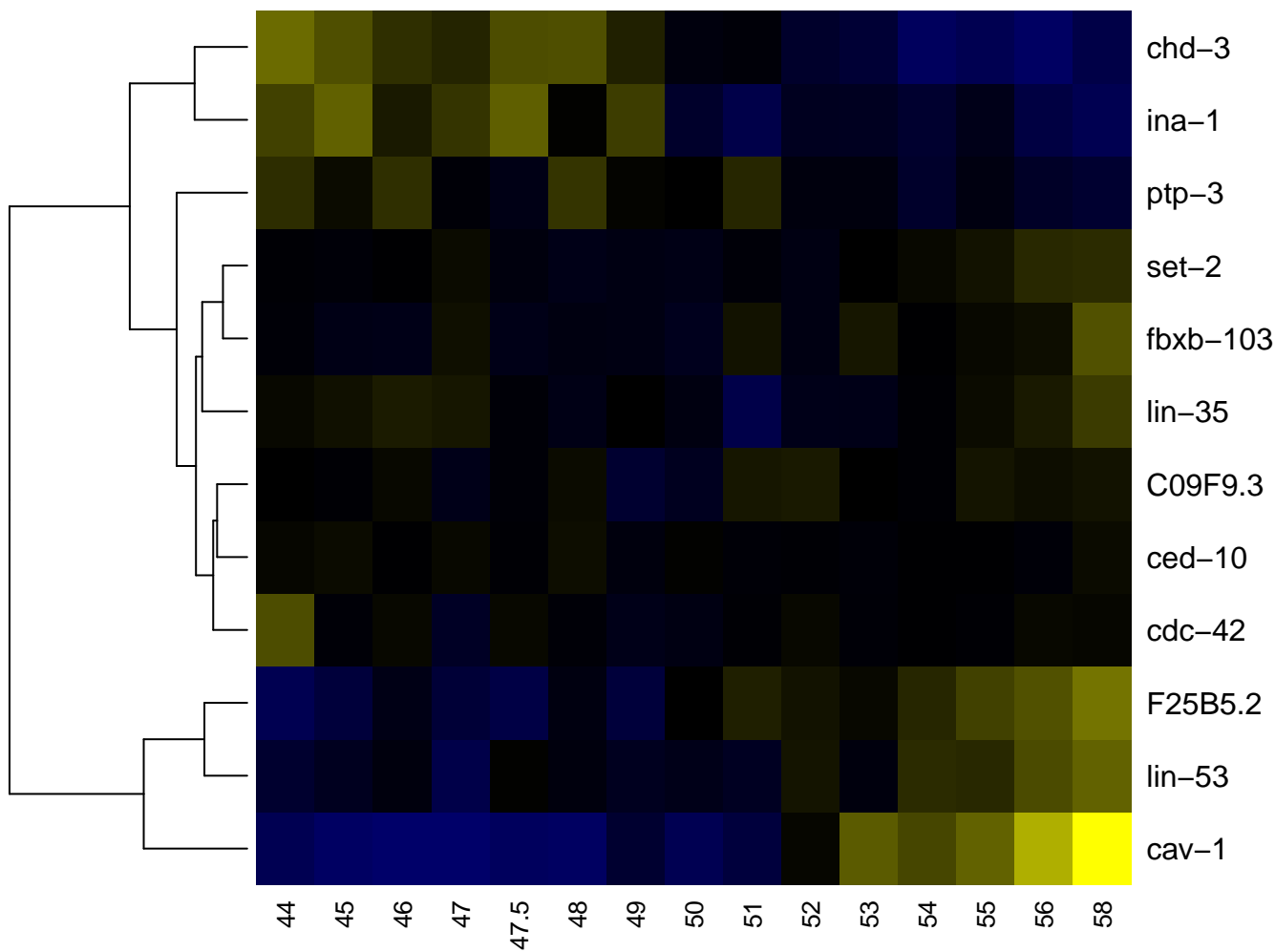
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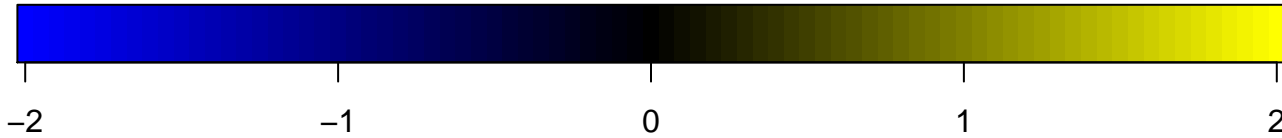
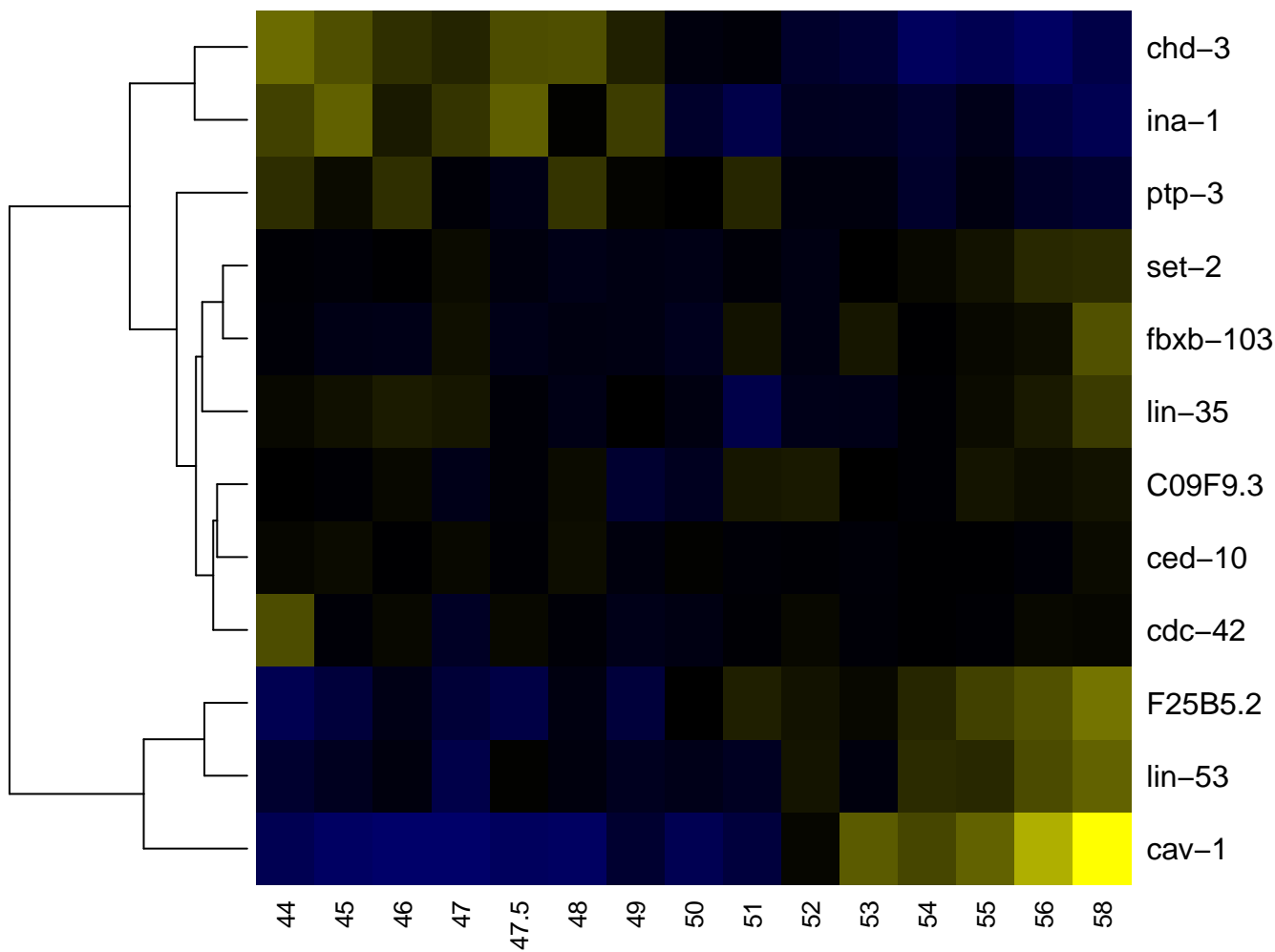
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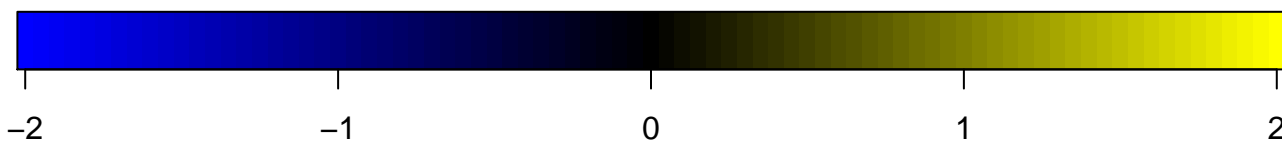
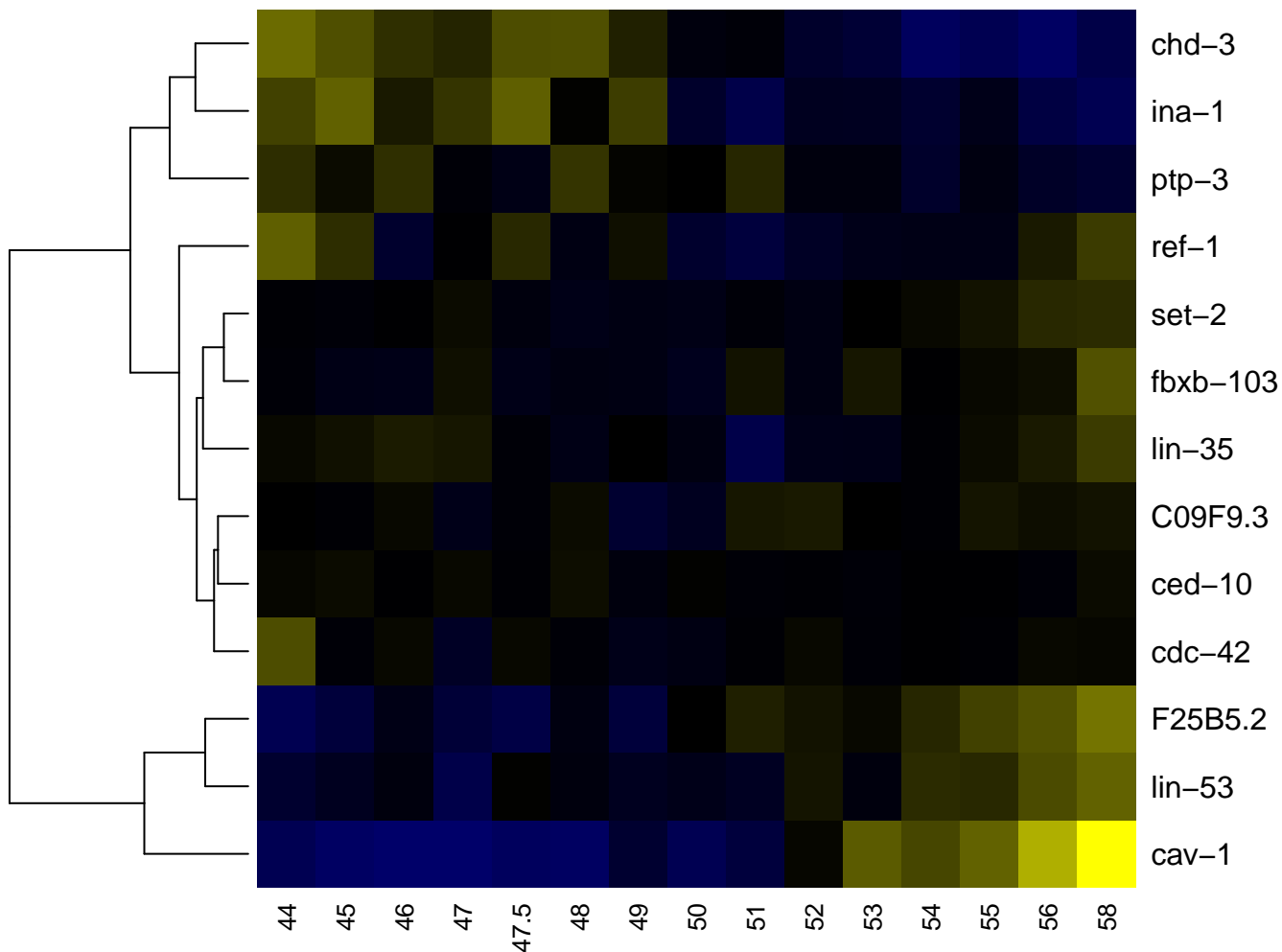
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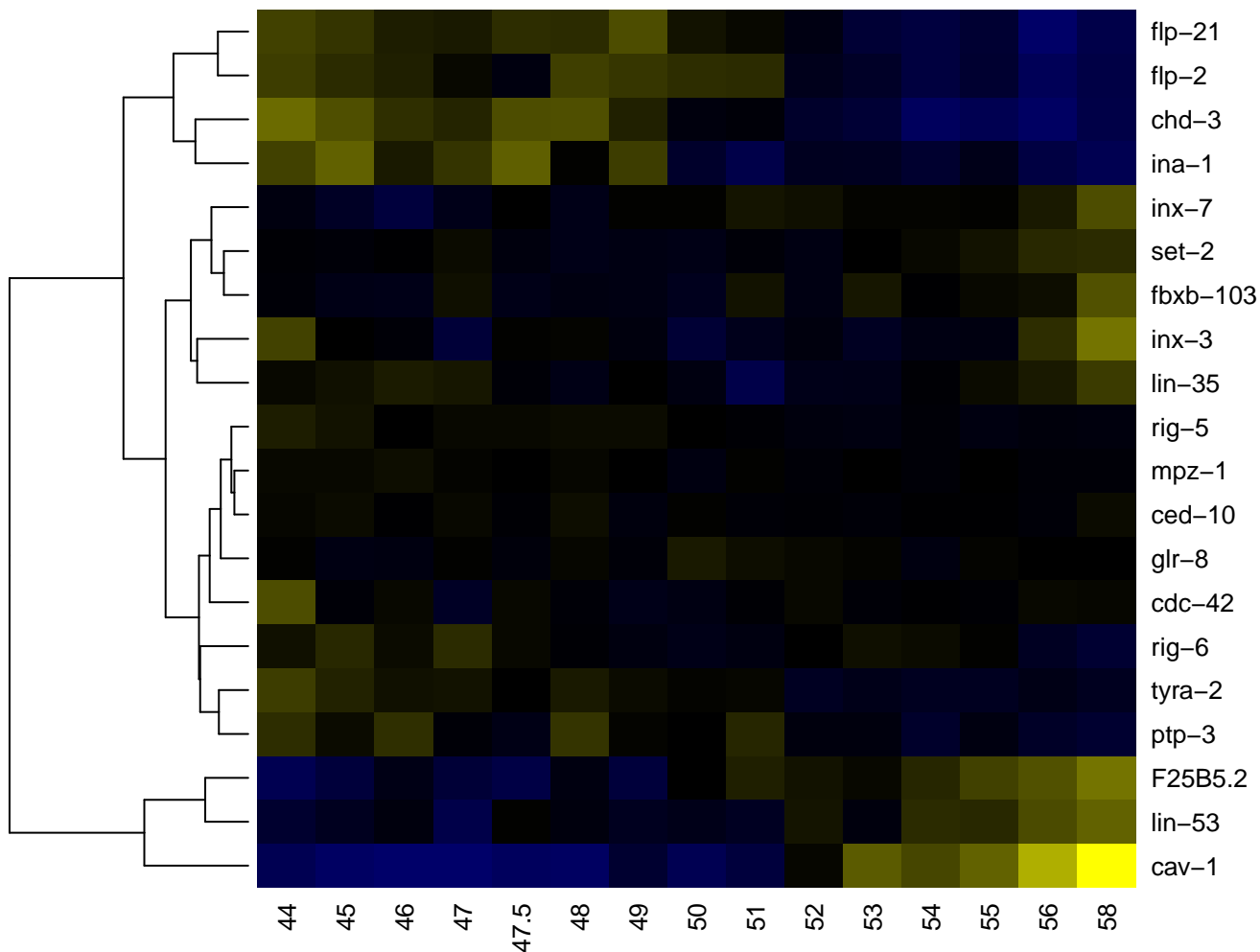
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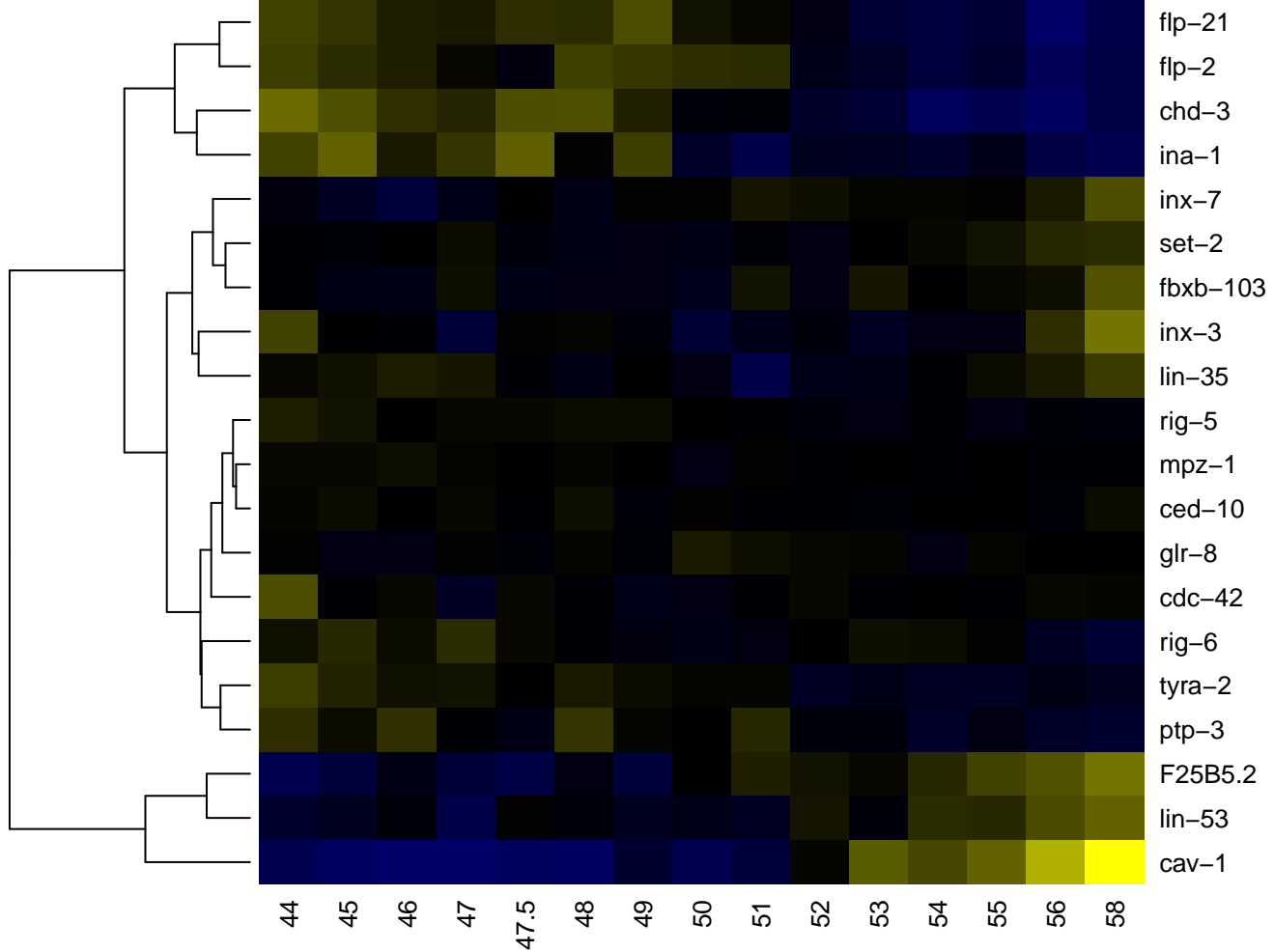
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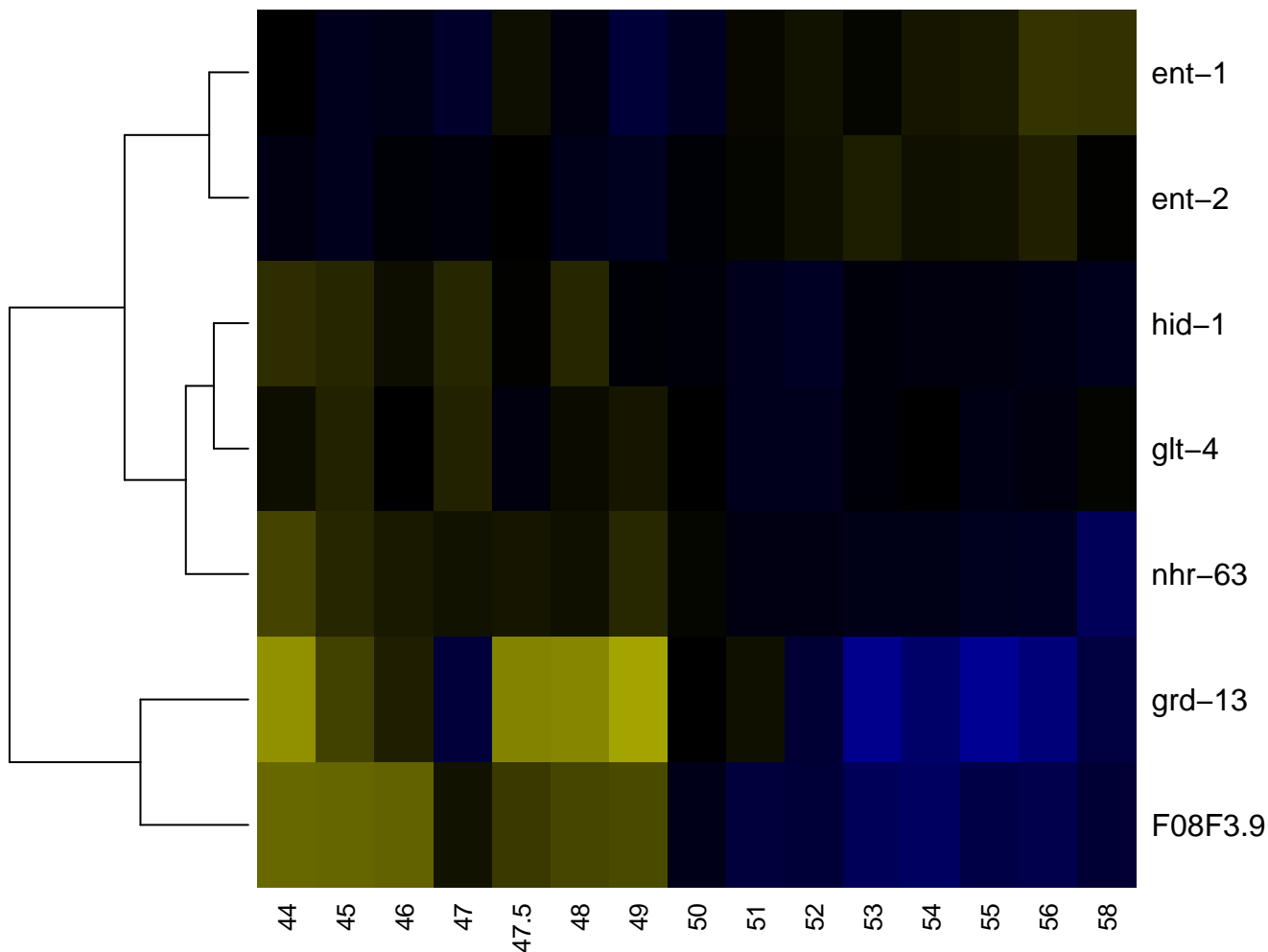
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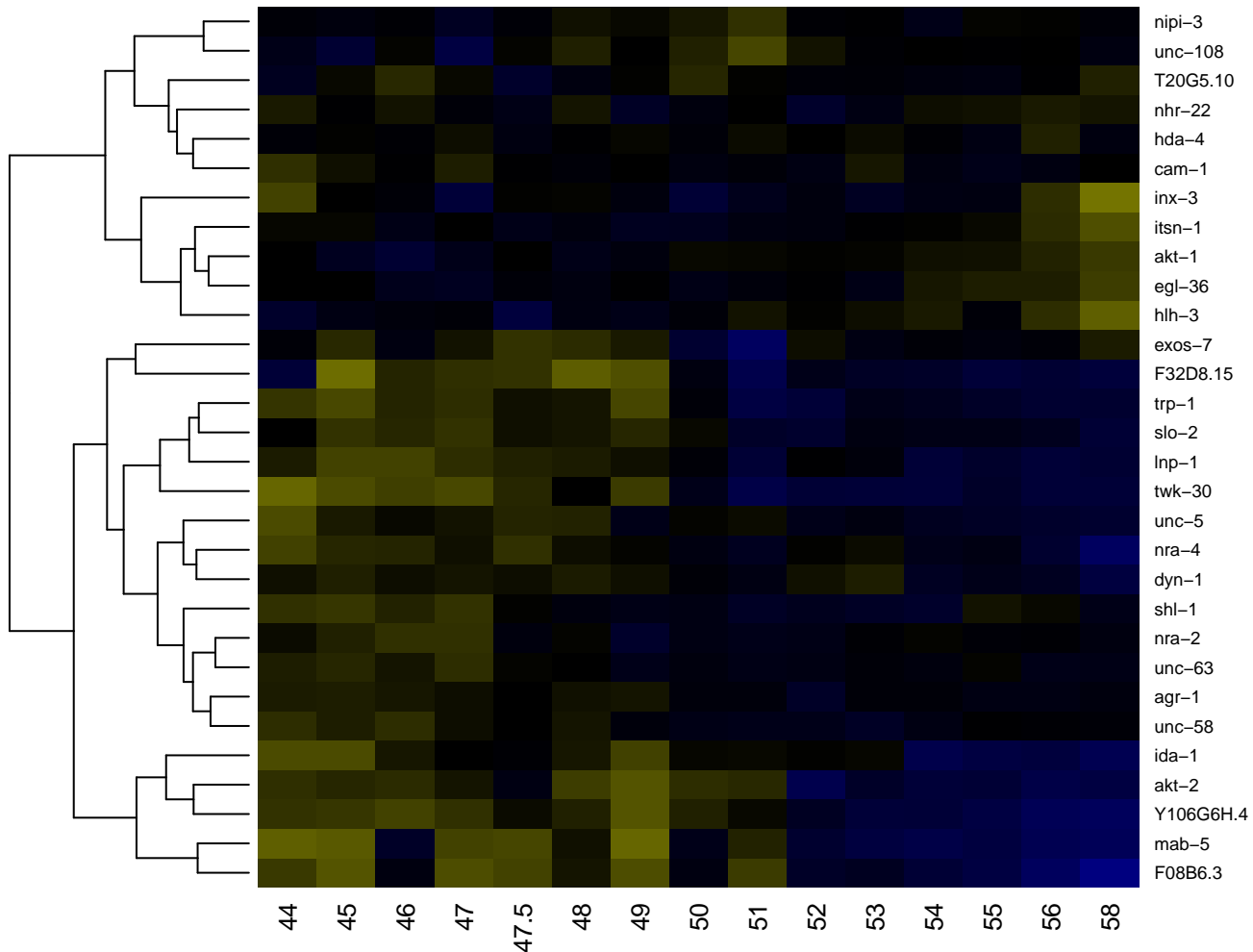
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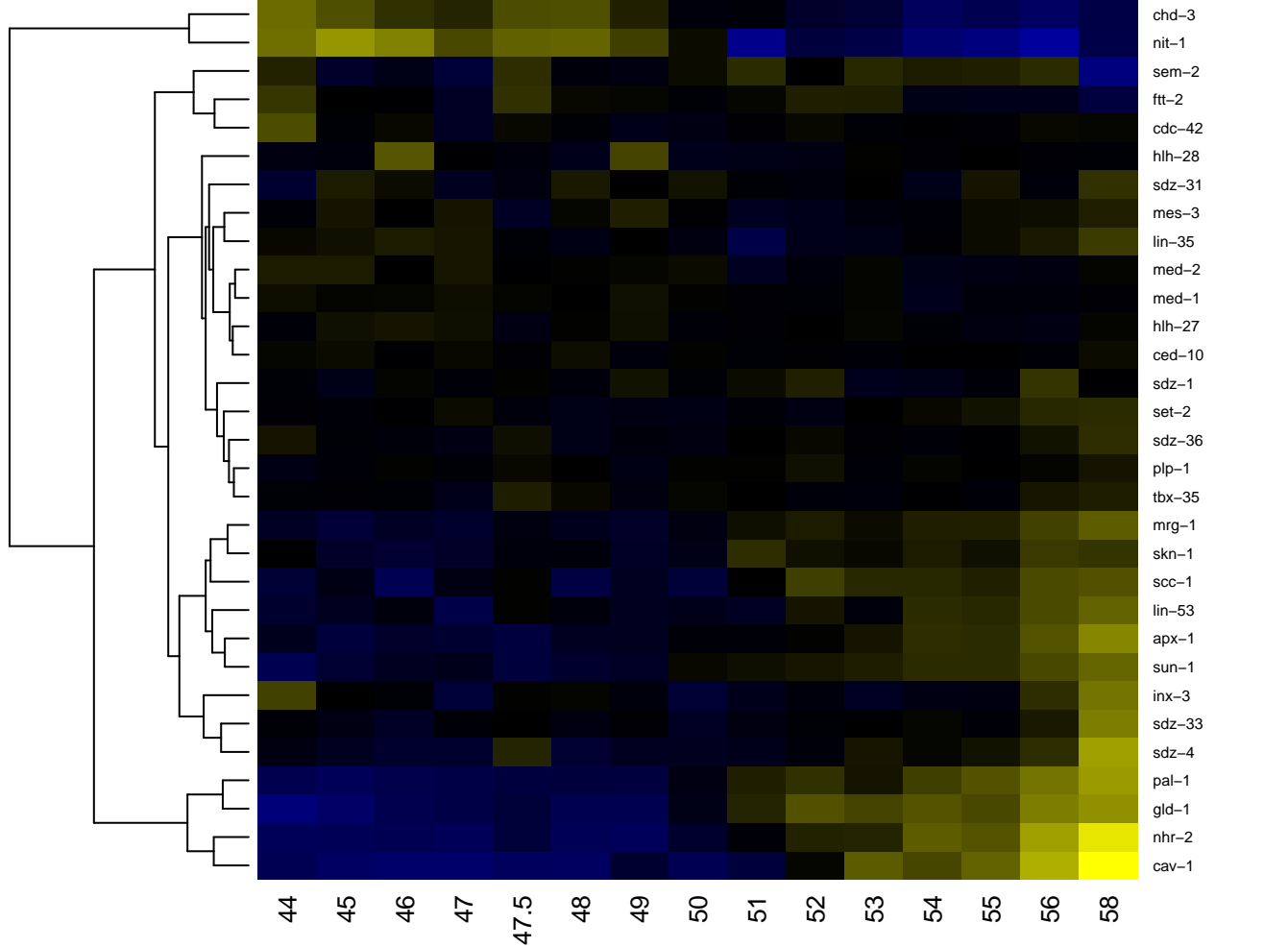
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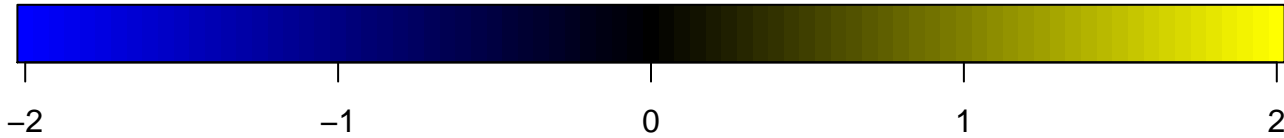
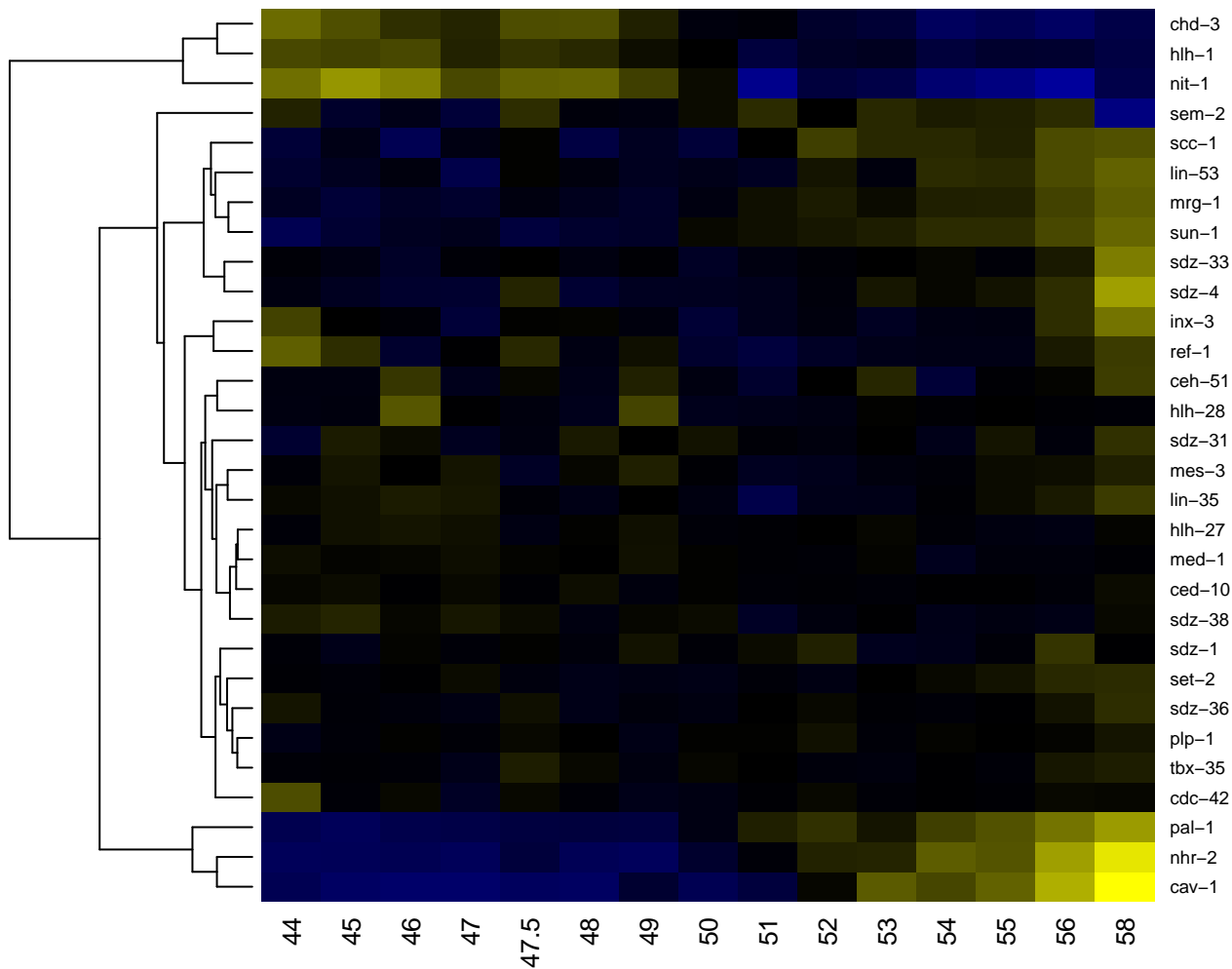
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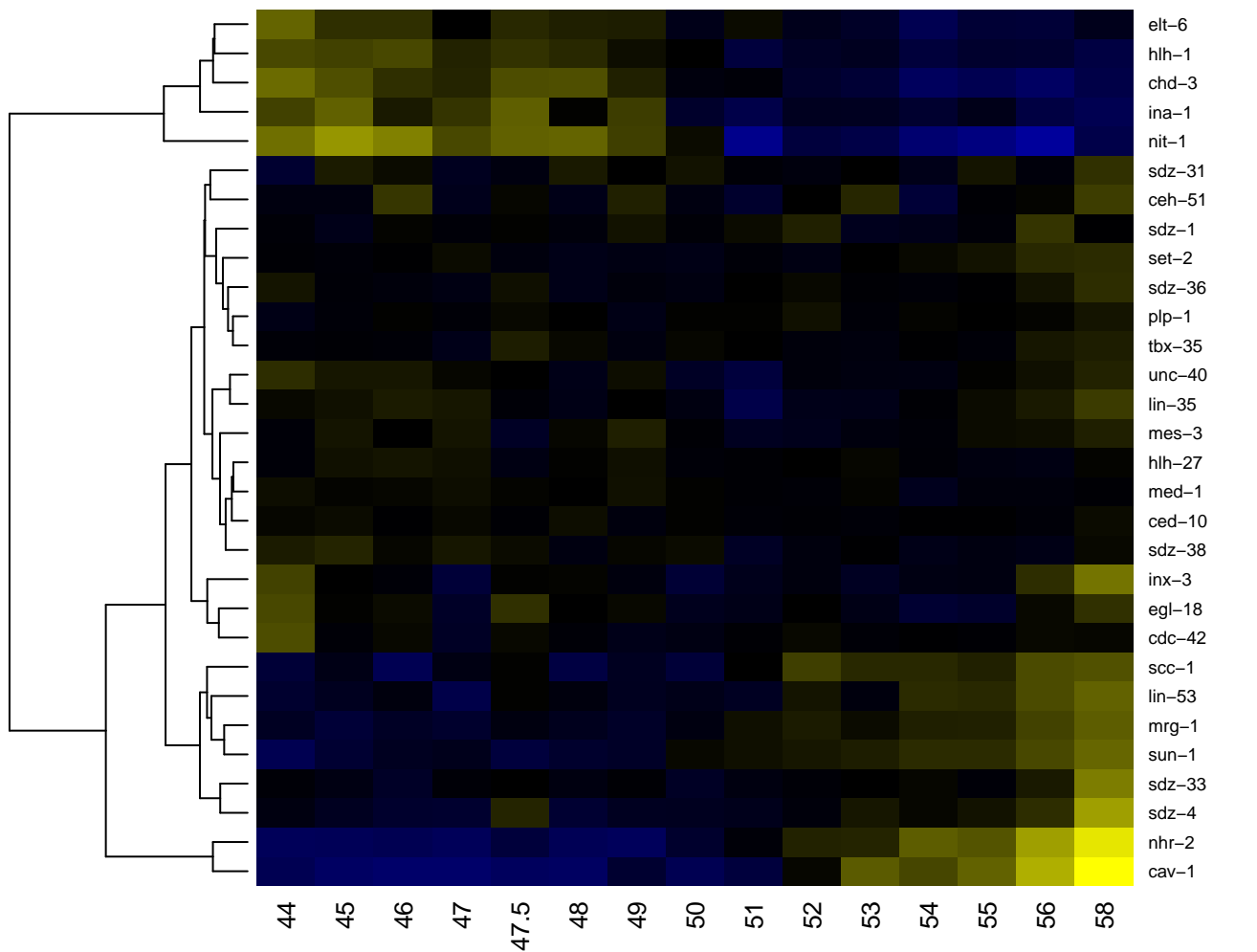
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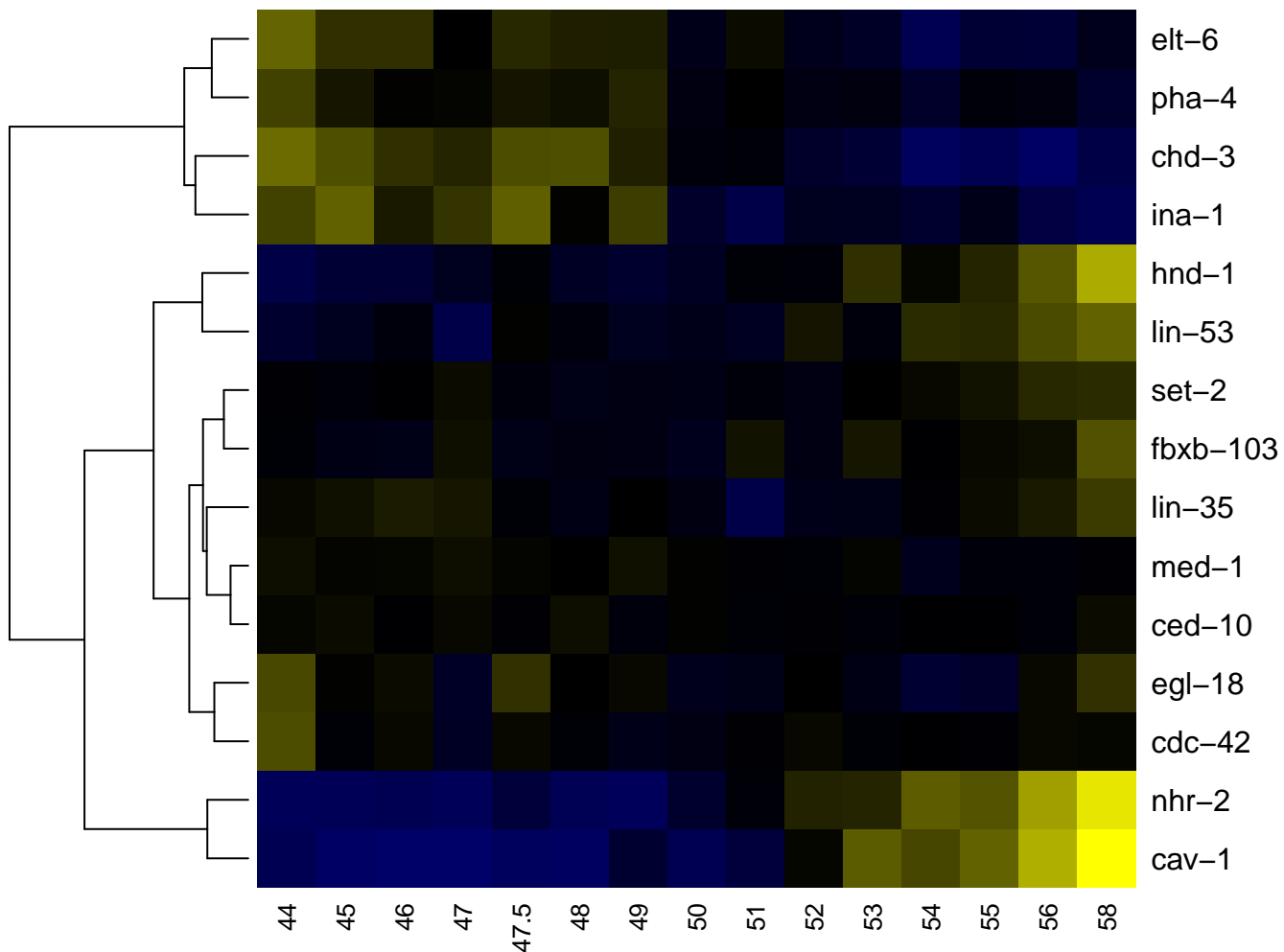
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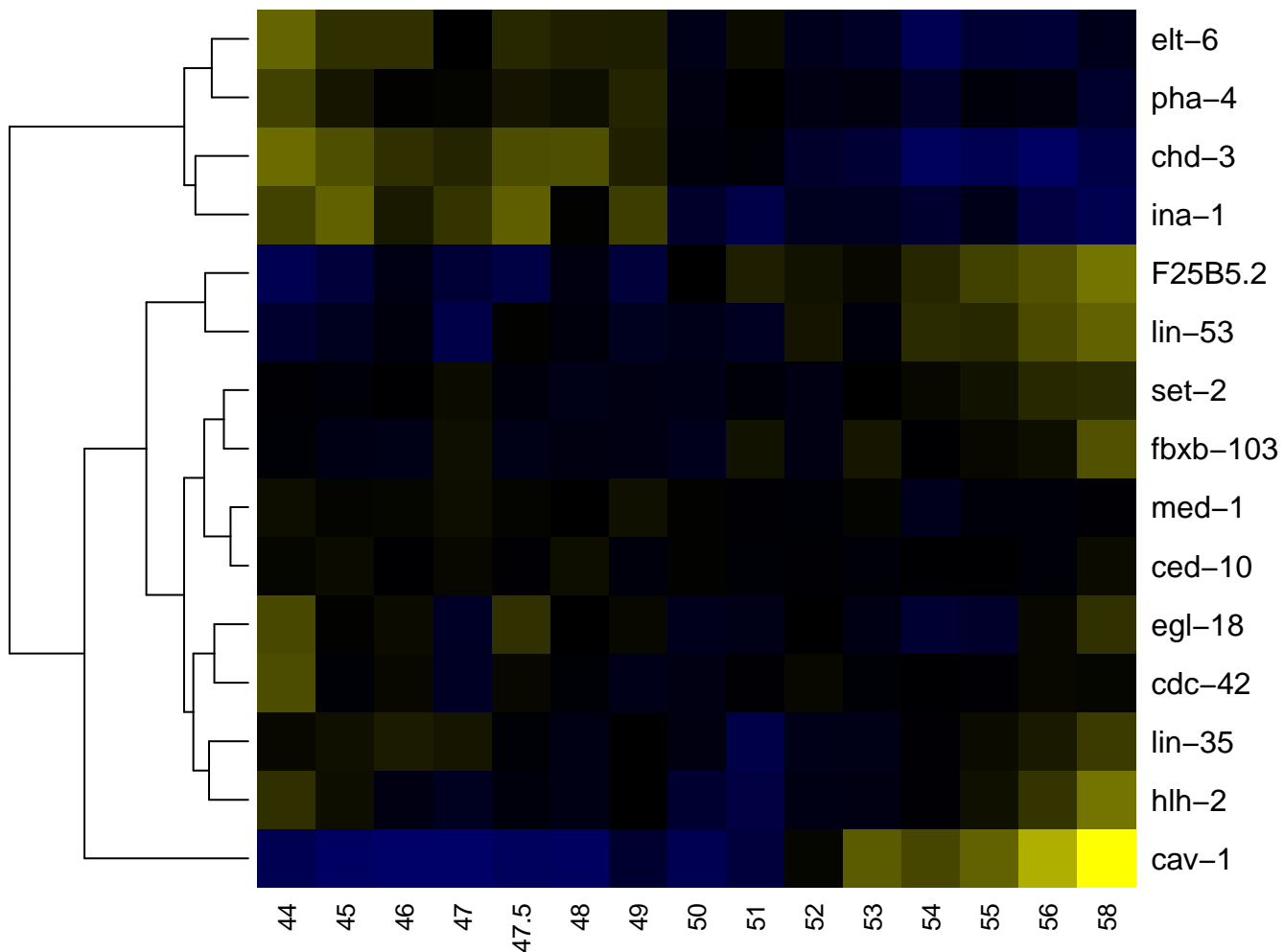
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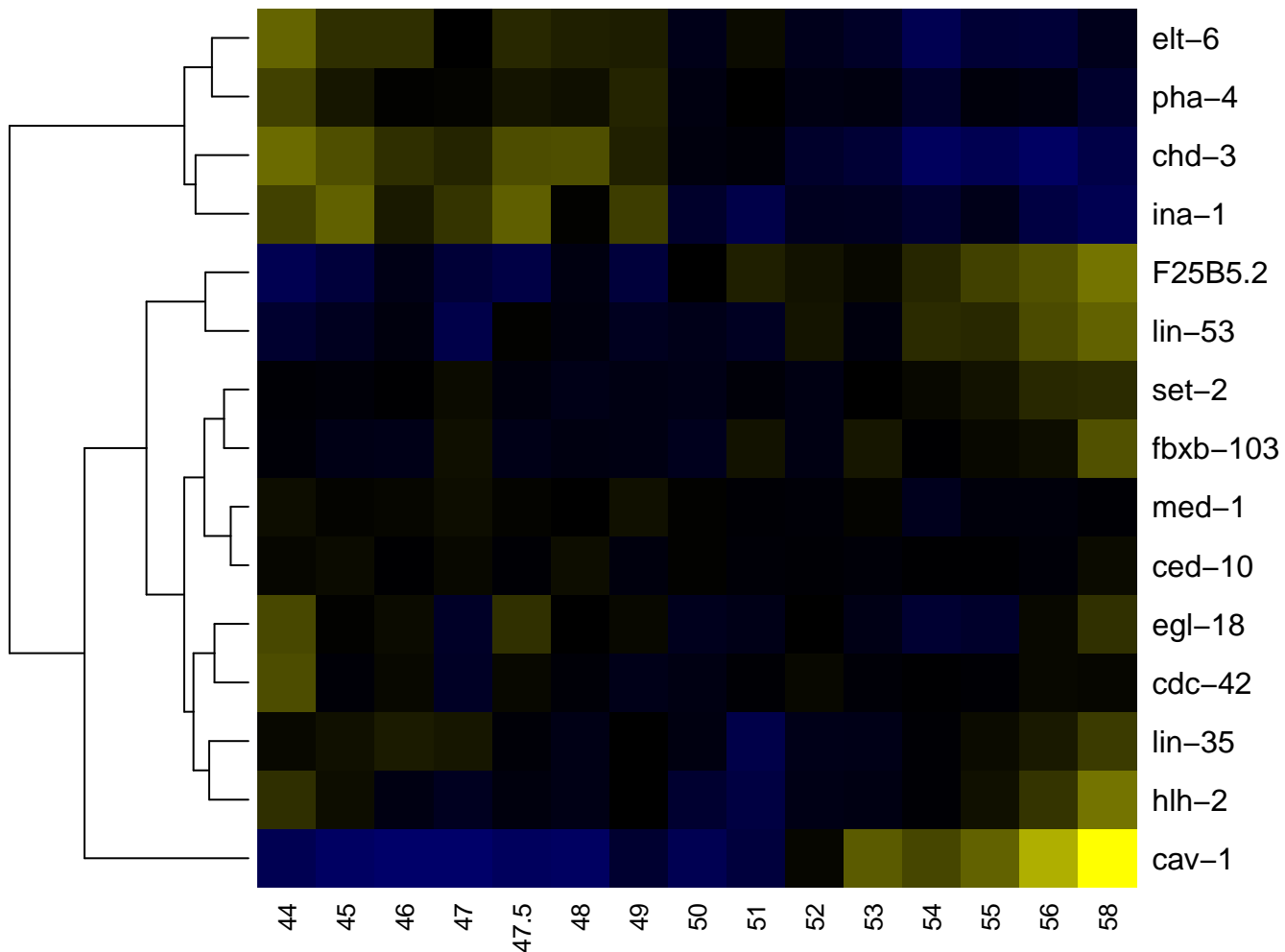
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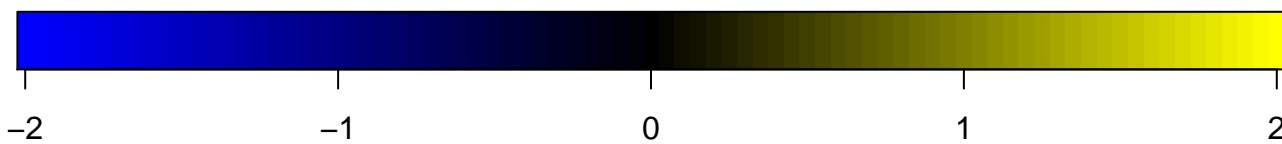
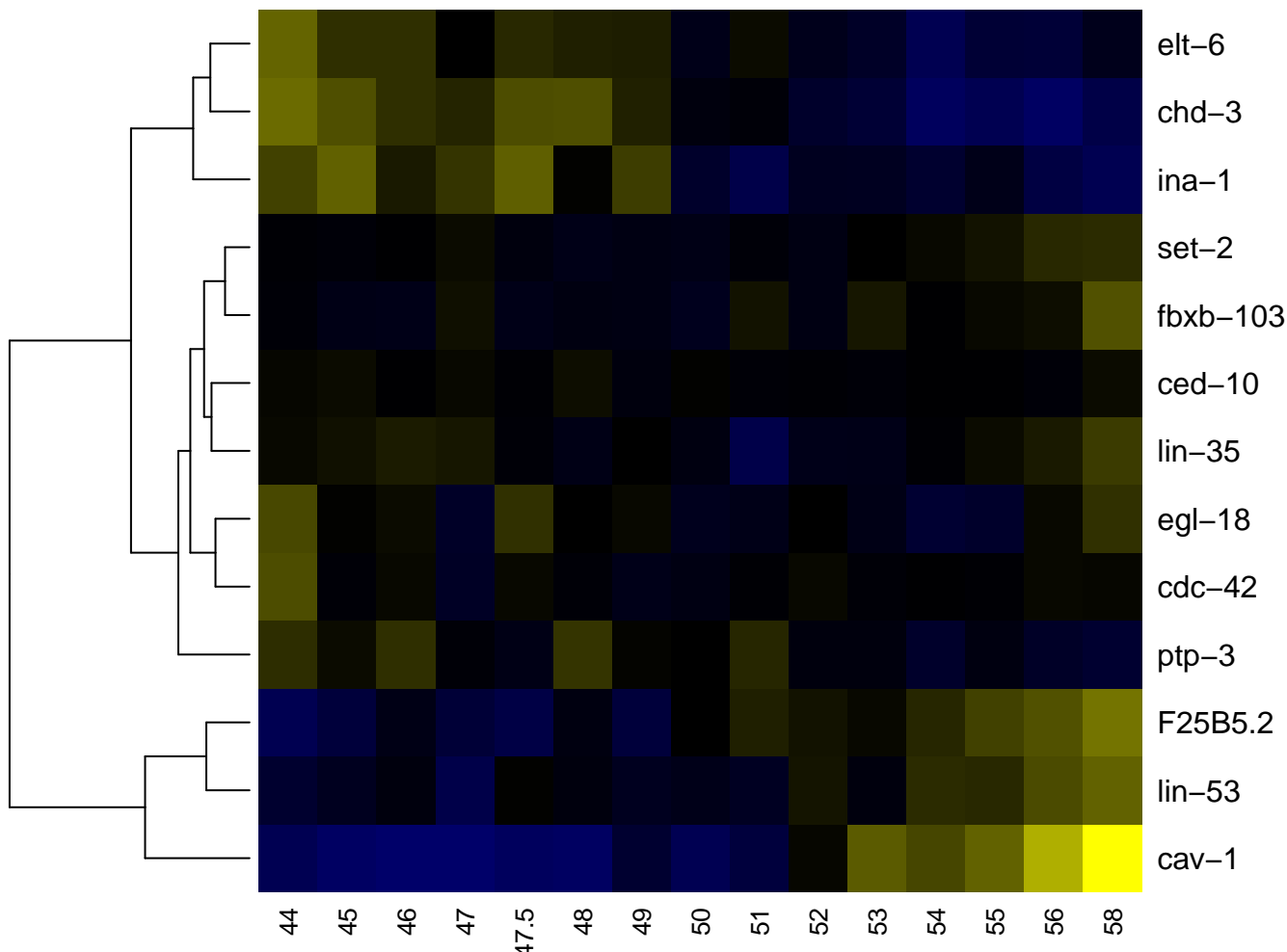
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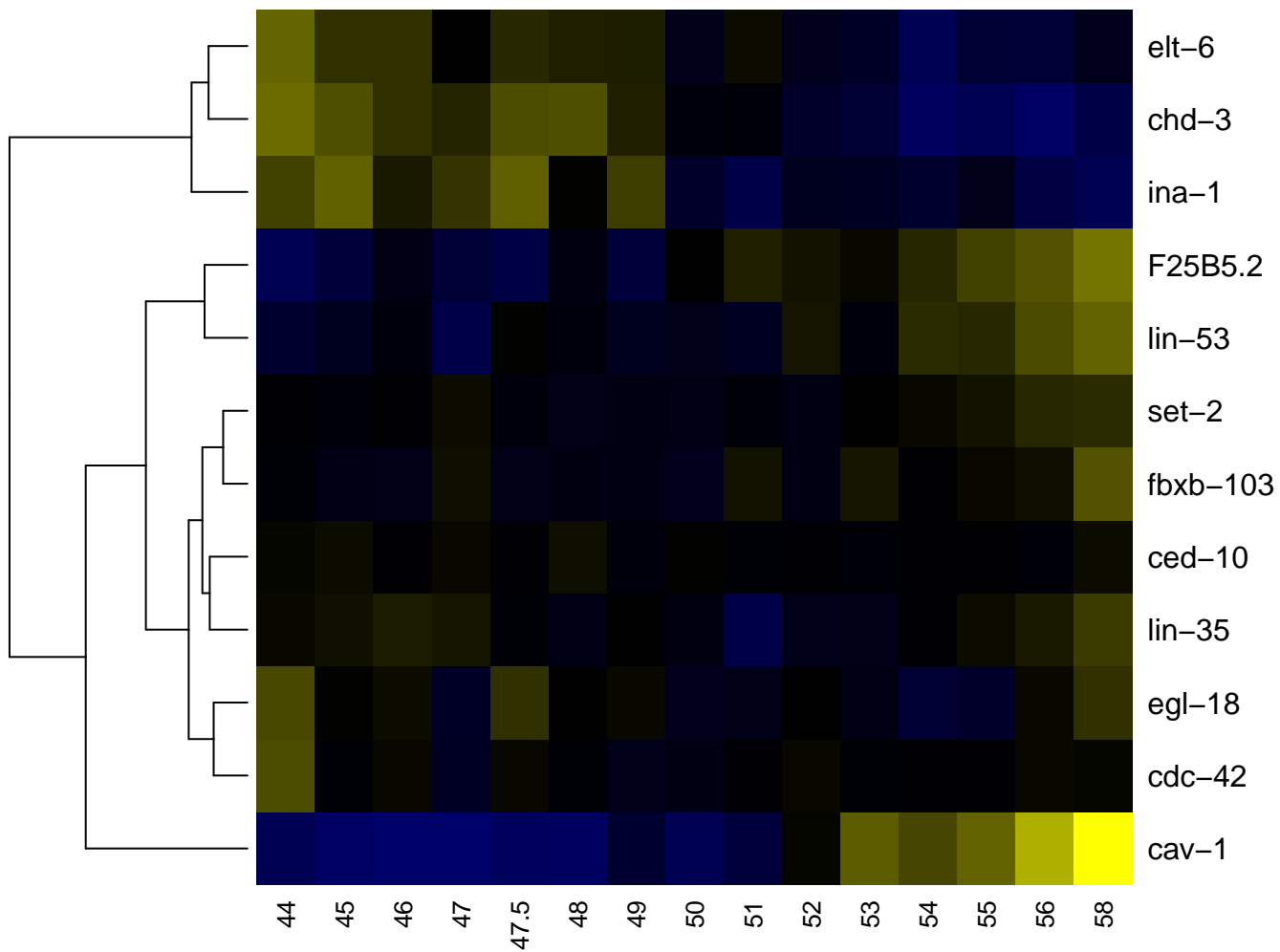
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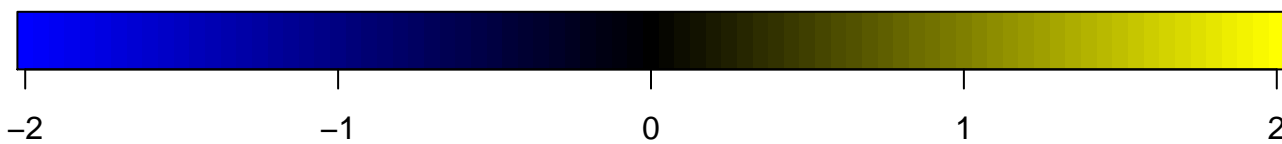
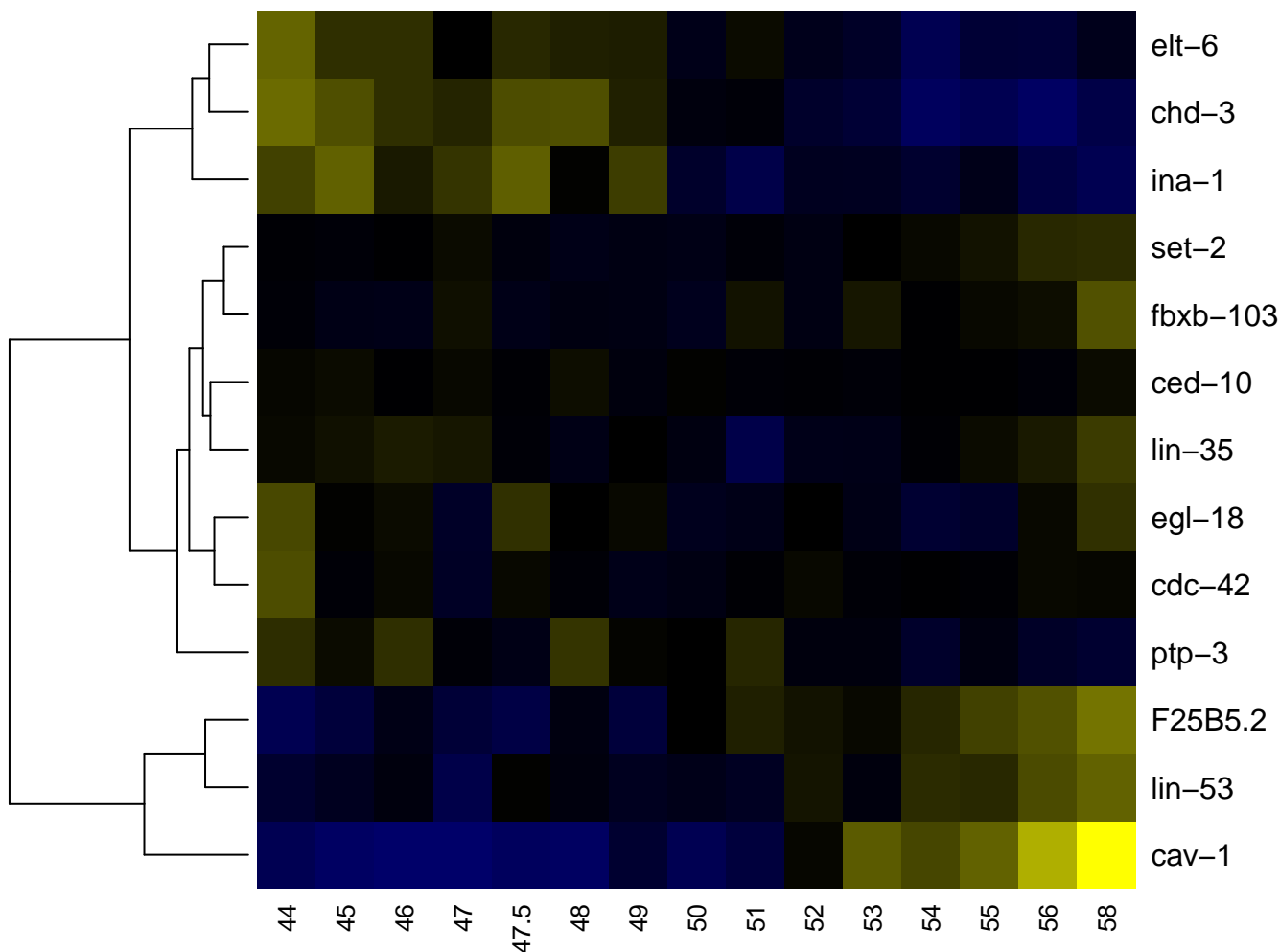
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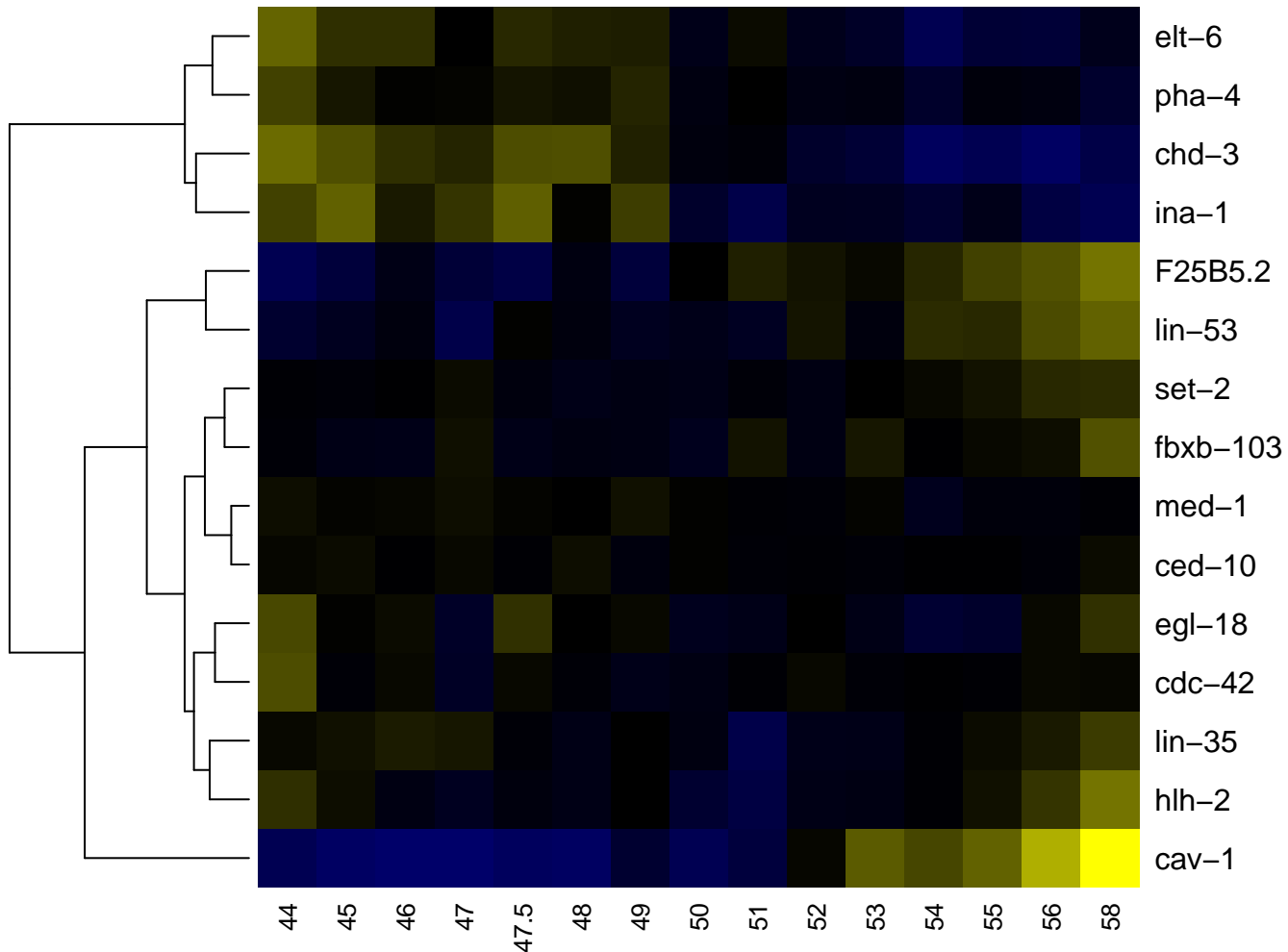
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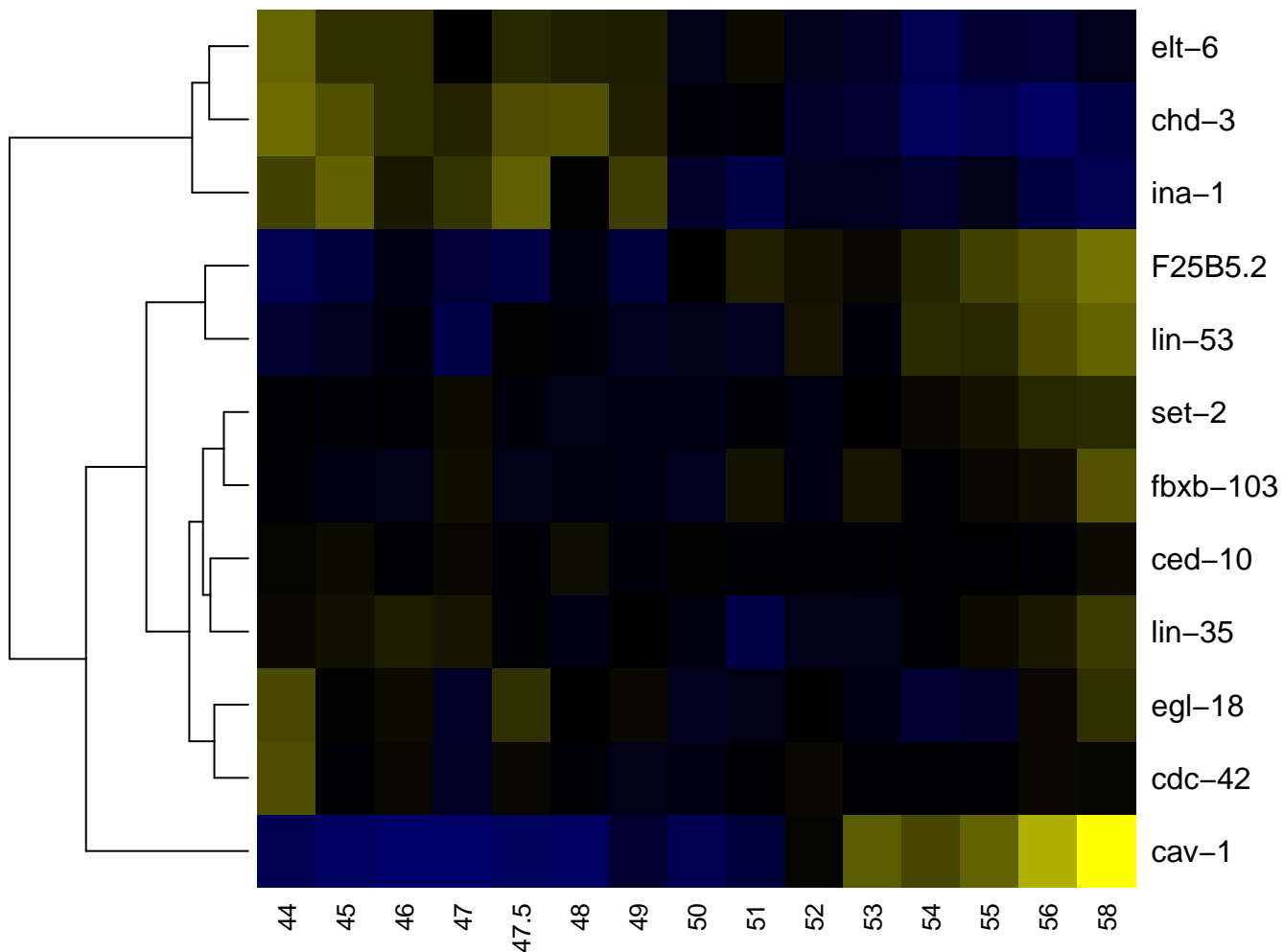
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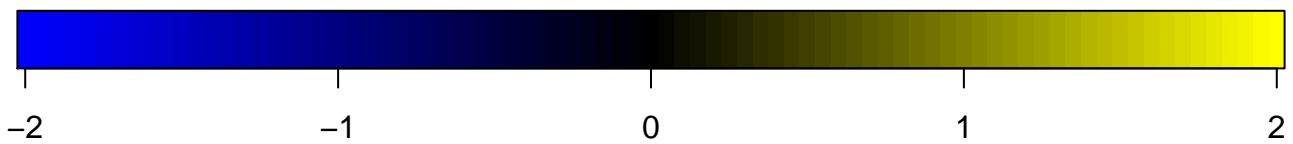
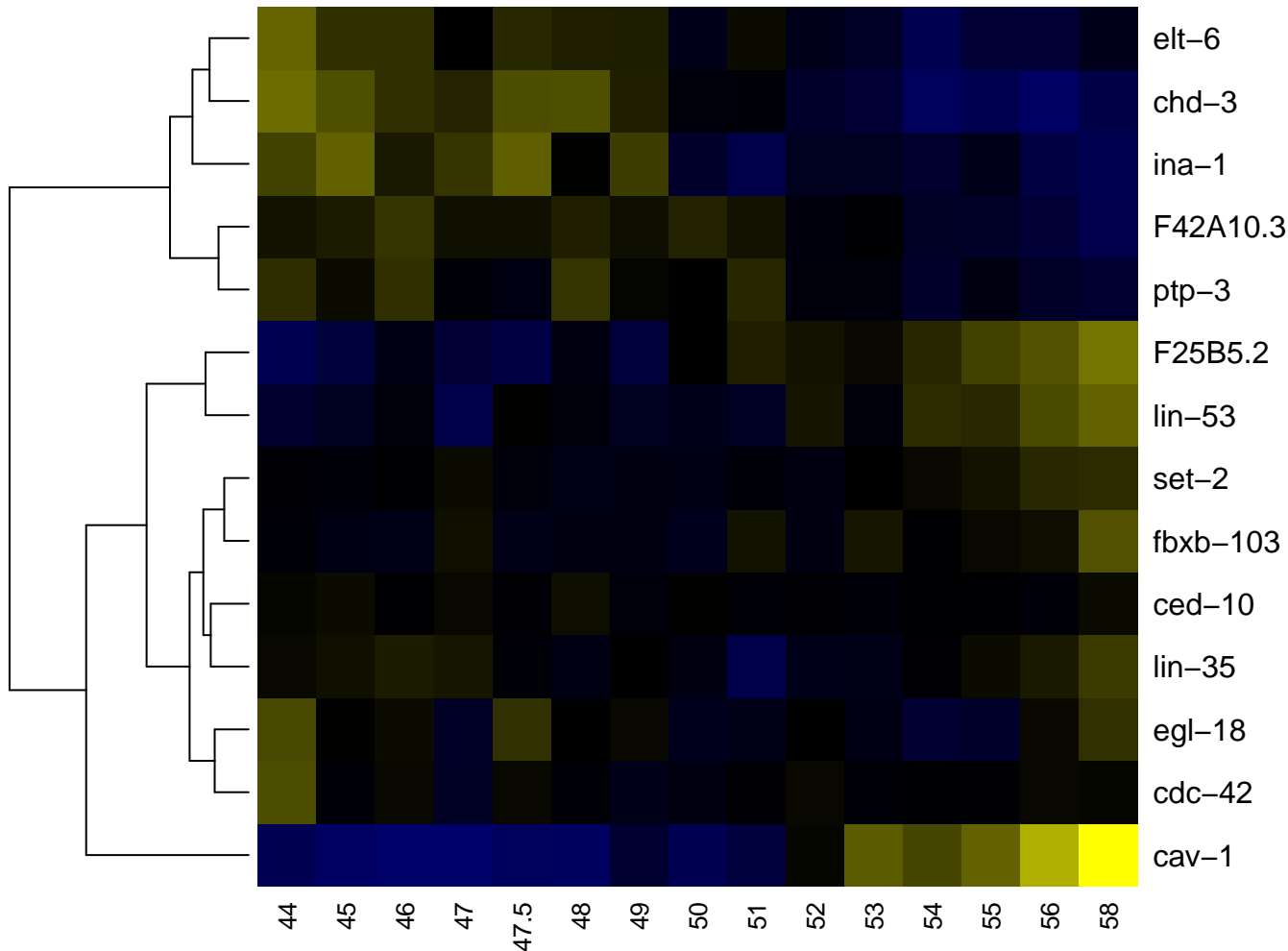
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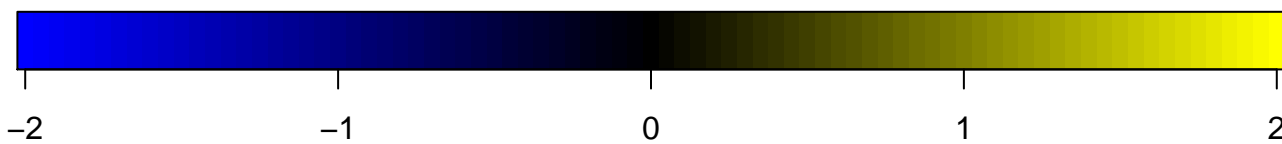
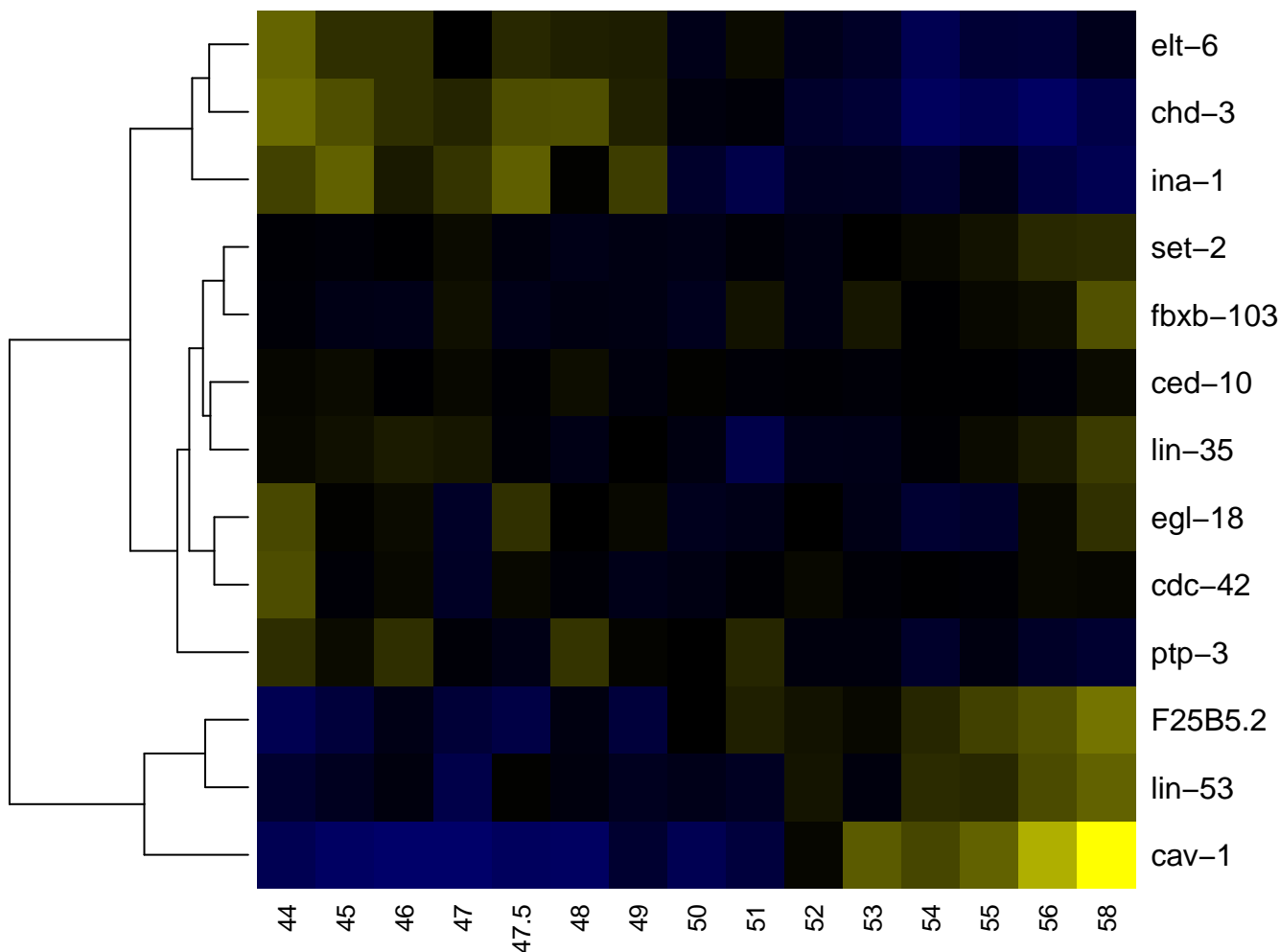
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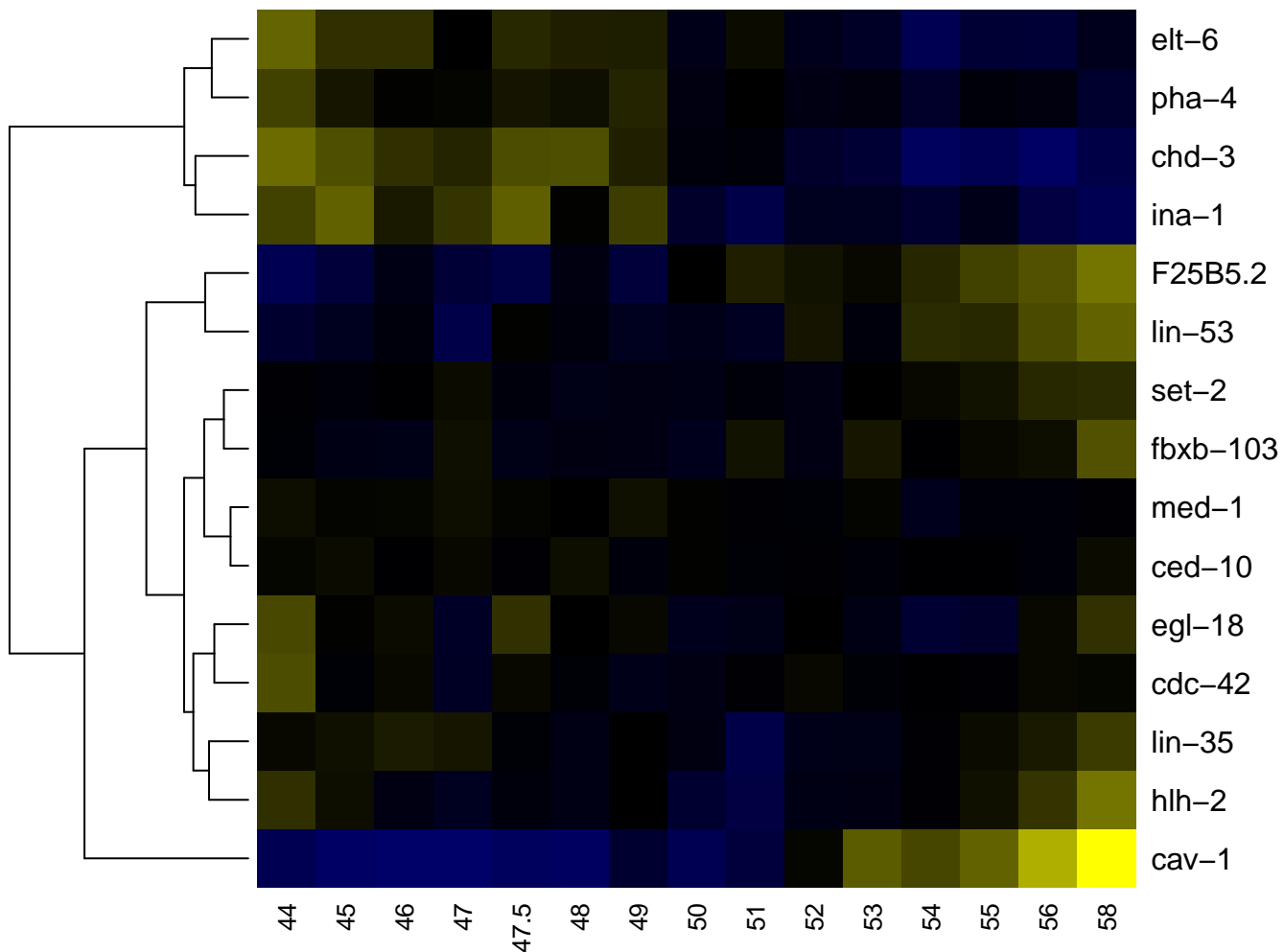
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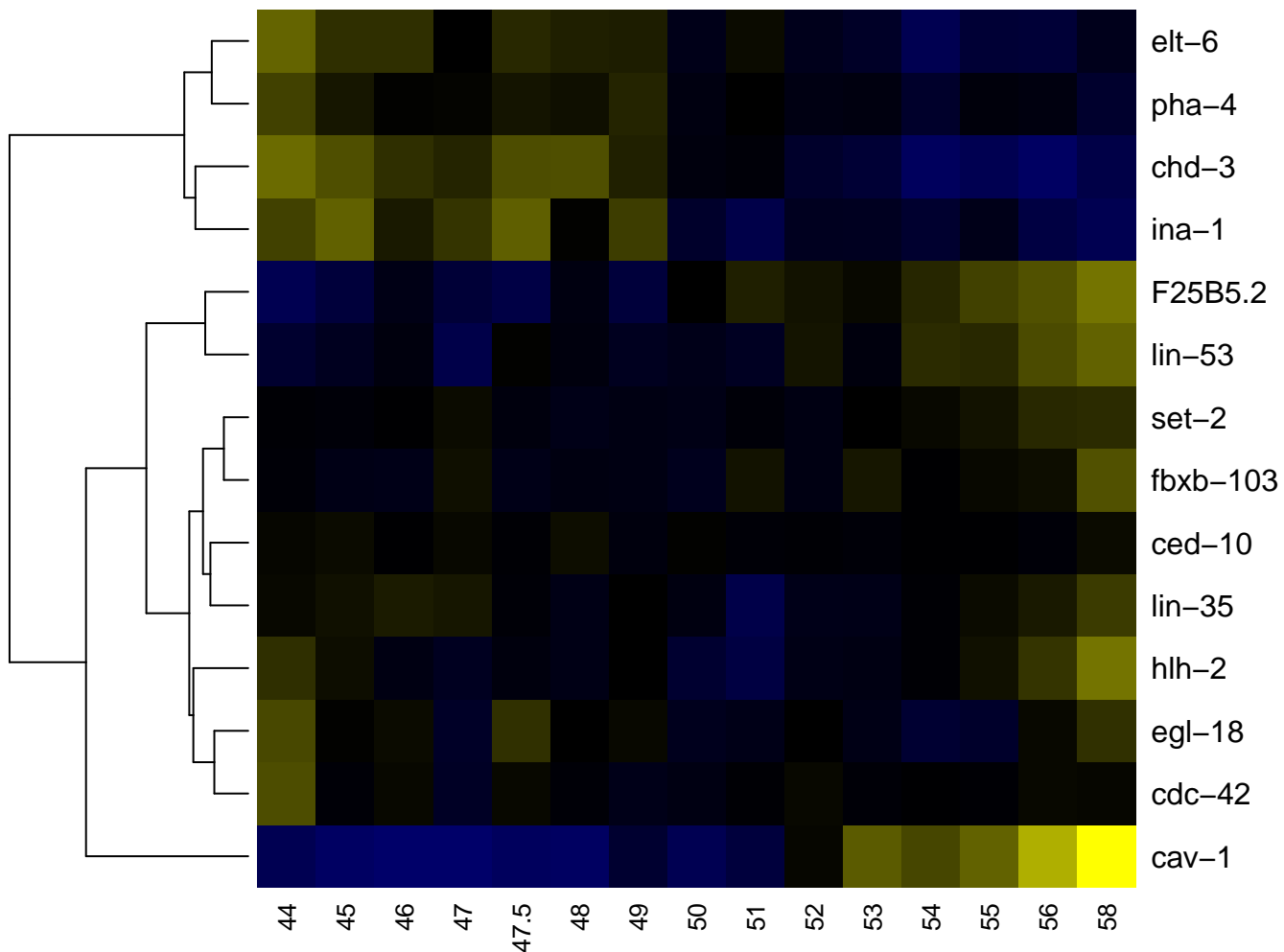
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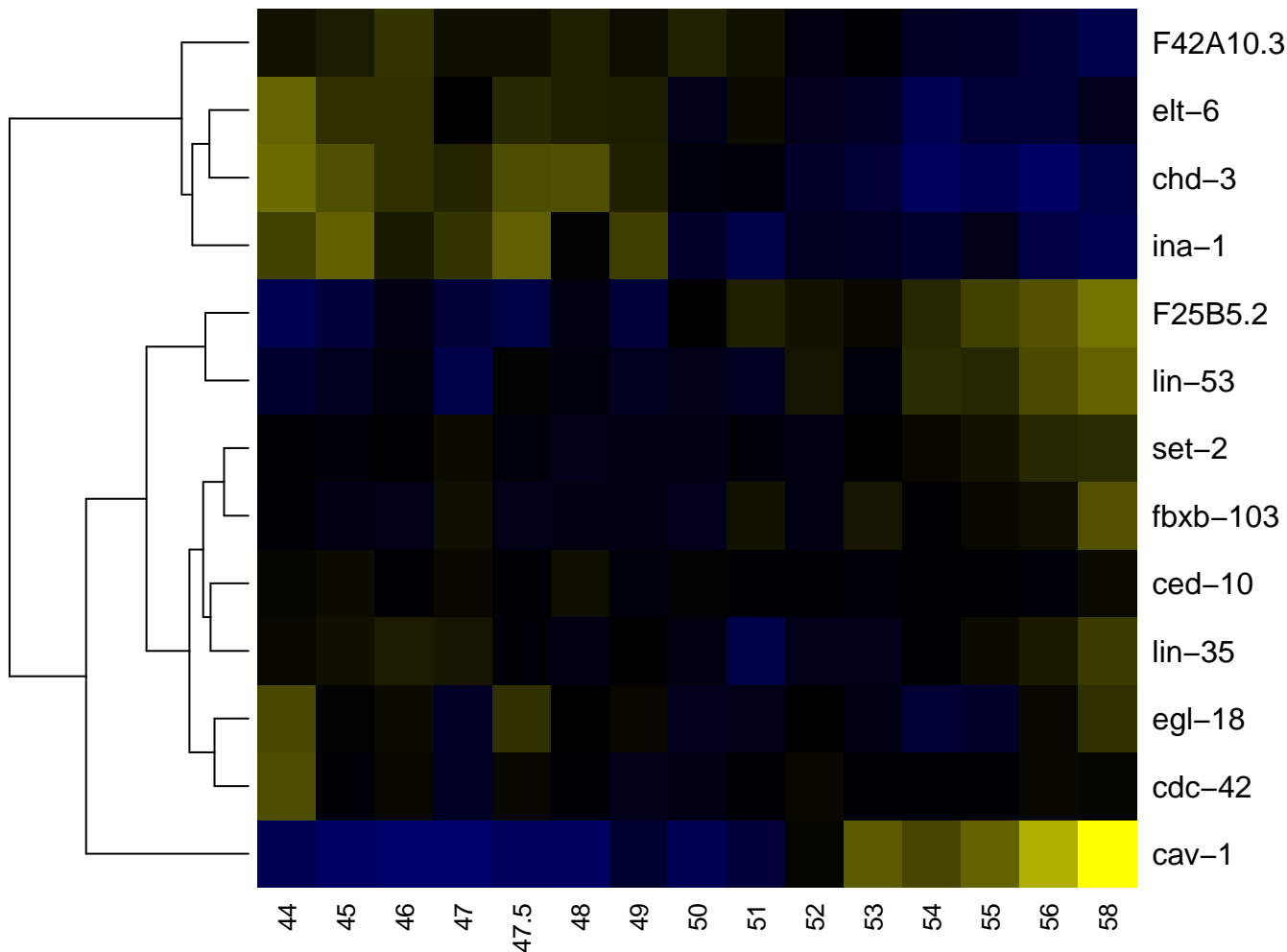
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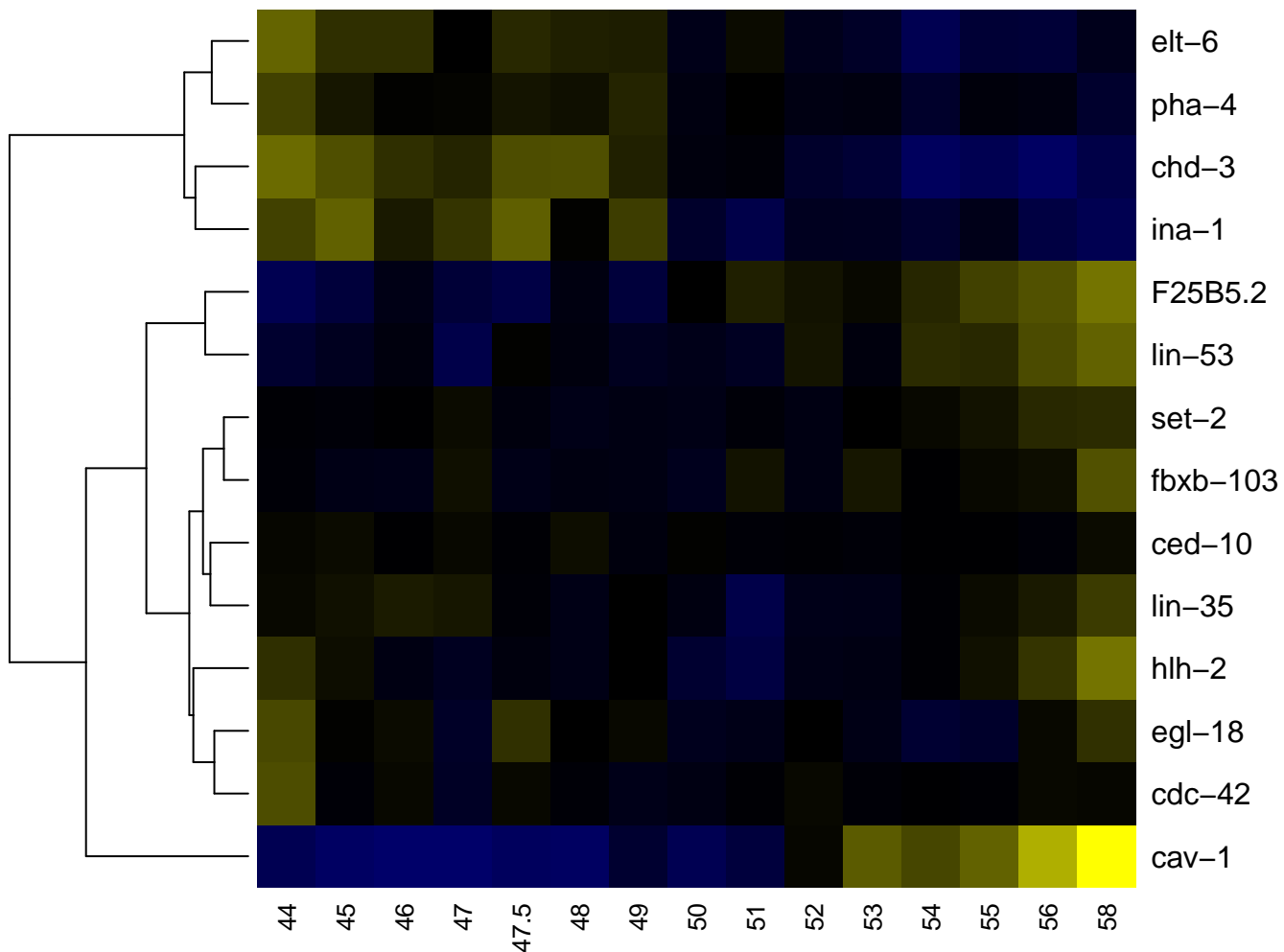
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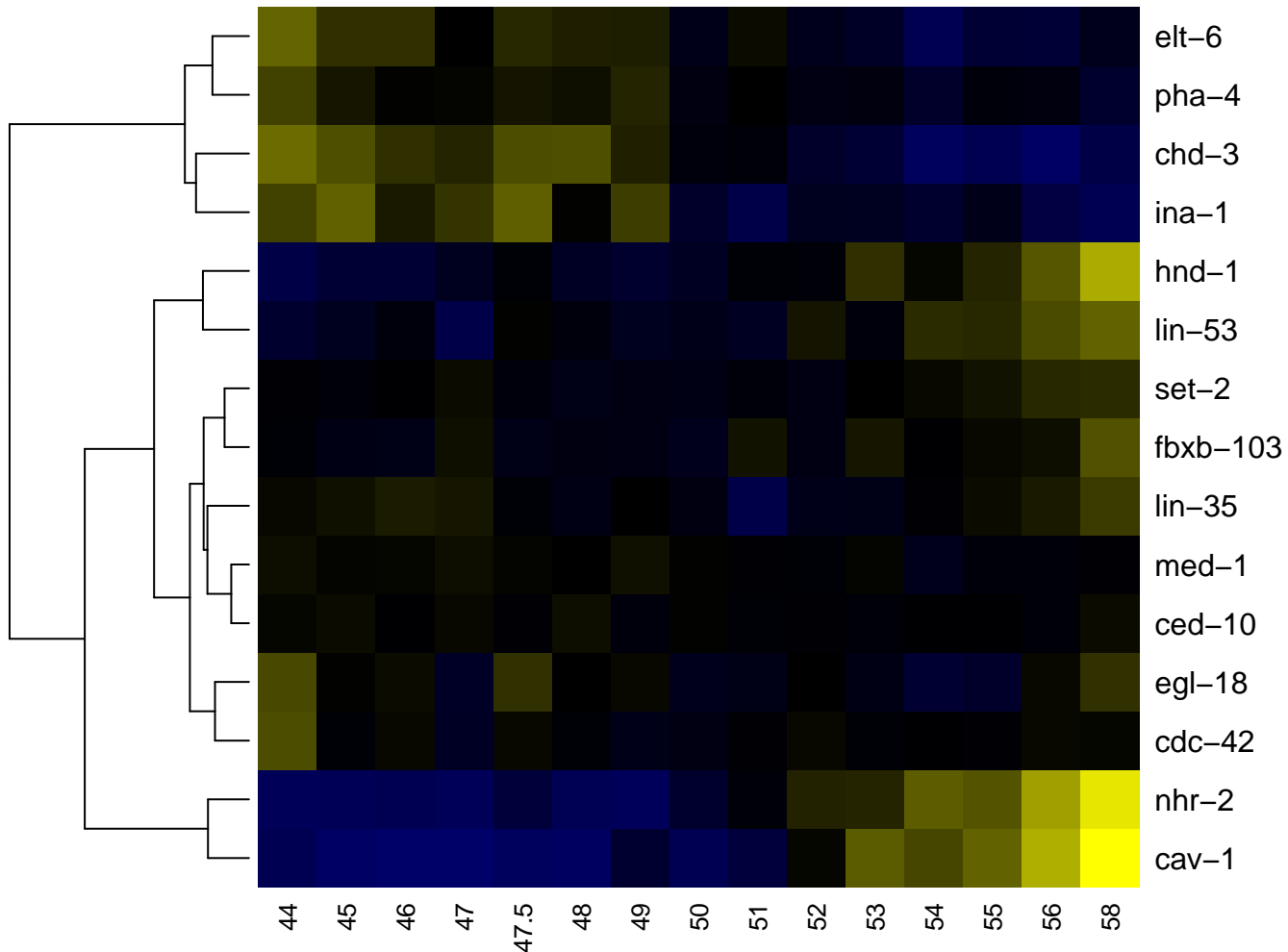
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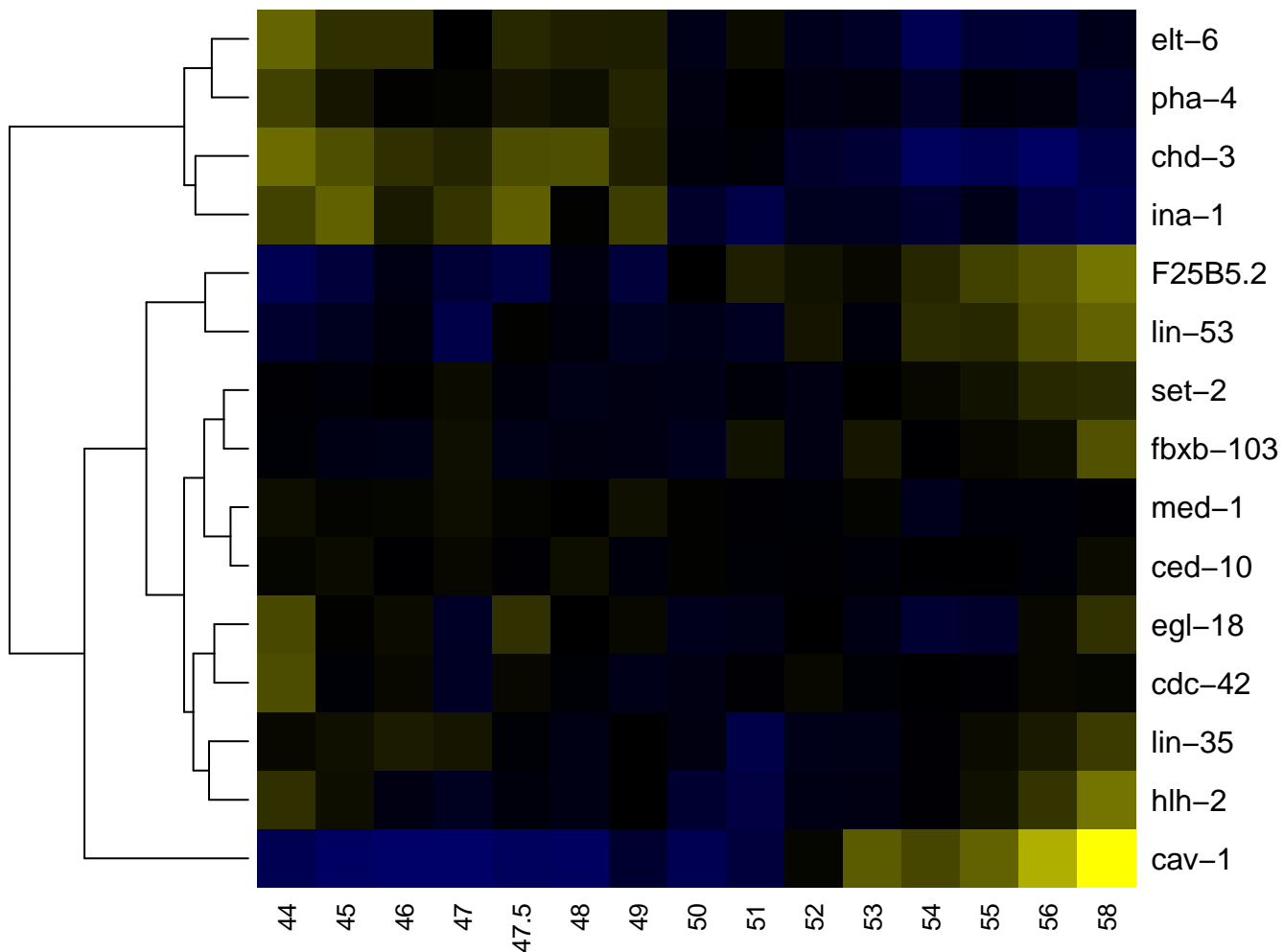
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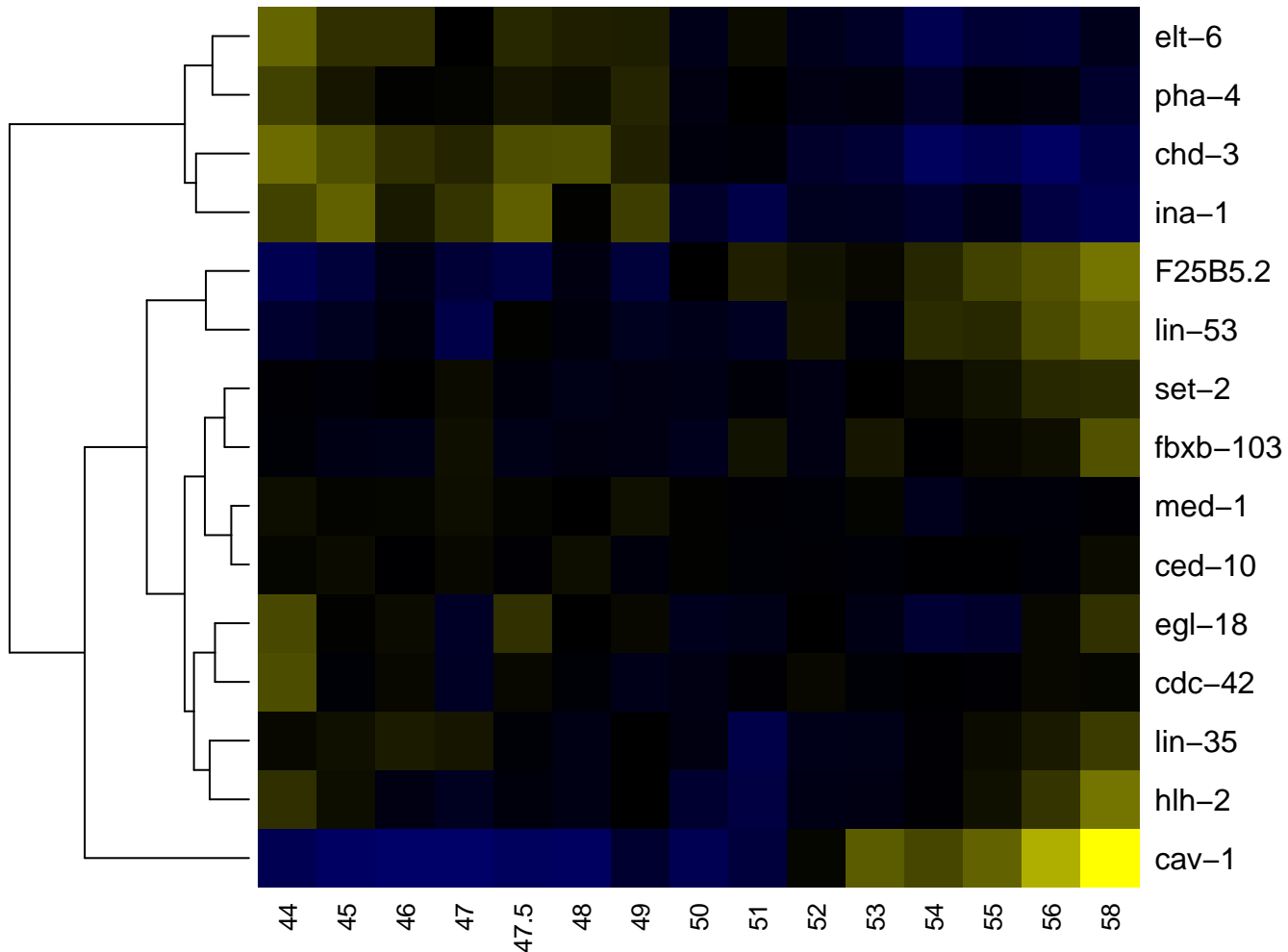
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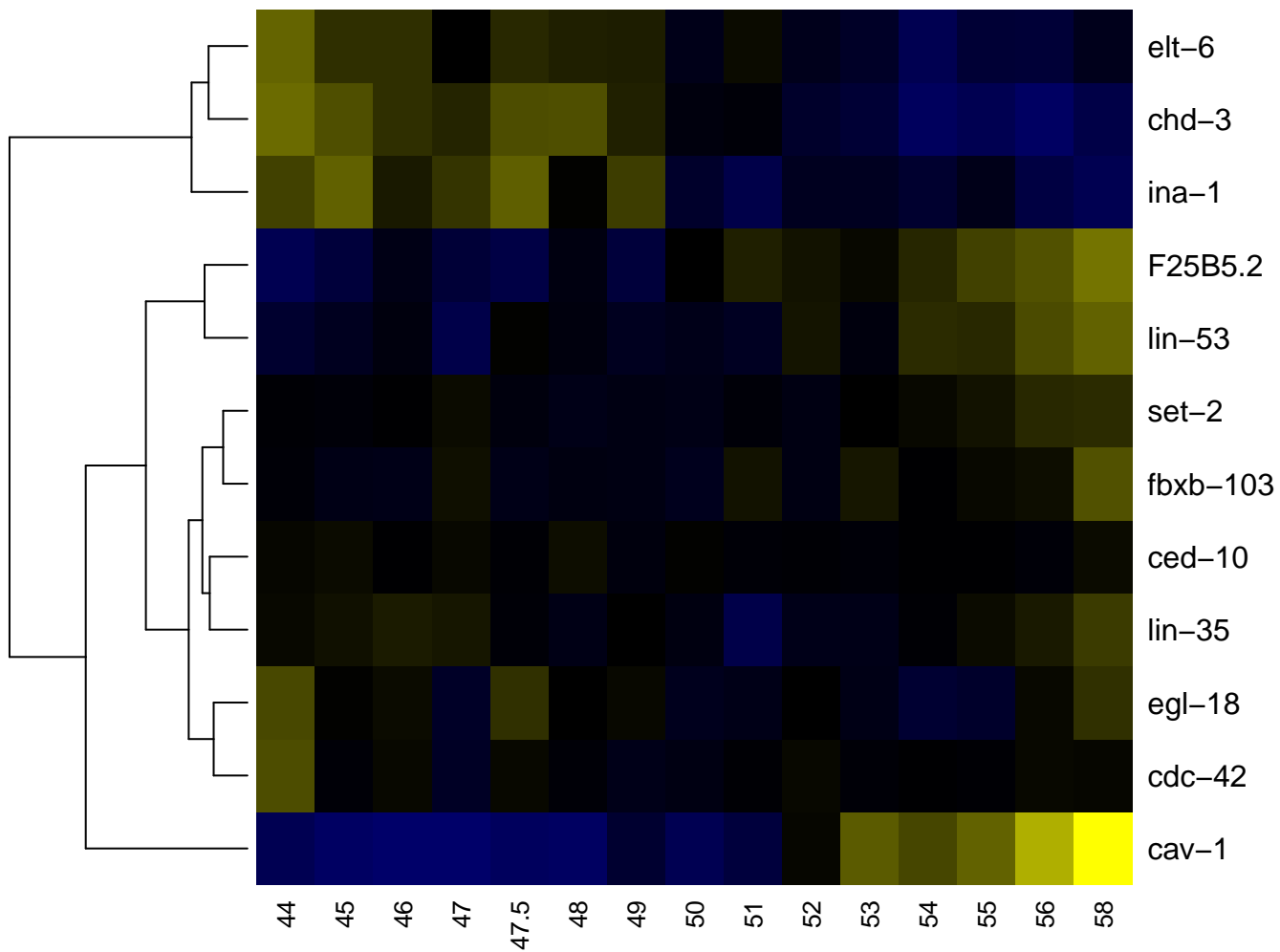
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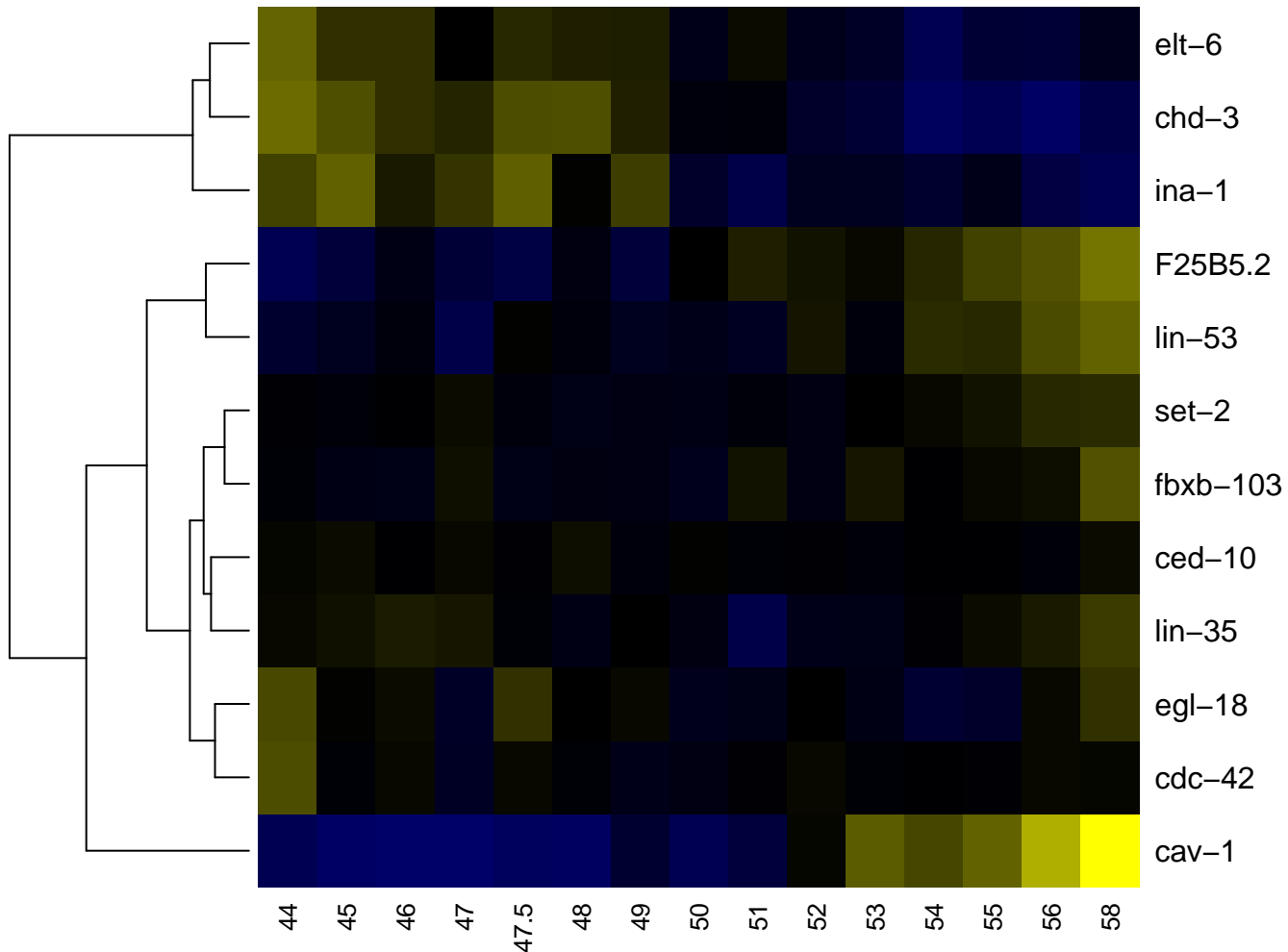
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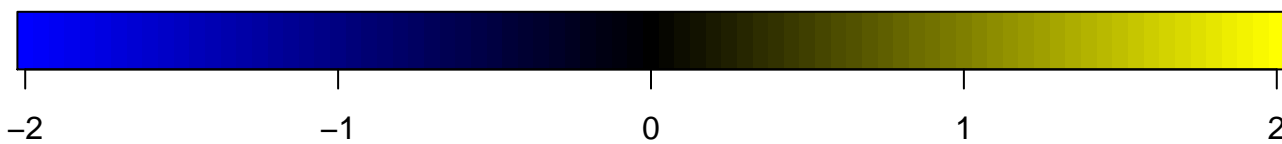
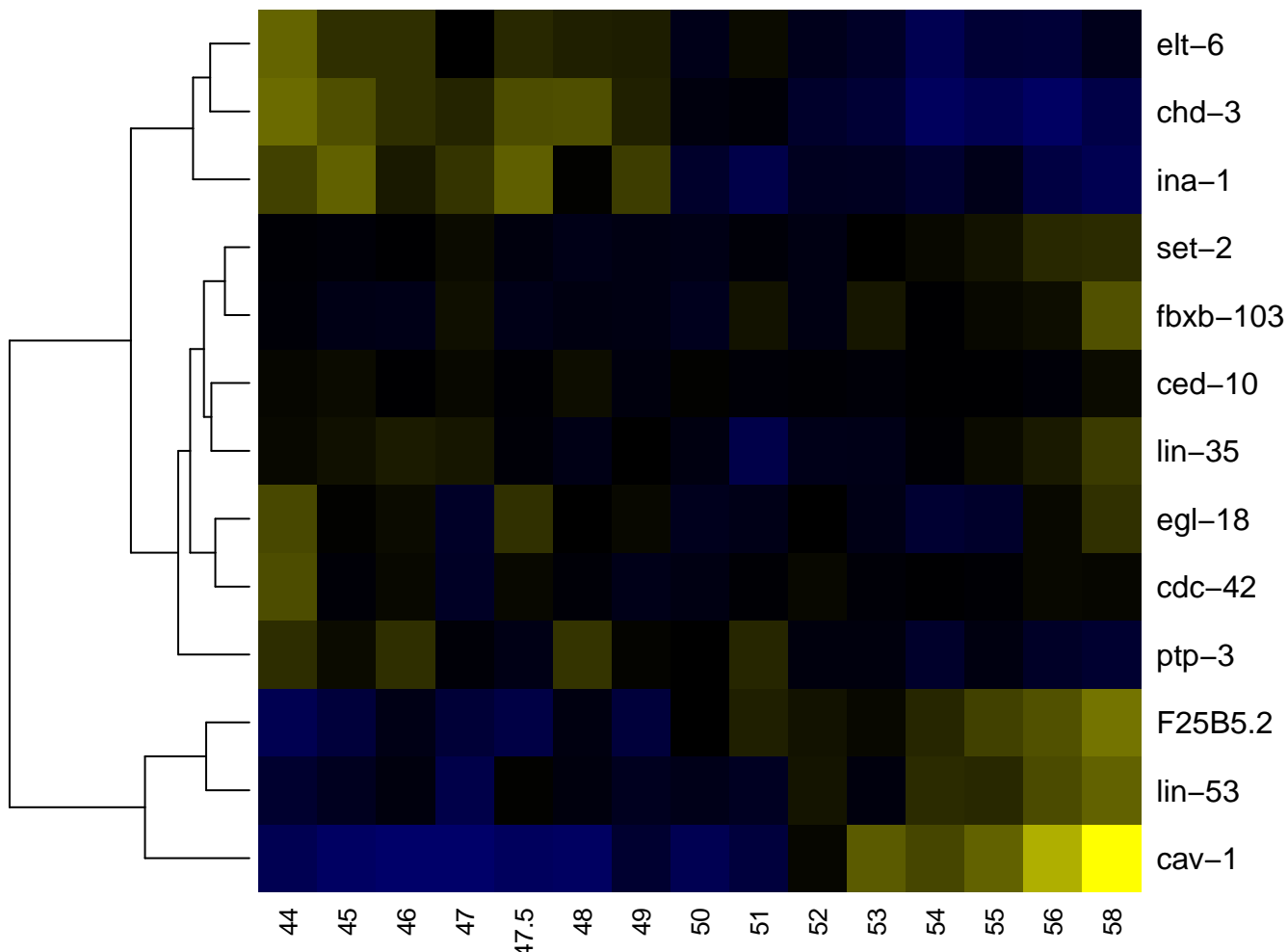
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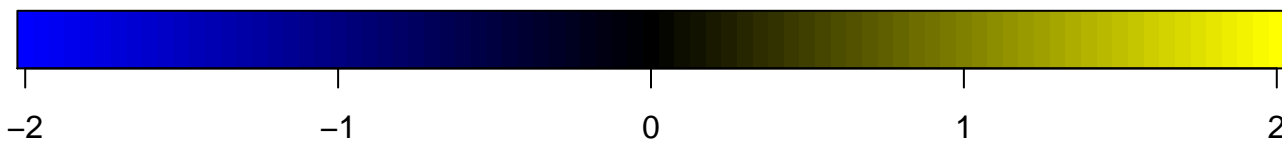
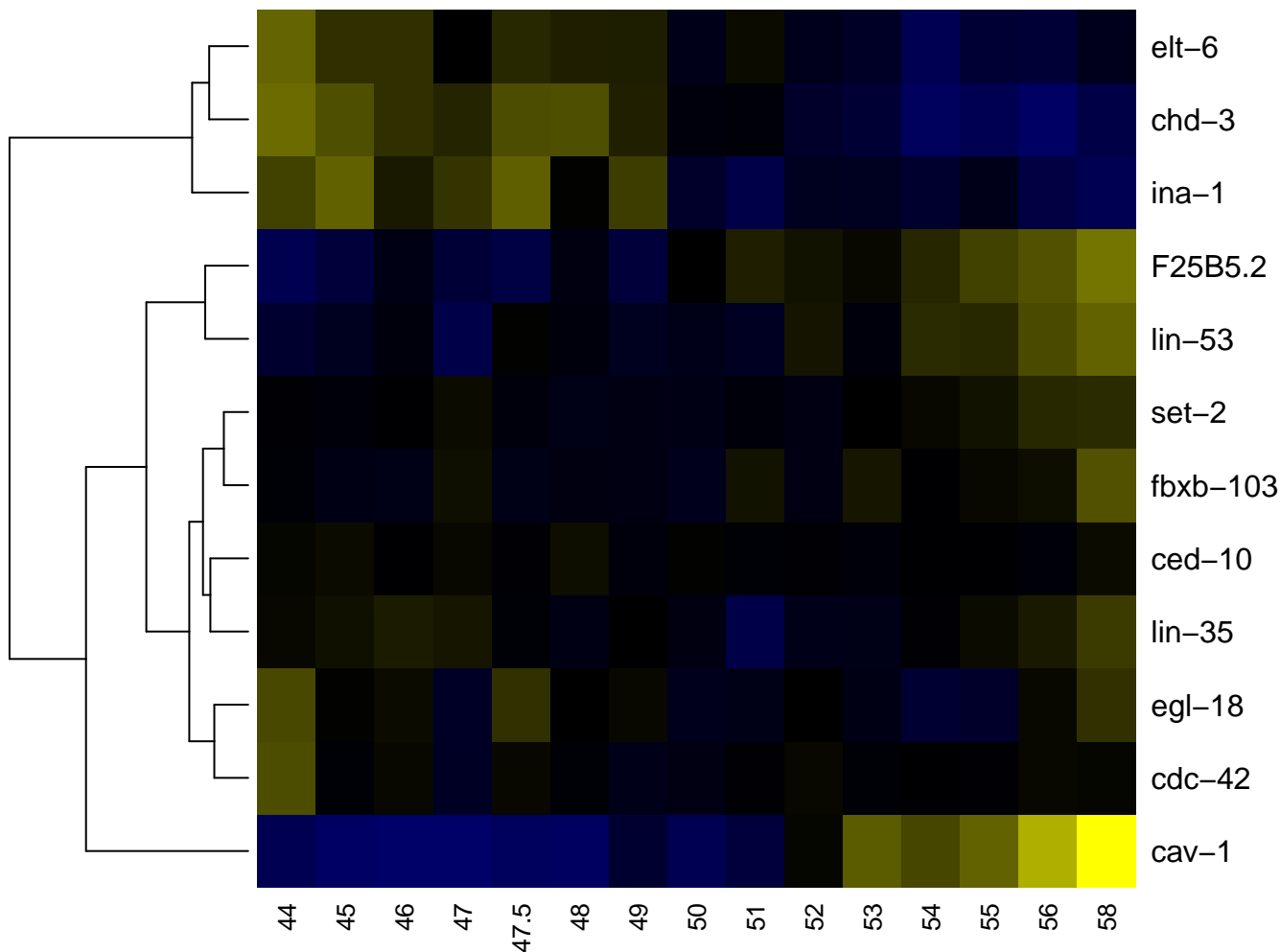
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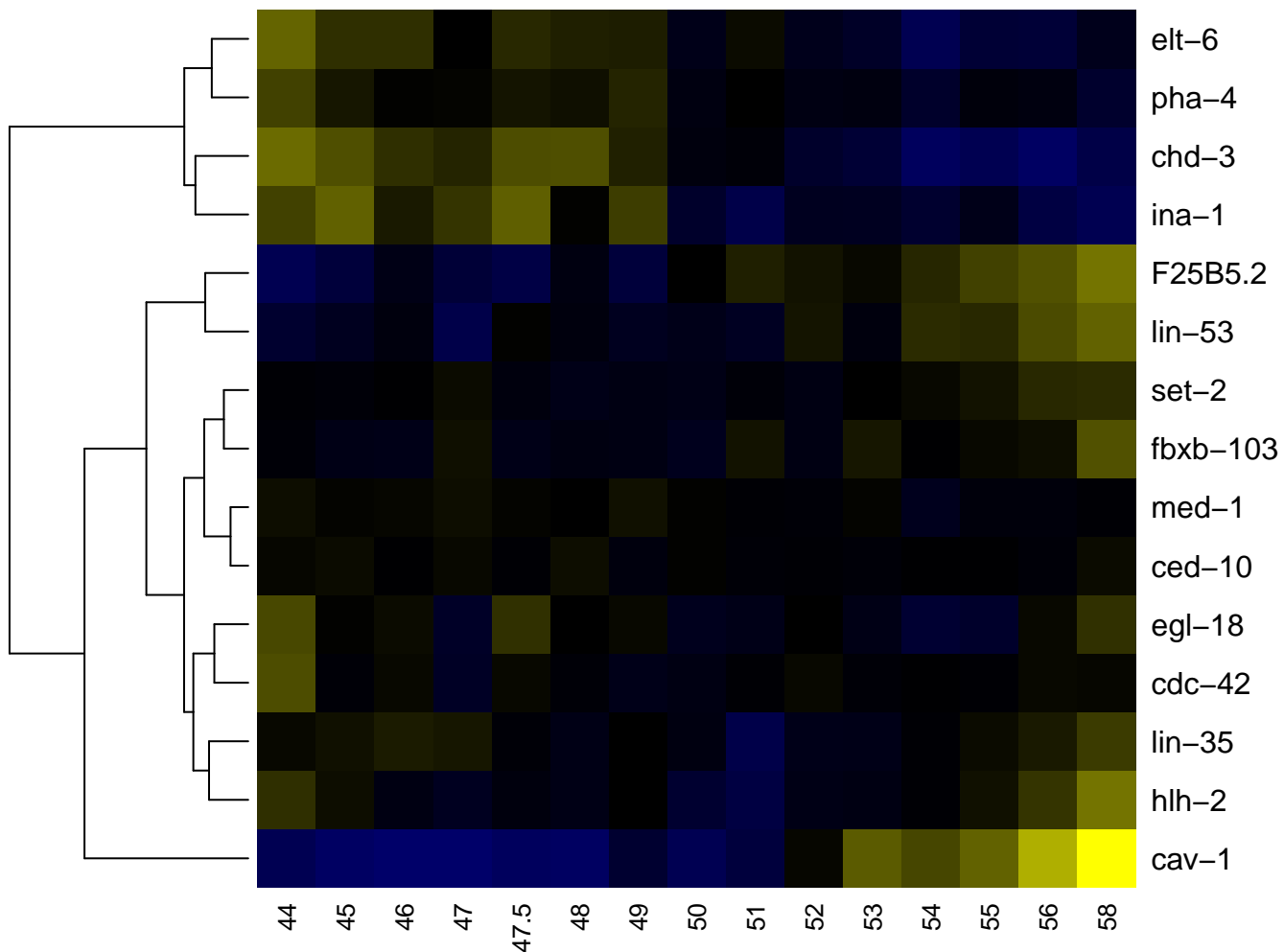
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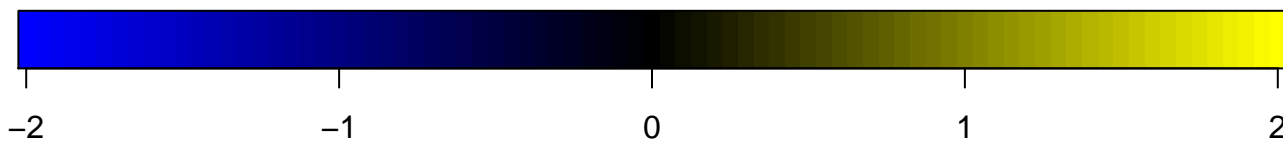
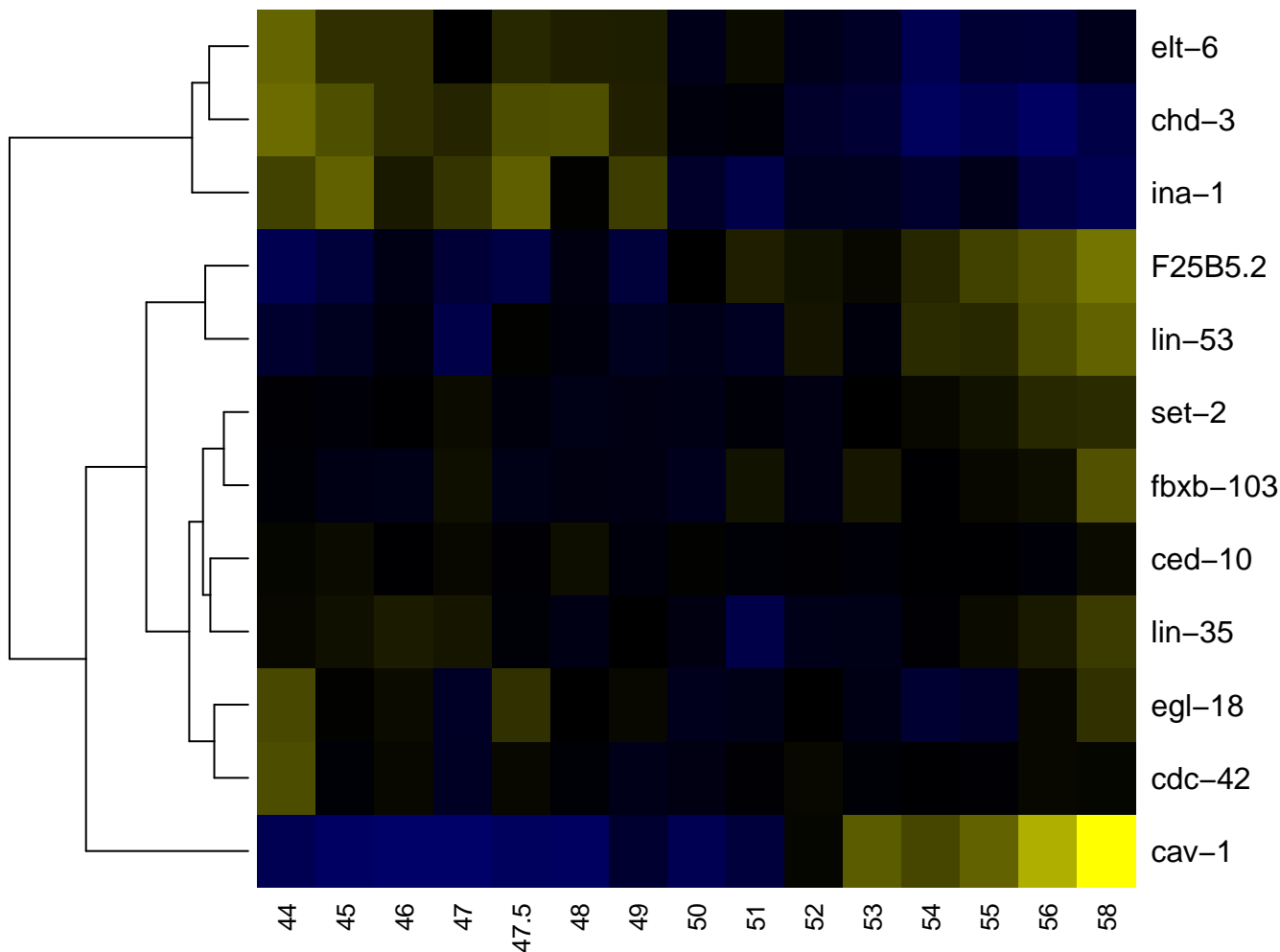
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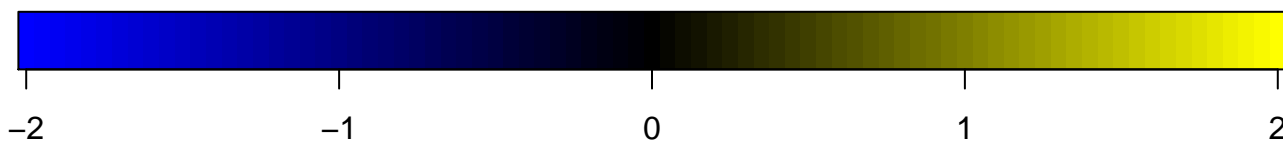
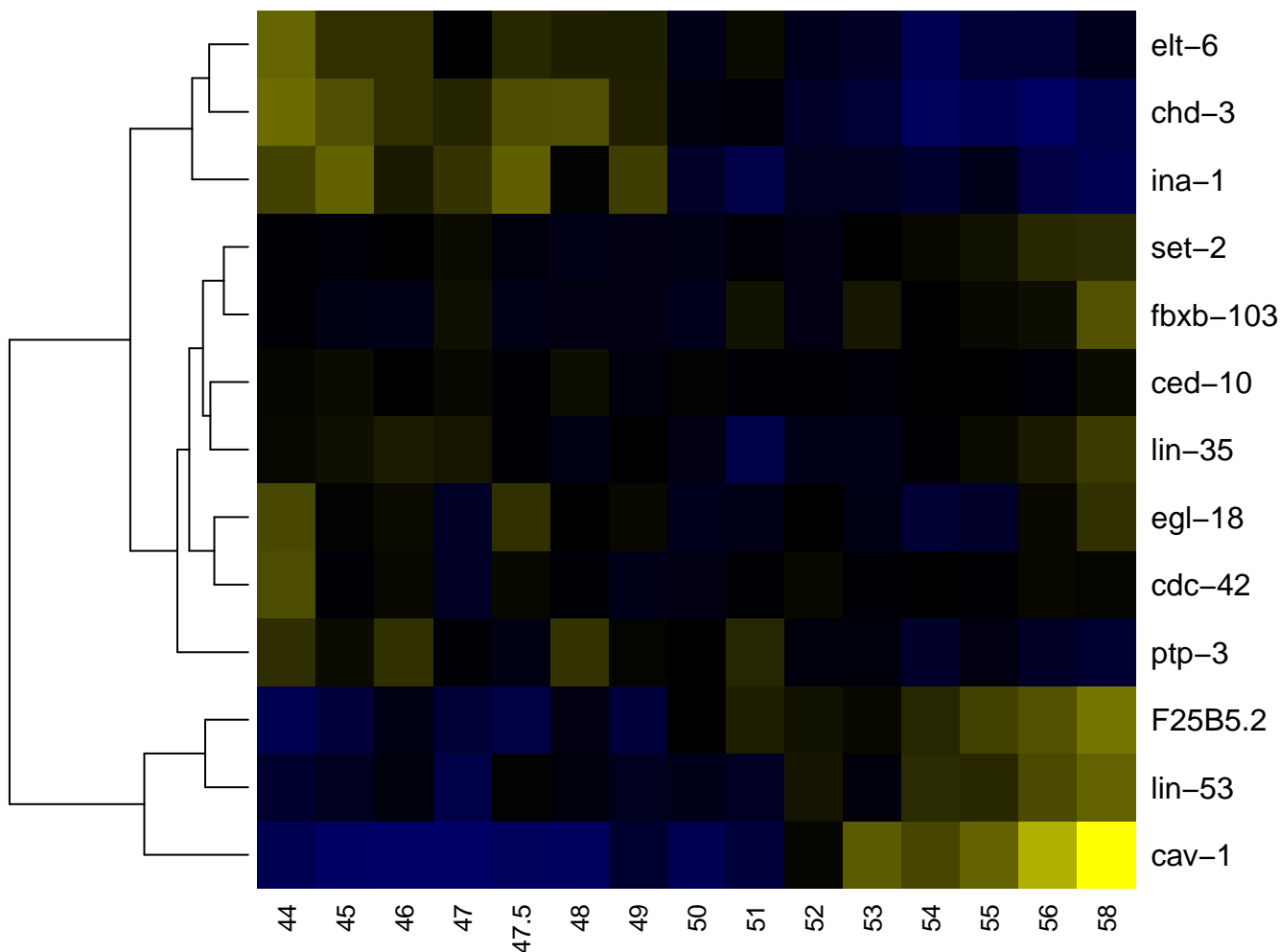
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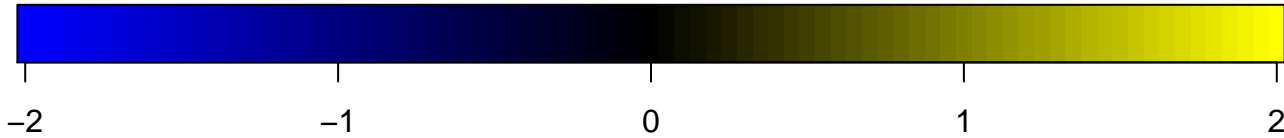
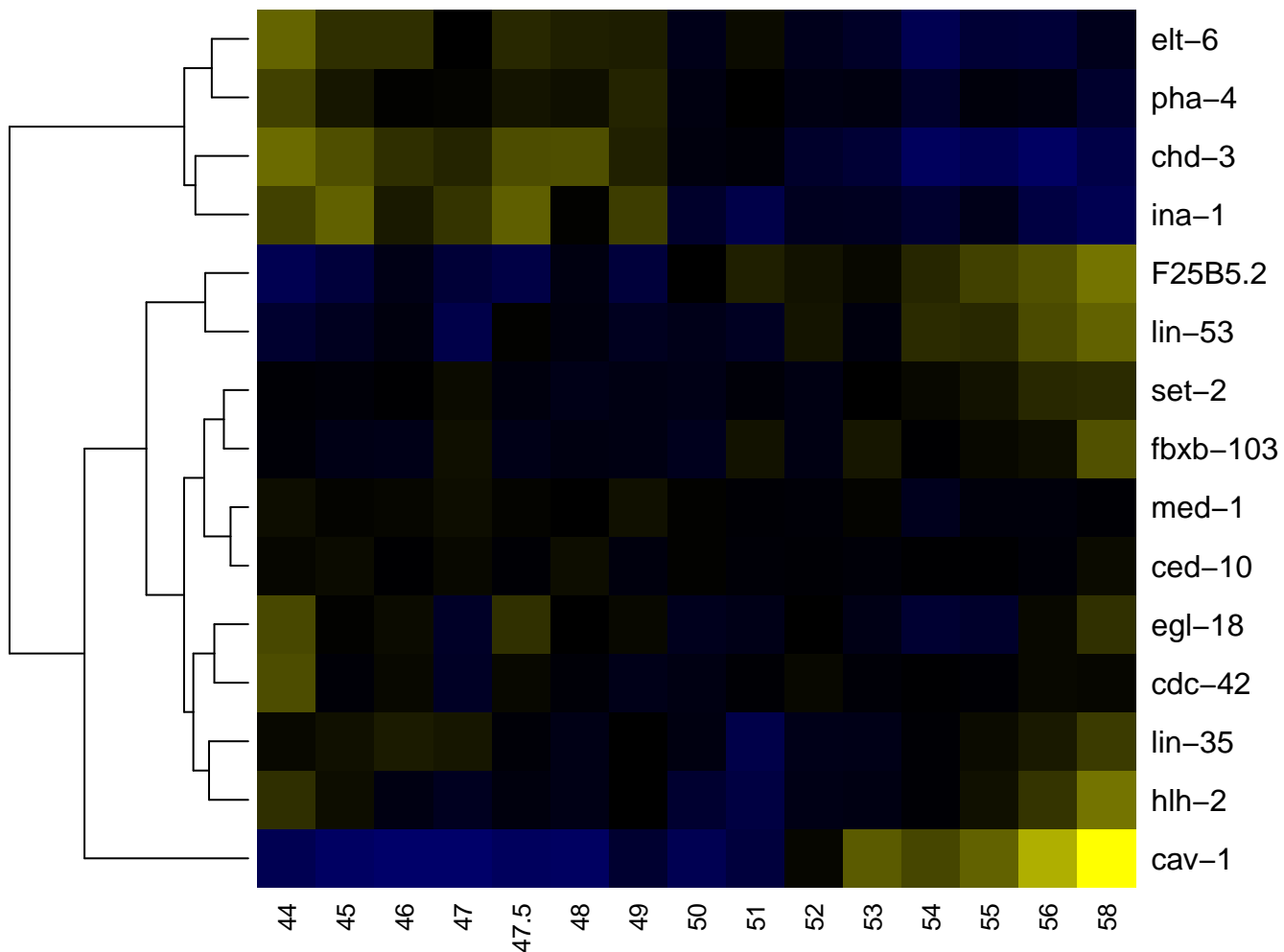
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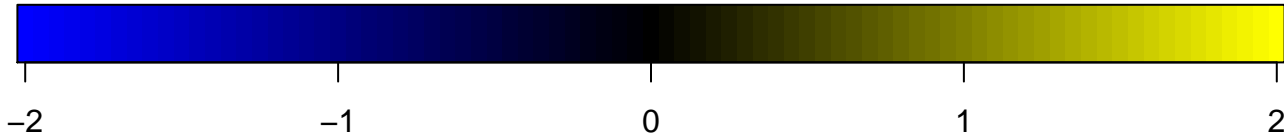
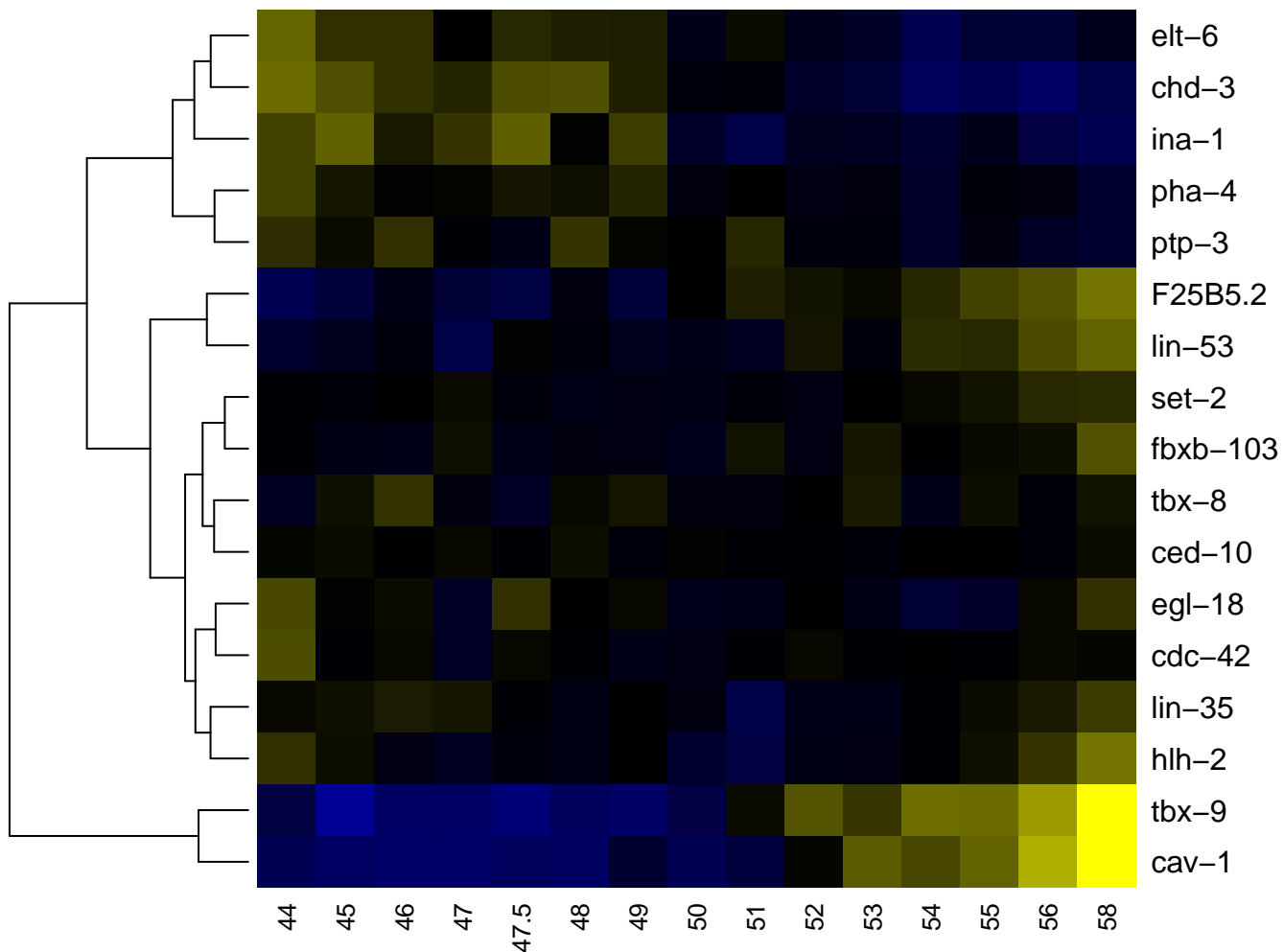
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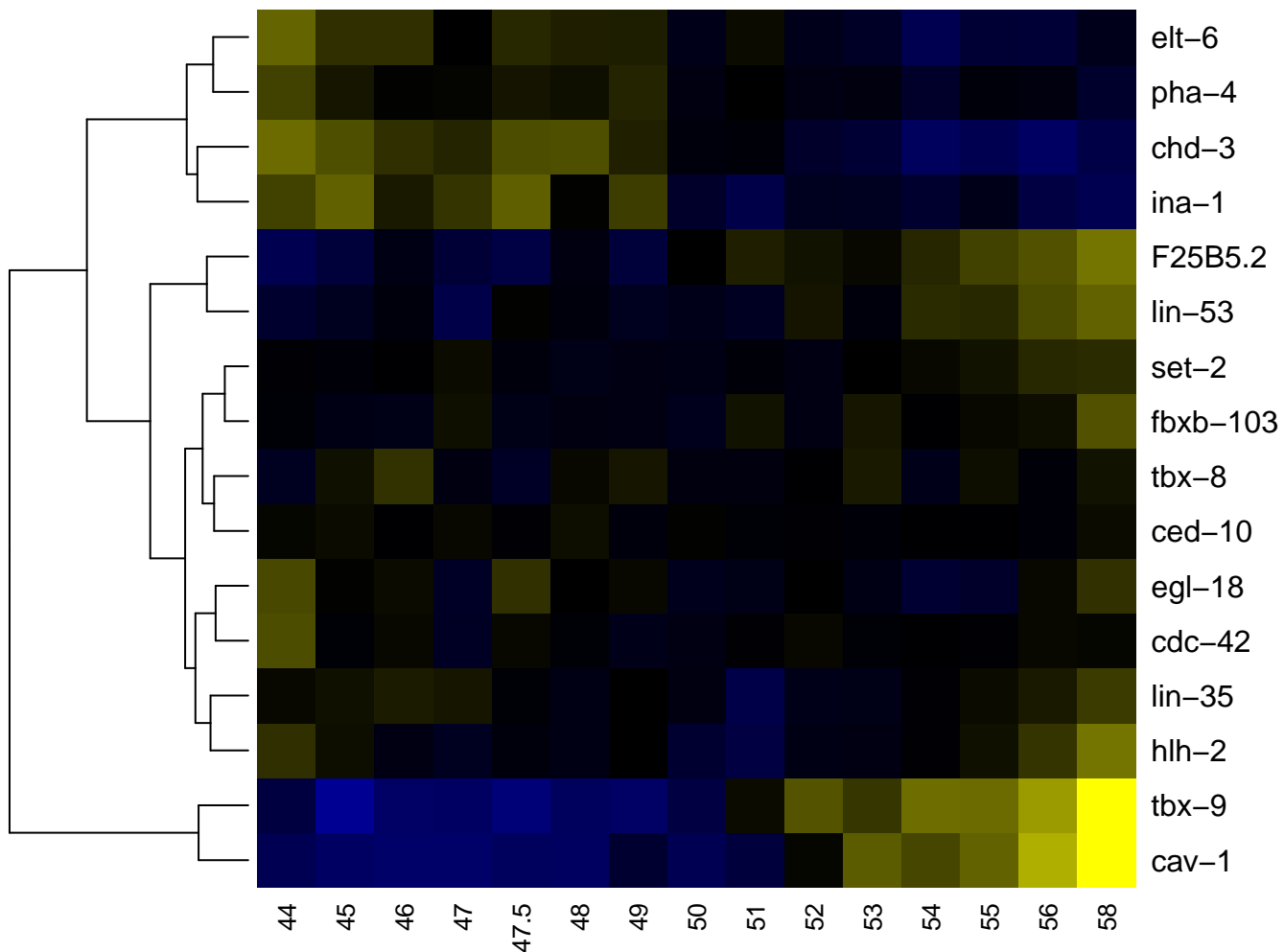
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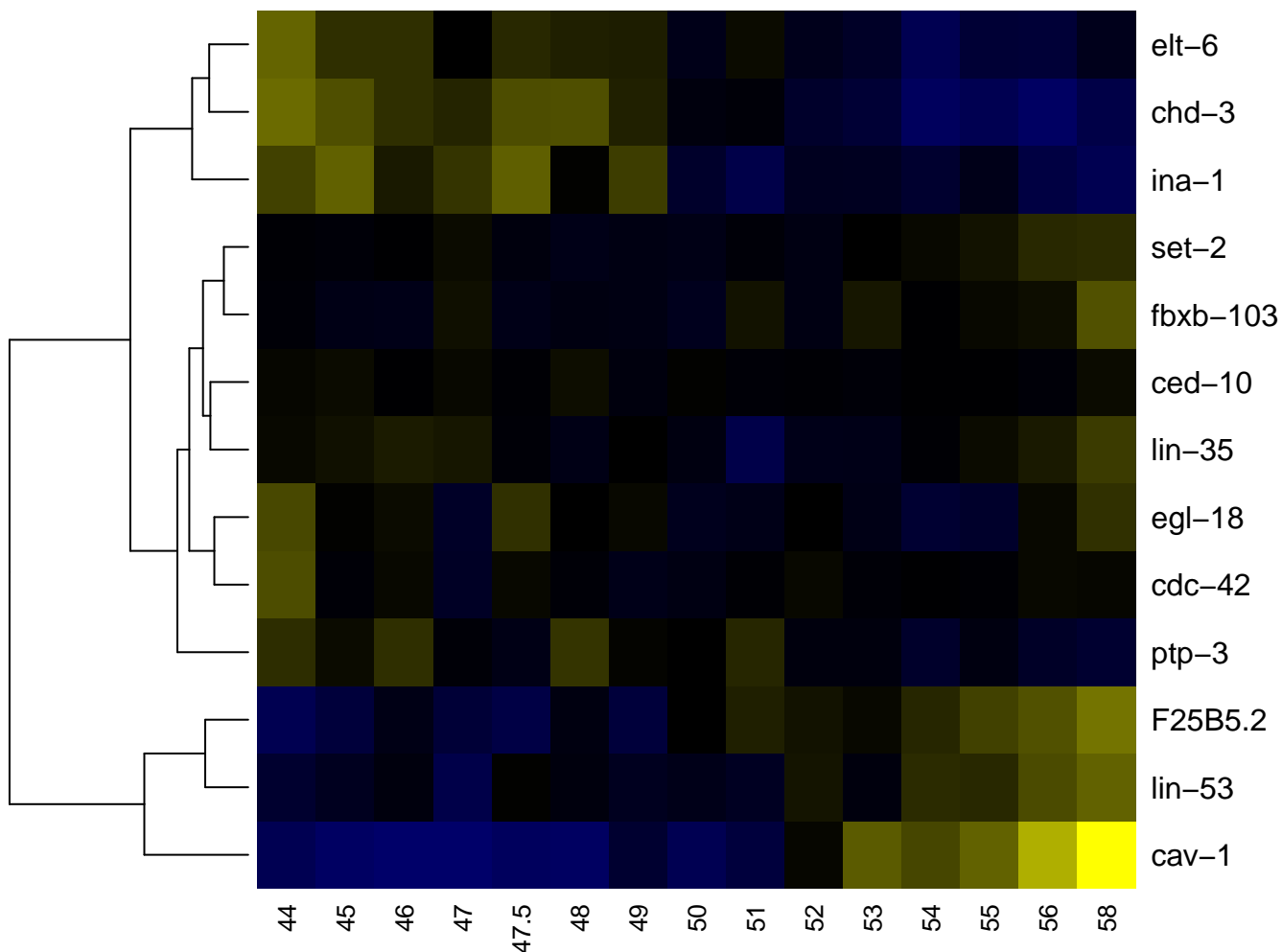
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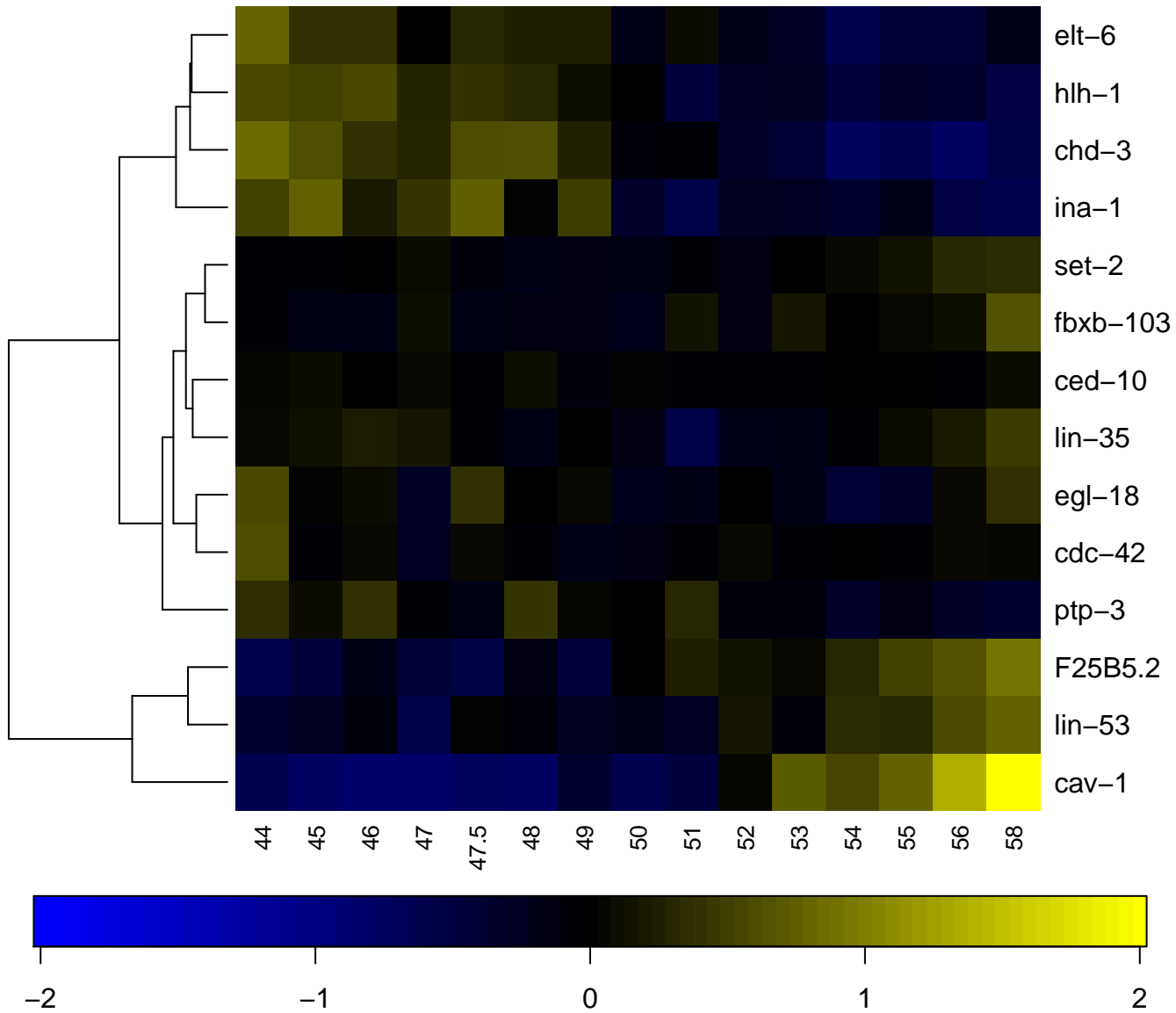
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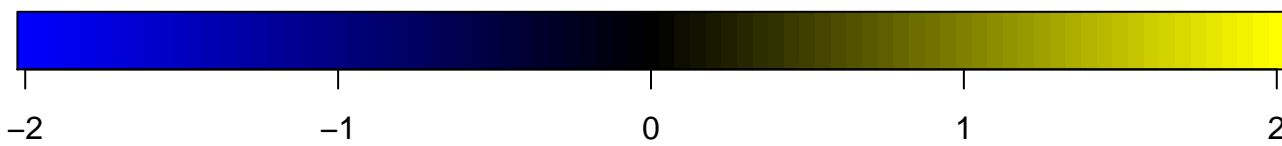
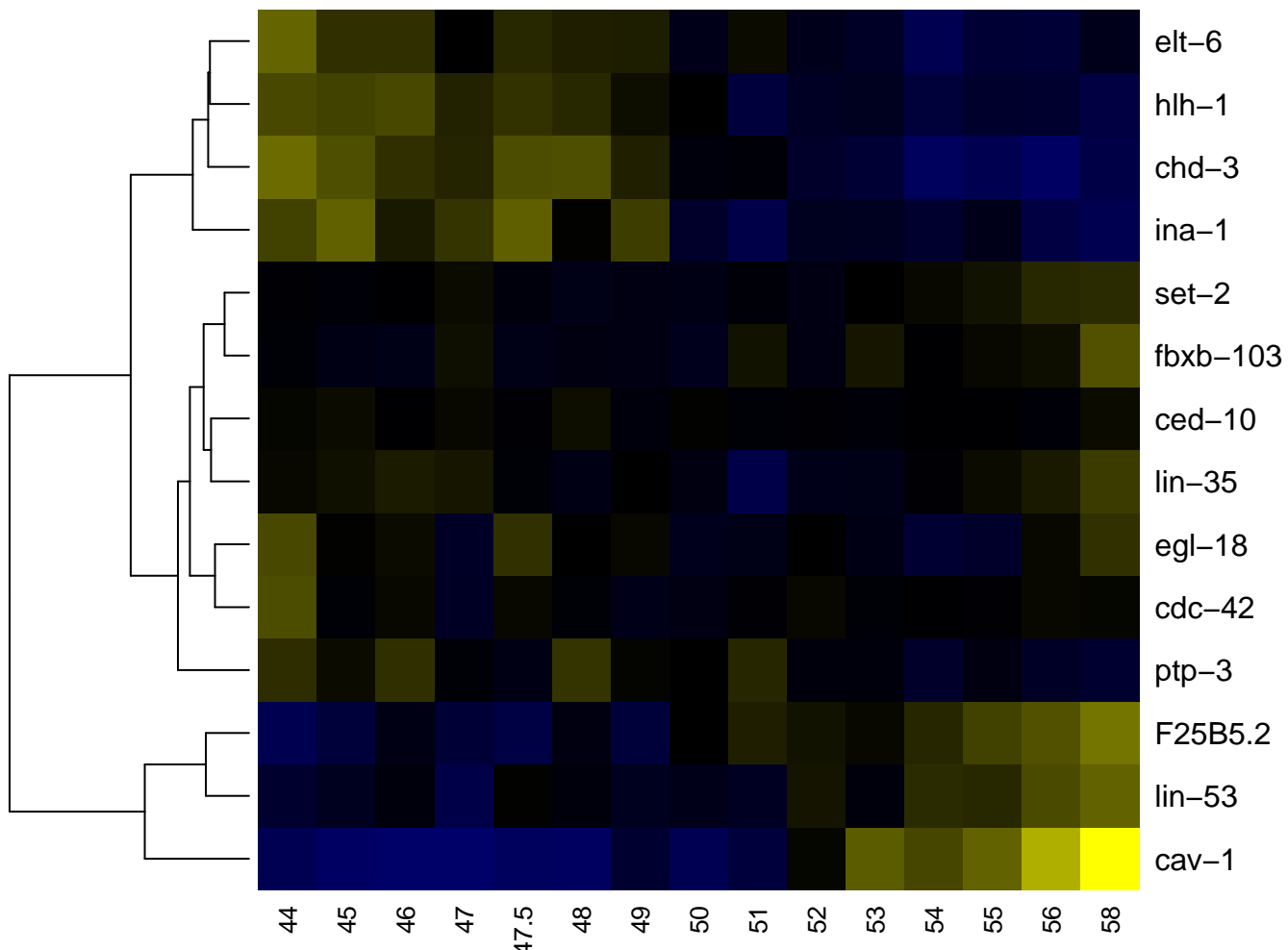
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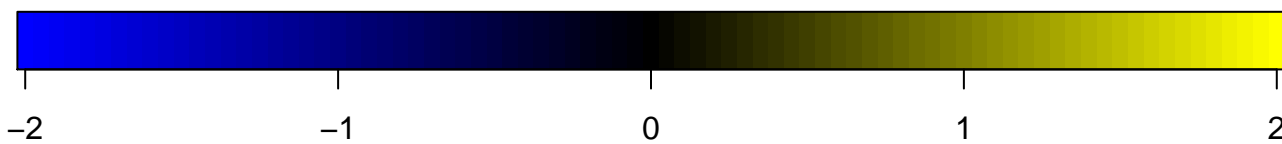
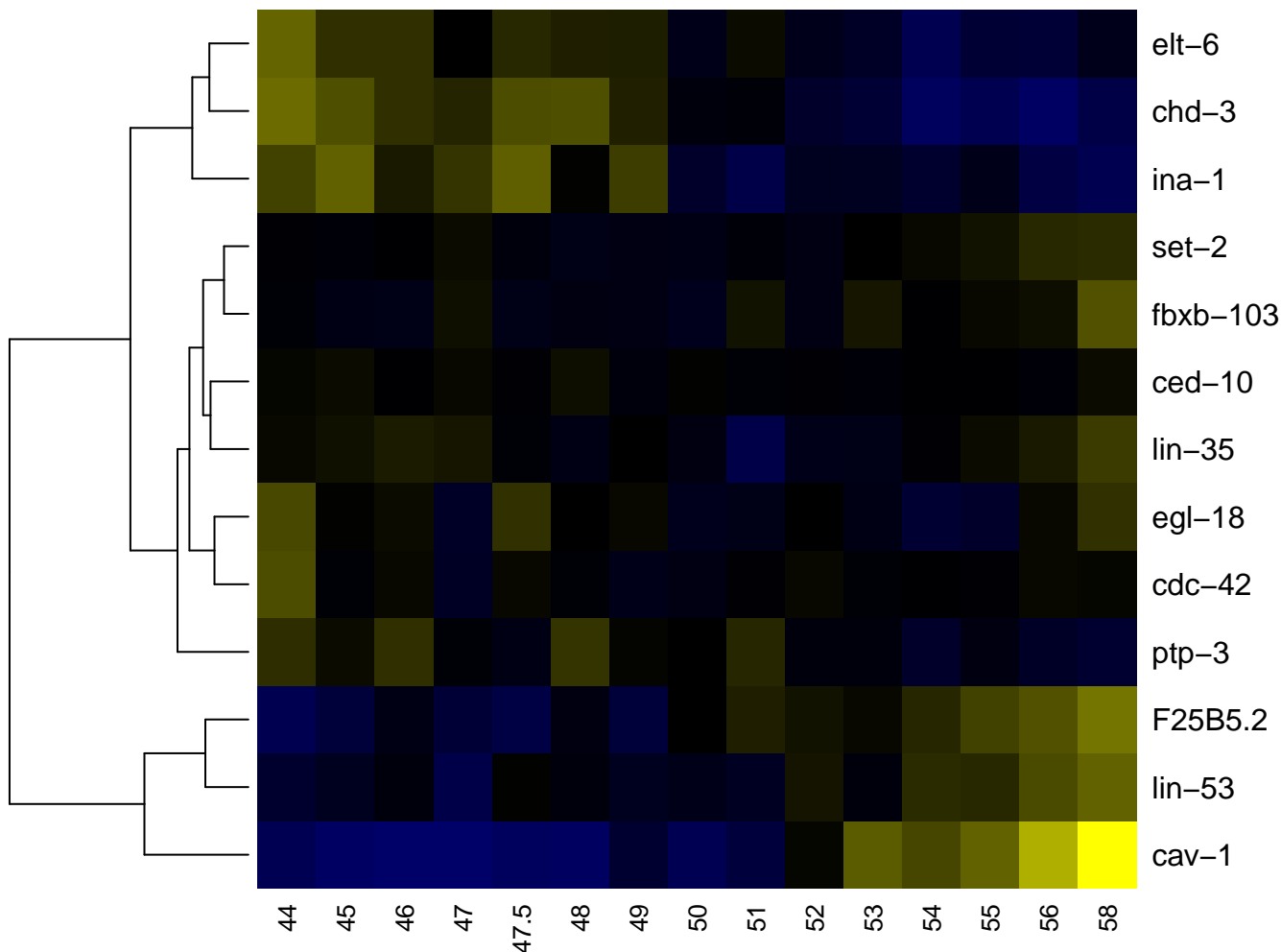
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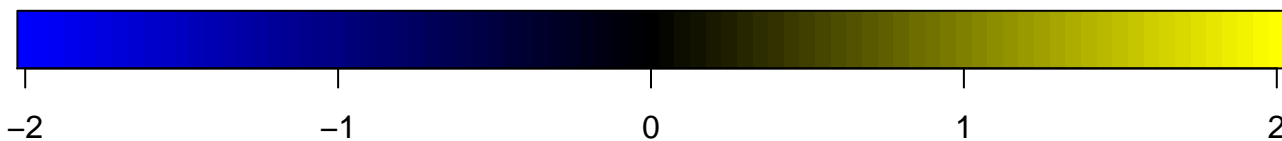
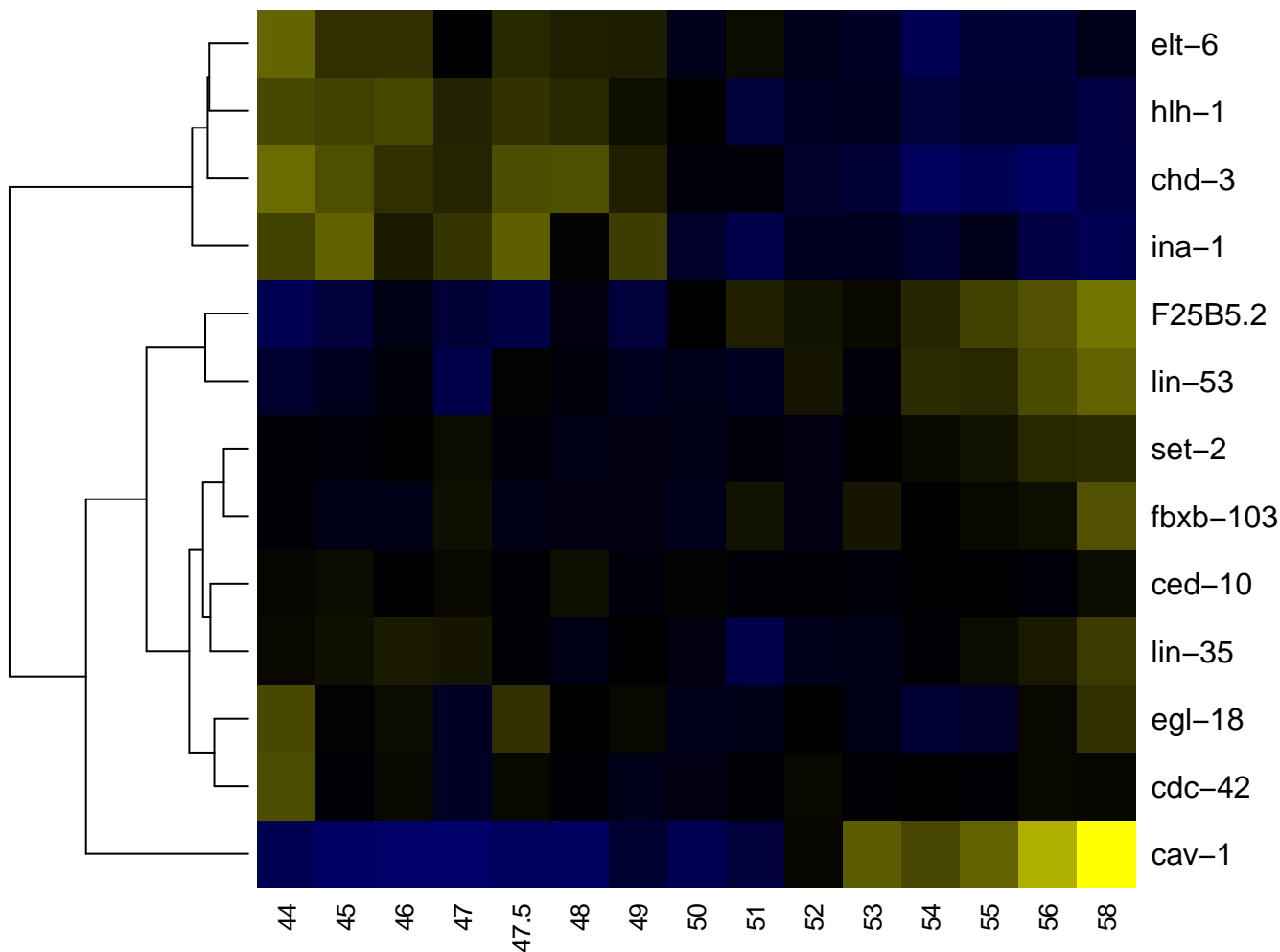
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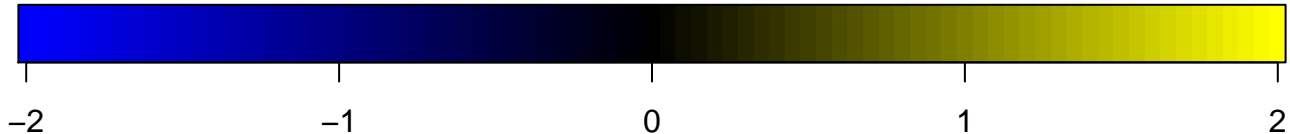
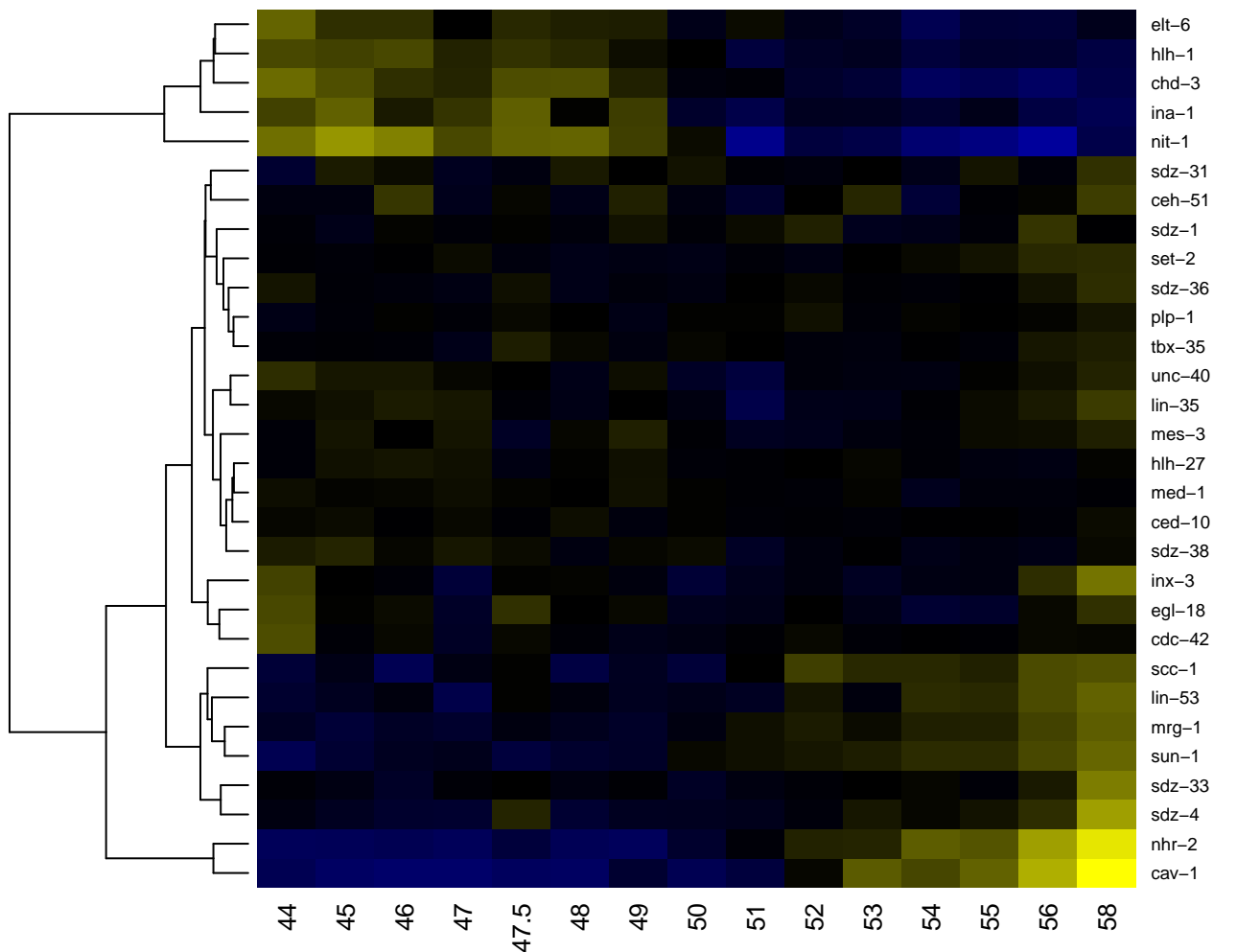
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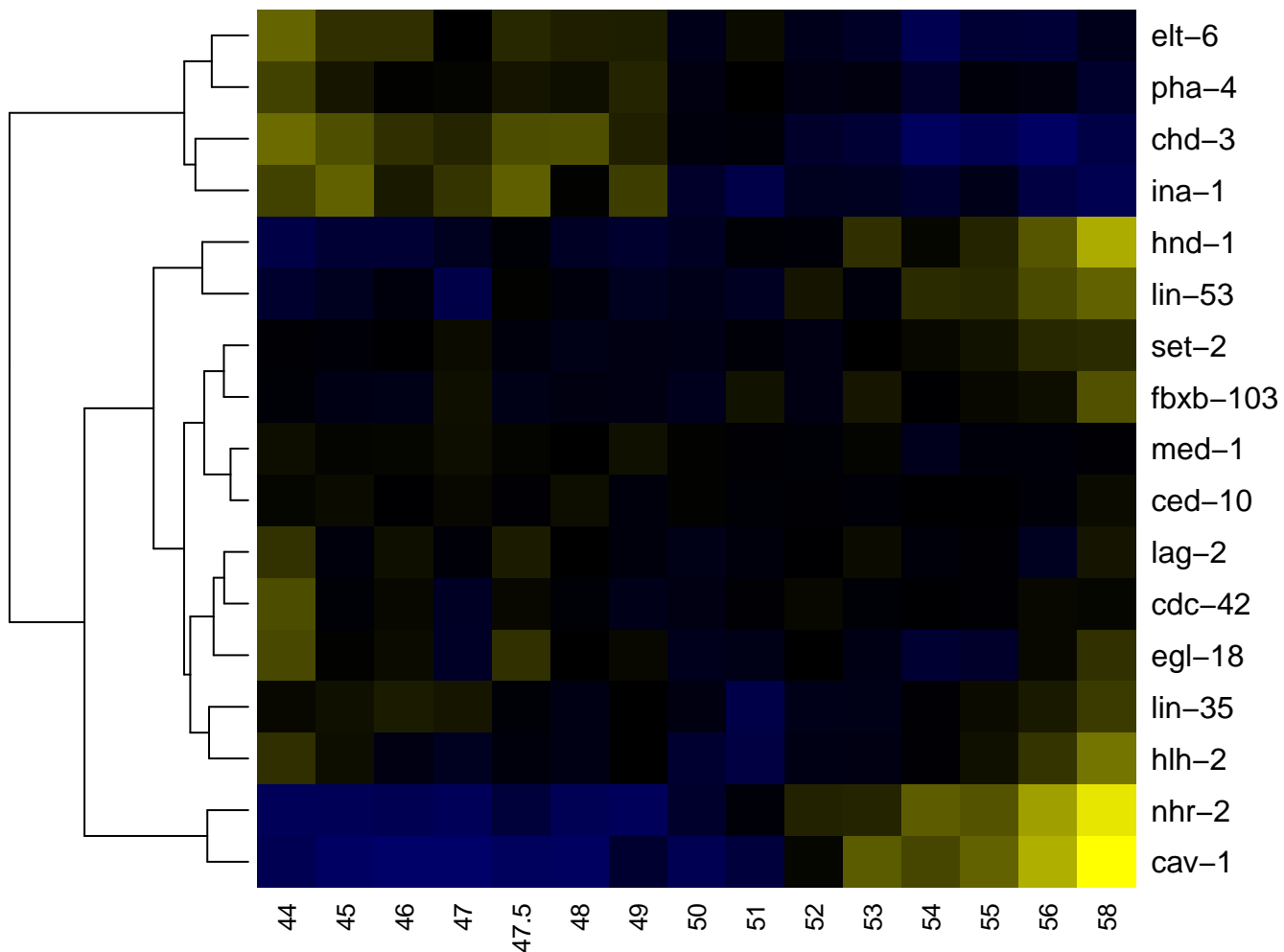
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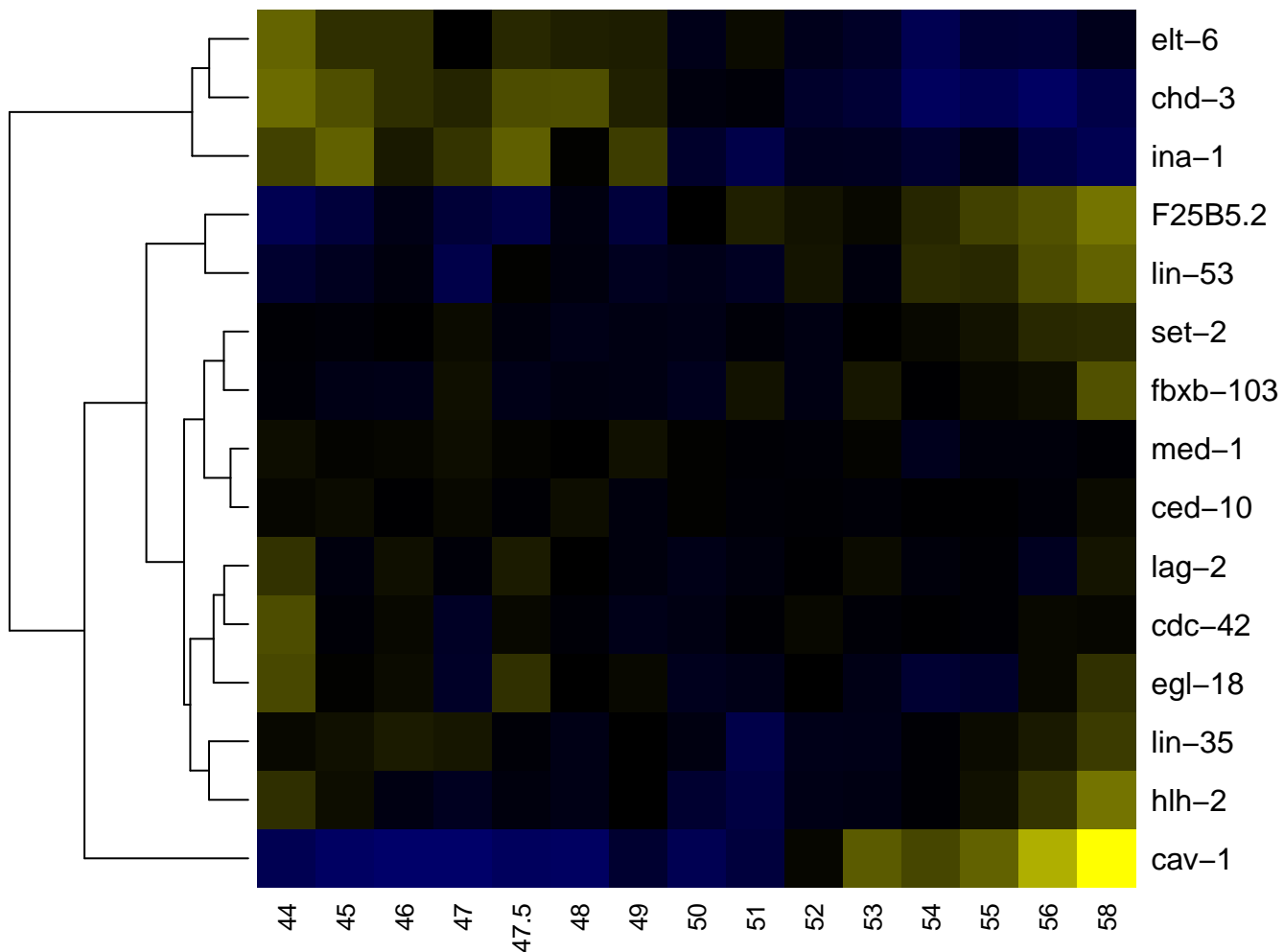
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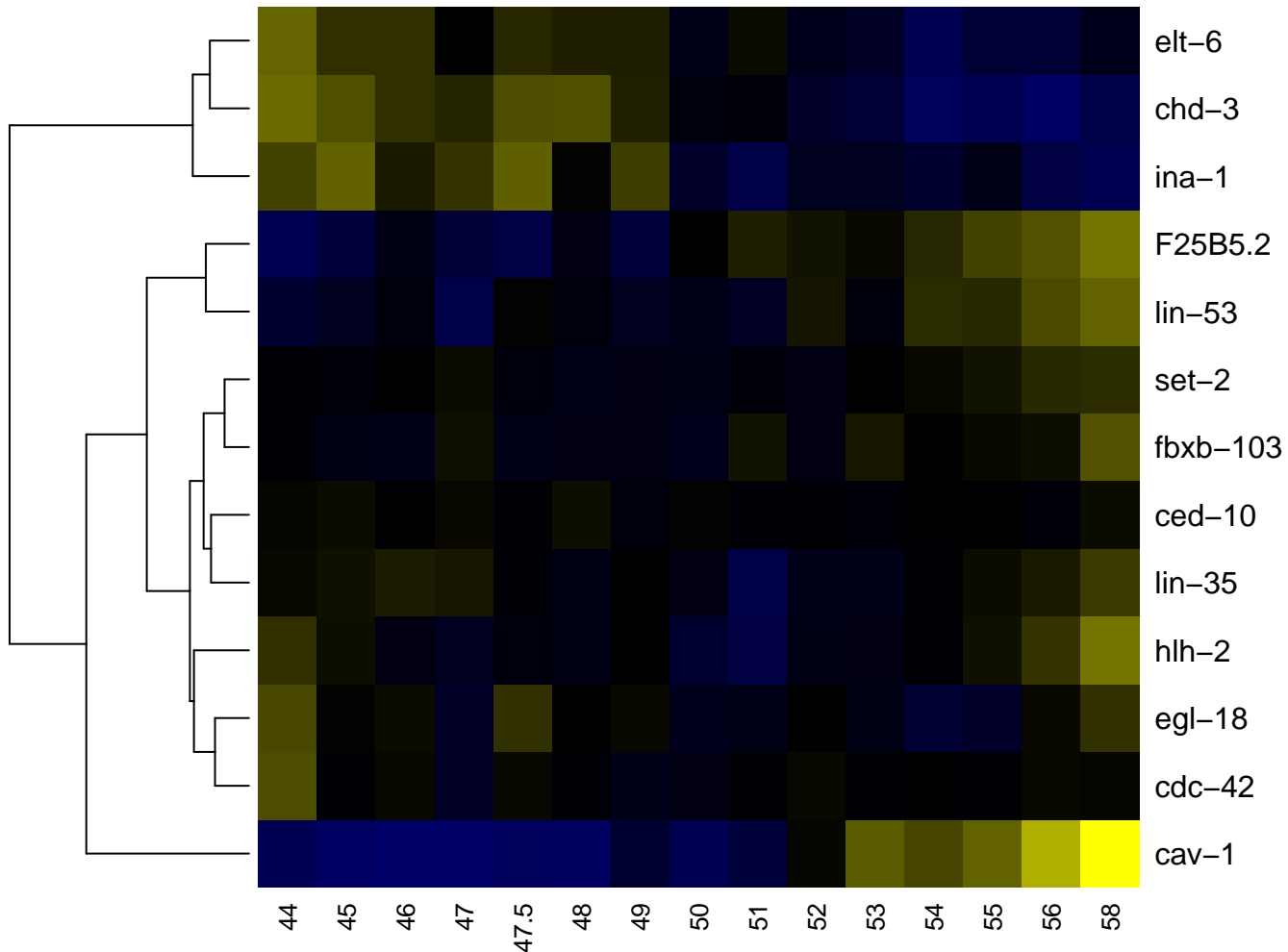
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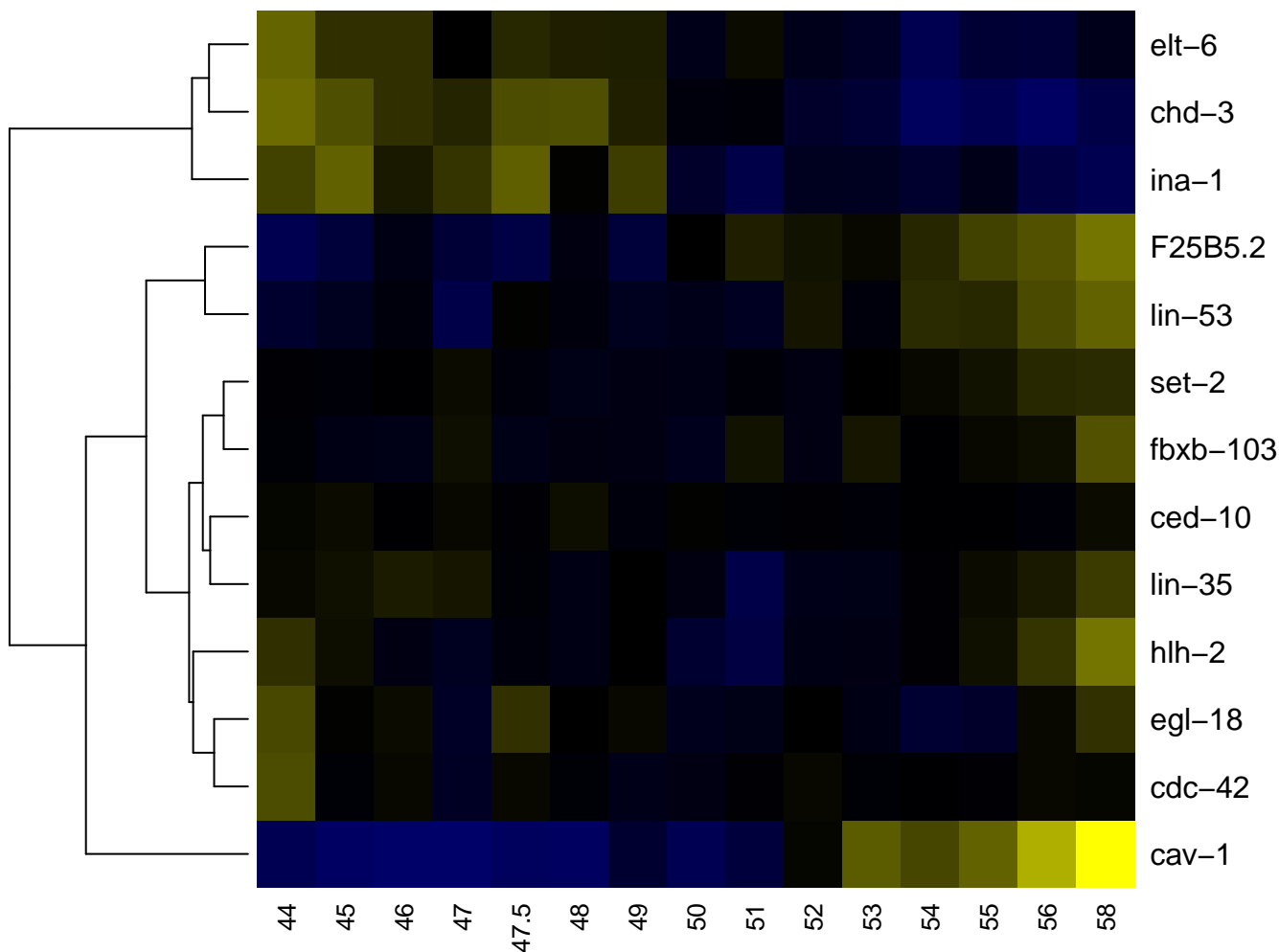
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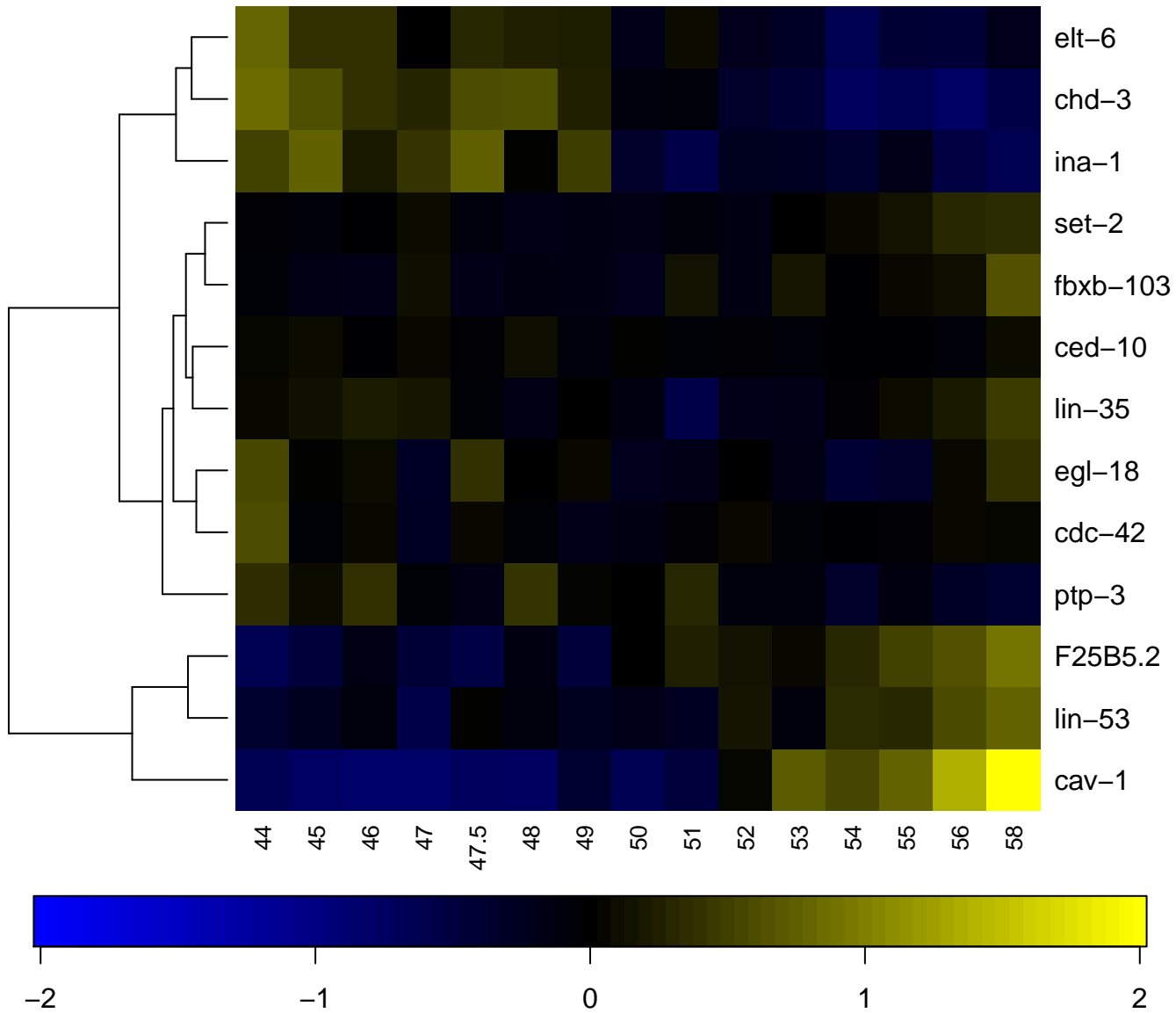
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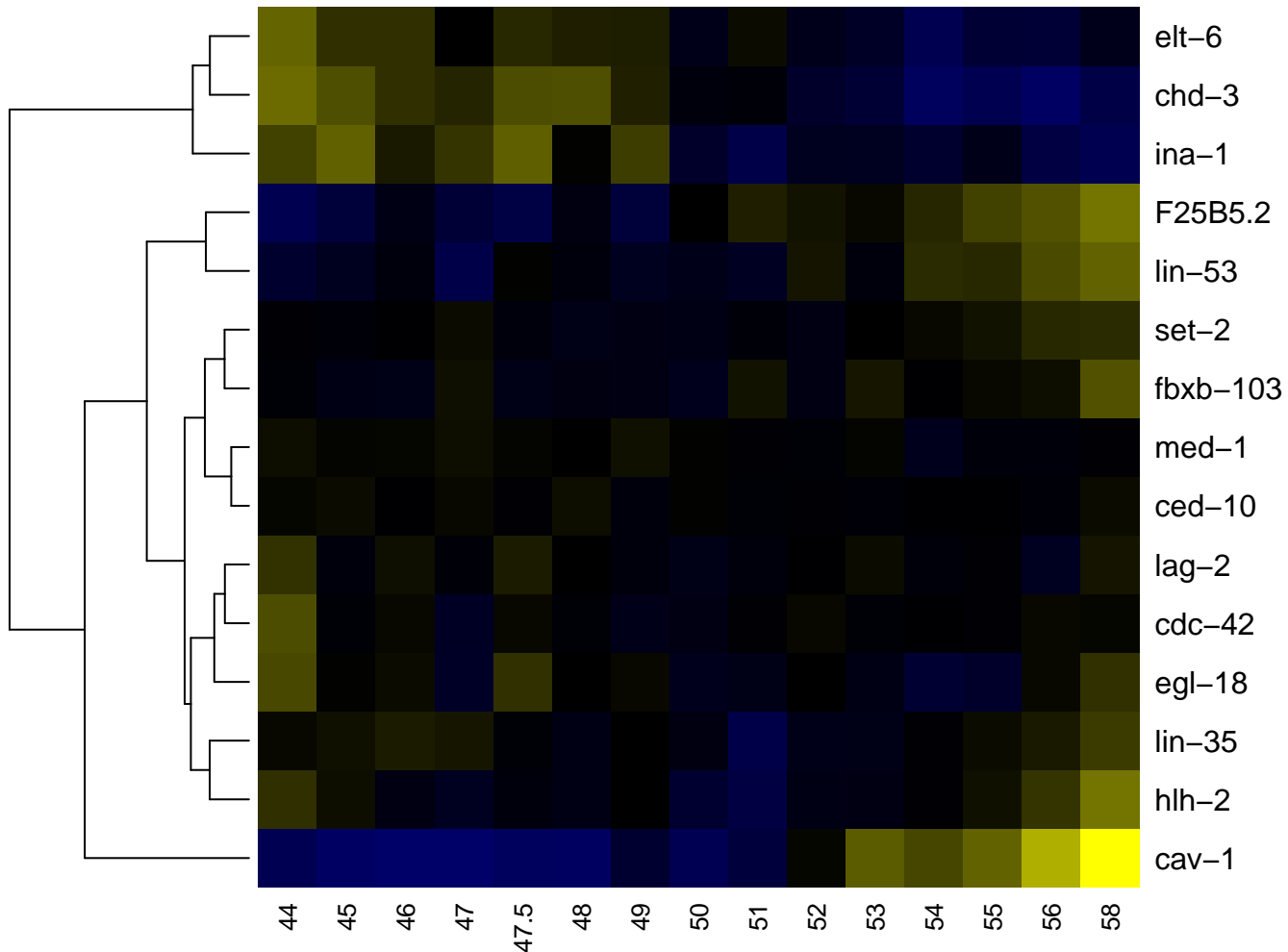
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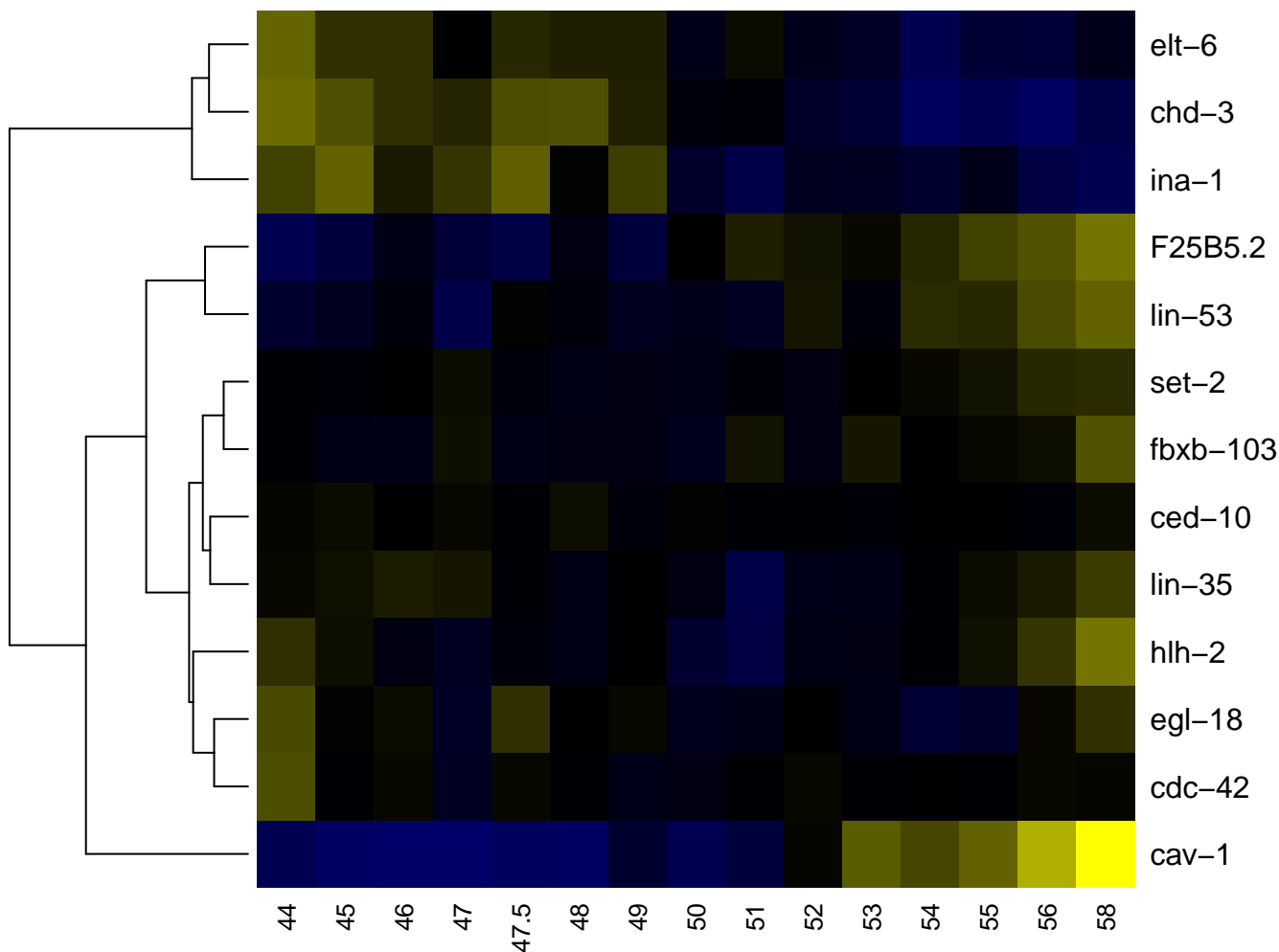
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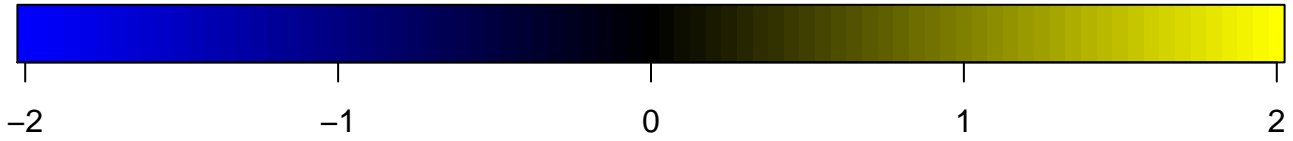
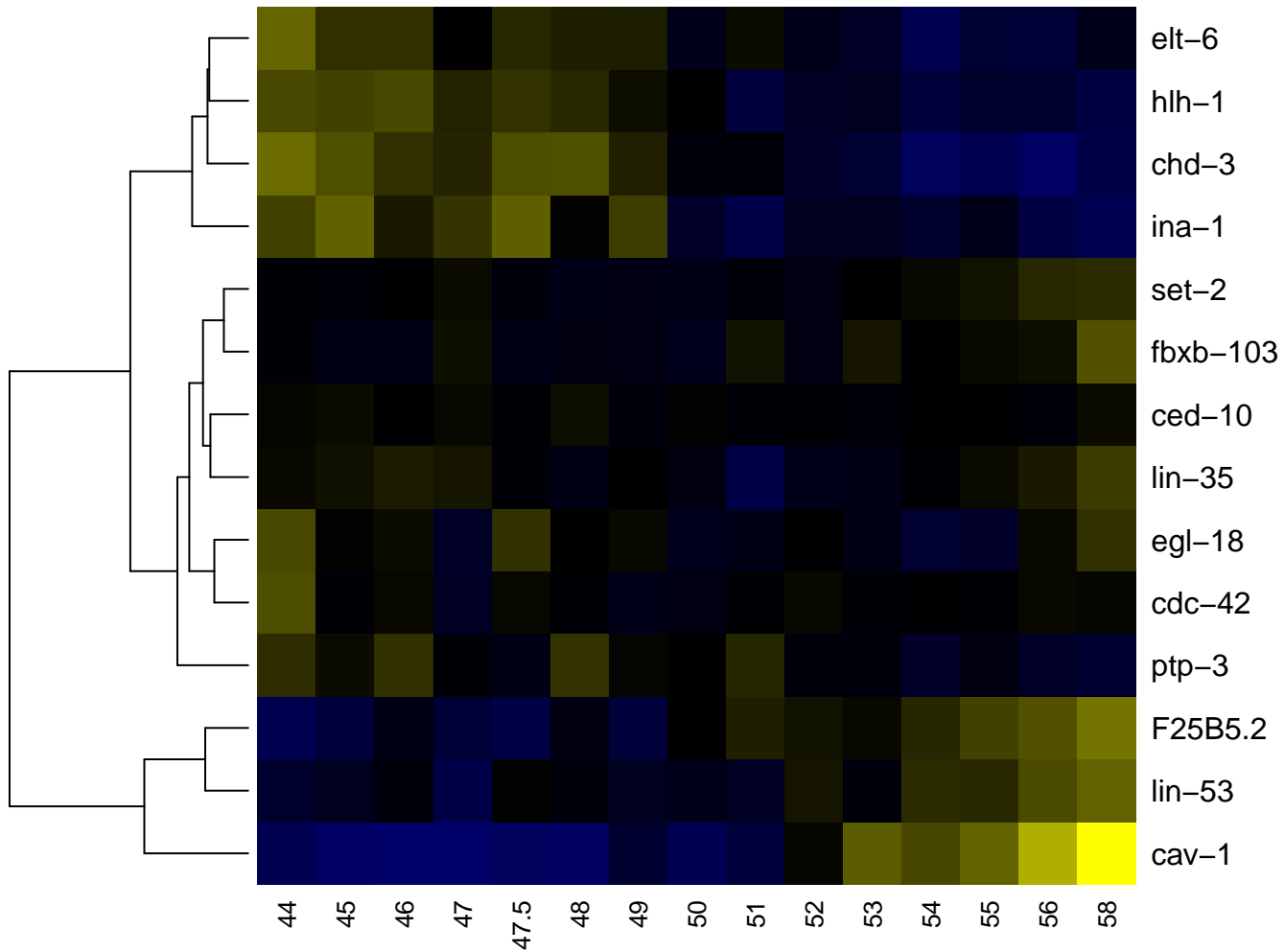
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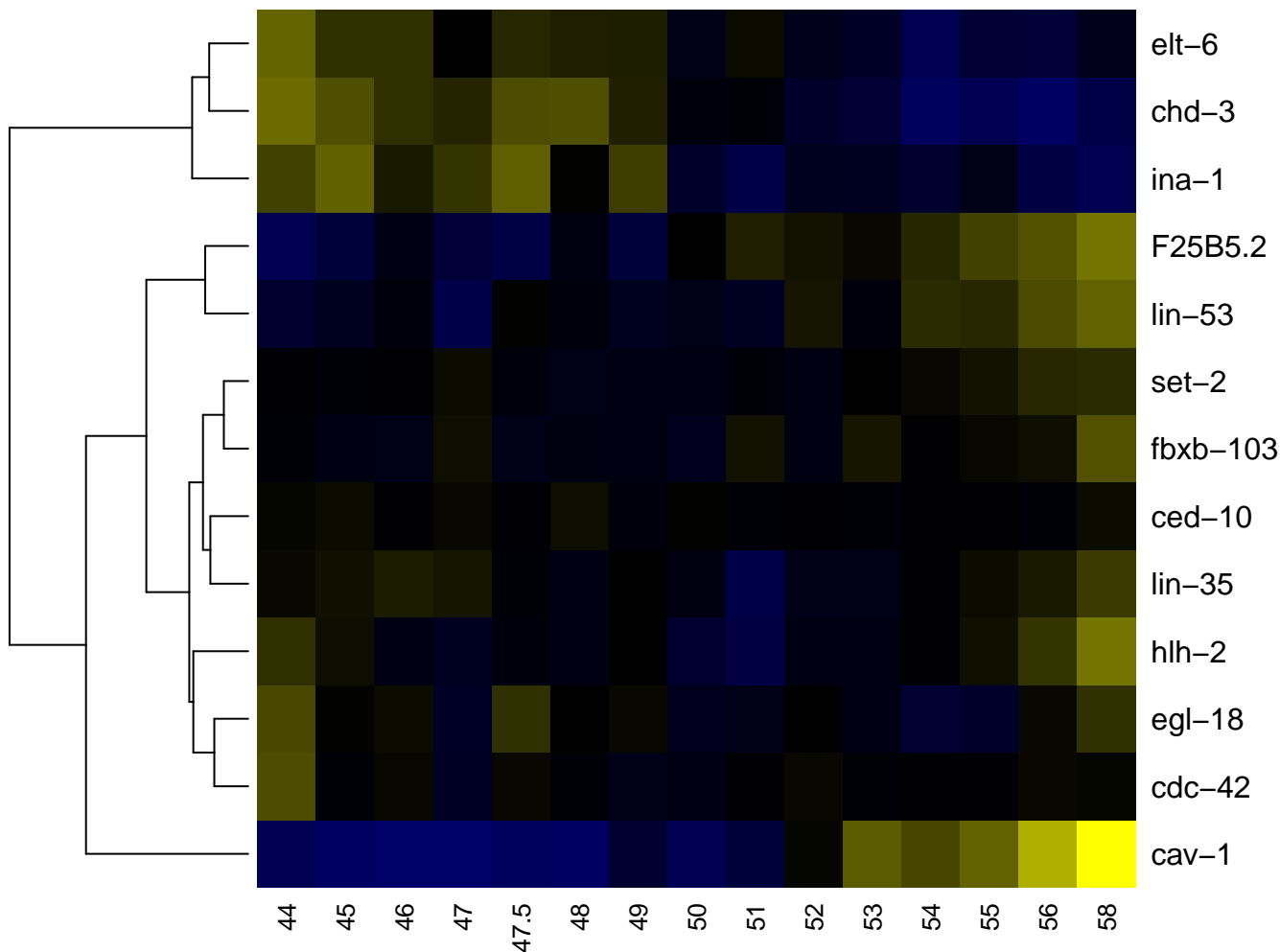
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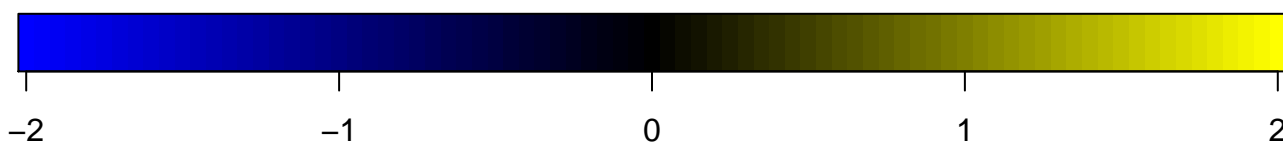
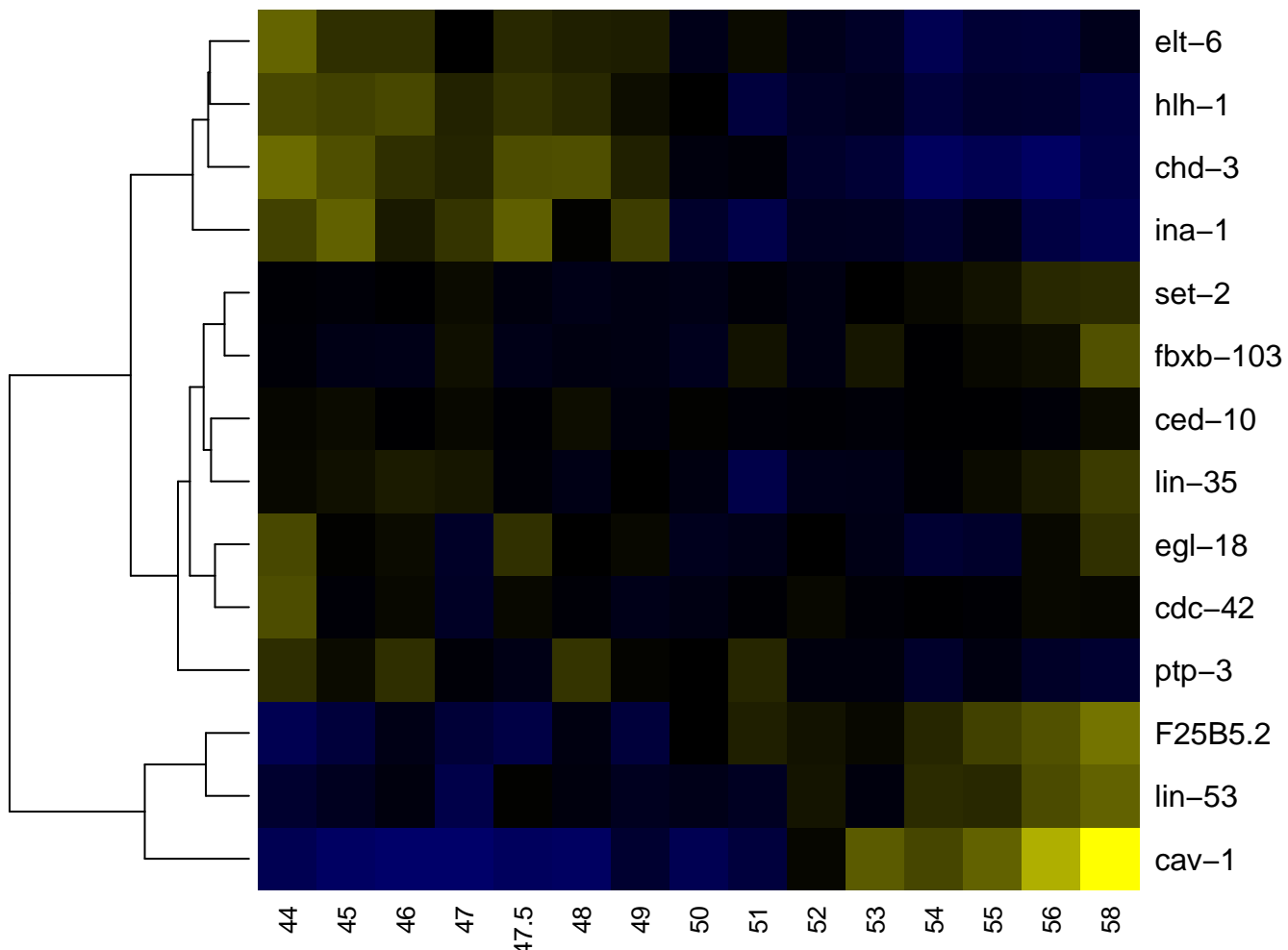
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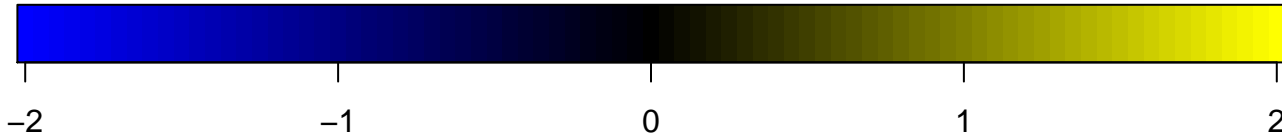
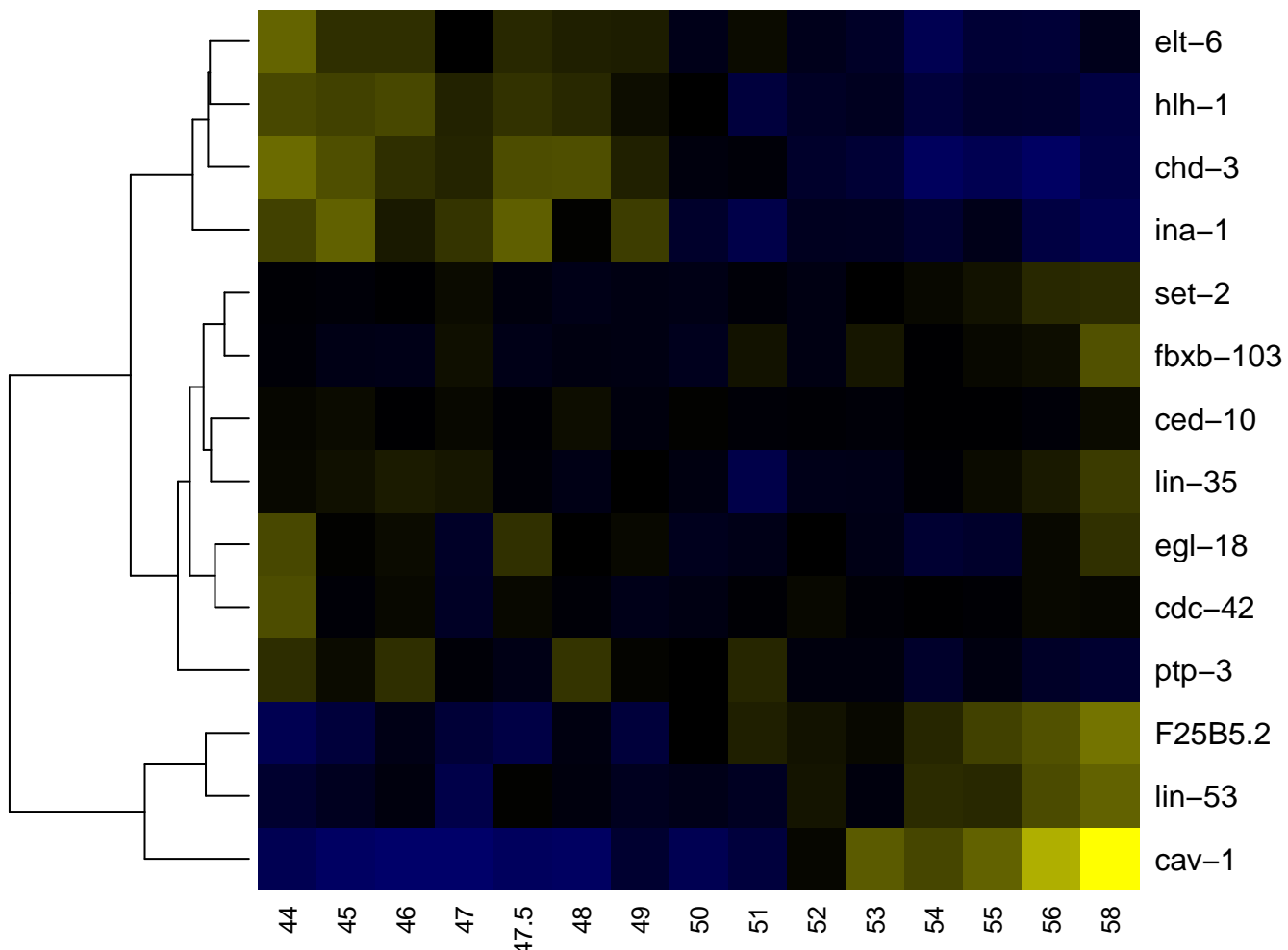
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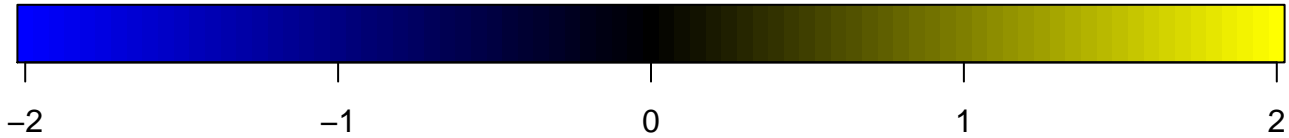
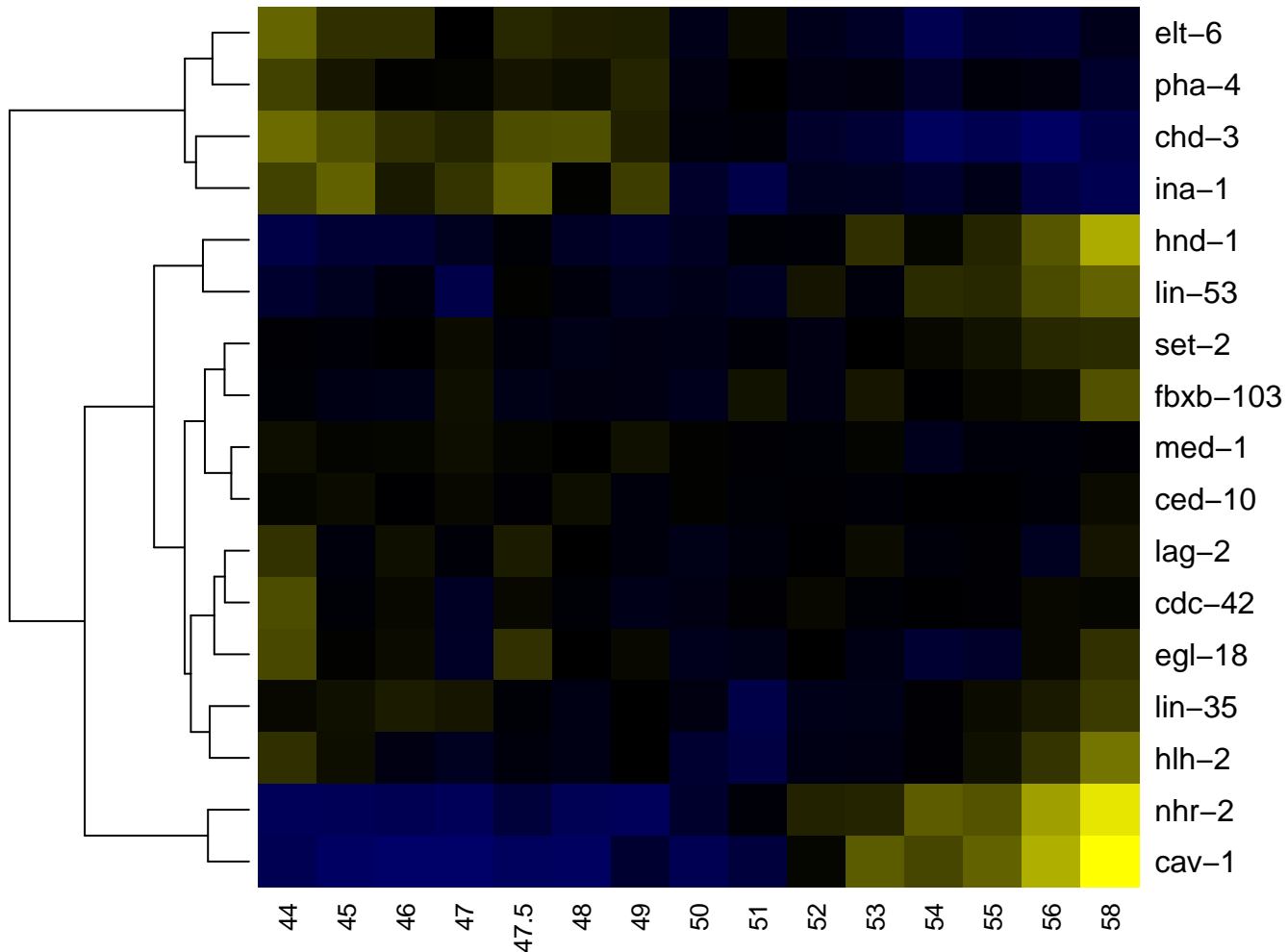
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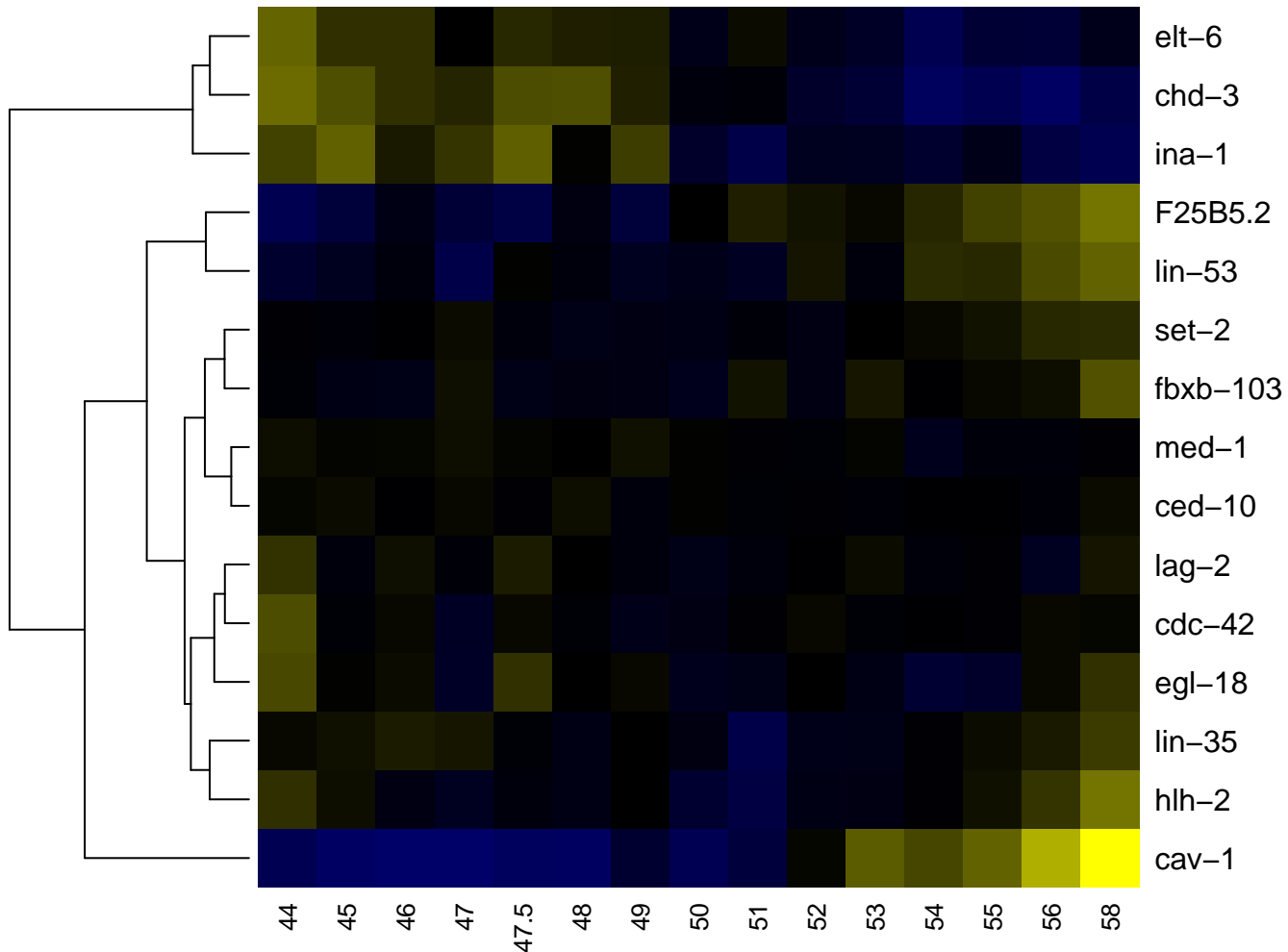
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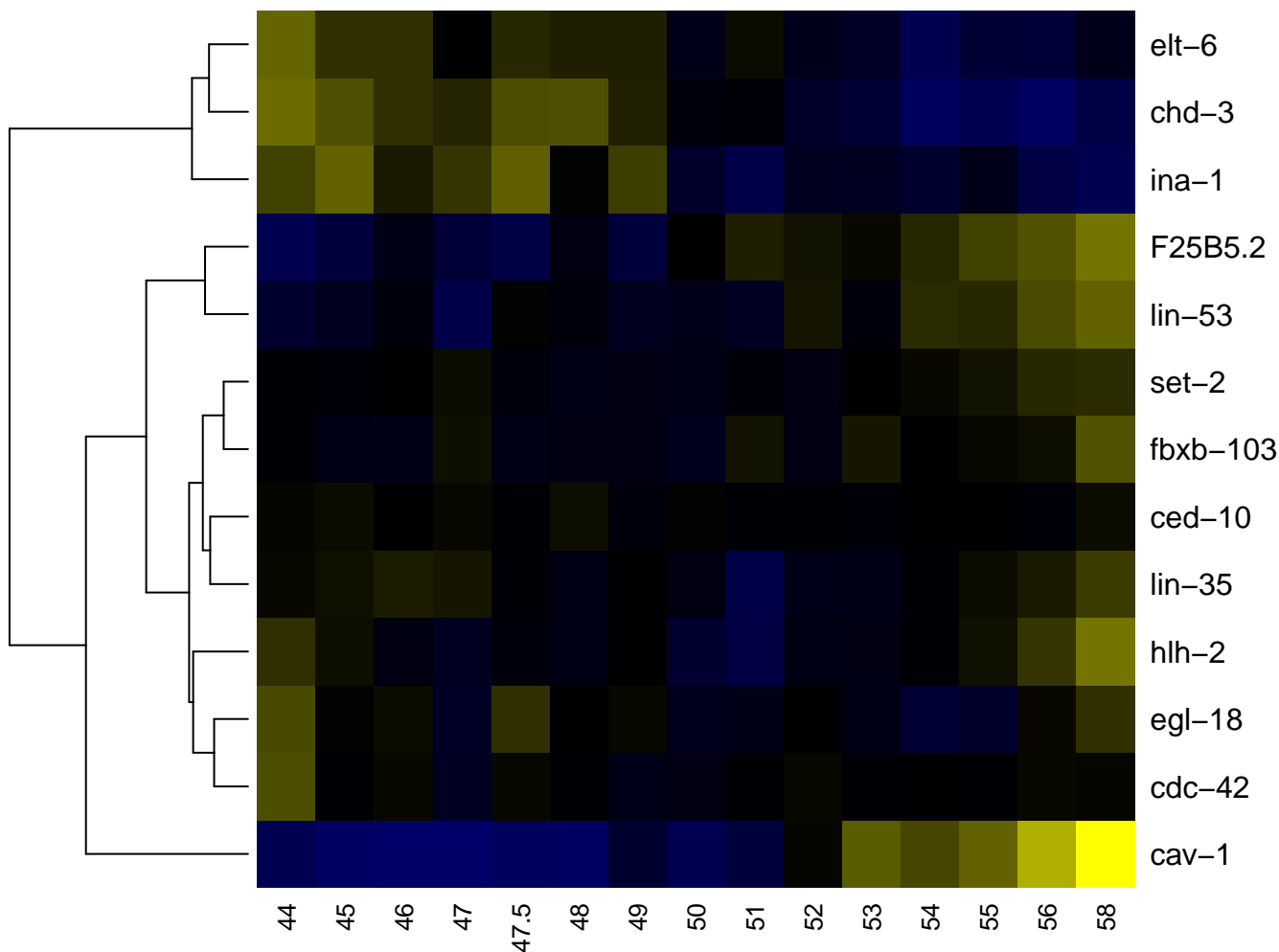
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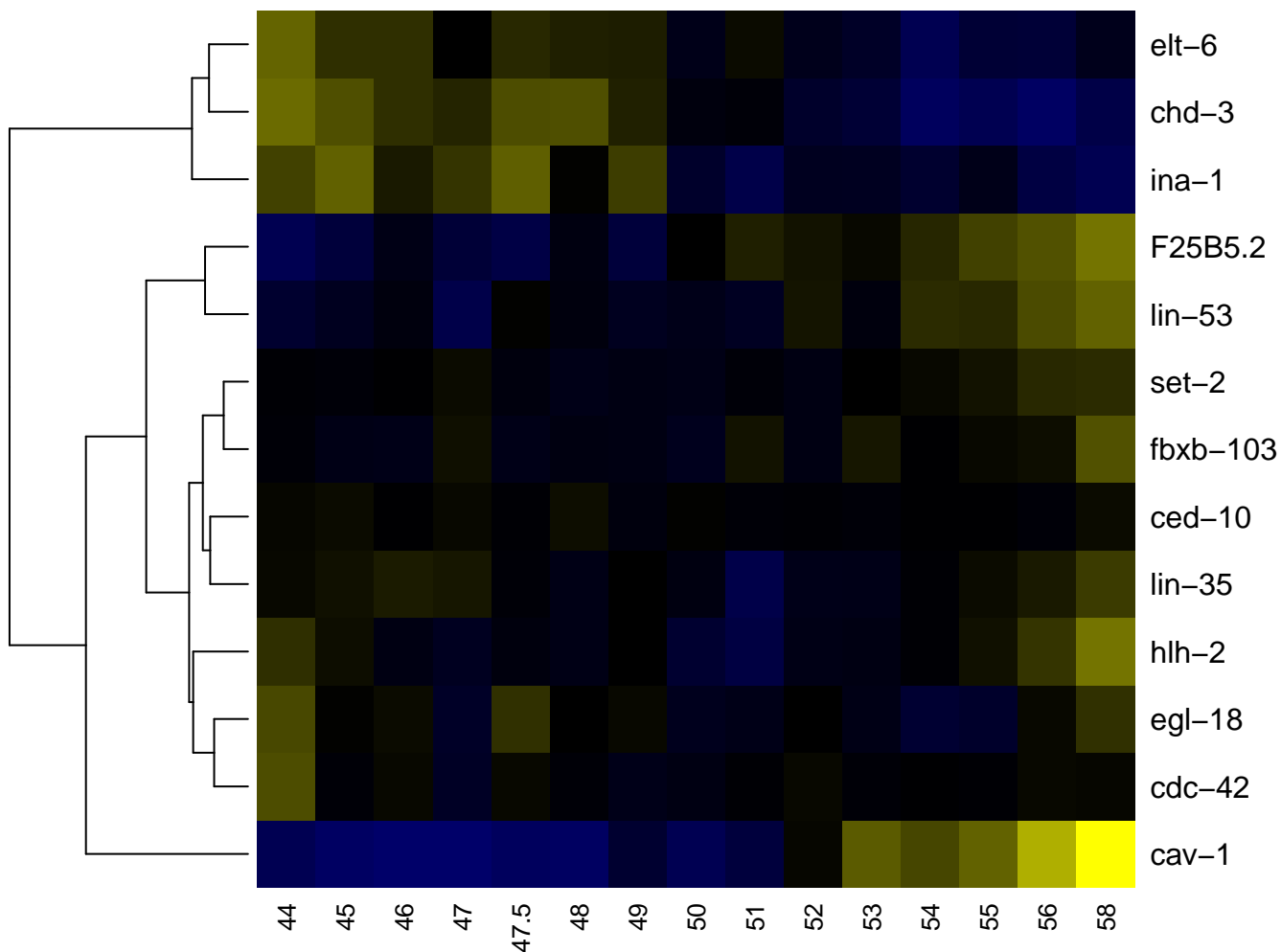
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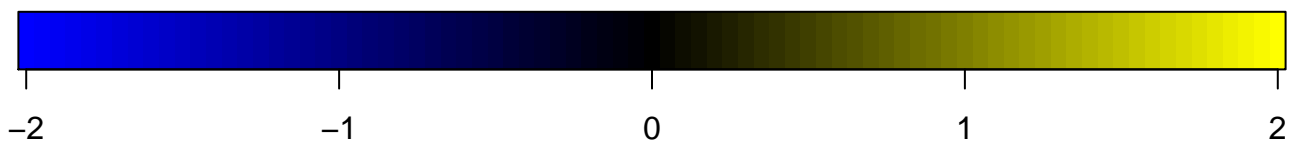
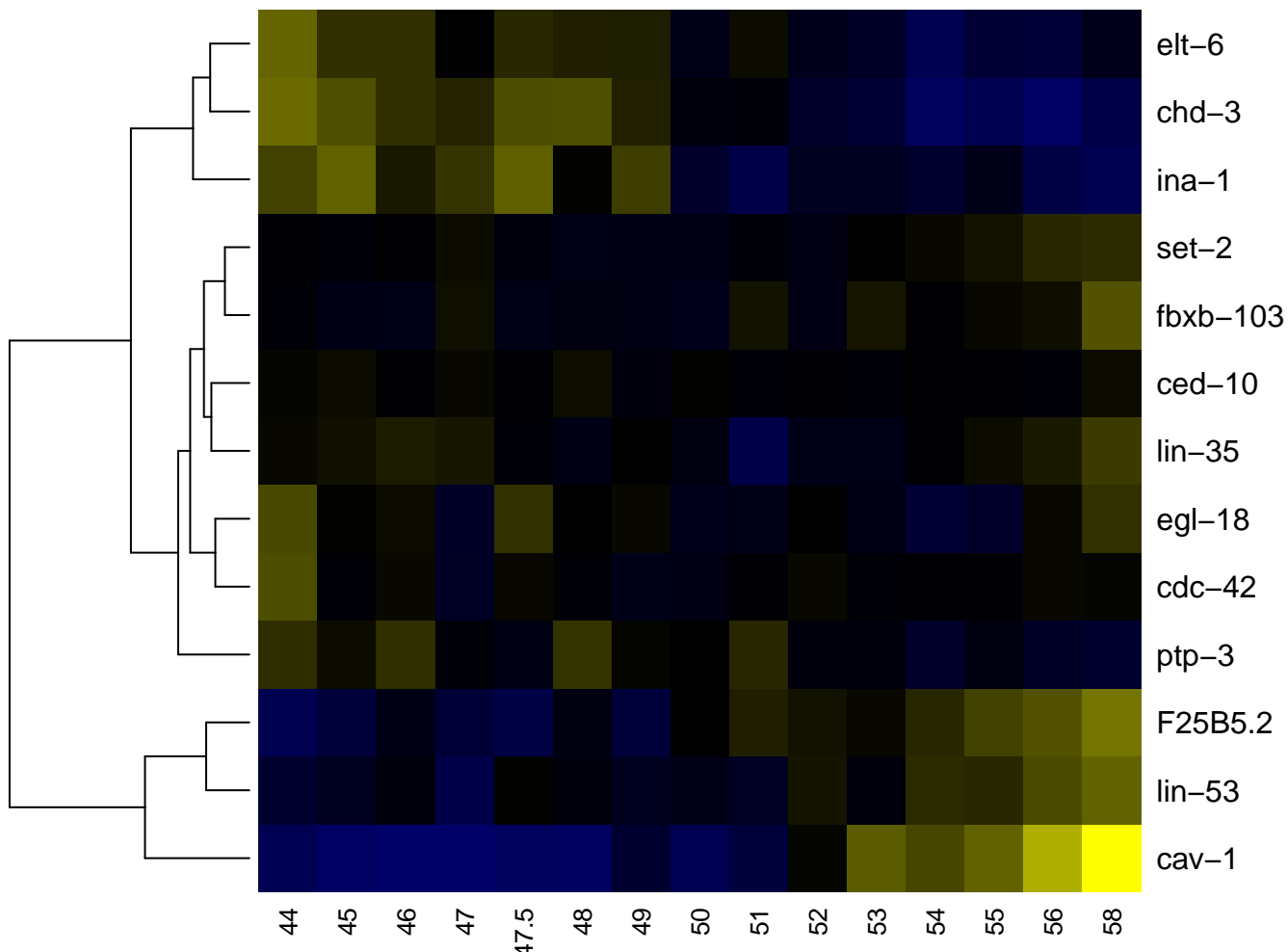
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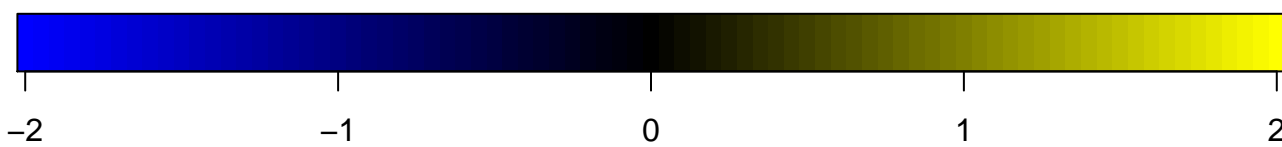
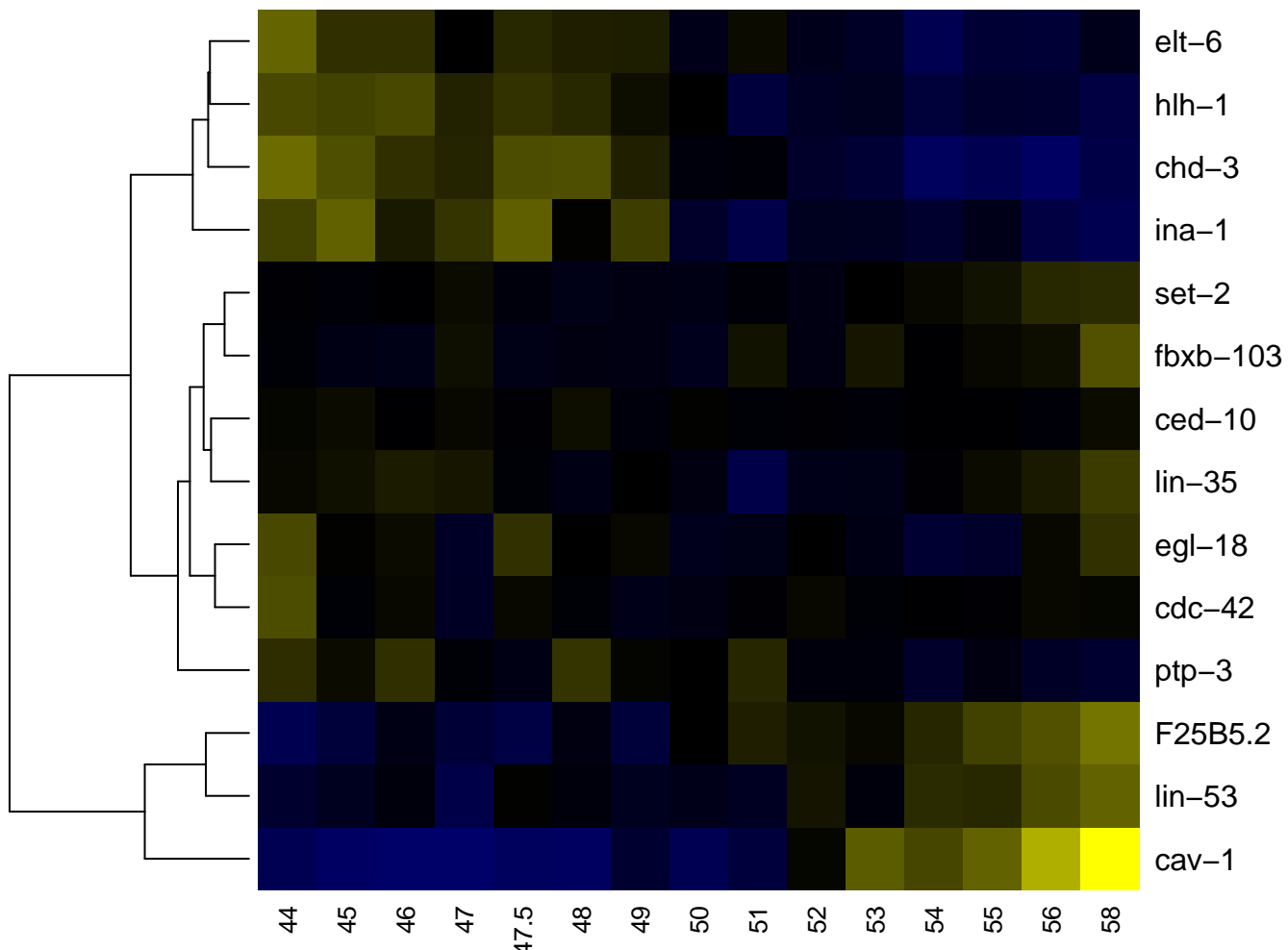
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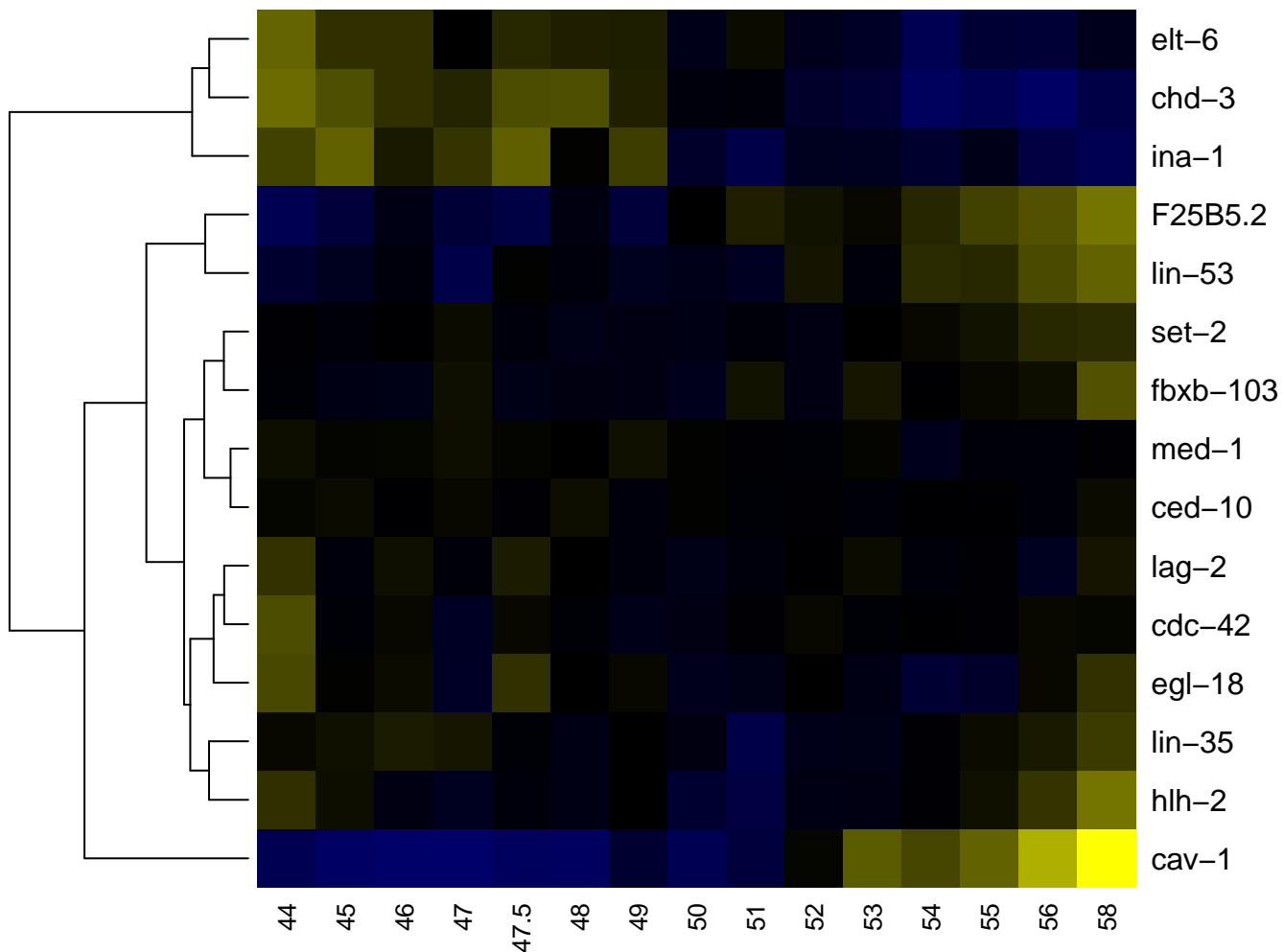
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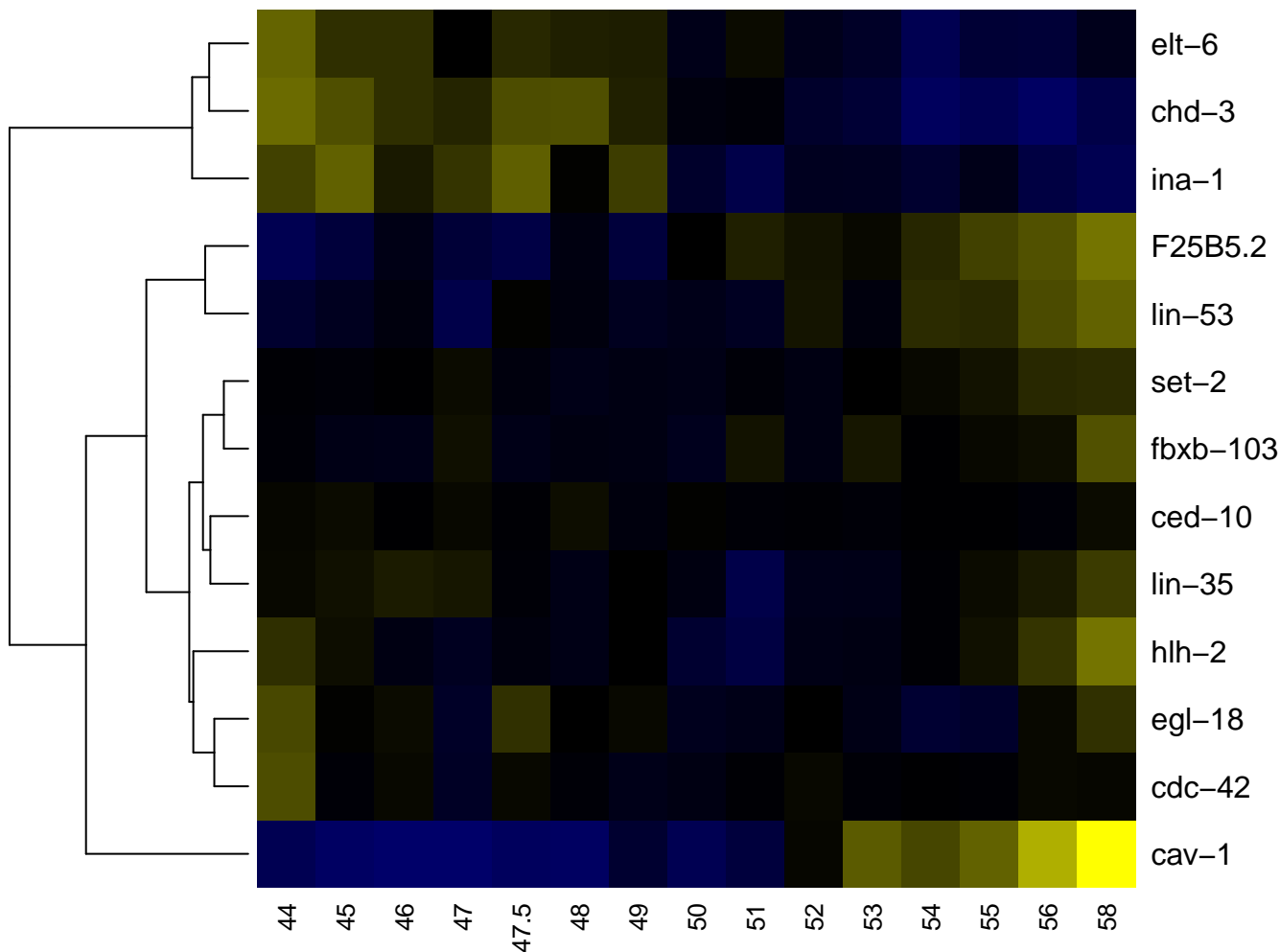
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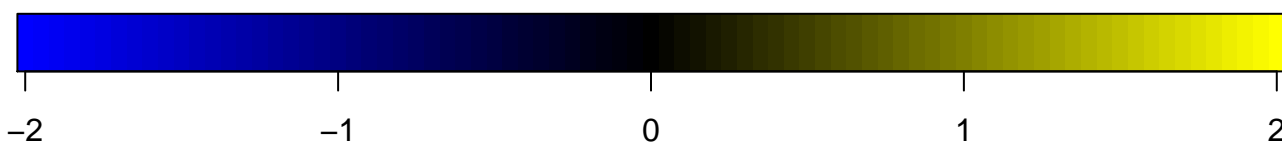
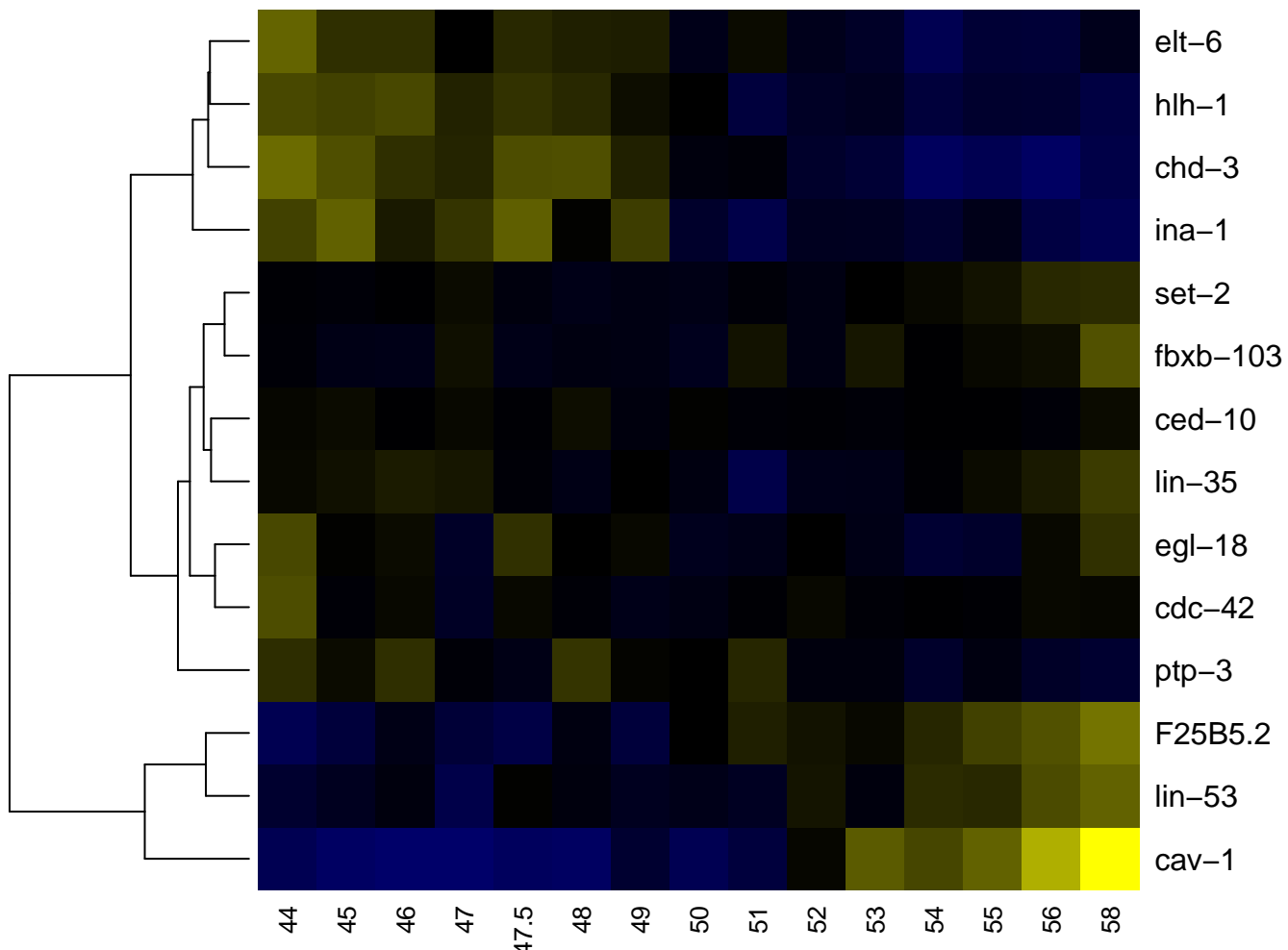
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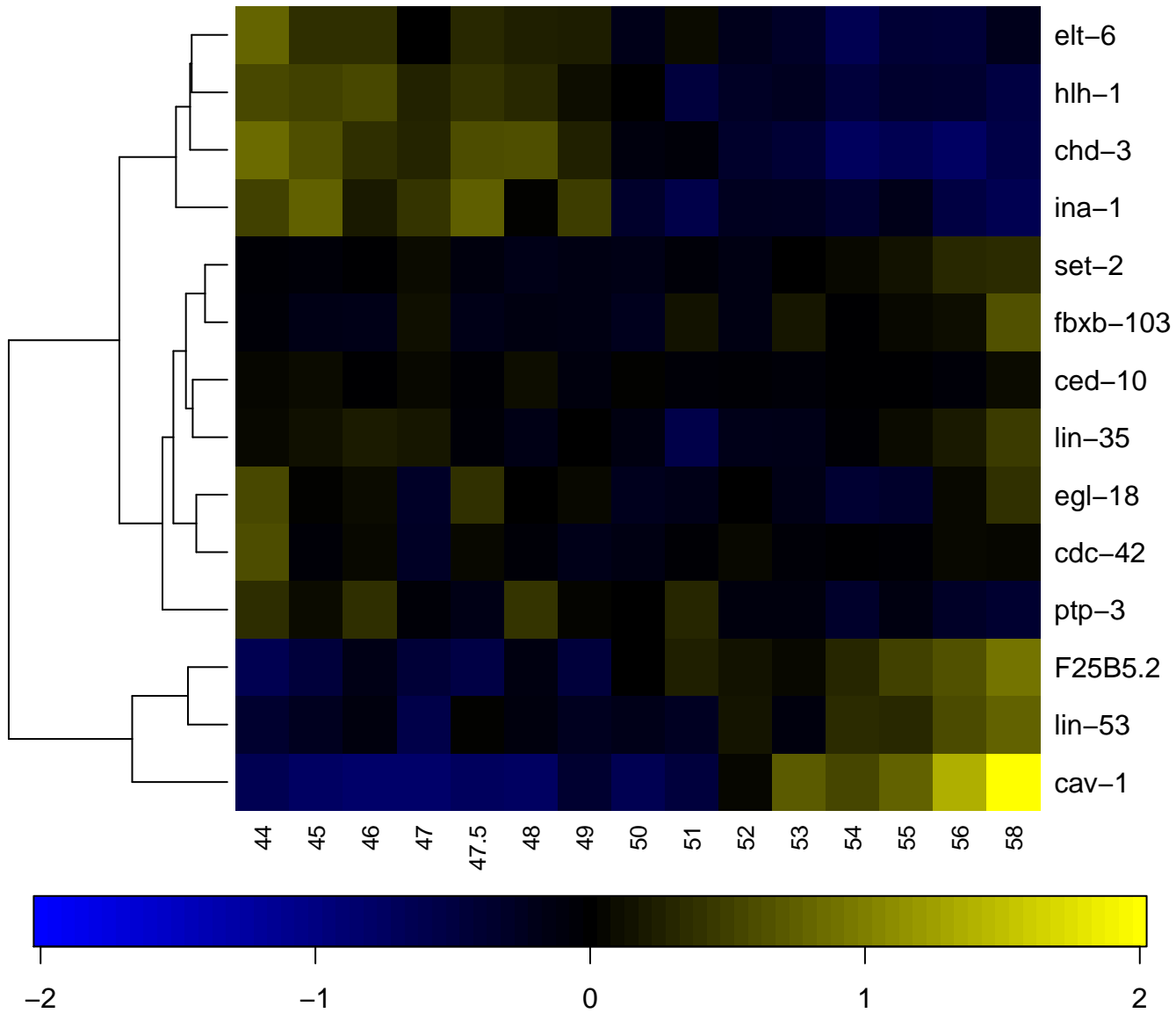
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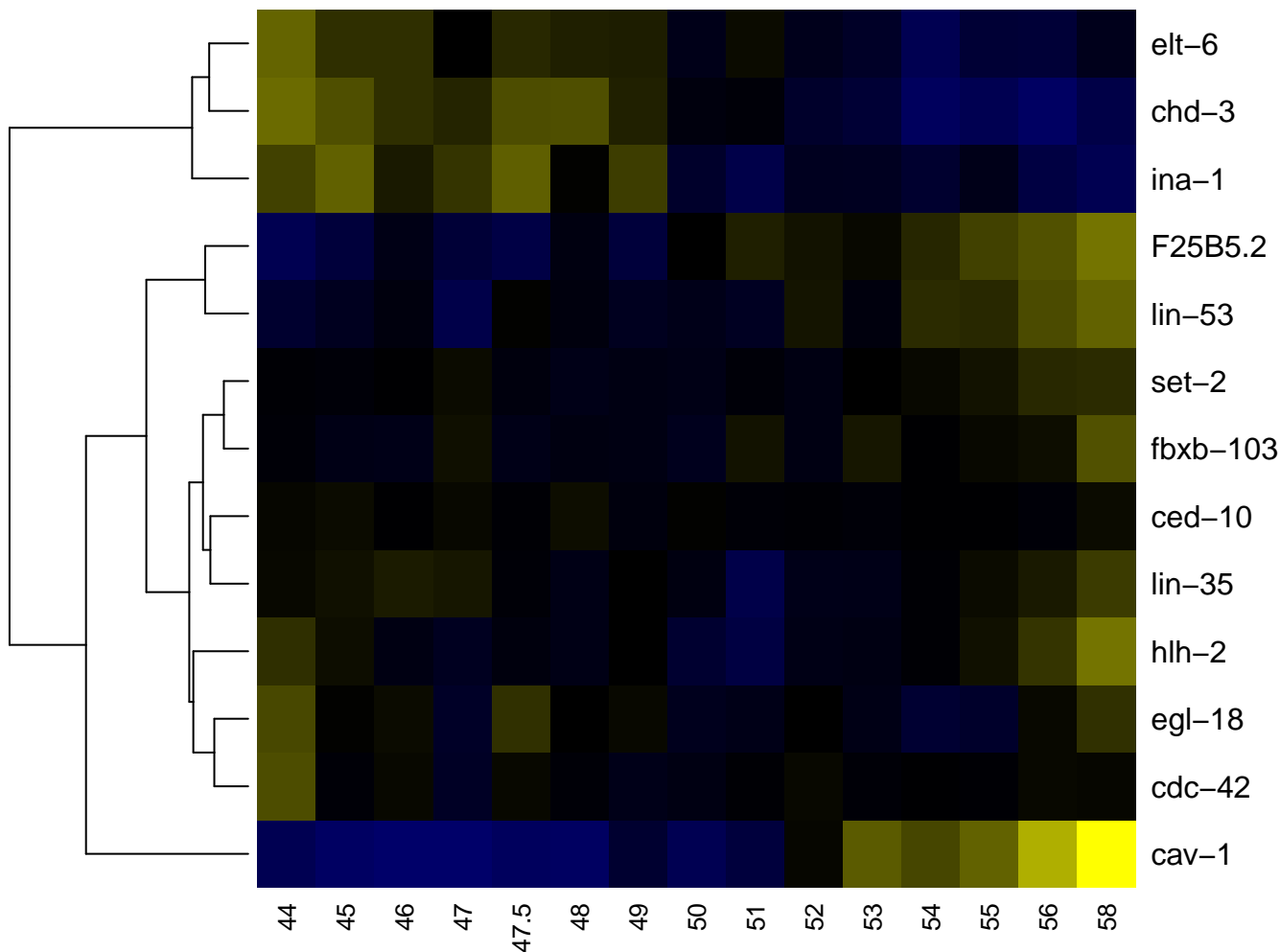
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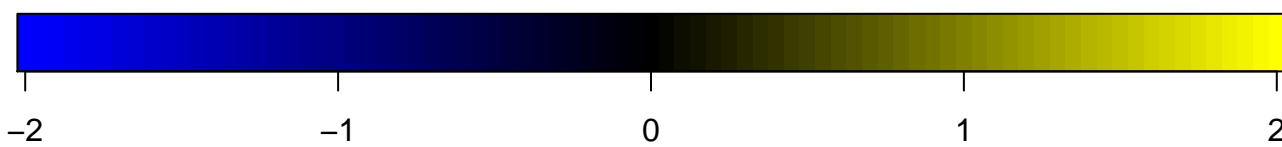
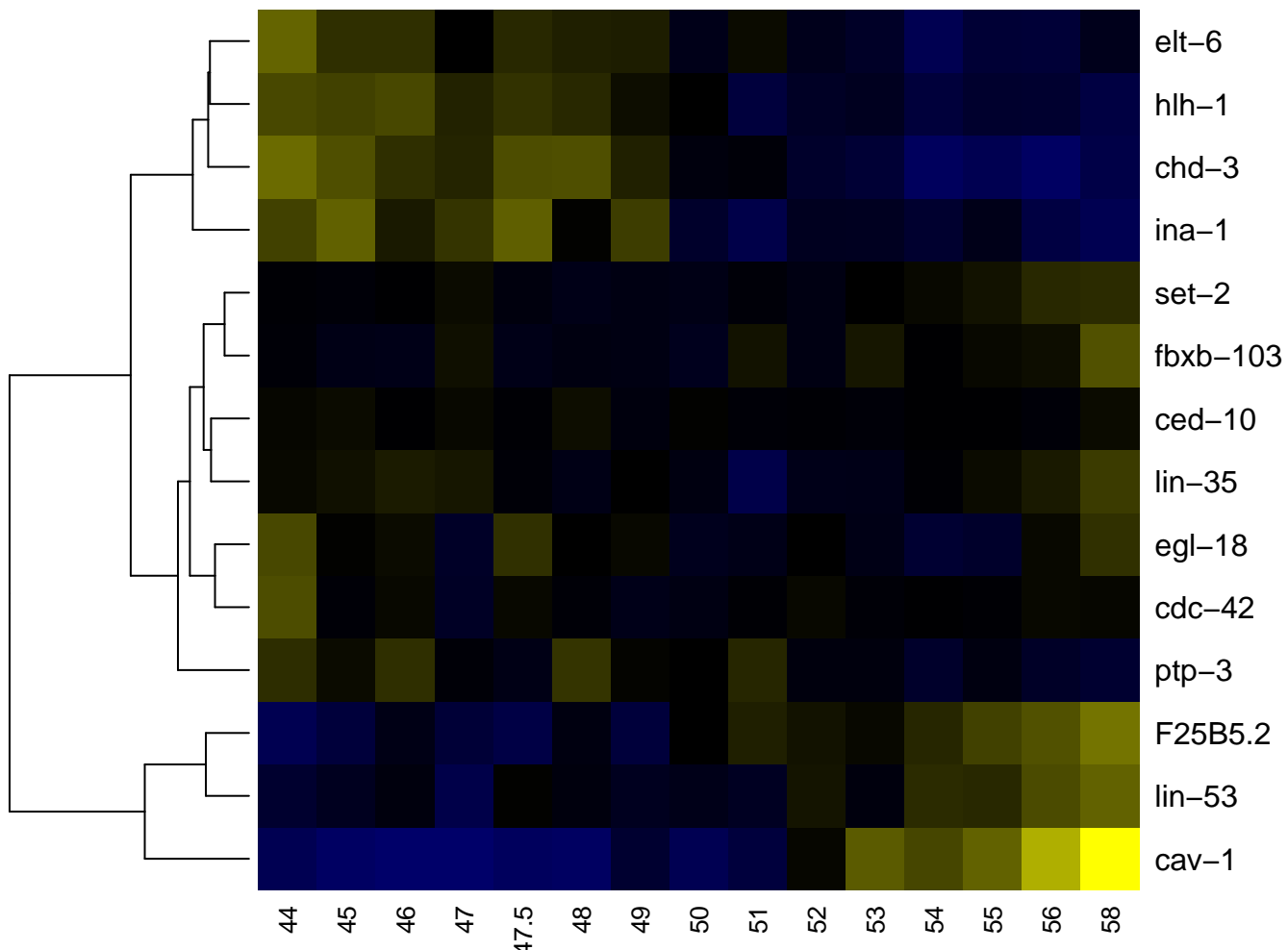
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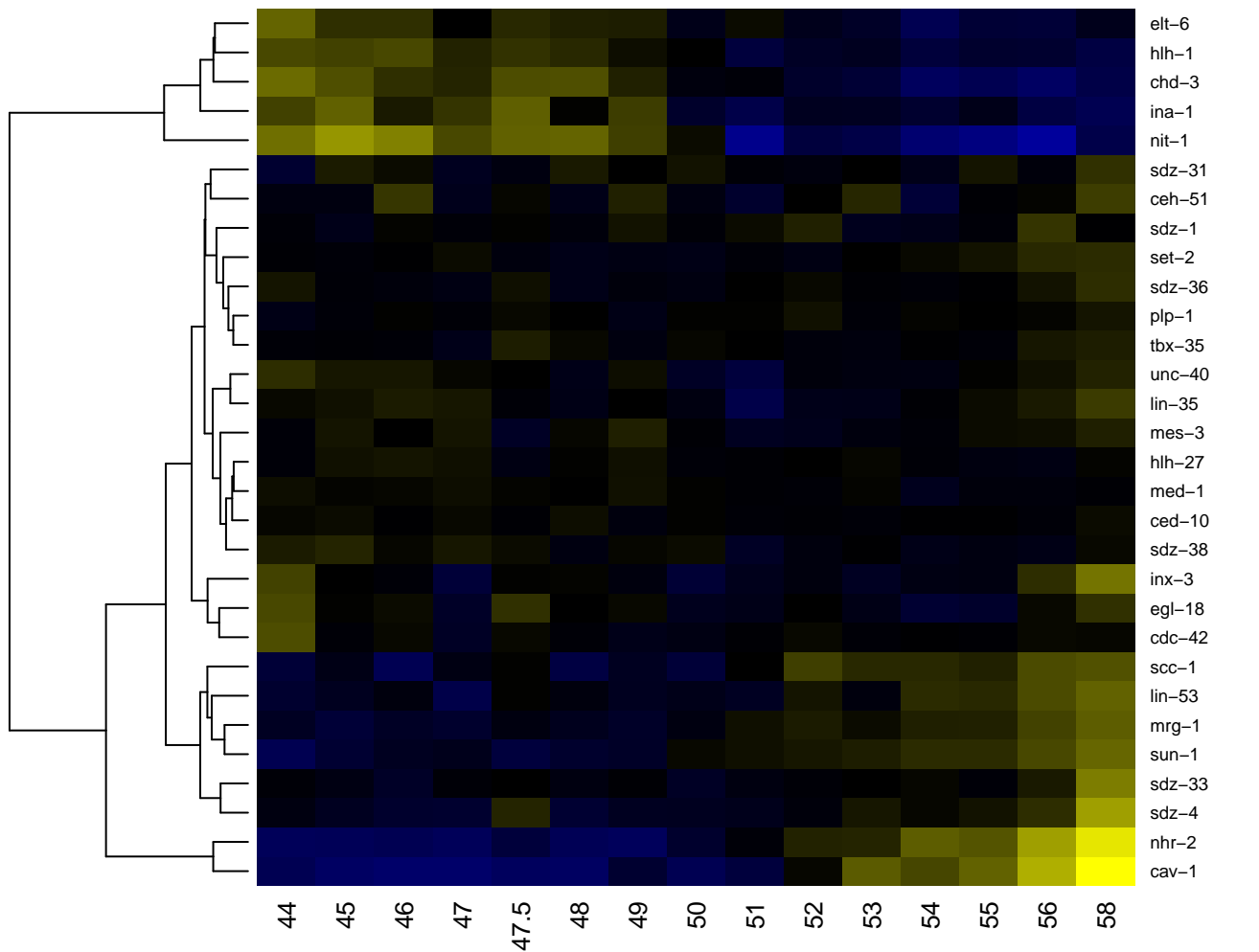
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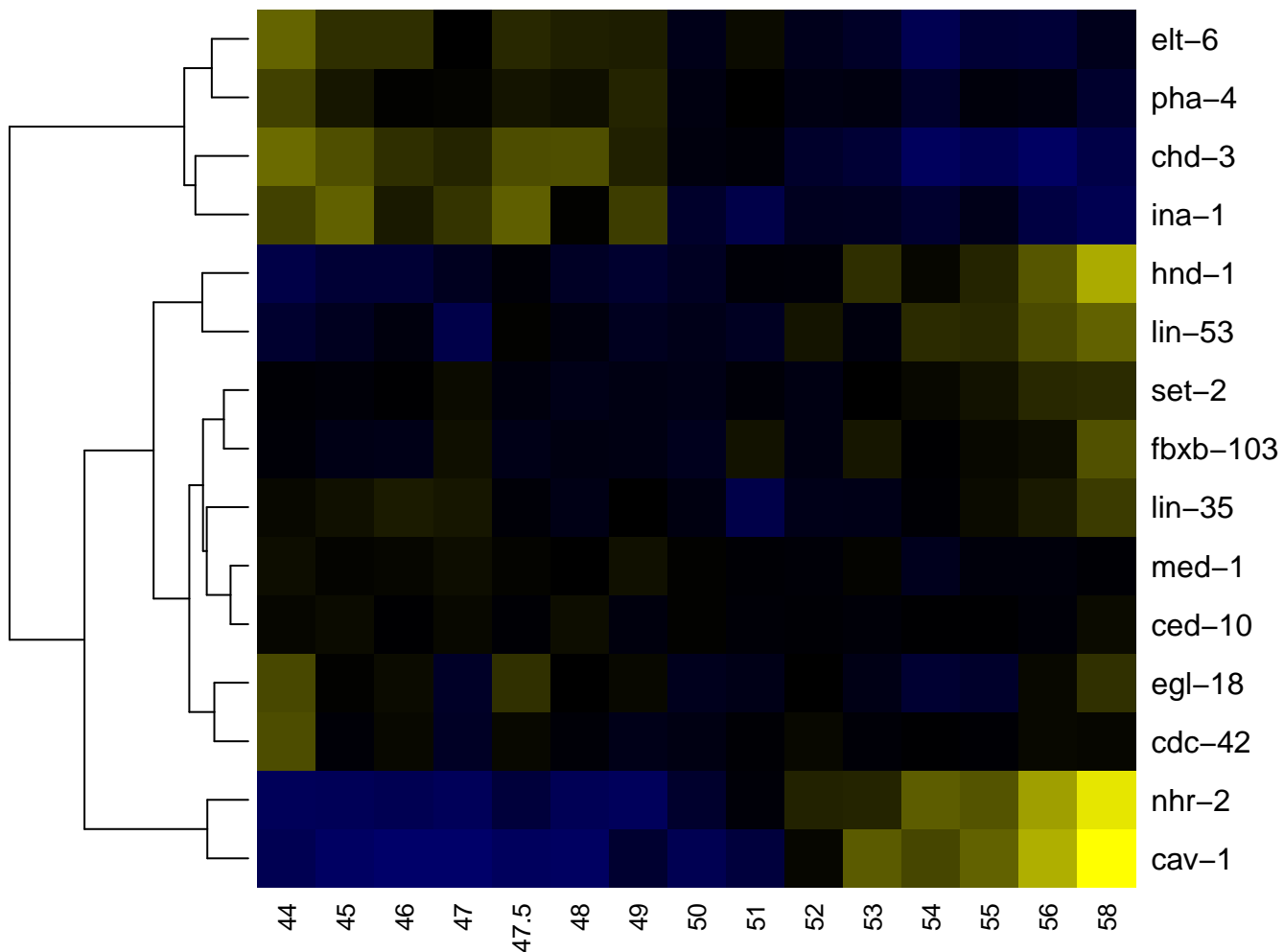
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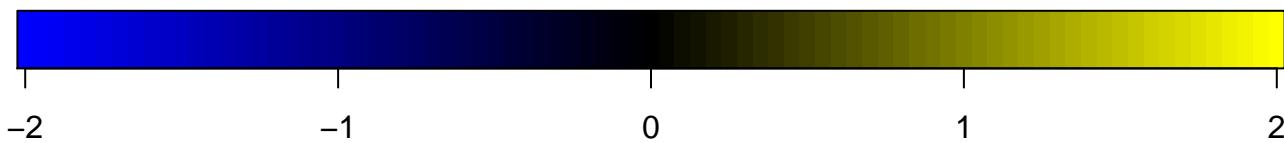
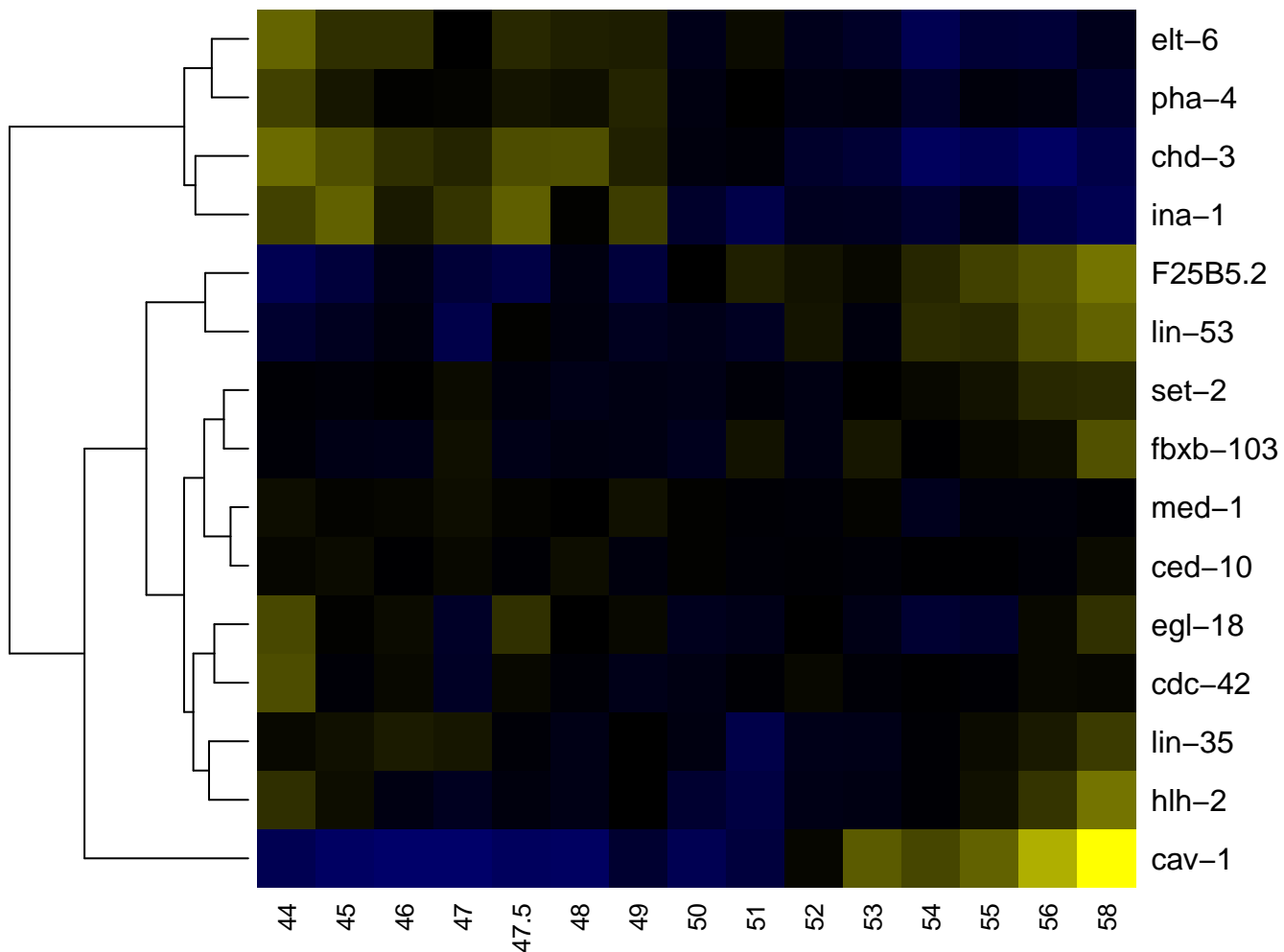
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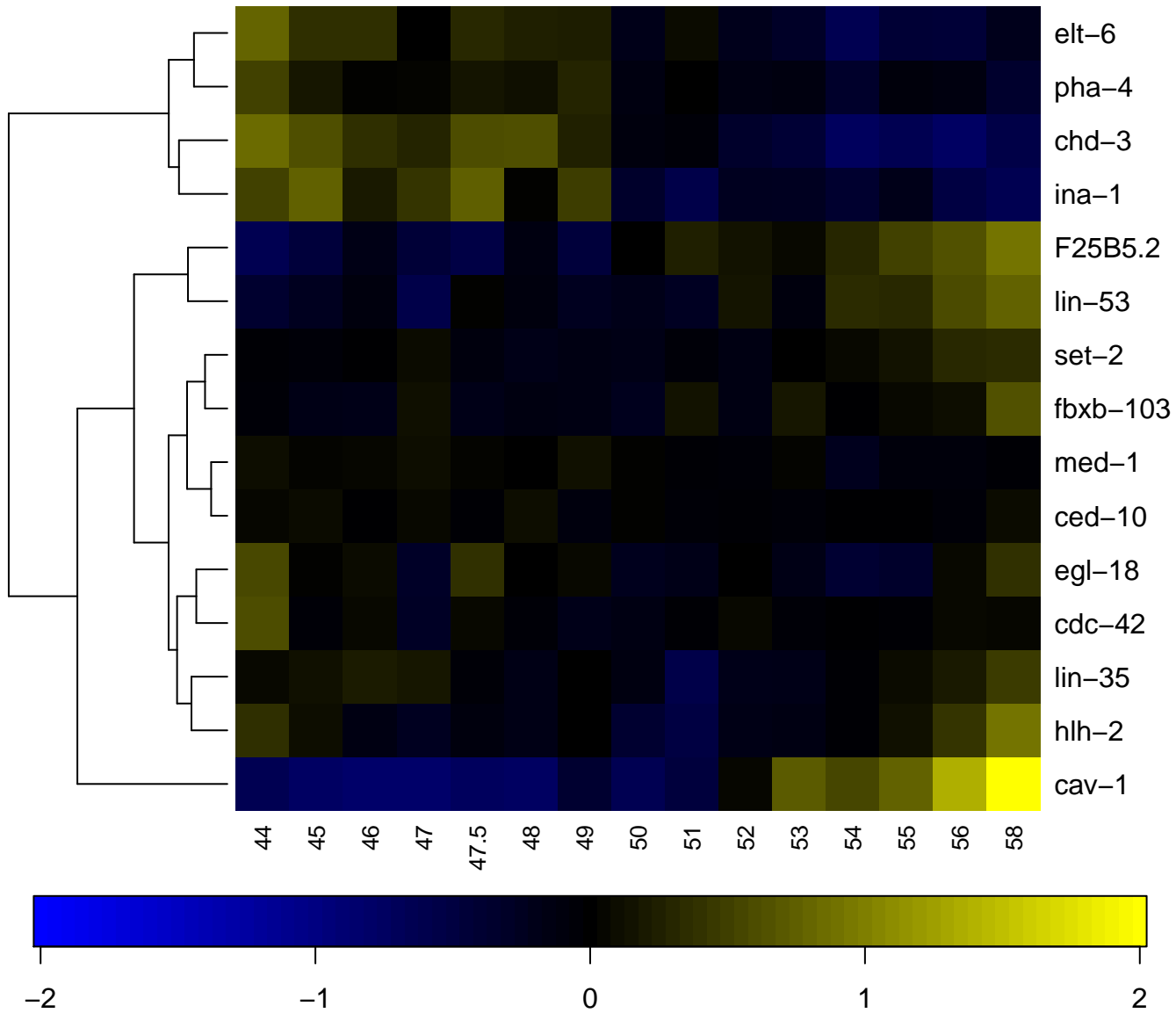
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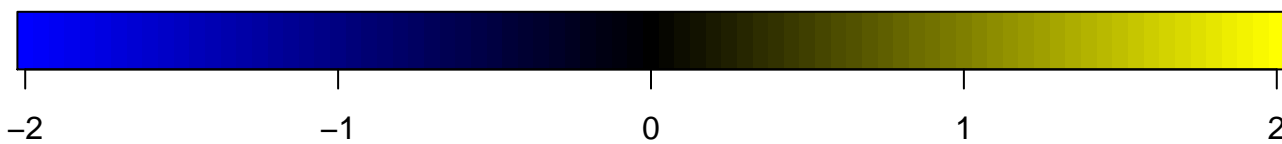
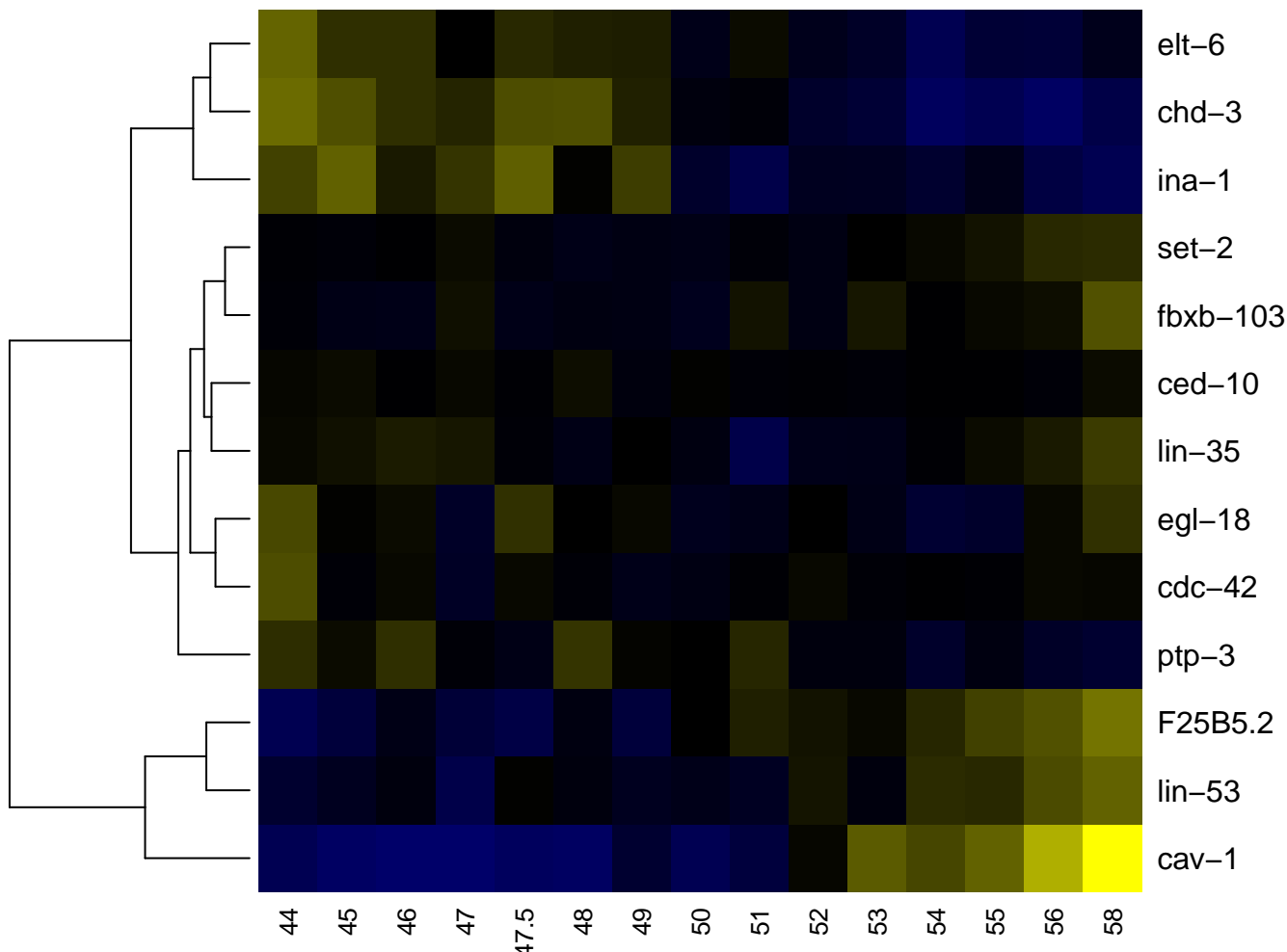
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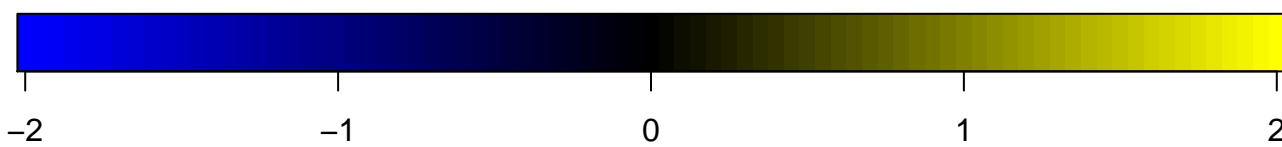
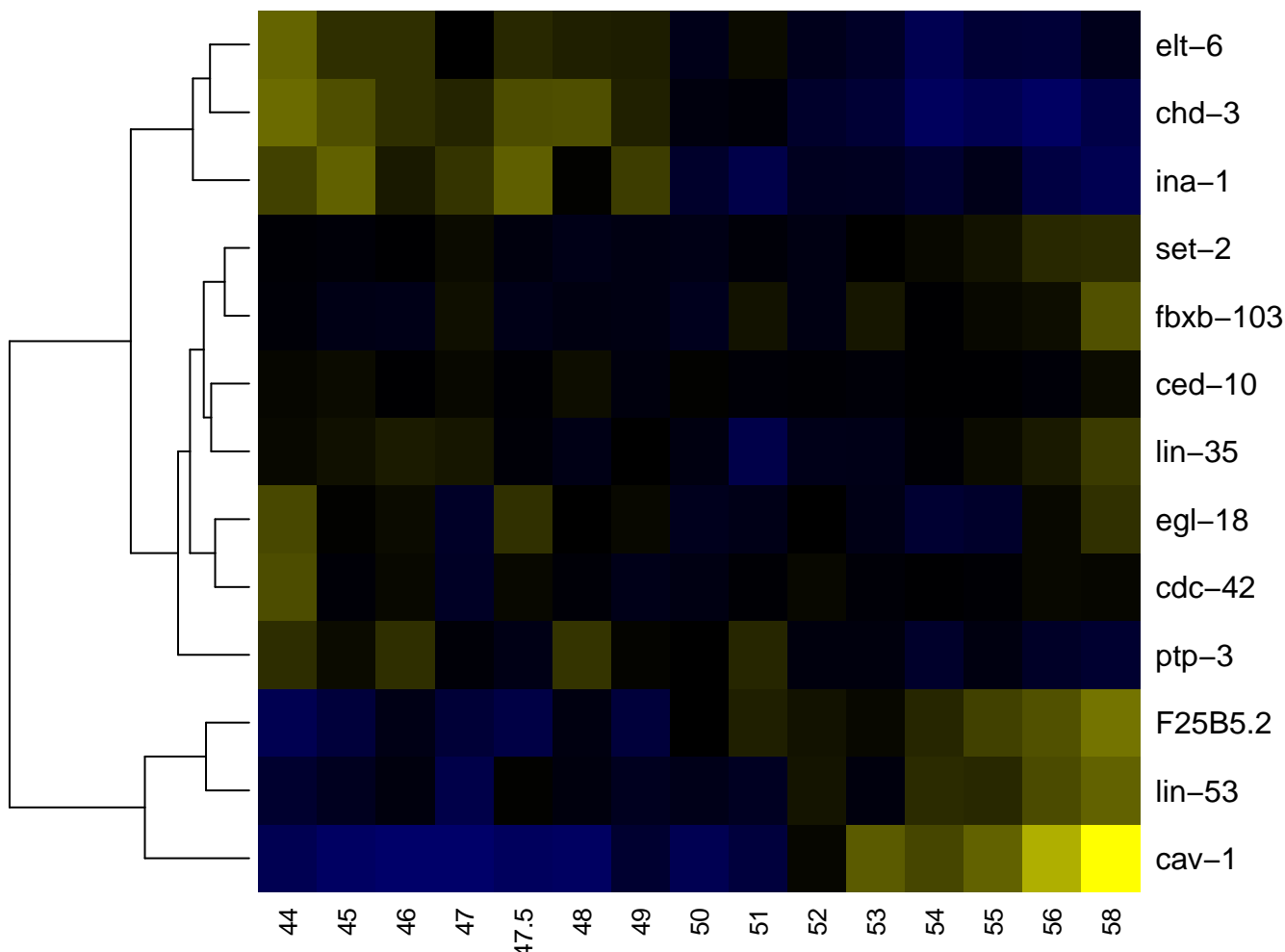
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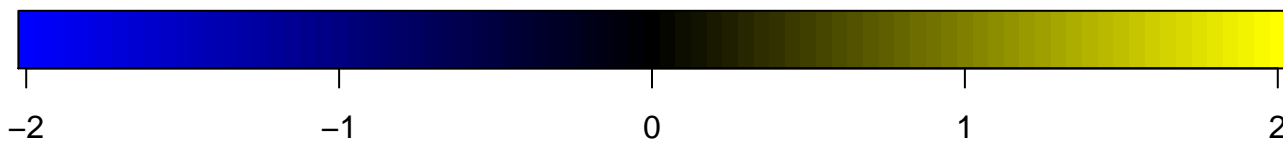
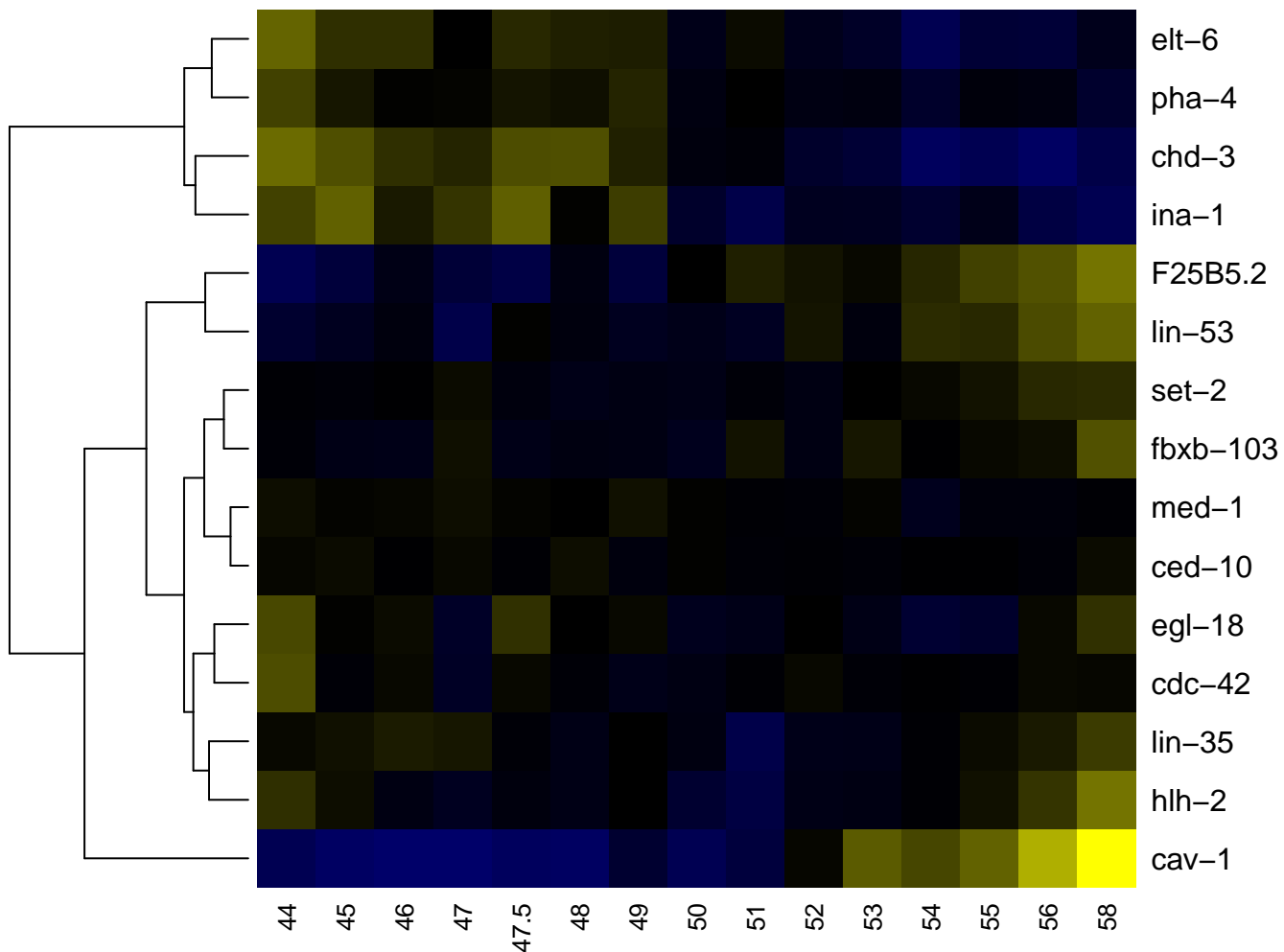
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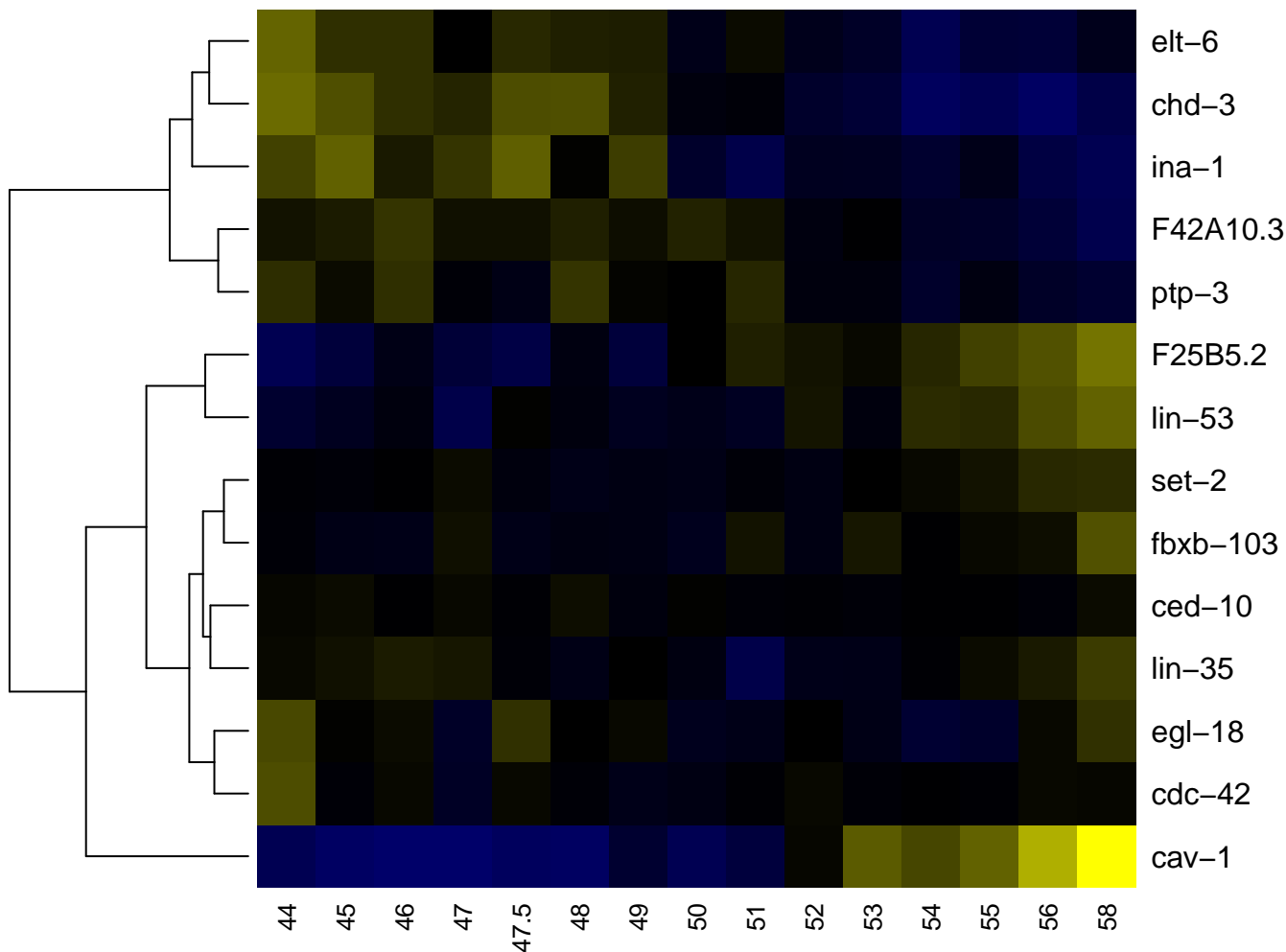
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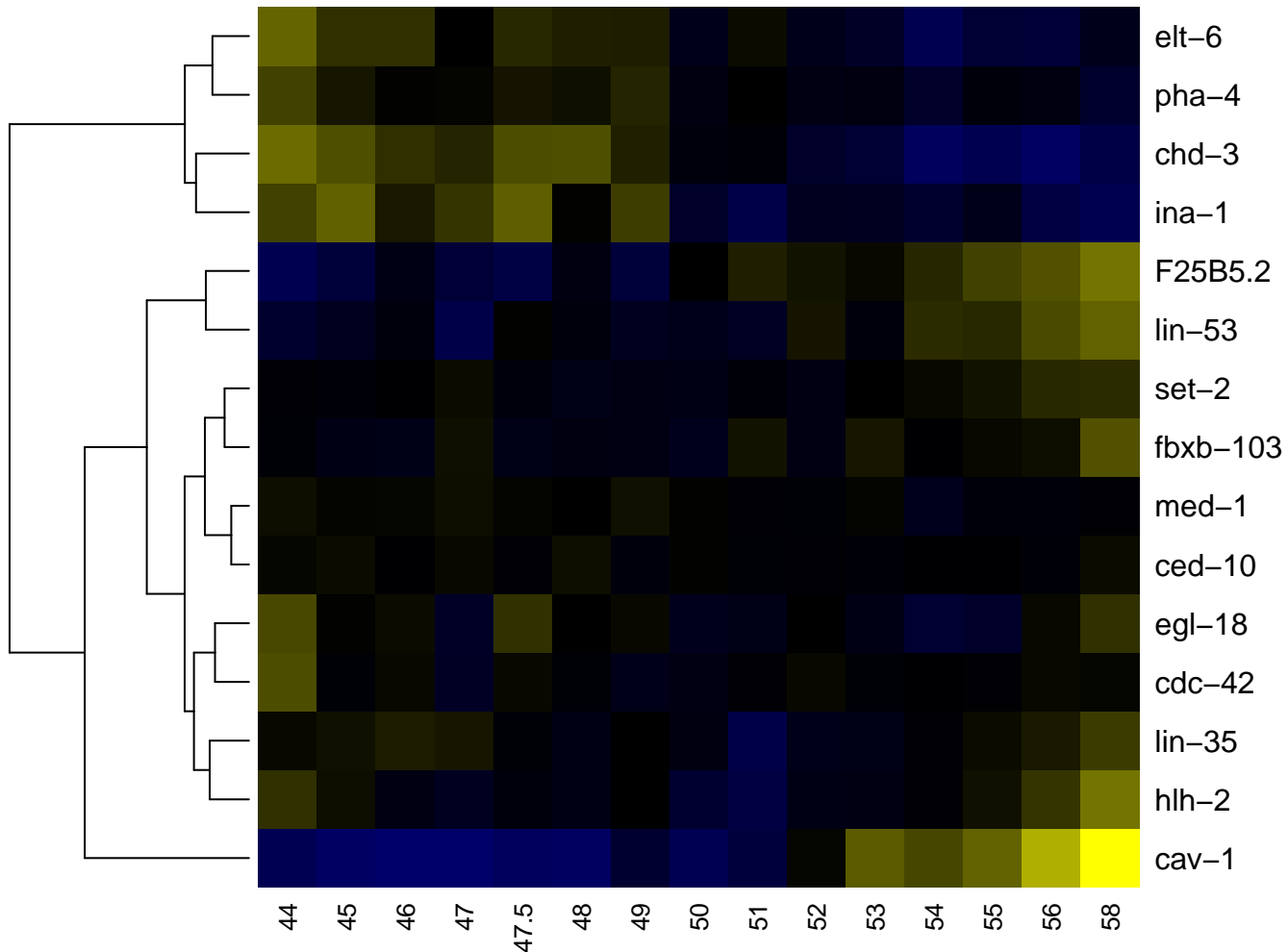
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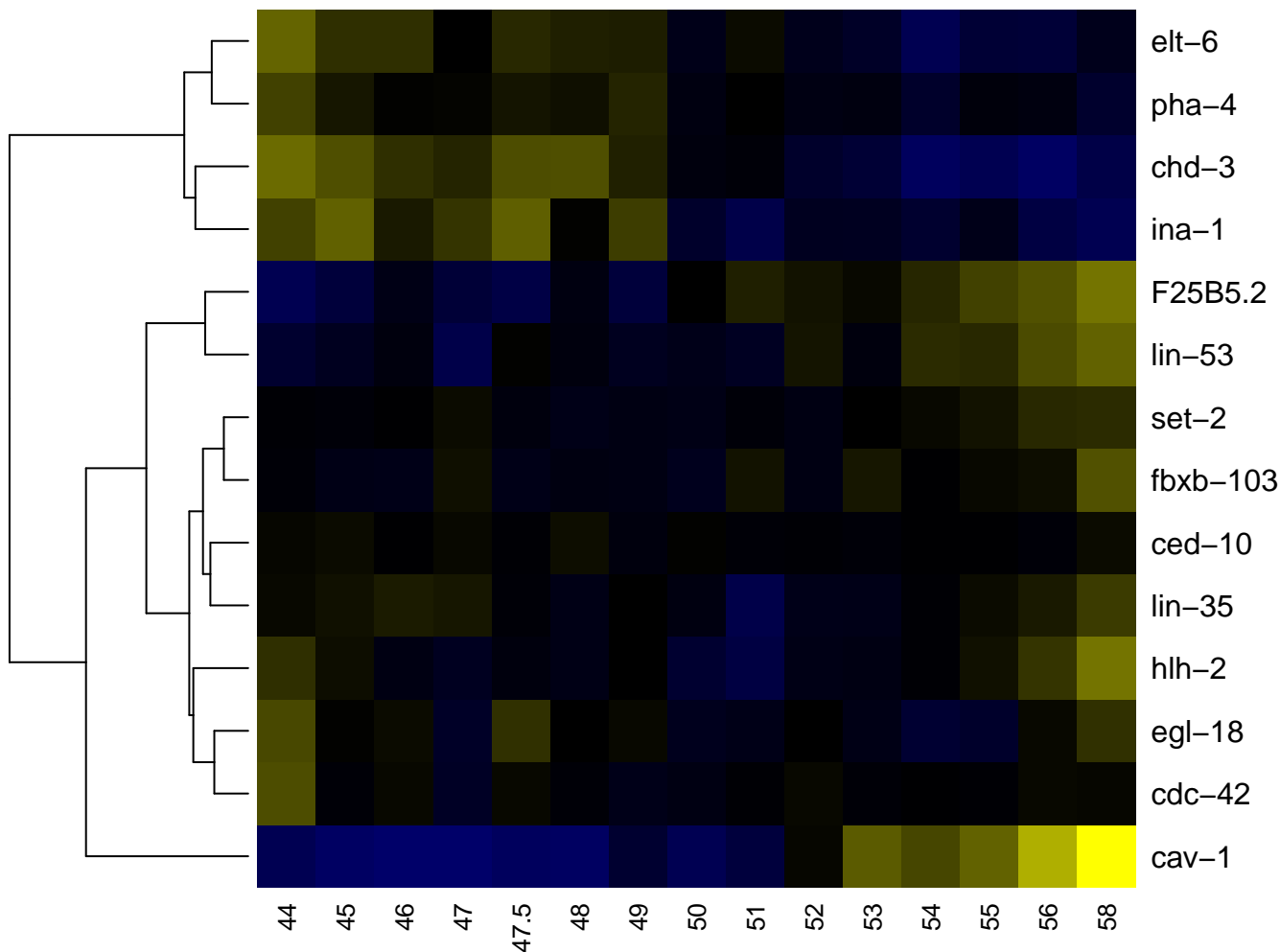
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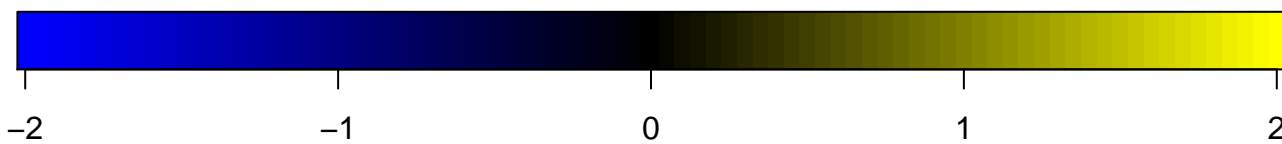
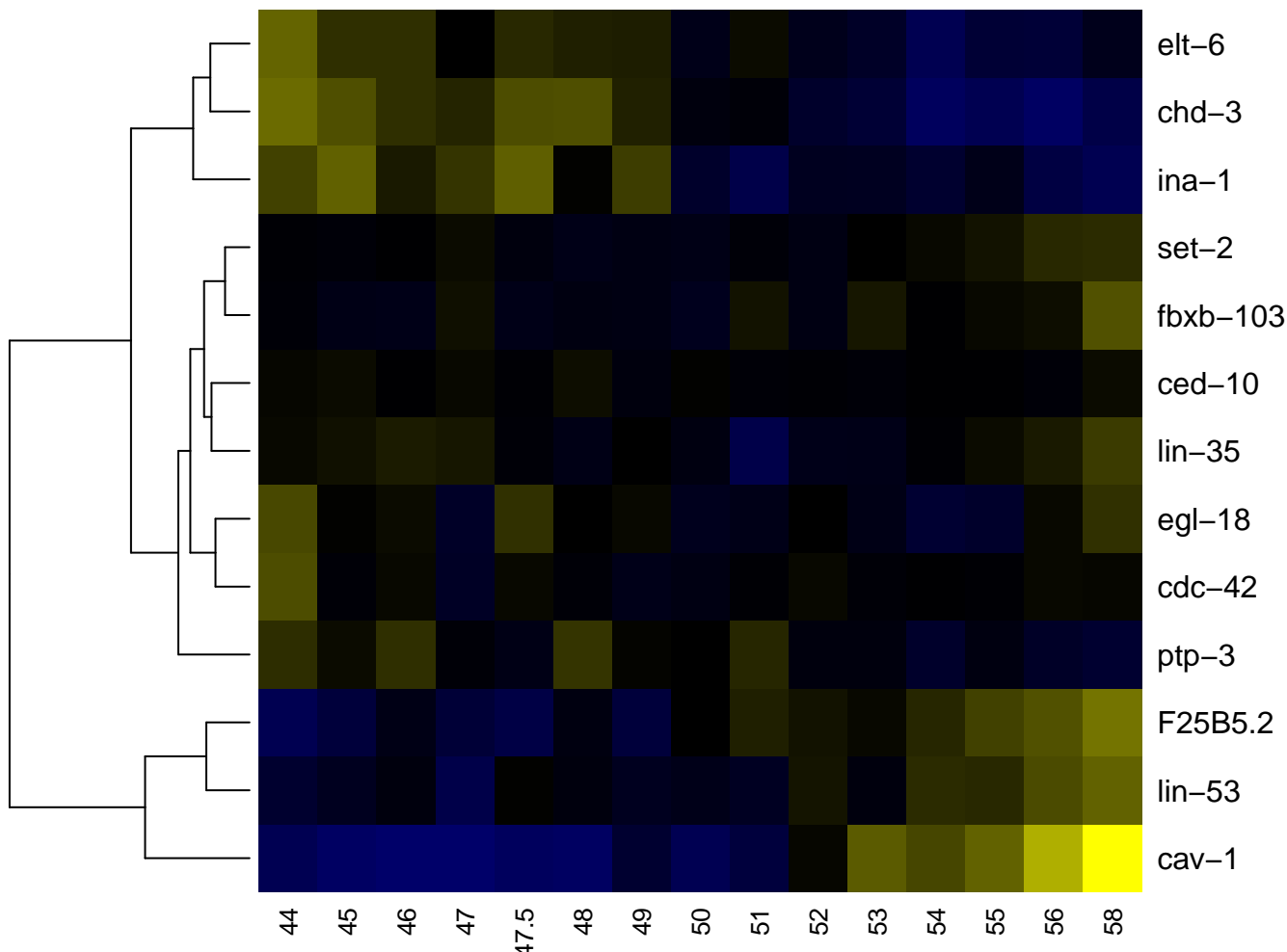
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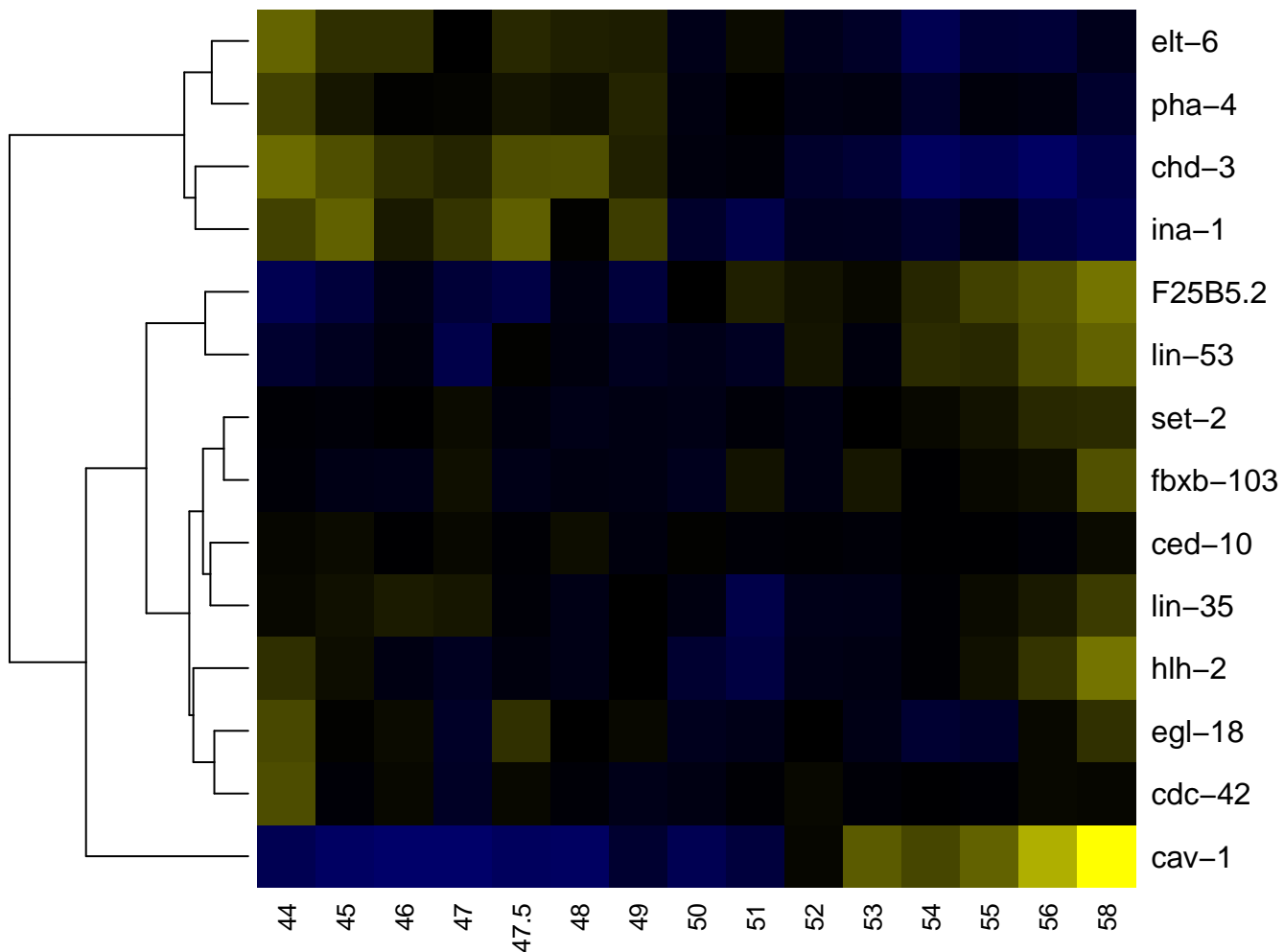
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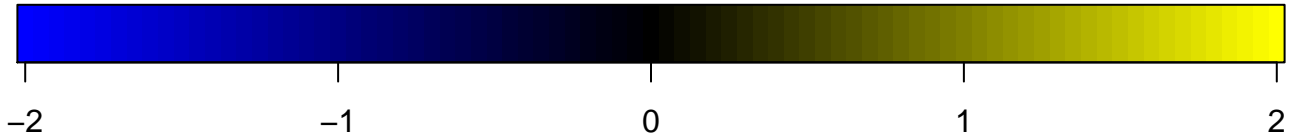
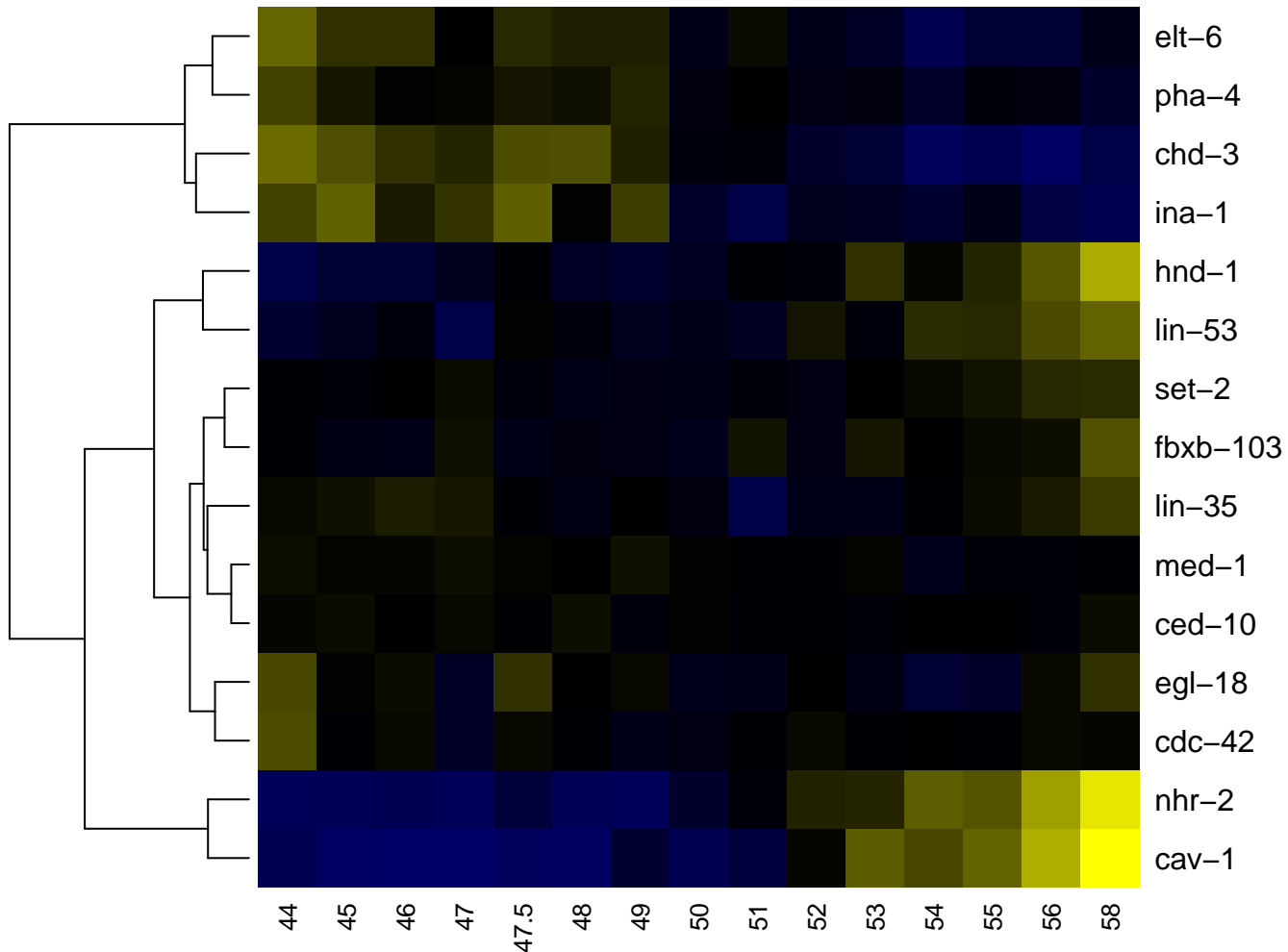
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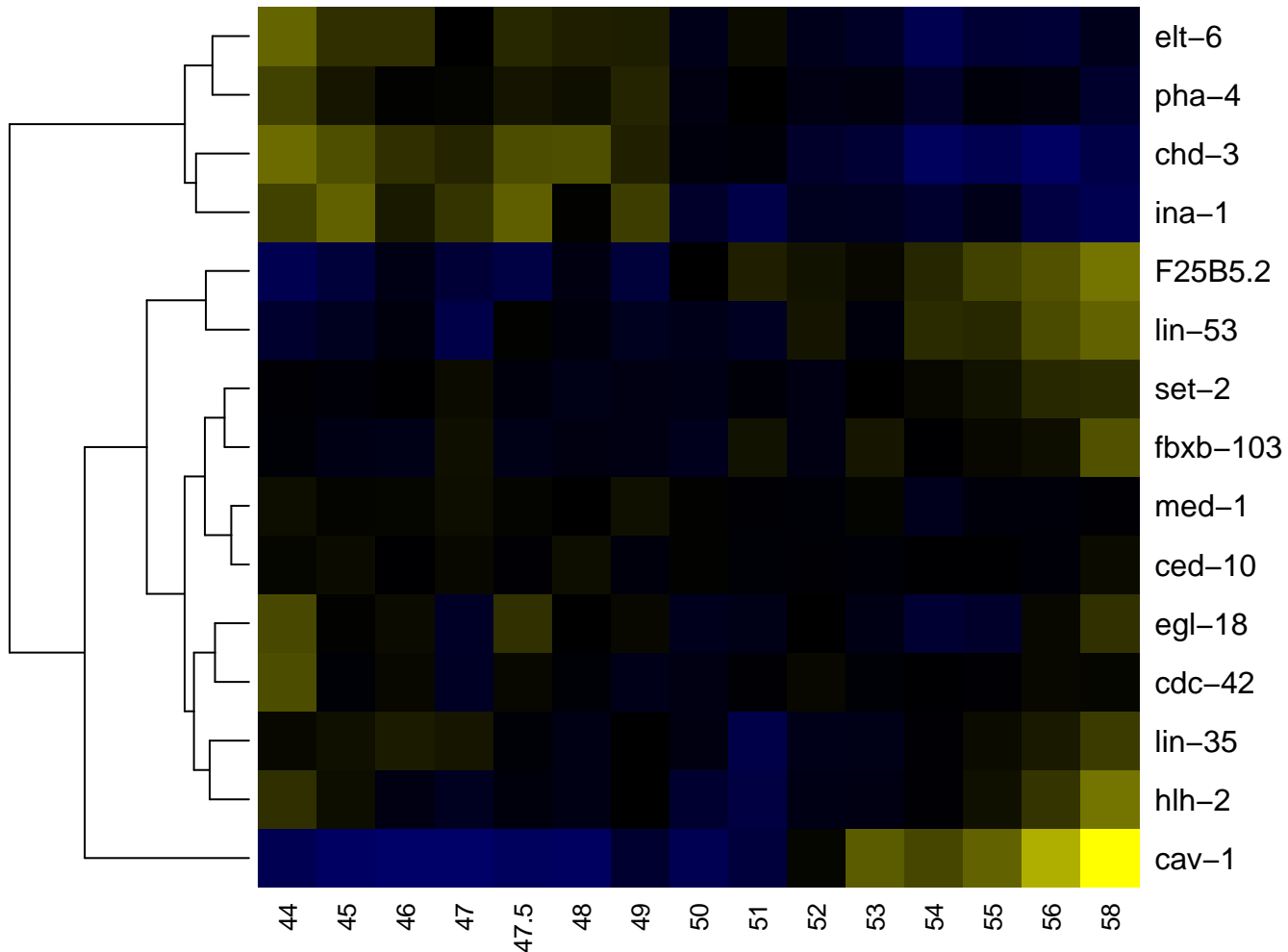
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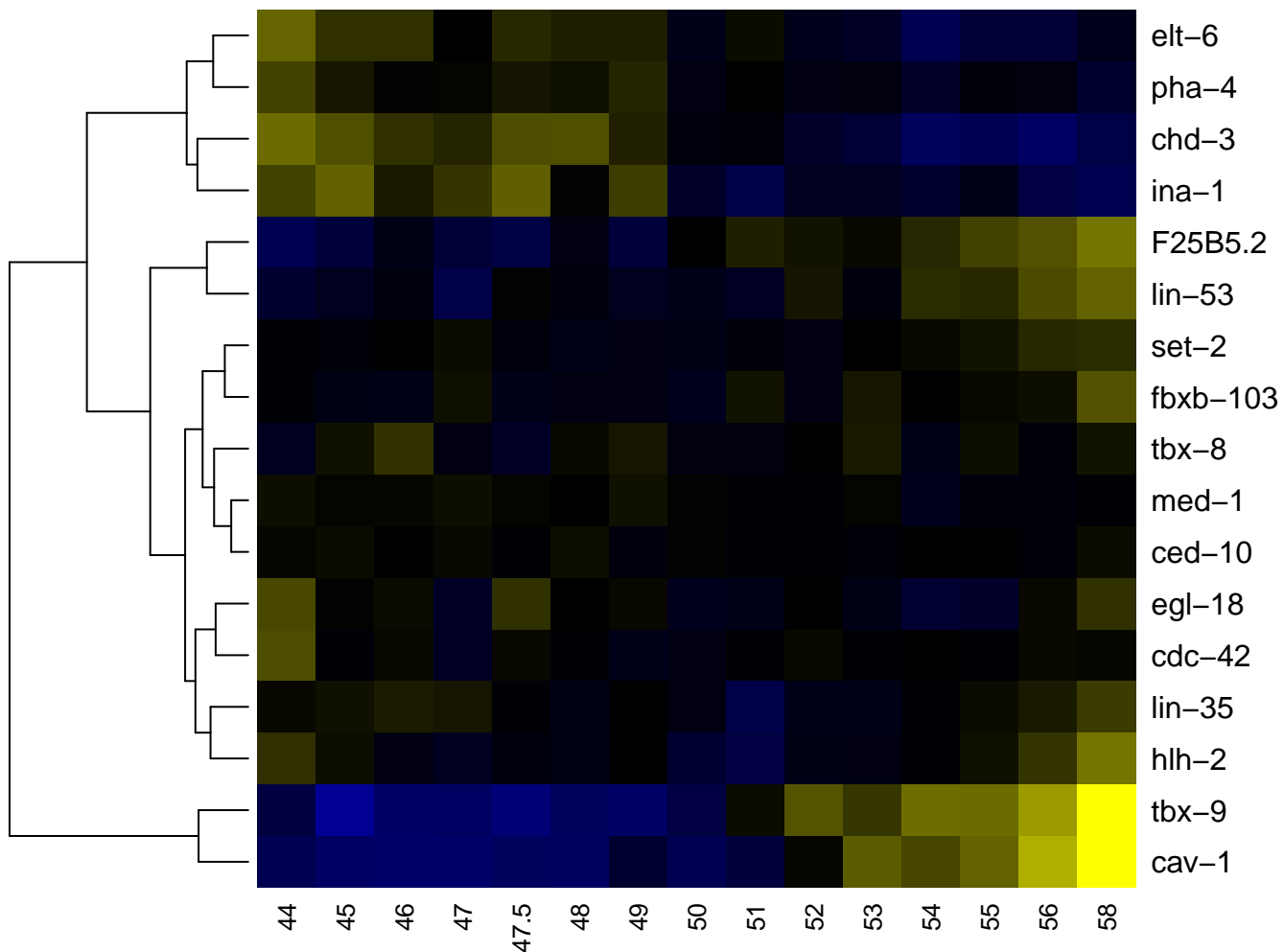
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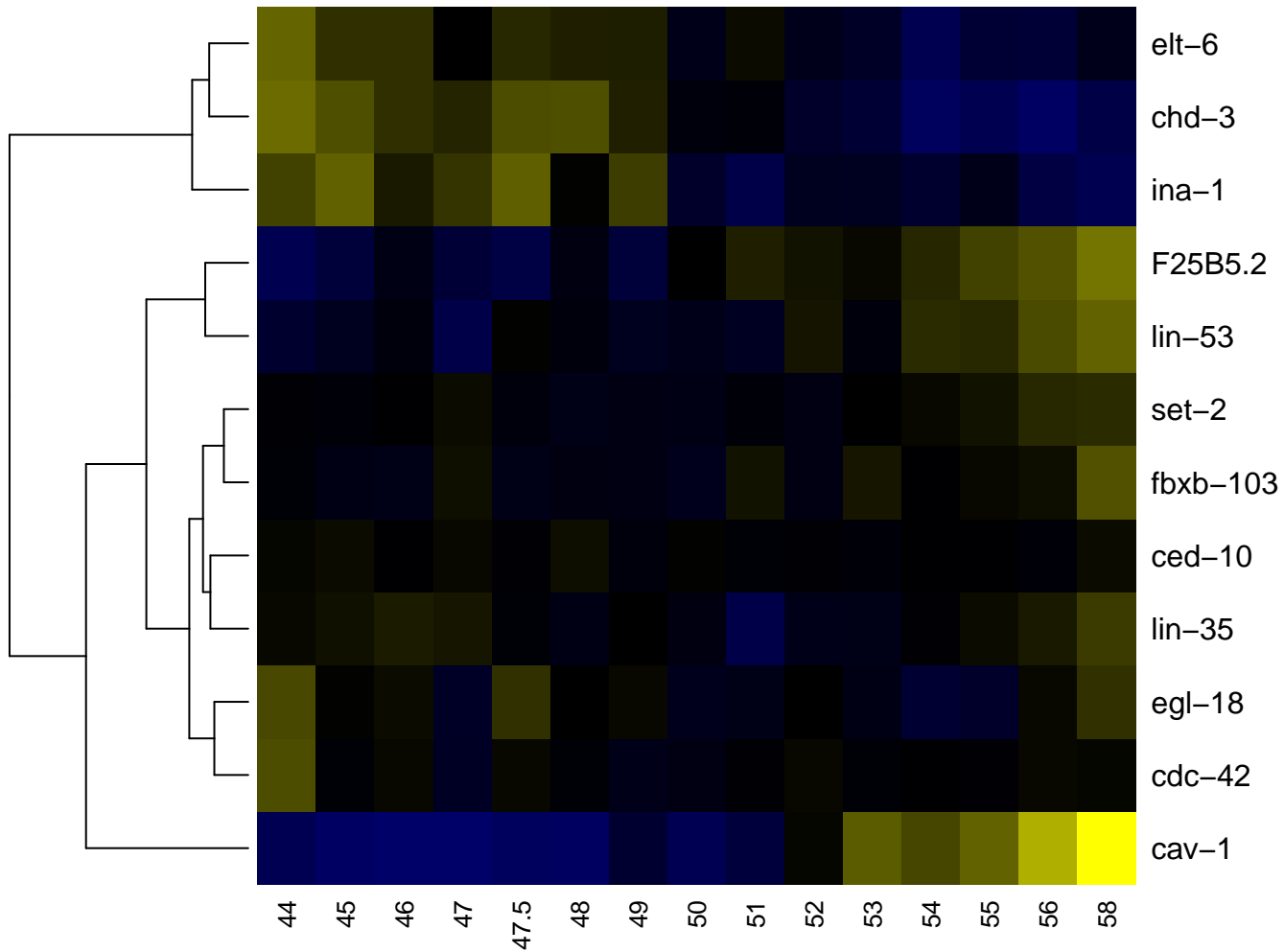
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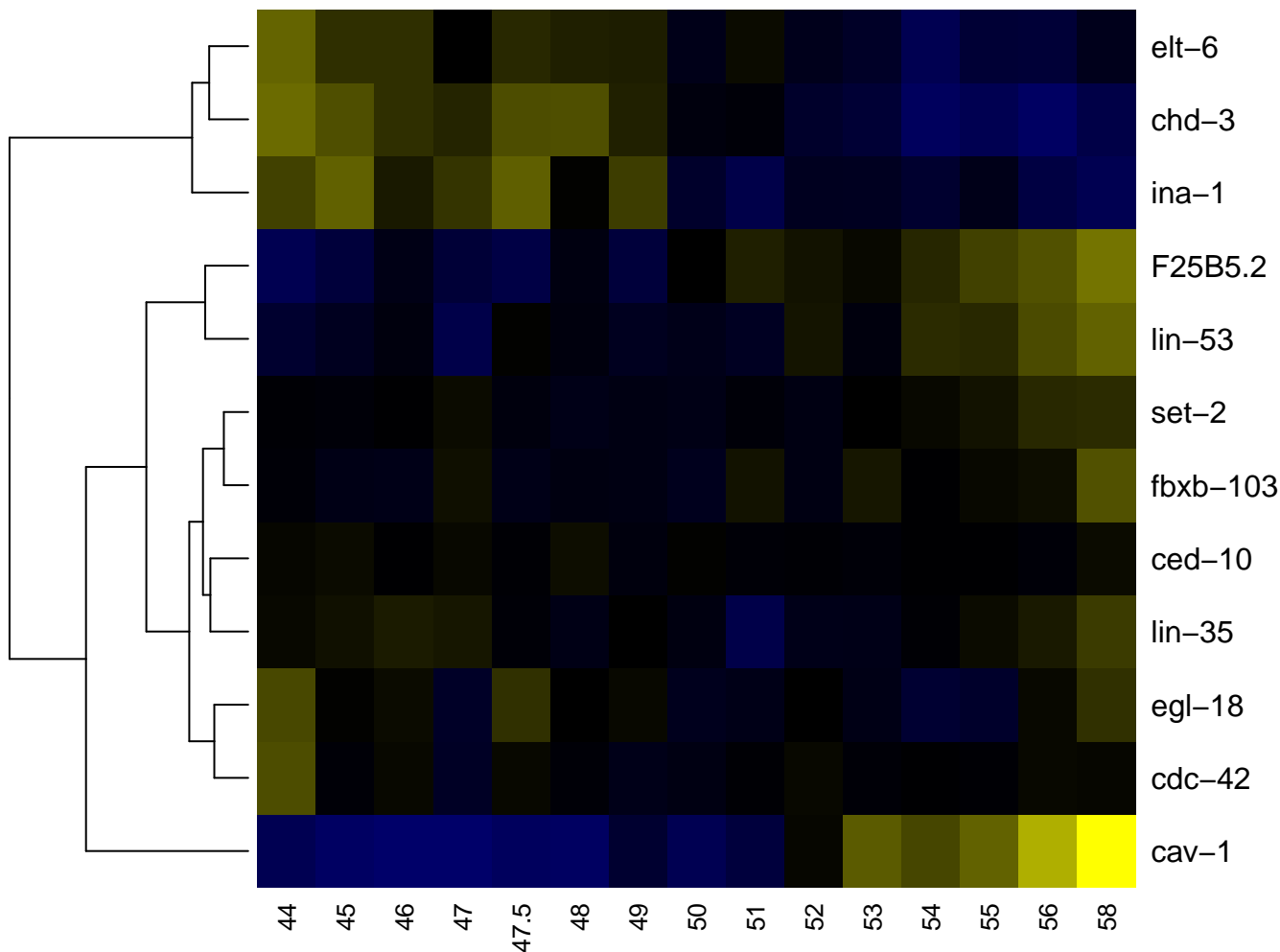
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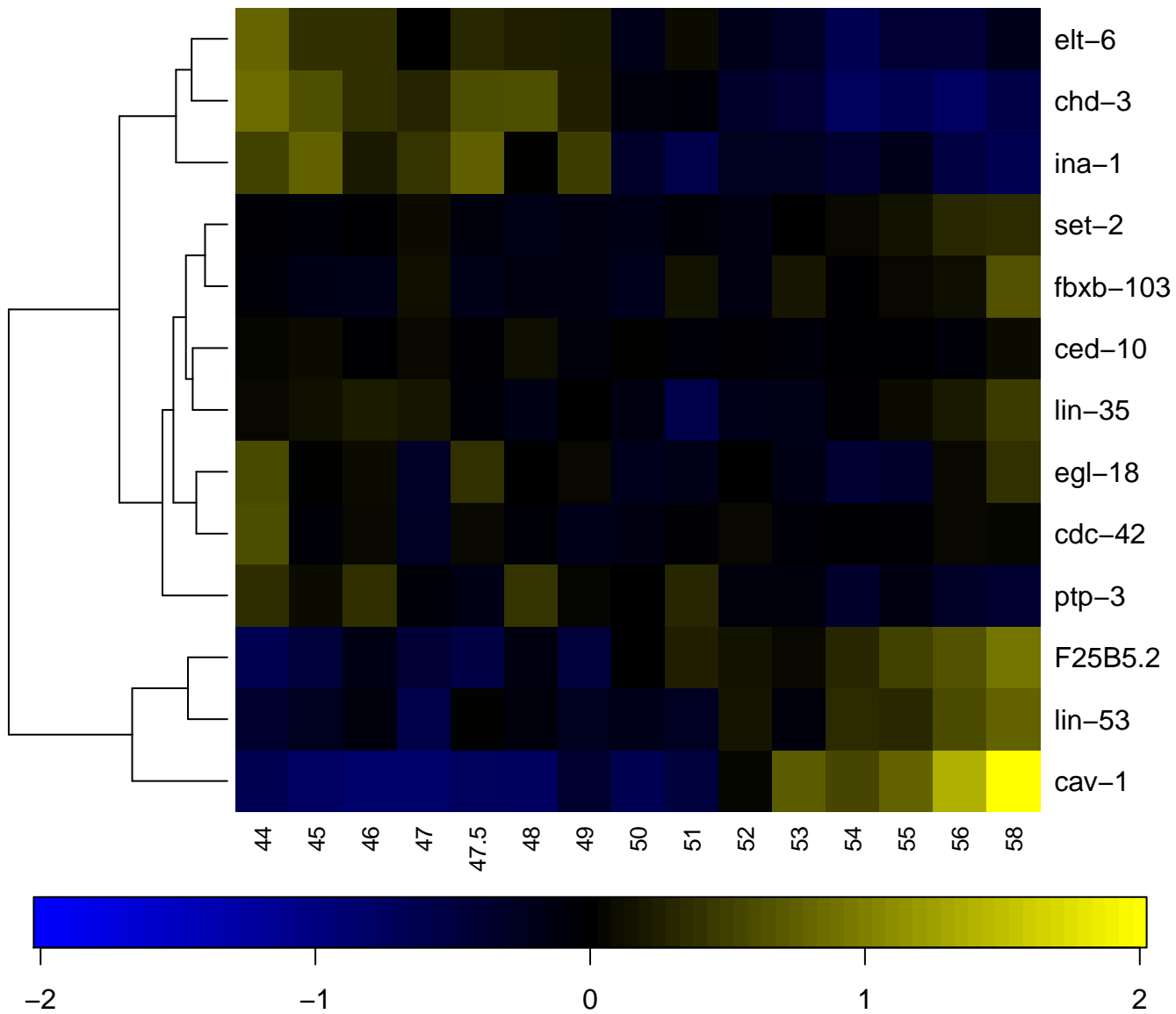
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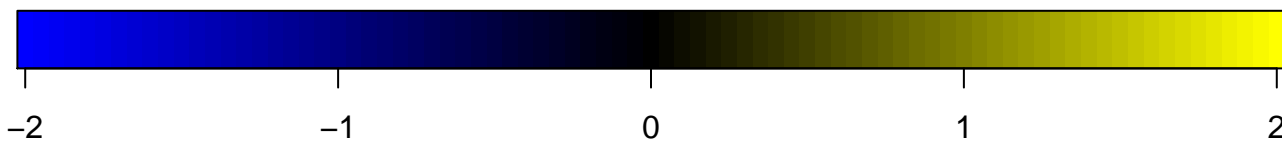
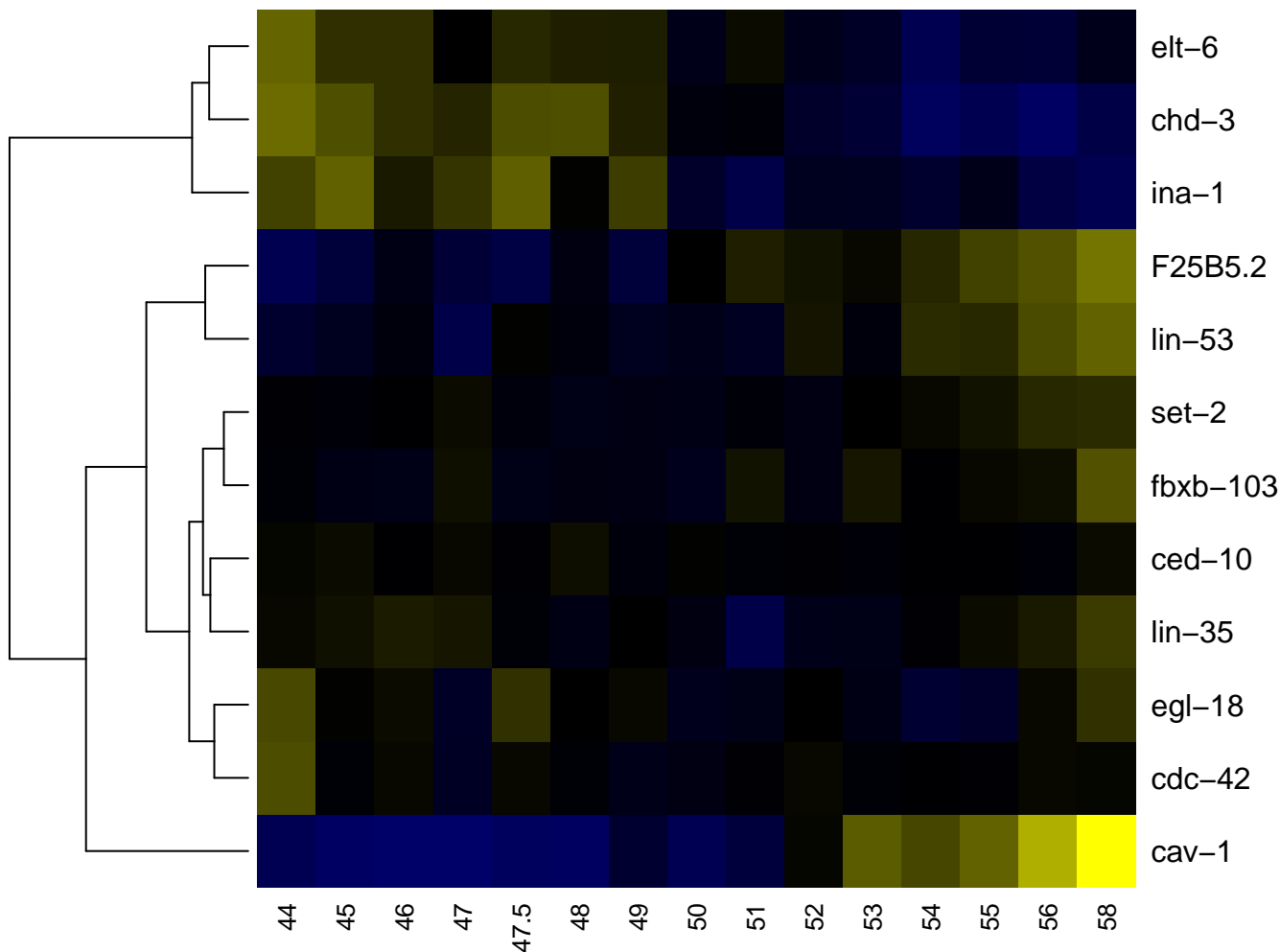
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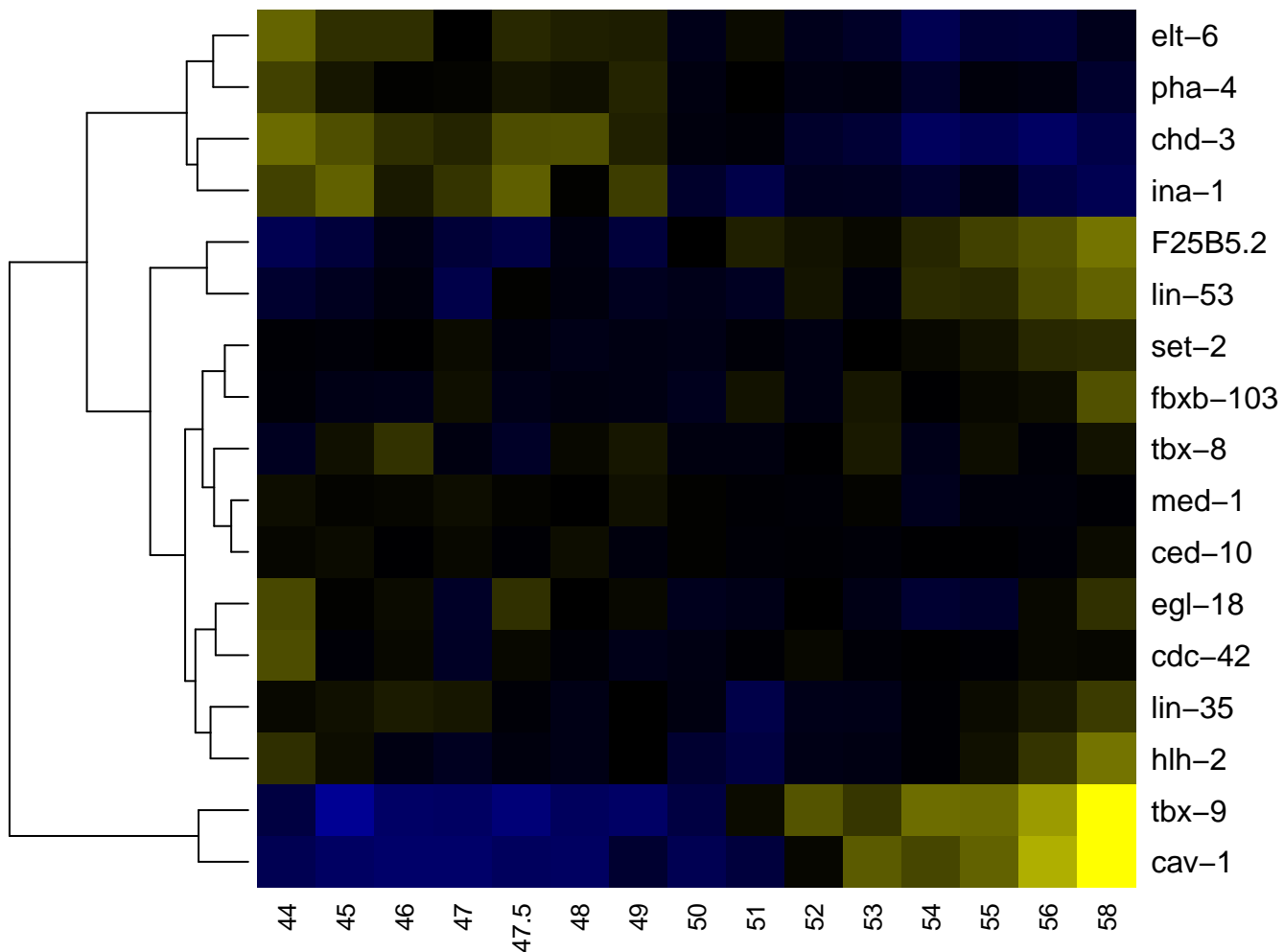
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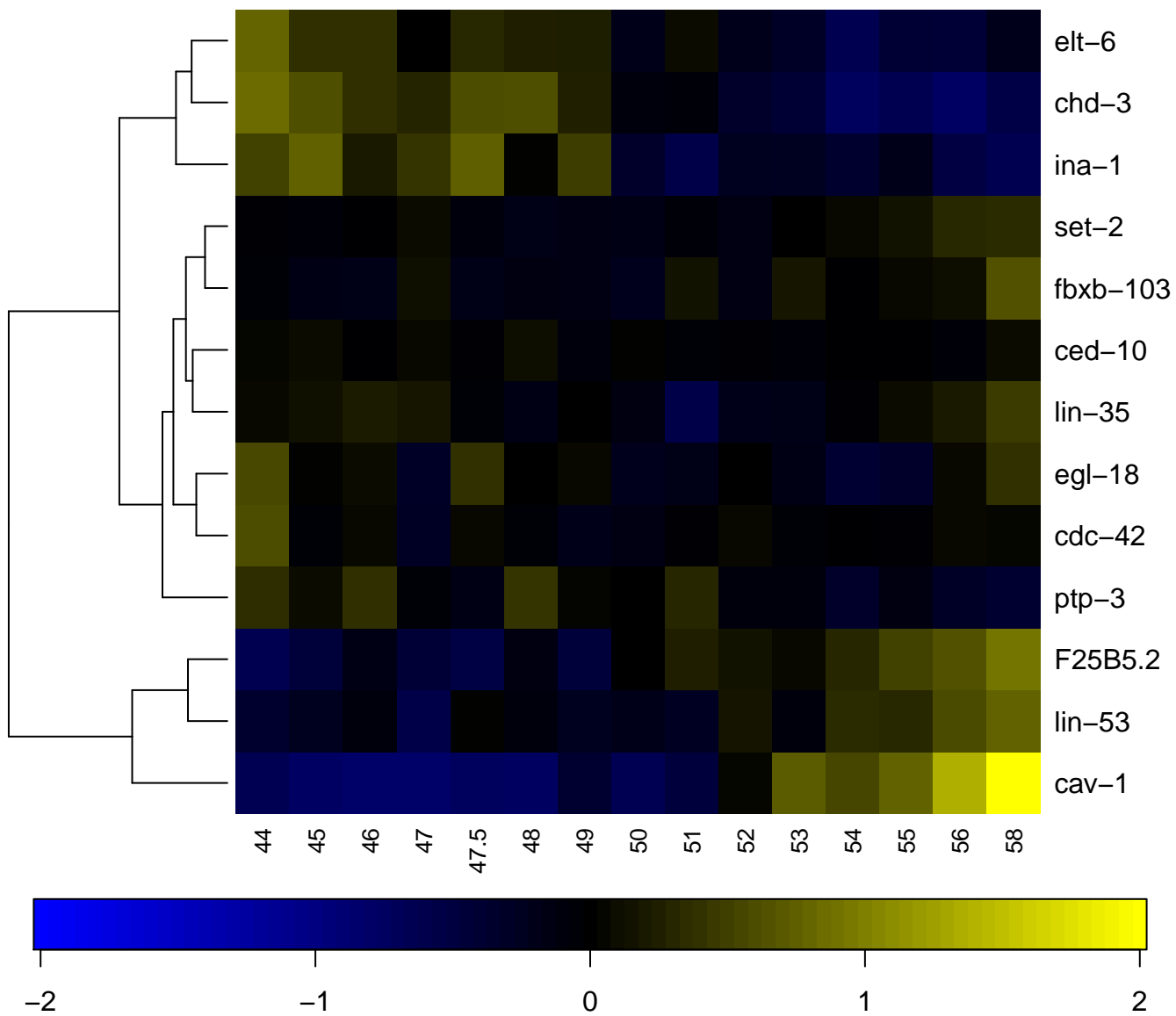
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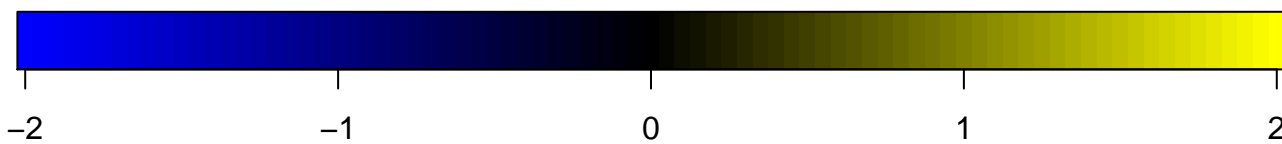
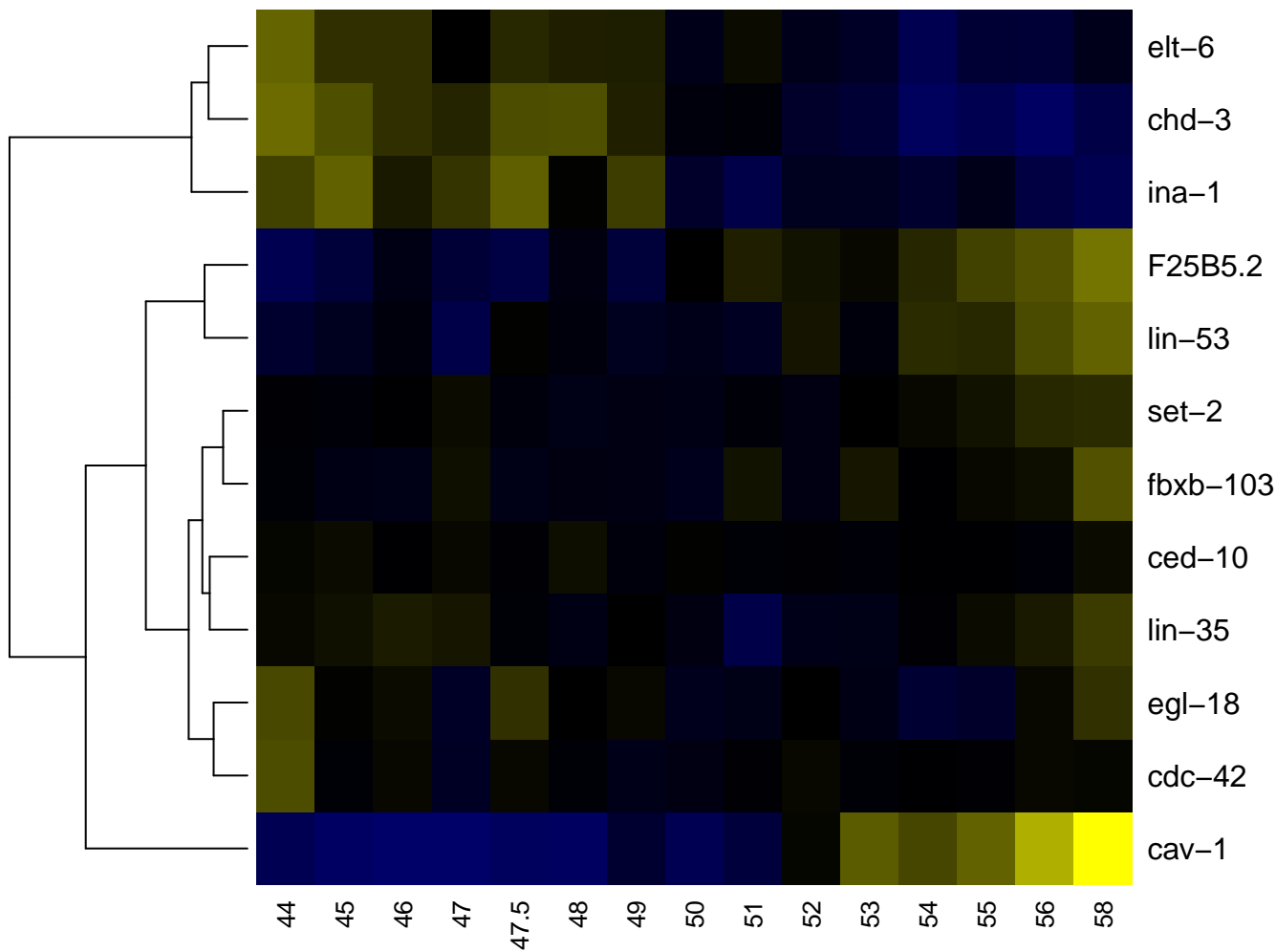
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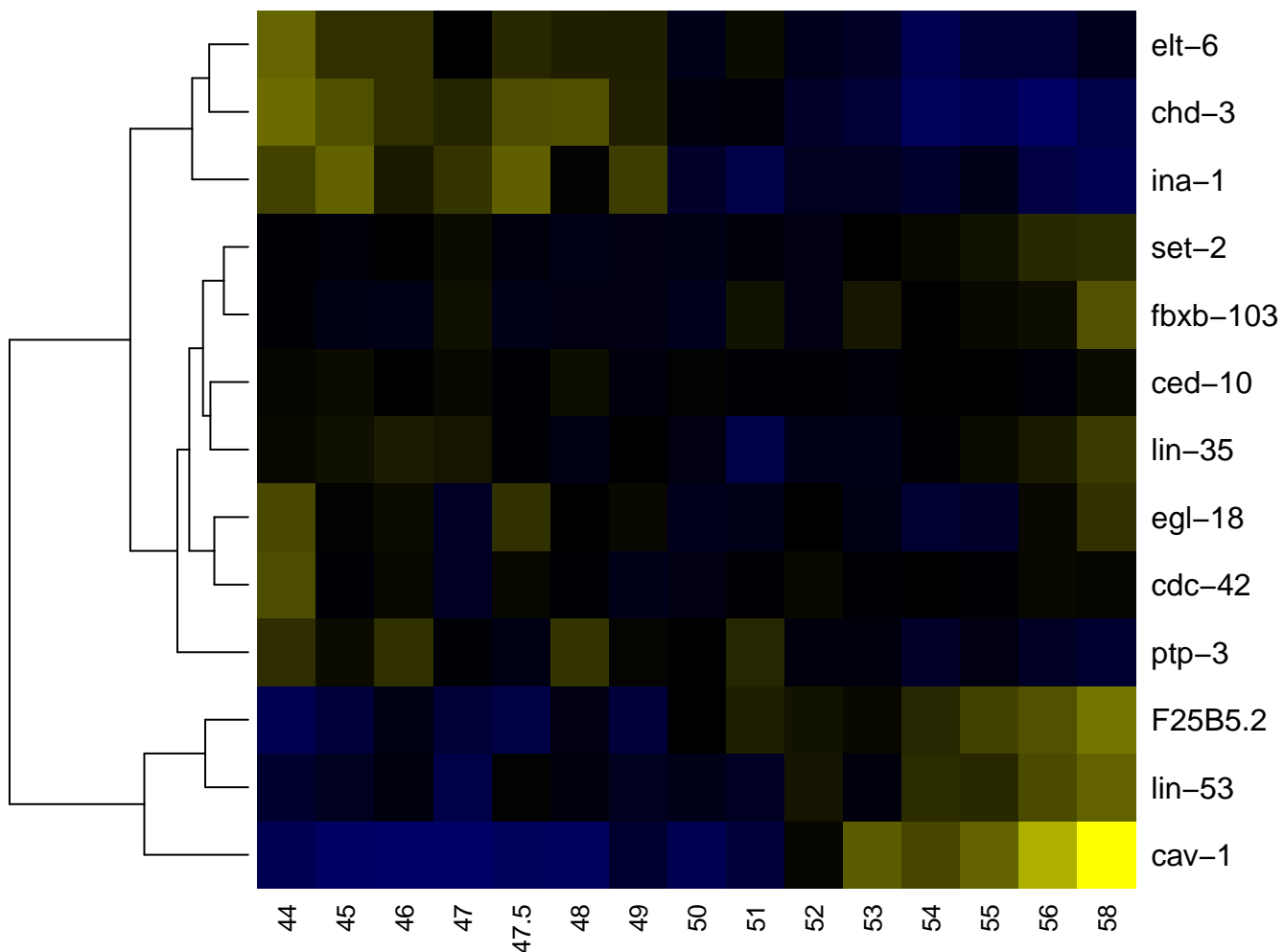
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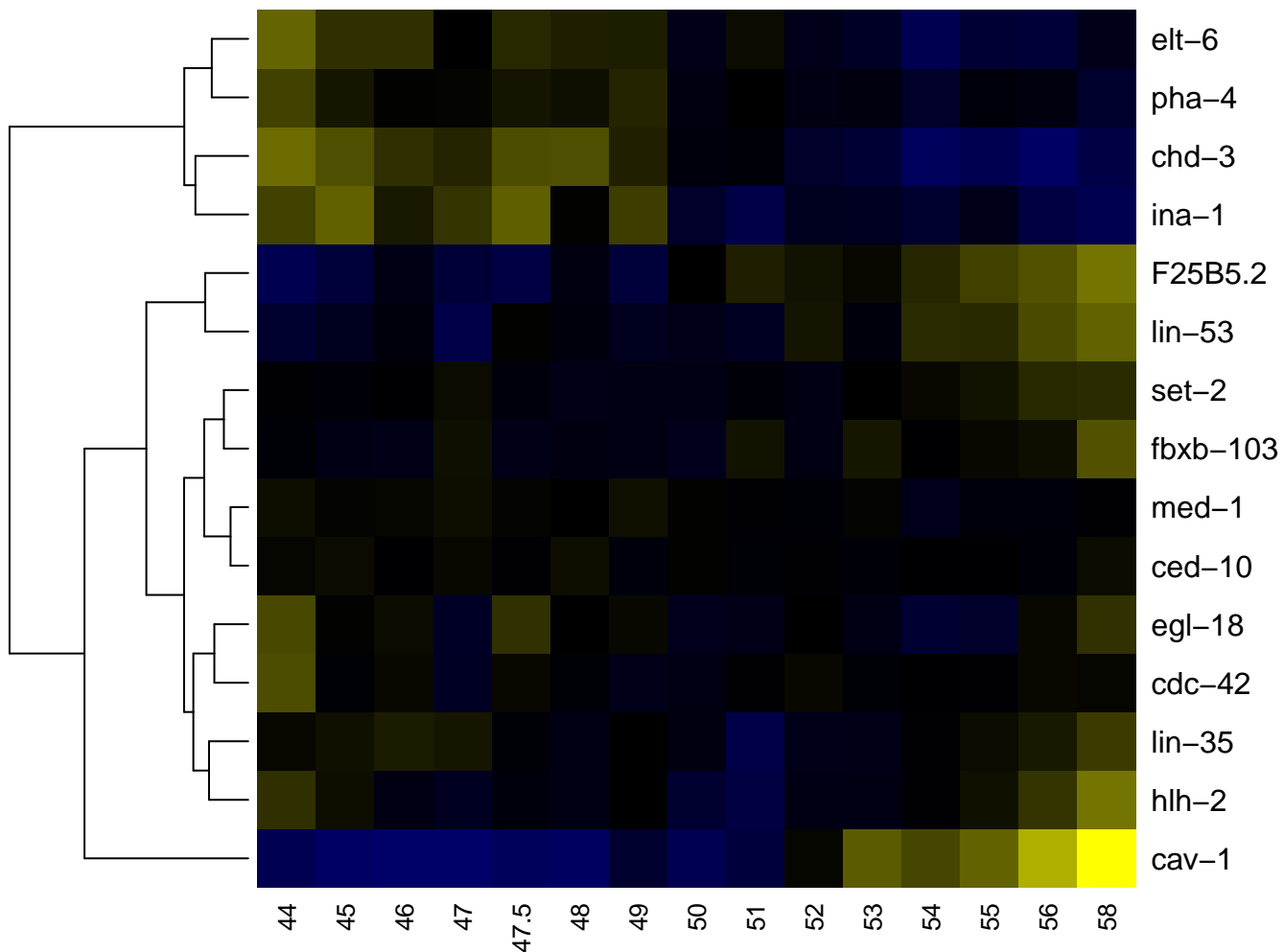
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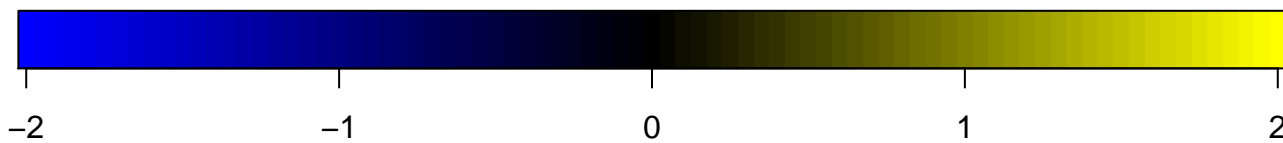
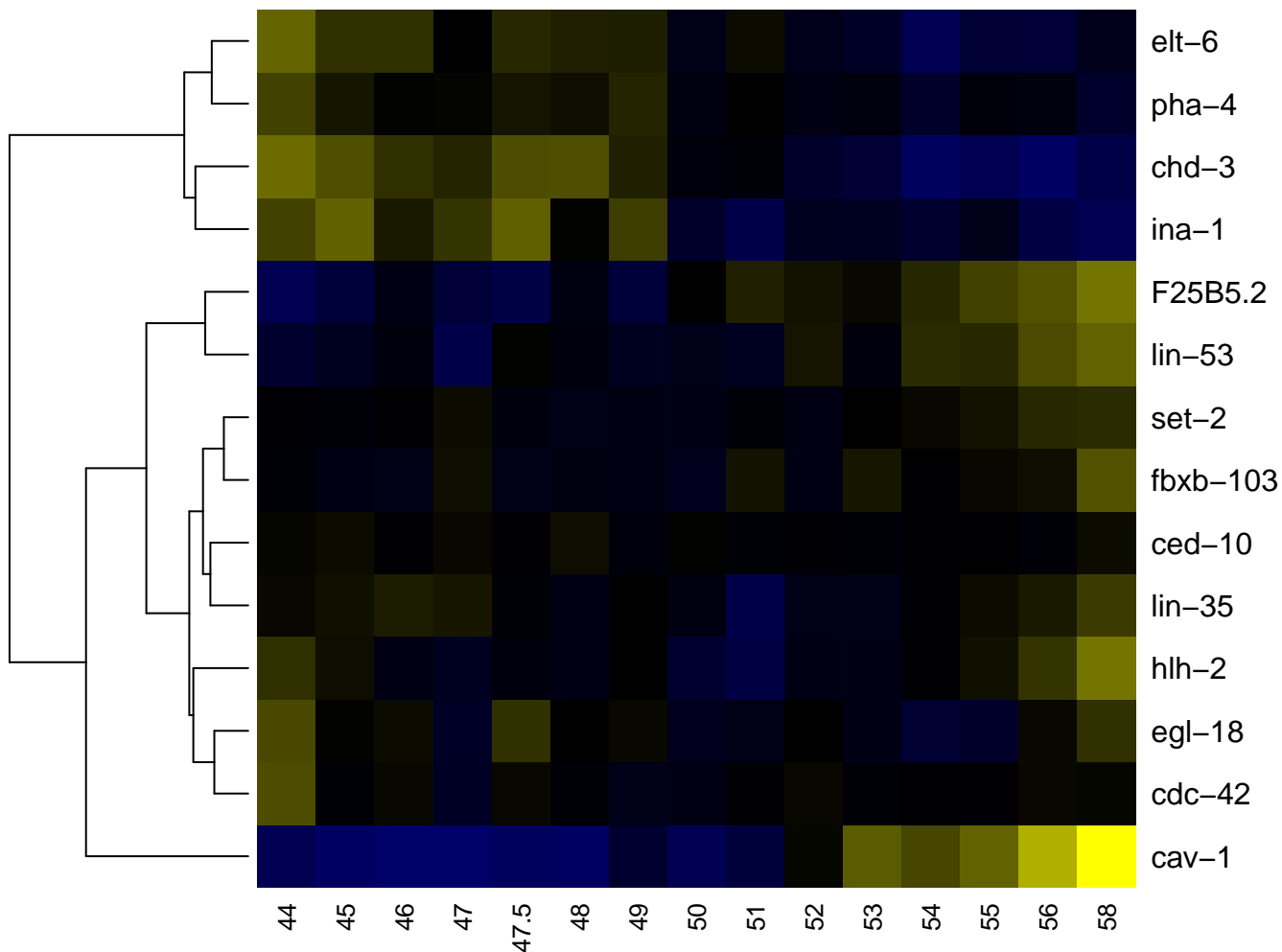
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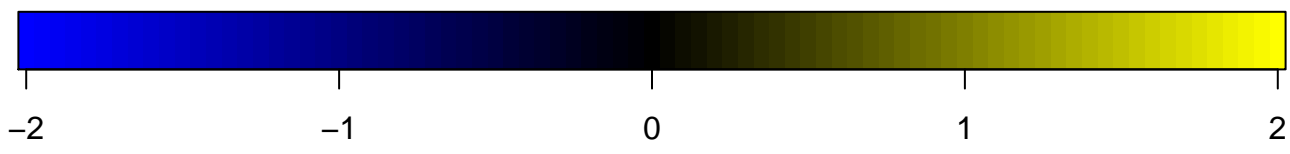
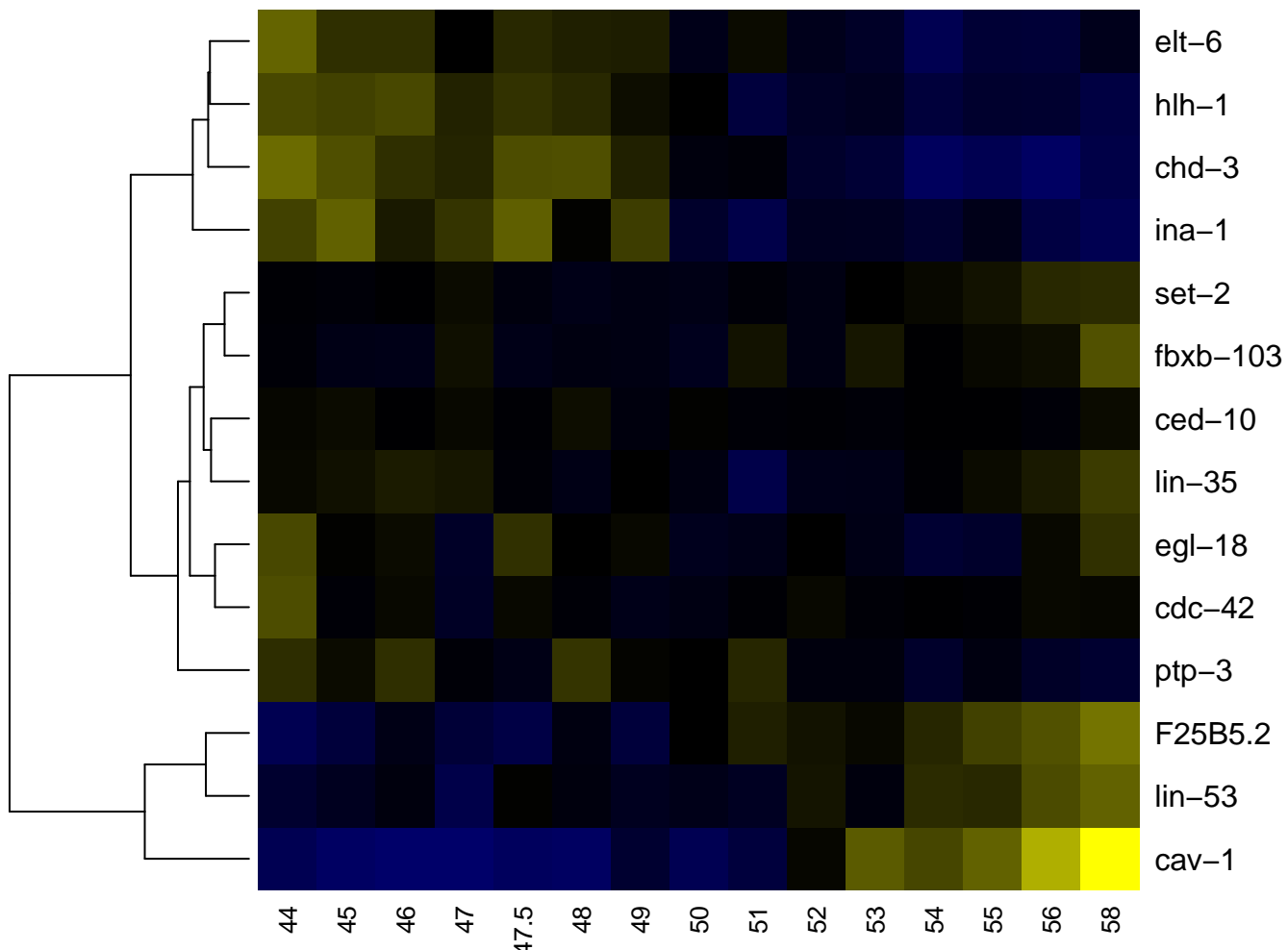
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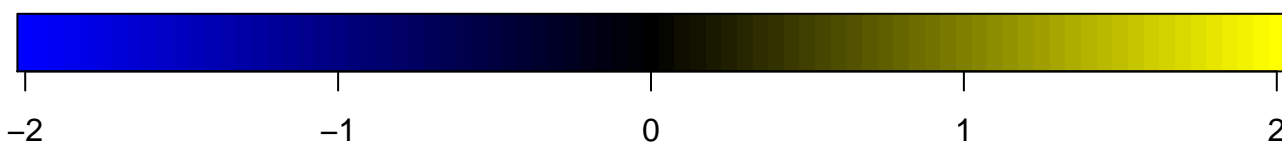
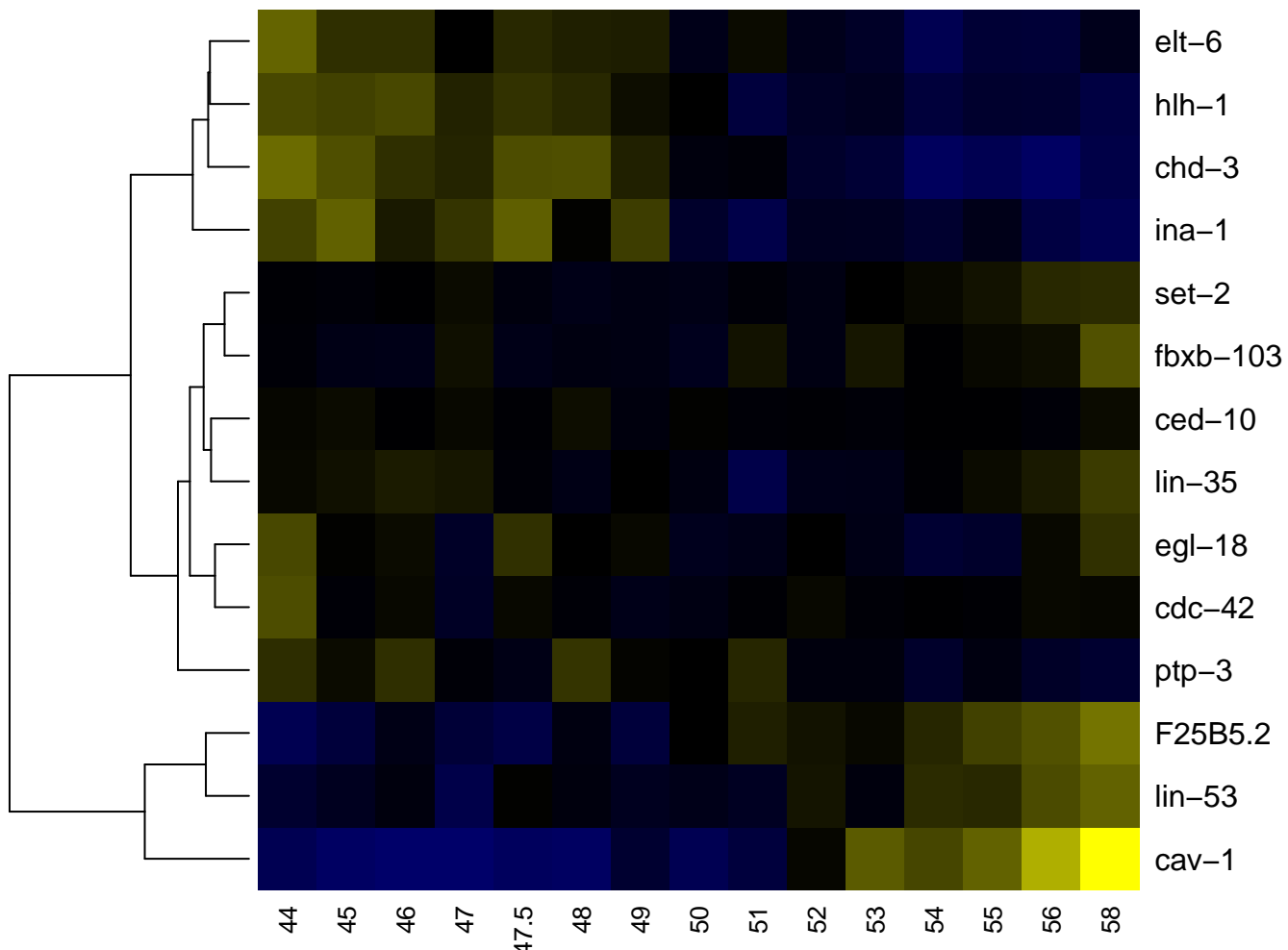
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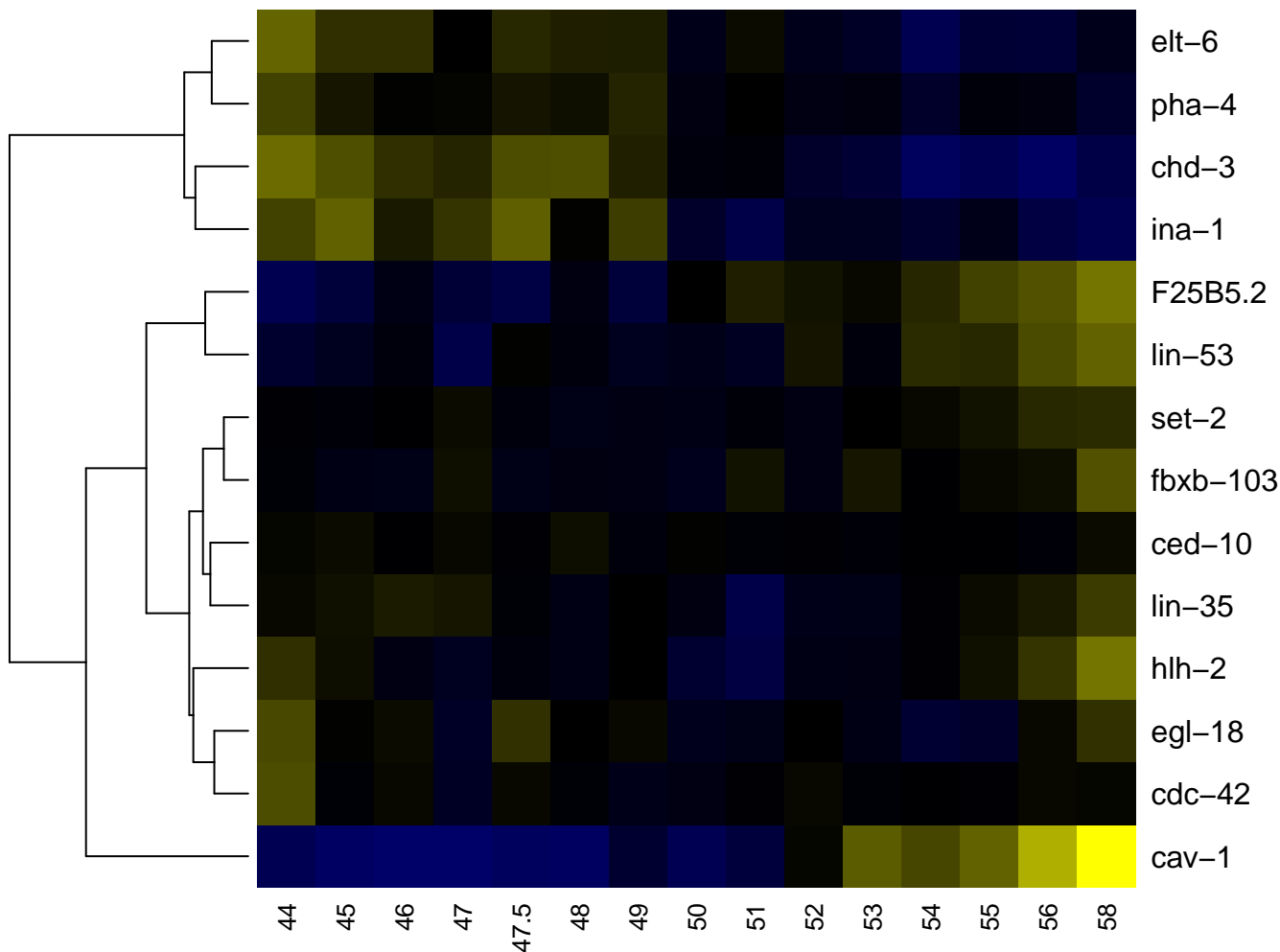
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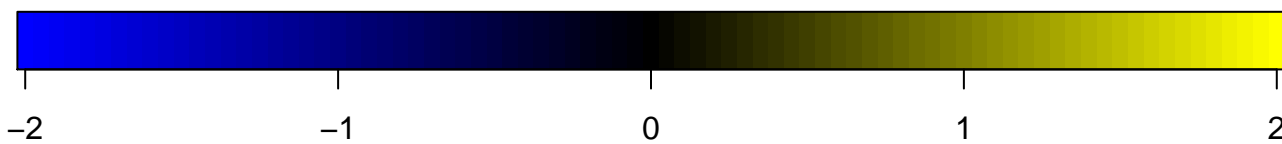
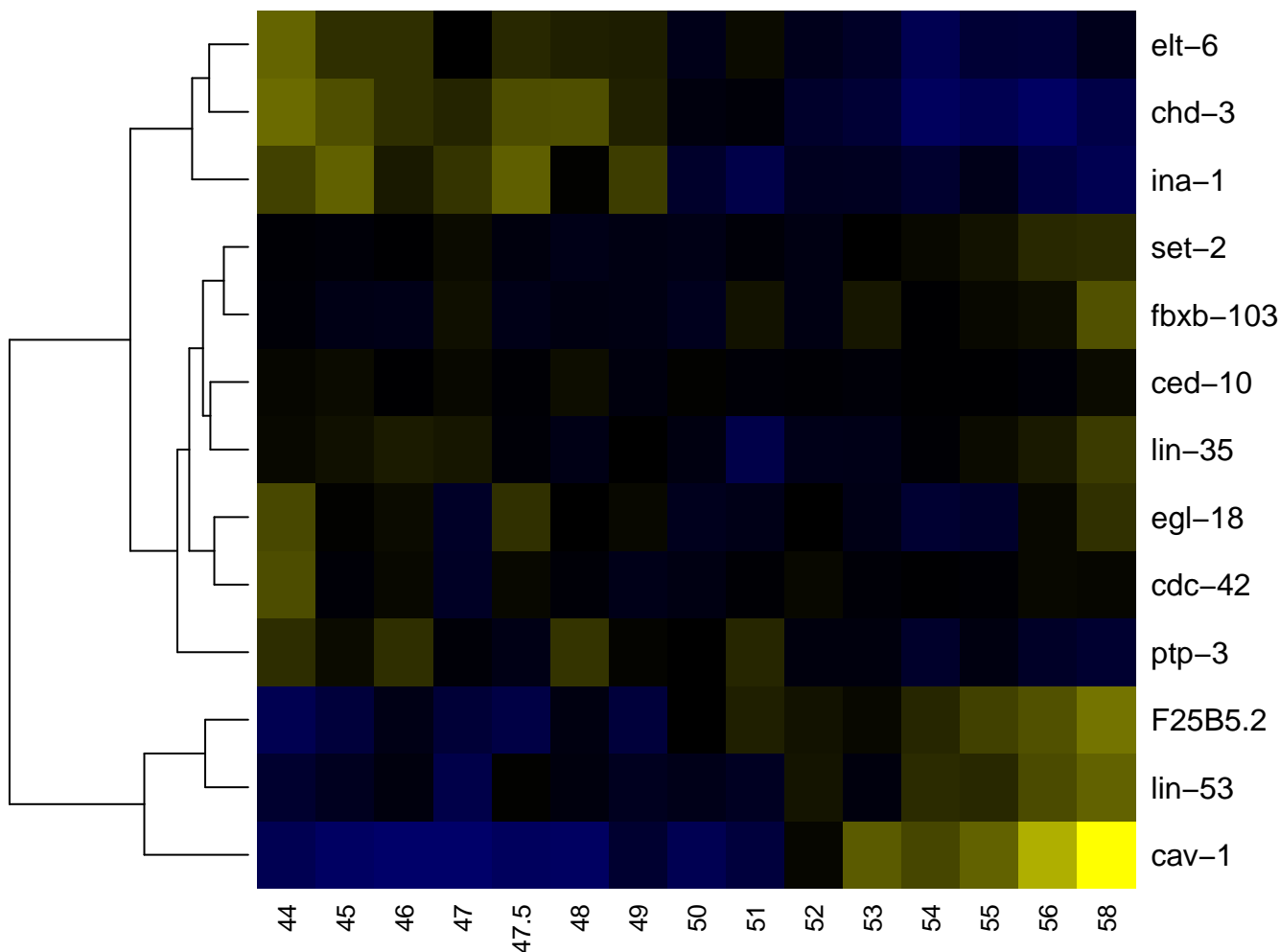
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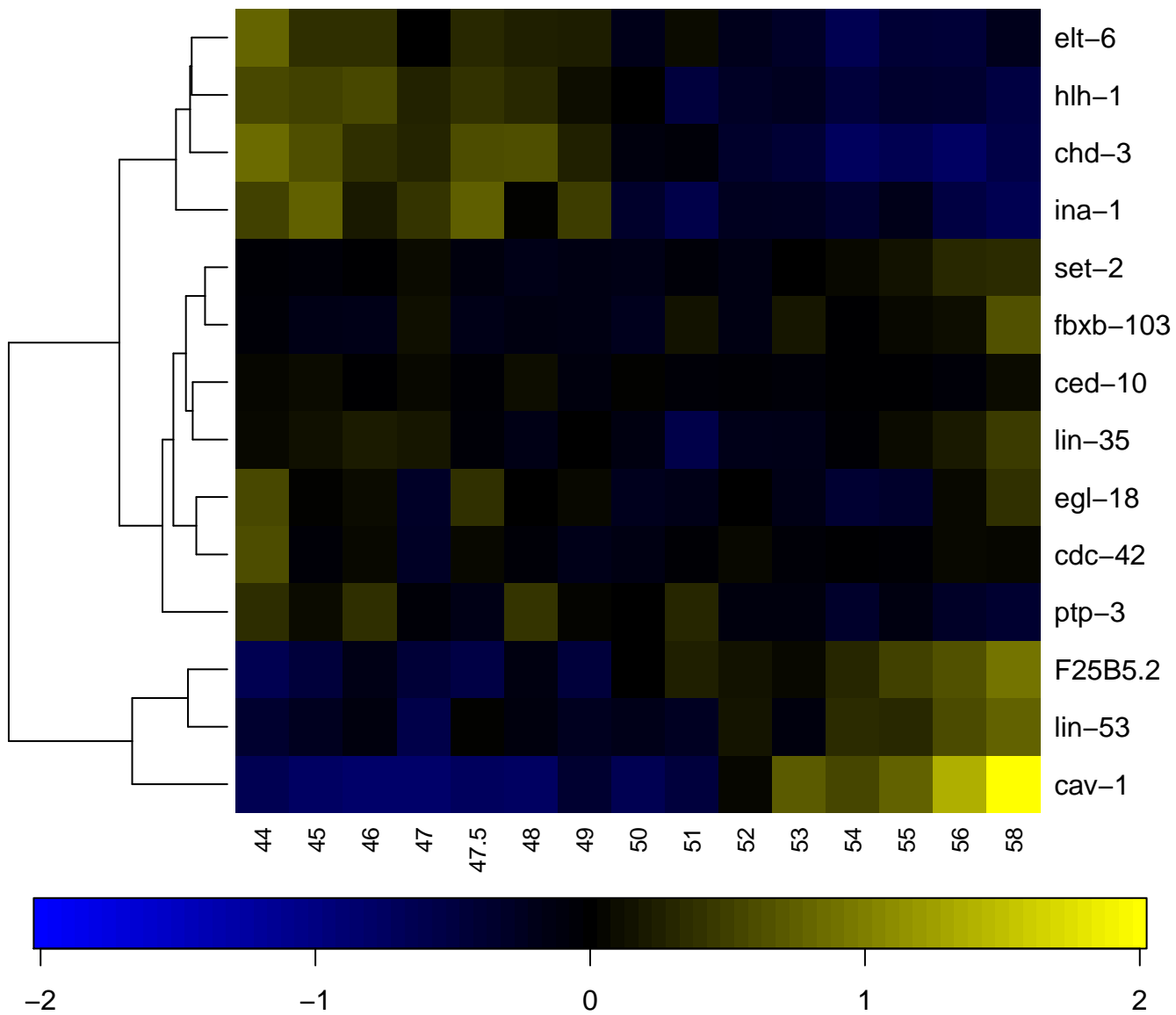
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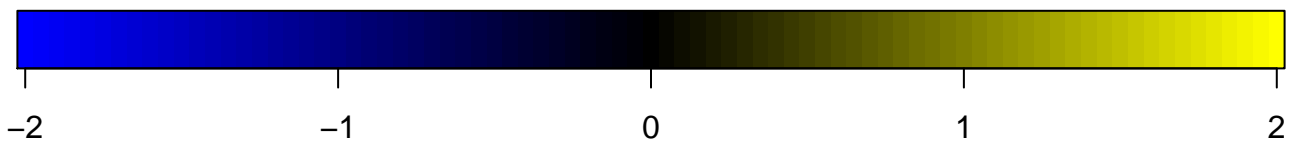
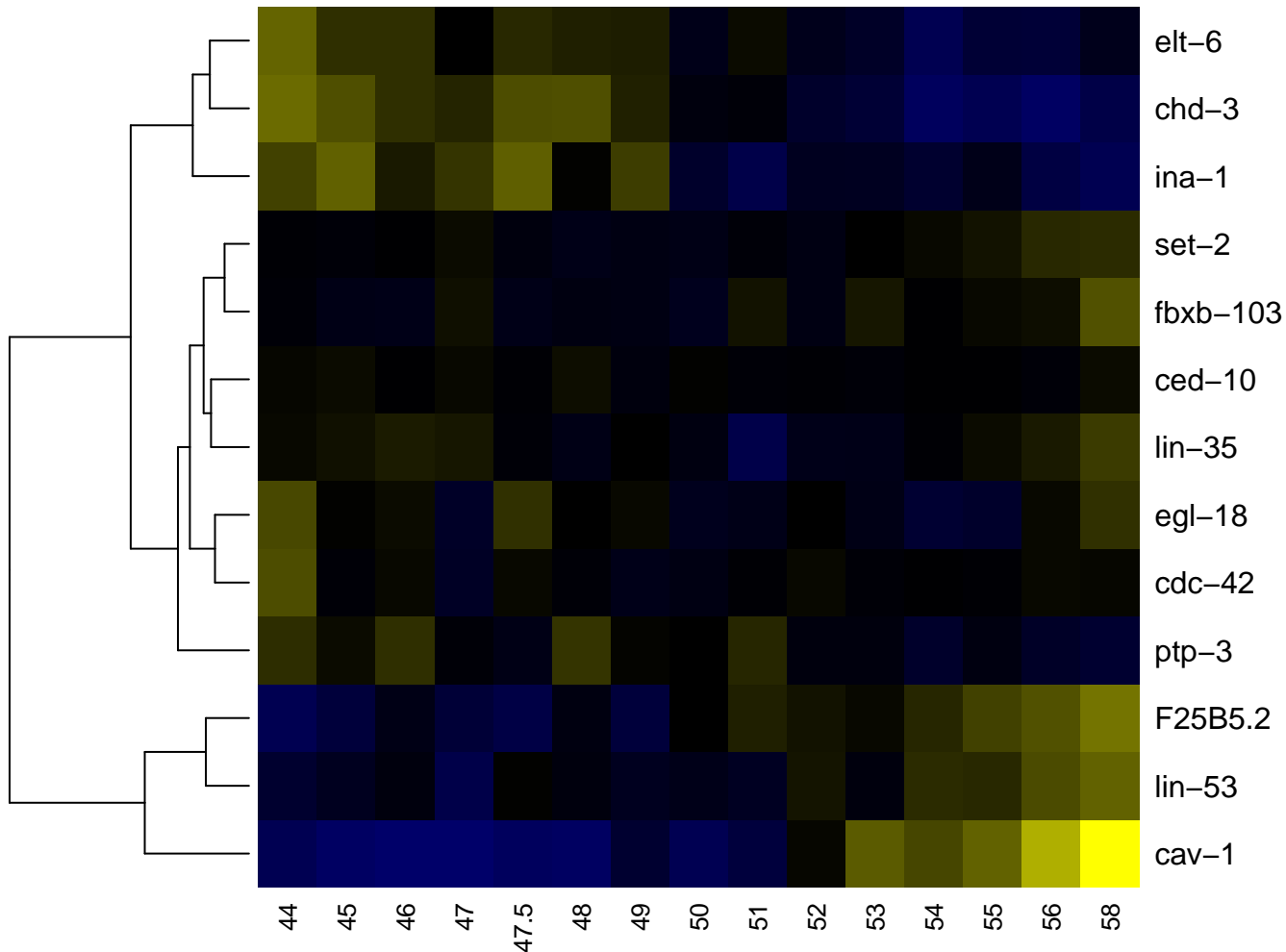
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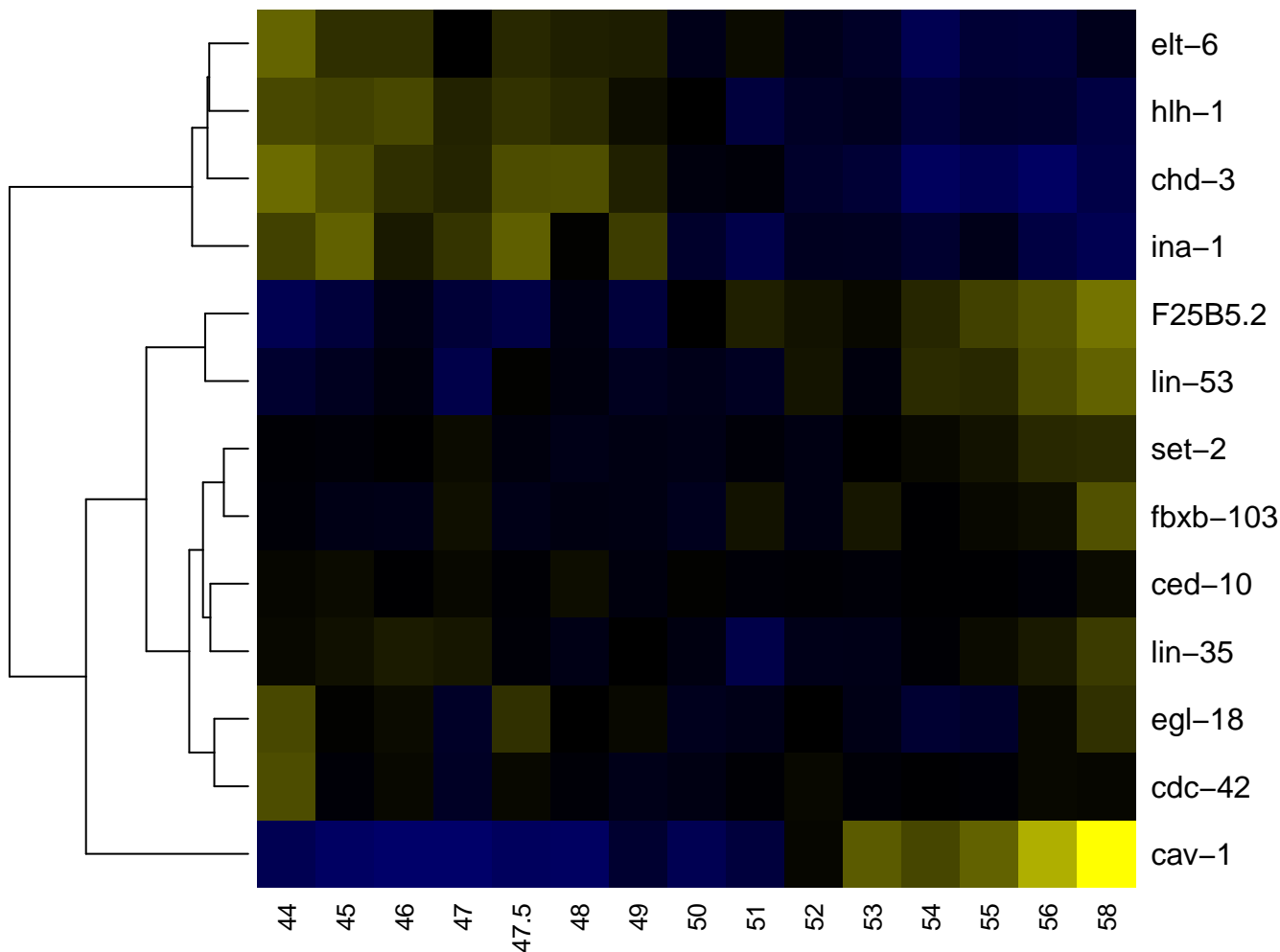
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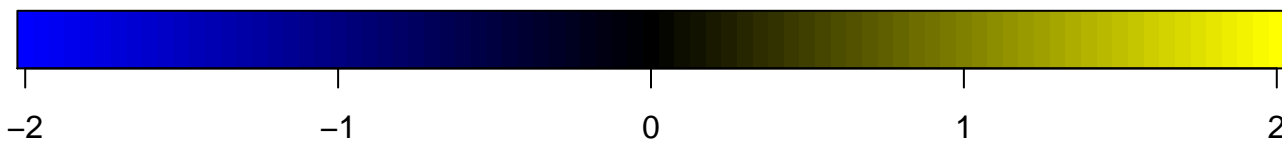
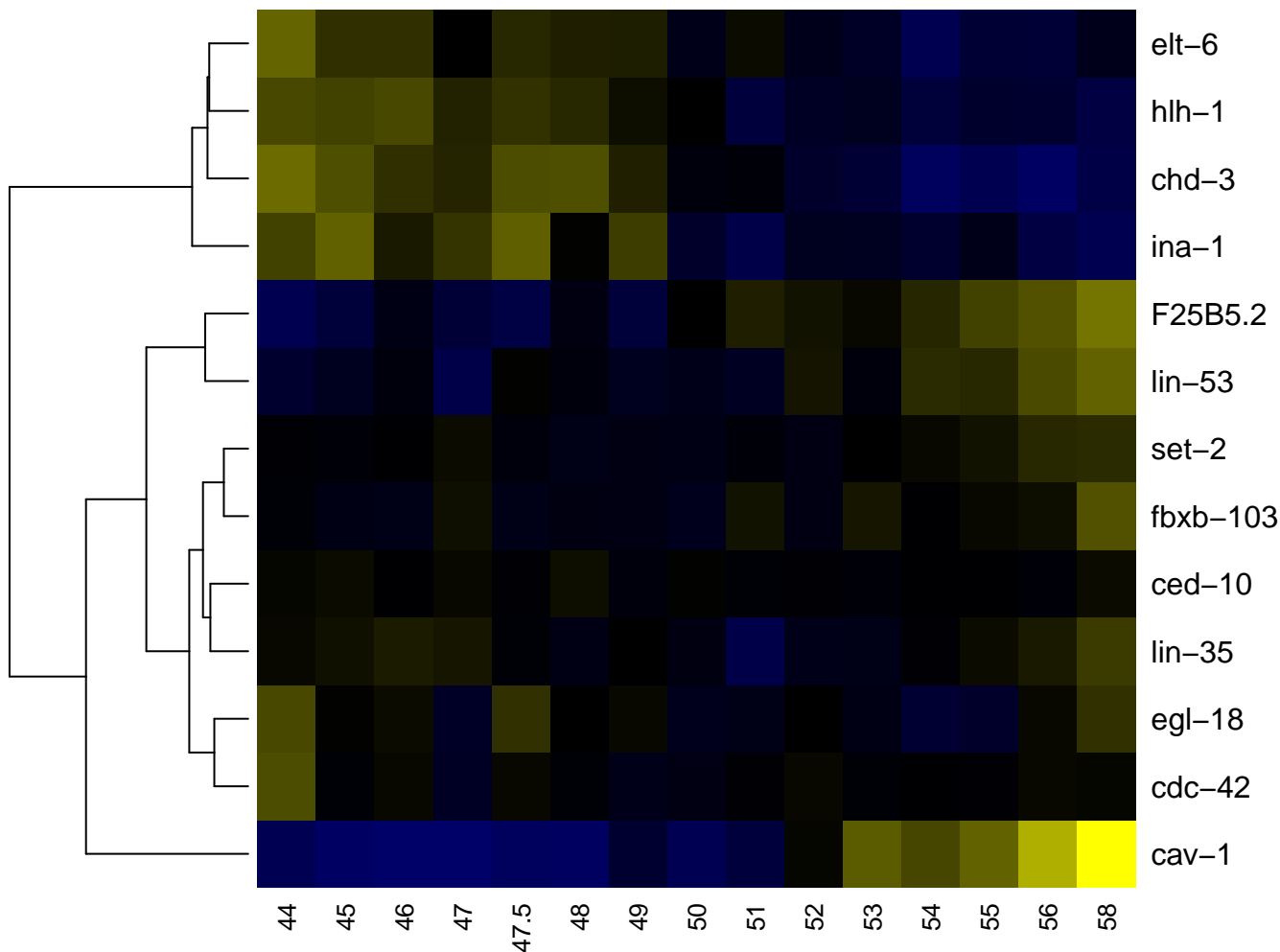
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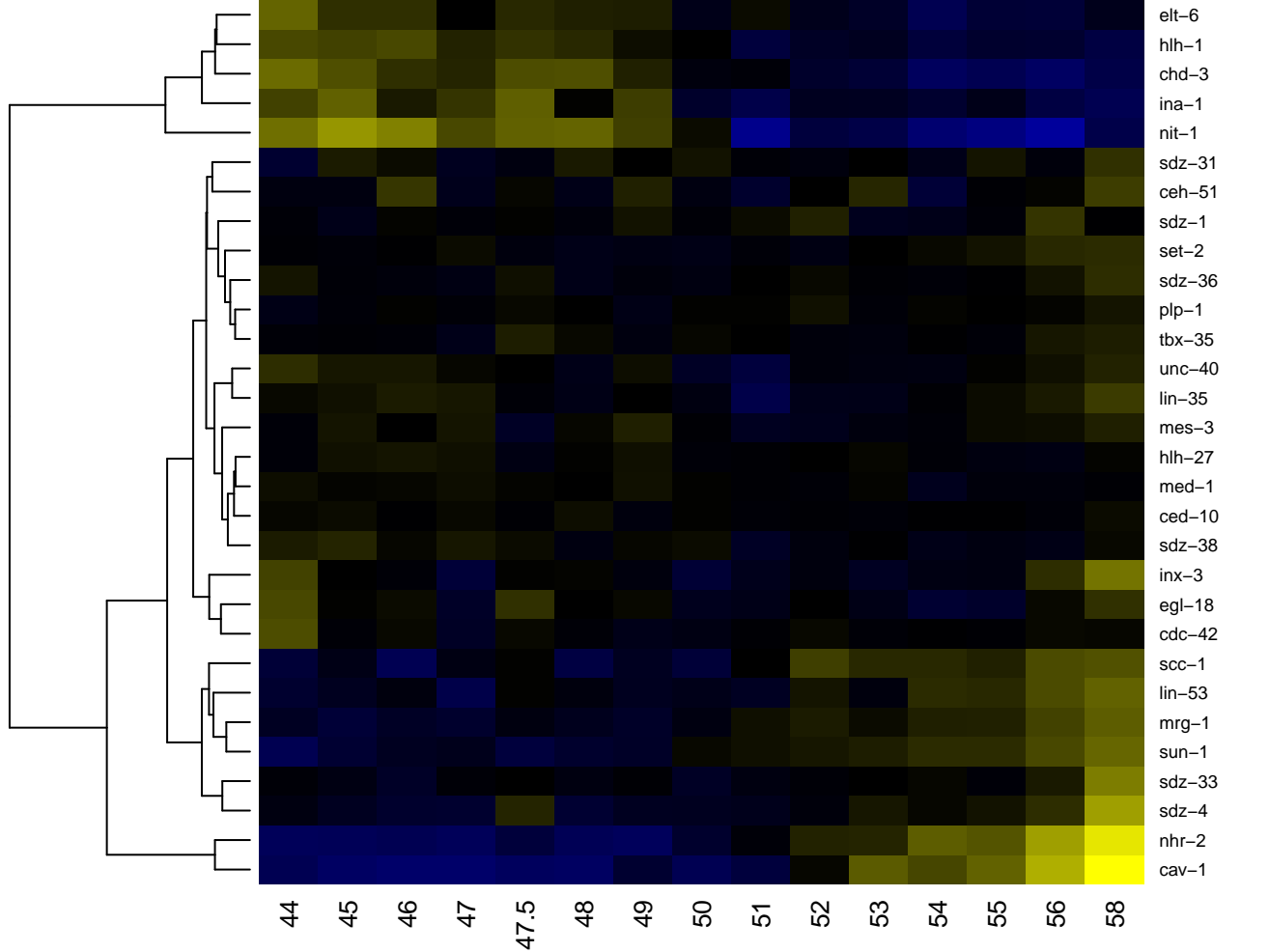
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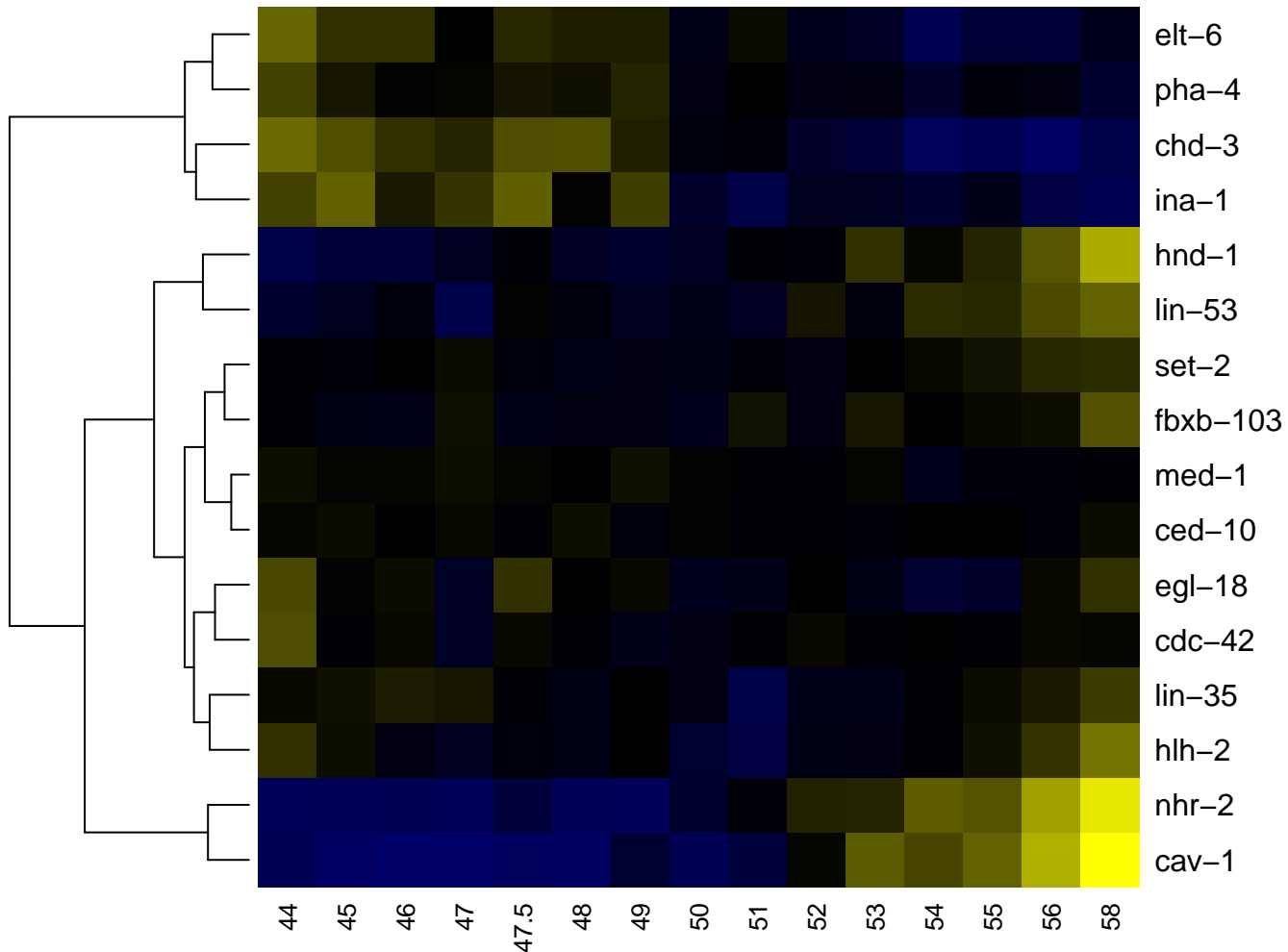
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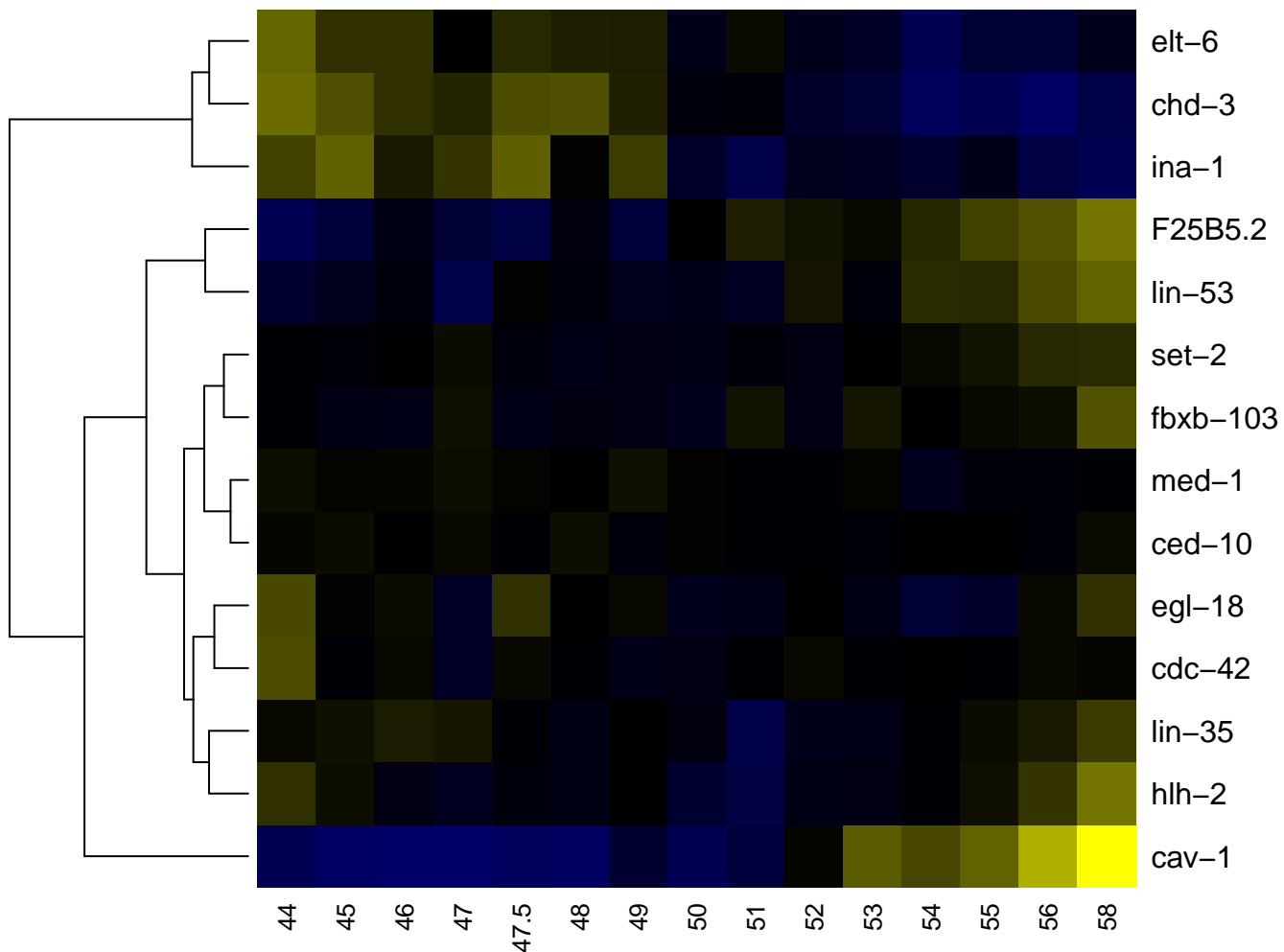
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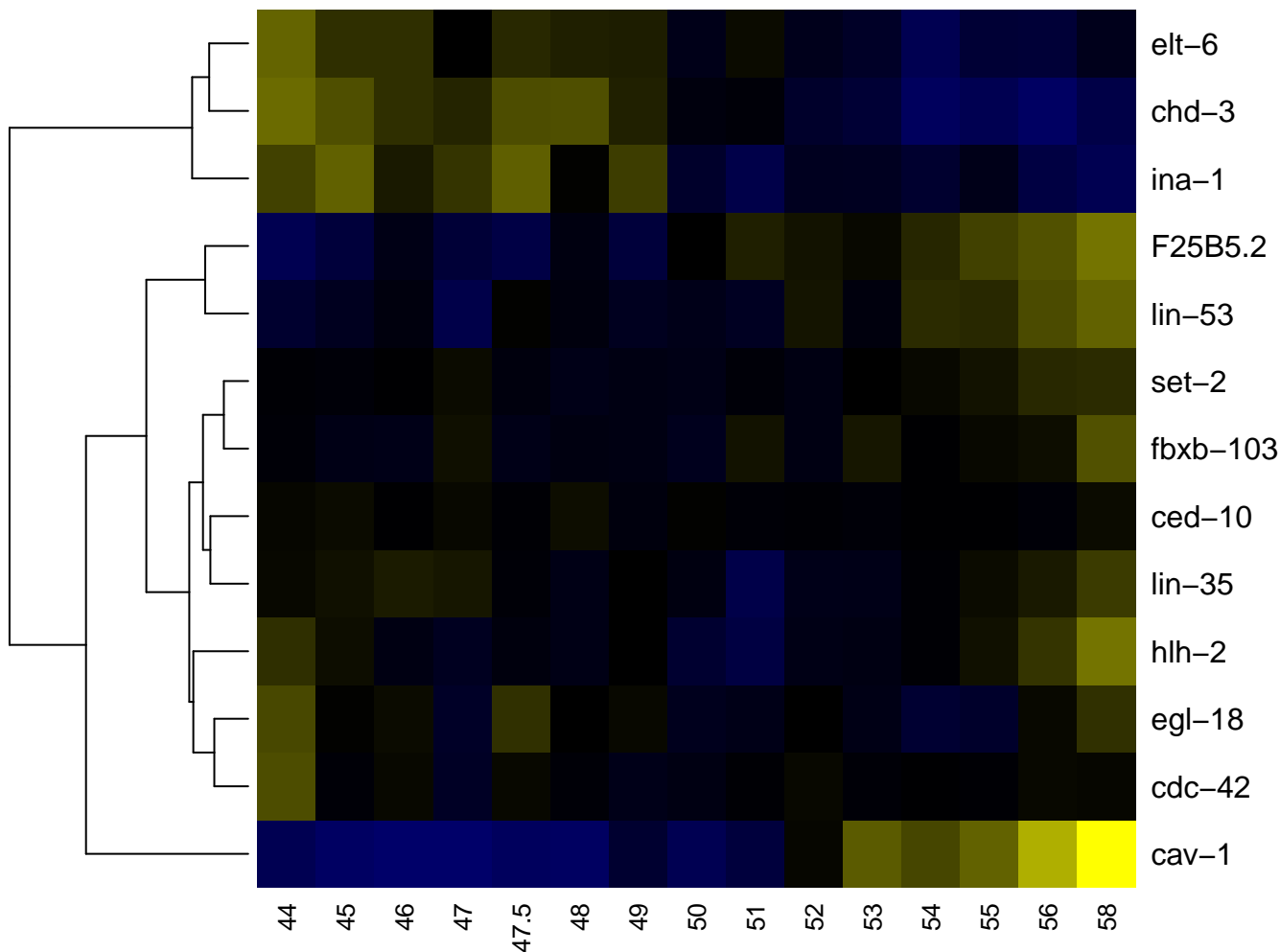
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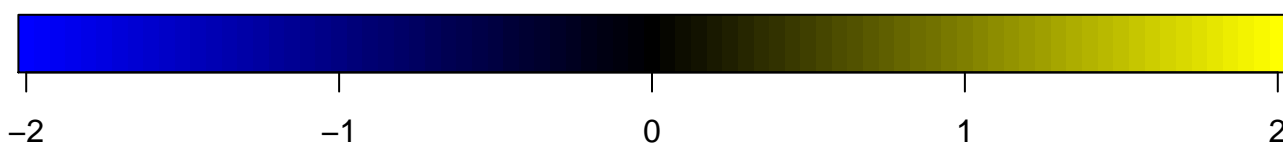
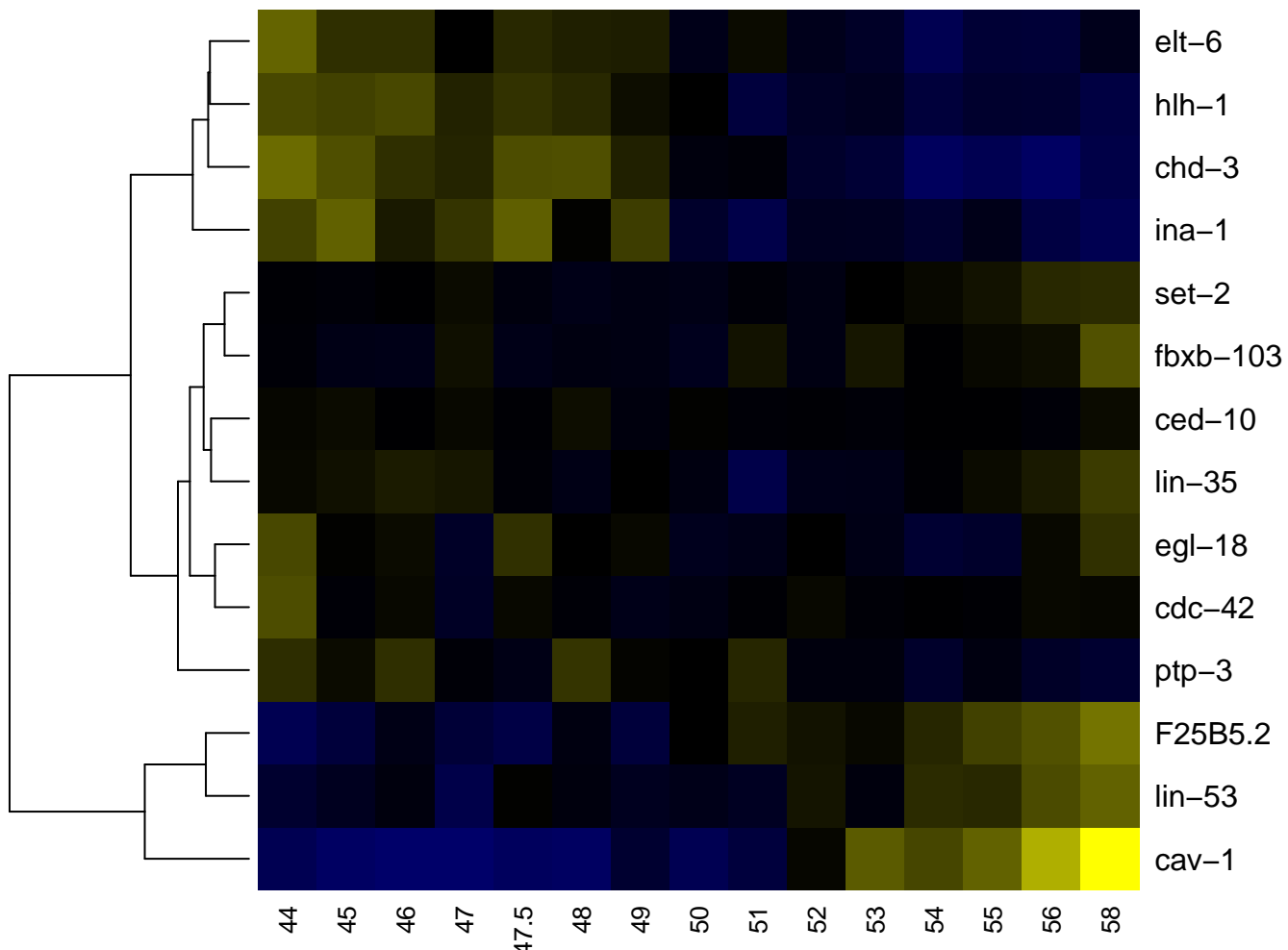
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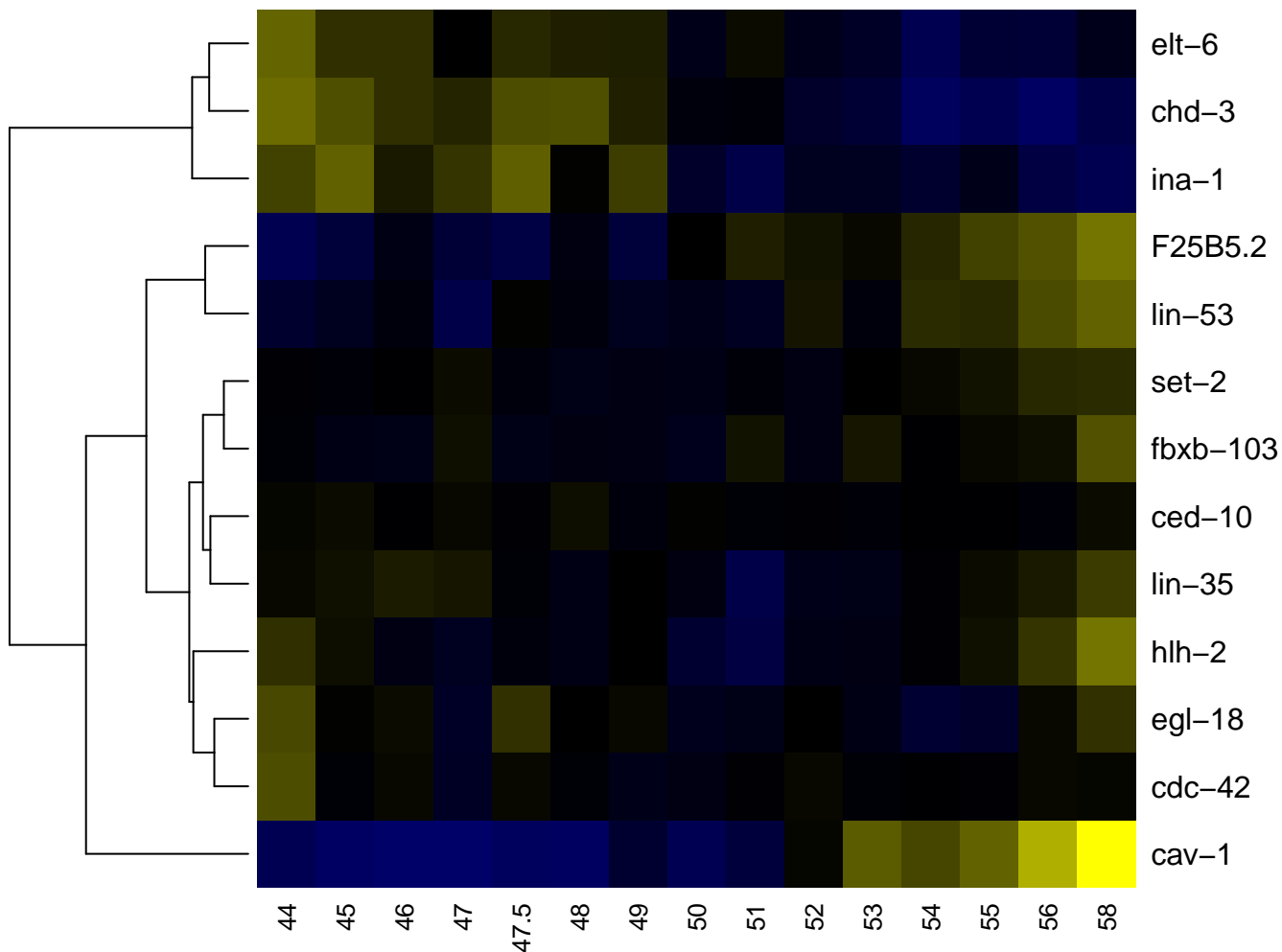
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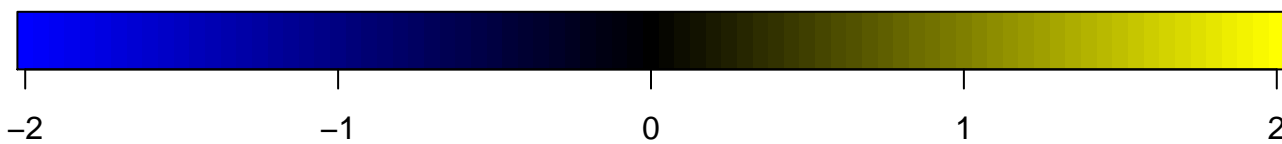
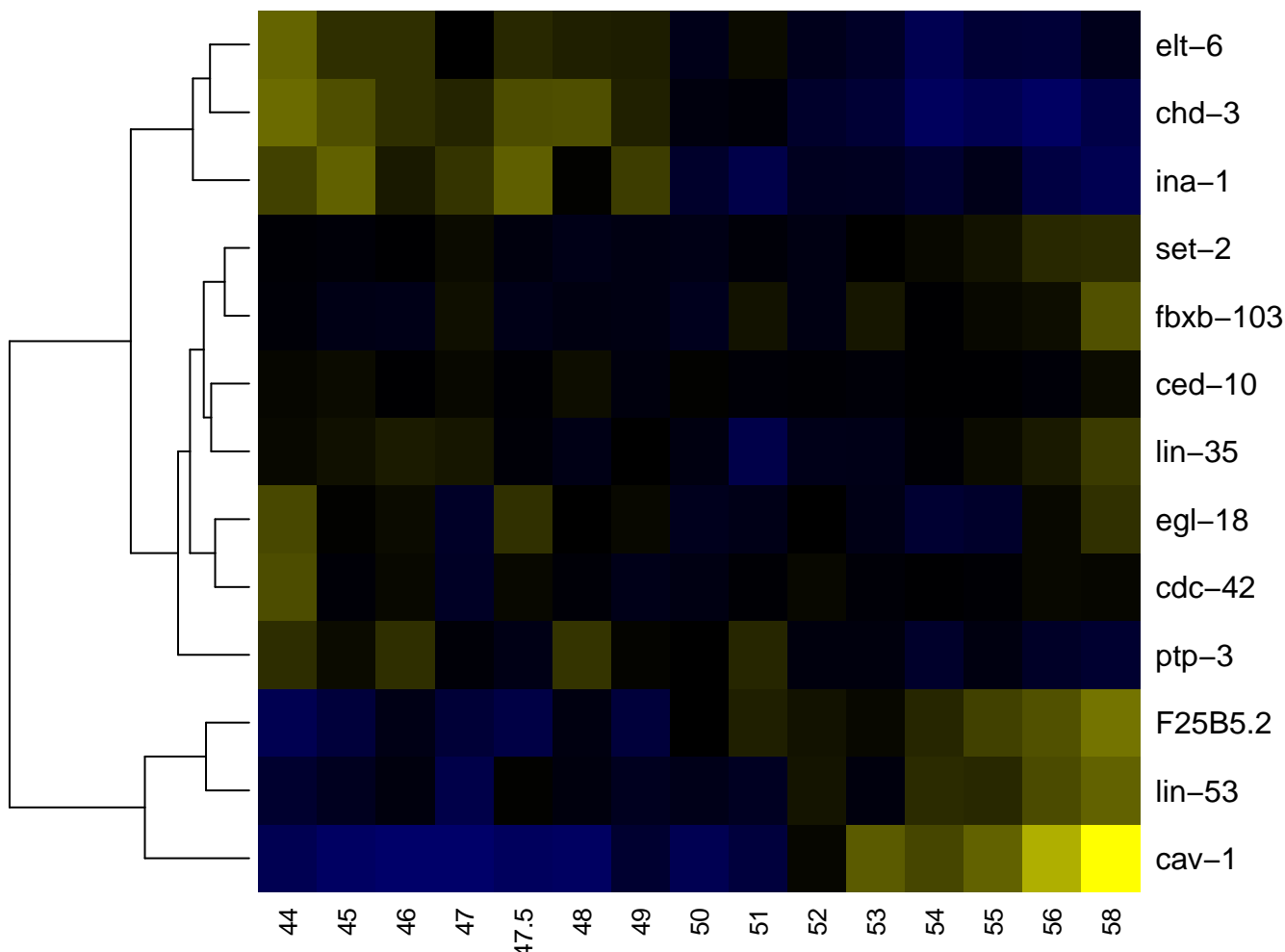
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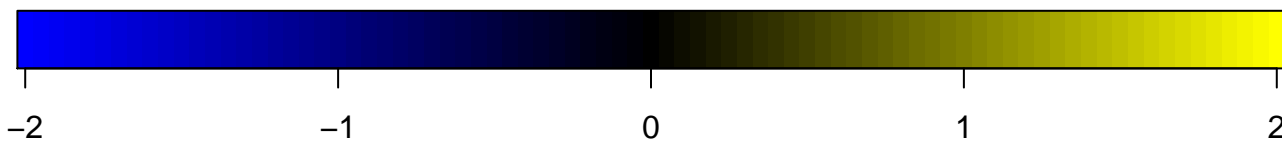
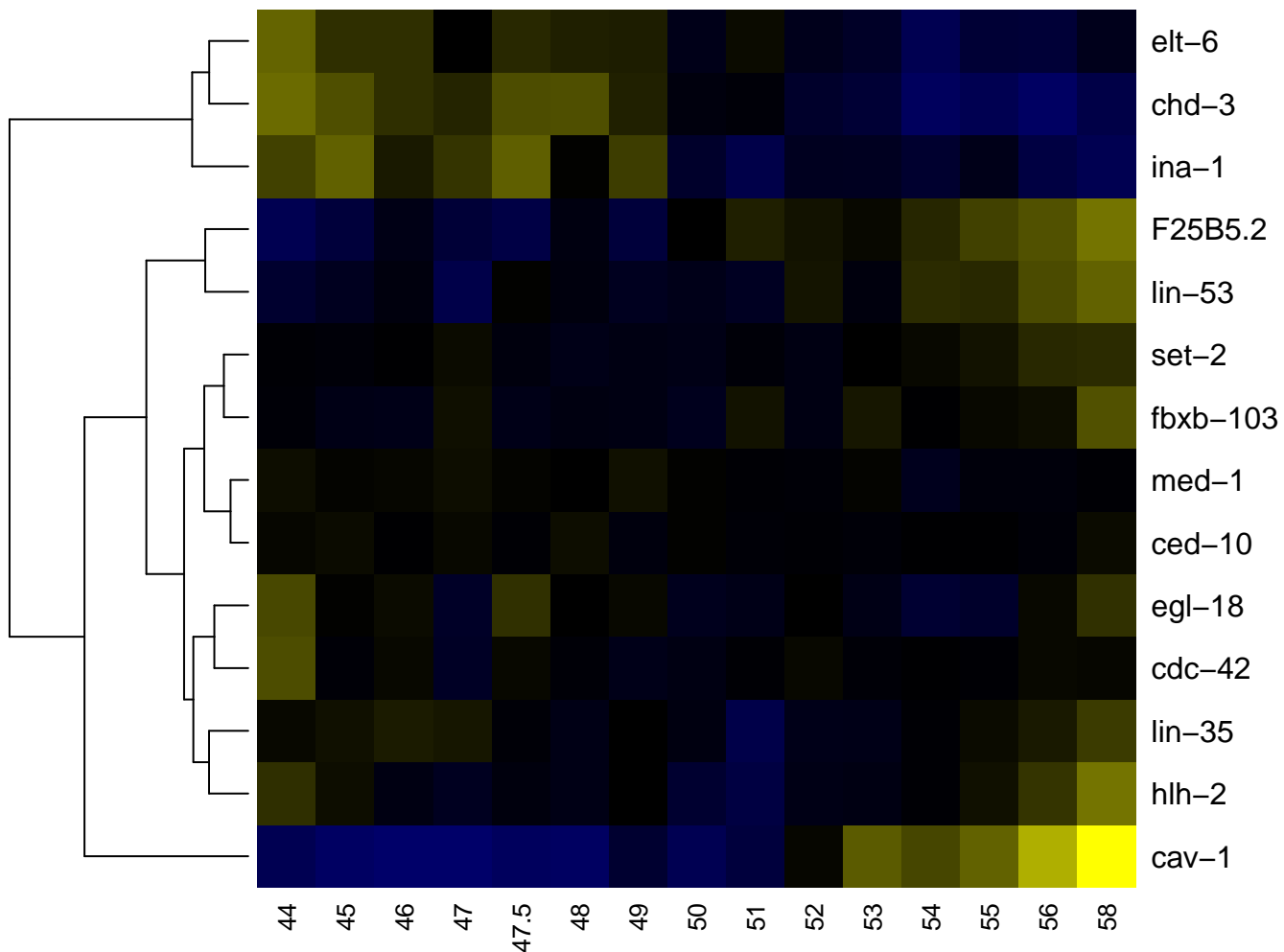
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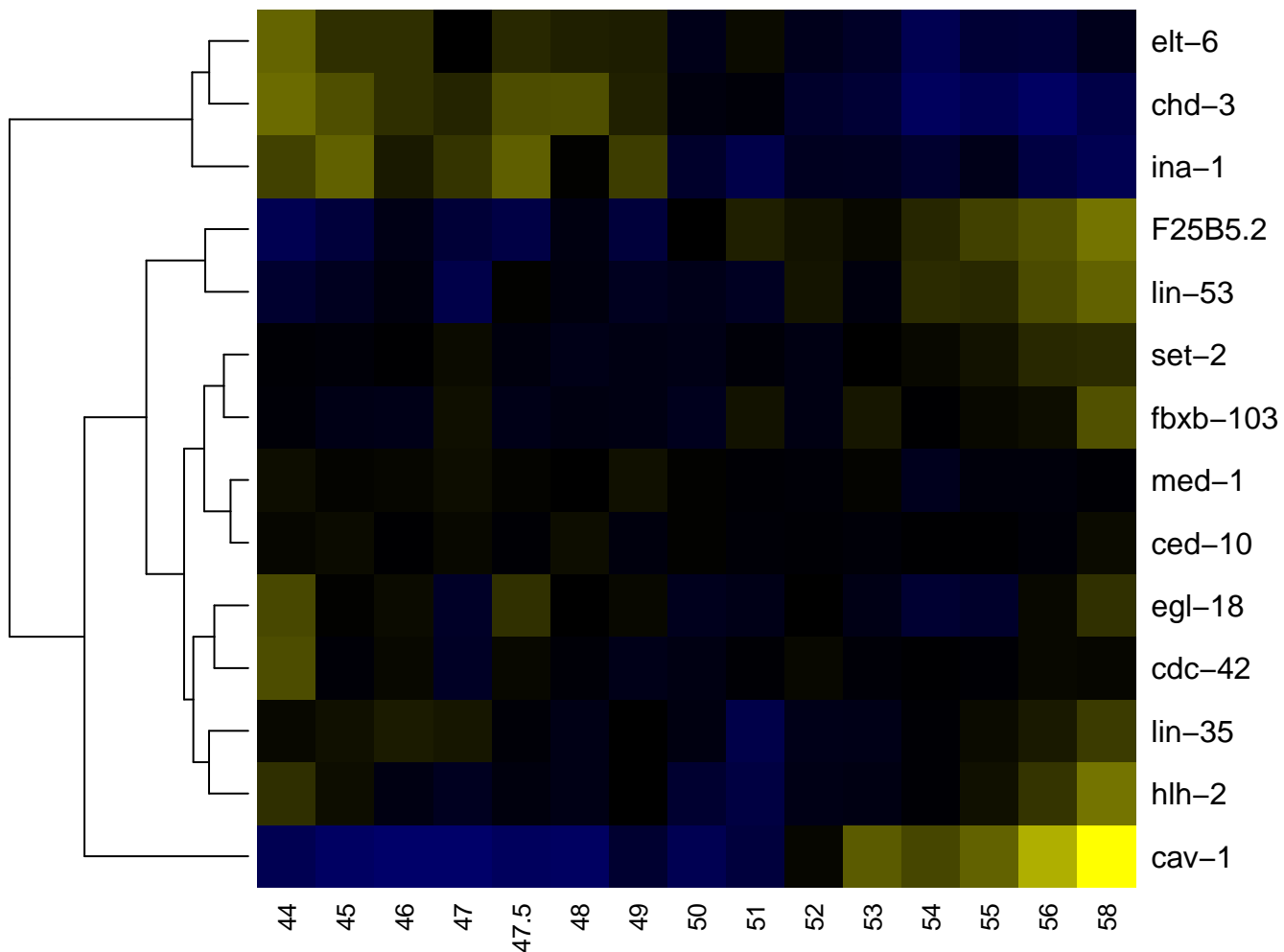
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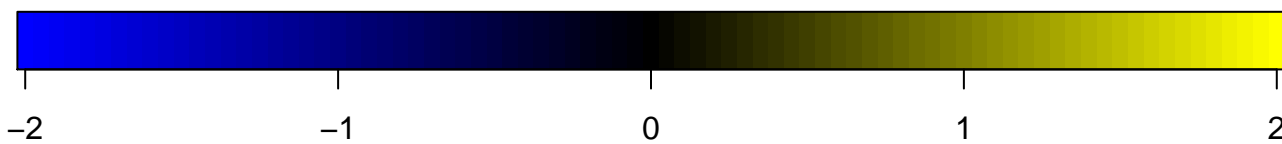
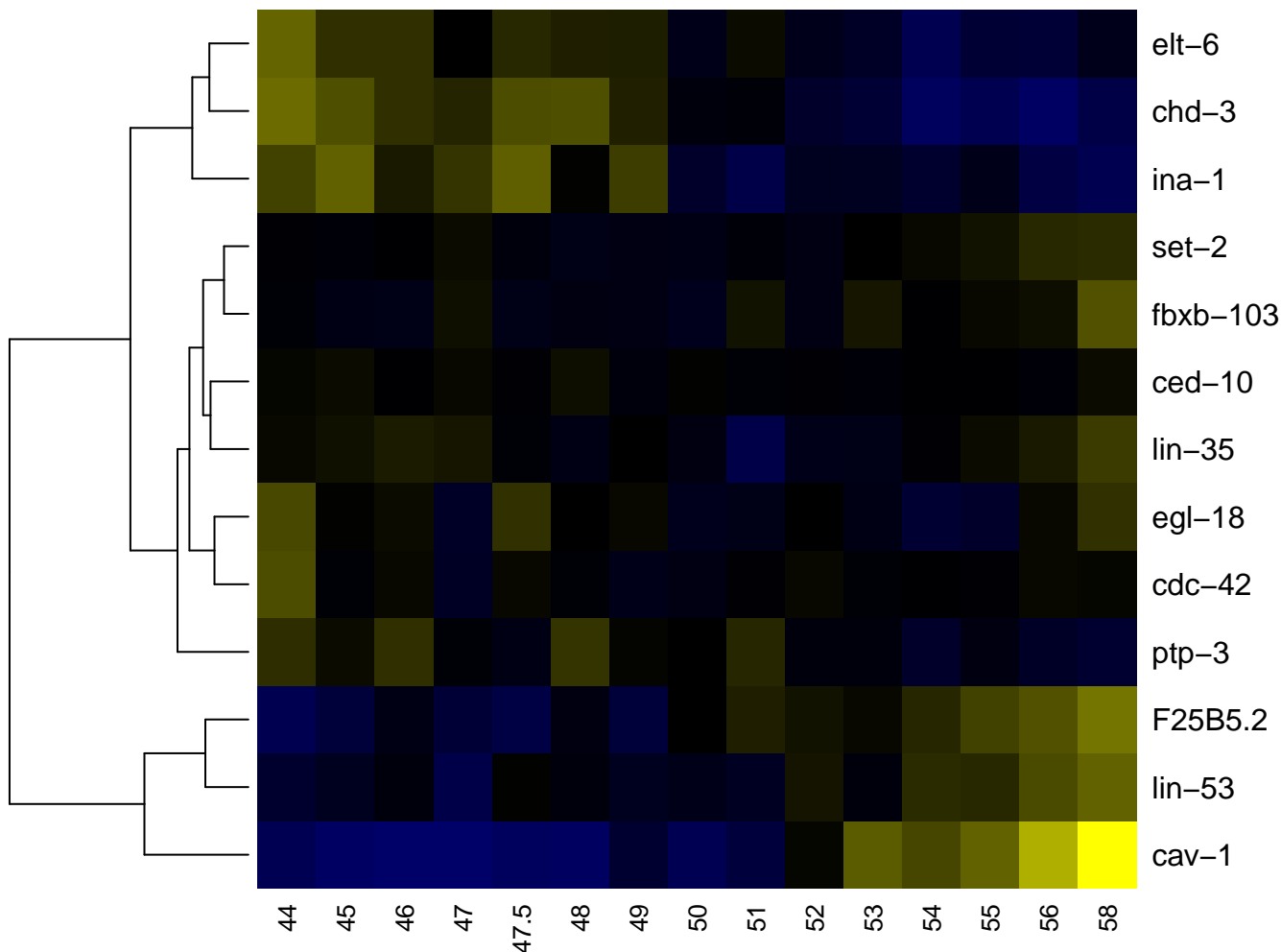
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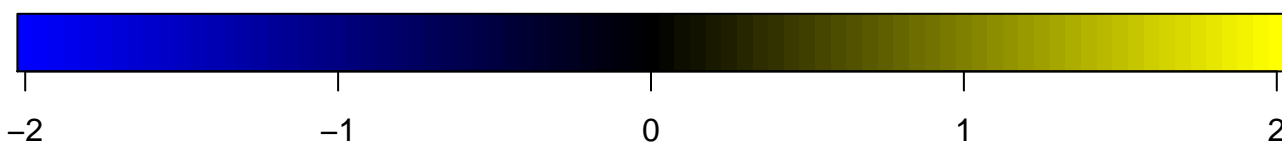
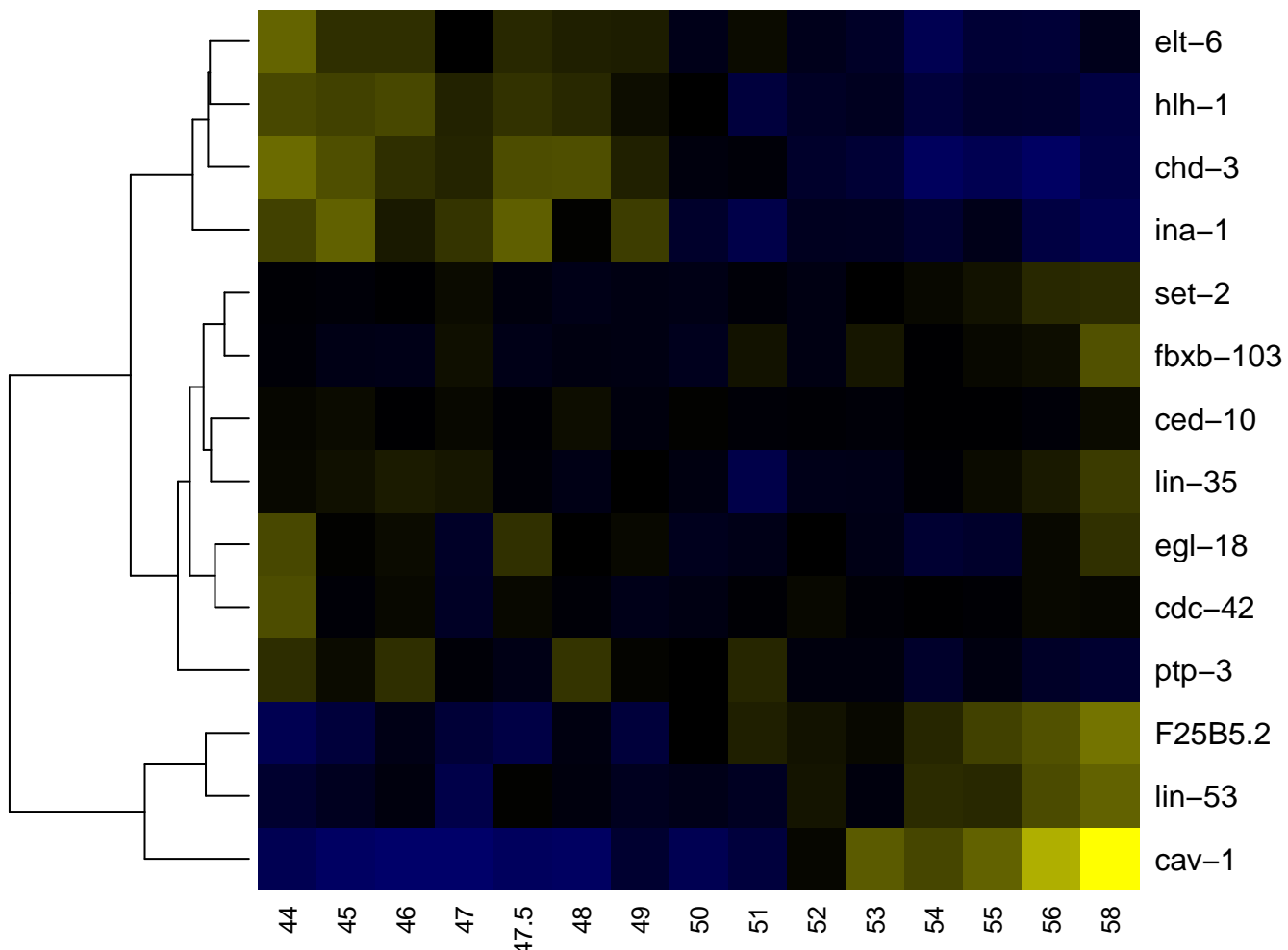
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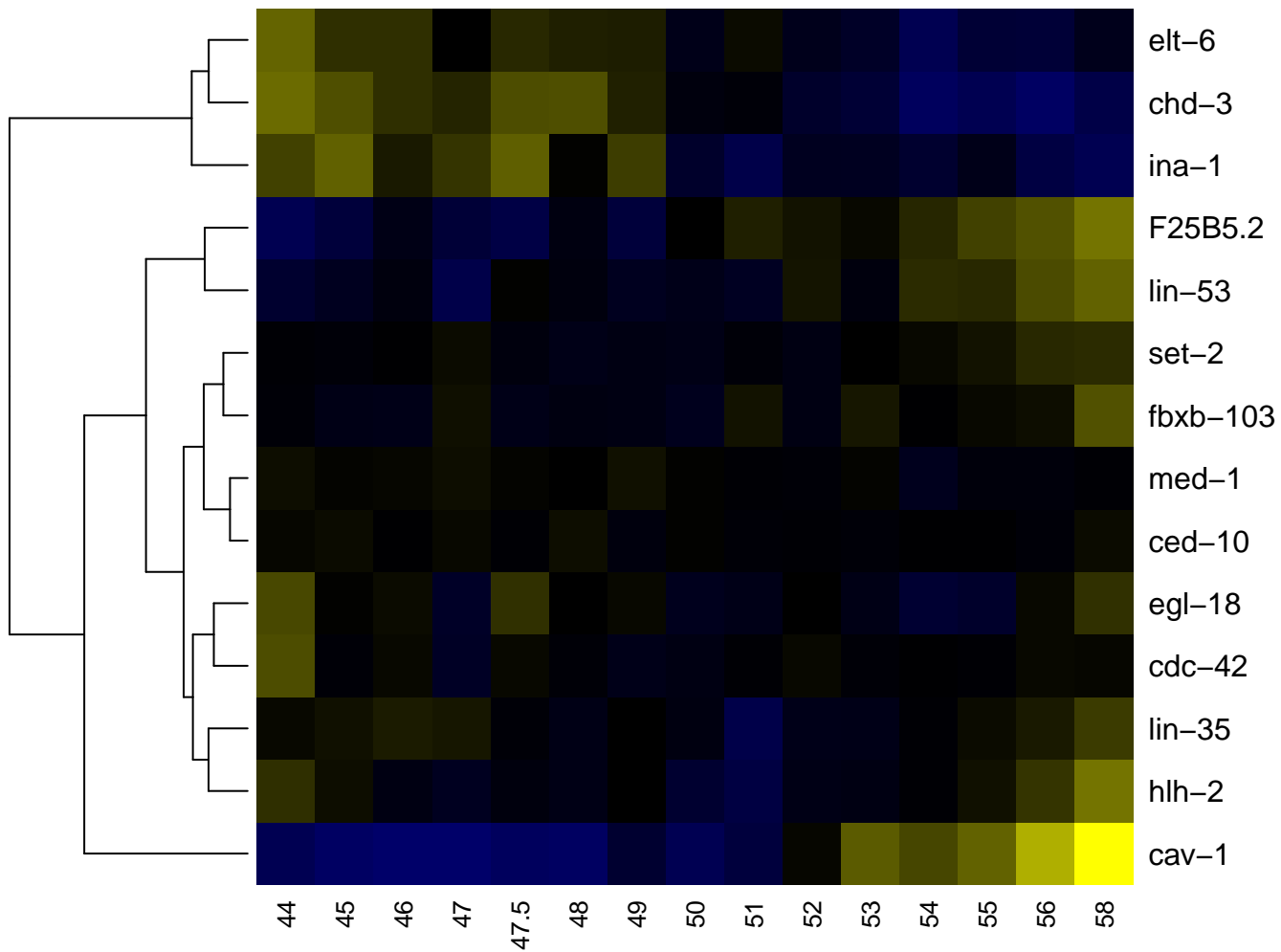
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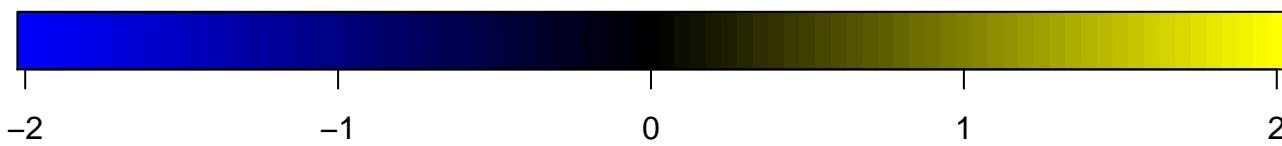
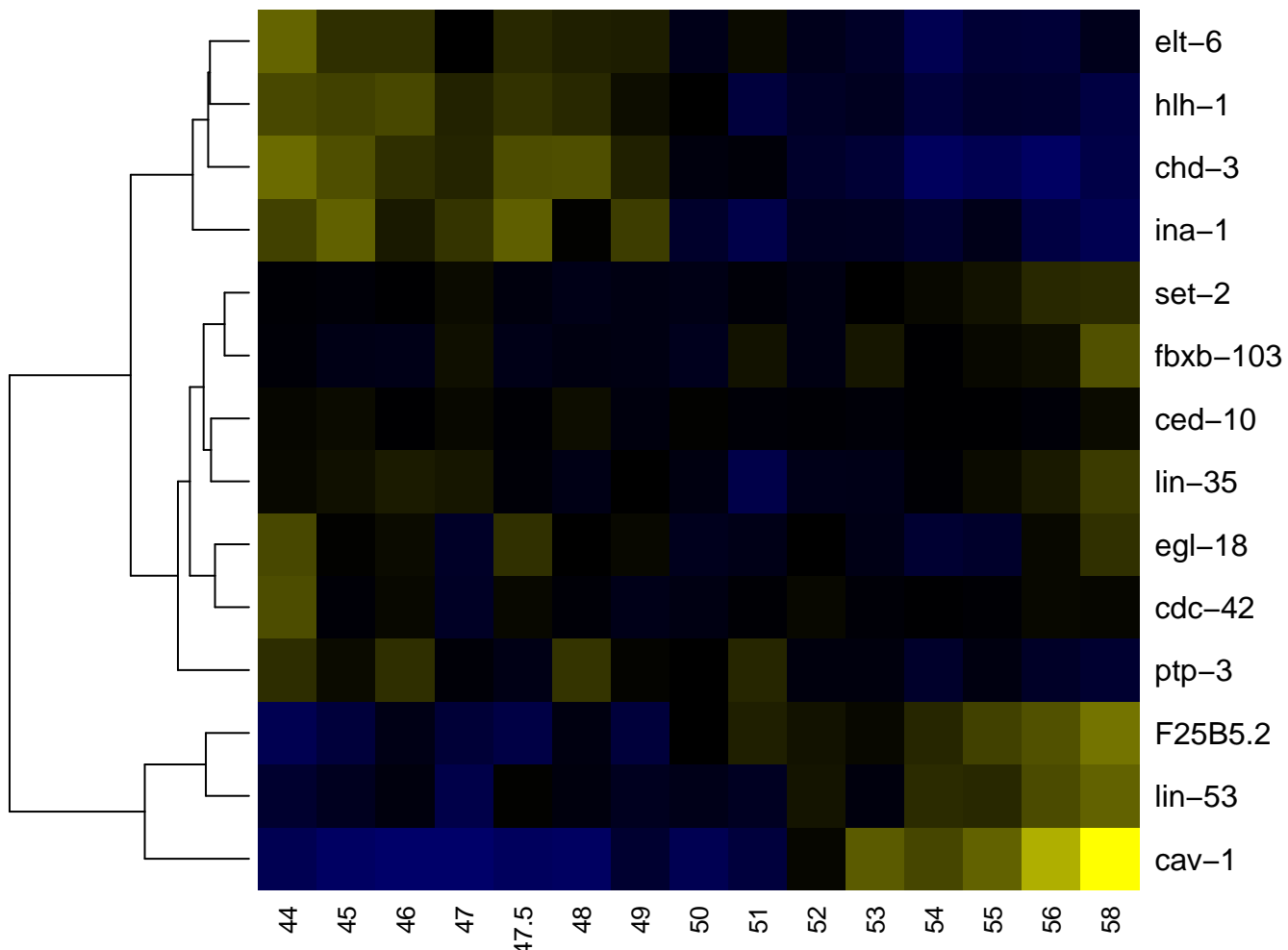
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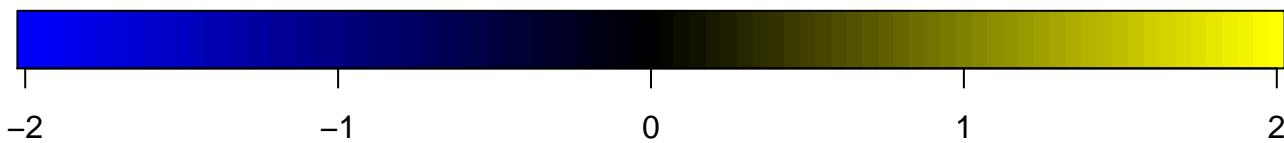
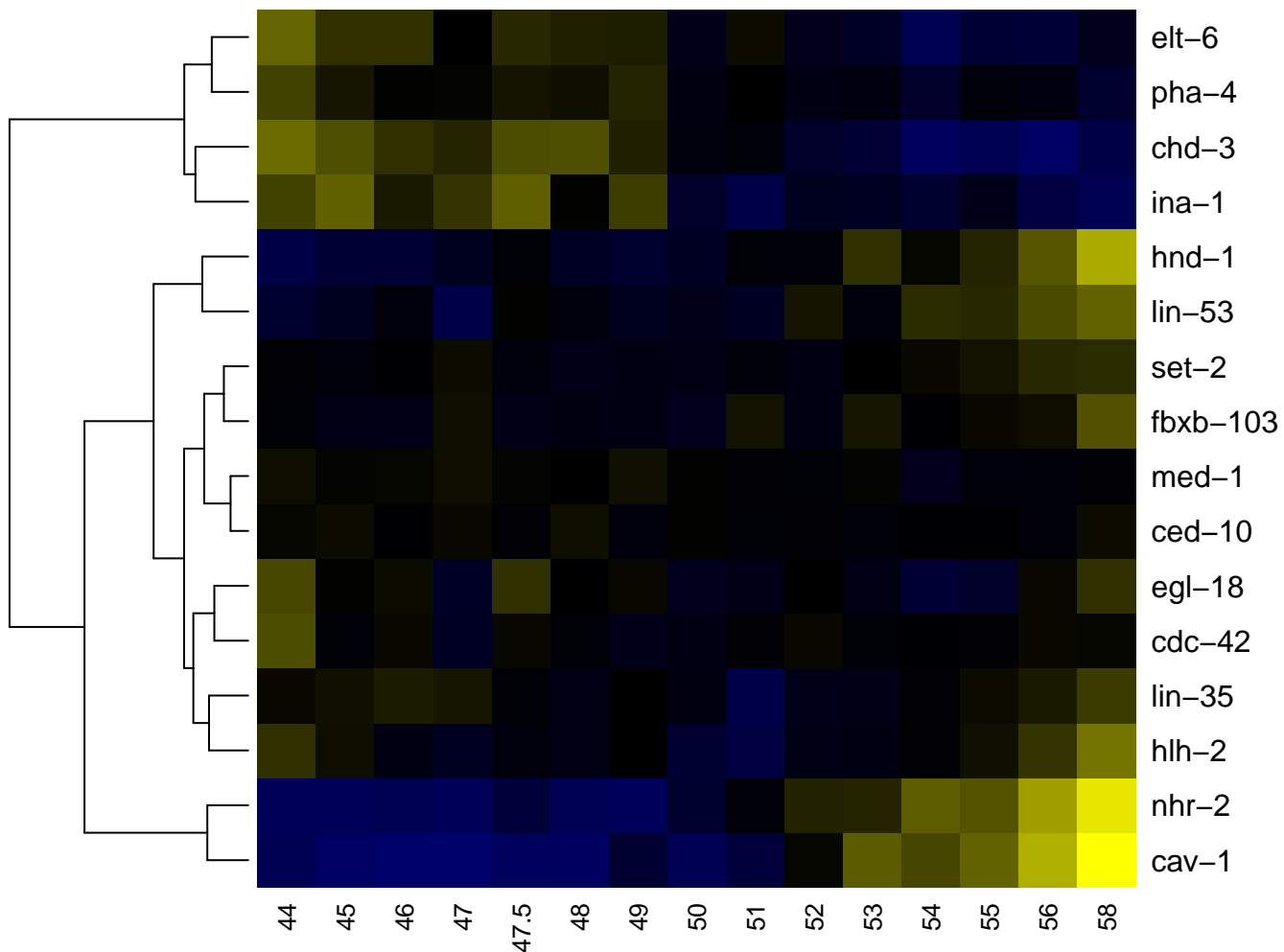
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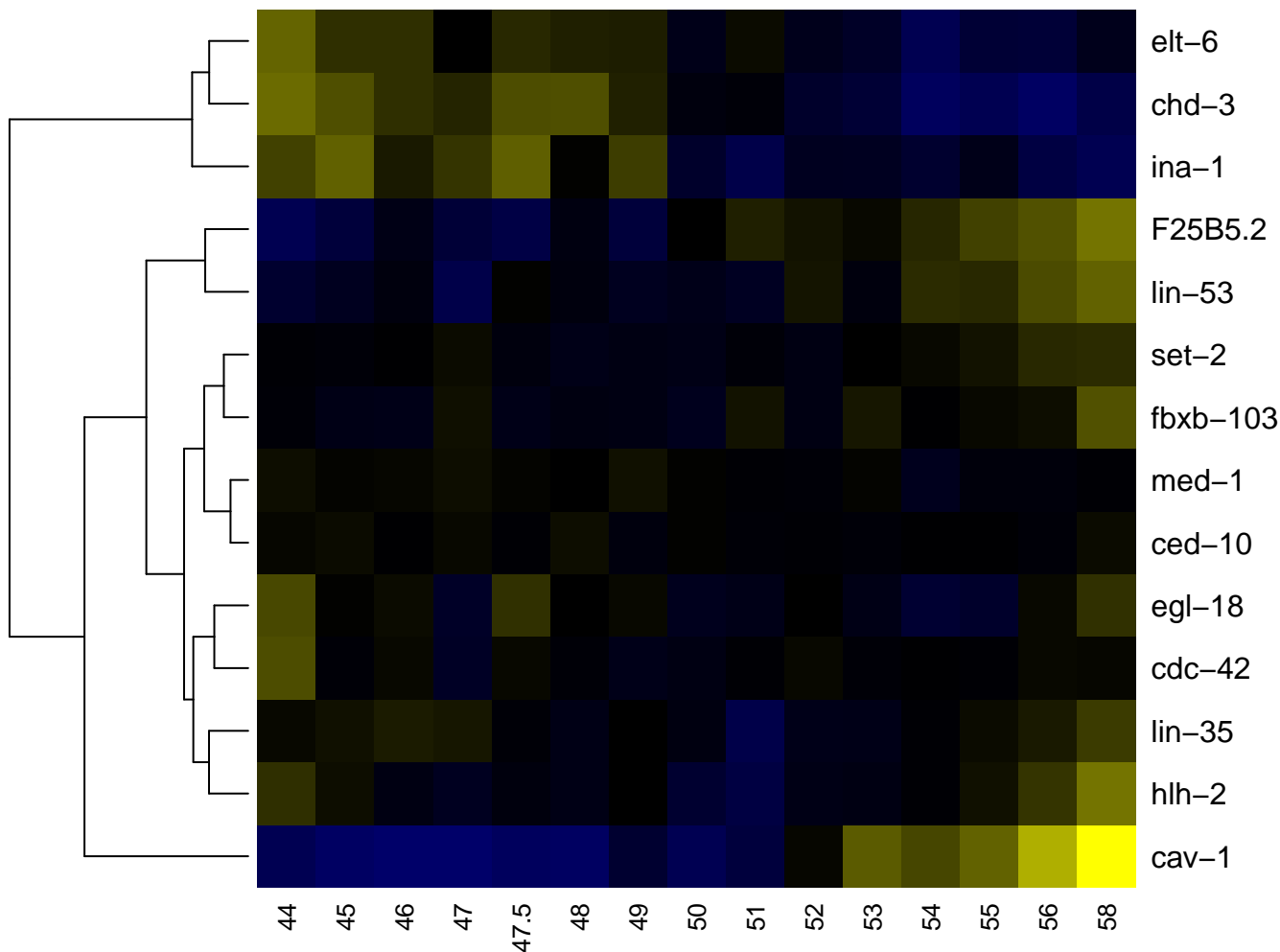
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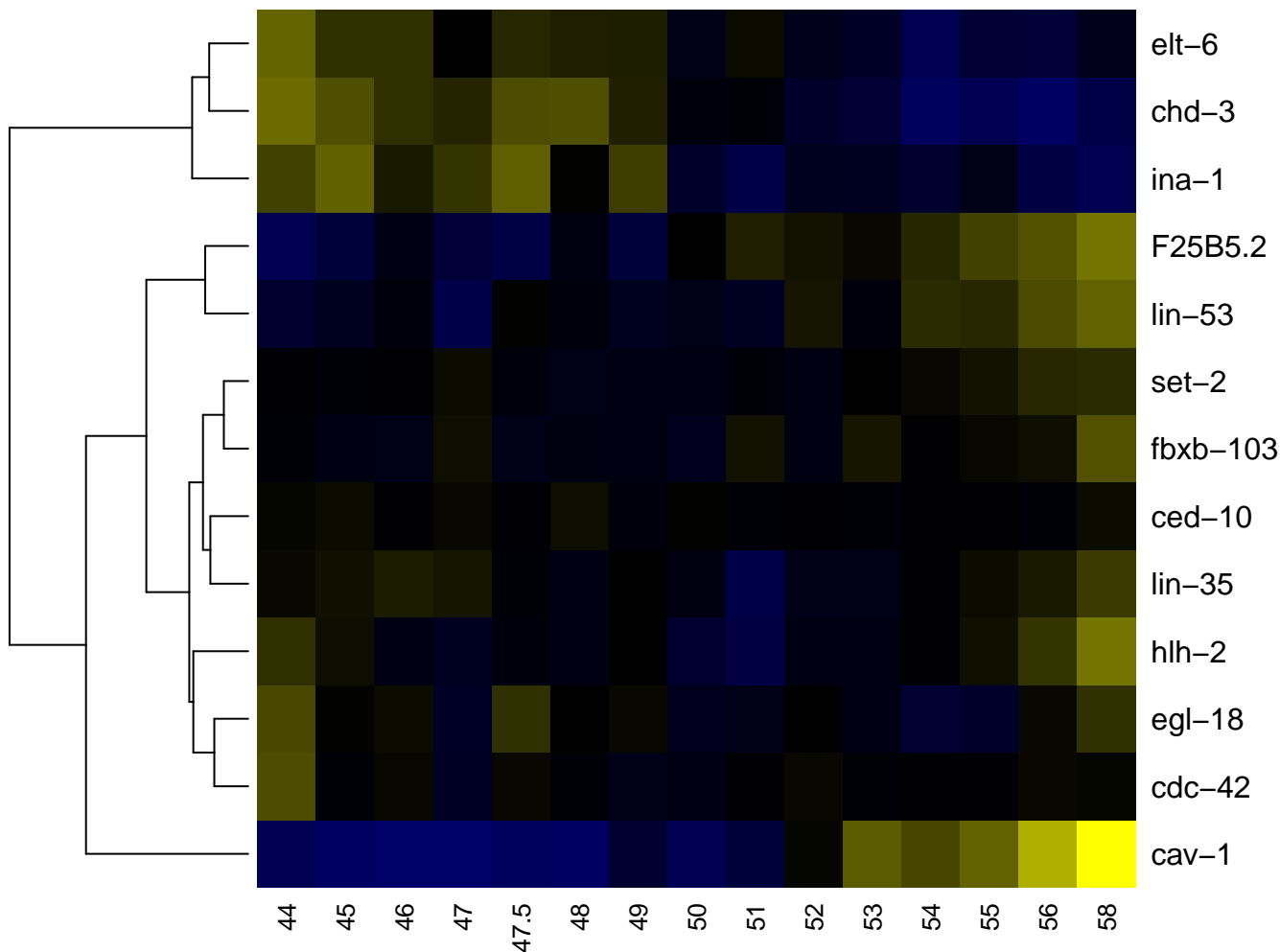
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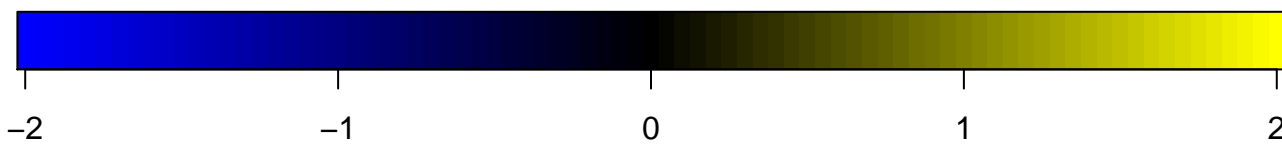
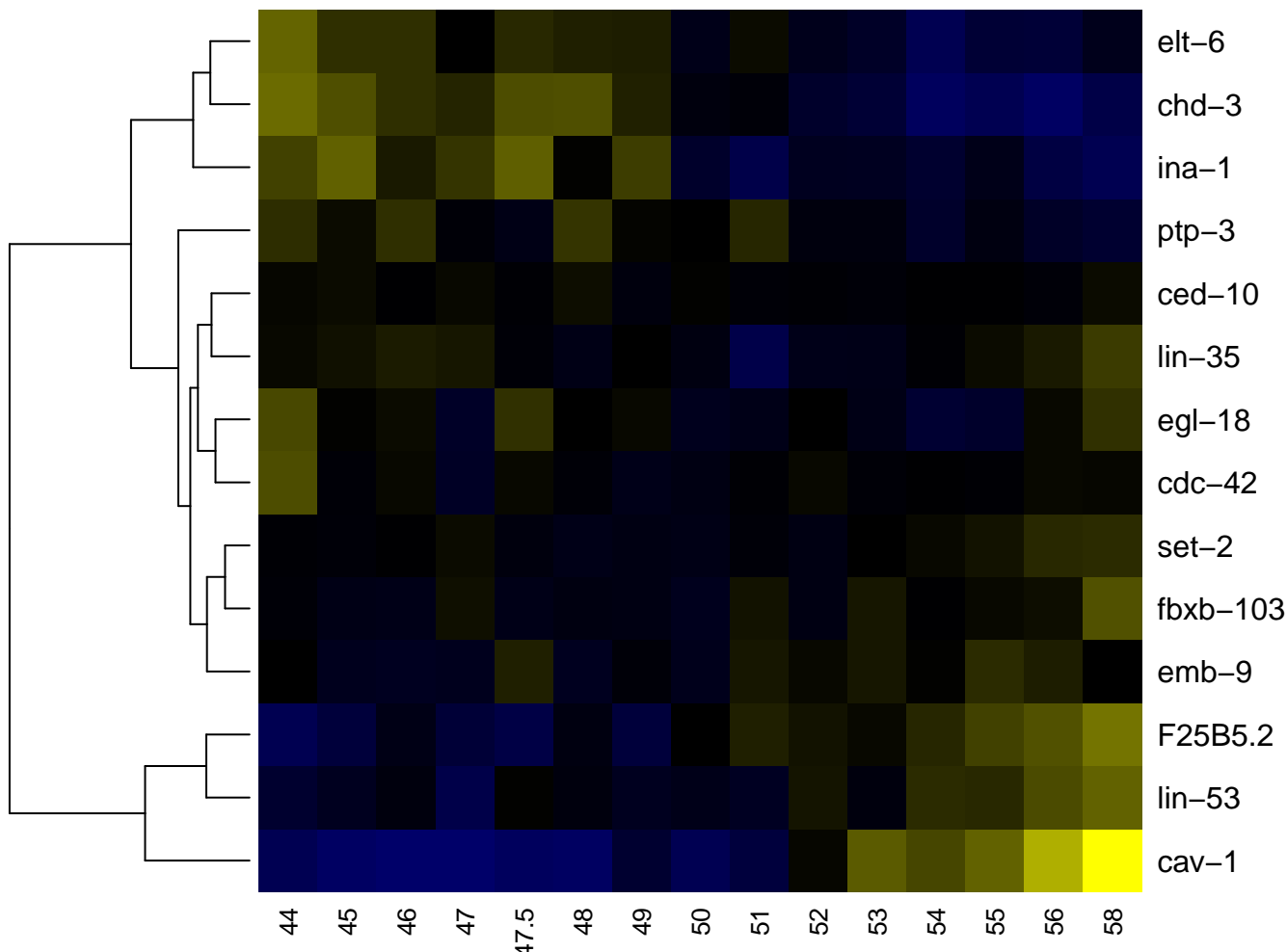
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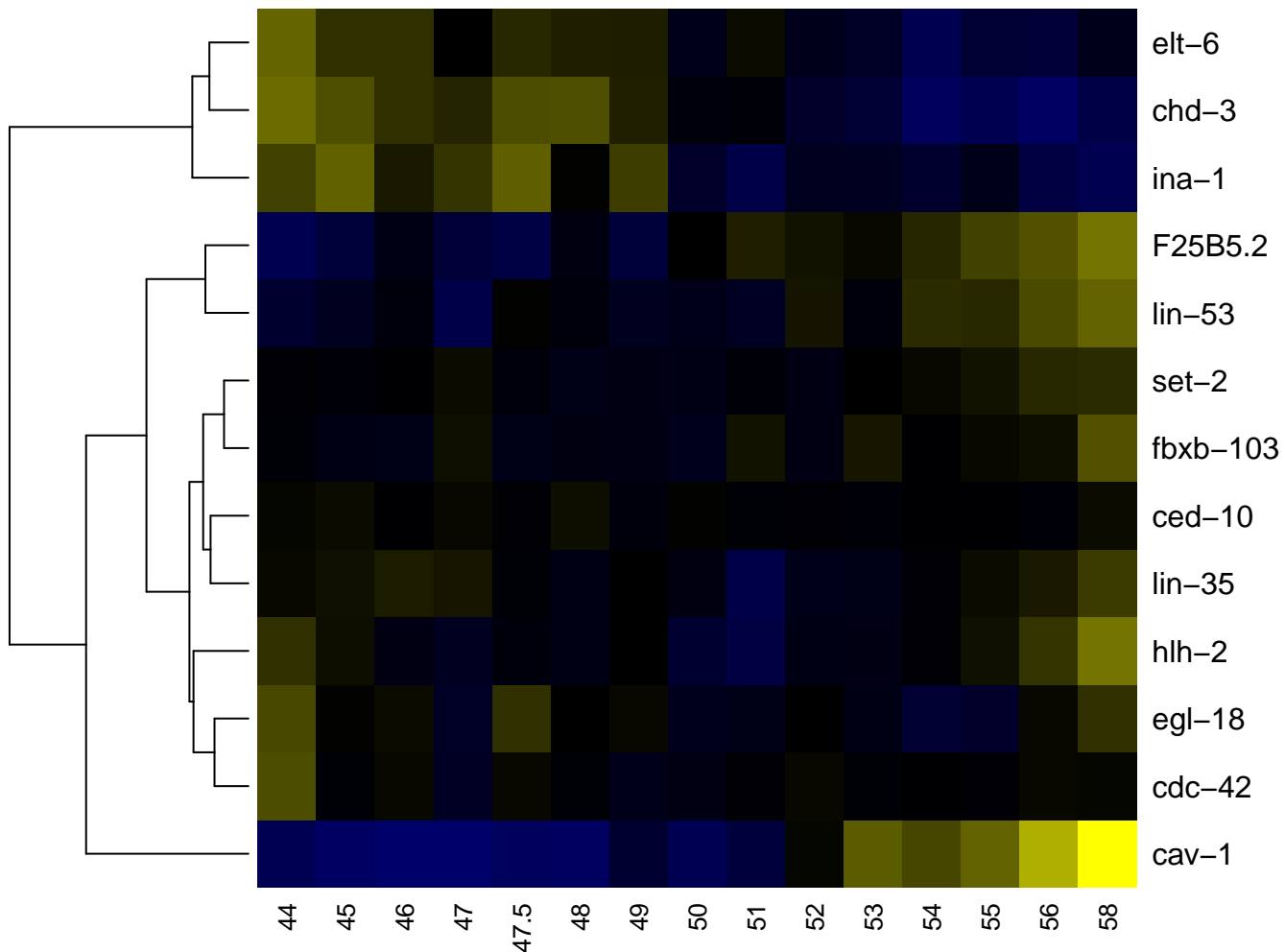
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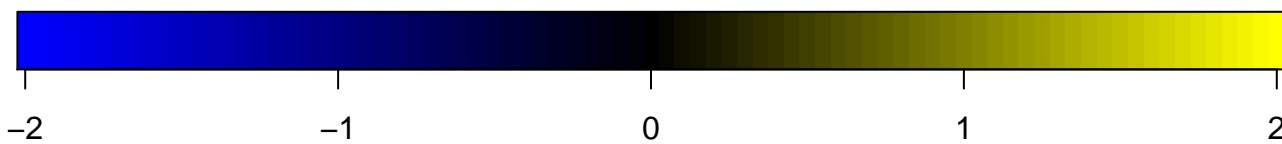
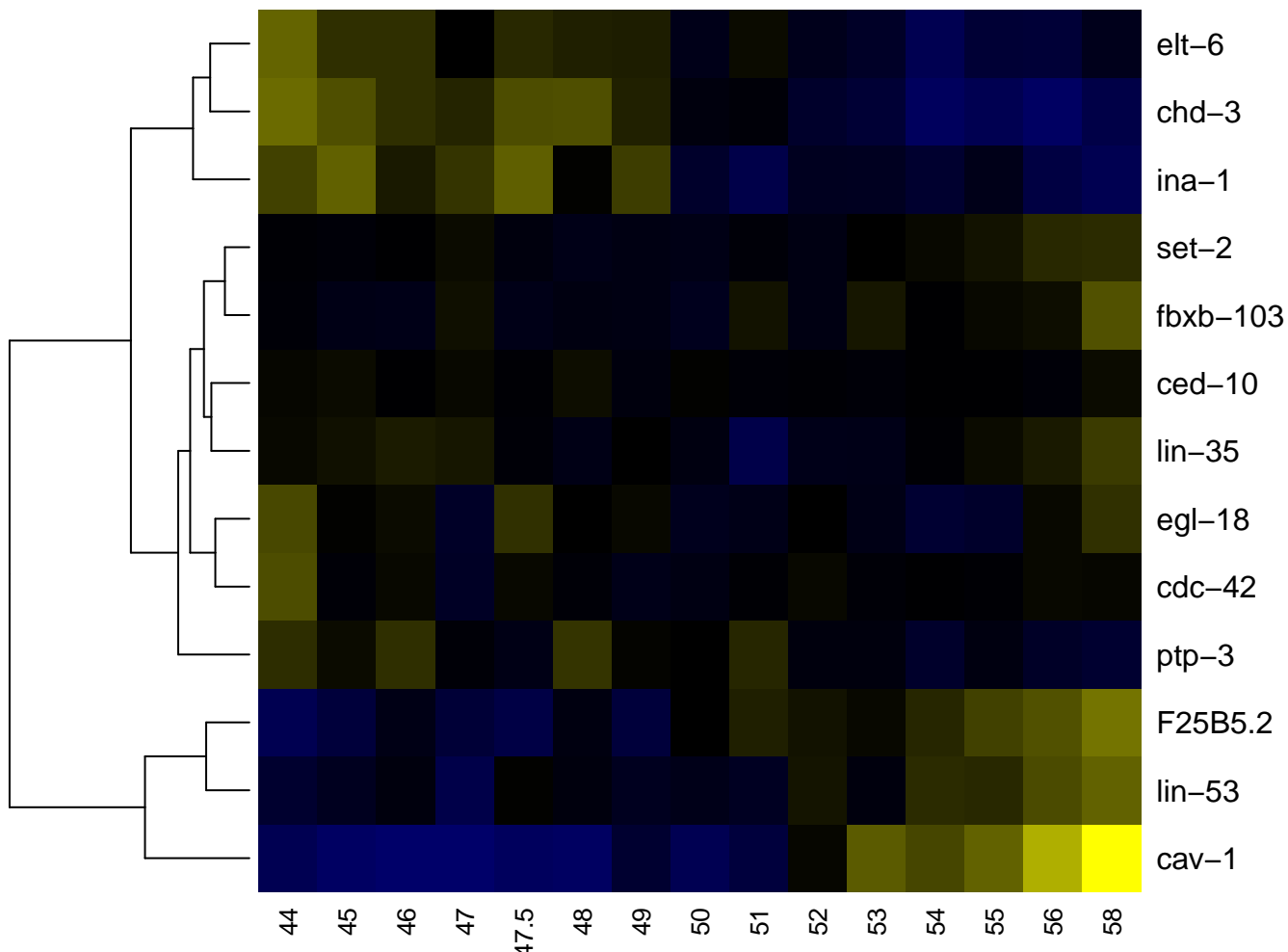
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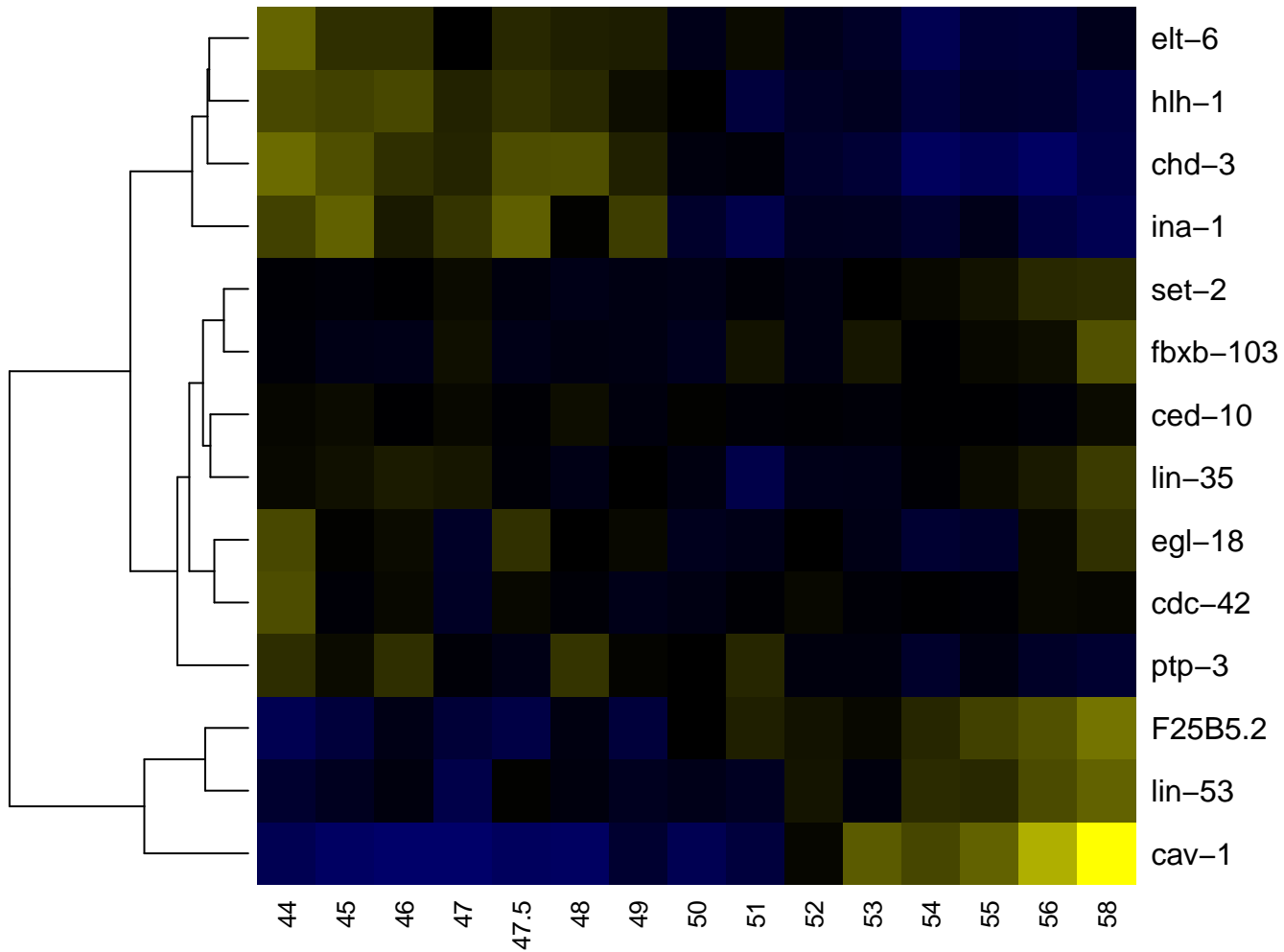
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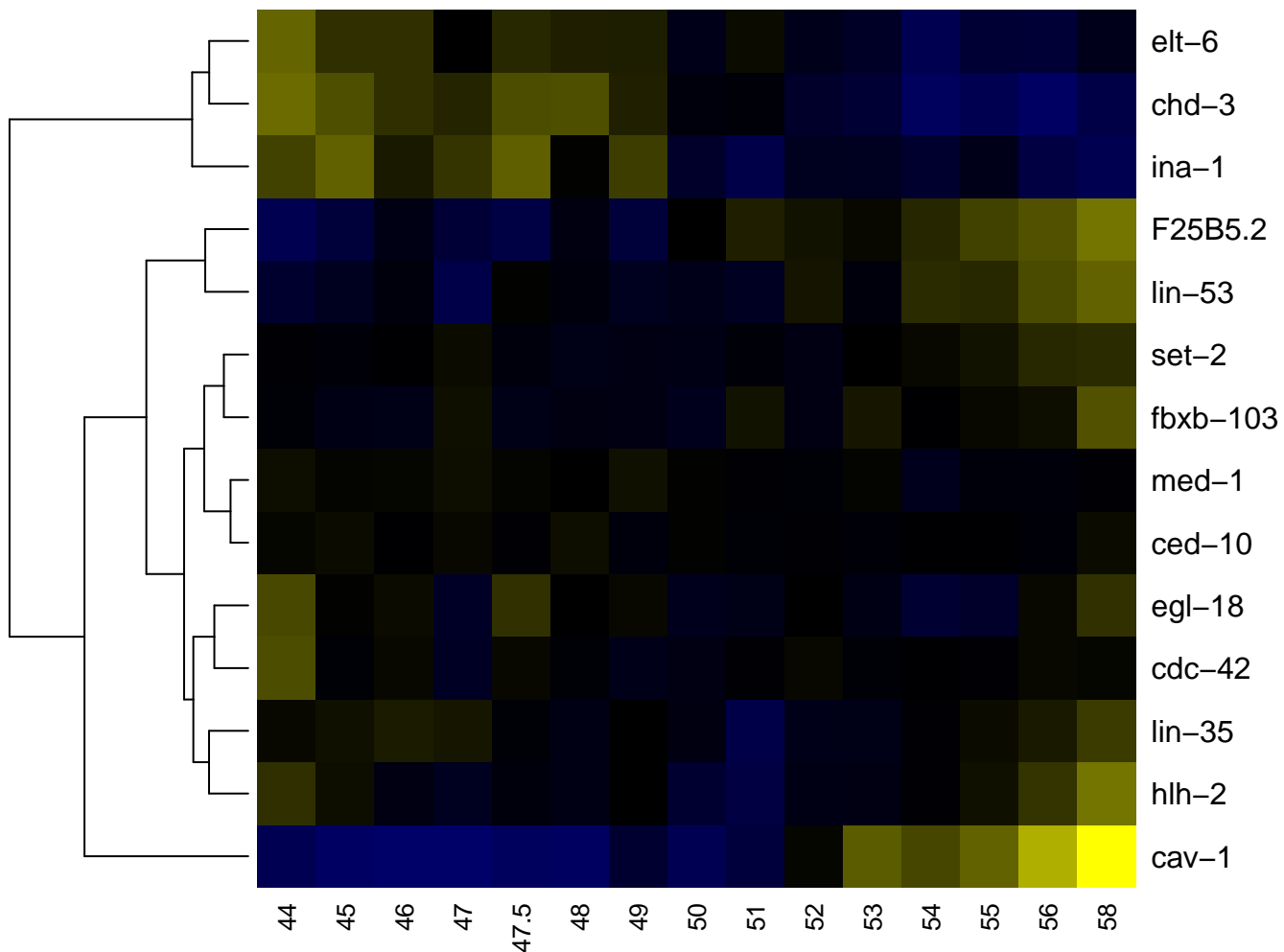
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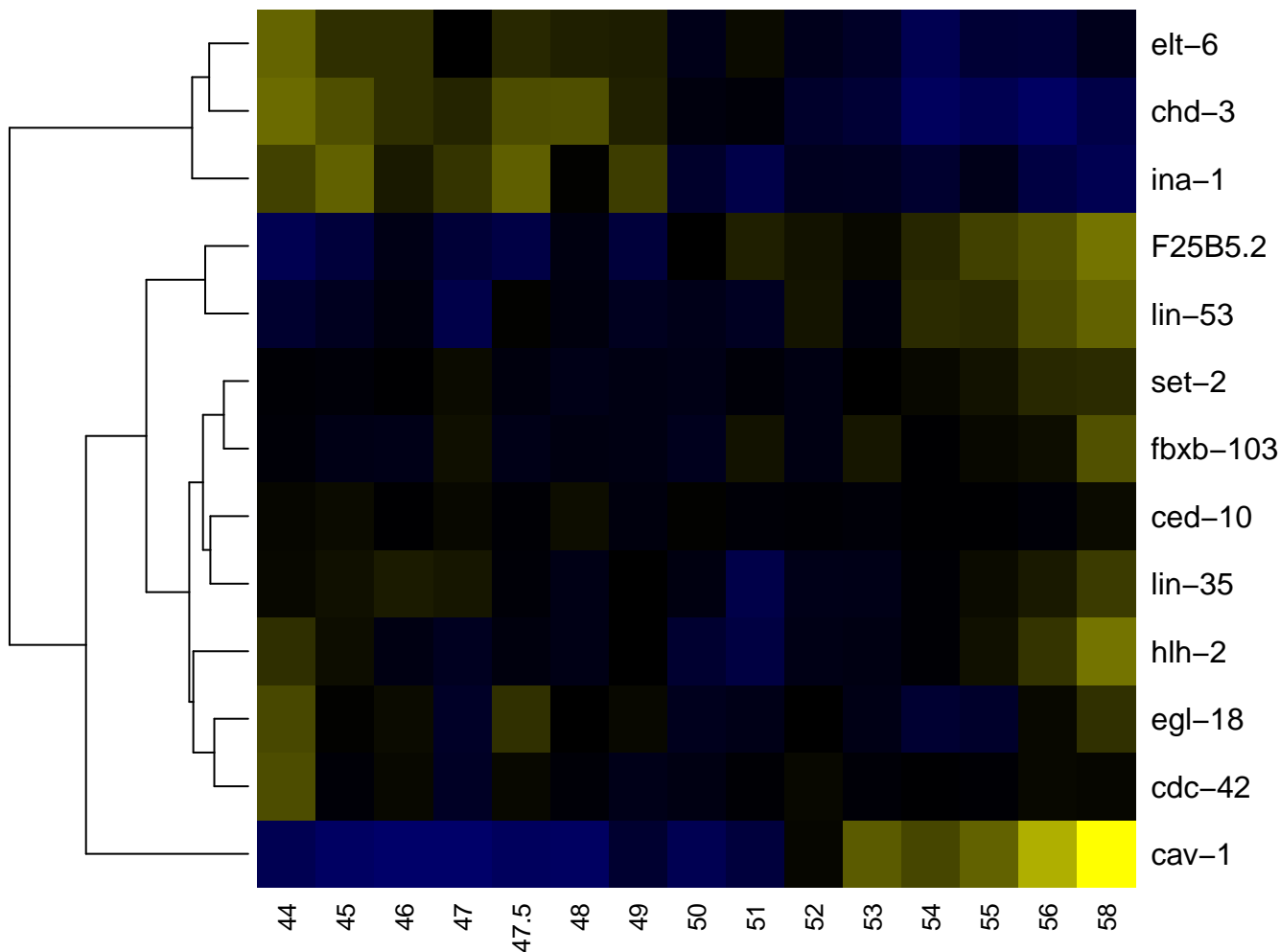
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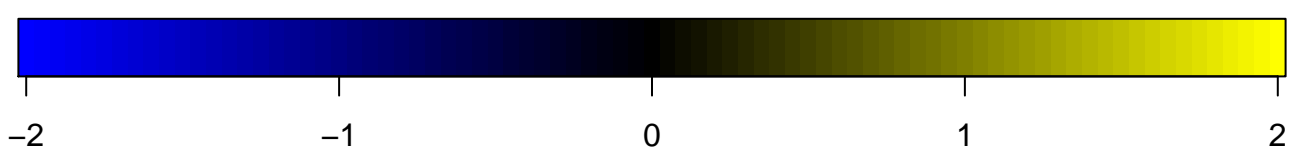
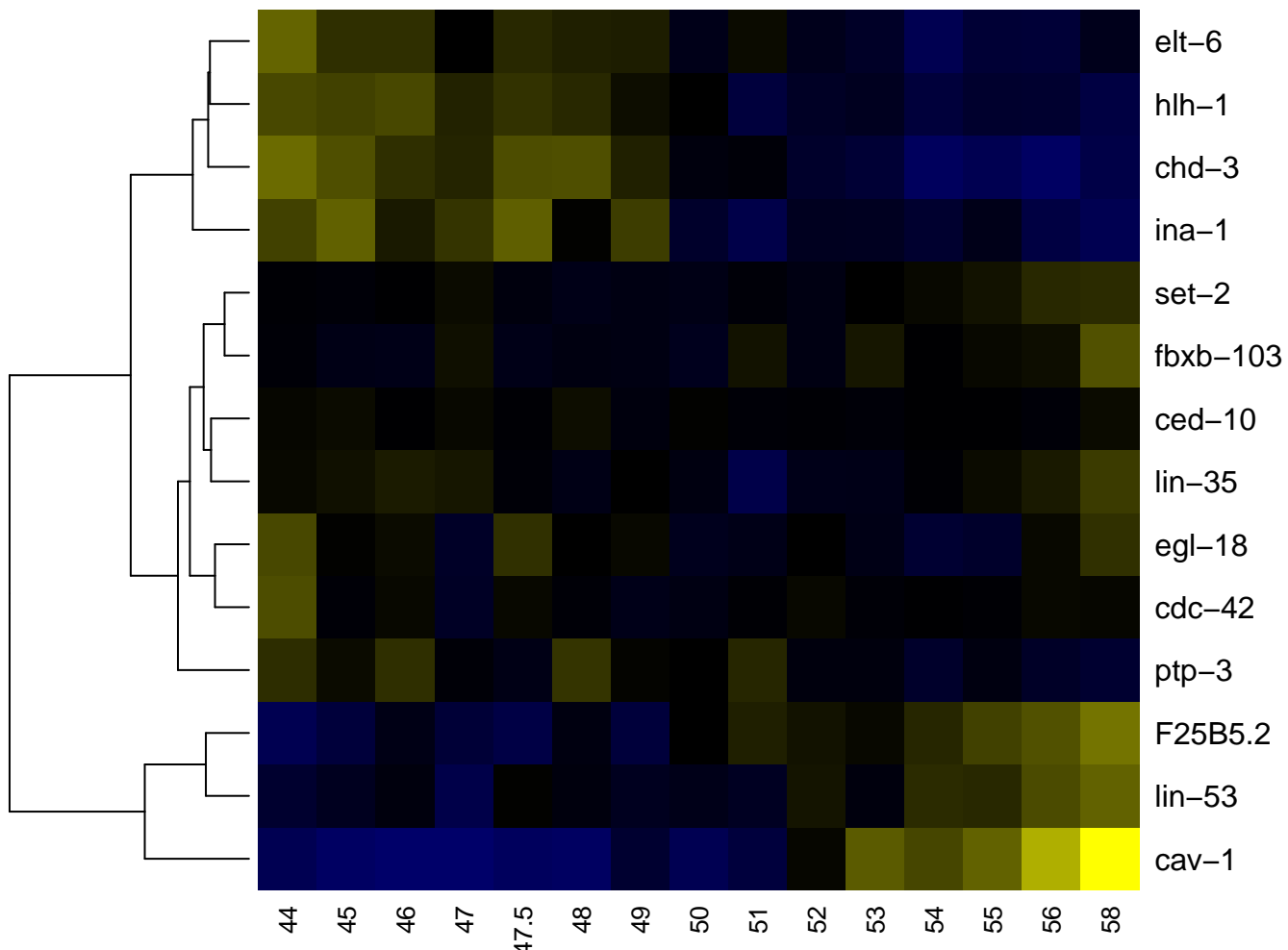
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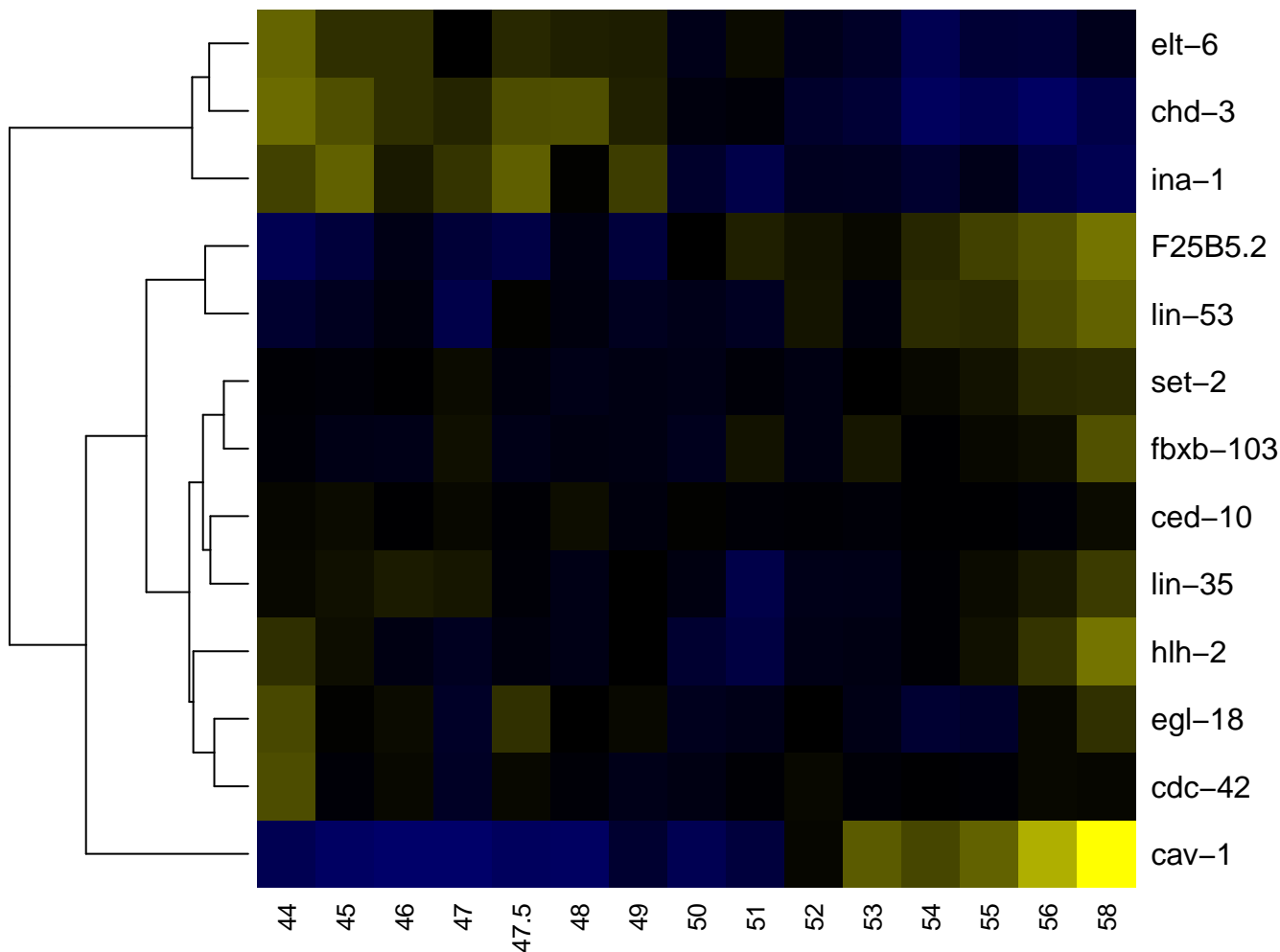
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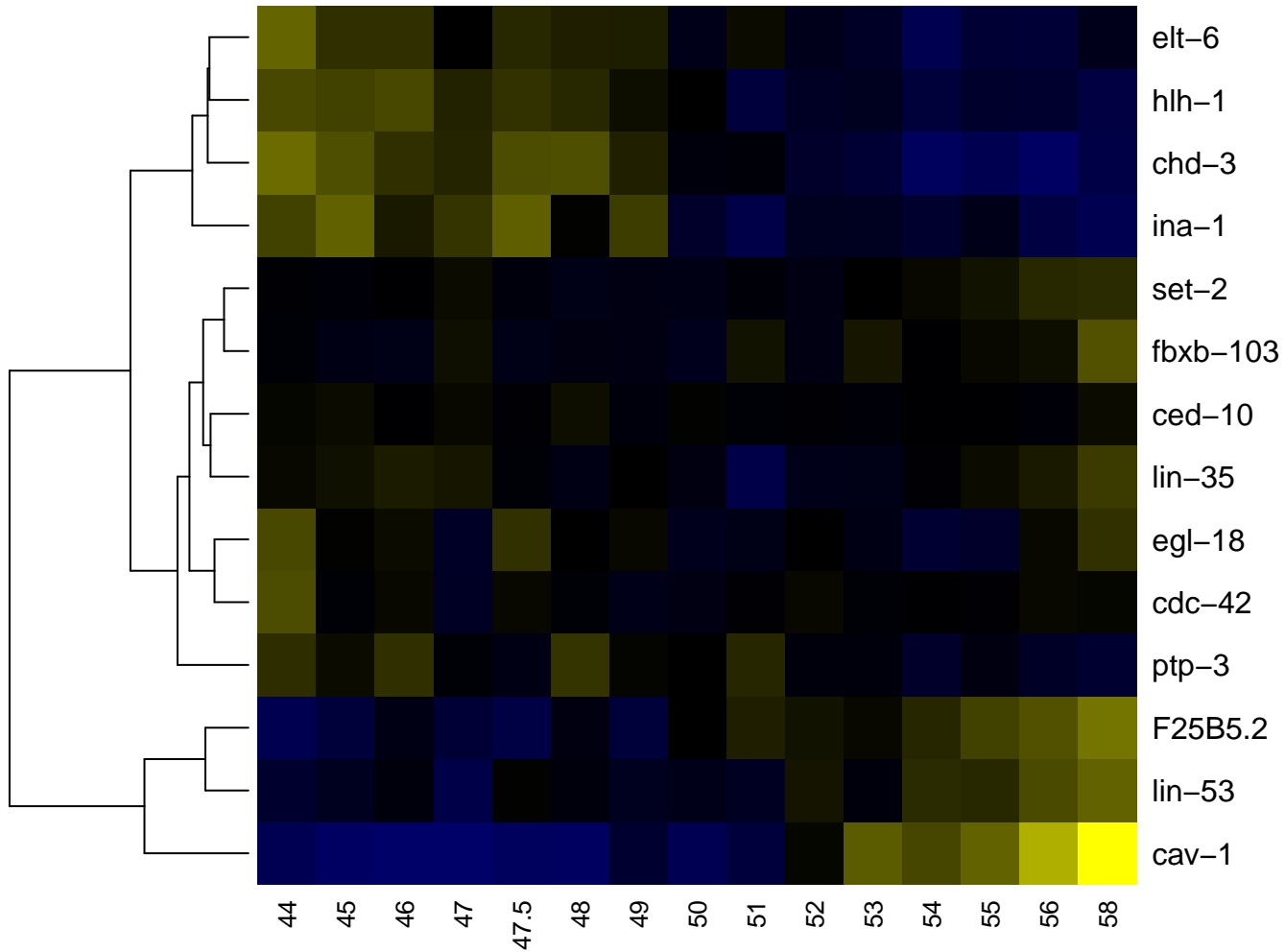
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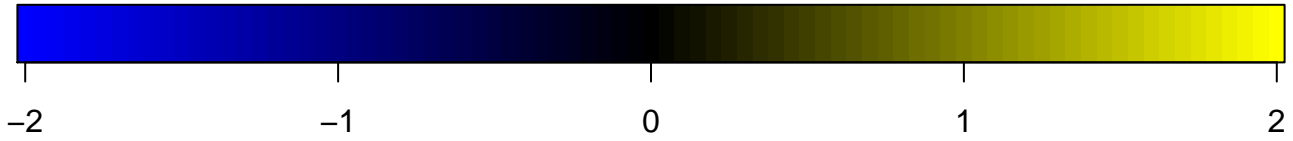
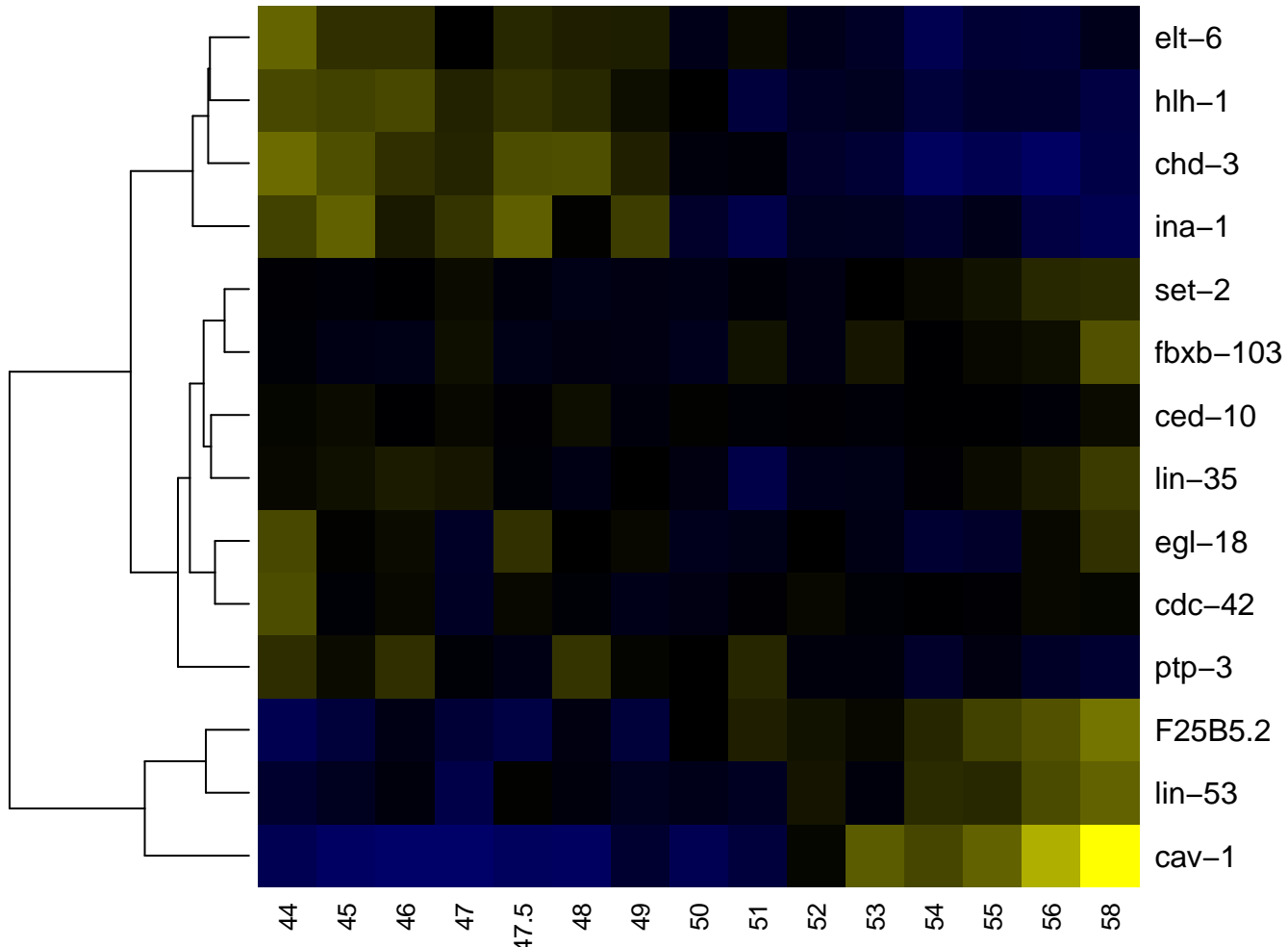
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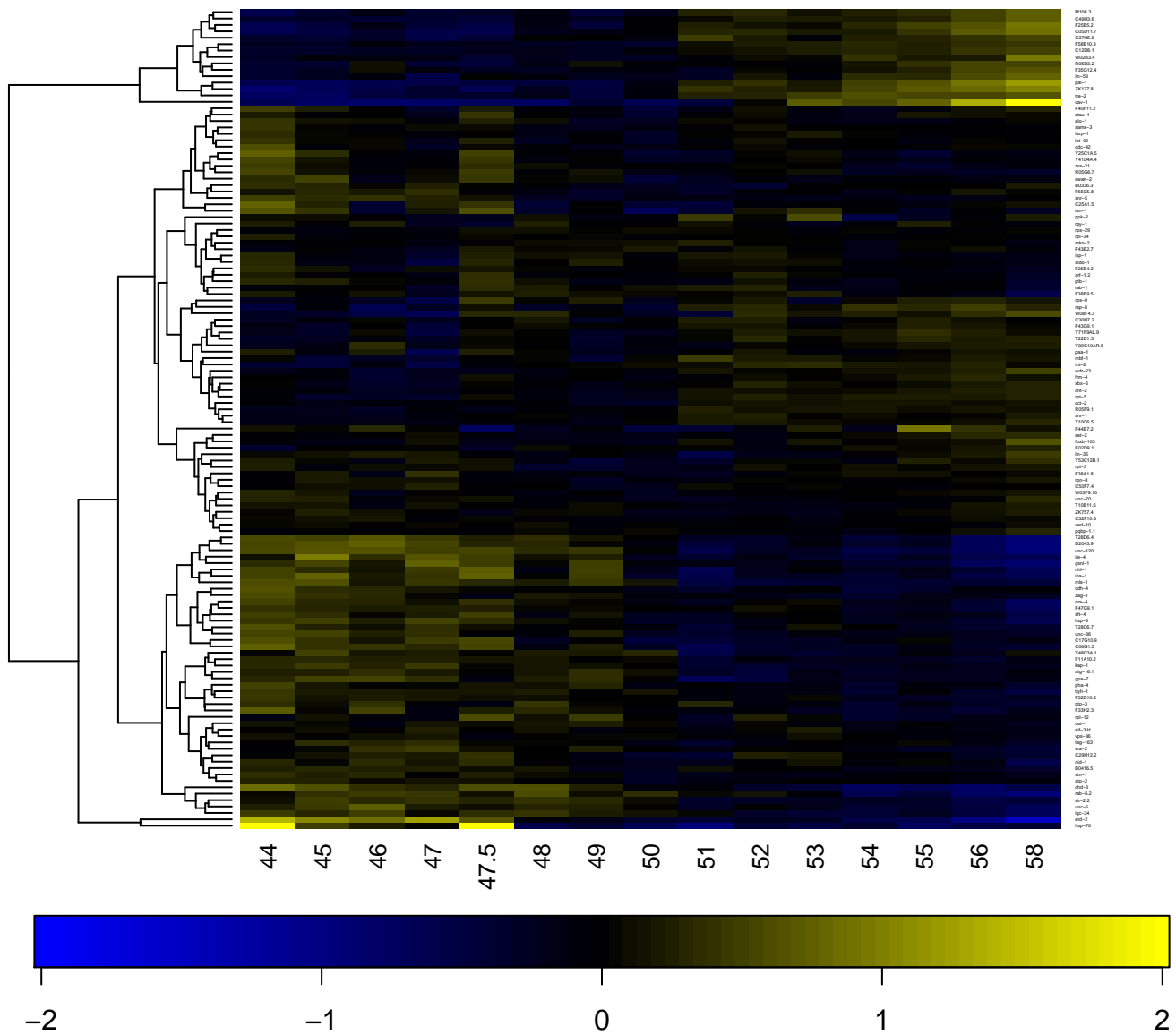
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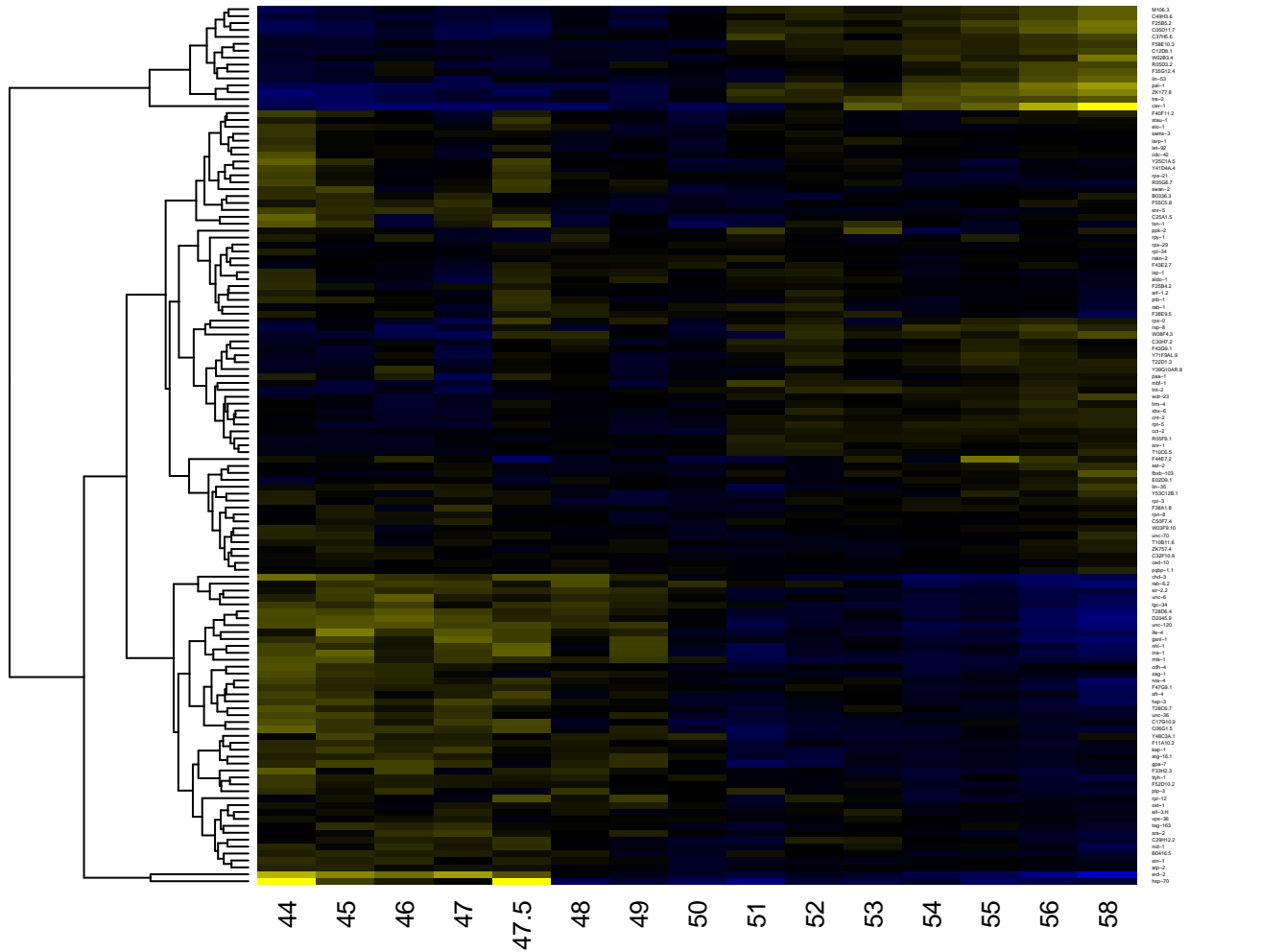
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mu_int_R



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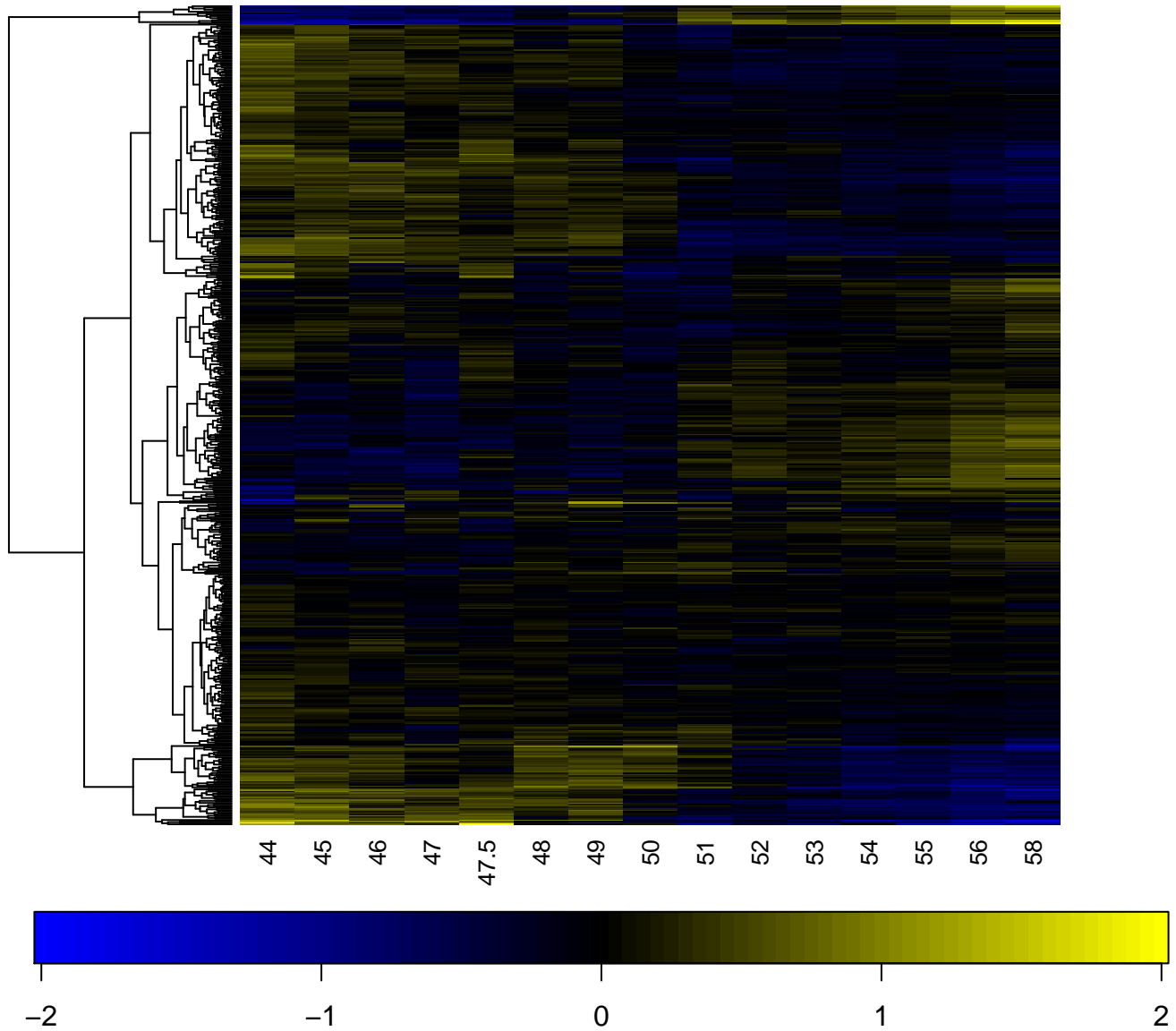
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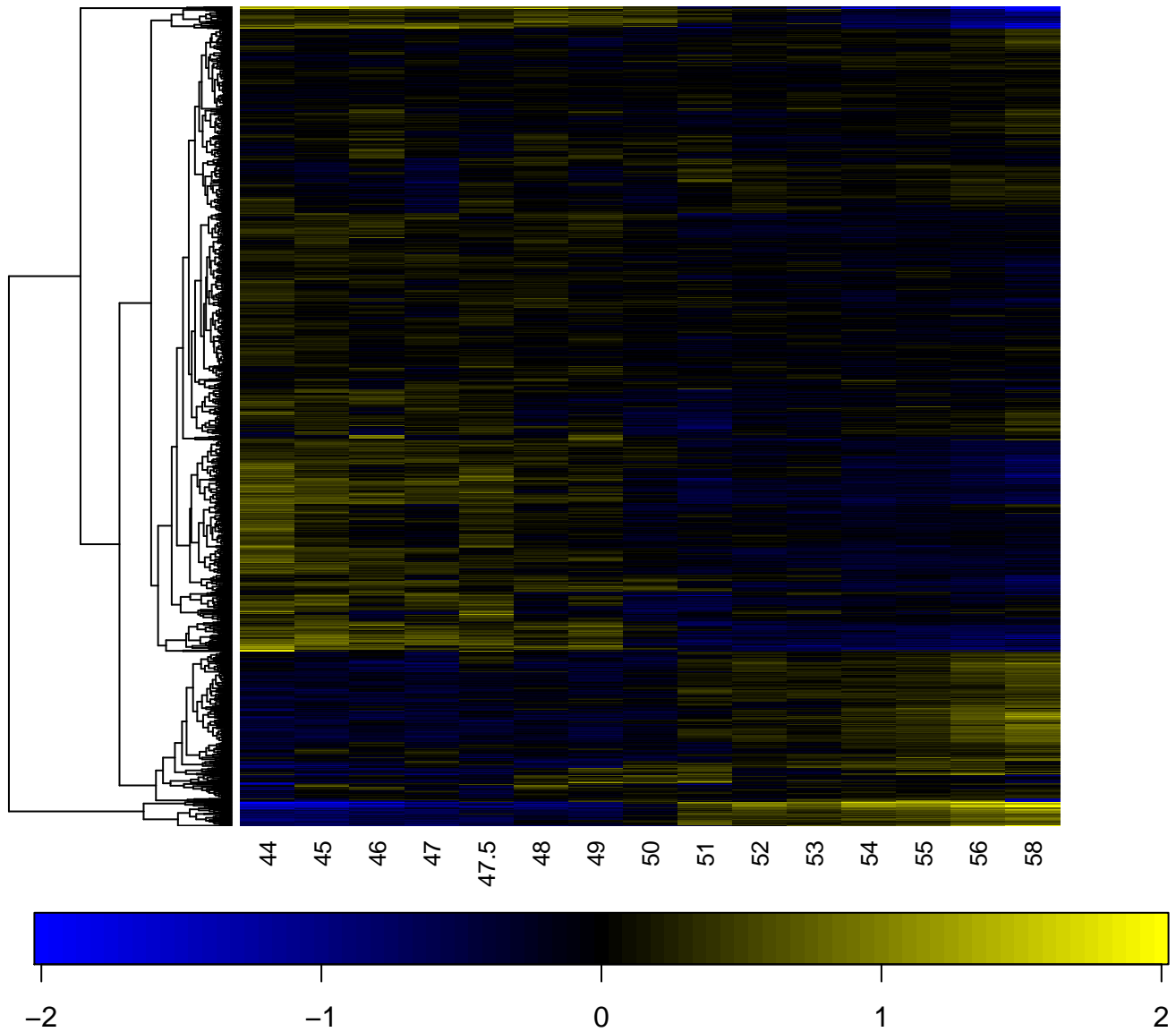
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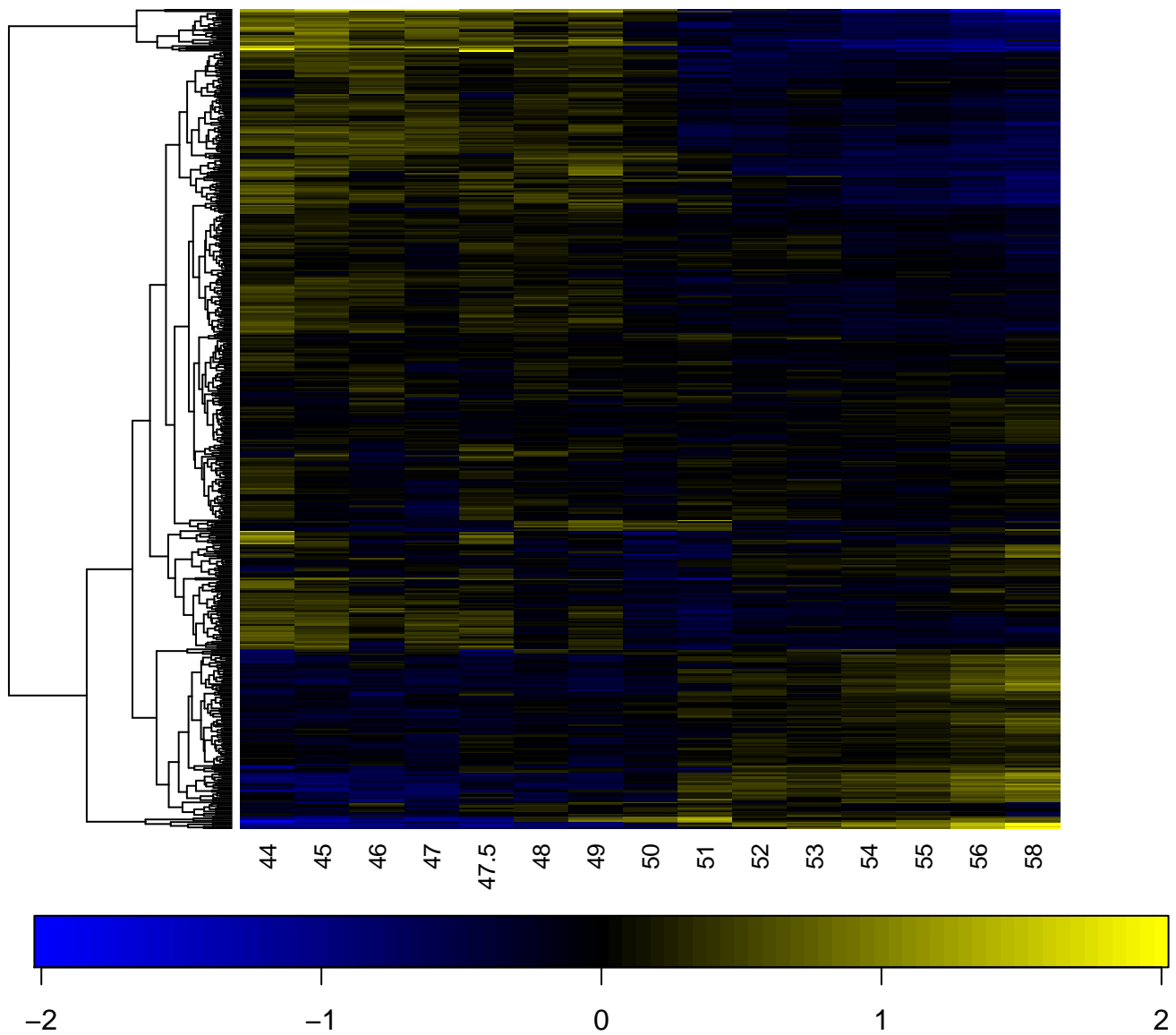
nerve ring



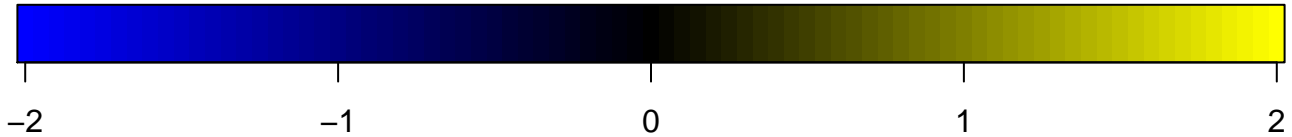
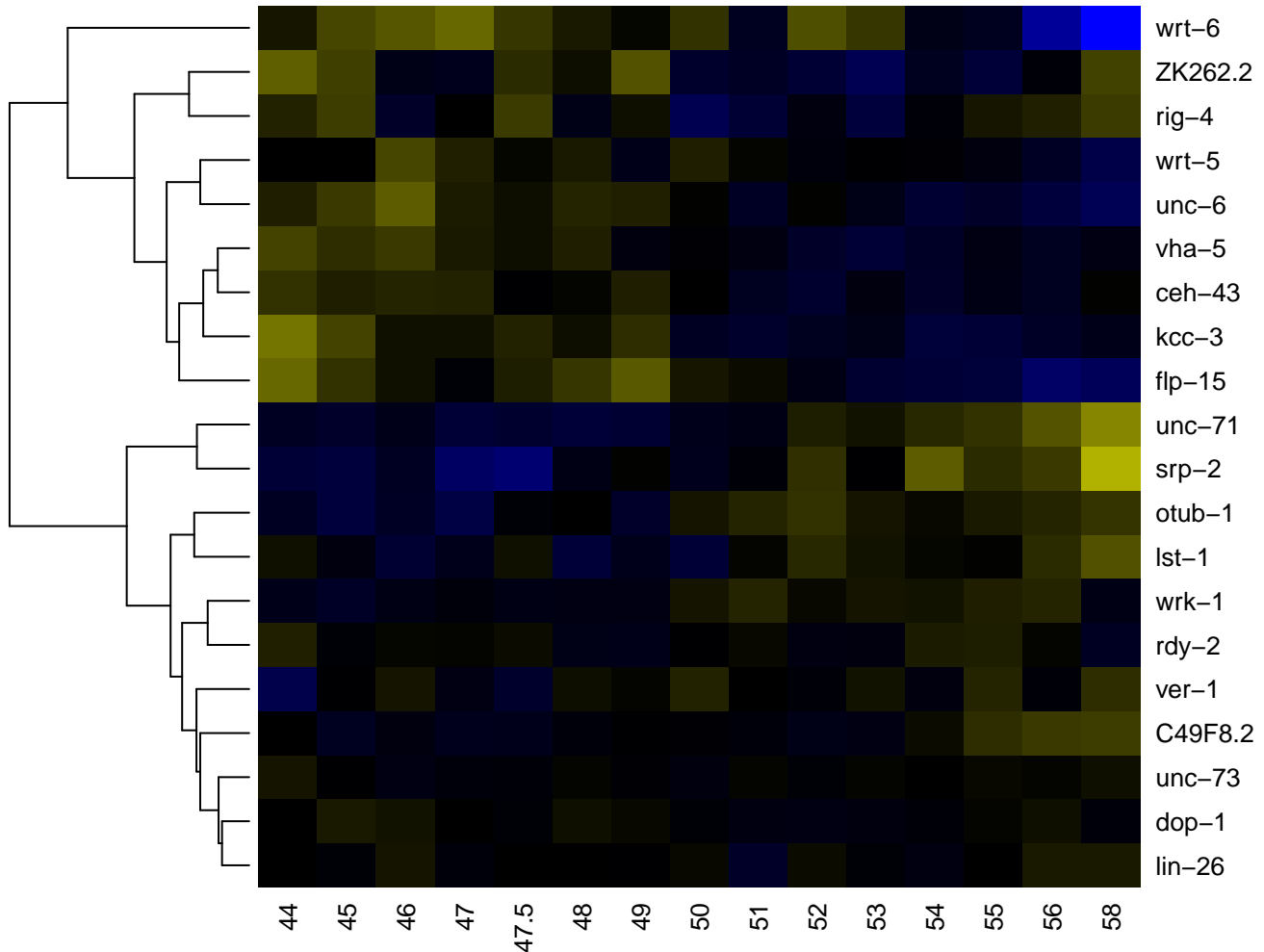
nervous system



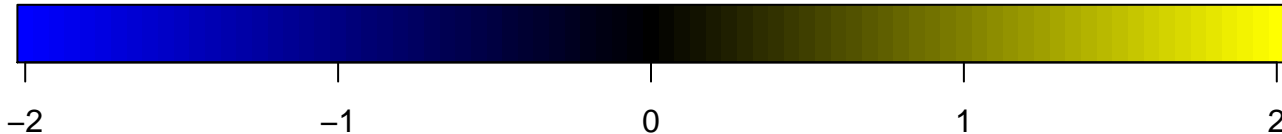
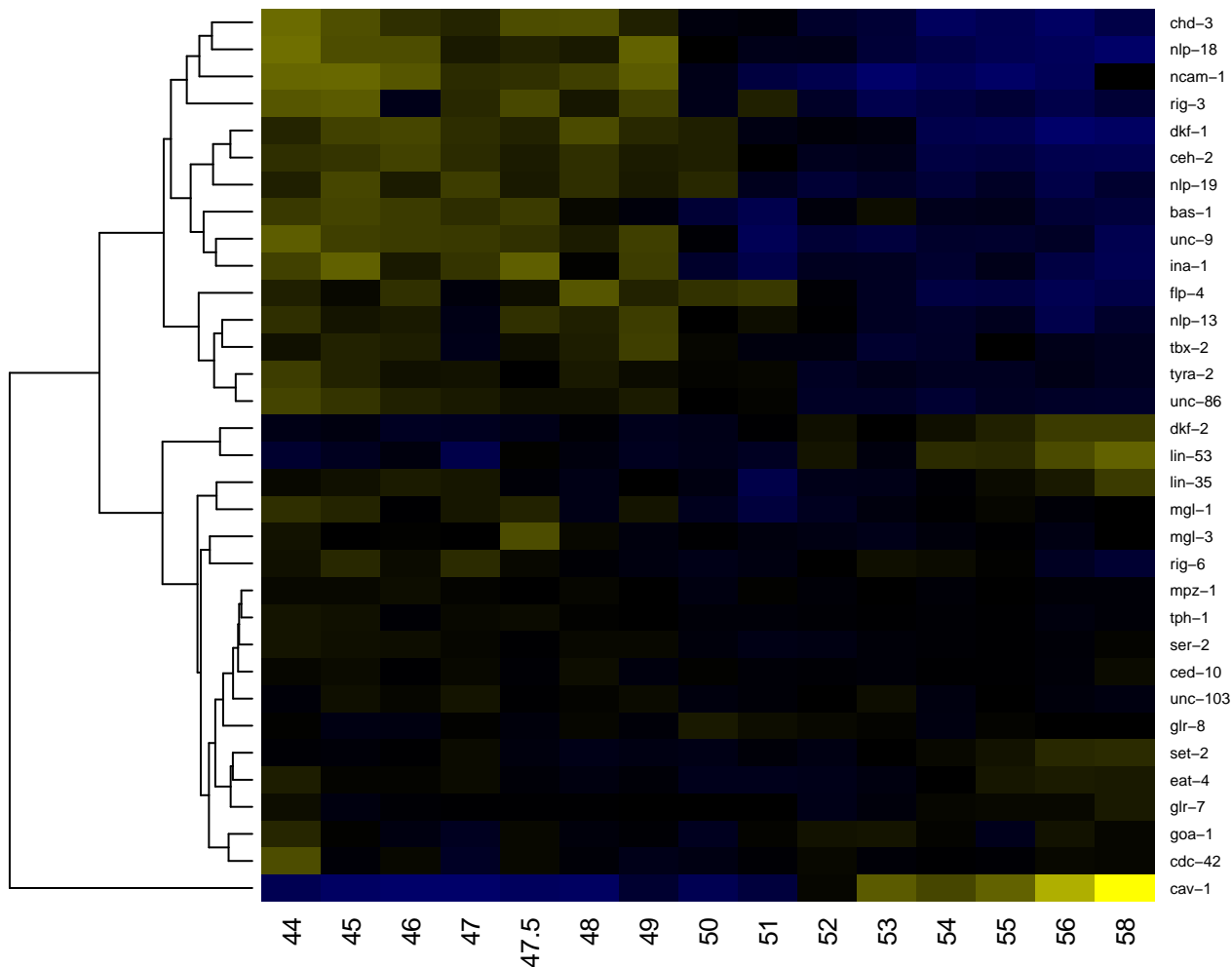
neuron



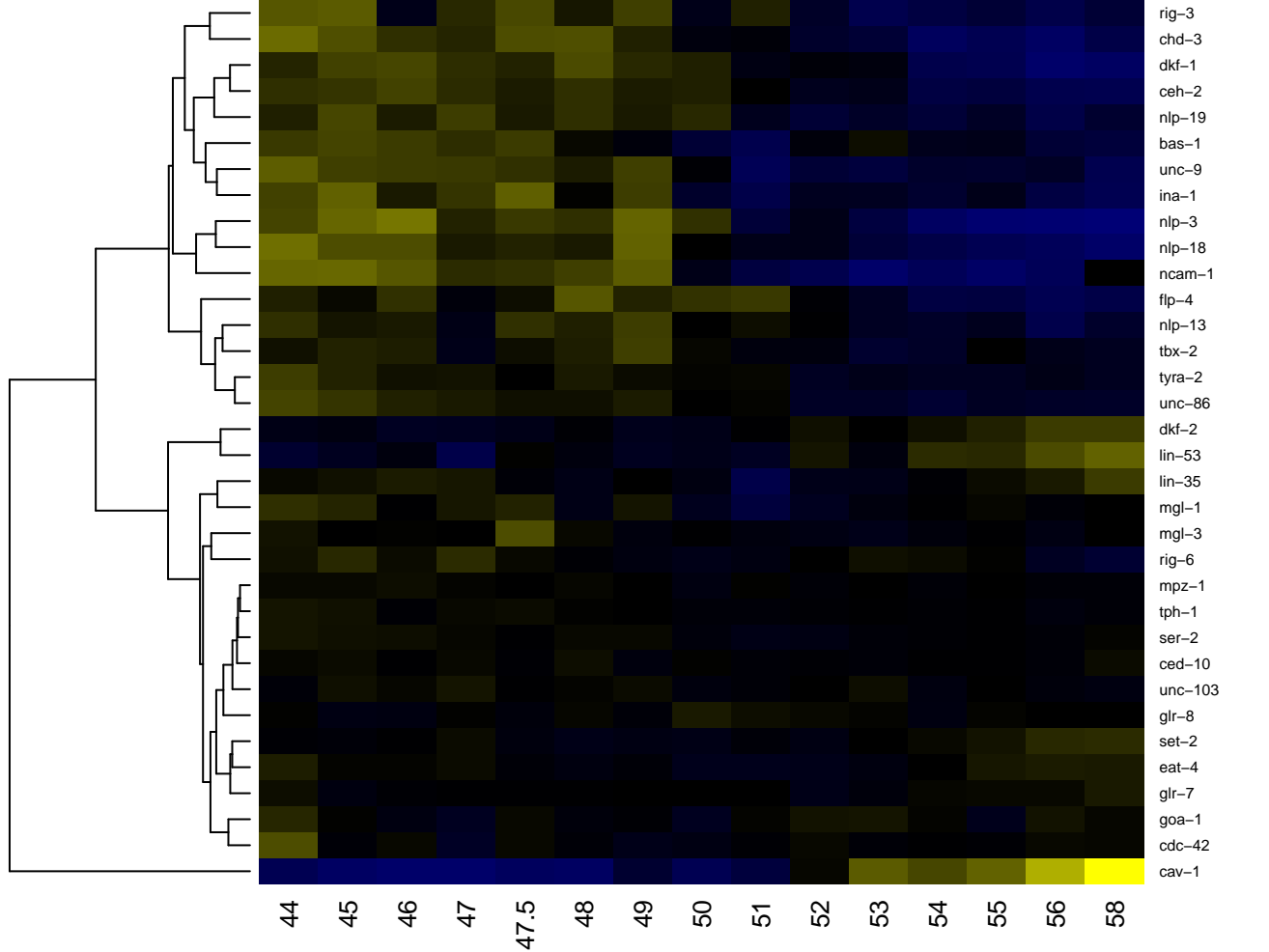
neuronal sheath cell



NSML



NSMR



-2

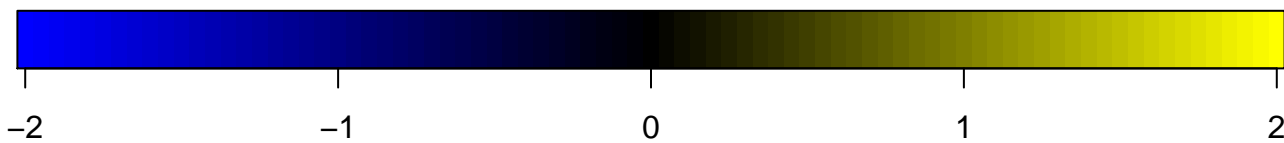
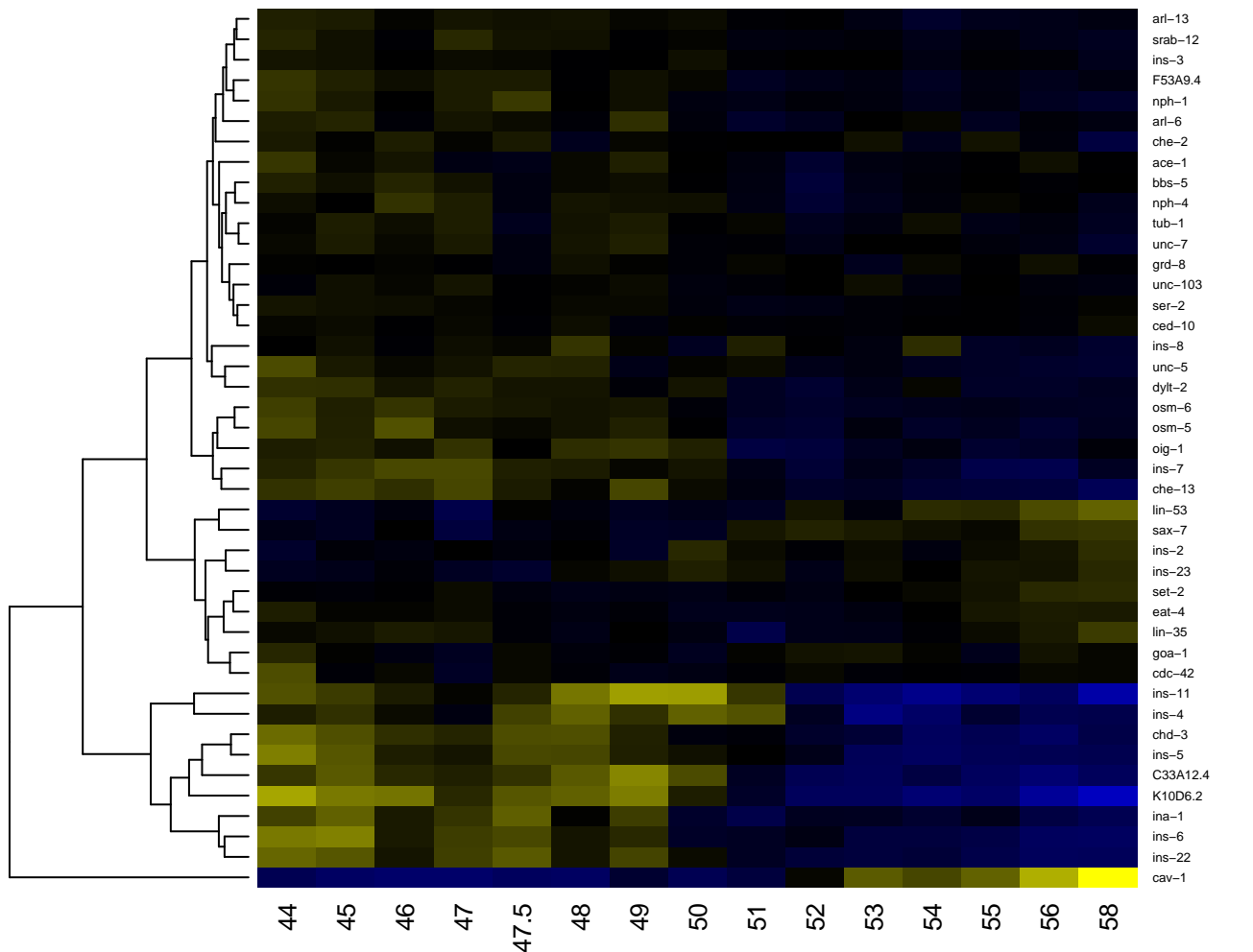
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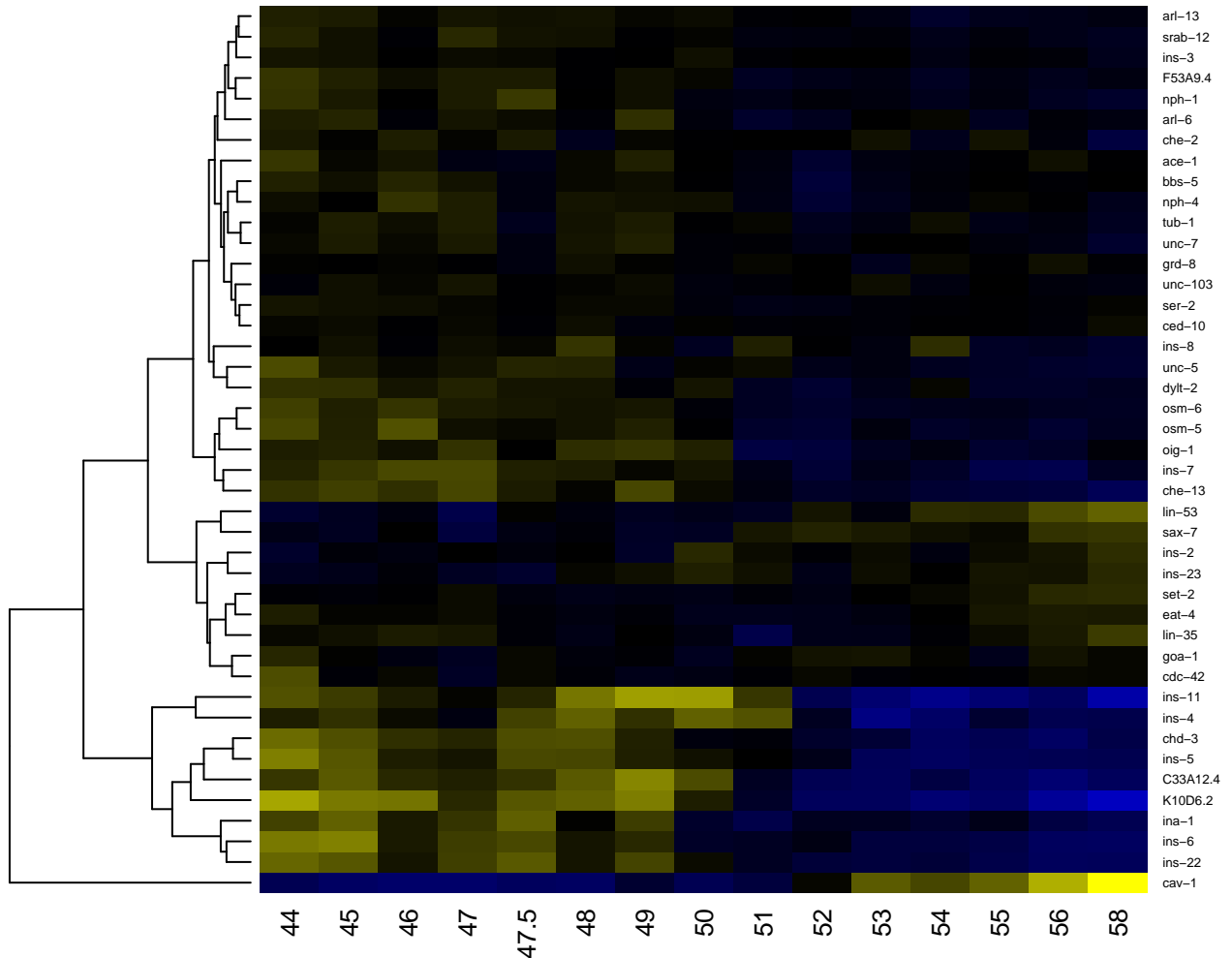
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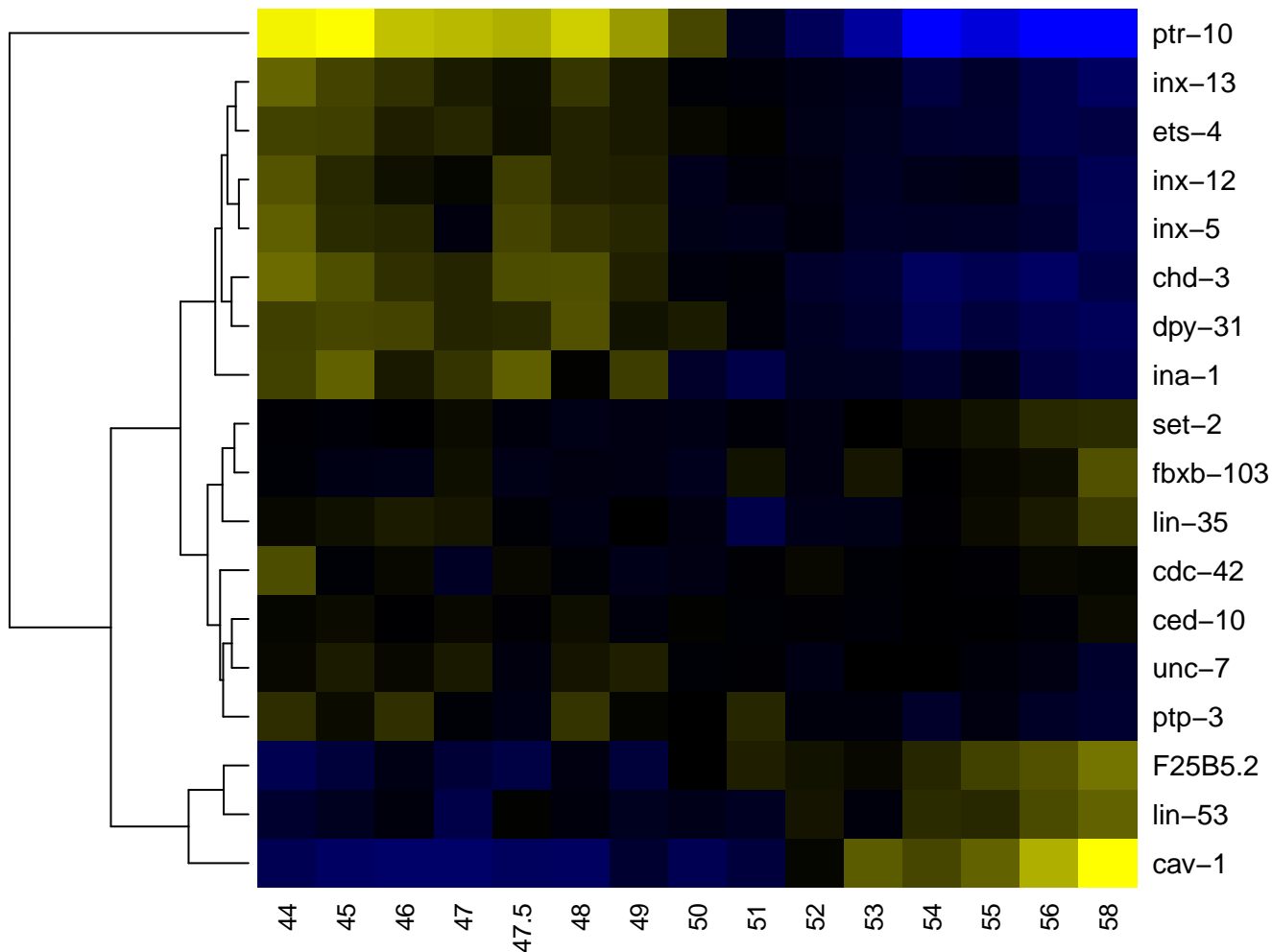
OLLL



OLLR



OLLsol



-2

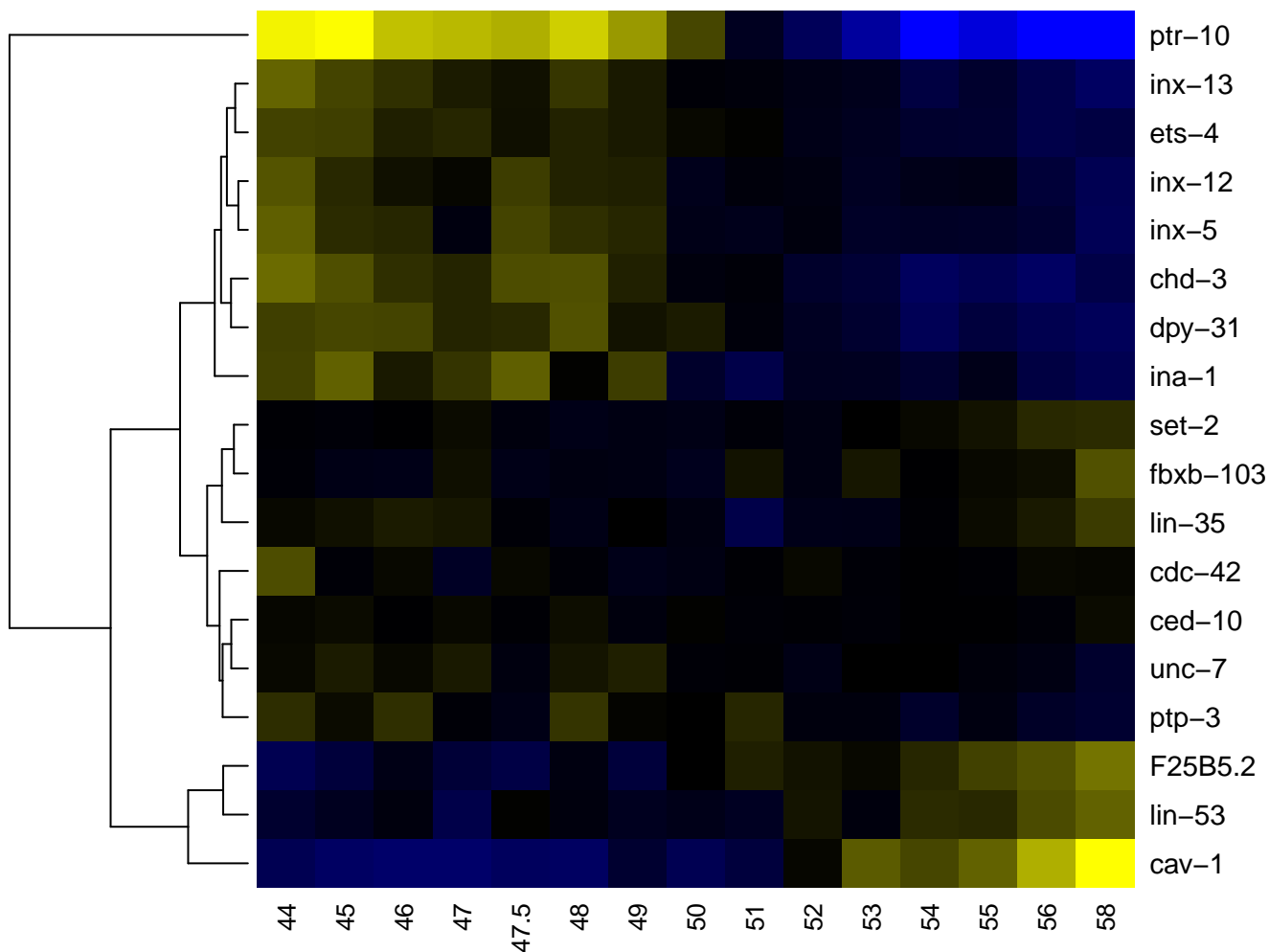
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OLLsoR



-2

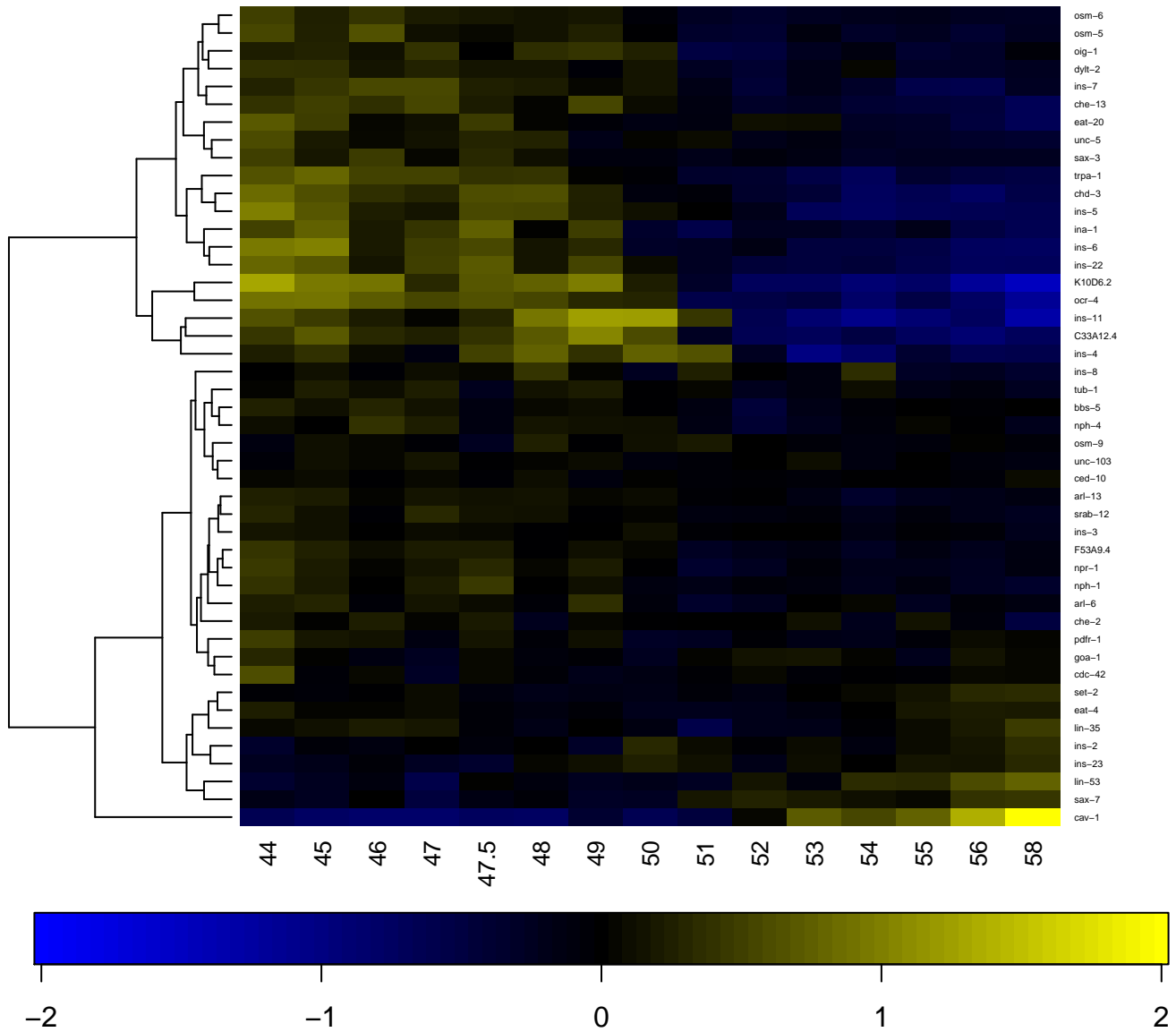
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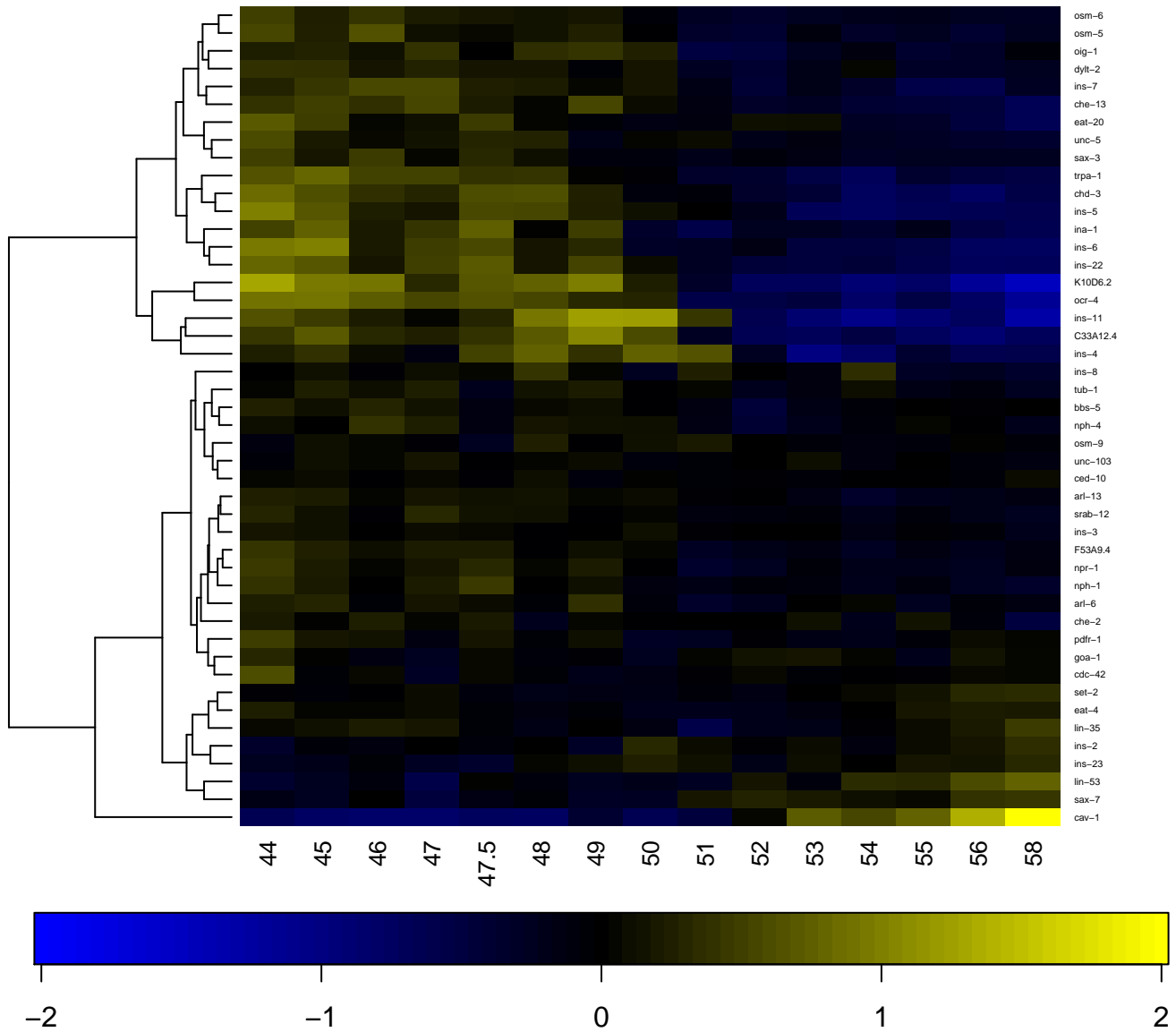
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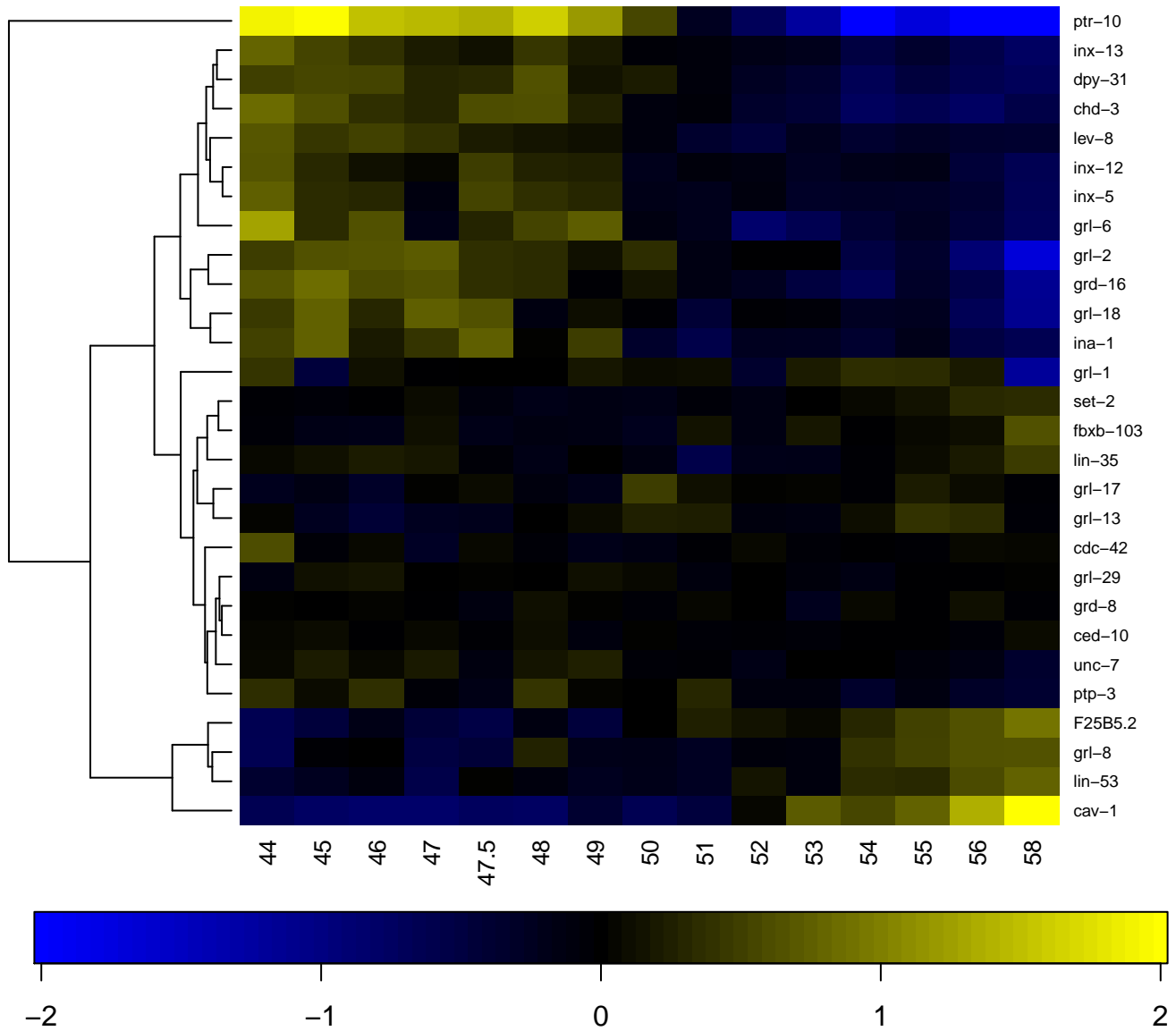
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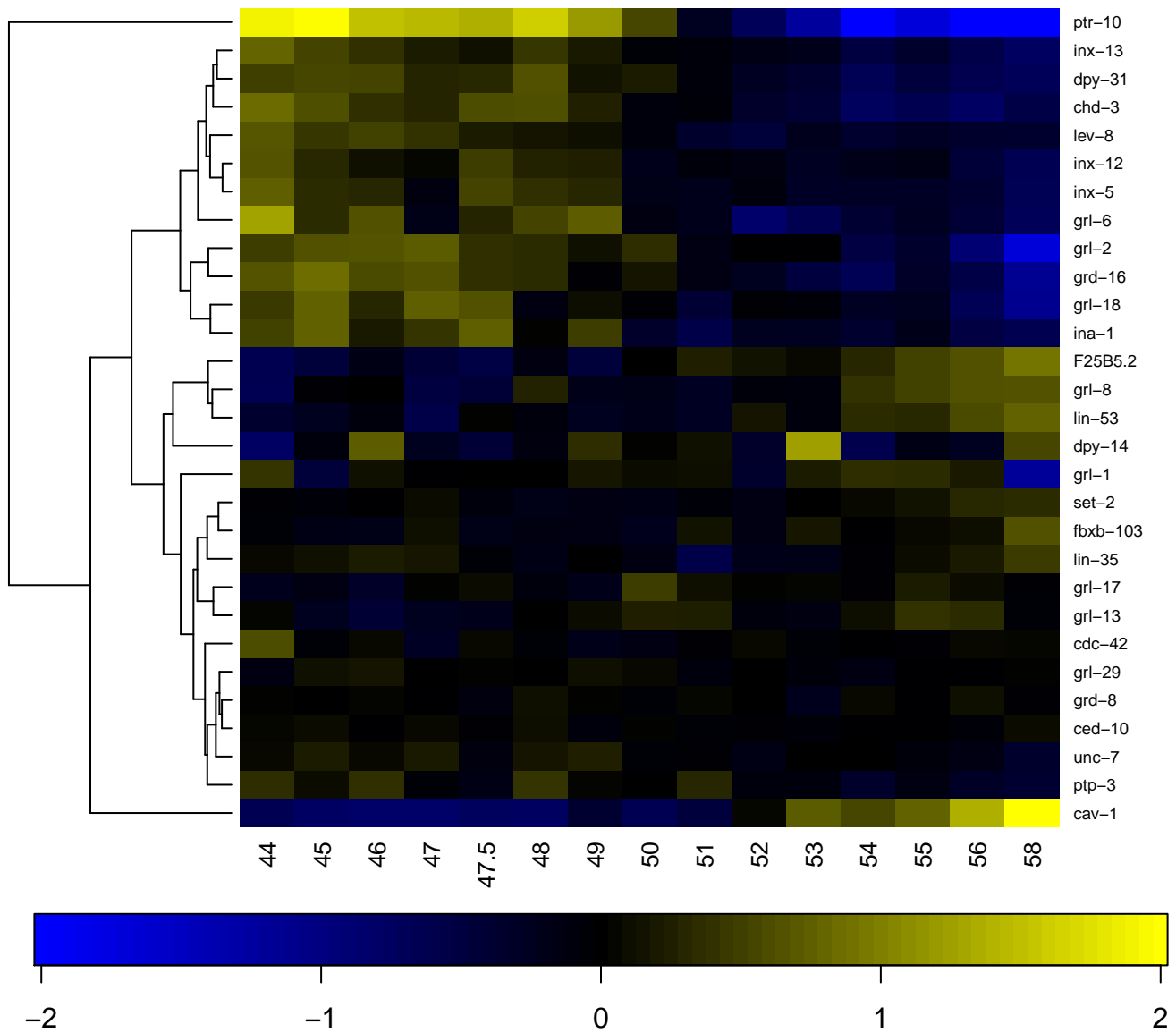
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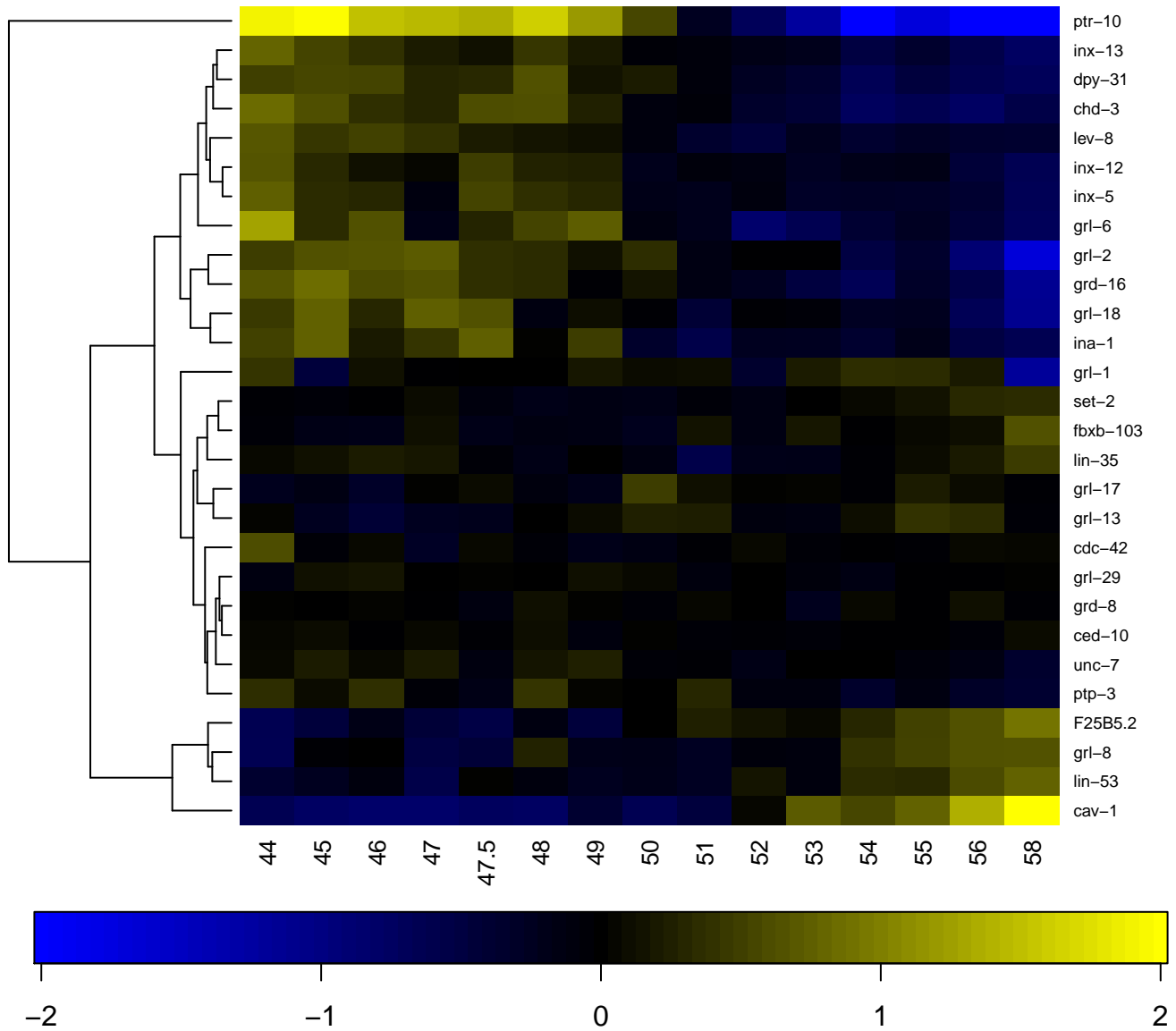
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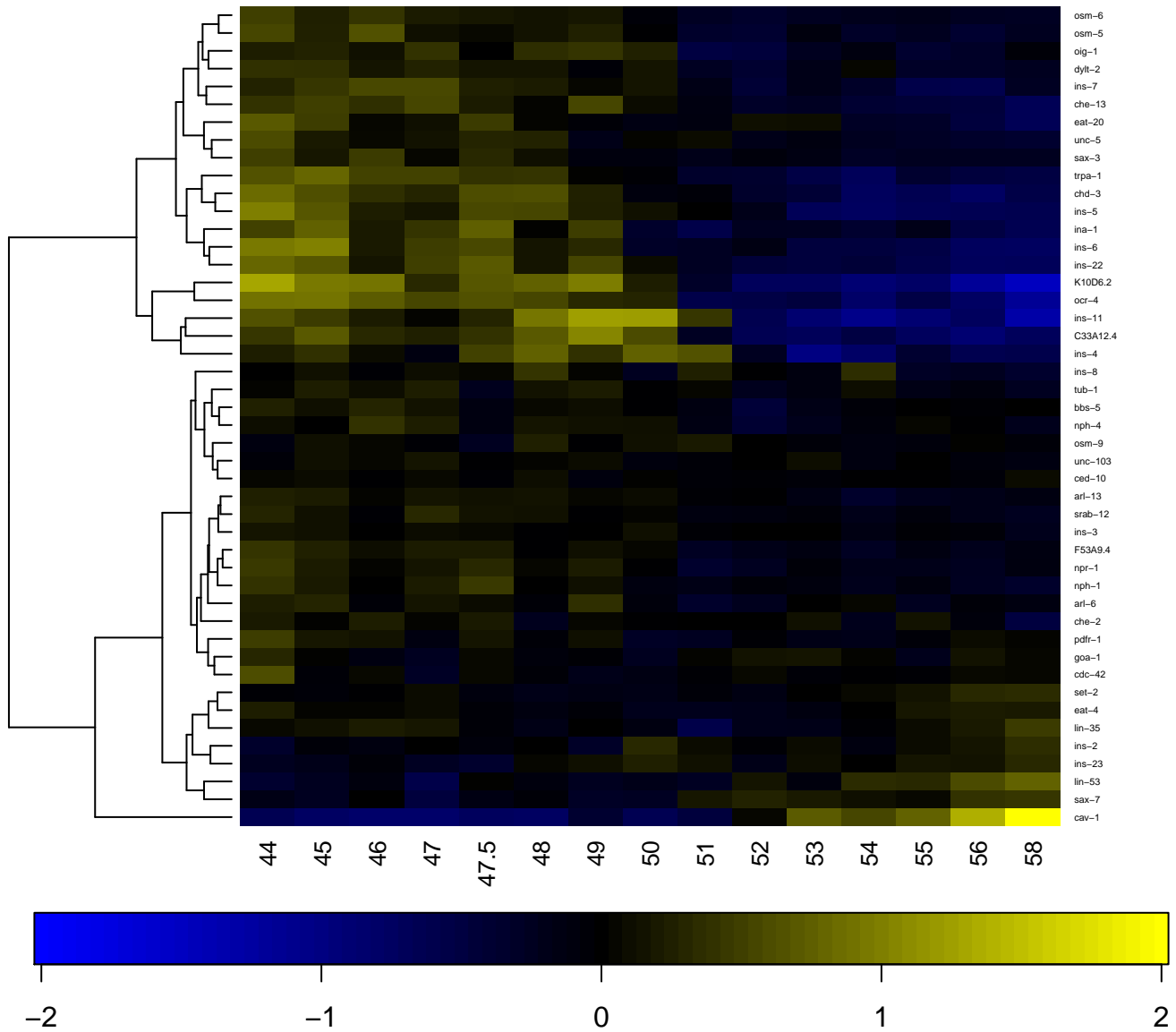
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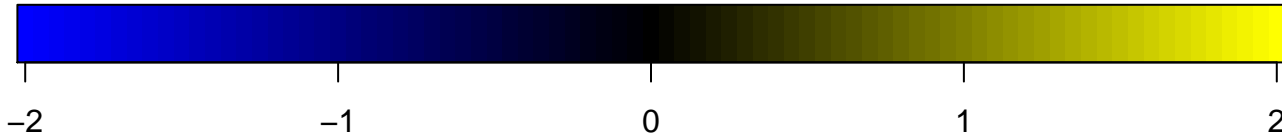
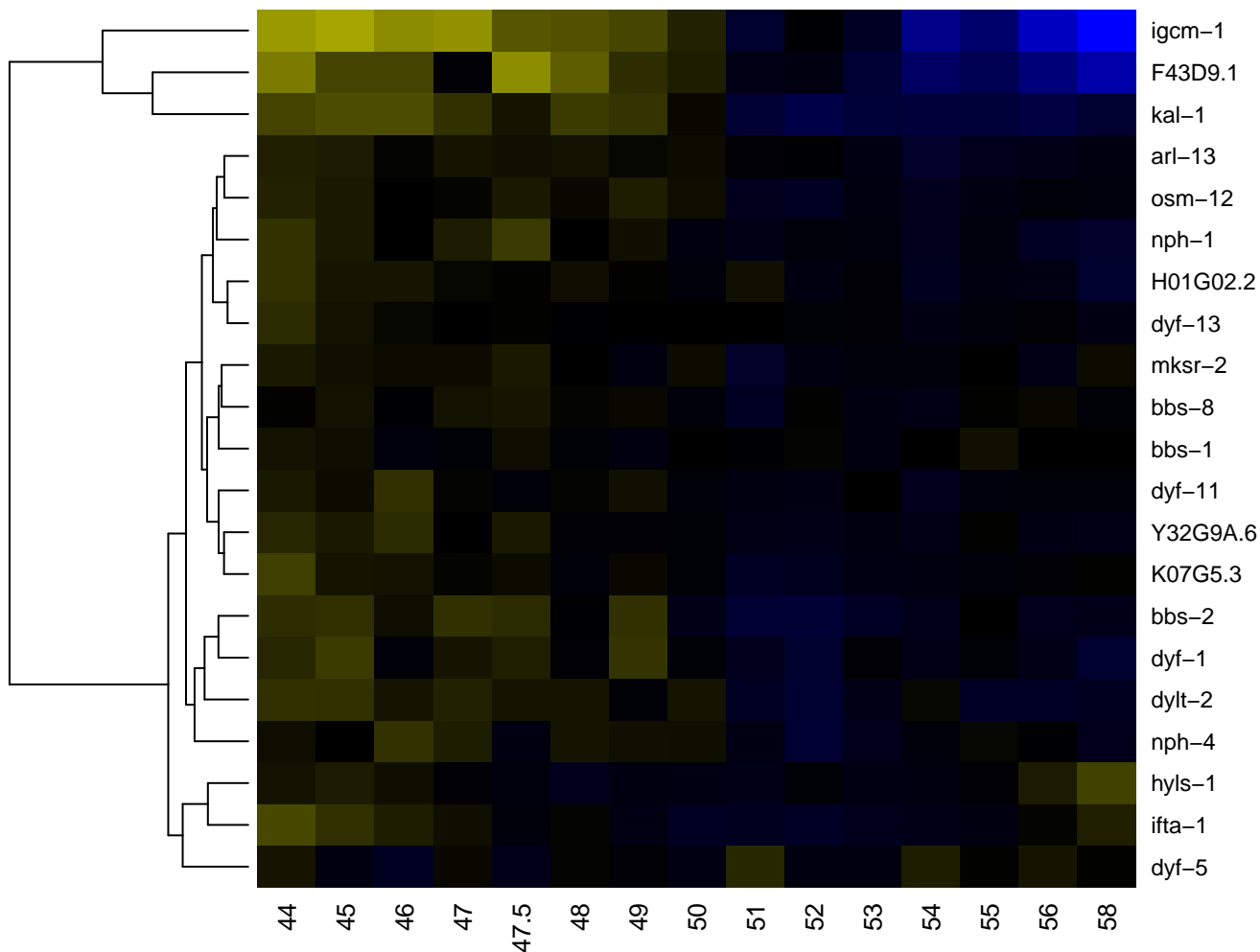
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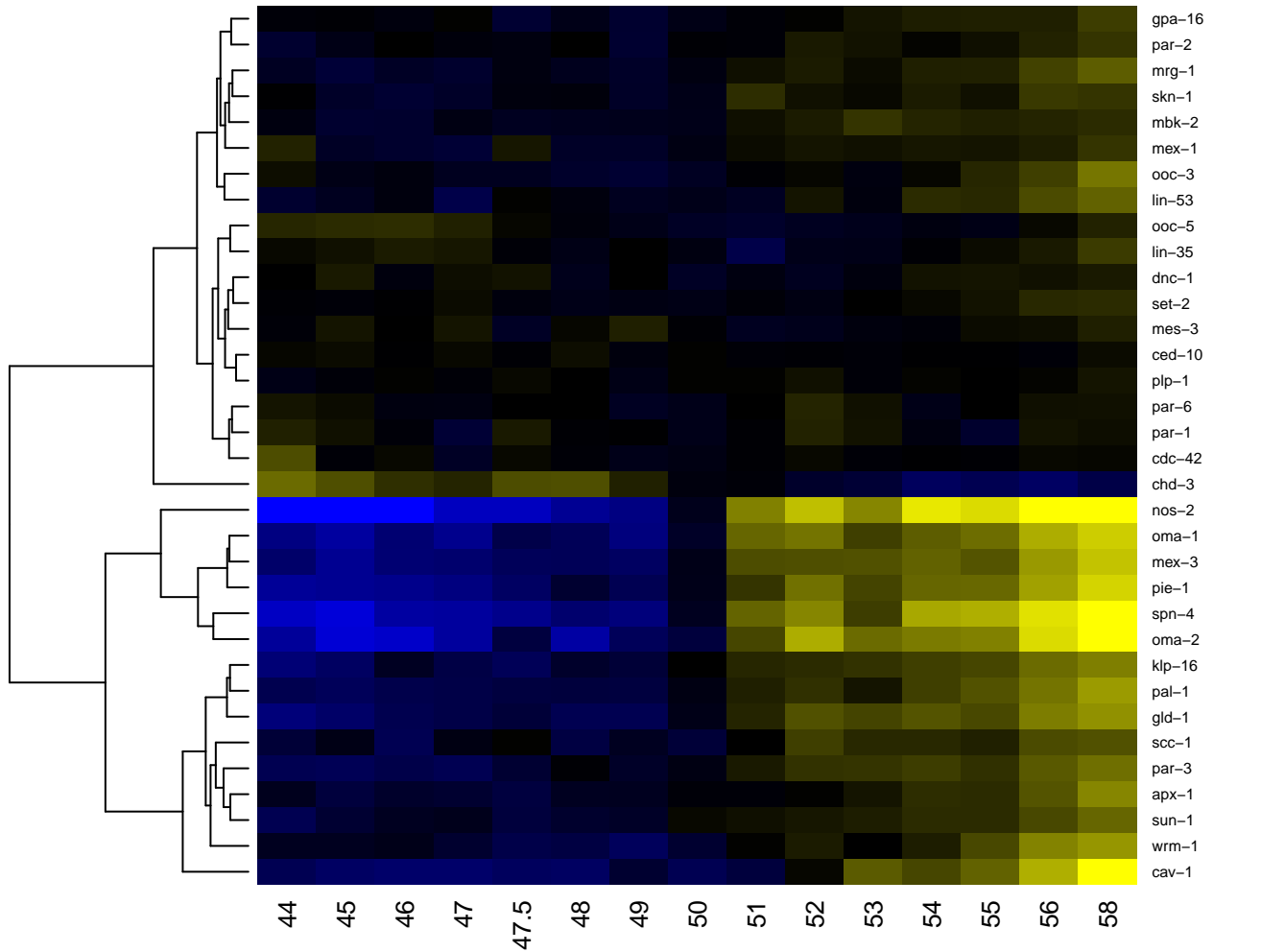
OLQVL



outer labial neuron



P0



-2

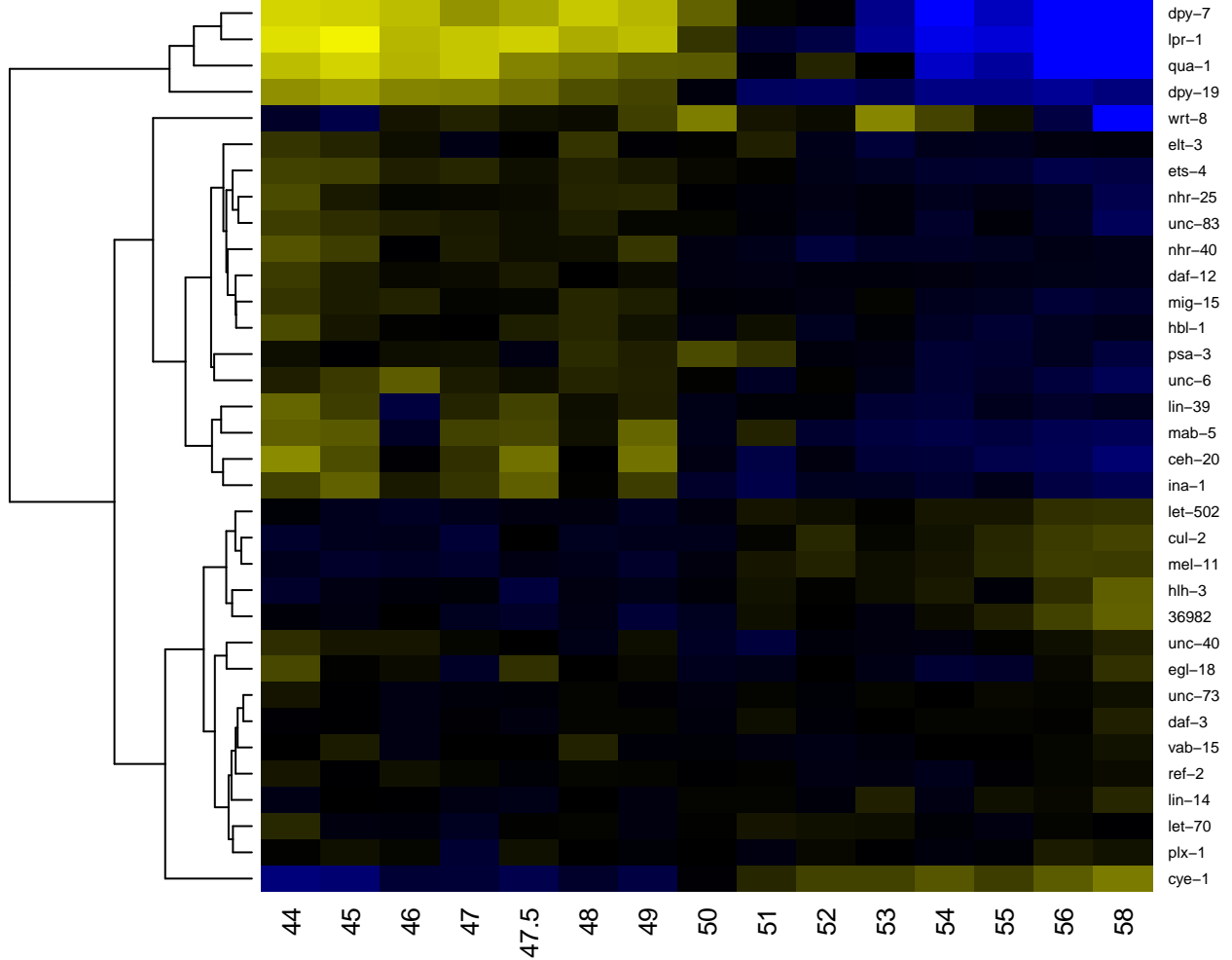
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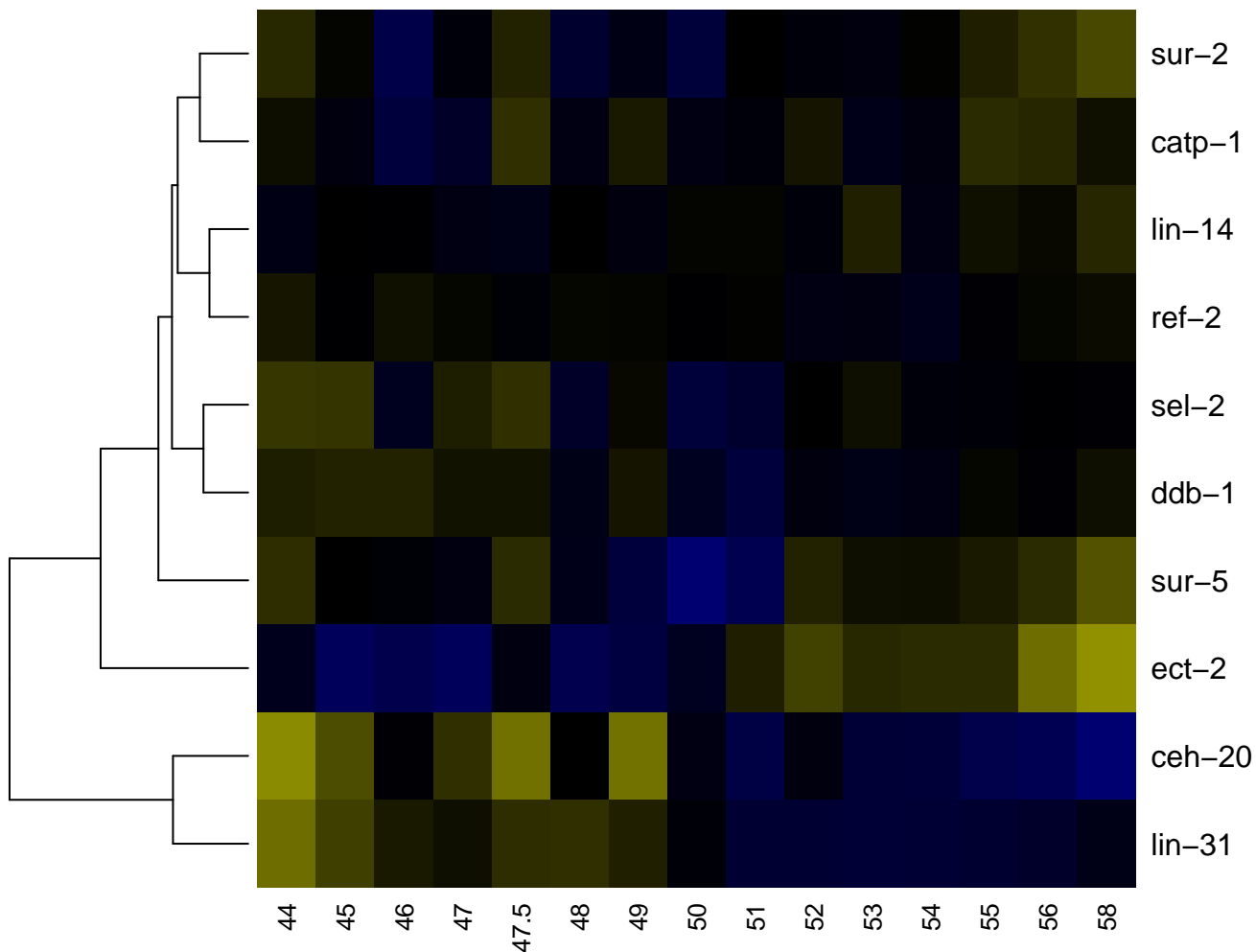
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2

P1



P1.p



-2

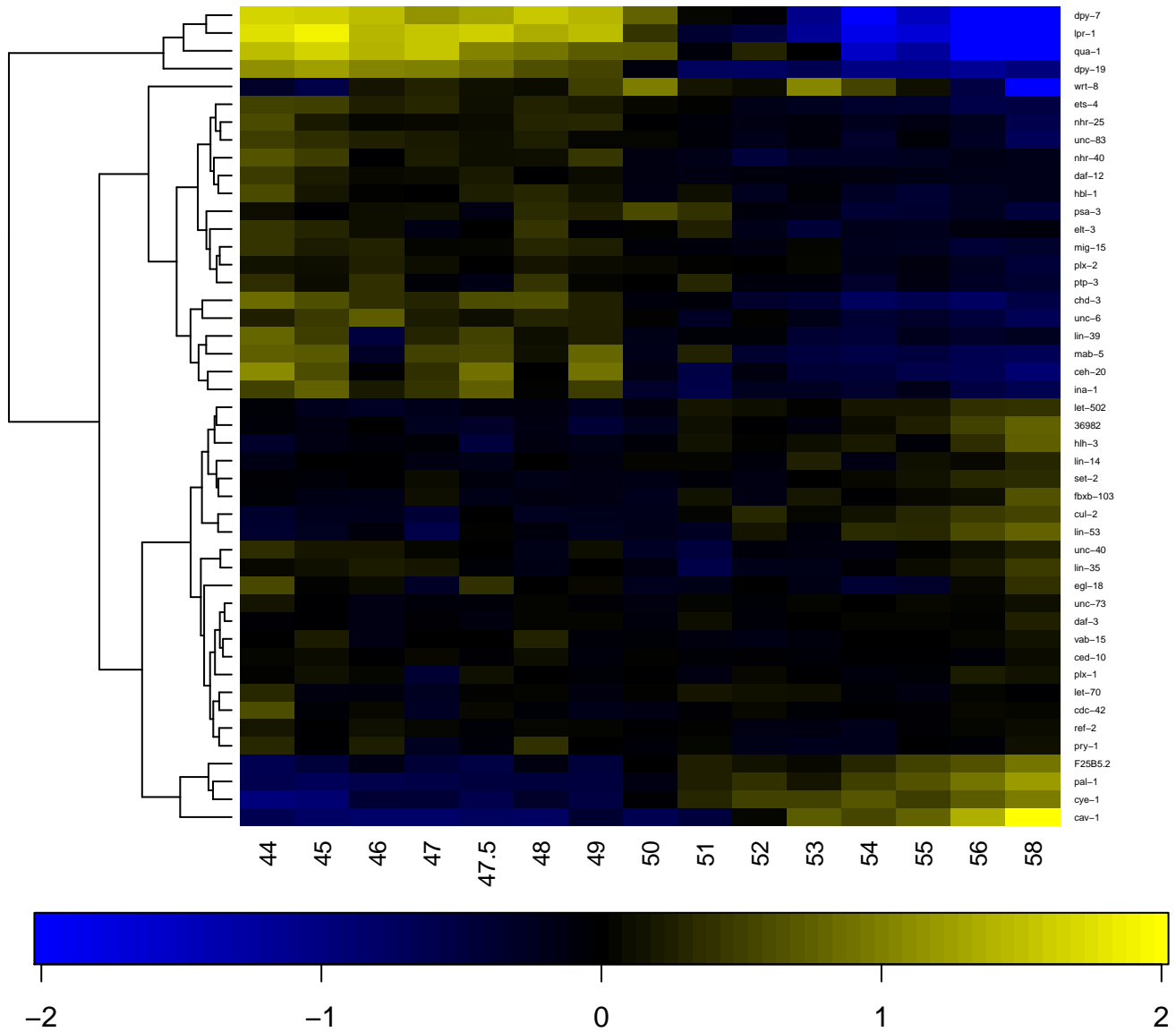
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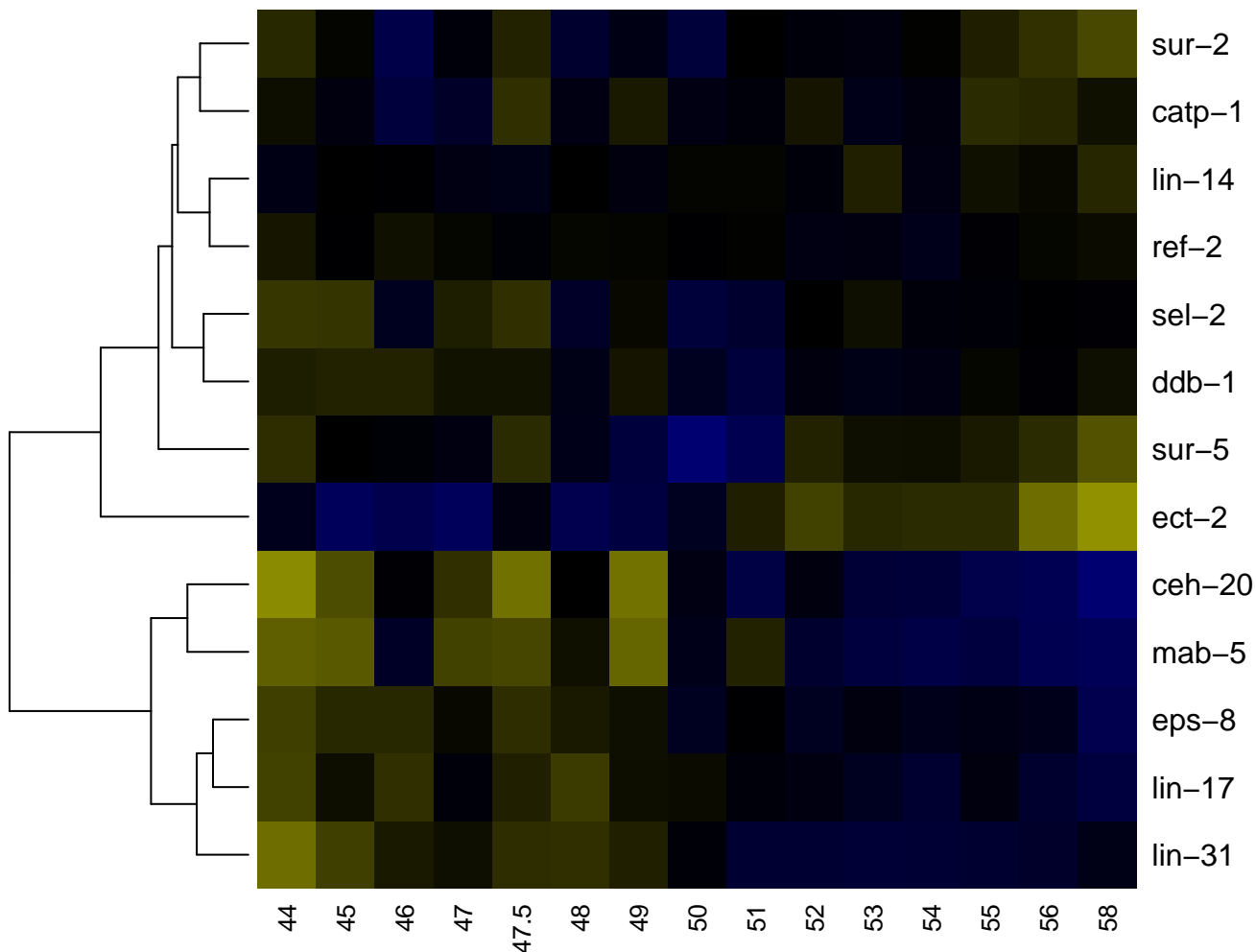
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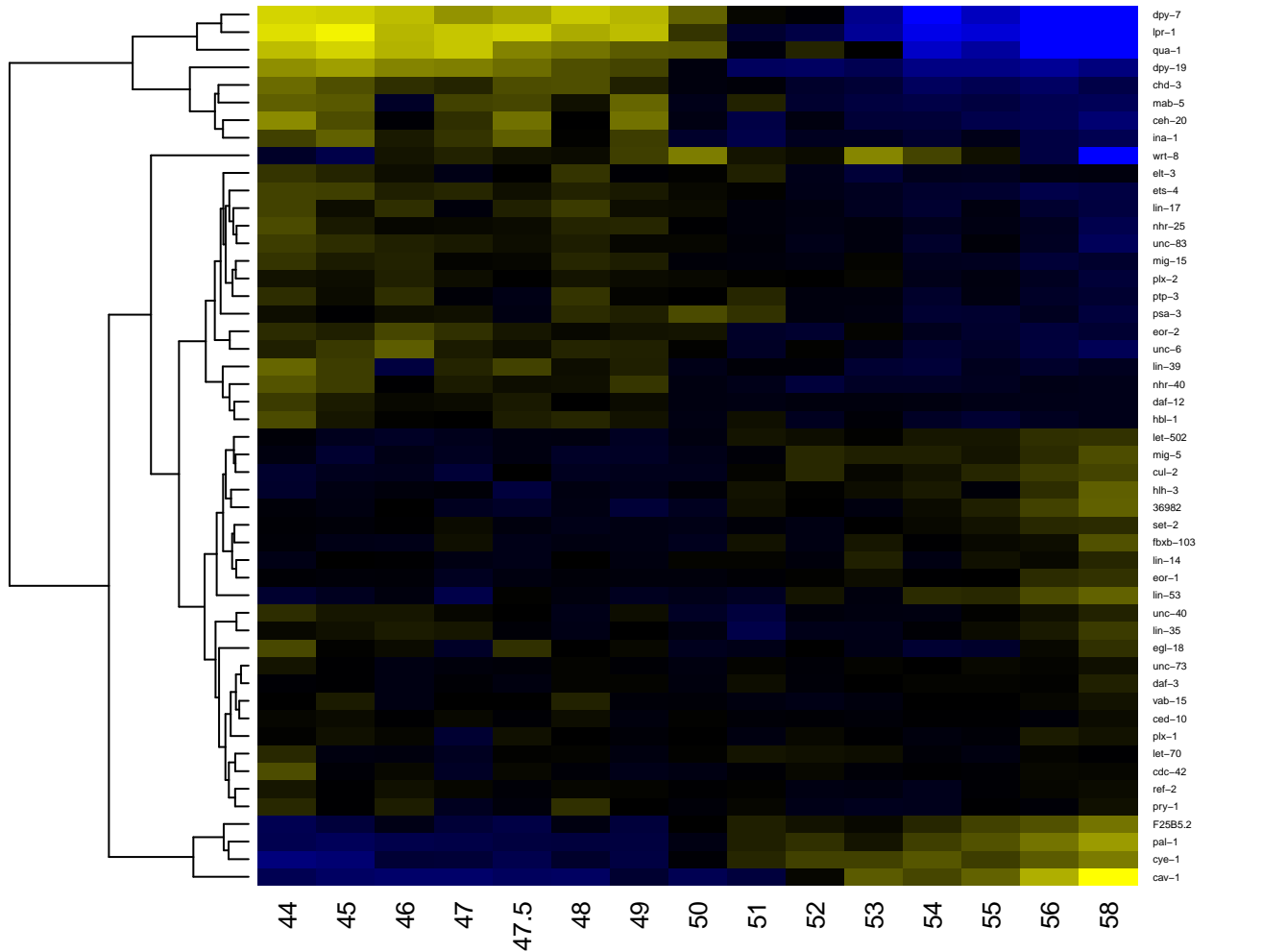
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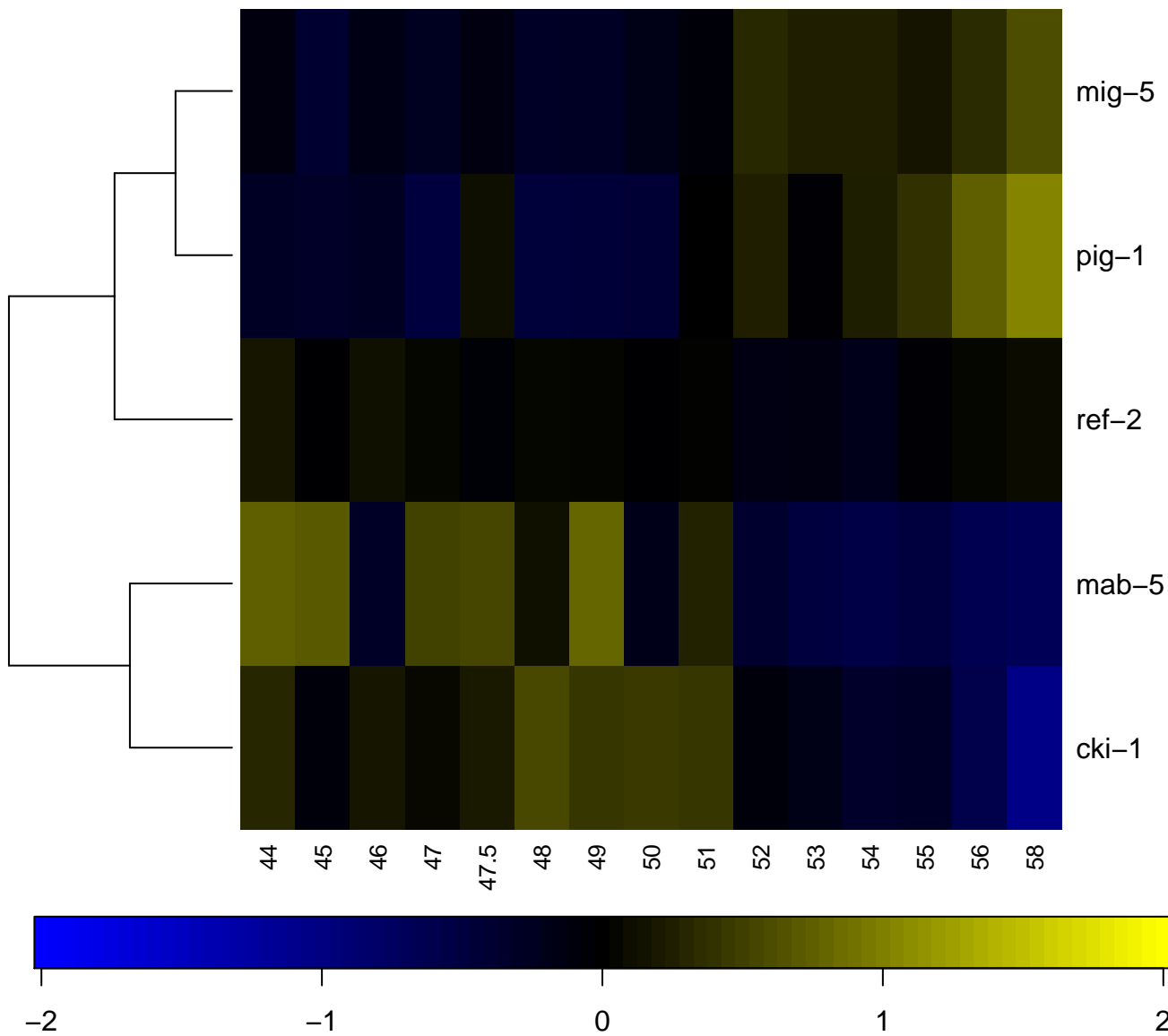
P10.p



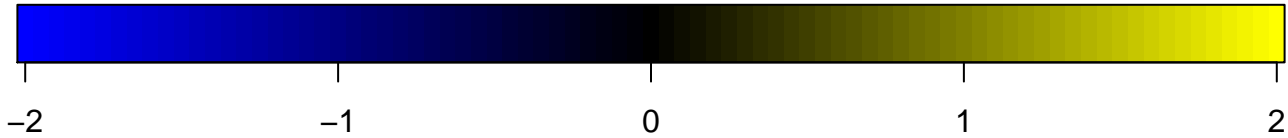
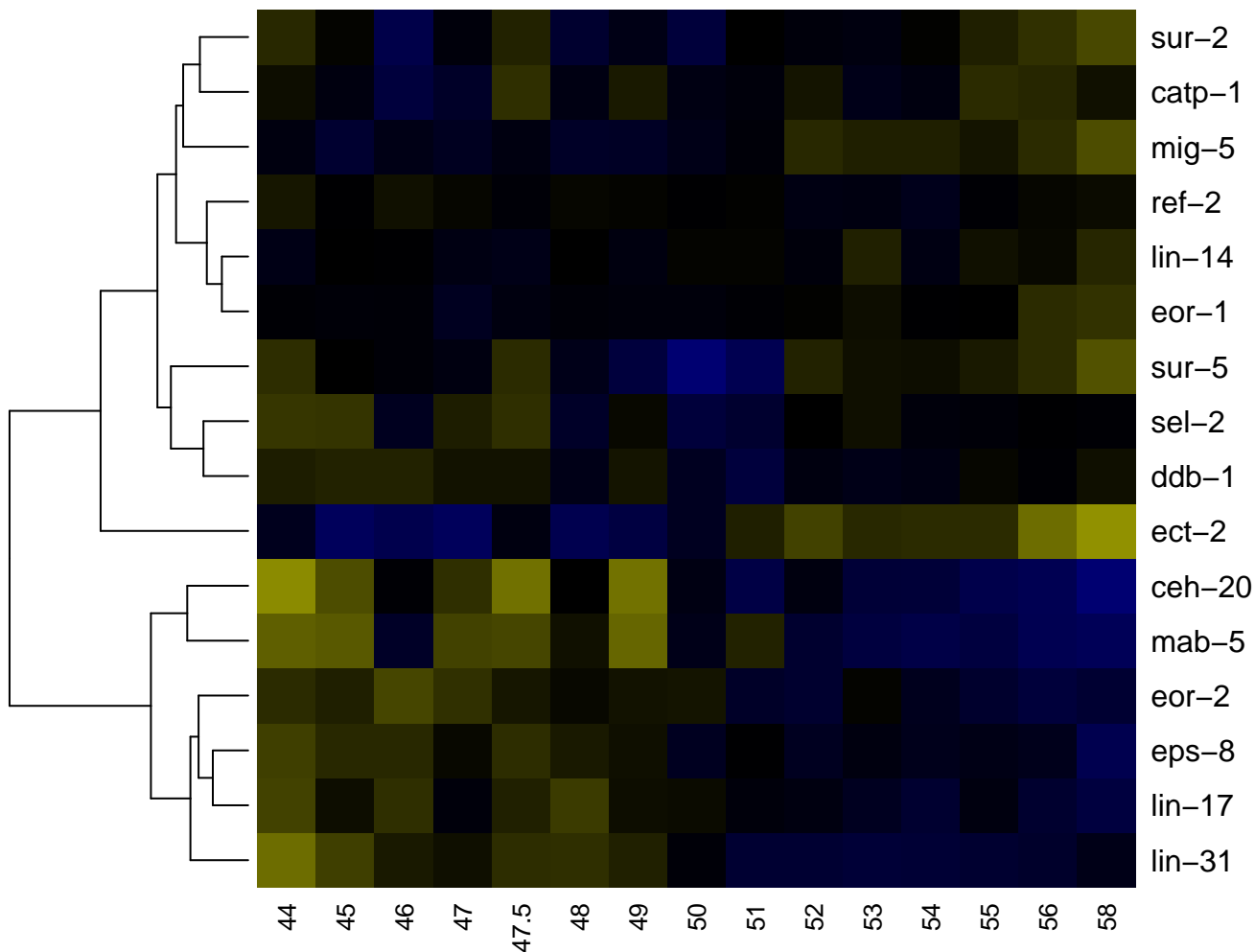
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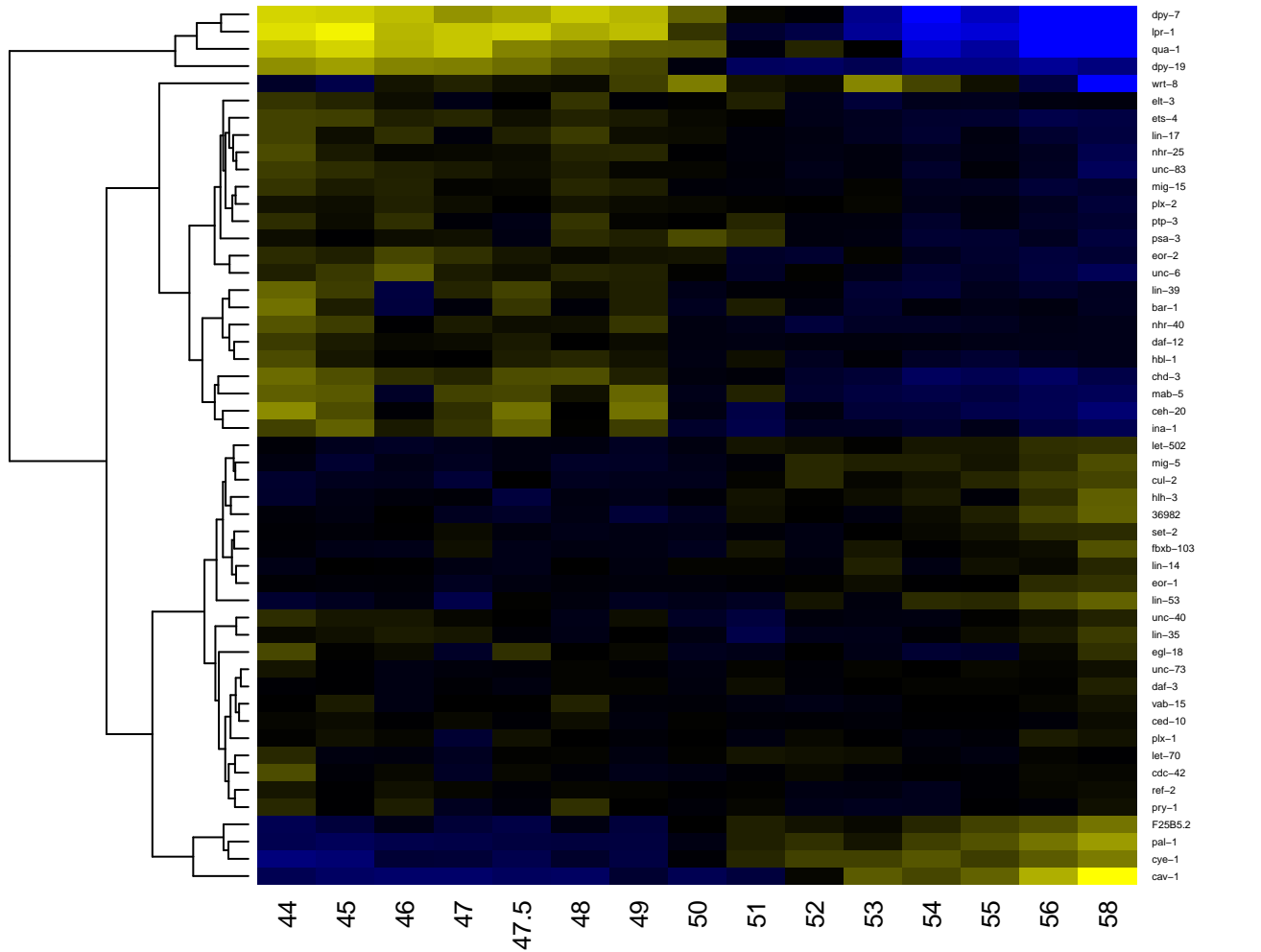
P11.a



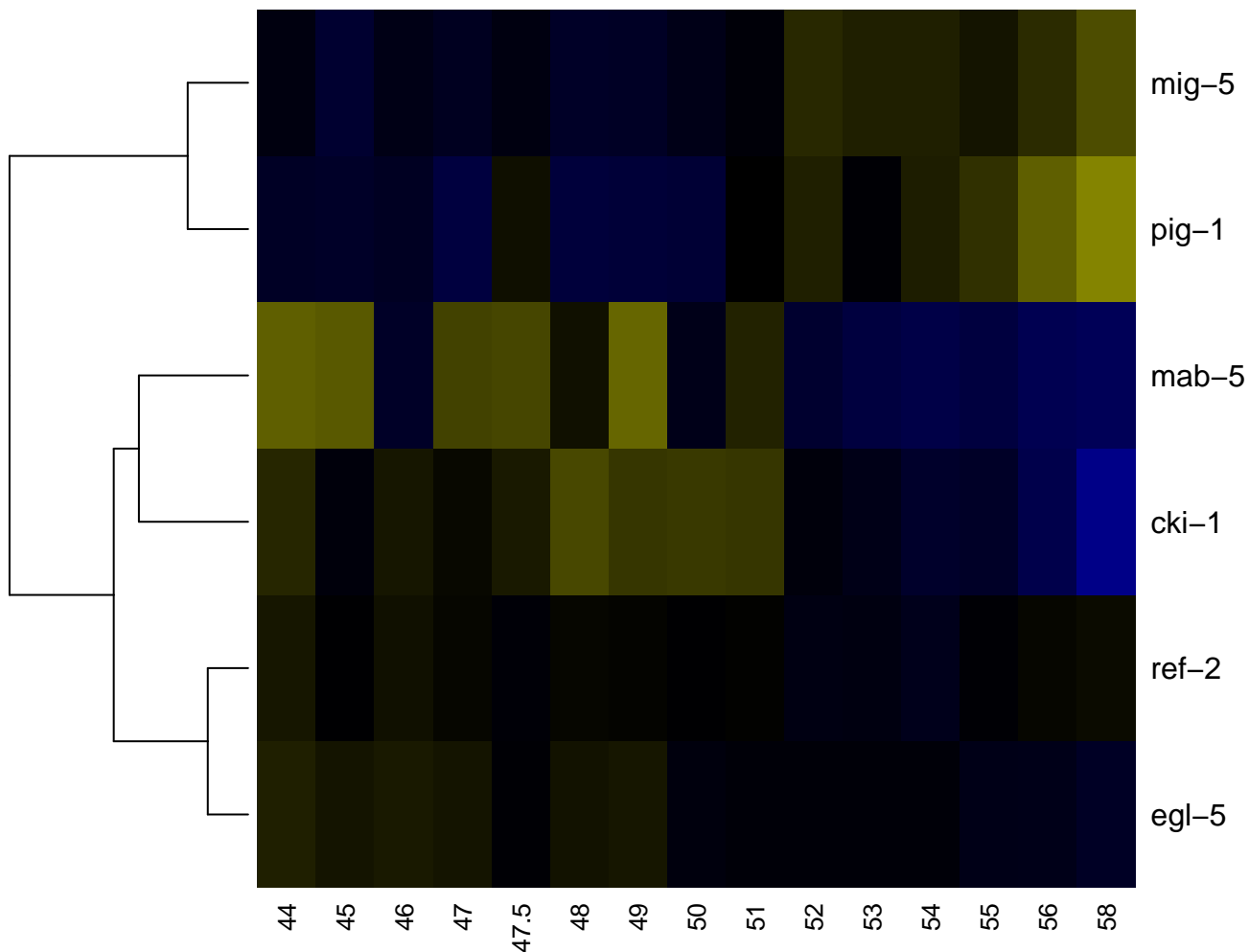
P11.p



P12



P12.a



-2

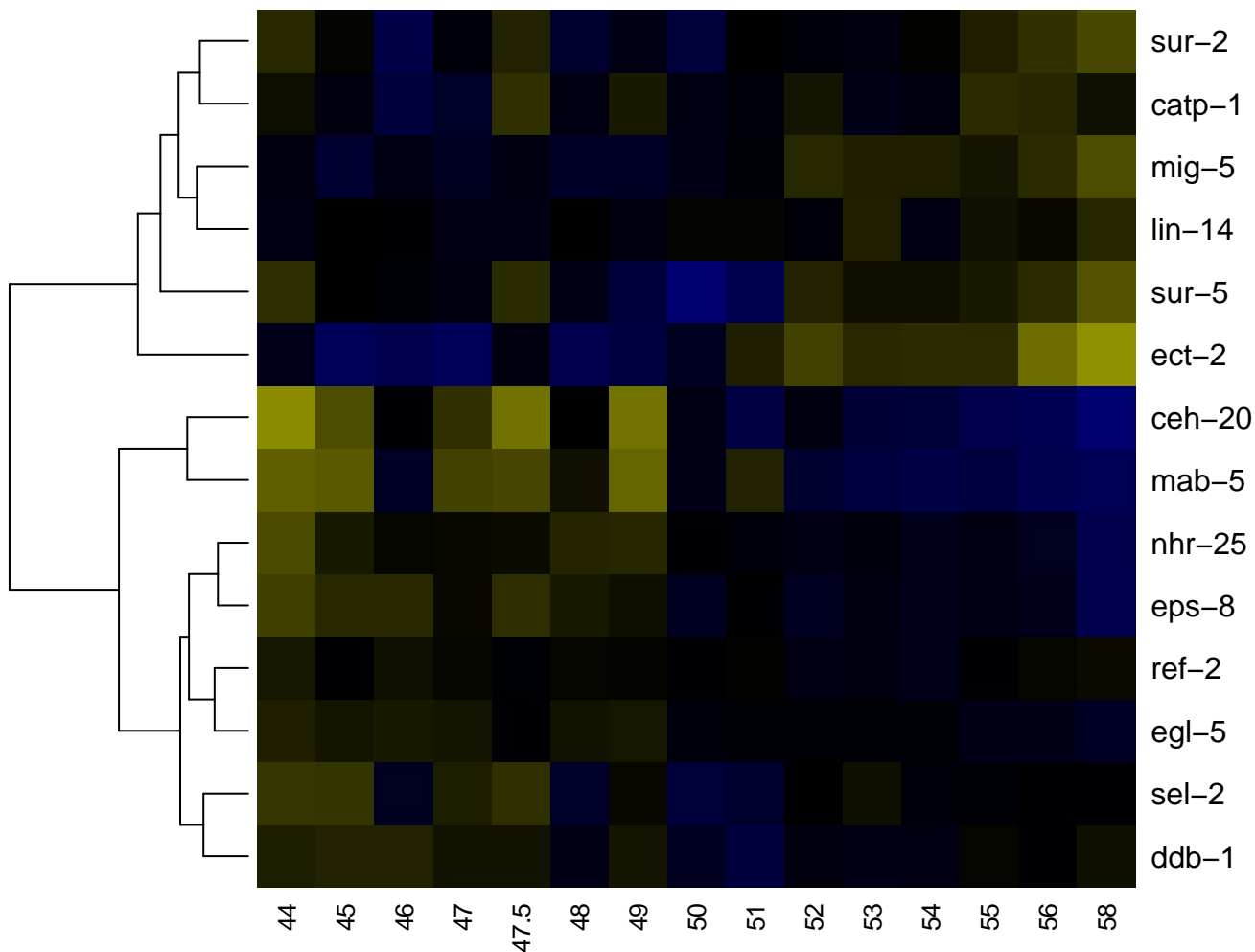
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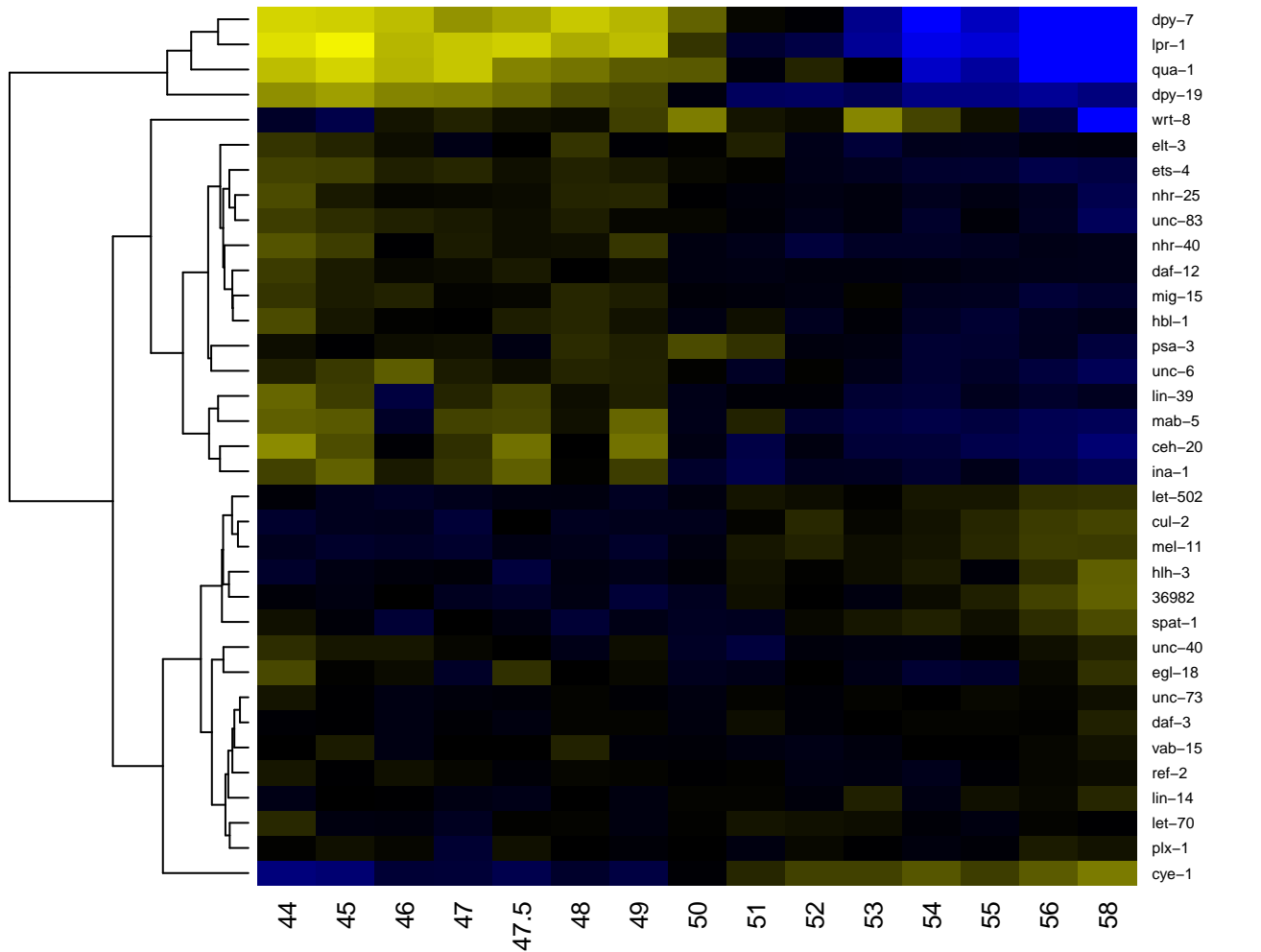
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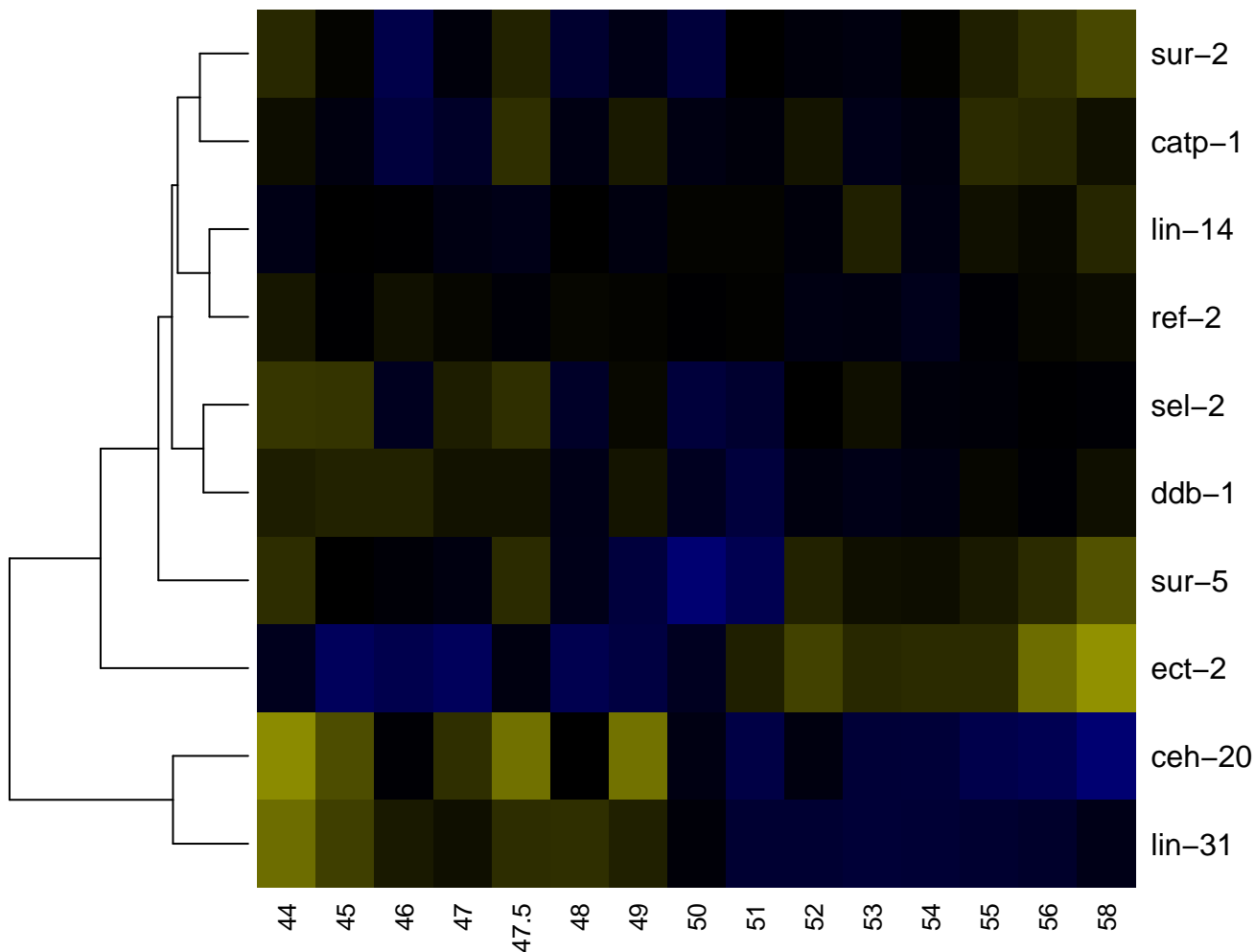
P12.p



P2



P2.p



-2

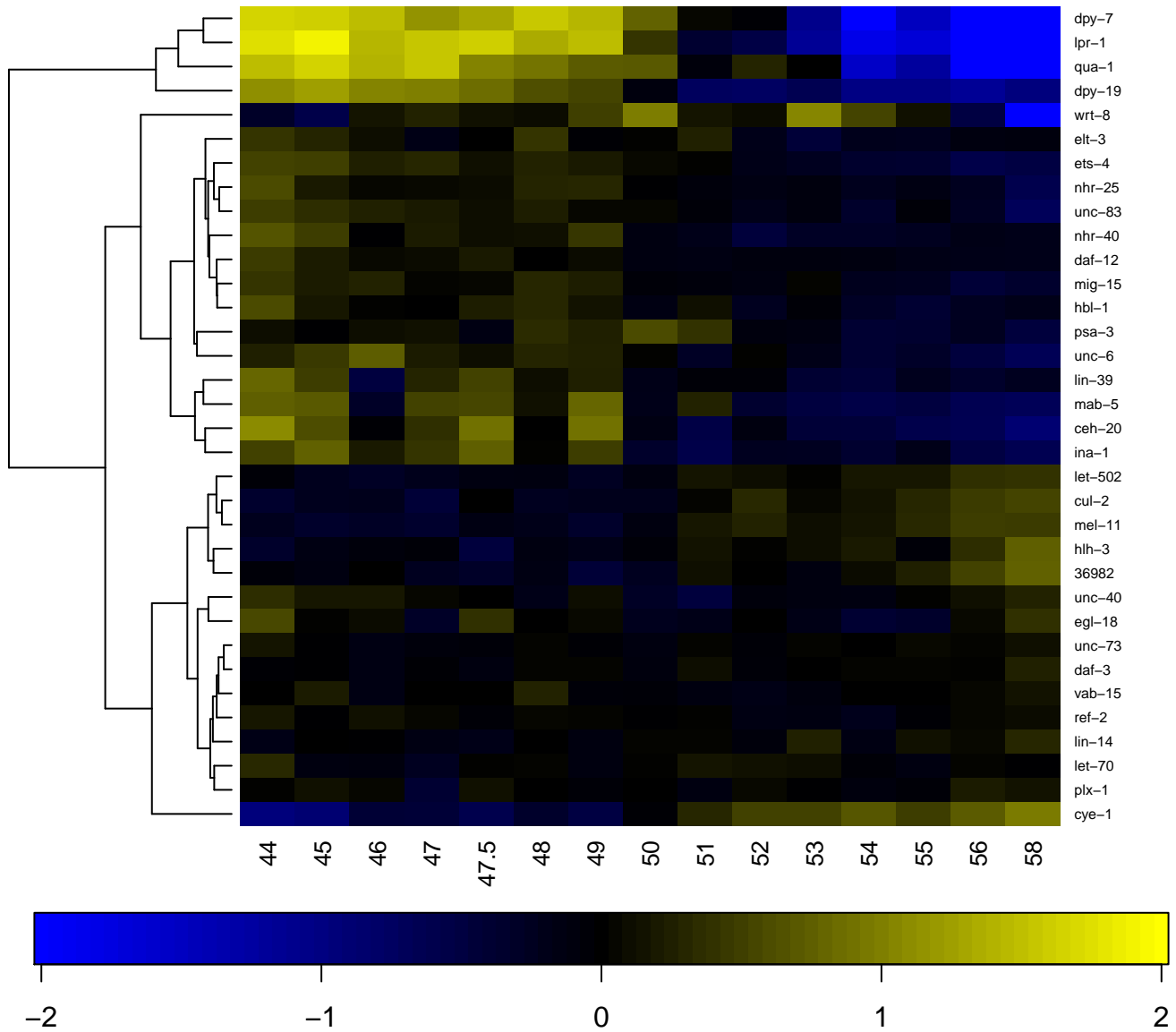
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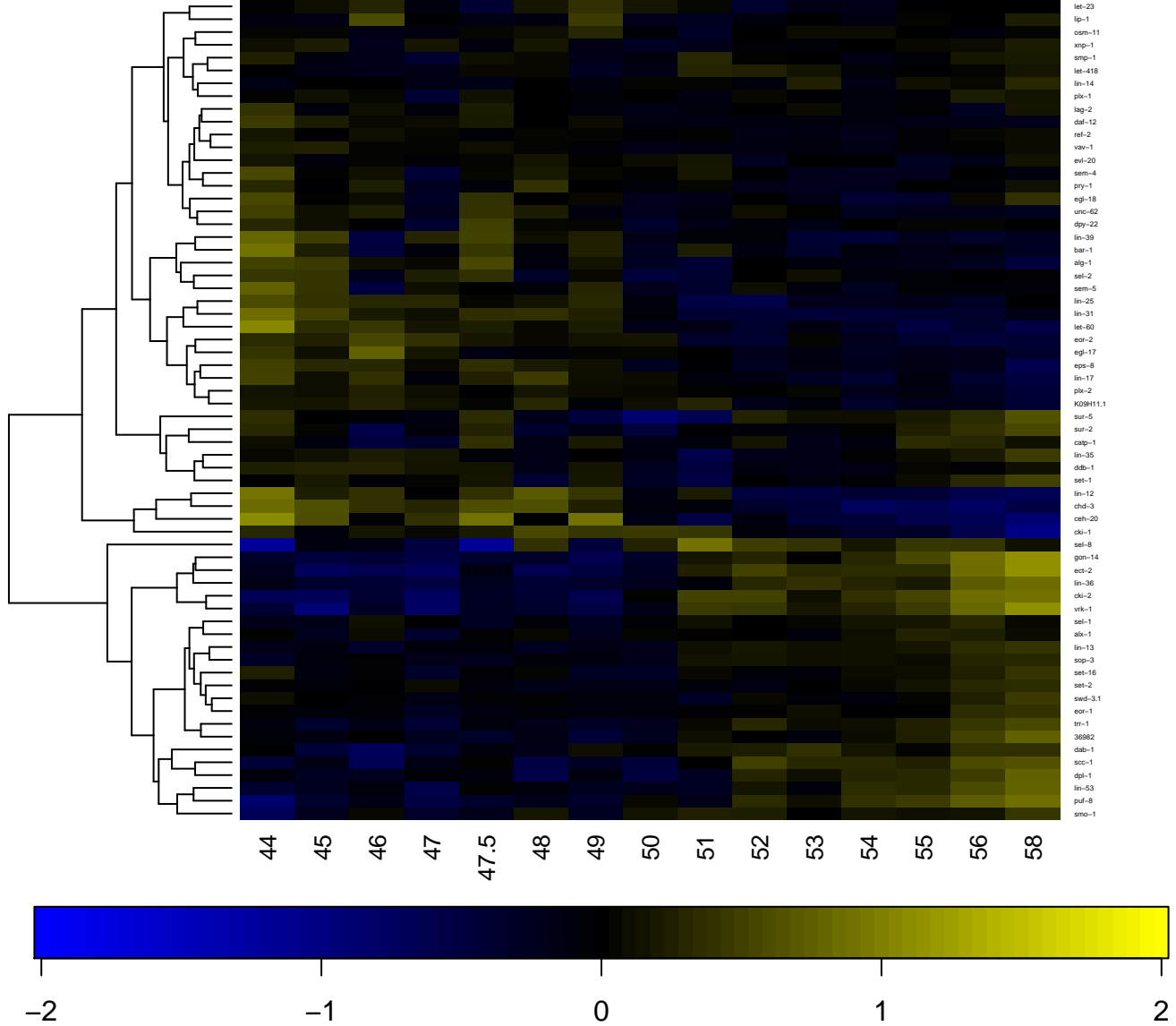
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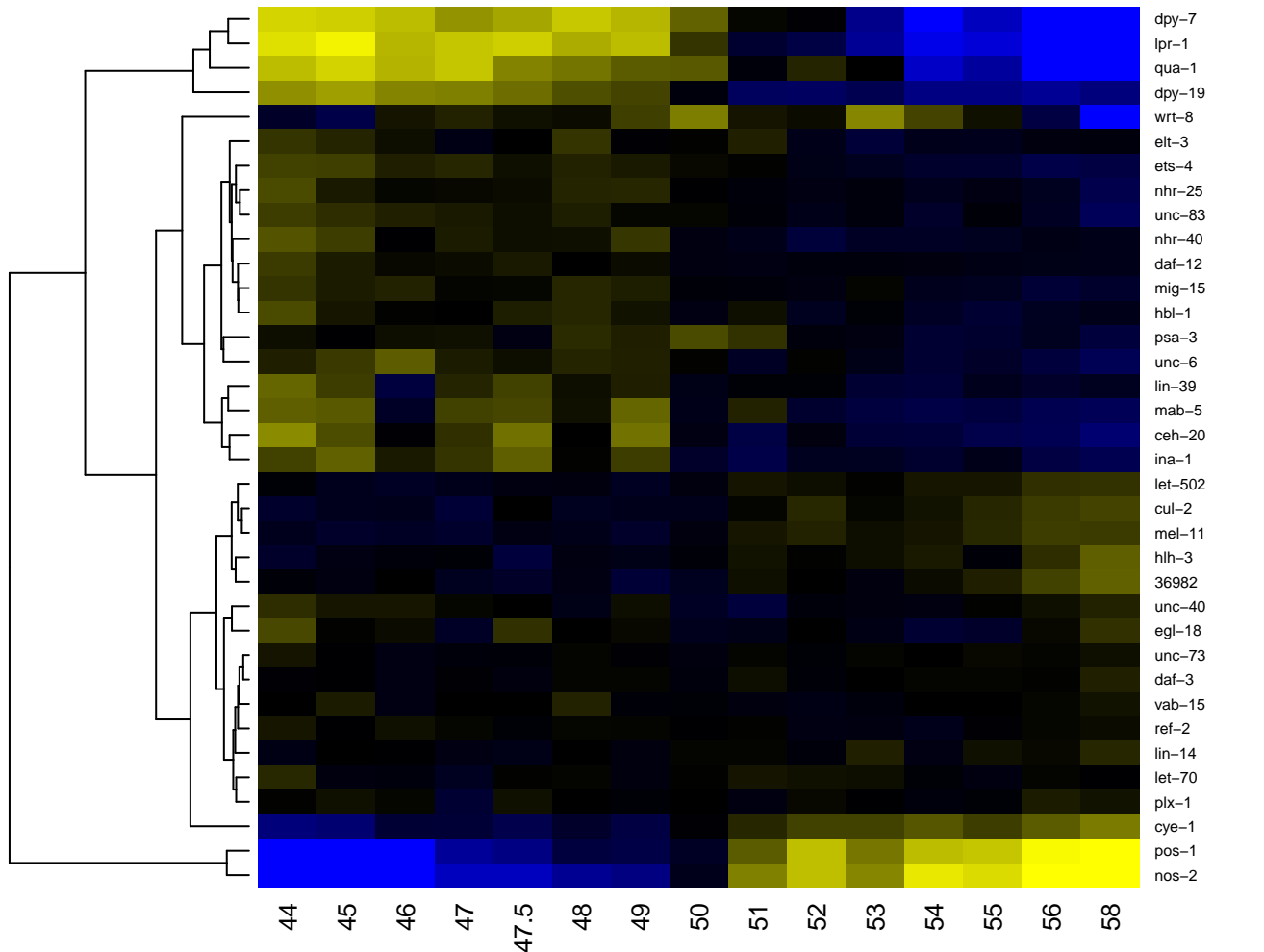
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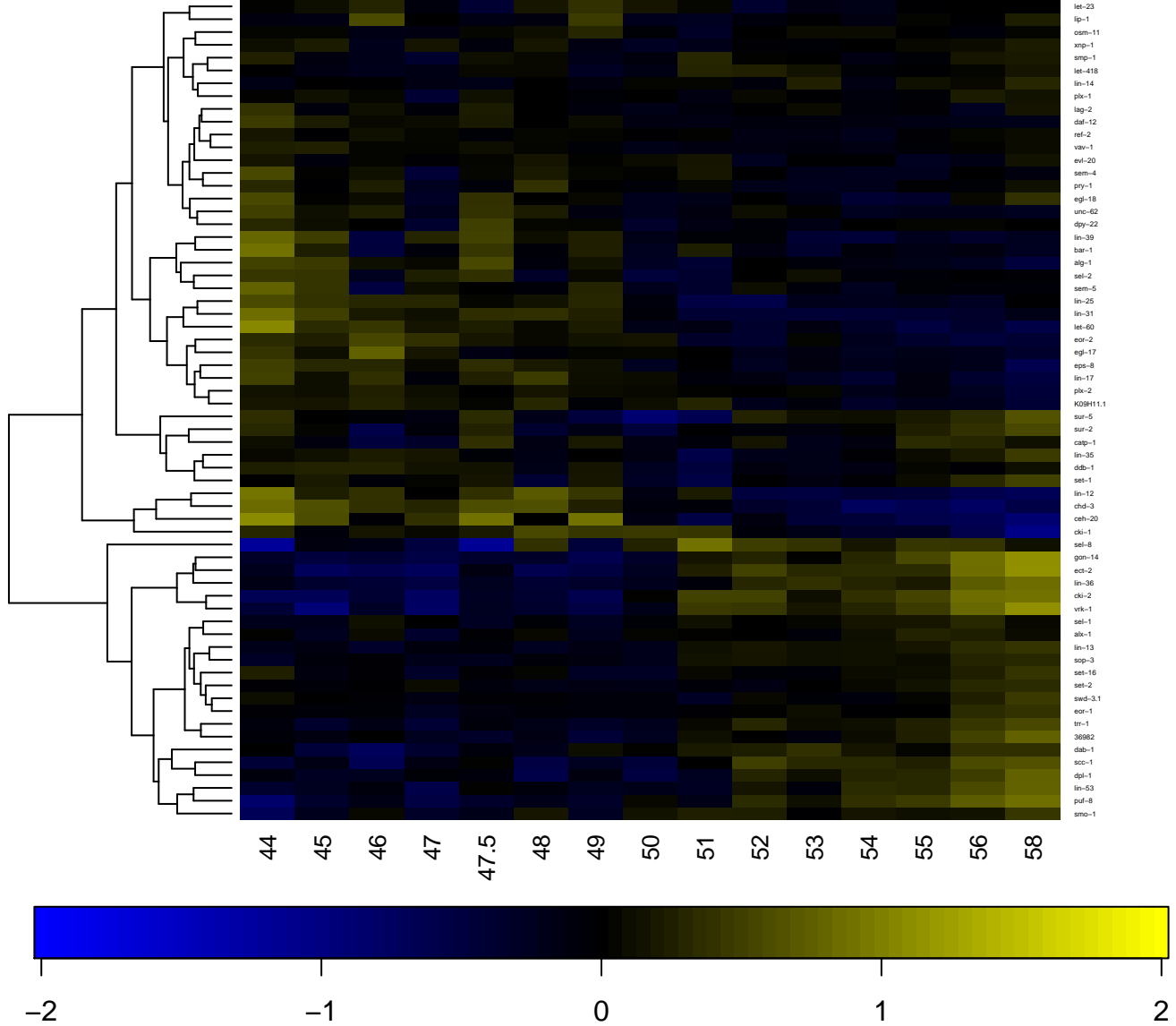
P3.p



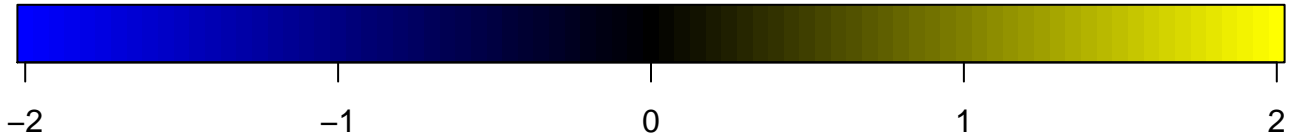
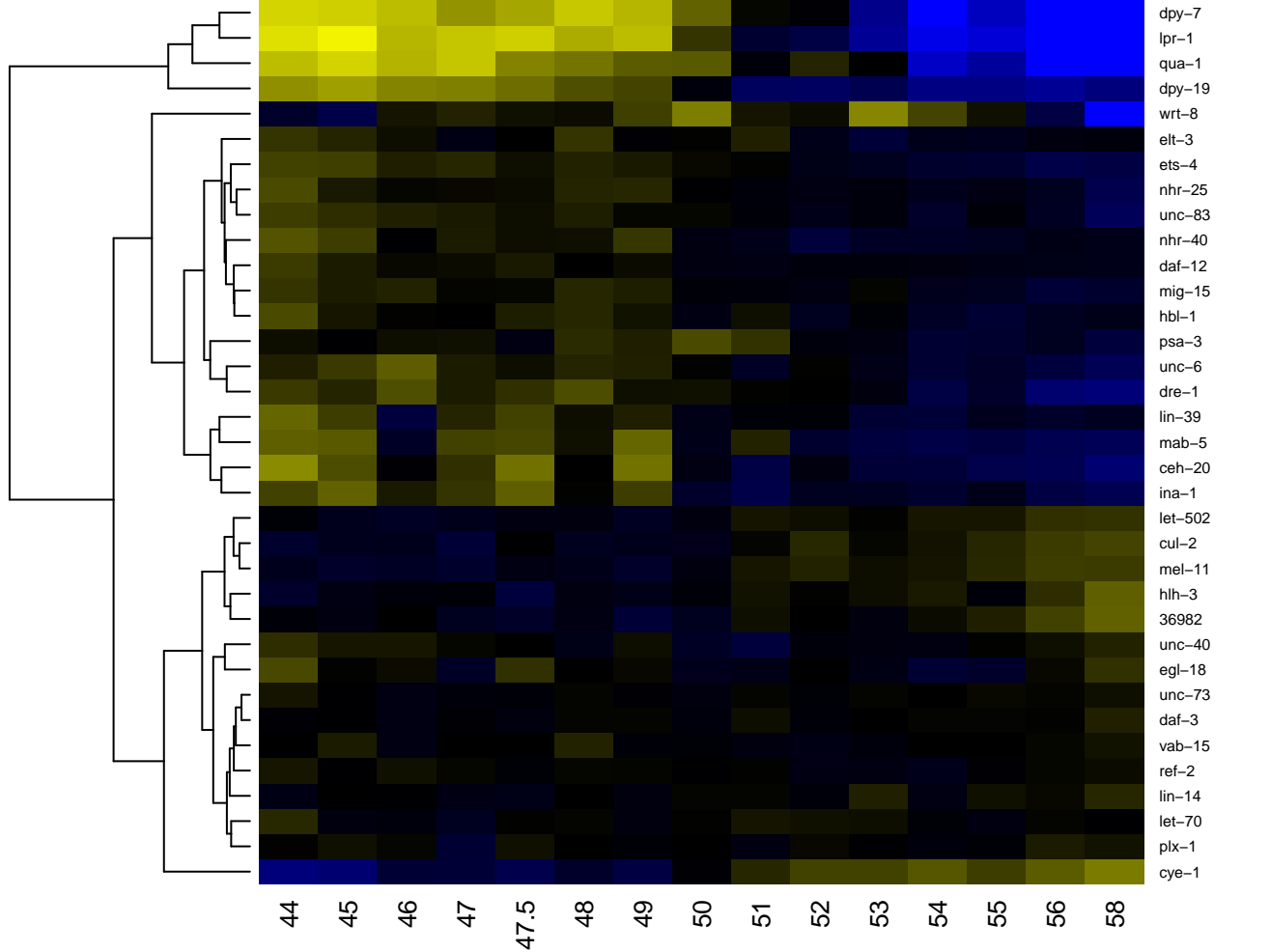
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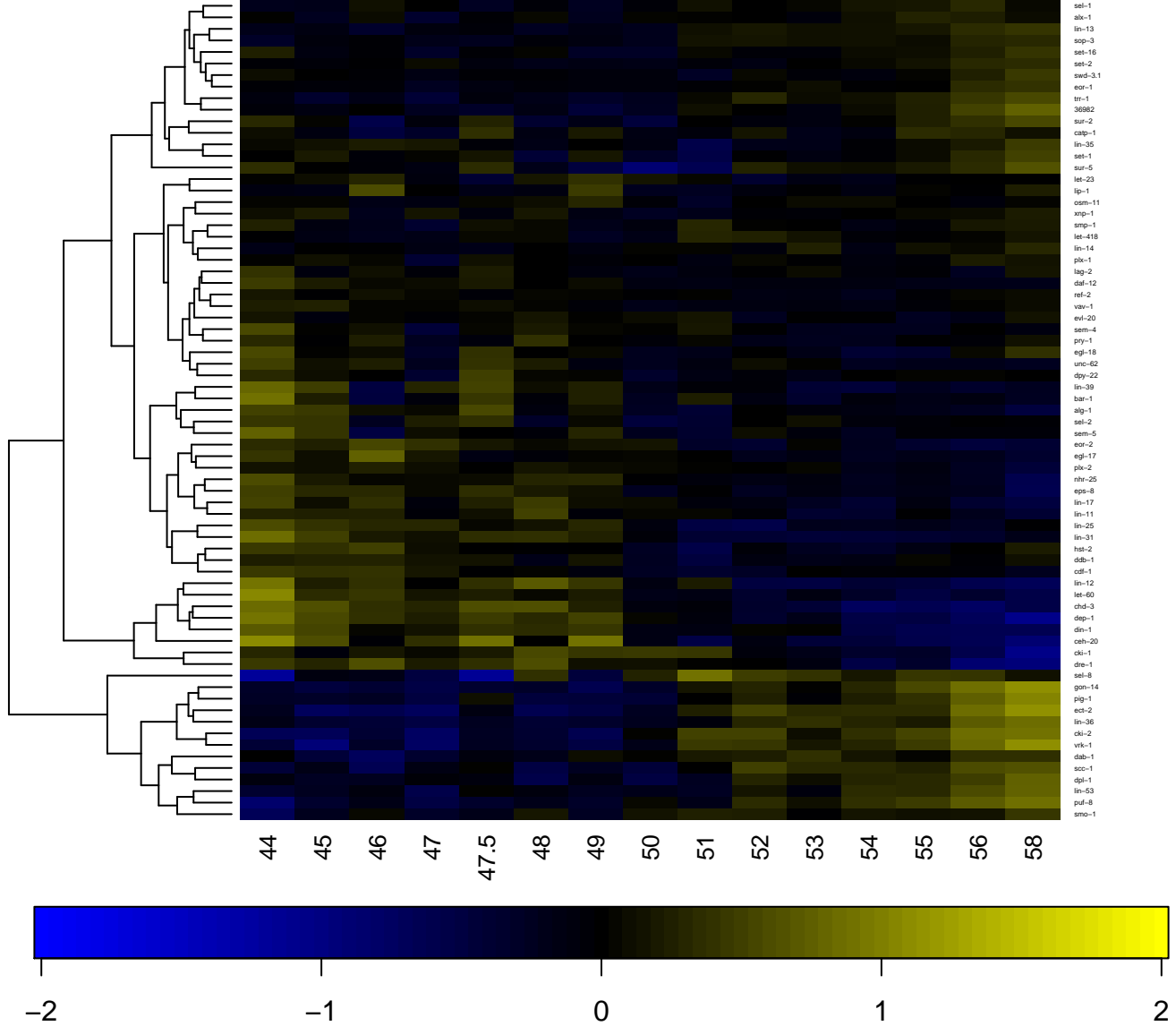
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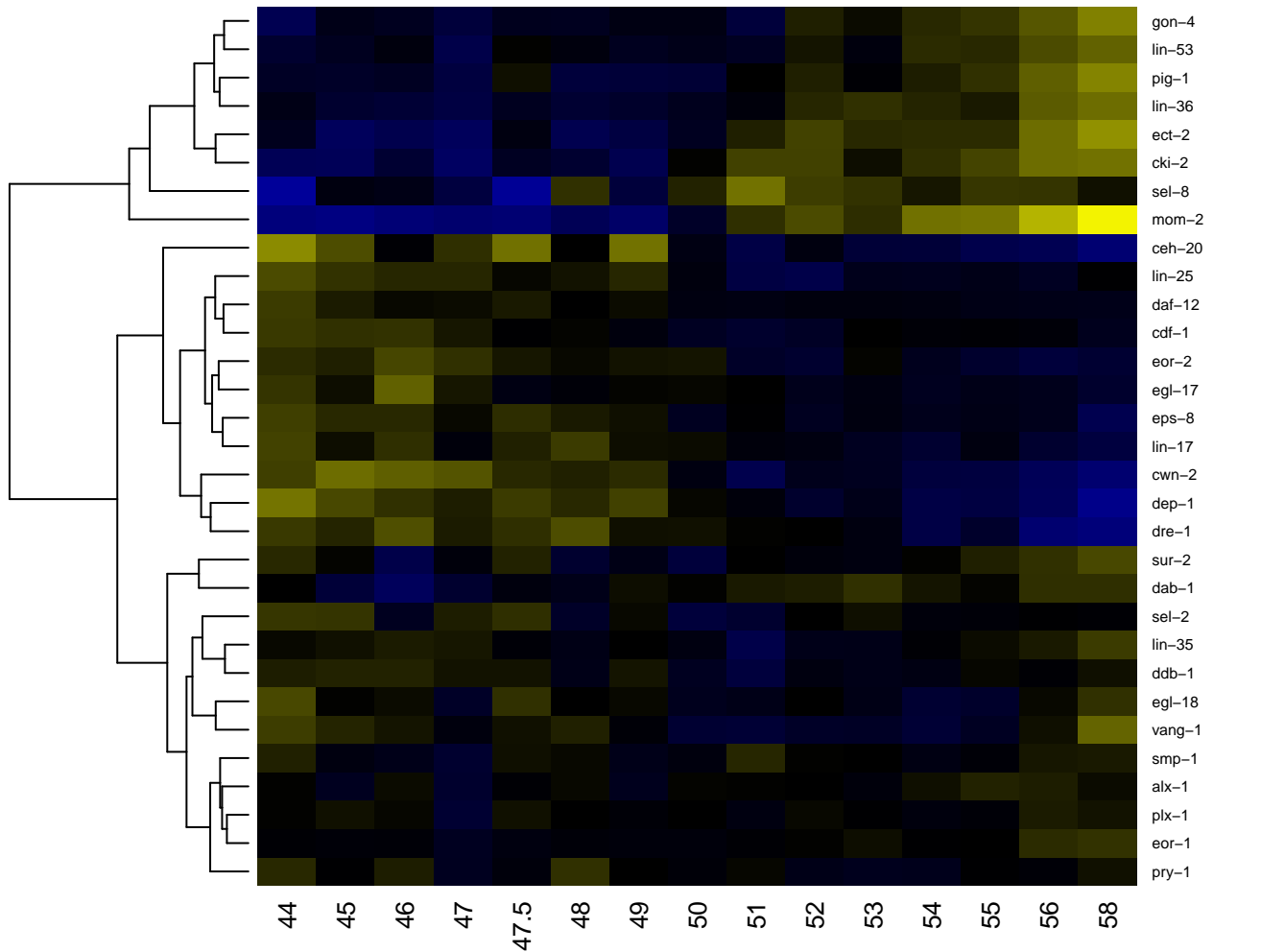
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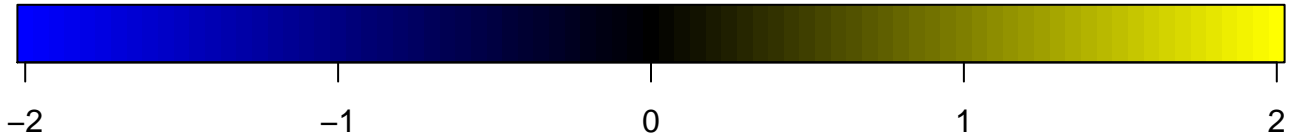
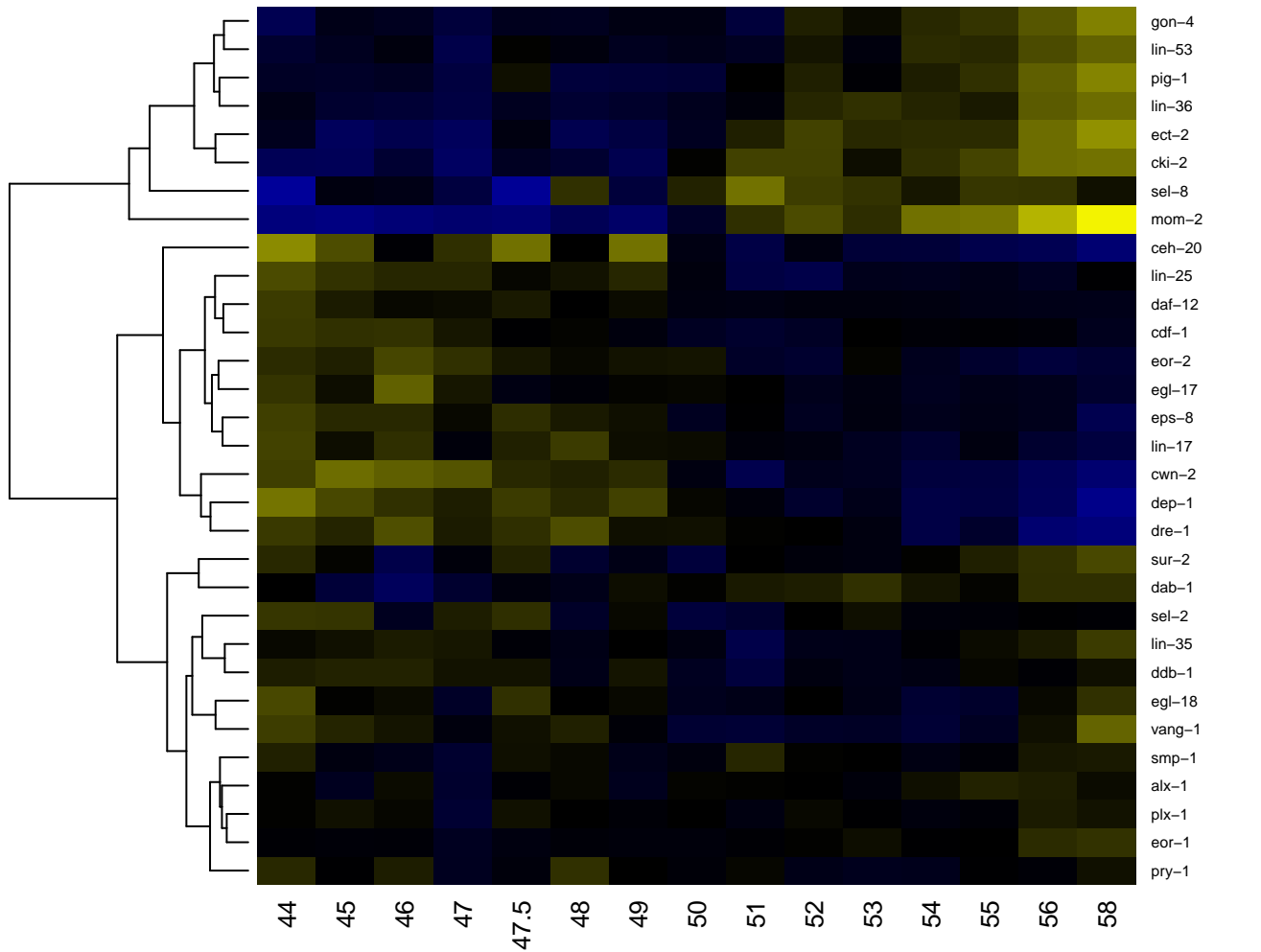
P5.p



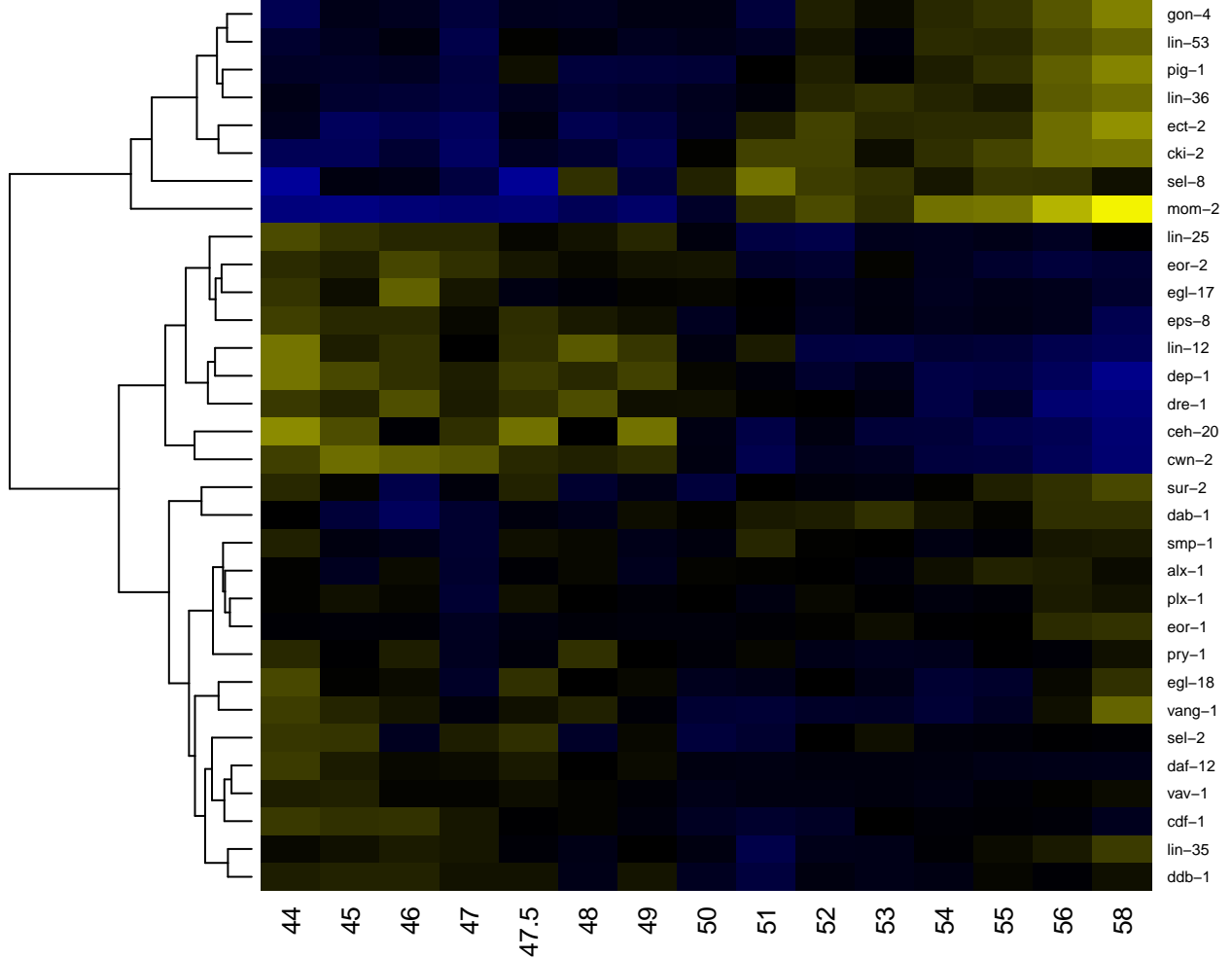
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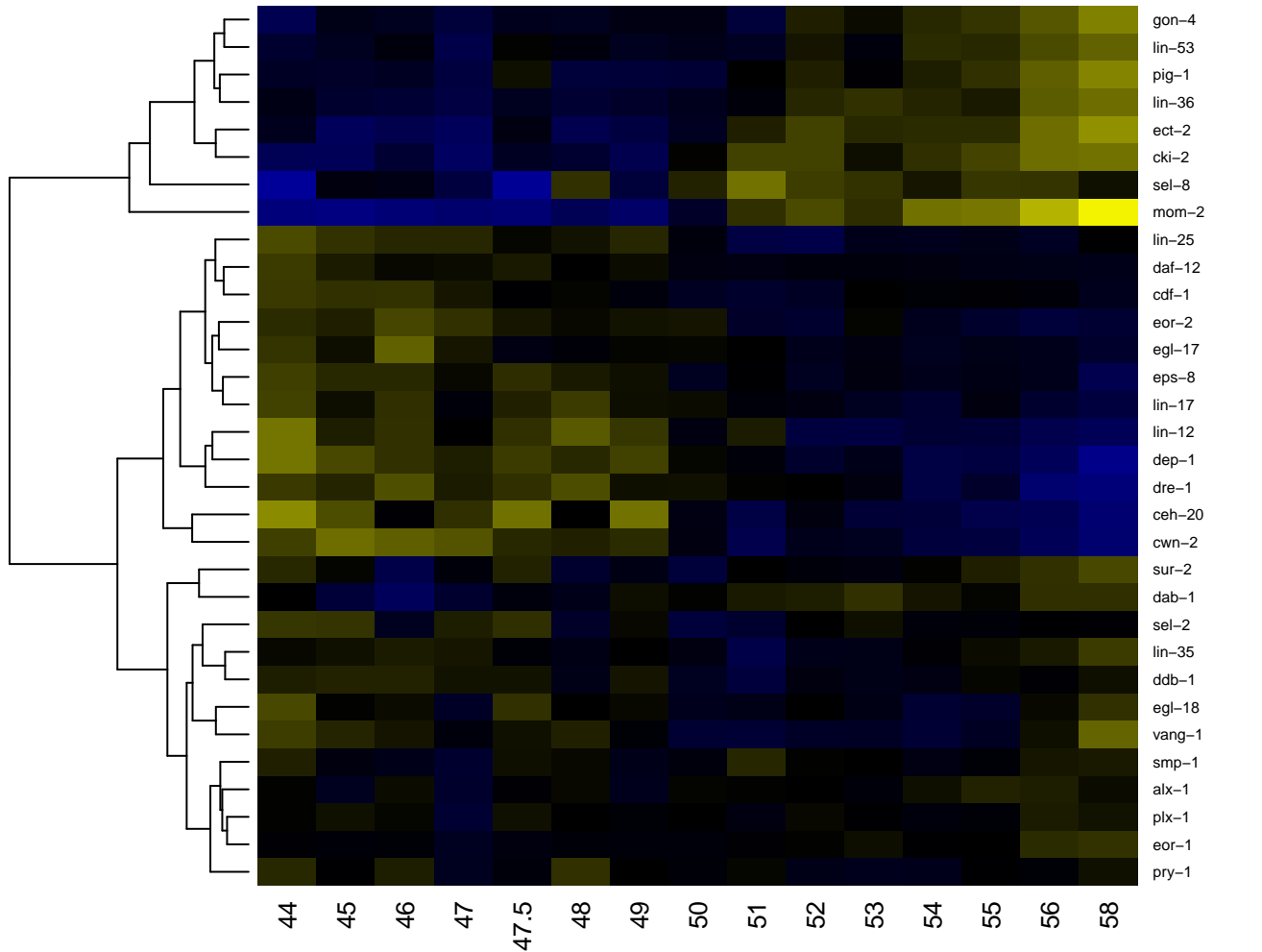
P5.pap



P5.pp



P5.ppa



-2

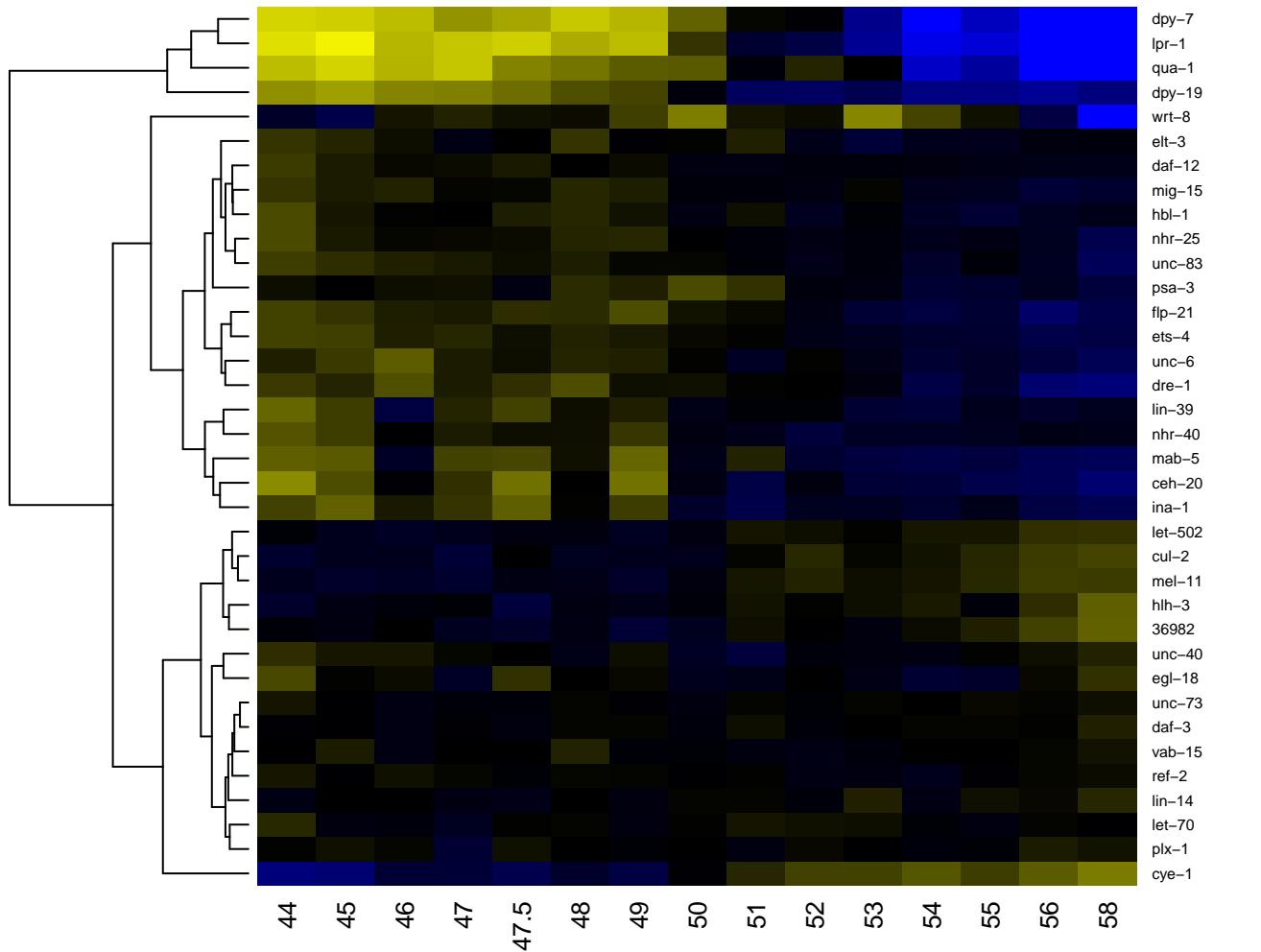
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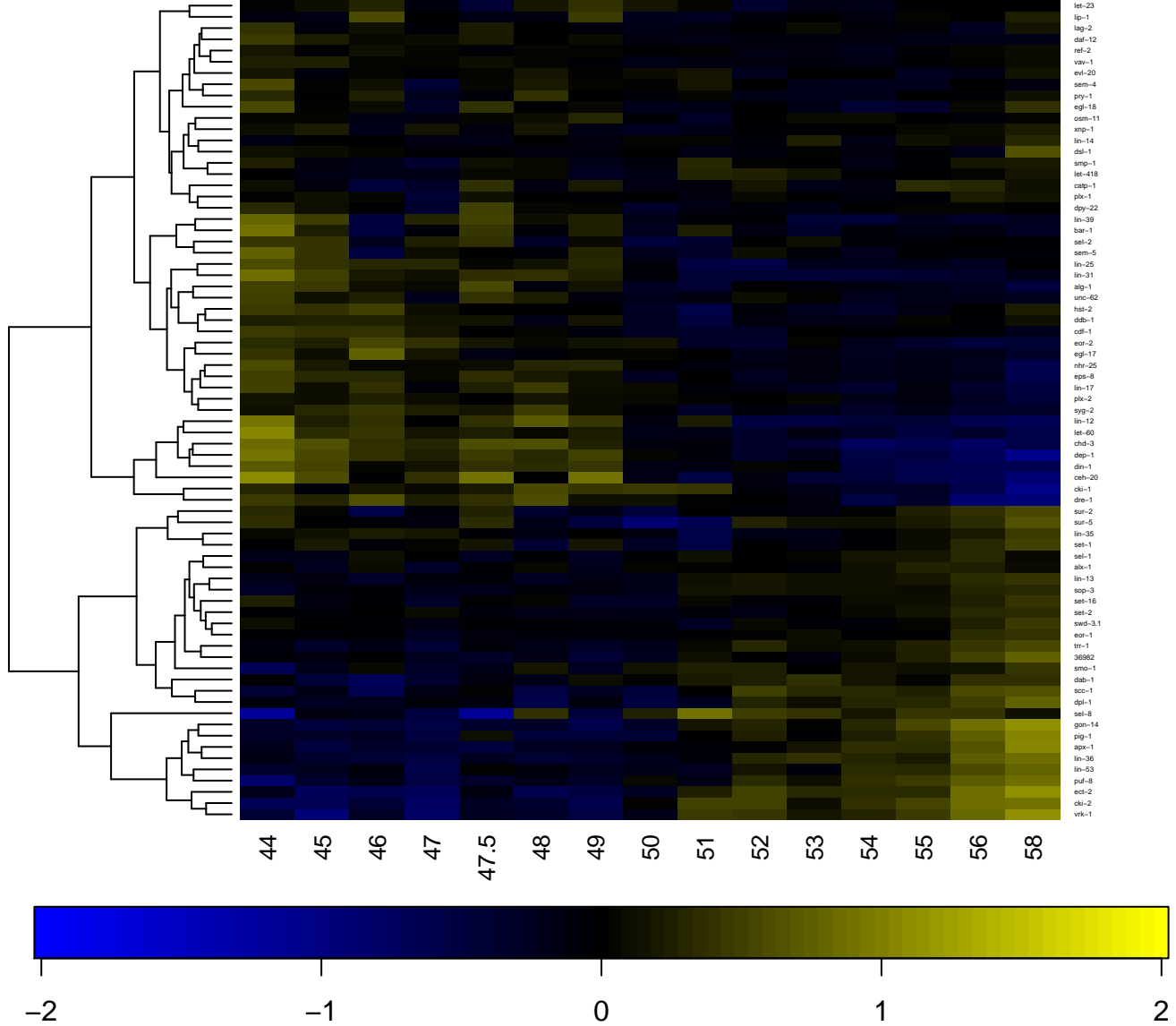
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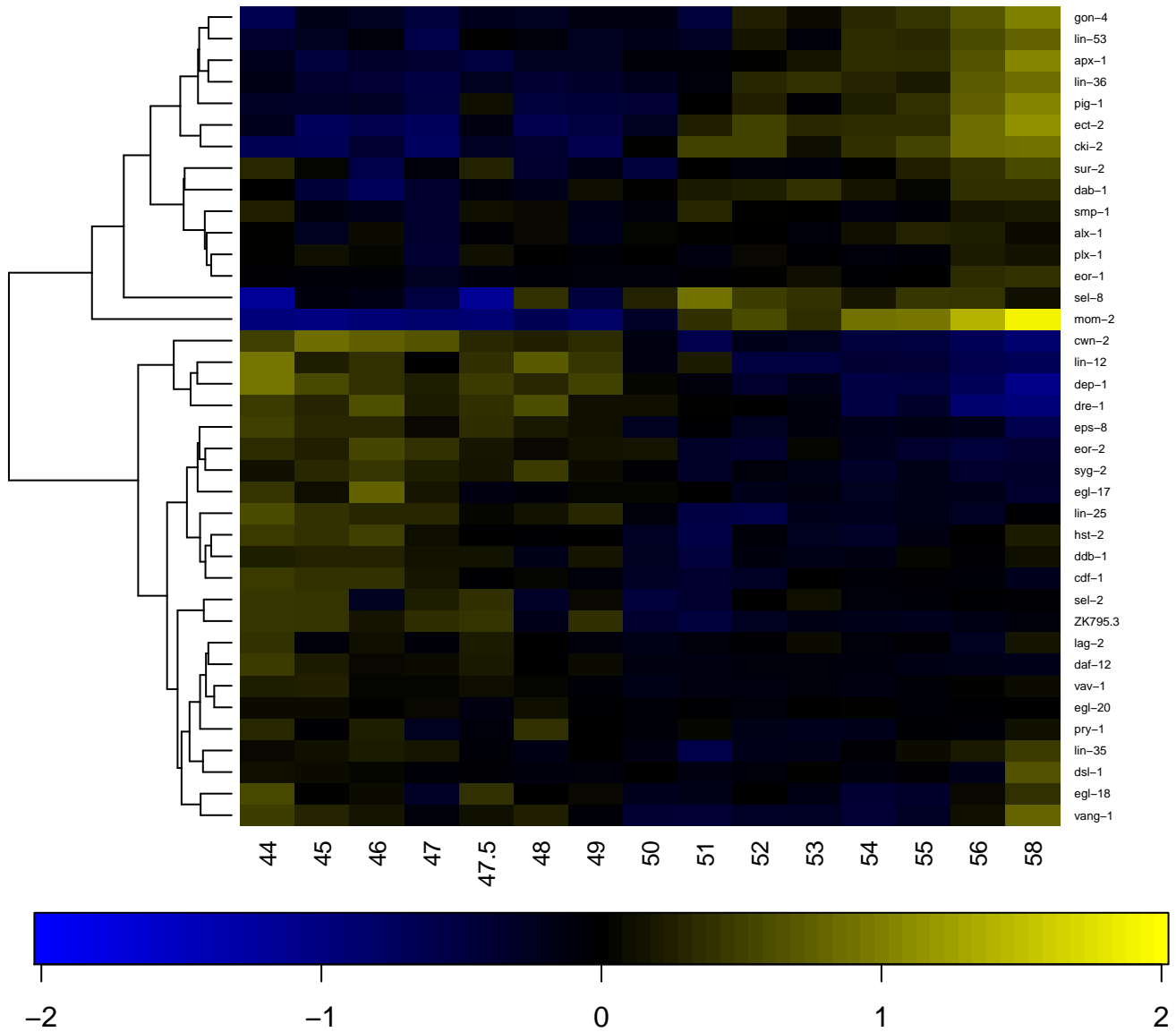
P6



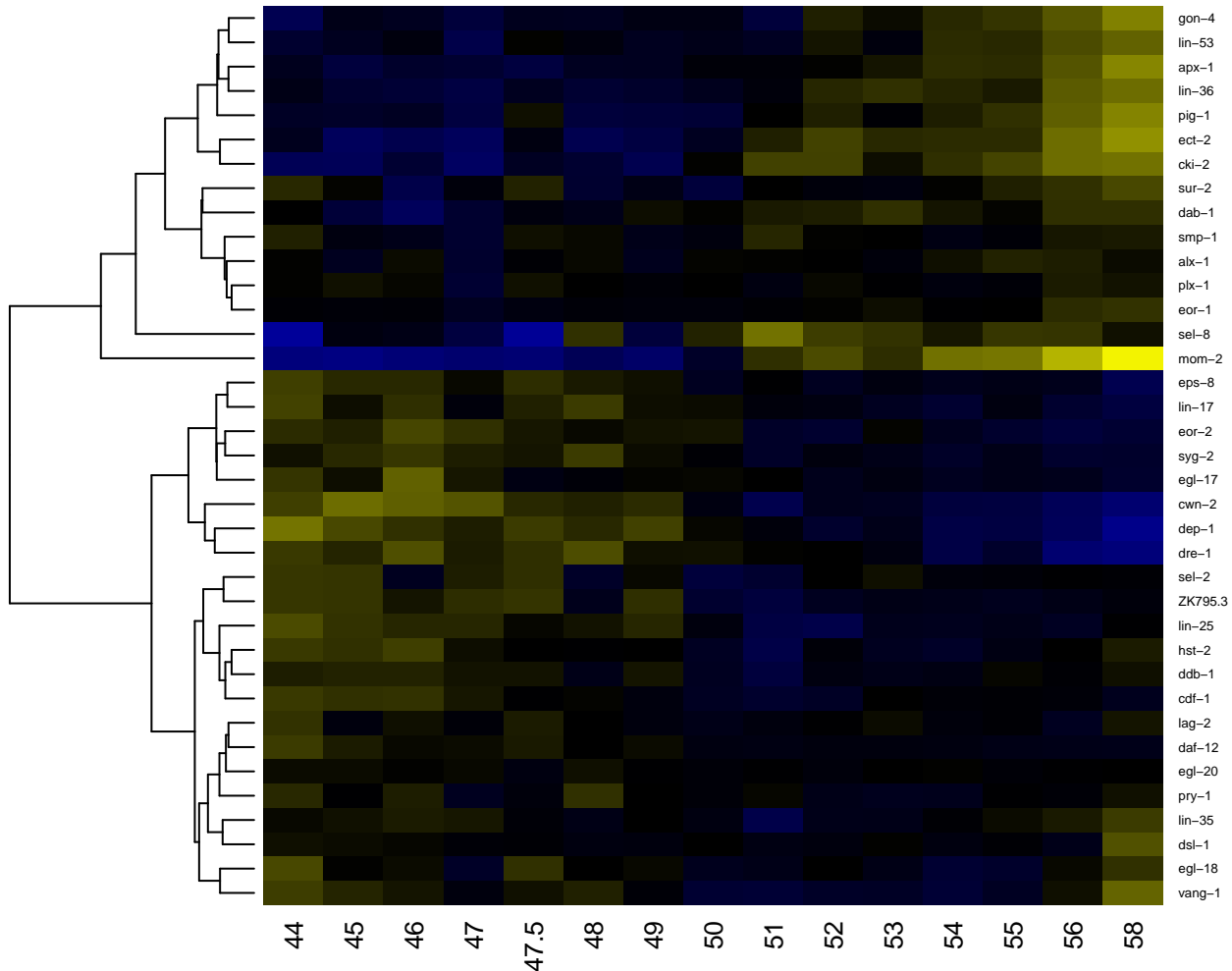
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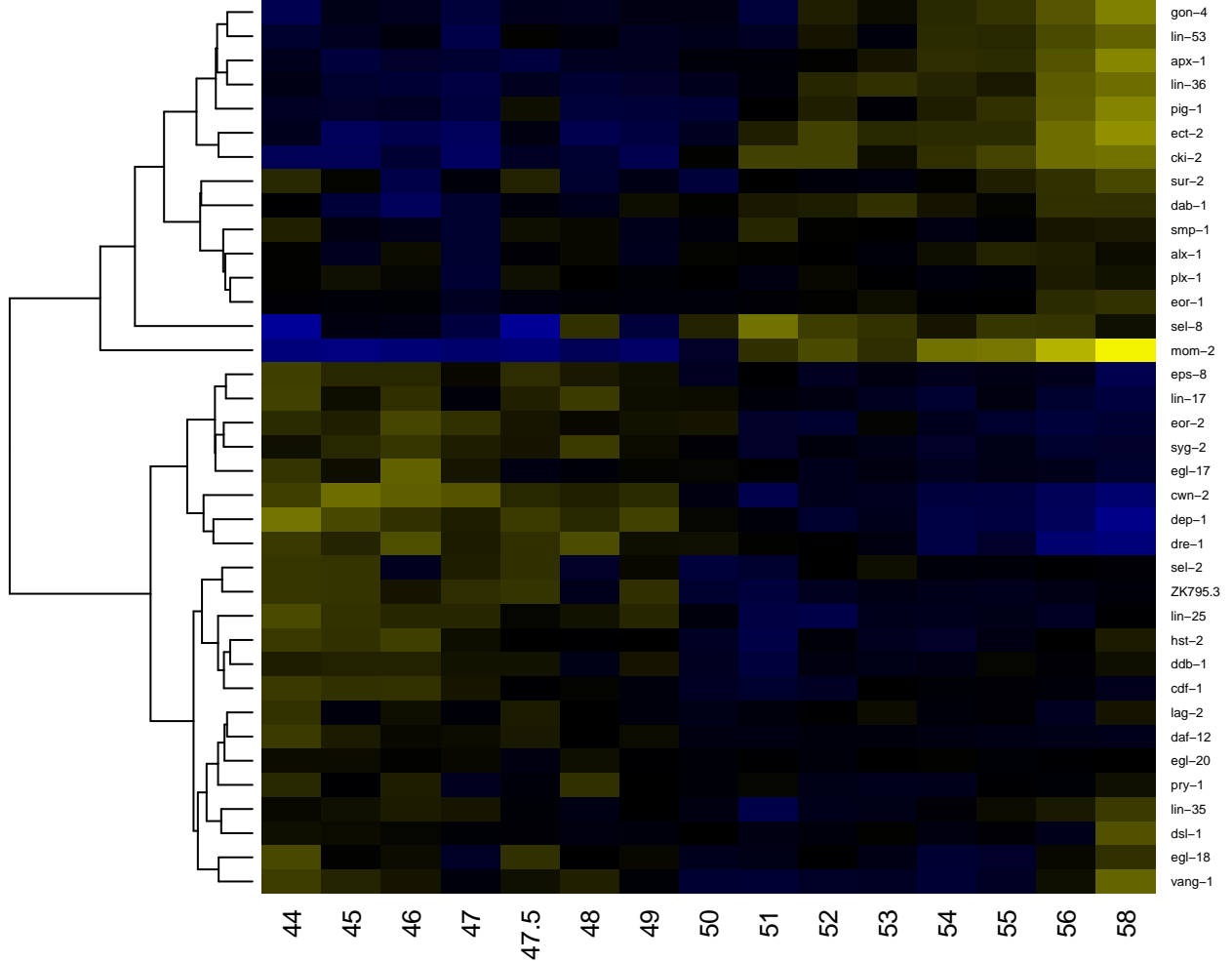
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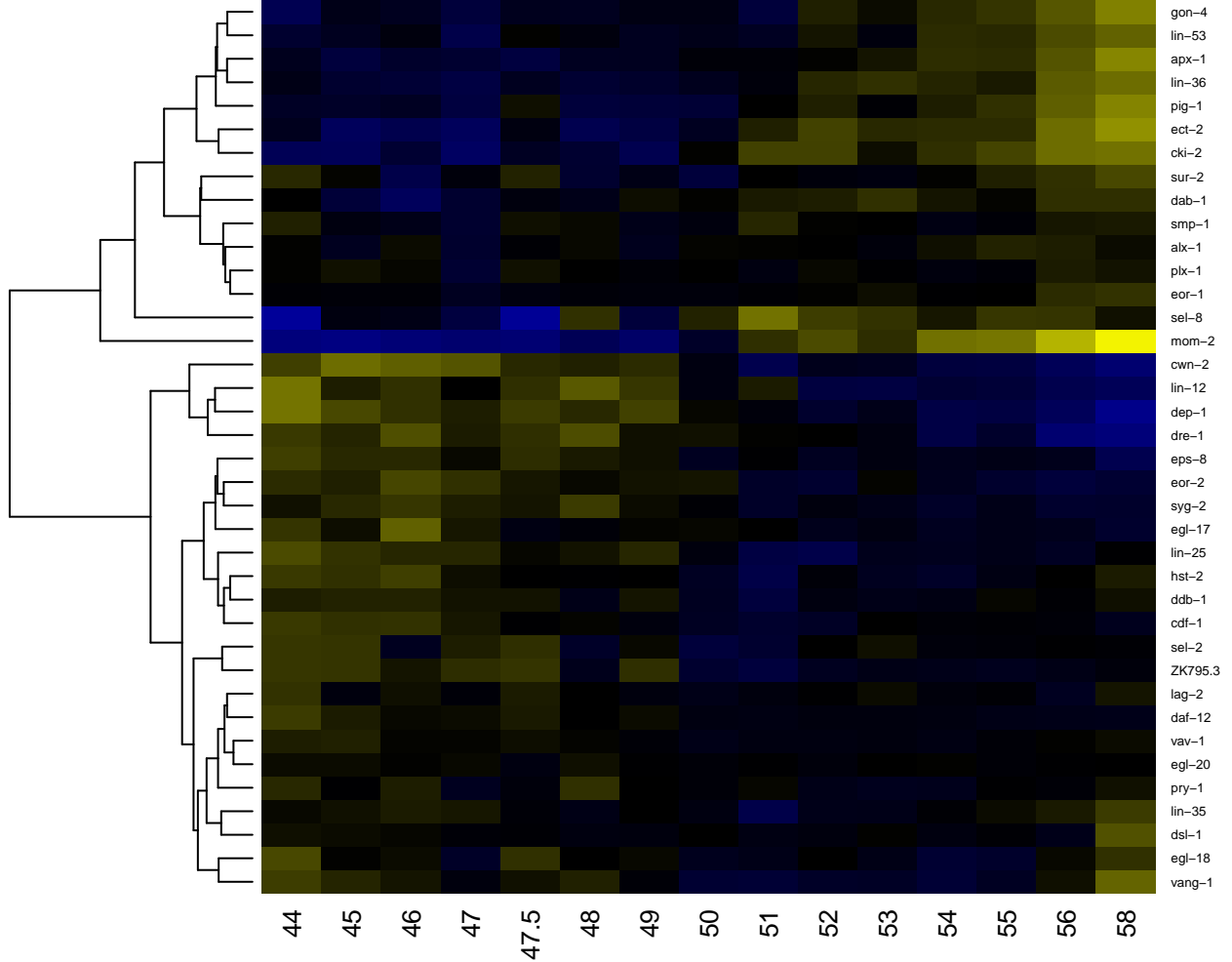
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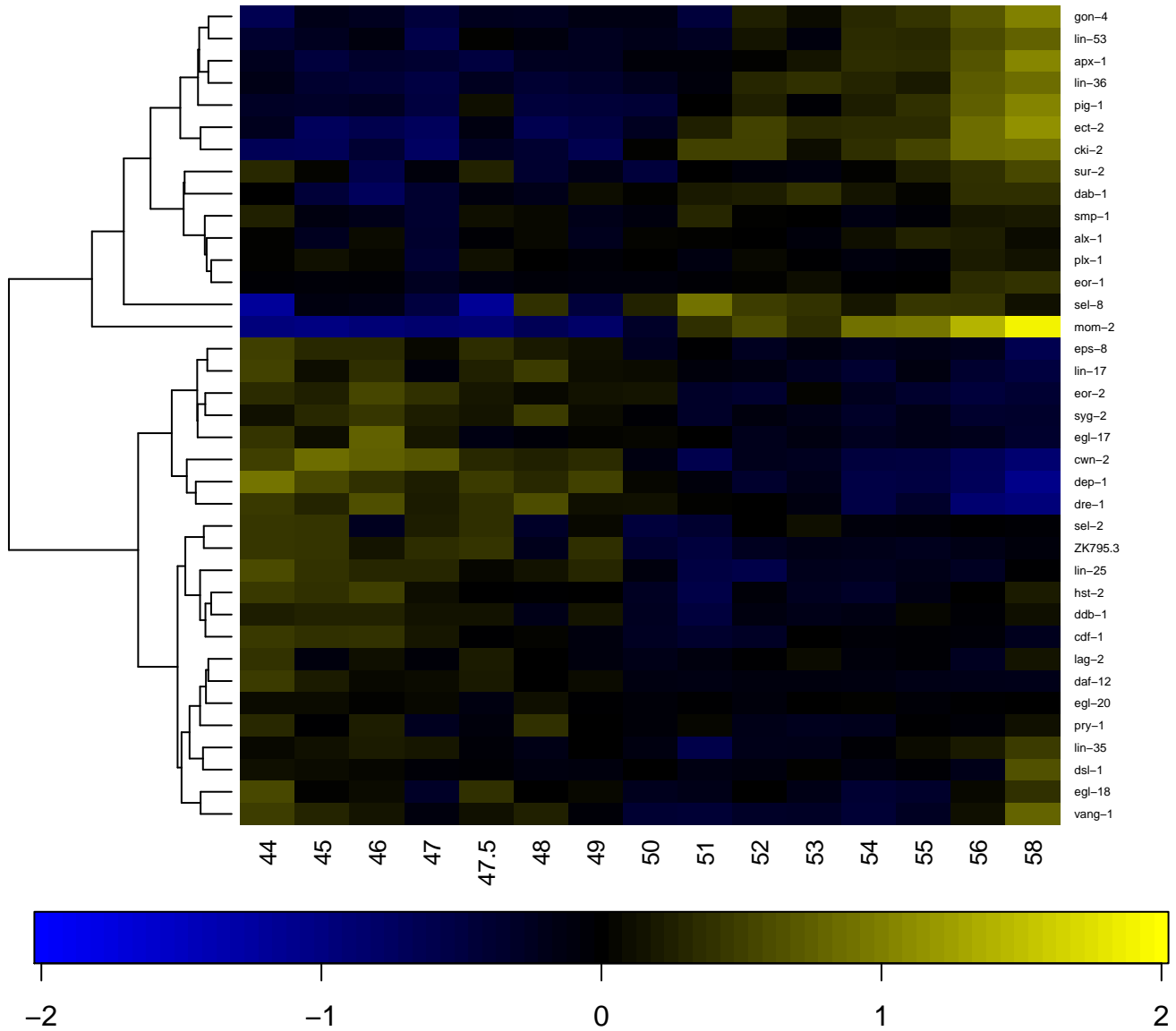
P6.pap



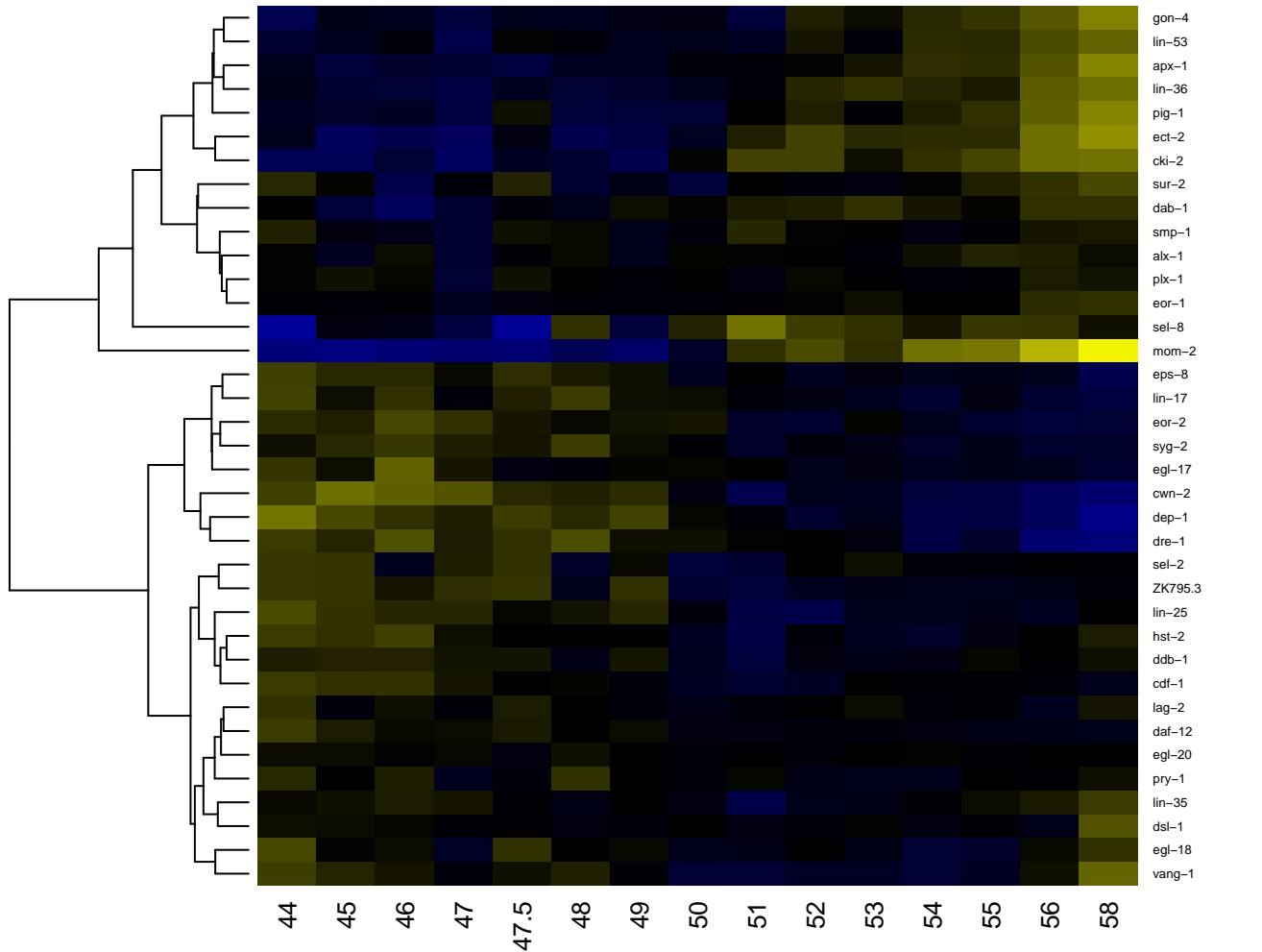
P6.pp



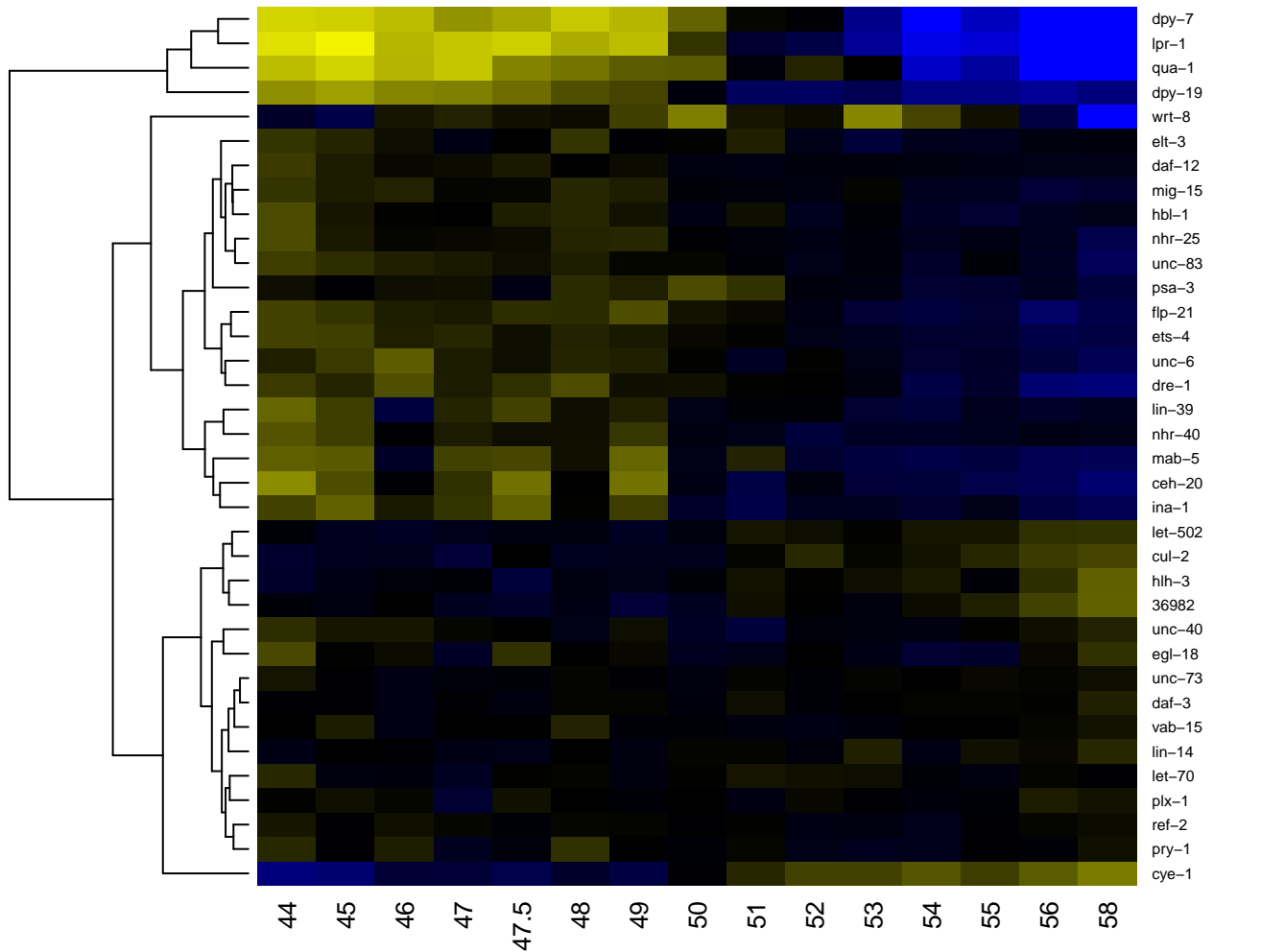
P6.ppa



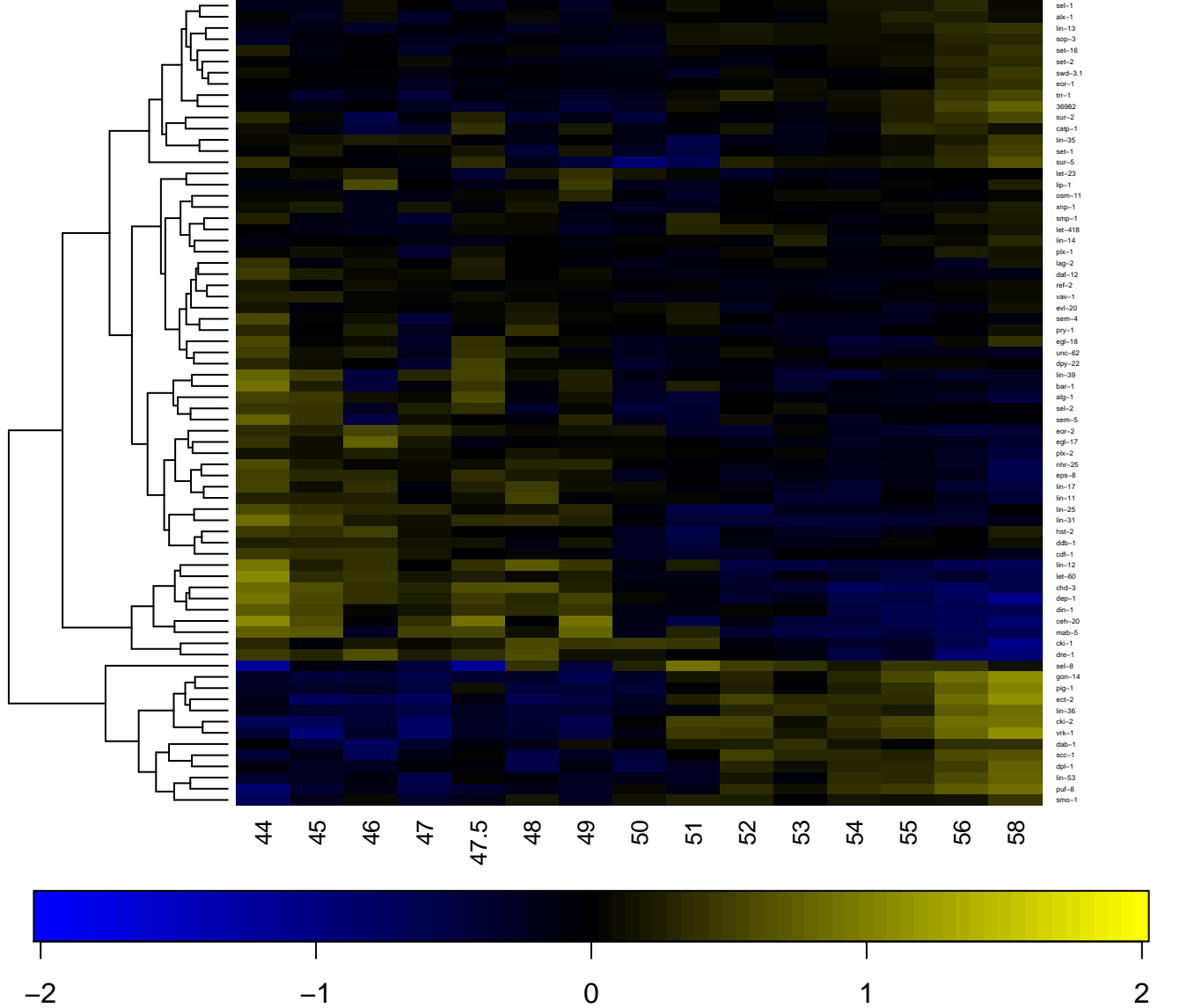
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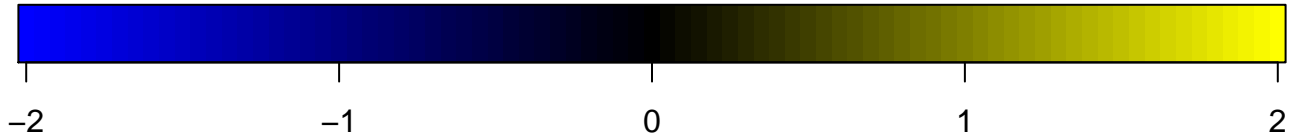
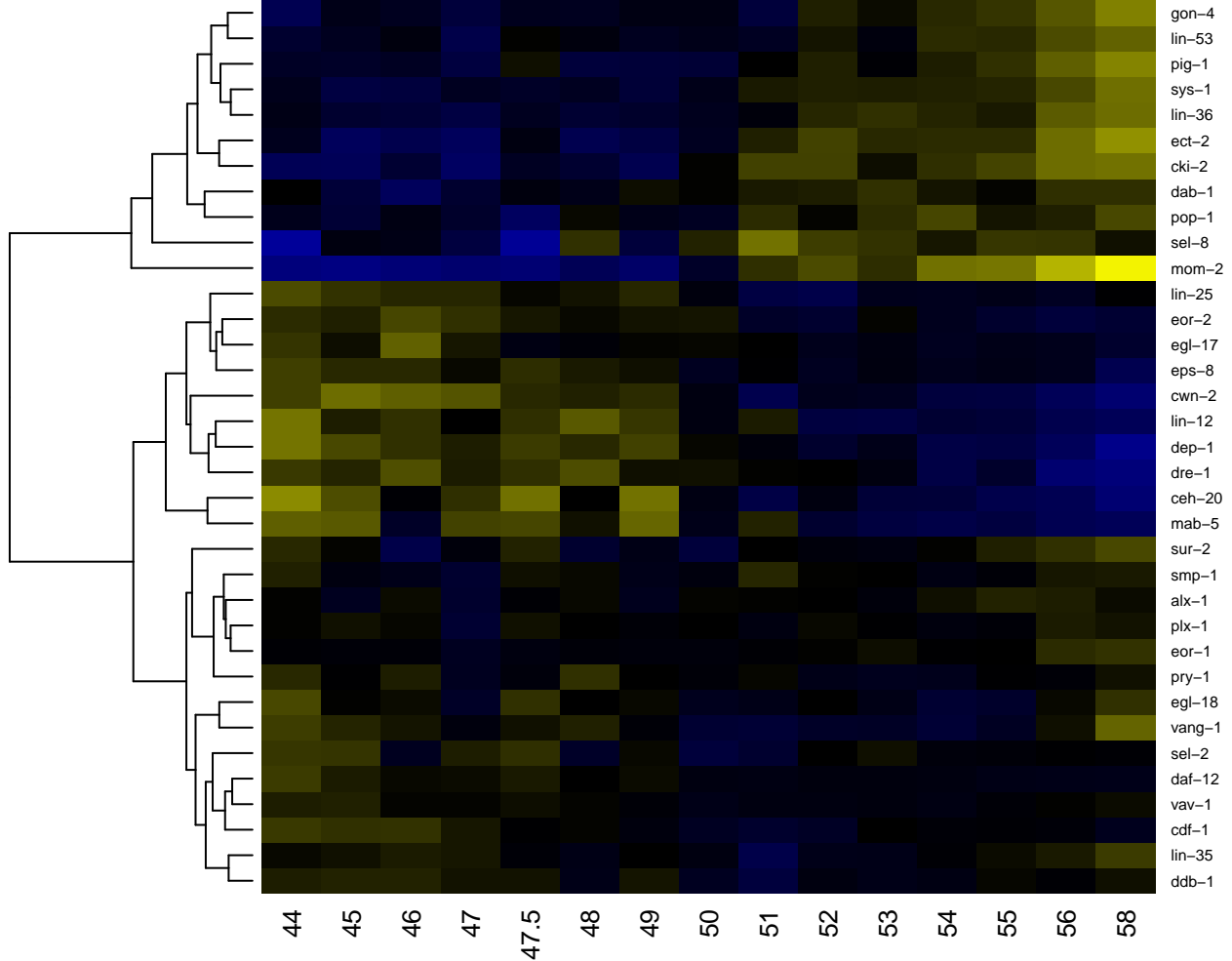
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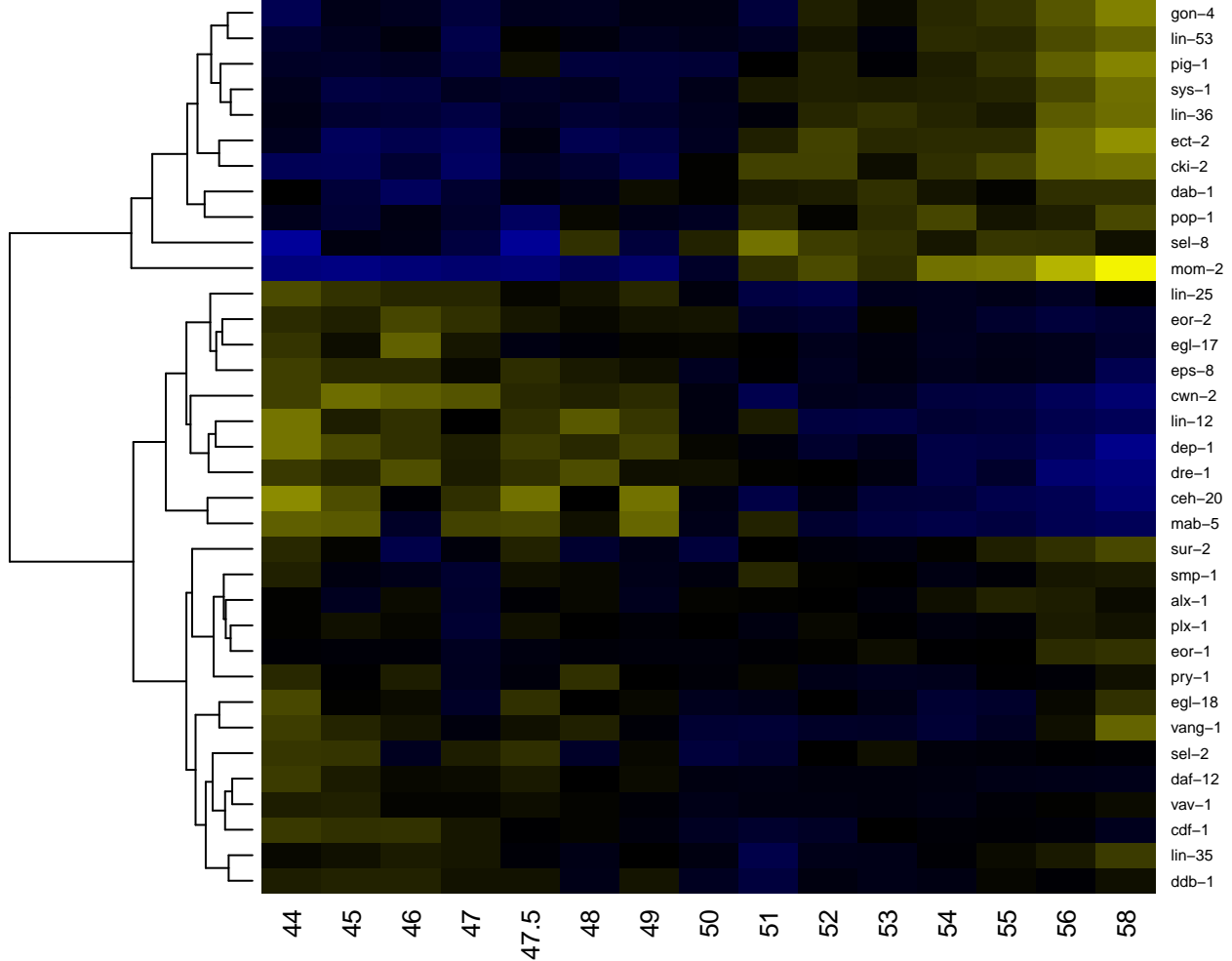
P7.p



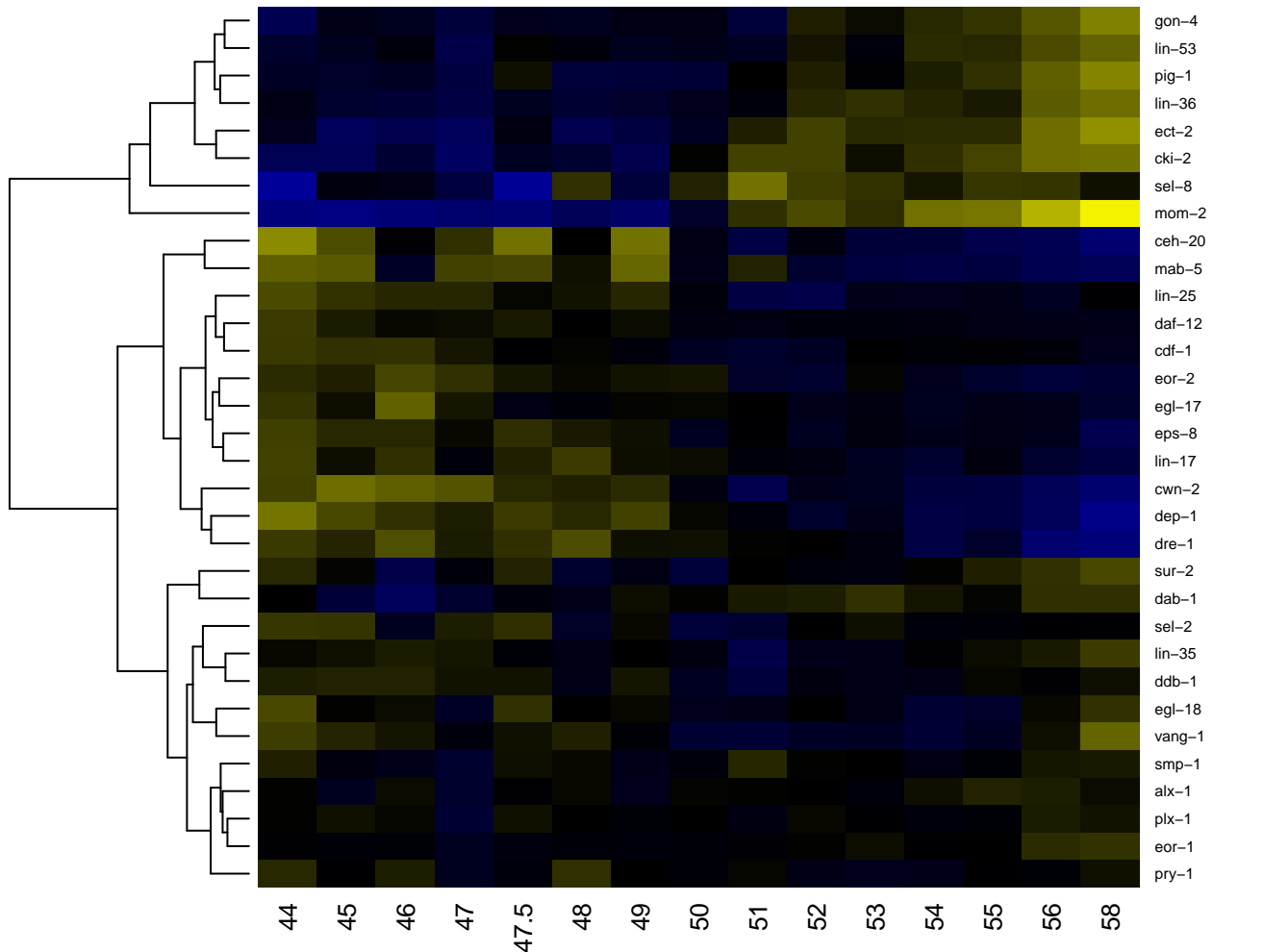
P7.pa



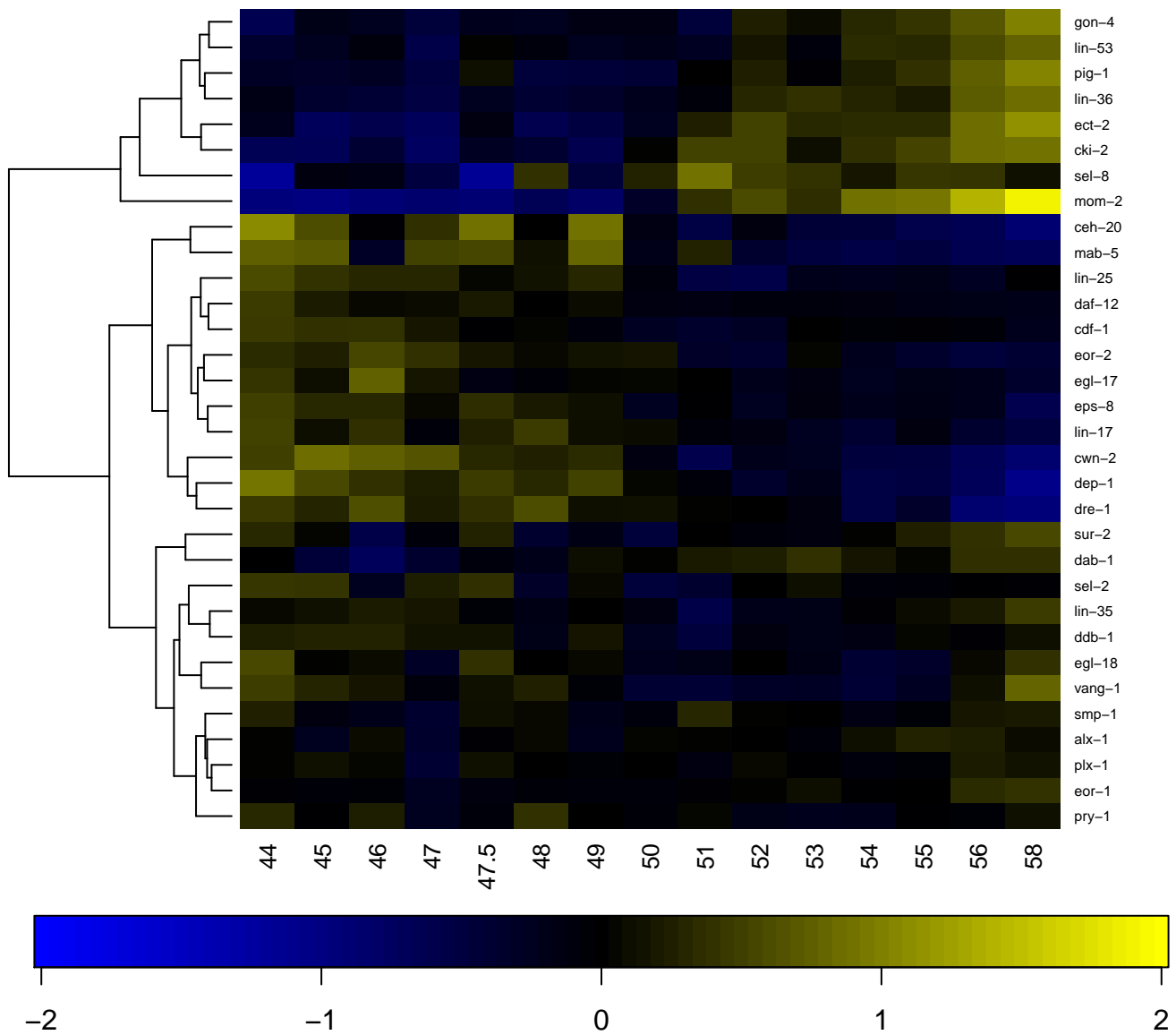
P7.pp



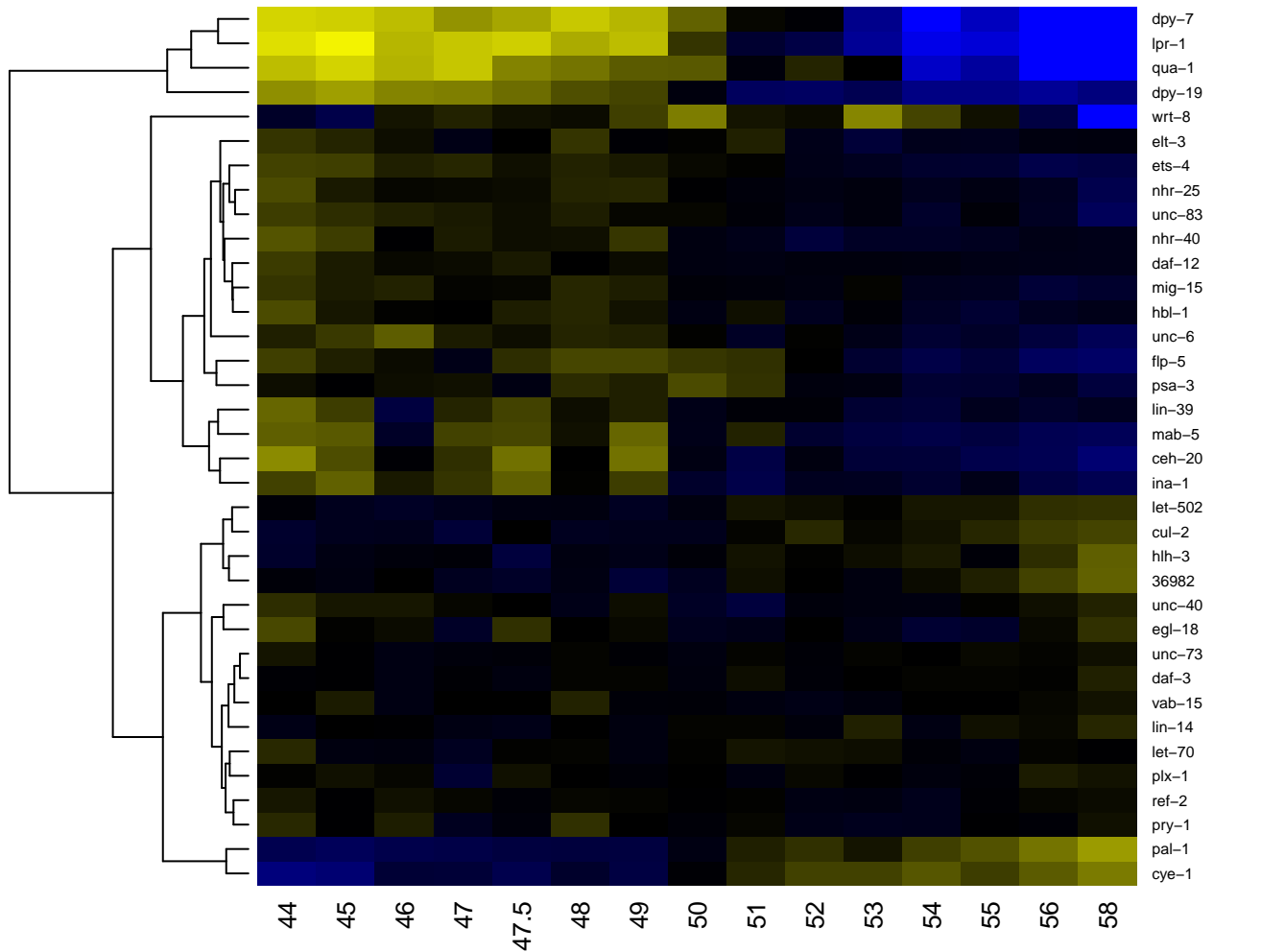
P7.ppa



P7.ppp



P8



-2

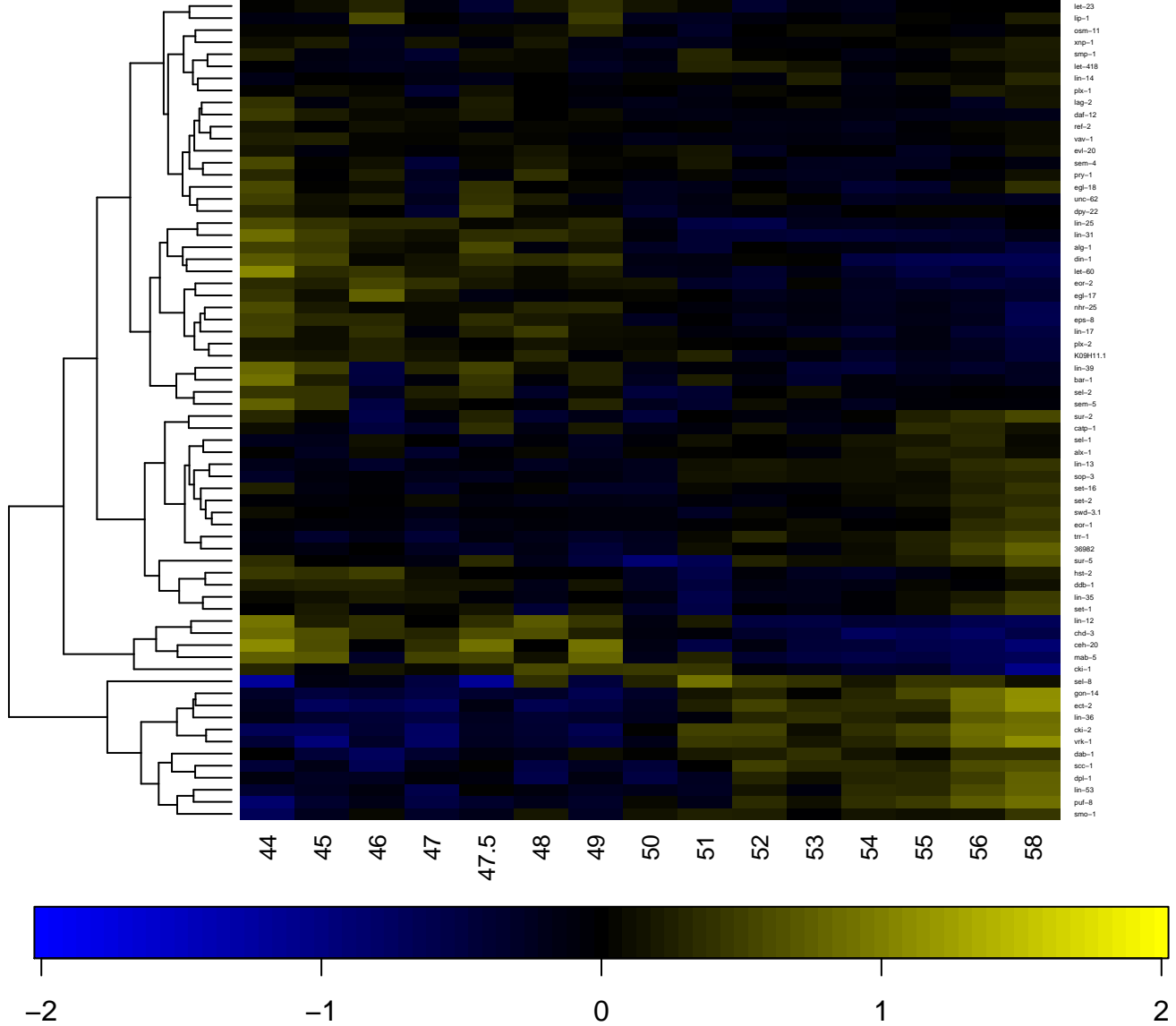
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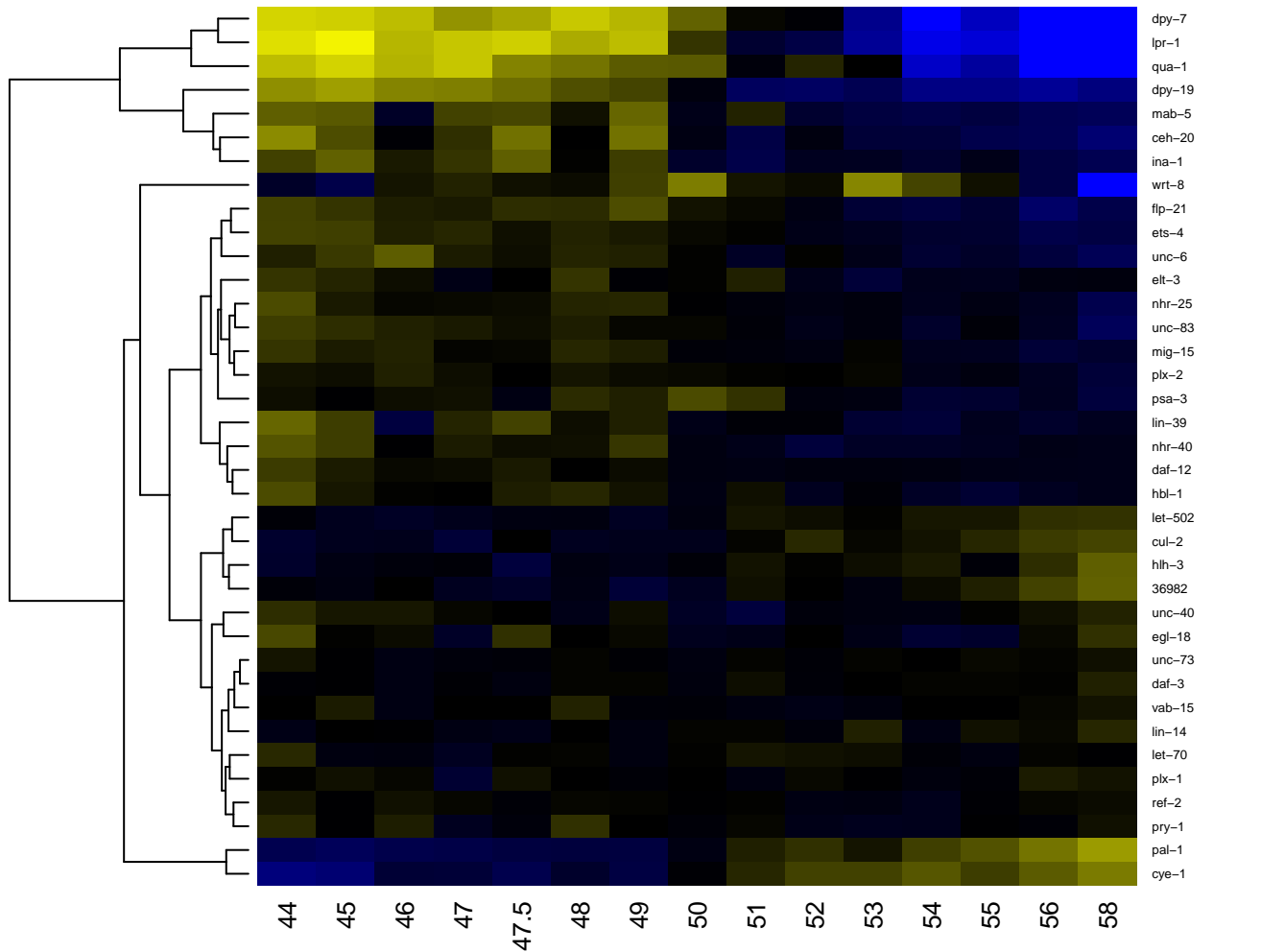
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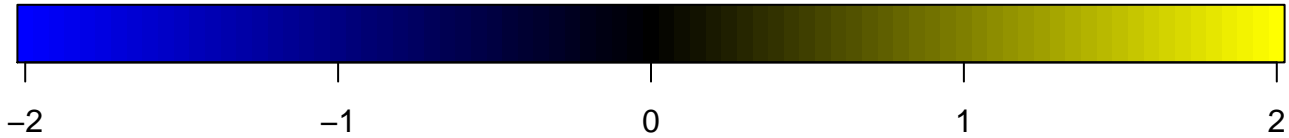
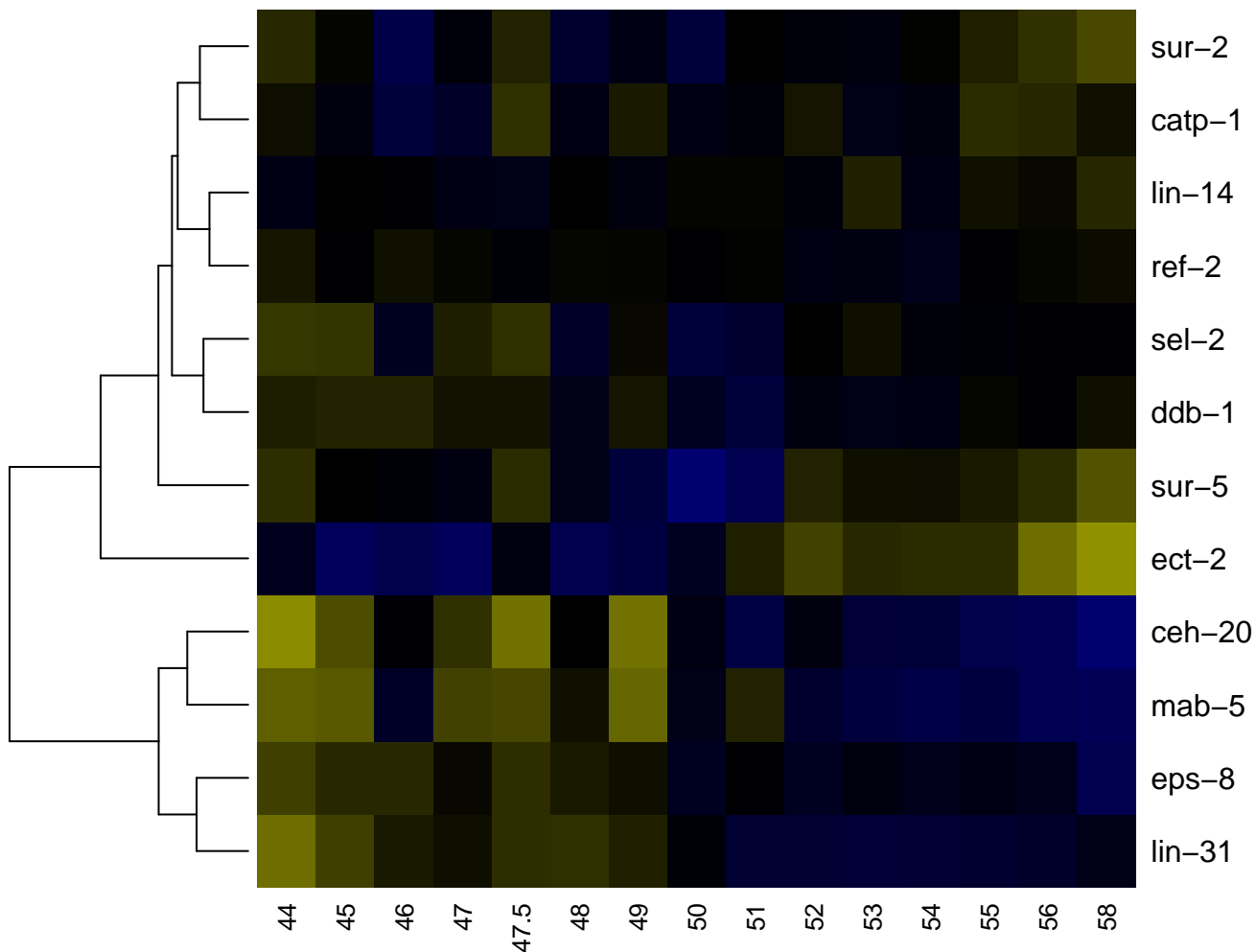
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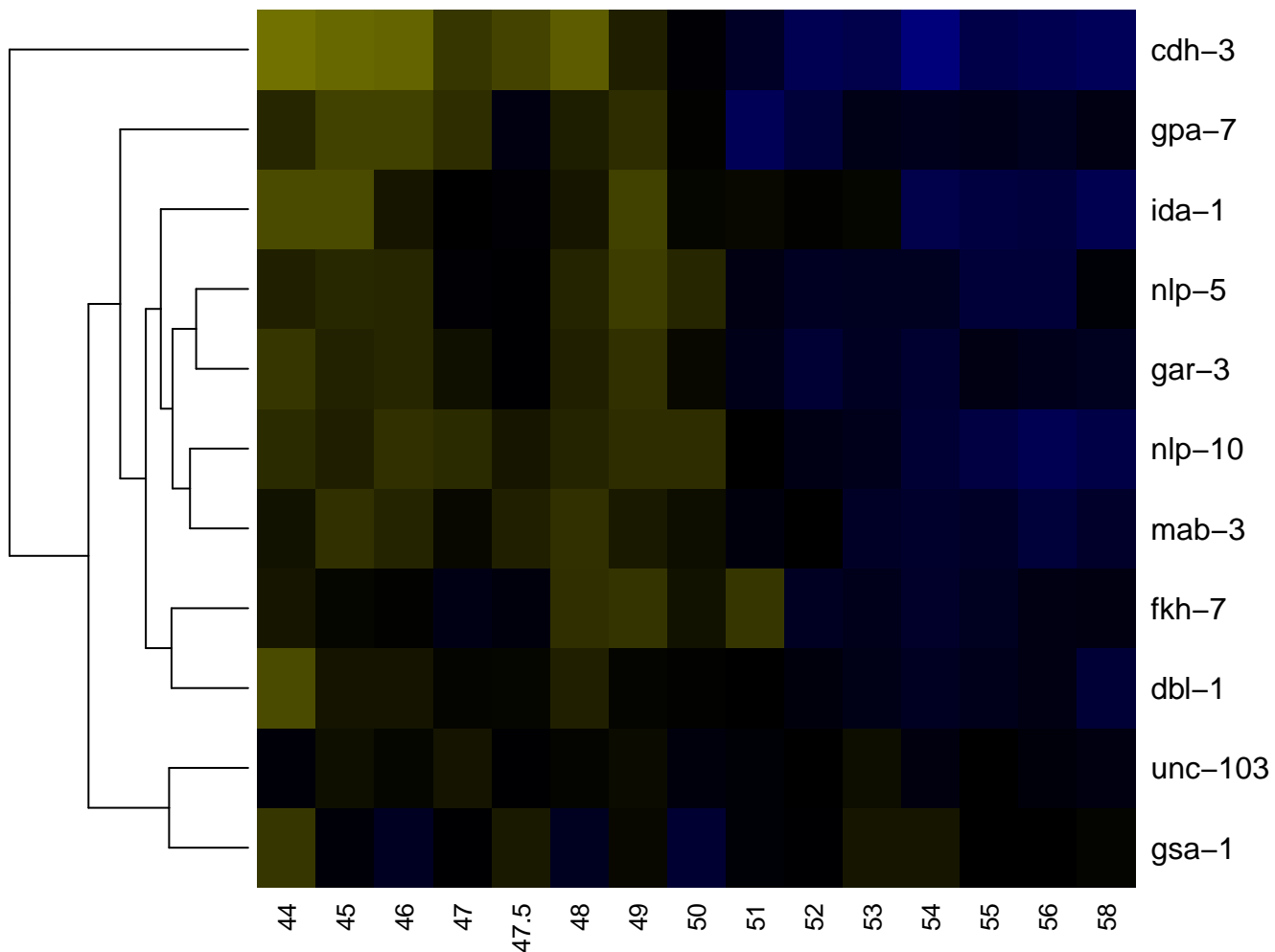
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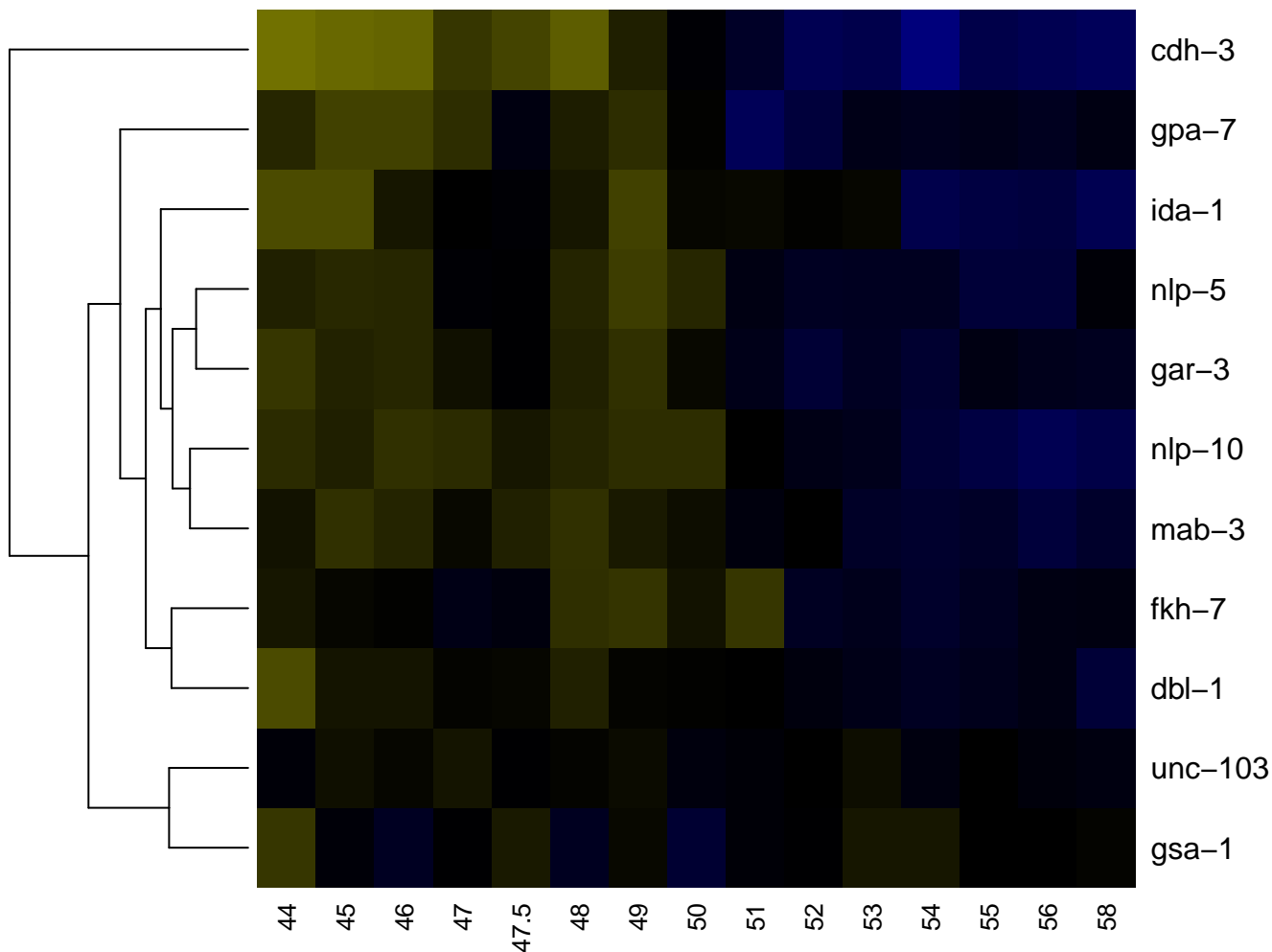
P9.p



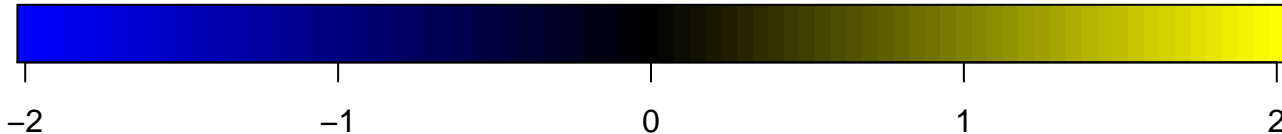
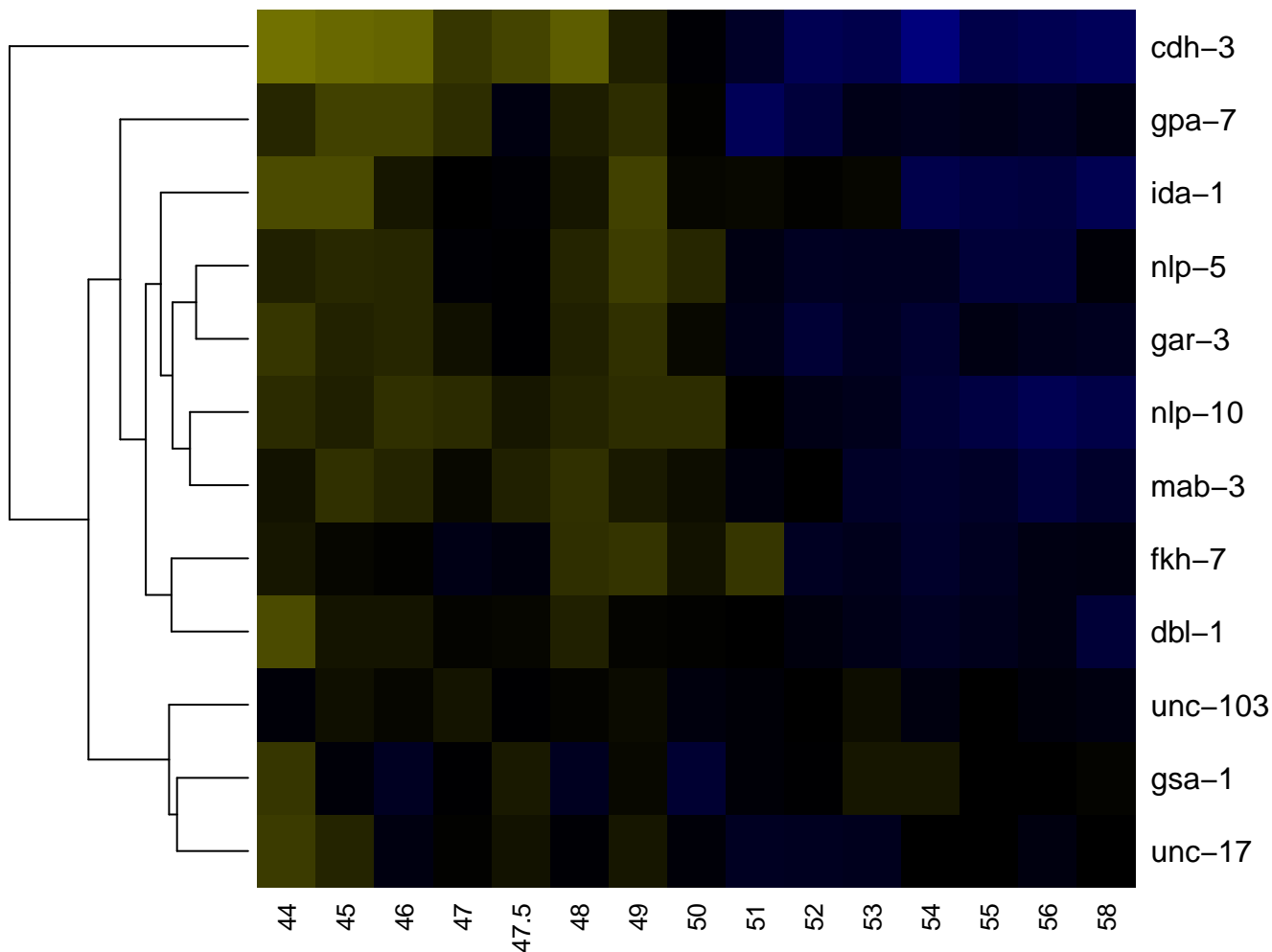
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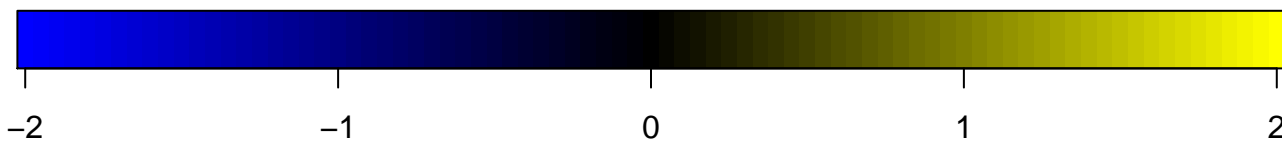
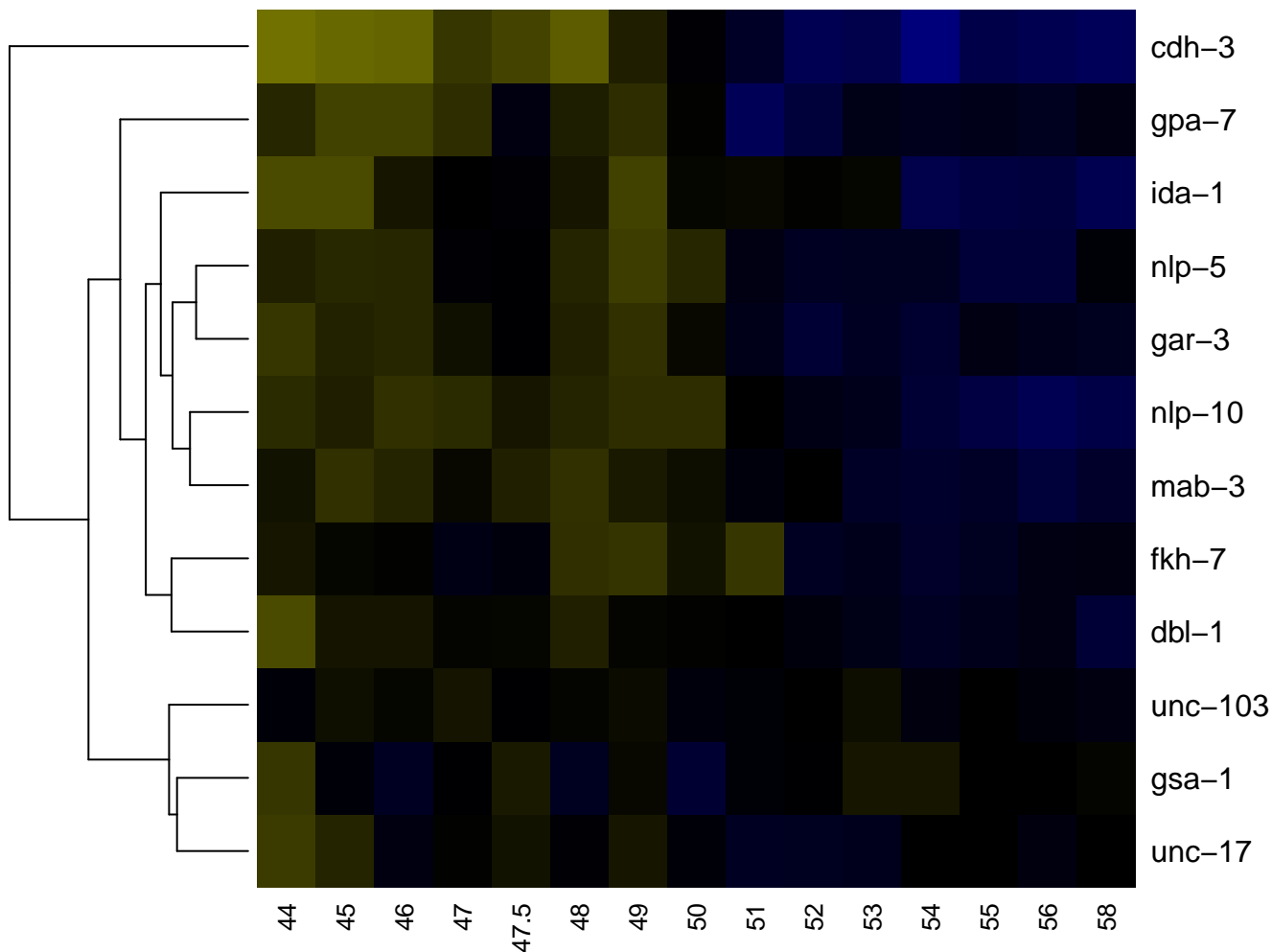
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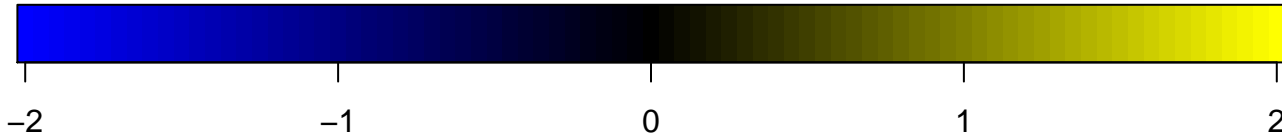
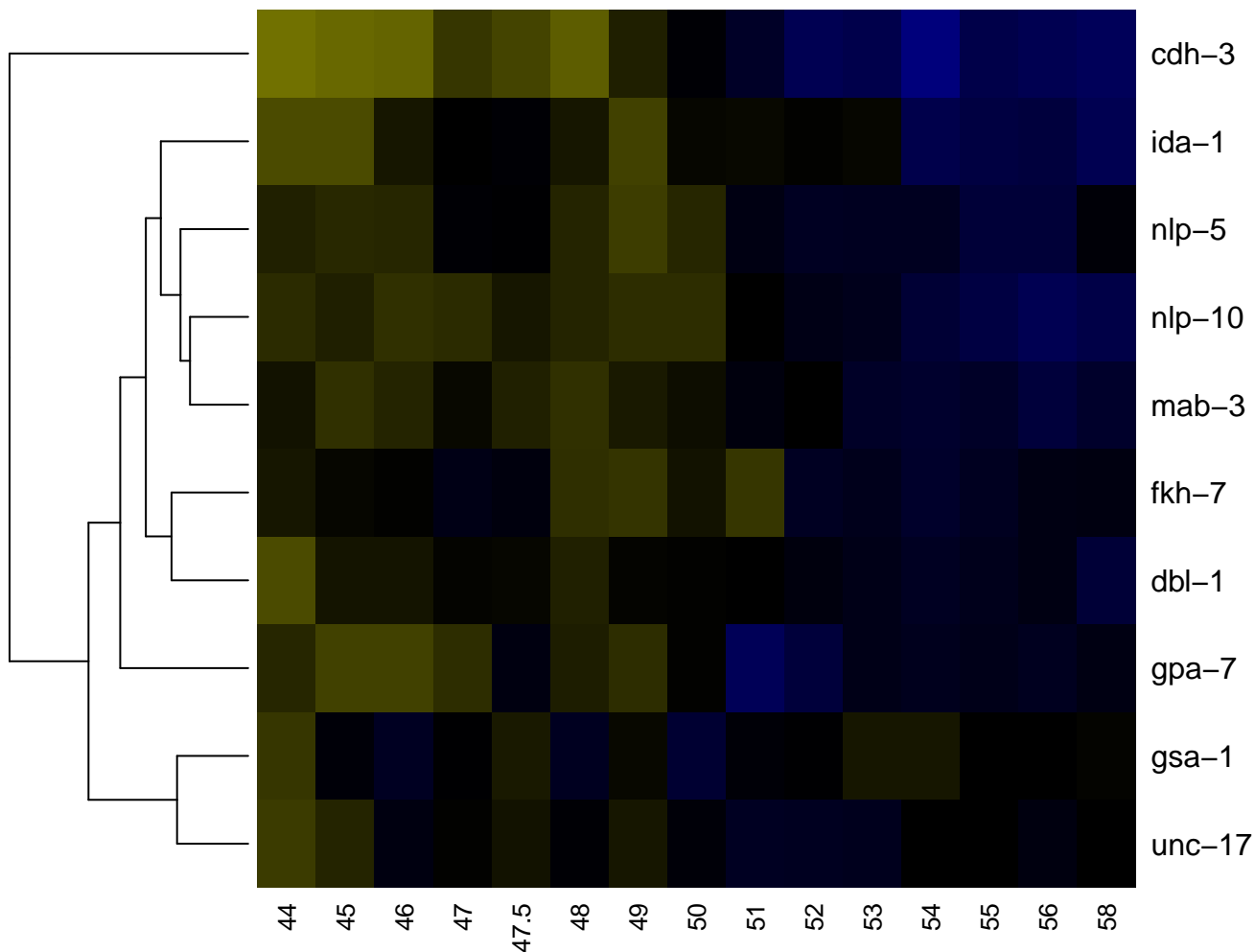
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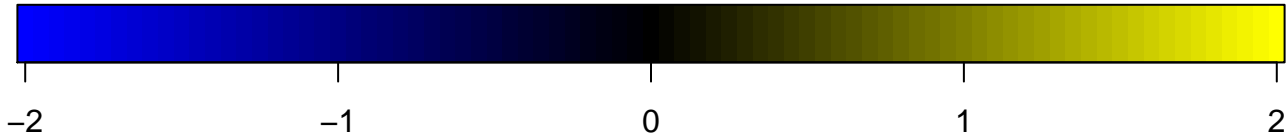
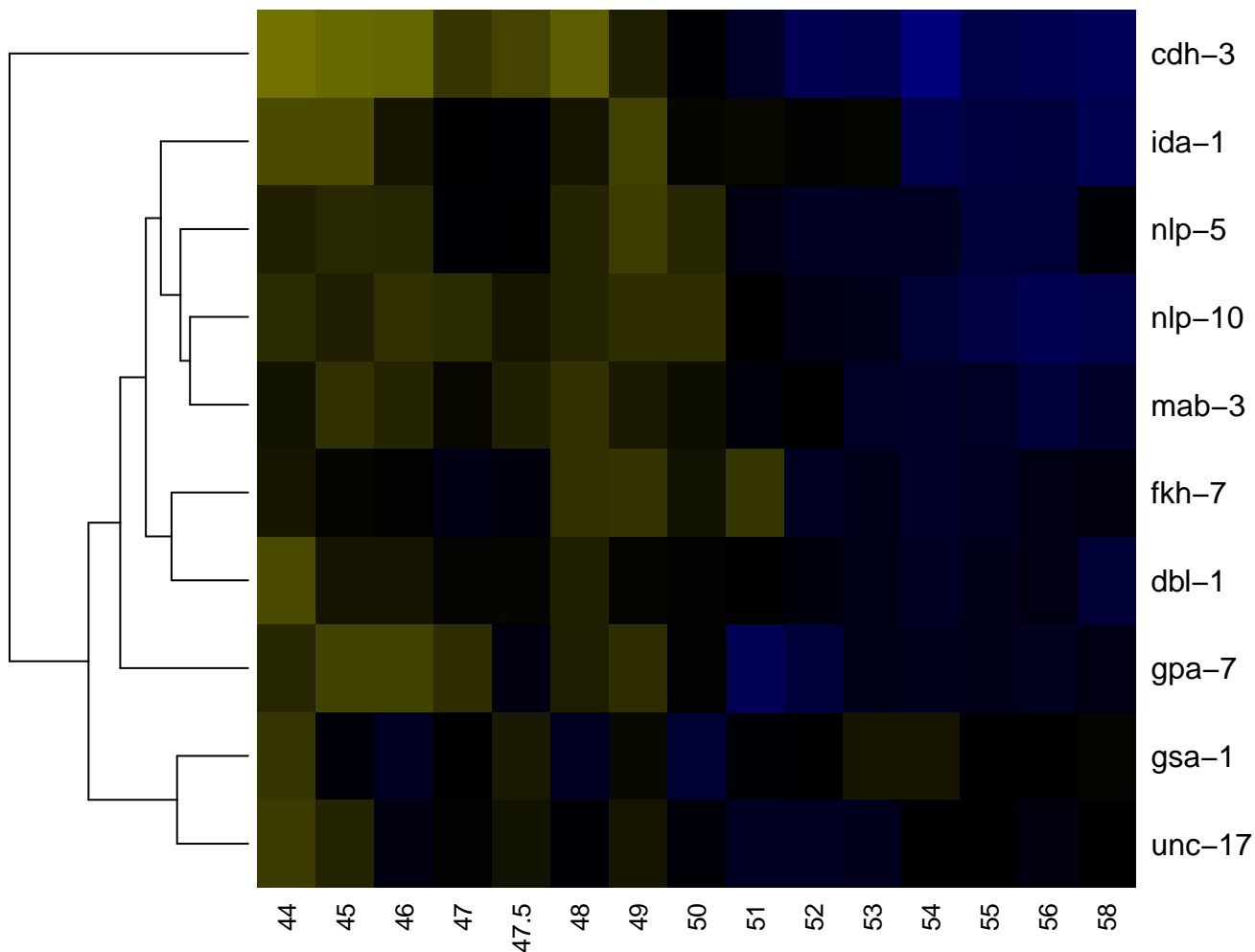
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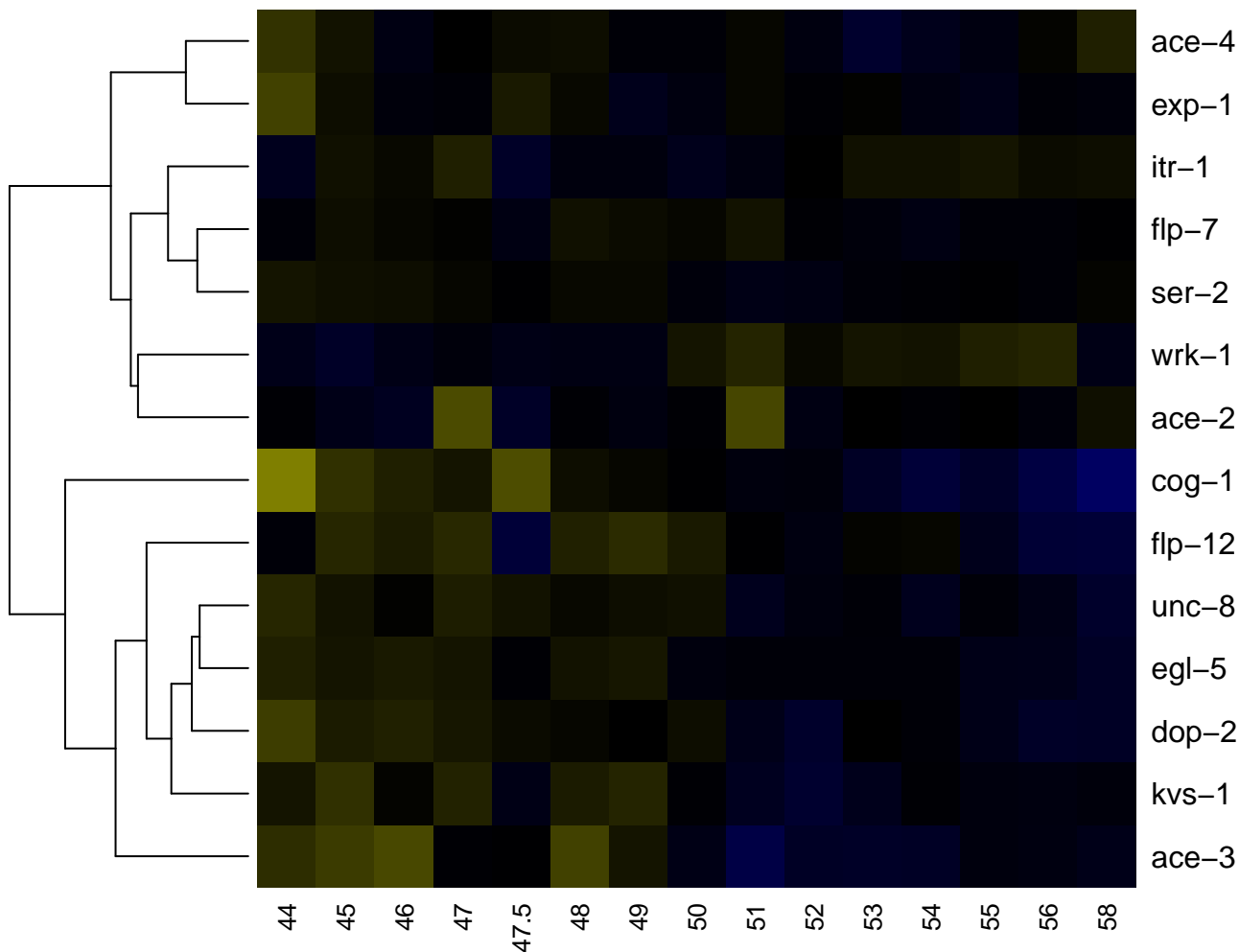
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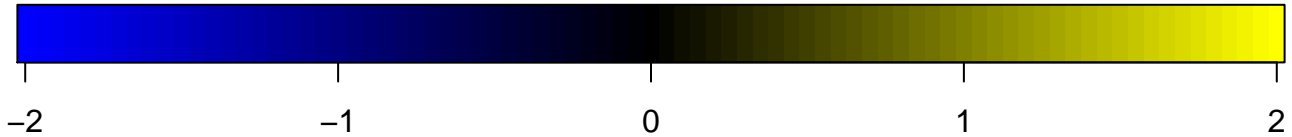
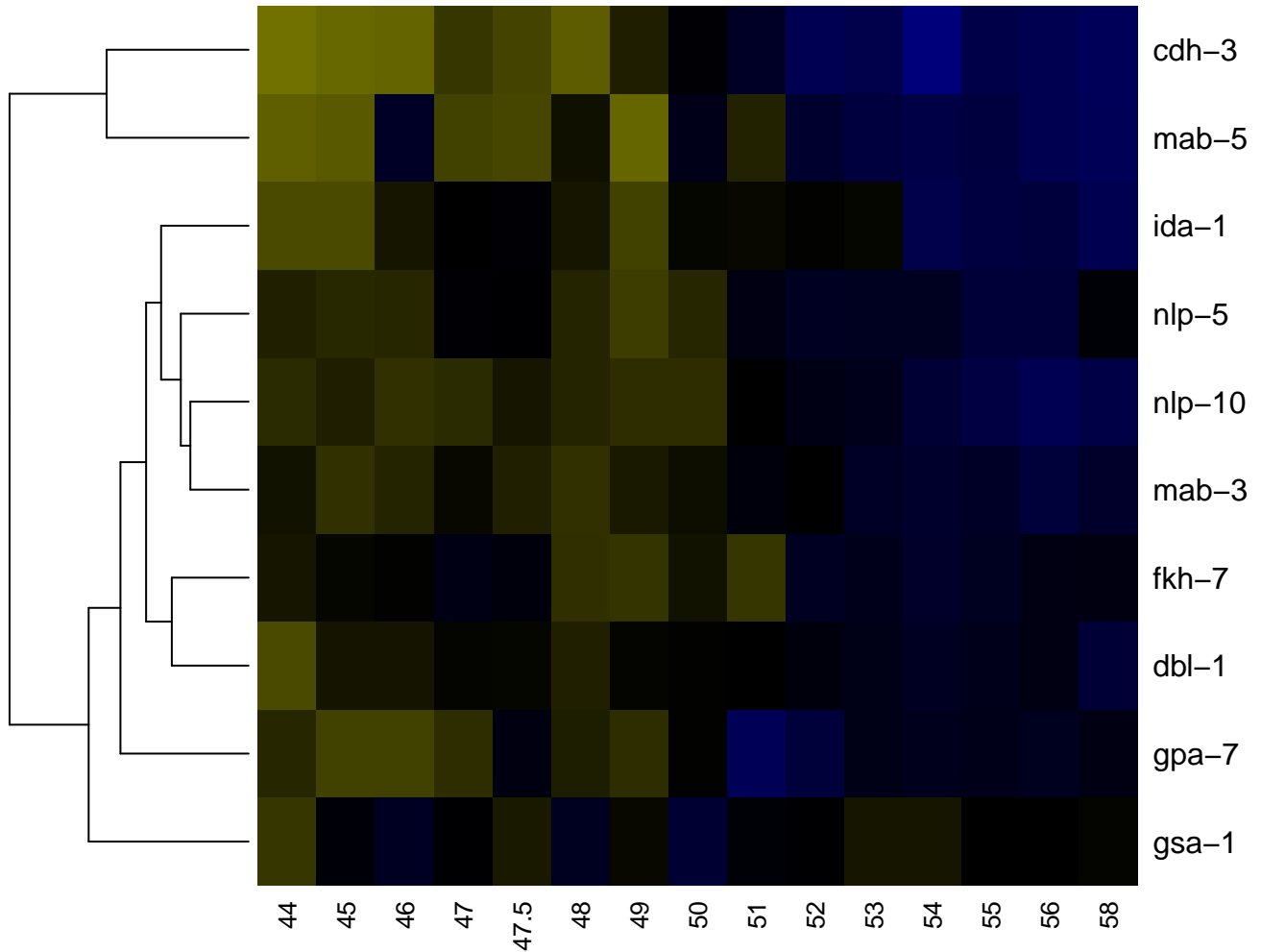
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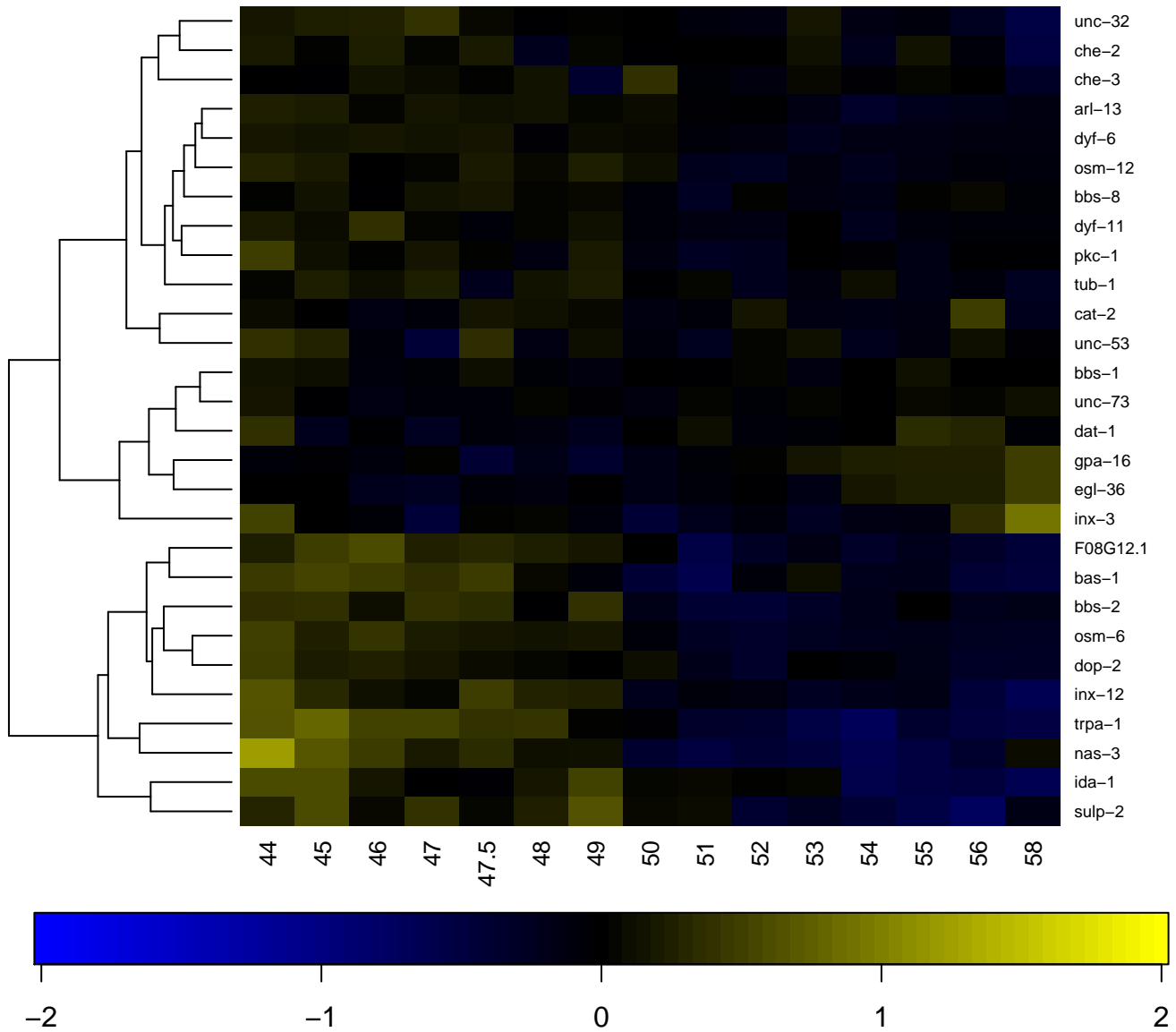
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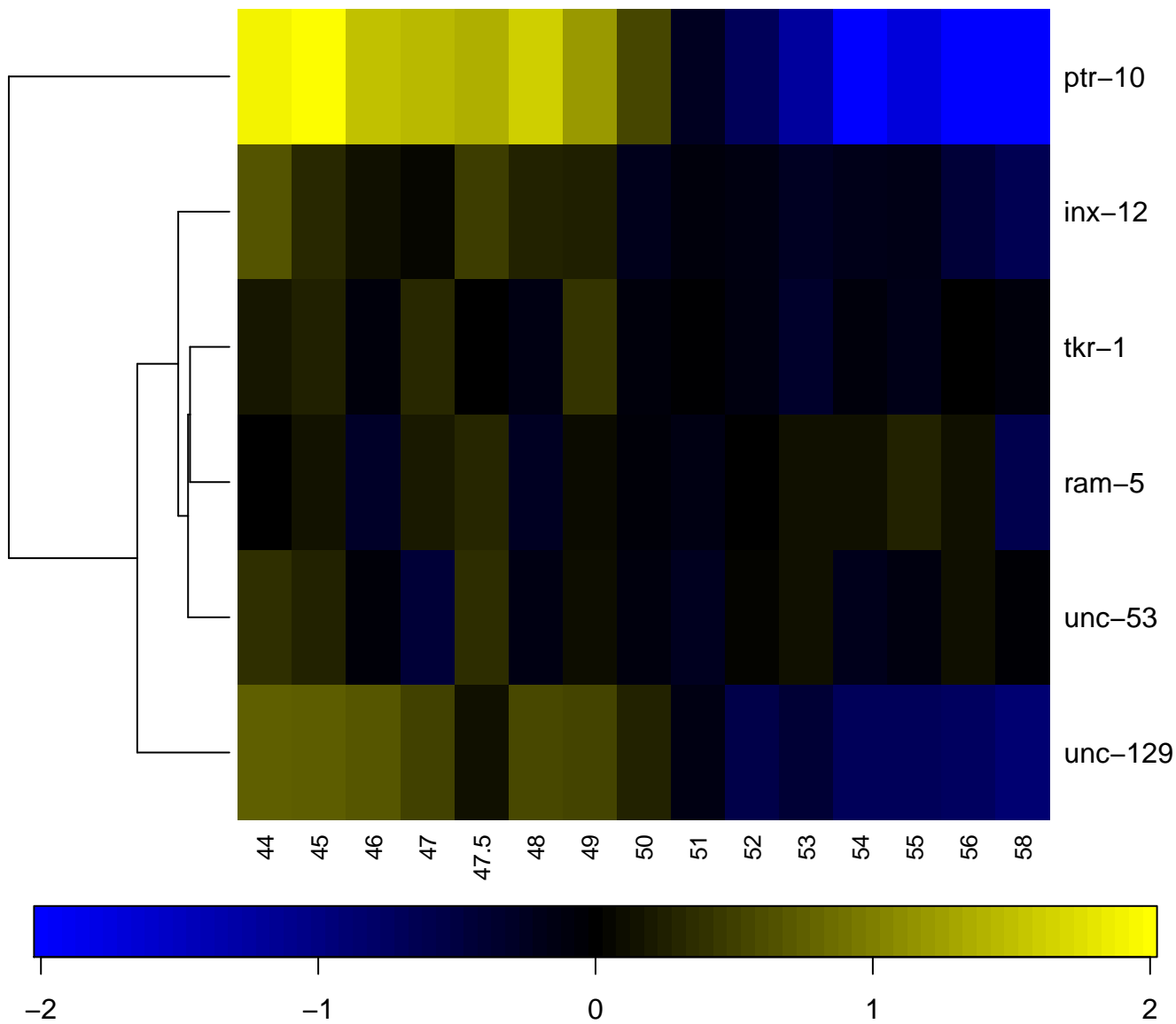
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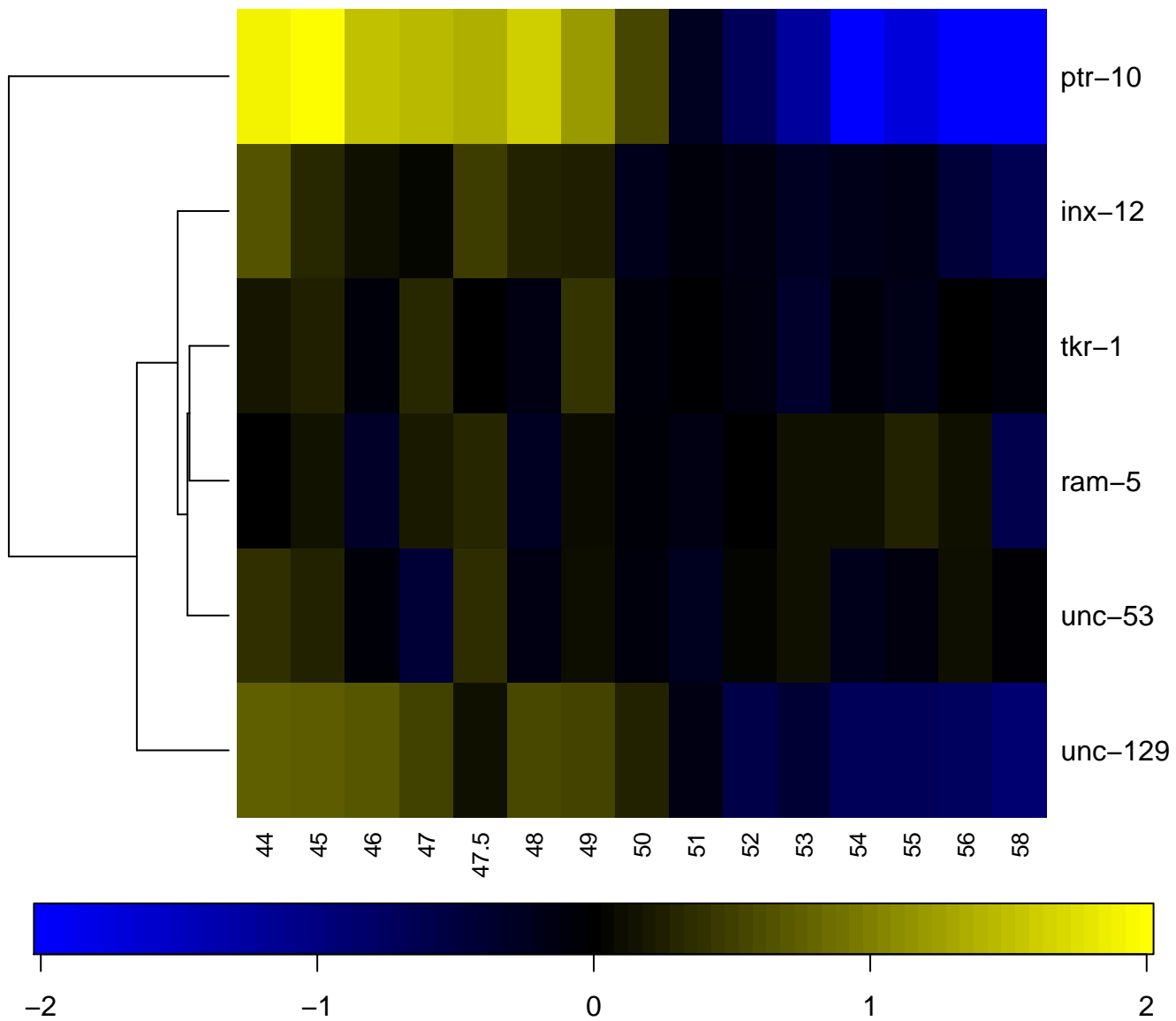
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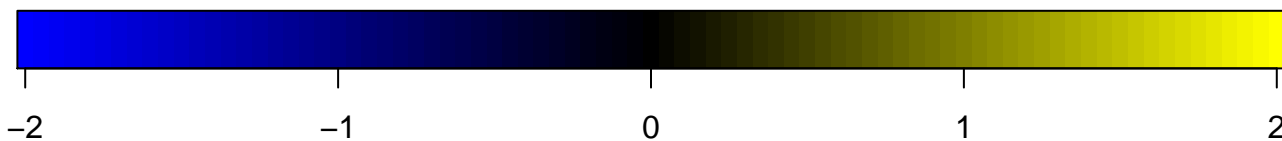
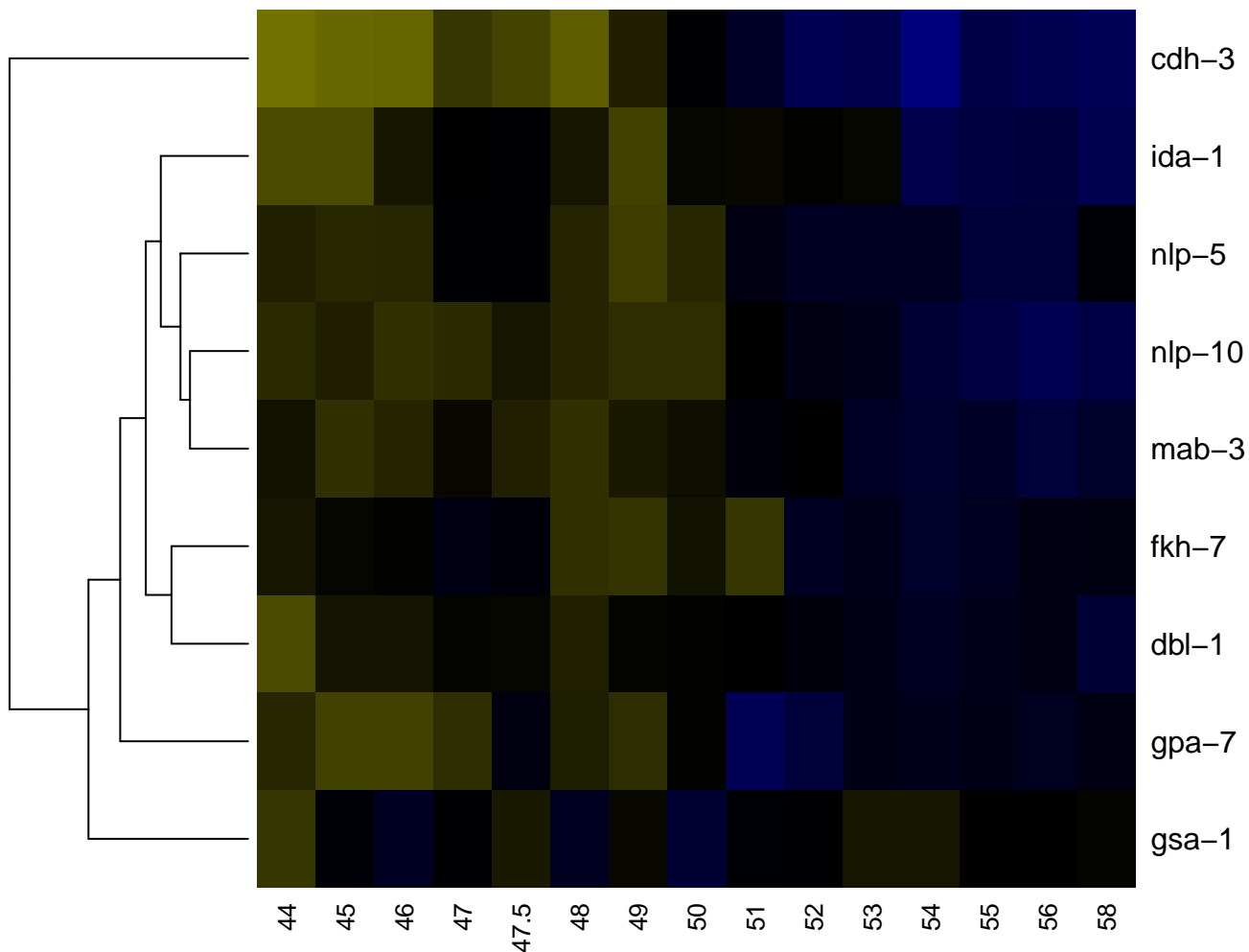
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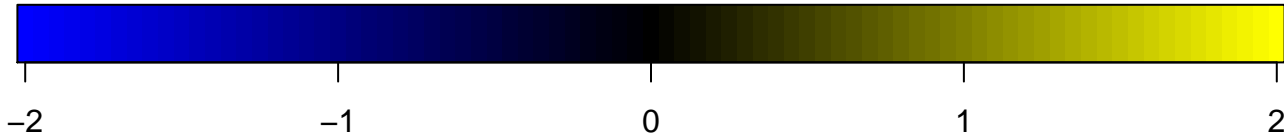
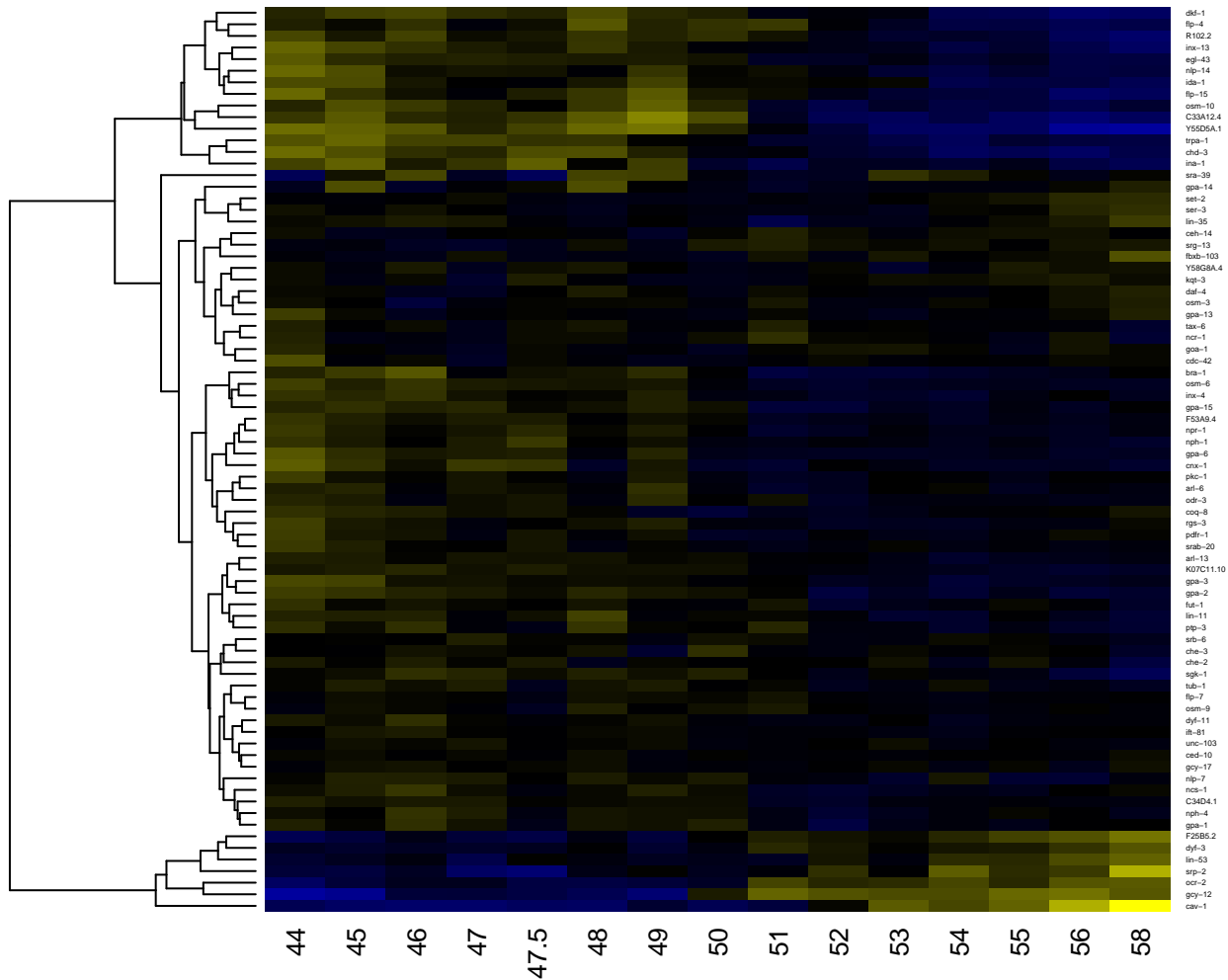
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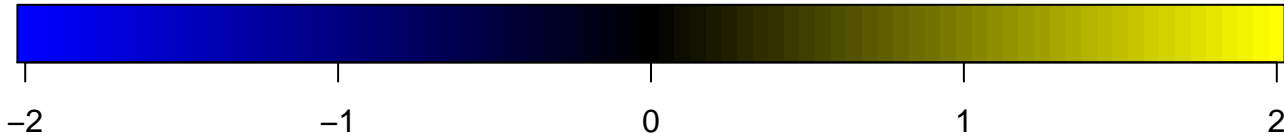
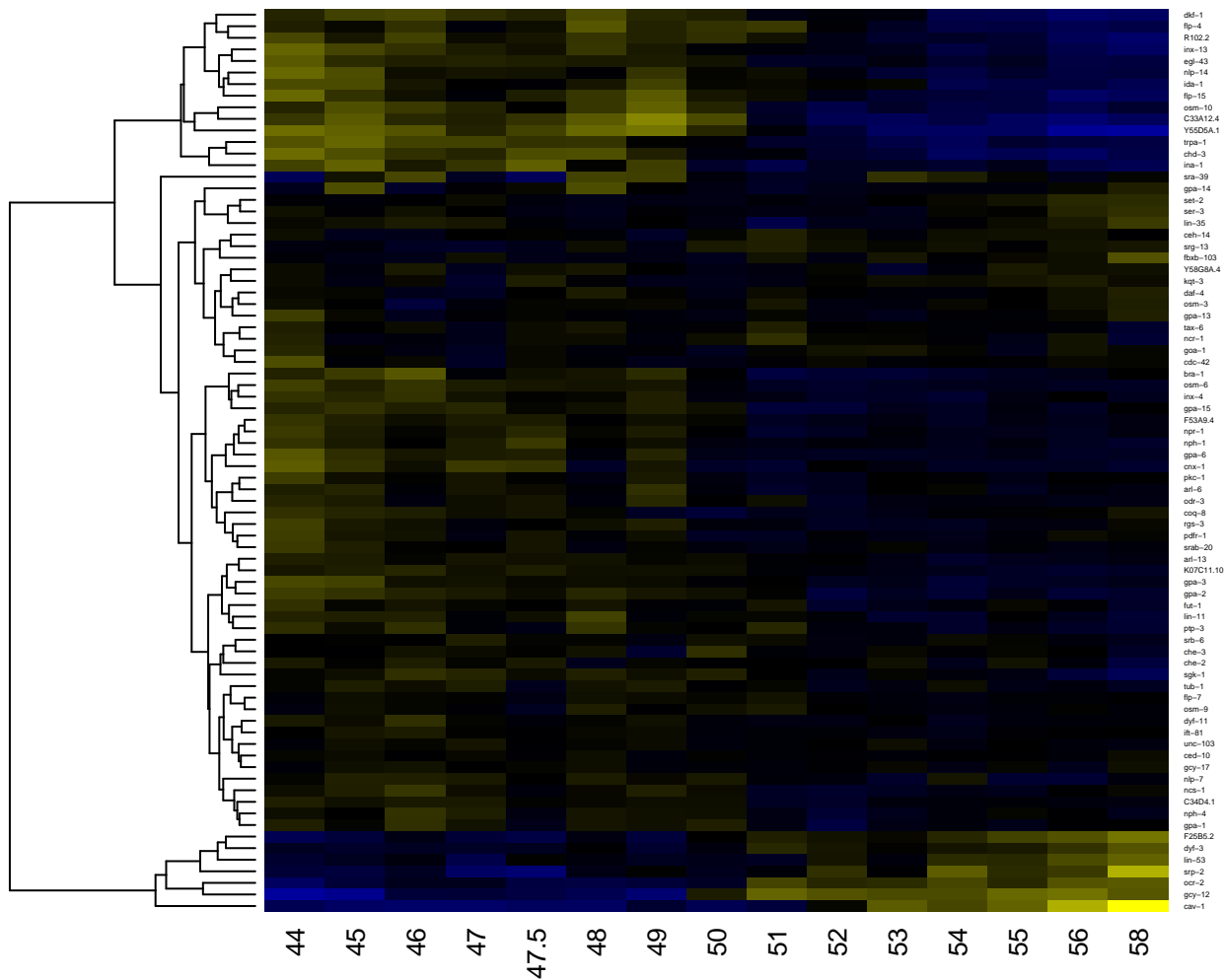
PGA



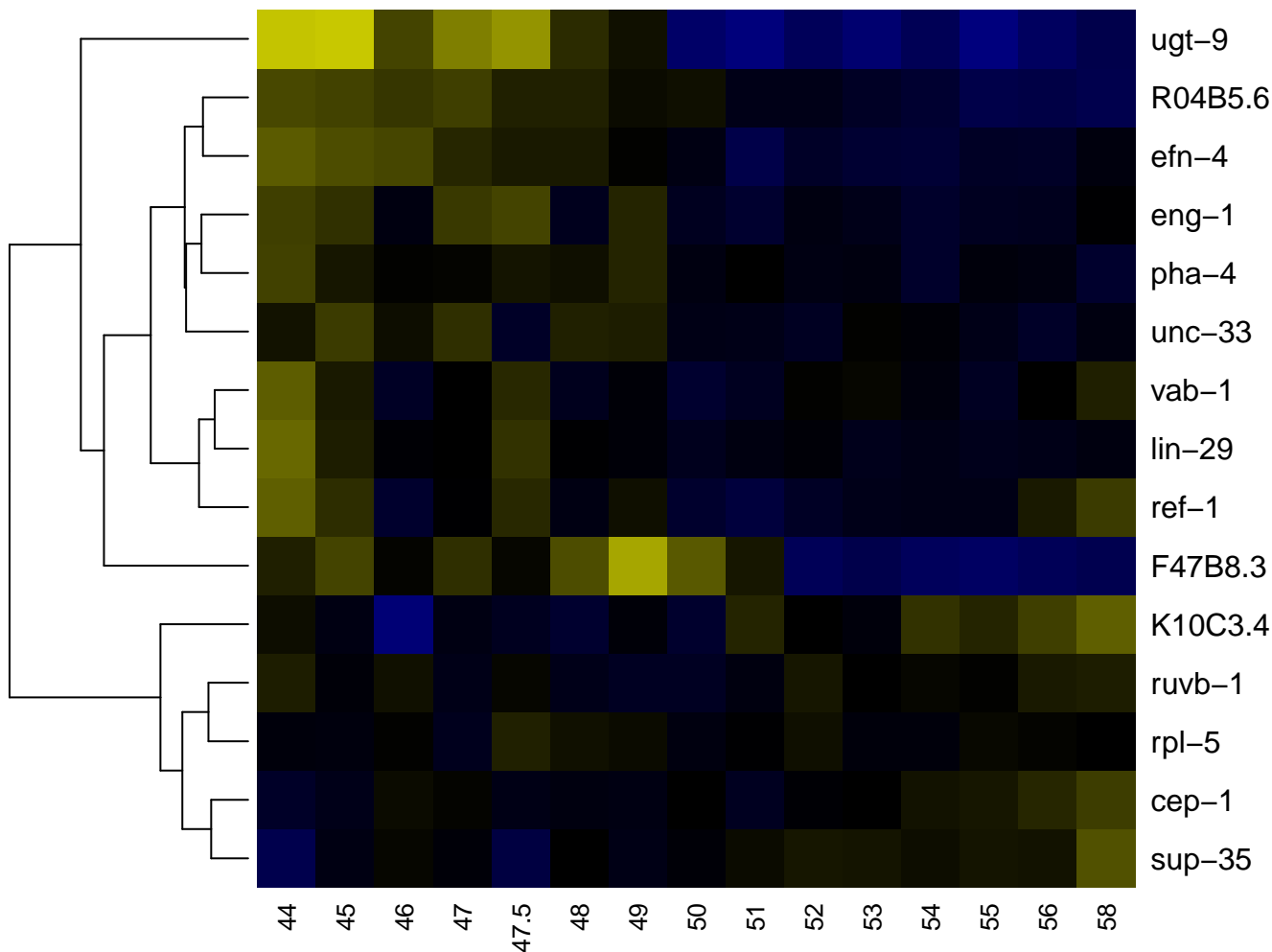
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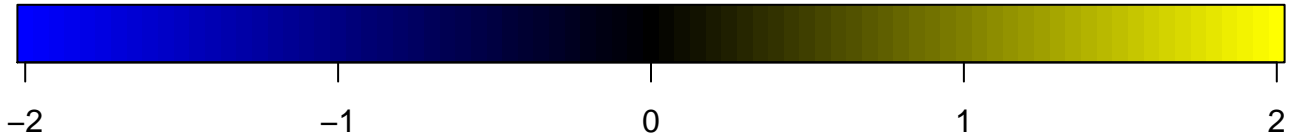
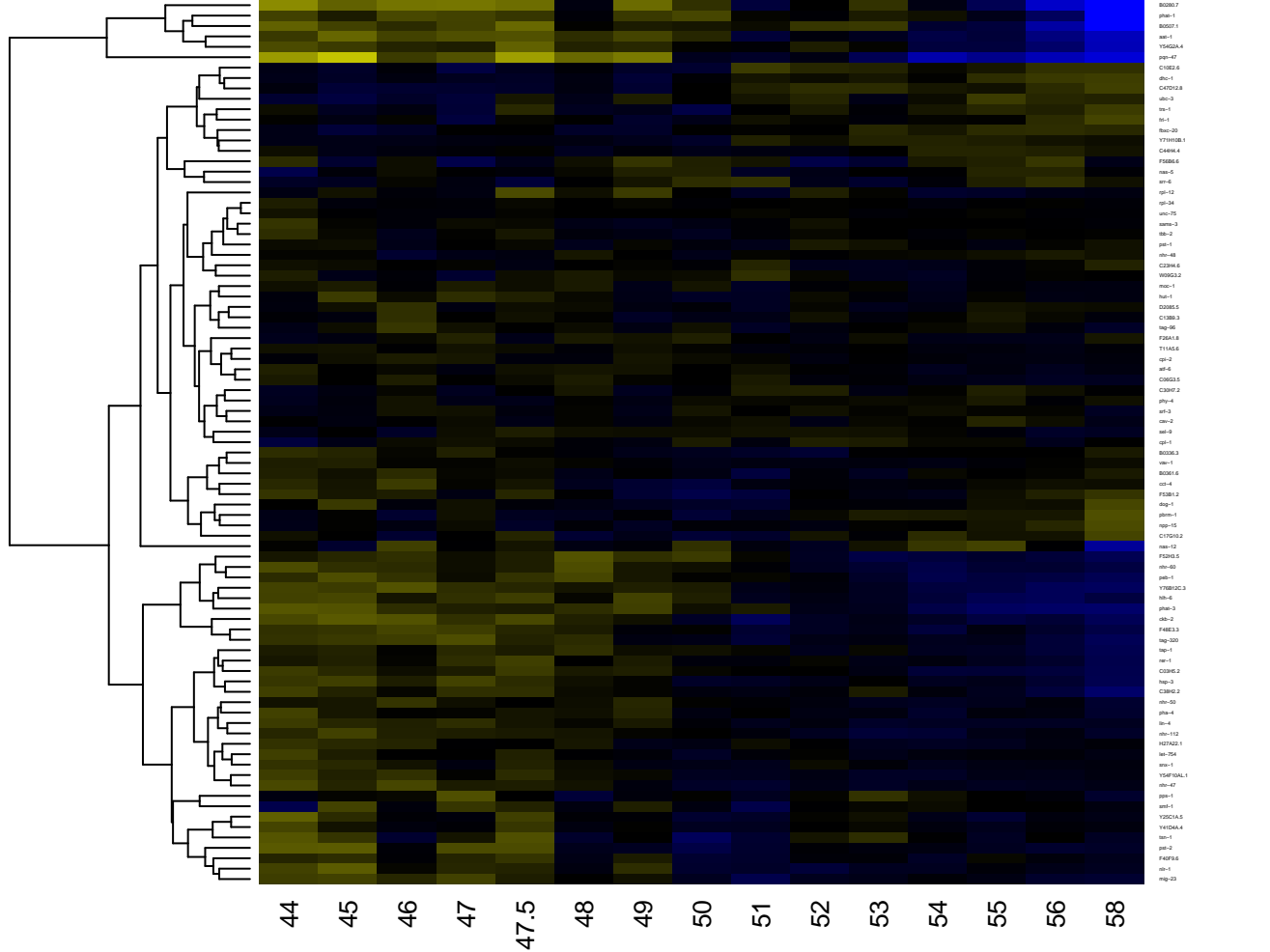
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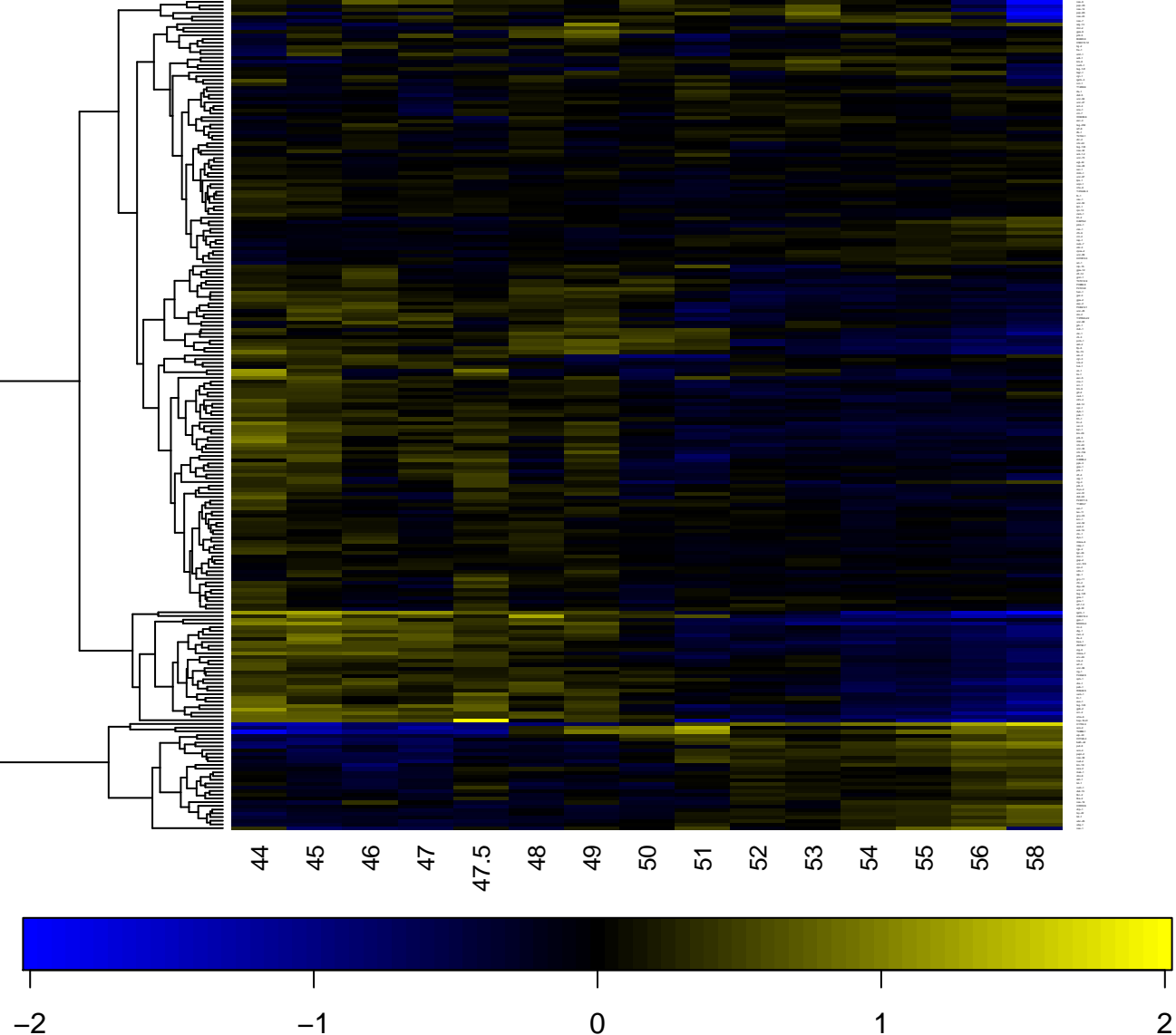
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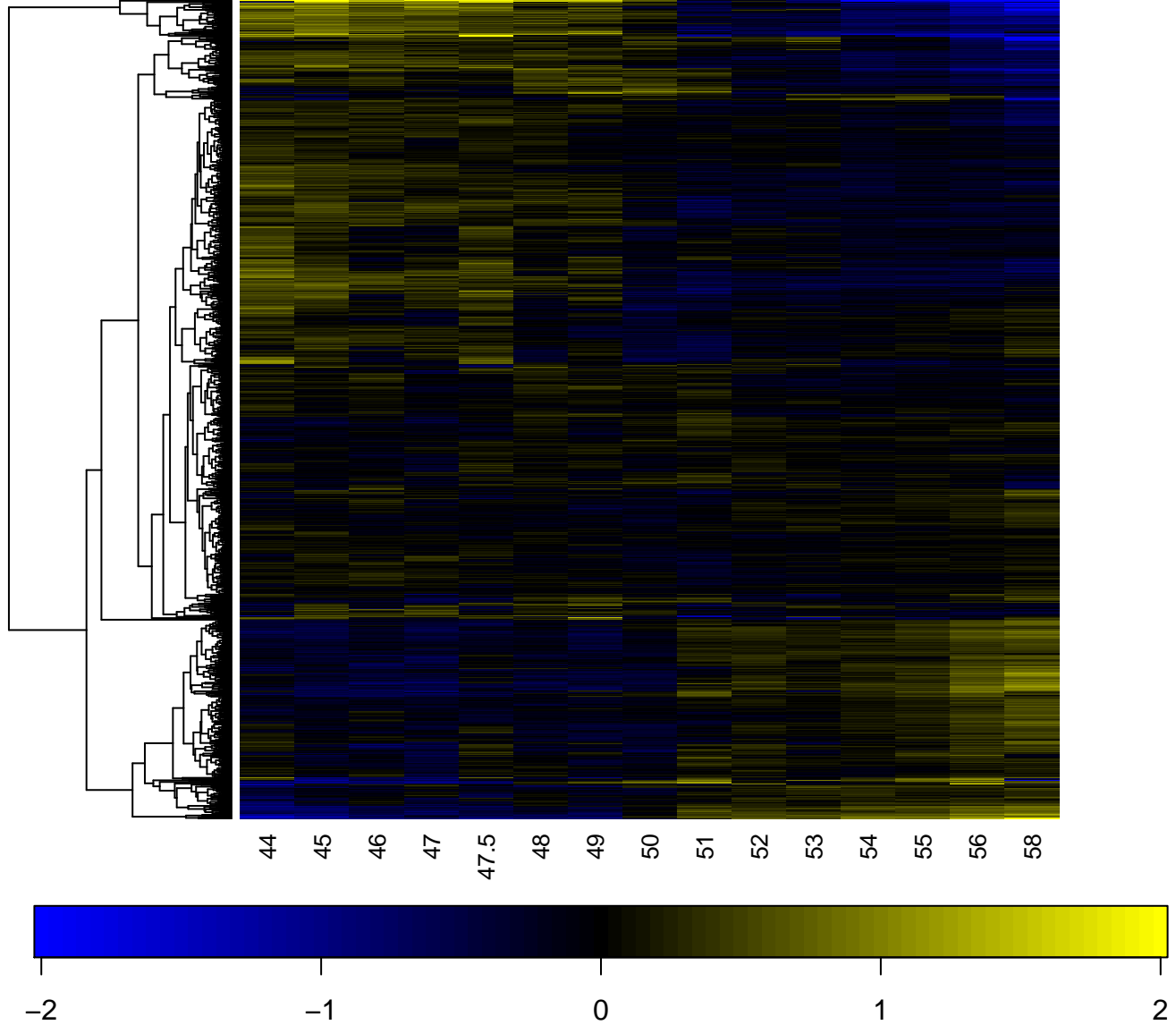
Pharyngeal gland cell



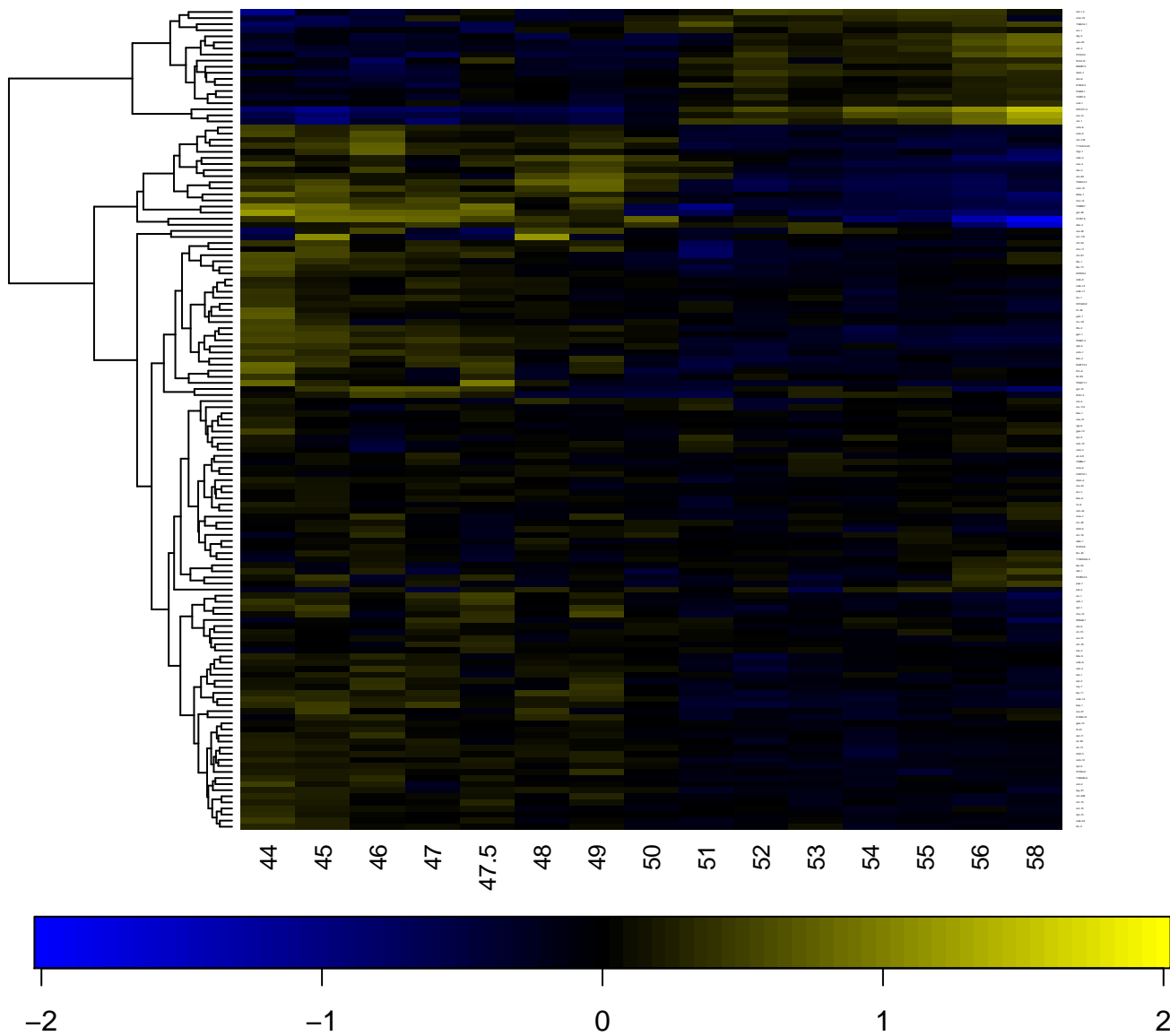
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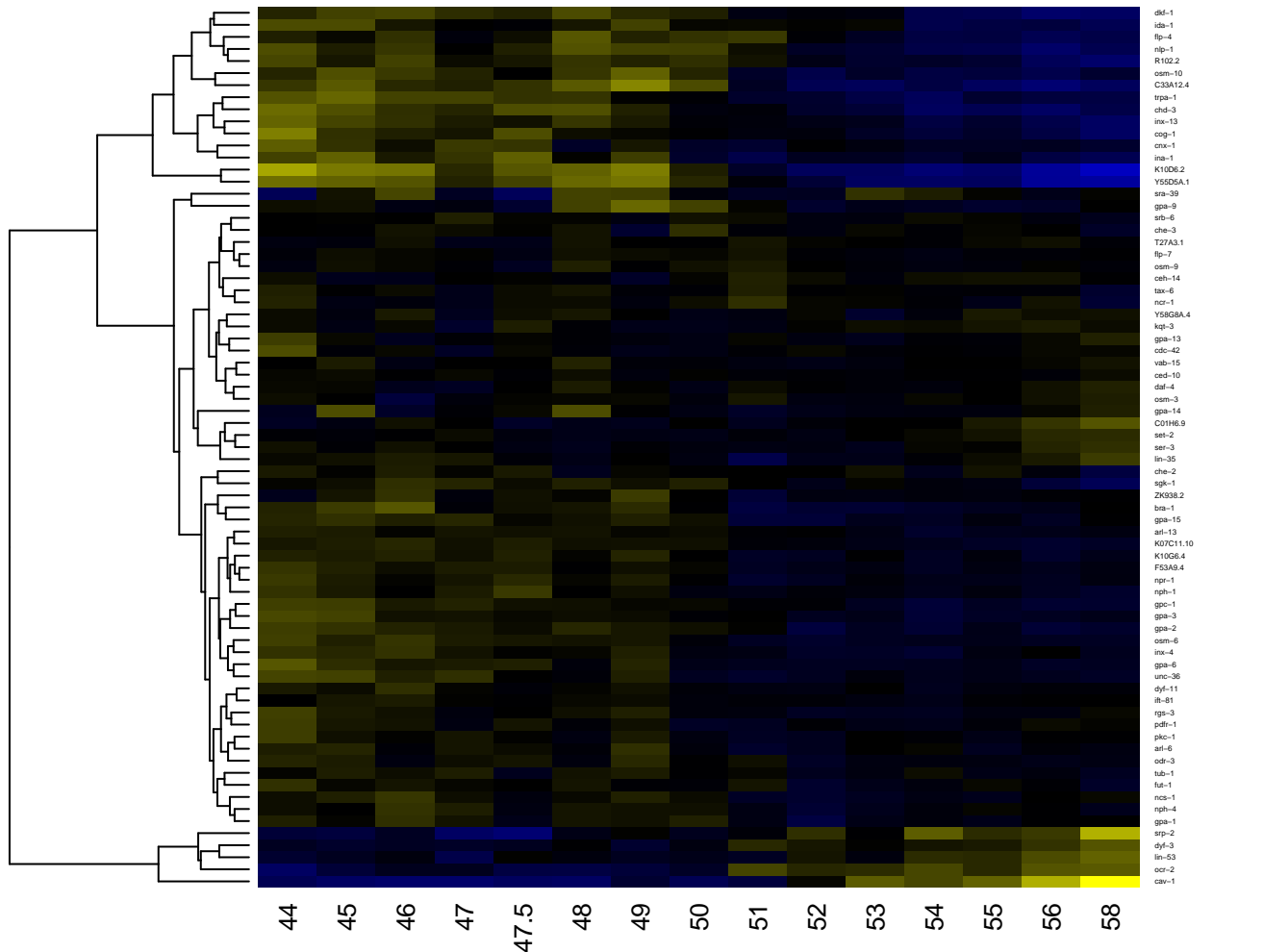
pharynx



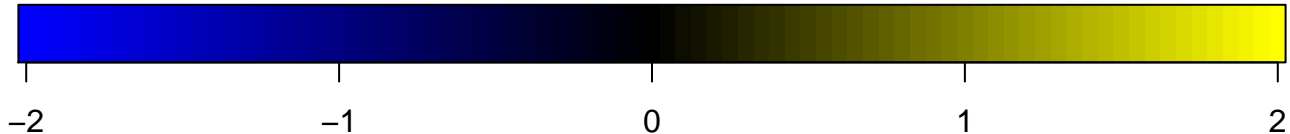
phasmid neuron



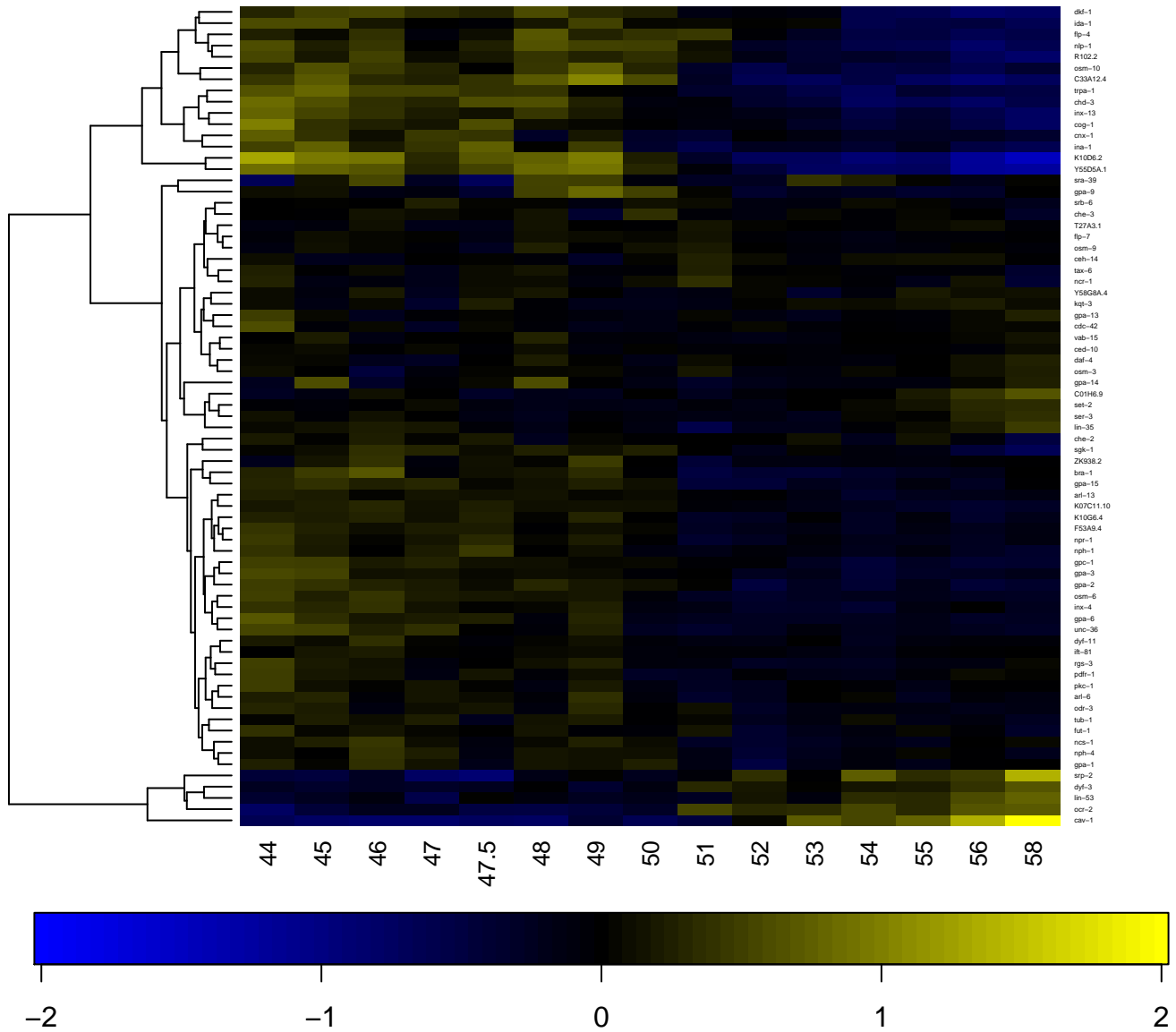
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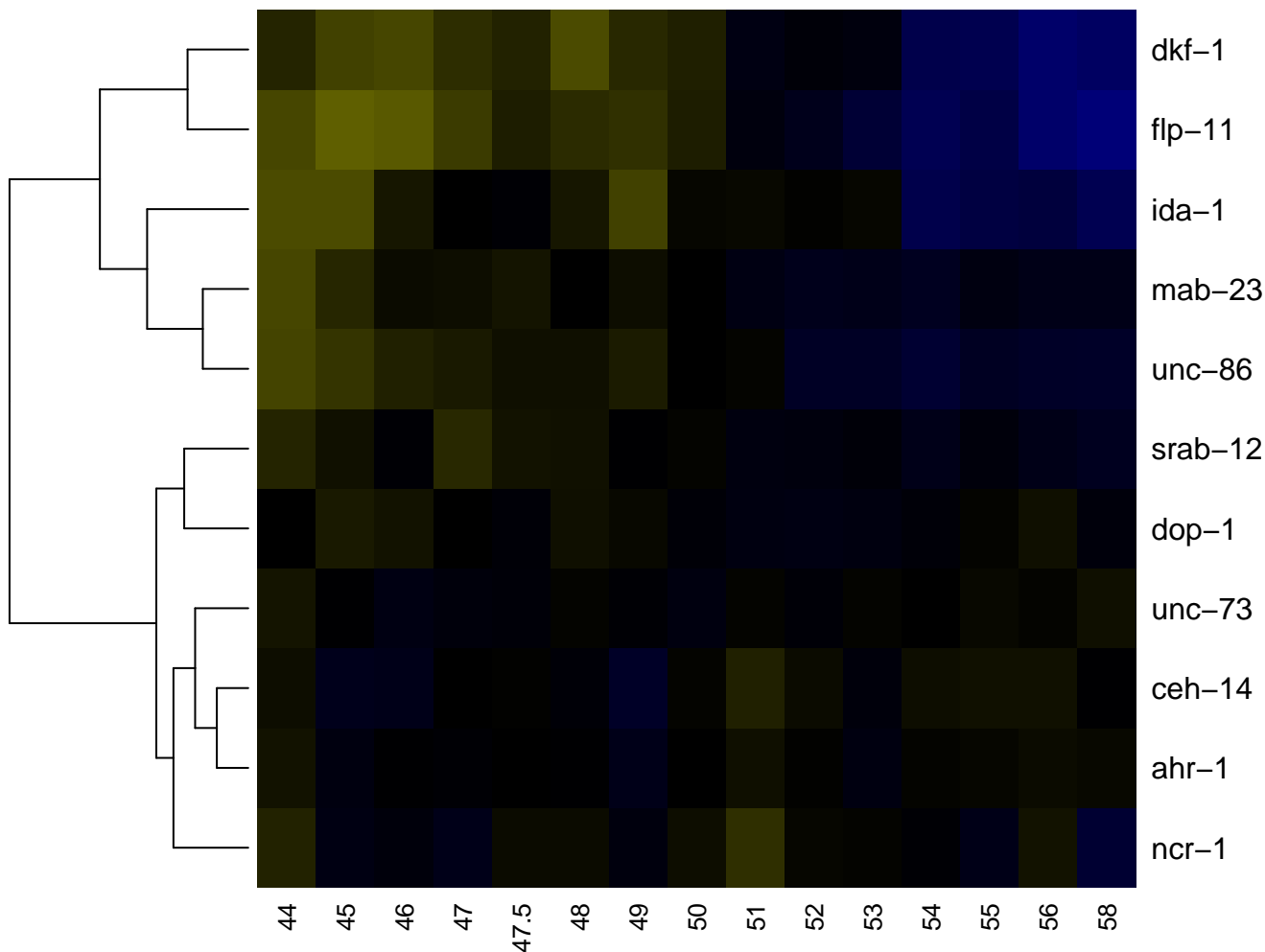
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ina-1
K1026.2
Y55DA.1
sra-39
gaa-9
srb-6
che-3
T27A3.1
fp-7
osm-9
ceh-14
tax-6
ncr-1
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kqt-3
gaa-13
cdt-42
vab-15
ced-10
daf-4
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set-2
set-3
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che-2
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gaa-15
arl-13
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gaa-3
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inx-4
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unc-36
dyf-11
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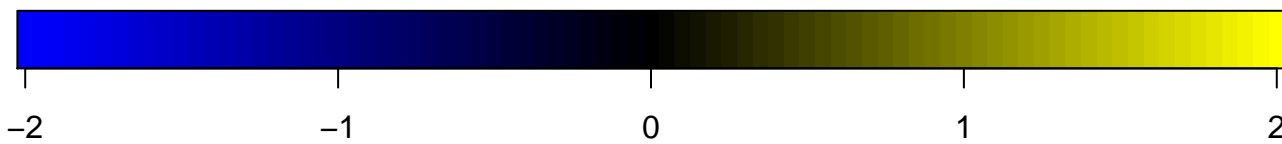
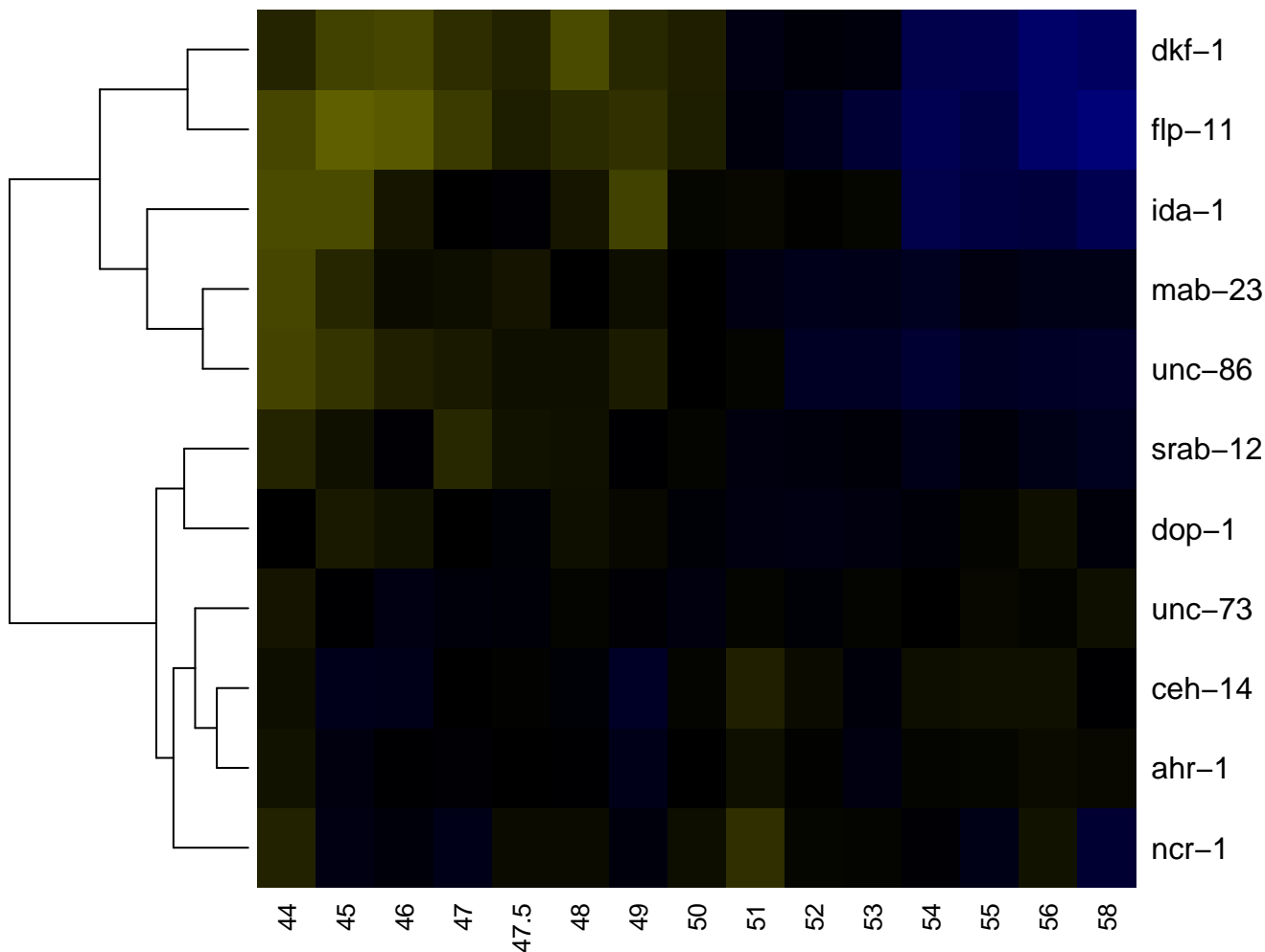
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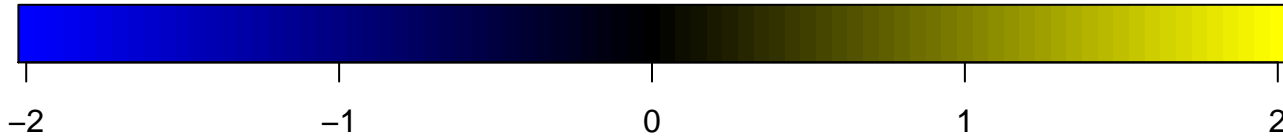
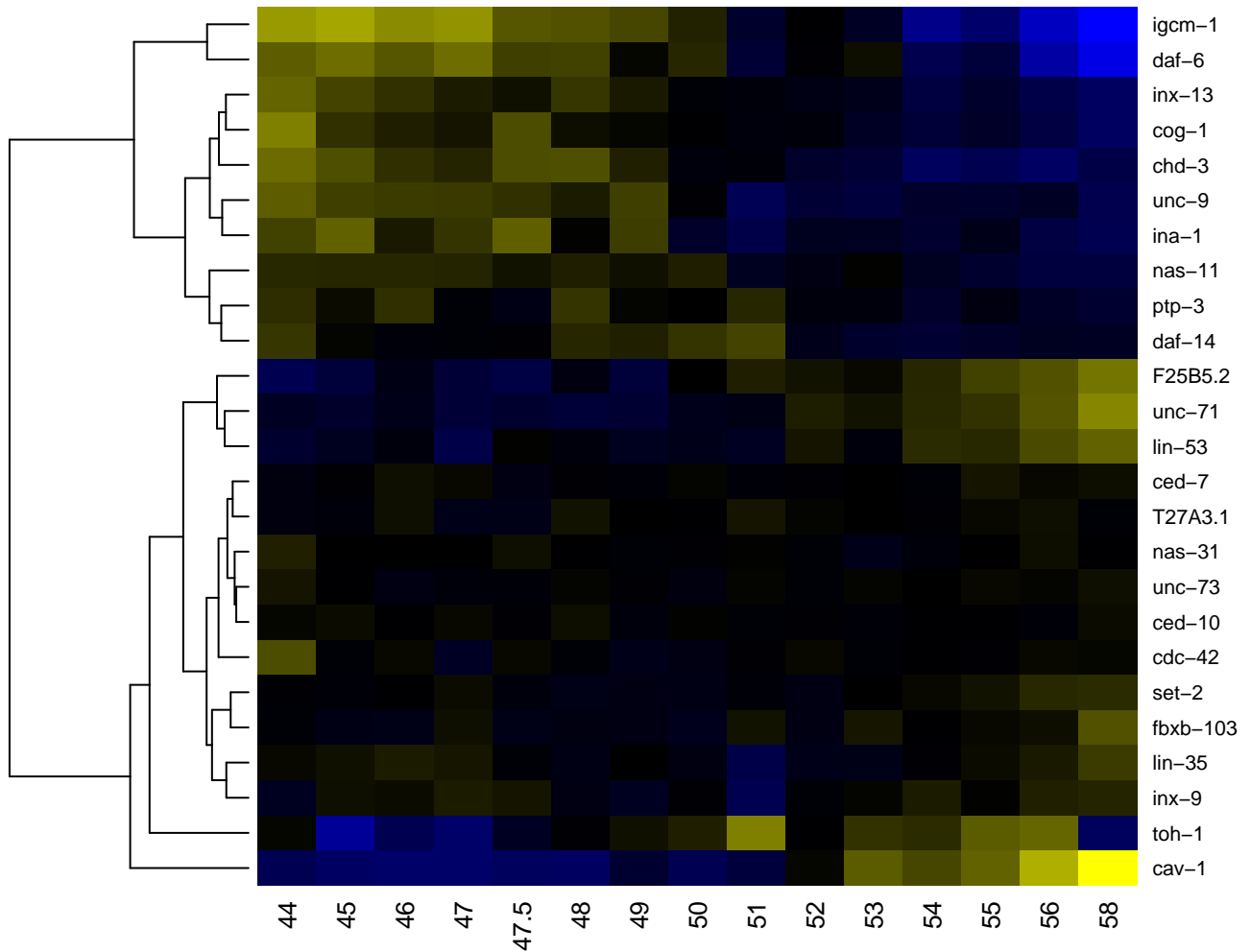
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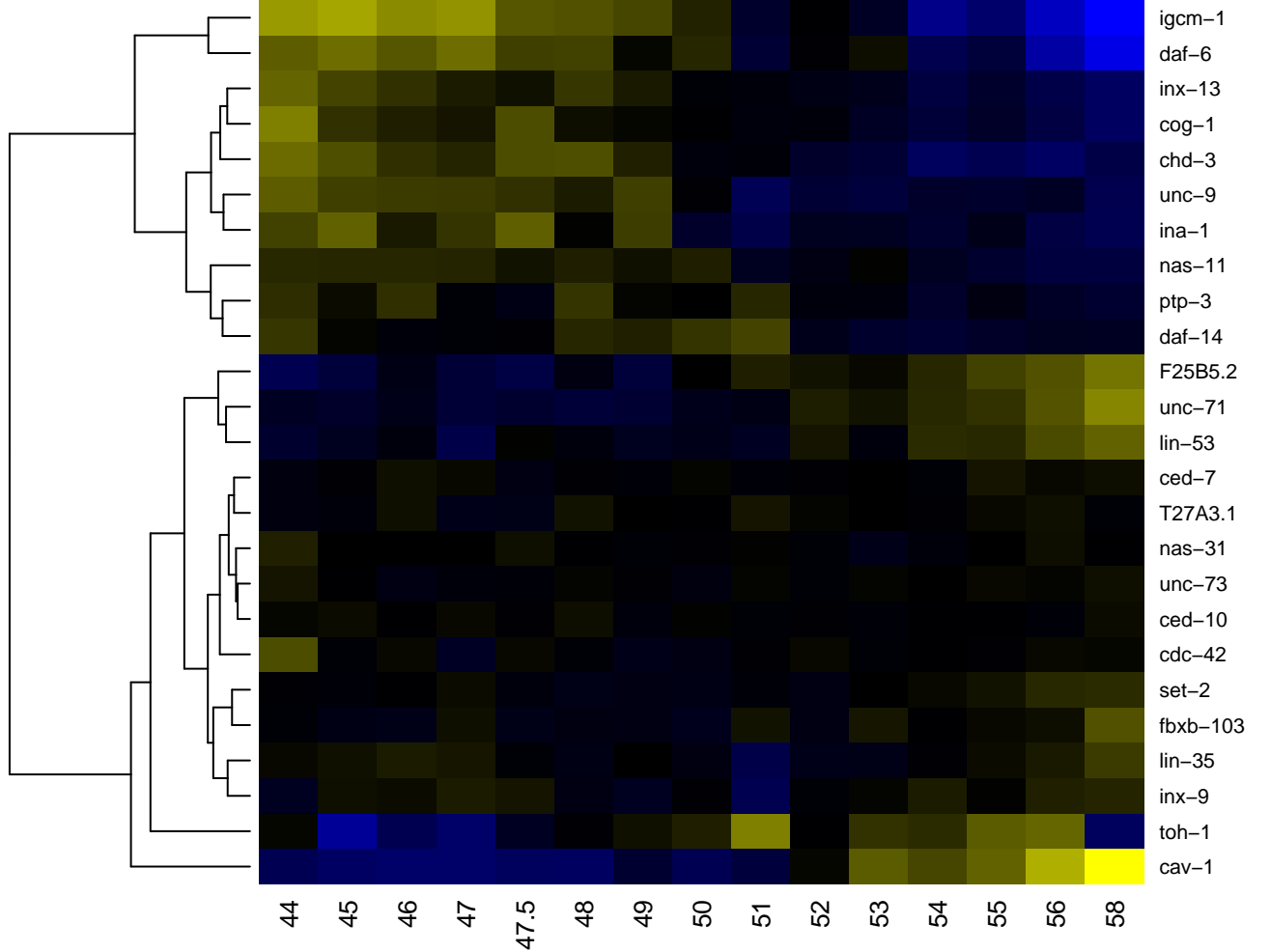
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PHshL



PHshR



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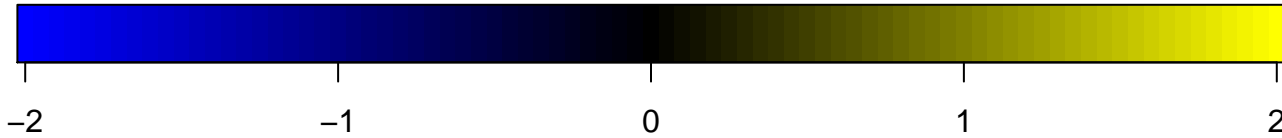
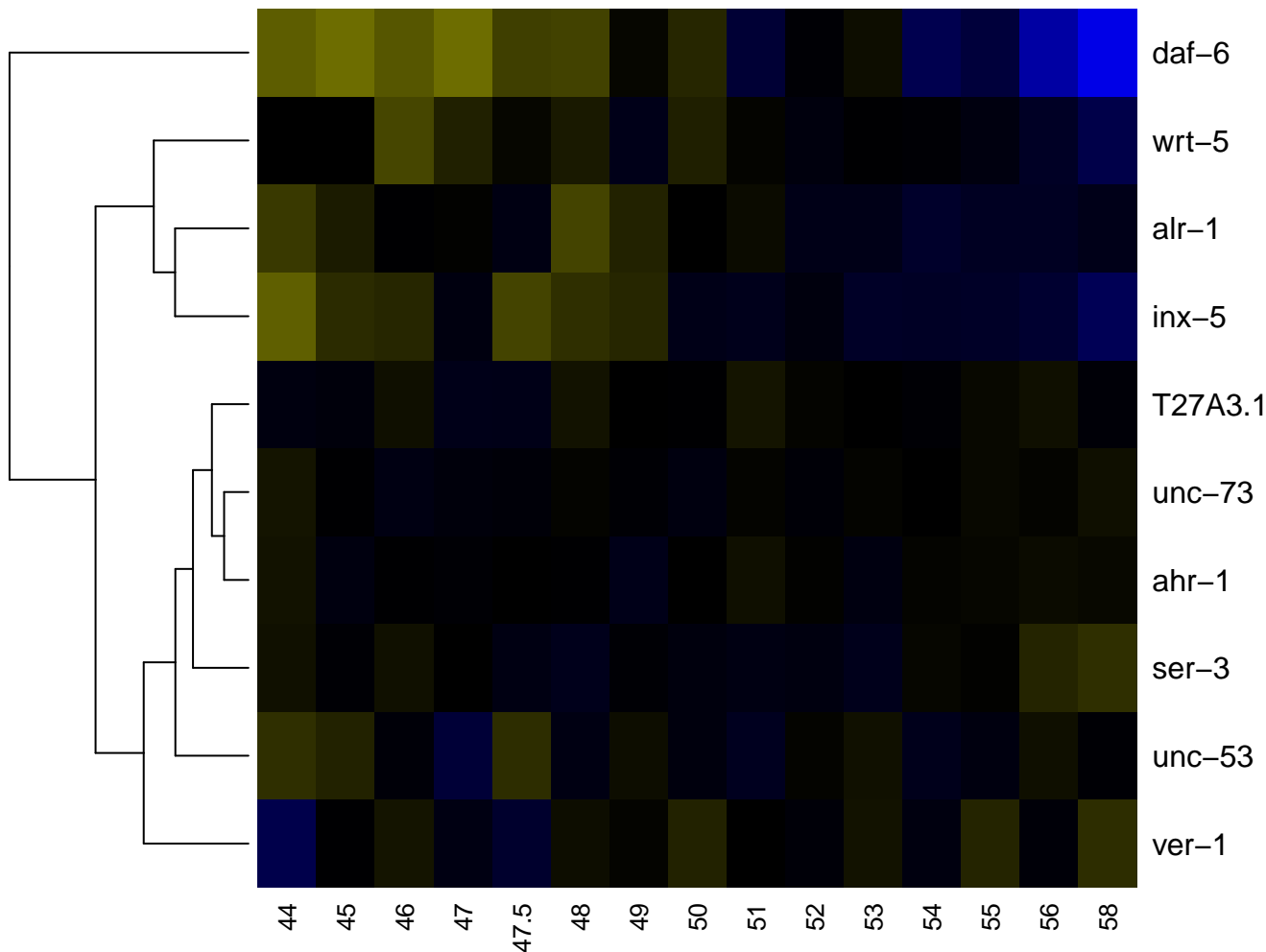
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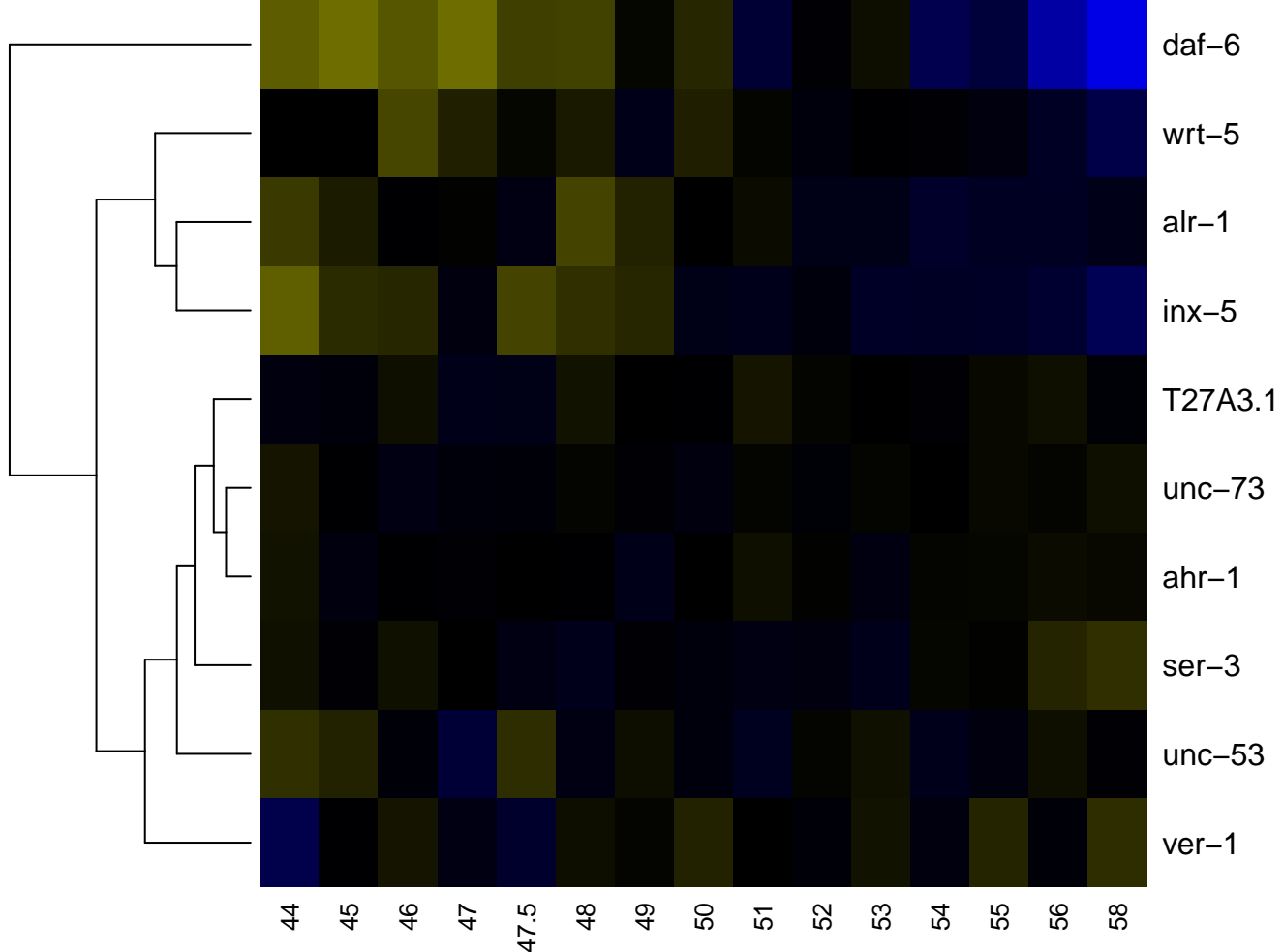
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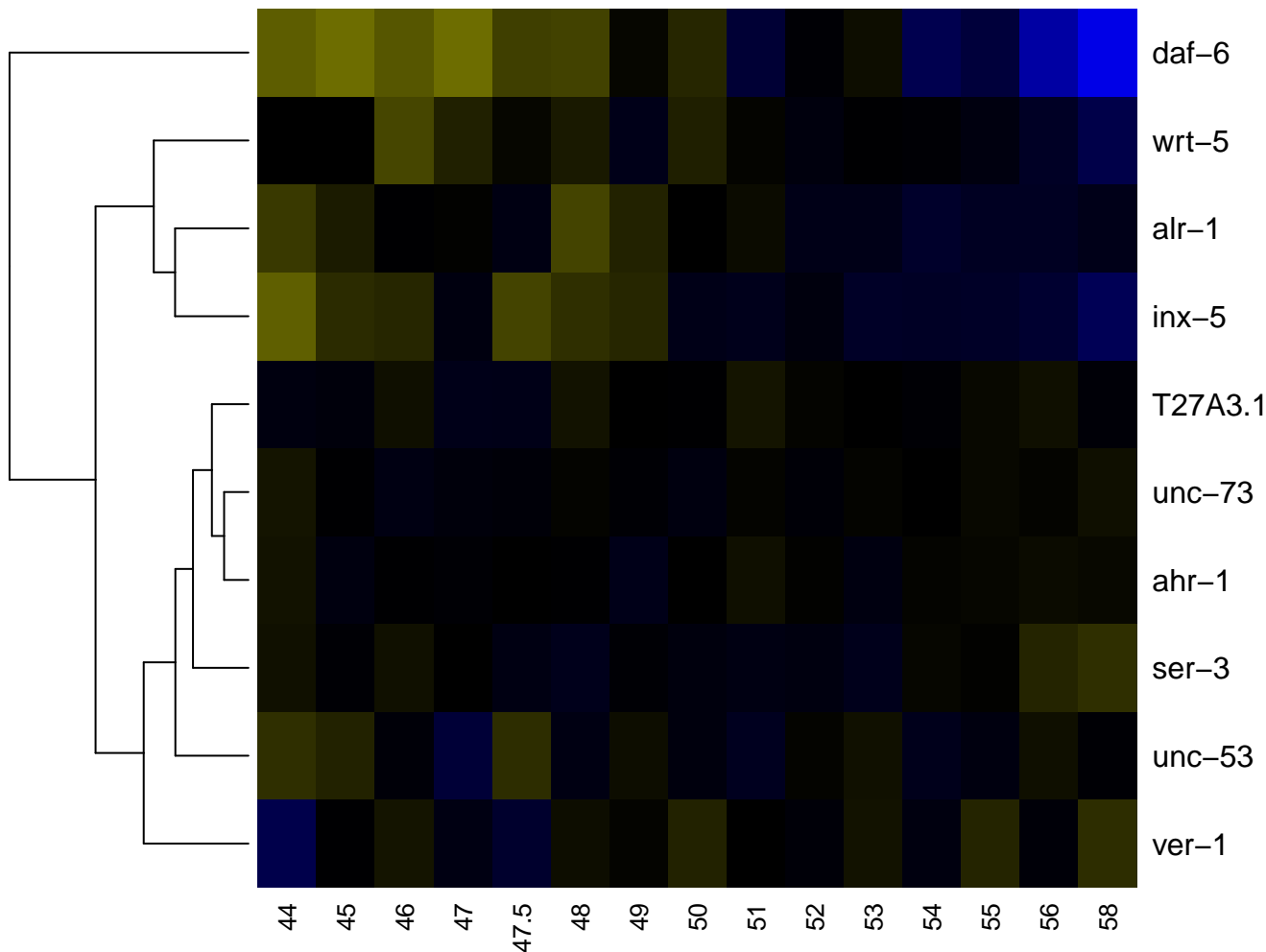
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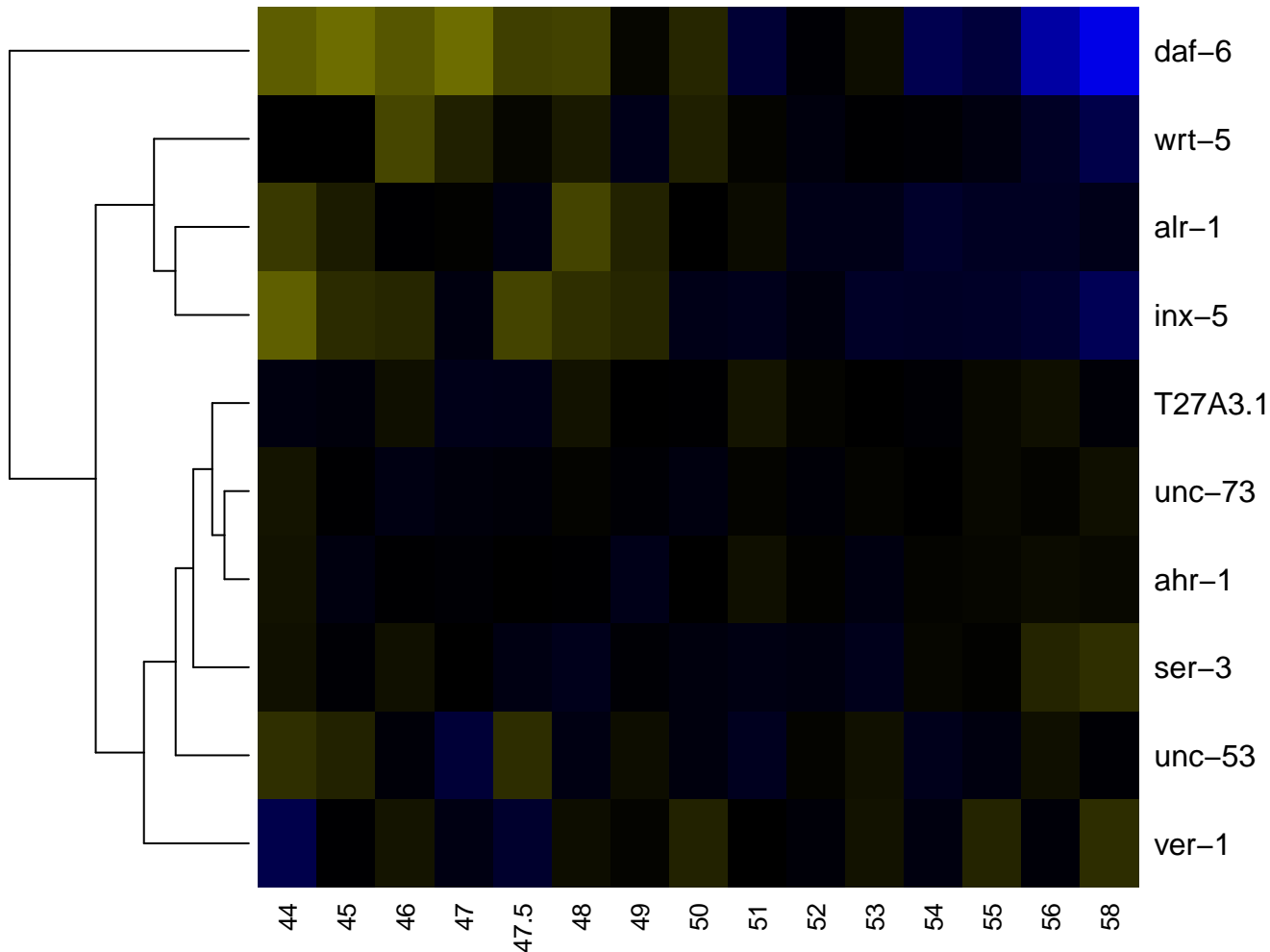
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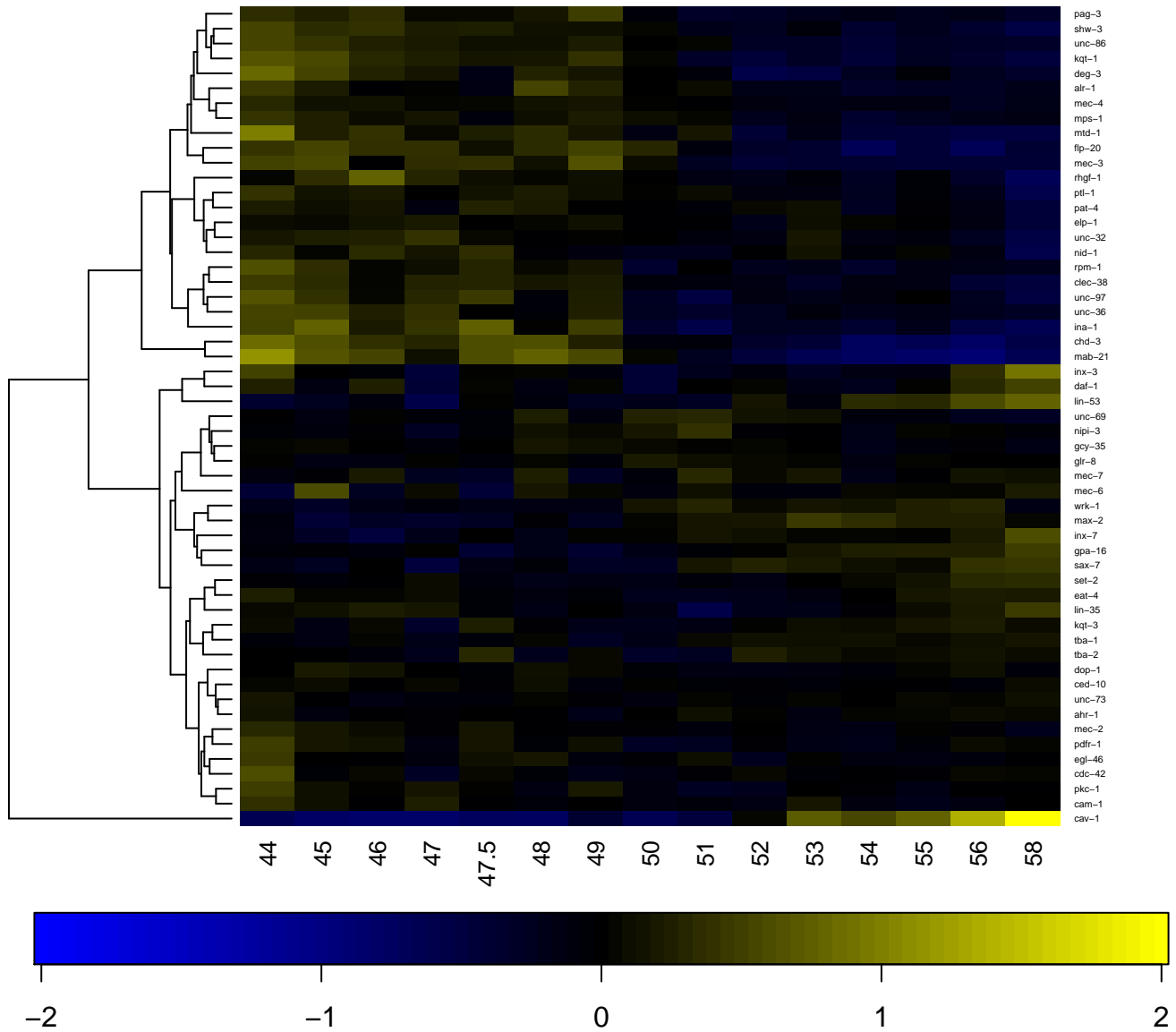
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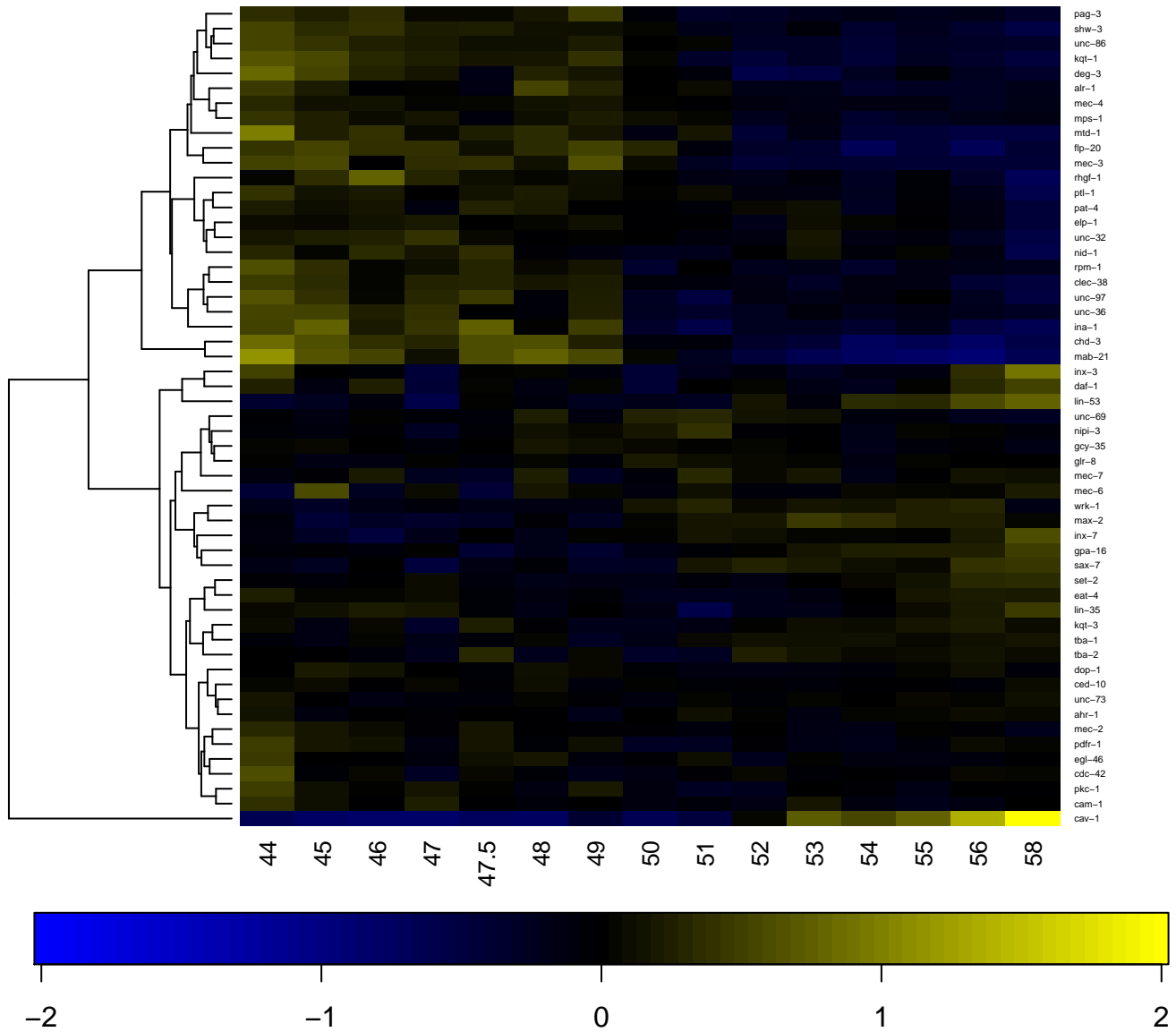
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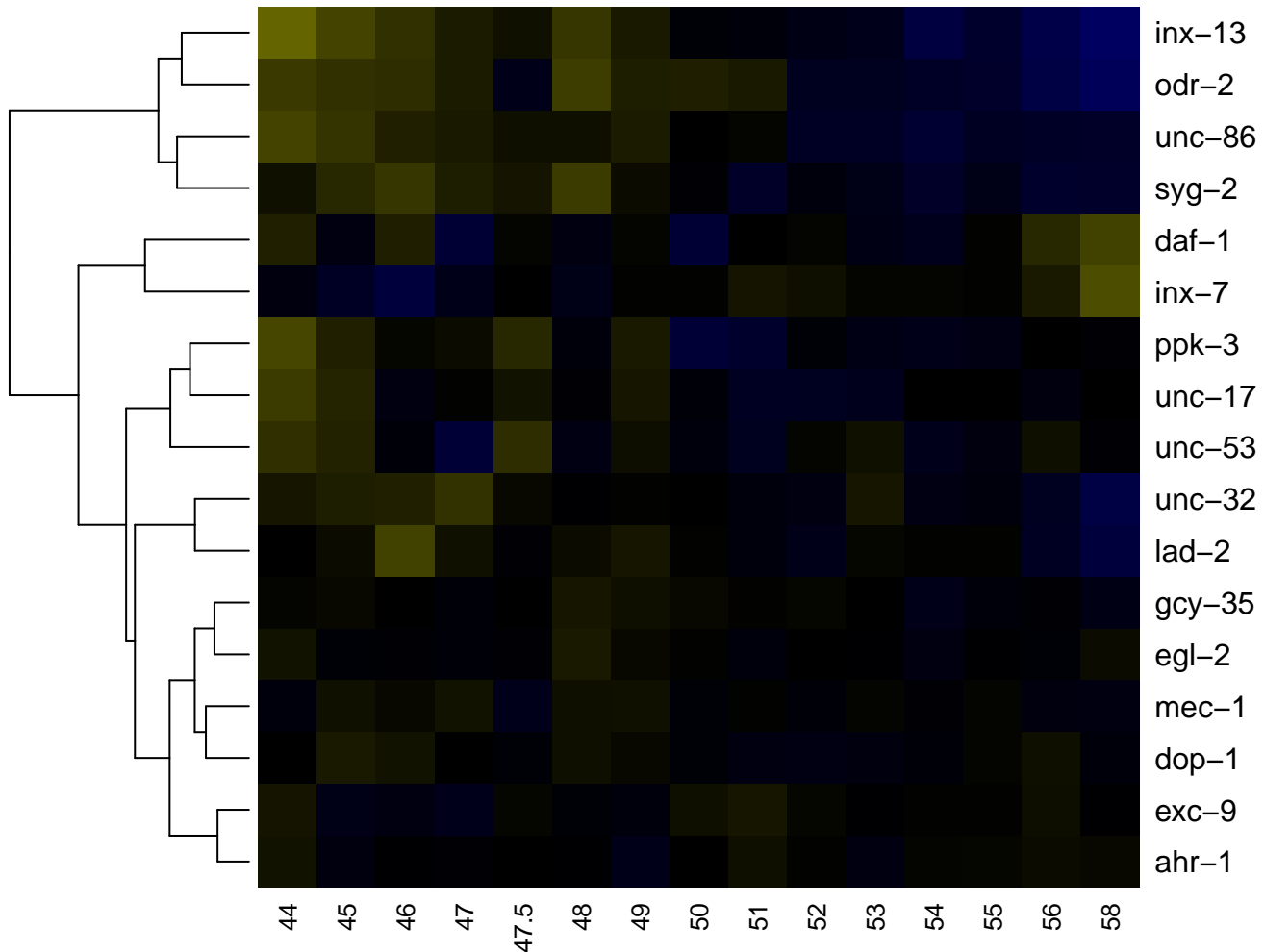
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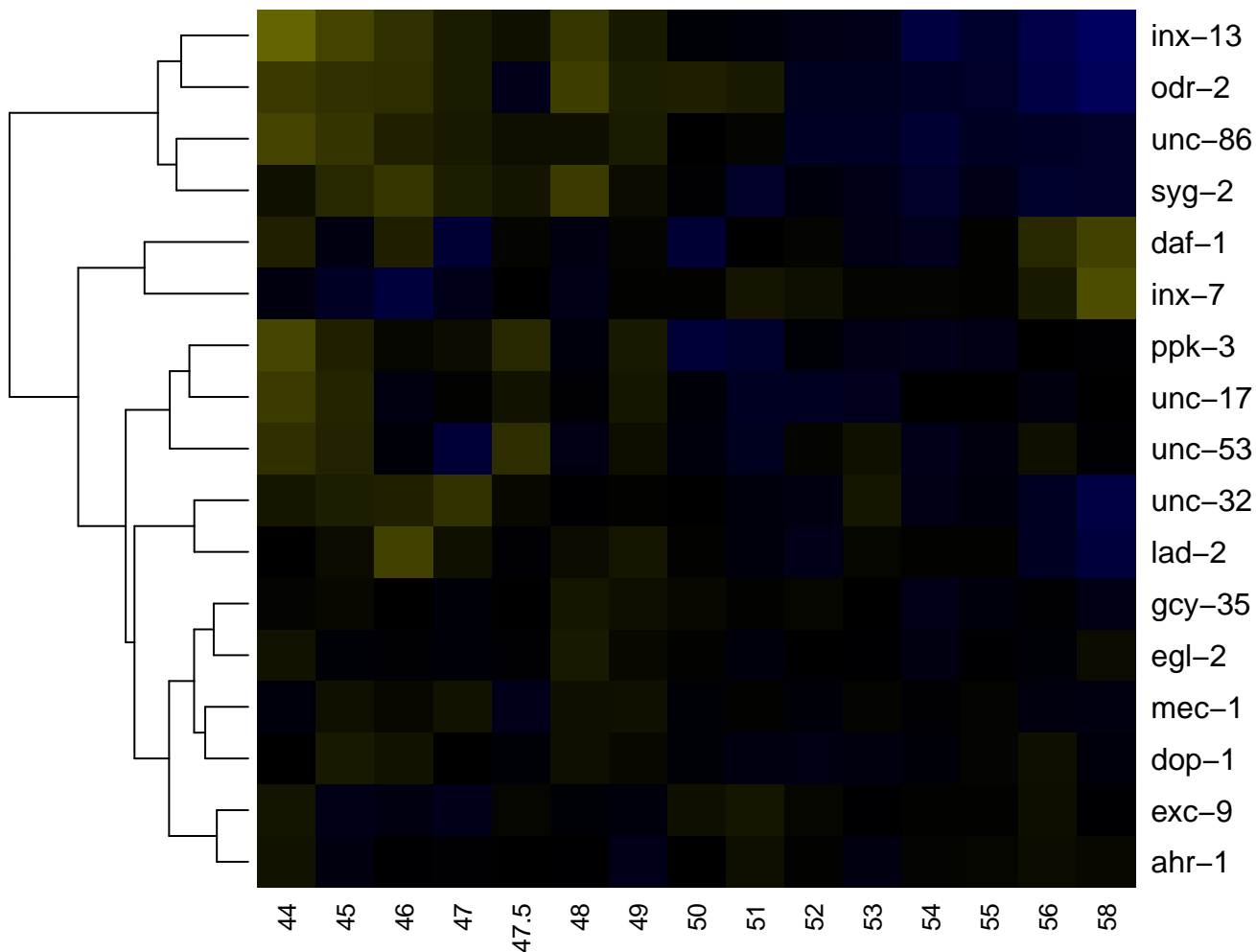
PLMR



PLNL



PLNR



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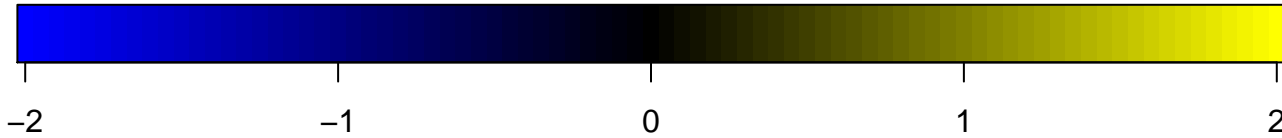
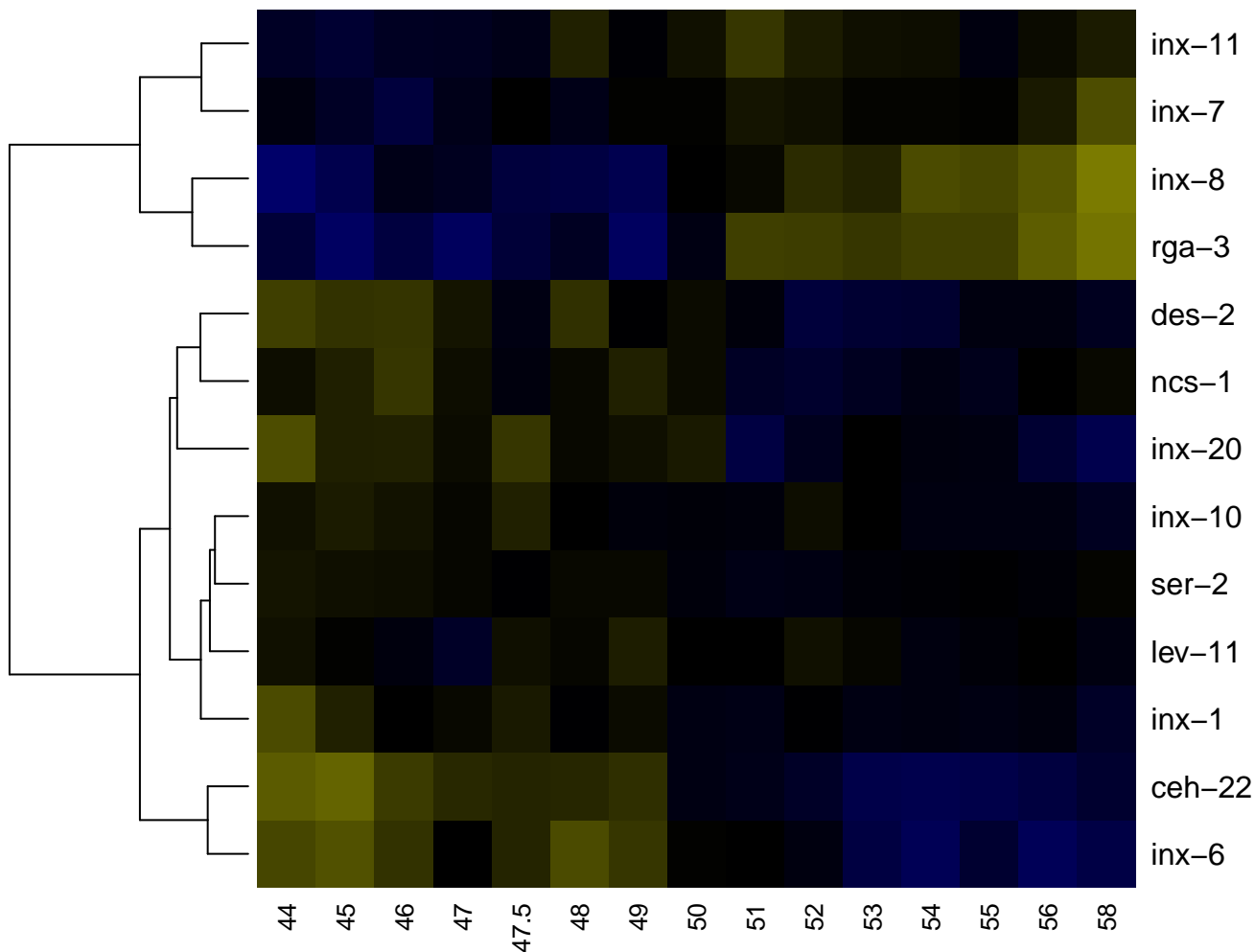
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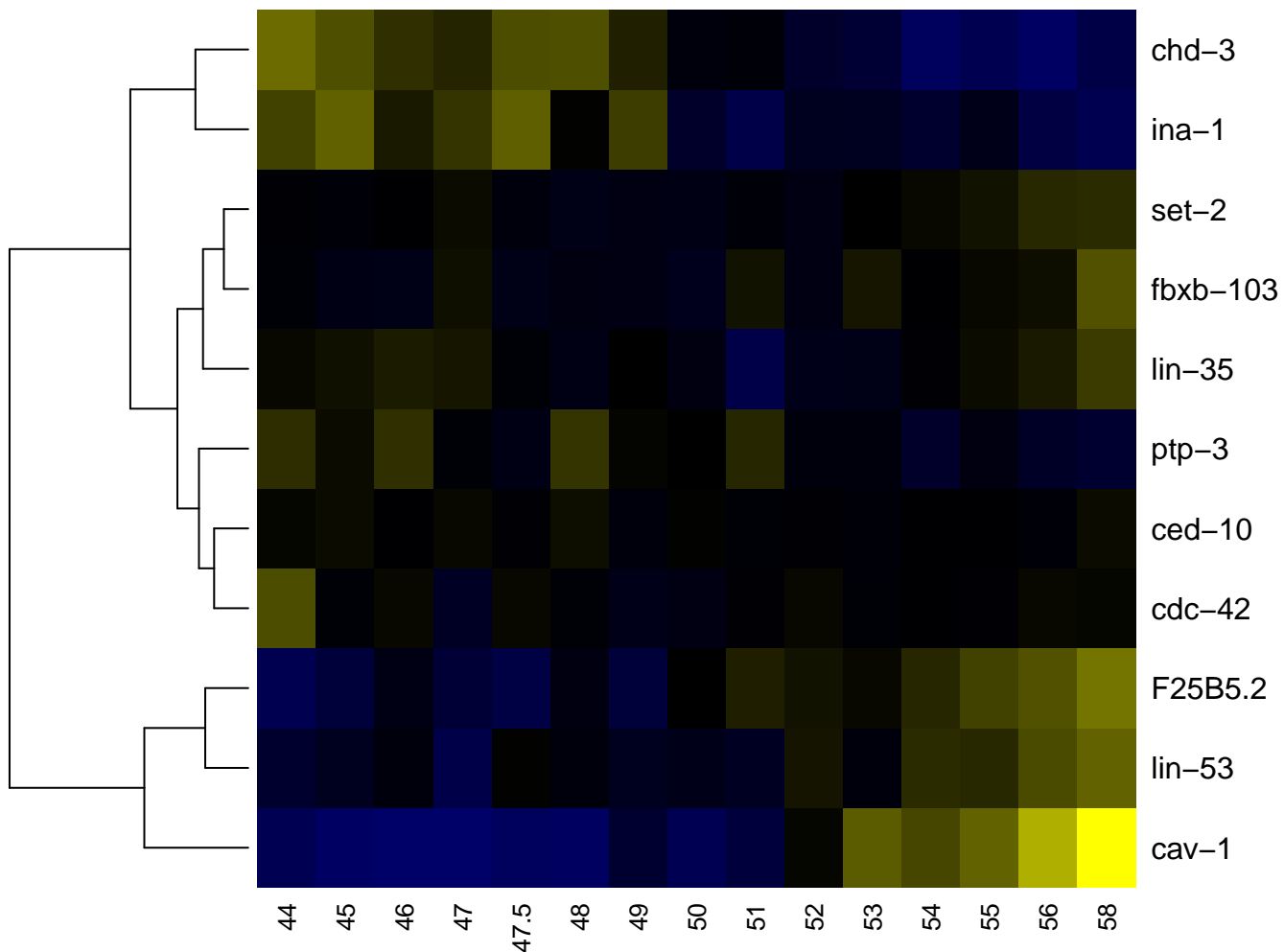
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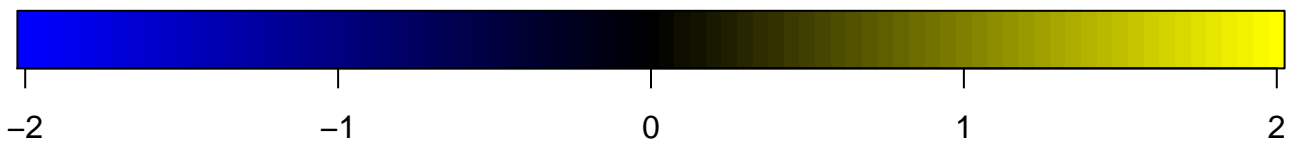
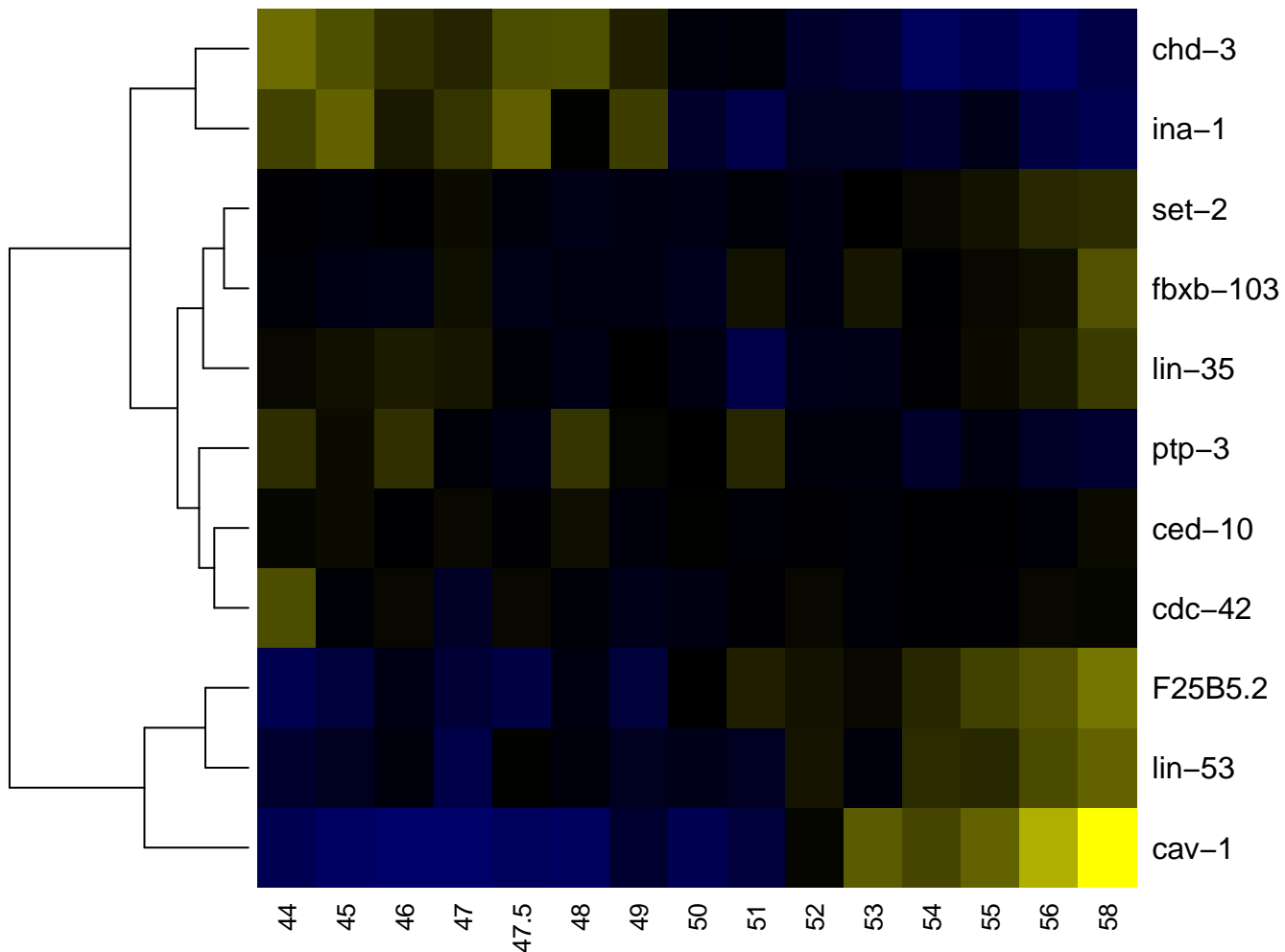
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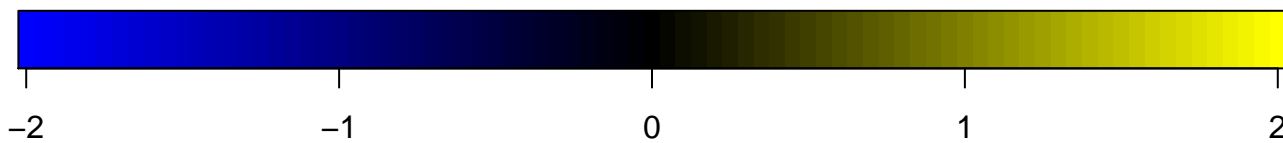
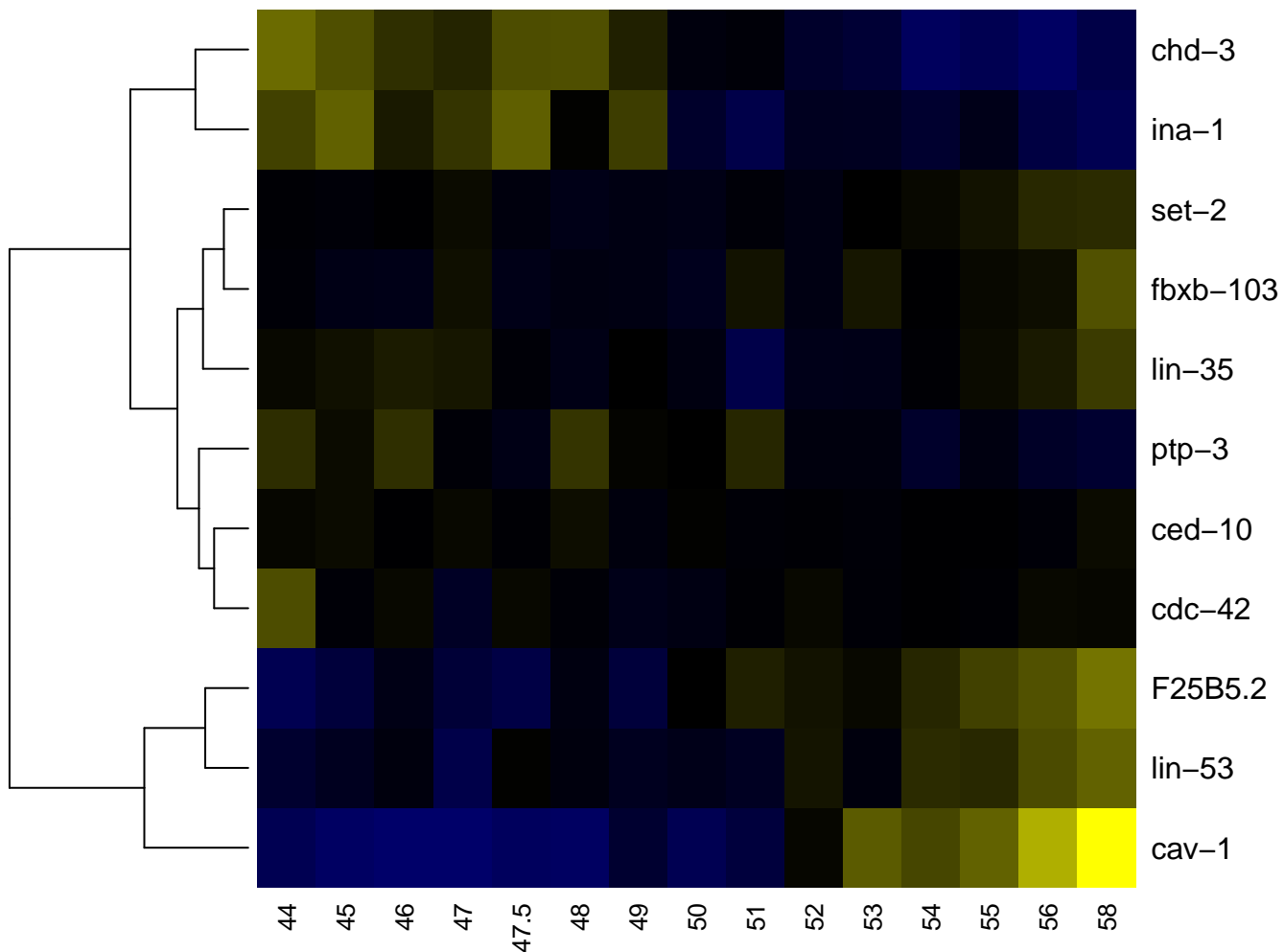
pm1DL



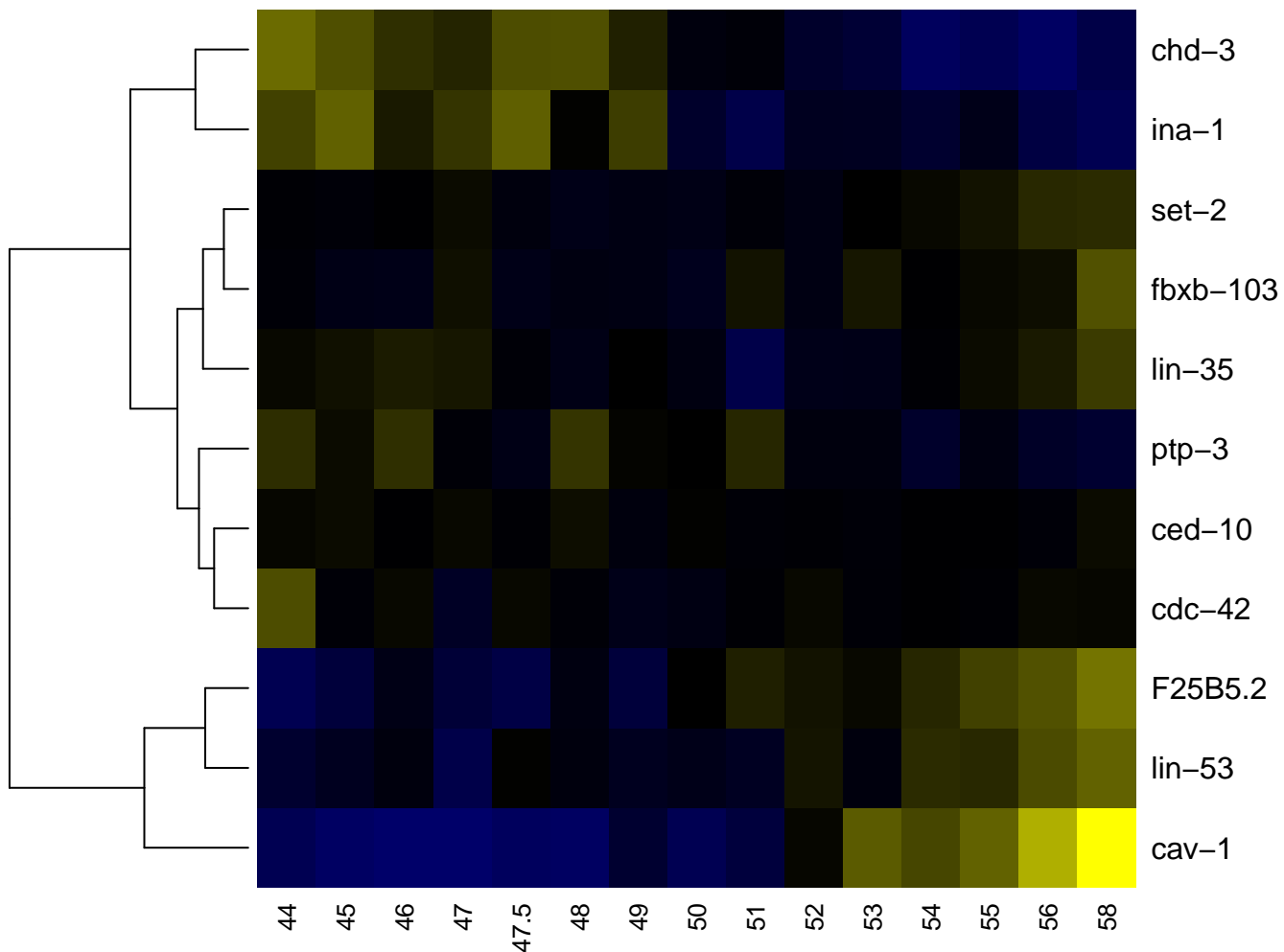
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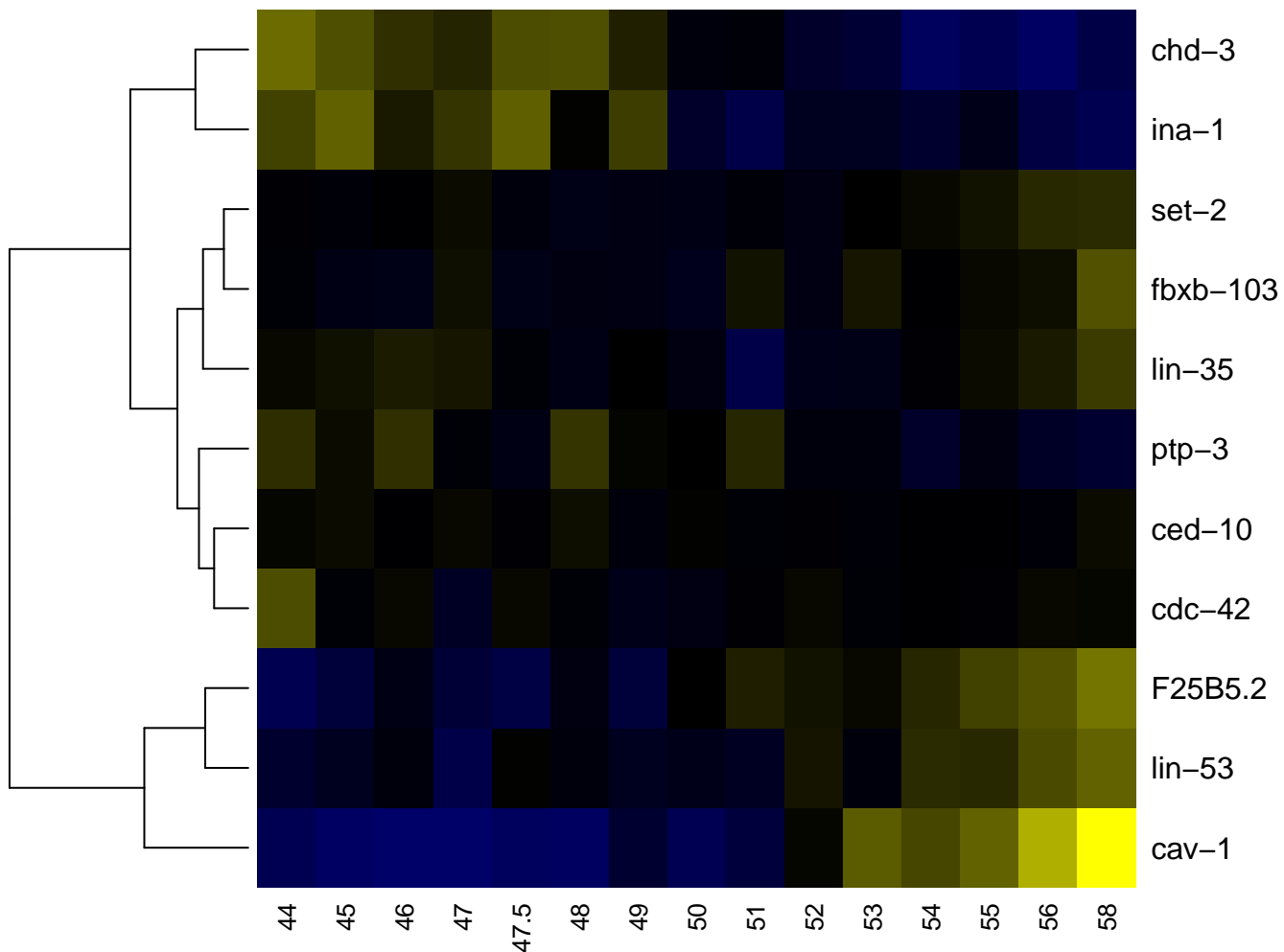
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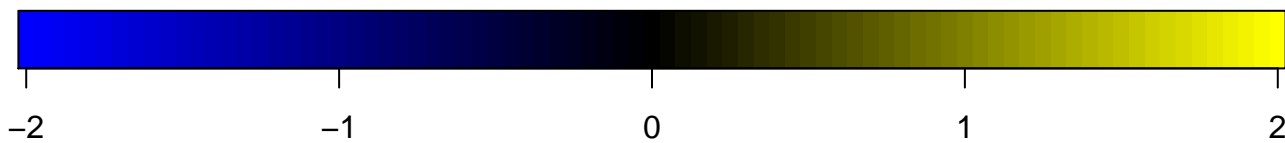
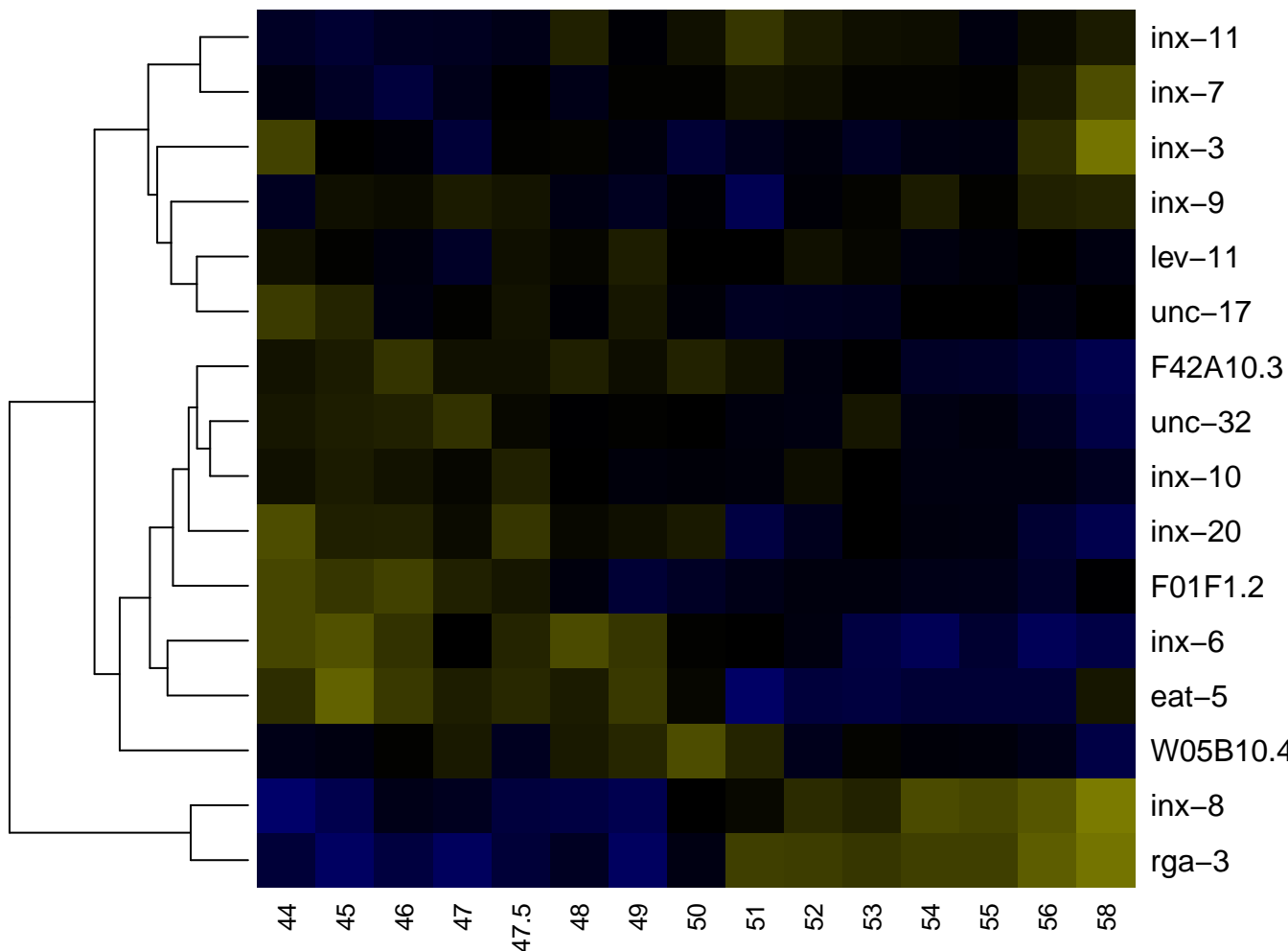
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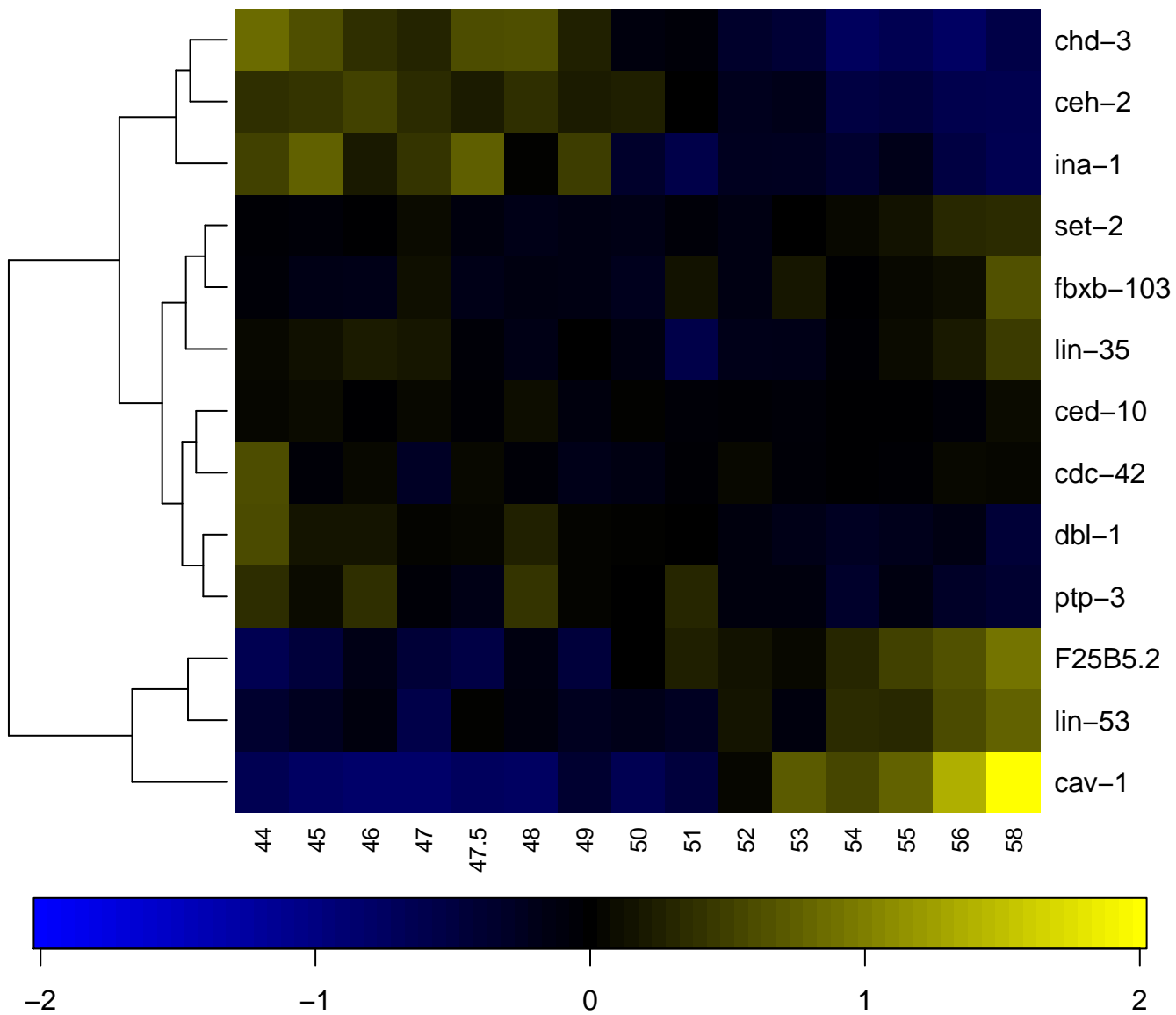
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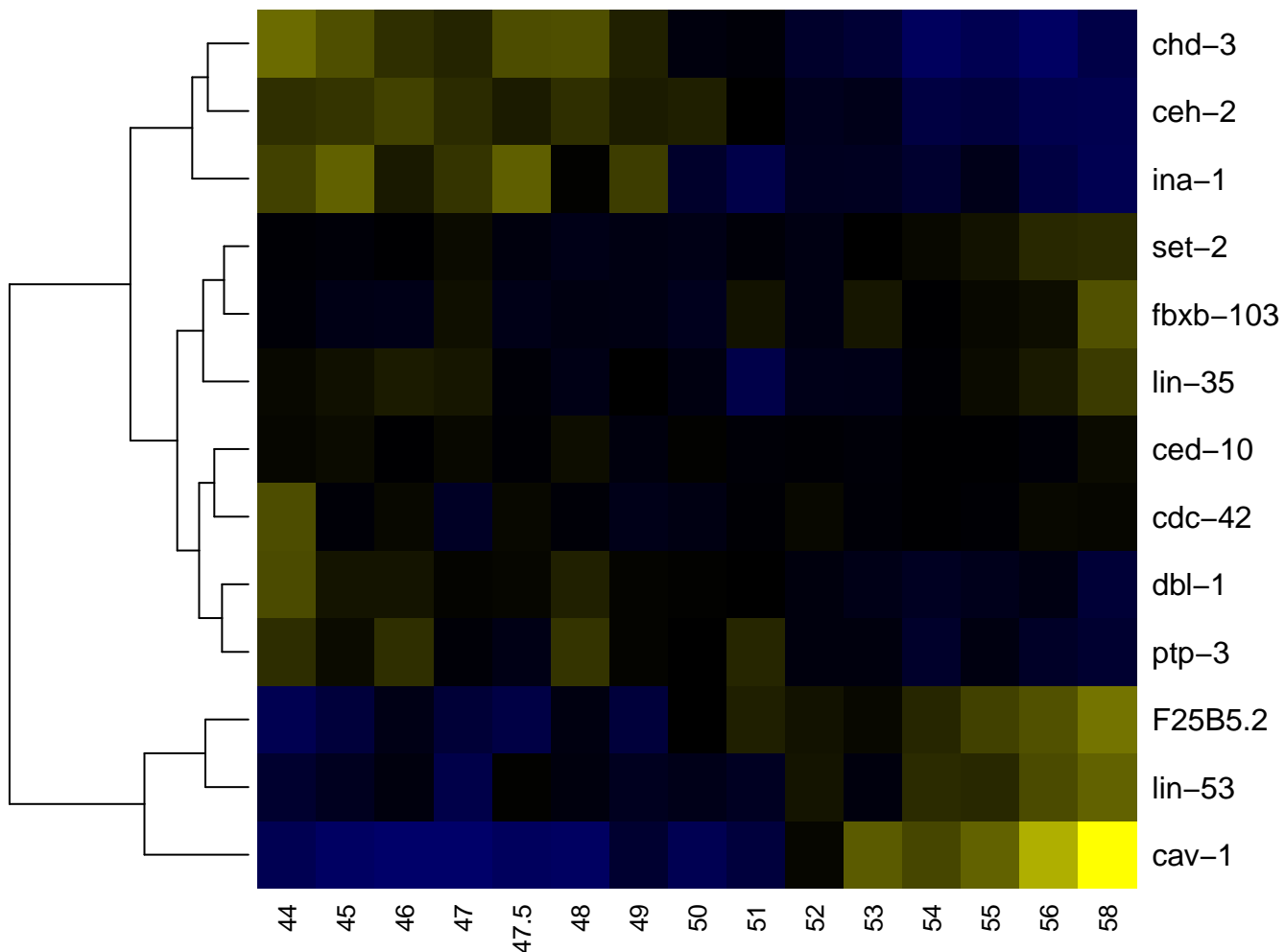
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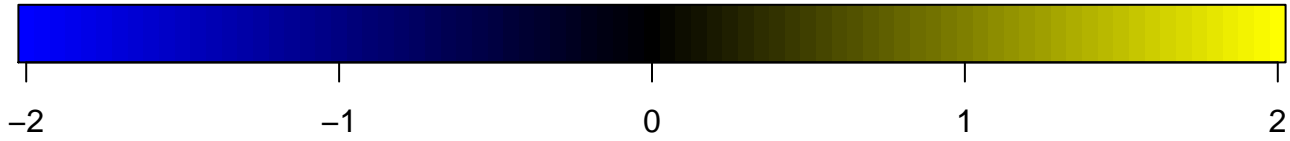
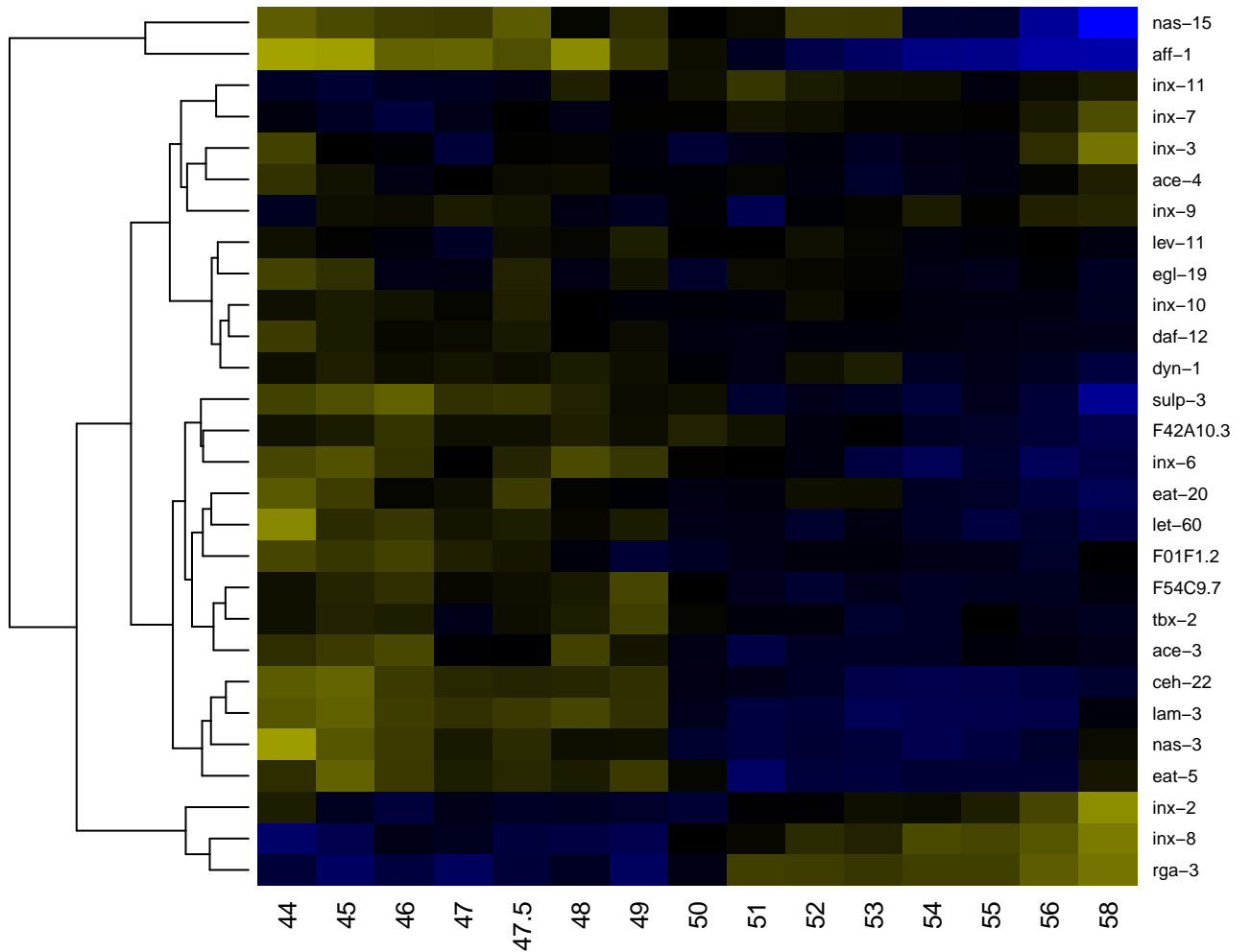
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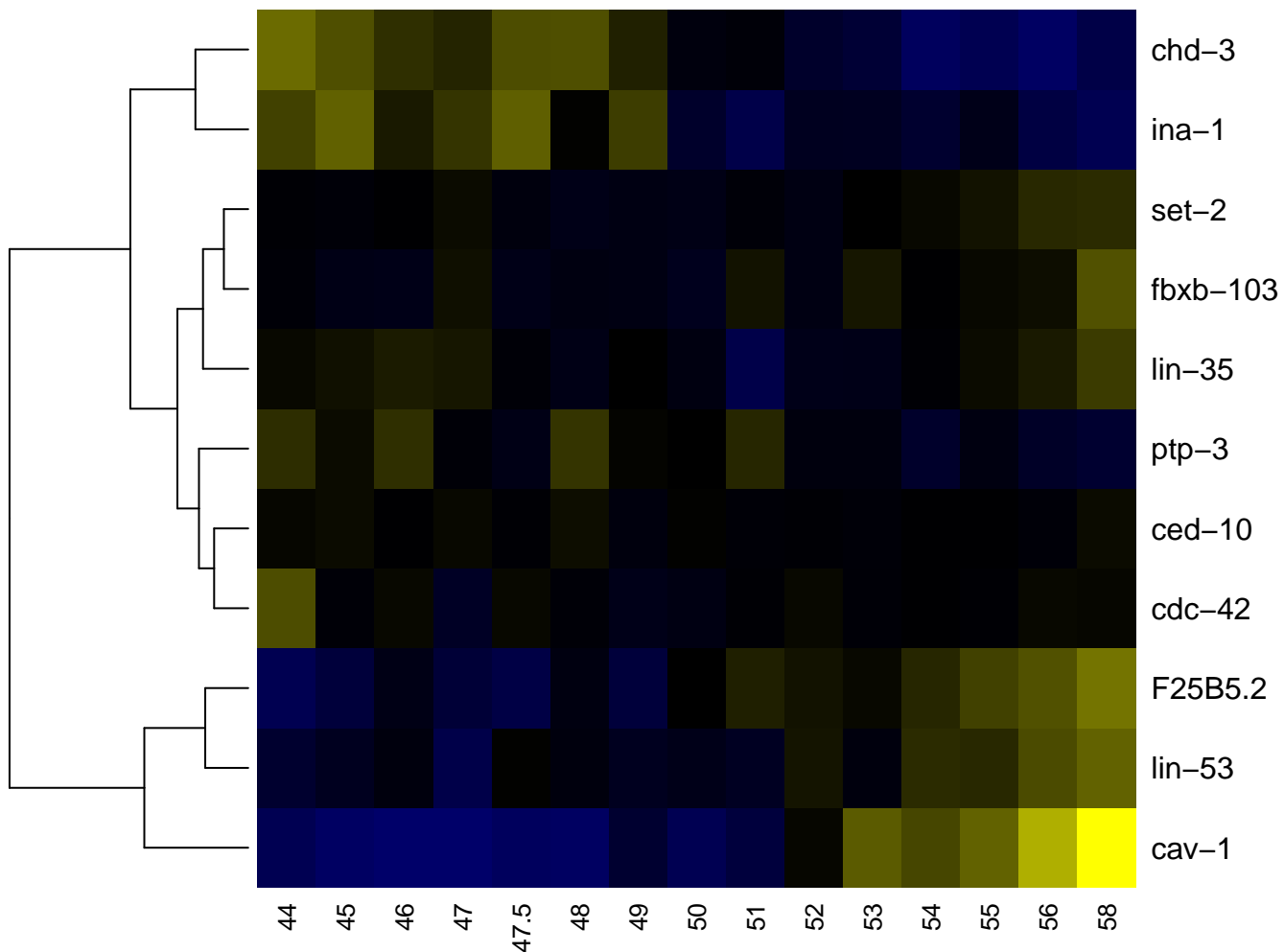
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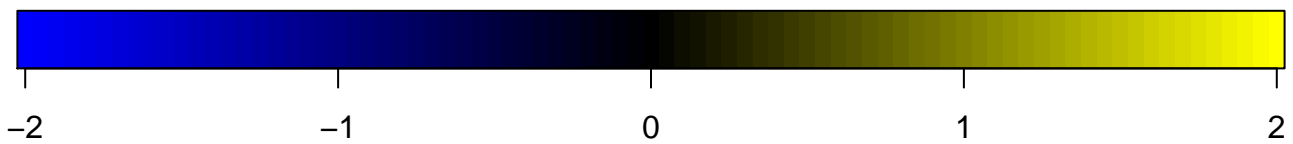
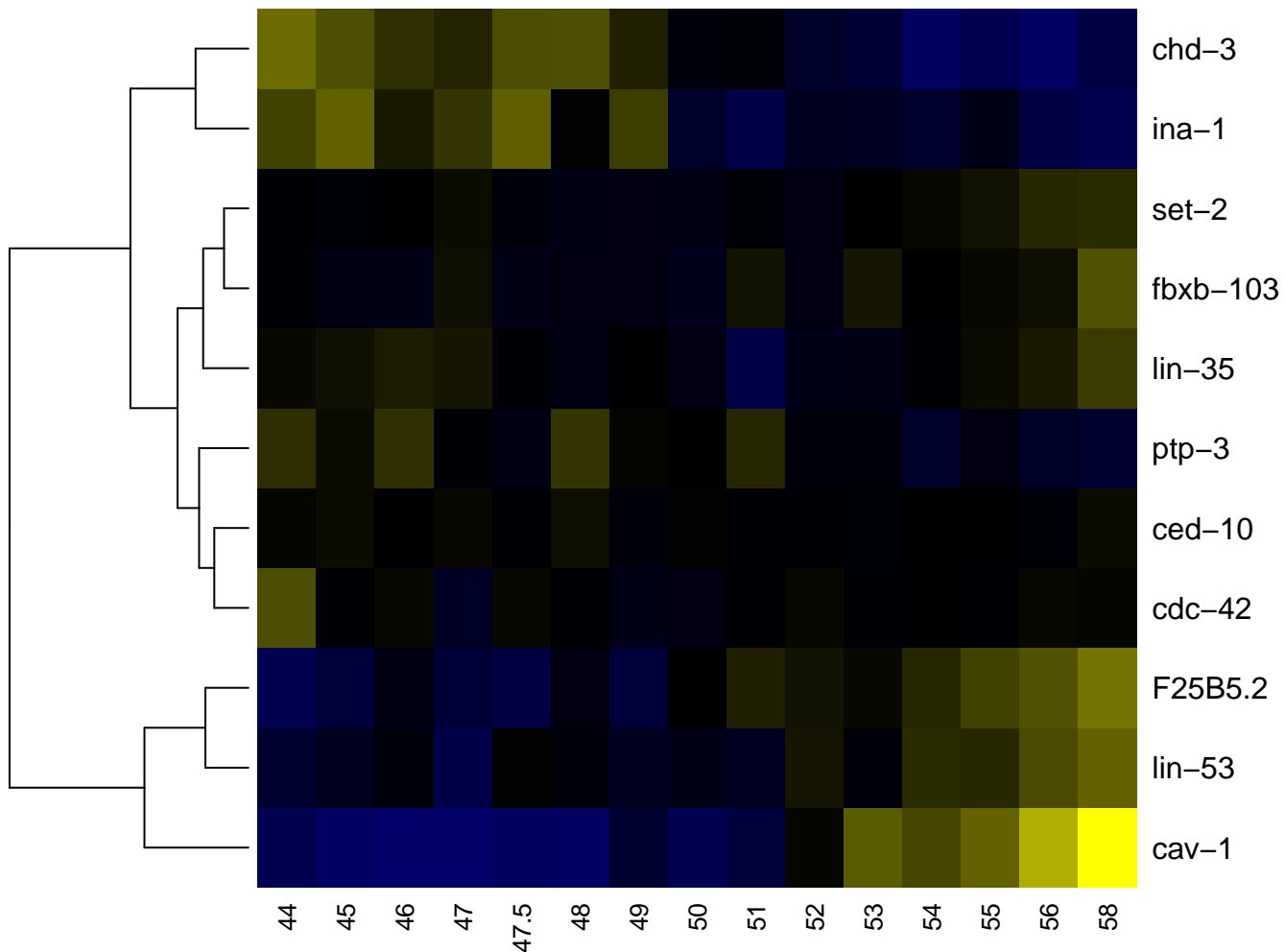
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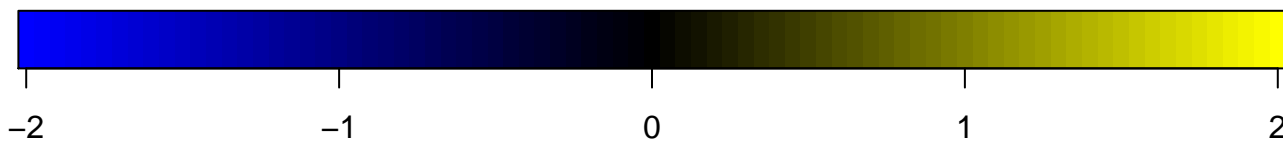
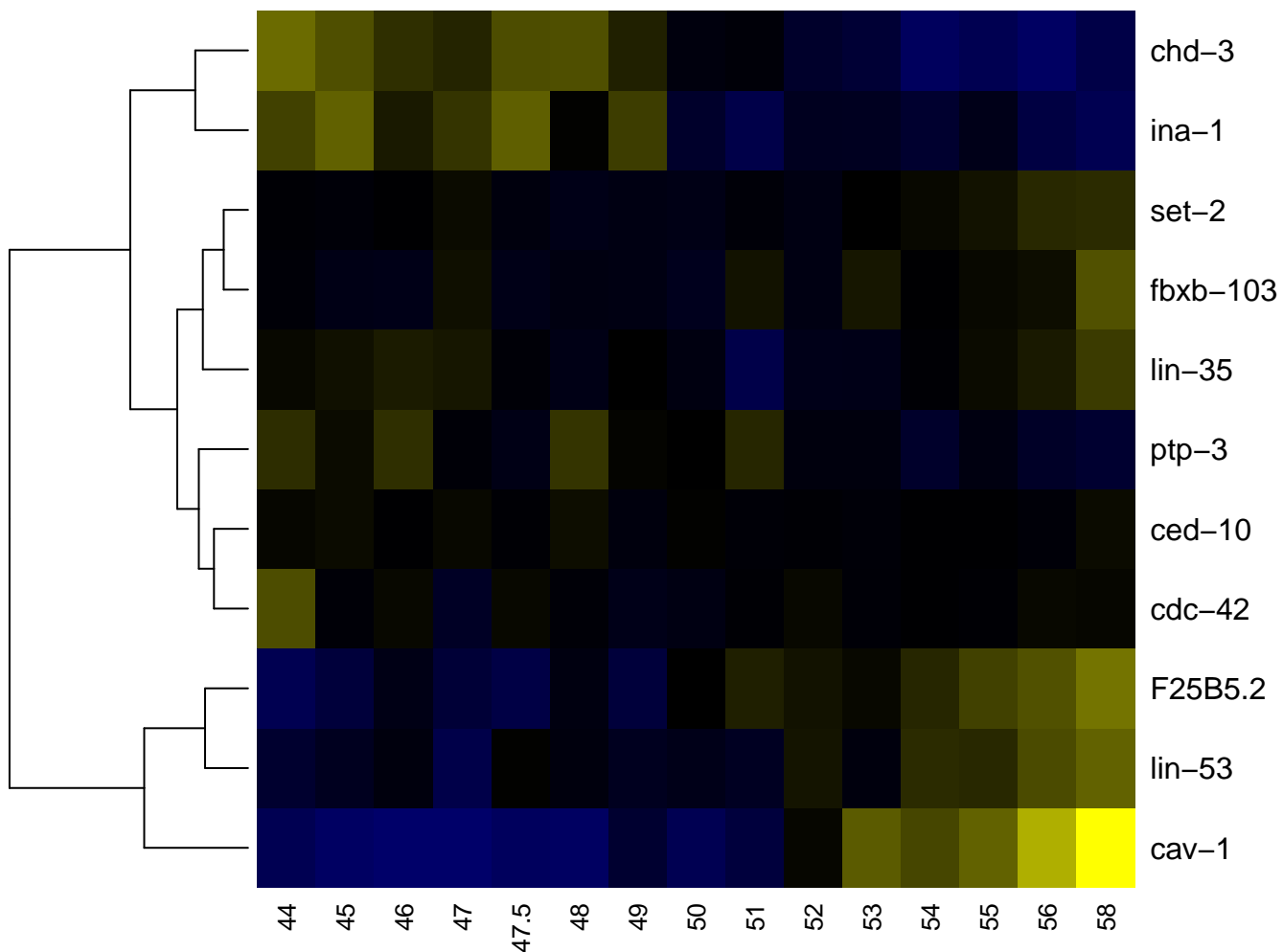
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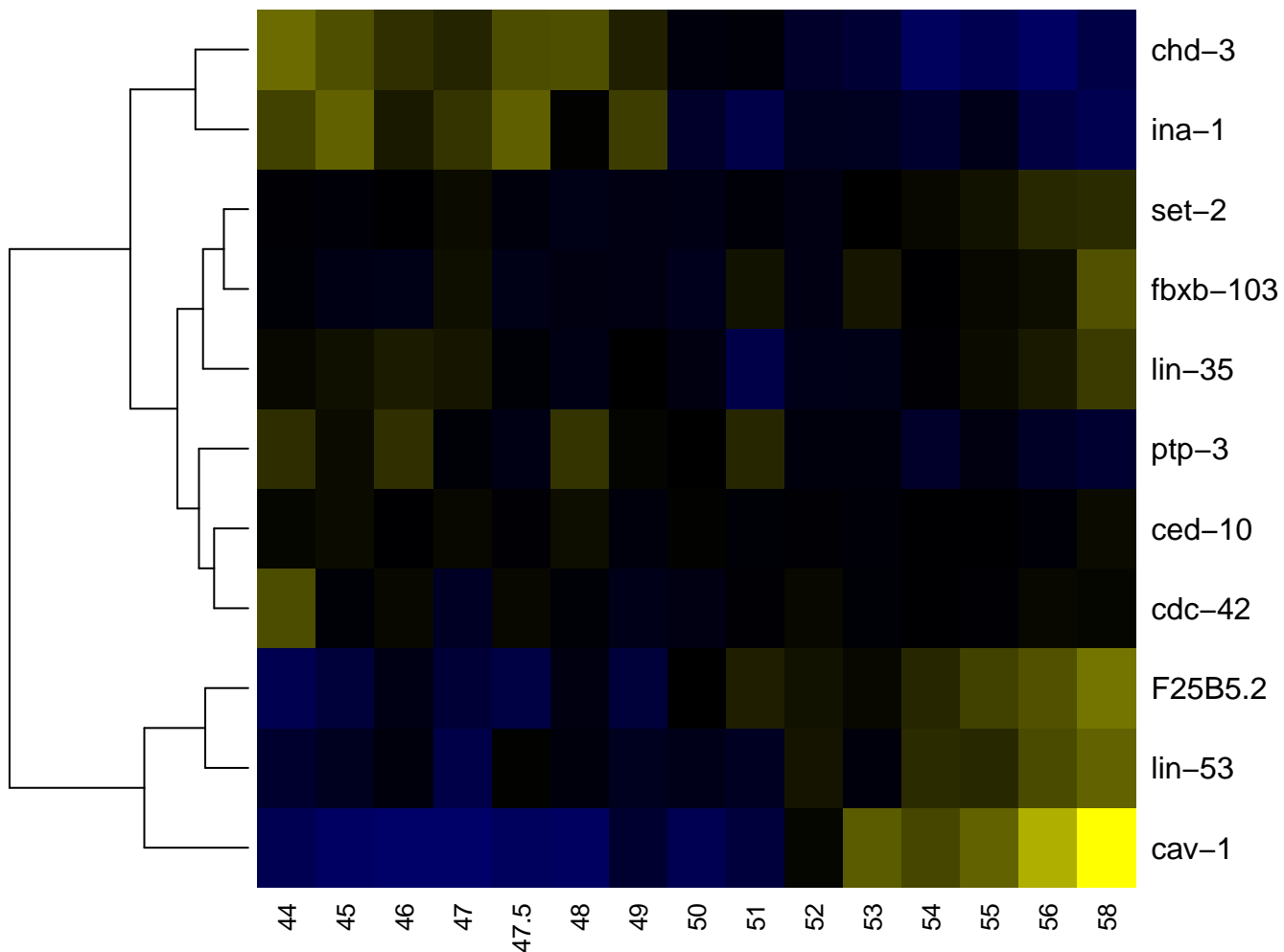
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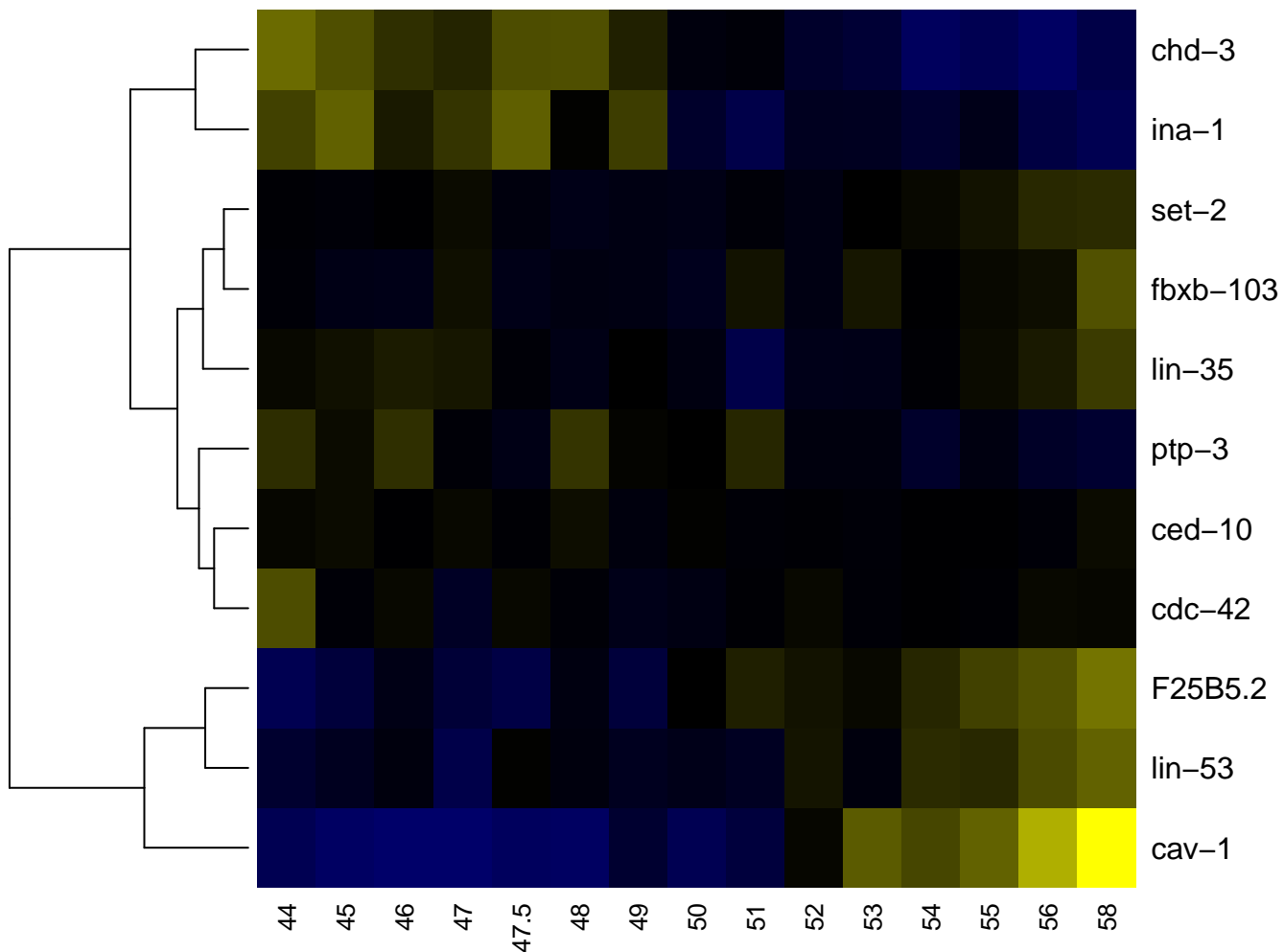
pm3L



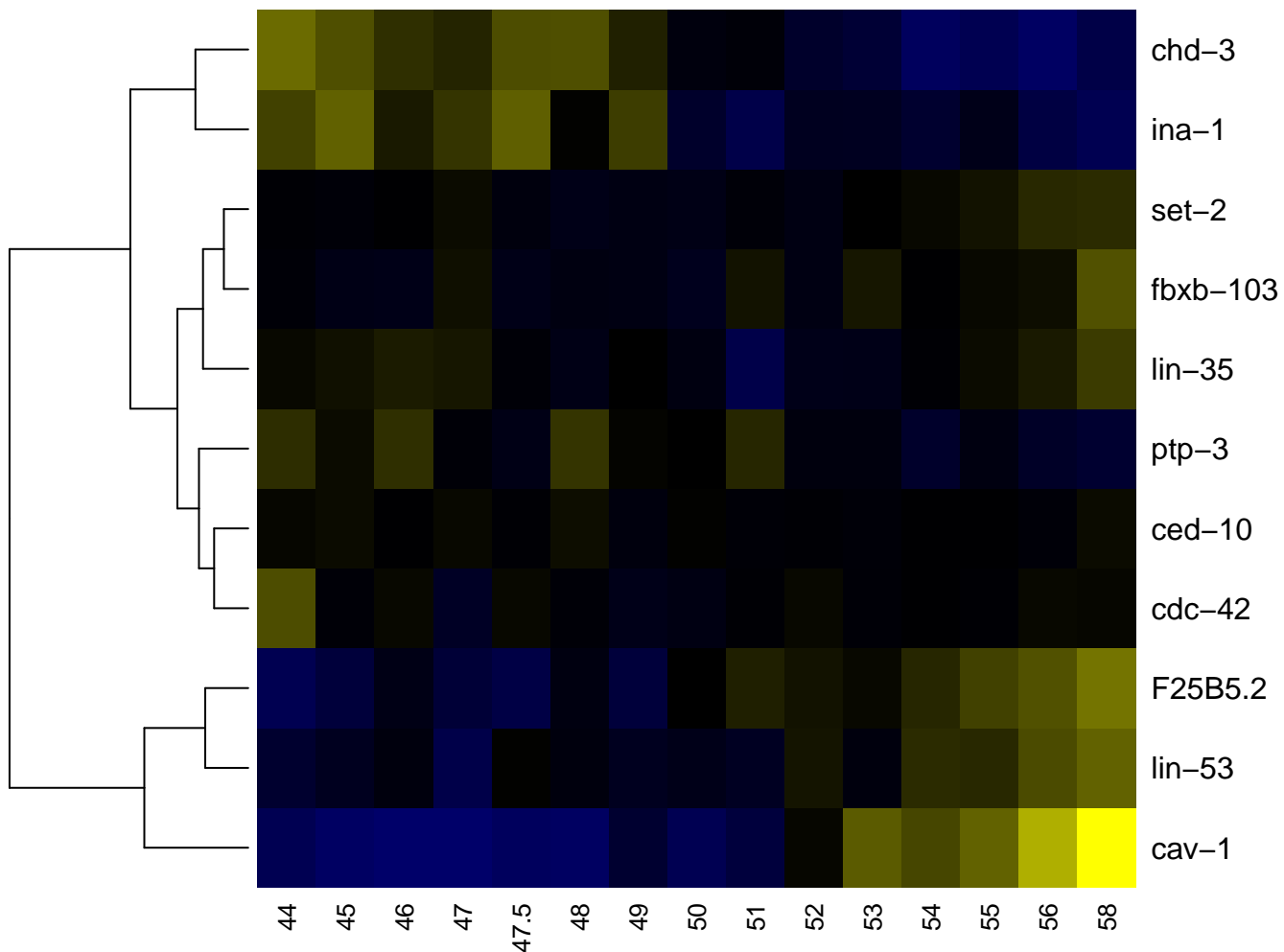
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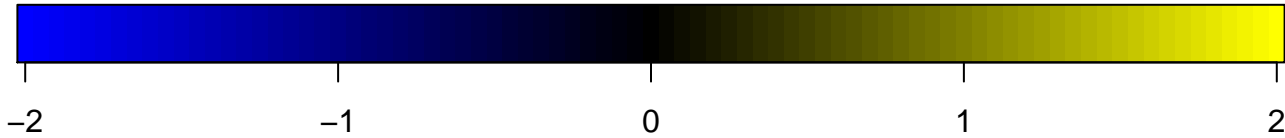
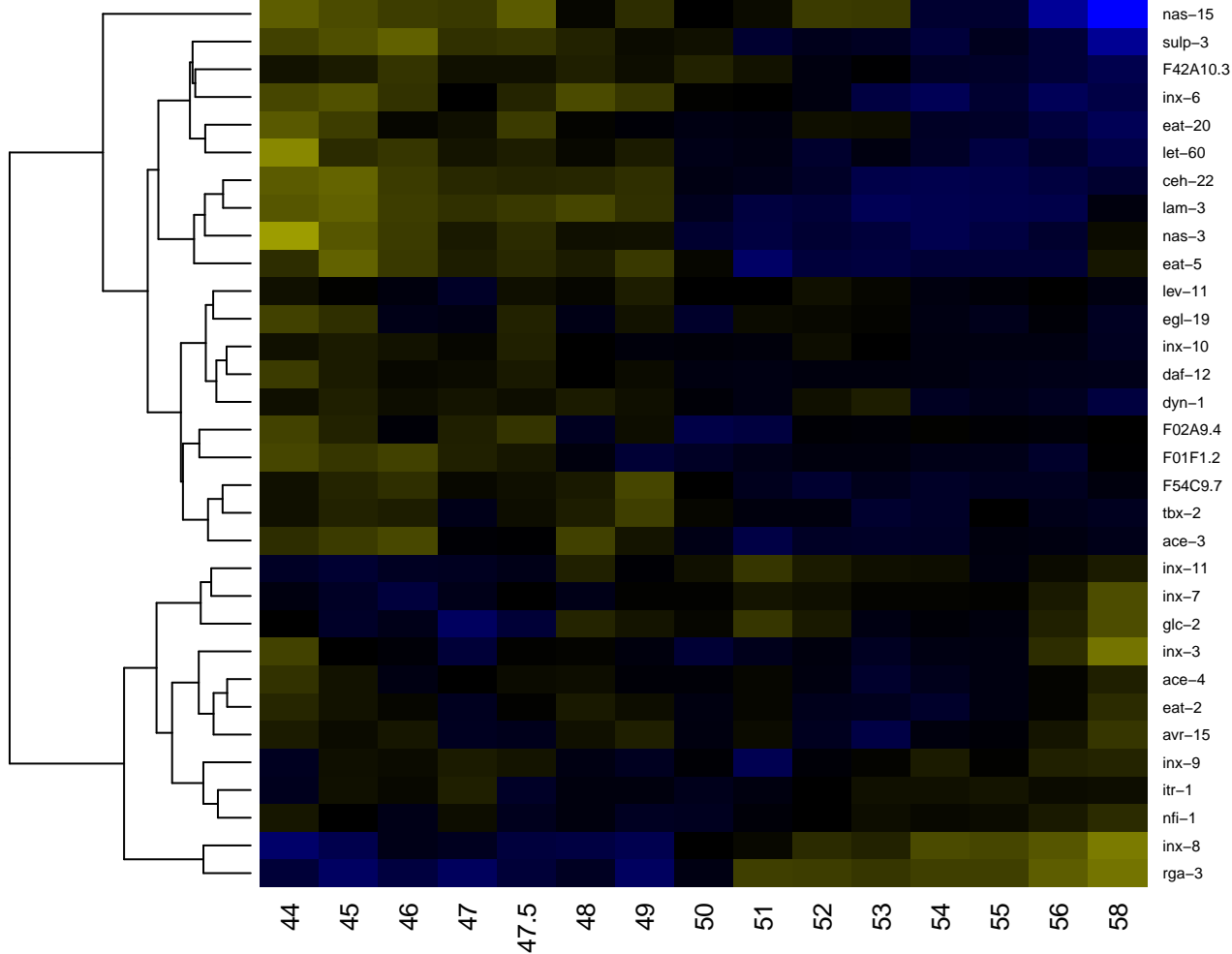
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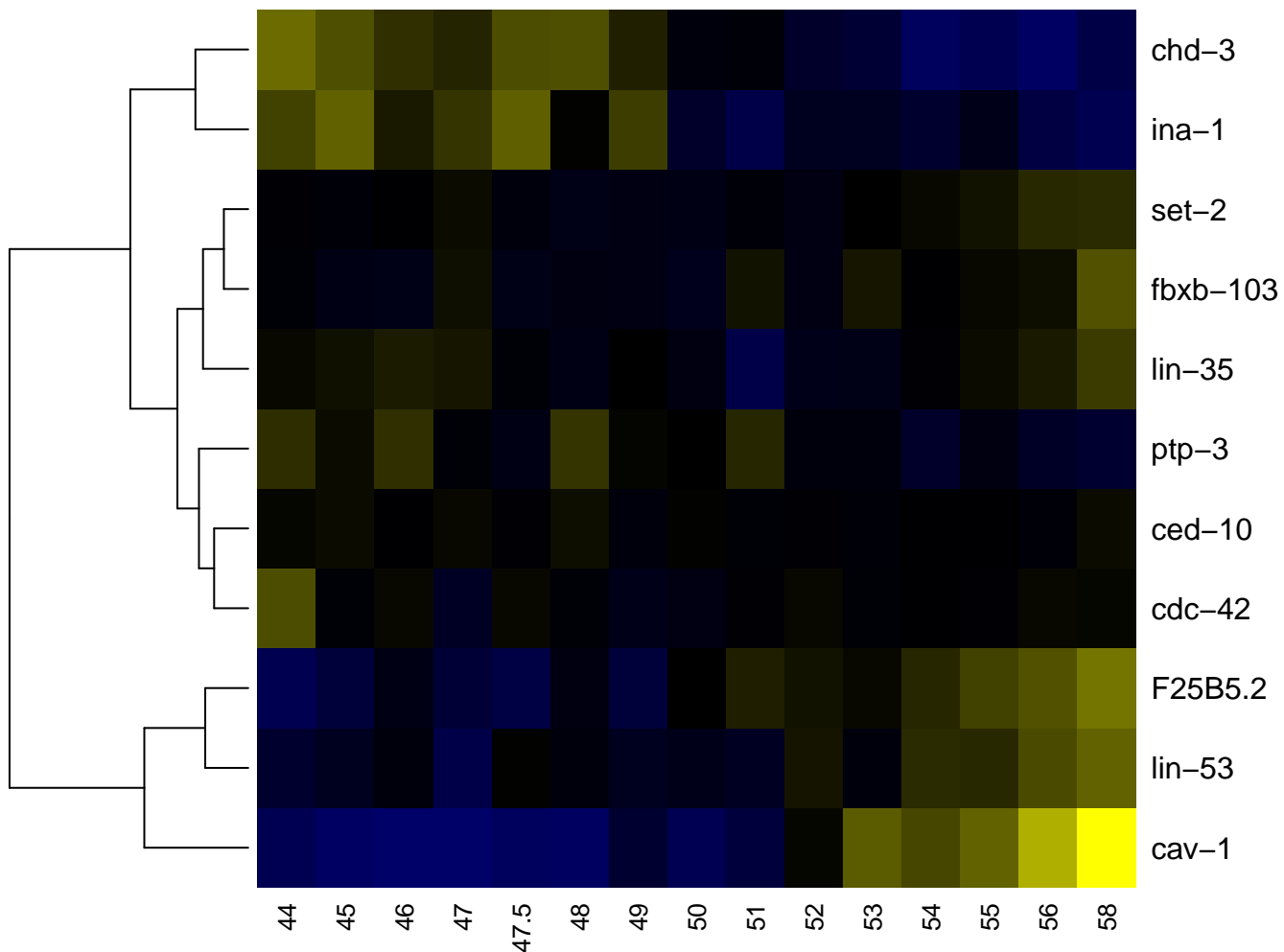
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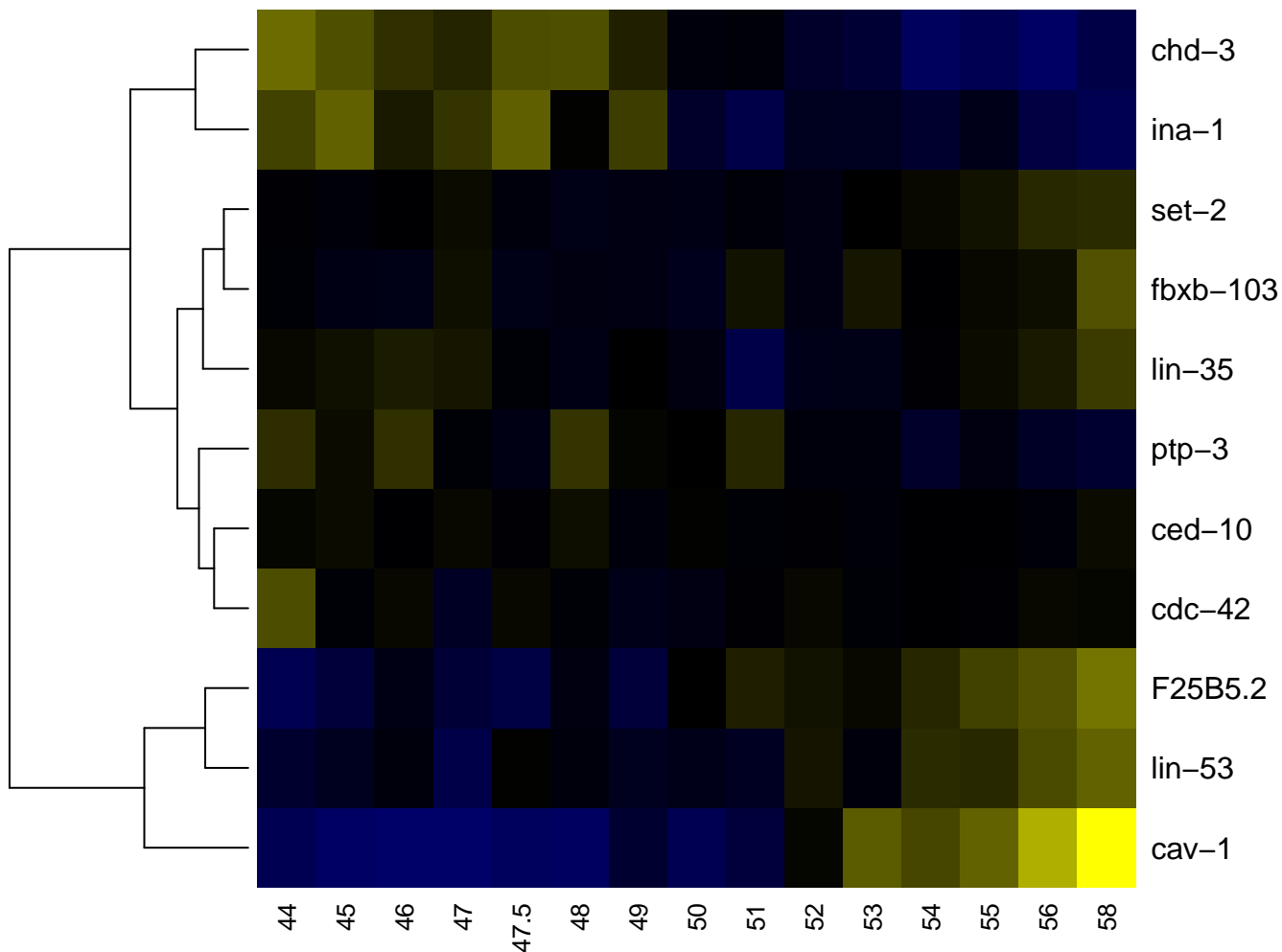
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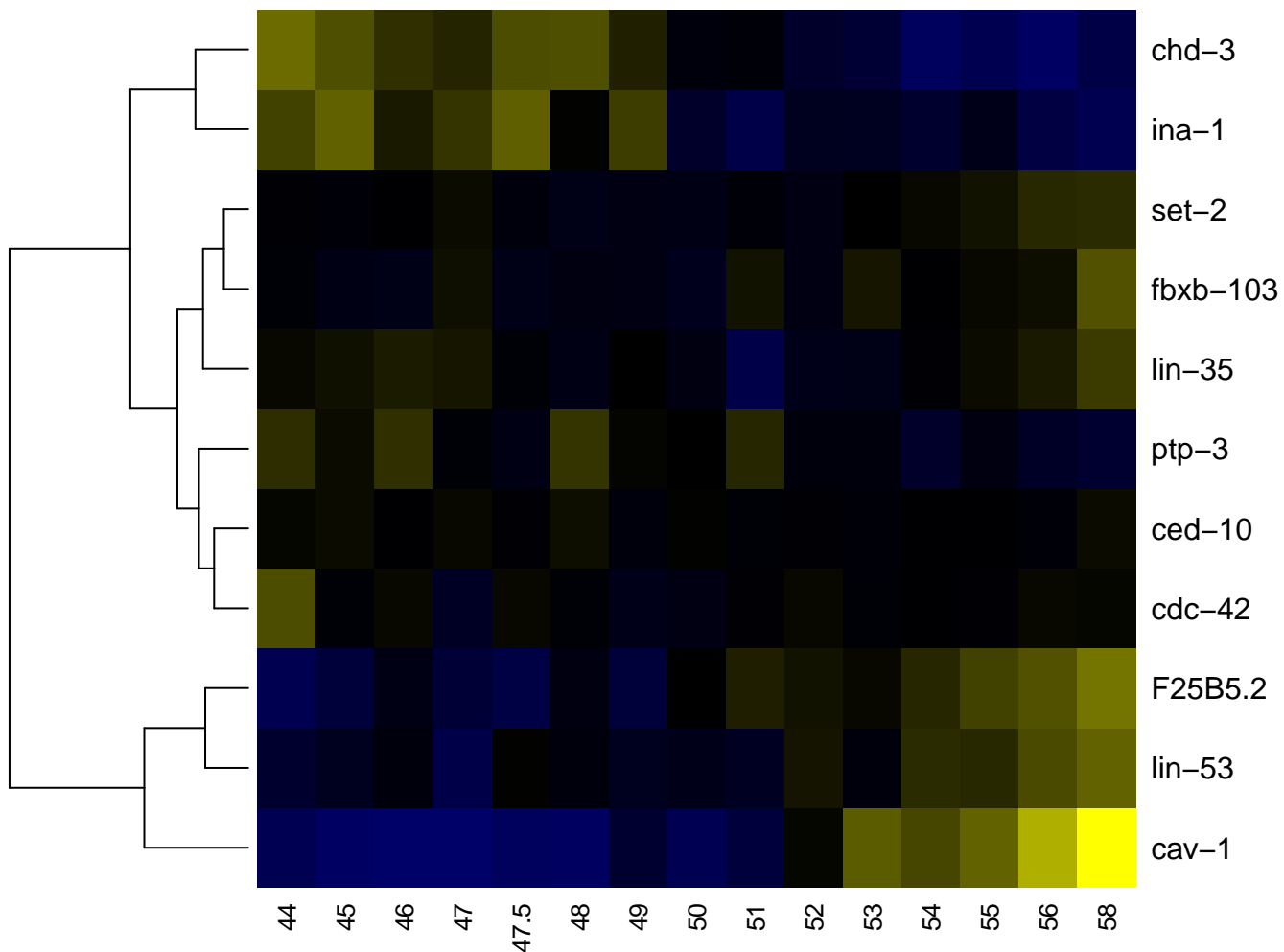
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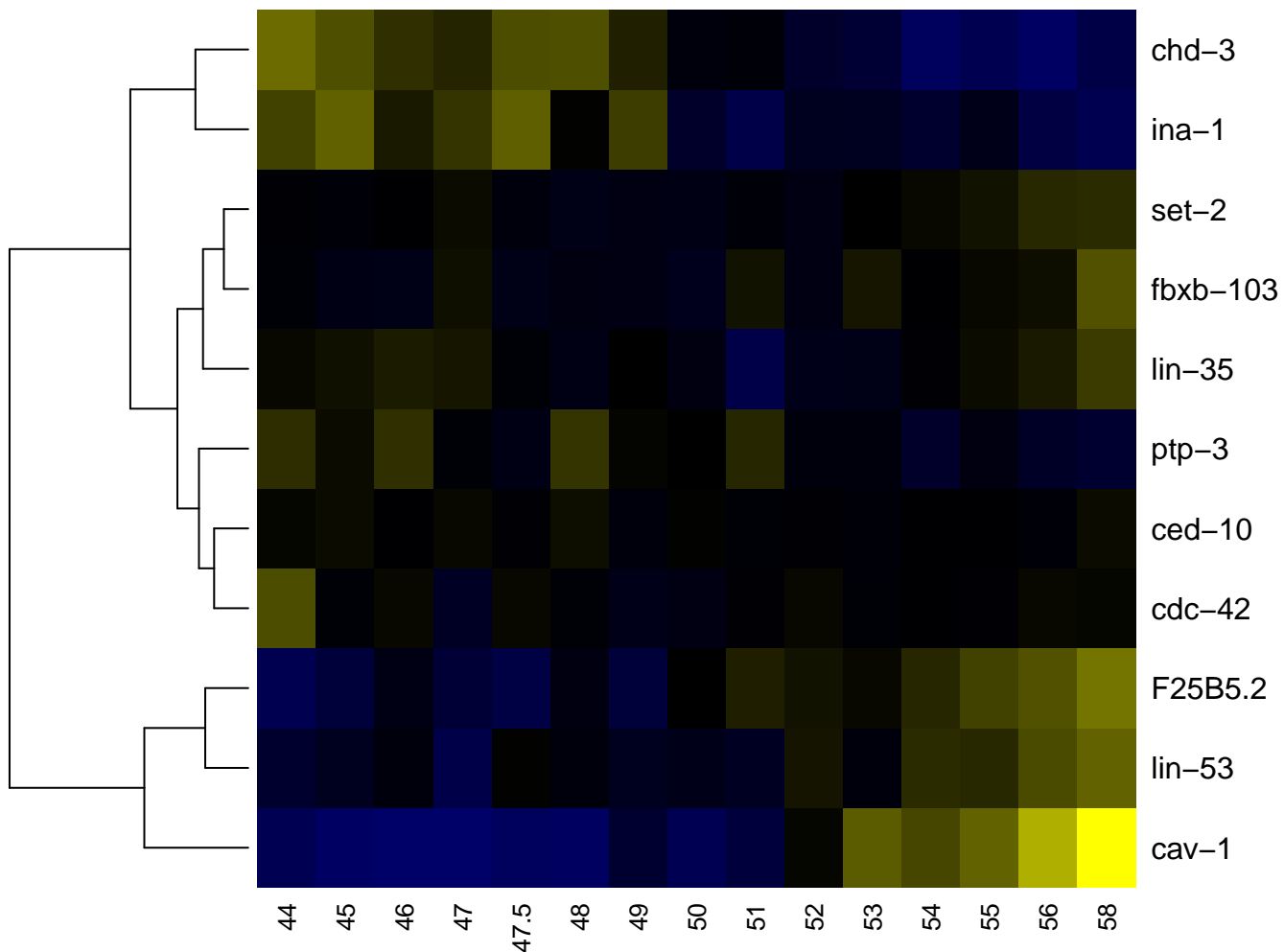
pm4DR



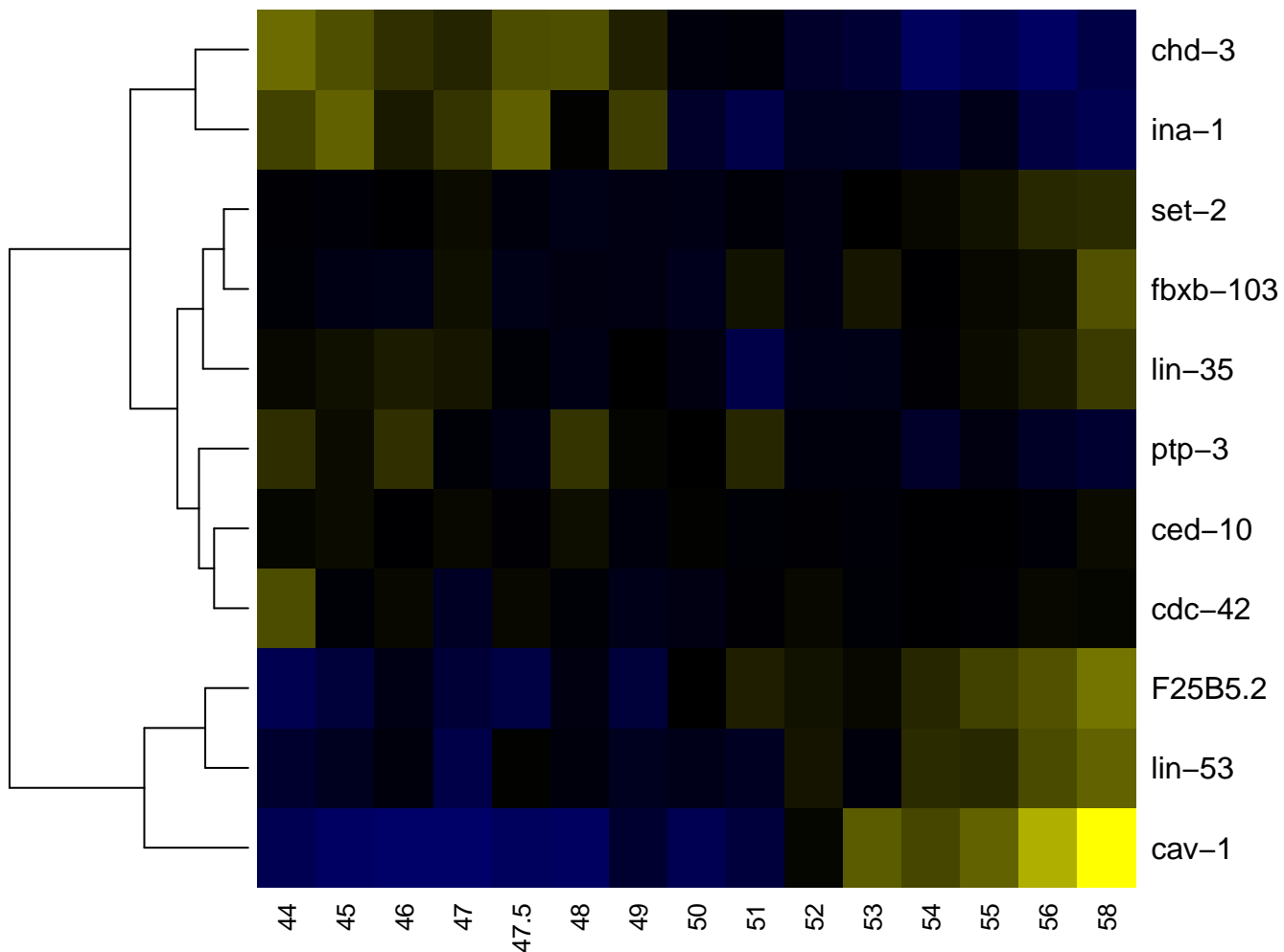
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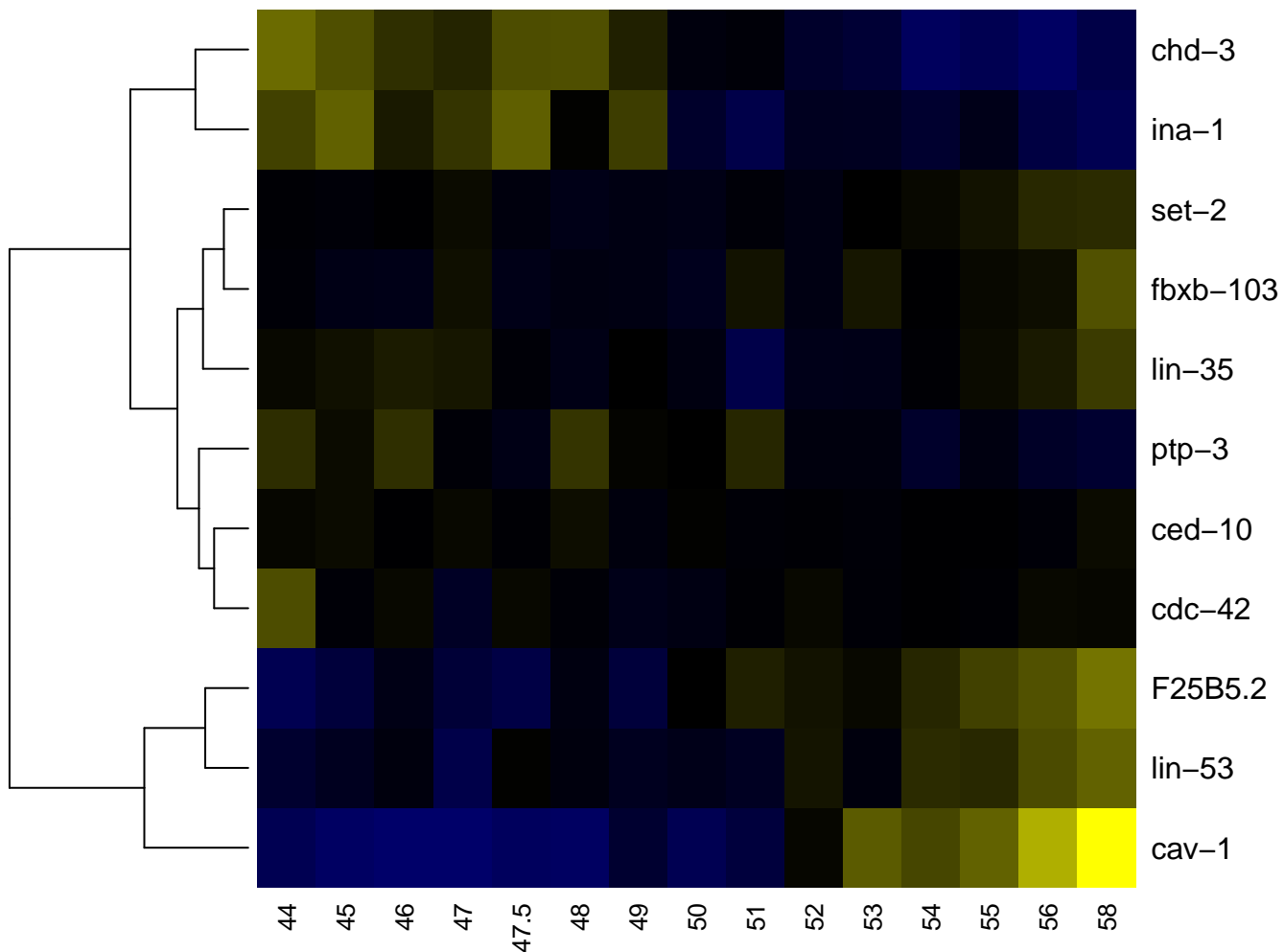
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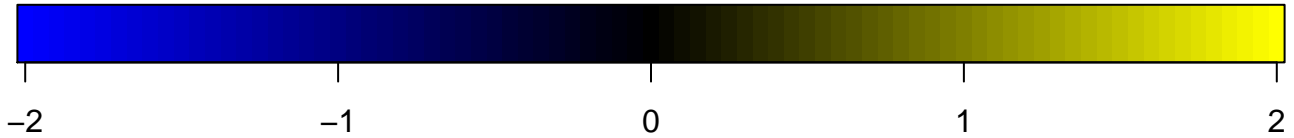
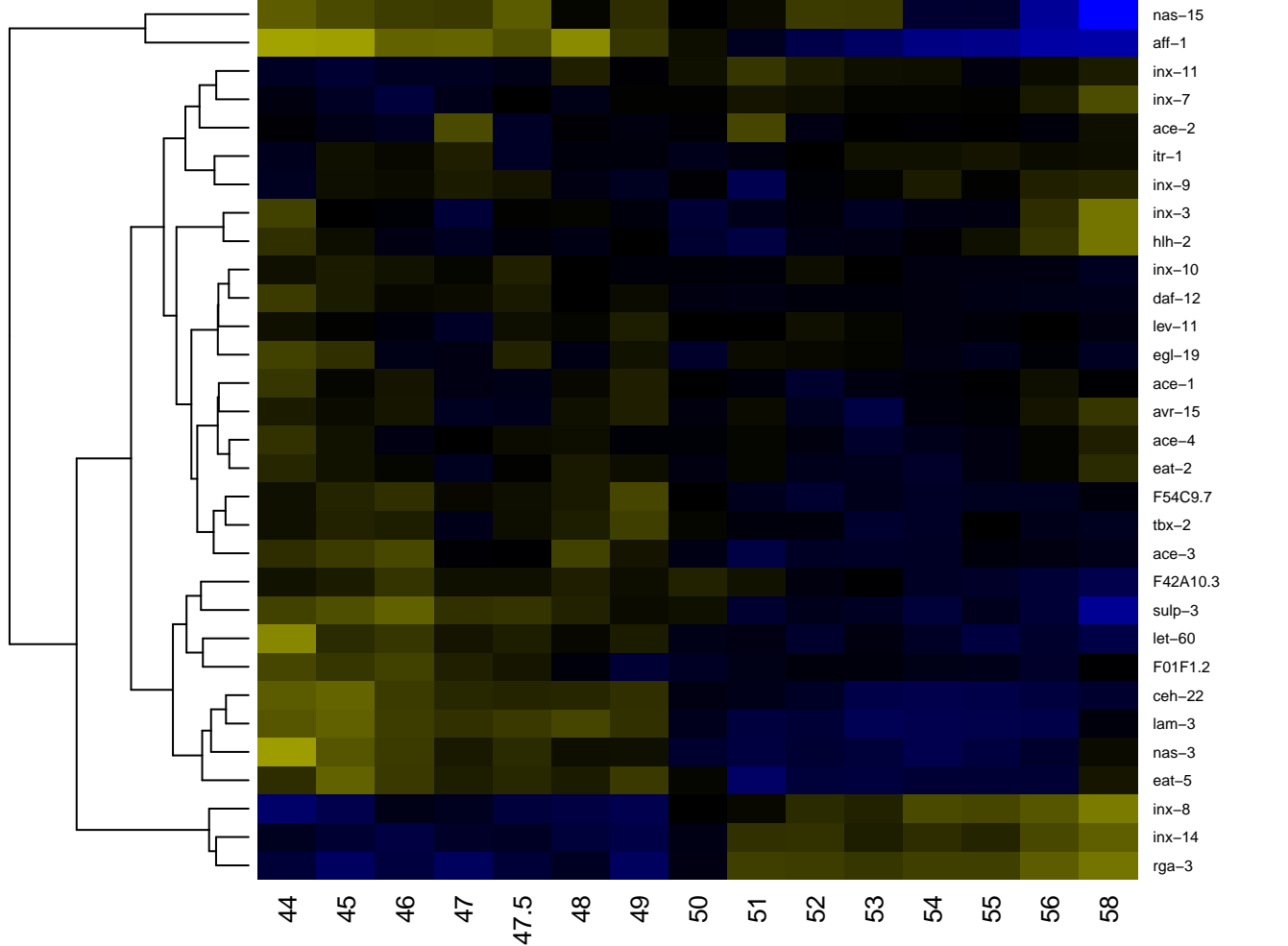
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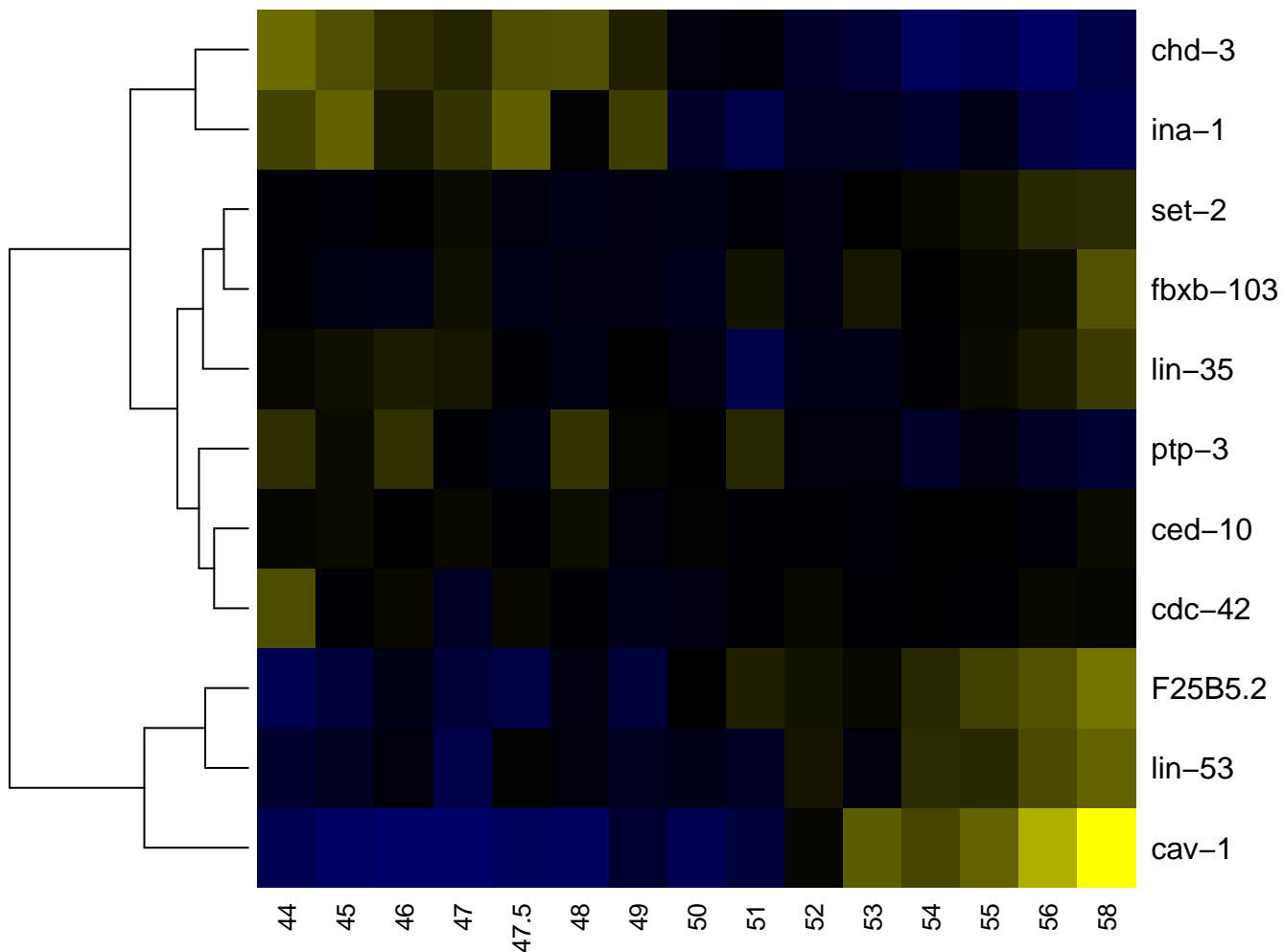
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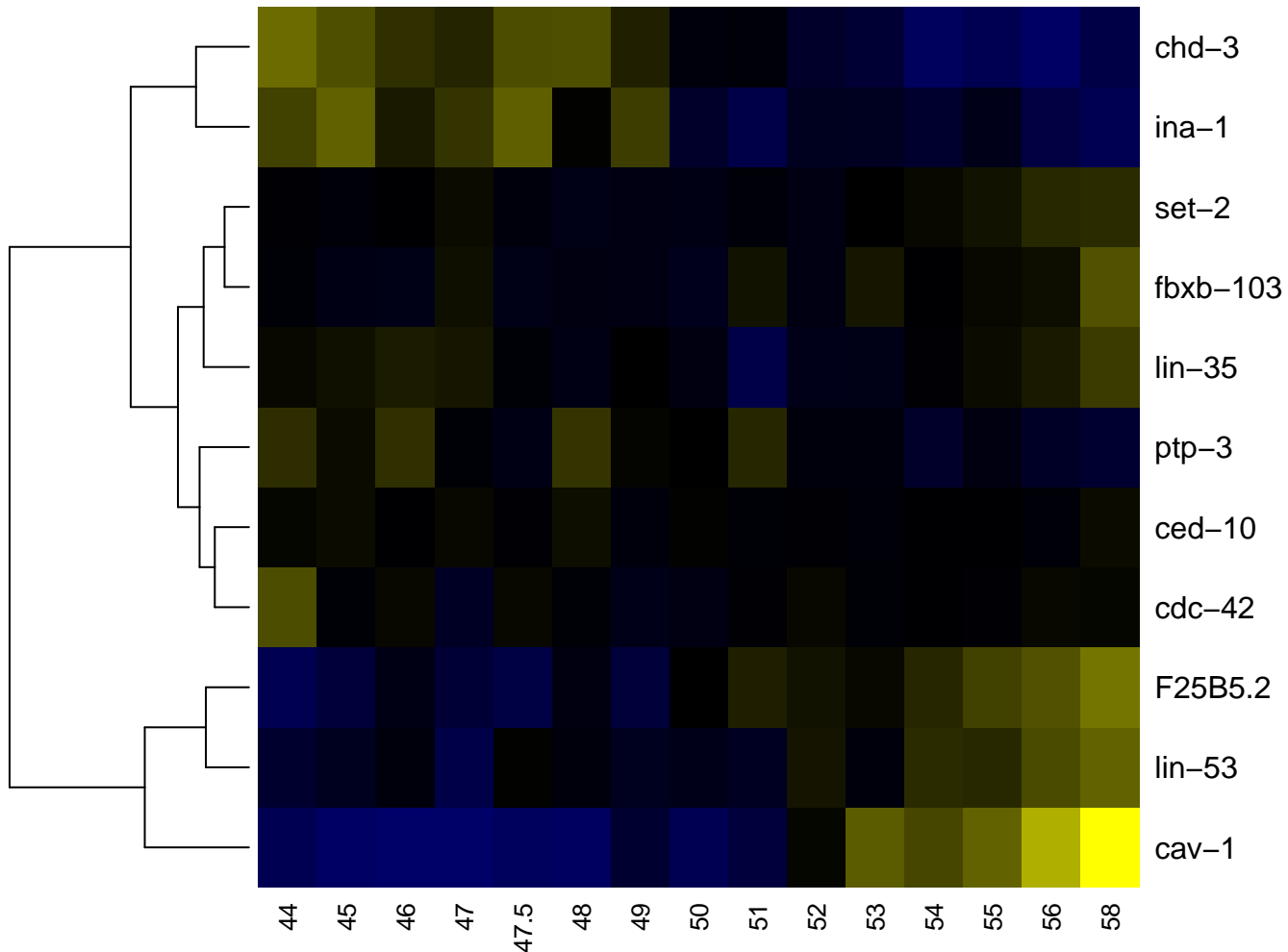
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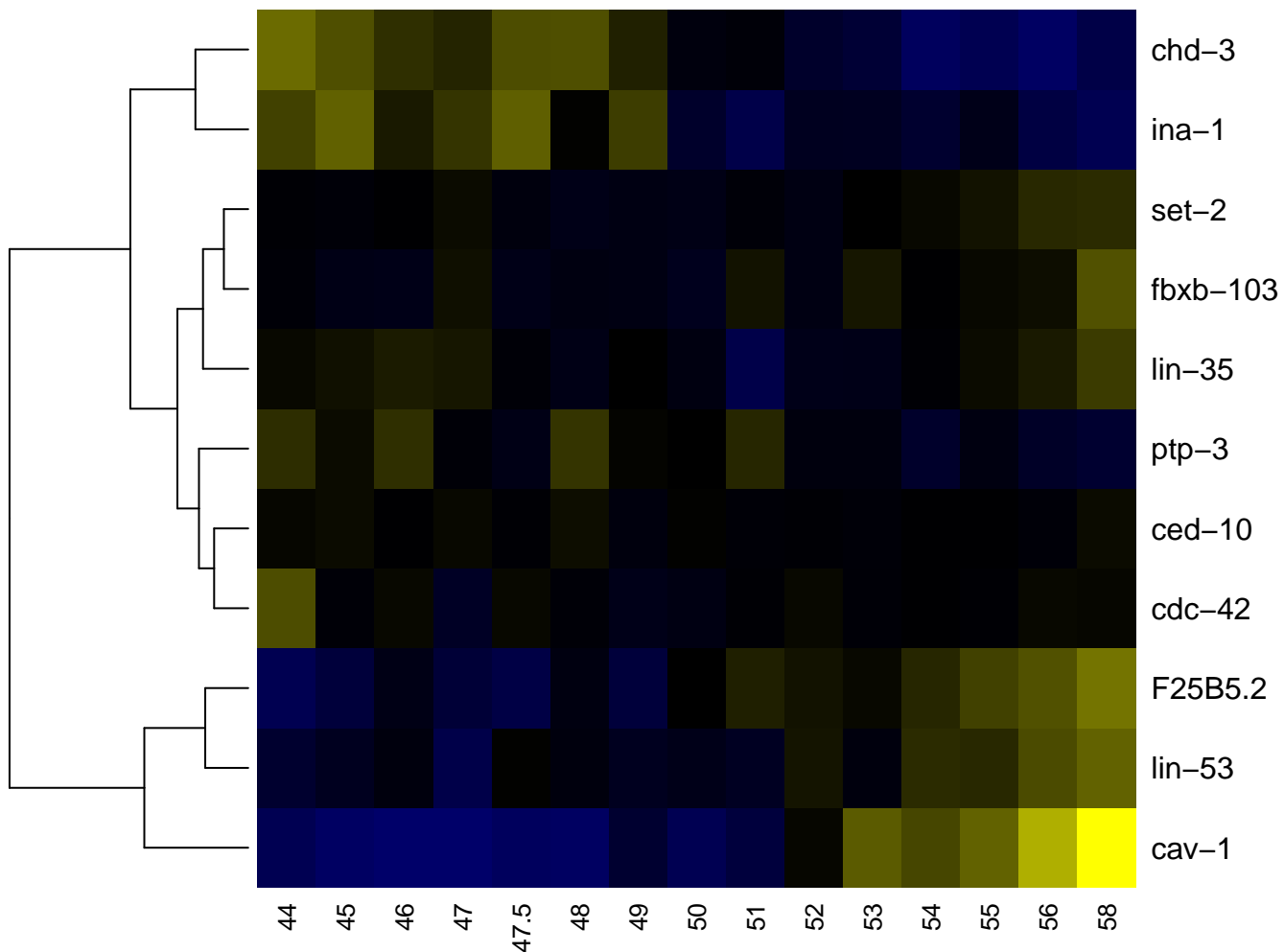
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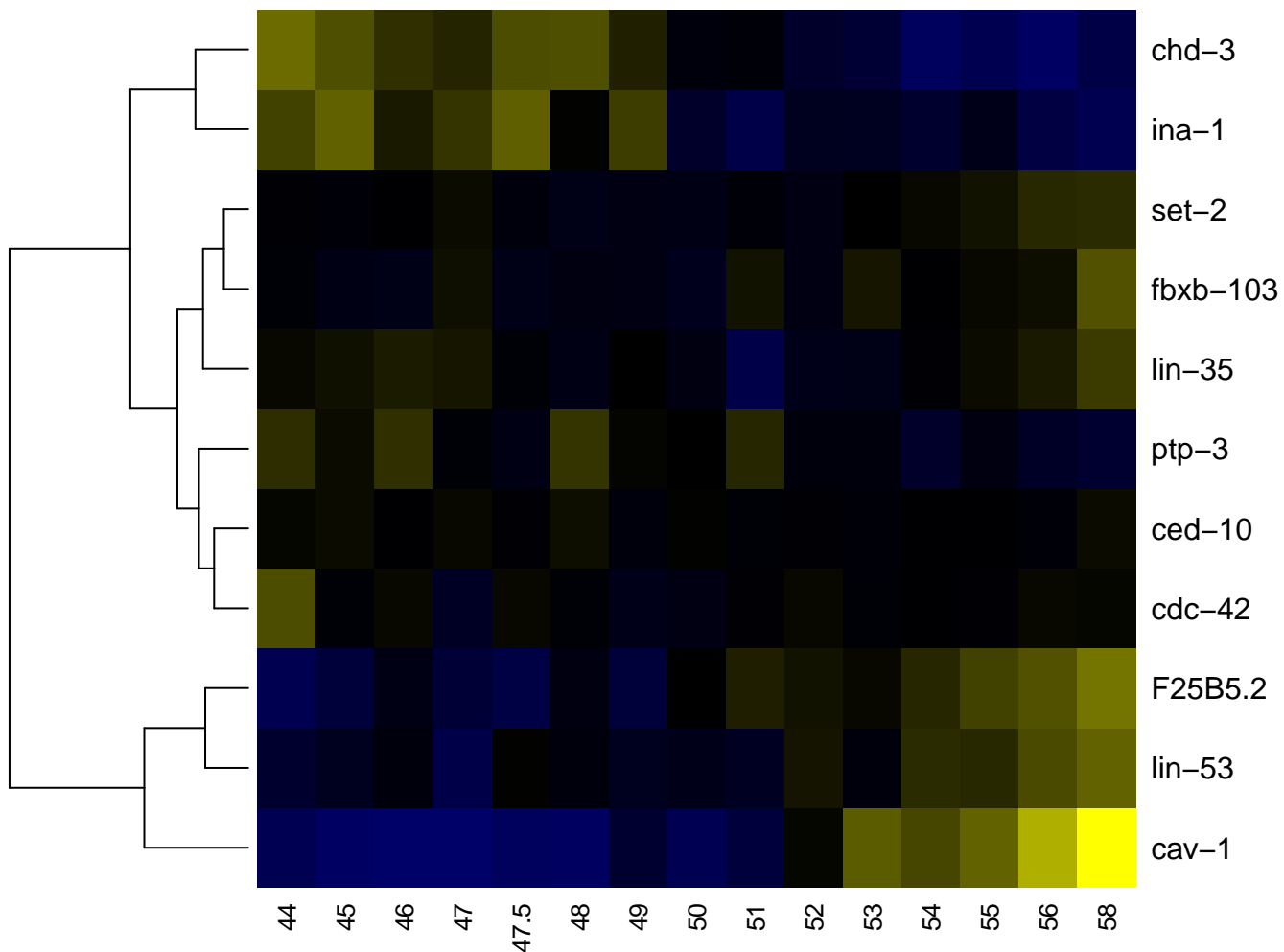
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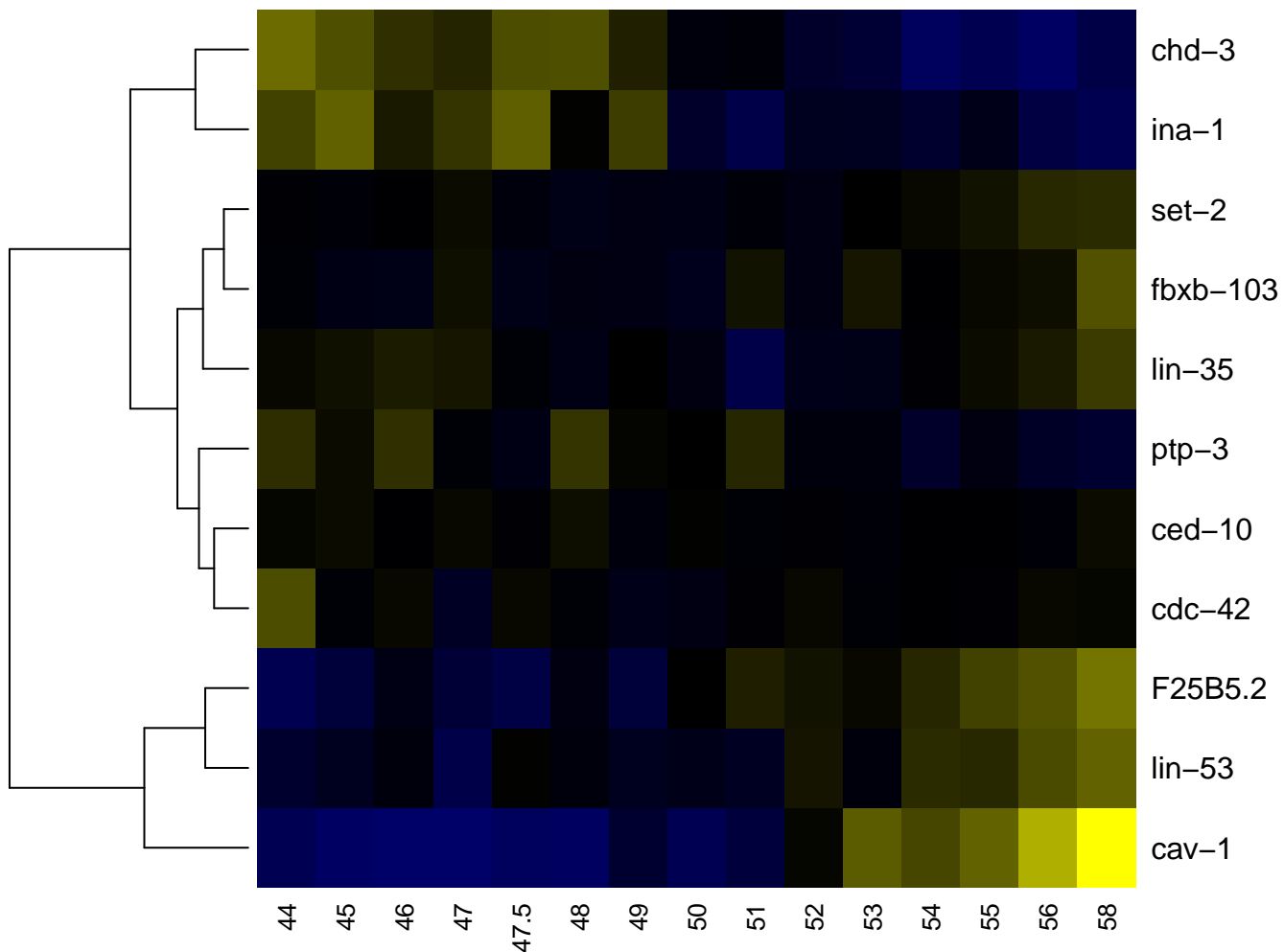
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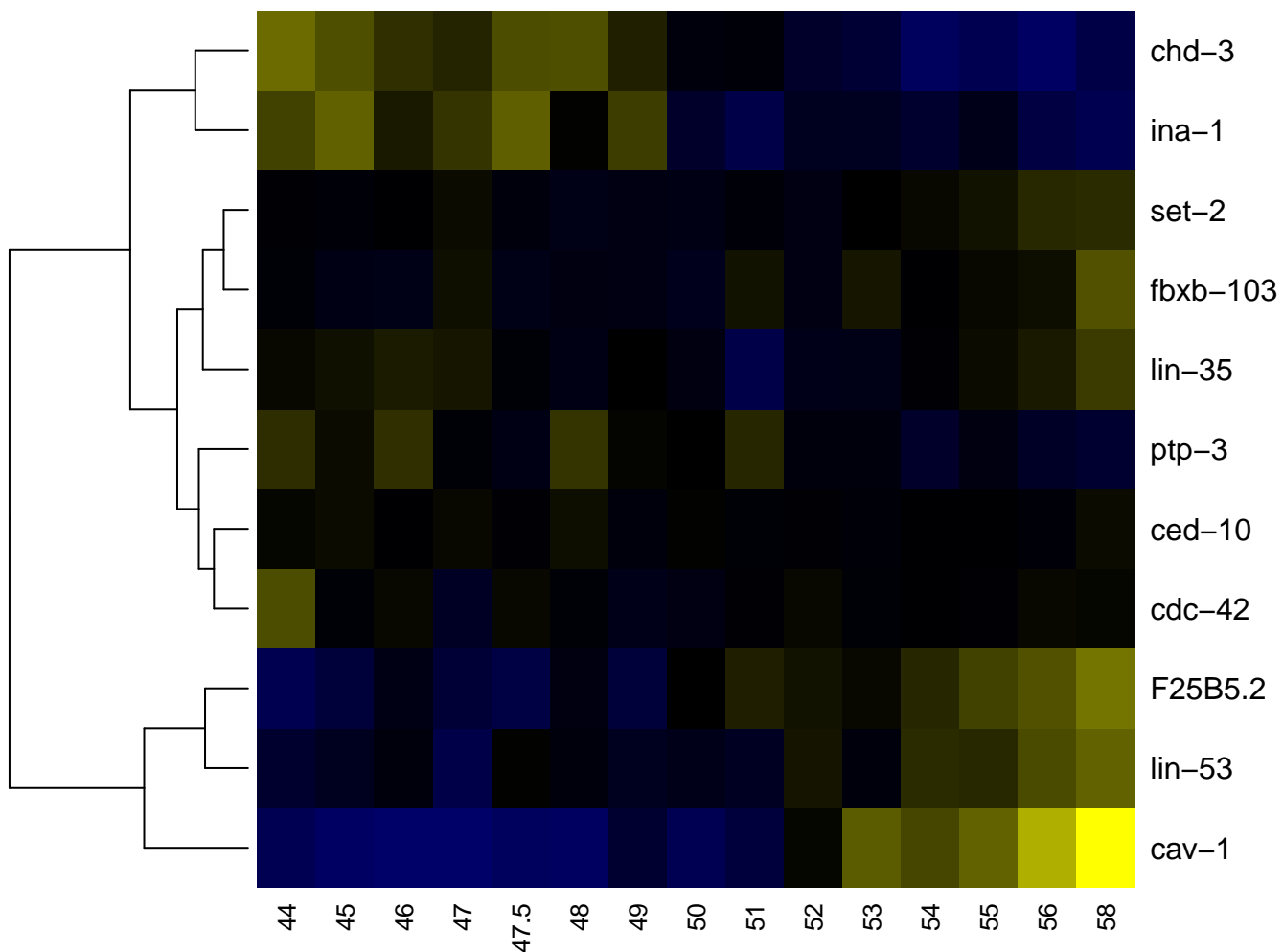
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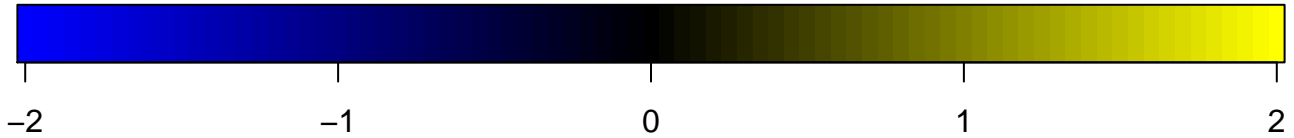
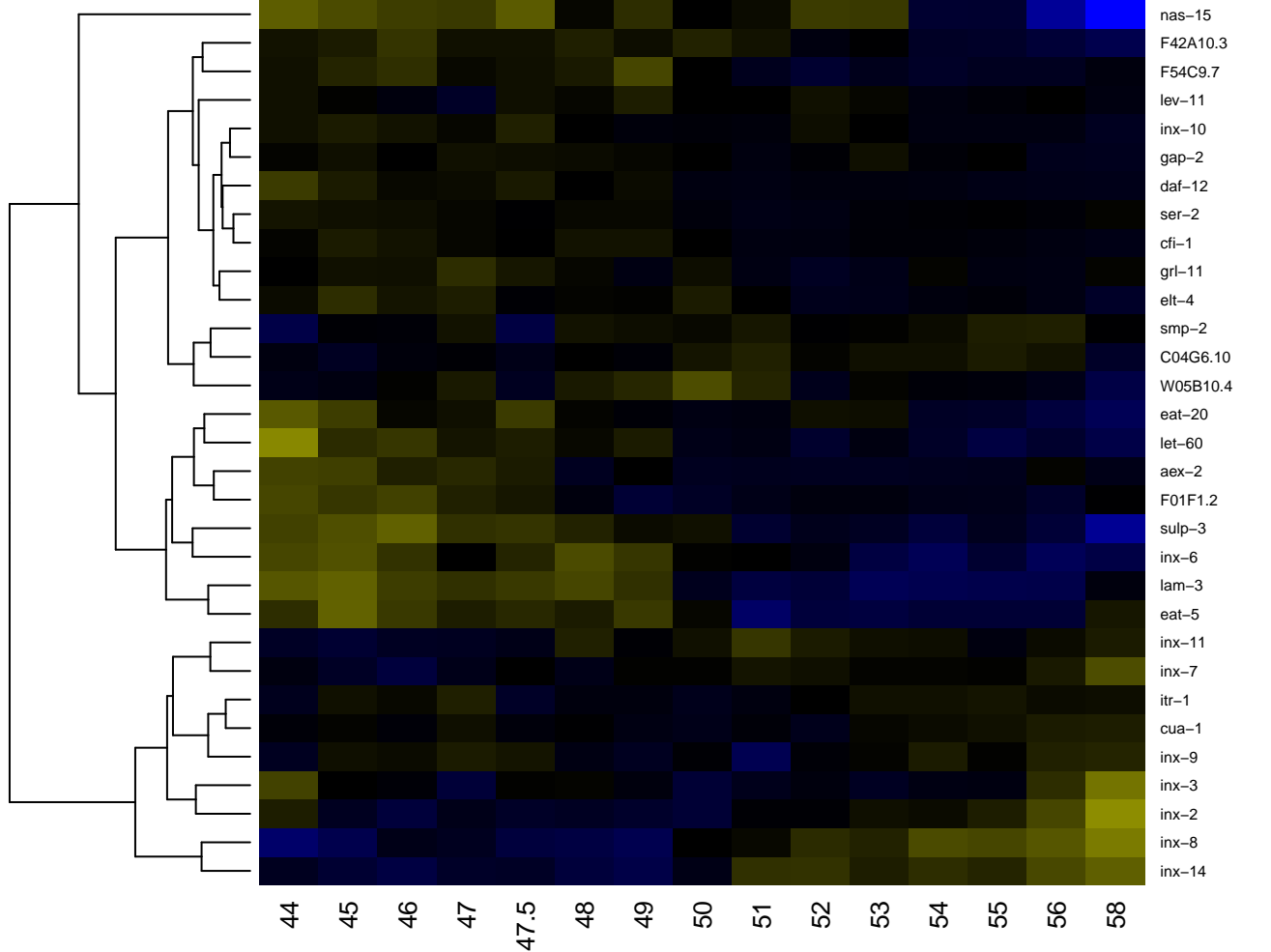
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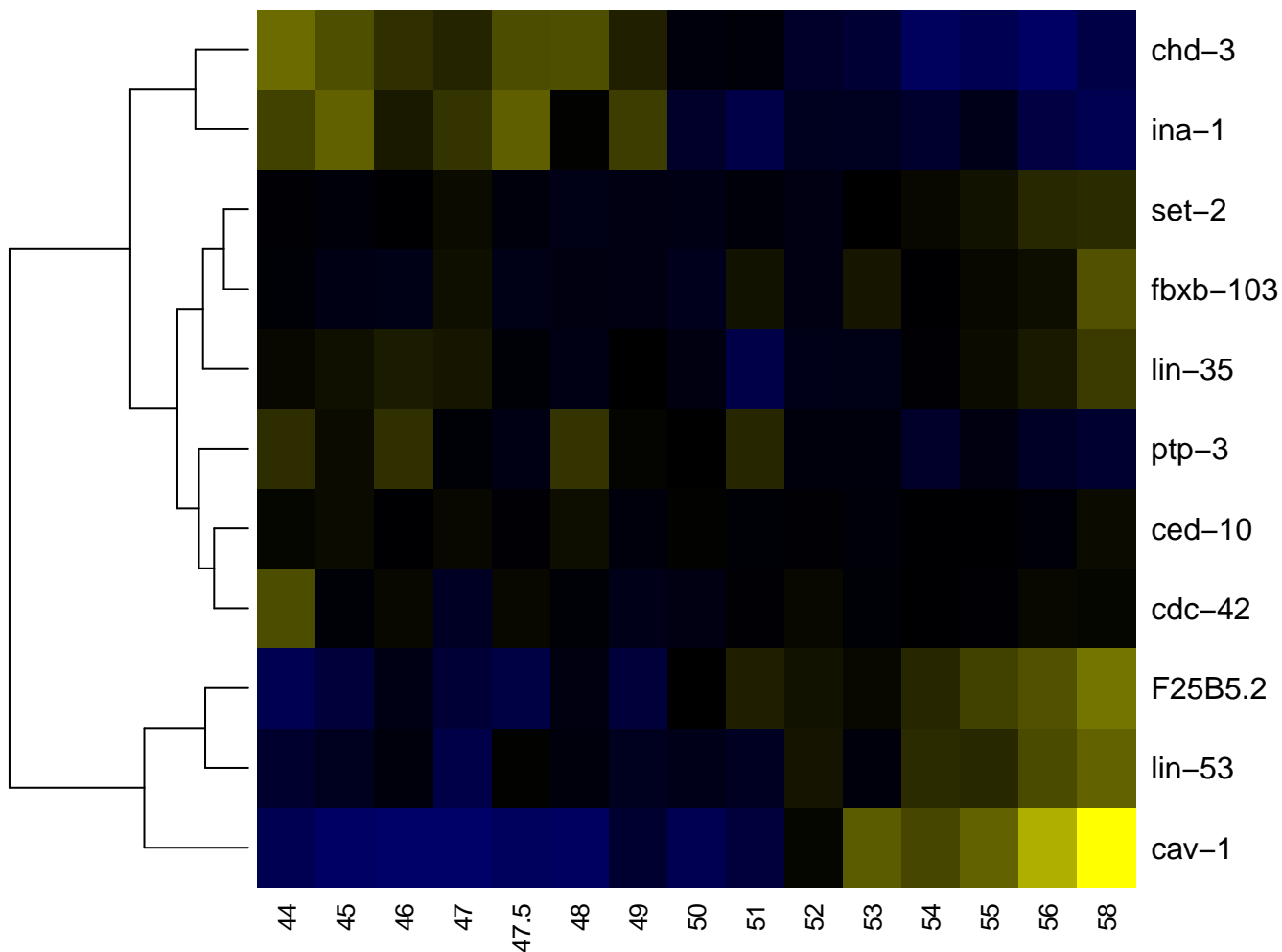
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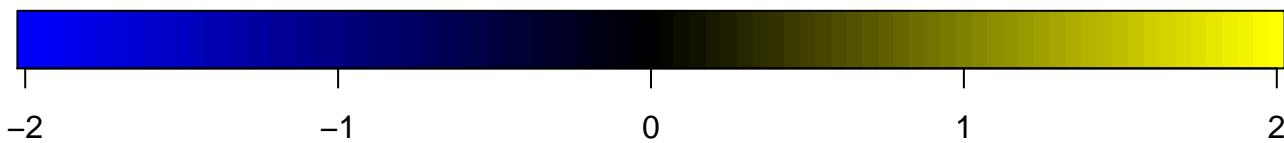
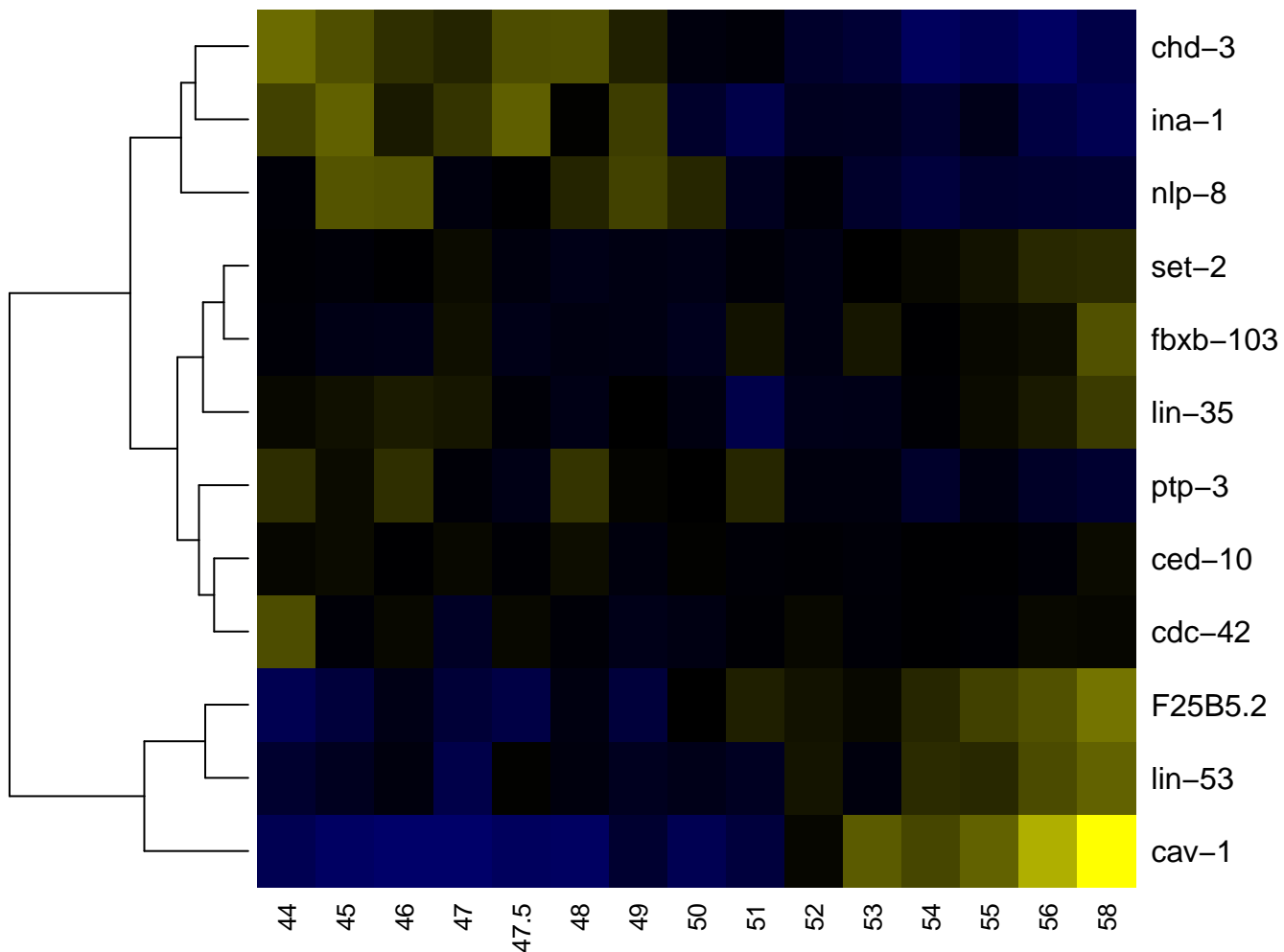
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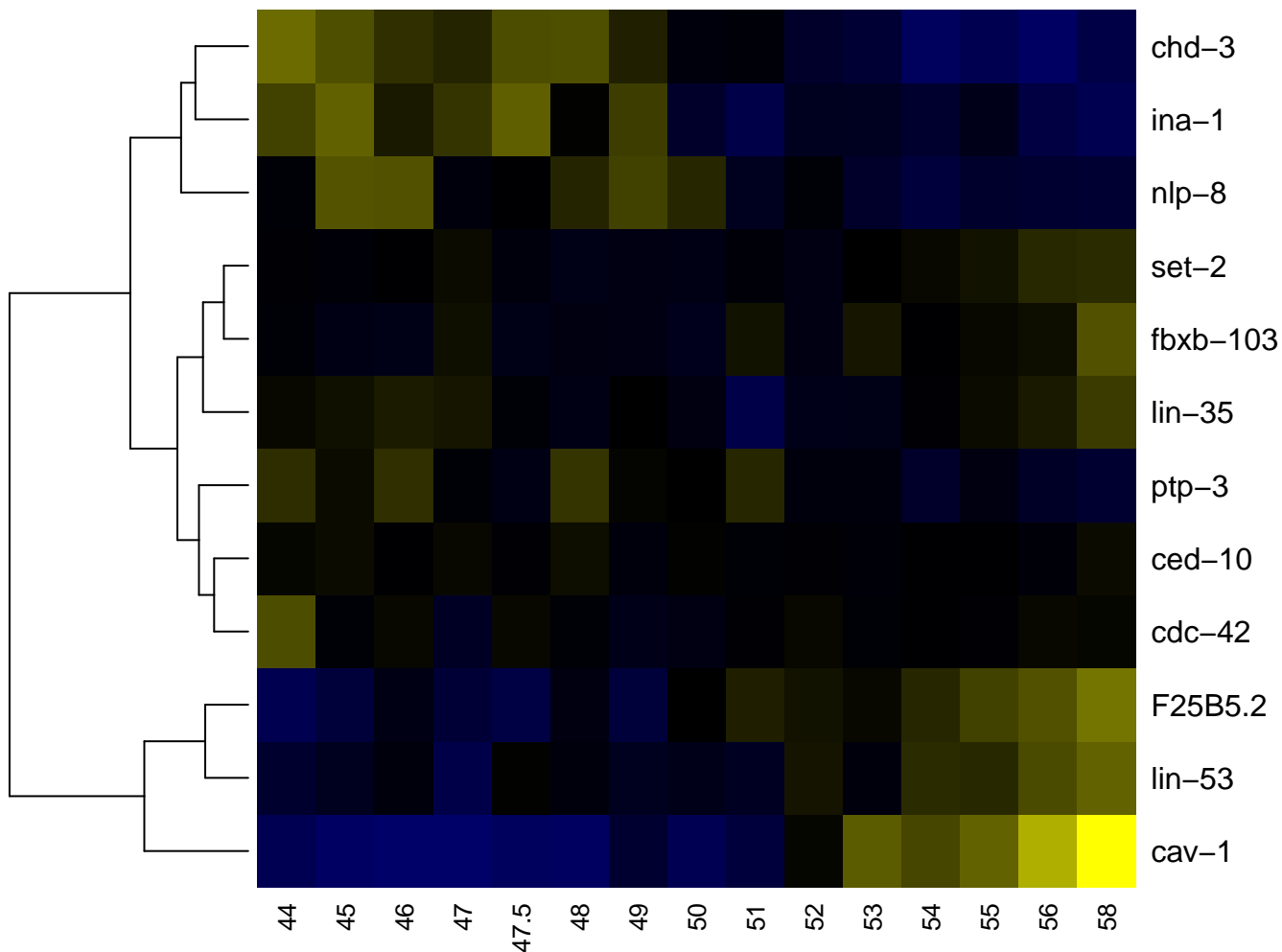
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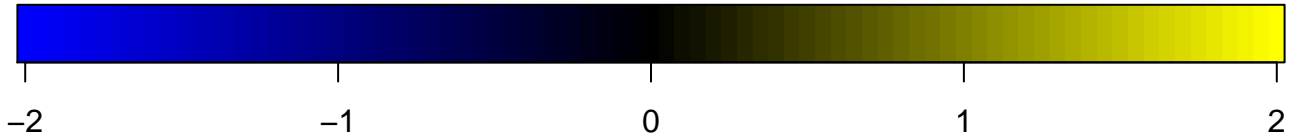
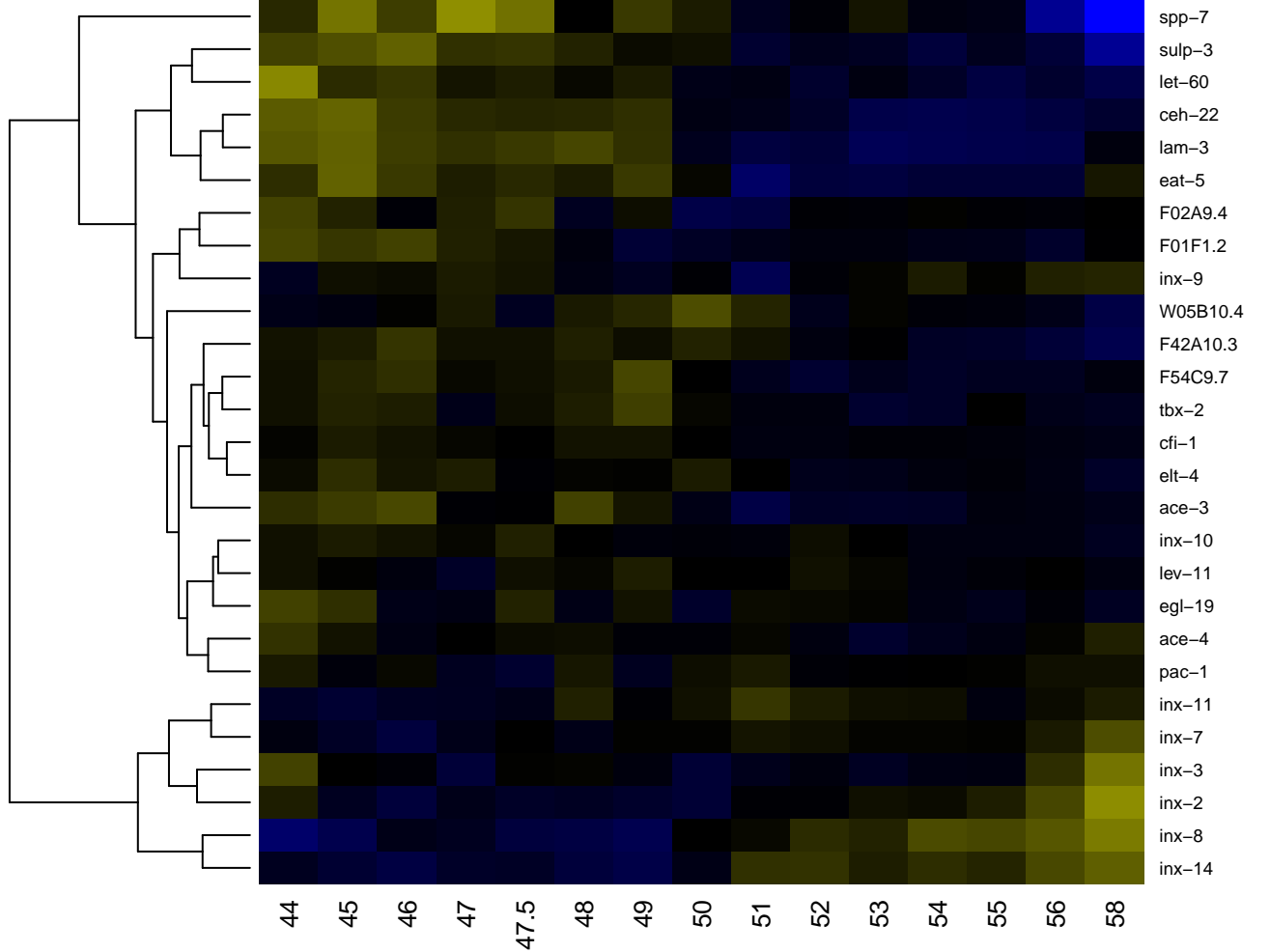
pm6VL



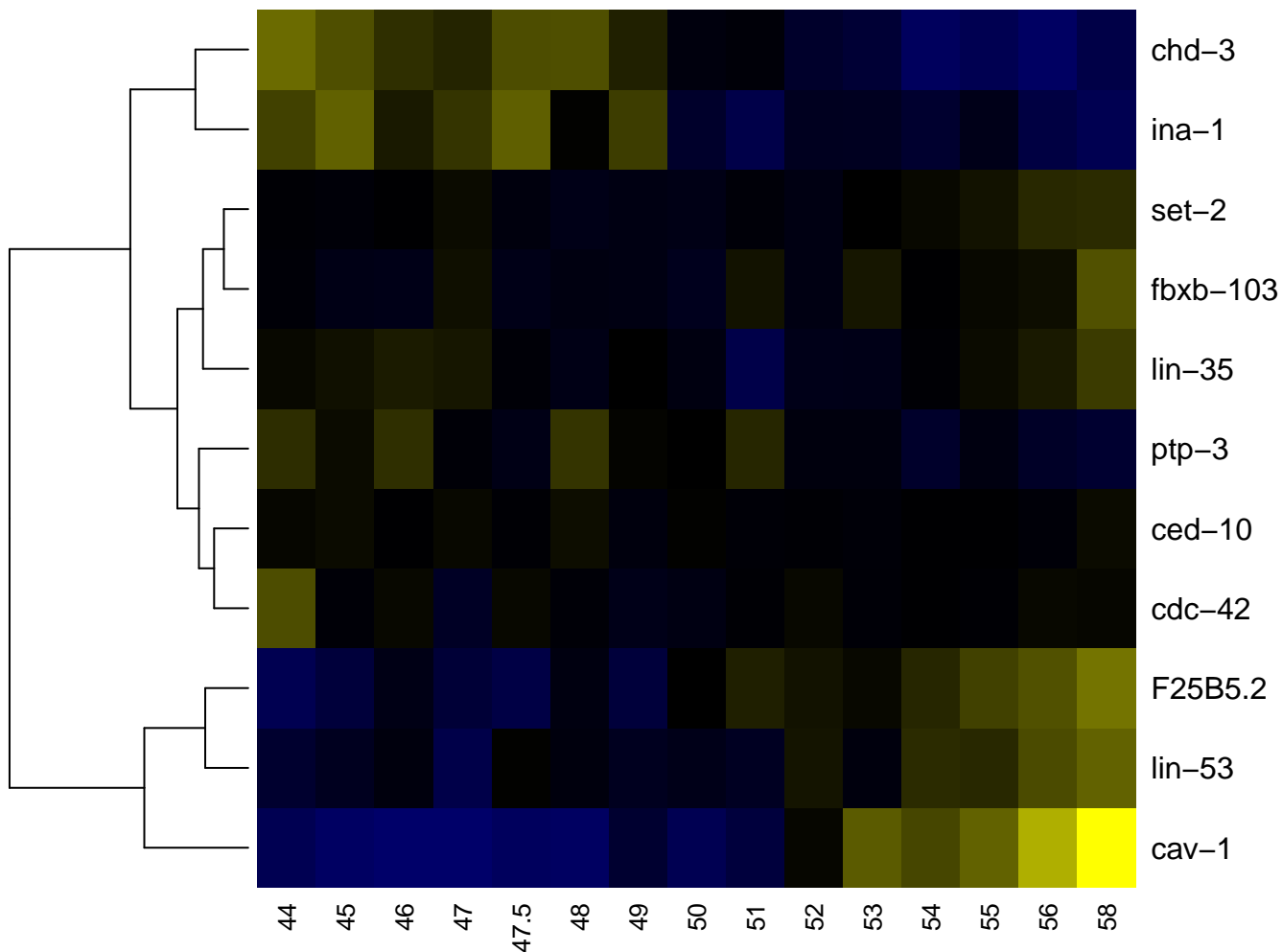
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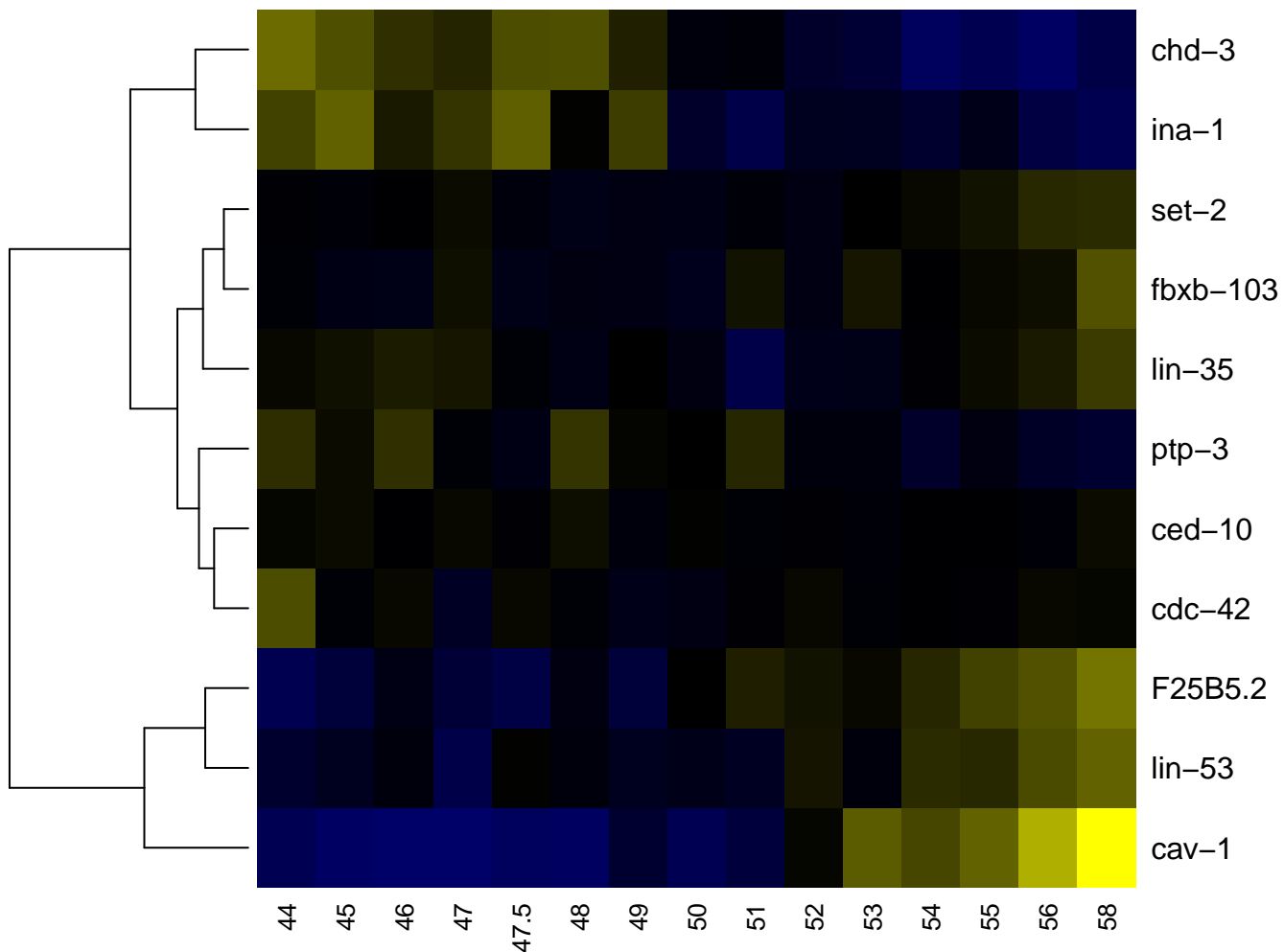
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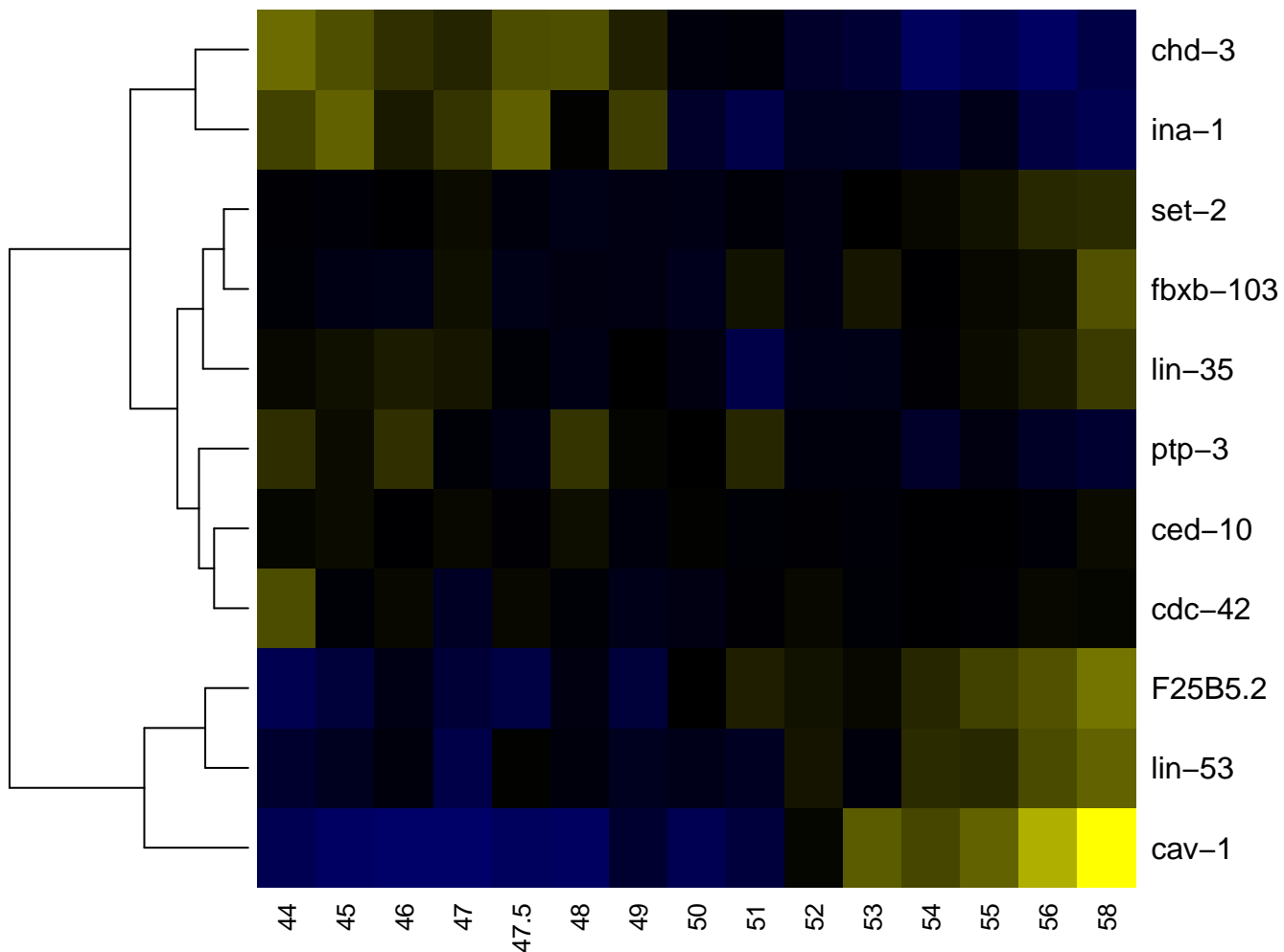
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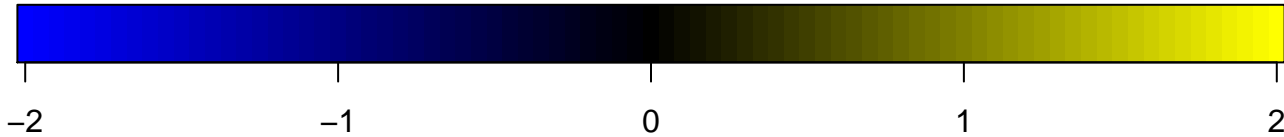
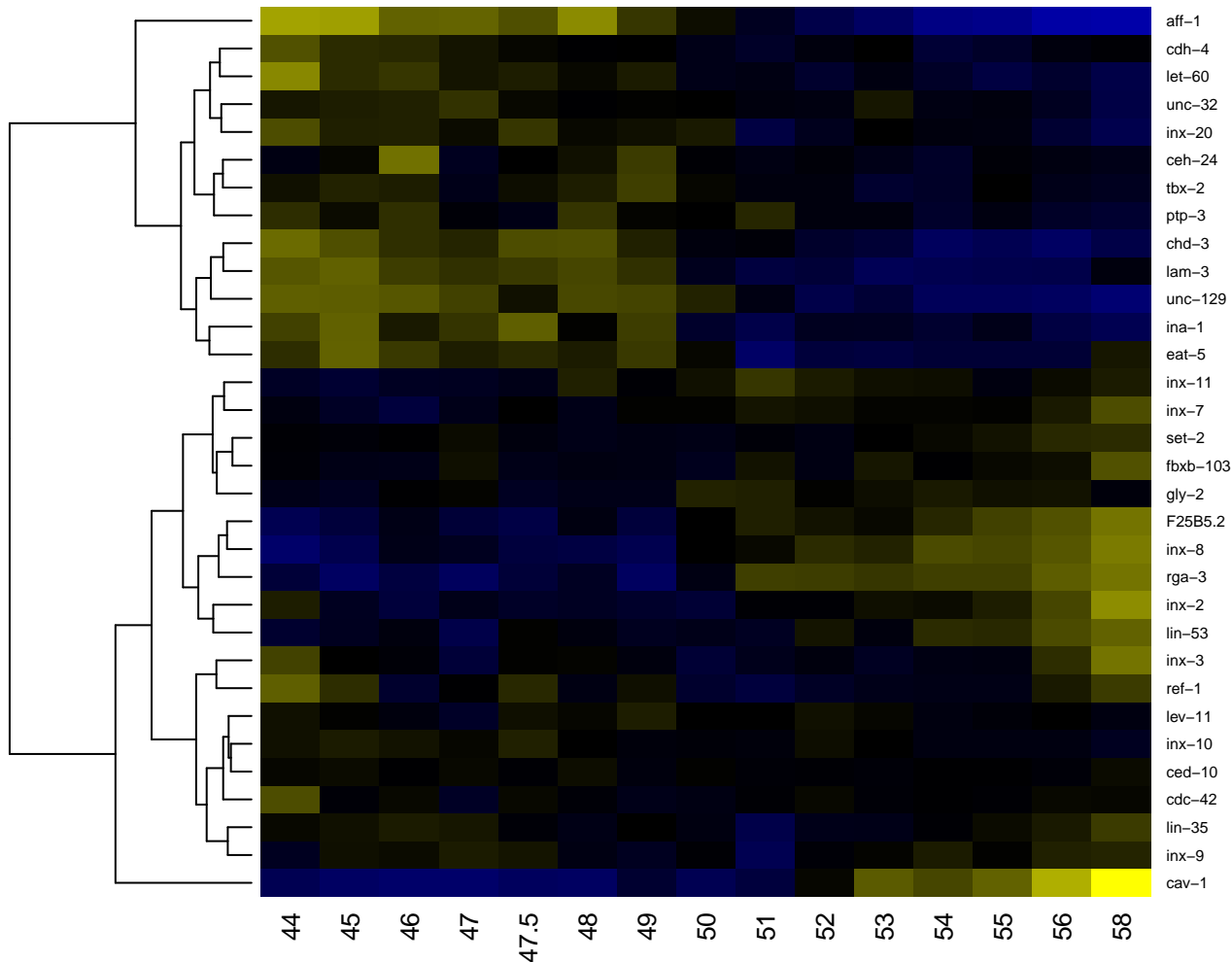
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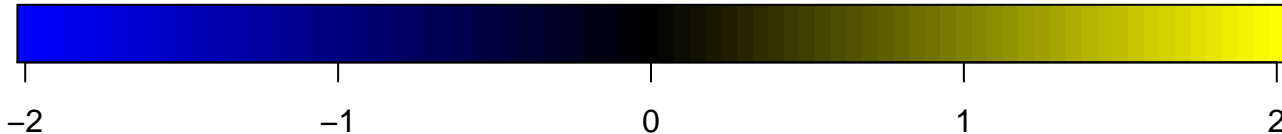
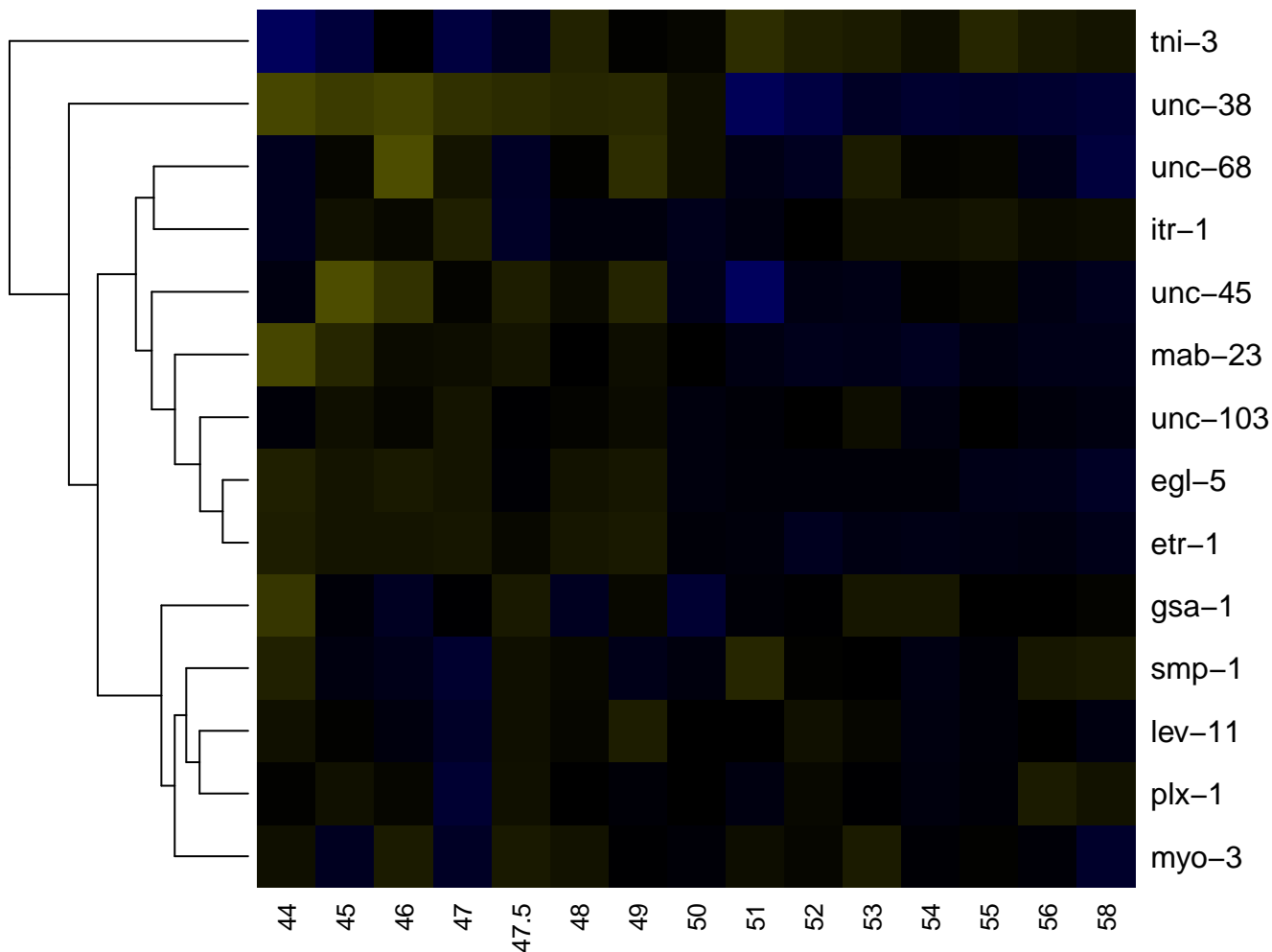
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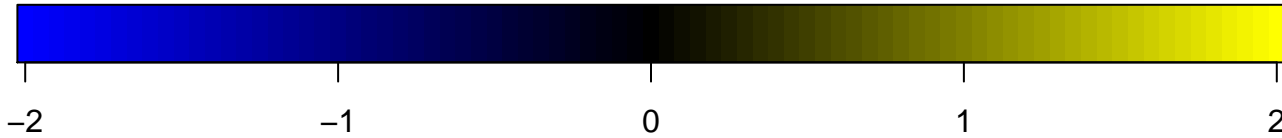
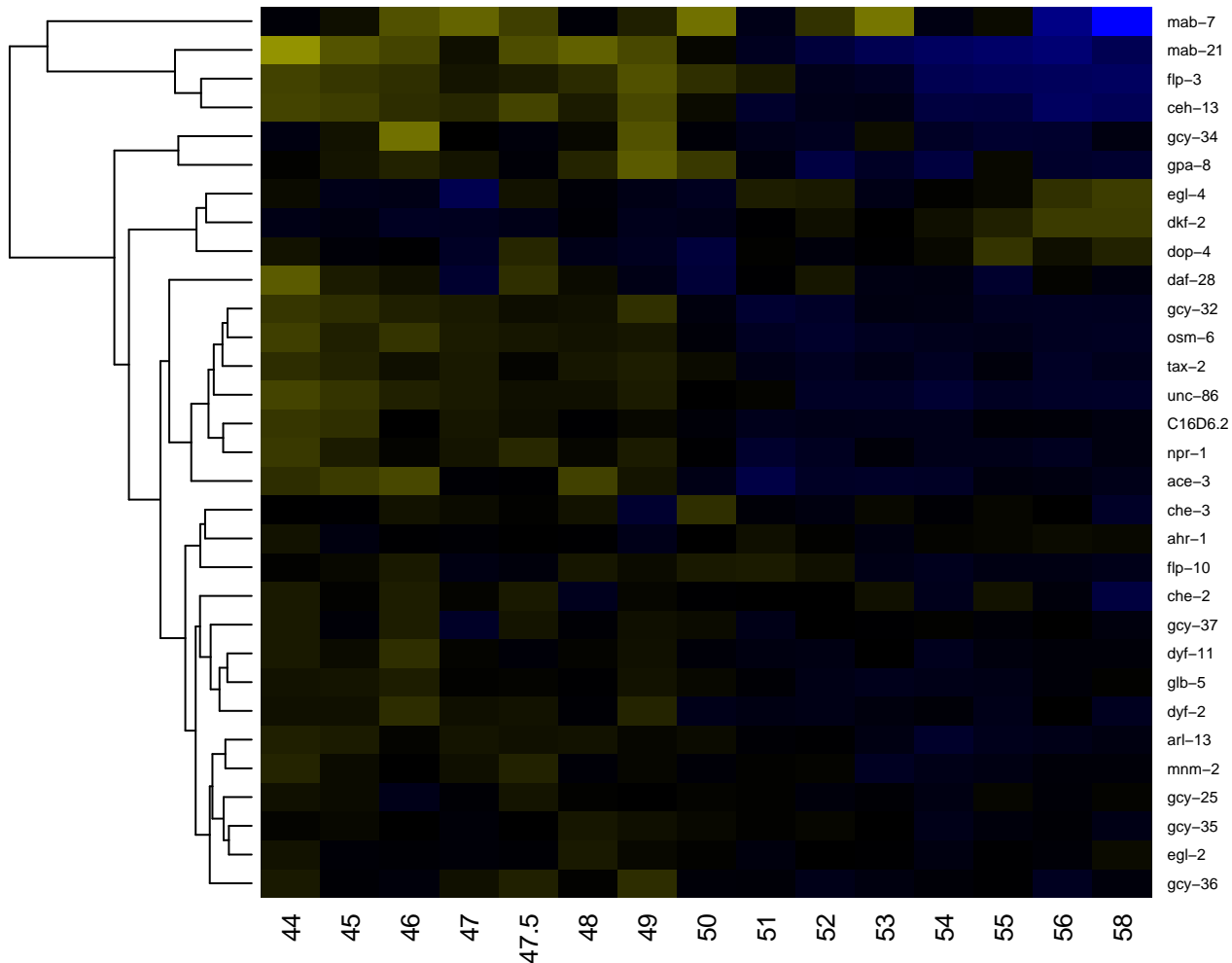
pm8



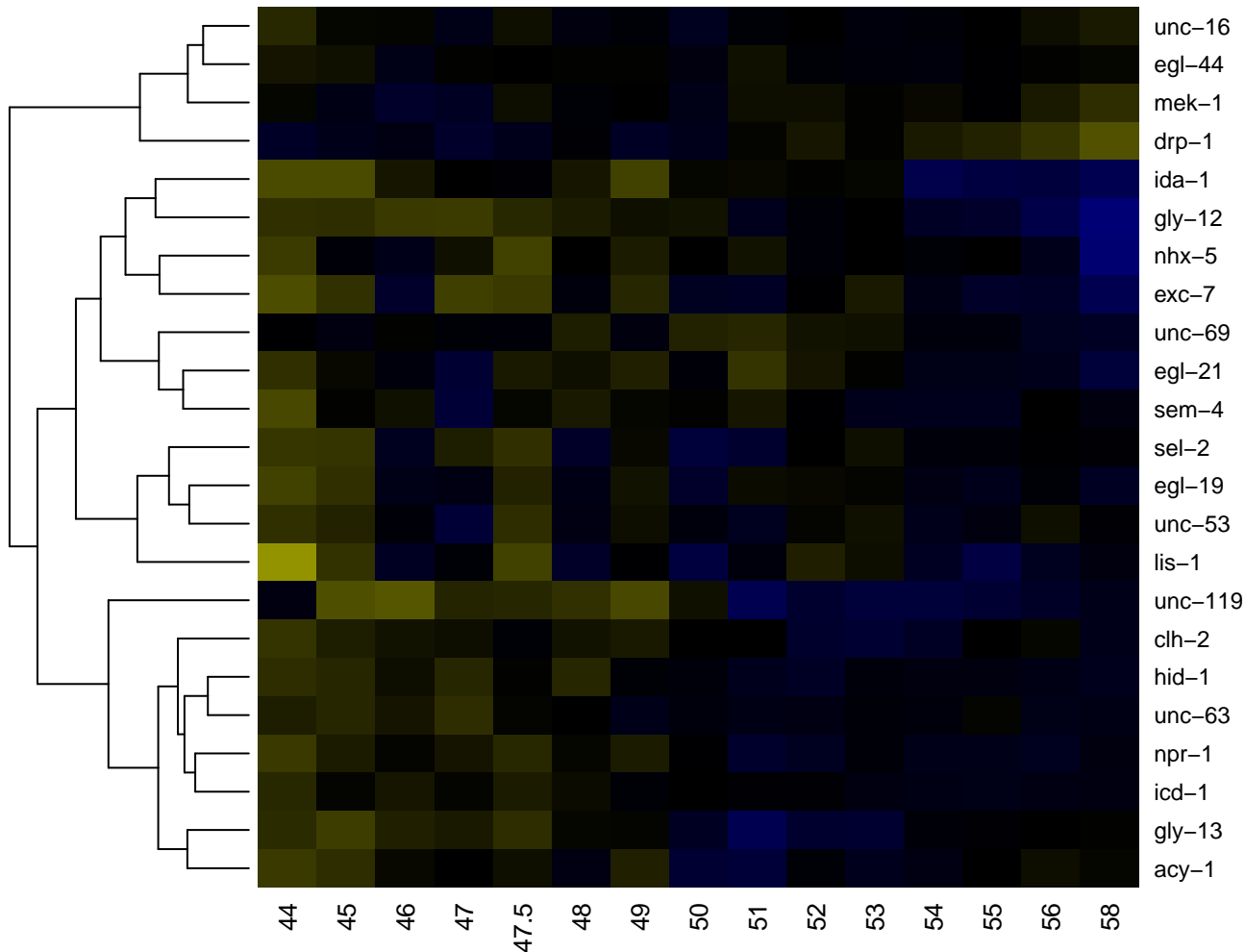
posterior oblique muscle



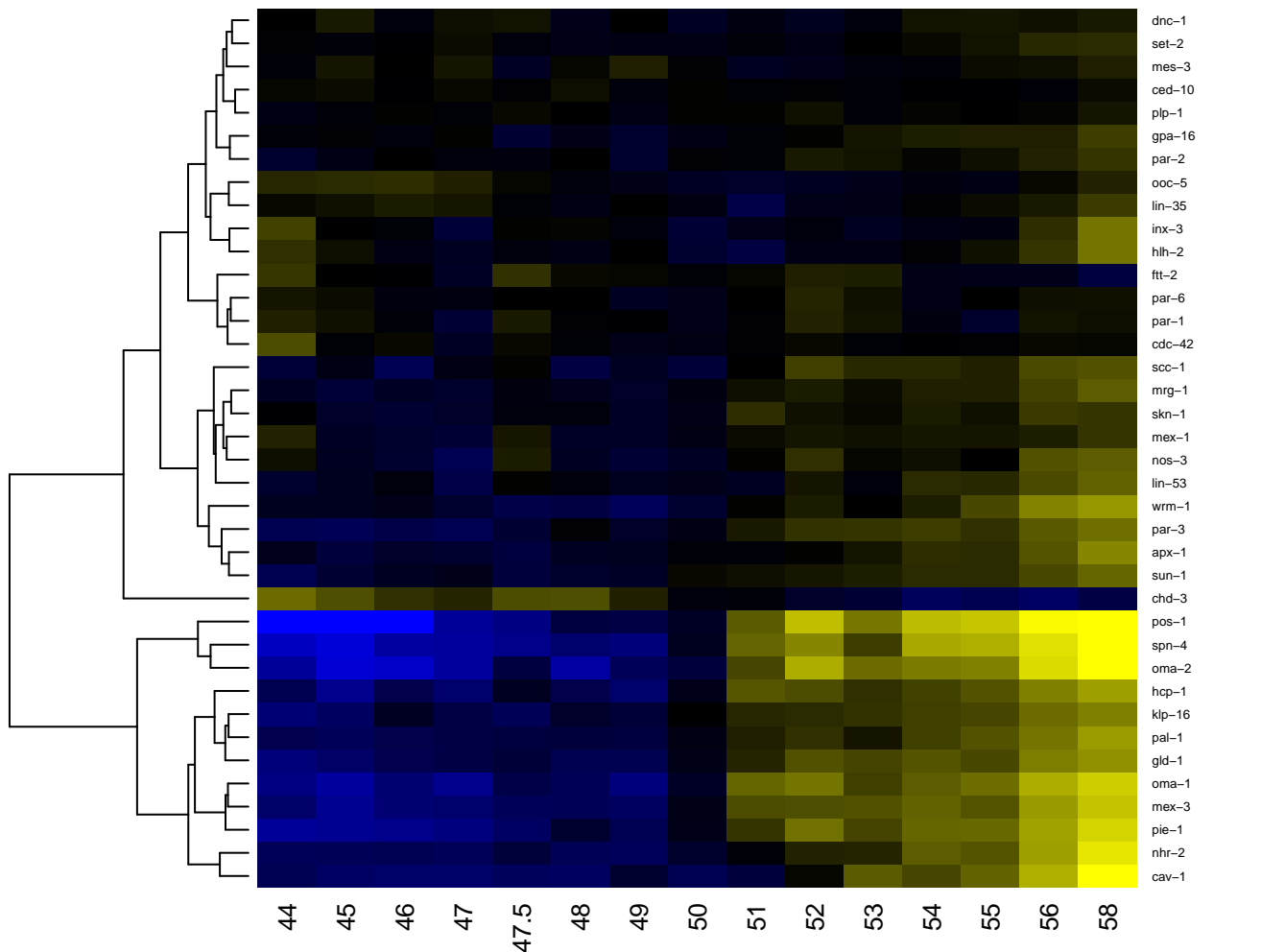
PQR



preanal ganglion



Psub1



-2

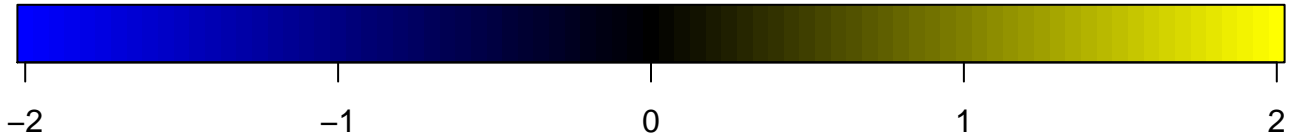
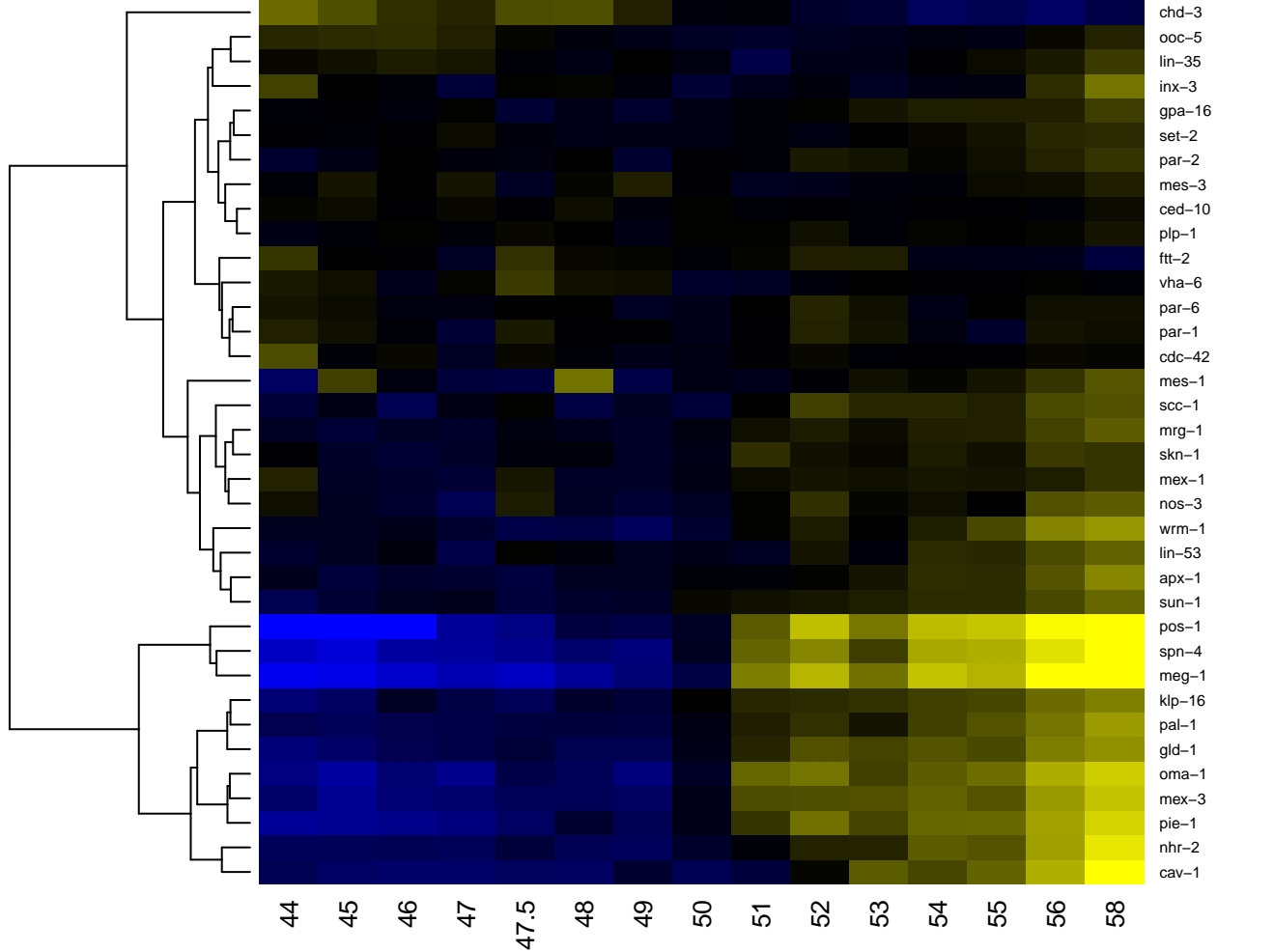
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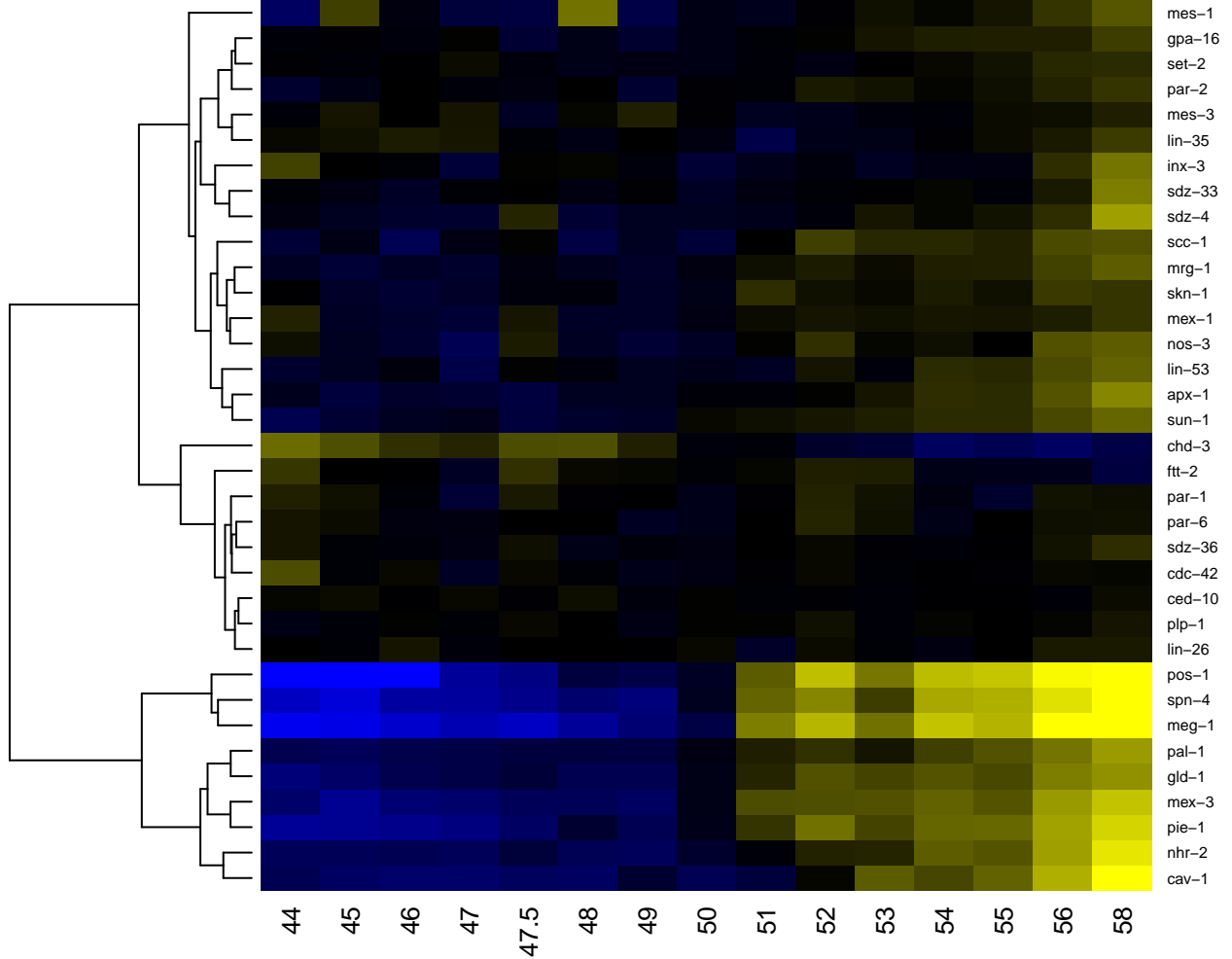
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2

Psub2



Psub3



-2

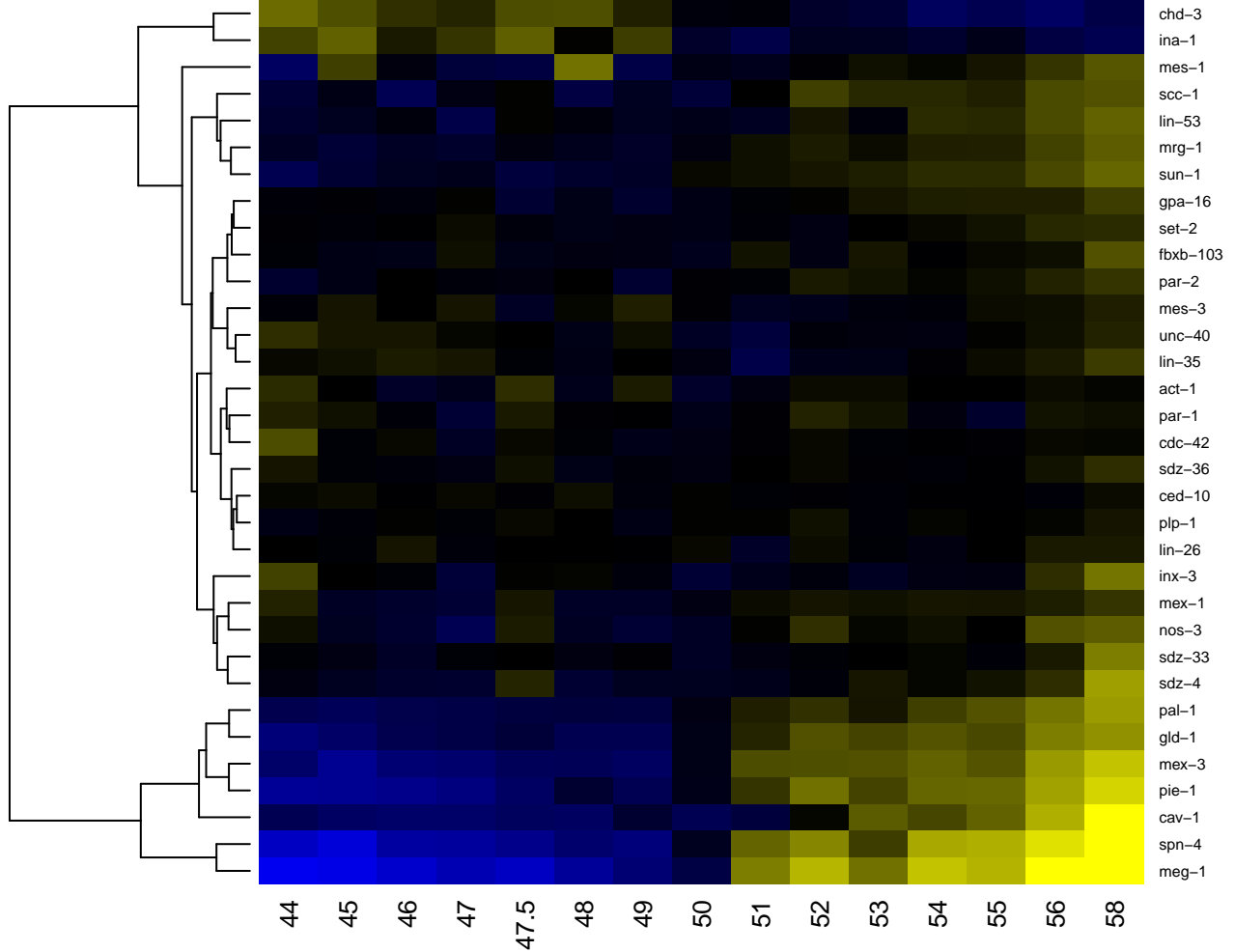
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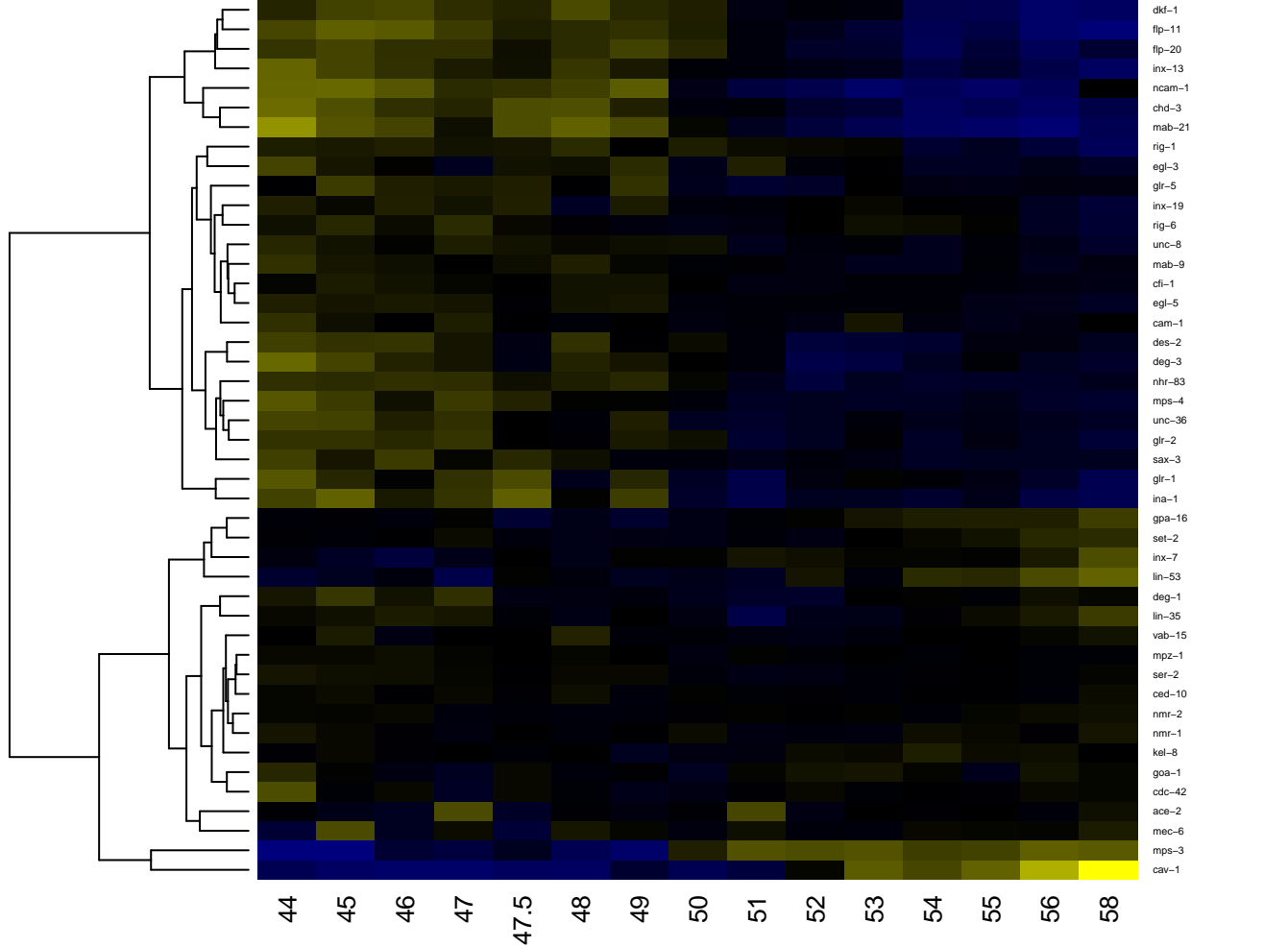
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Psub4



PVCL



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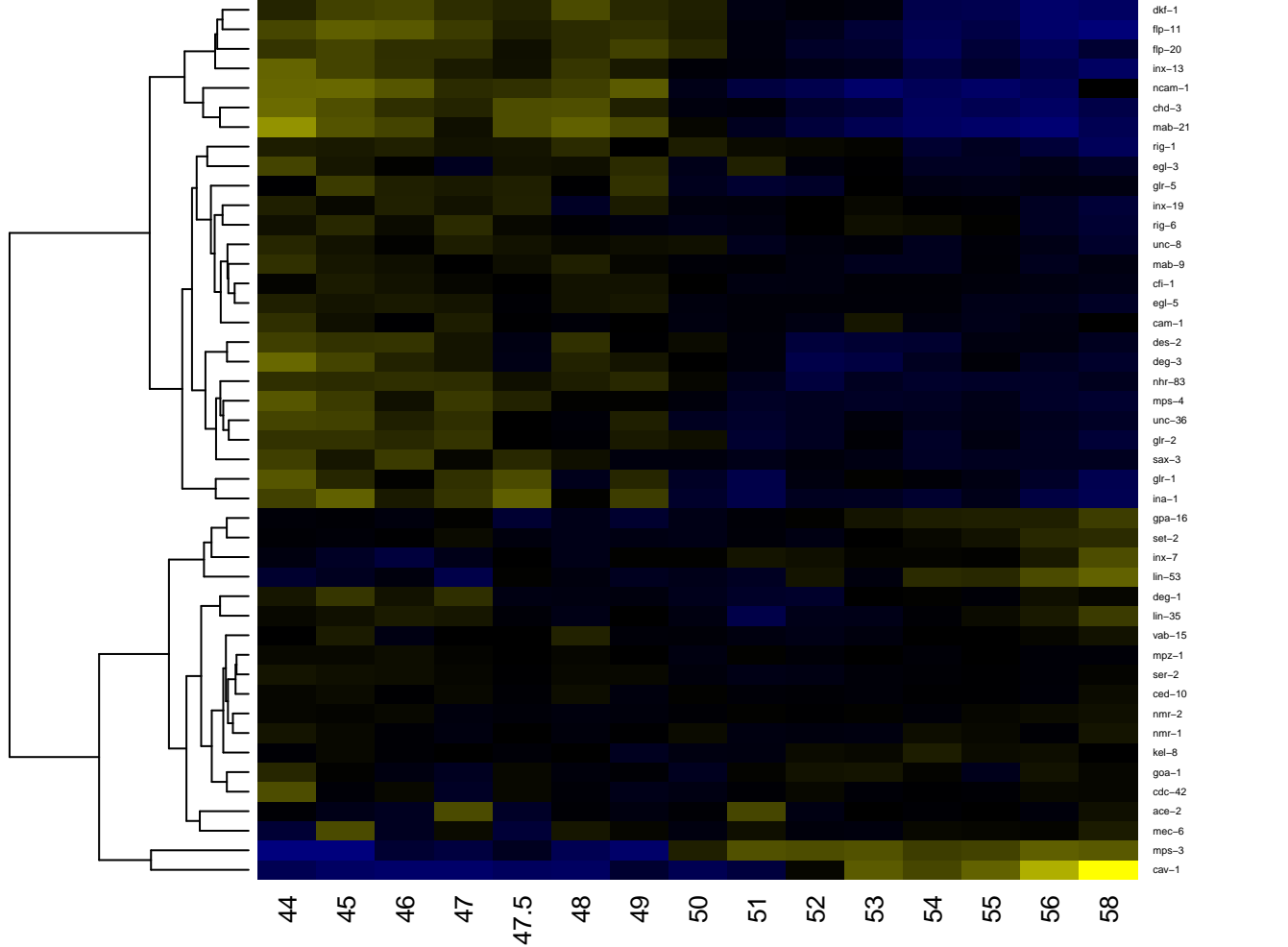
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PVCR



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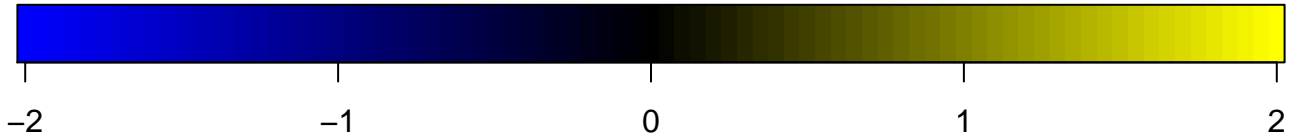
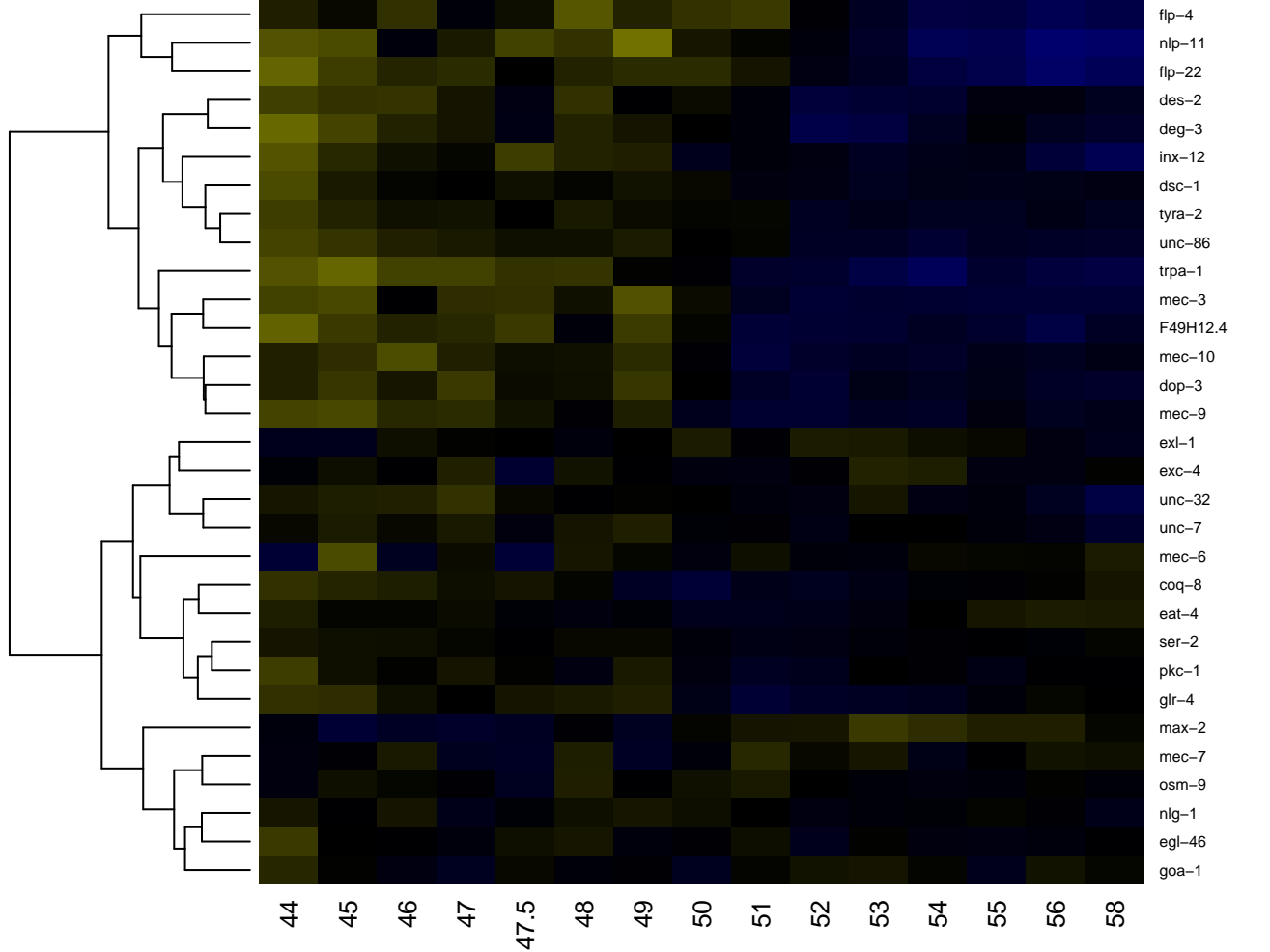
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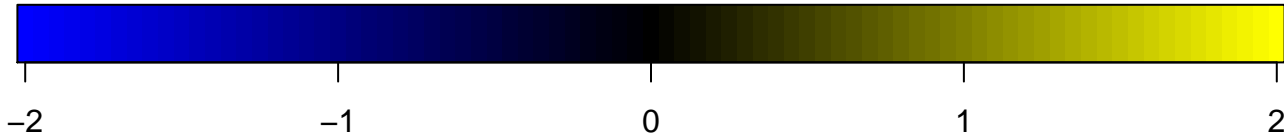
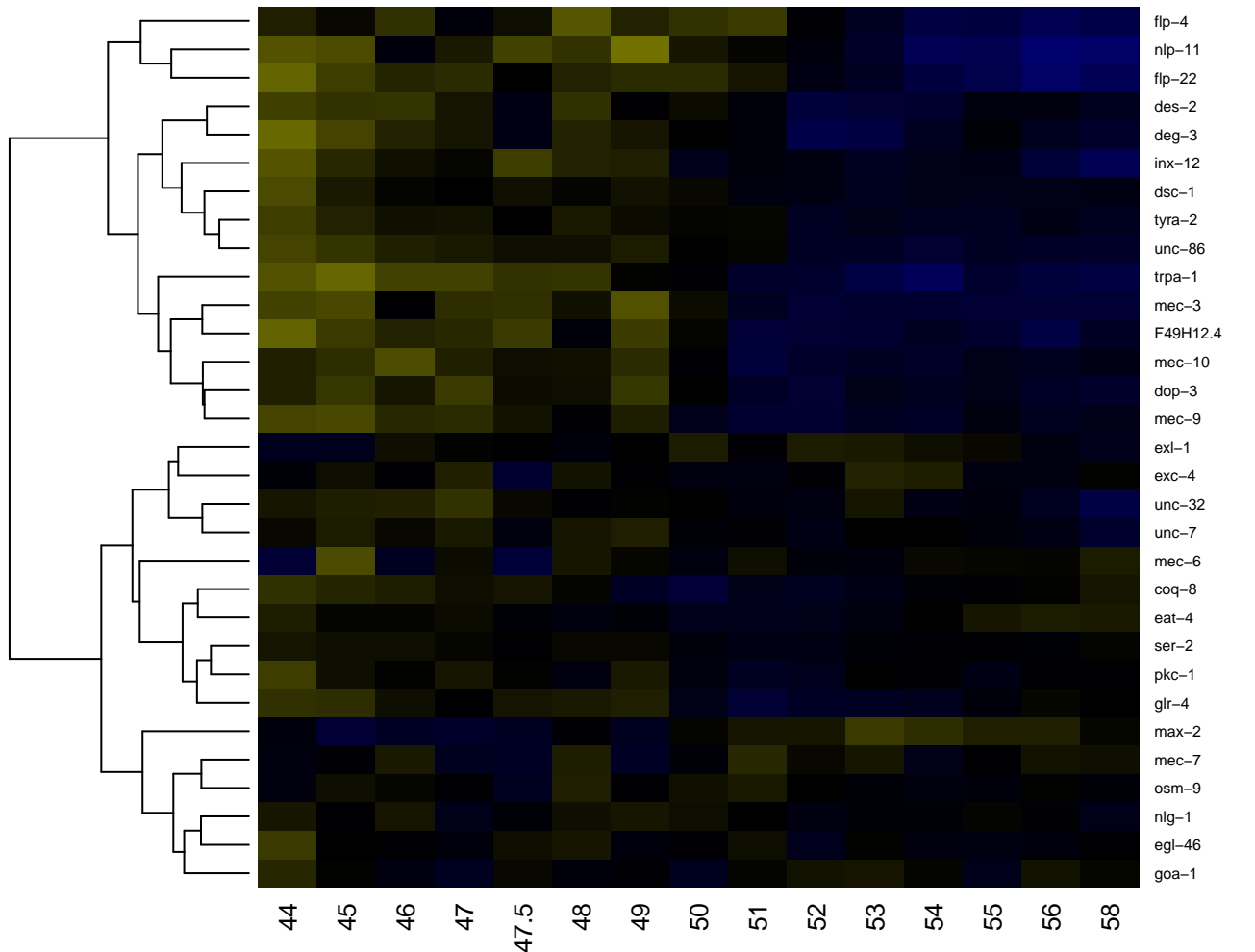
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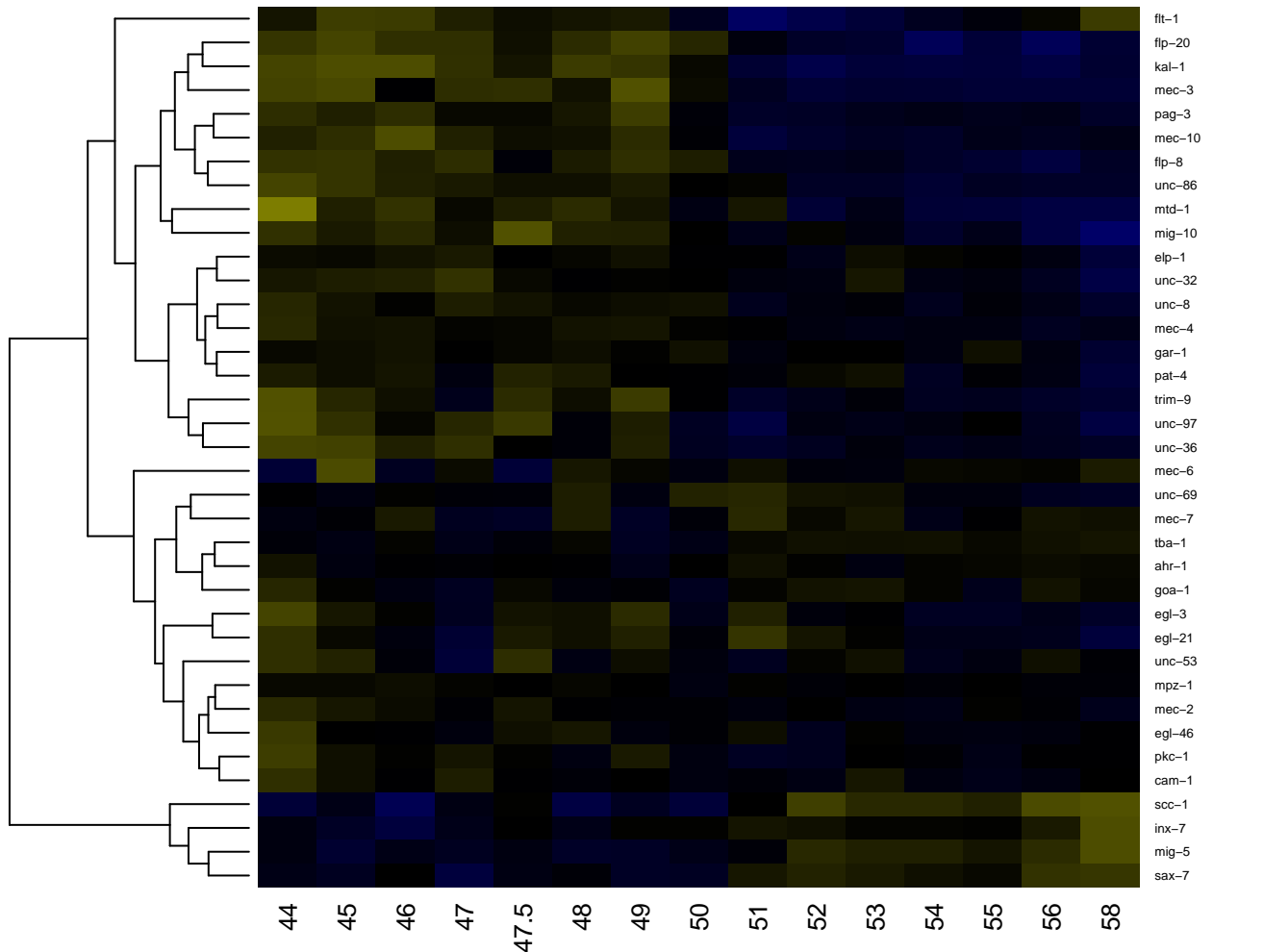
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PVDR



PVM



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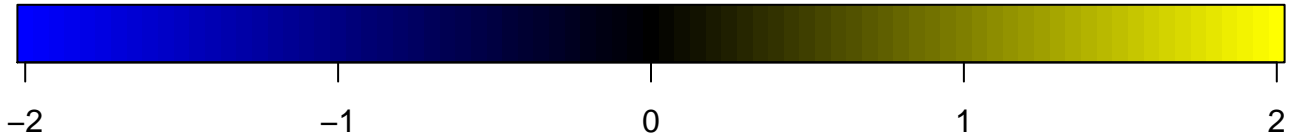
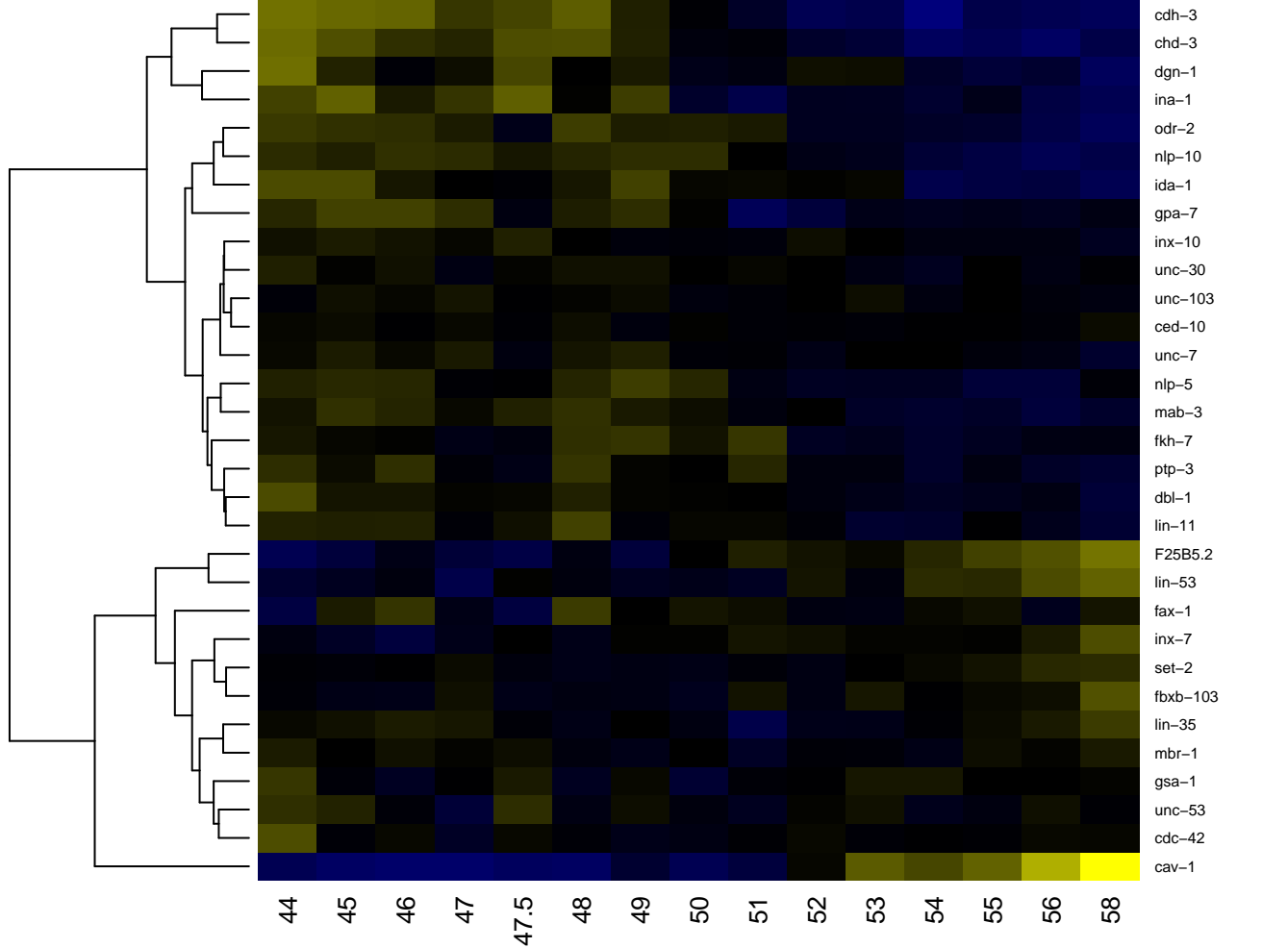
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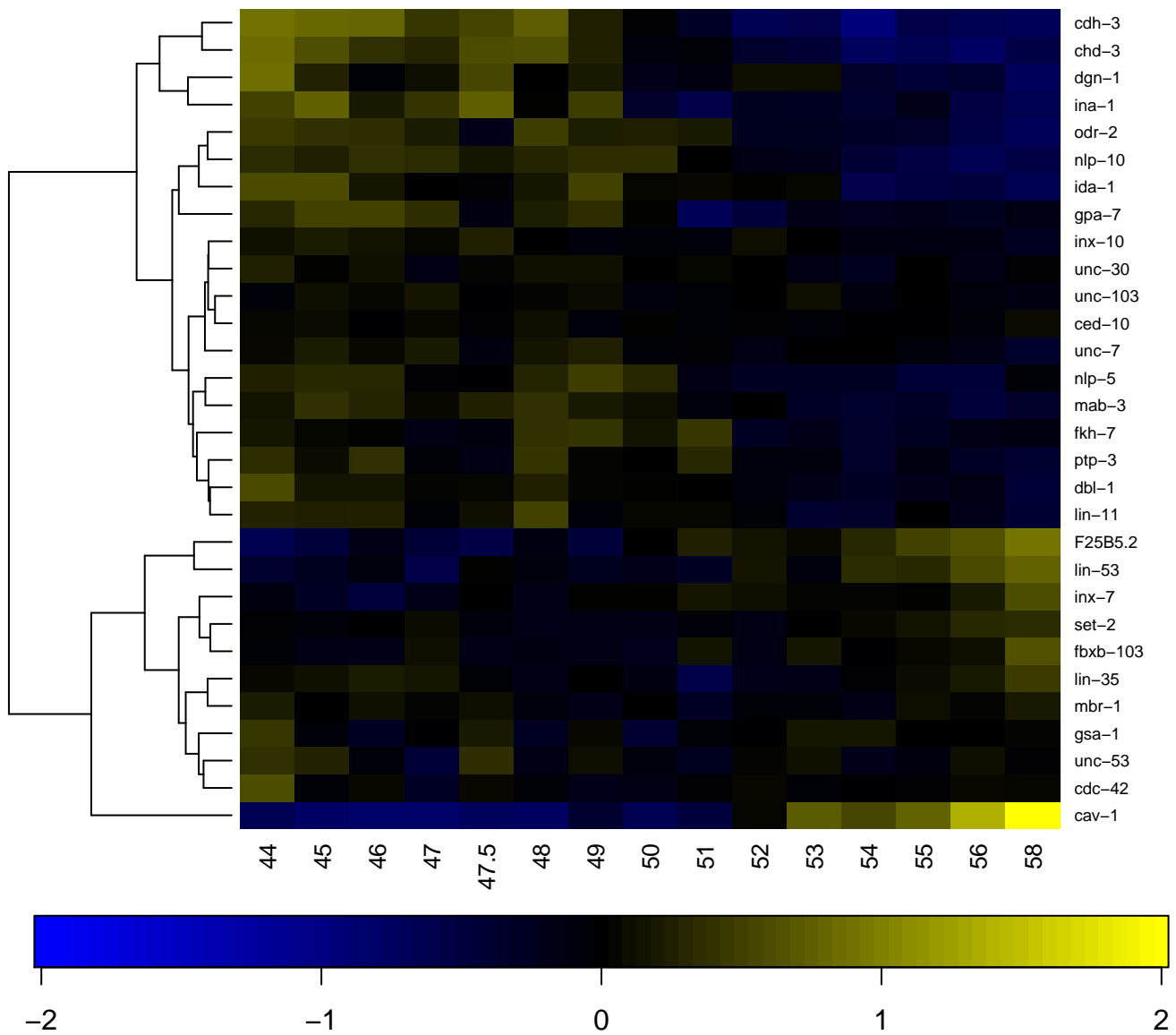
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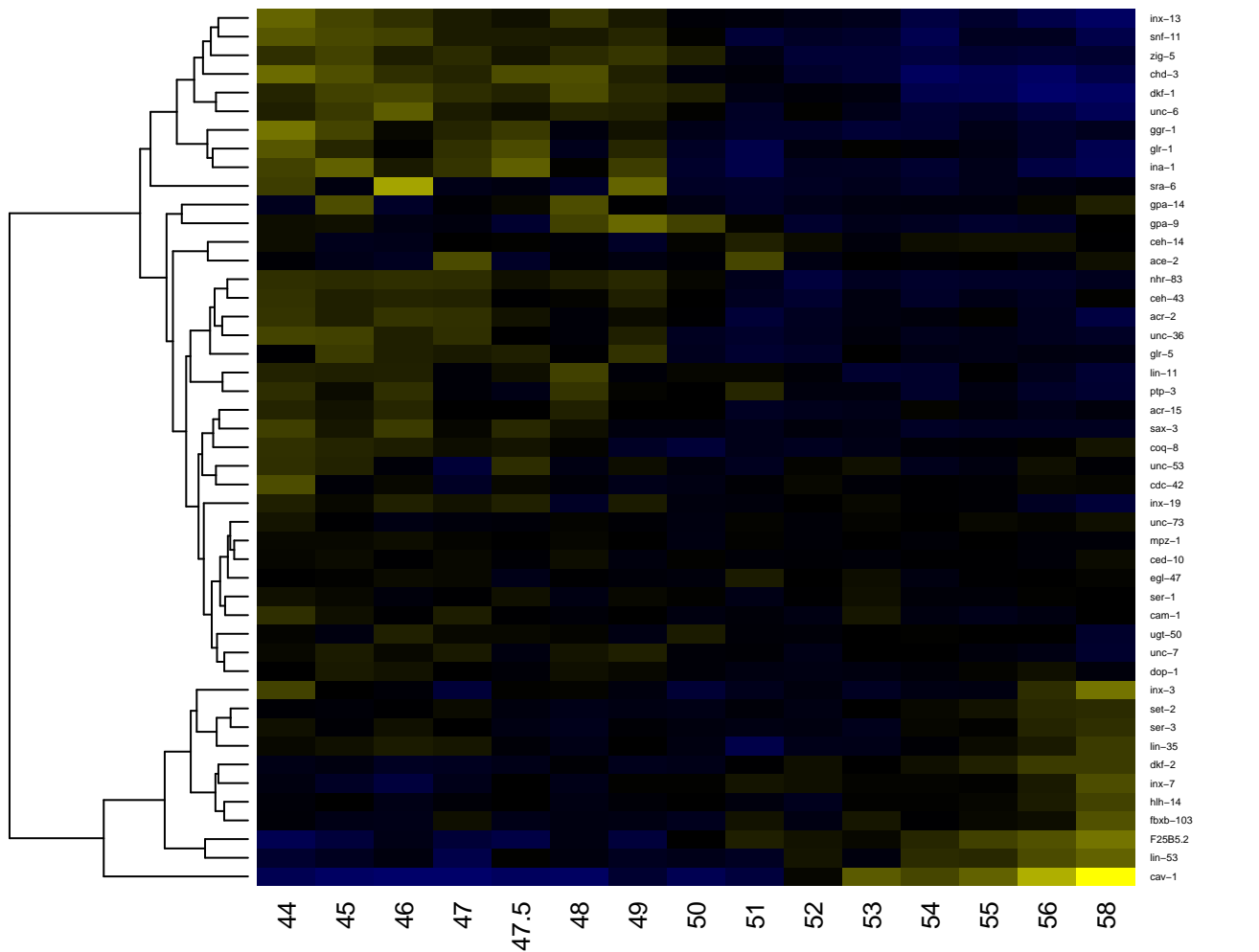
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PVPR



PVQL



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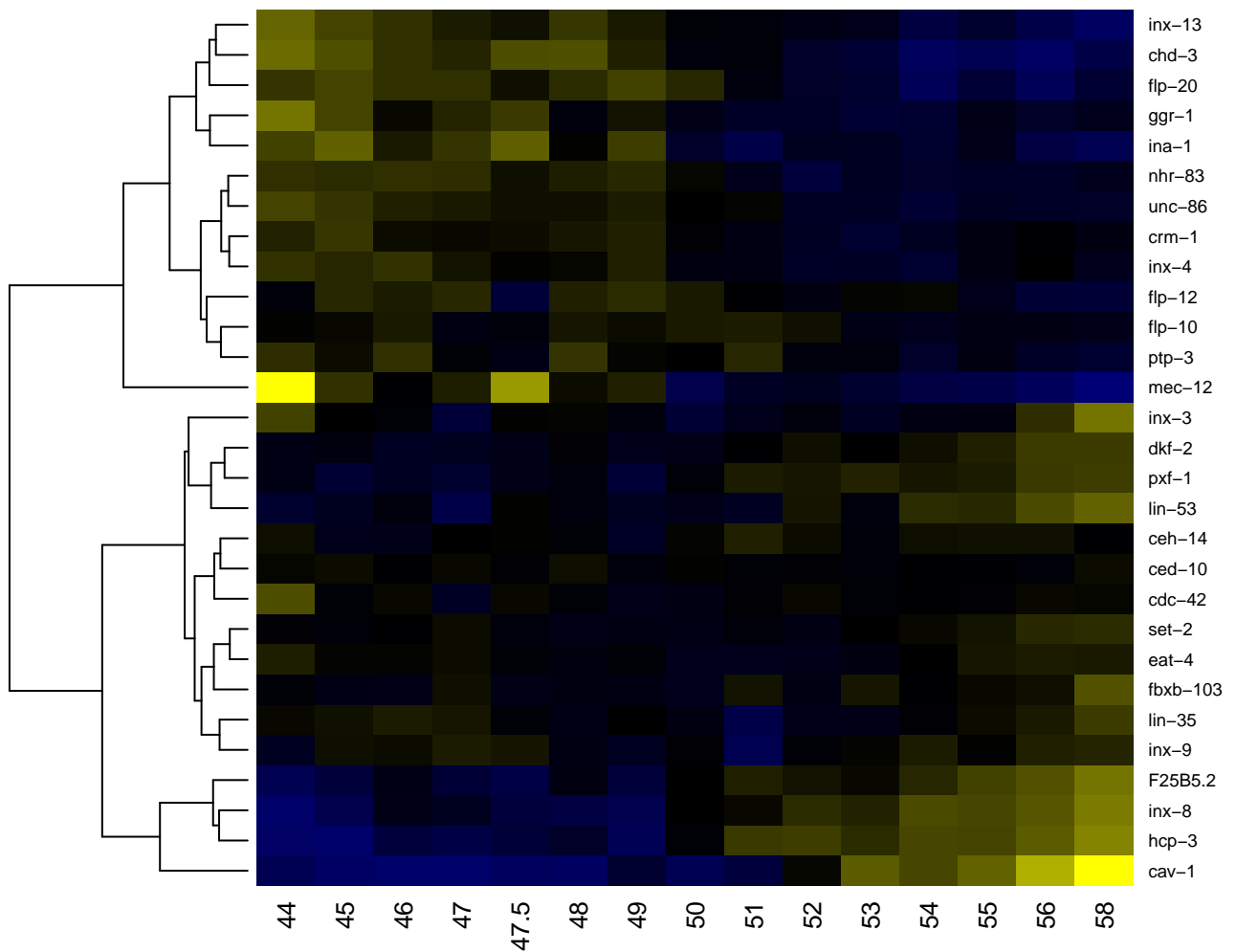
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PVR



-2

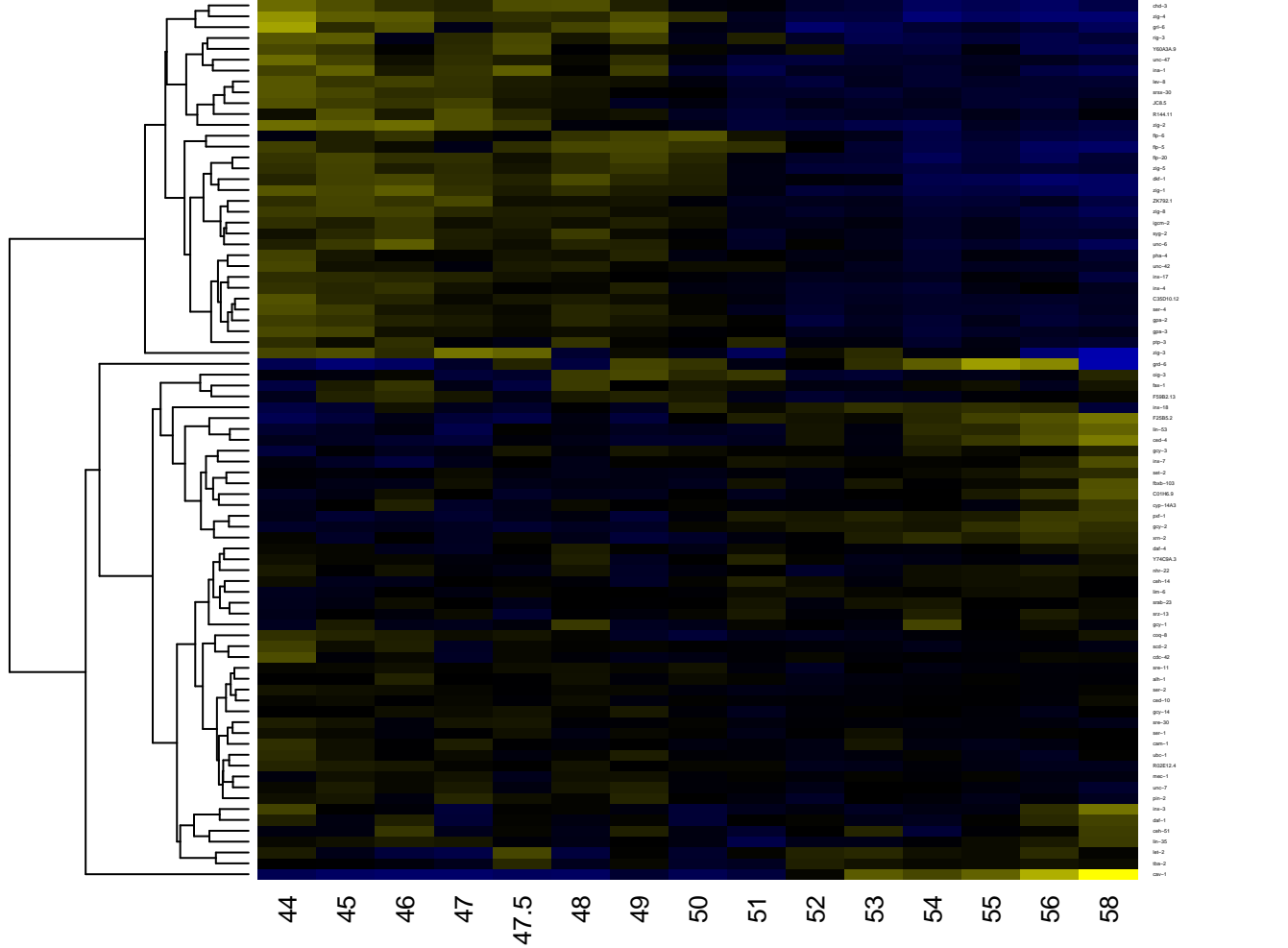
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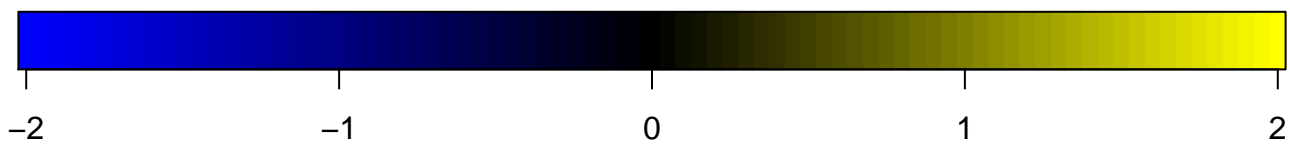
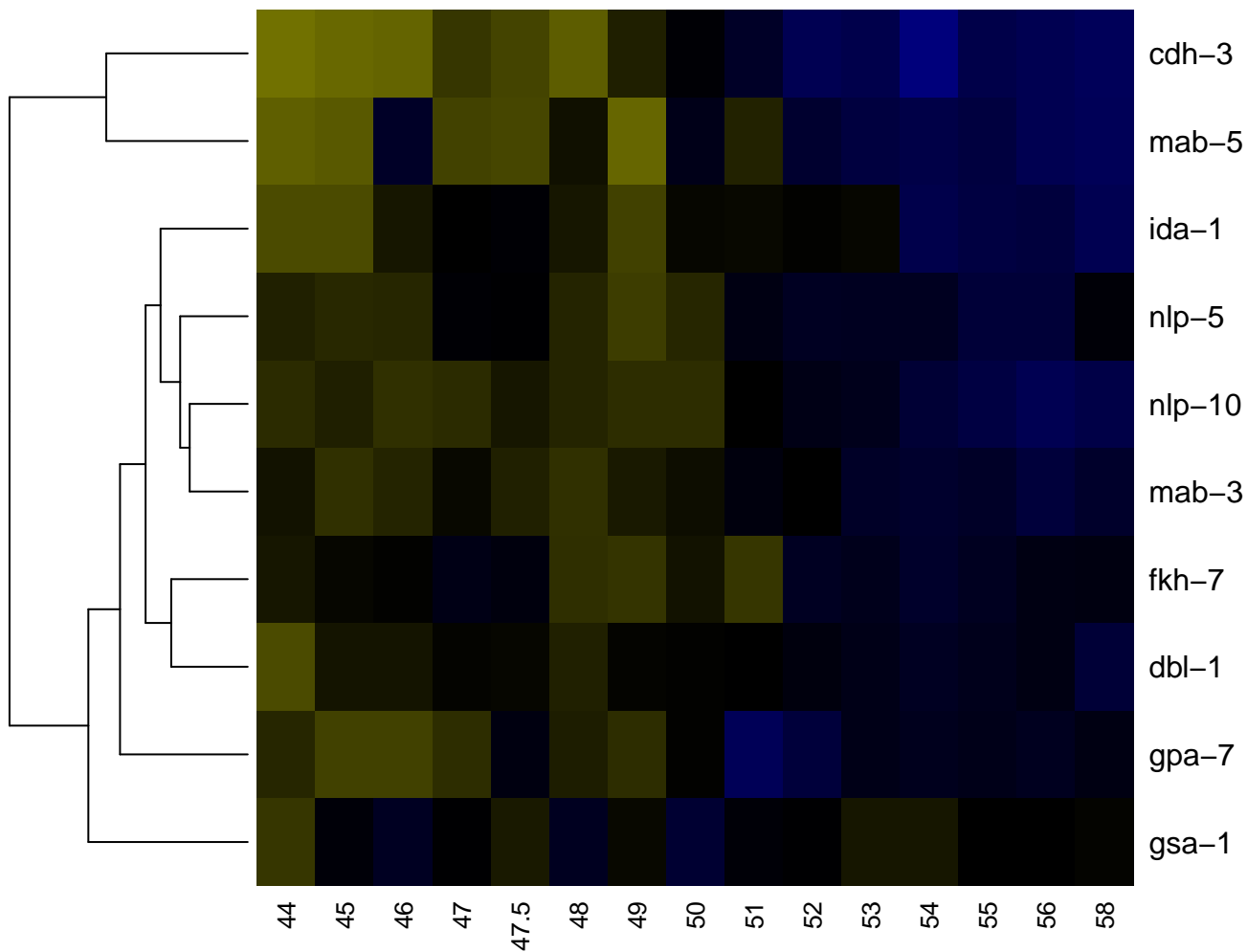
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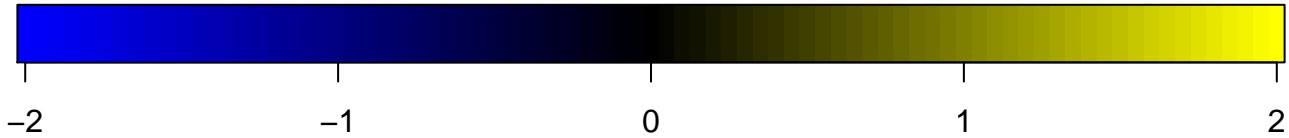
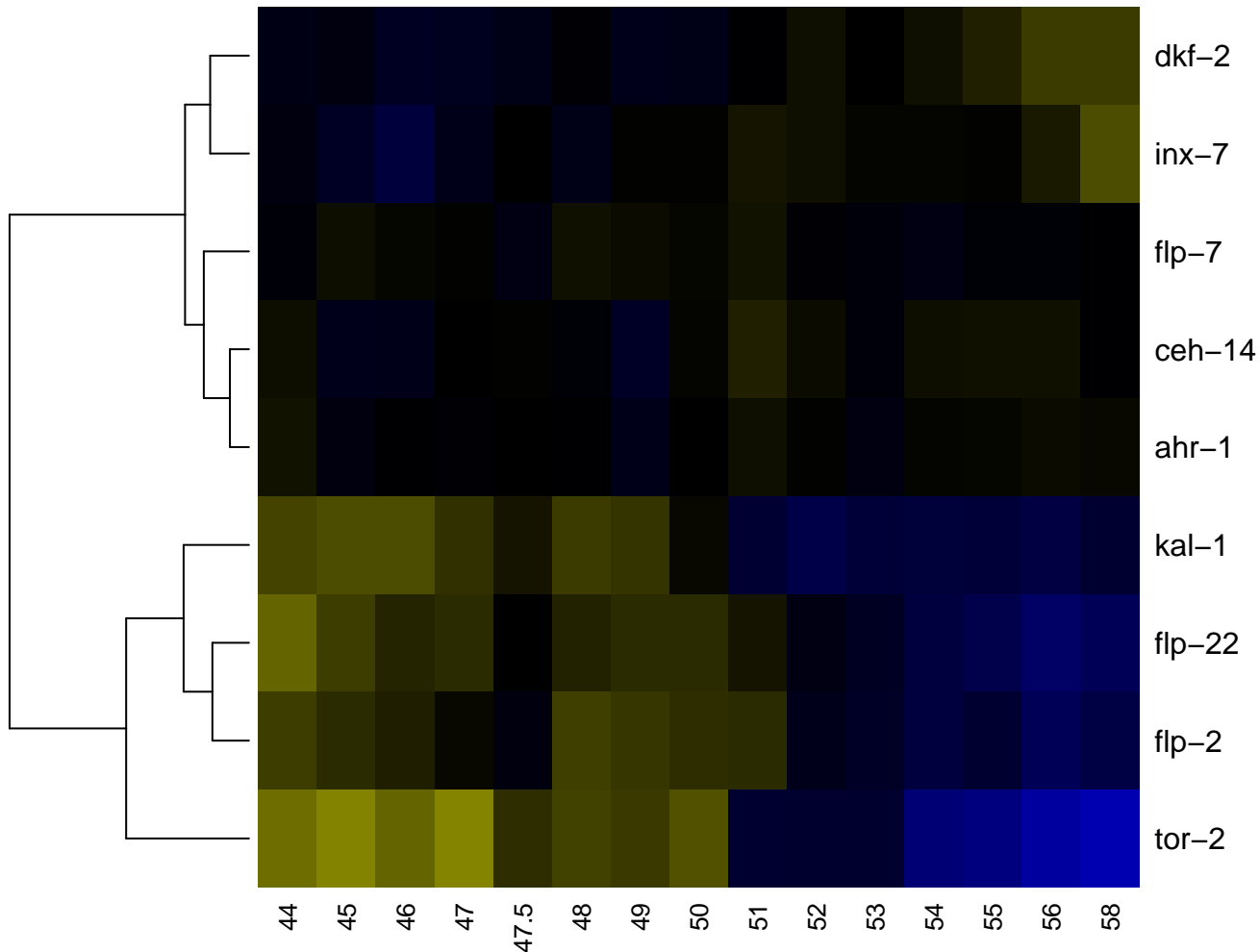
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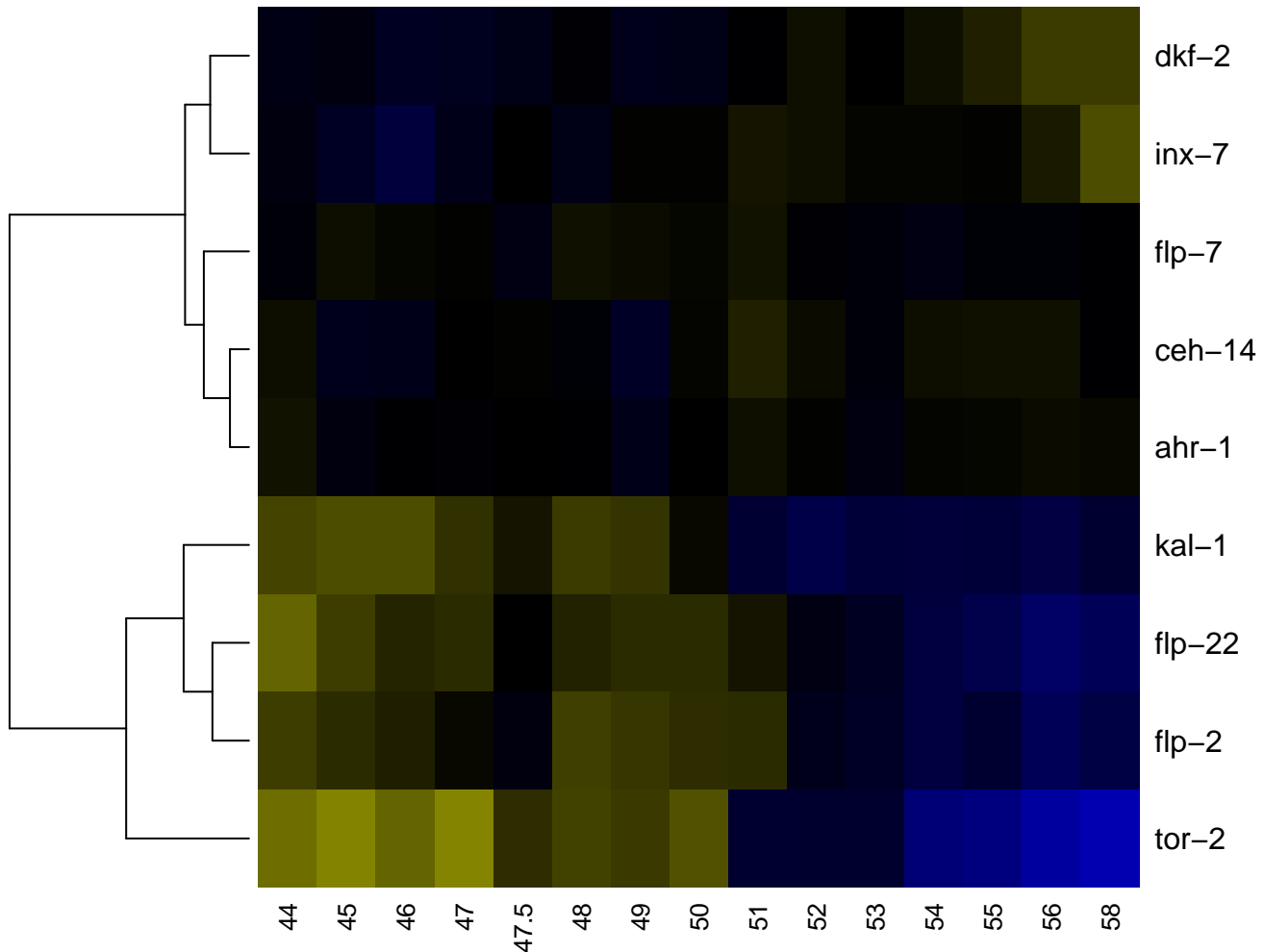
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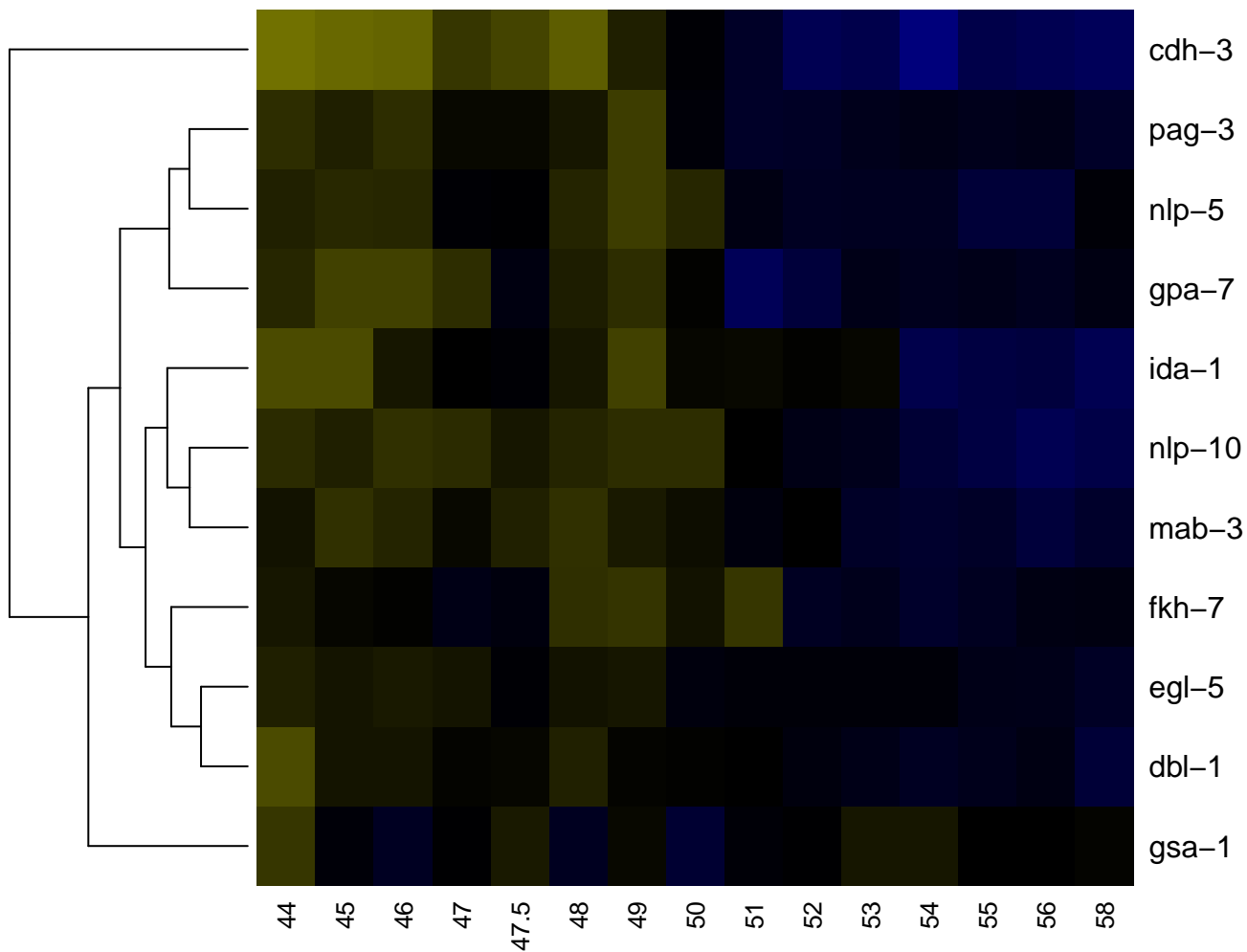
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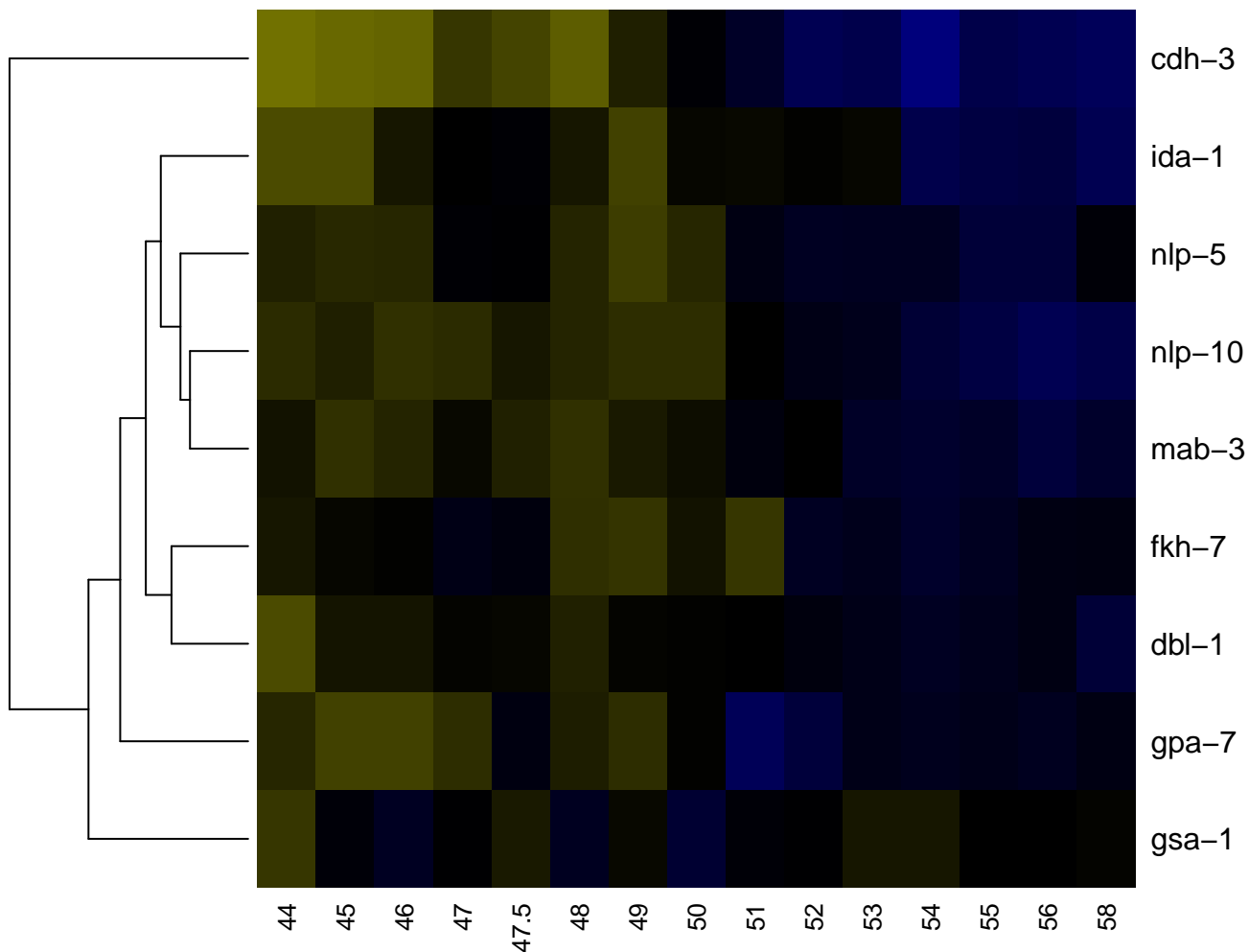
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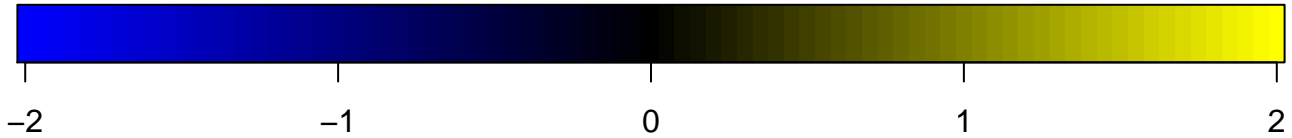
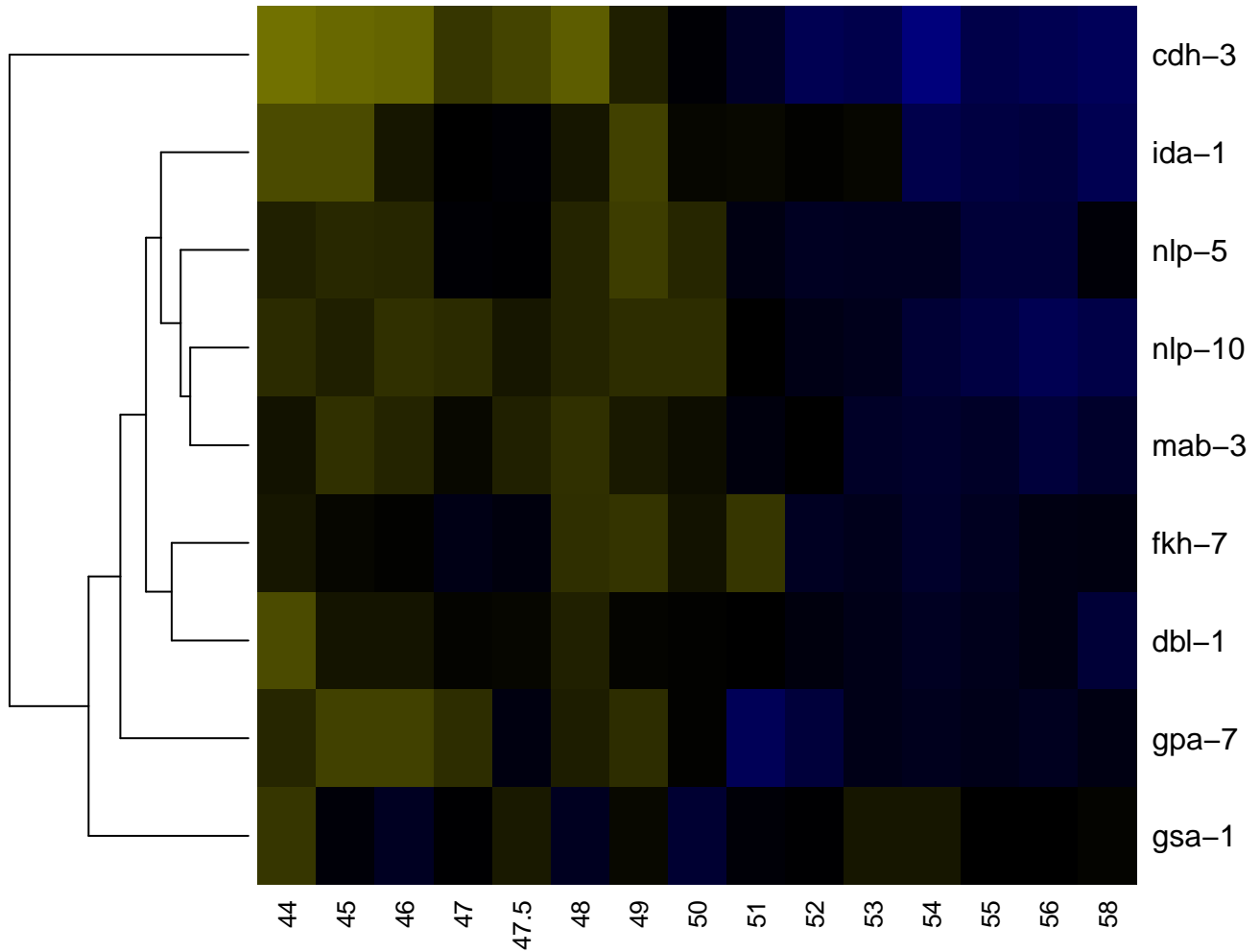
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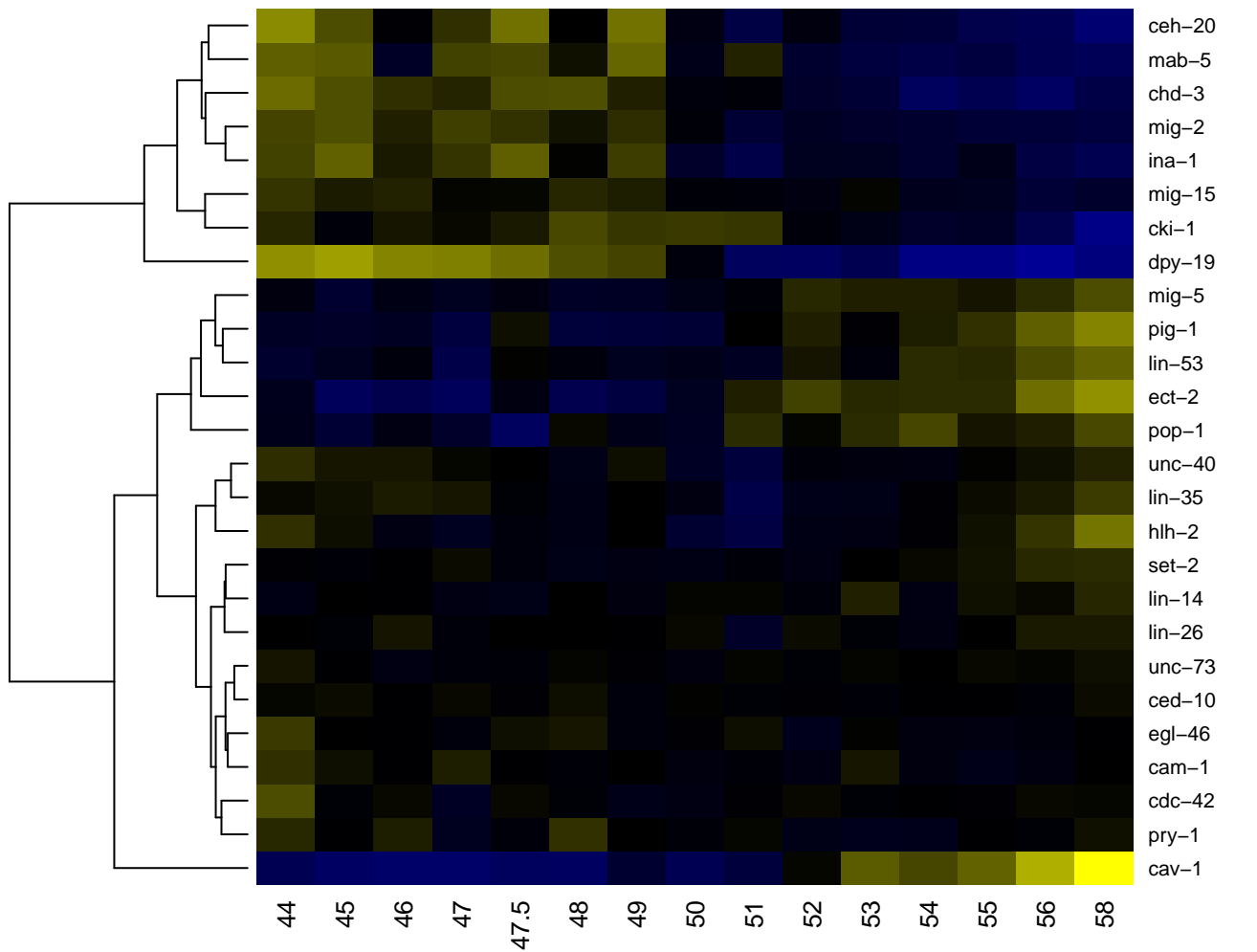
PVY



PVZ



QL



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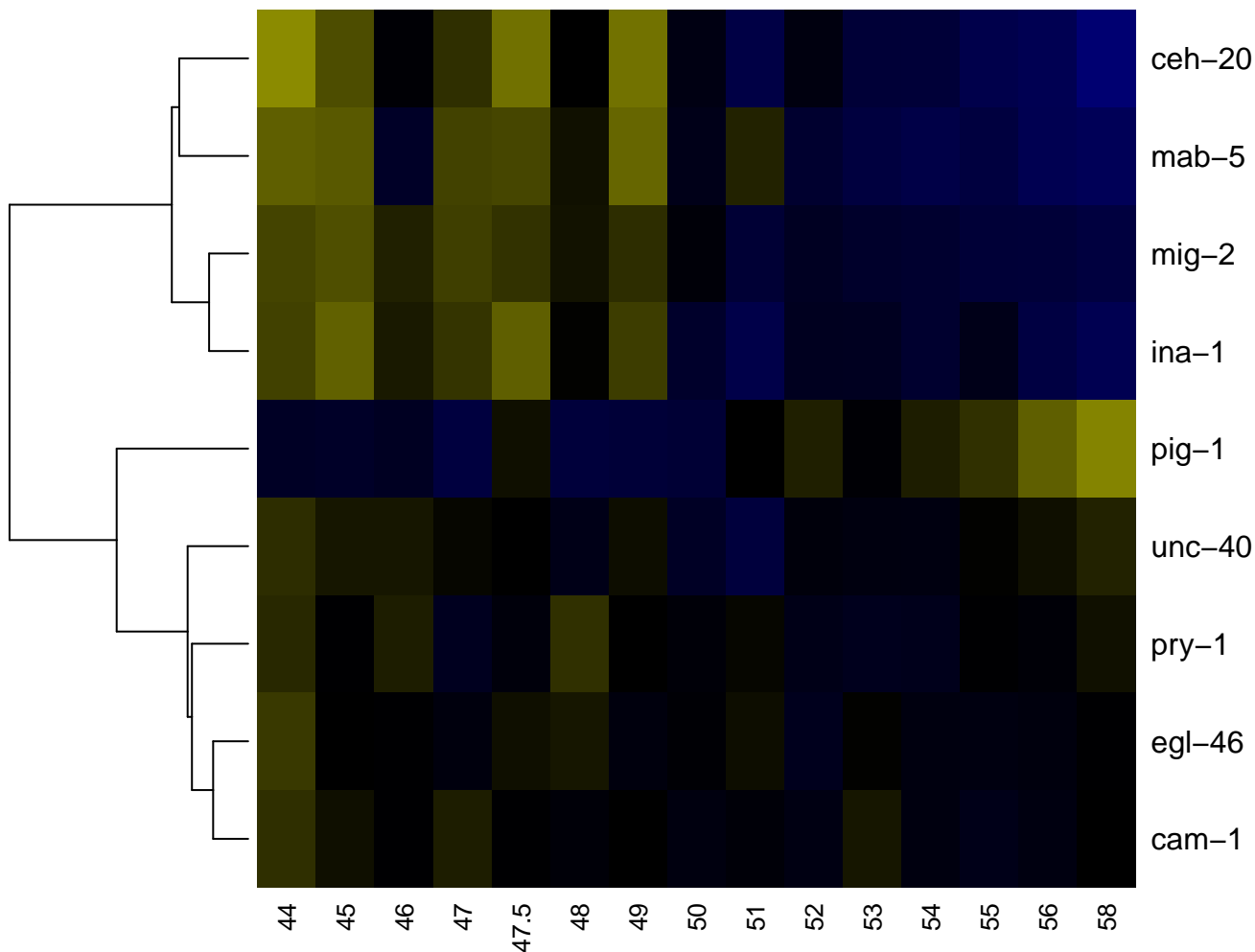
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QL.a



-2

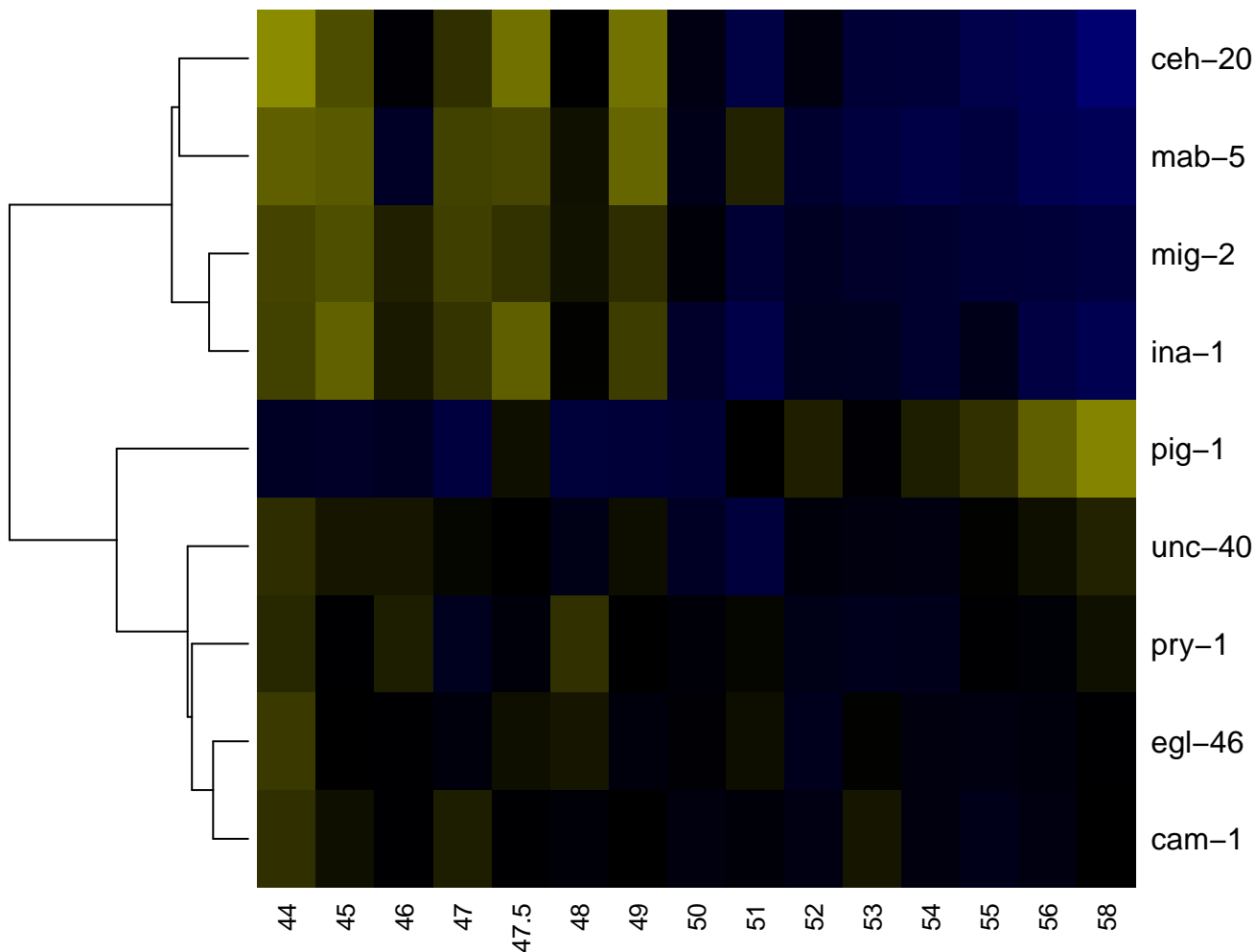
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QL.p



-2

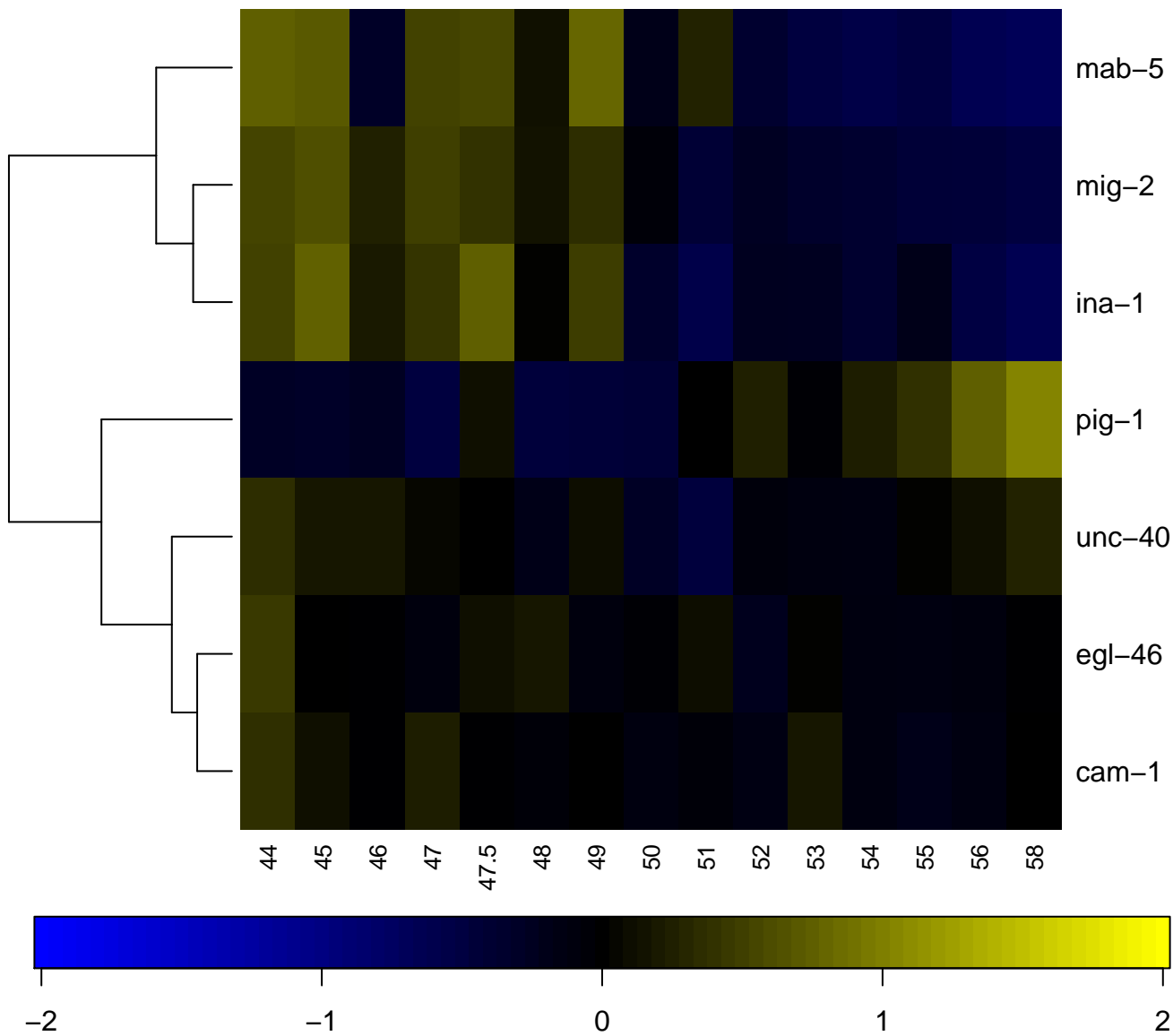
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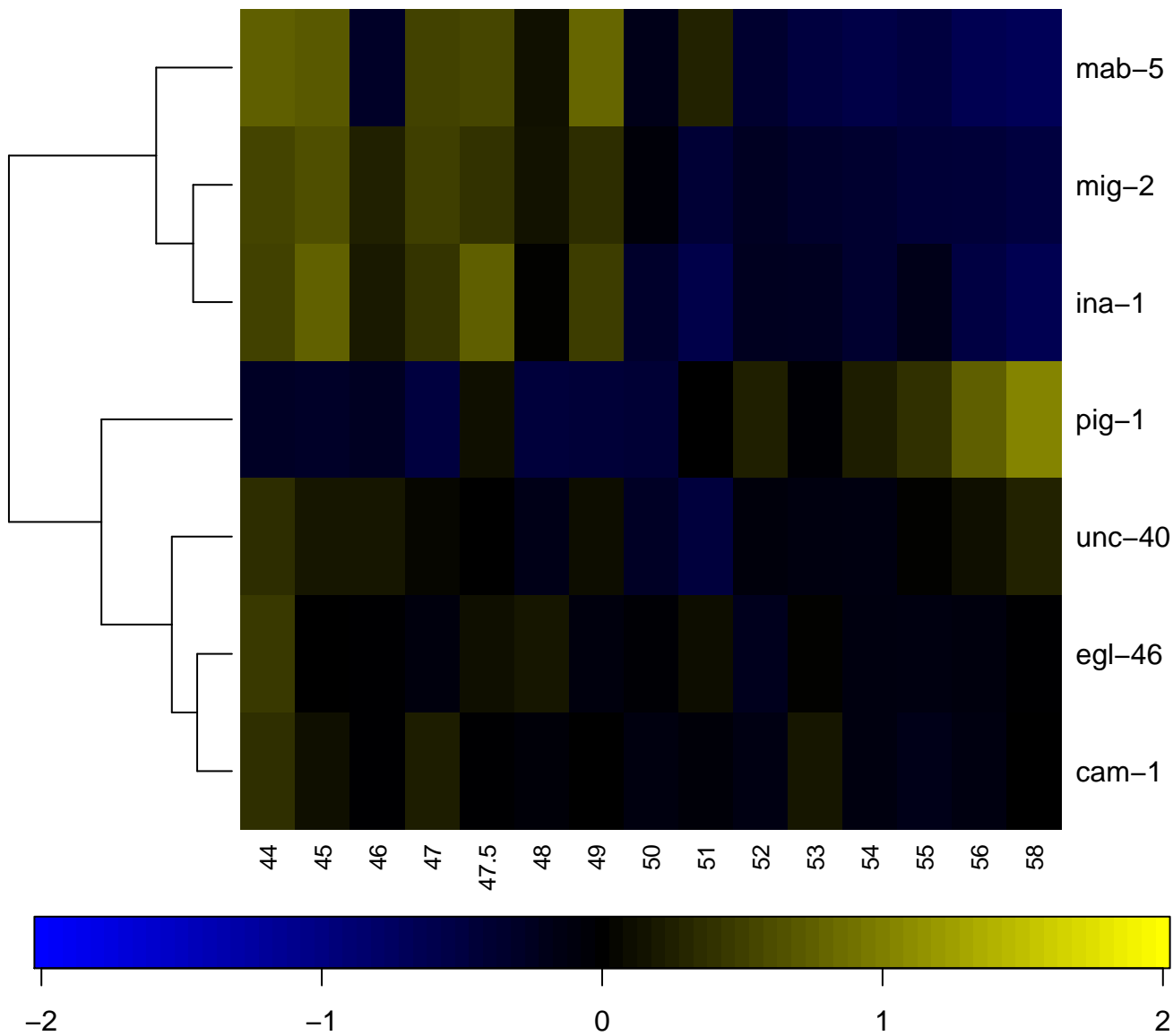
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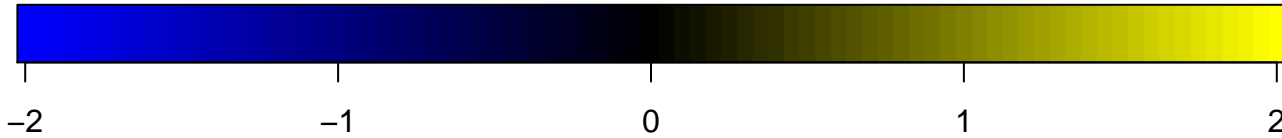
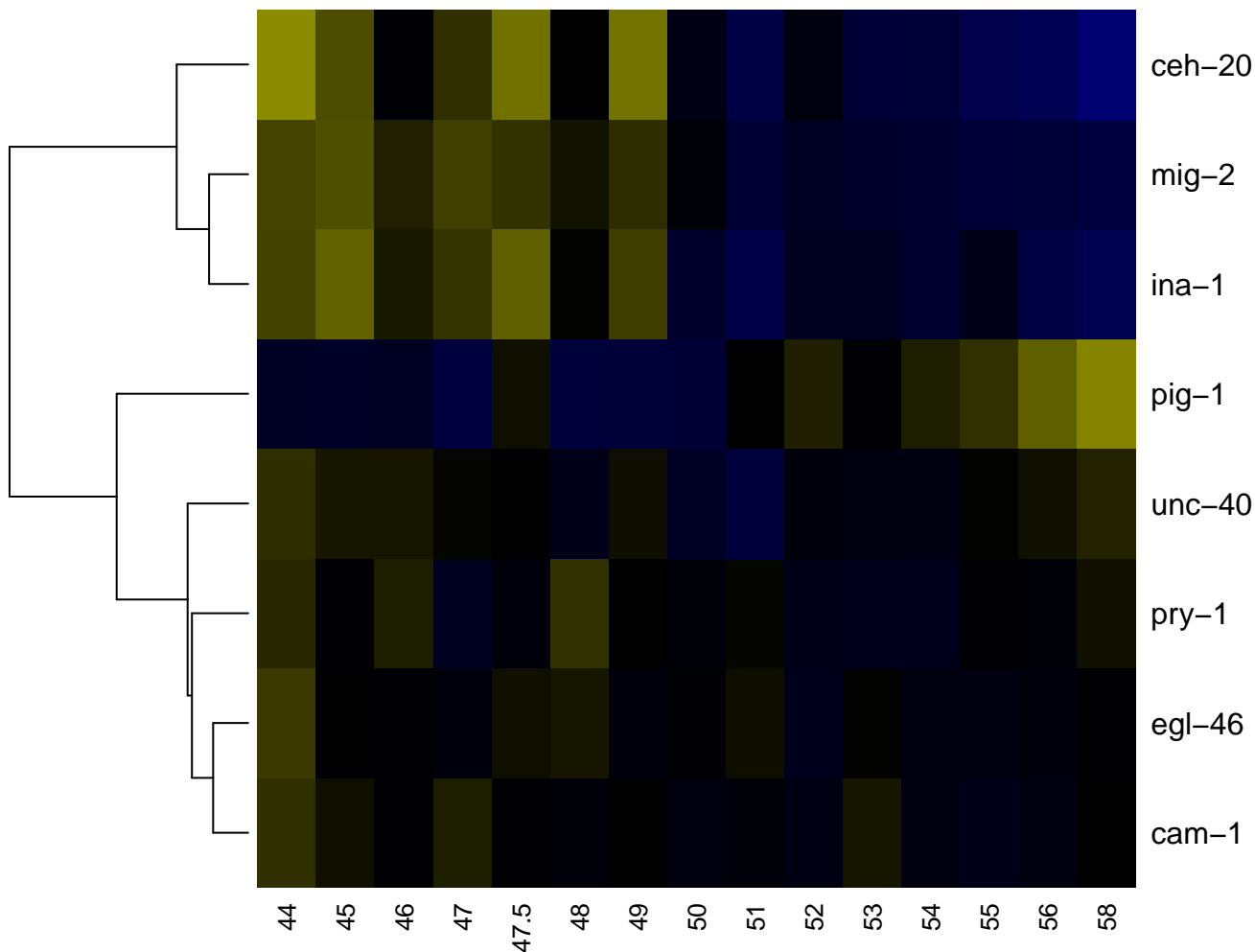
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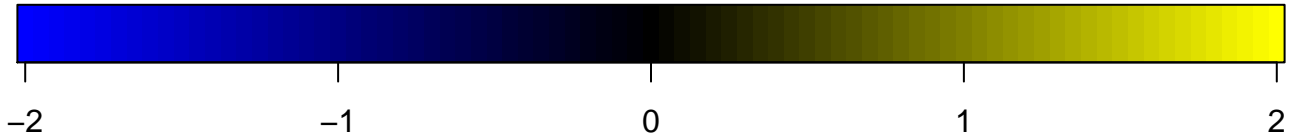
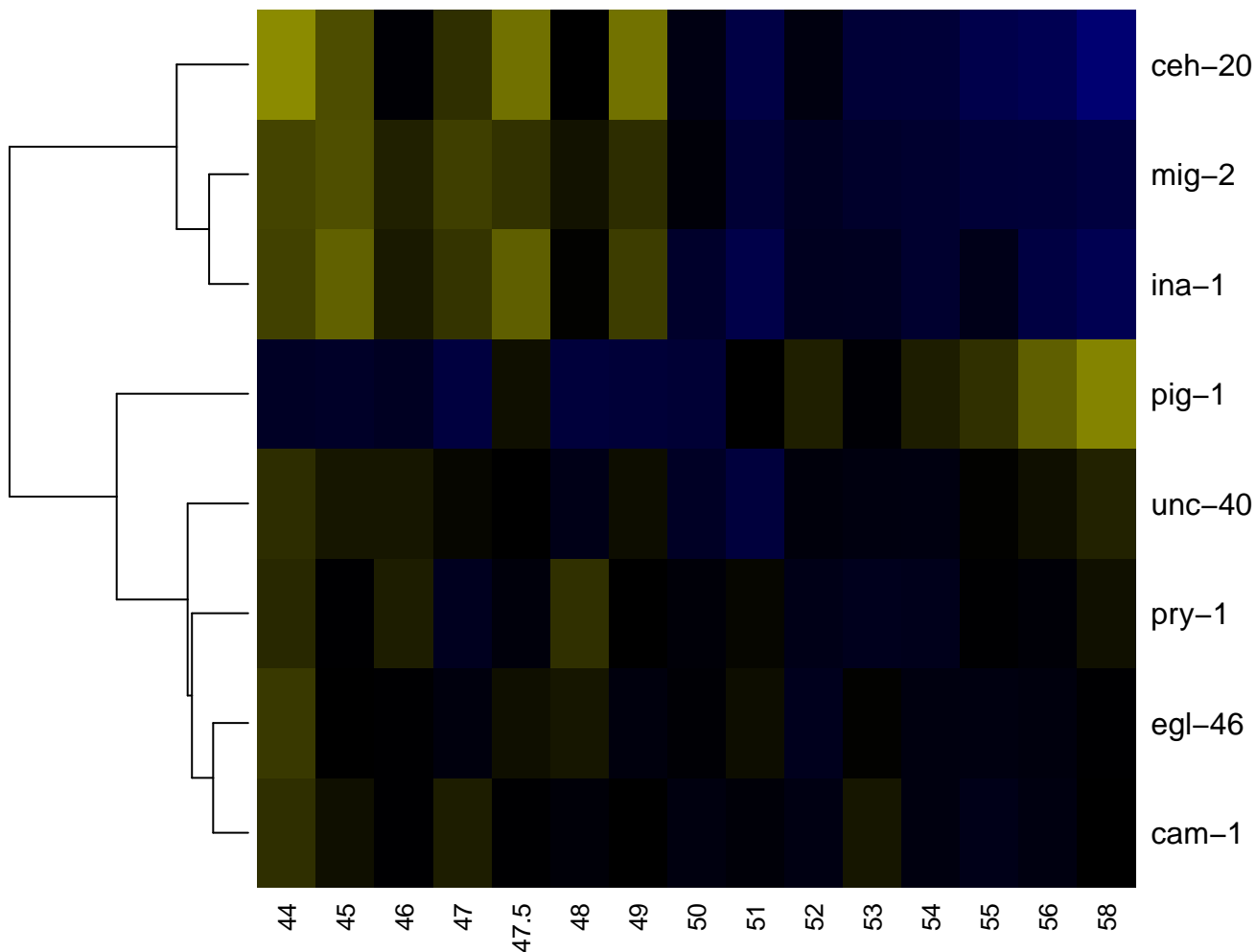
QL.pp



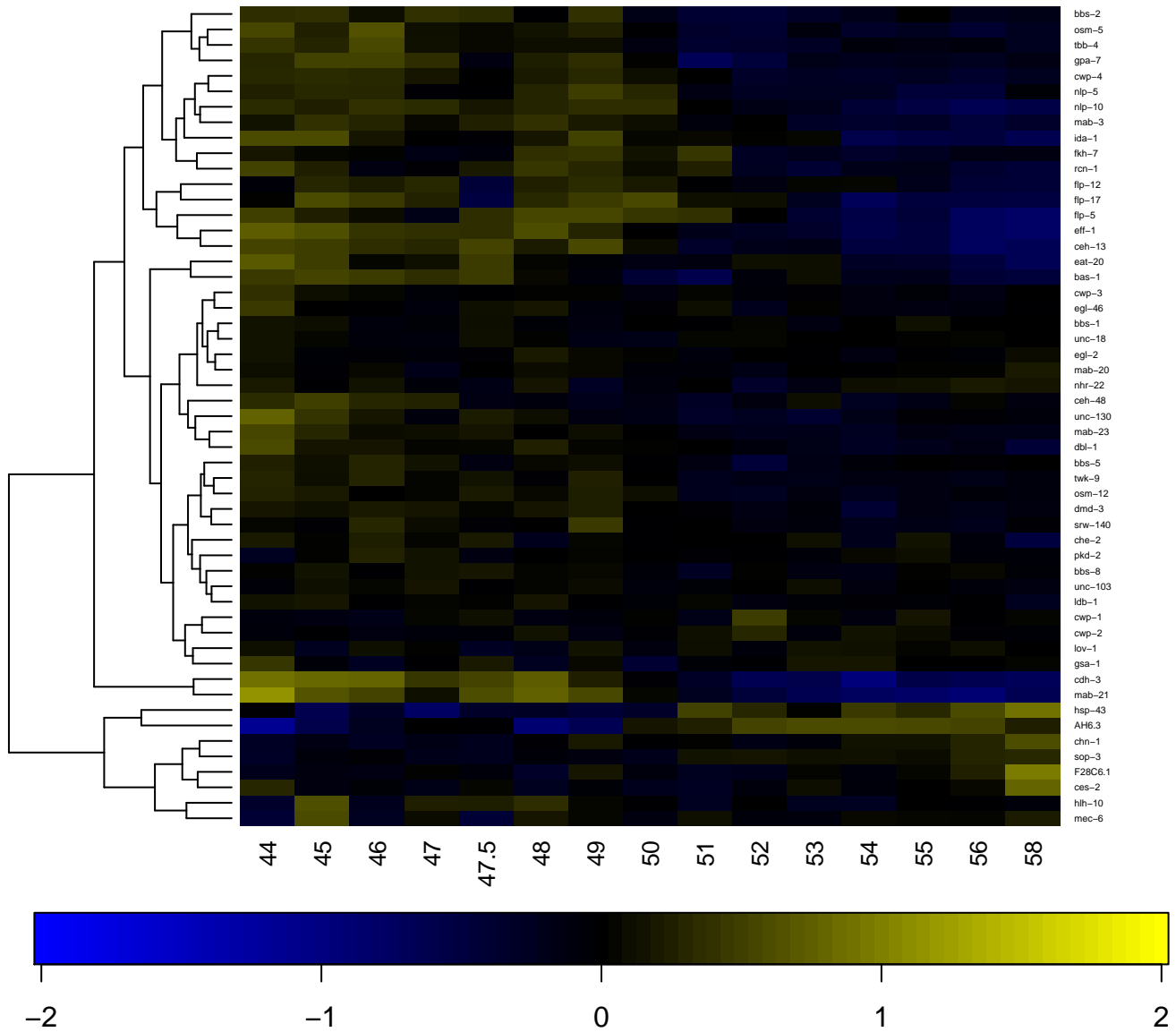
QR.a



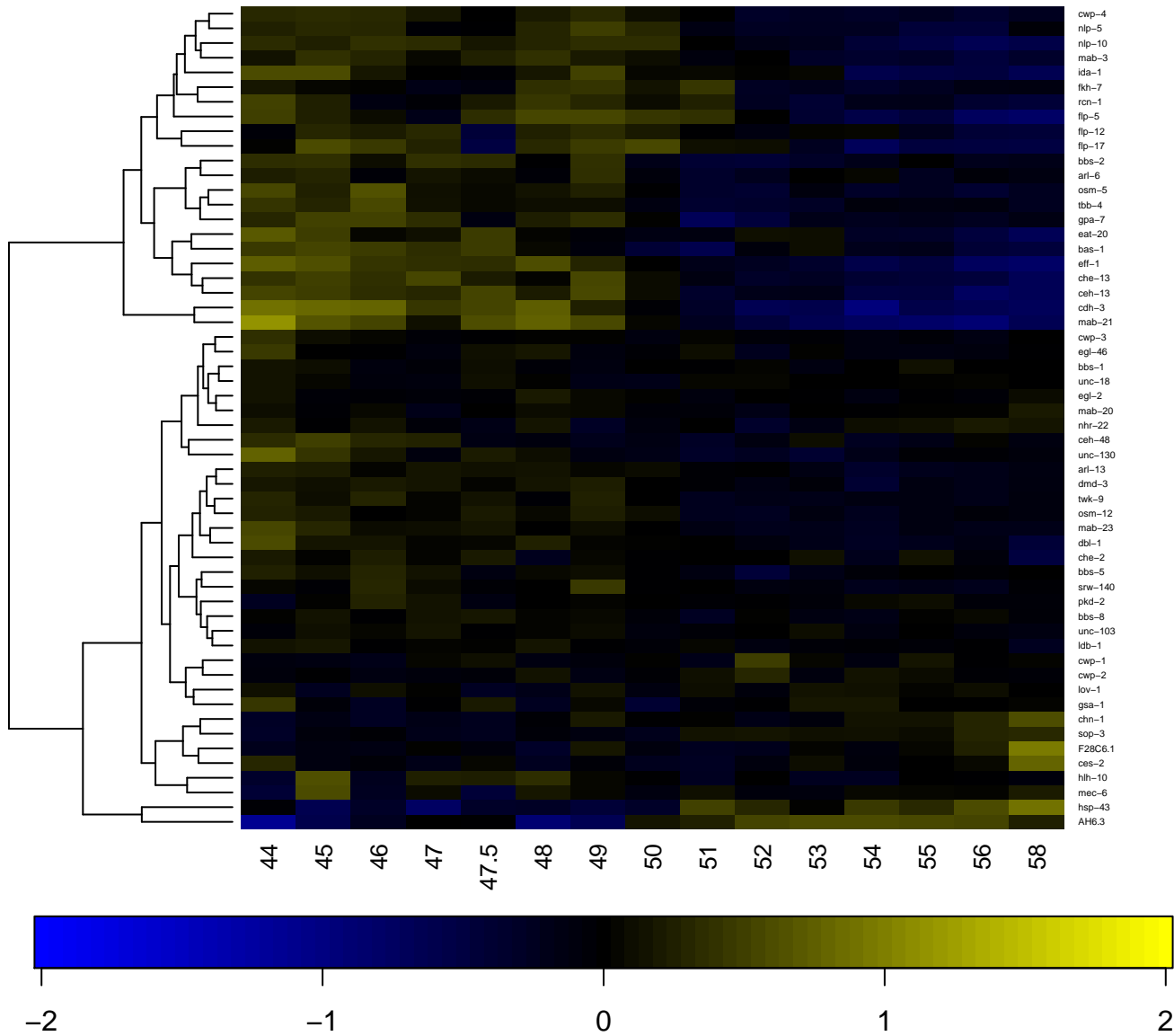
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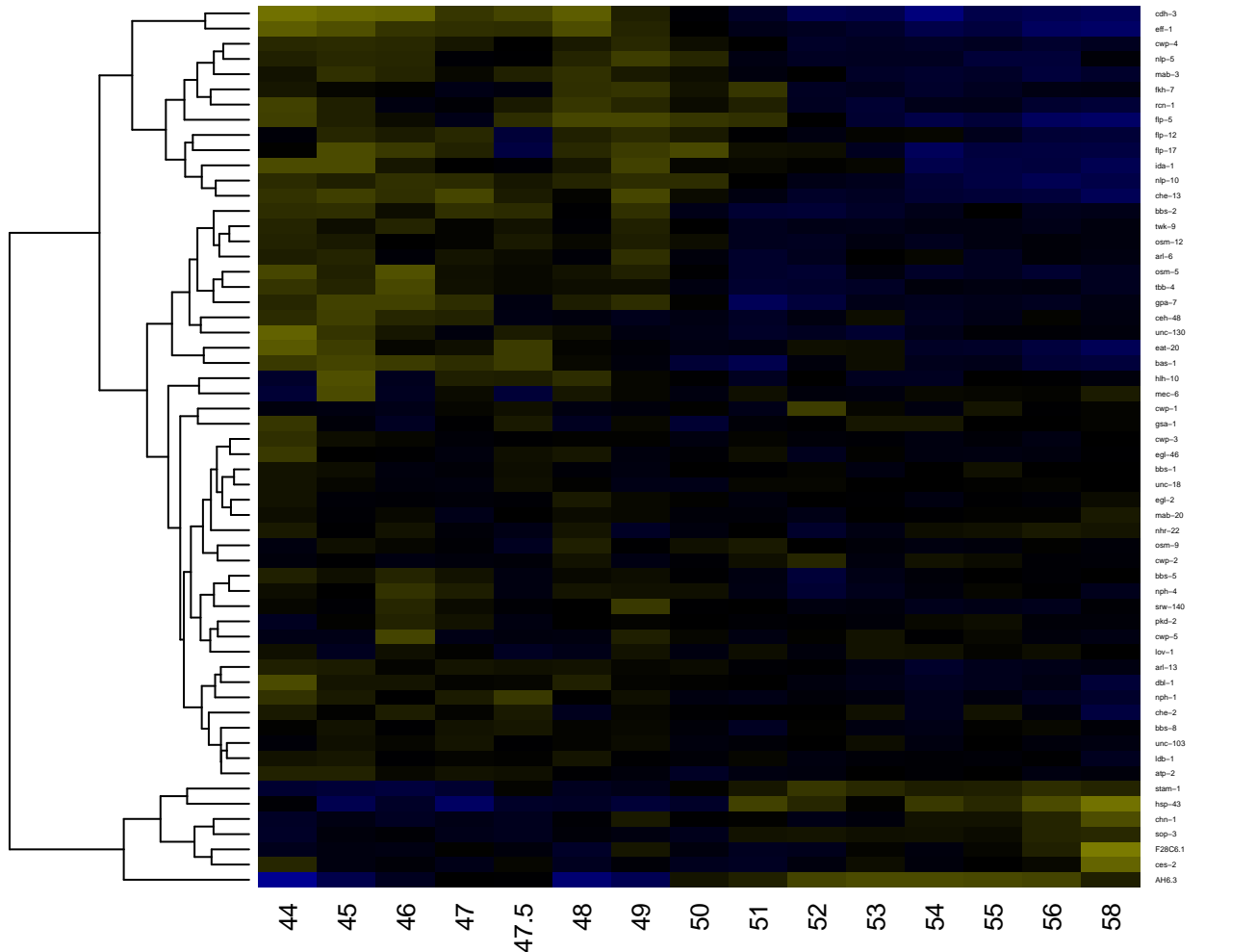
R1AL



R1AR



R1BL



-2

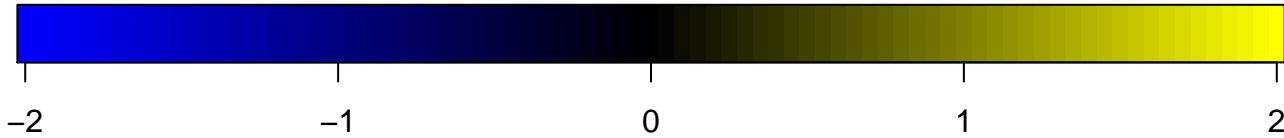
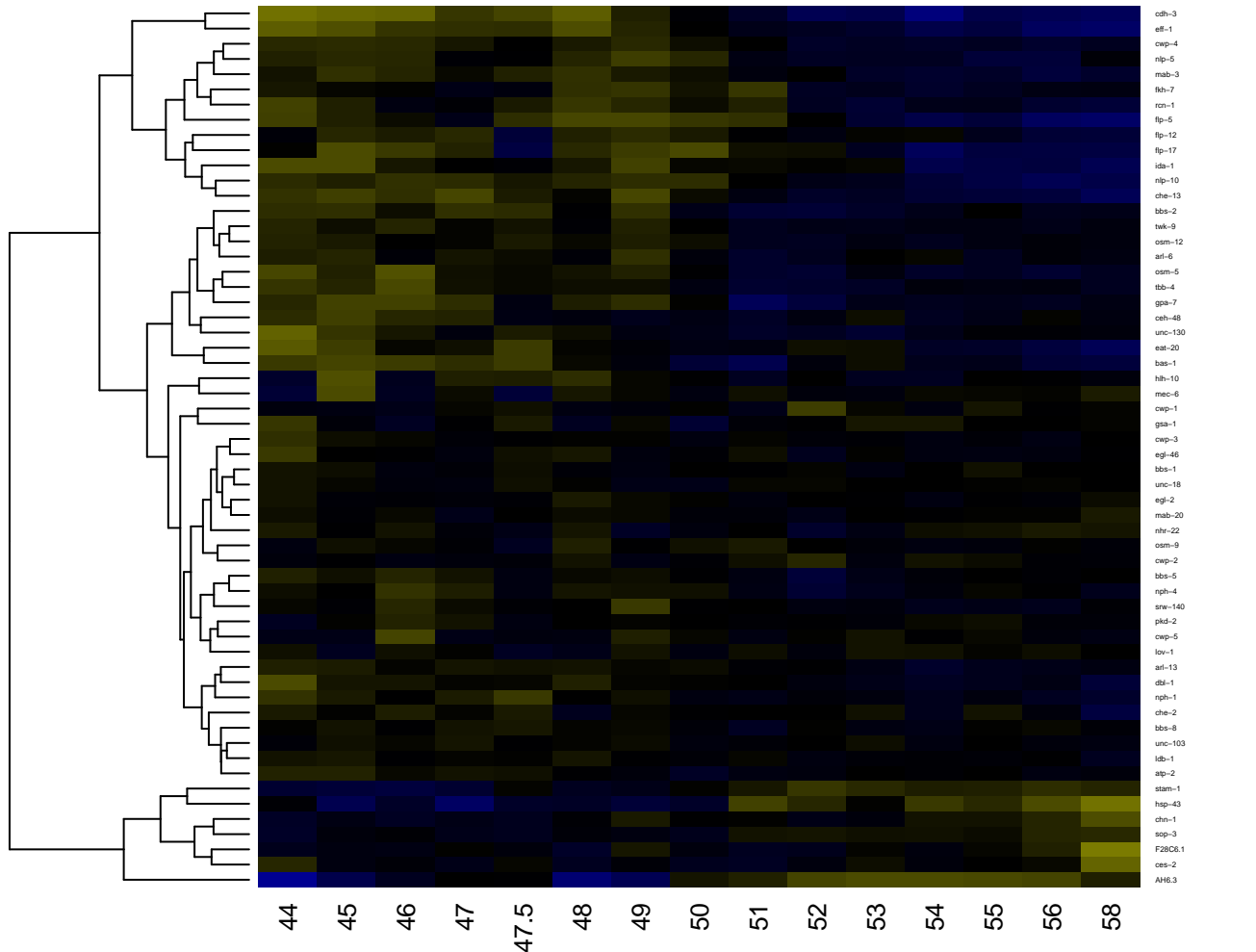
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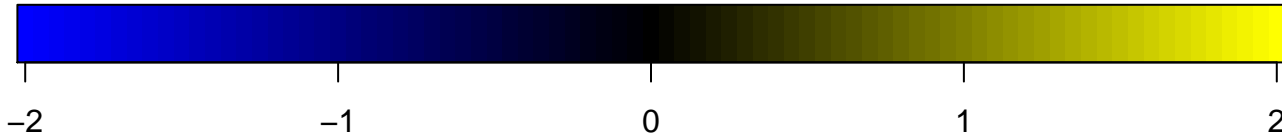
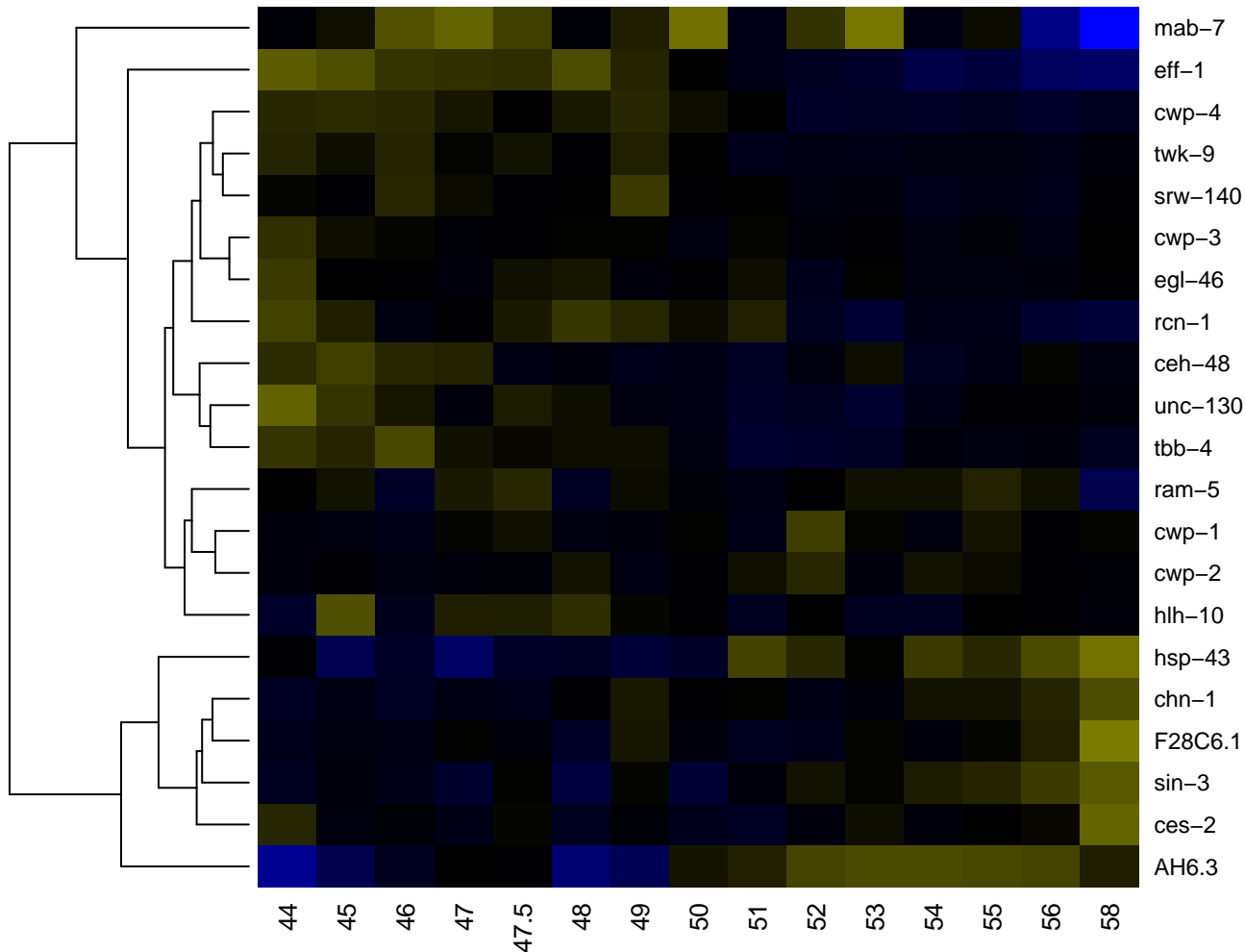
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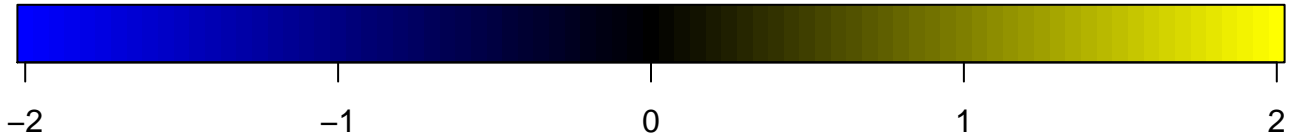
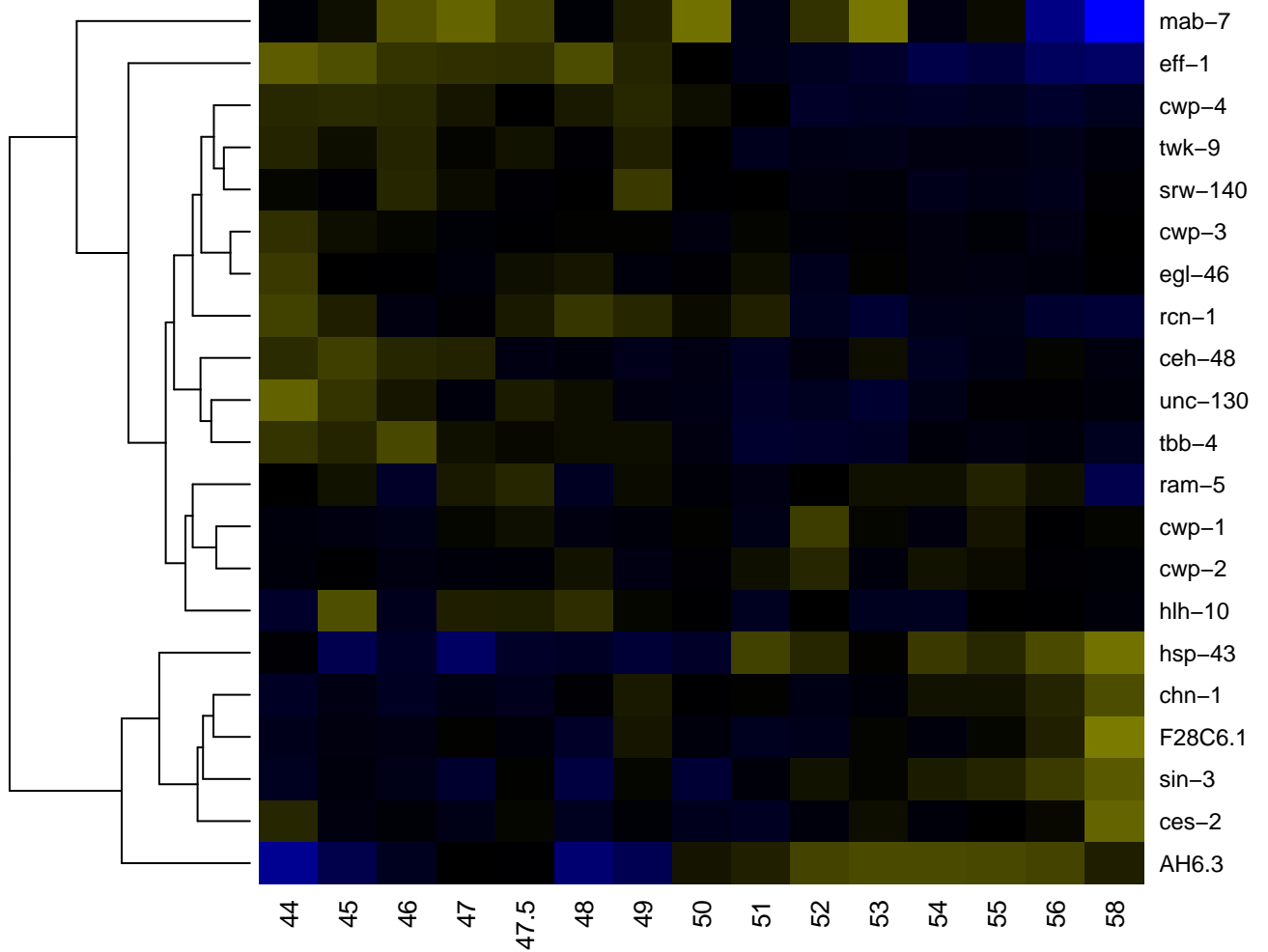
R1BR



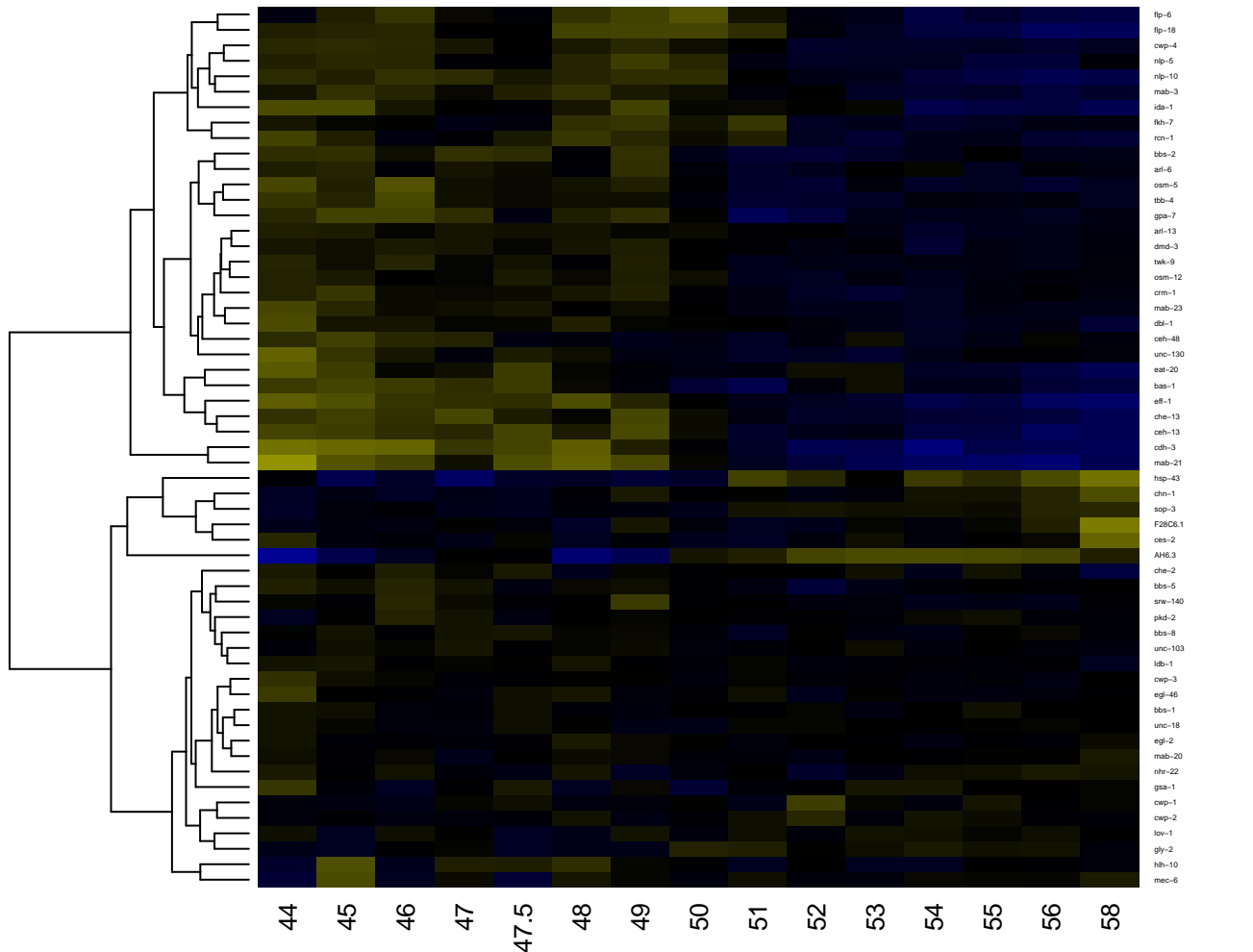
R1stL



R1stR



R2AL



-2

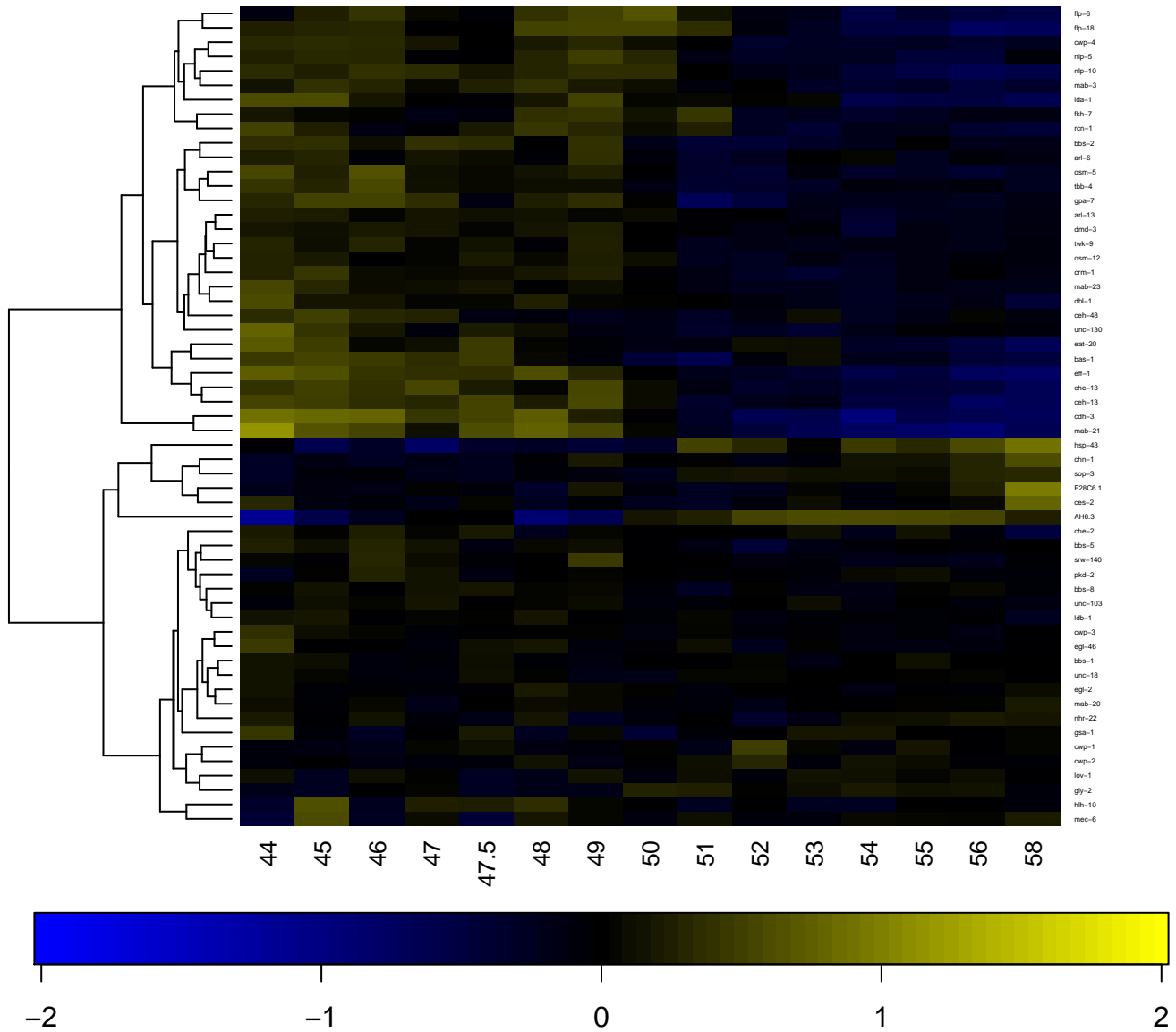
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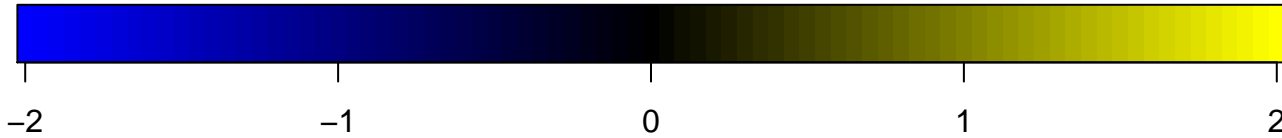
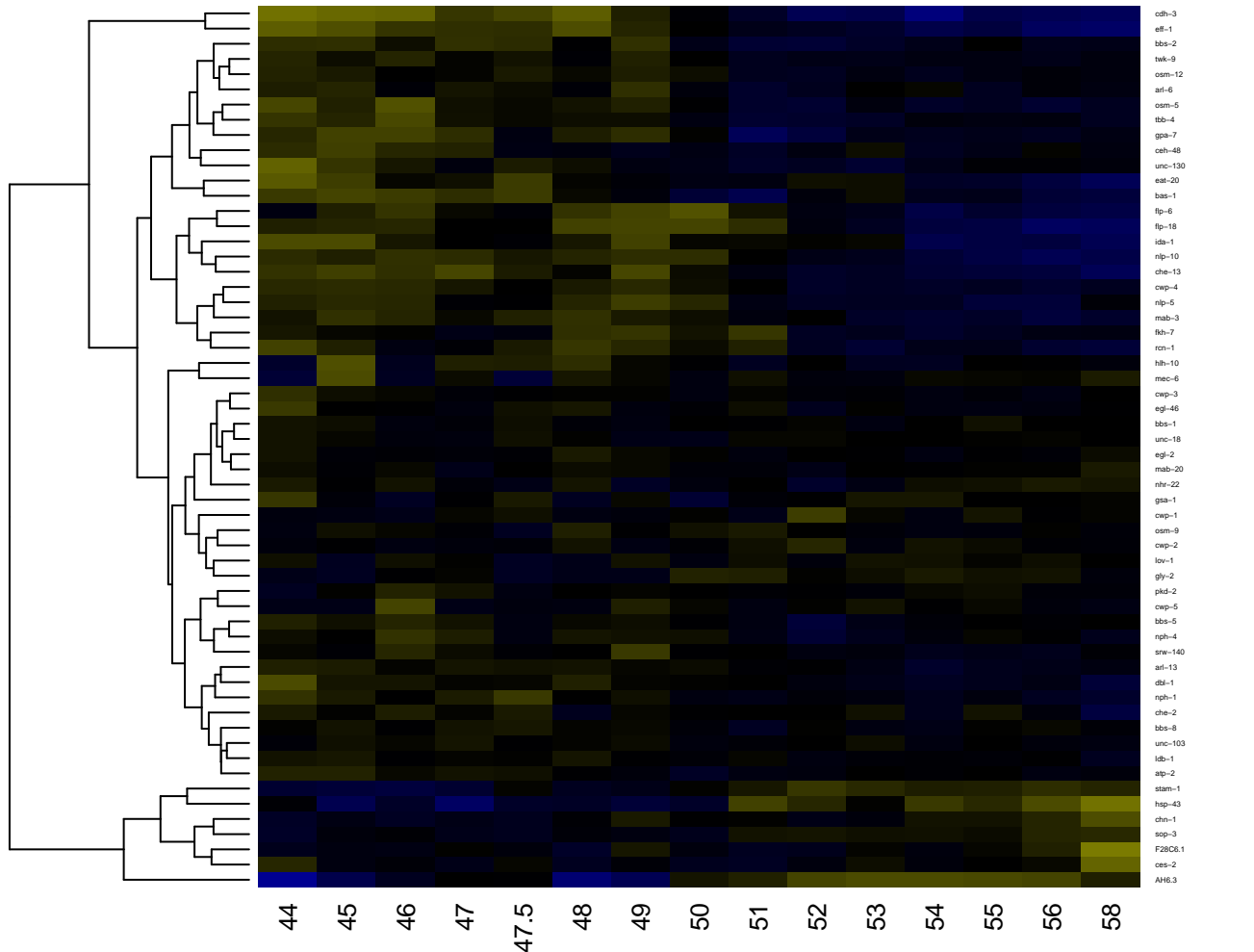
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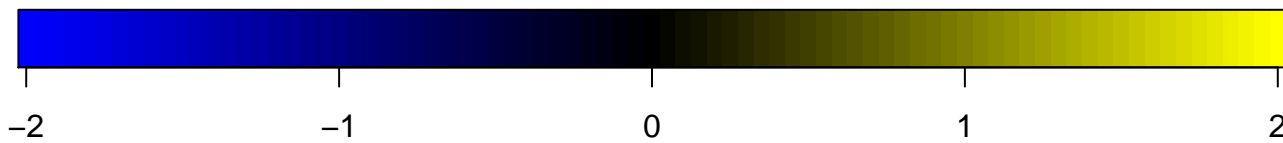
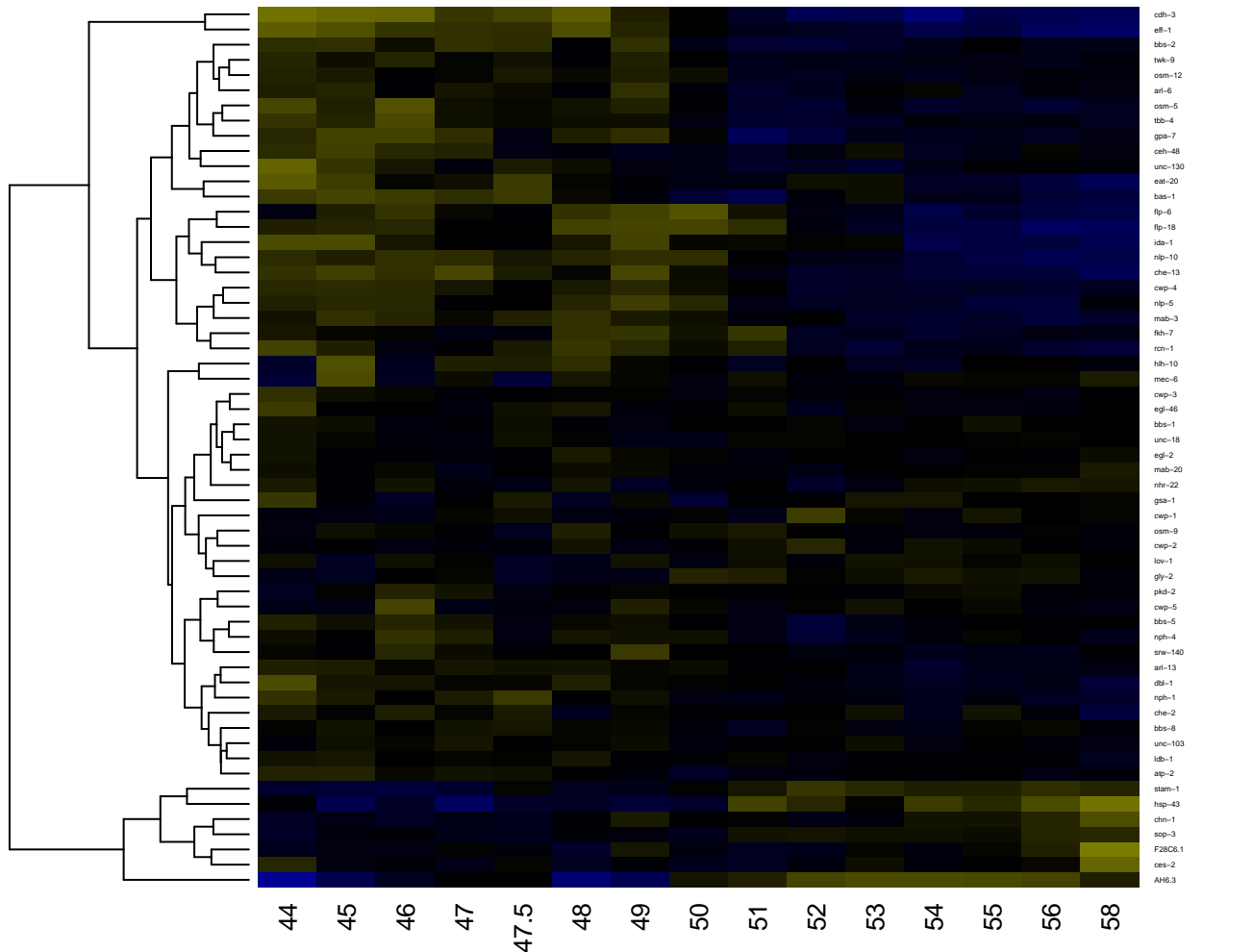
R2AR



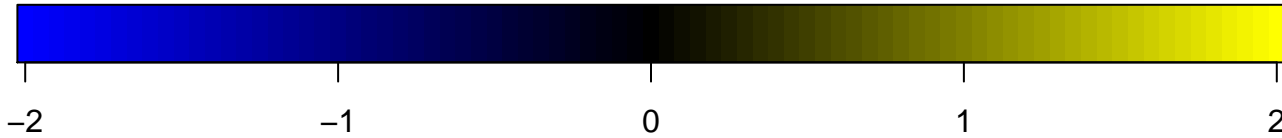
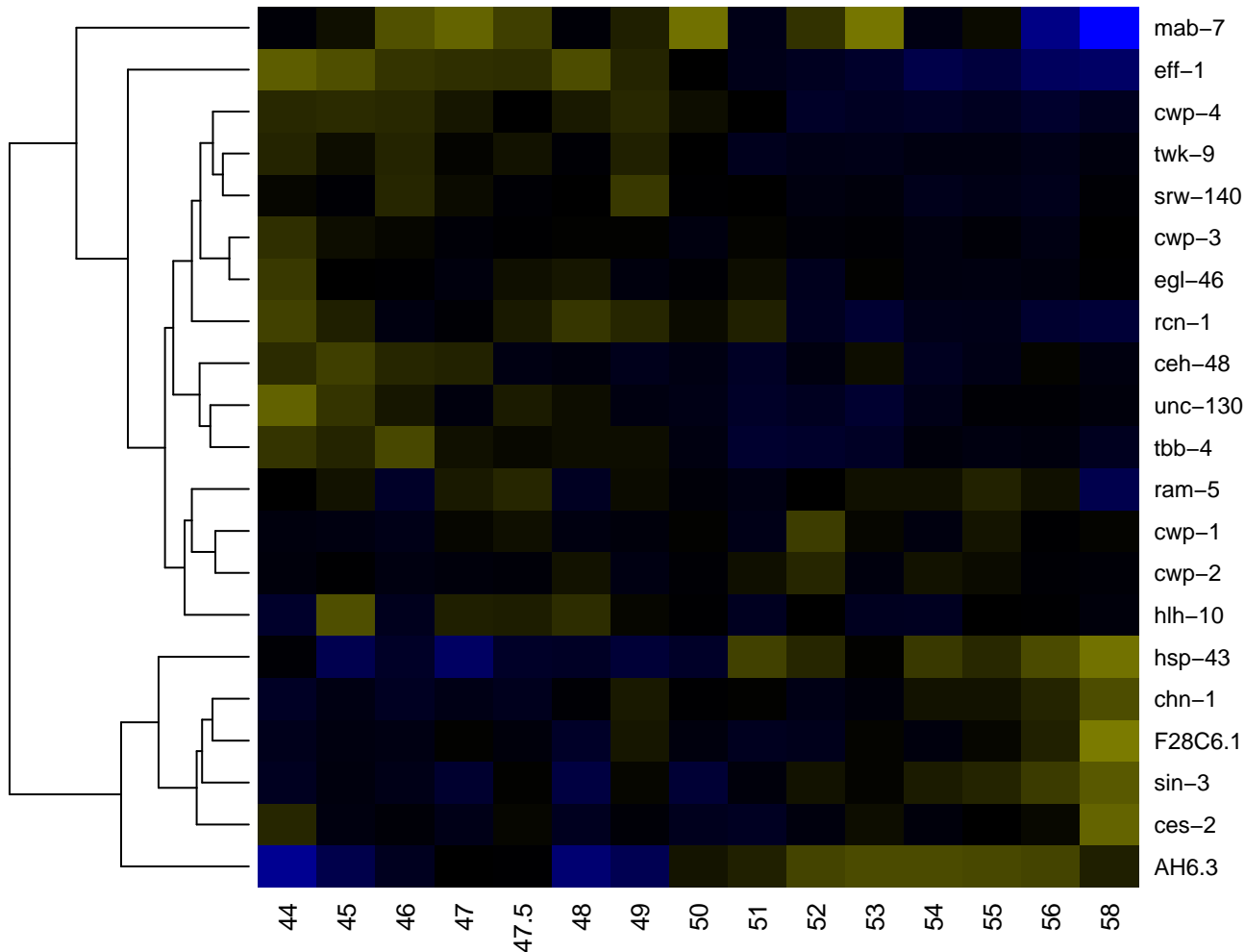
R2BL



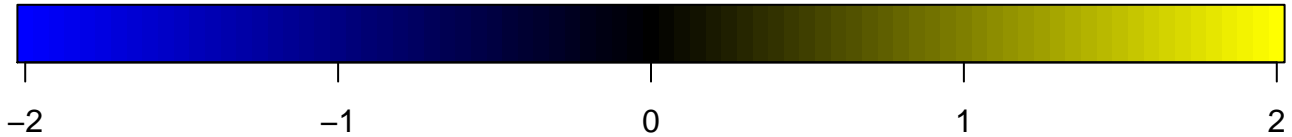
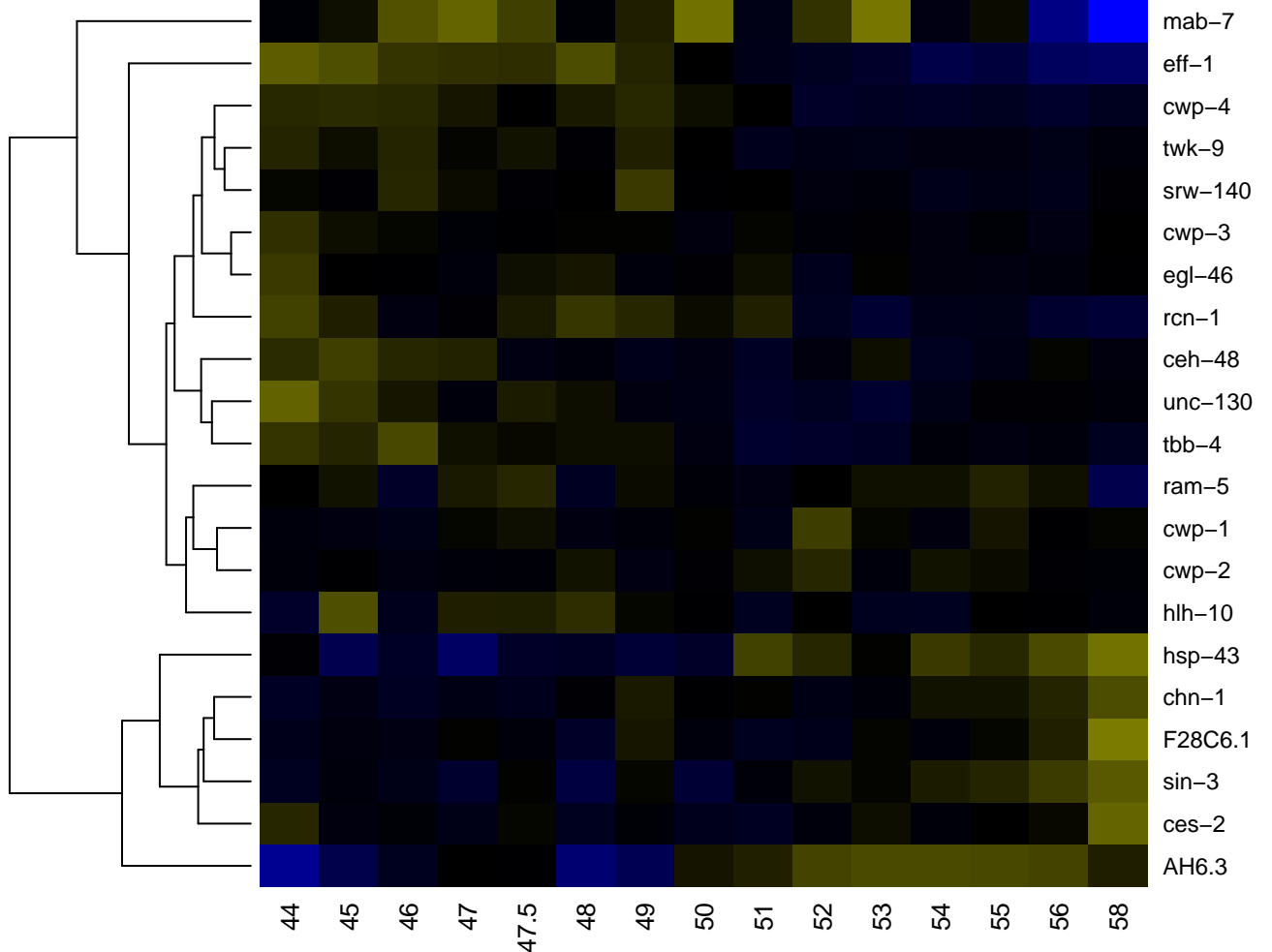
R2BR



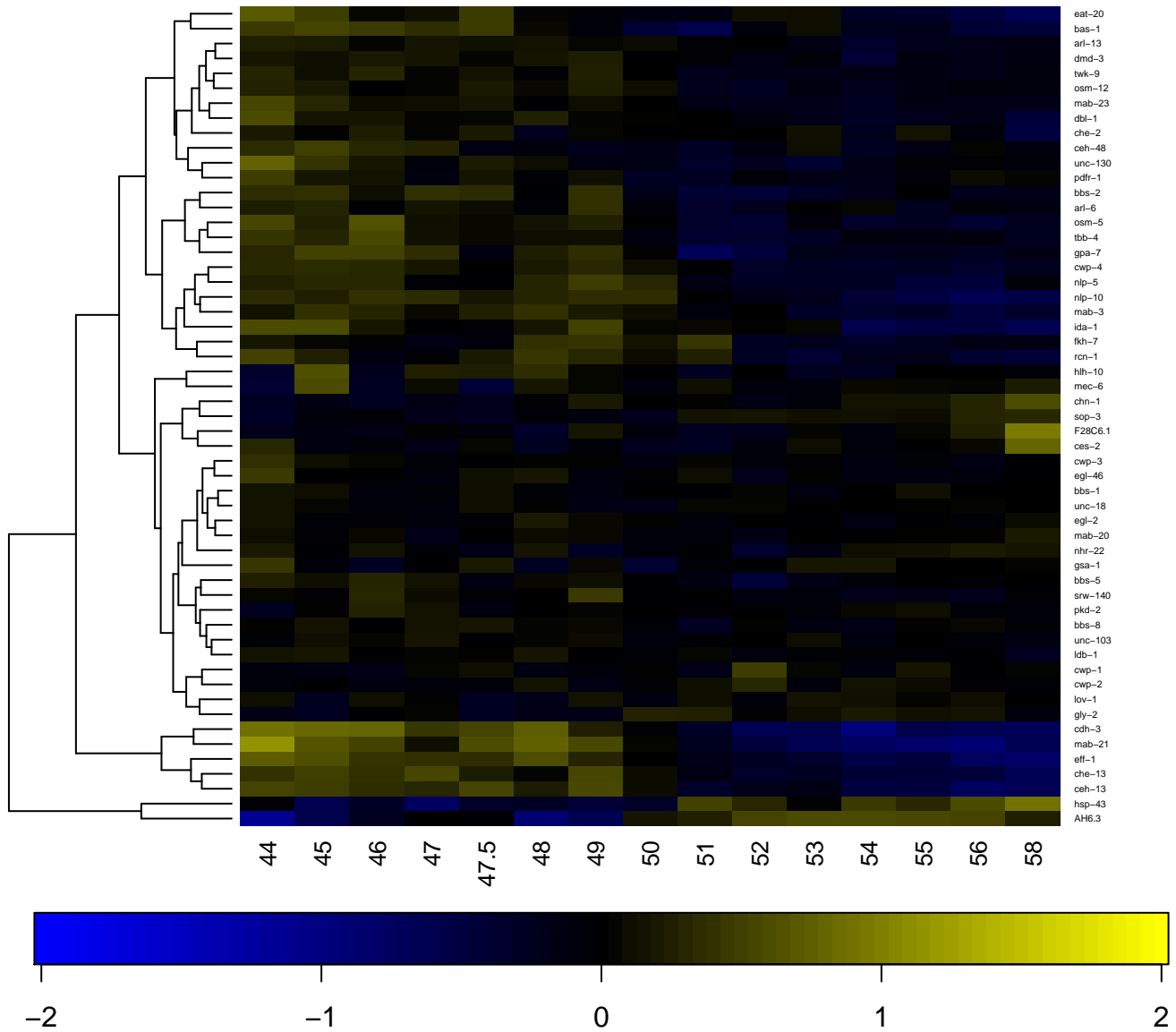
R2stL



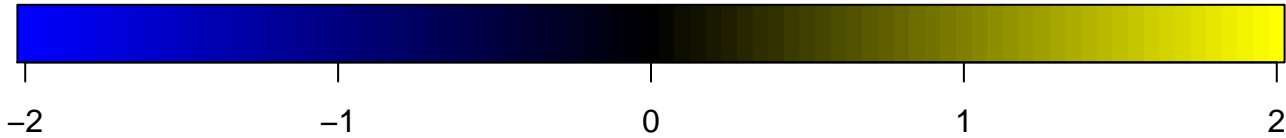
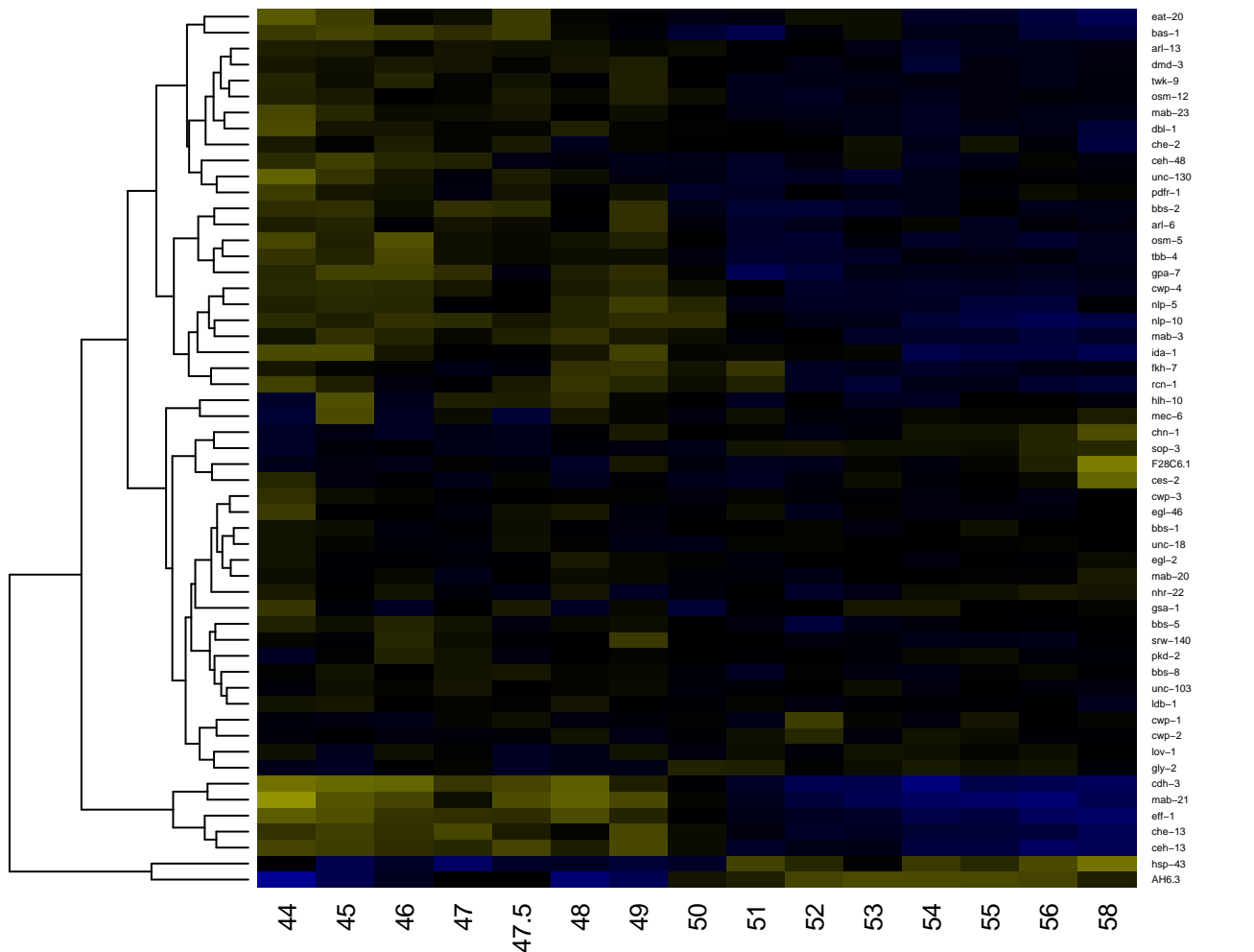
R2stR



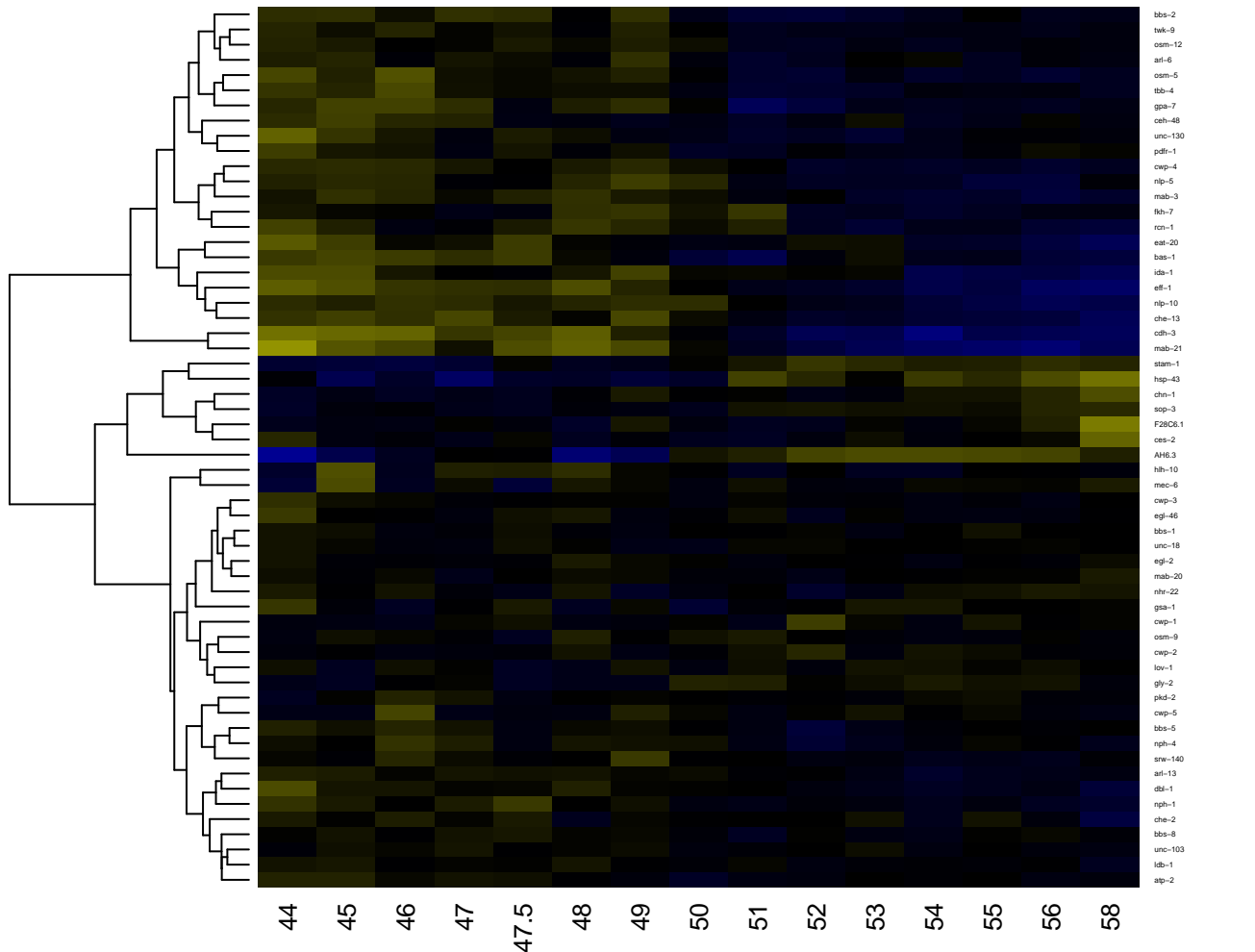
R3AL



R3AR



R3BL



-2

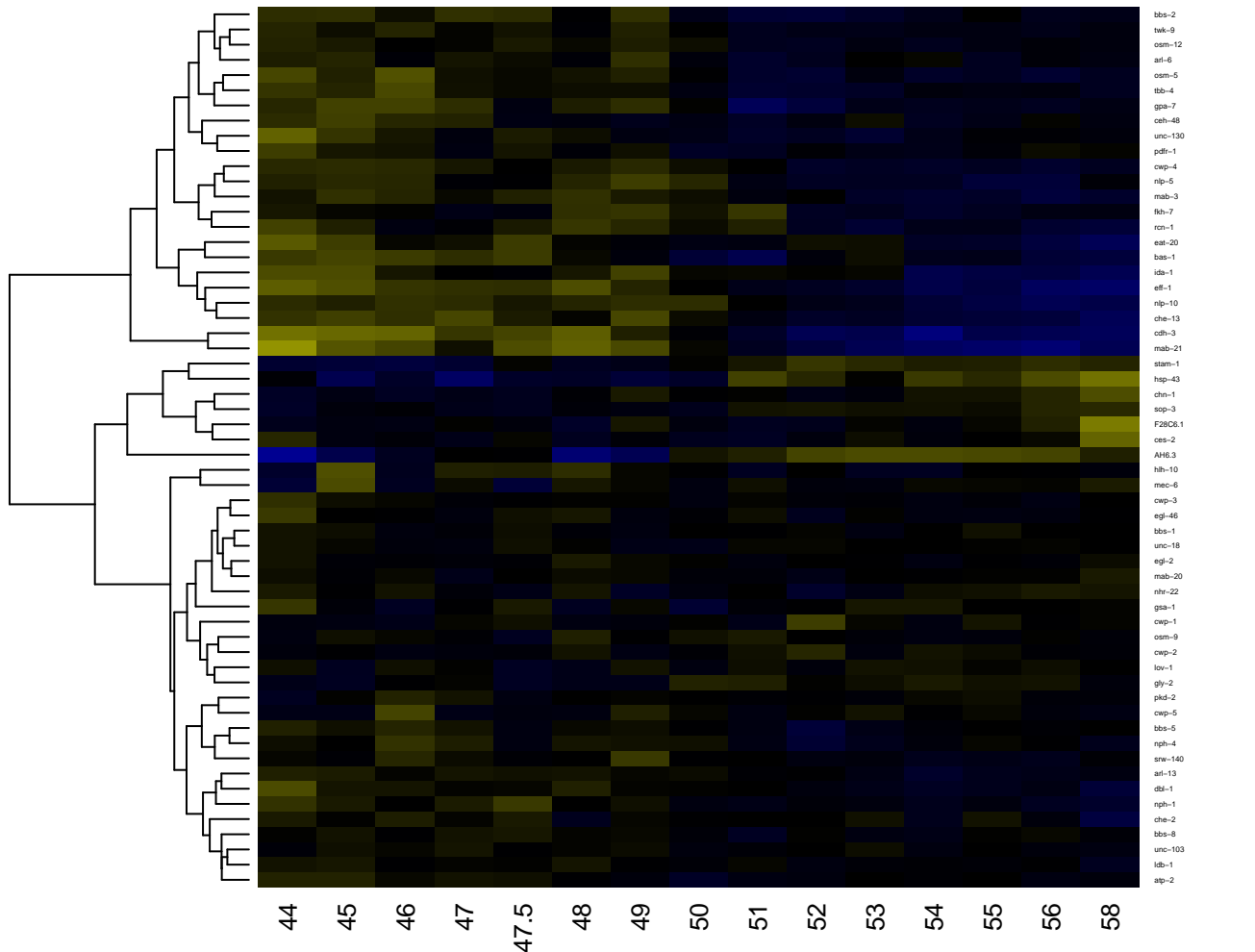
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R3BR



-2

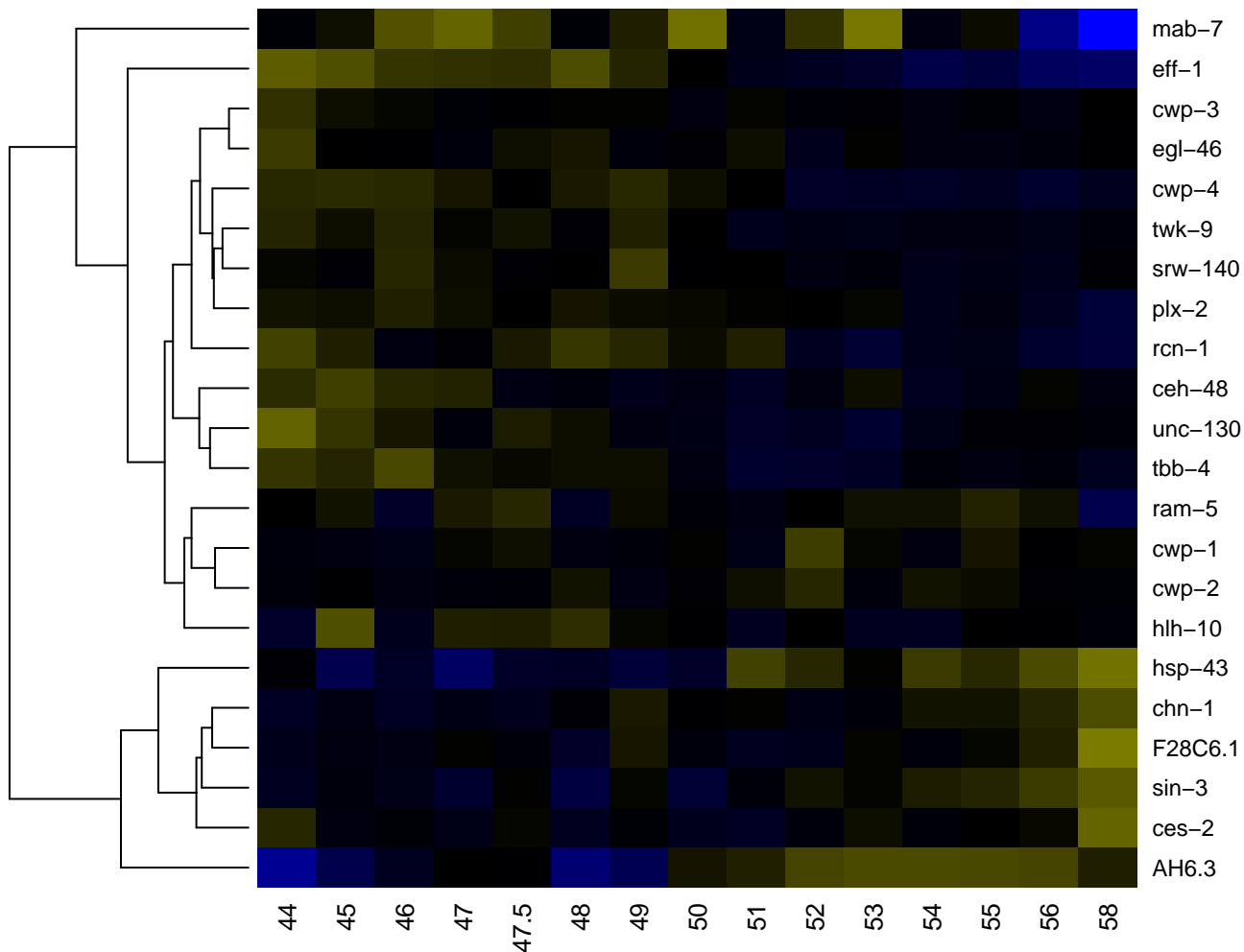
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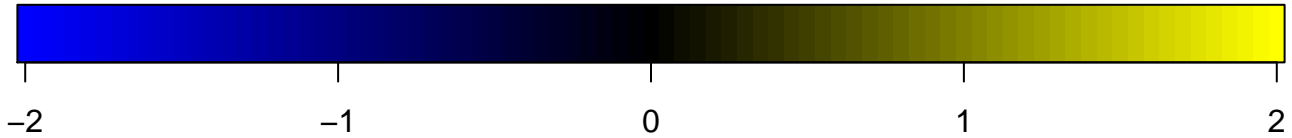
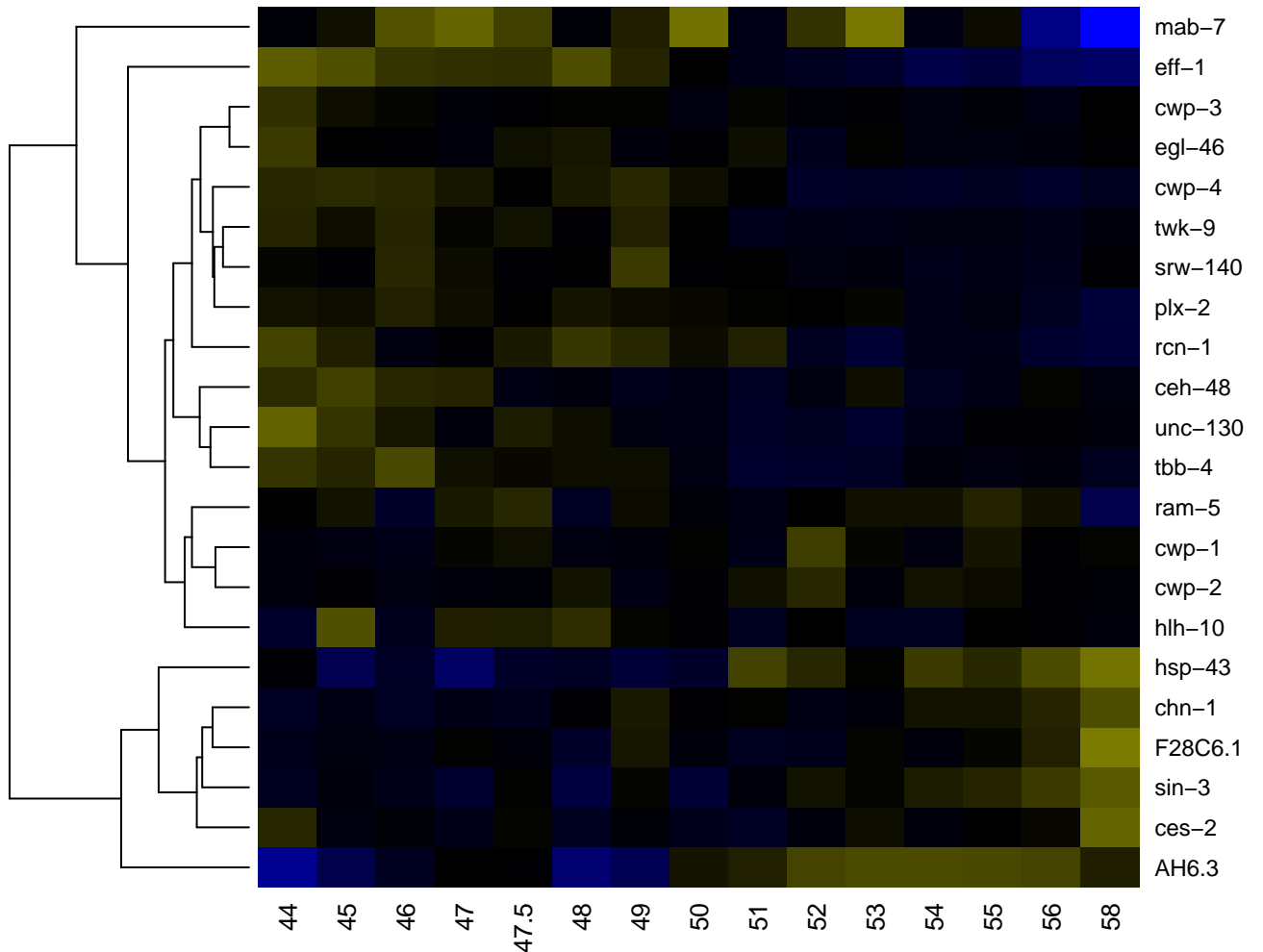
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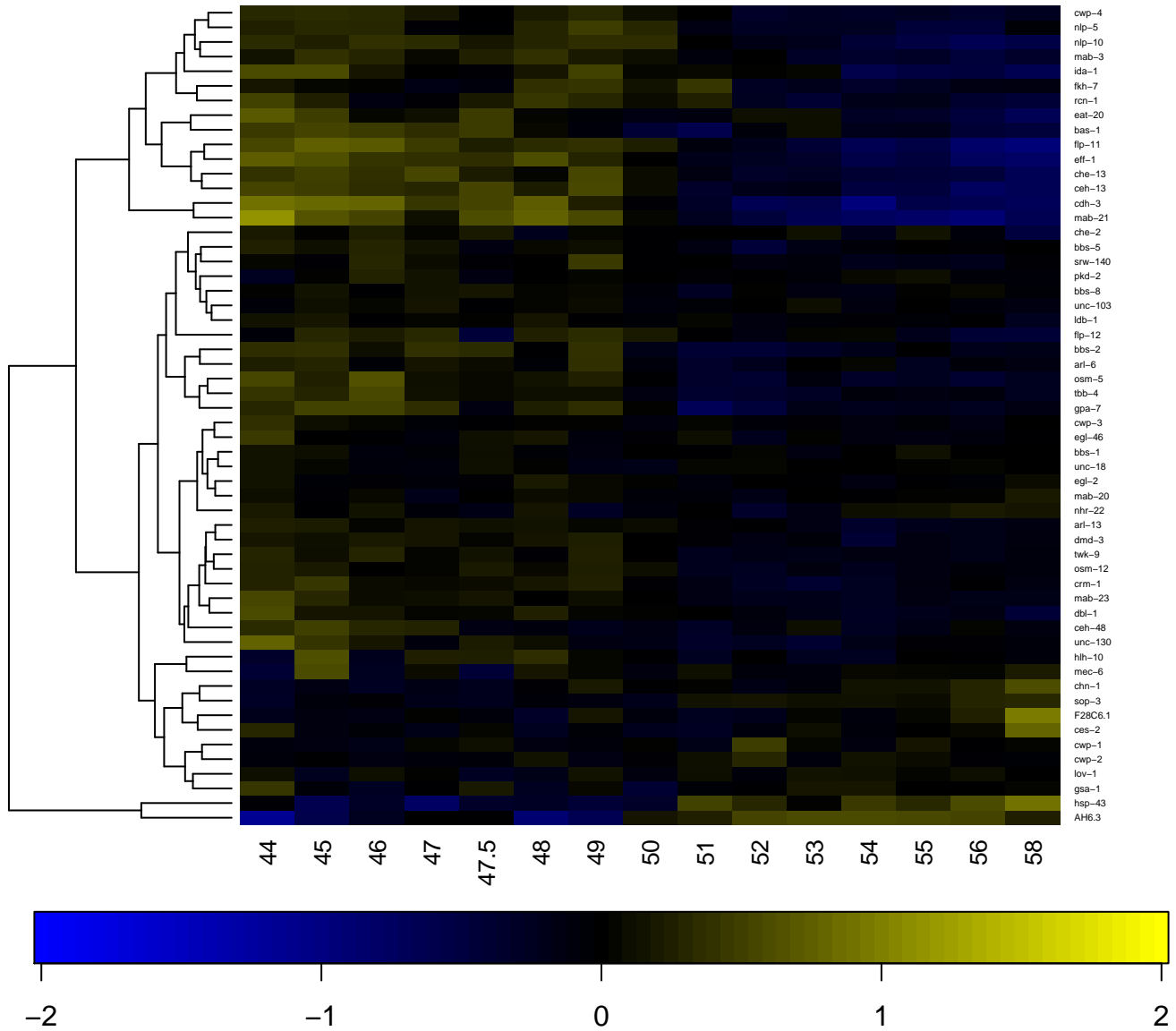
R3stL



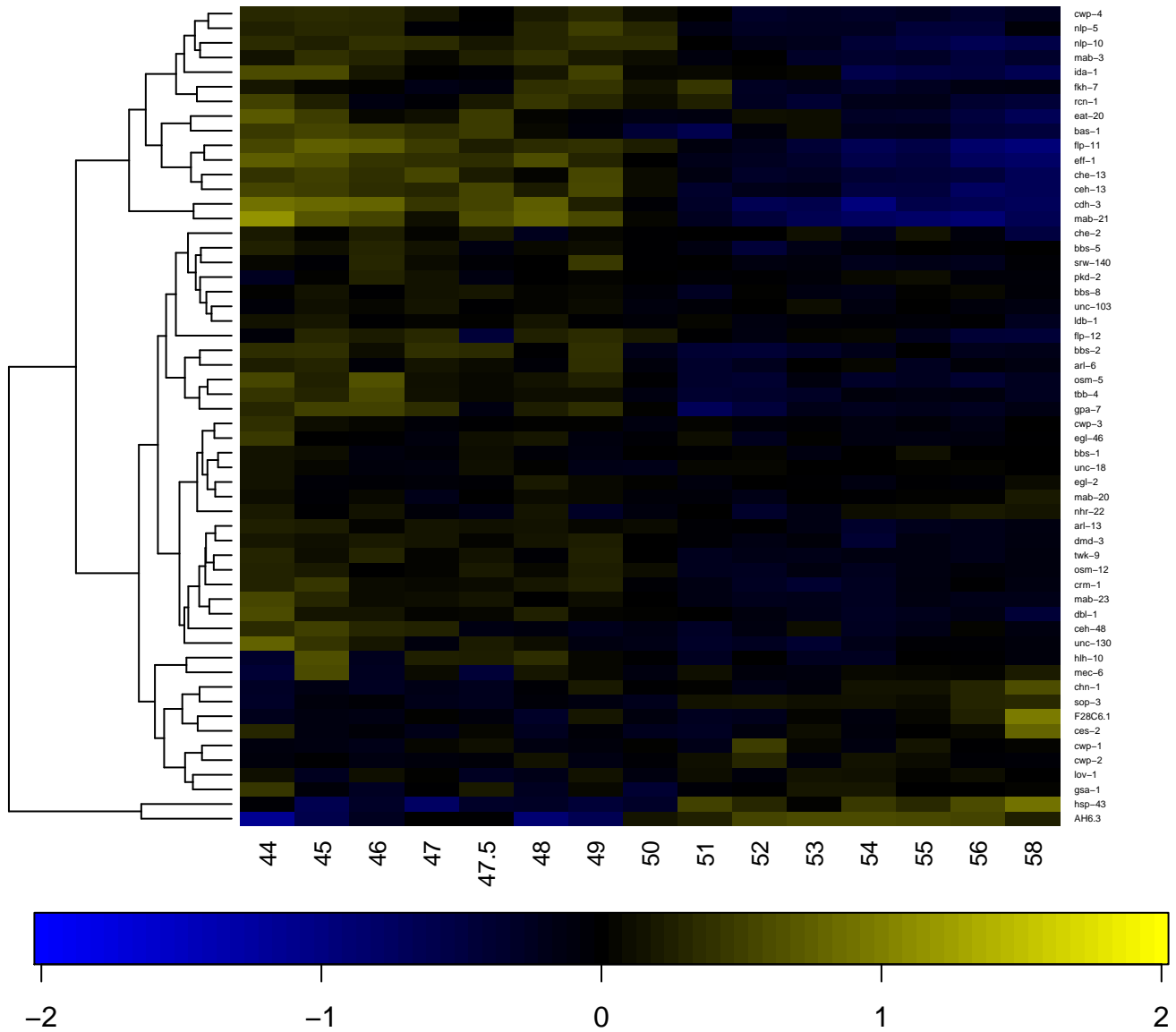
R3stR



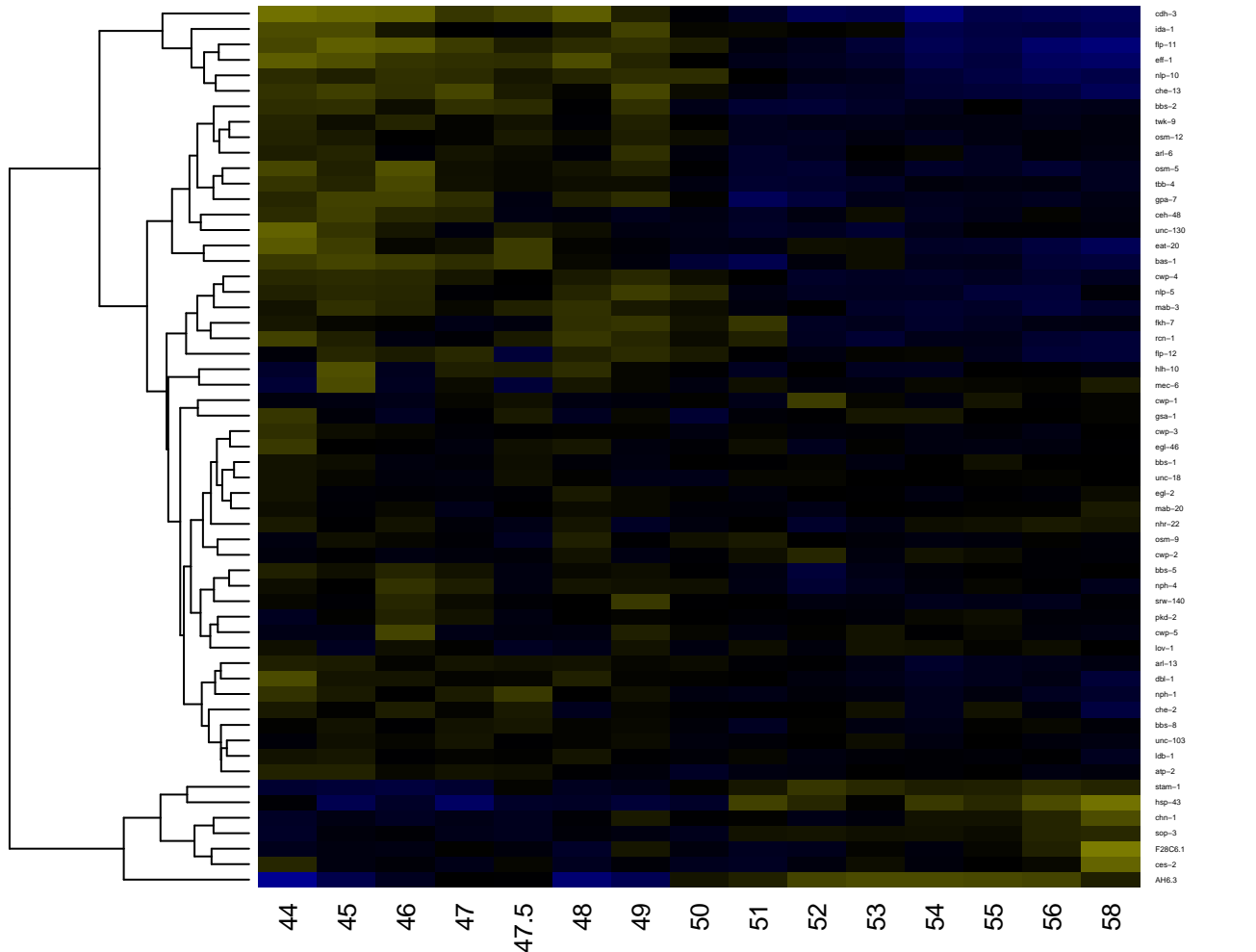
R4AL



R4AR



R4BL



-2

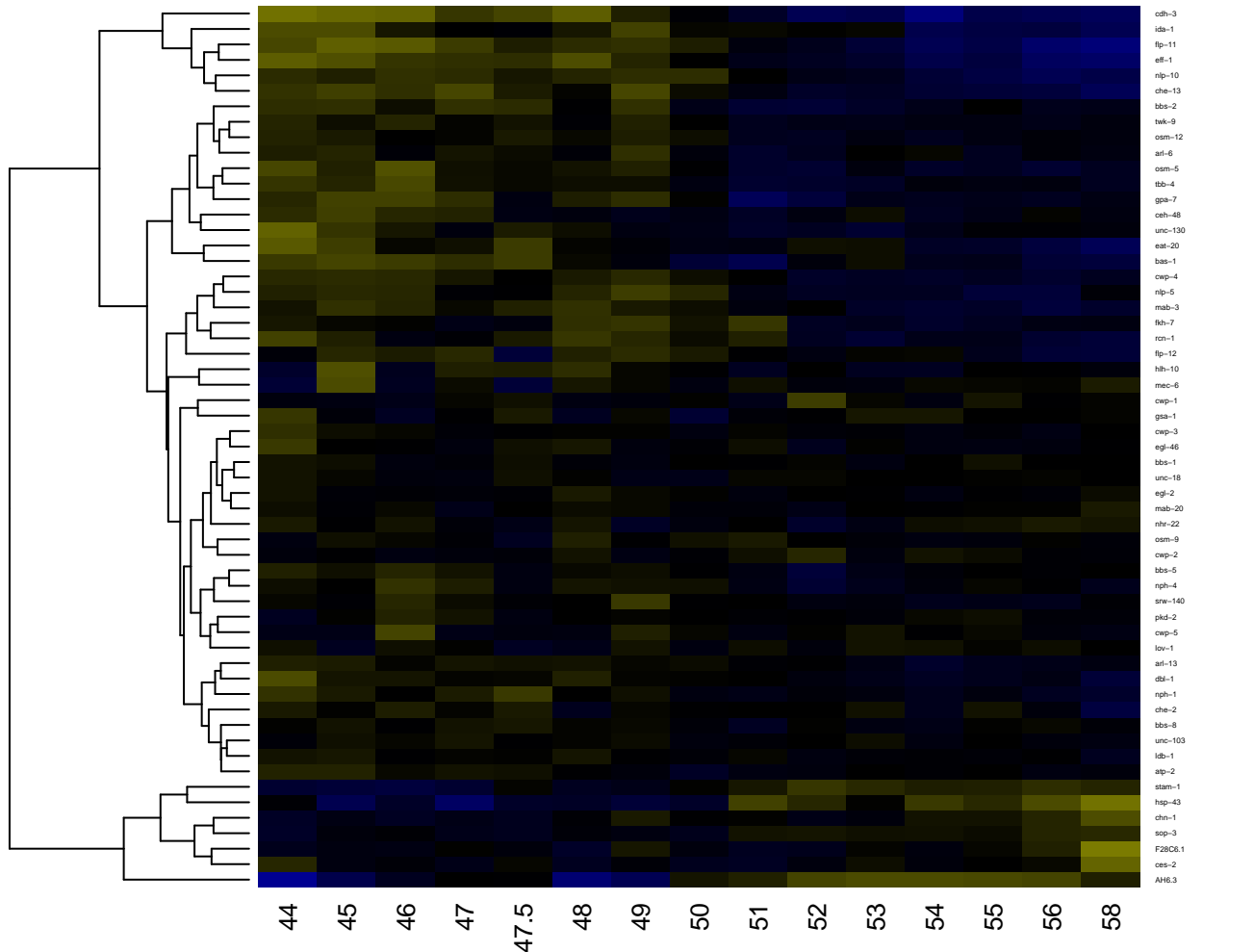
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R4BR



-2

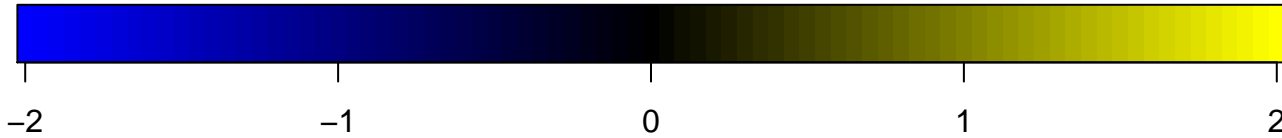
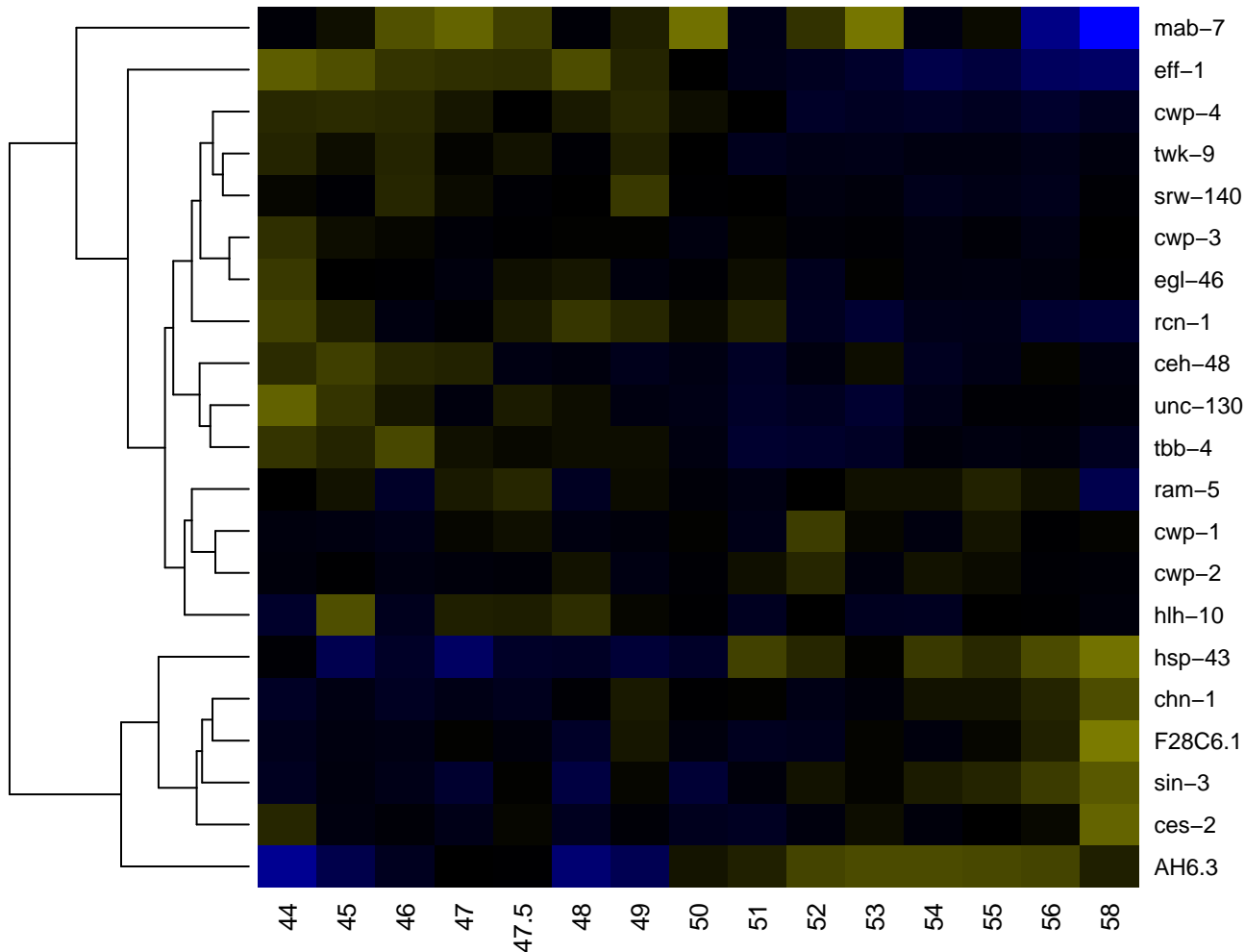
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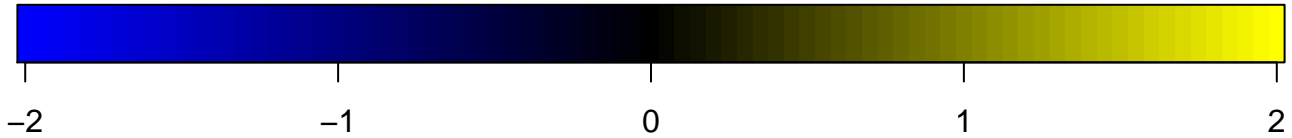
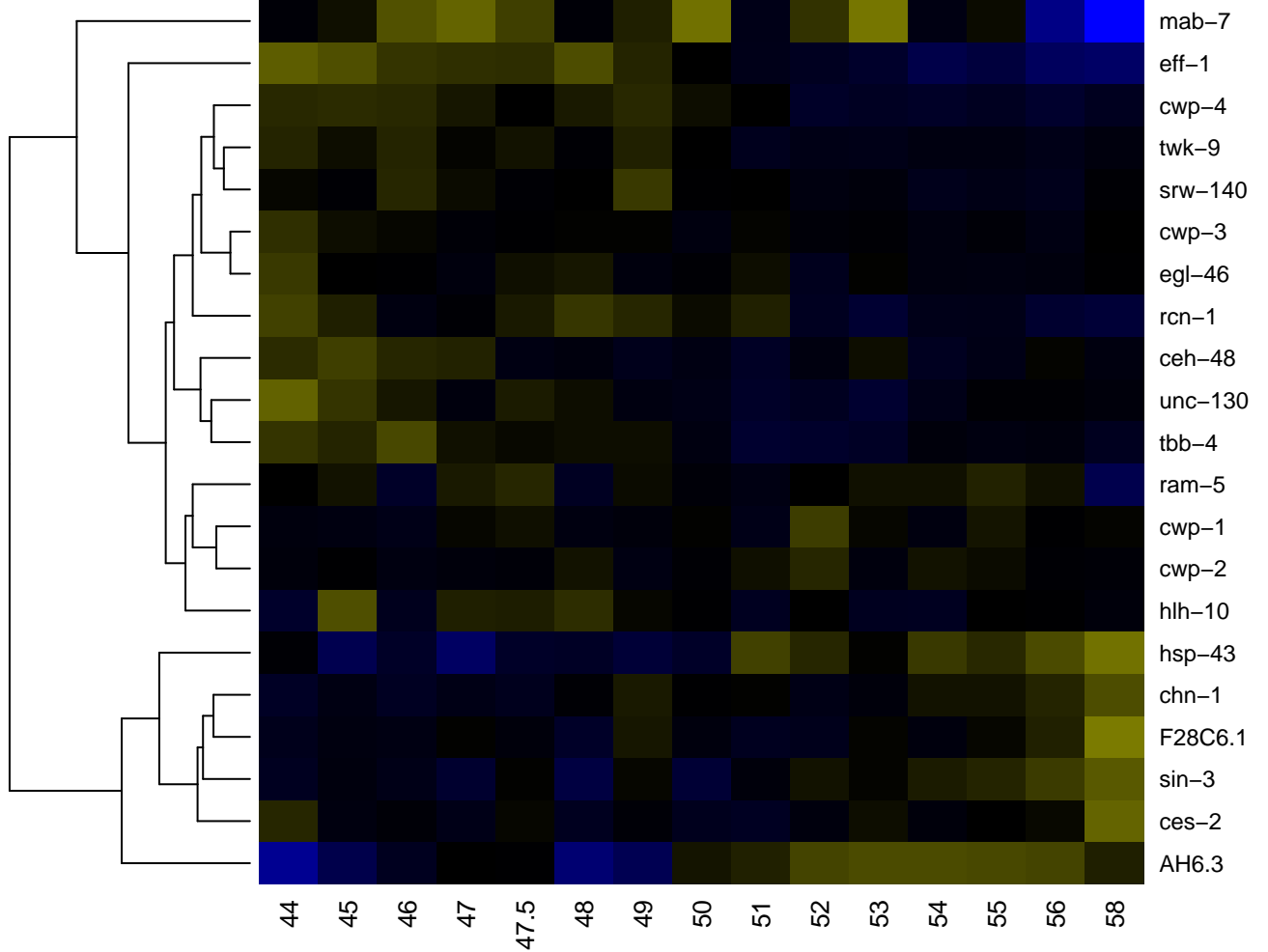
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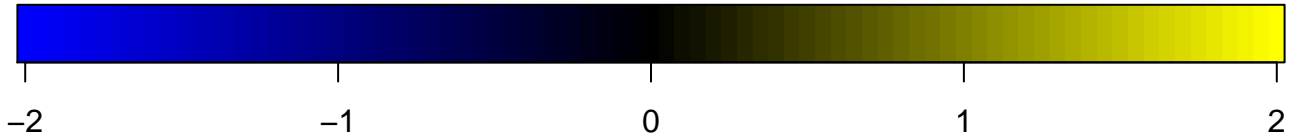
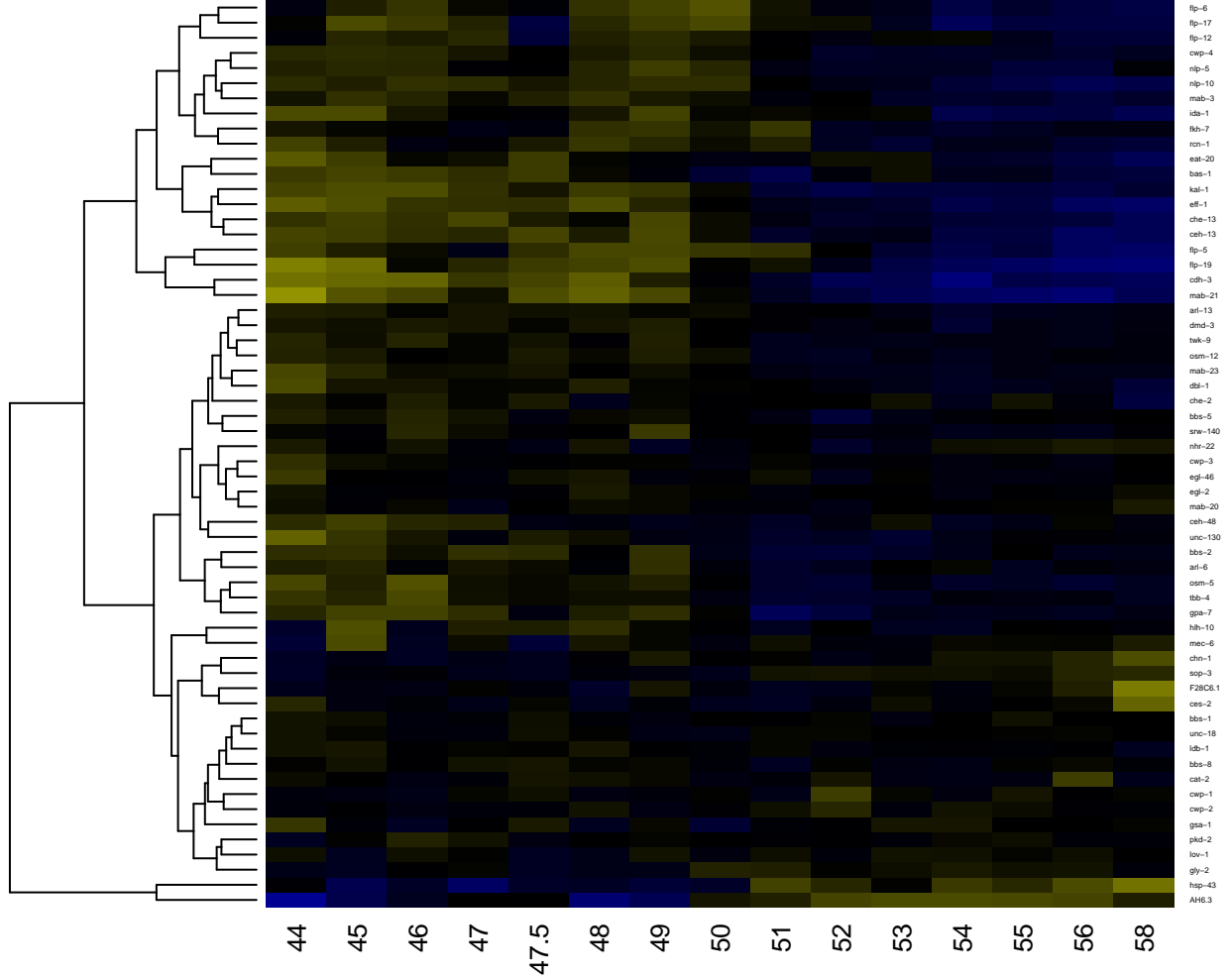
R4stL



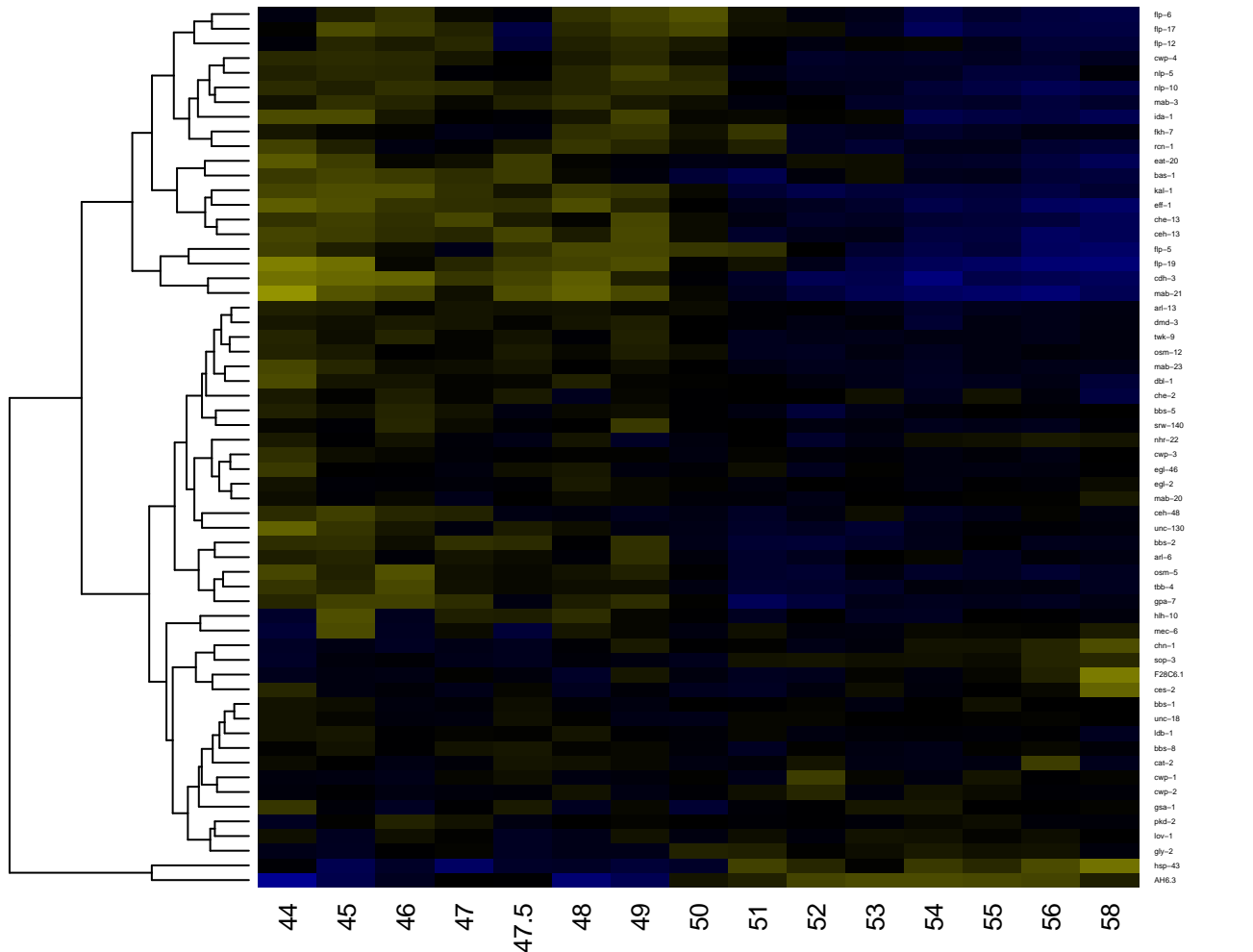
R4stR



R5AL



R5AR



-2

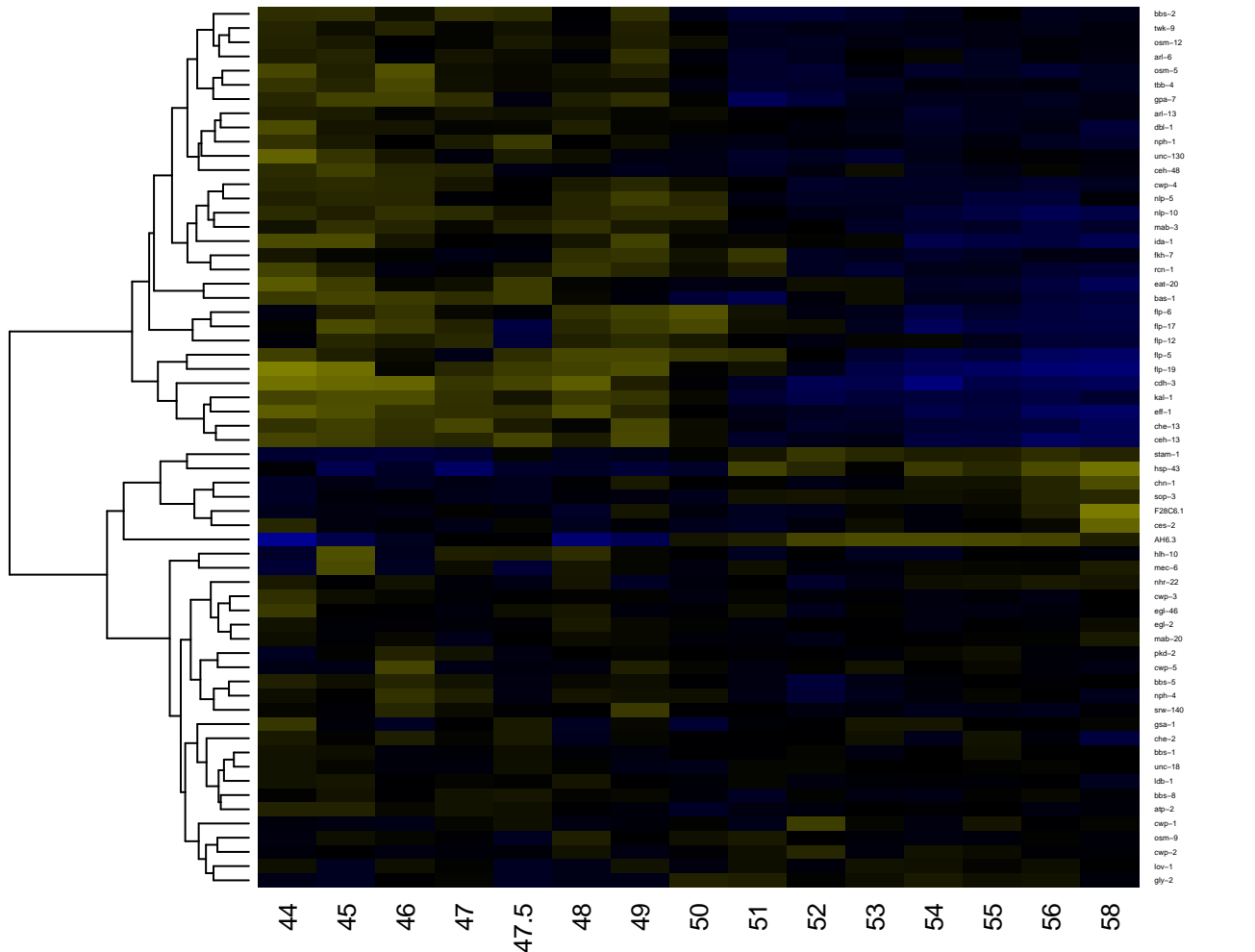
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1

2

R5BL



-2

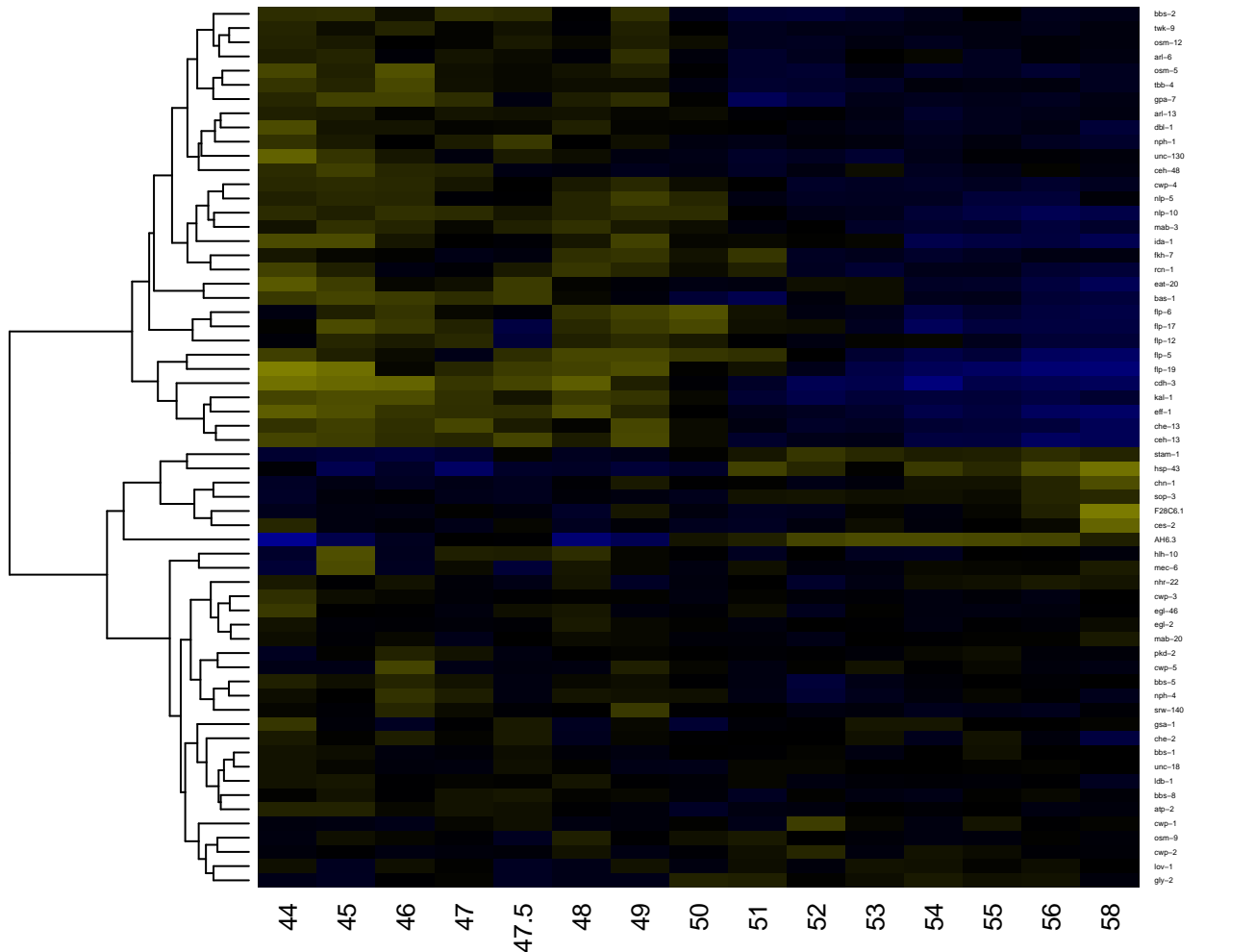
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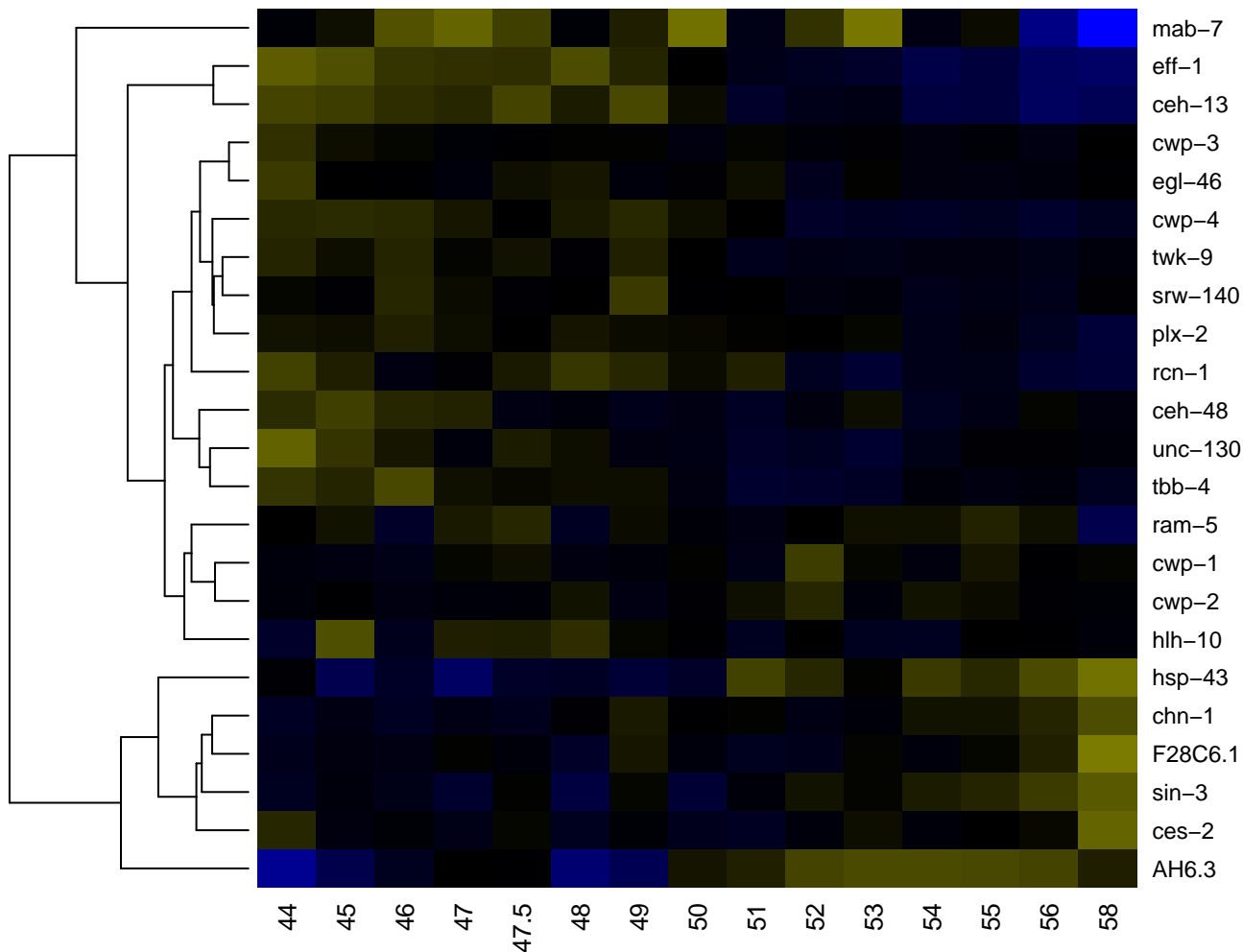
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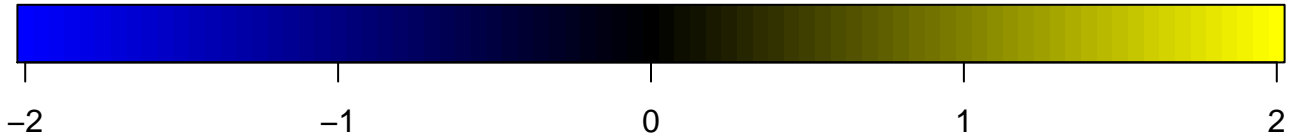
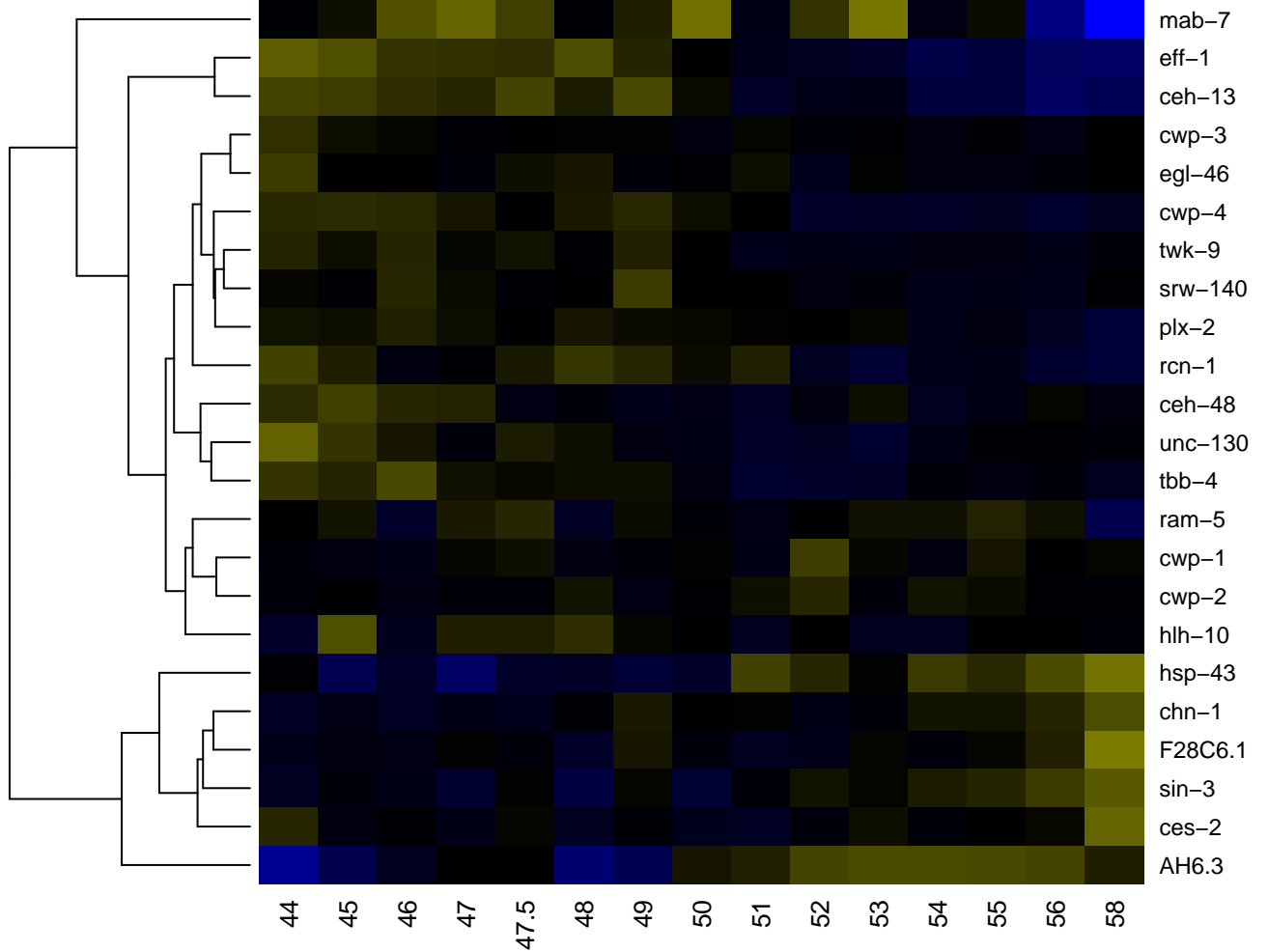
R5BR



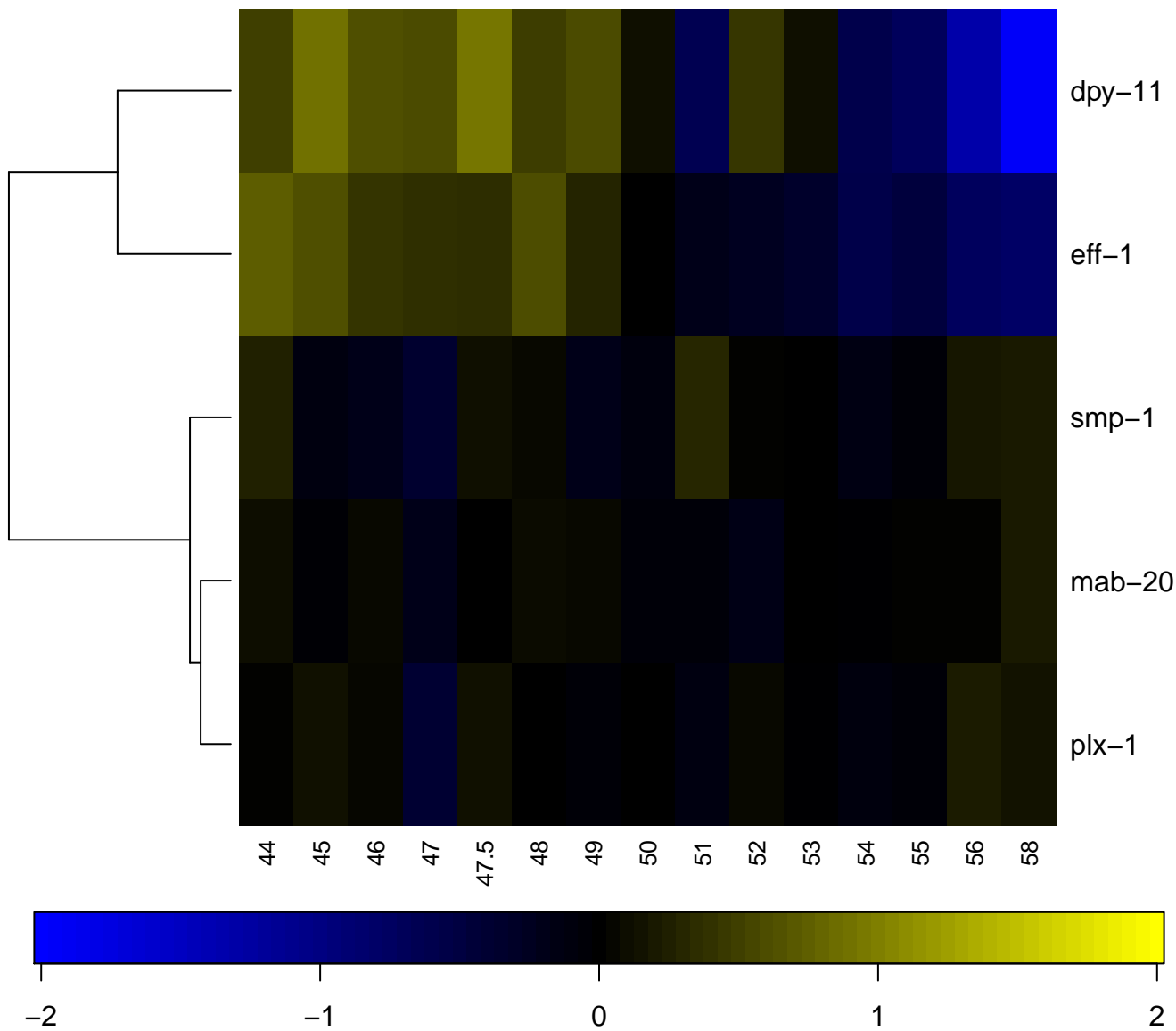
R5stL



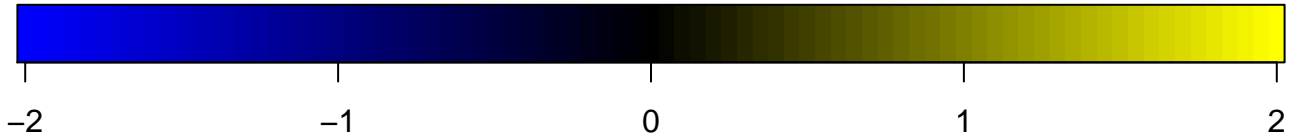
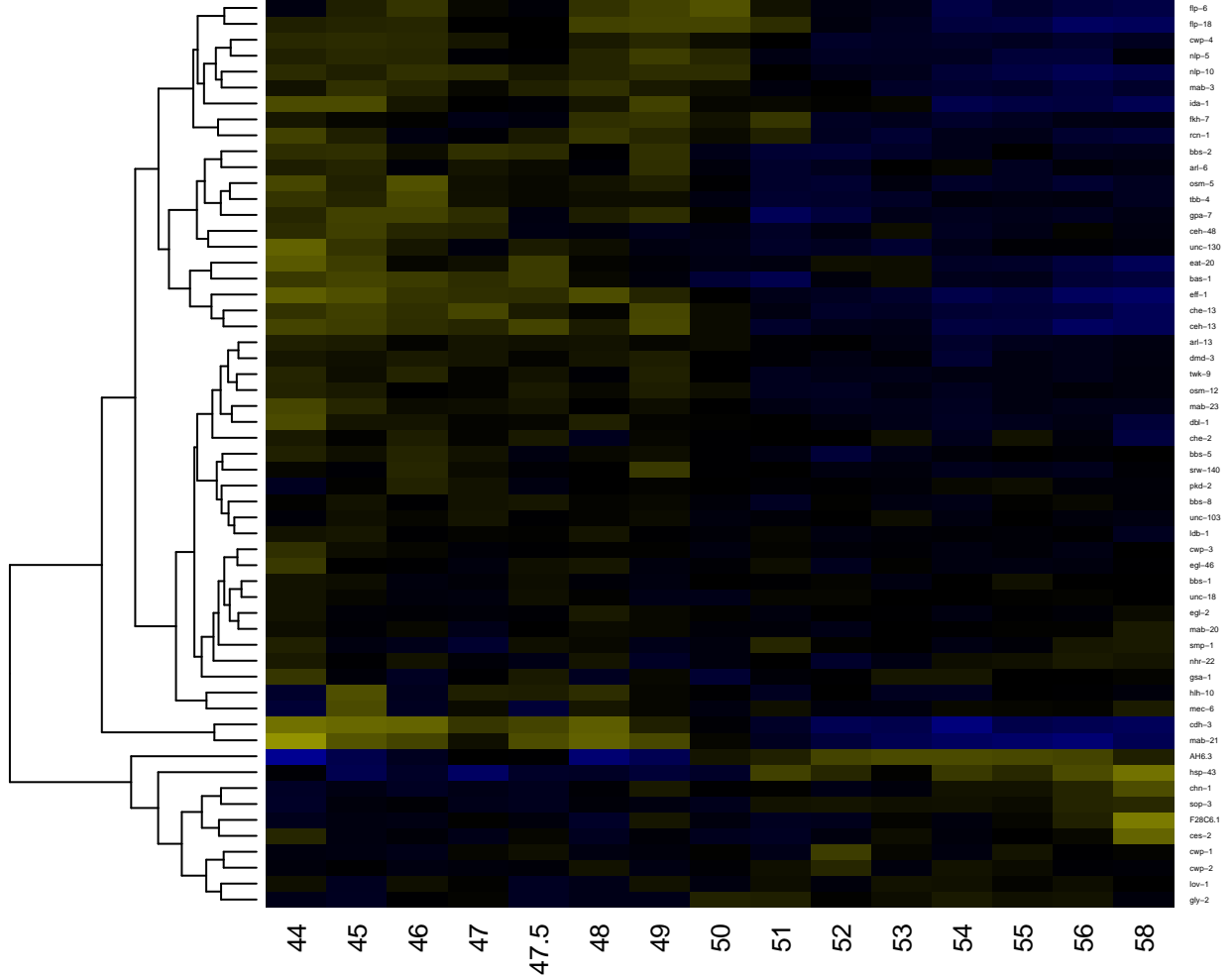
R5stR



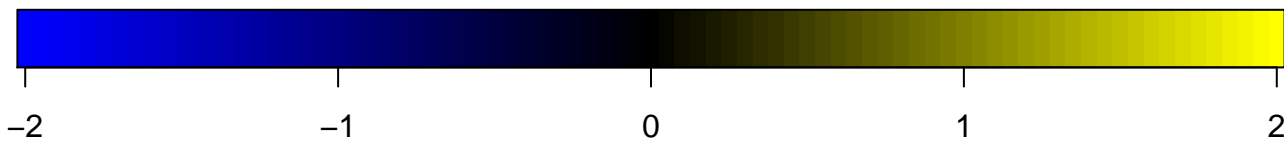
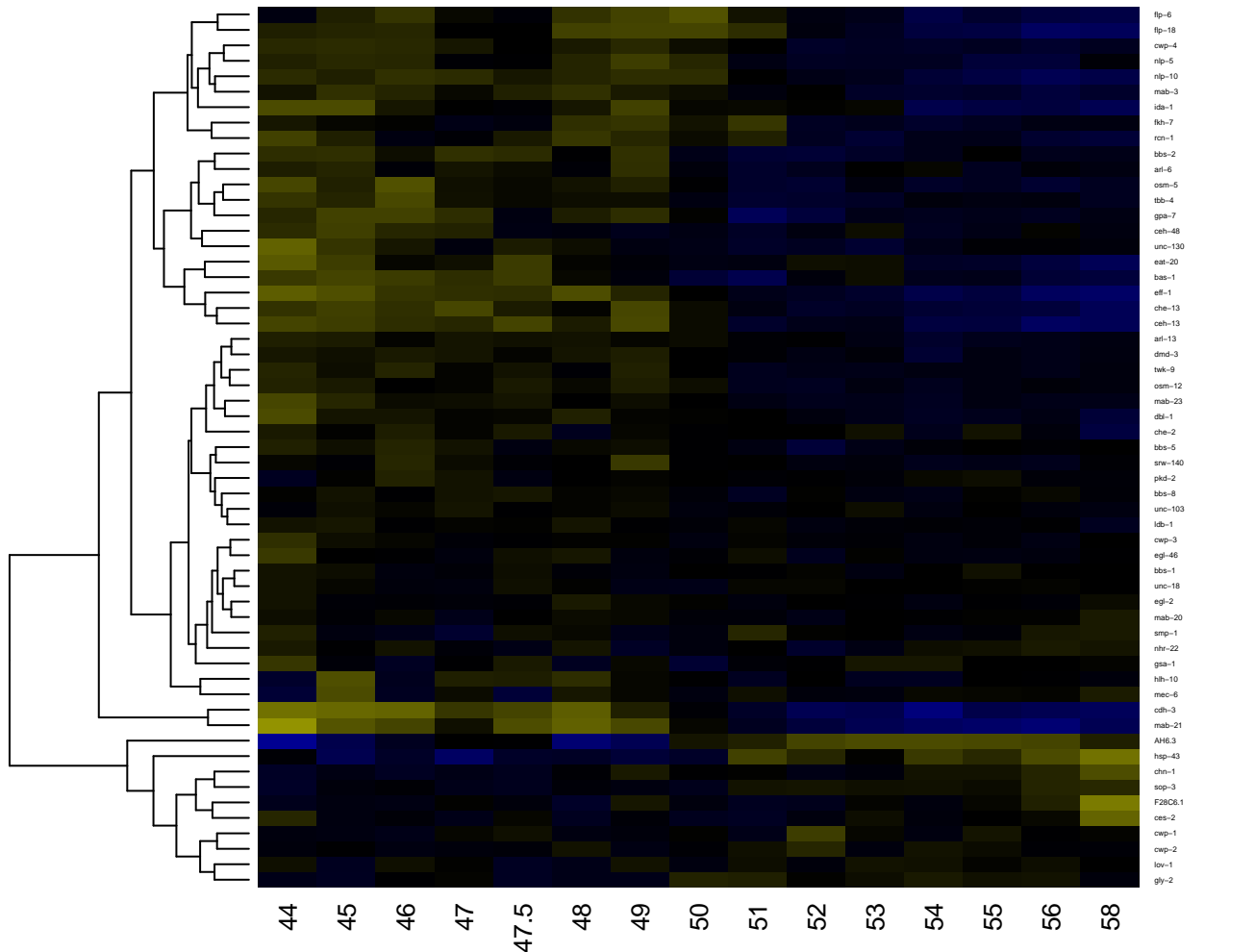
R6_hyp



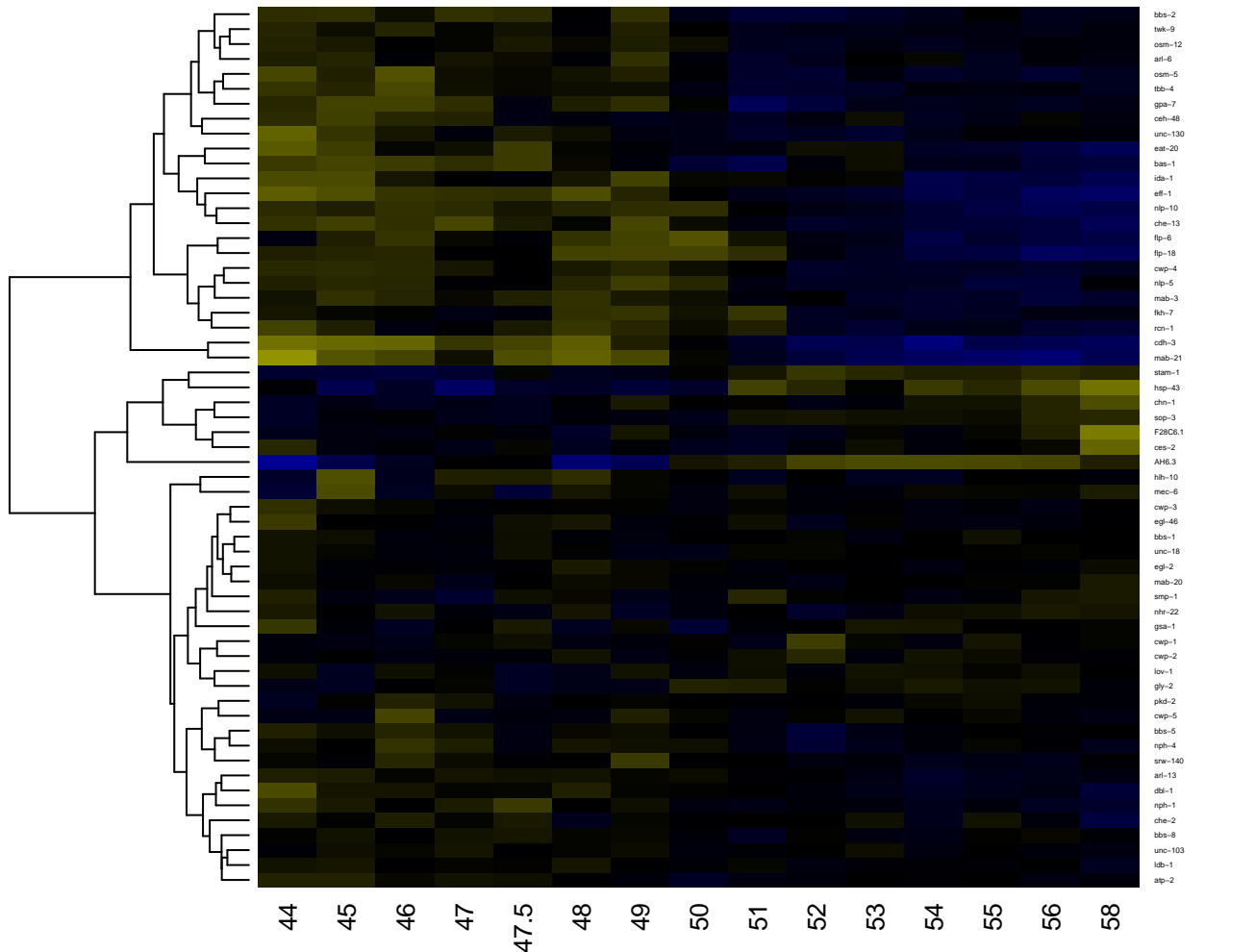
R6AL



R6AR



R6BL



-2

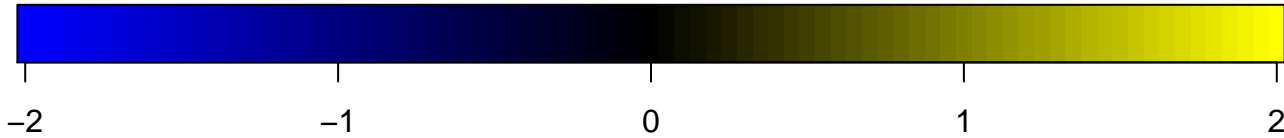
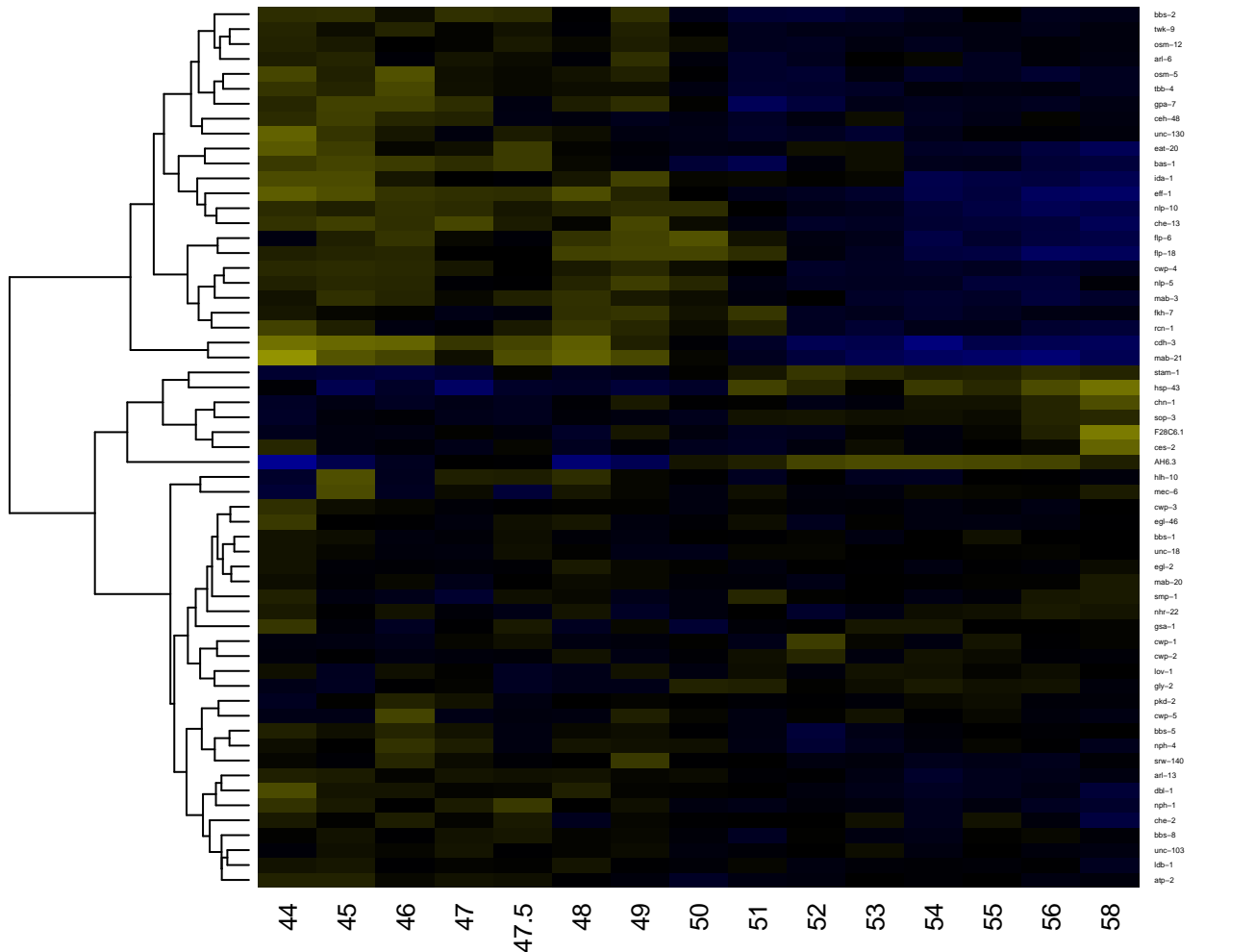
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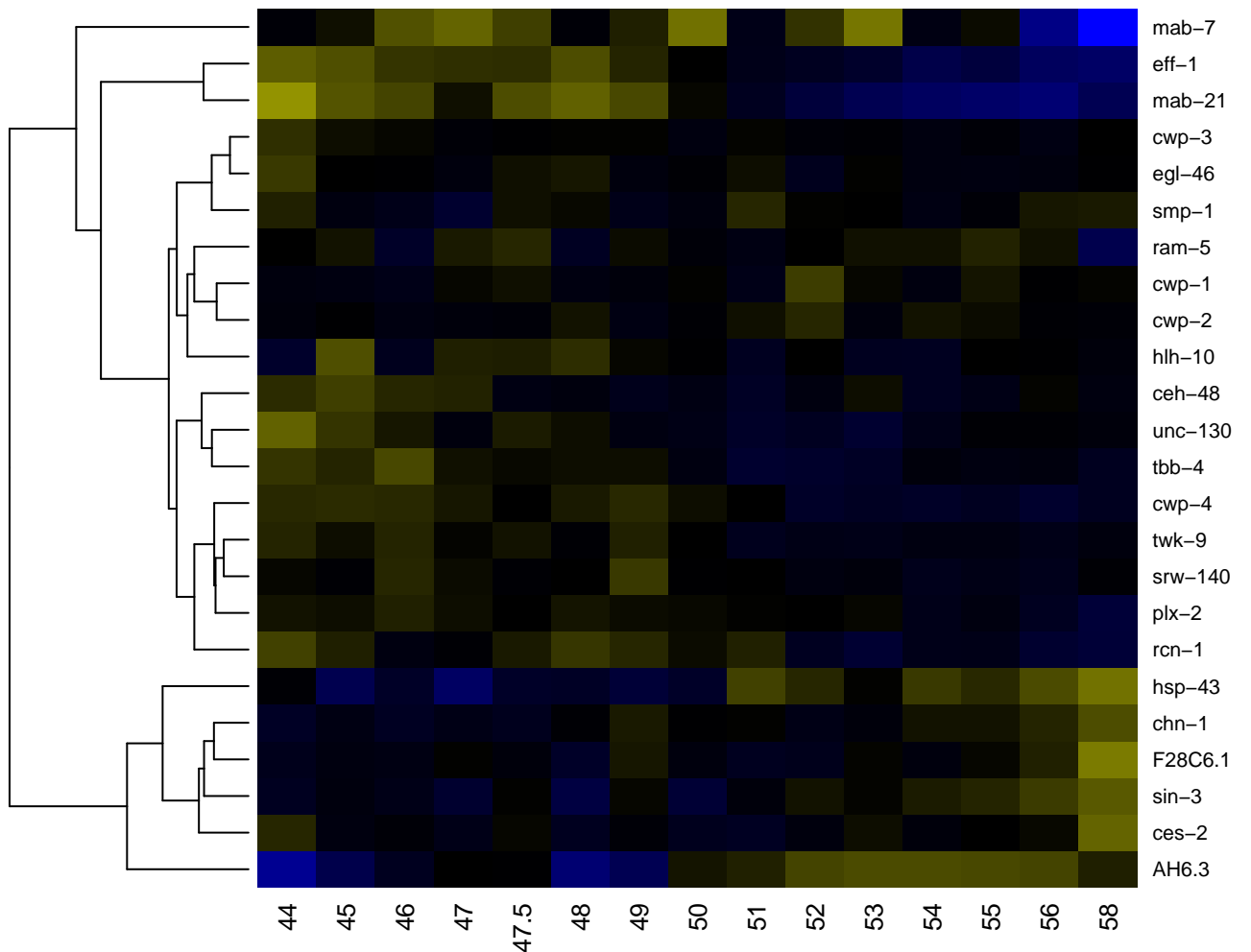
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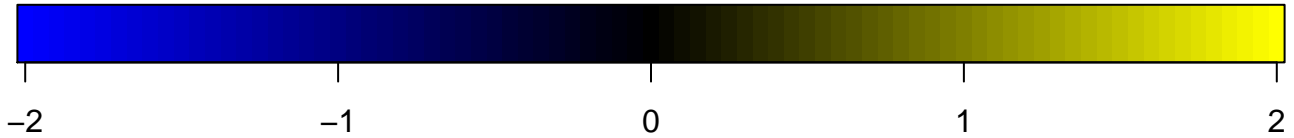
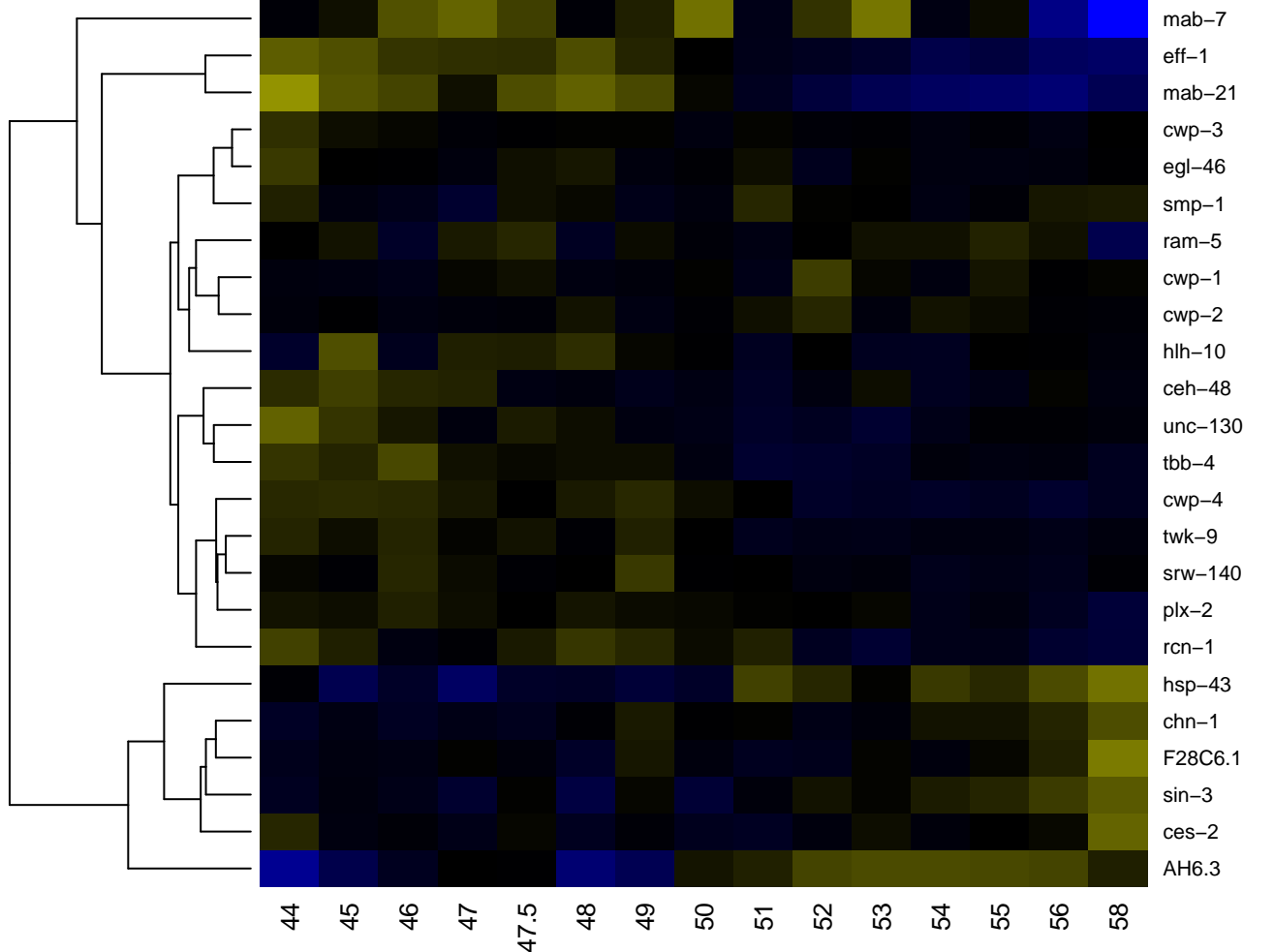
R6BR



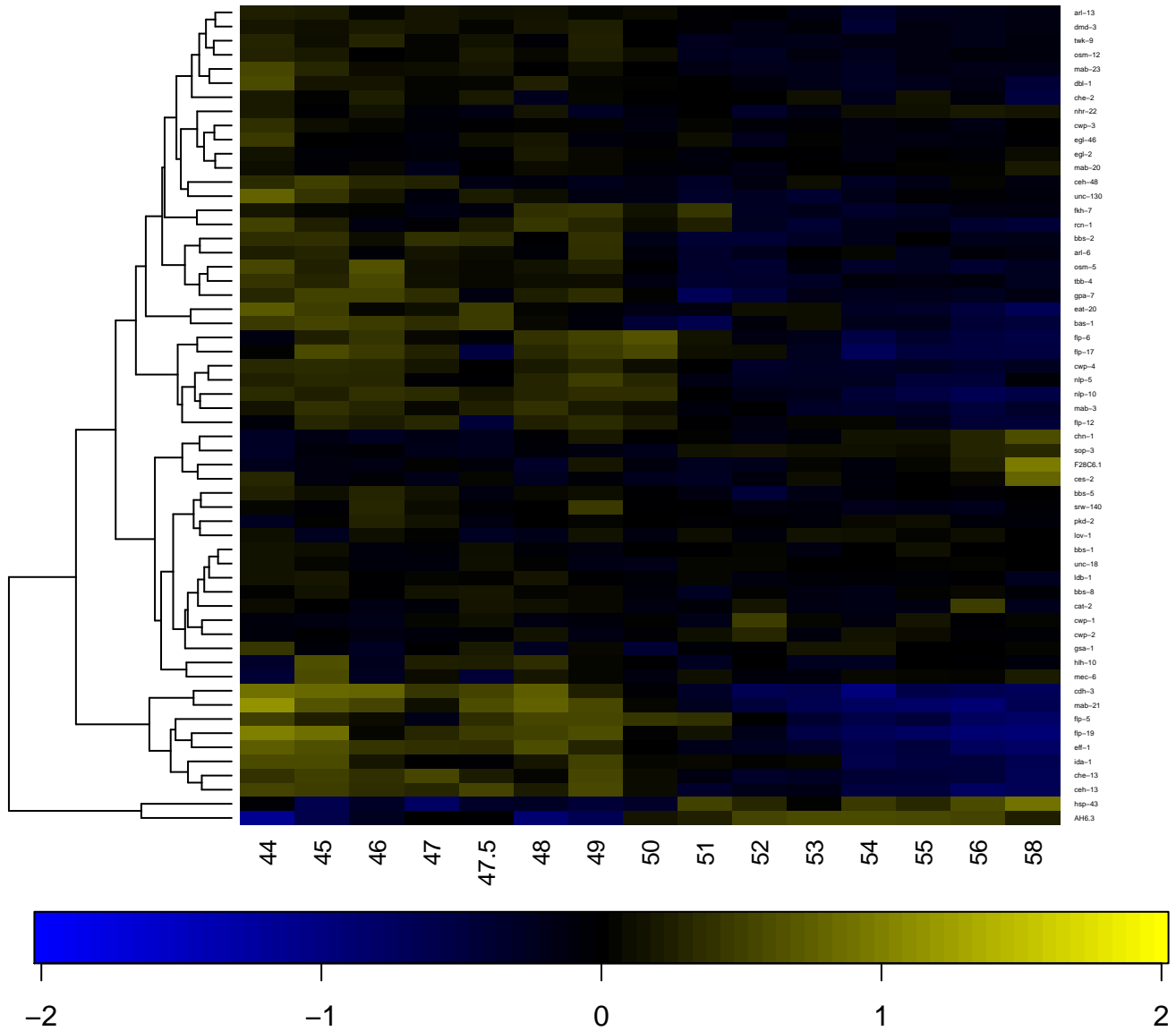
R6stL



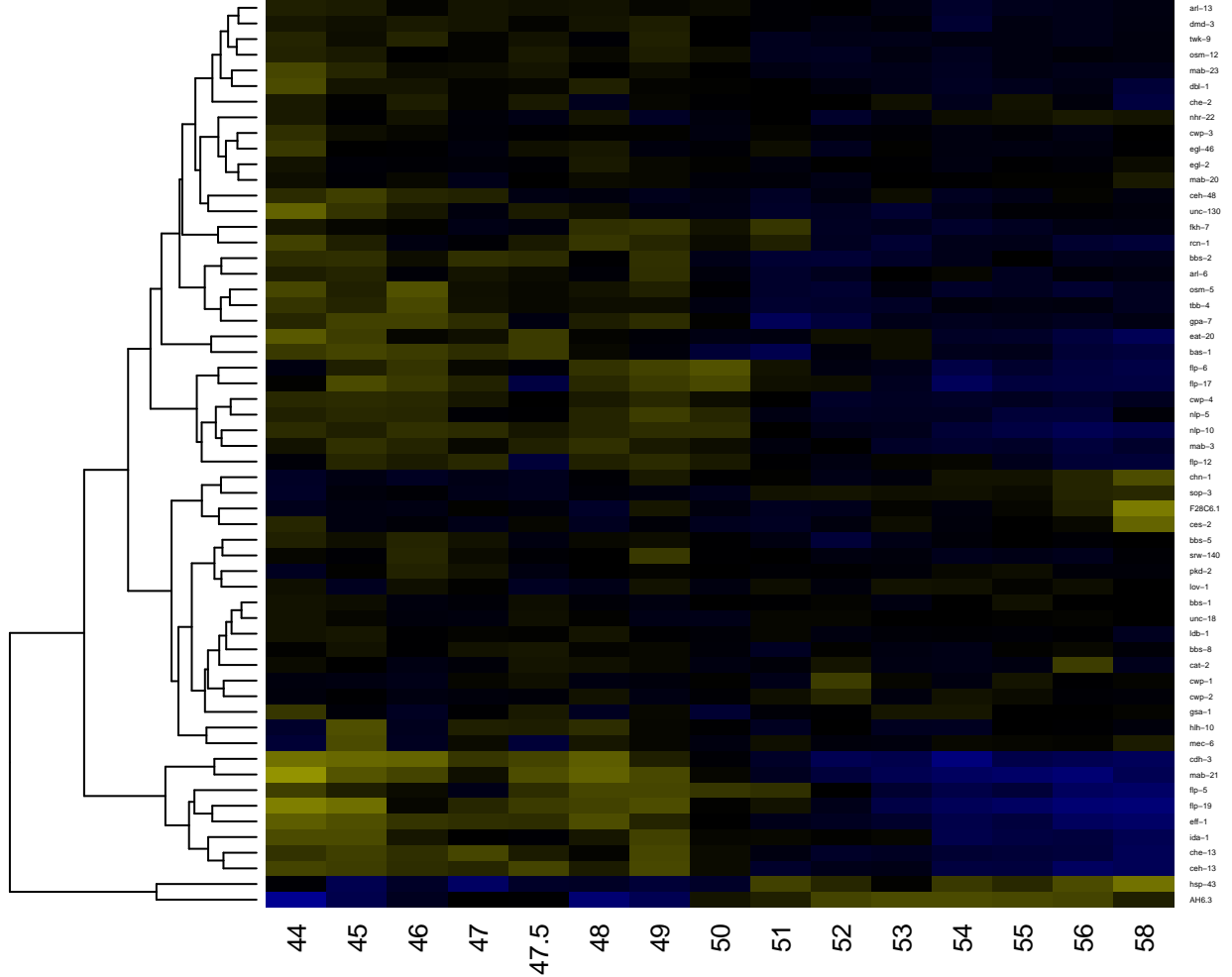
R6stR



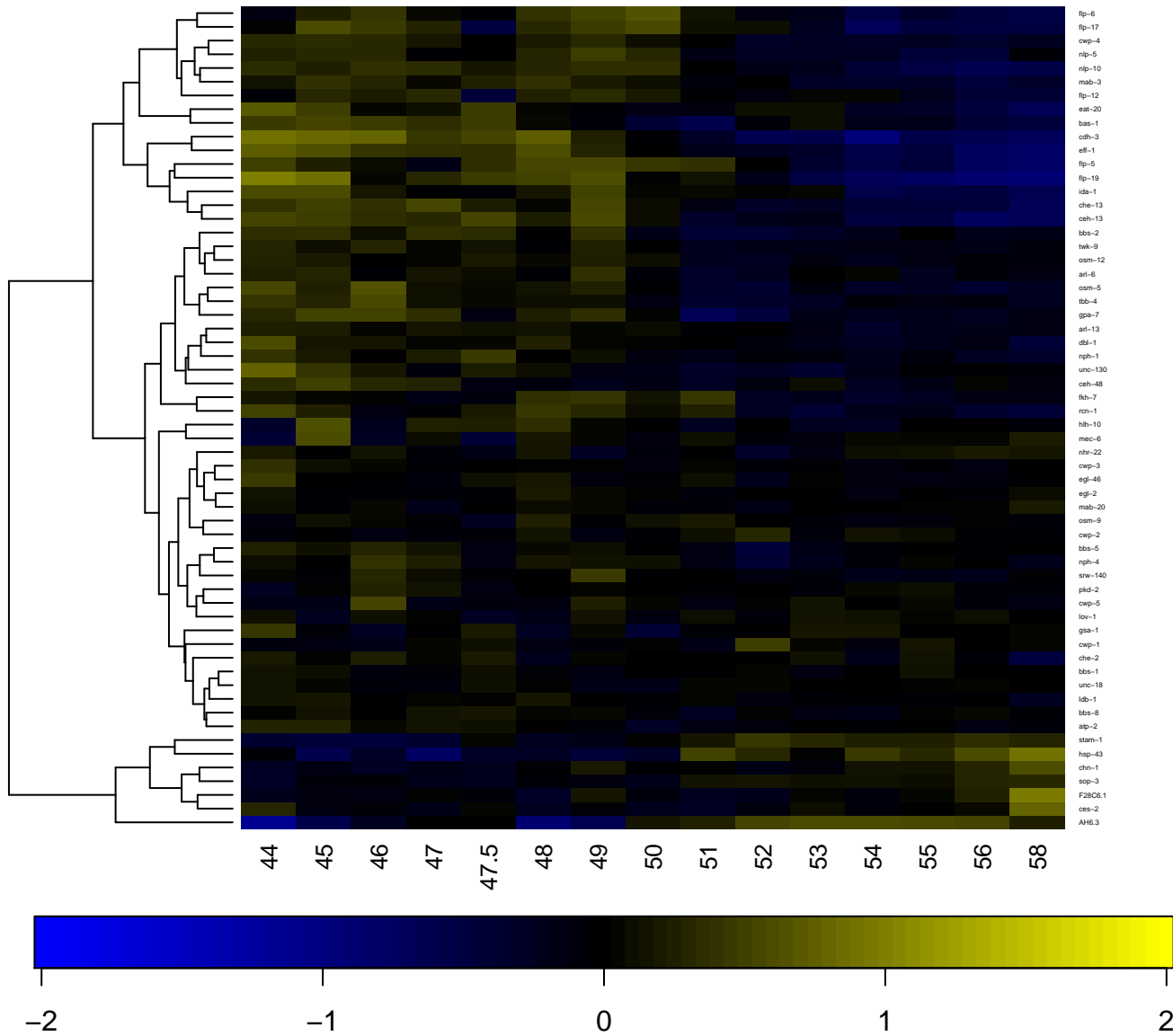
R7AL



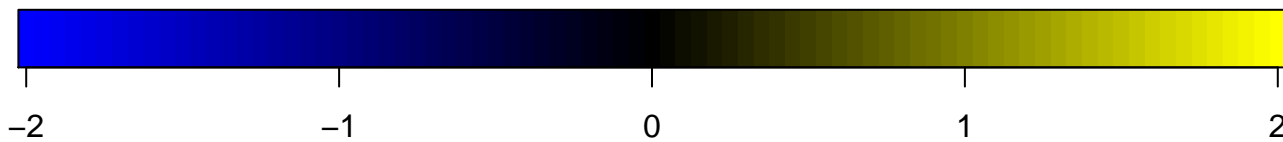
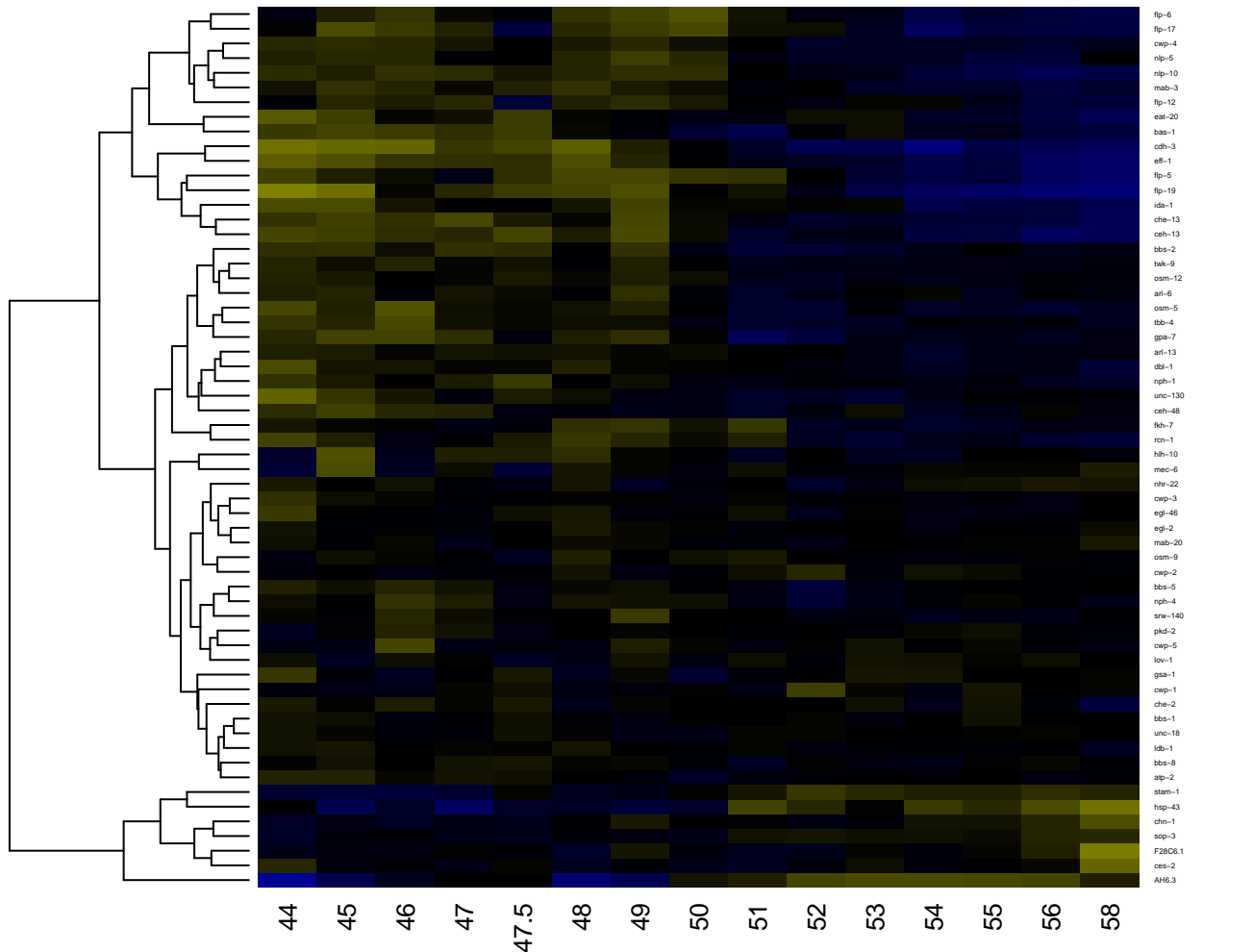
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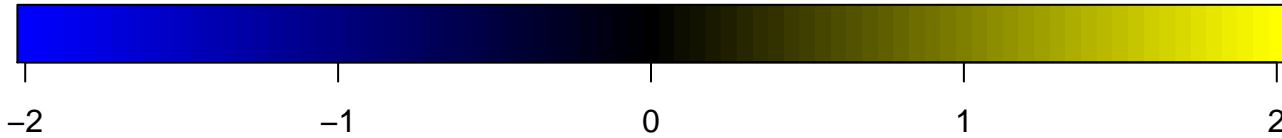
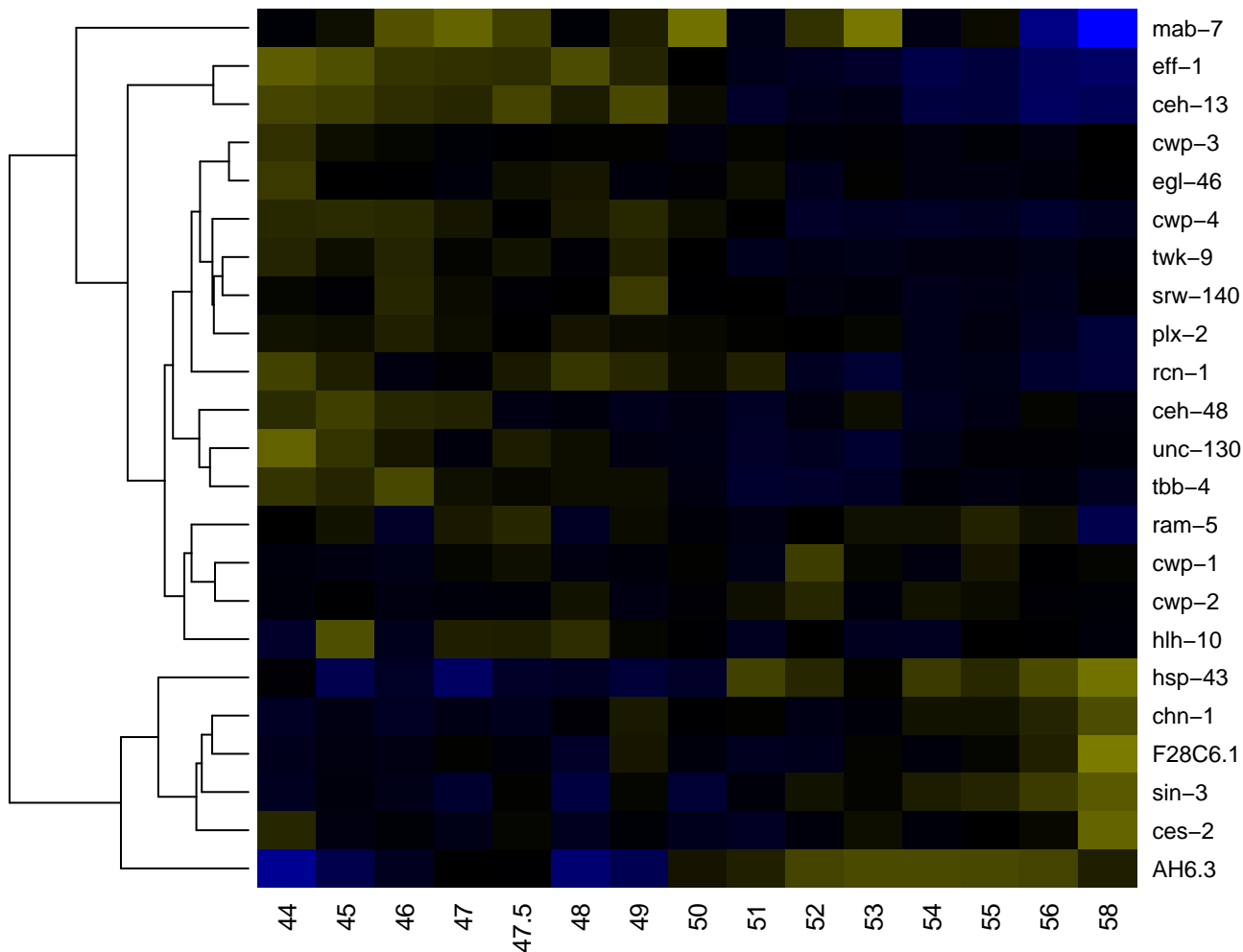
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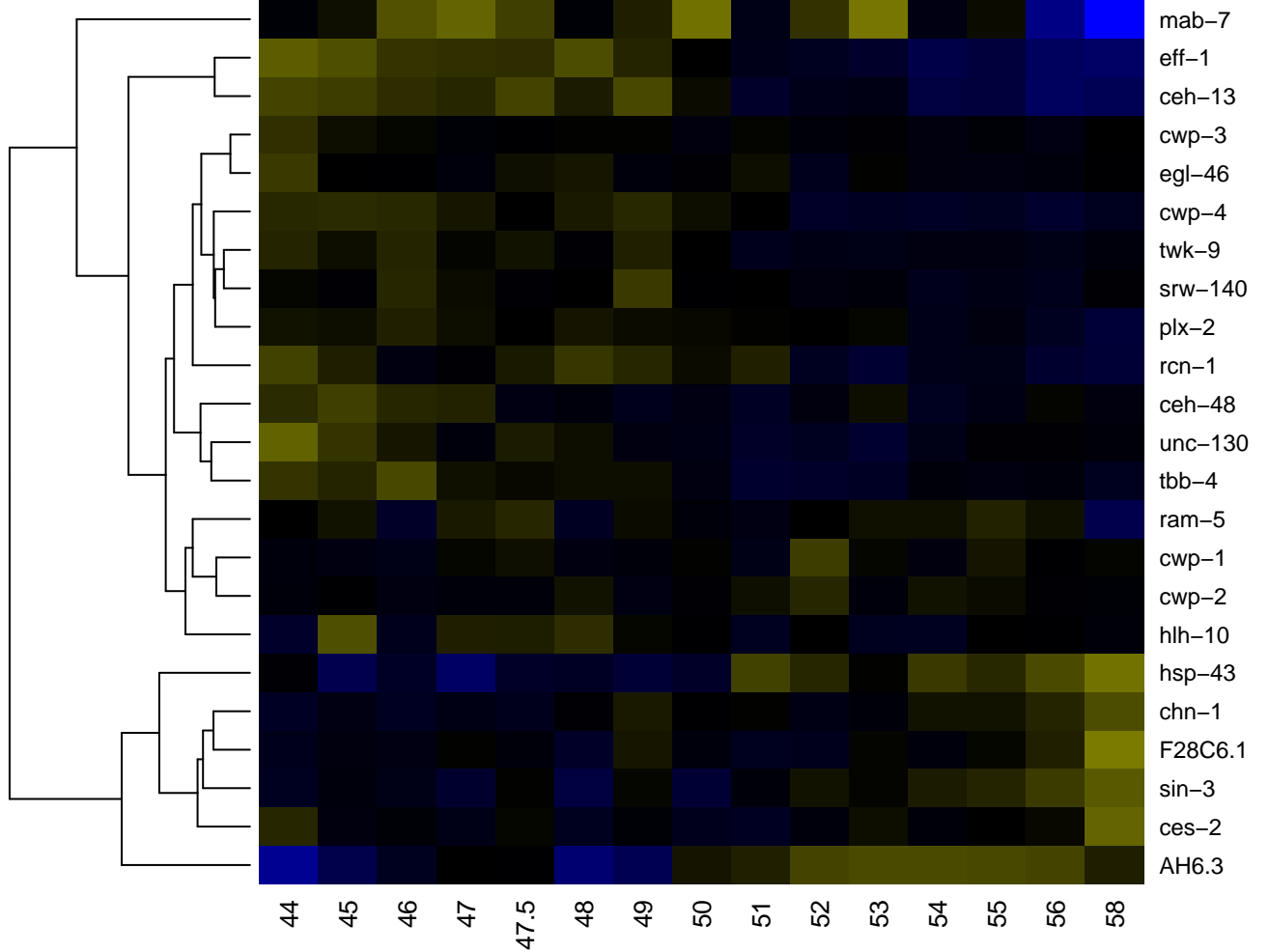
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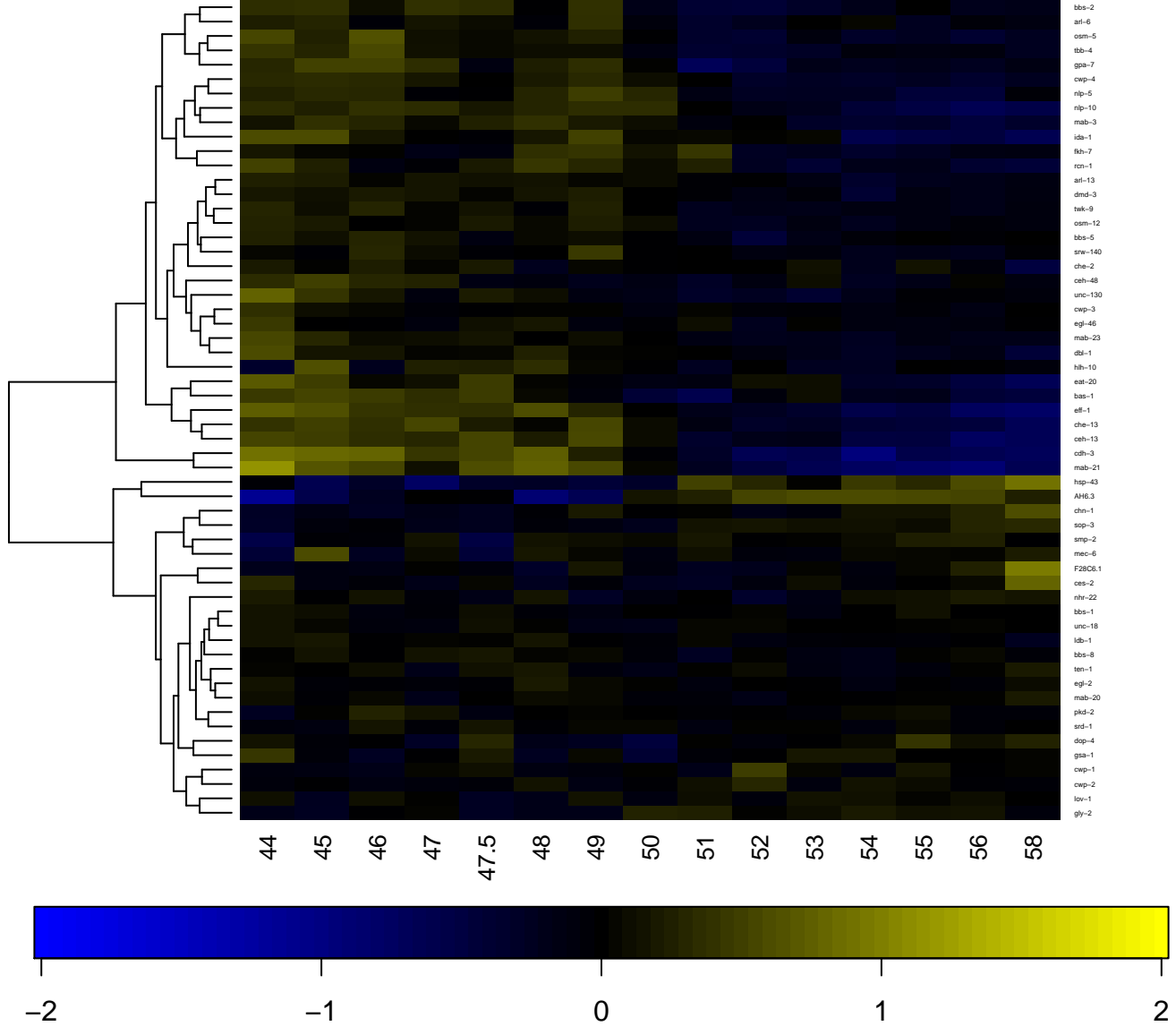
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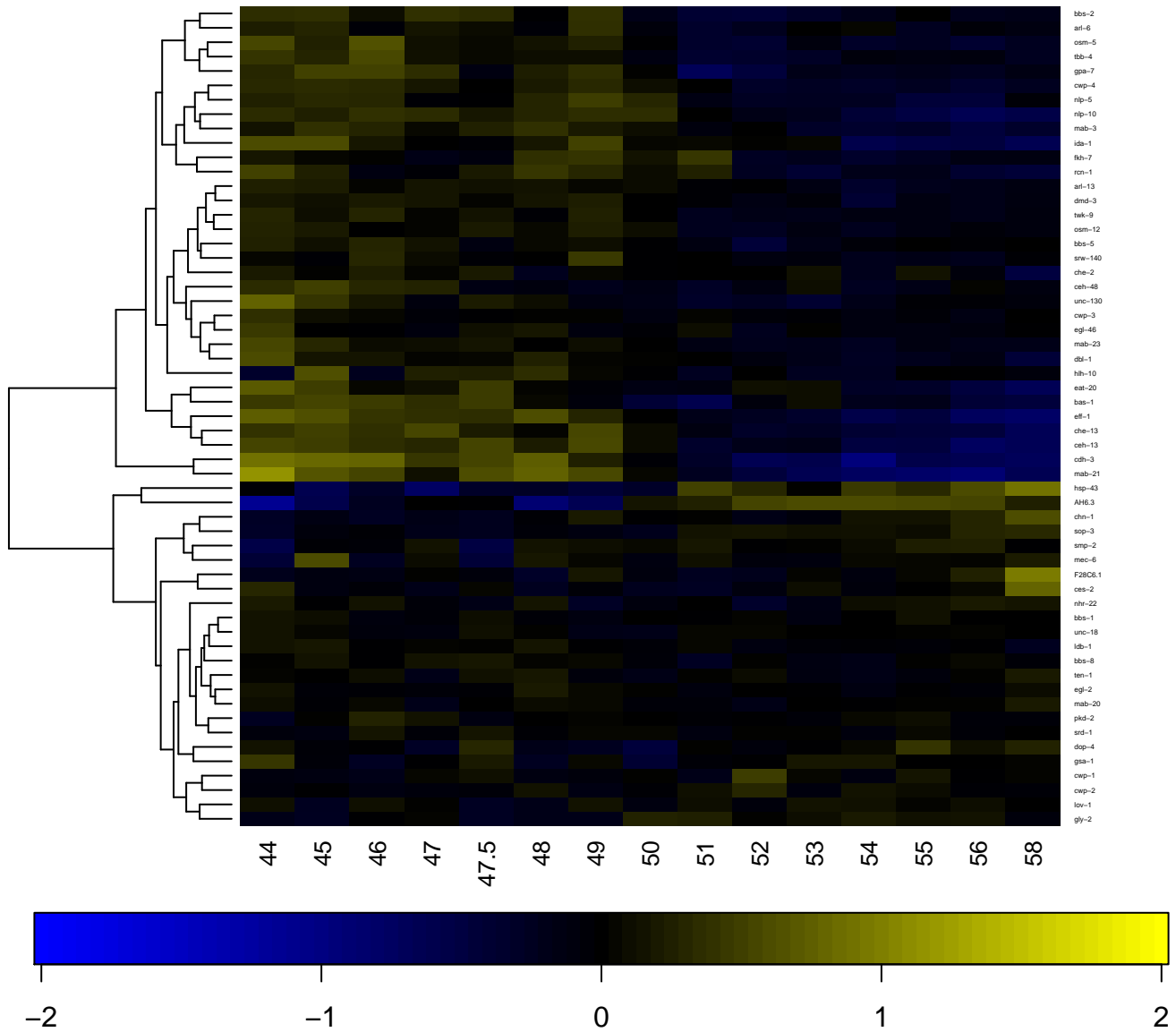
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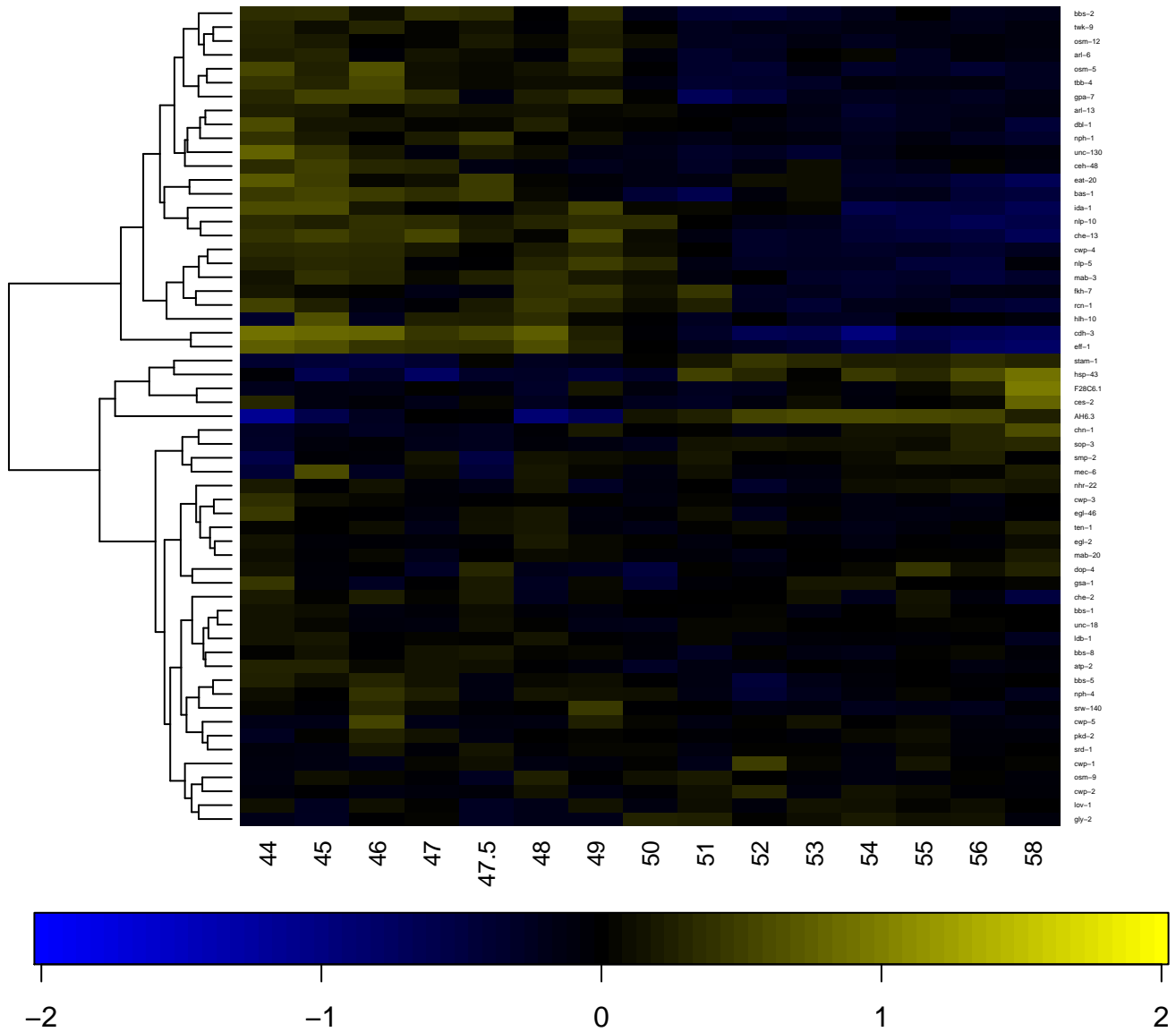
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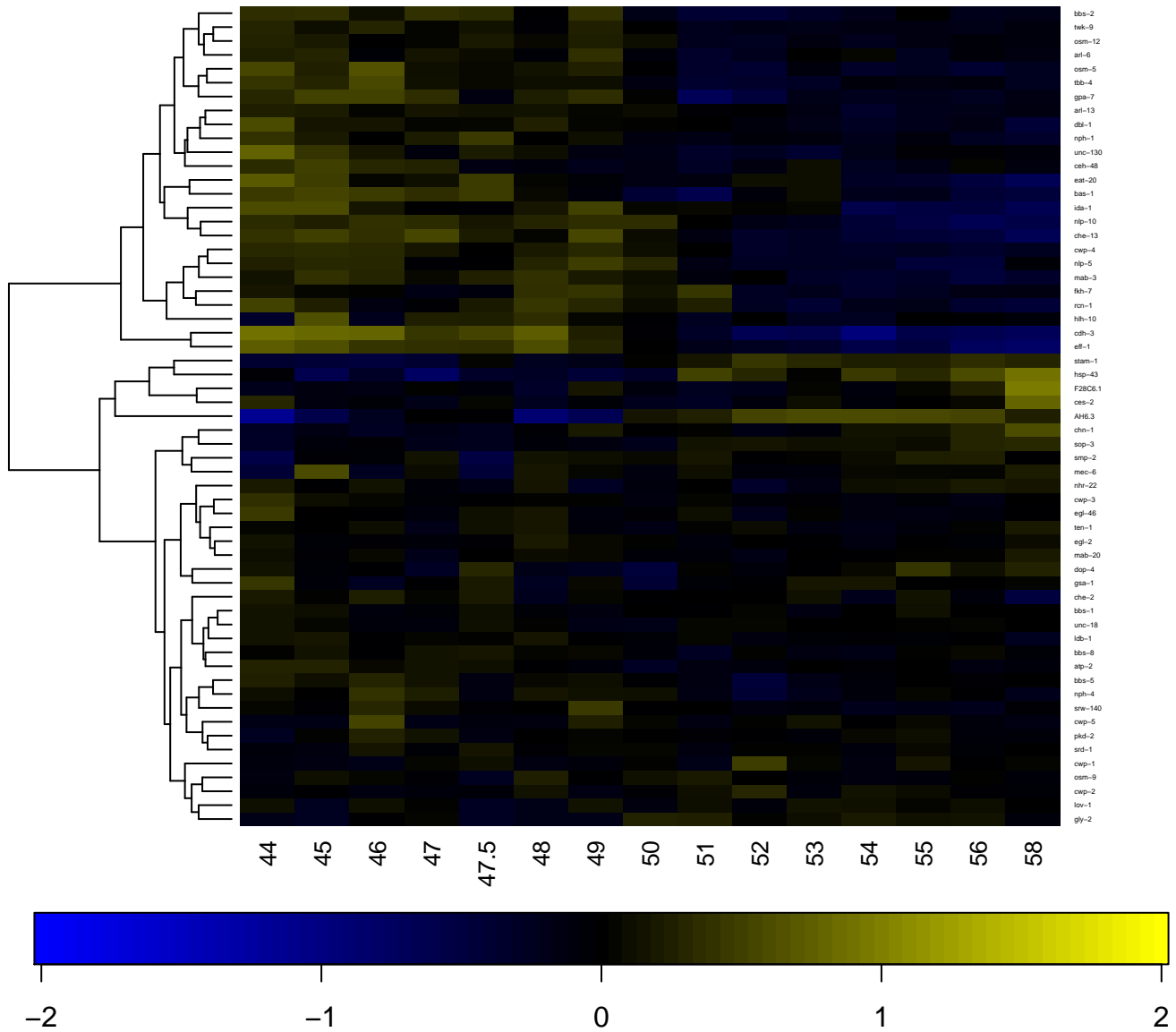
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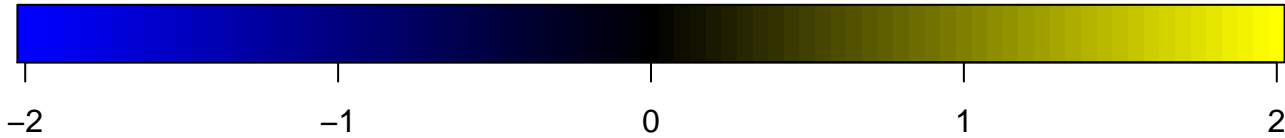
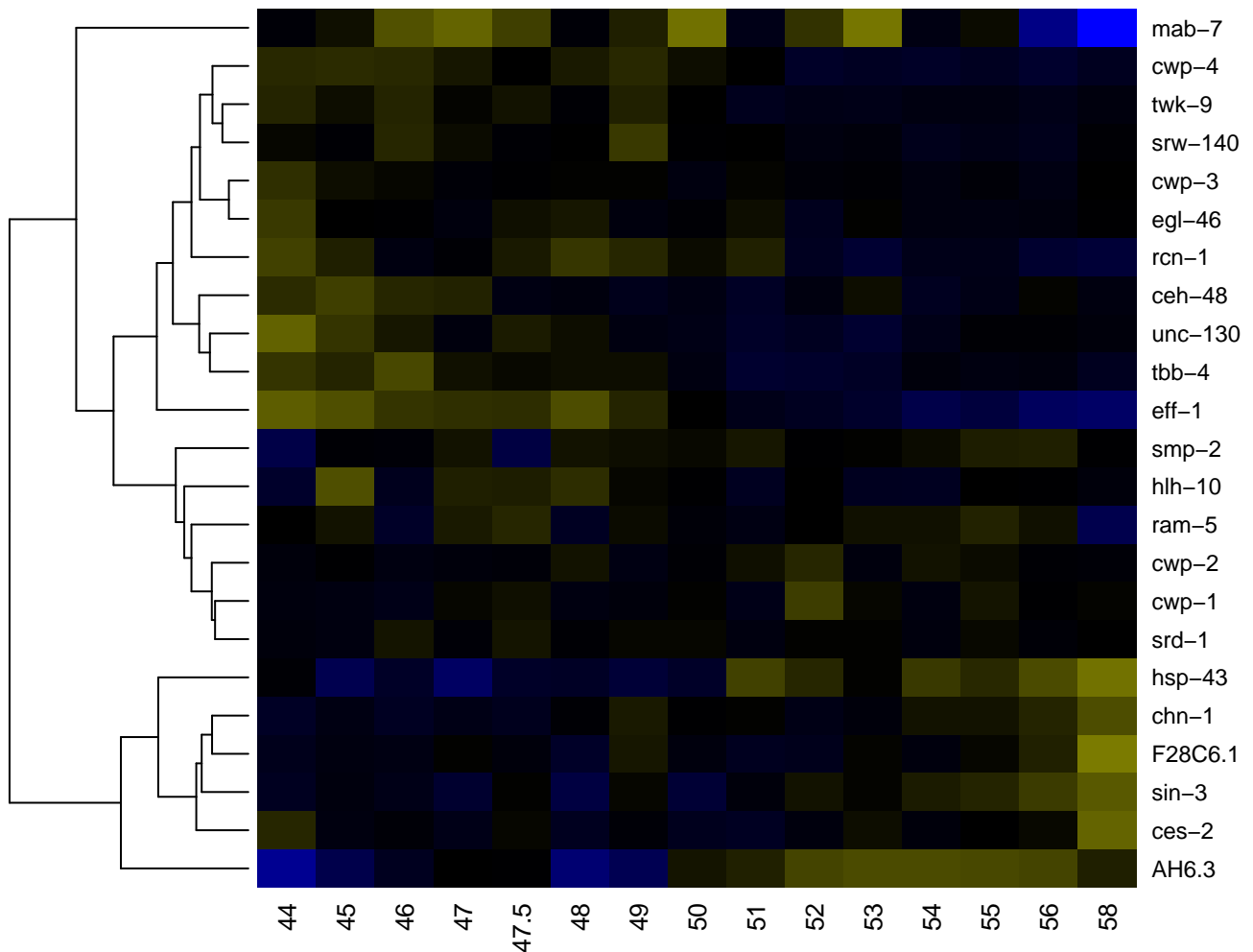
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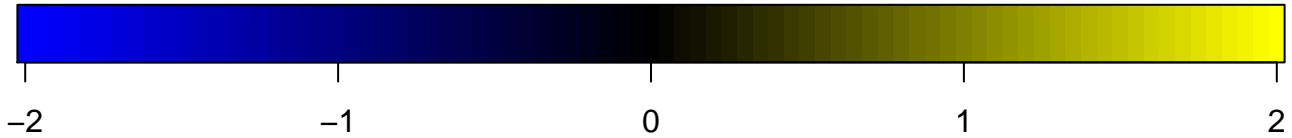
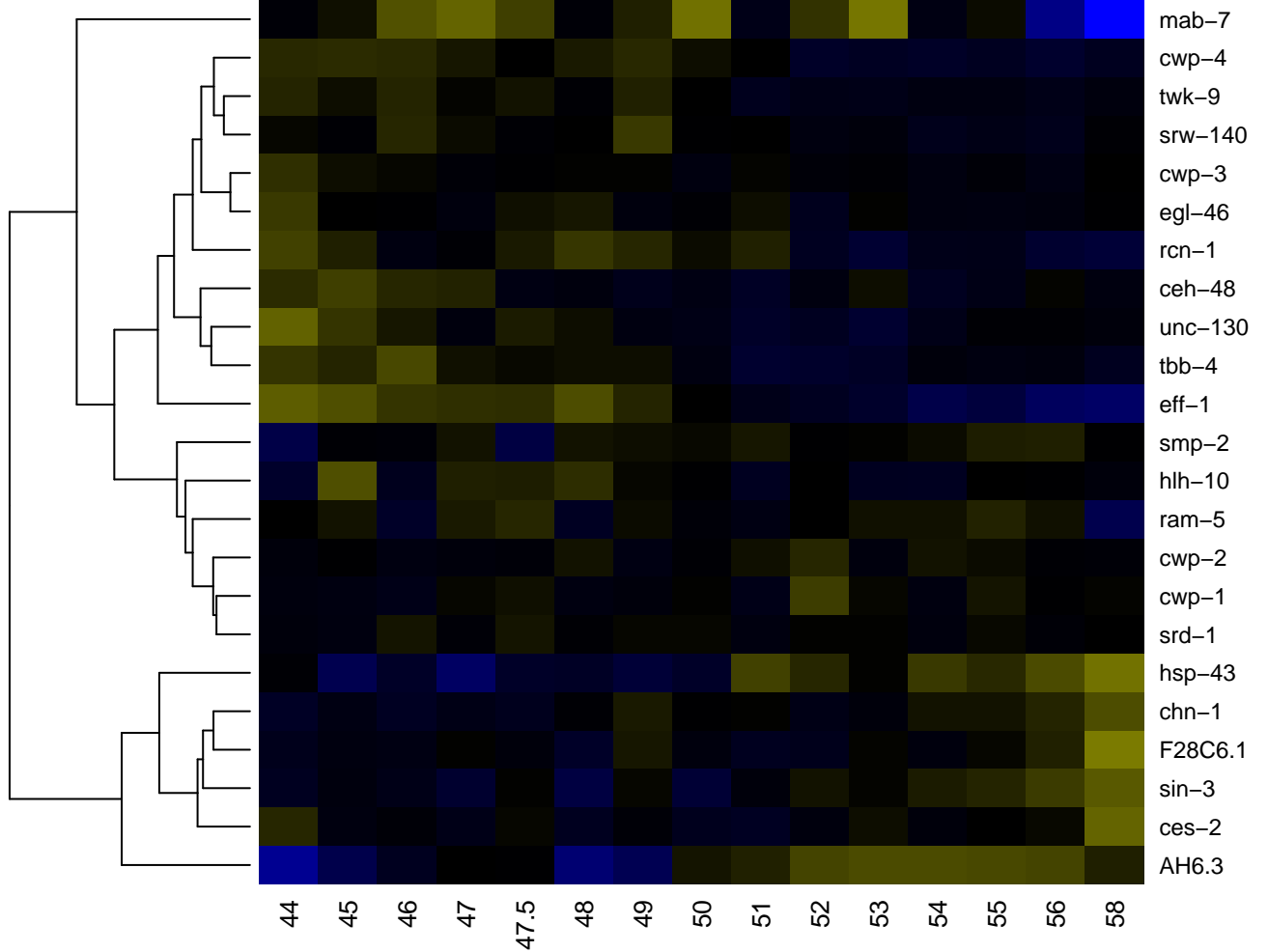
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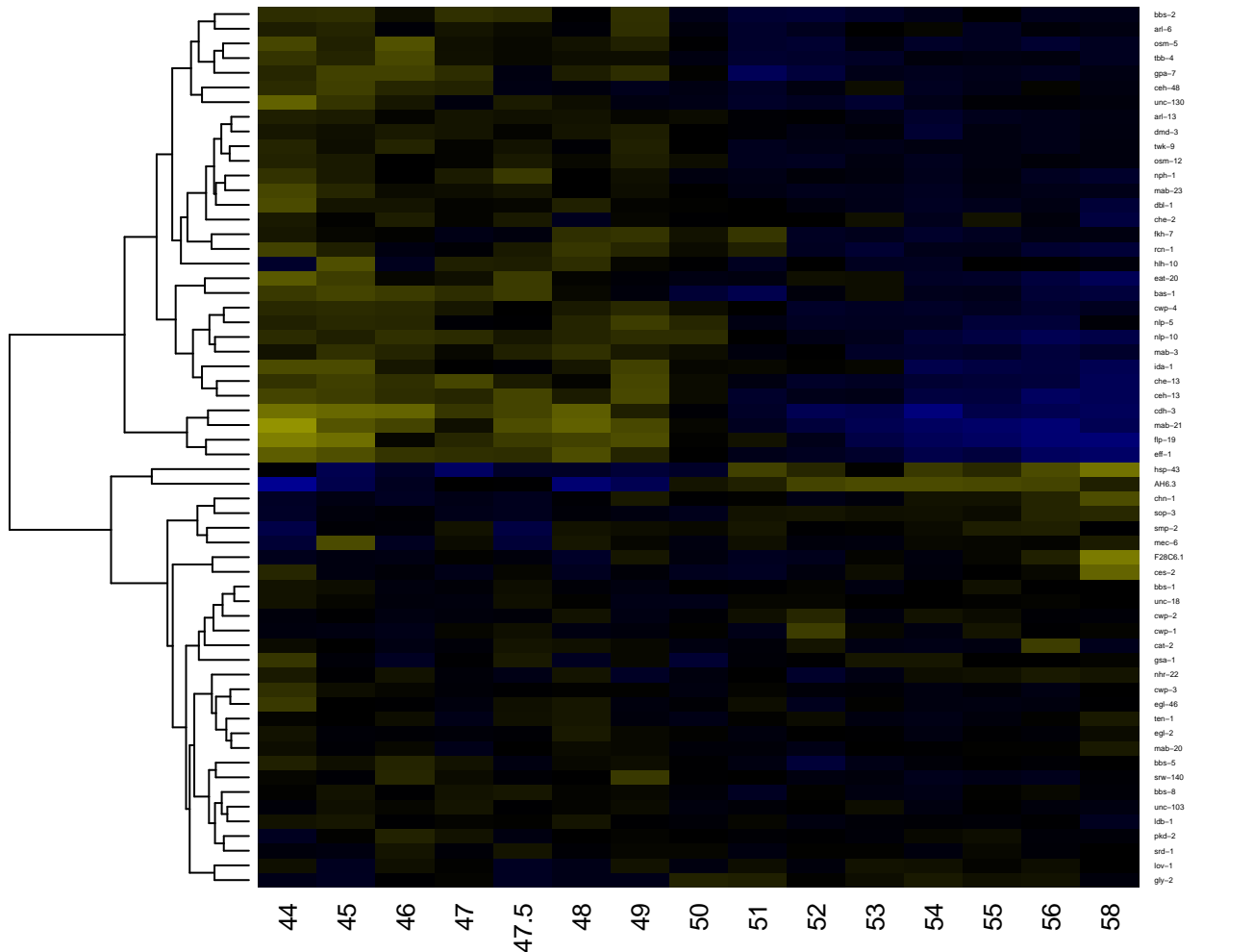
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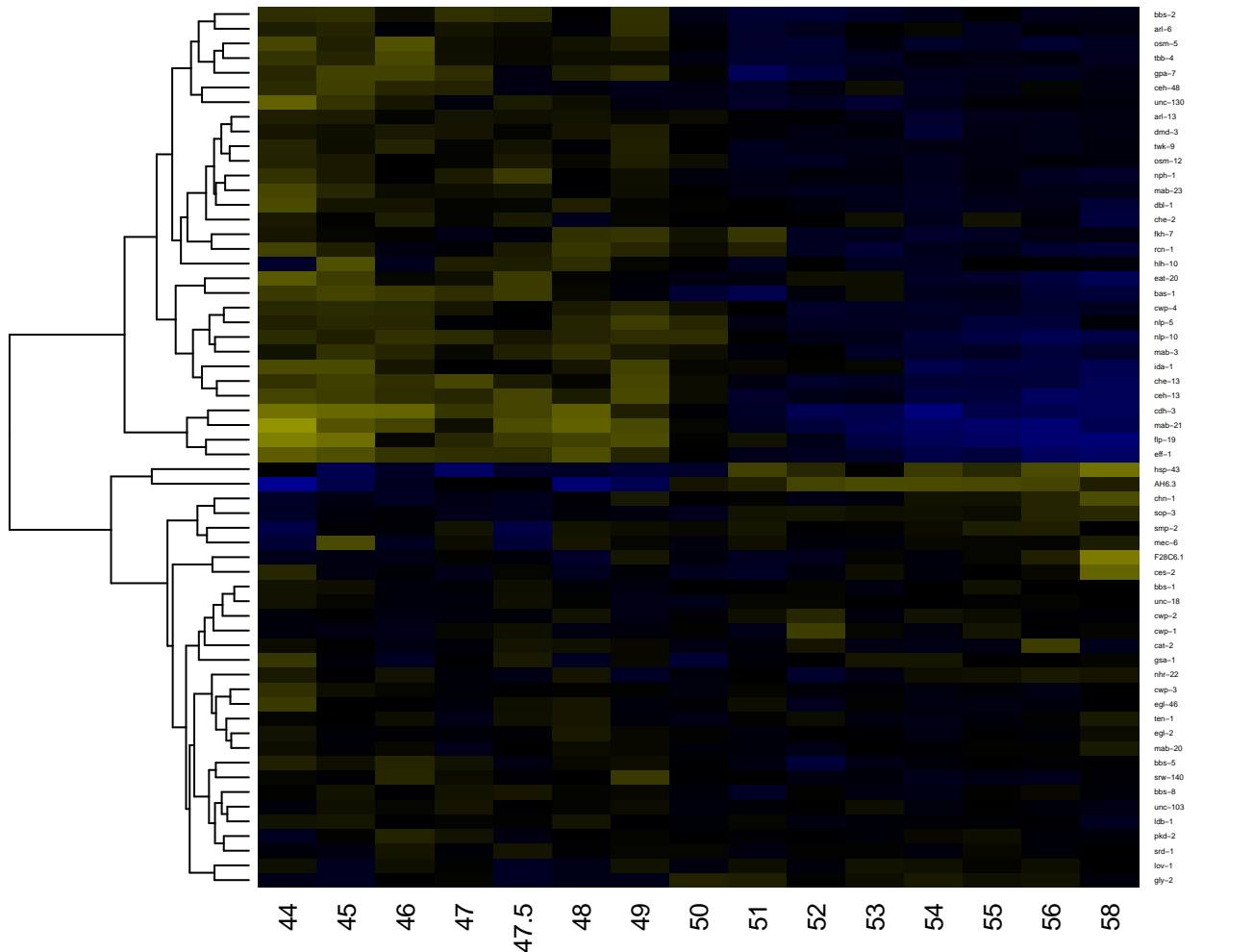
R8stR



R9AL



R9AR



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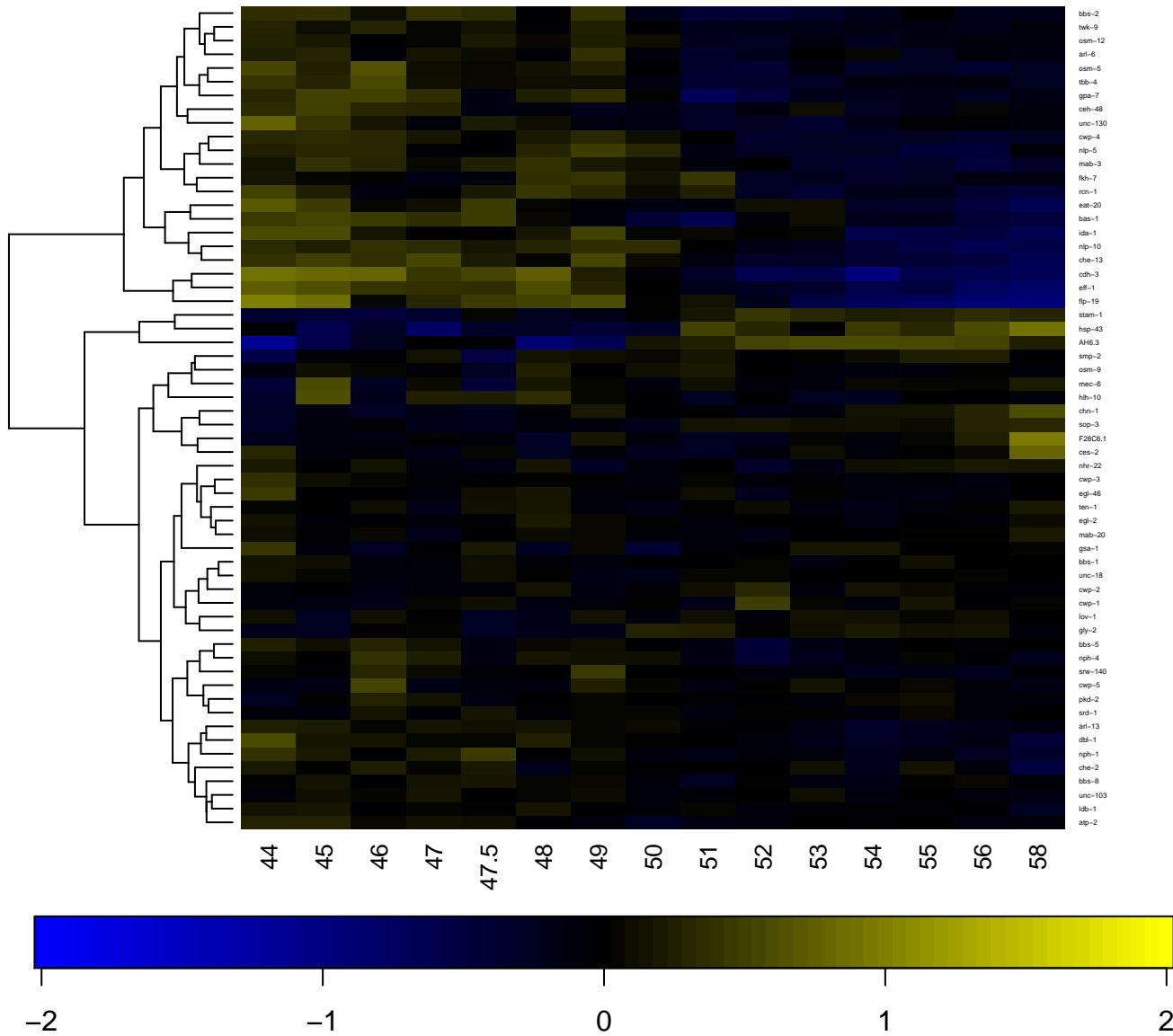
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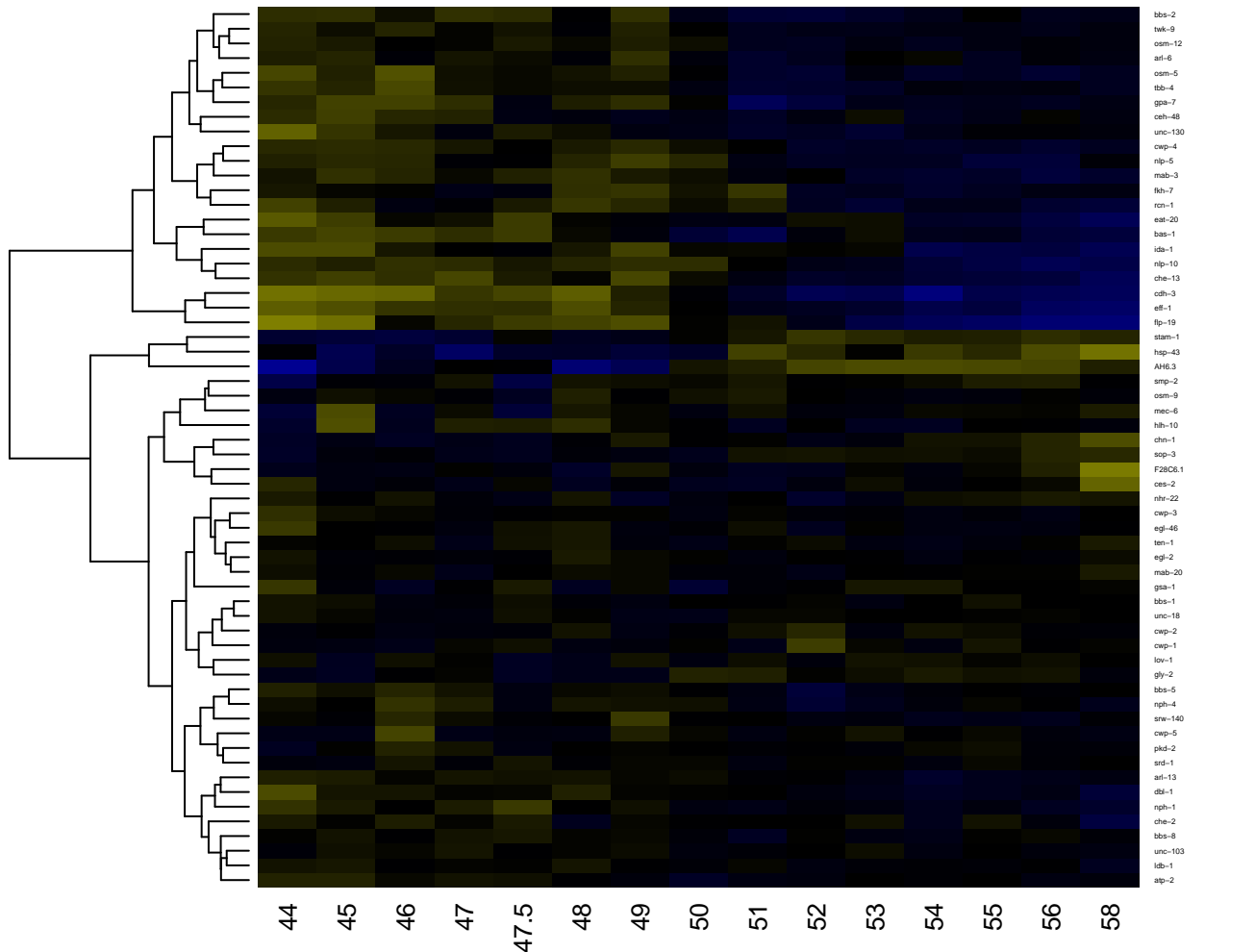
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R9BL



R9BR



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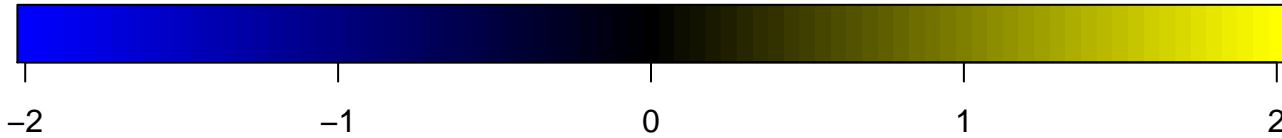
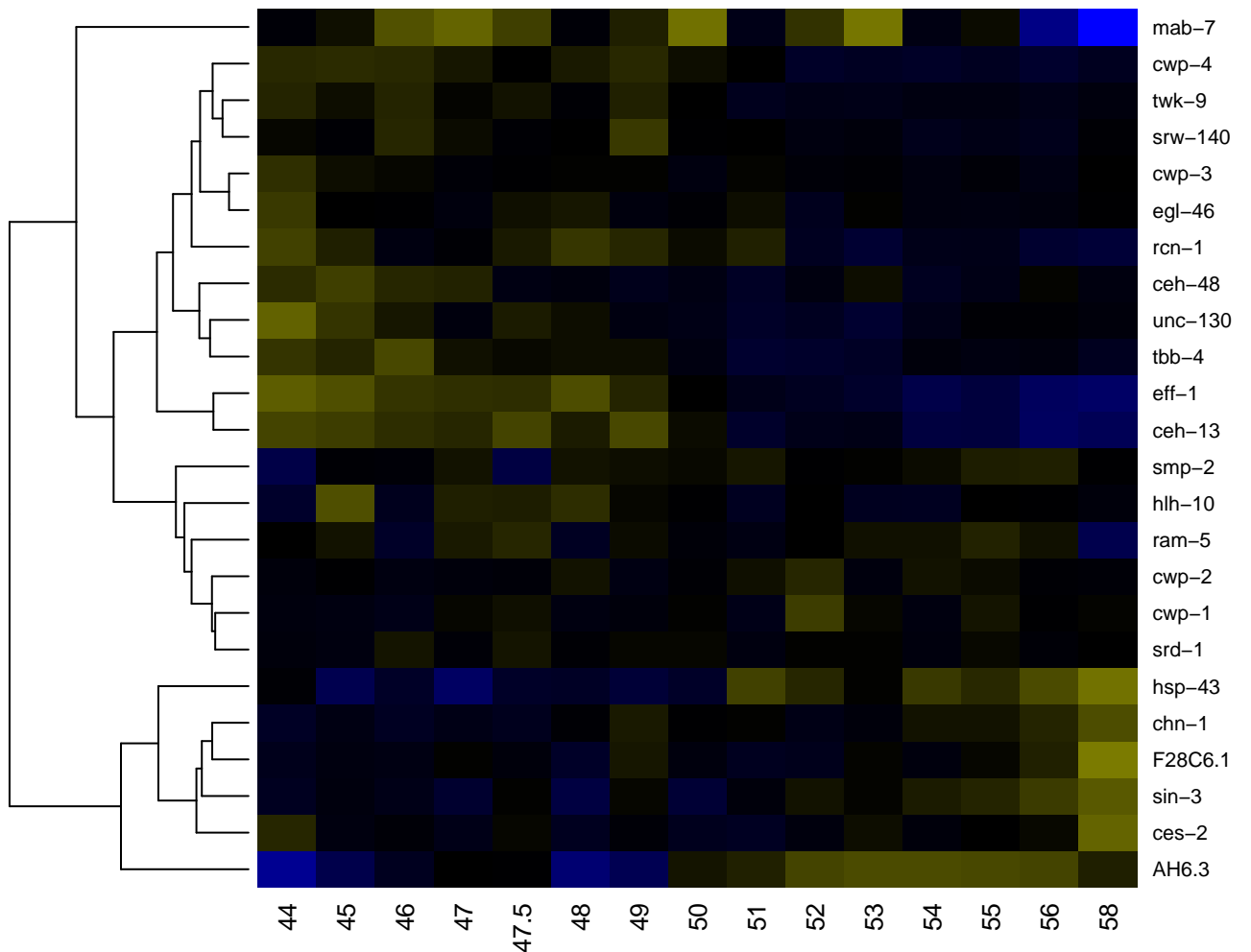
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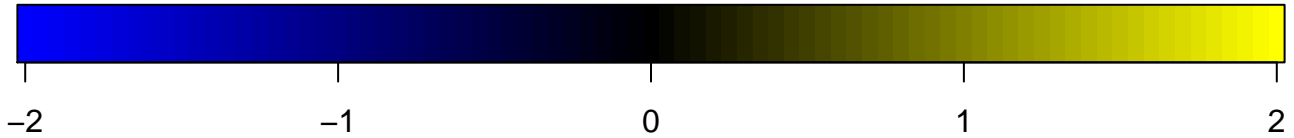
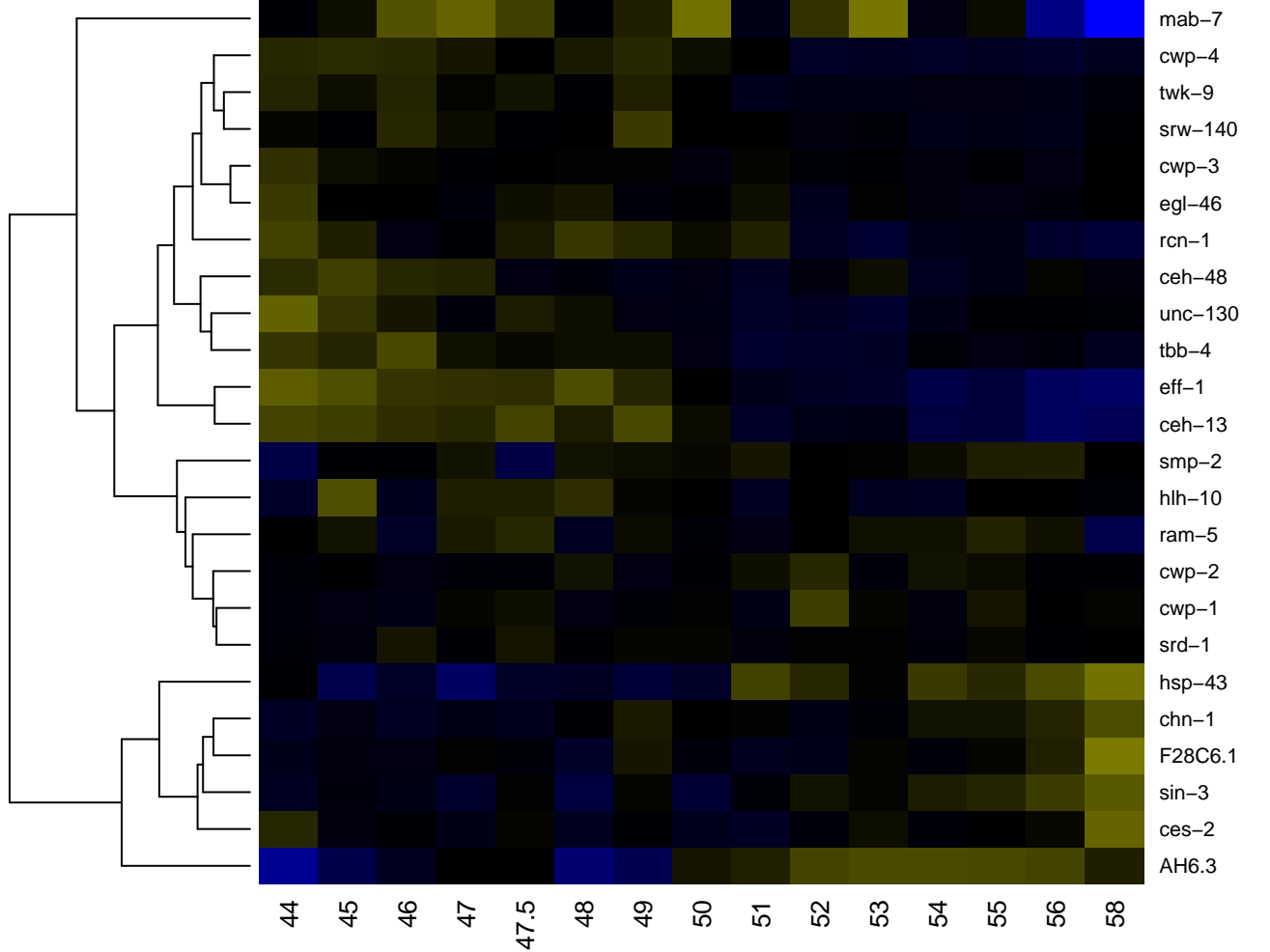
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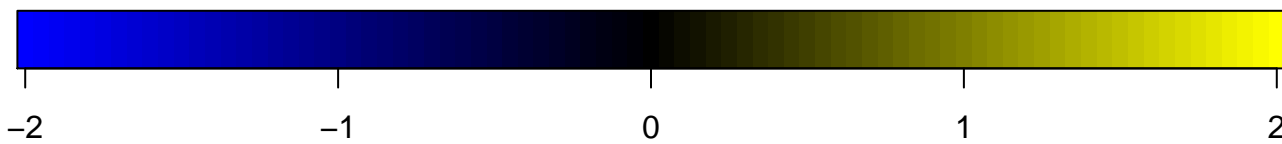
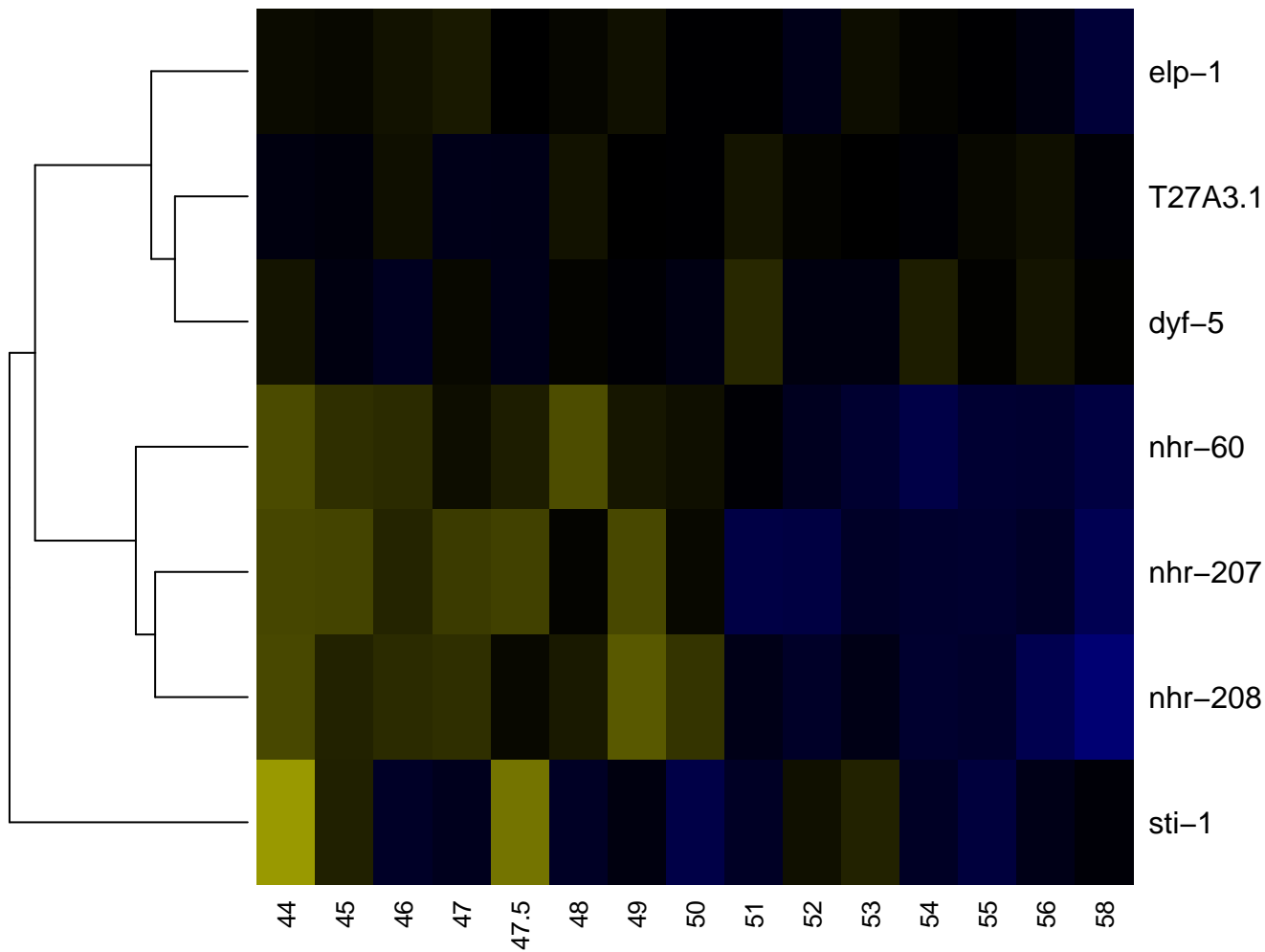
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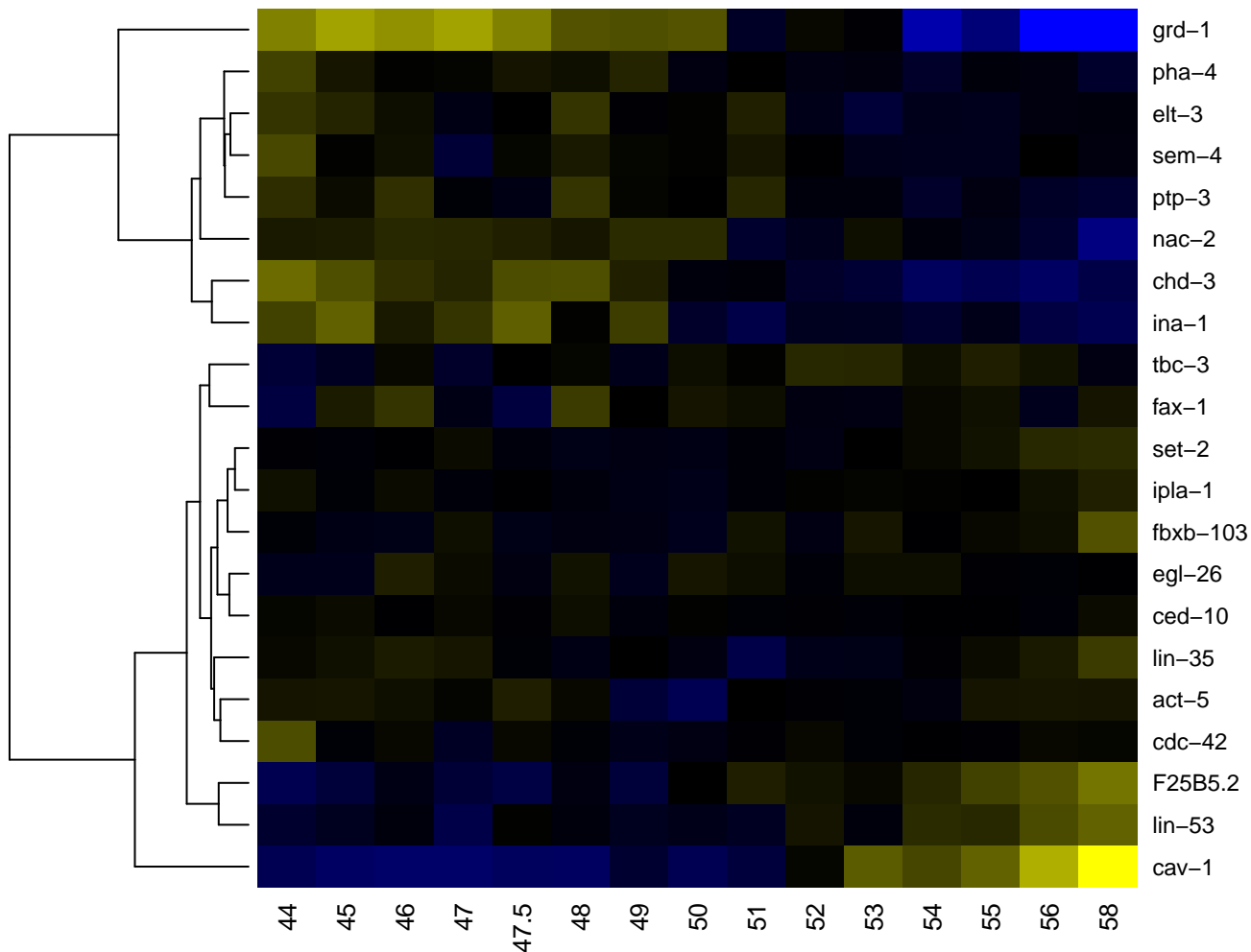
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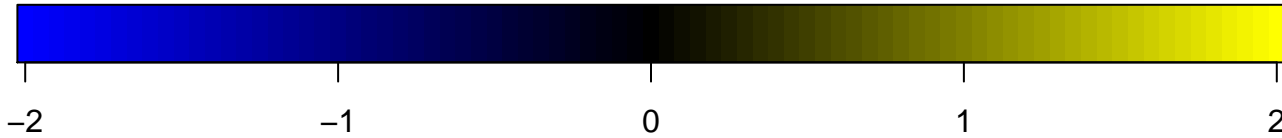
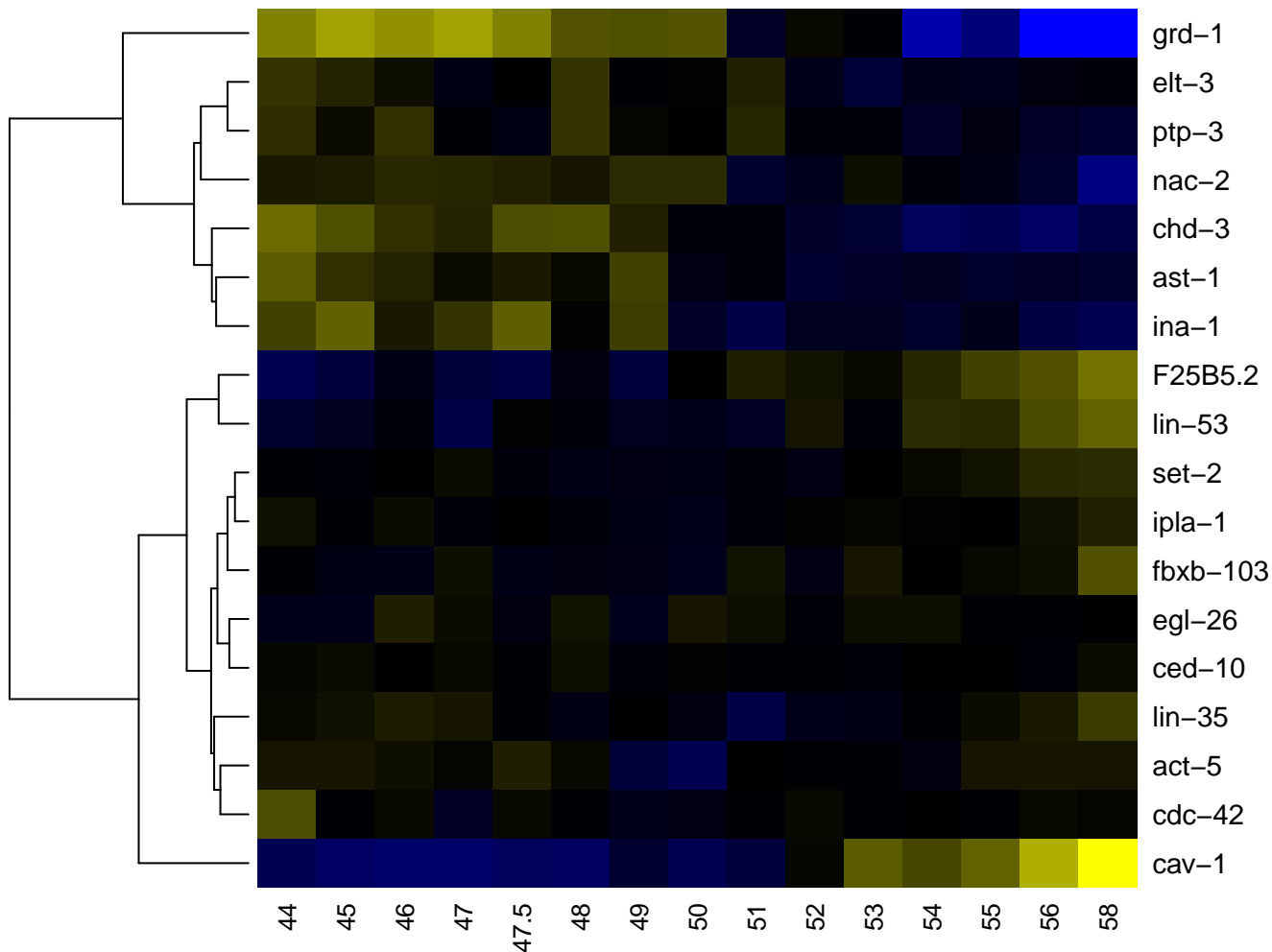
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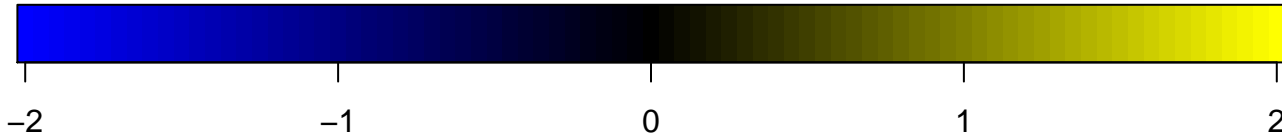
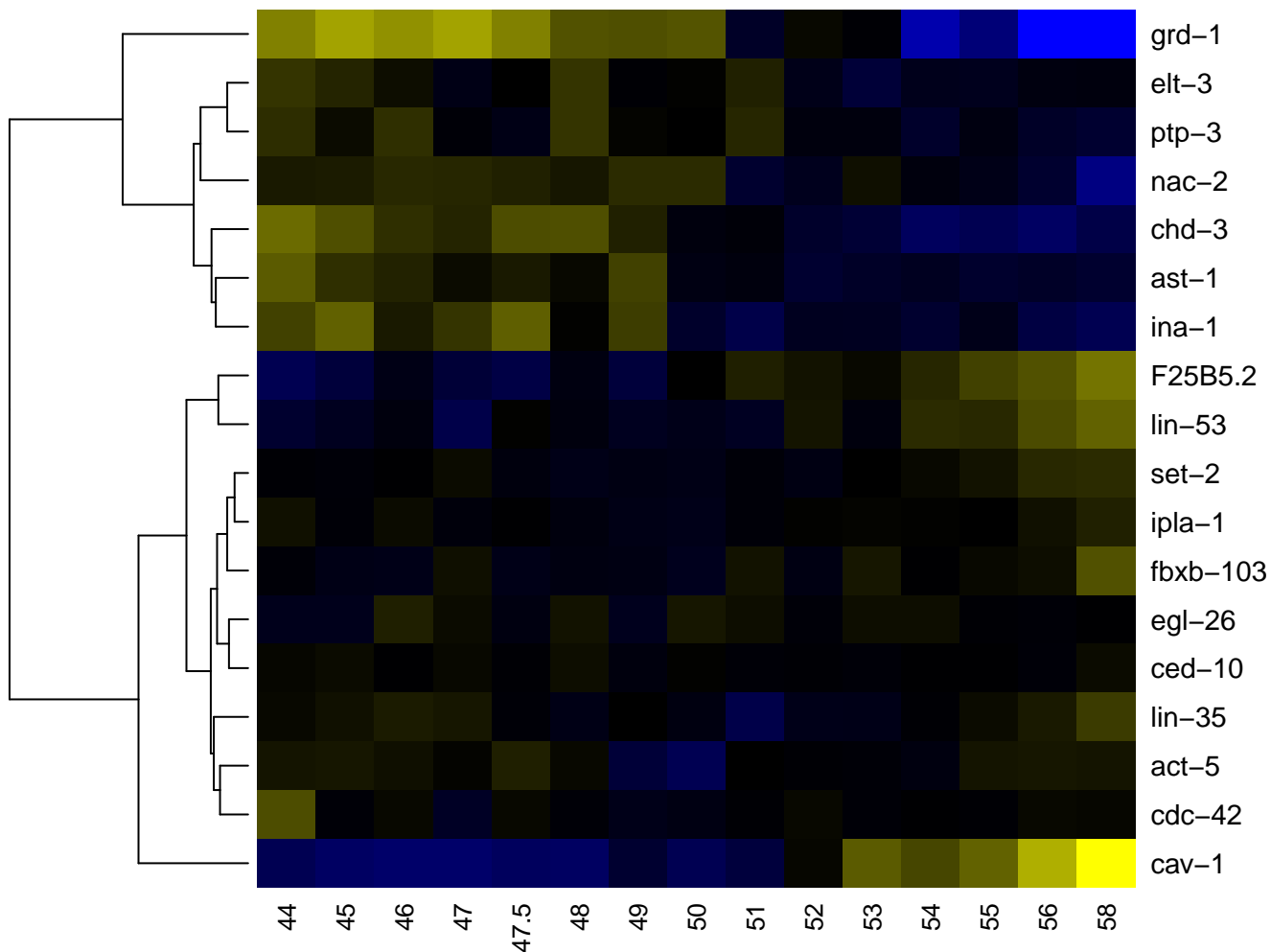
rect_D



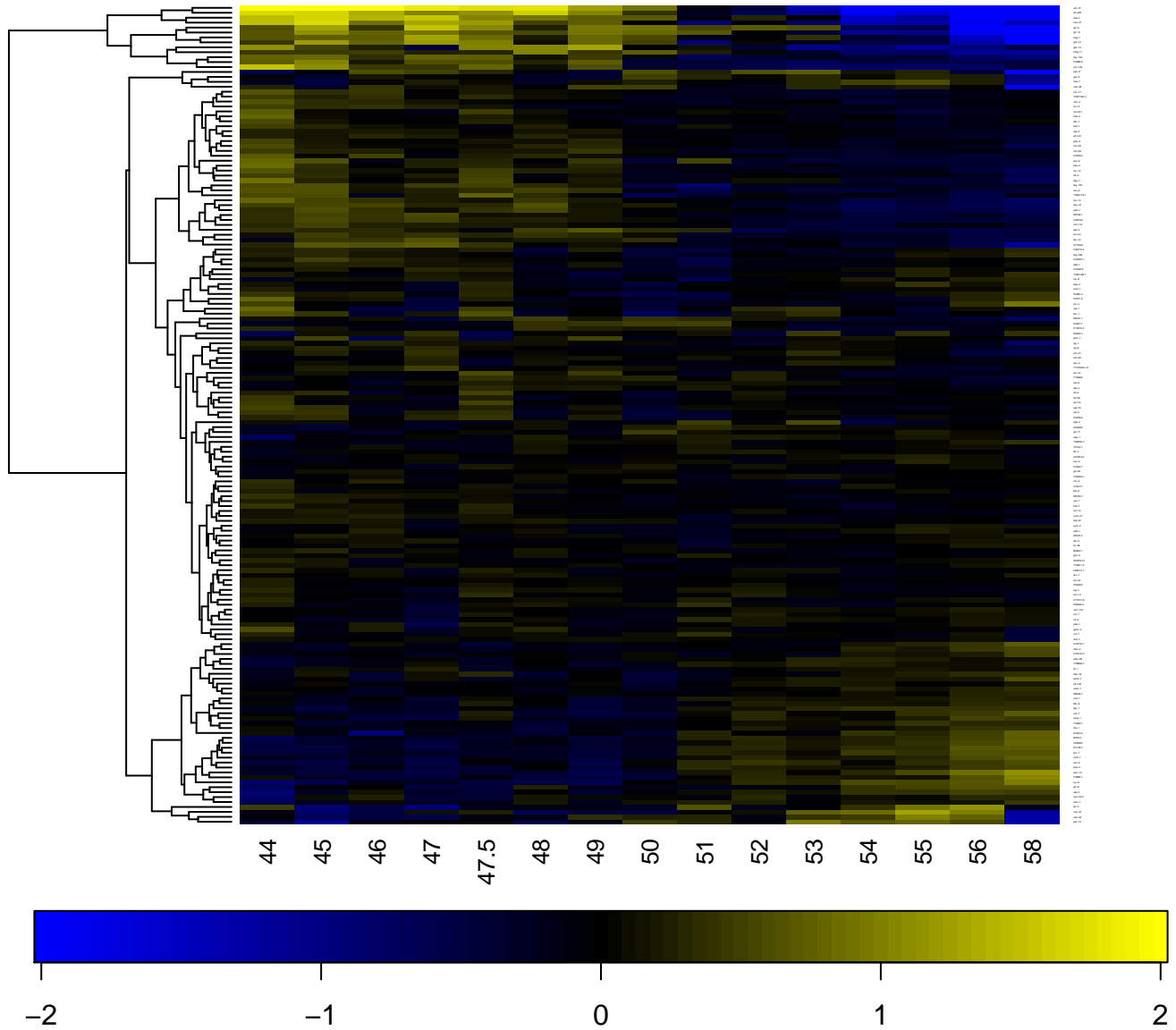
rect_VL



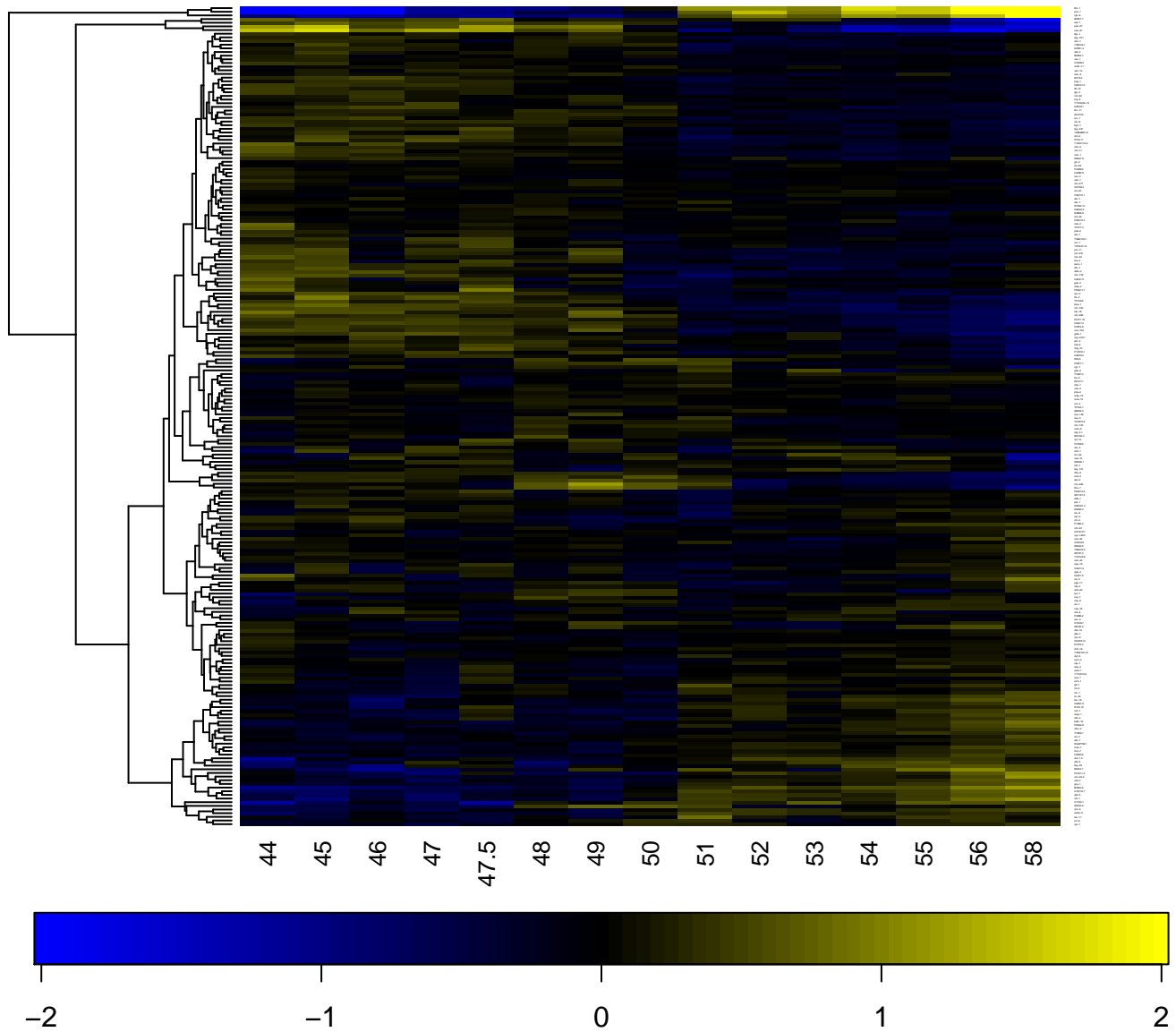
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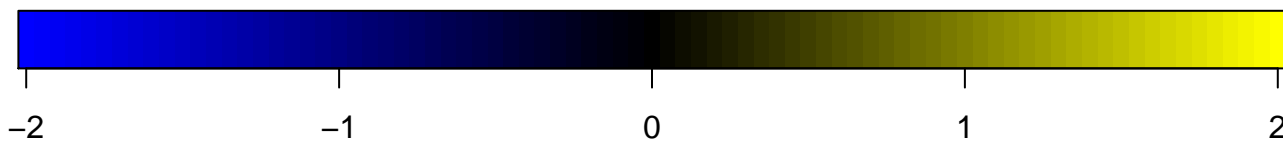
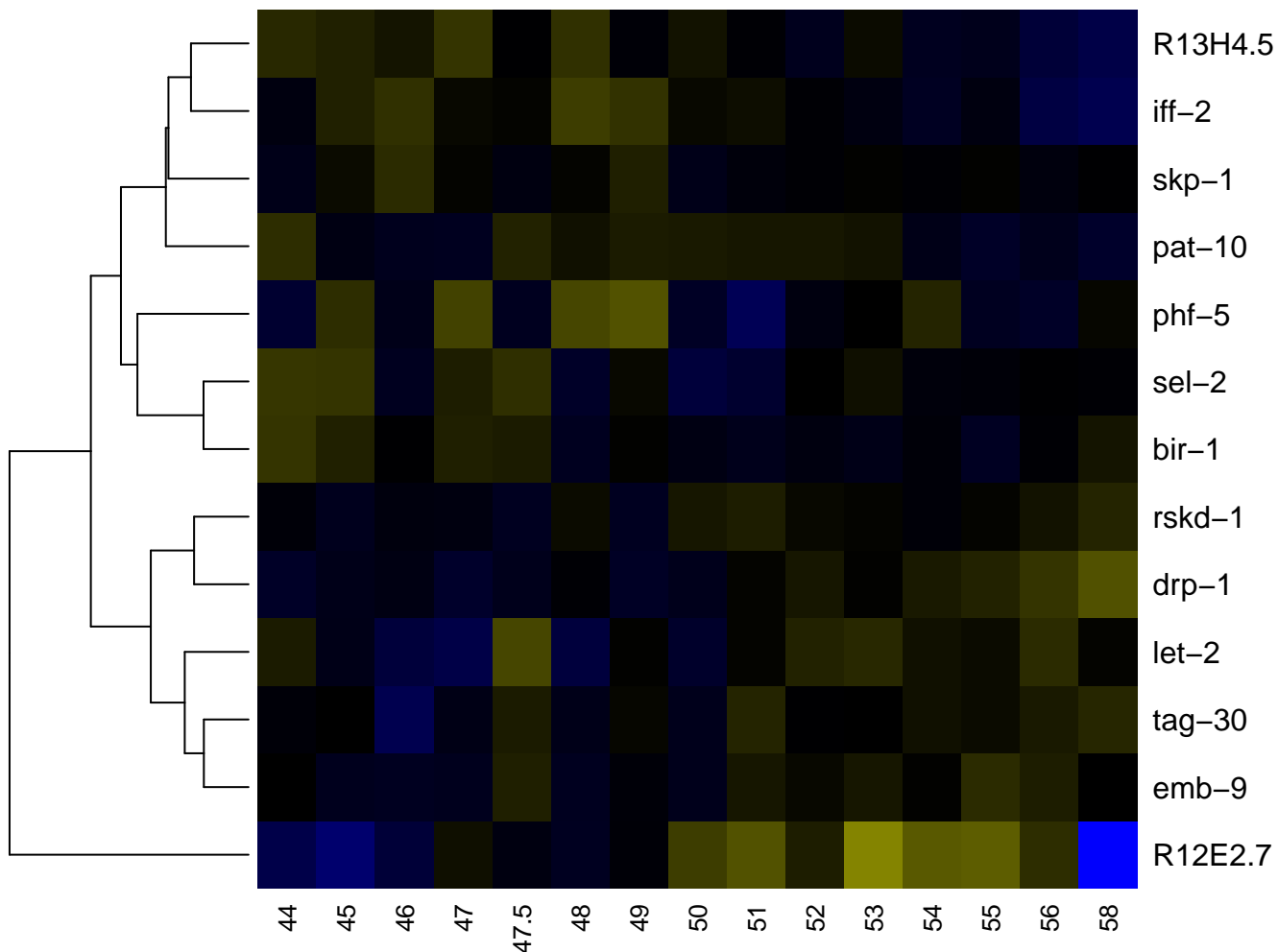
rectal epithelium



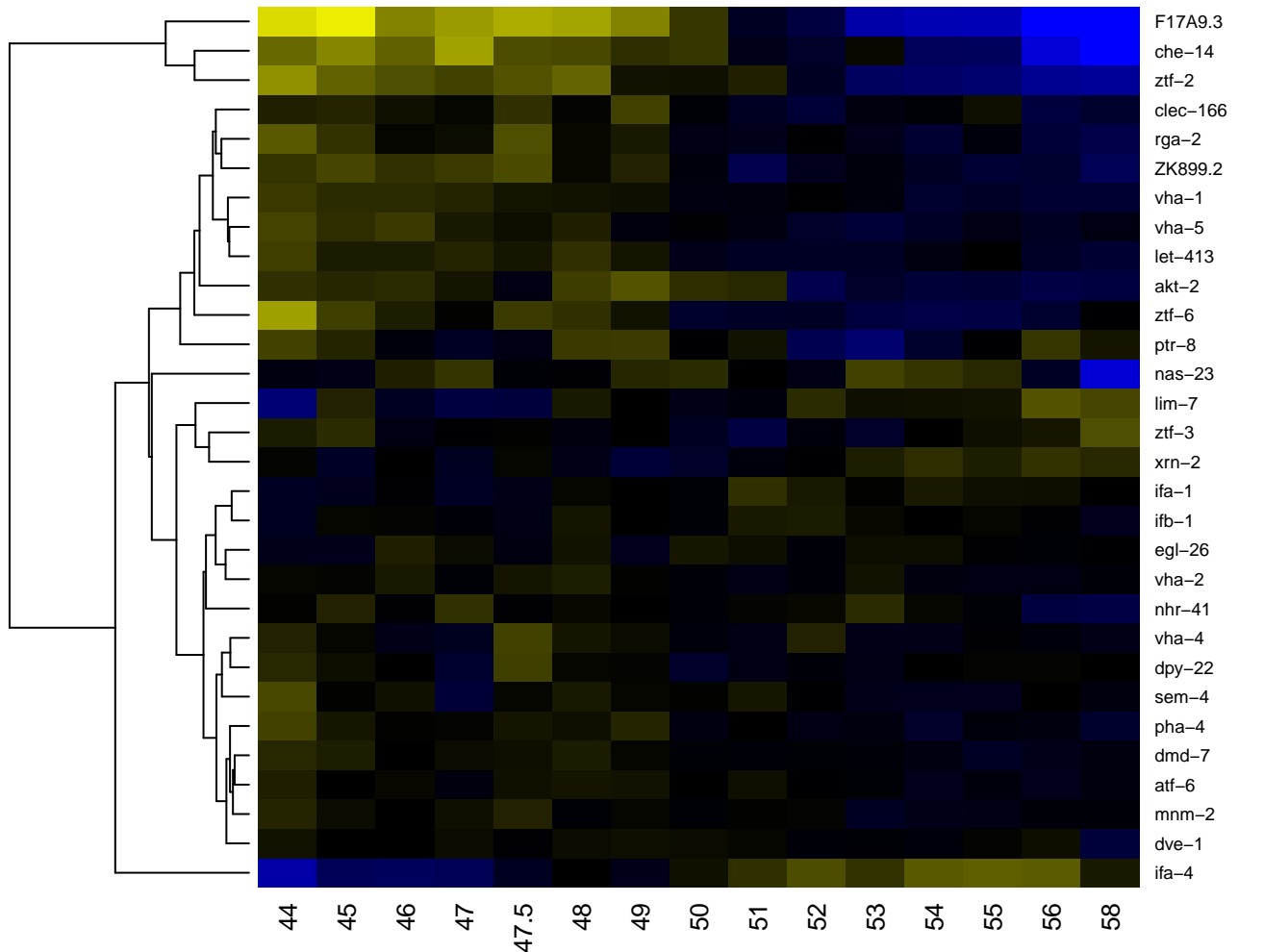
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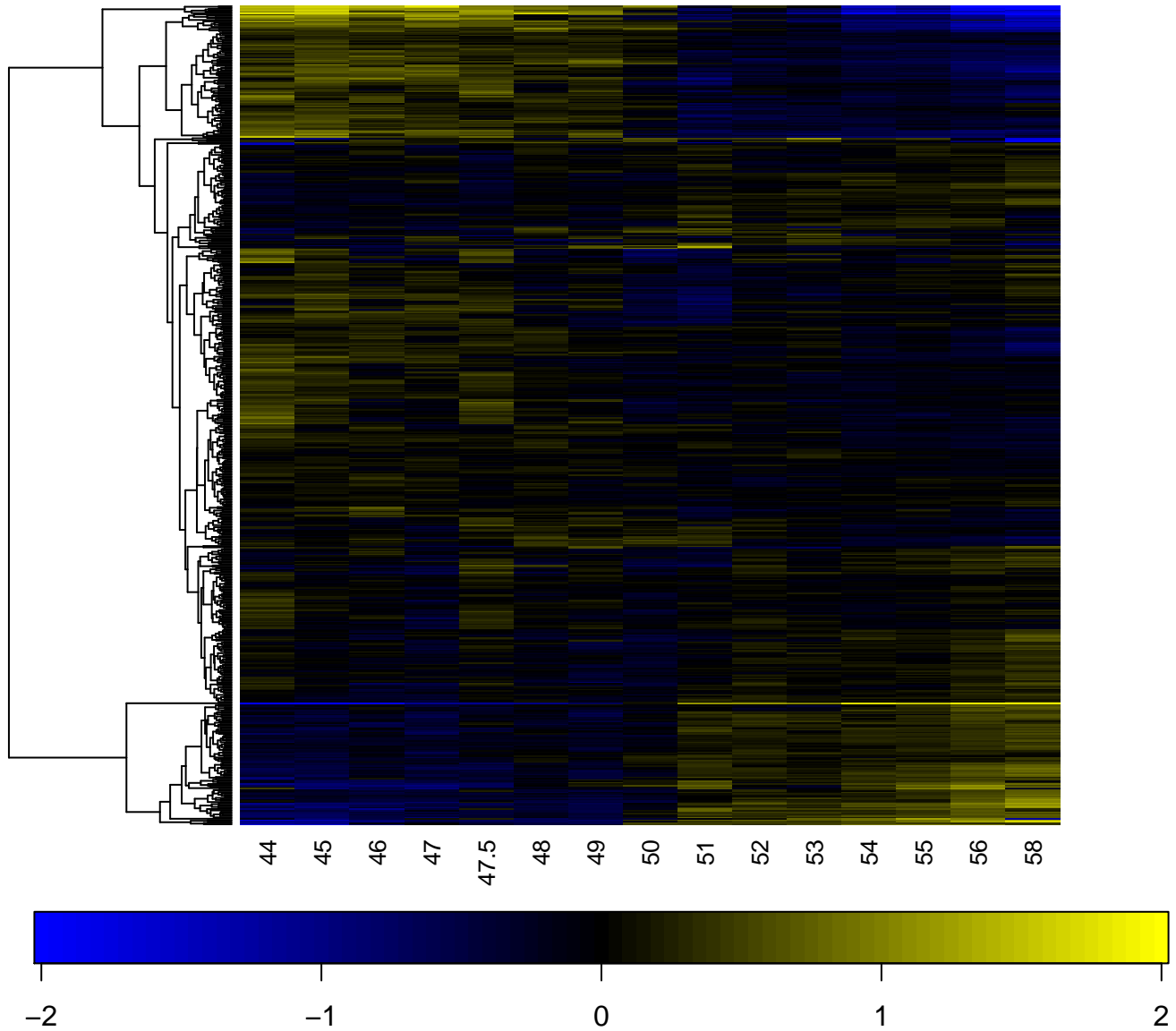
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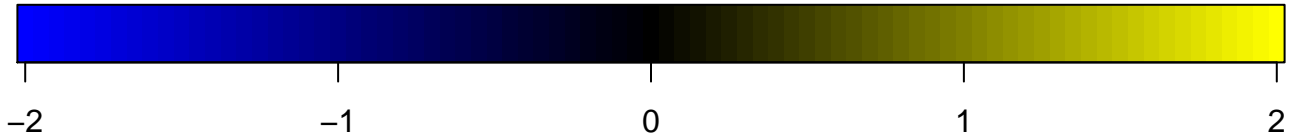
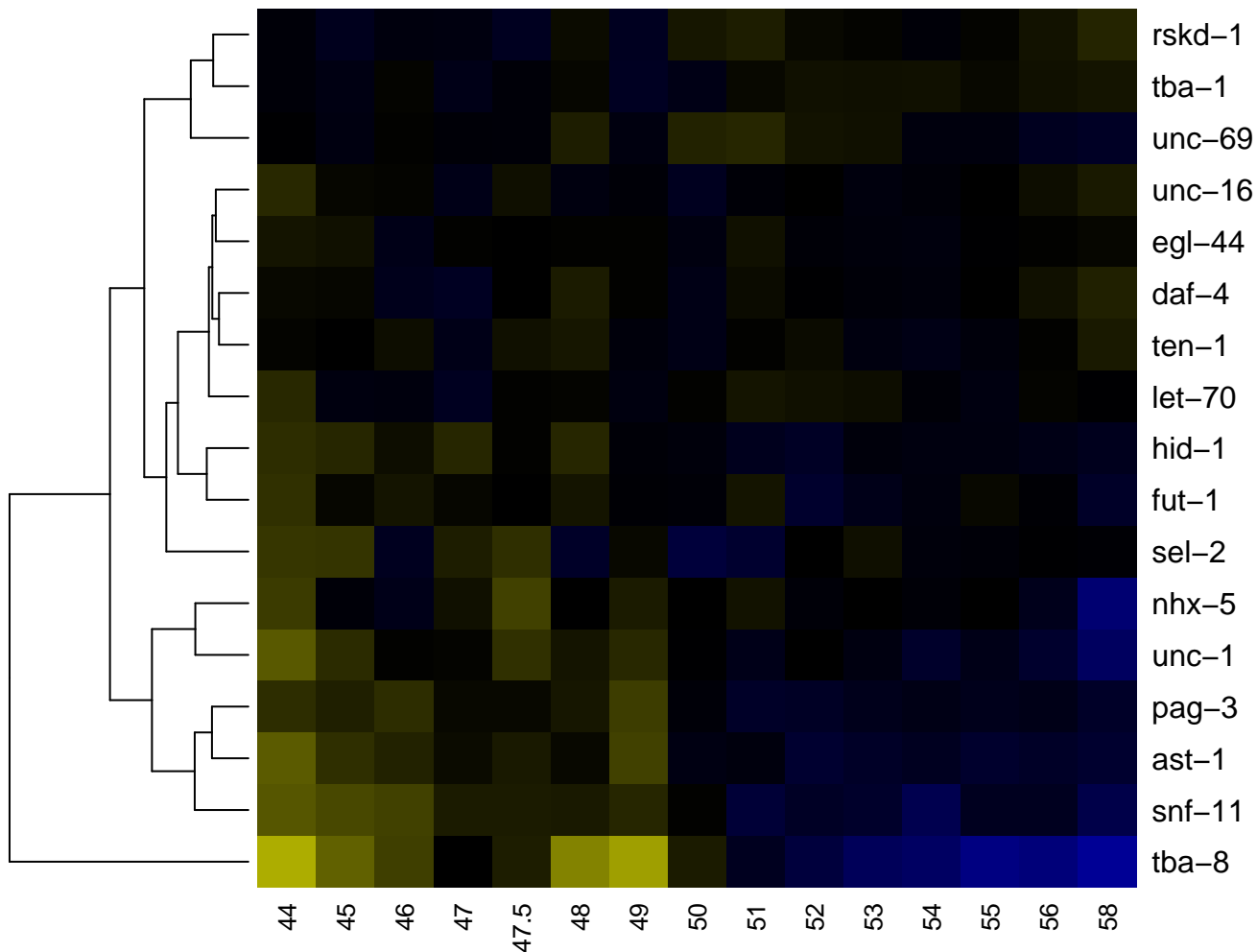
rectum



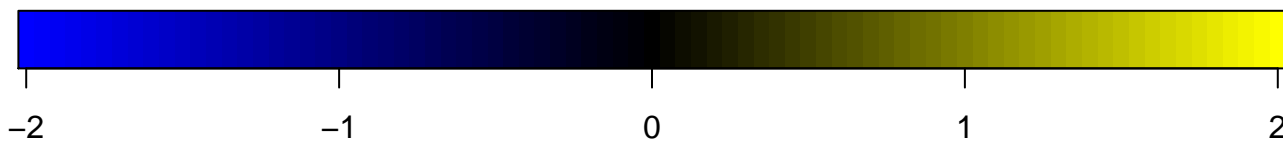
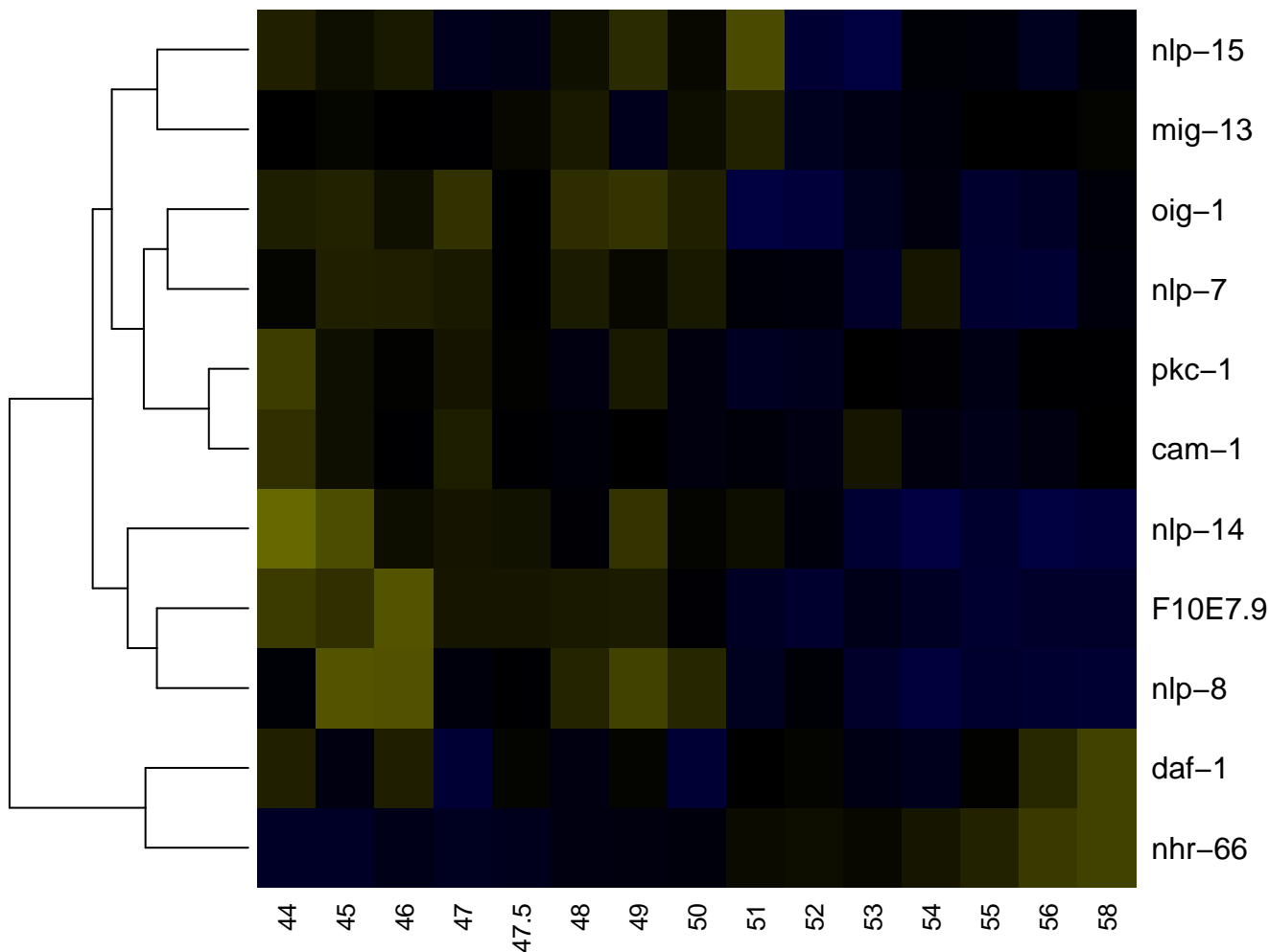
reproductive system



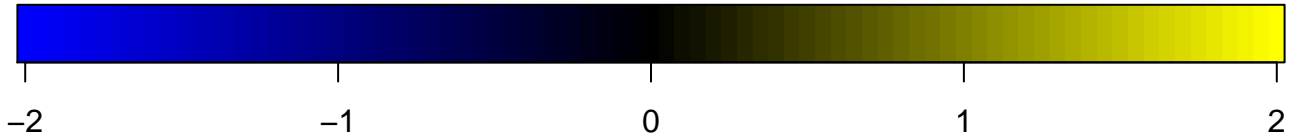
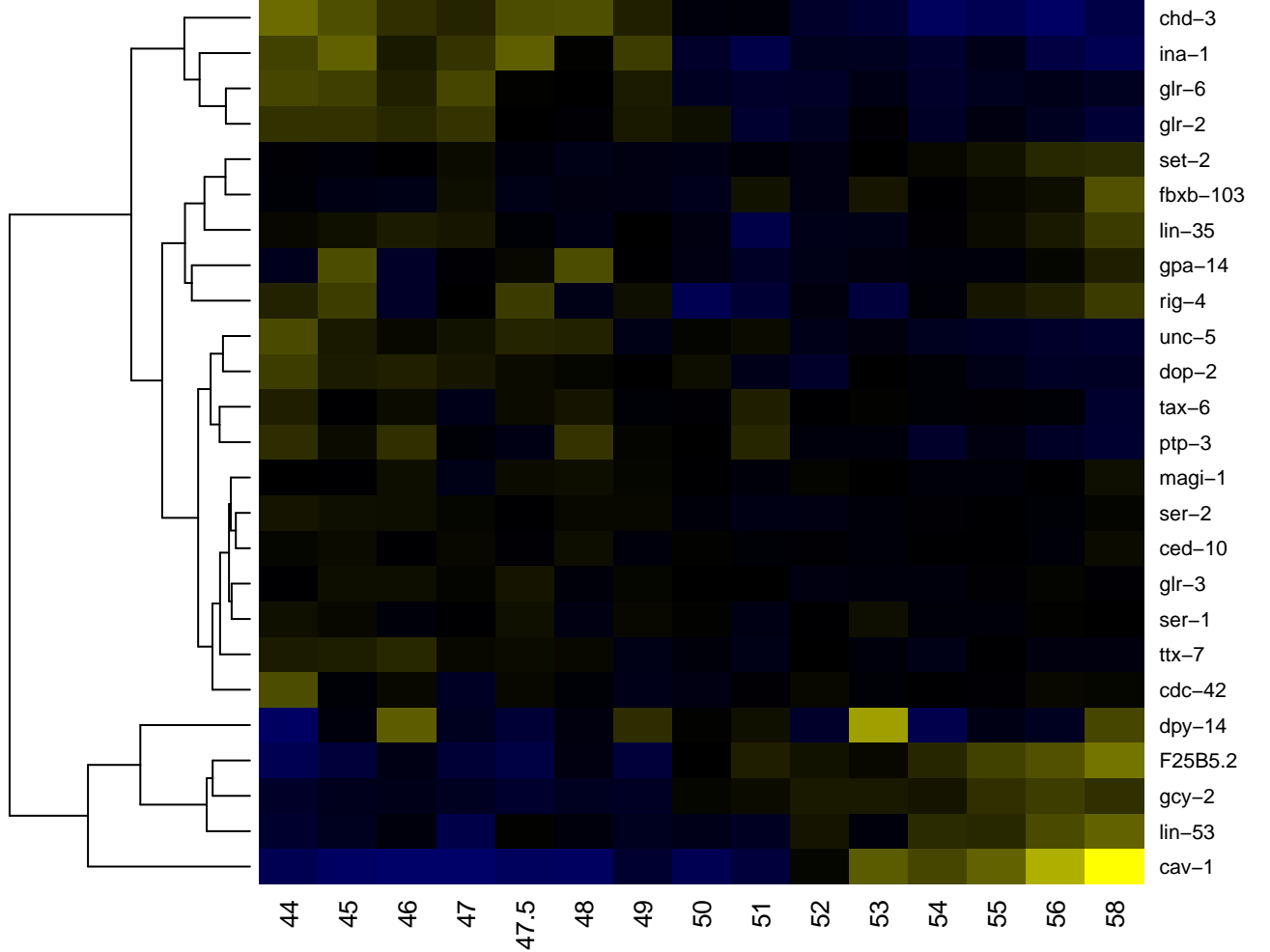
retrovesicular ganglion



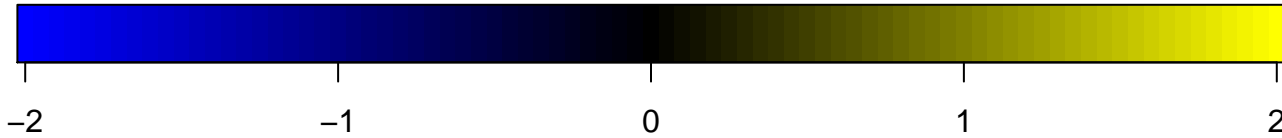
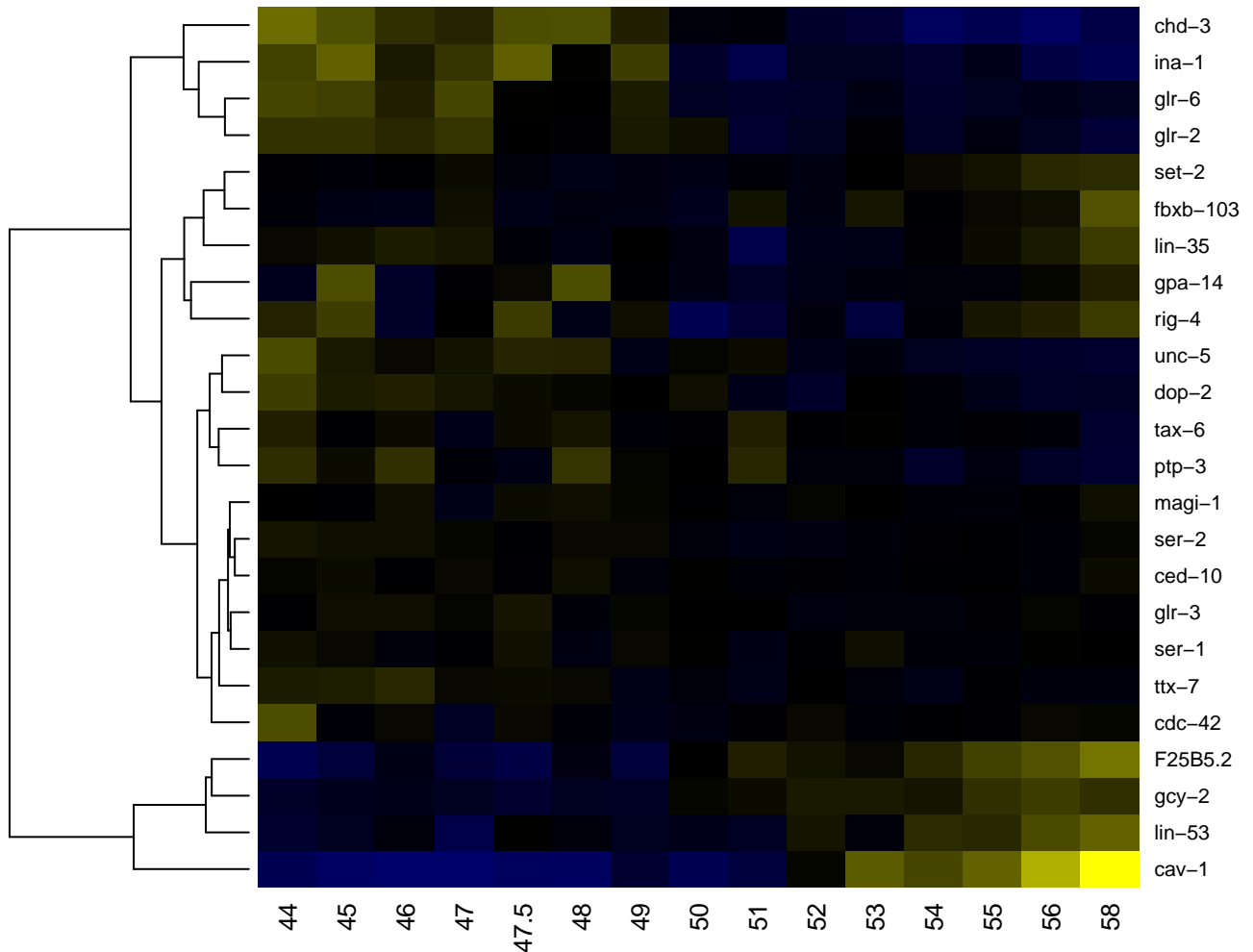
retrovesicular ganglion neuron



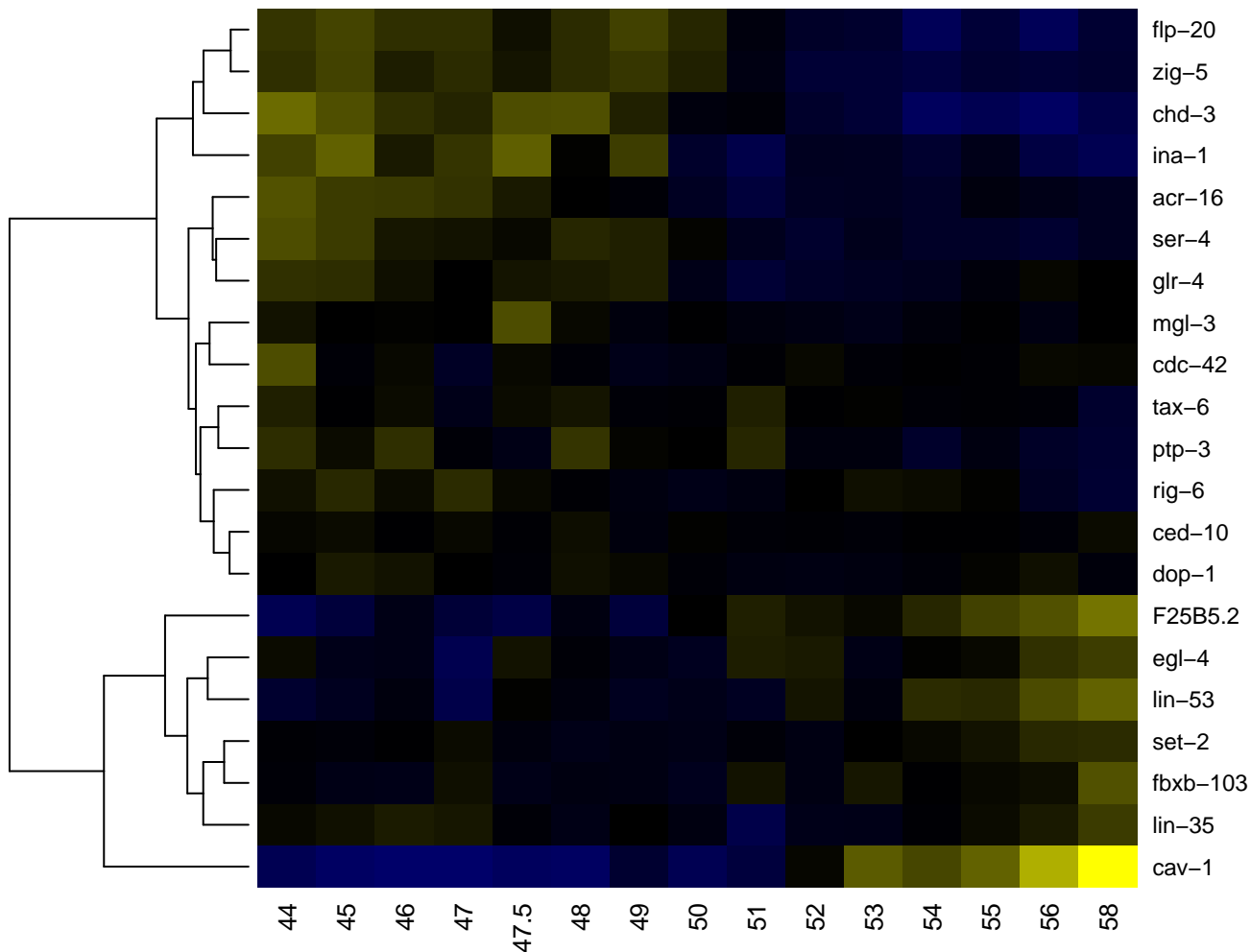
RIAL



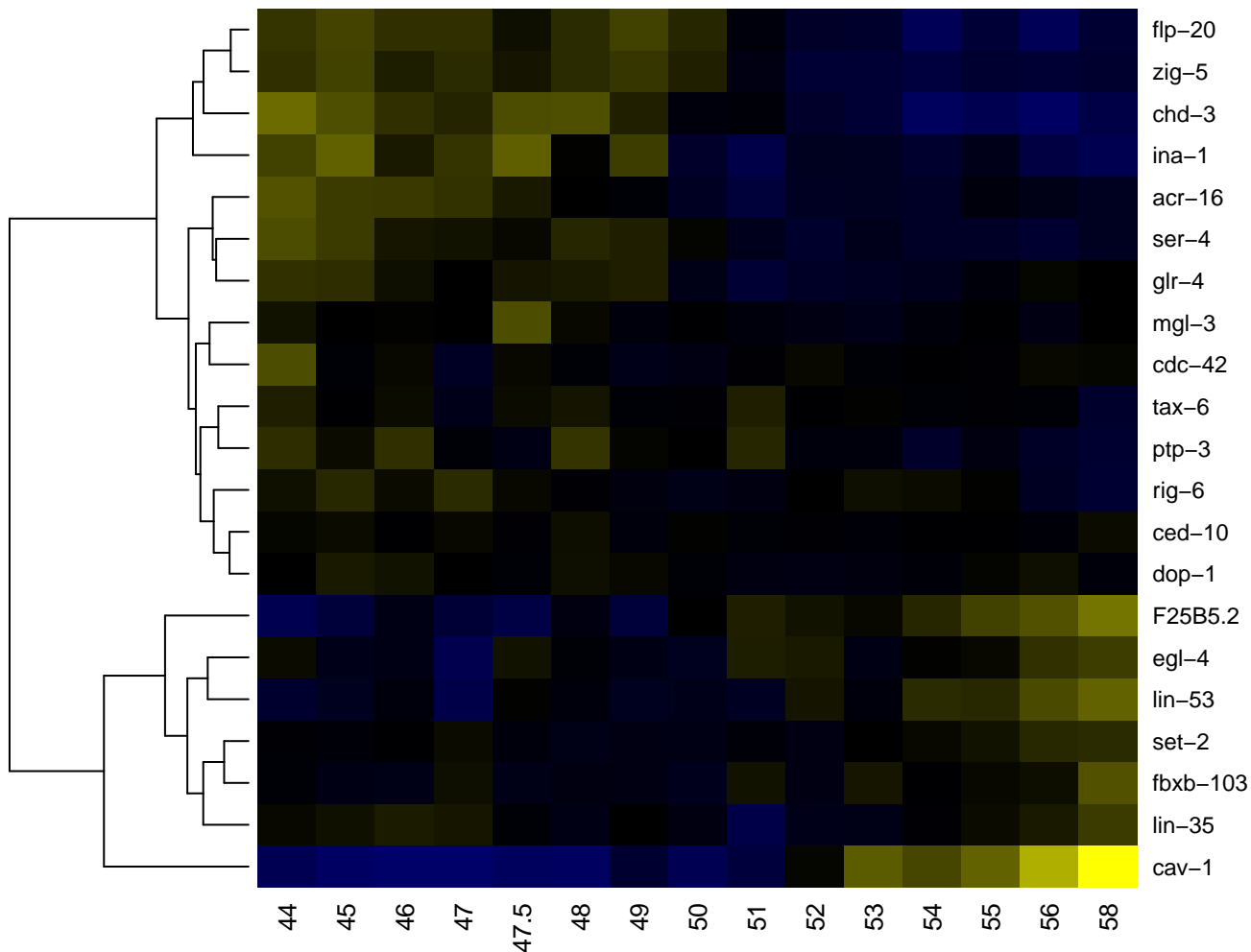
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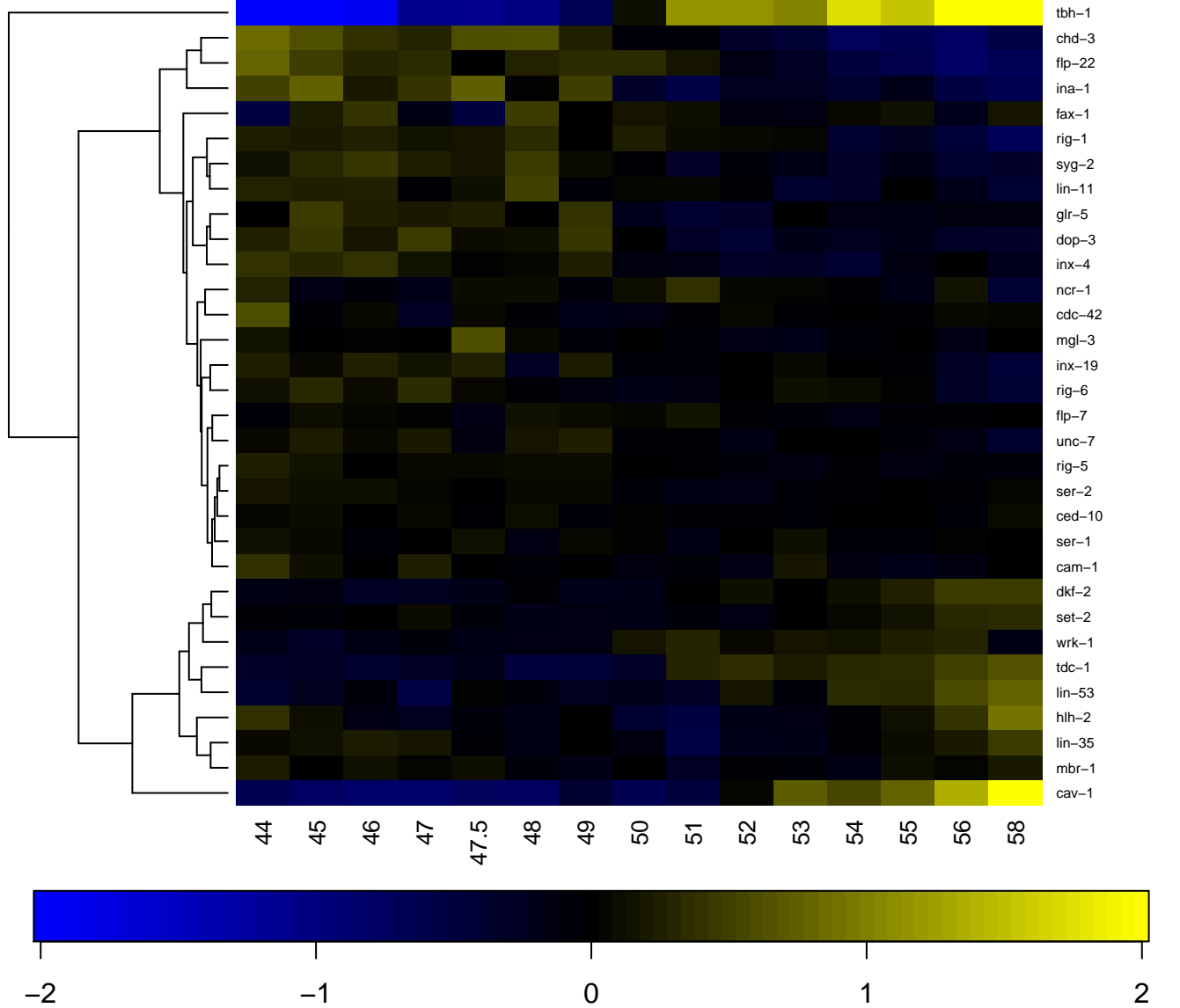
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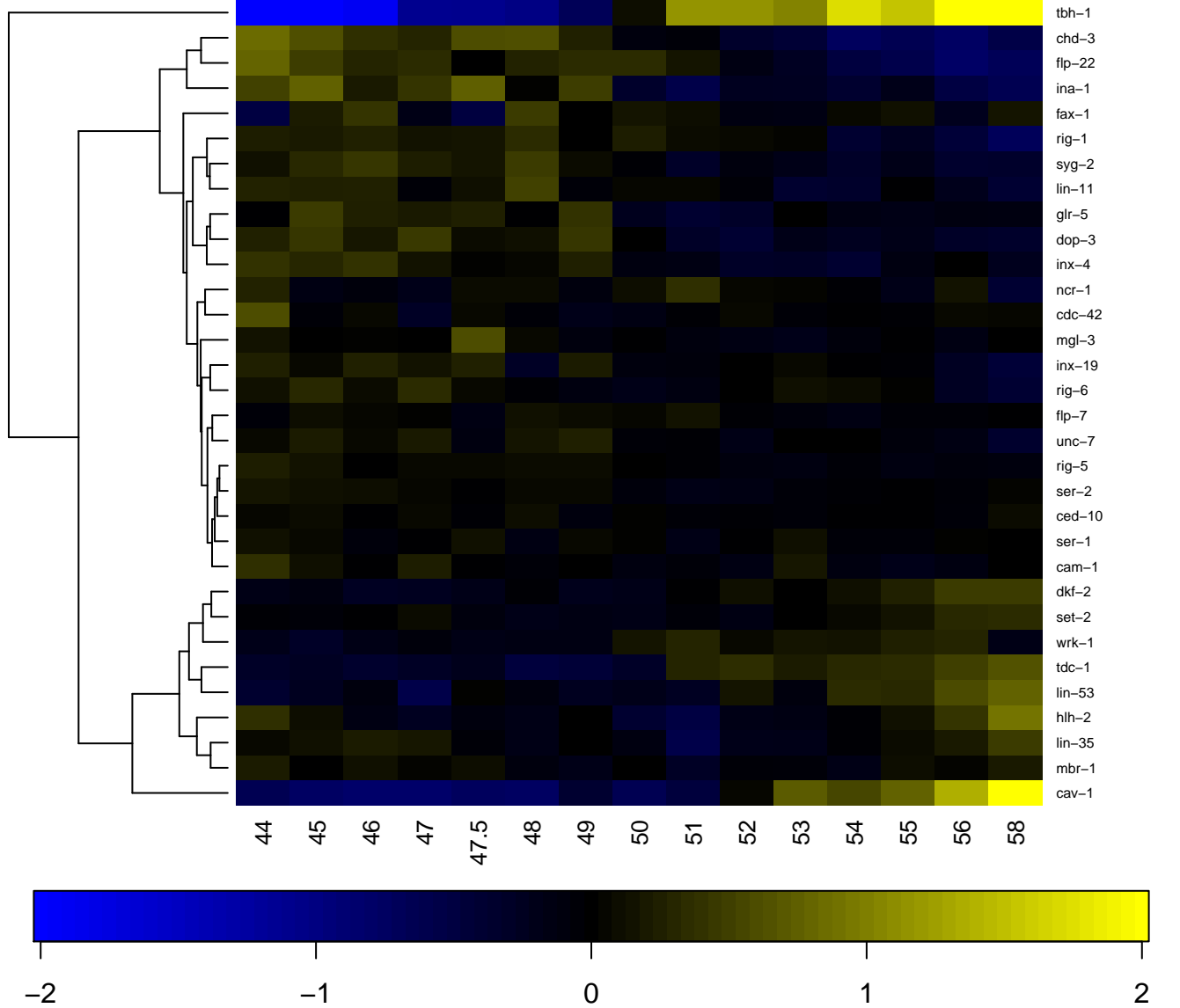
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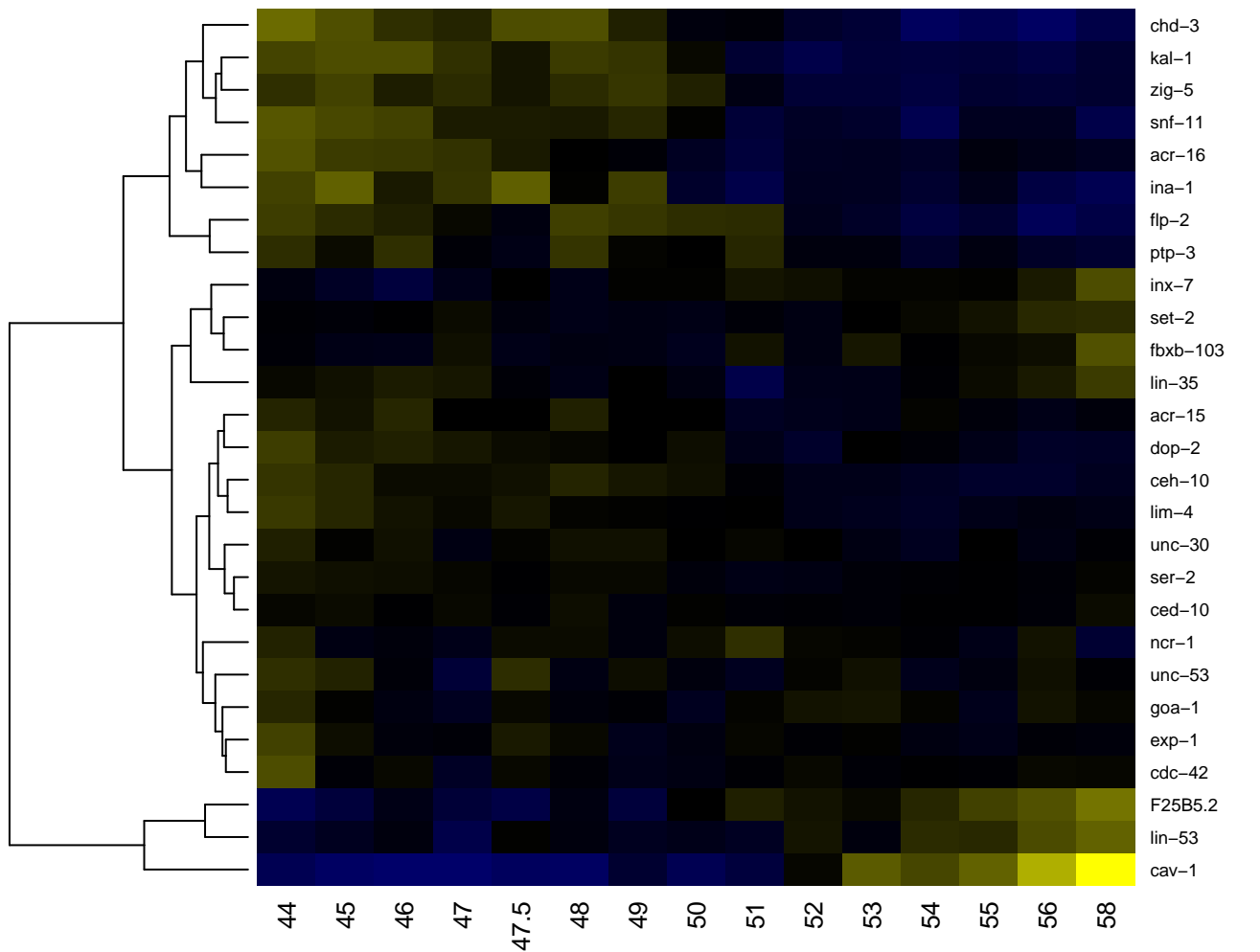
RICL



RICR



RID



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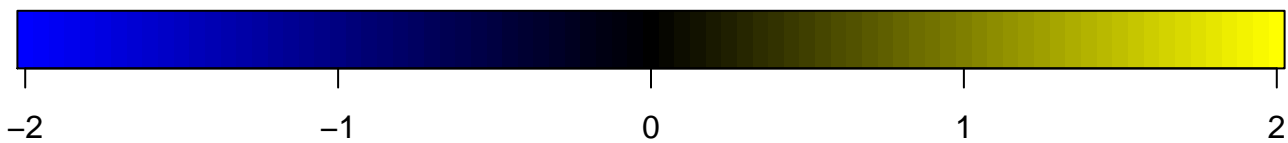
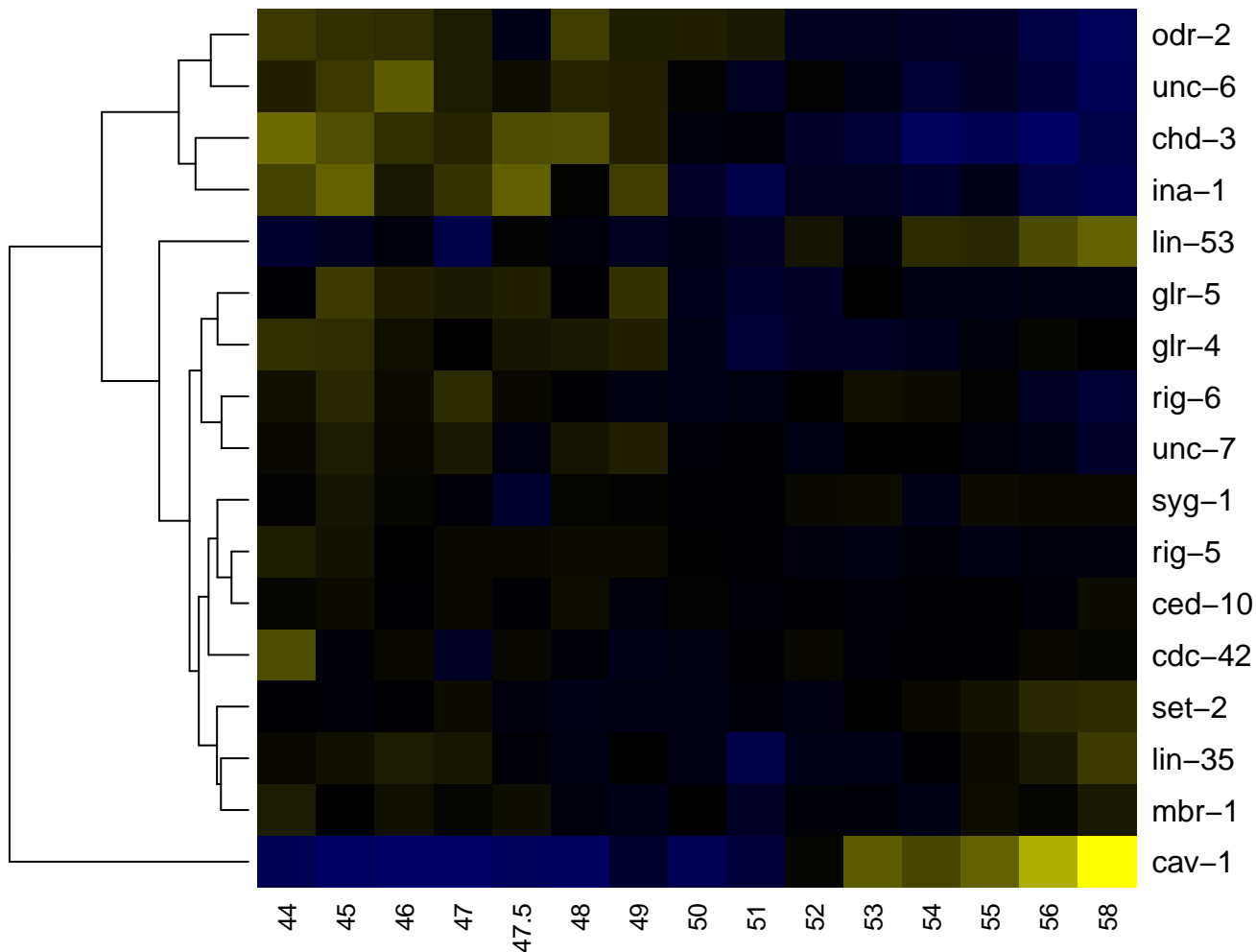
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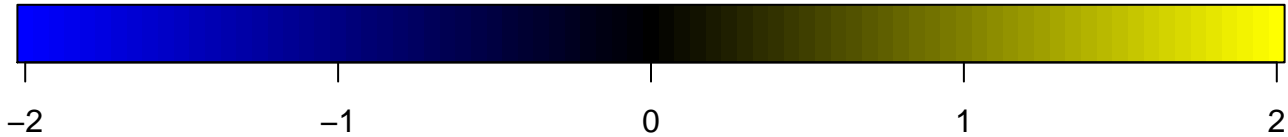
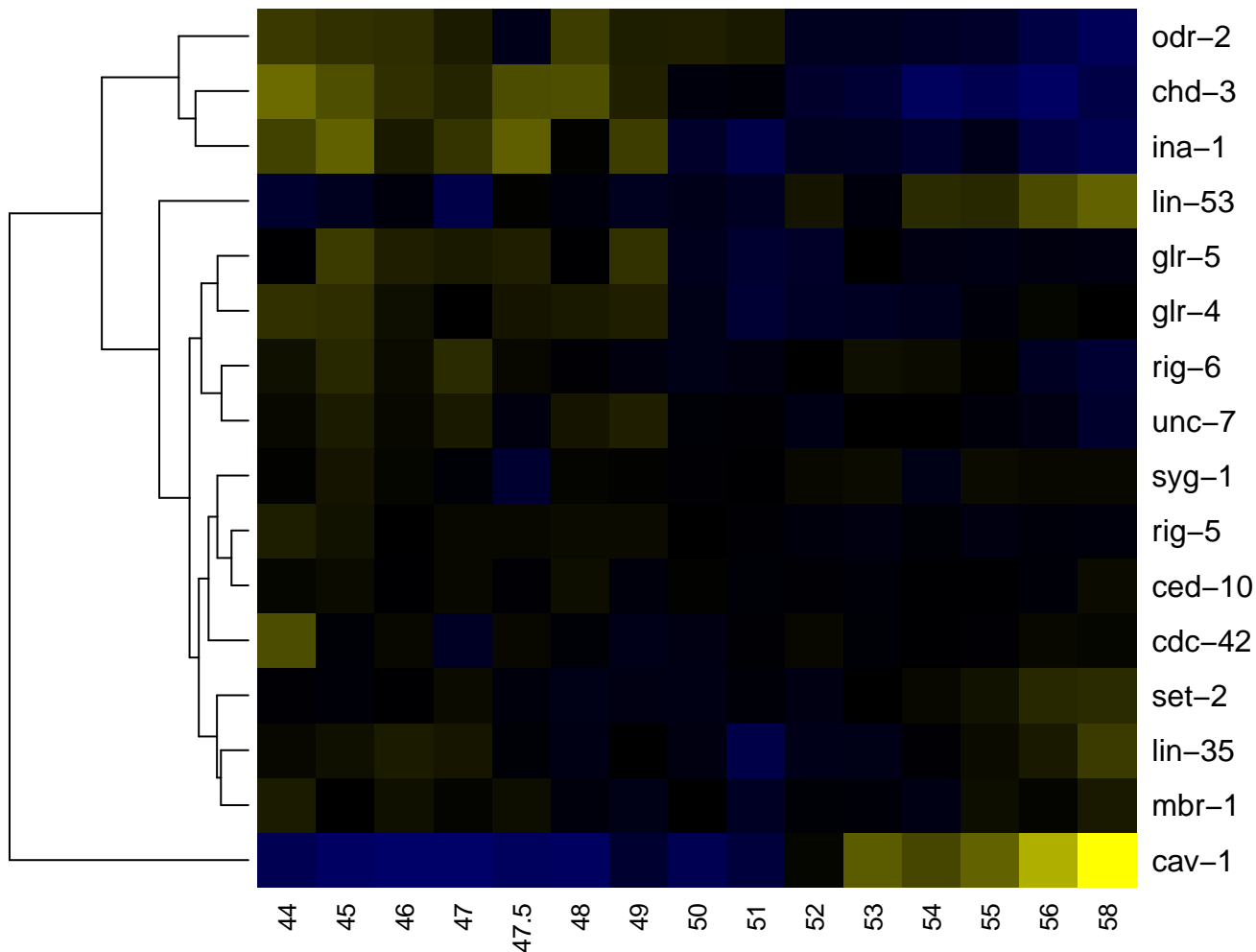
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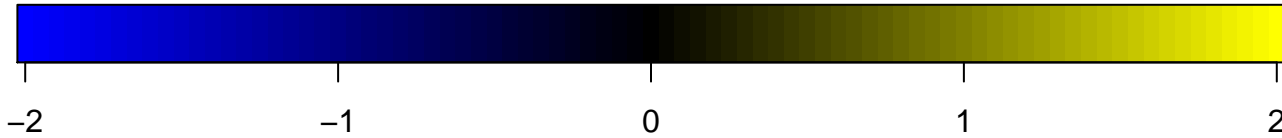
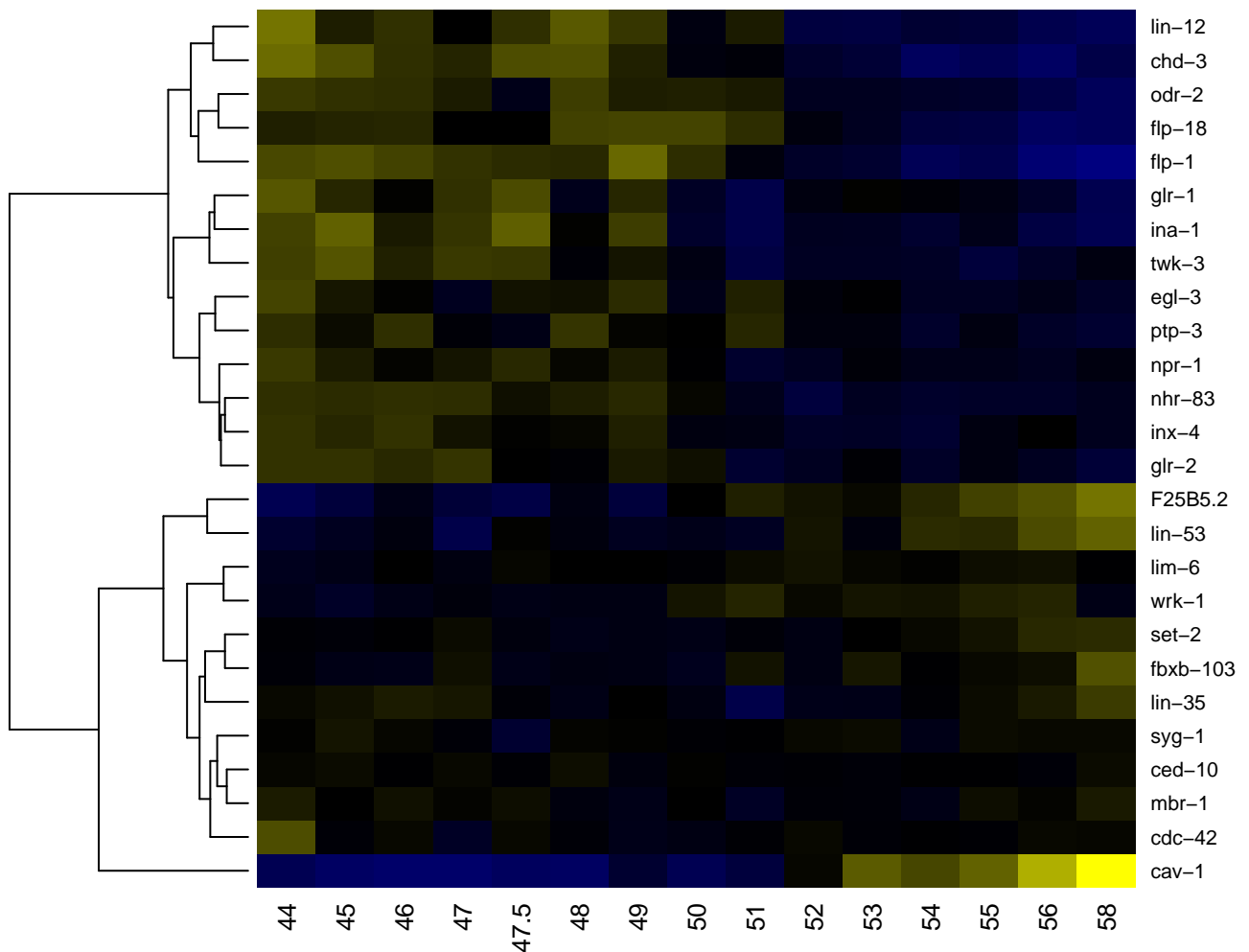
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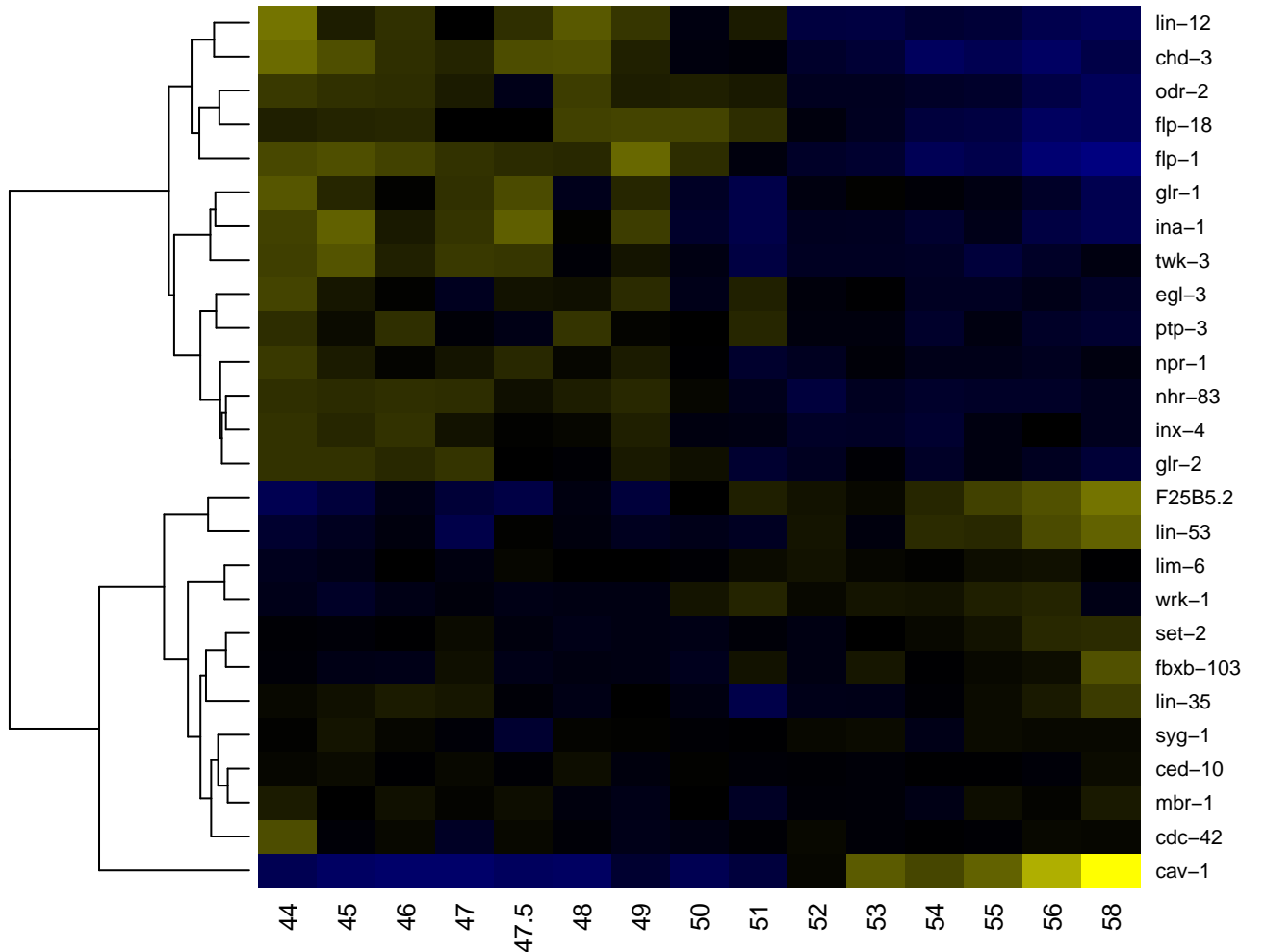
RIFR



RIGL



RIGR



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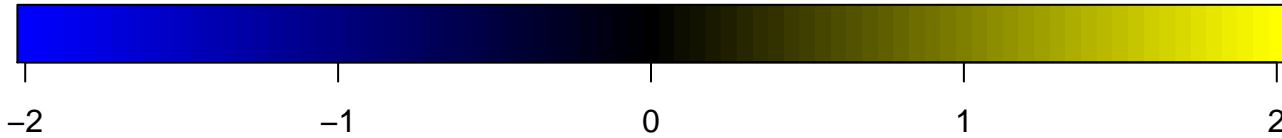
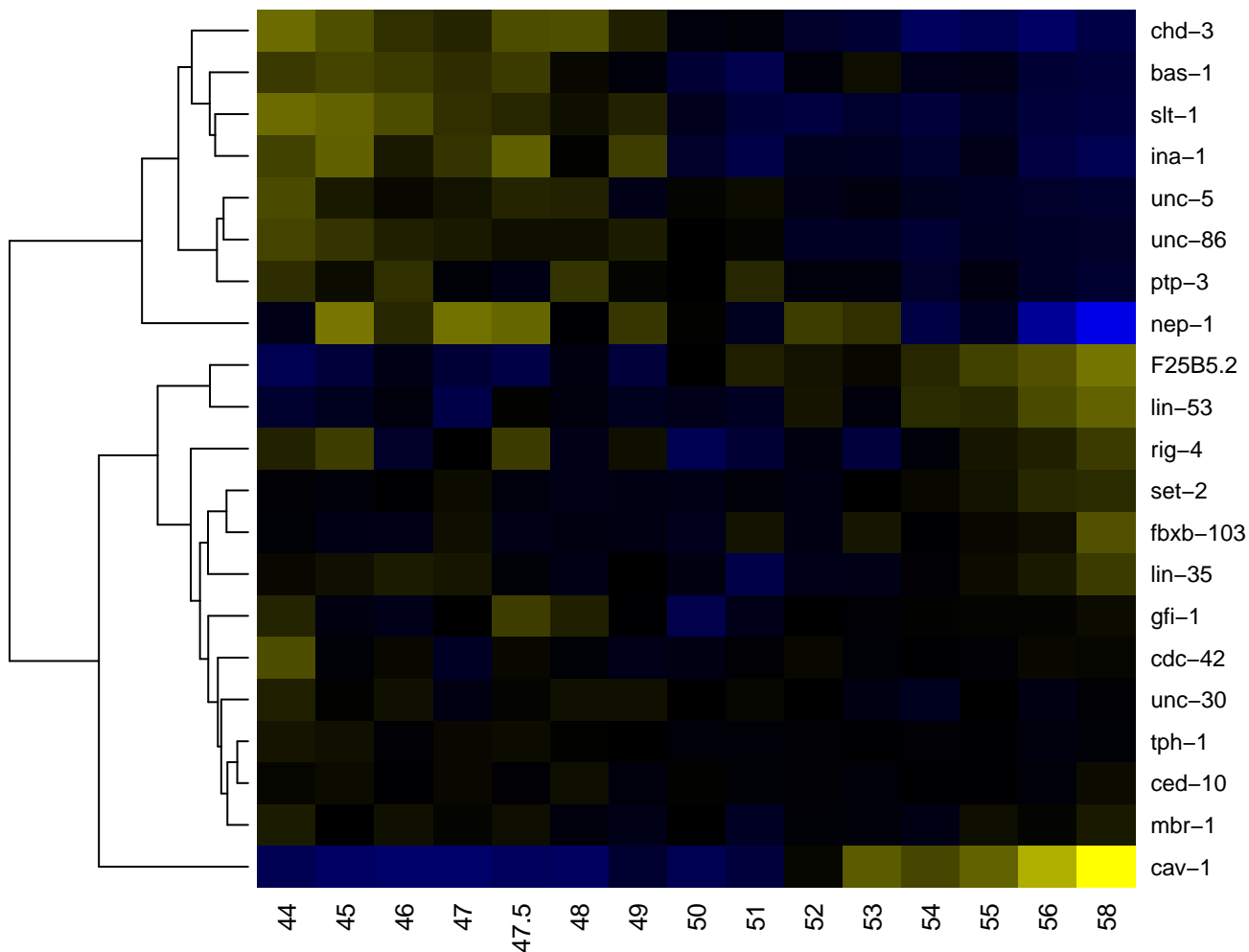
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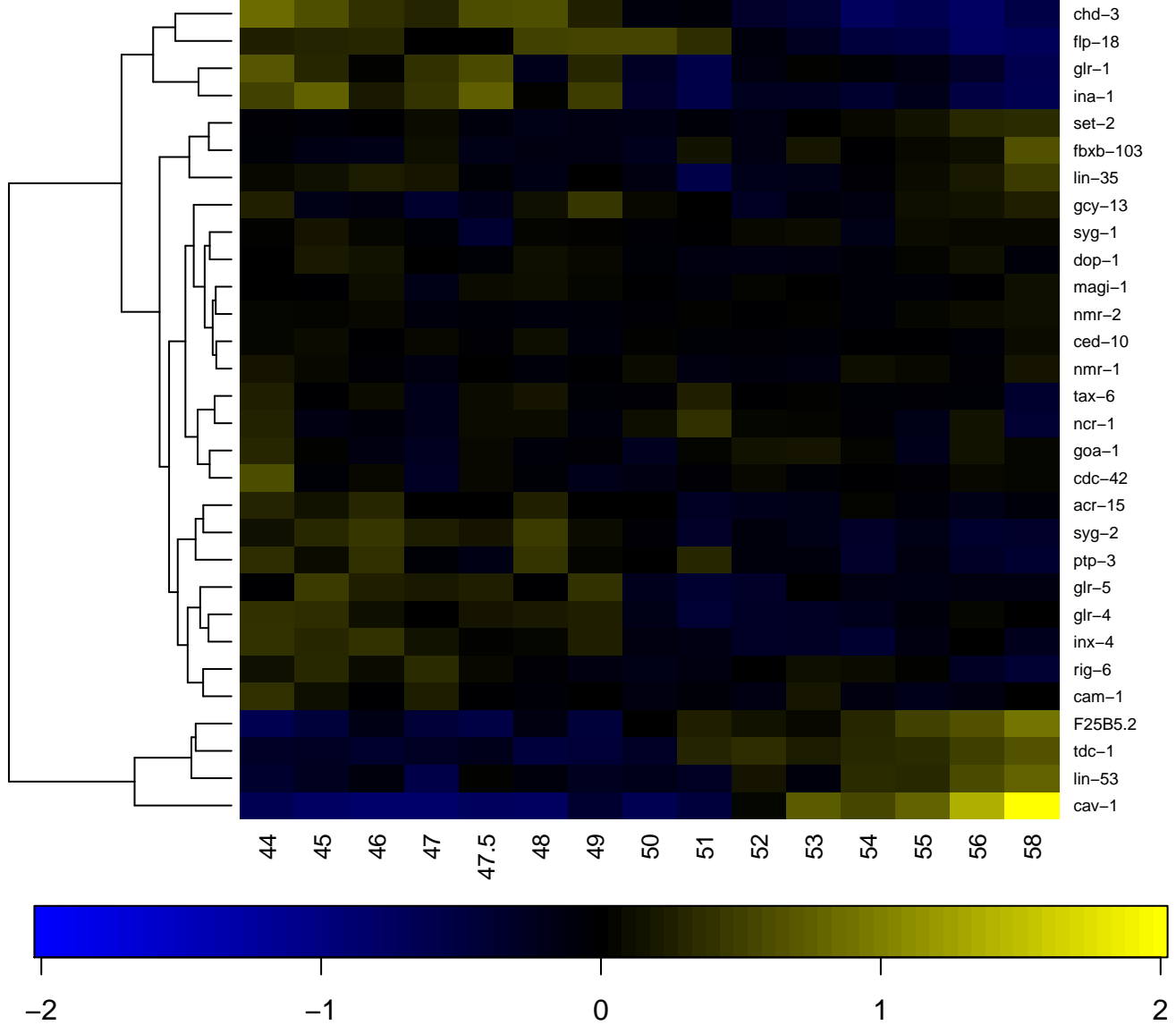
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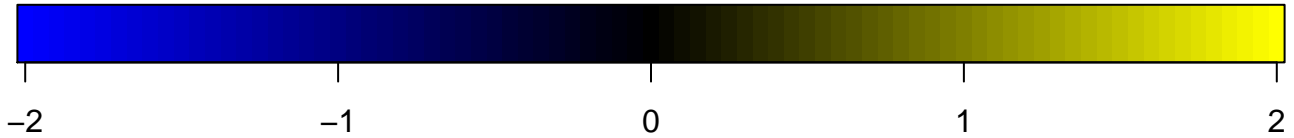
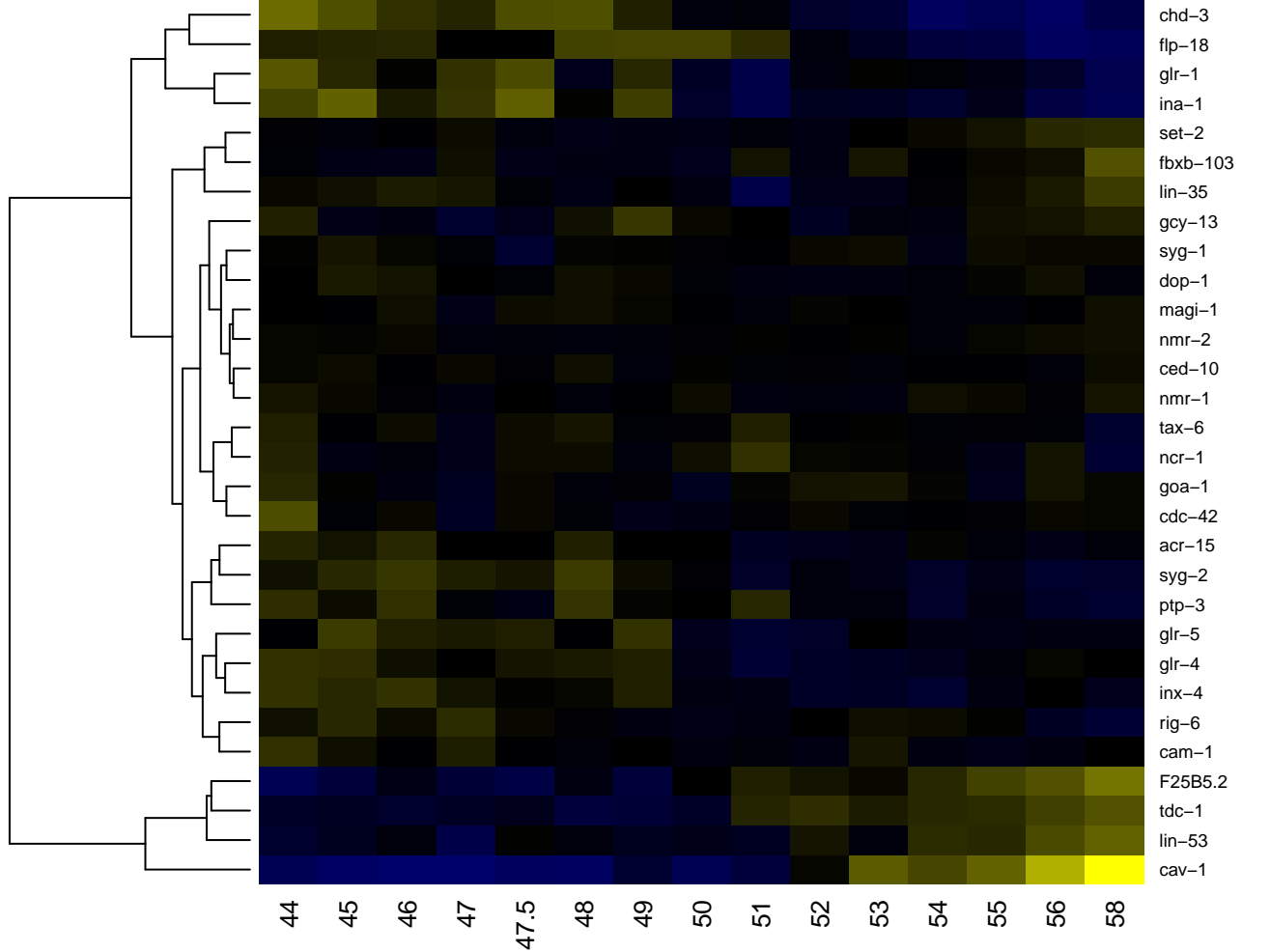
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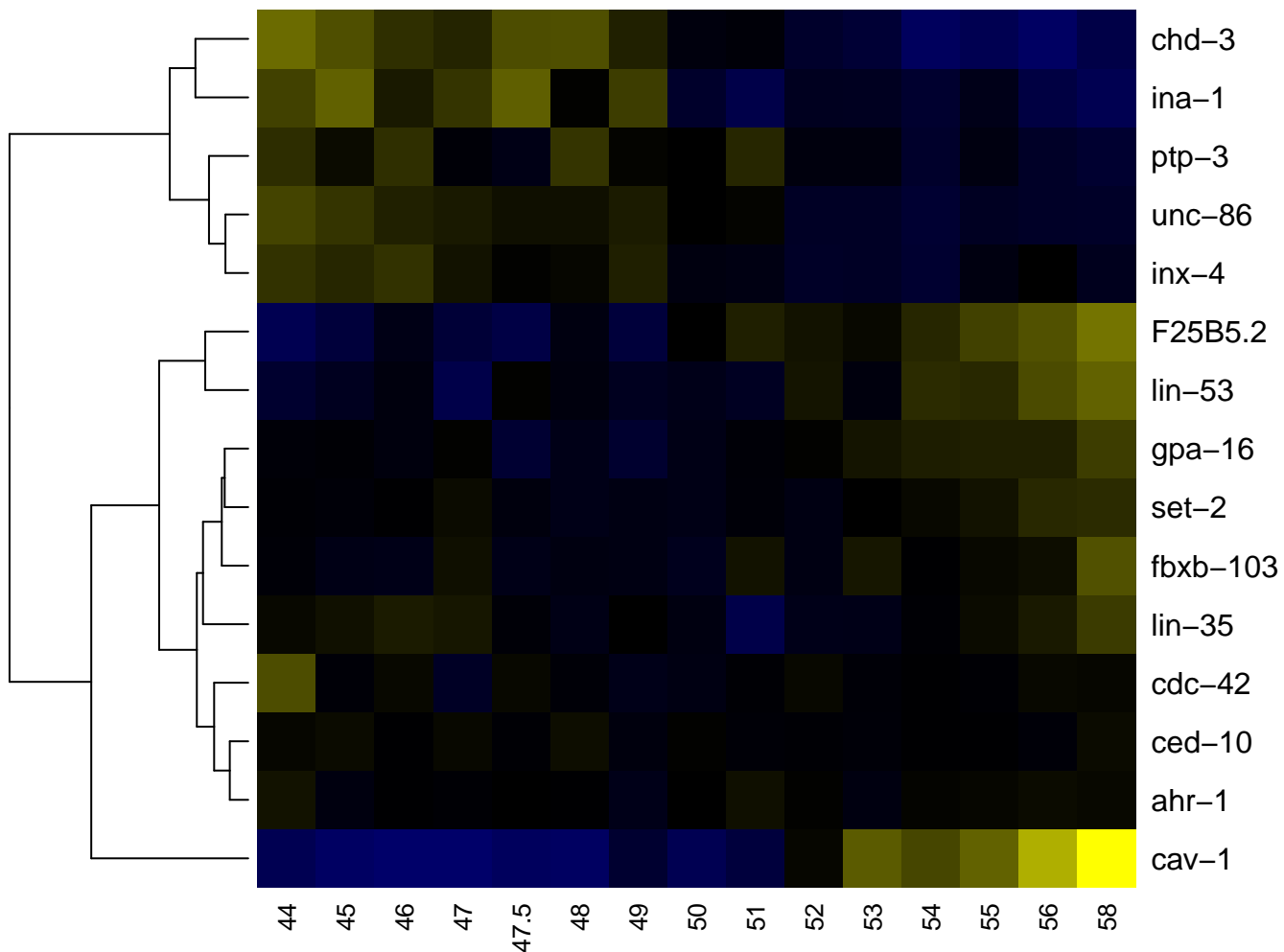
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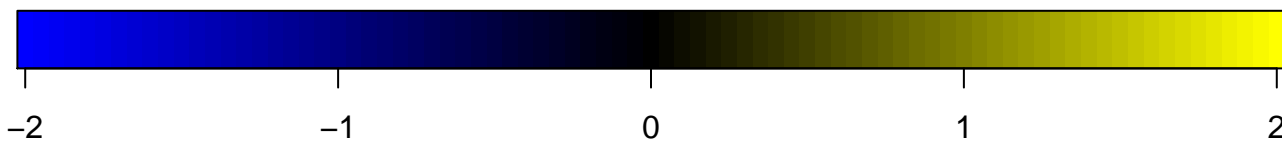
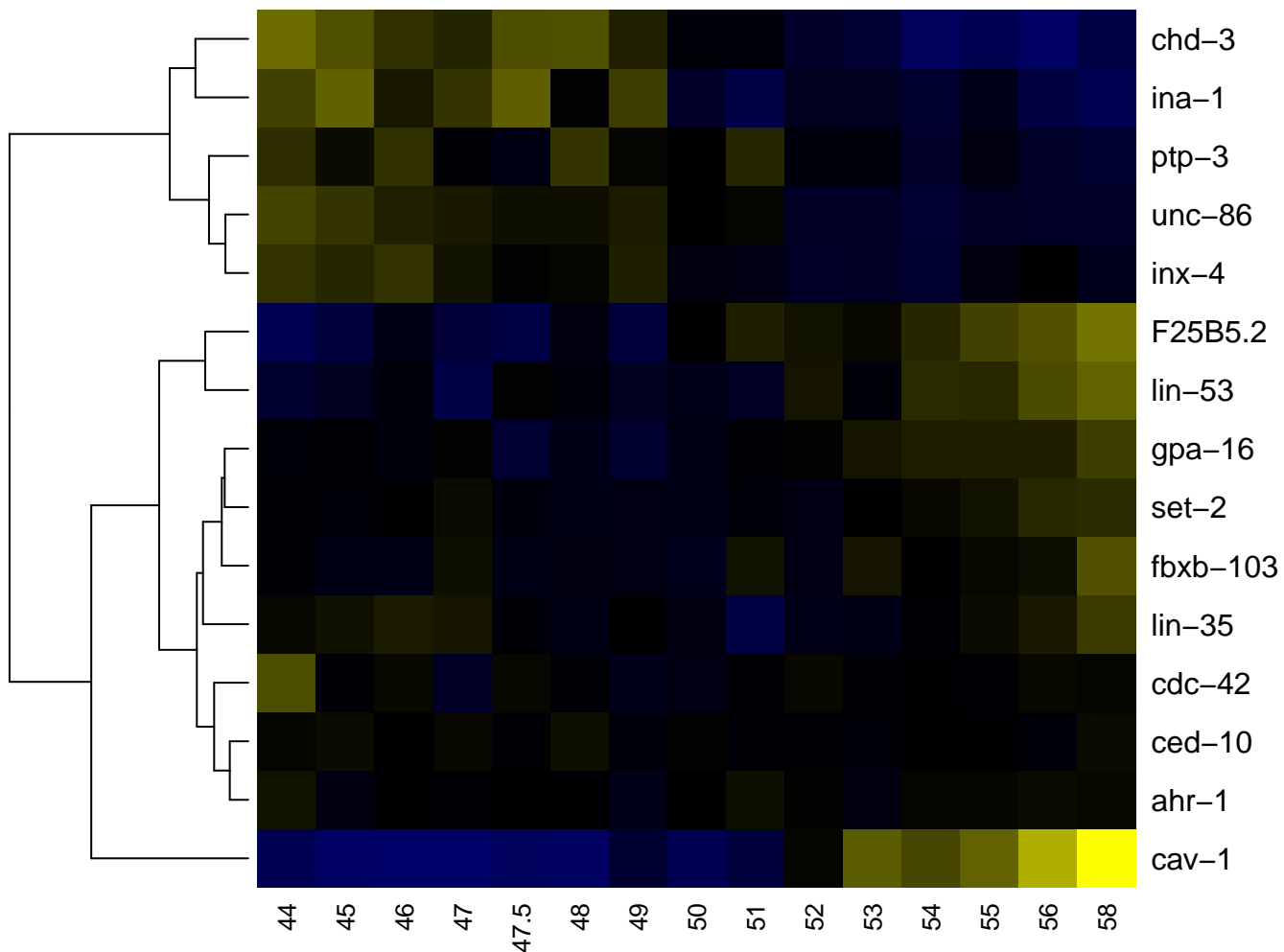
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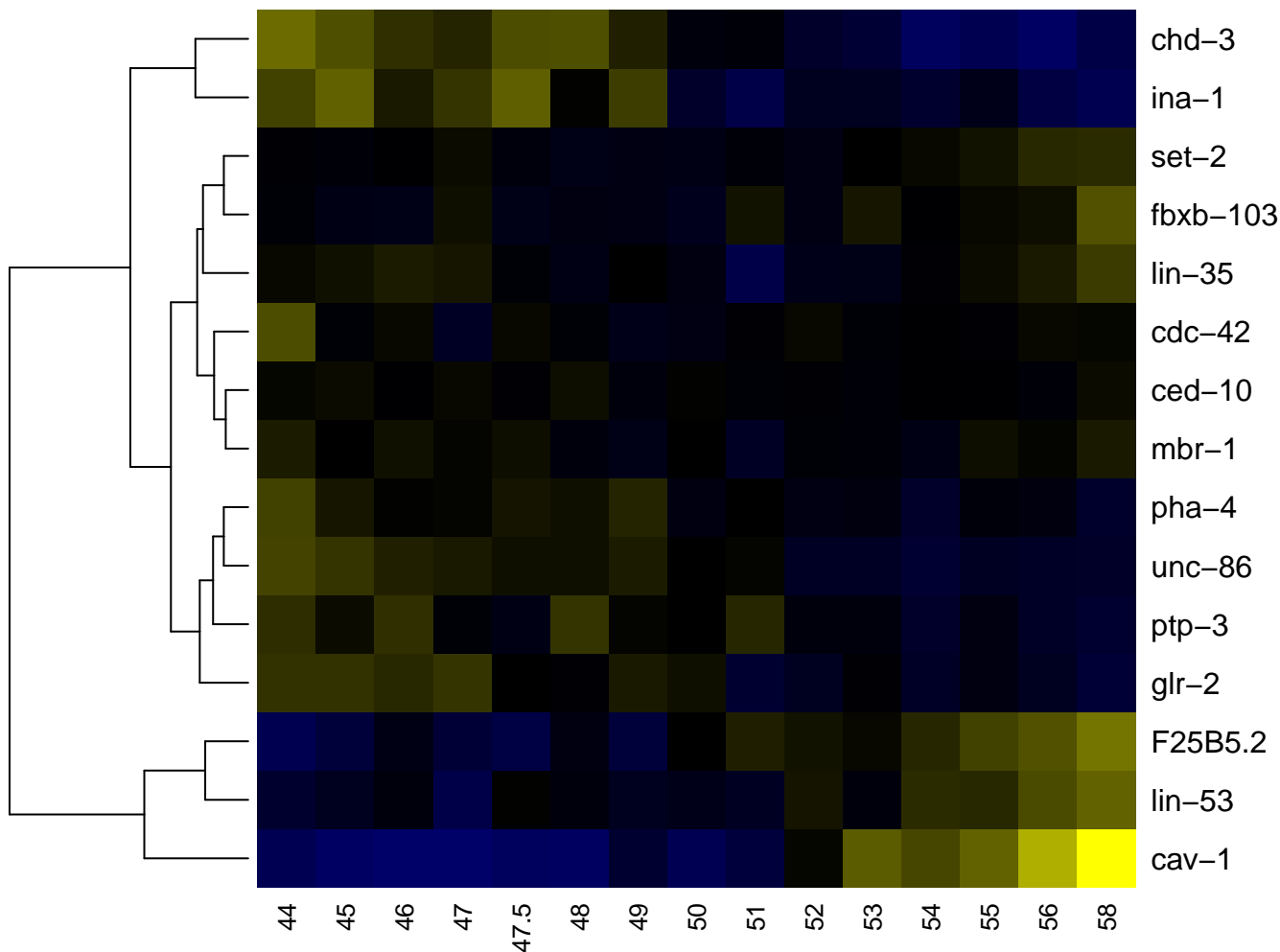
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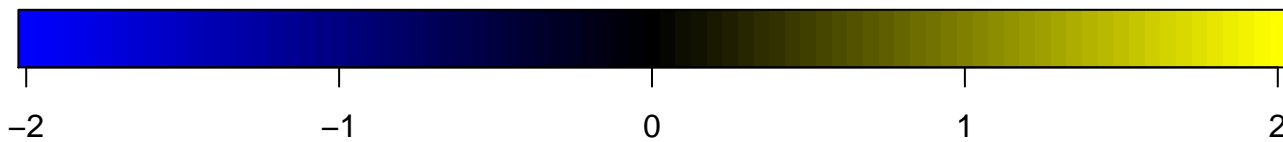
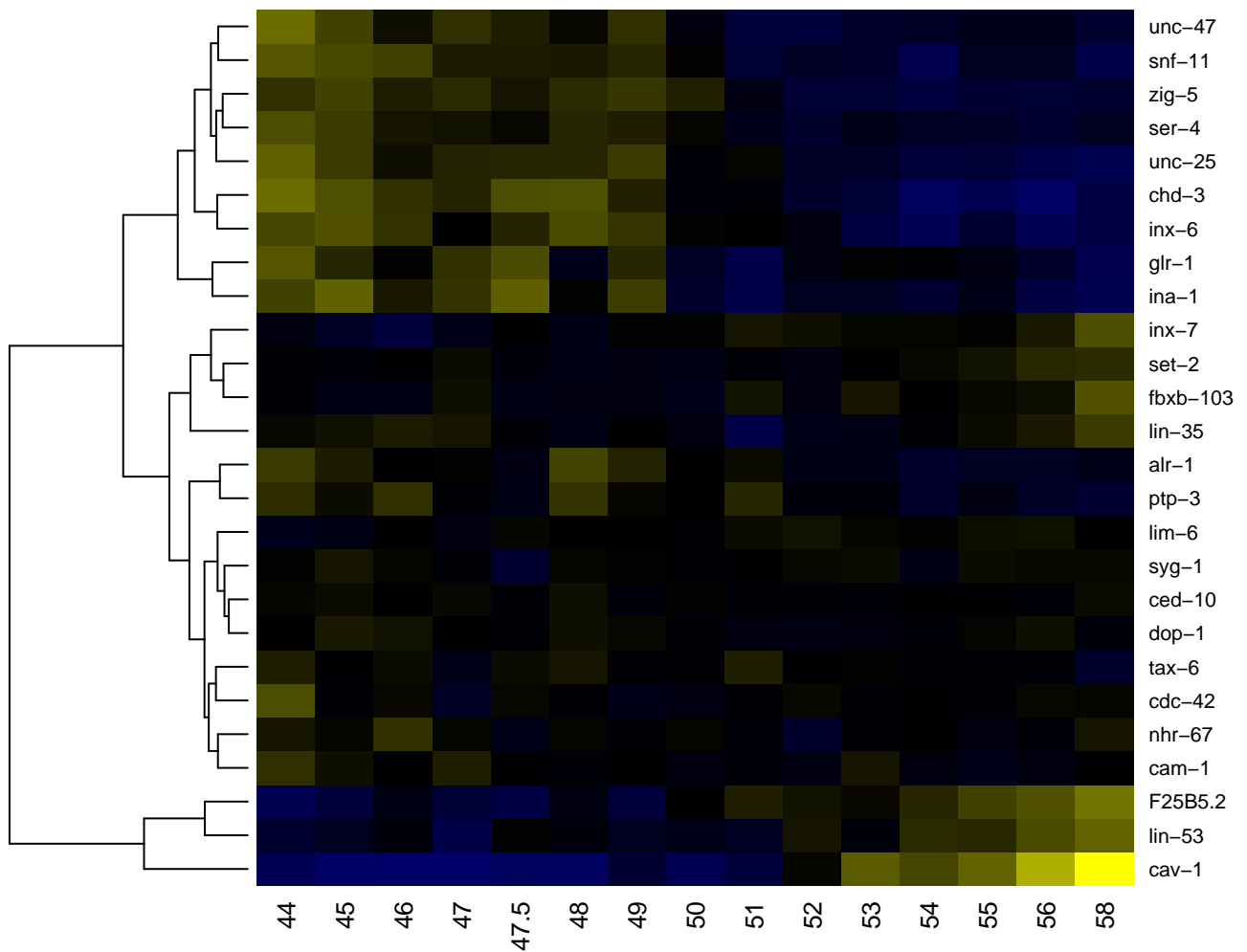
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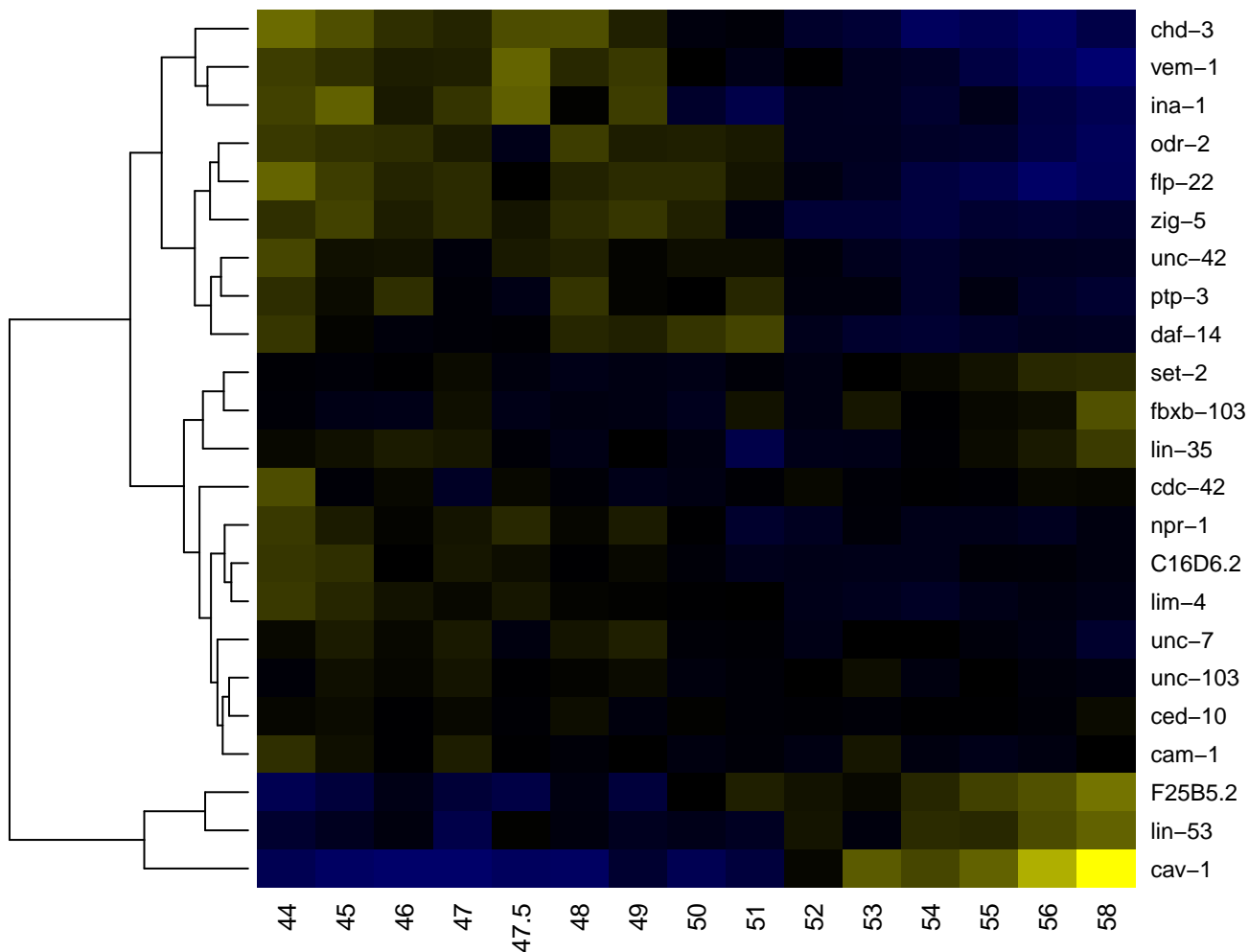
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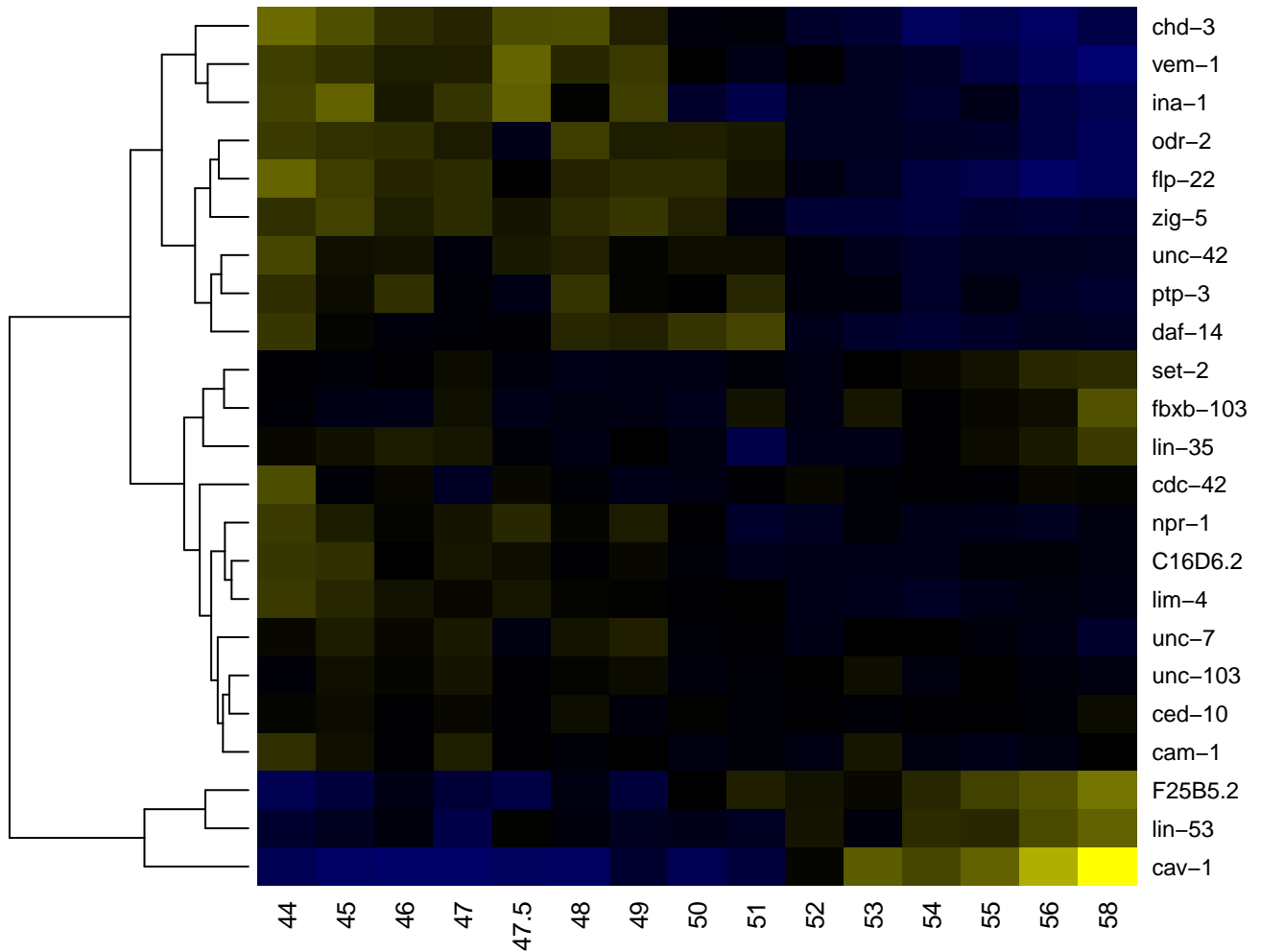
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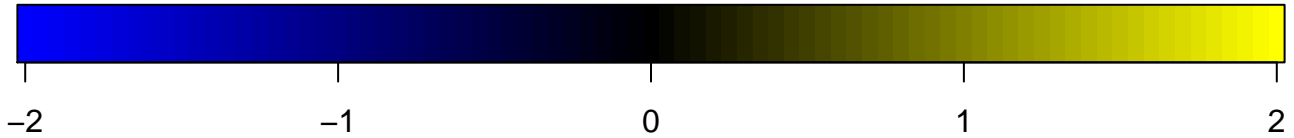
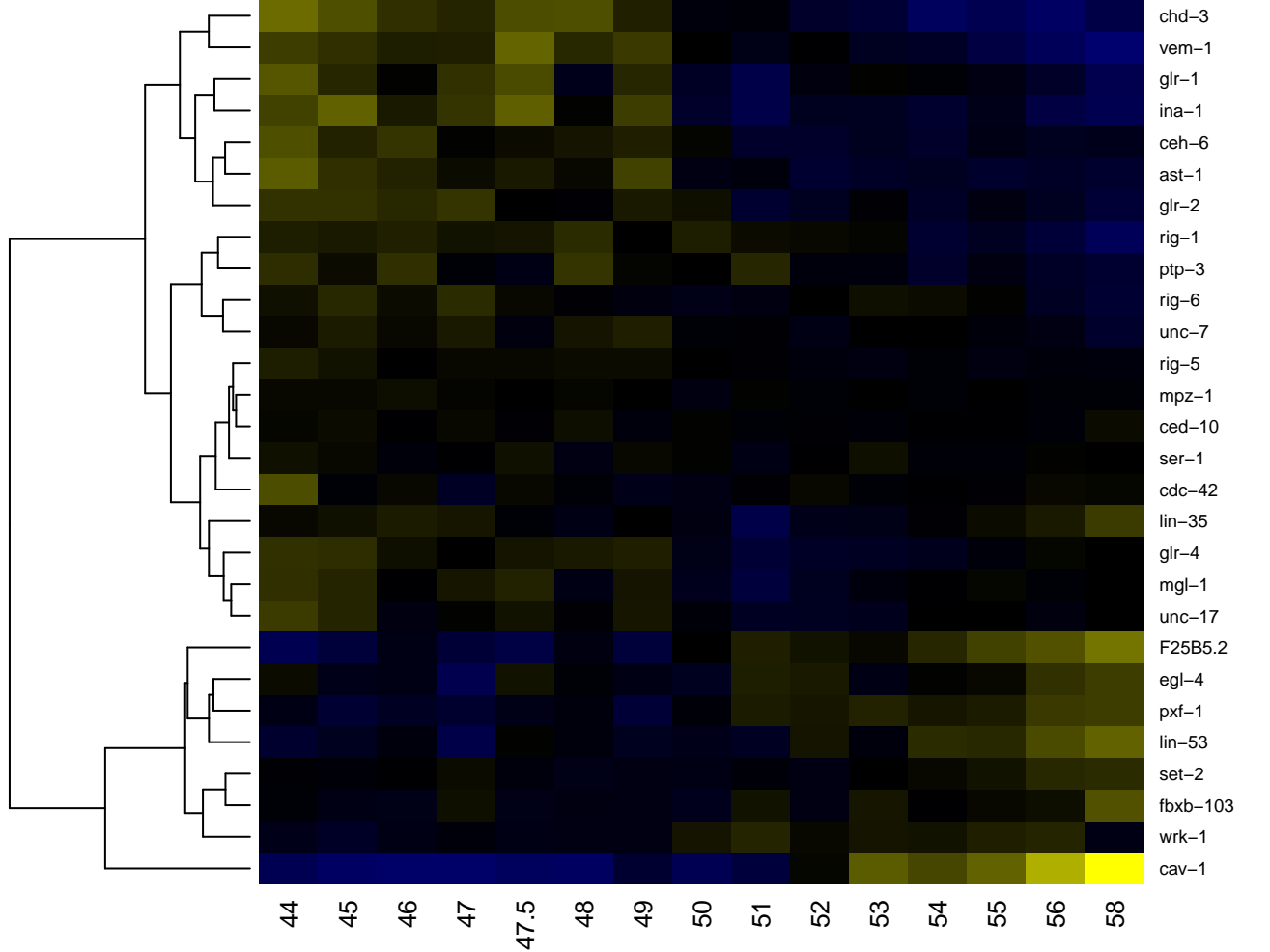
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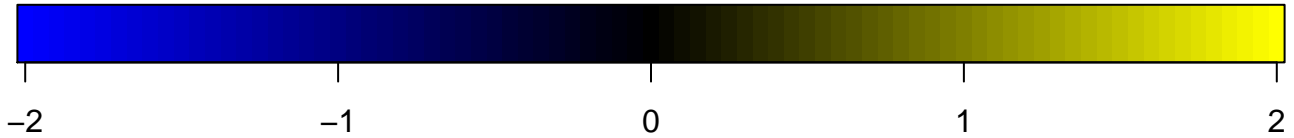
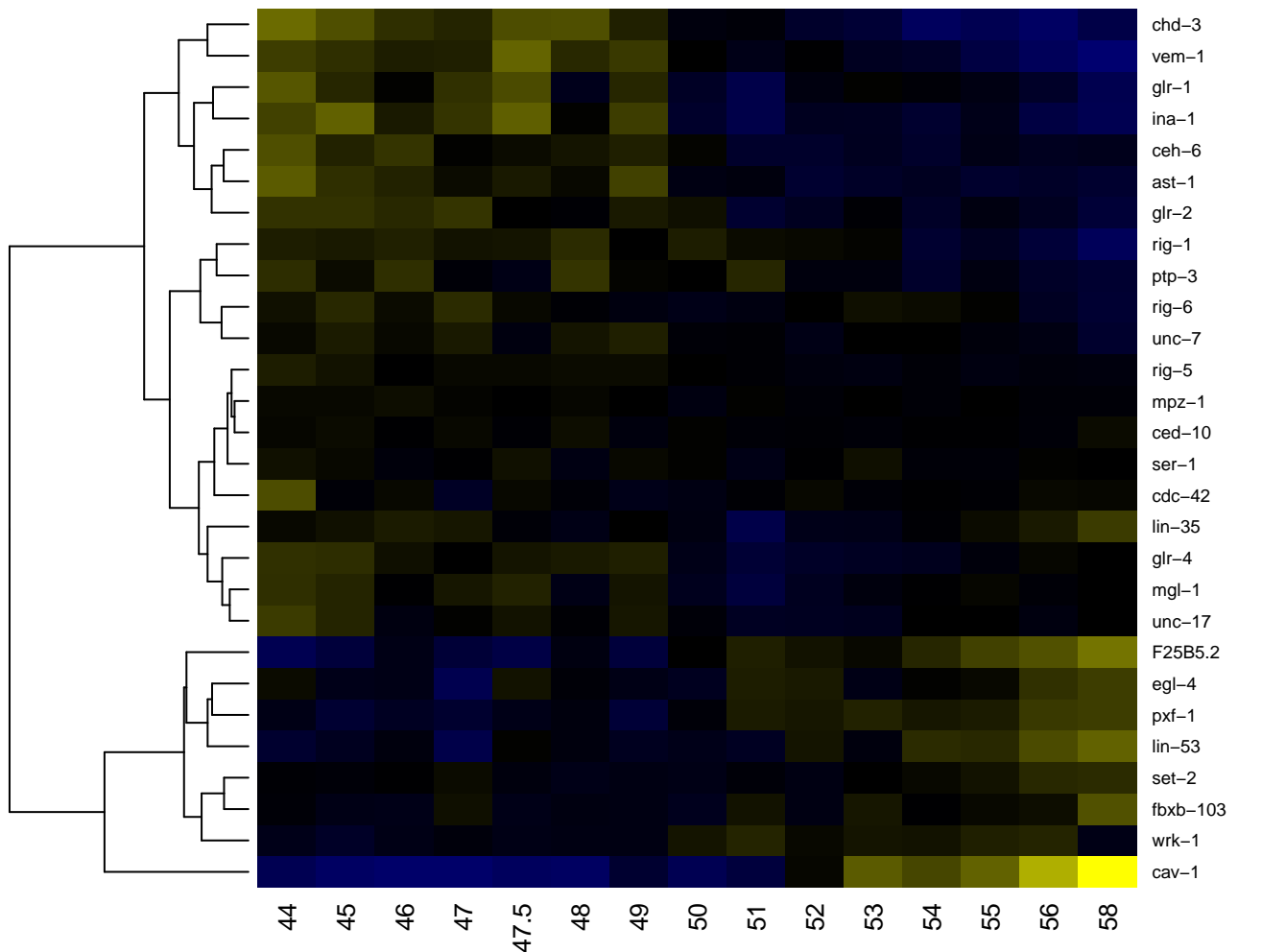
RIVR



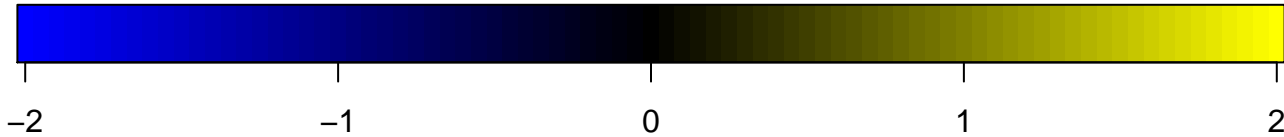
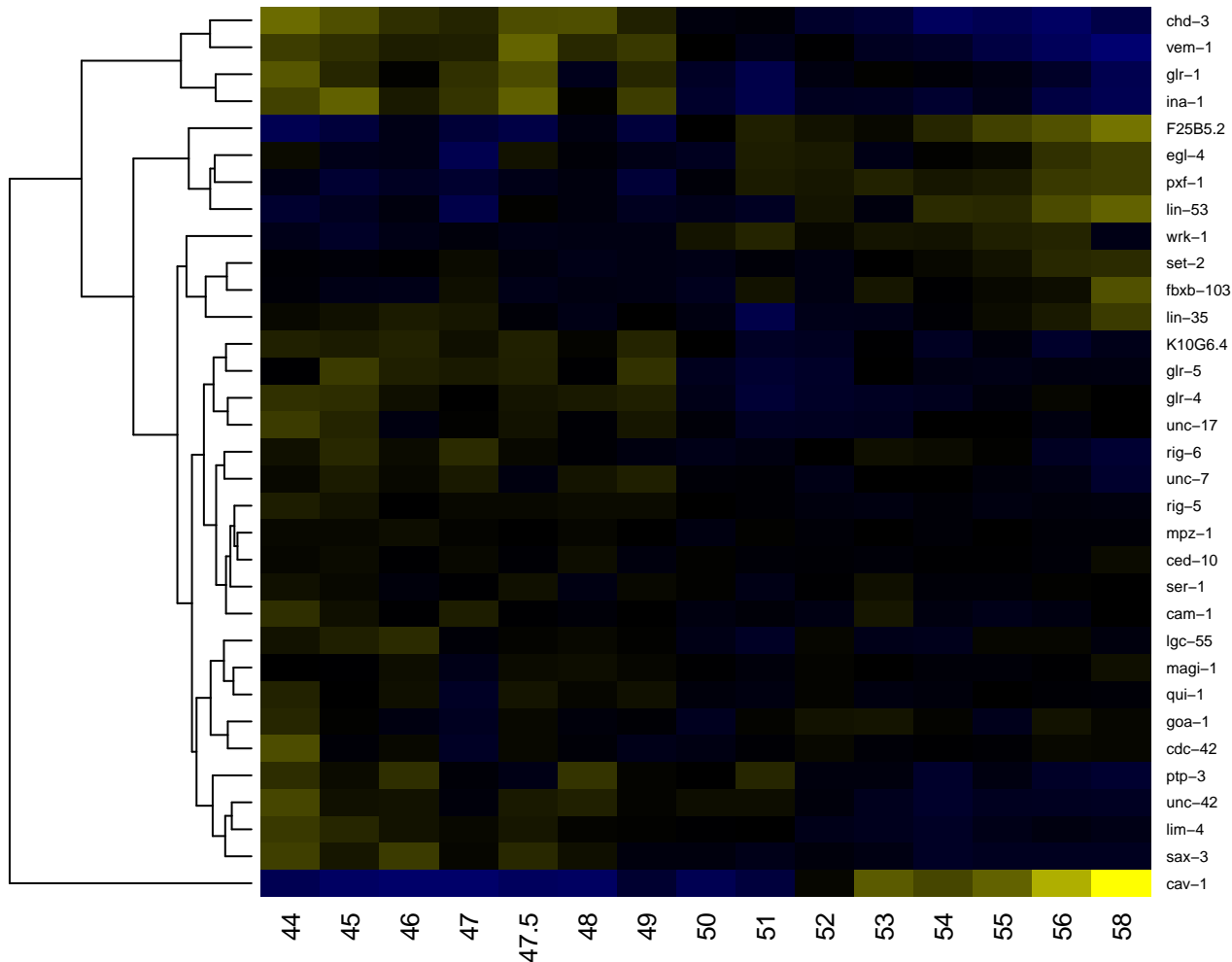
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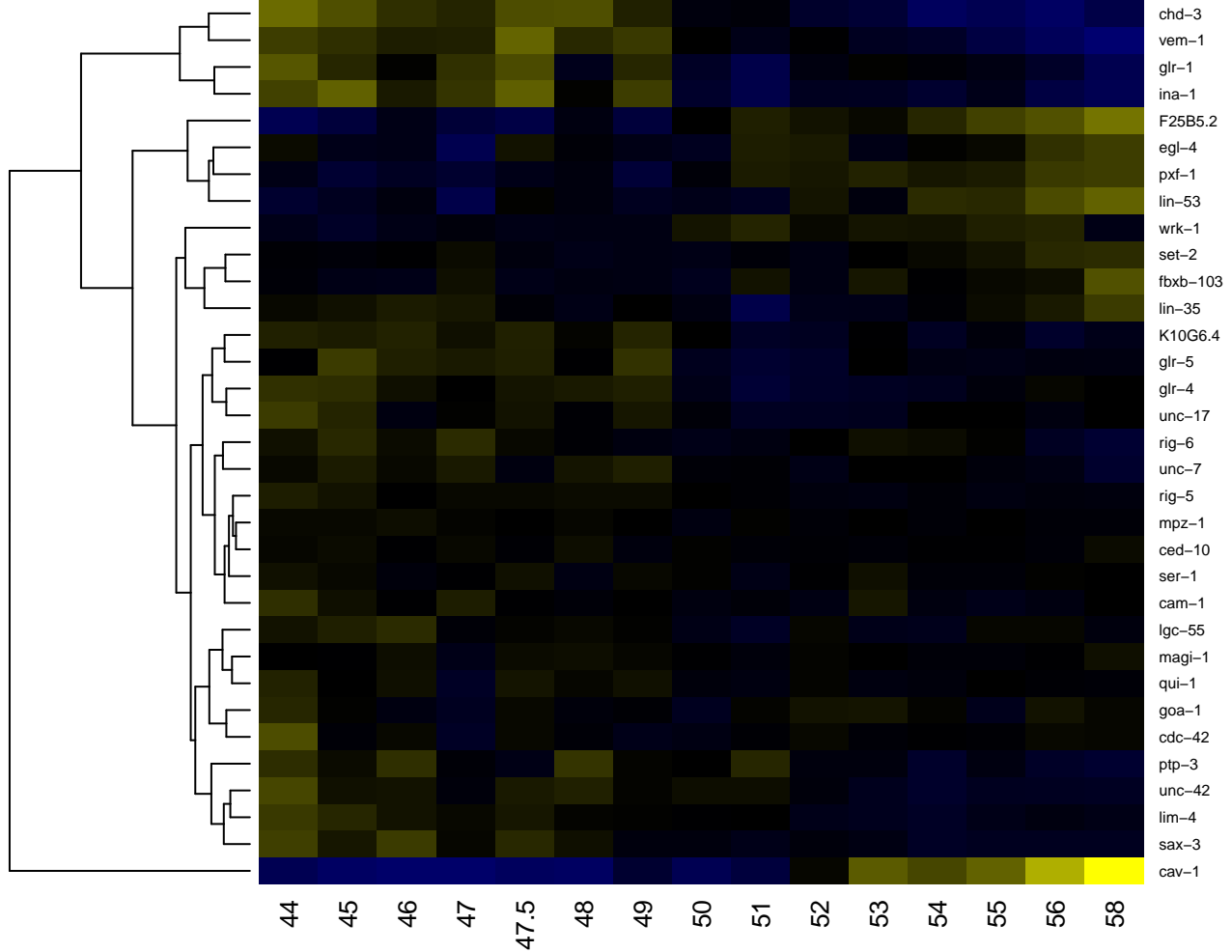
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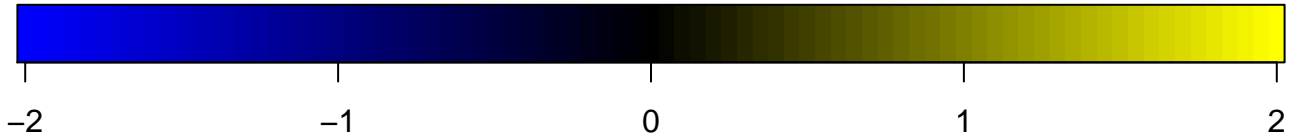
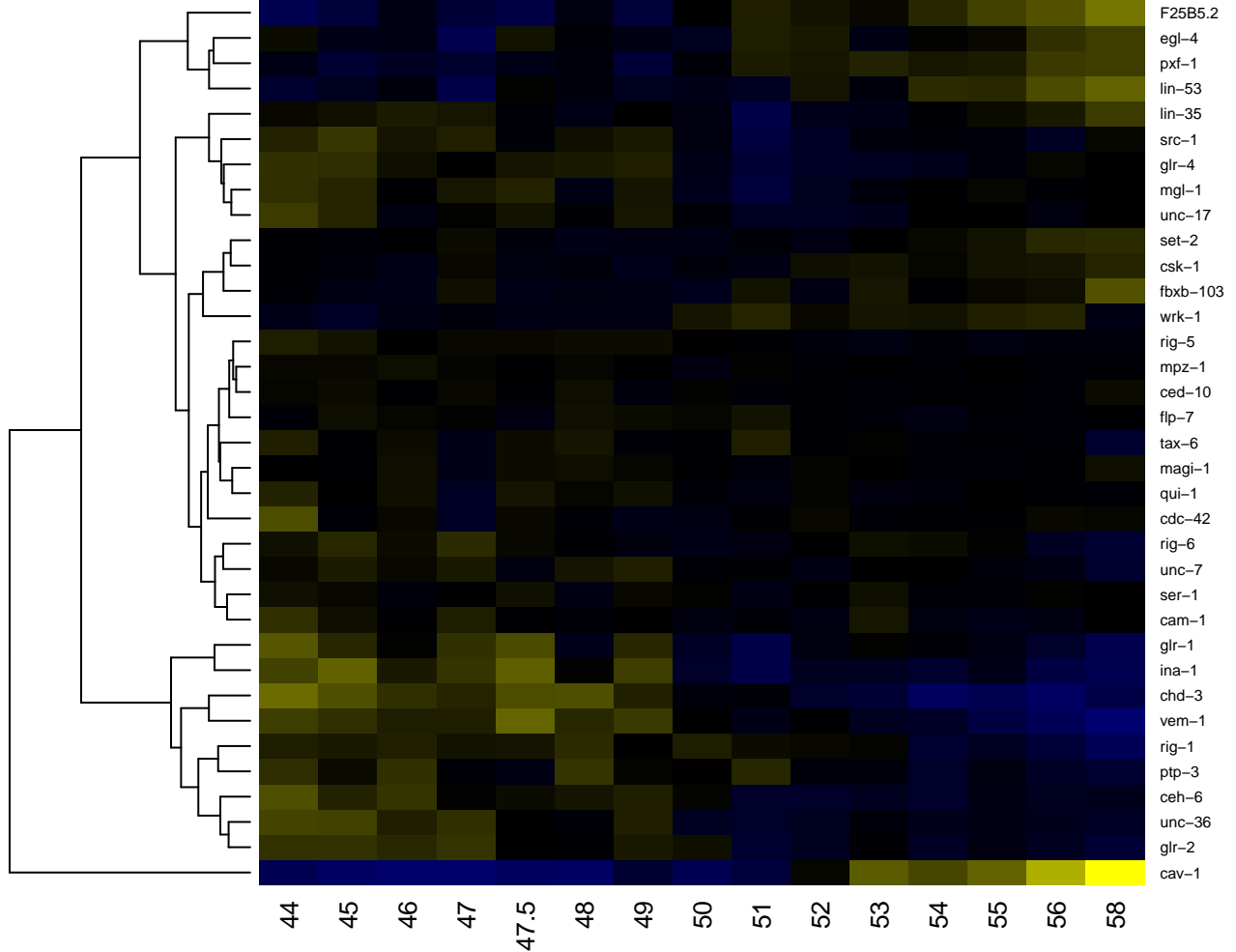
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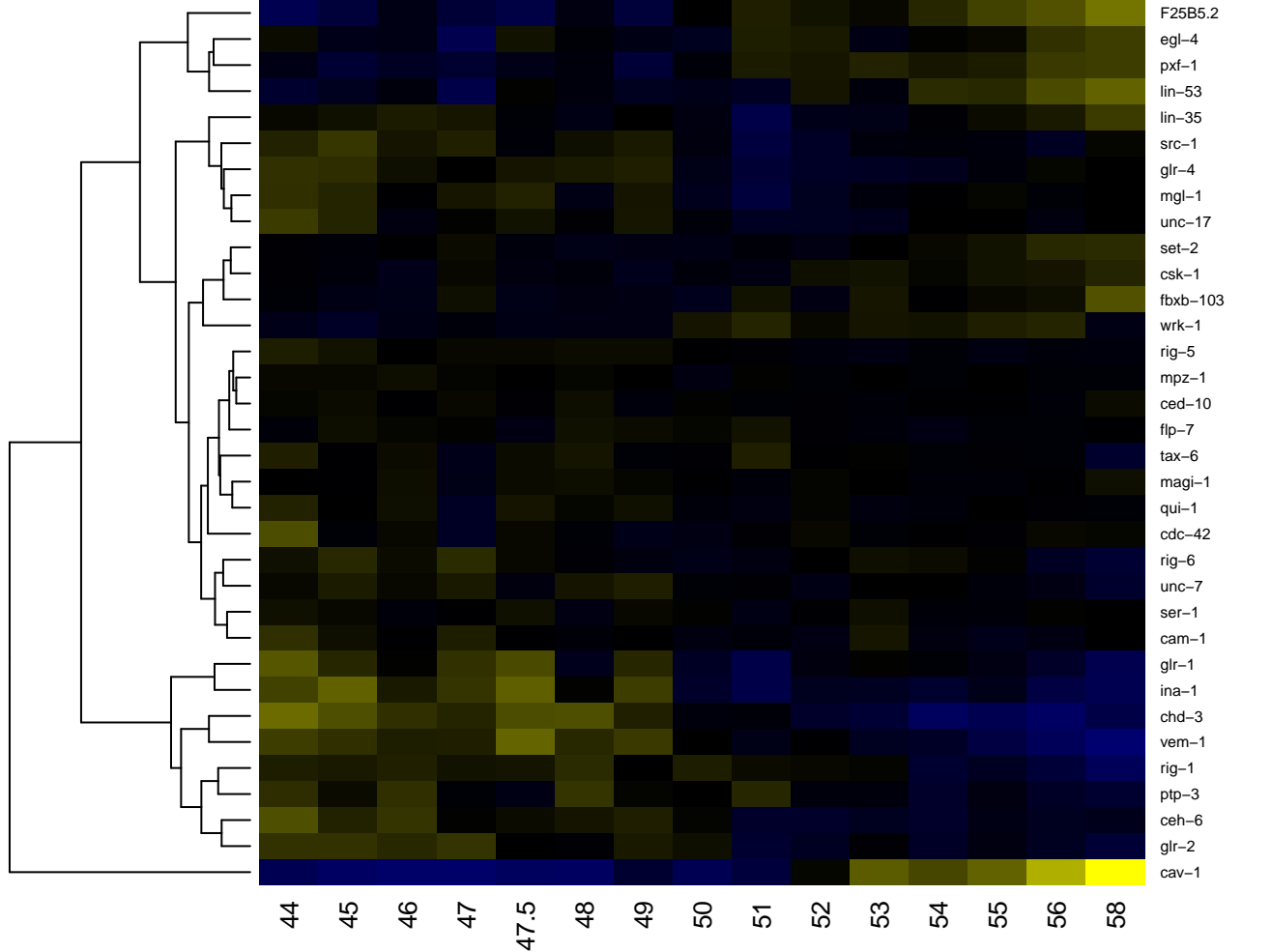
RMDR



RMDVL



RMDVR



-2

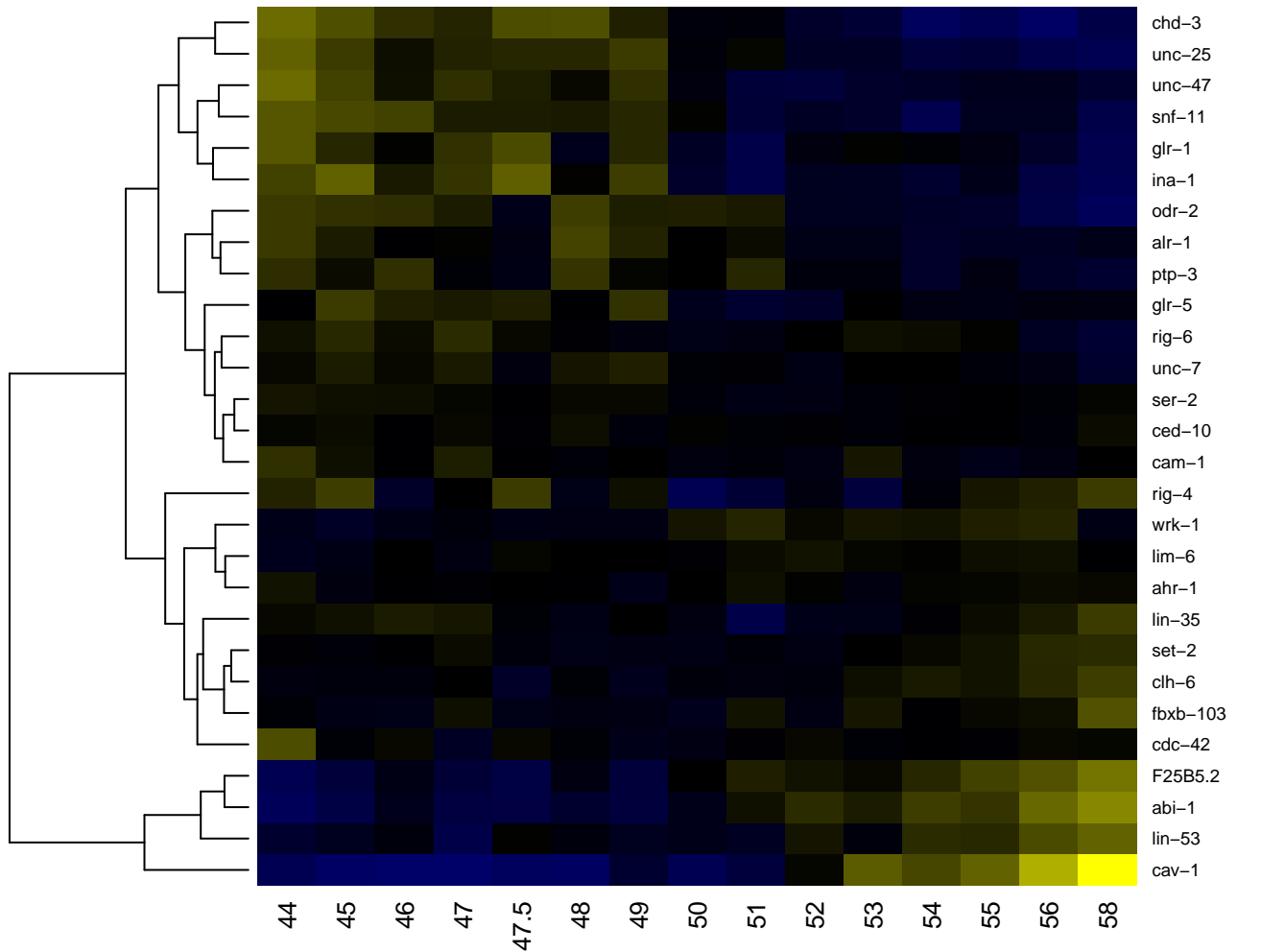
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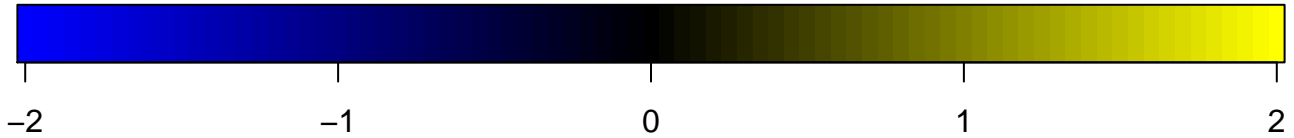
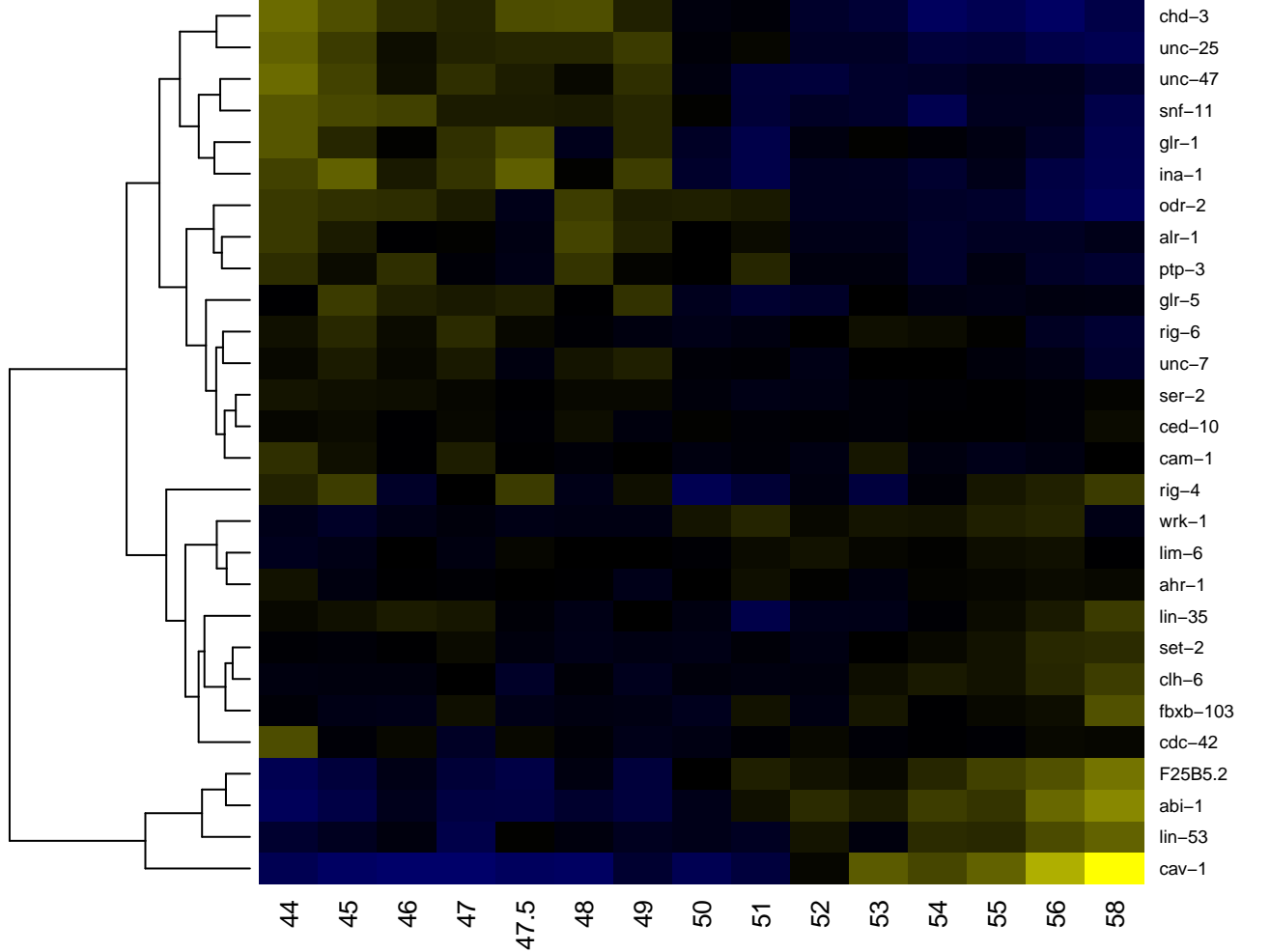
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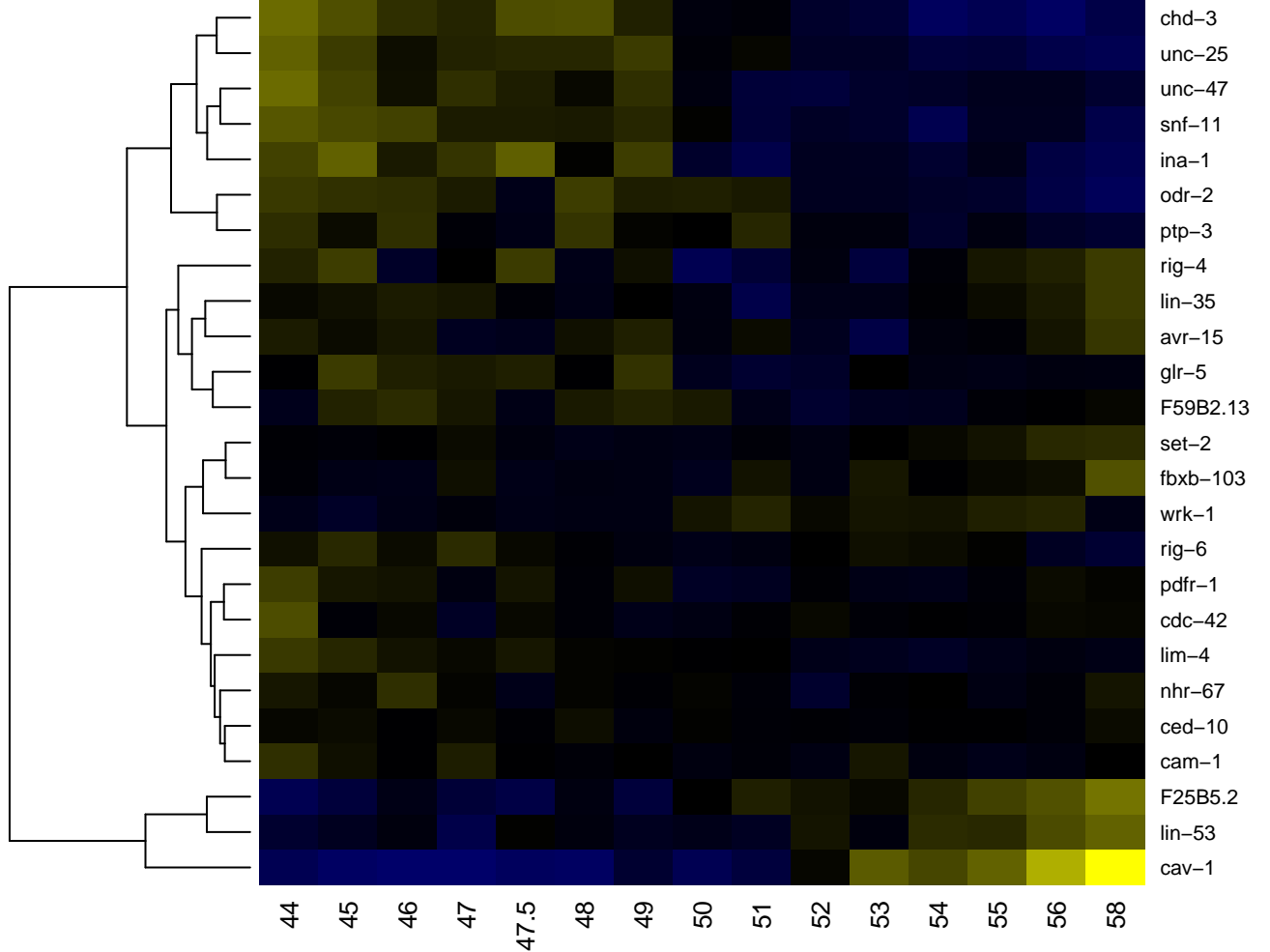
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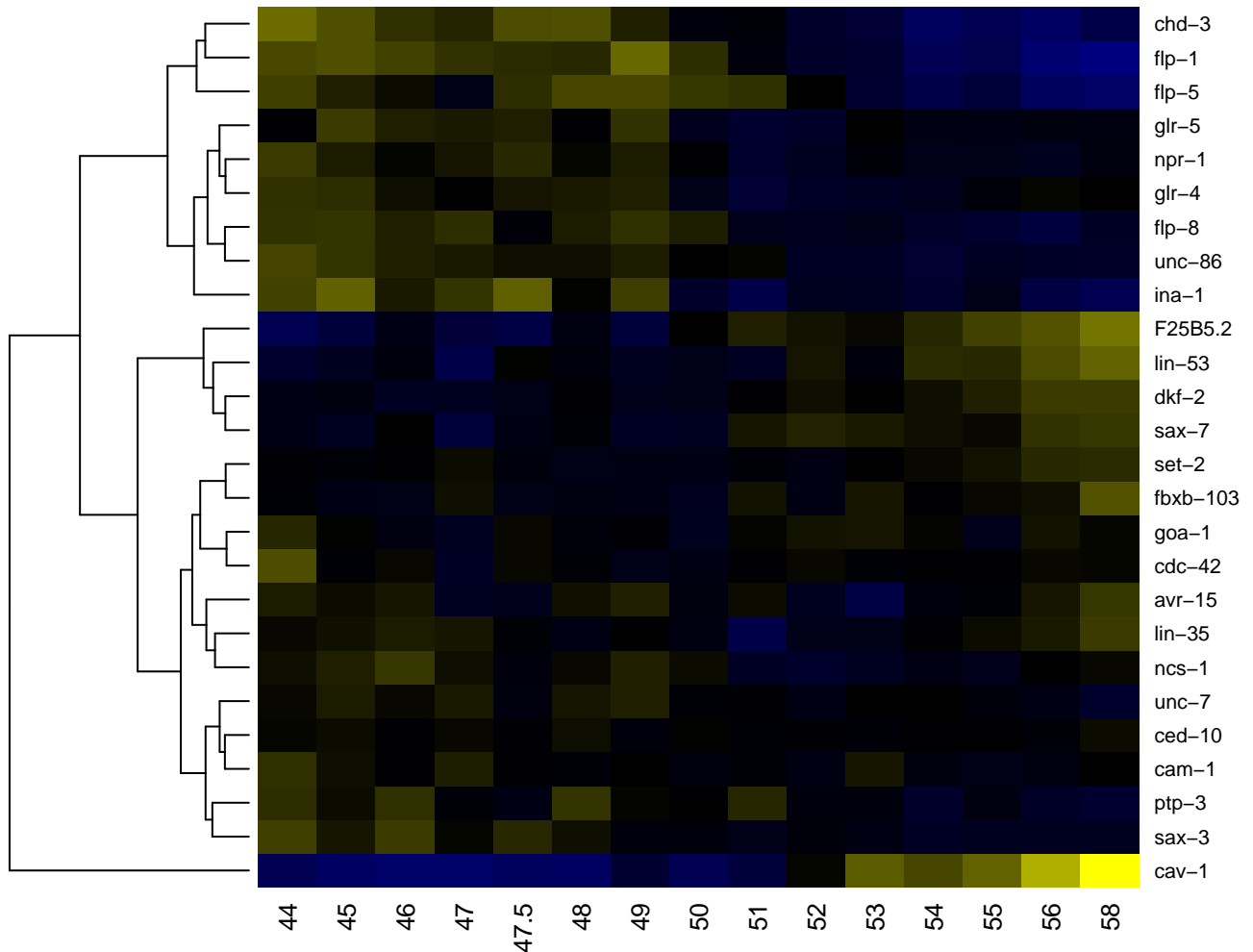
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RMEV



RMGL



-2

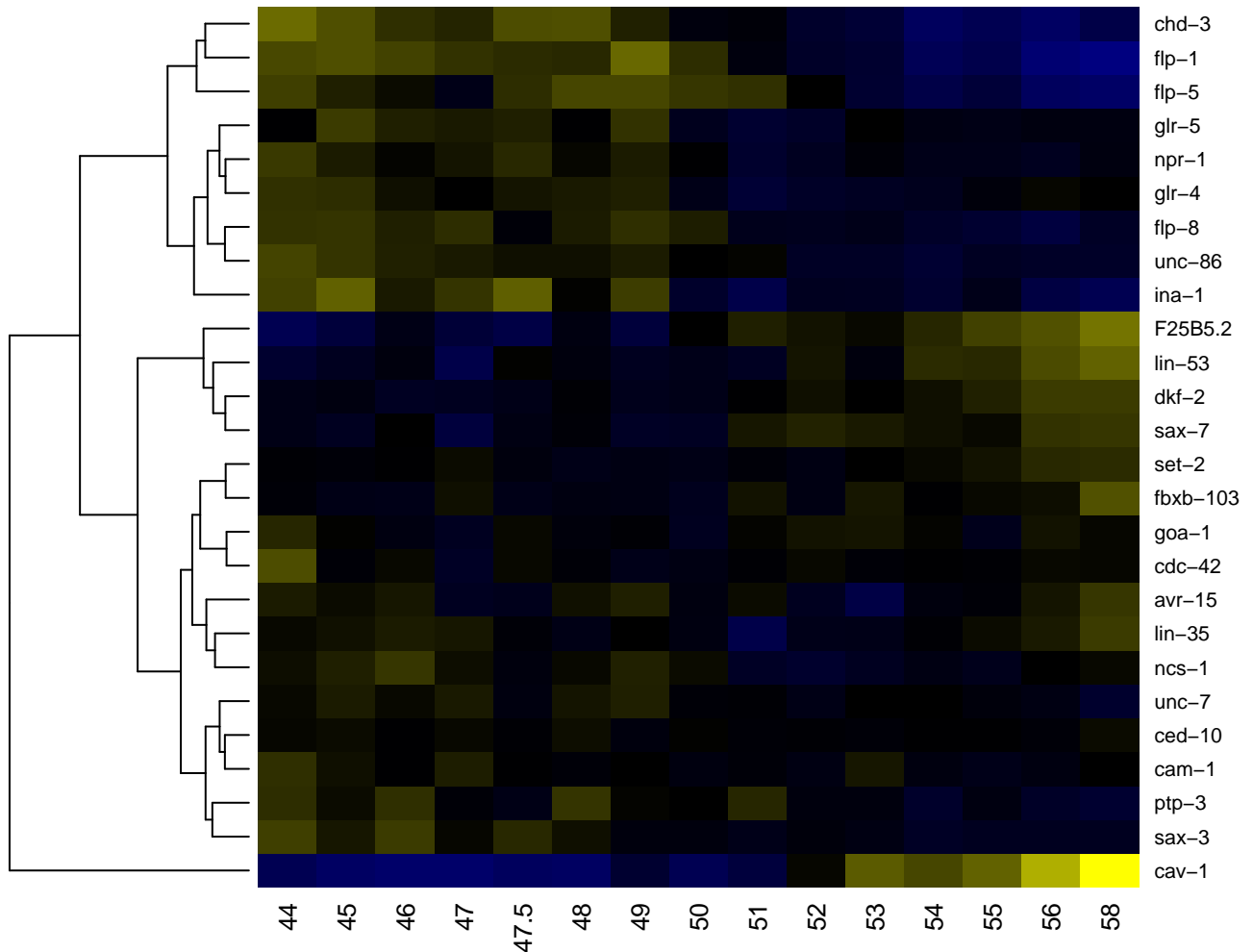
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RMGR



-2

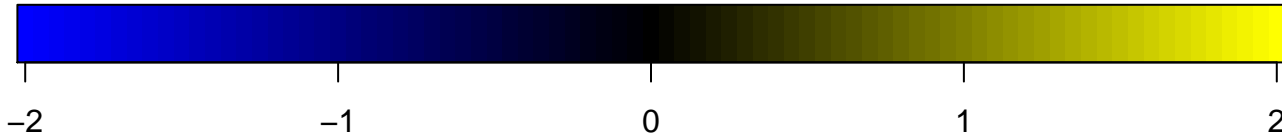
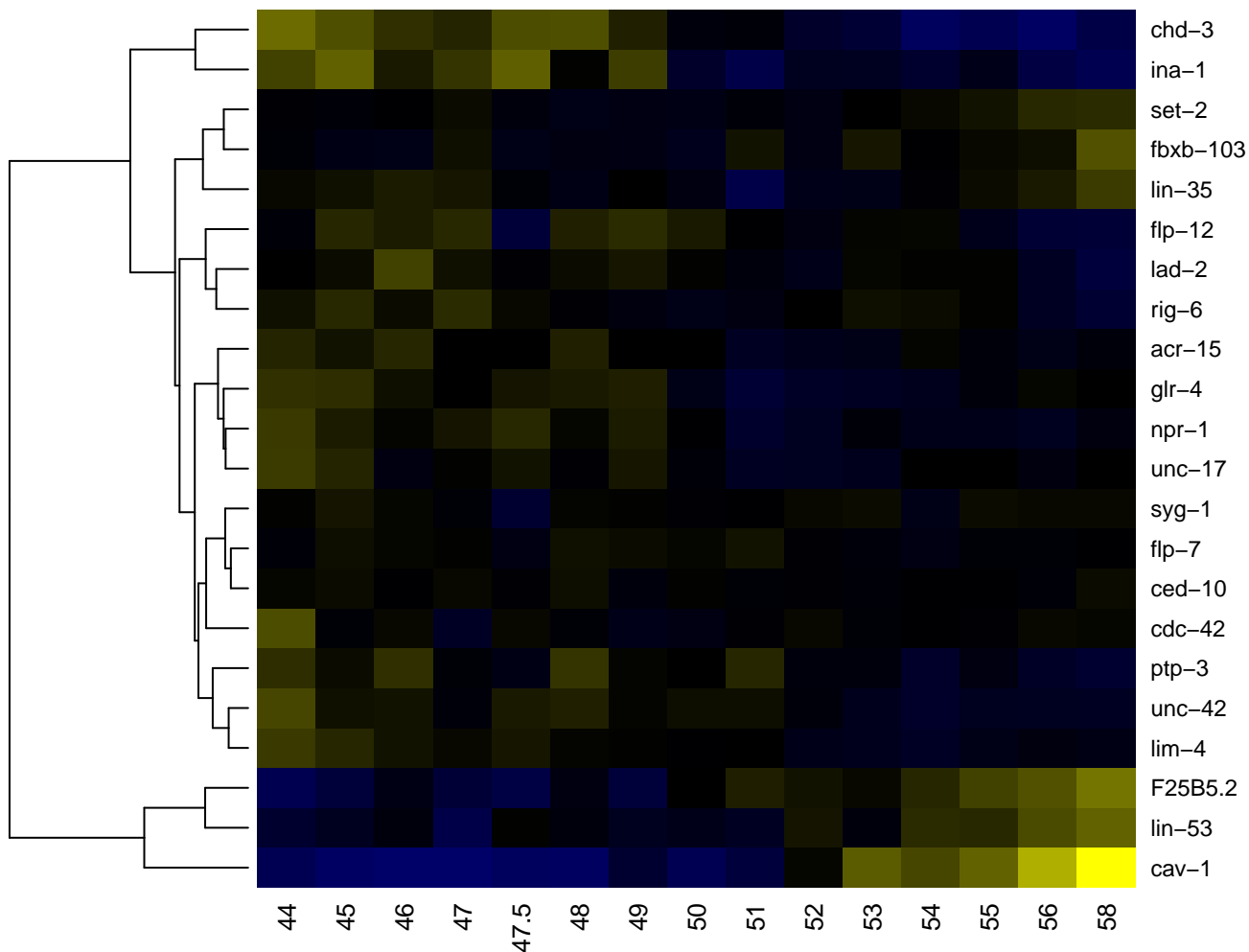
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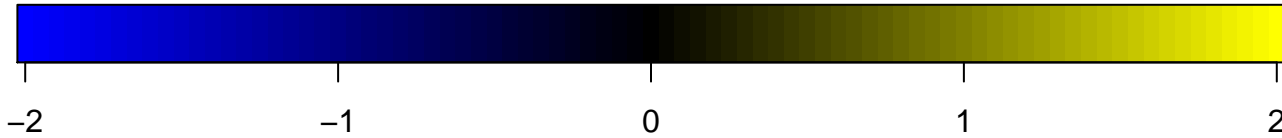
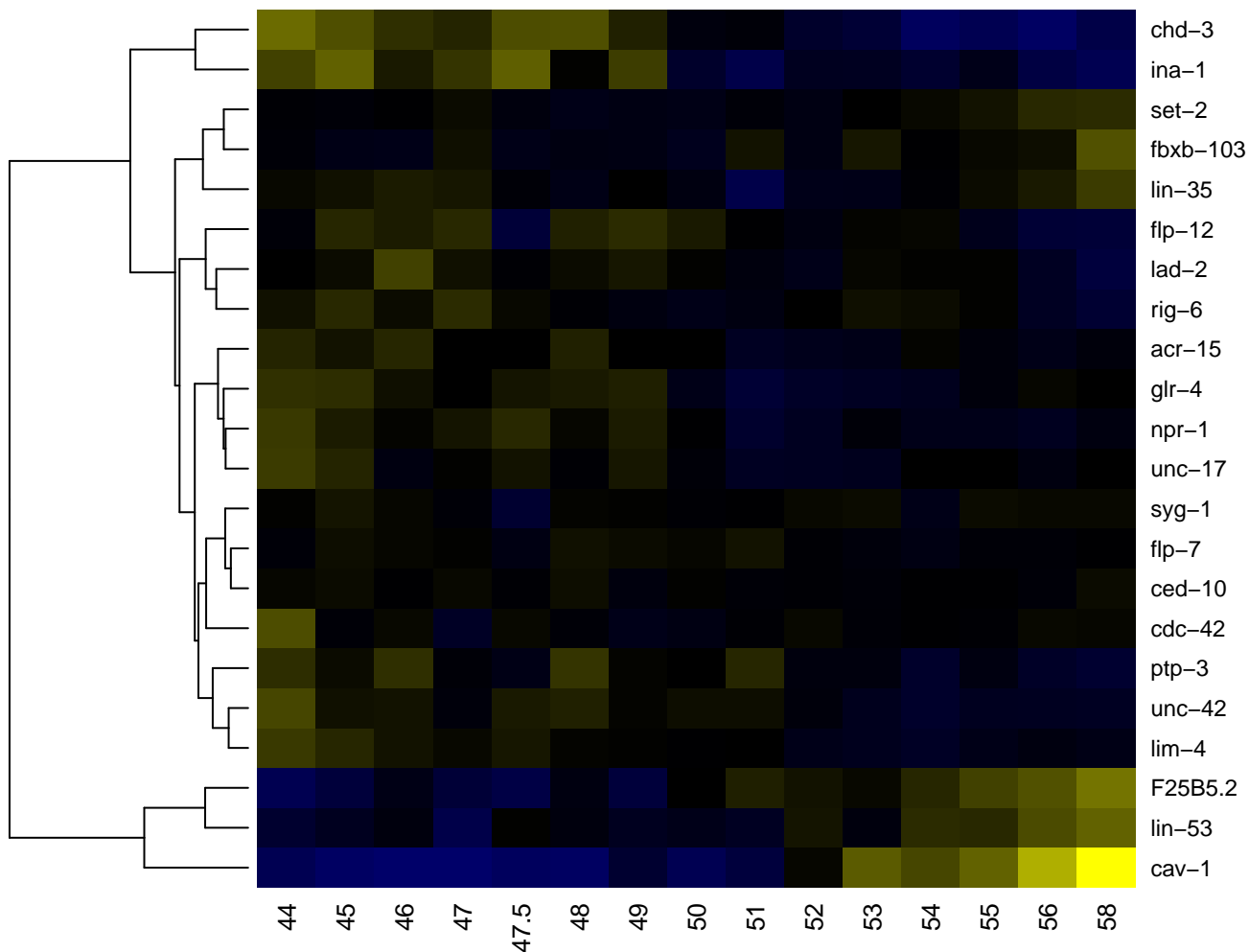
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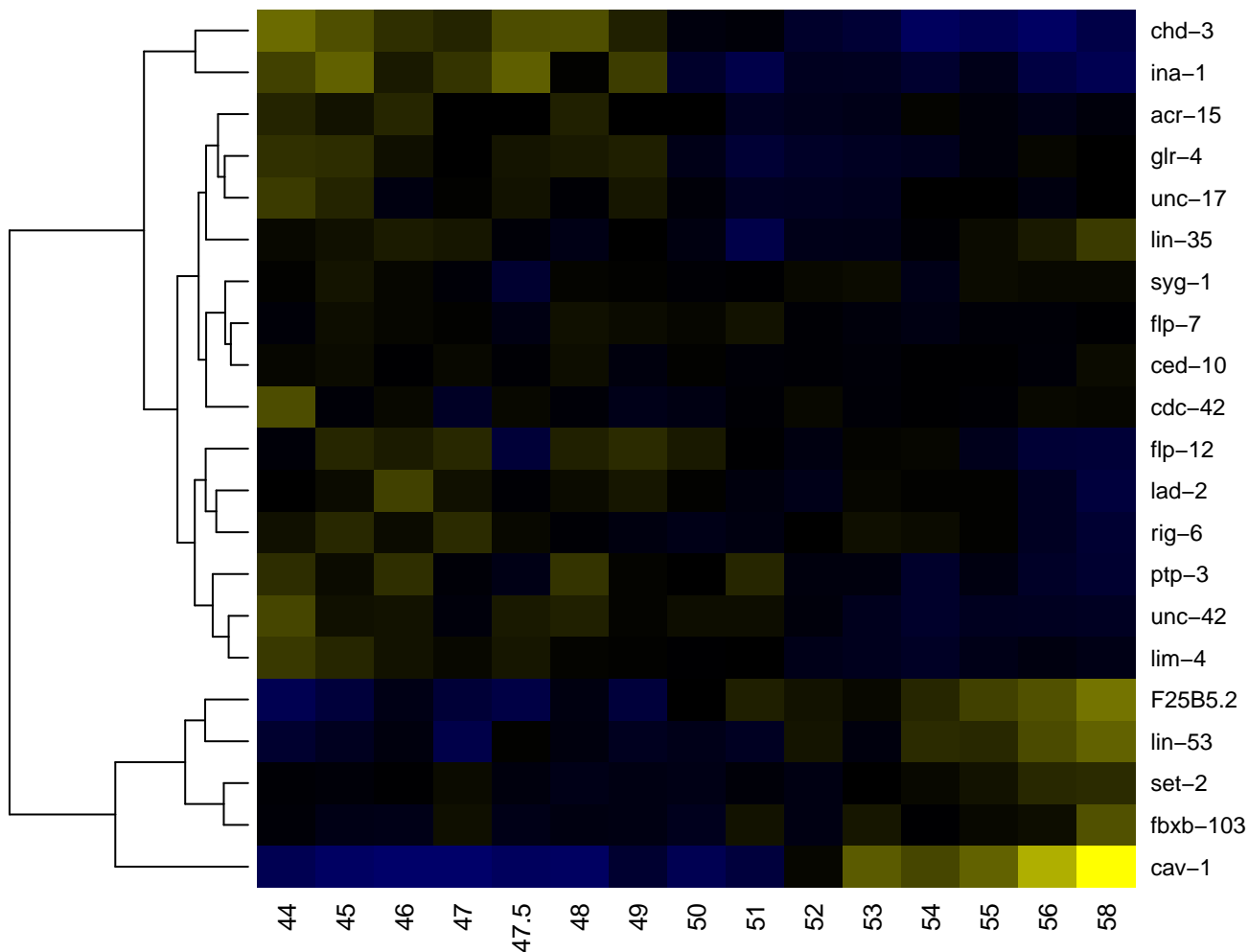
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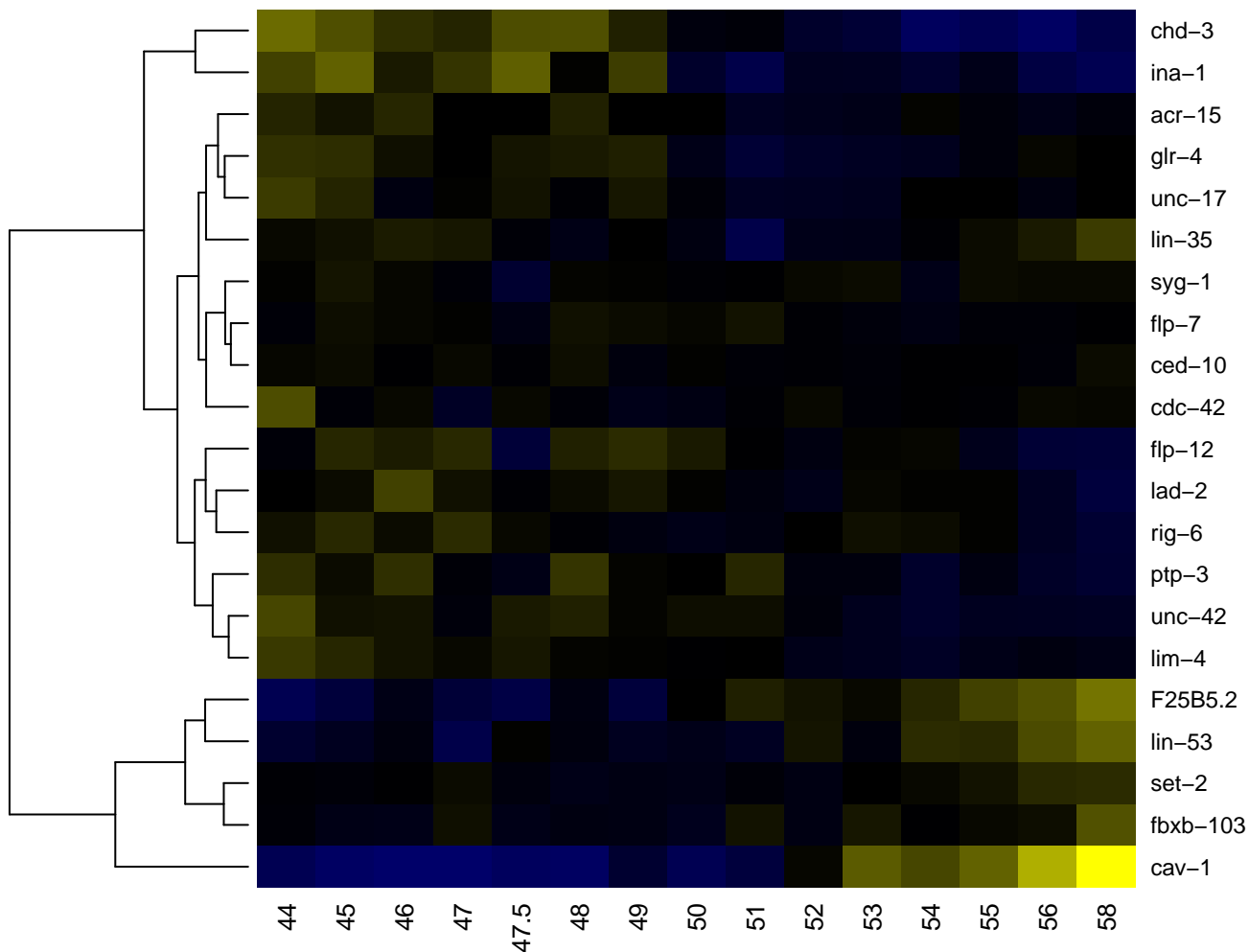
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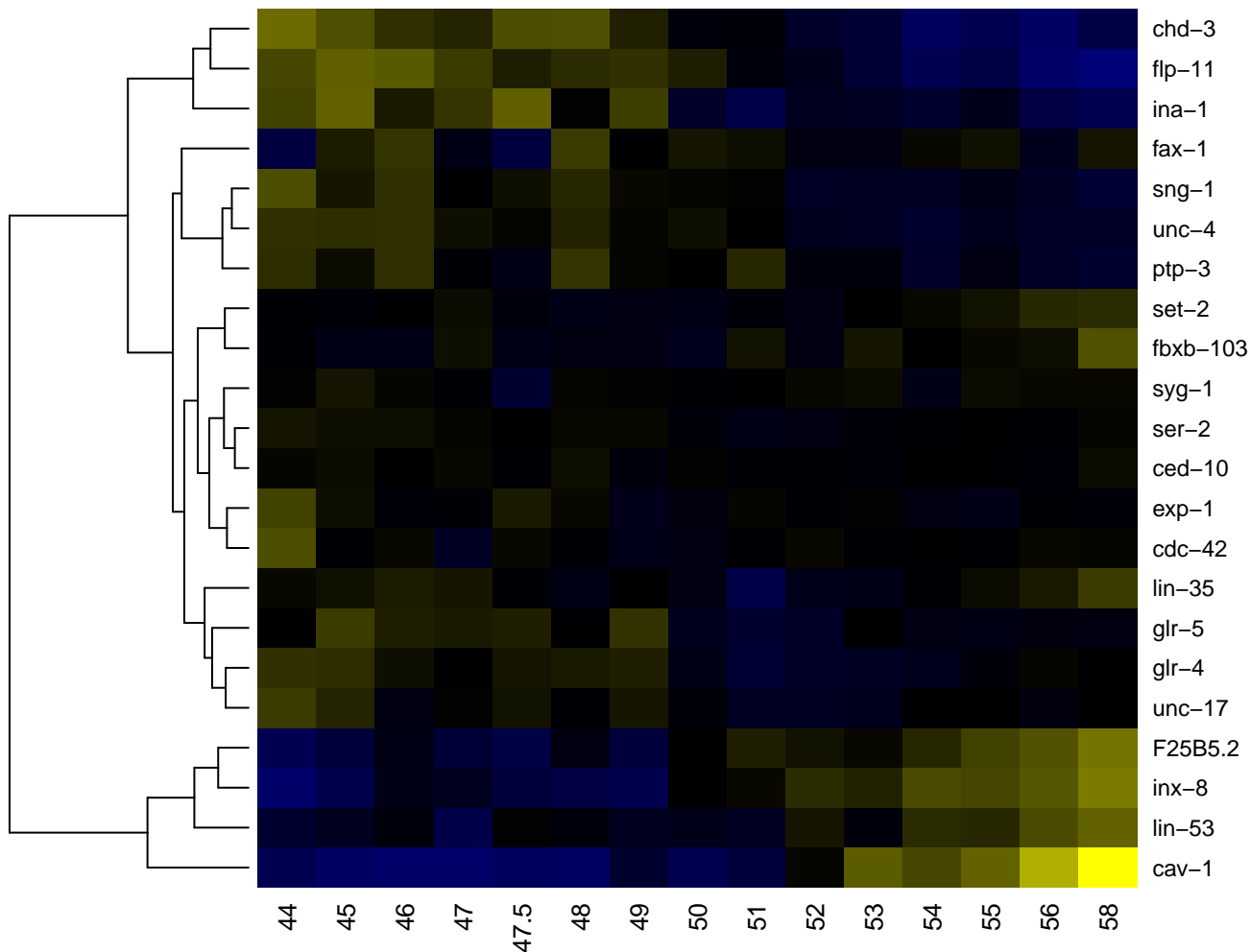
SAAVL



SAAVR



SABD



-2

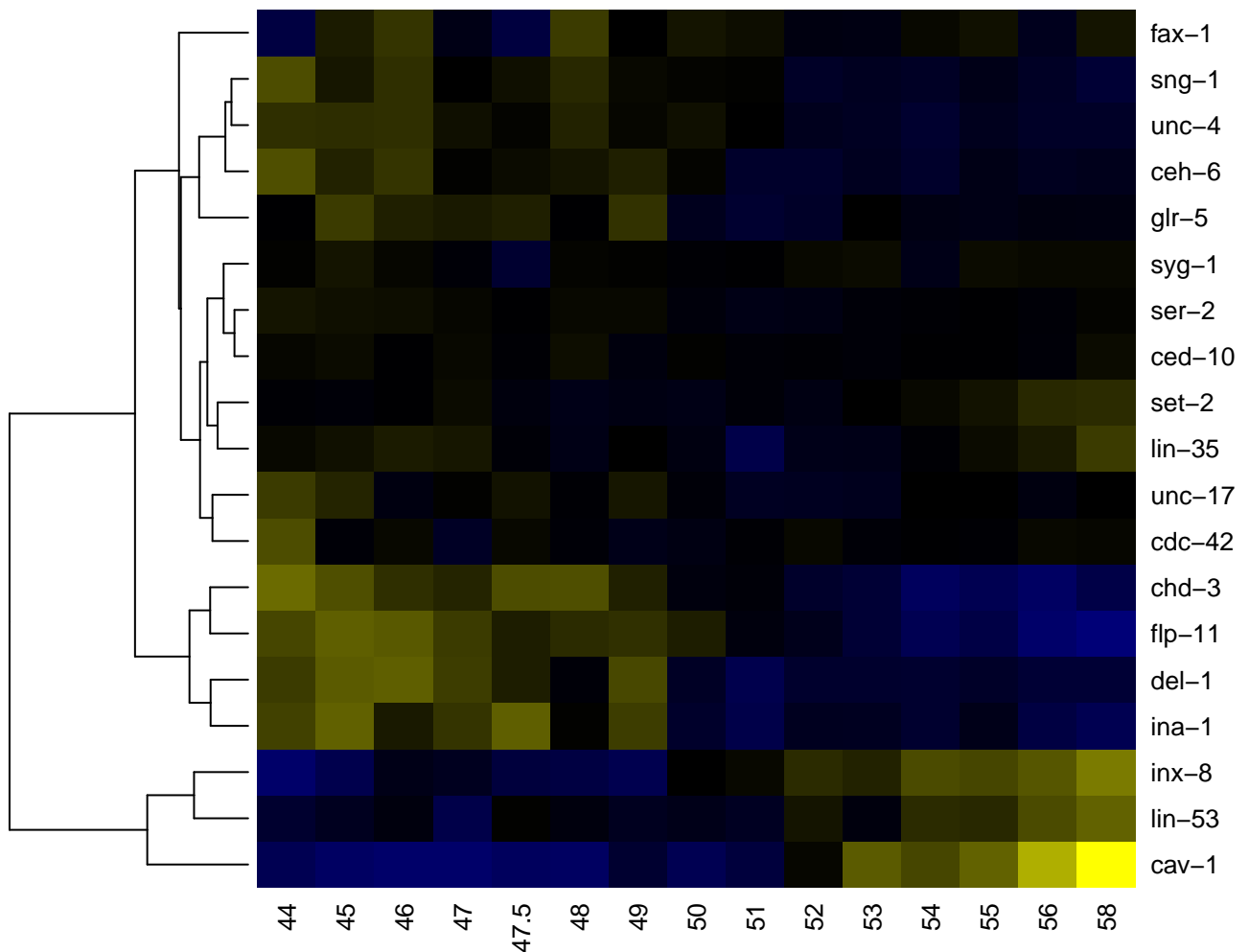
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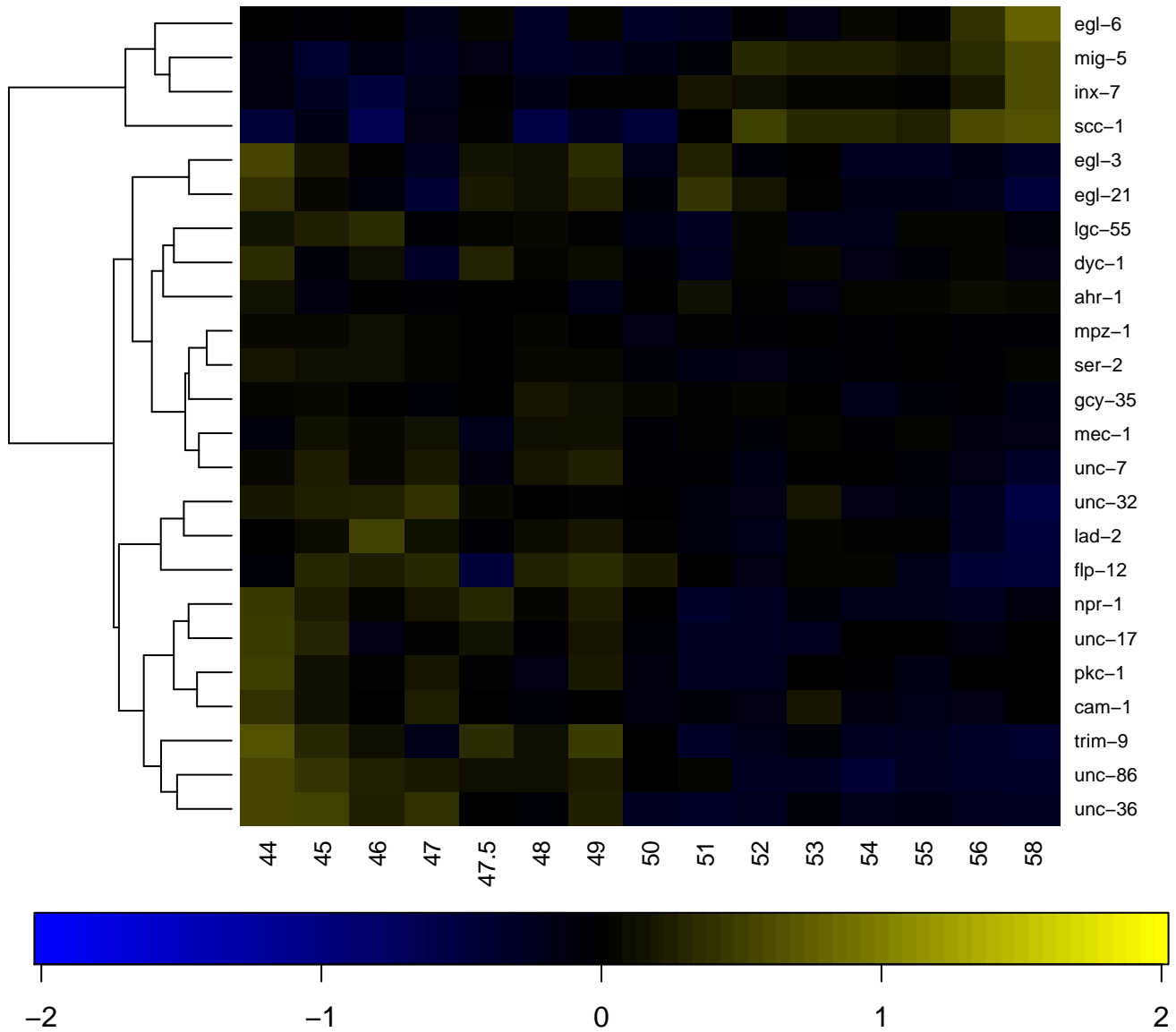
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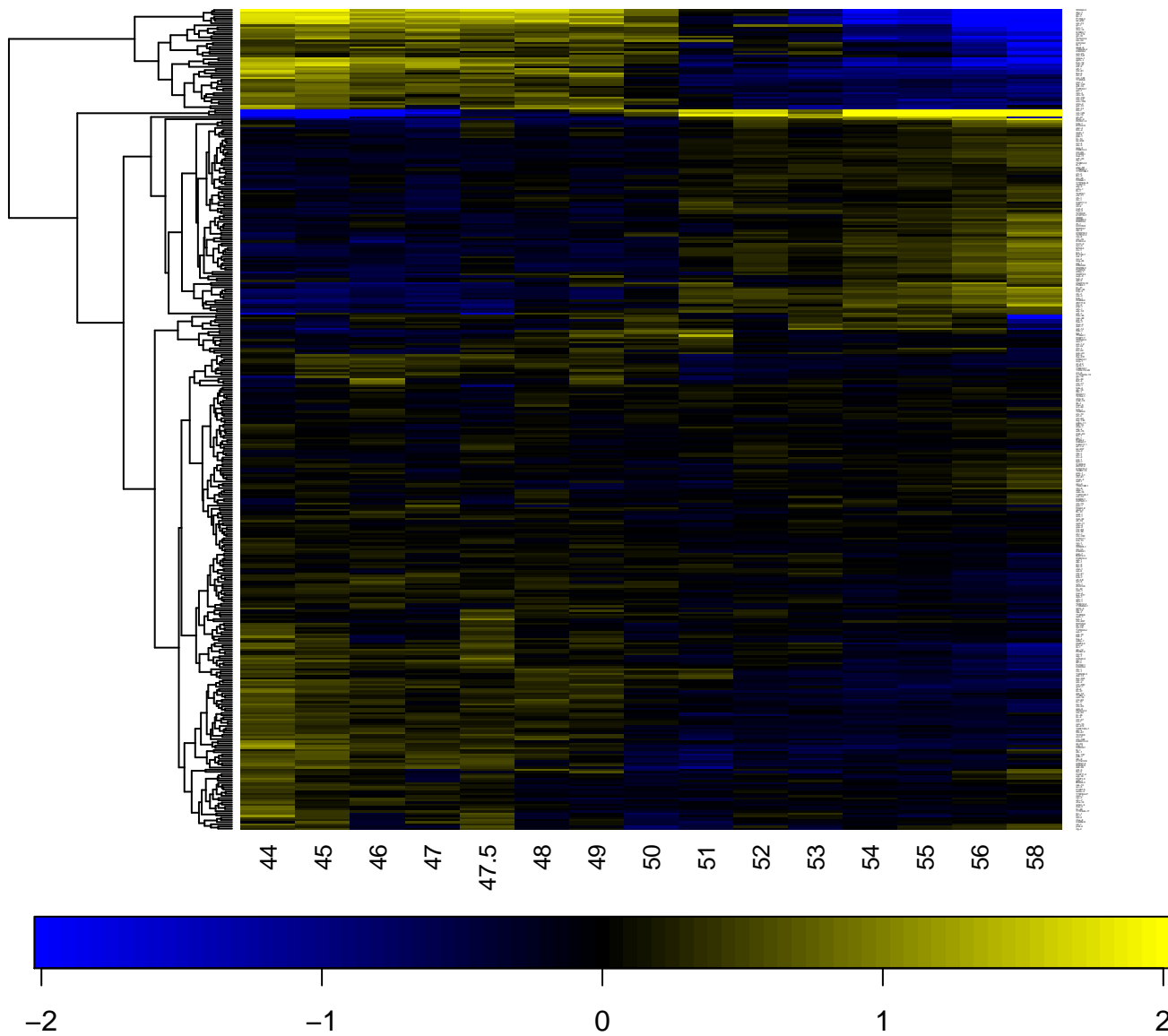
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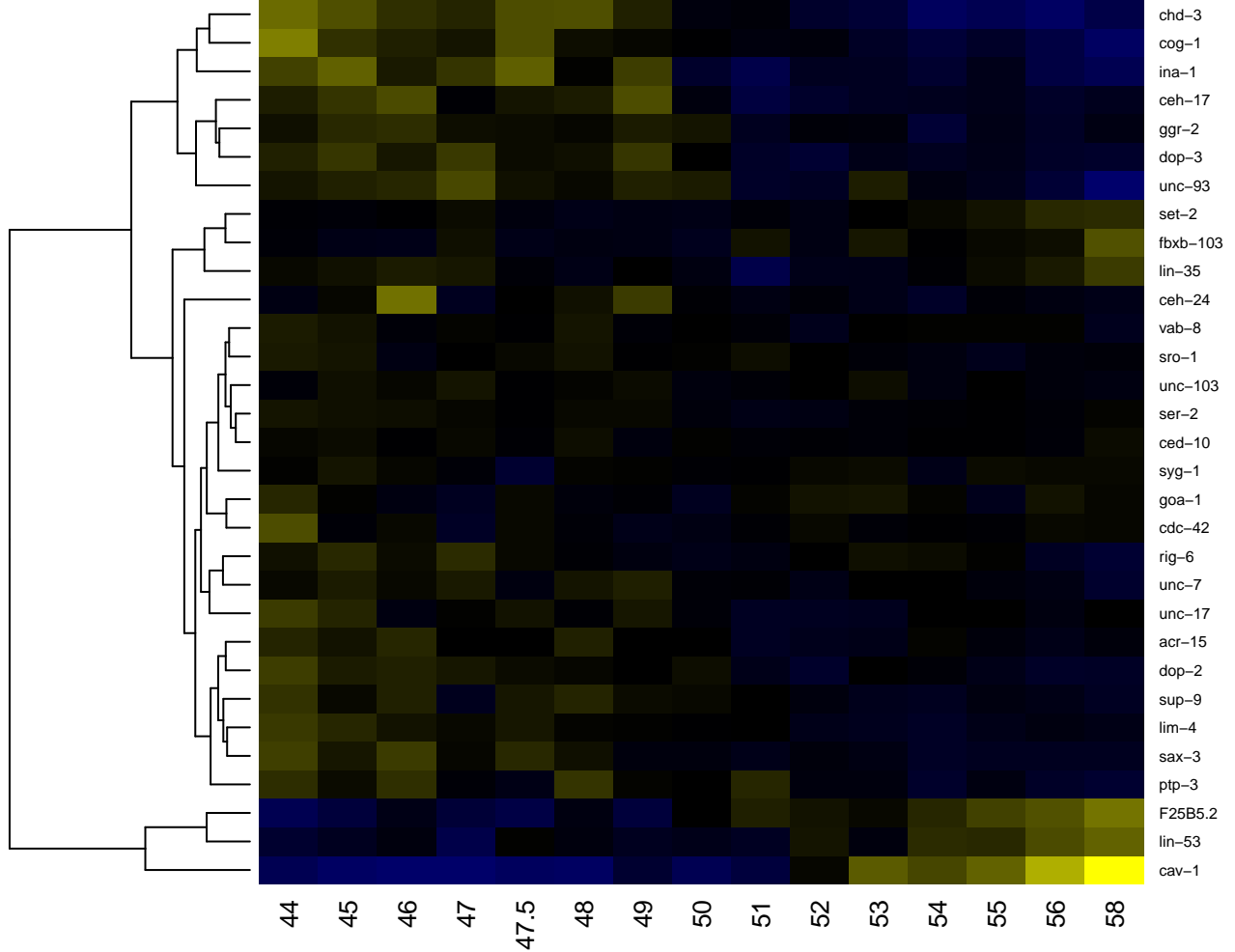
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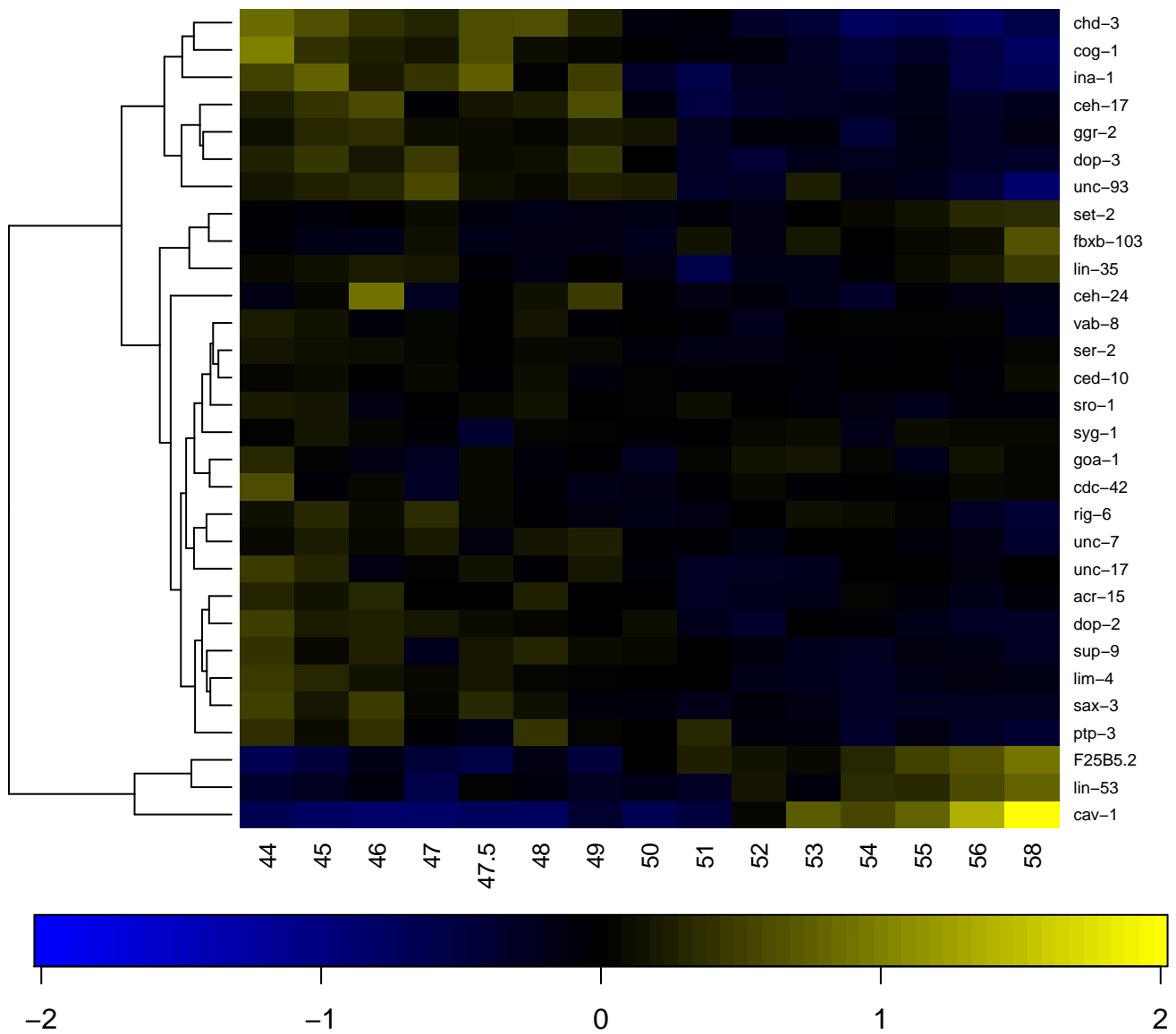
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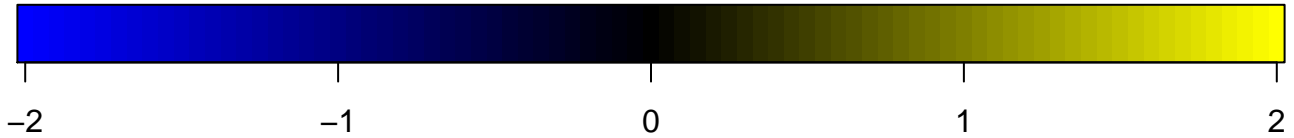
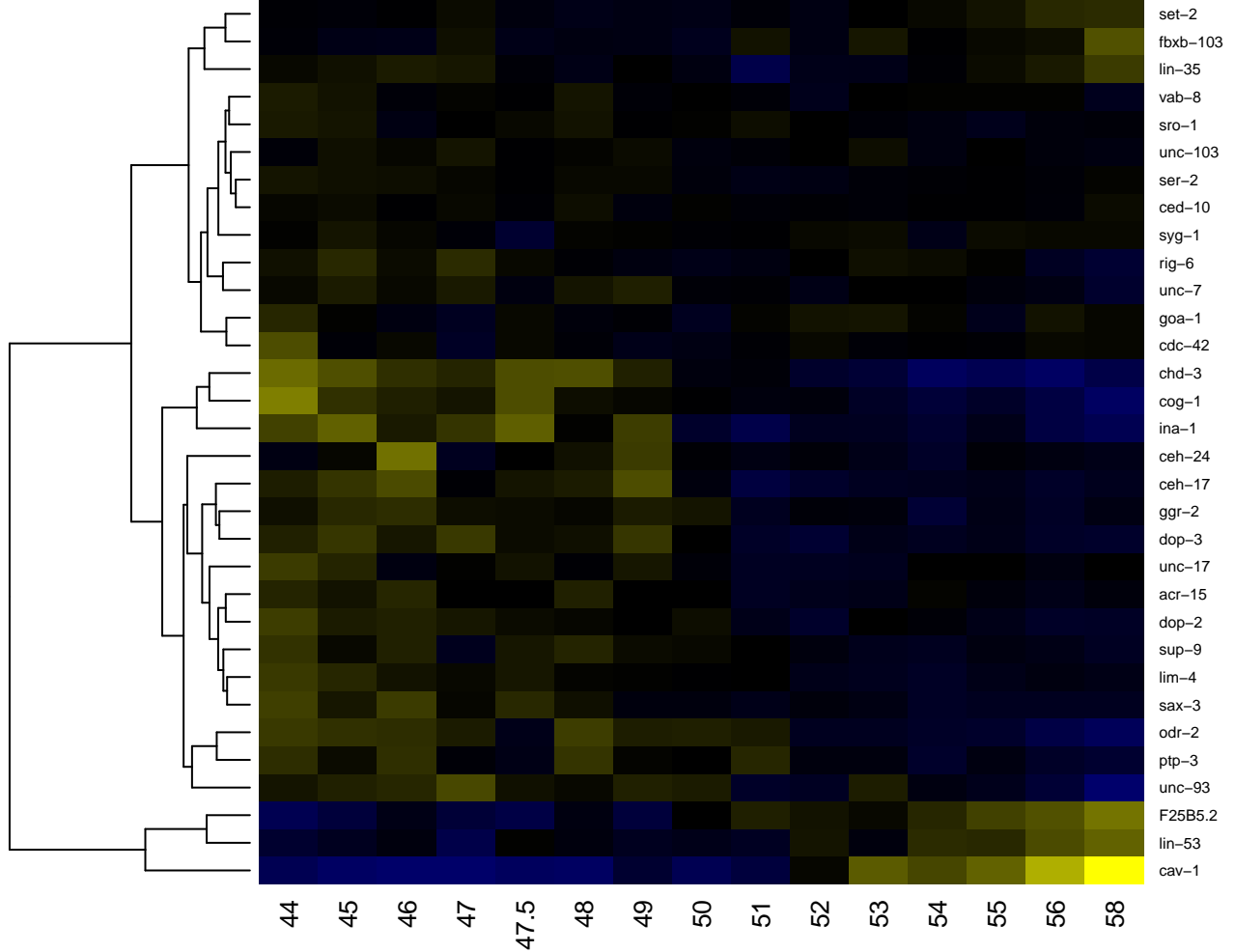
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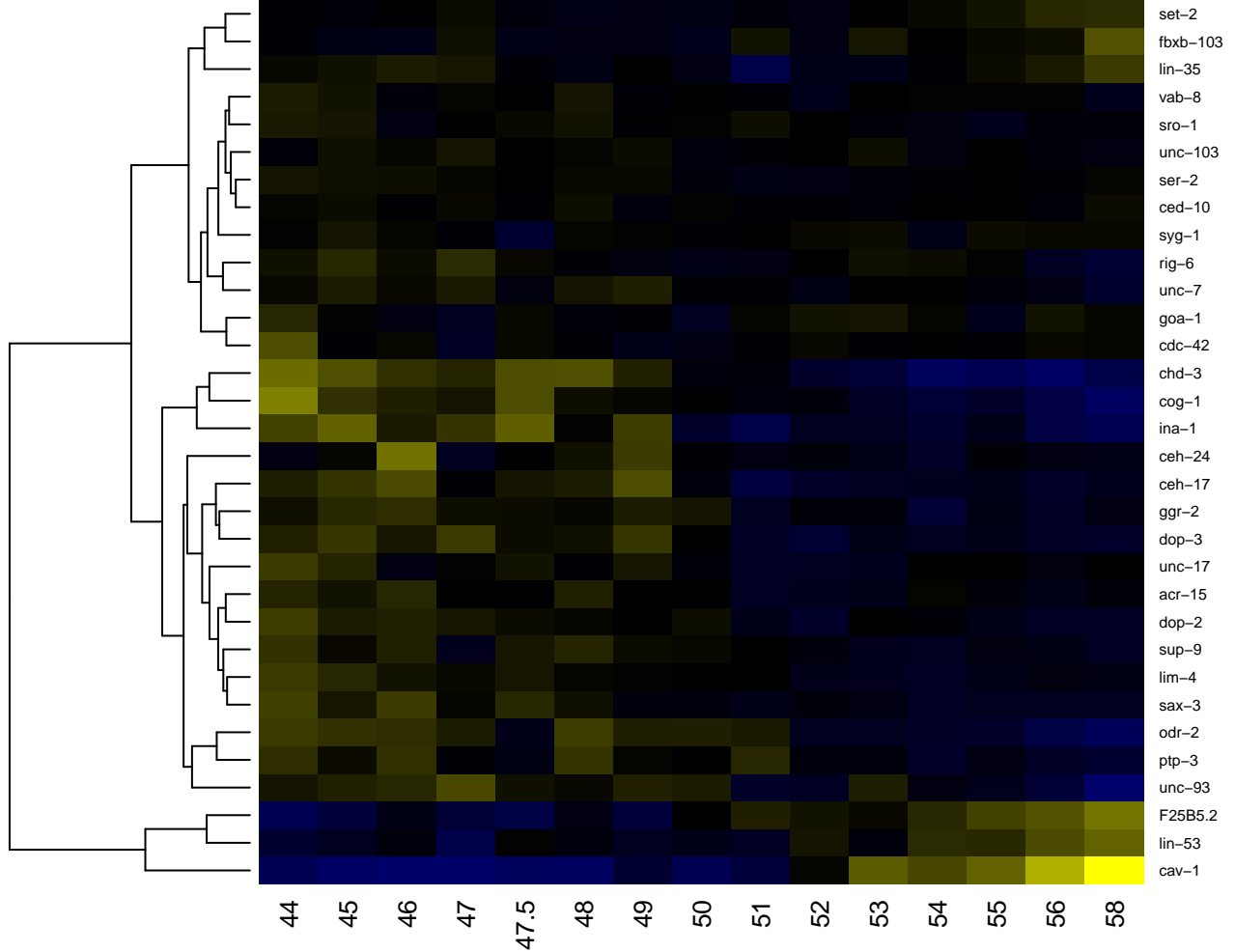
SIADR



SI AVL



SIAVR



-2

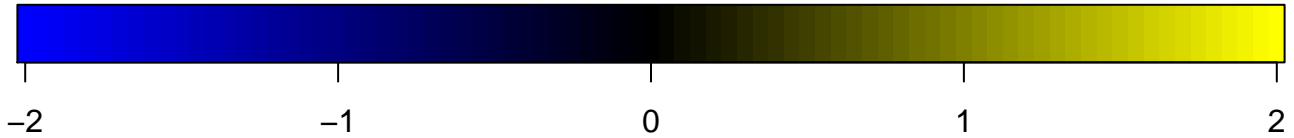
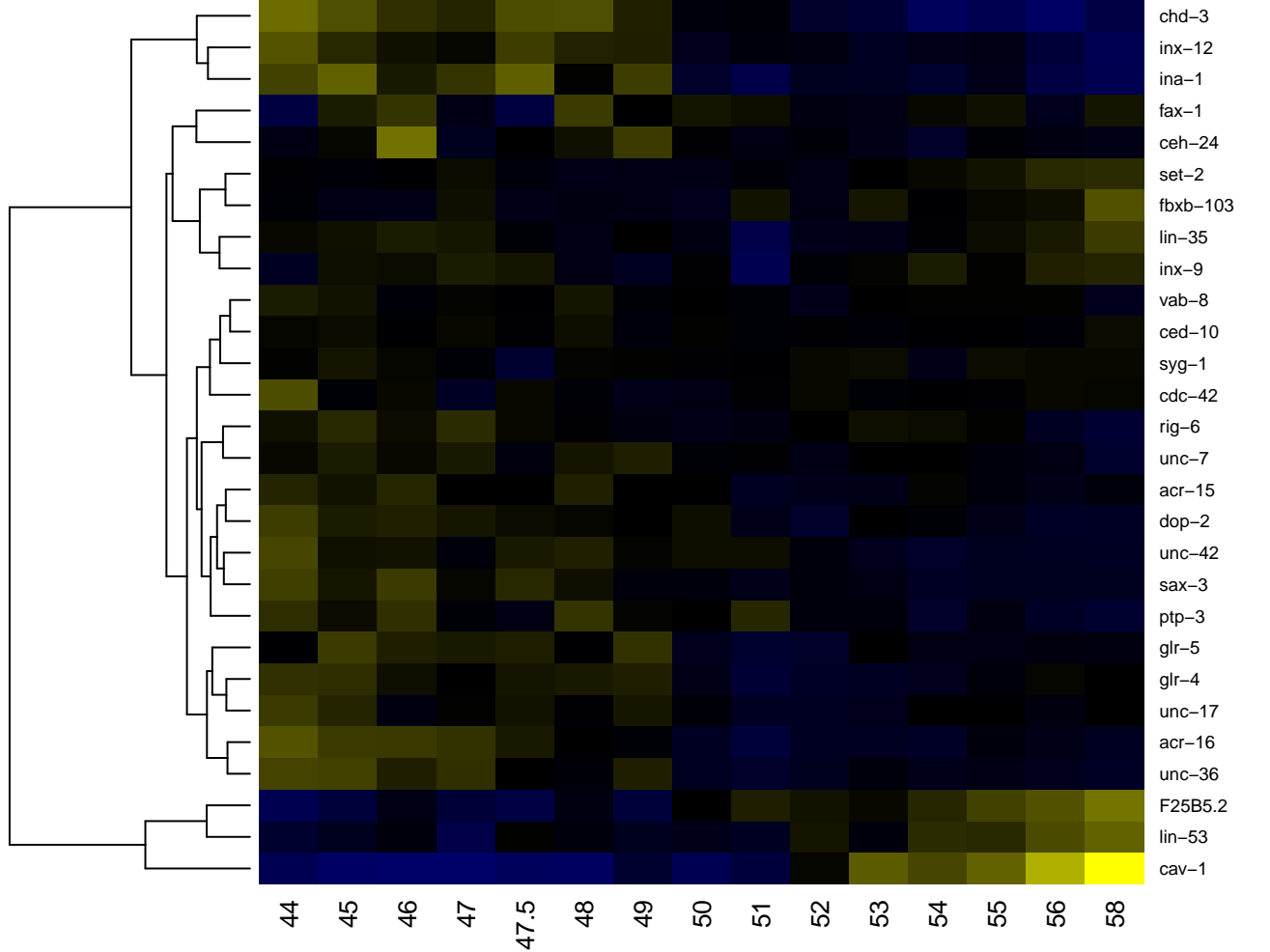
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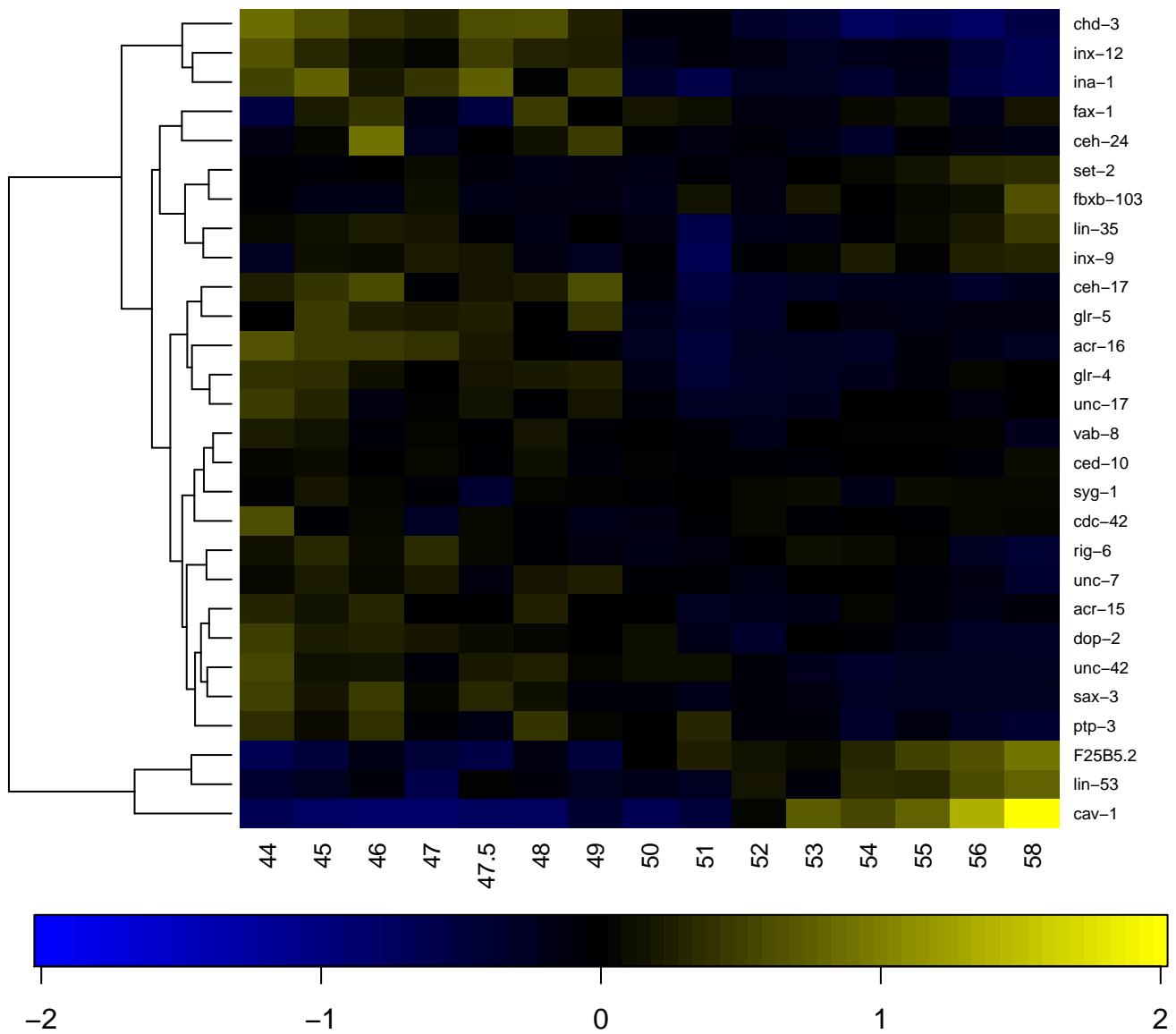
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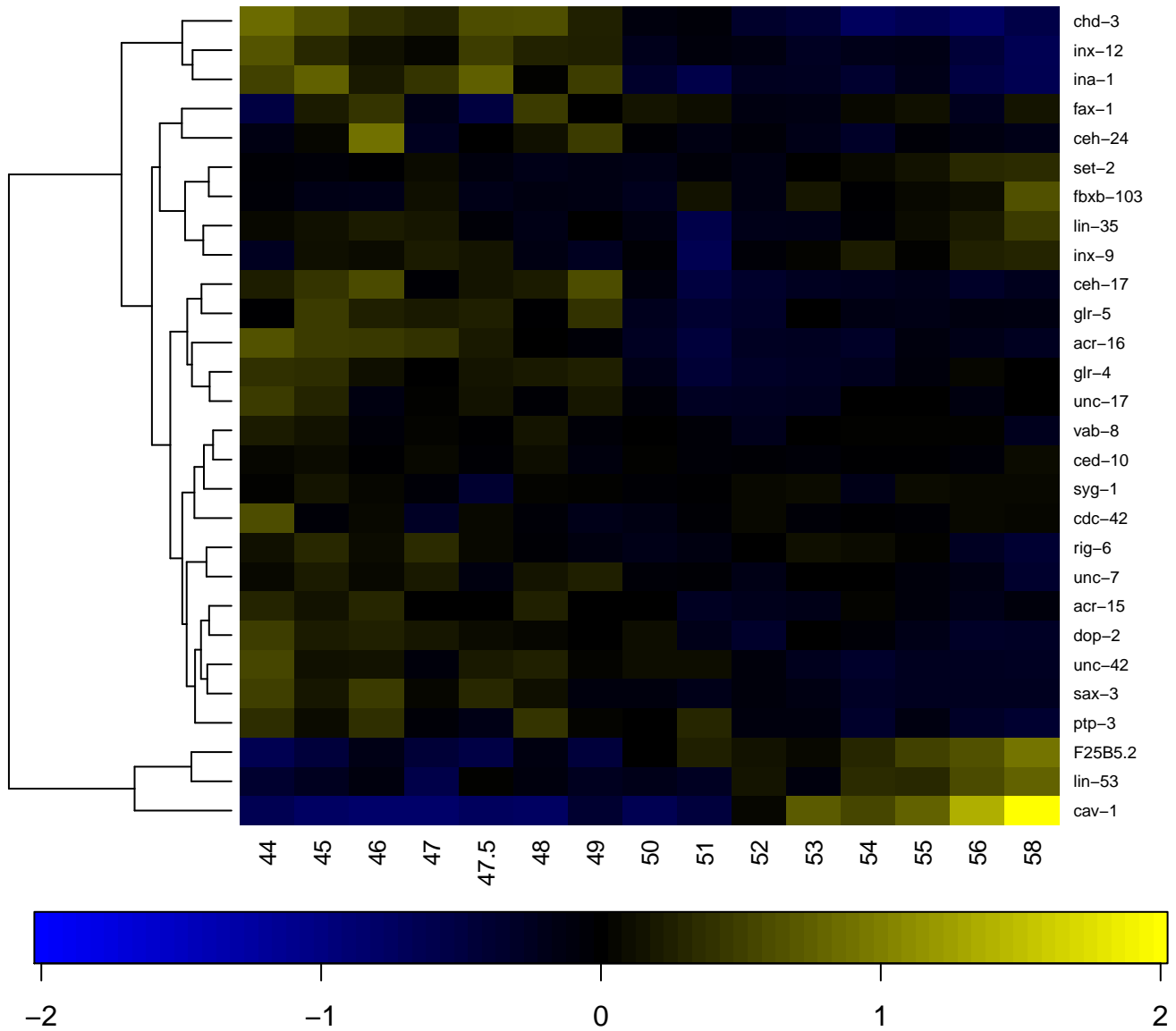
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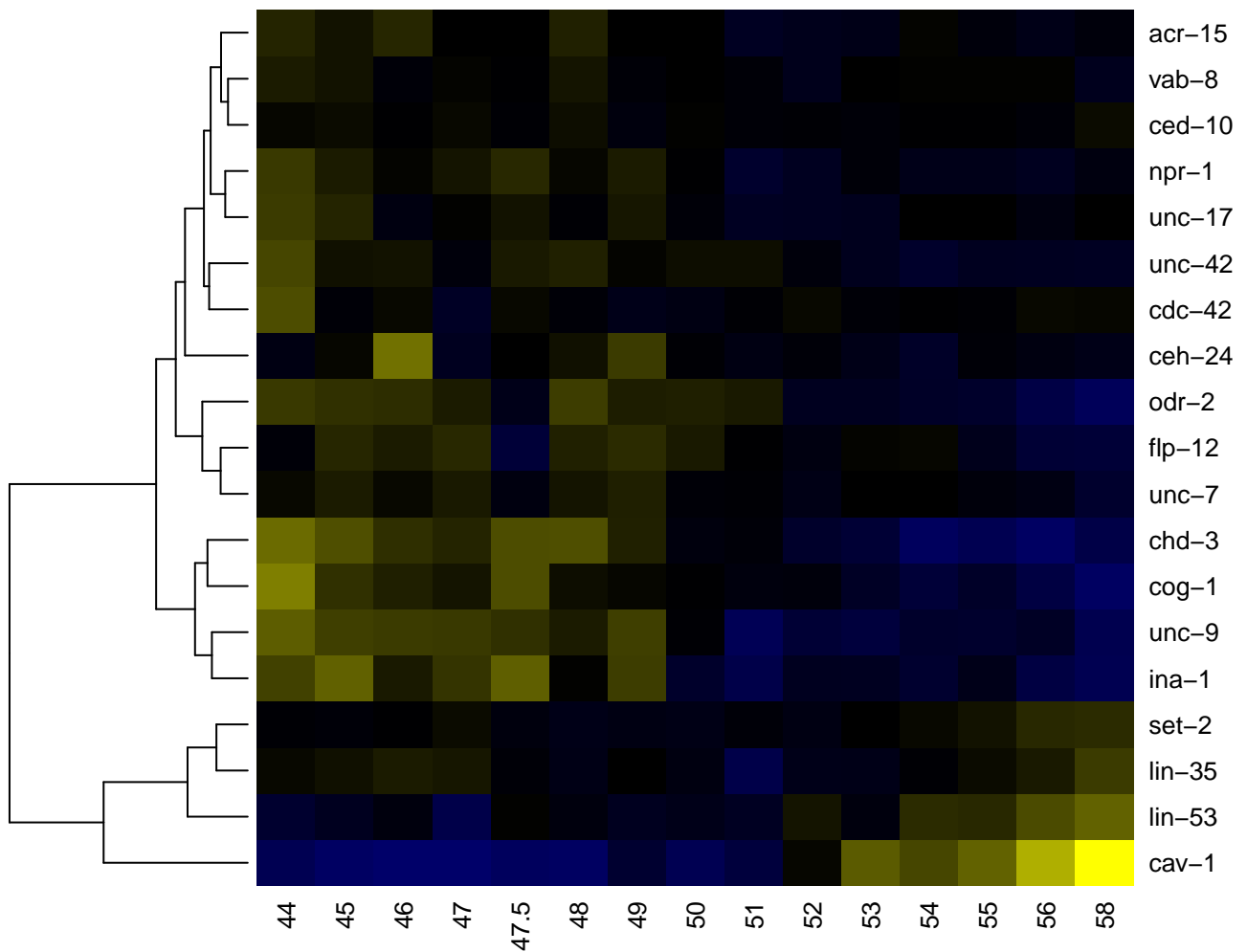
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SIBVR



SMBDL



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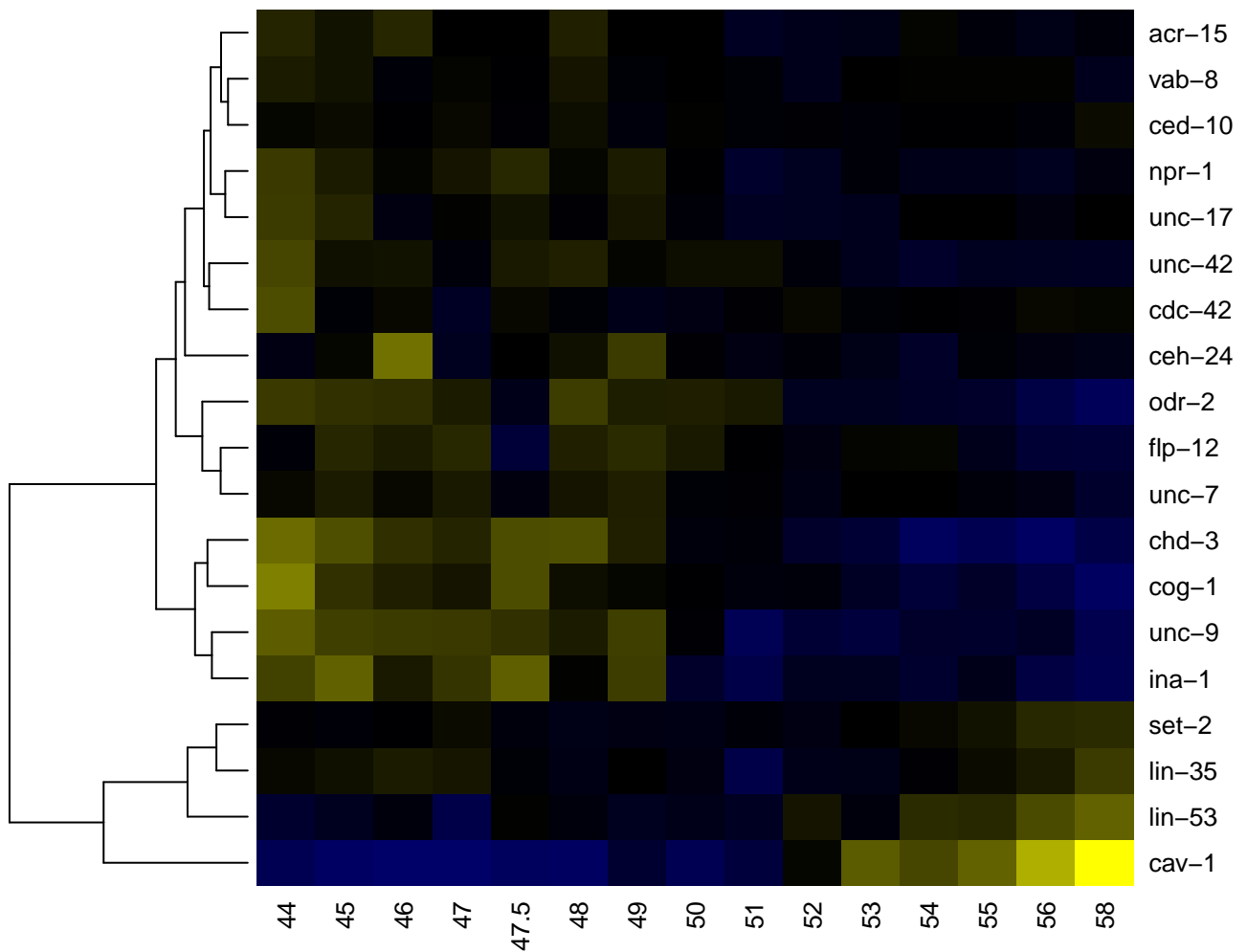
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SMBDR



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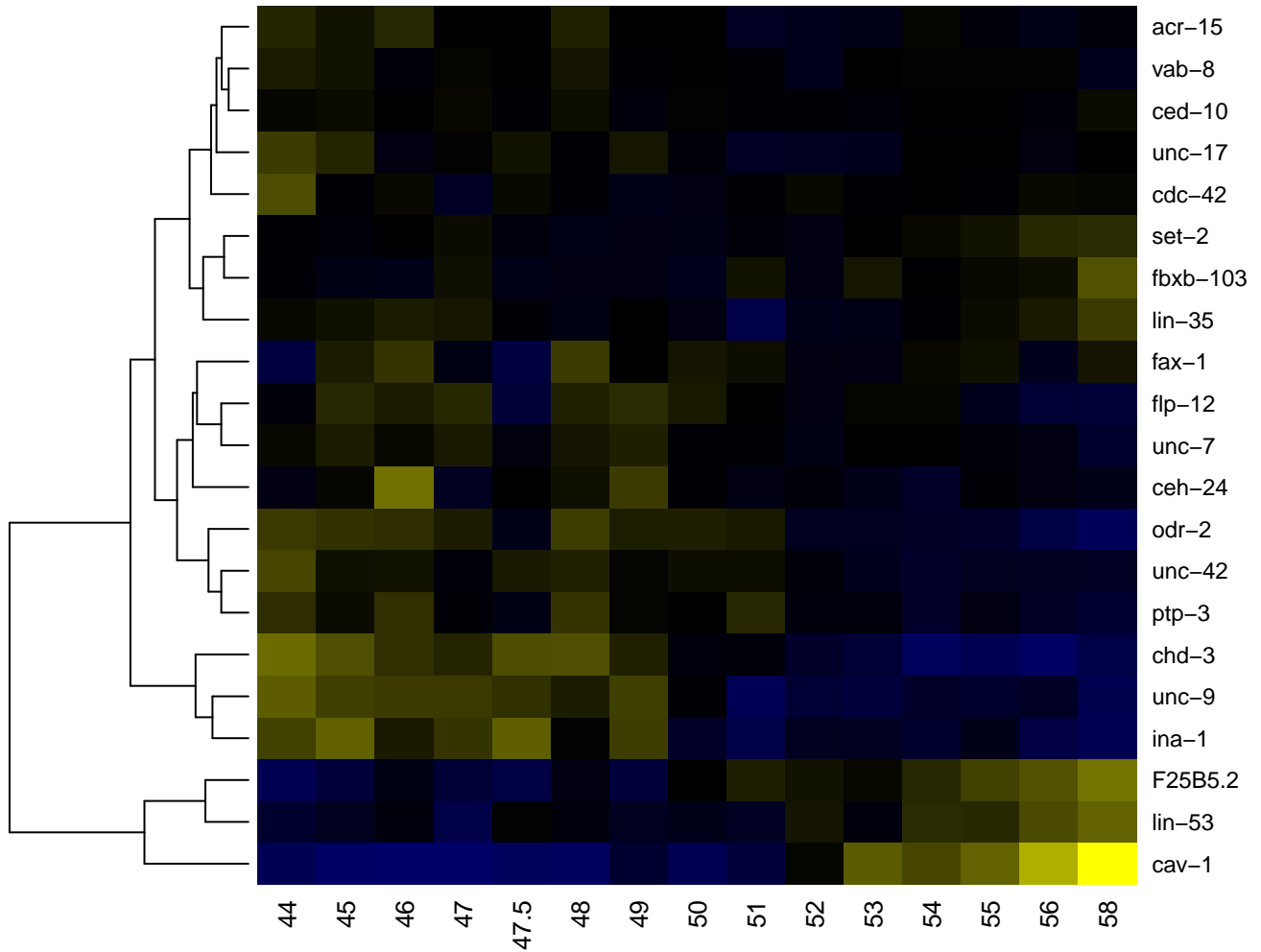
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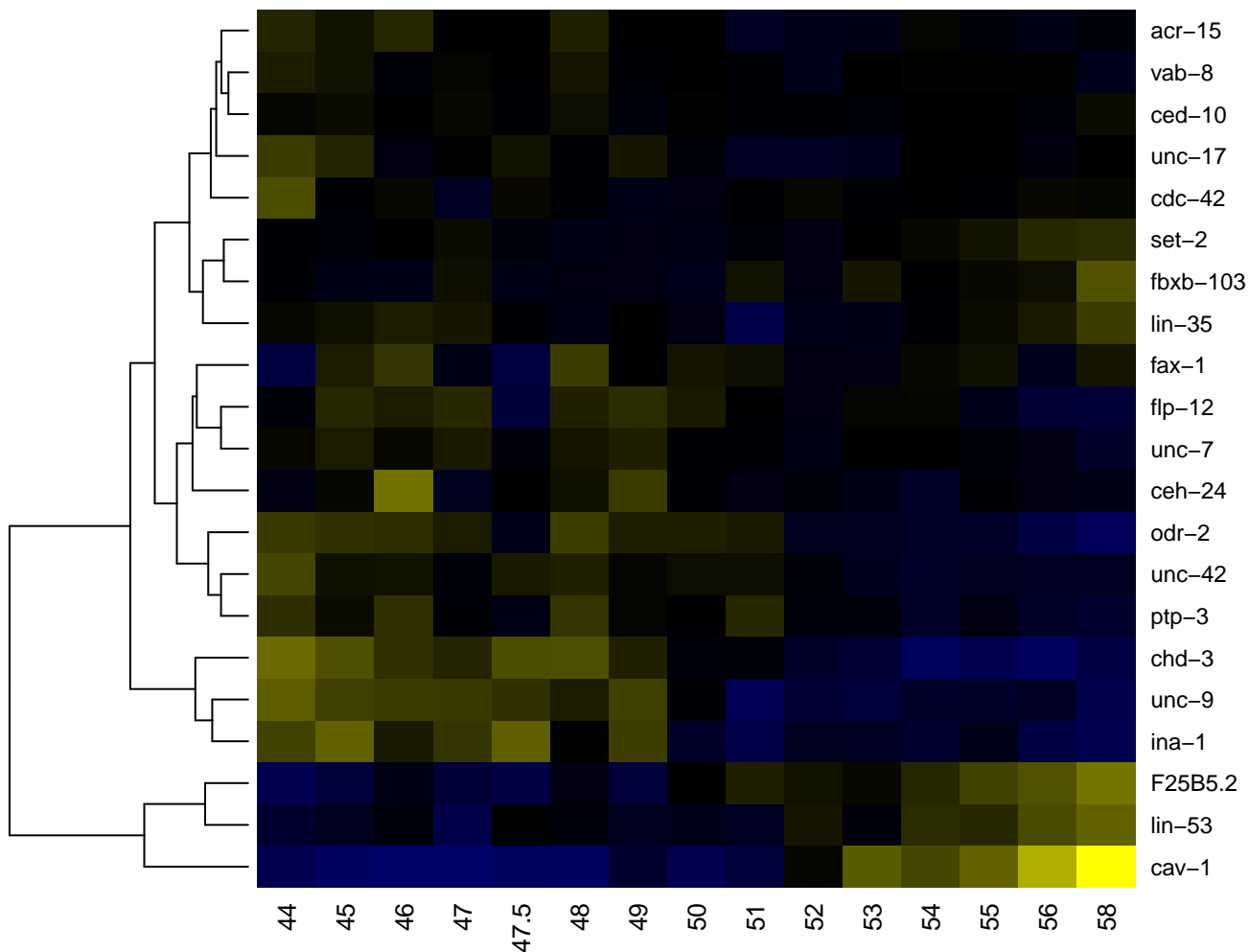
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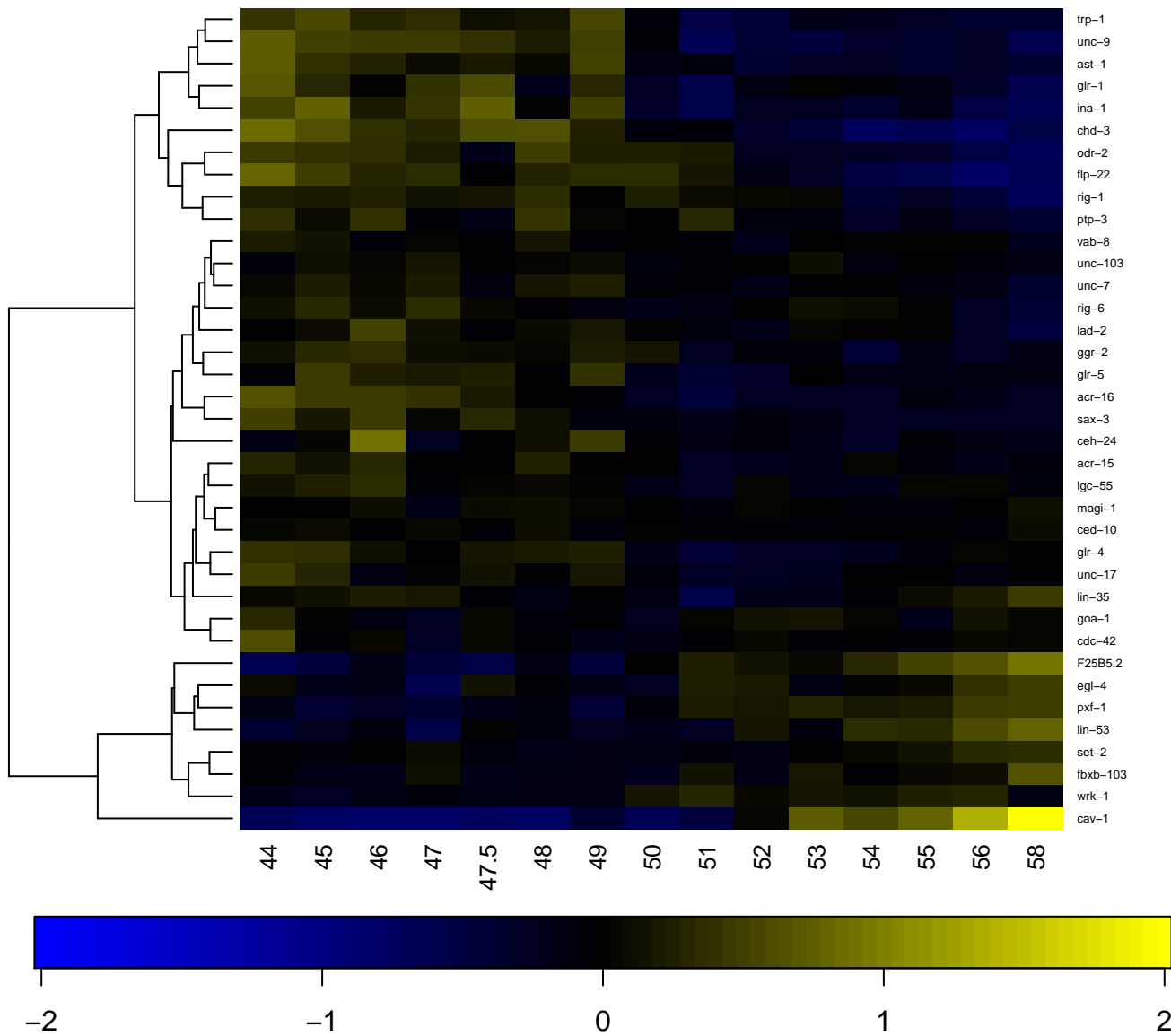
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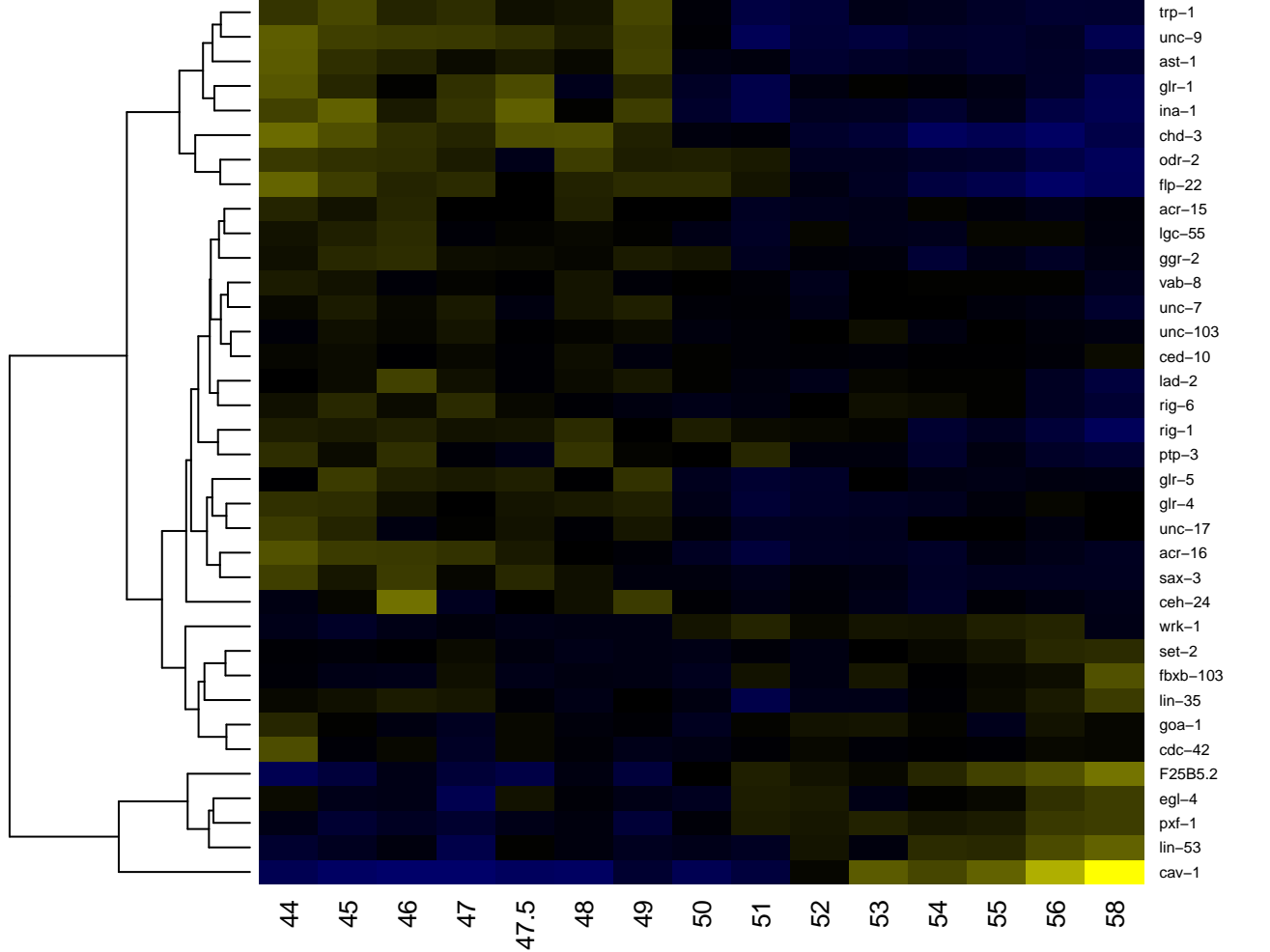
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SMDDL



SMDDR



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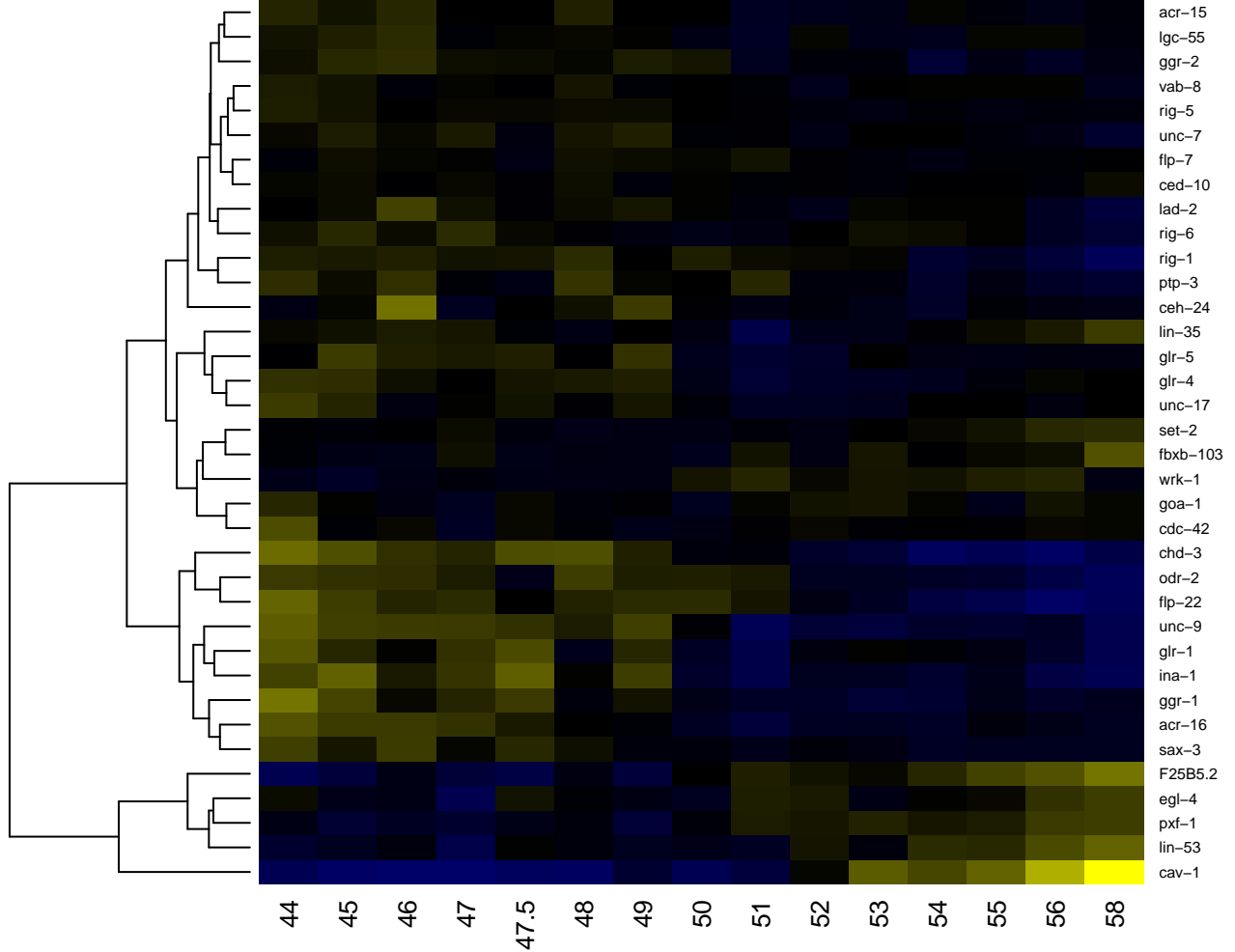
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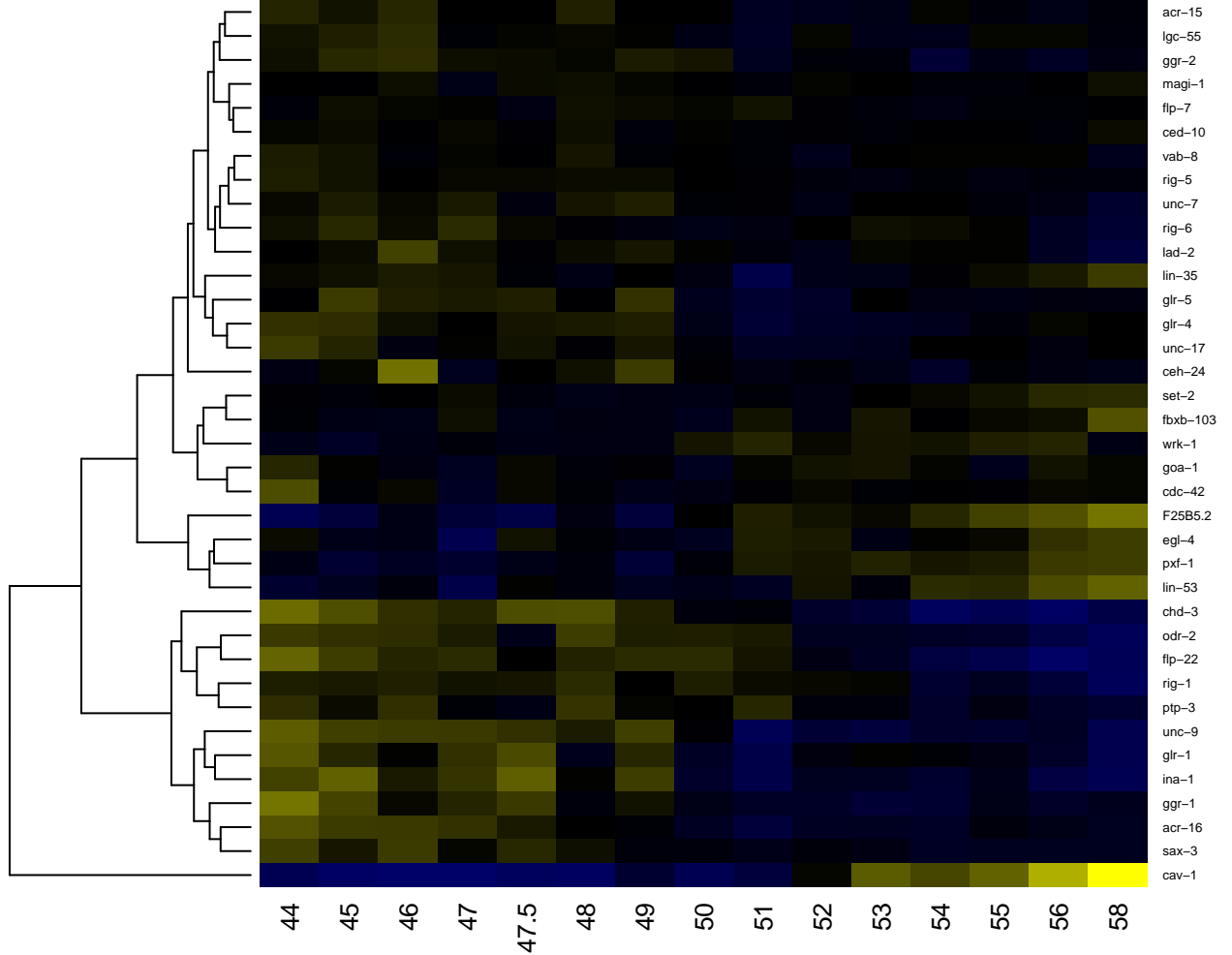
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SMDVL



SMDVR



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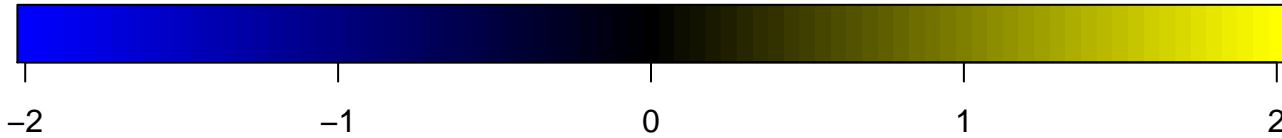
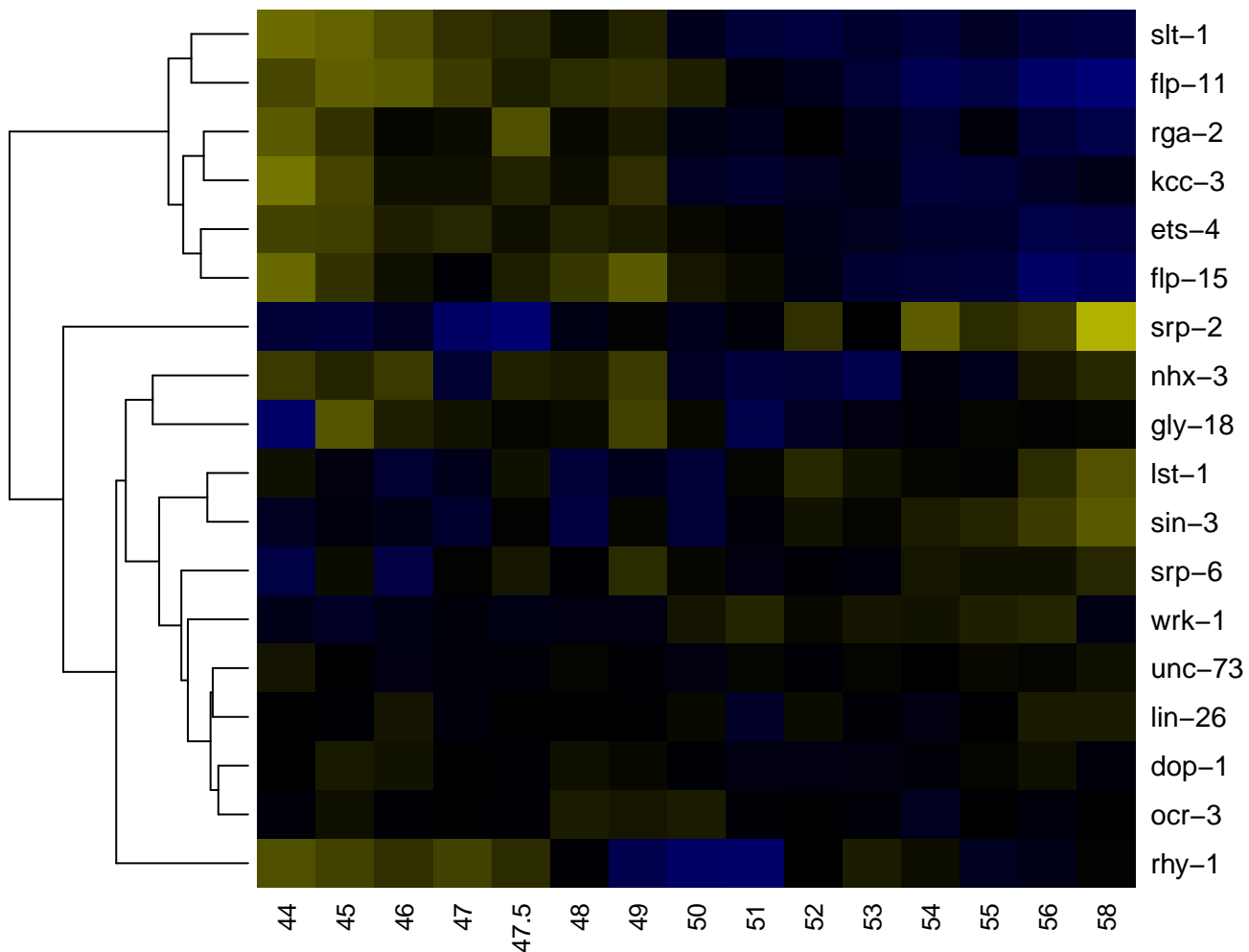
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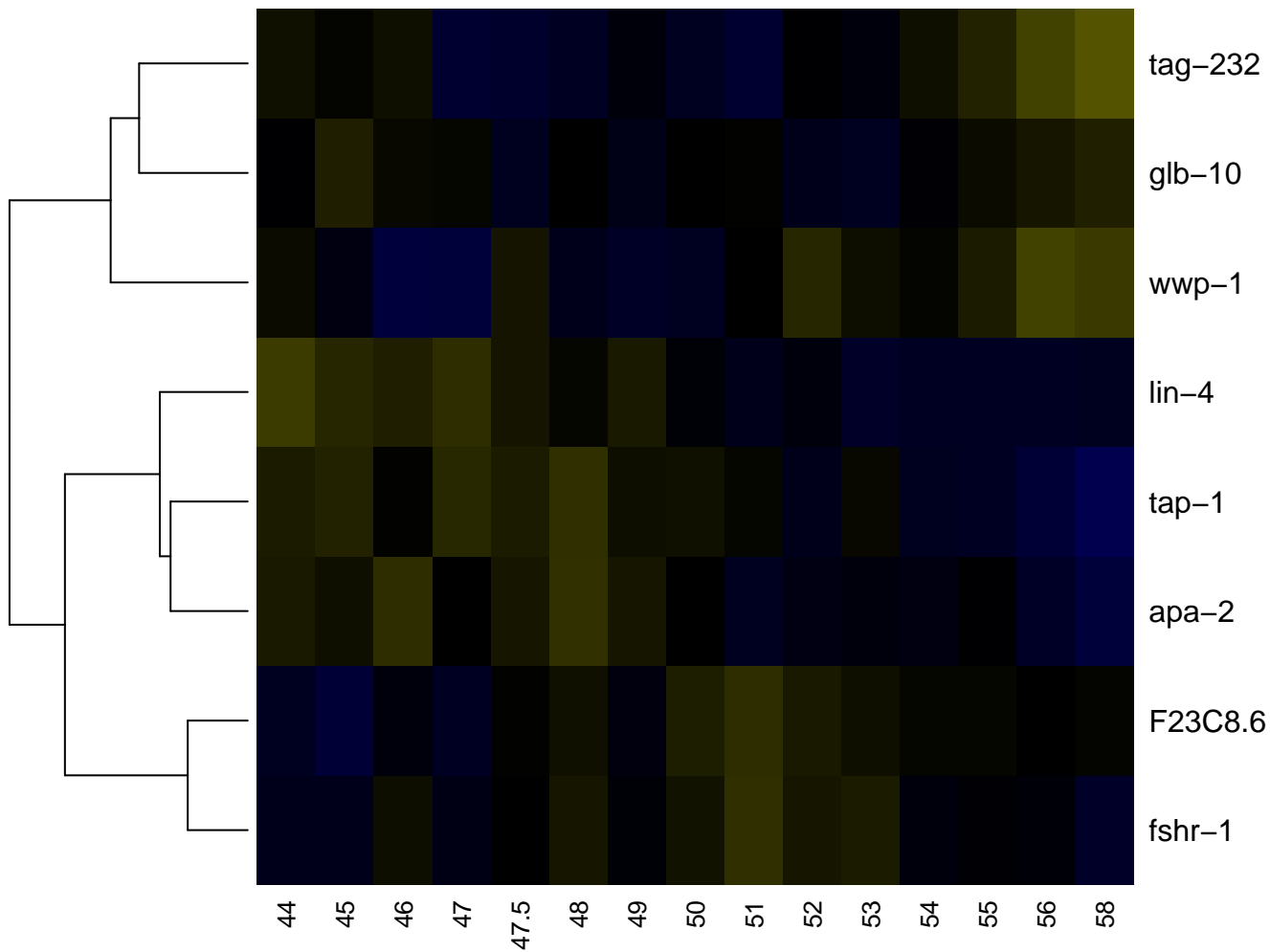
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socket cell



somatic neuron



-2

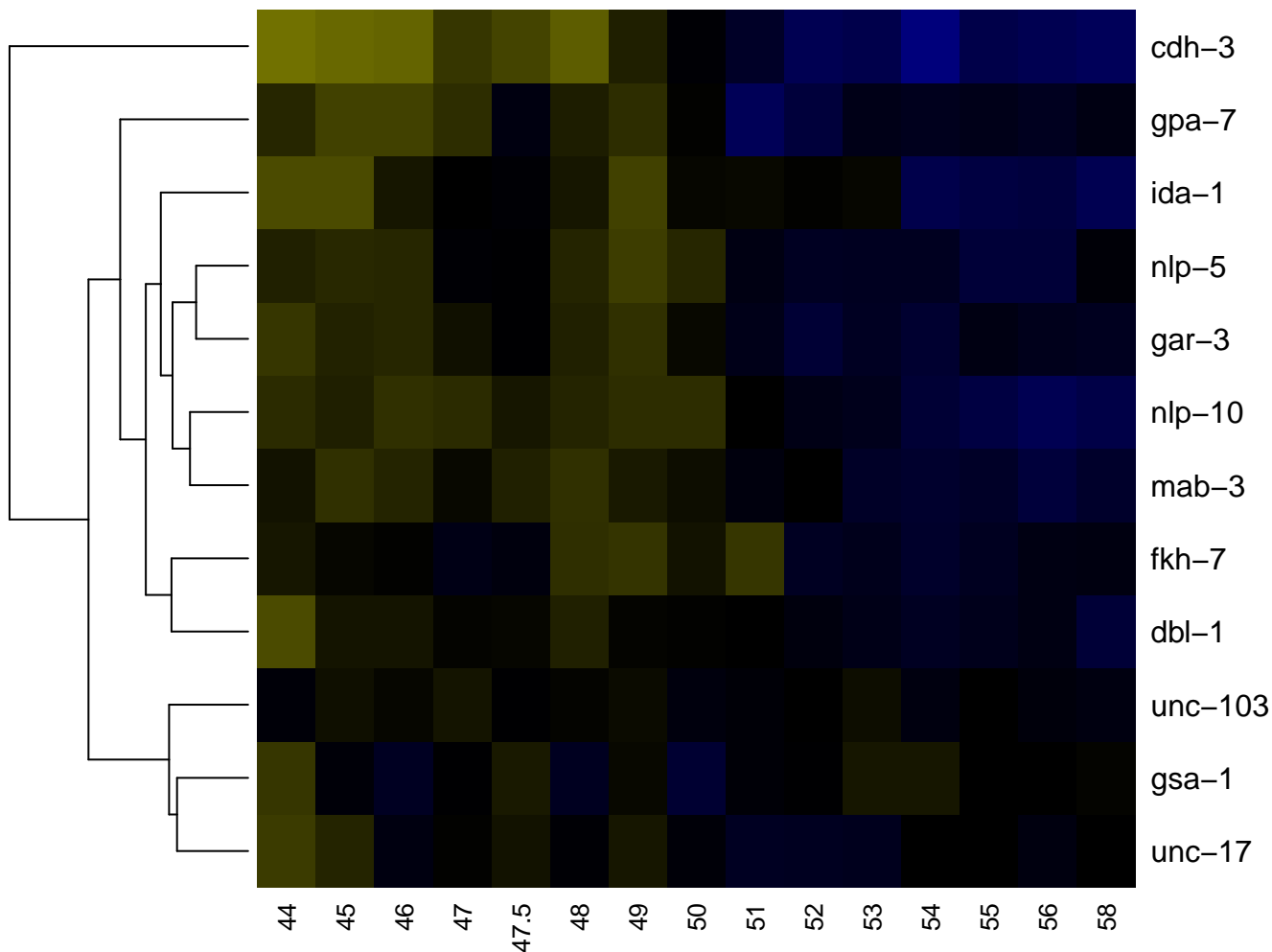
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SPCL



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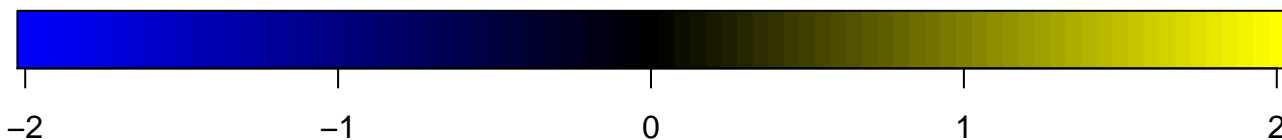
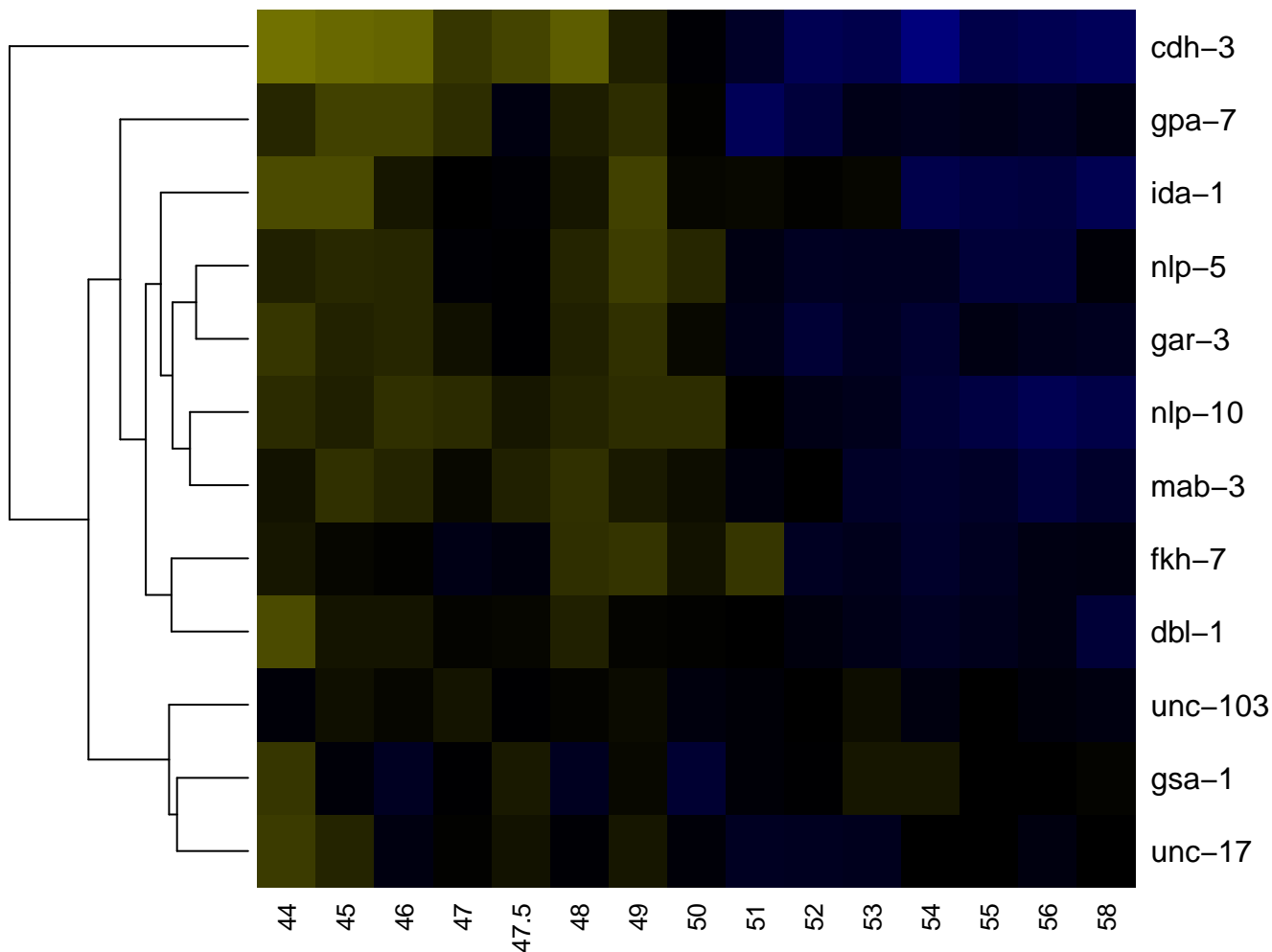
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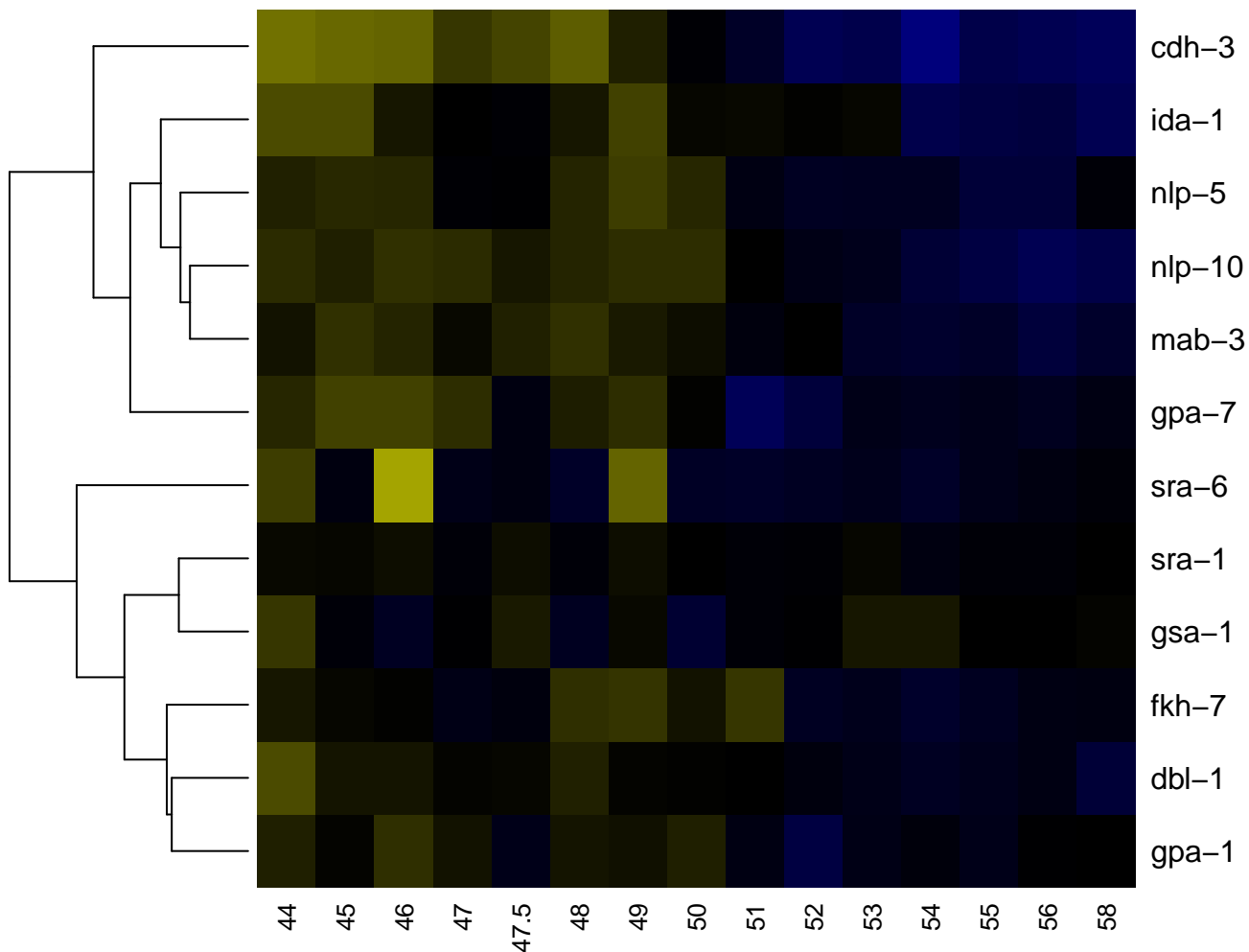
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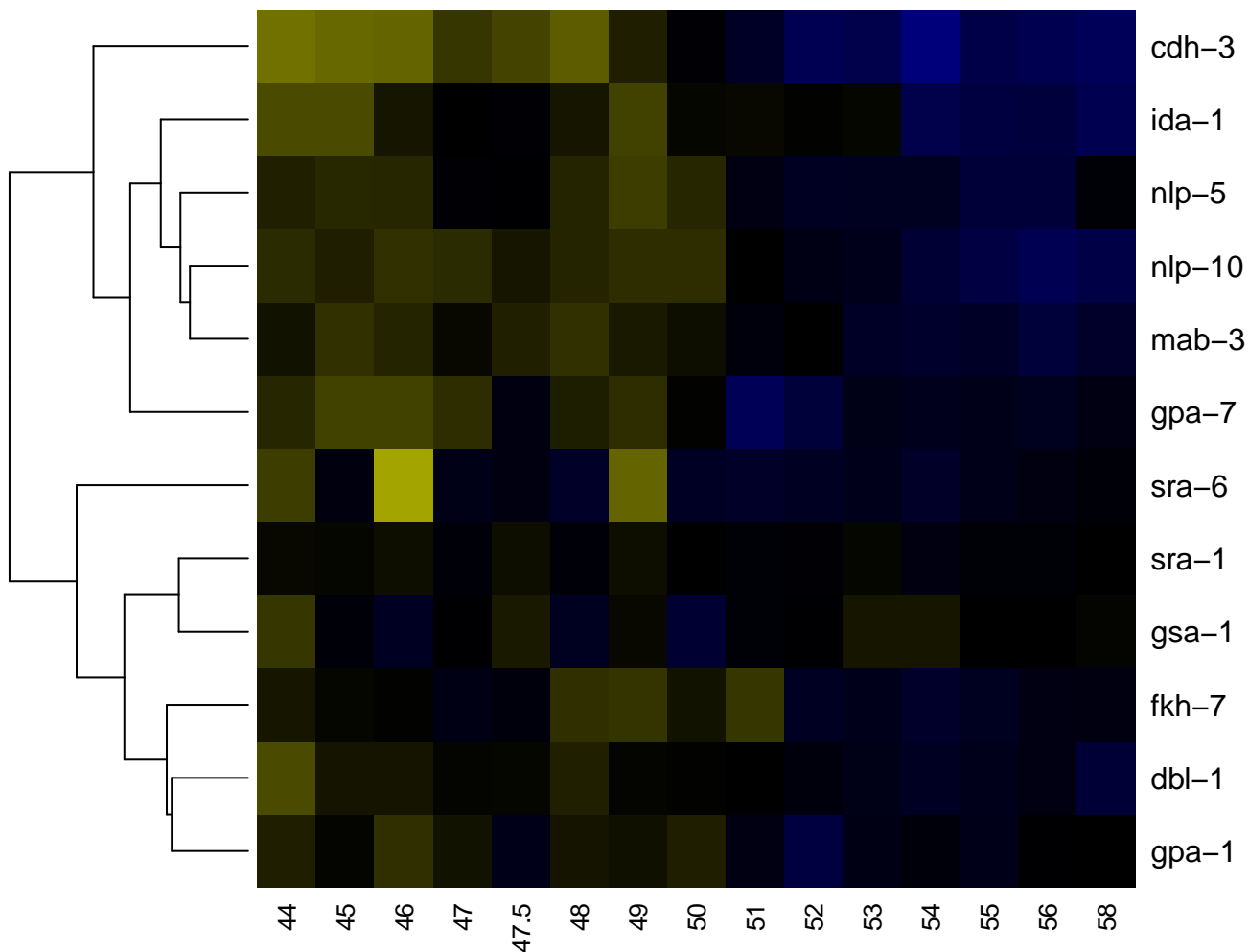
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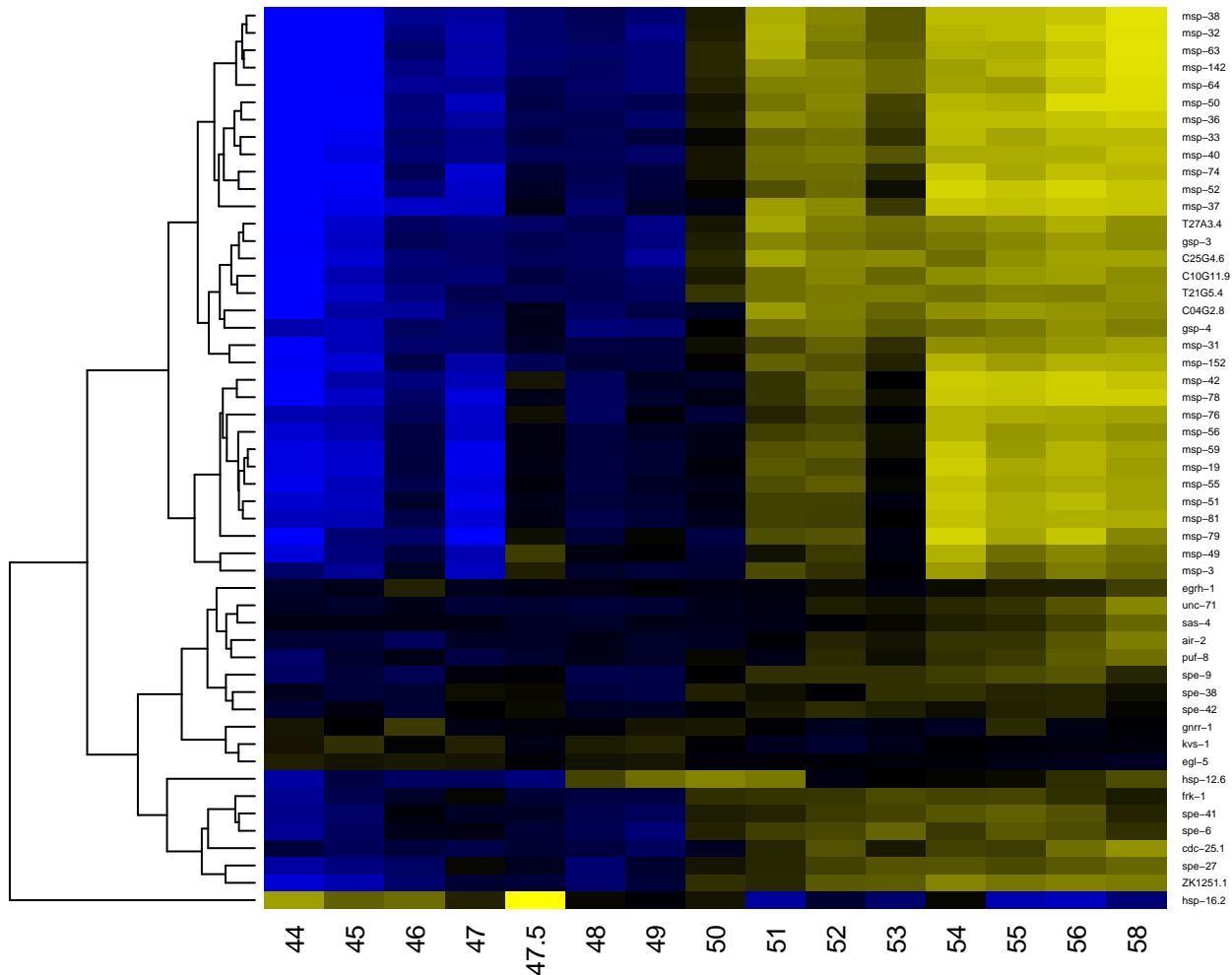
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SPDR



sperm



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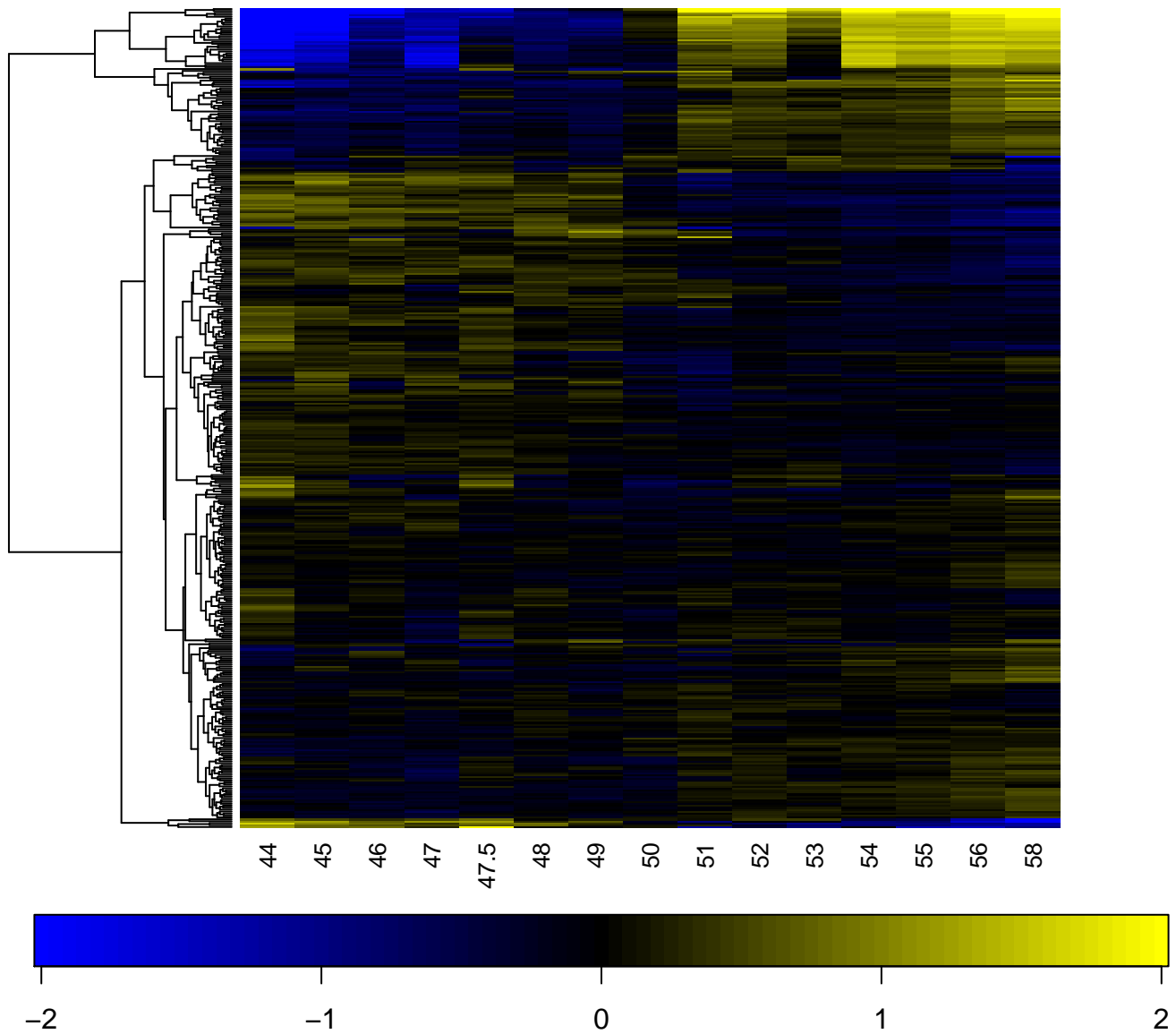
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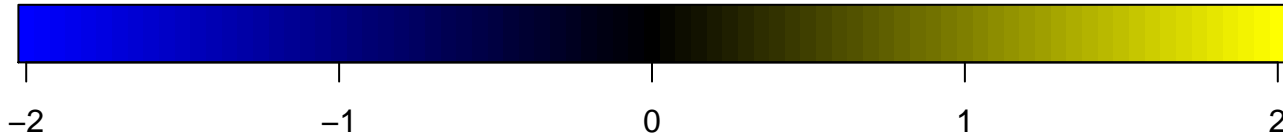
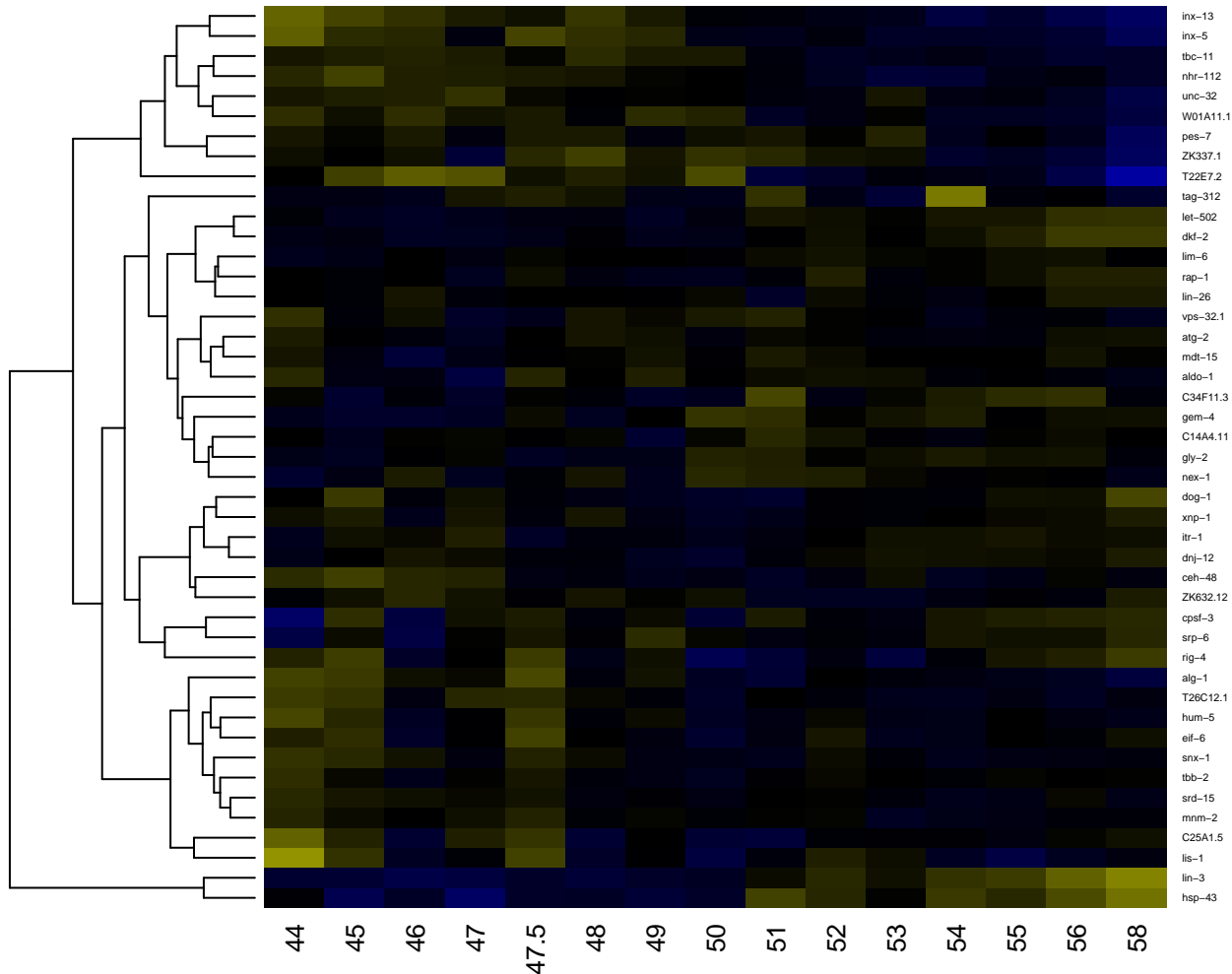
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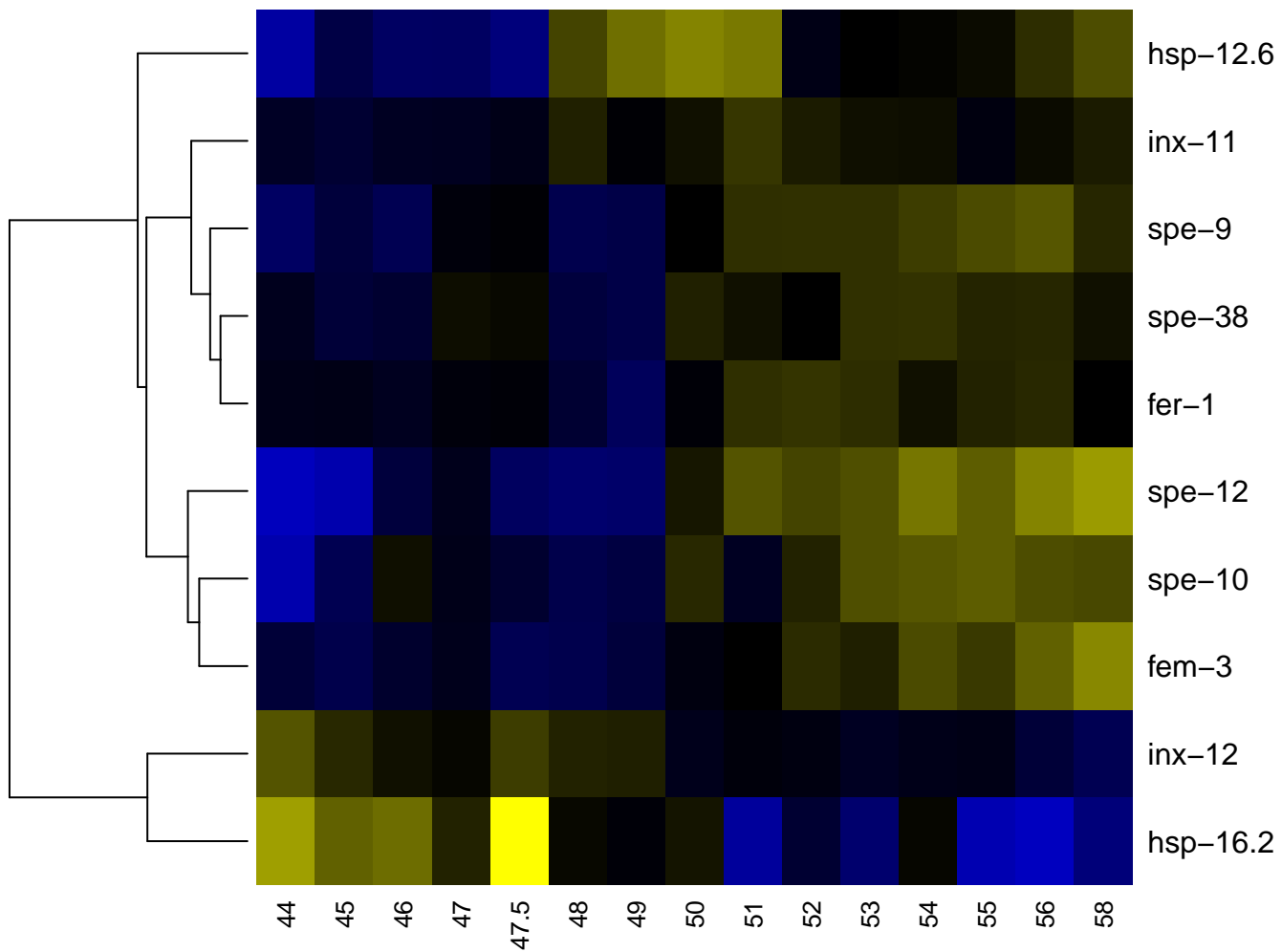
spermatheca



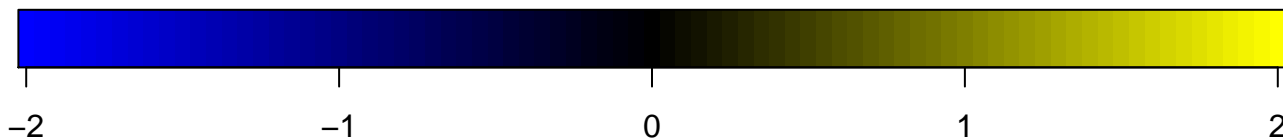
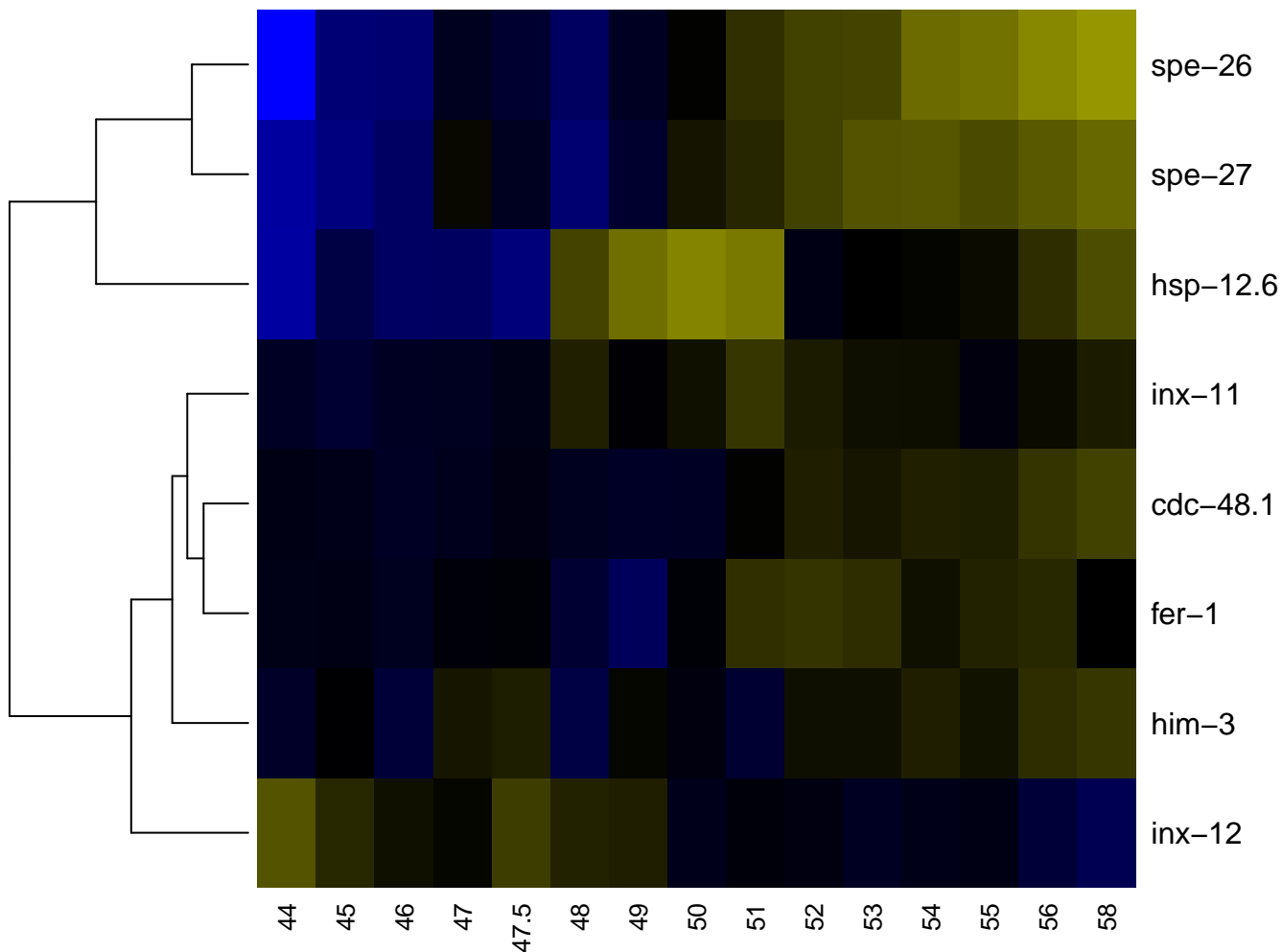
spermathecal-uterine junction



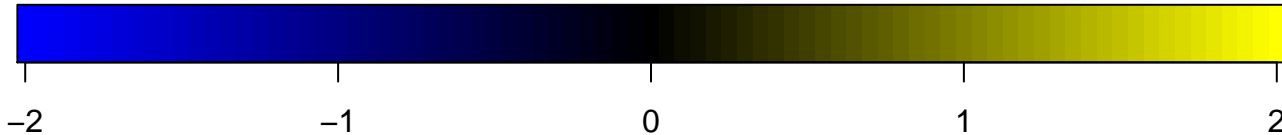
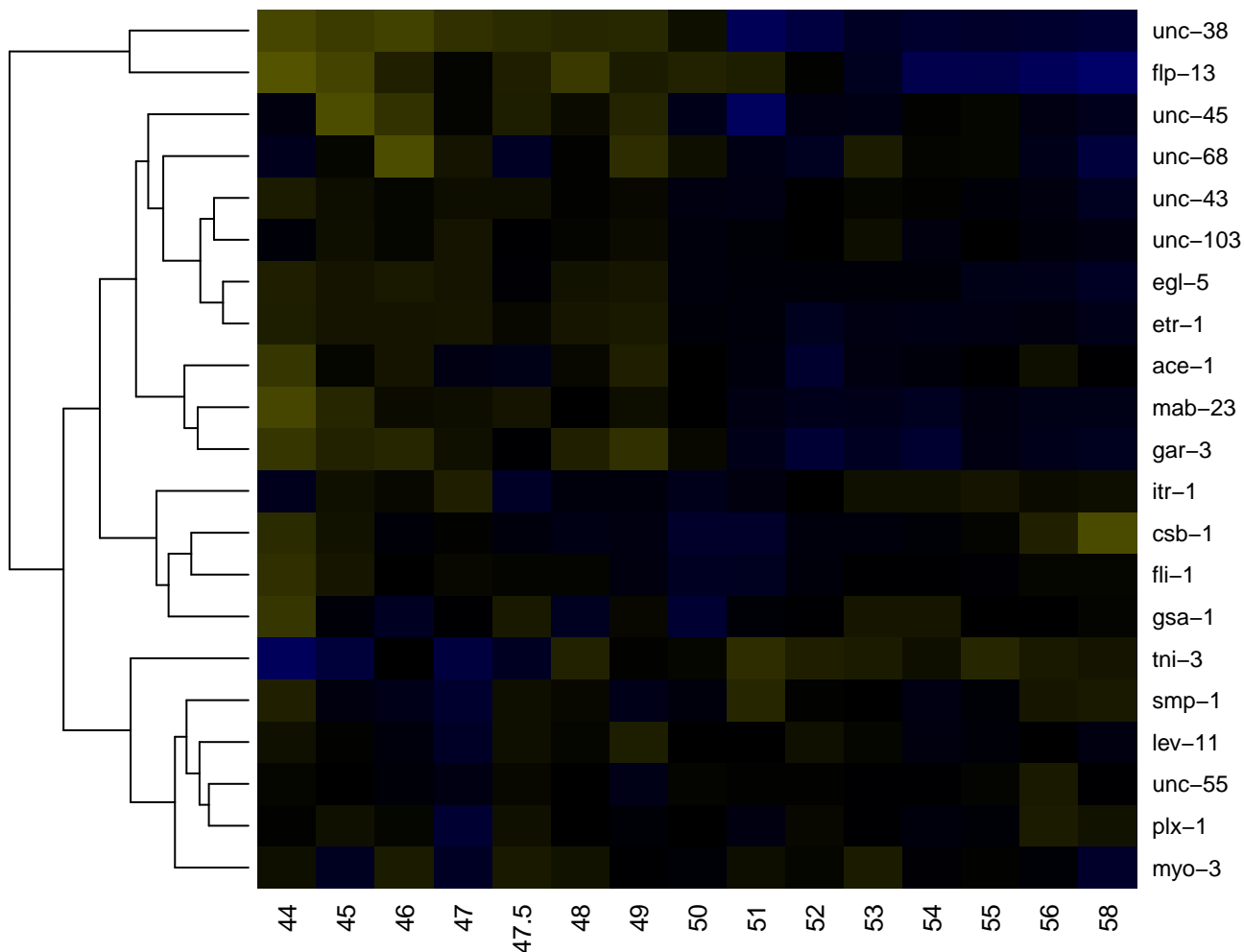
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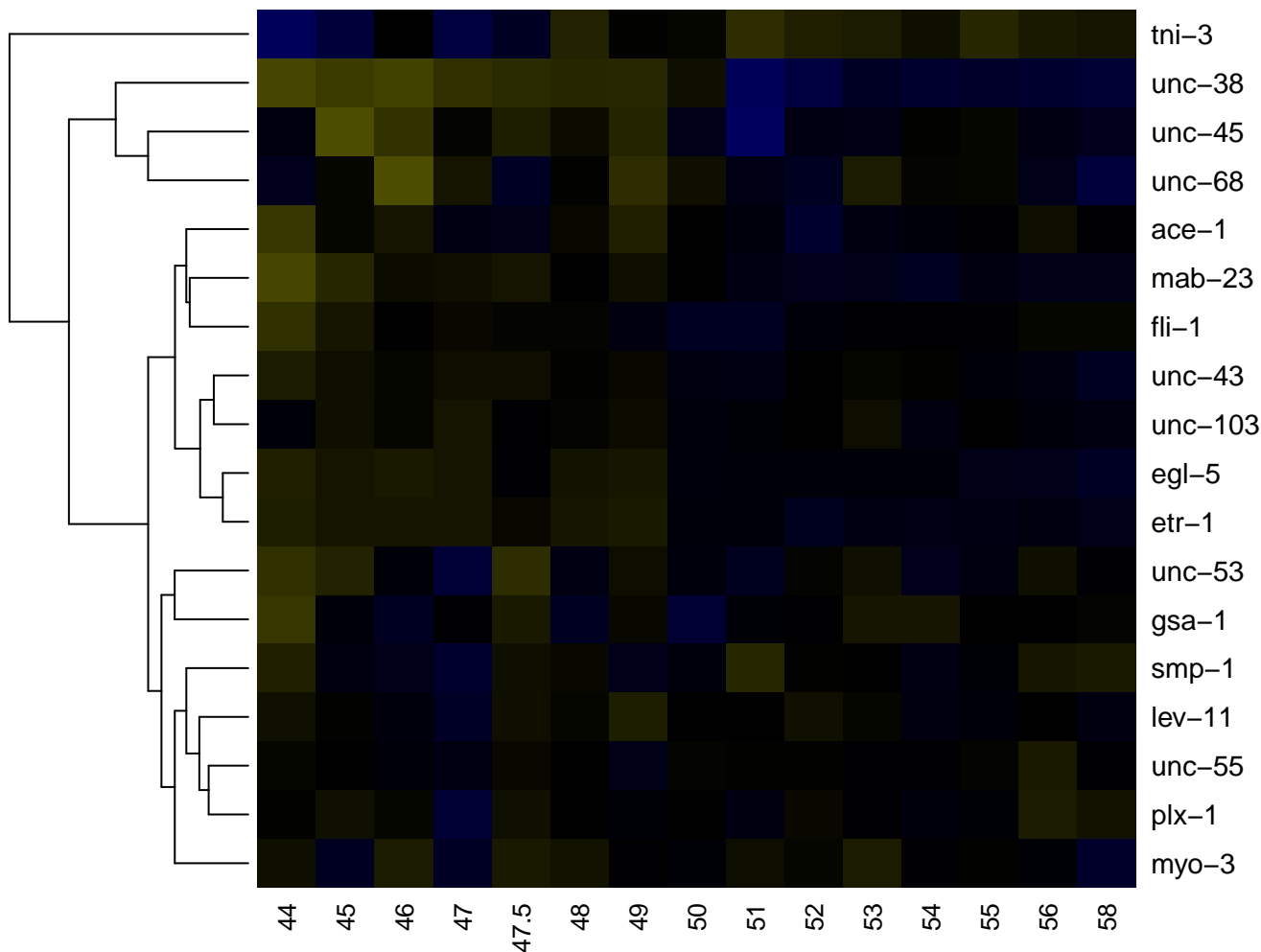
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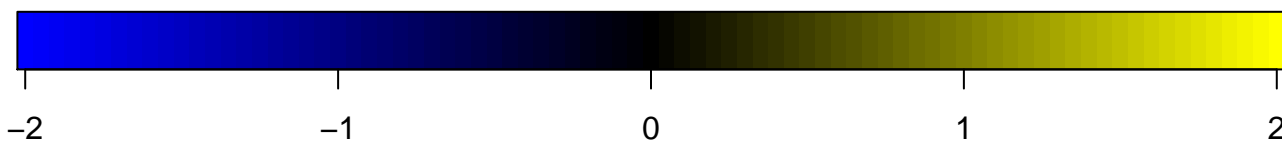
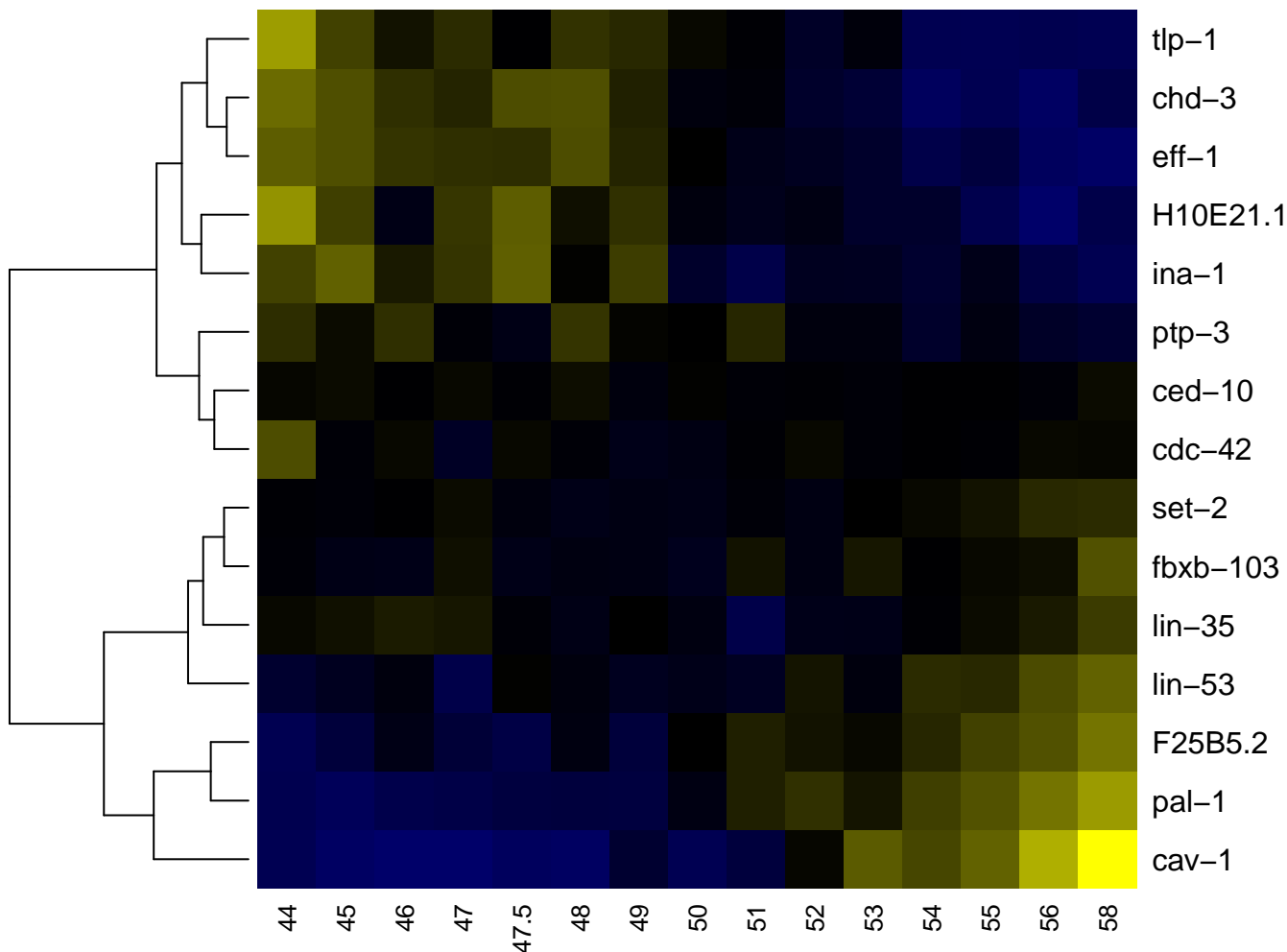
spicule protractor muscle



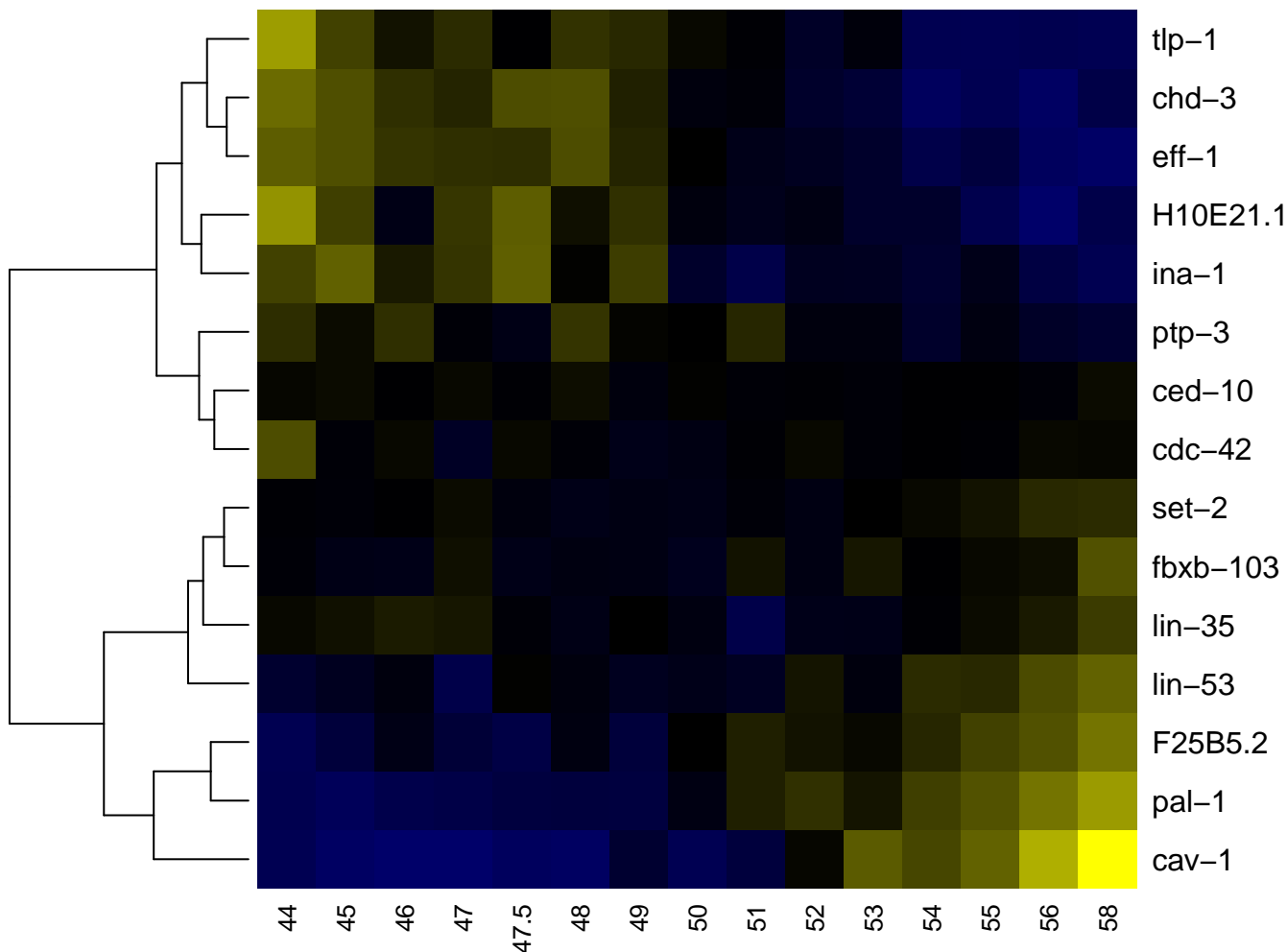
spicule retractor muscle



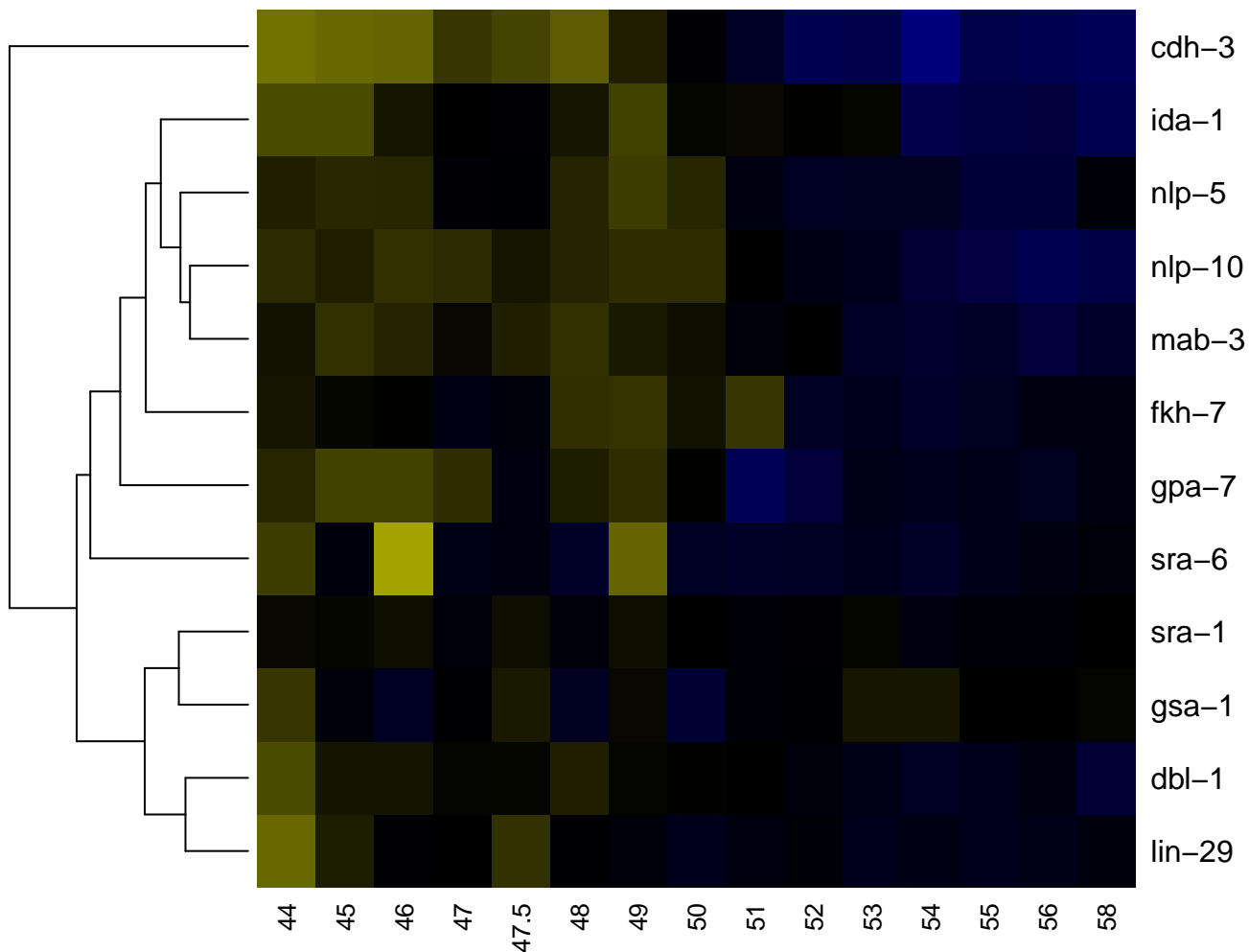
spike precursor left



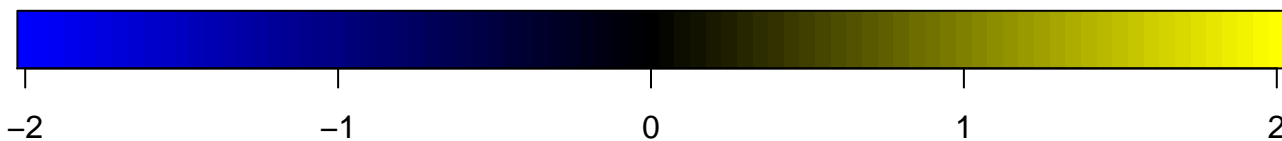
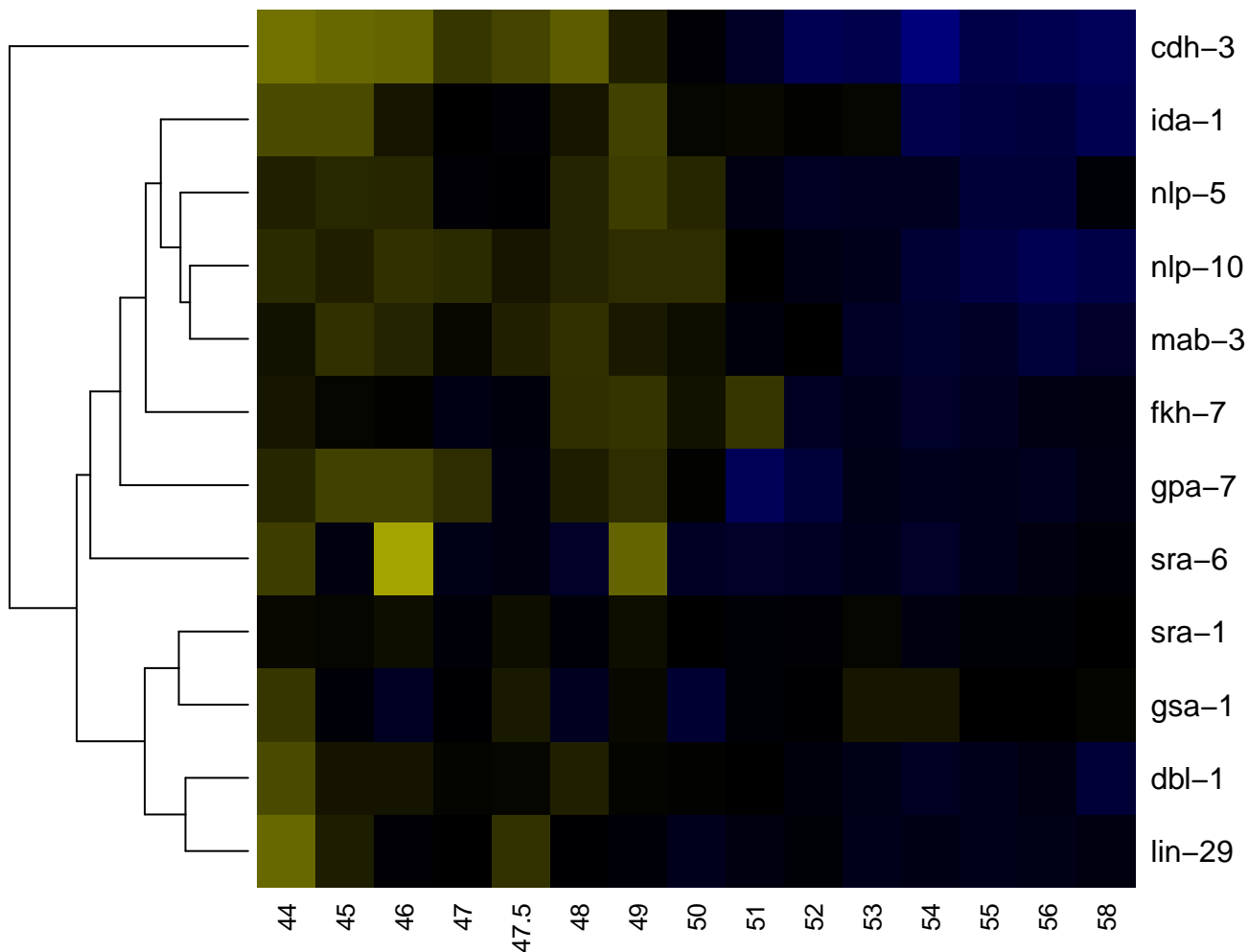
spike precursor right



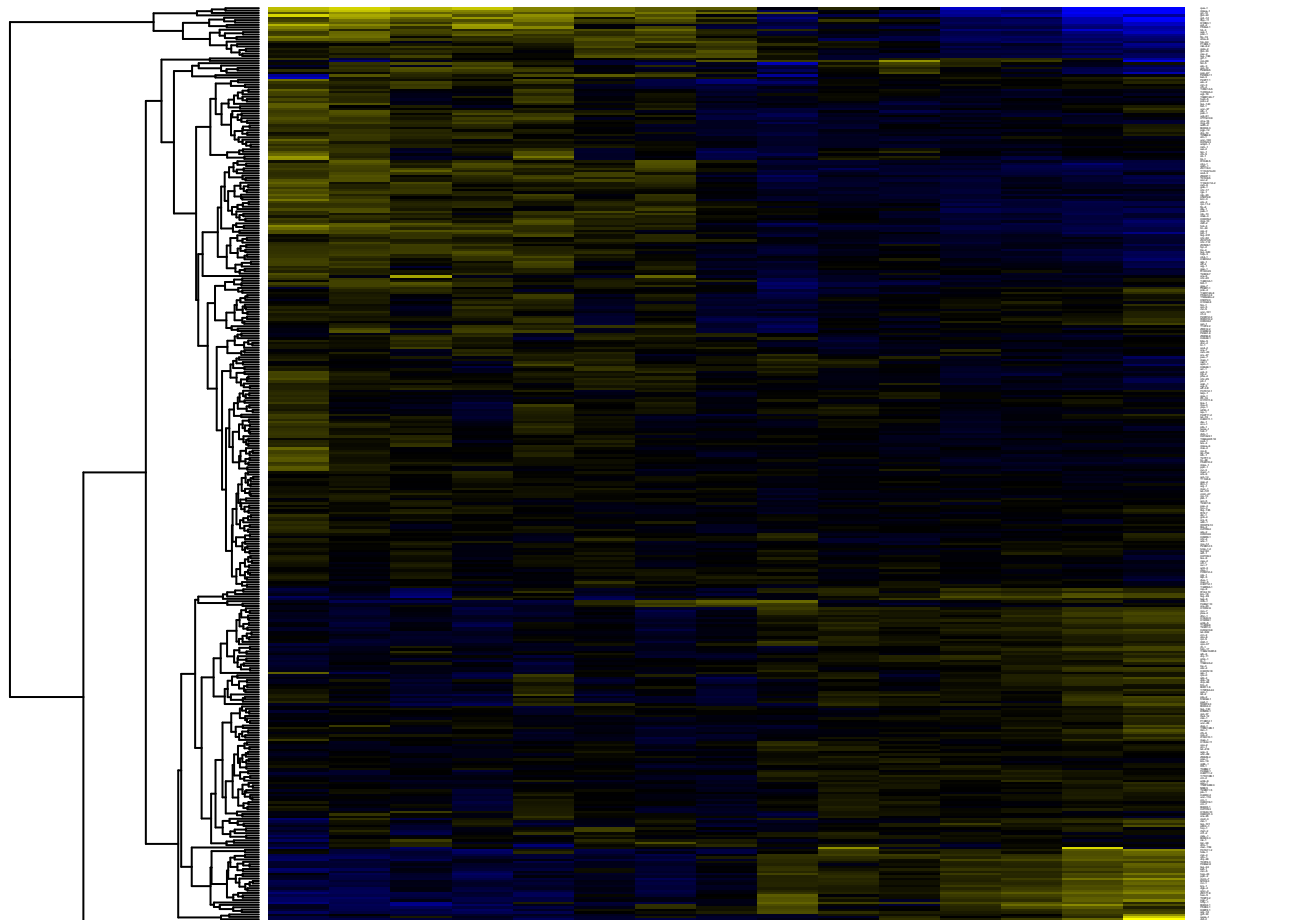
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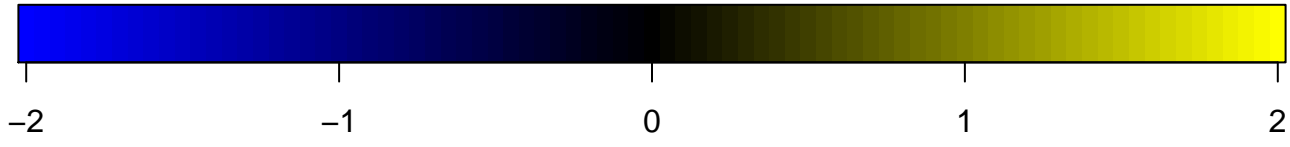
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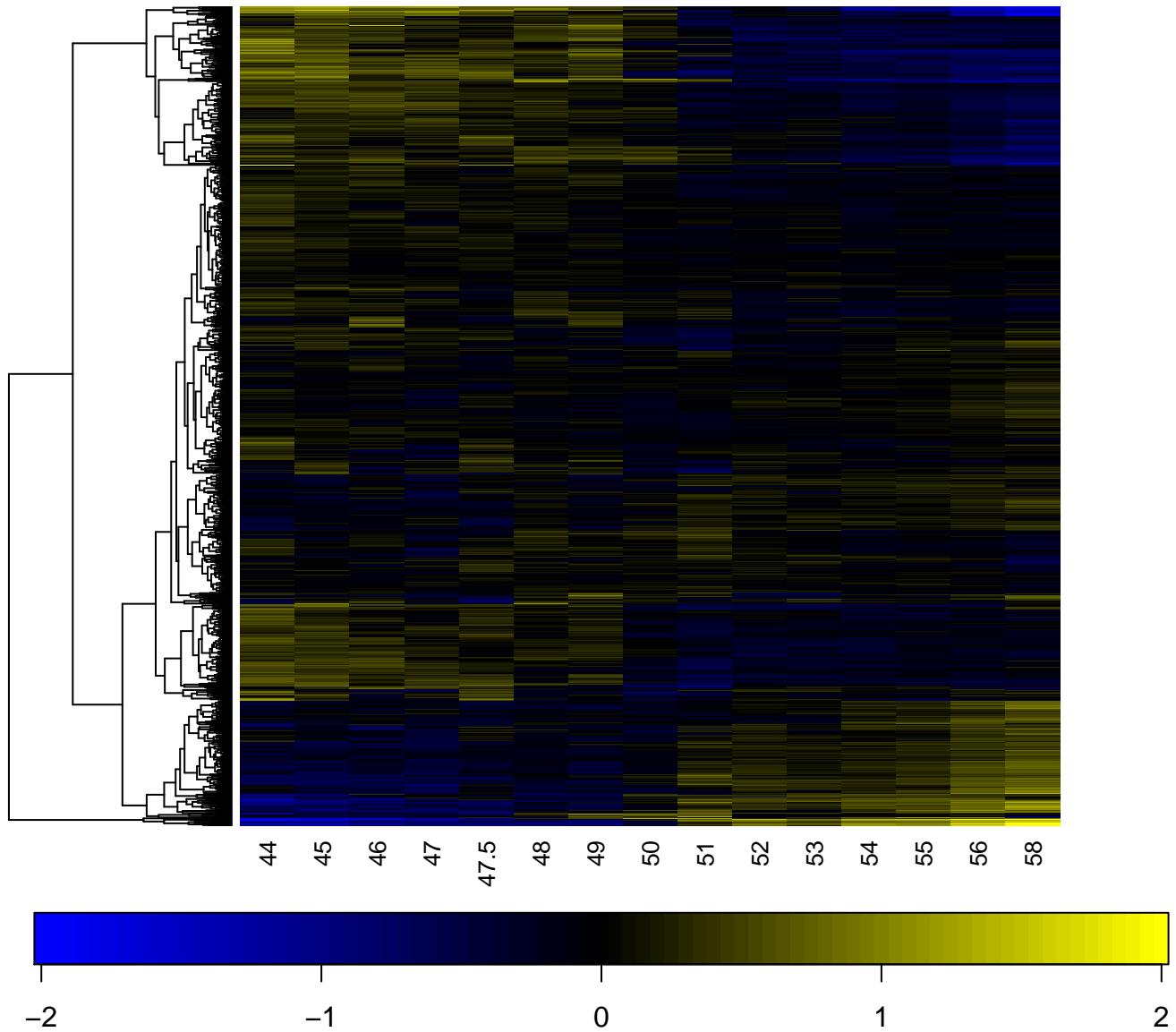
tail



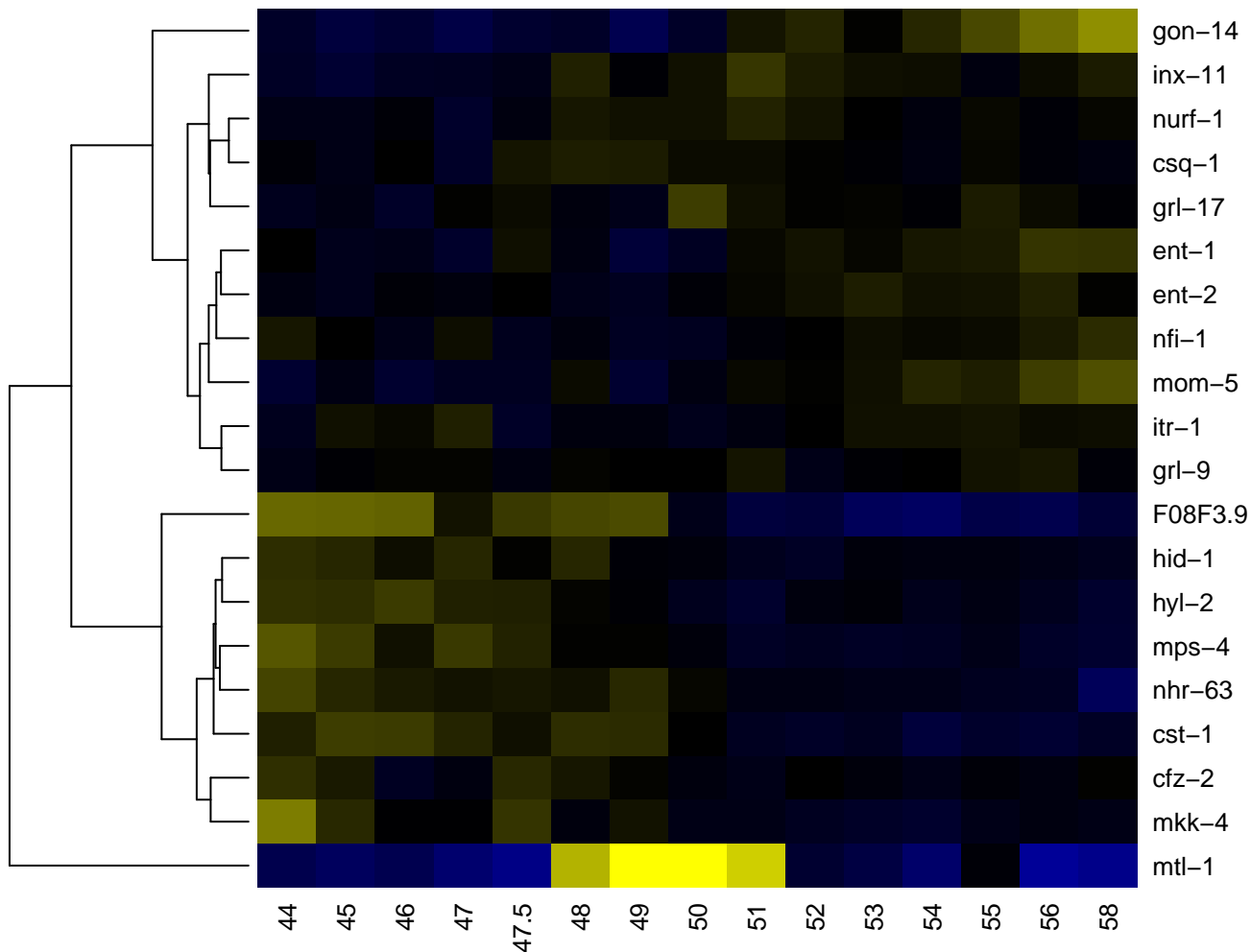
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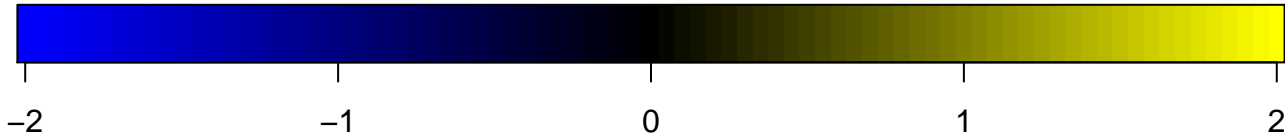
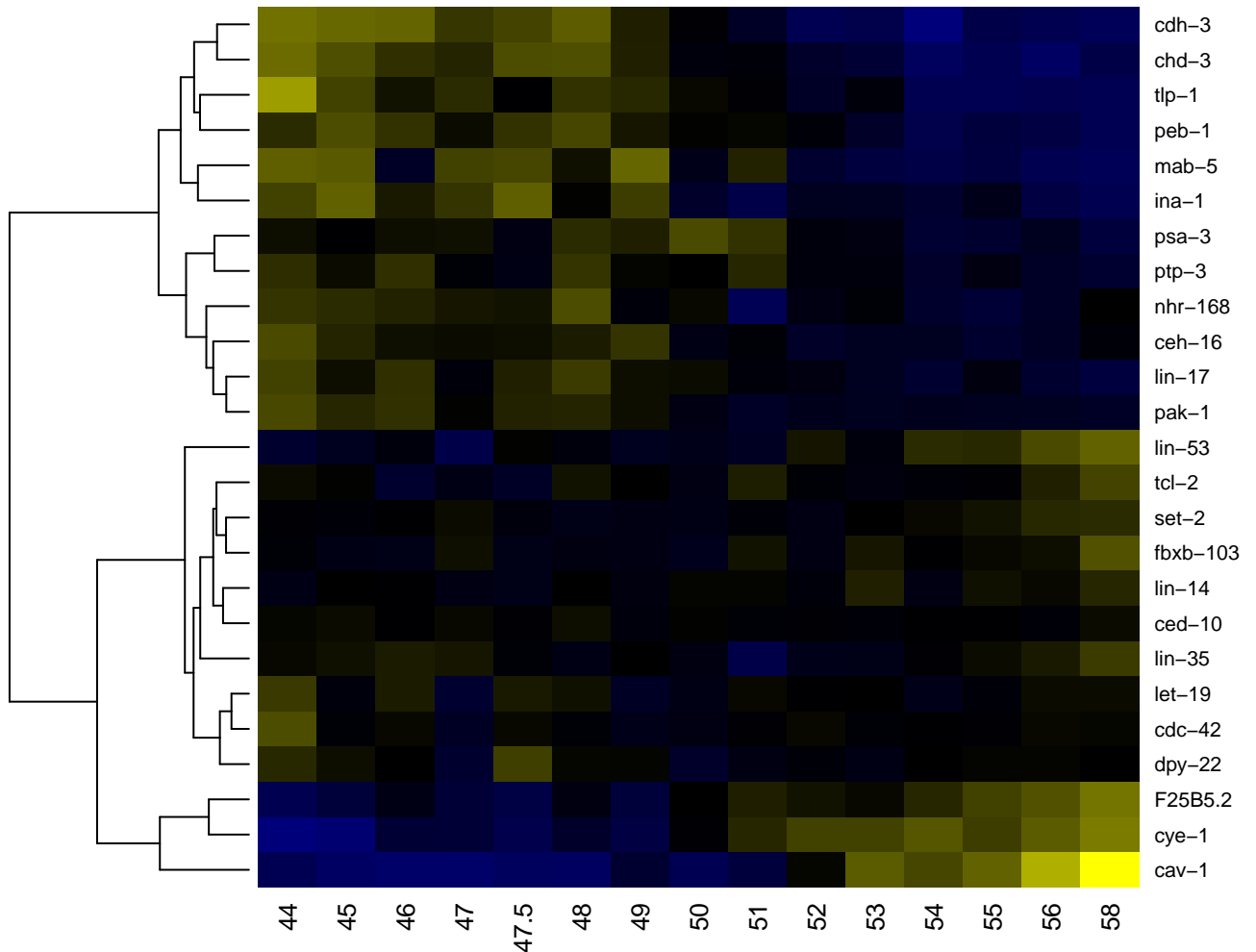
tail neuron



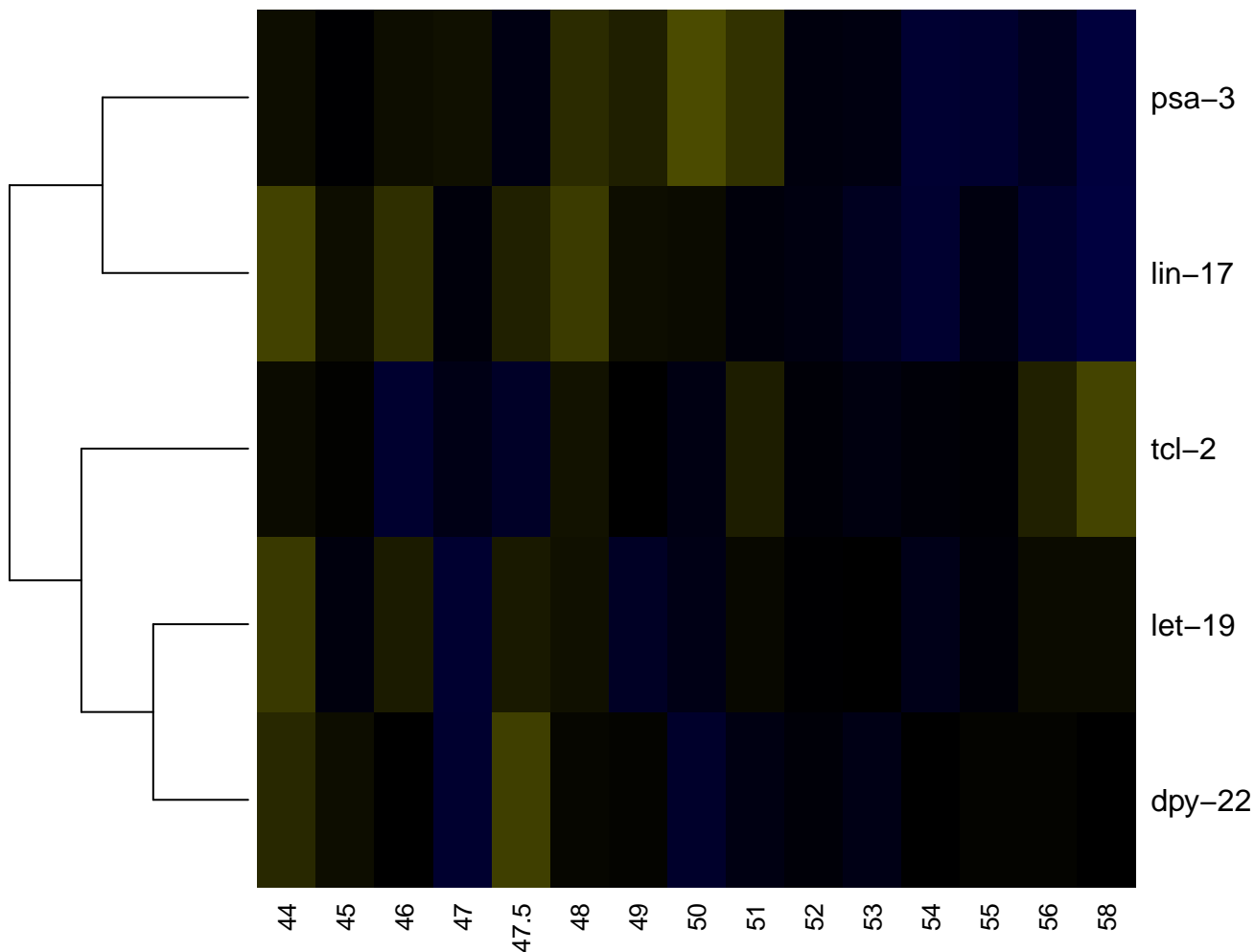
terminal bulb



TL



TL.a



-2

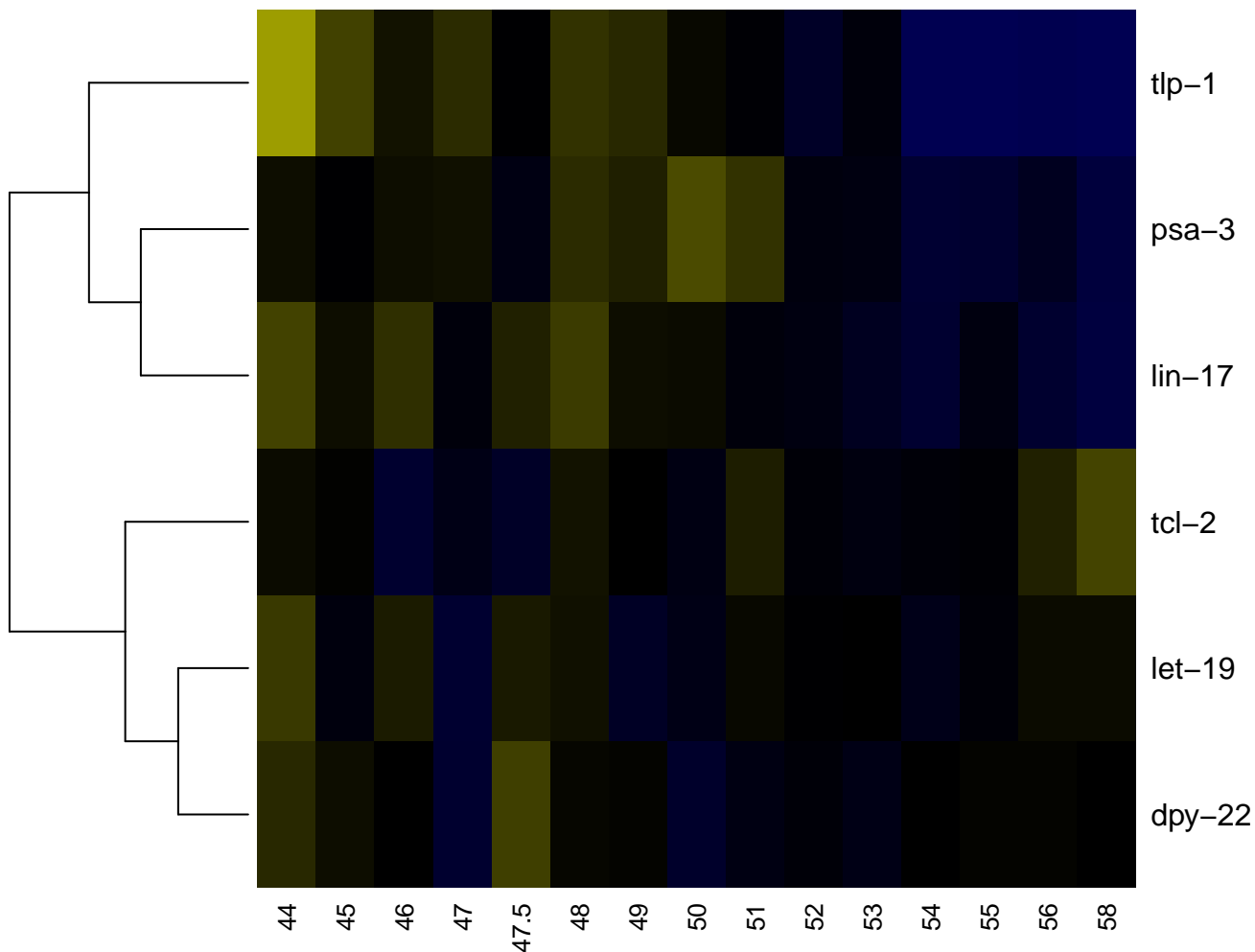
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TL.p



-2

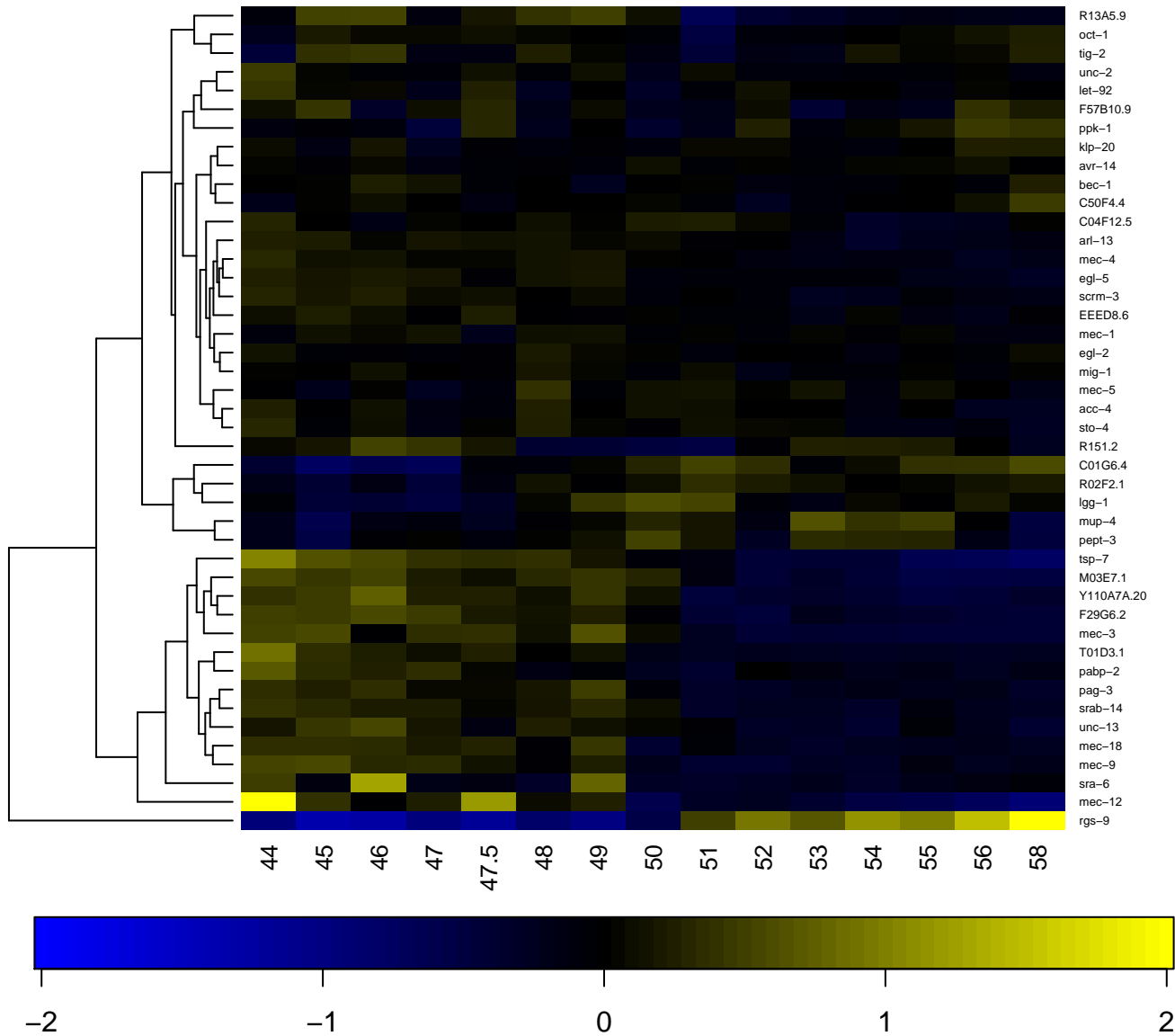
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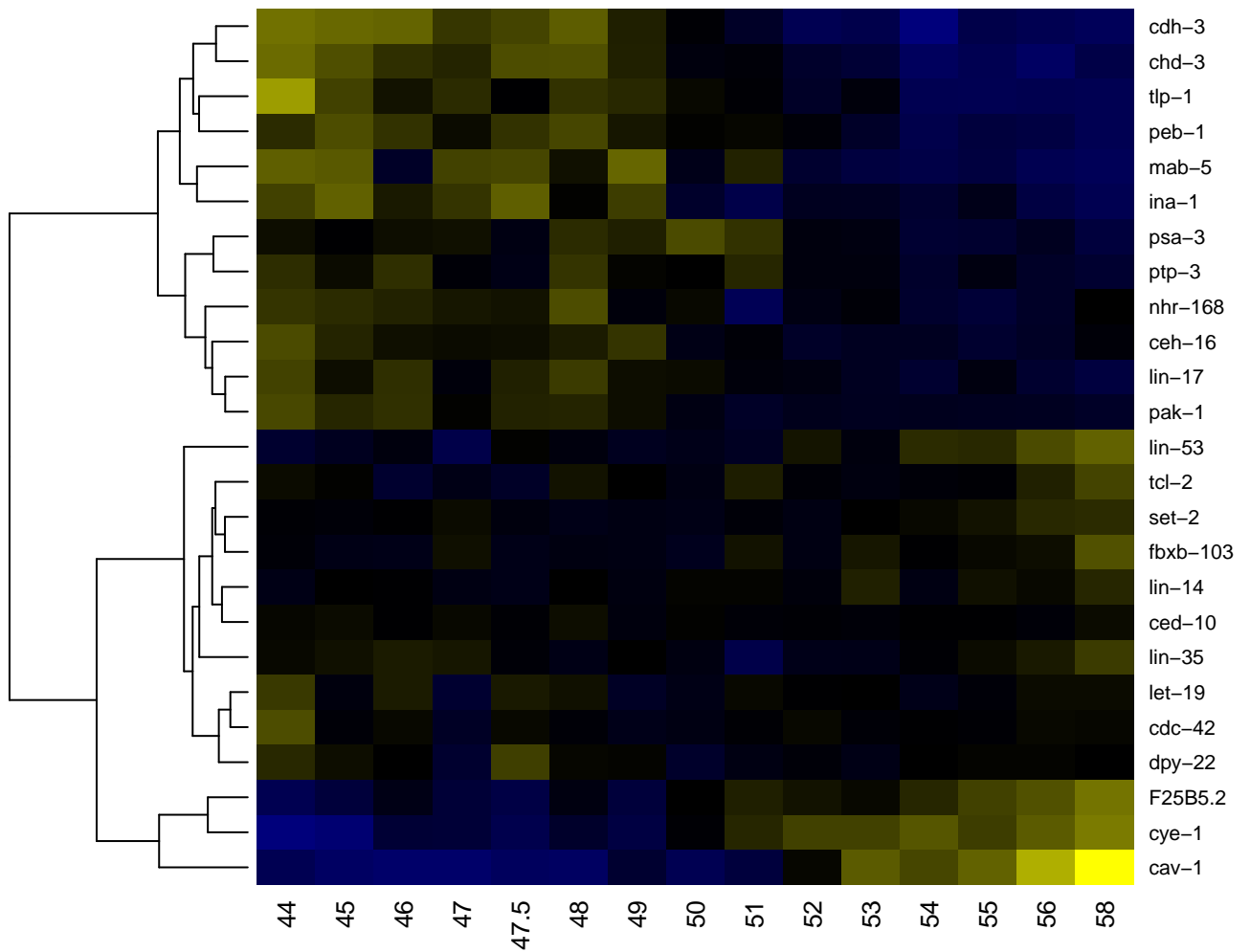
1

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touch receptor neuron



TR



-2

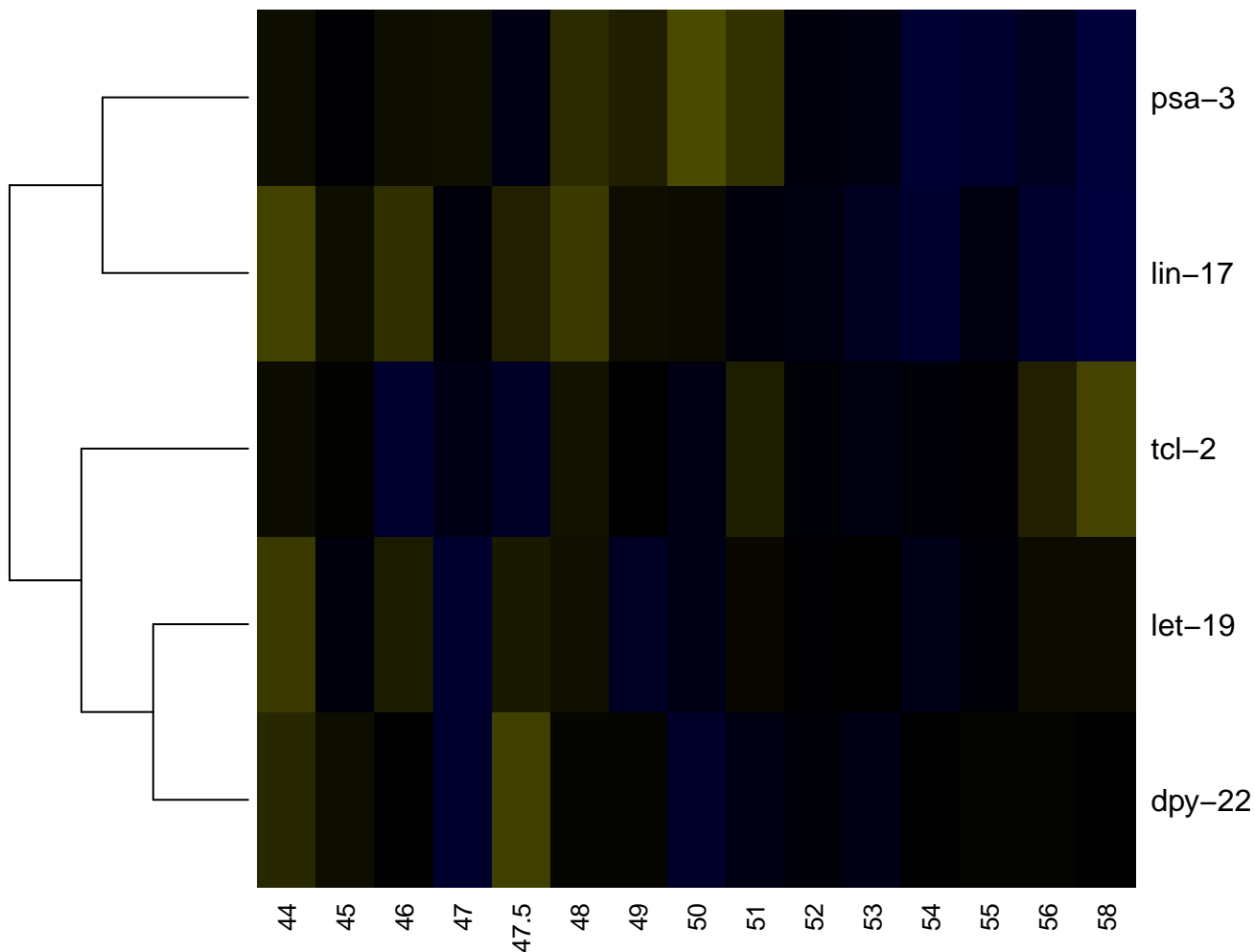
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TR.a



-2

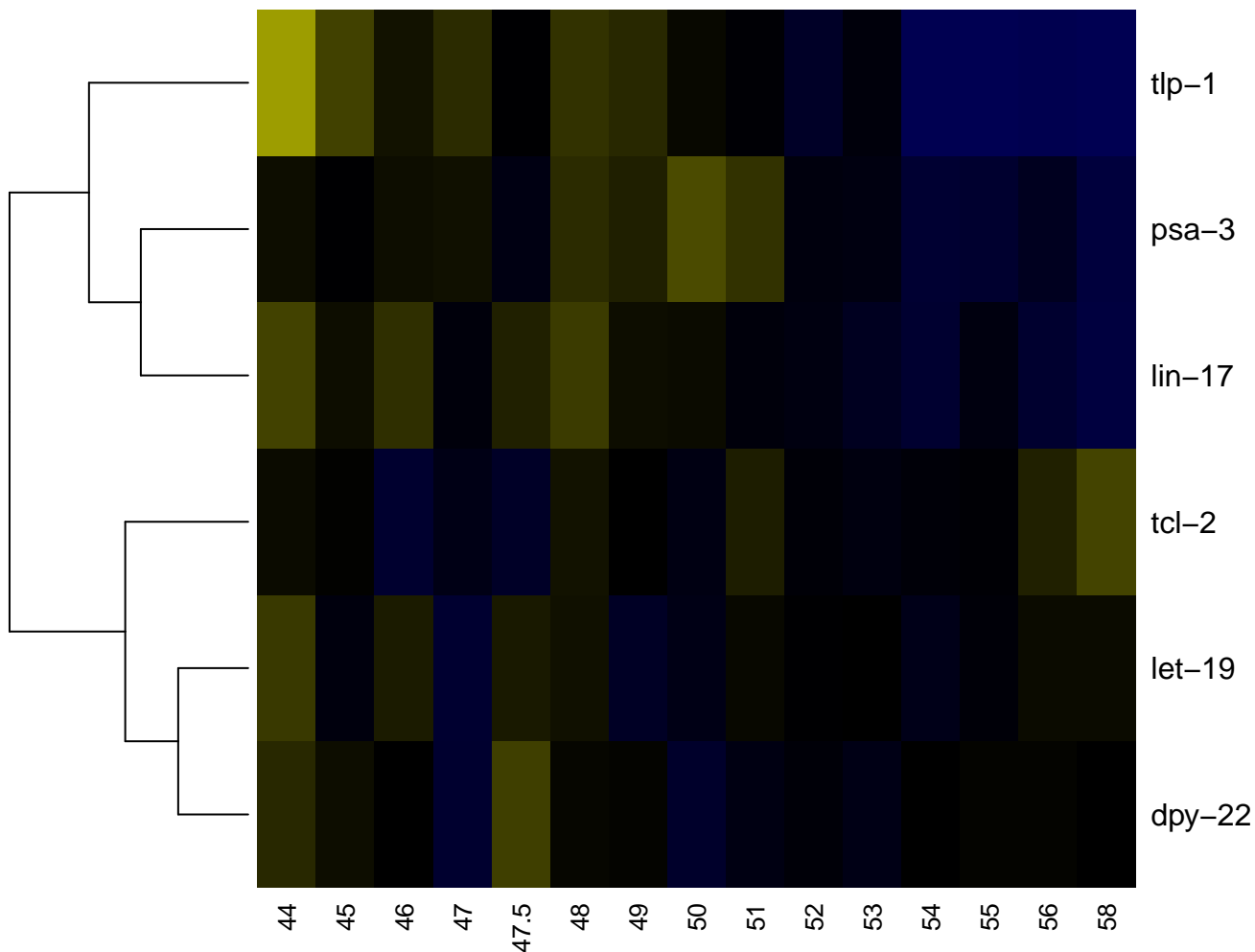
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TR.p



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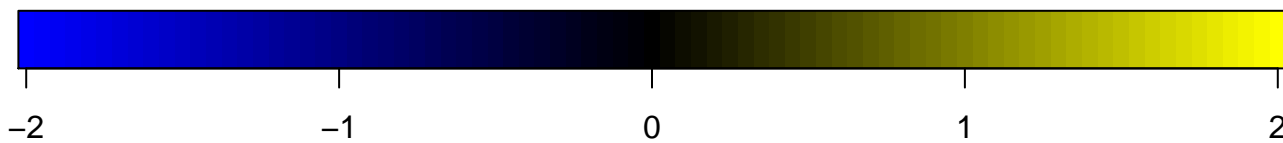
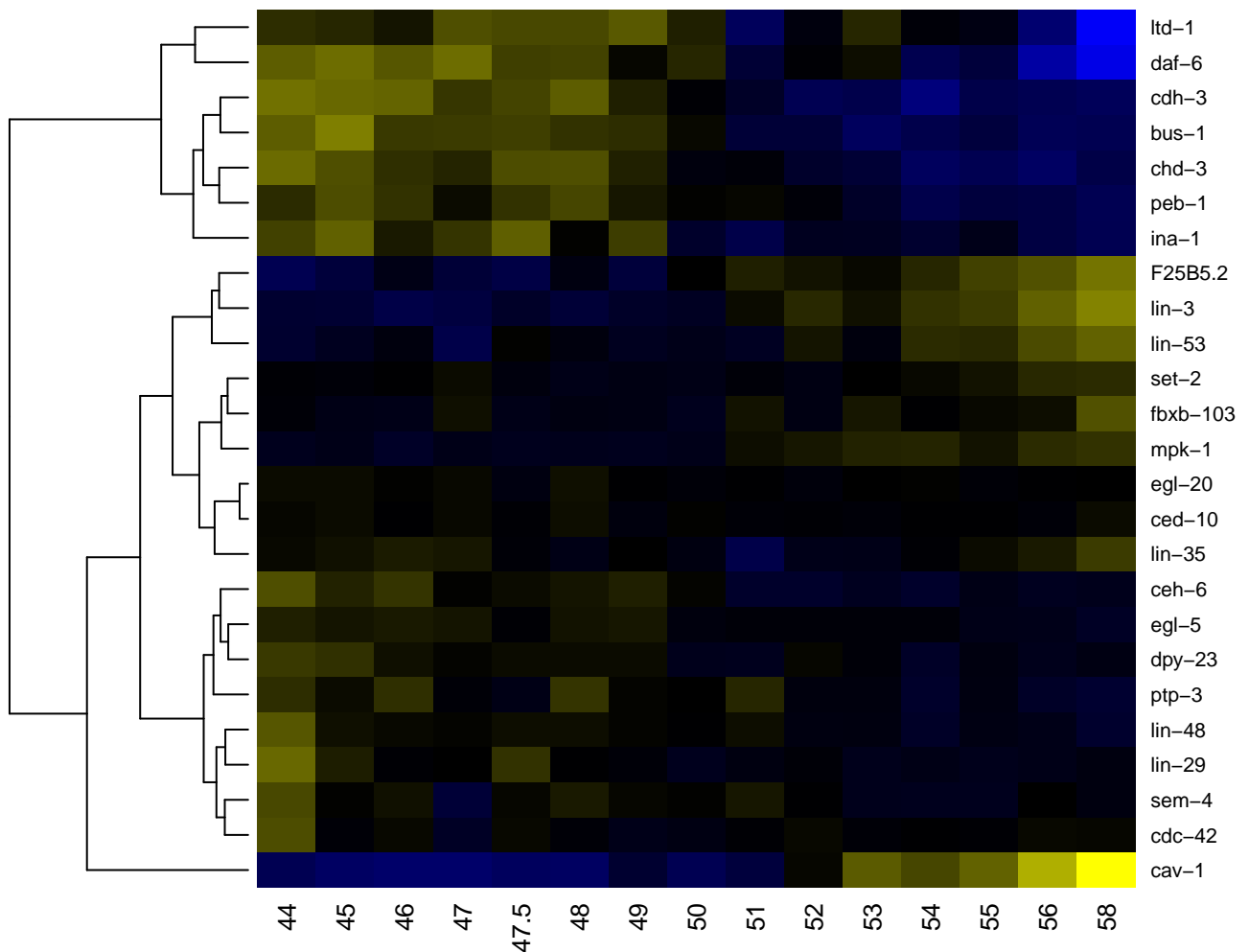
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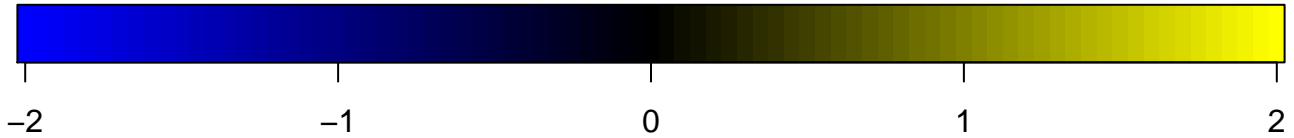
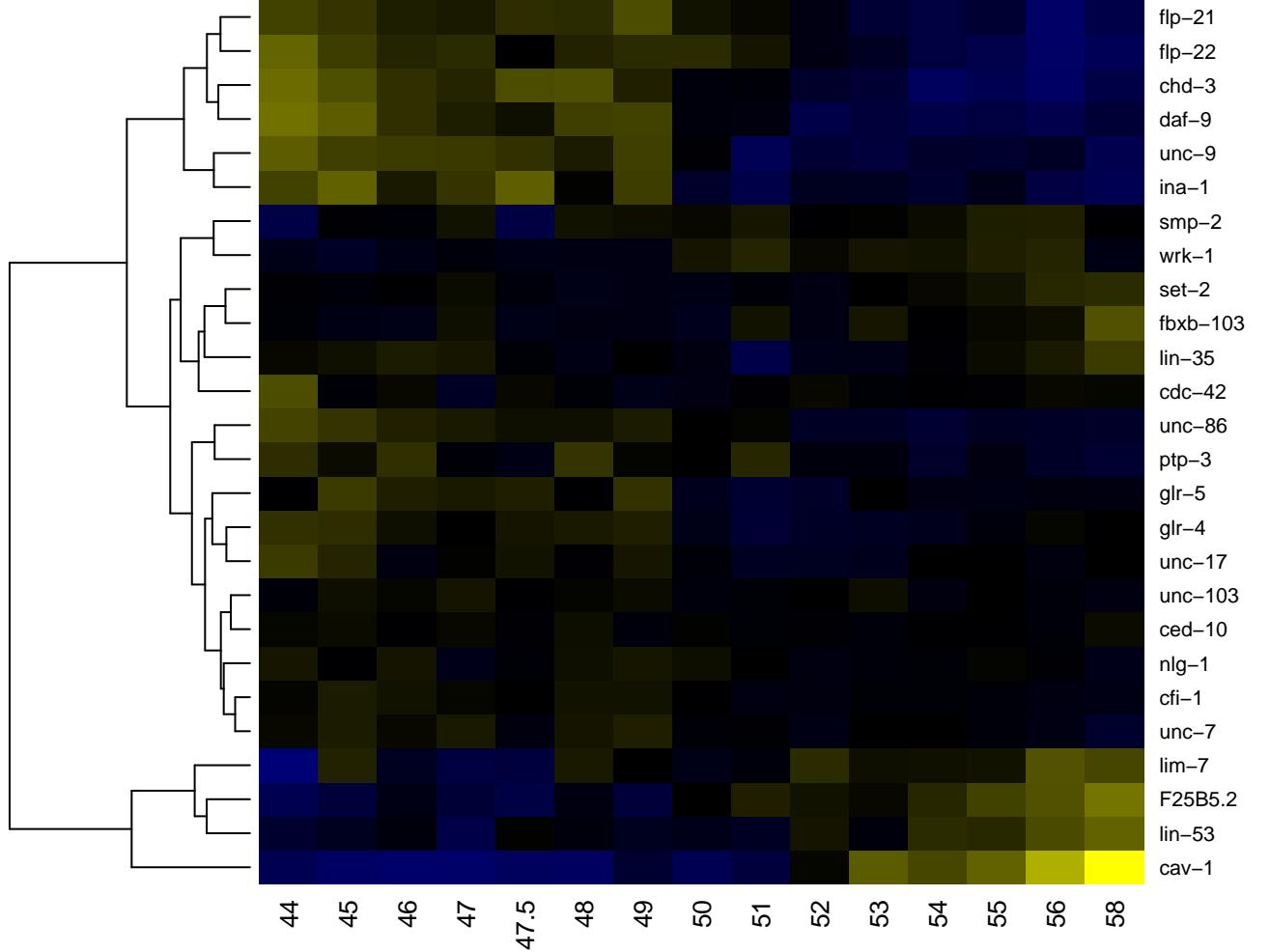
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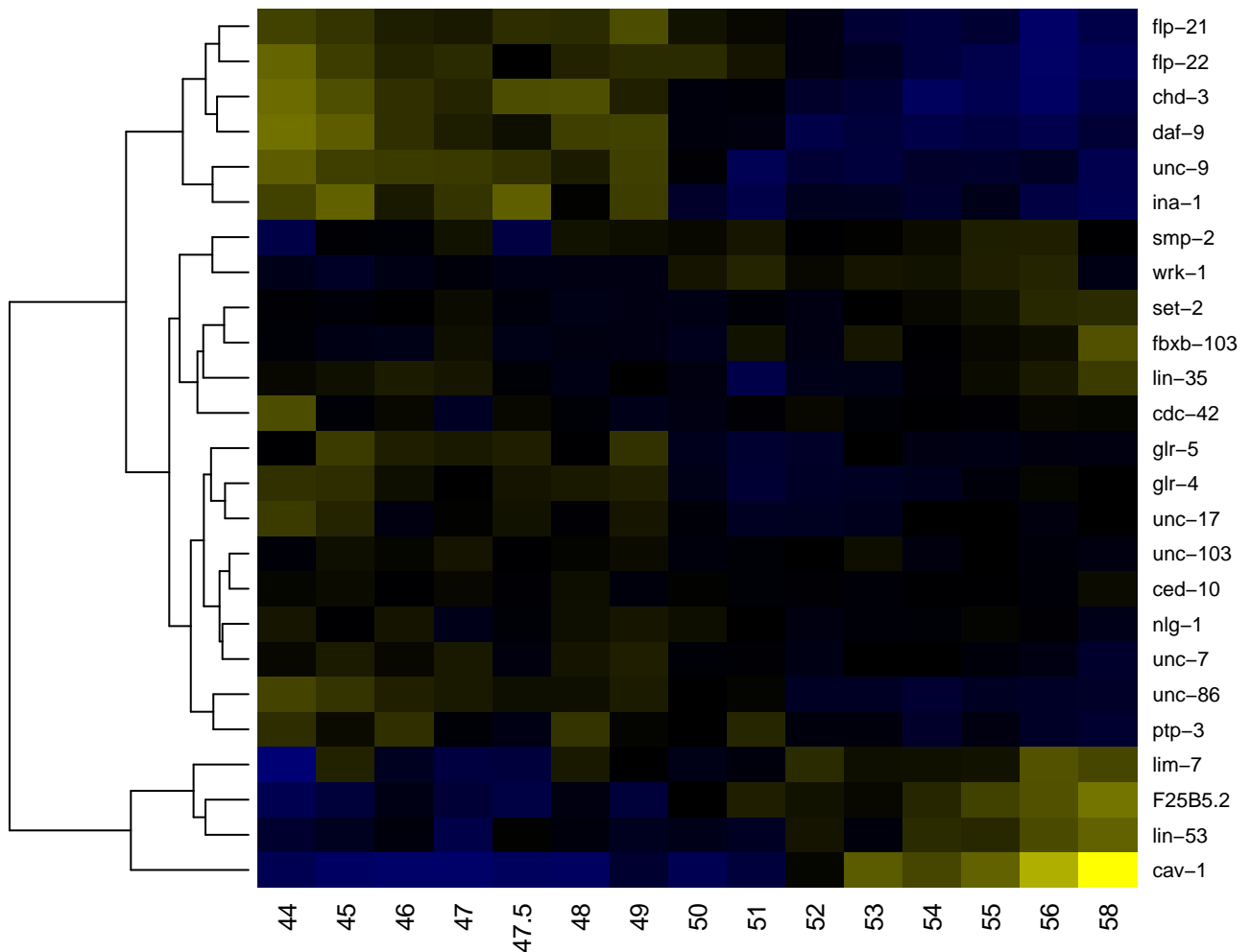
U cell



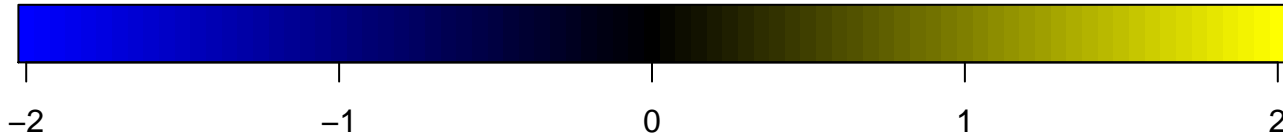
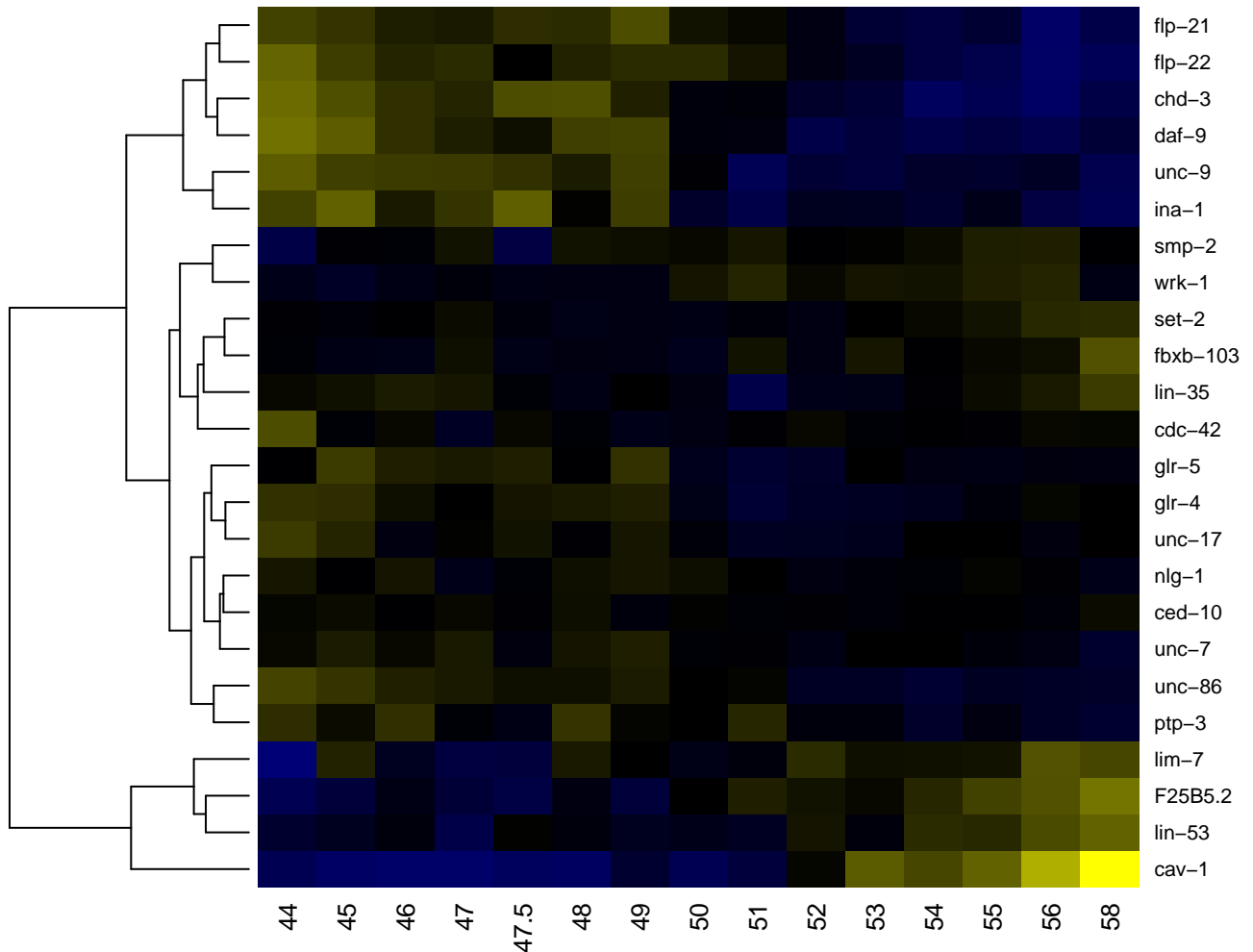
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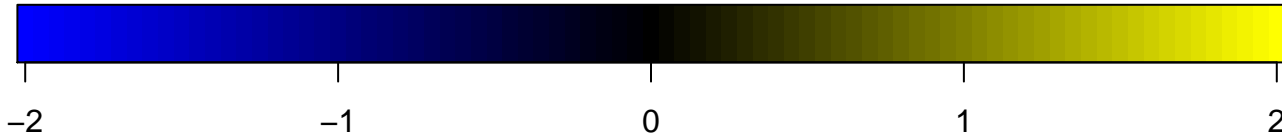
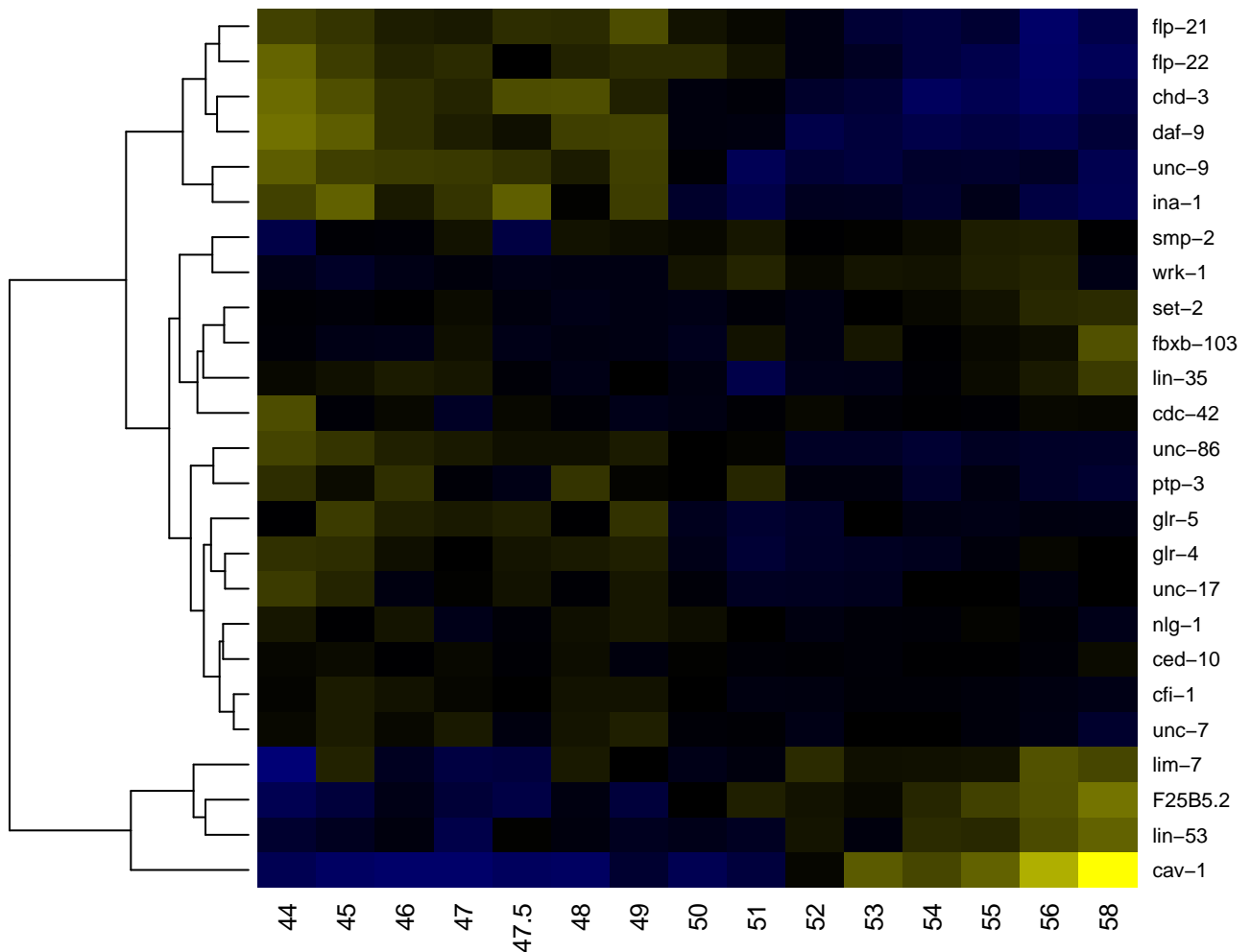
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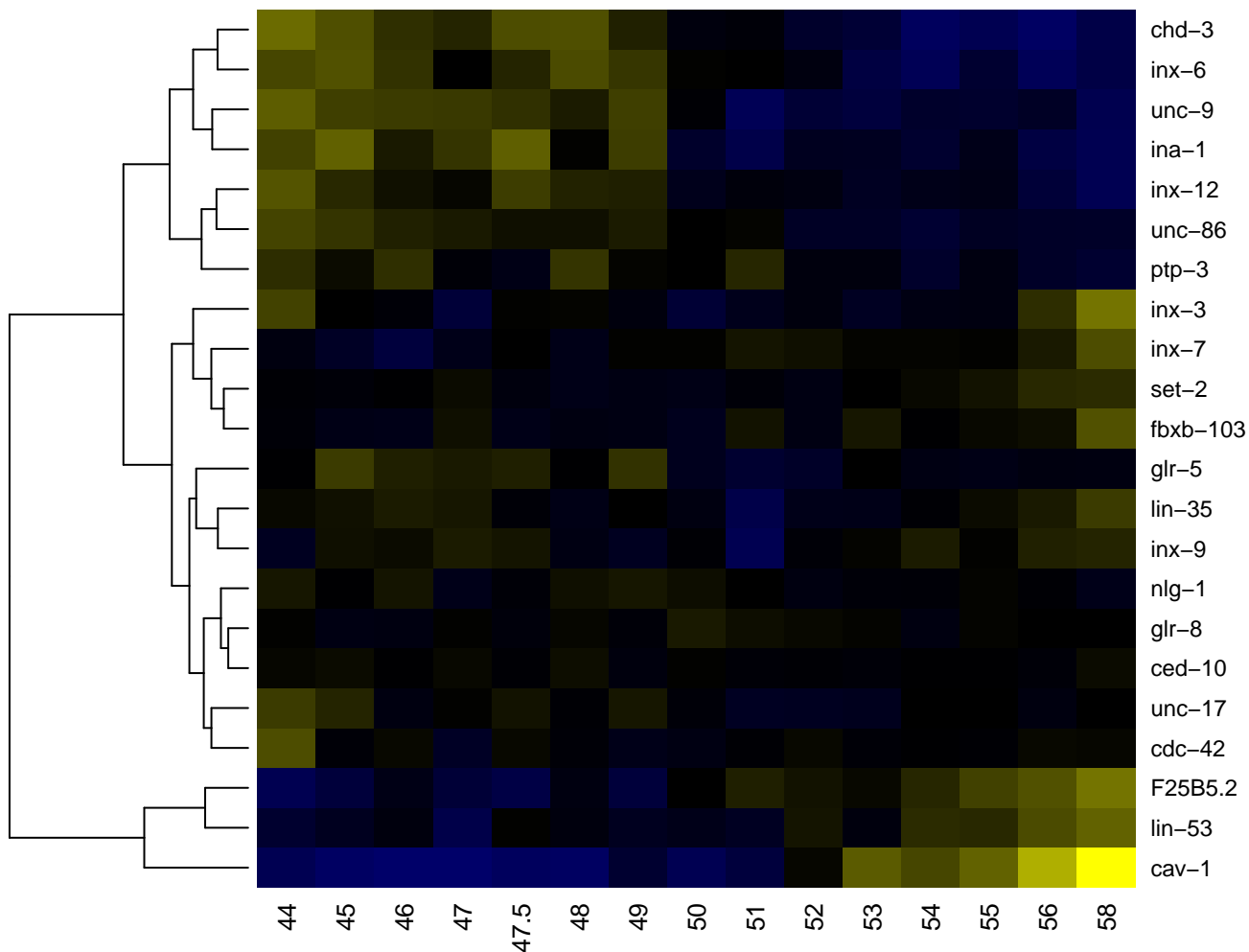
URAVL



URAVR



URBL



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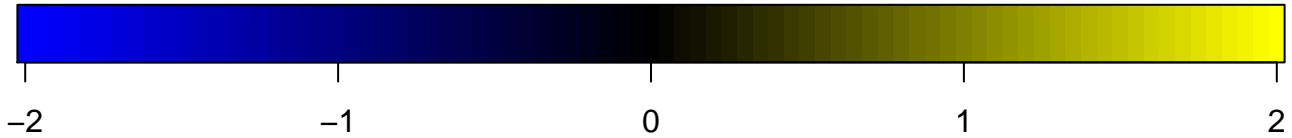
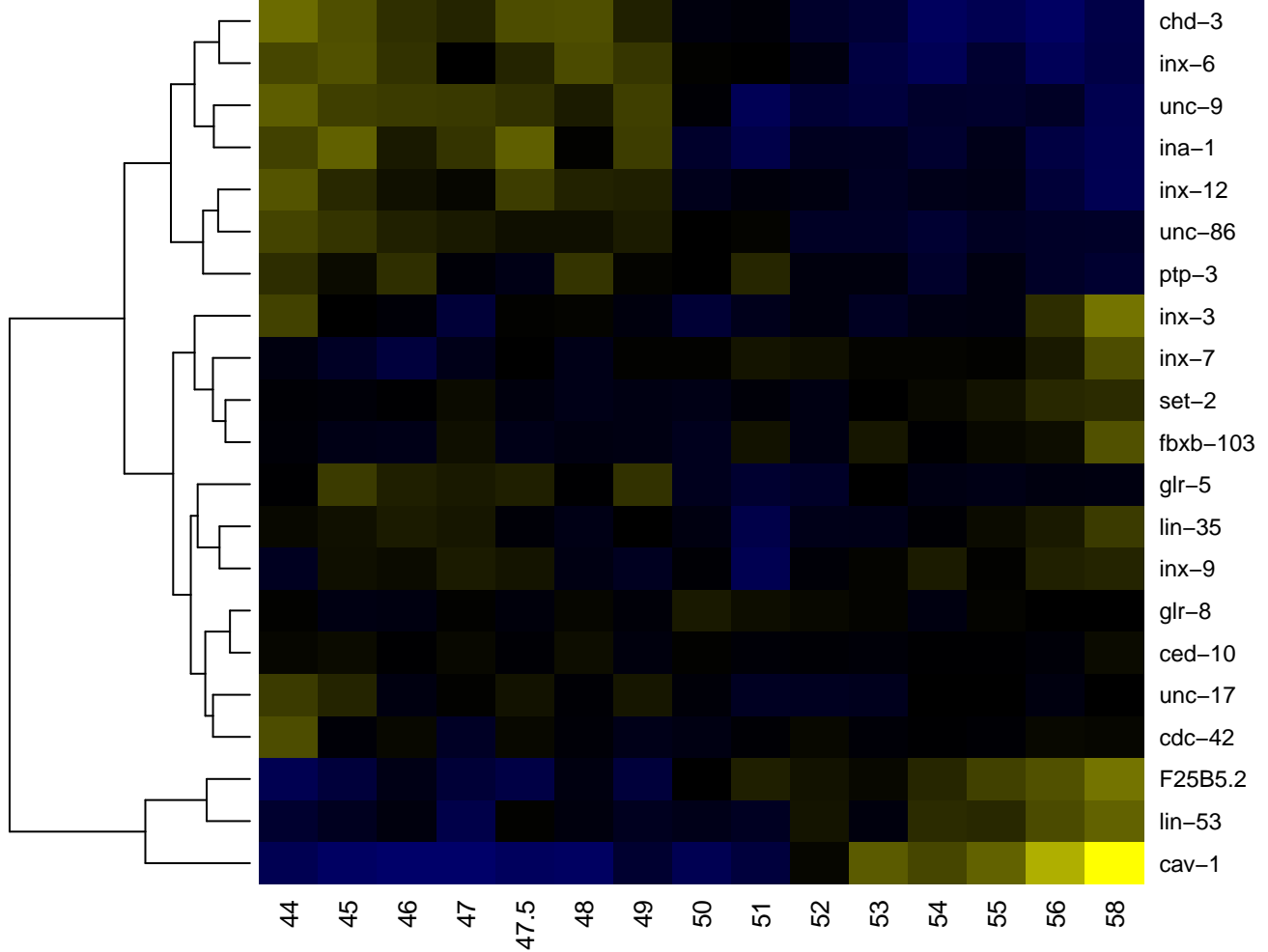
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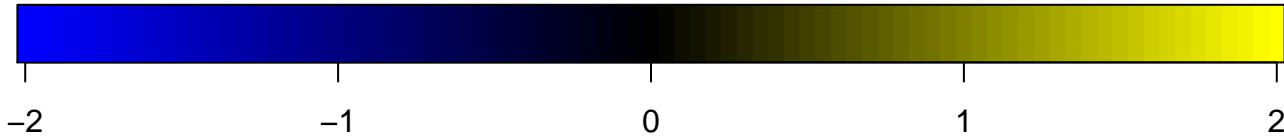
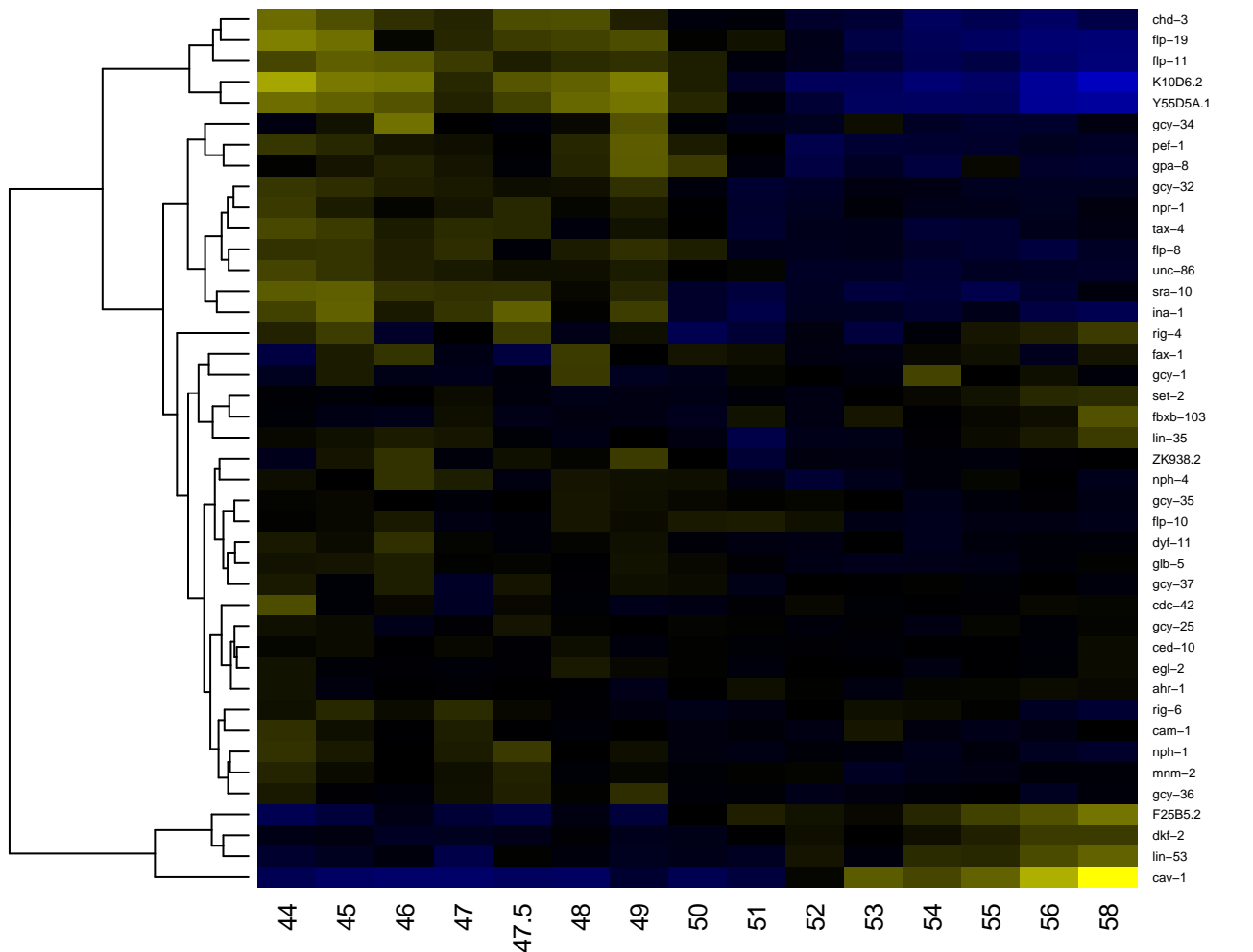
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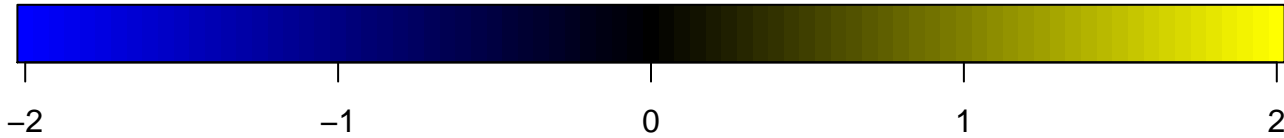
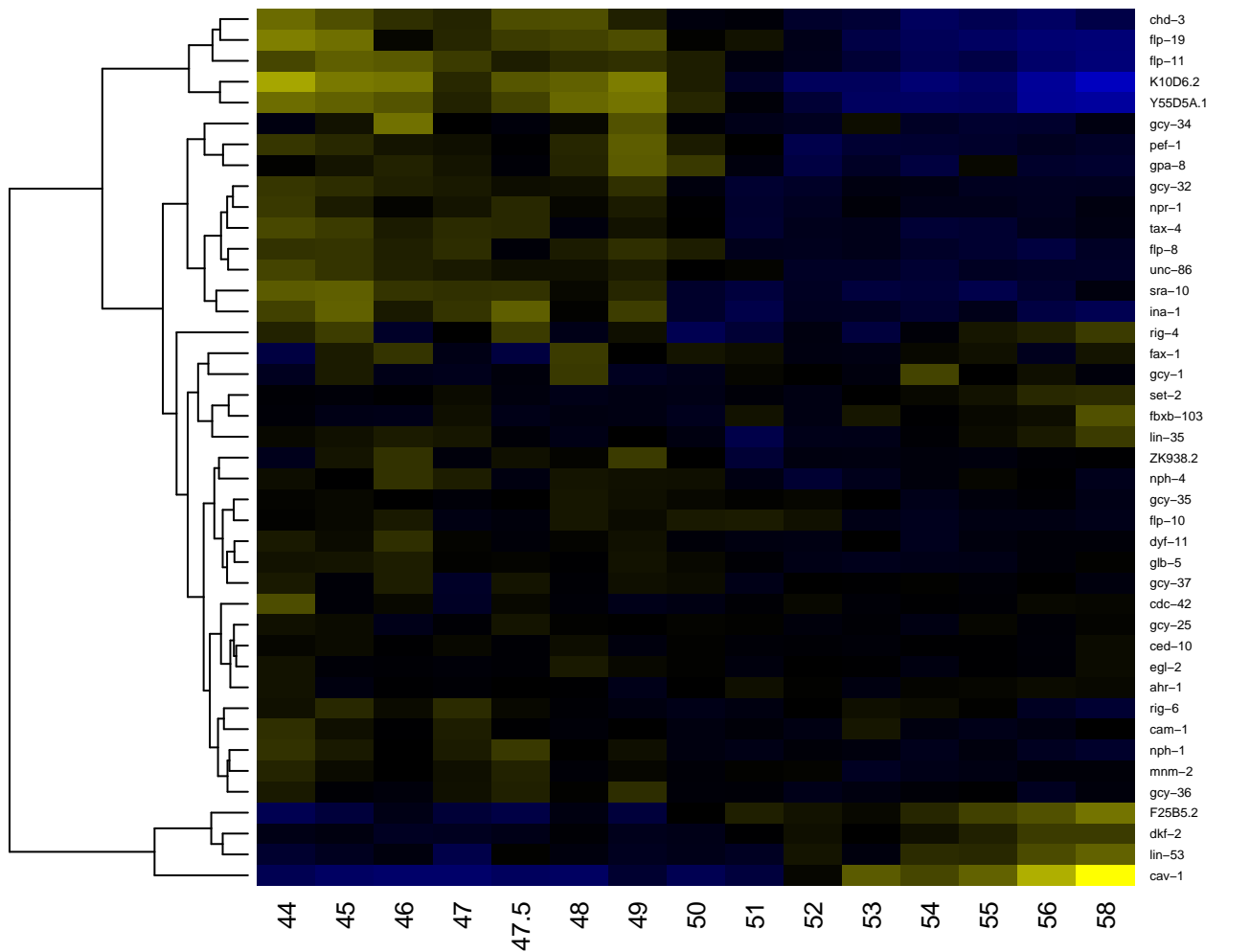
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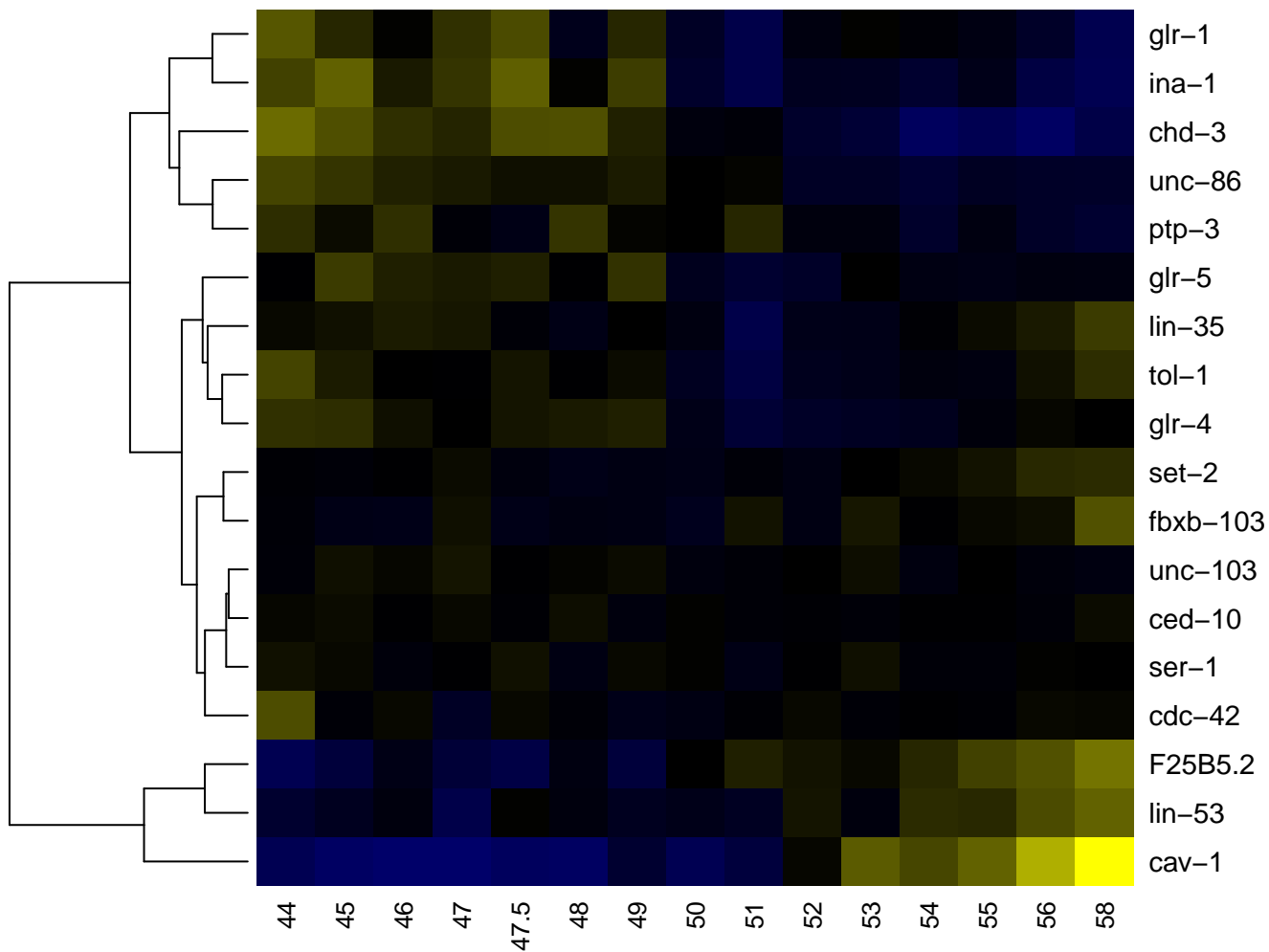
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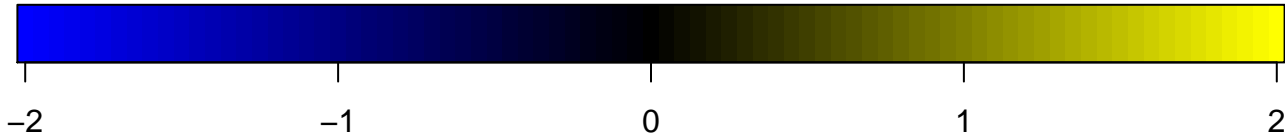
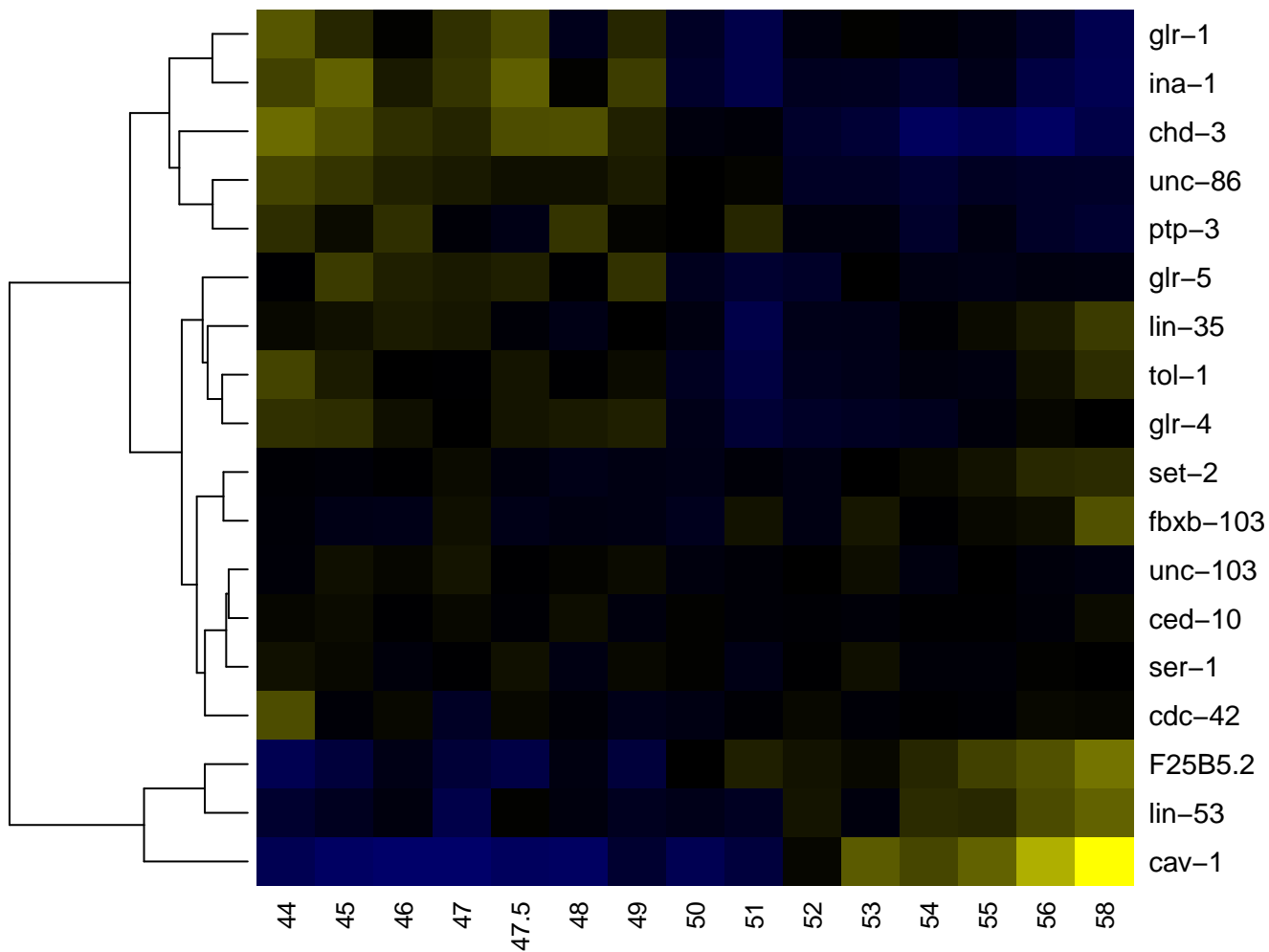
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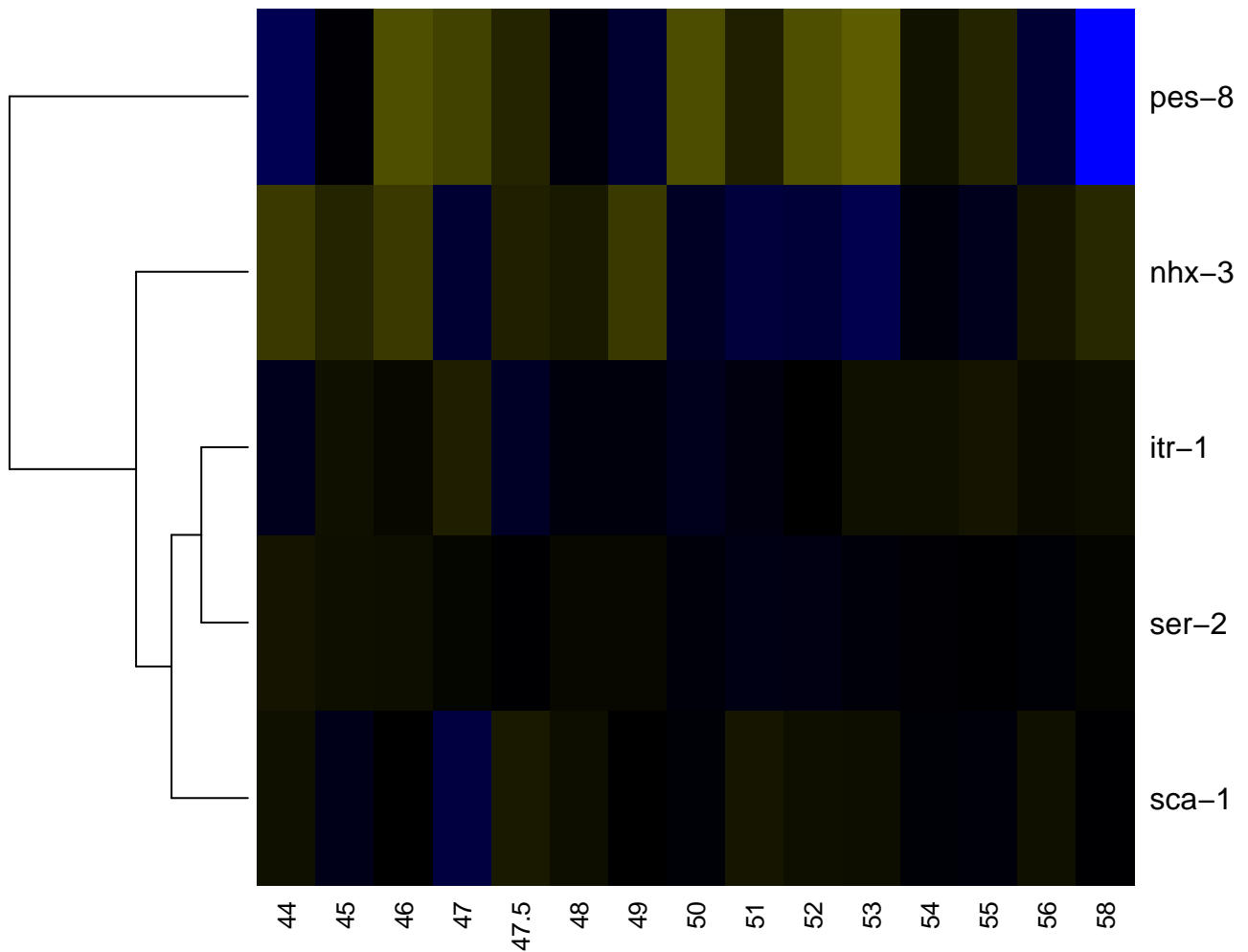
URYVL



URYVR



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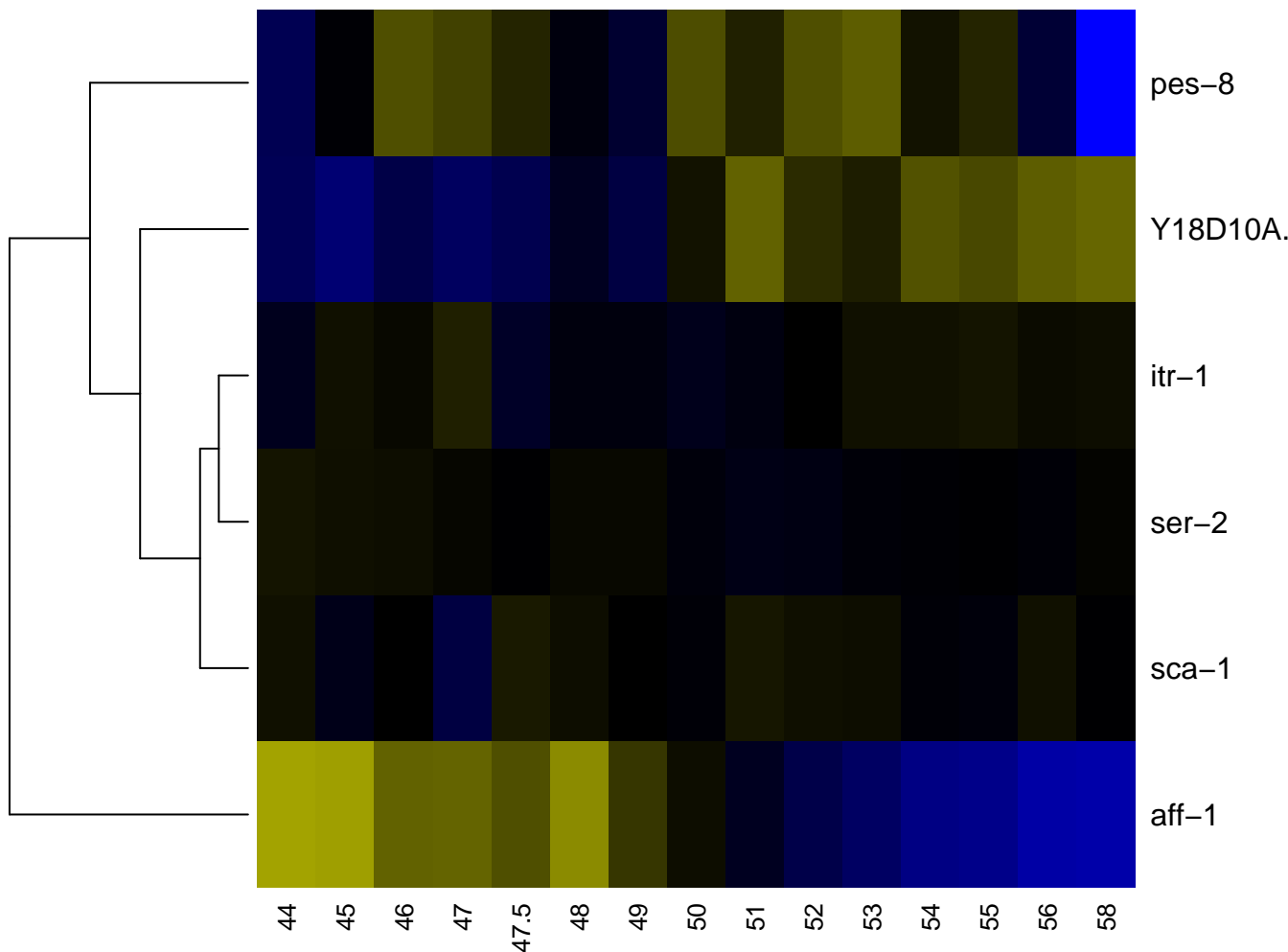
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ut2



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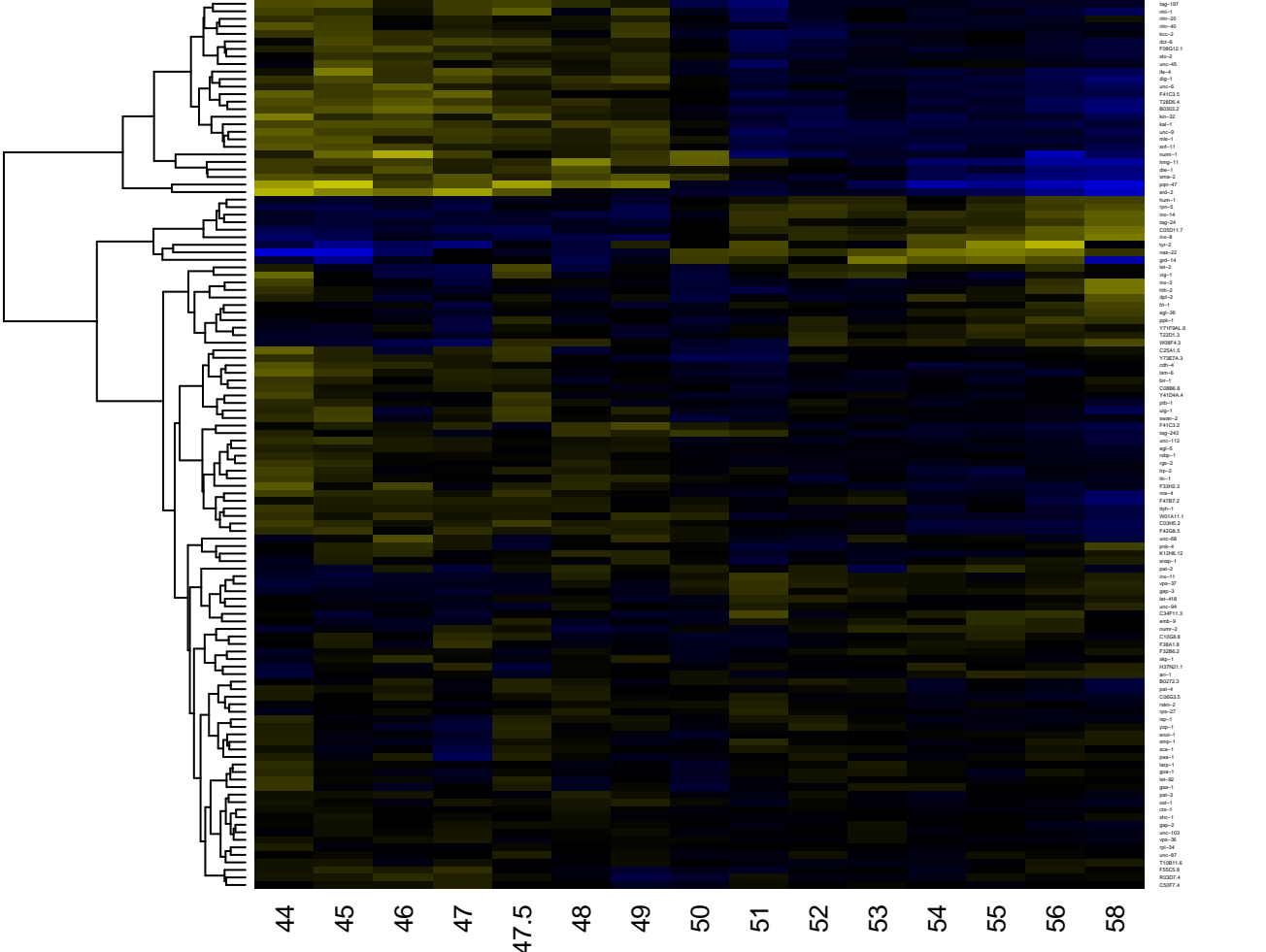
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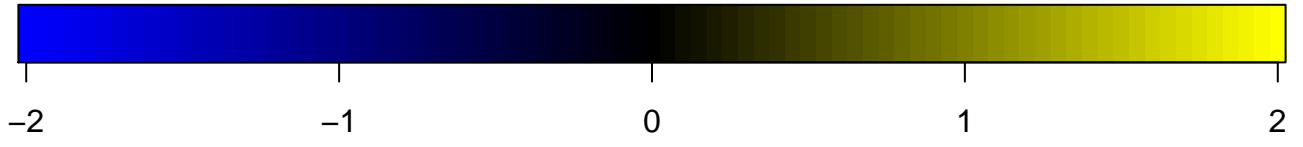
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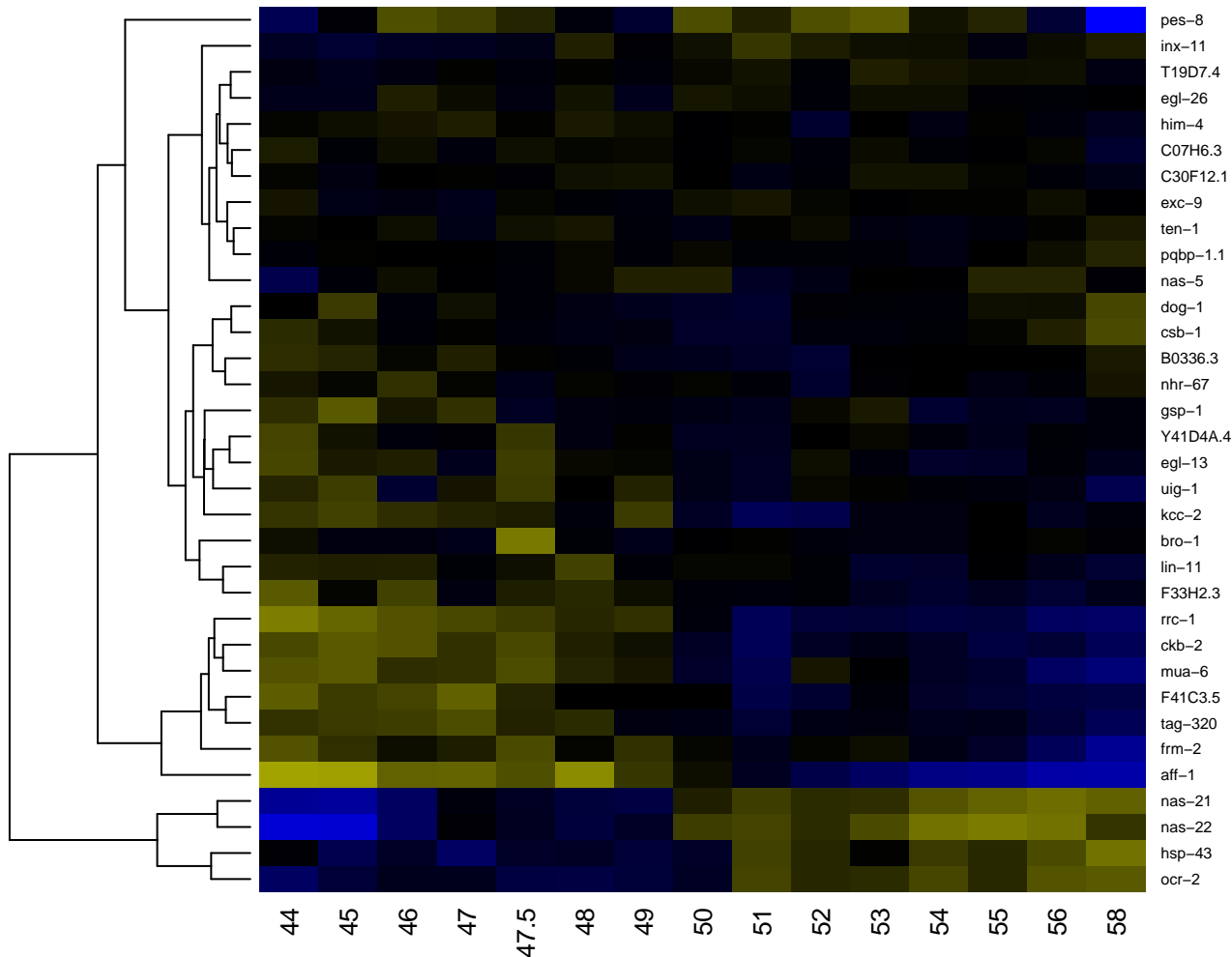
uterine muscle



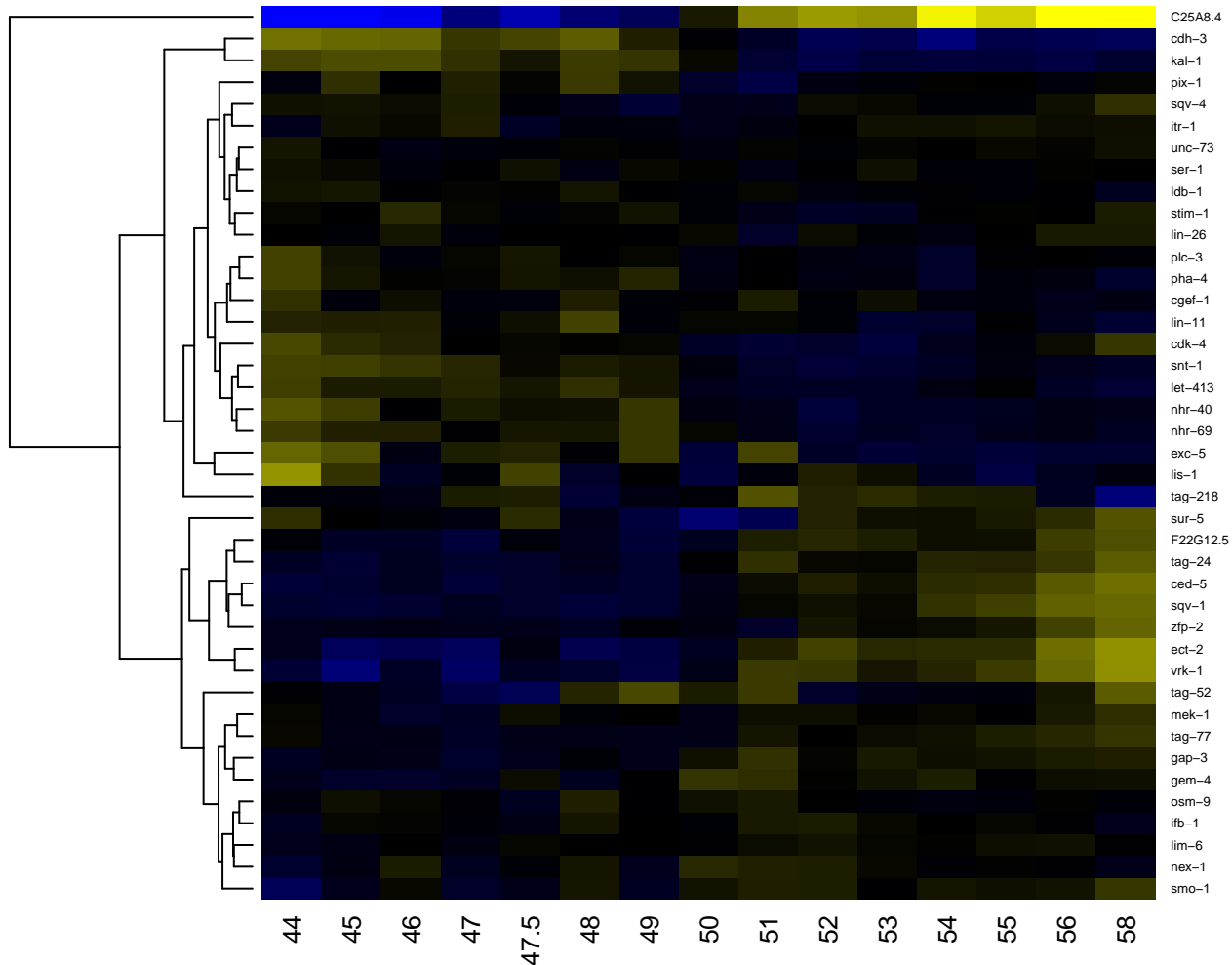
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- mtl-98
- mtl-99
- mtl-100



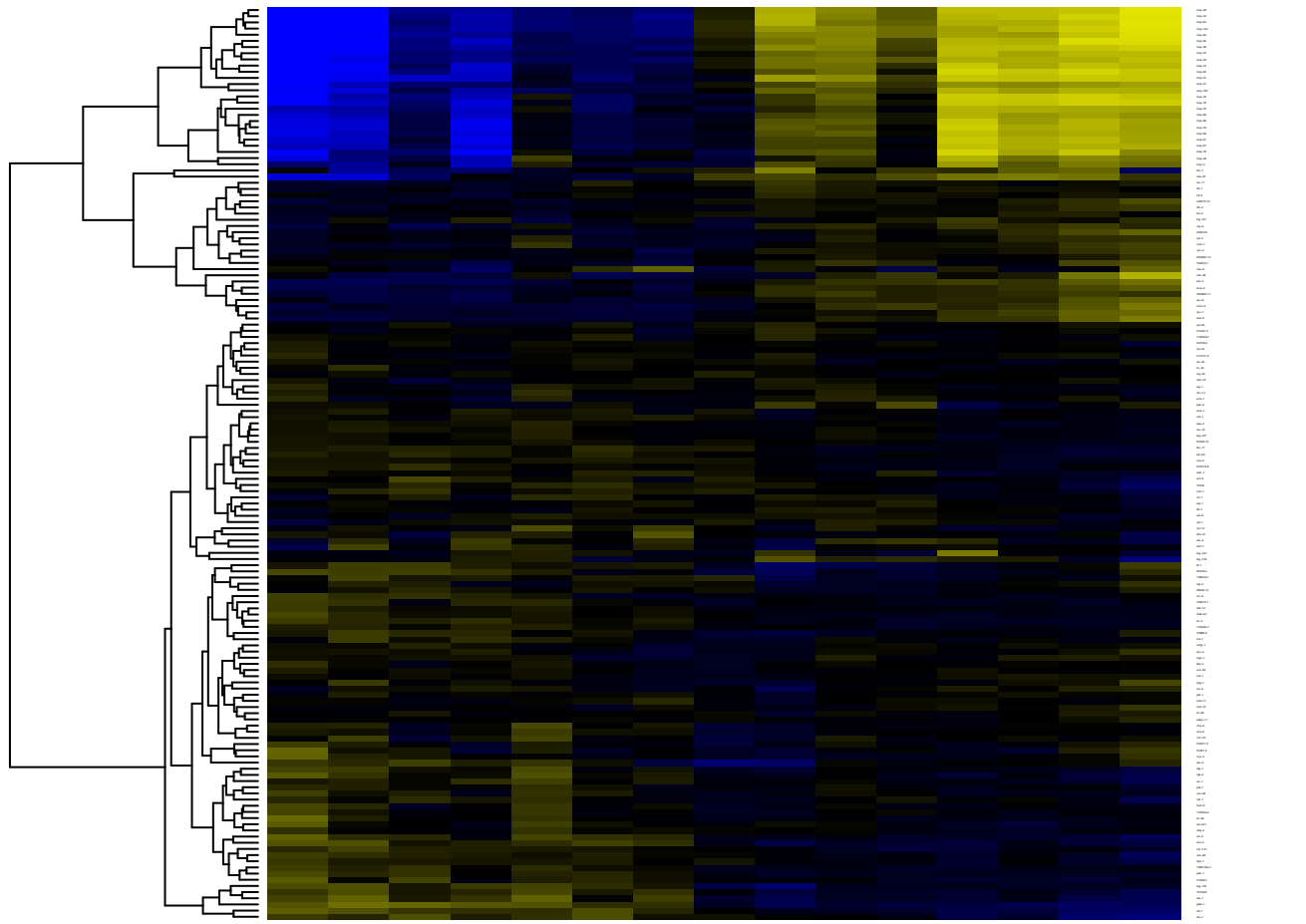
uterine seam cell



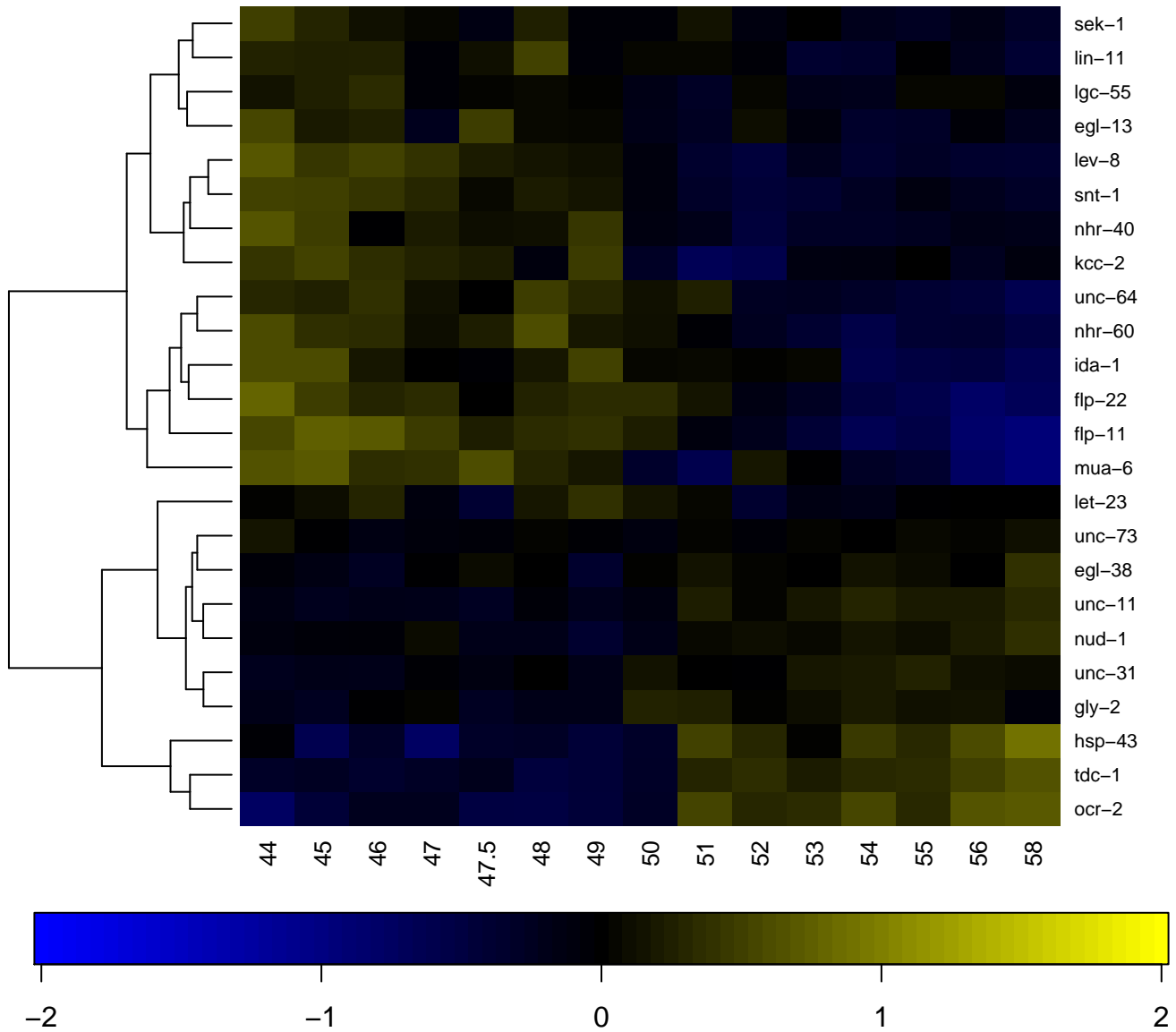
uterine toroidal epithelial cell



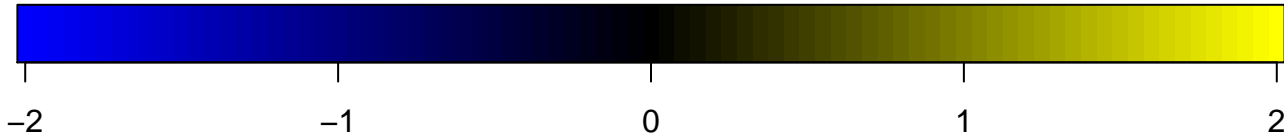
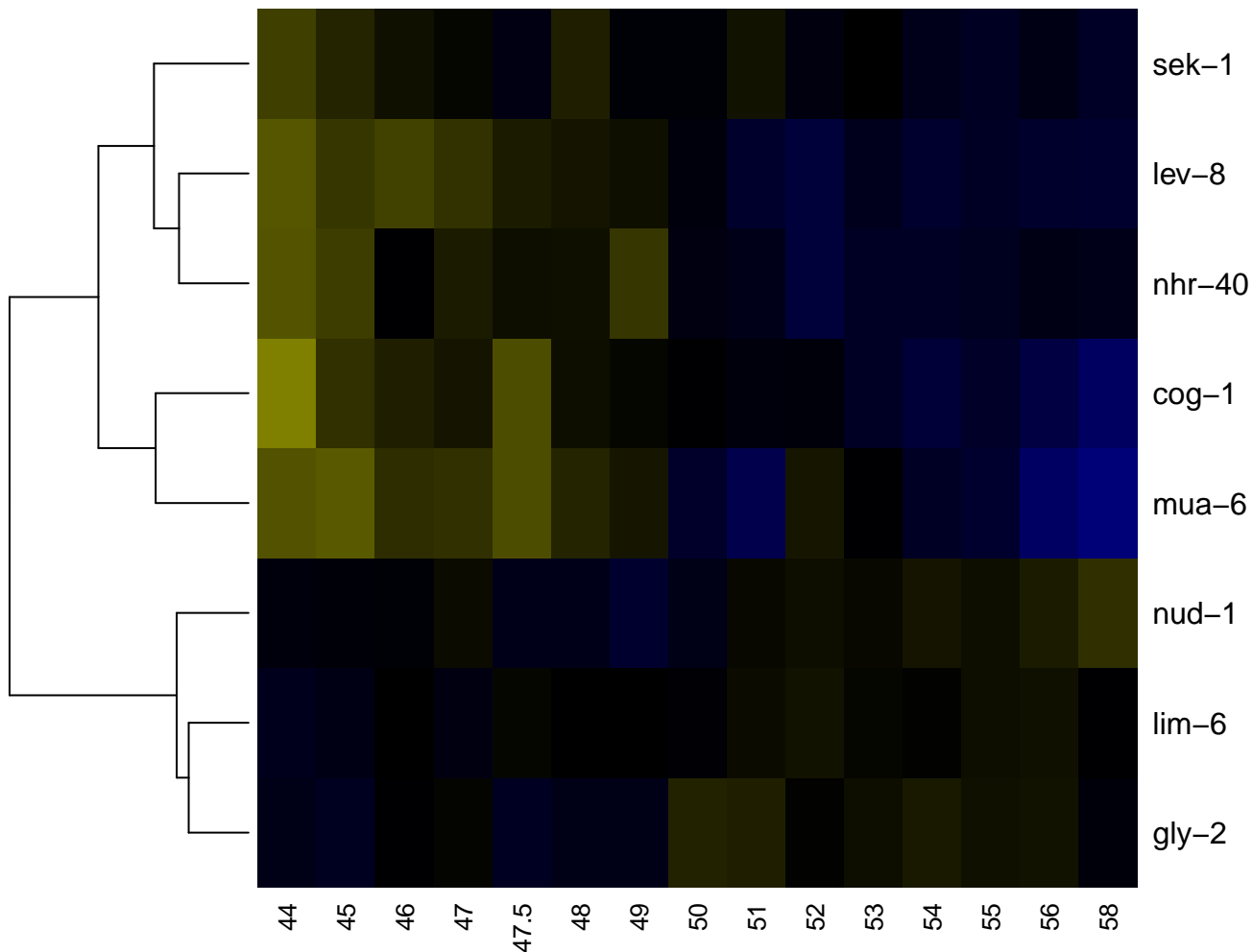
uterus



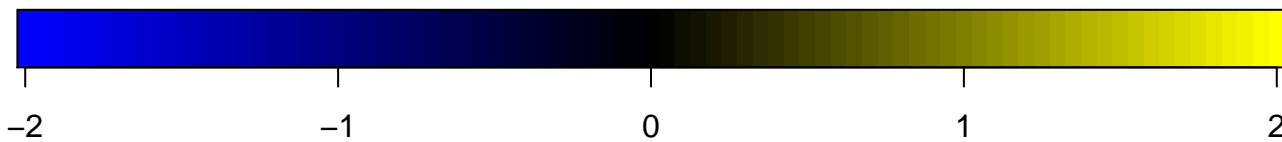
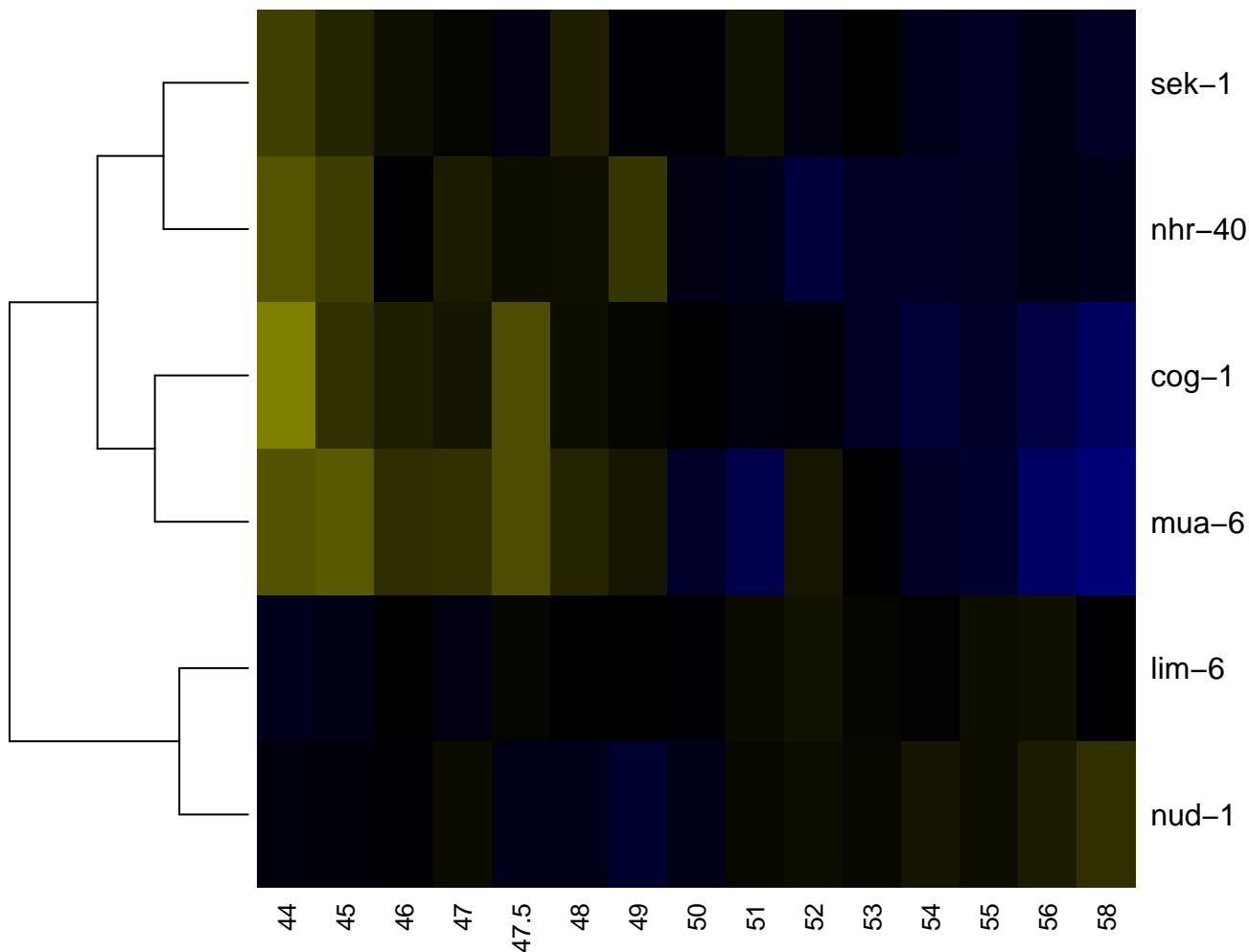
uv1



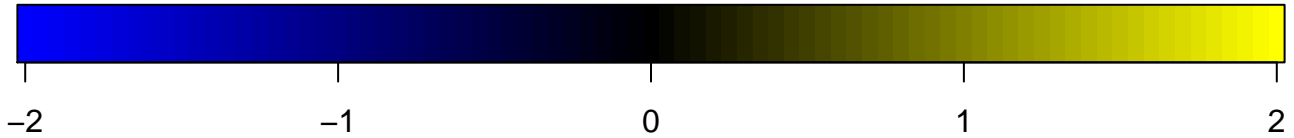
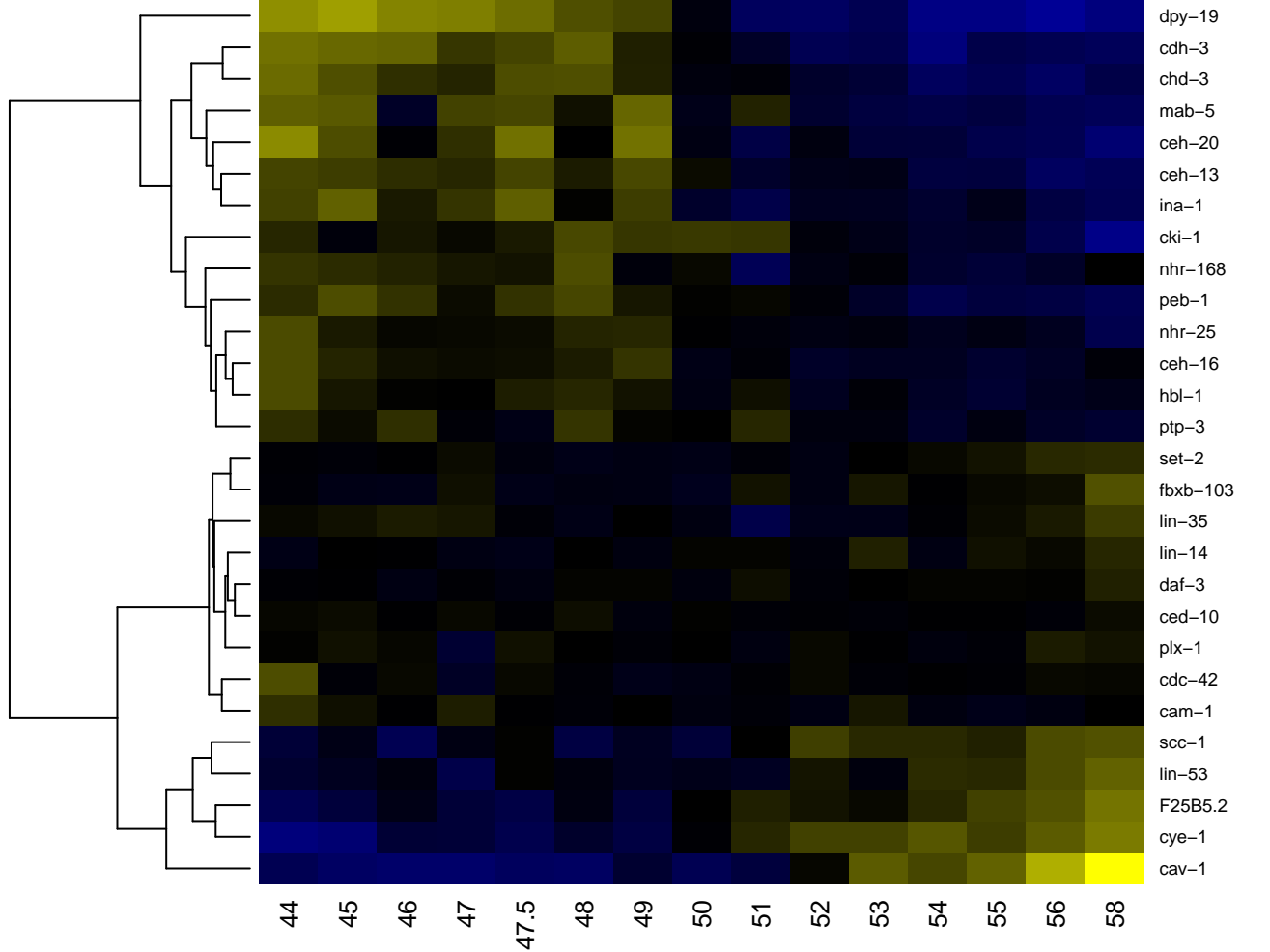
uv2



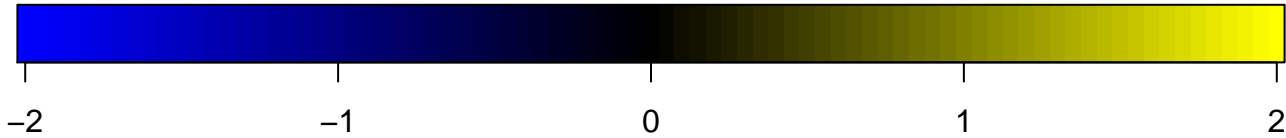
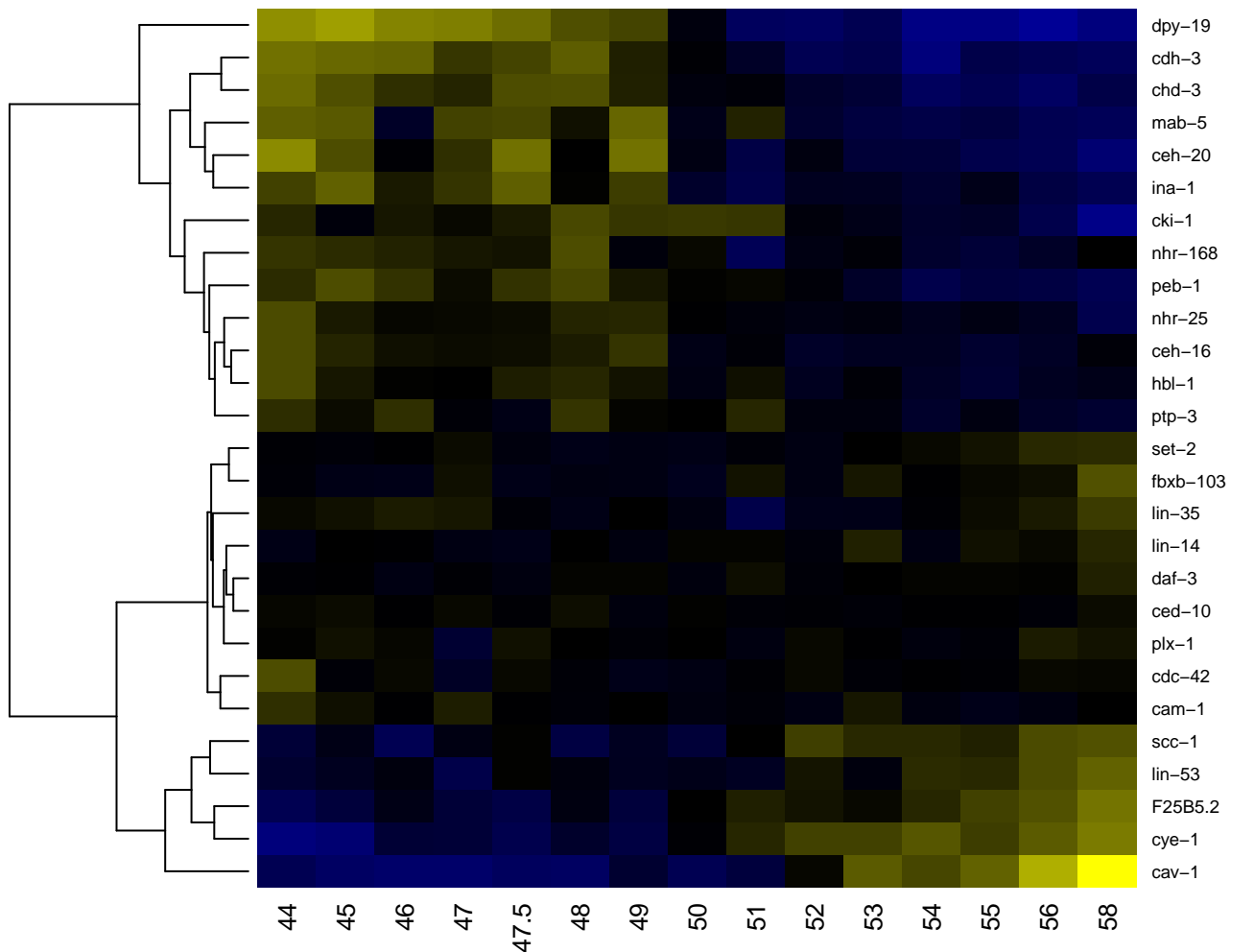
uv3



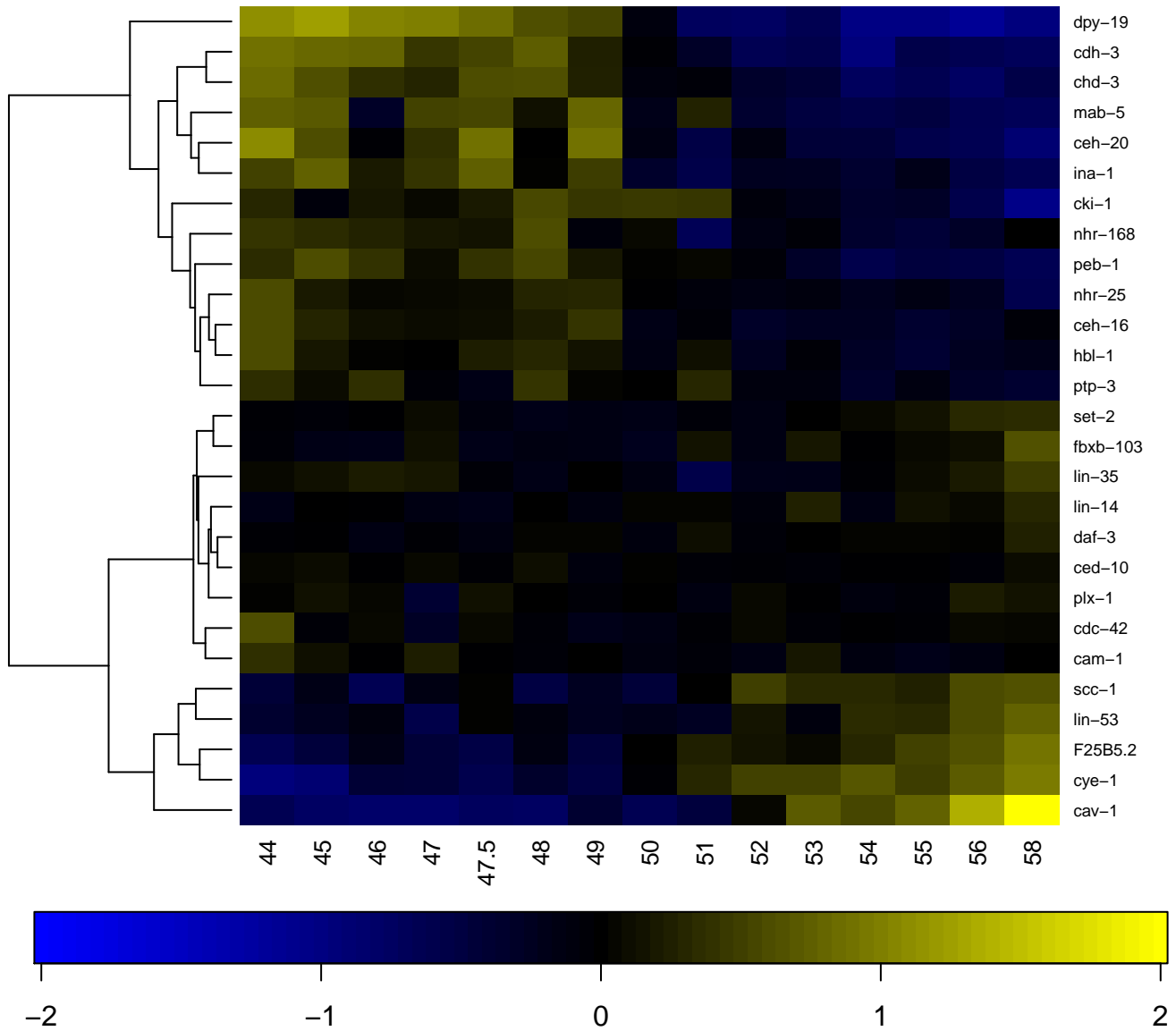
V1L



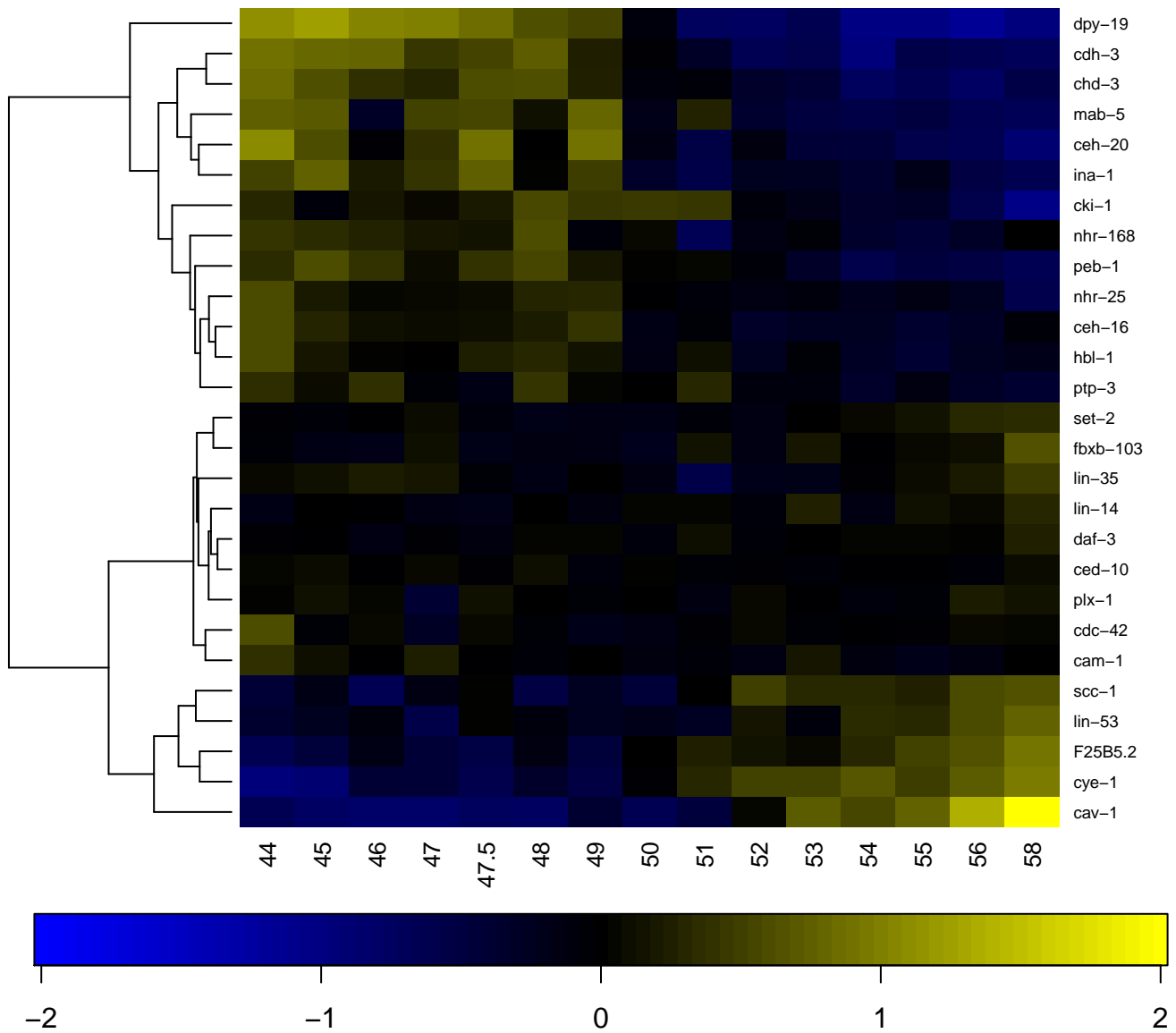
V1R



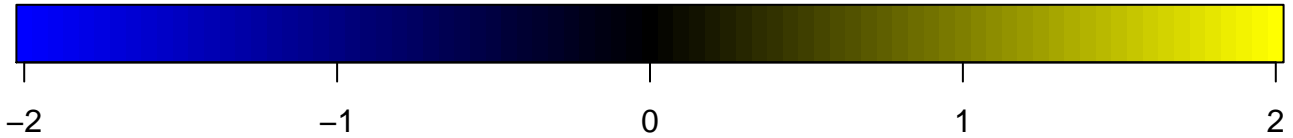
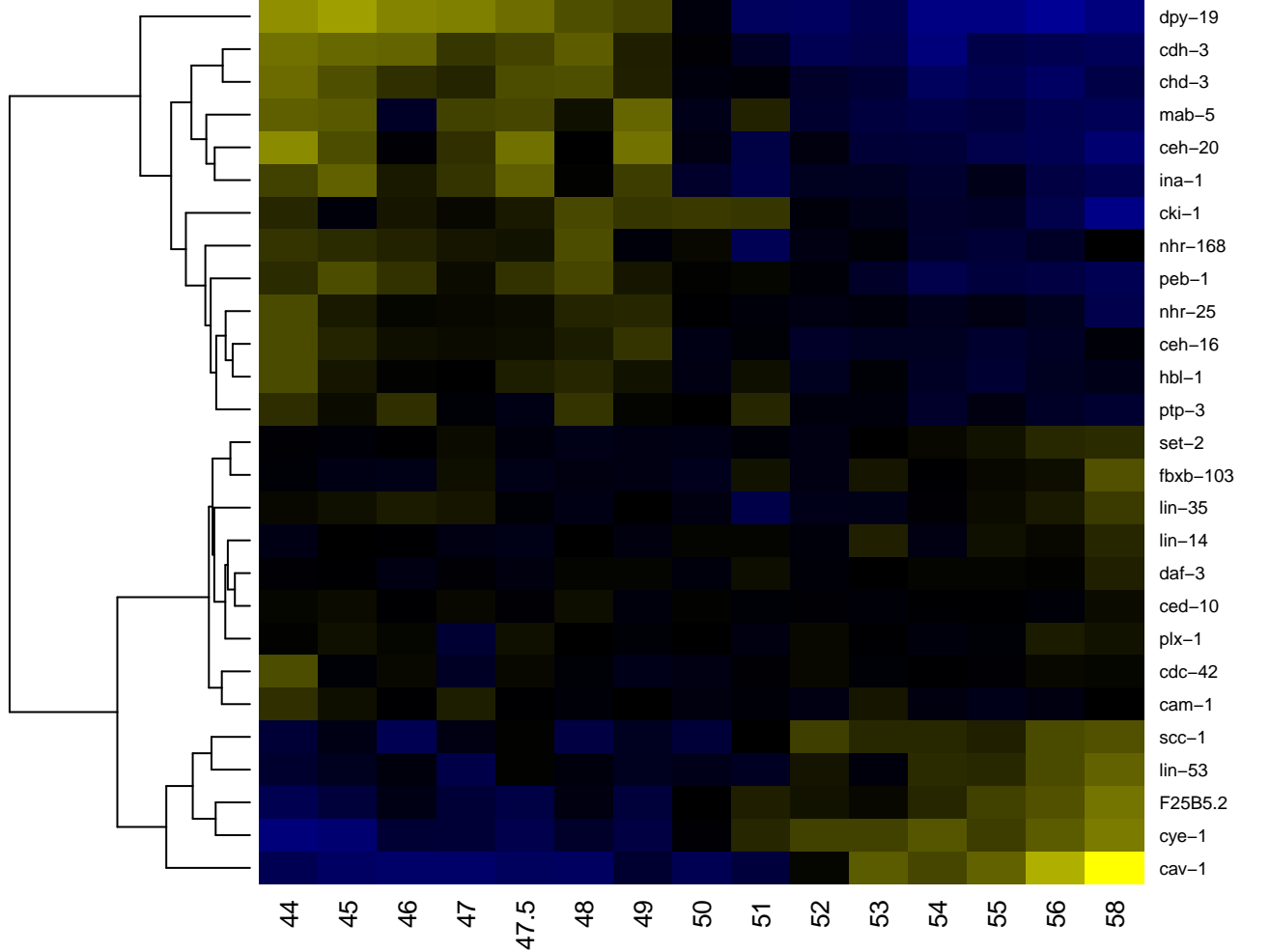
V2L



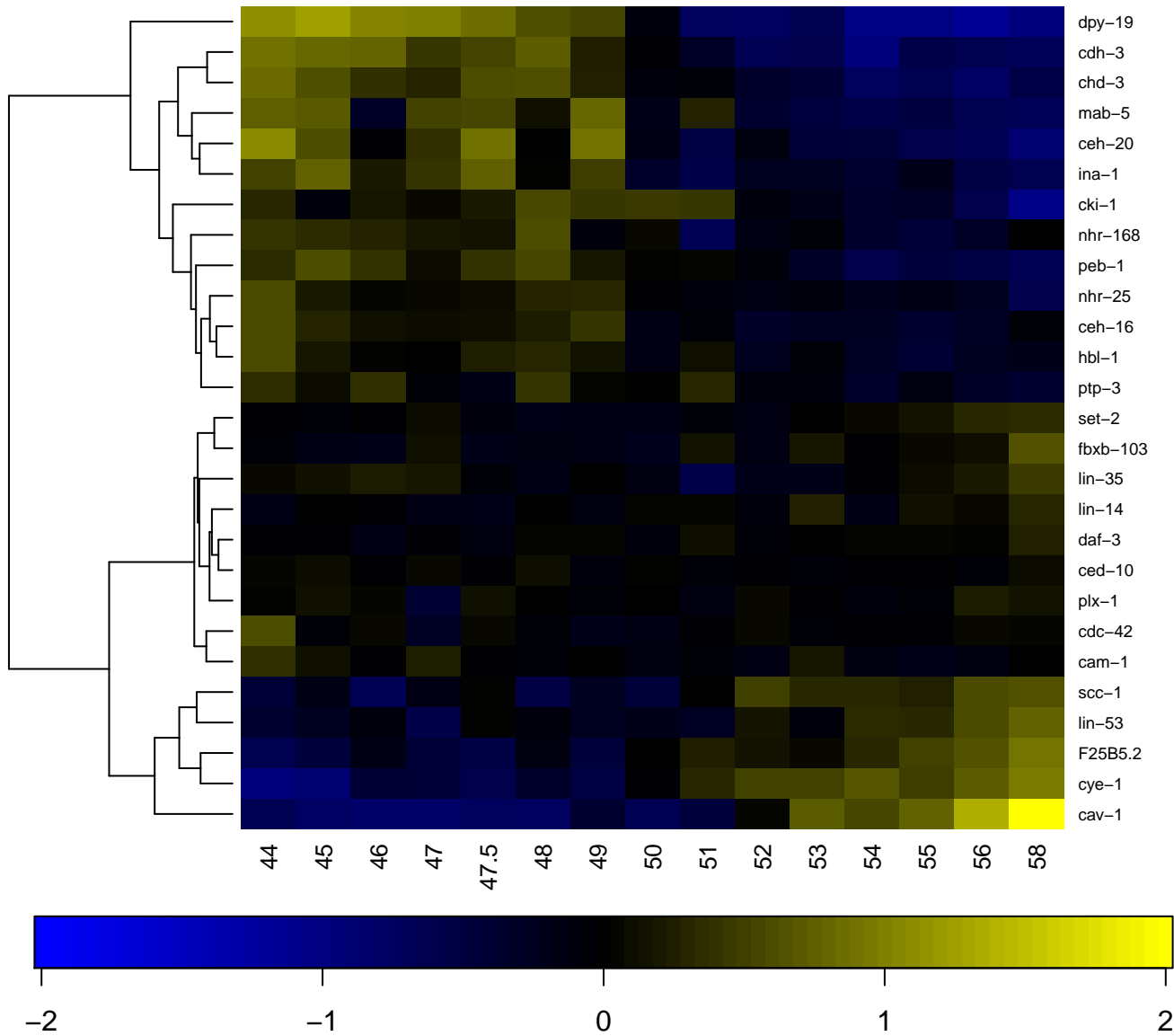
V3R



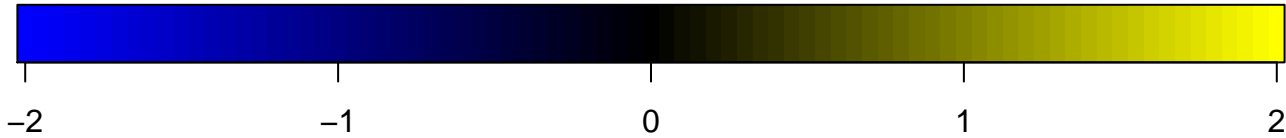
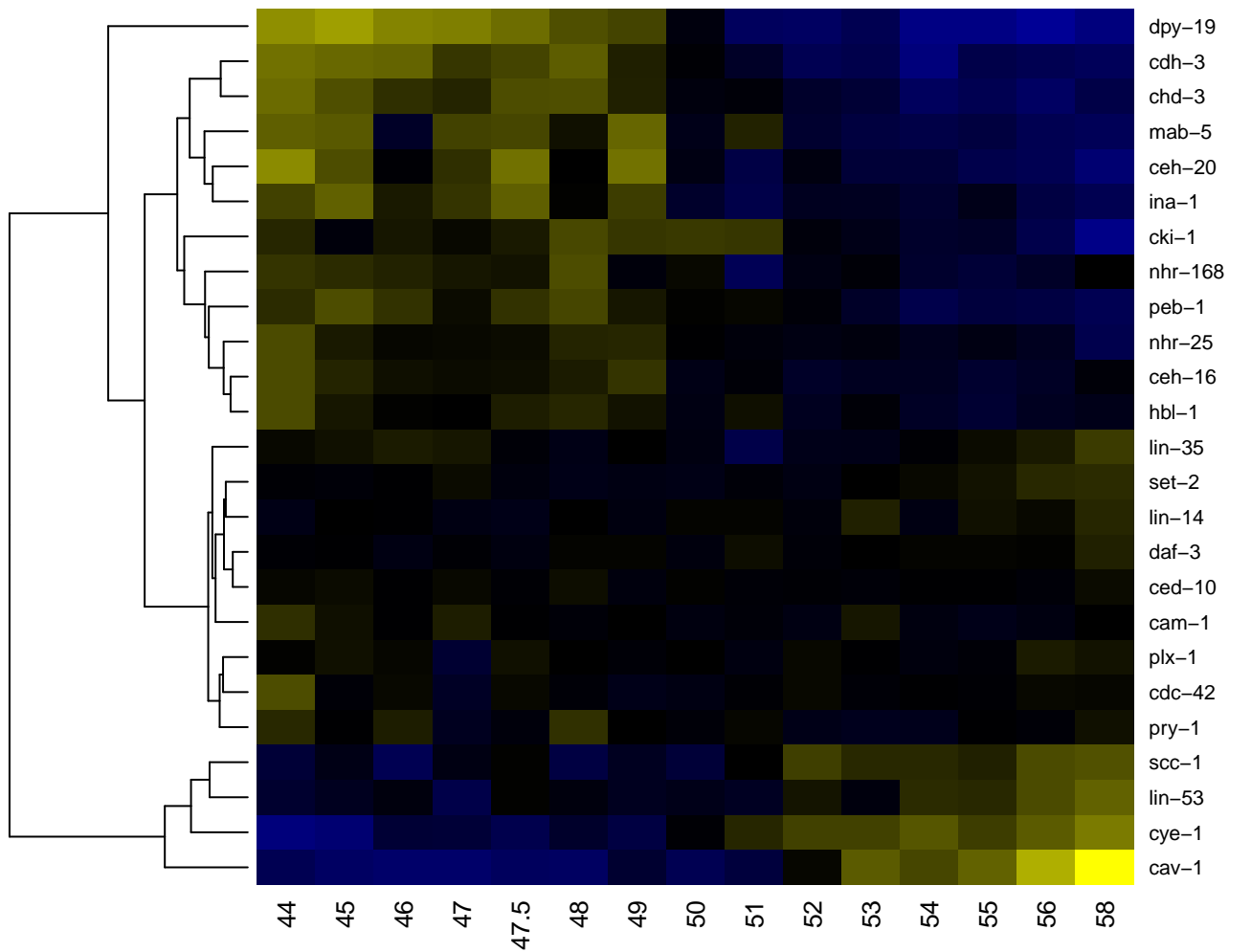
V4L



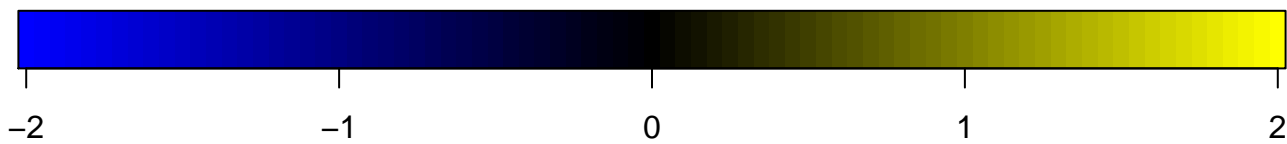
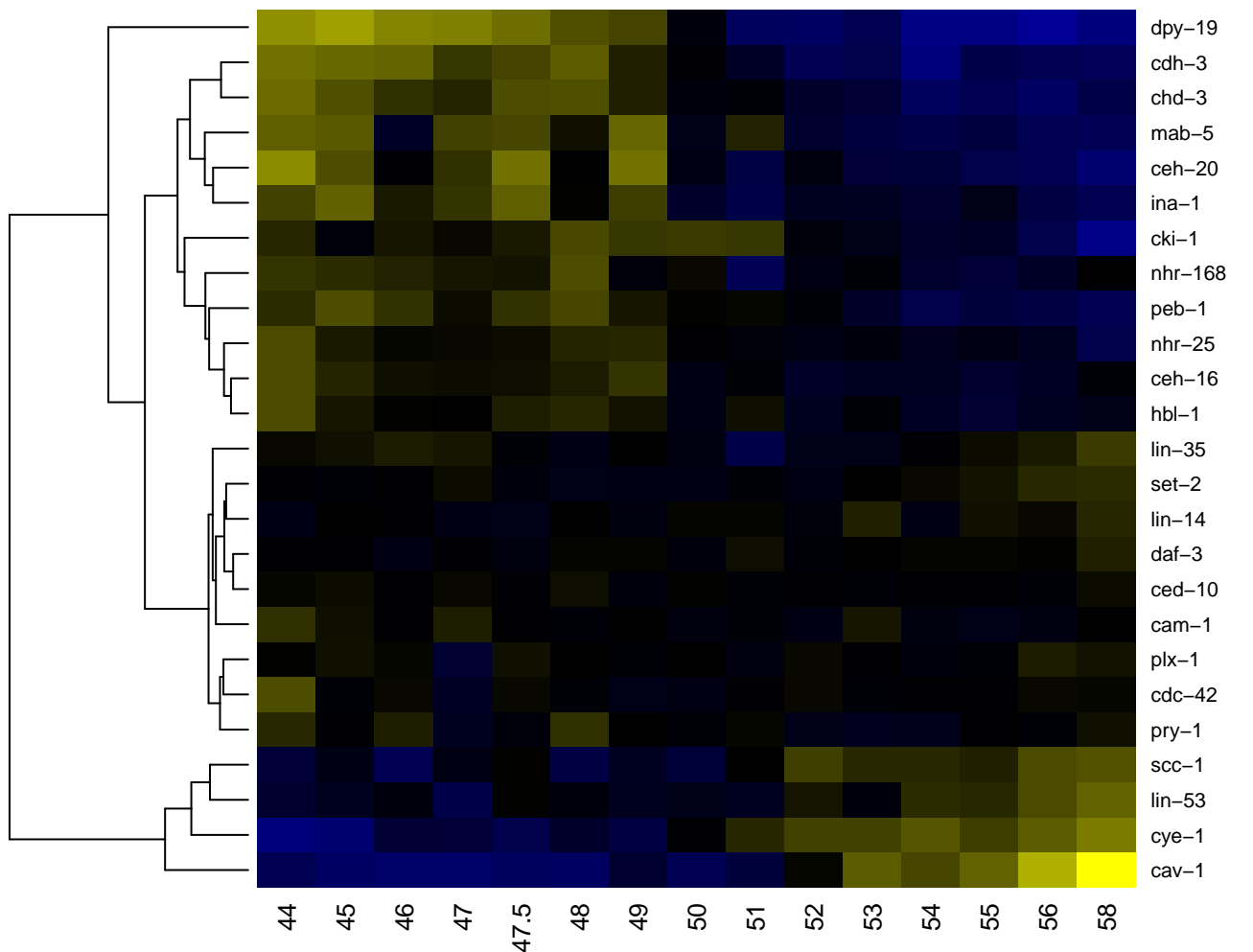
V4R



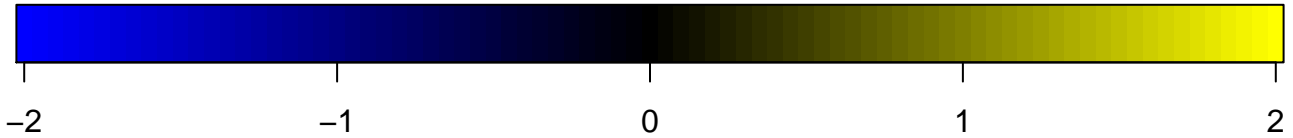
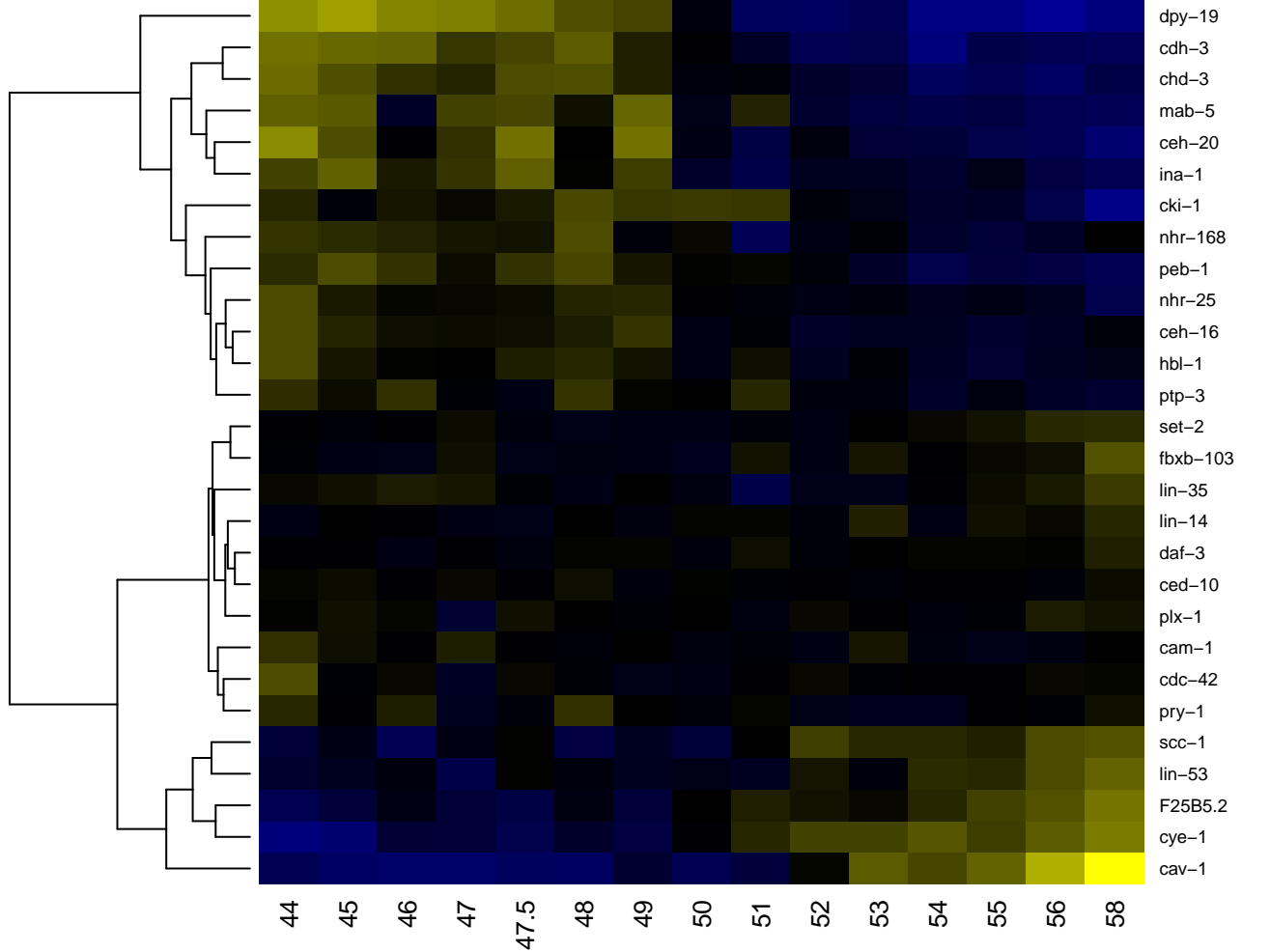
V5L



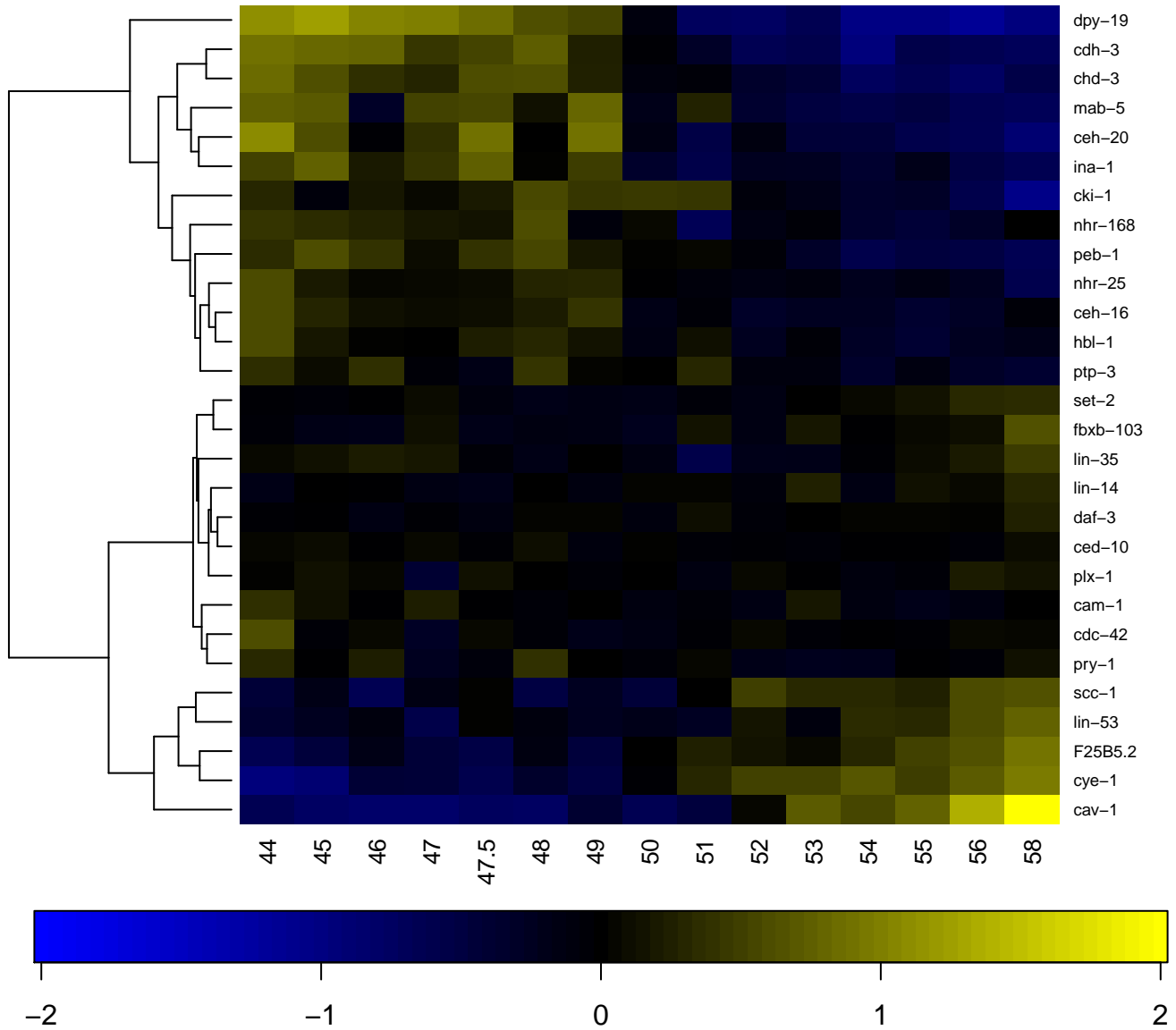
V5R



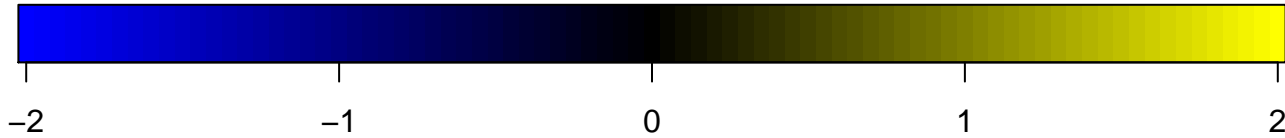
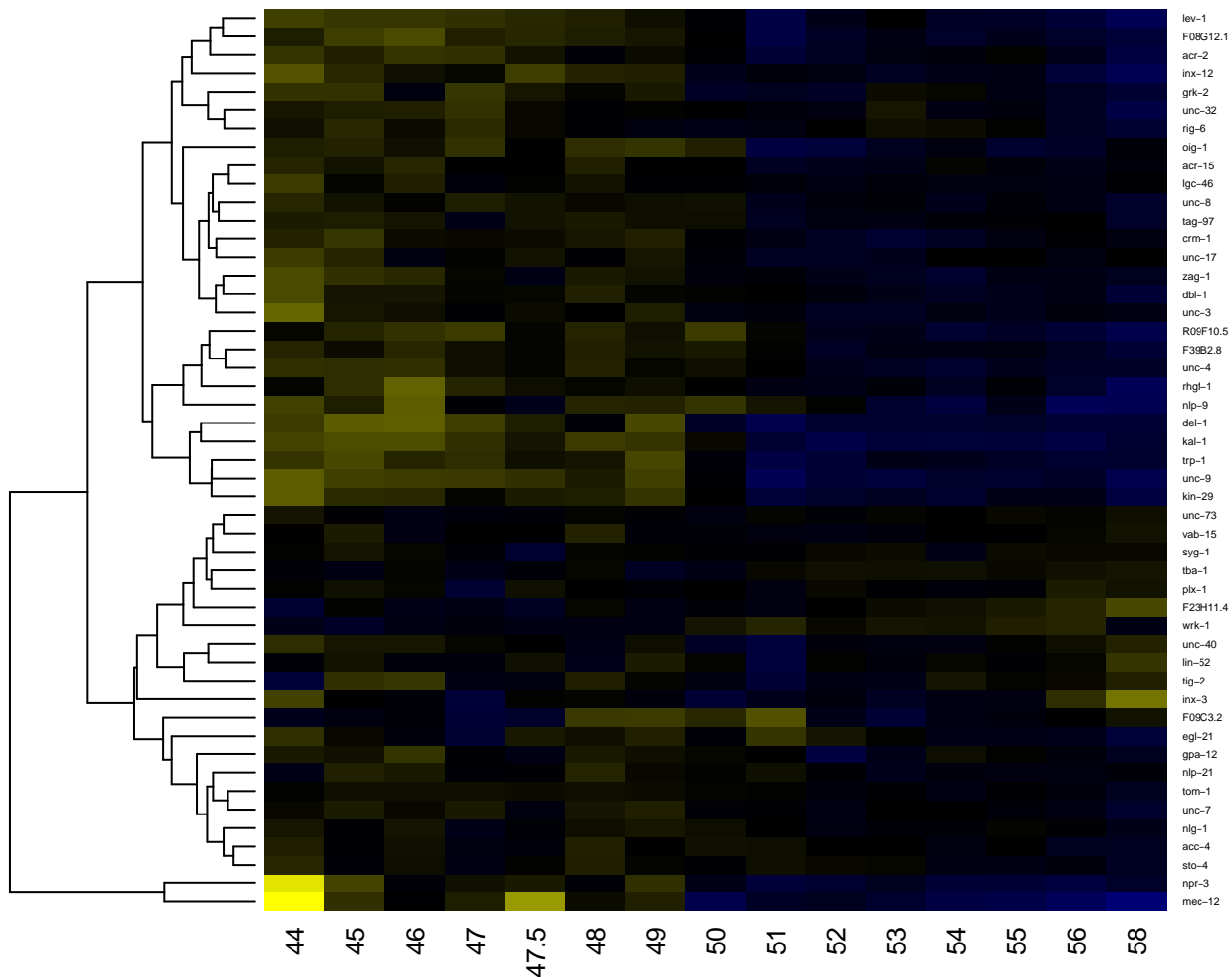
V6L



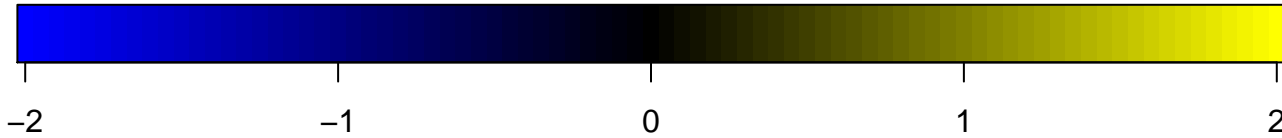
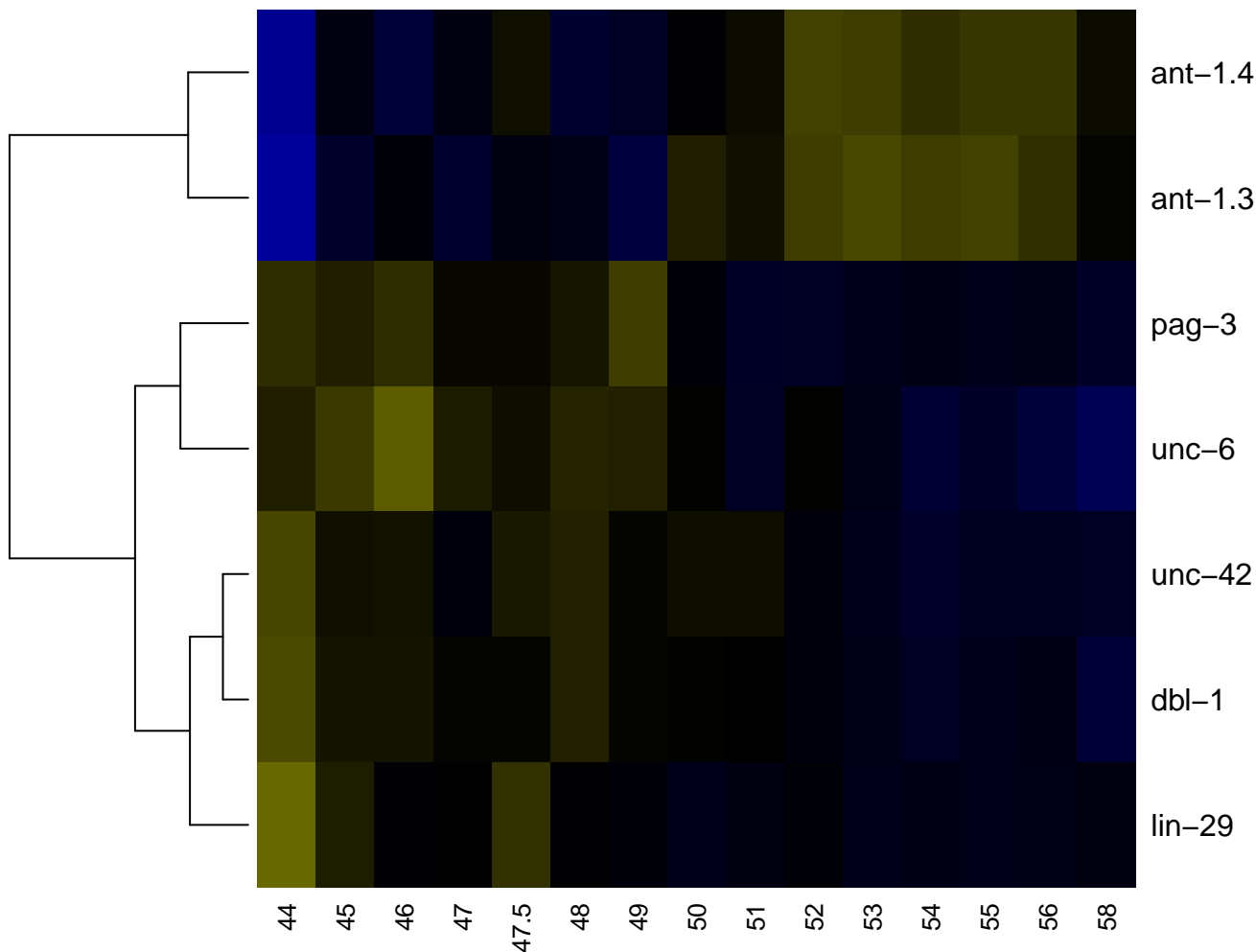
V6R



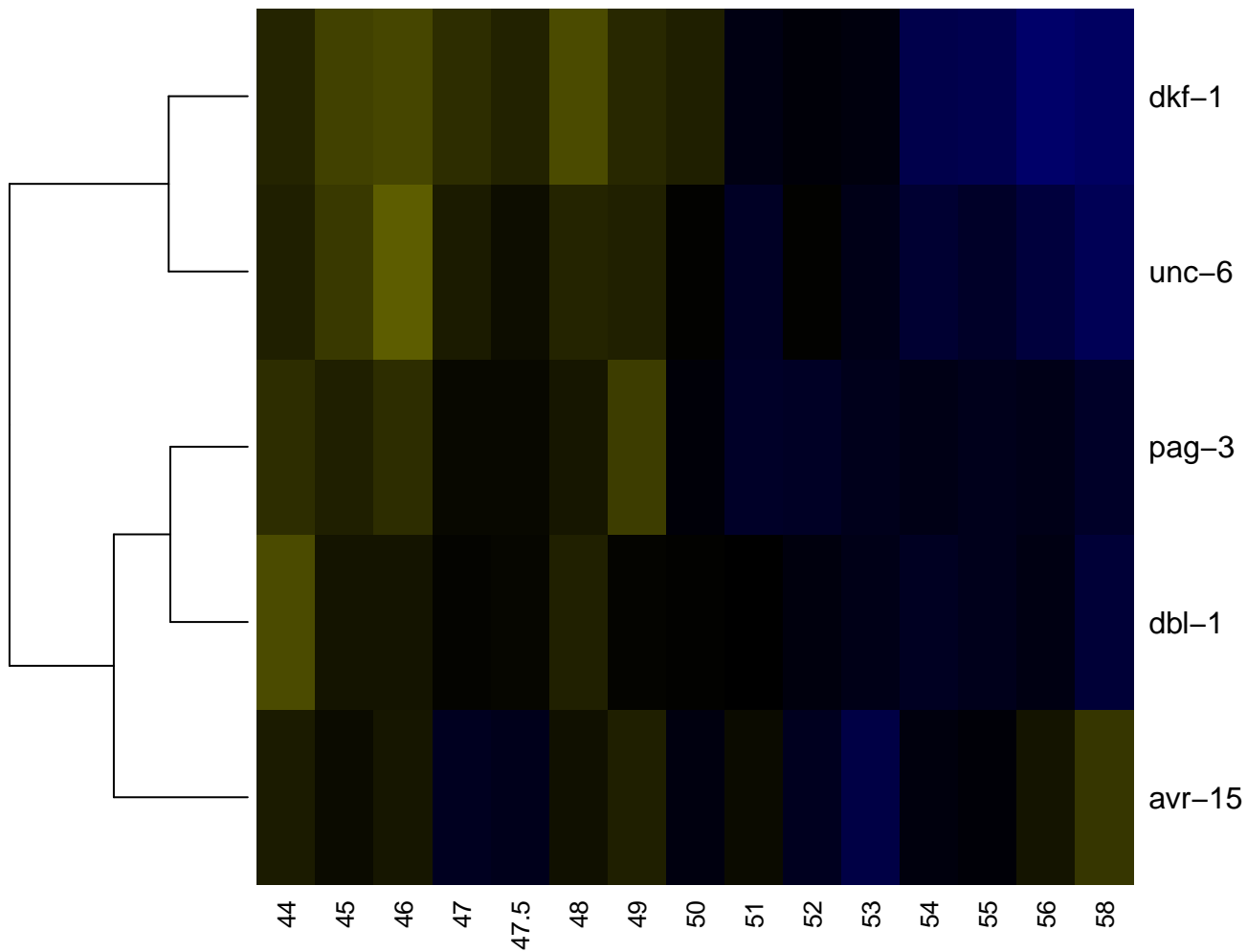
VA neuron



VA11



VA12



-2

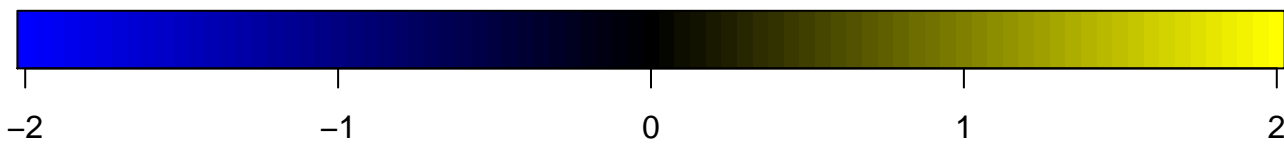
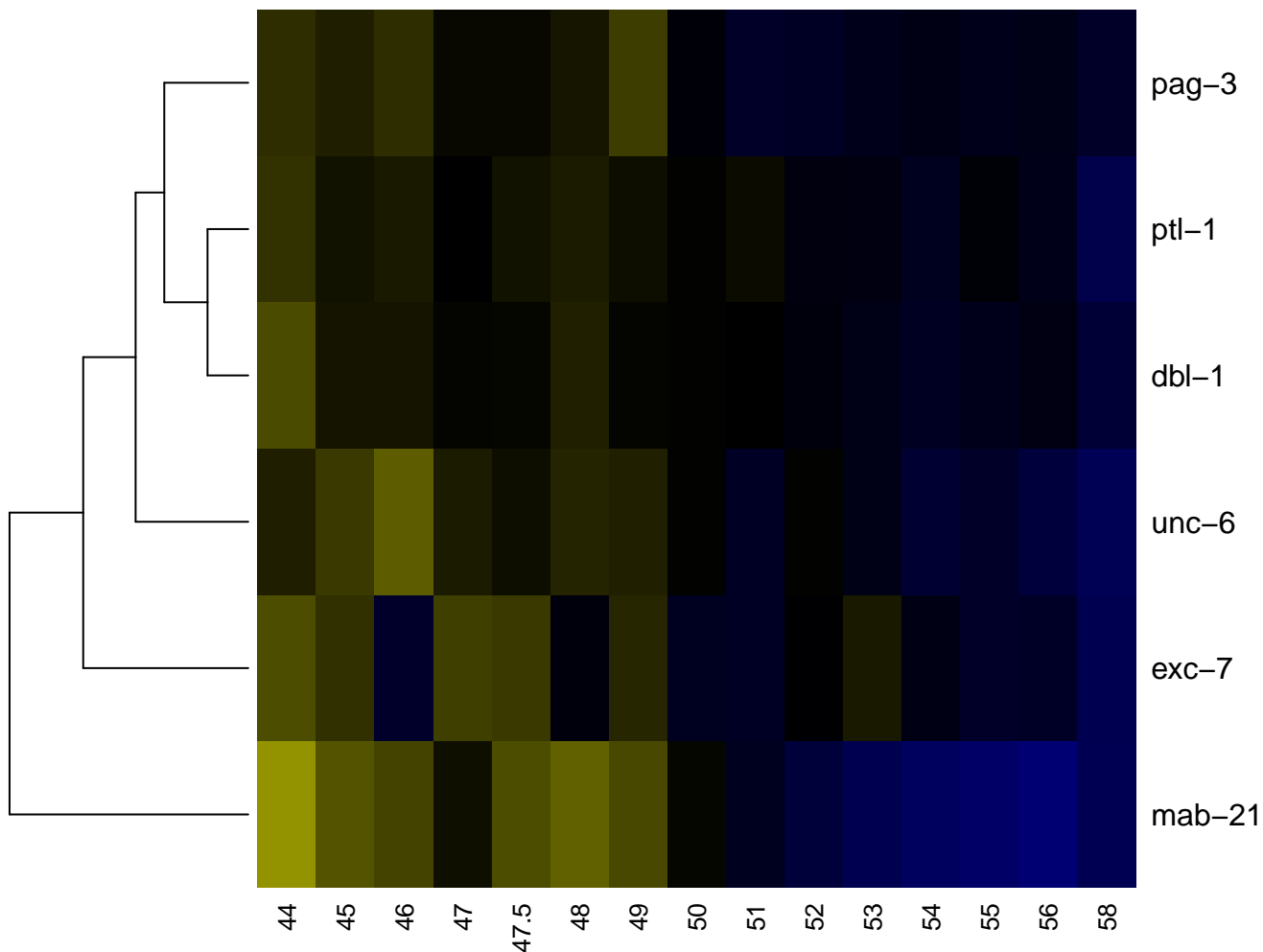
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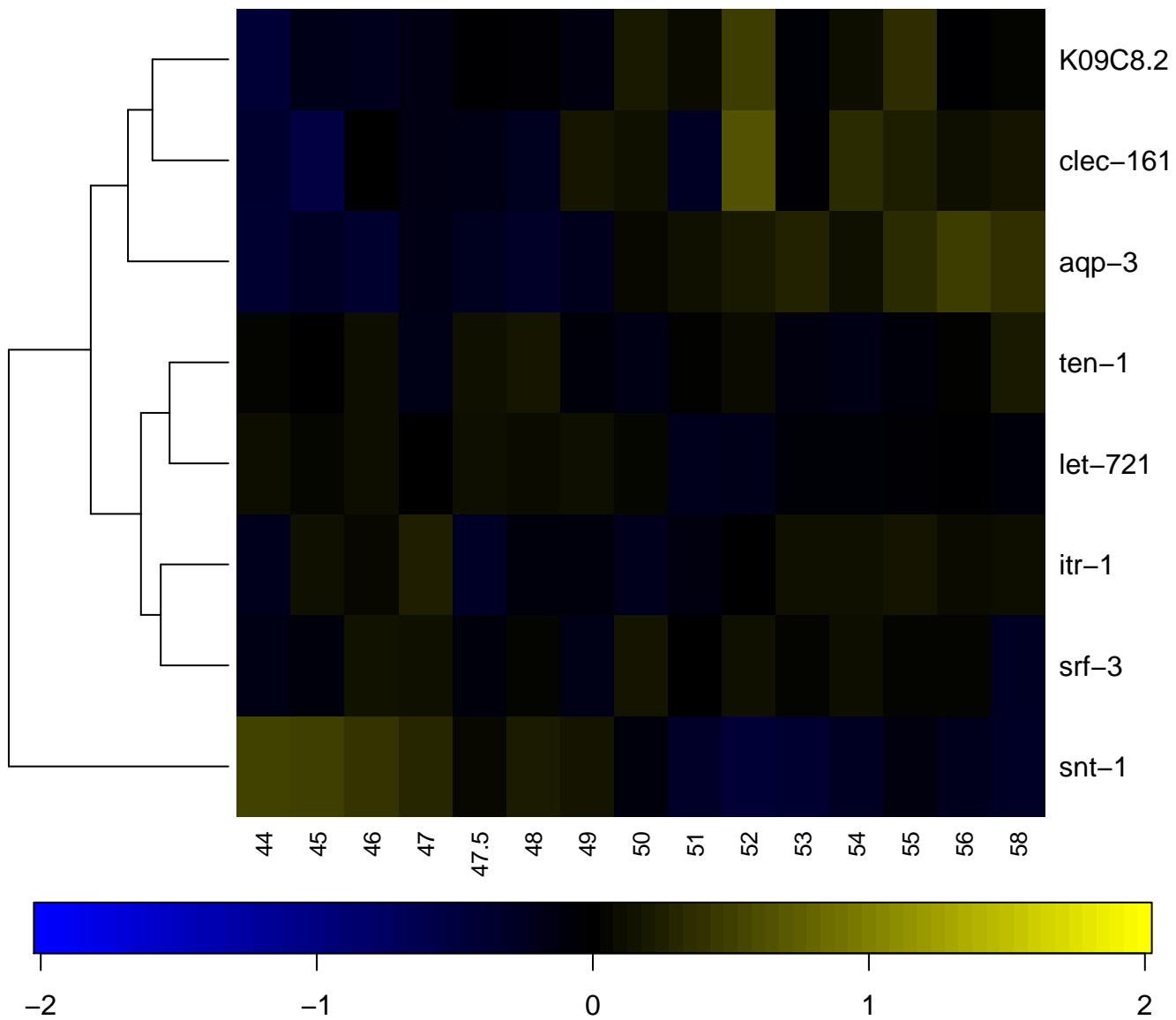
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2

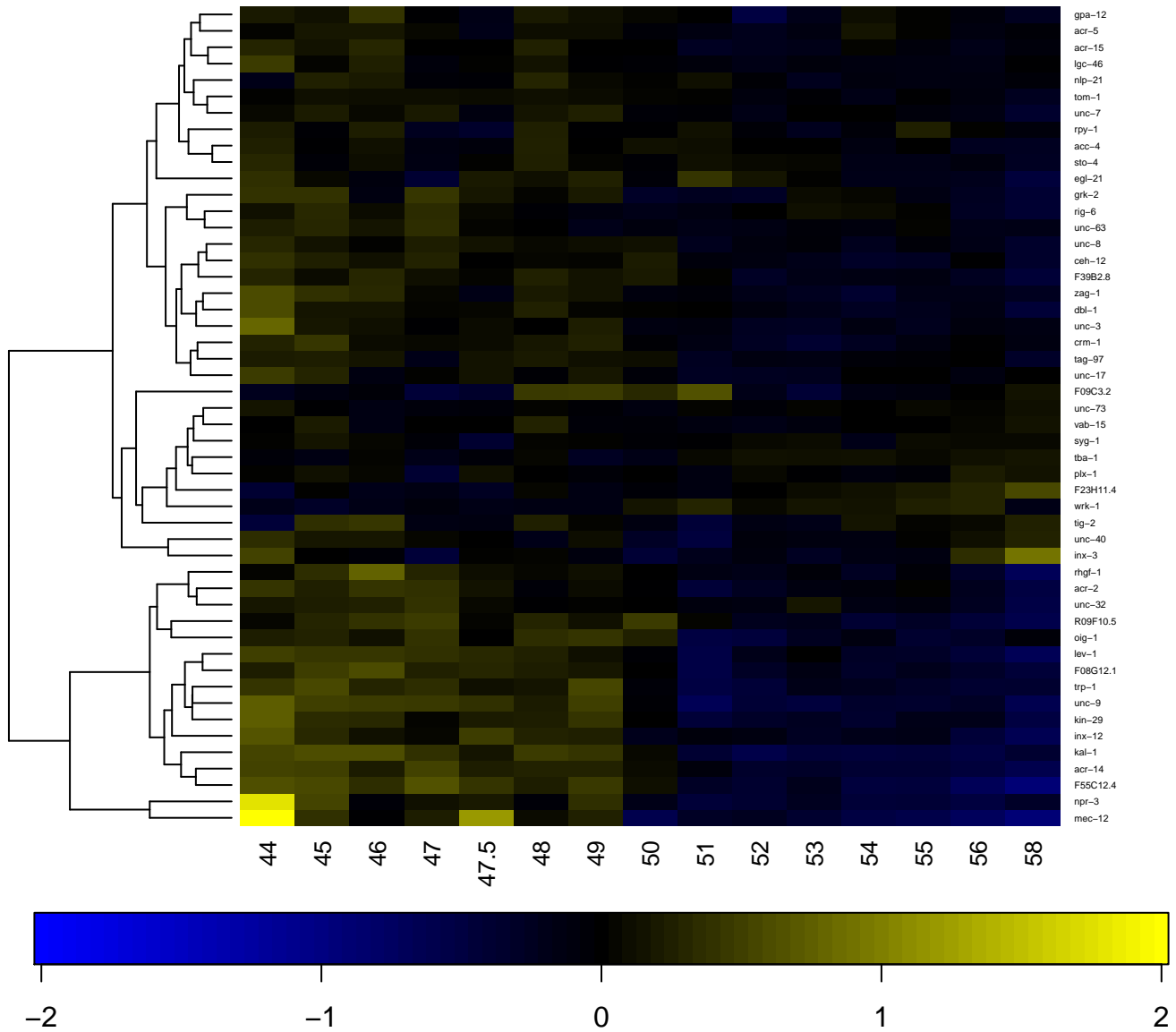
VA2



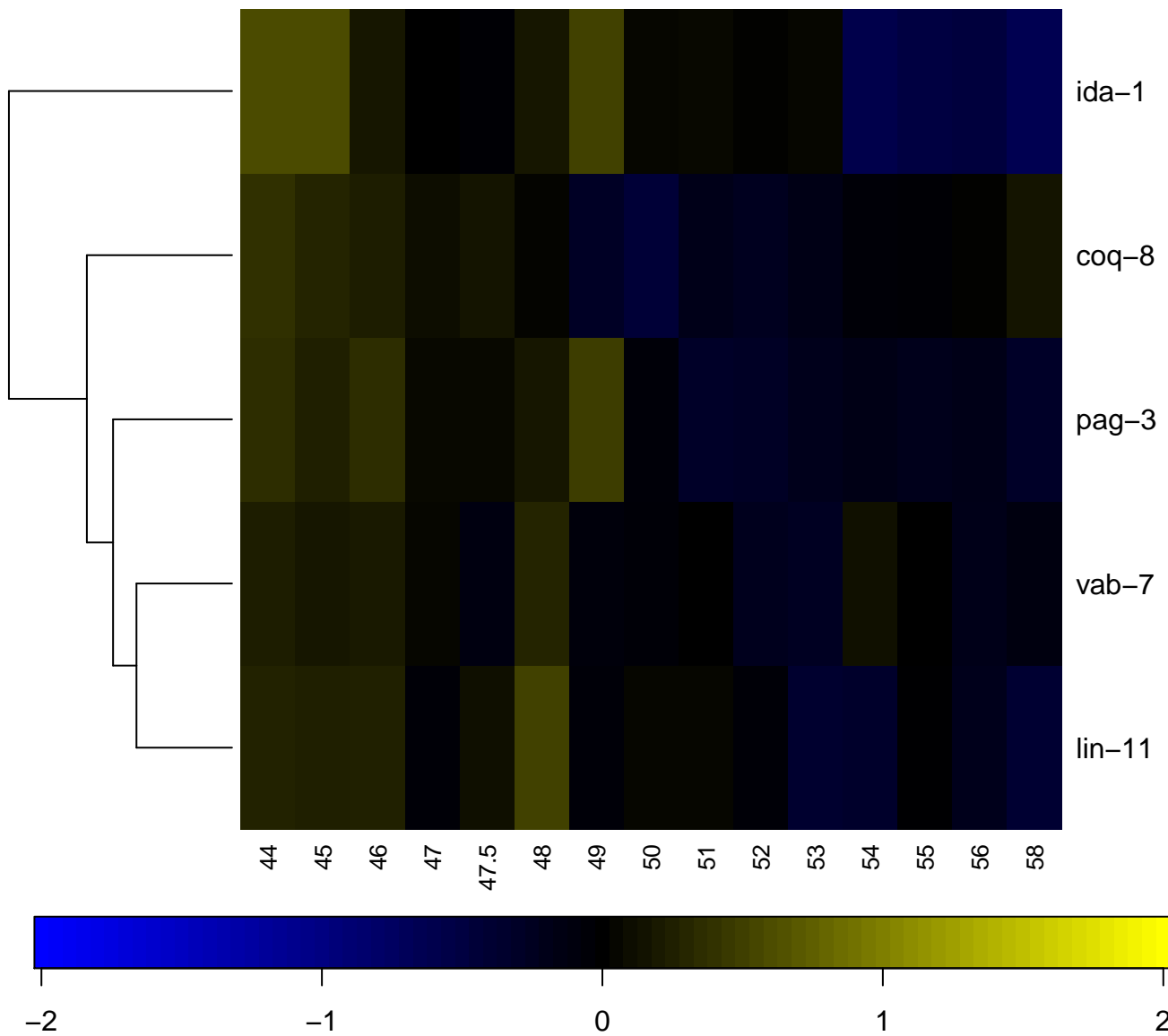
vas deferens



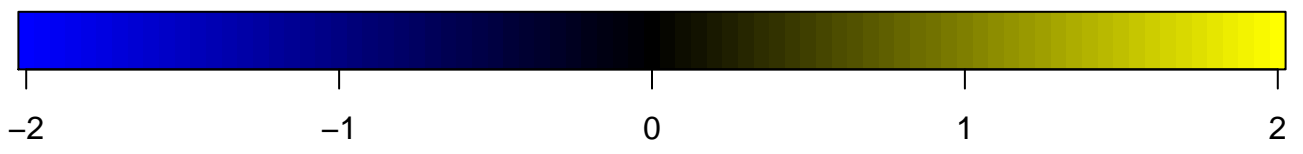
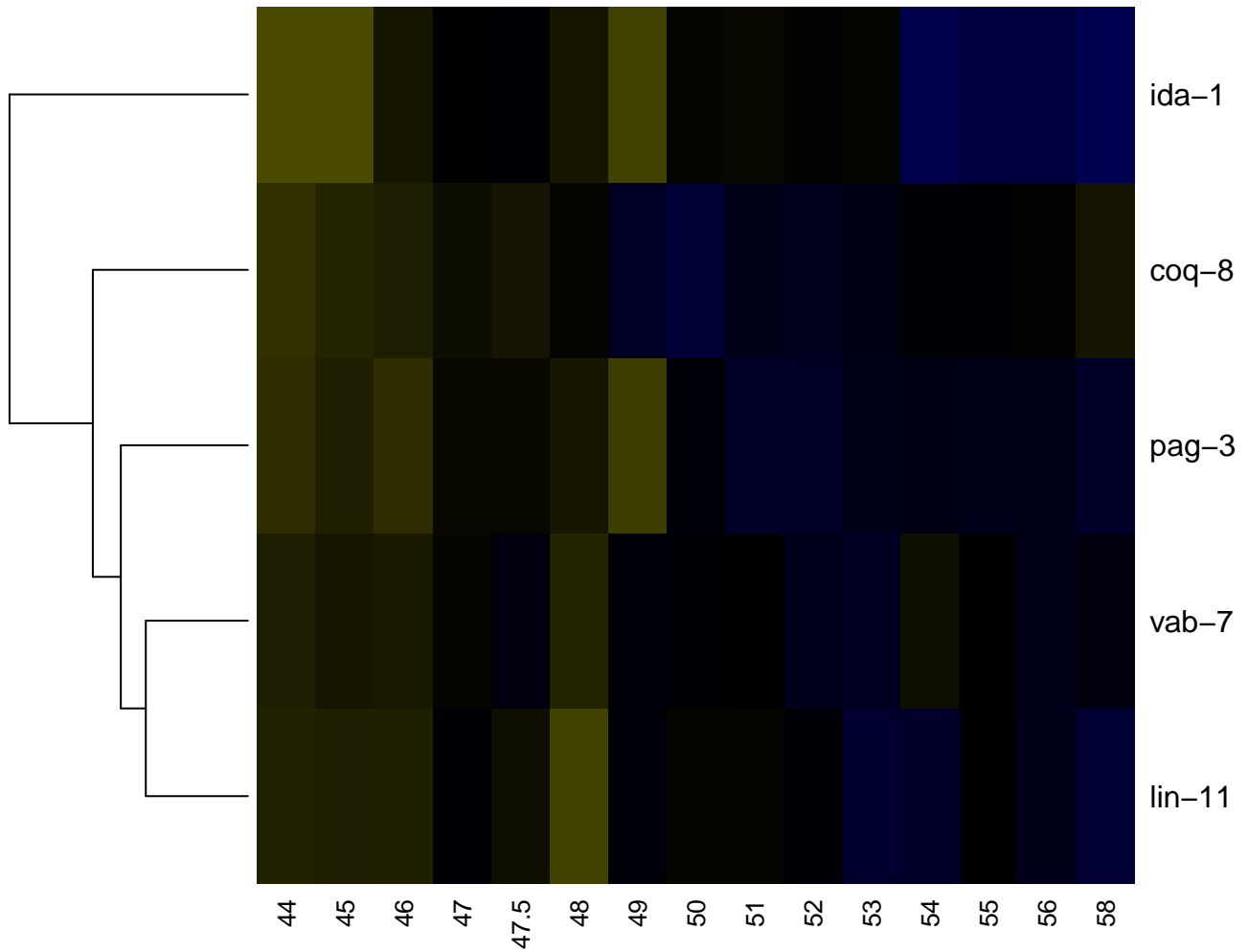
VB neuron



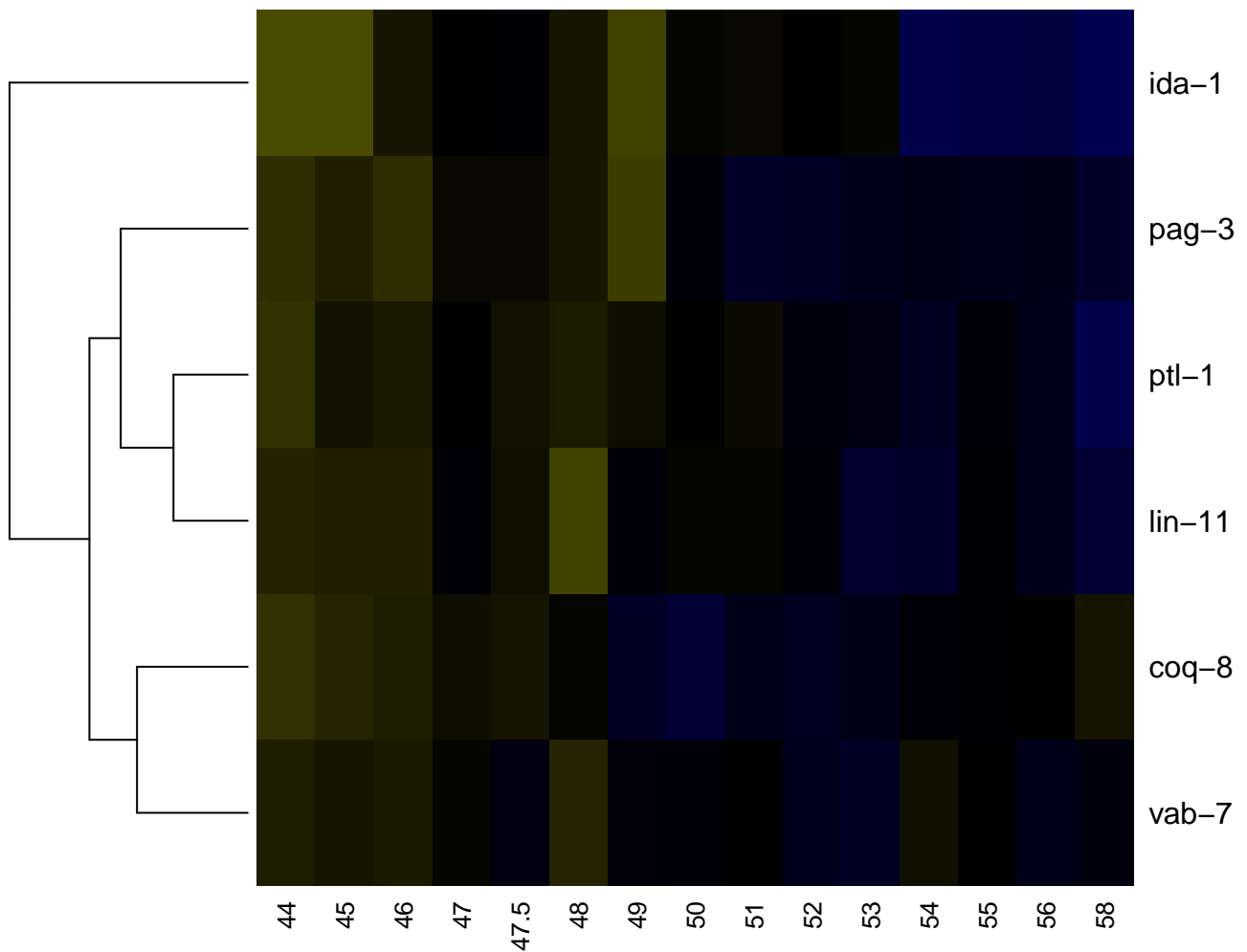
VC1



VC2



VC3



-2

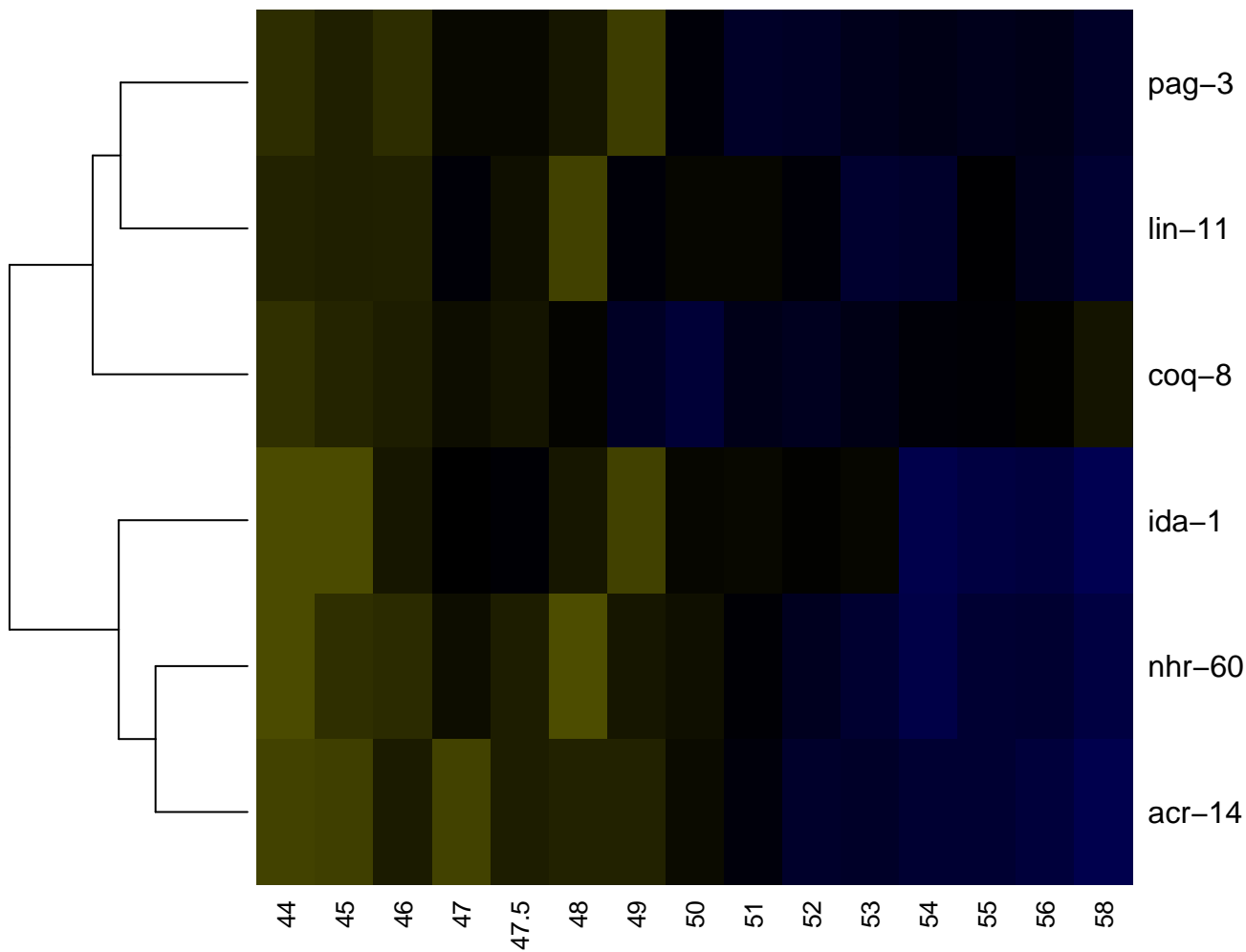
-1

0

1

2

VC4



-2

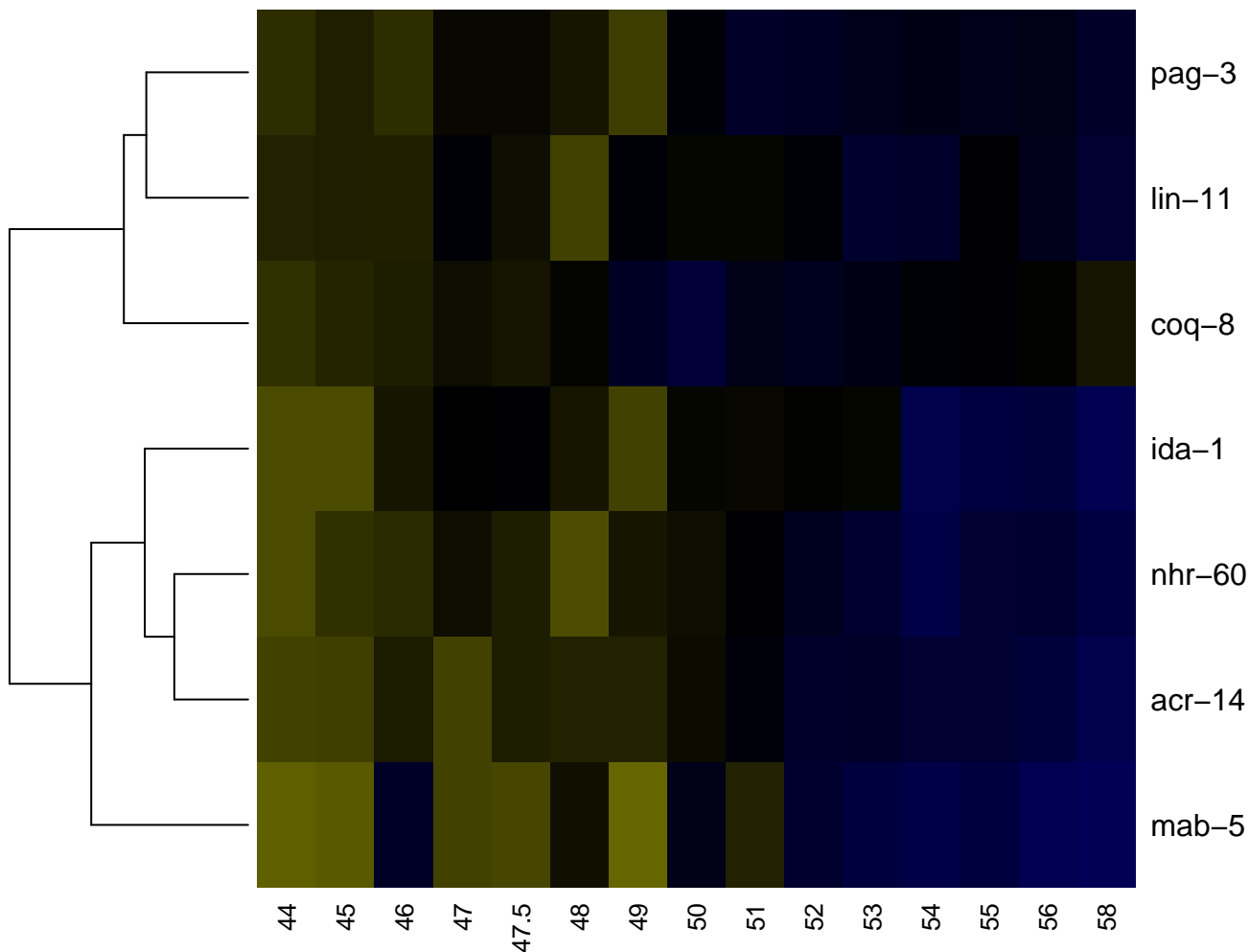
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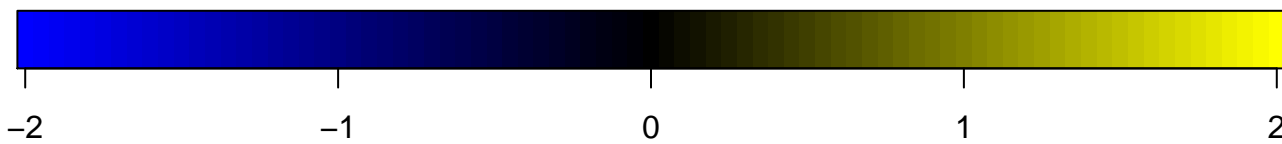
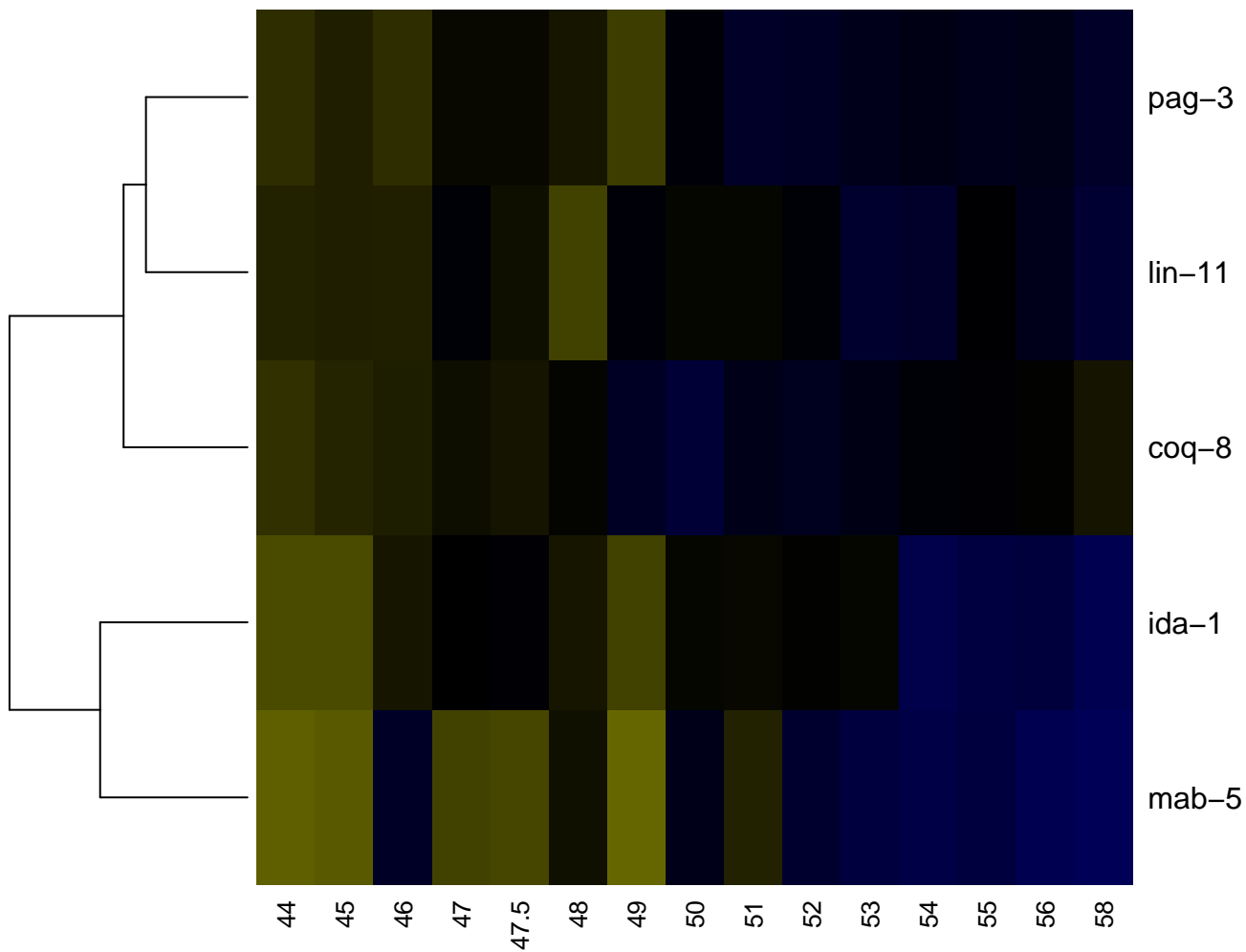
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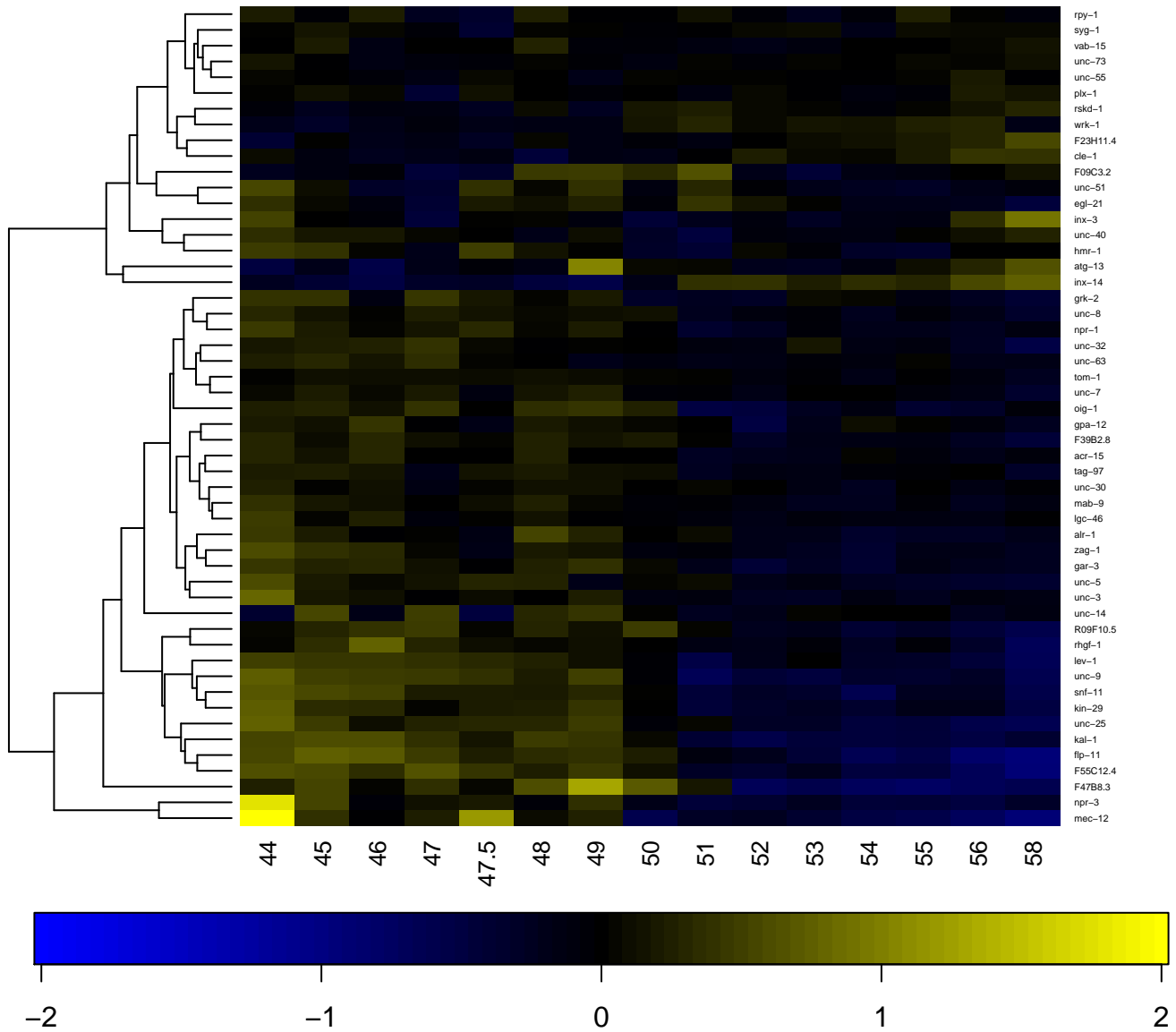
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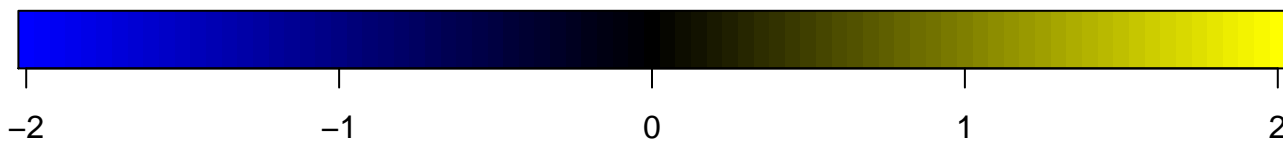
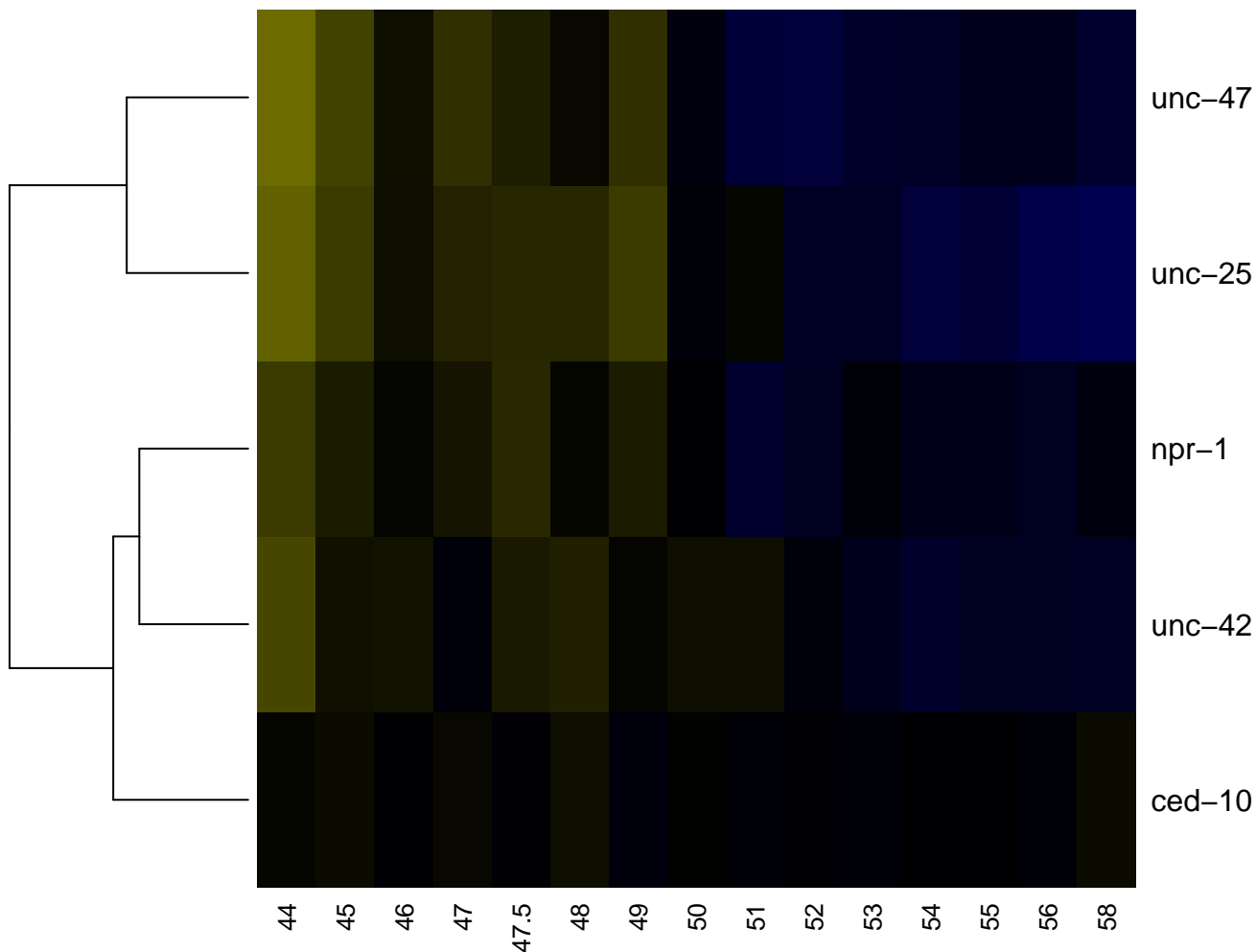
VC6



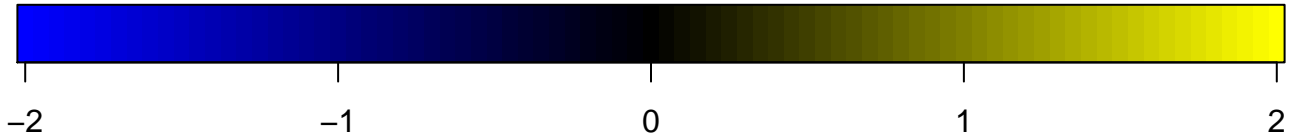
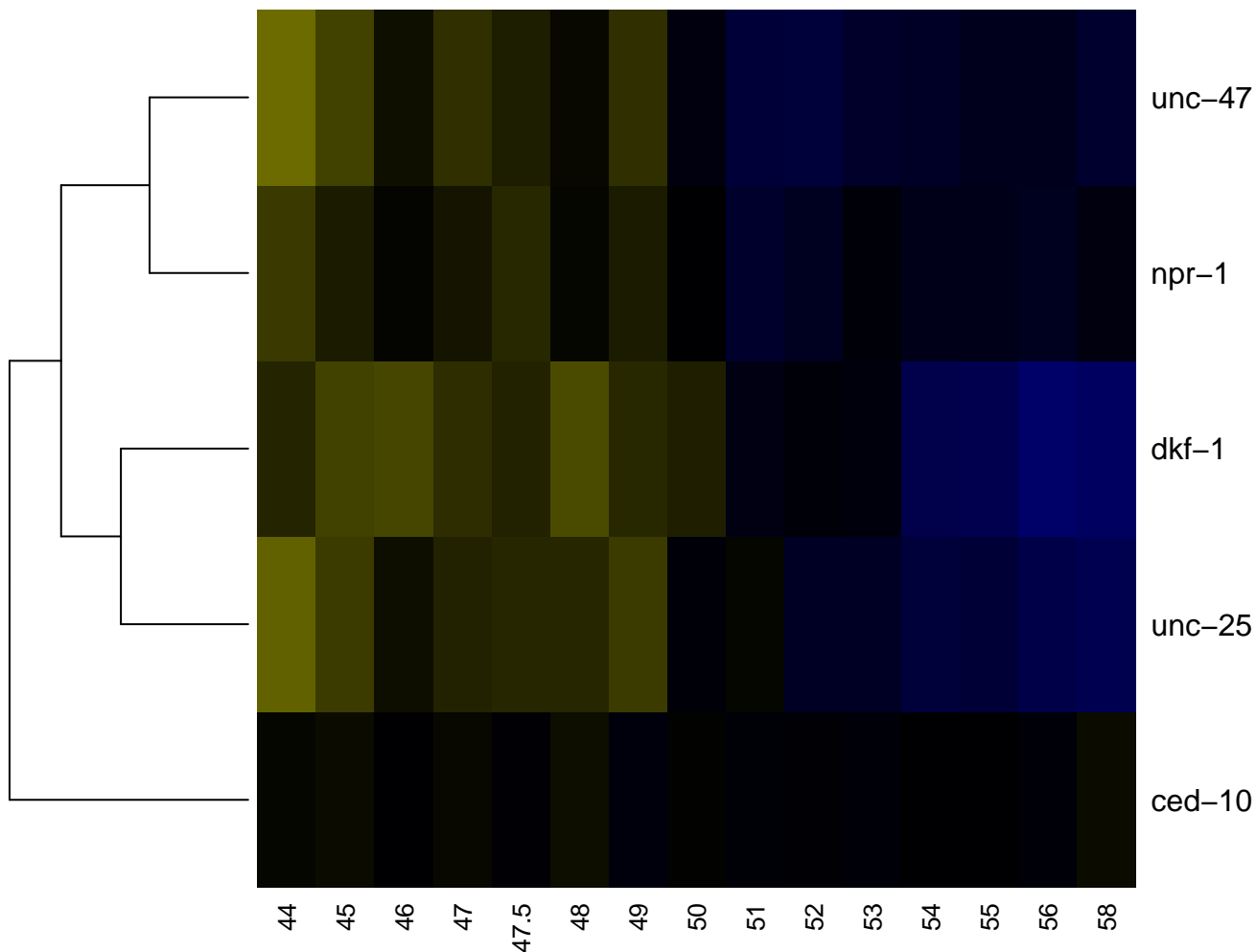
VD neuron



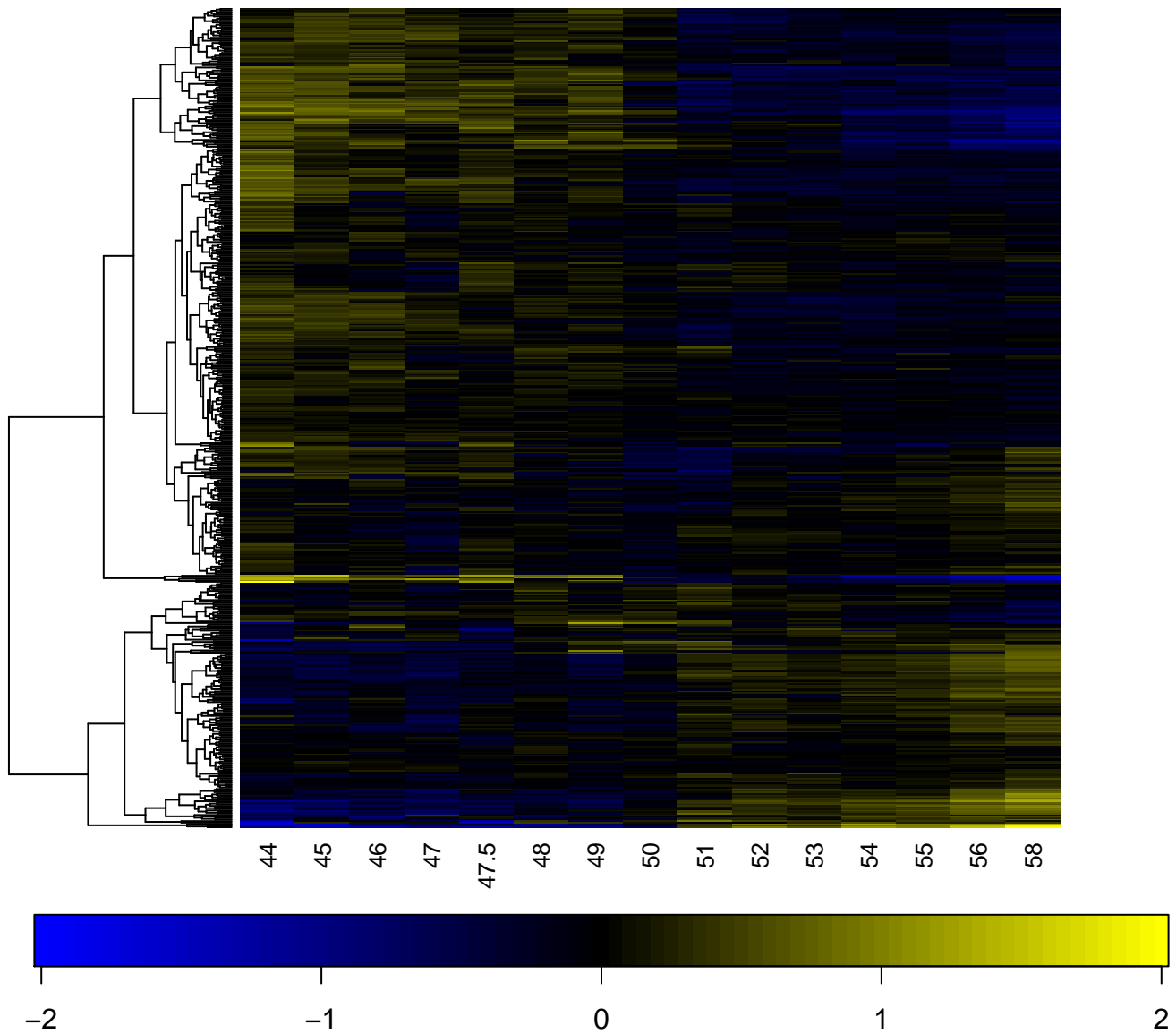
VD12



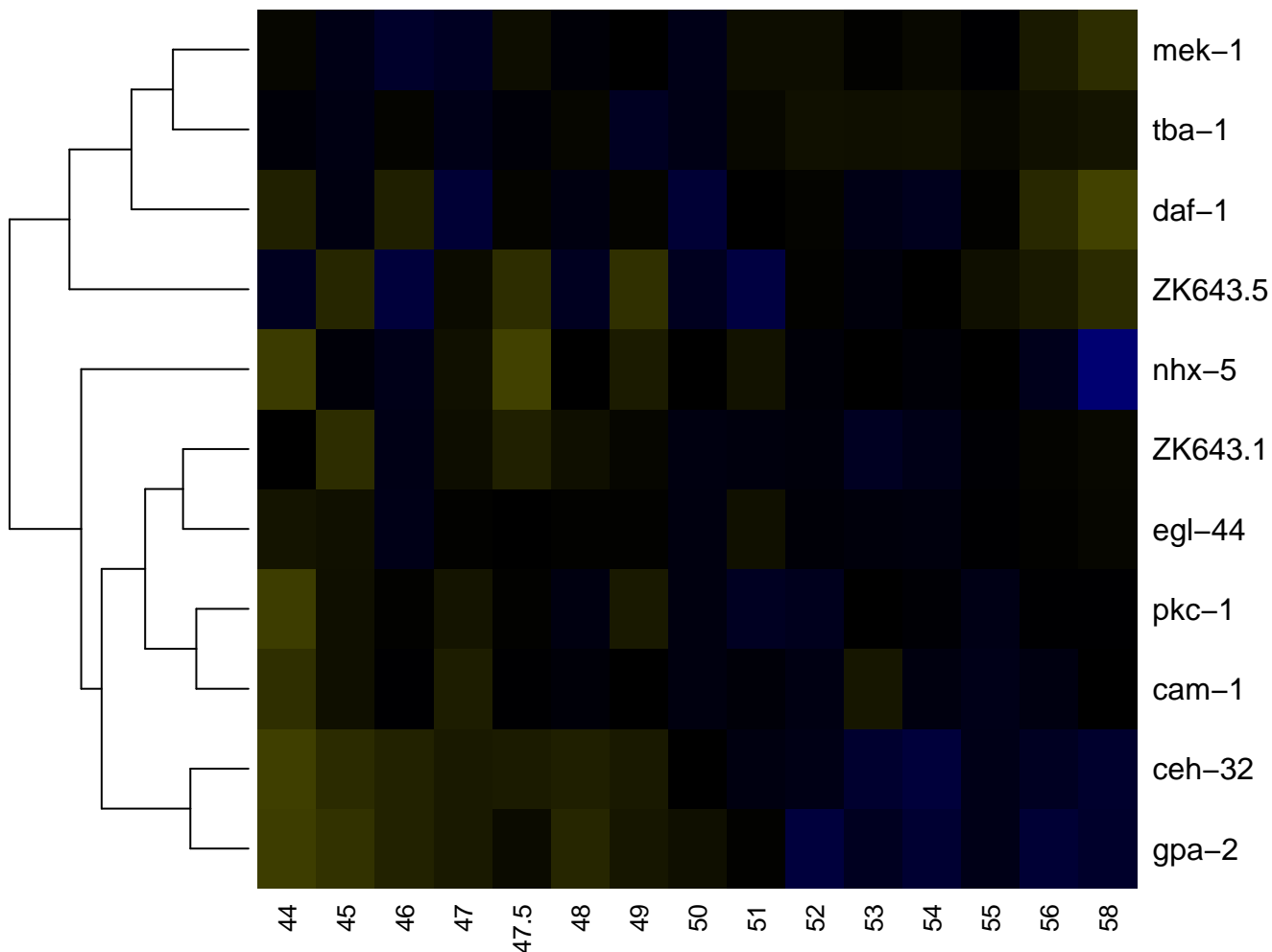
VD13



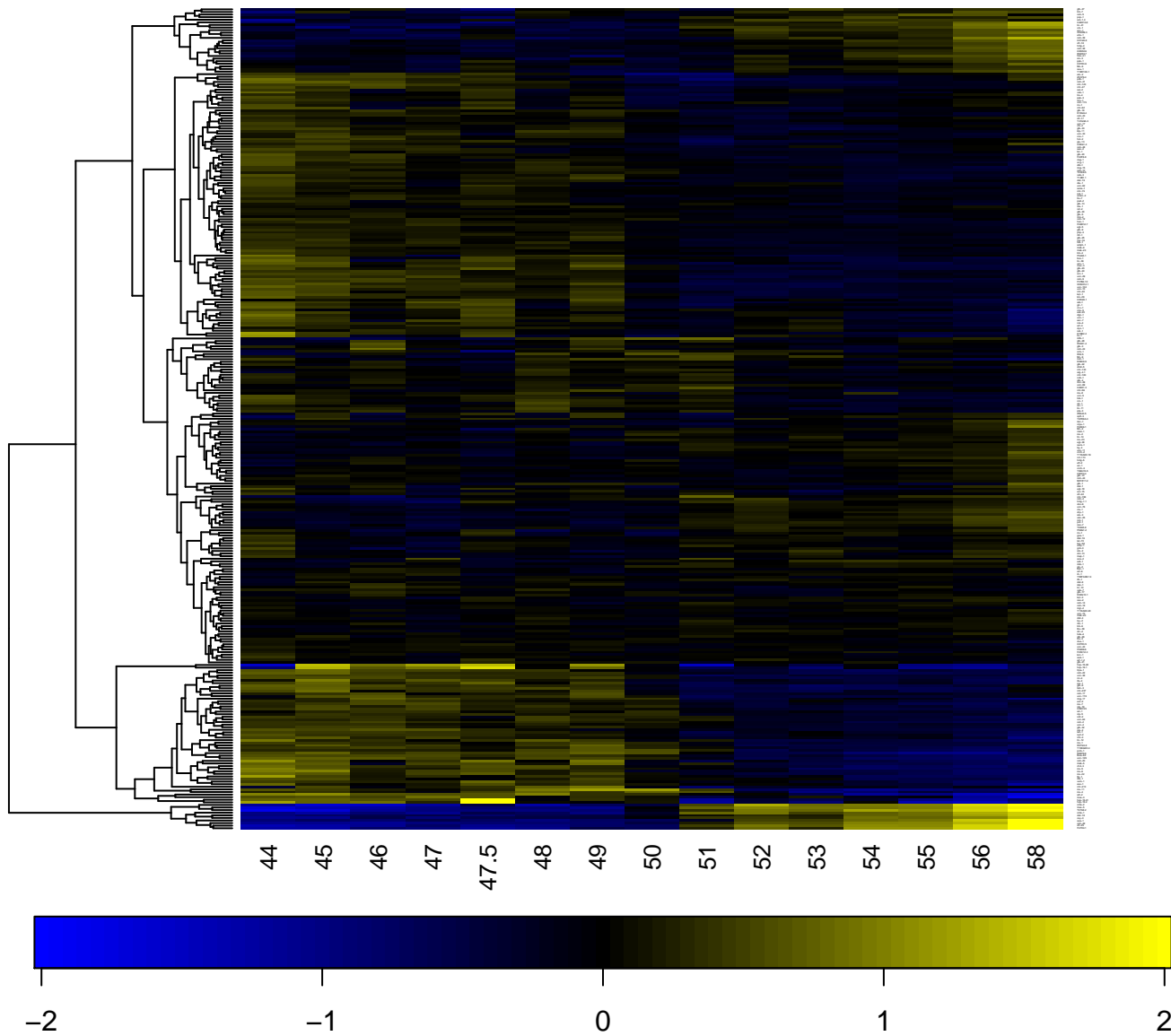
ventral cord neuron



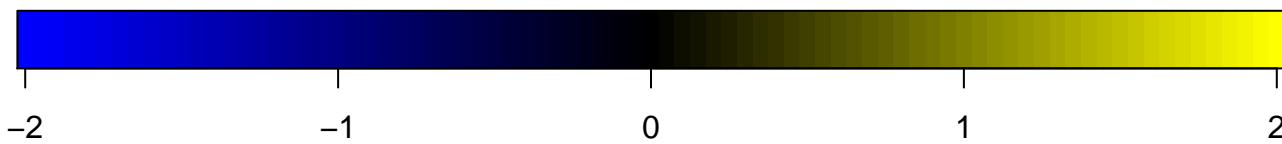
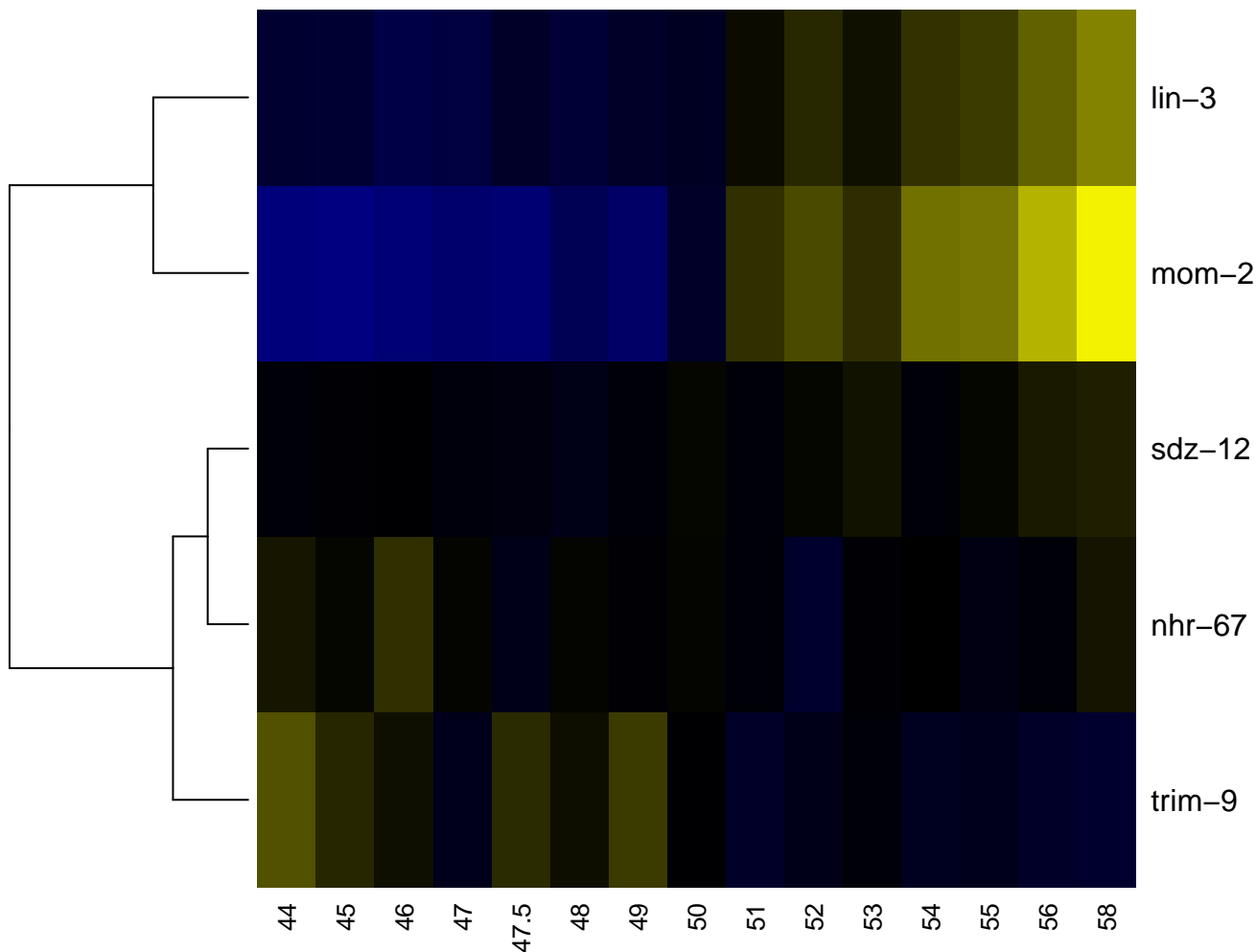
ventral ganglion



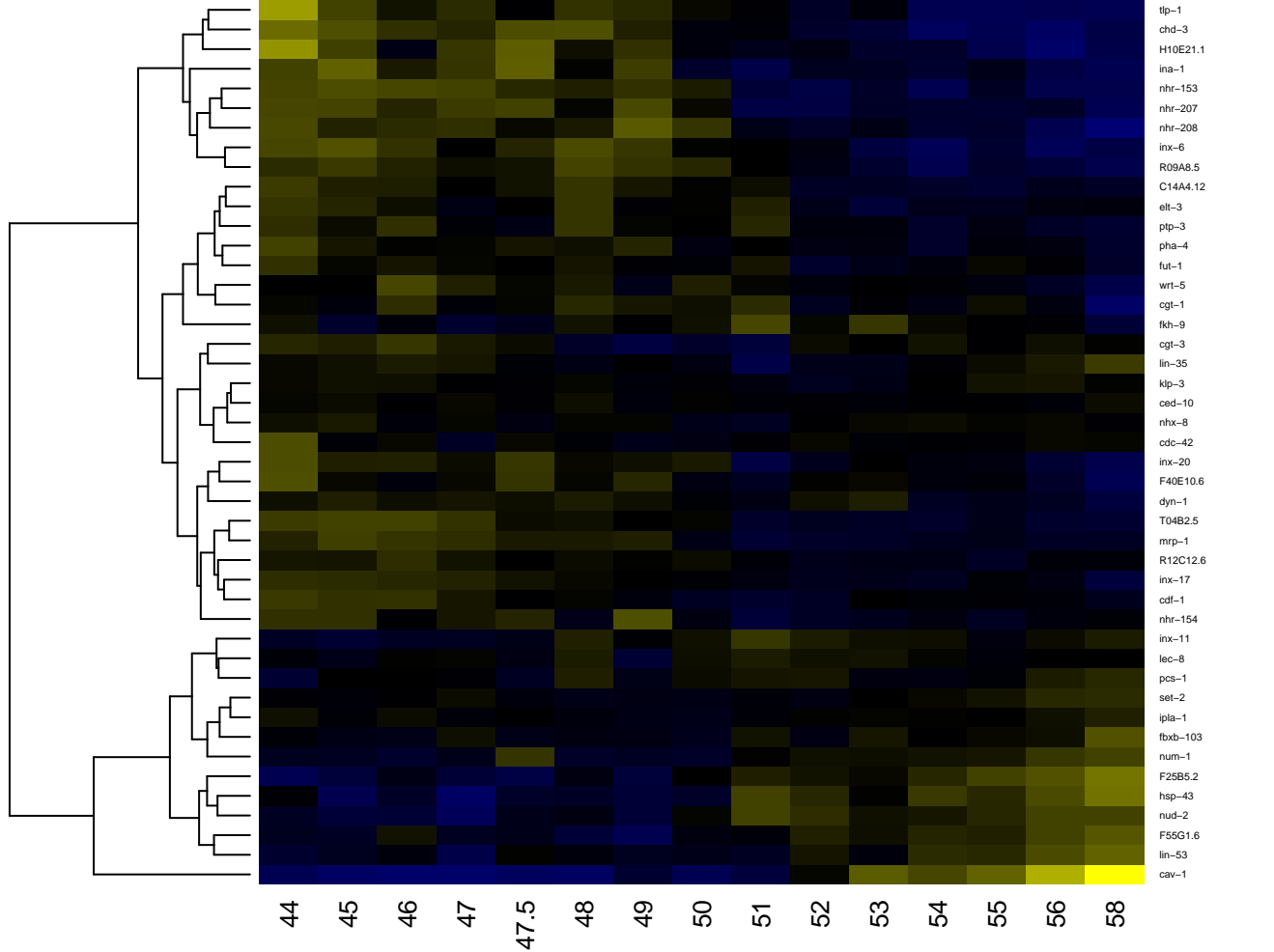
ventral nerve cord



ventral uterine precursor



virL



-2

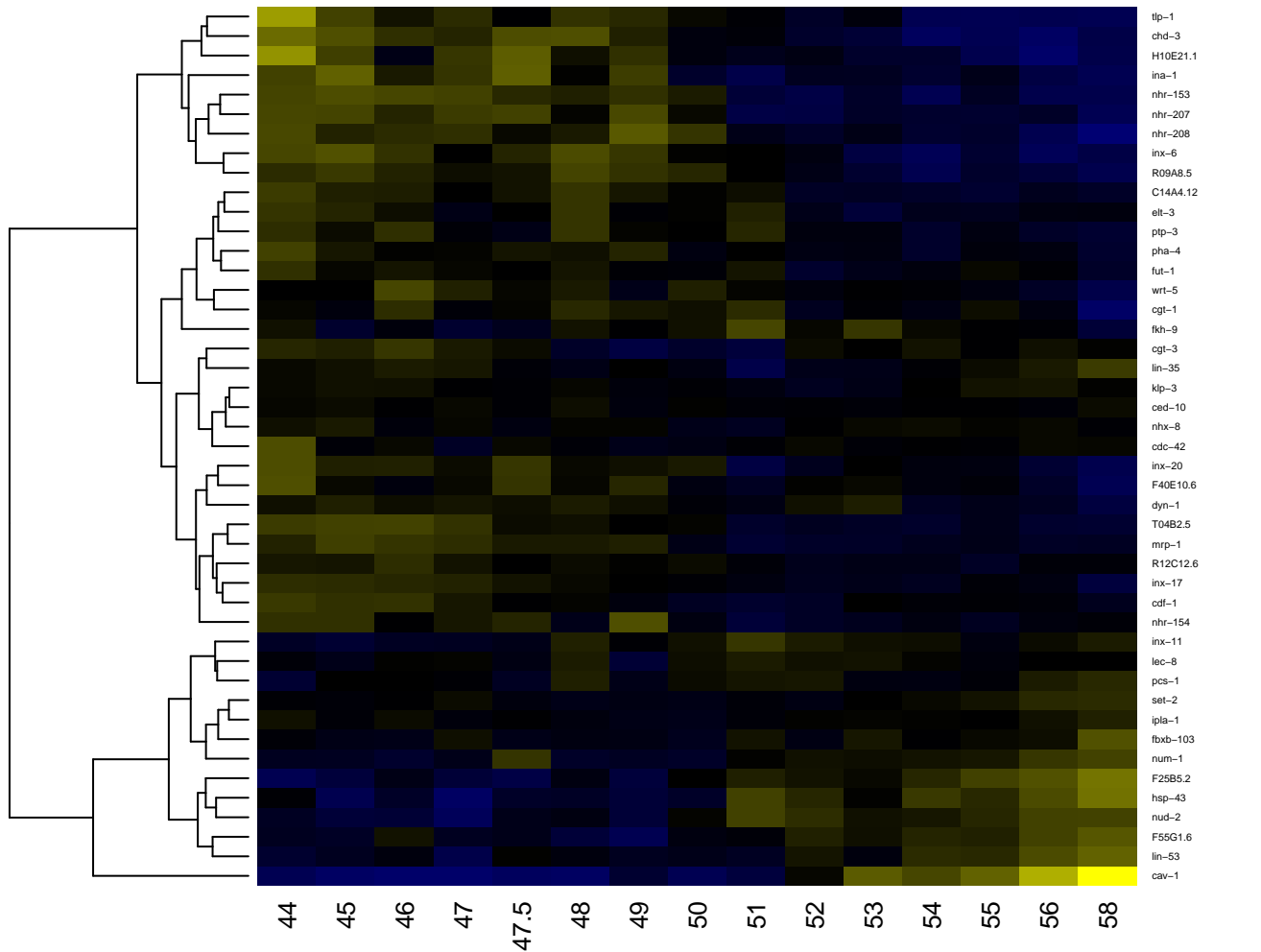
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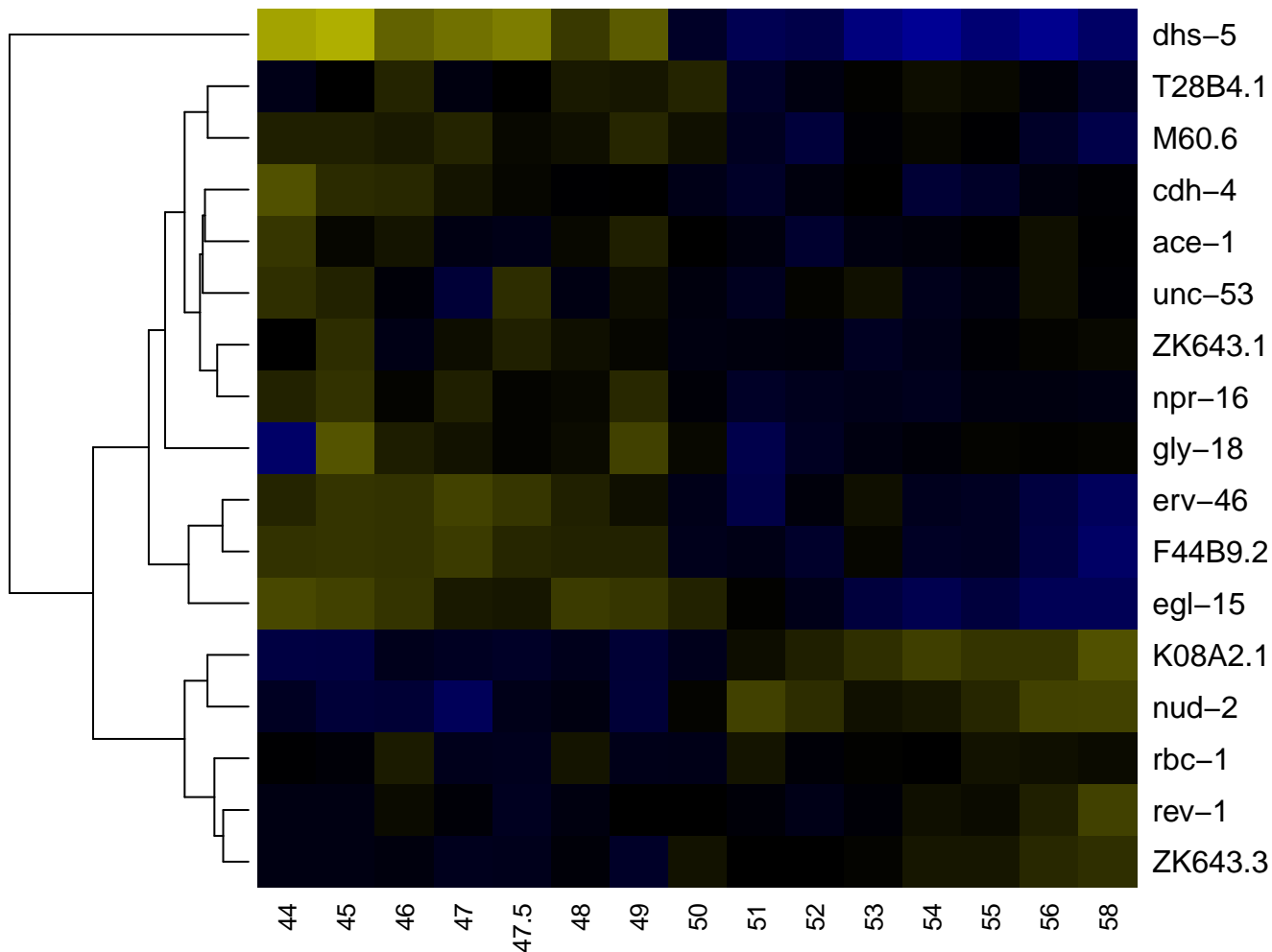
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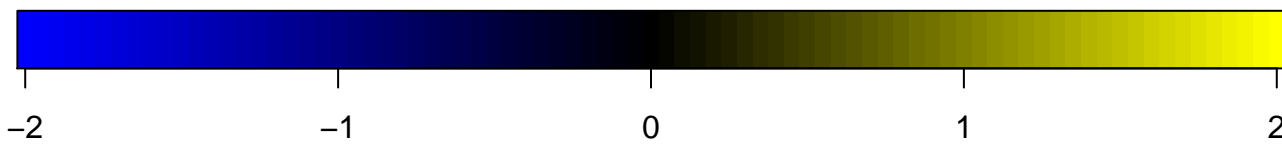
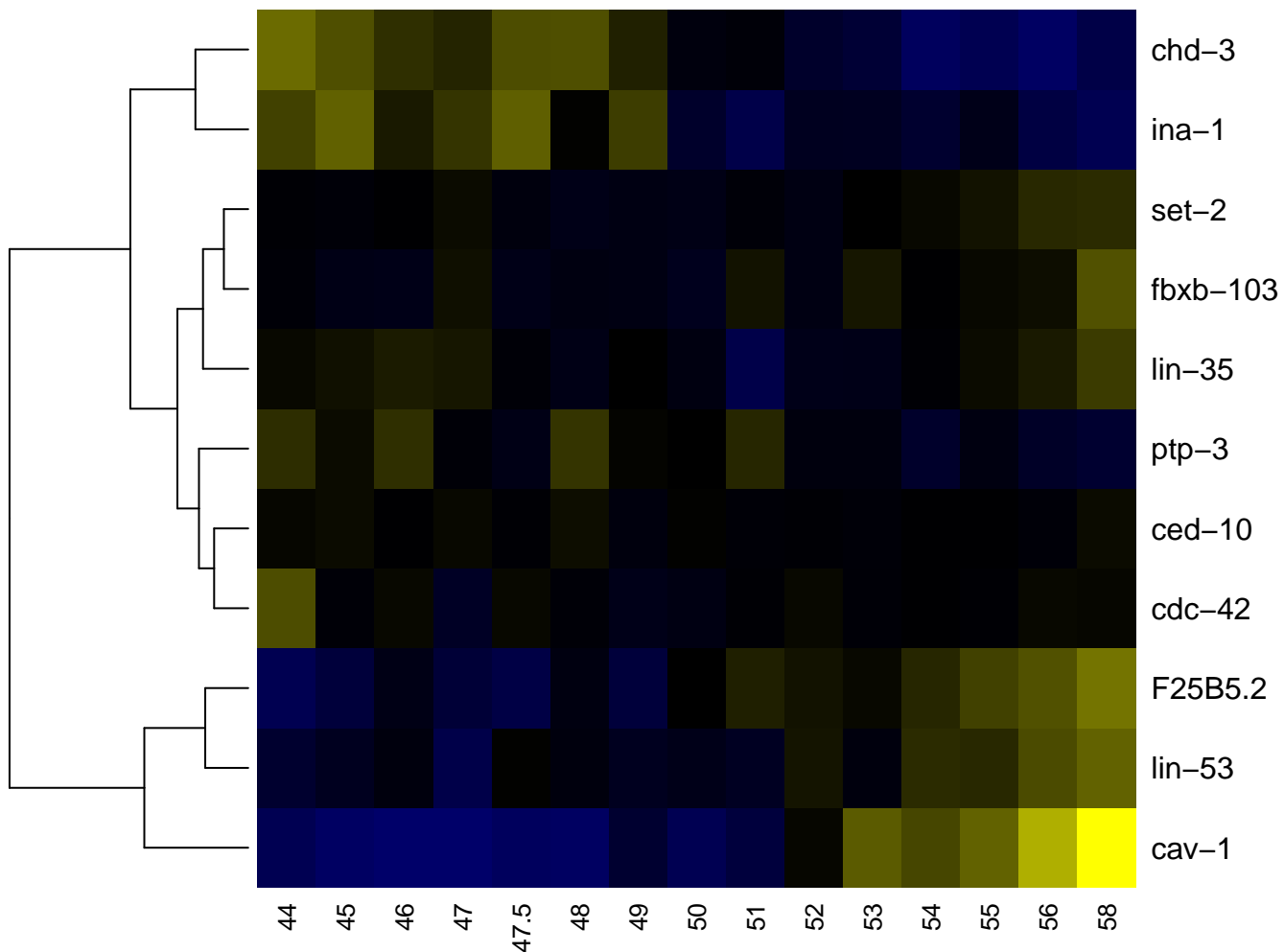
virR



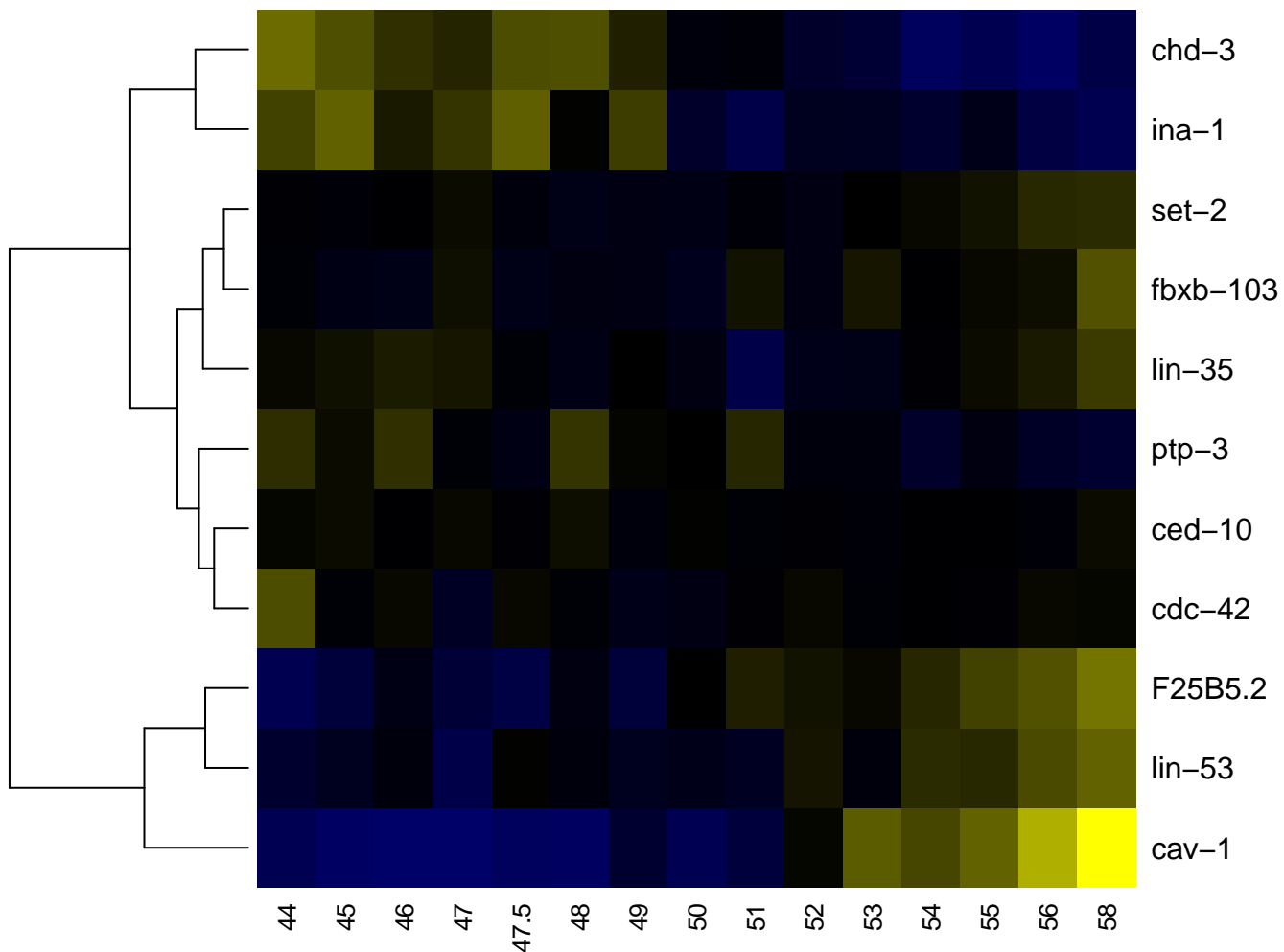
vm1



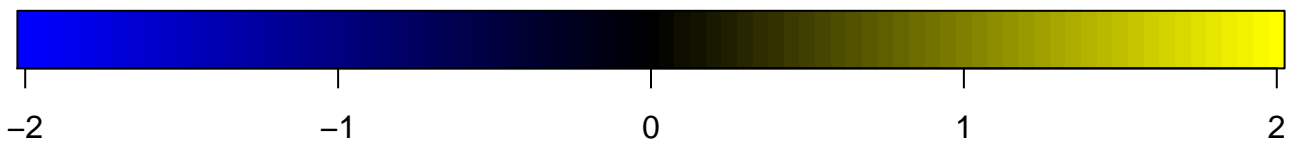
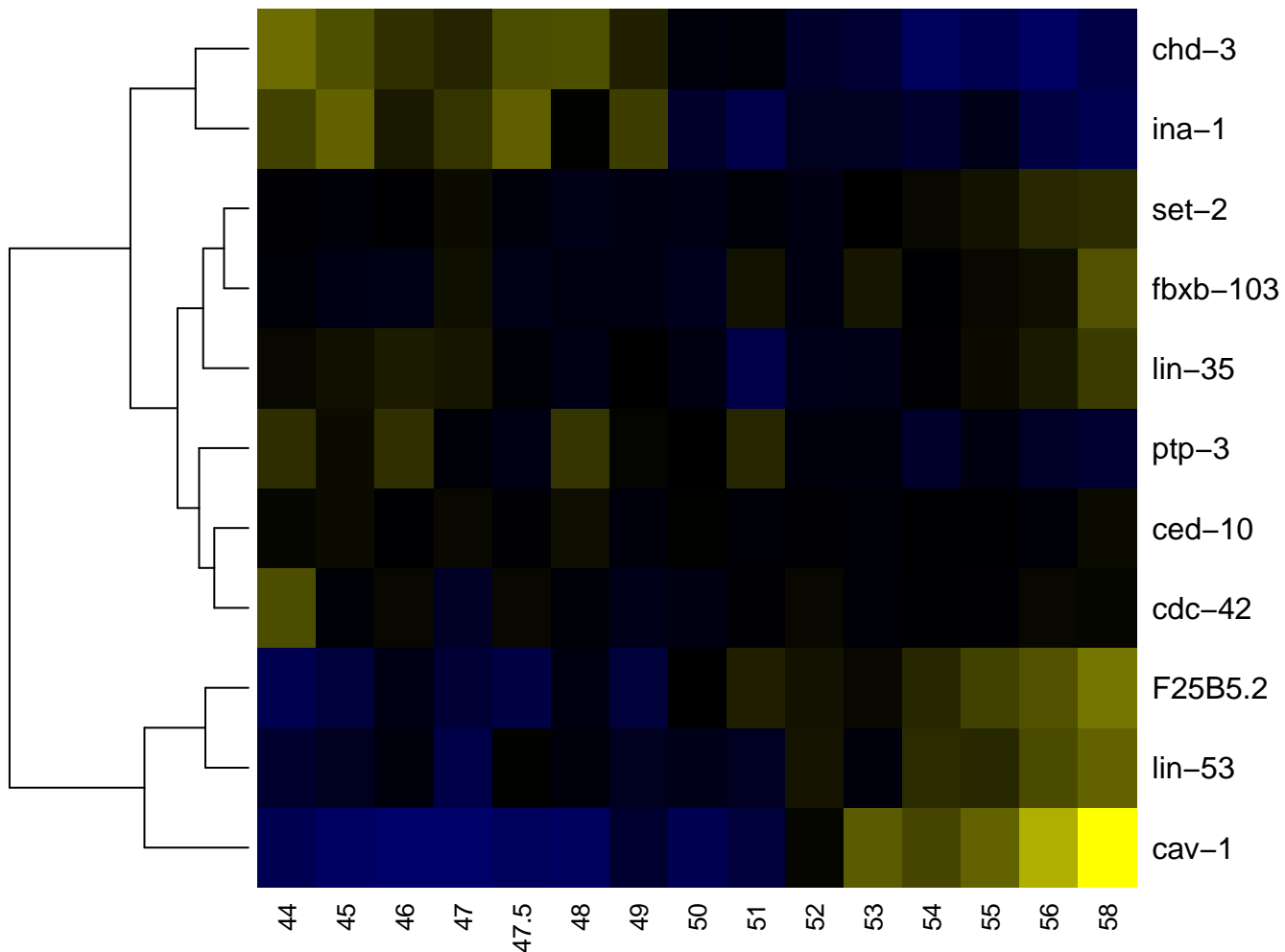
vpi1



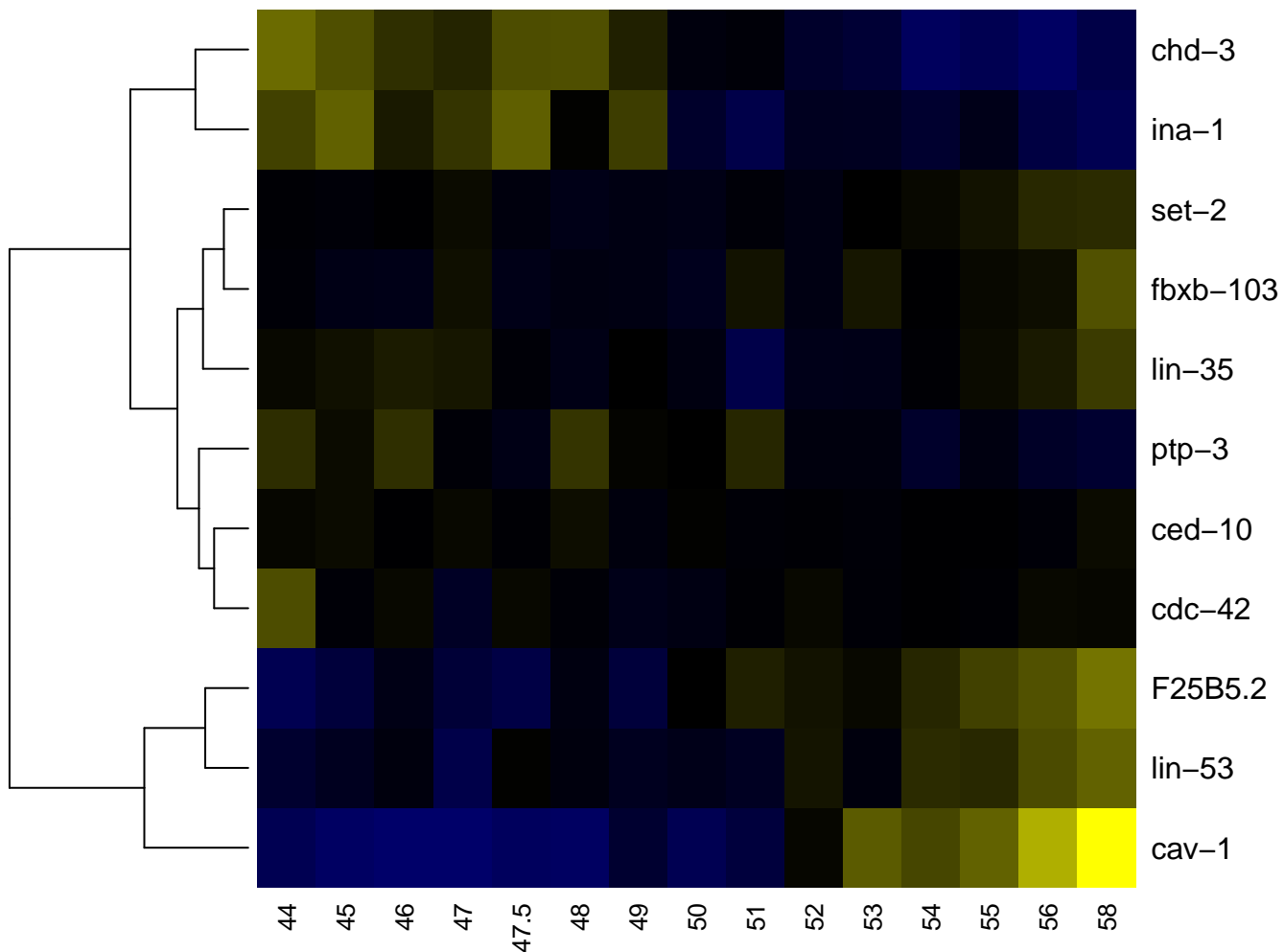
vpi2DL



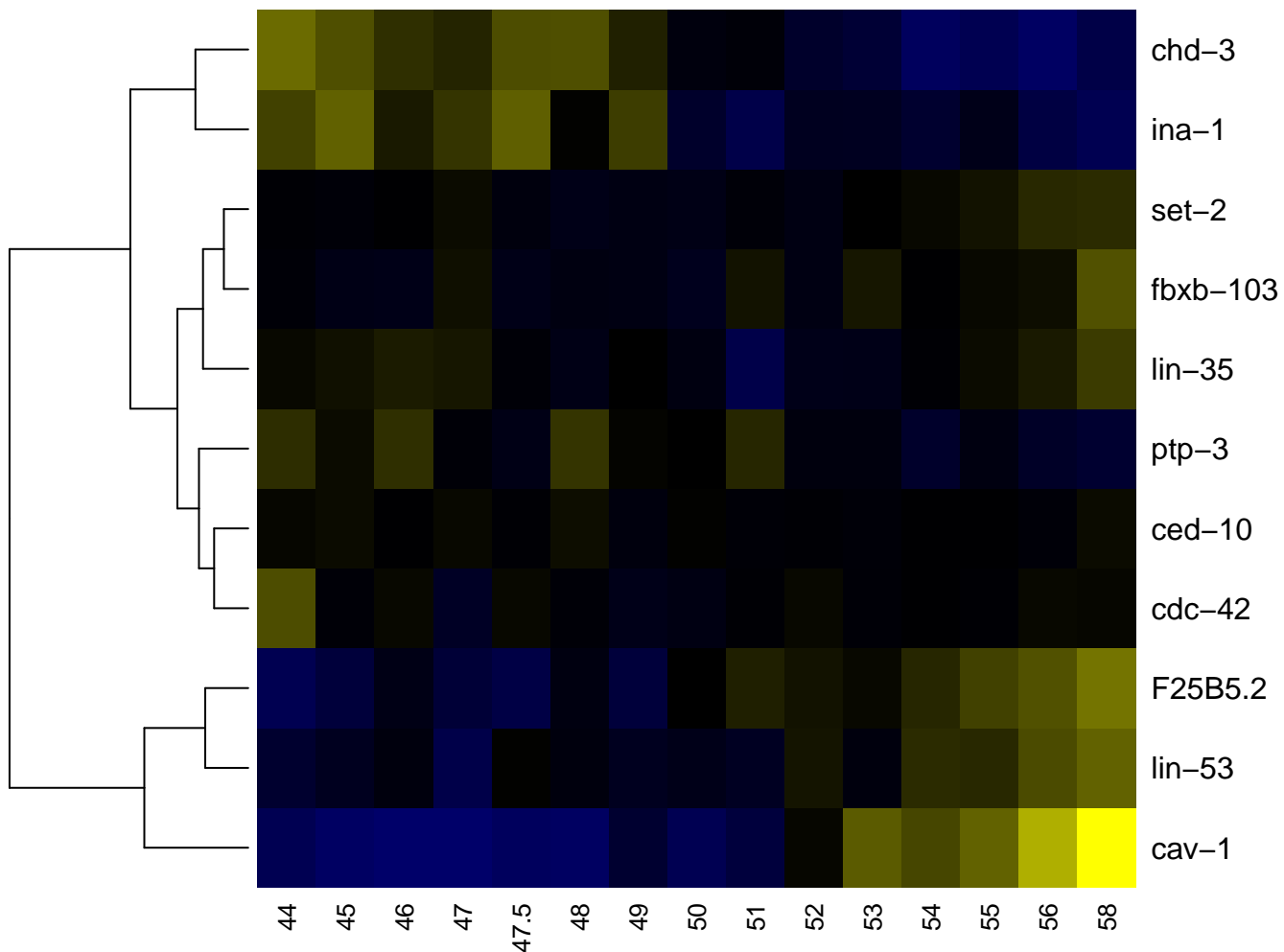
vpi2V



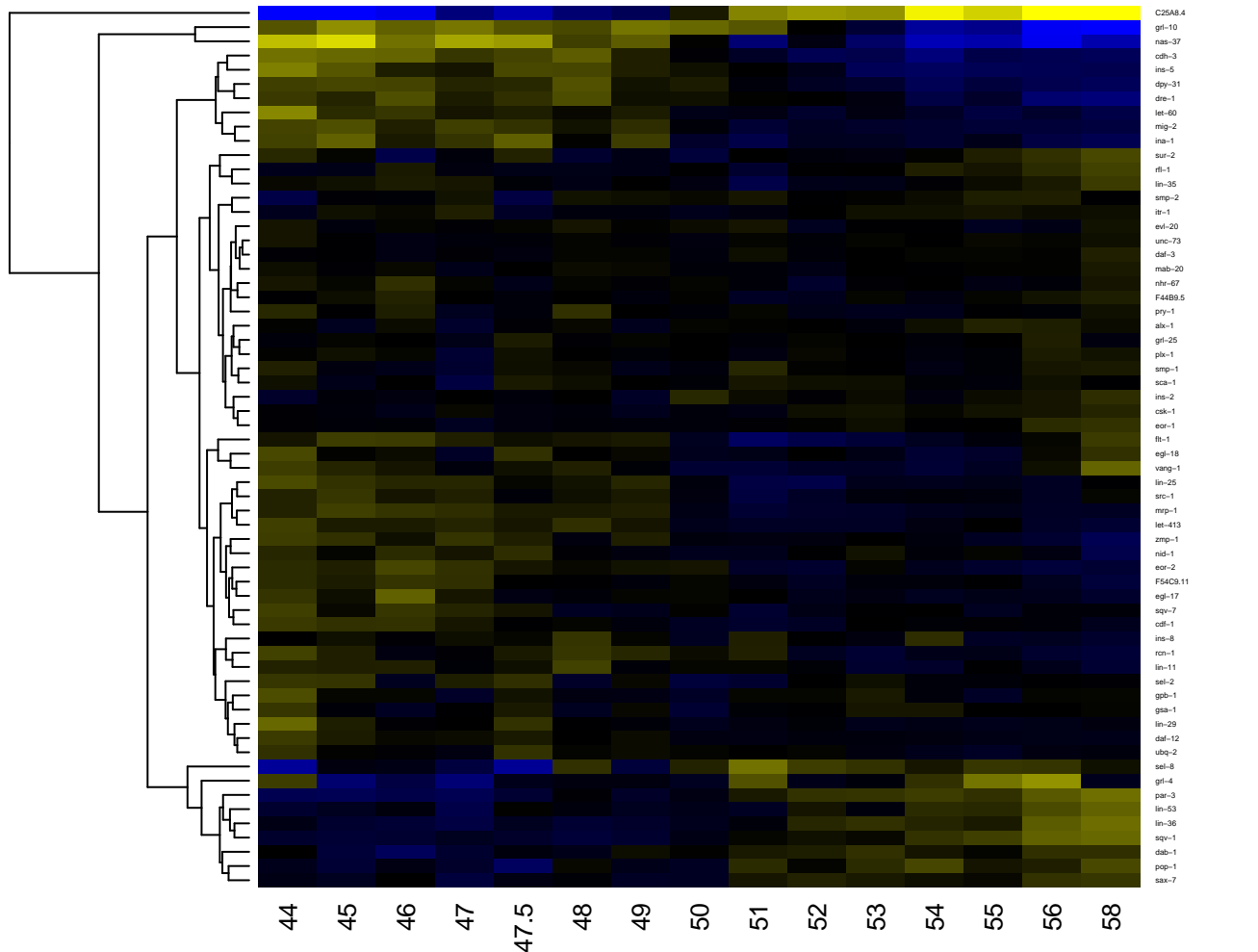
vpi3D



vpi3V



vulA



-2

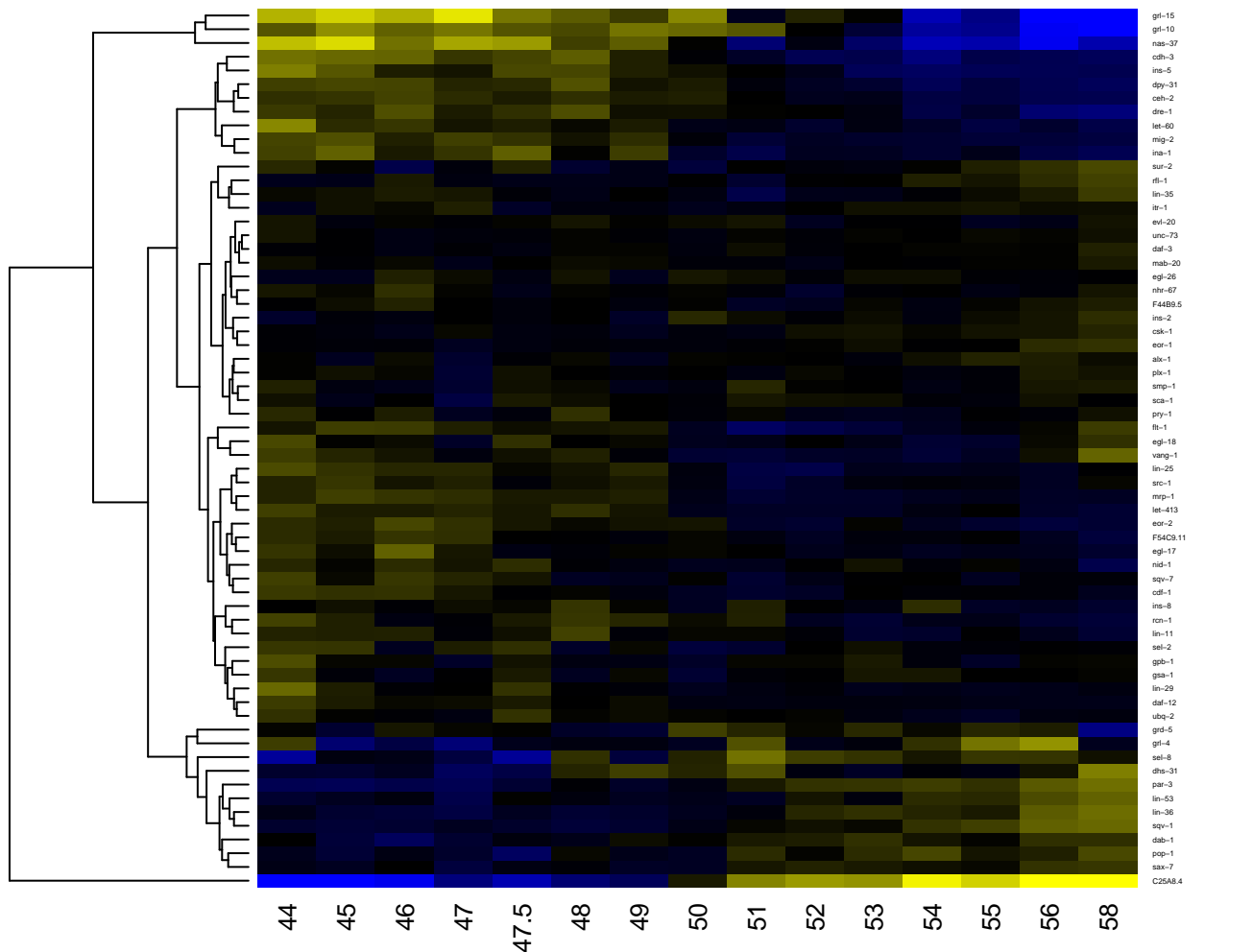
-1

0

1

2

vulB1



-2

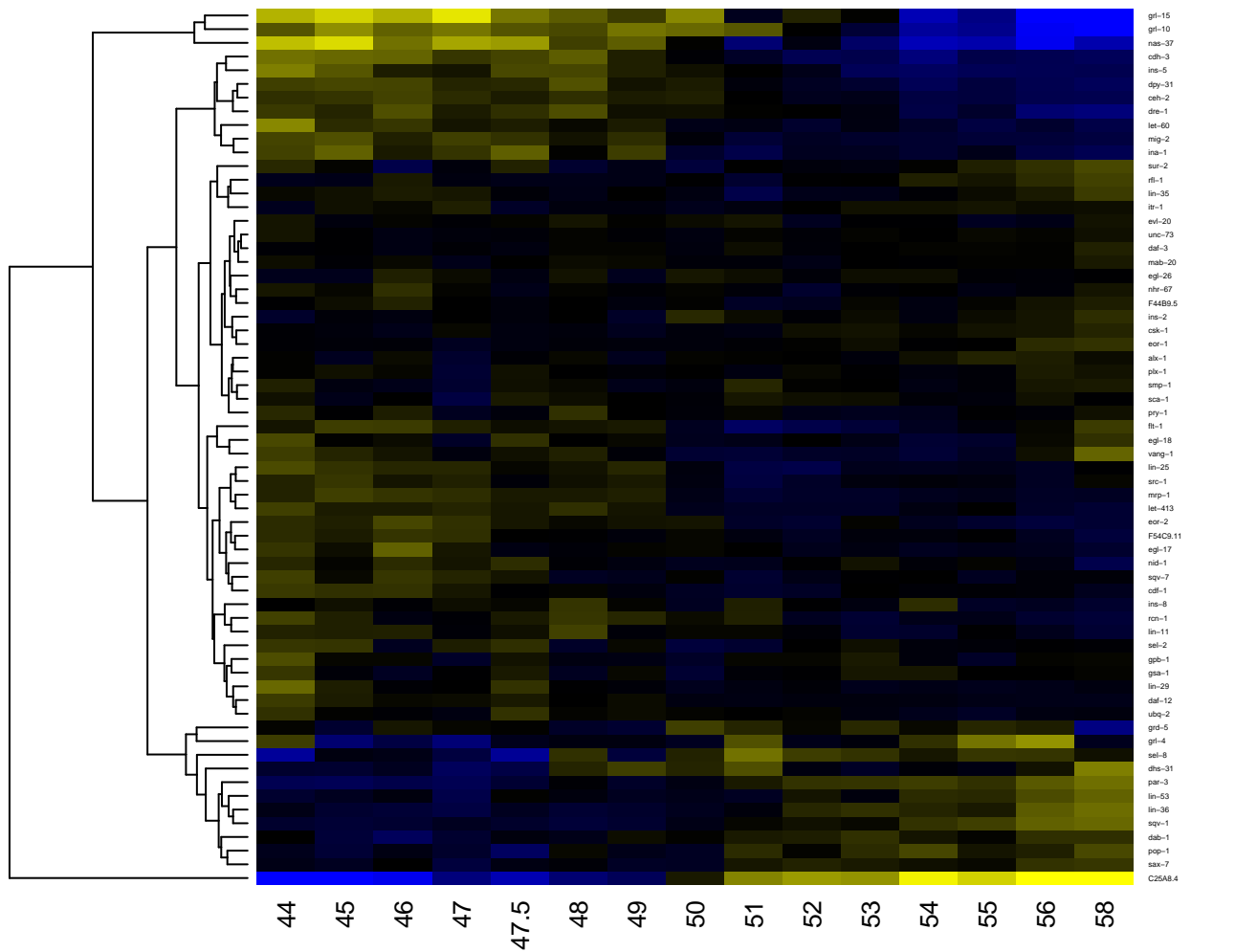
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1

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vulB2



-2

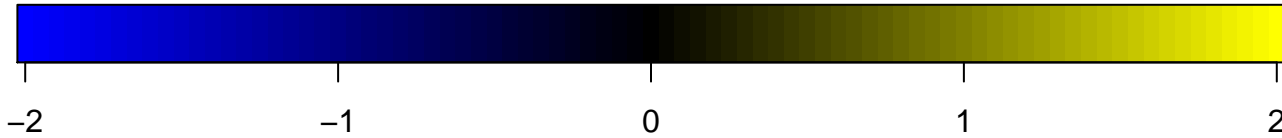
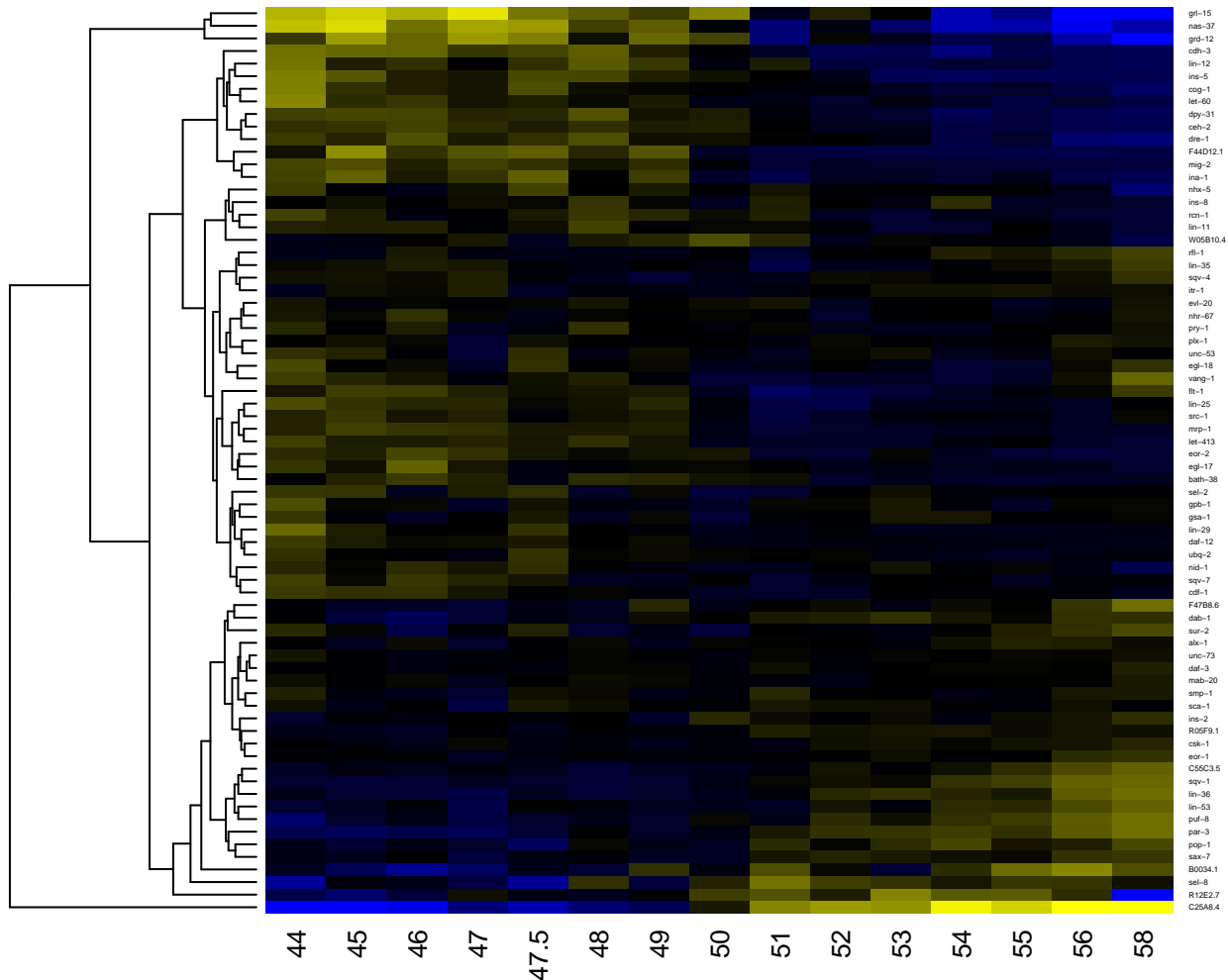
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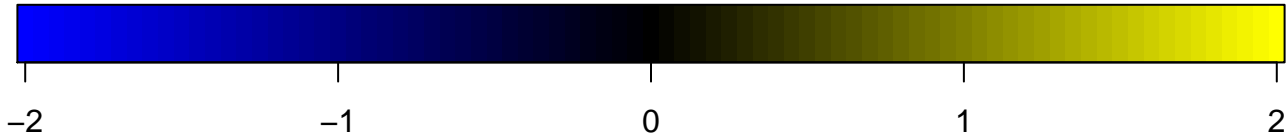
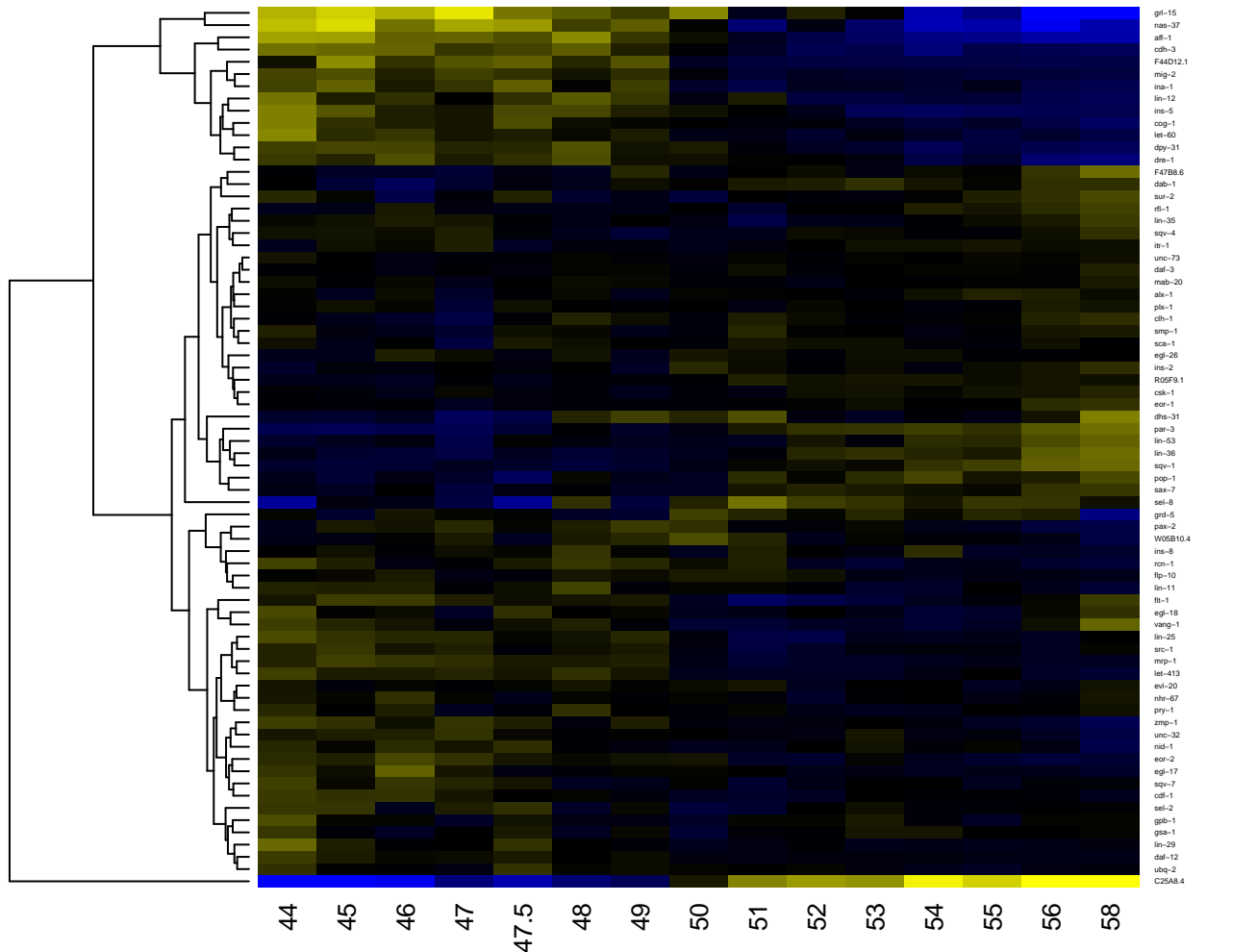
1

2

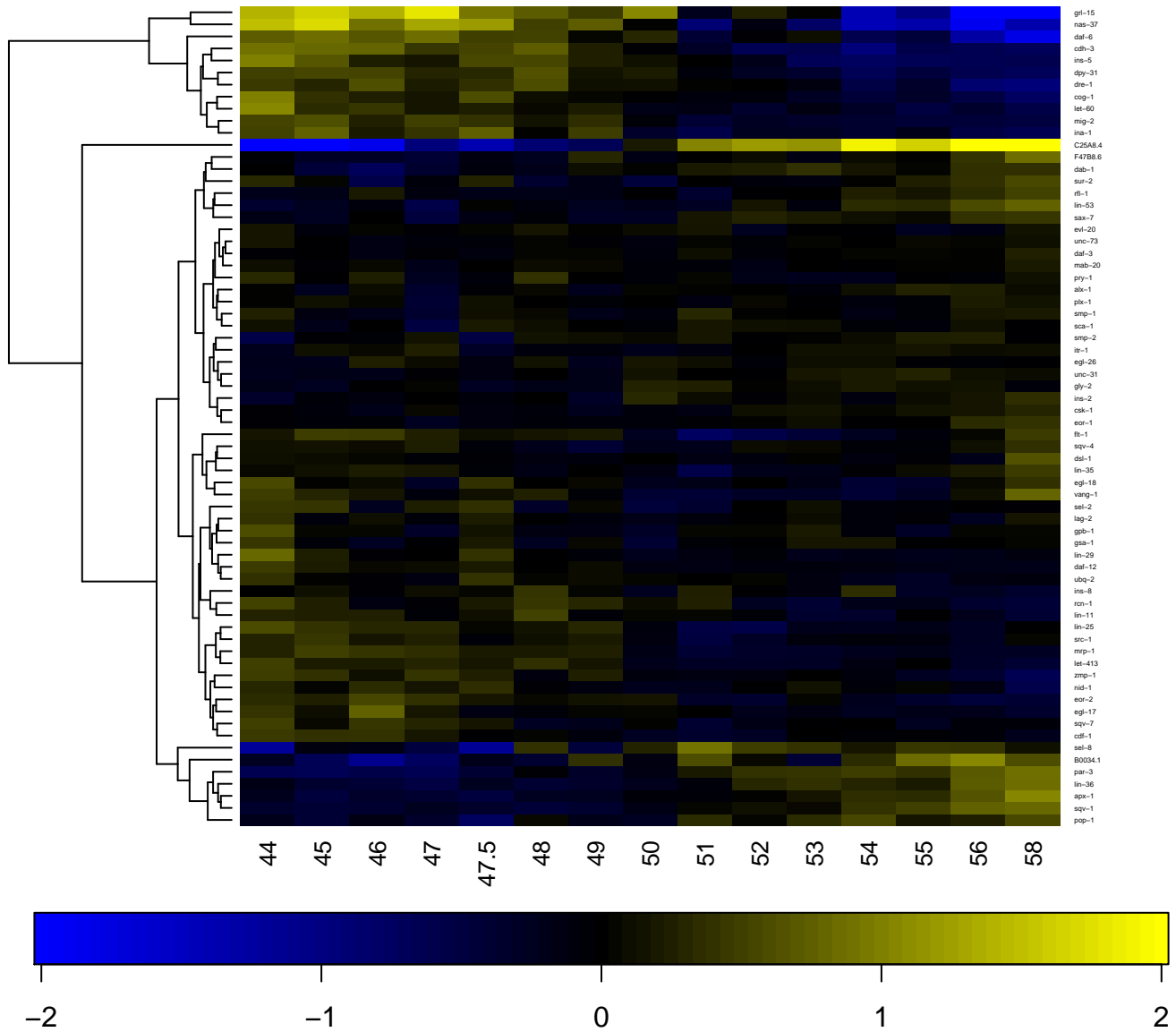
vulC



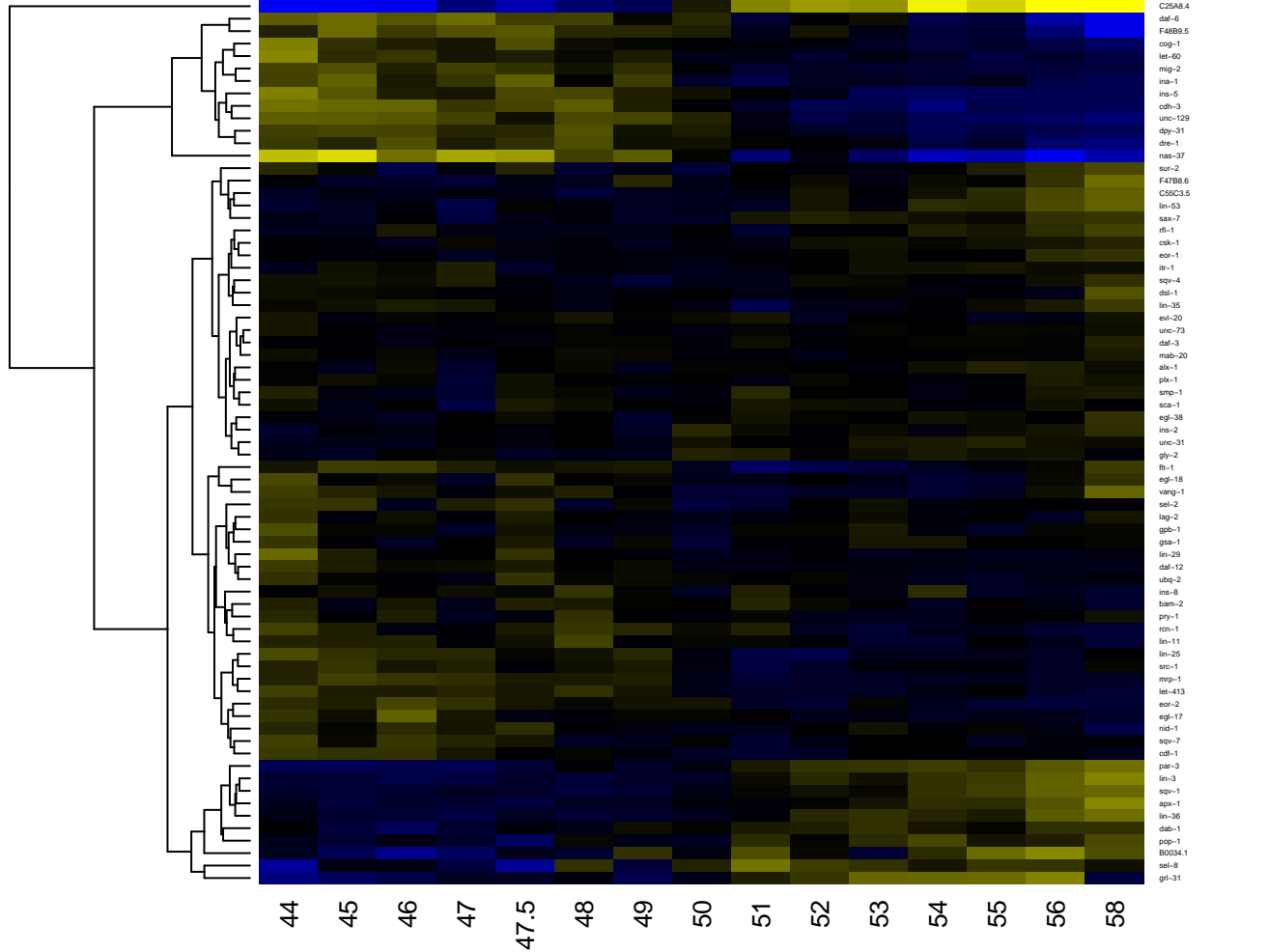
vulD



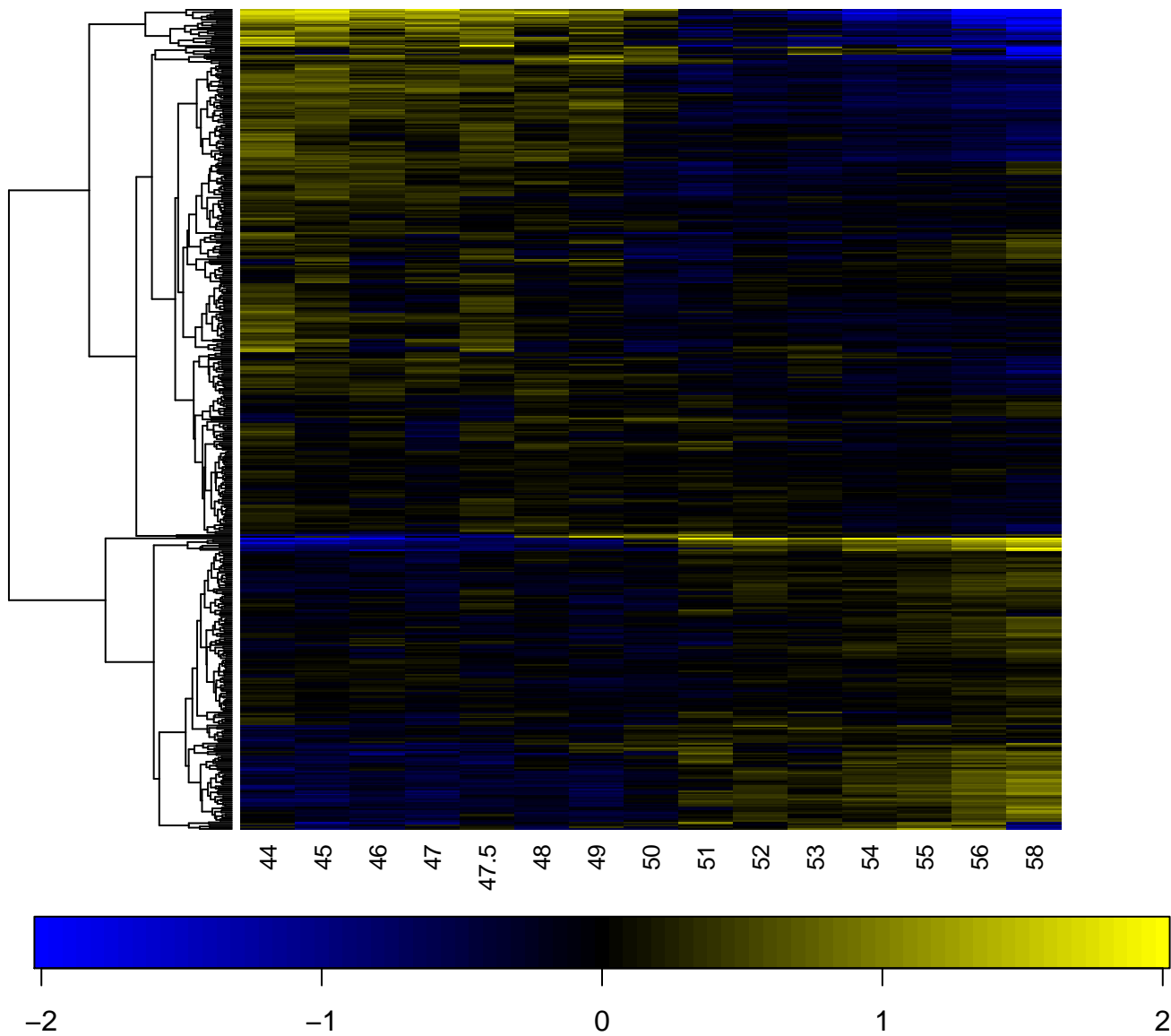
vulE



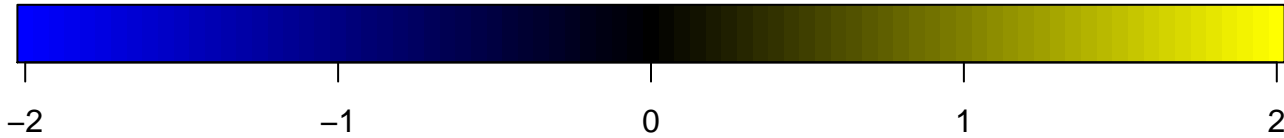
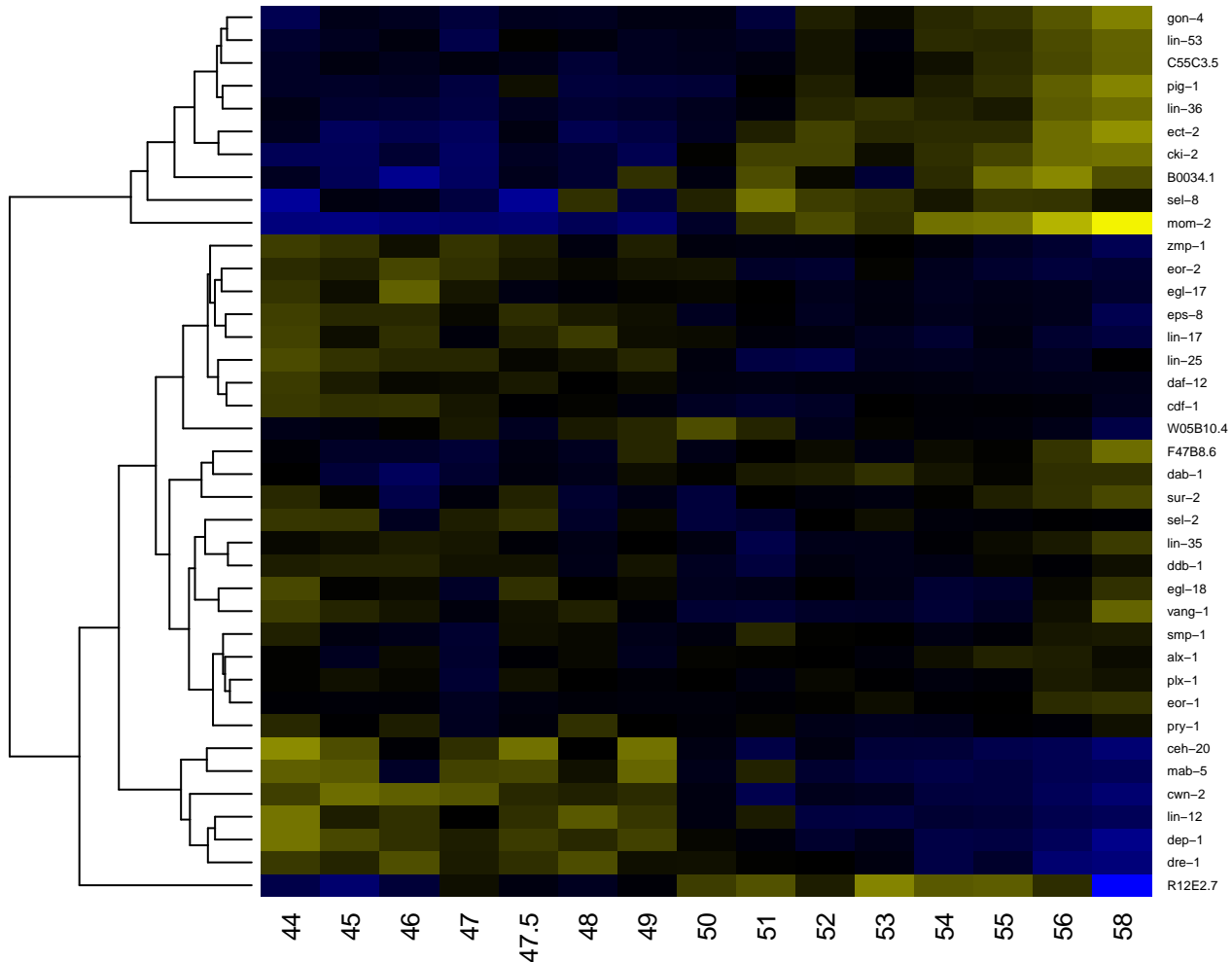
vulF



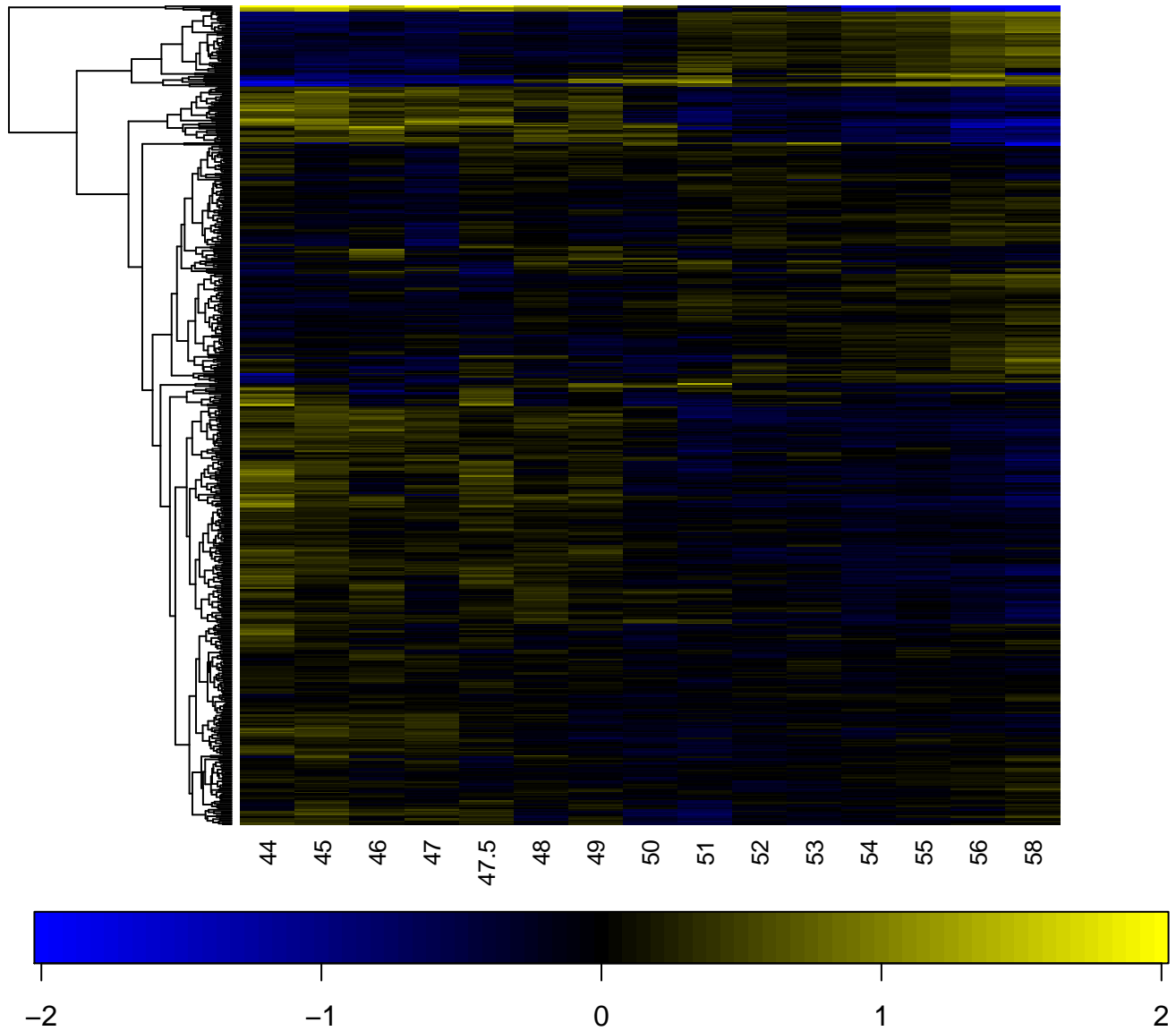
vulva



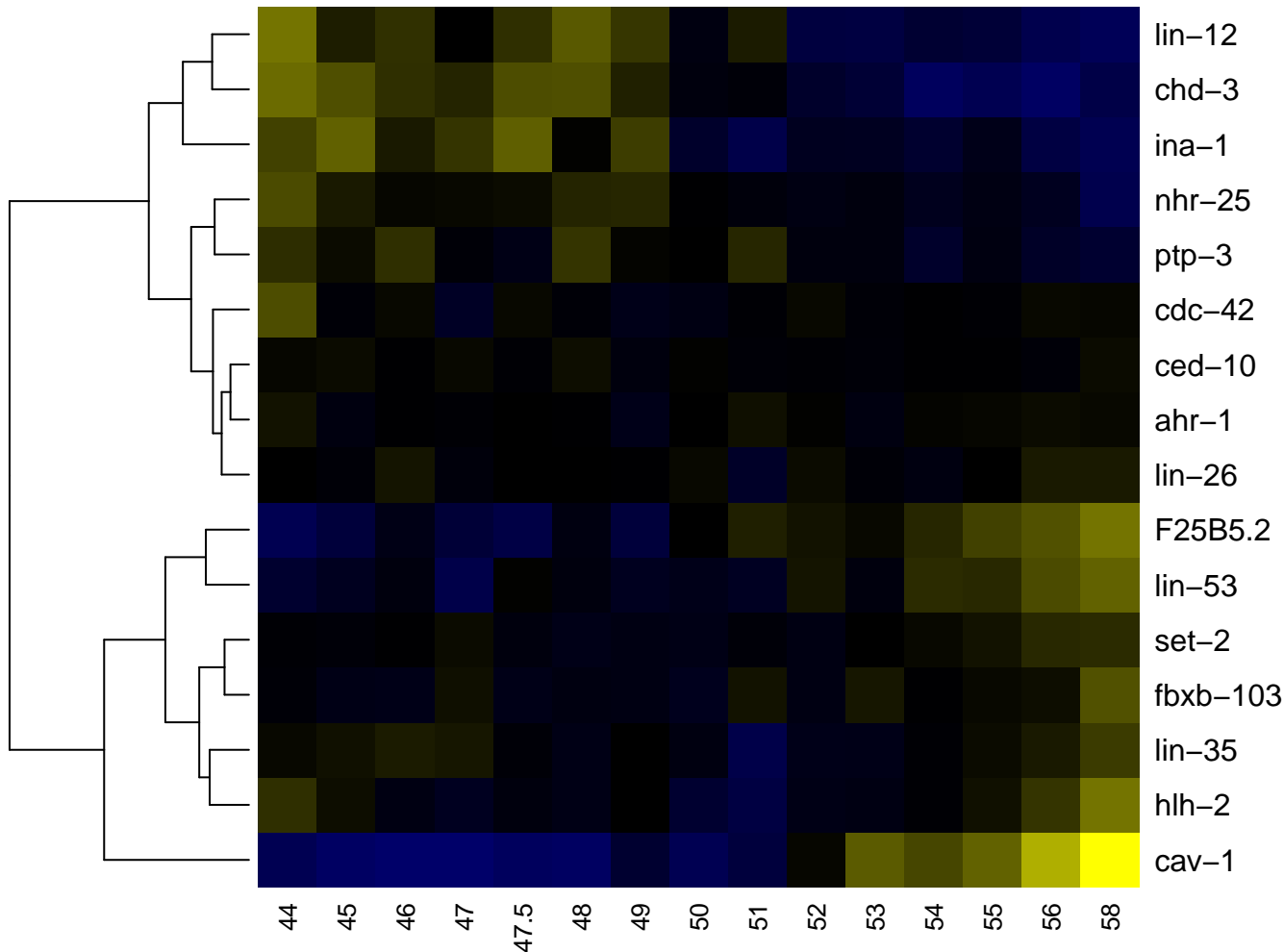
vulval cell



vulval muscle



W



-2

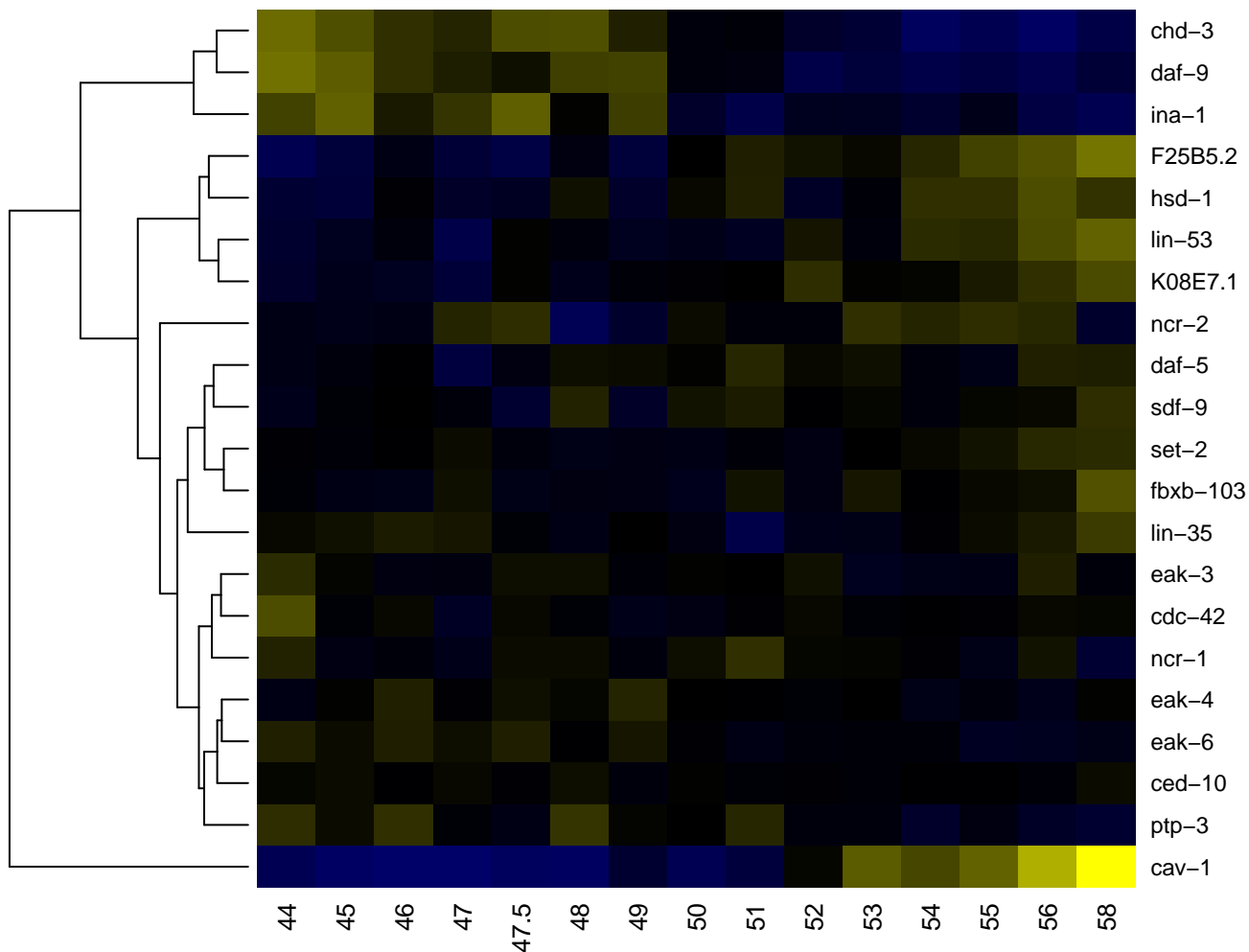
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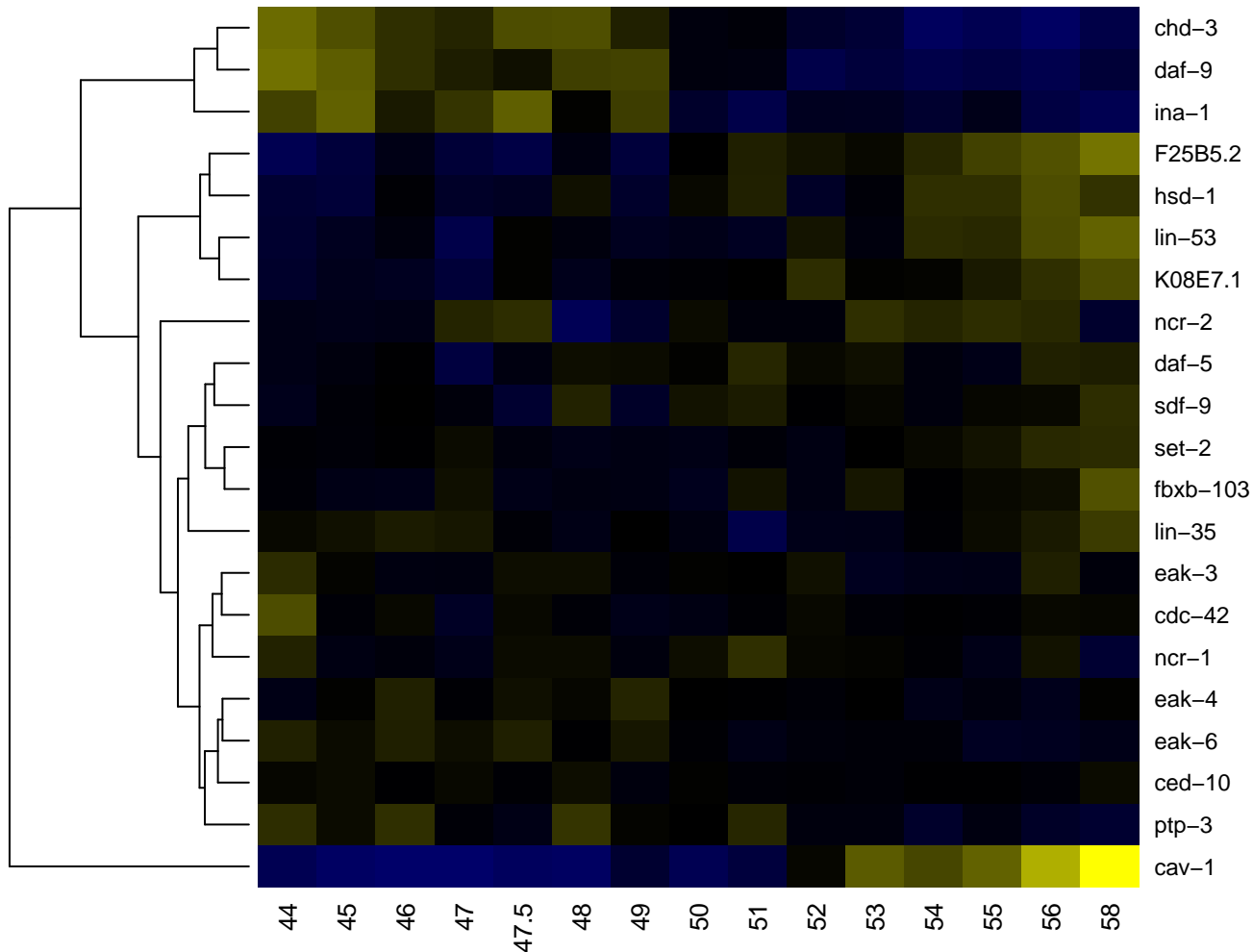
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2

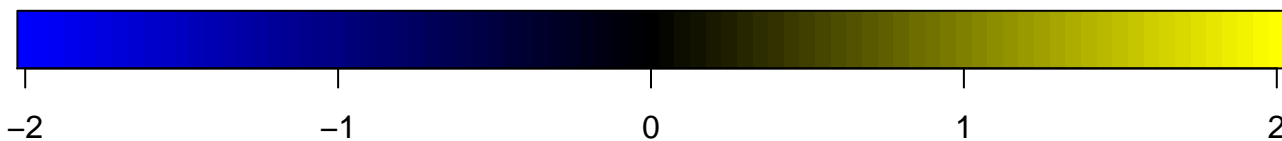
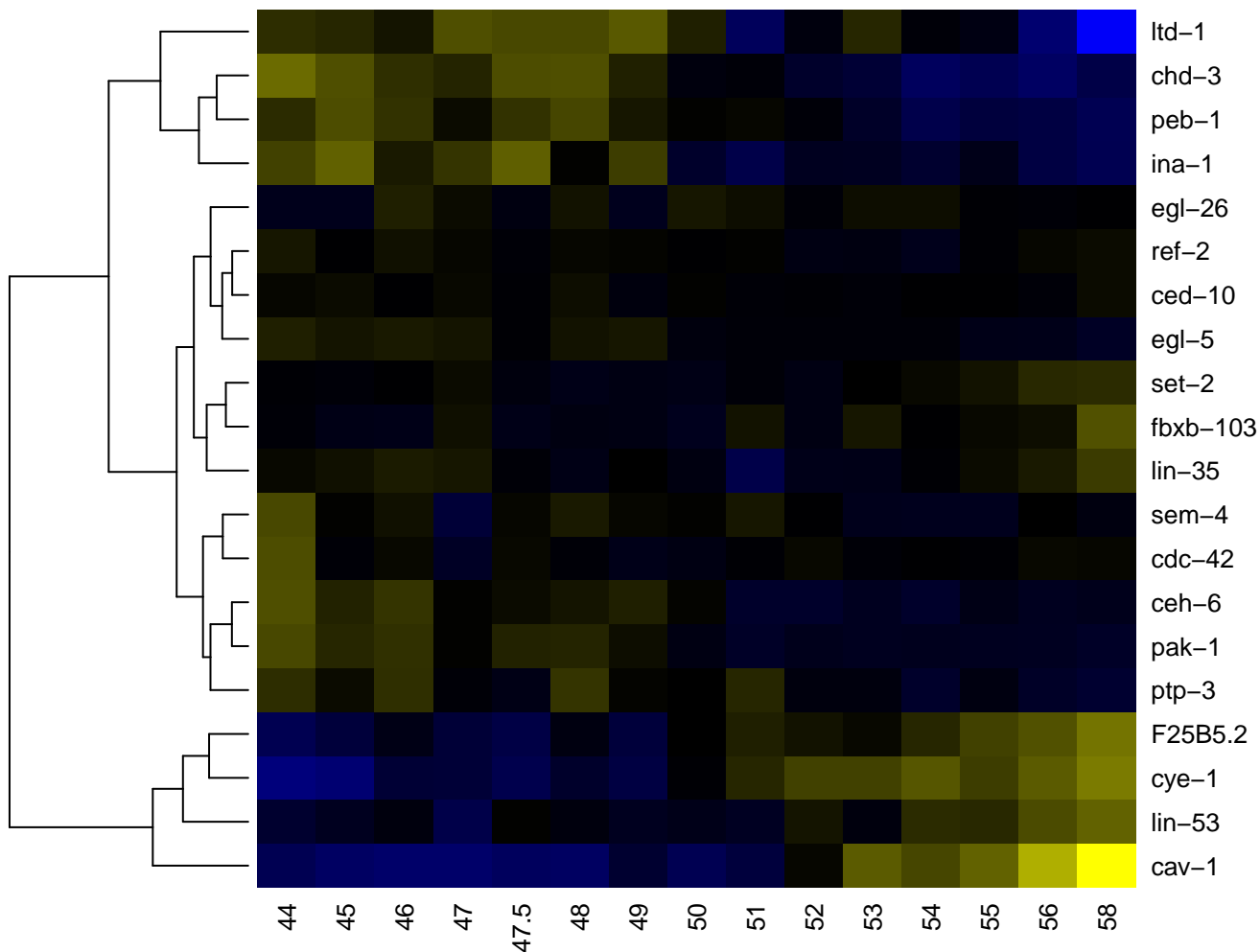
XXXL



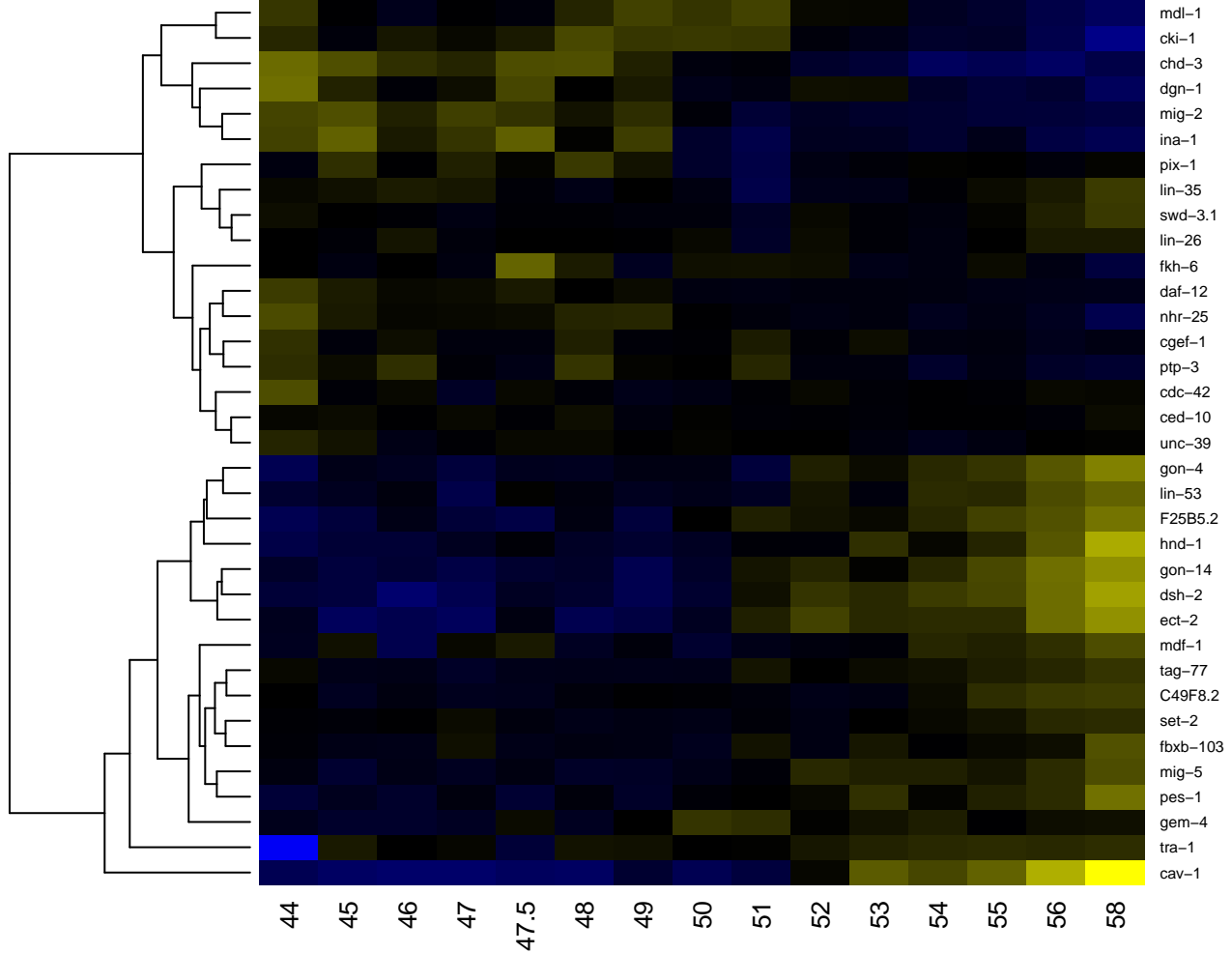
XXXR



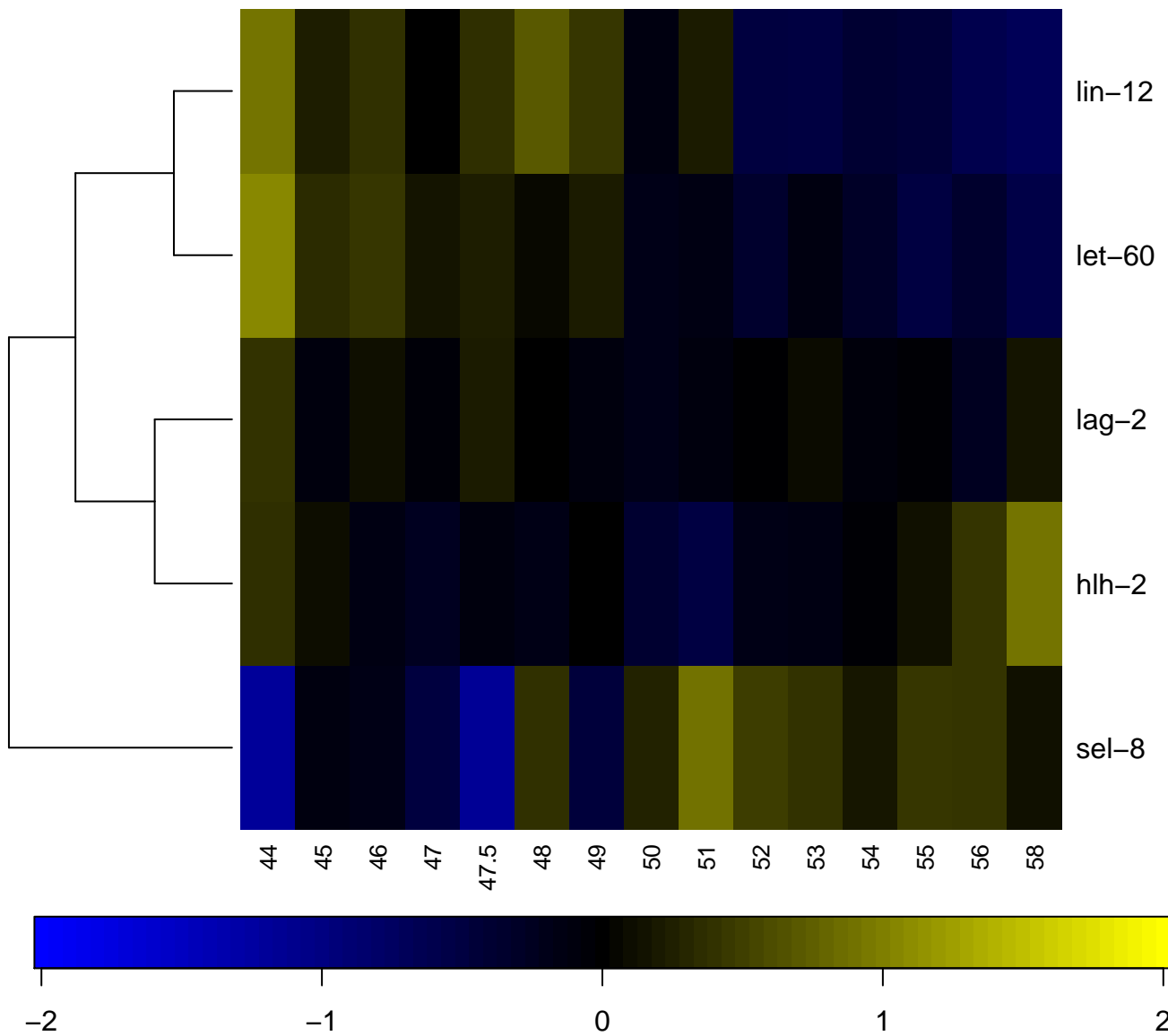
Y cell



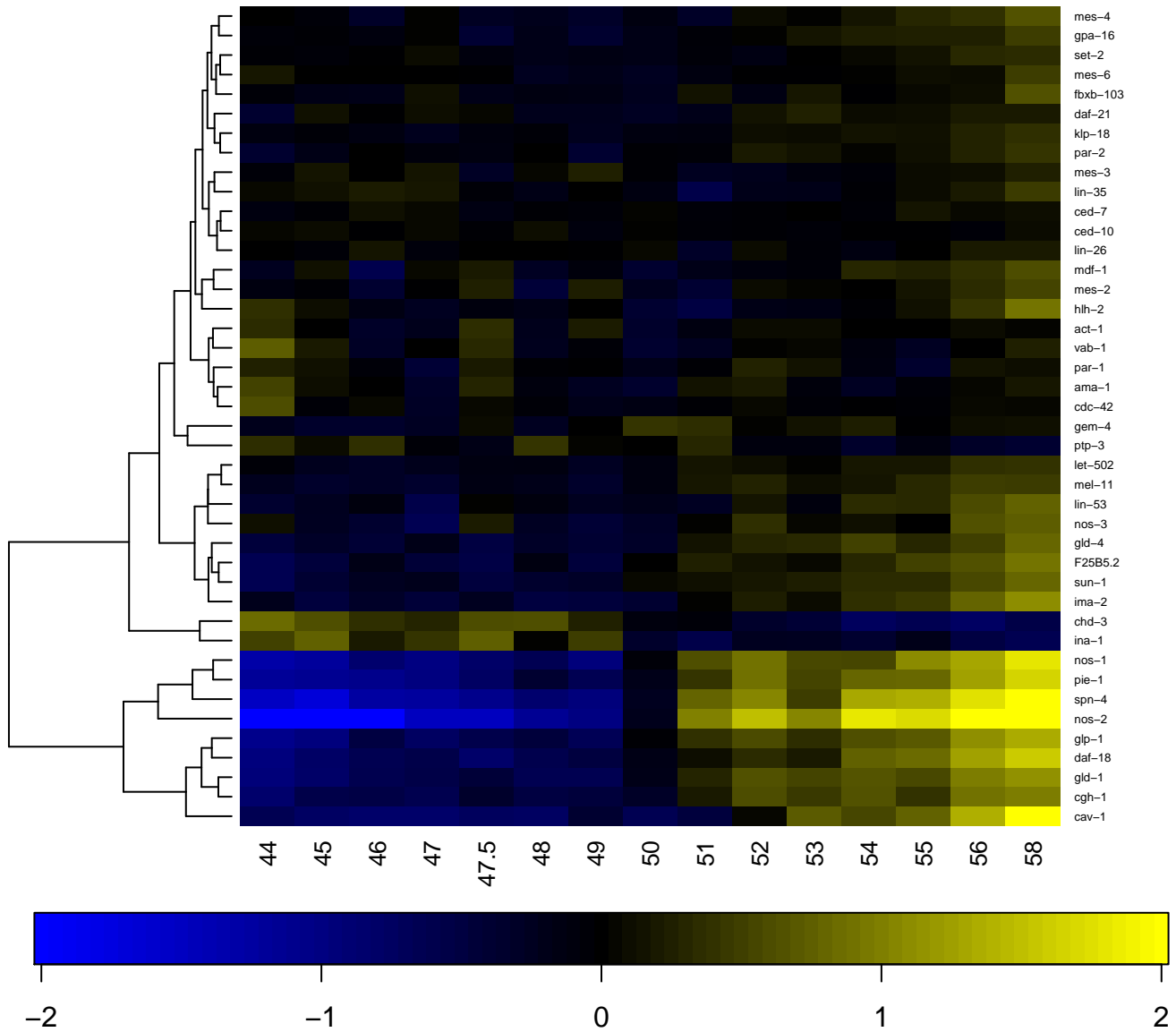
Z1



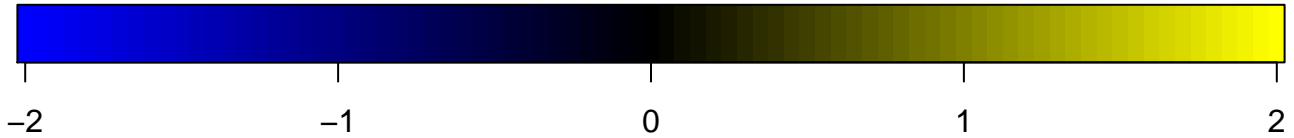
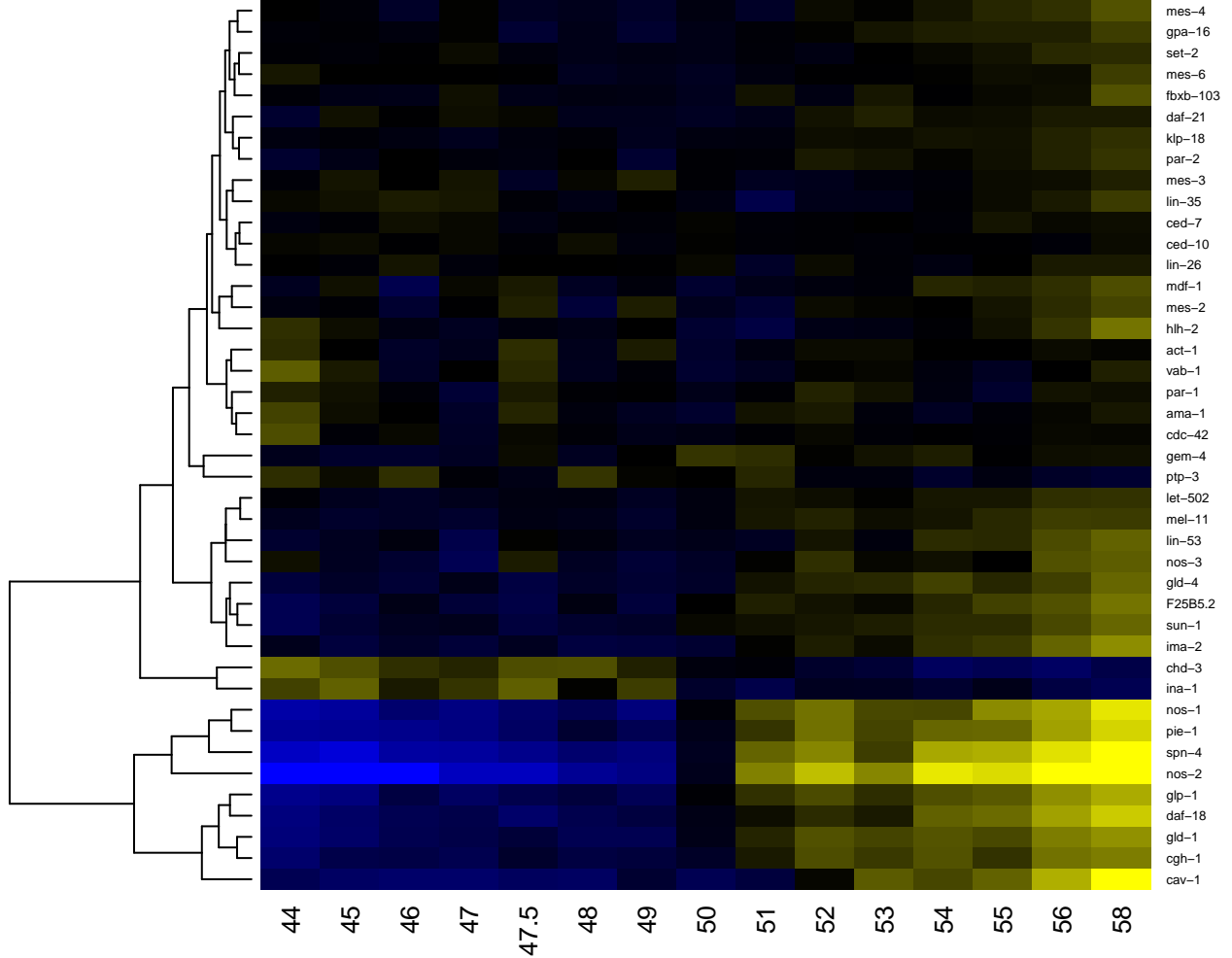
Z1.ppp



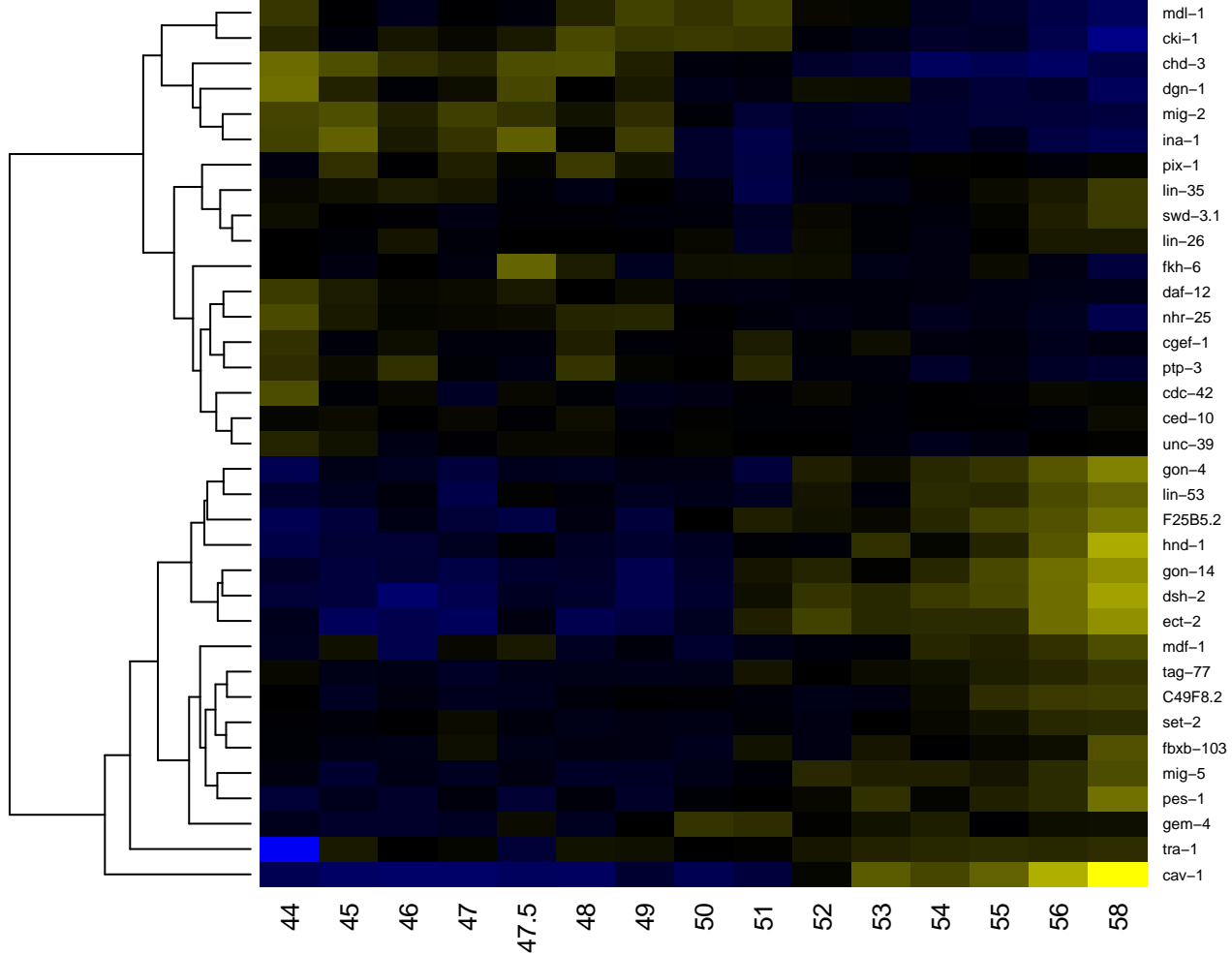
Z2



Z3



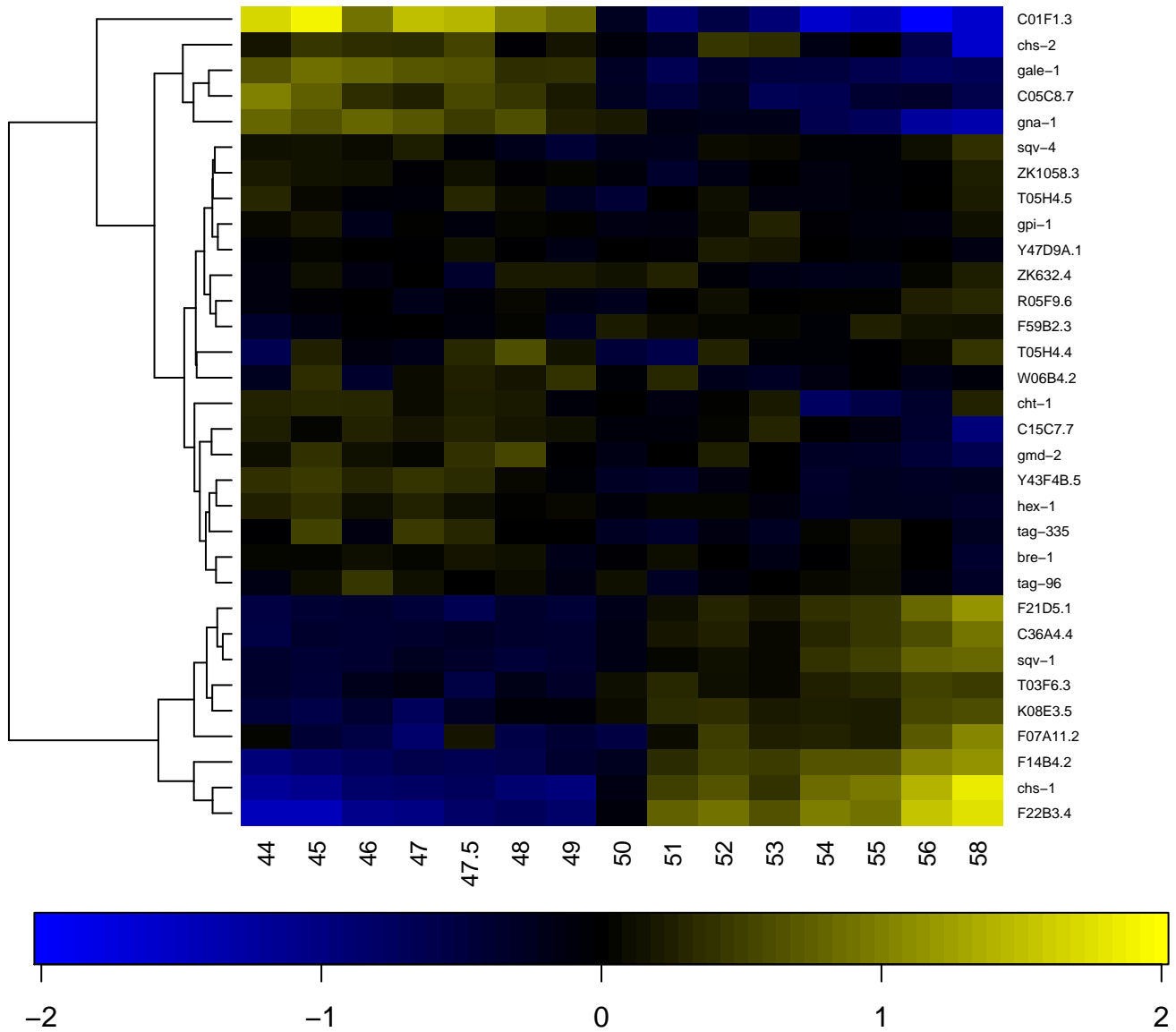
Z4



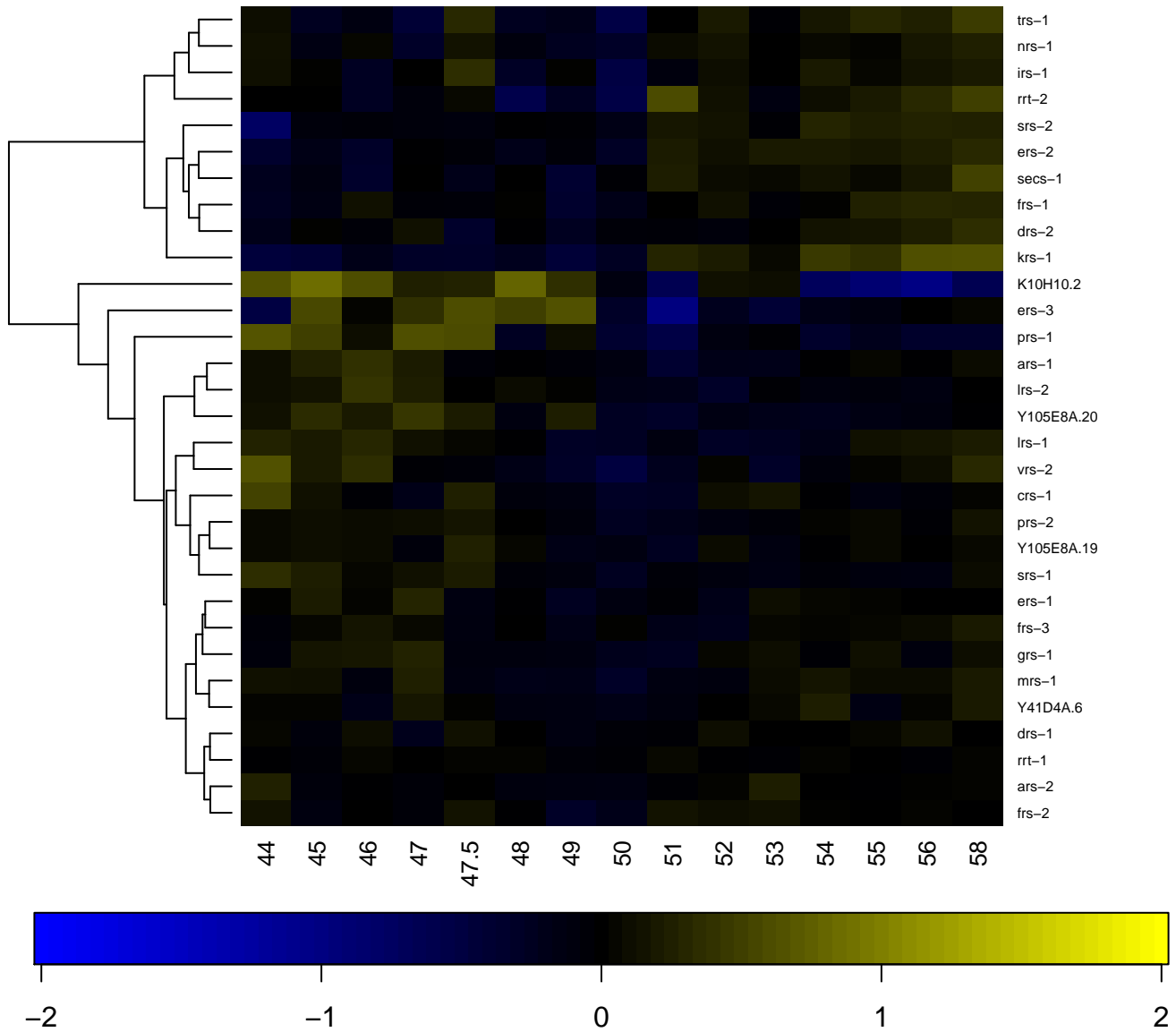
Supplementary file G | Dynamic gene expression patterns of all KEGG pathways.

The “heatmap” function of “R” was used to cluster genes of each individual KEGG pathway terms according to their expression pattern. KEGG pathway name is shown per page as figure title. The time in hours is shown on the x-axis. Gene names are shown on the y-axis. The scale bar shows the log₂ ratio with the mean for each time-point. Blue is lower than the mean and yellow is higher than the mean.

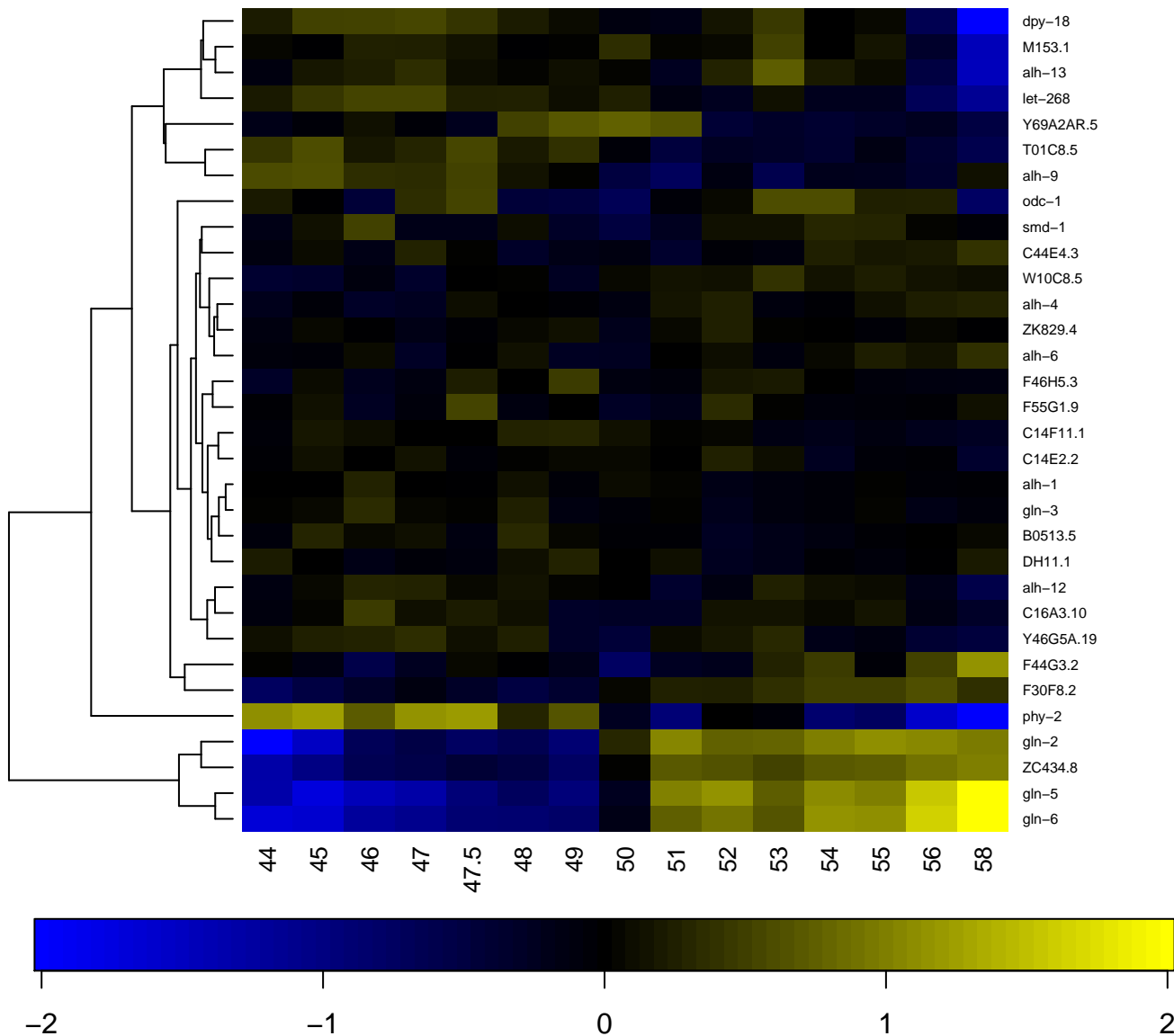
Amino sugar and nucleotide sugar metabolism



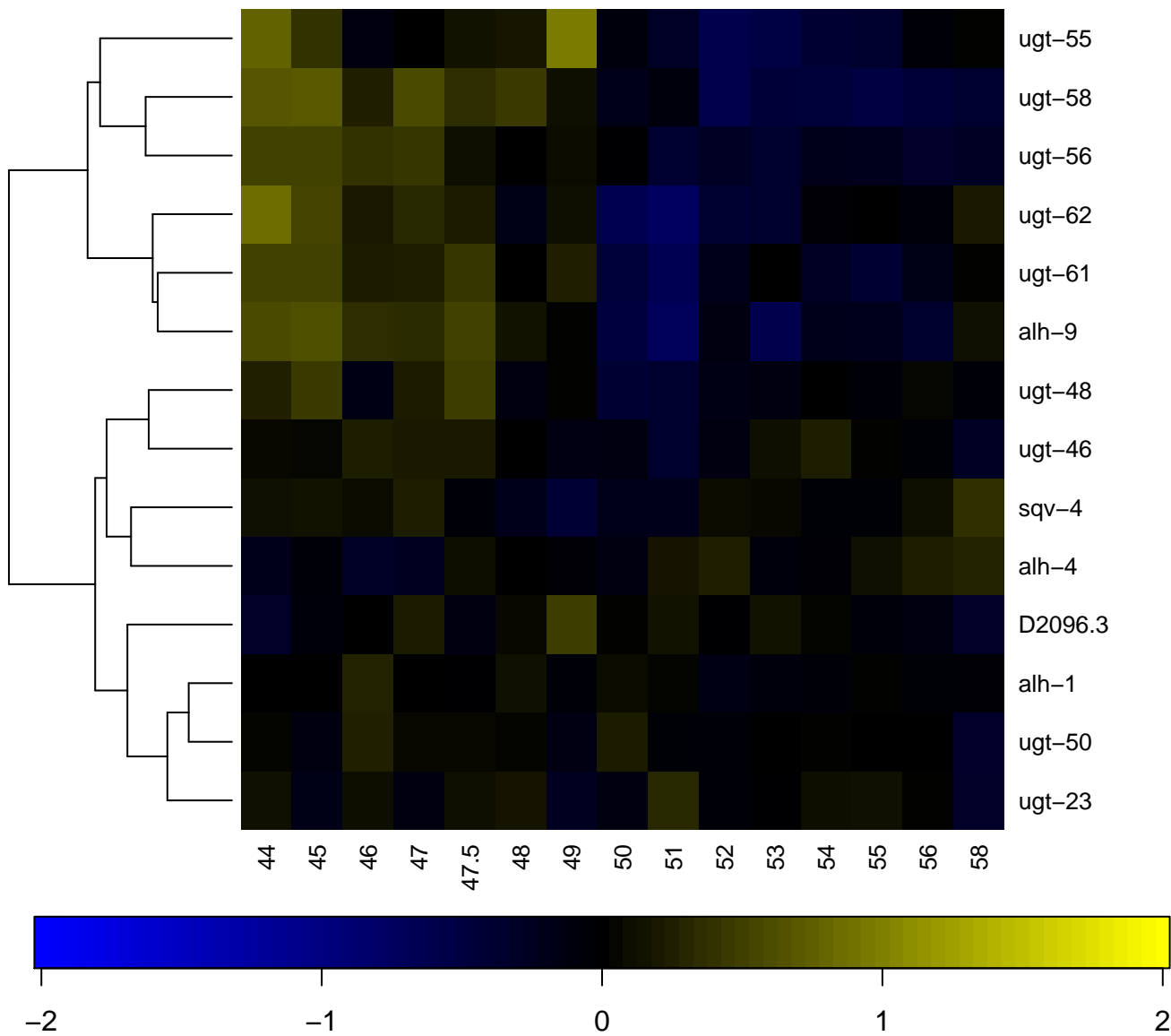
Aminoacyl-tRNA biosynthesis



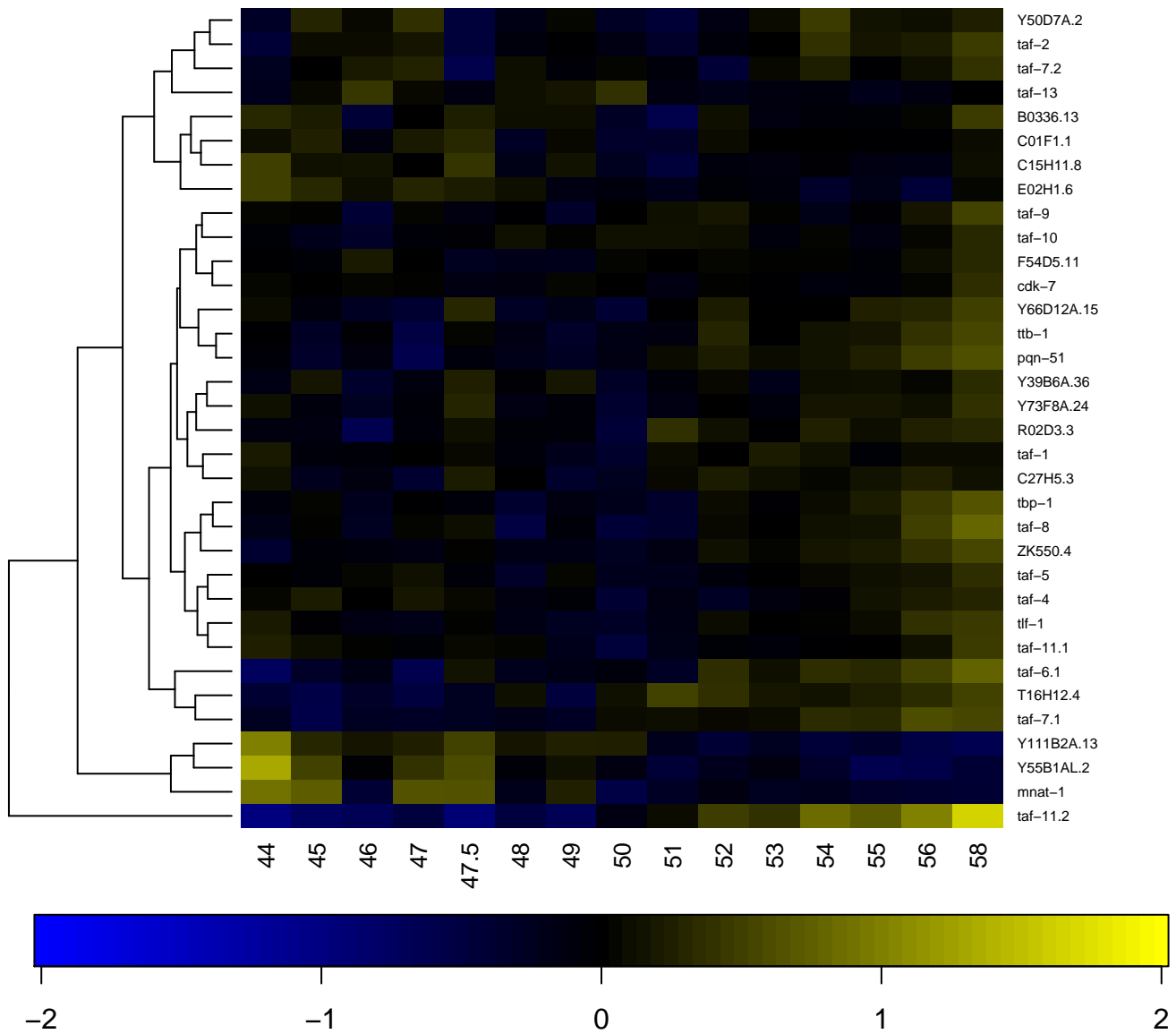
Arginine and proline metabolism



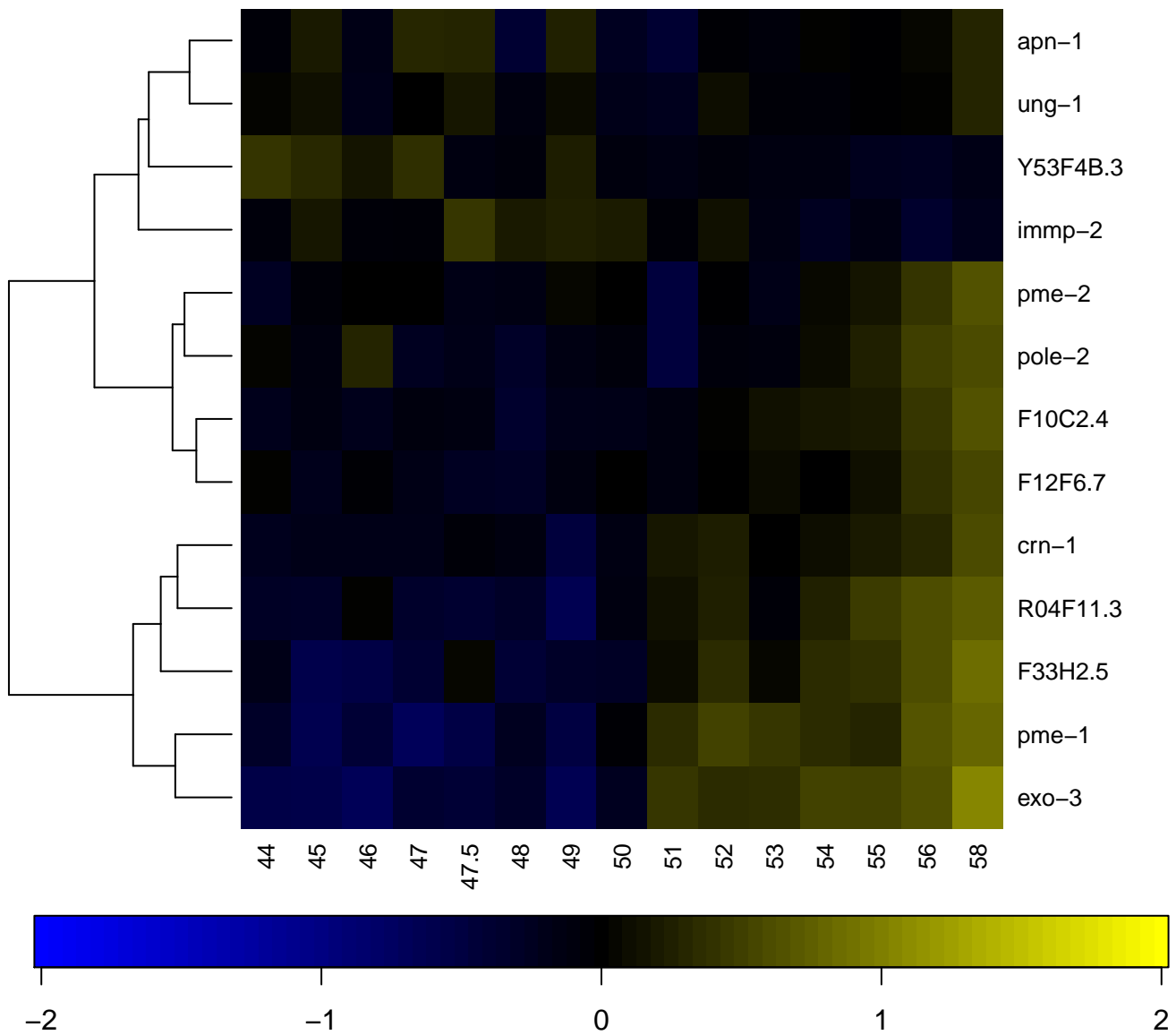
Ascorbate and aldrate metabolism



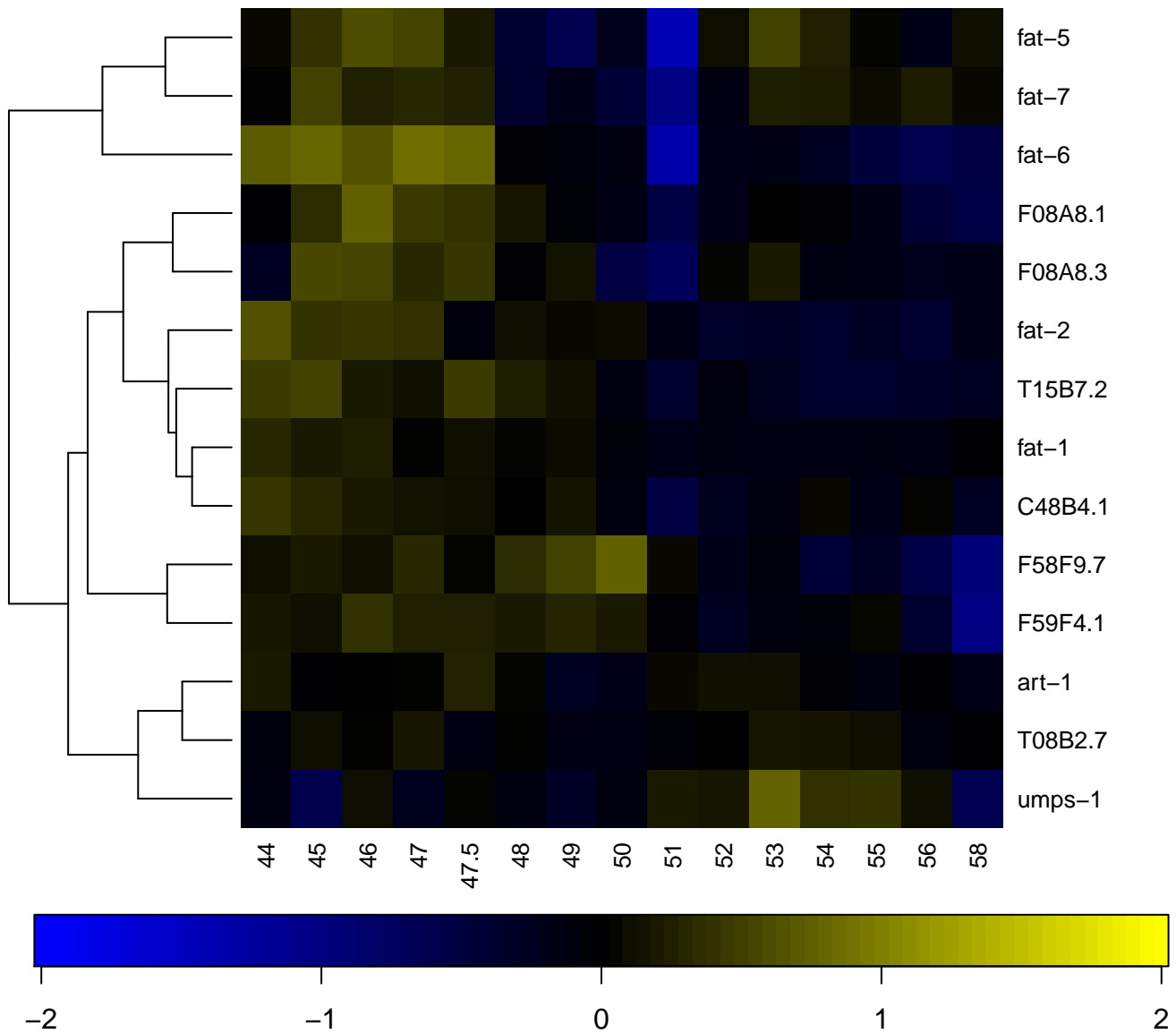
Basal transcription factors (eukaryotes)



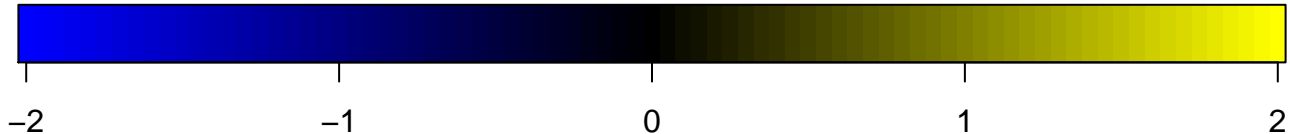
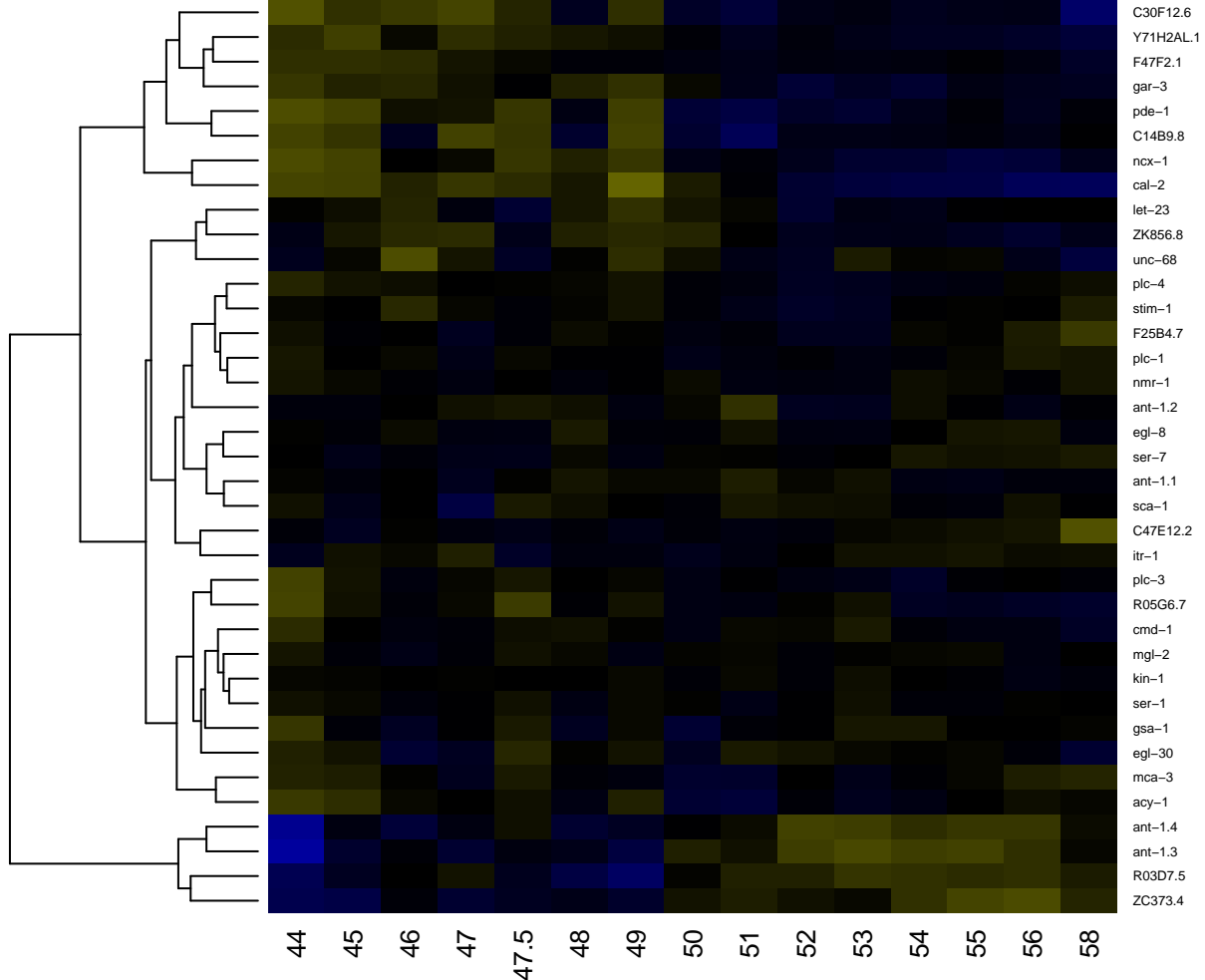
Base excision repair



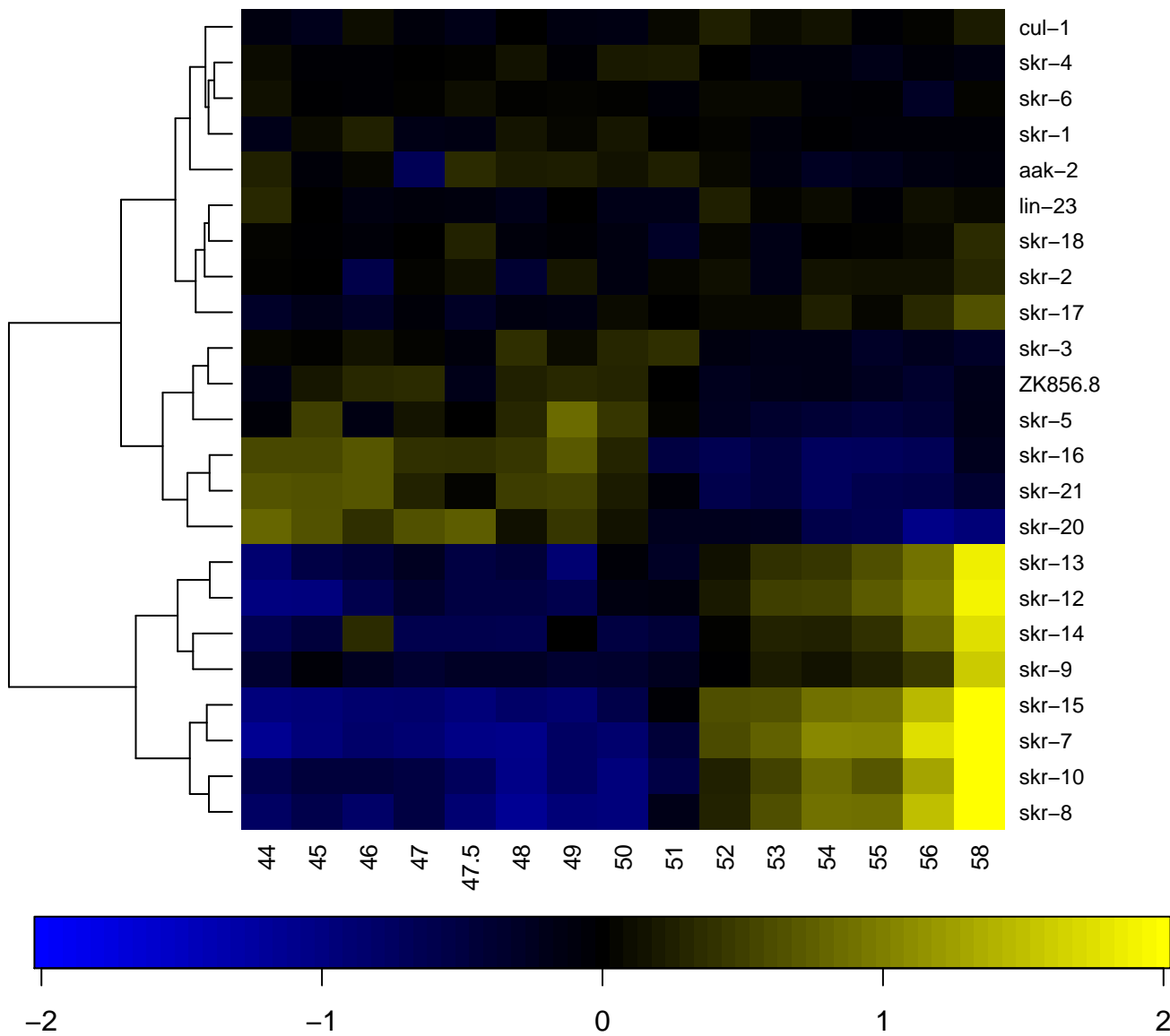
Biosynthesis of unsaturated fatty acids



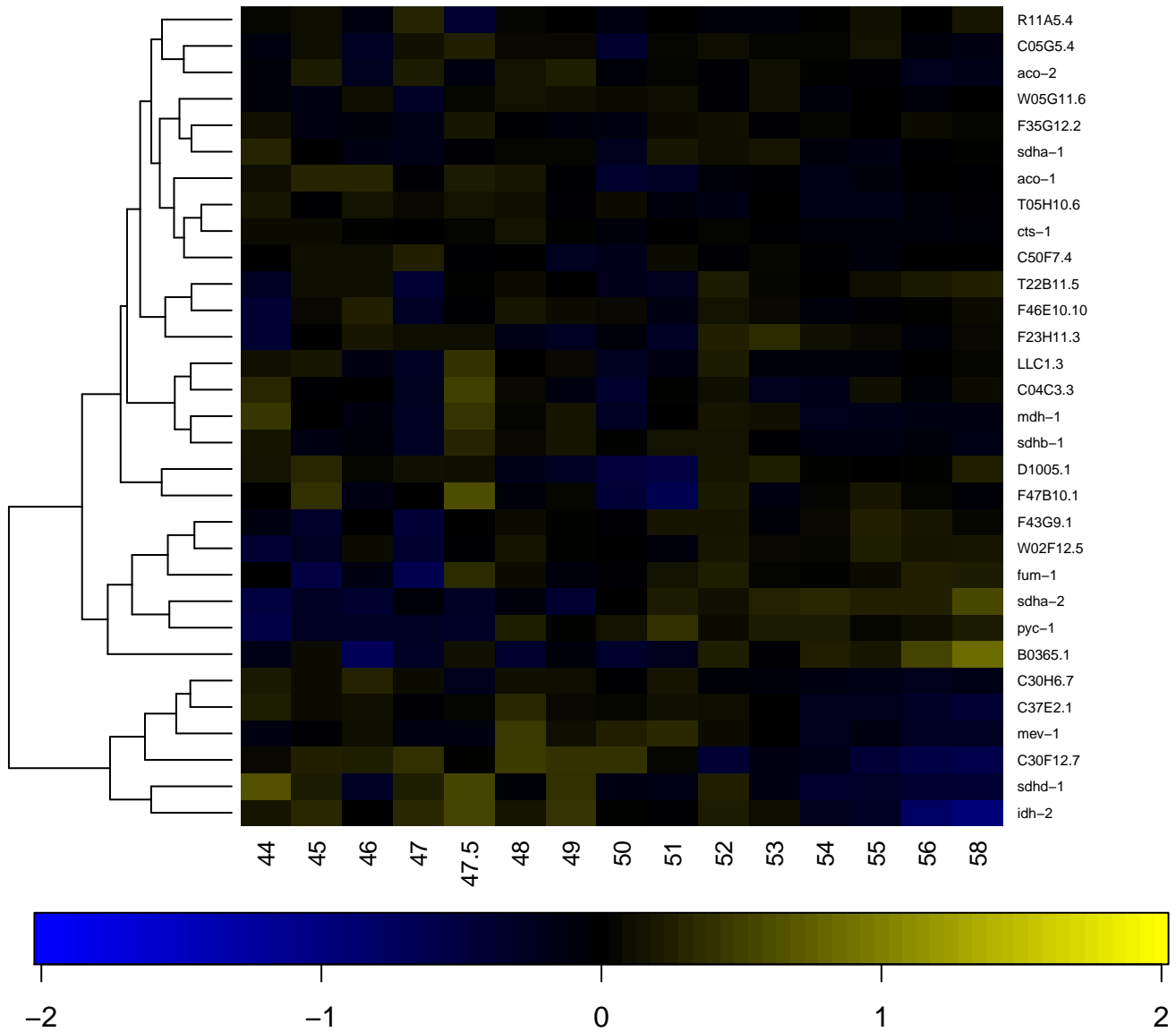
Calcium signaling pathway



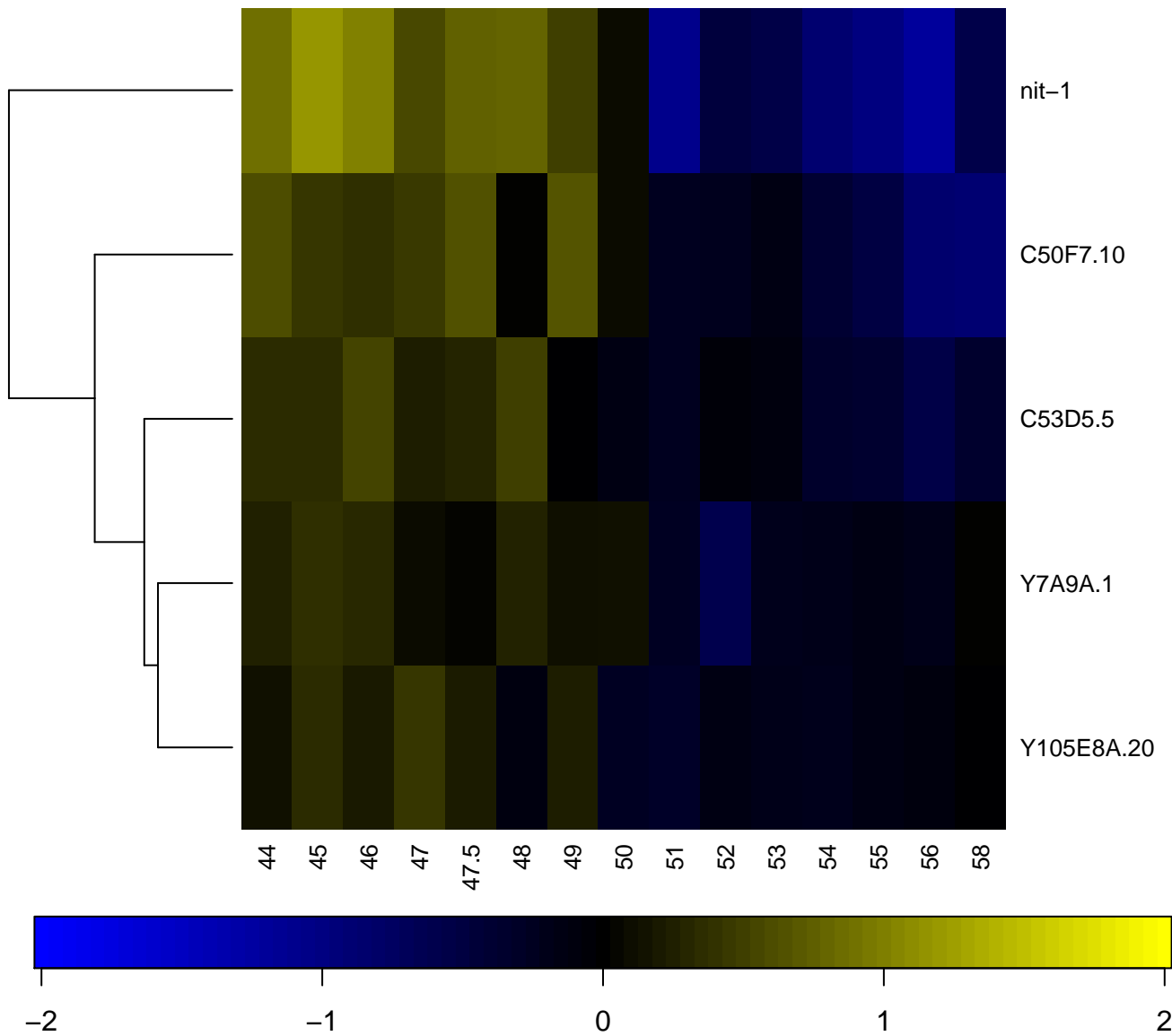
Circadian rhythm



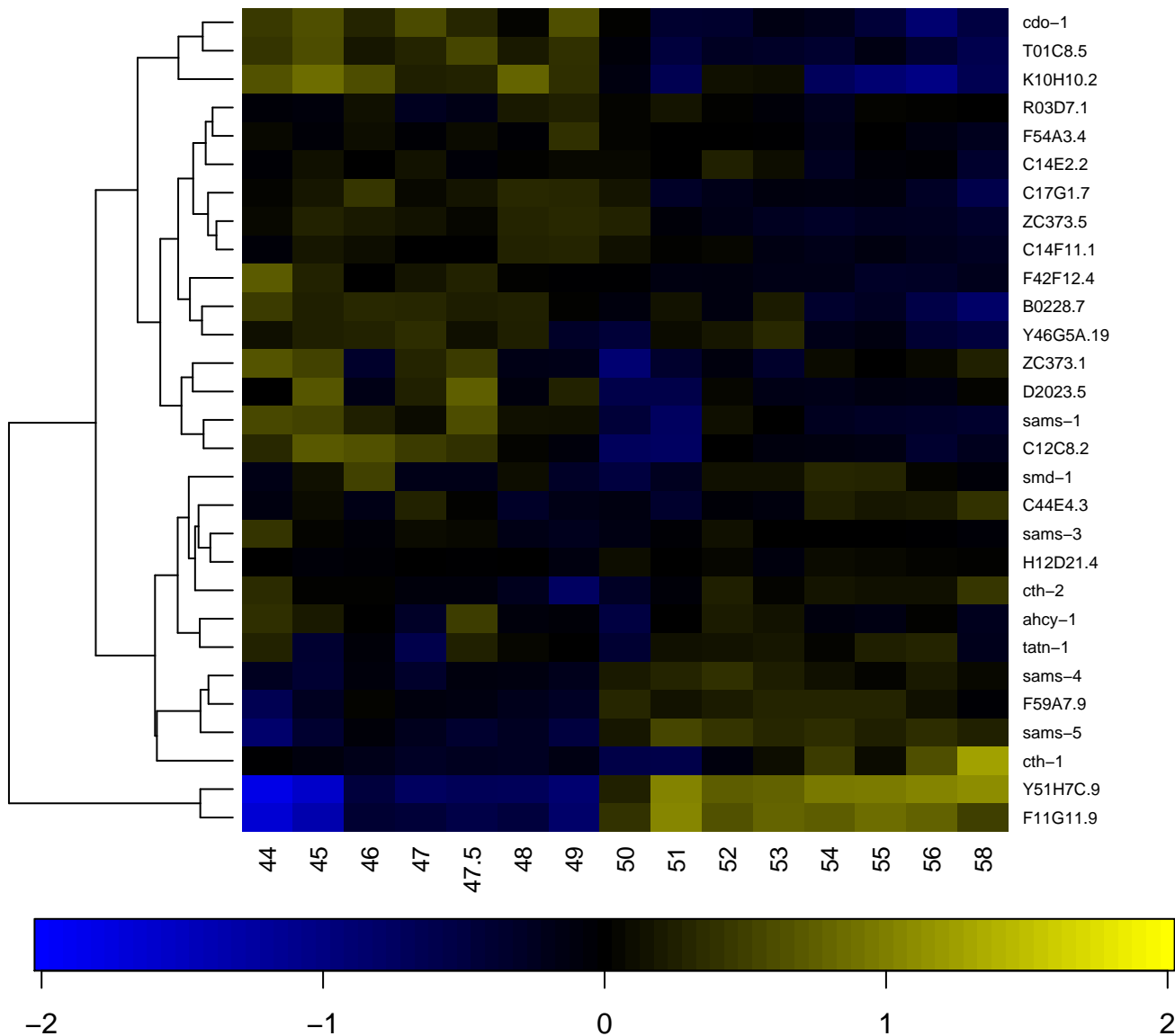
Citrate cycle (TCA cycle)



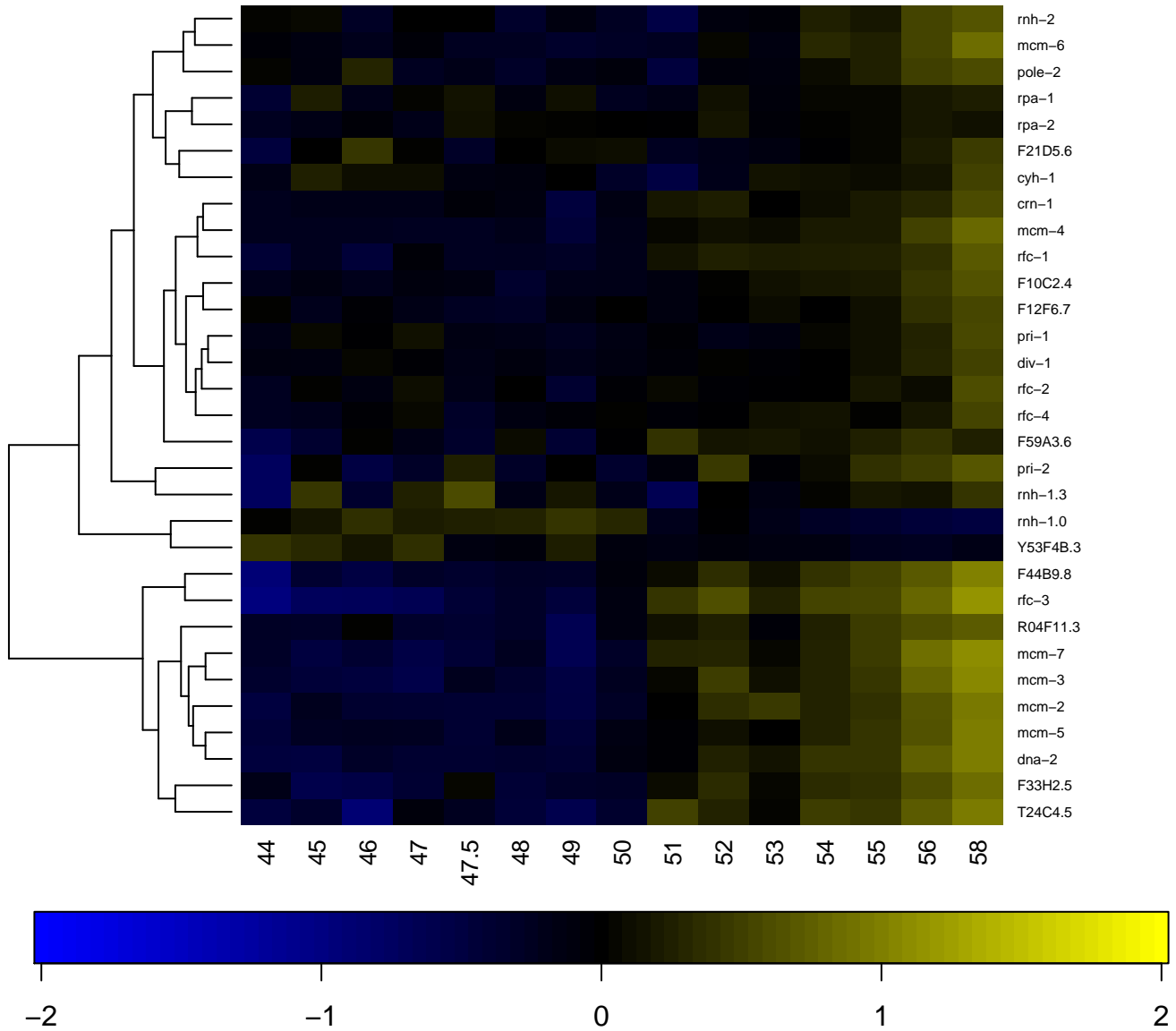
Cyanoamino acid metabolism



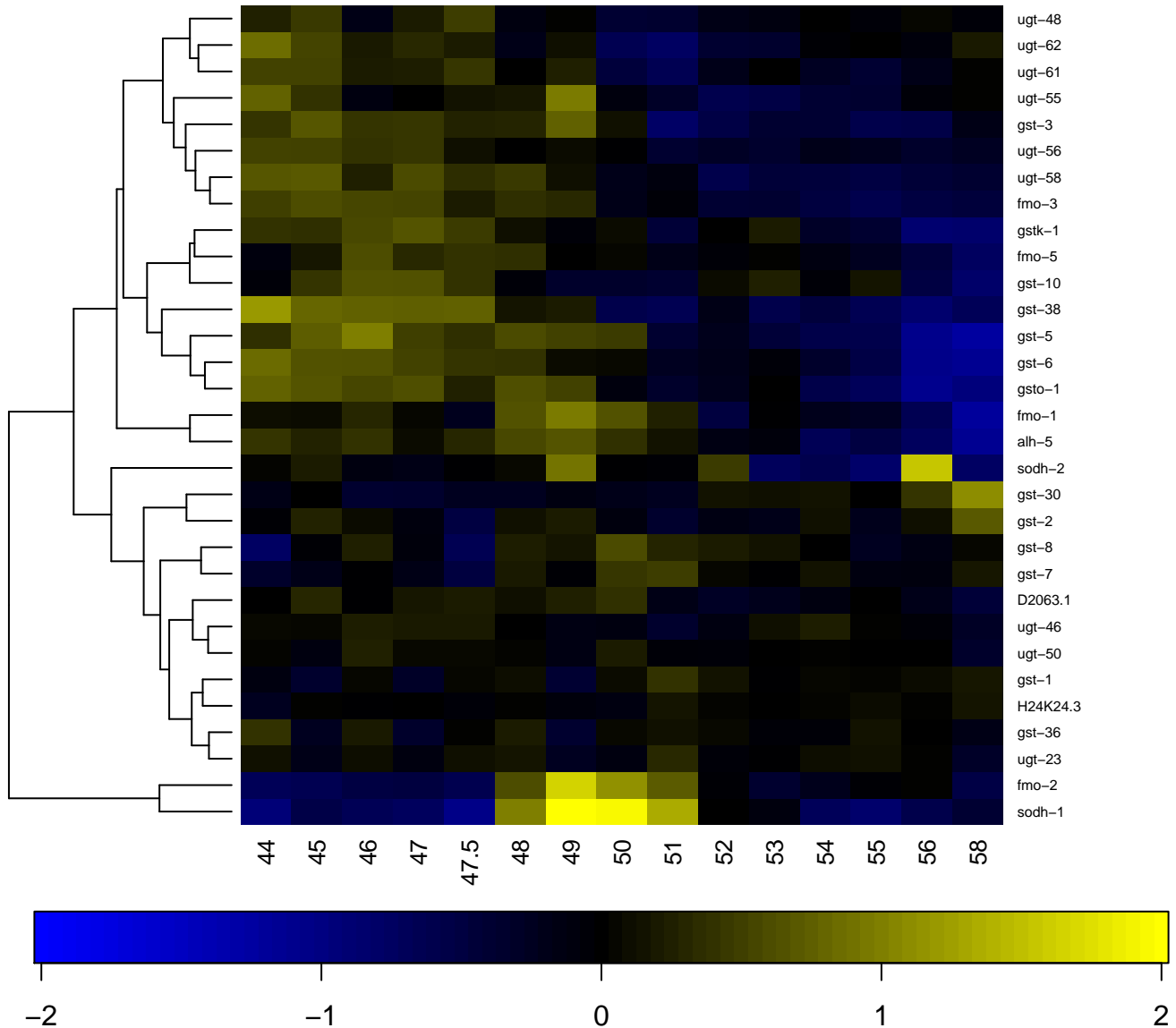
Cysteine and methionine metabolism



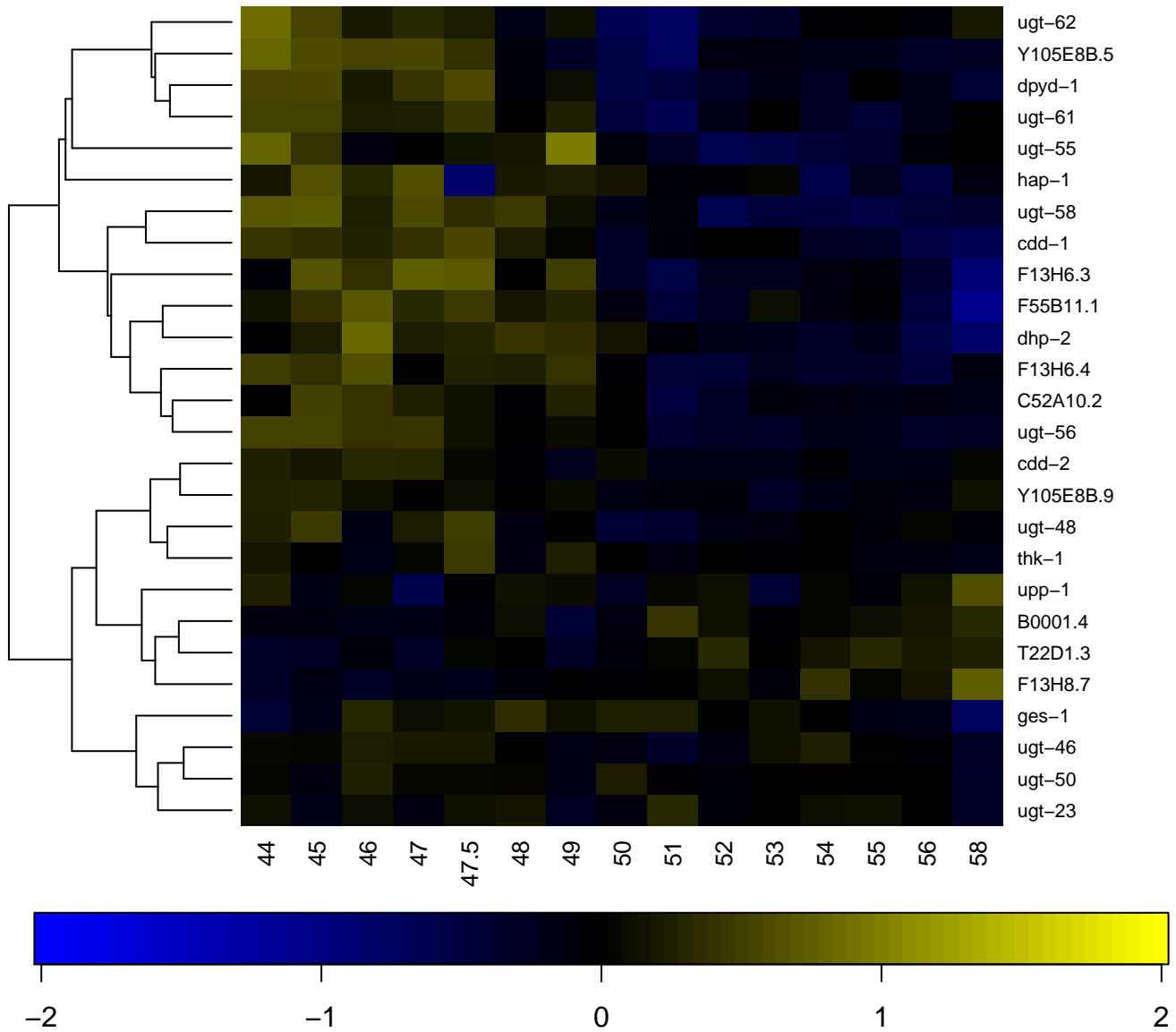
DNA replication



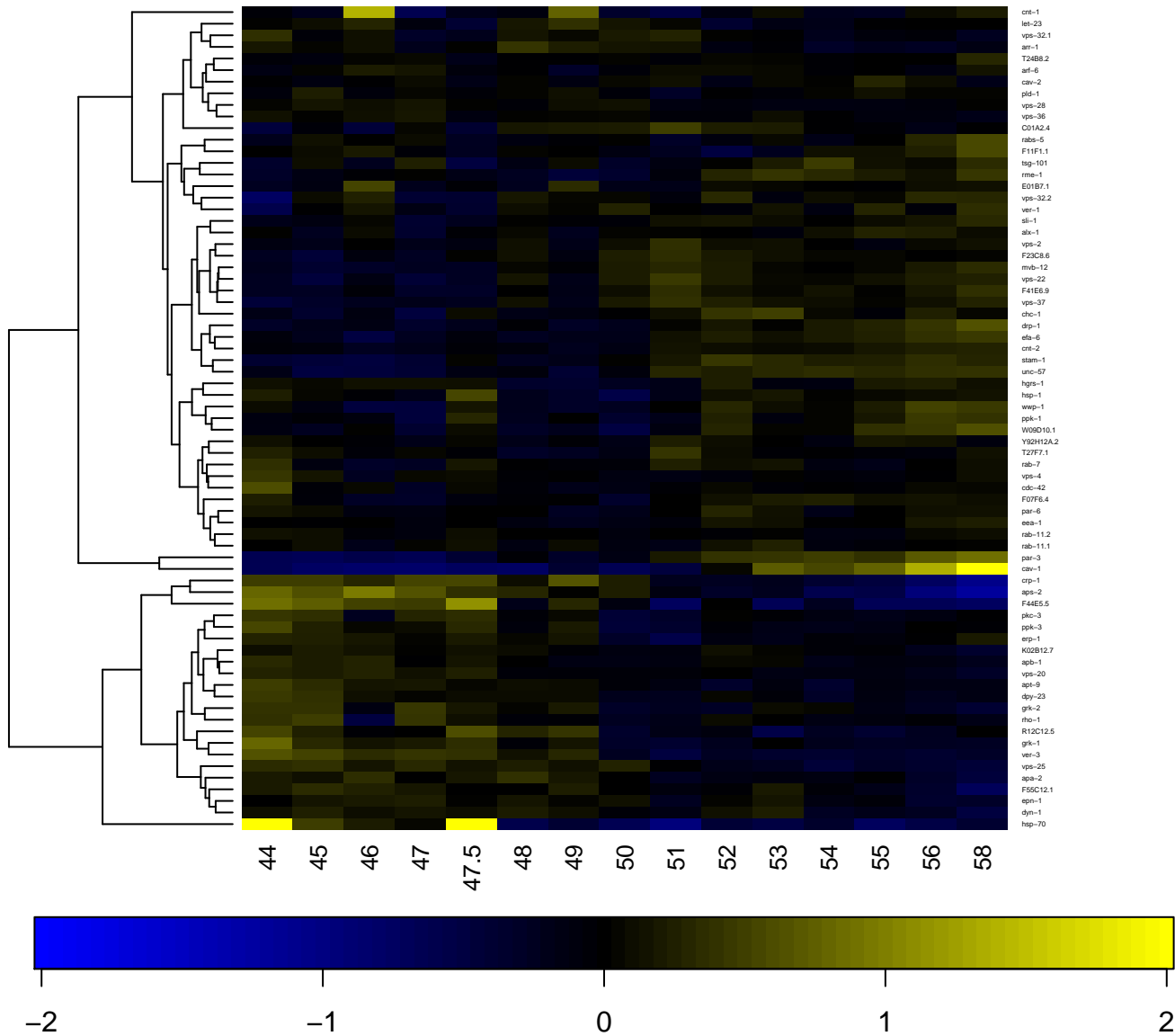
Drug metabolism – cytochrome P450



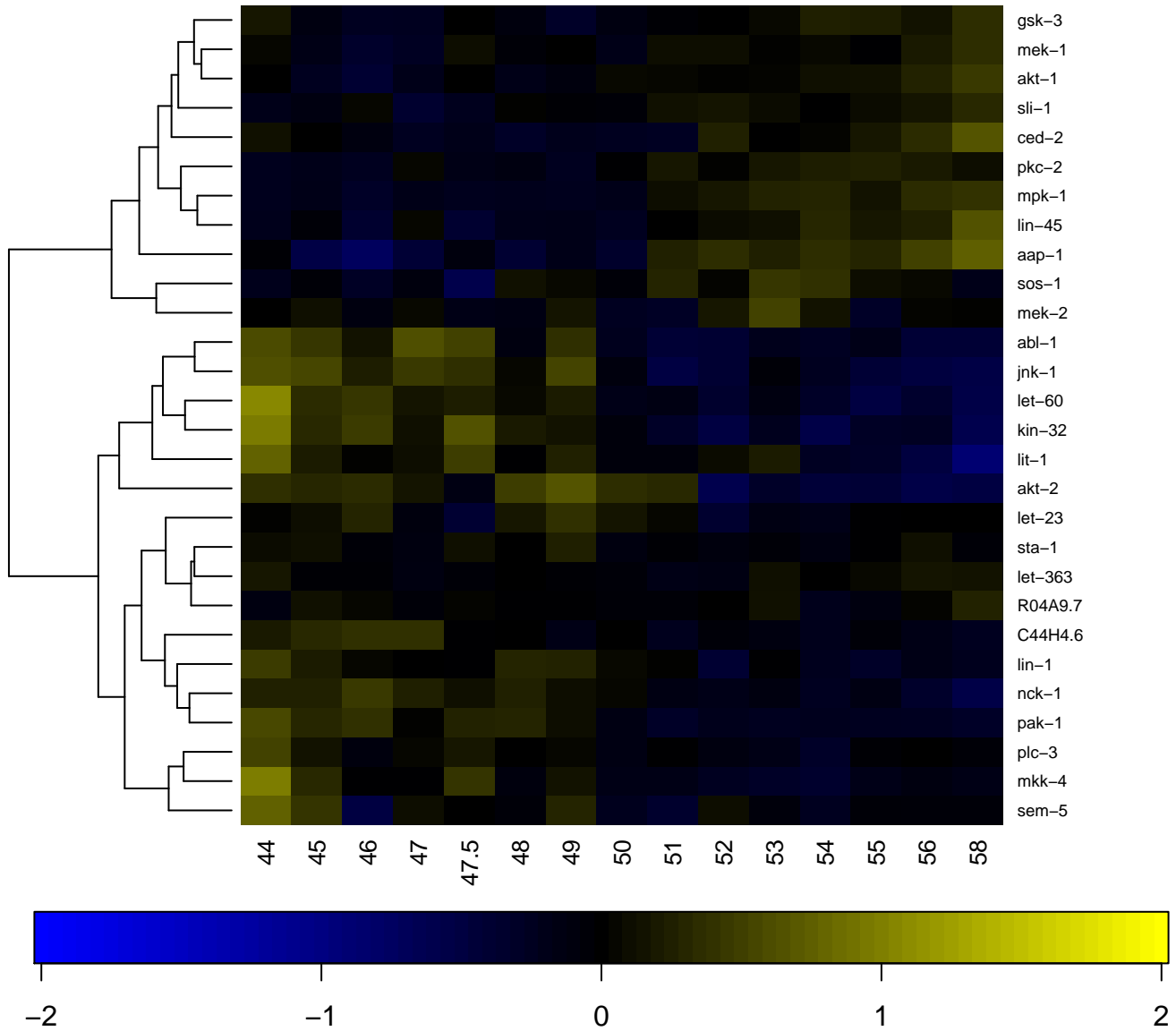
Drug metabolism – other enzymes



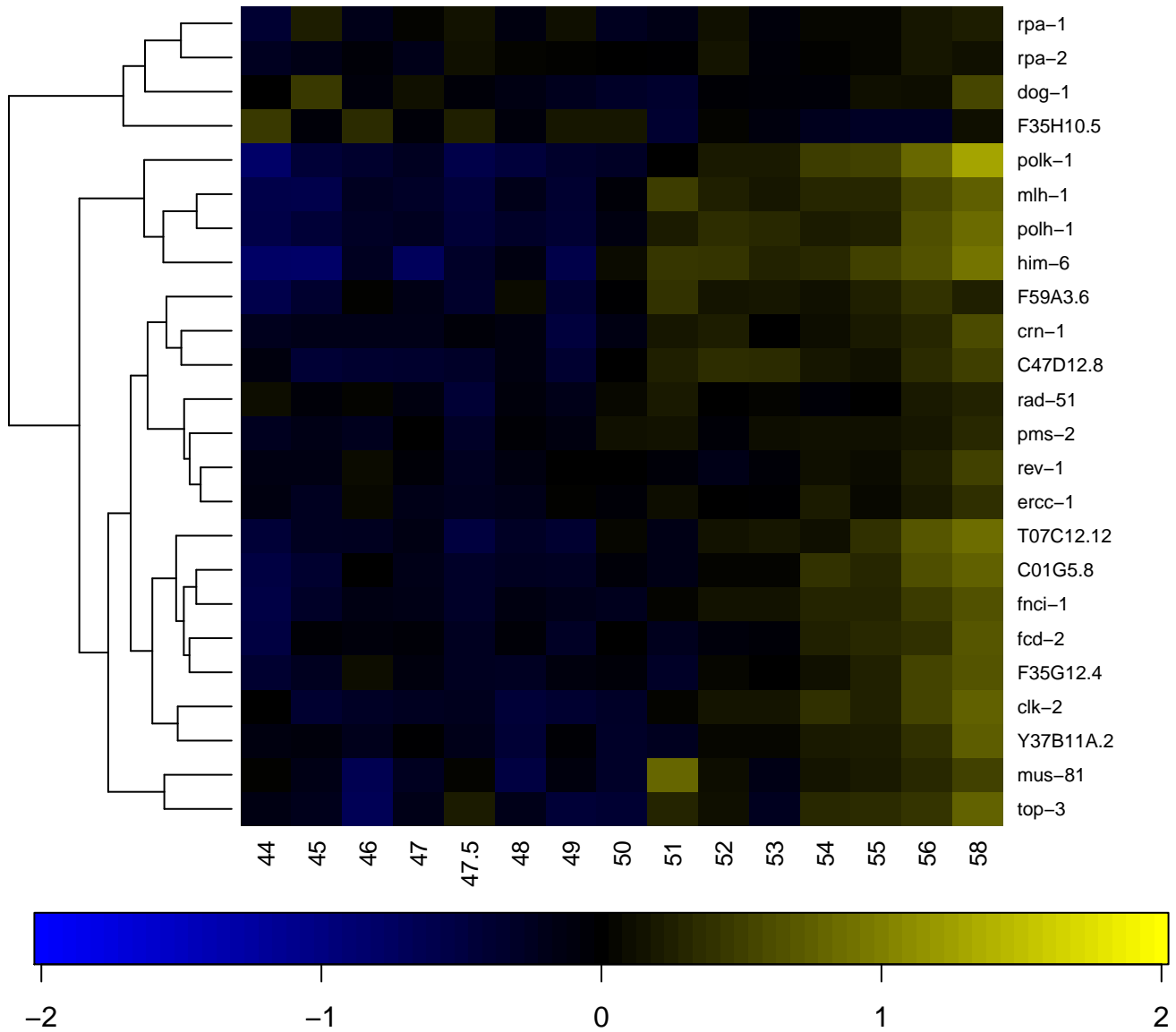
Endocytosis



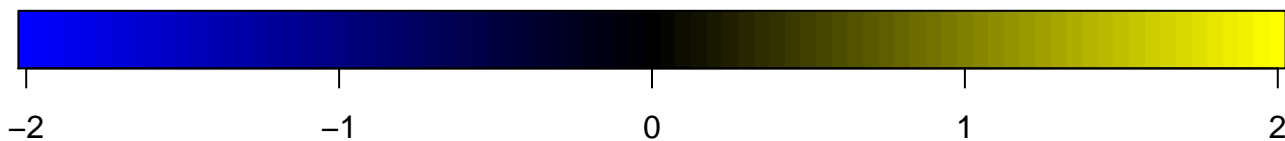
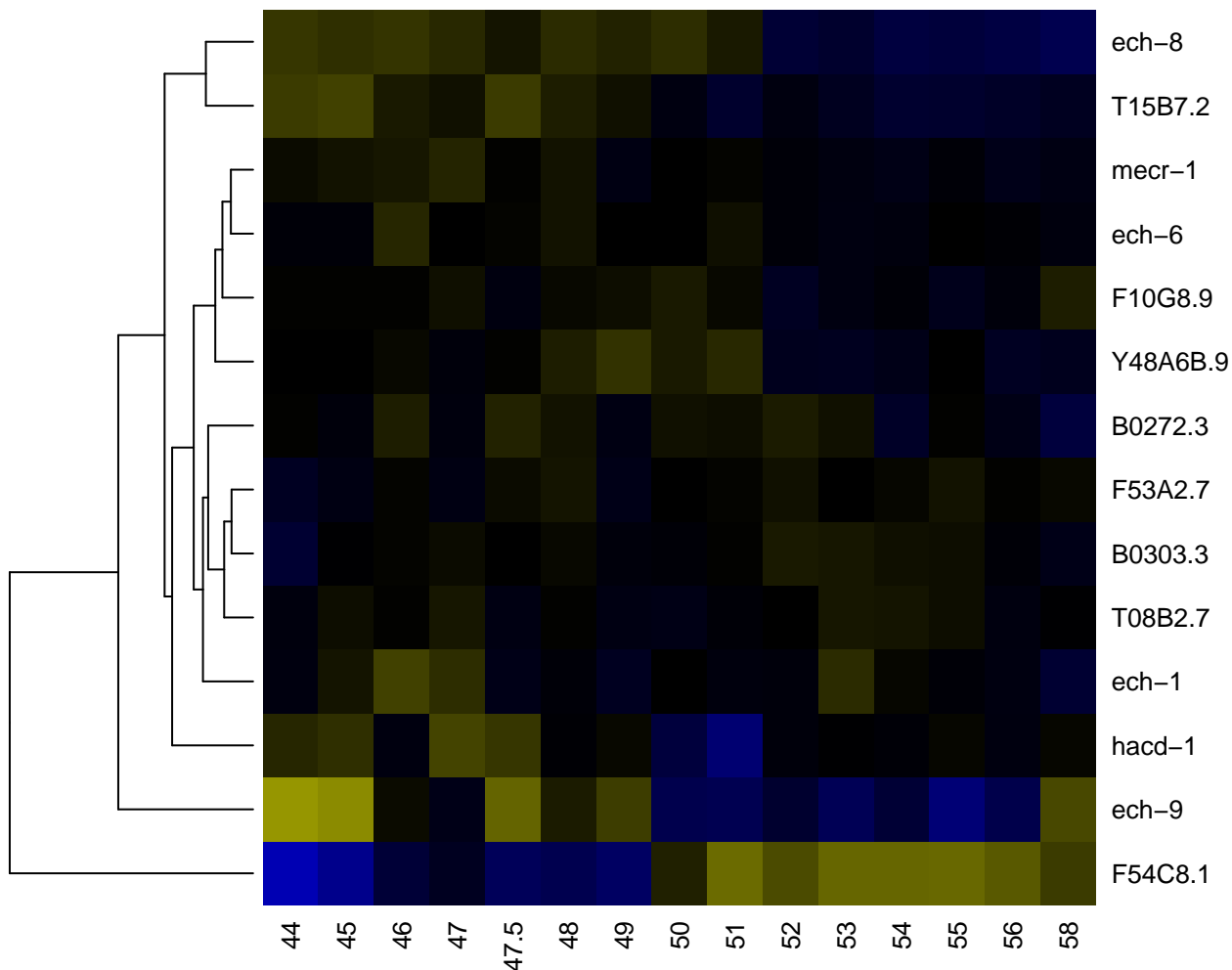
ERBB signaling pathway



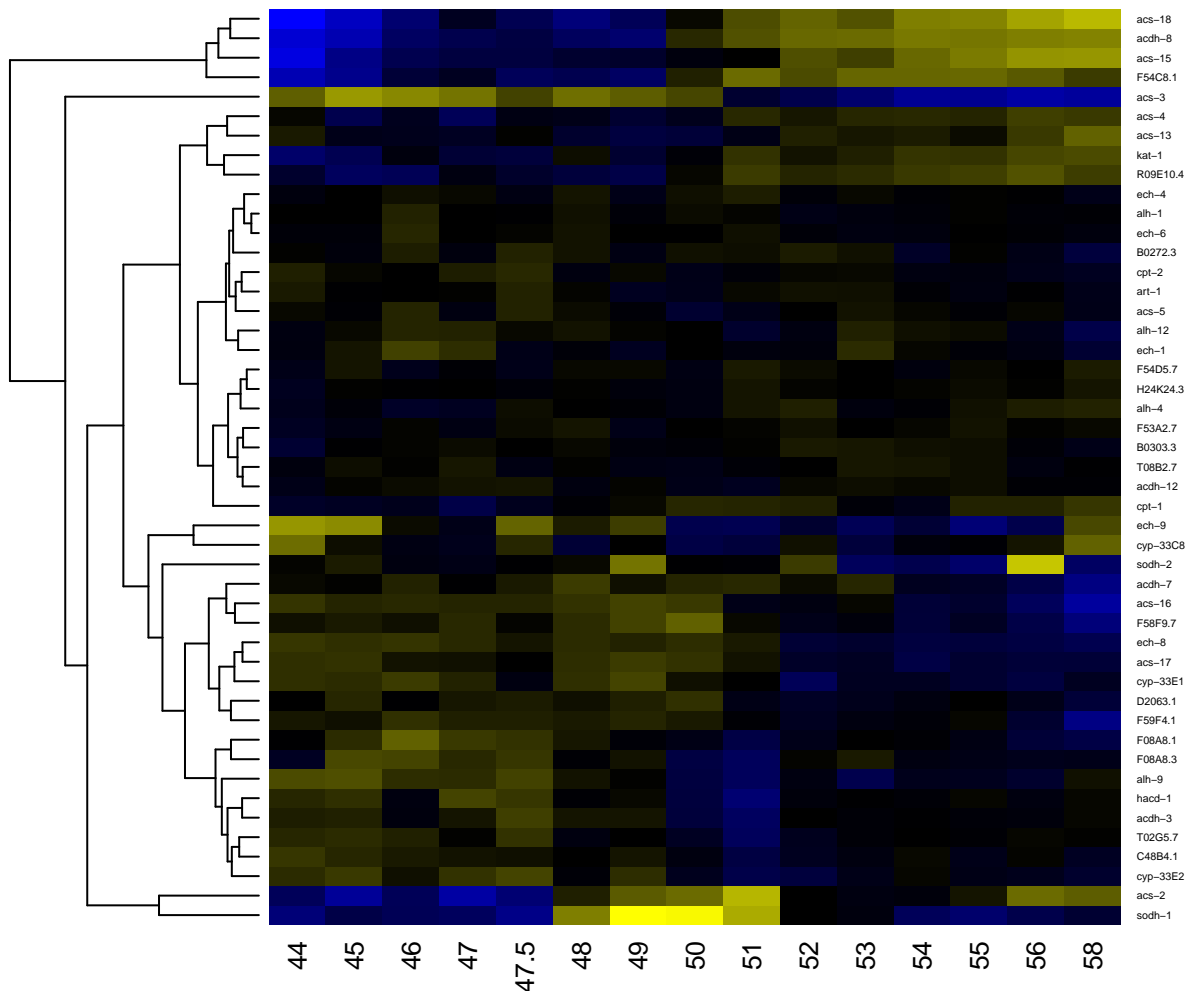
Fanconi anemia pathway



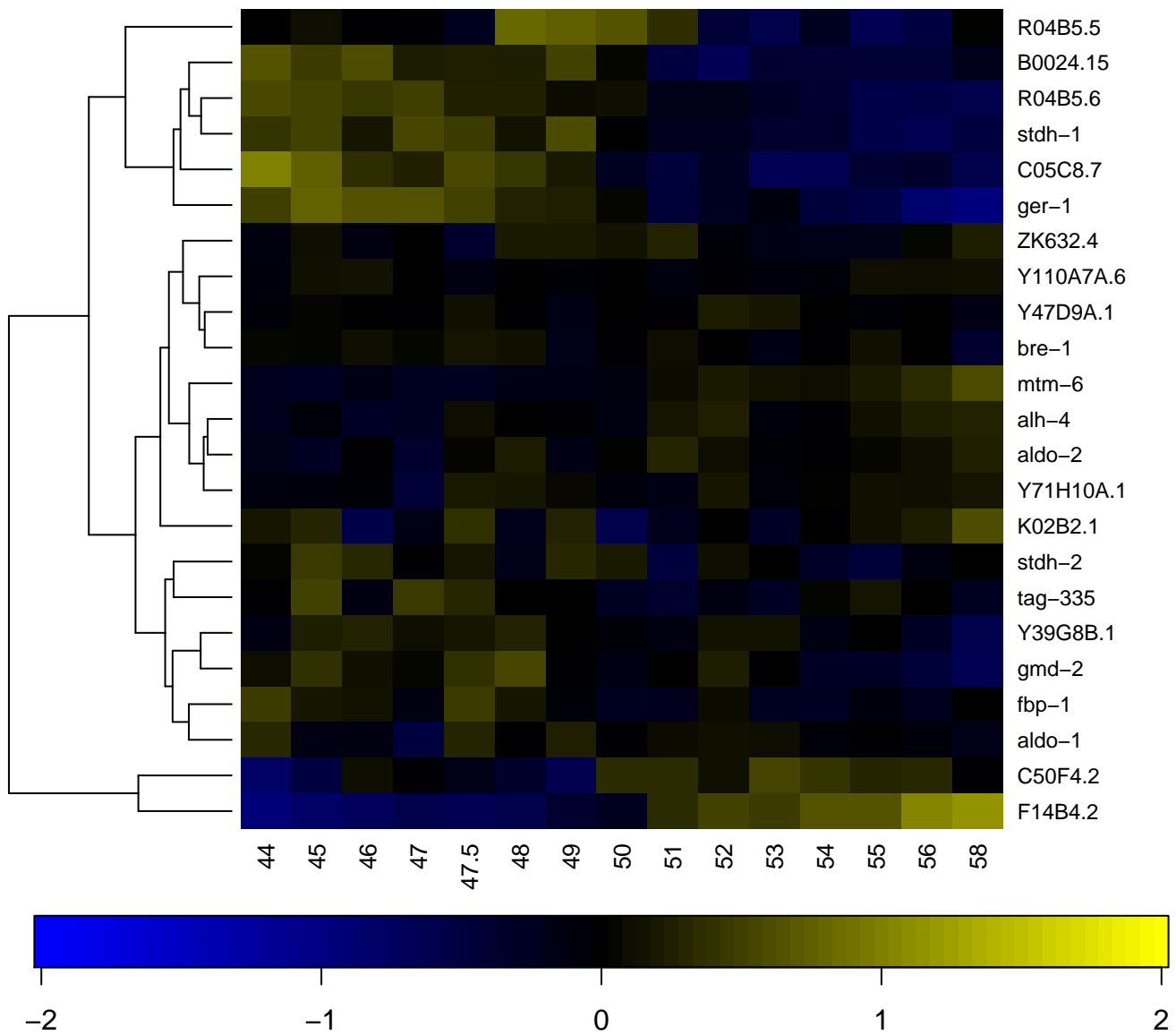
Fatty acid elongation



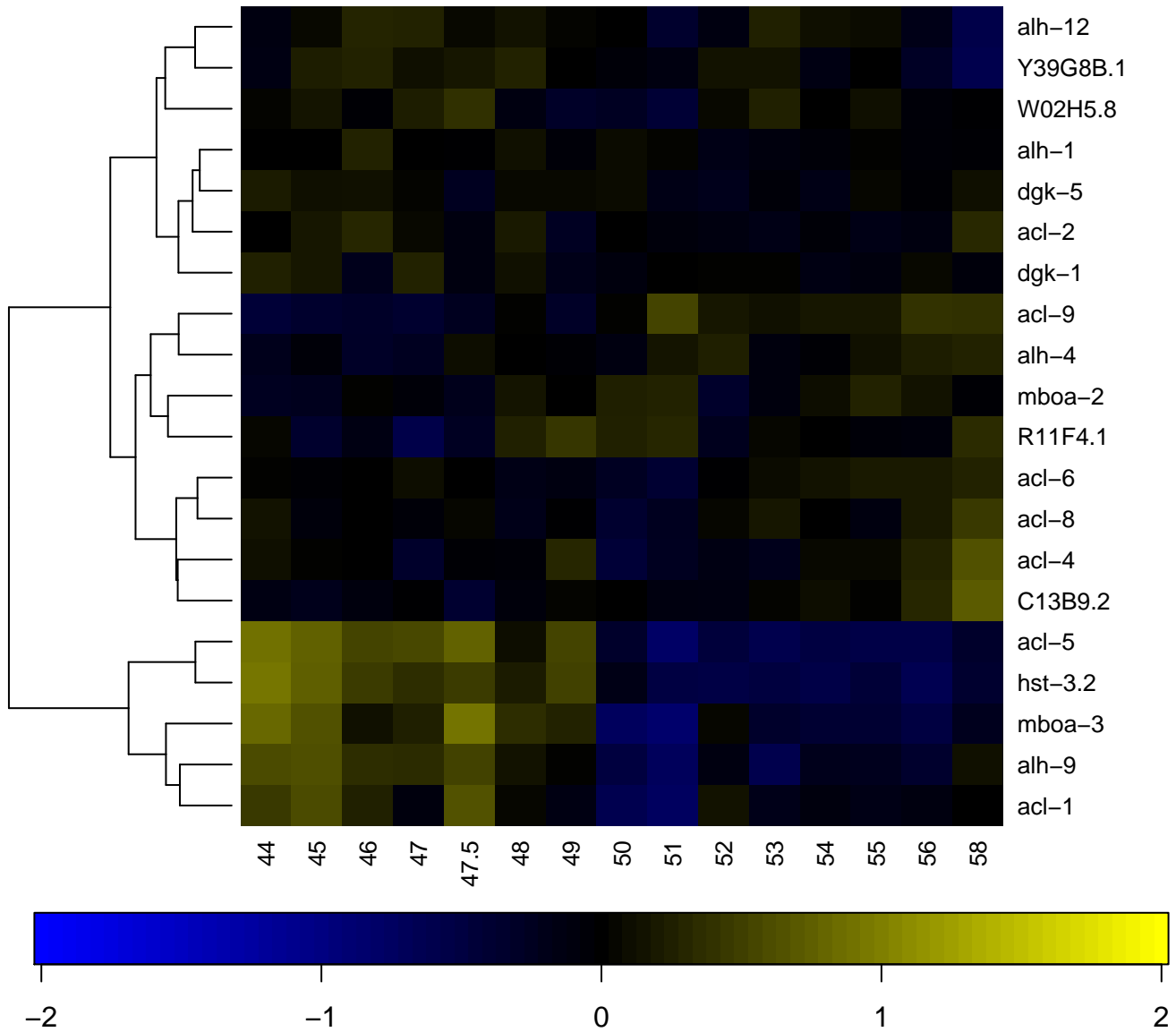
Fatty acid metabolism



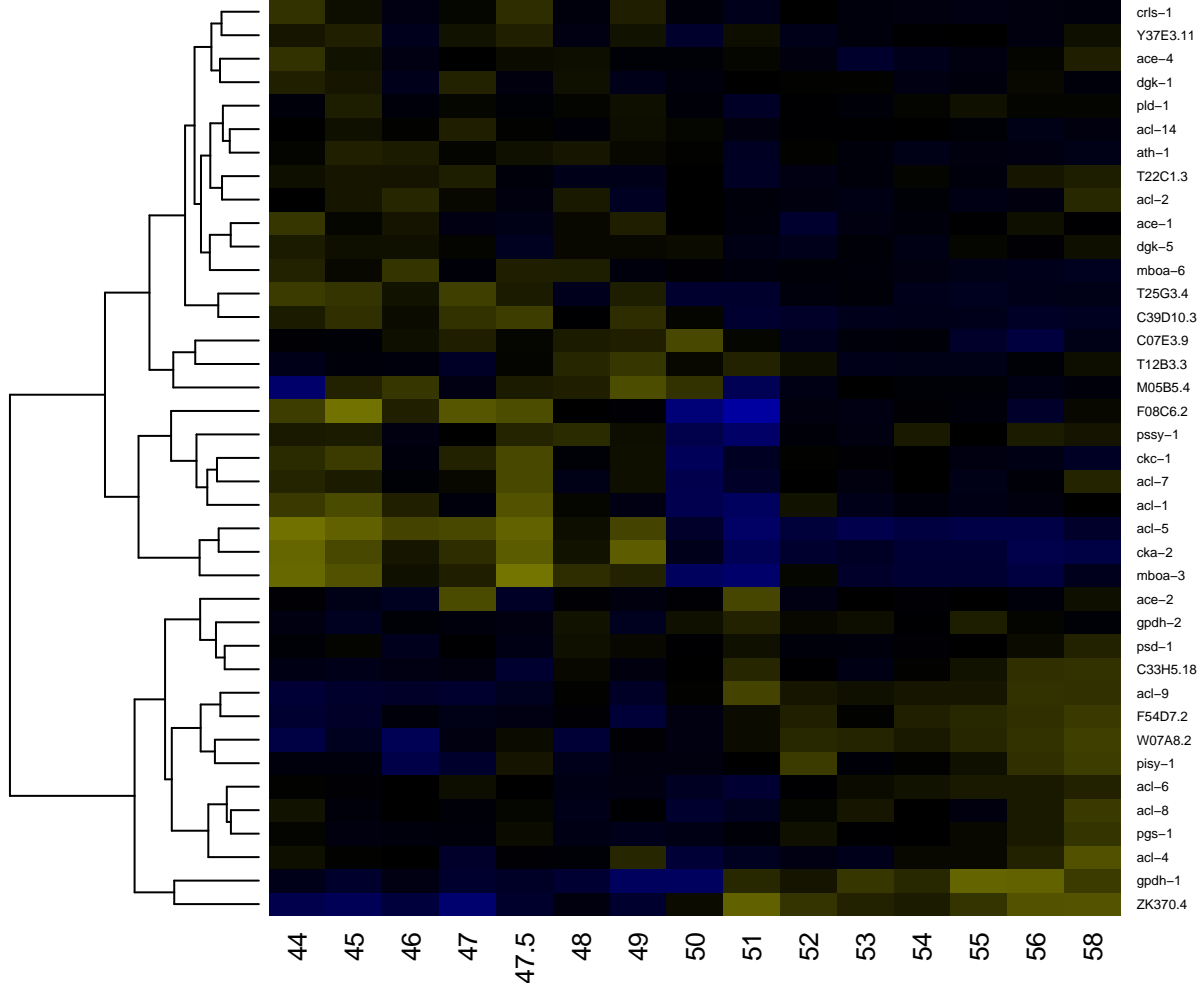
Fructose and mannose metabolism



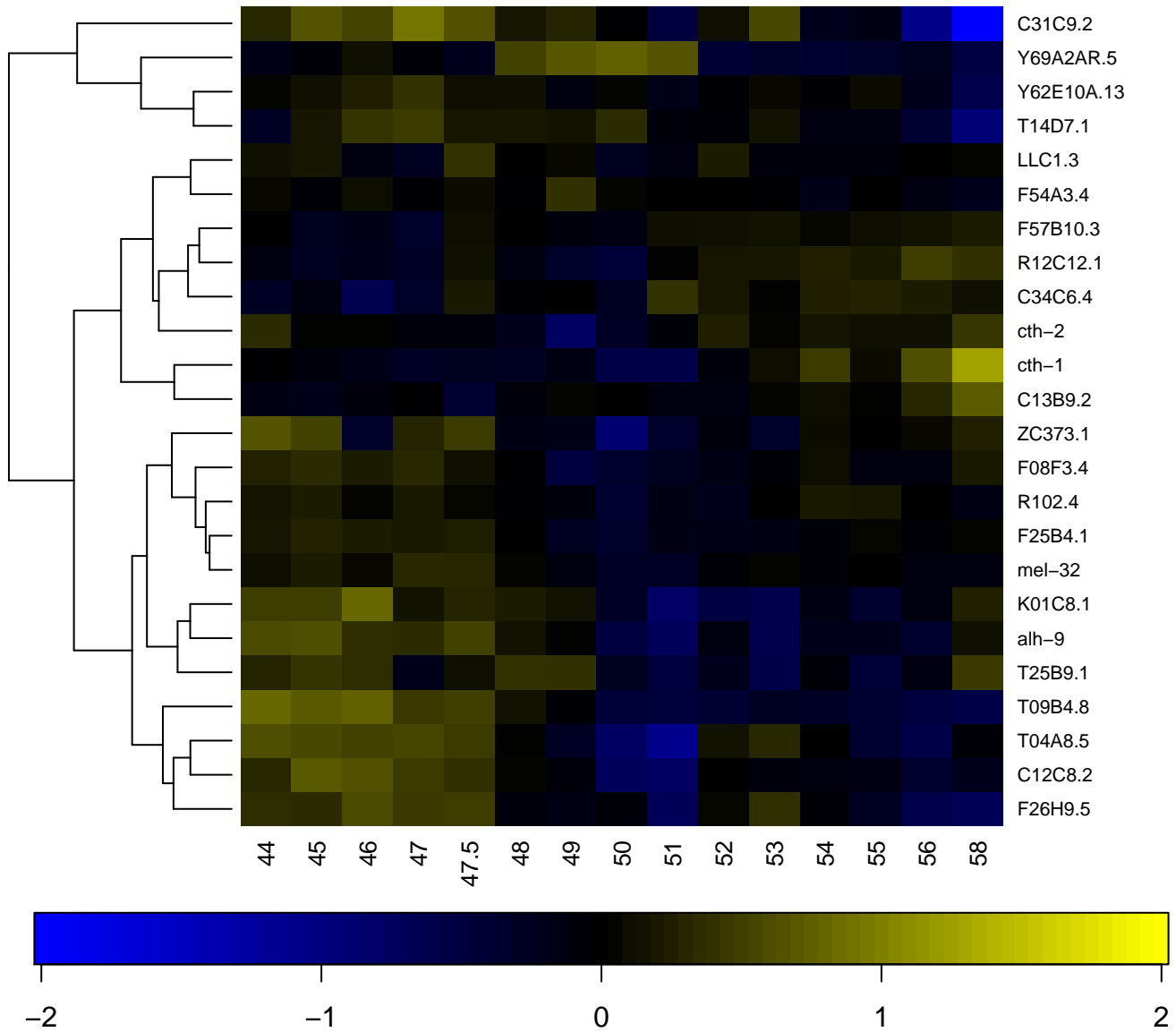
Glycerolipid metabolism



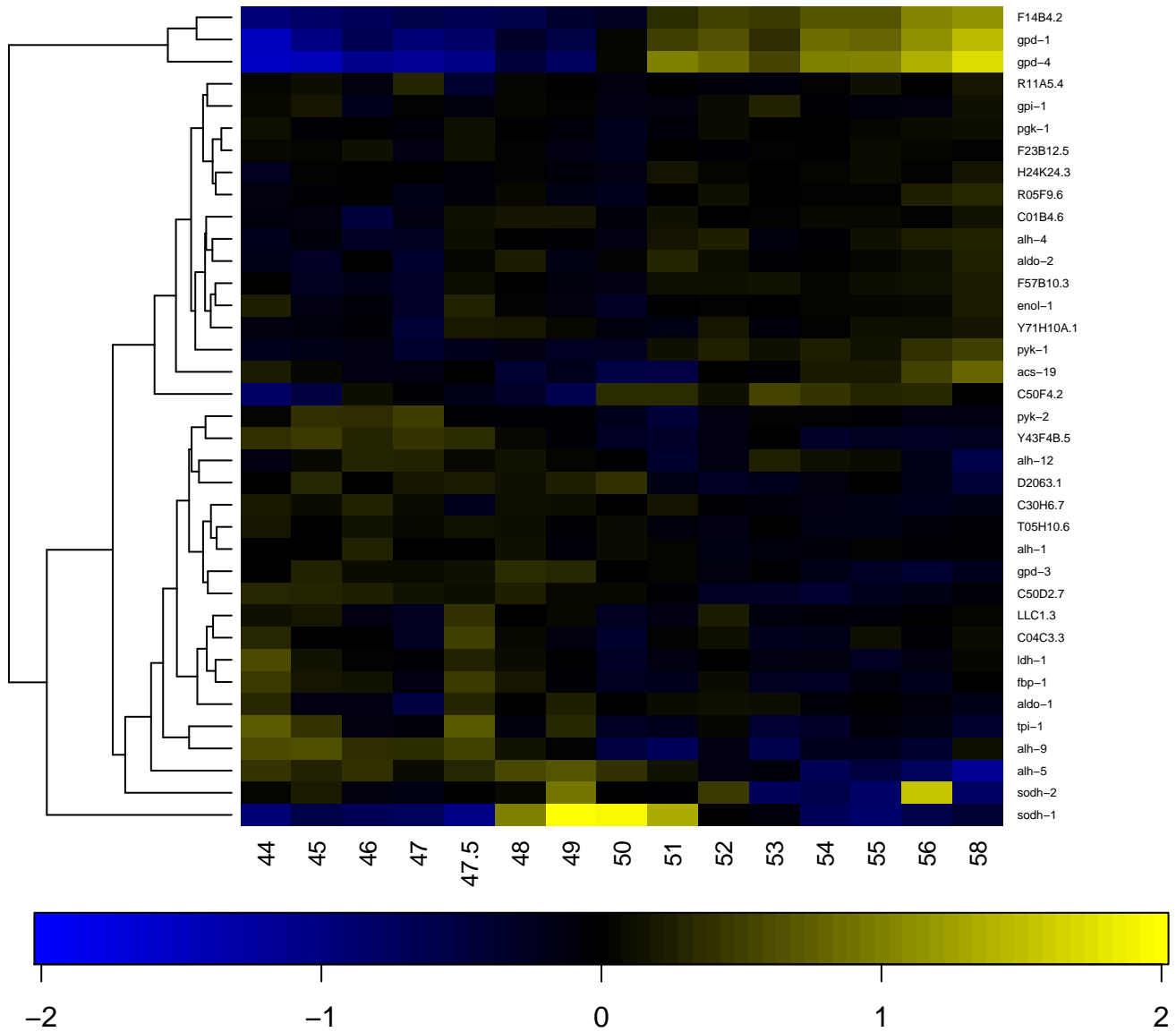
Glycerophospholipid metabolism



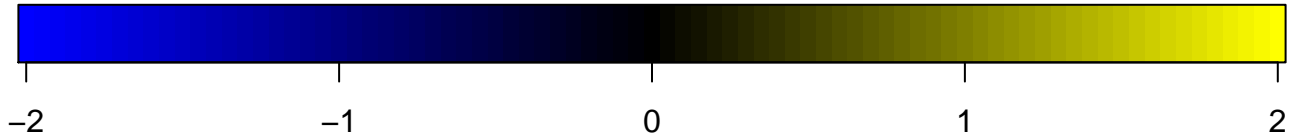
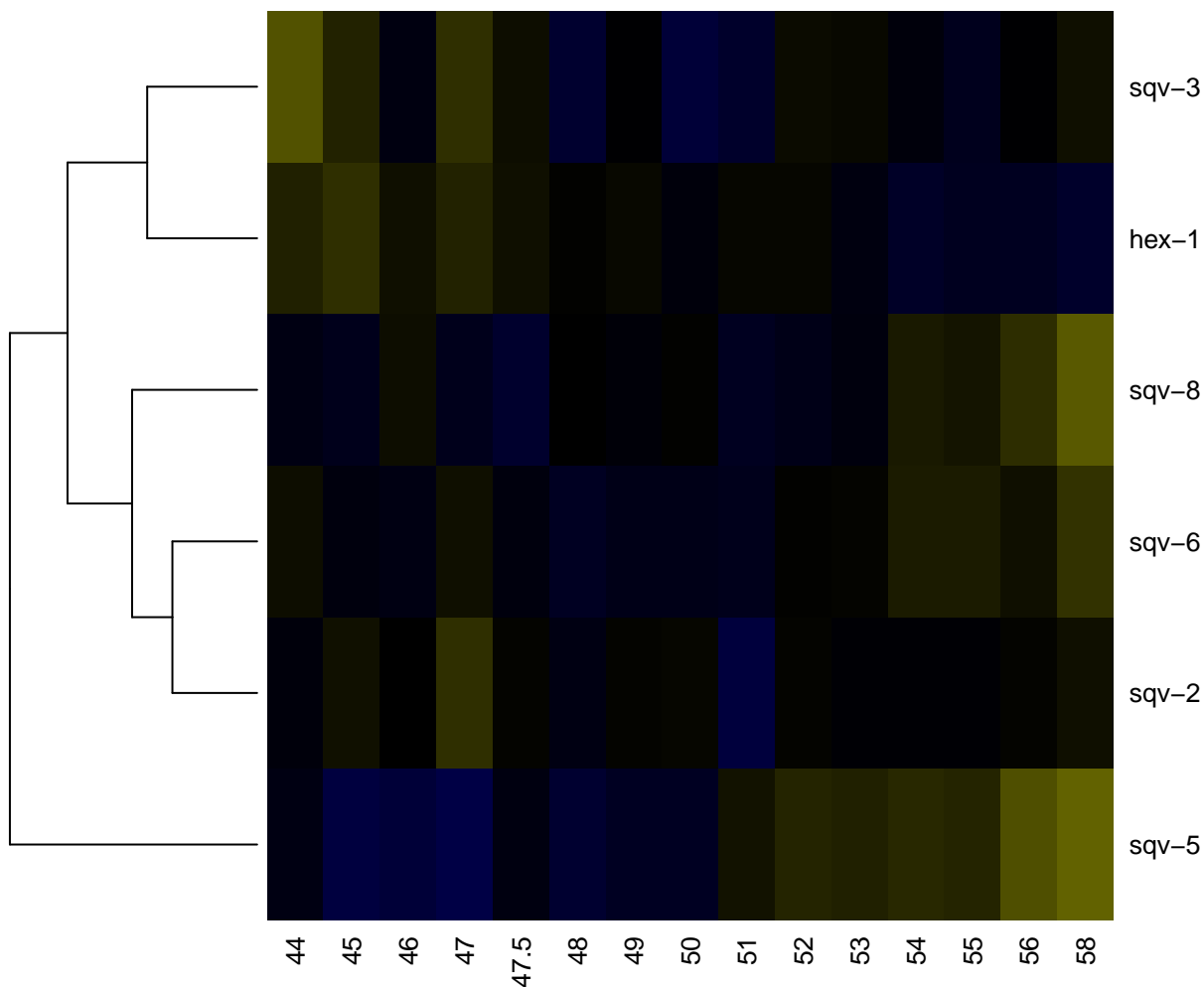
Glycine, serine and threonine metabolism



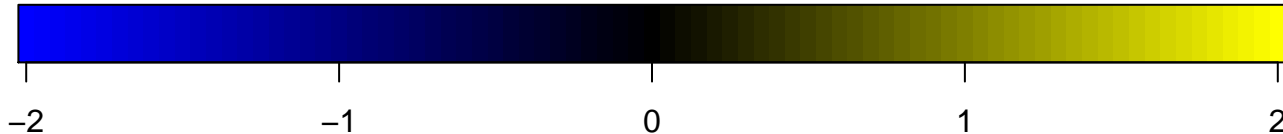
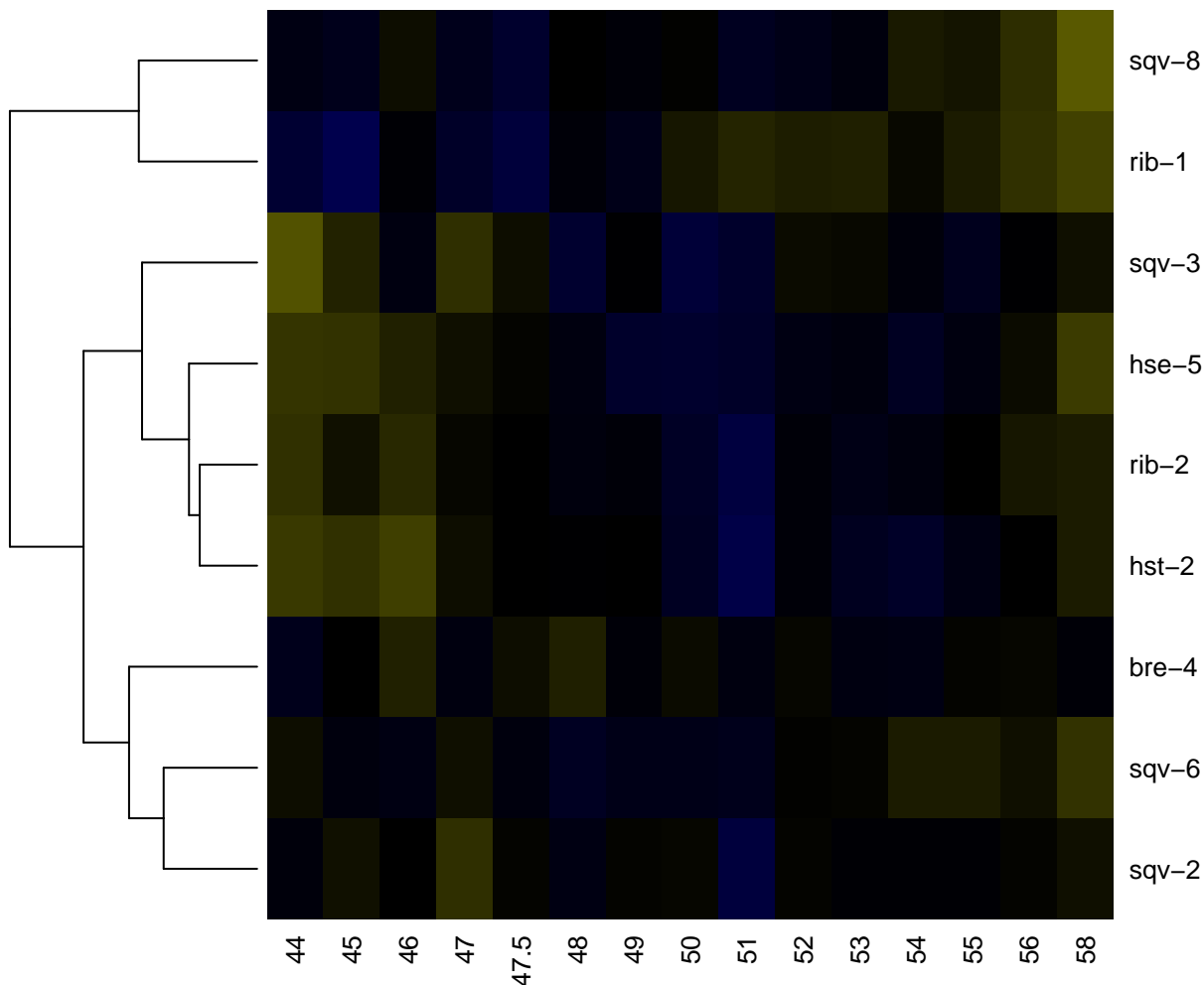
Glycolyse / Gluconeogenesis



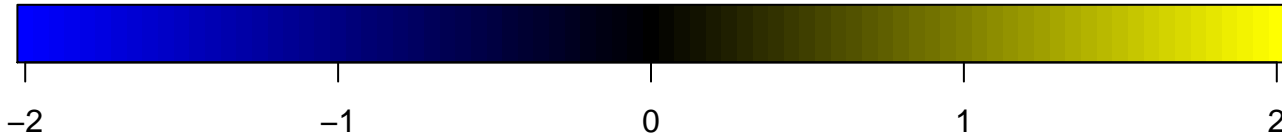
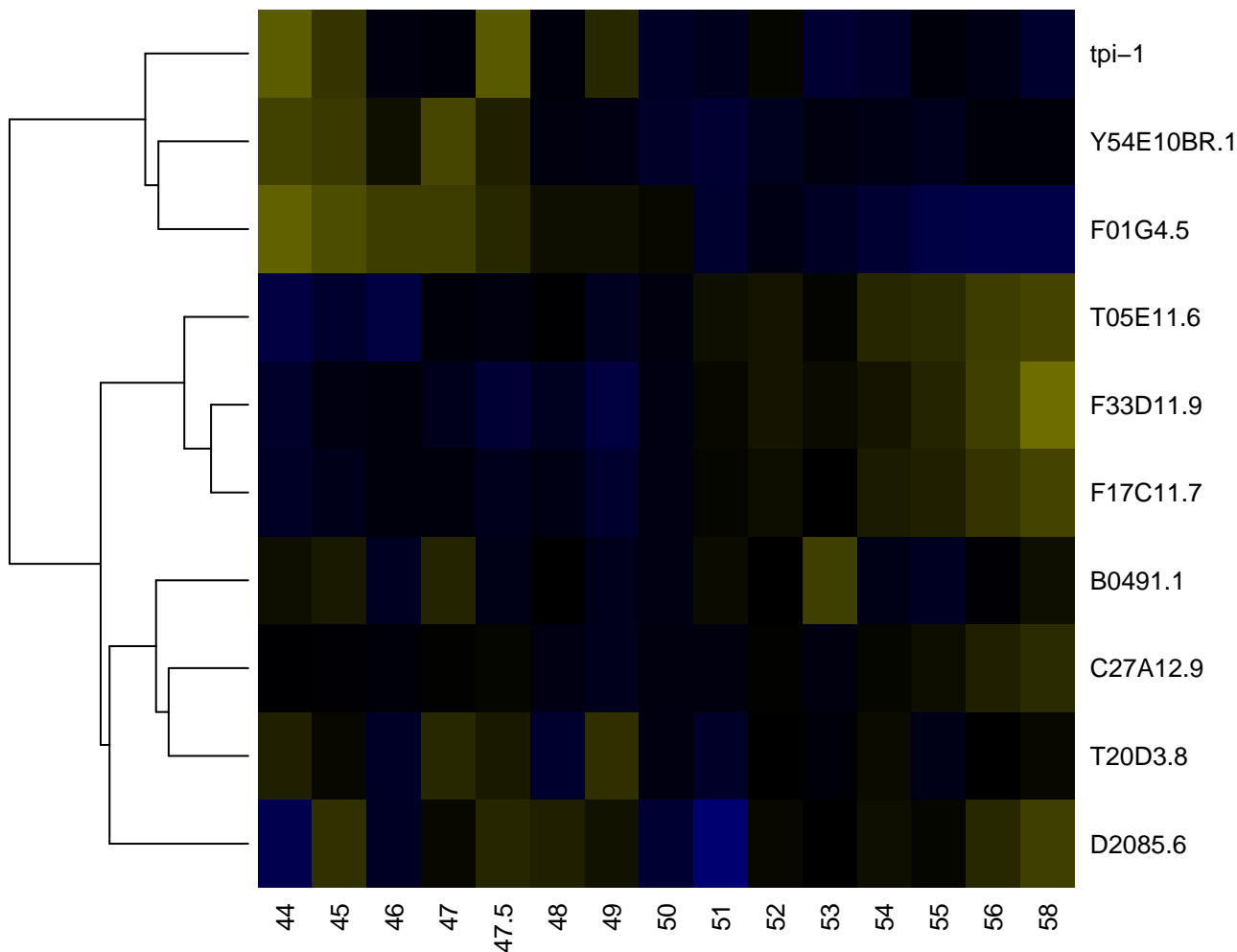
saminoglycan biosynthesis – chondroitin sulfate / dermatan



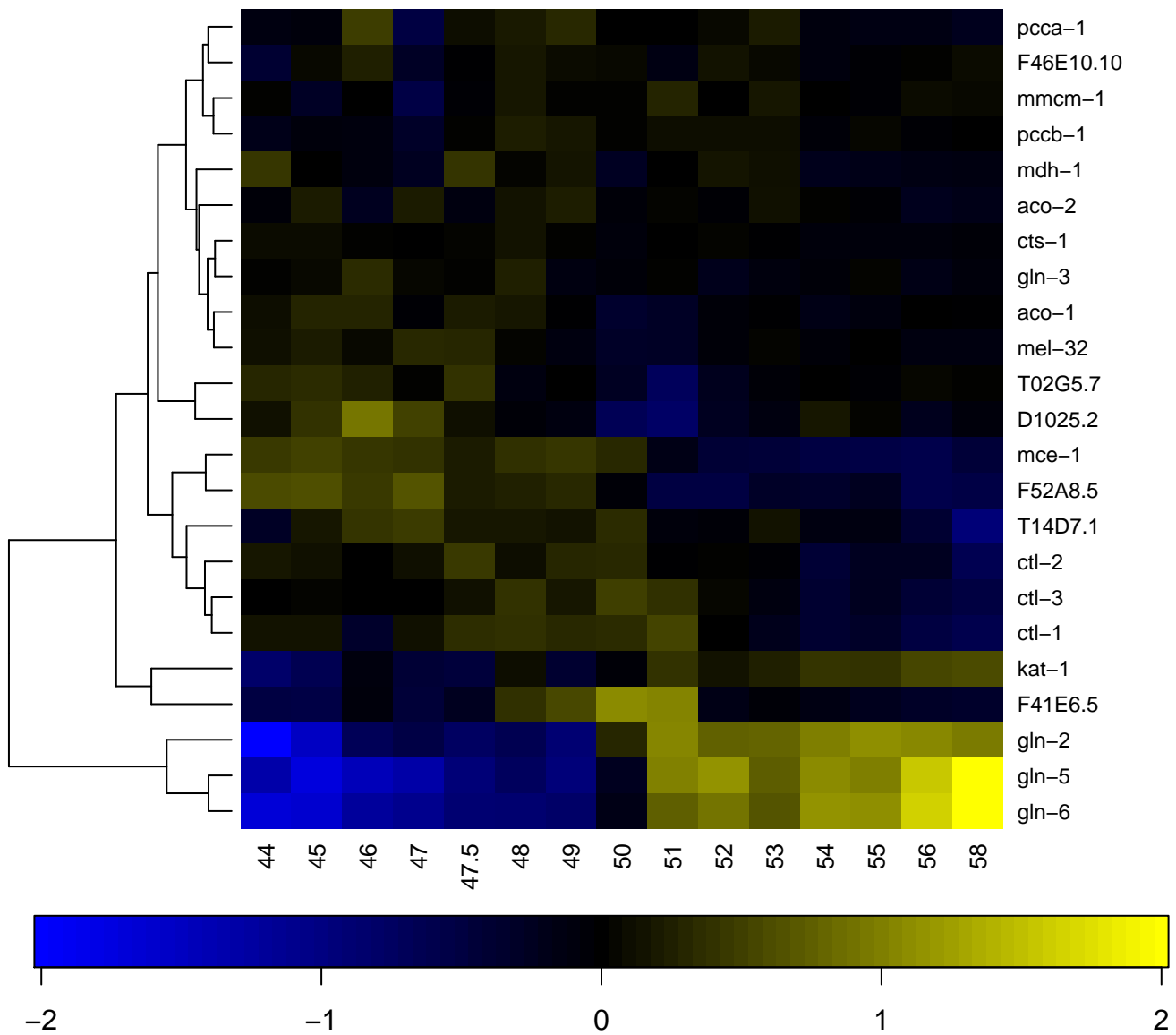
Glycosaminoglycan biosynthesis – heparan sulfate / heparin



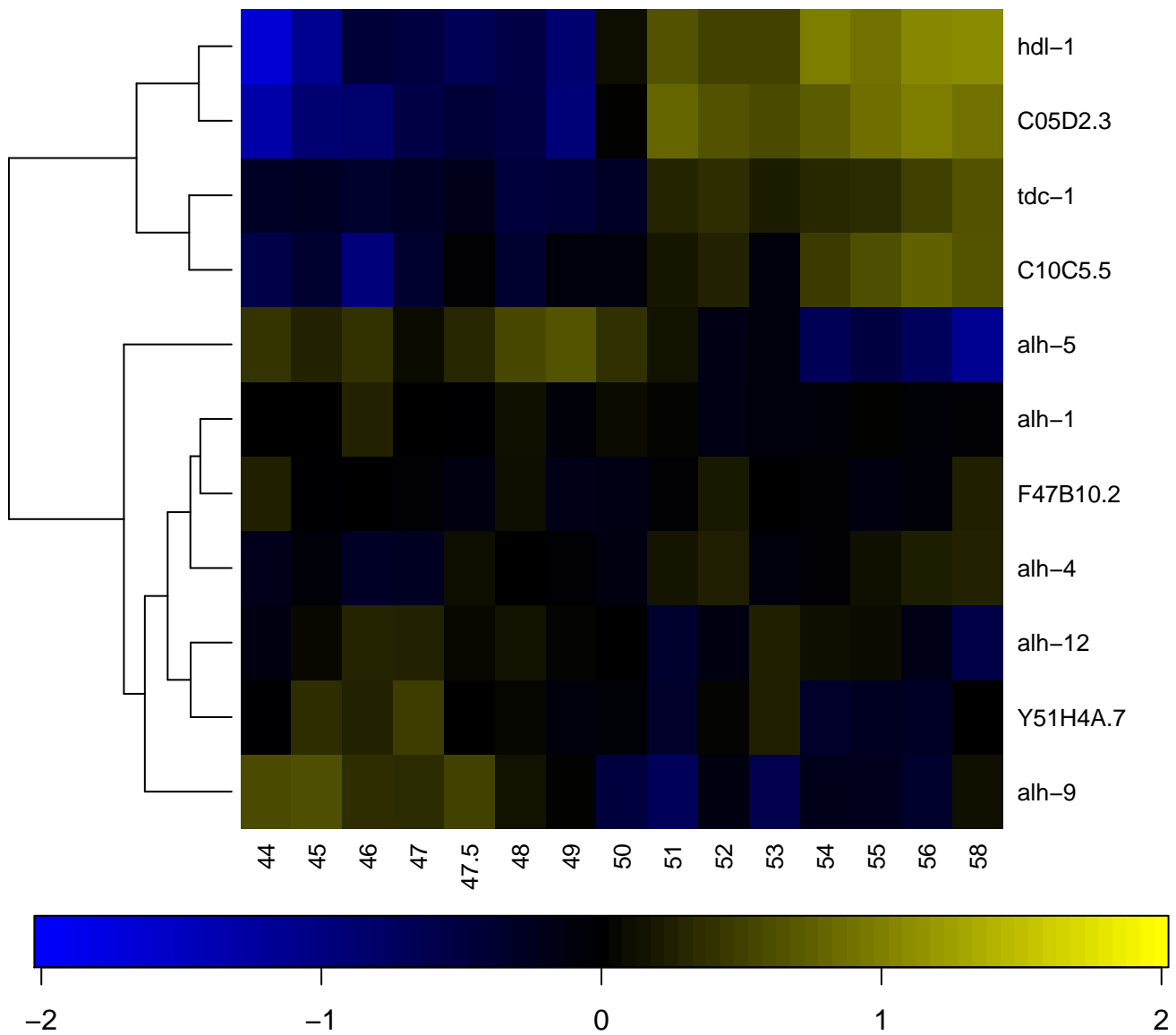
Glycosylphosphatidylinositol (GPI) – anchor biosynthesis



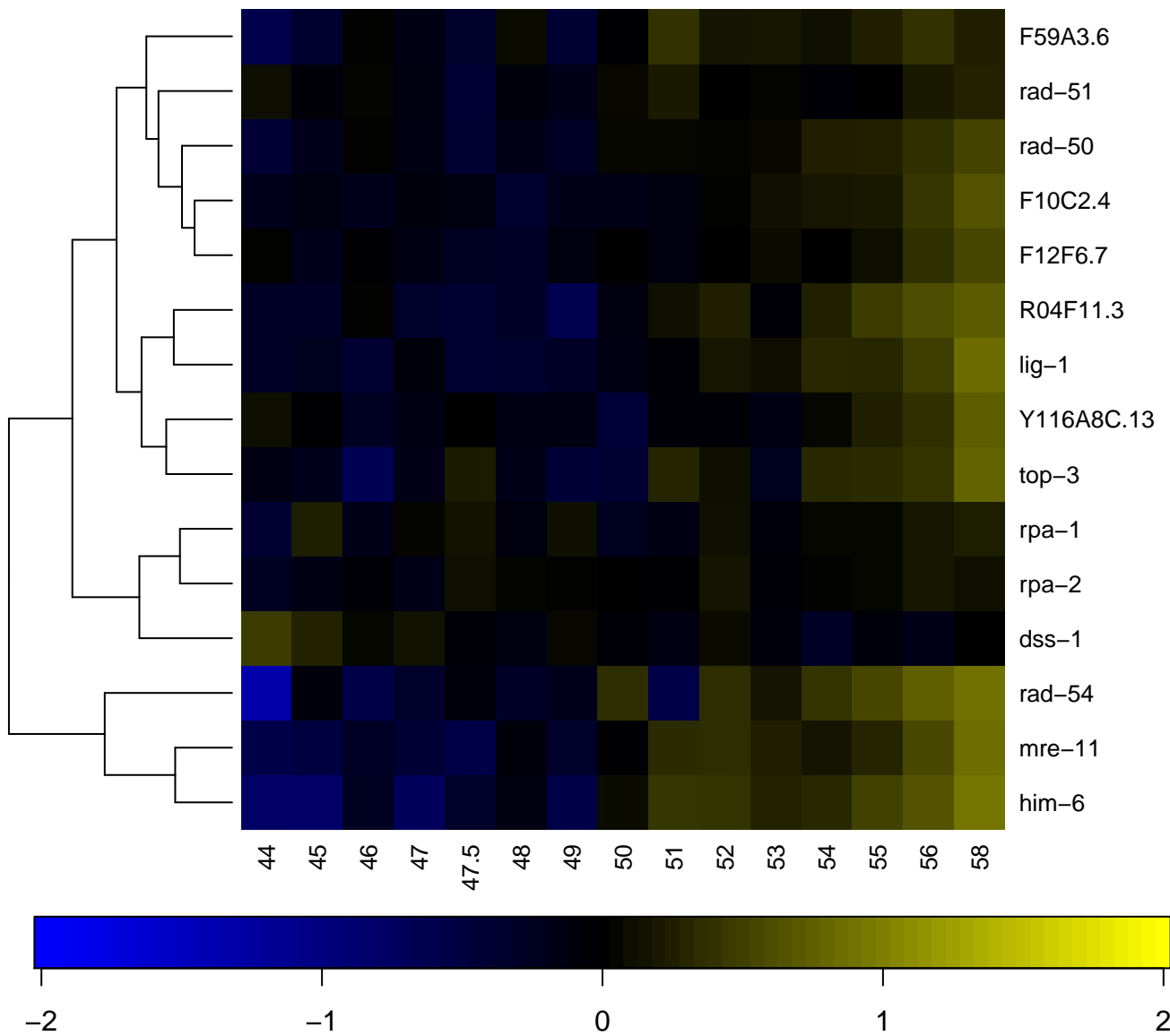
Glyoxylate and dicarboxylate metabolism



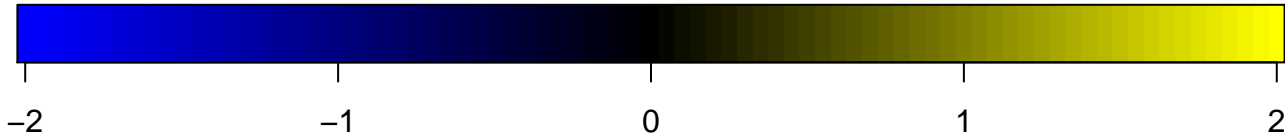
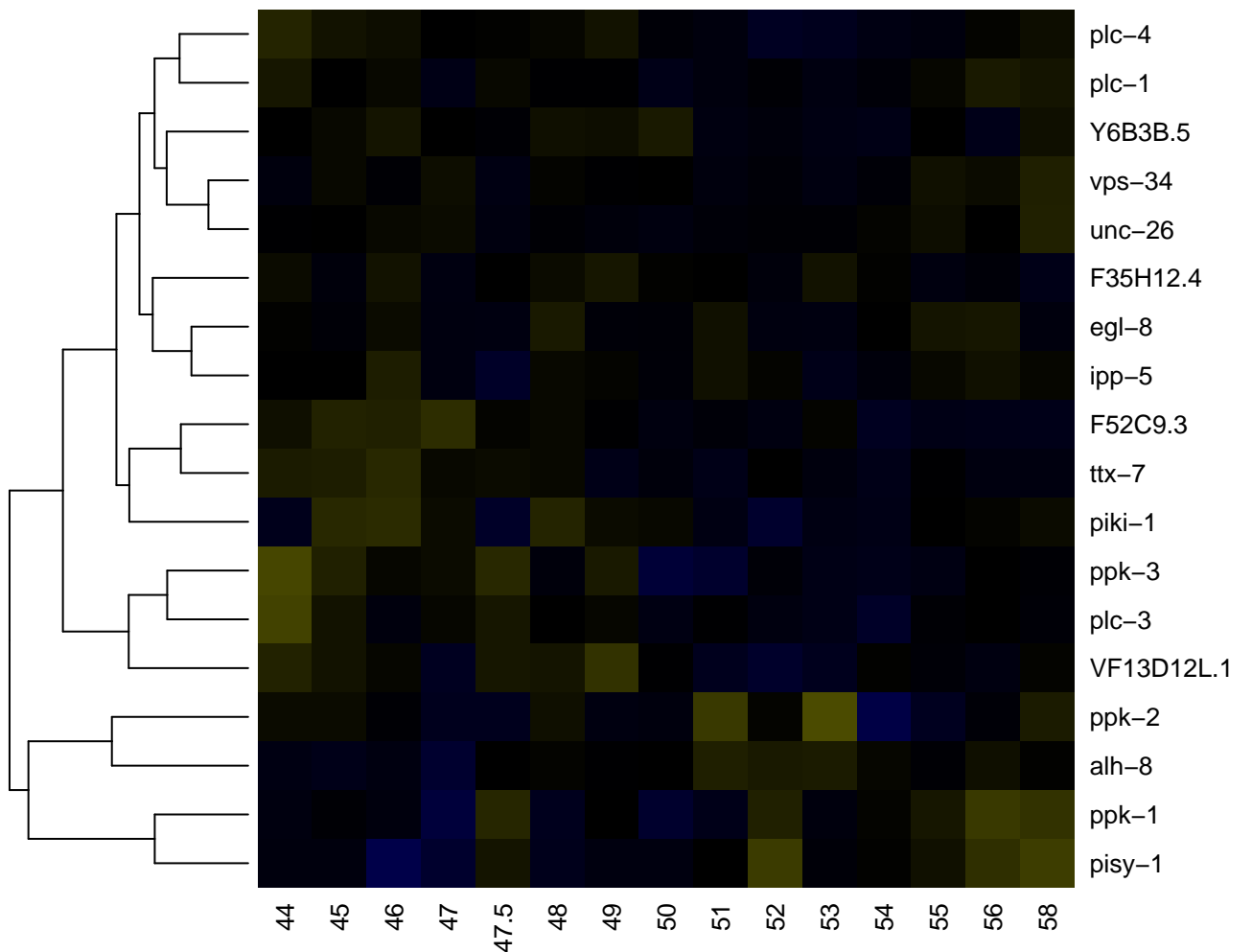
Histidine metabolism



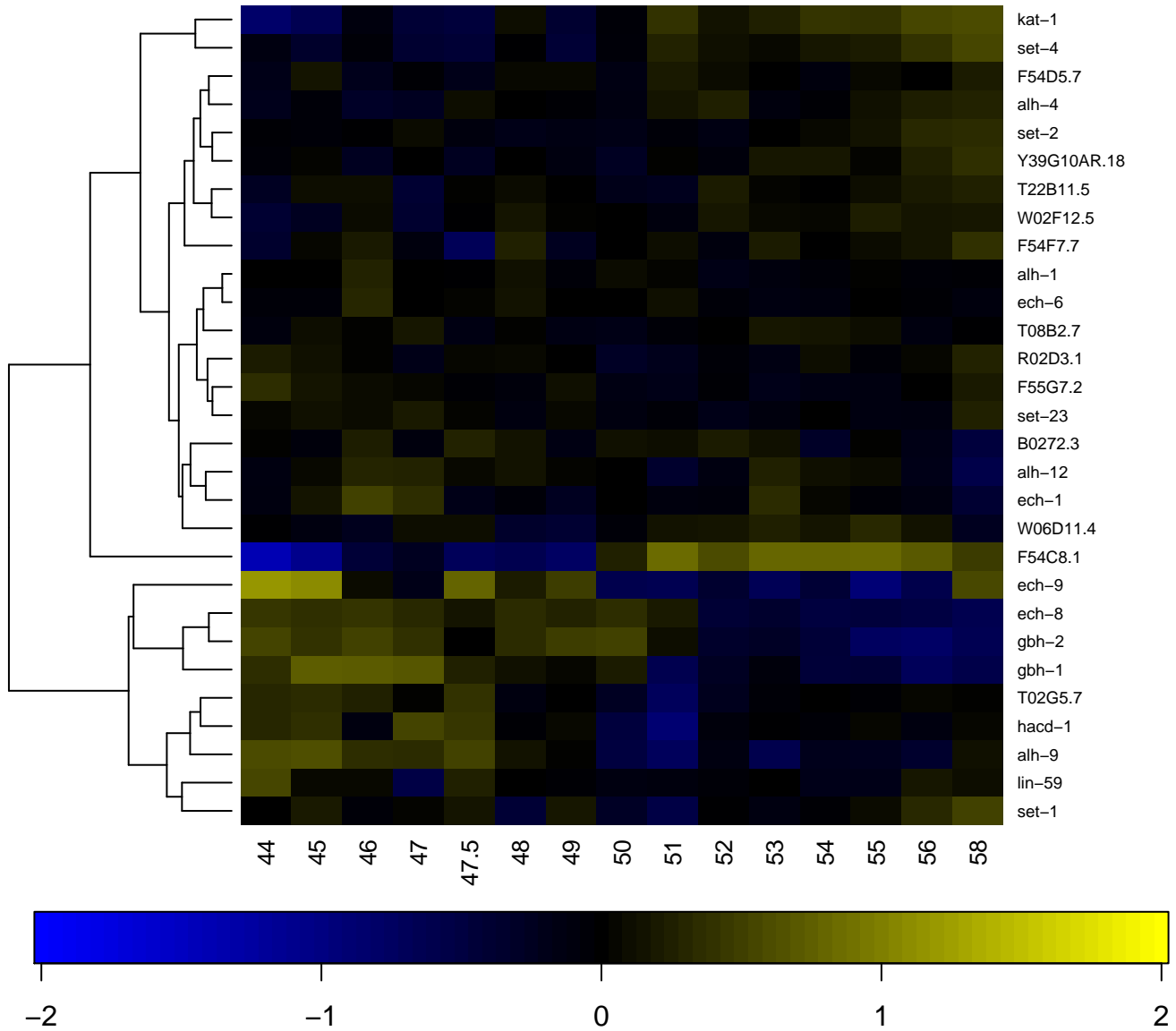
Homologous recombination



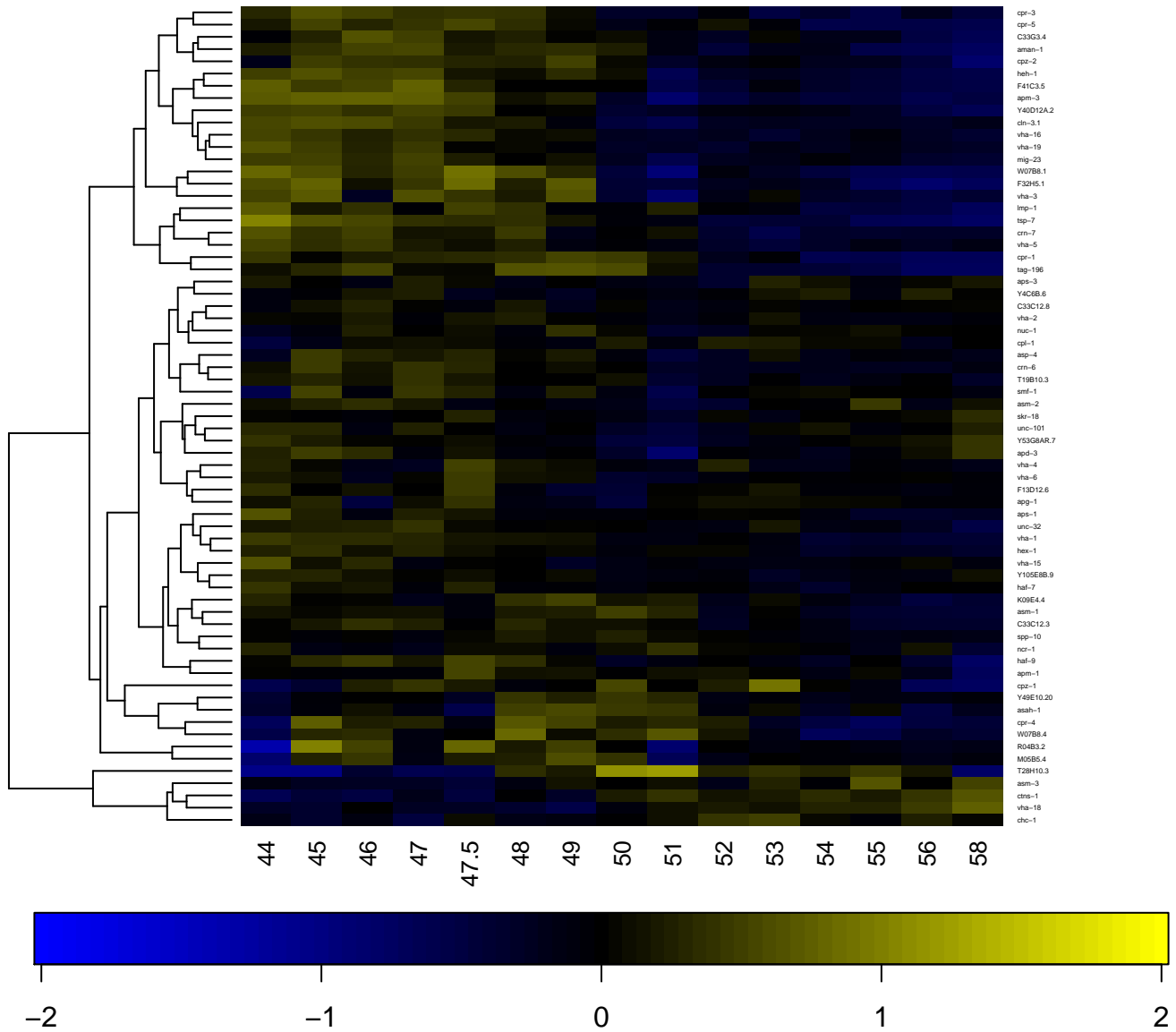
Inositol phosphate metabolism



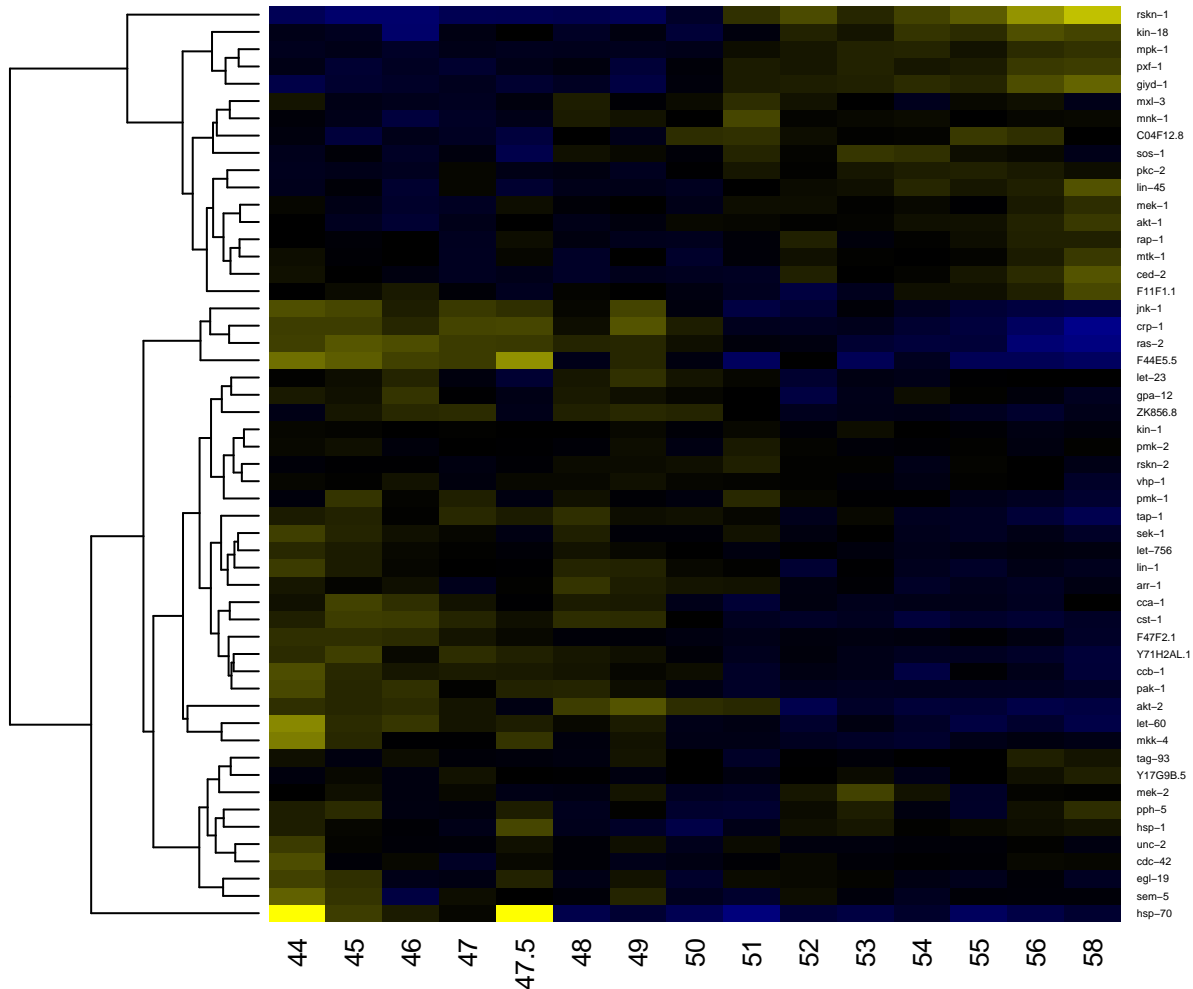
Lysine degradation



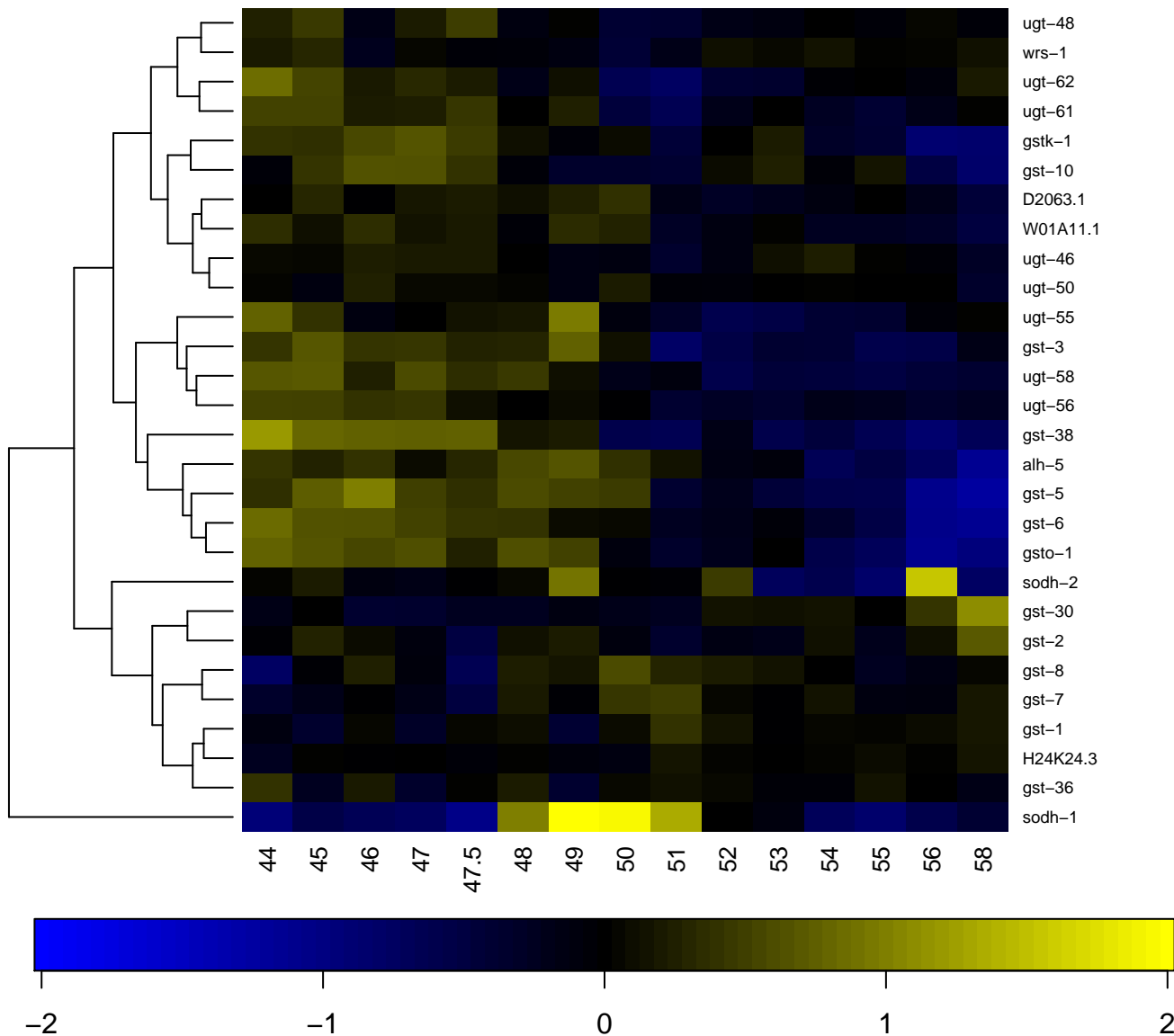
Lysosome



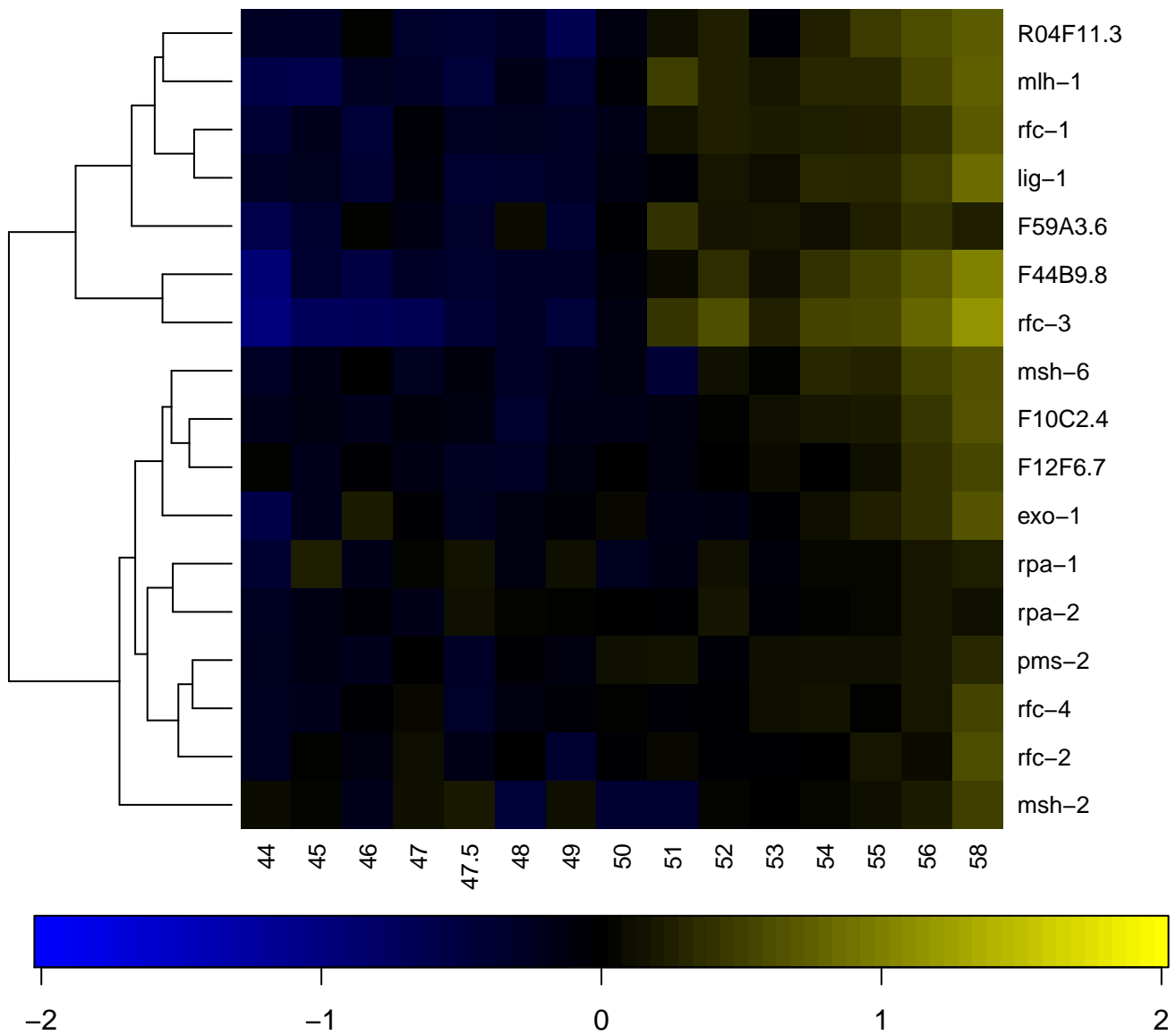
MAPK signaling pathway



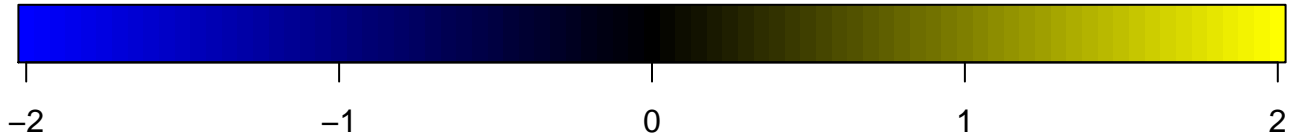
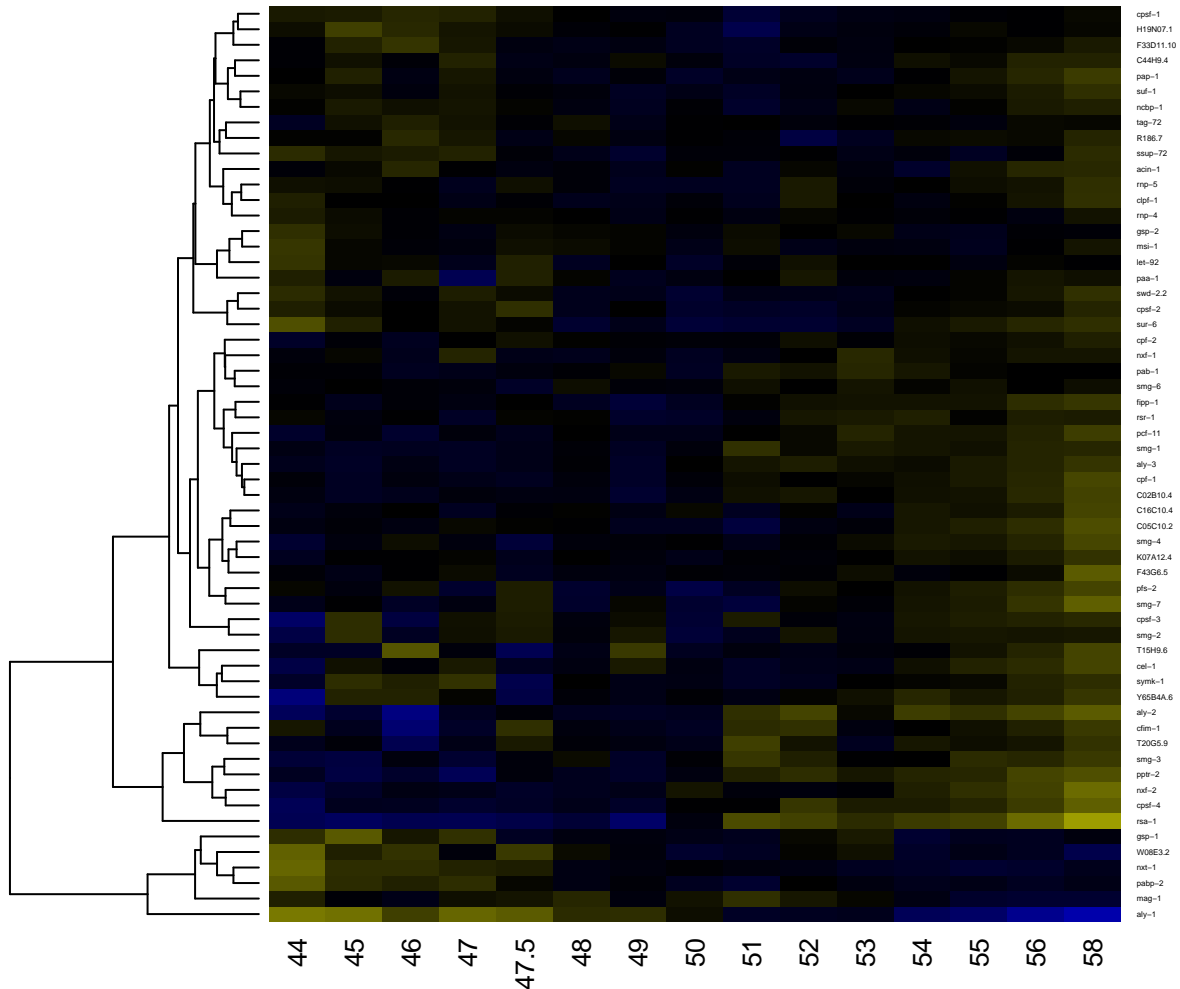
Metabolism of xenobiotics by cytochrome P450



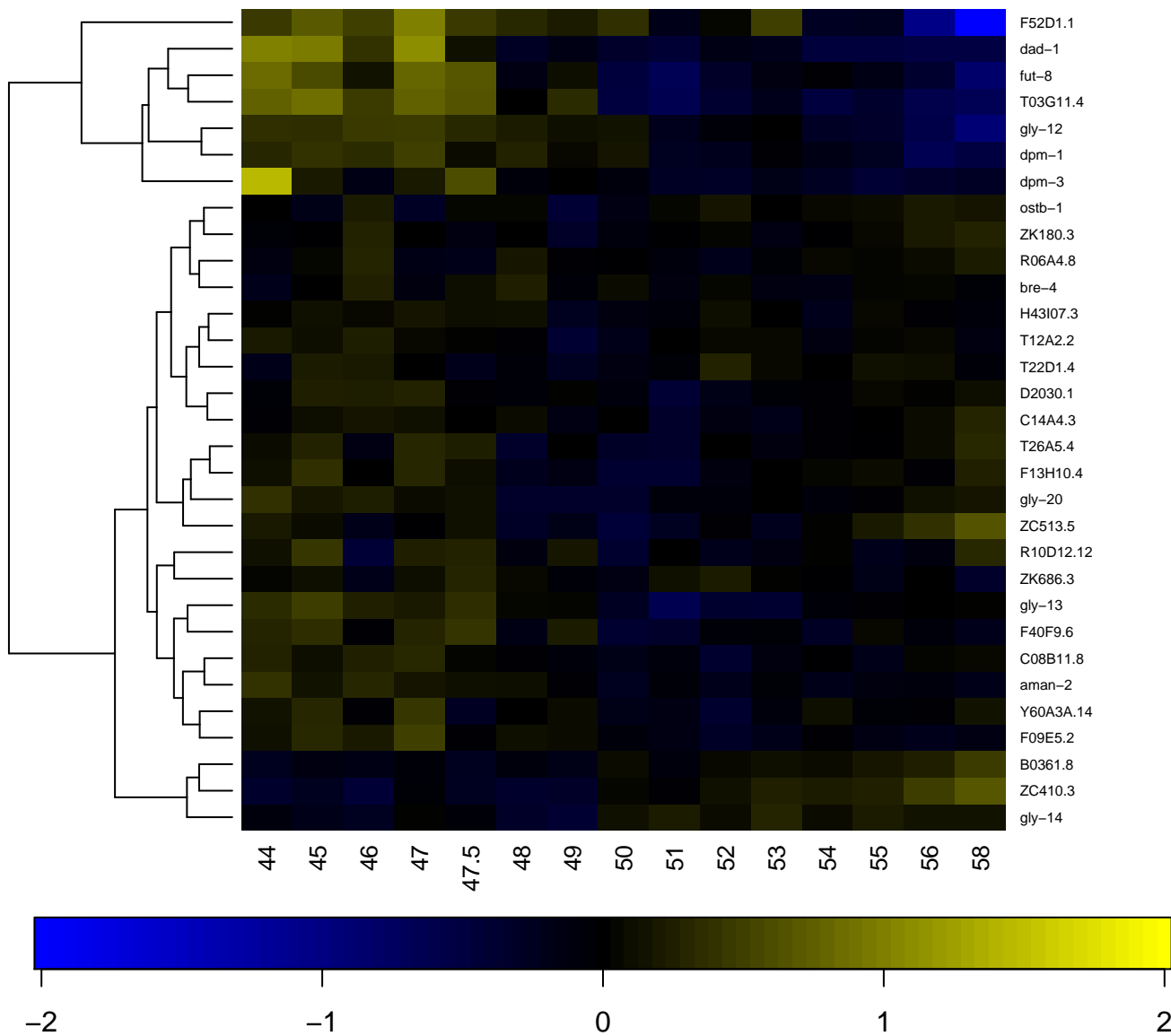
Mismatch repair



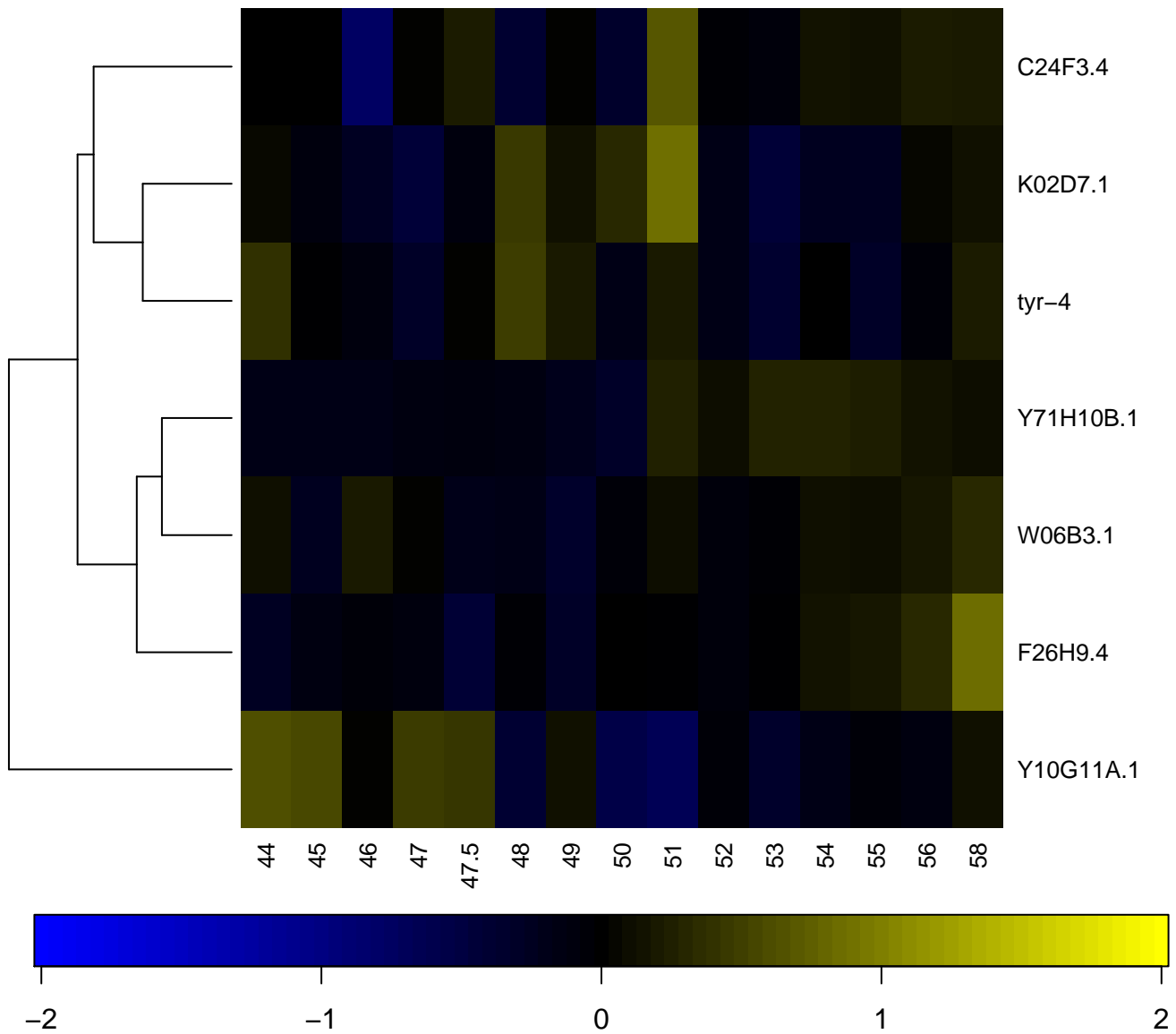
mRNA surveillance pathway



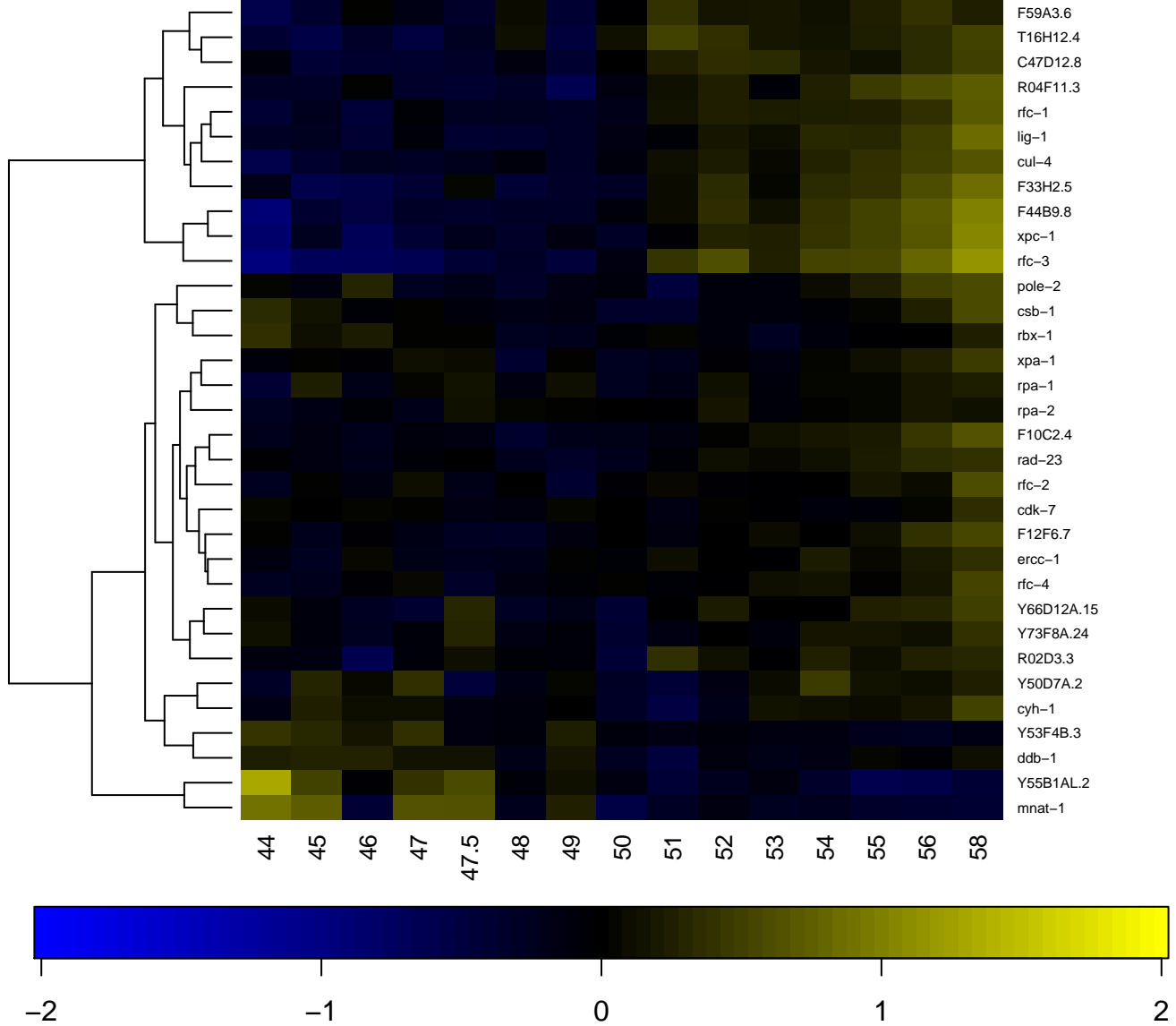
N-glycan biosynthesis



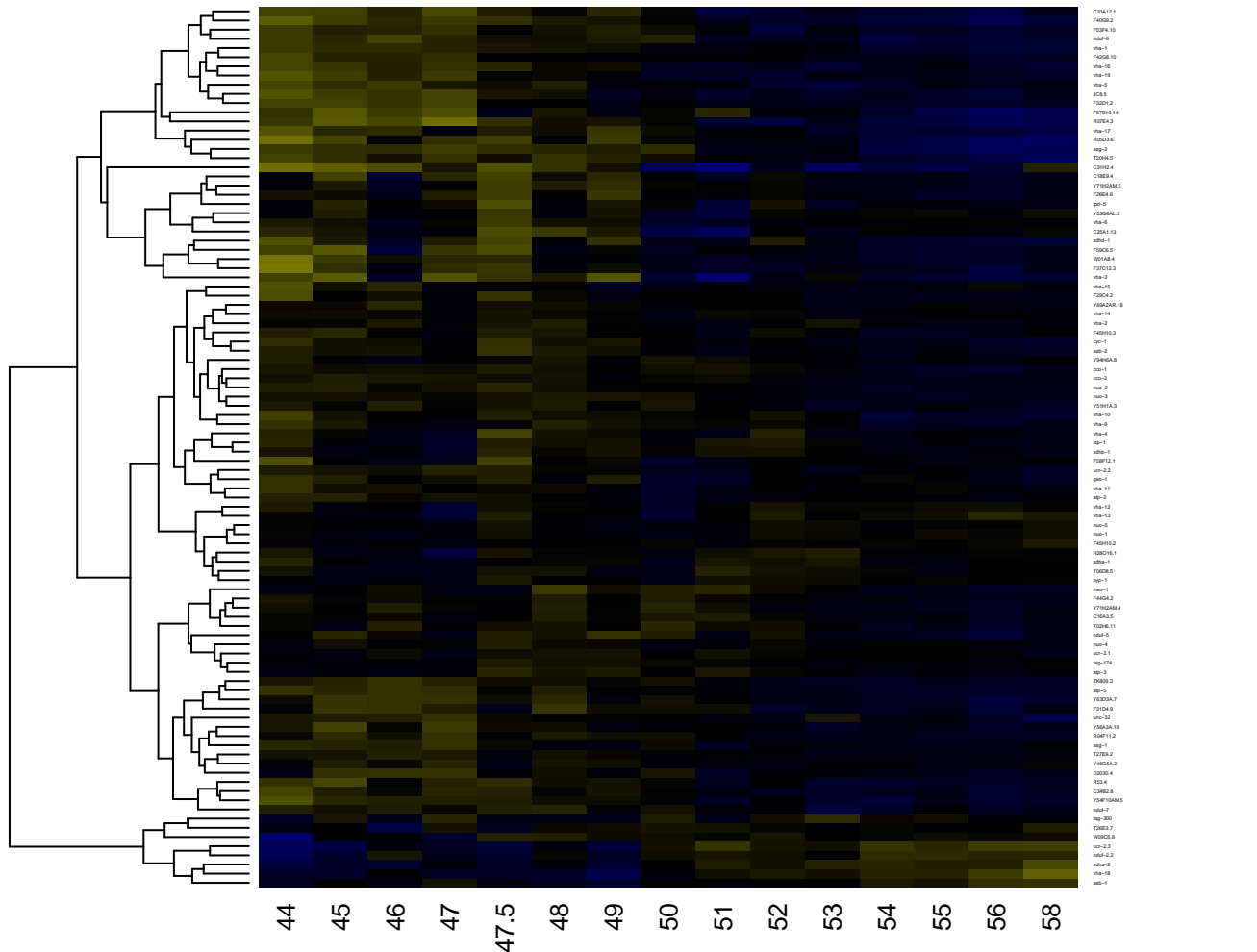
Nicotinate and nicotinamide metabolism



Nucleotide excision repair



Oxidative phosphorylation



-2

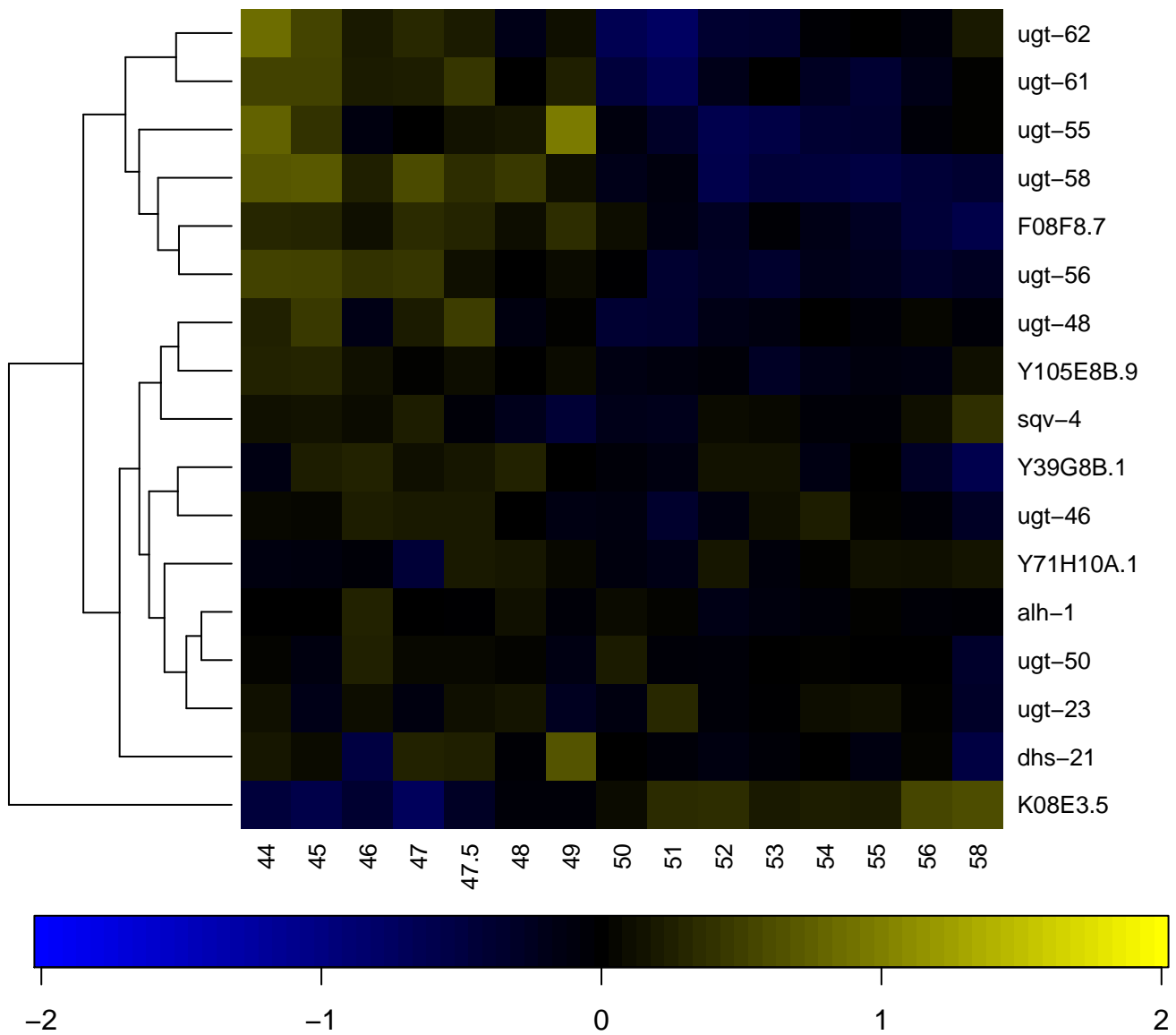
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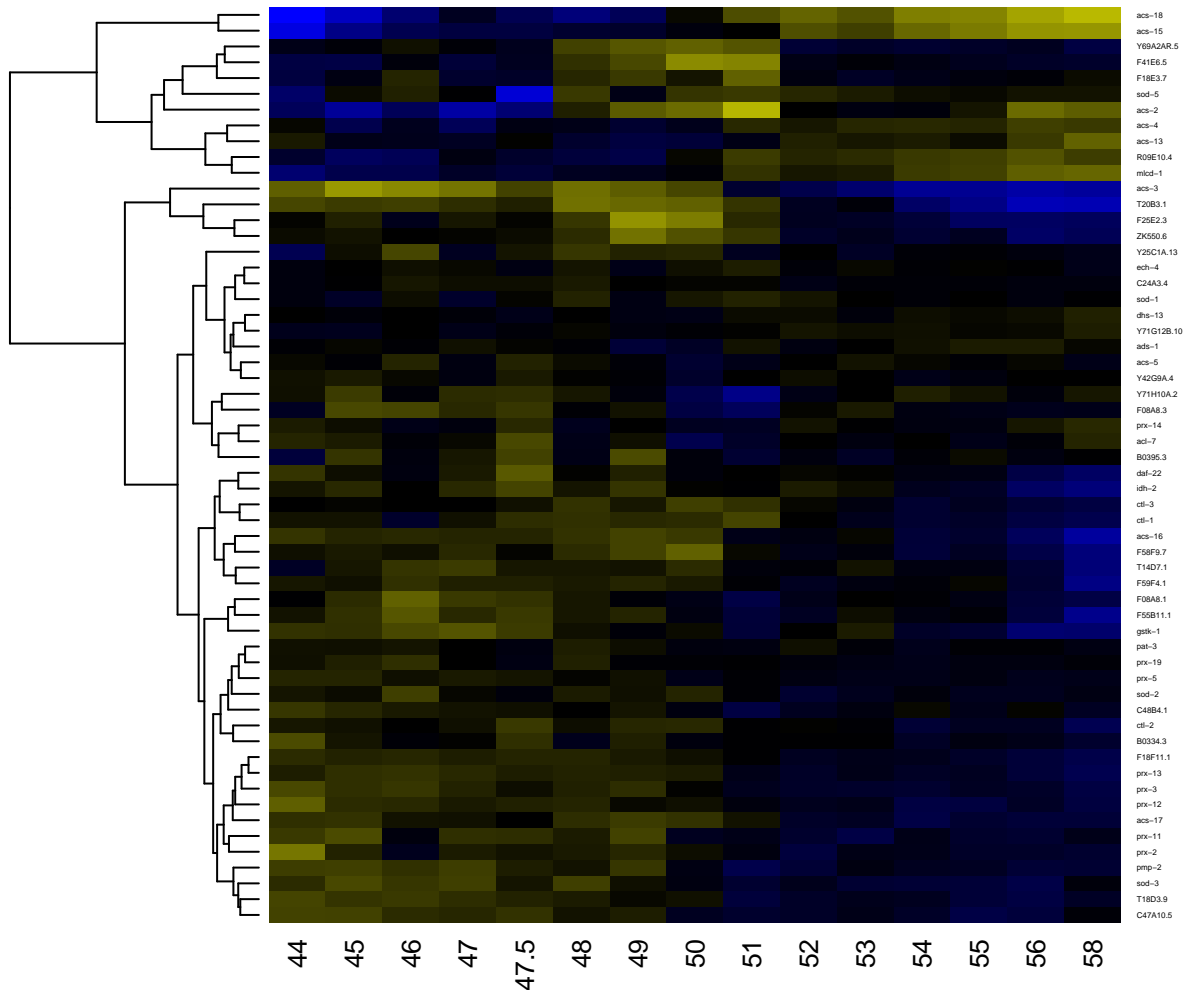
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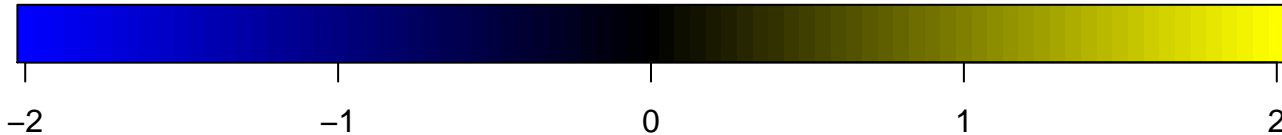
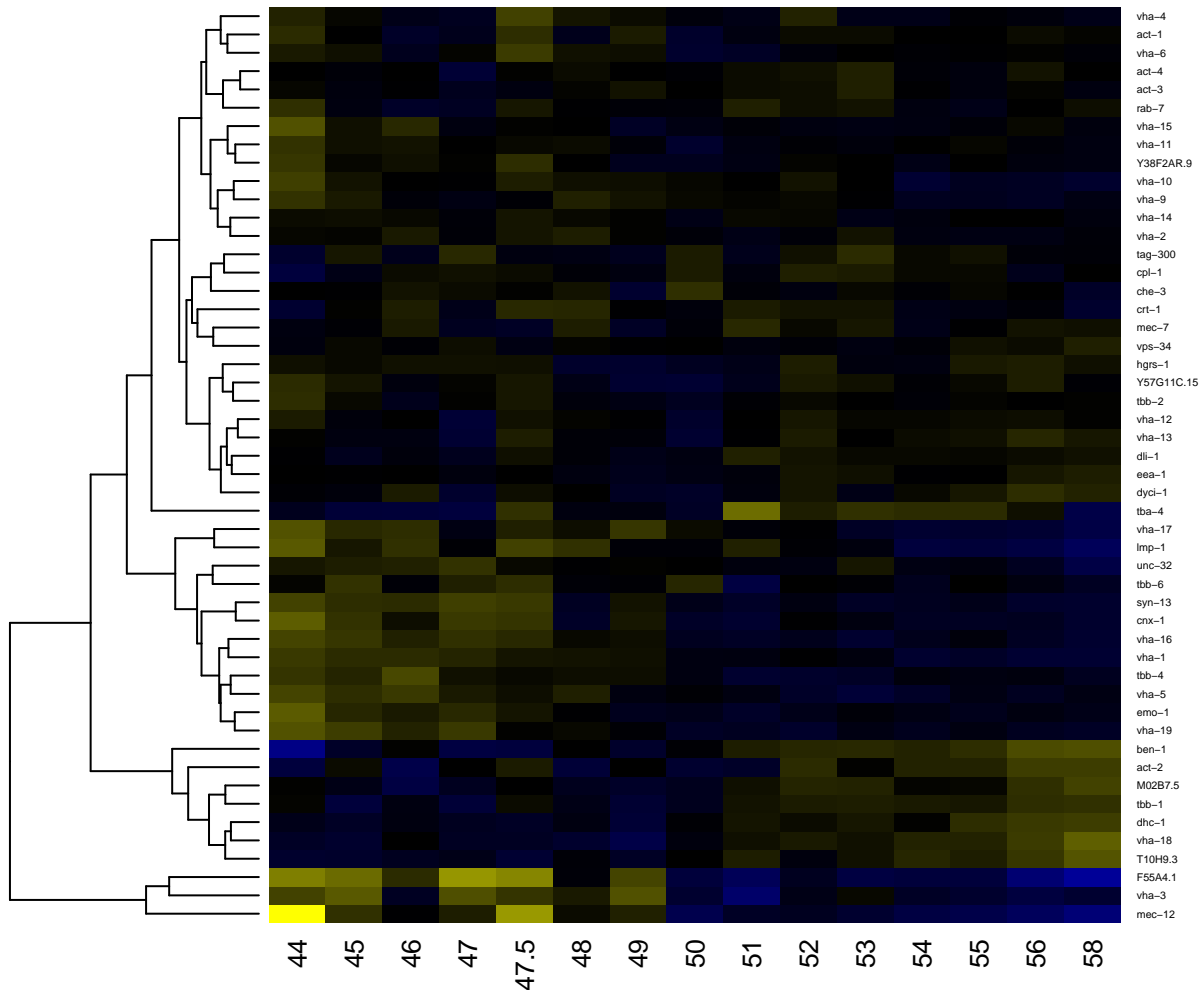
Pentose and glucuronate interconversions



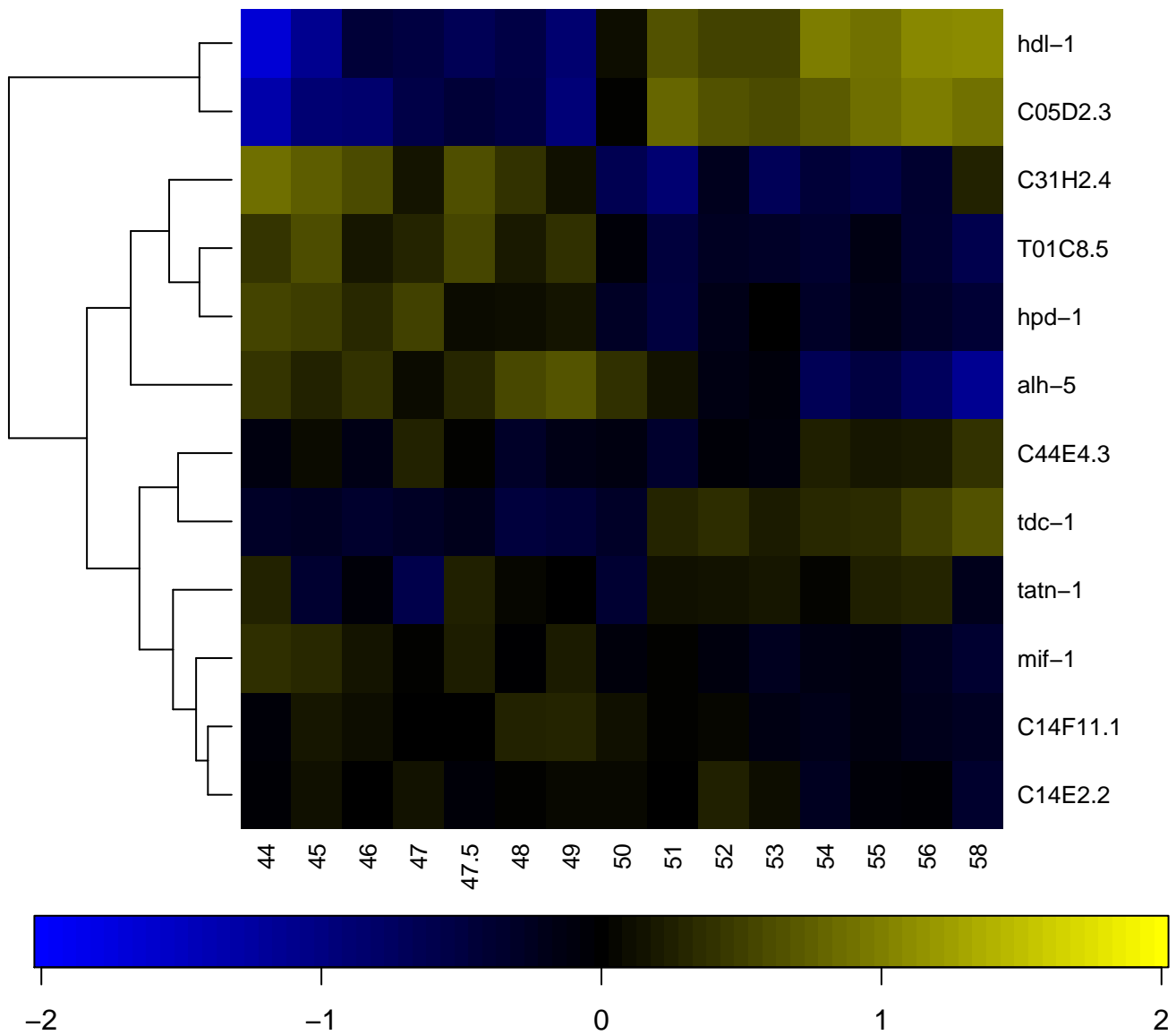
Peroxisome



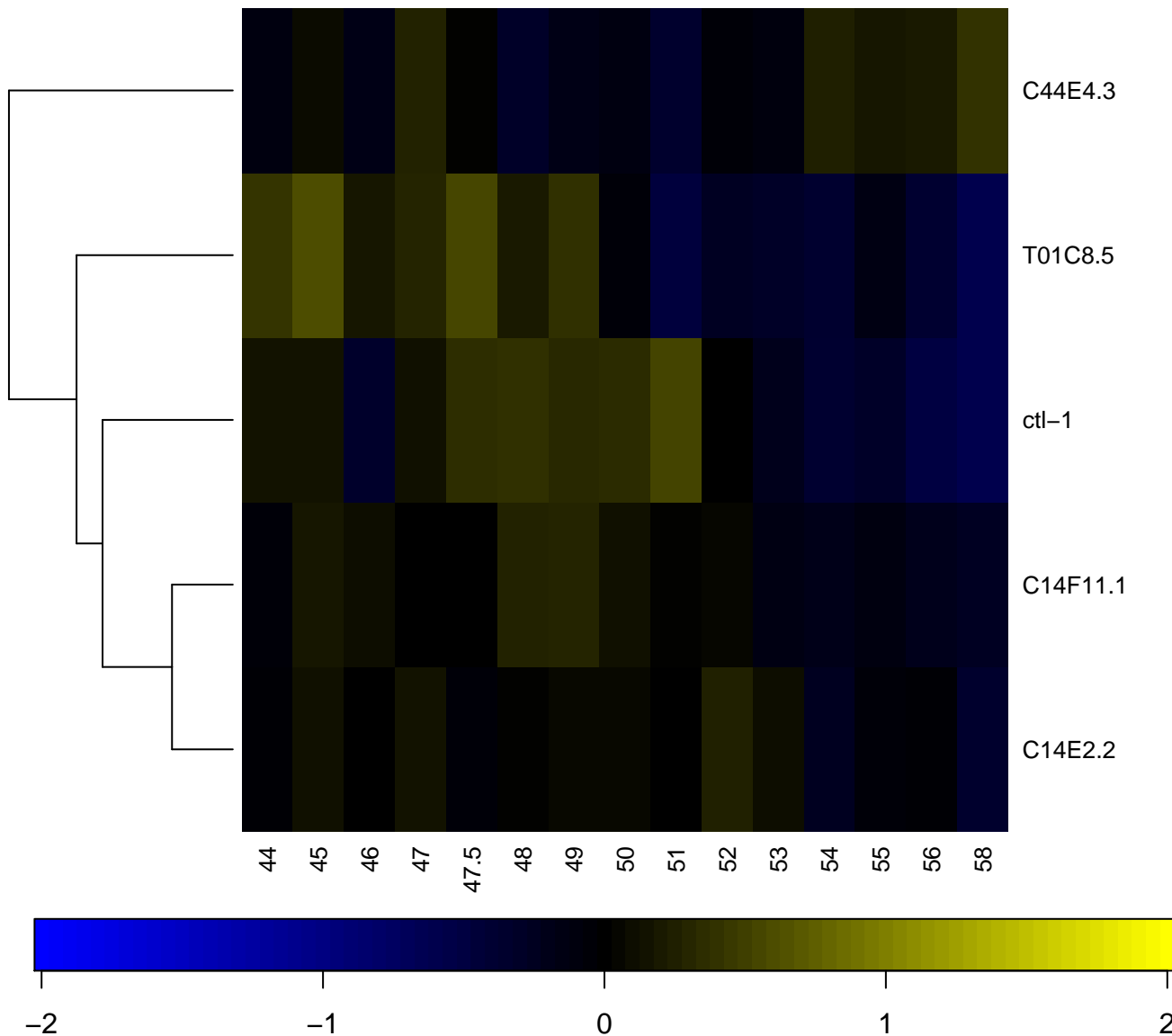
Phagosome



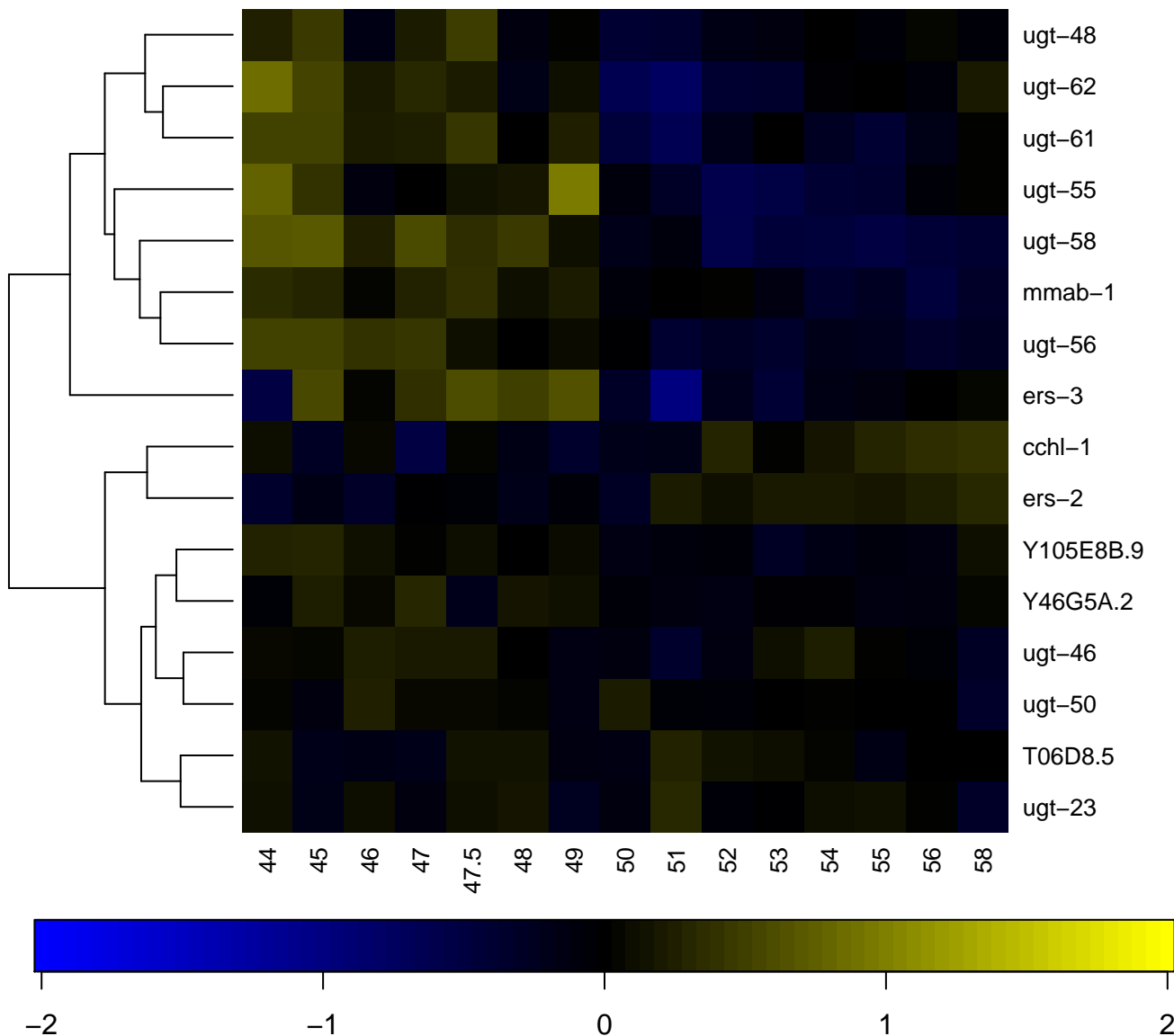
Phenylalanine metabolism



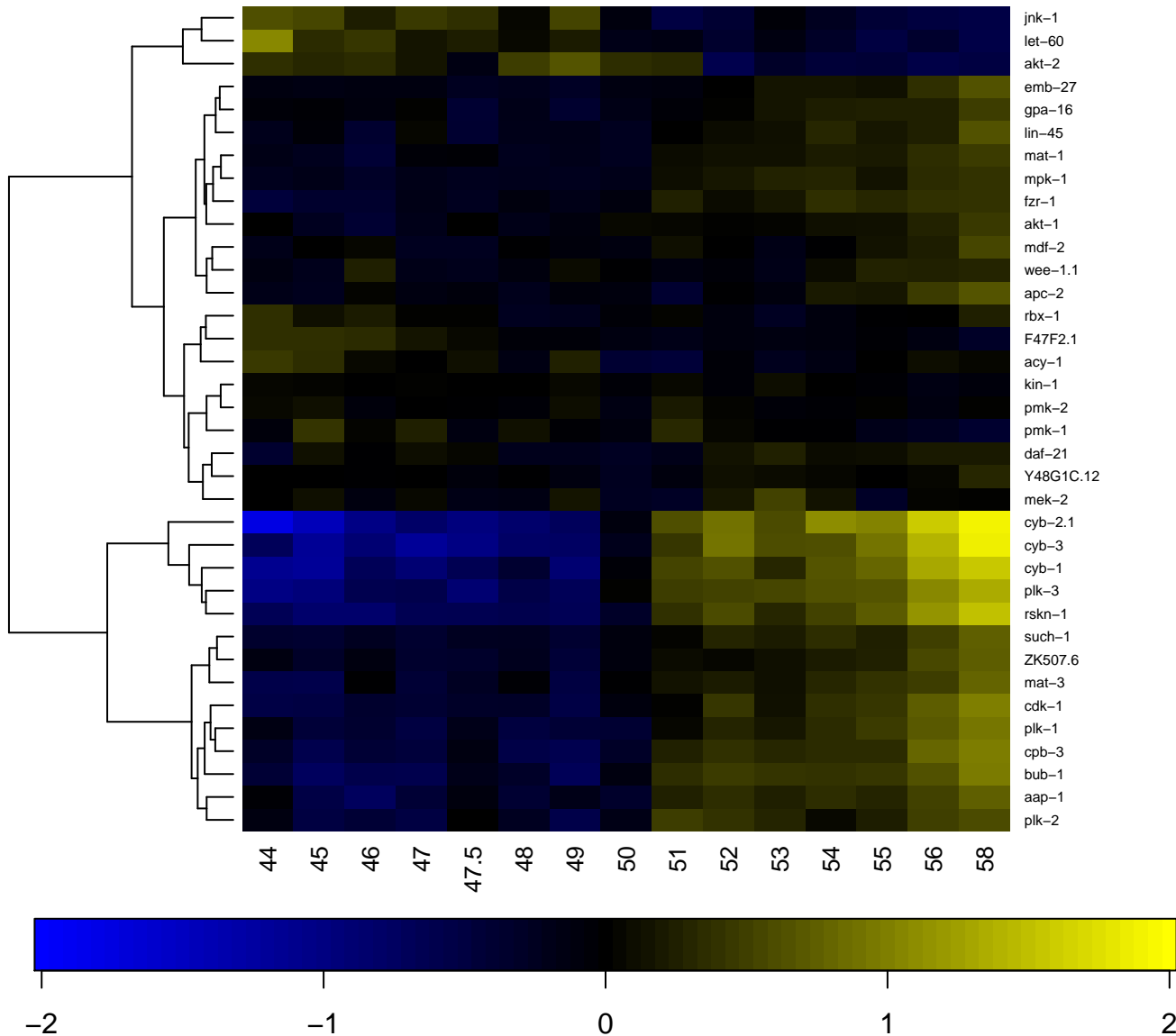
Phenylalanine, tyrosine and tryptophan biosynthesis



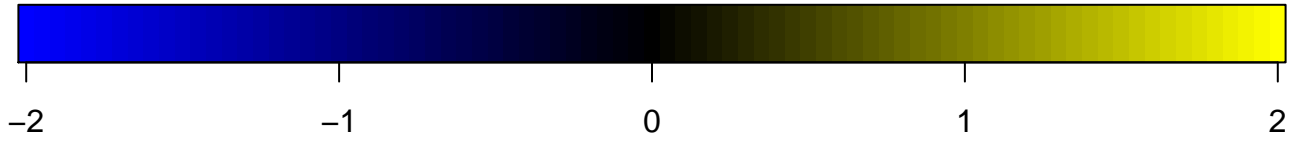
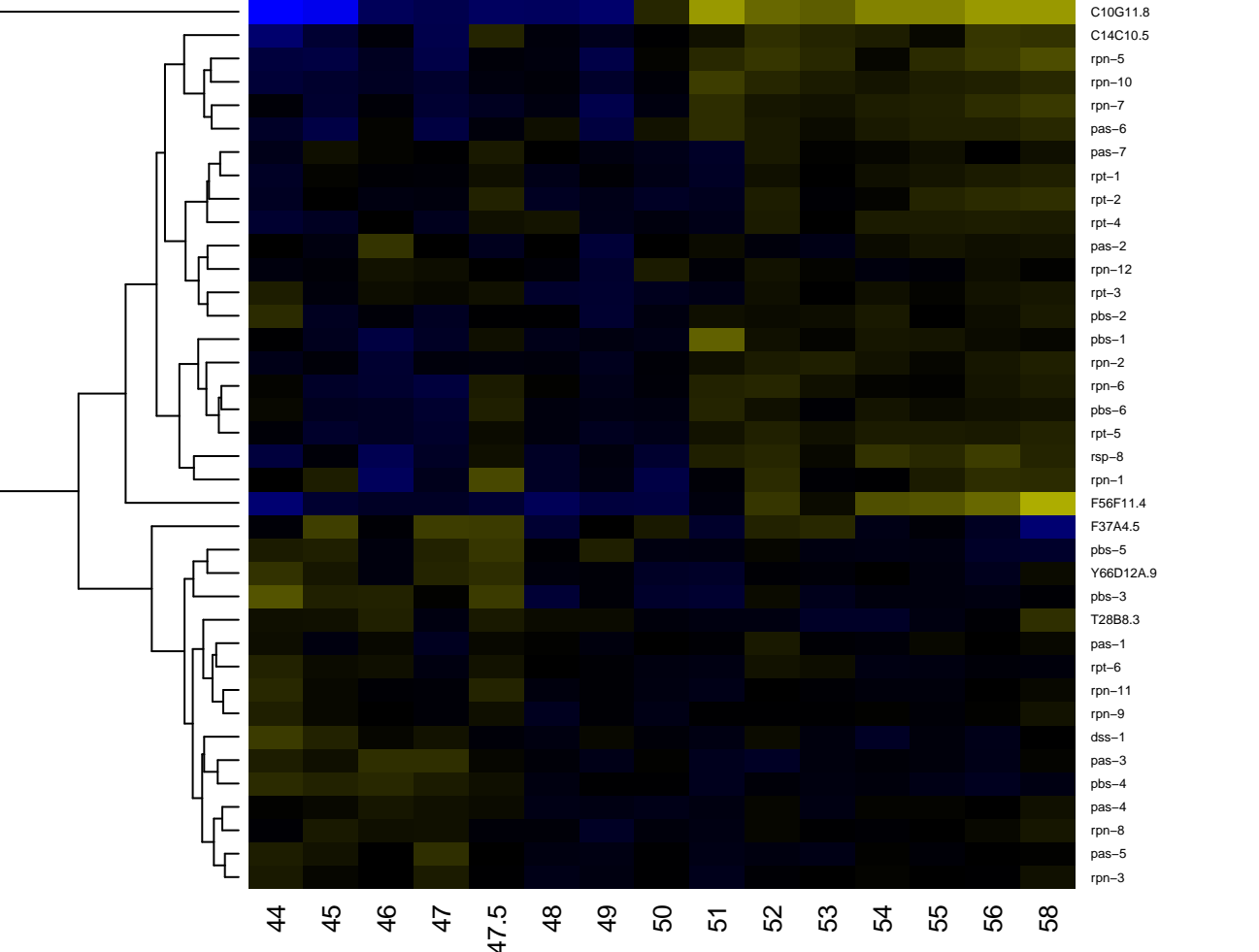
Porphyrin and chlorophyll metabolism



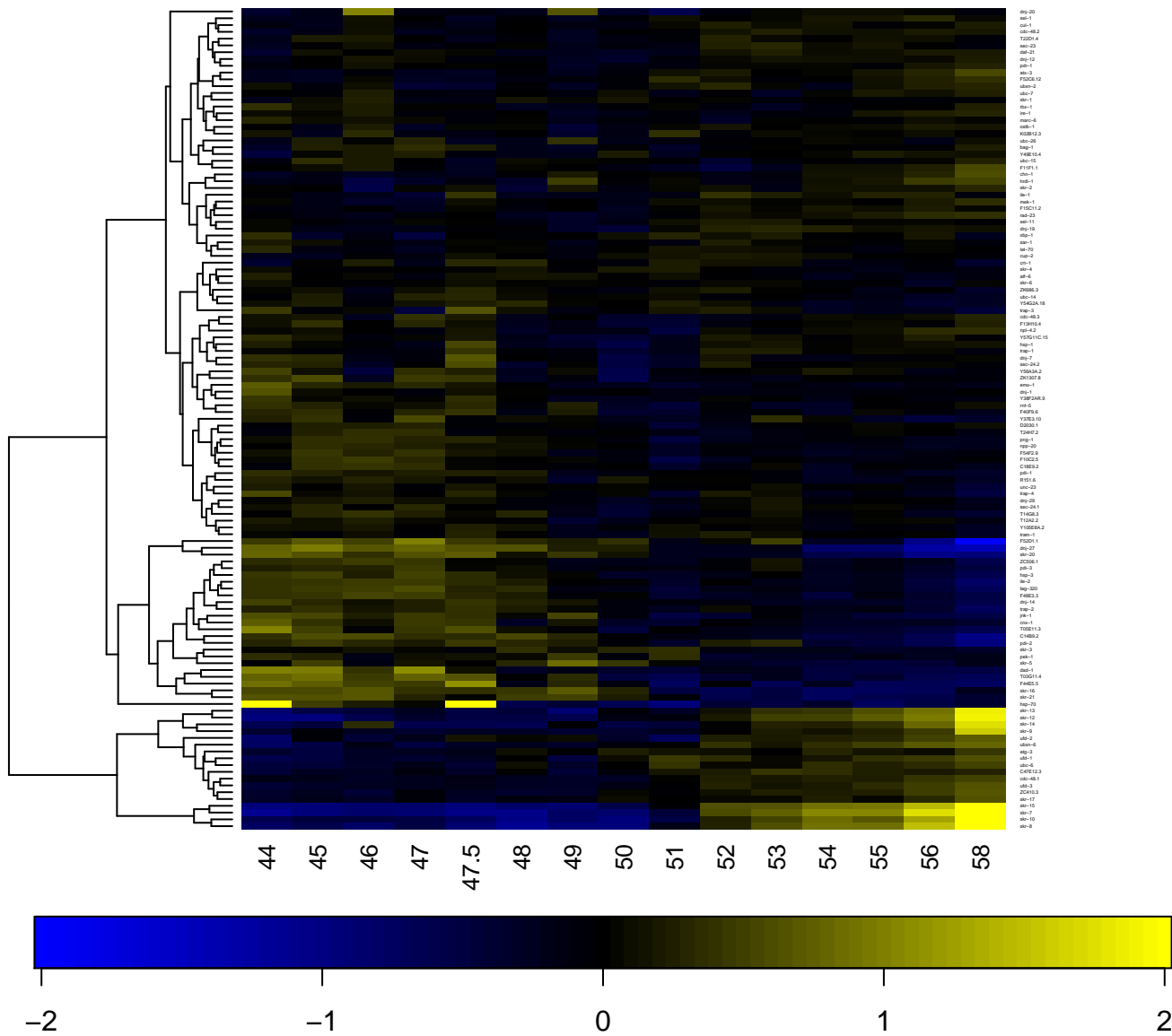
Progesterone-mediated oocyte maturation



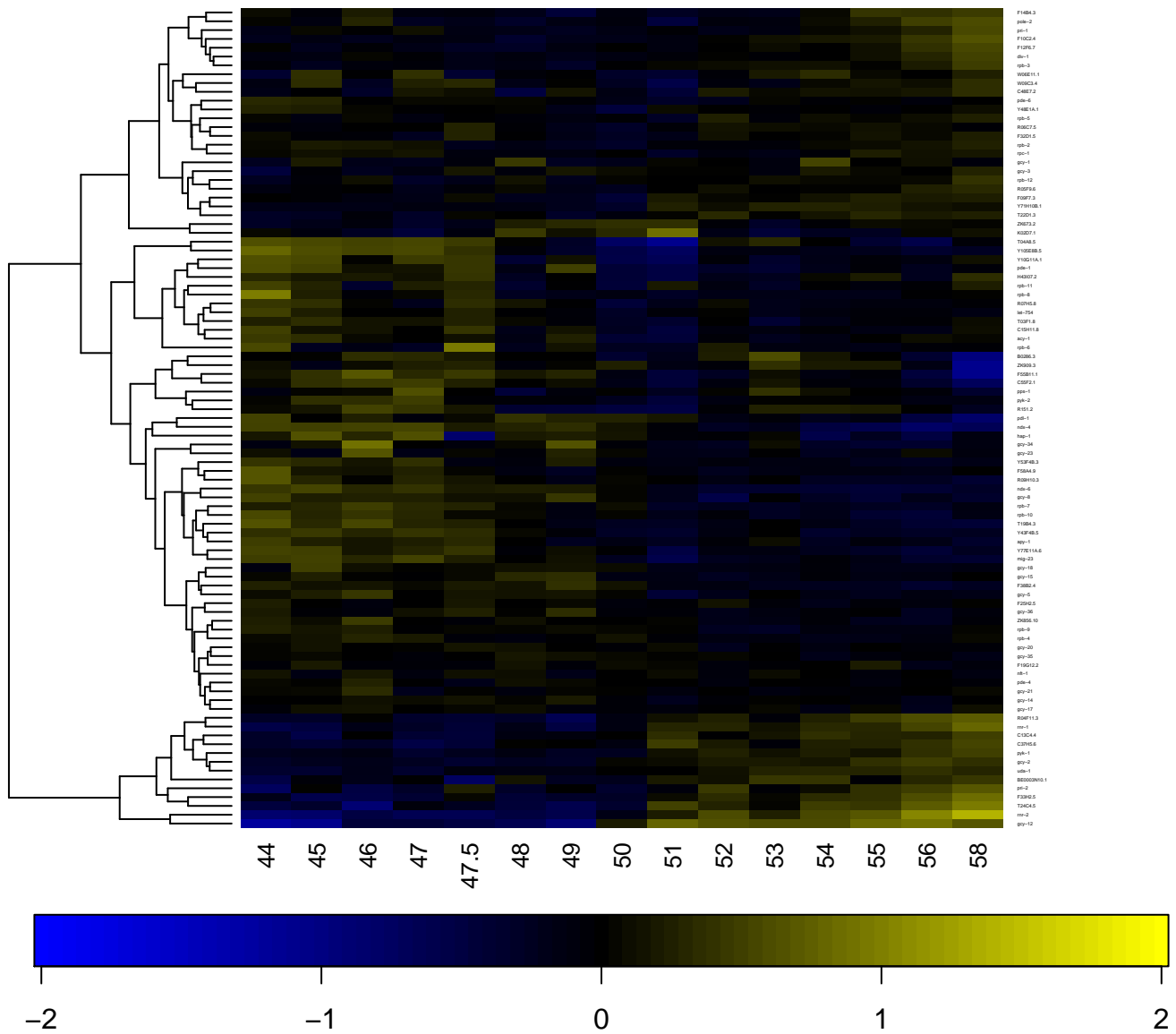
Proteasome



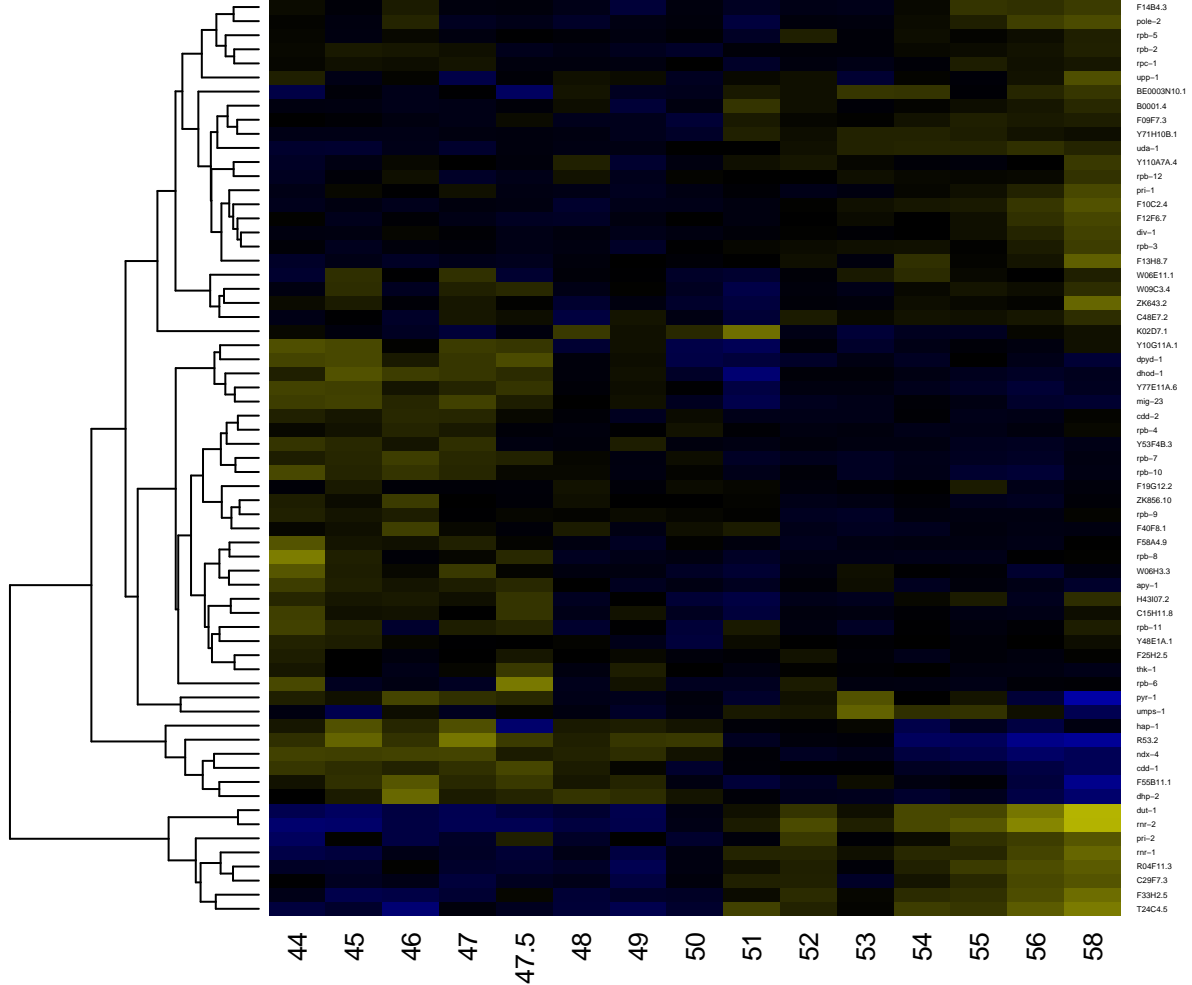
Protein processing in endoplasmic reticulum



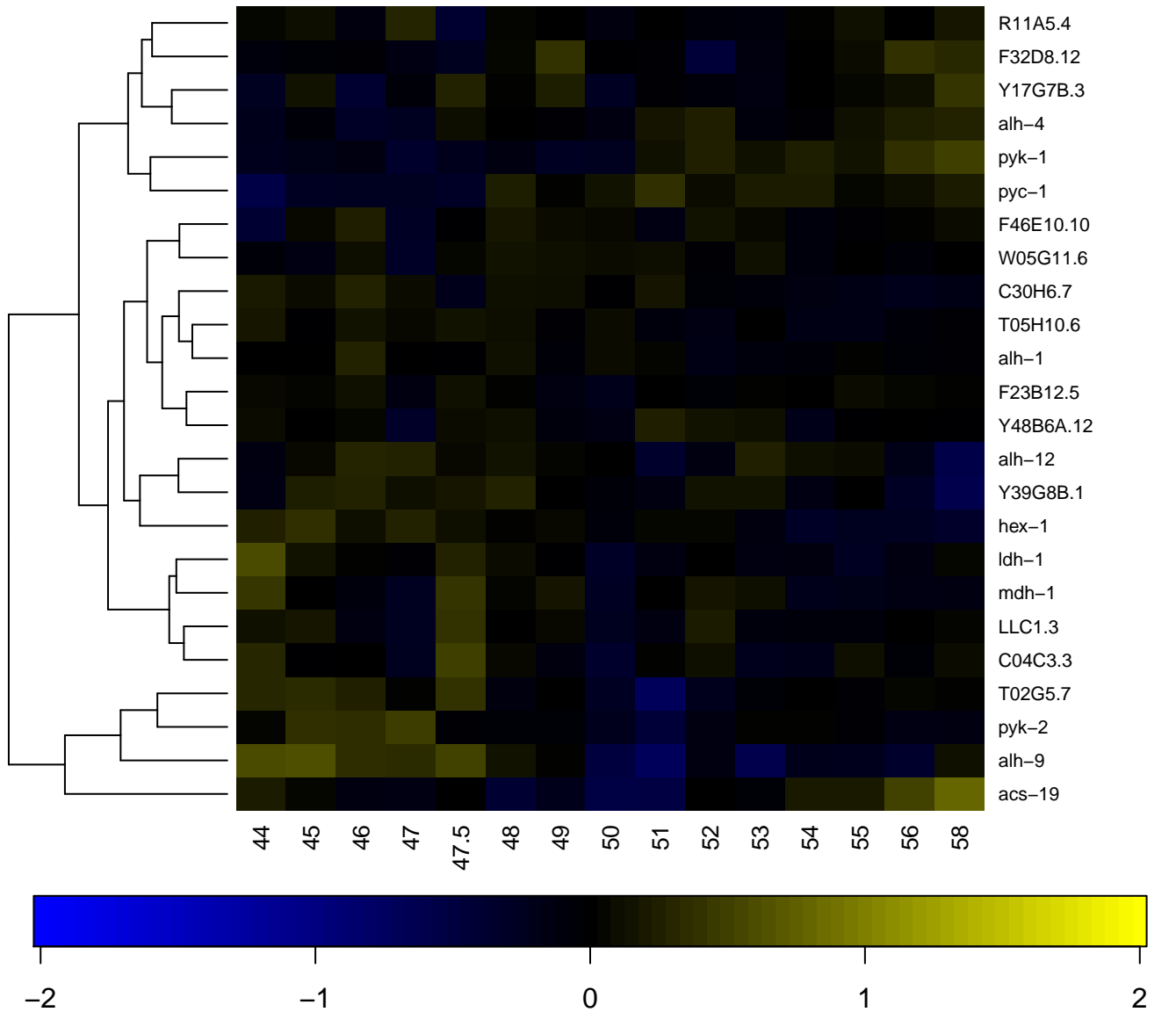
Purine metabolism



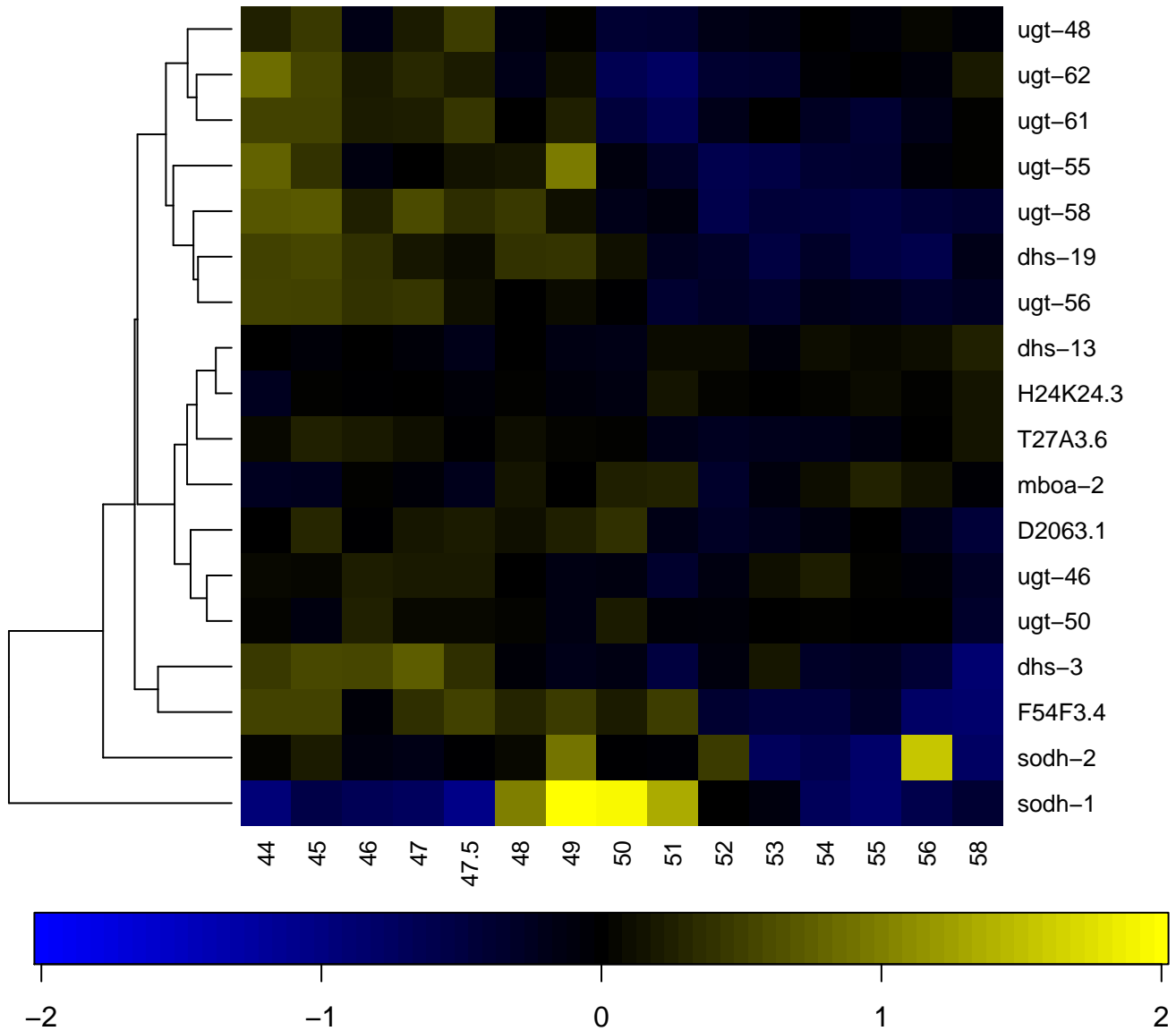
Pyrimidine metabolism



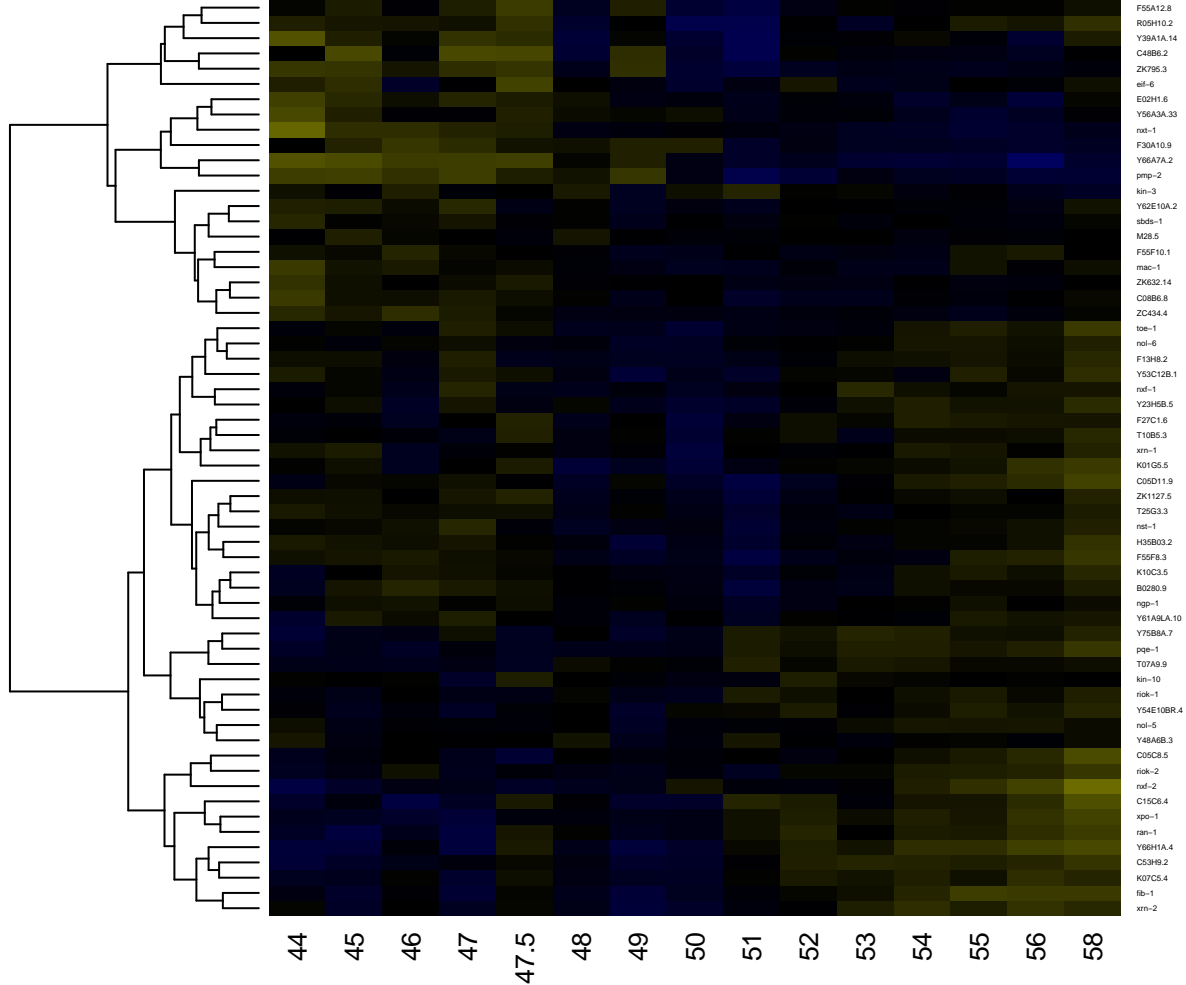
Pyruvate metabolism



Retinol metabolism in animal



Ribosome biogenesis in eukaryotes



-2

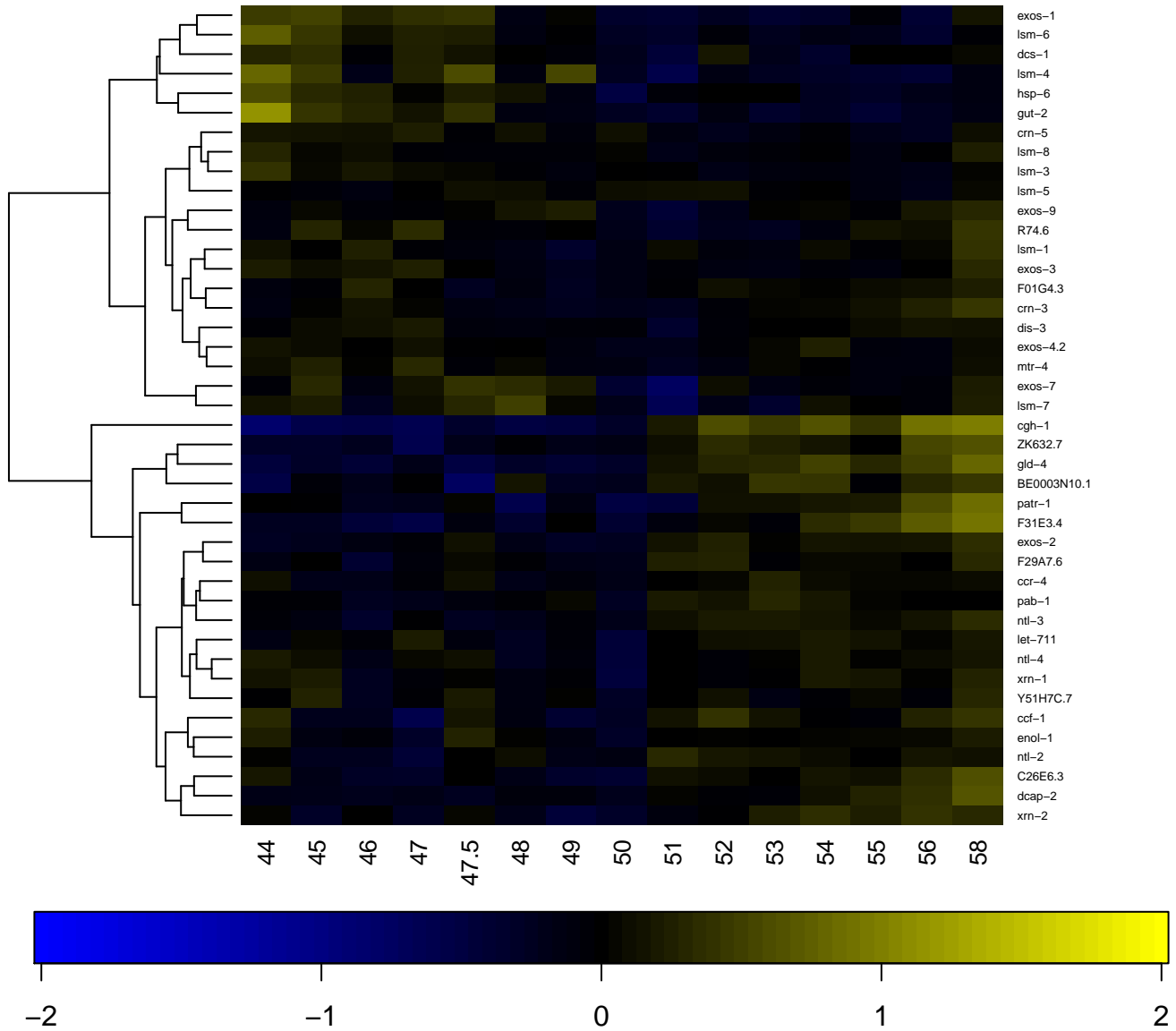
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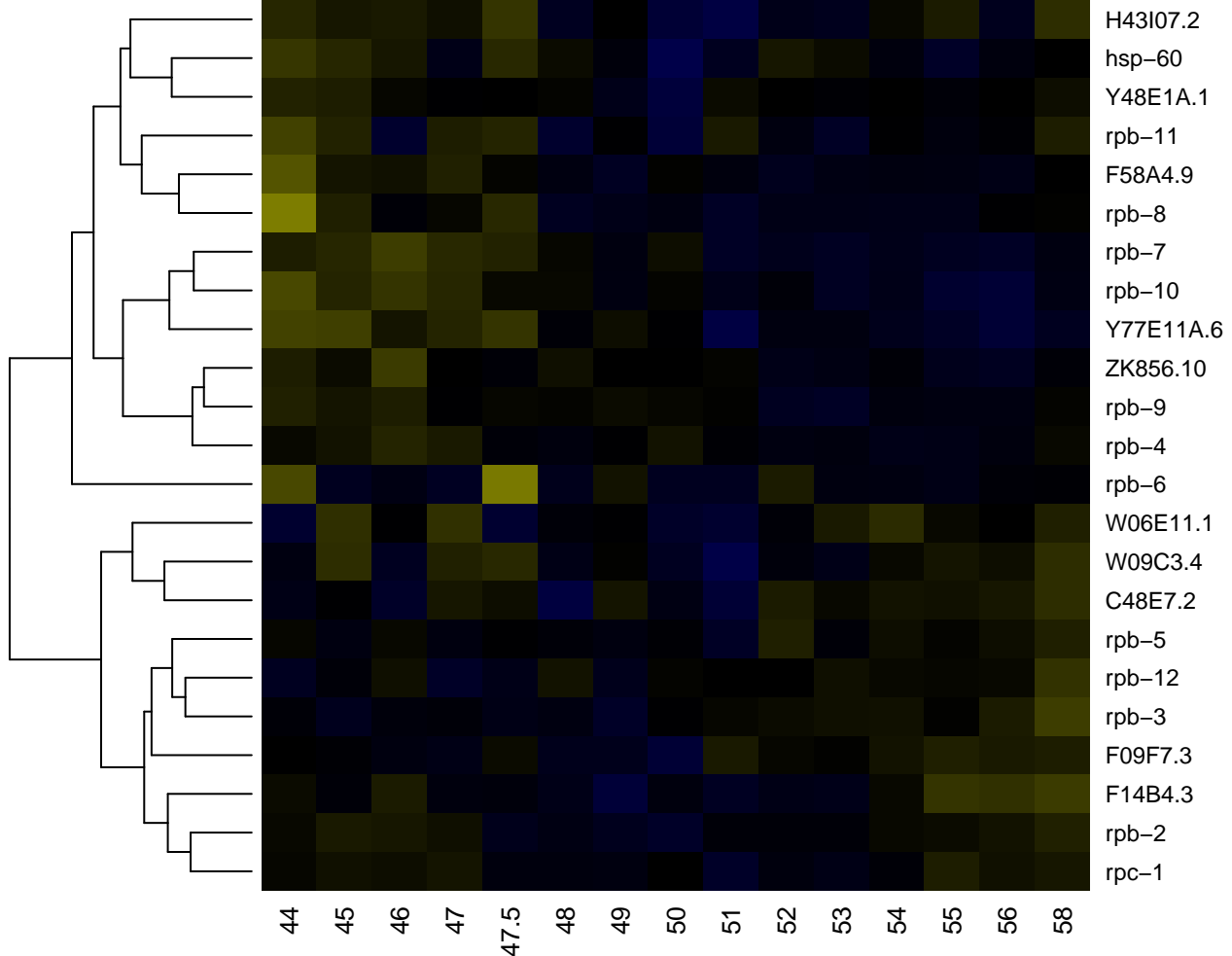
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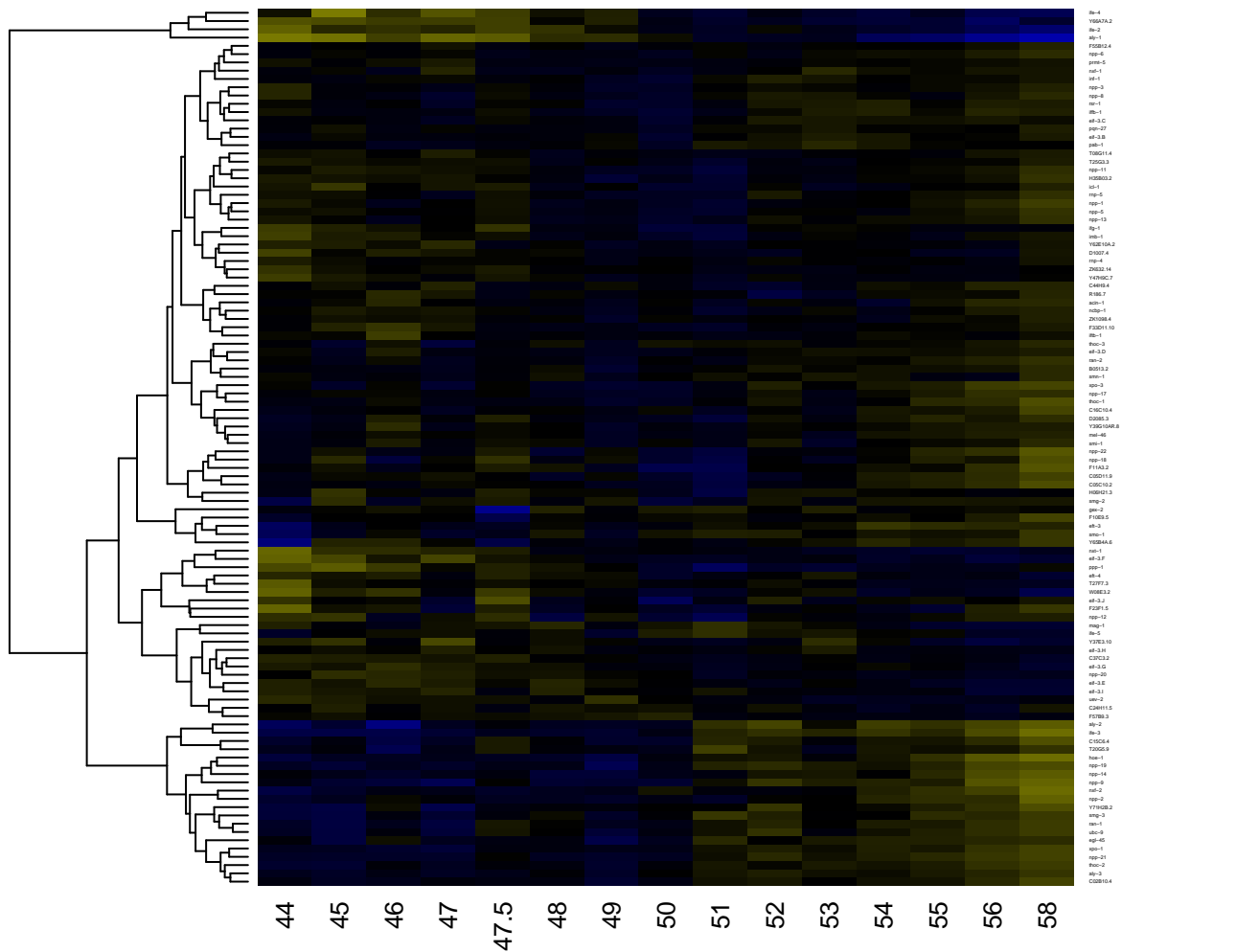
RNA degradation



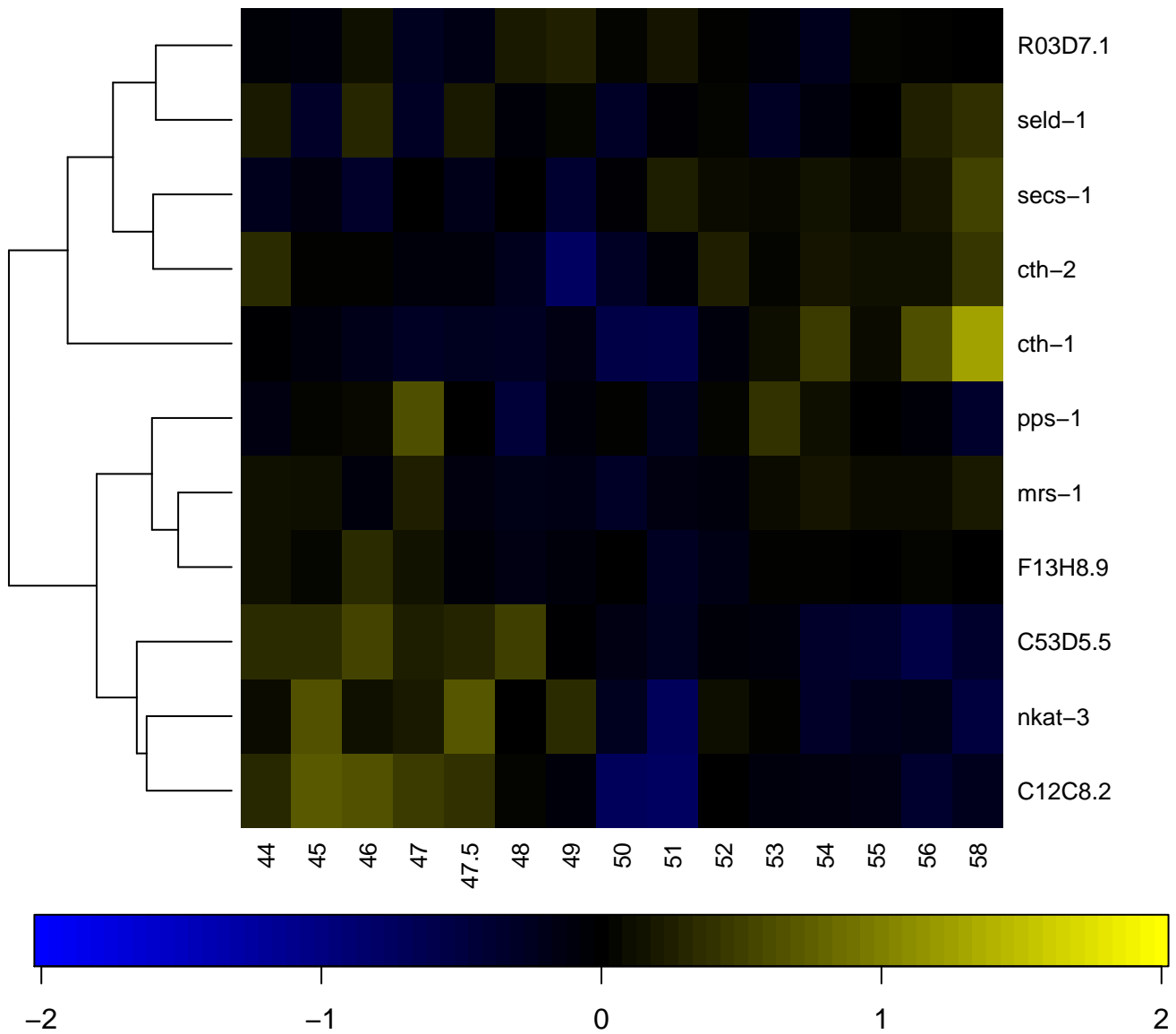
RNA polymerase



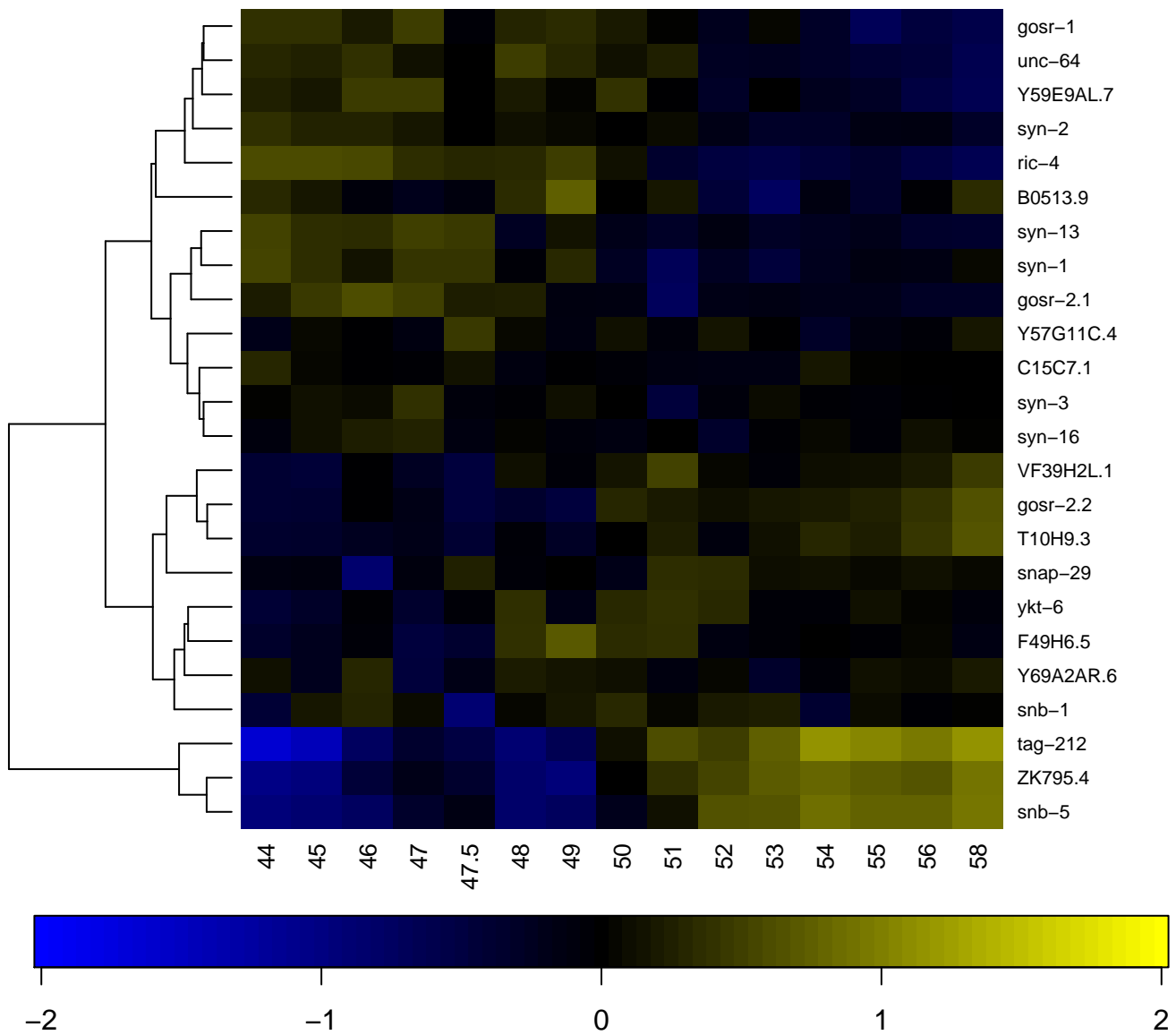
RNA transport



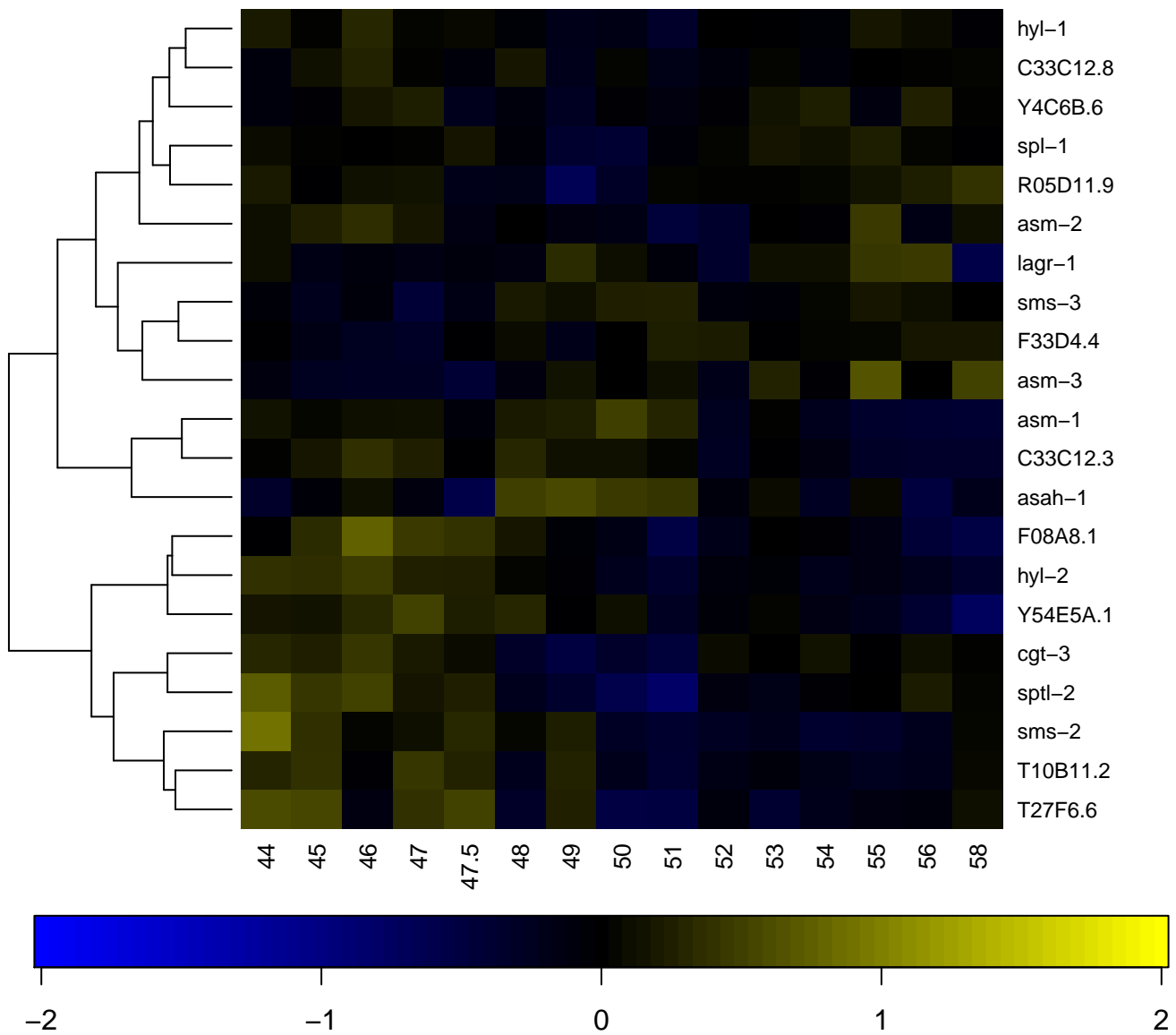
Selenocompound metabolism



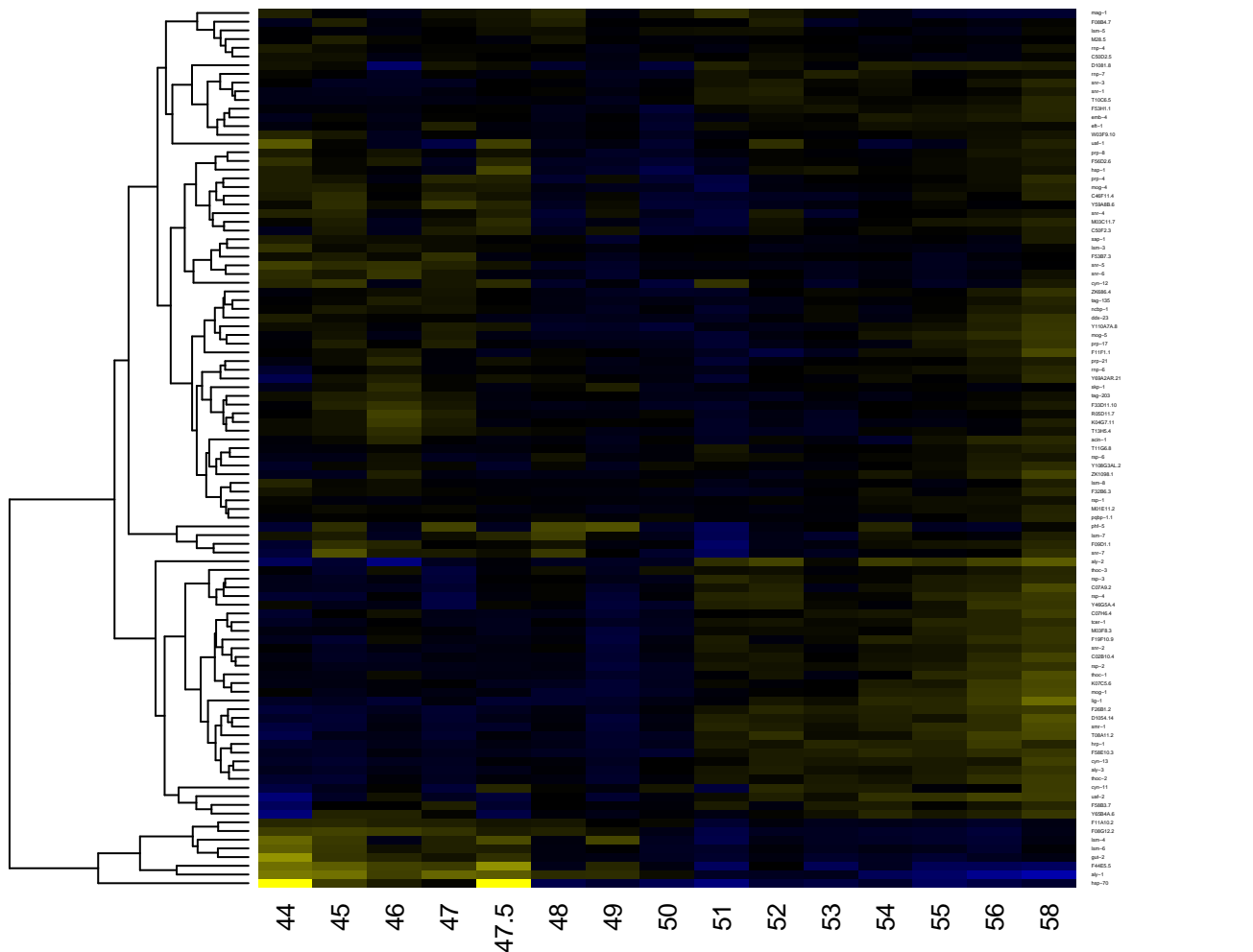
Snare interactions in vesicular transport



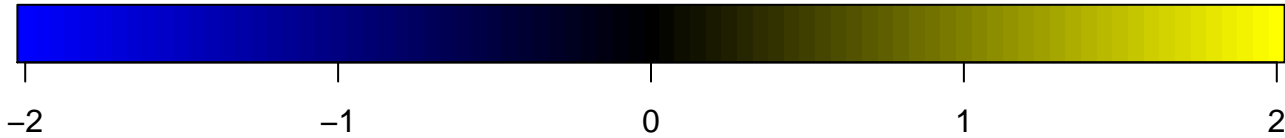
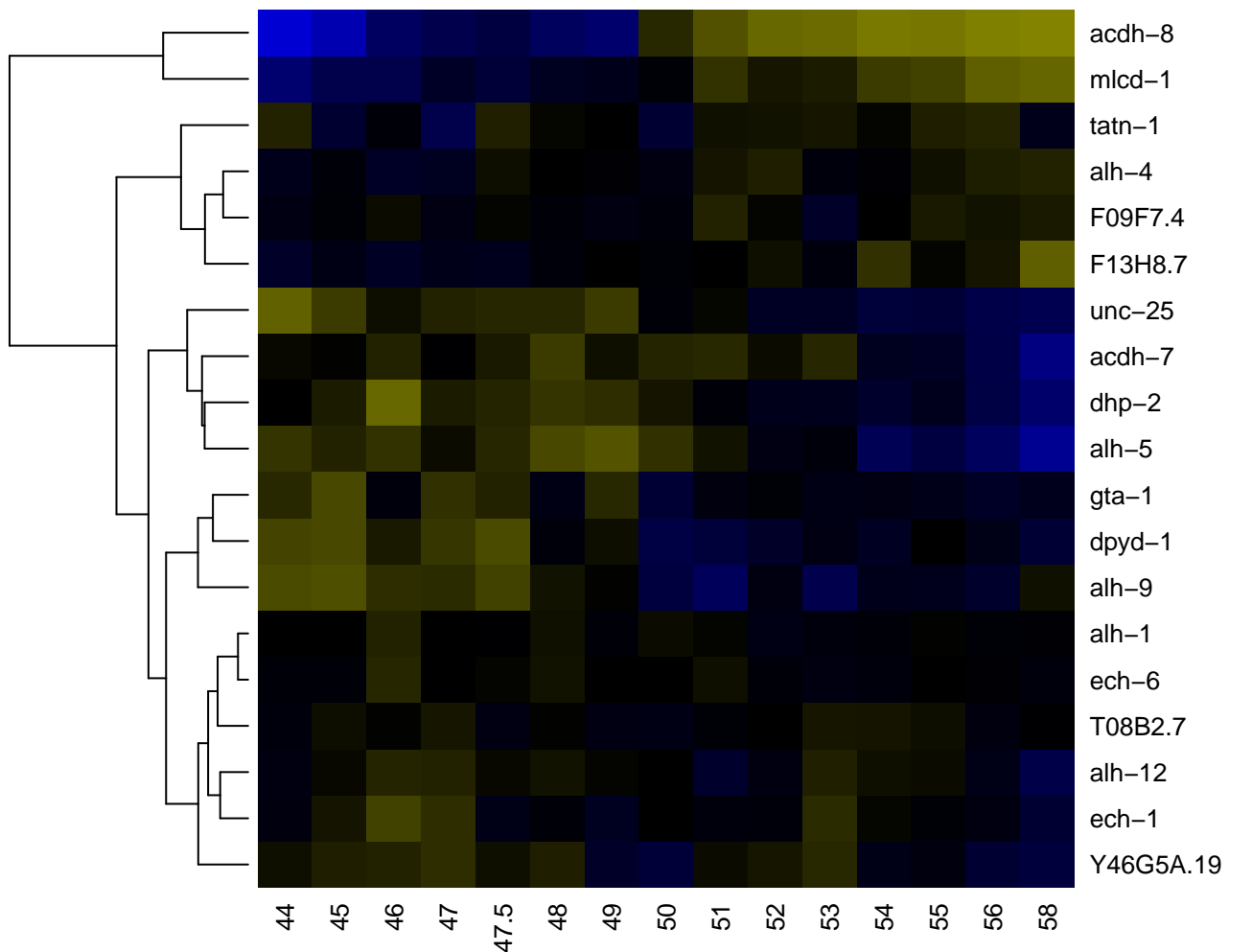
Spingolipid metabolism



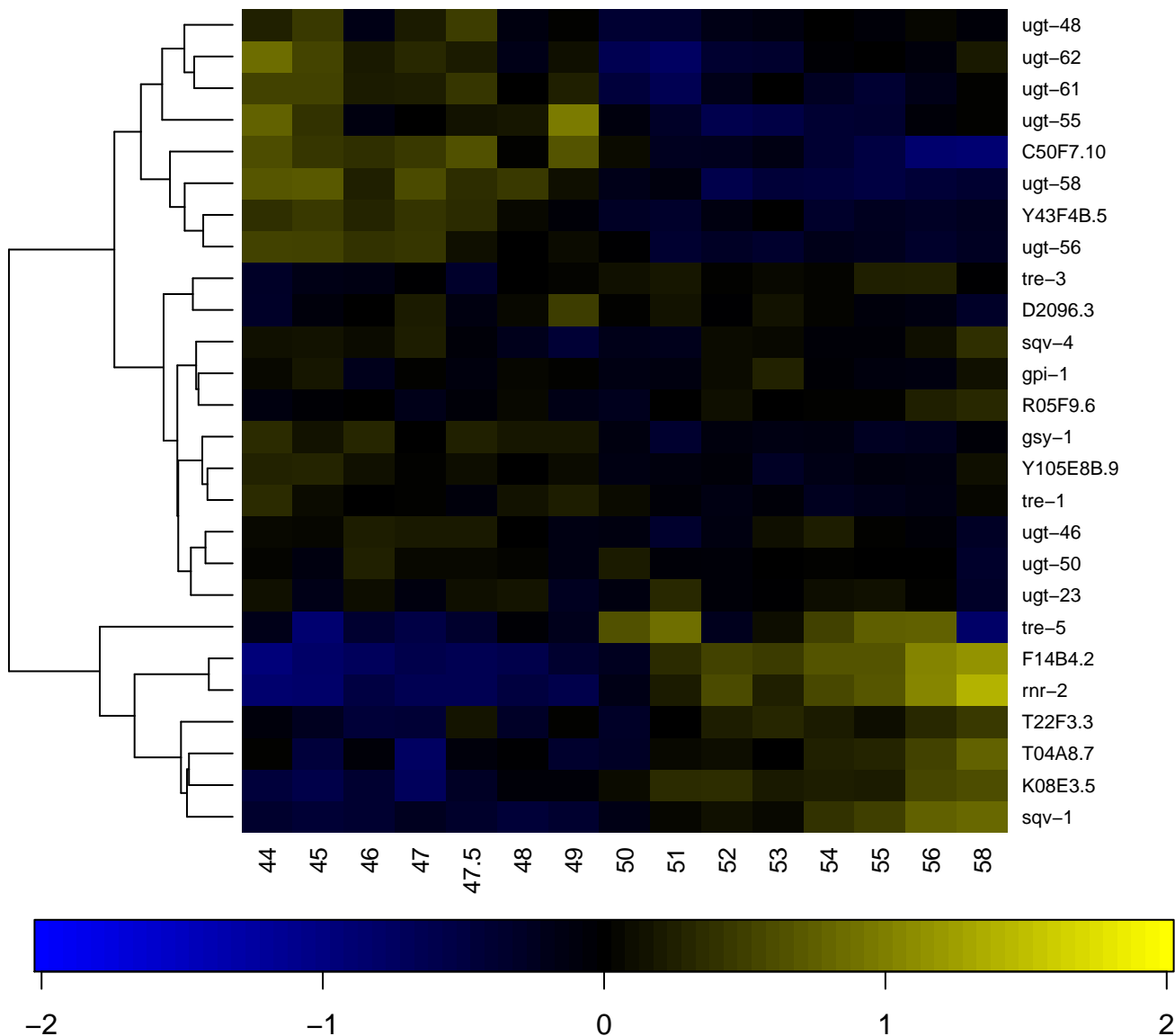
Spliceosome



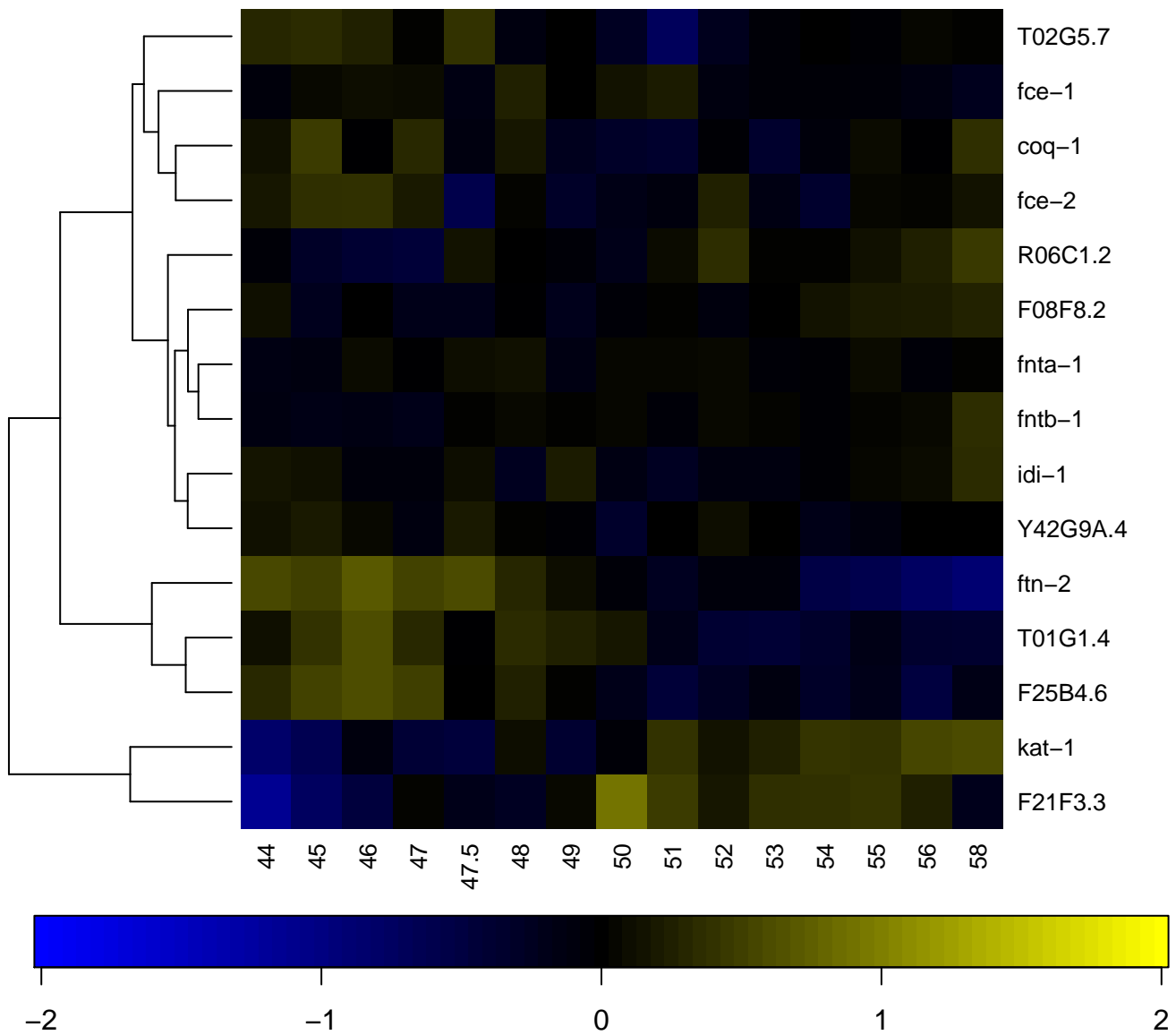
β -alanine metabolism



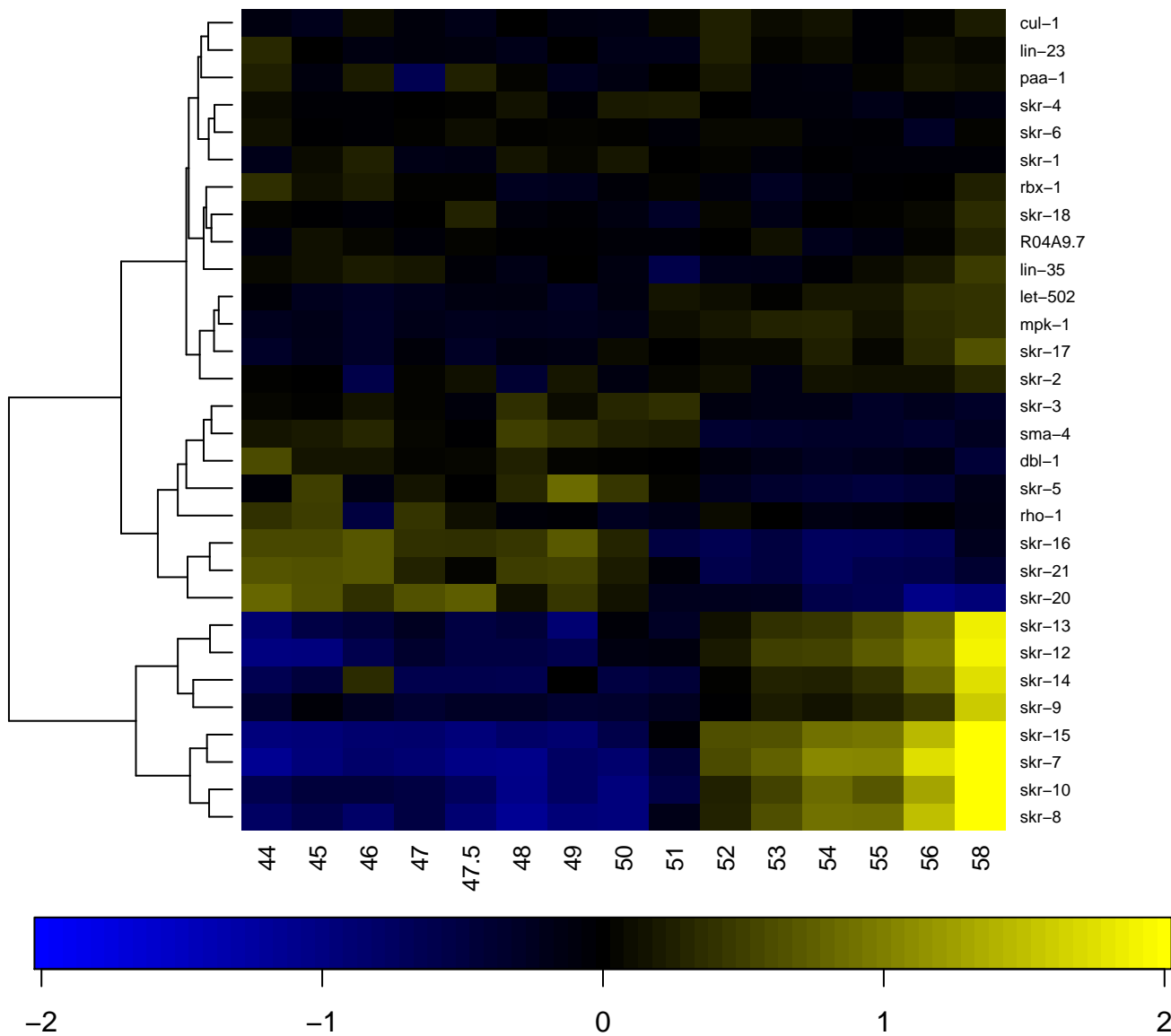
Starch and sucrose metabolism



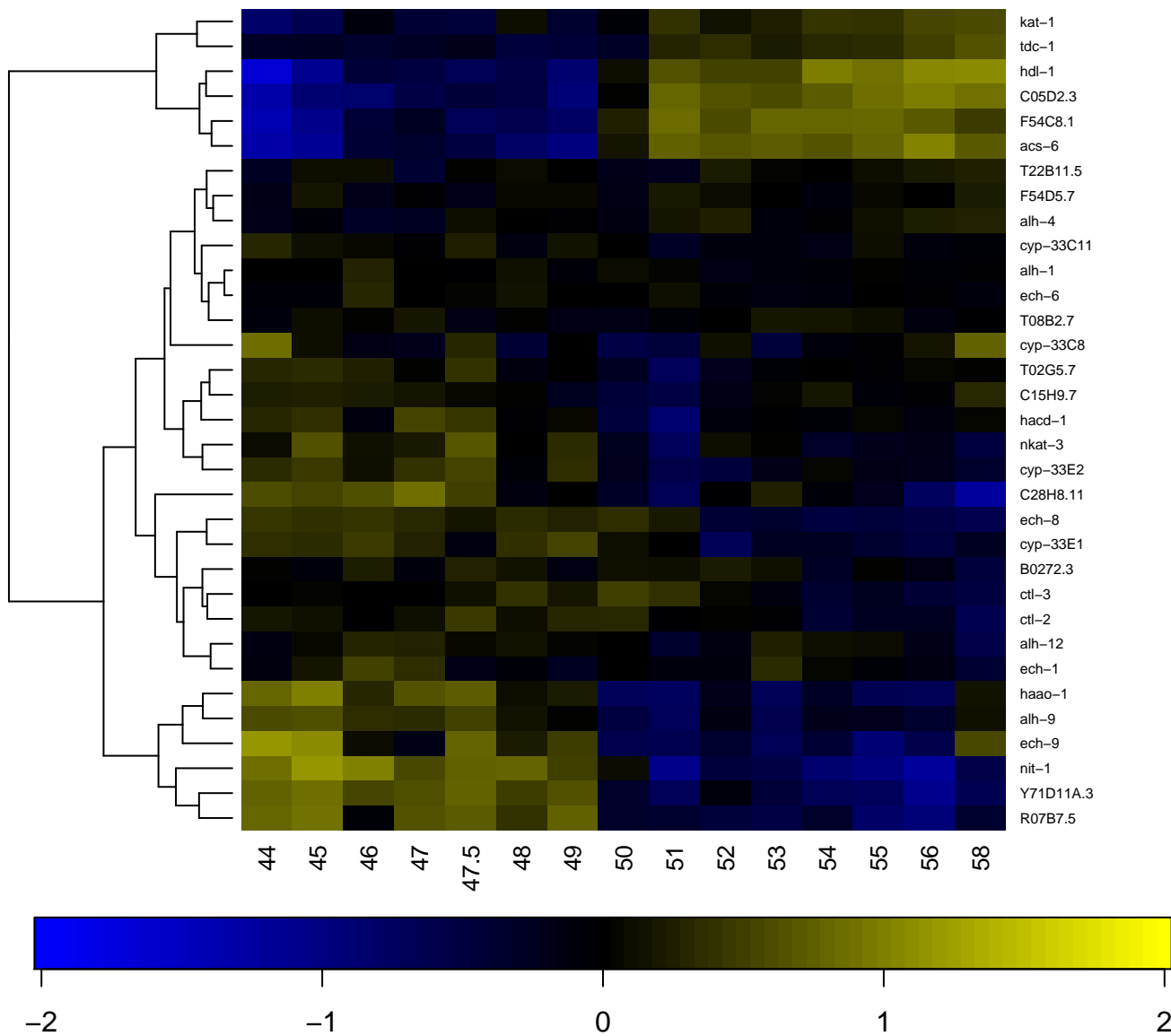
Terpenoid backbone biosynthesis



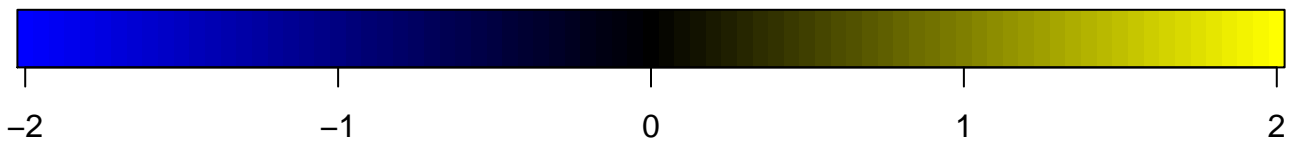
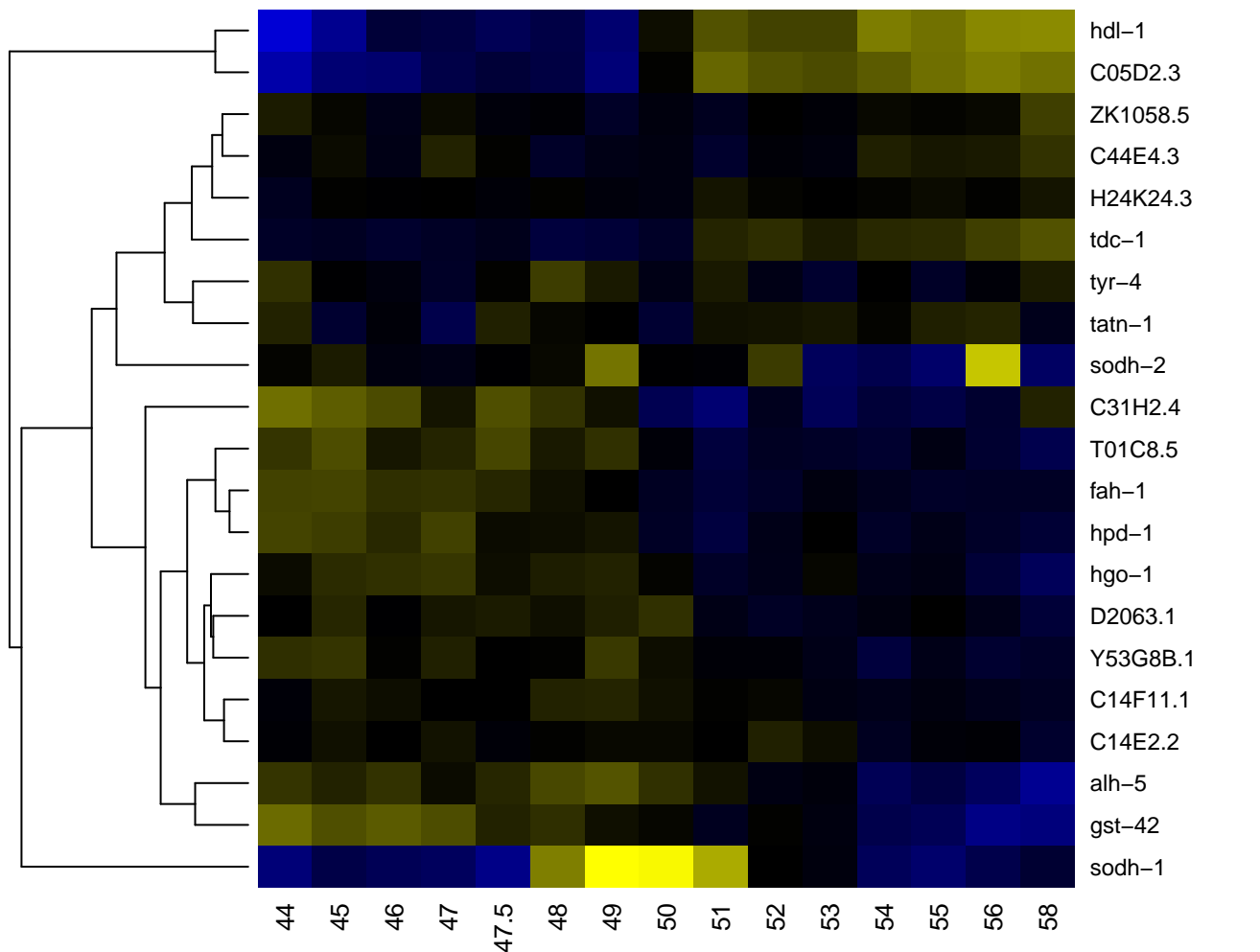
TGF-beta signaling pathway



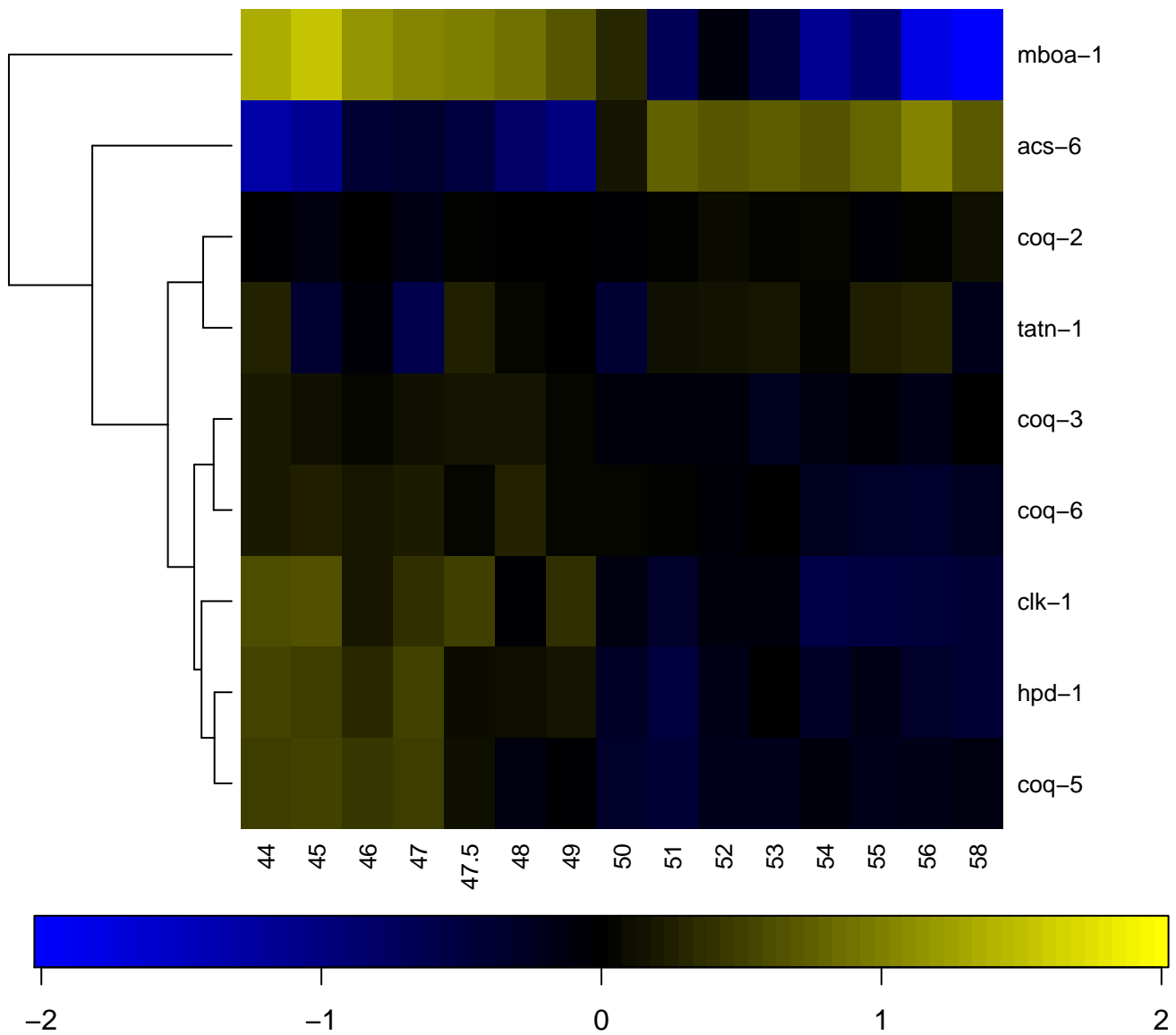
Tryptophan metabolism



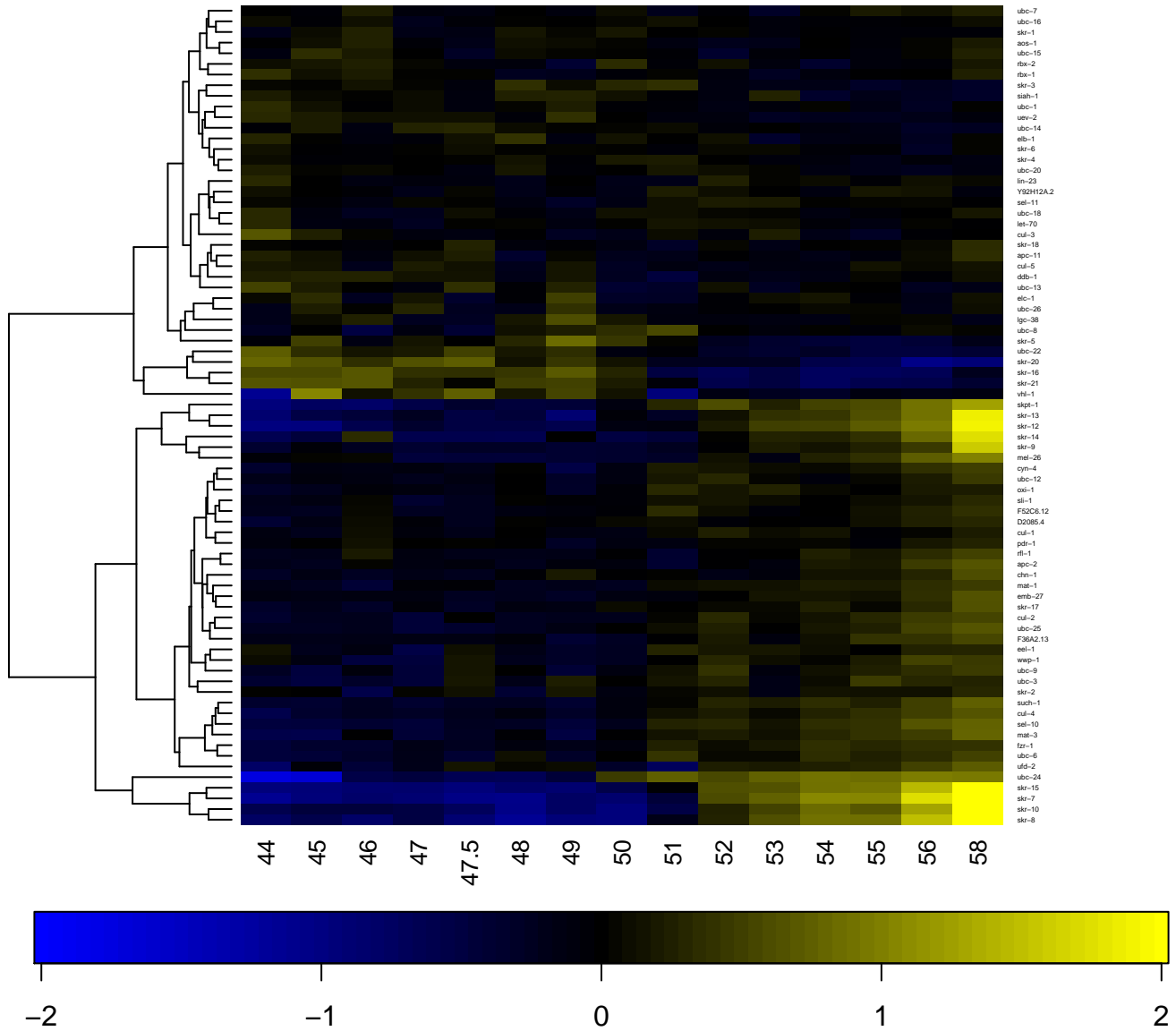
Tyrosine metabolism



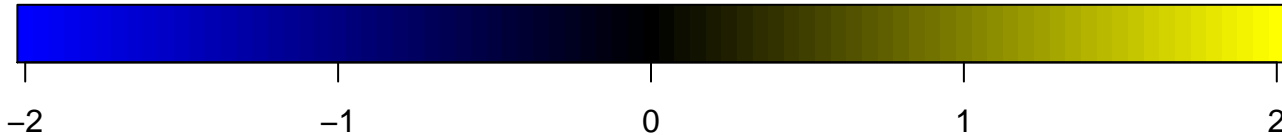
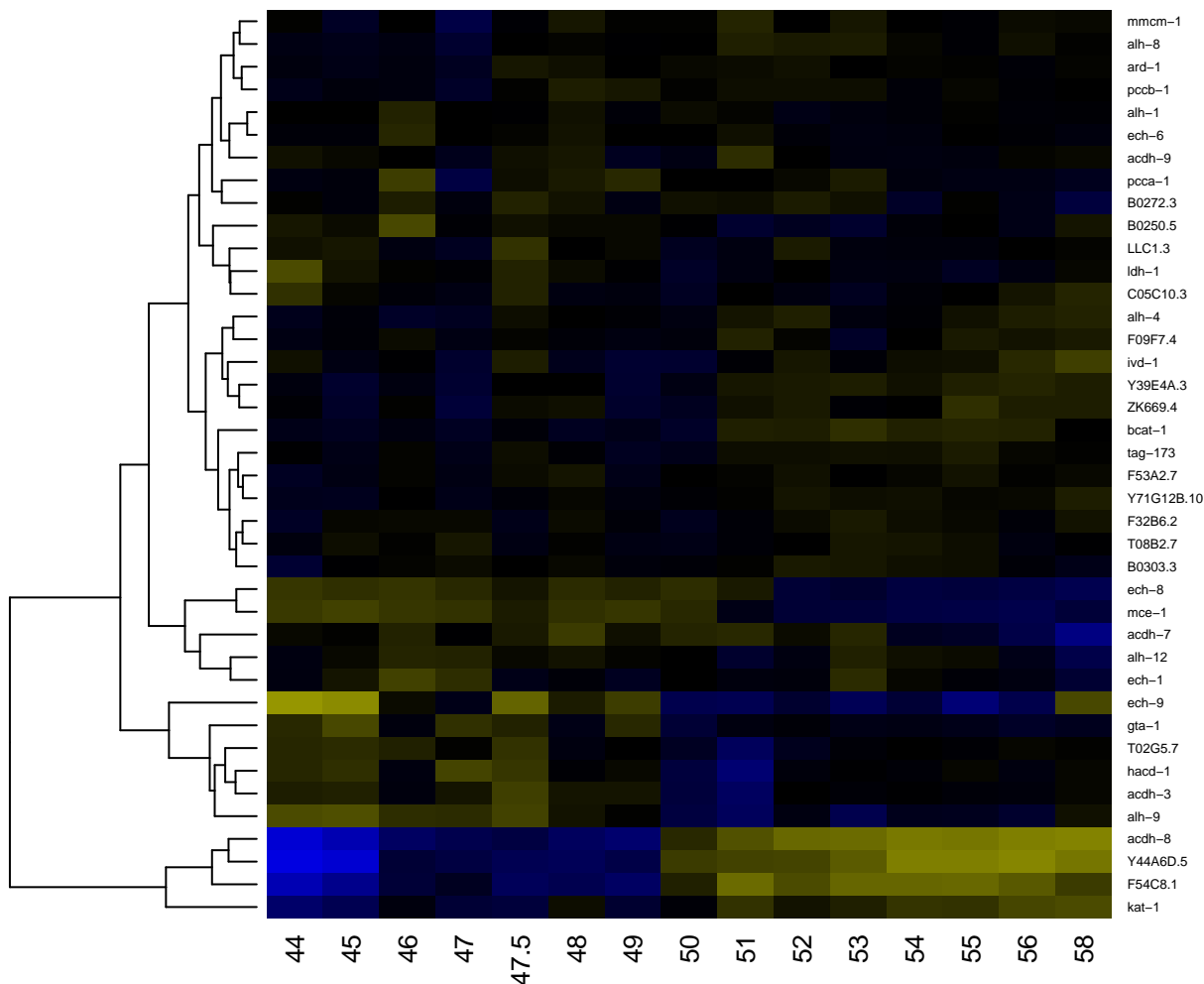
Ubiquinone and other terpenoid-quinone biosynthesis



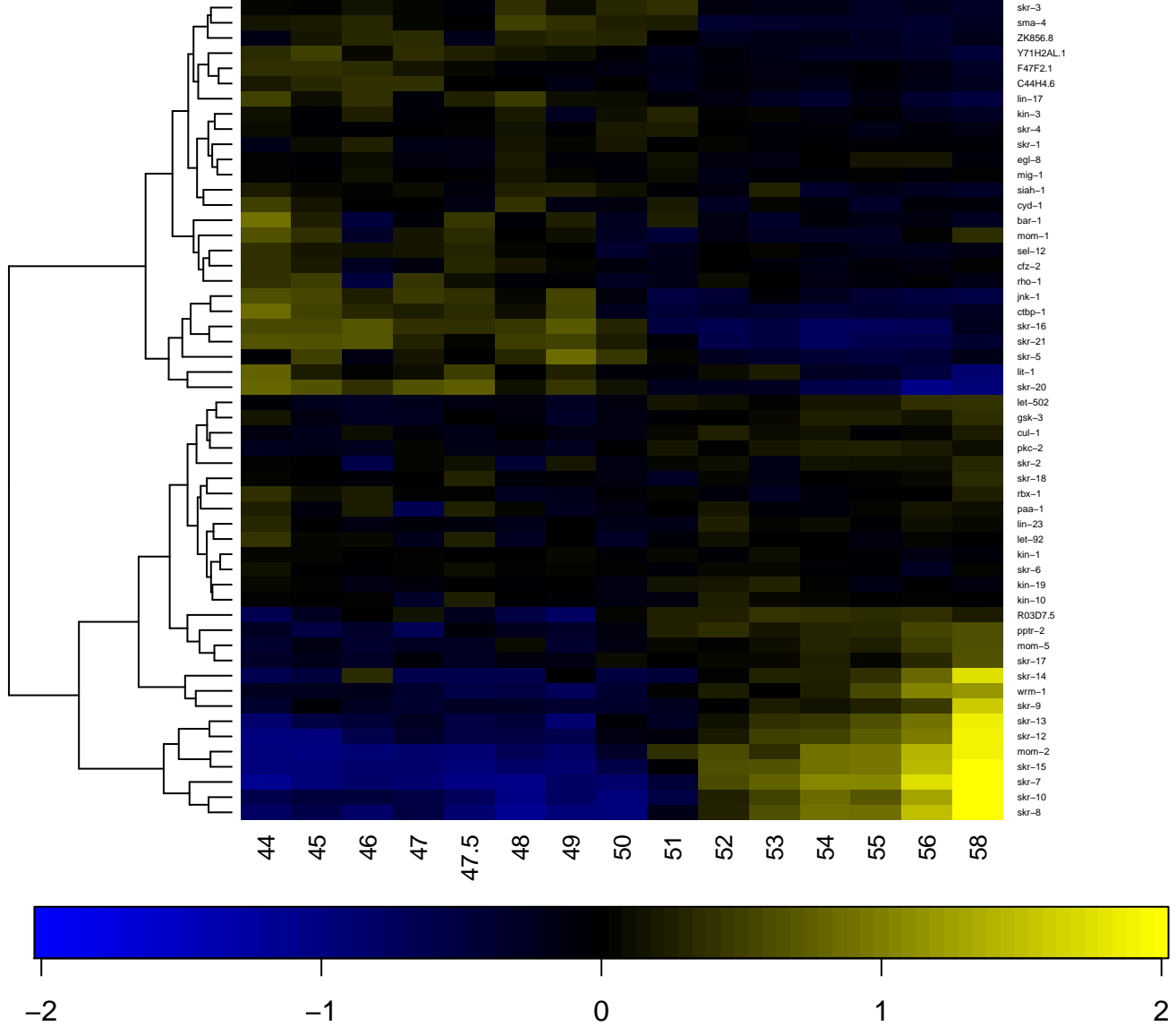
Ubiquitin mediated proteolysis



Valine, leucine and isoleucine degradation

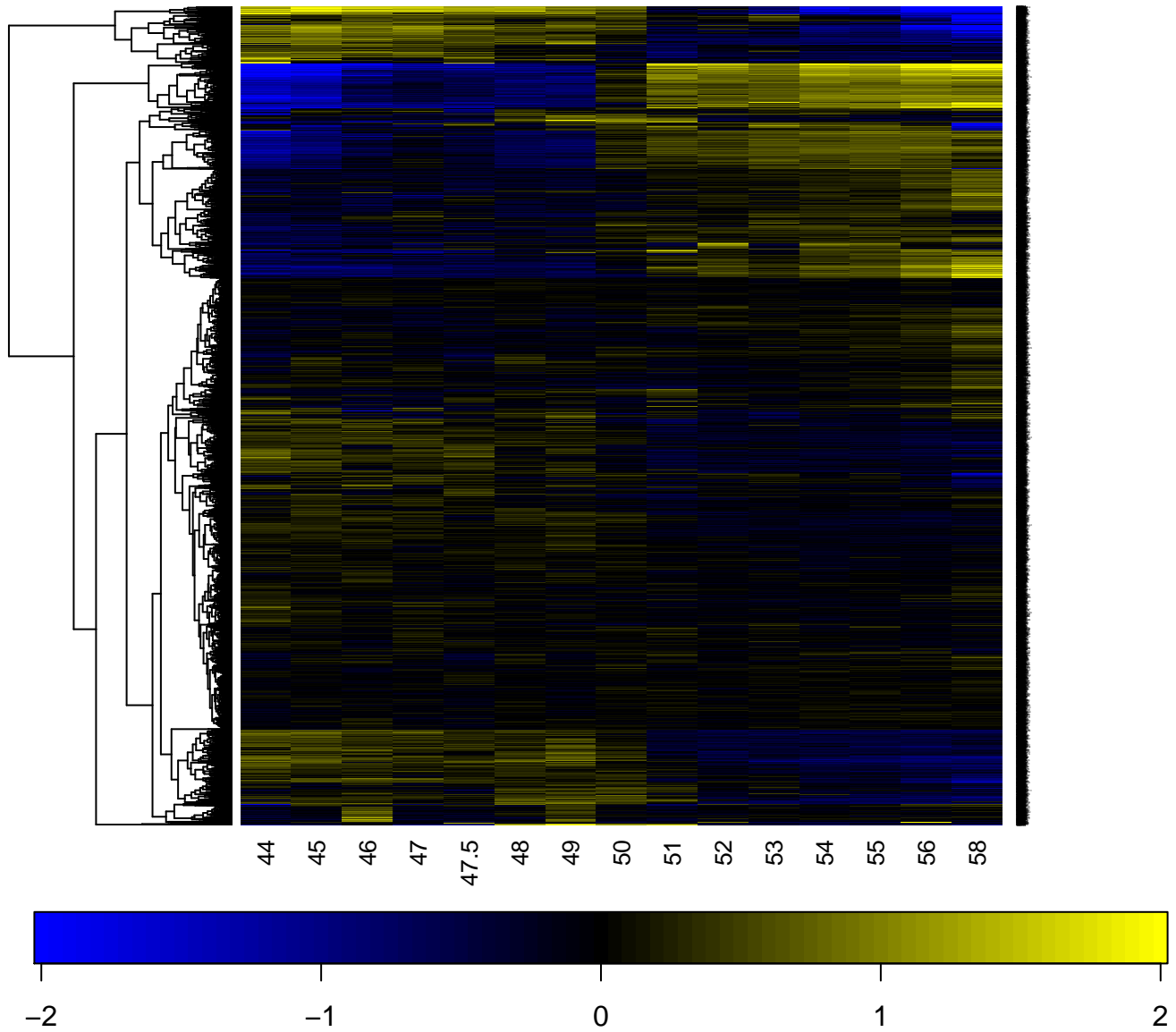


WNT signaling pathway

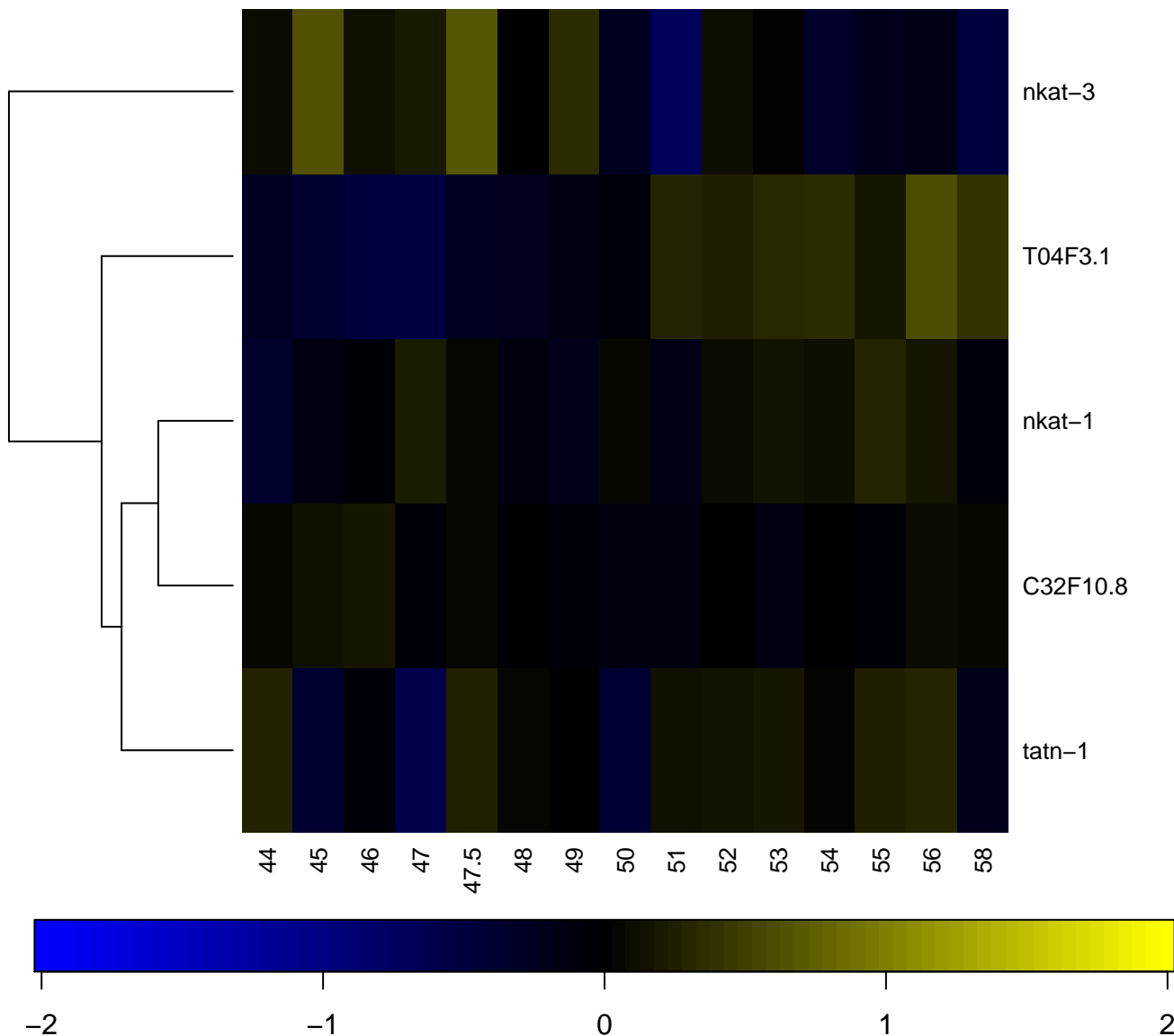


Supplementary file H. Dynamic gene expression patterns of all Protein Domains.

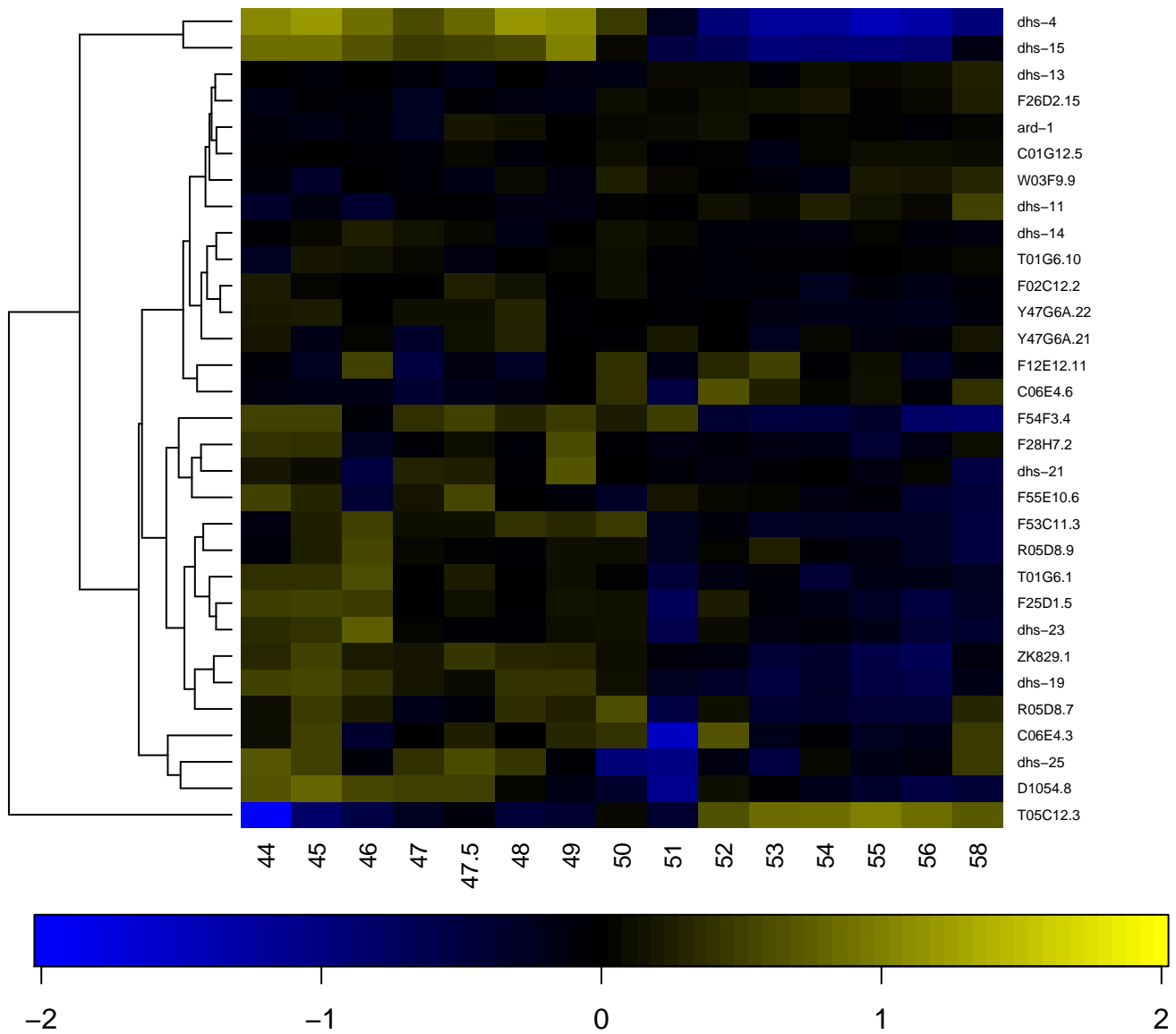
The “heatmap” function of “R” was used to cluster genes of each individual Protein Domain according to their expression pattern. Protein Domain name is shown per page as figure title. The time in hours is shown on the *x*-axis. Gene names are shown on the *y*-axis. The scale bar shows the log₂ ratio with the mean for each time-point. Blue is lower than the mean and yellow is higher than the mean.



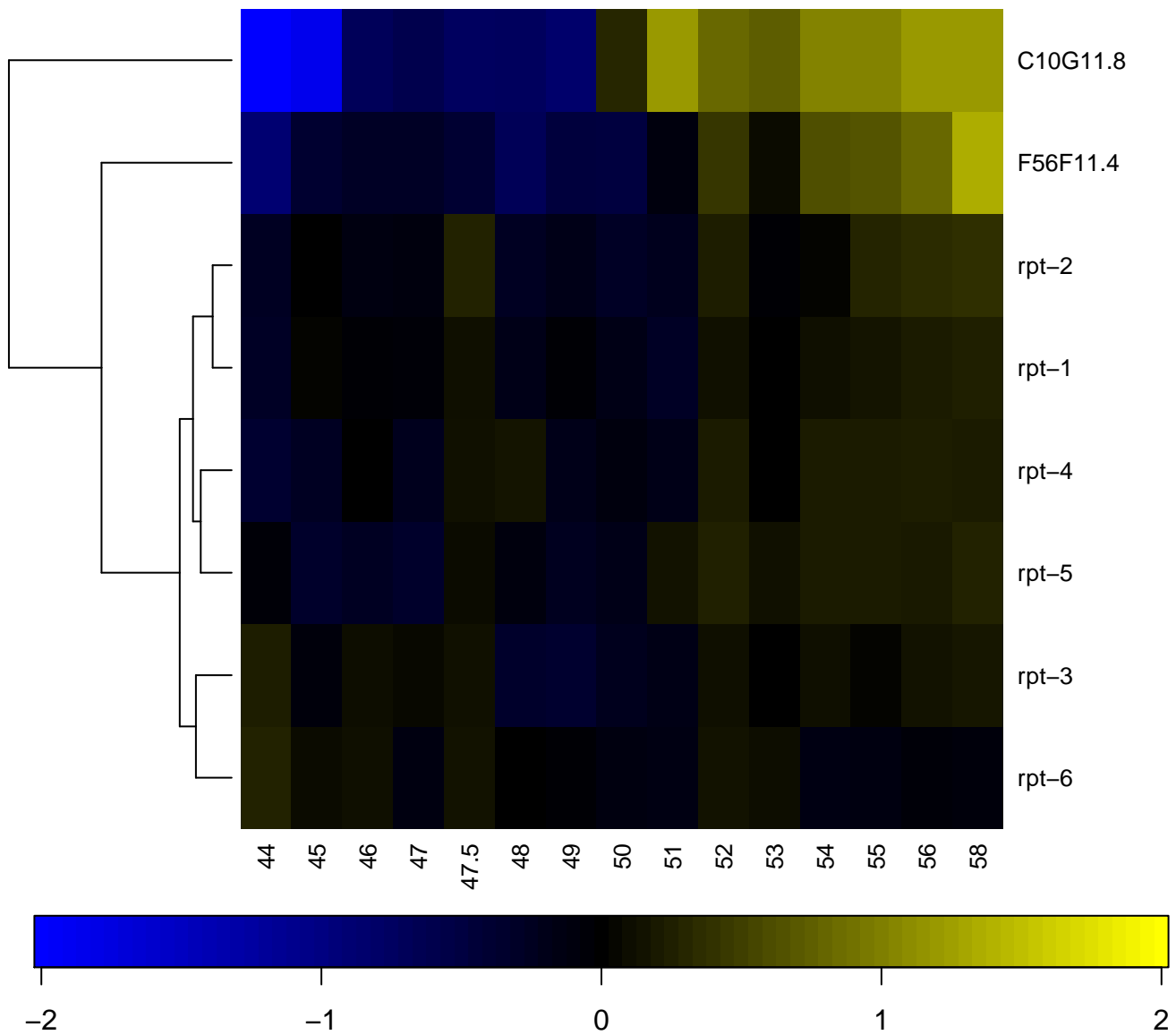
1-aminocyclopropane-1-carboxylate synthase



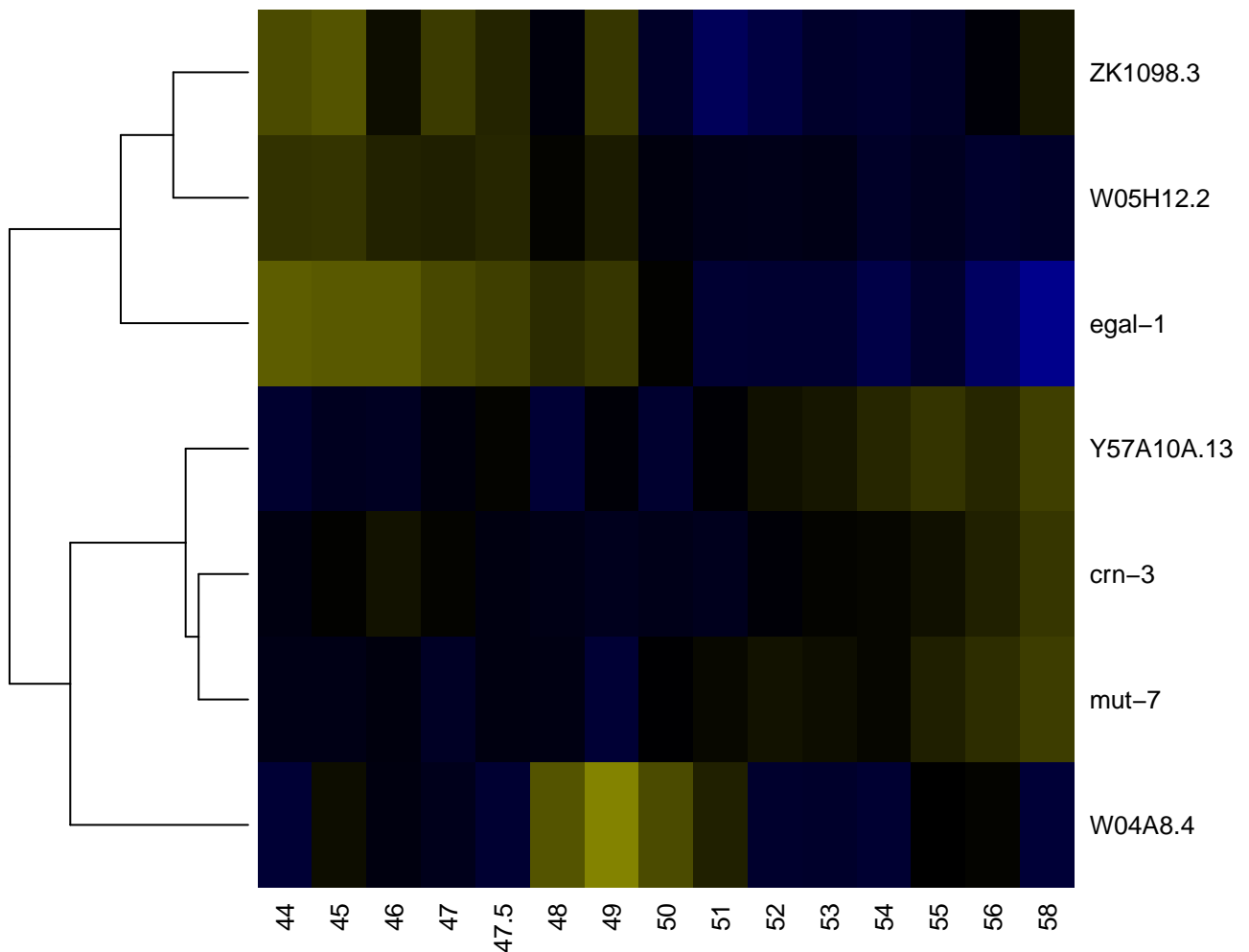
2,3-dihydro-2,3-dihydroxybenzoate dehydrogenase



26S proteasome subunit P45



3'-5' exonuclease



-2

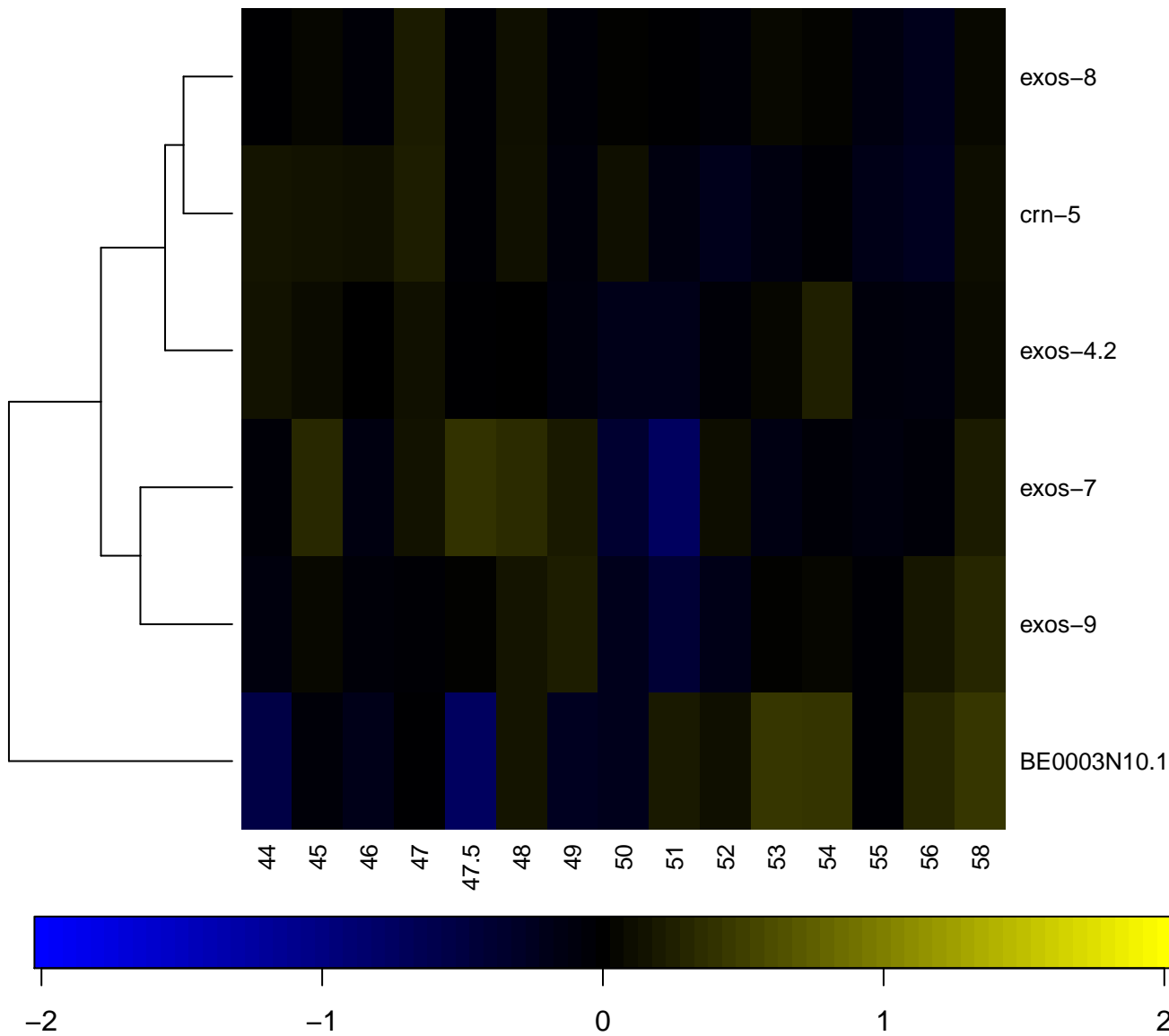
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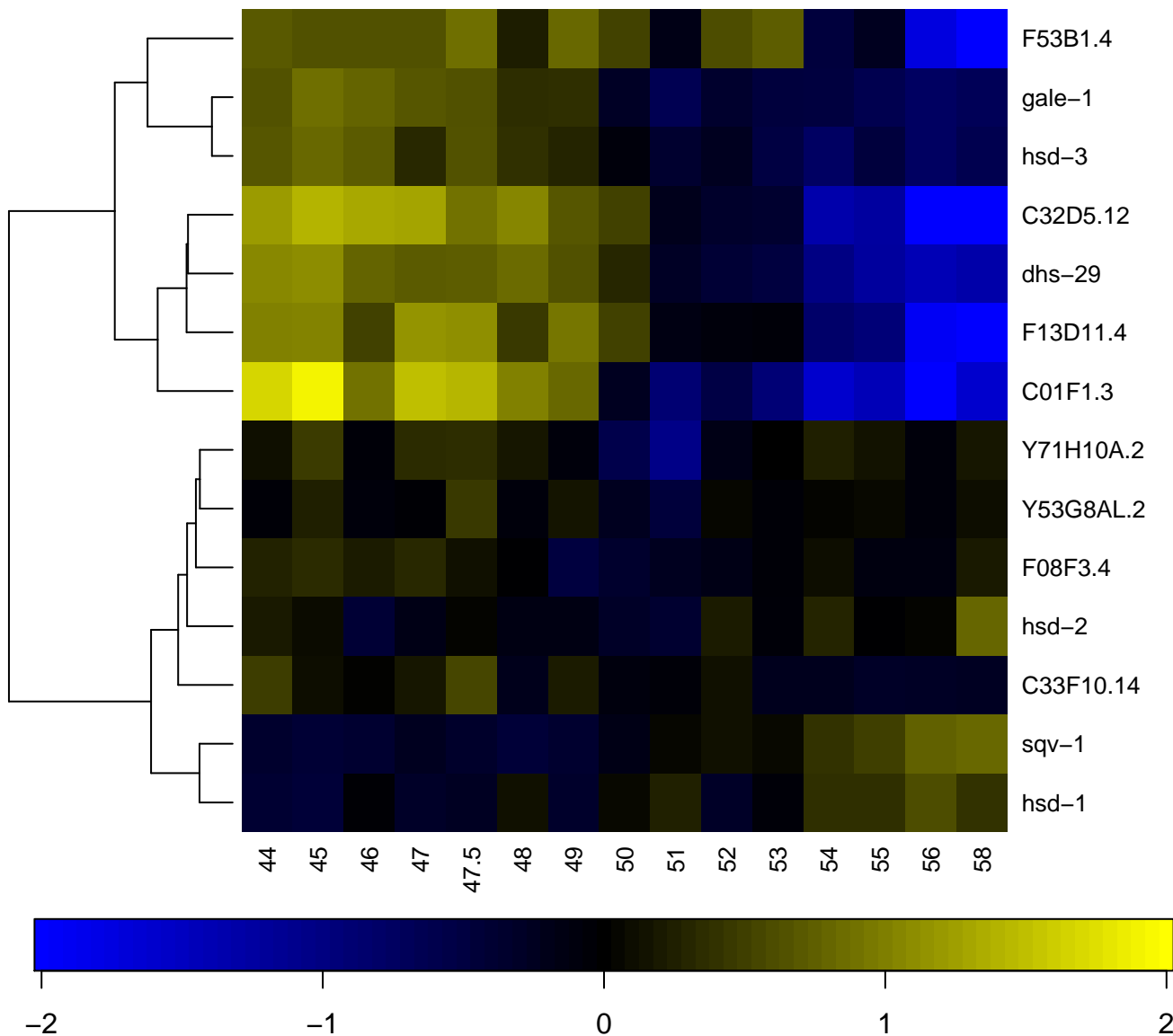
1

2

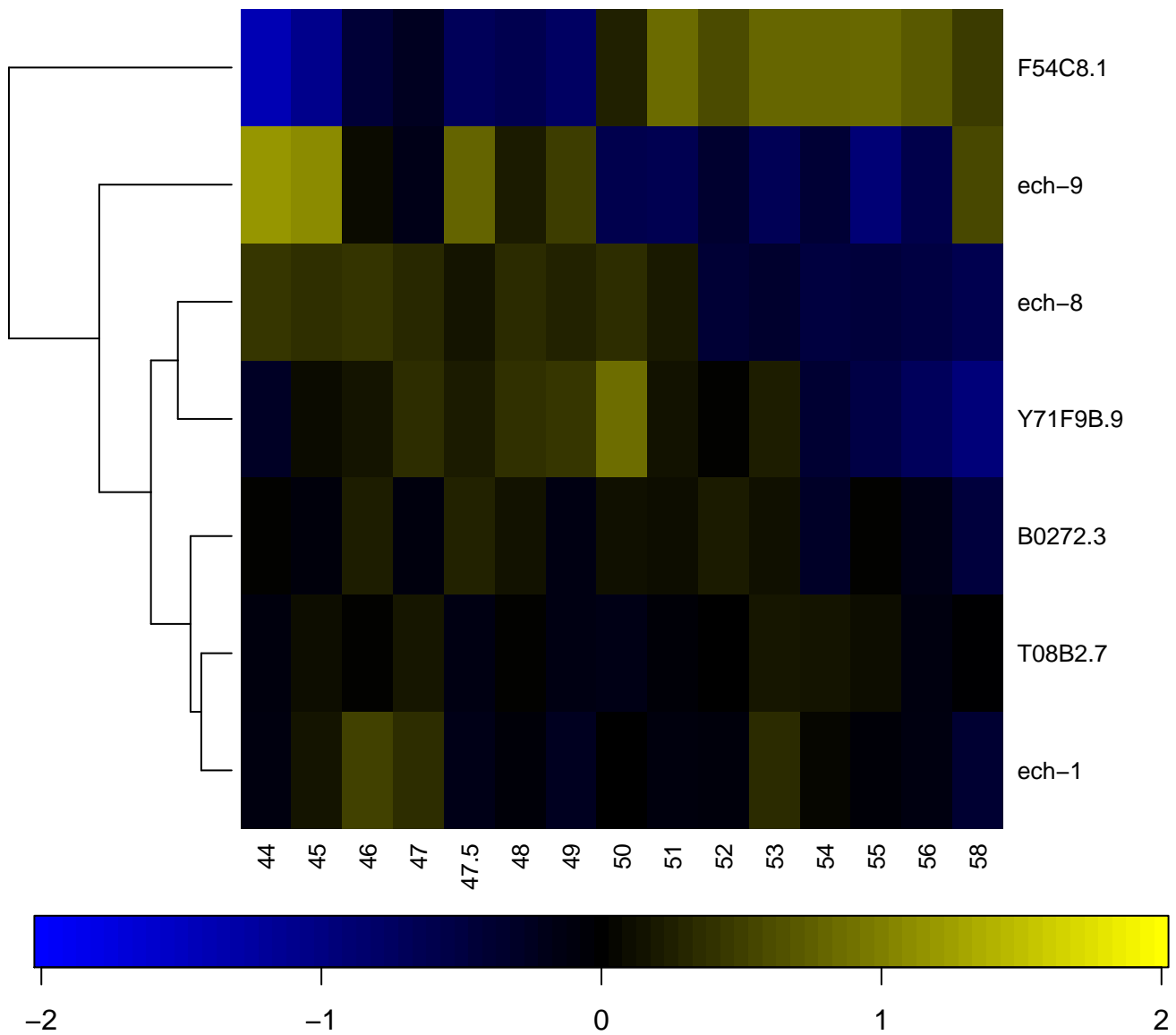
3' exoribonuclease family, domain 1



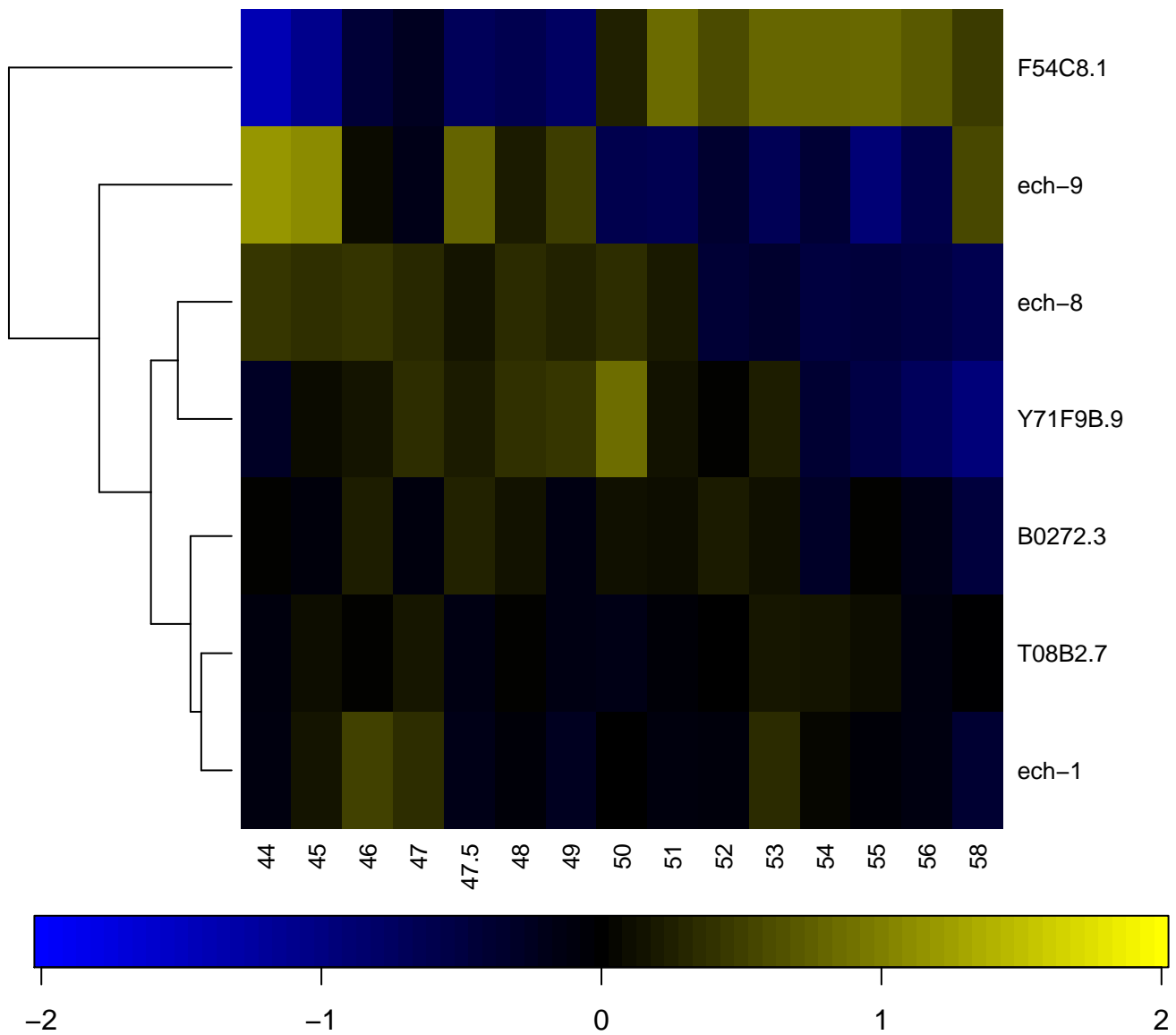
3-beta hydroxysteroid dehydrogenase/isomerase



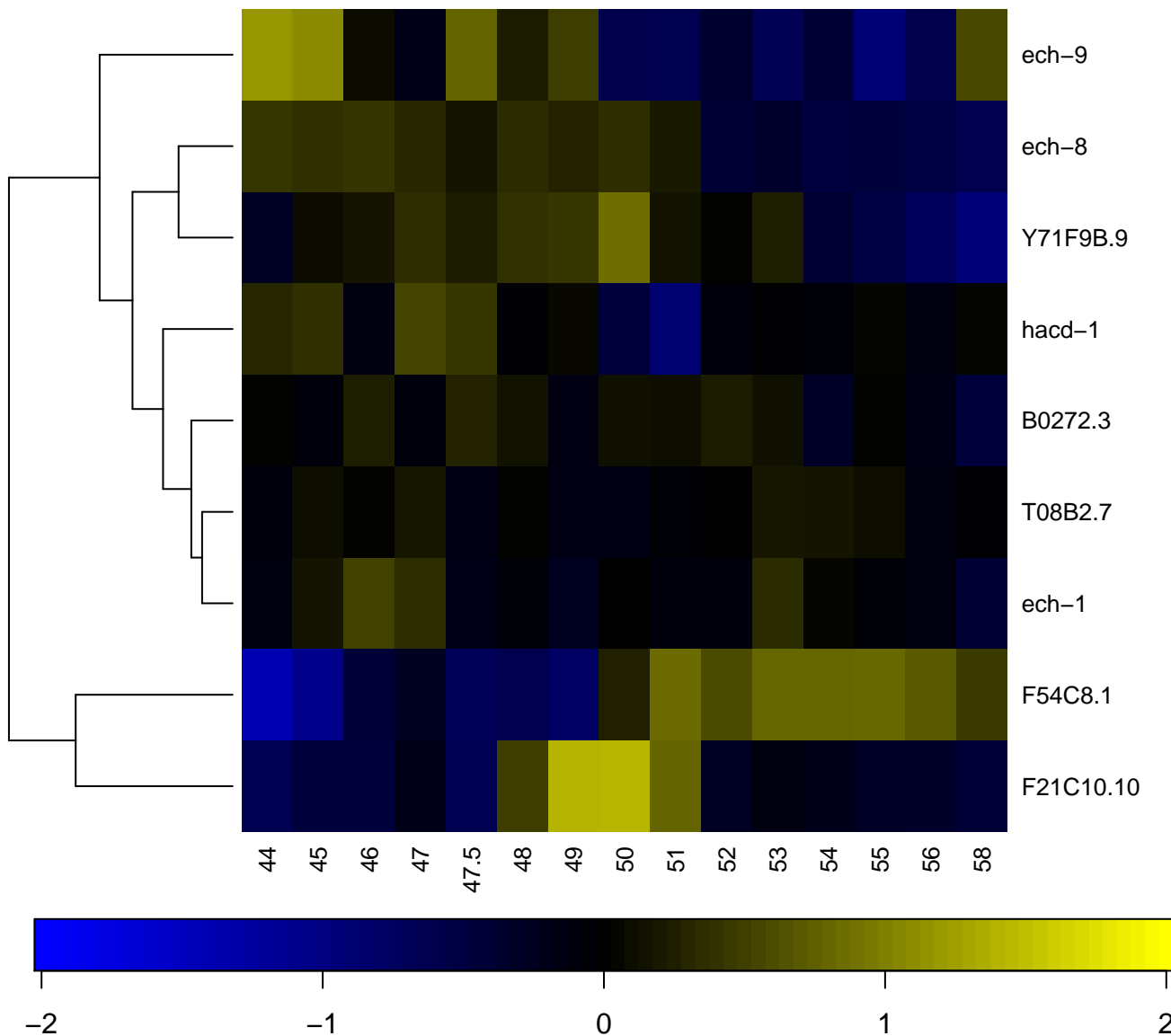
3-hydroxyacyl-CoA dehydrogenase, C-terminal



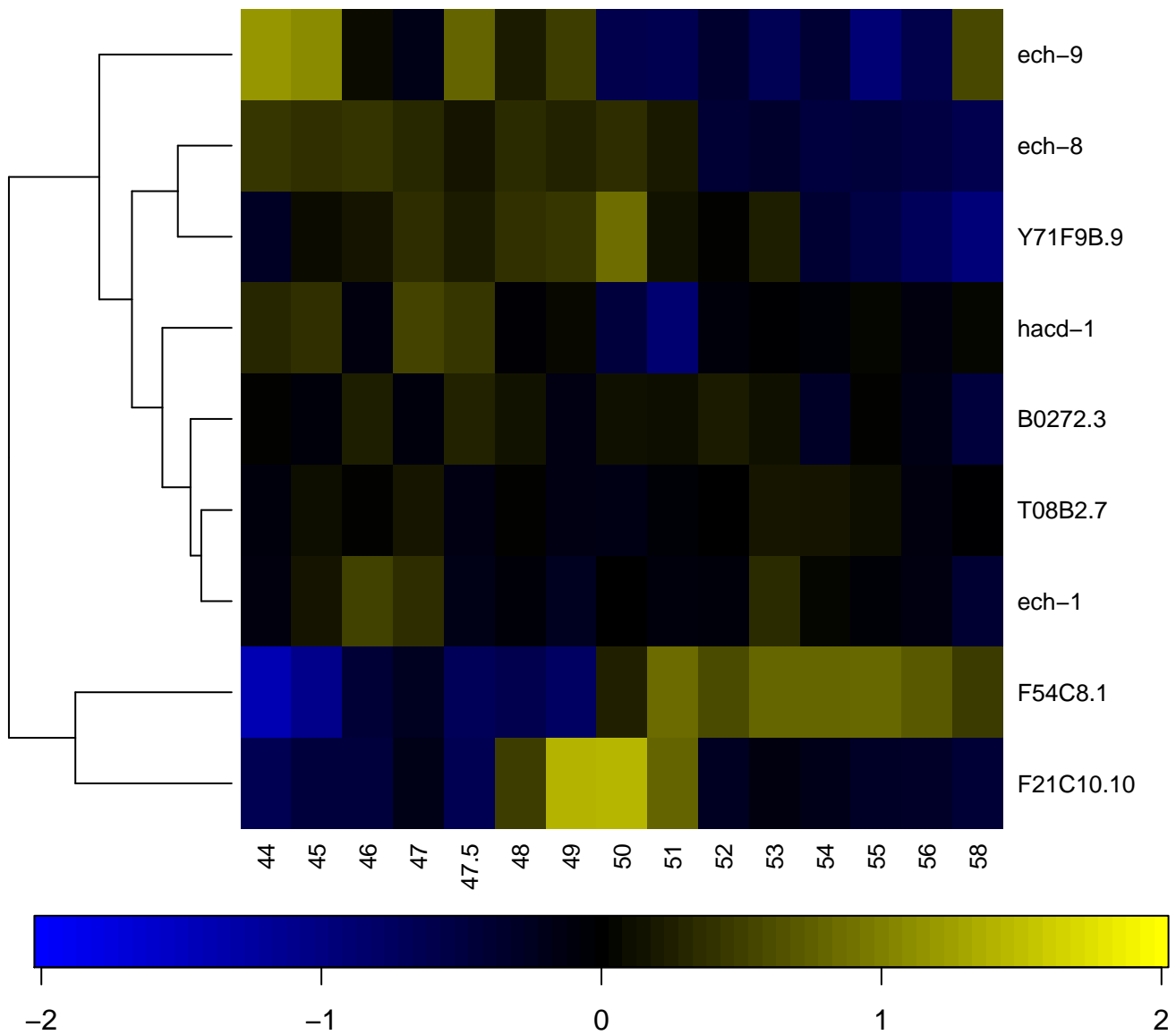
3-hydroxyacyl-CoA dehydrogenase, C-terminal domain



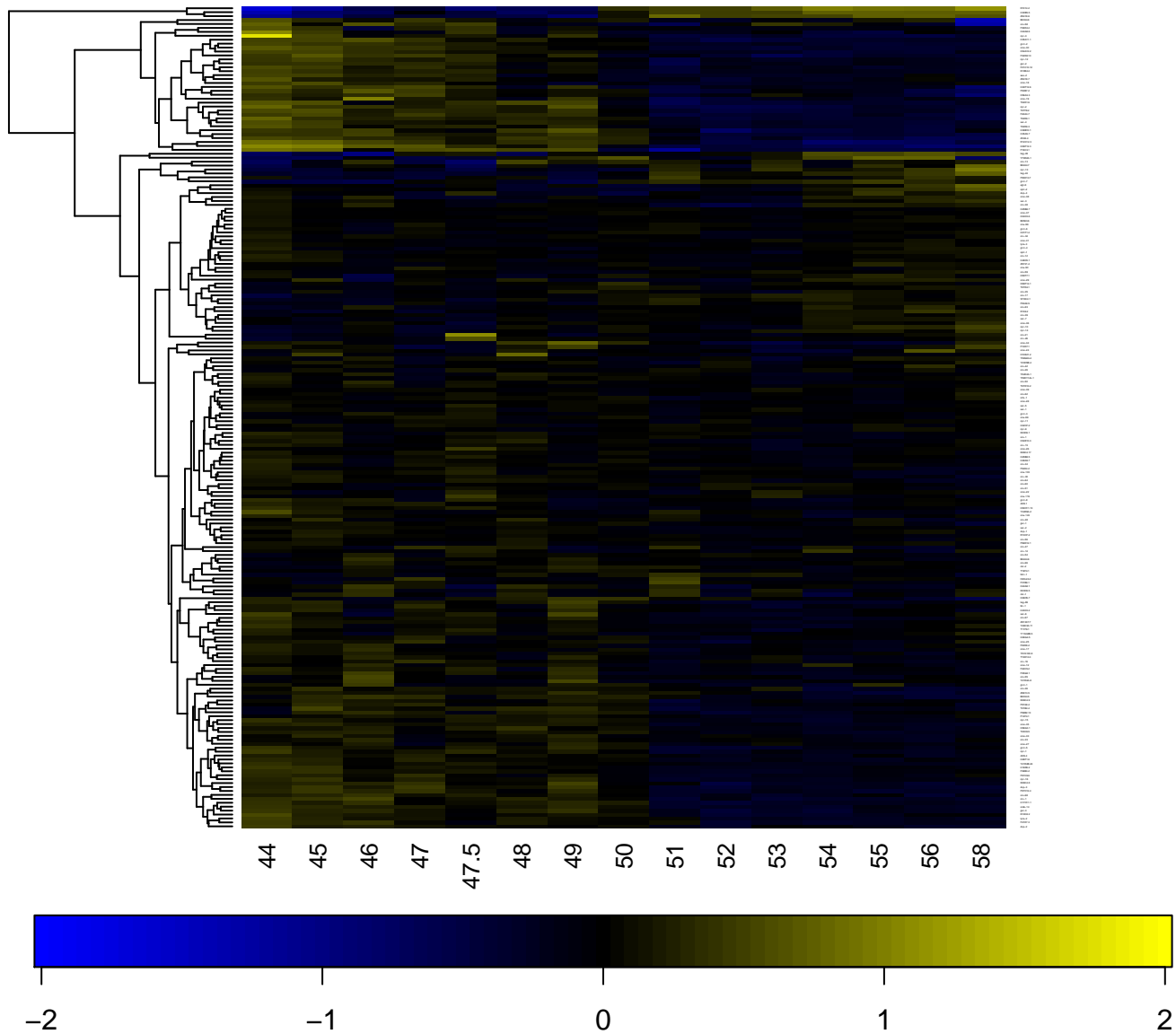
3-hydroxyacyl-CoA dehydrogenase, NAD binding



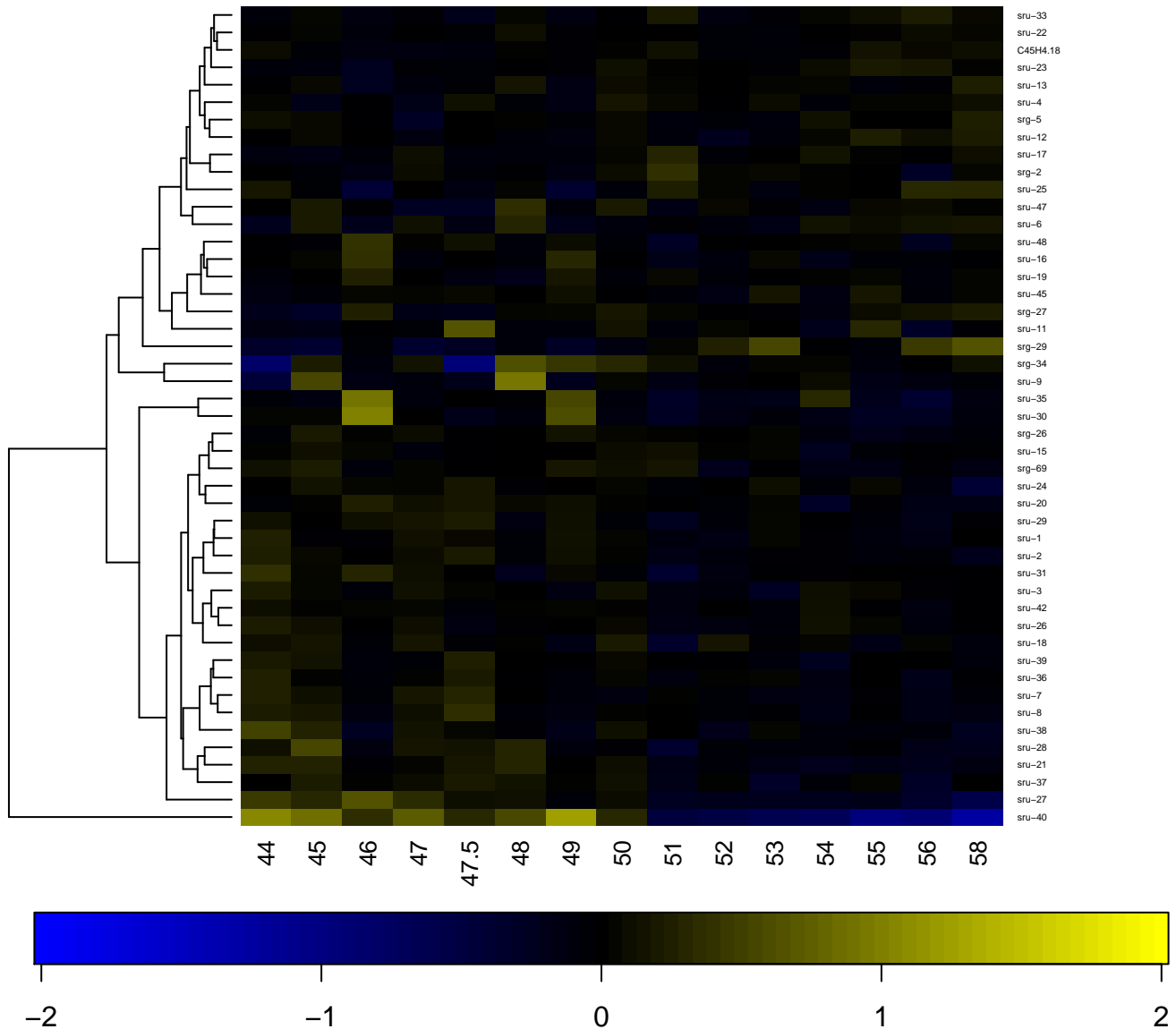
3-hydroxyacyl-CoA dehydrogenase, NAD binding domain



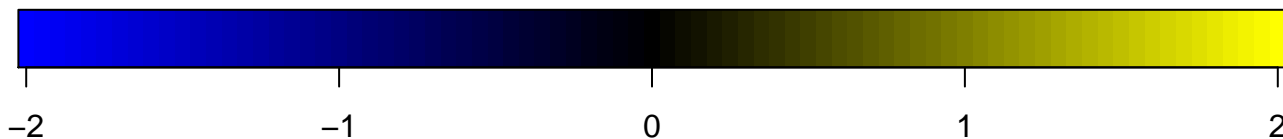
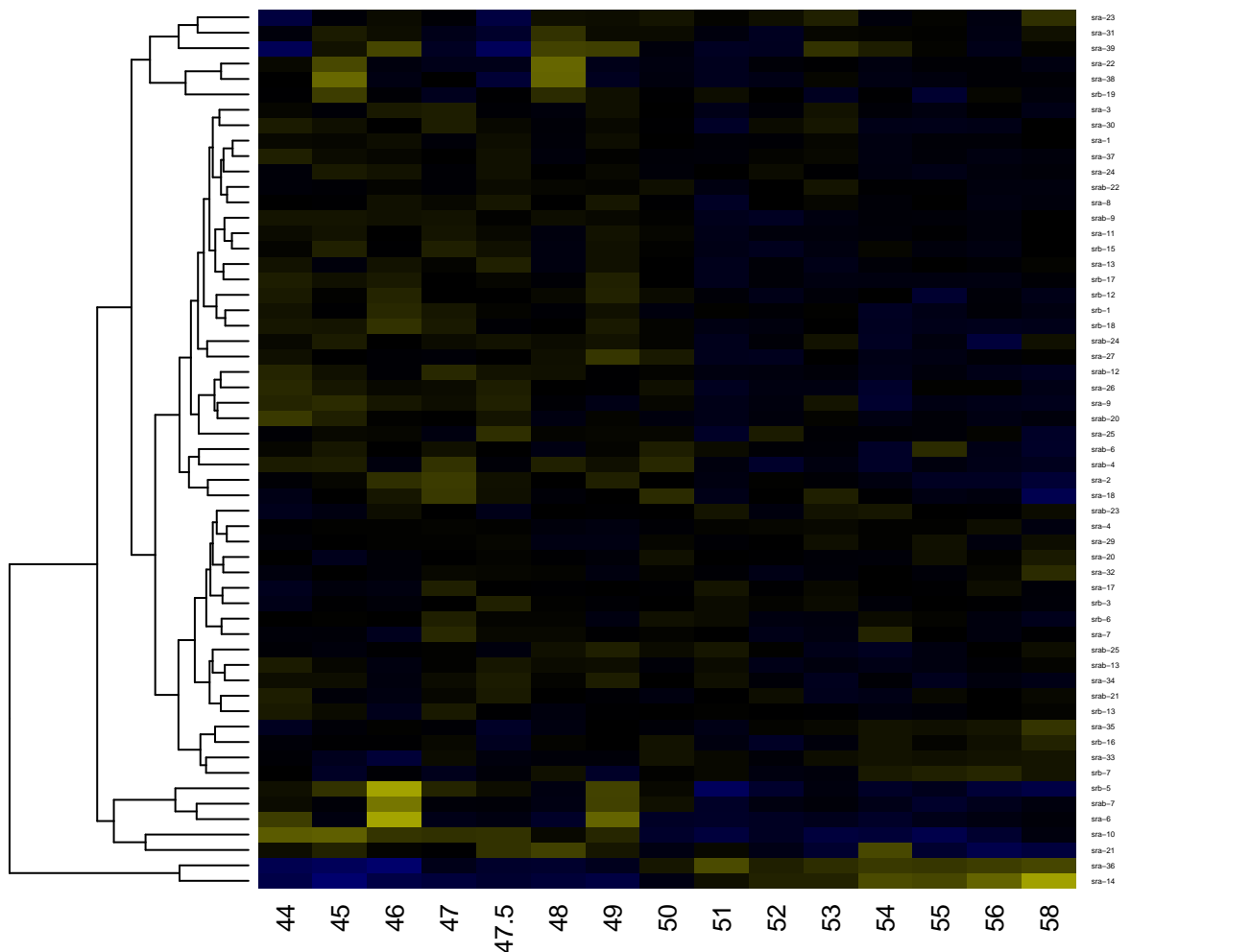
7 transmembrane receptor (rhodopsin family)



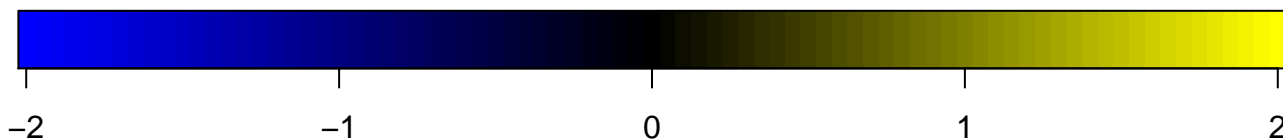
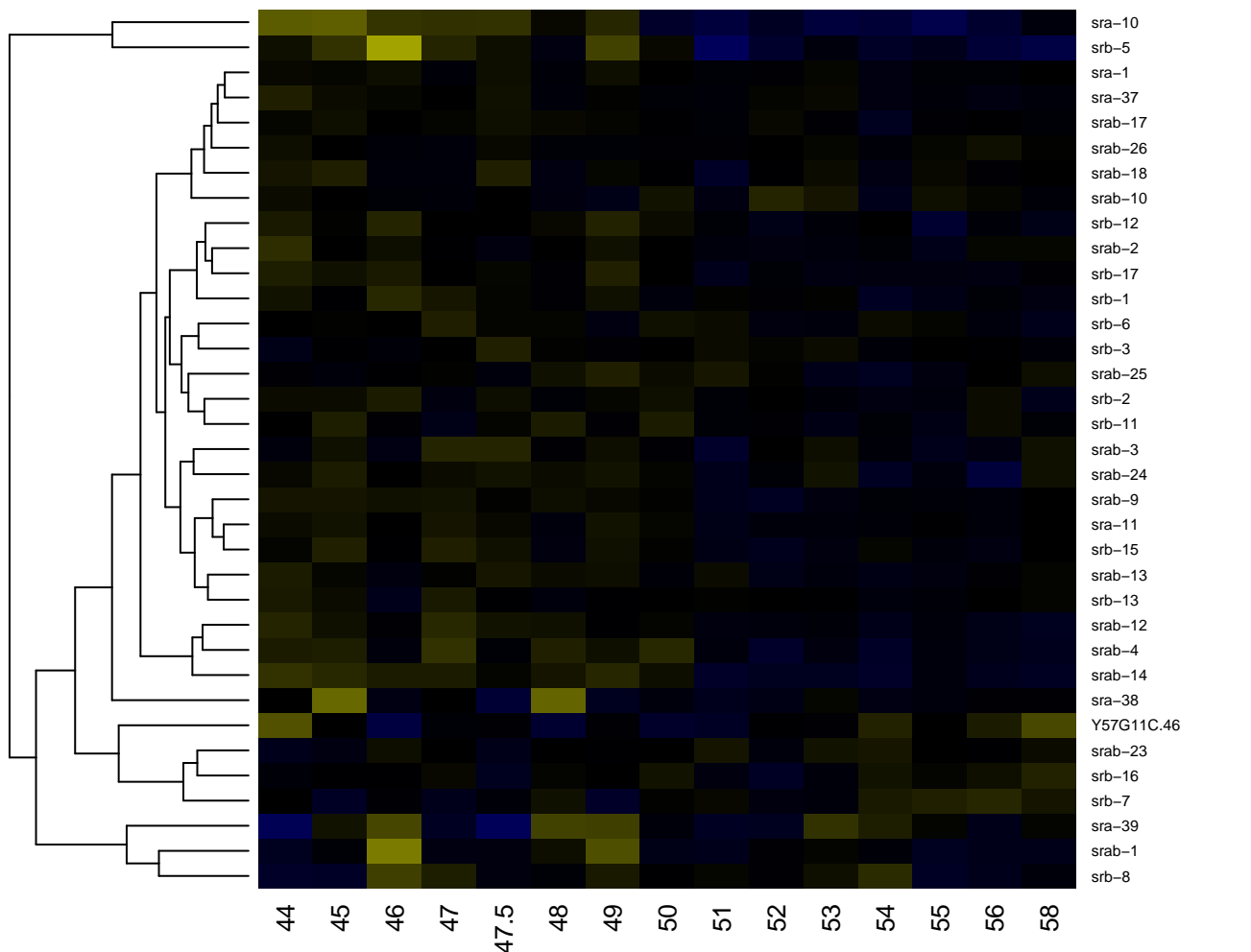
7TM GPCR , serpentine receptor class u (Sru), Nematode



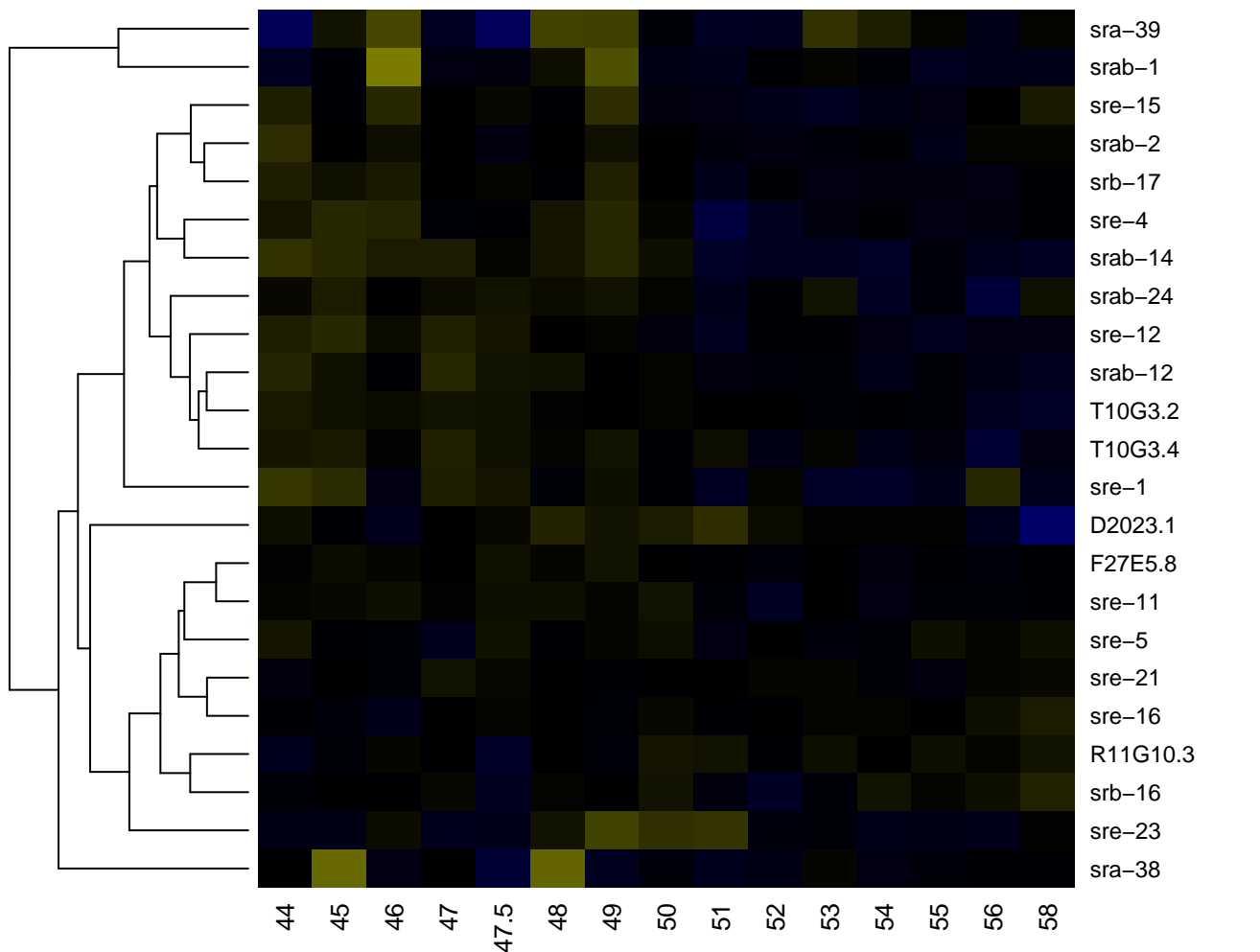
7TM GPCR , serpentine receptor class a (Sra), Nematode



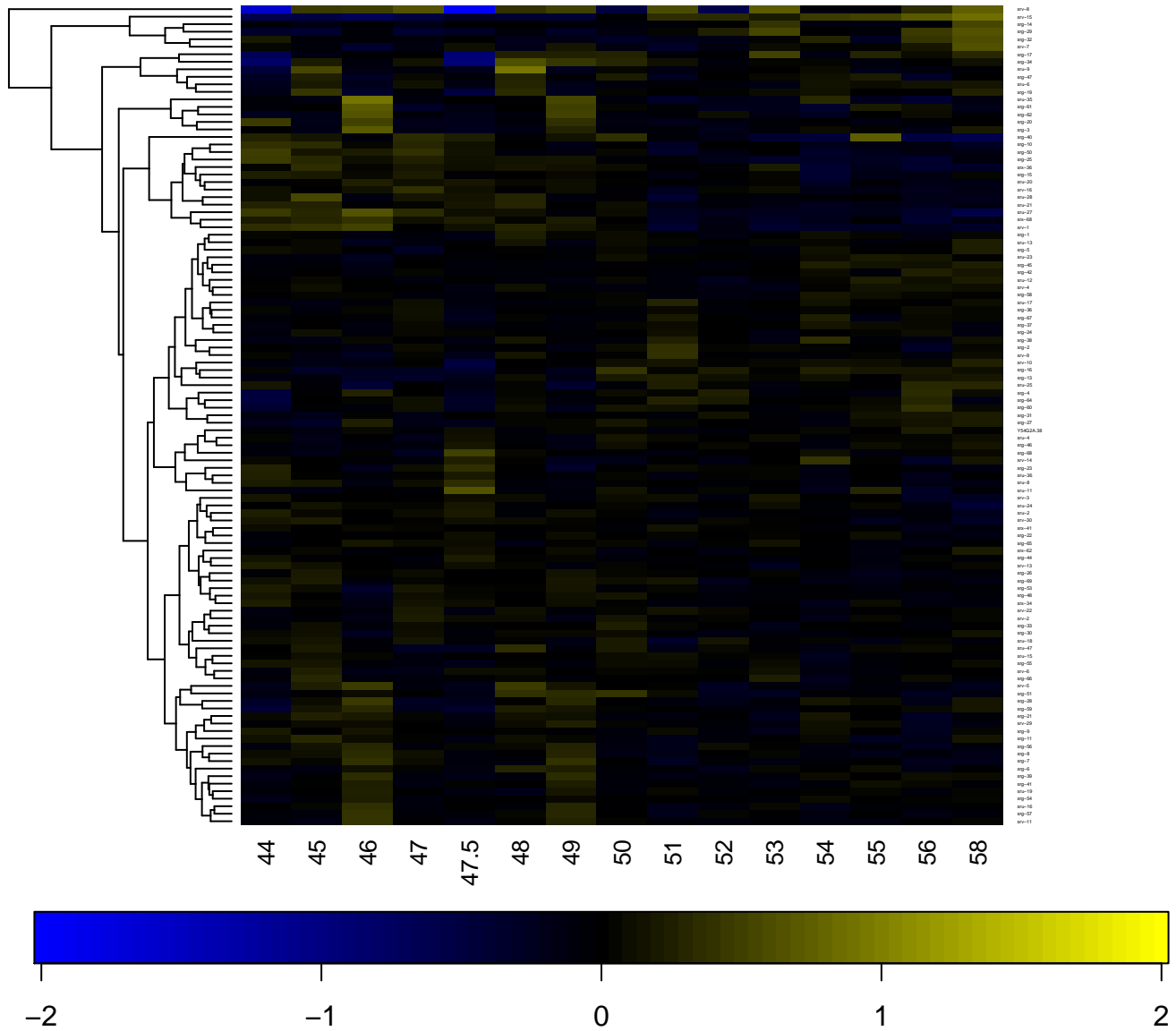
7TM GPCR , serpentine receptor class b (Srb), Nematode



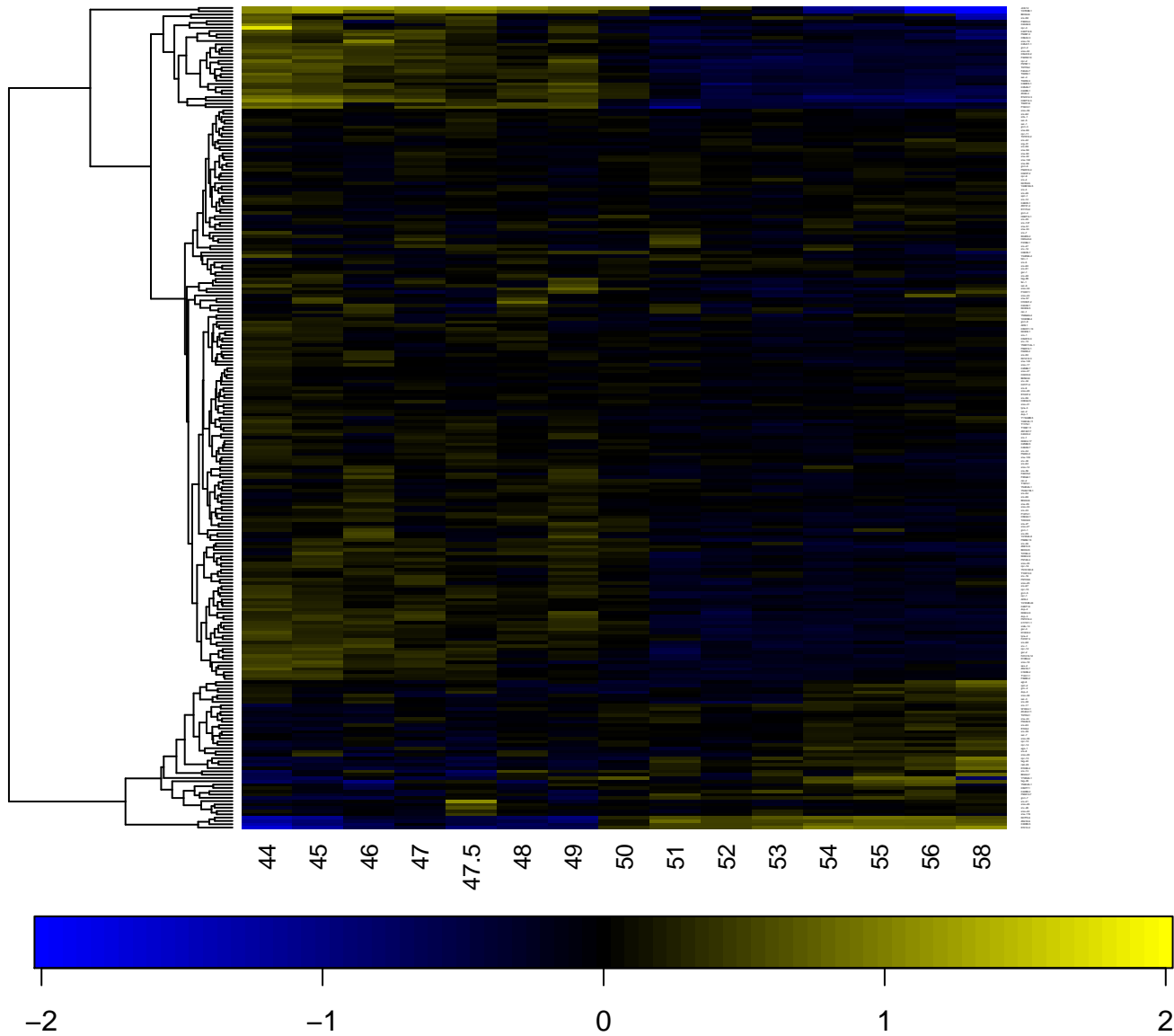
7TM GPCR , serpentine receptor class e (Sre), Nematode



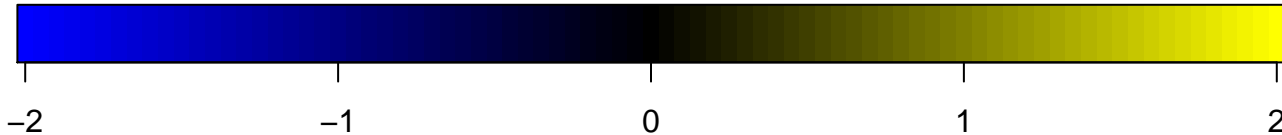
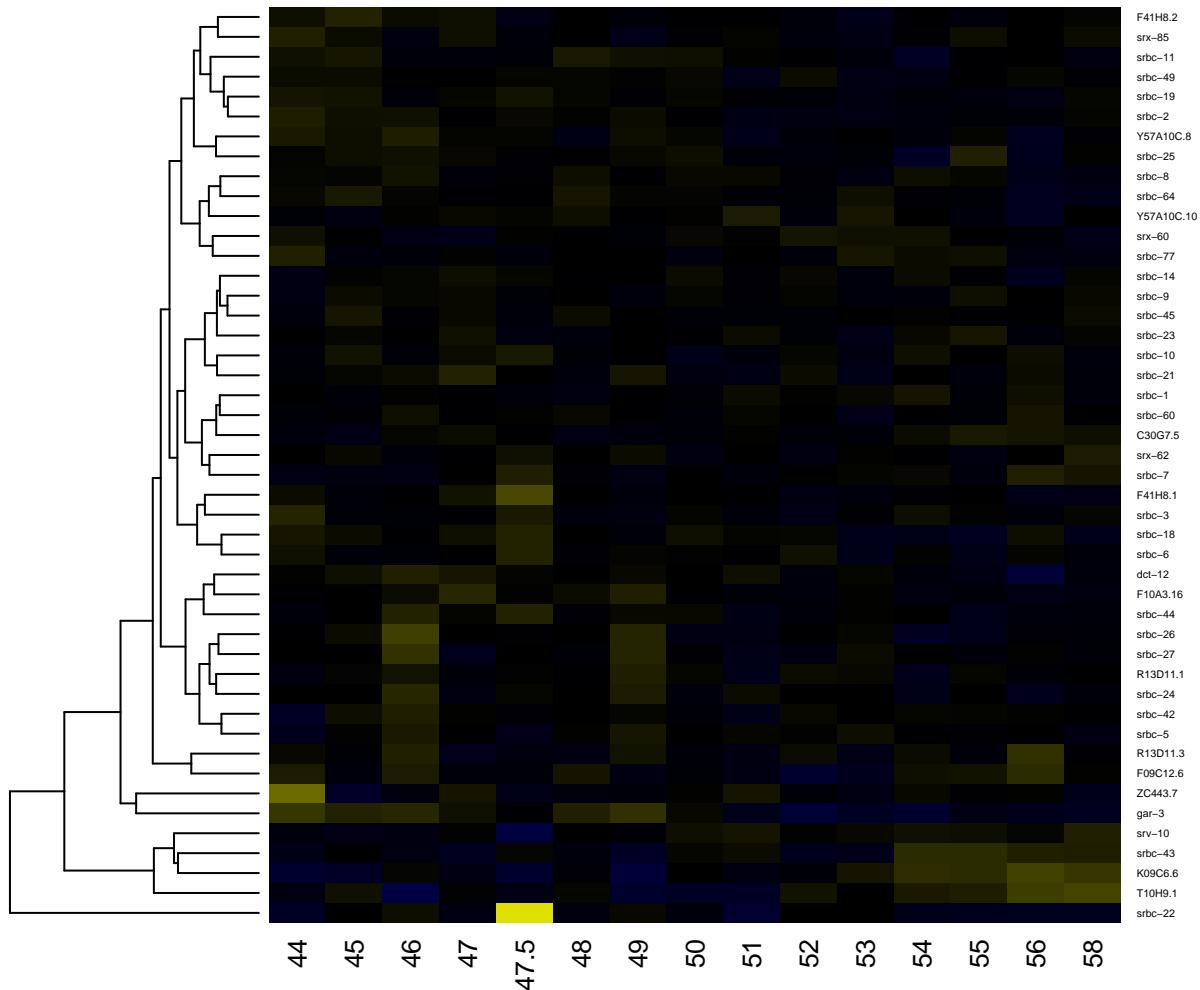
7TM GPCR , serpentine receptor class g (Srg), Nematode



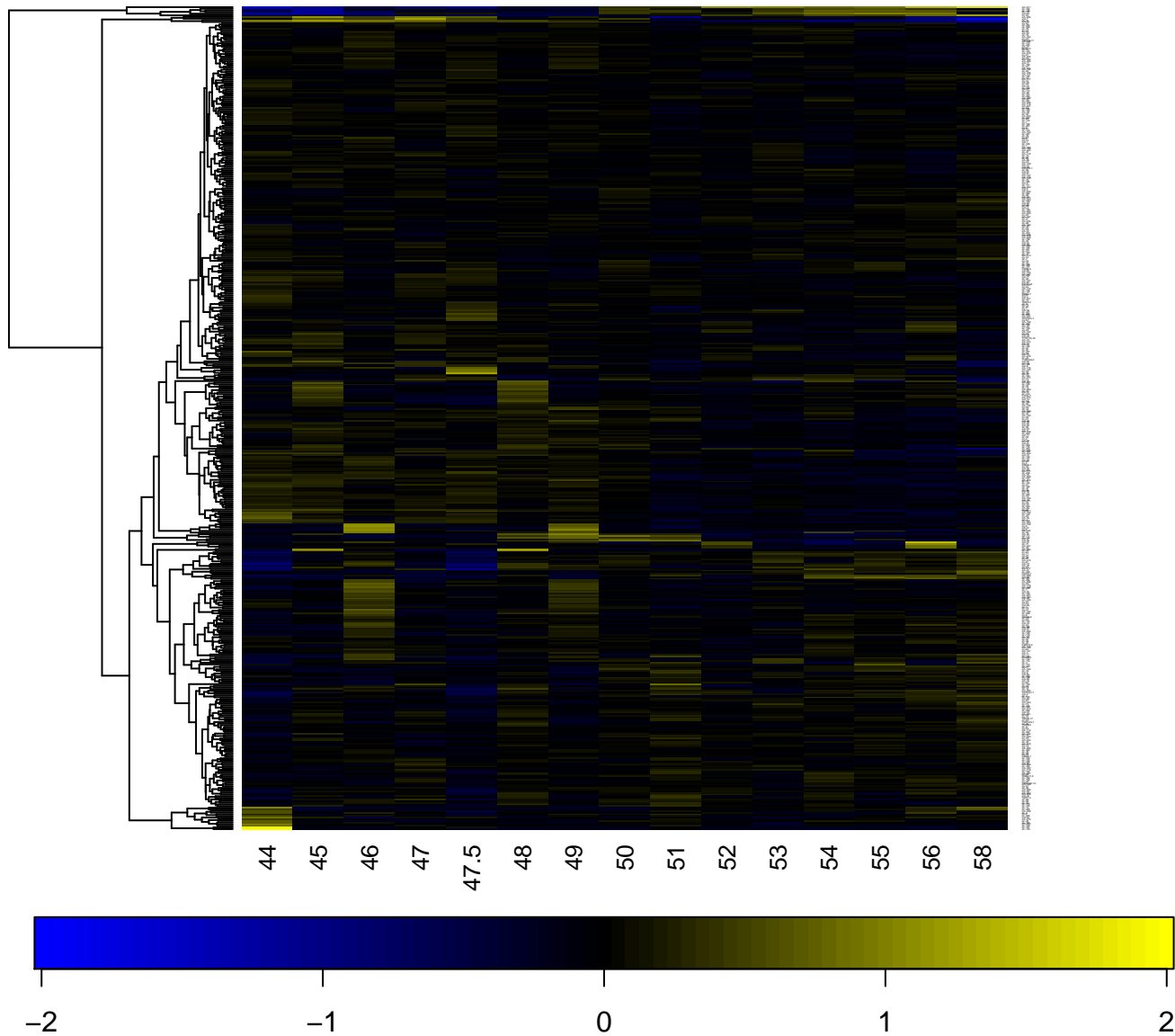
7TM GPCR, rhodopsin-like



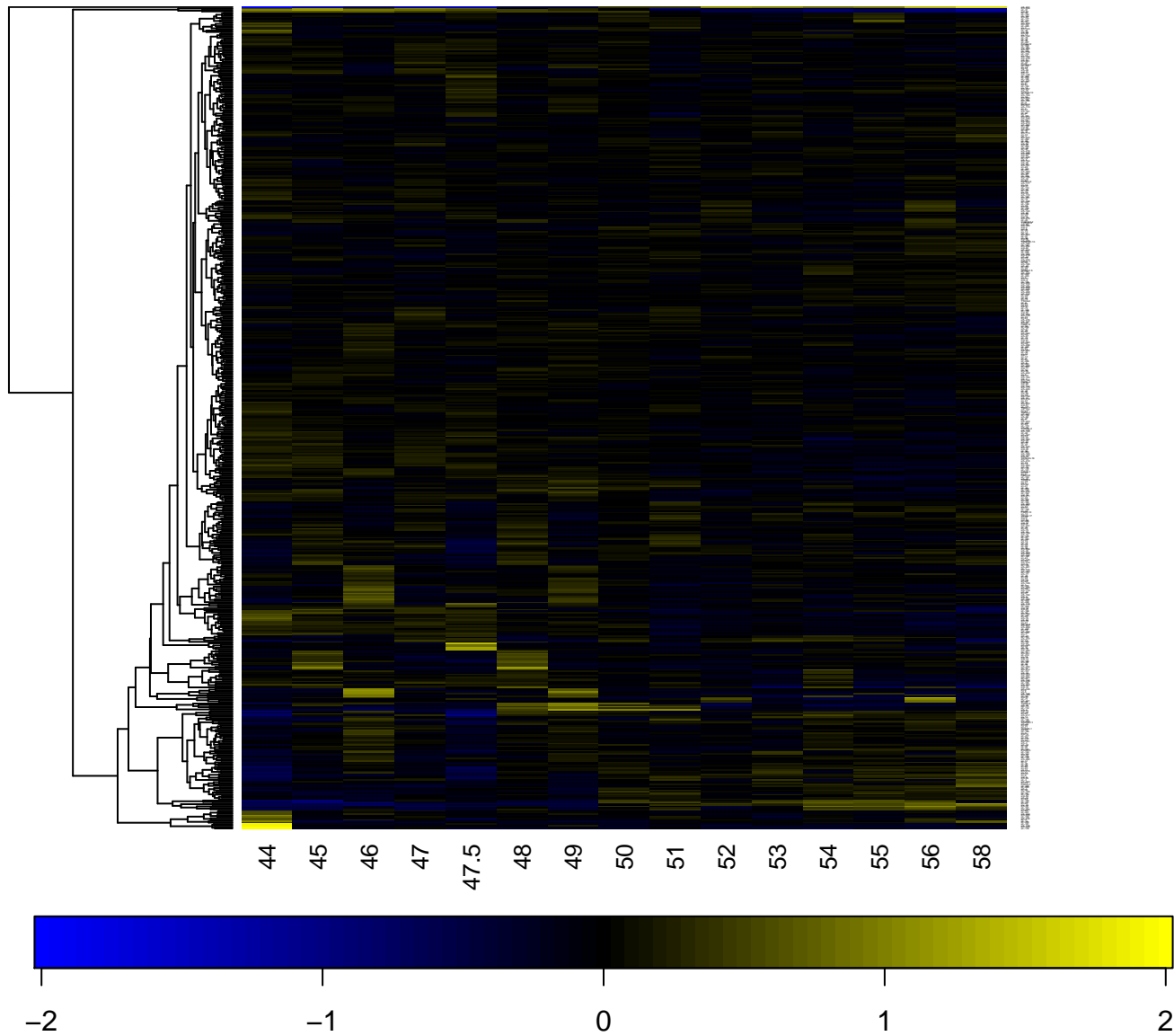
7TM GPCR, serpentine chemoreceptor Srbc



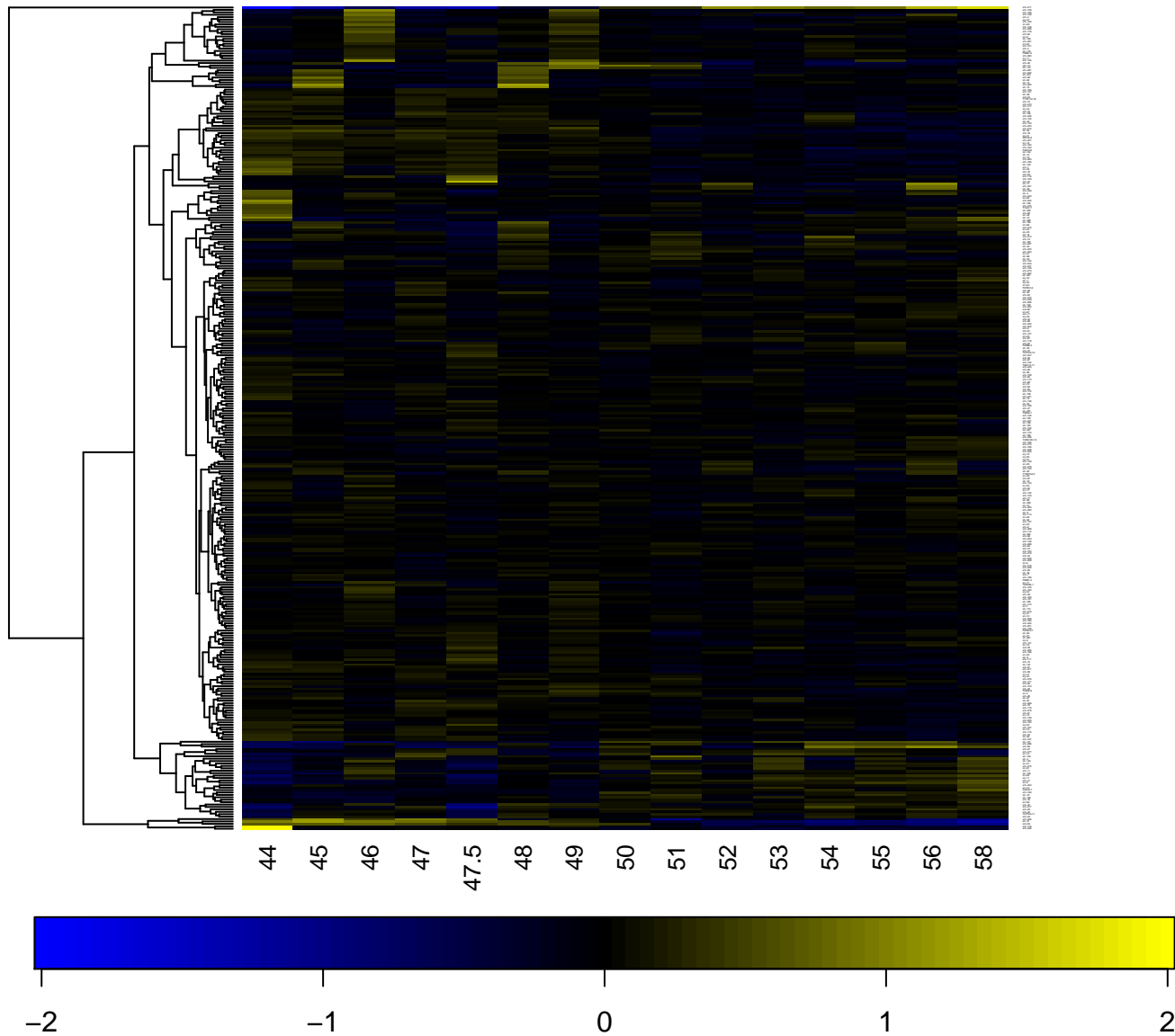
7TM GPCR, serpentine chemoreceptor Srd



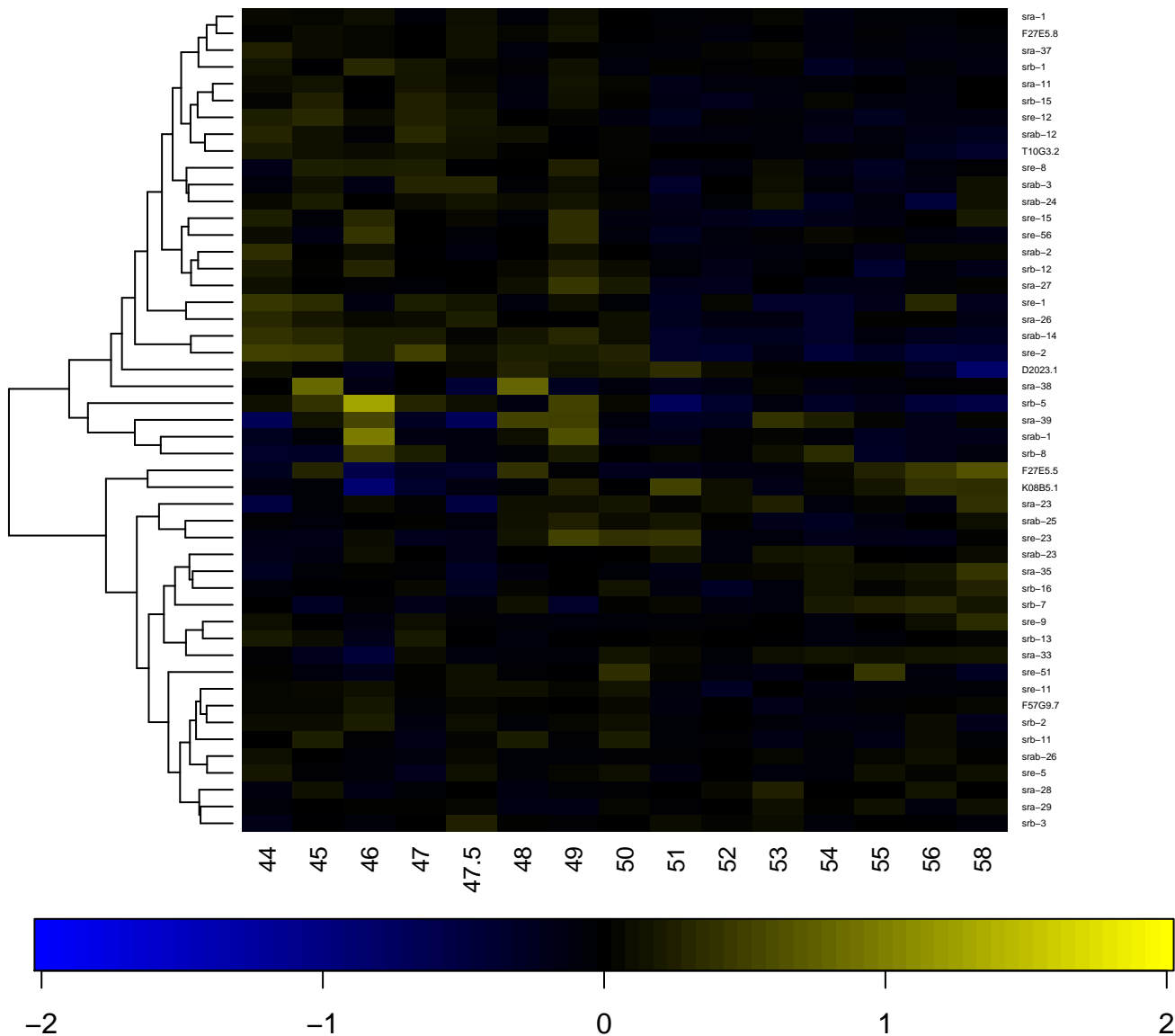
7TM GPCR, serpentine chemoreceptor Srh



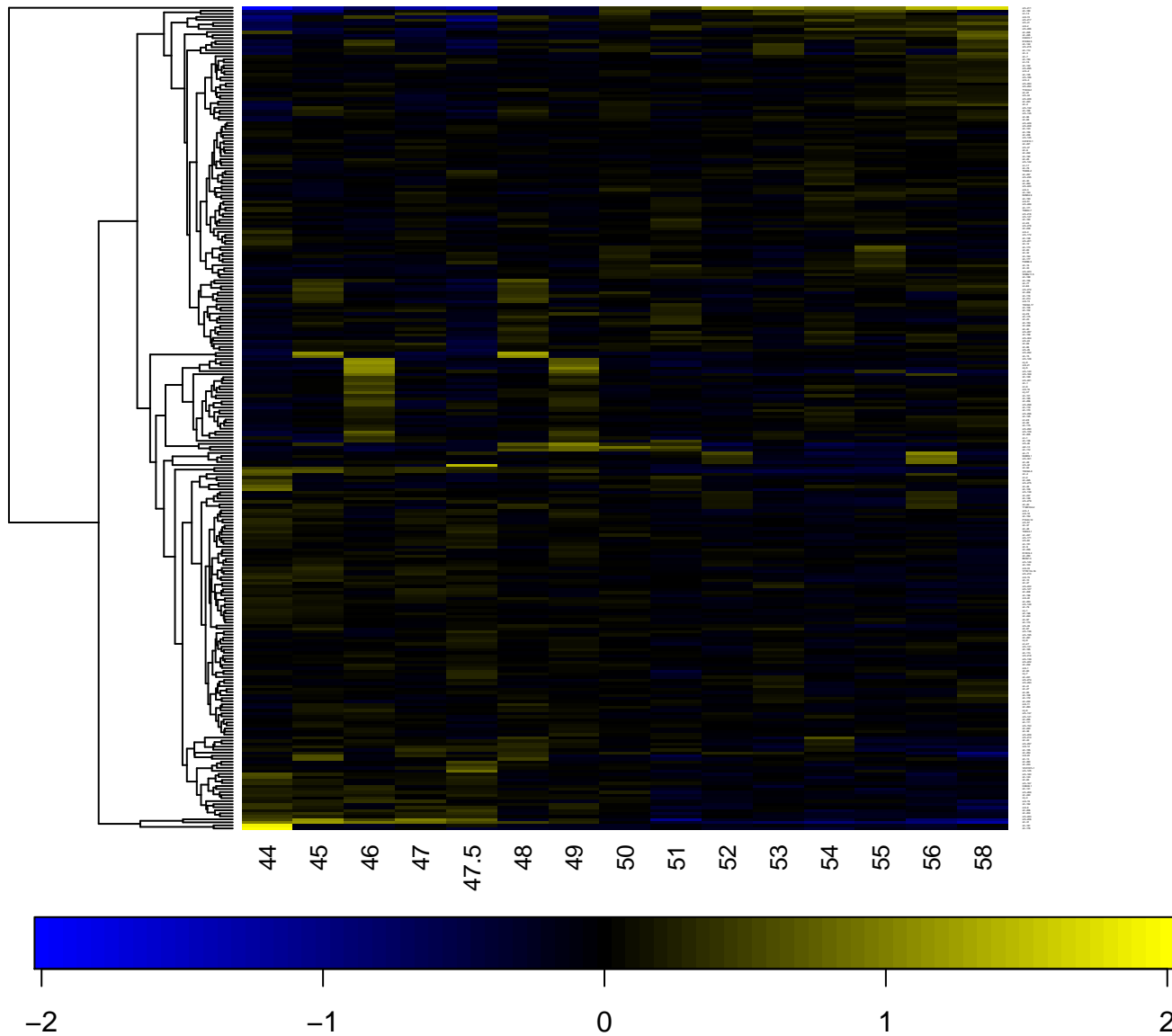
7TM GPCR, serpentine chemoreceptor Sri



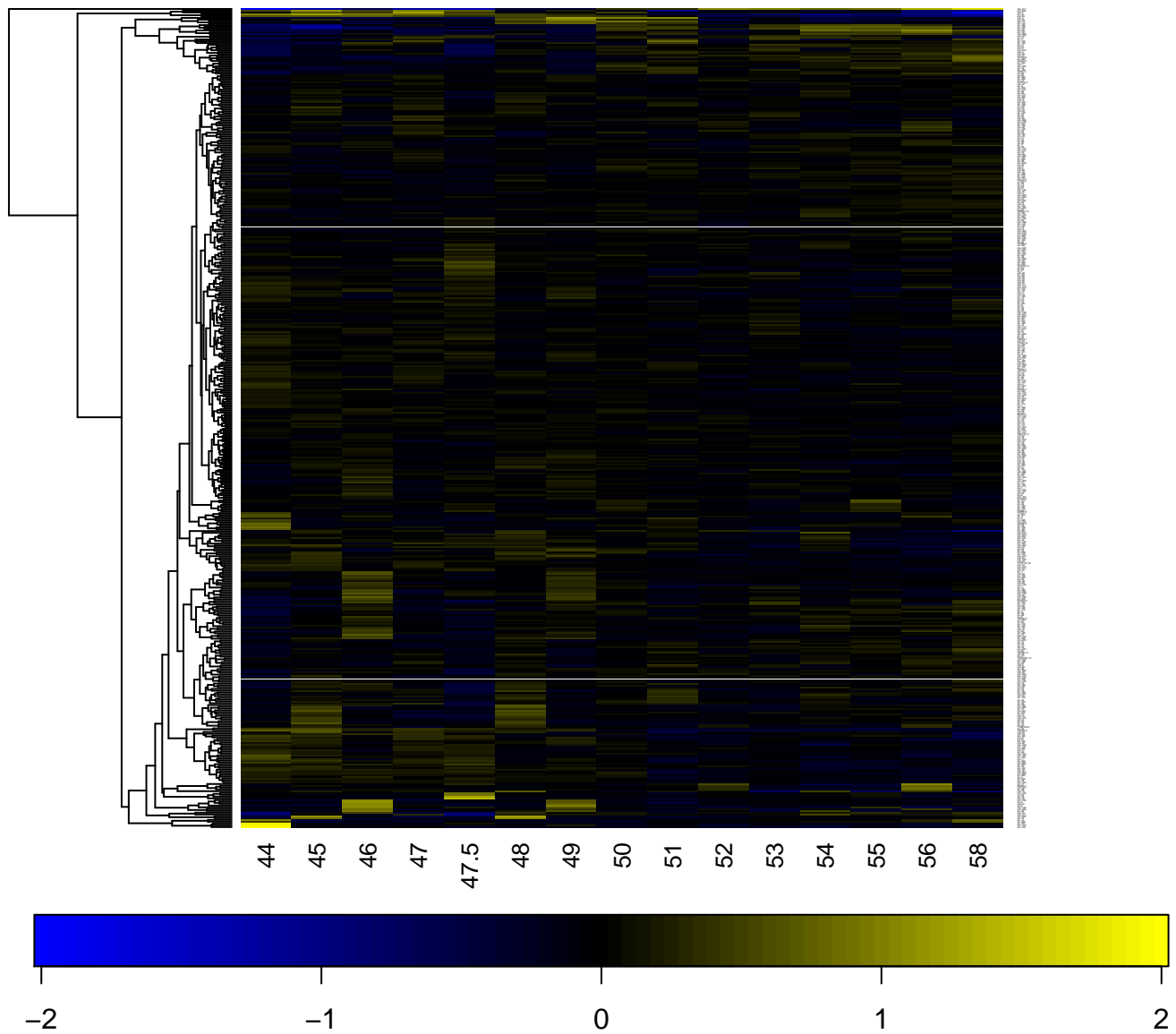
7TM GPCR, serpentine chemoreceptor, Srab



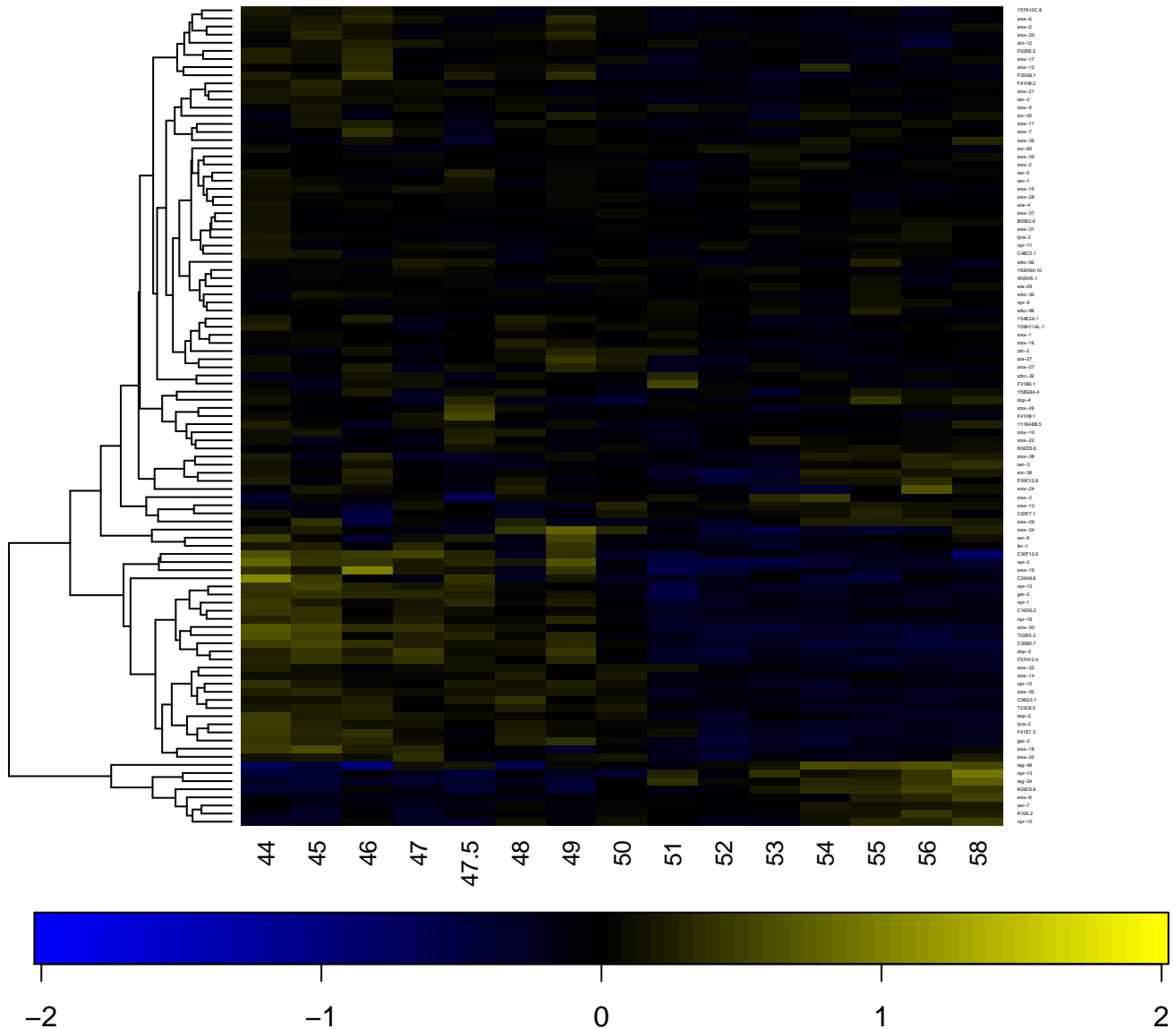
7TM GPCR, serpentine receptor class j (Srj), Nematode



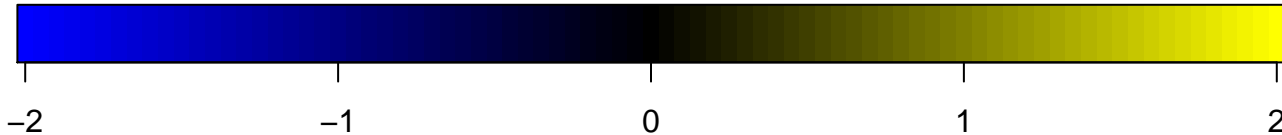
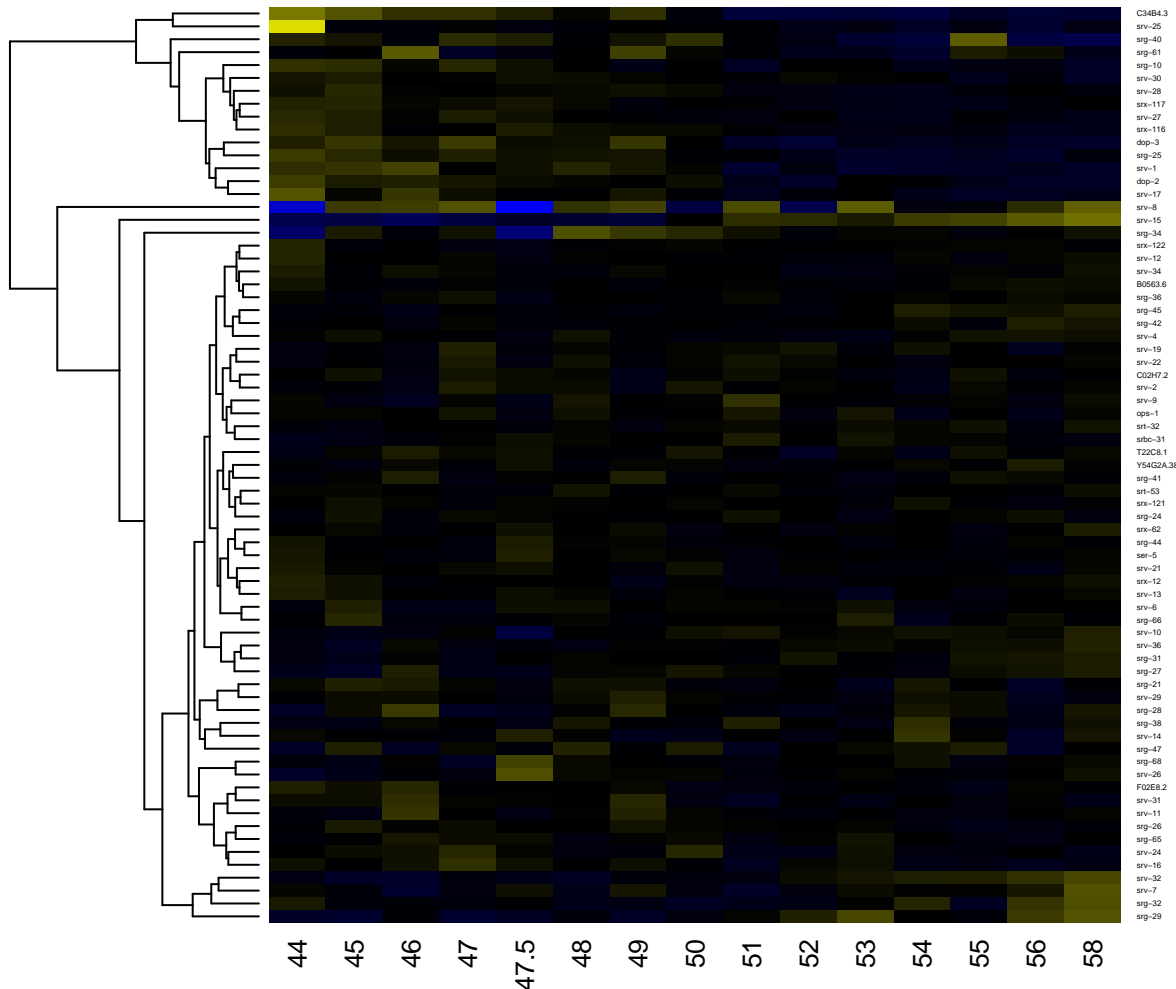
7TM GPCR, serpentine receptor class r (Str), Nematode



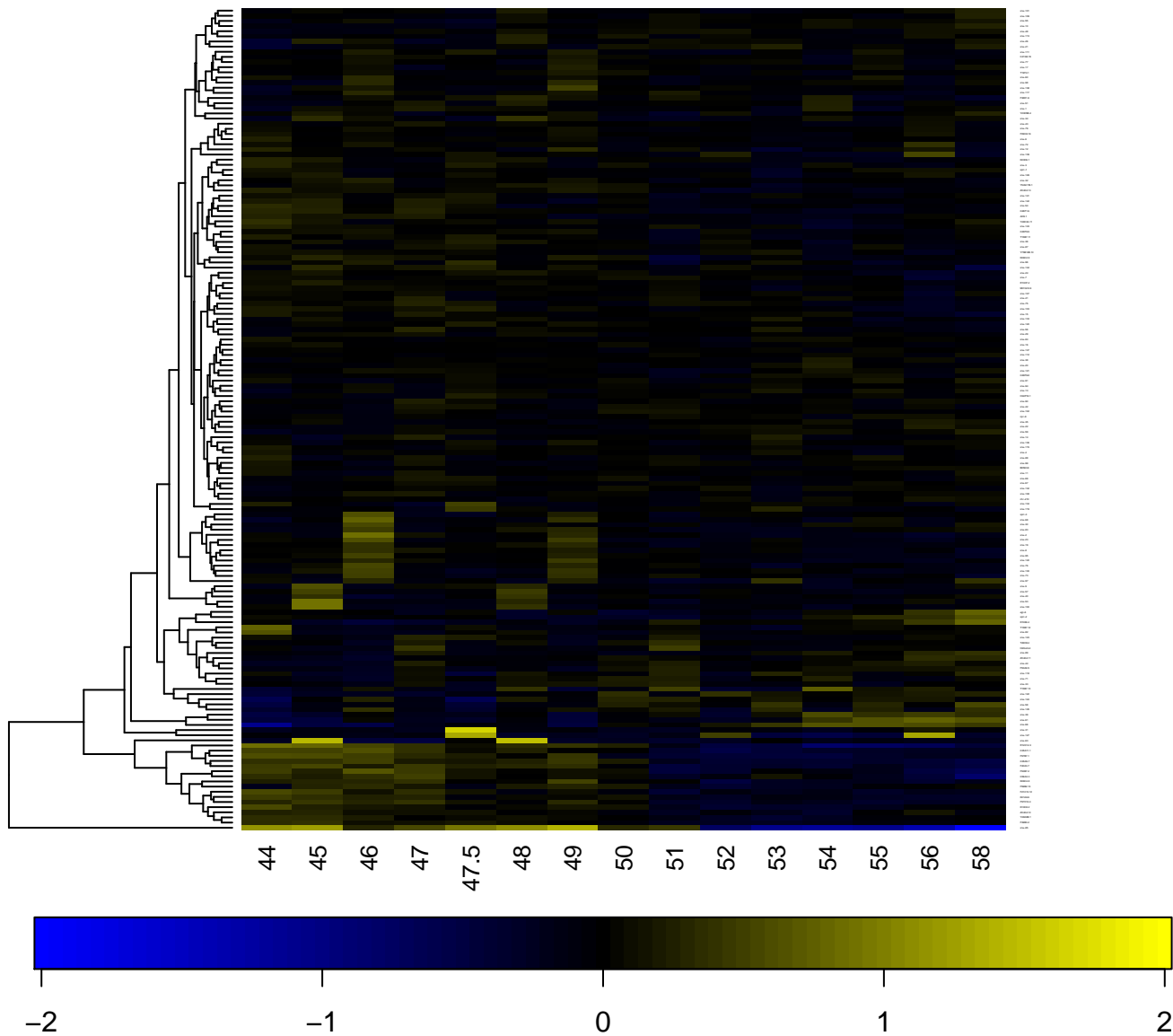
7TM GPCR, serpentine receptor class sx (Srsx)



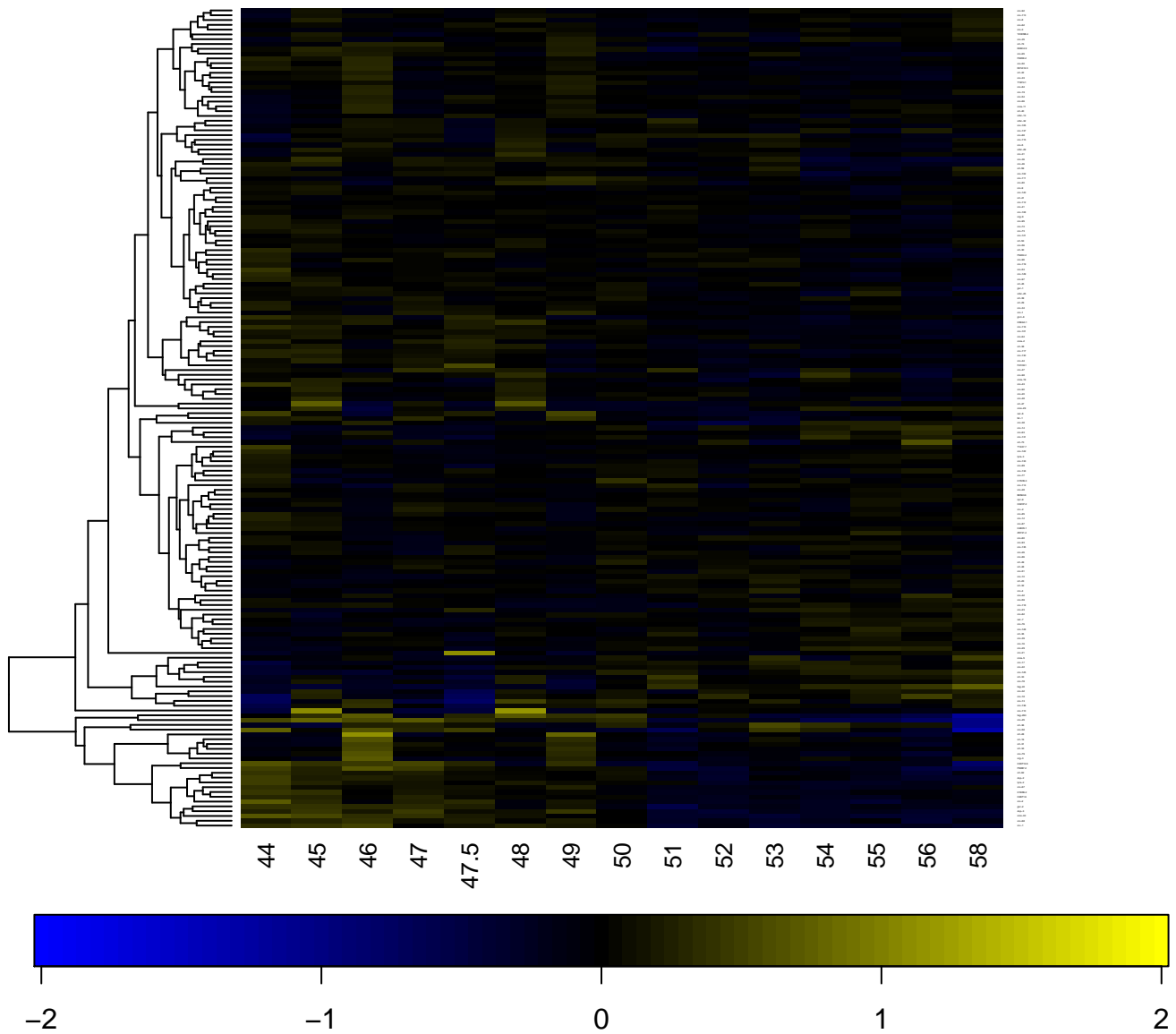
7TM GPCR, serpentine receptor class v (Srv), Nematode



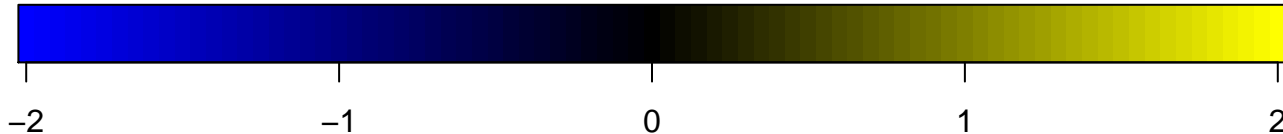
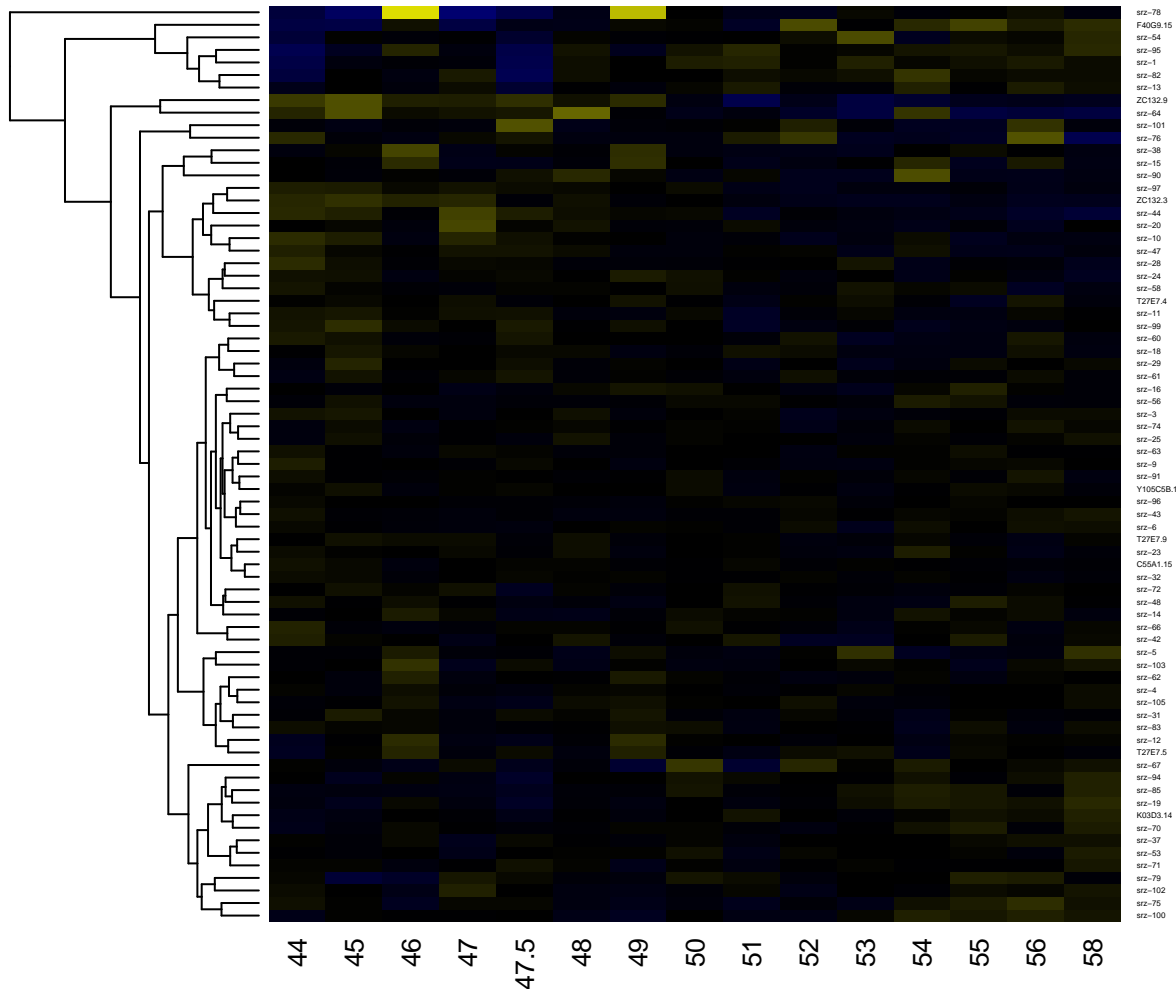
7TM GPCR, serpentine receptor class w (Srw)



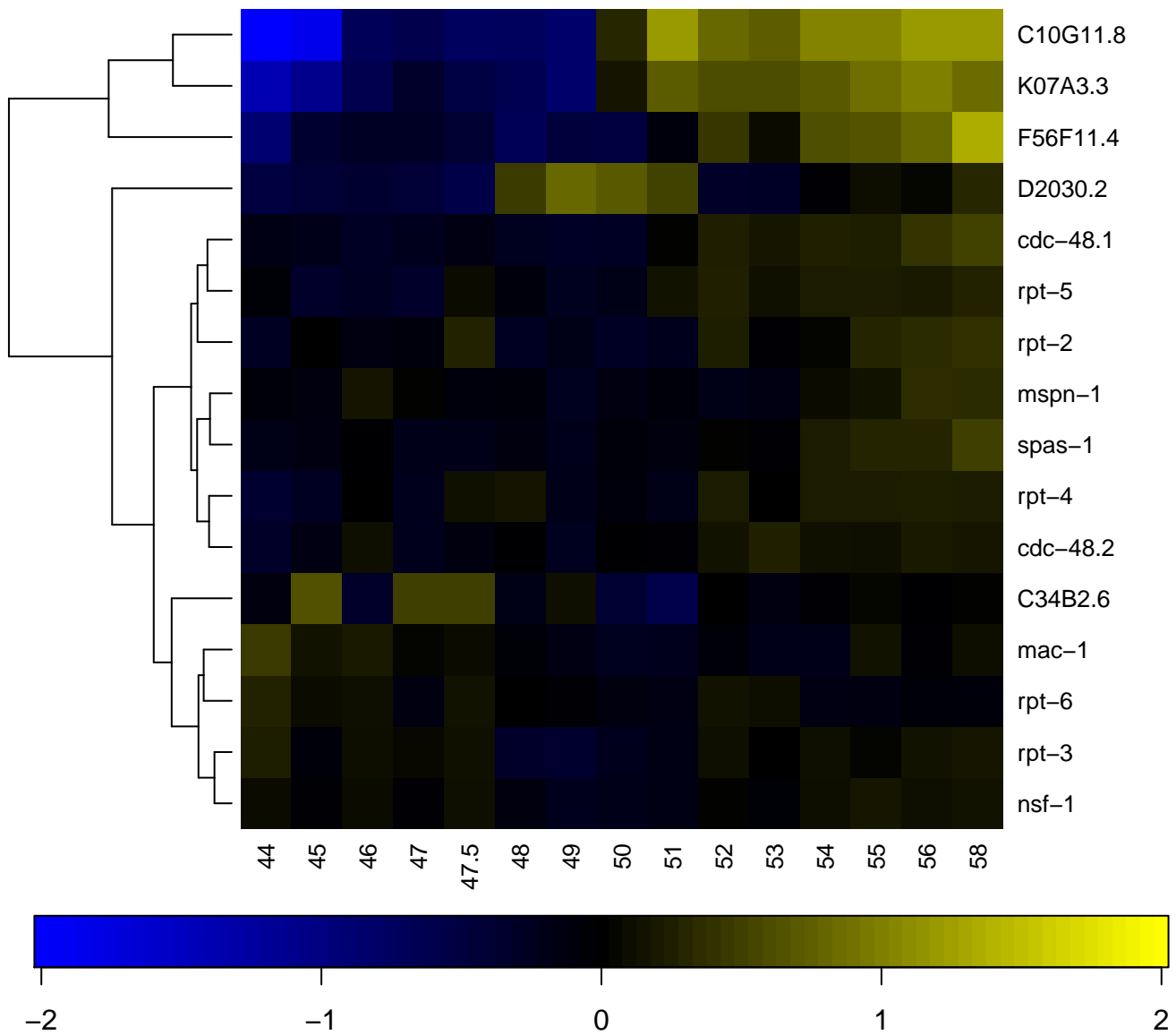
7TM GPCR, serpentine receptor class x (Srx)



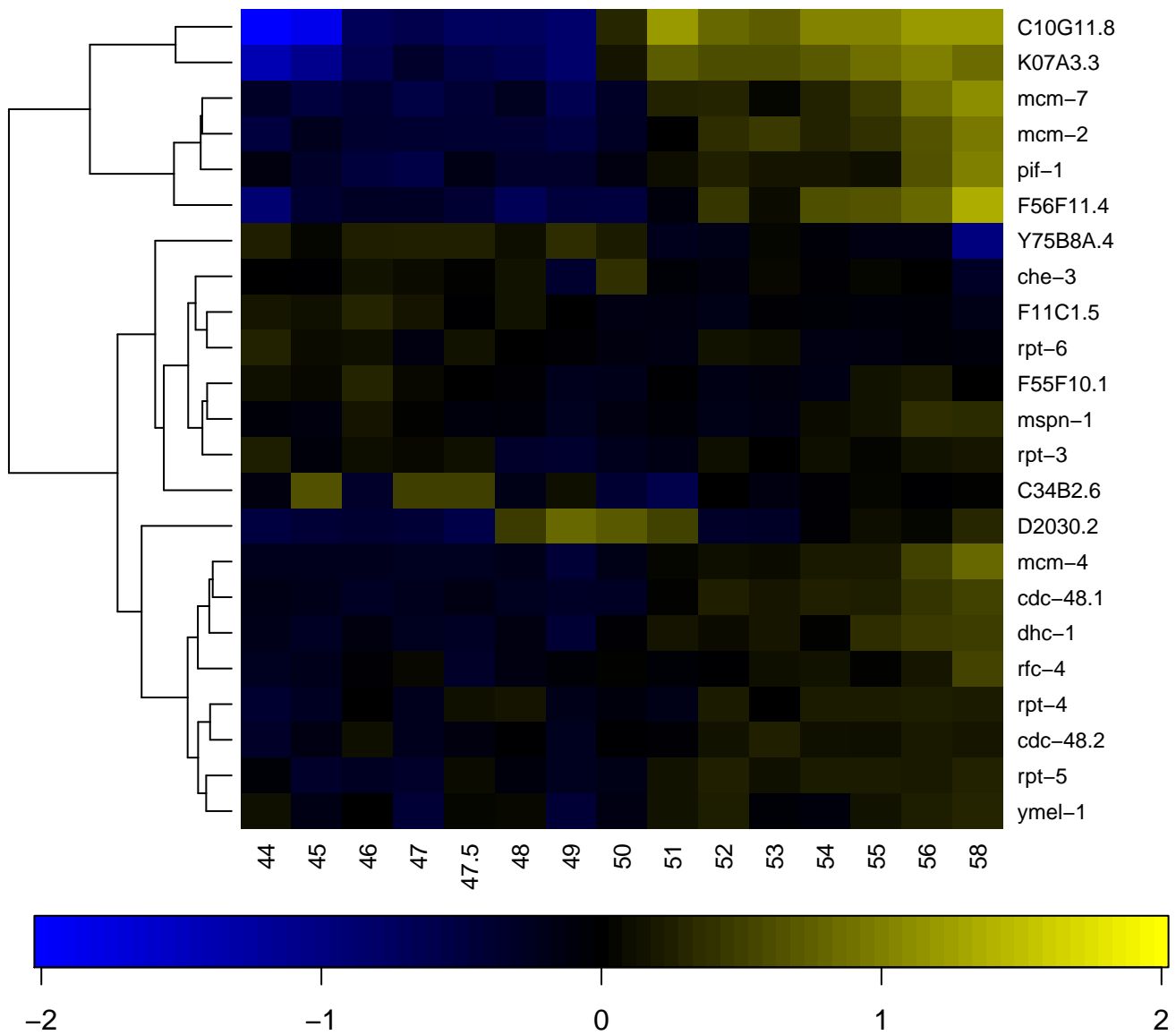
7TM GPCR, serpentine receptor class z (Srz), Nematode



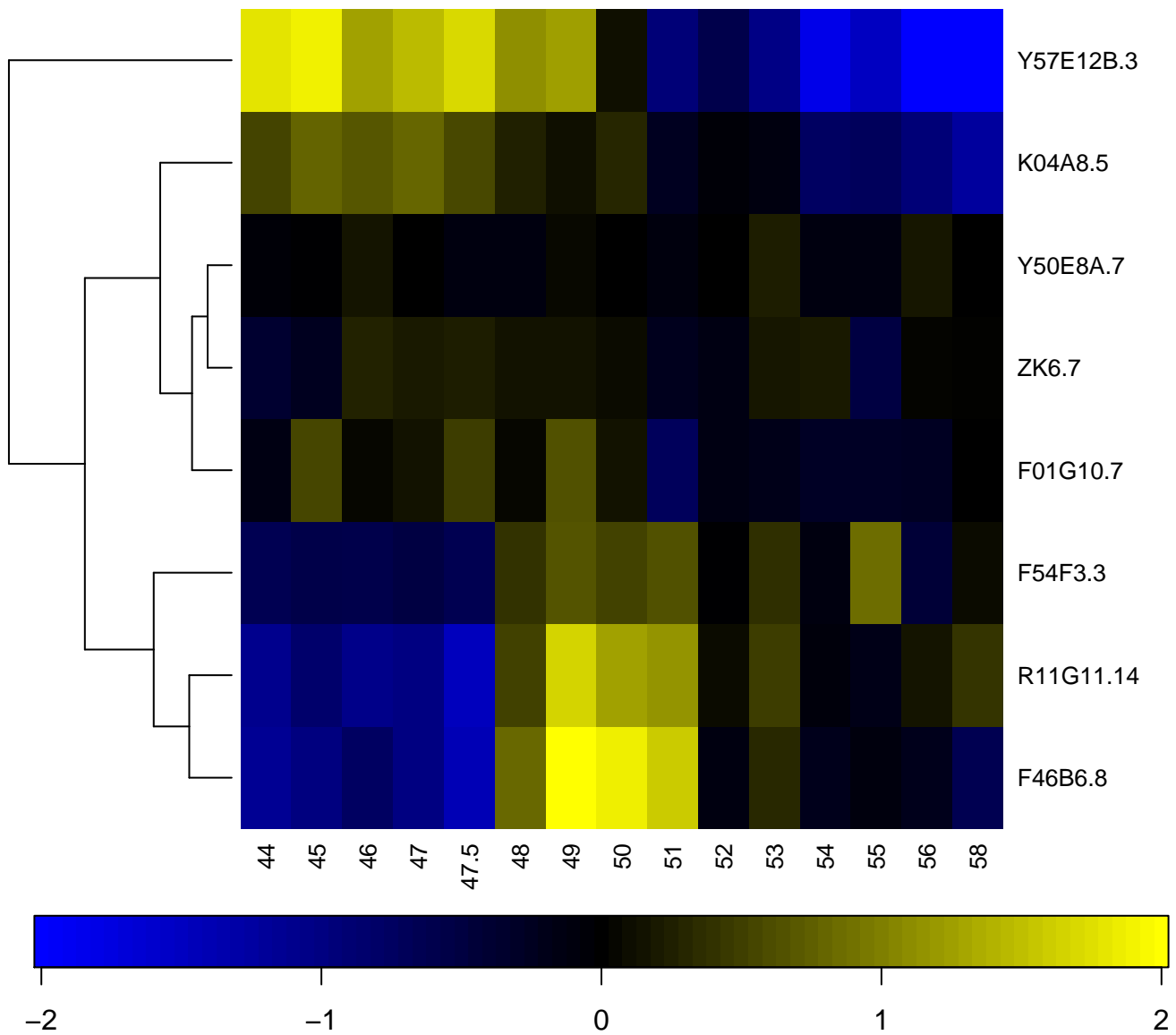
AAA domain (Cdc48 subfamily)



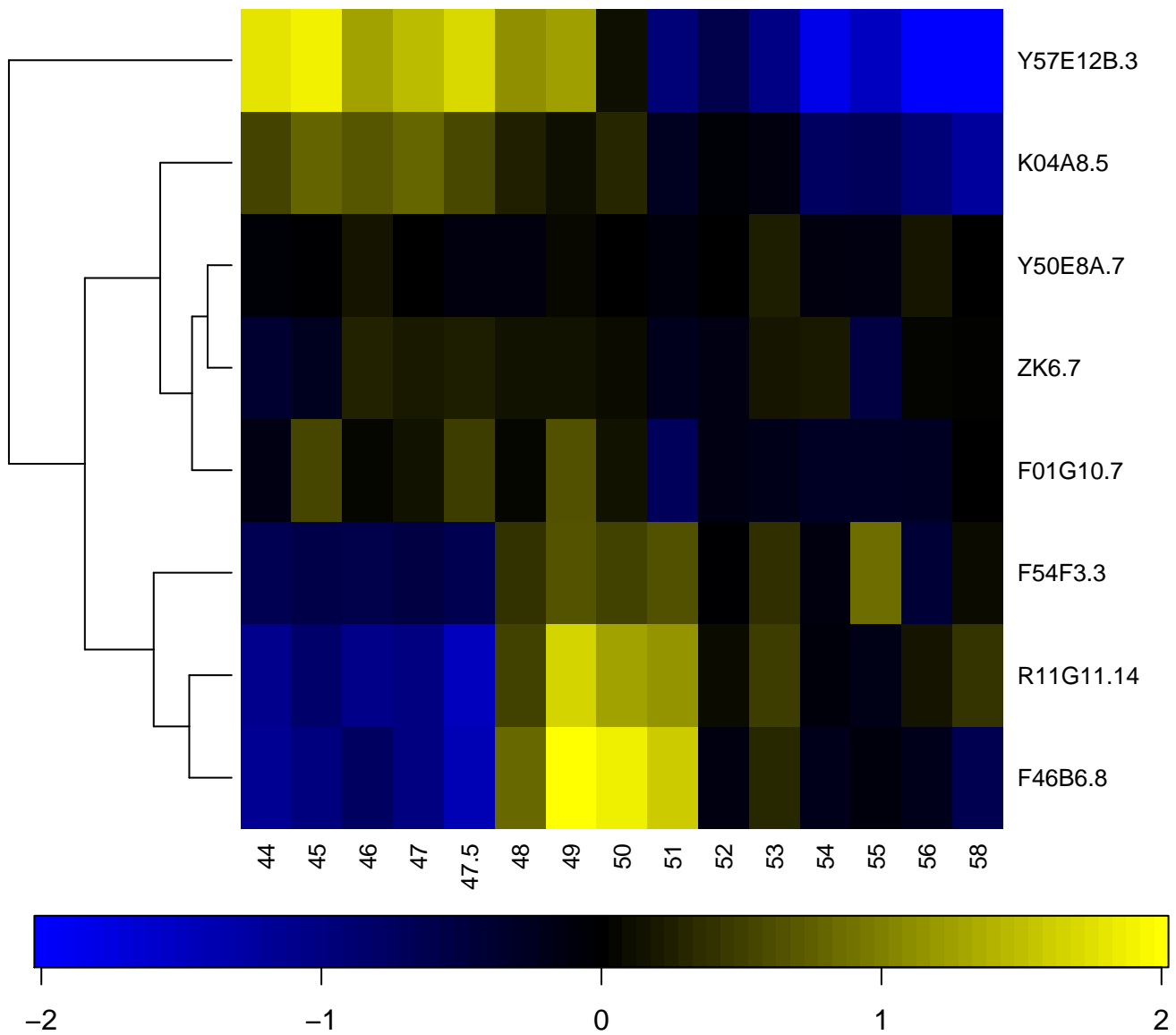
AAA domain (dynein-related subfamily)



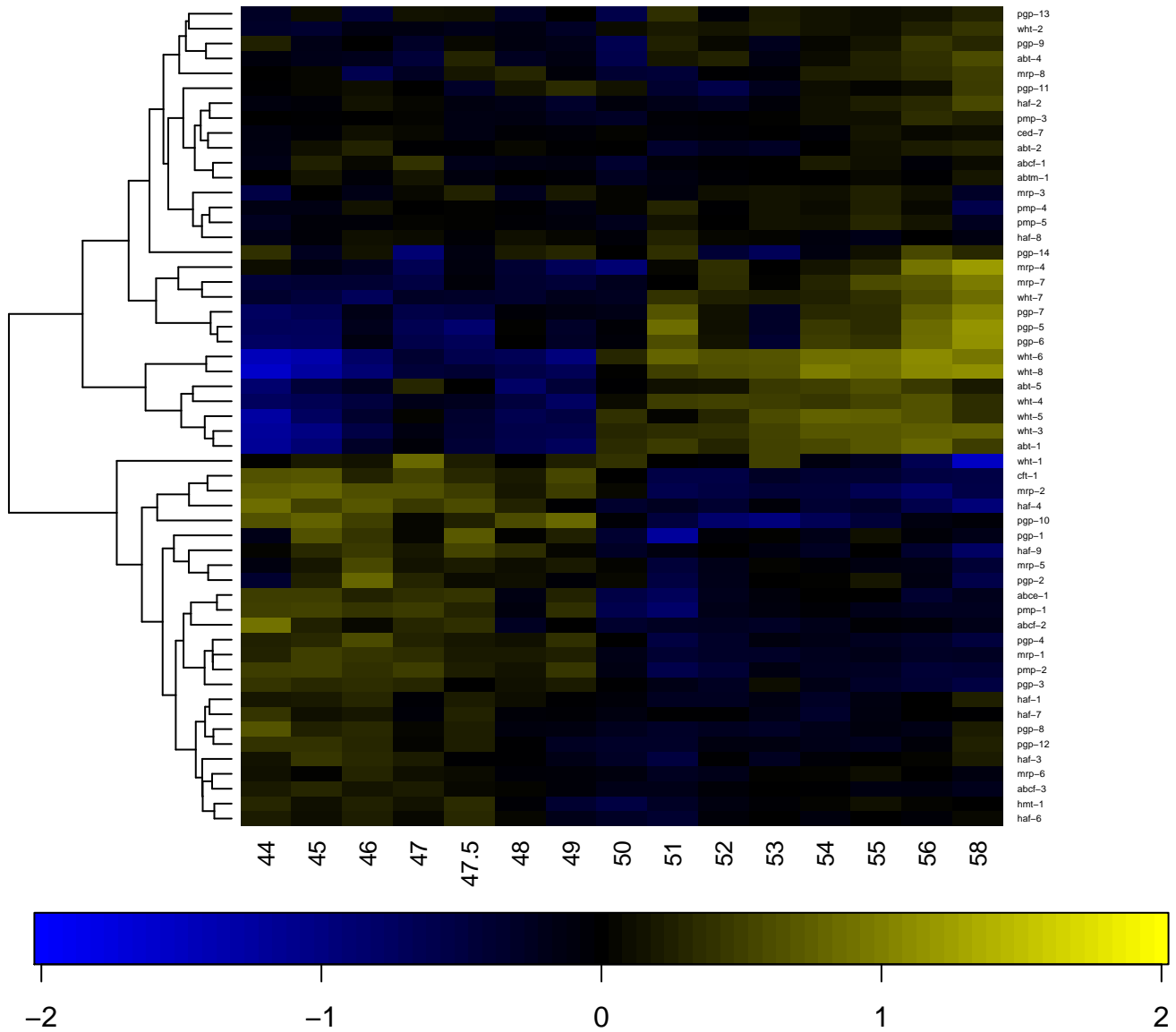
AB-hydrolase-associated lipase region



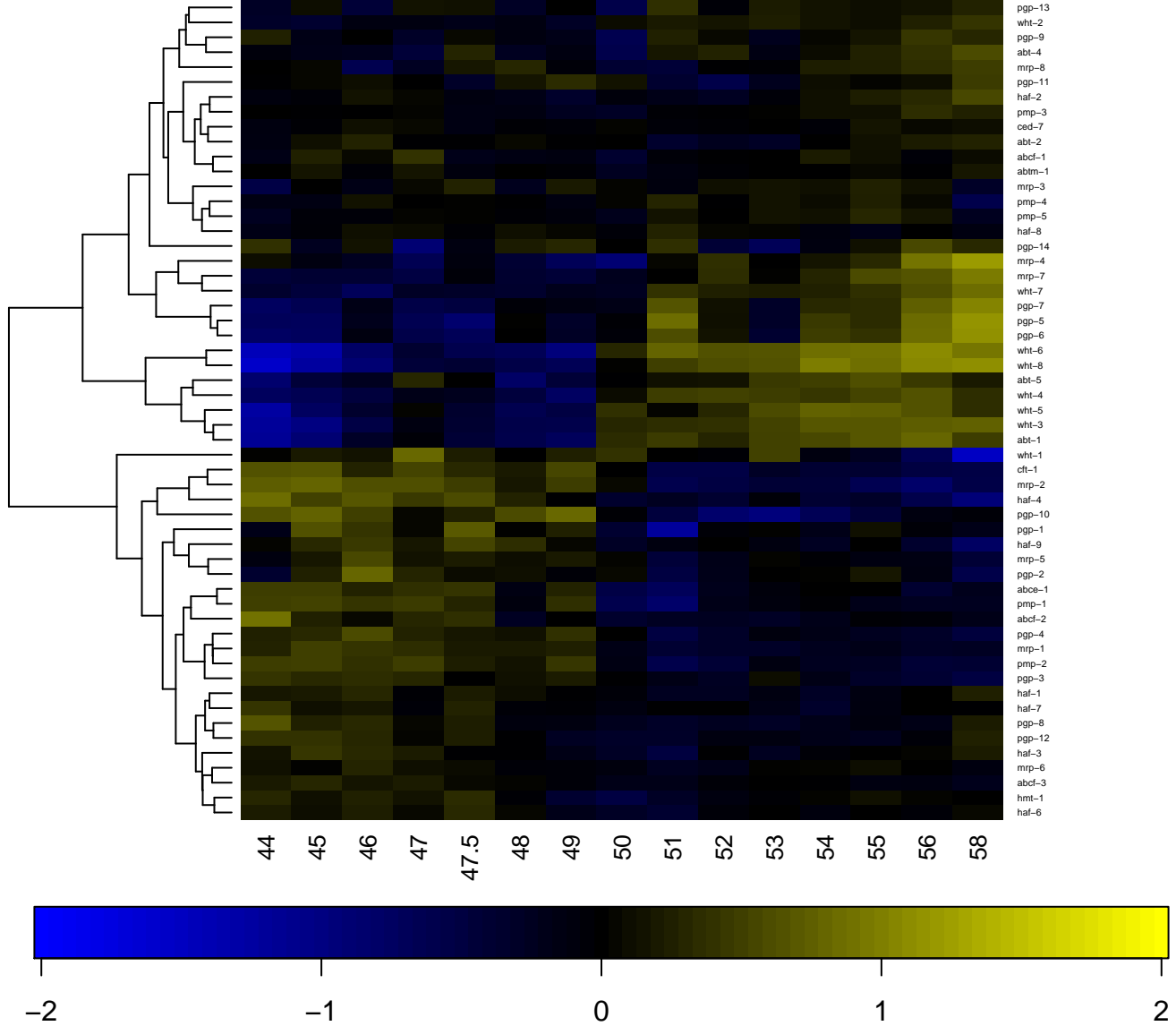
ab-hydrolase associated lipase region



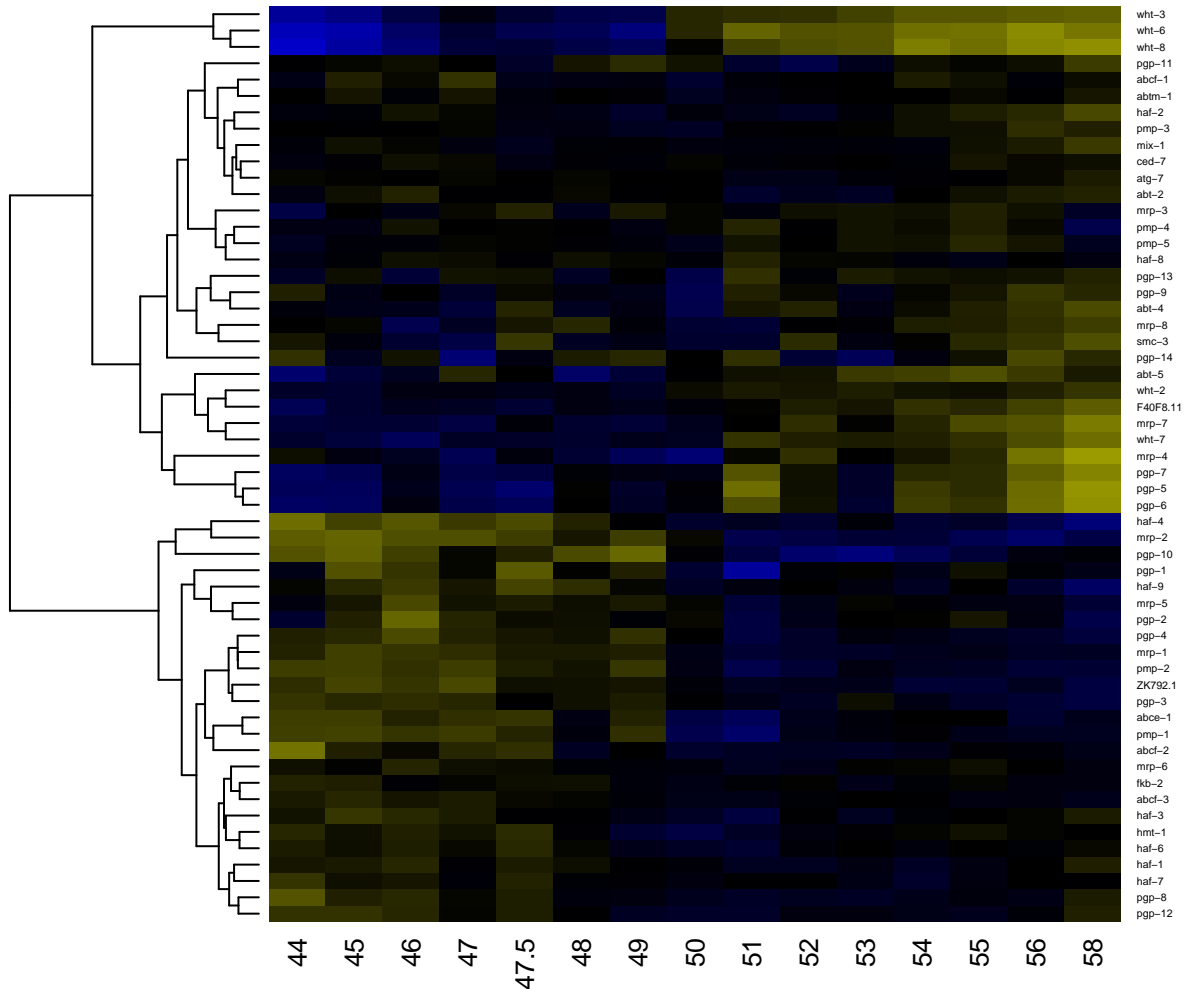
ABC transporter



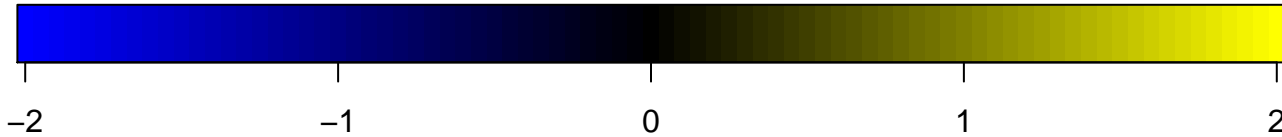
ABC transporter-like



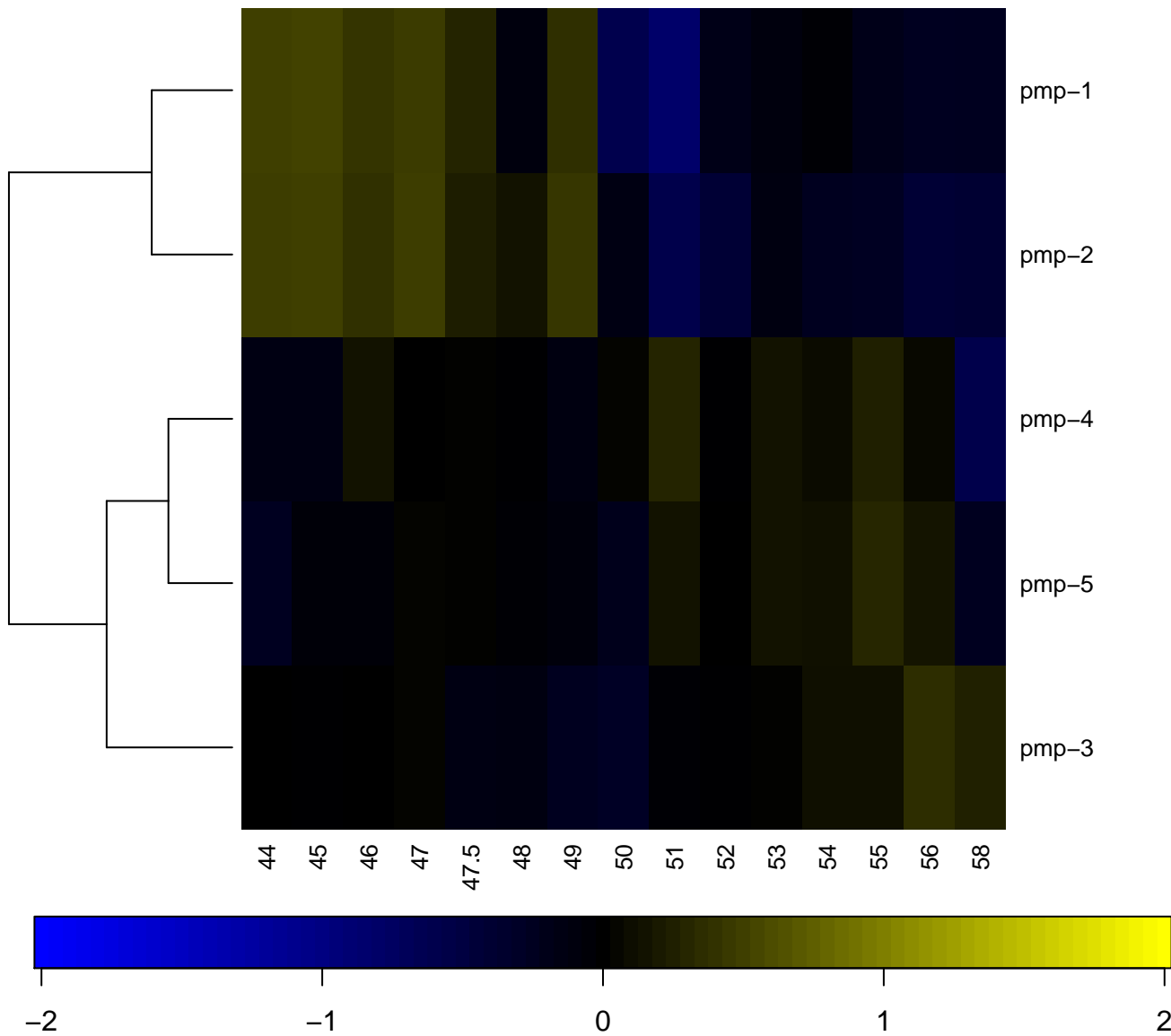
ABC transporter, conserved site



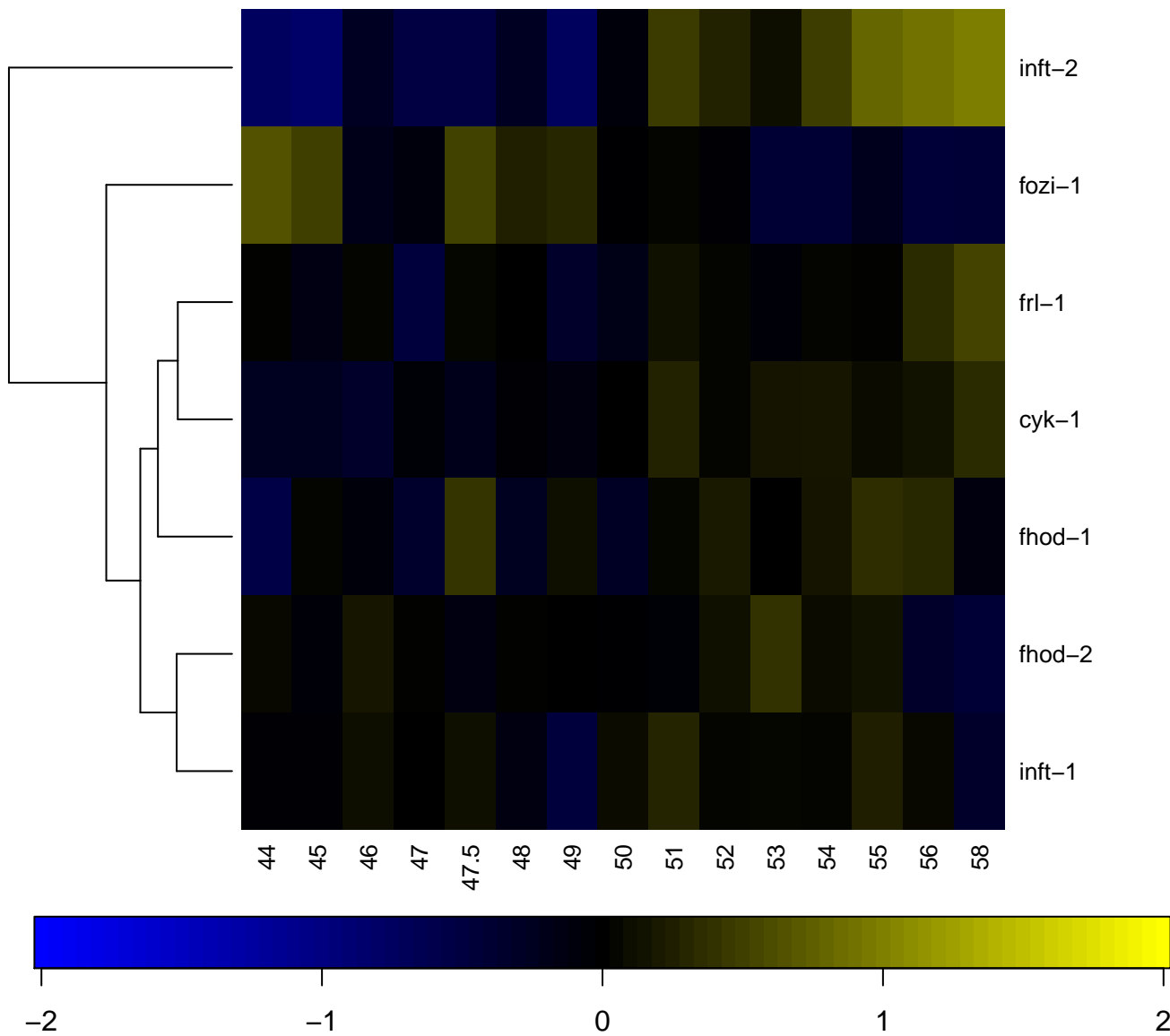
wht-3
wht-6
wht-8
pgp-11
abcf-1
abtm-1
haf-2
pmp-3
mix-1
ced-7
atg-7
abt-2
mrp-3
pmp-4
pmp-5
haf-8
pgp-13
pgp-9
abt-4
mrp-8
smc-3
pgp-14
abt-5
wht-2
F40F8.11
mrp-7
wht-7
mrp-4
pgp-7
pgp-5
pgp-6
haf-4
mrp-2
pgp-10
pgp-1
haf-9
mrp-5
pgp-2
pgp-4
mrp-1
pmp-2
ZK792.1
pgp-3
abce-1
pmp-1
abcf-2
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pgp-8
pgp-12



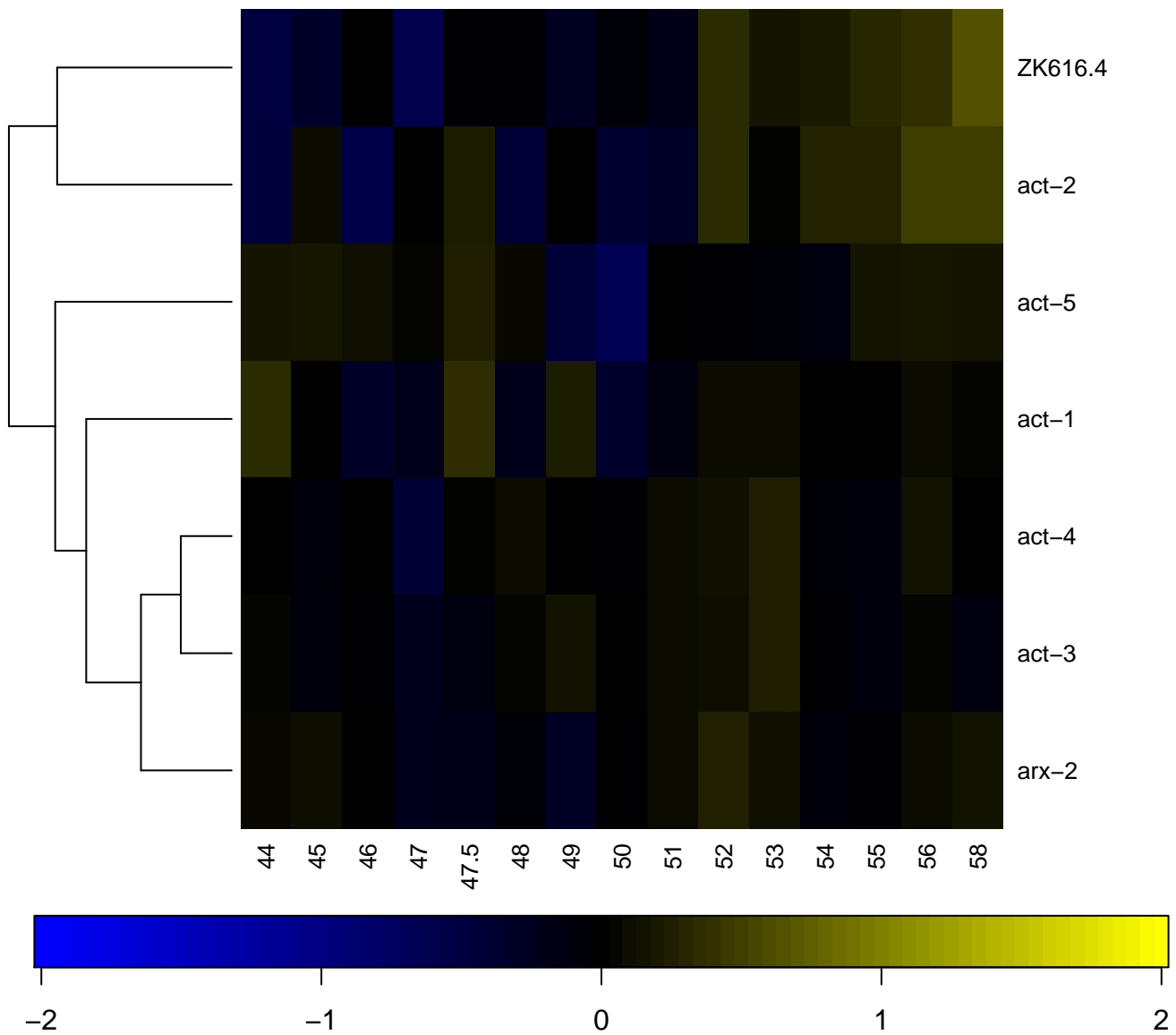
ABC transporter, N-terminal



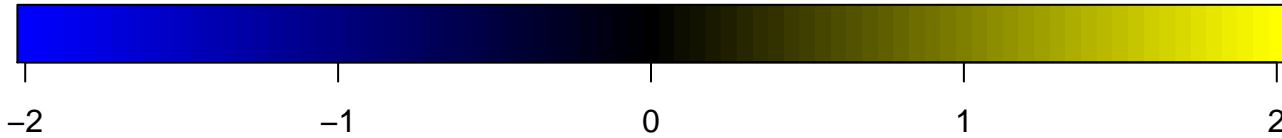
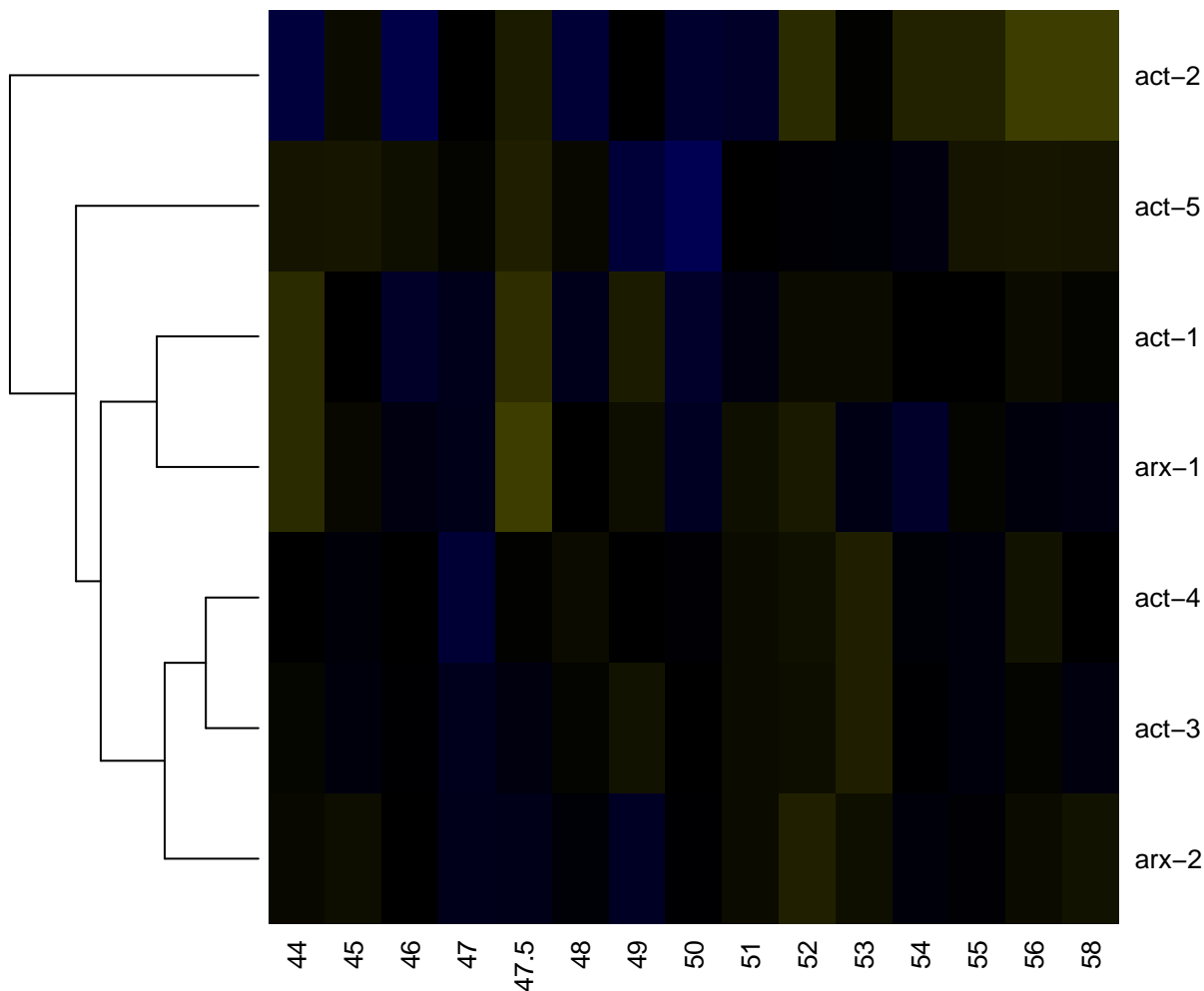
Actin-binding FH2



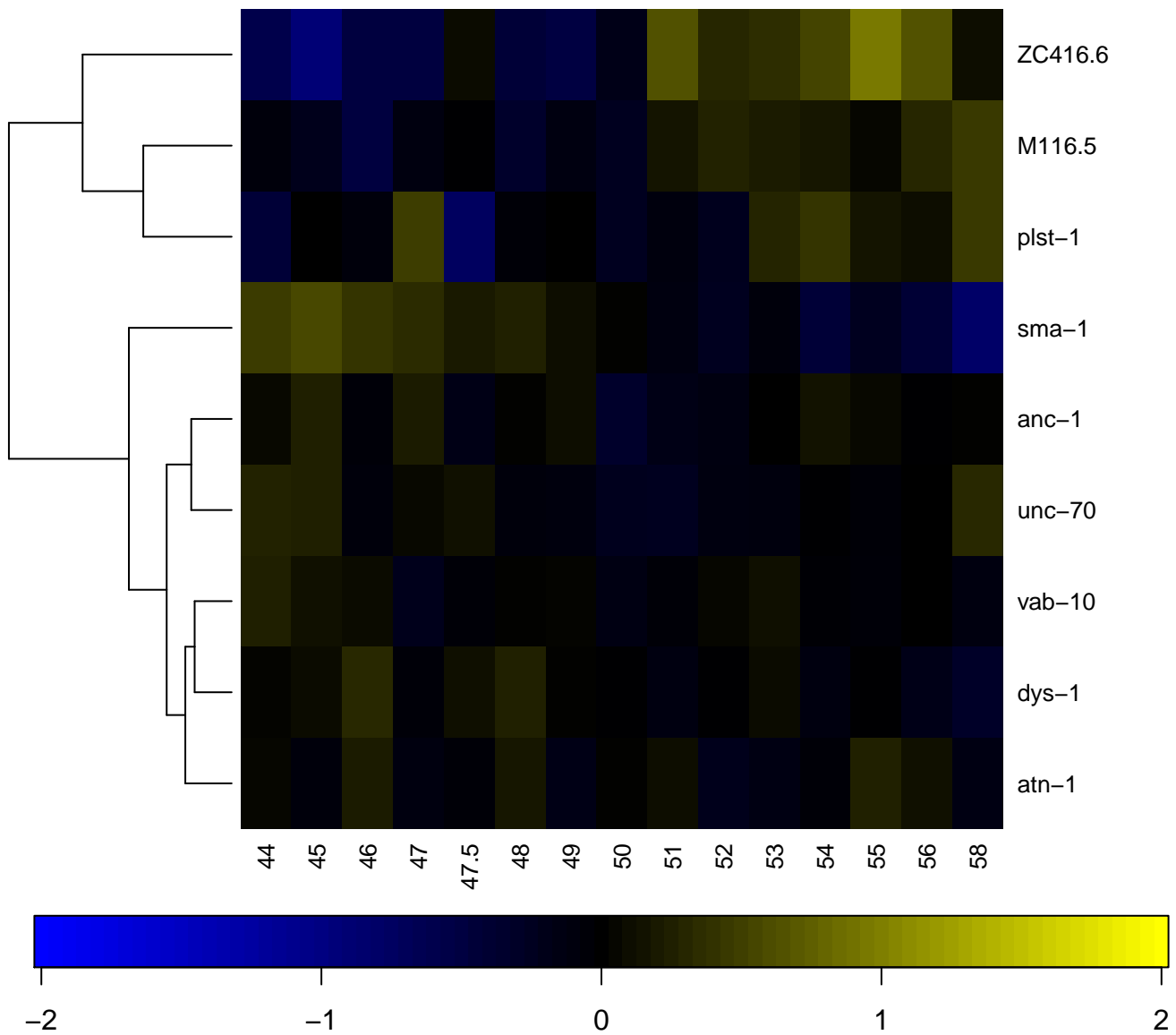
Actin, conserved site



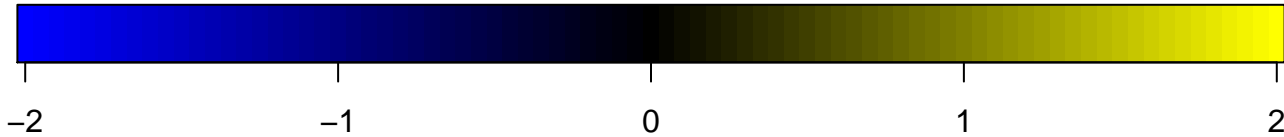
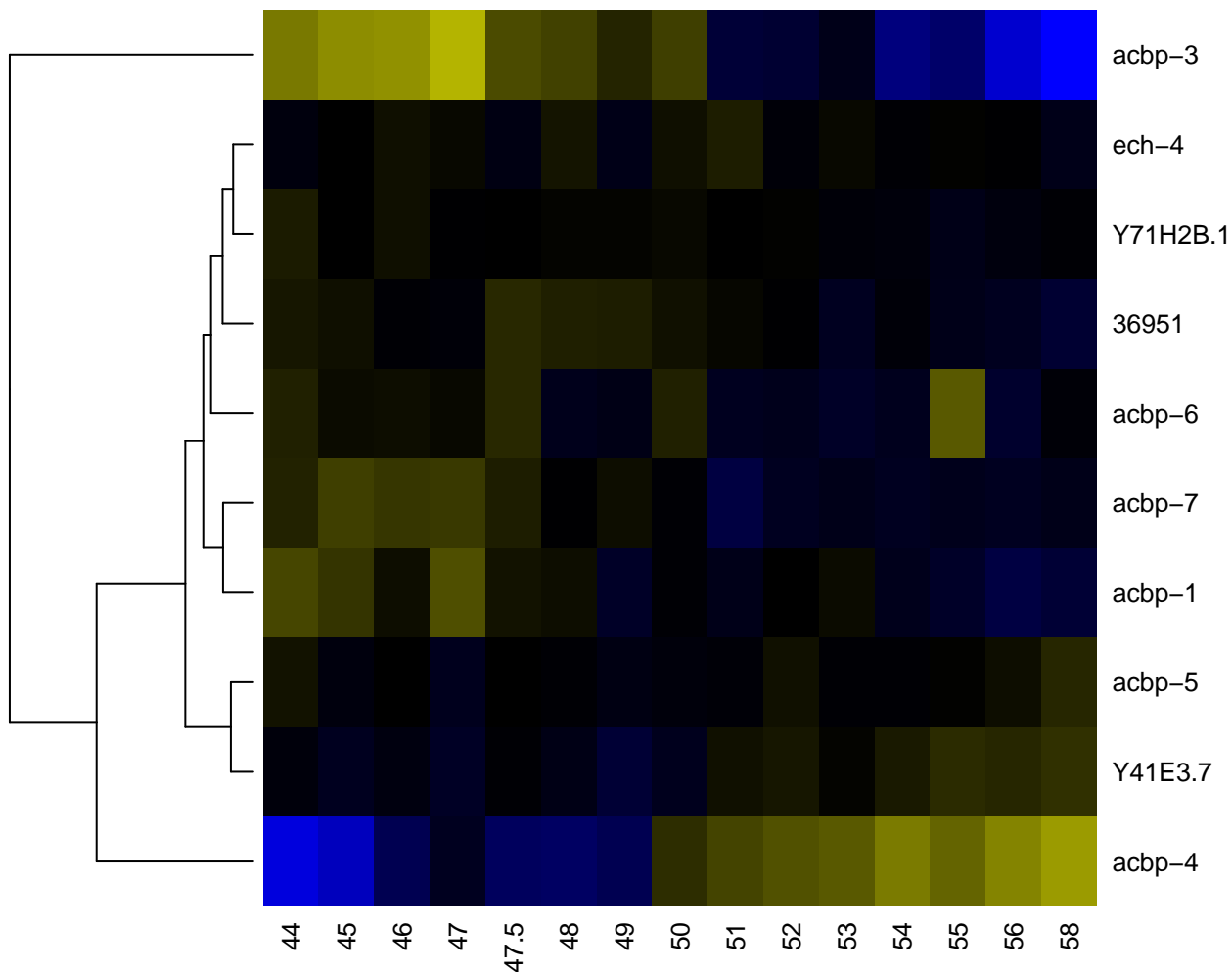
Actin/actin-like conserved site



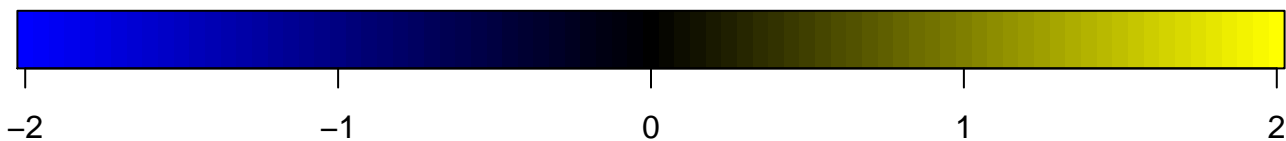
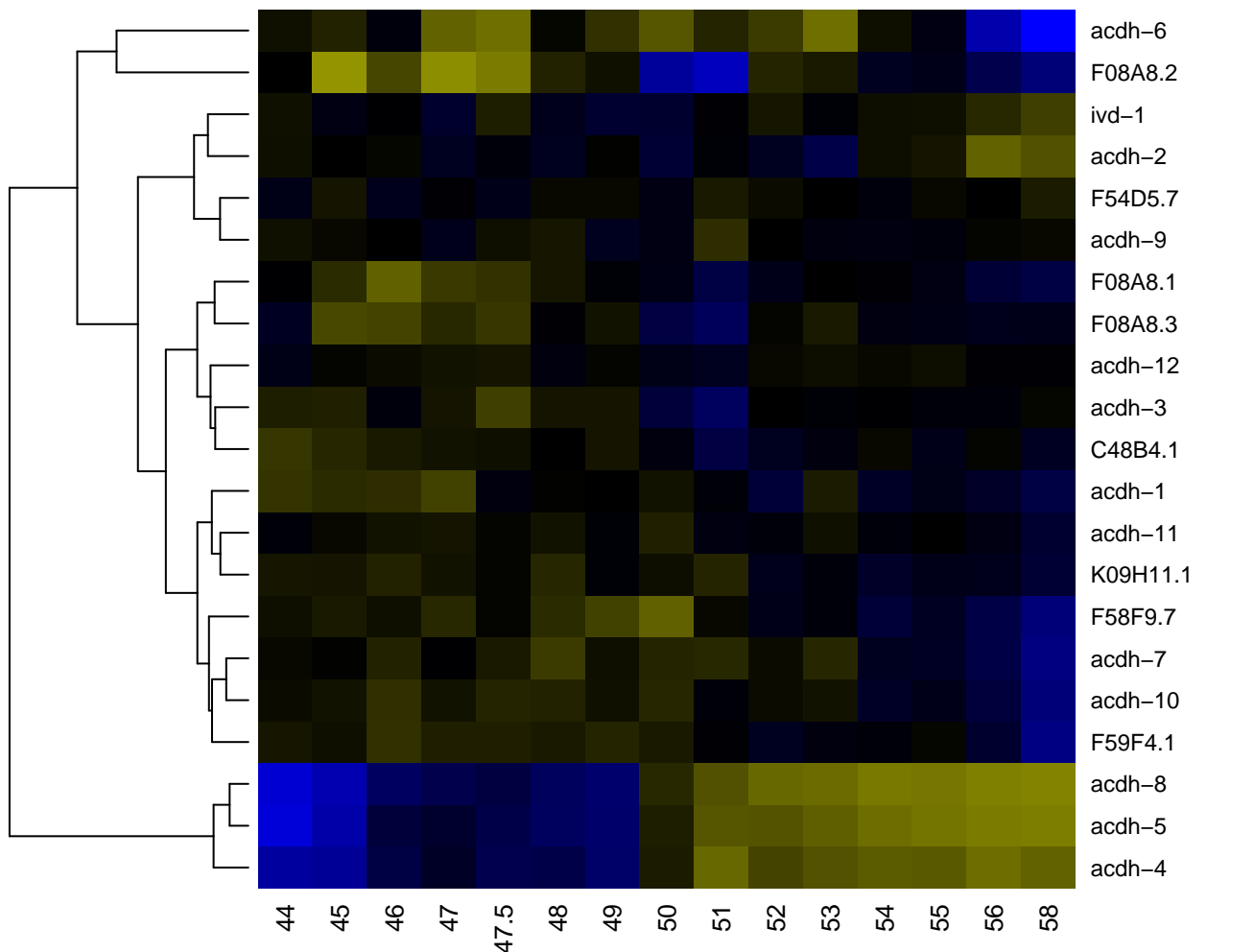
Actinin-type, actin-binding, conserved site



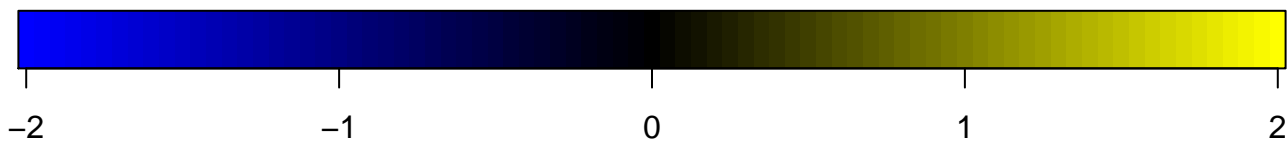
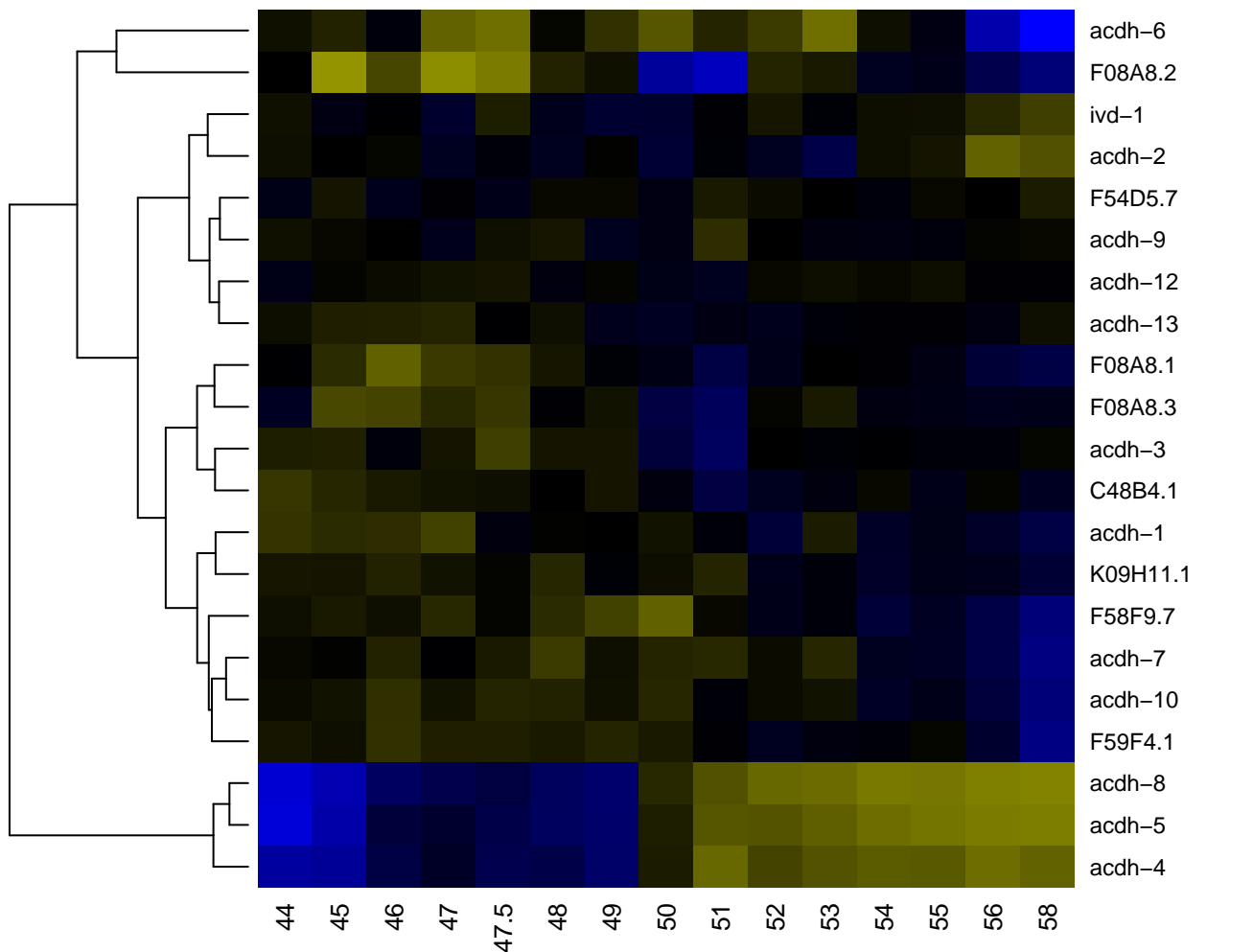
Acyl-CoA-binding protein, ACBP



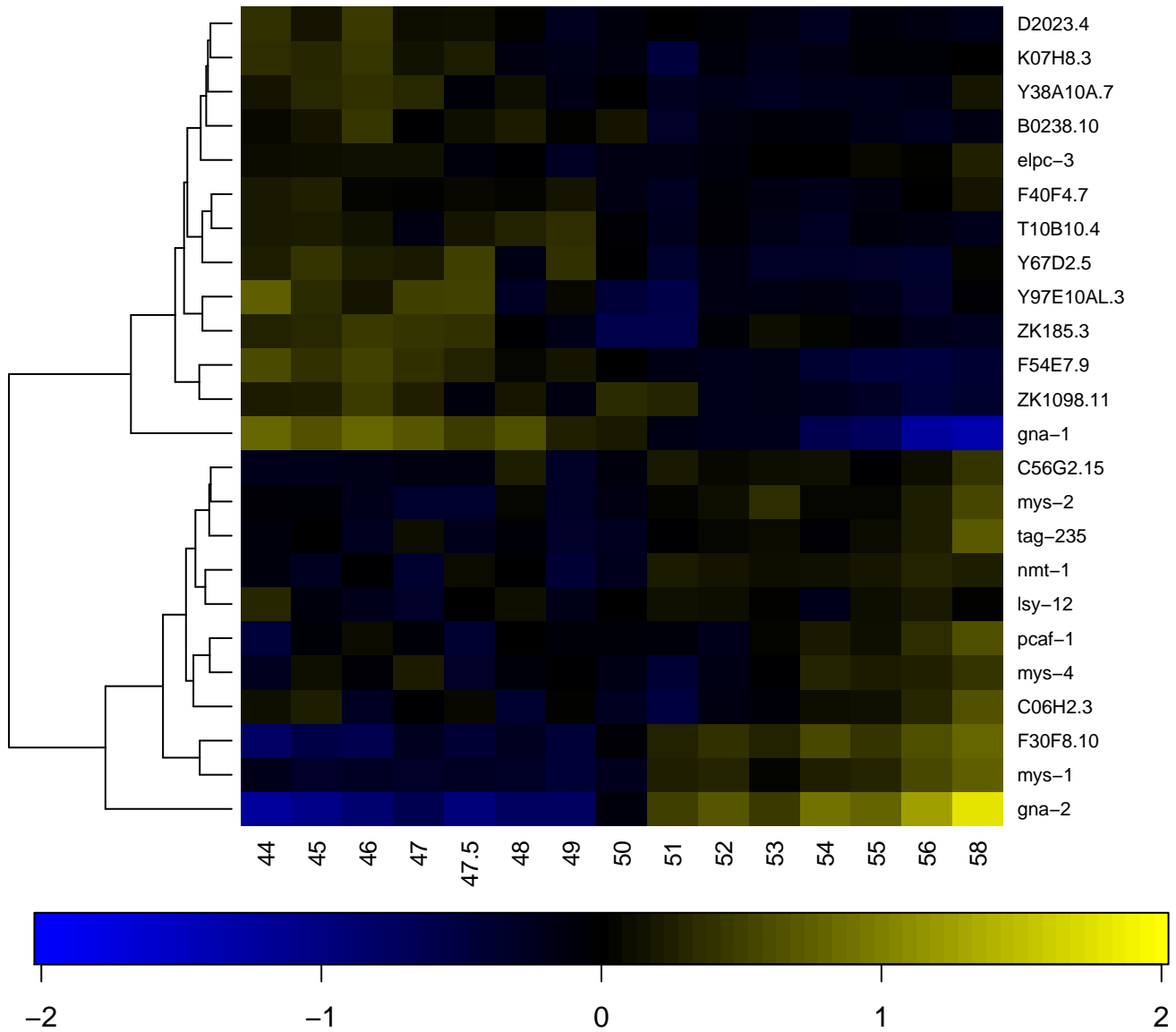
Acyl-CoA dehydrogenase, middle domain



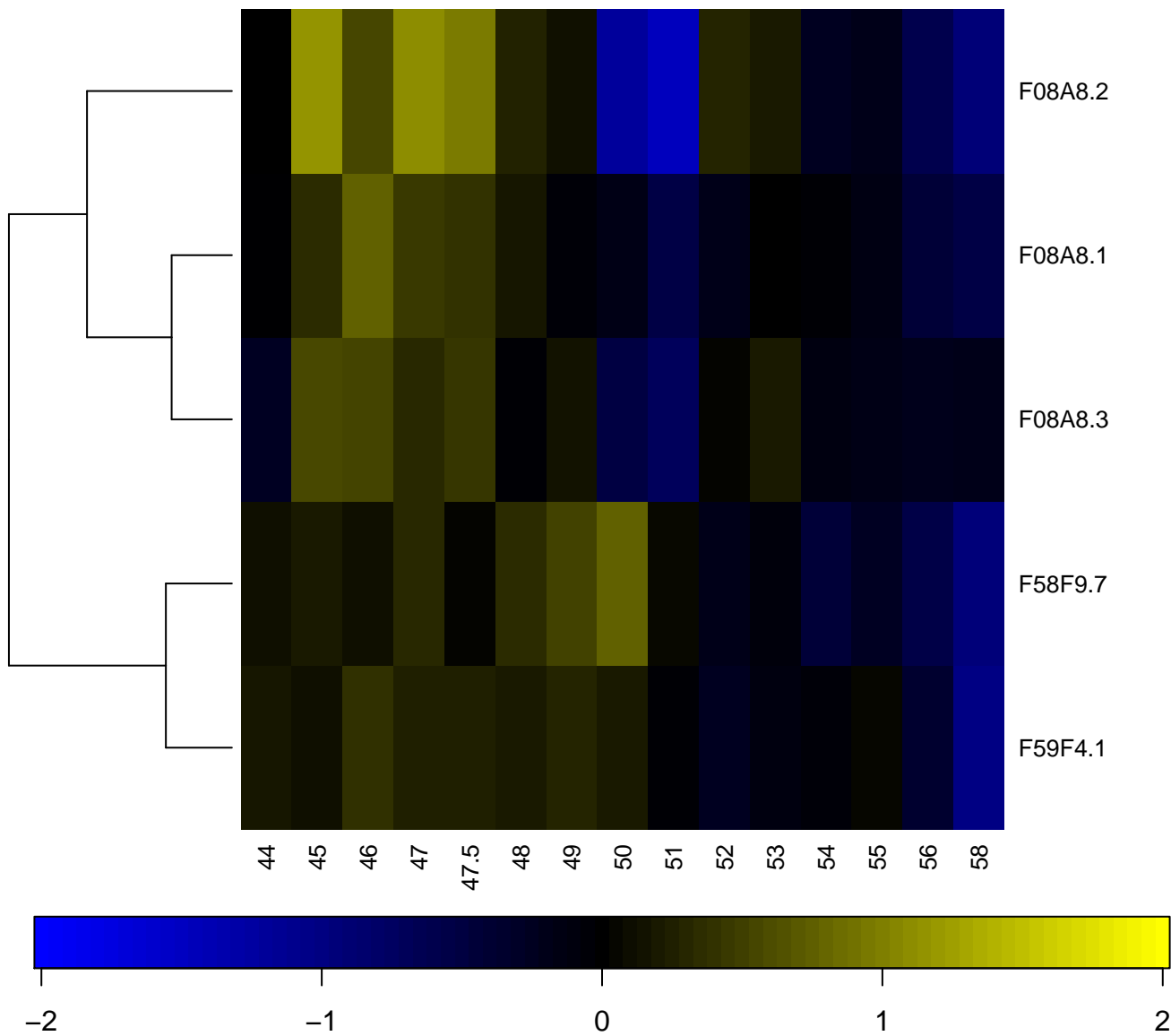
Acyl-CoA dehydrogenase/oxidase, N-terminal



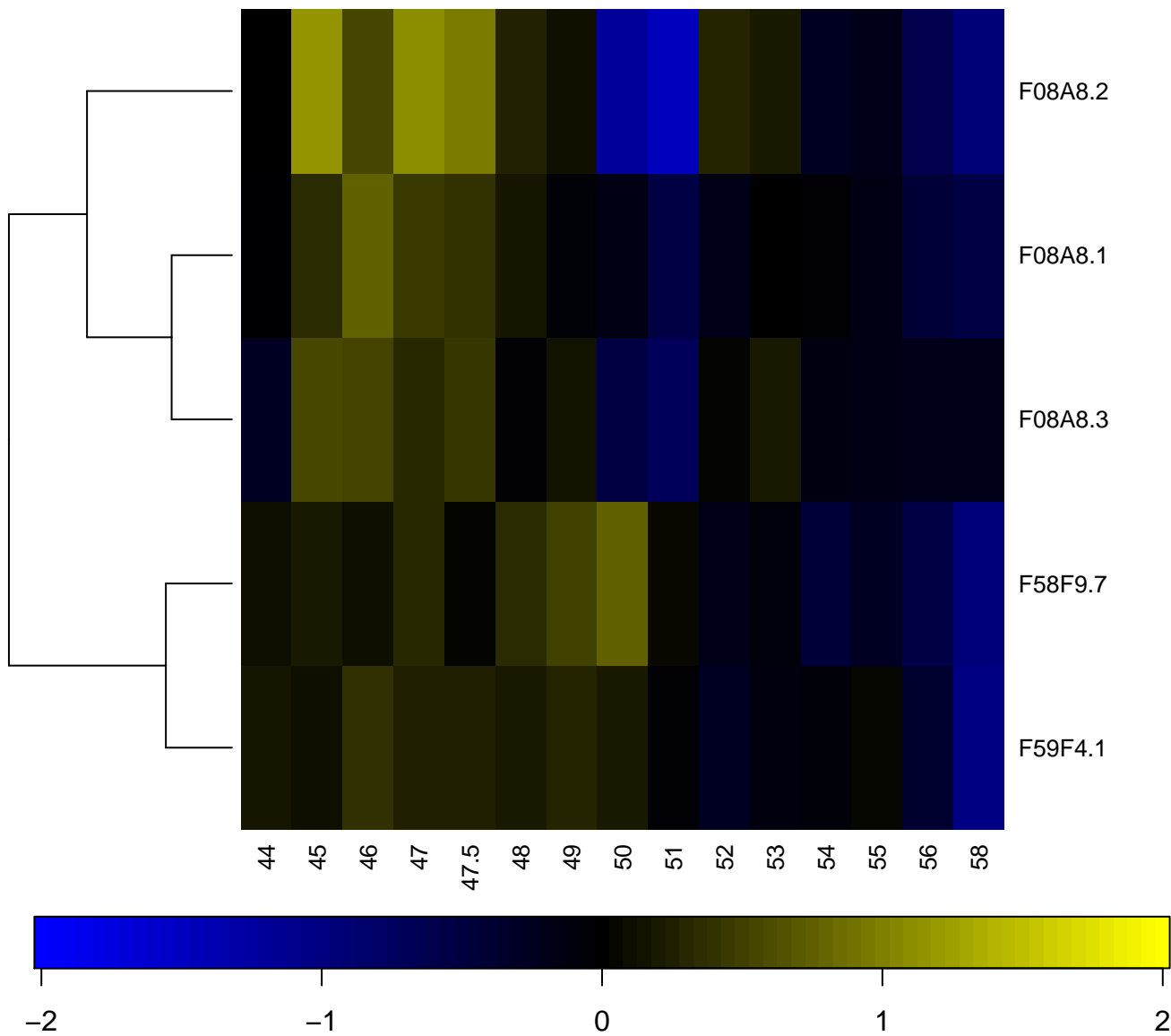
Acyl-CoA N-acyltransferase



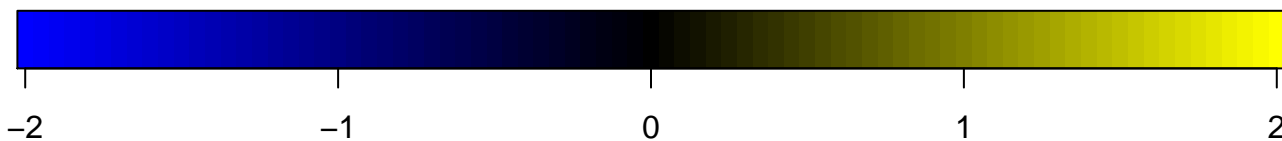
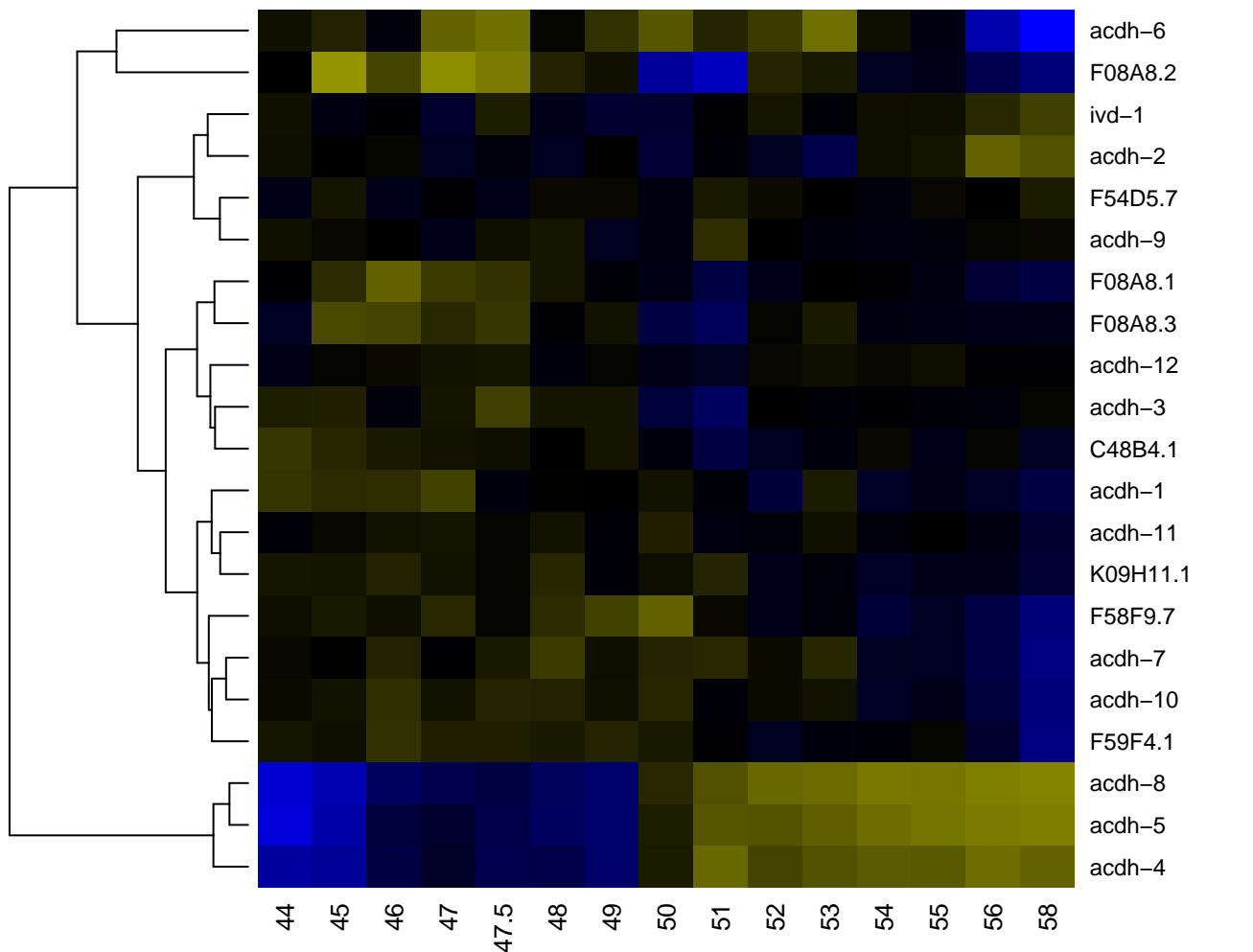
Acyl-CoA oxidase



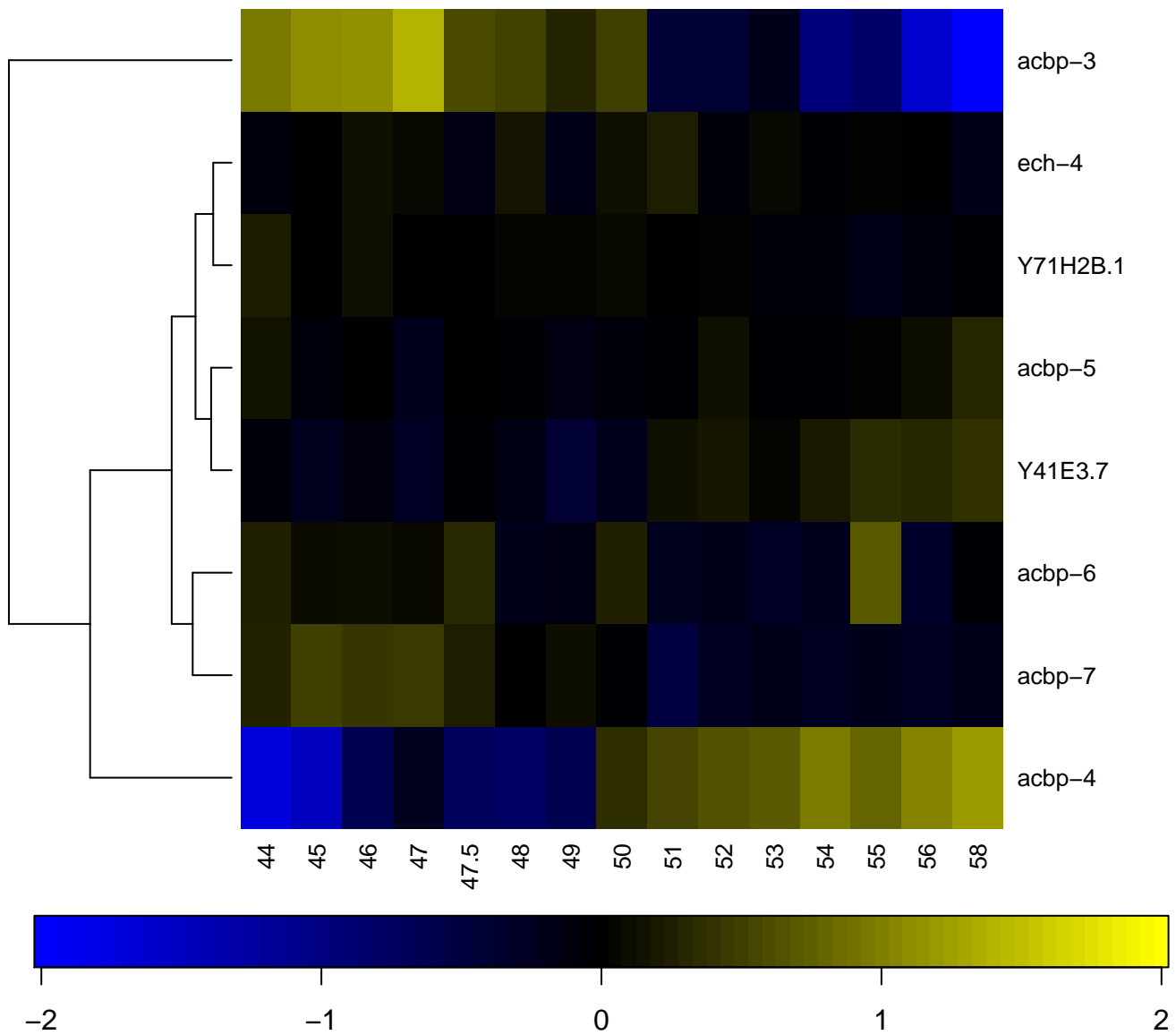
Acyl-CoA oxidase, C-terminal



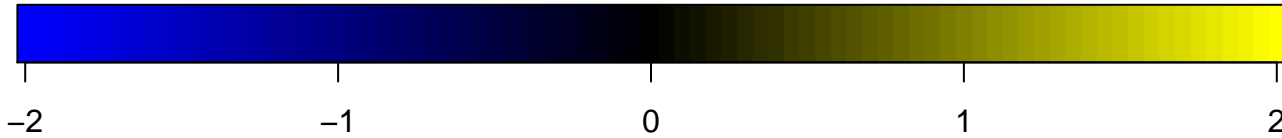
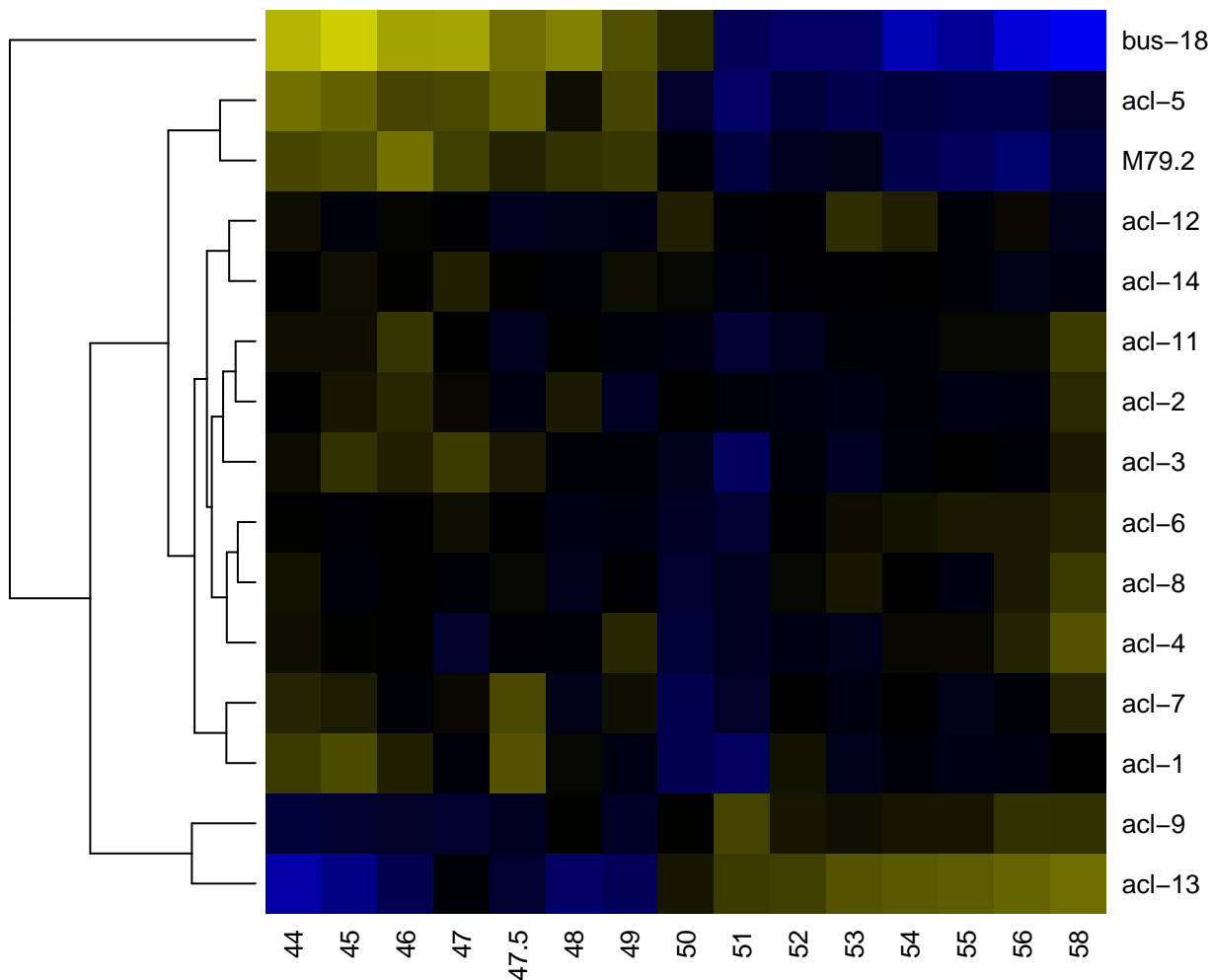
Acyl-CoA oxidase/dehydrogenase, central domain



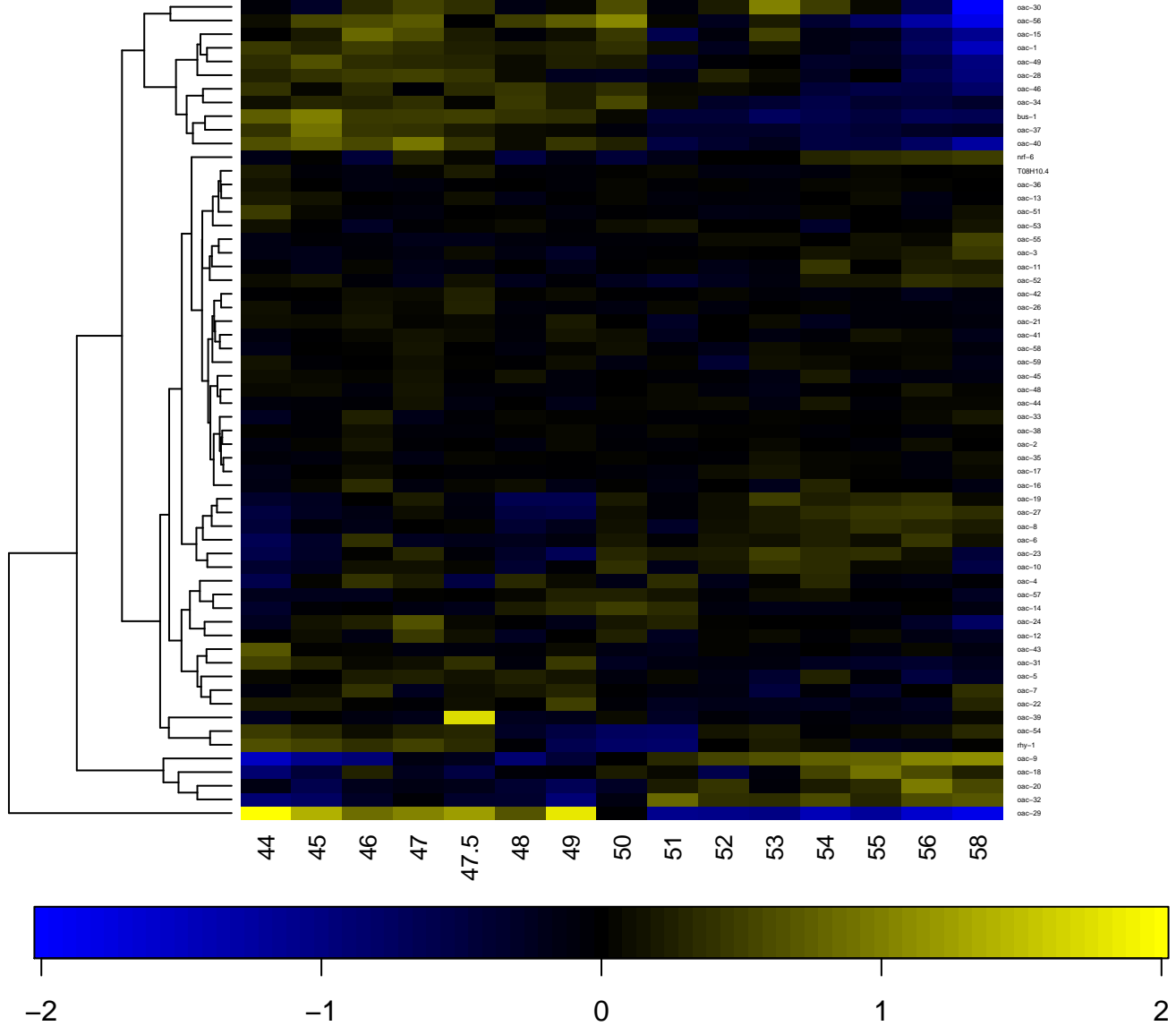
Acyl CoA binding protein



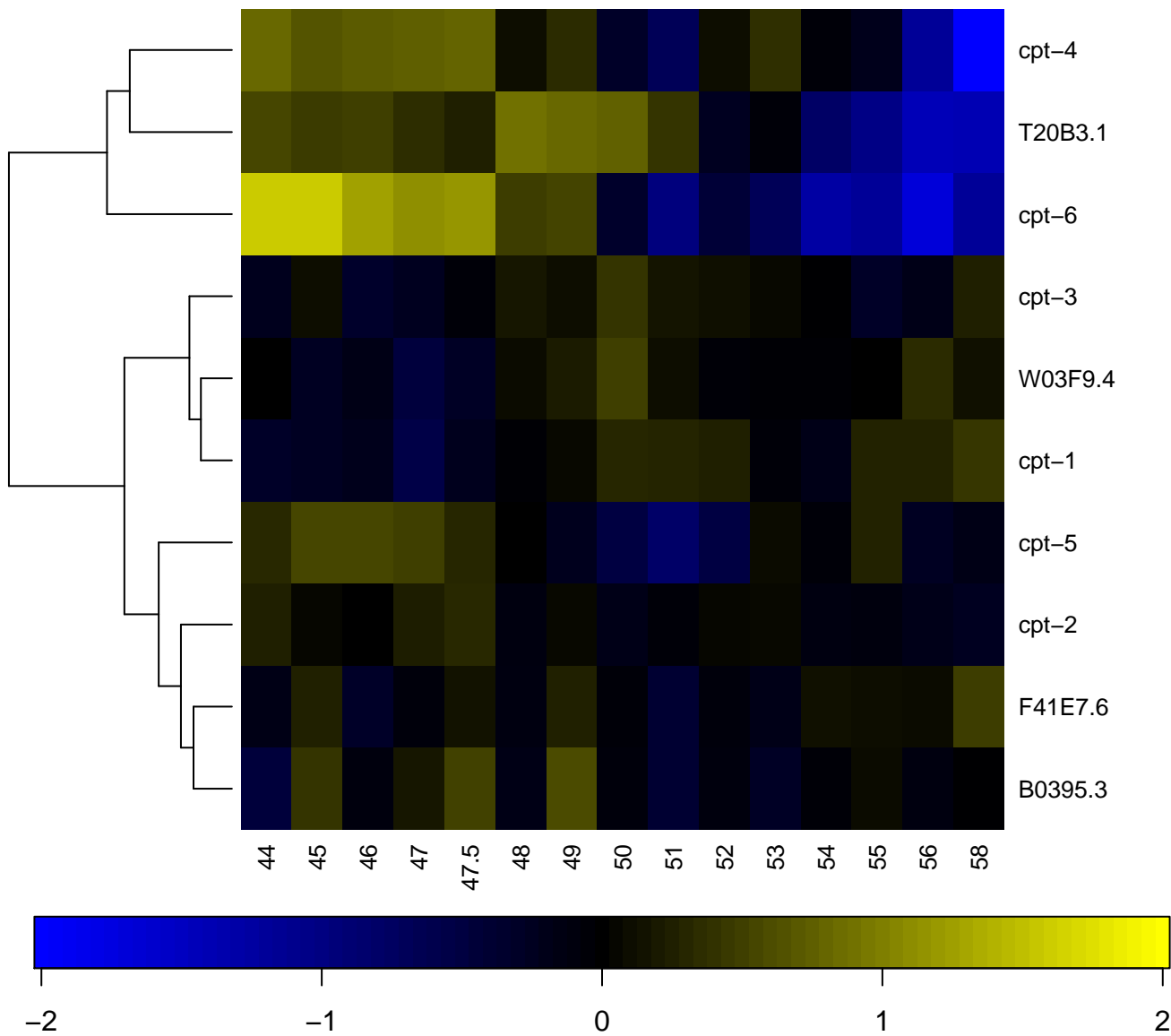
Acyltransferase



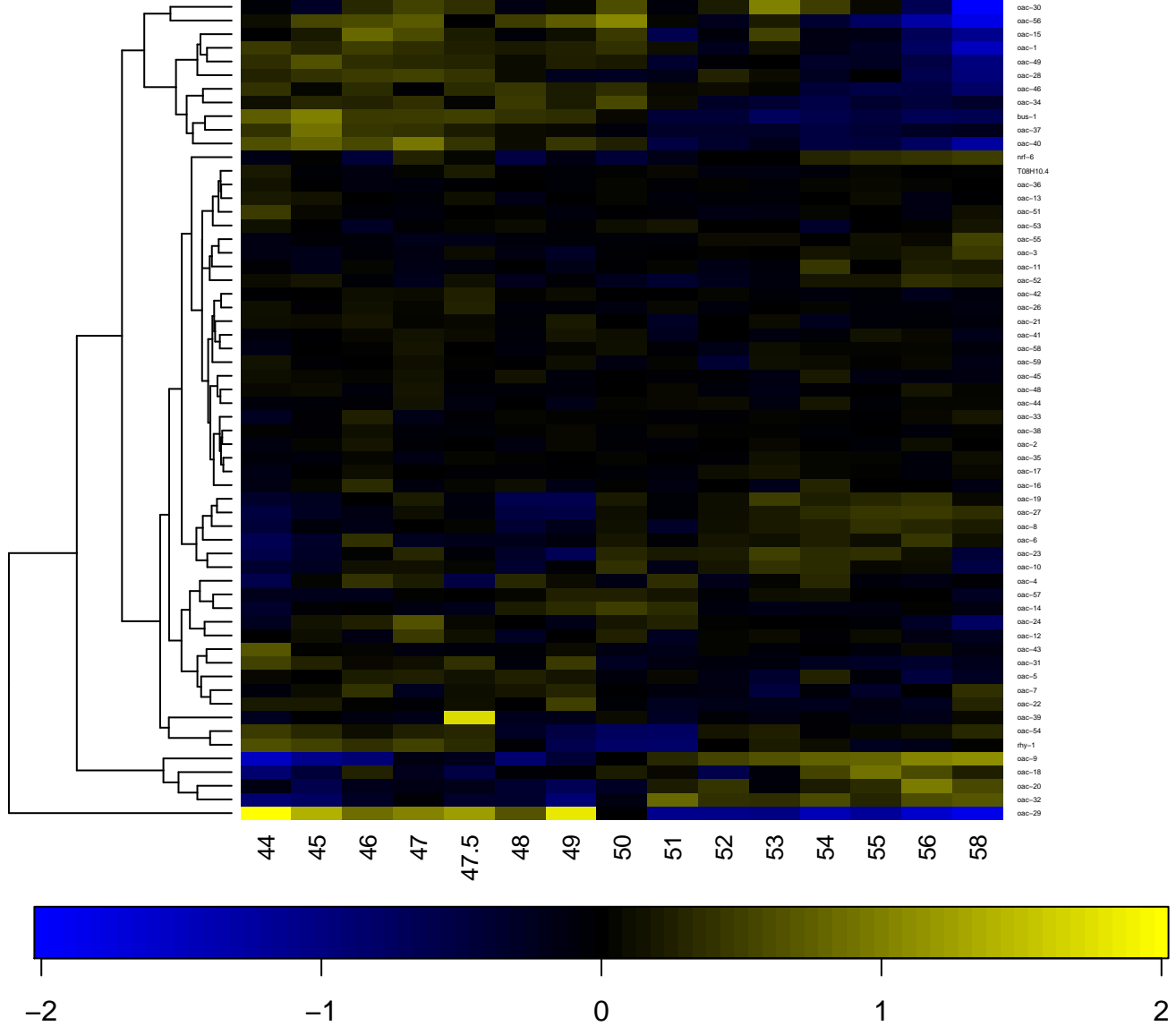
Acyltransferase 3



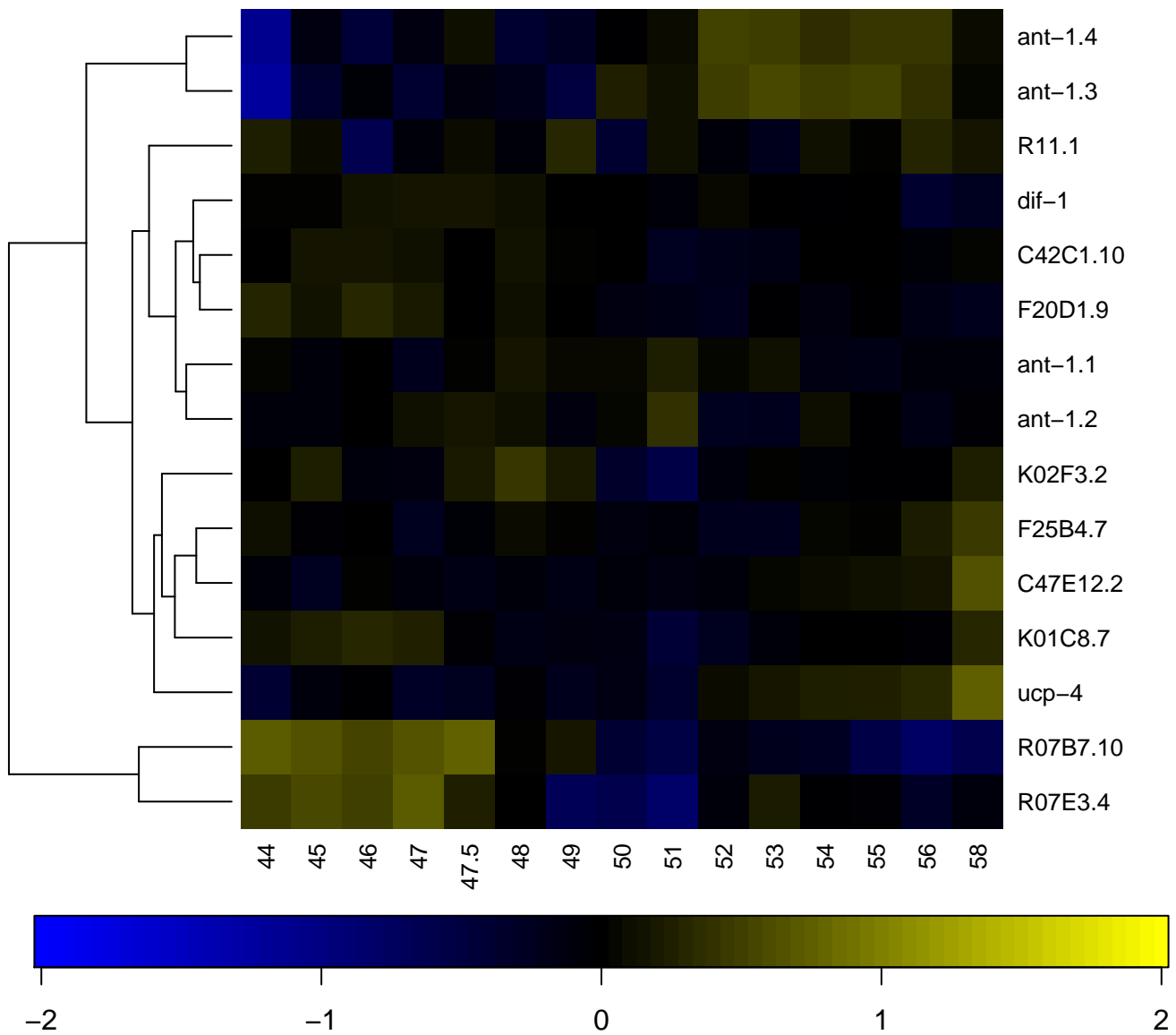
Acyltransferase ChoActase/COT/CPT



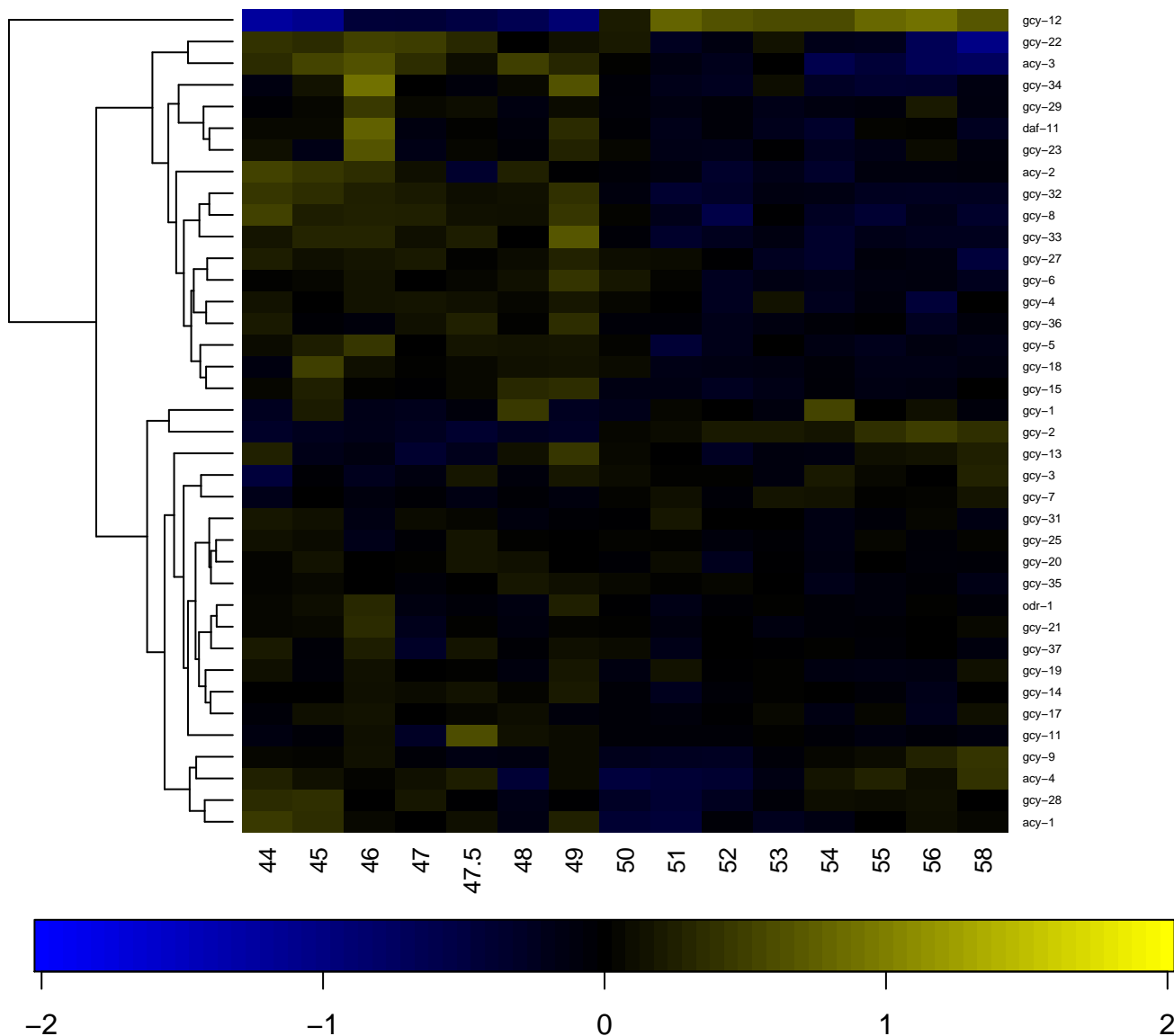
Acyltransferase family



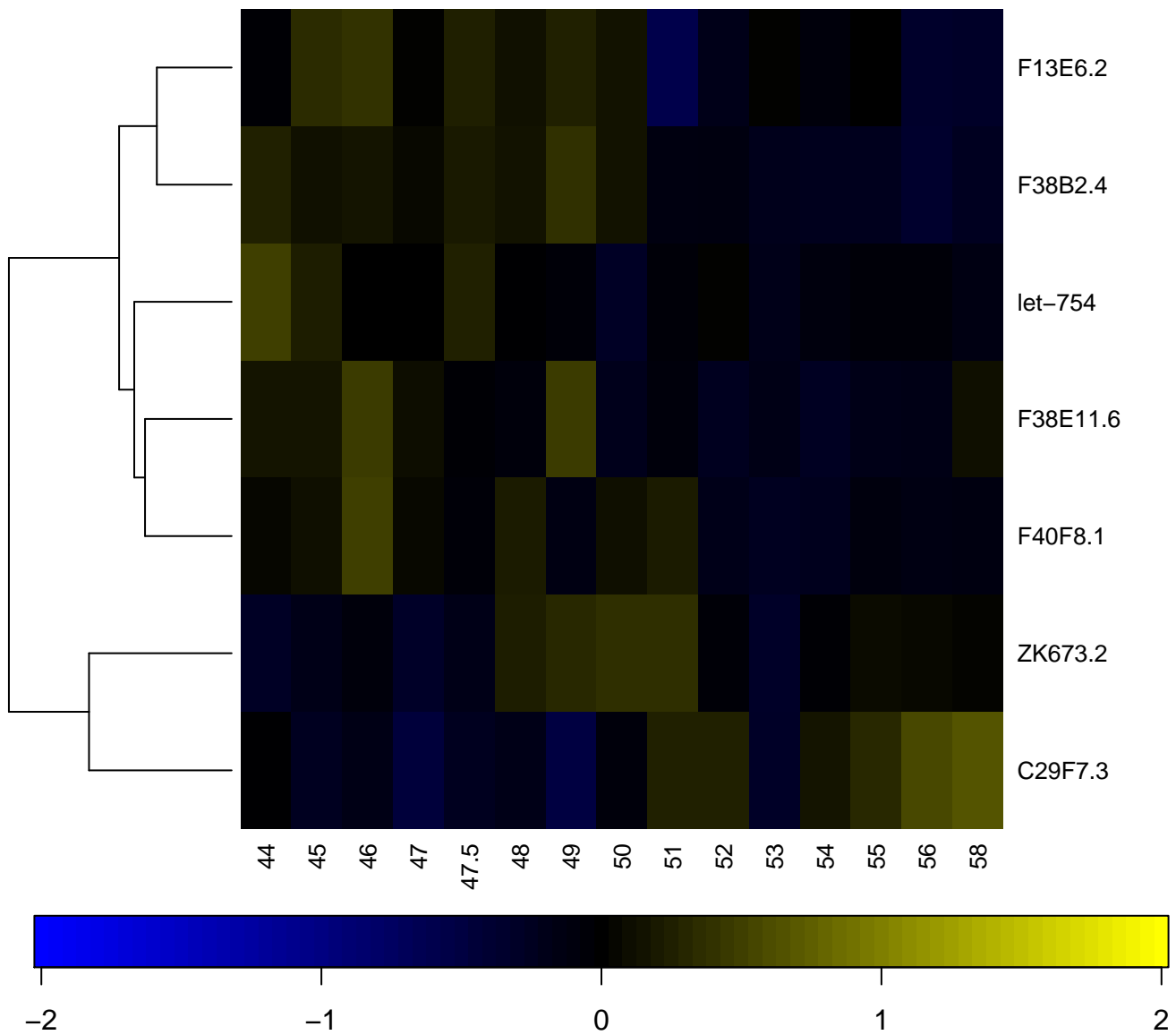
Adenine nucleotide translocator 1



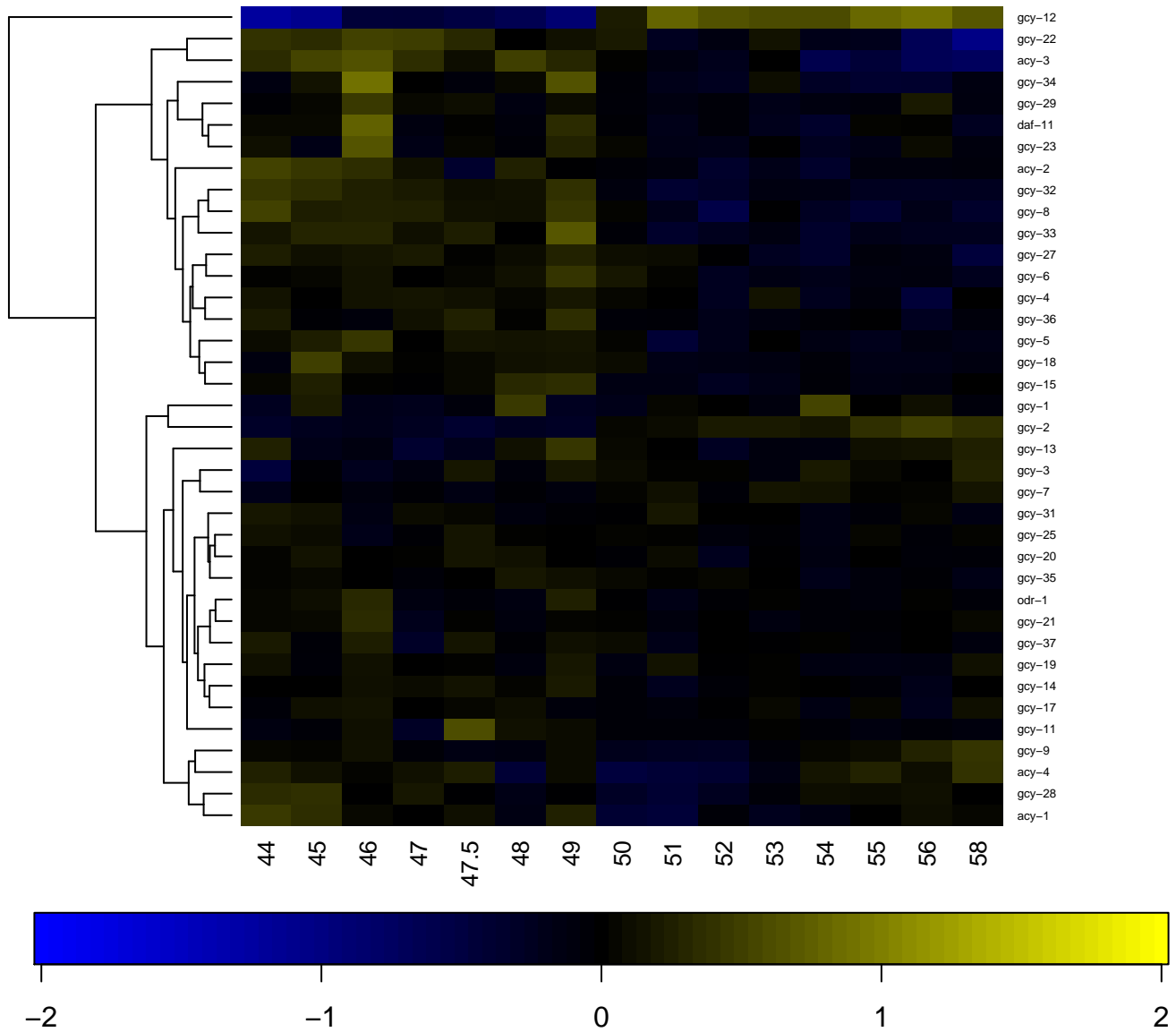
Adenylate and Guanylate cyclase catalytic domain



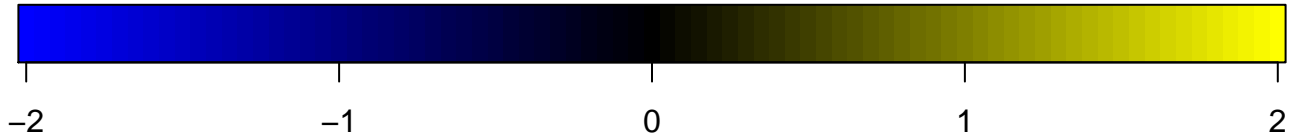
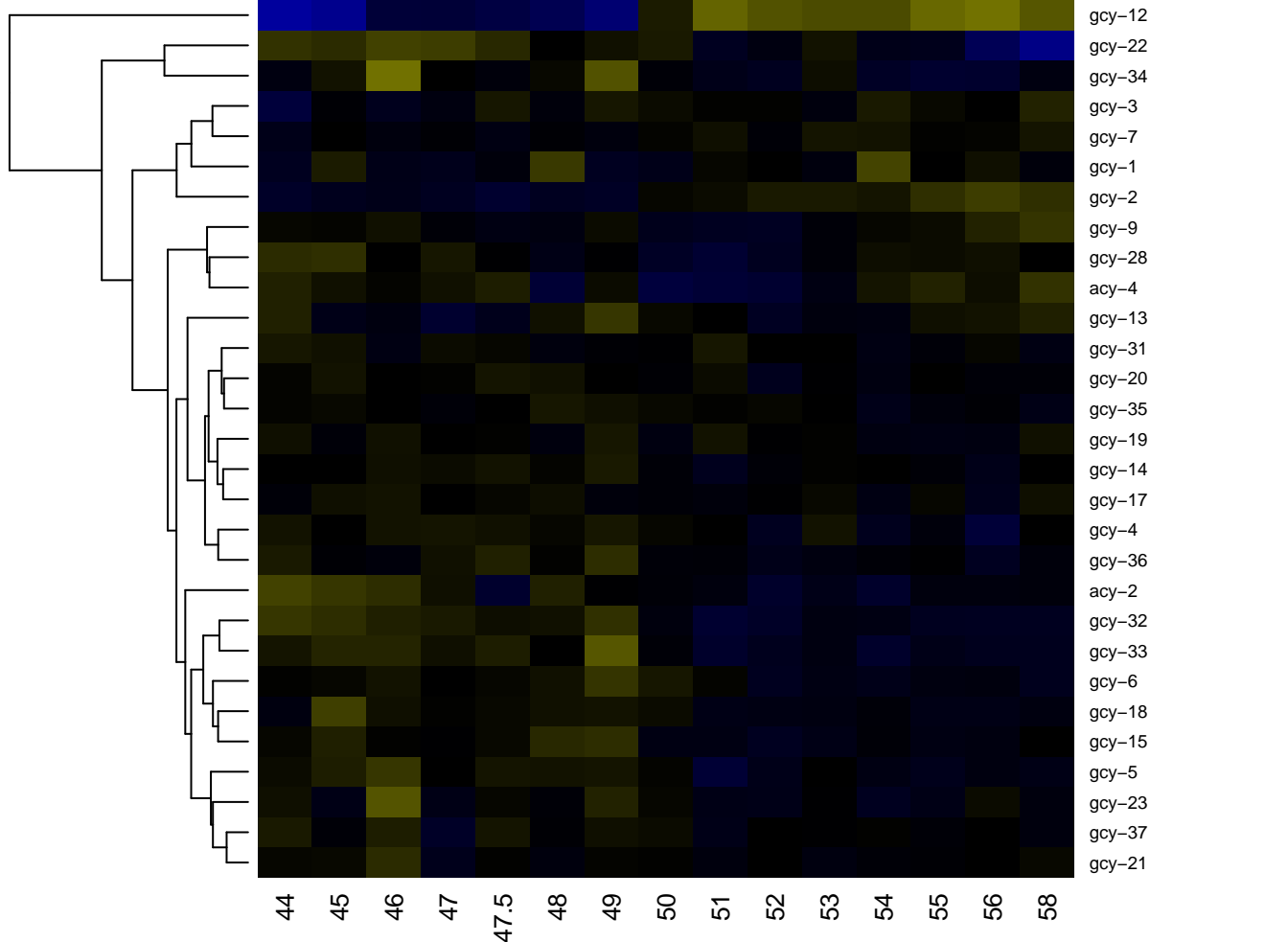
Adenylate kinase



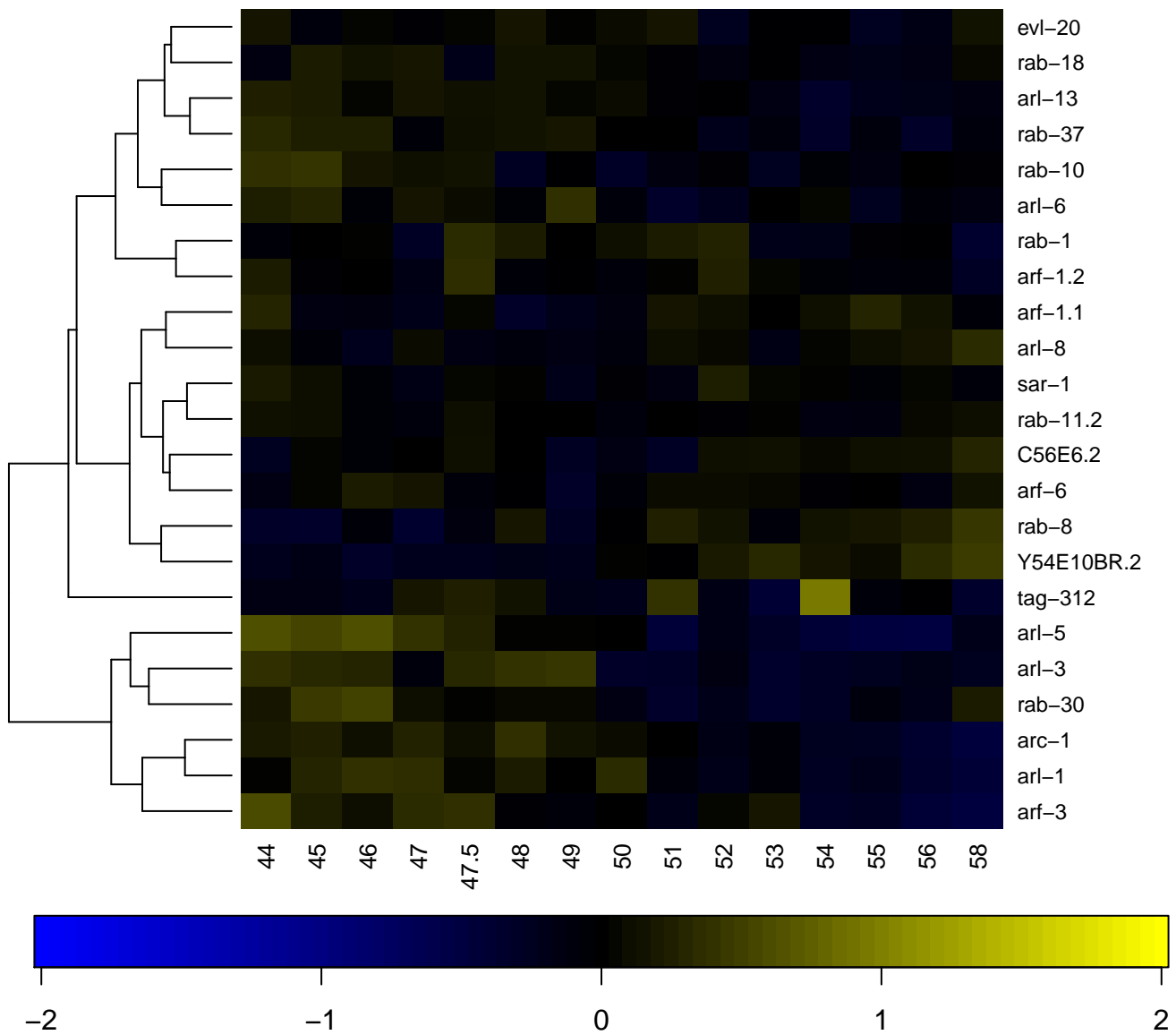
Adenylyl cyclase class-3/4/guanylyl cyclase



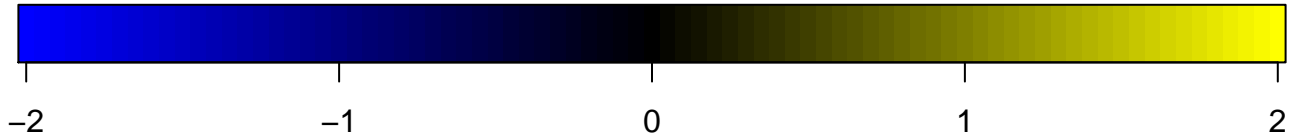
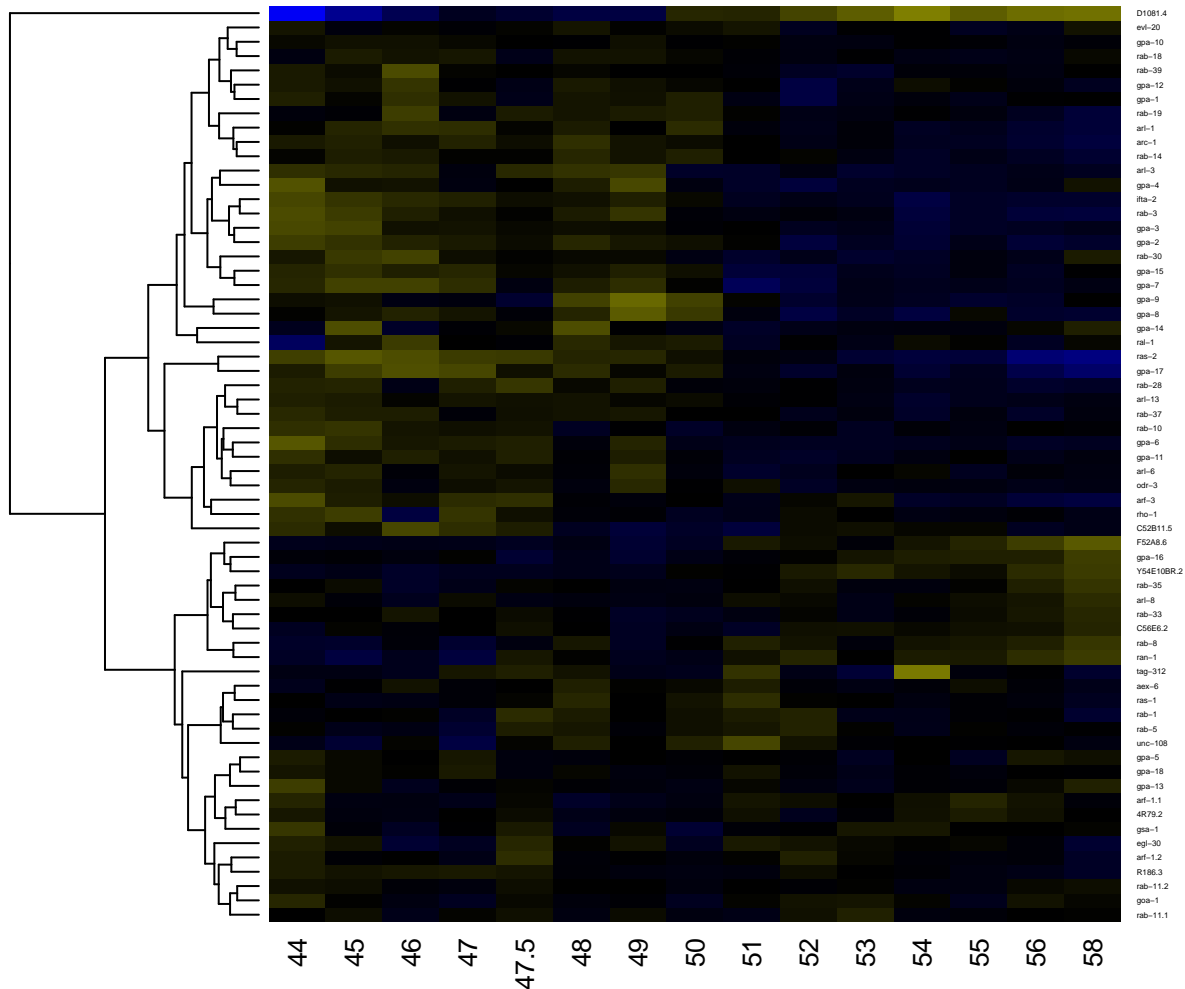
Adenylyl cyclase class-3/4/guanylyl cyclase, conserved sites



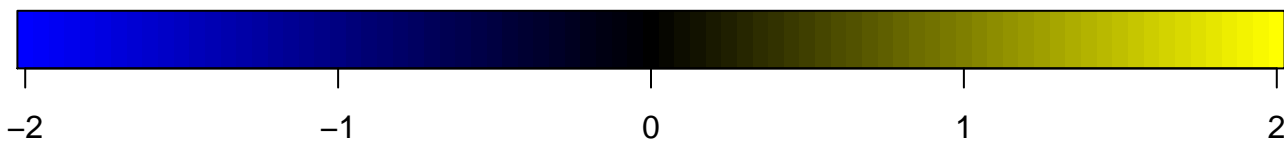
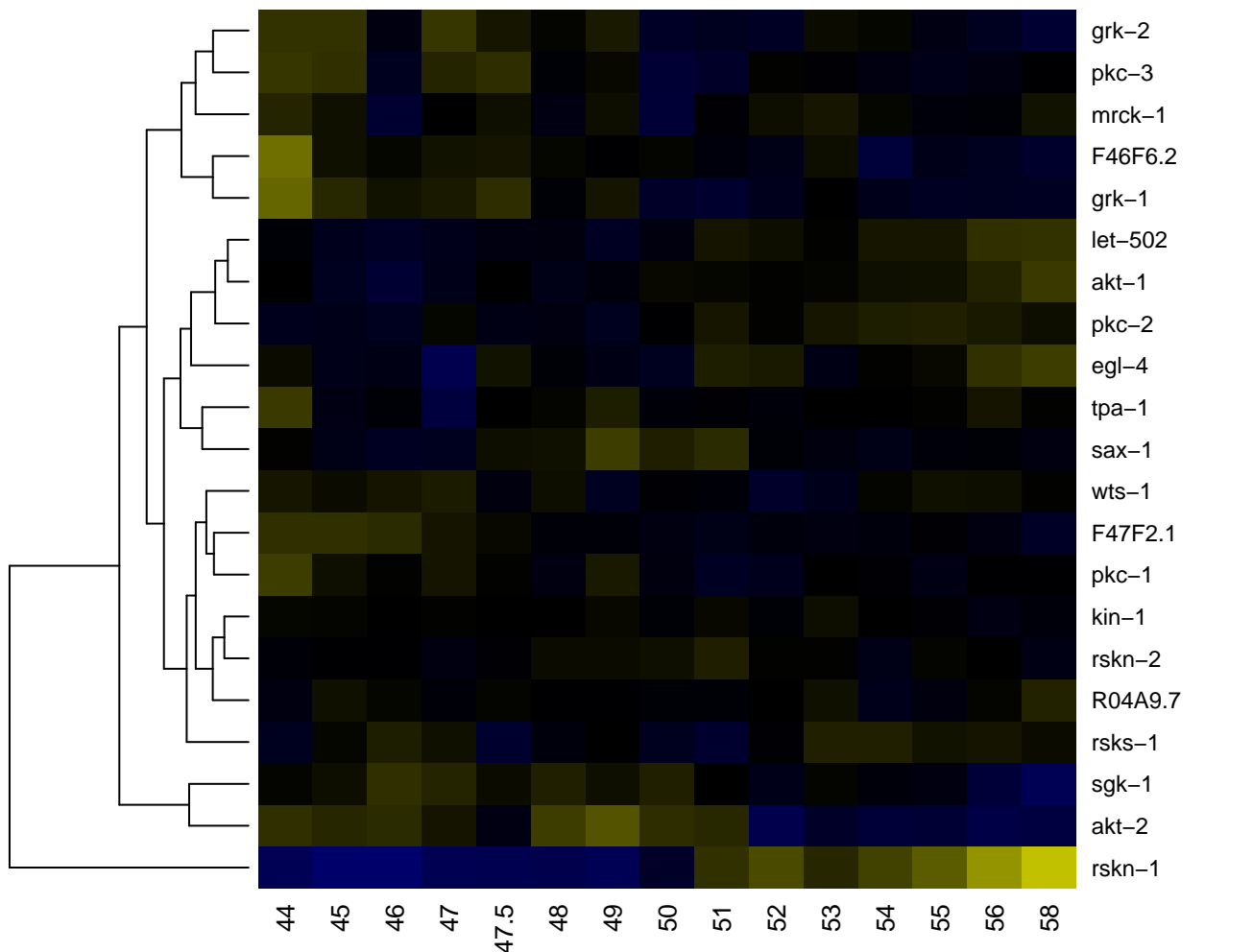
ADP-ribosylation factor



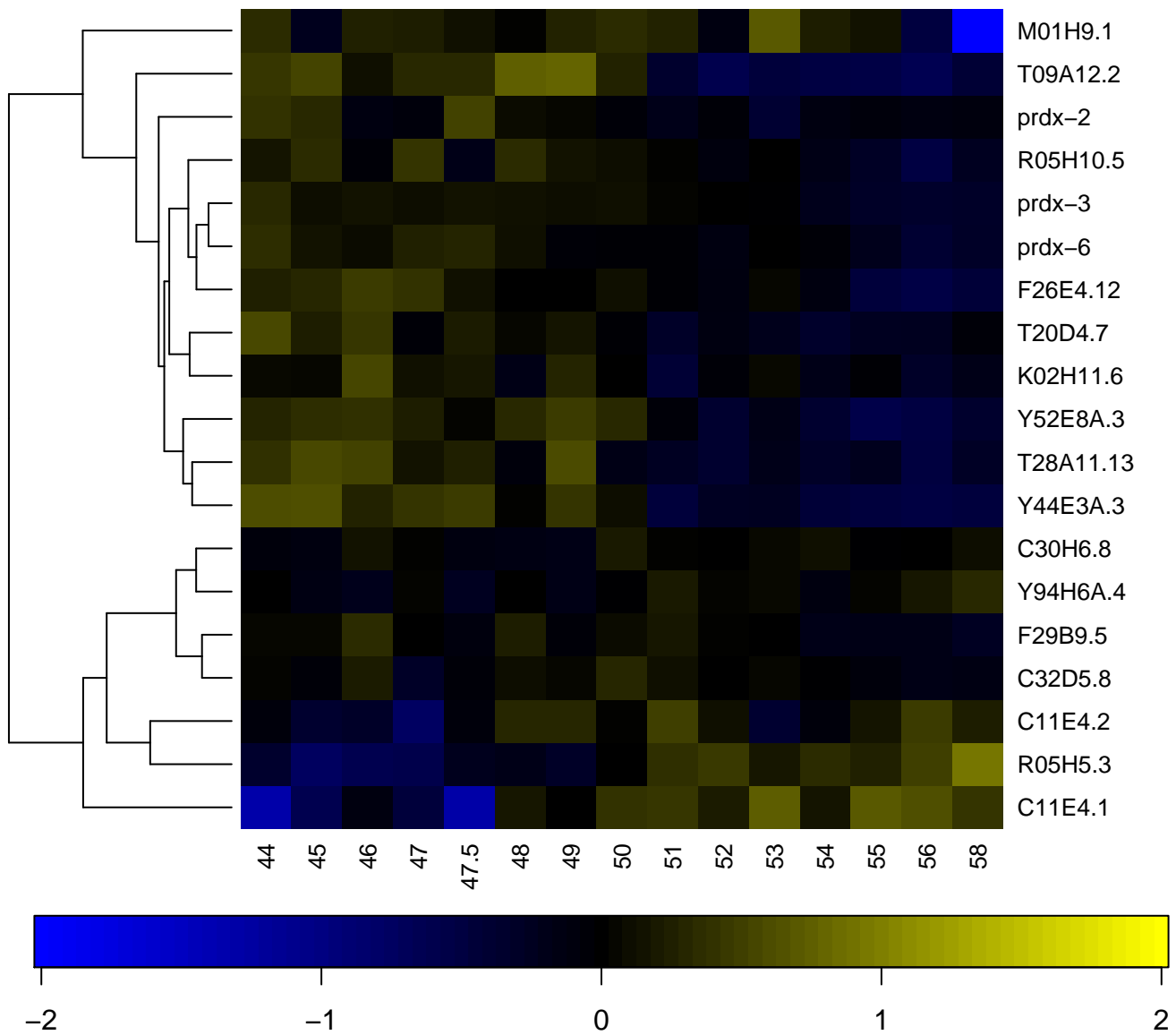
ADP-ribosylation factor family



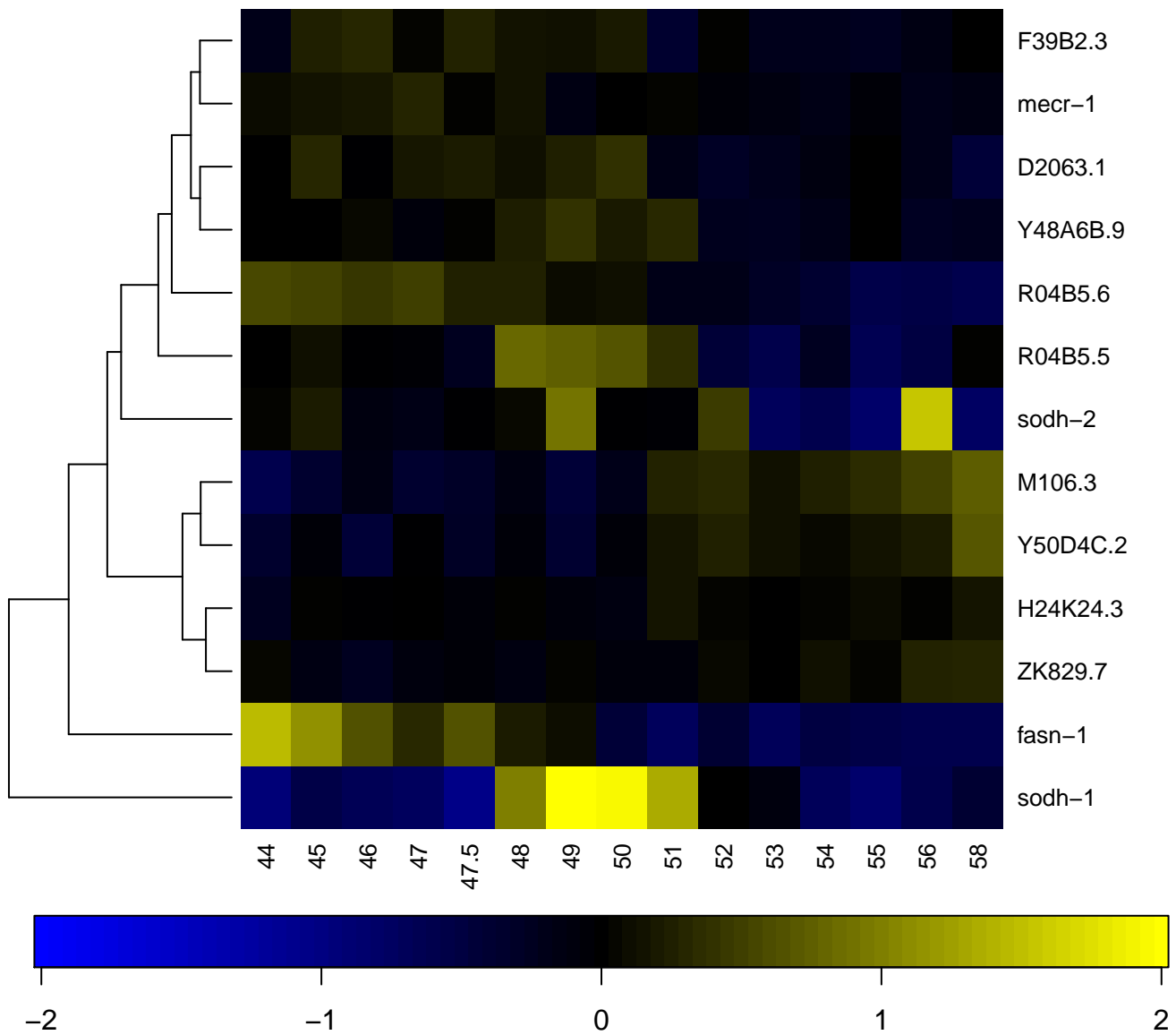
AGC-kinase, C-terminal



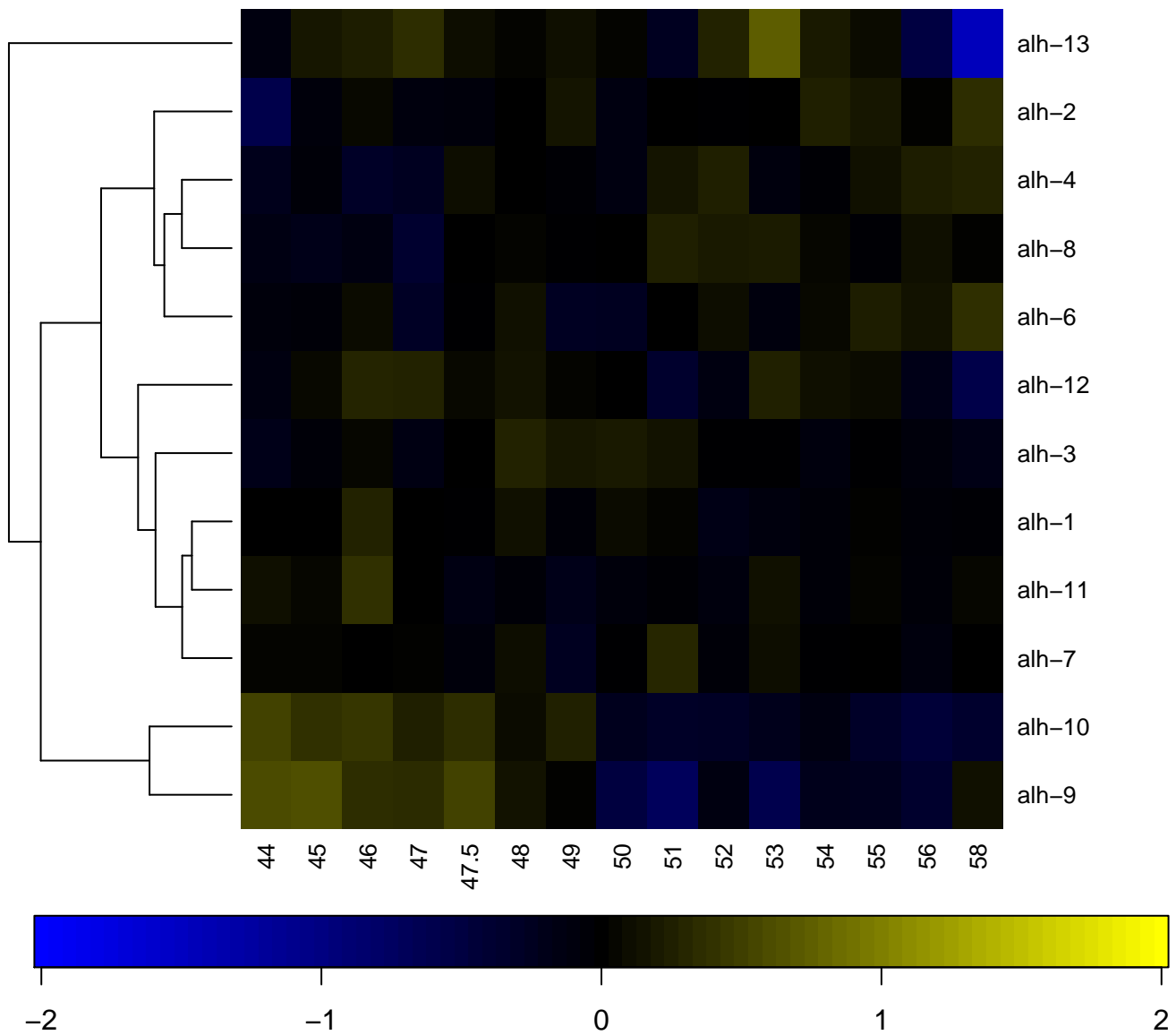
AhpC/TSA family



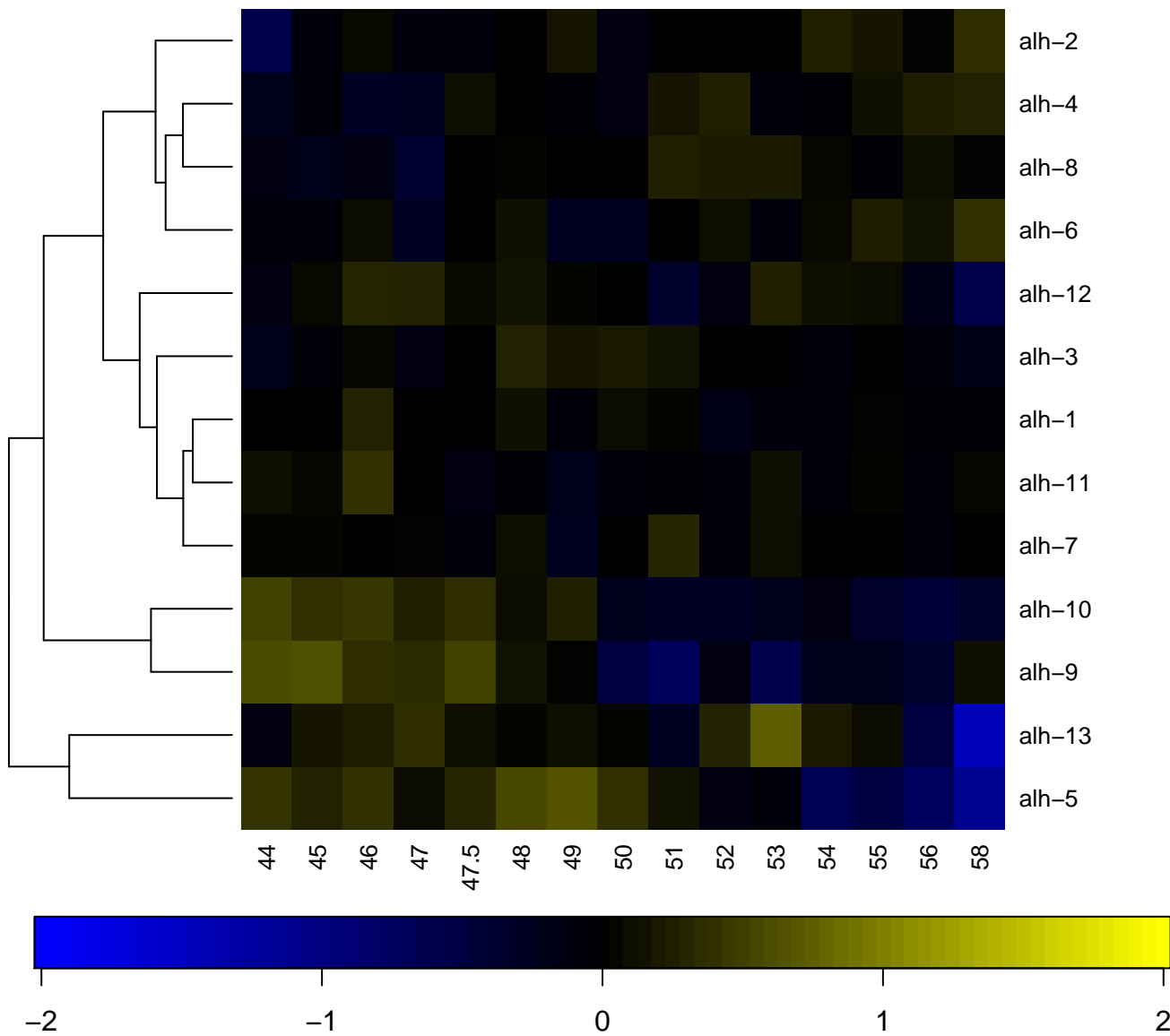
Alcohol dehydrogenase, C-terminal



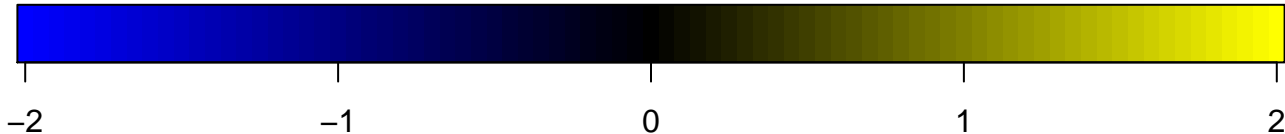
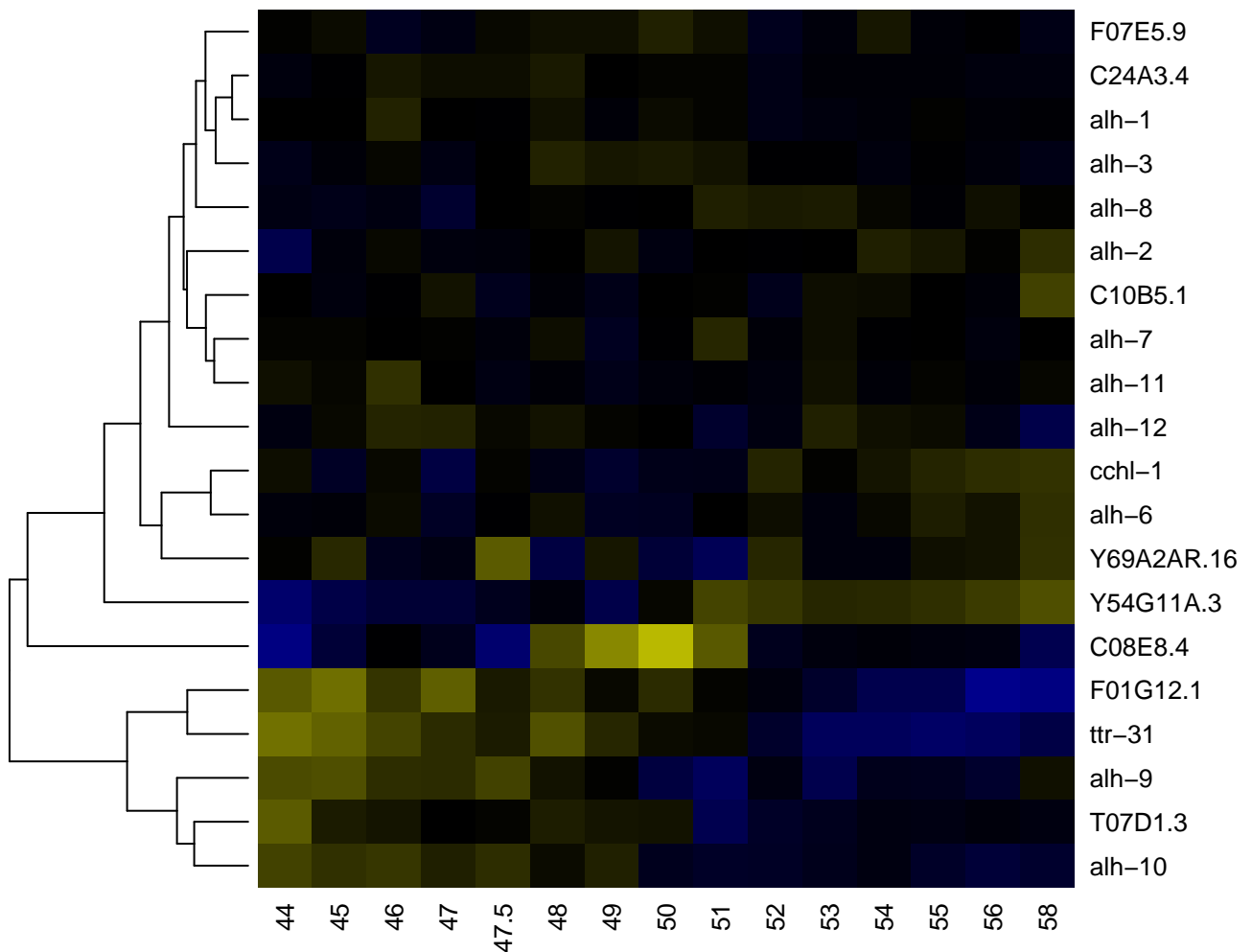
Aldehyde dehydrogenase family



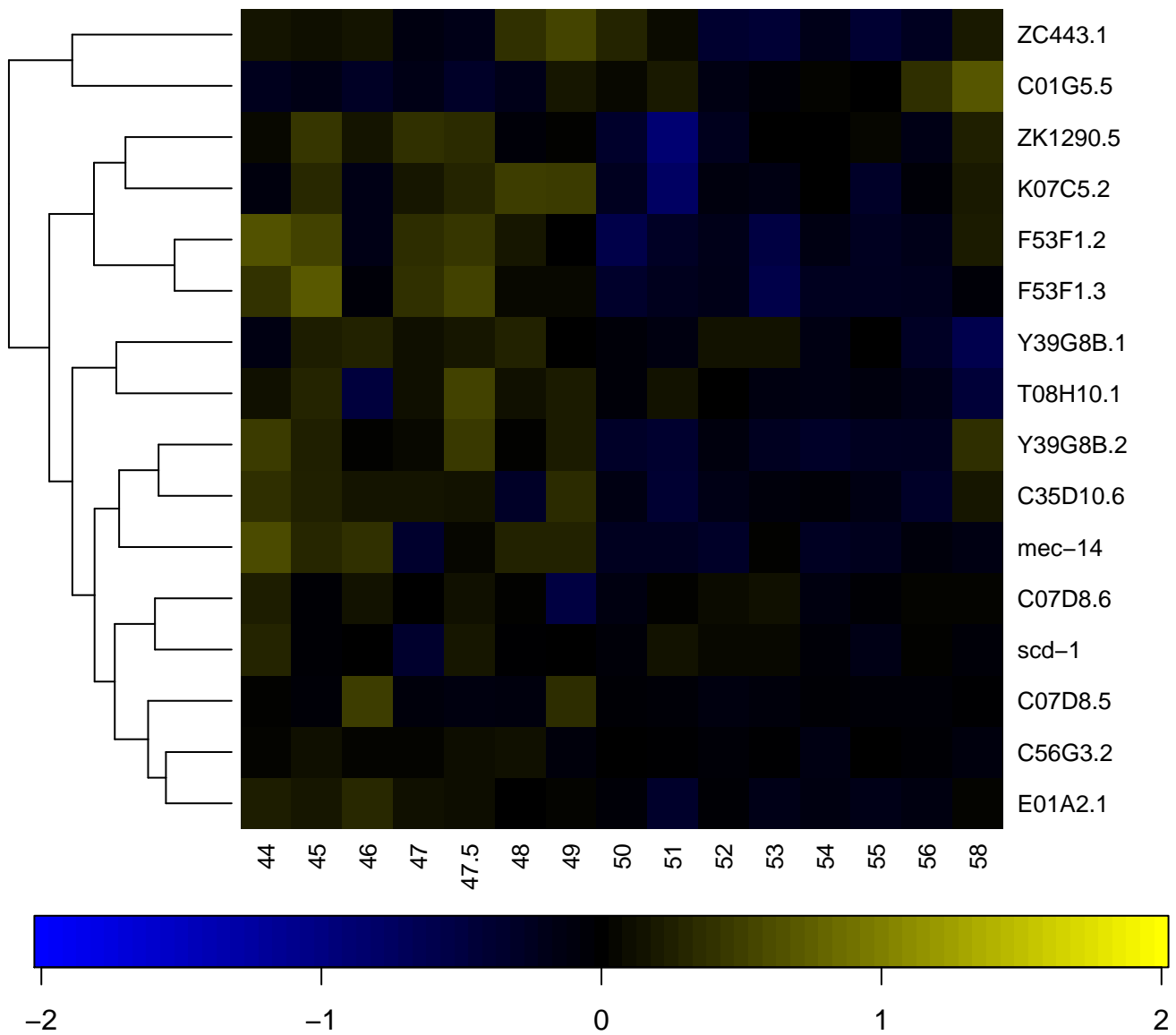
Aldehyde dehydrogenase, C-terminal



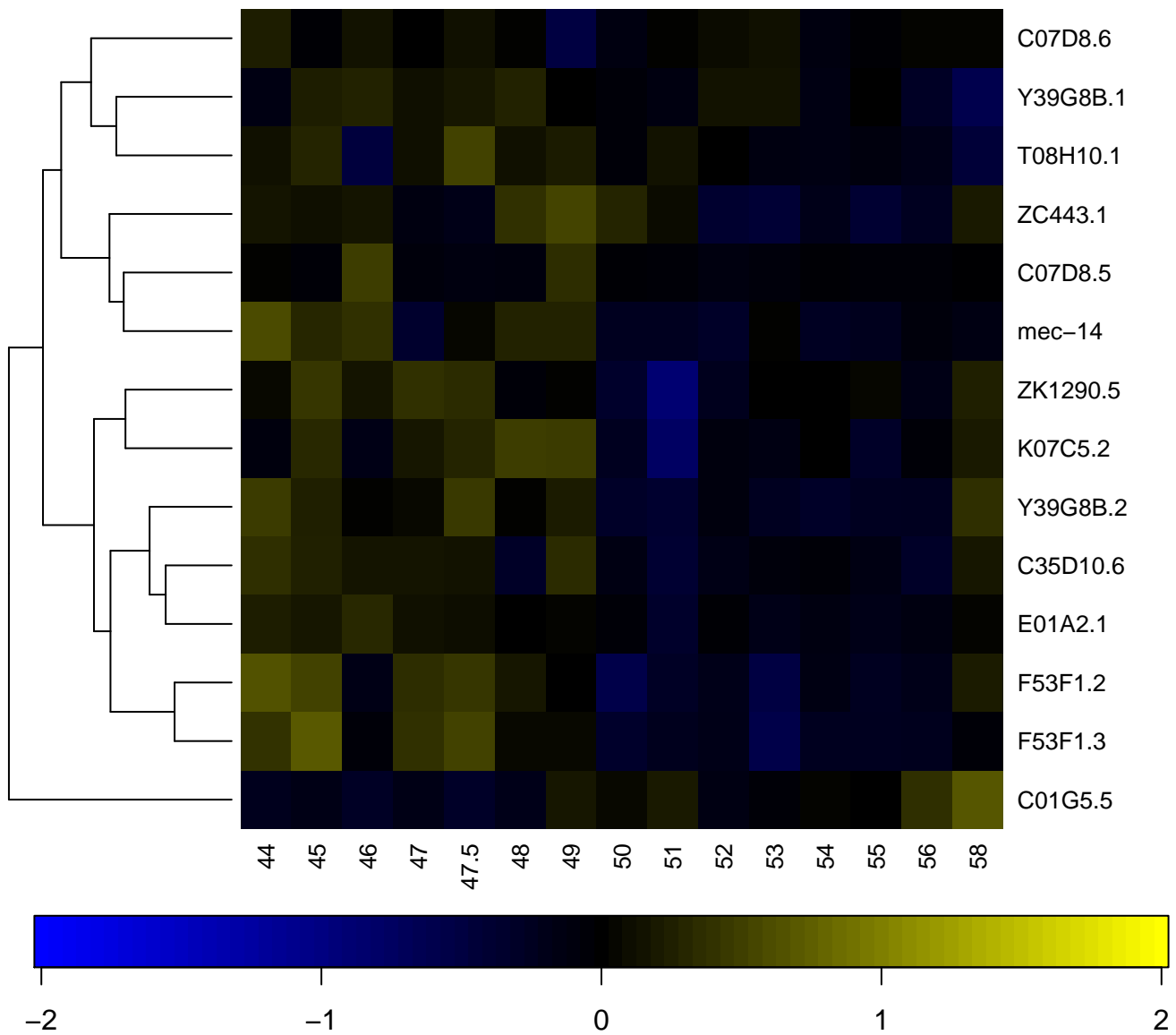
Aldehyde dehydrogenase, conserved site



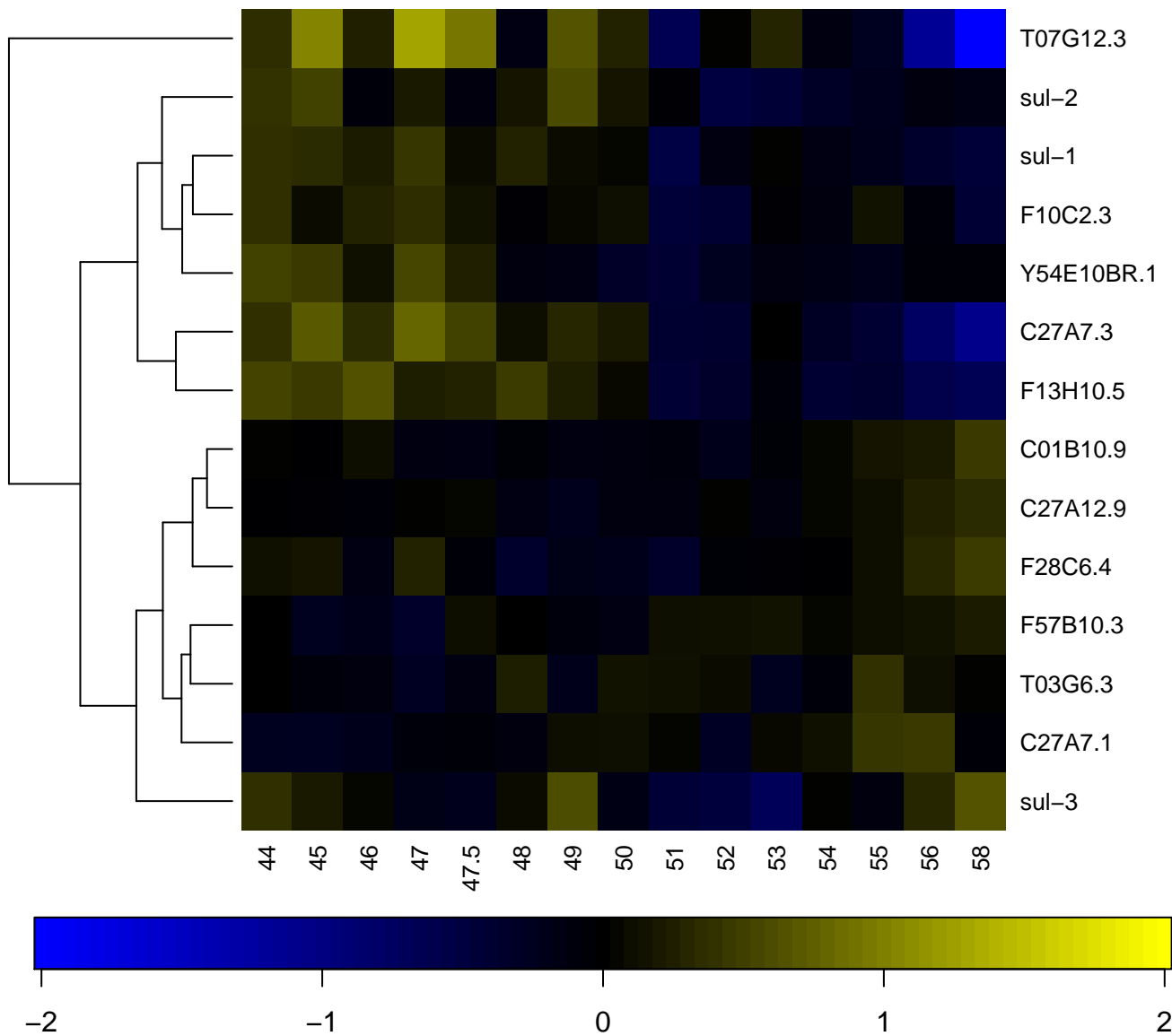
Aldo/keto reductase



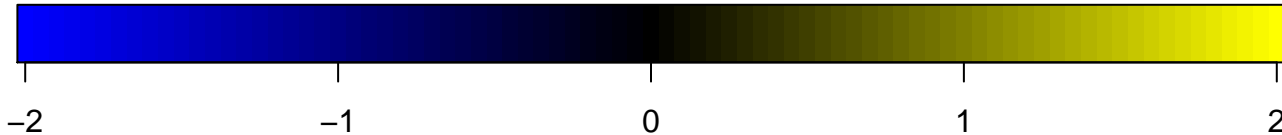
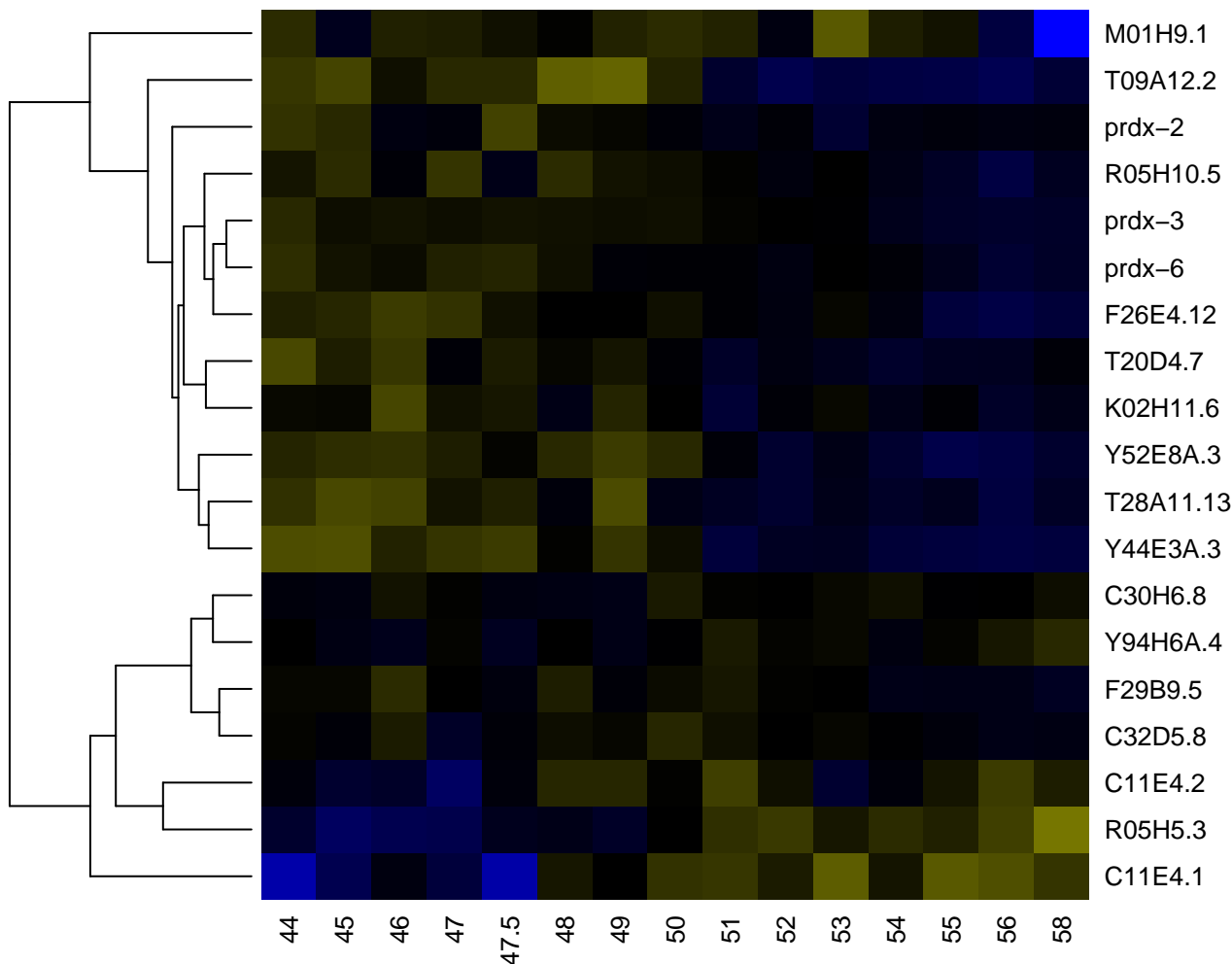
Aldo/keto reductase family



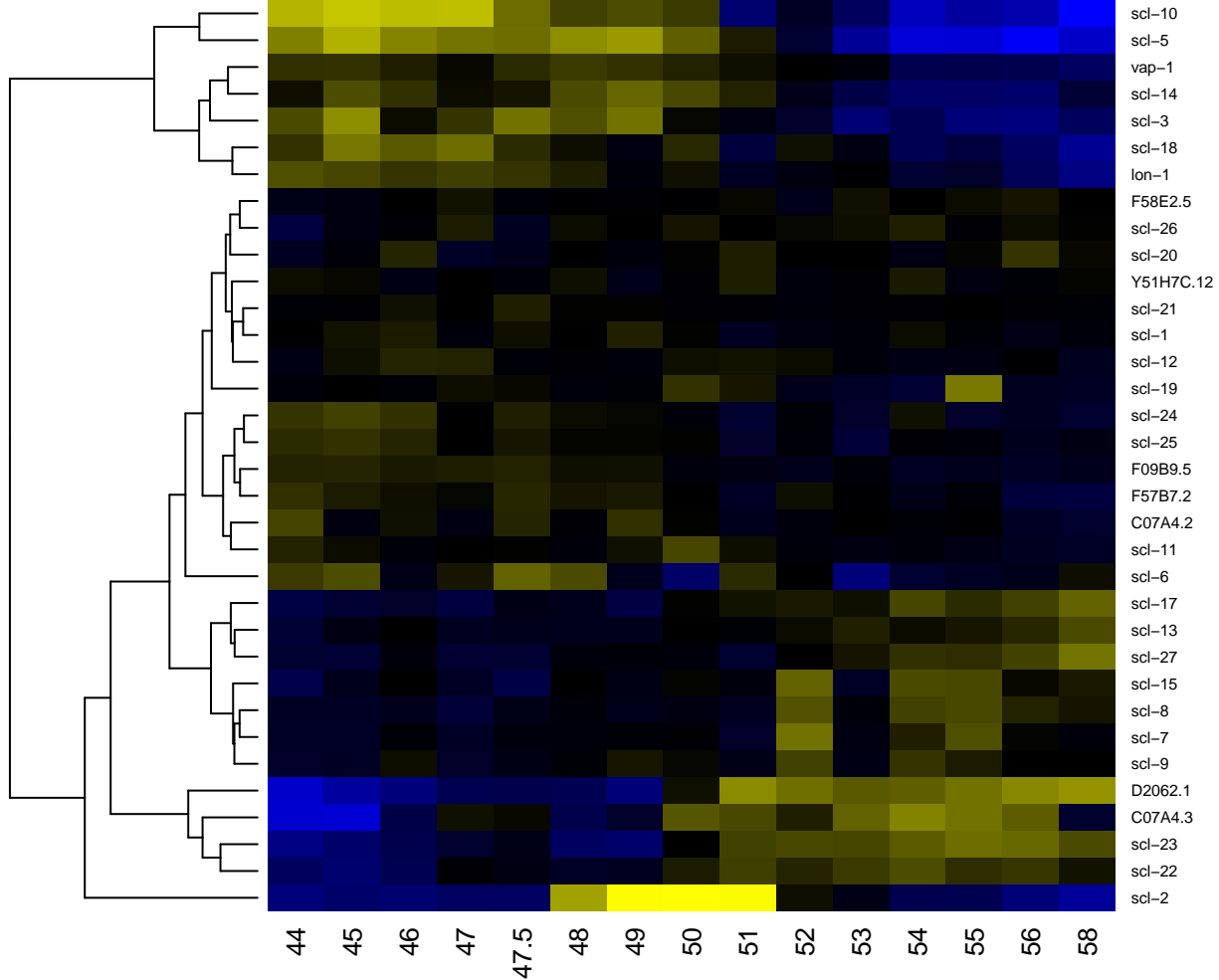
Alkaline phosphatase-like, alpha/beta/alpha



hydroperoxide reductase/ Thiol specific antioxidant/ Mal a



Allergen V5/Tpx-1 related



-2

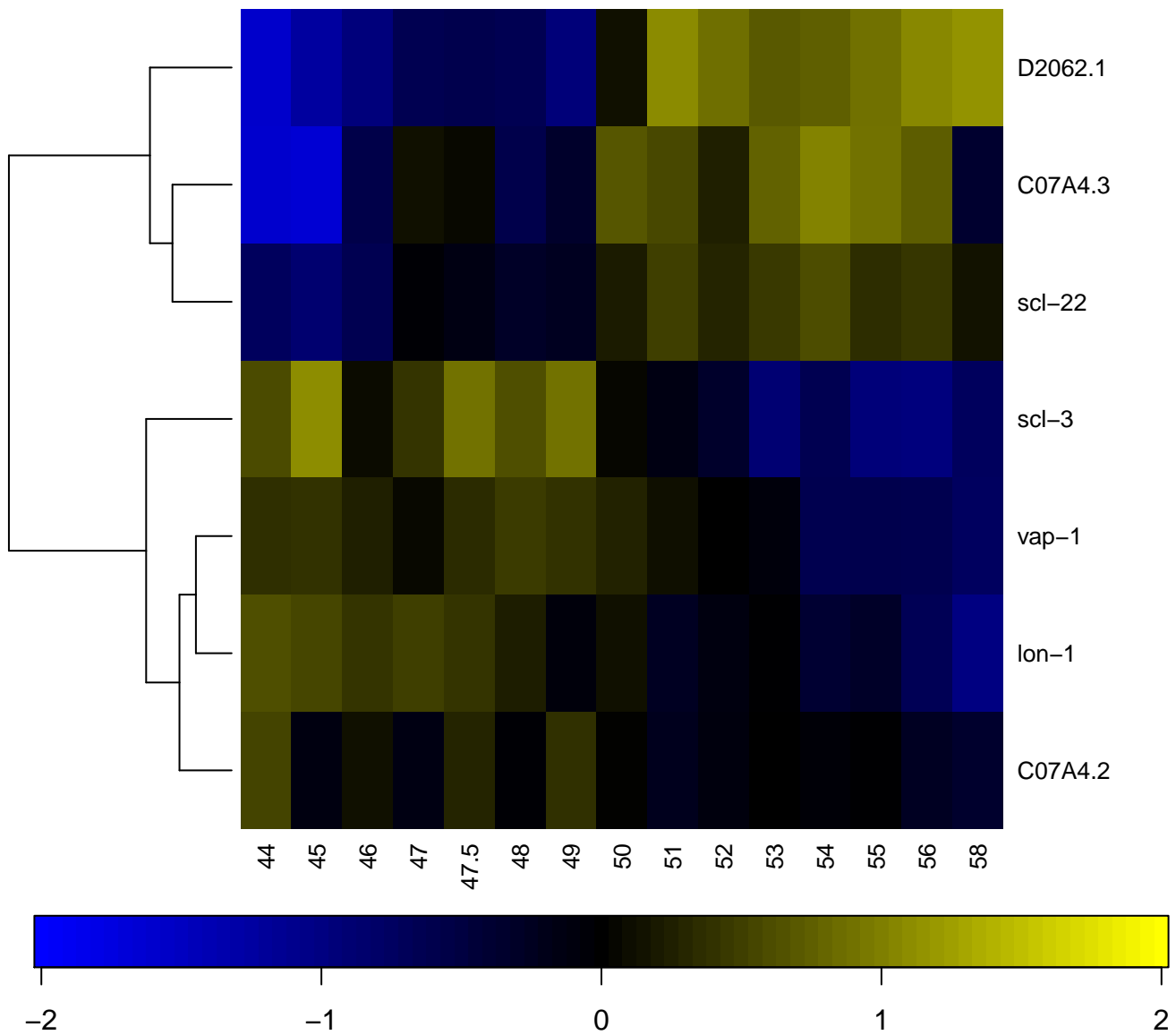
-1

0

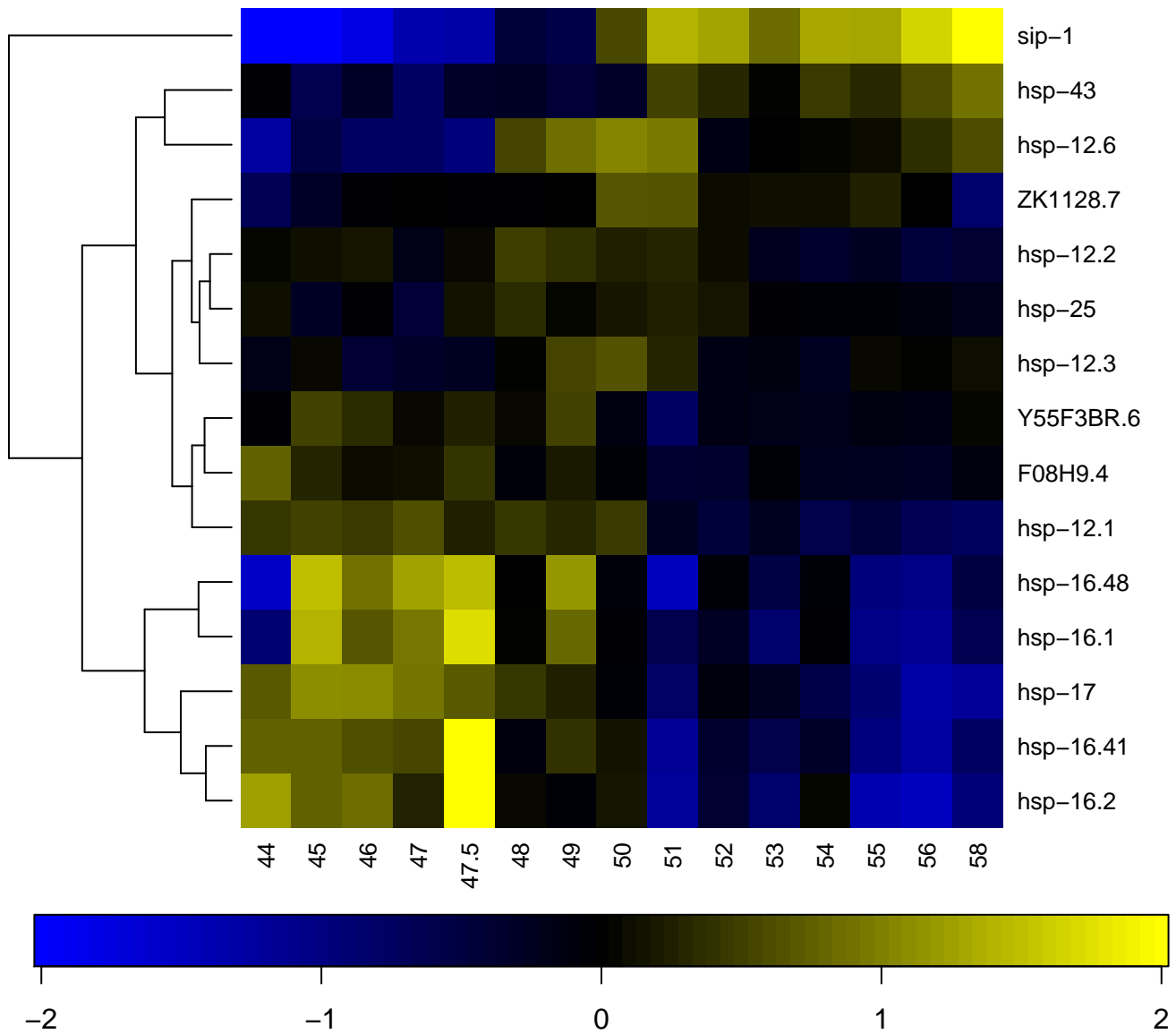
1

2

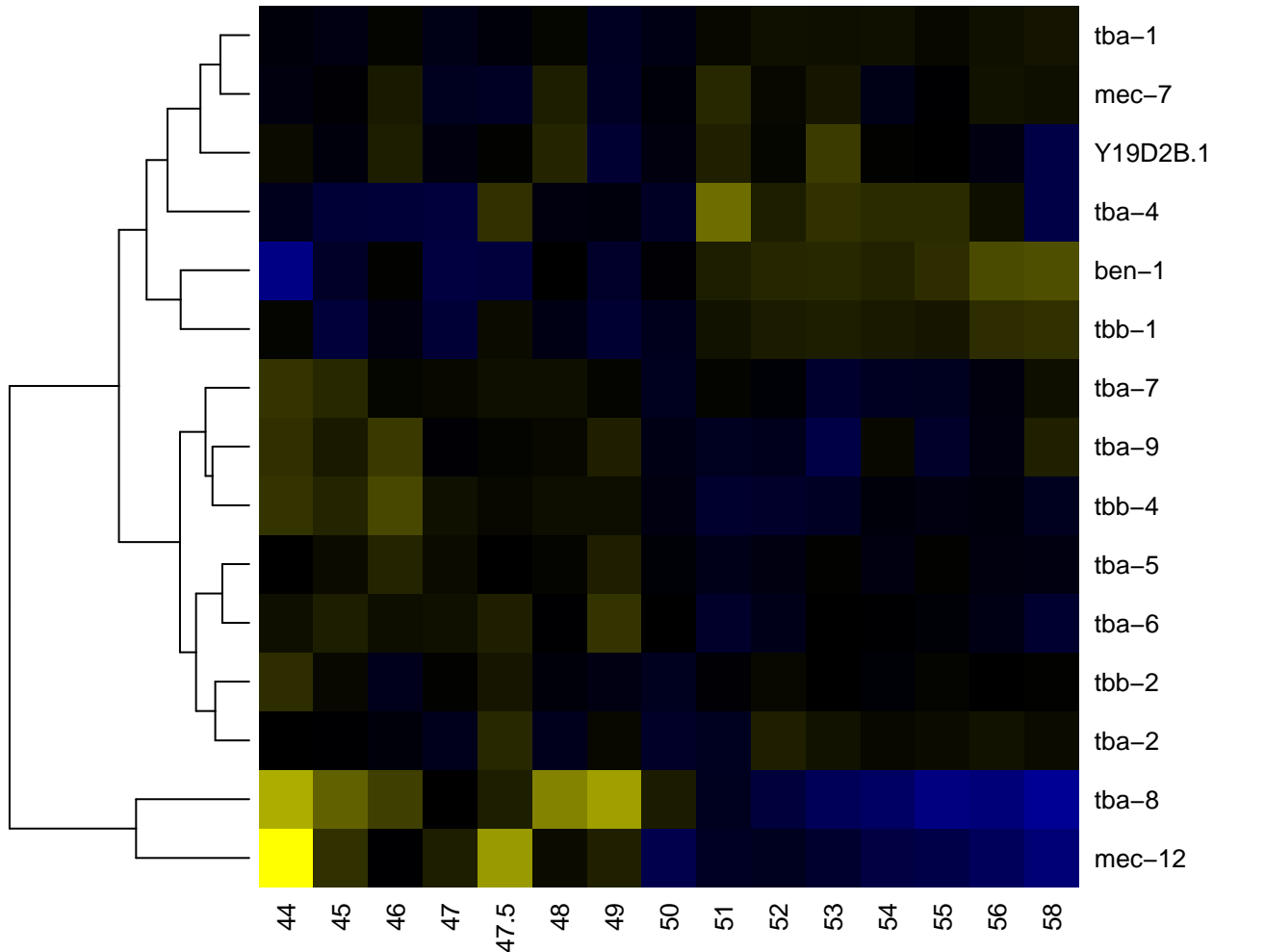
Allergen V5/Tpx-1 related, conserved site



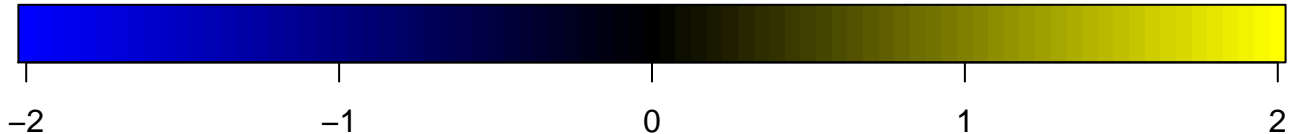
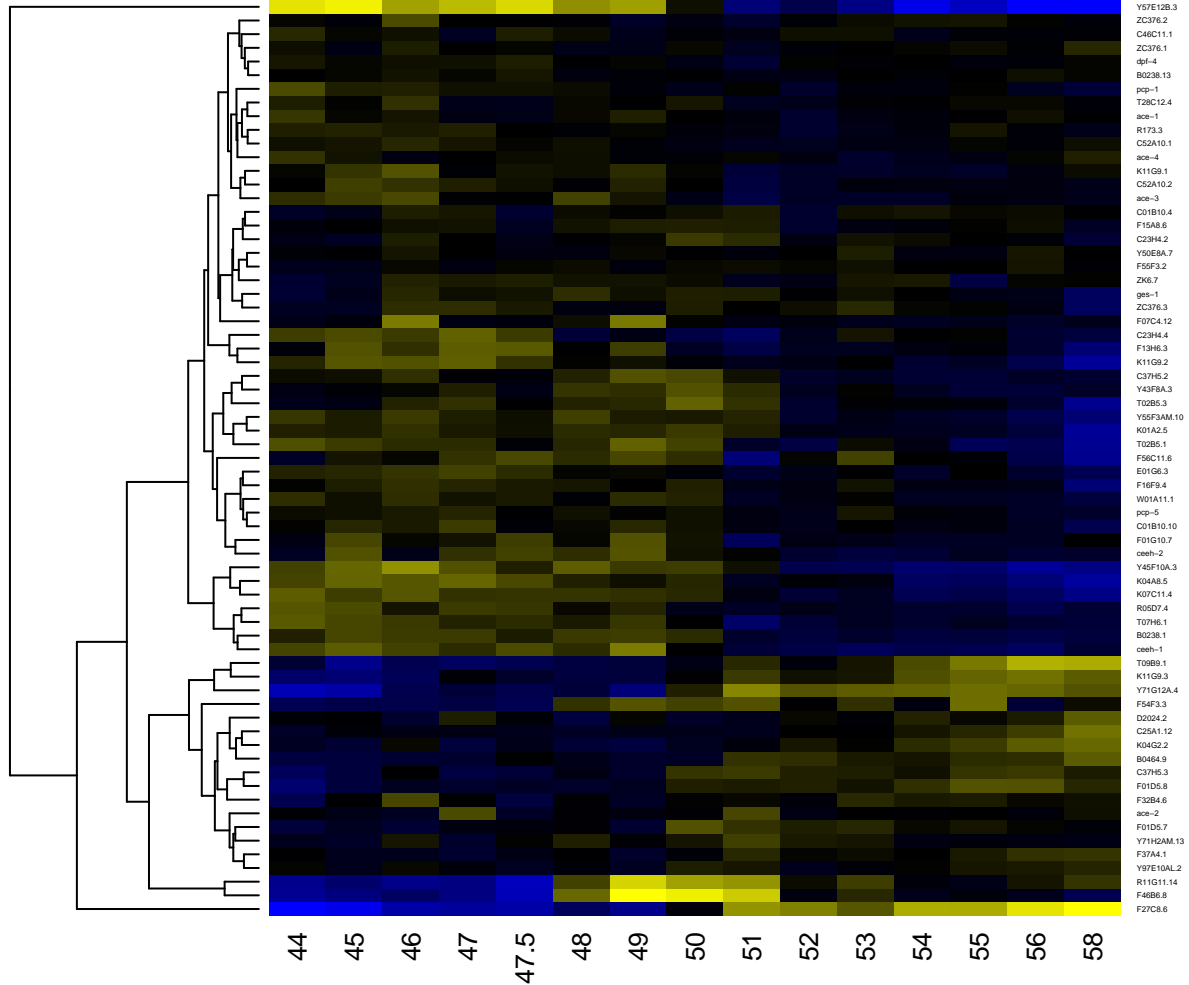
Alpha crystallin/Heat shock protein



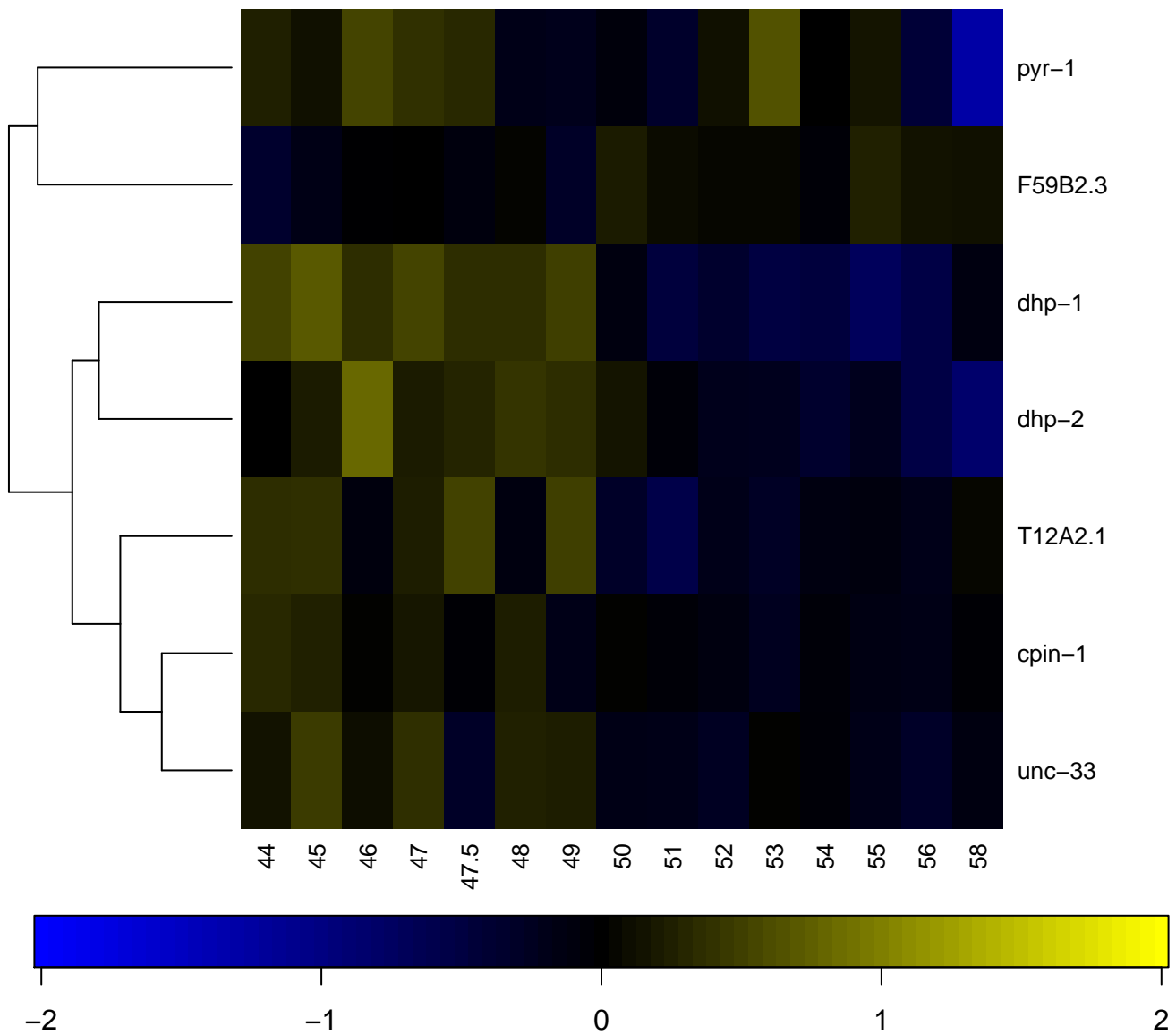
Alpha tubulin



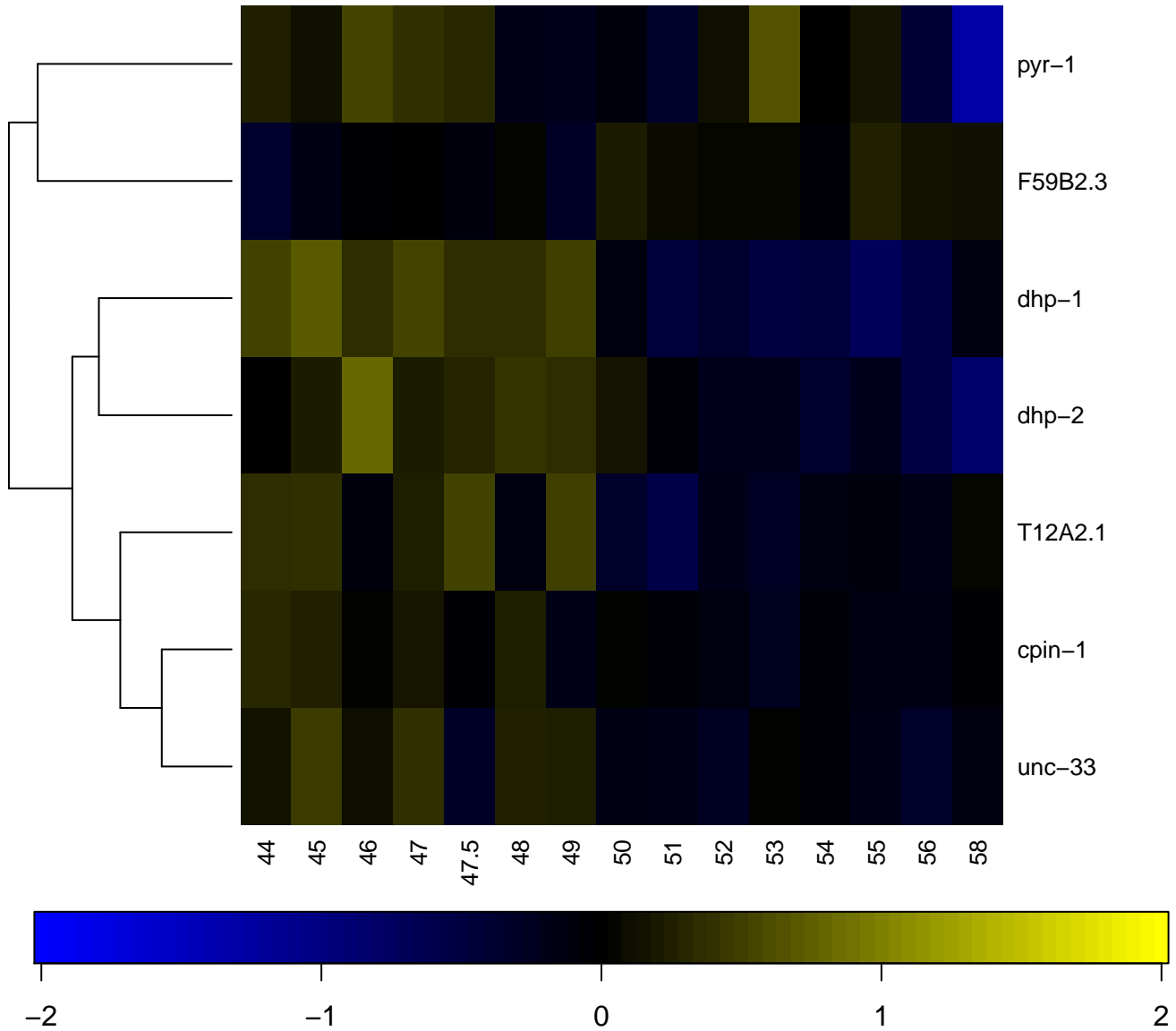
alpha/beta hydrolase fold



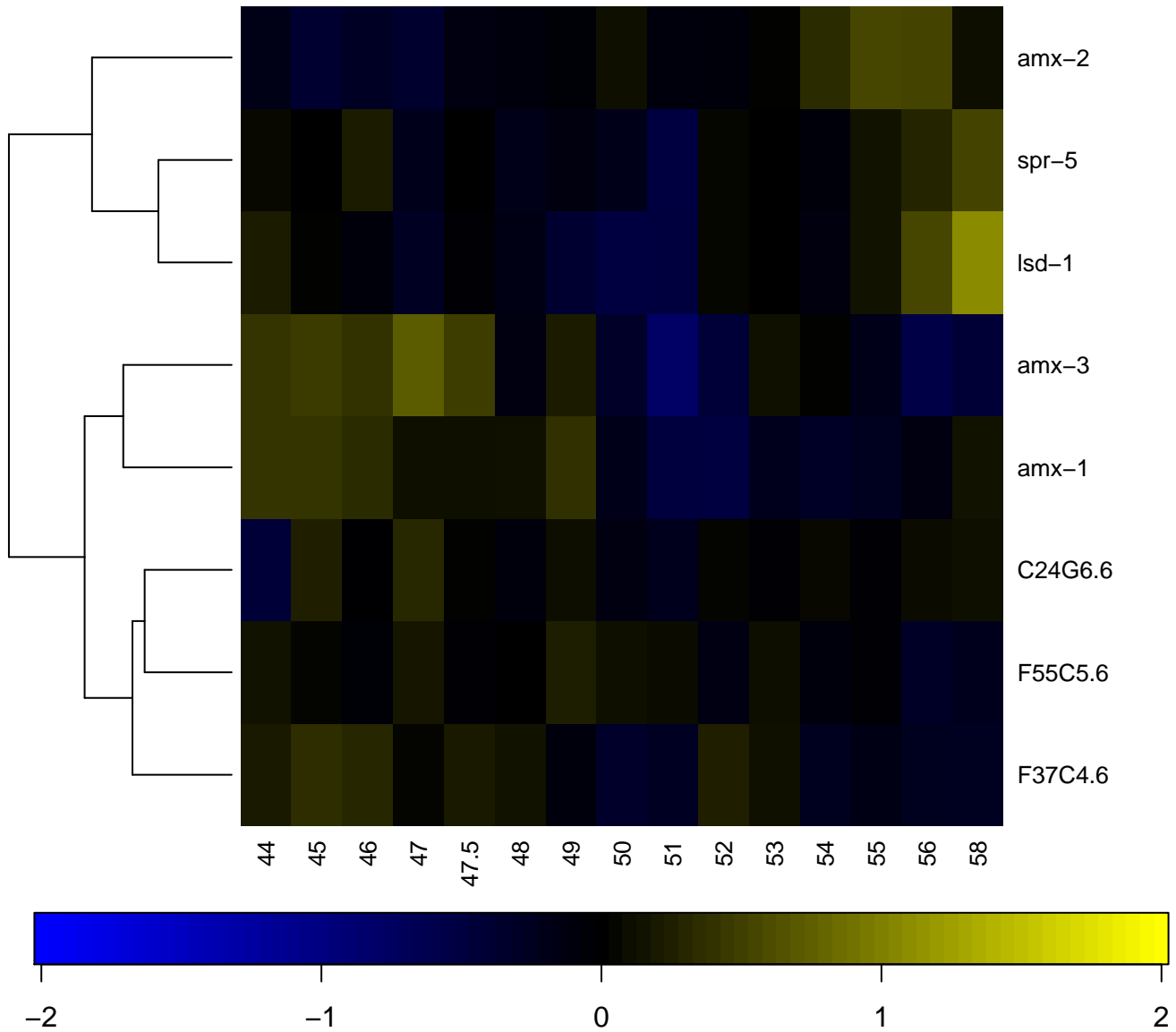
Amidohydrolase 1



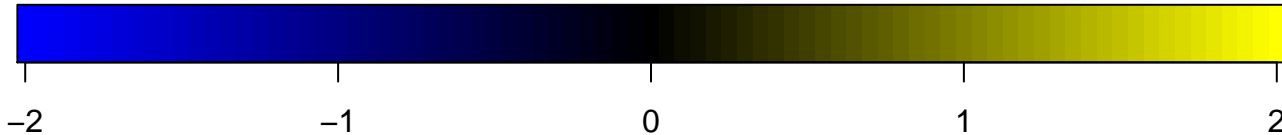
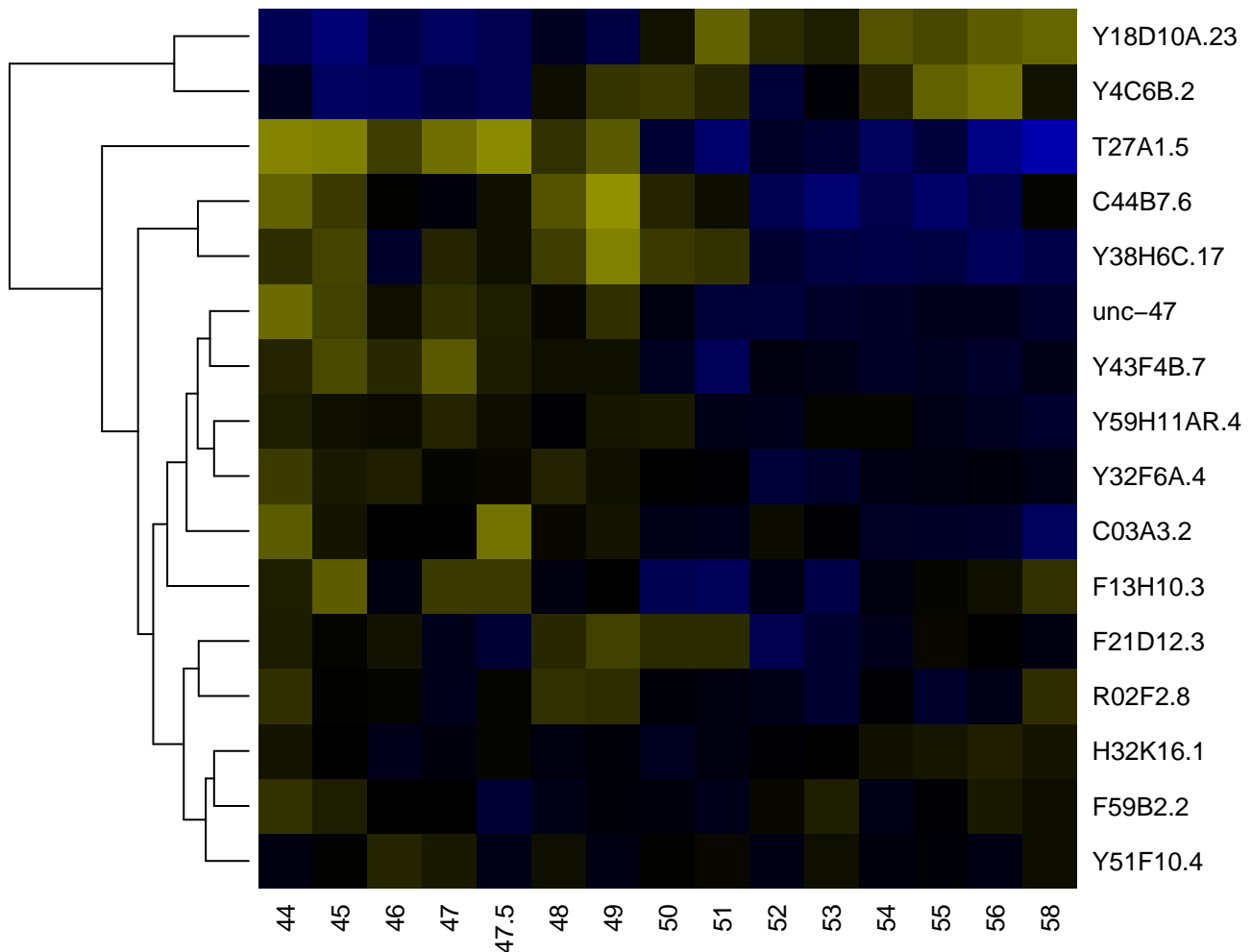
Amidohydrolase family



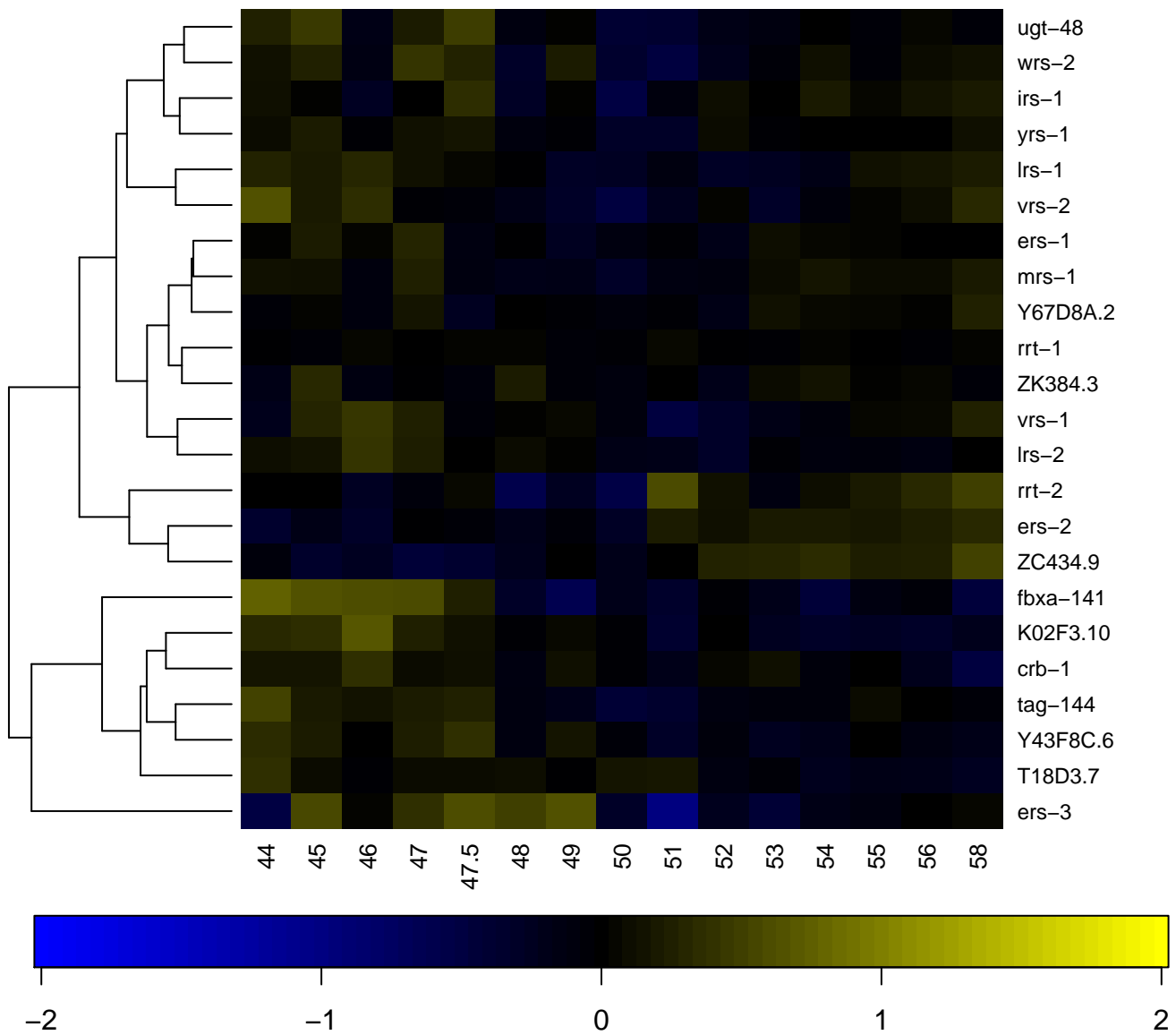
Amine oxidase



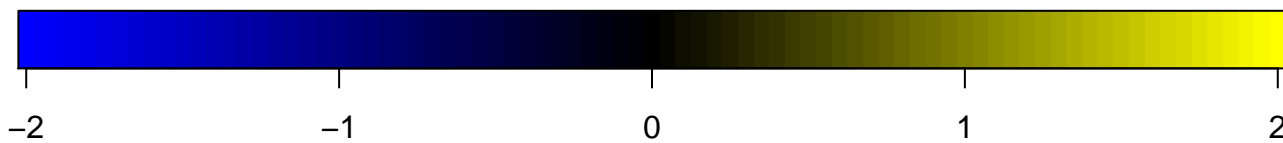
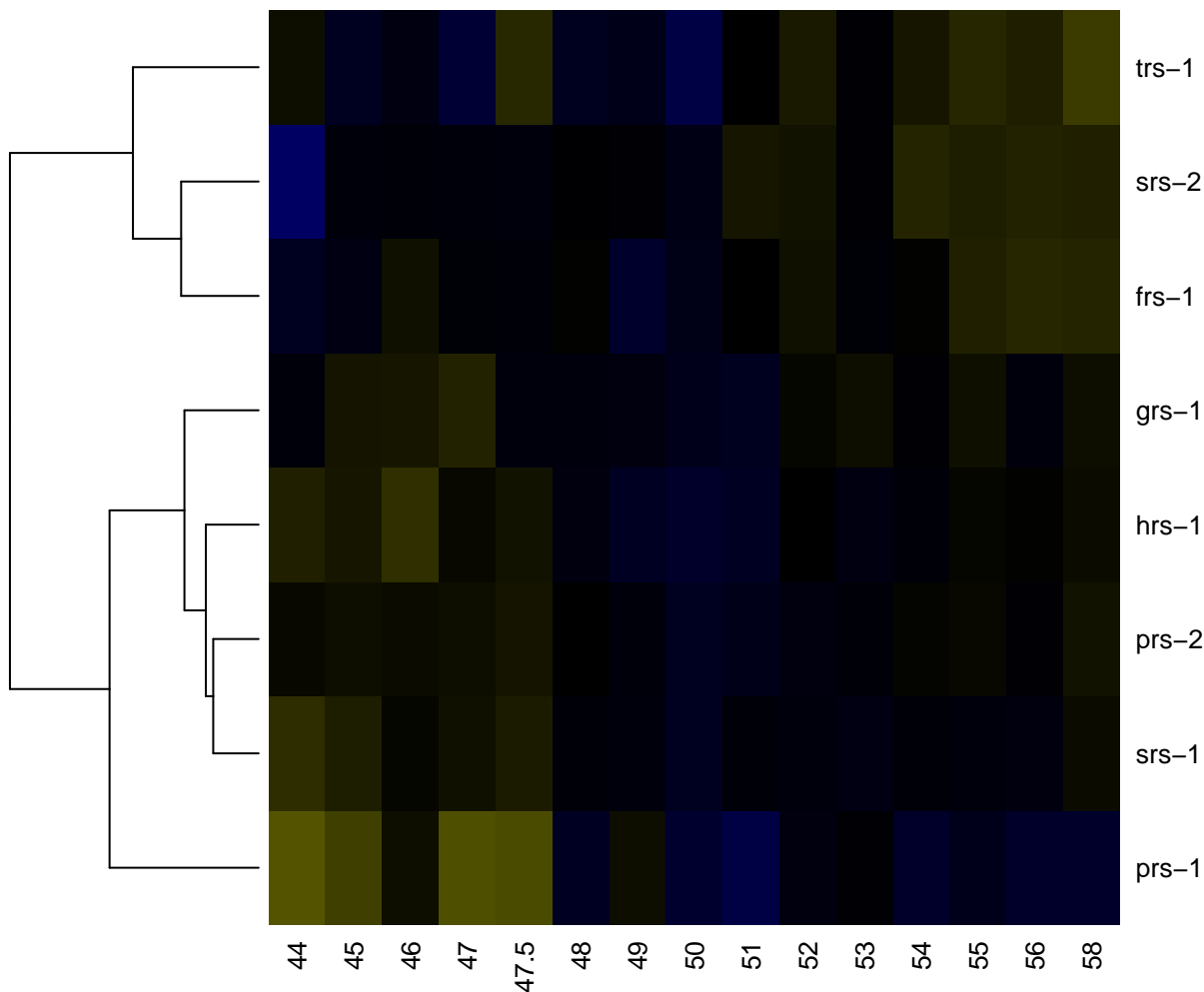
Amino acid transporter, transmembrane



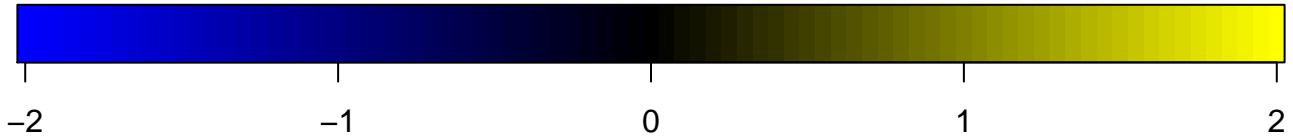
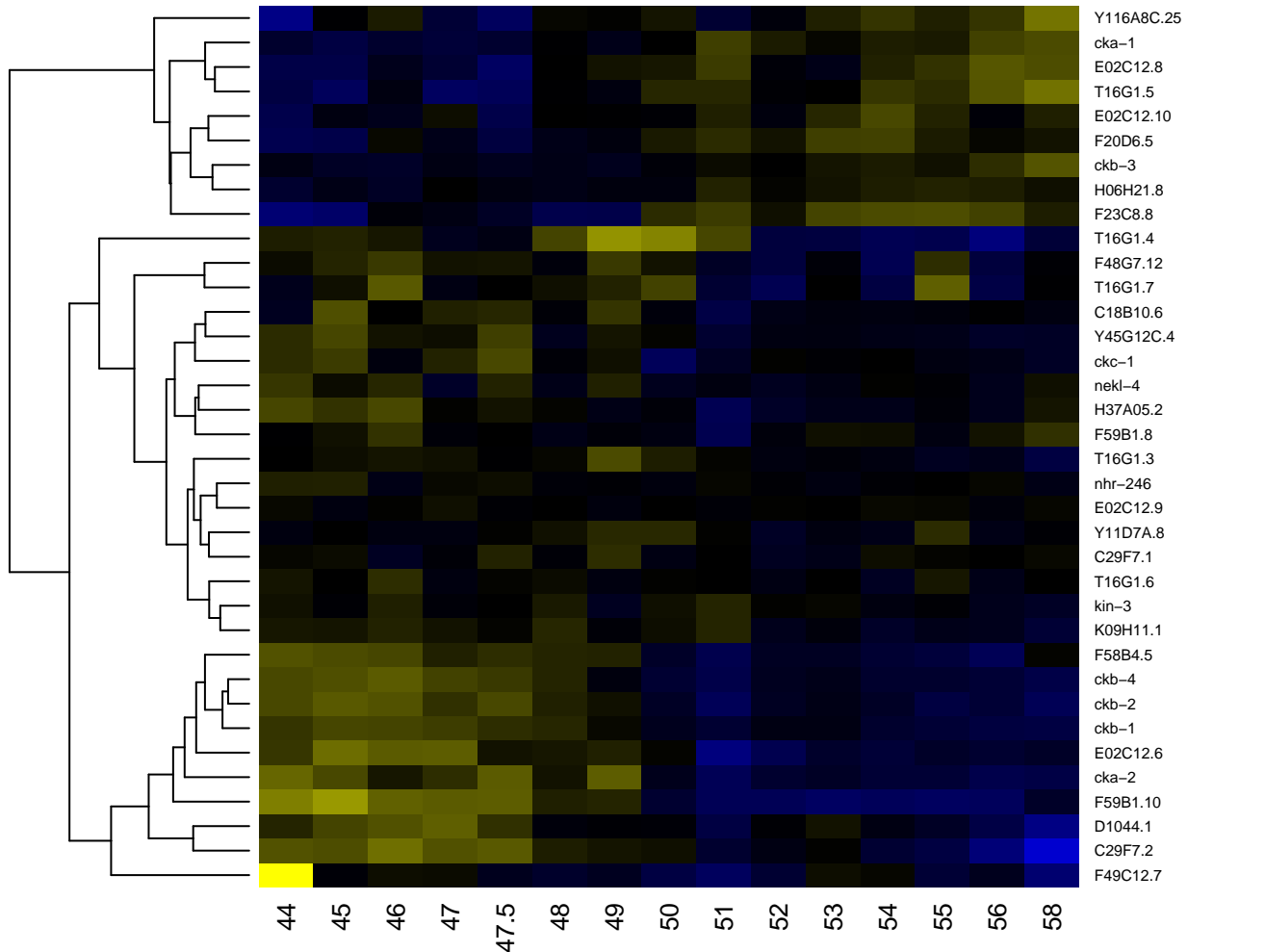
Aminoacyl-tRNA synthetase, class I, conserved site



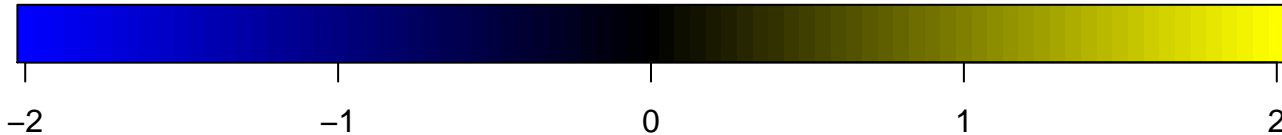
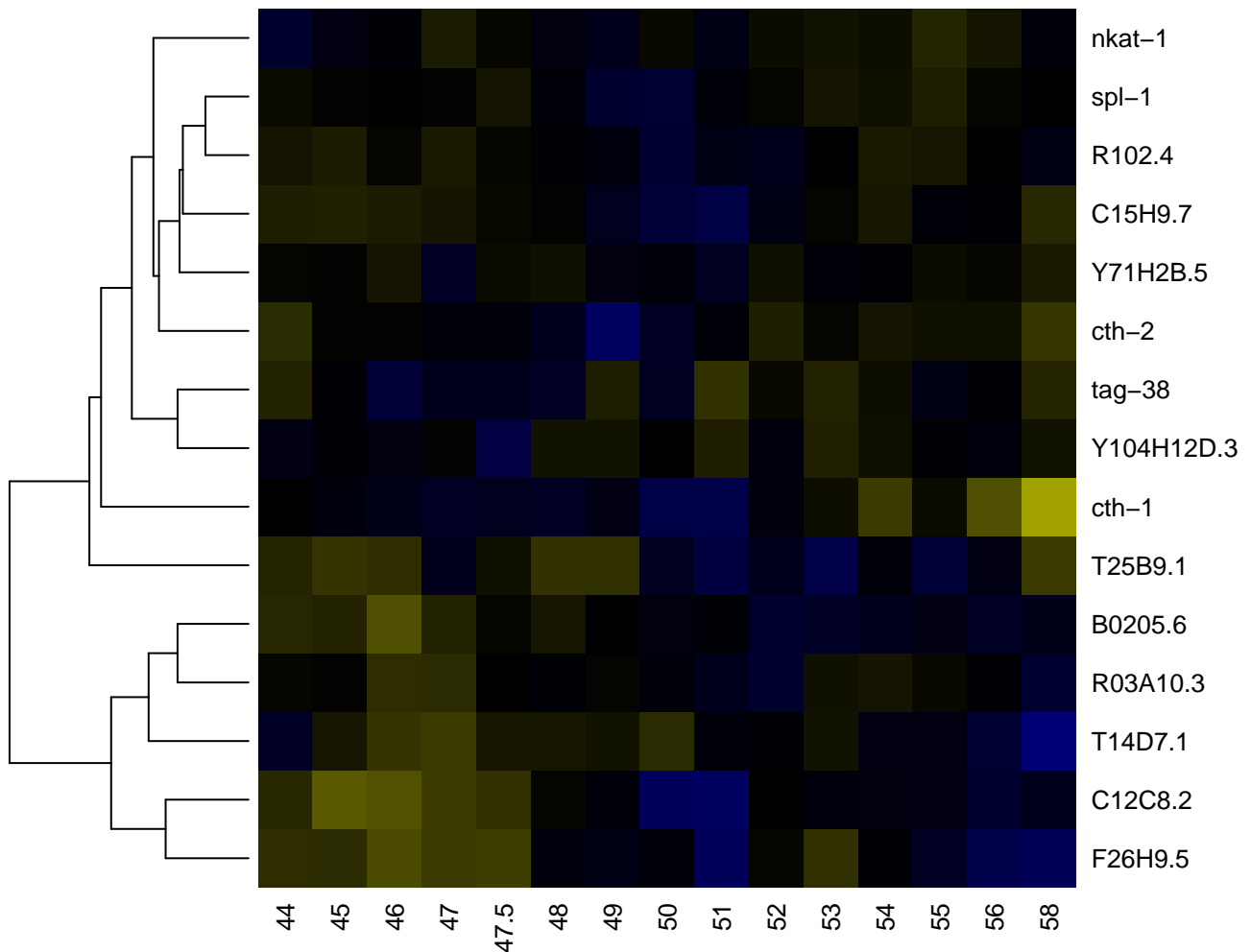
inoacyl-tRNA synthetase, class II (G/ H/ P/ S), conserved do



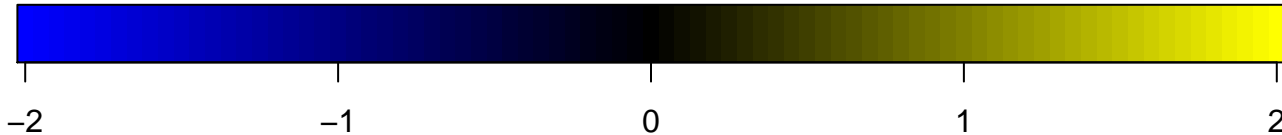
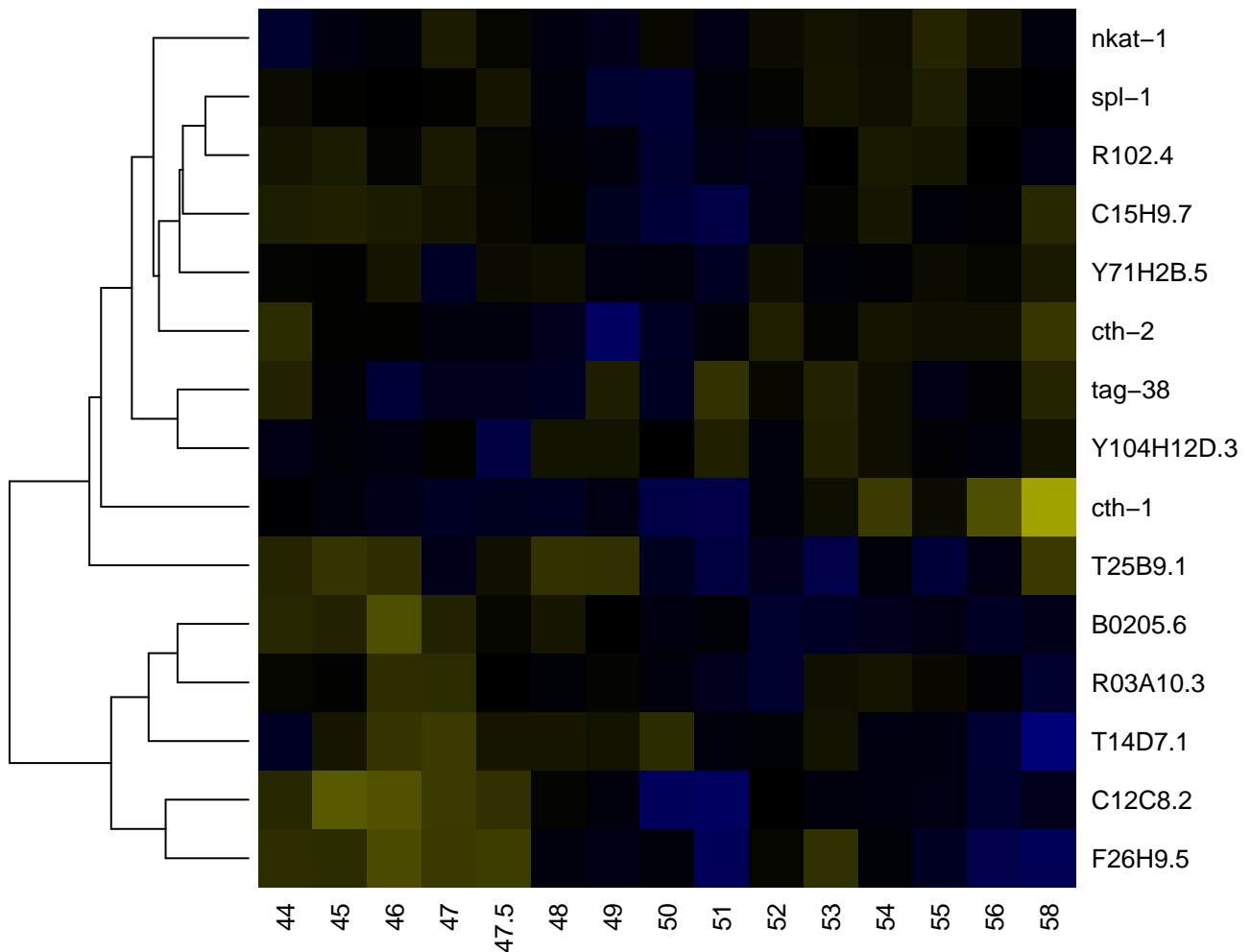
Aminoglycoside phosphotransferase



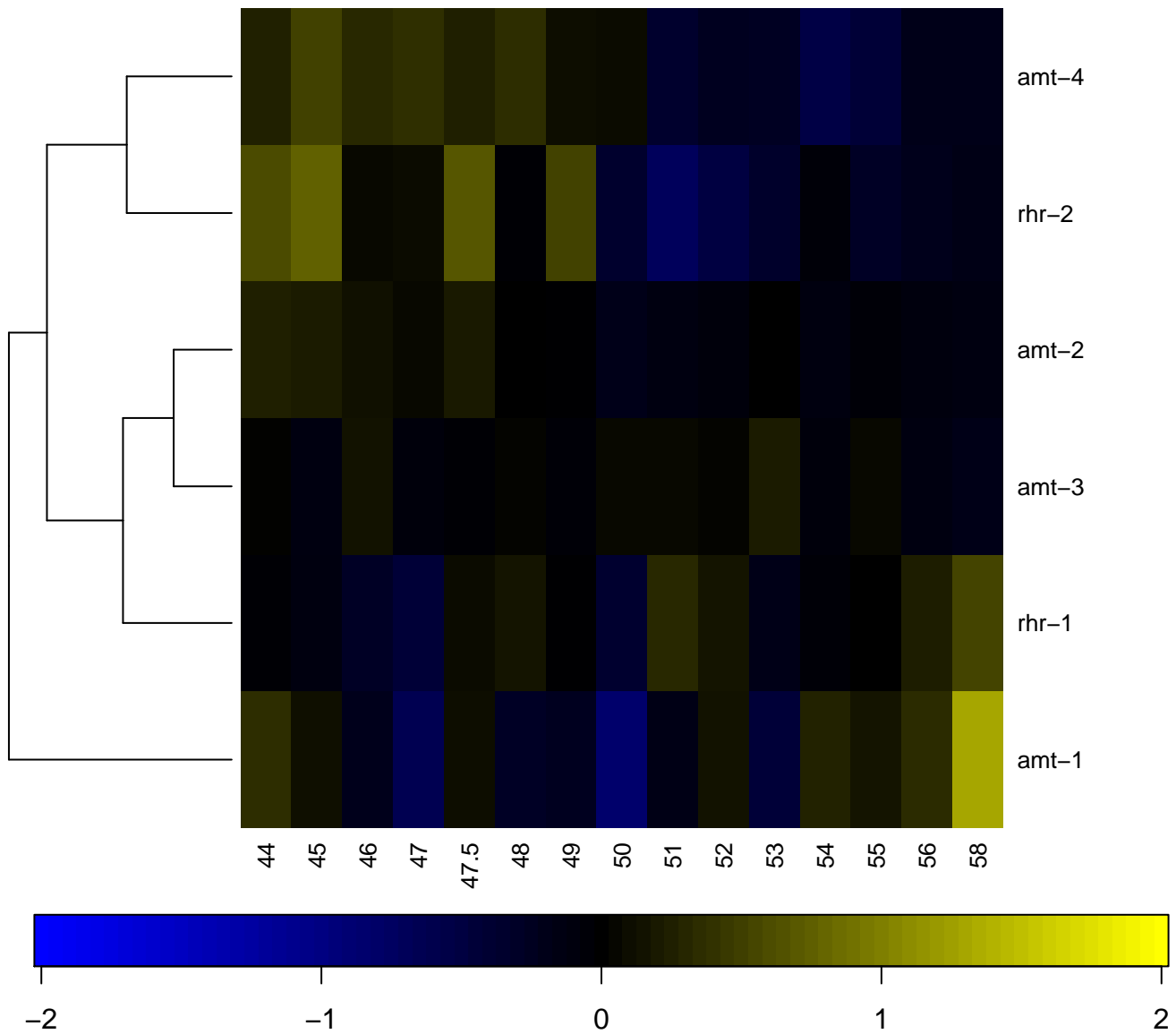
Aminotransferase class-V



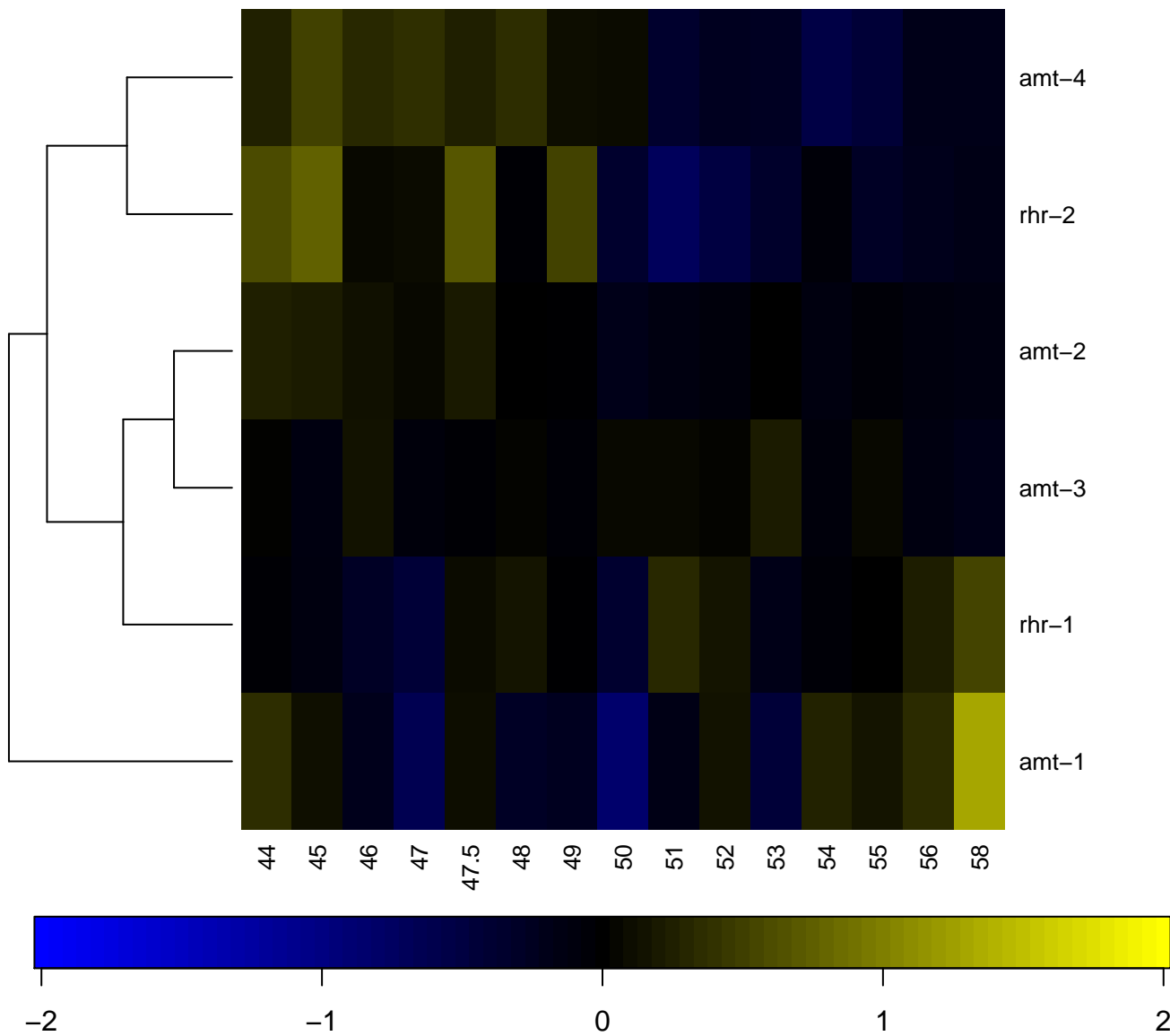
Aminotransferase, class V/Cysteine desulfurase



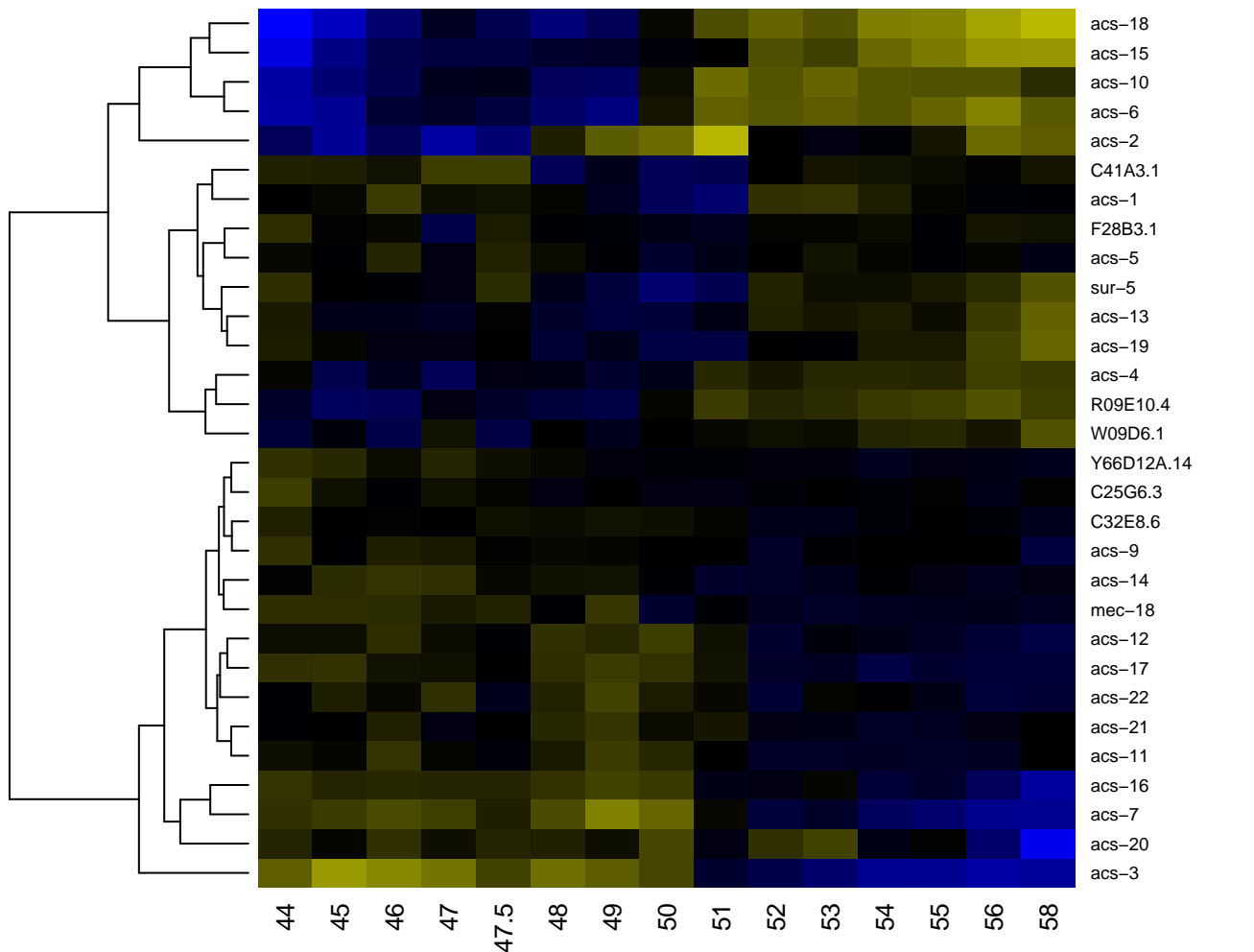
Ammonium transporter



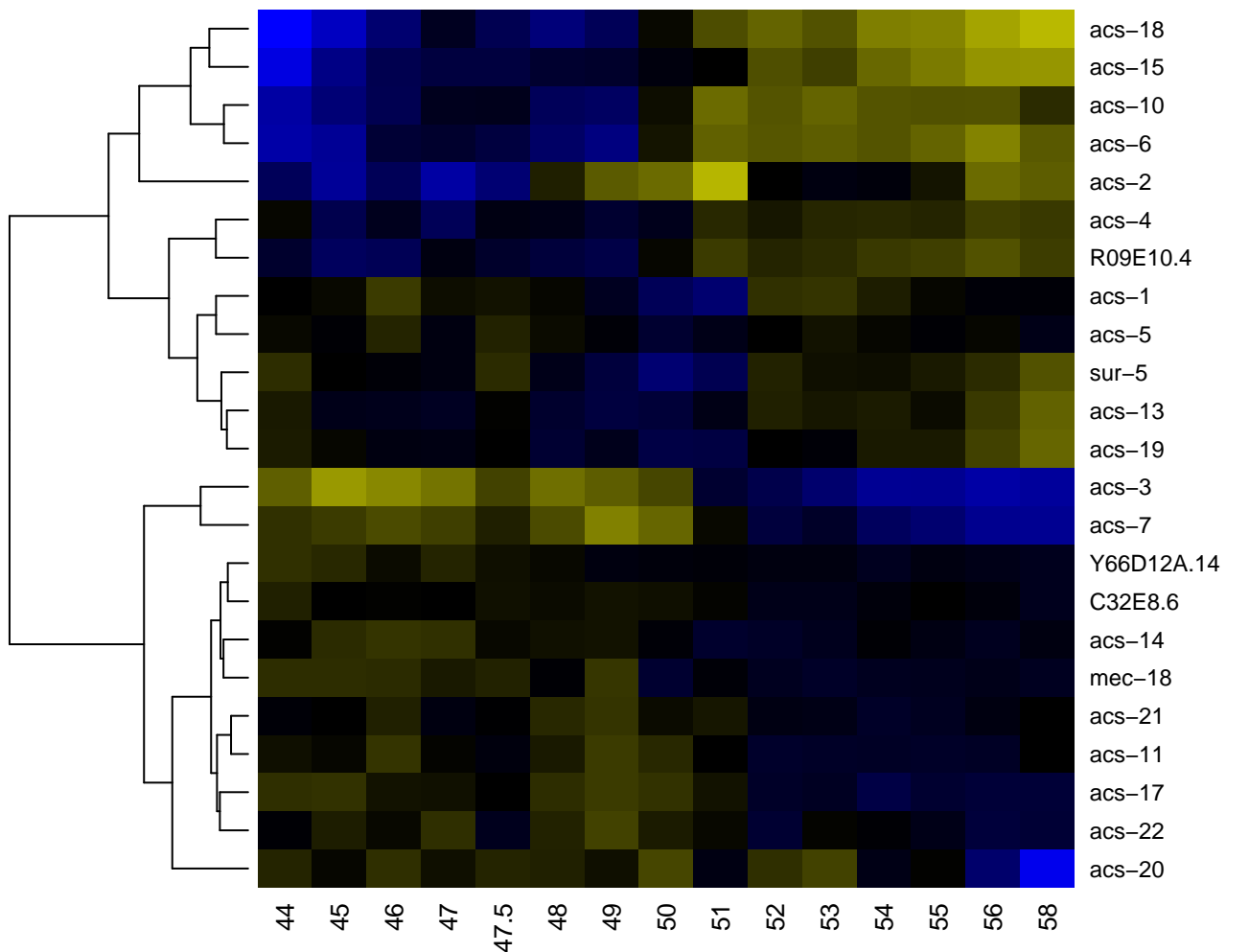
Ammonium Transporter Family



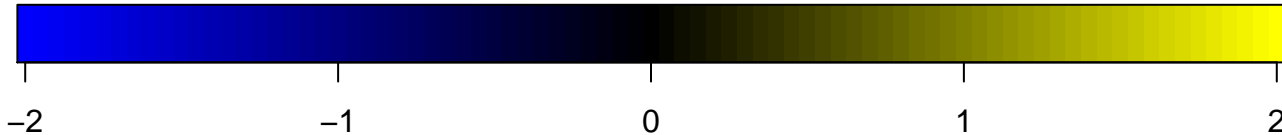
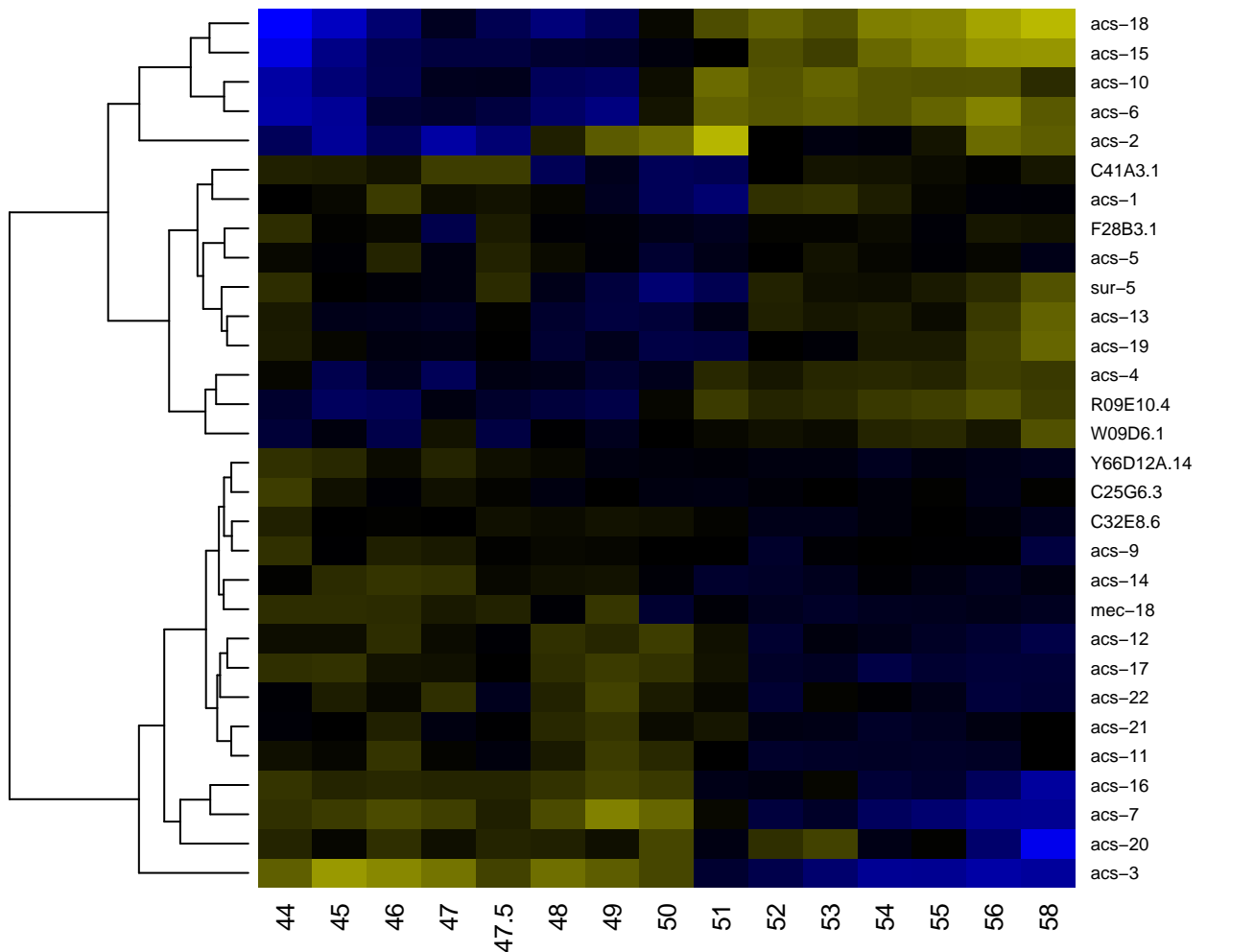
AMP-binding enzyme



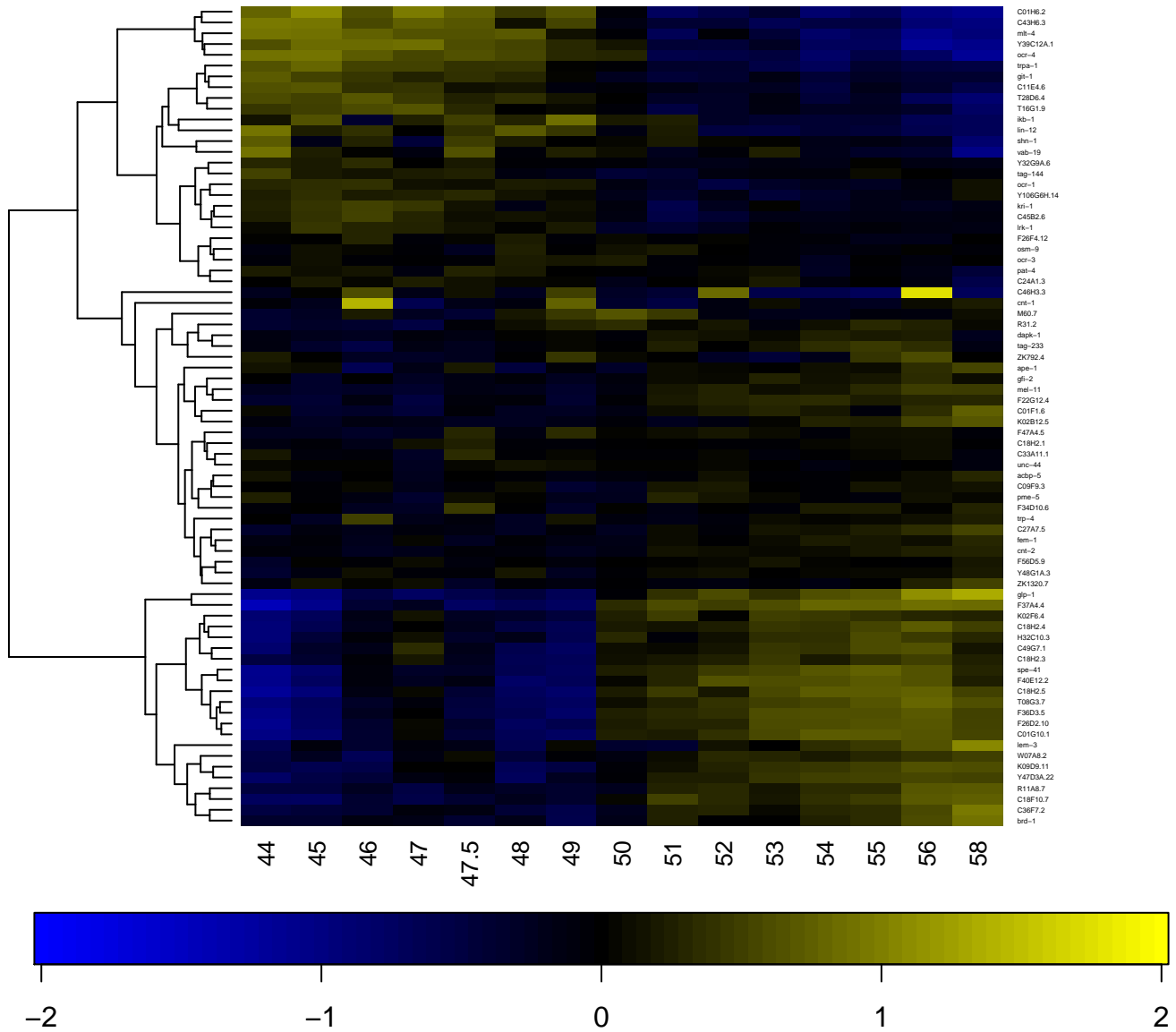
AMP-binding, conserved site



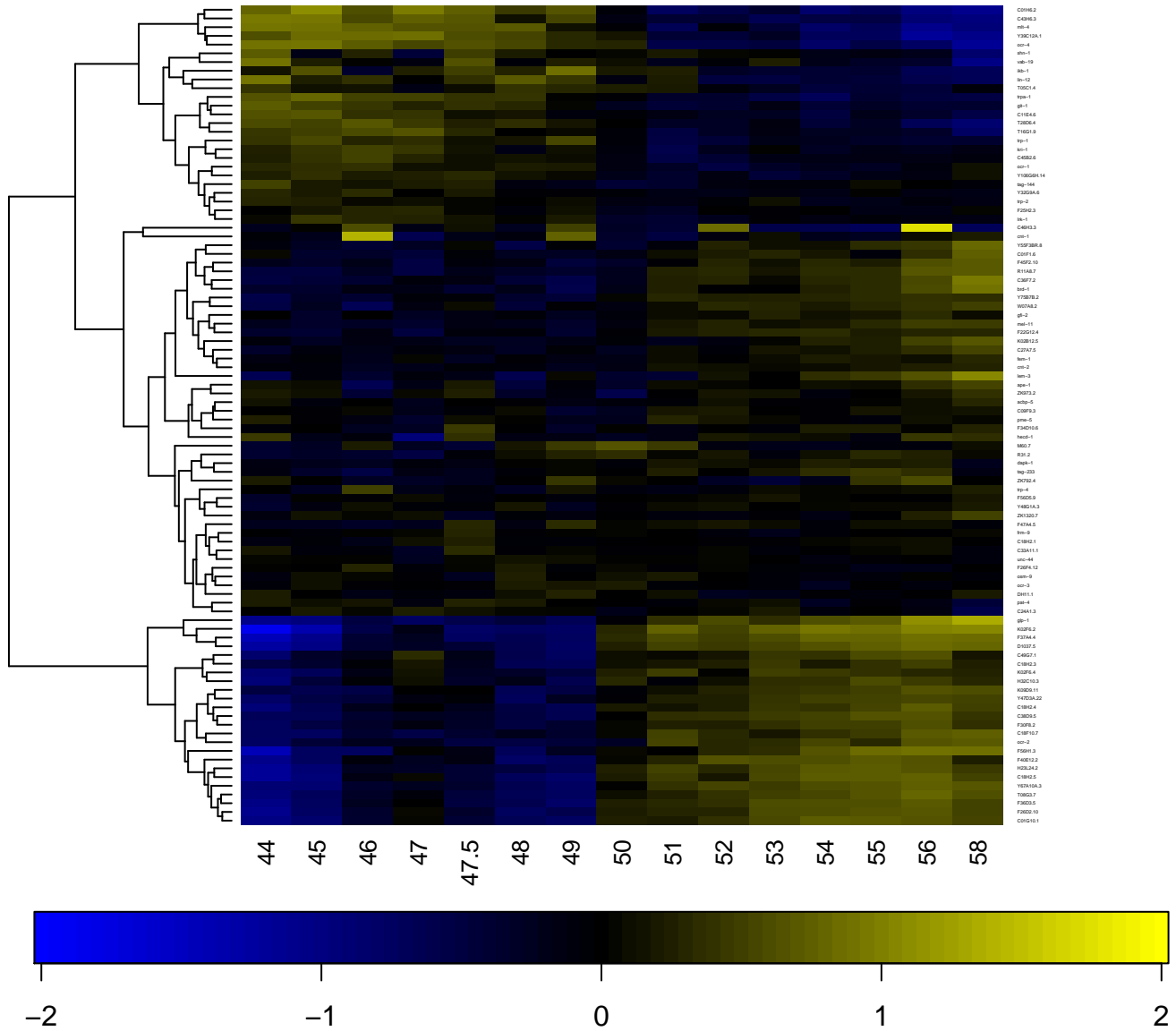
AMP-dependent synthetase/ligase



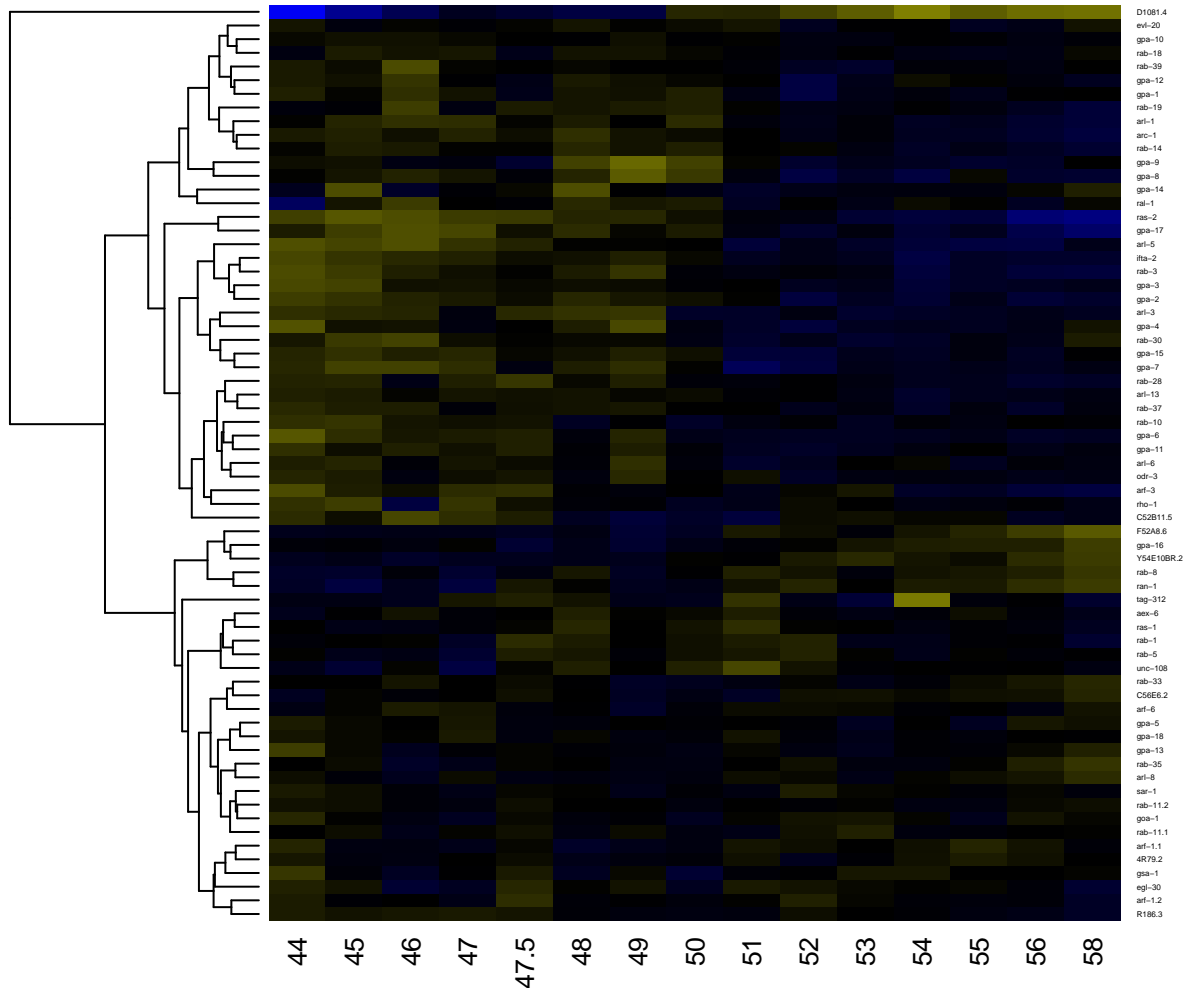
Ankyrin repeat



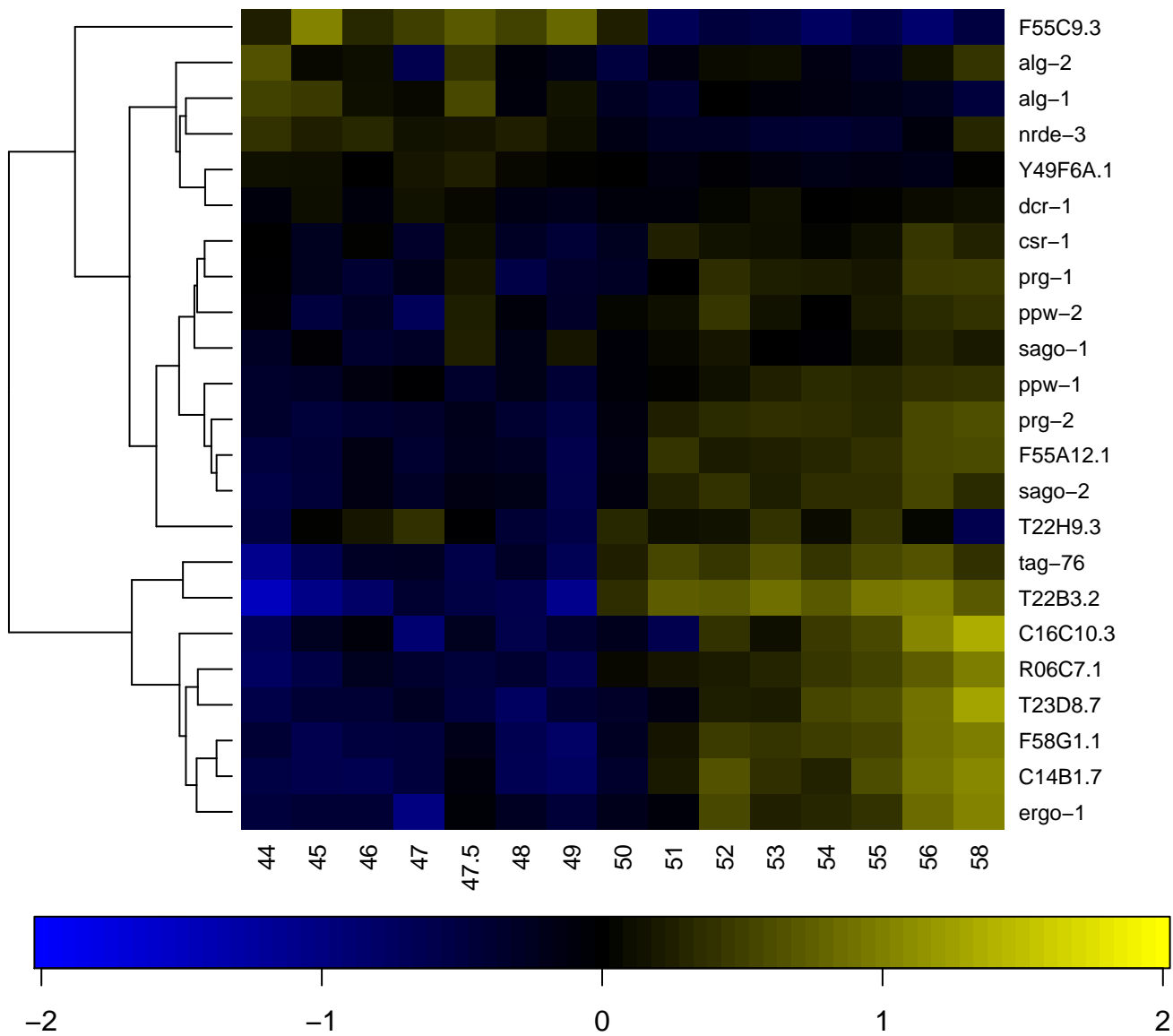
Ankyrin repeat-containing domain



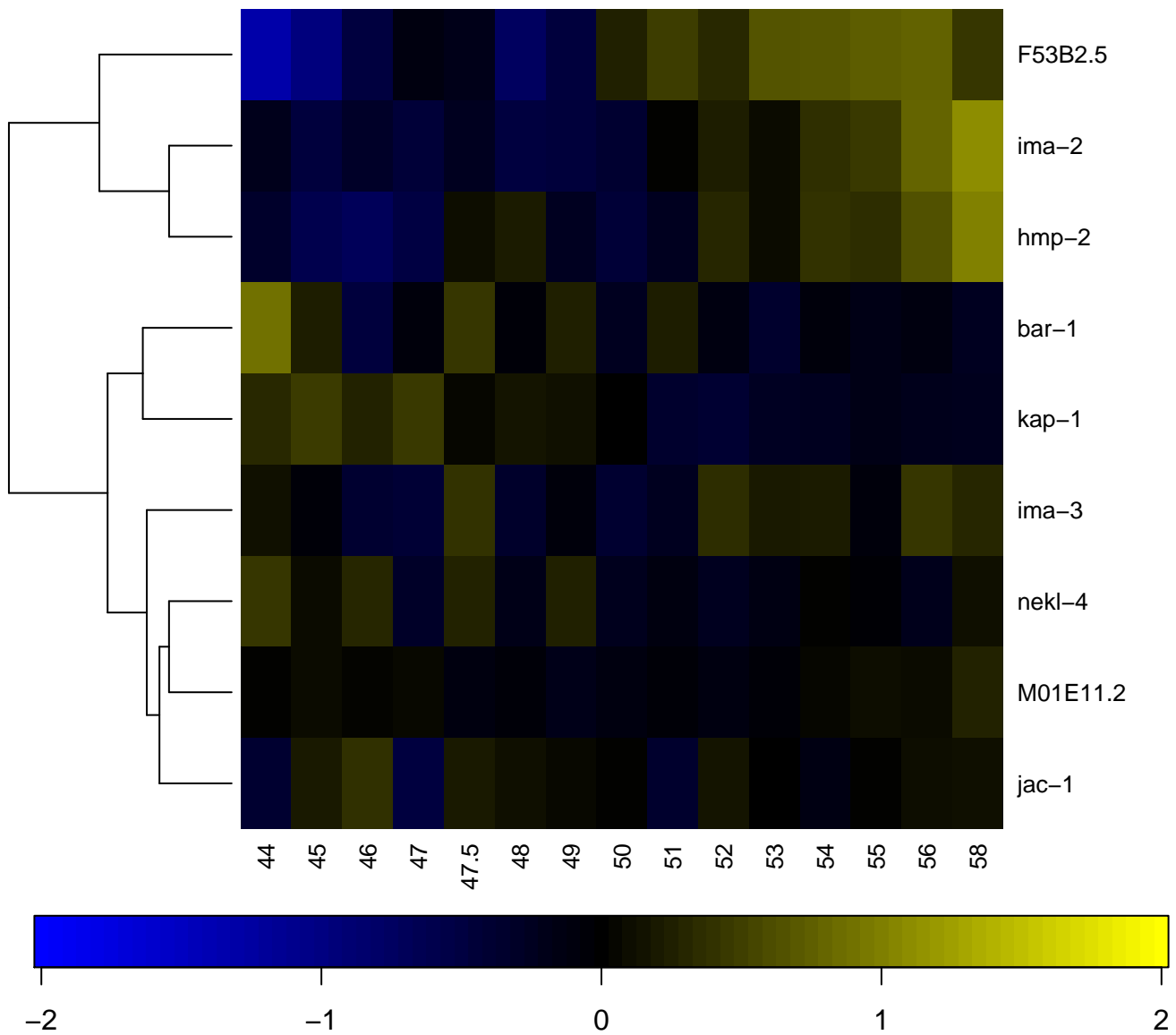
ARF/SAR superfamily



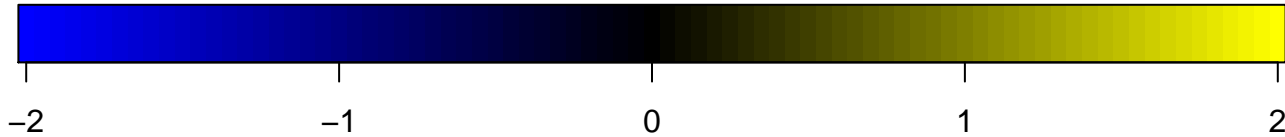
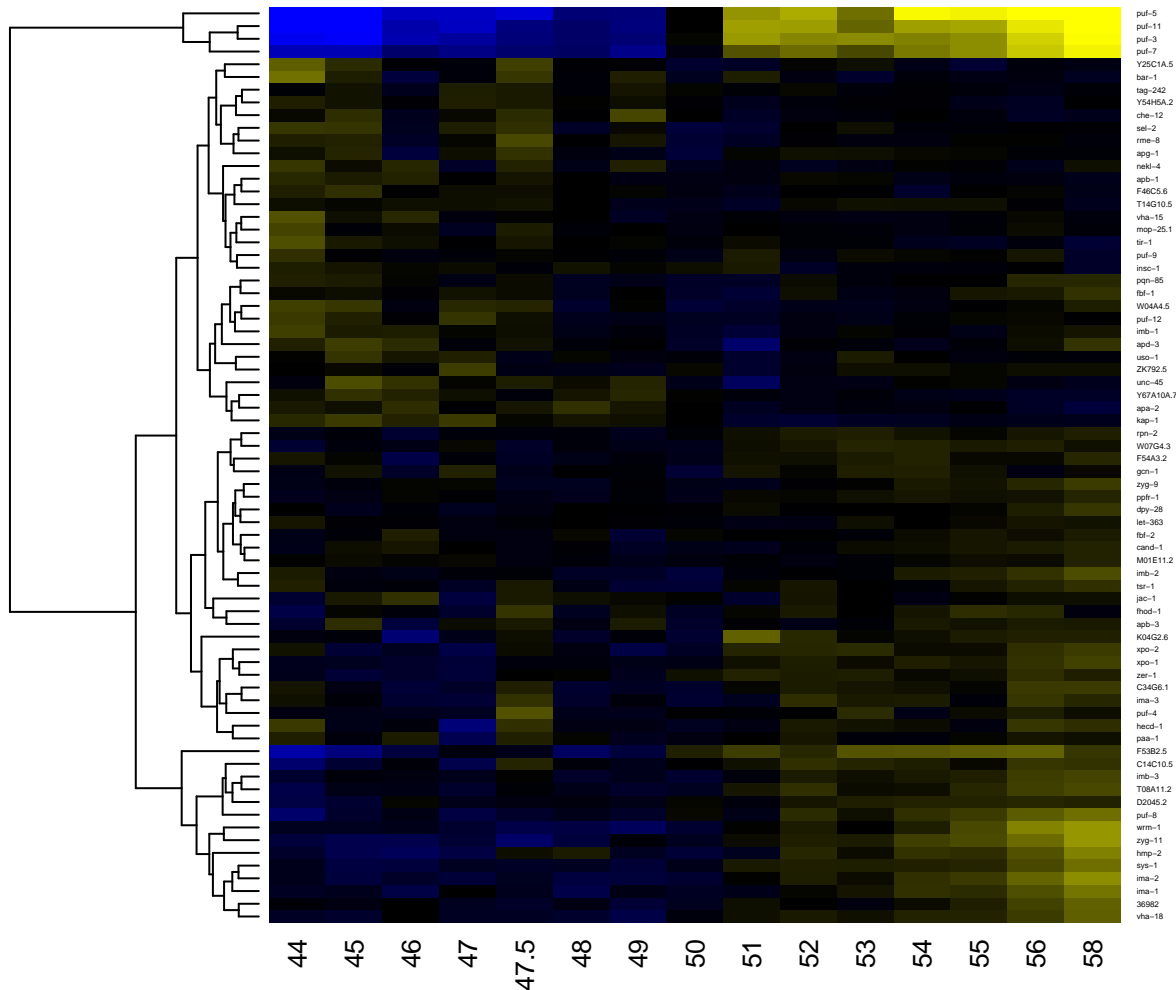
Argonaute/Dicer protein, PAZ



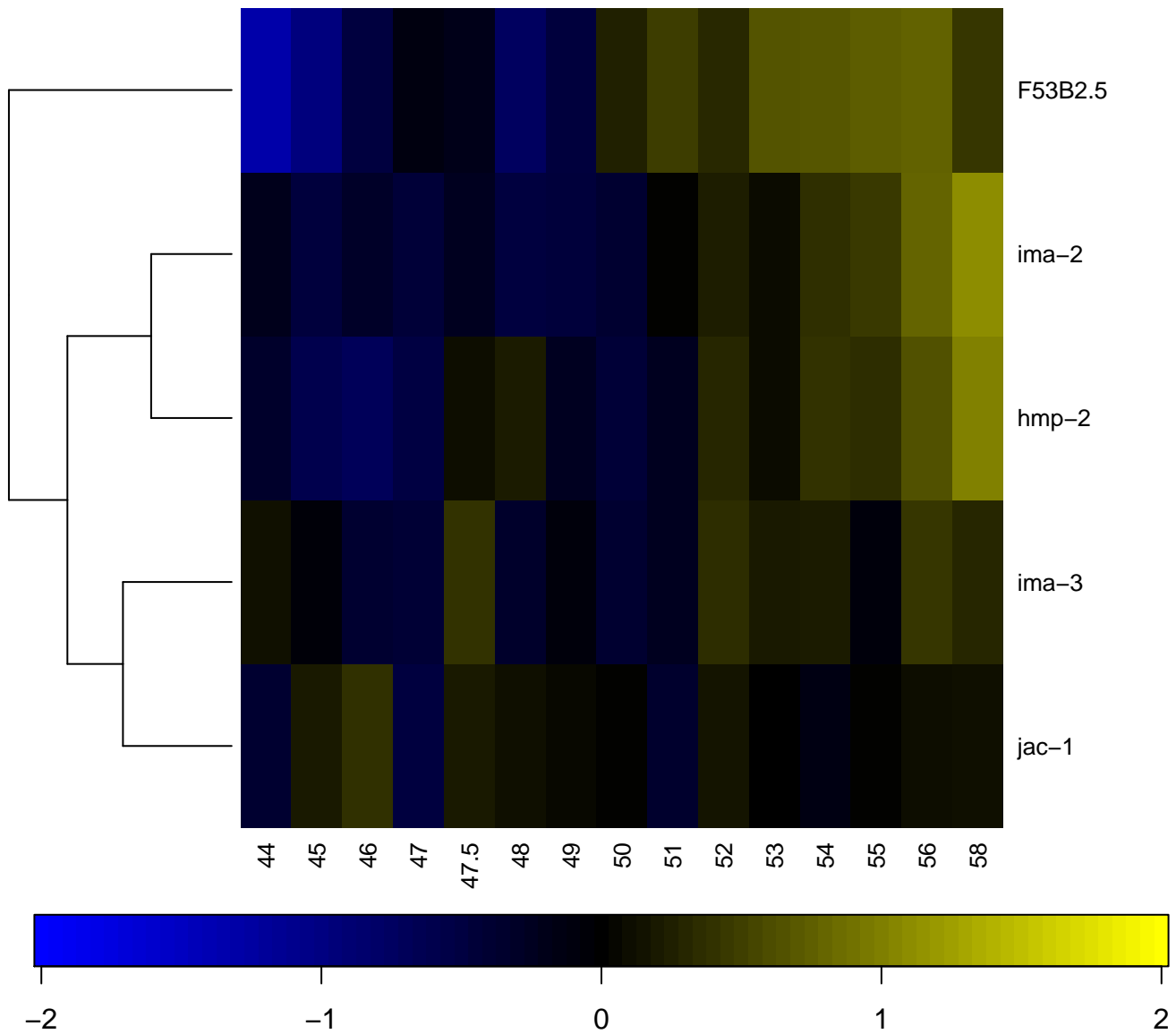
Armadillo



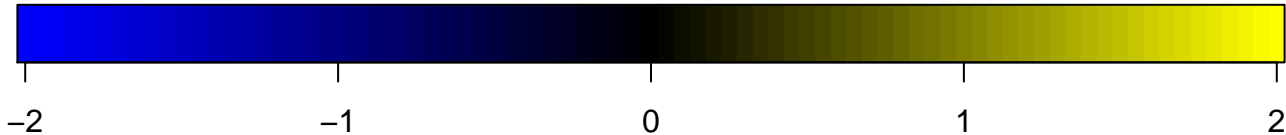
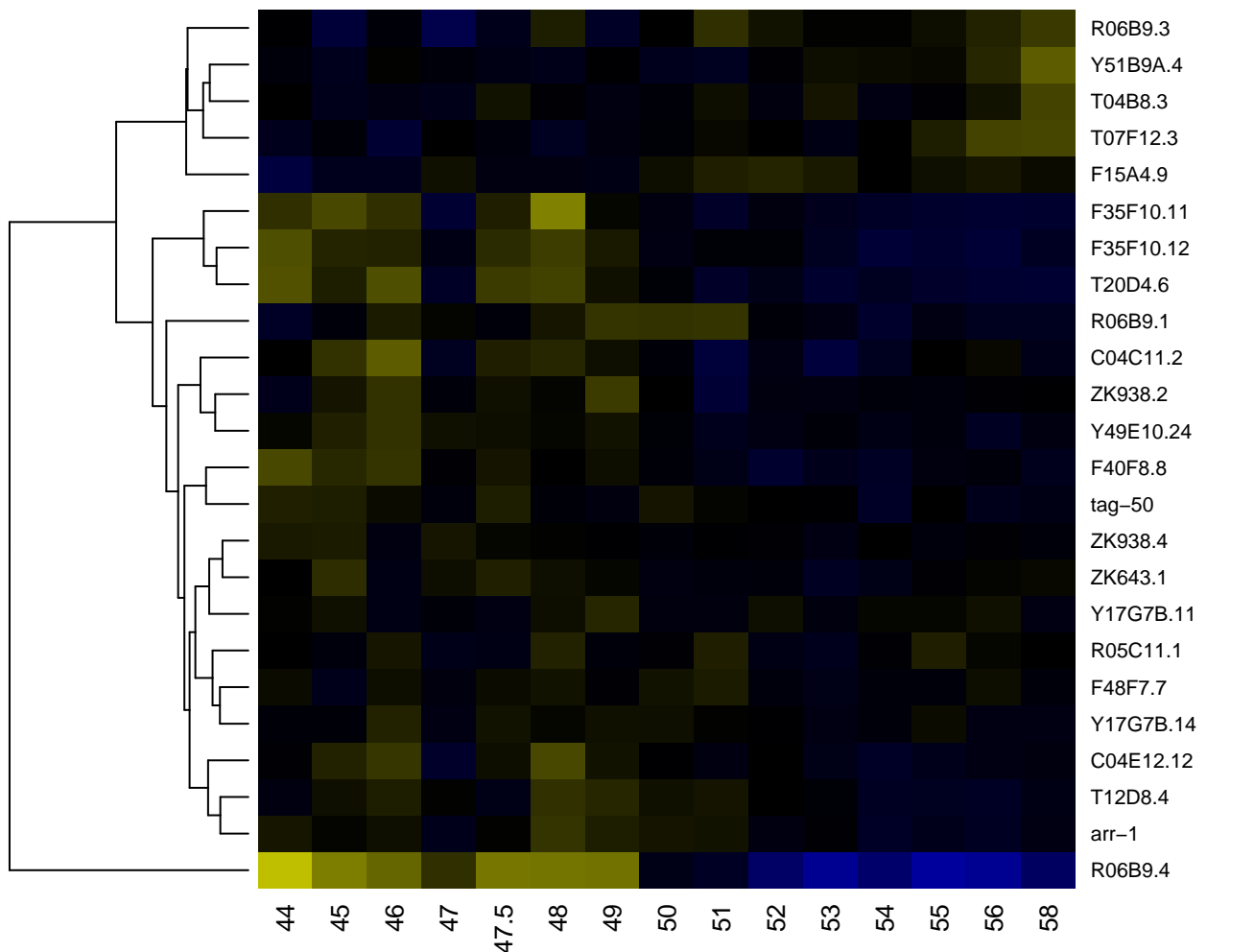
Armadillo-like helical



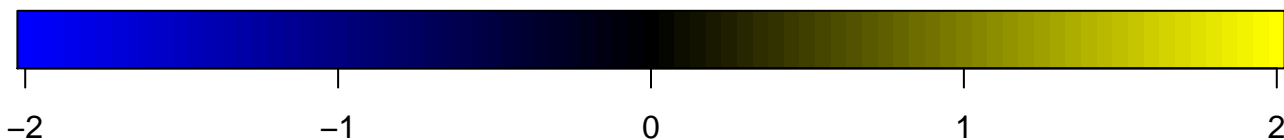
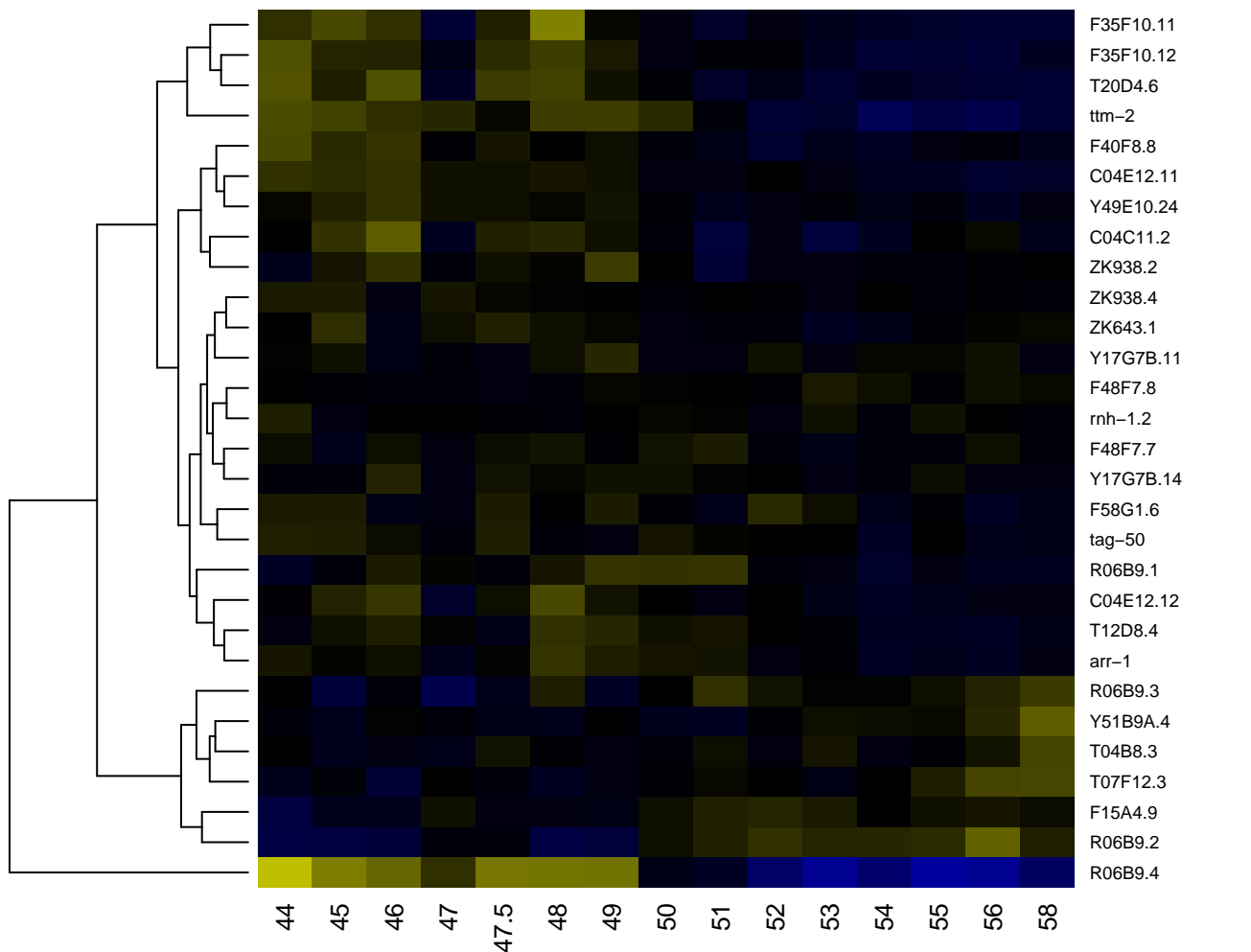
Armadillo/beta-catenin-like repeat



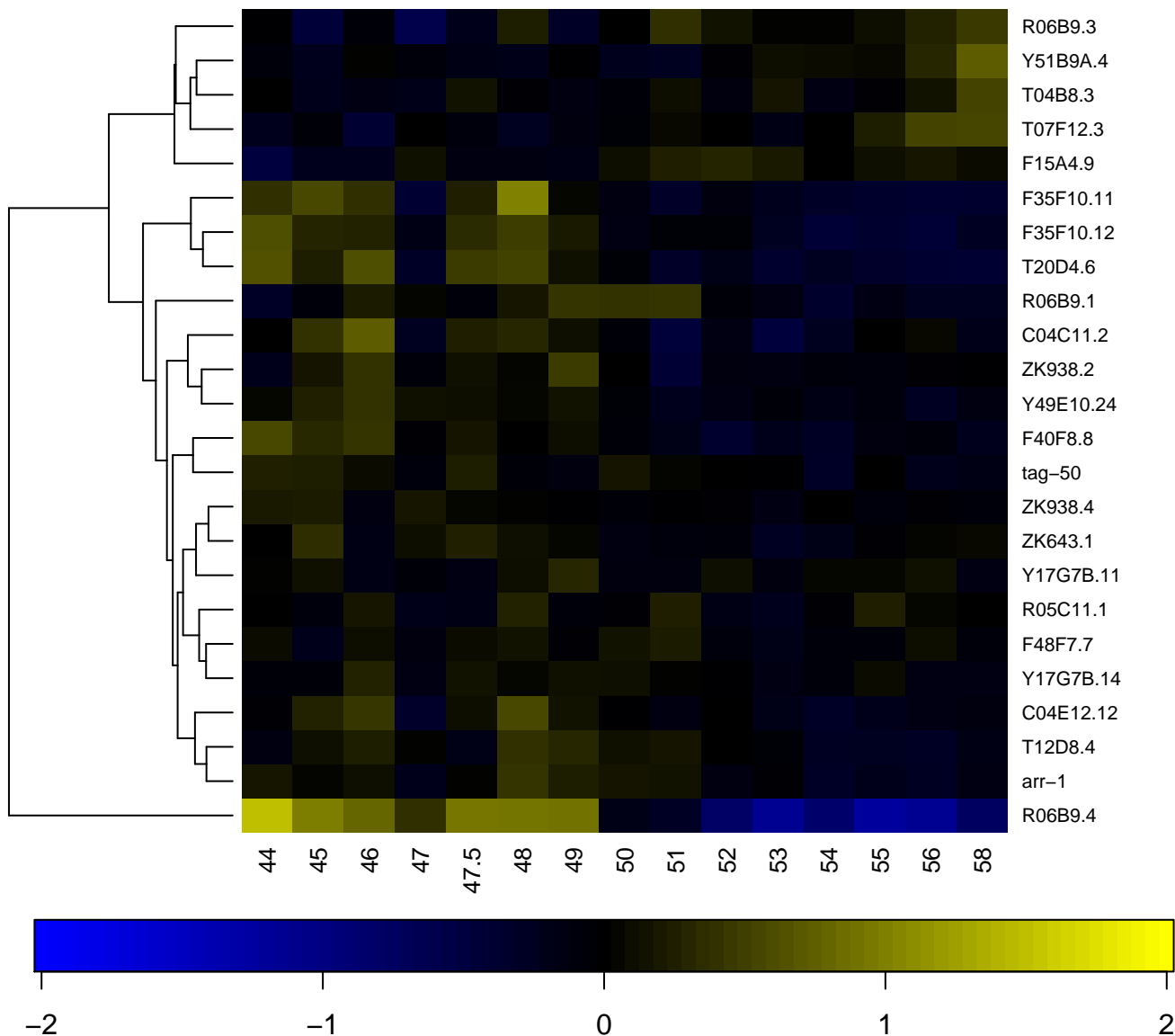
Arrestin-like, C-terminal



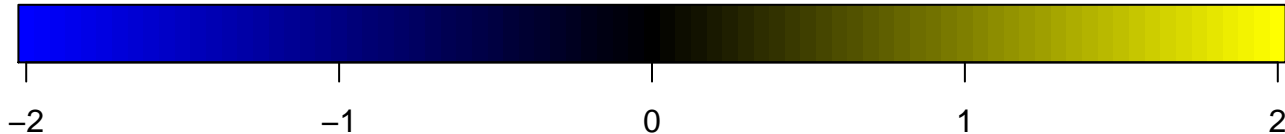
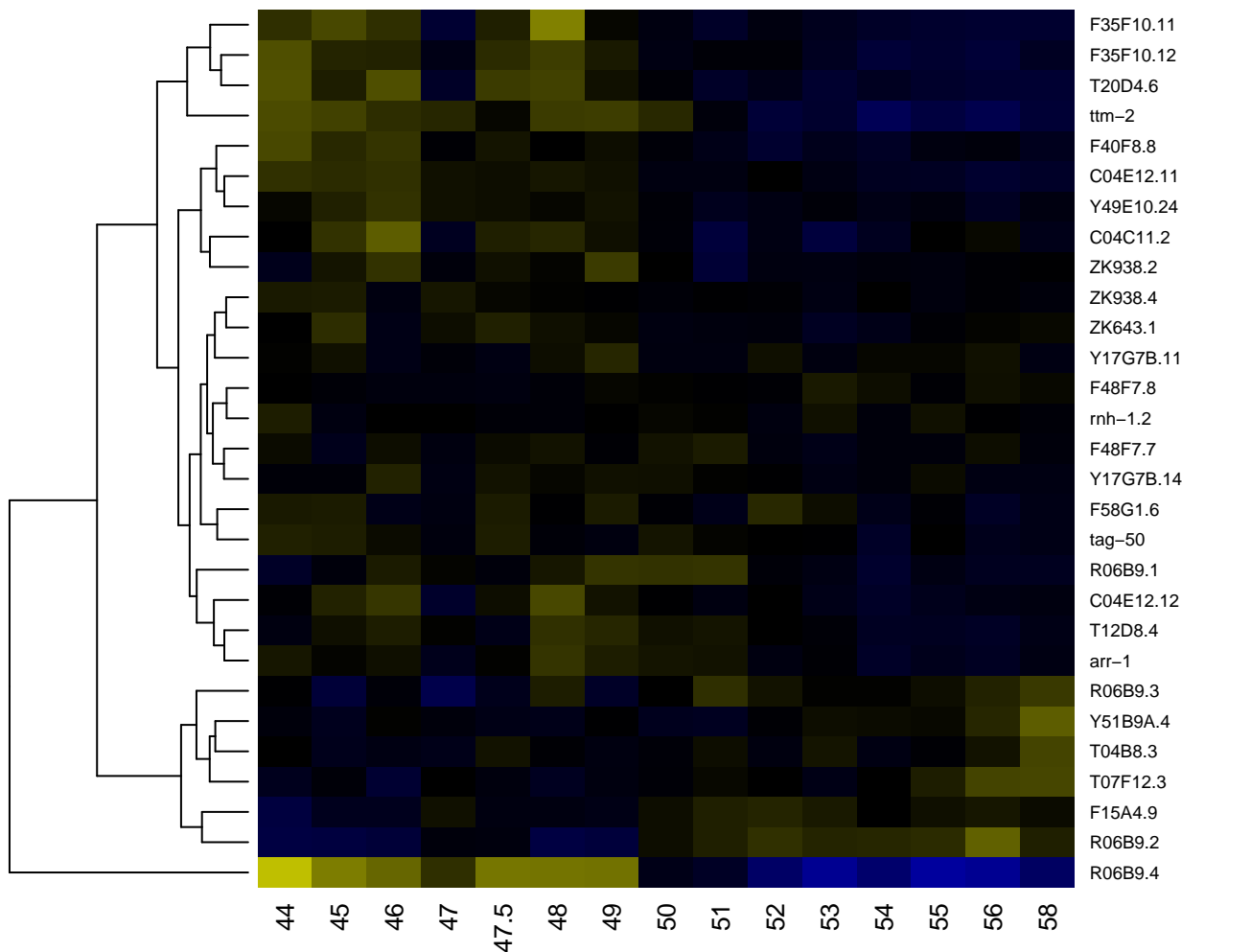
Arrestin-like, N-terminal



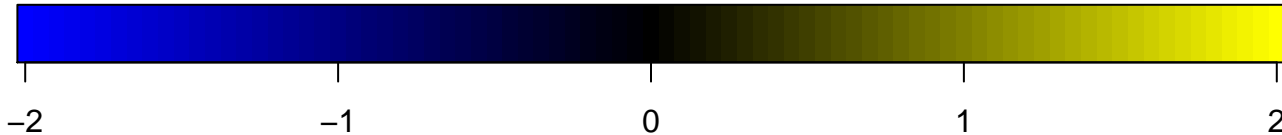
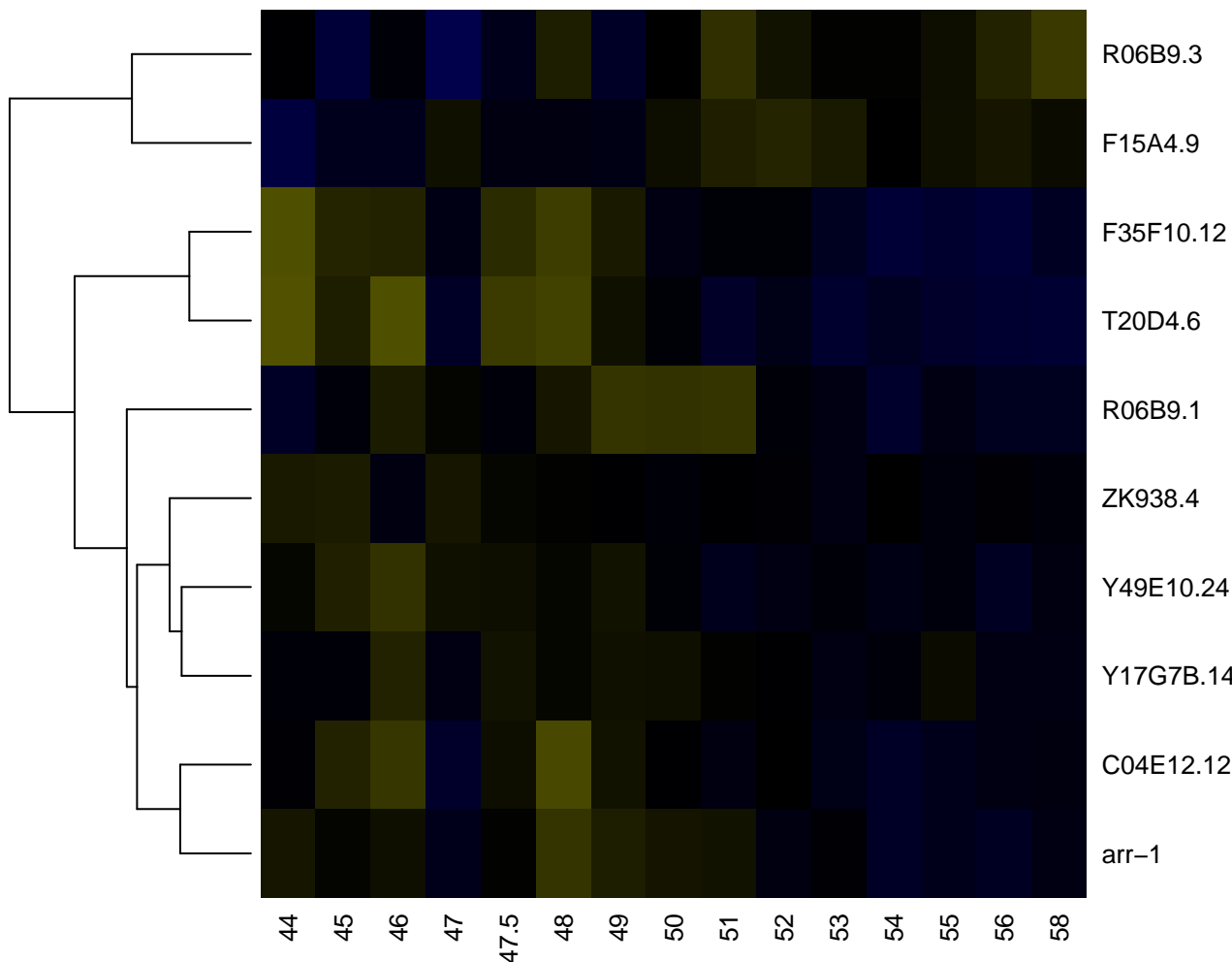
Arrestin (or S-antigen), C-terminal domain



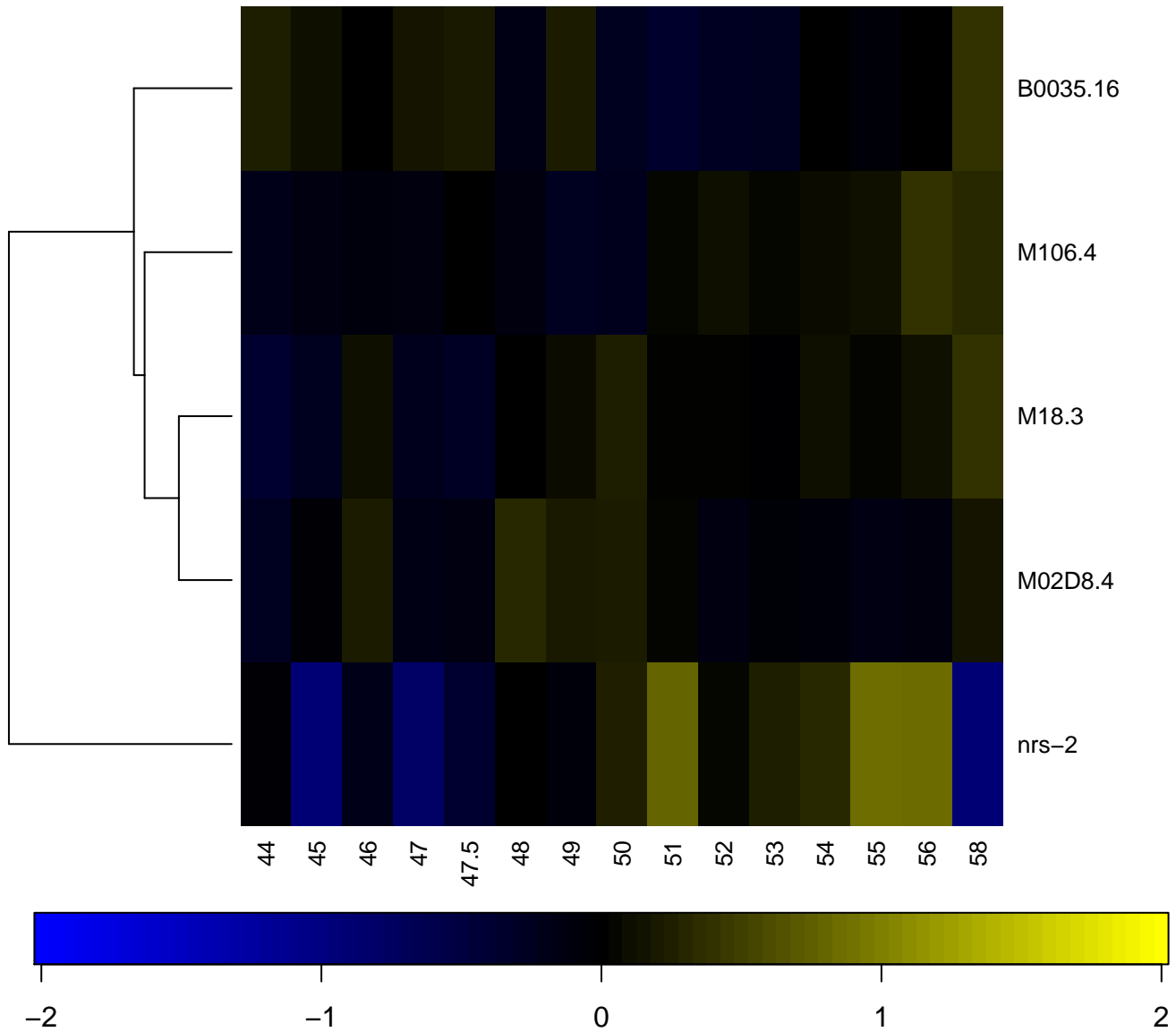
Arrestin (or S-antigen), N-terminal domain



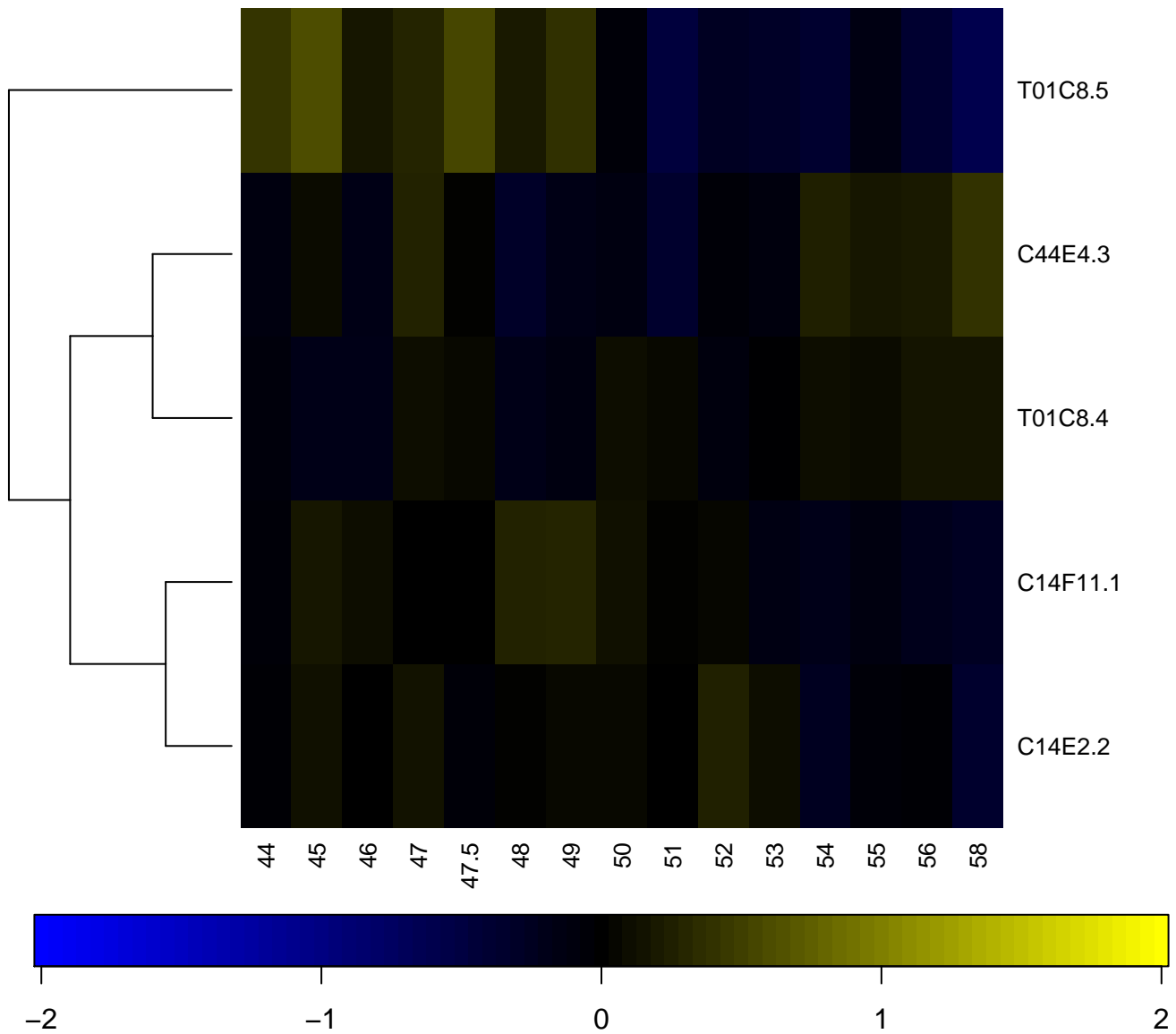
Arrestin, C-terminal



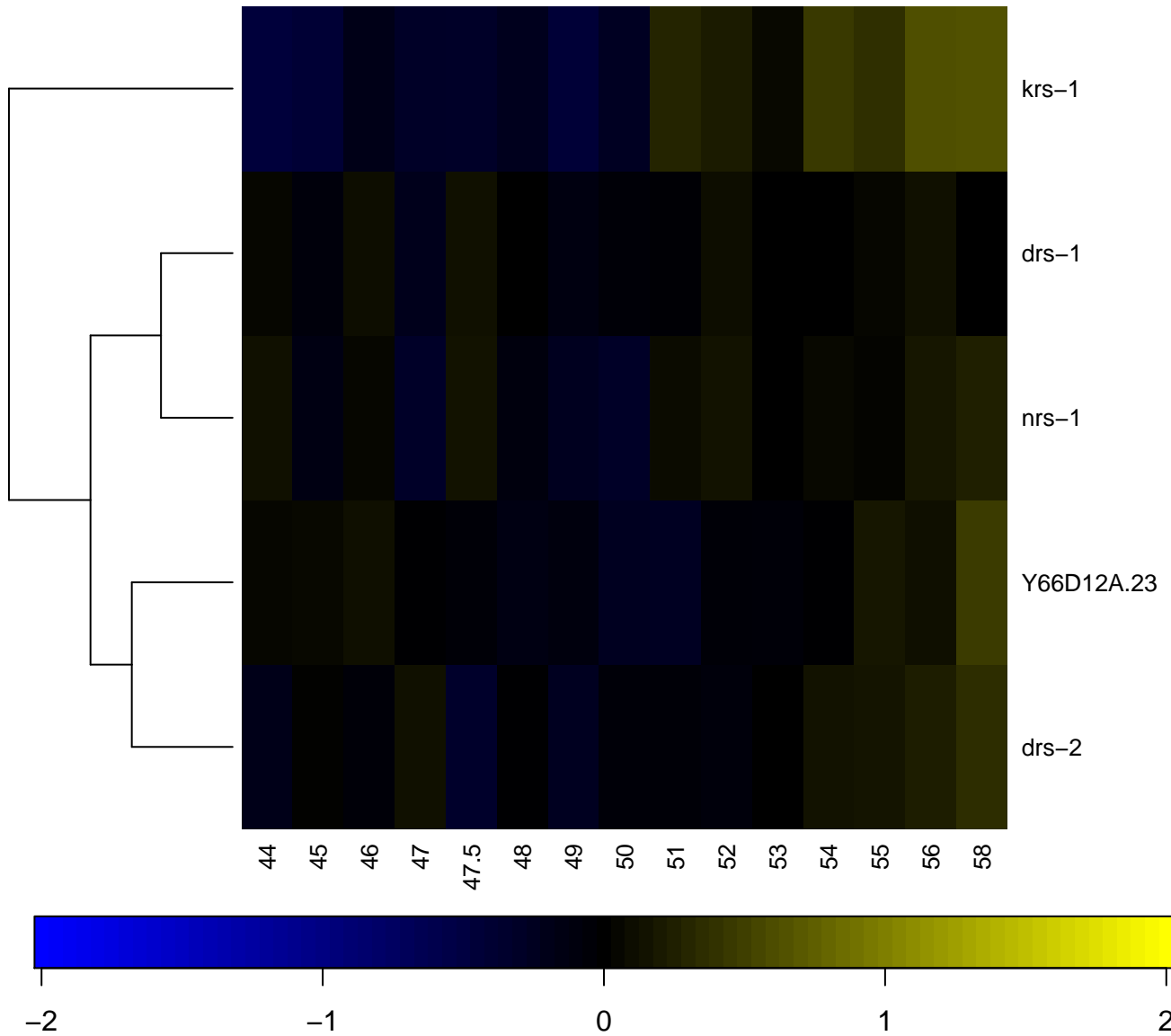
Asparagine synthase



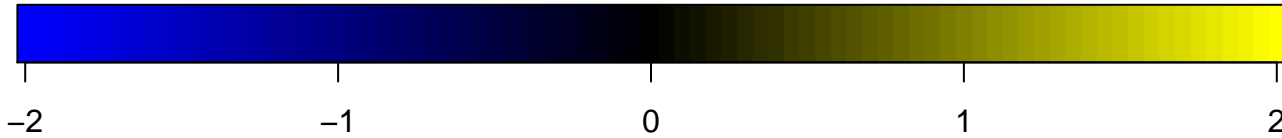
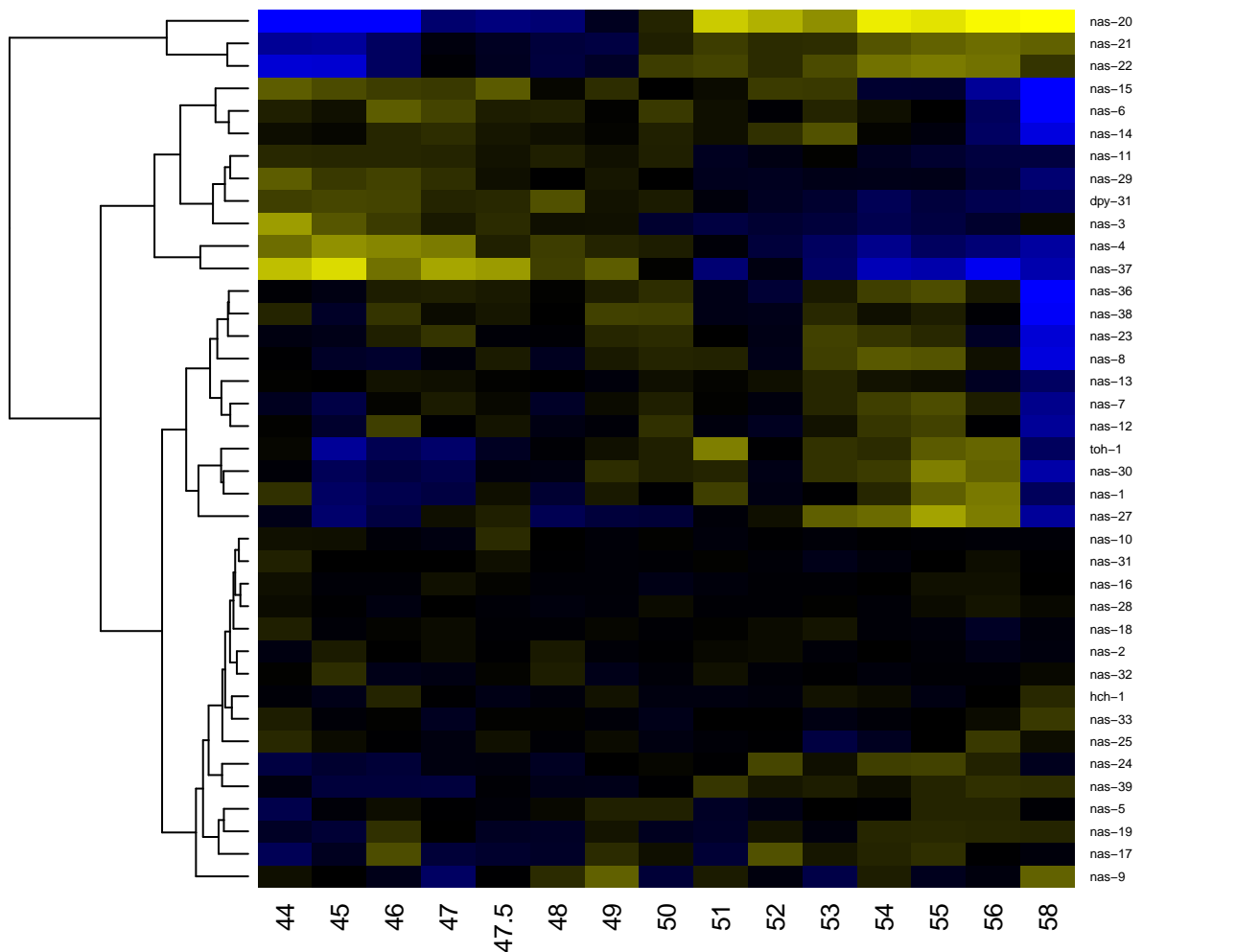
Aspartate/other aminotransferase



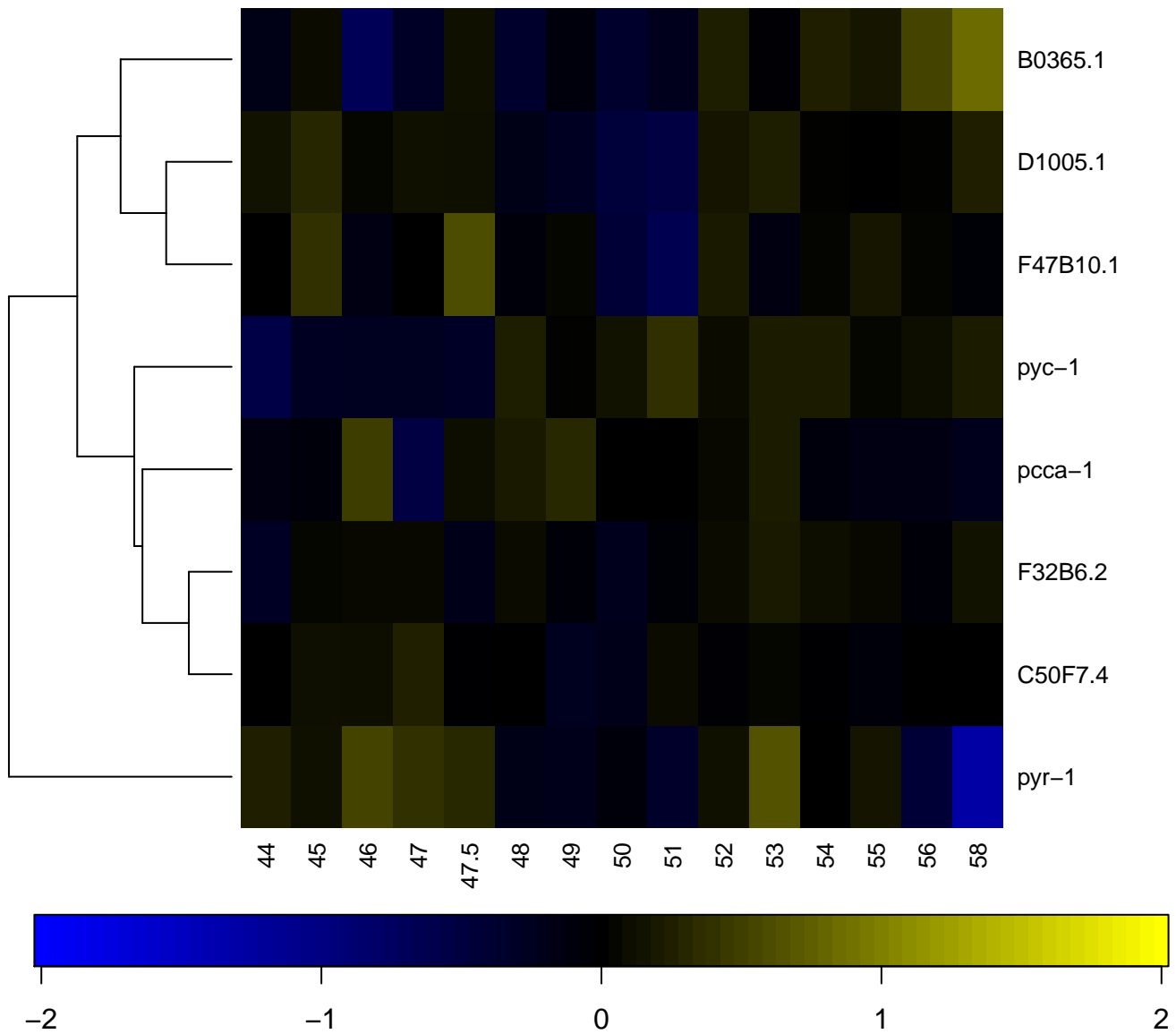
Aspartyl/Asparaginyl-tRNA synthetase, class IIb



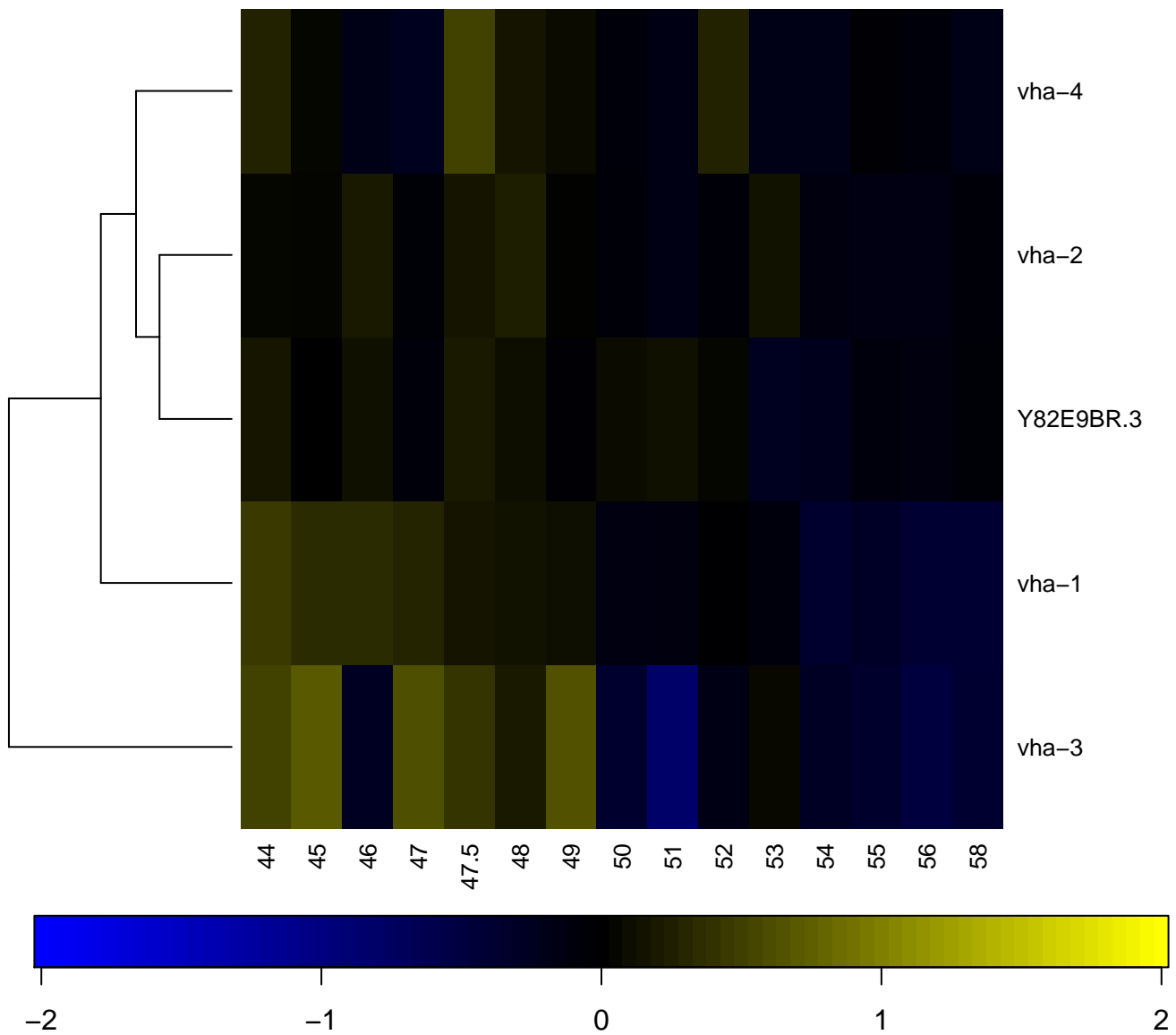
Astacin (Peptidase family M12A)



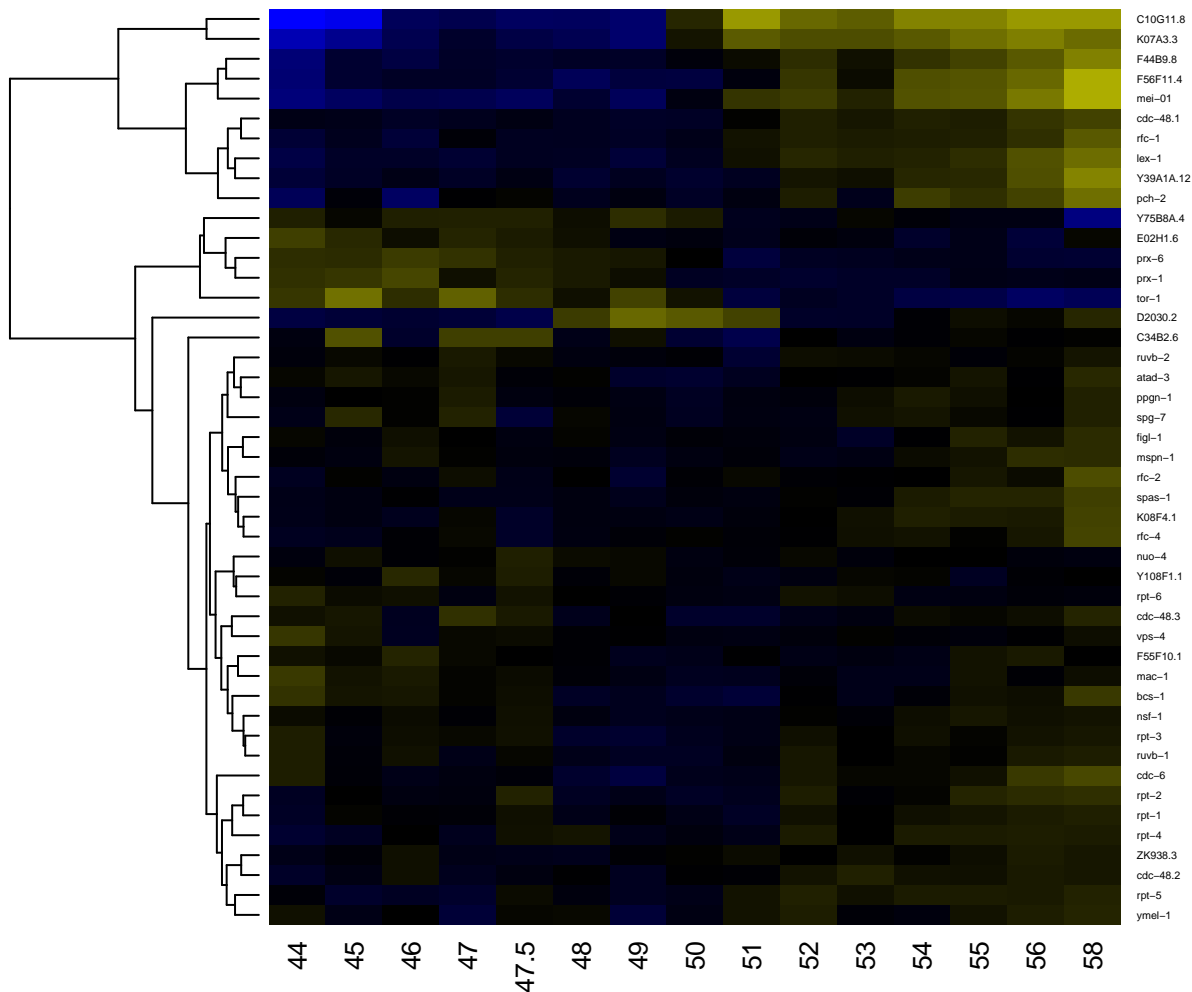
ATP-grasp domain



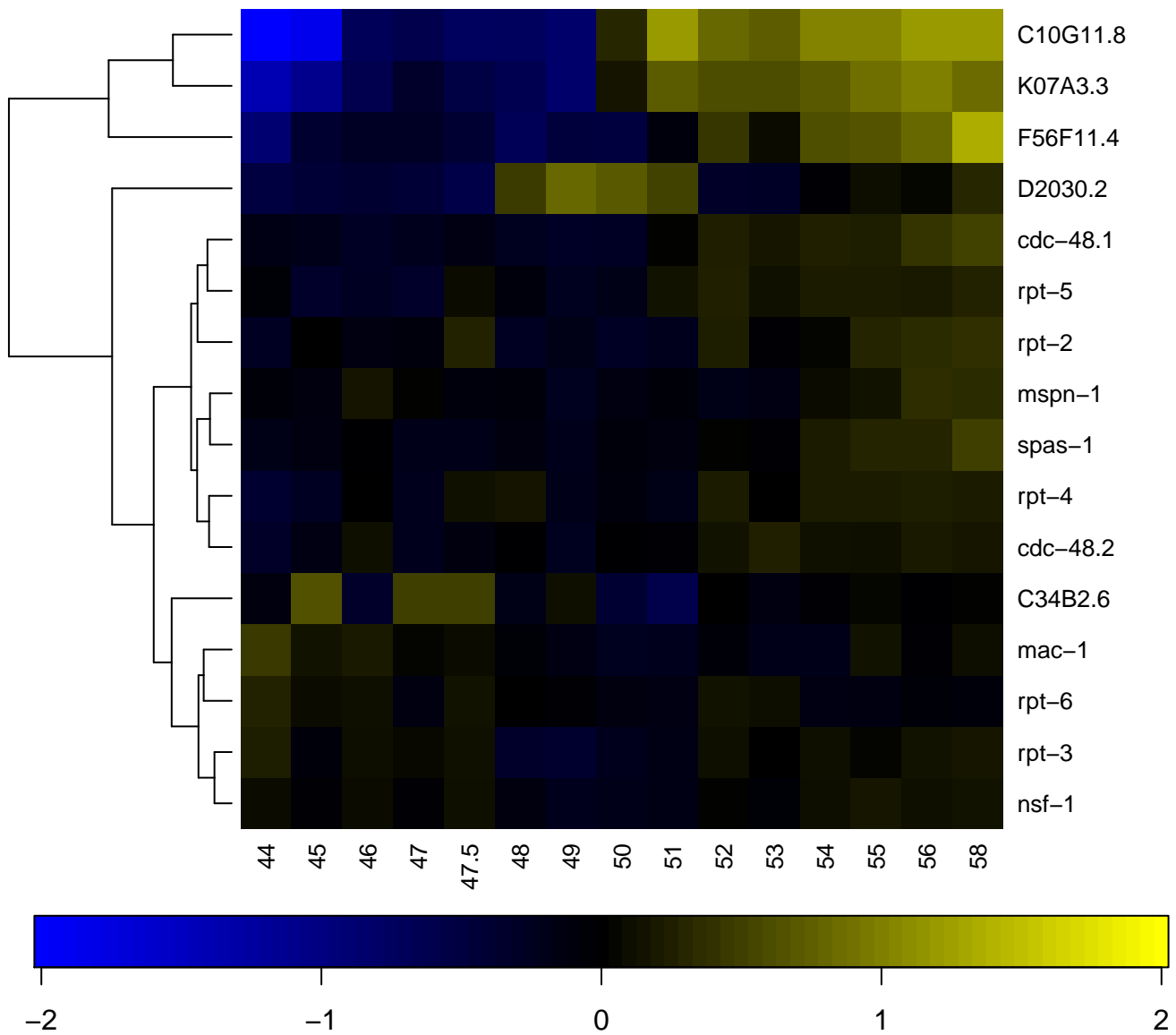
ATP synthase subunit C



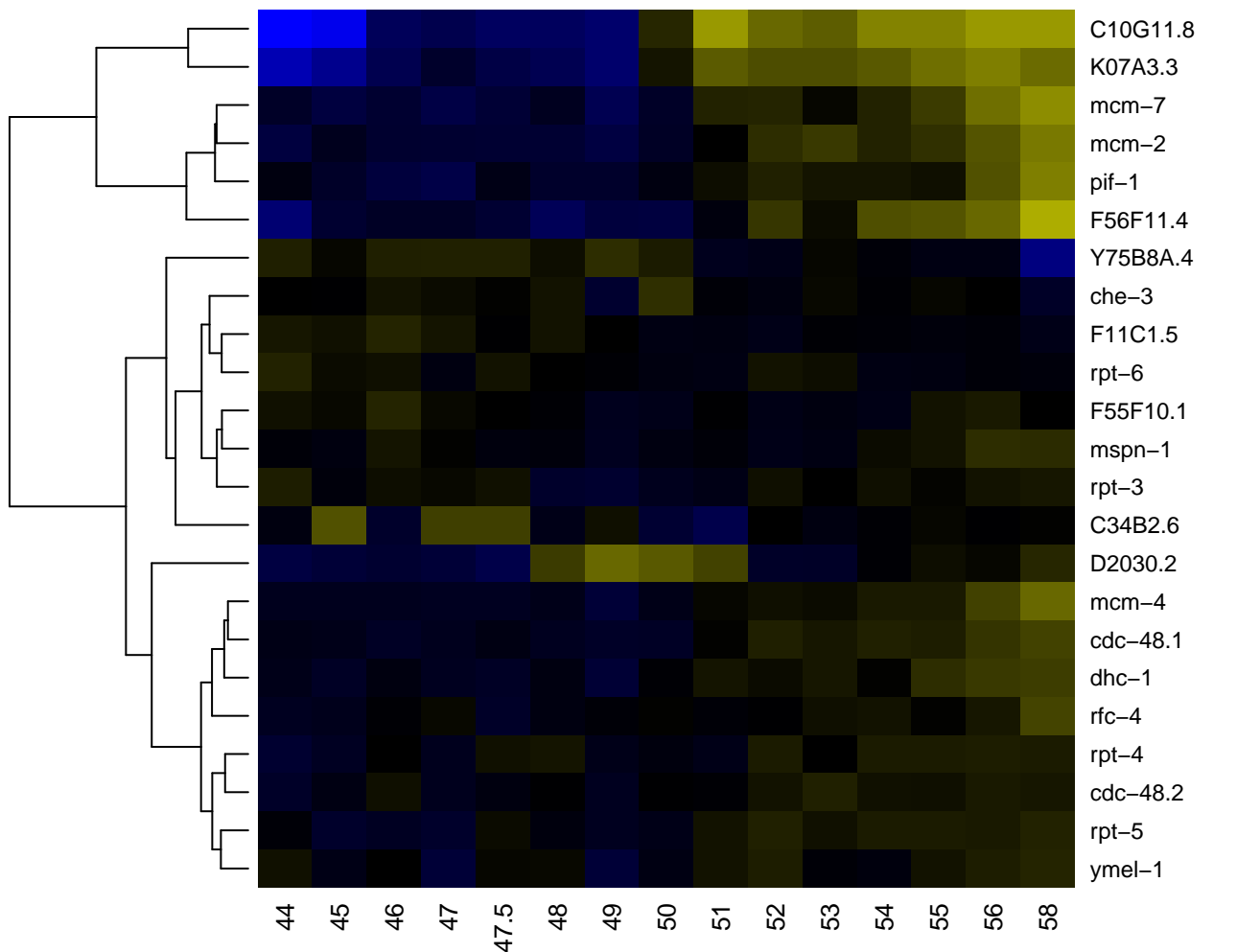
ATPase family associated with various cellular activities (AA



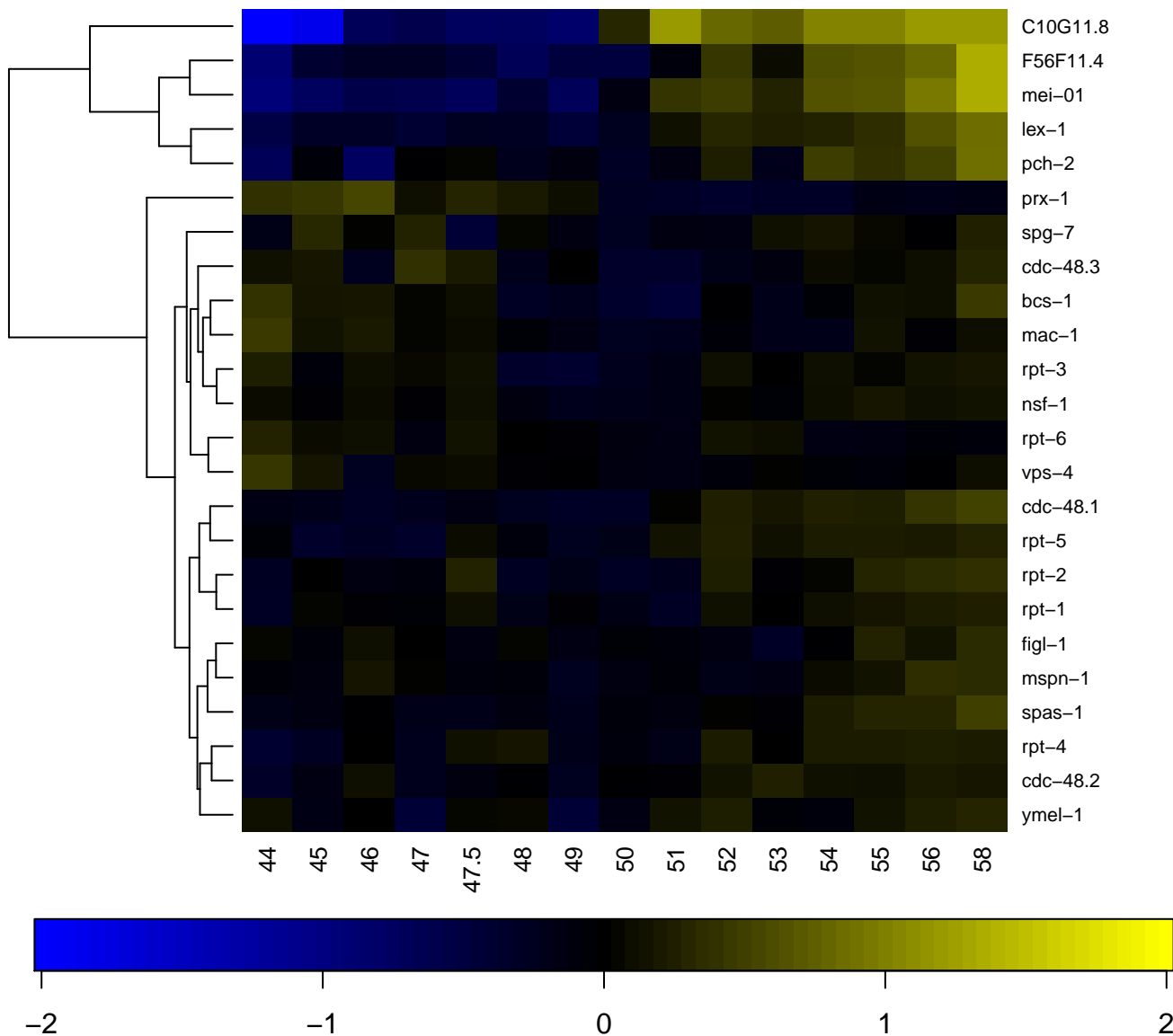
ATPase, AAA-2



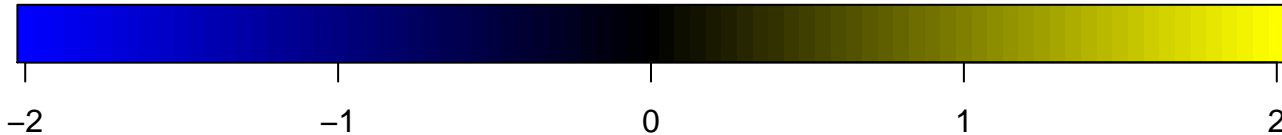
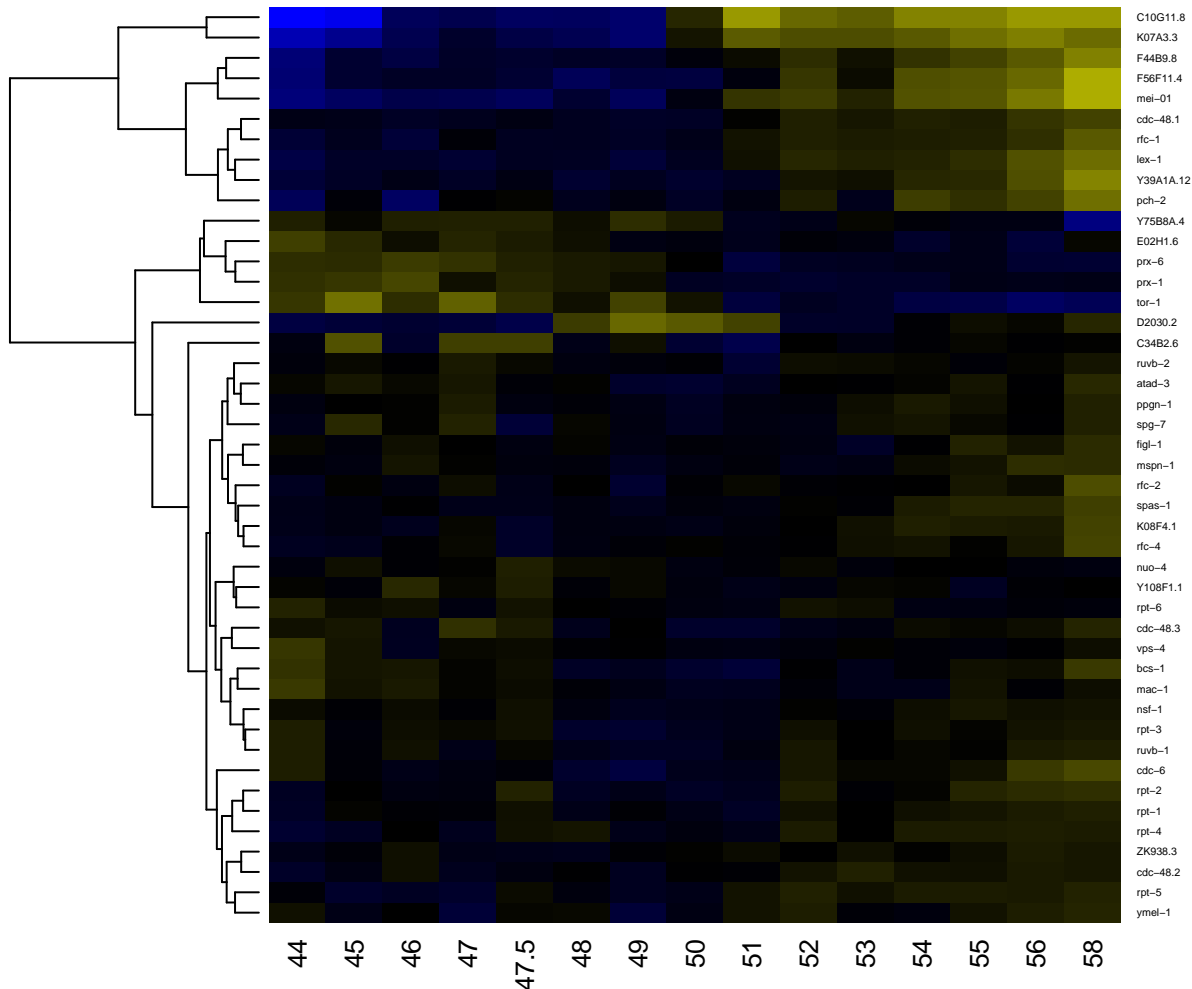
ATPase, AAA-5



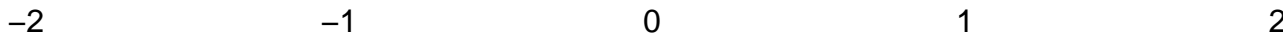
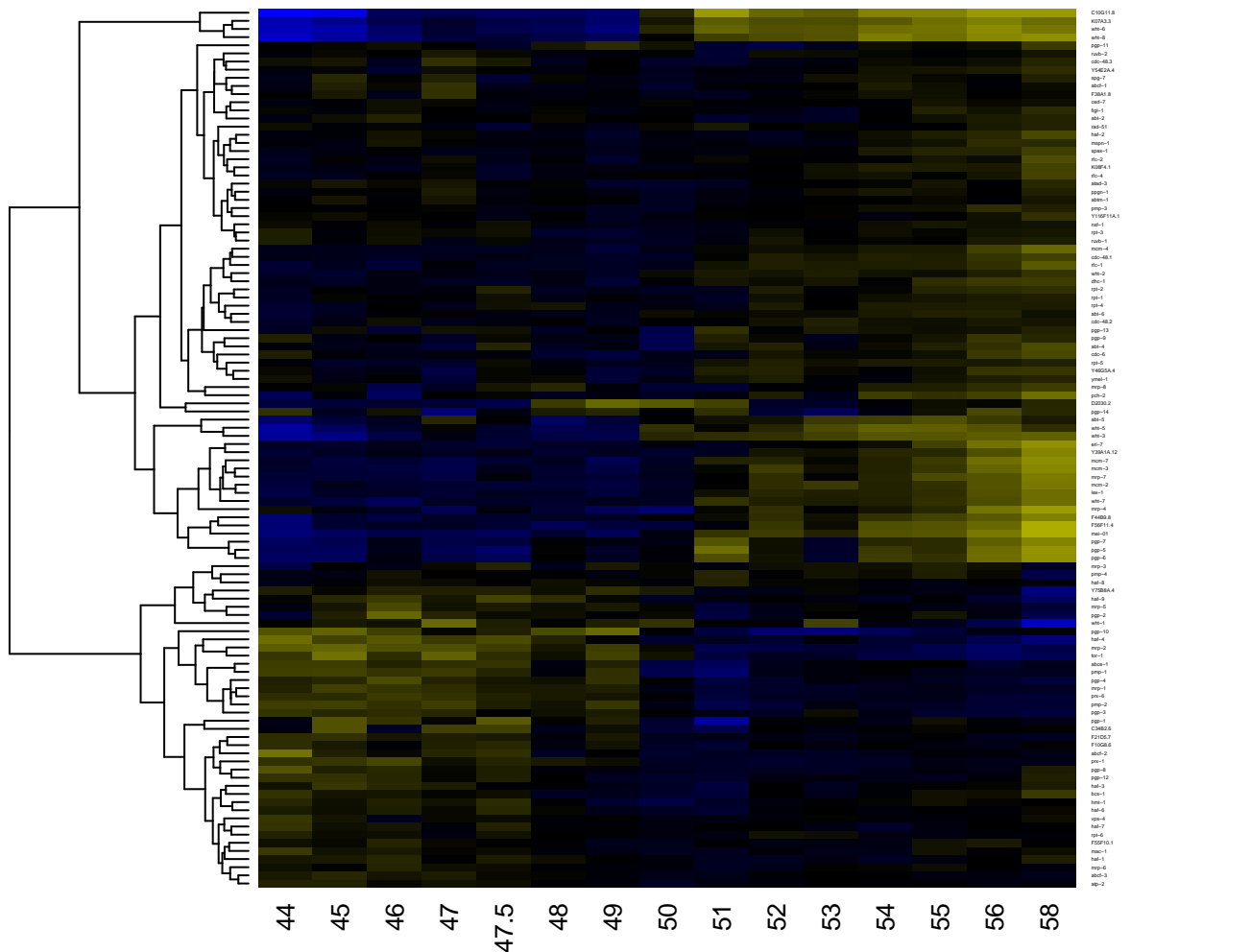
ATPase, AAA-type, conserved site



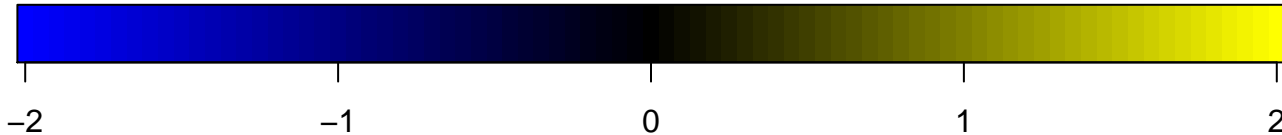
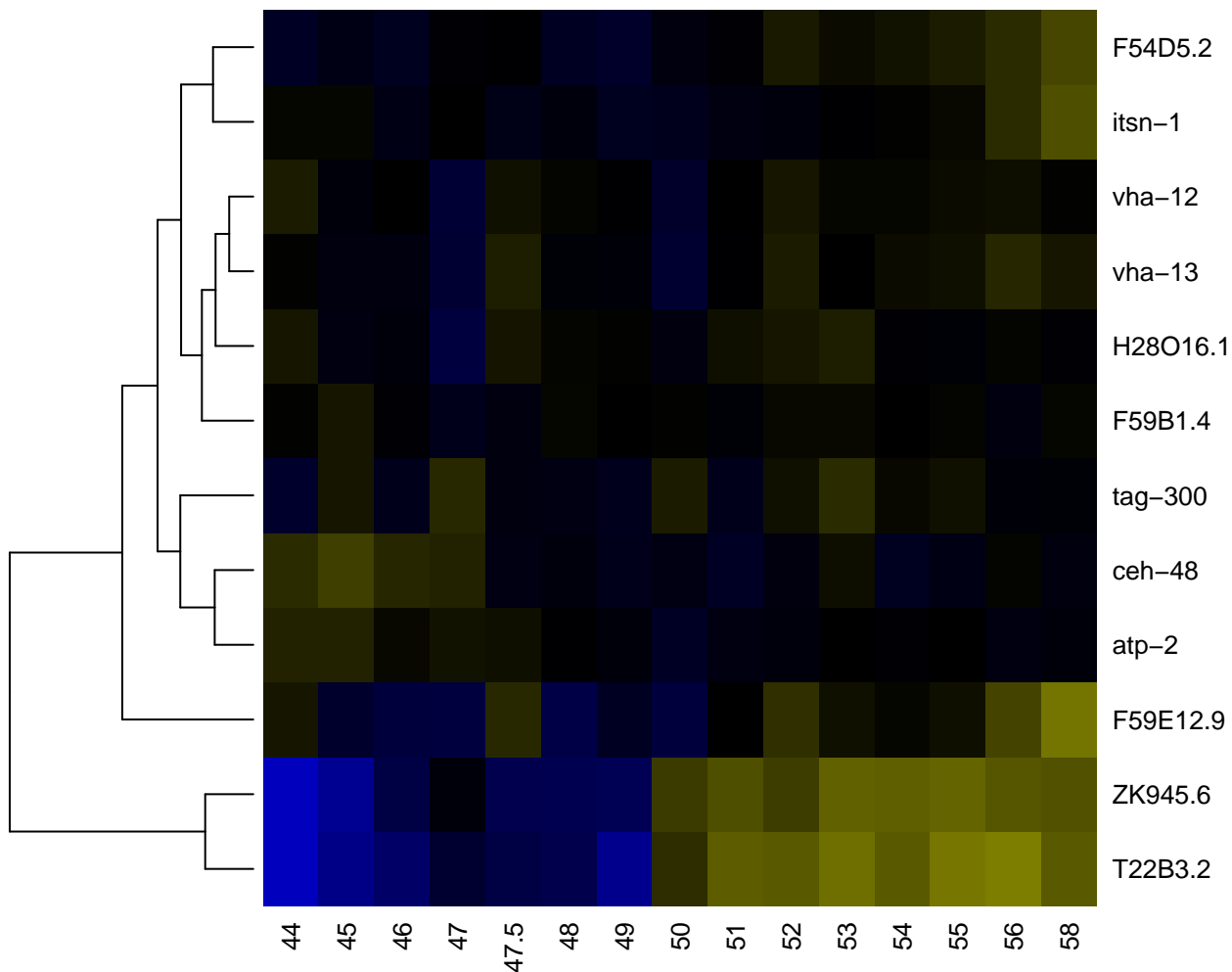
ATPase, AAA-type, core



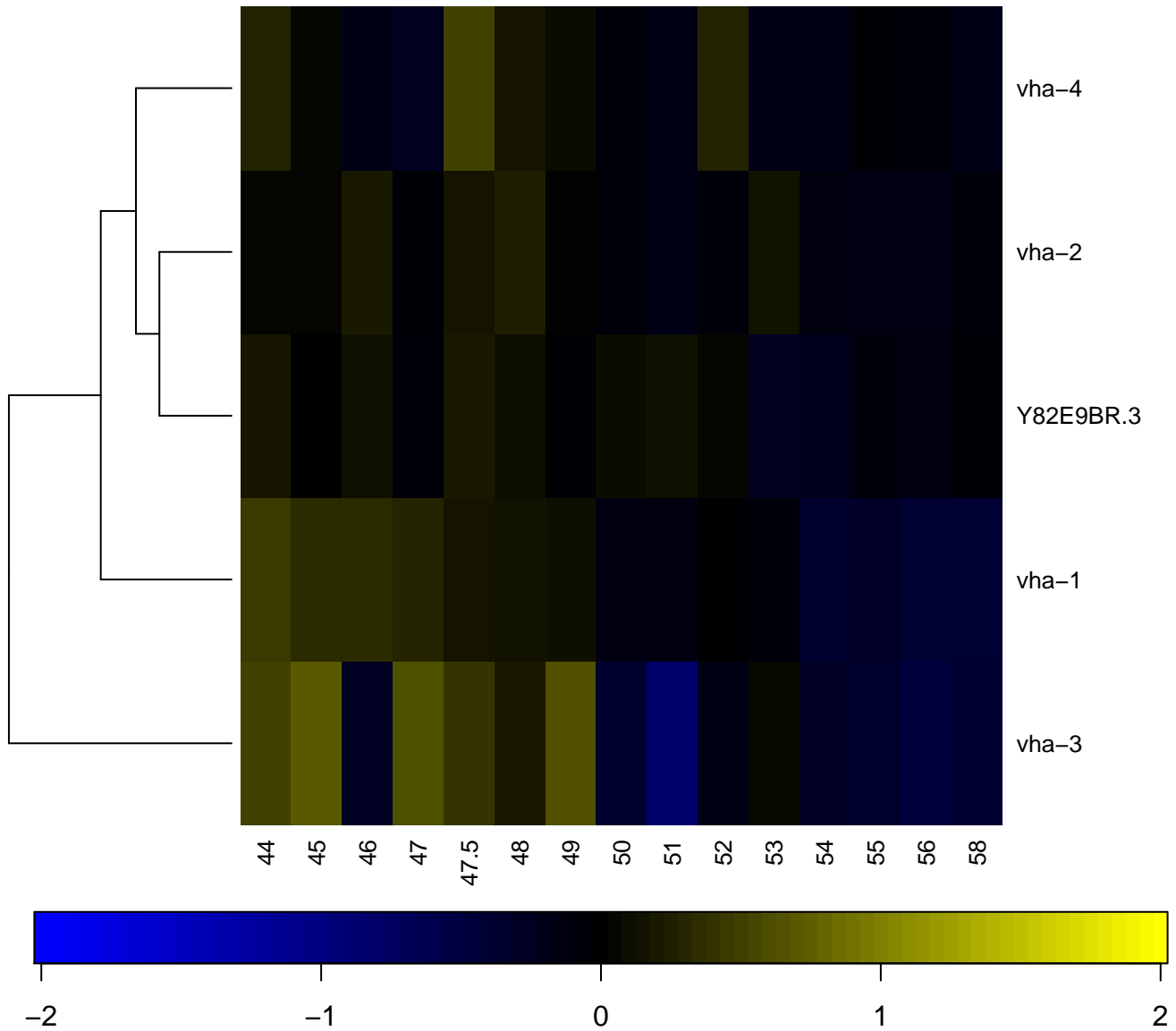
ATPase, AAA+ type, core



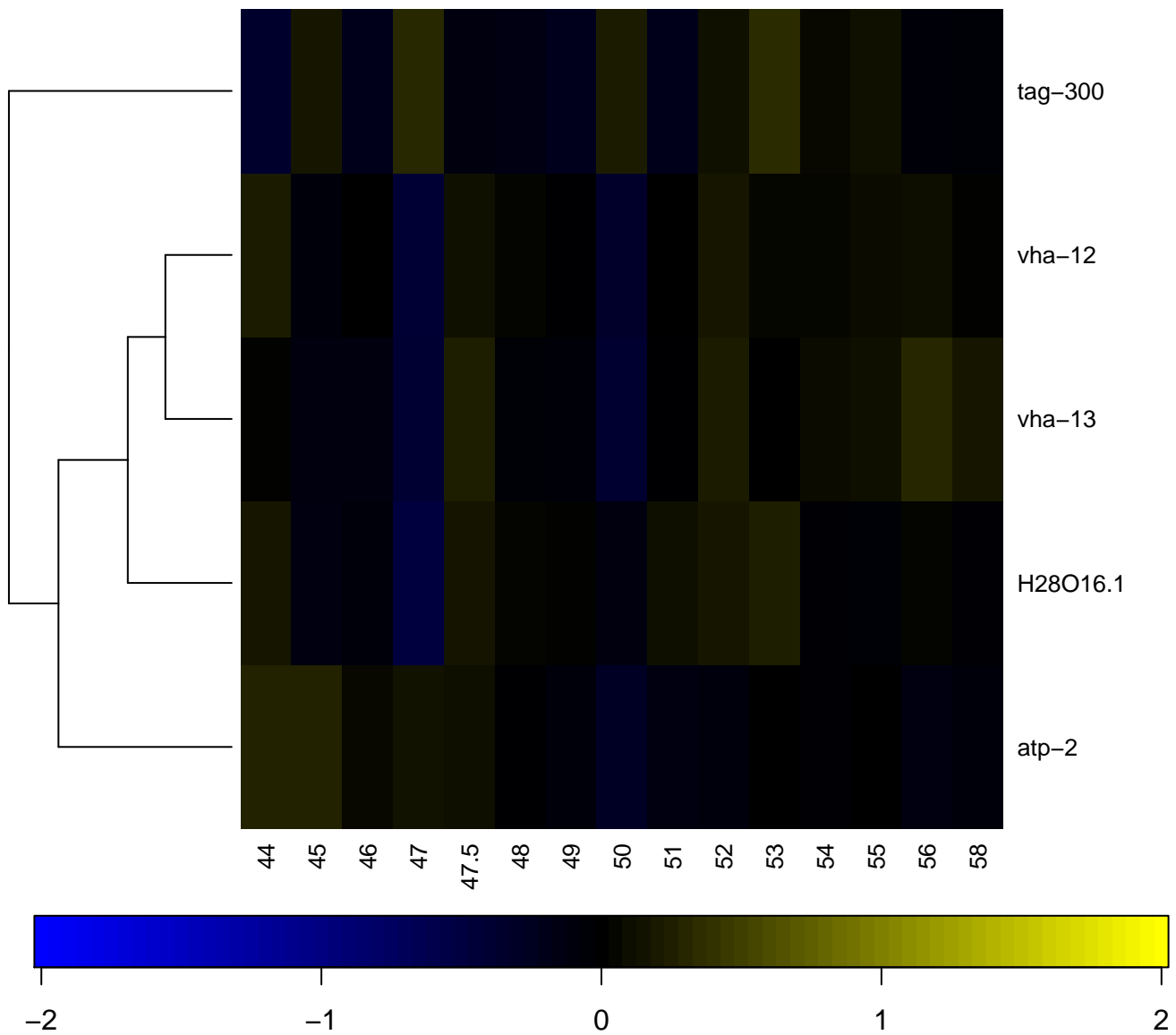
Pase, alpha/beta subunit, nucleotide-binding domain, active



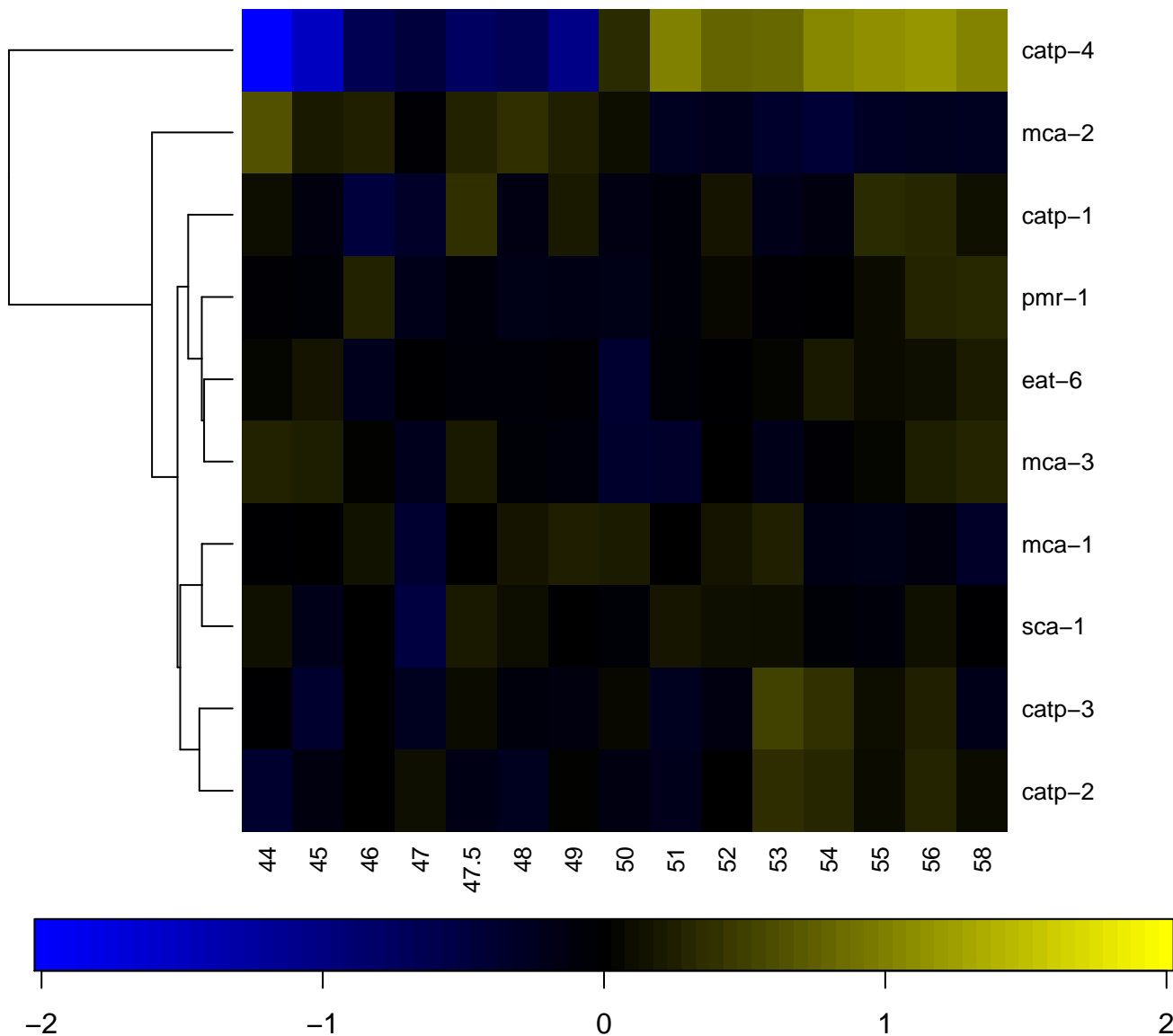
ATPase, F0/V0 complex, subunit C



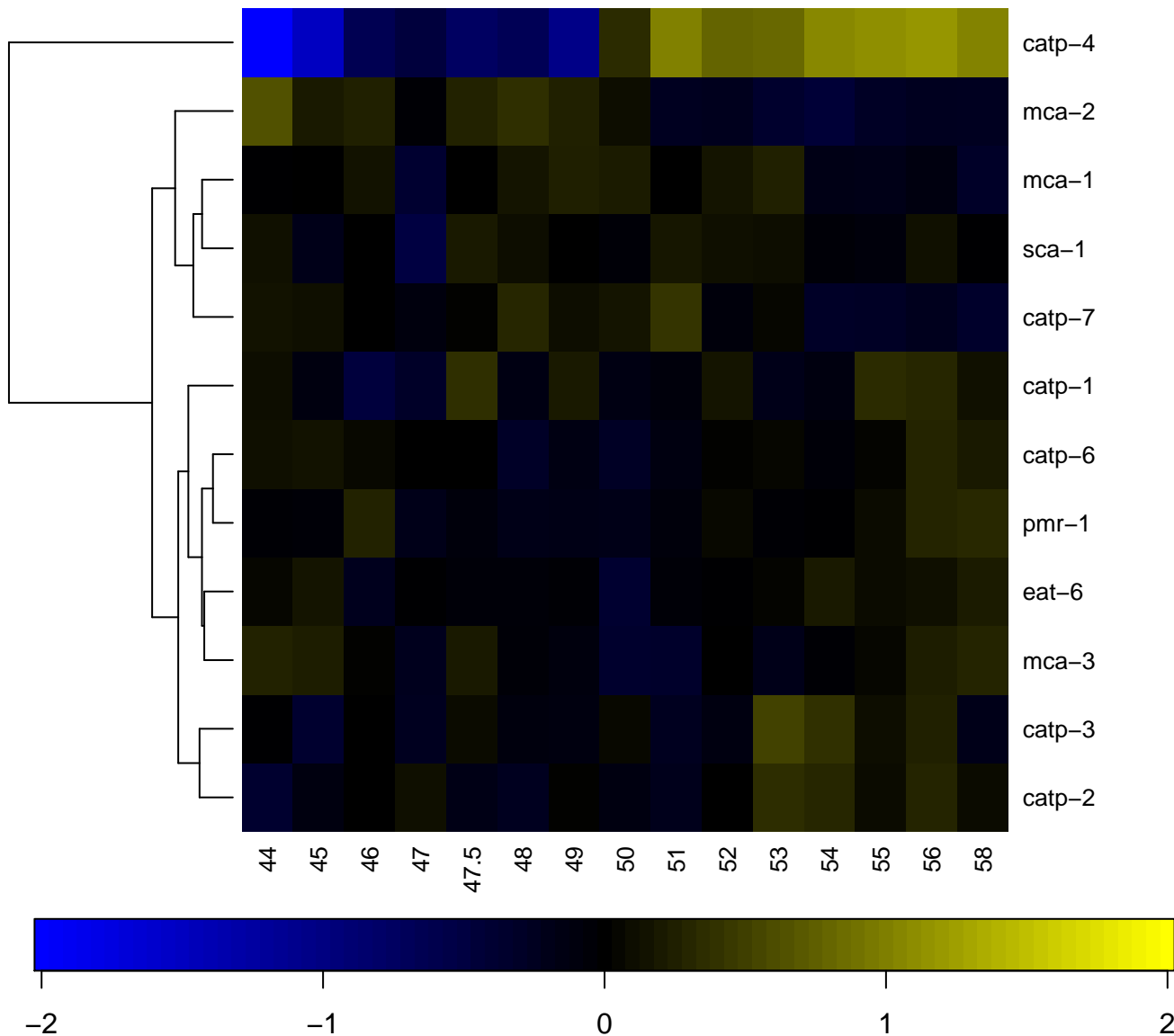
ATPase, F1/V1/A1 complex, alpha/beta subunit, N-termina



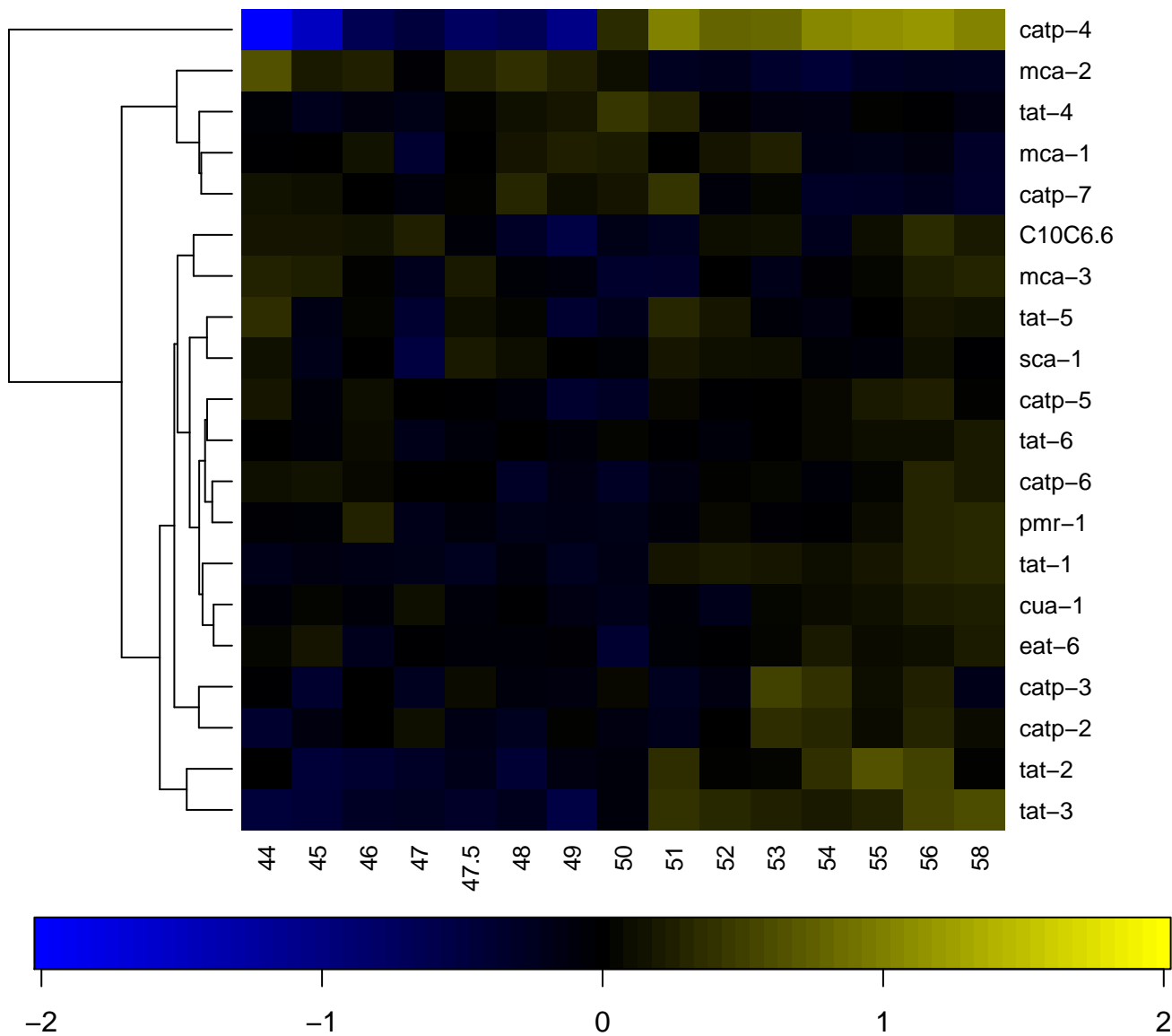
ATPase, P-type cation-transporter, C-terminal



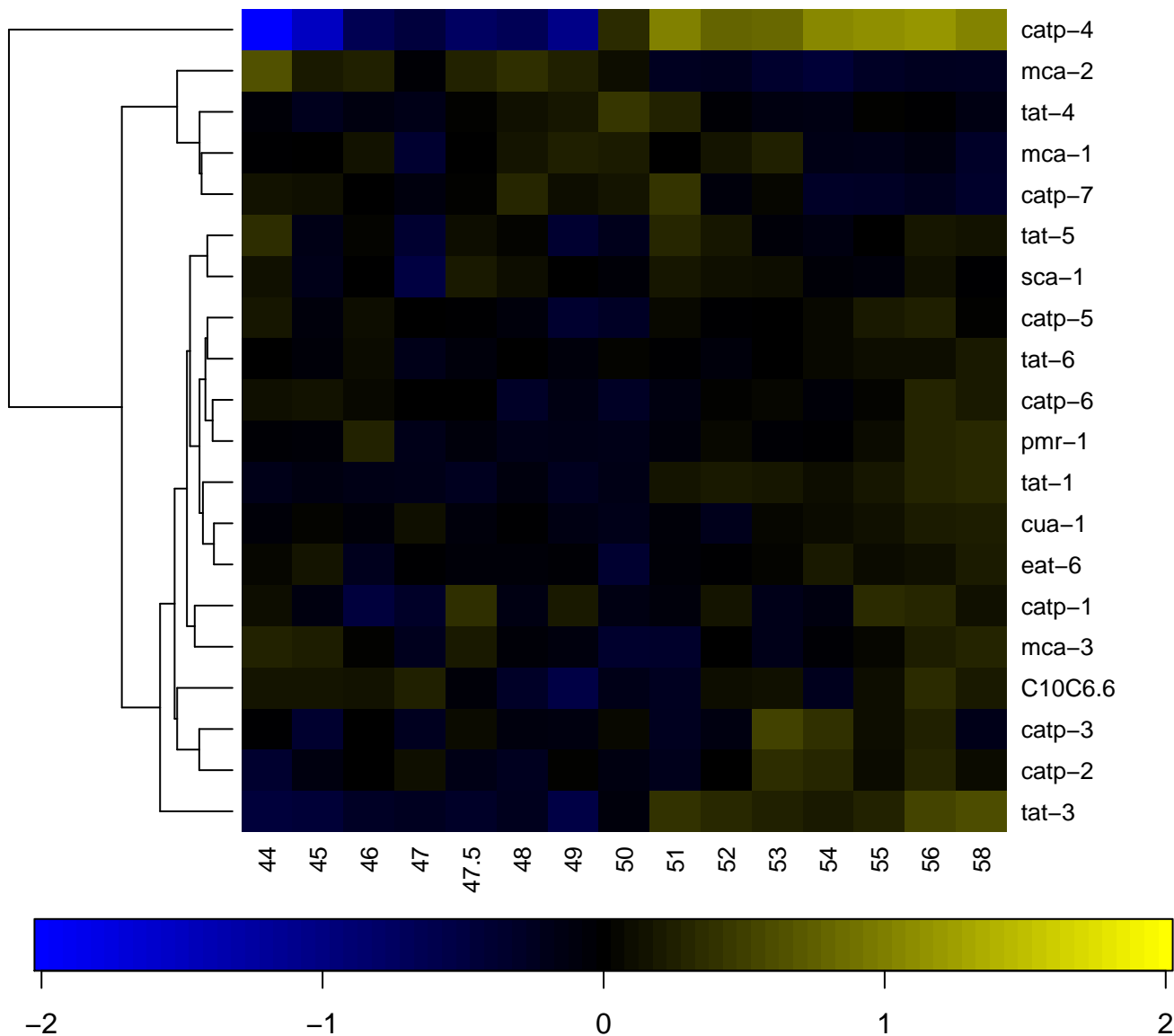
ATPase, P-type cation-transporter, N-terminal



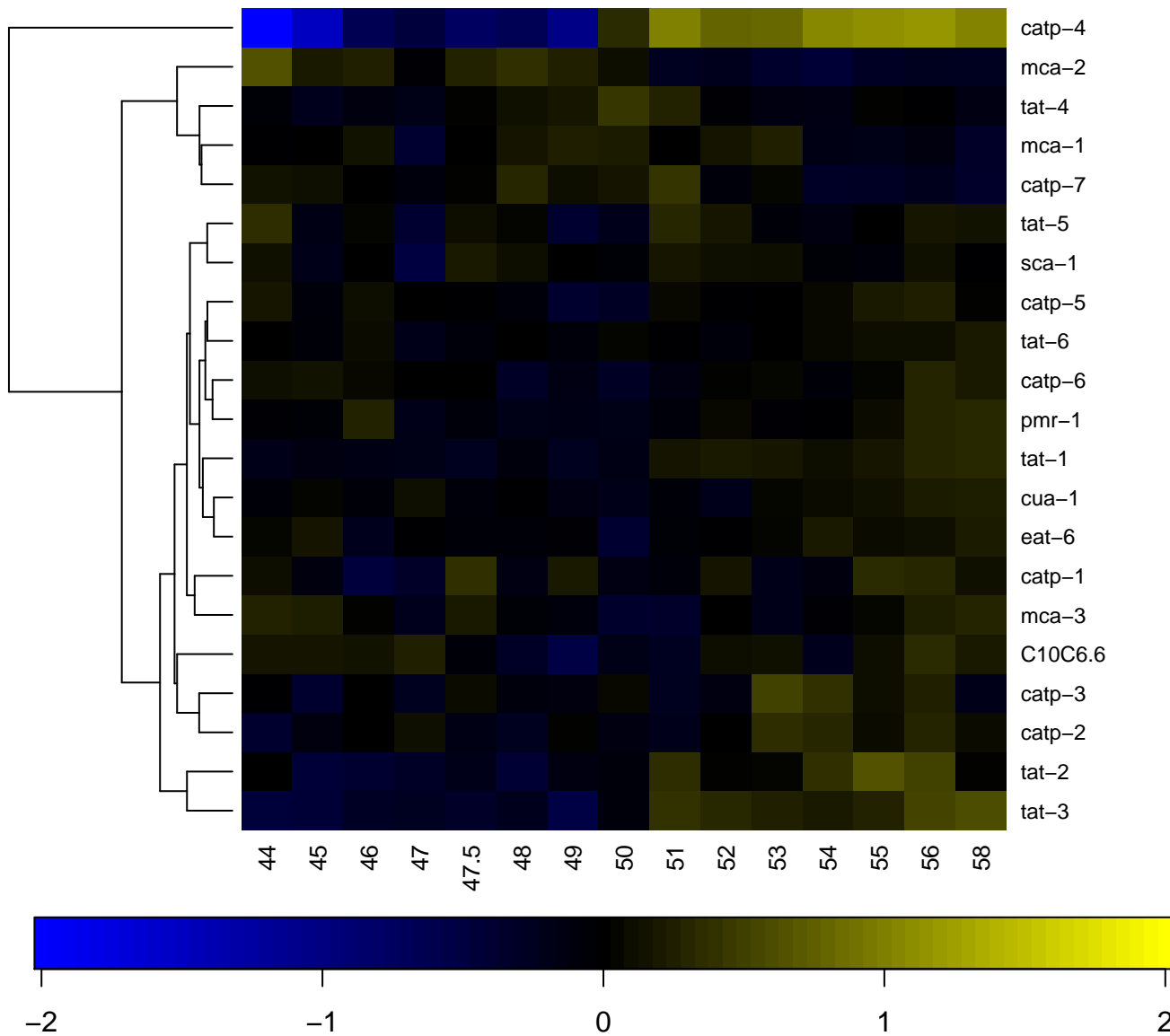
ATPase, P-type phosphorylation site



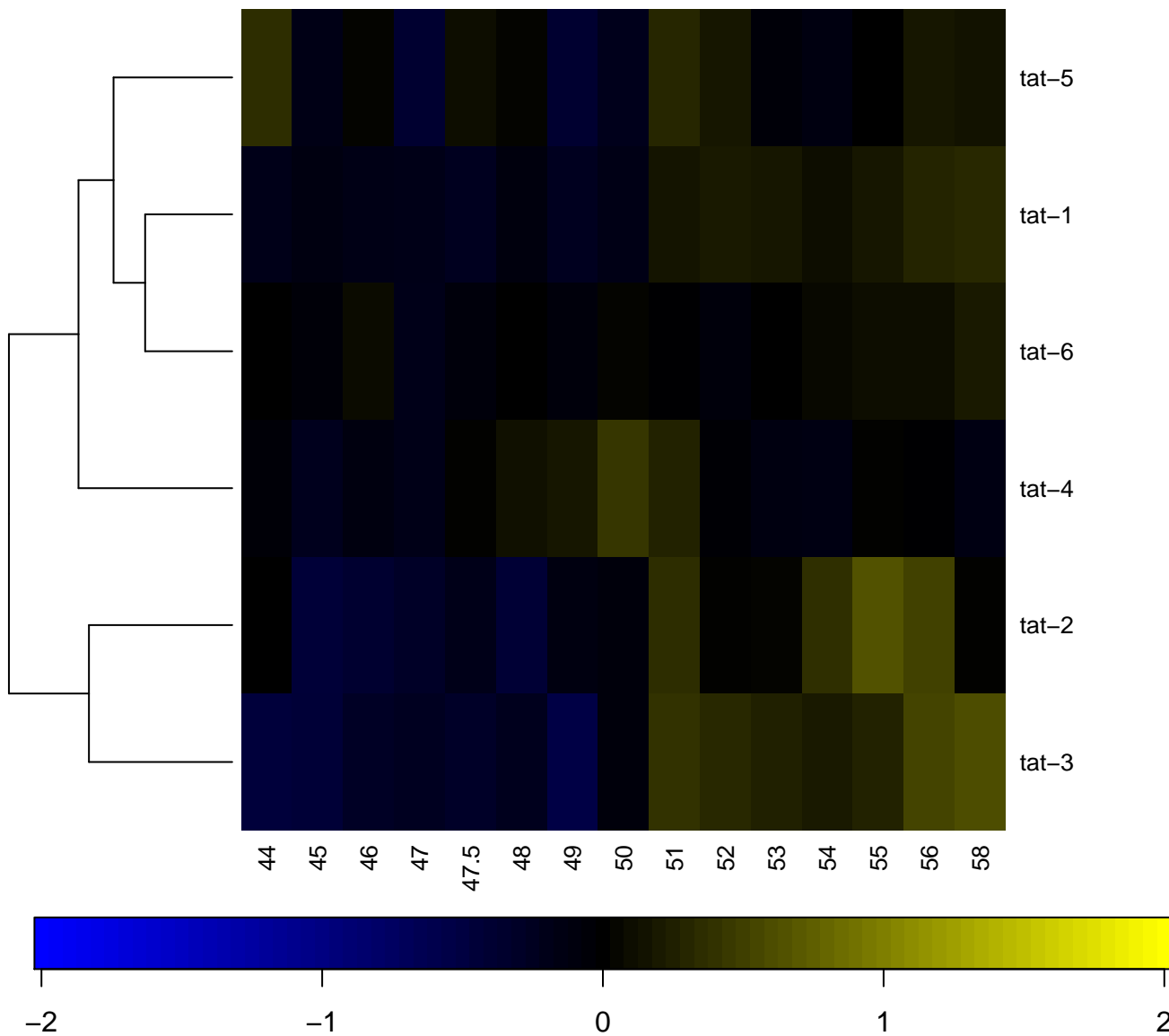
ATPase, P-type, ATPase-associated domain



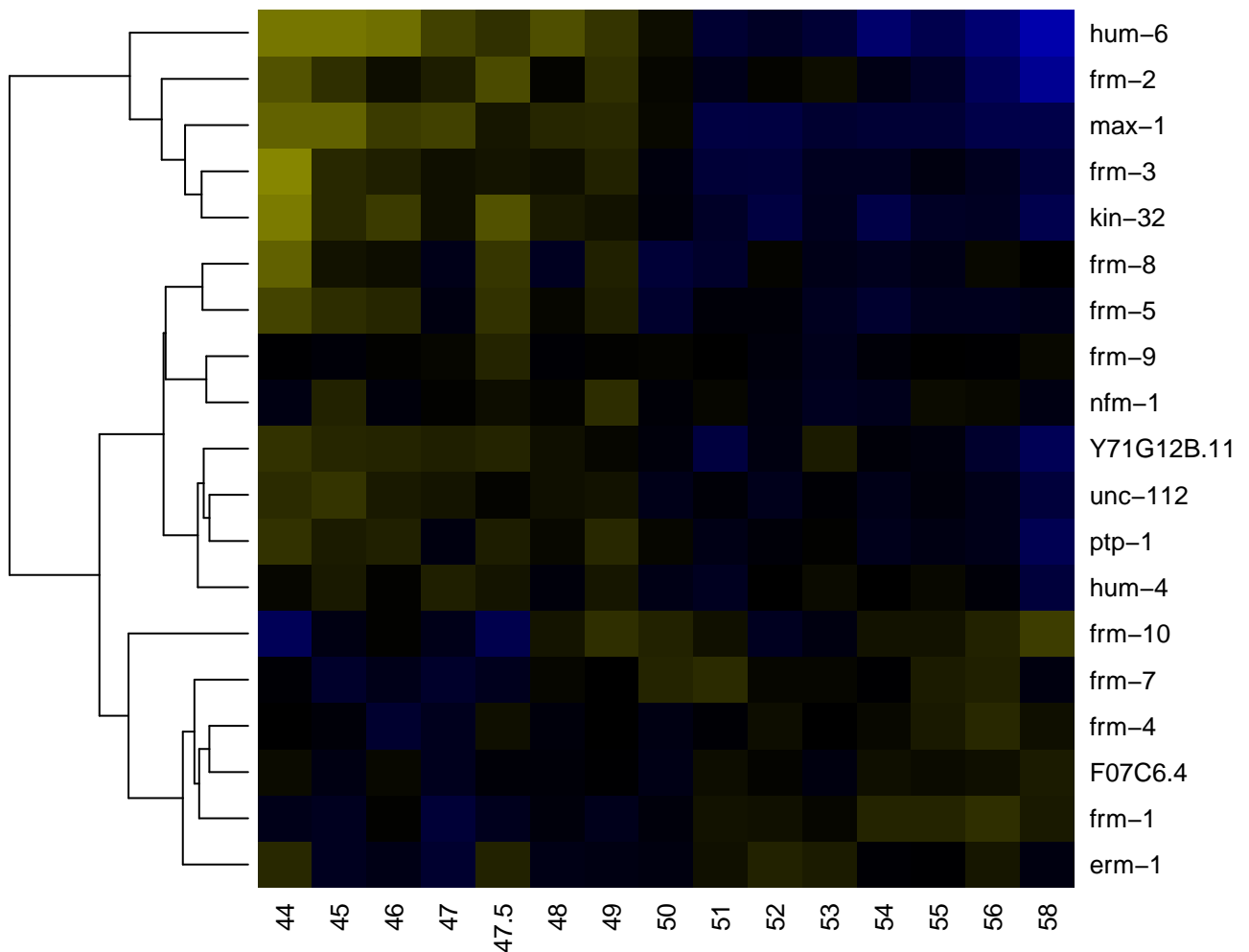
ATPase, P-type, K/Mg/Cd/Cu/Zn/Na/Ca/Na/H-transporter



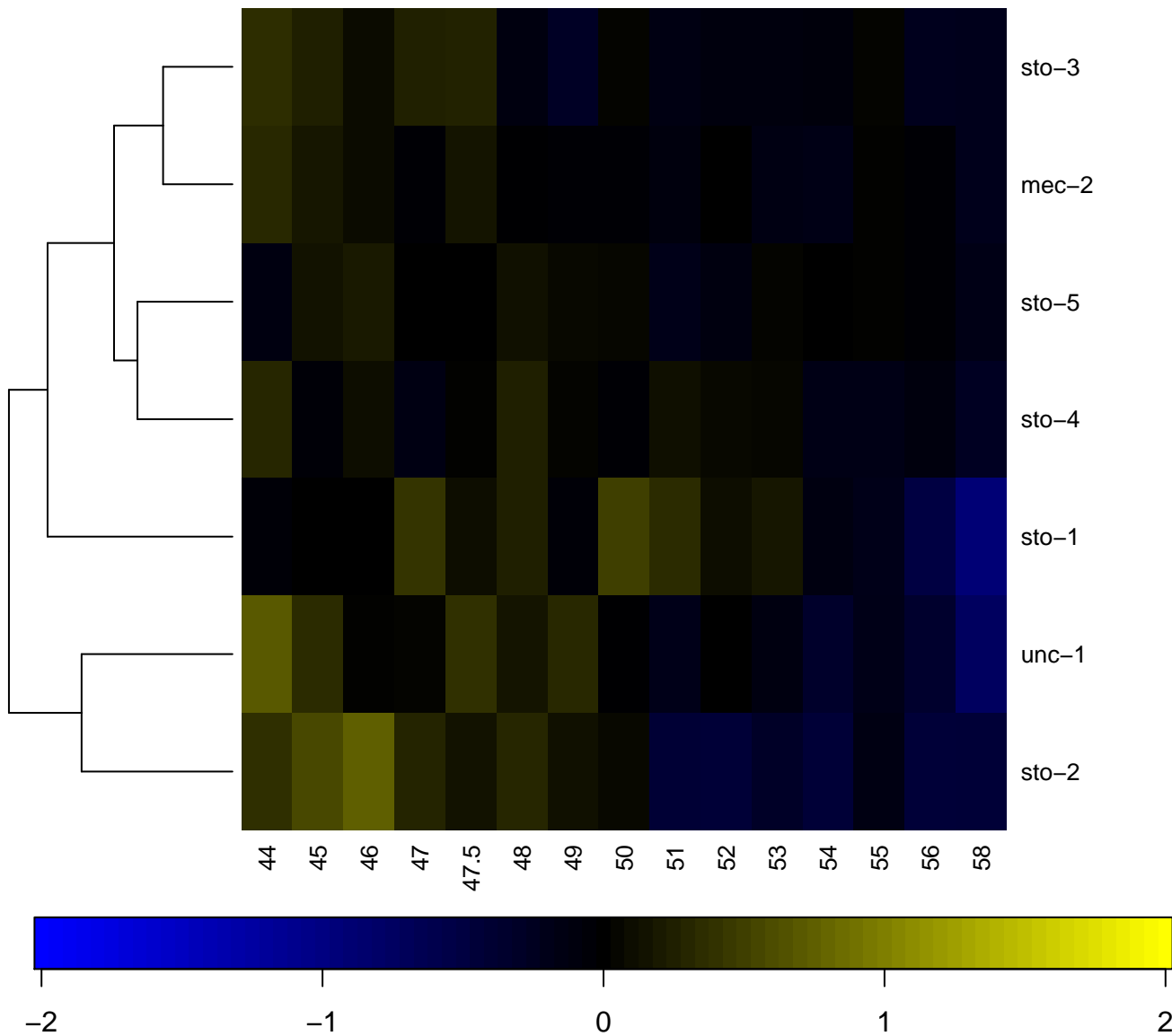
ATPase, P-type, phospholipid-translocating, flippase



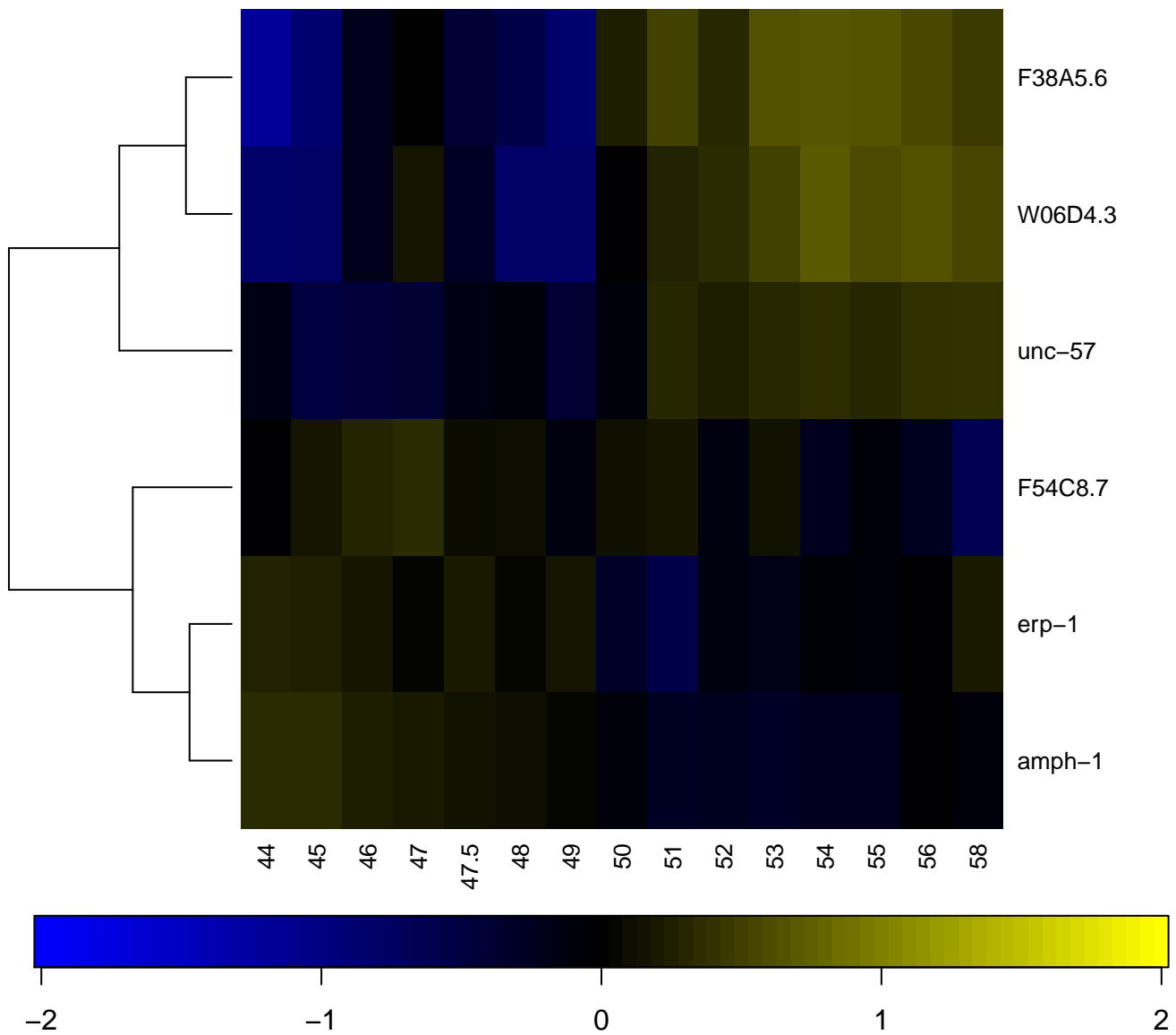
Band 4.1 domain



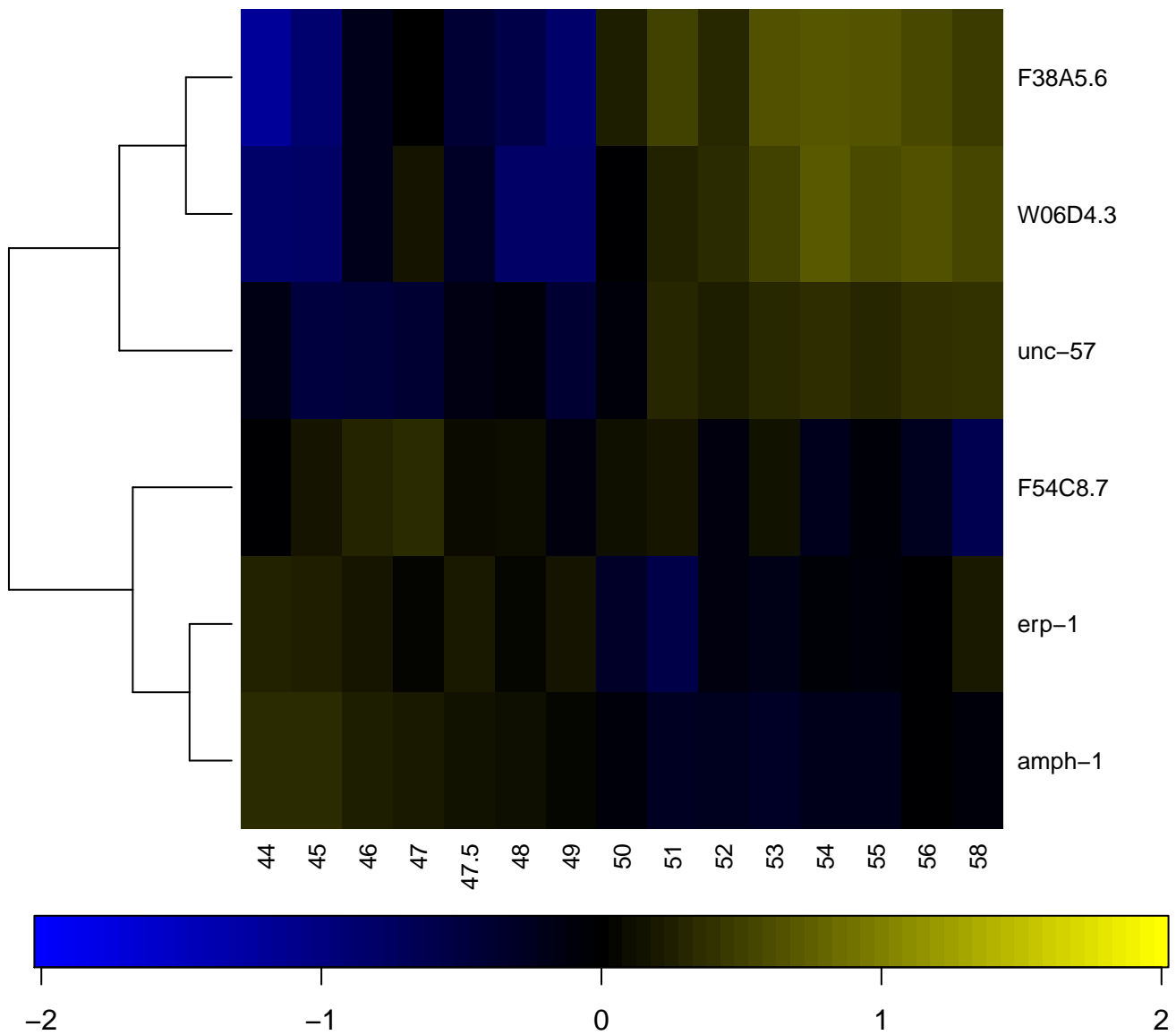
Band 7/stomatin-like, conserved site



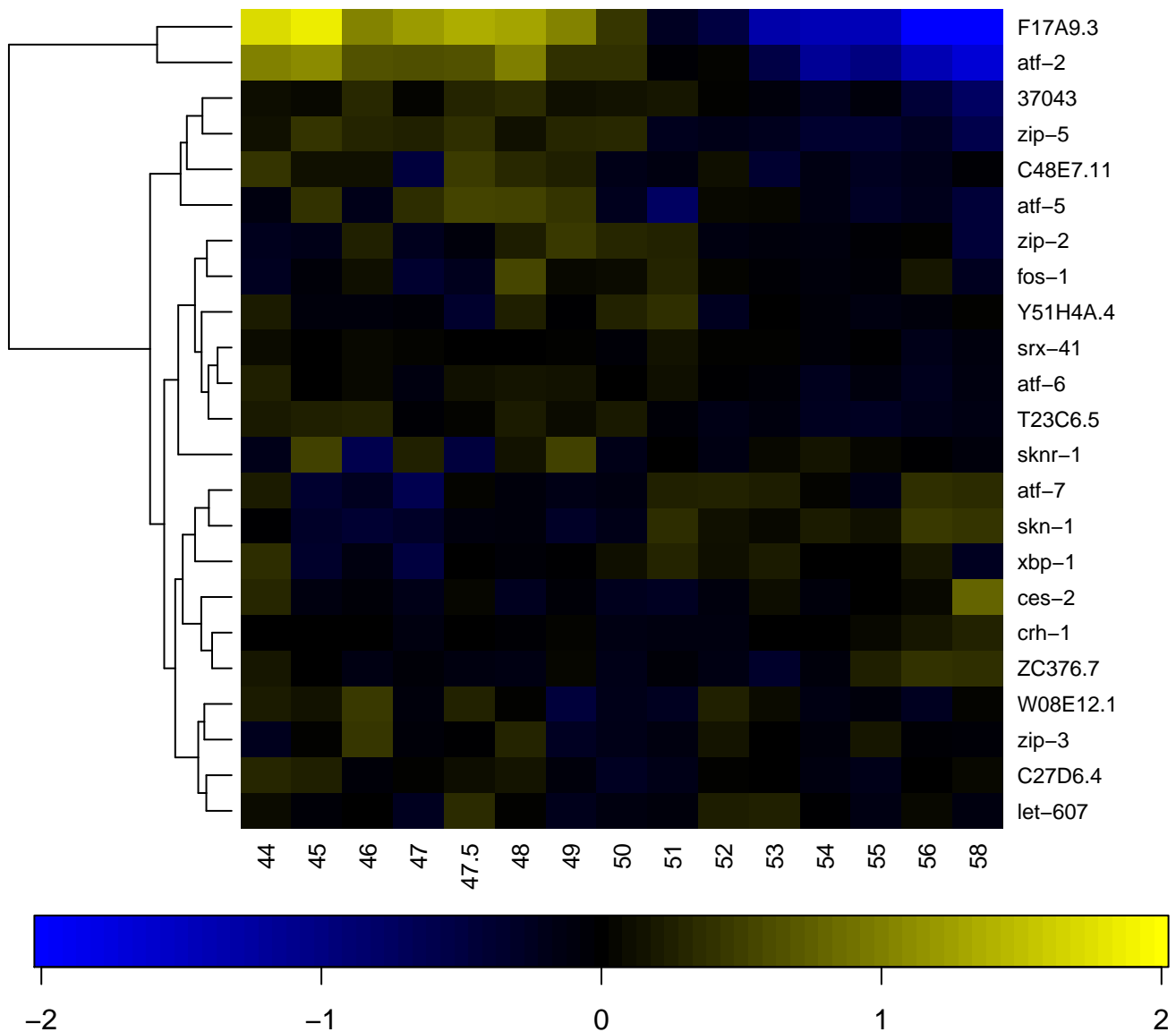
BAR



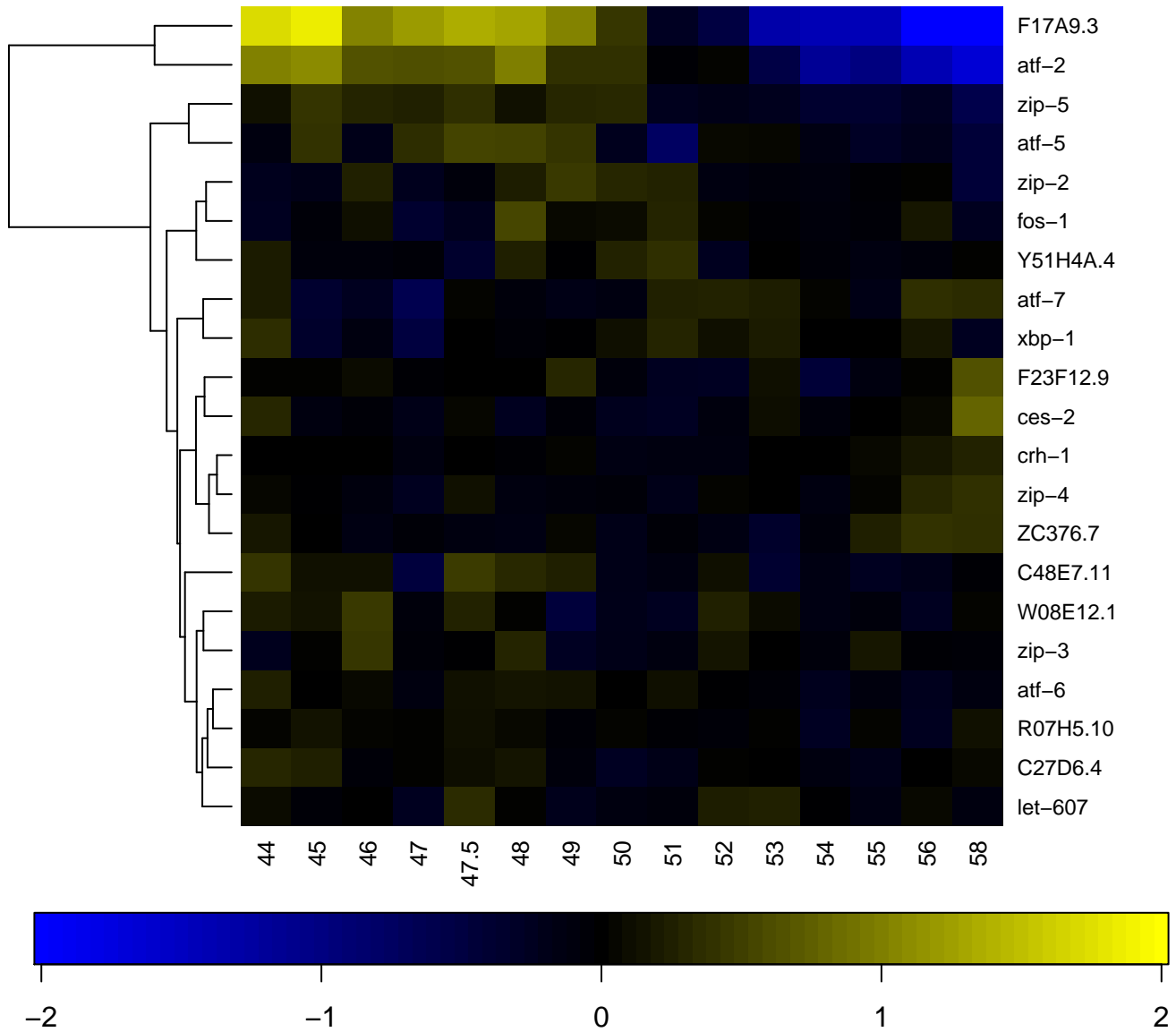
BAR domain



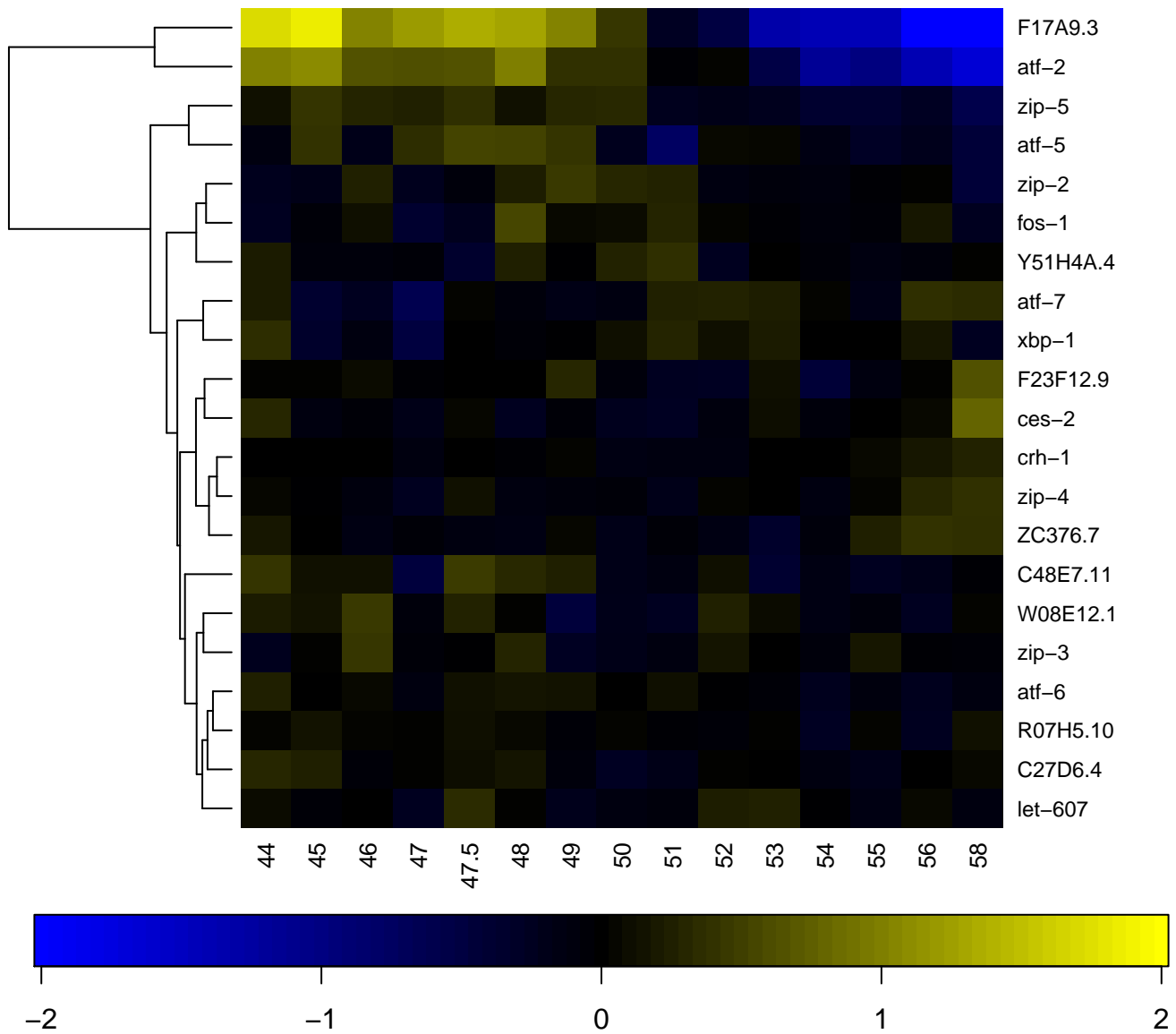
Basic-leucine zipper (bZIP) transcription factor



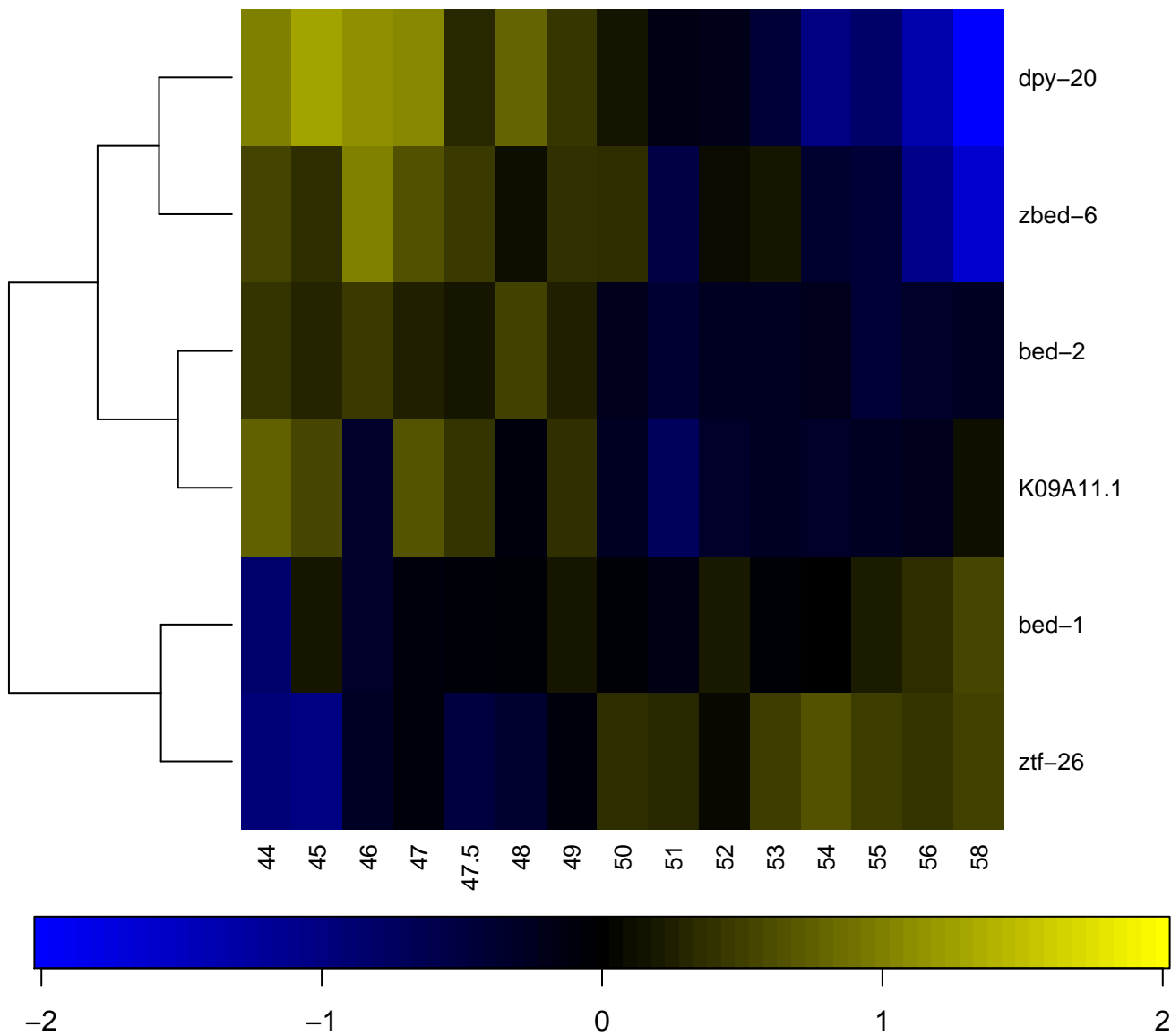
Basic leucine zipper



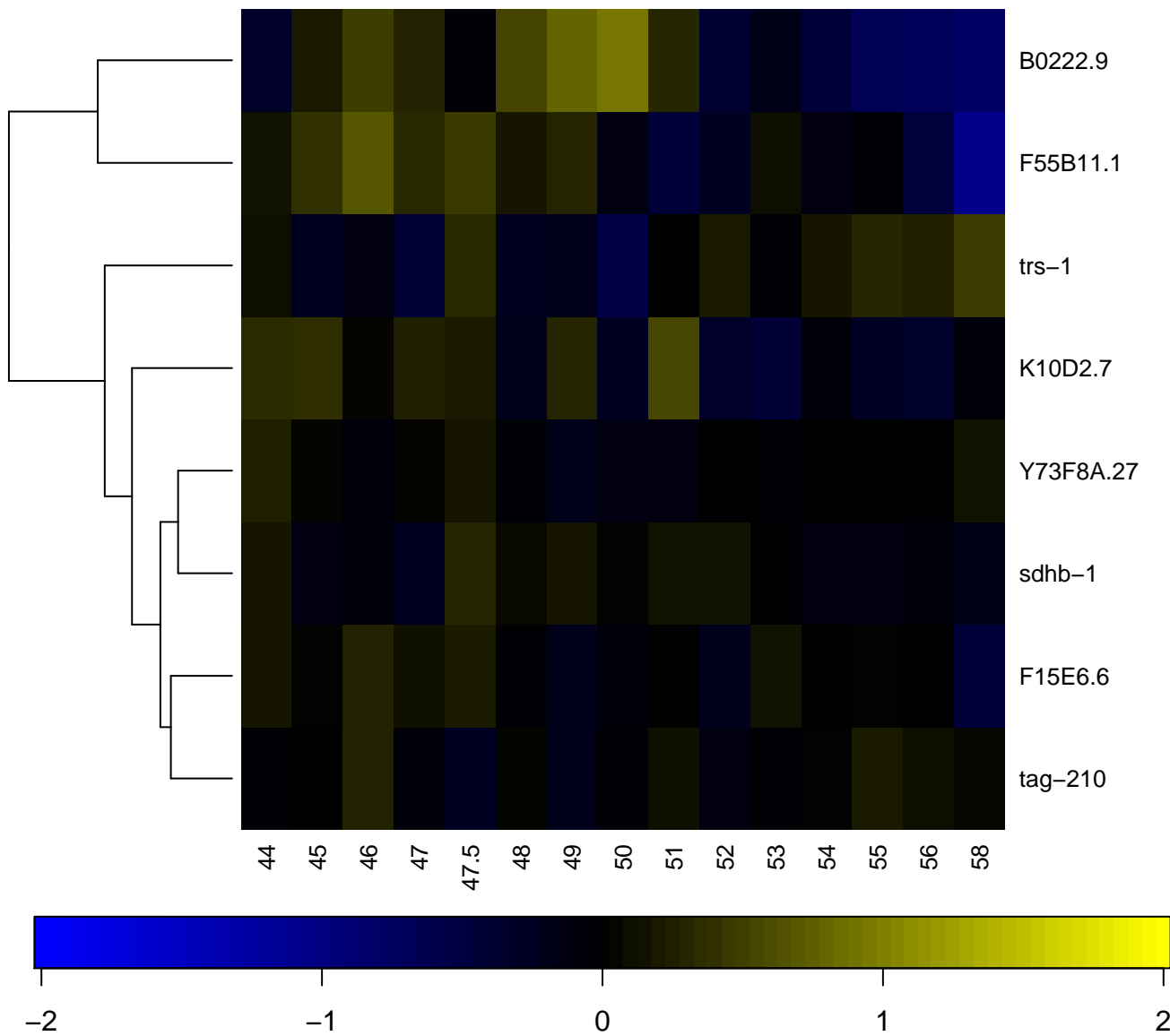
Basic region leucine zipper



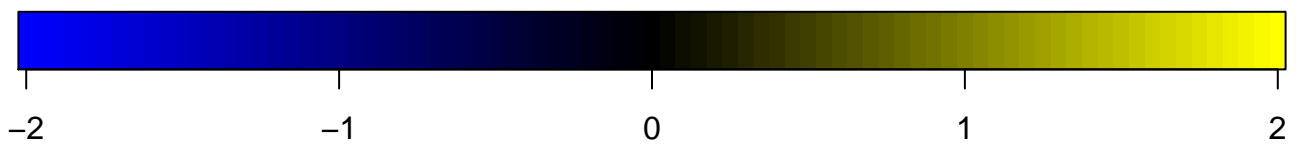
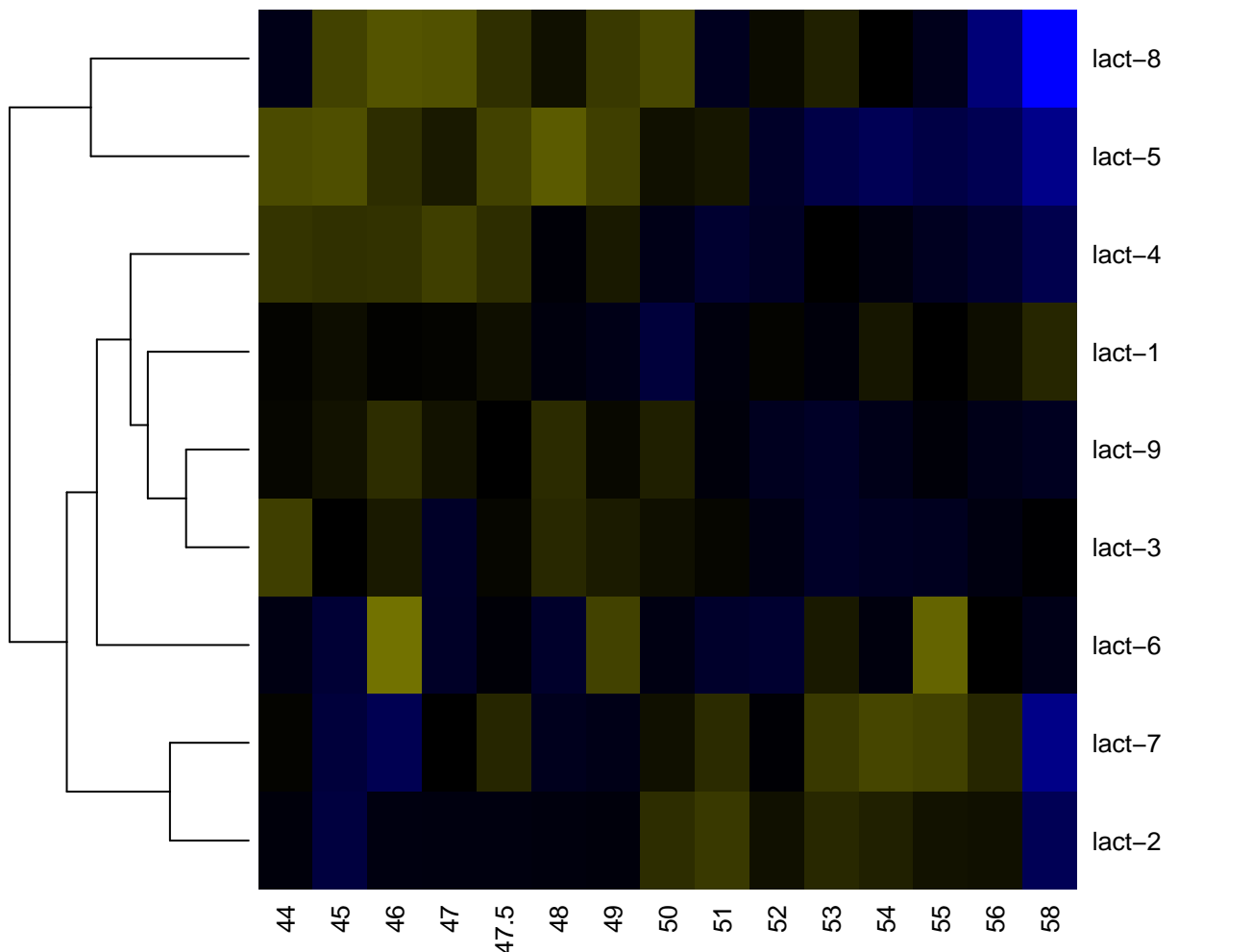
BED zinc finger



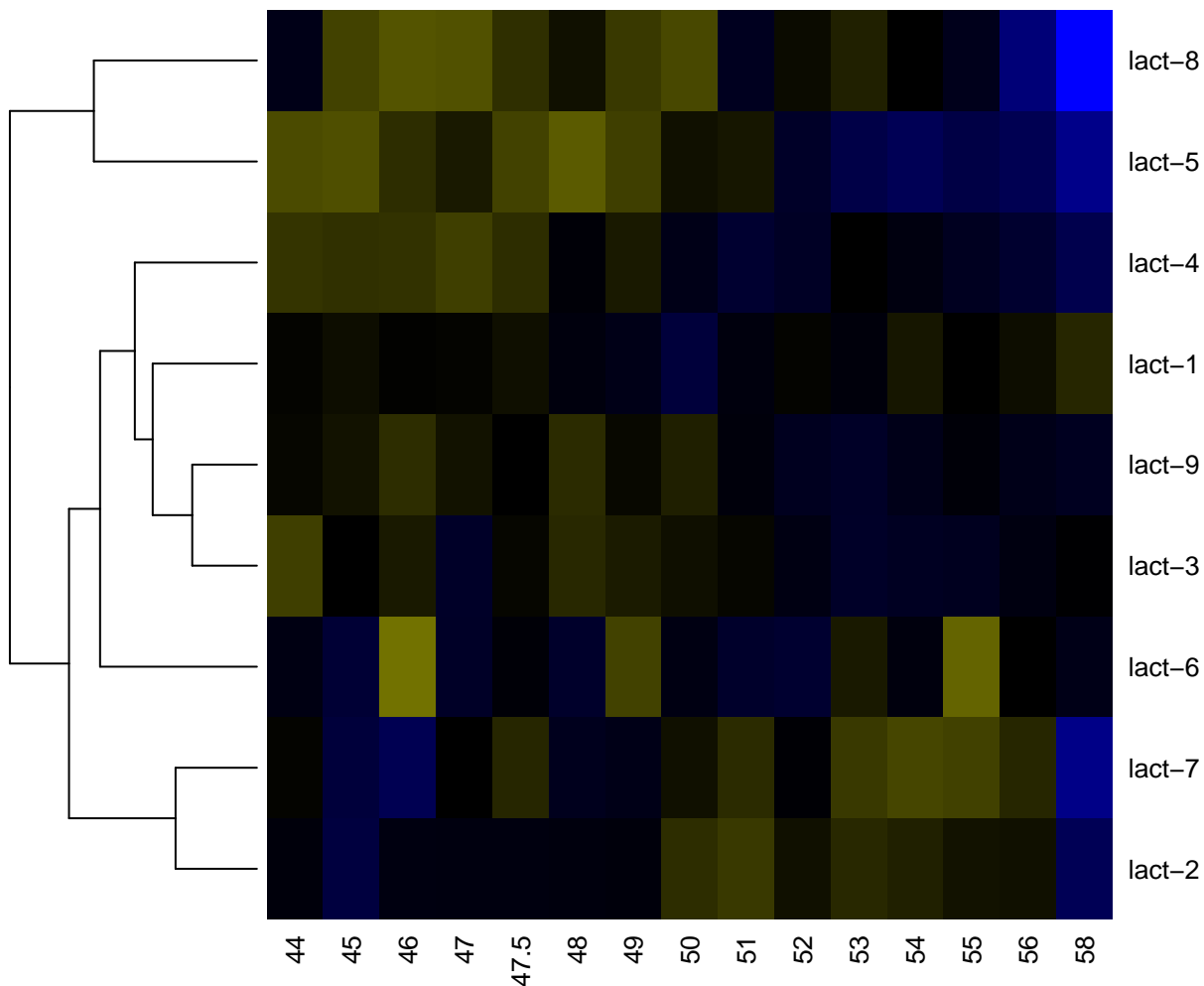
Beta-grasp fold, ferredoxin-type



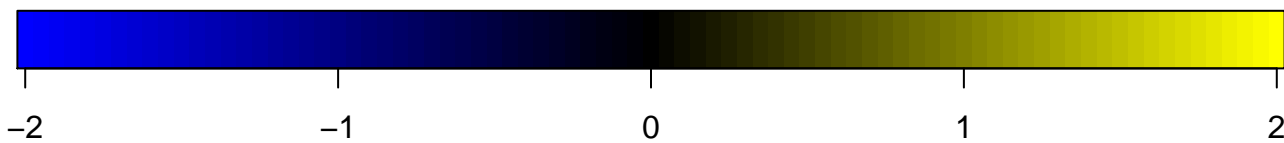
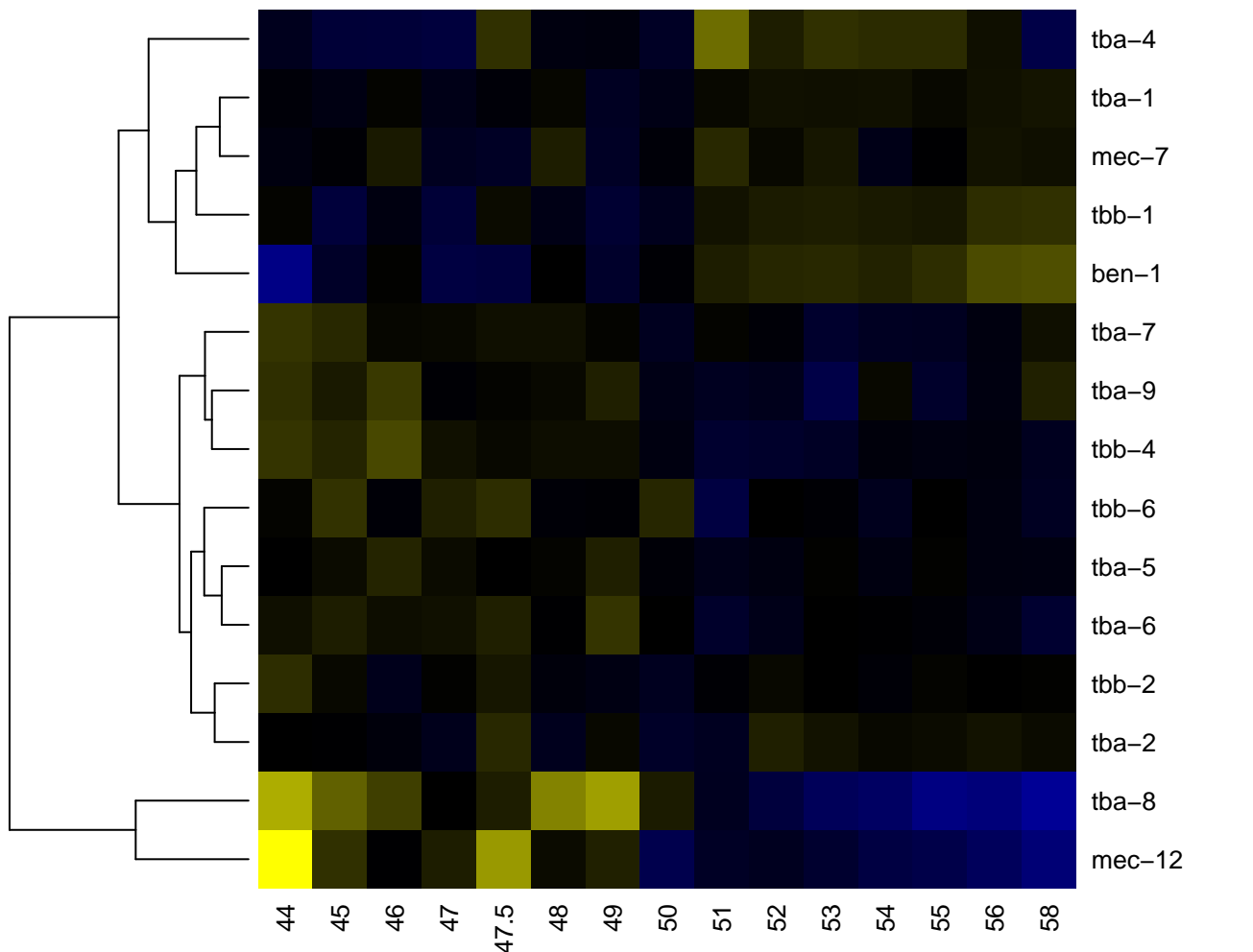
Beta-lactamase



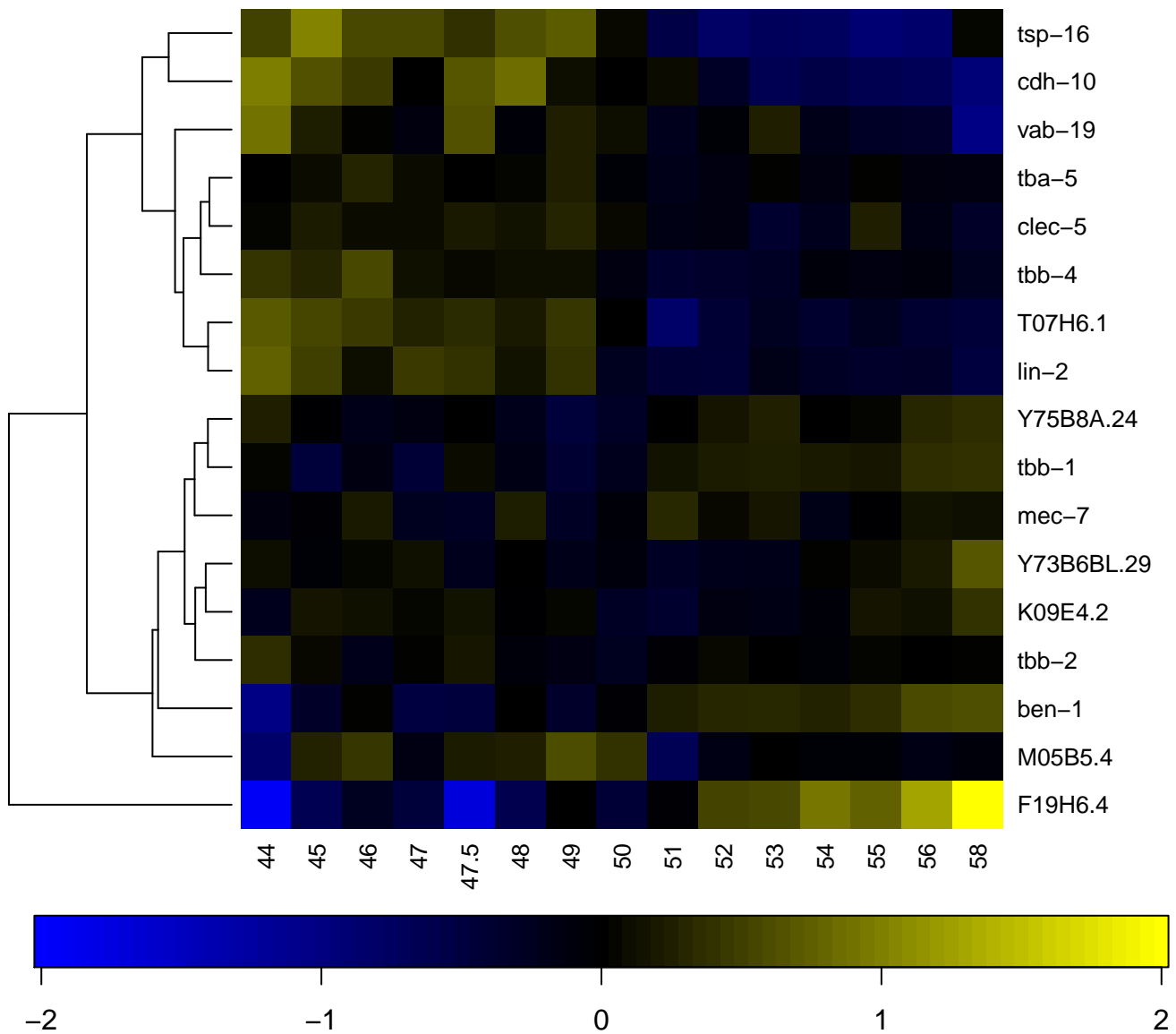
Beta-lactamase-related



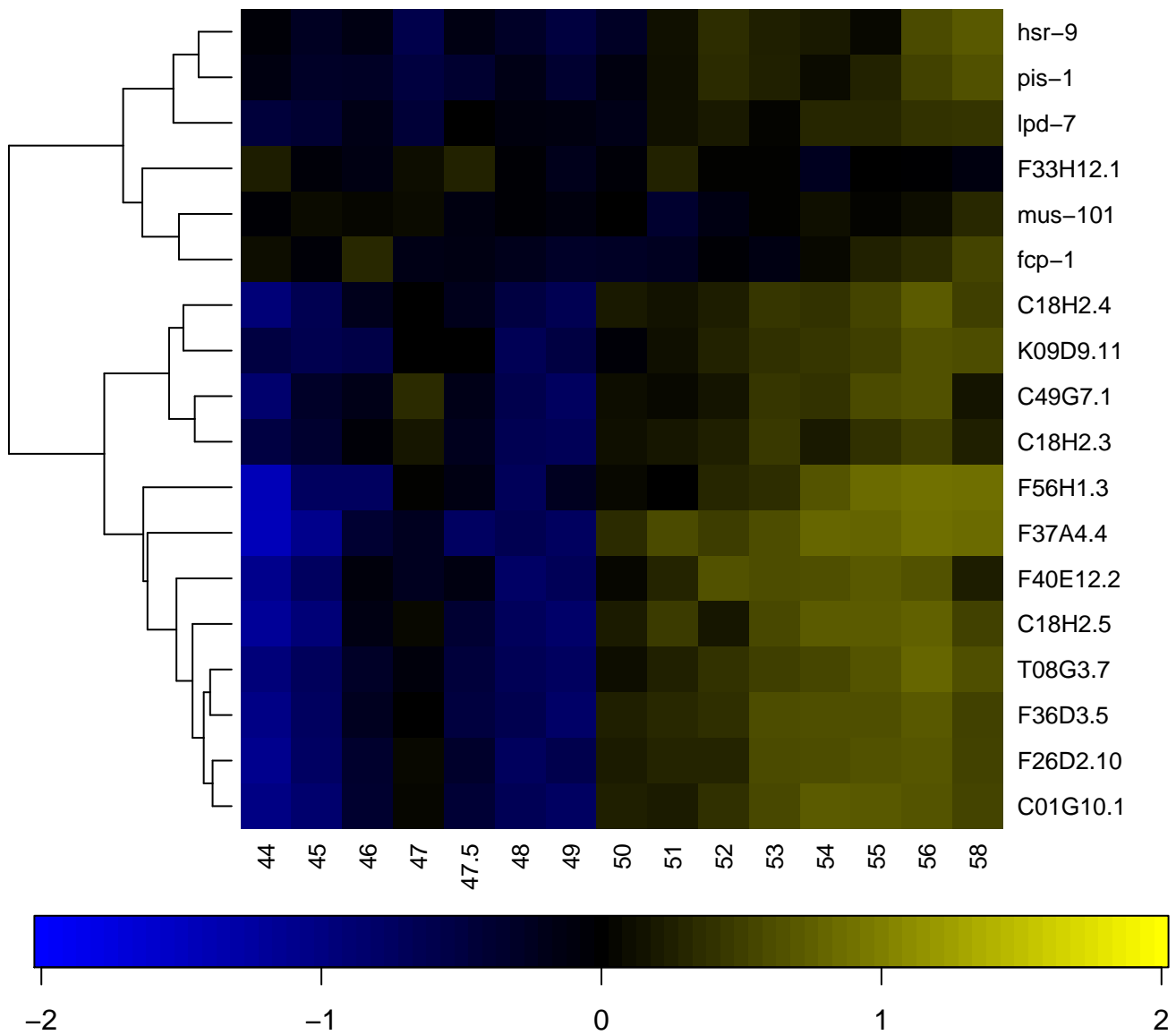
Beta tubulin



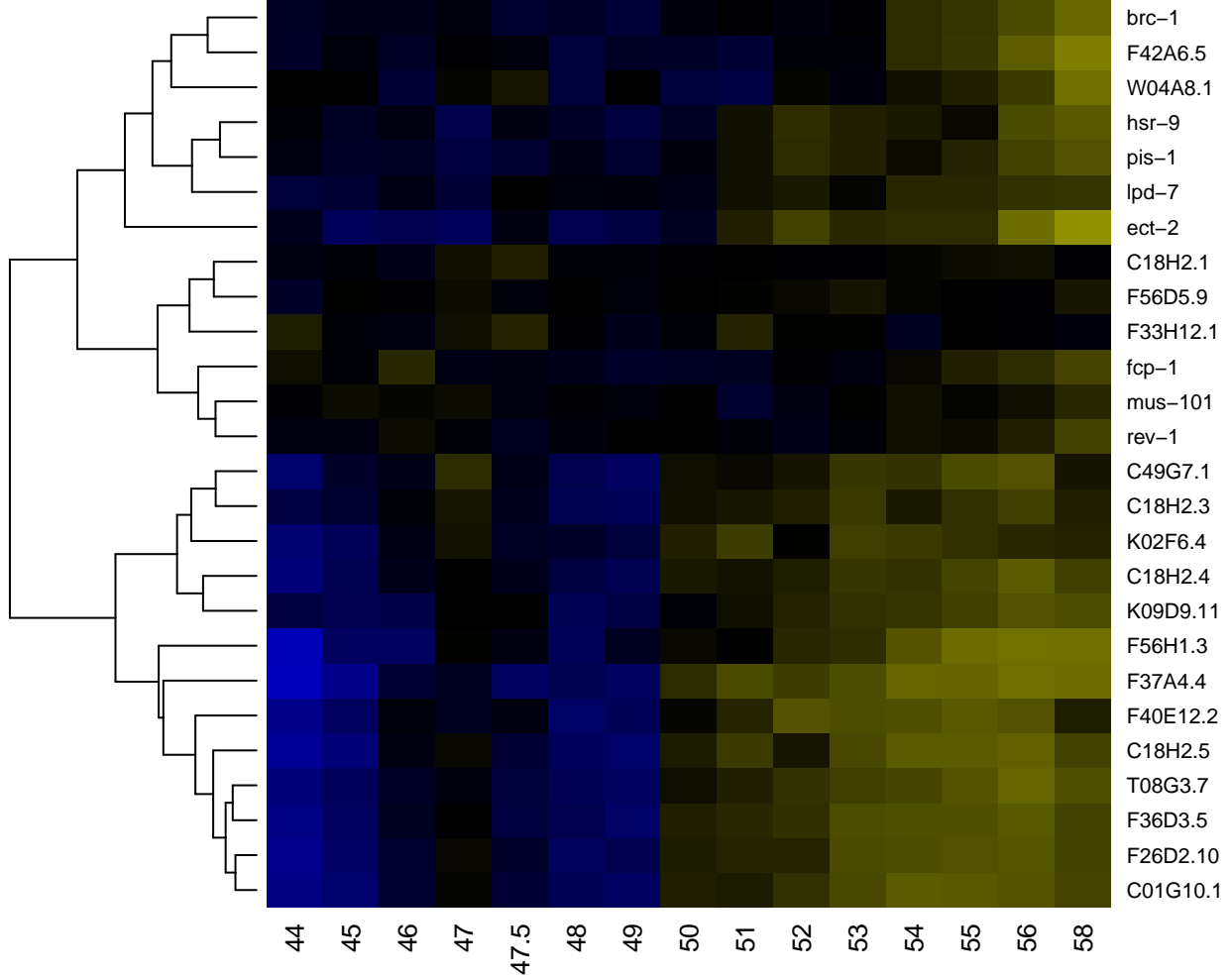
Beta tubulin, autoregulation binding site



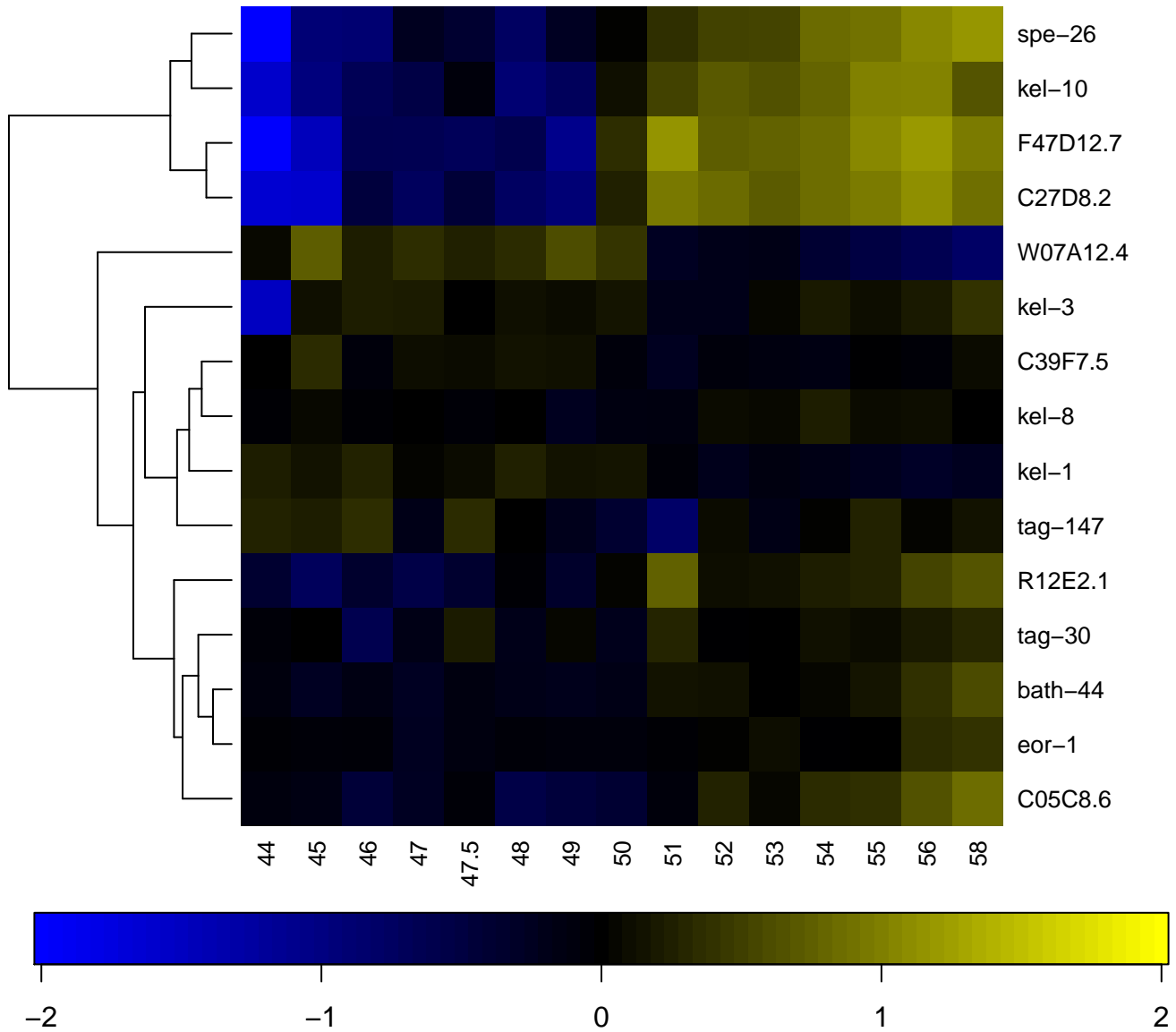
BRCA1 C Terminus (BRCT) domain



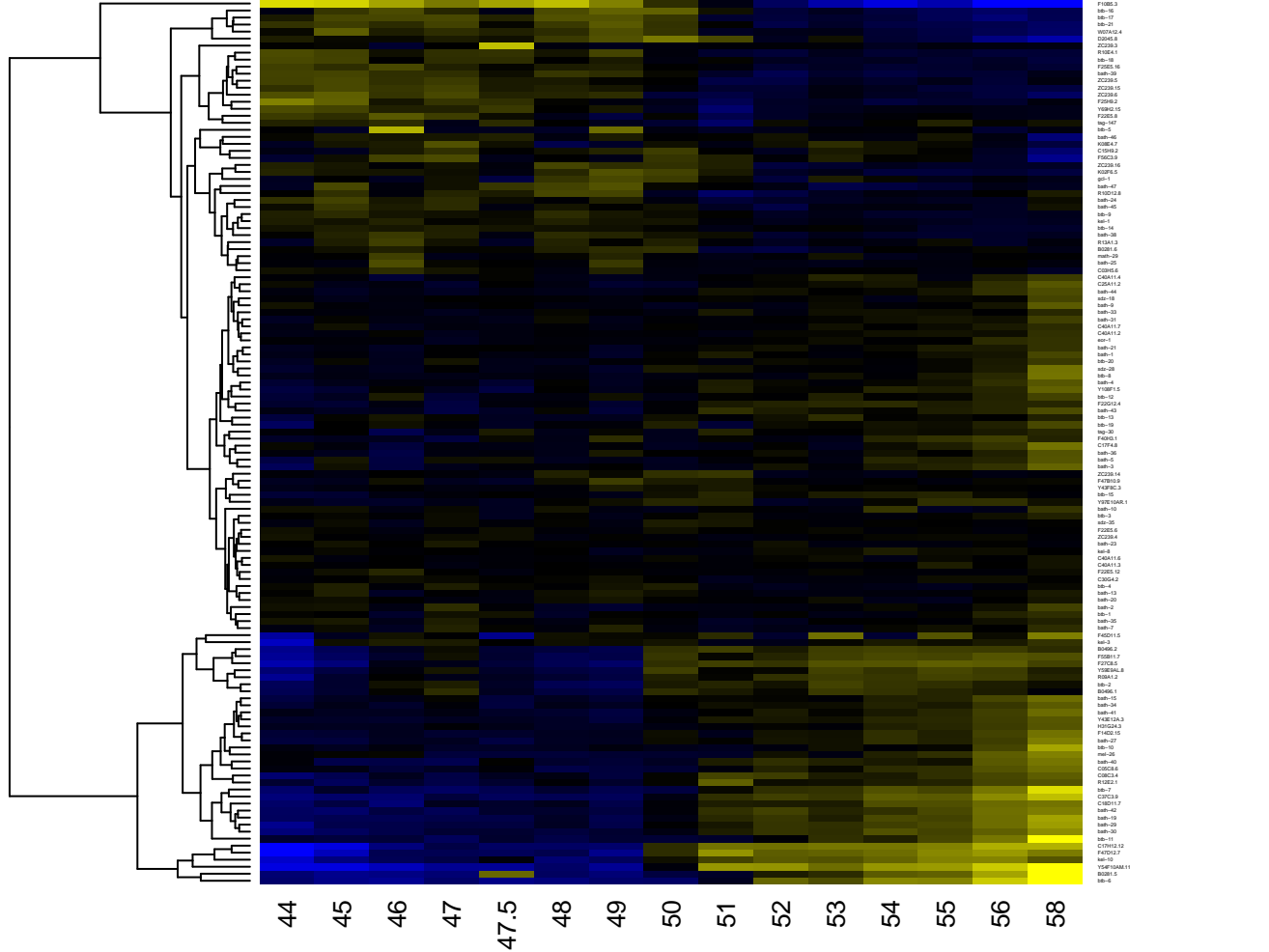
BRCT



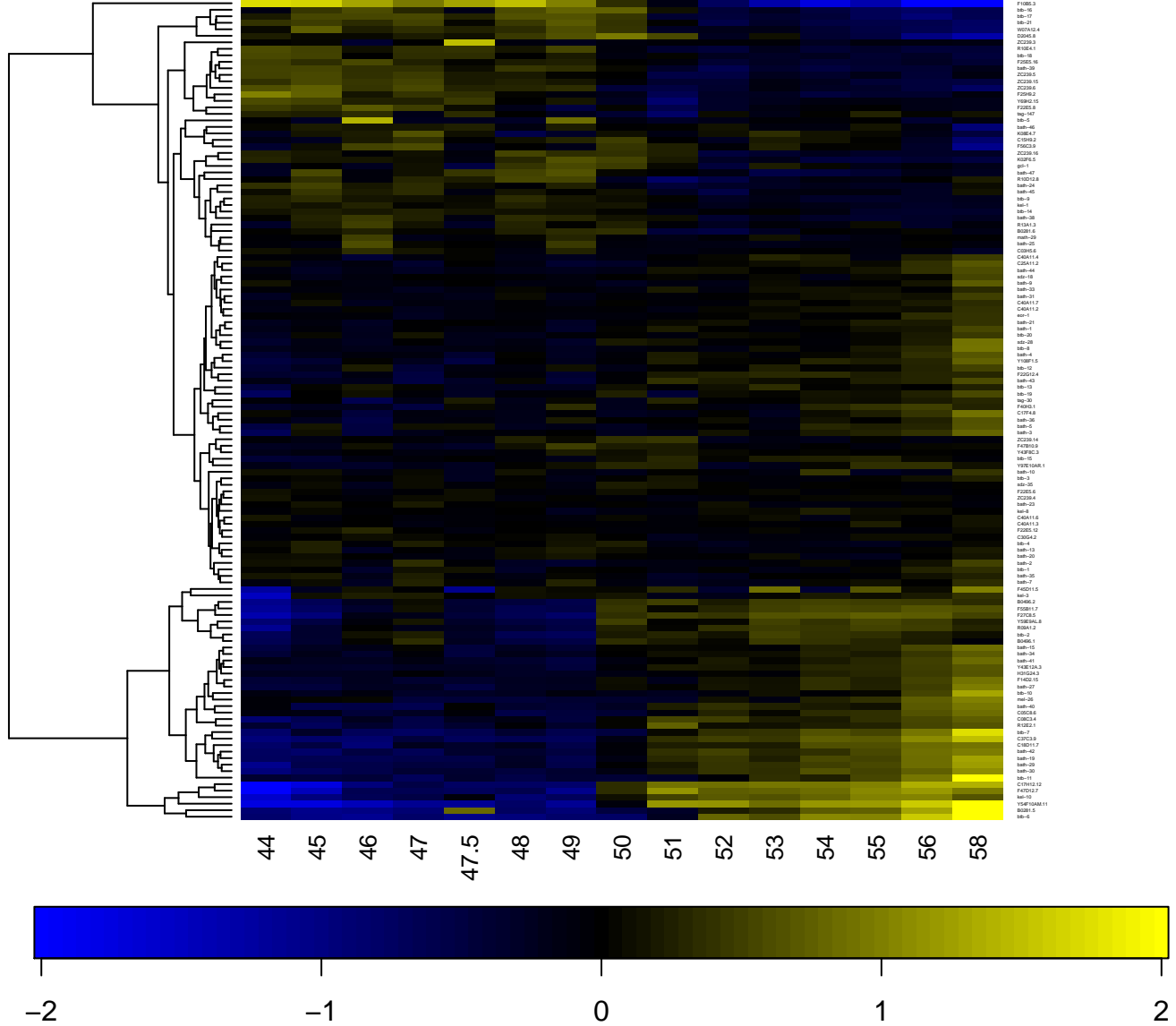
BTB/Kelch-associated



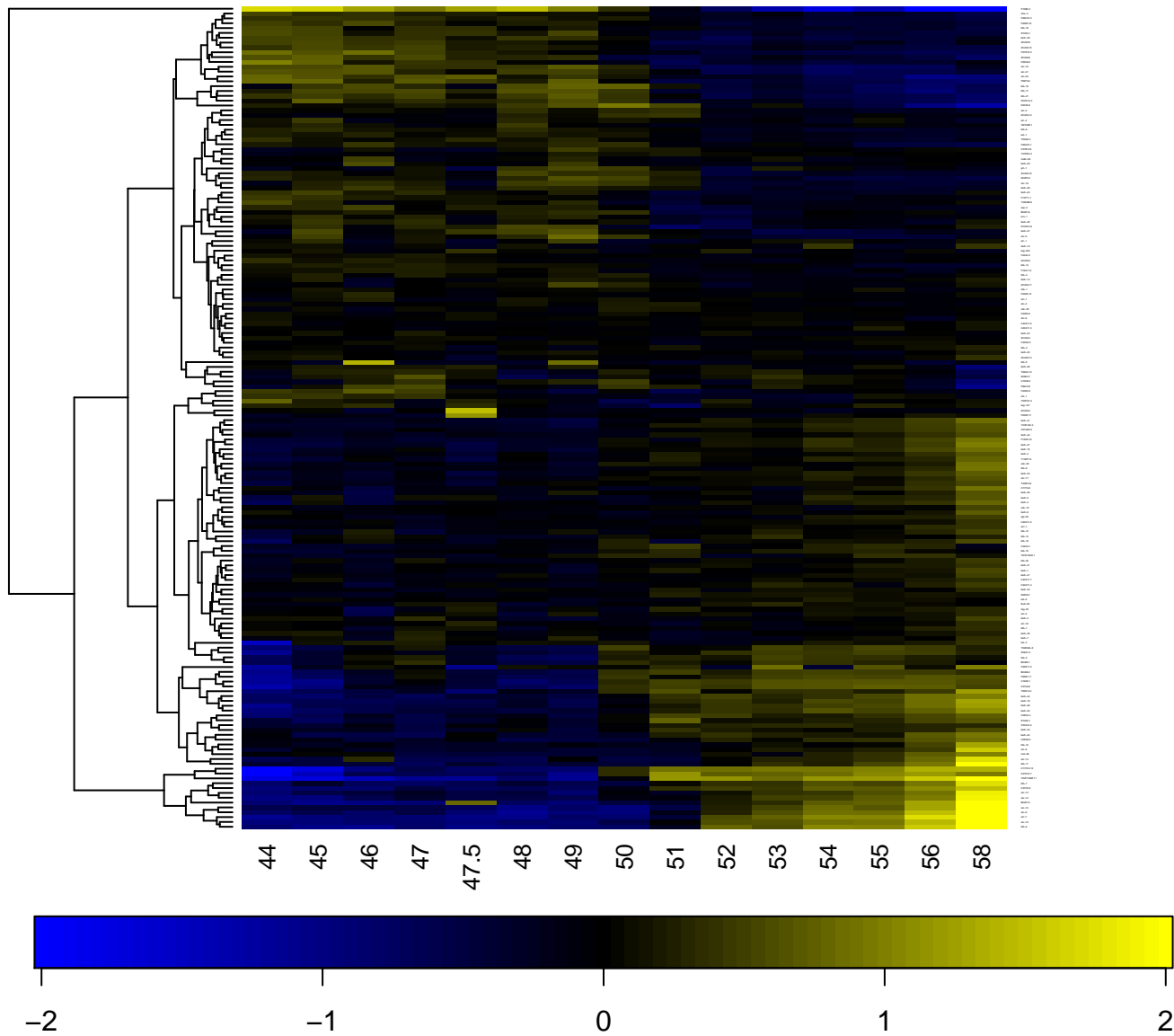
BTB/POZ



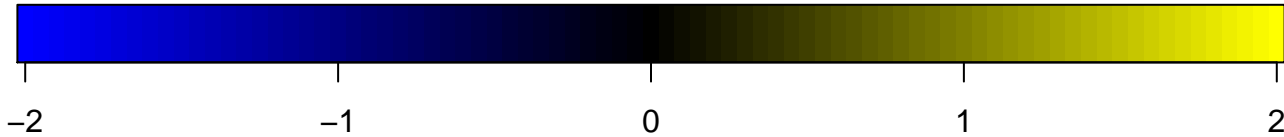
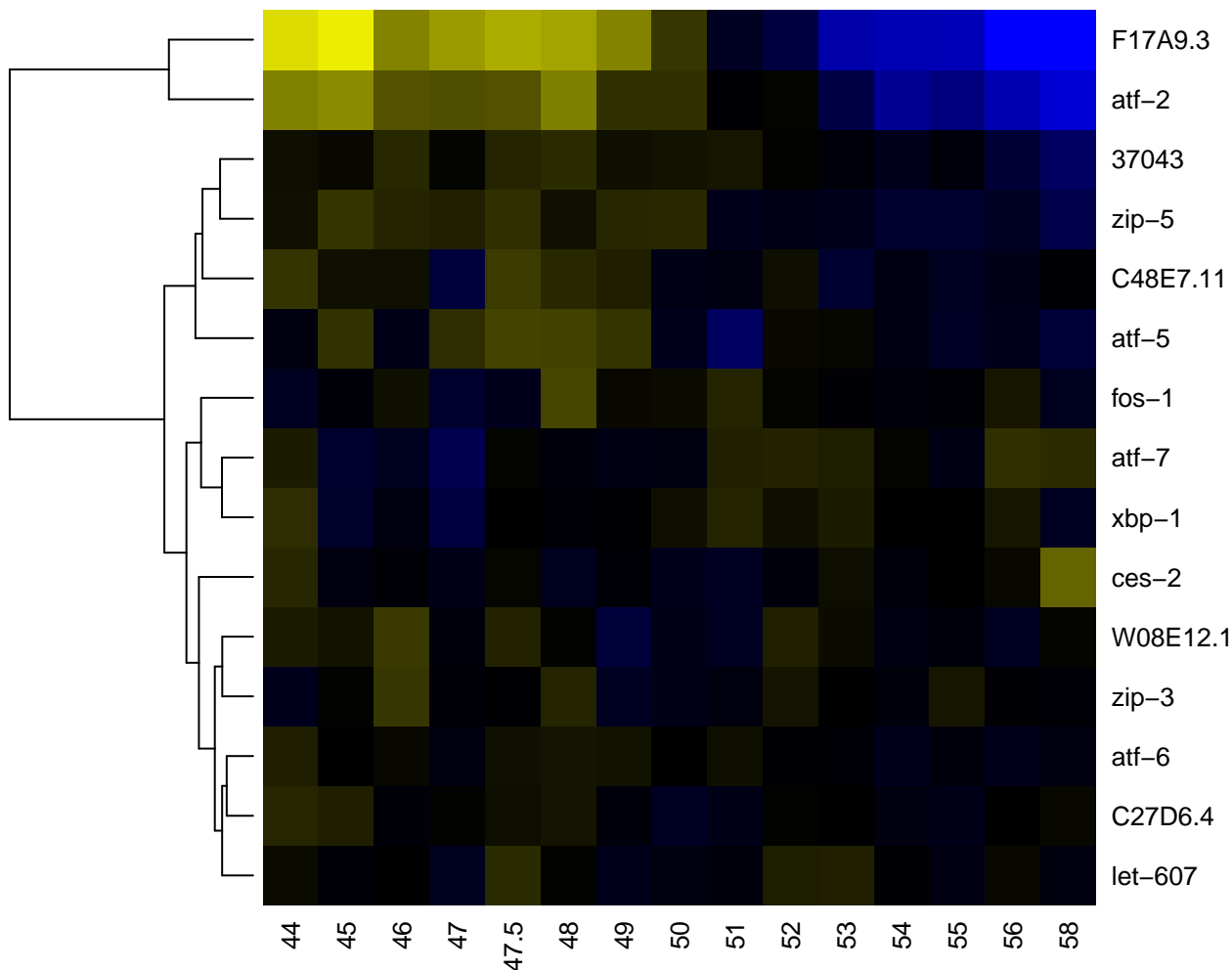
BTB/POZ domain



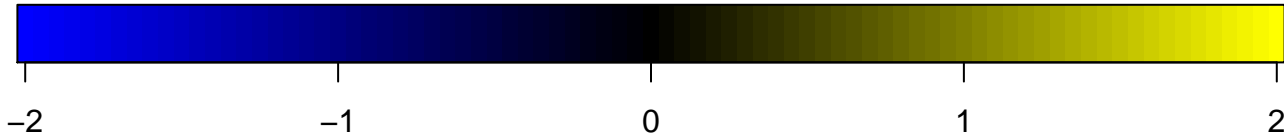
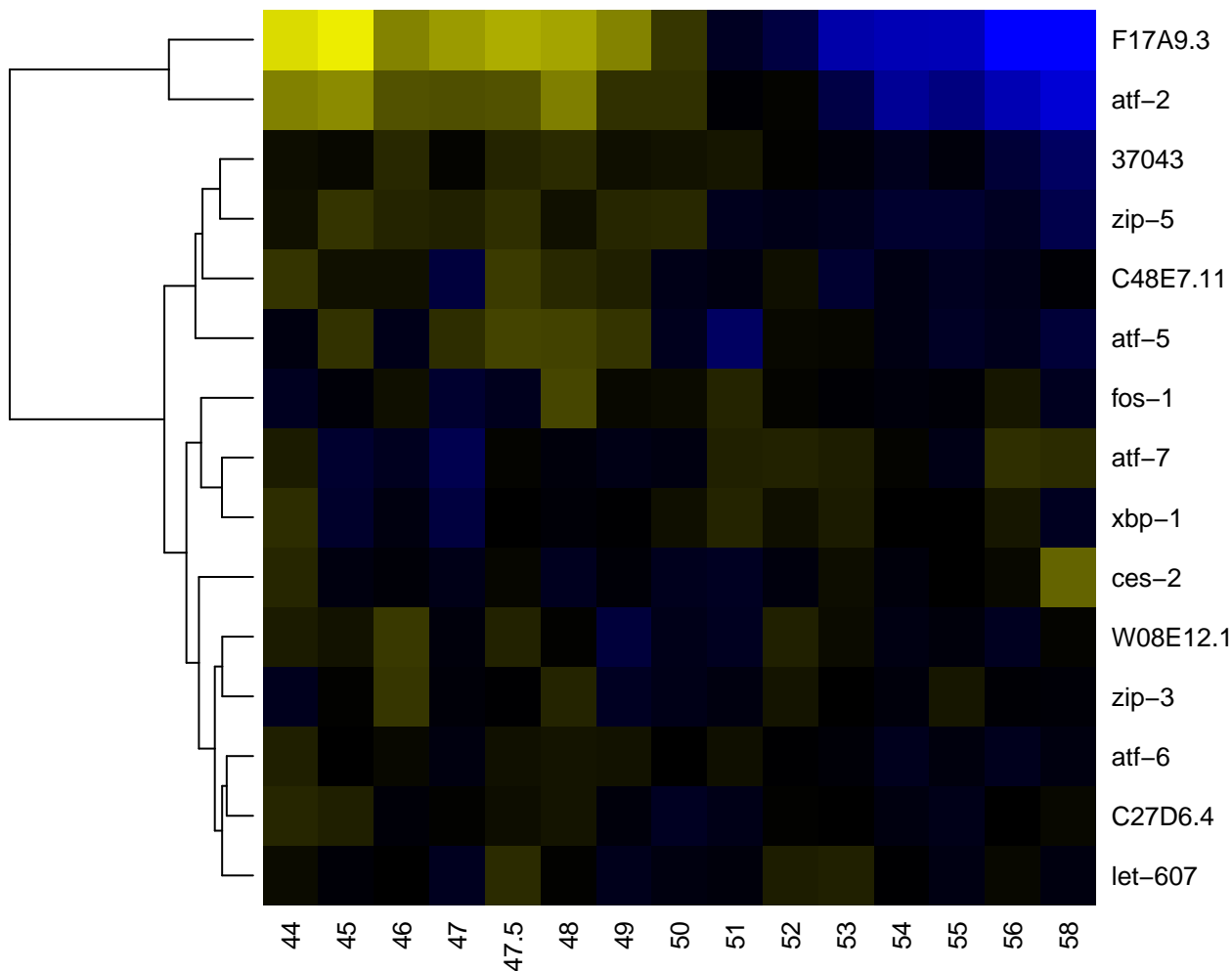
BTB/POZ fold



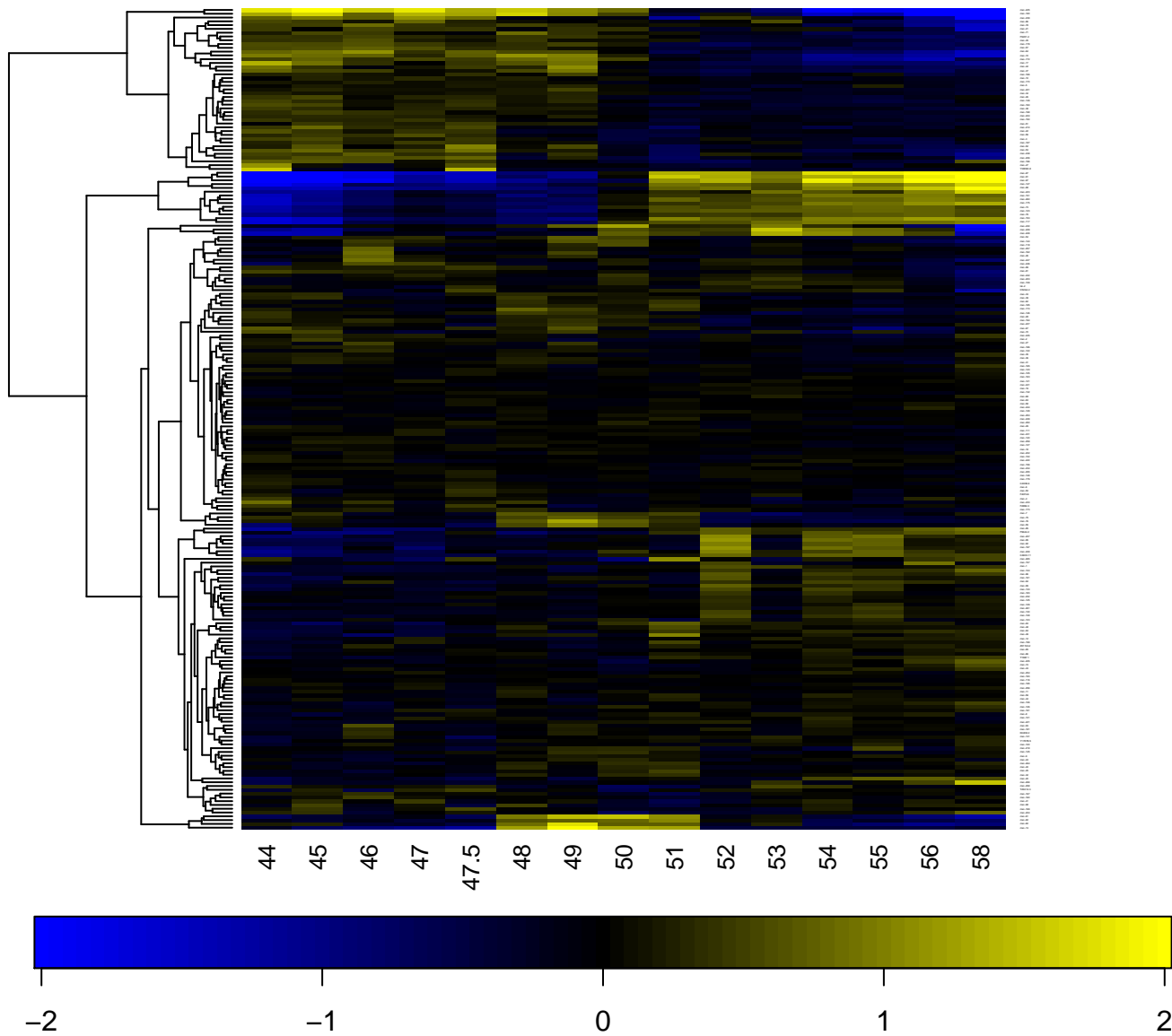
bZIP transcription factor



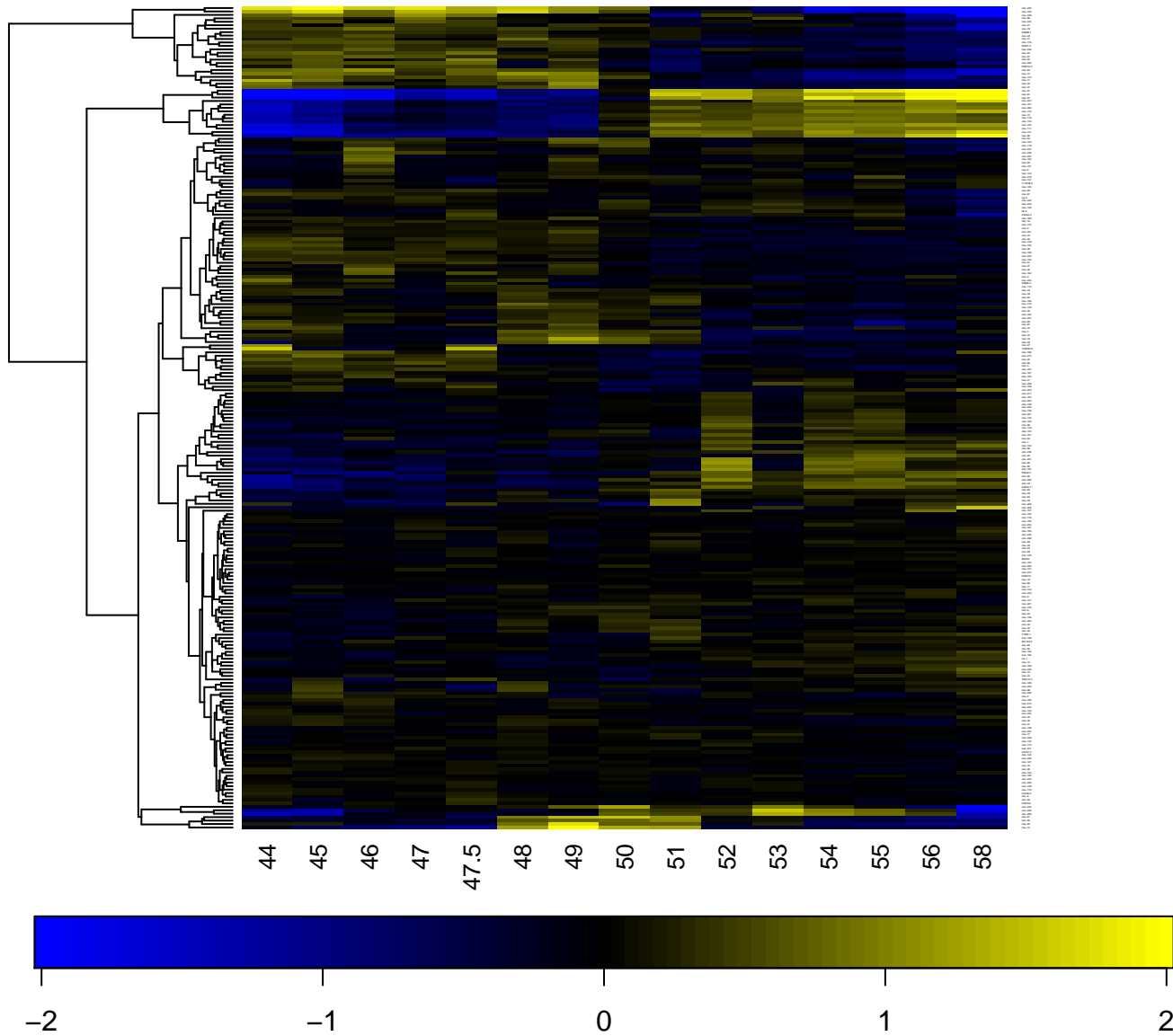
bZIP transcription factor, bZIP-1



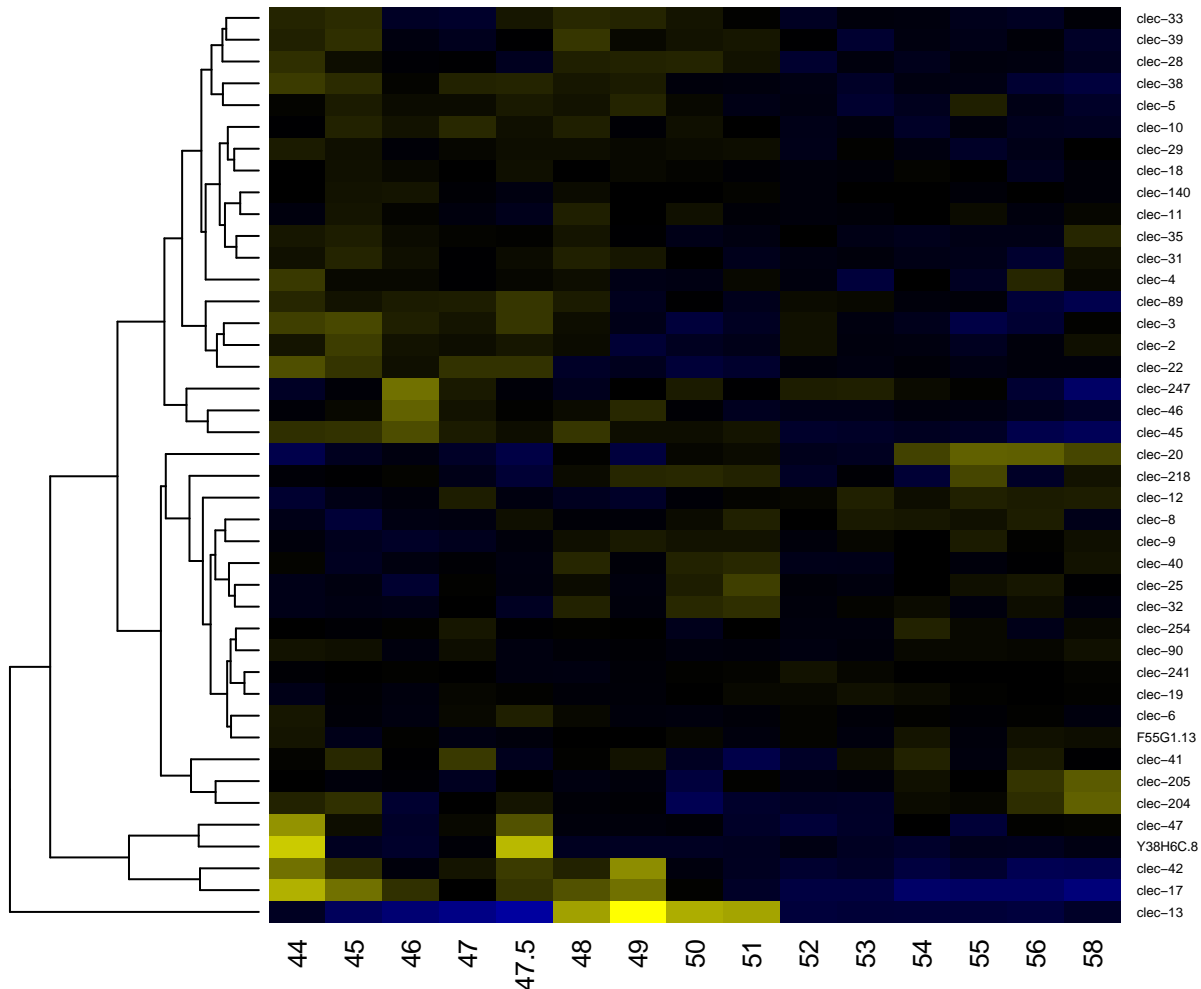
C-type lectin



C-type lectin-like



C-type lectin, conserved site



-2

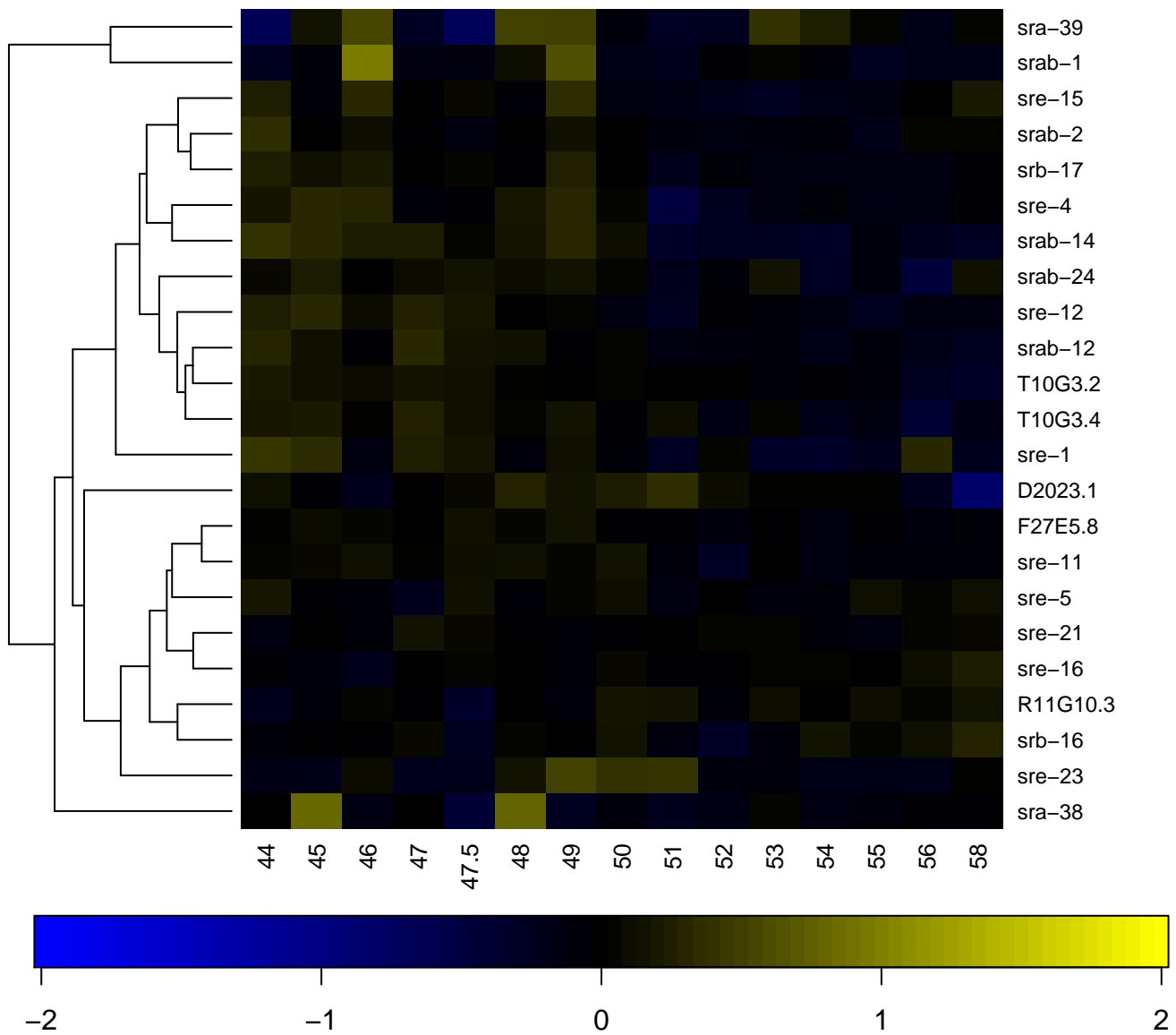
-1

0

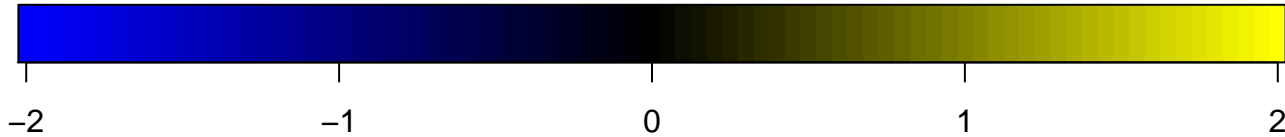
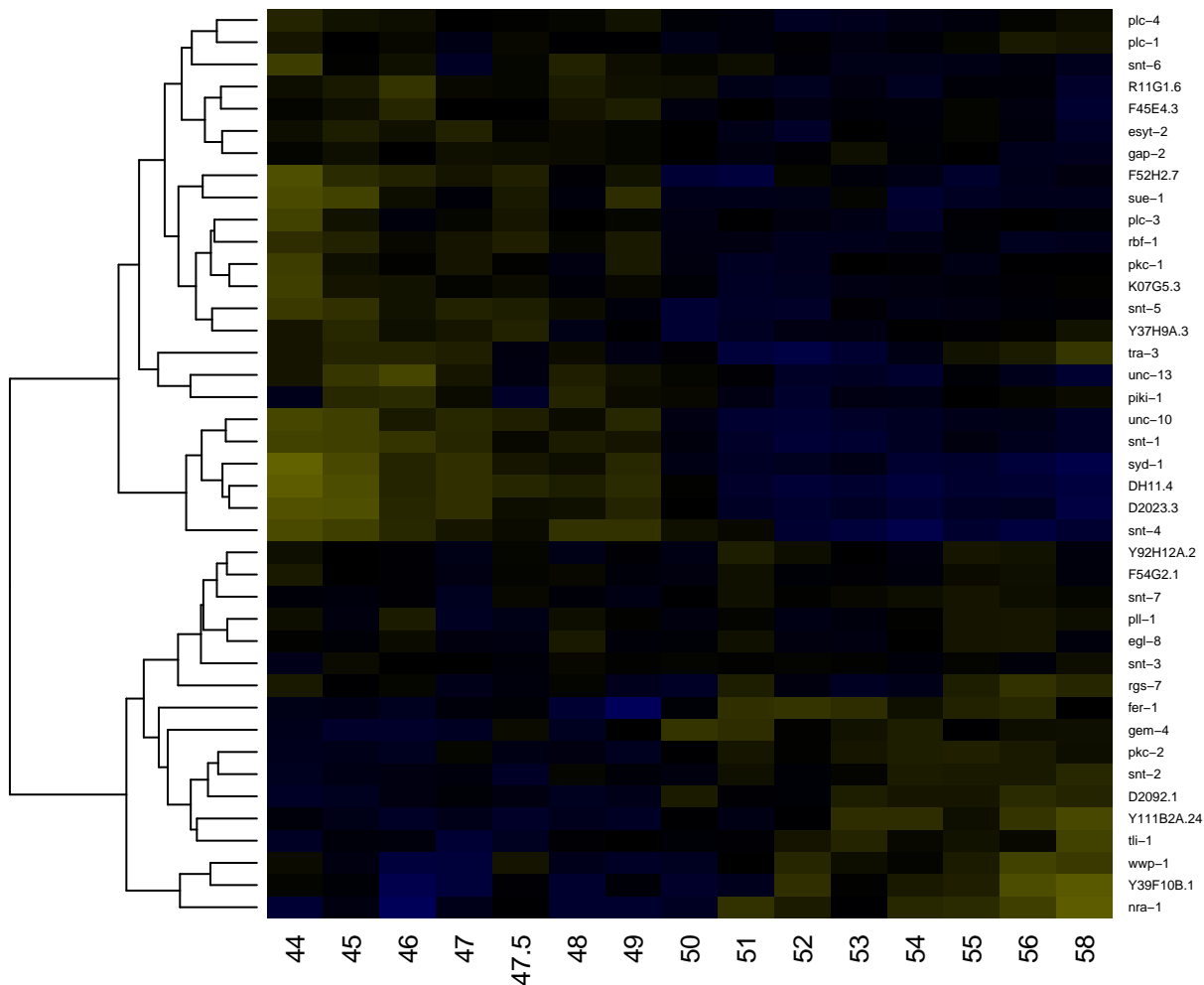
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2

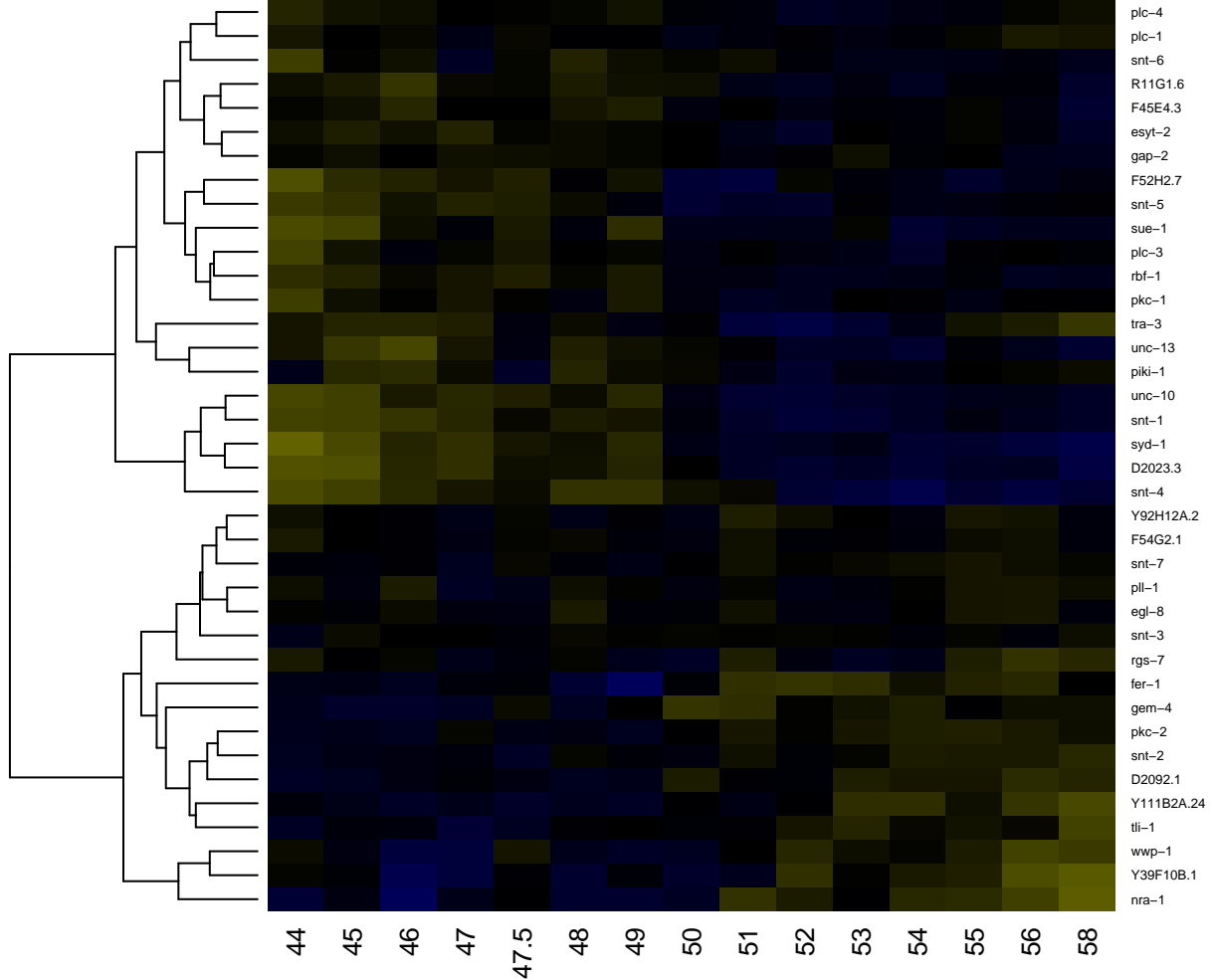
C. elegans Sre G protein-coupled chemoreceptor



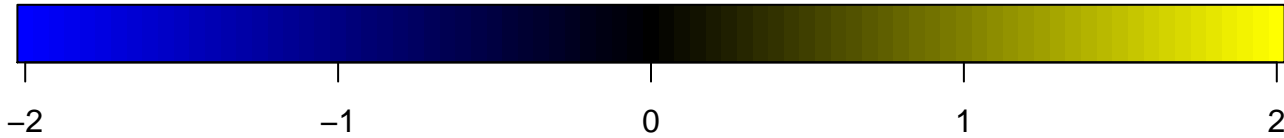
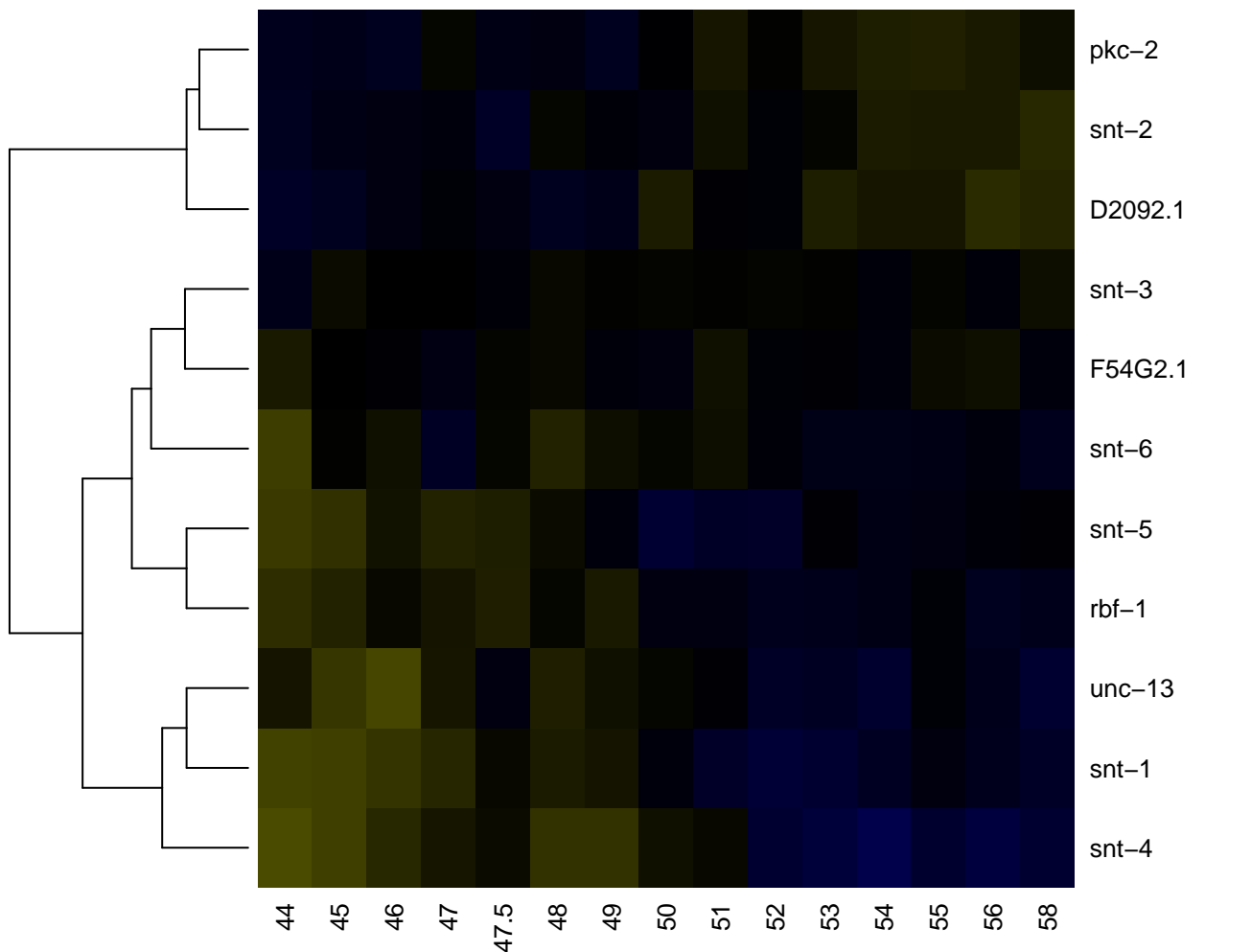
C2 calcium-dependent membrane targeting



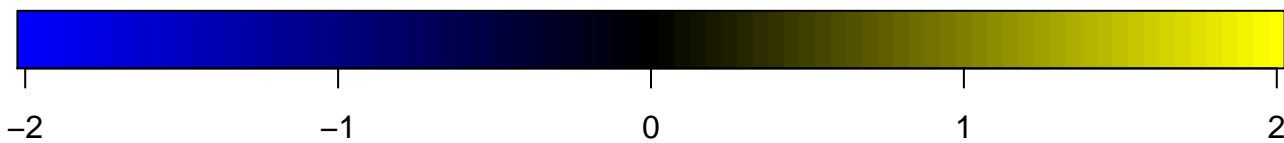
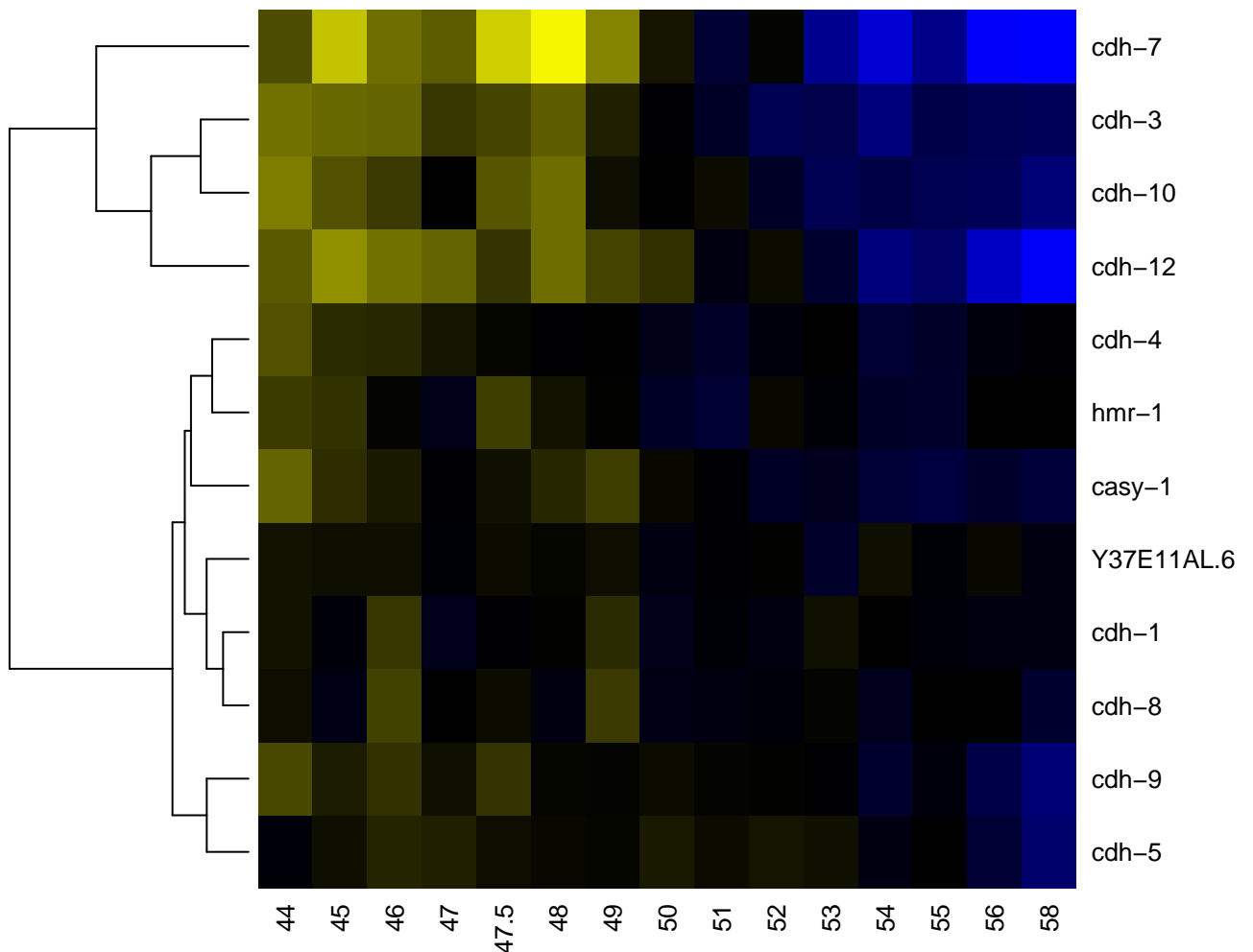
C2 domain



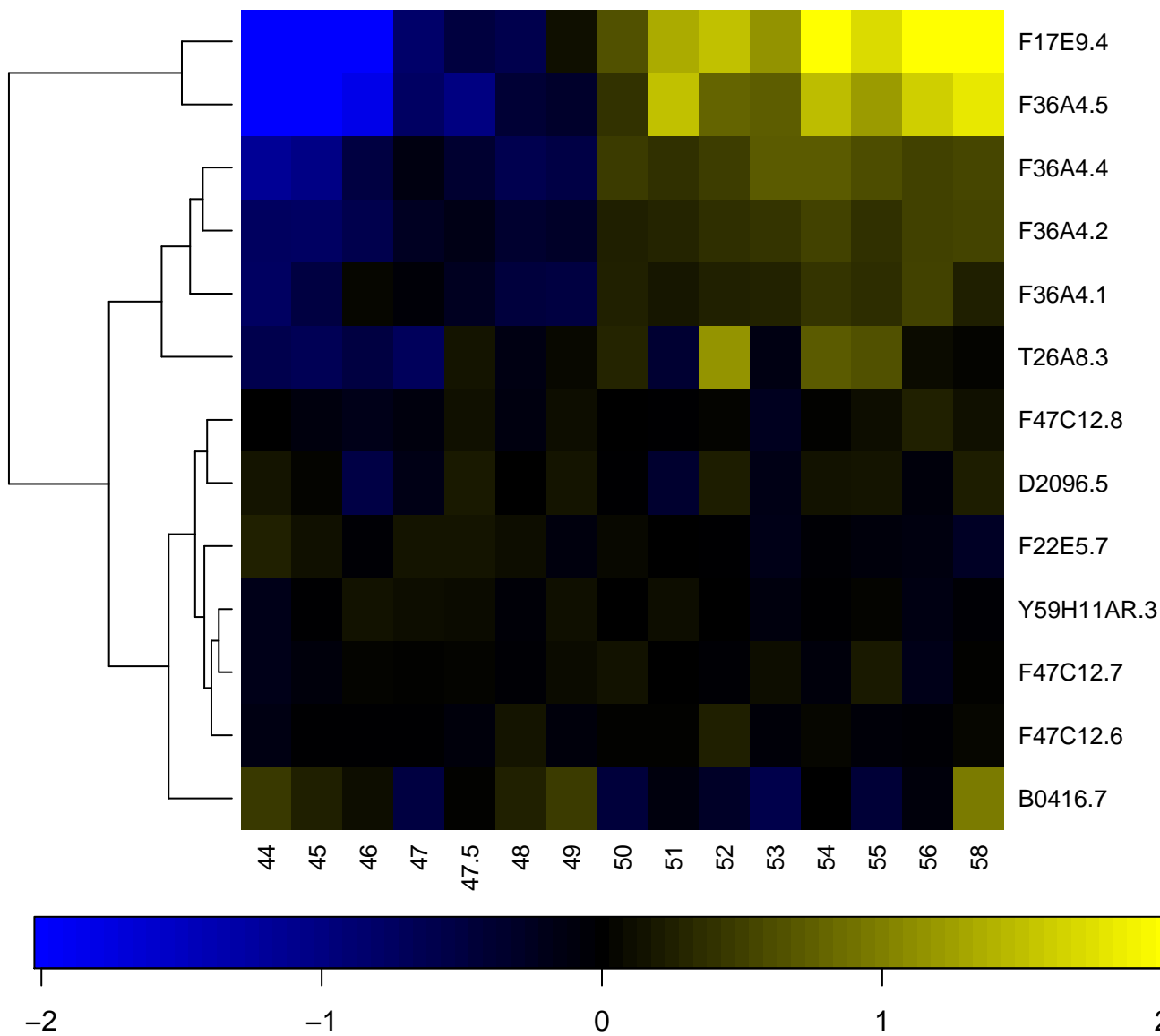
C2 region



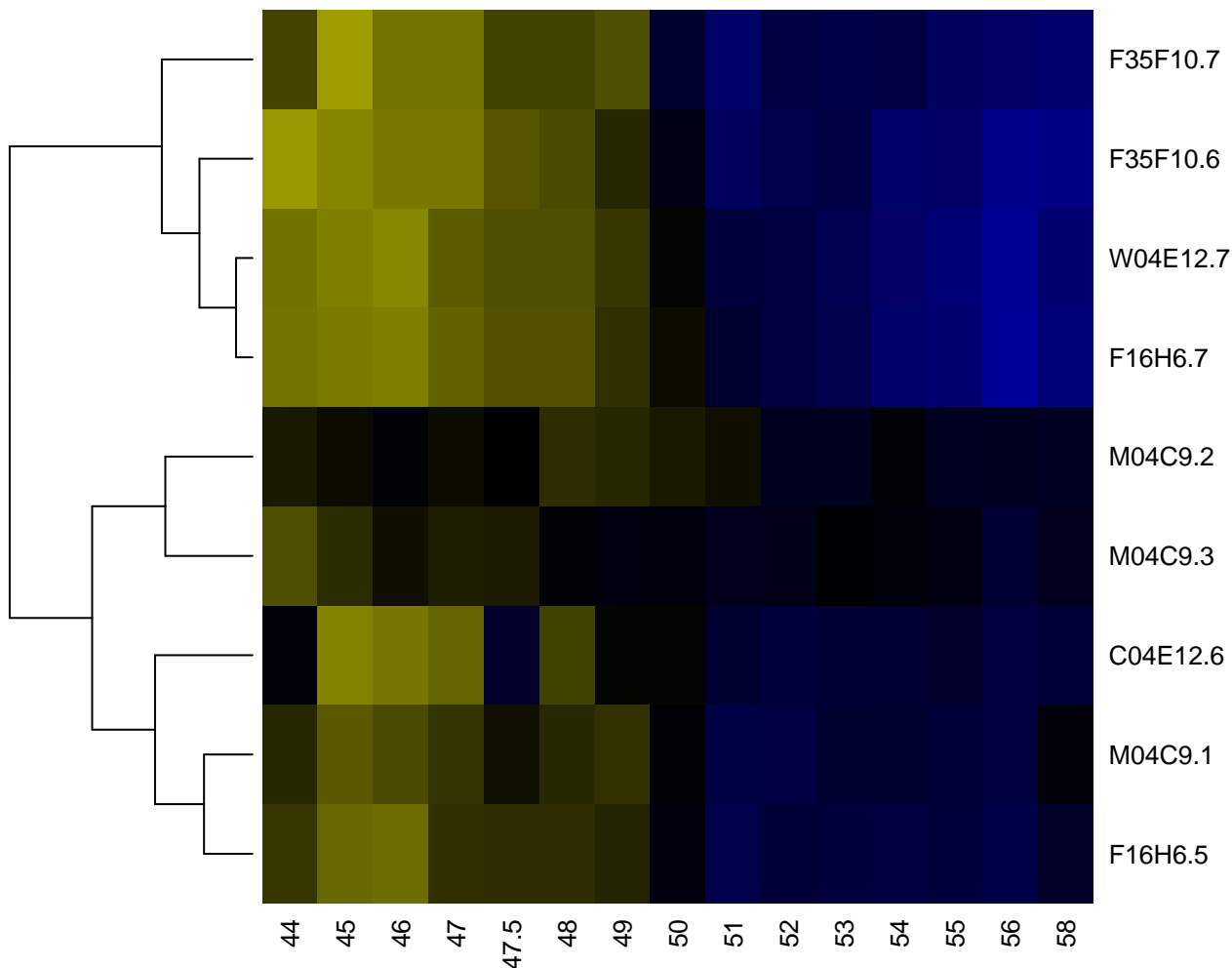
Cadherin



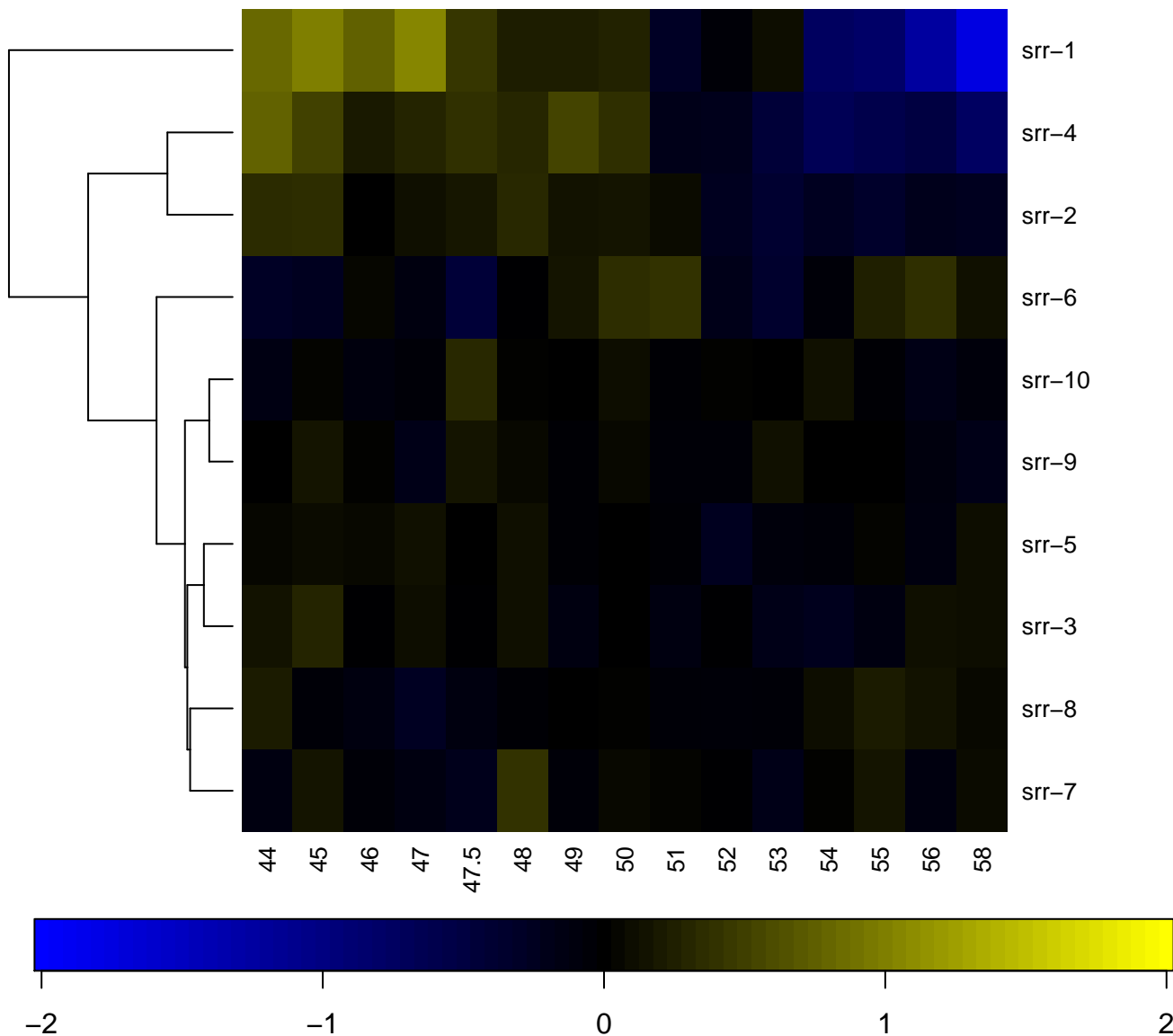
Caenorhabditis elegans protein of unknown function (DUF8



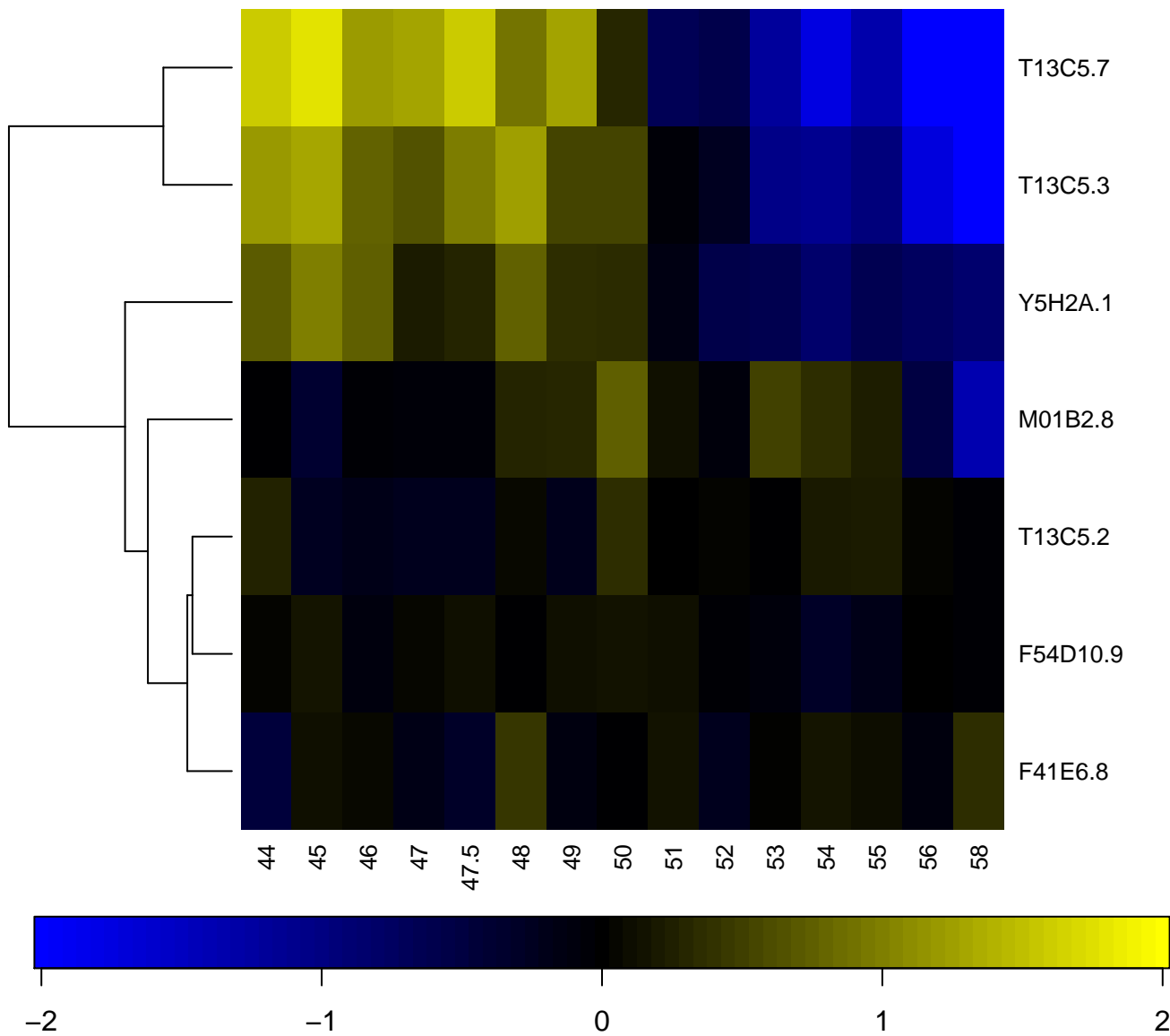
Caenorhabditis elegans protein of unknown function (DUF9



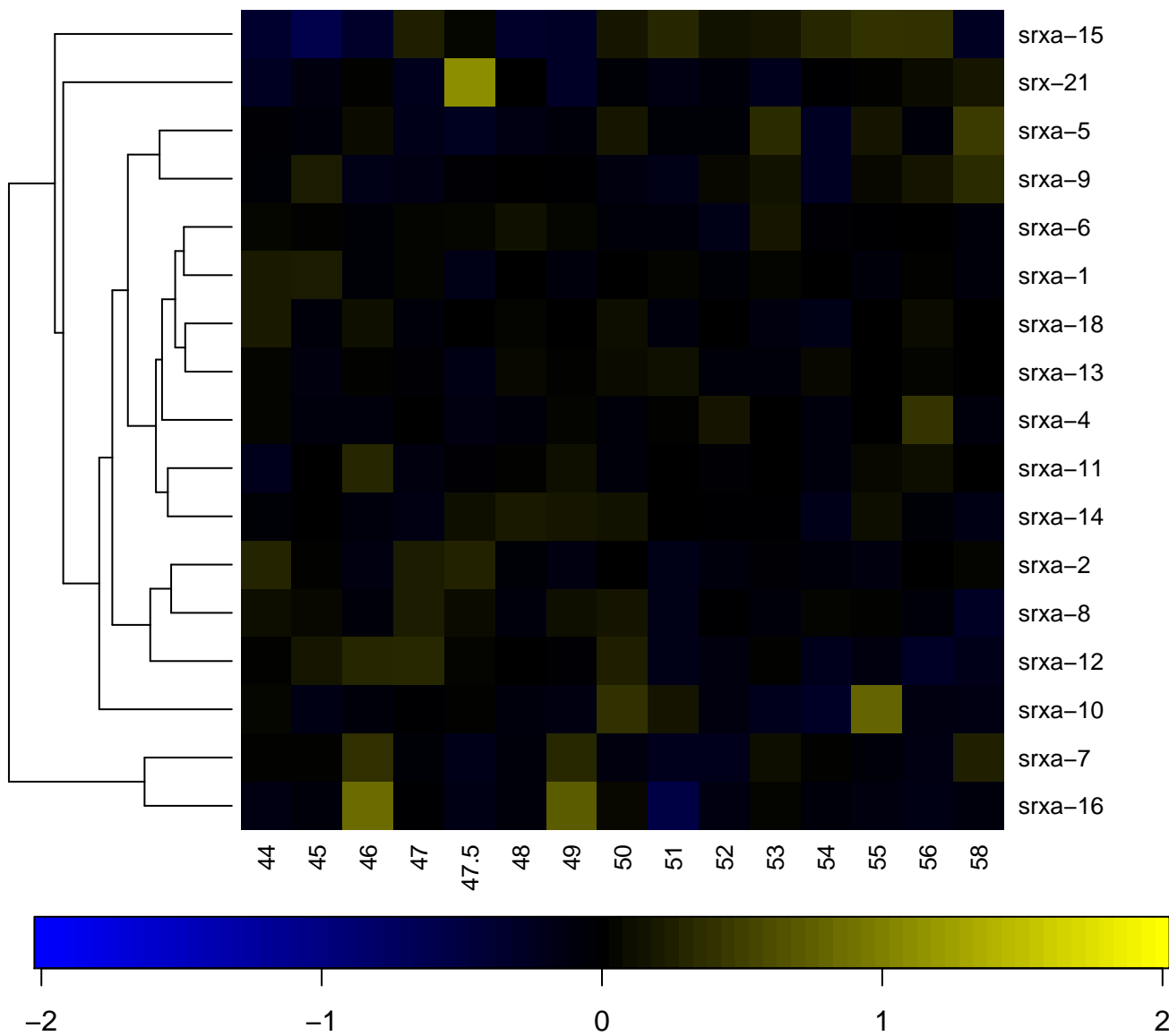
Caenorhabditis protein of unknown function, DUF267



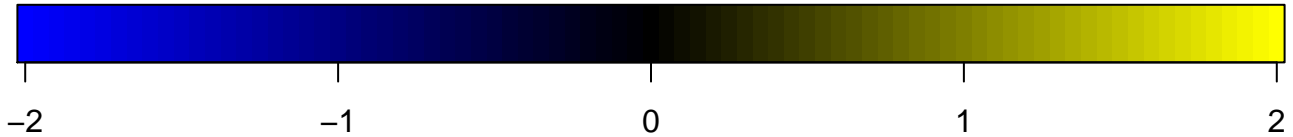
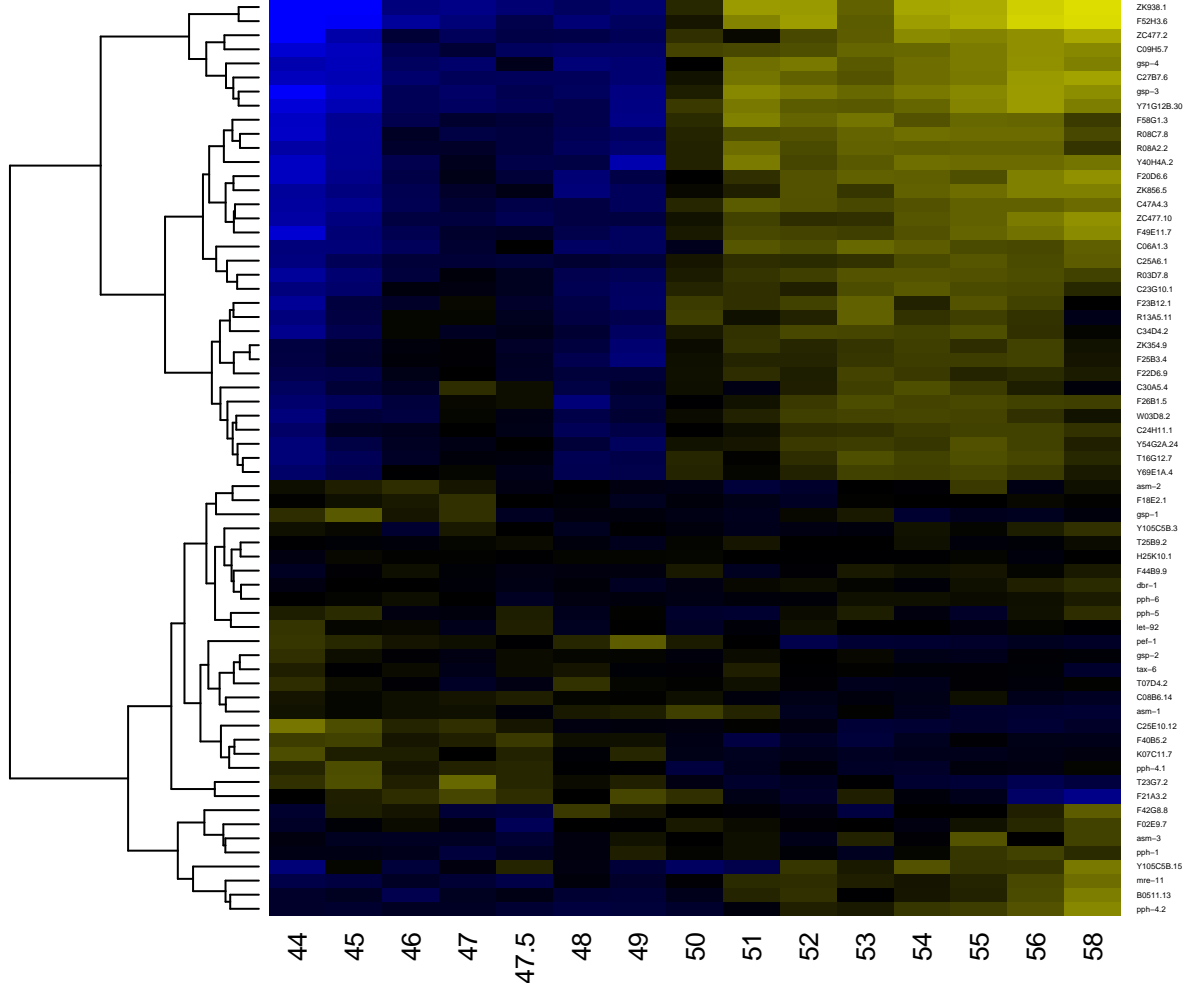
Caenorhabditis protein of unknown function, DUF282



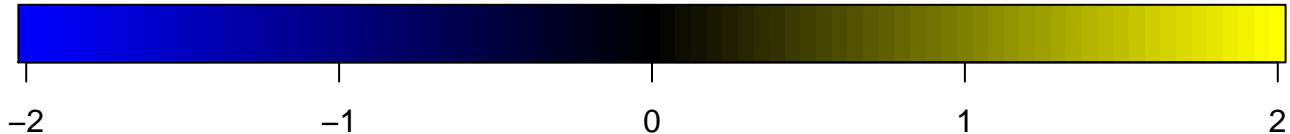
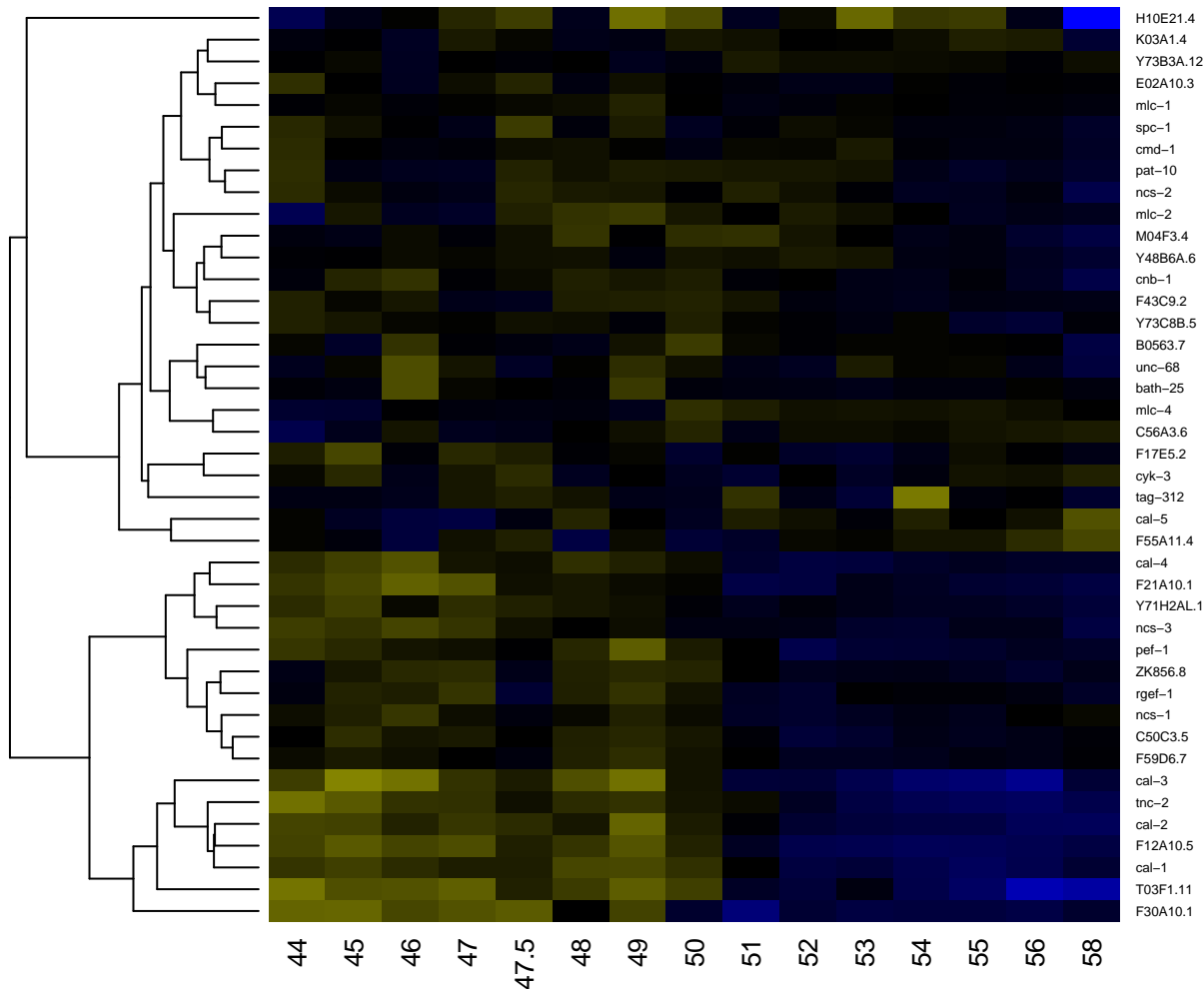
Caenorhabditis serpentine receptor-like protein, class xa



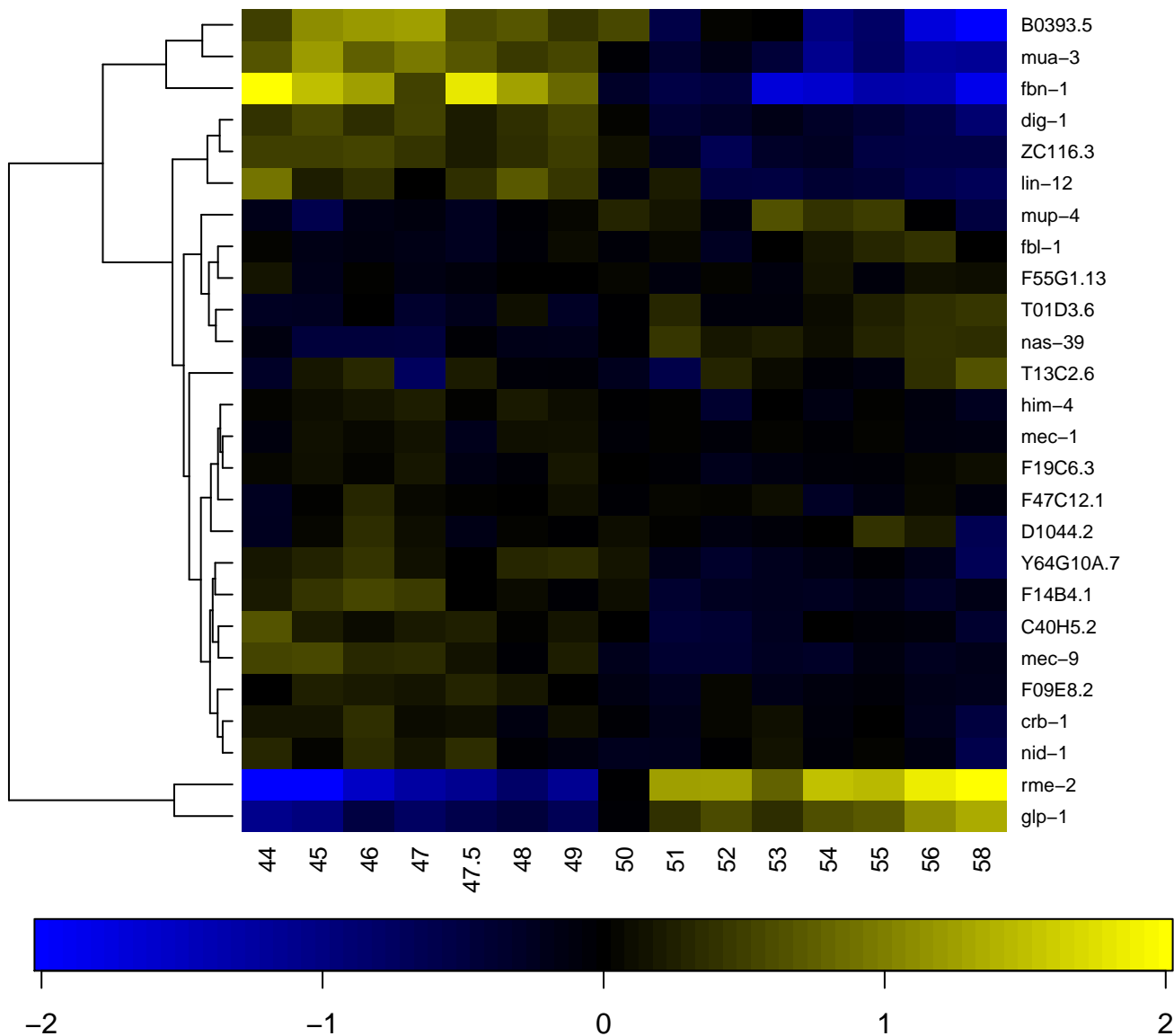
Calcineurin-like phosphoesterase



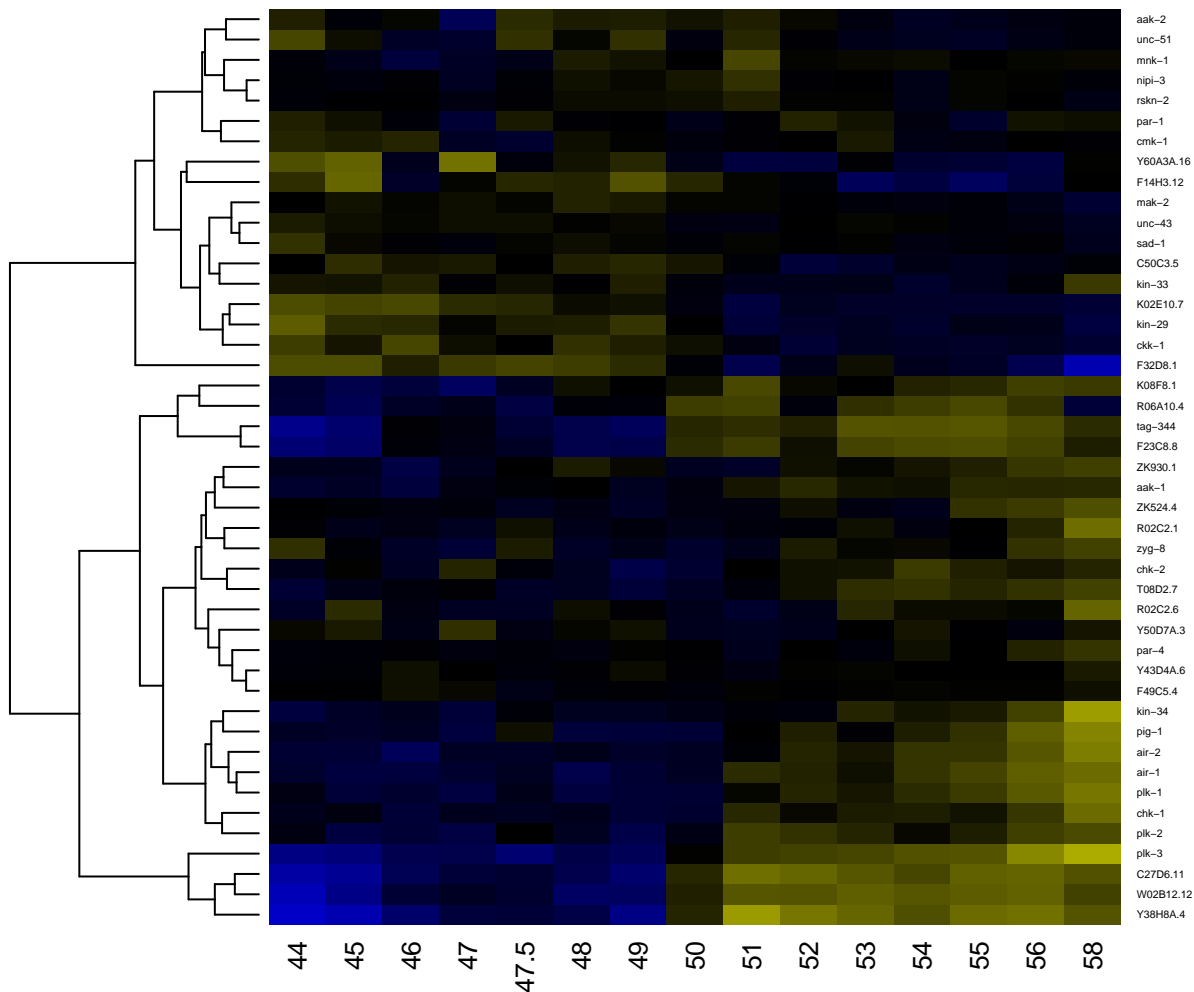
Calcium-binding EF-hand



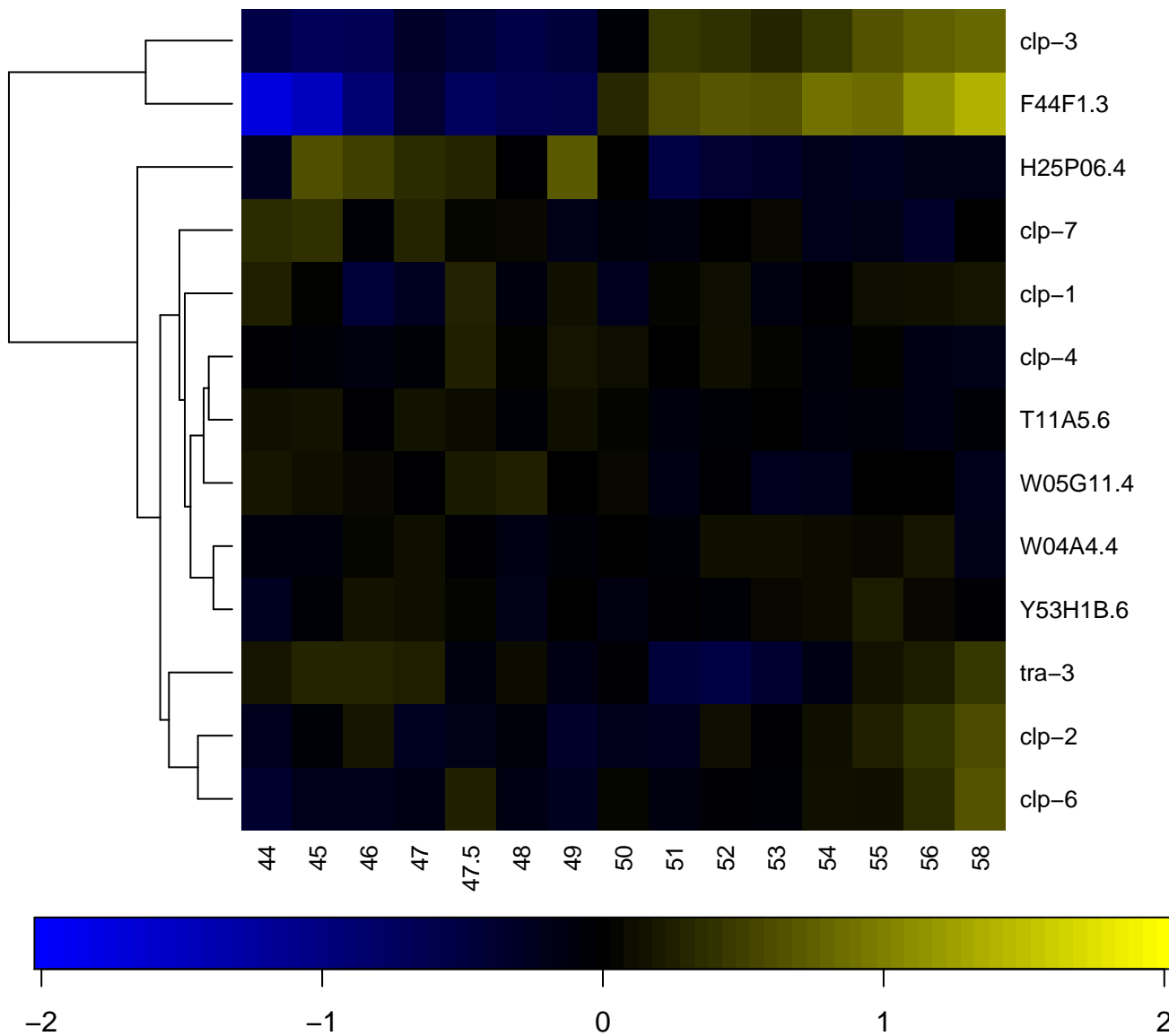
Calcium-binding EGF domain



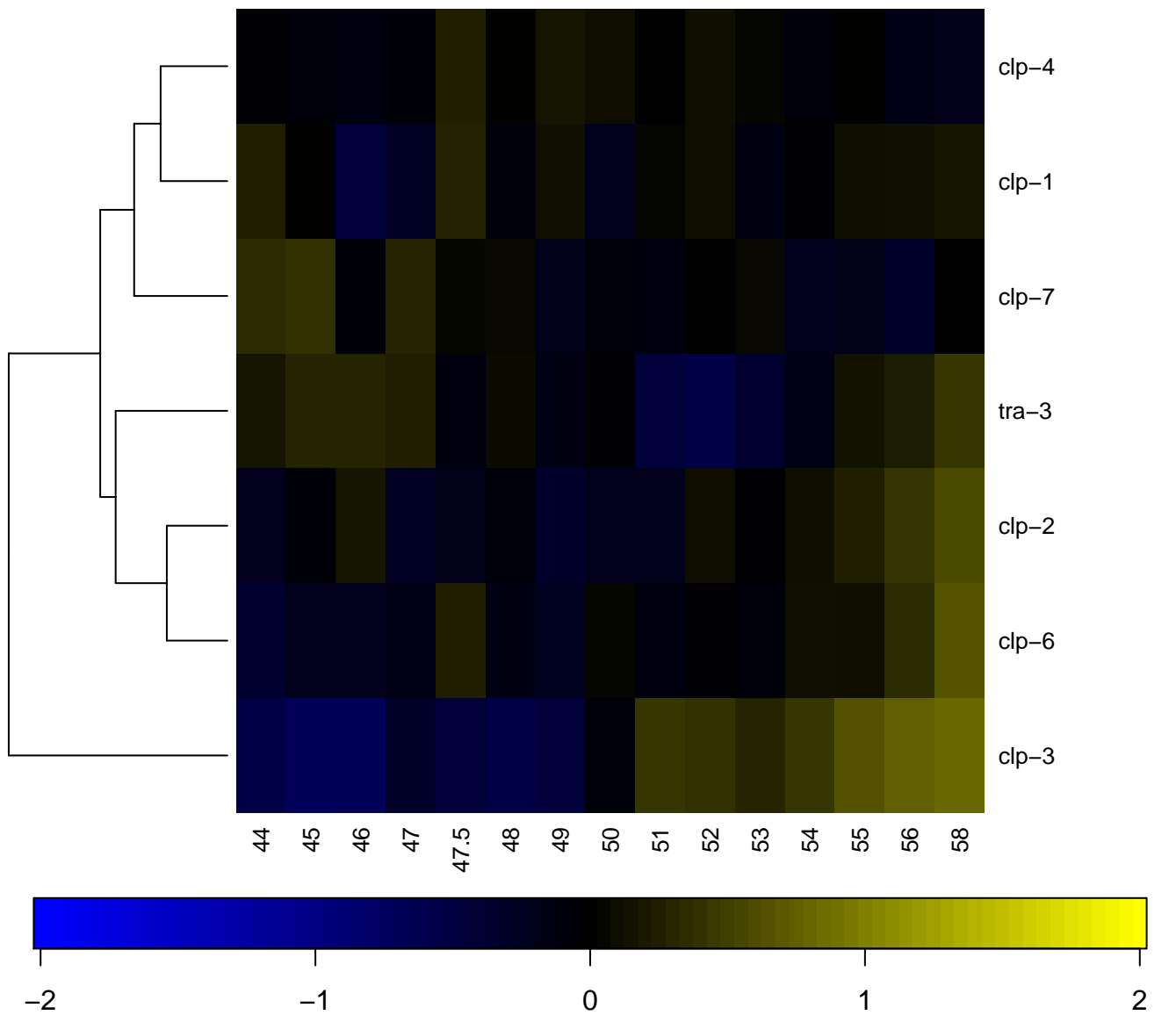
Calcium/calmodulin-dependent protein kinase-like



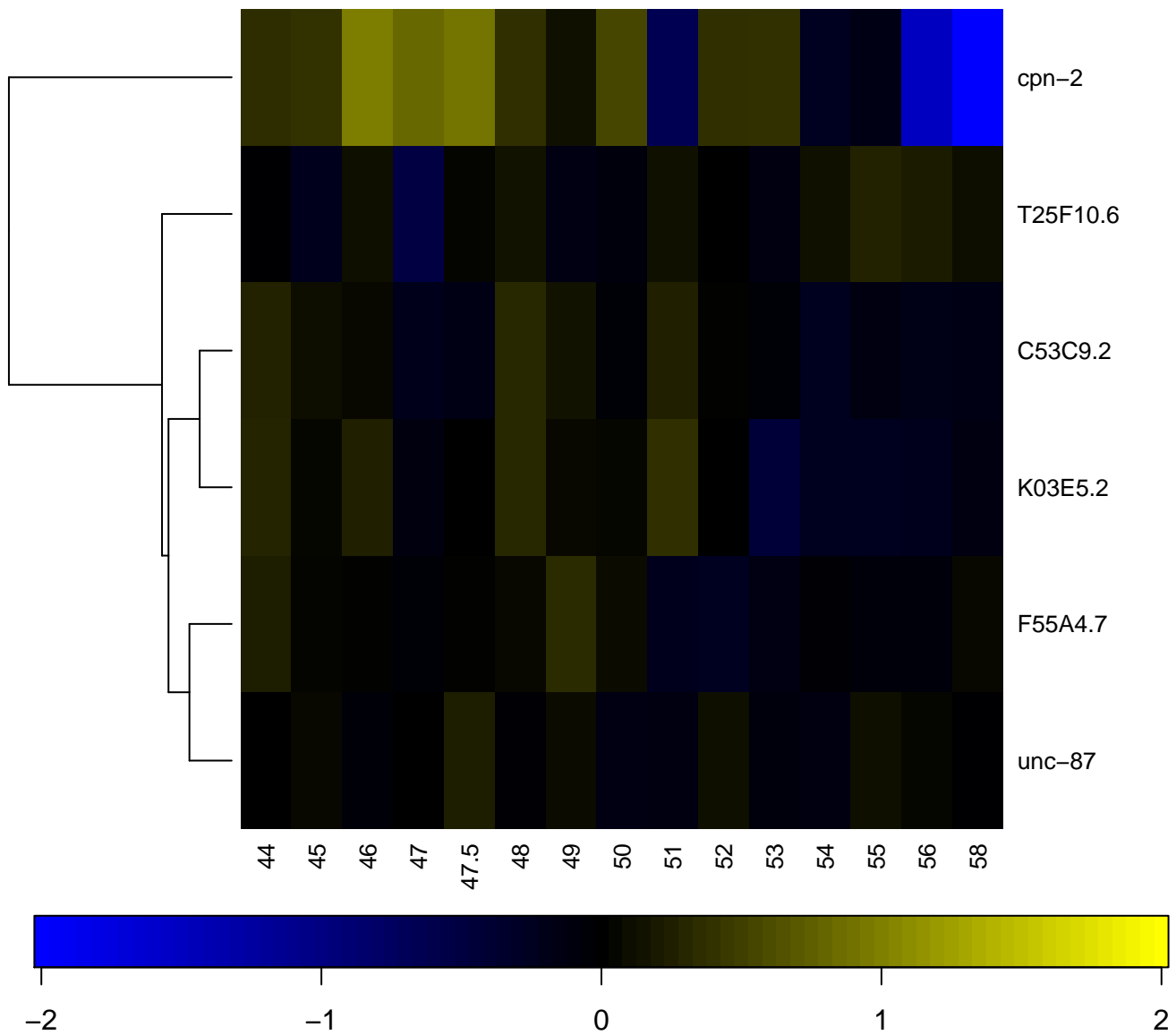
Calpain family cysteine protease



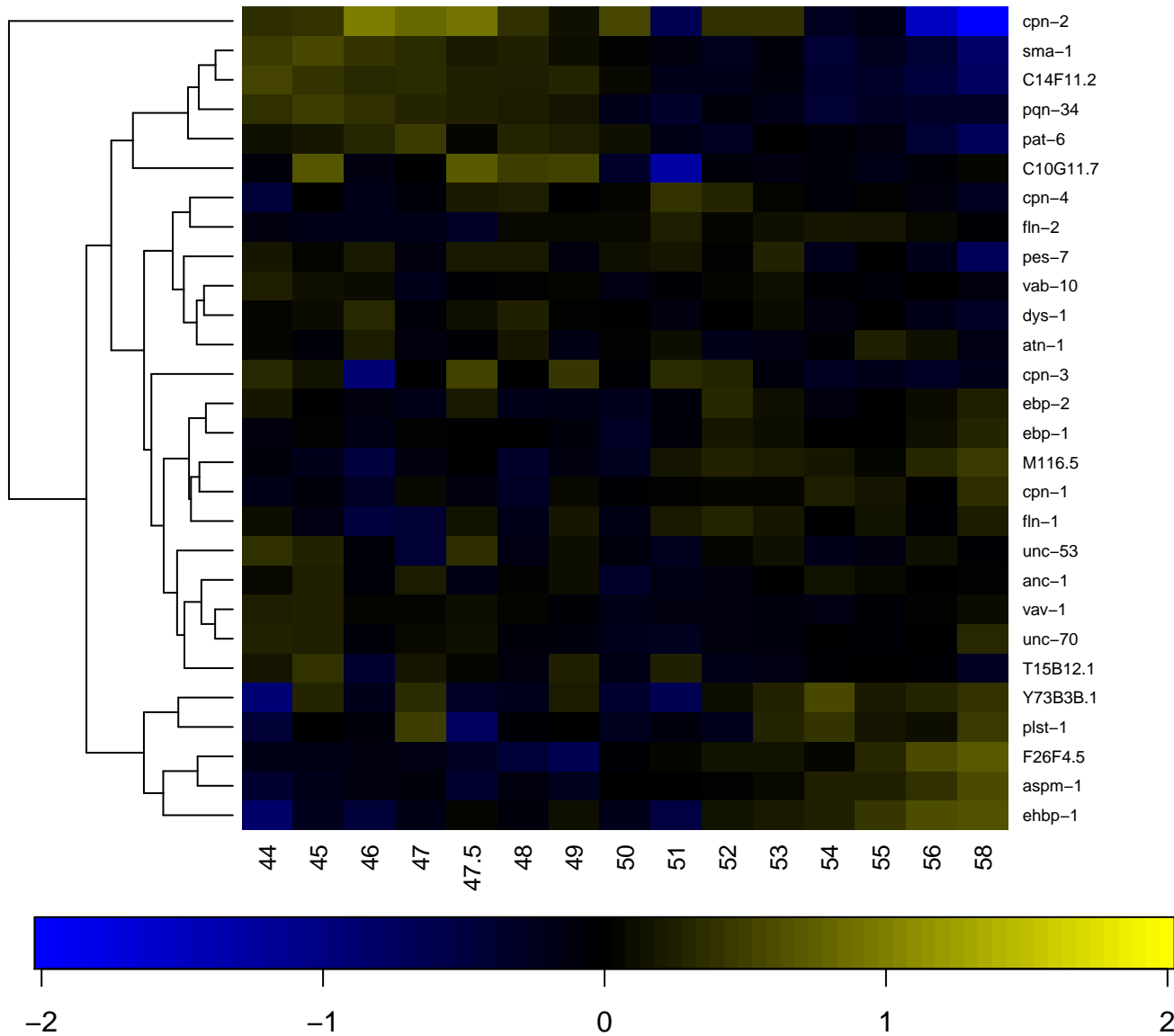
Calpain large subunit, domain III



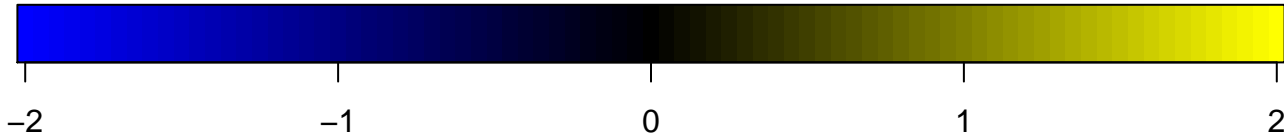
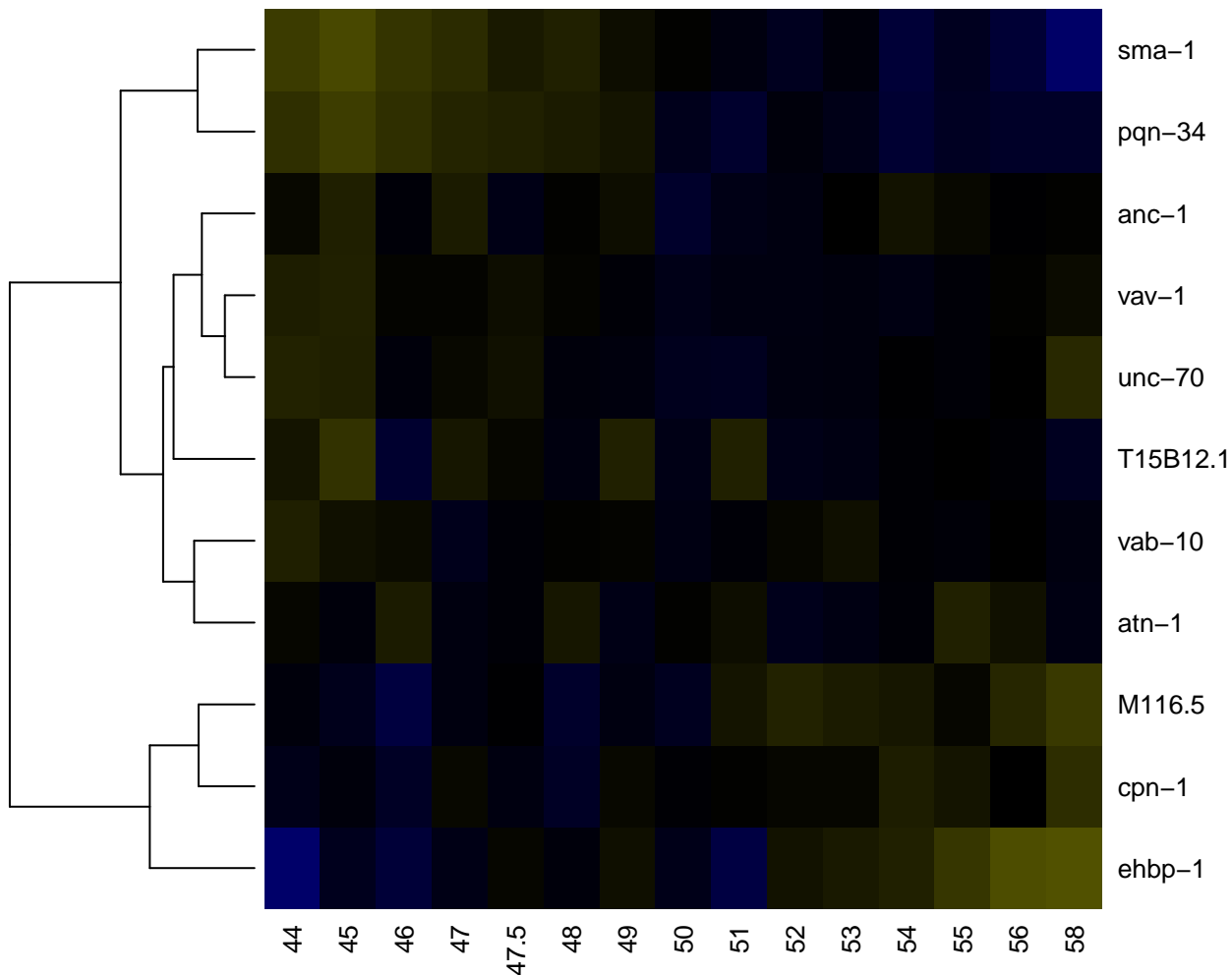
Calponin family repeat



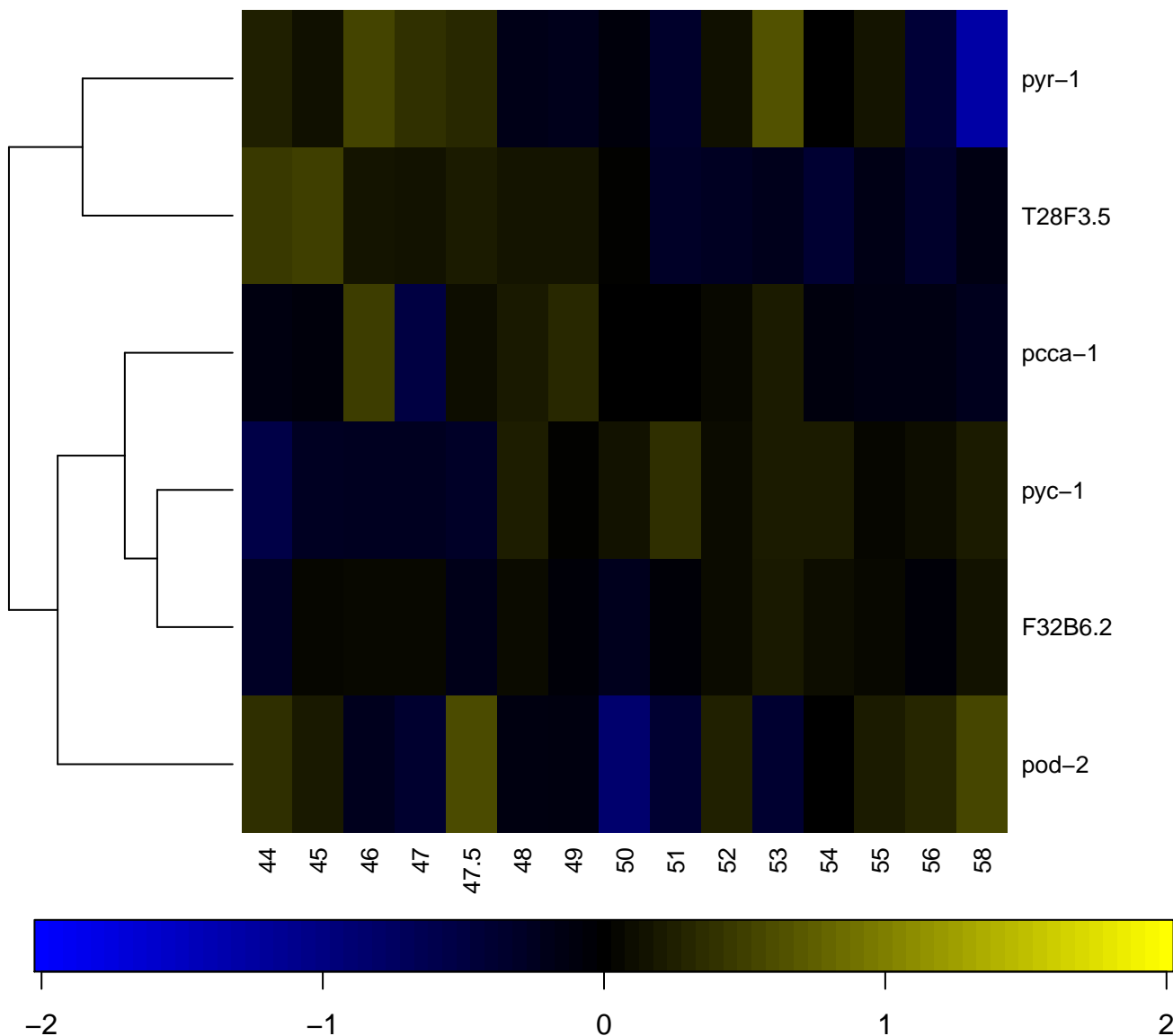
Calponin homology (CH) domain



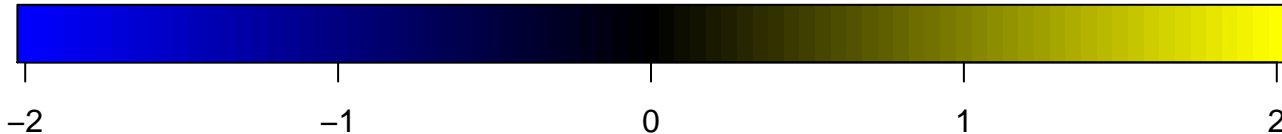
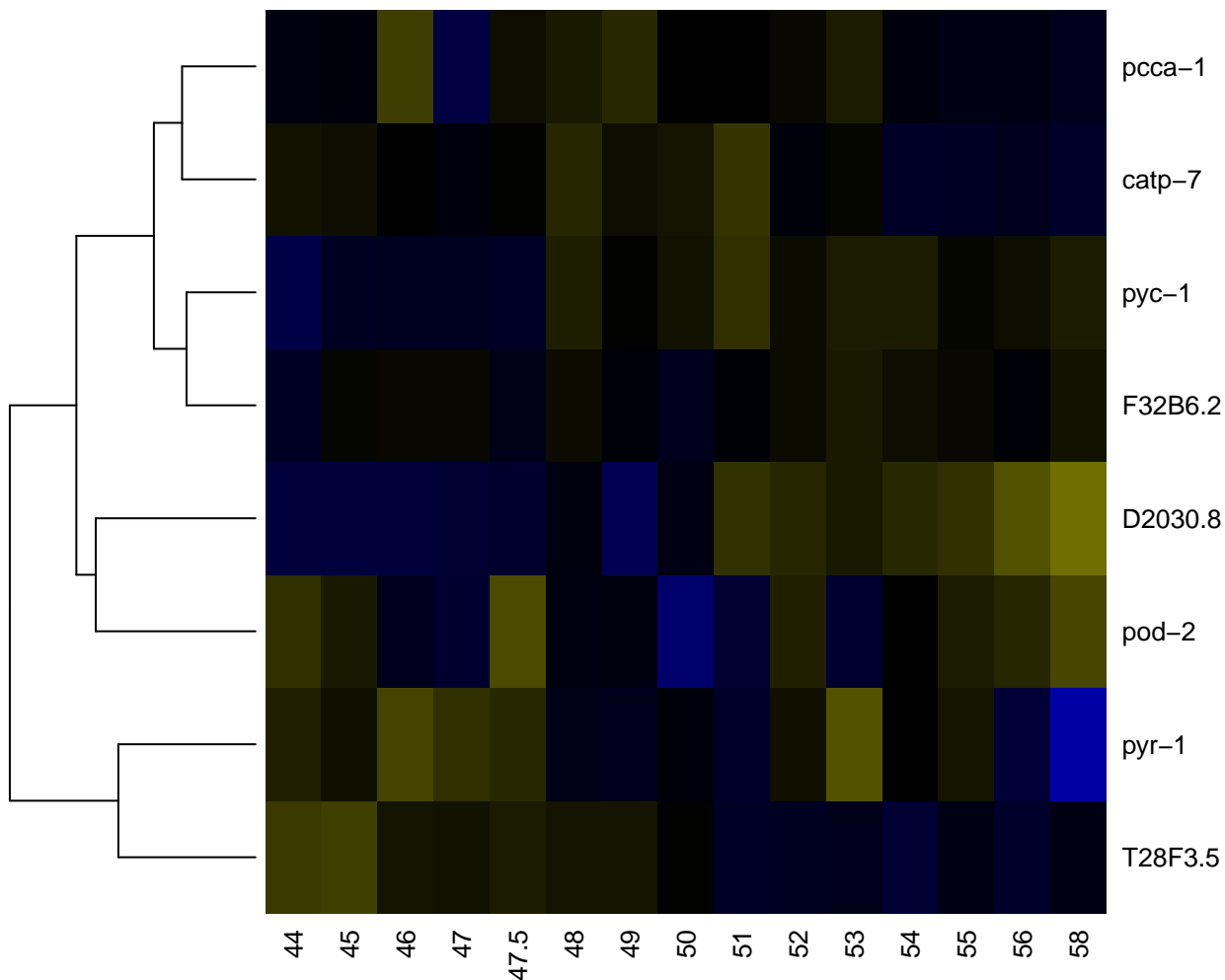
CAMSAP CH domain



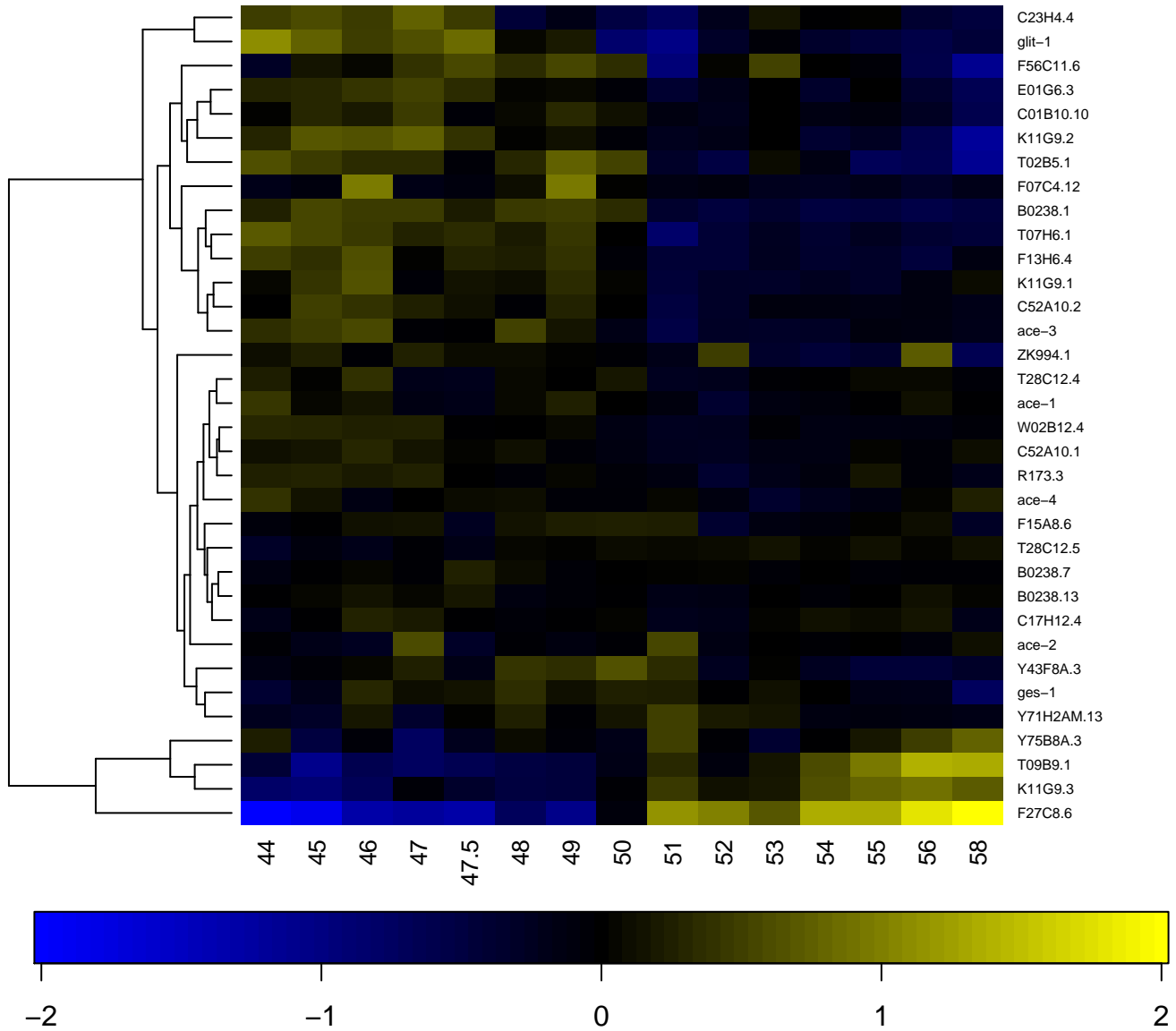
Carbamoyl phosphate synthase, large subunit, N-termina



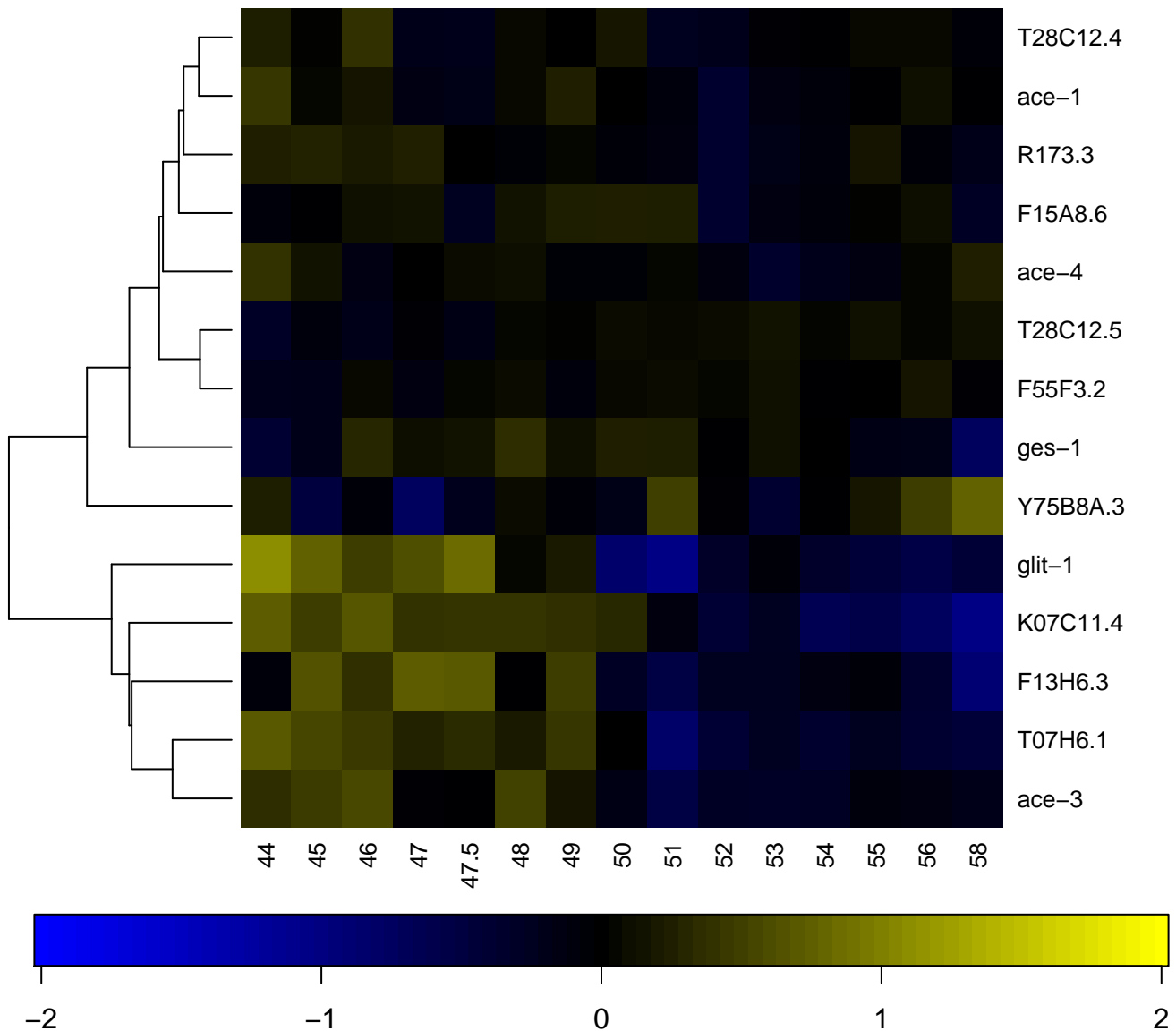
Carbamoyl phosphate synthetase, large subunit, ATP-binding



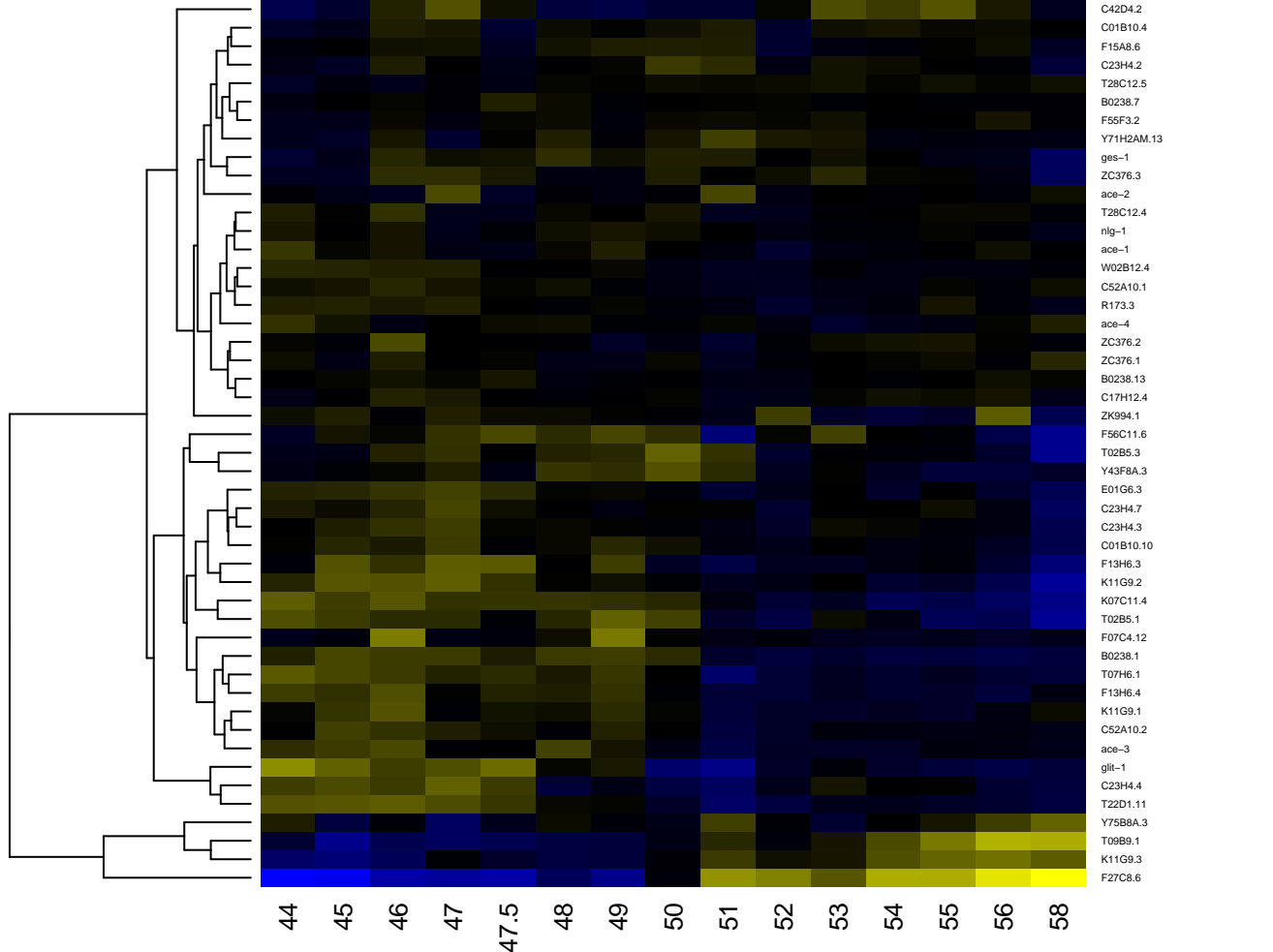
Carboxylesterase



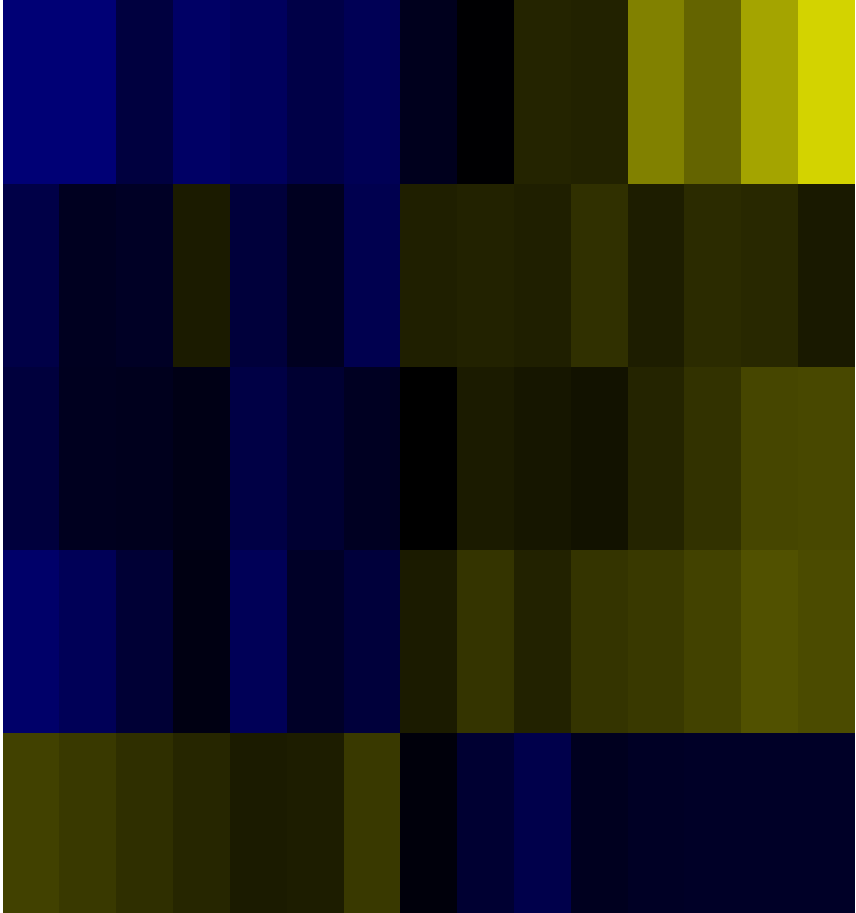
Carboxylesterase type B, conserved site



Carboxylesterase, type B



Caspase domain



ced-3

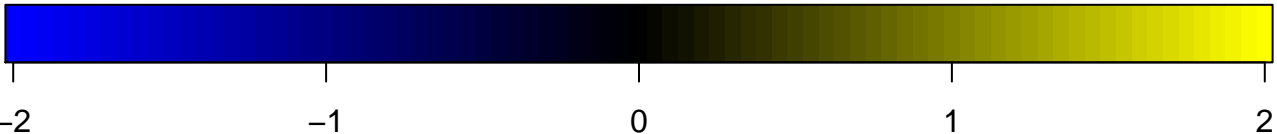
csp-3

csp-1

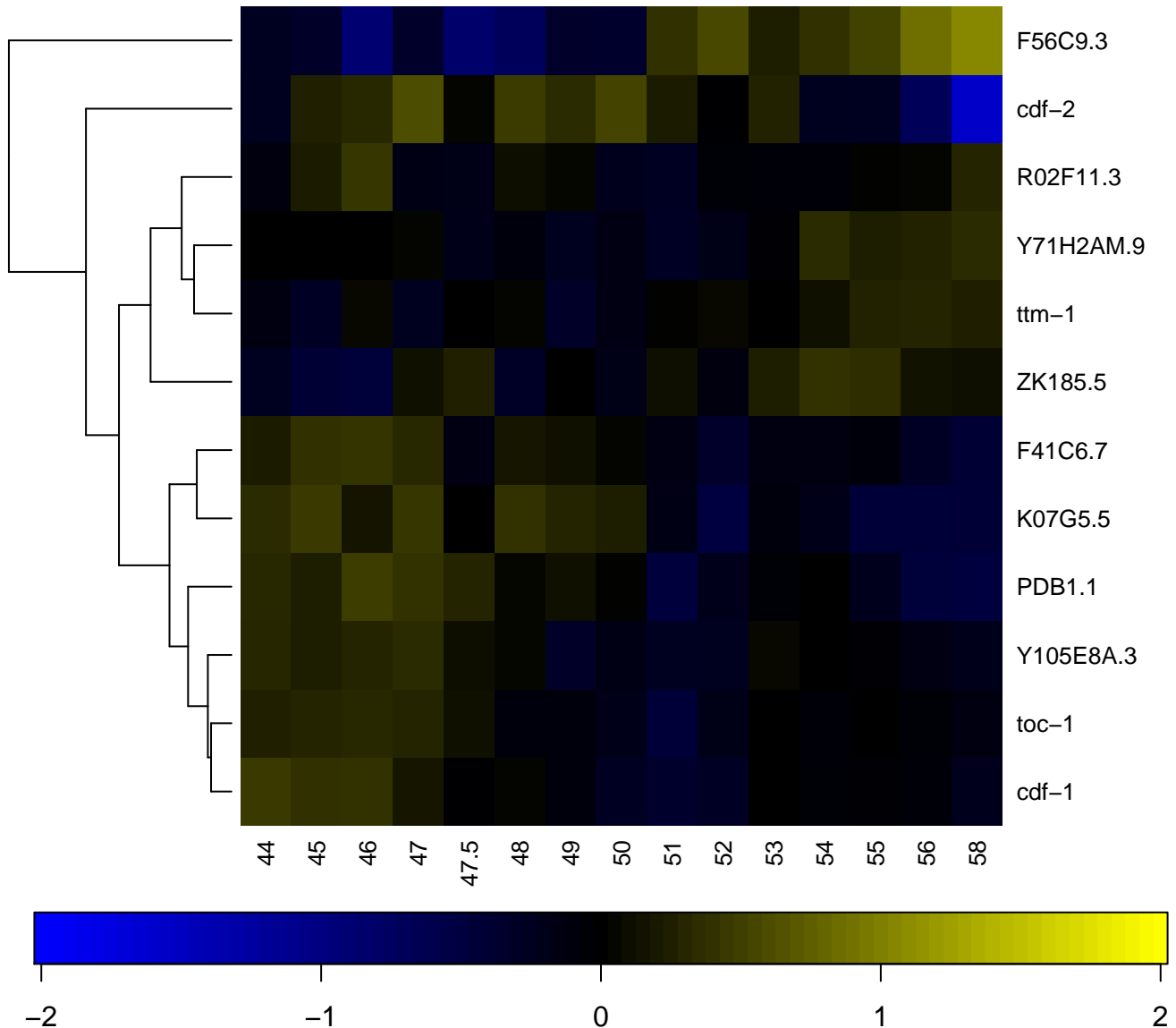
csp-2

F22D3.6

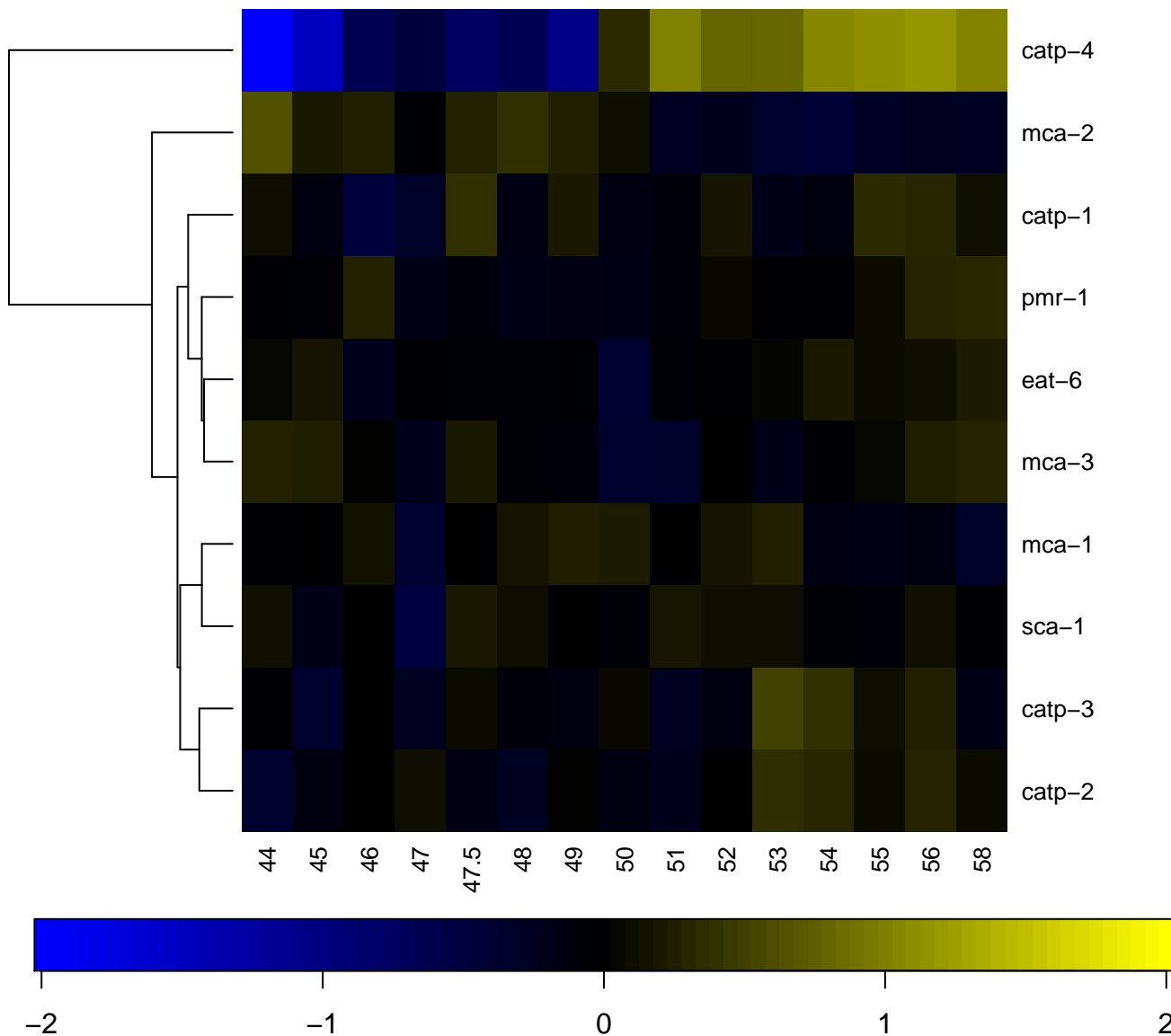
44 45 46 47 47.5 48 49 50 51 52 53 54 55 56 58



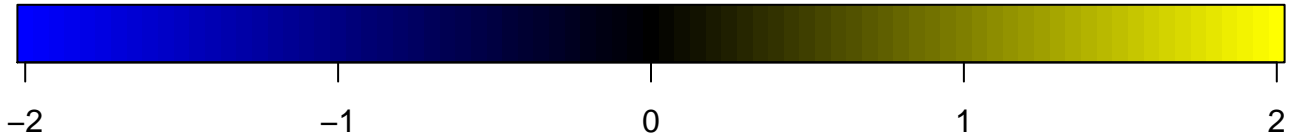
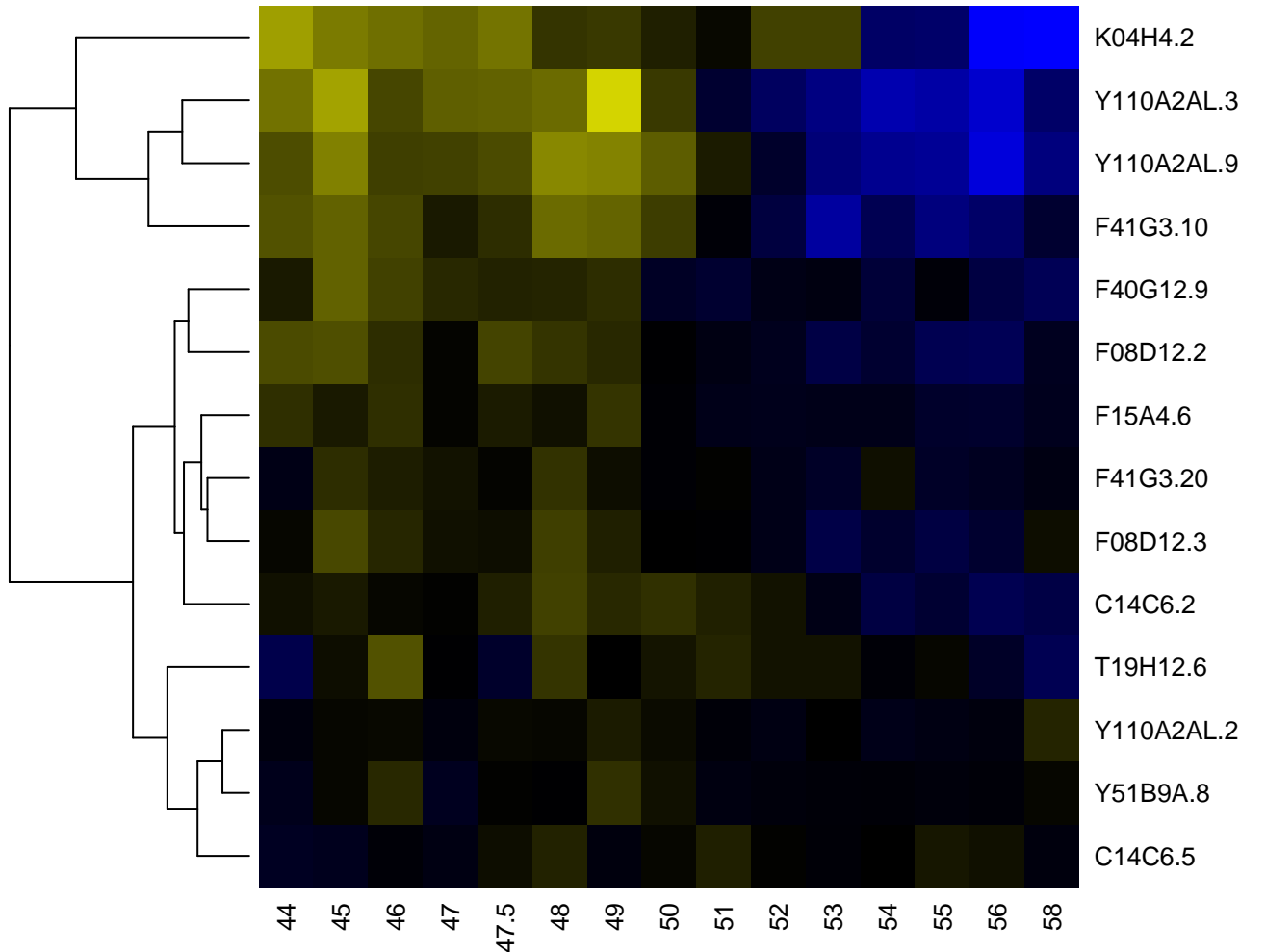
Cation efflux protein



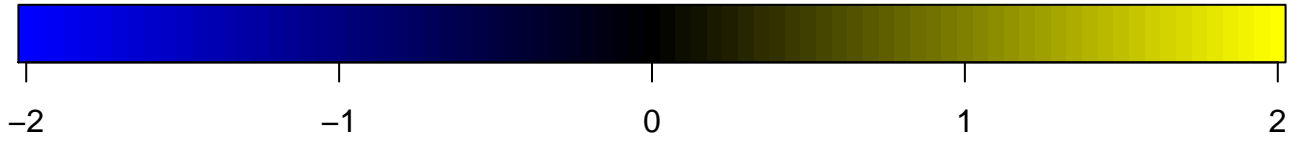
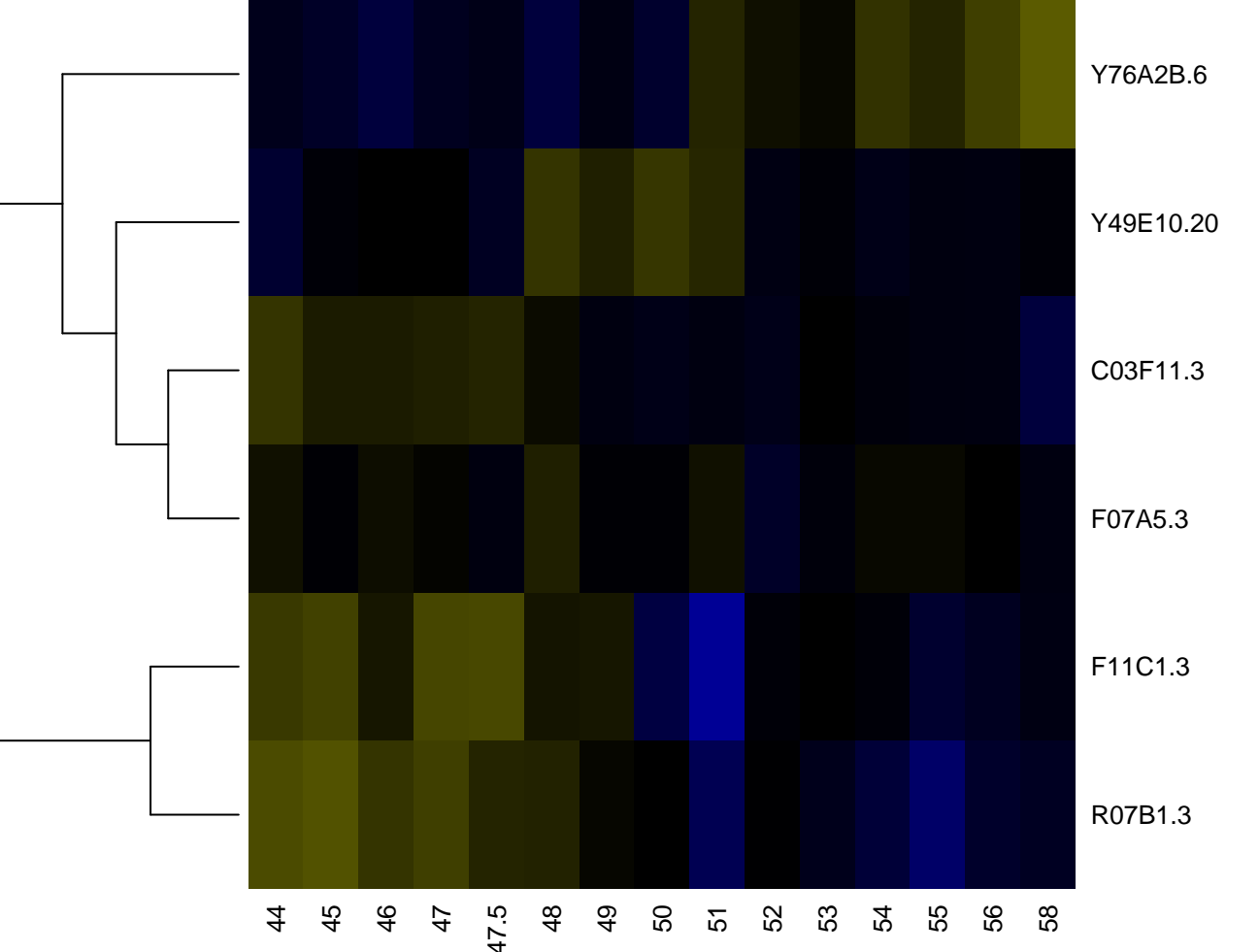
Cation transporting ATPase, C-terminus



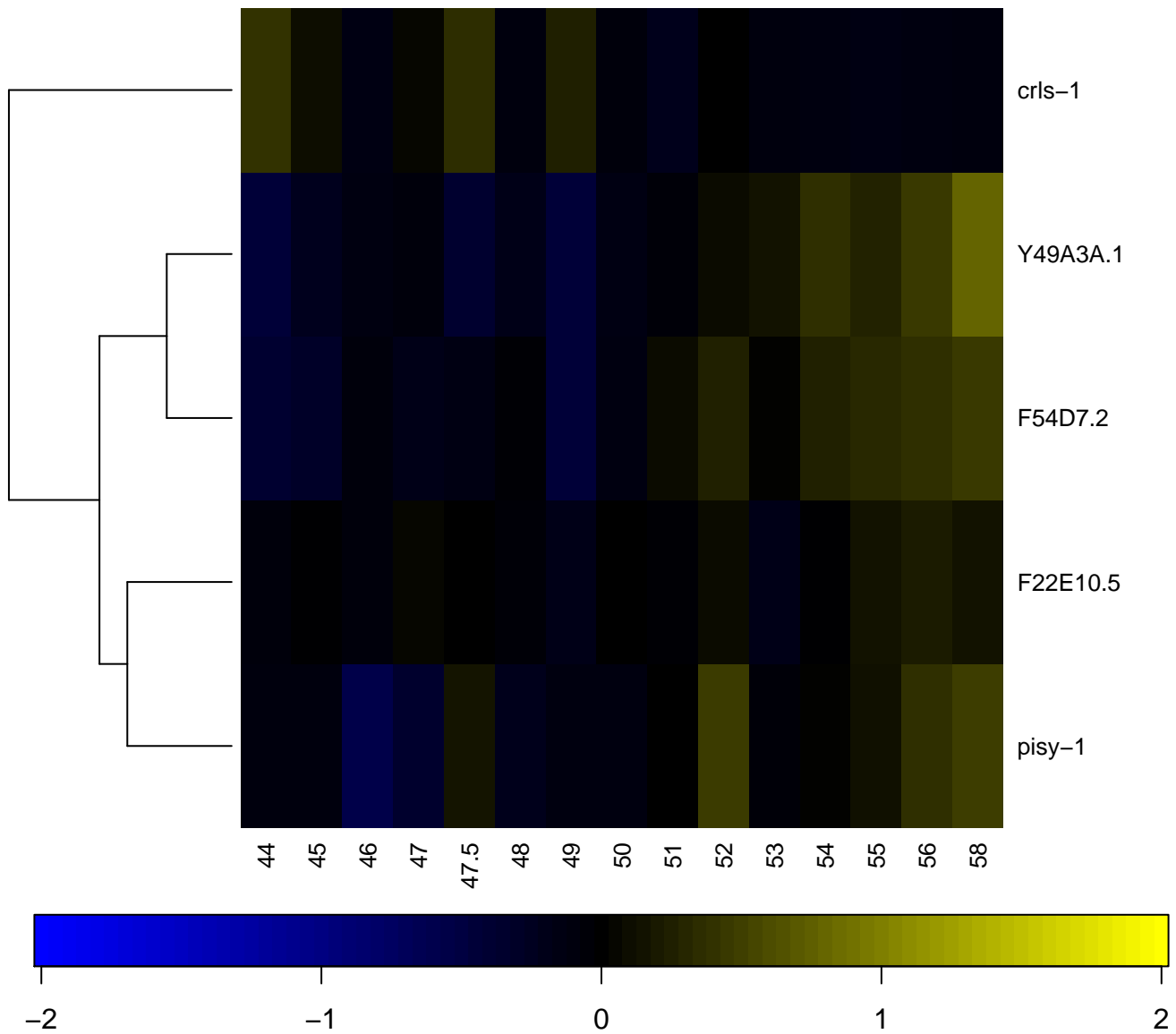
CC domain



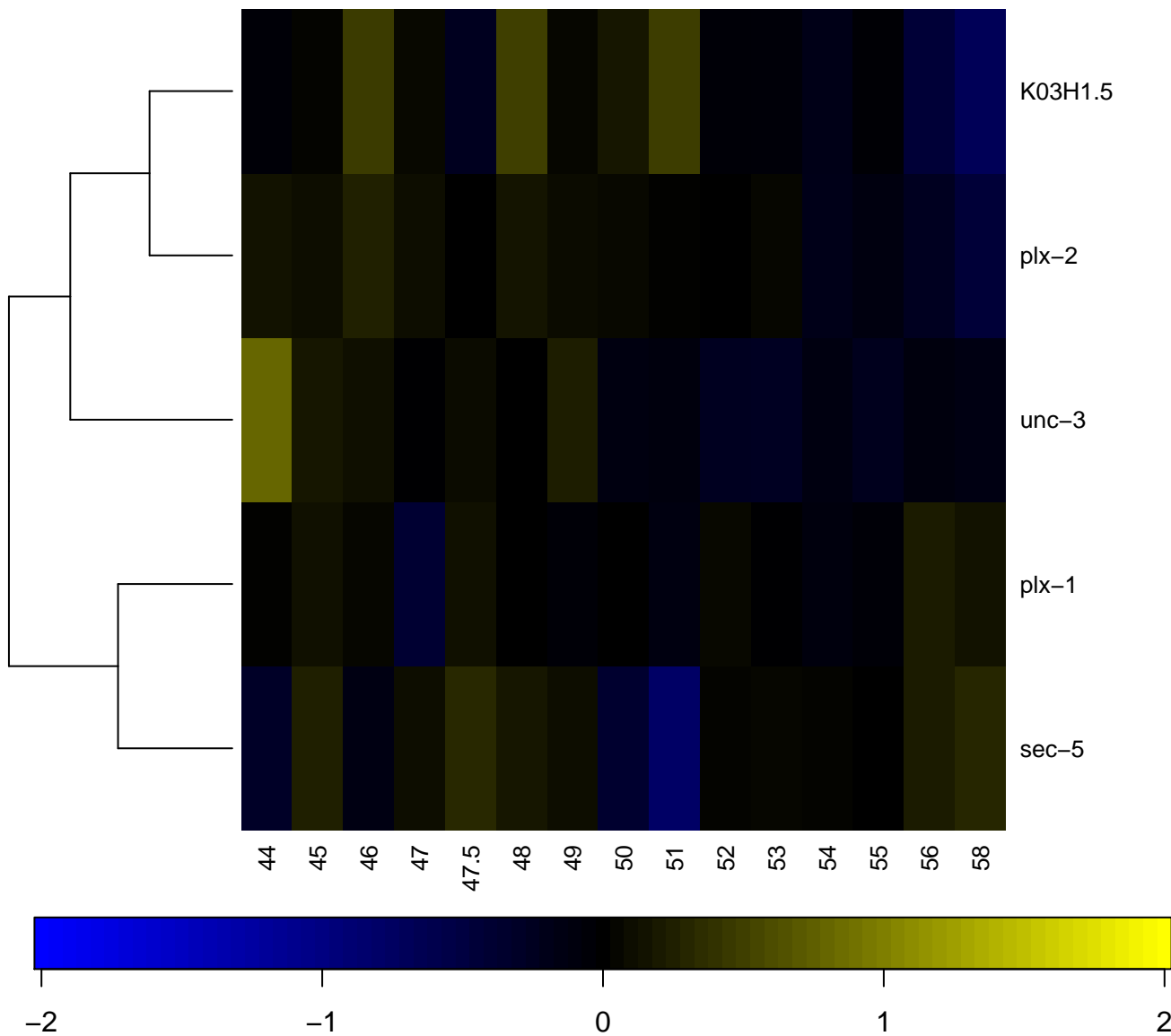
CD36 family



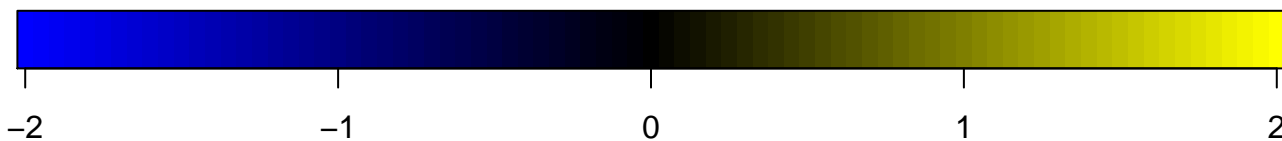
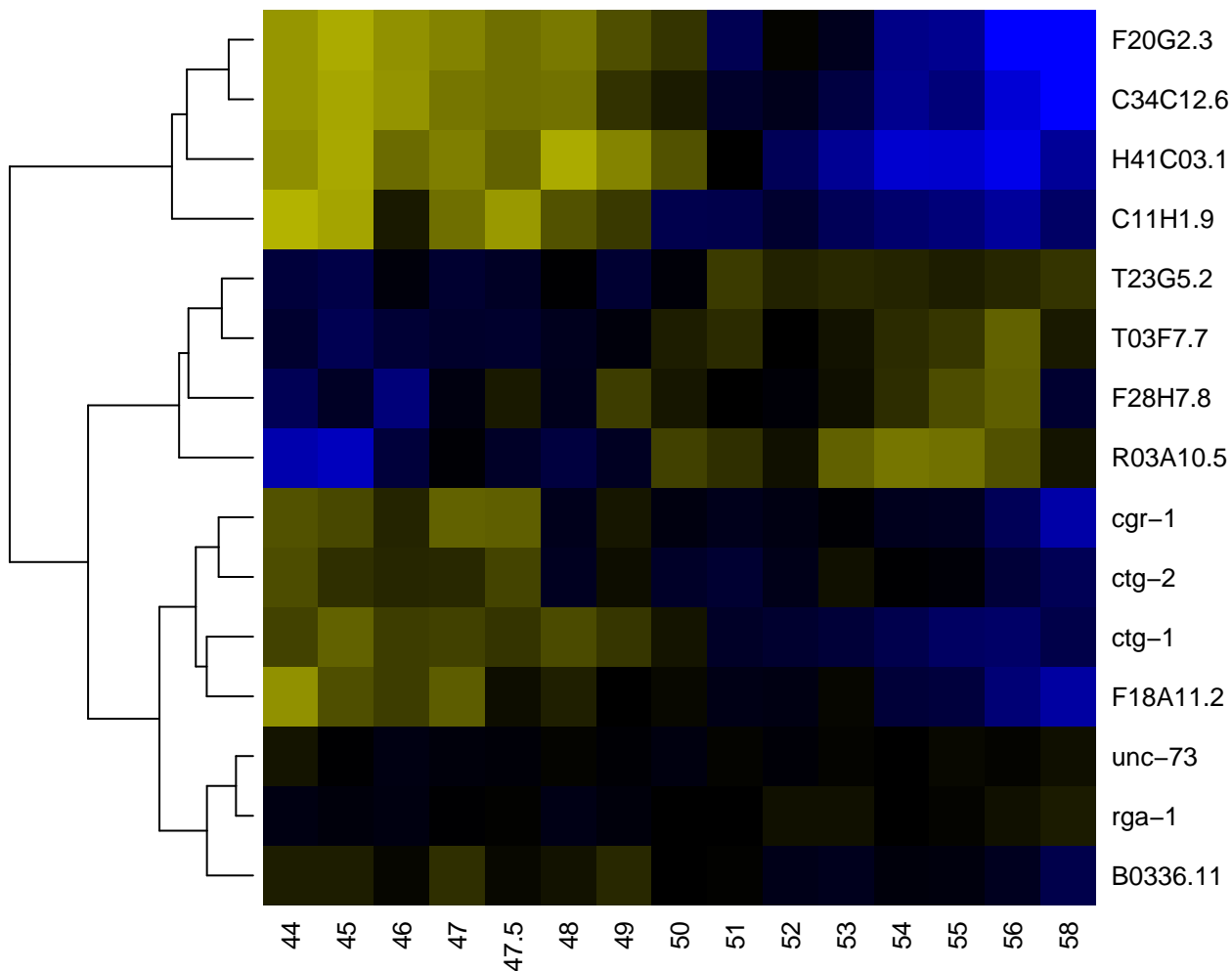
CDP-alcohol phosphatidyltransferase



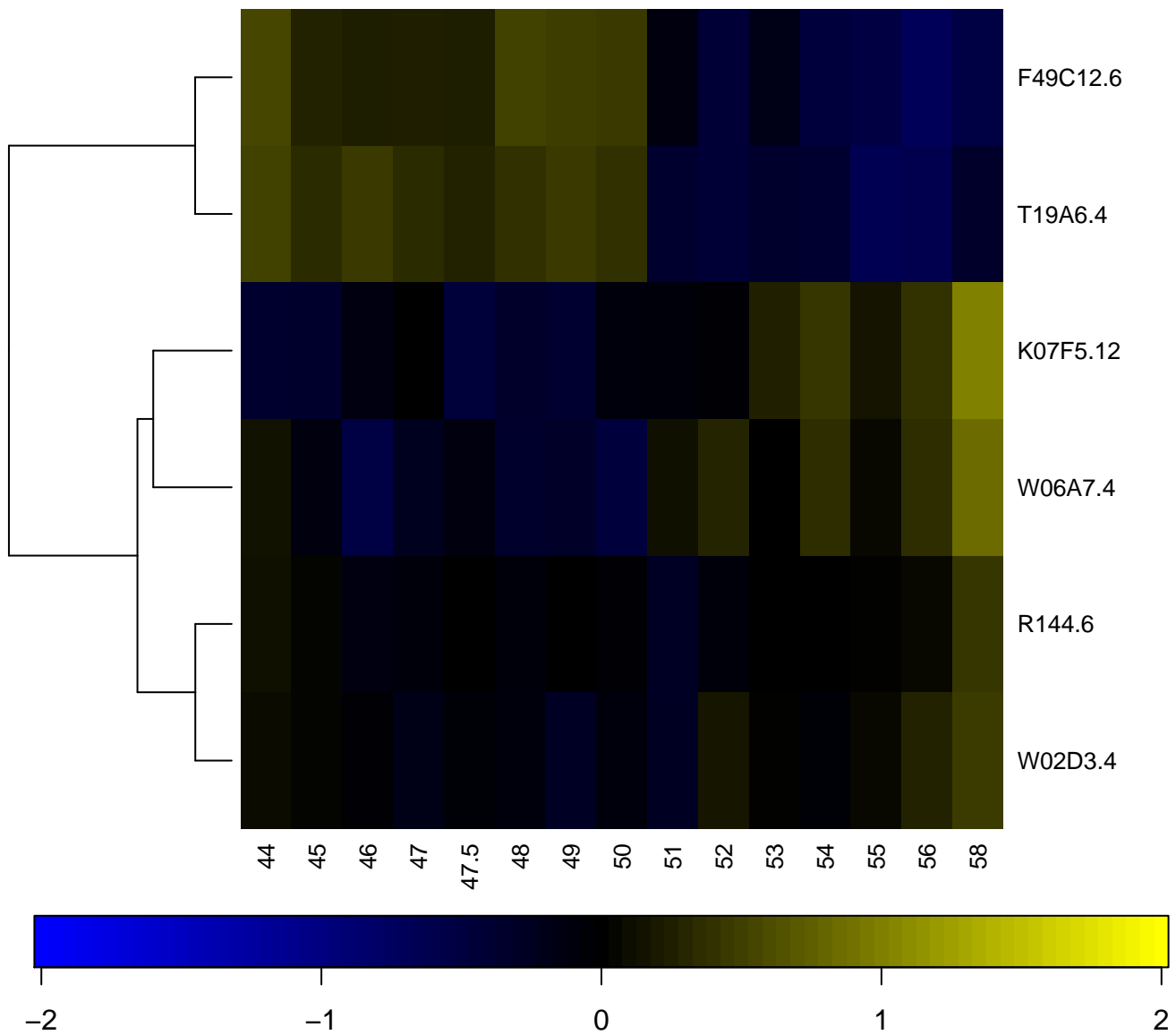
Cell surface receptor IPT/TIG



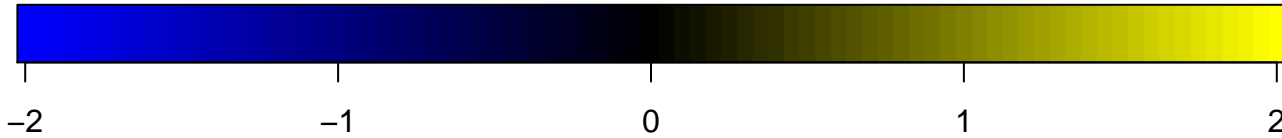
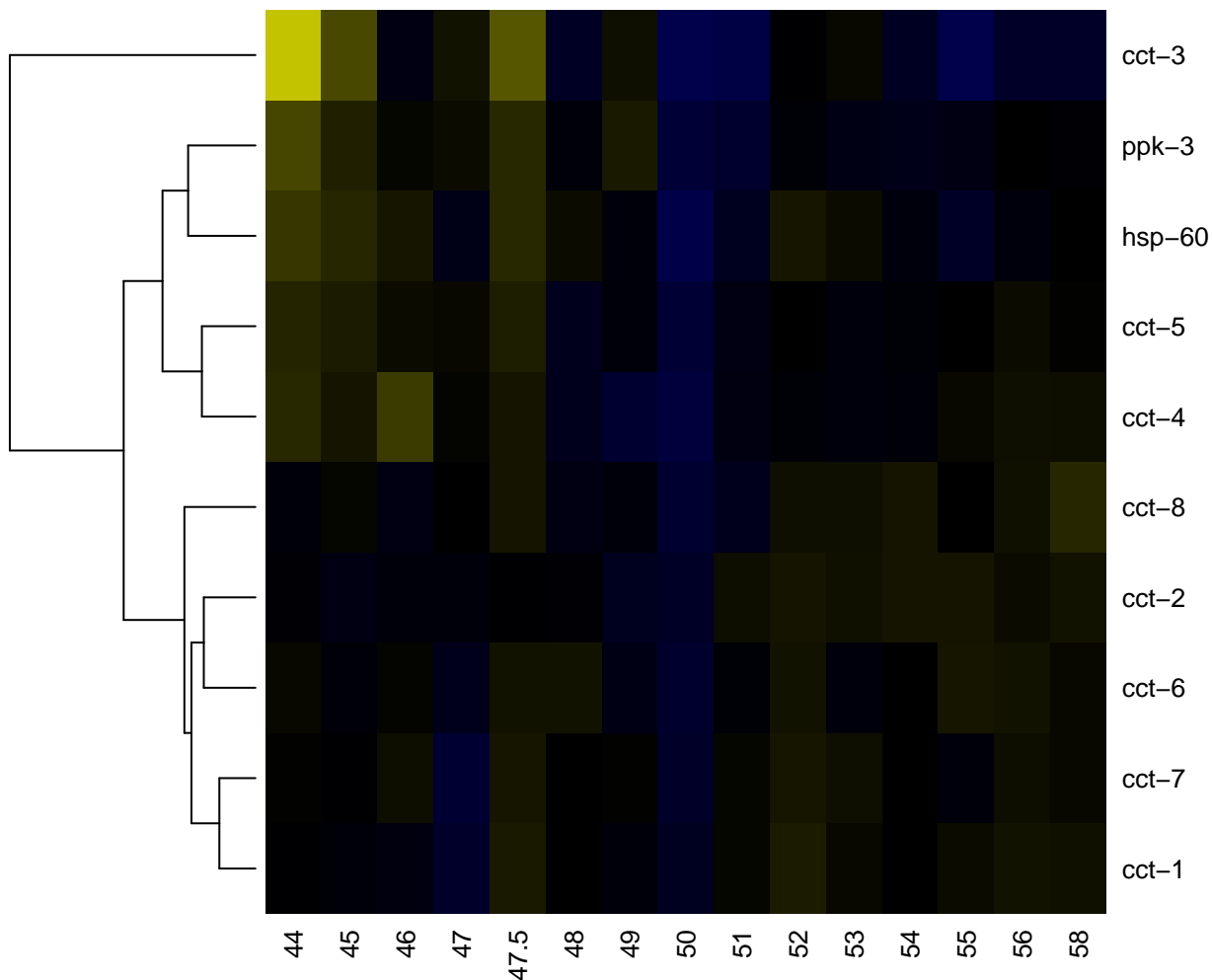
Cellular retinaldehyde-binding/triple function, C-terminal



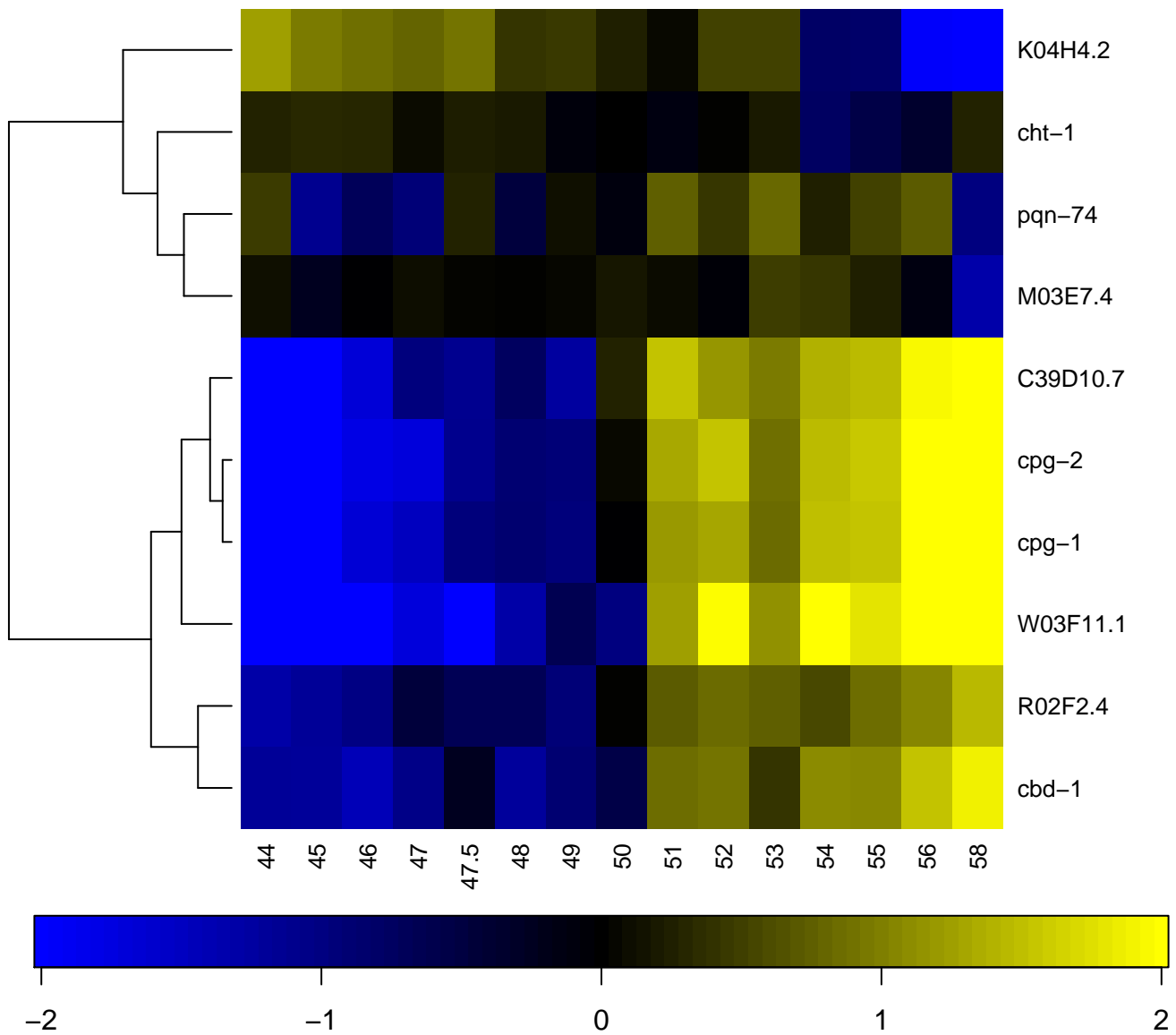
CEO family (DUF1632)



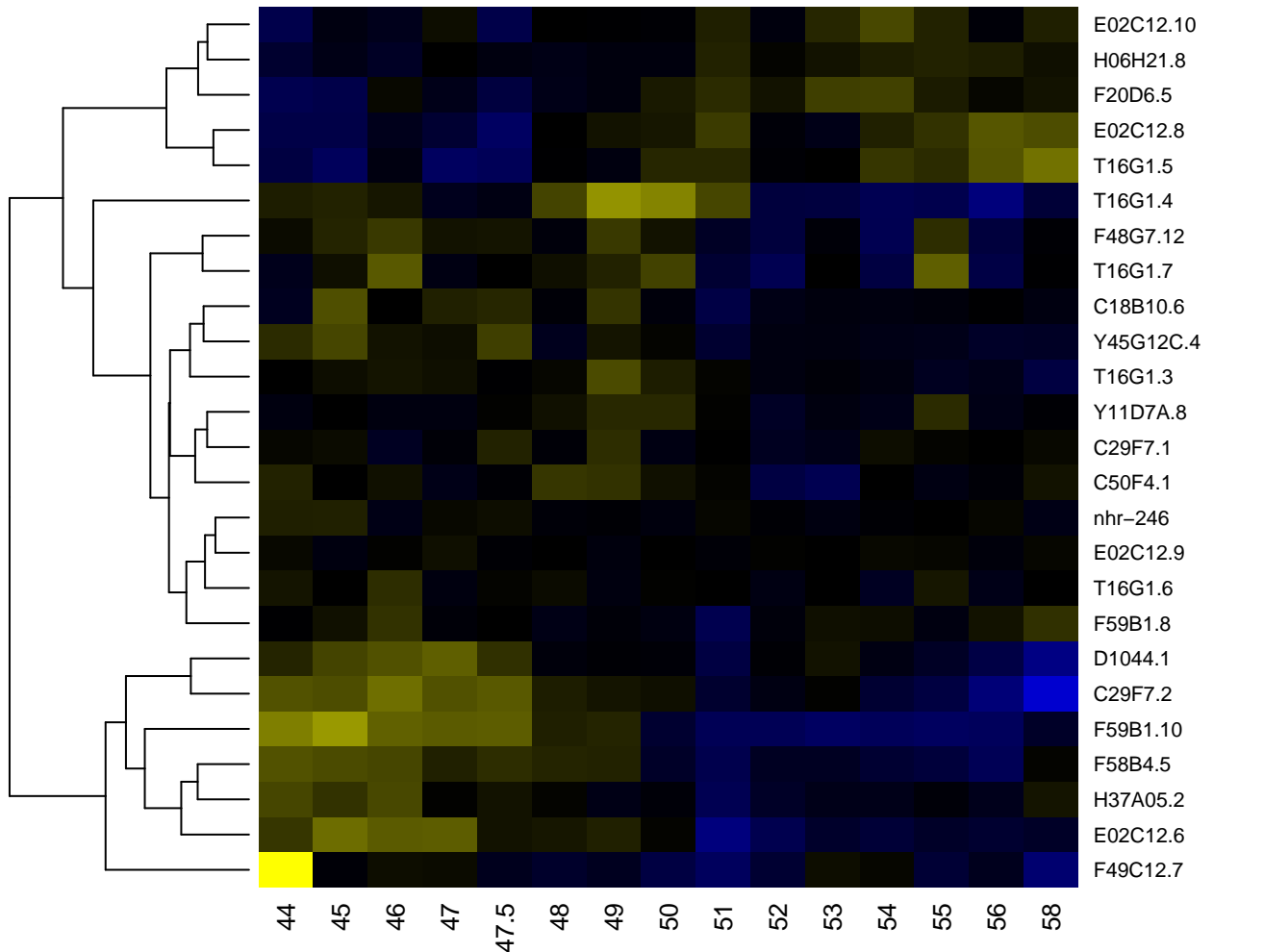
Chaperonin Cpn60/TCP-1



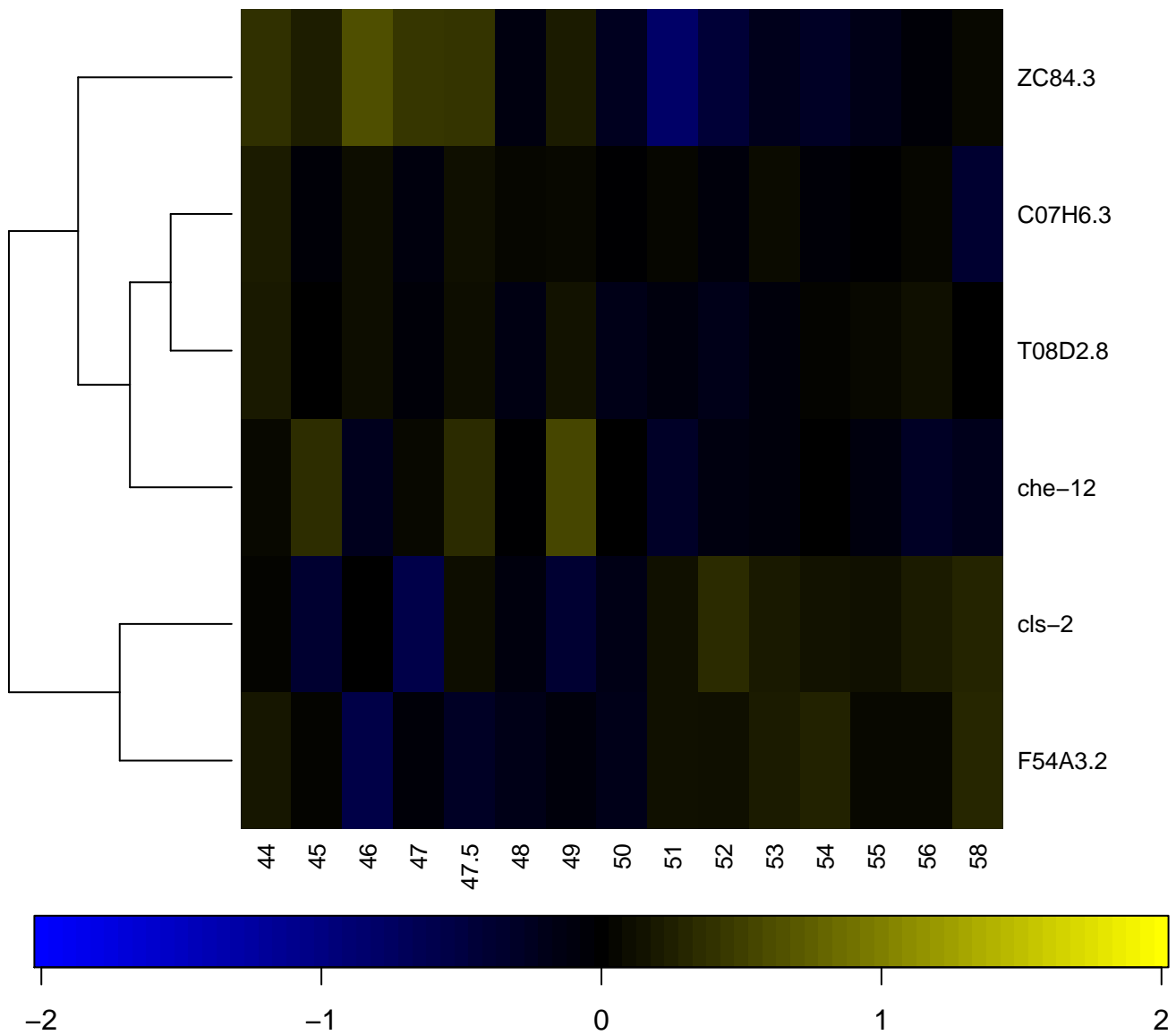
Chitin binding protein, peritrophin-A



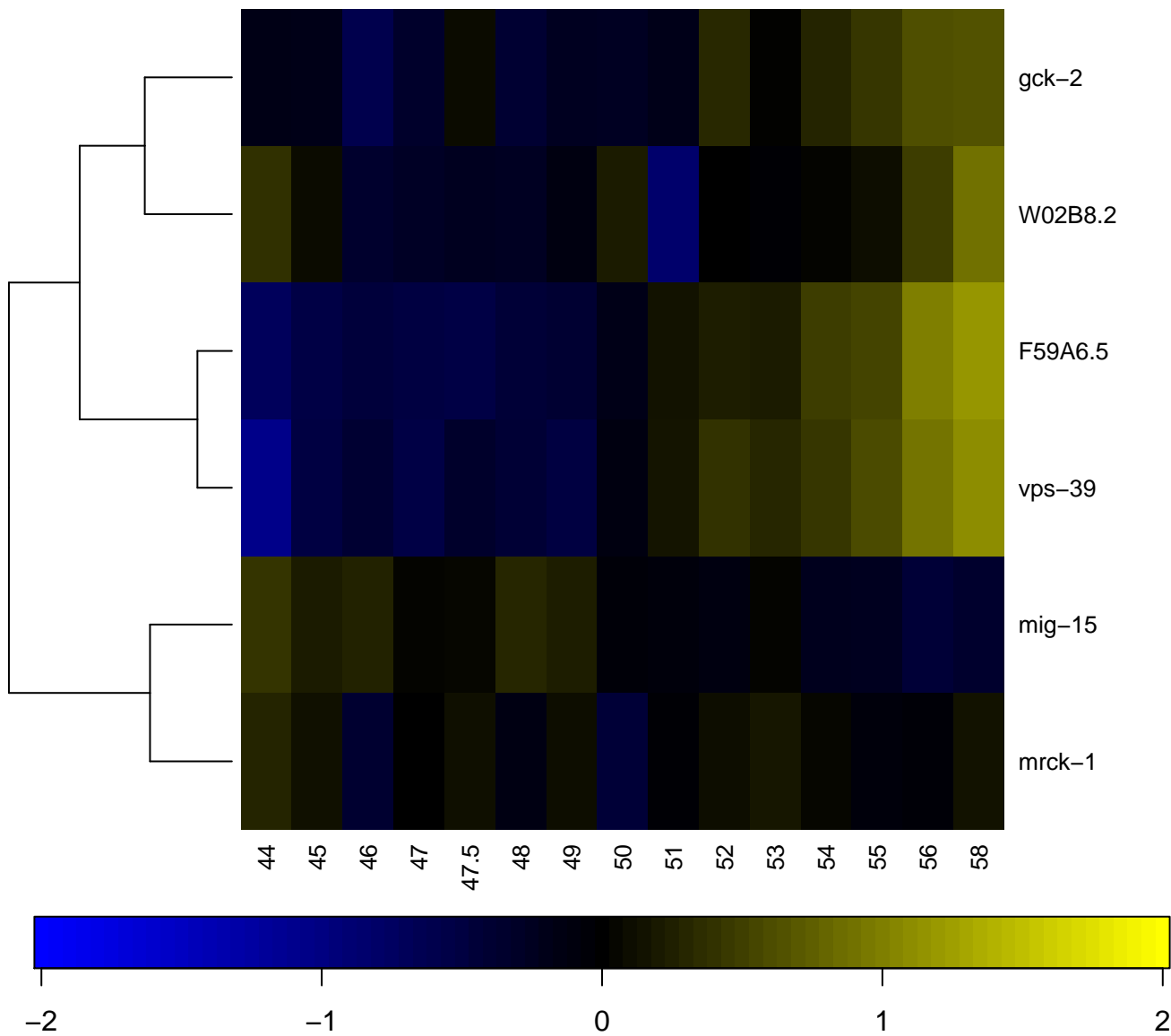
CHK kinase-like



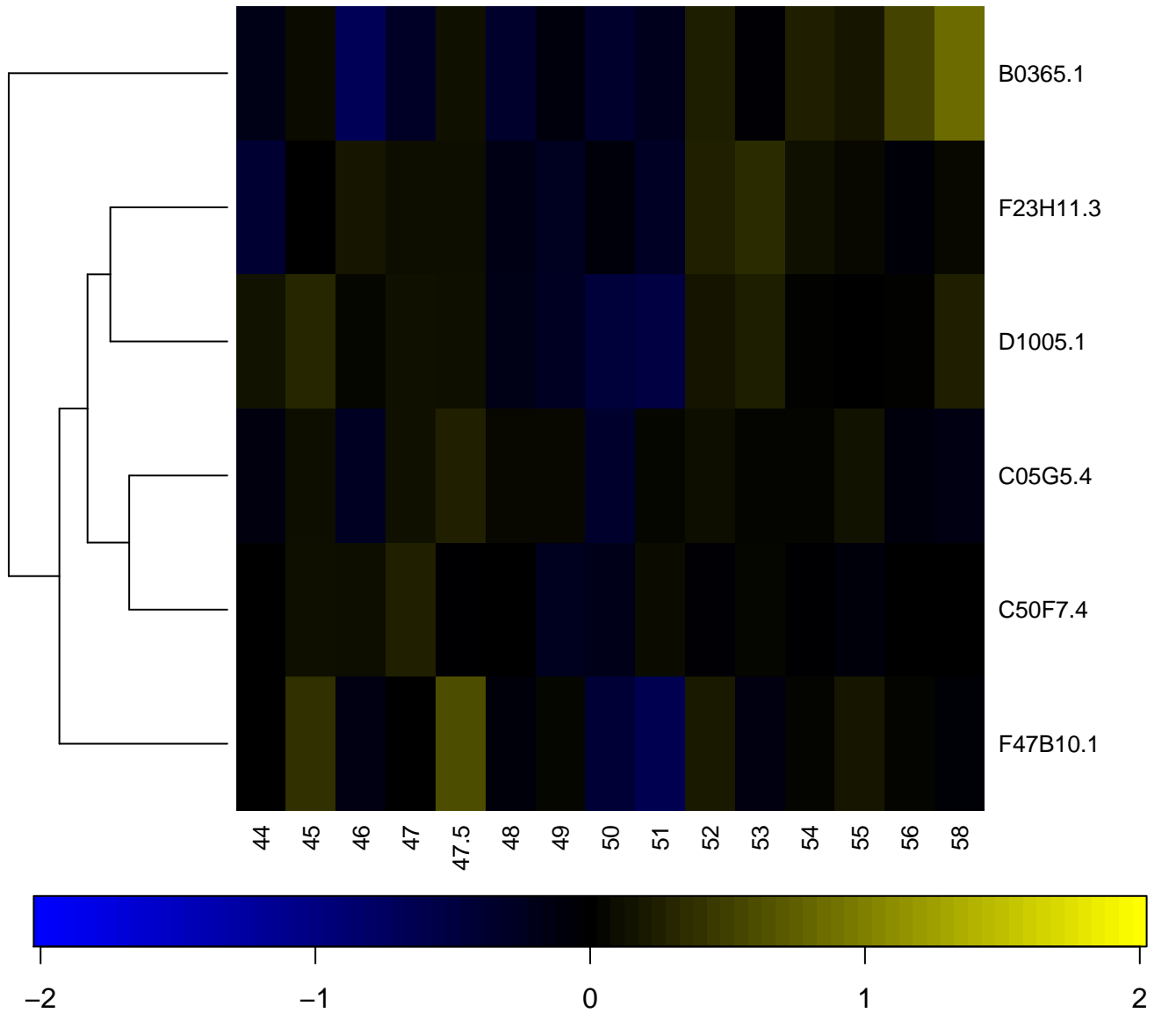
CLASP N terminal



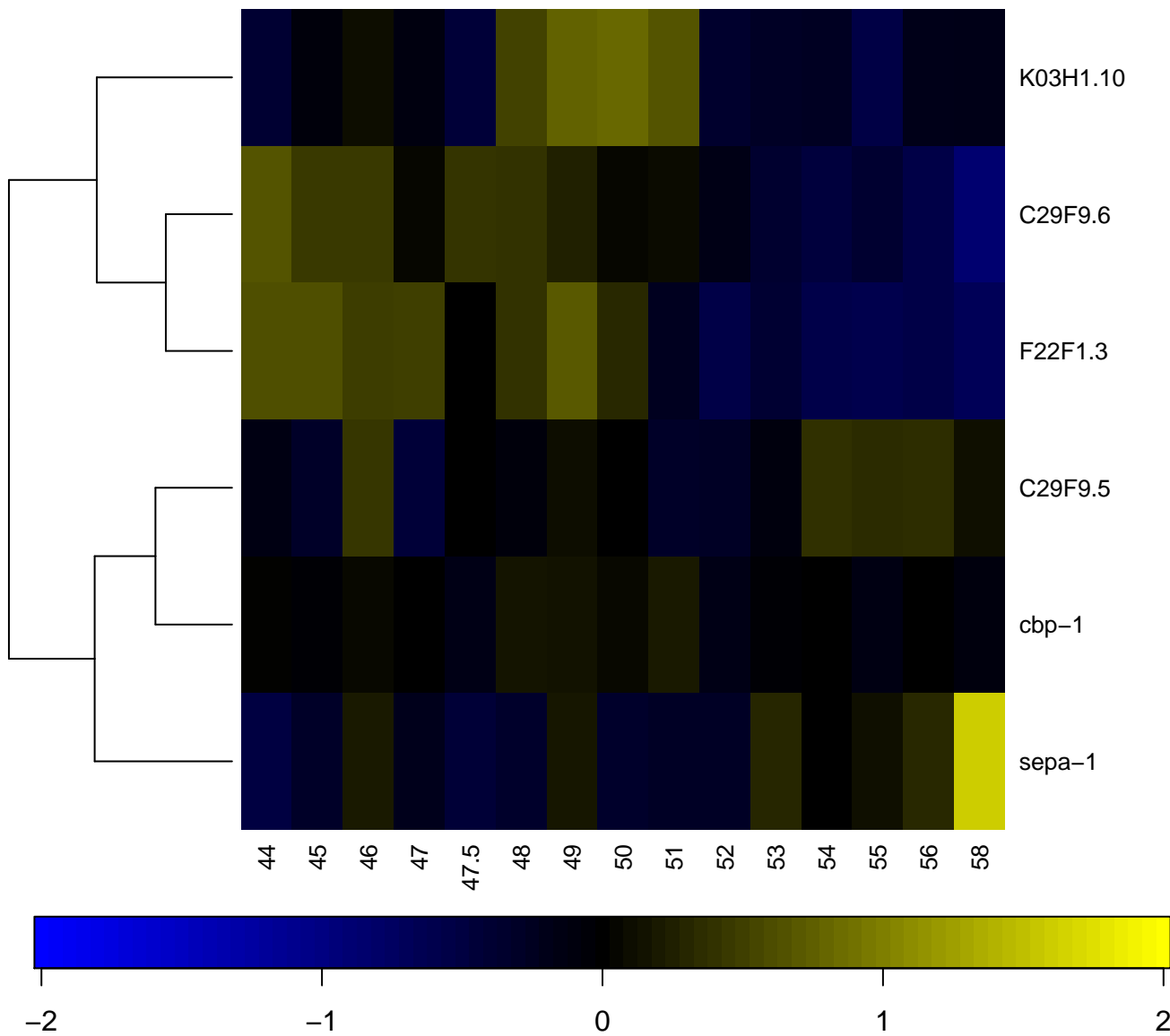
CNH domain



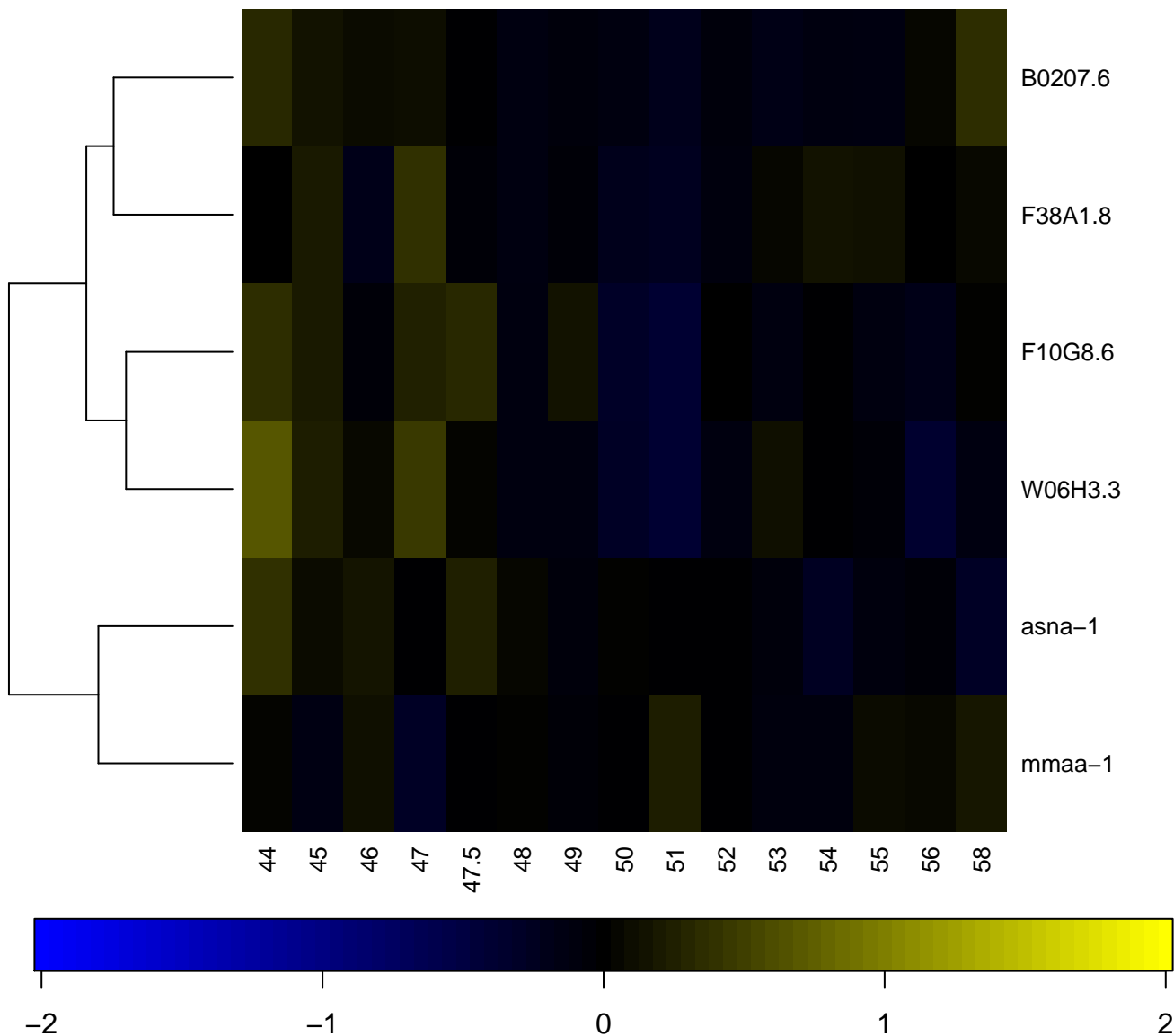
CoA-ligase



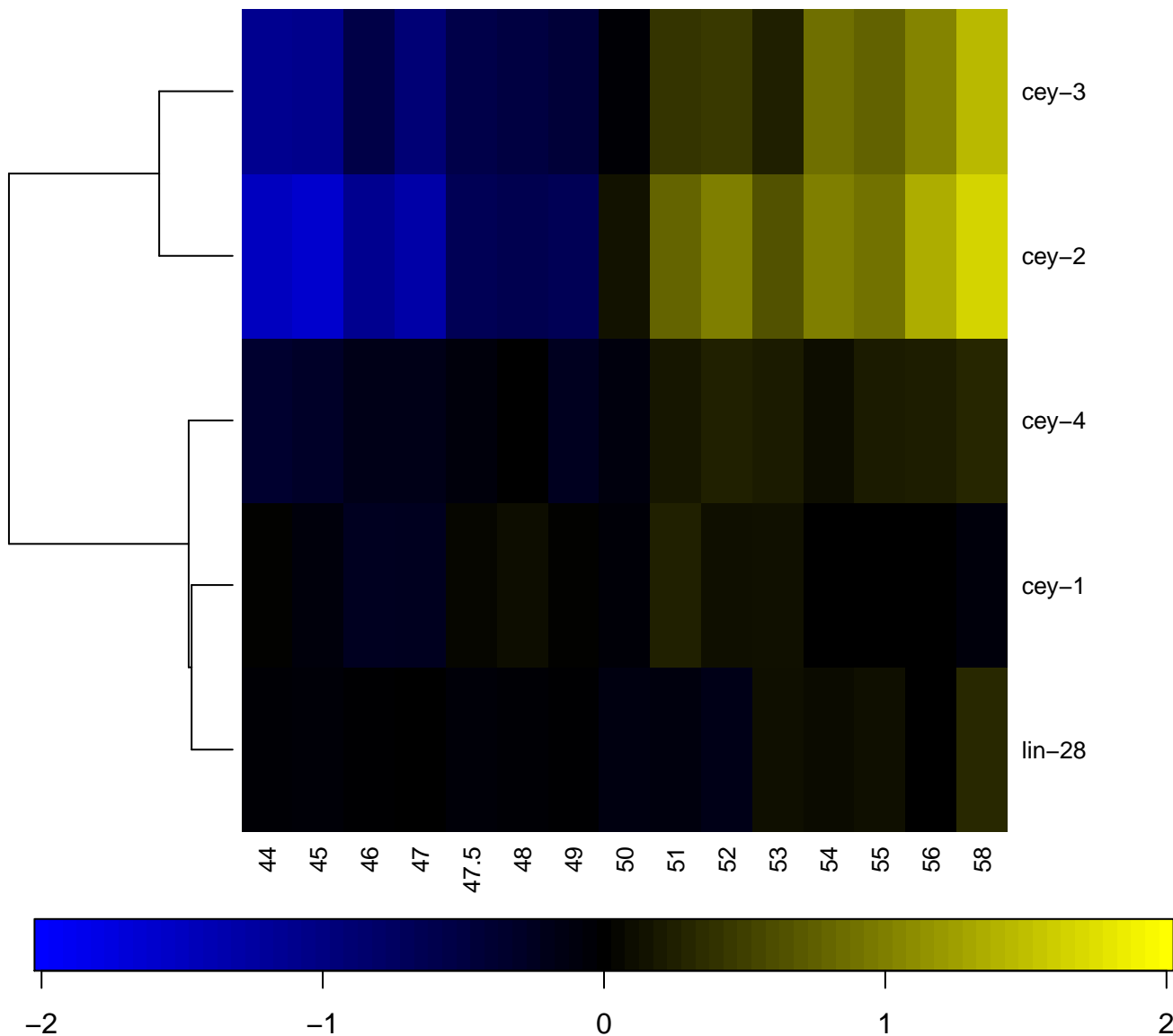
Coactivator CBP, KIX



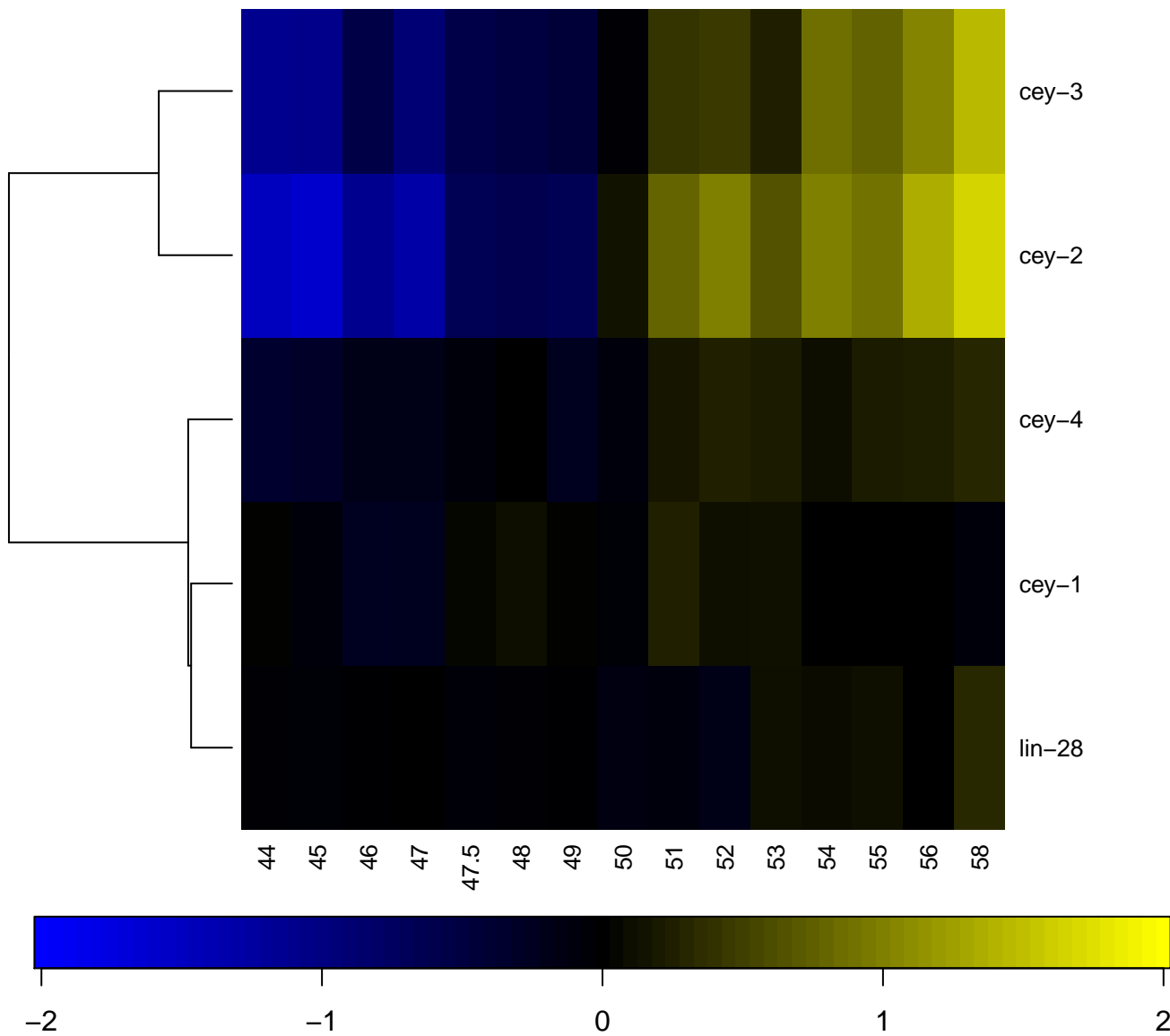
CobQ/CobB/MinD/ParA nucleotide binding domain



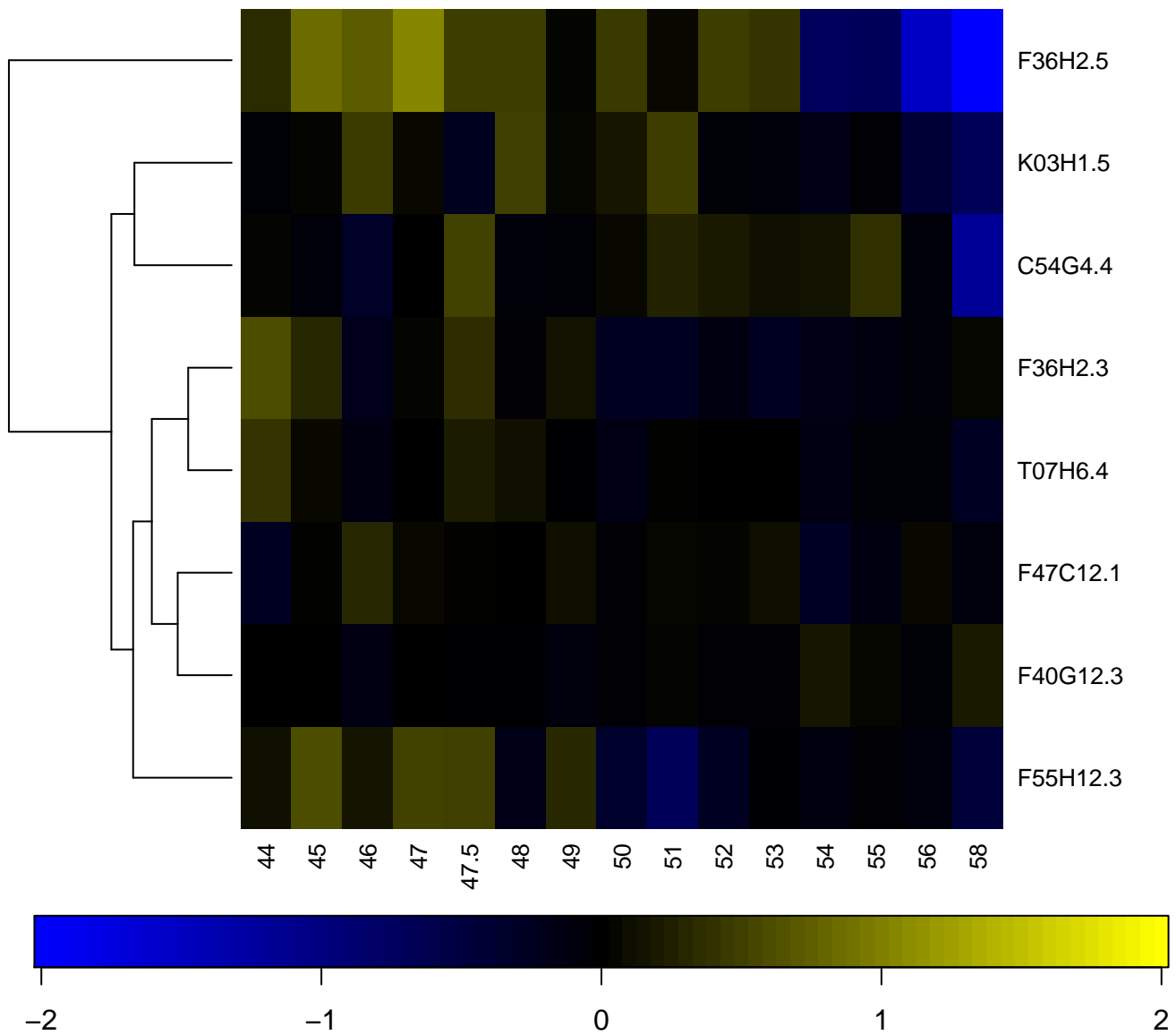
Cold-shock protein, DNA-binding



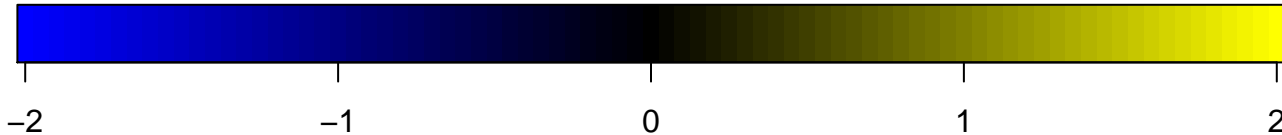
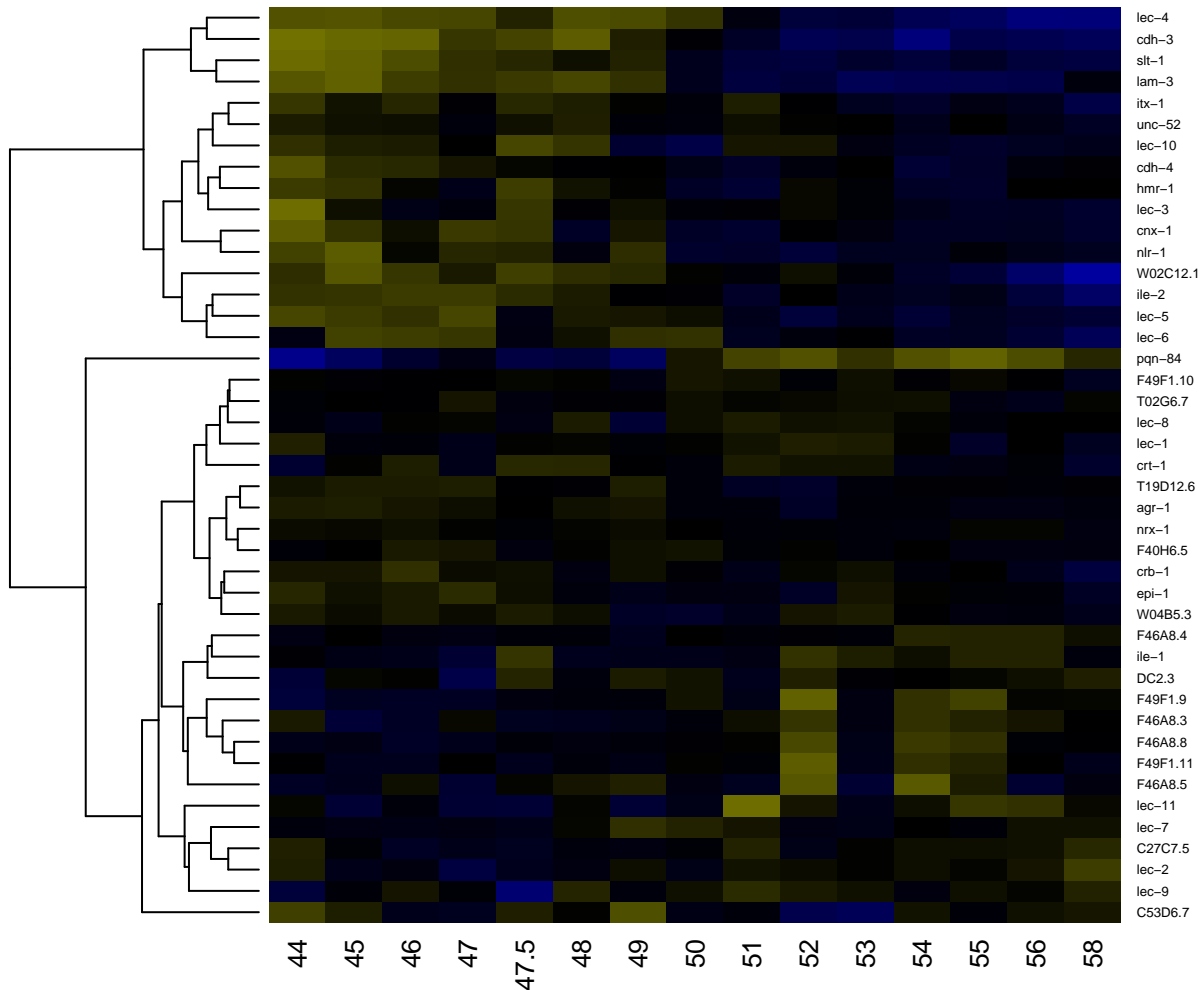
Cold shock protein



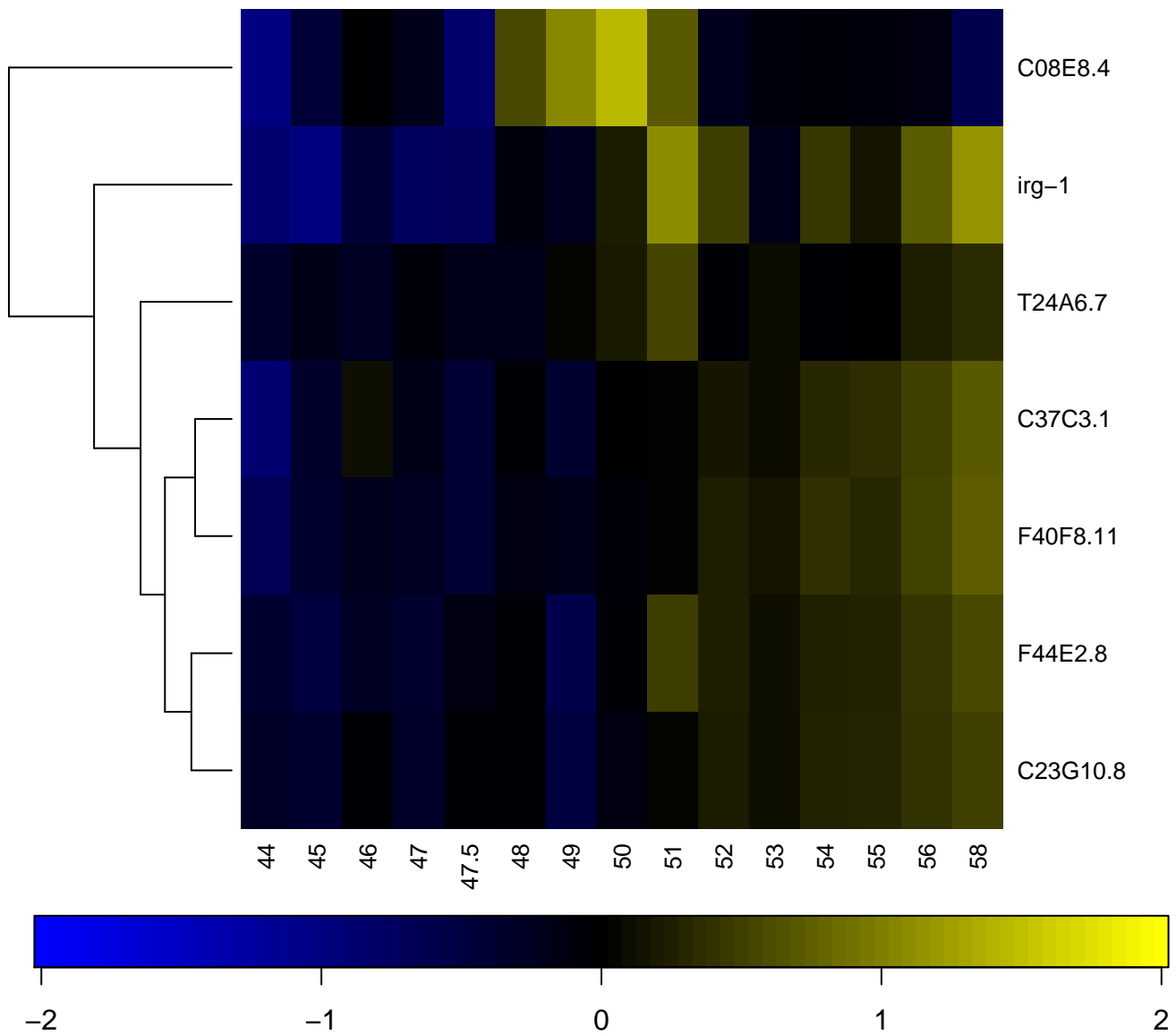
Complement control module



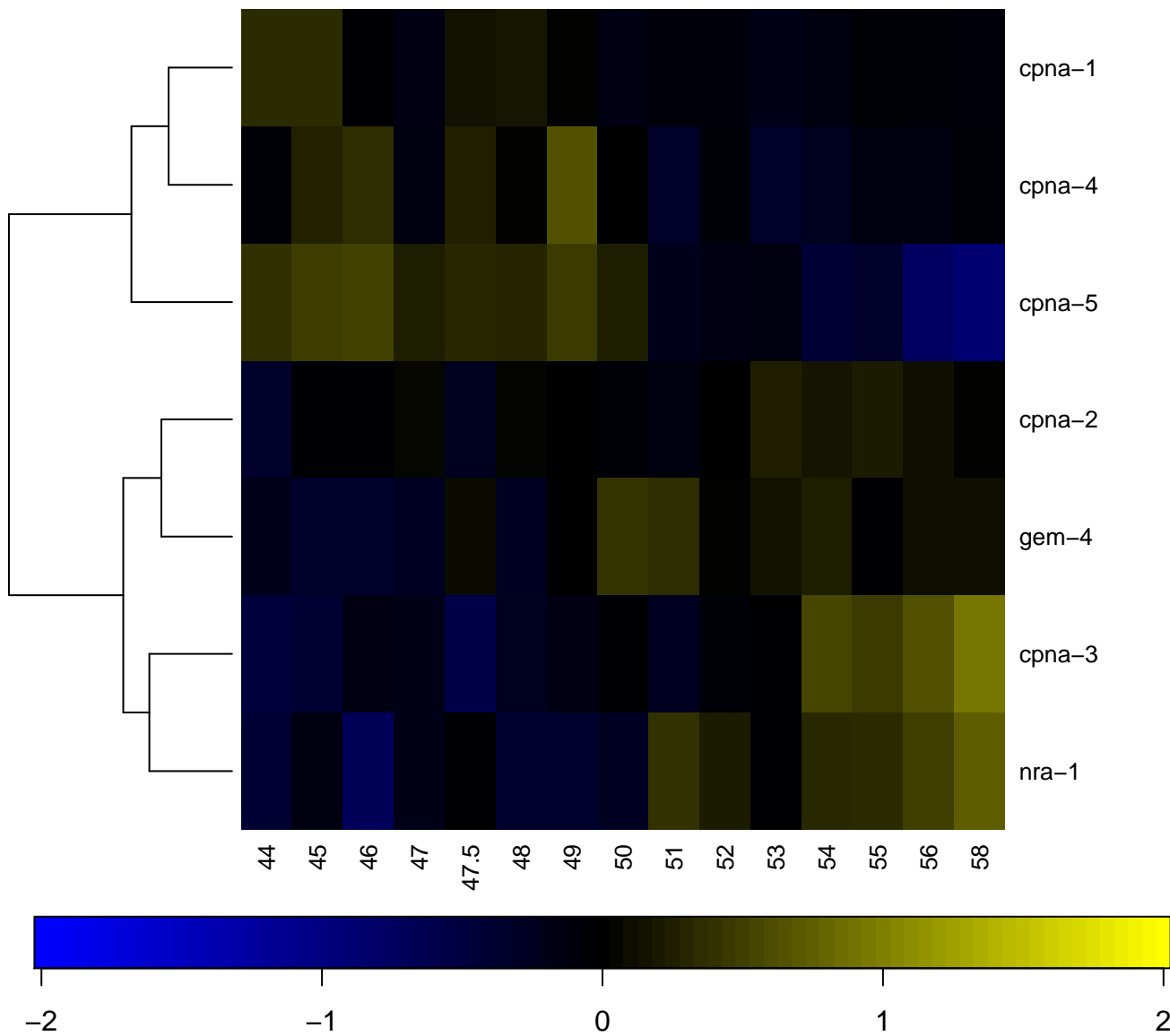
Concanavalin A-like lectin/glucanase, subgroup



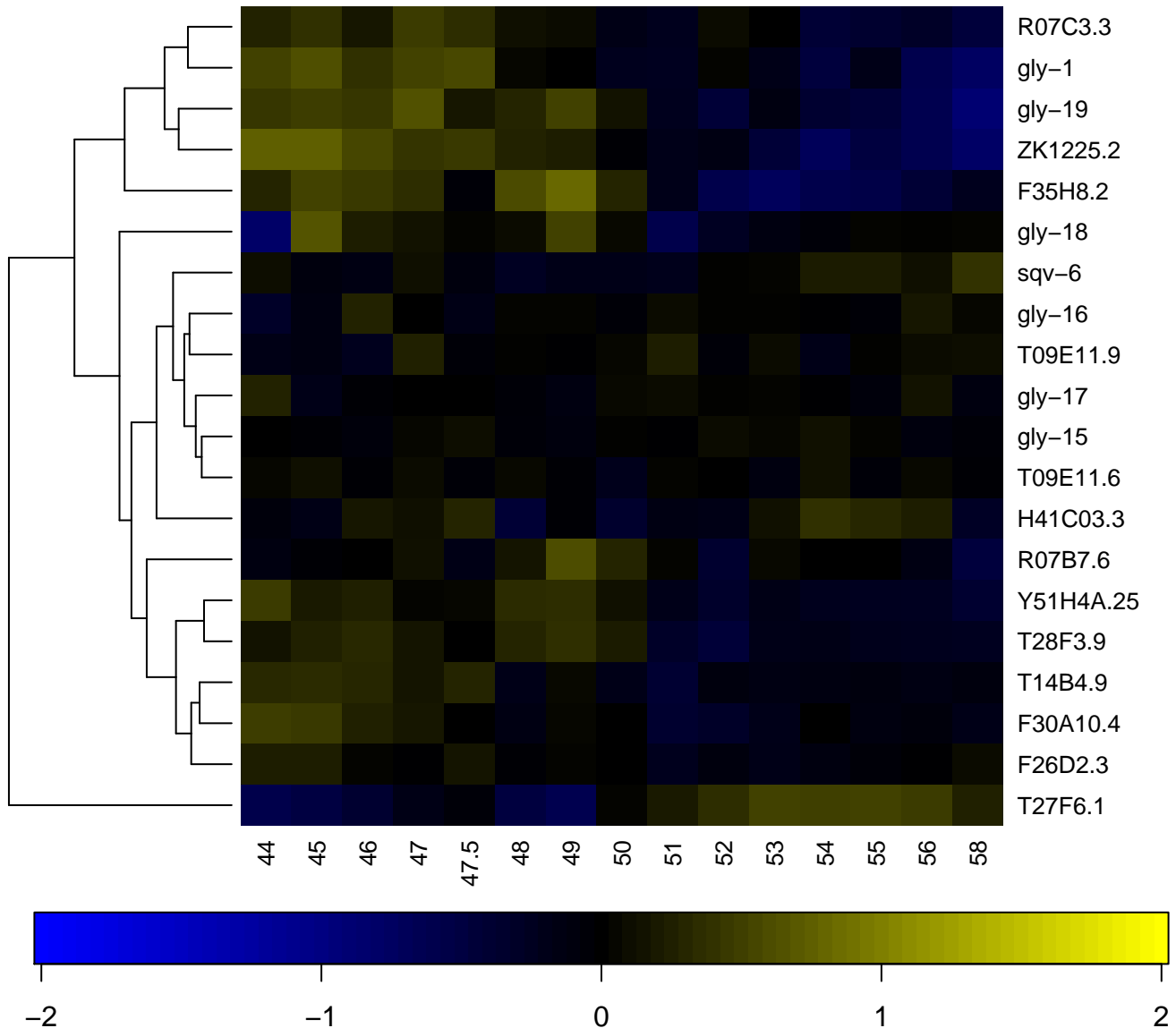
Conserved hypothetical protein CHP02464



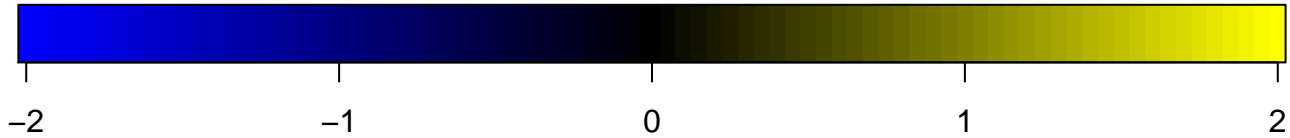
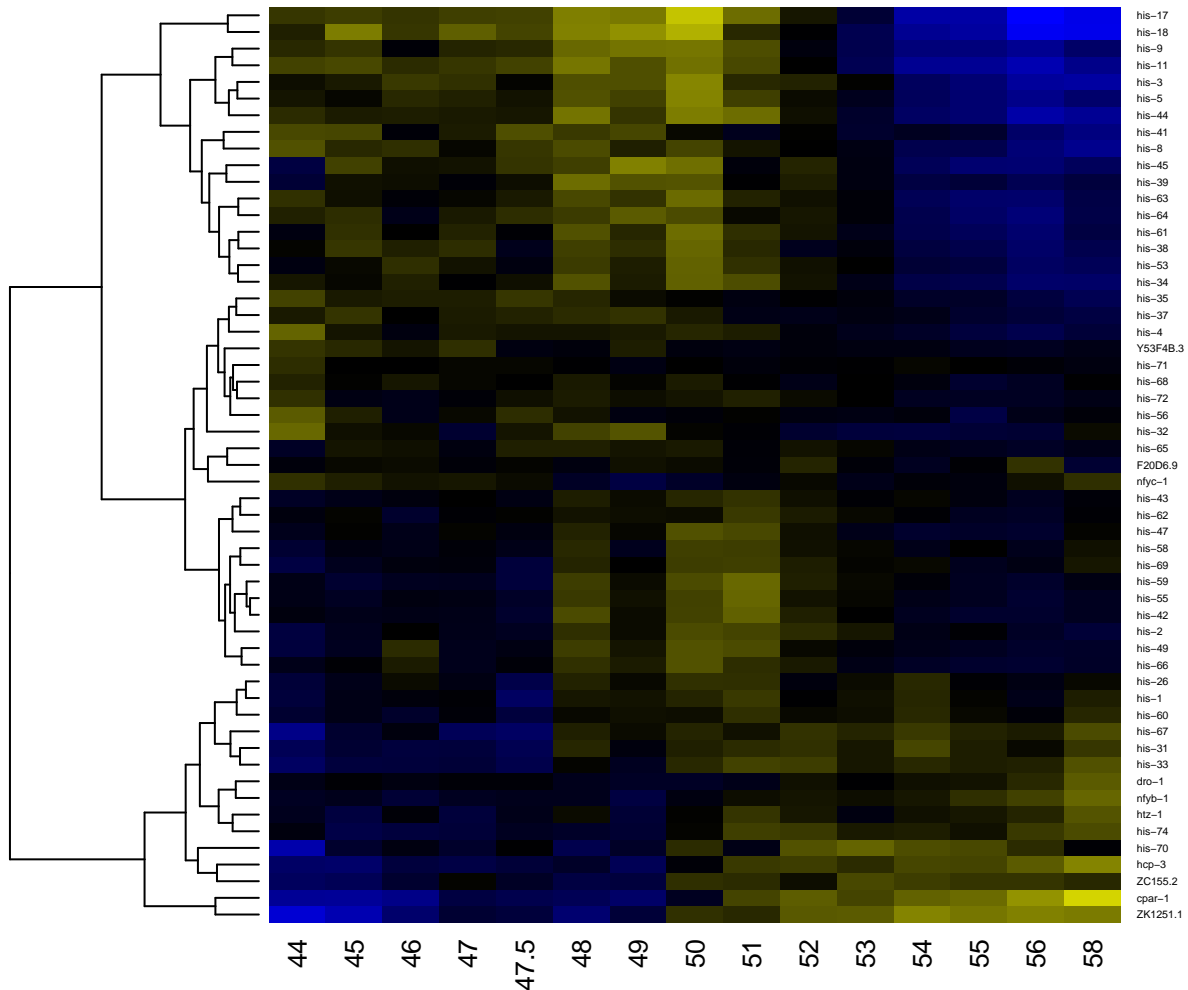
Copine



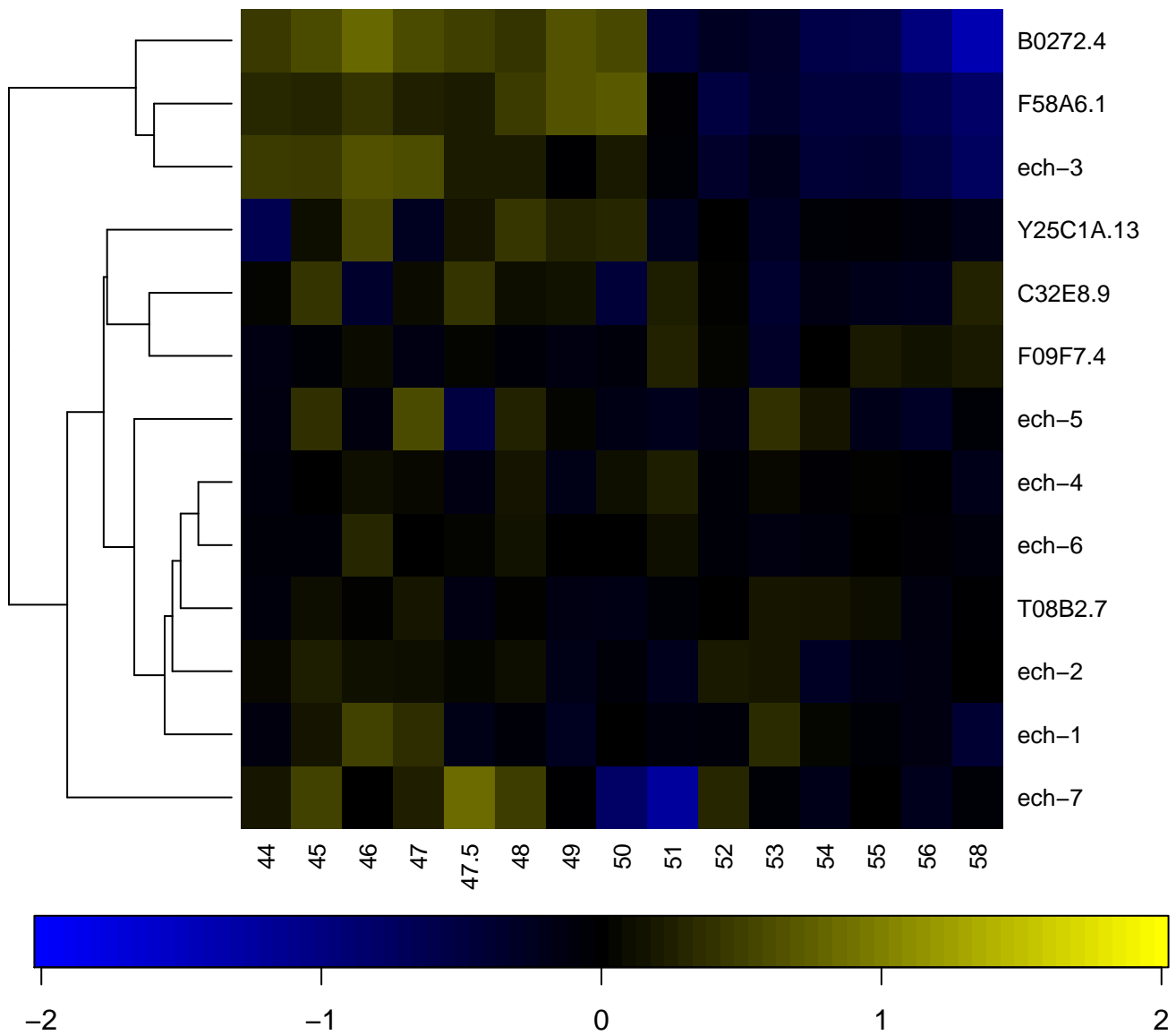
Core-2/I-Branching enzyme



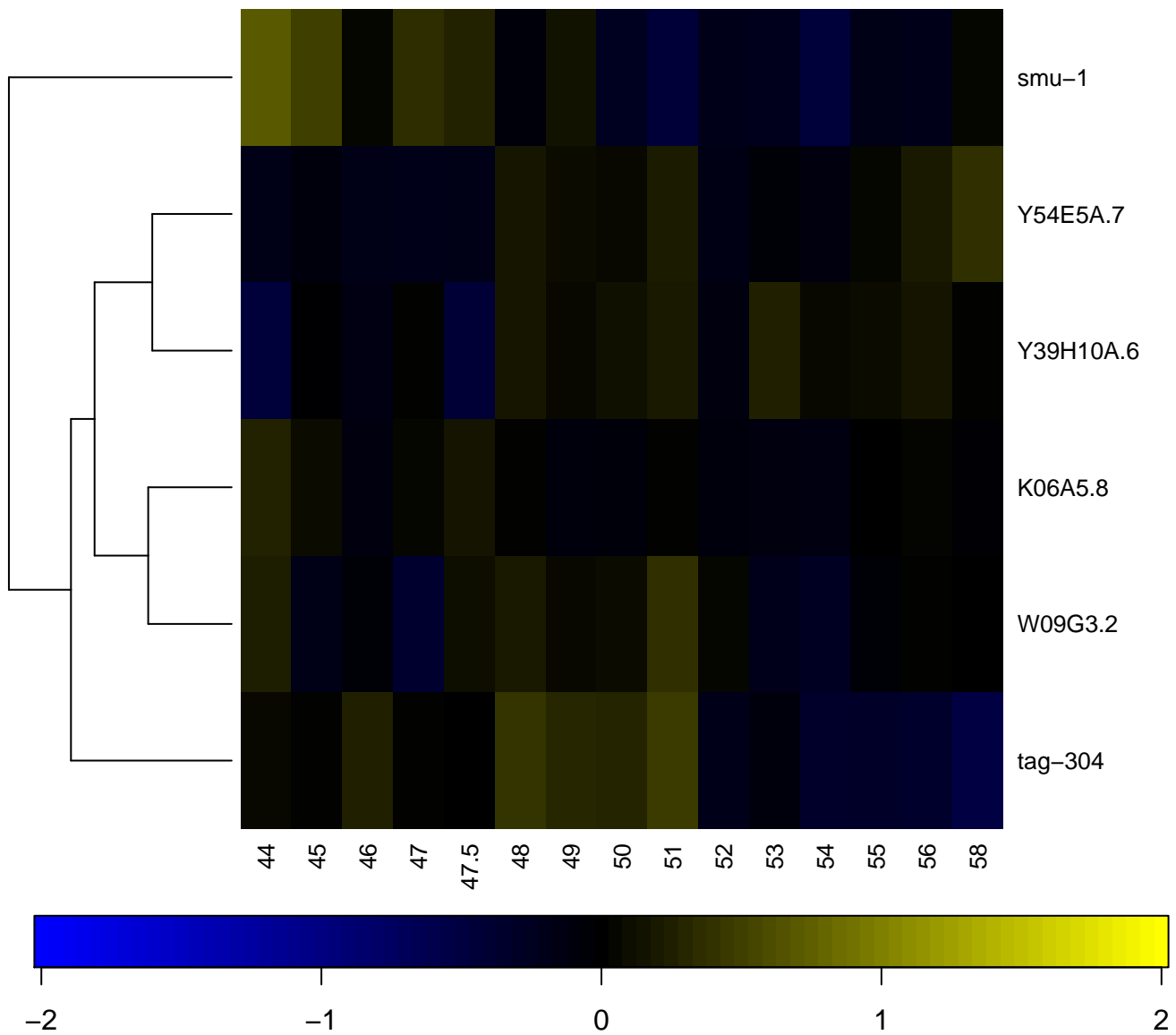
Core histone H2A/H2B/H3/H4



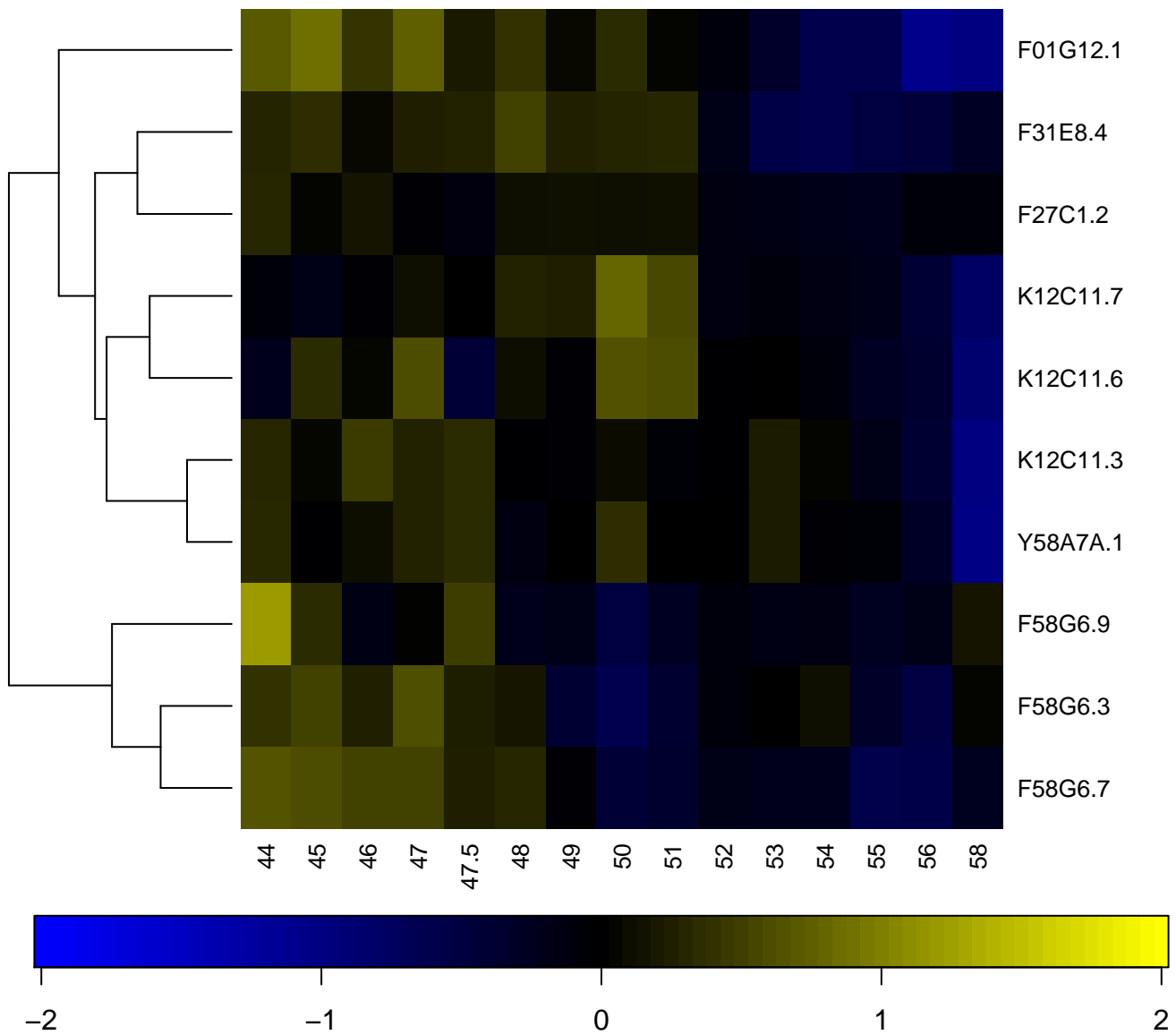
Crotonase, core



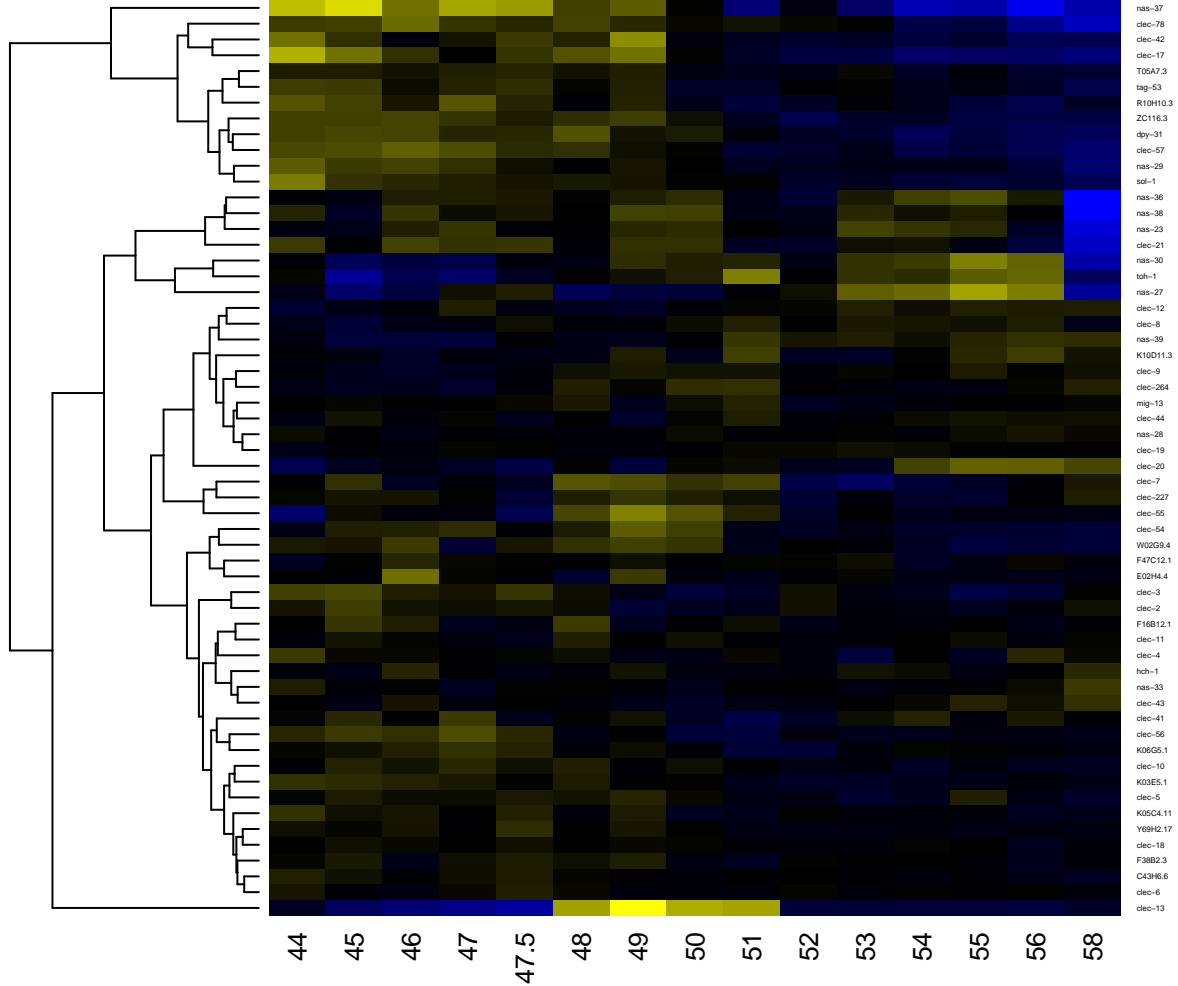
CTLH, C-terminal LisH motif



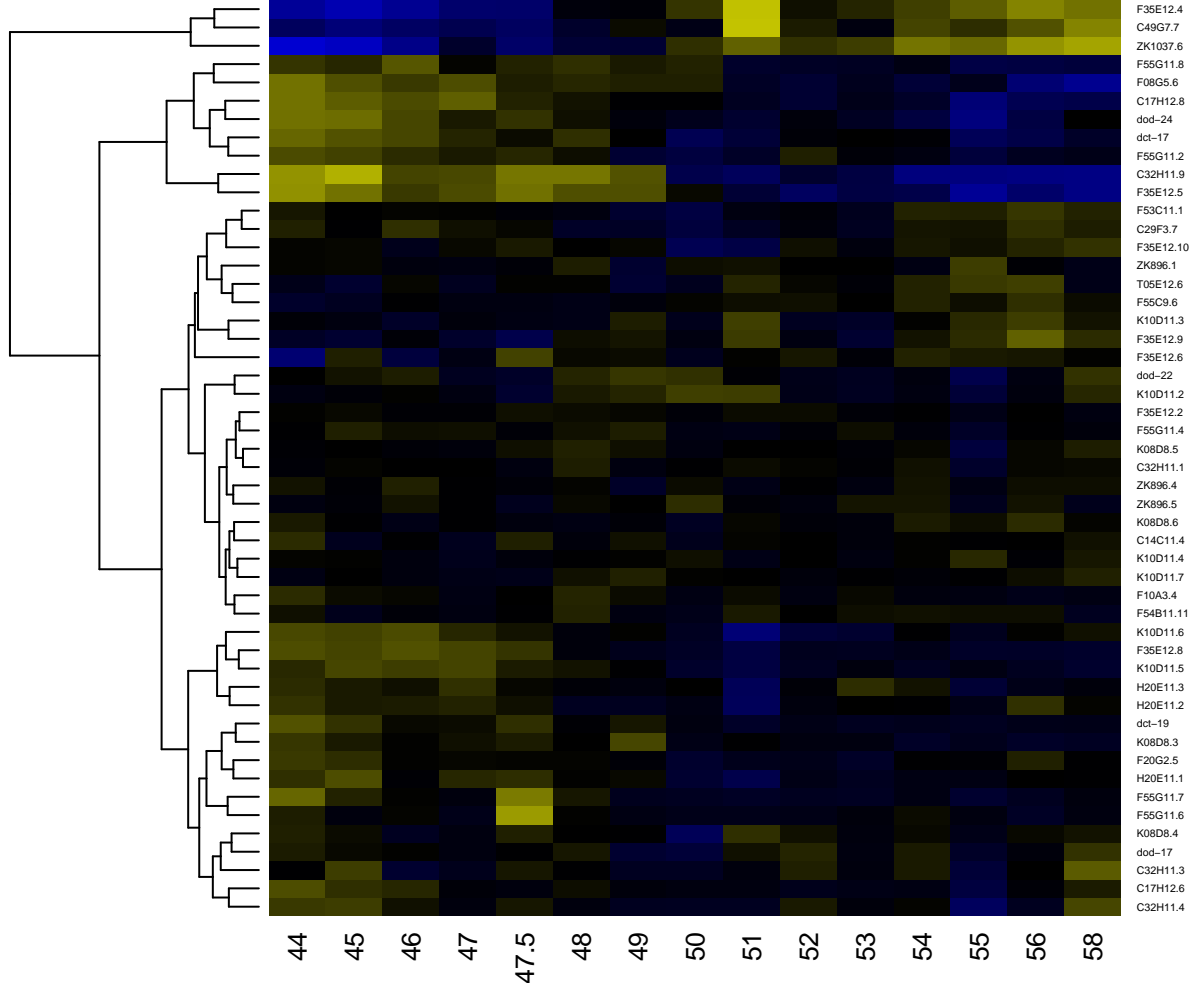
Ctr copper transporter family



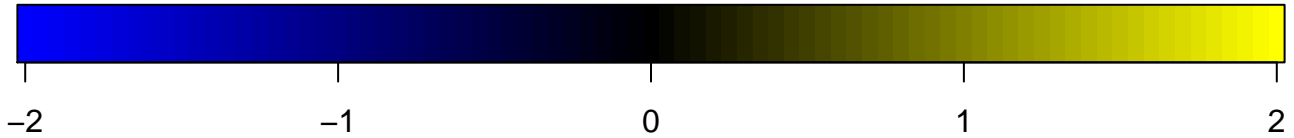
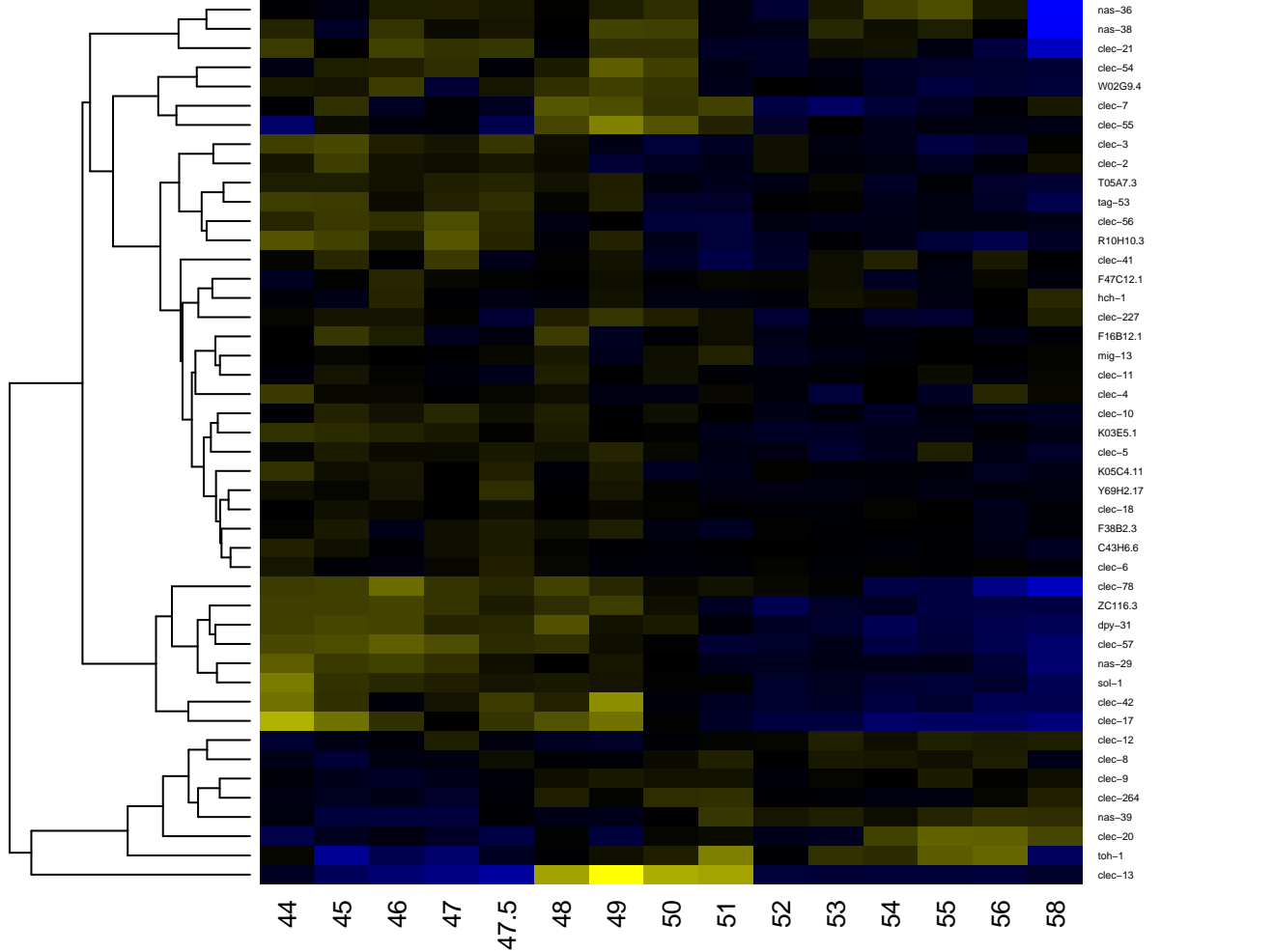
CUB



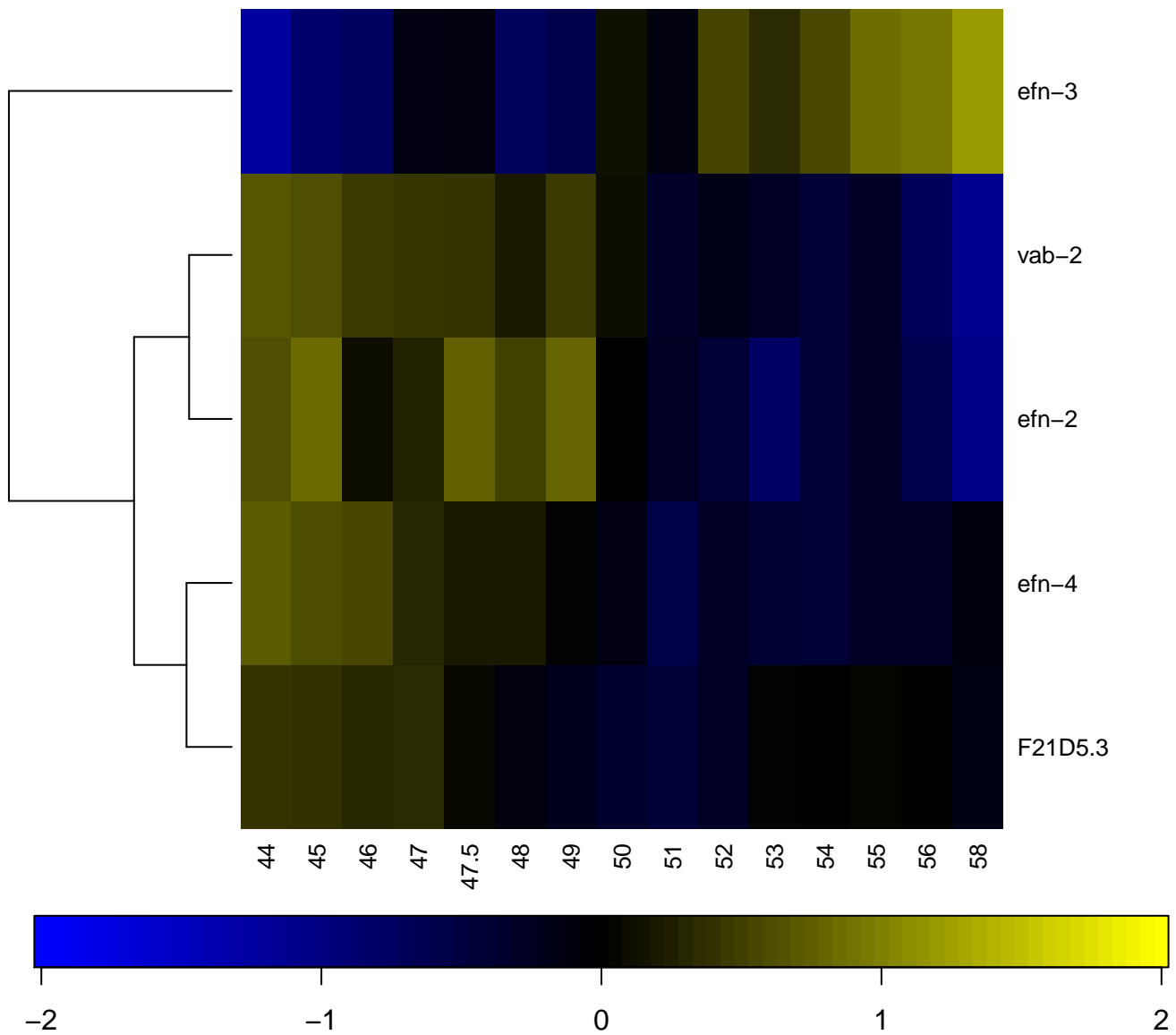
CUB-like domain



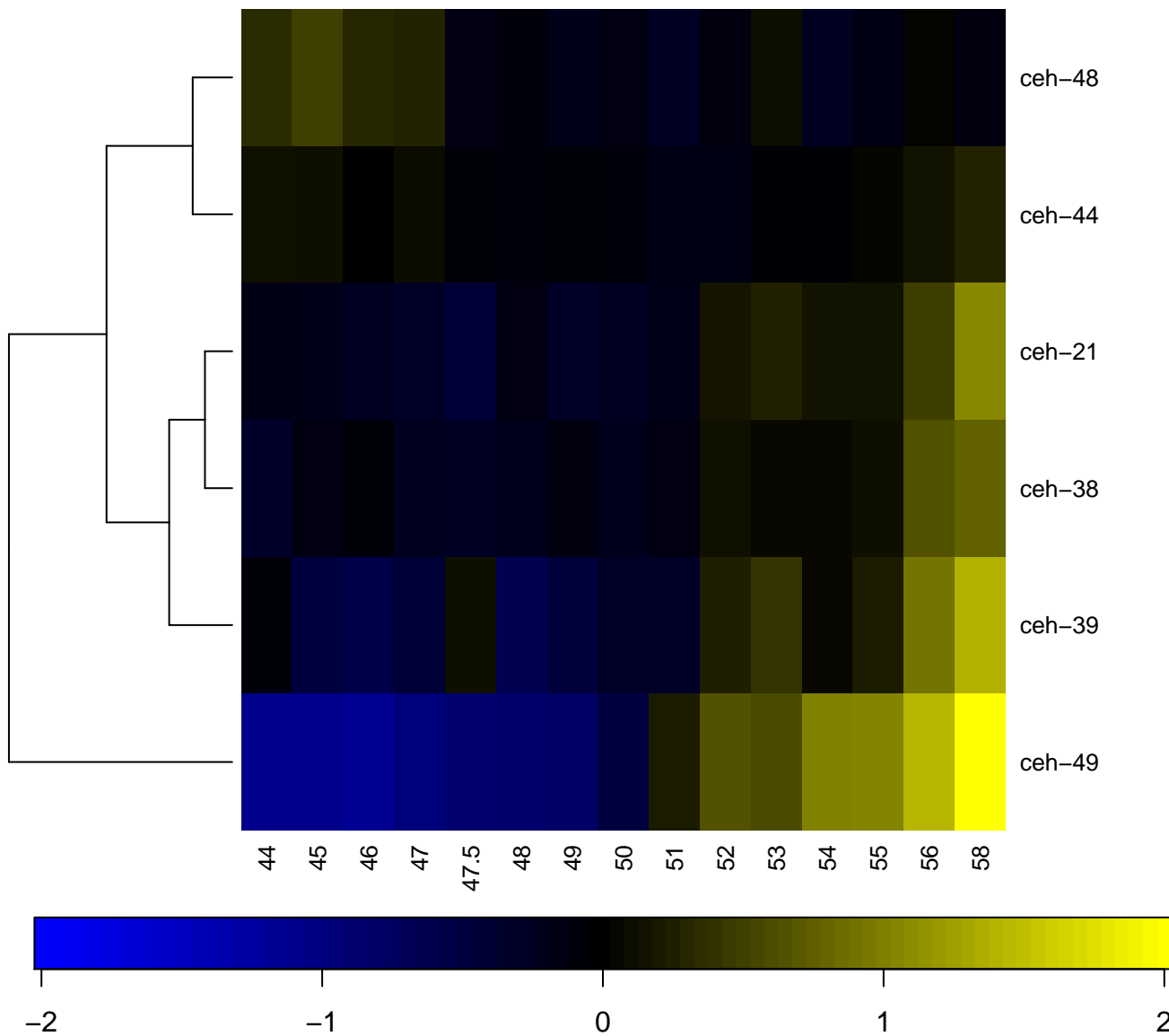
CUB domain



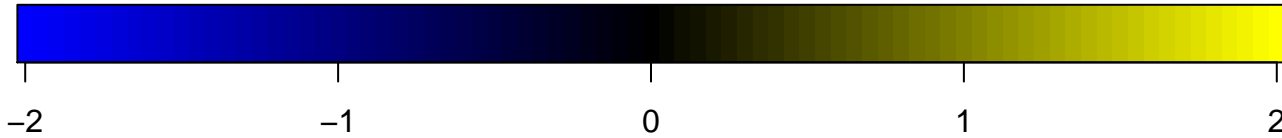
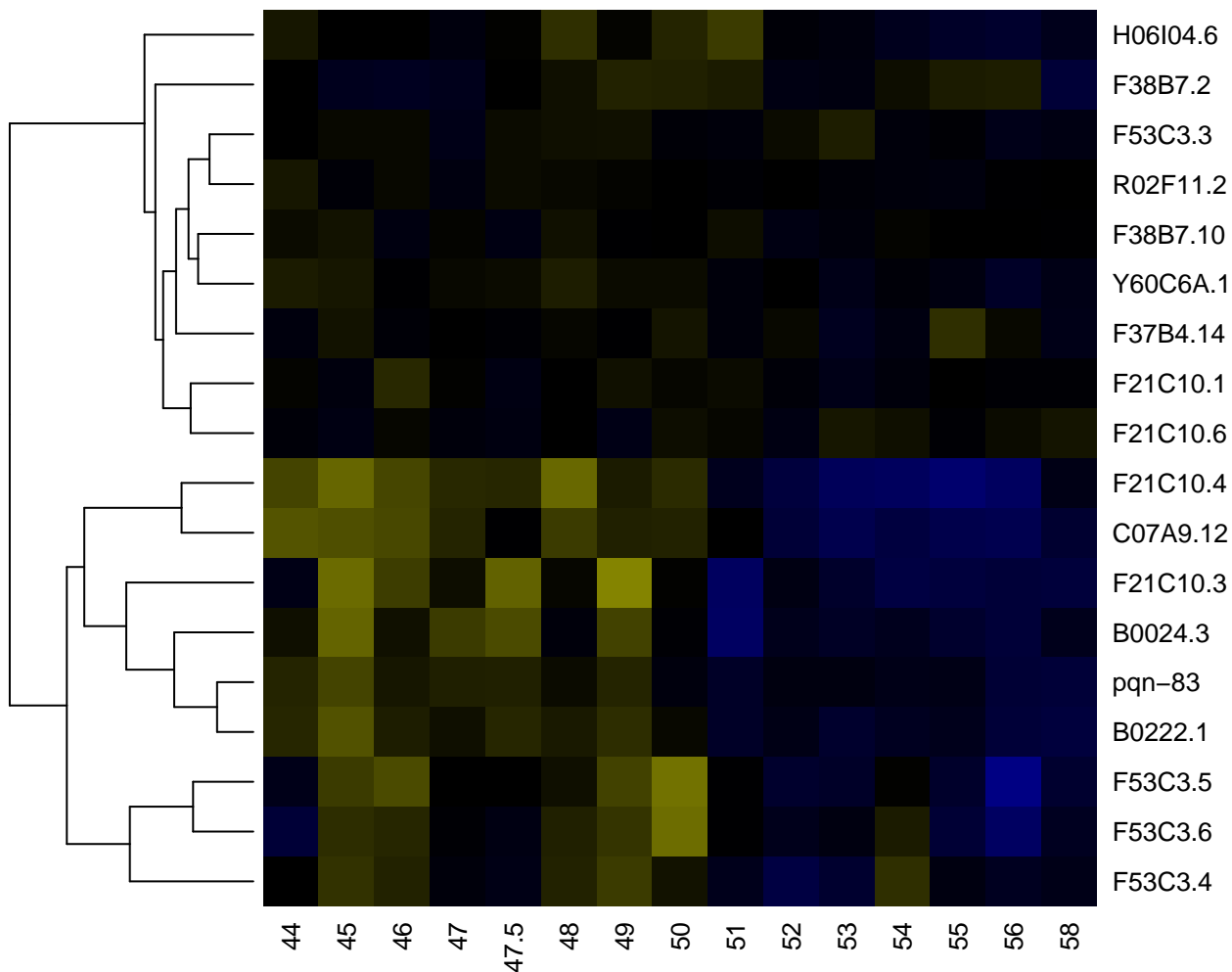
Cupredoxin



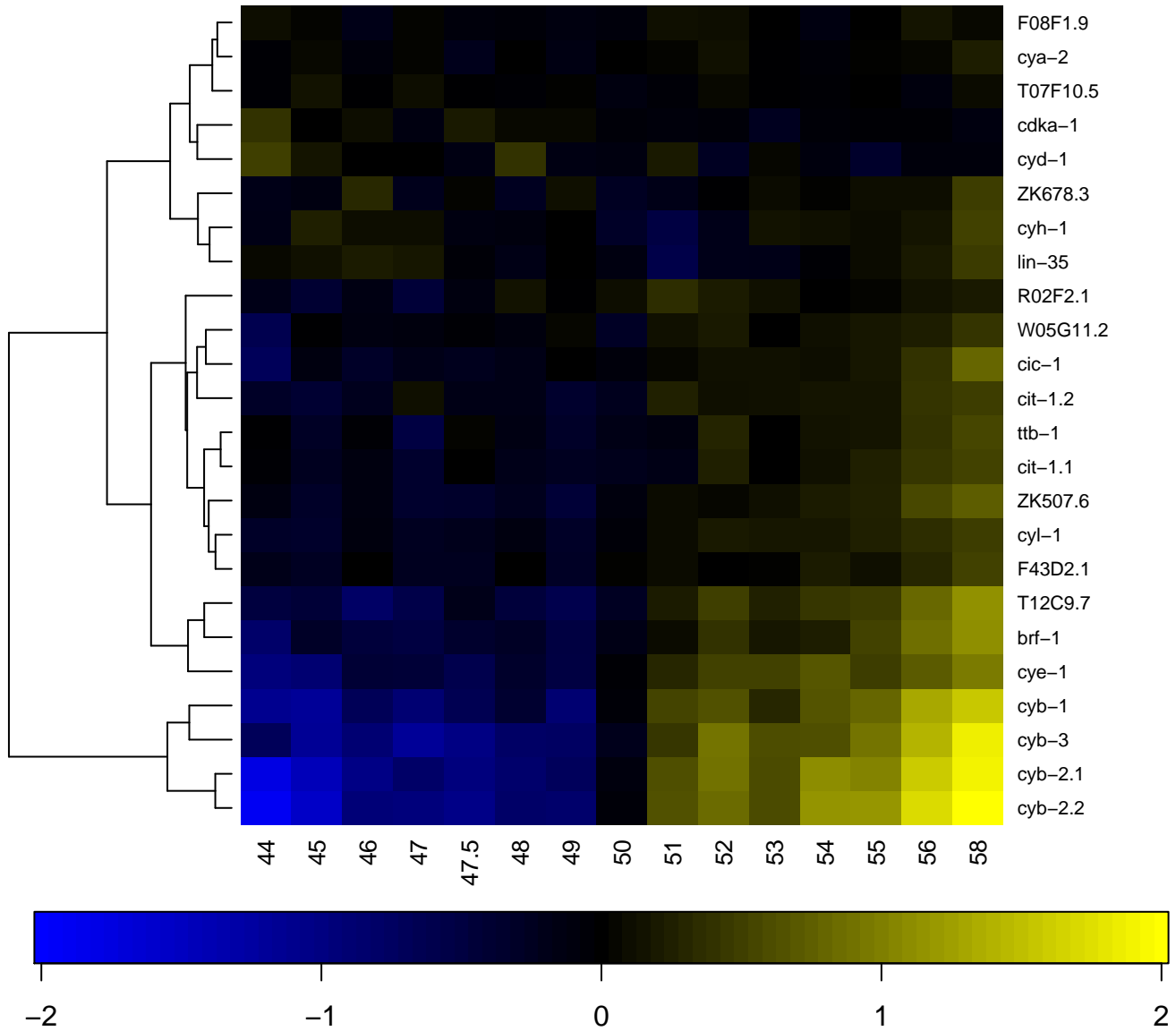
CUT domain



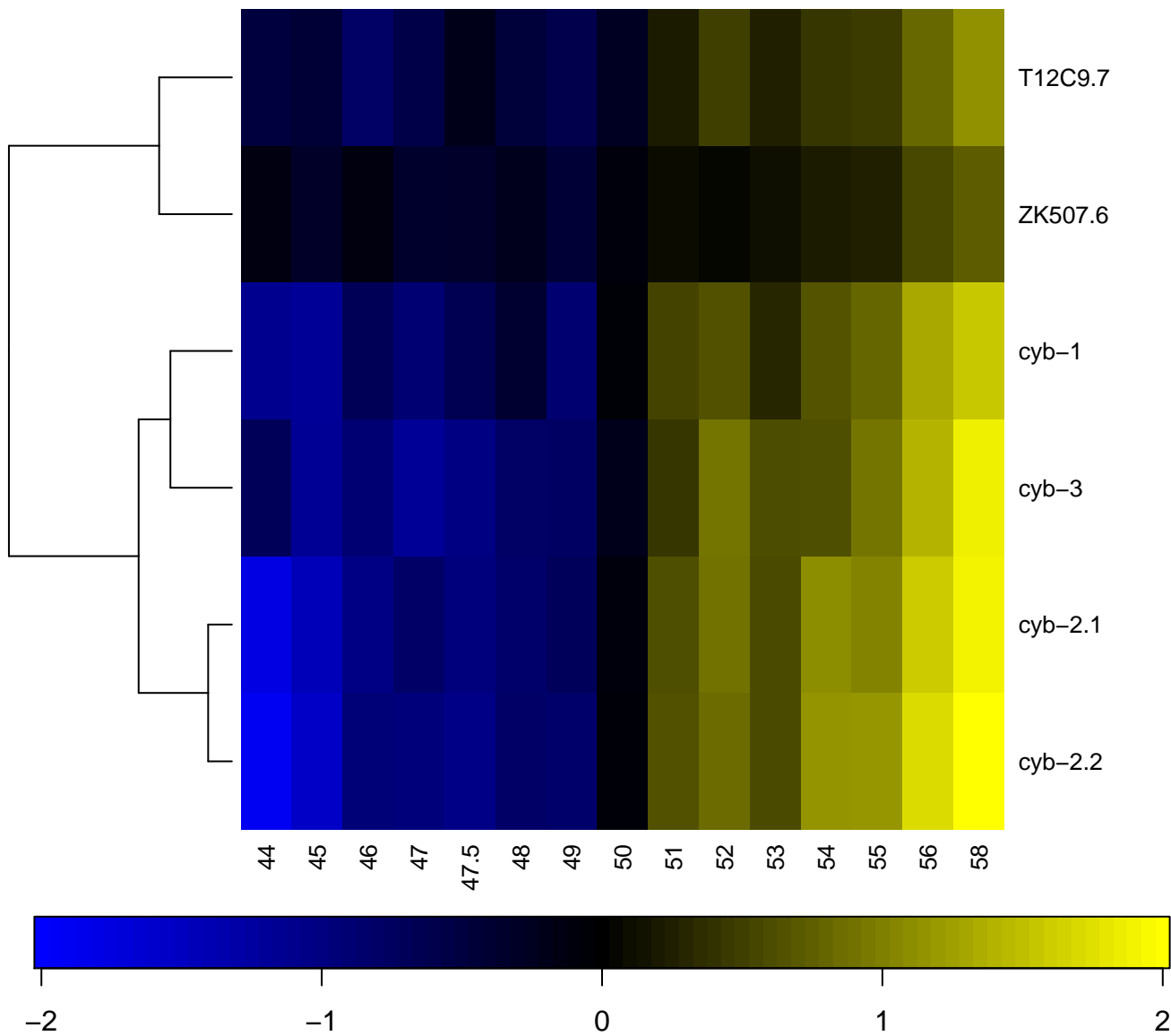
CX module



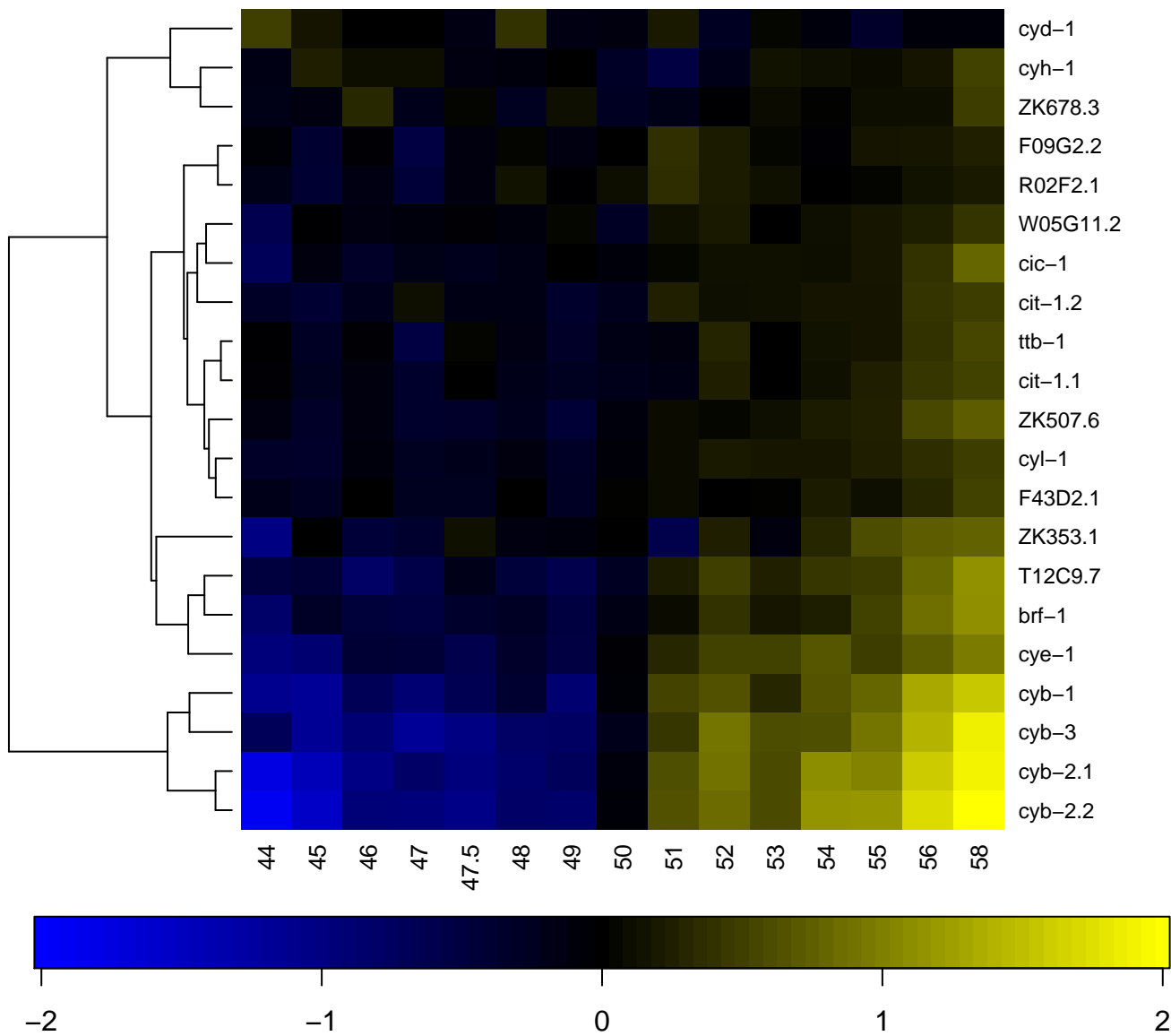
Cyclin-related



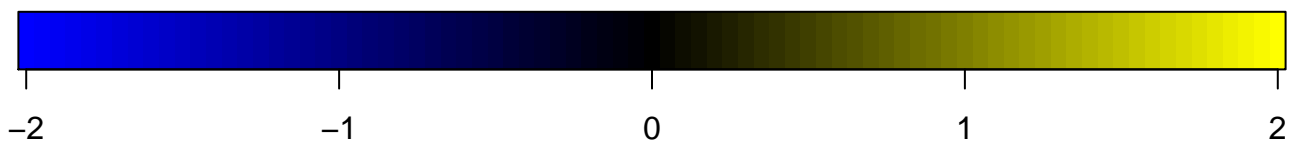
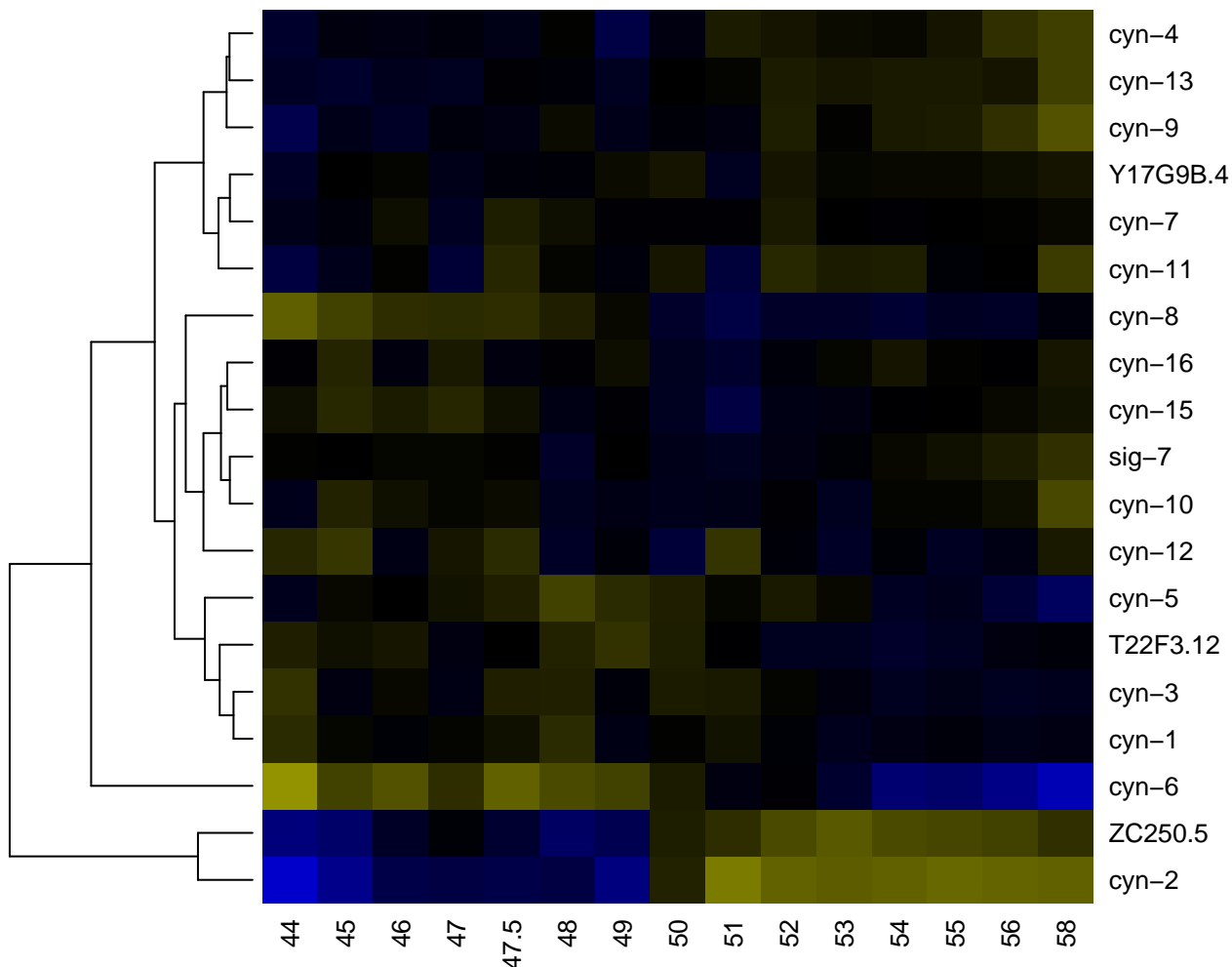
Cyclin, C-terminal



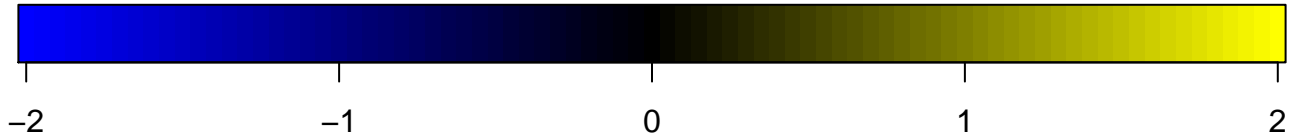
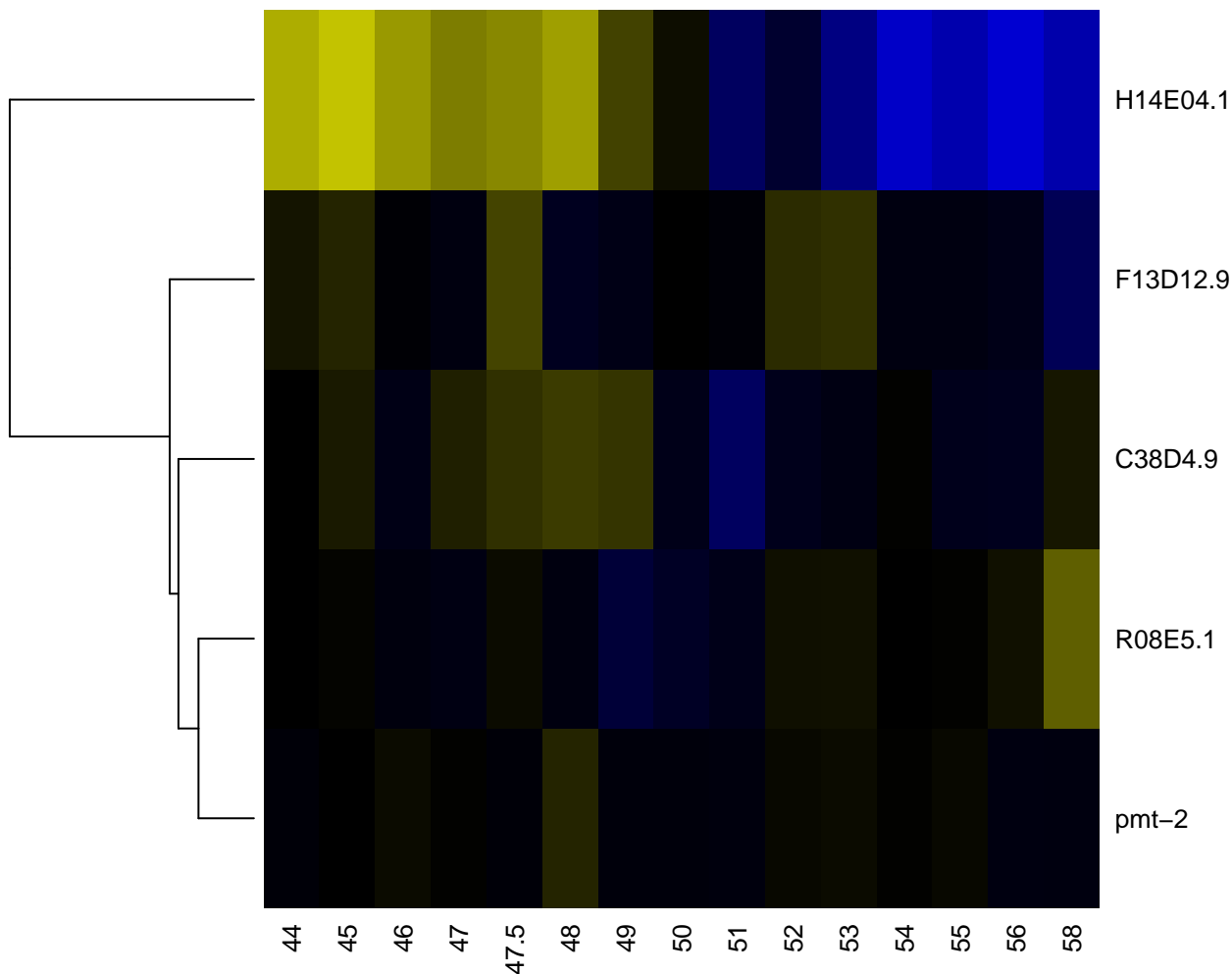
Cyclin, N-terminal



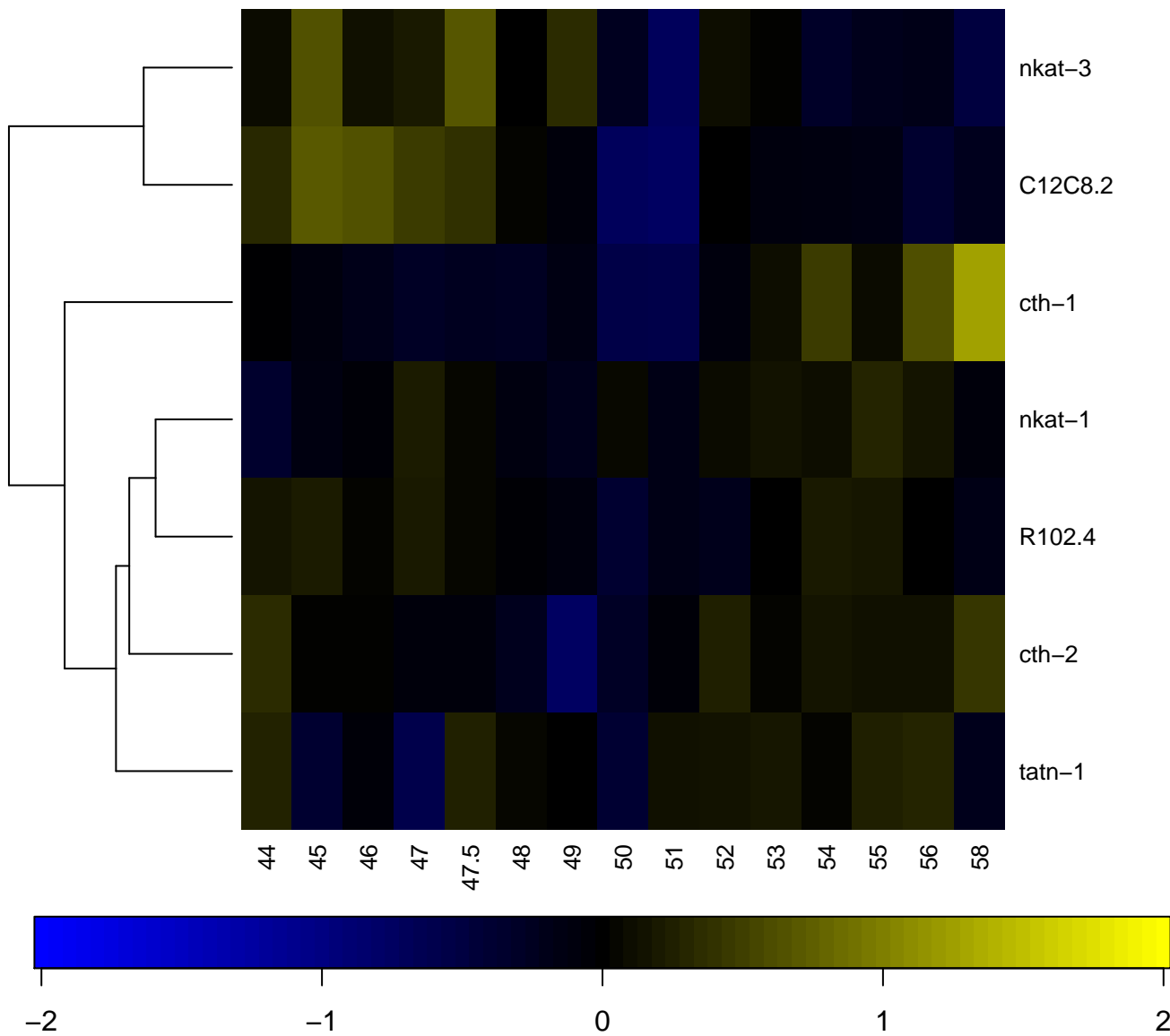
Cyclophilin type peptidyl–prolyl cis–trans isomerase/CLD



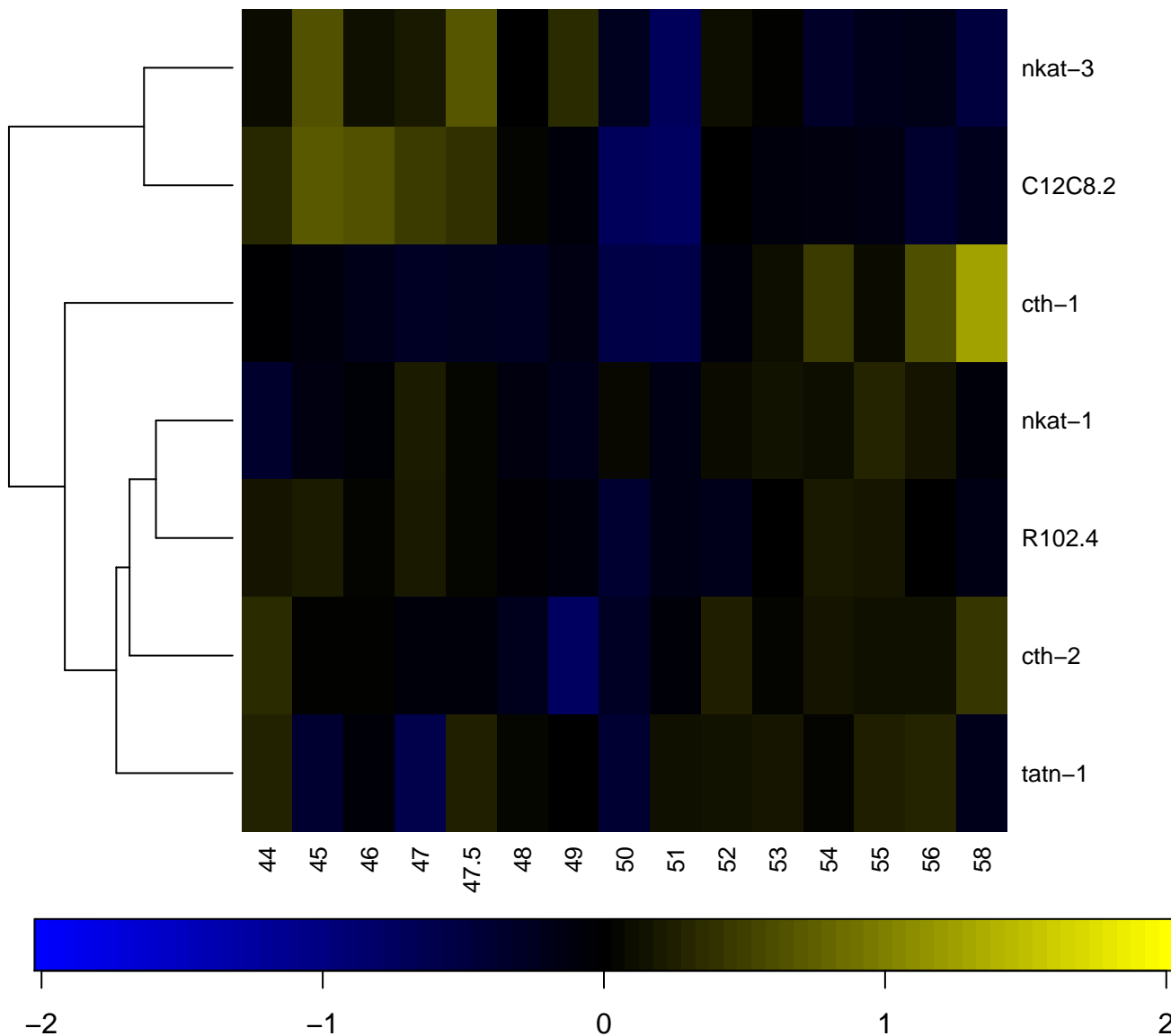
Cyclopropane-fatty-acyl-phospholipid/mycolic acid synthase



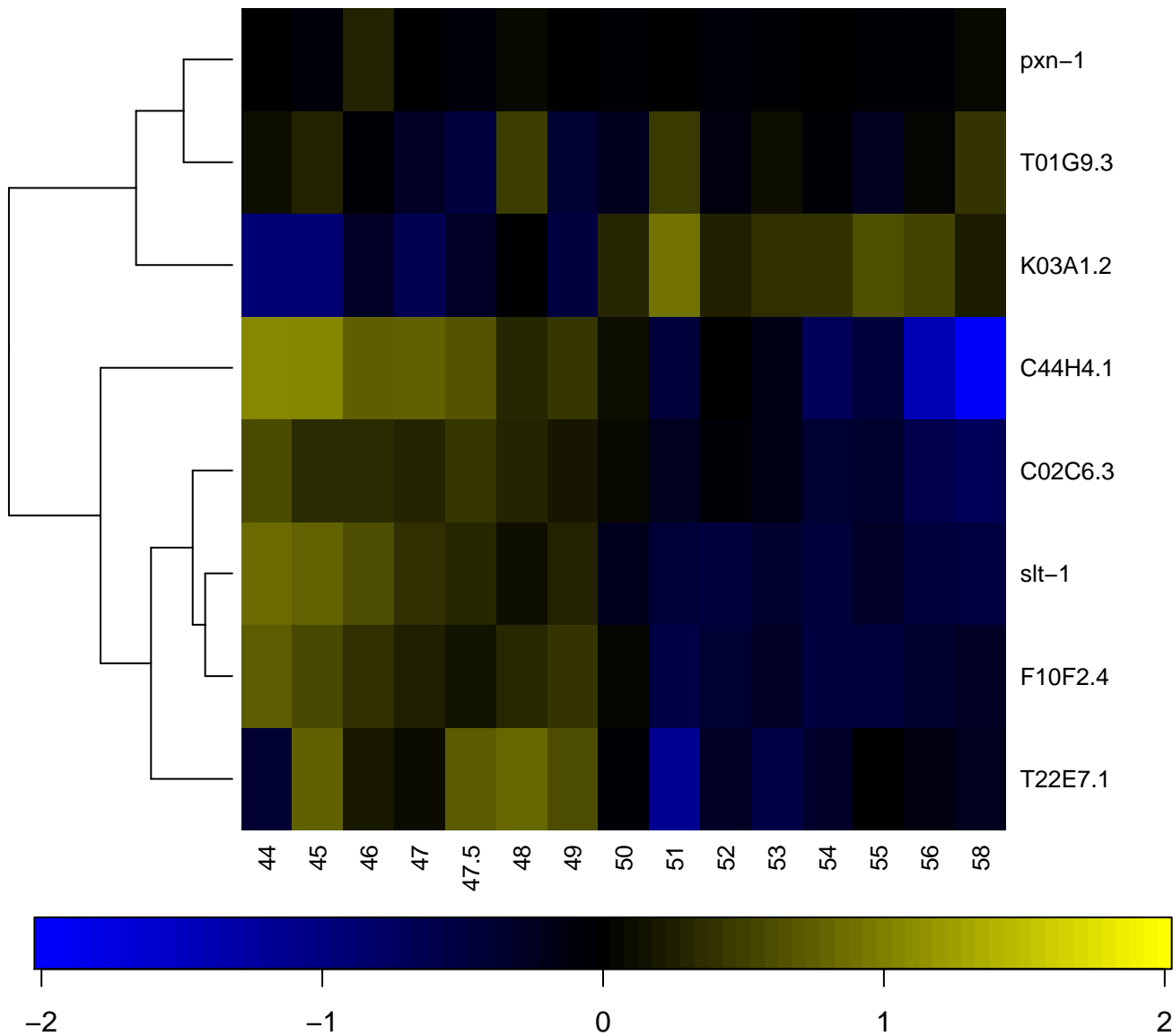
Cys/Met metabolism PLP-dependent enzyme



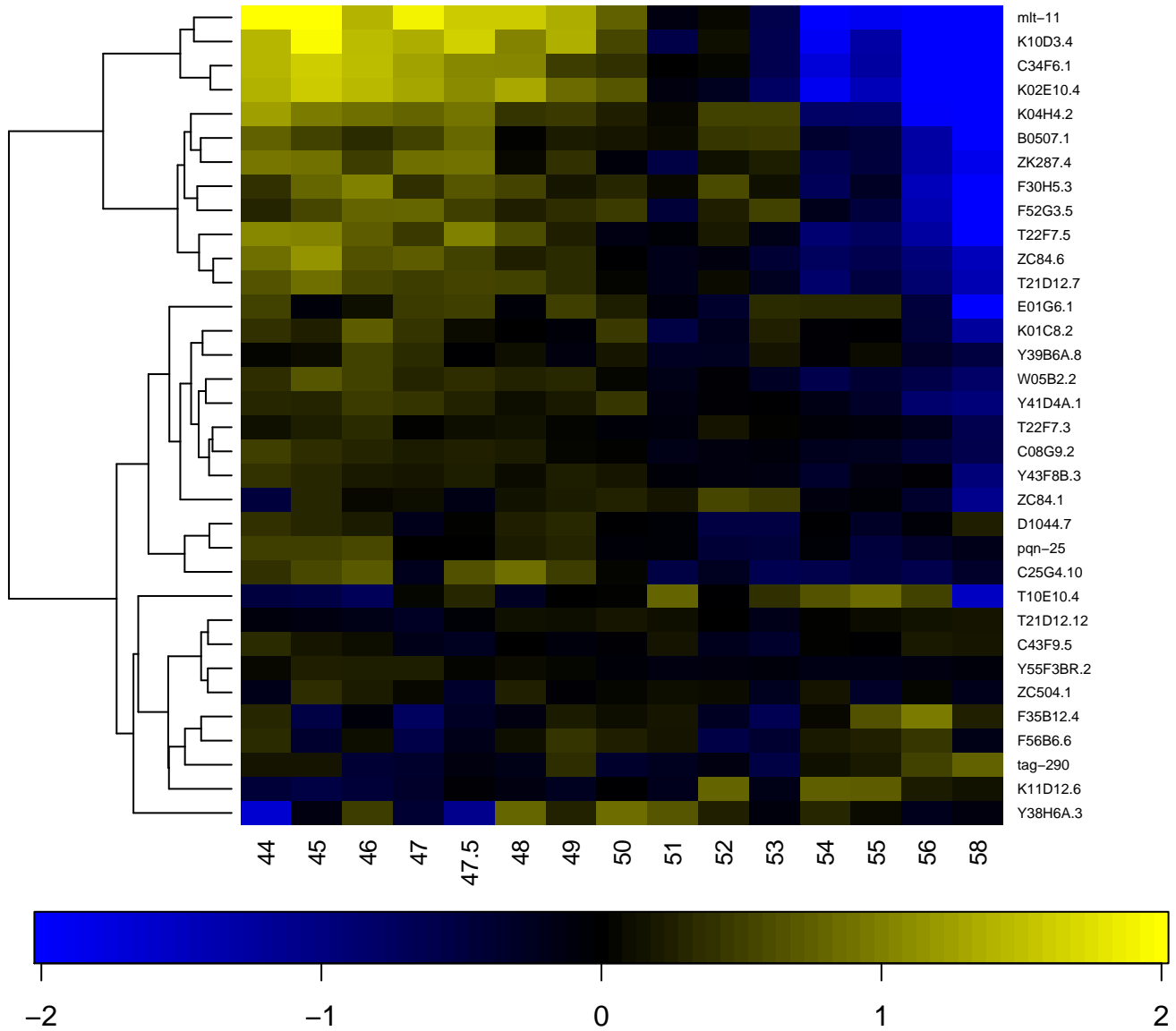
Cys/Met metabolism, pyridoxal phosphate–dependent enzyme



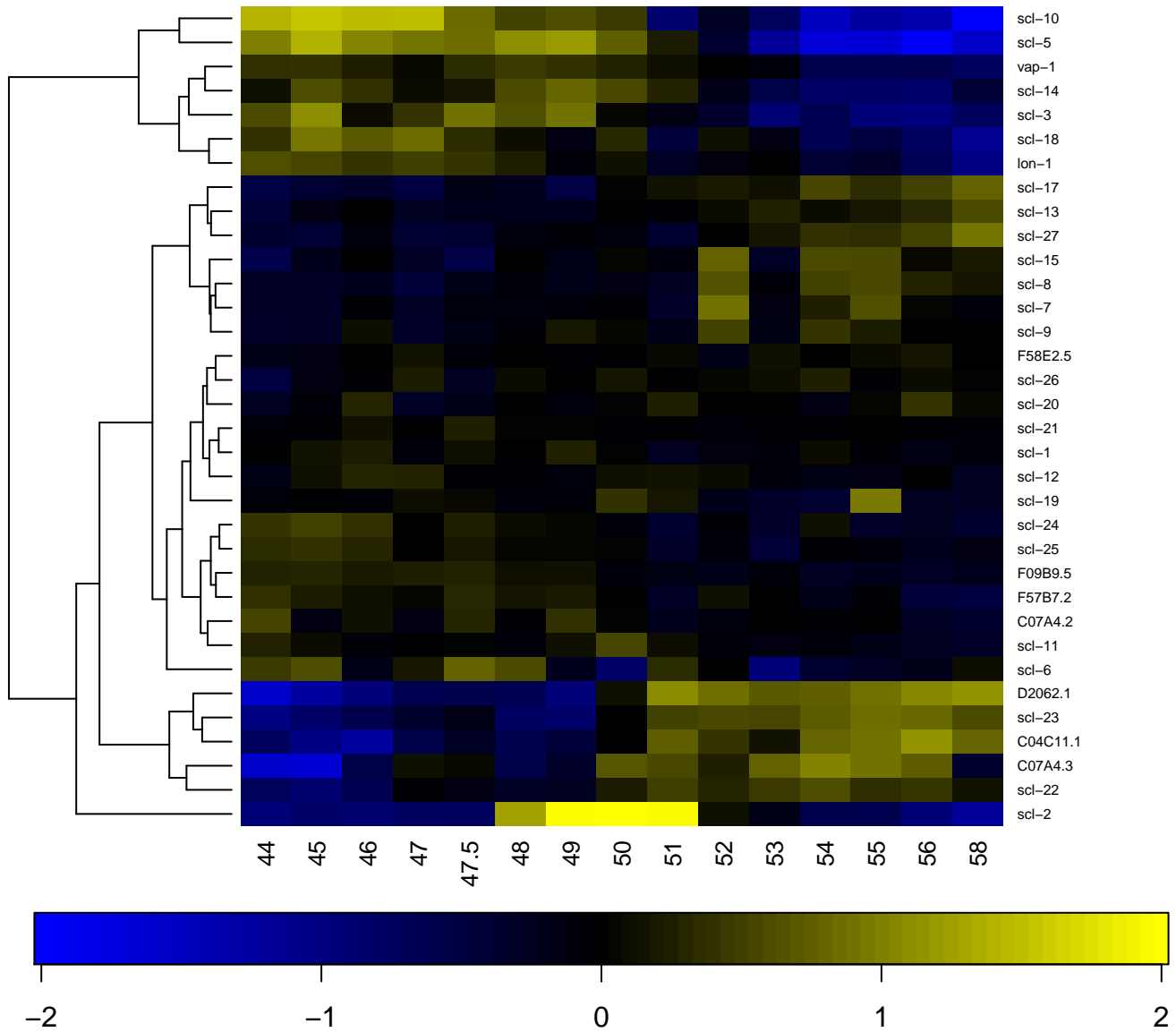
Cysteine-rich flanking region, C-terminal domain



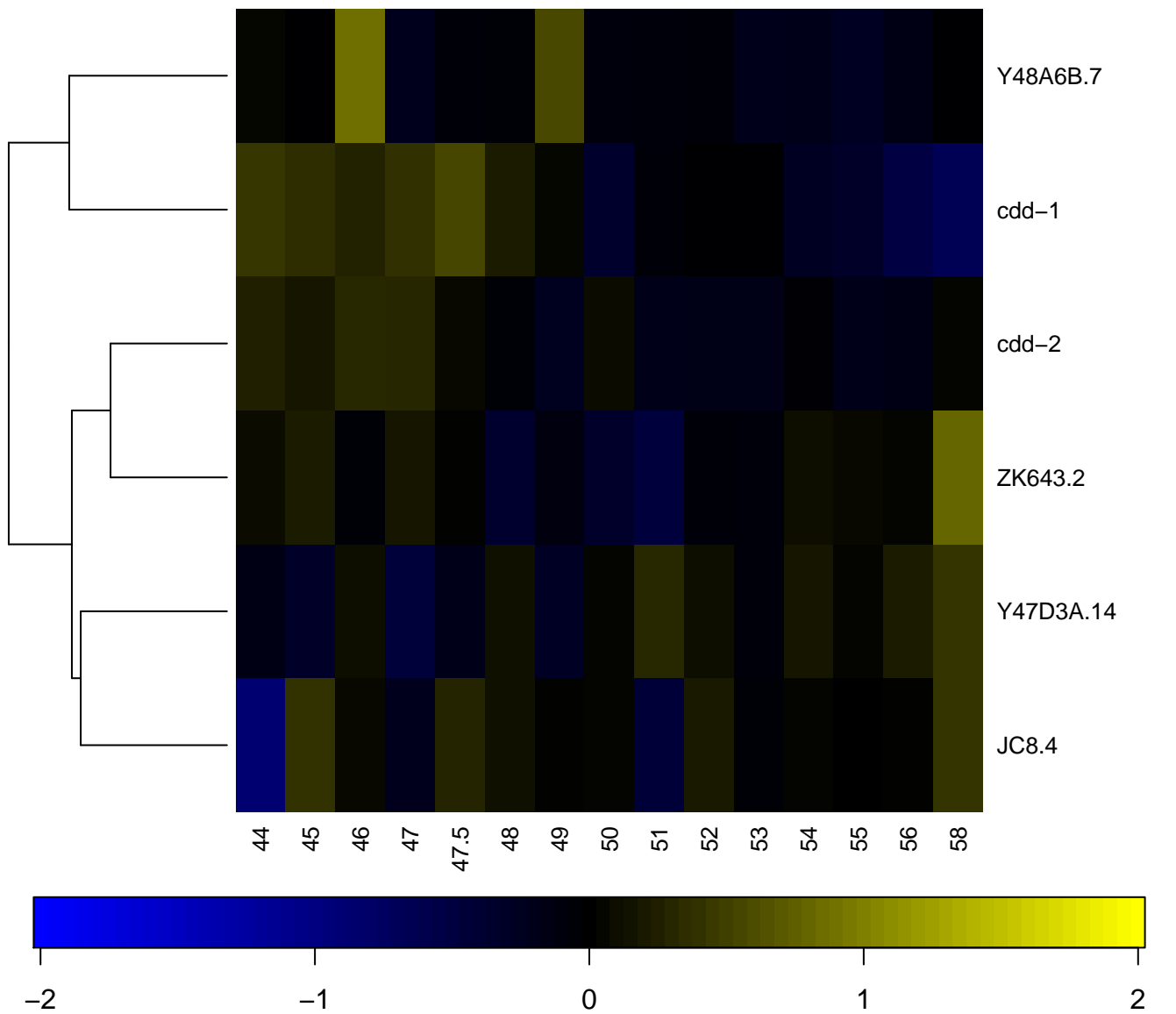
Cysteine-rich repeat



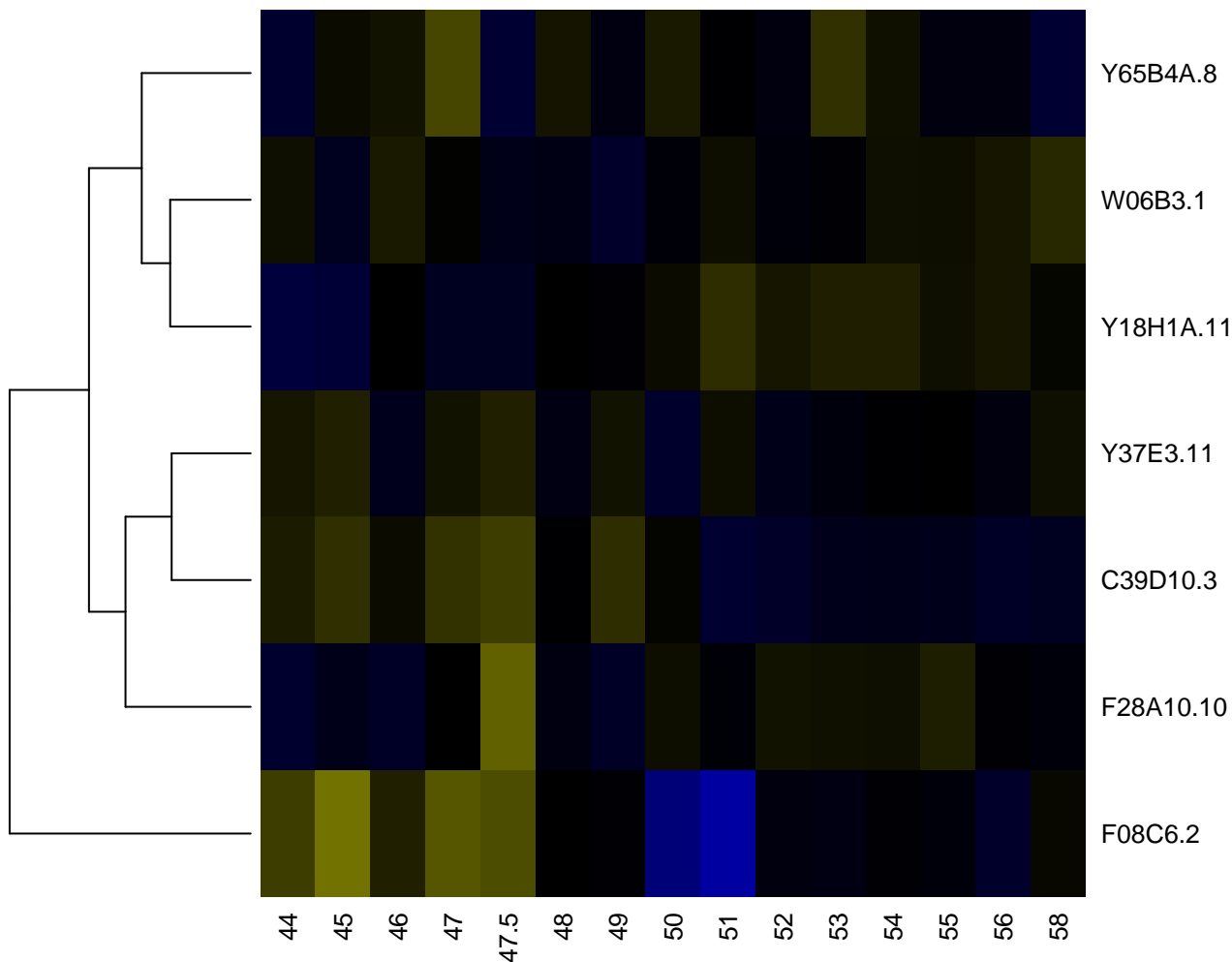
Cysteine-rich secretory protein family



Cytidine and deoxycytidylate deaminase zinc-binding region



Cytidyltransferase-related



-2

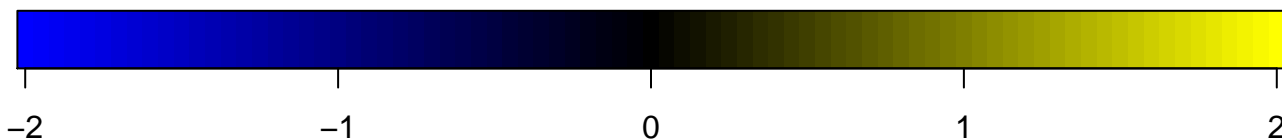
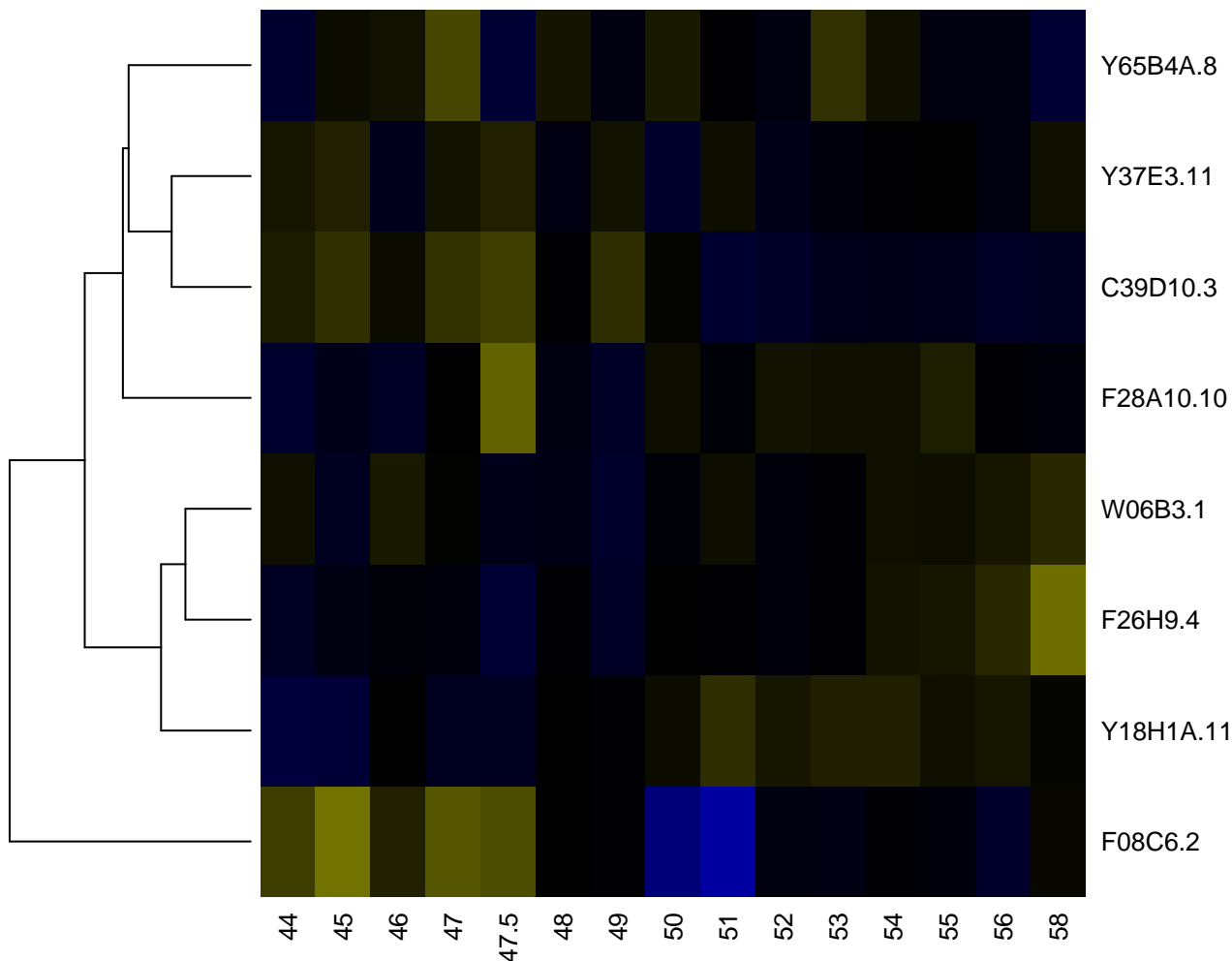
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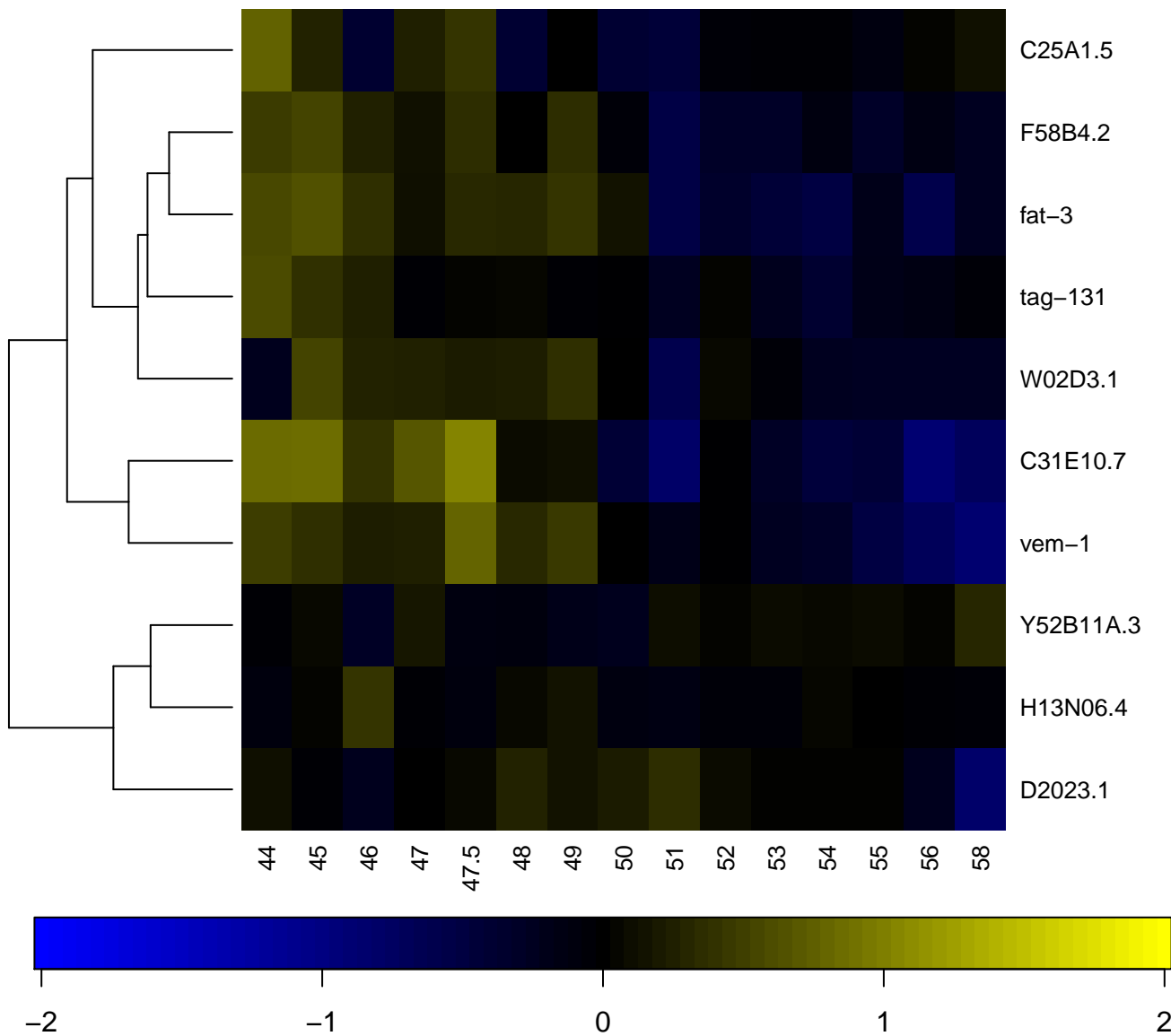
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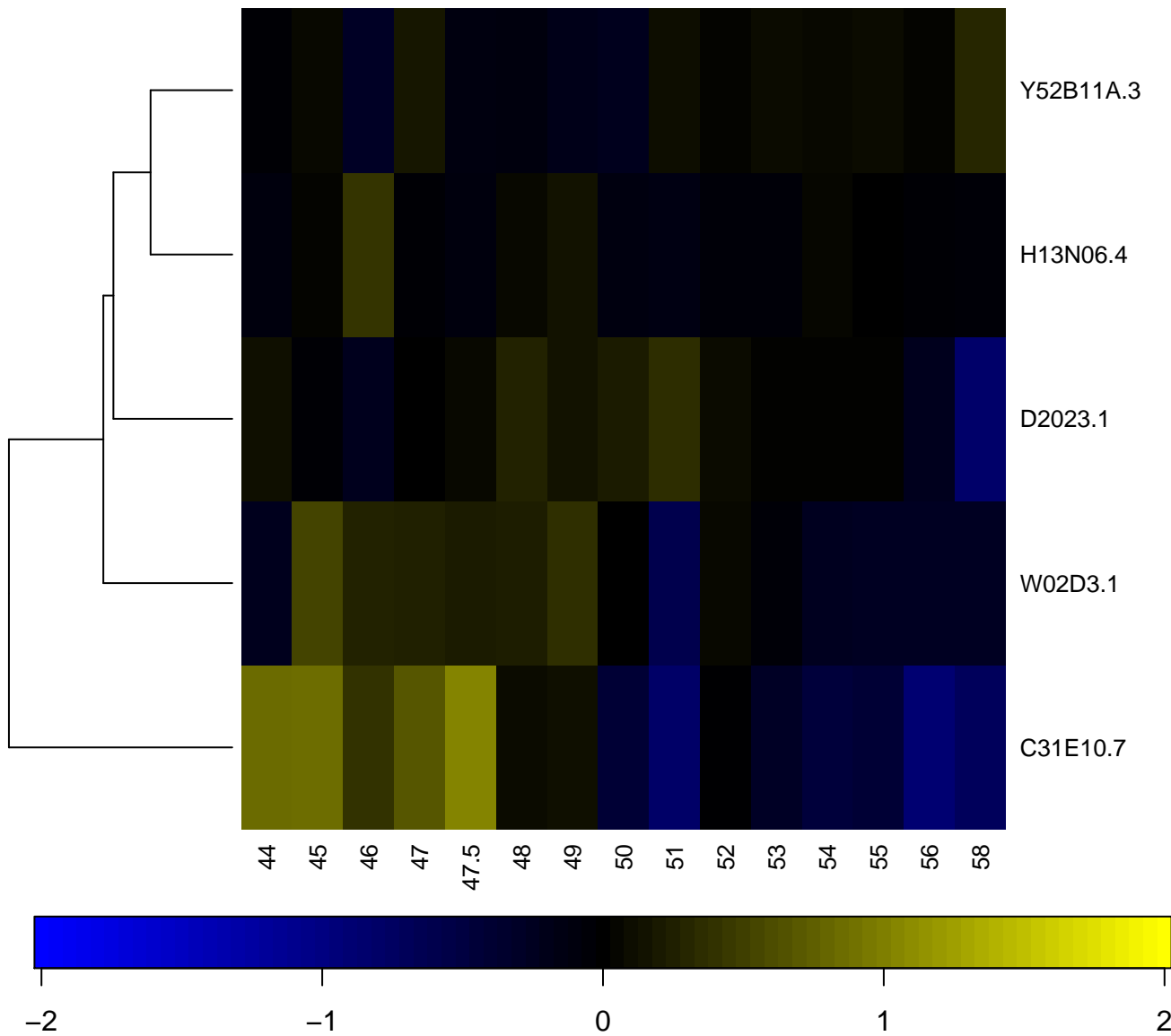
Cytidylyltransferase



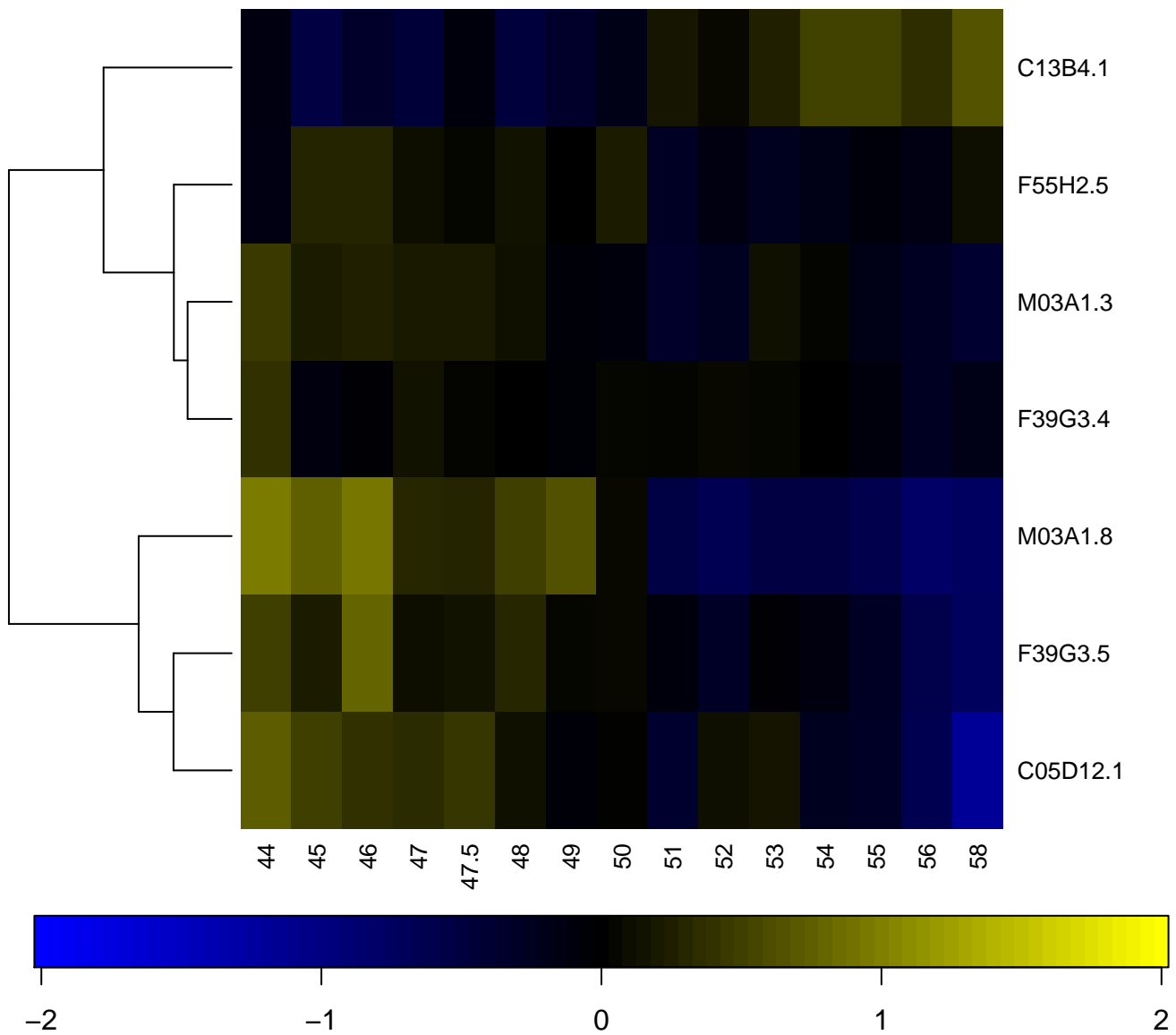
Cytochrome b5-like Heme/Steroid binding domain



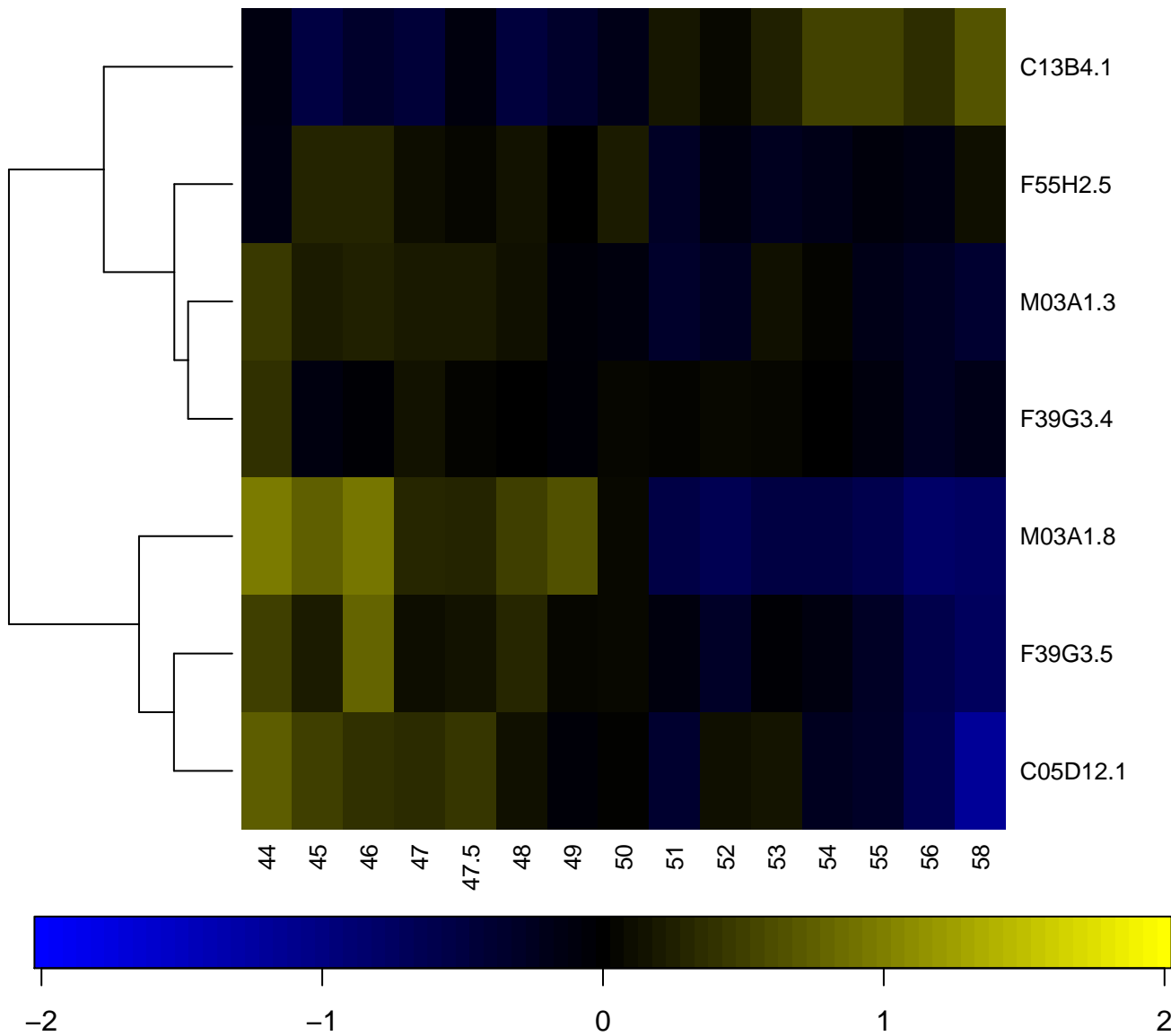
Cytochrome b5, heme-binding site



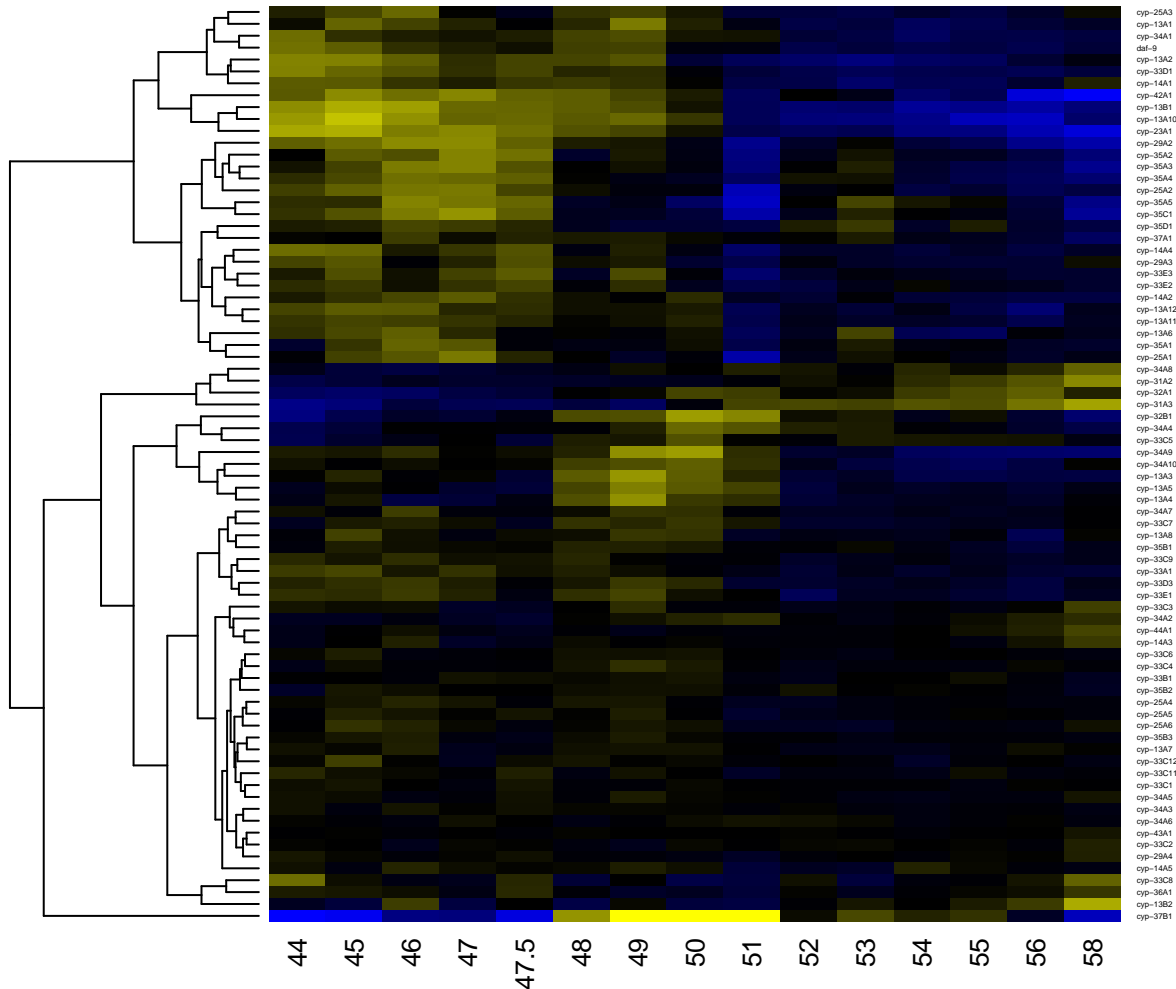
Cytochrome b561, eukaryote



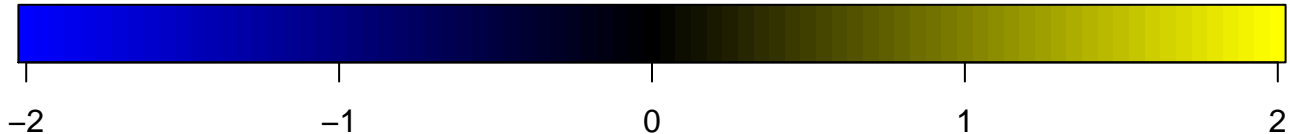
Cytochrome b561/ferric reductase transmembrane



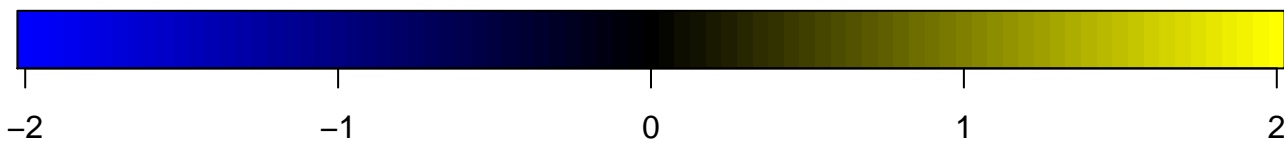
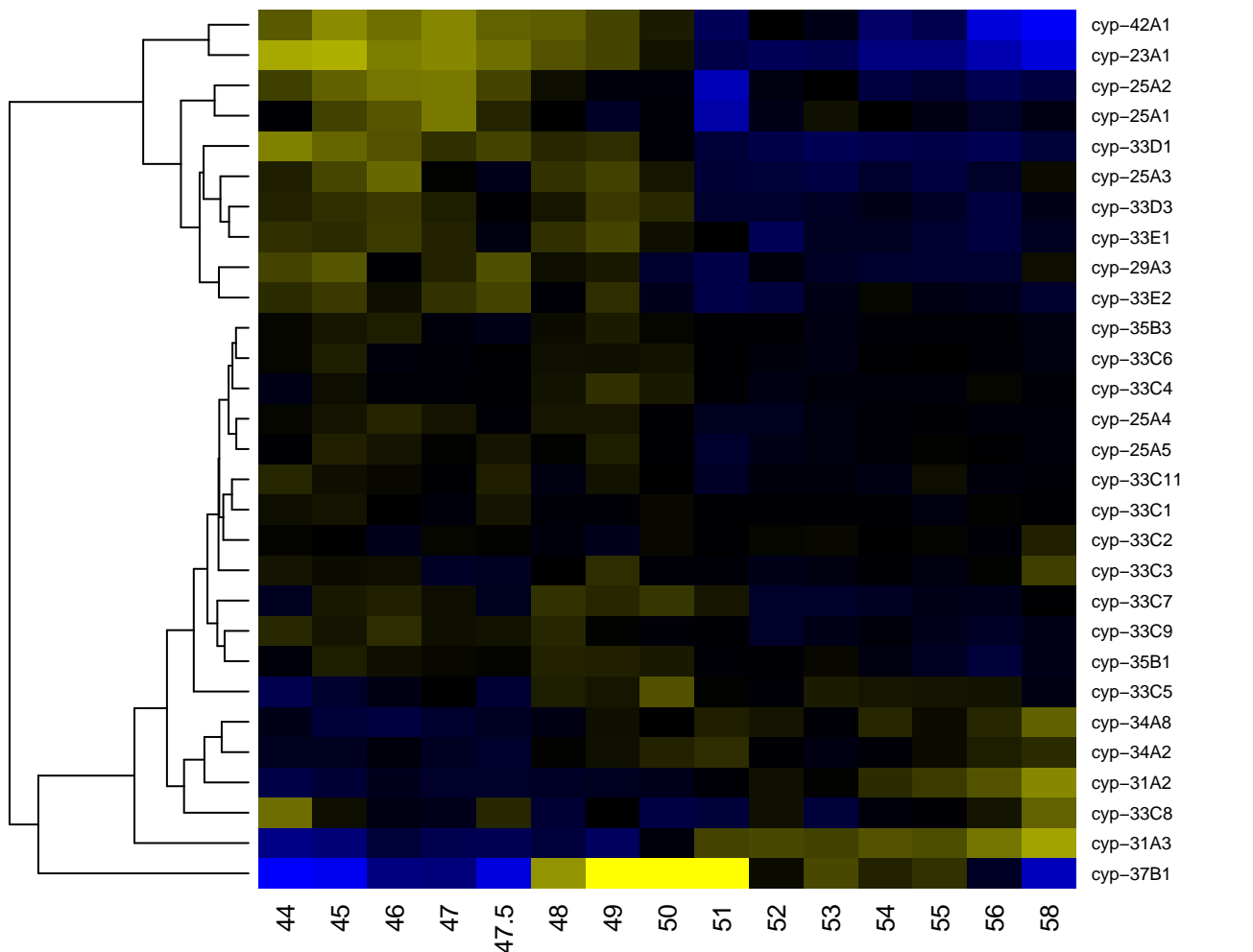
Cytochrome P450



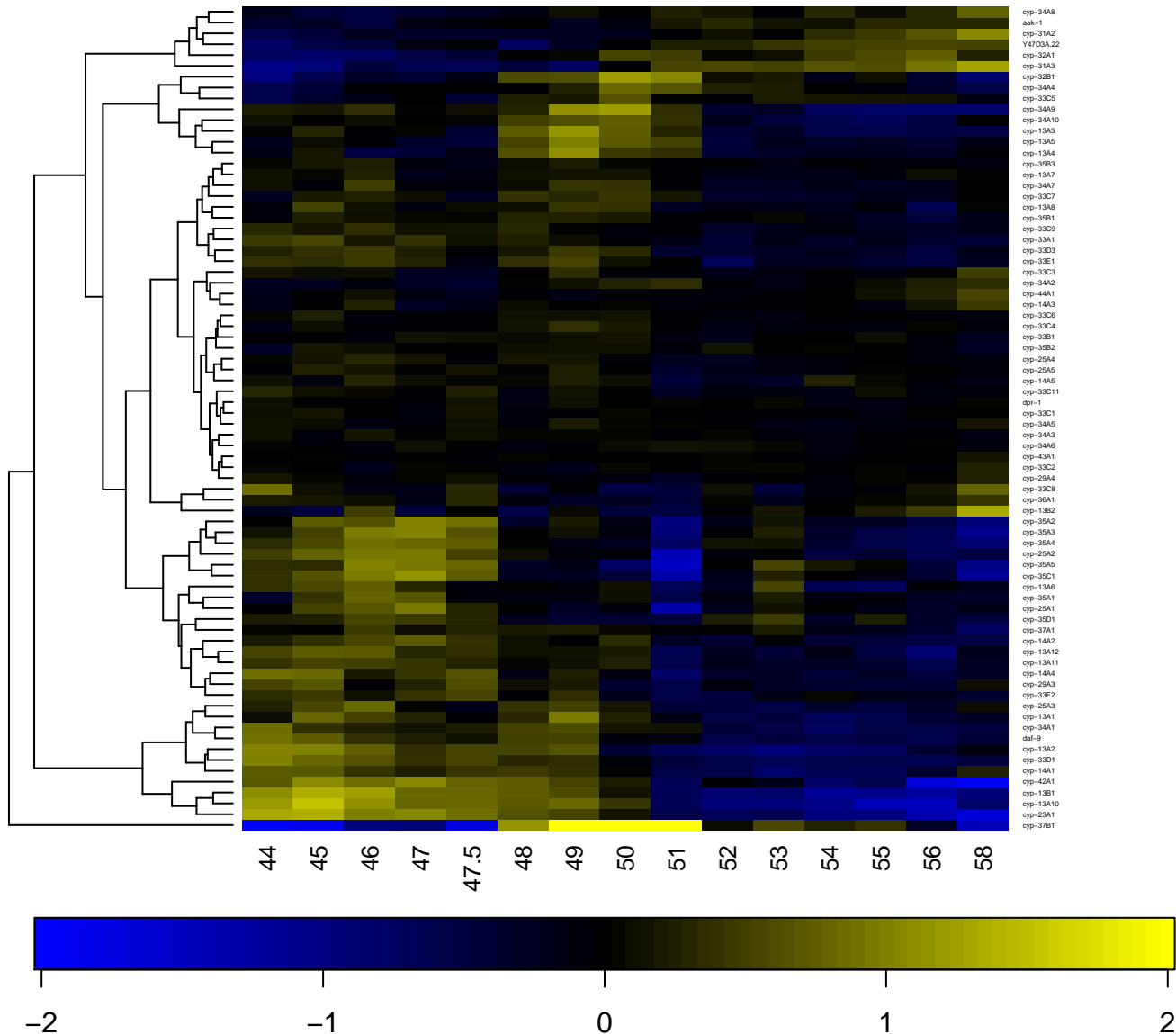
cyp-25A3
cyp-13A1
cyp-34A1
dab-9
cyp-13A2
cyp-33D1
cyp-14A1
cyp-42A1
cyp-13B1
cyp-13A10
cyp-23A1
cyp-29A2
cyp-35C2
cyp-35A3
cyp-35A4
cyp-25A2
cyp-35A6
cyp-35C1
cyp-35D1
cyp-37A1
cyp-14A4
cyp-29A3
cyp-33E3
cyp-33E2
cyp-14A2
cyp-13A12
cyp-13A11
cyp-13A6
cyp-35A1
cyp-25A1
cyp-34A8
cyp-31A2
cyp-32A1
cyp-31A3
cyp-32B1
cyp-34A4
cyp-33C5
cyp-34A9
cyp-34A10
cyp-13A3
cyp-13A5
cyp-13A4
cyp-34A7
cyp-33C7
cyp-13A8
cyp-35B1
cyp-33C9
cyp-33A1
cyp-33D3
cyp-33E1
cyp-33C3
cyp-34A2
cyp-44A1
cyp-14A3
cyp-33C6
cyp-33C4
cyp-33B1
cyp-35B2
cyp-25A4
cyp-25A5
cyp-25A6
cyp-35B3
cyp-13A7
cyp-33C12
cyp-33C11
cyp-33C1
cyp-34A5
cyp-34A3
cyp-34A6
cyp-43A1
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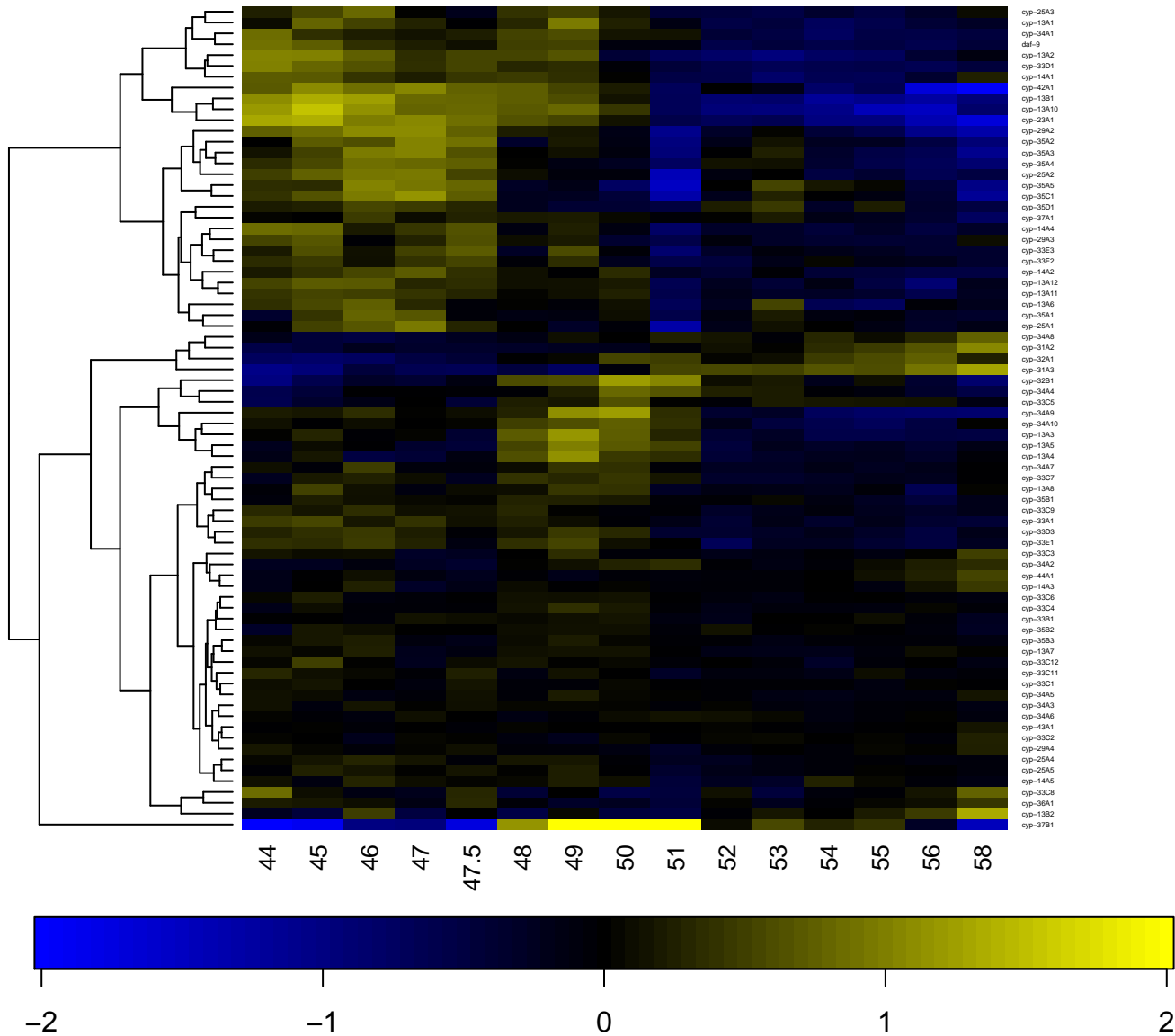
Cytochrome P450, B-class



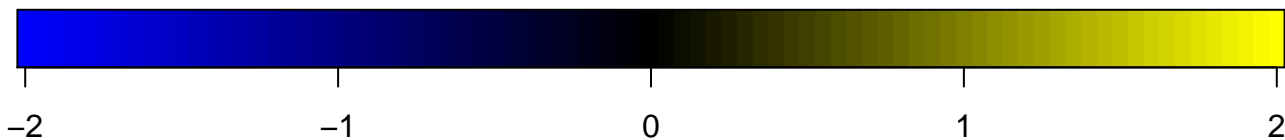
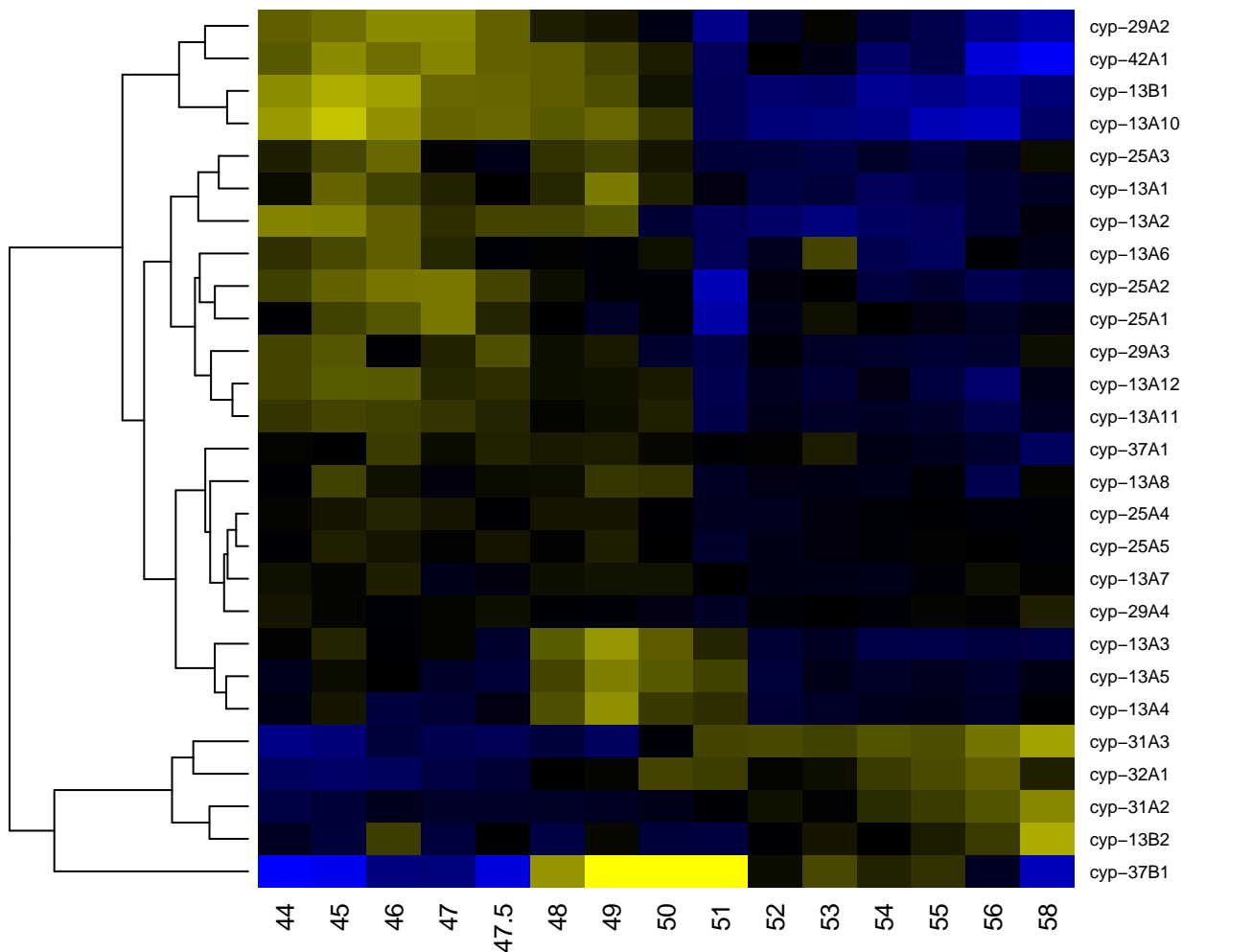
Cytochrome P450, conserved site



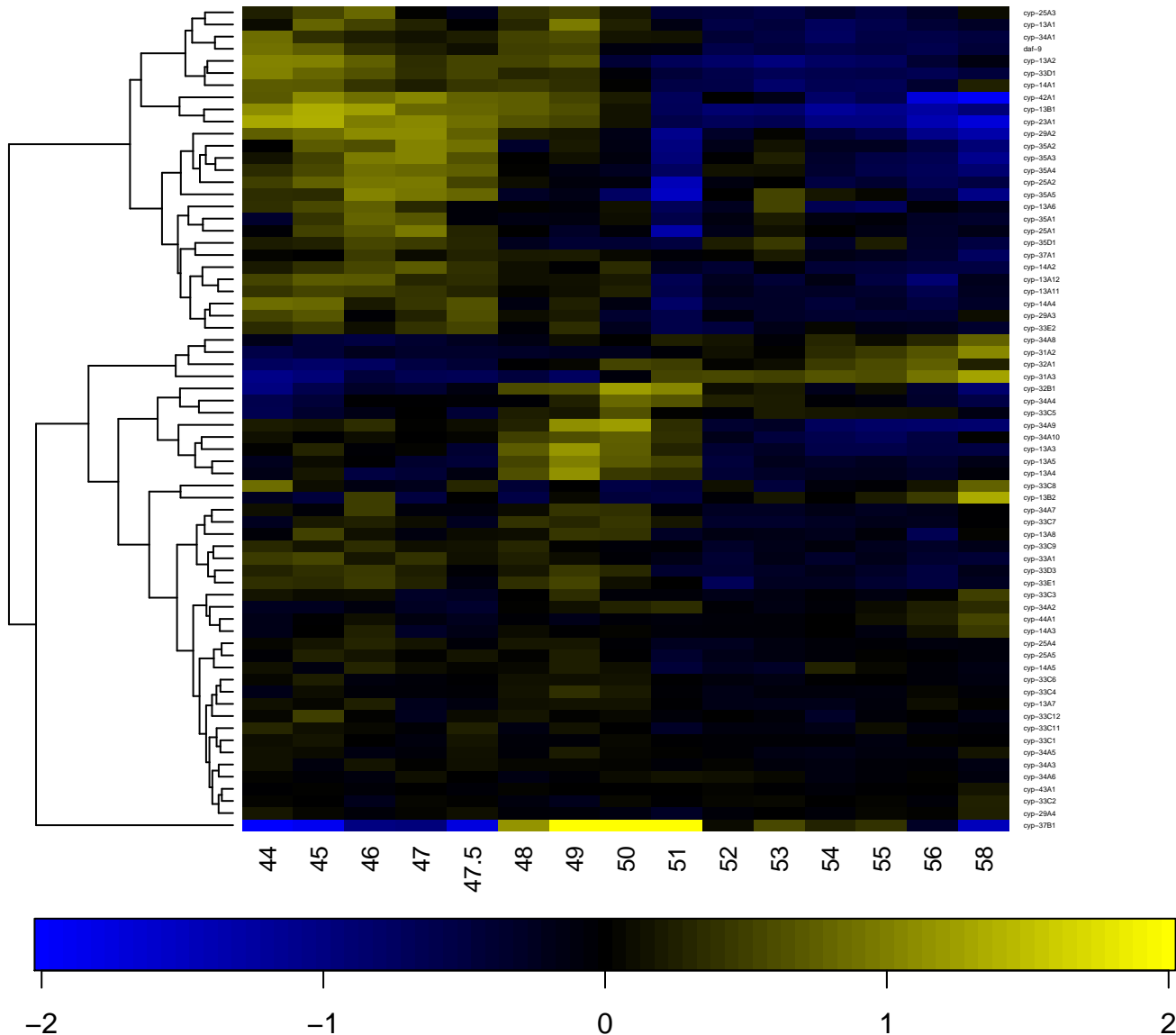
Cytochrome P450, E-class, group I



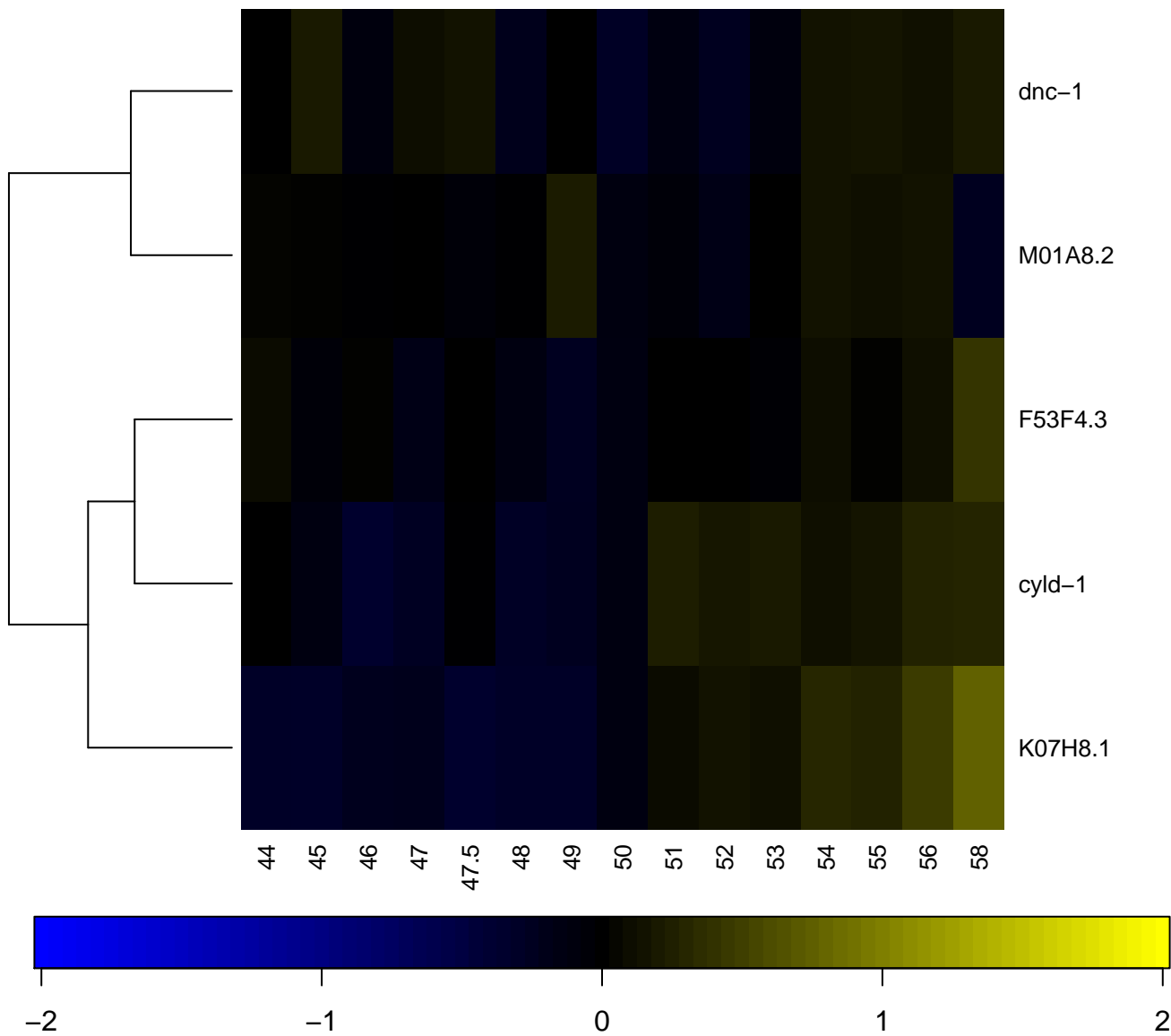
Cytochrome P450, E-class, group II



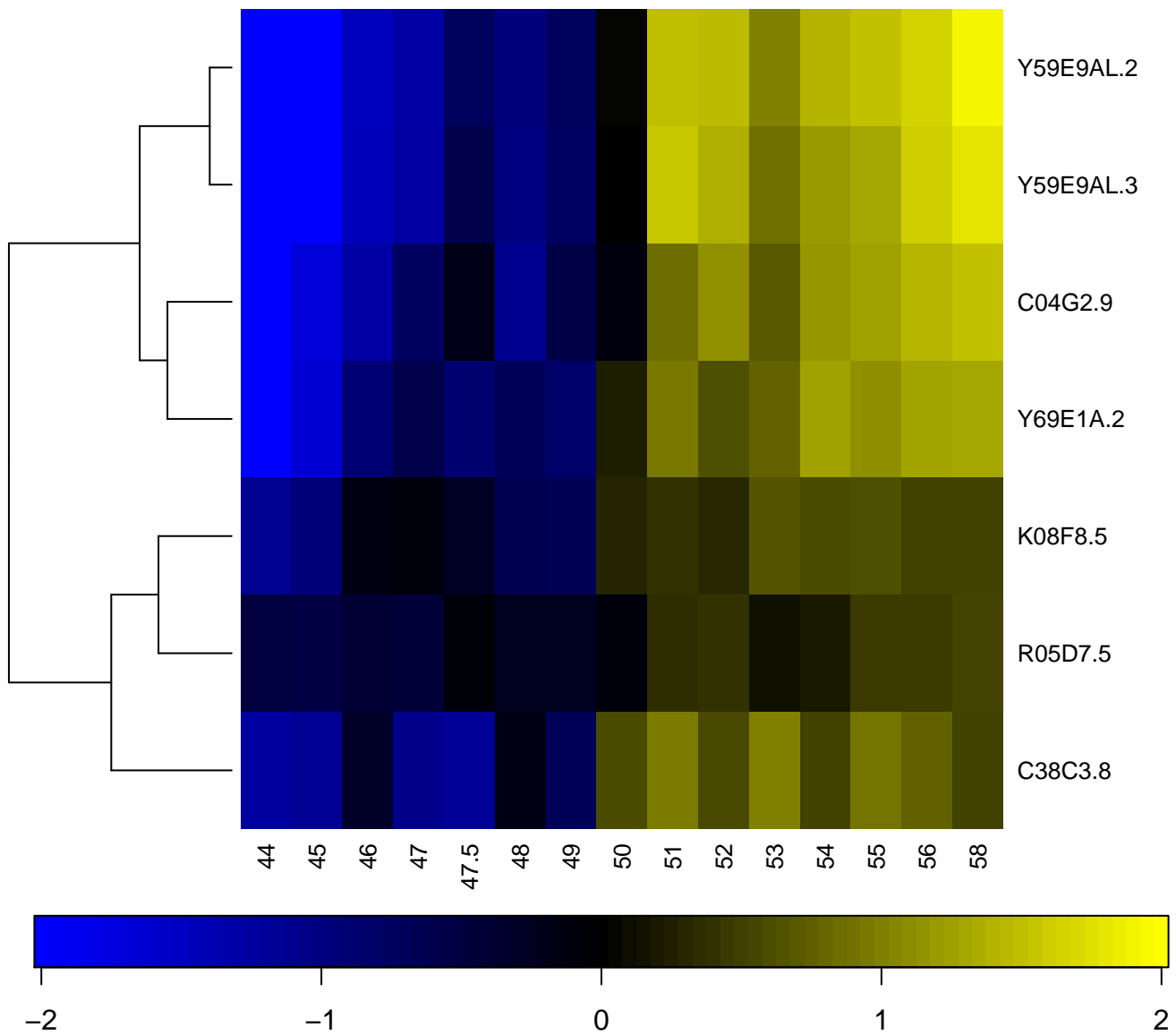
Cytochrome P450, E-class, group IV



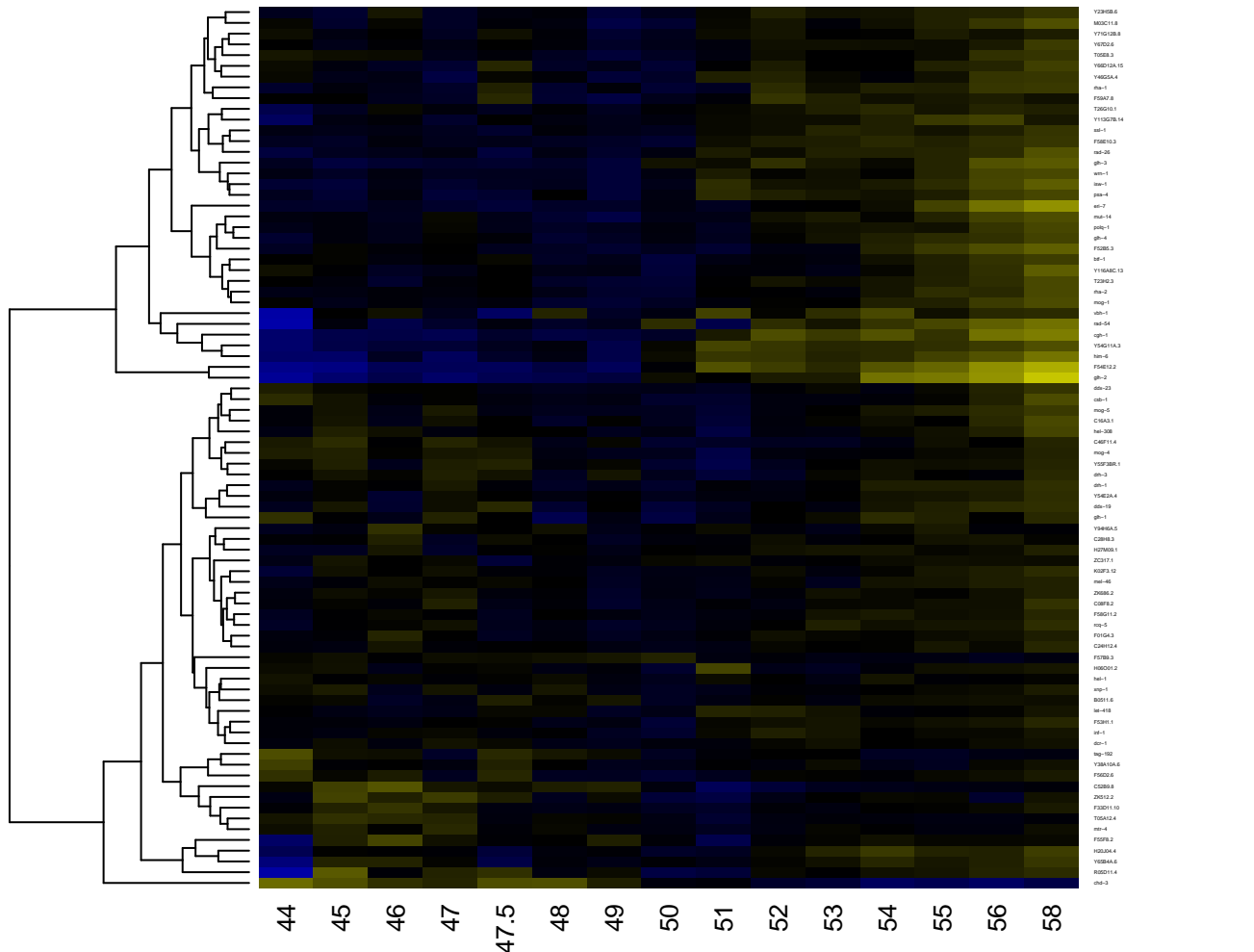
Cytoskeleton-associated protein, CAP-Gly



Cytosolic motility protein



DEAD-like helicase, N-terminal



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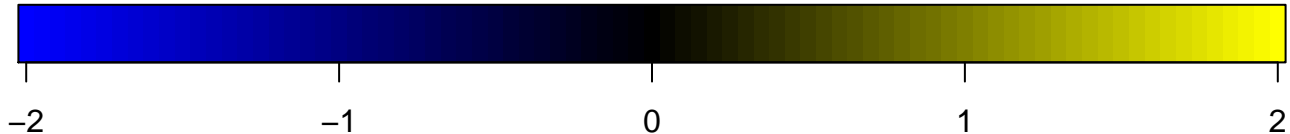
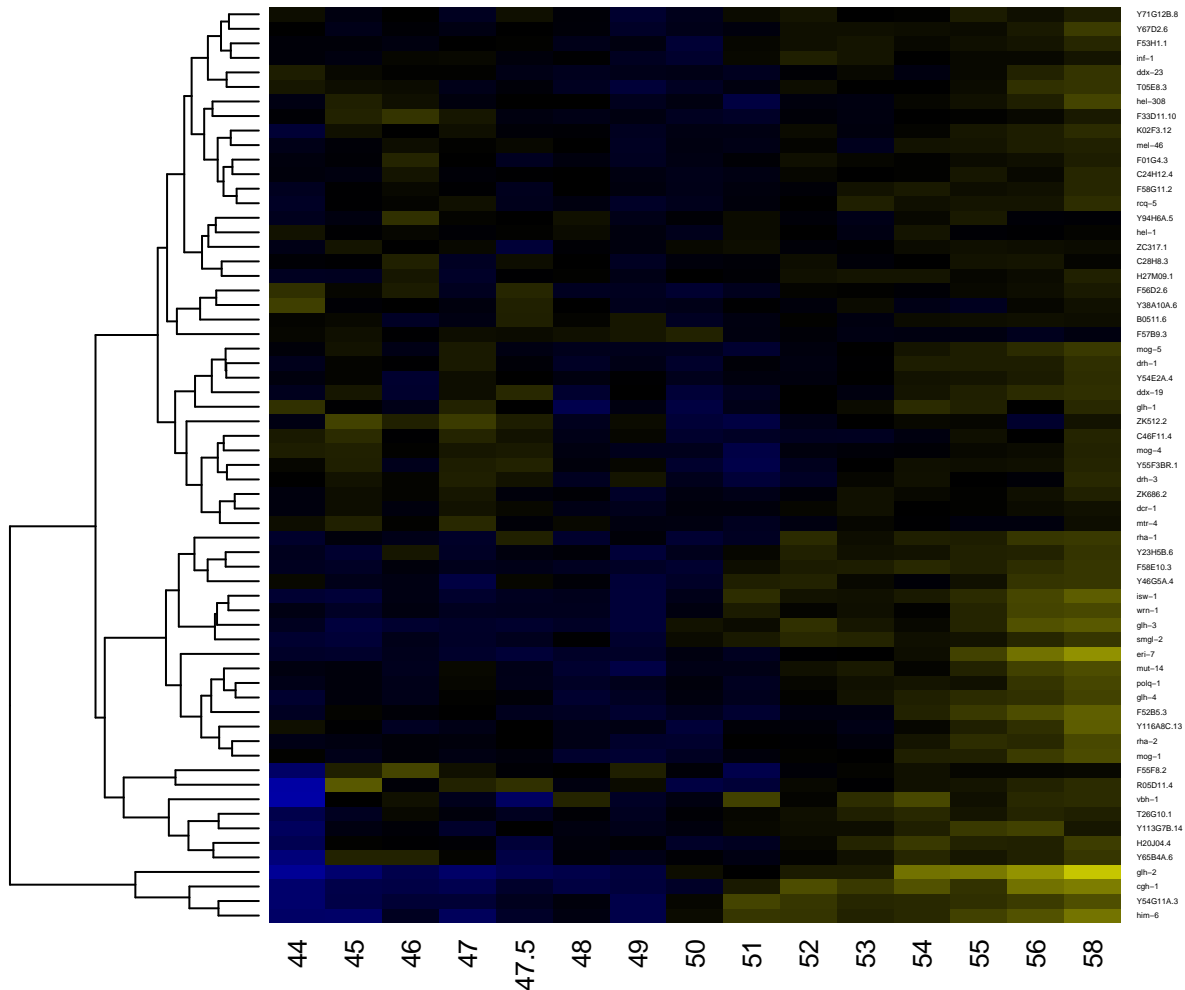
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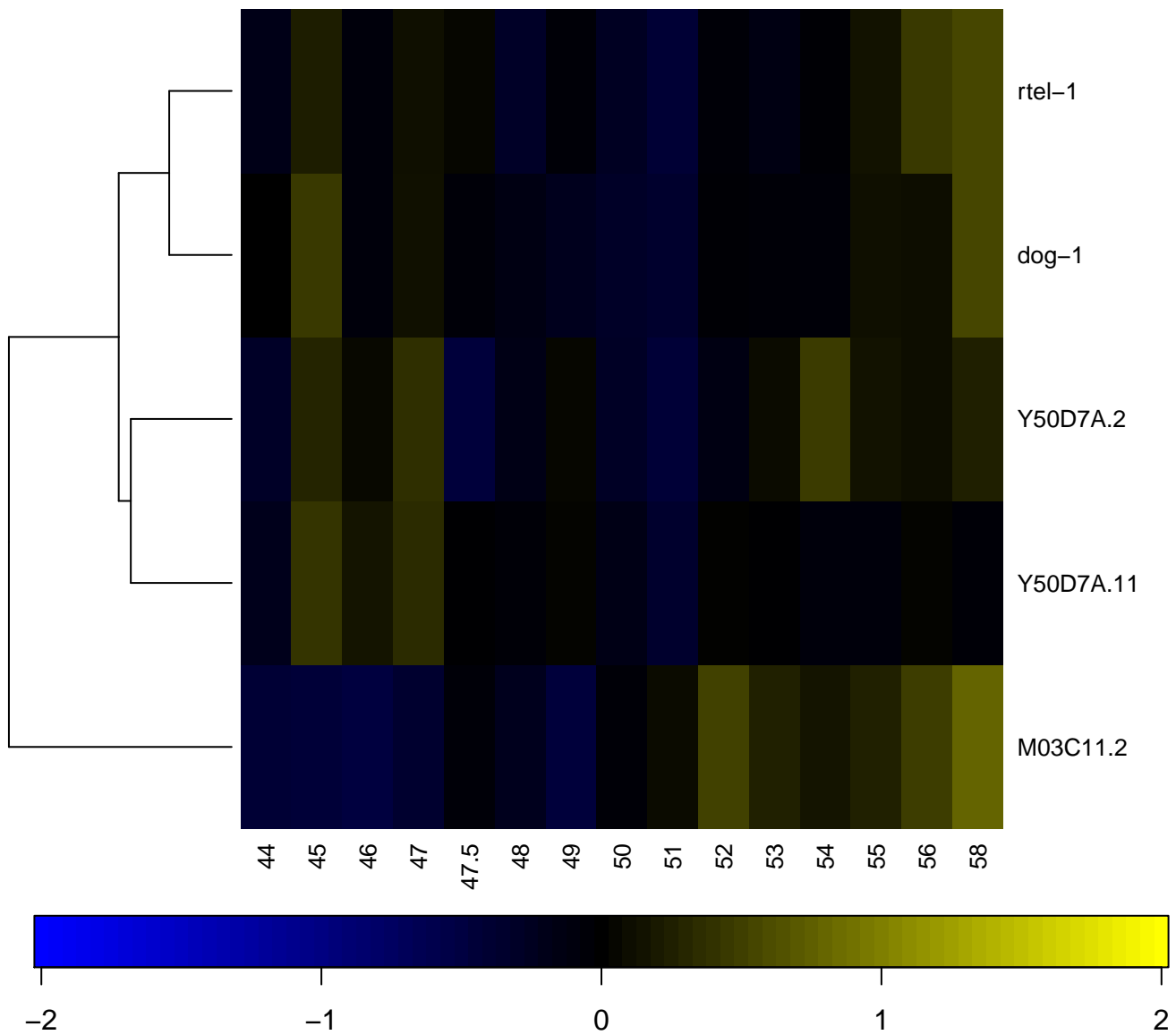
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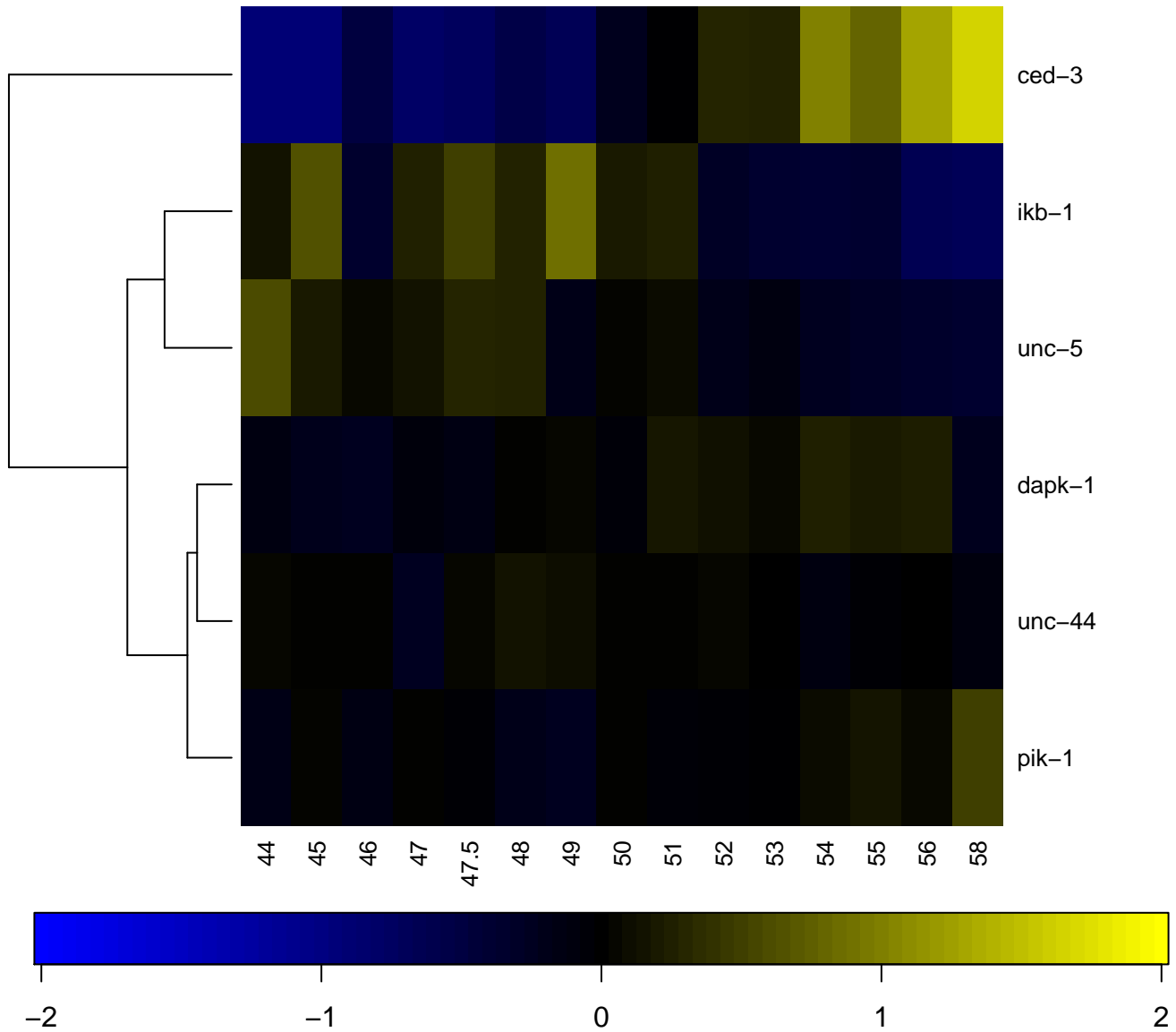
DEAD/DEAH box helicase



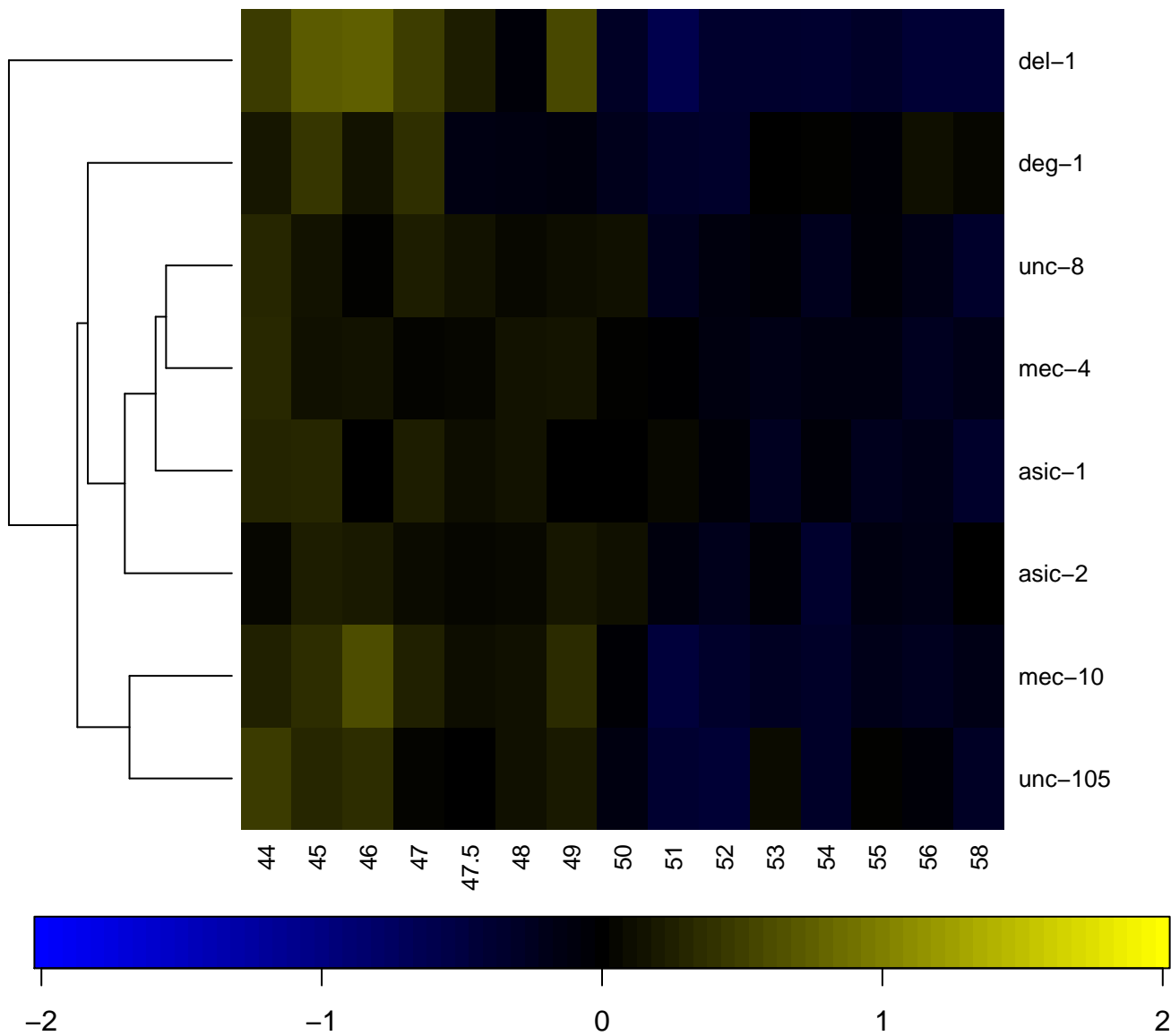
DEAD2



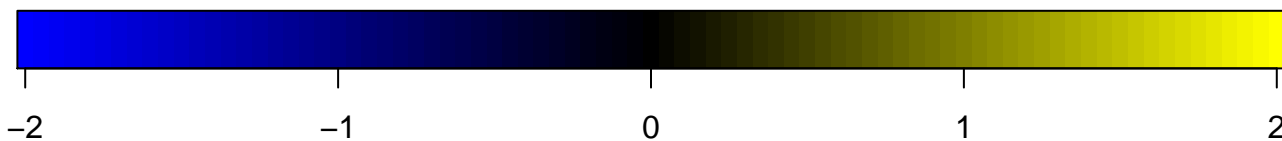
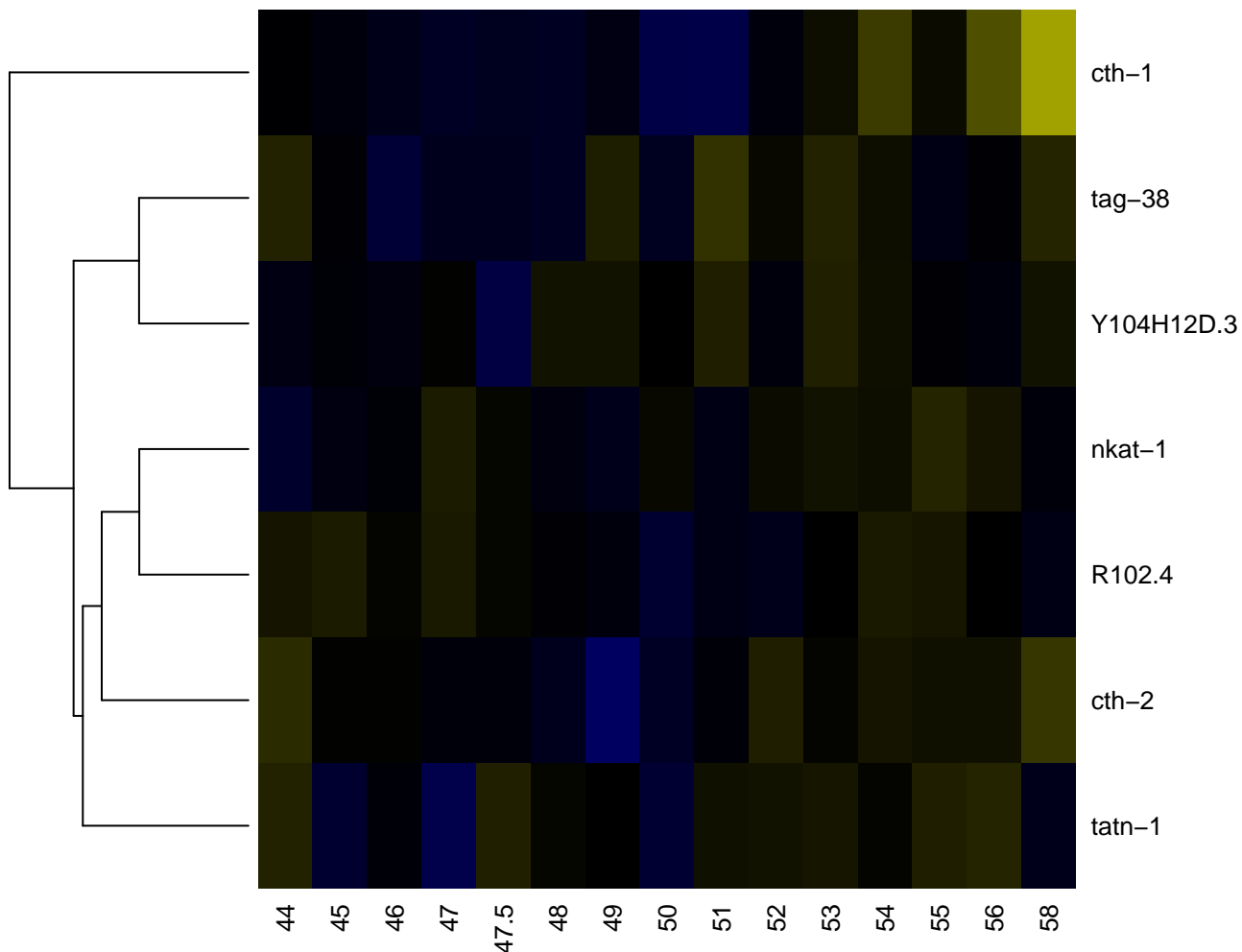
DEATH-like



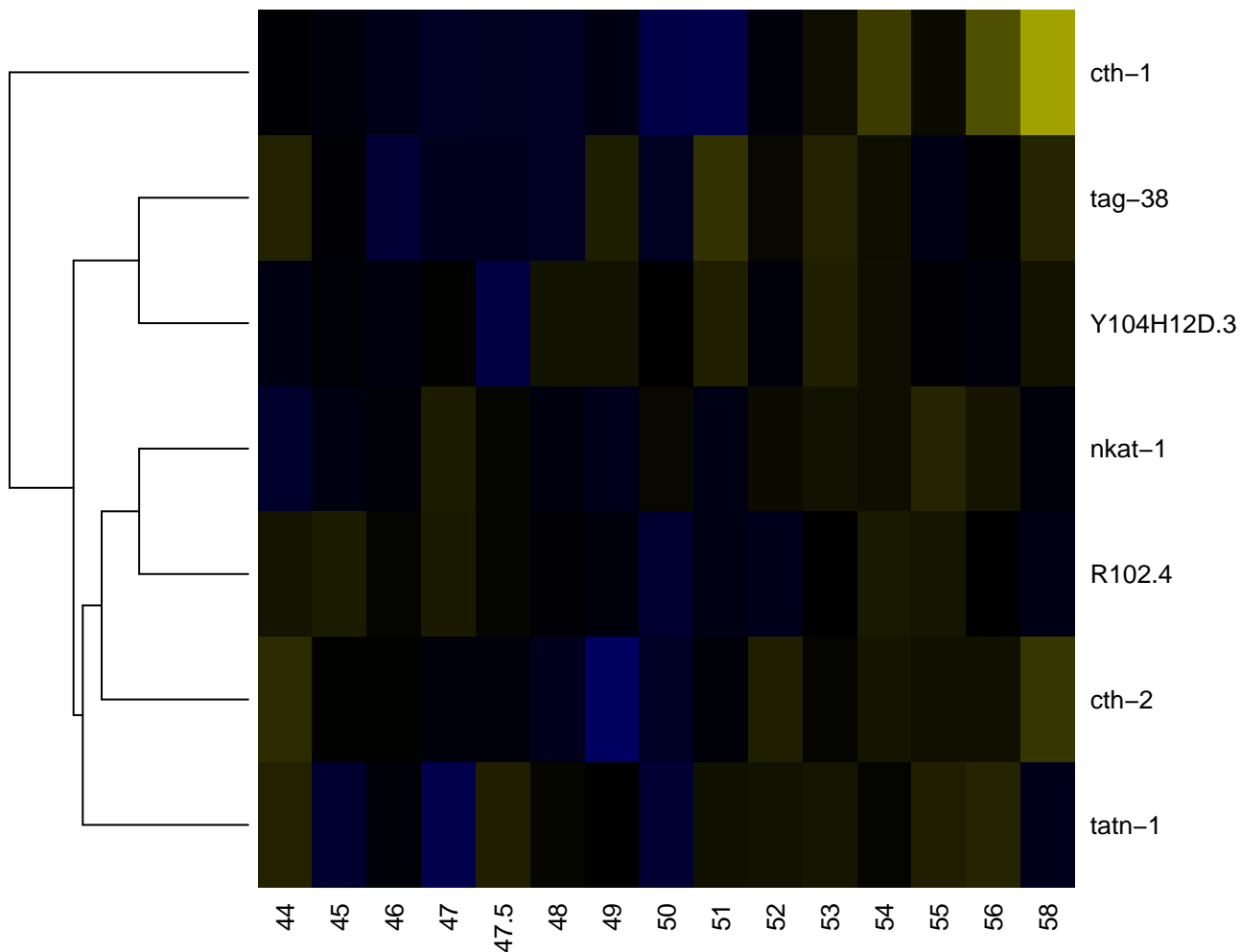
Degenerin



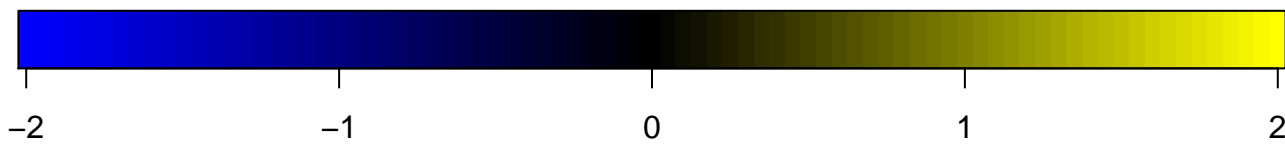
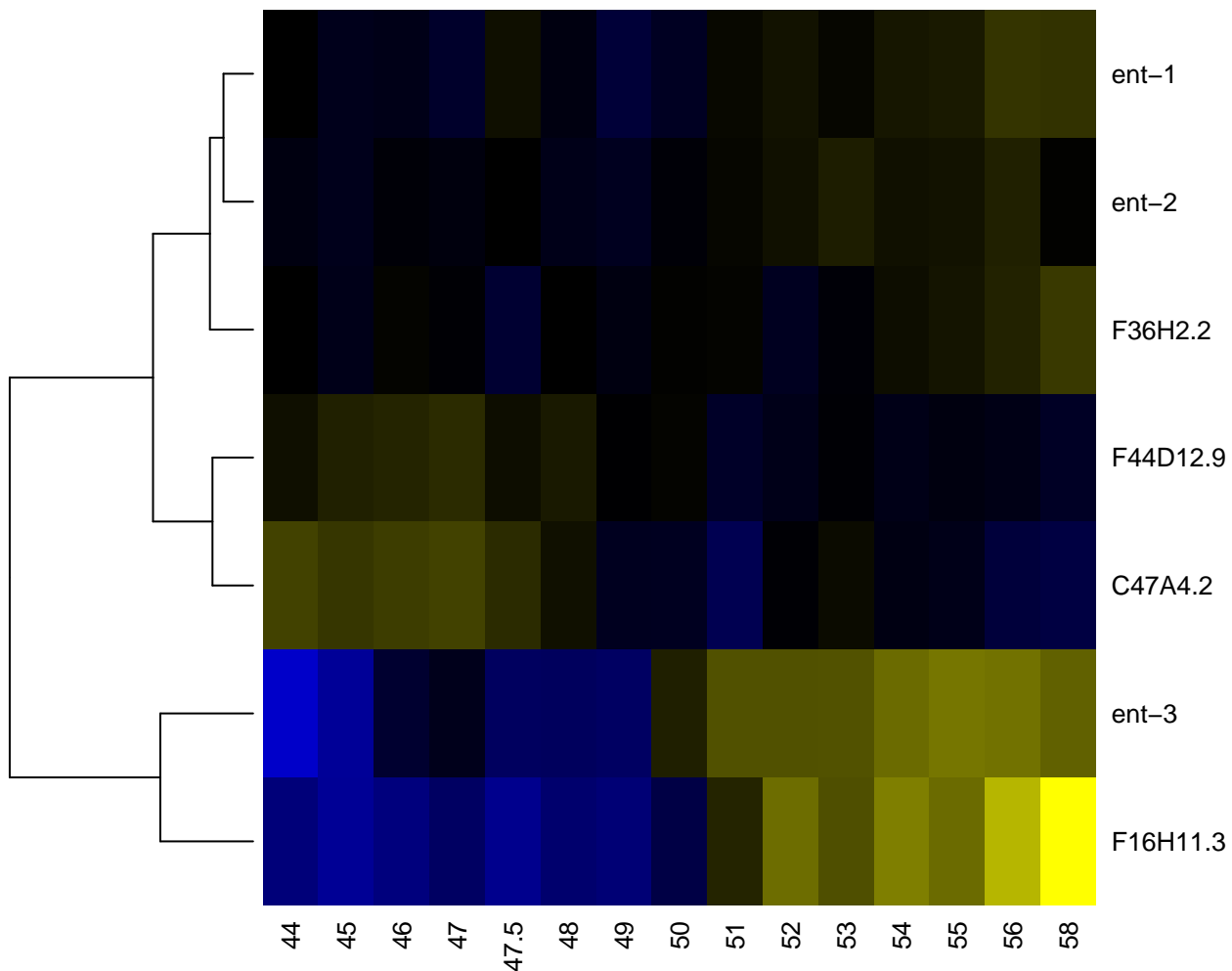
DegT/DnrJ/EryC1/StrS aminotransferase



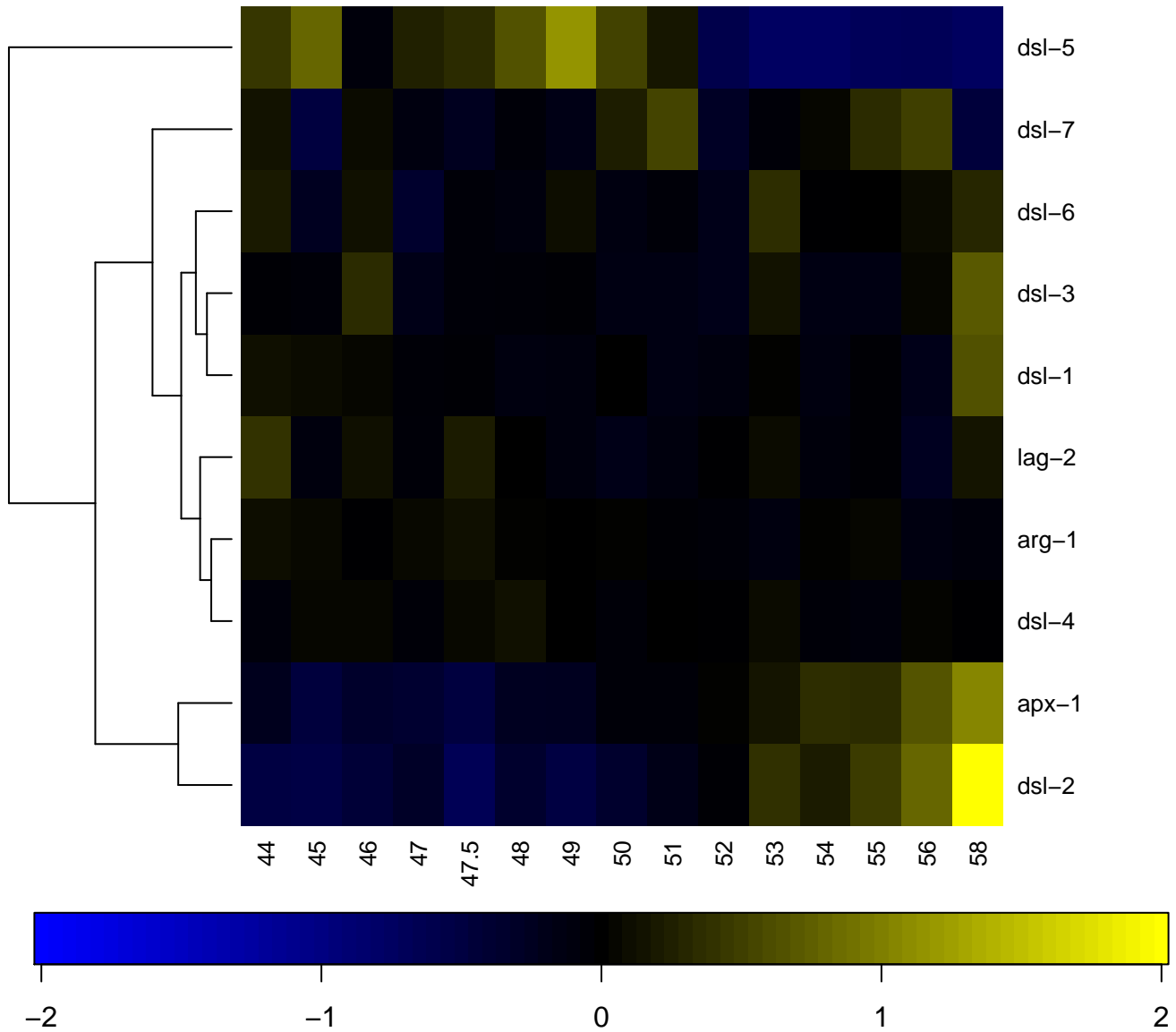
DegT/DnrJ/EryC1/StrS aminotransferase family



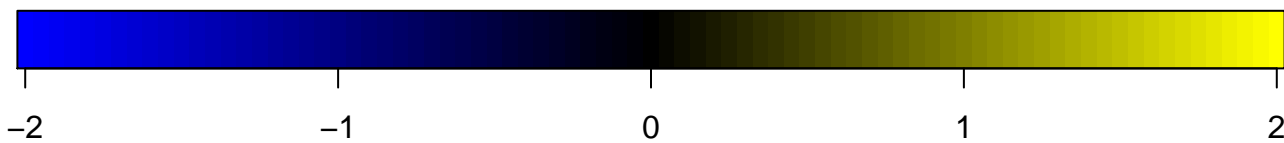
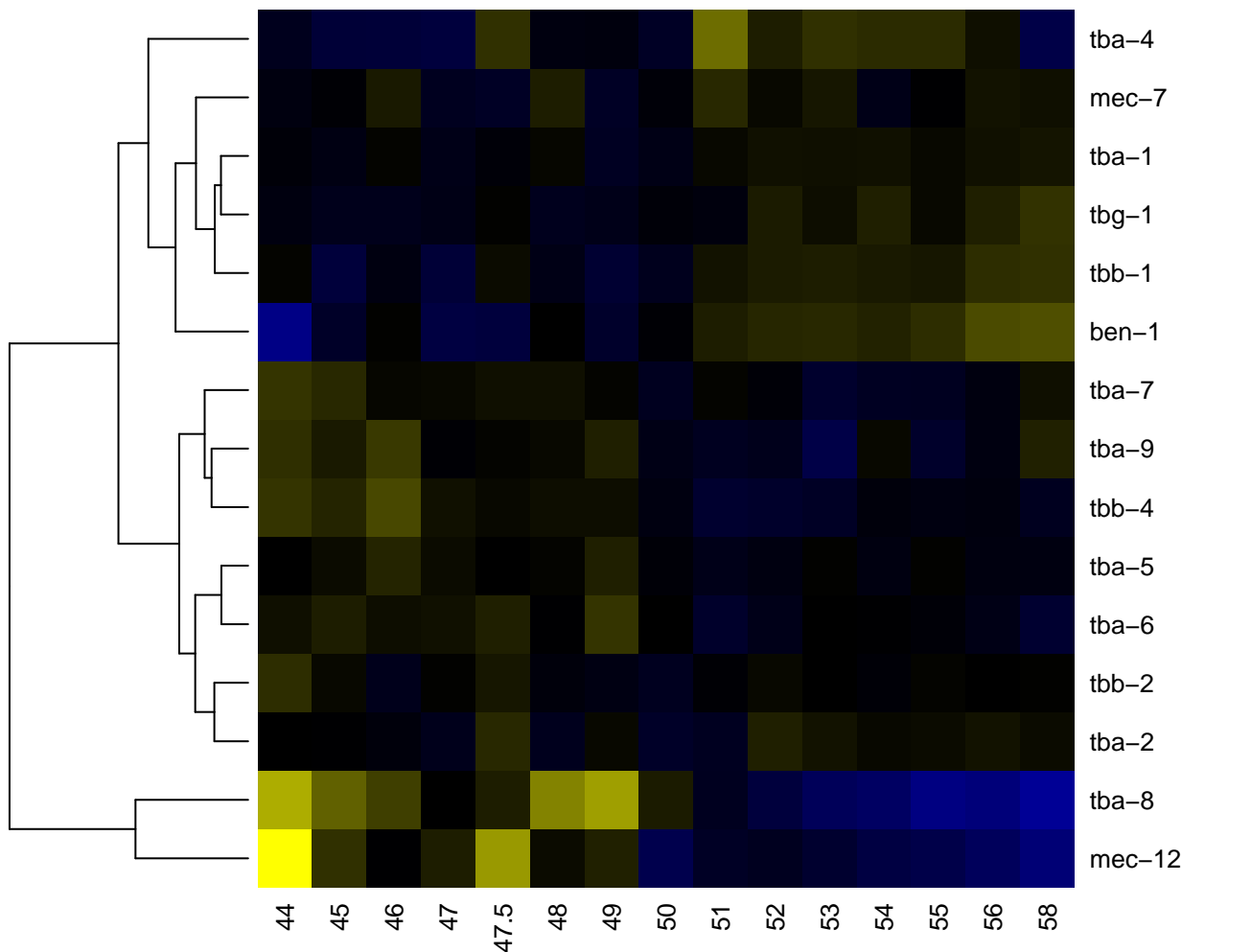
Delayed-early response protein/equilibrative nucleoside transp



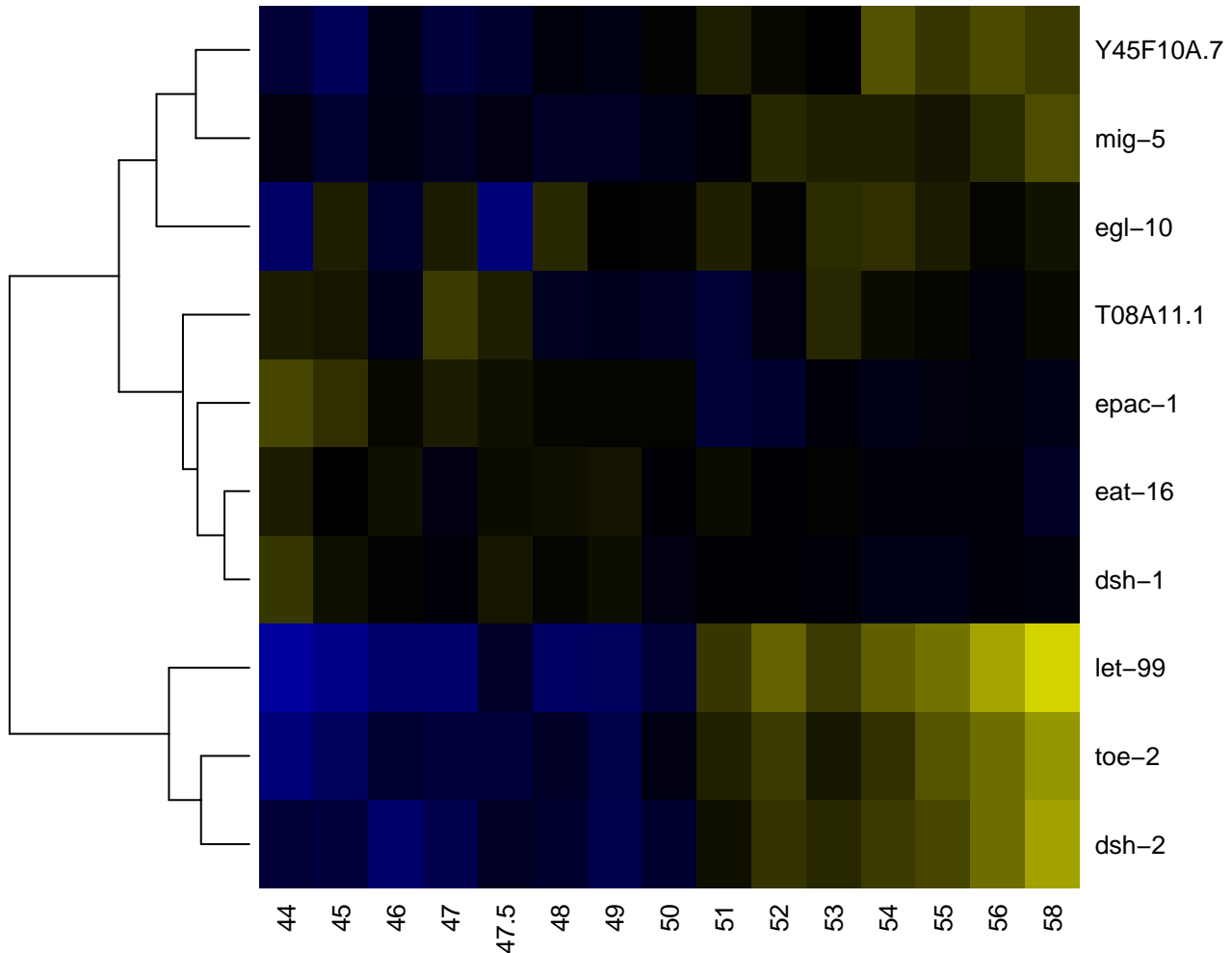
Delta serrate ligand



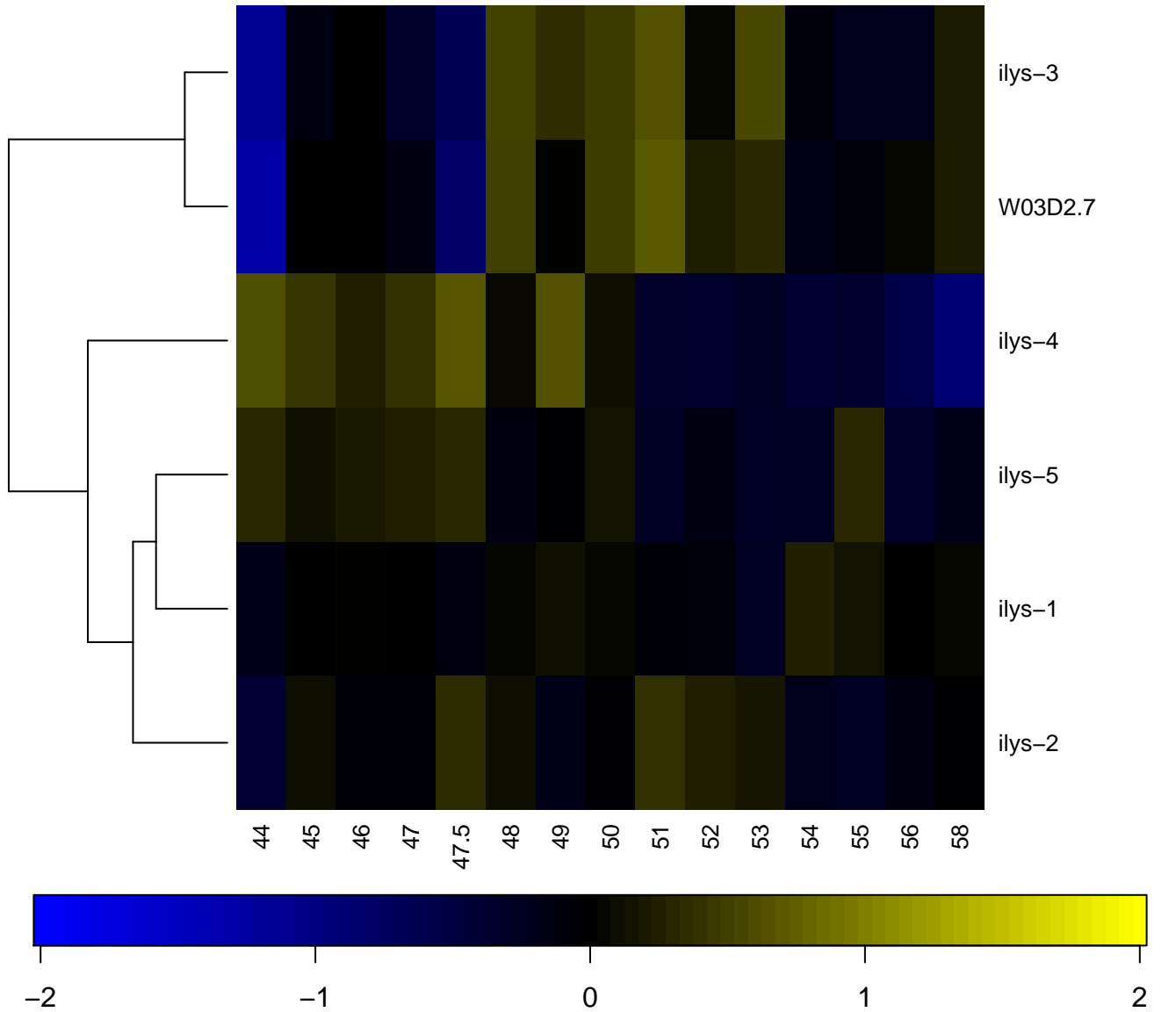
Delta tubulin



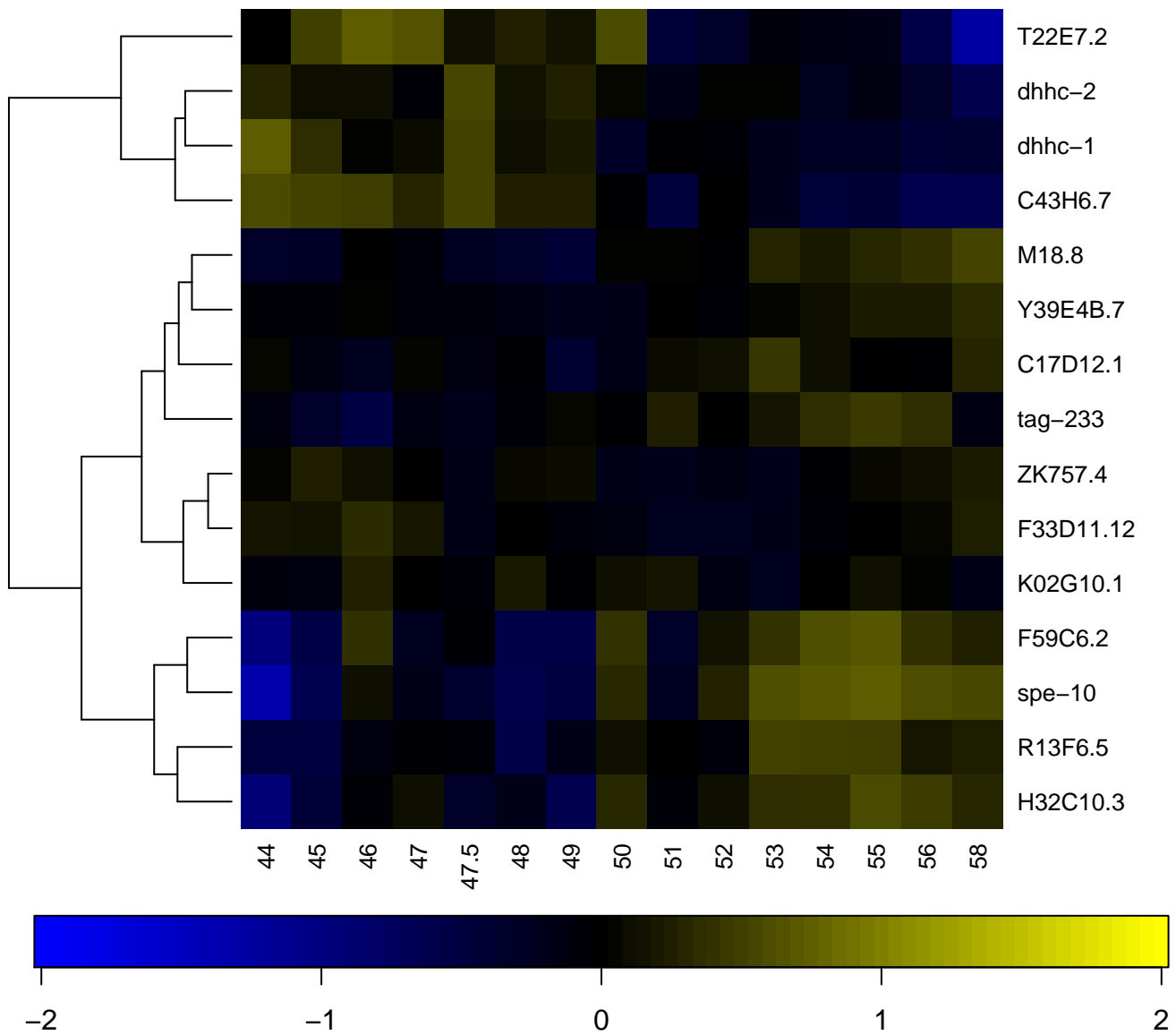
DEP domain



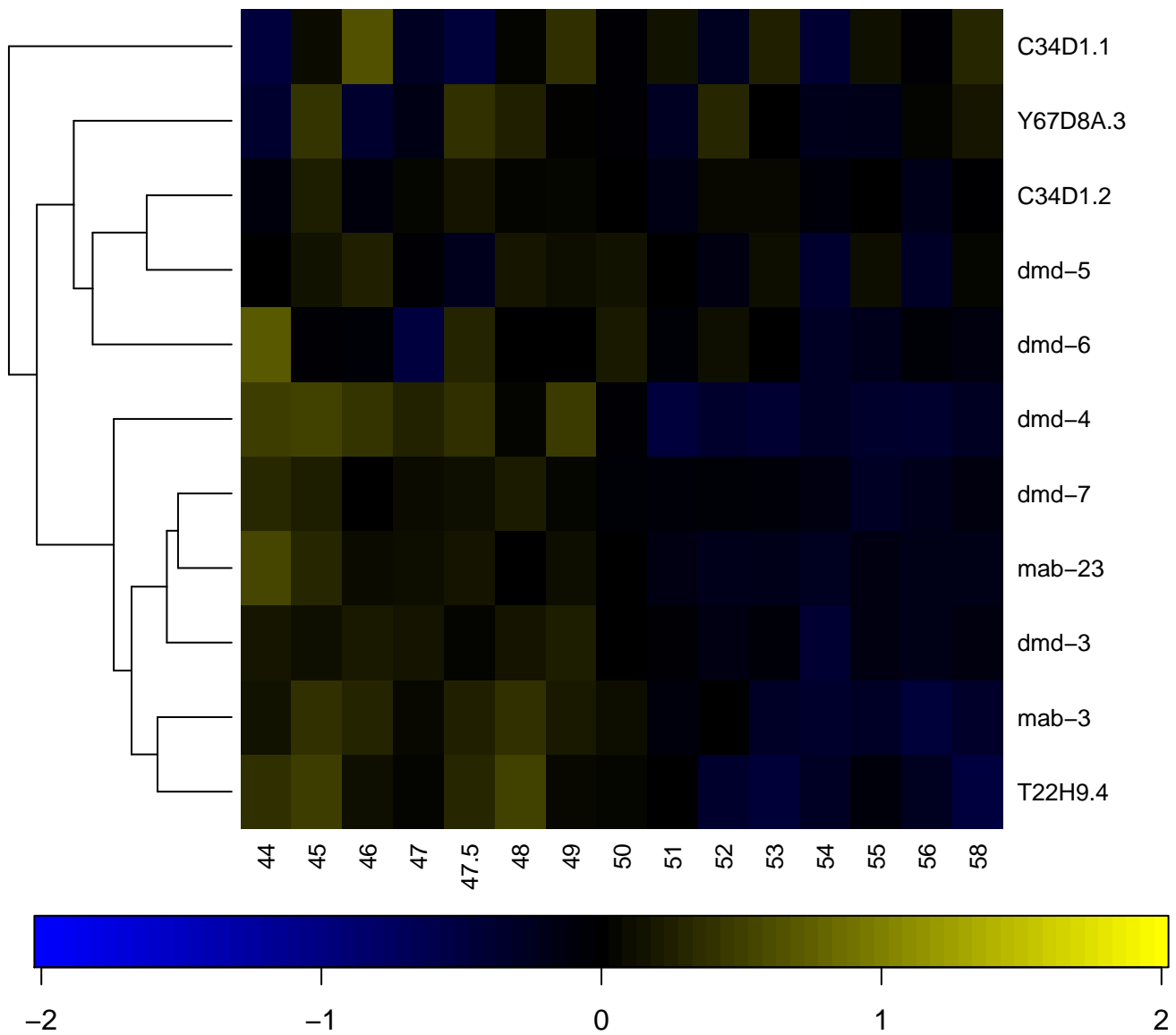
Destabilase



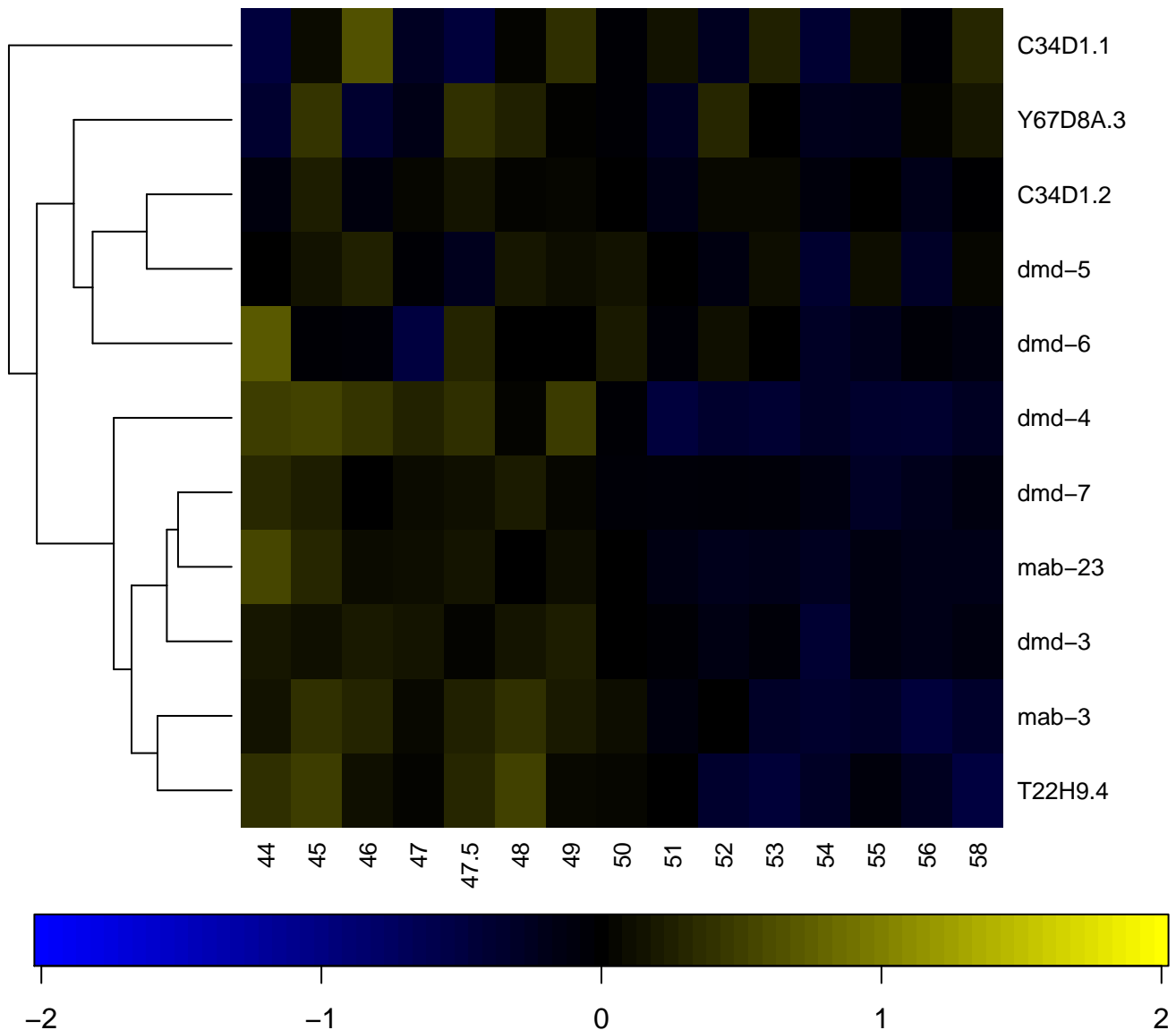
DHHC zinc finger domain



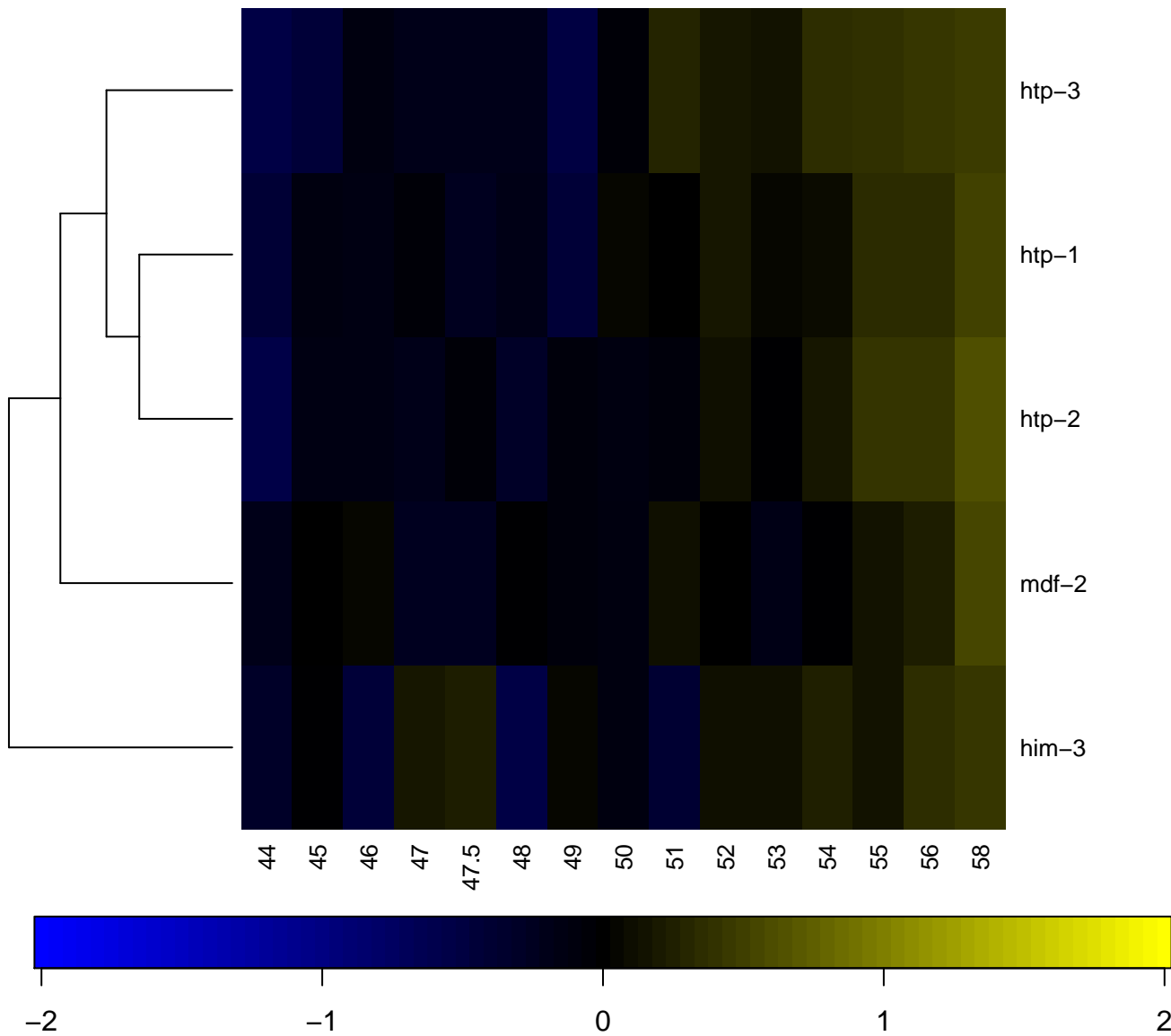
DM DNA-binding



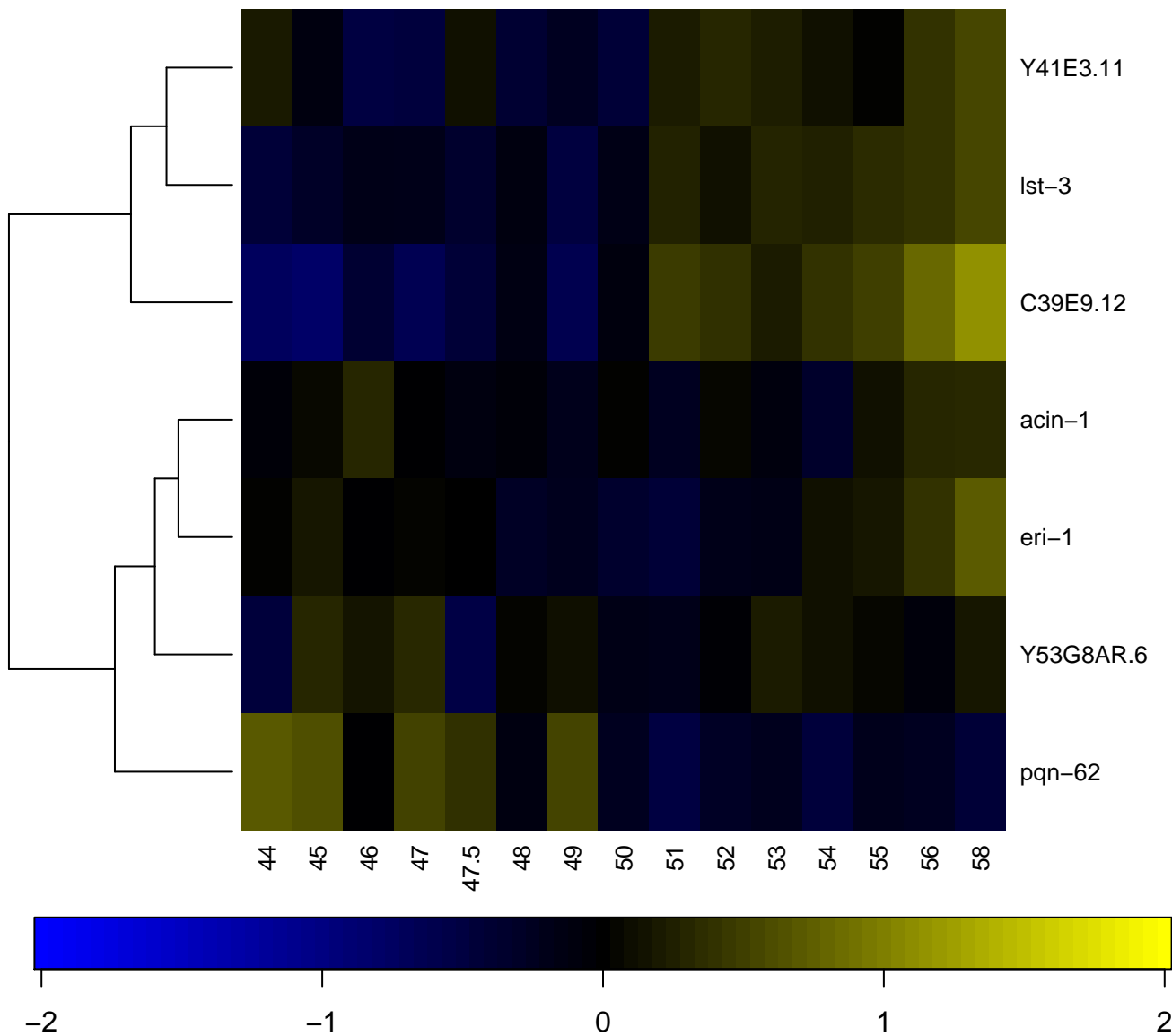
DM DNA binding domain



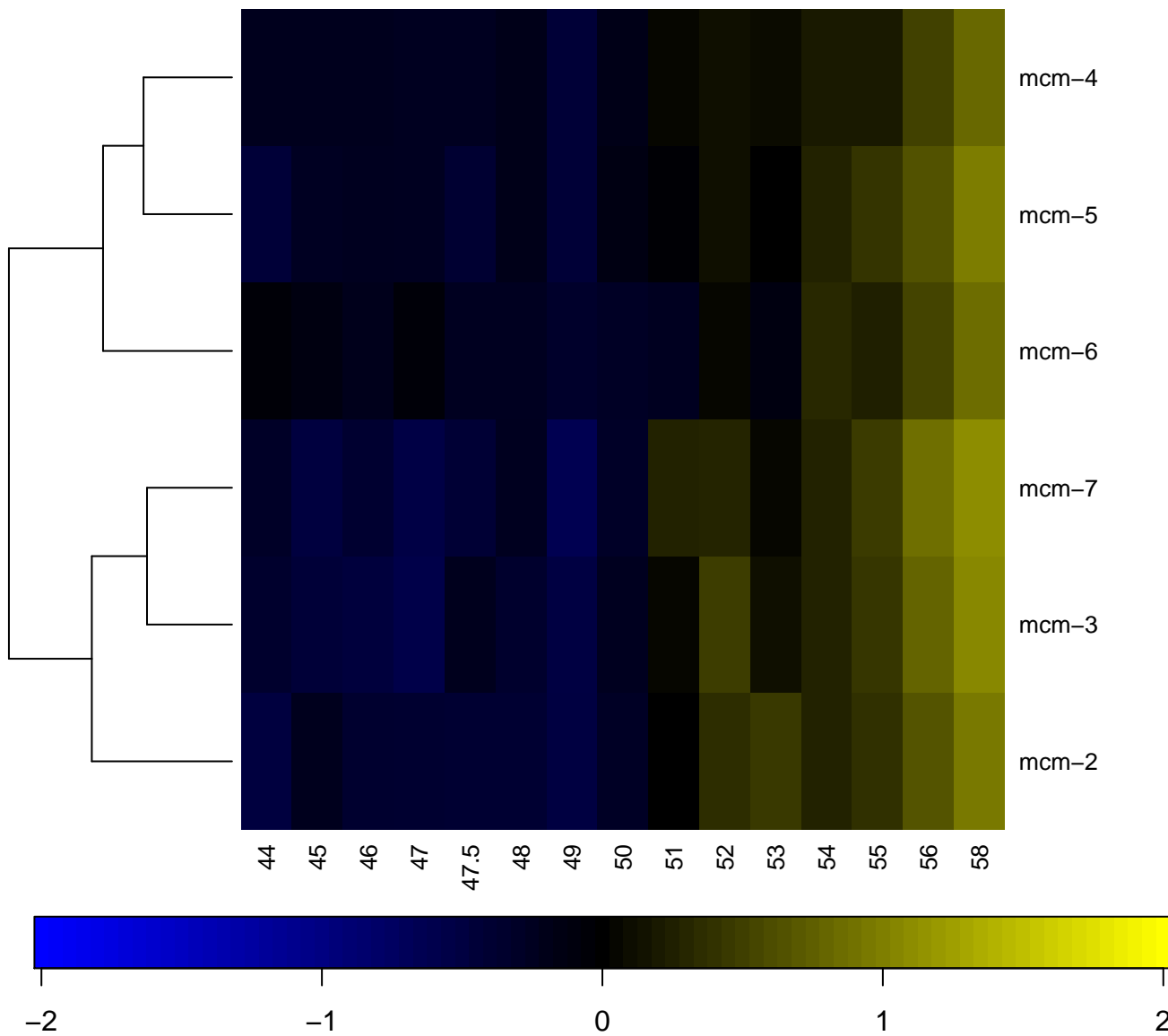
DNA-binding HORMA



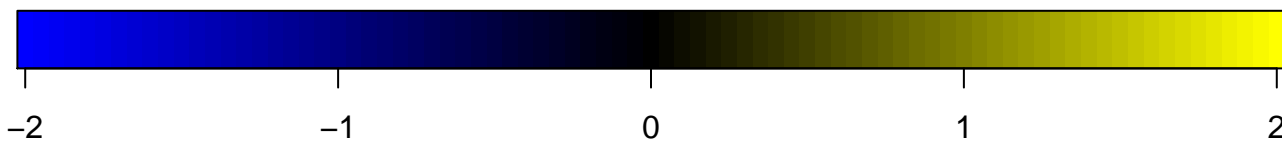
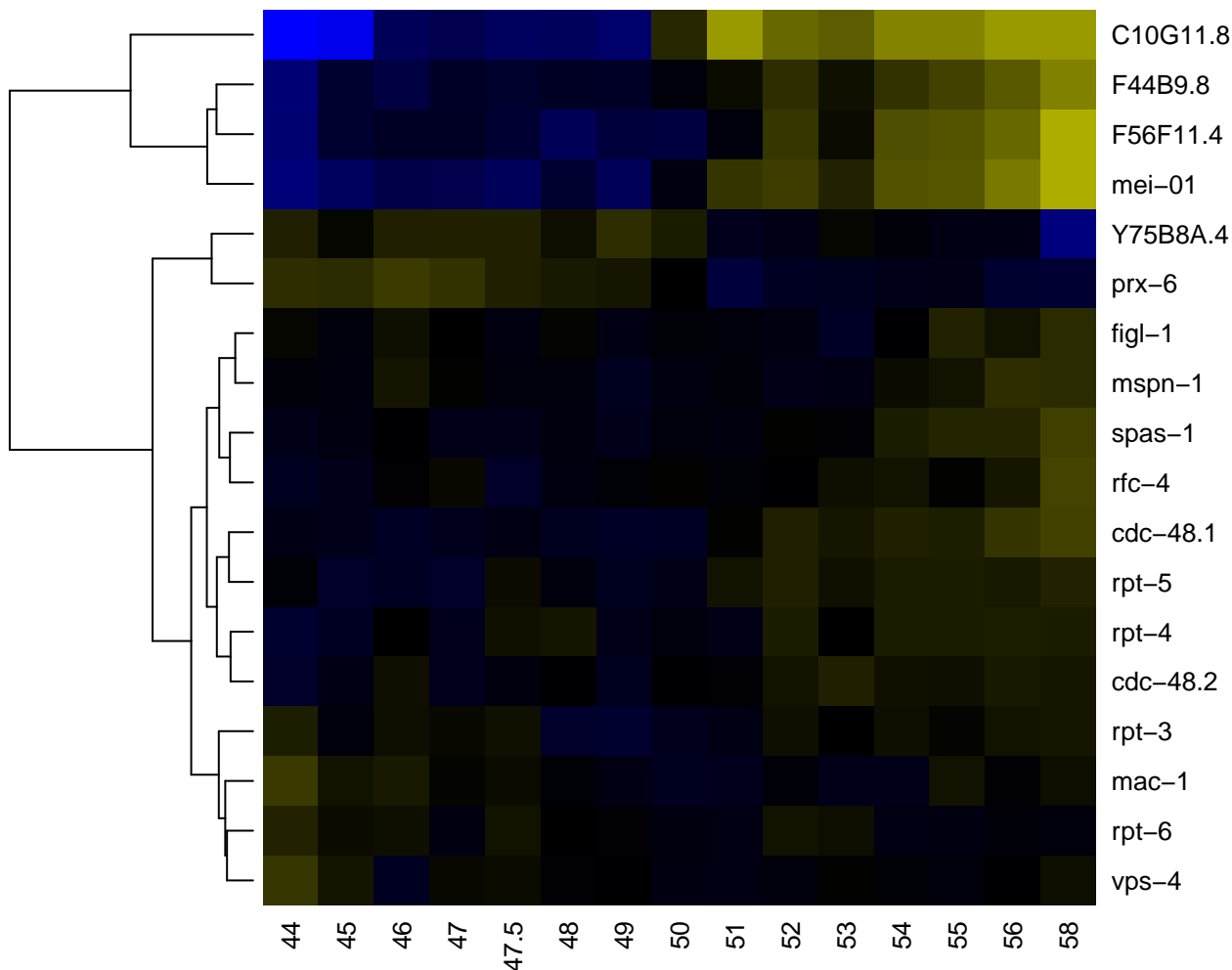
DNA-binding SAP



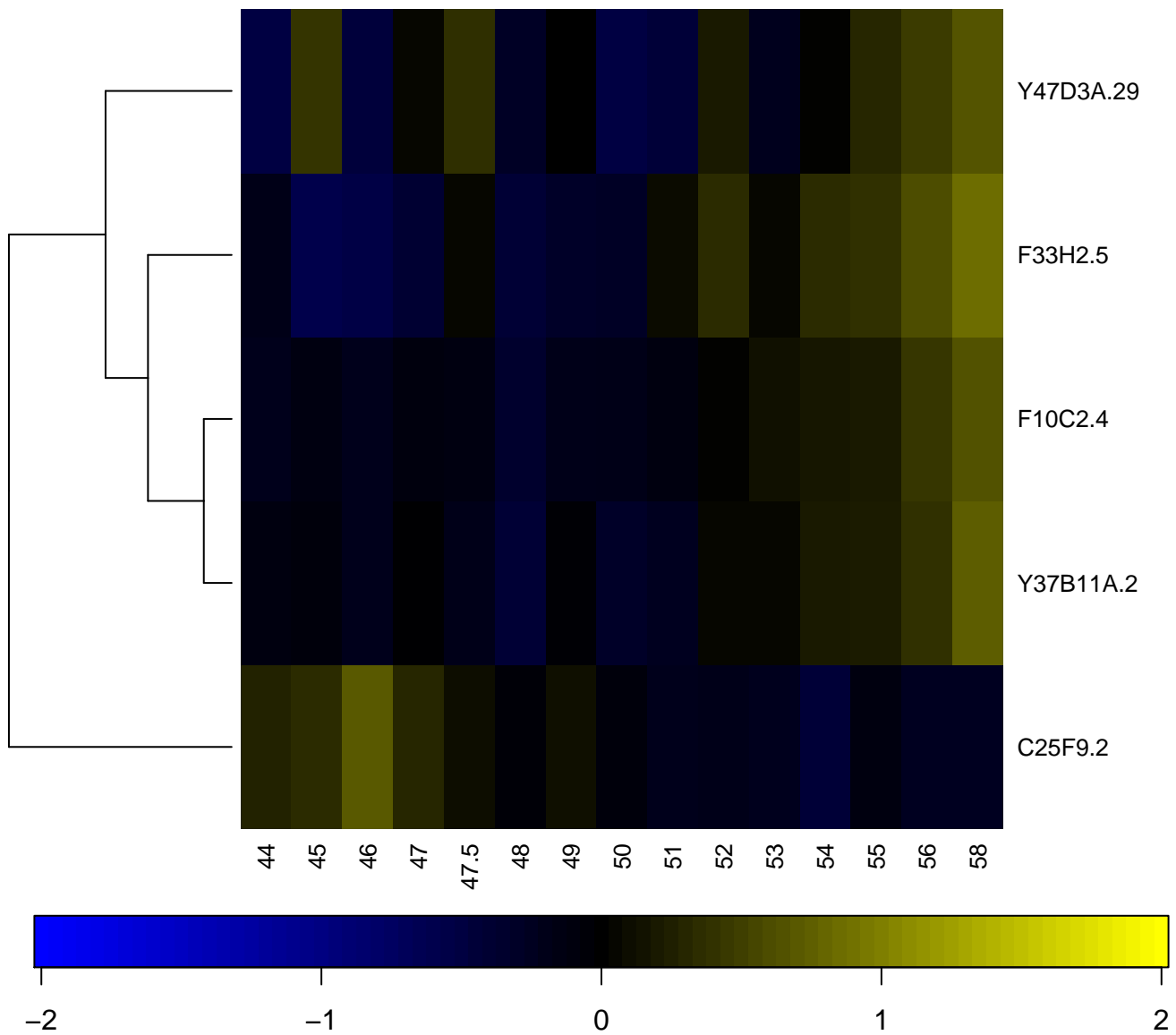
DNA-dependent ATPase MCM



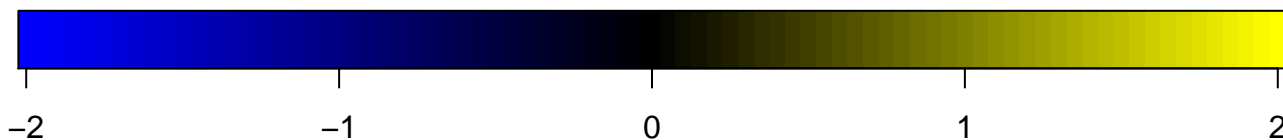
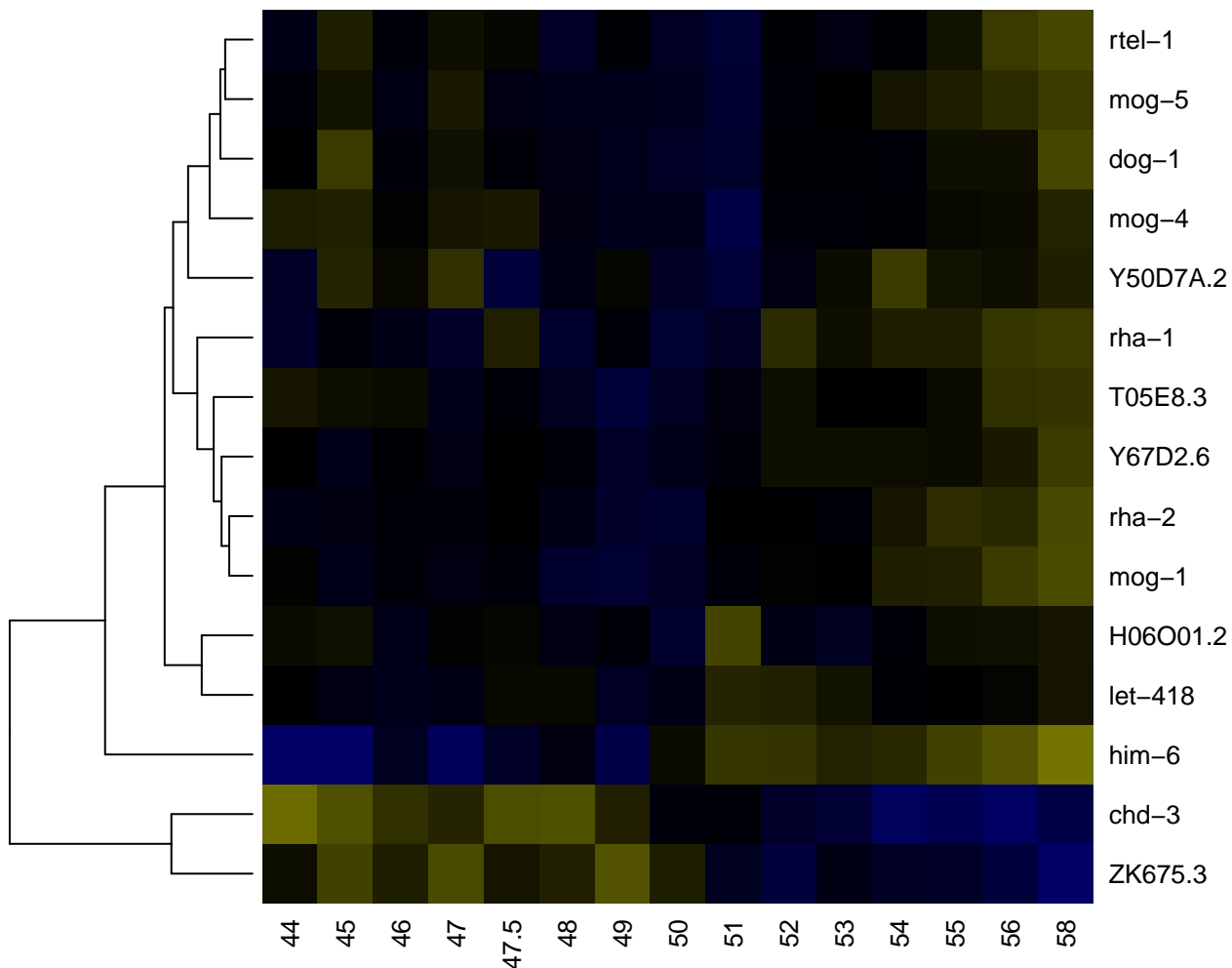
DNA helicase, Holliday junction RuvB type, N-terminal



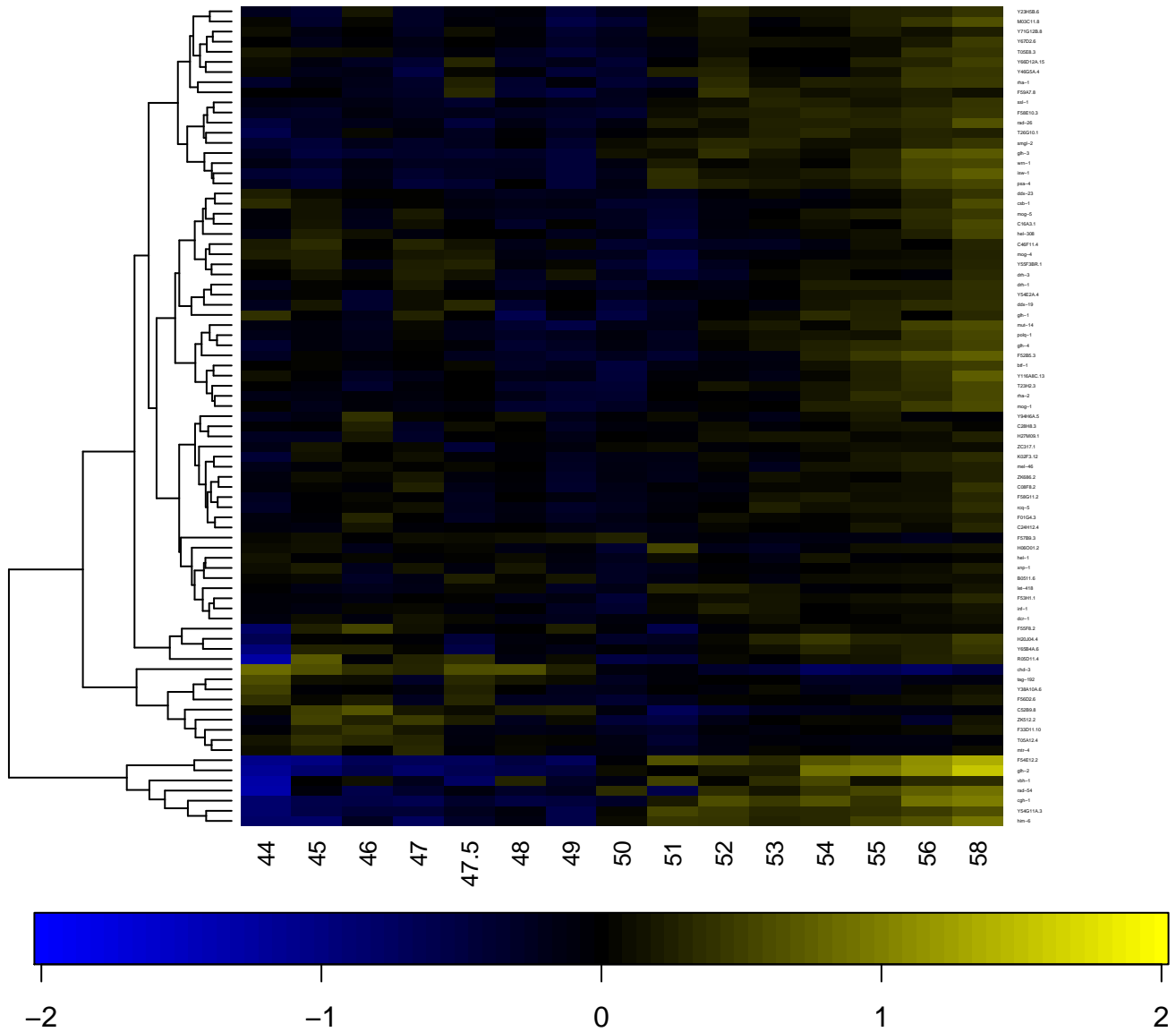
DNA polymerase, family B



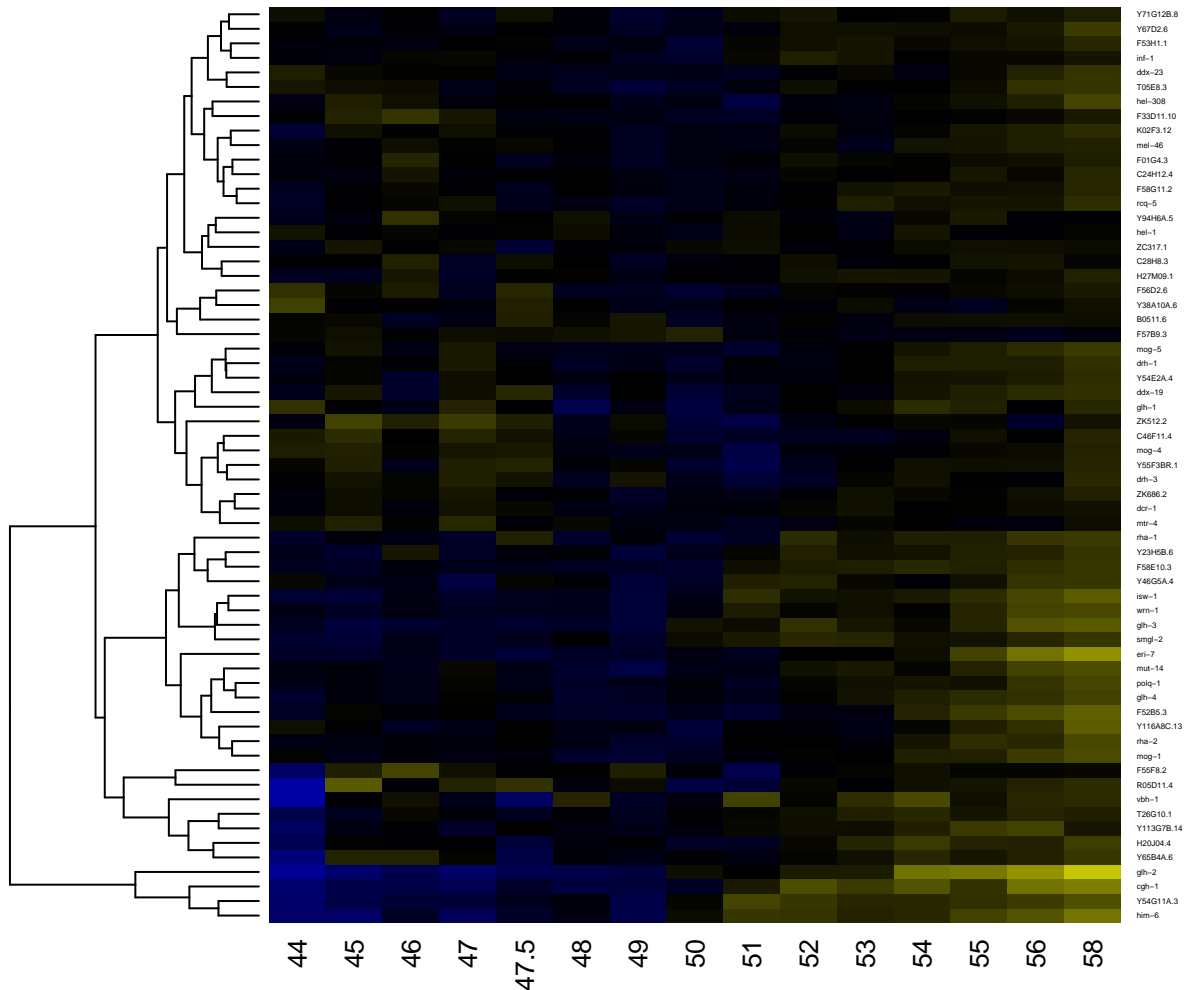
5'UTR RNA helicase, ATP-dependent, DEAH-box type, conserved



DNA/RNA helicase, C-terminal



DNA/RNA helicase, DEAD/DEAH box type, N-terminal



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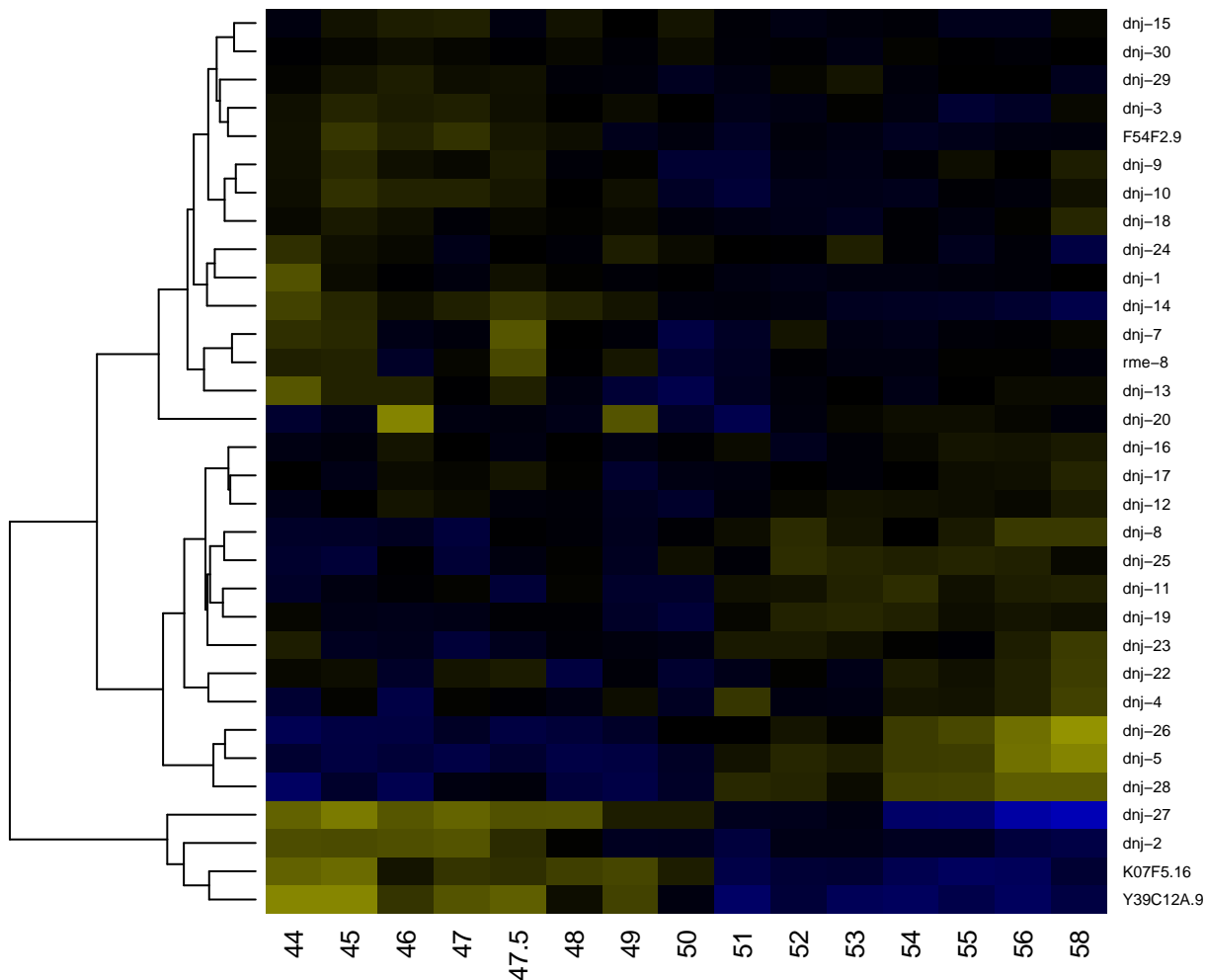
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DnaJ domain



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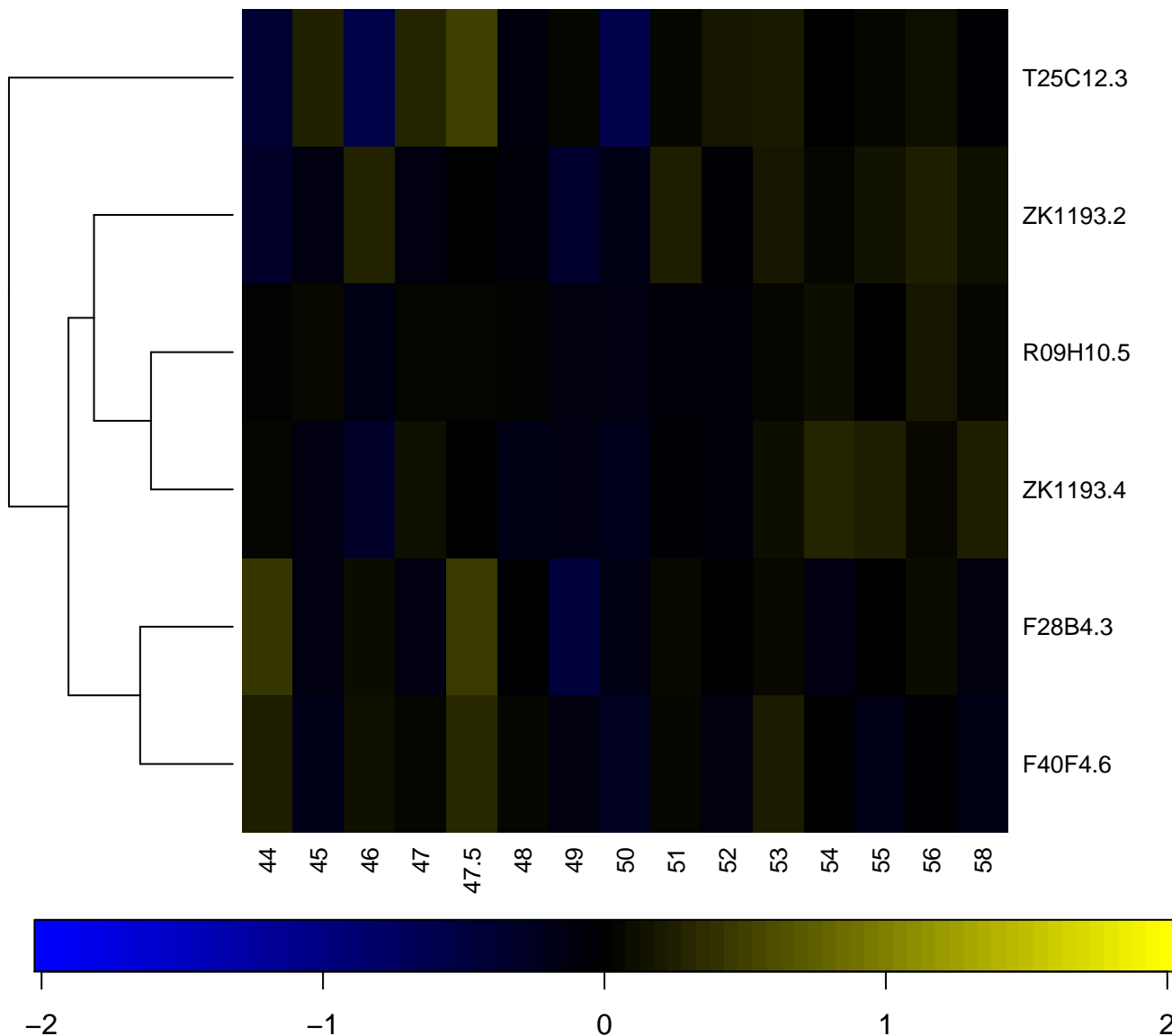
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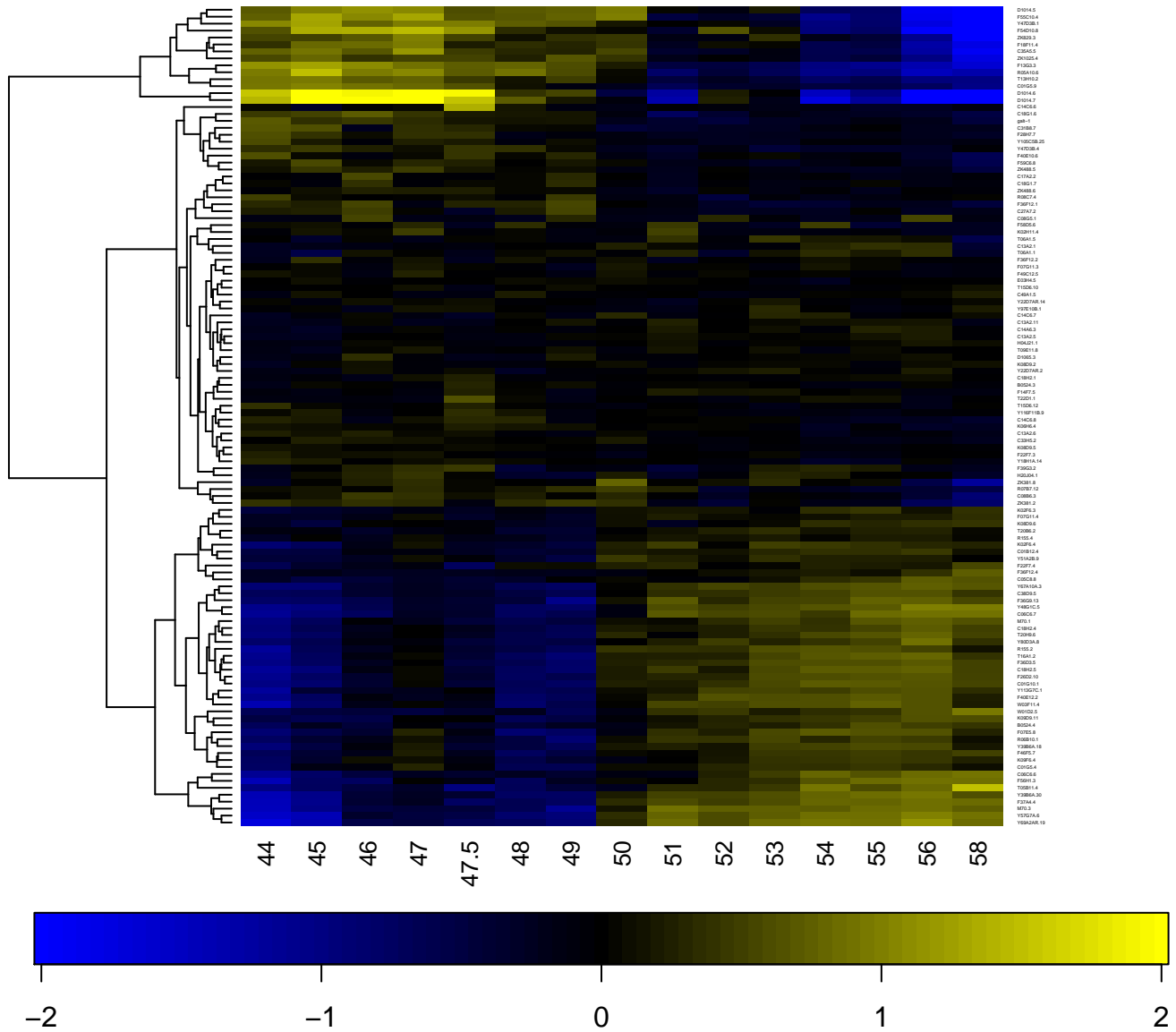
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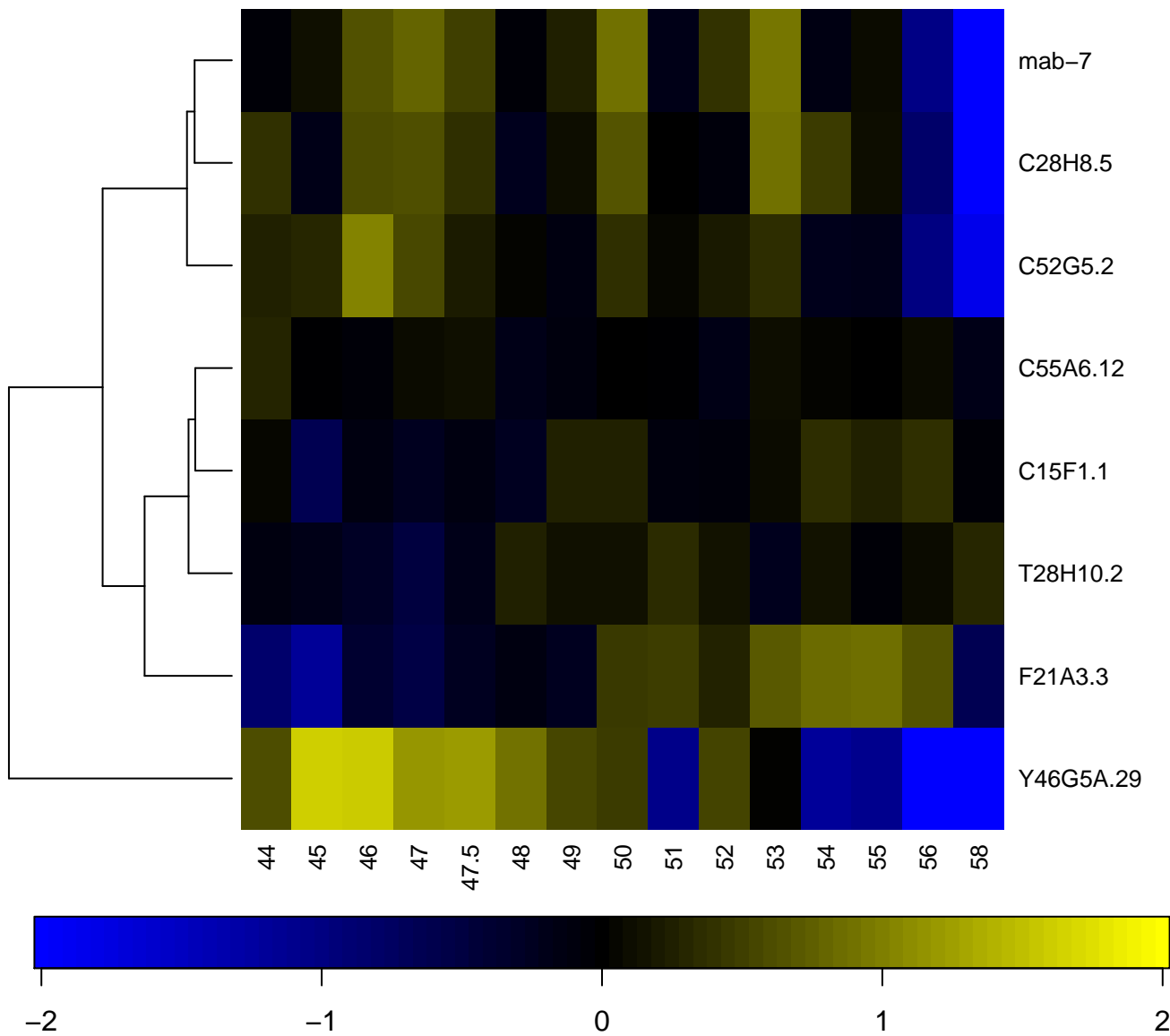
Domain of unknown function MD, *Caenorhabditis elegans*



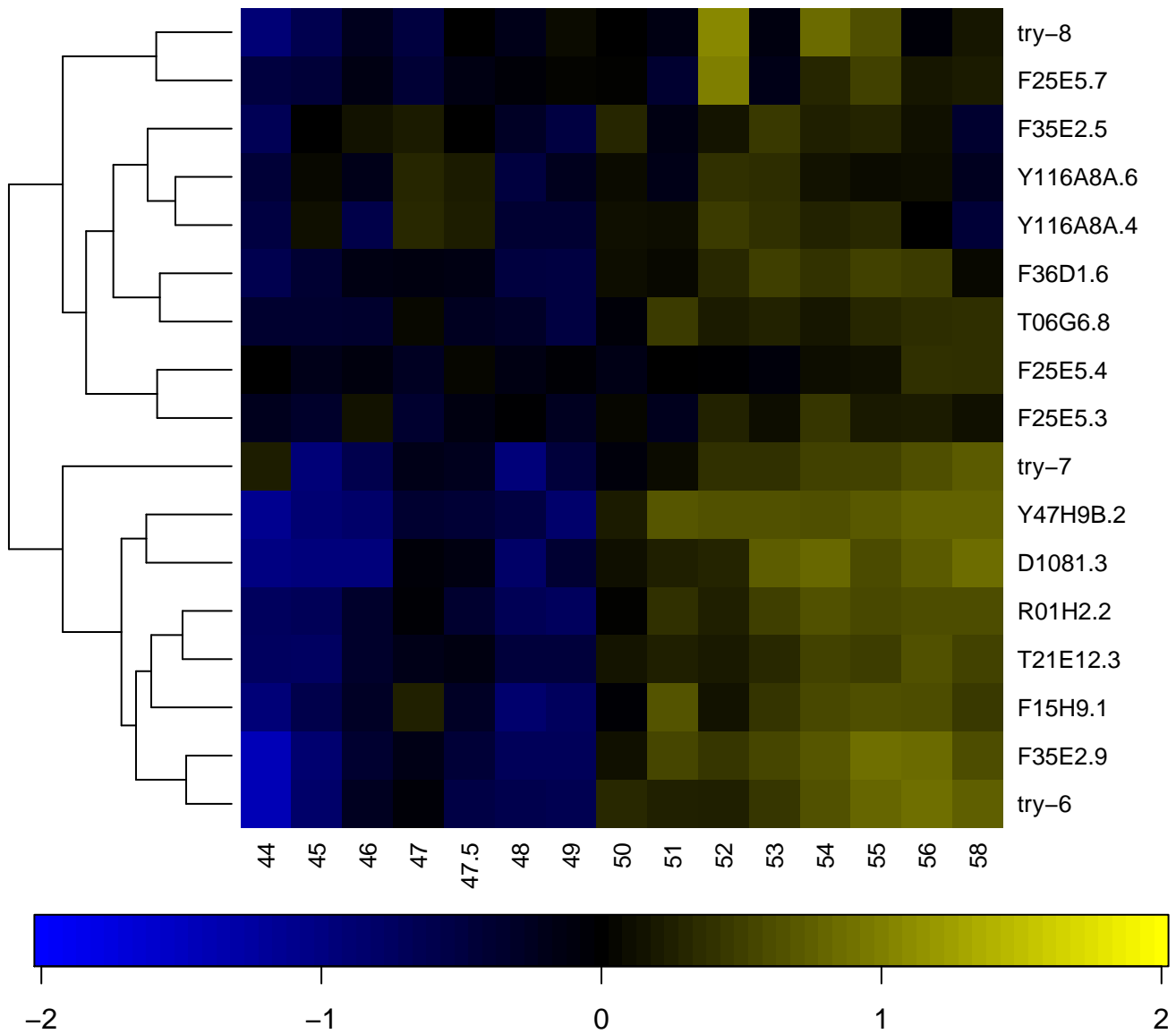
Domain of unknown function



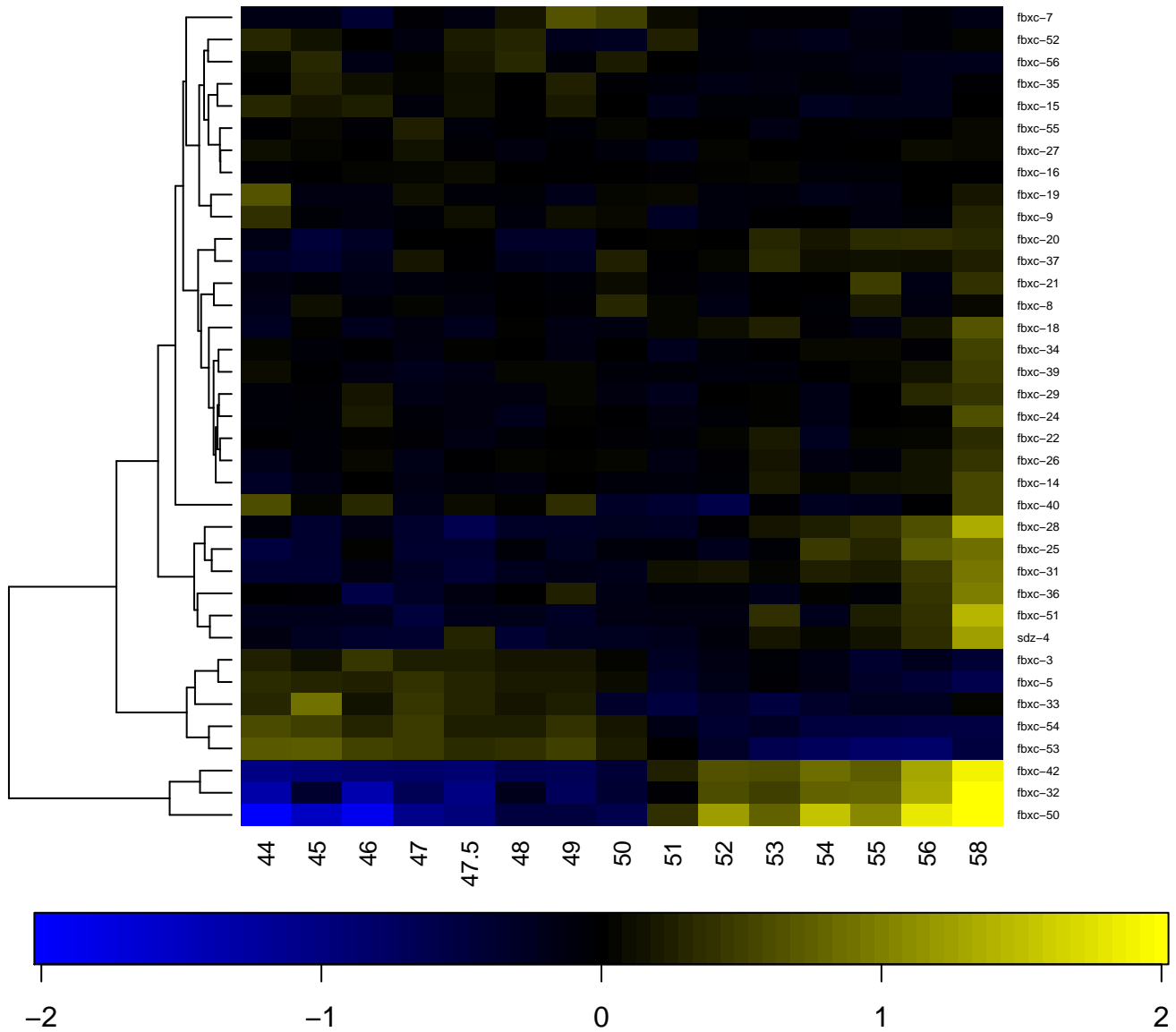
Domain of unknown function (DUF1794)



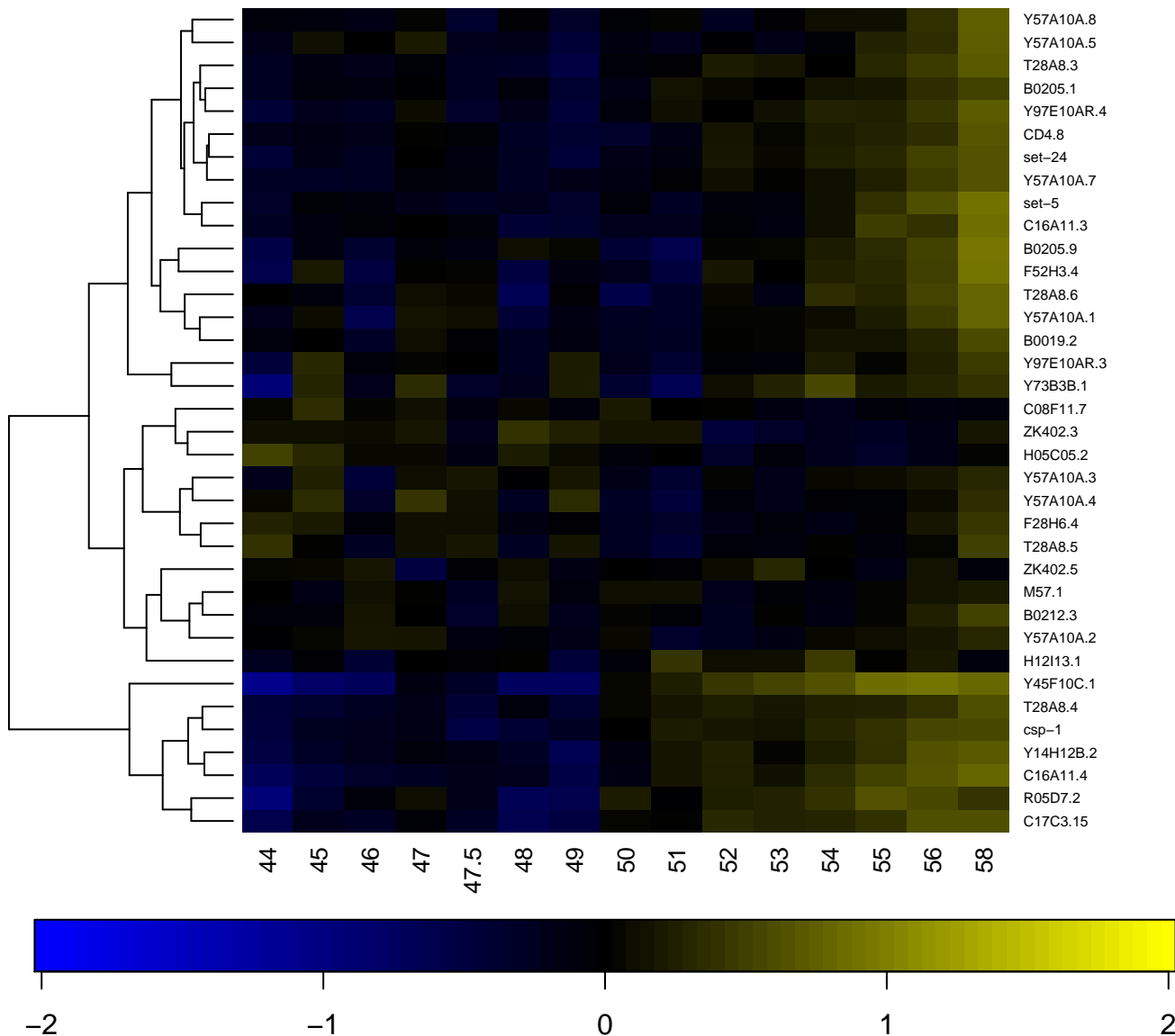
Domain of unknown function (DUF316)



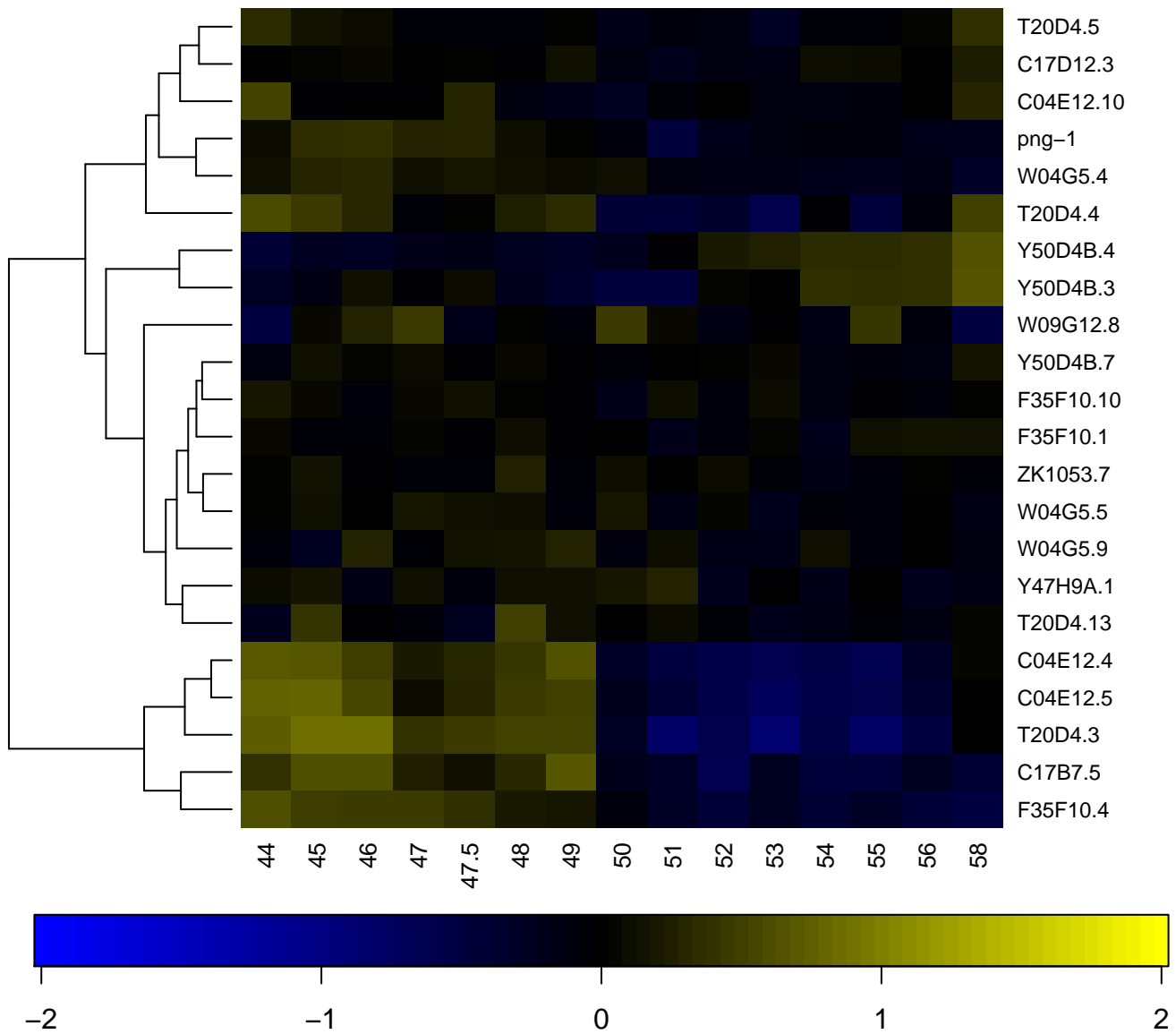
Domain of unknown function (DUF3557)



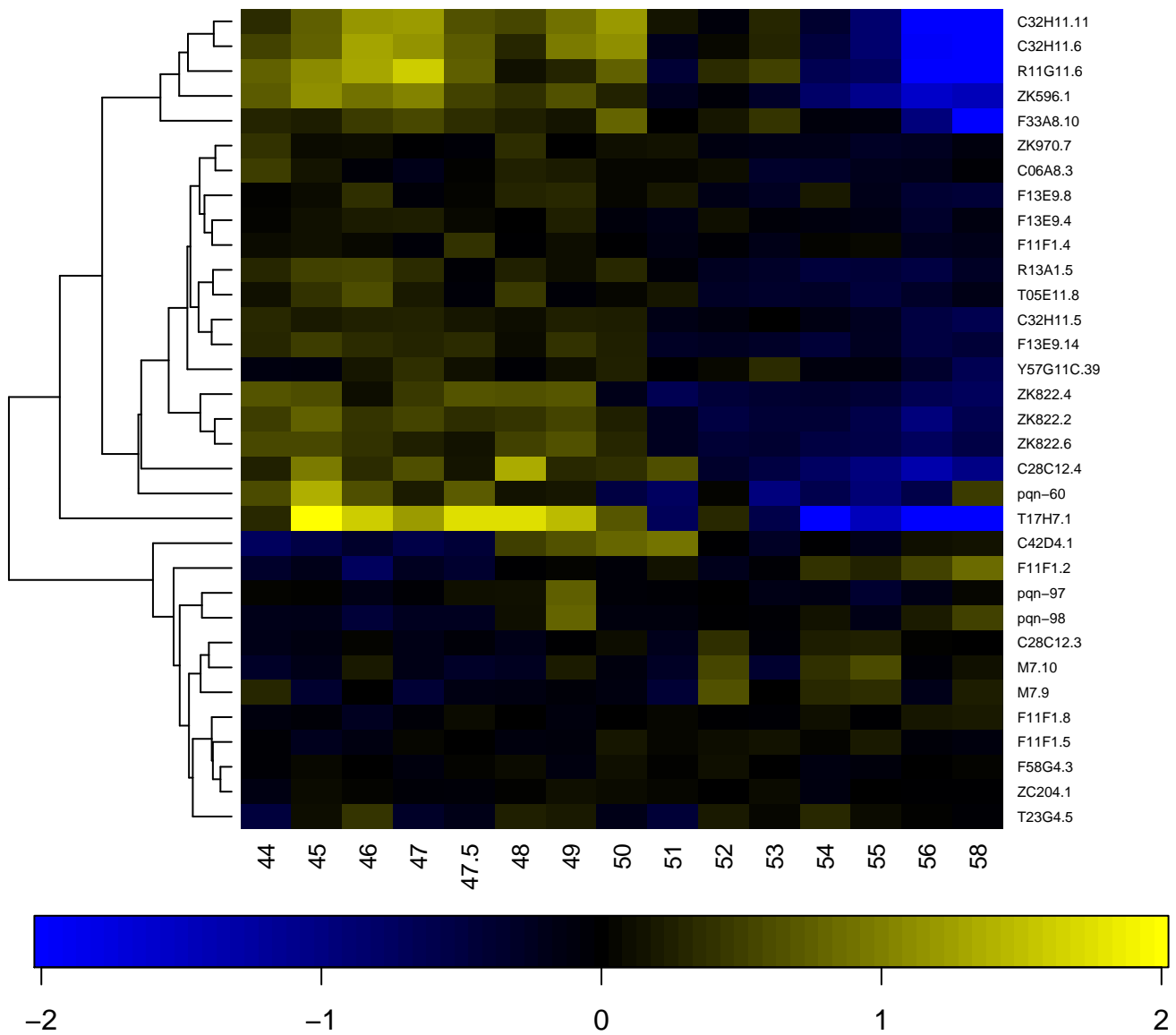
Domain of unknown function (DUF545)



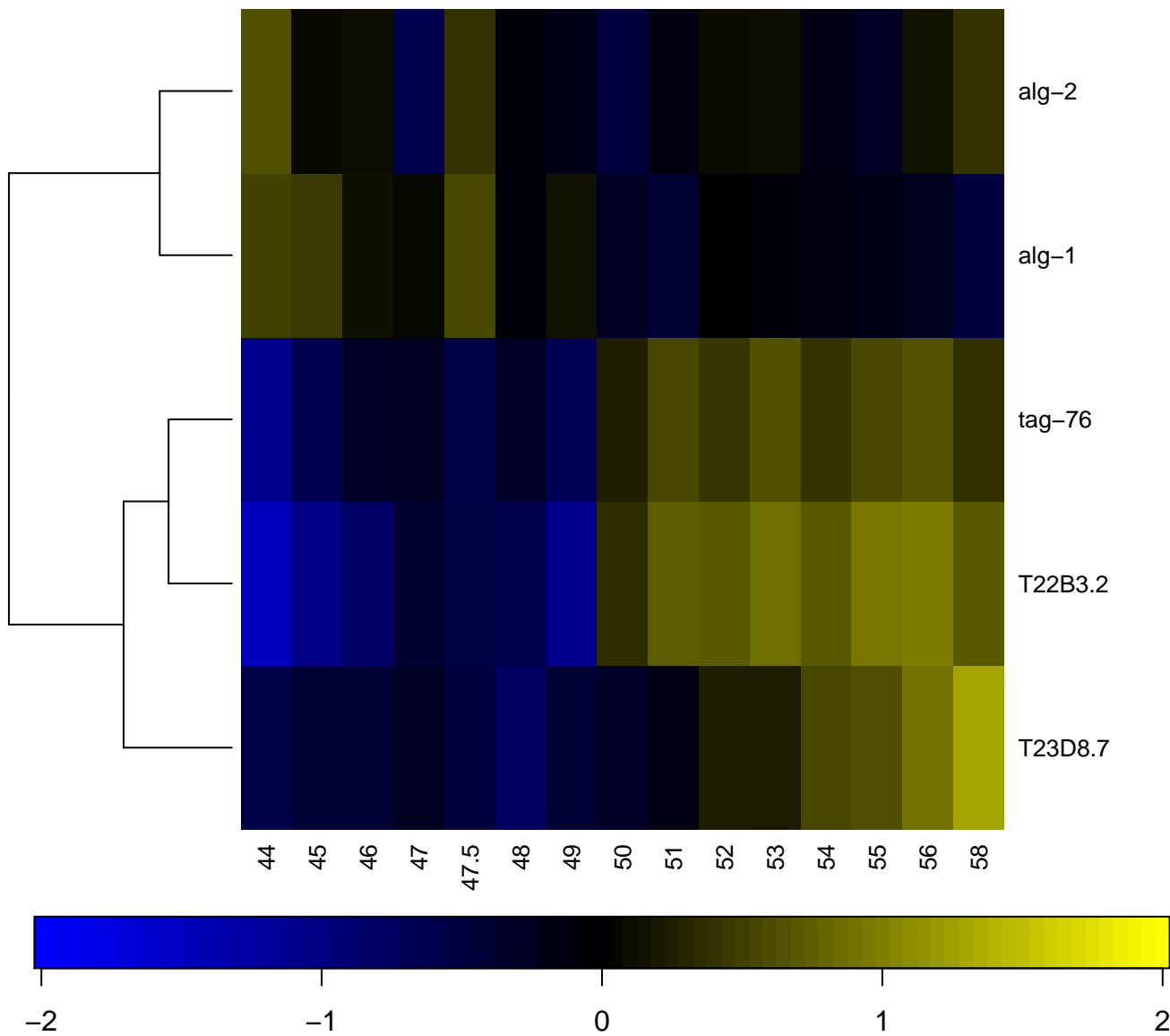
Domain of unknown function (DUF750)



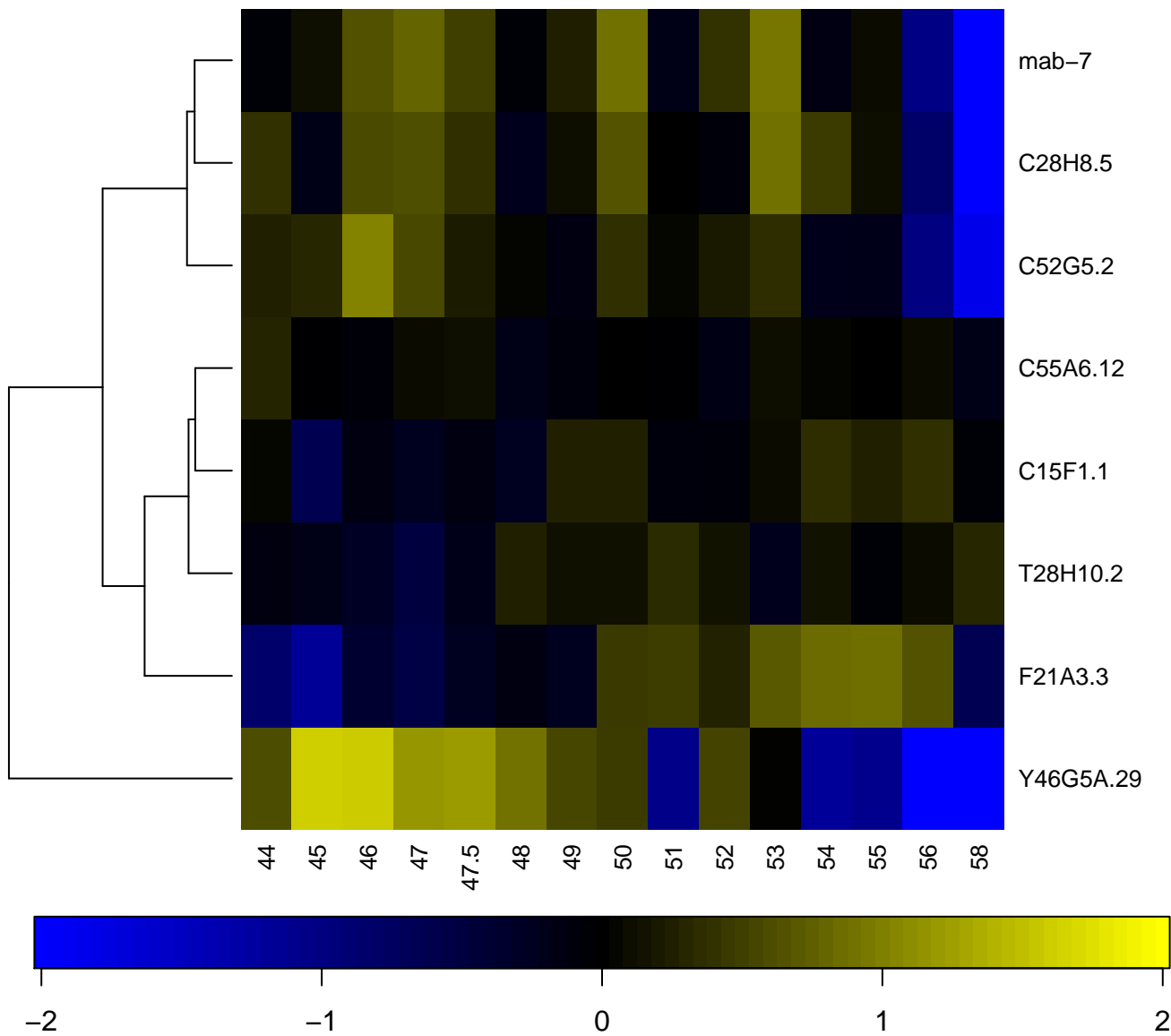
Domain of unknown function DUF148



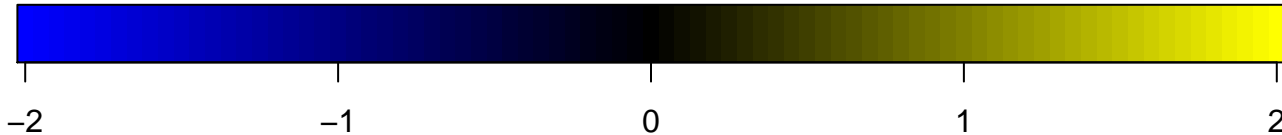
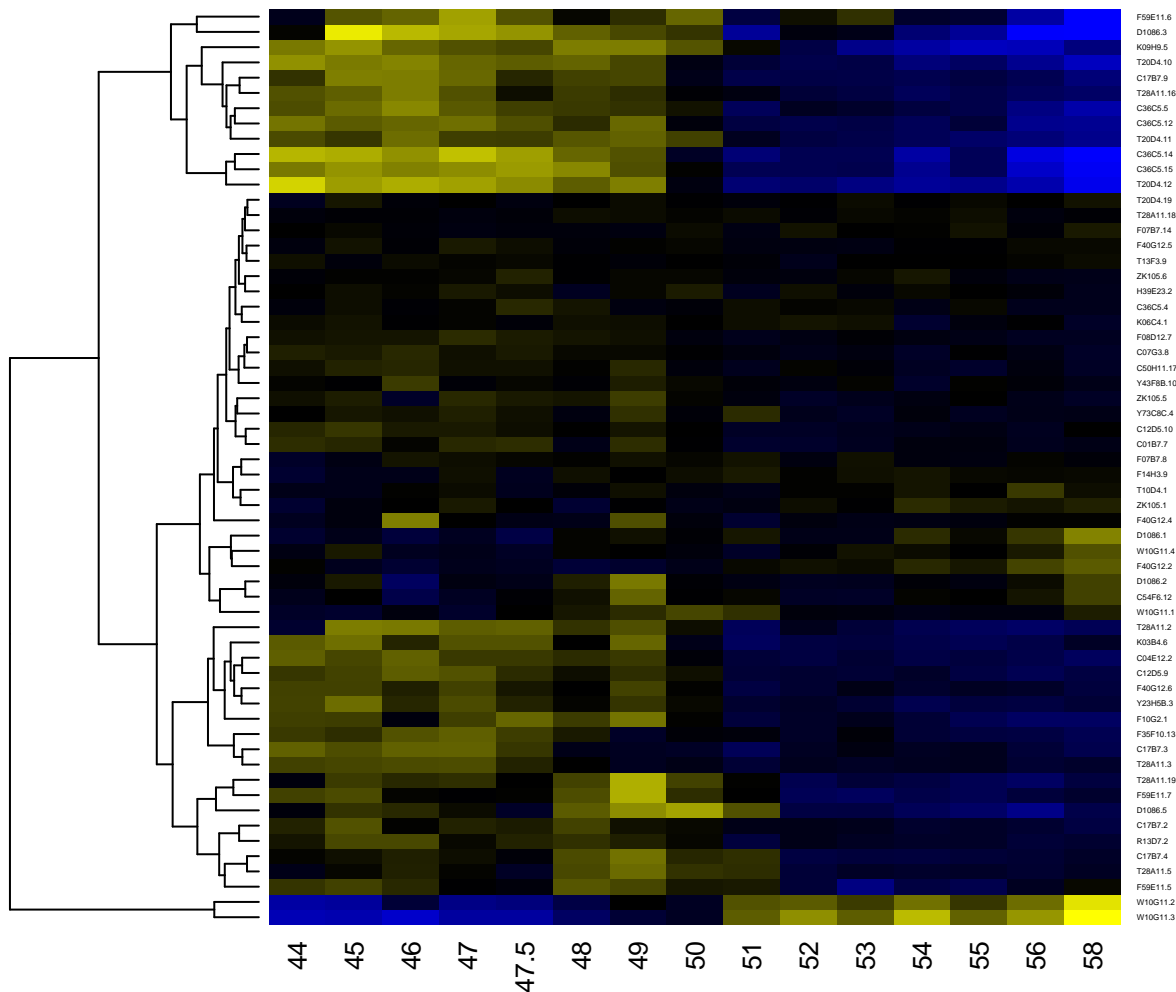
Domain of unknown function DUF1785



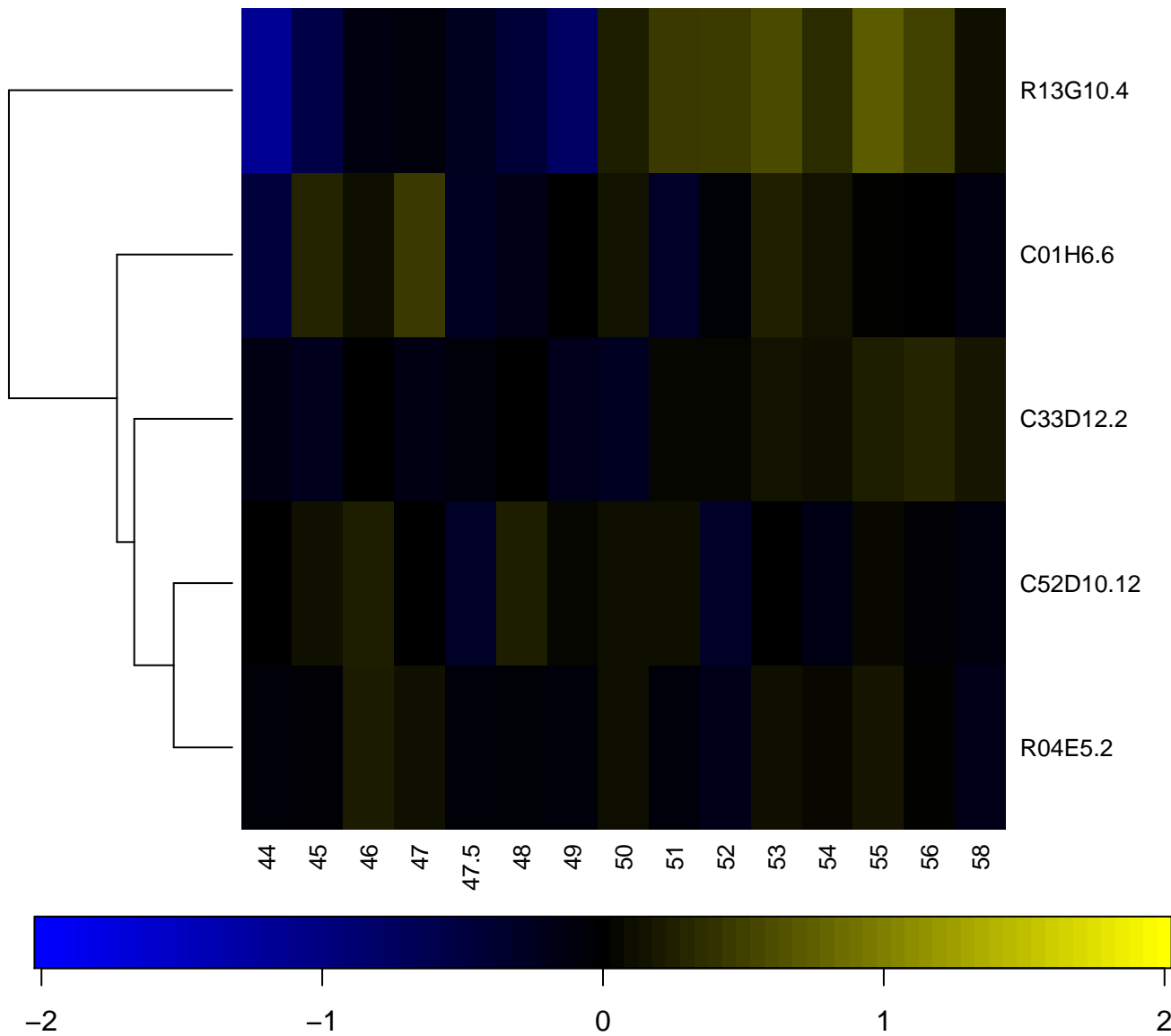
Domain of unknown function DUF1794



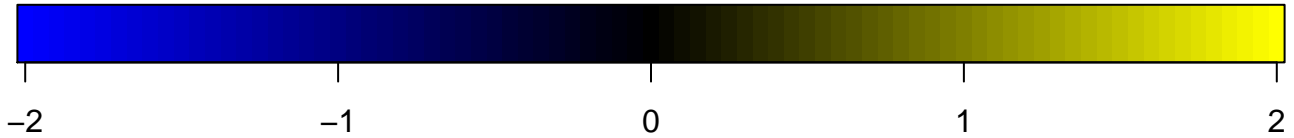
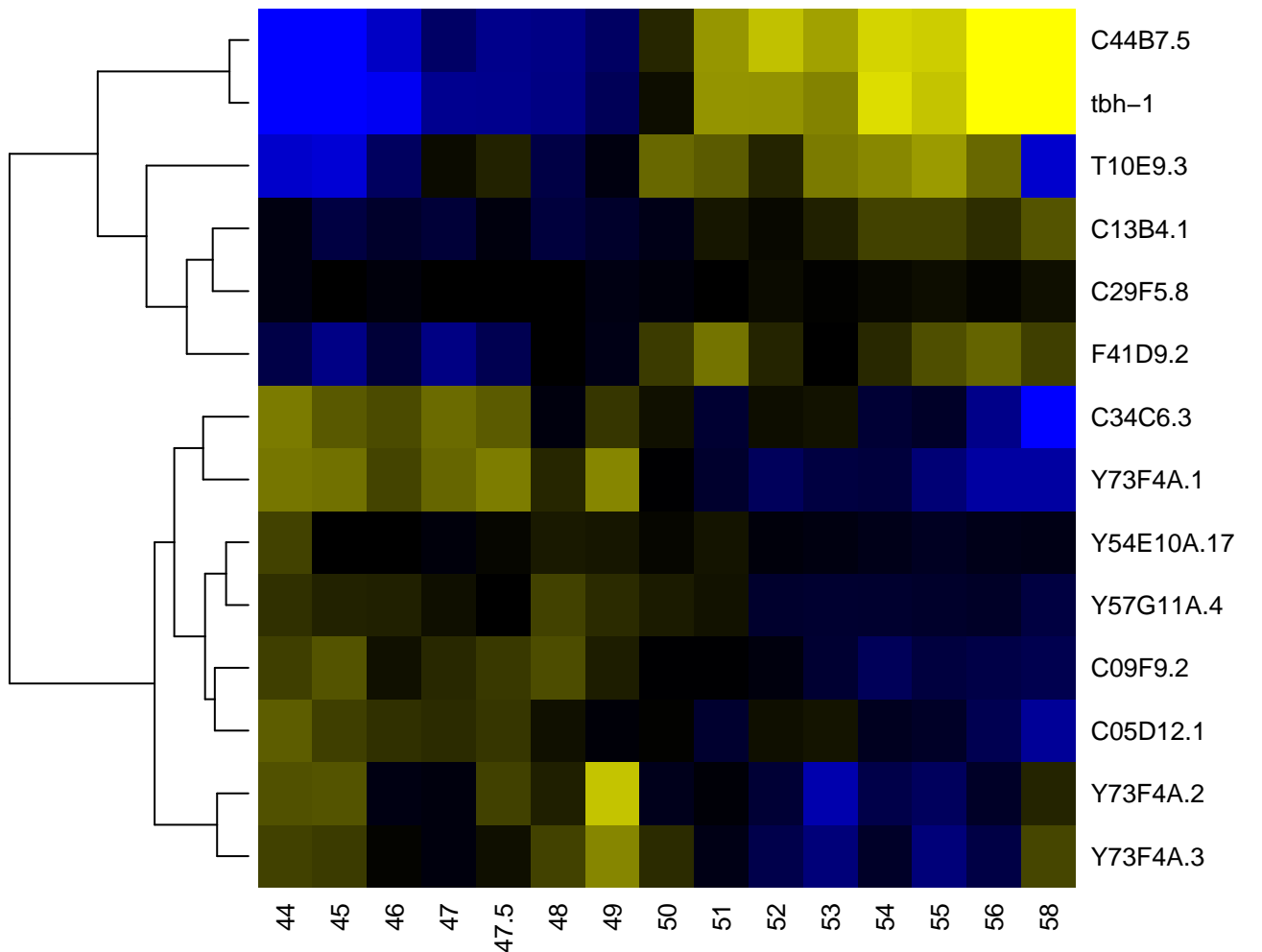
Domain of unknown function DUF19



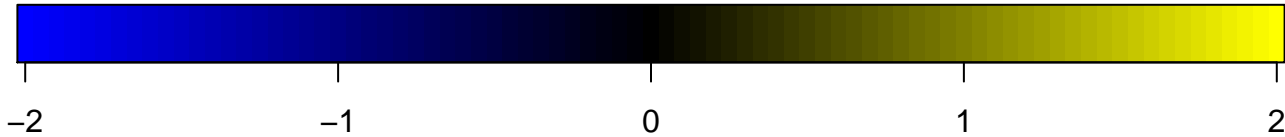
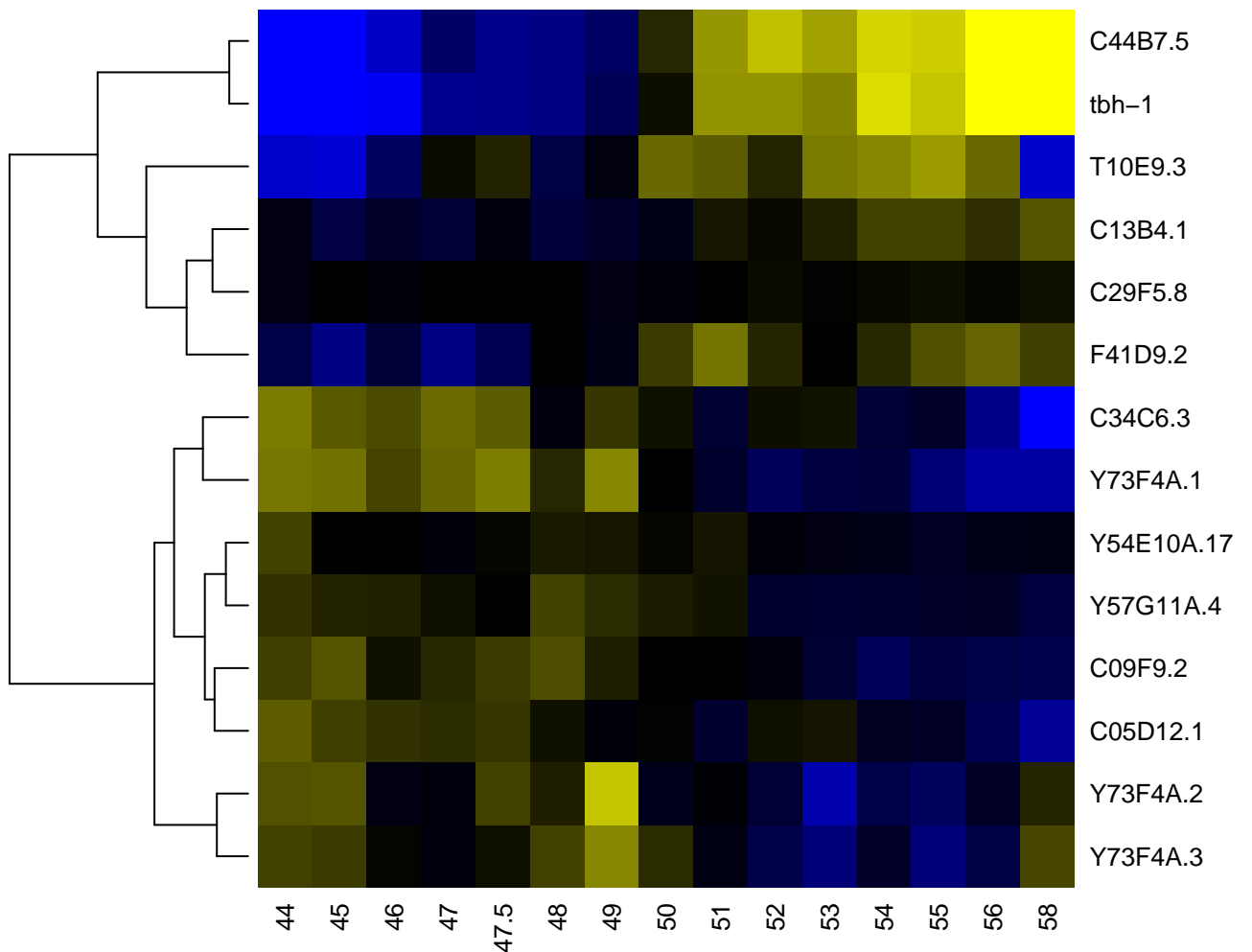
Domain of unknown function DUF21



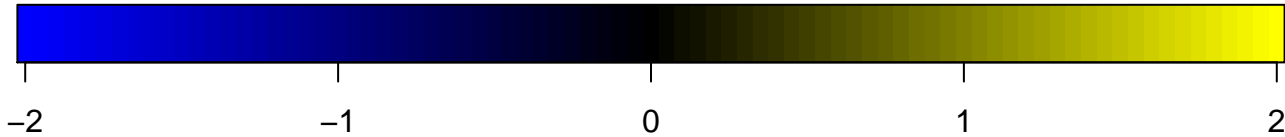
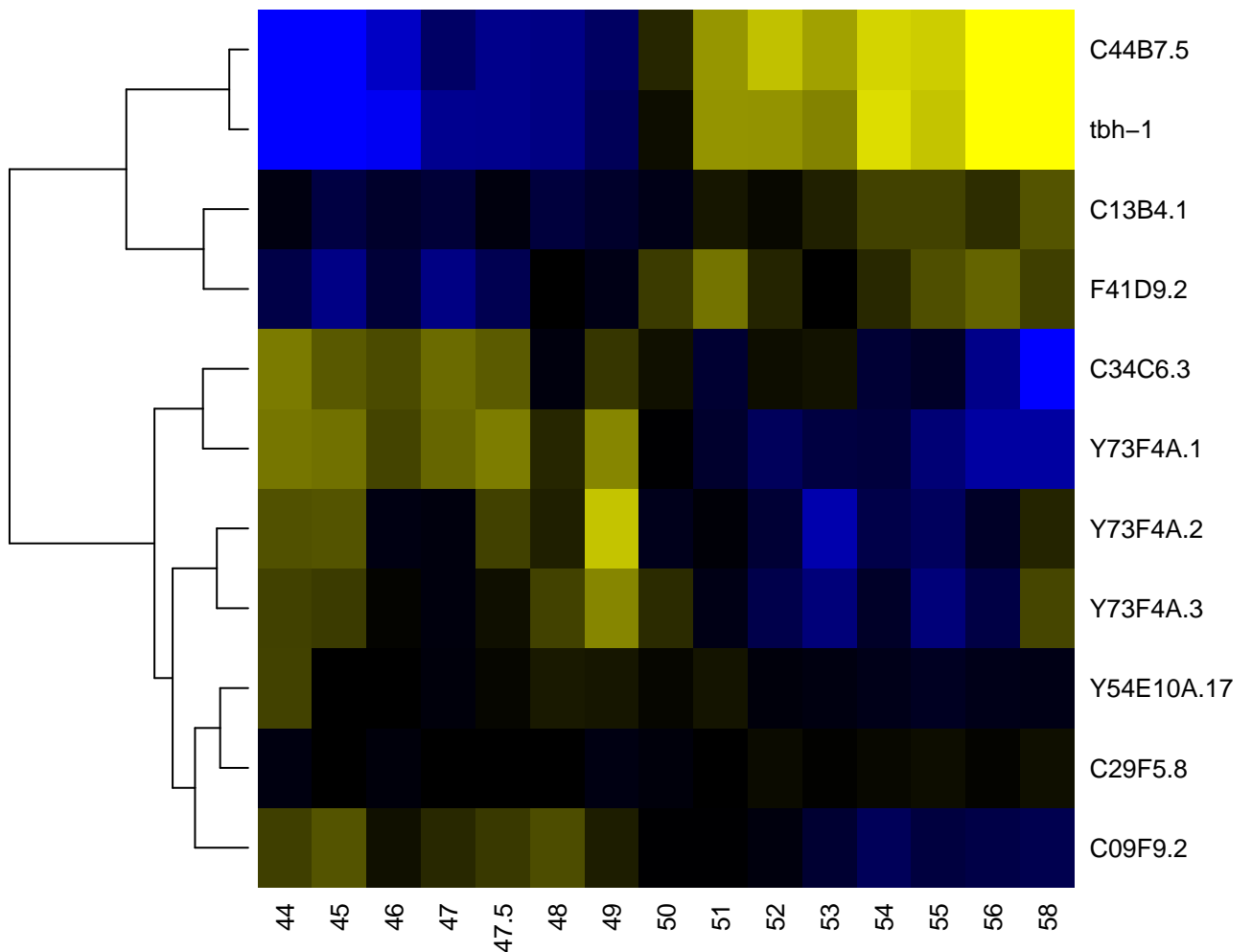
DOMON



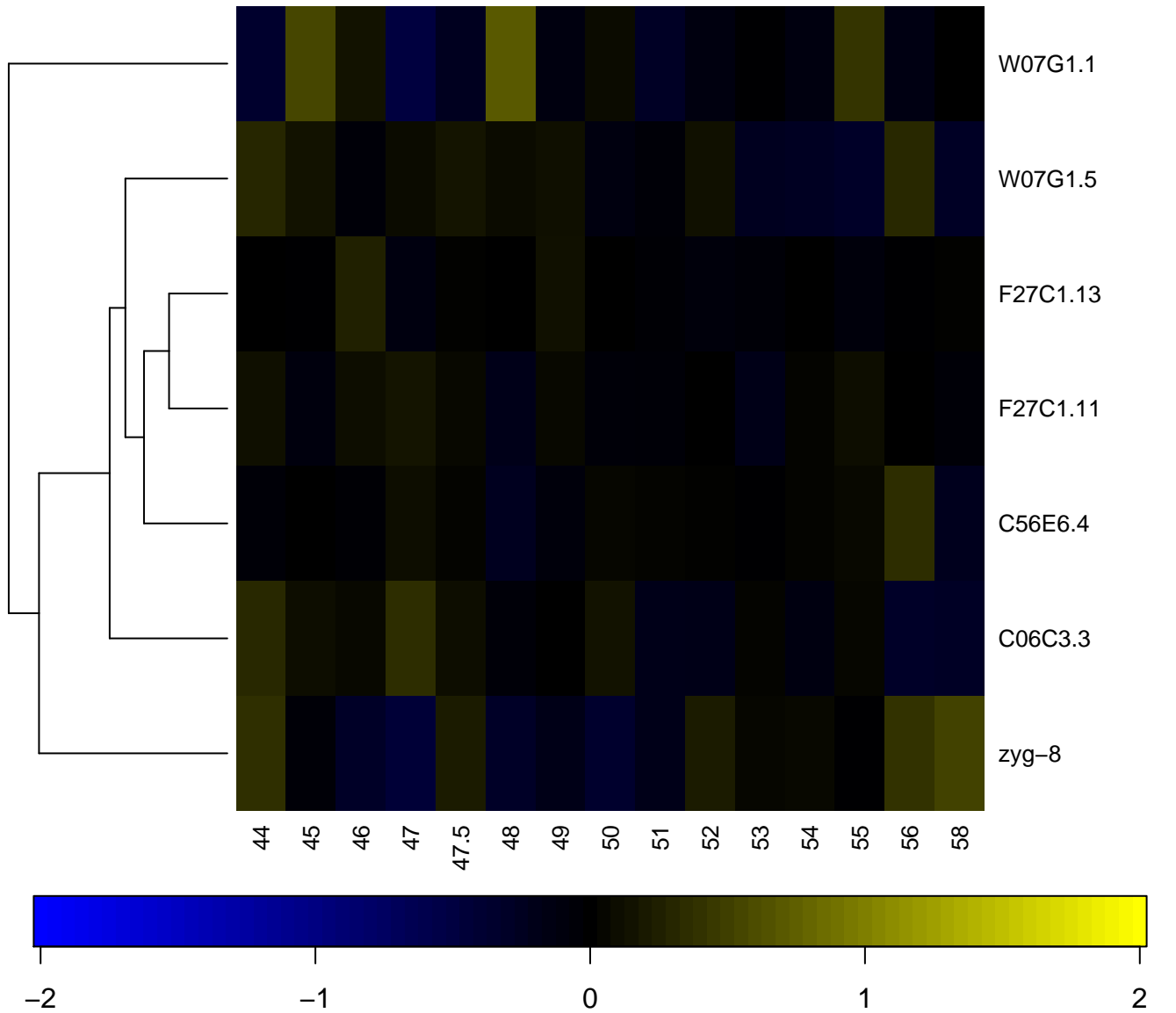
DOMON domain



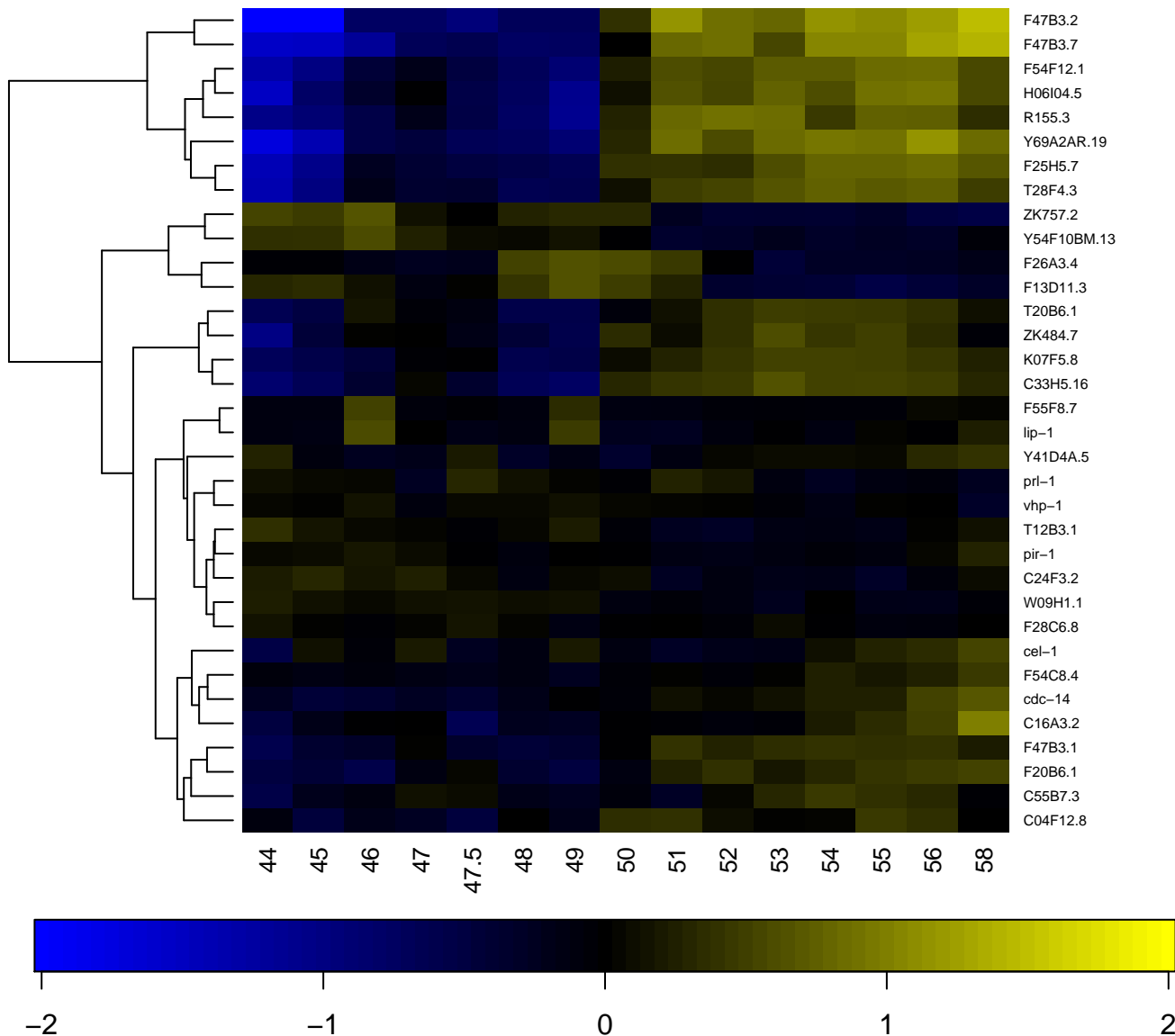
DOMON related



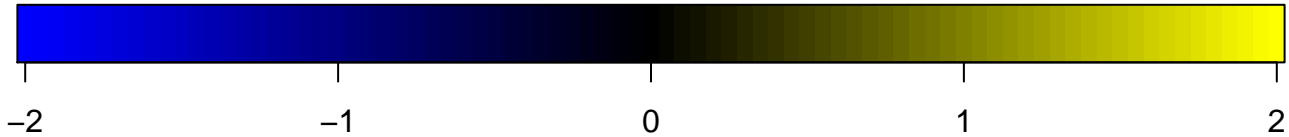
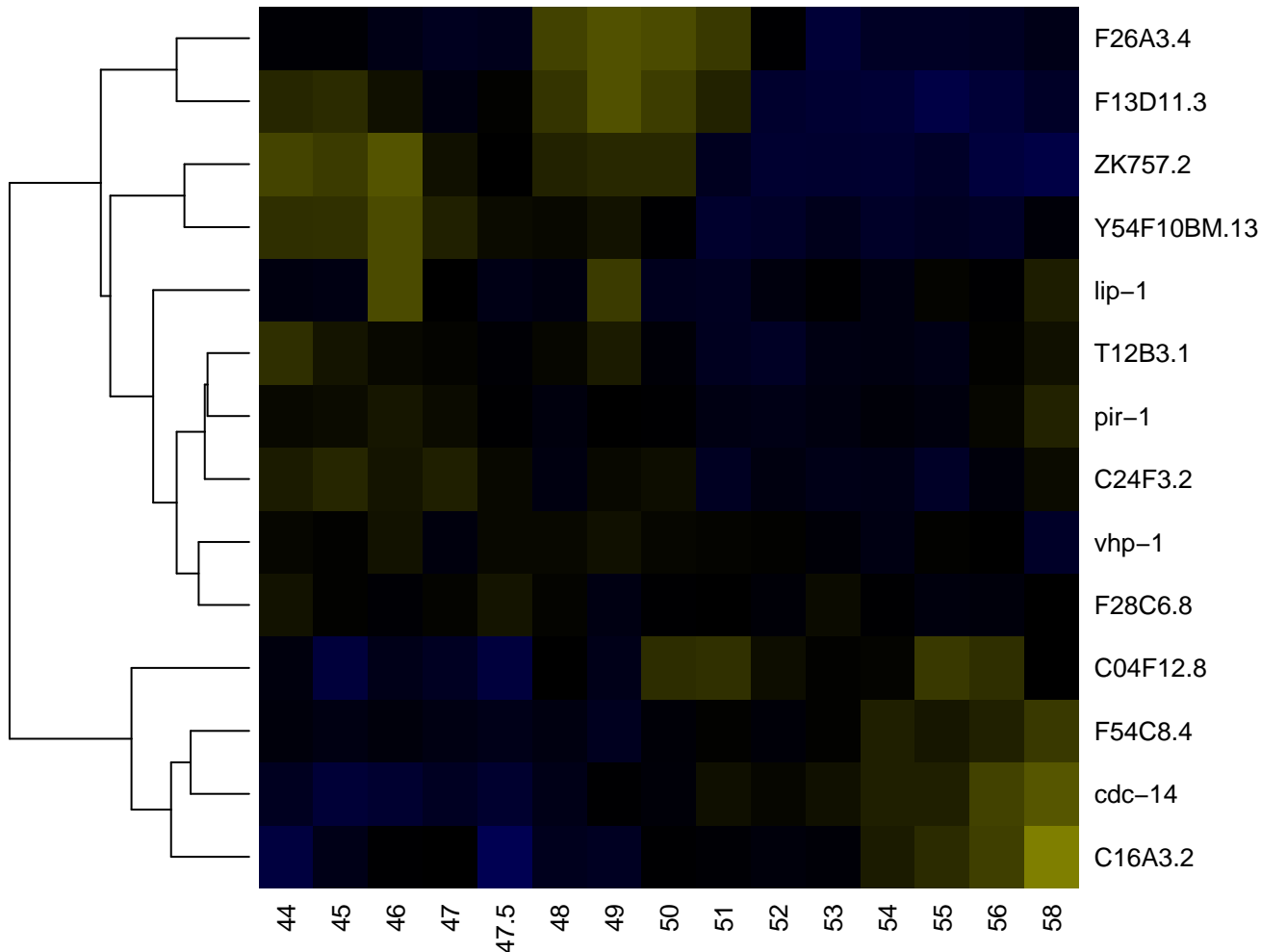
Doublecortin



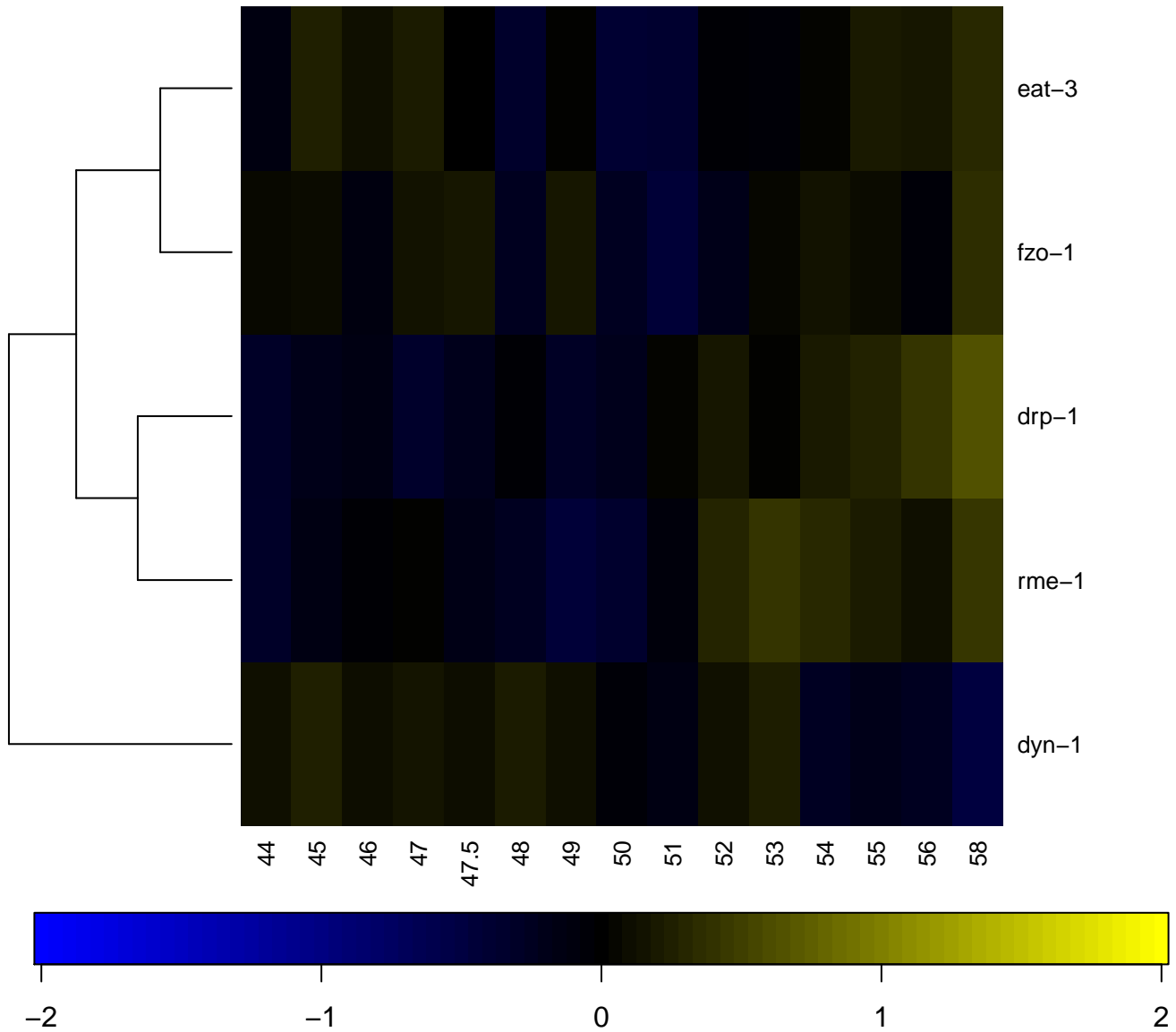
Dual specificity phosphatase, catalytic domain



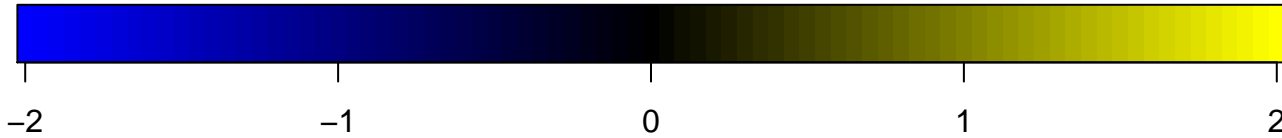
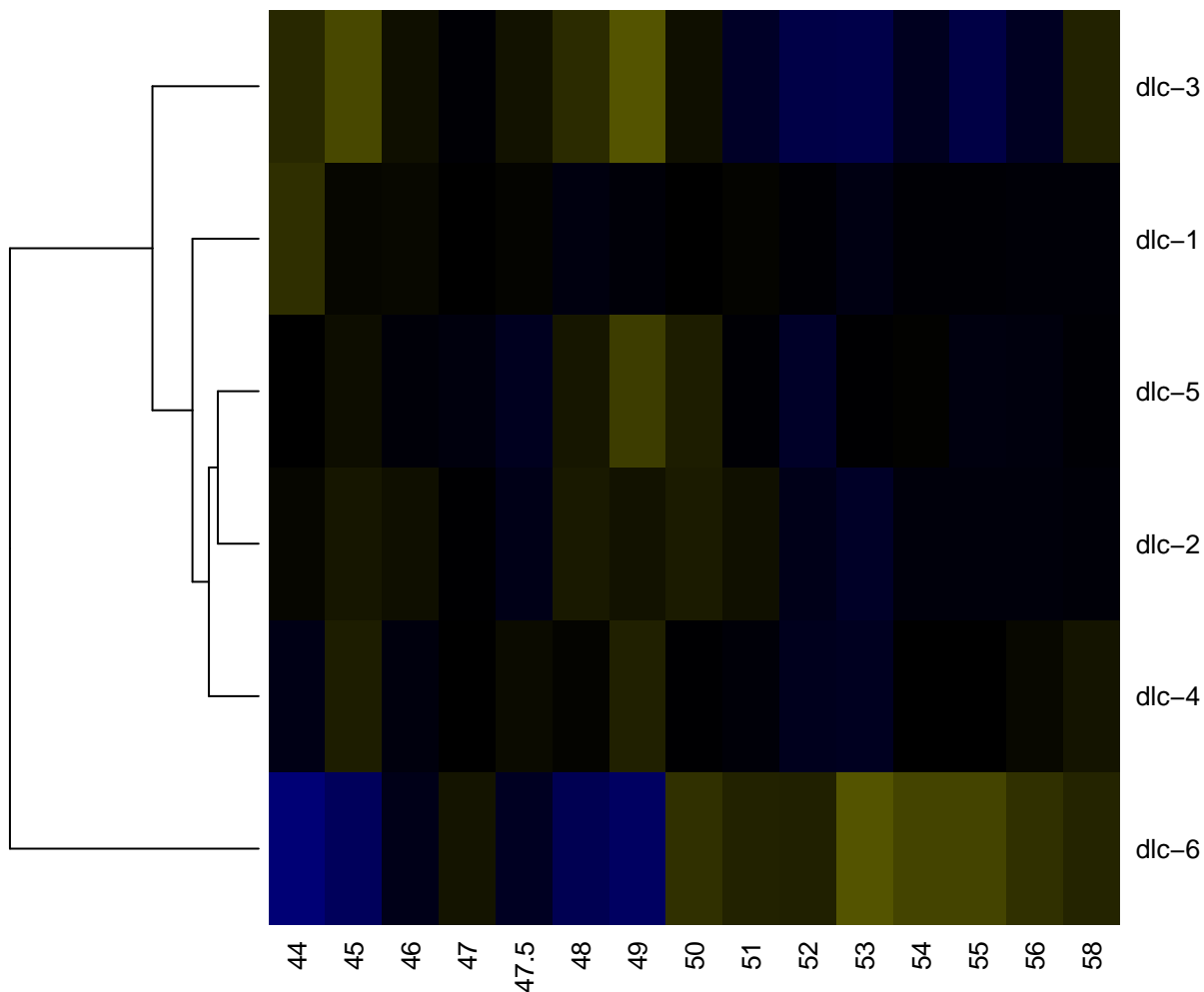
Dual specificity phosphatase, subgroup, catalytic domain



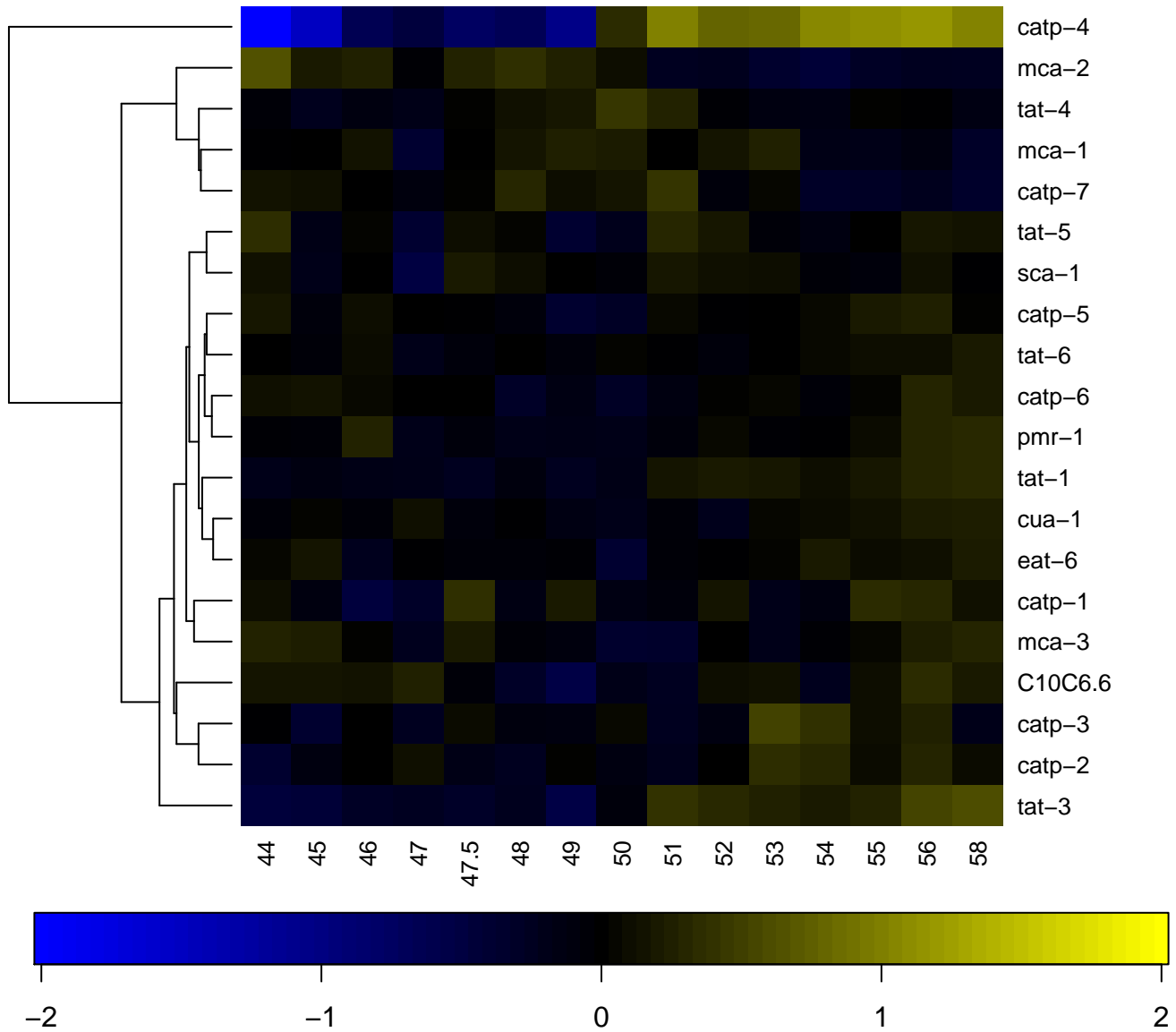
Dynamin, GTPase domain



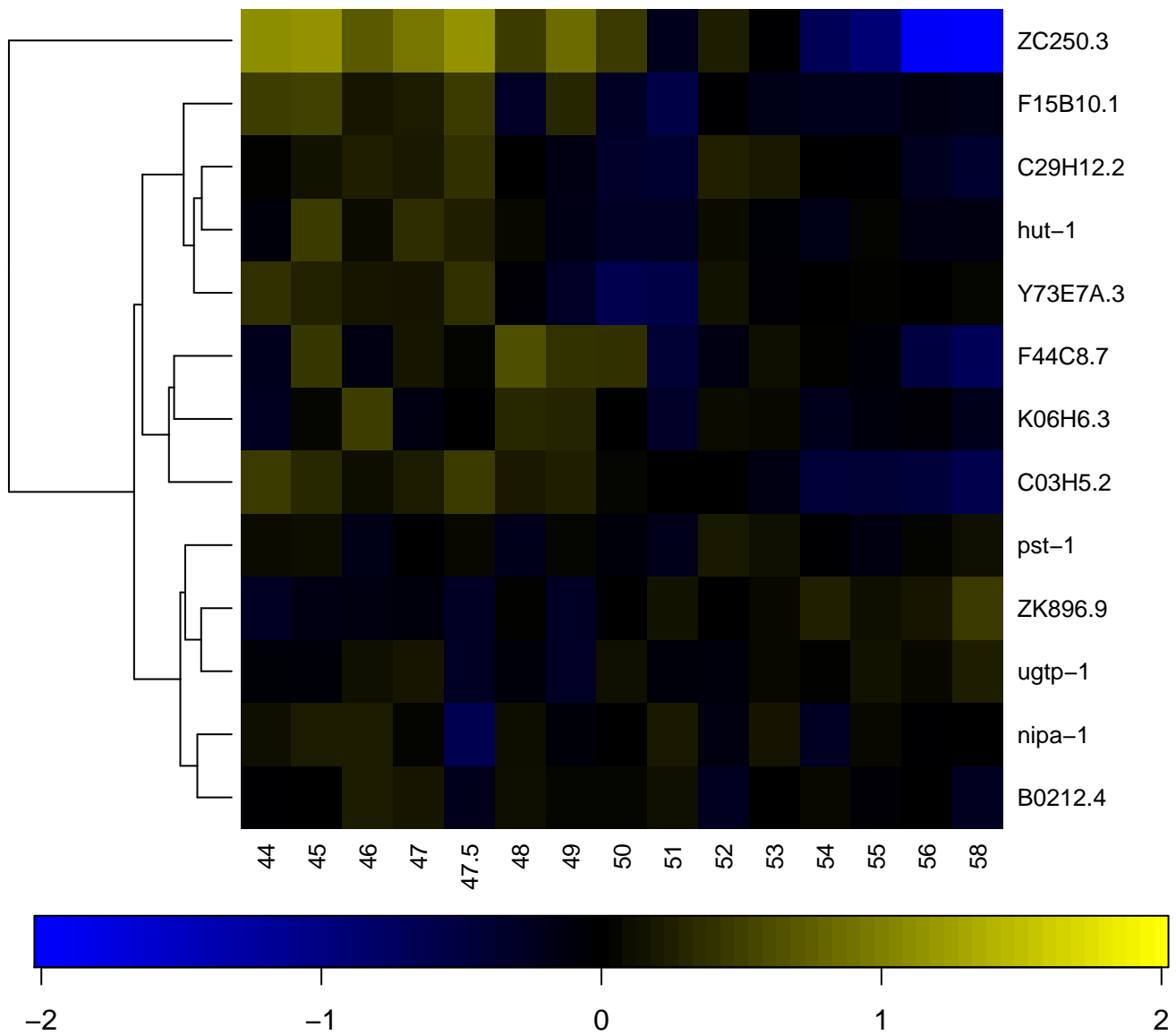
Dynein light chain, type 1/2



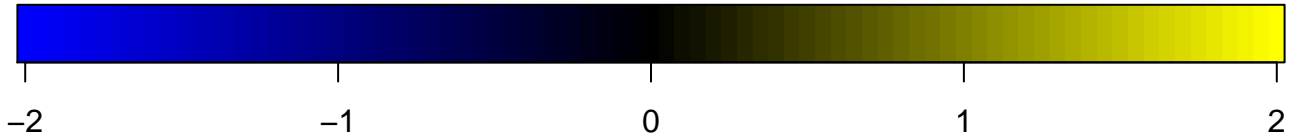
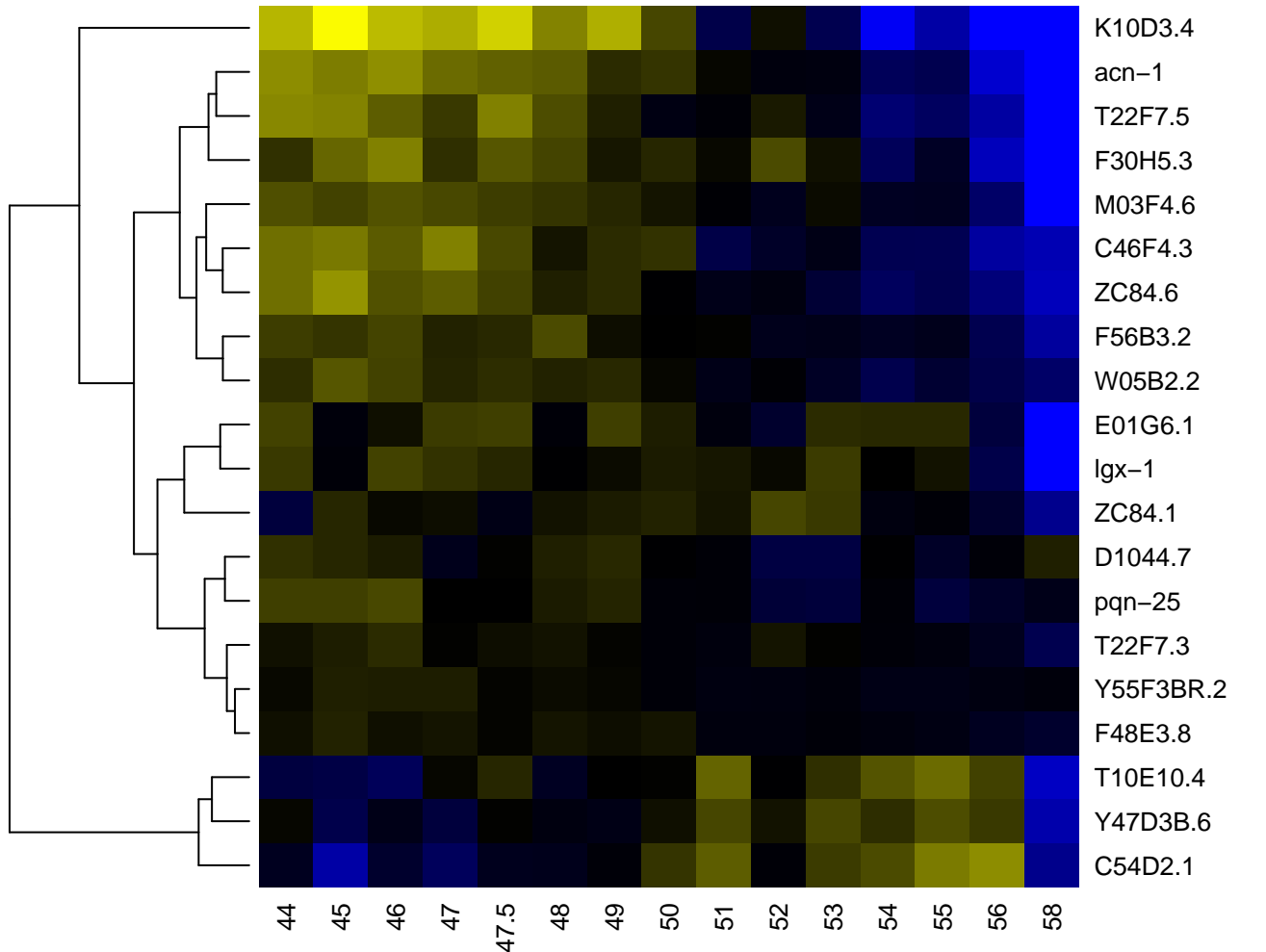
E1-E2 ATPase



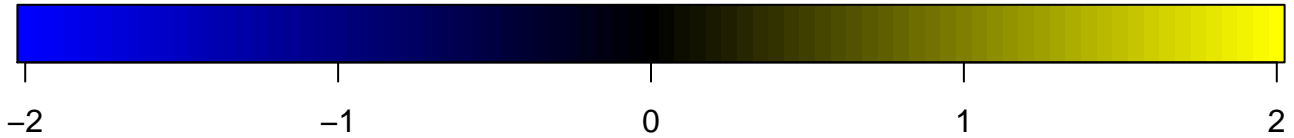
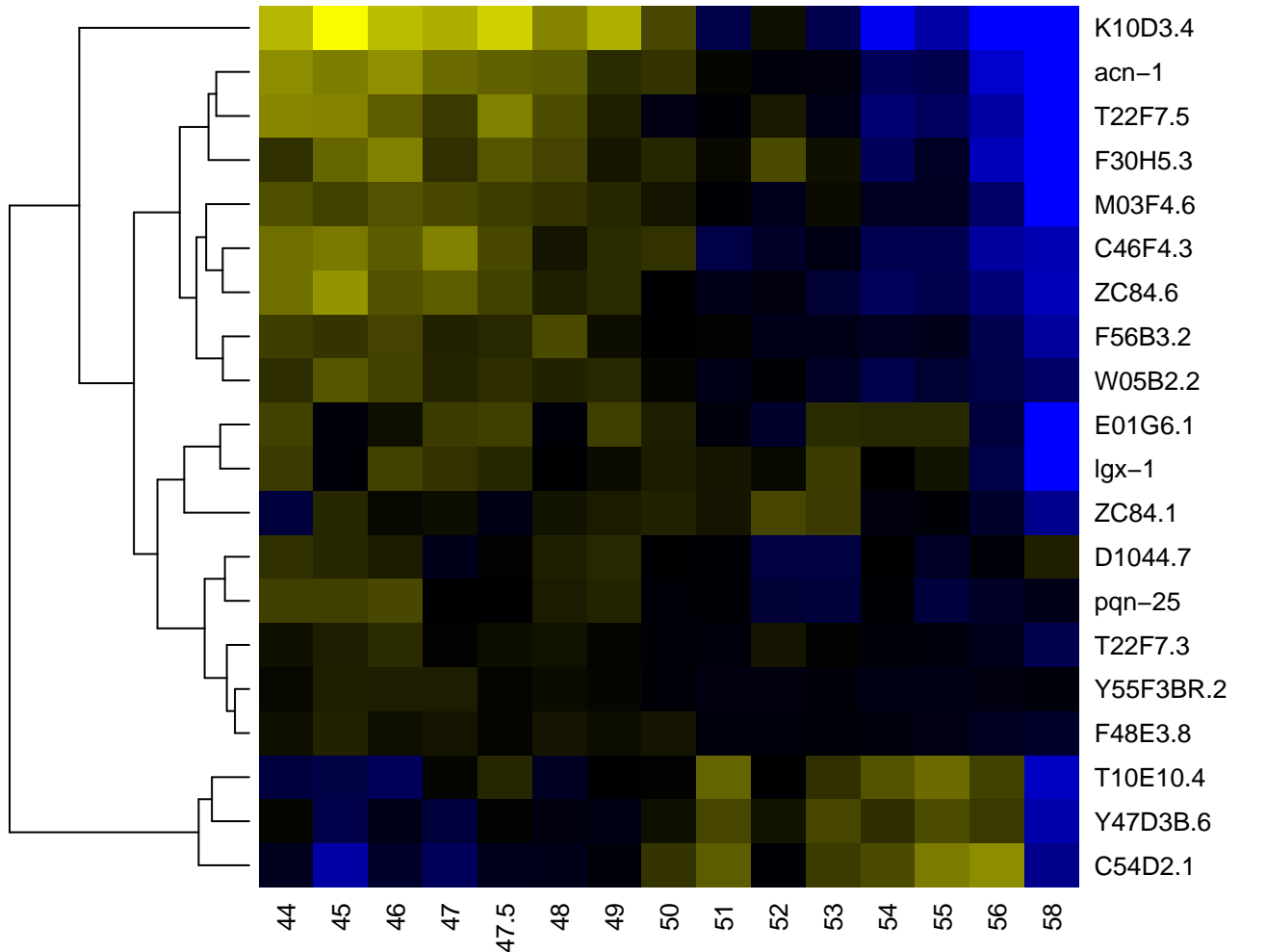
EamA-like transporter family



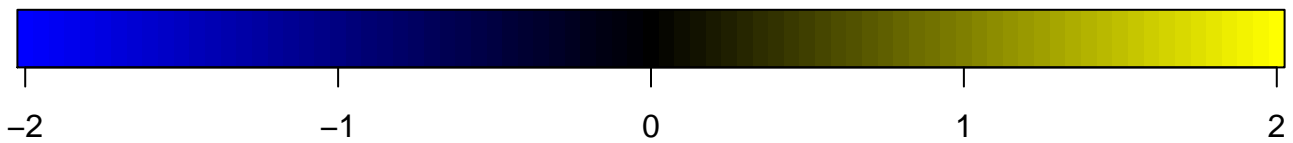
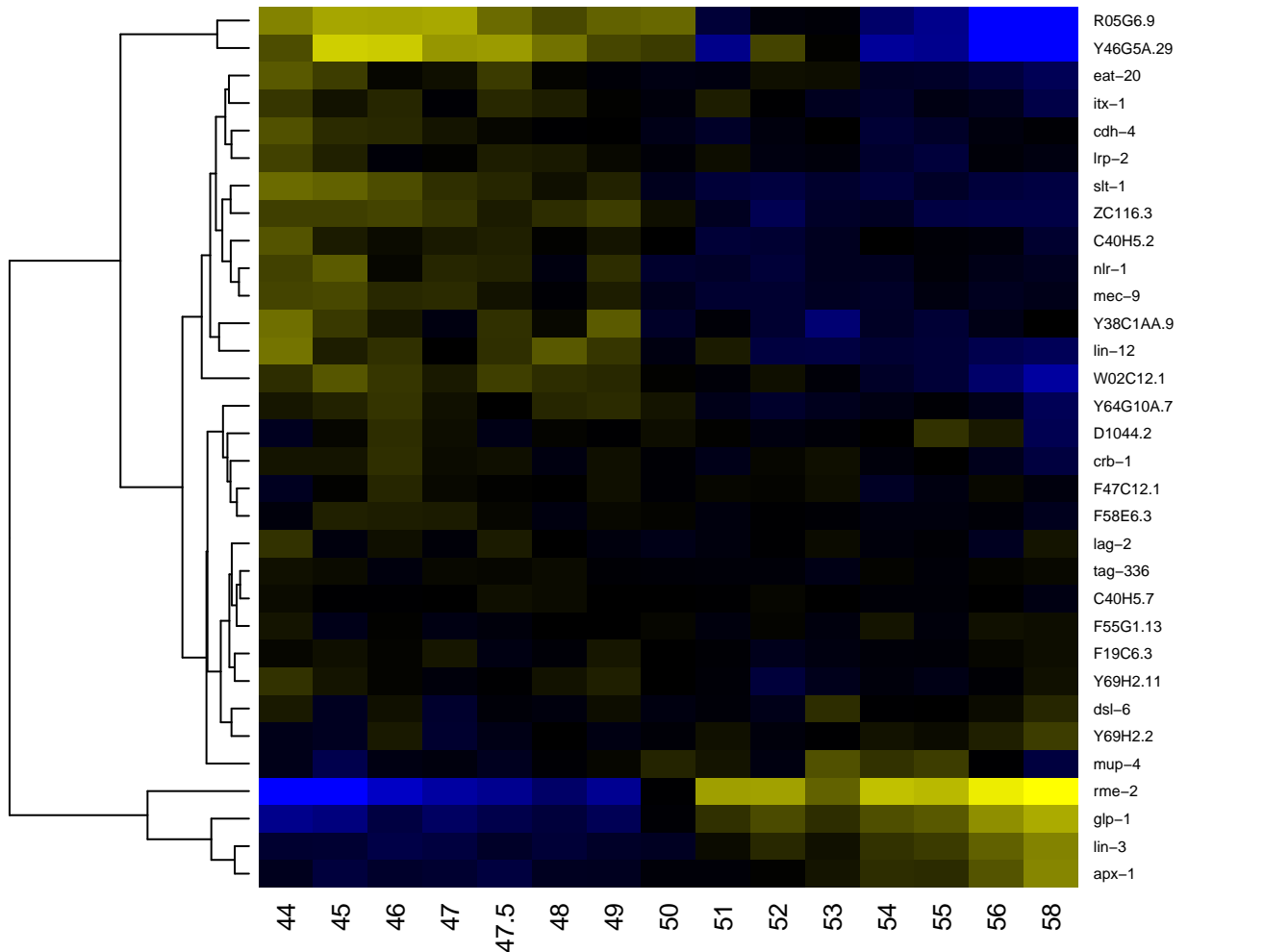
EB domain



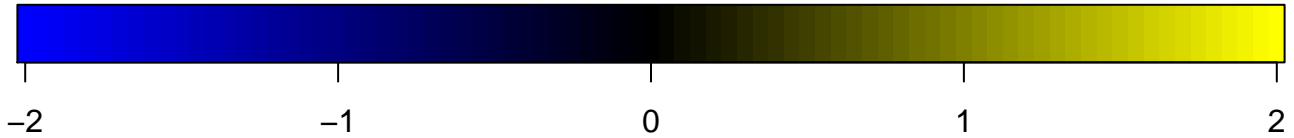
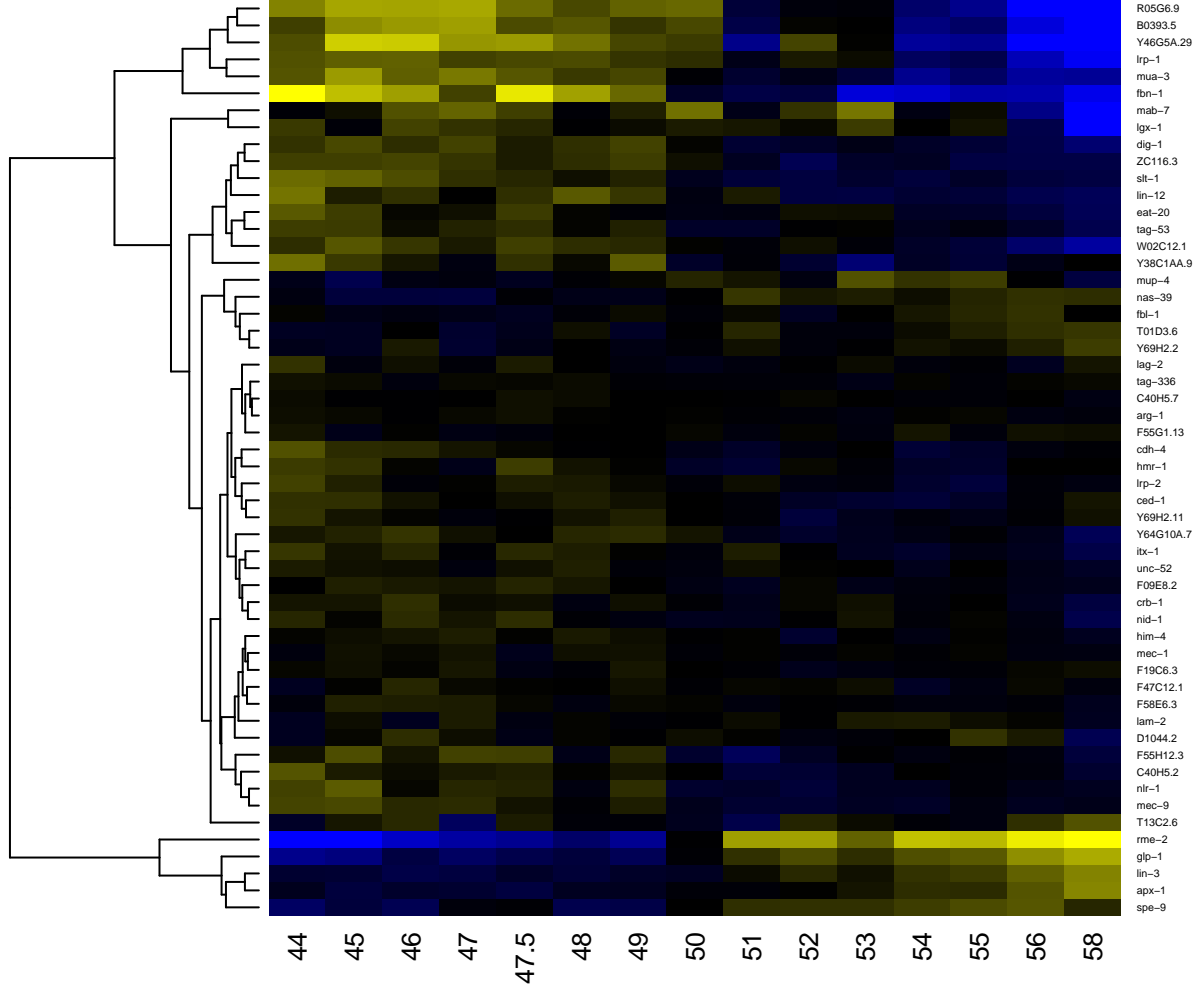
EB module



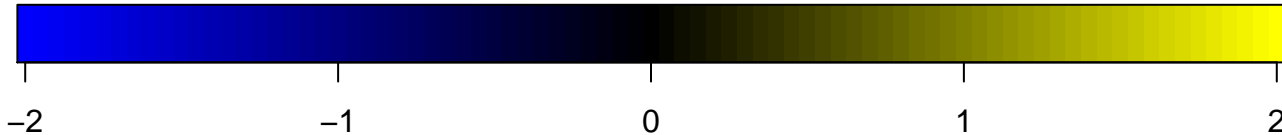
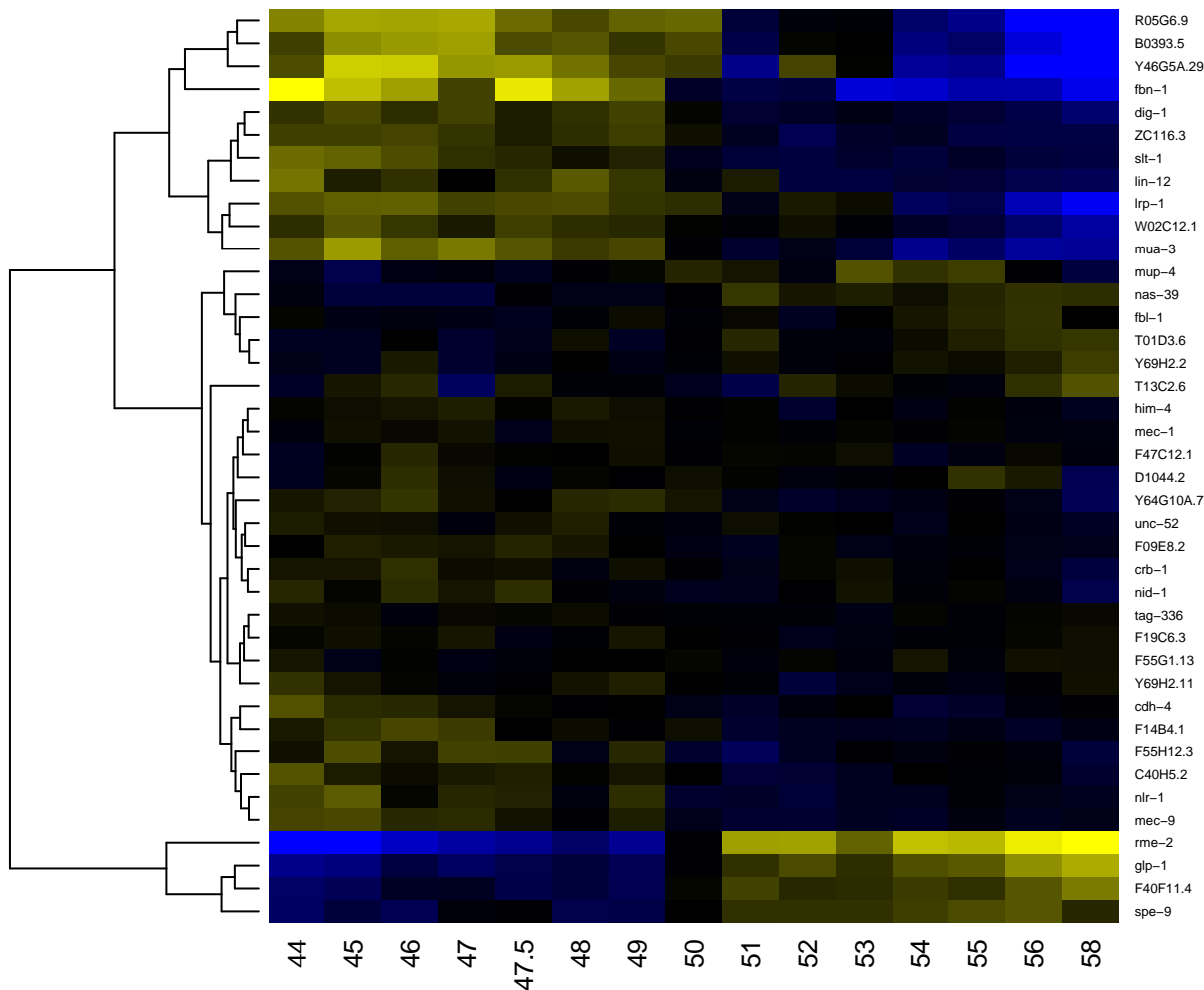
EGF



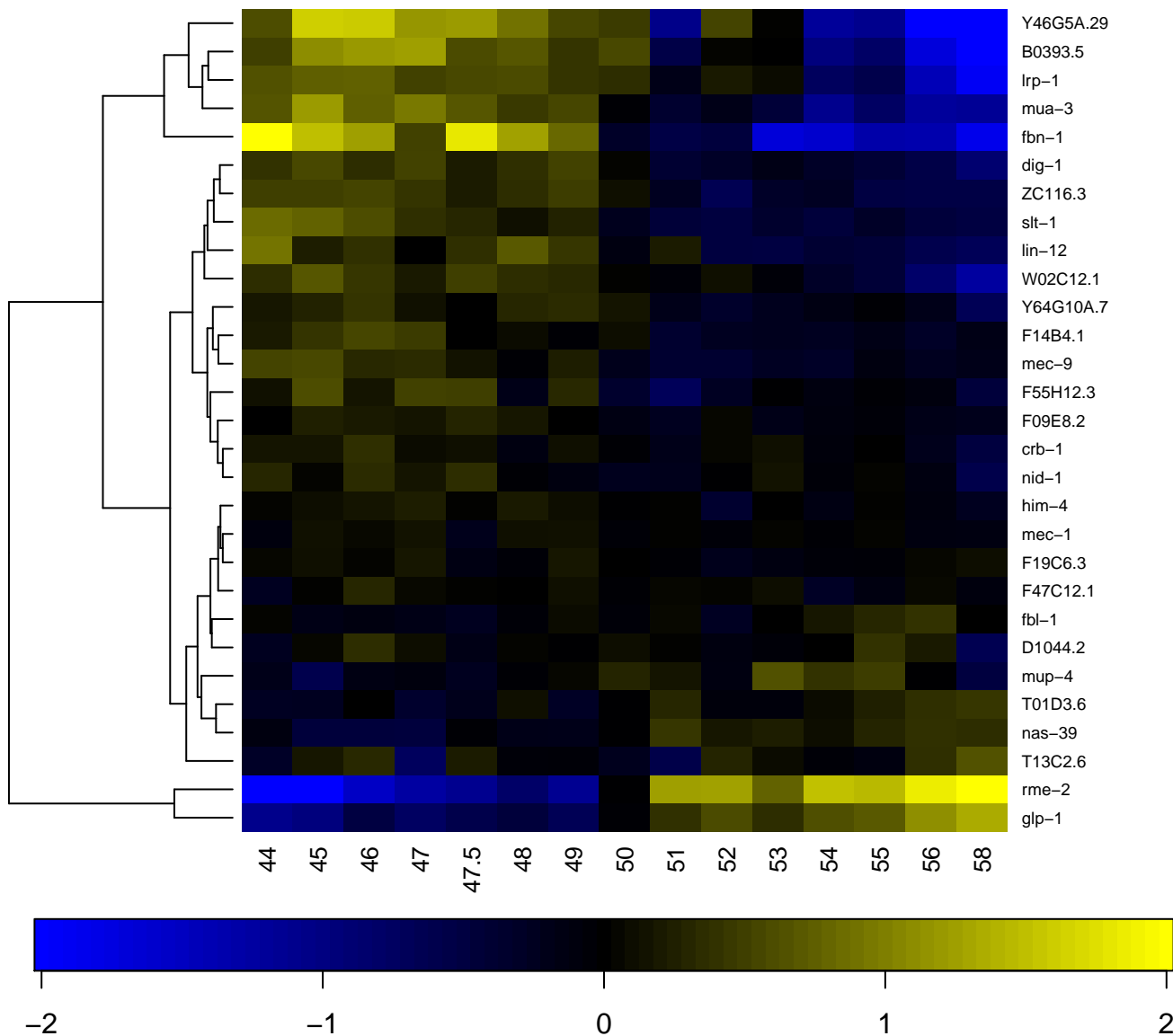
EGF-like



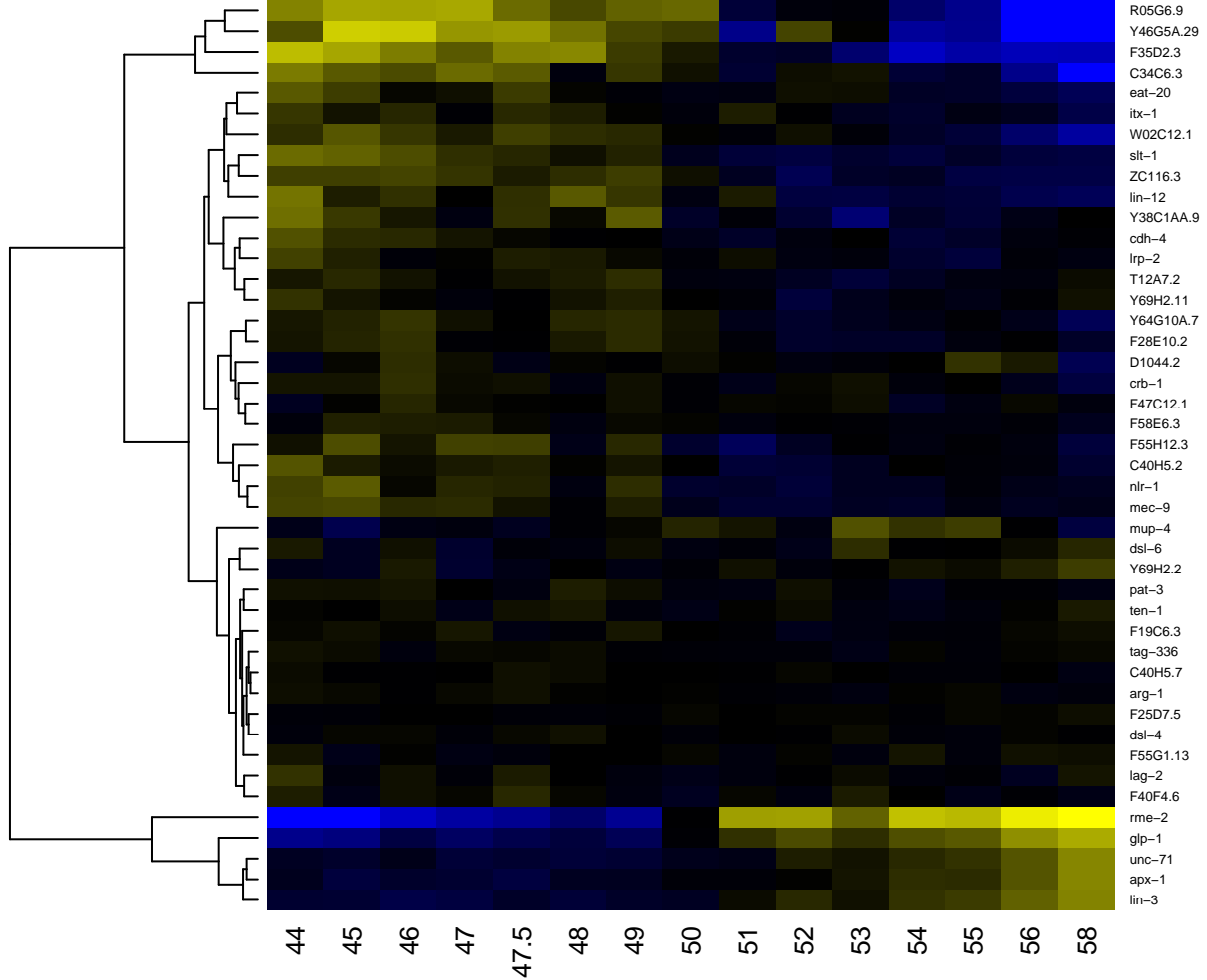
EGF-like calcium-binding



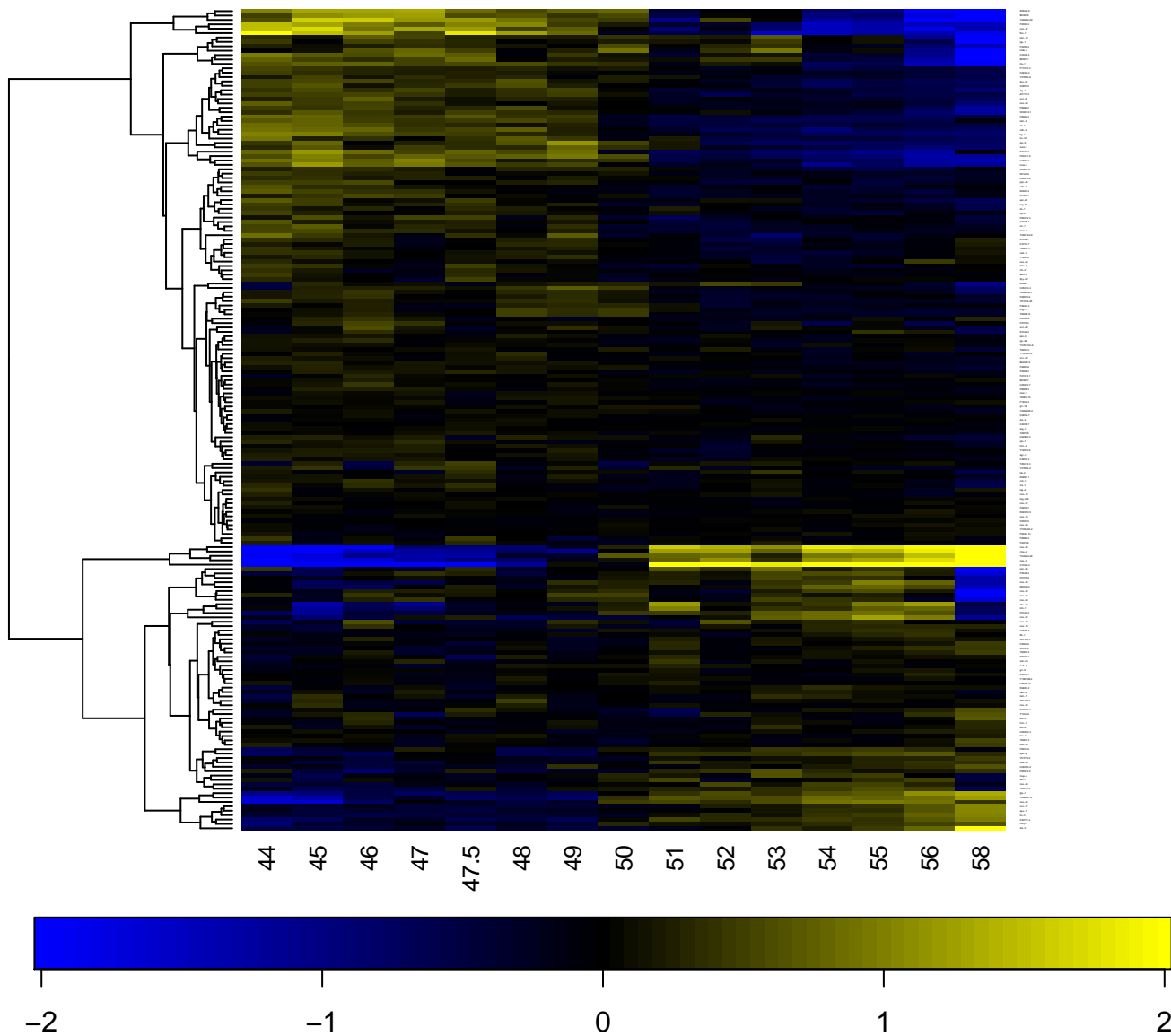
EGF-like calcium-binding, conserved site



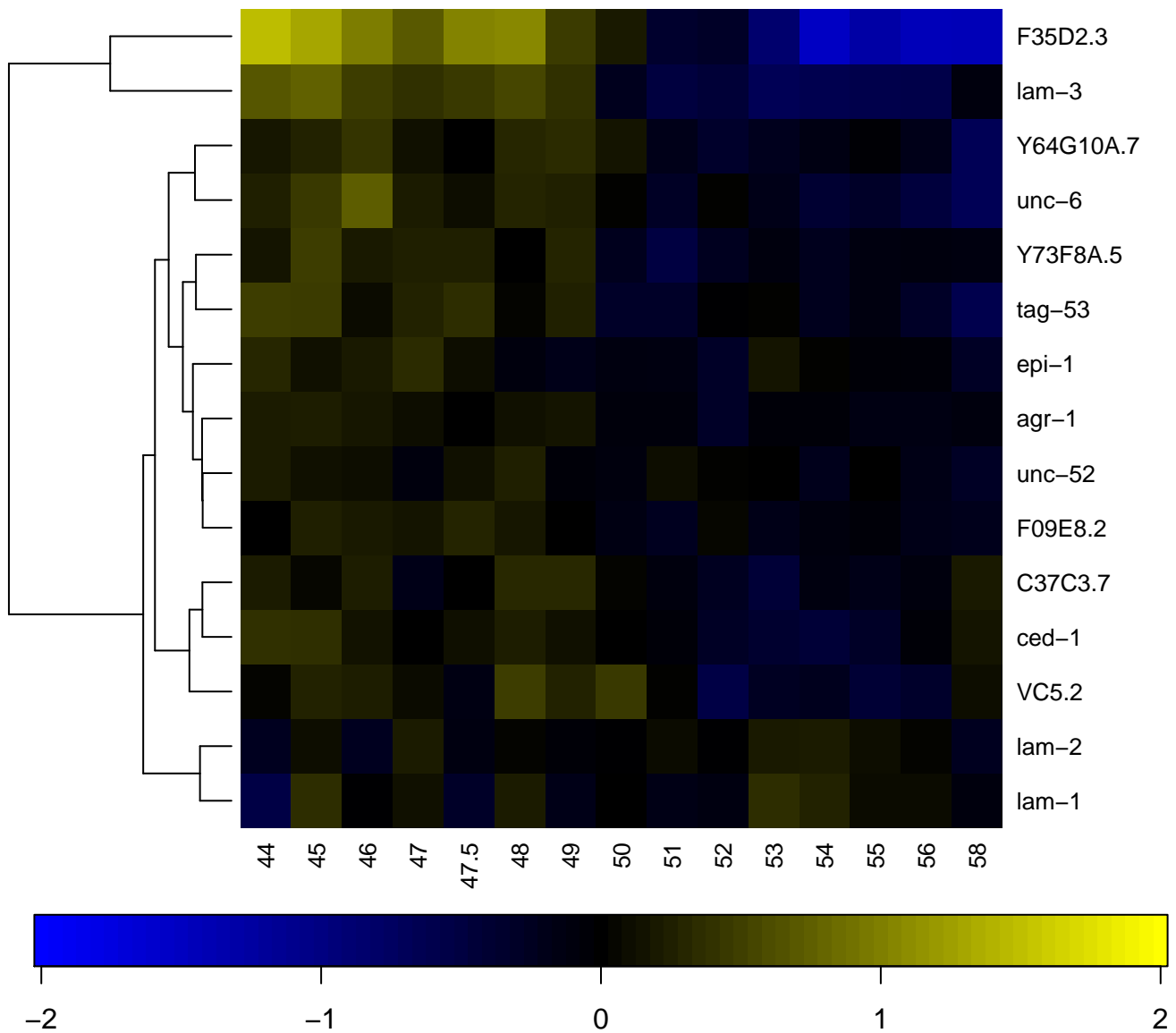
EGF-like domain



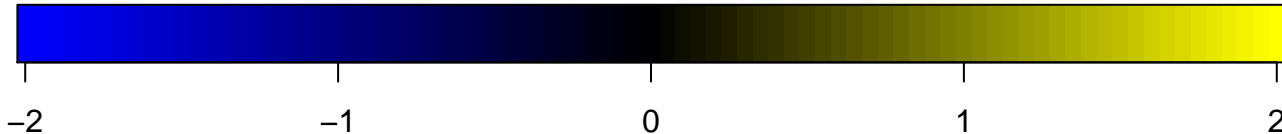
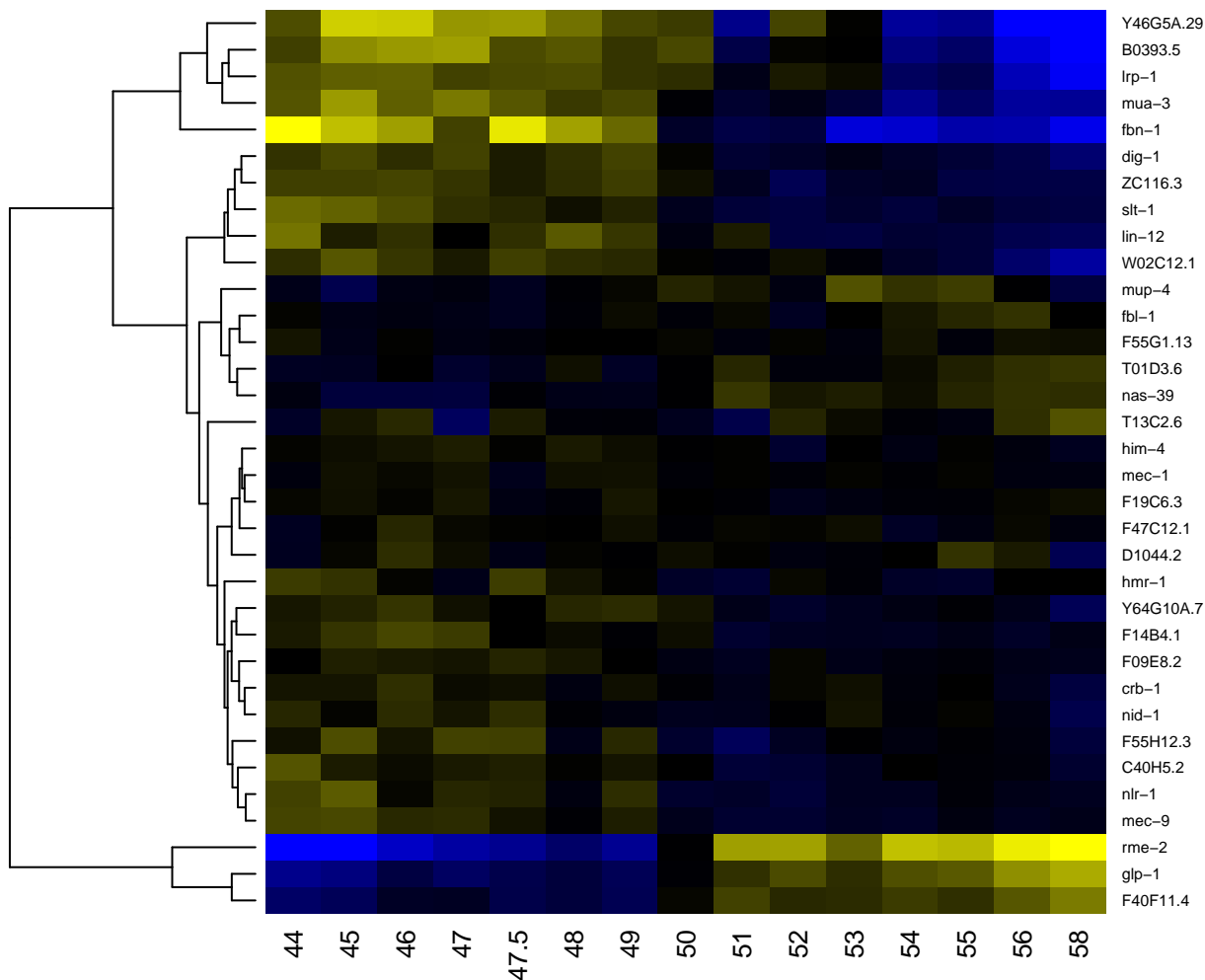
EGF-like region, conserved site



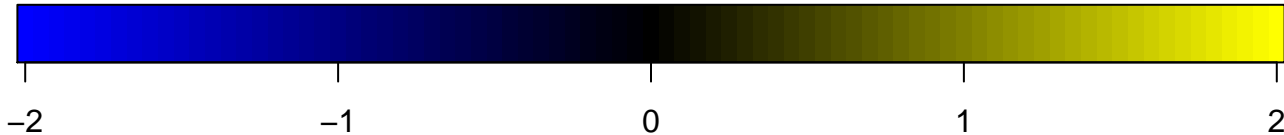
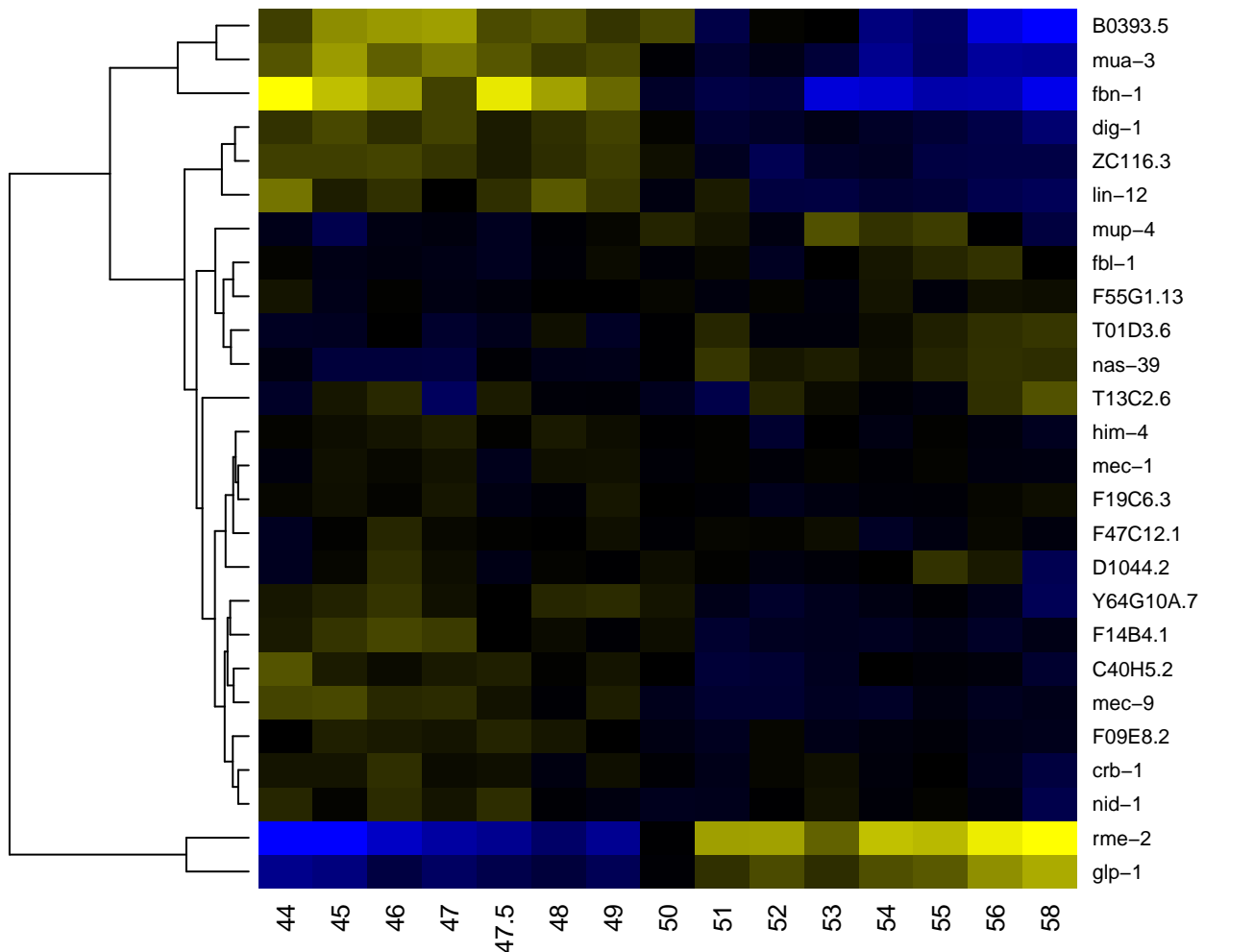
EGF-like, laminin



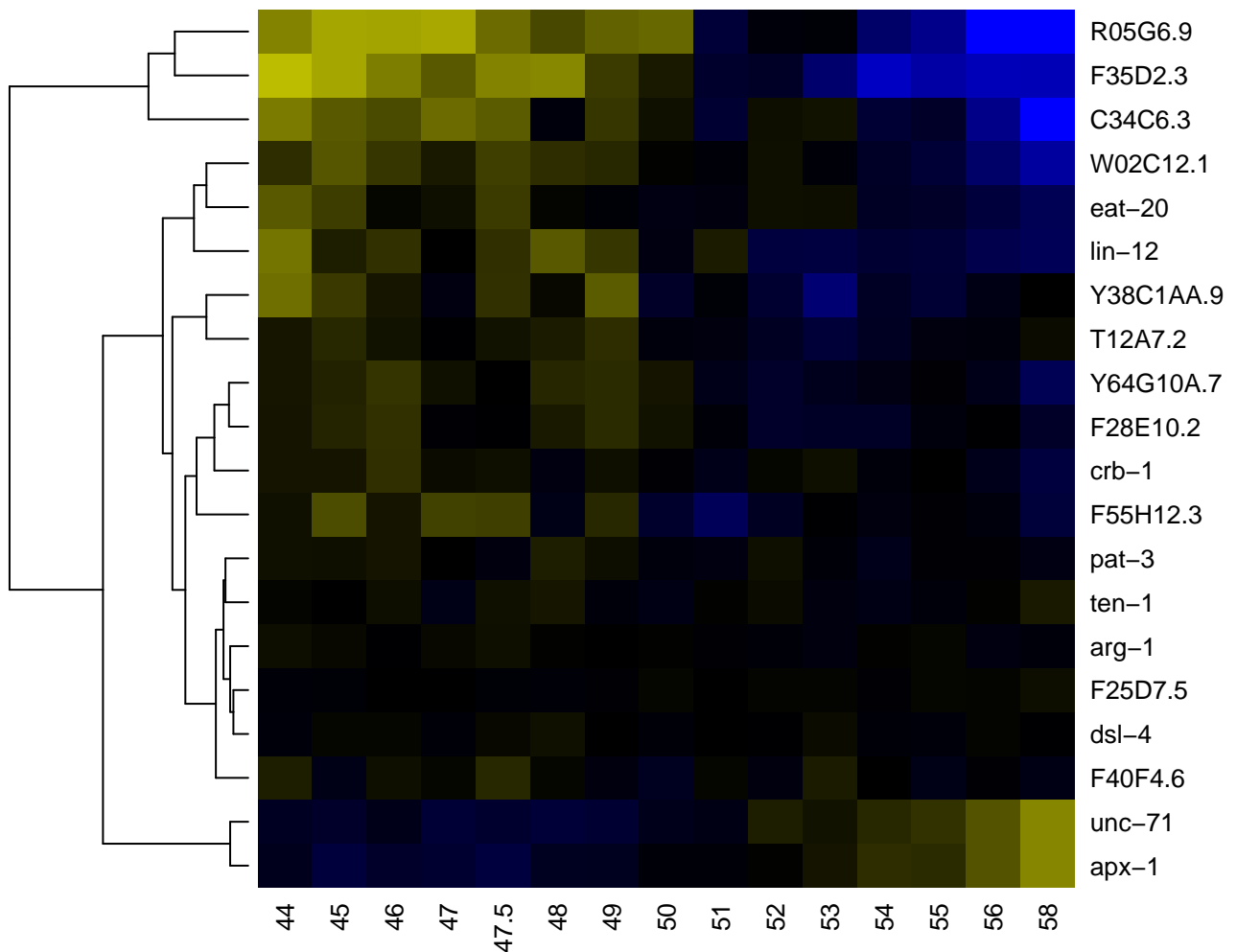
EGF-type aspartate/asparagine hydroxylation site



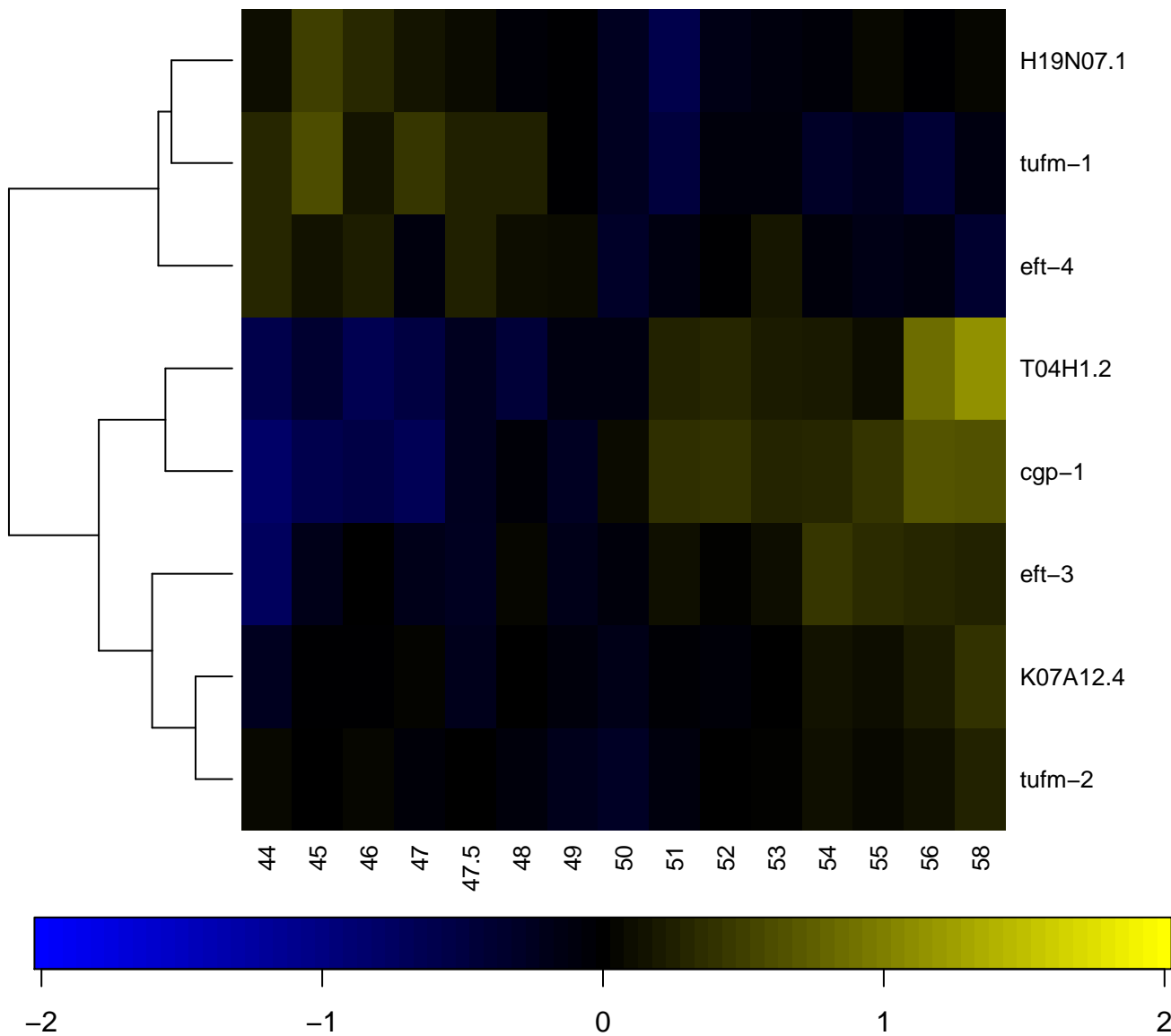
EGF calcium-binding



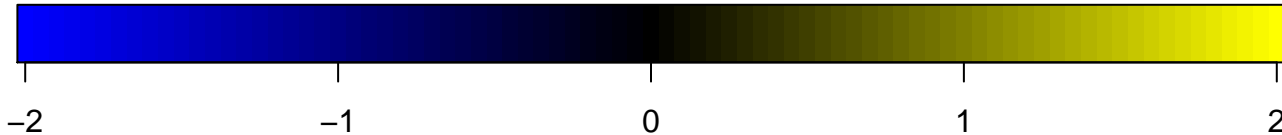
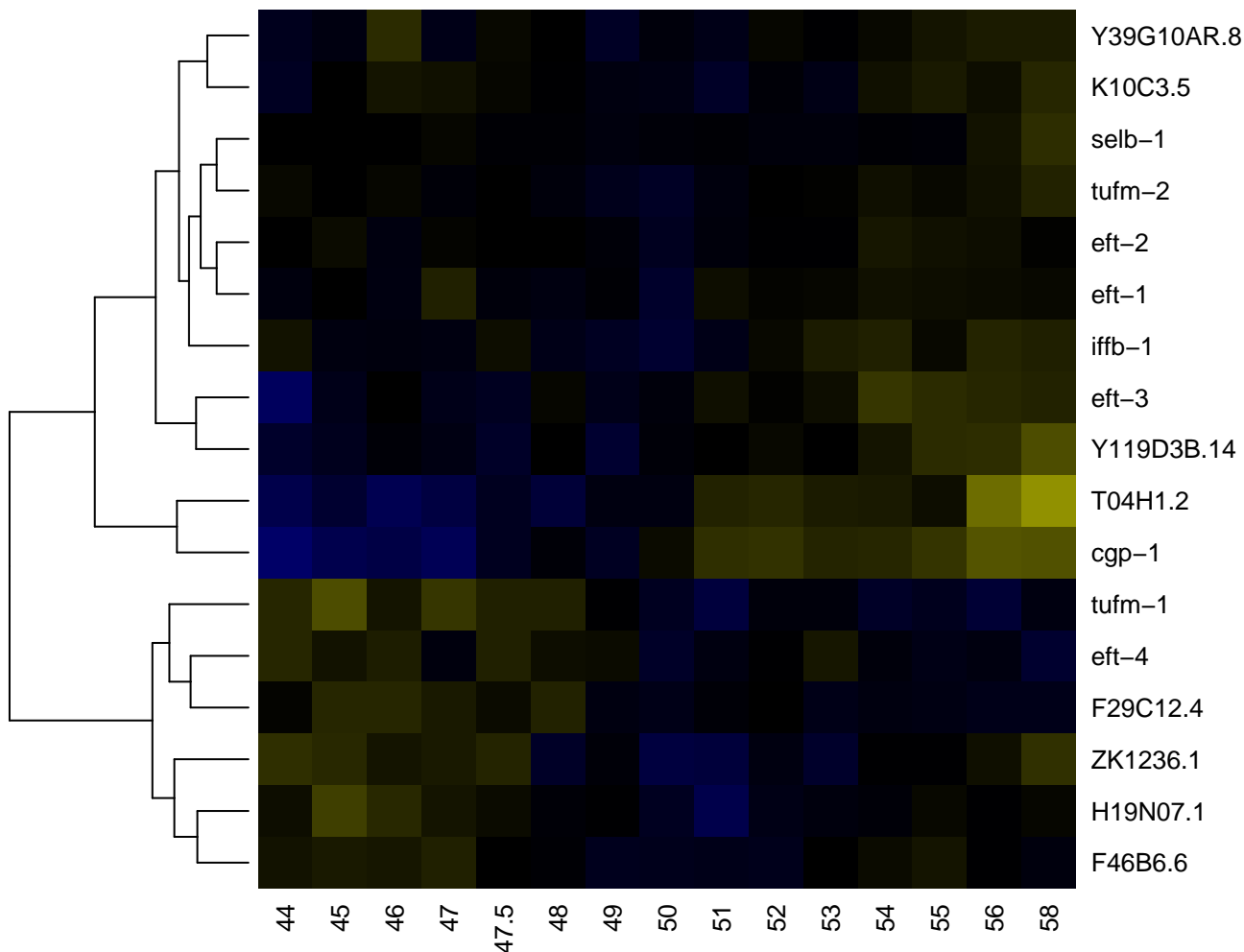
EGF, extracellular



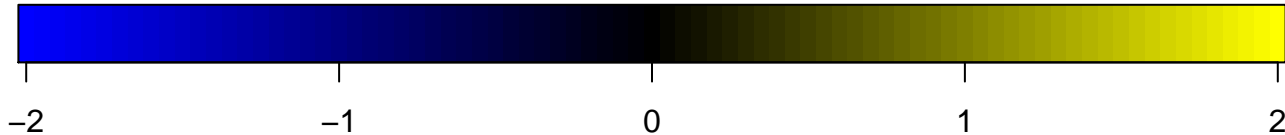
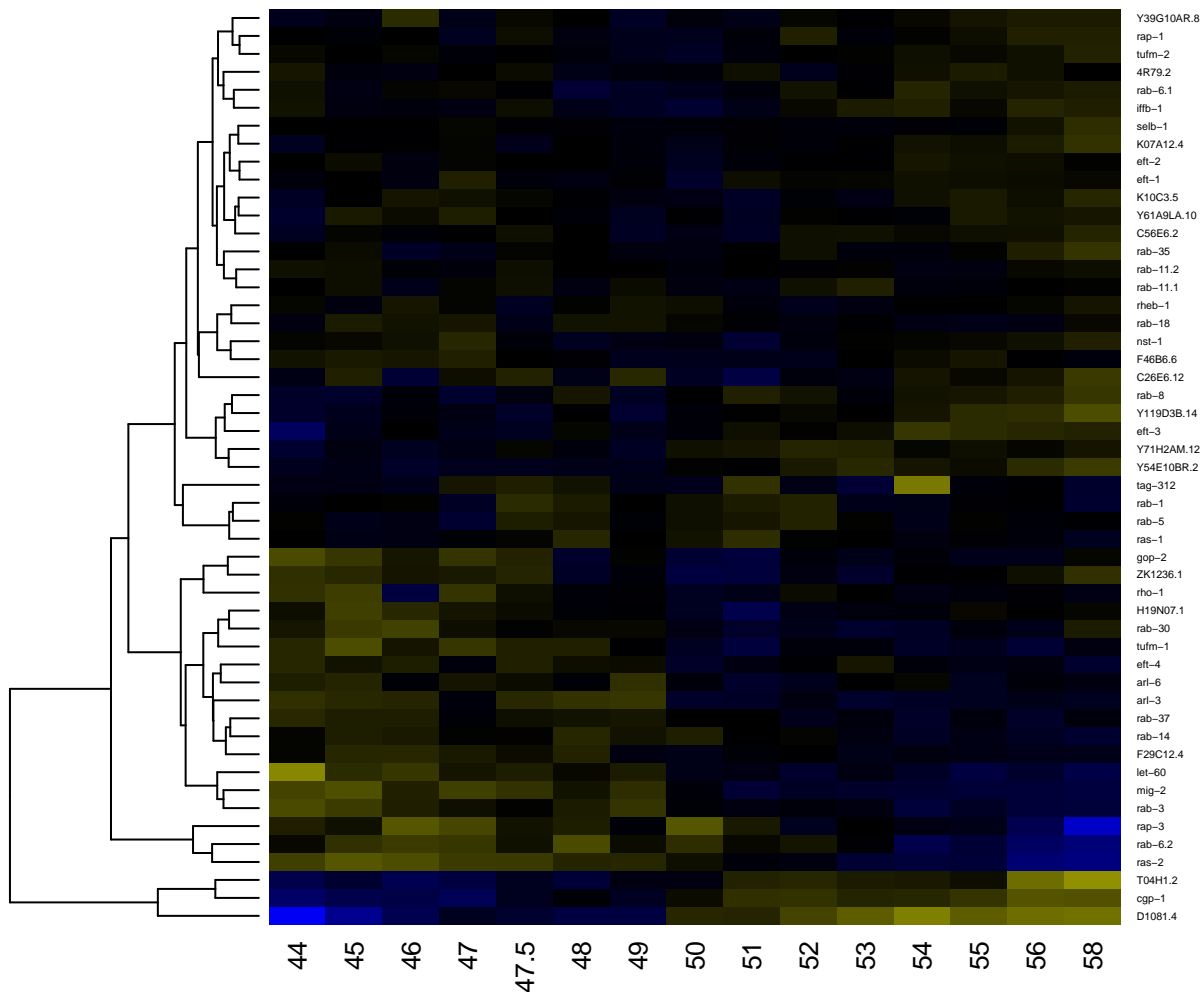
Elongation factor Tu C-terminal domain



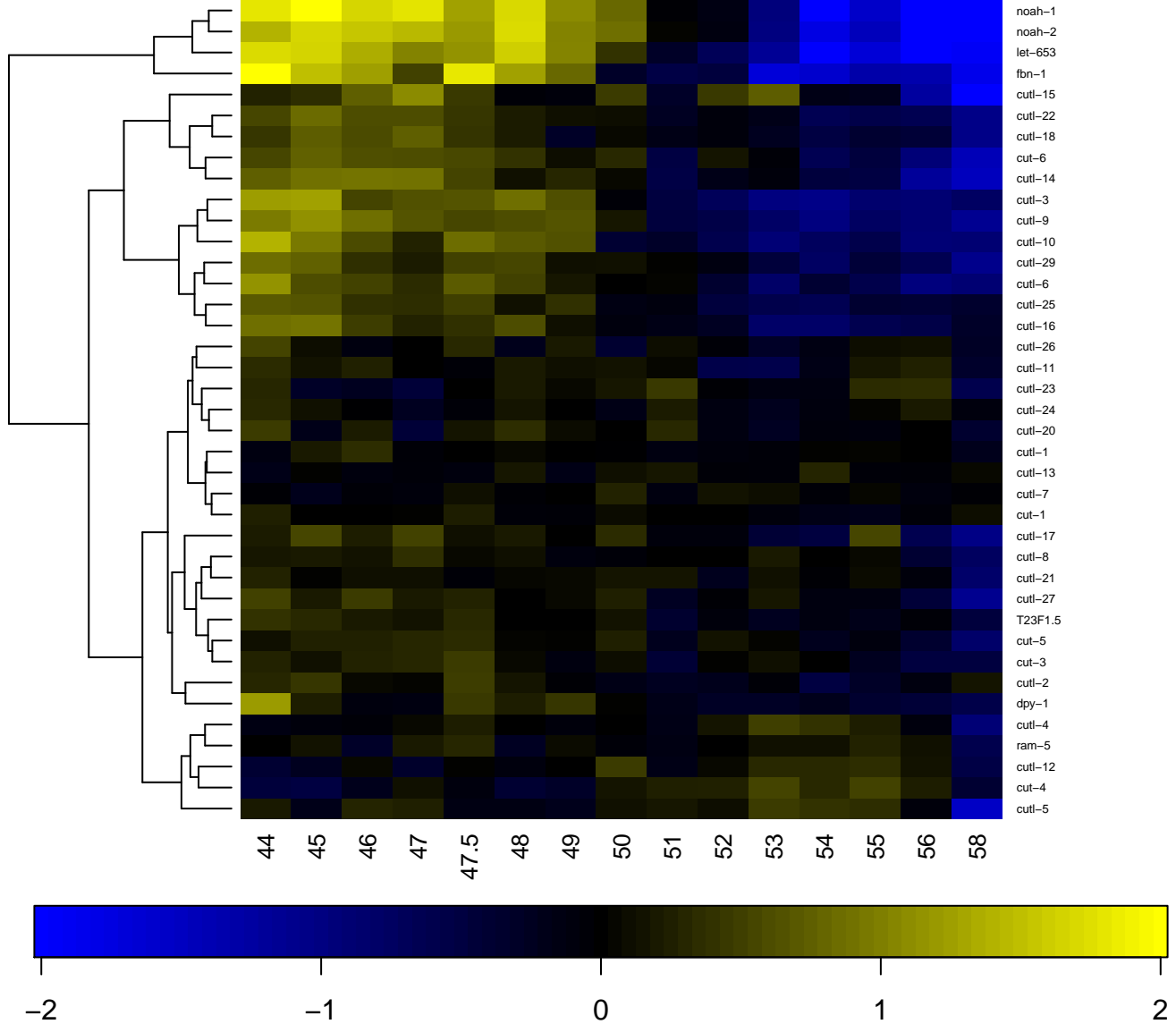
Elongation factor Tu domain 2



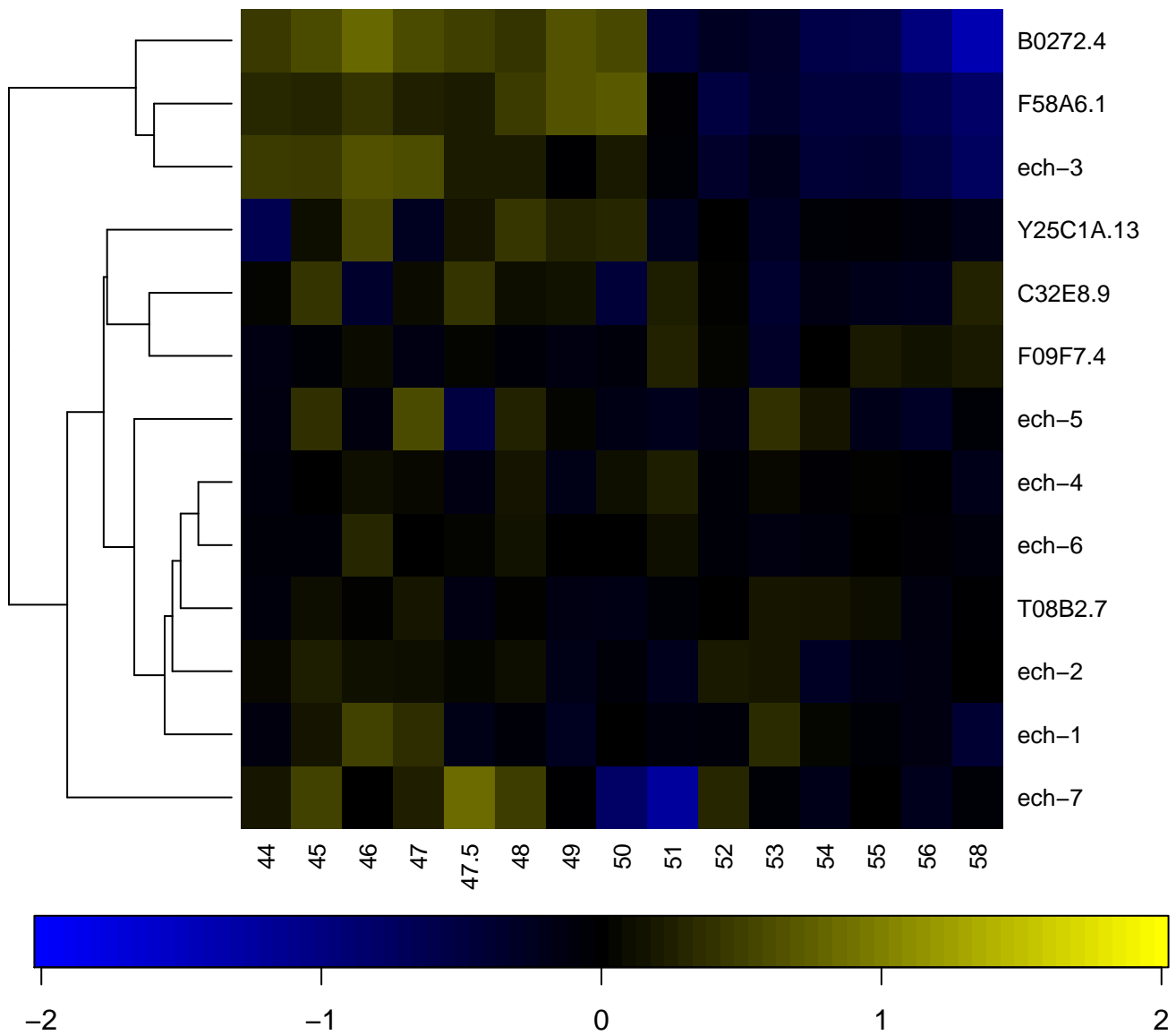
Elongation factor Tu GTP binding domain



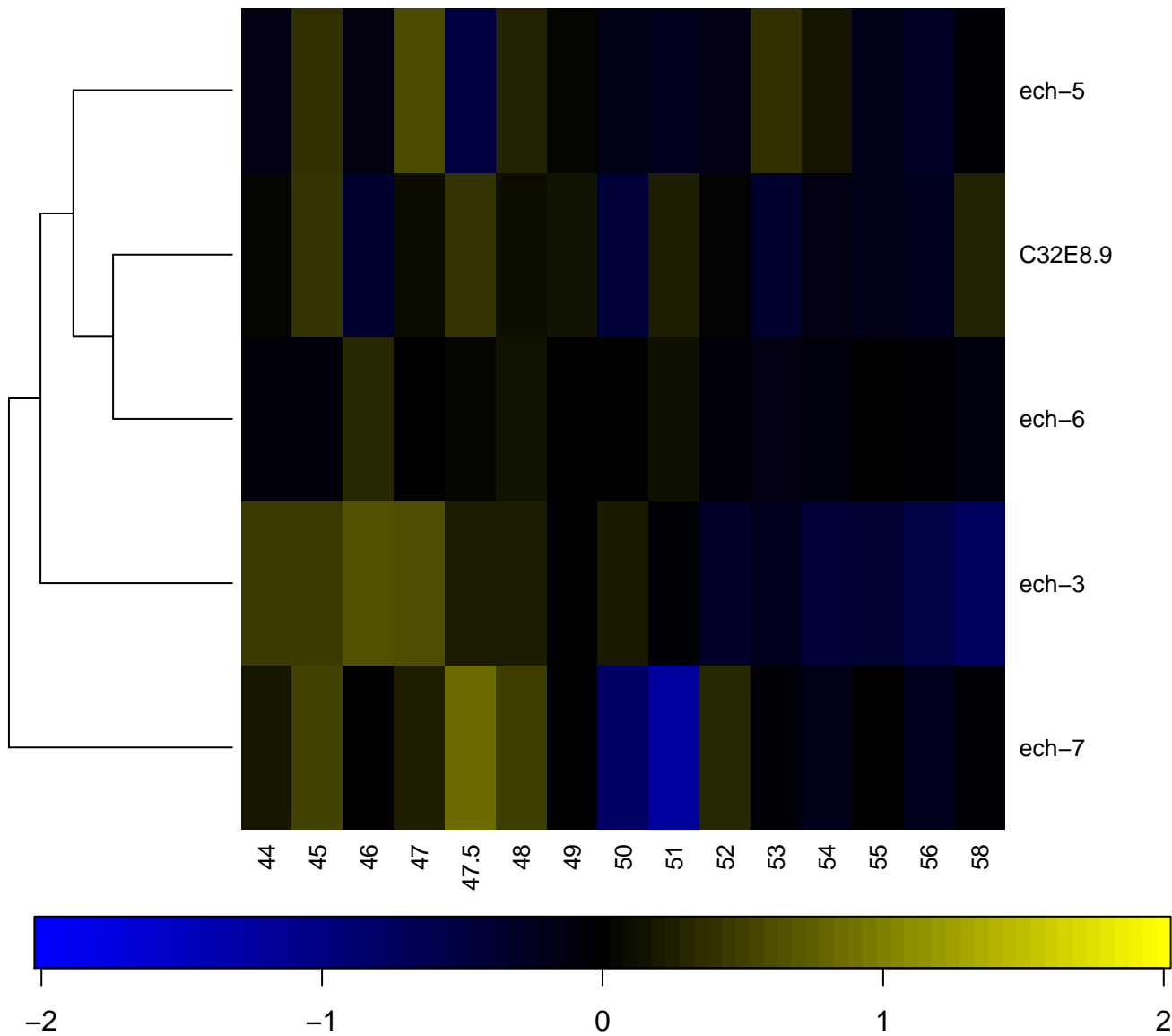
Endoglin/CD105 antigen



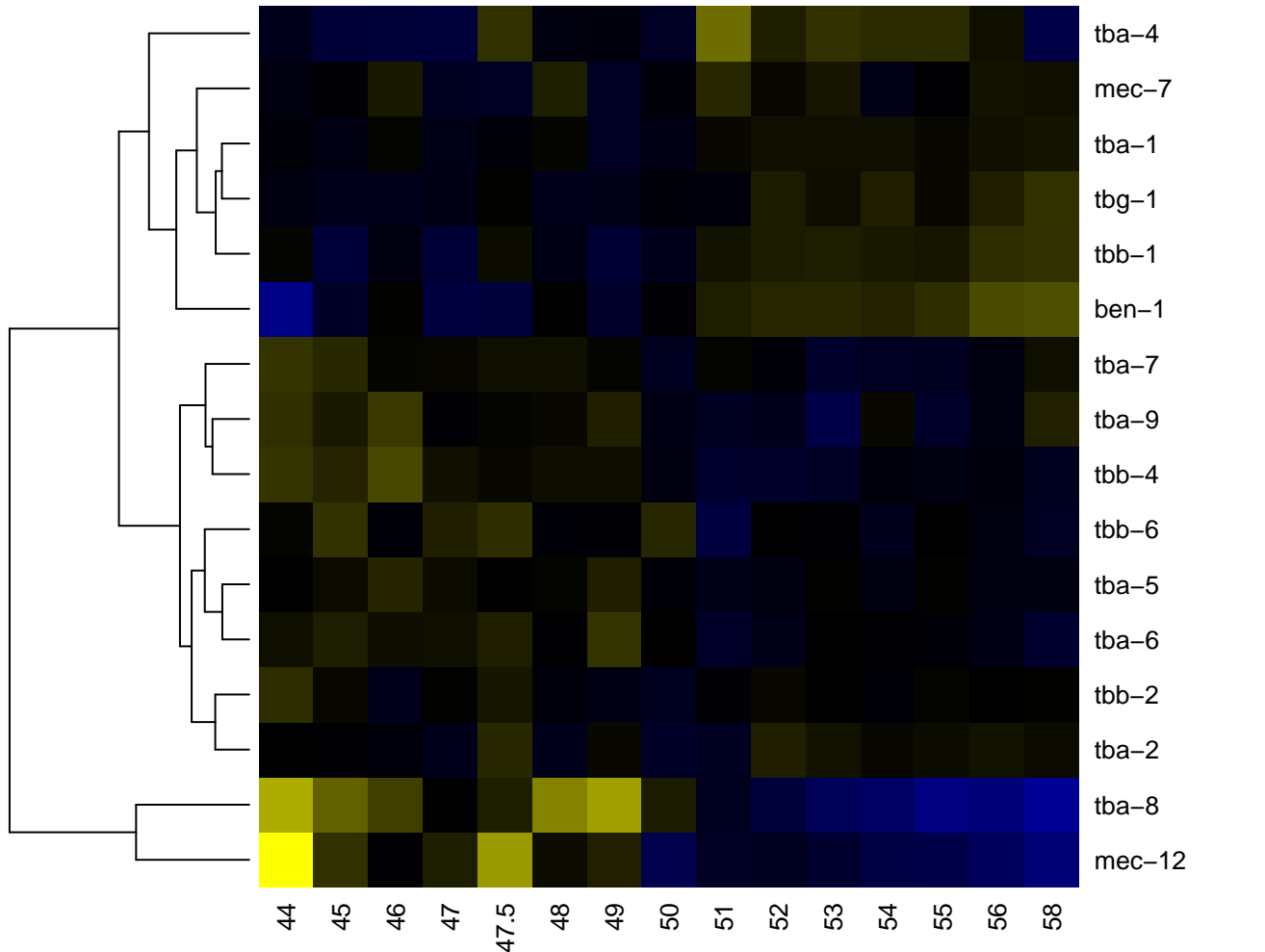
Enoyl-CoA hydratase/isomerase family



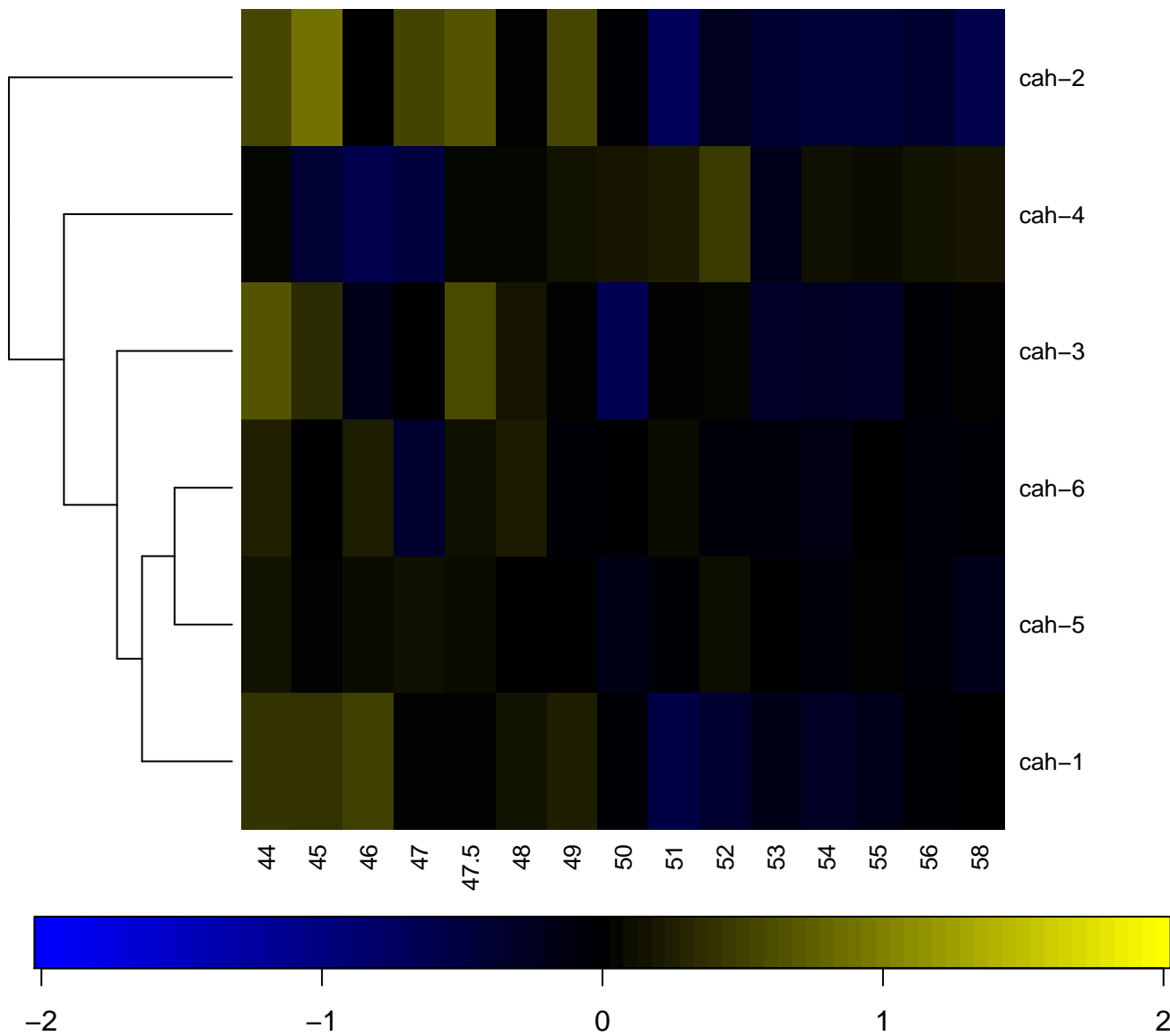
Enoyl-CoA hydratase/isomerase, conserved site



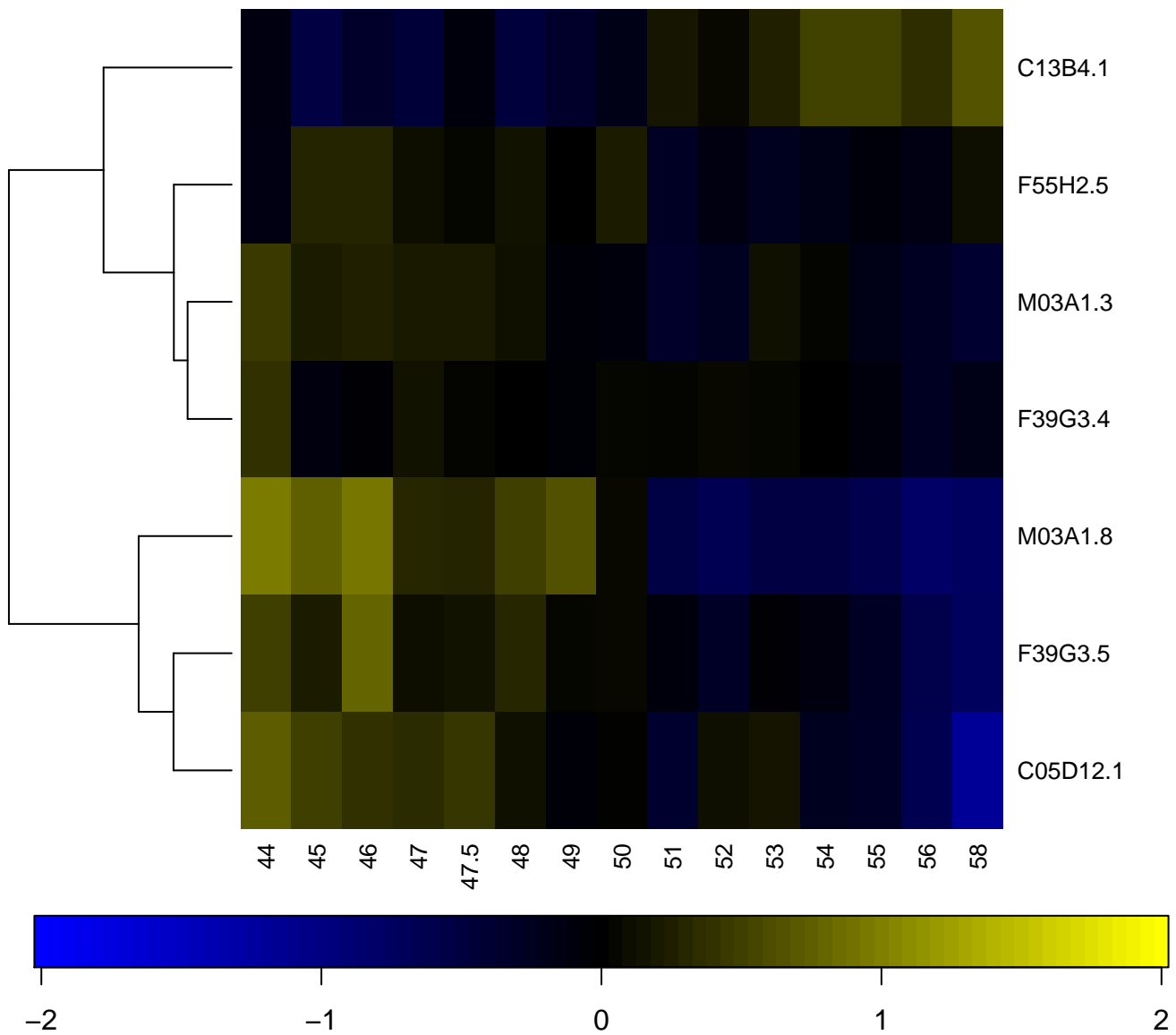
Epsilon tubulin



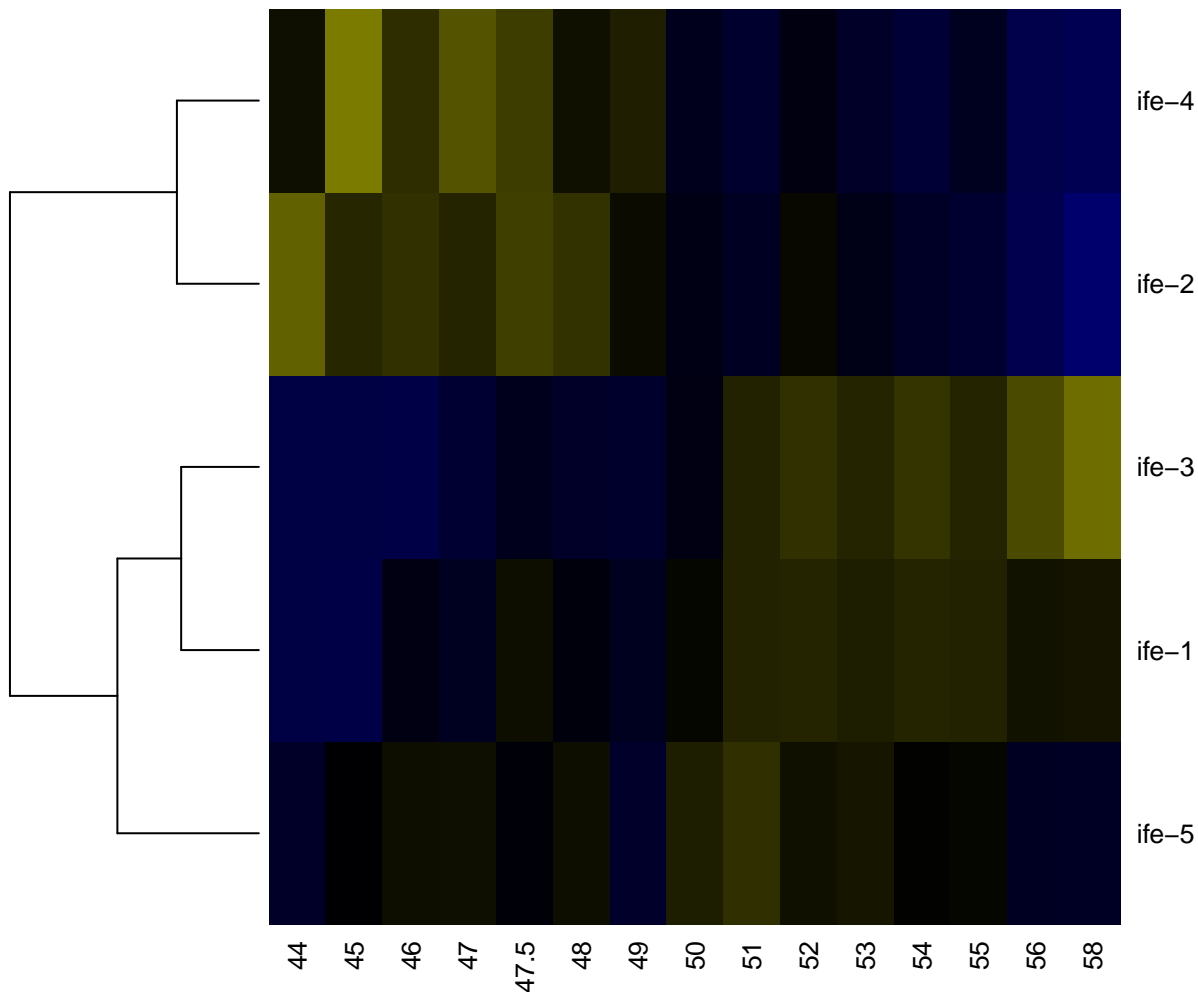
Eukaryotic-type carbonic anhydrase



Eukaryotic cytochrome b561



Eukaryotic initiation factor 4E



-2

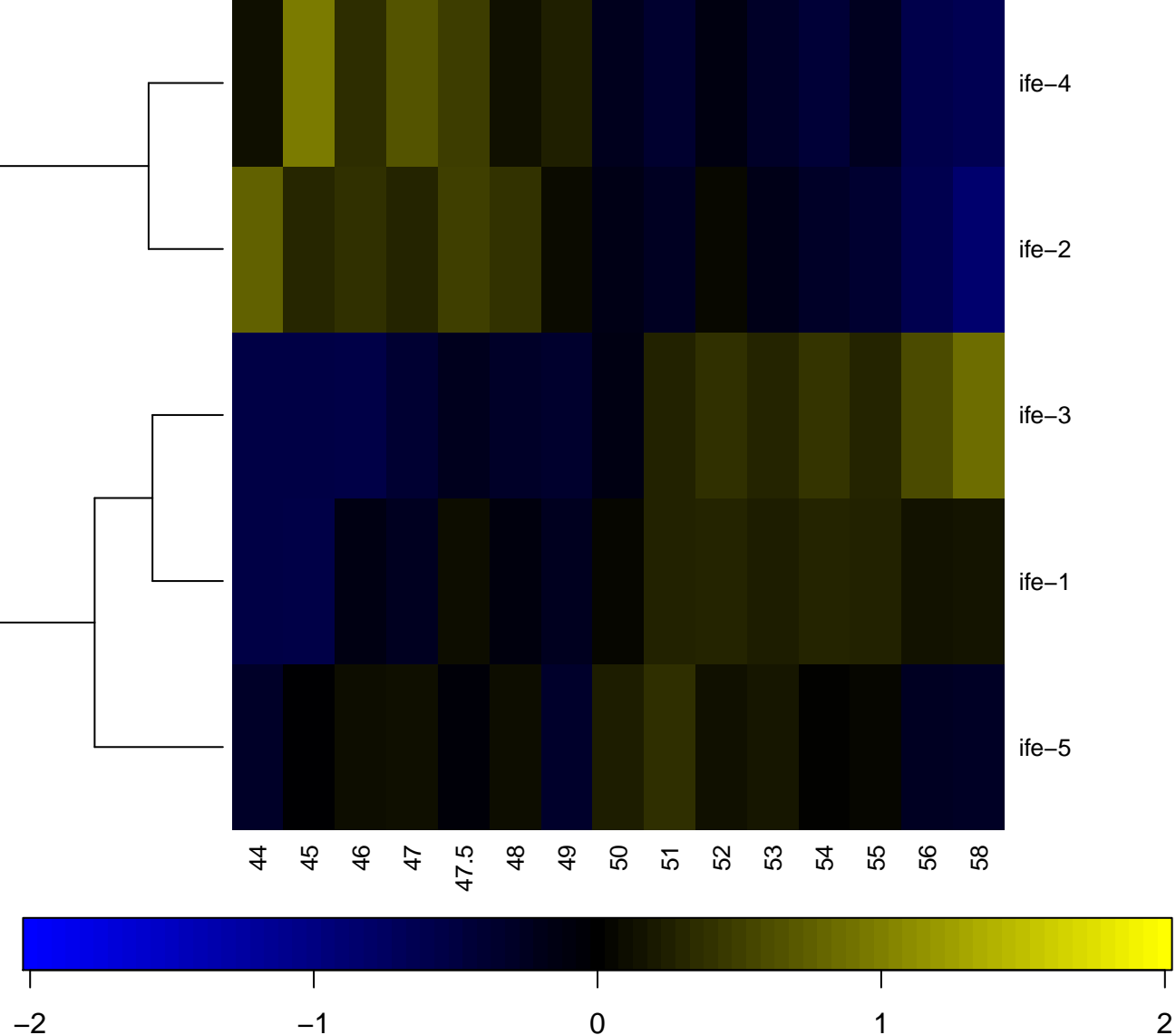
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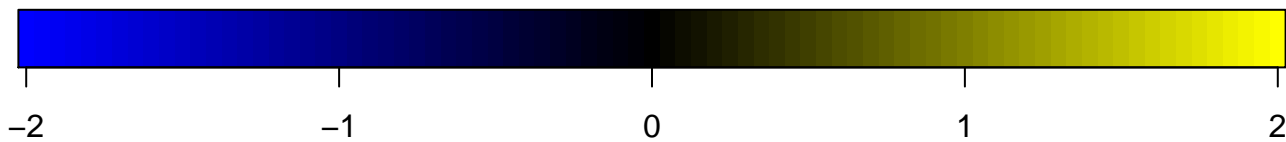
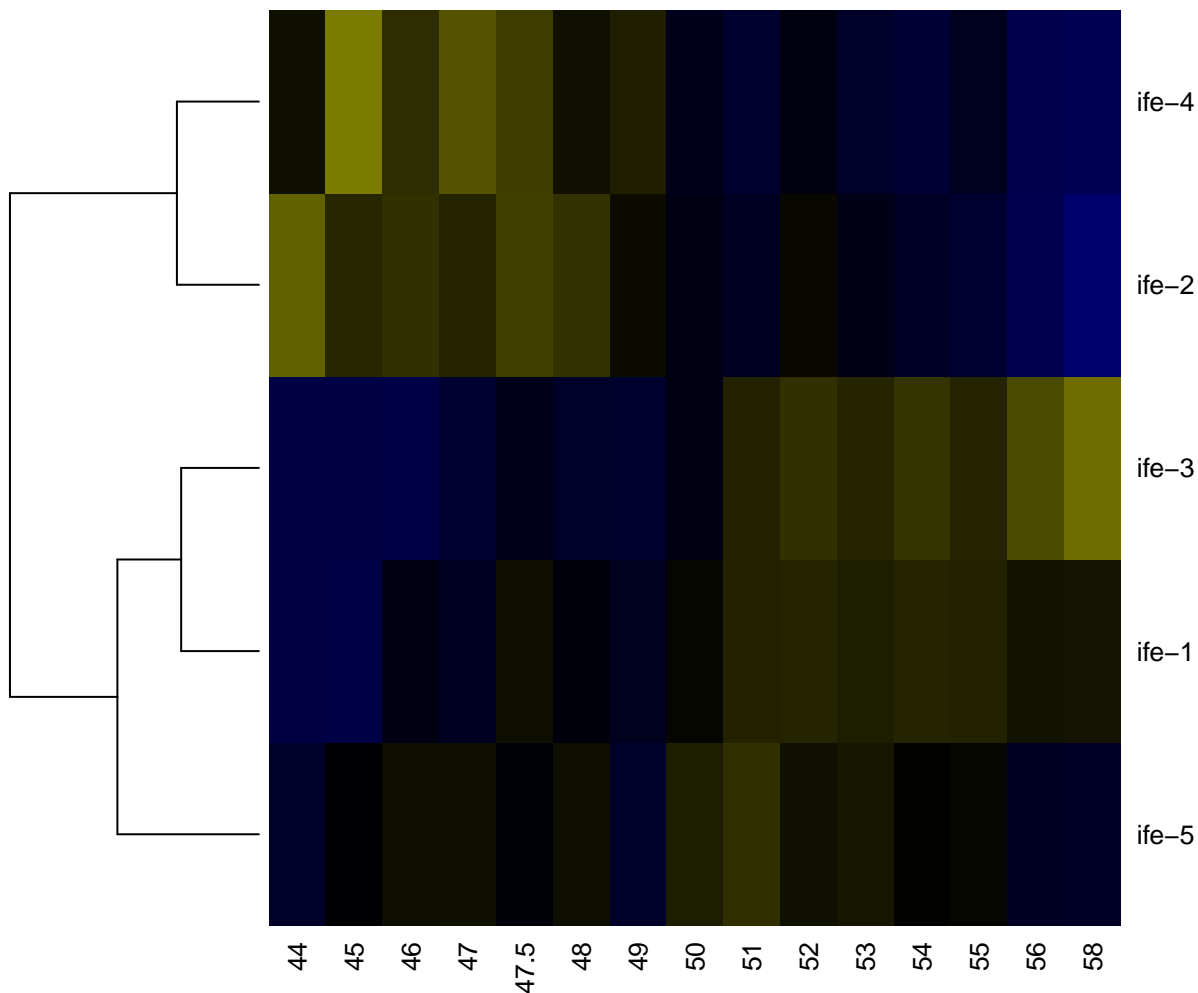
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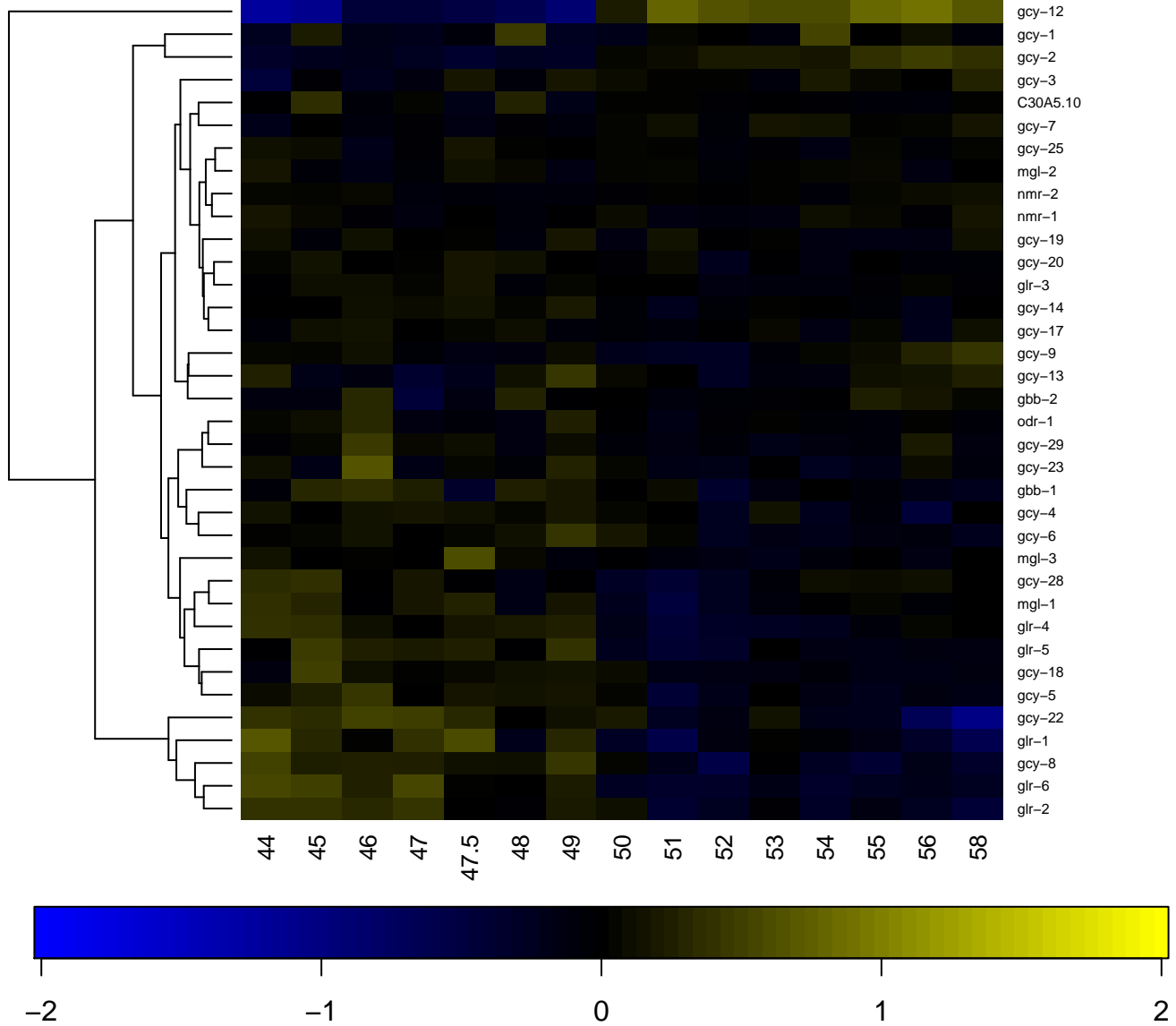
Eukaryotic translation initiation factor 4E (eIF-4E)



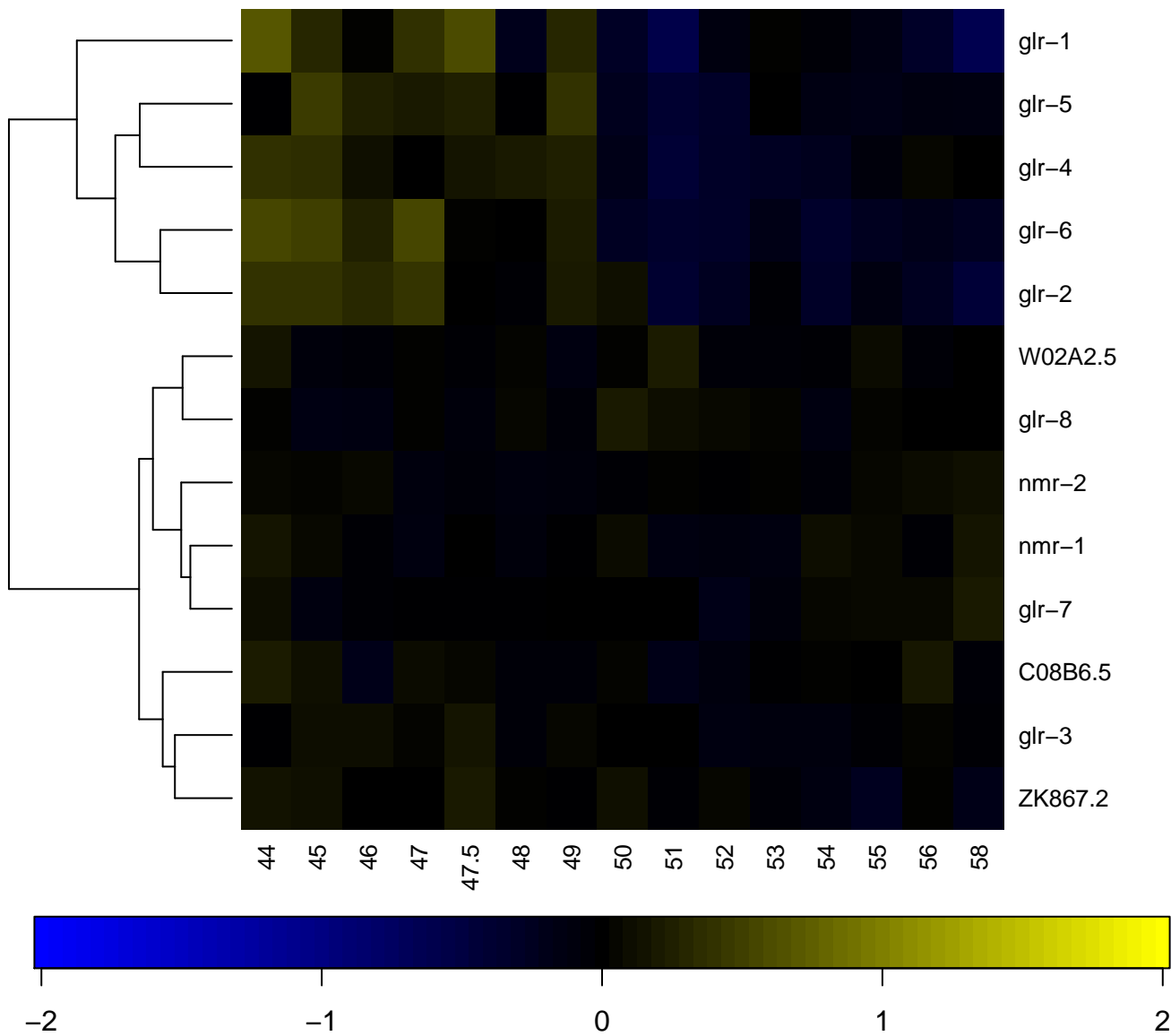
karyotic translation initiation factor 4E (eIF-4E), conserved



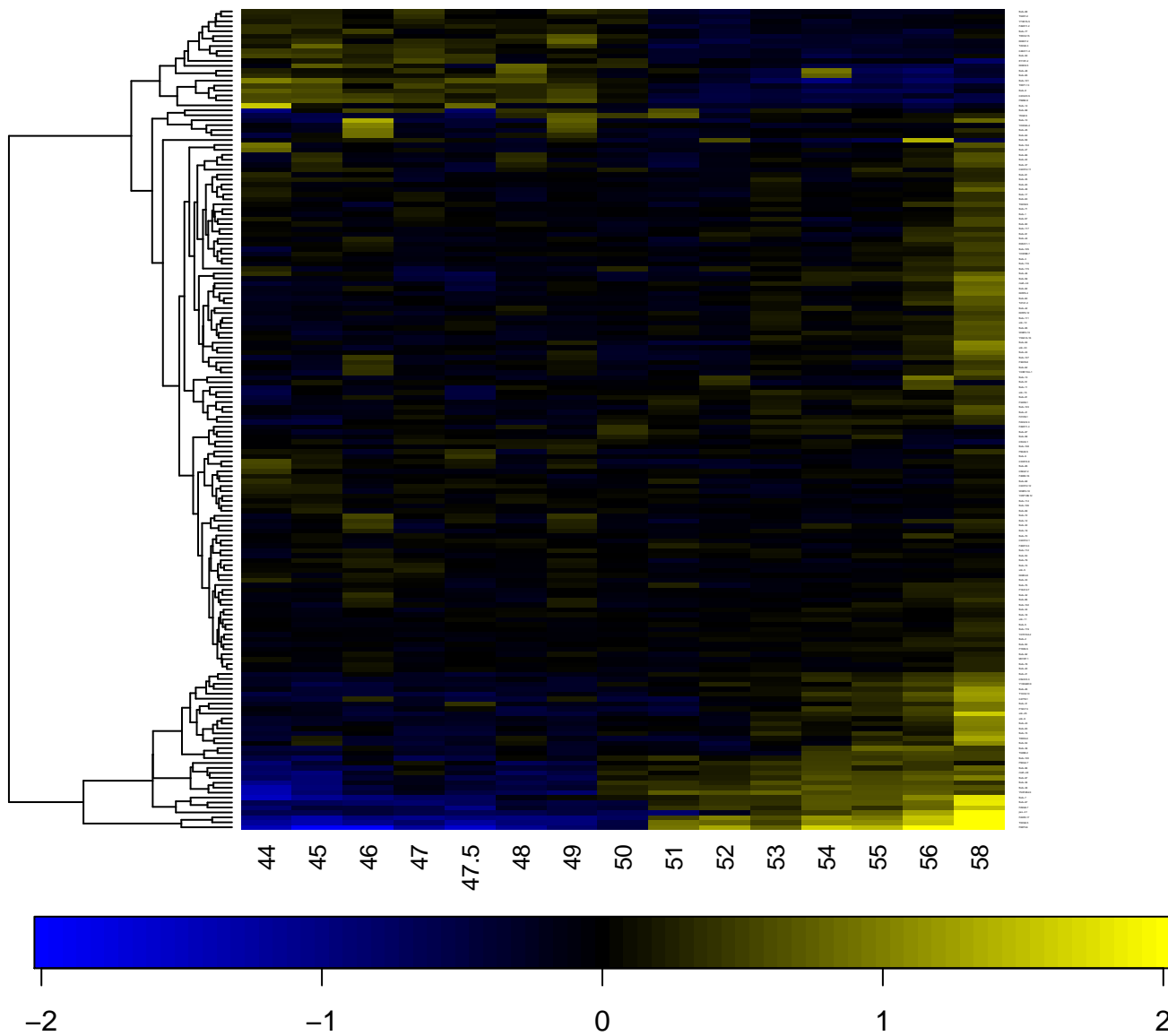
Extracellular ligand-binding receptor



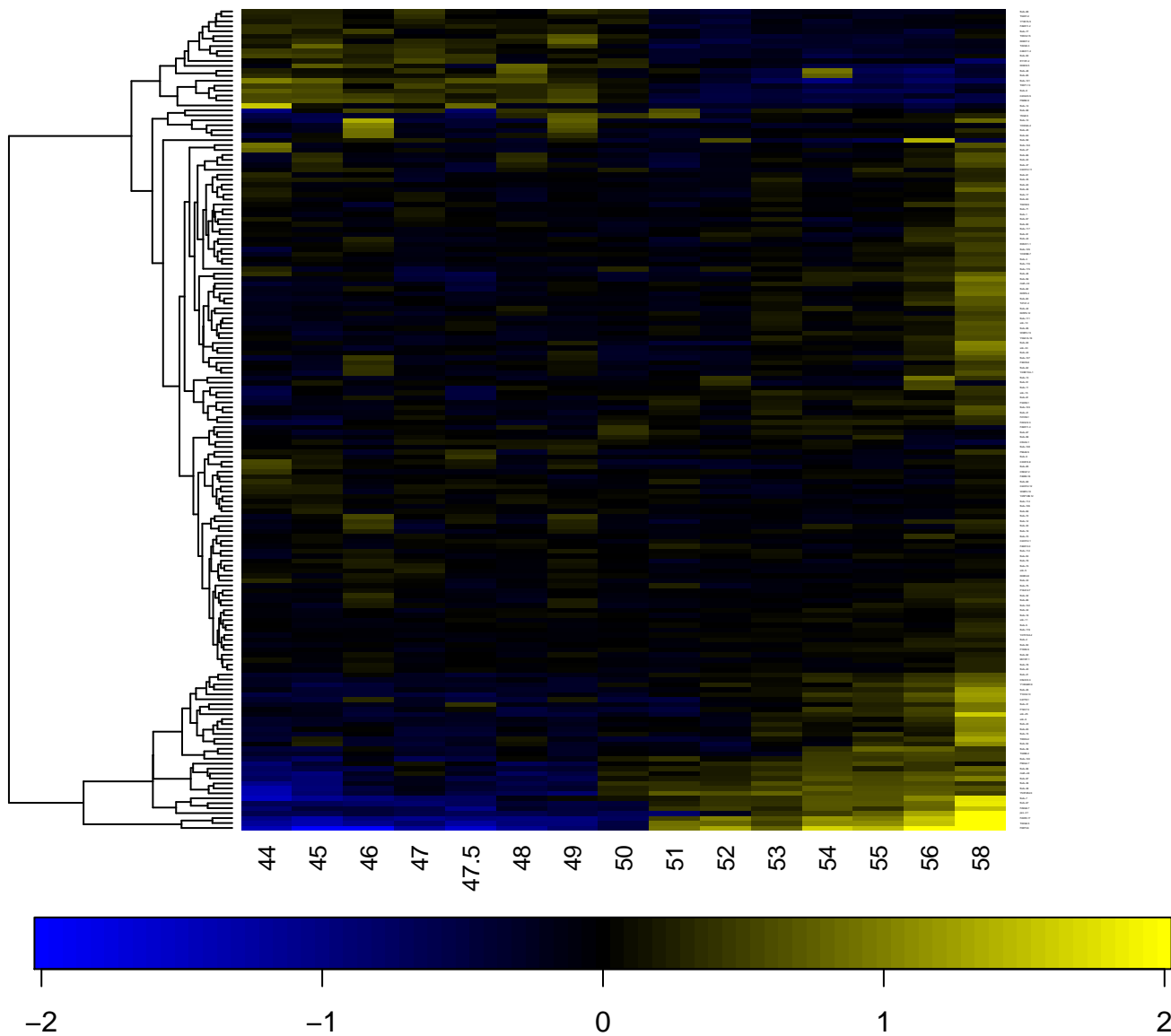
Extracellular solute-binding protein, family 3



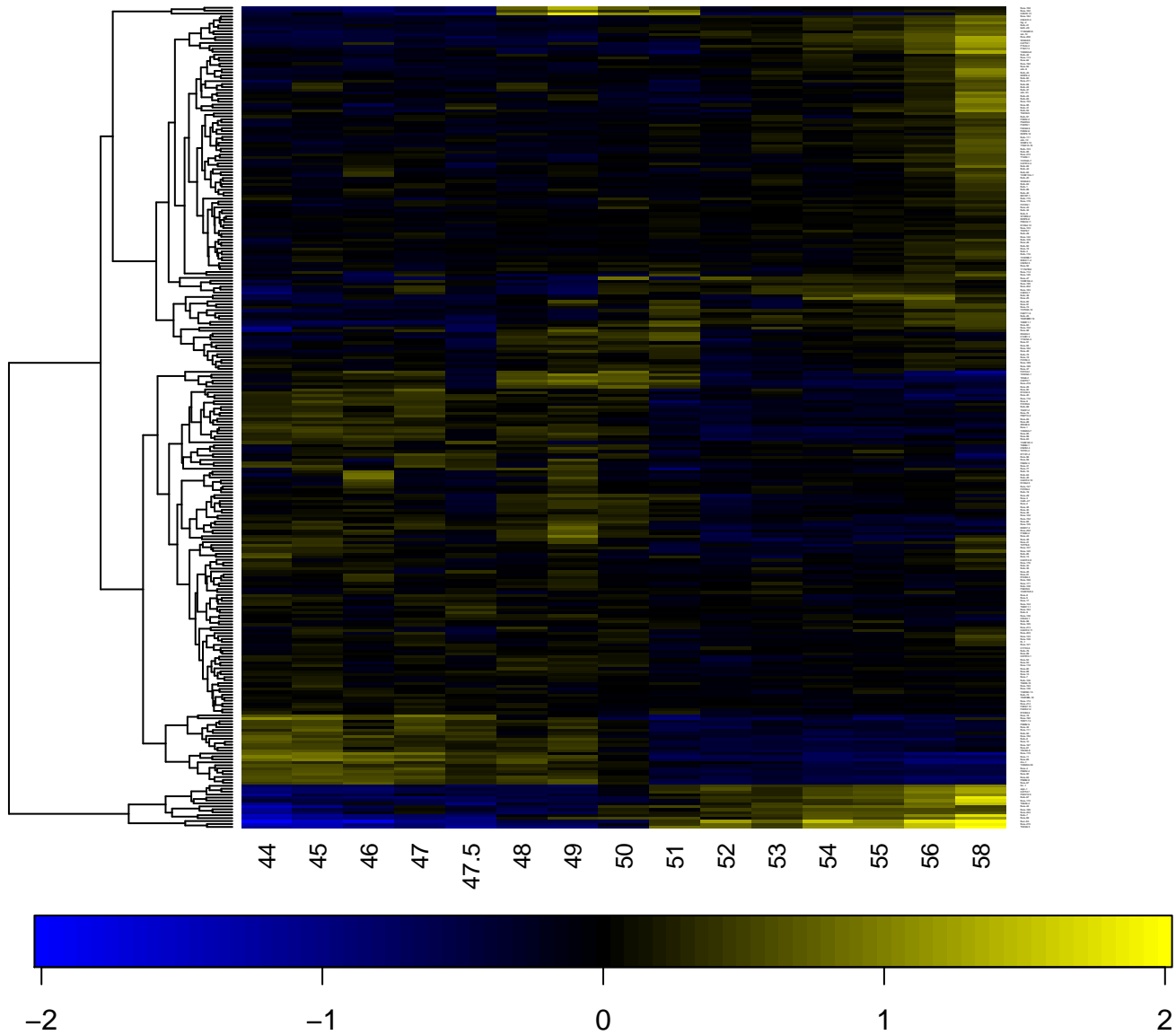
F-box associated



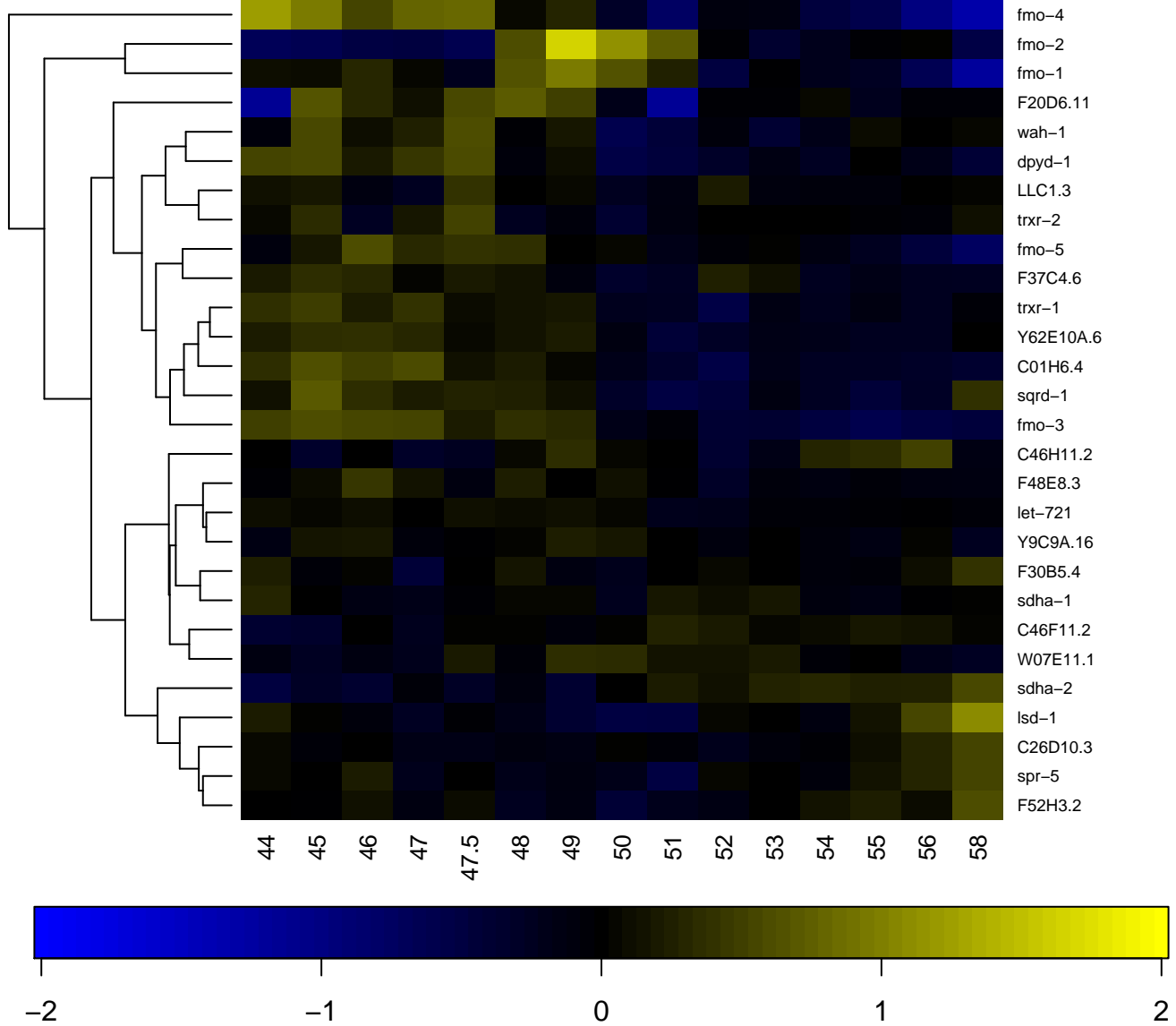
F-box associated domain, type 2



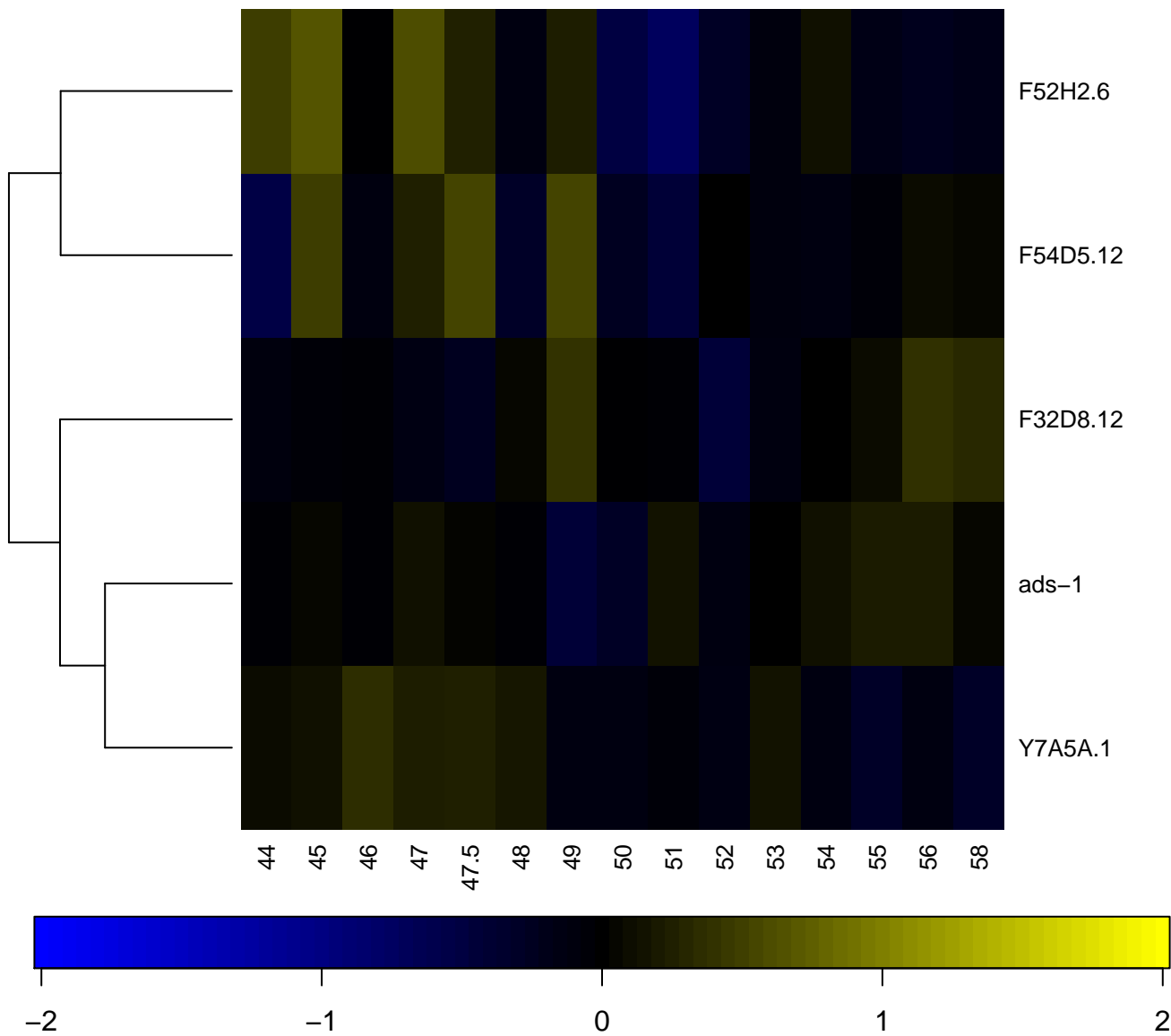
F-box domain



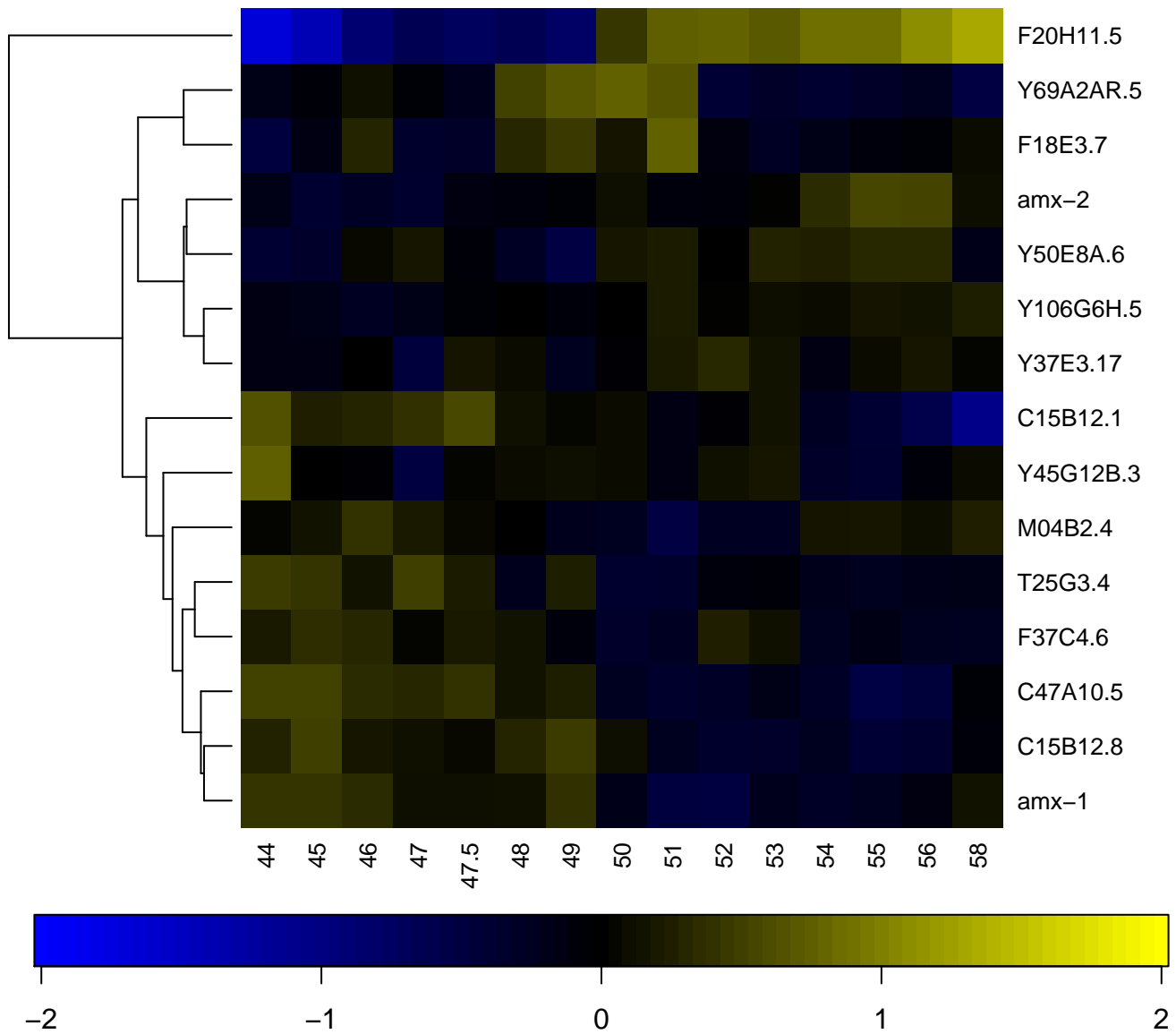
AD-dependent pyridine nucleotide-disulphide oxidoreduct



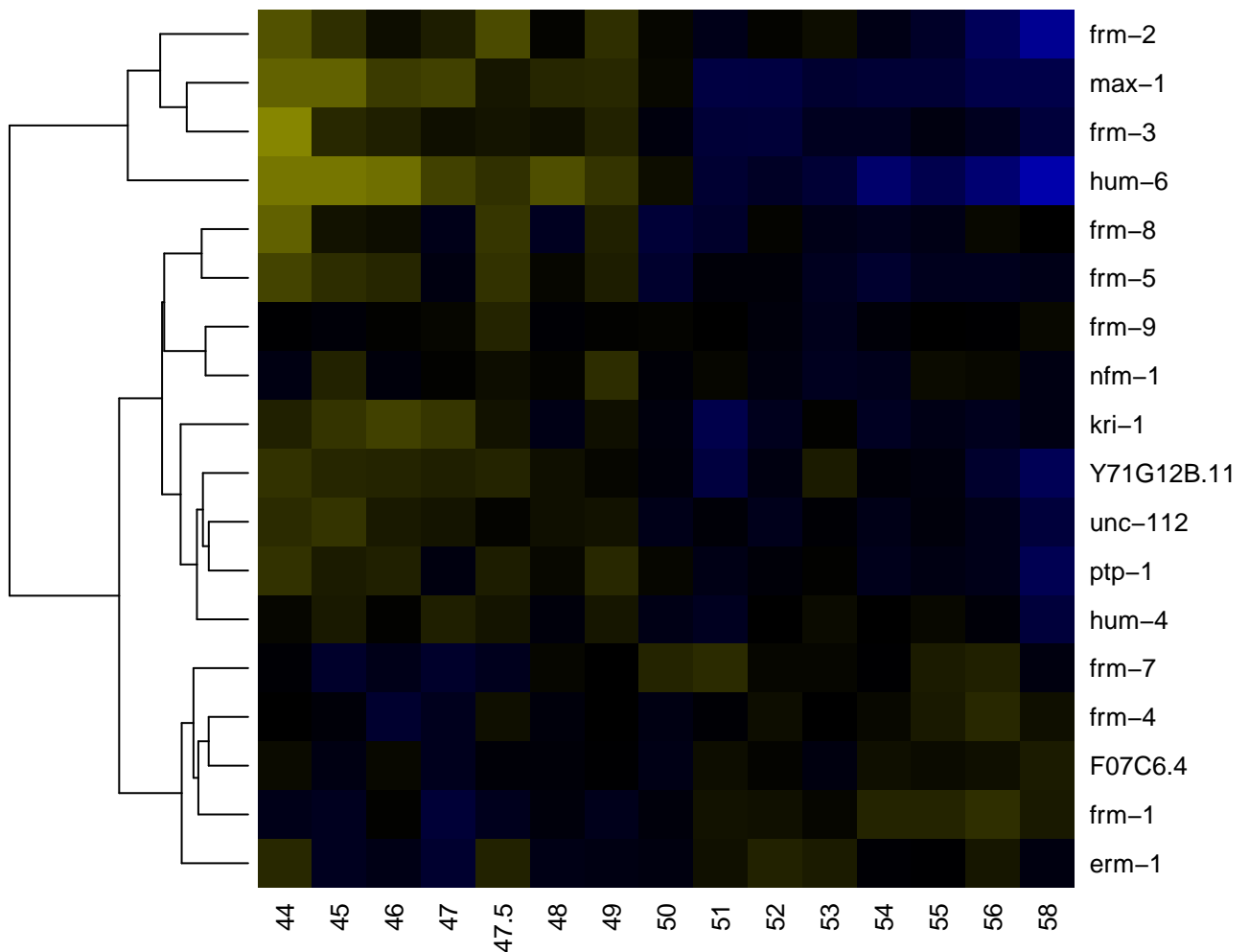
FAD-linked oxidase, FAD-binding, subdomain 2



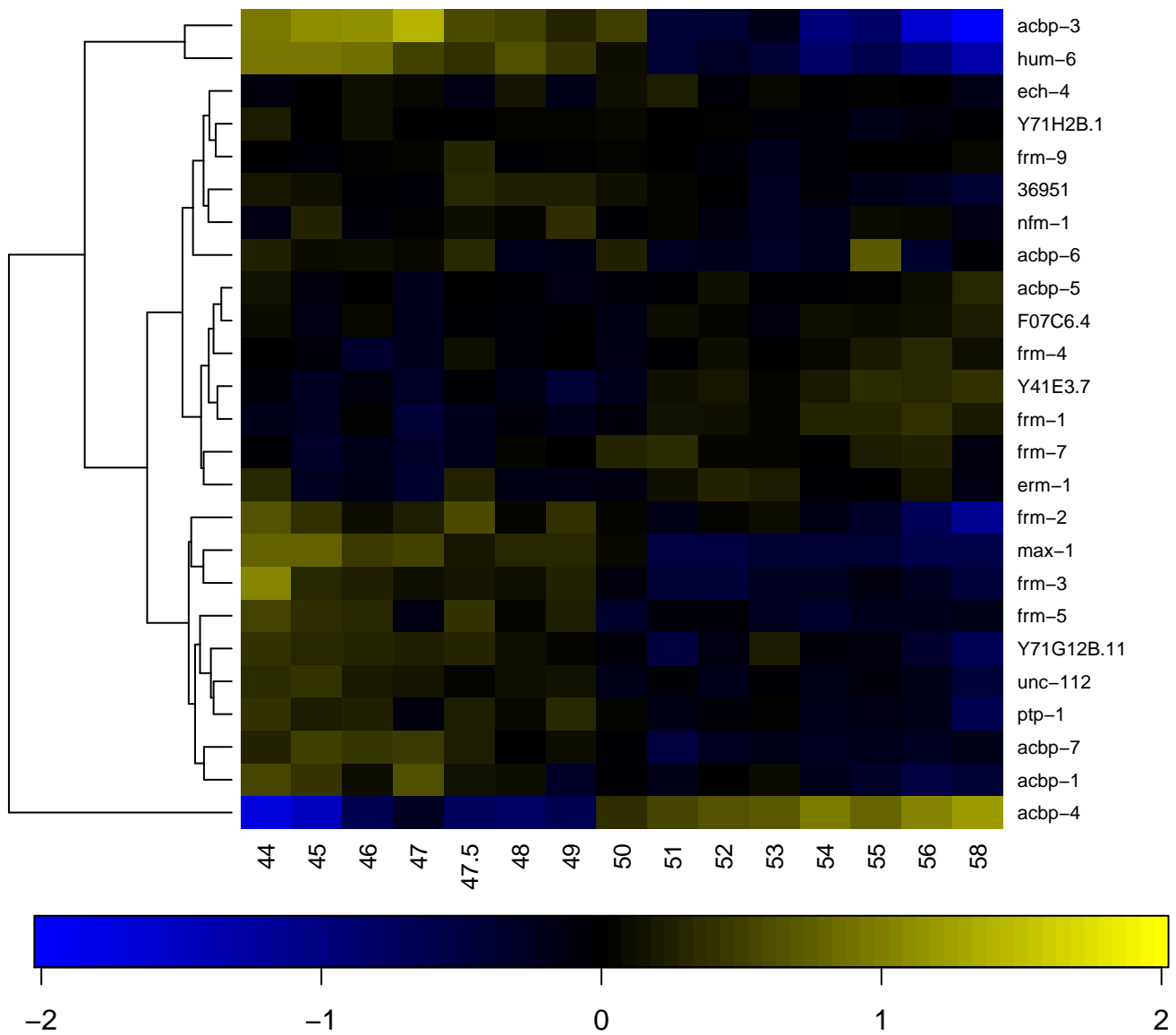
FAD dependent oxidoreductase



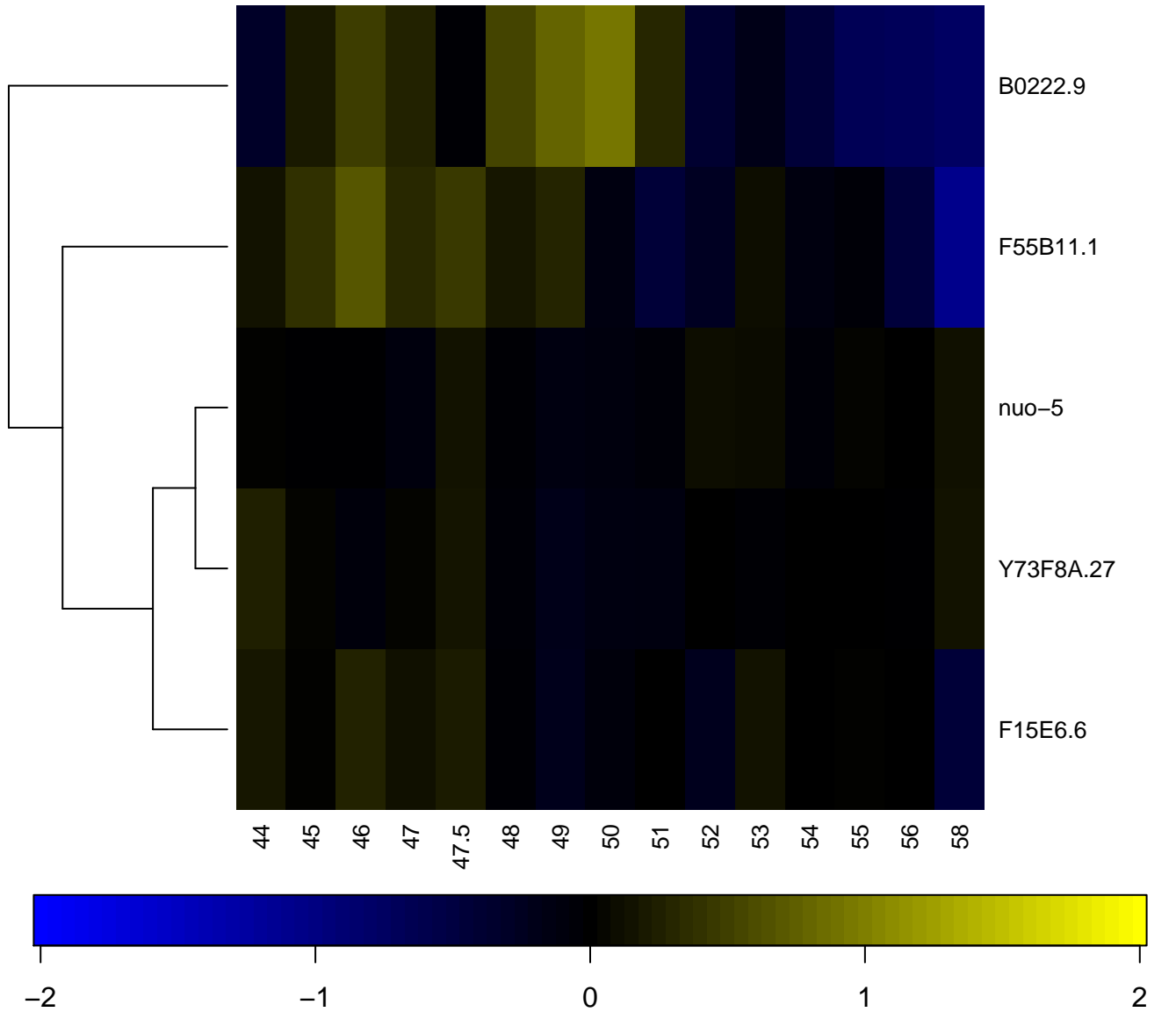
FERM central domain



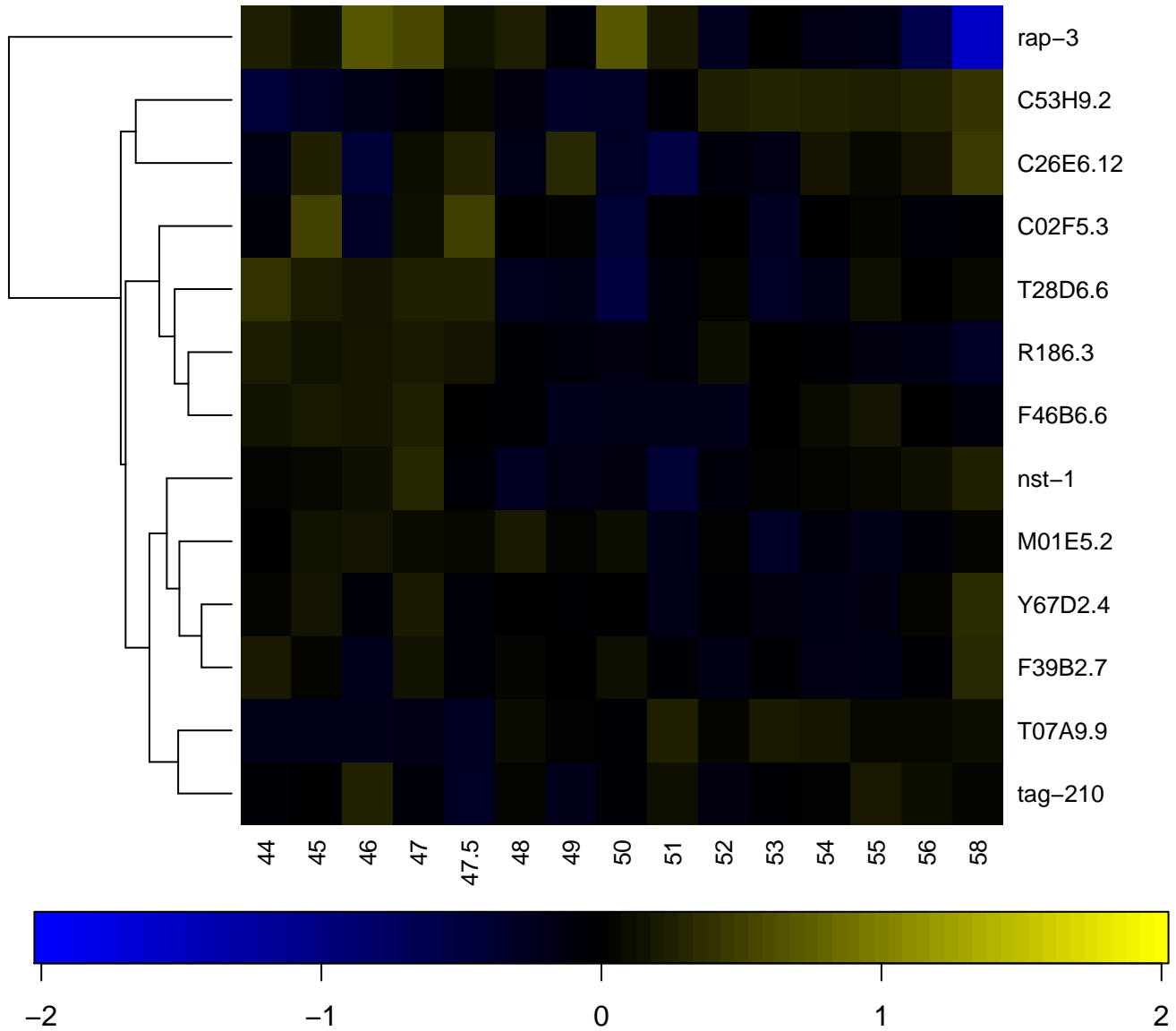
FERM/acyl-CoA-binding protein, 3-helical bundle



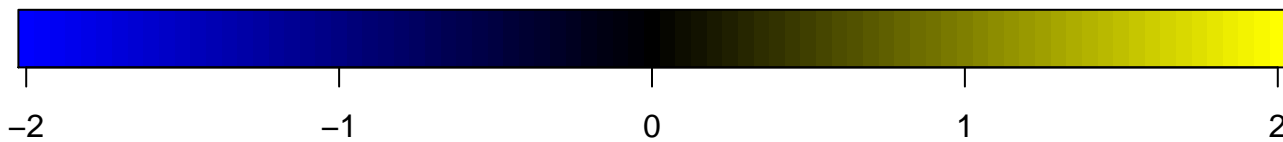
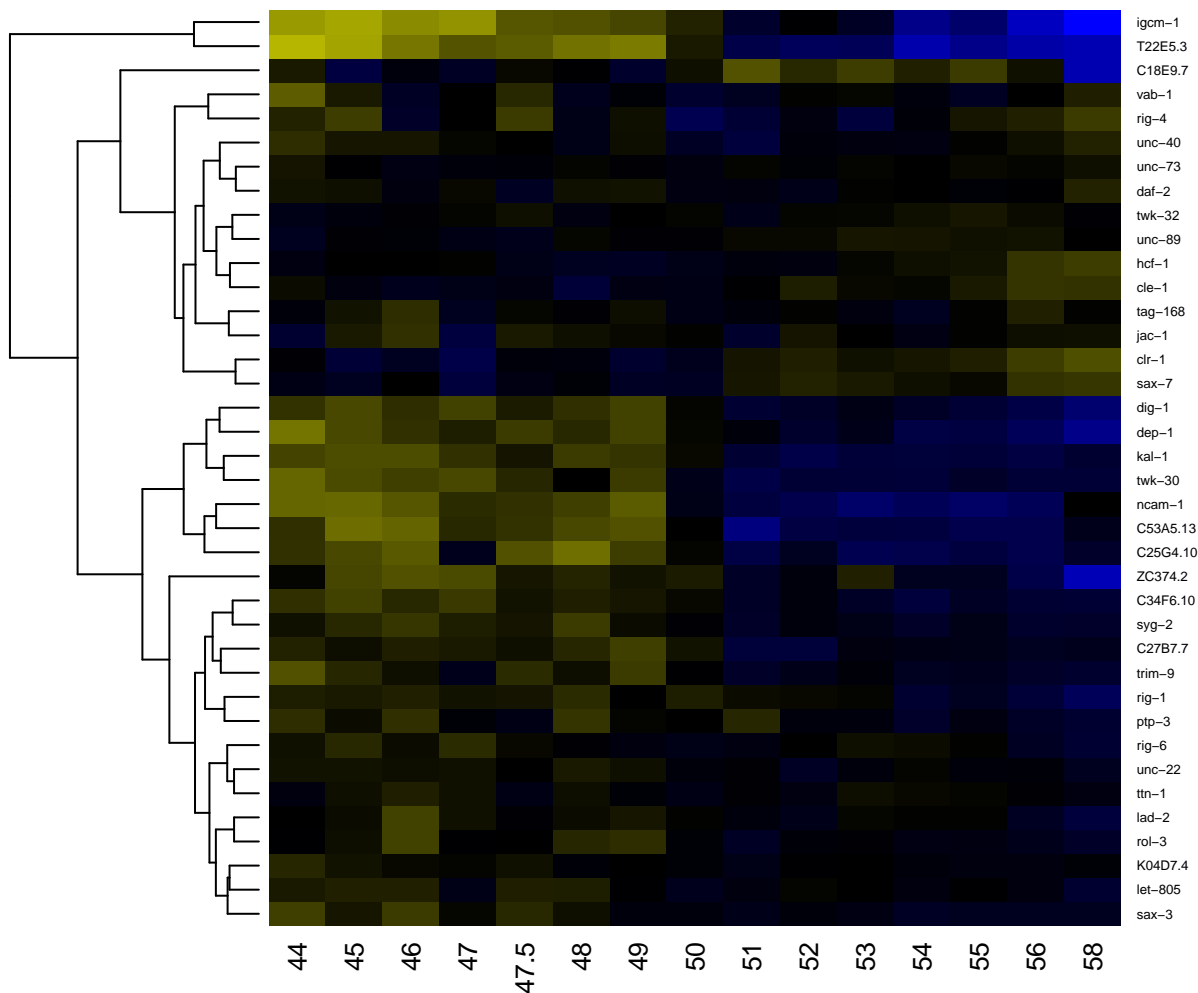
Ferredoxin



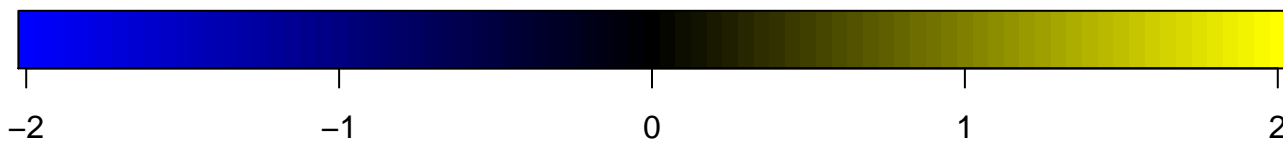
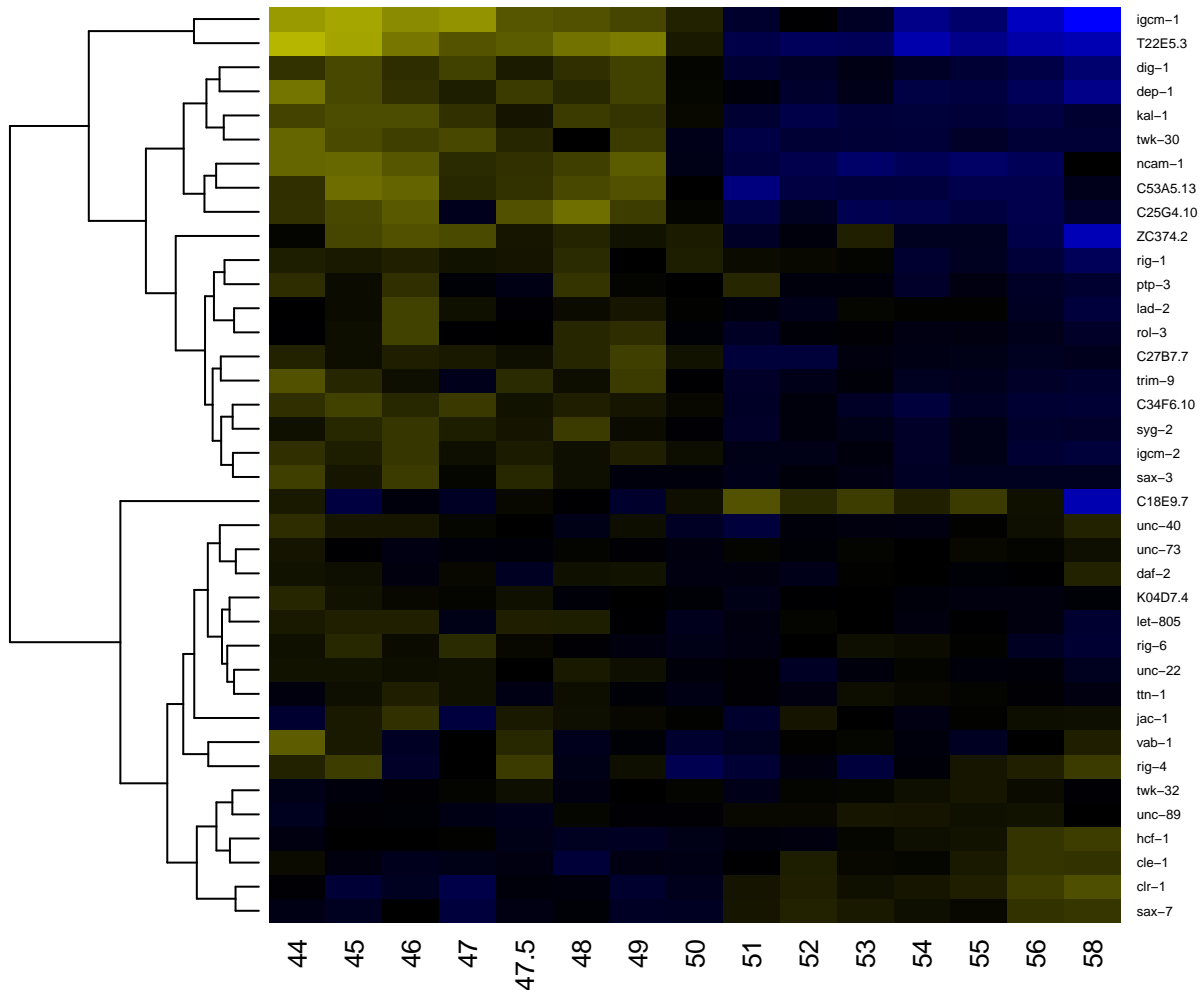
Ferrous iron transport protein B



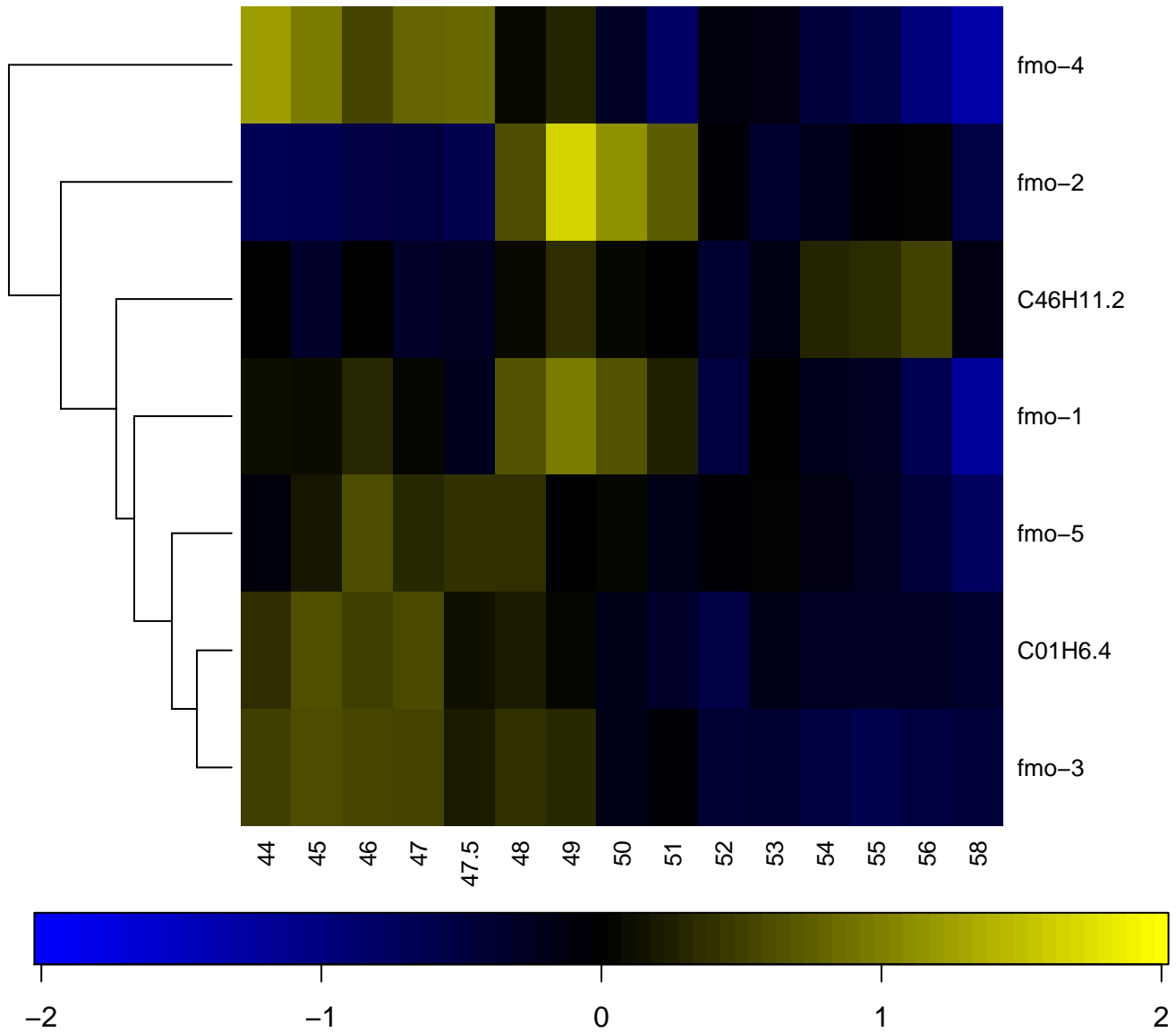
Fibronectin type III domain



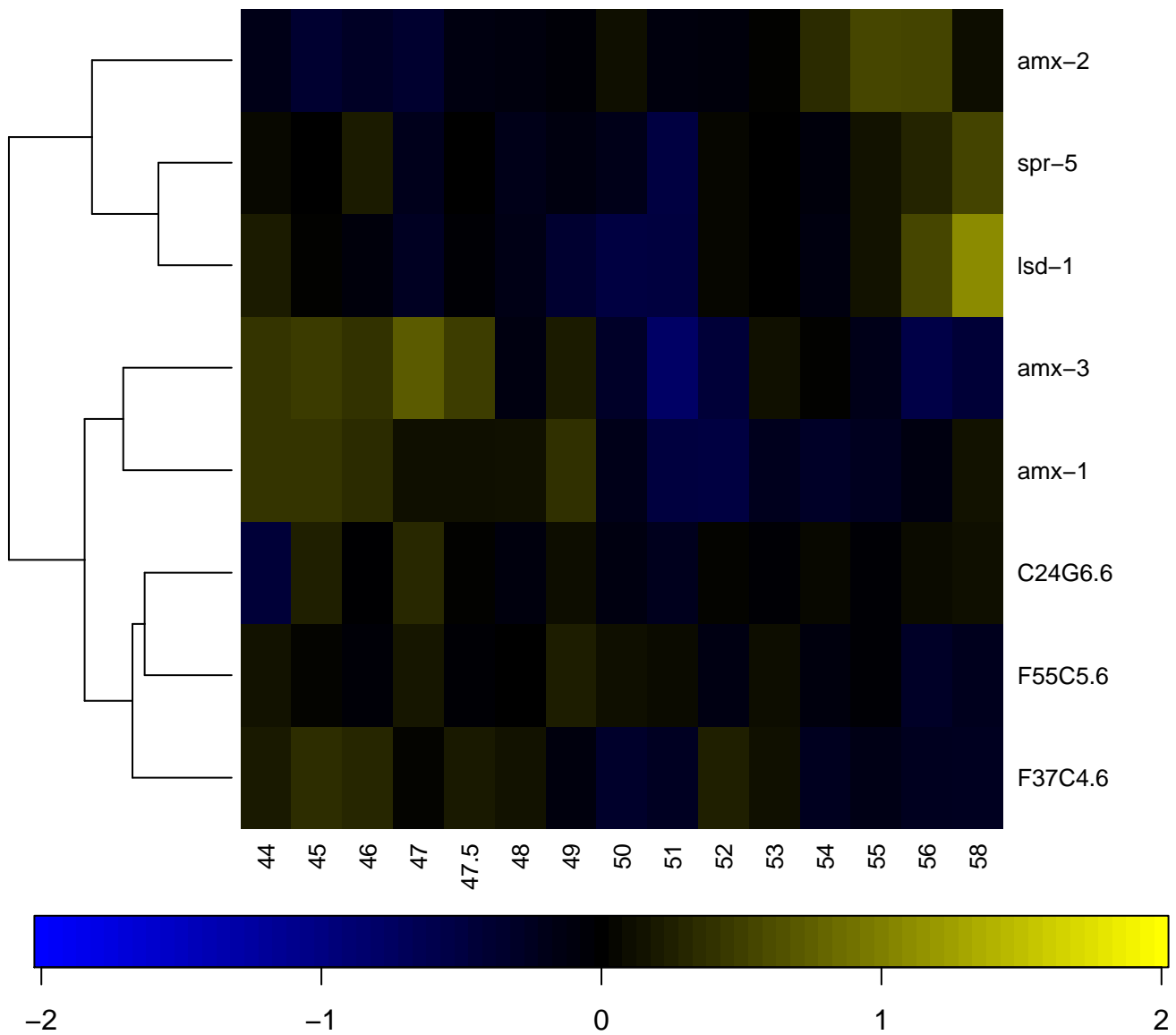
Fibronectin, type III



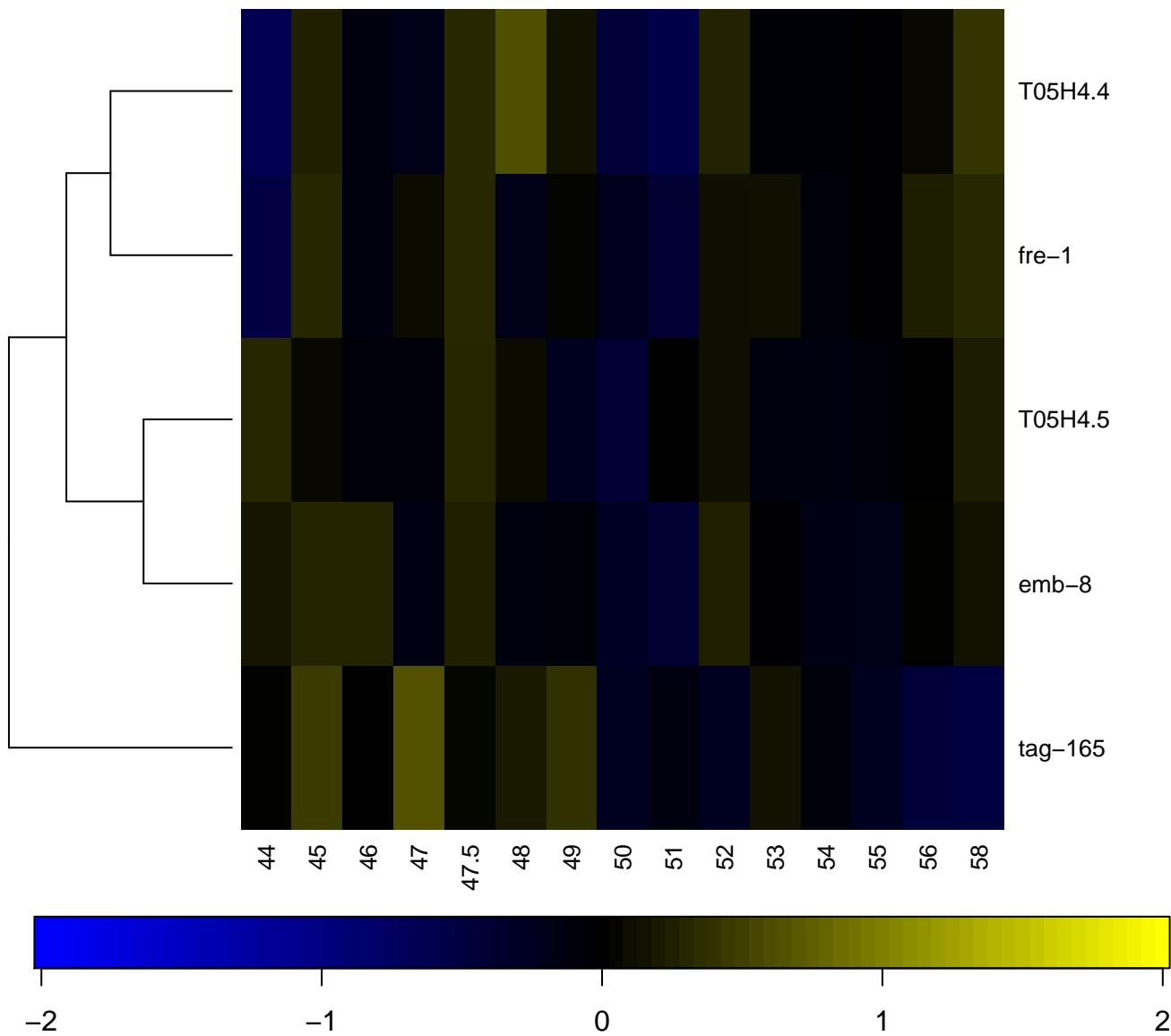
Flavin-containing monooxygenase FMO



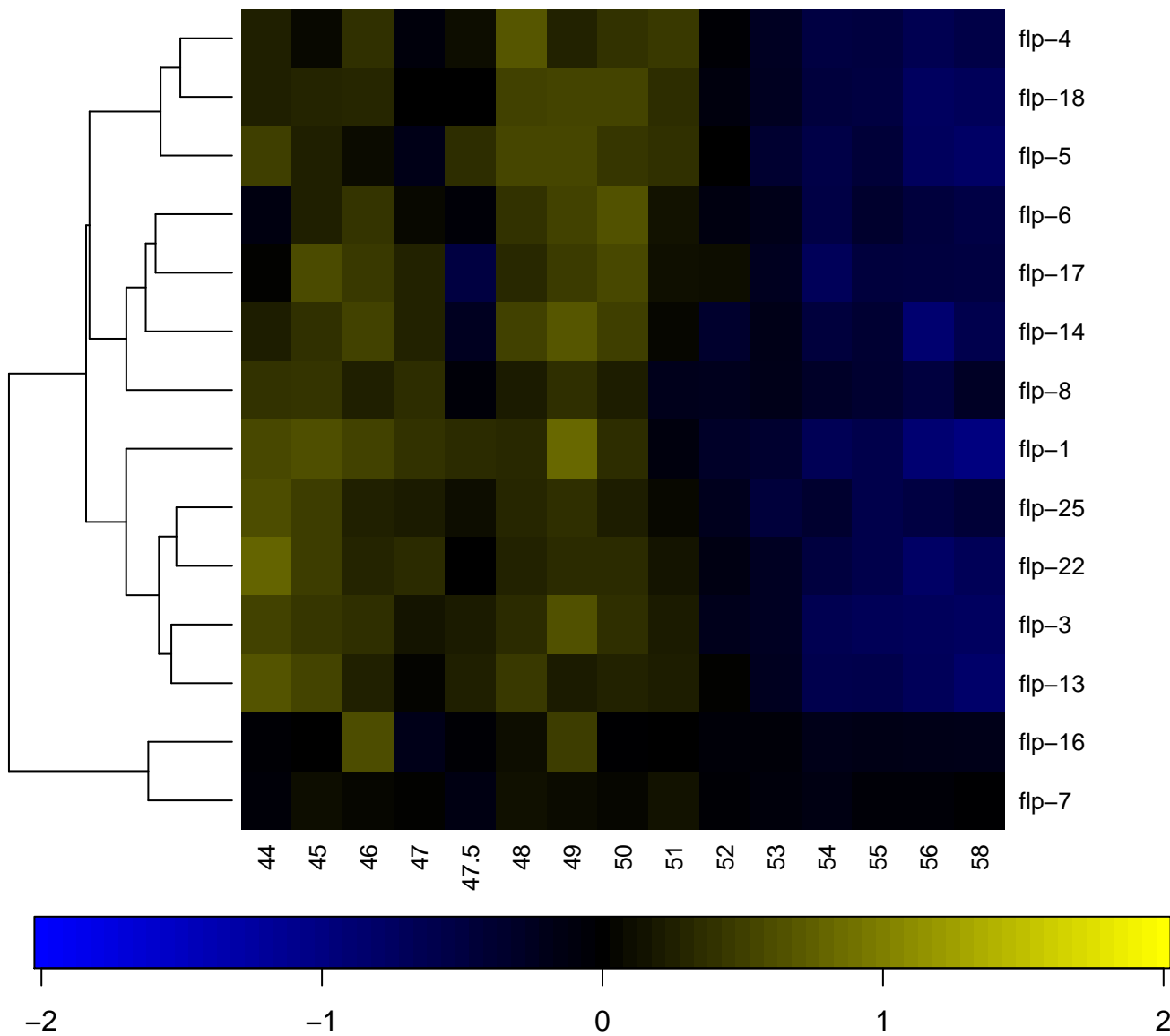
Flavin containing amine oxidoreductase



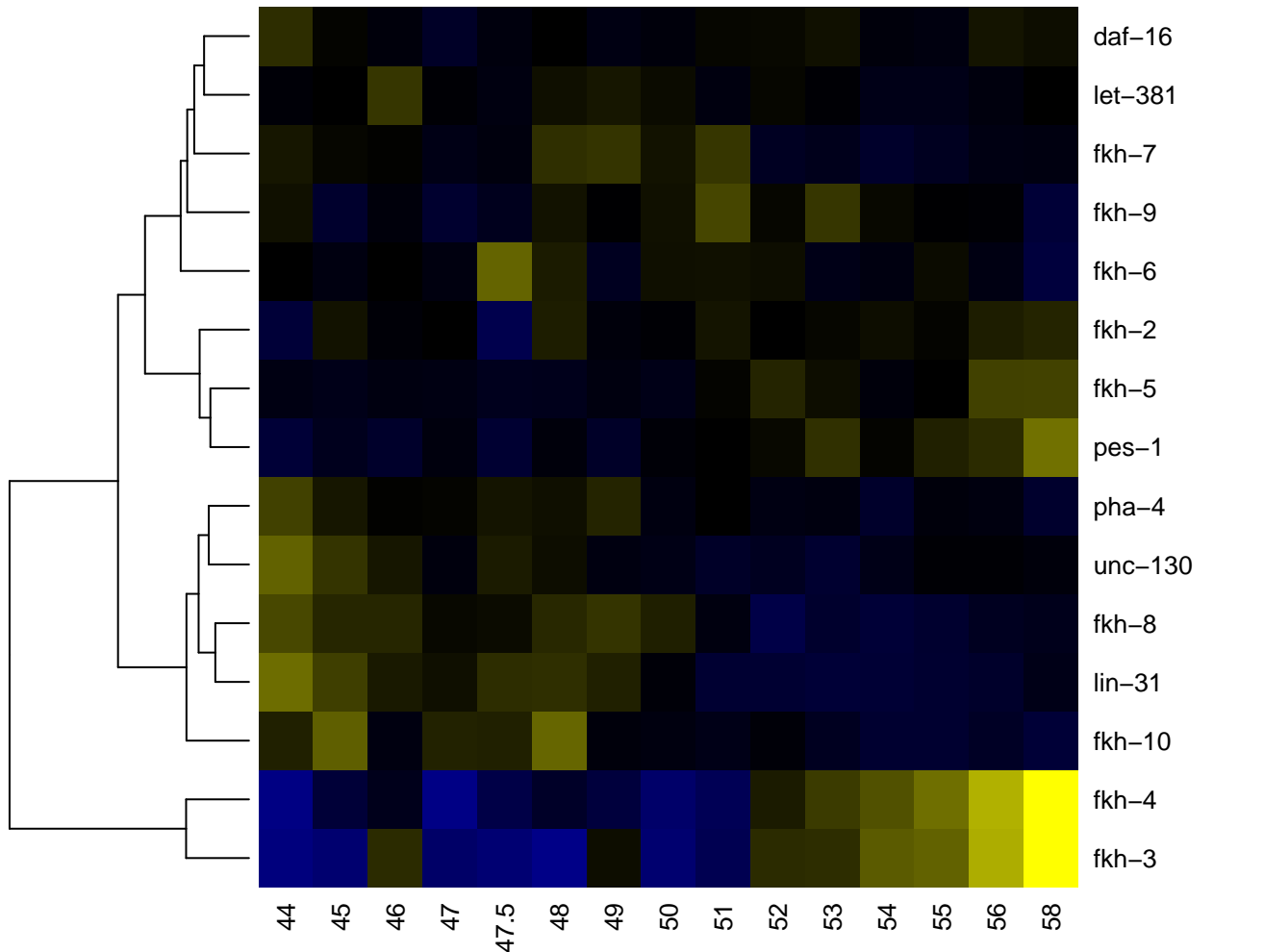
Flavoprotein pyridine nucleotide cytochrome reductase



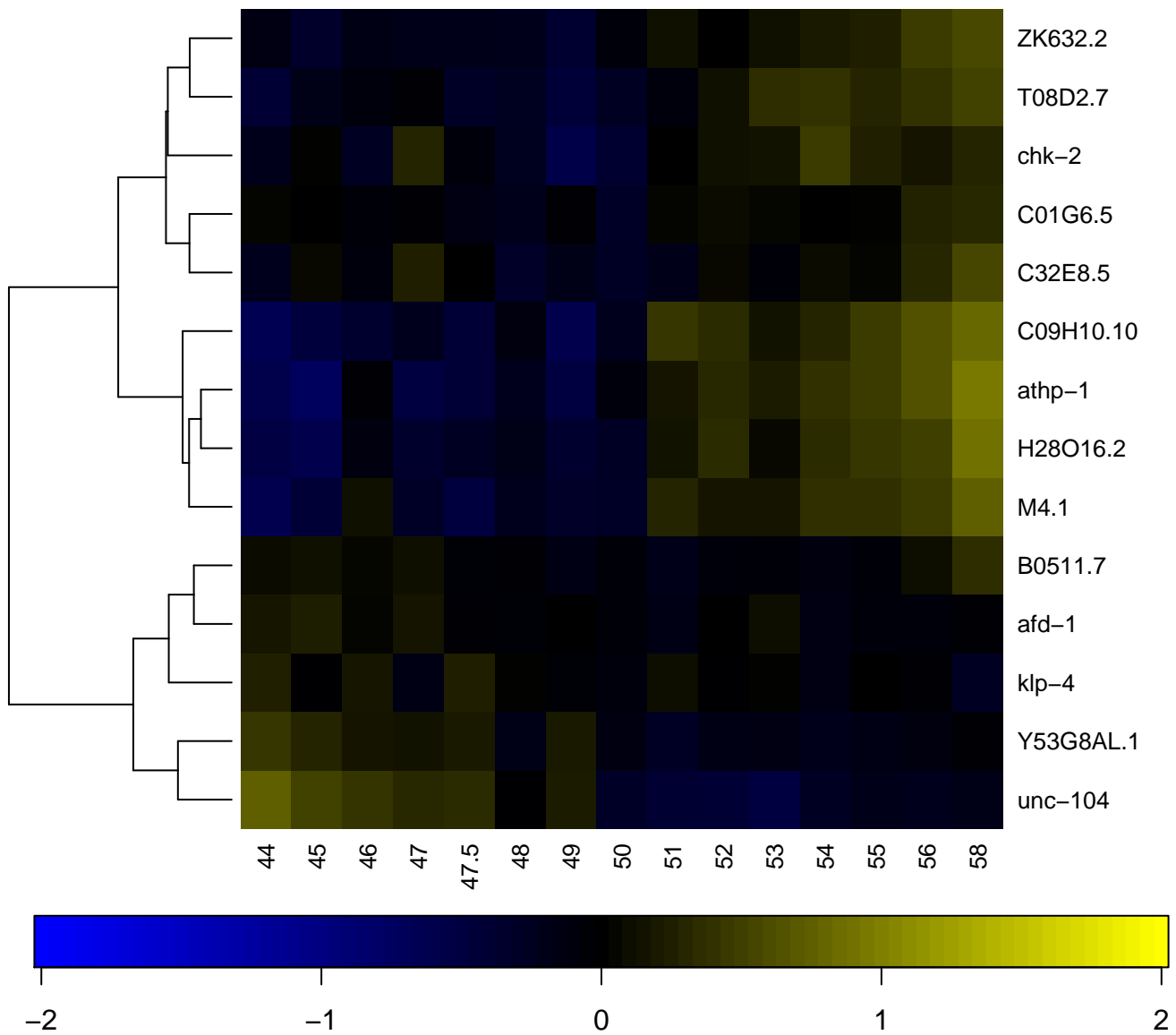
FMRFamide related peptide family



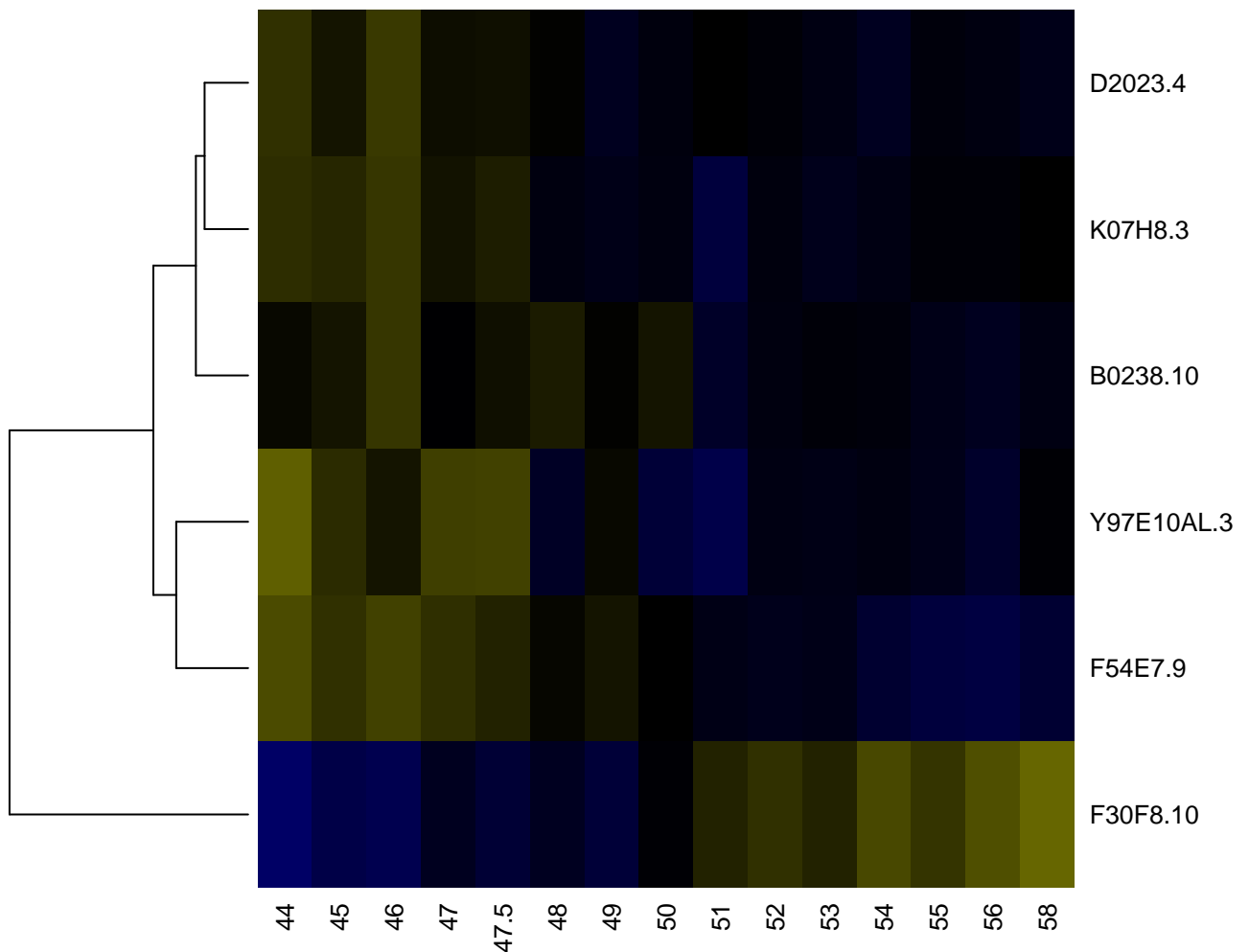
Fork head domain



Forkhead-associated (FHA) domain



FR47-like



-2

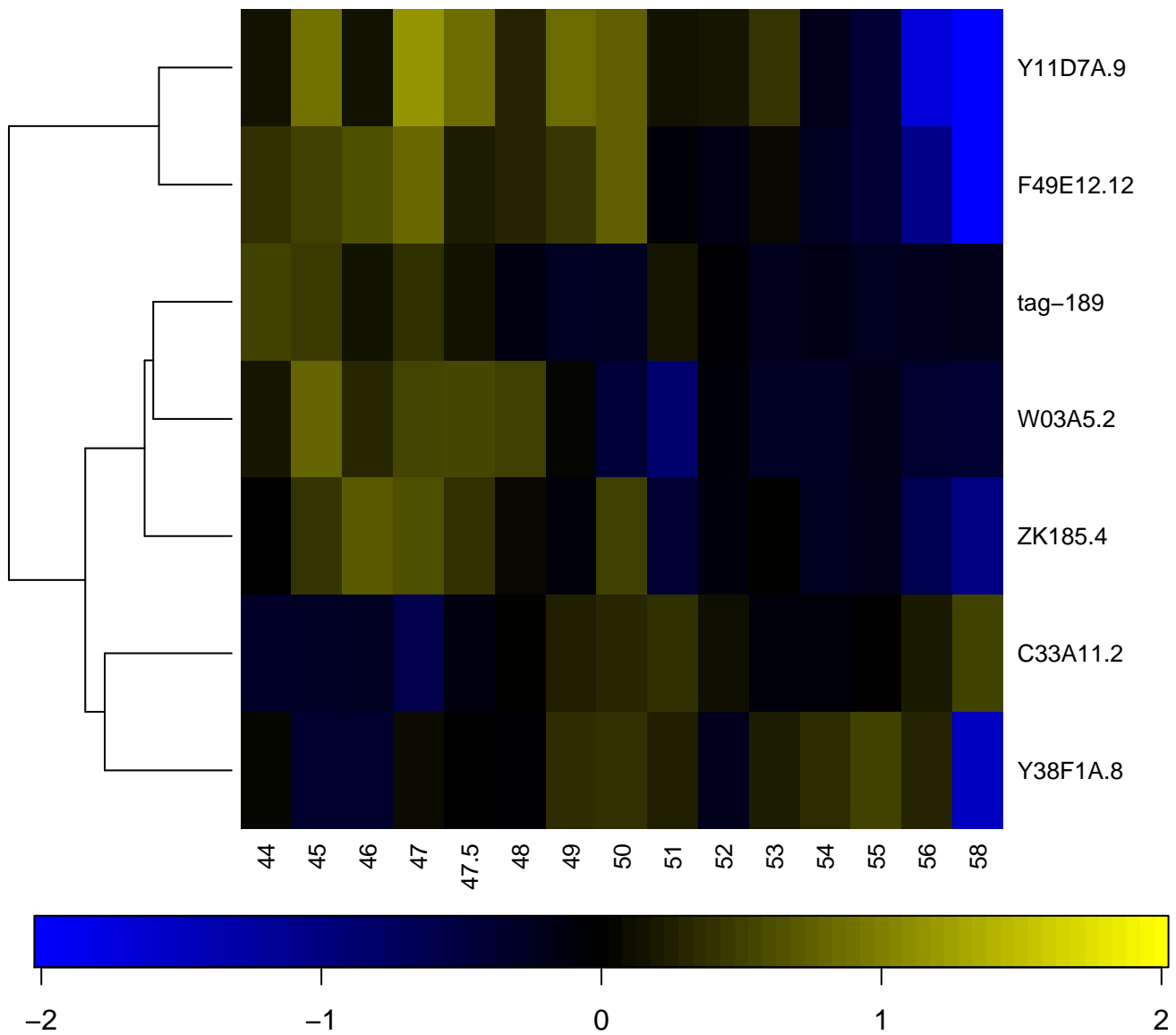
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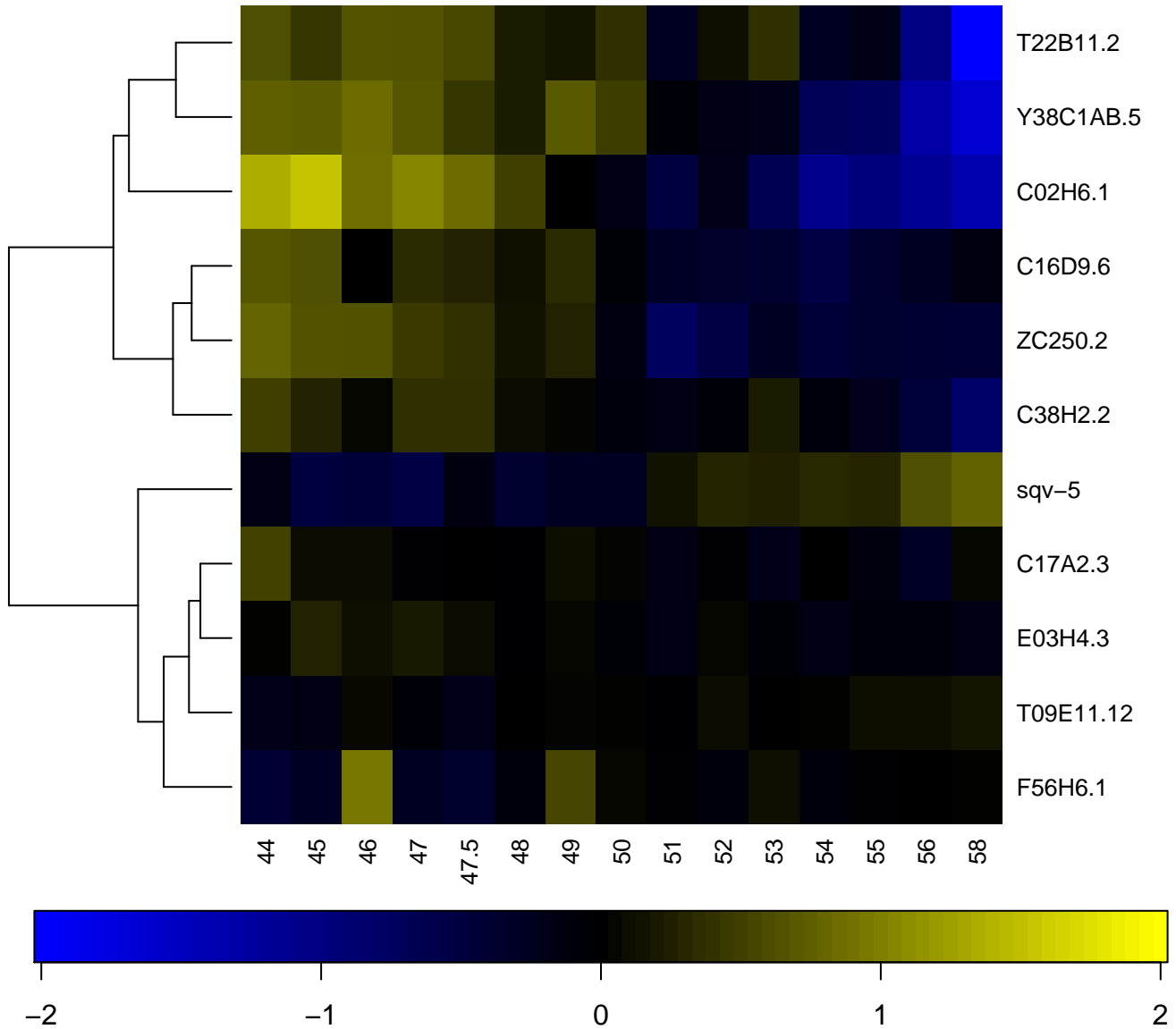
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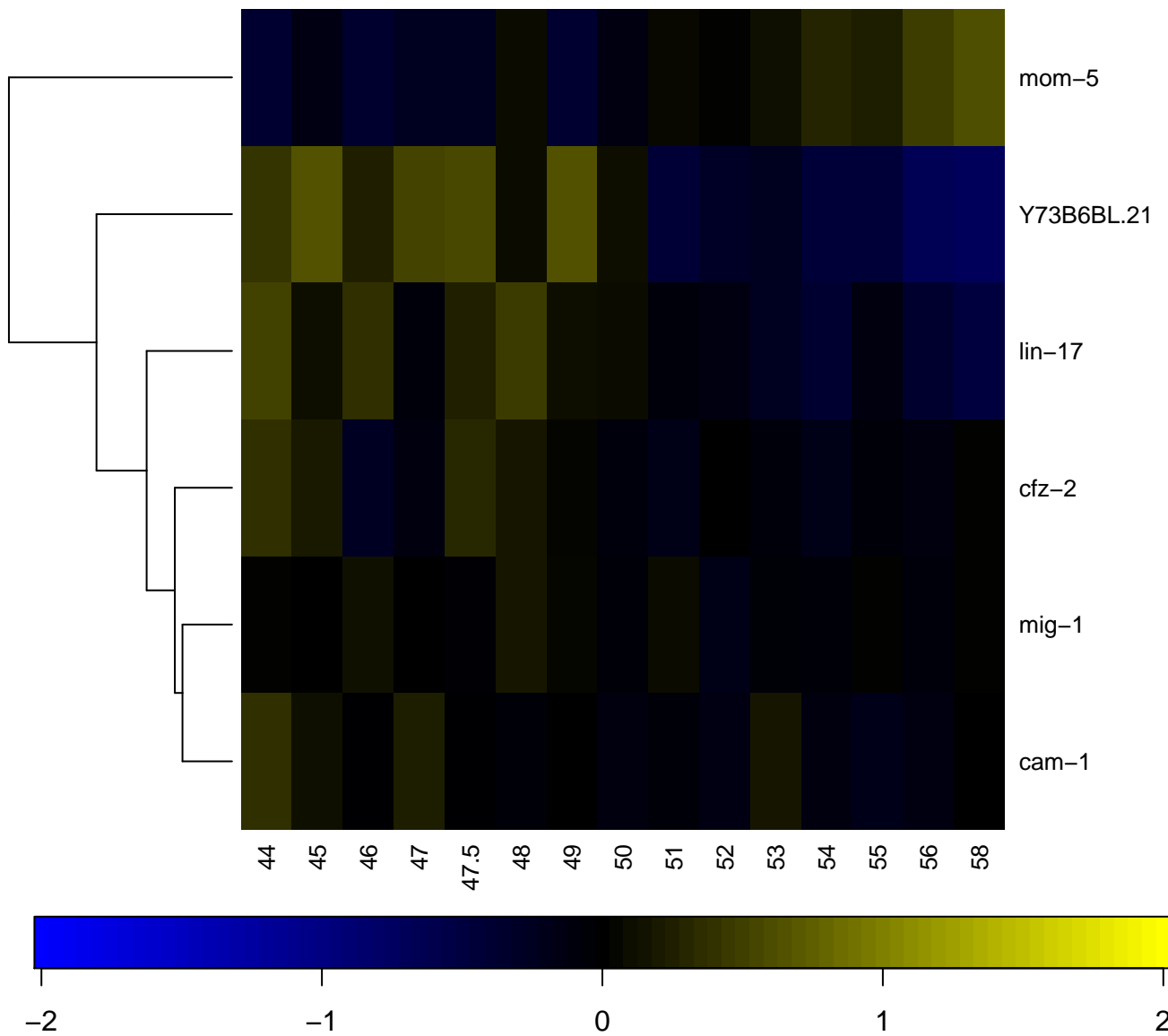
Frag1/DRAM/Sfk1



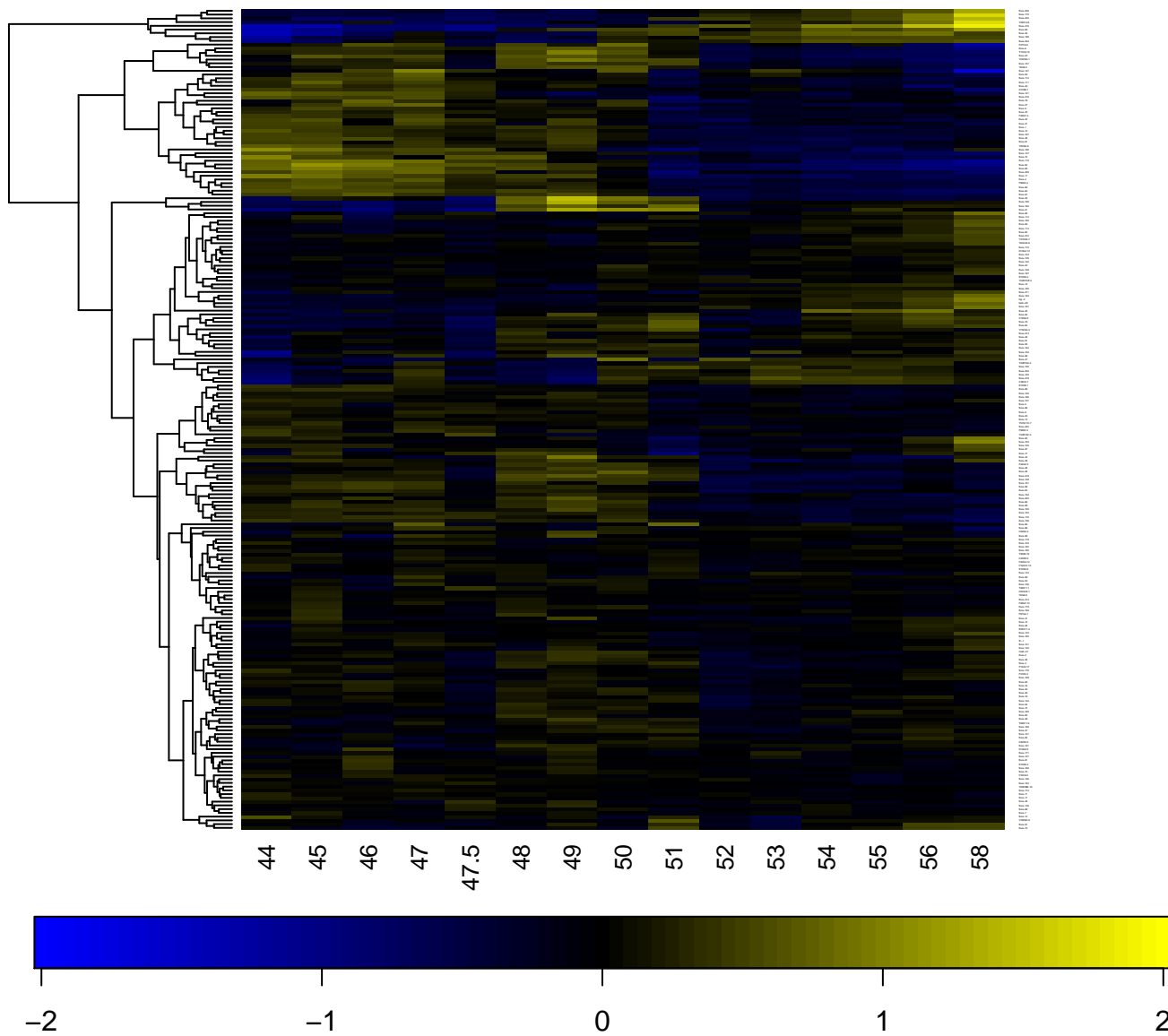
Fringe-like



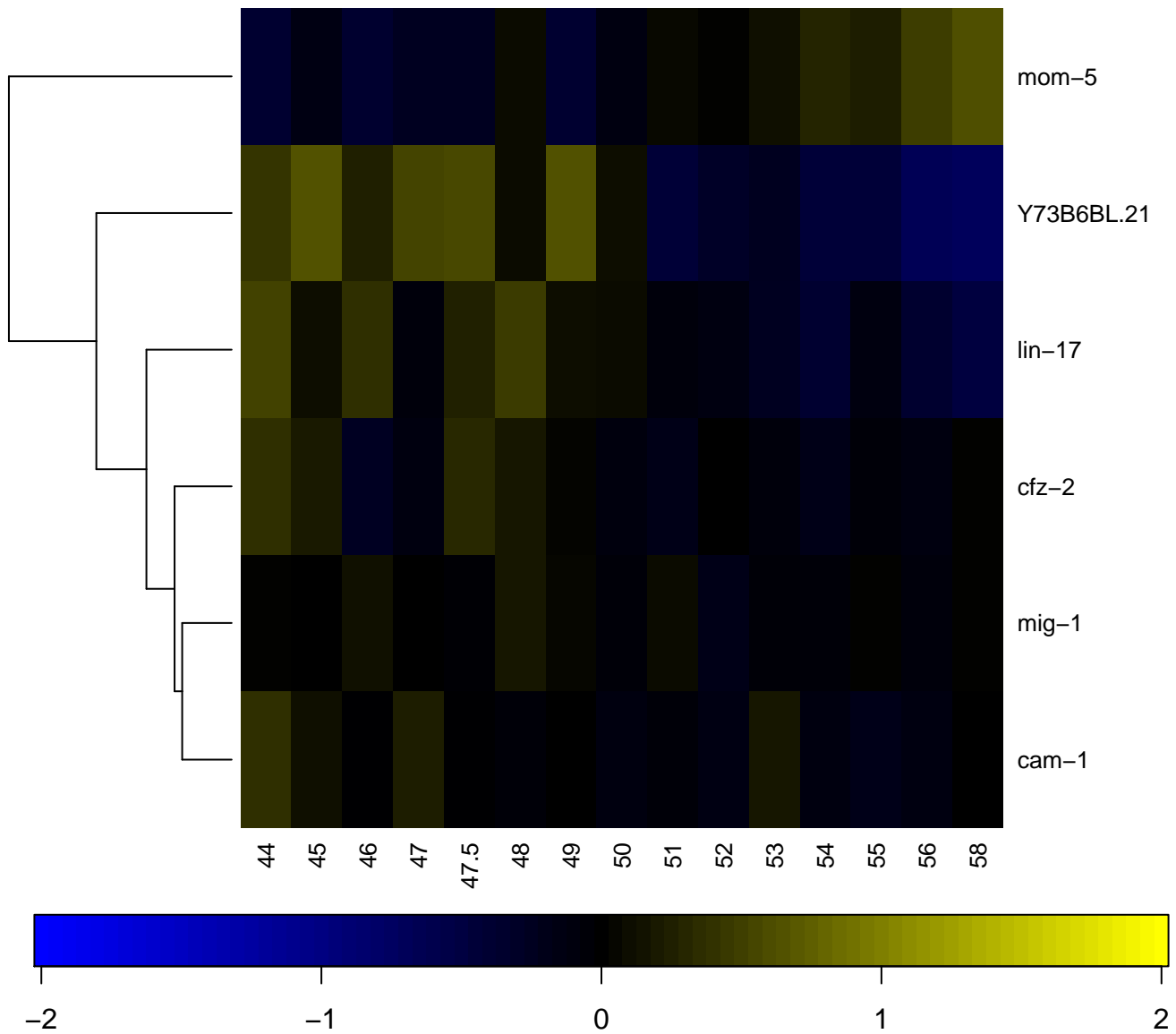
Frizzled domain



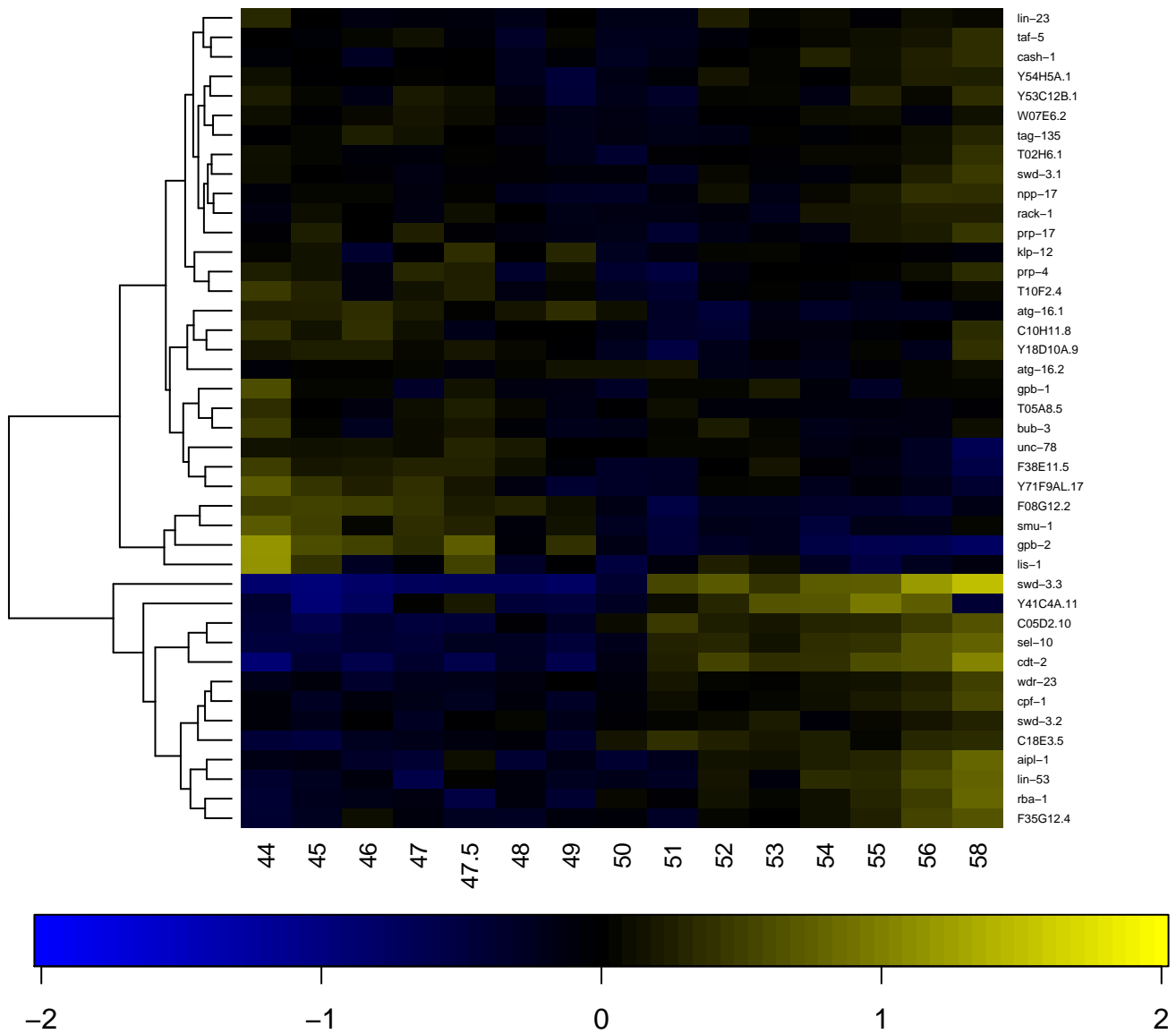
FTH domain



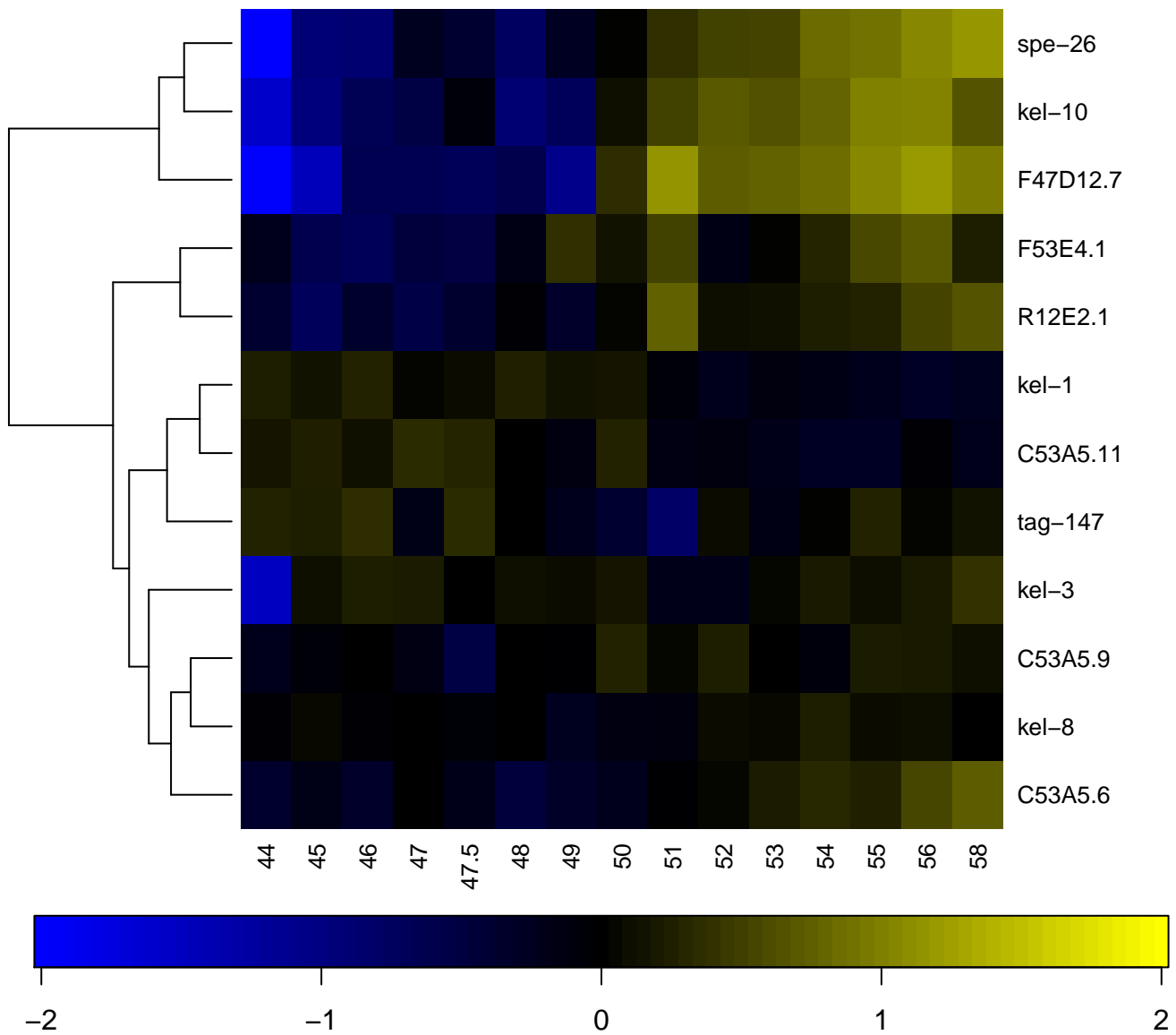
Fz domain



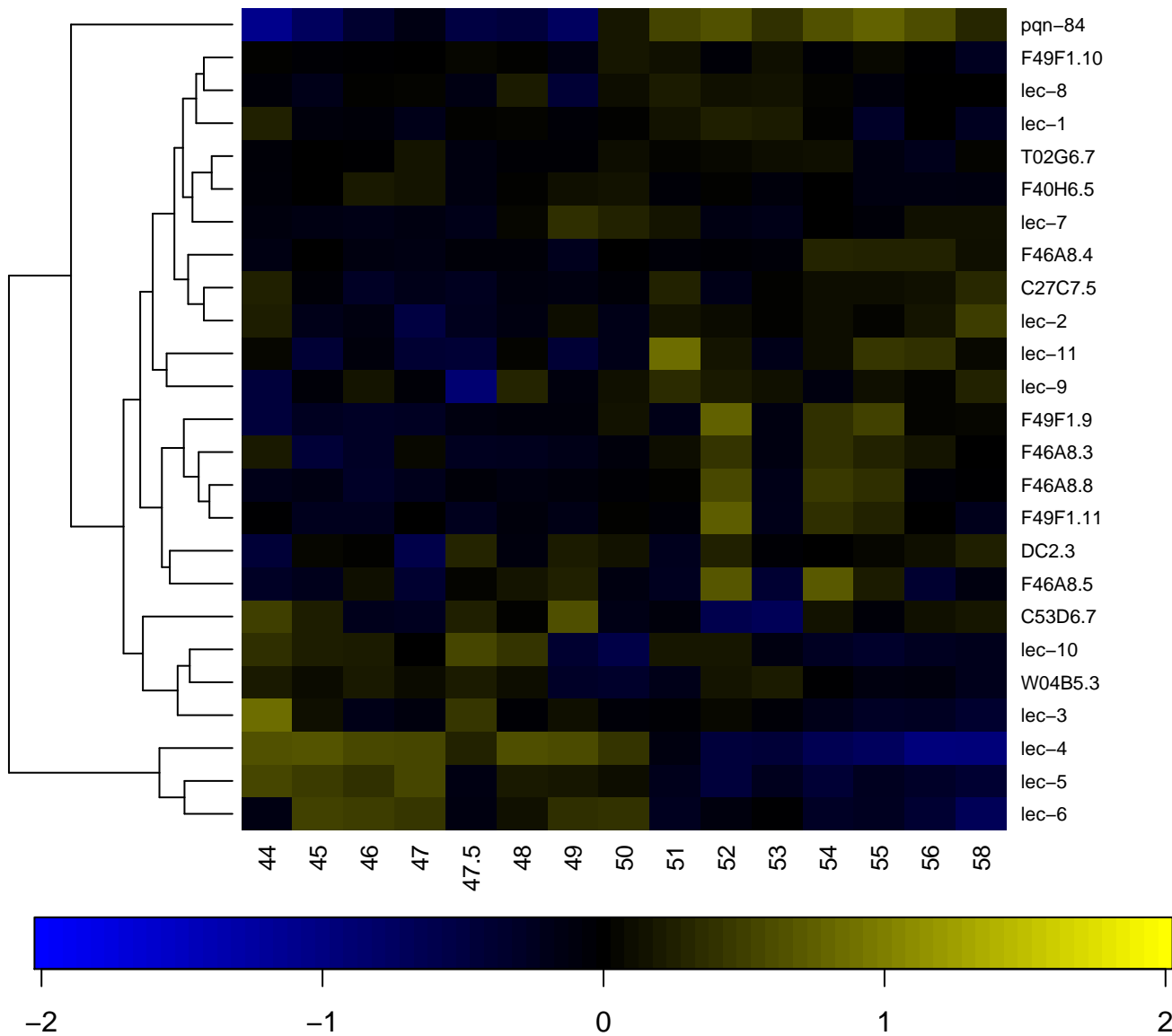
G-protein beta WD-40 repeat, region



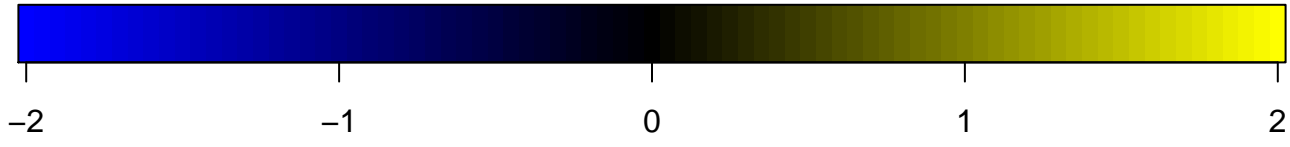
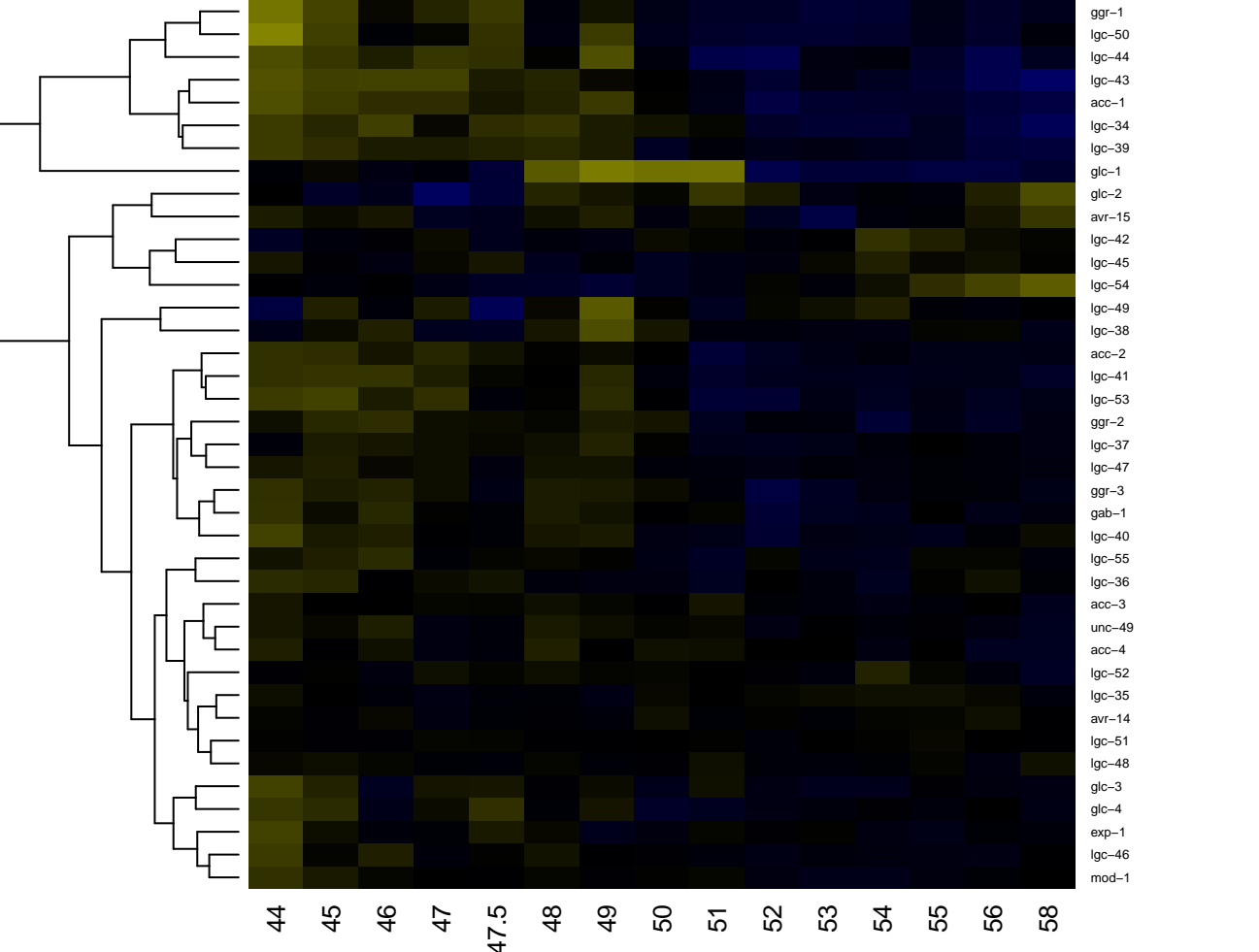
Galactose oxidase, beta-propeller



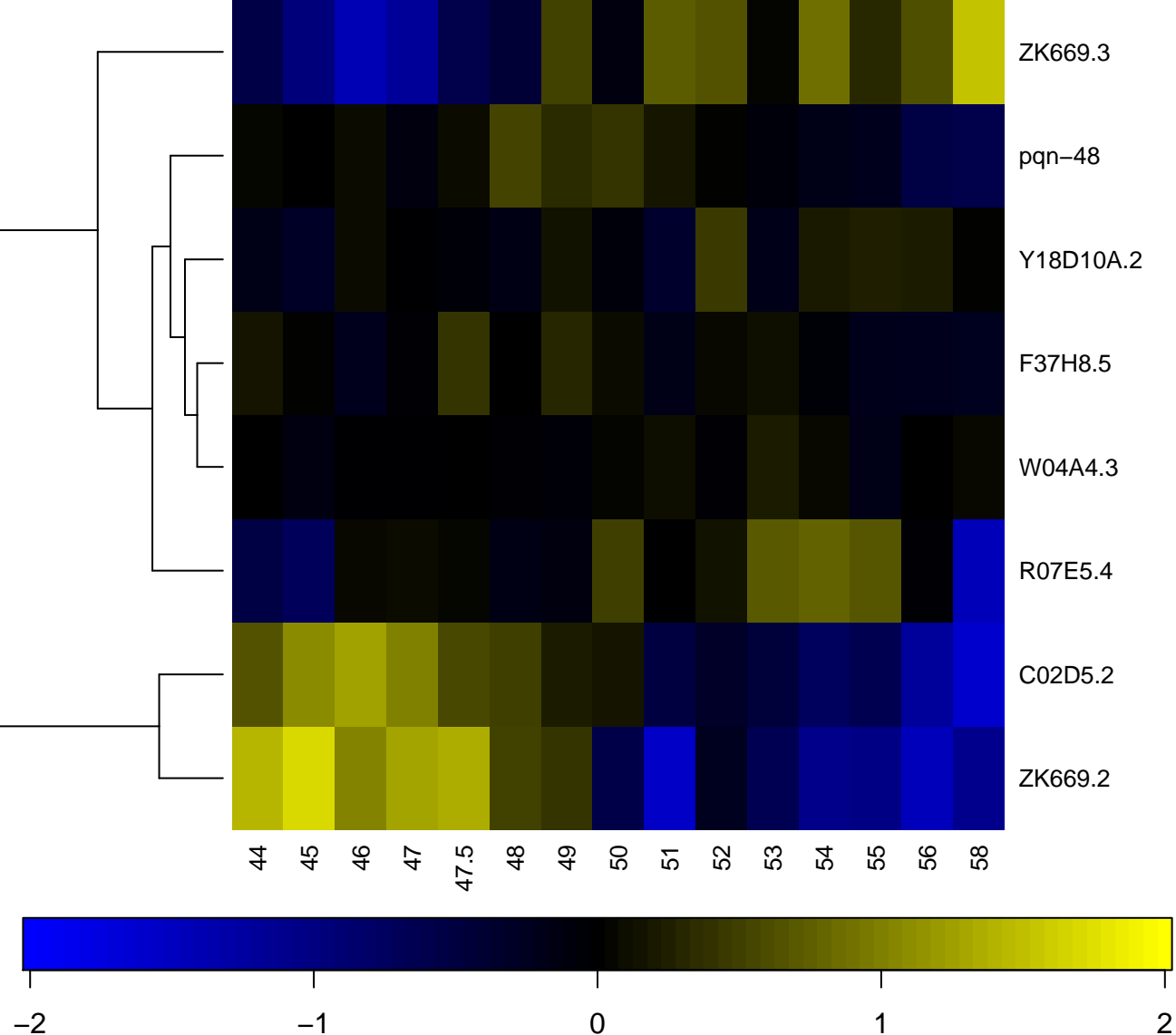
Galectin, carbohydrate recognition domain



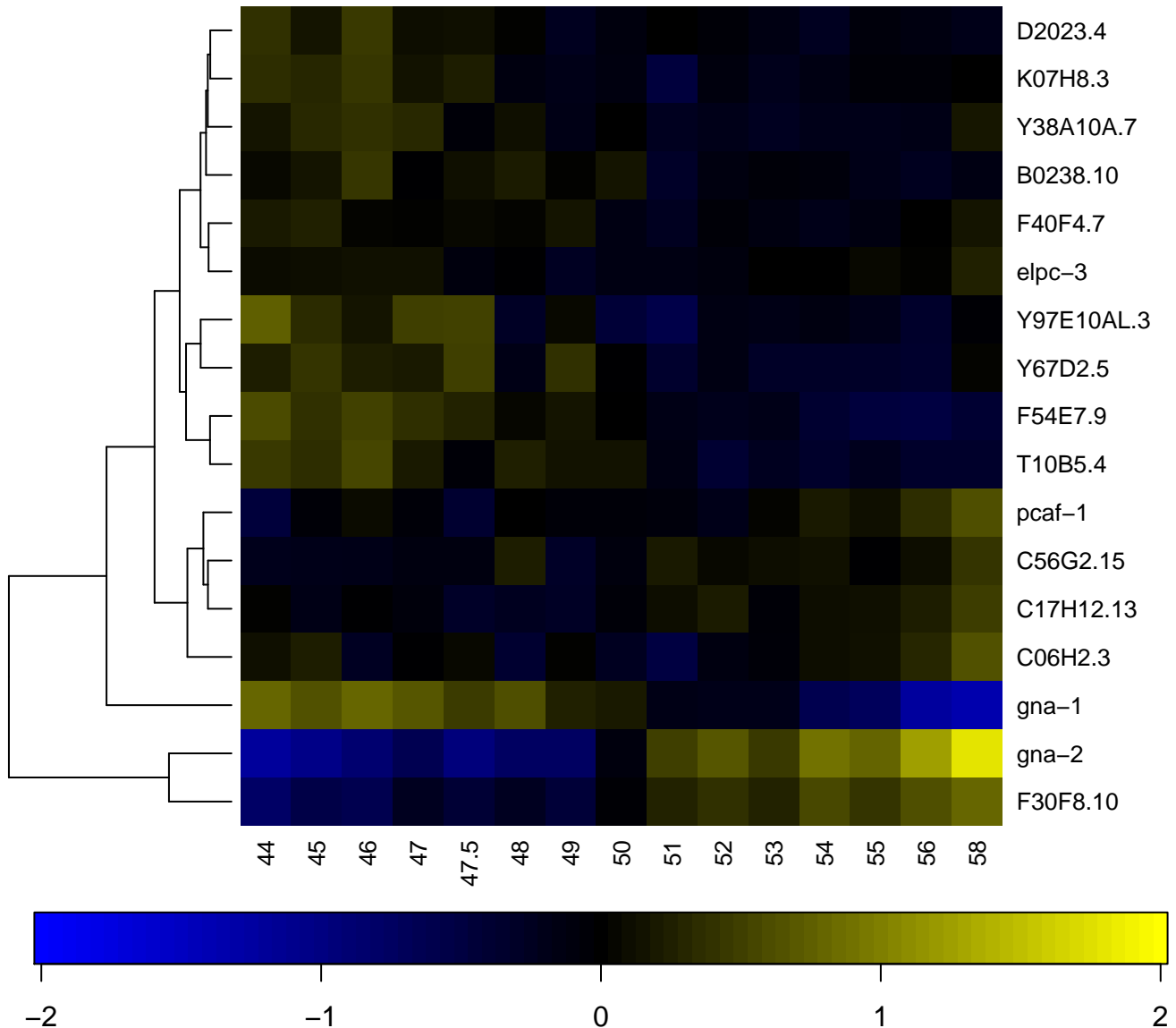
Gamma-aminobutyric acid A receptor



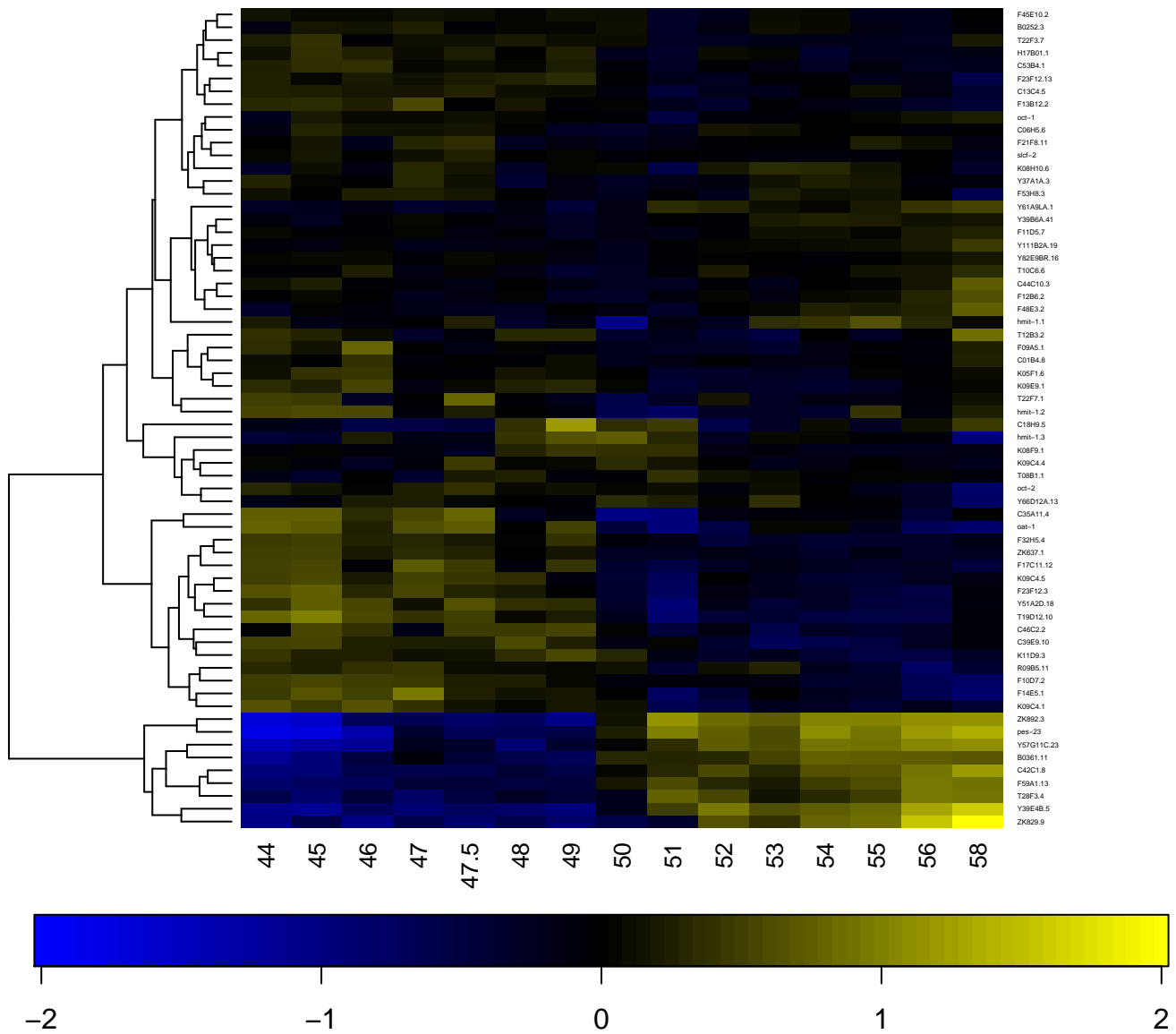
Gamma interferon inducible lysosomal thiol reductase GIL



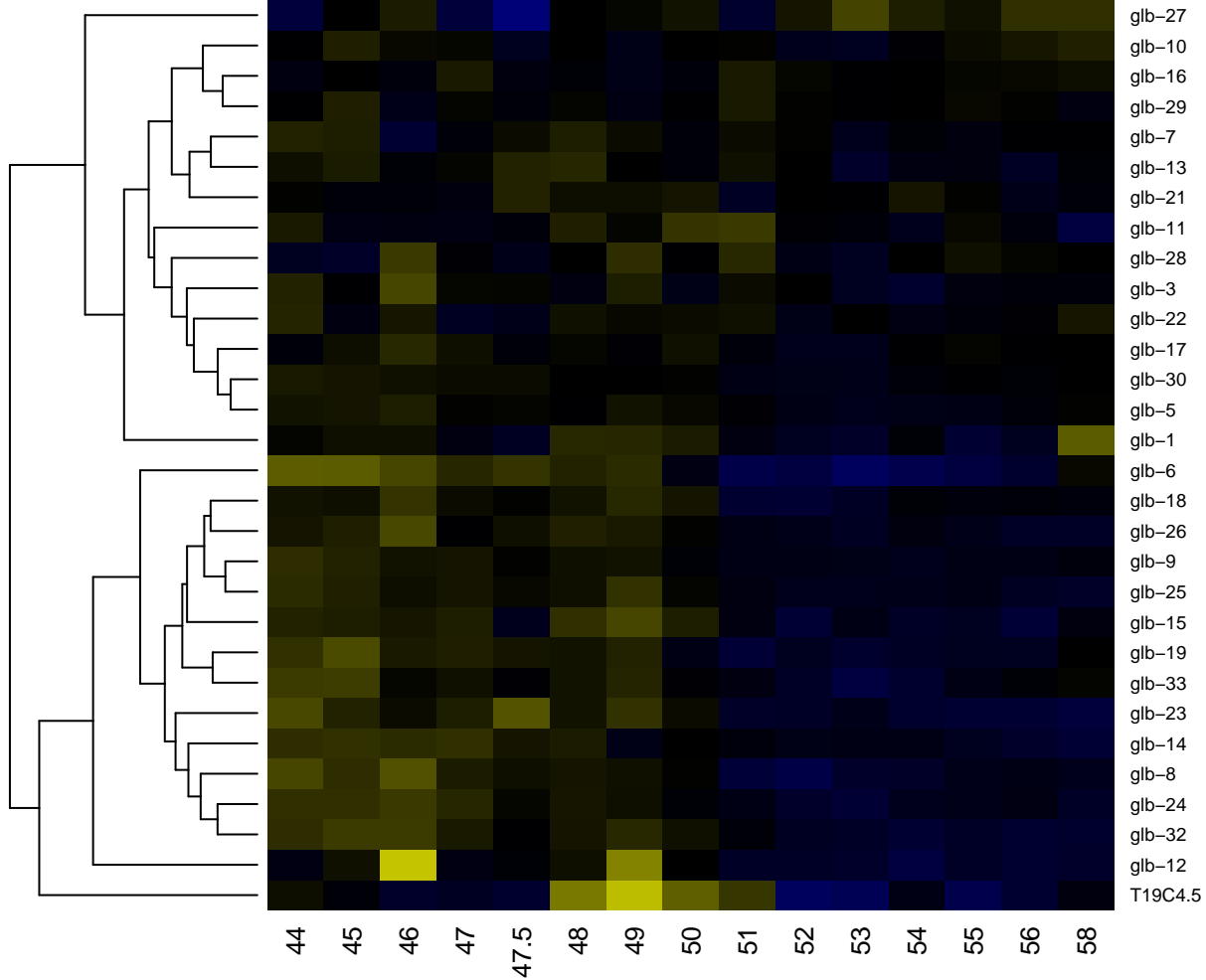
GCN5-related N-acetyltransferase, C-terminal



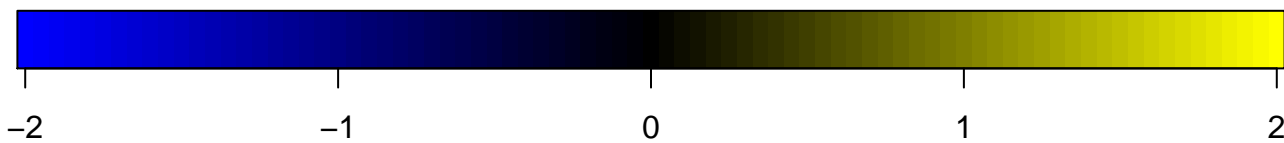
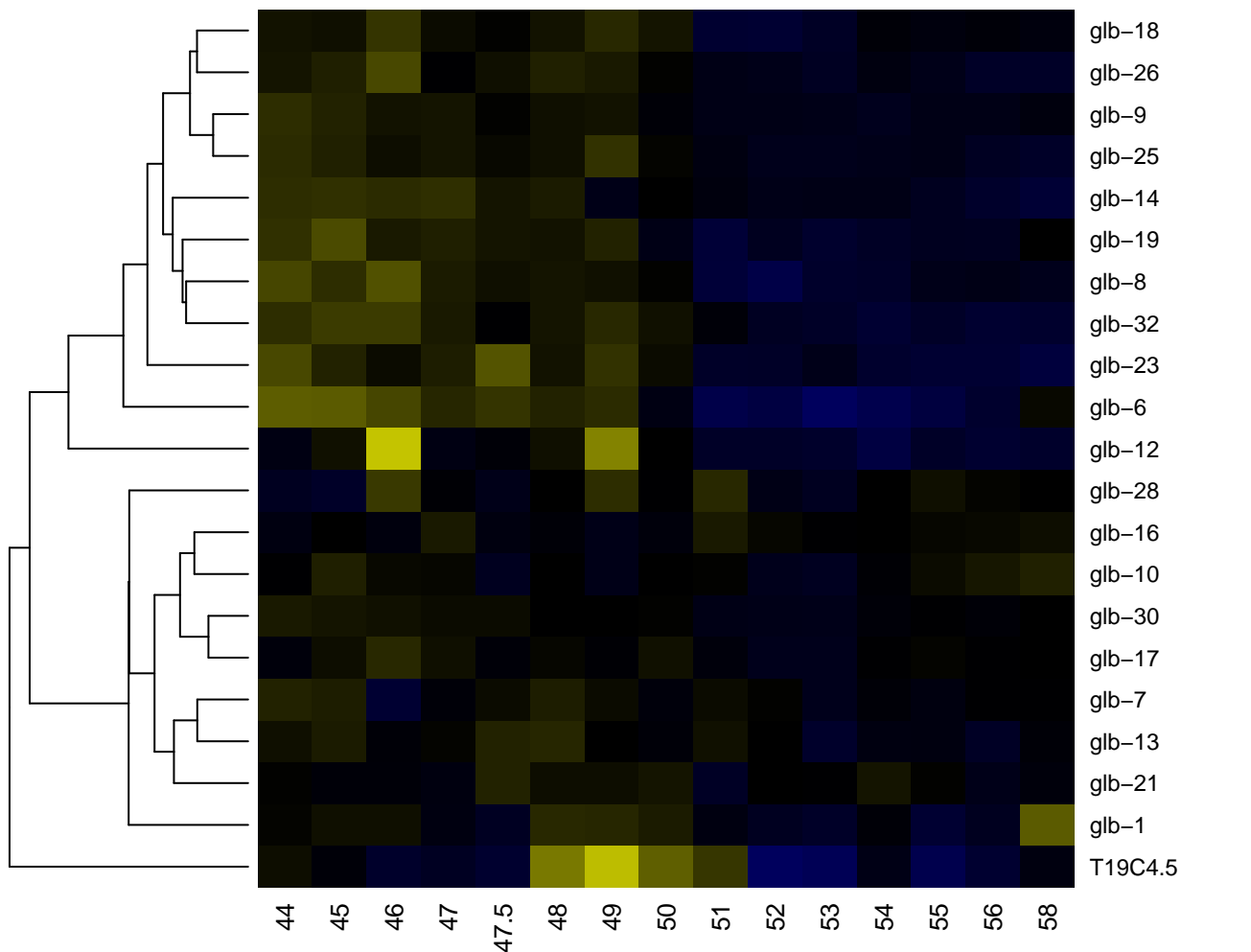
General substrate transporter



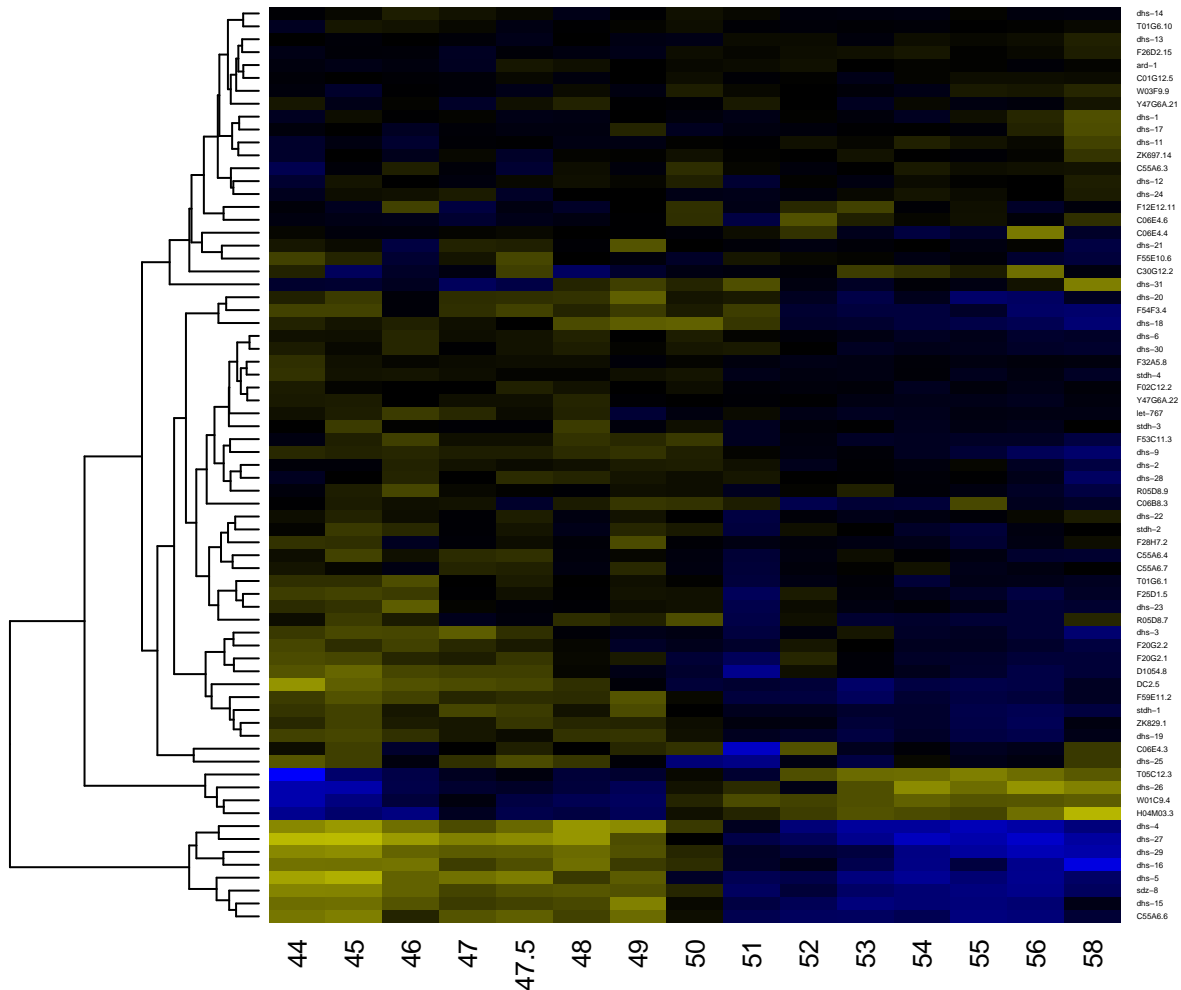
Globin



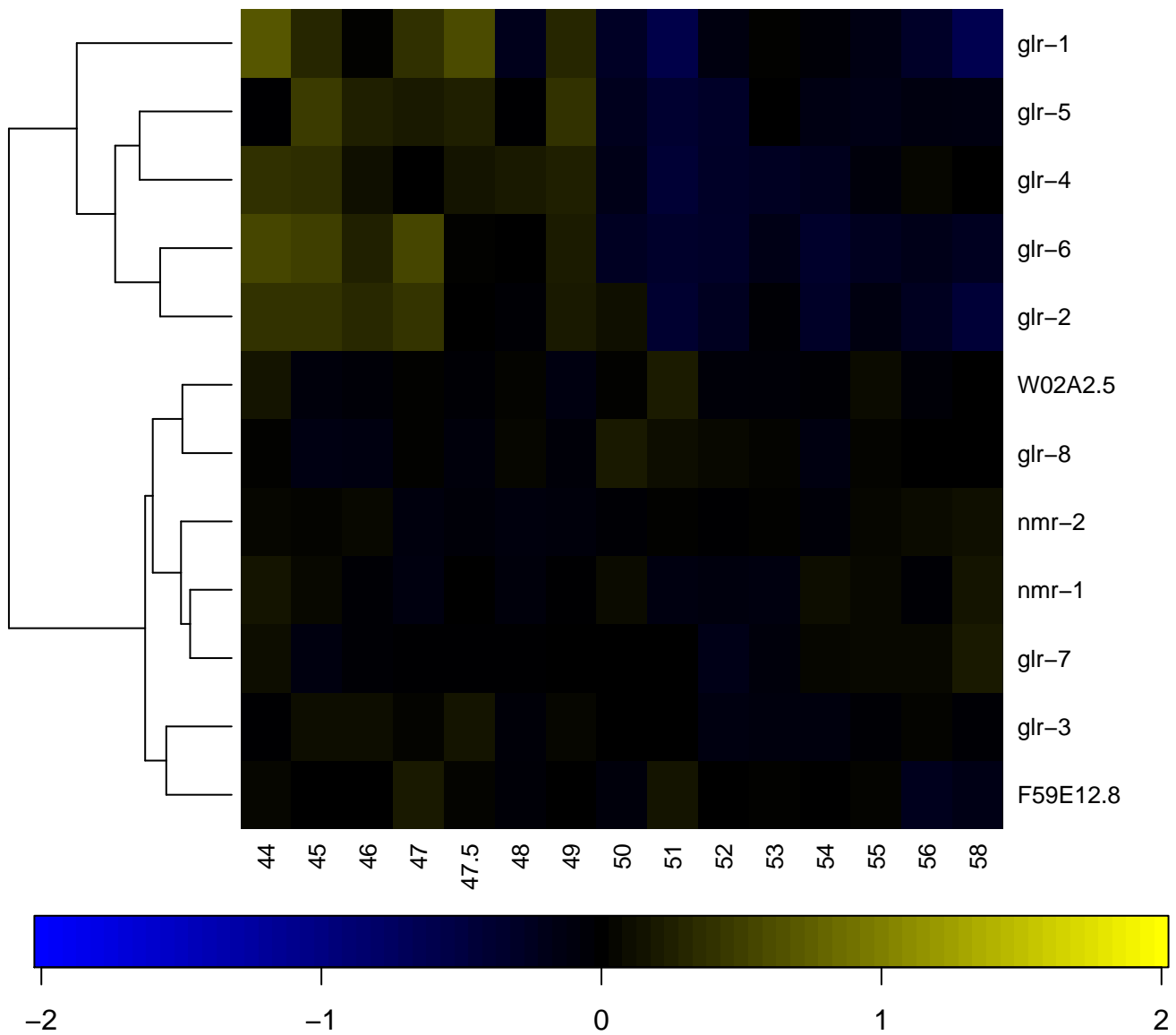
Globin, subset



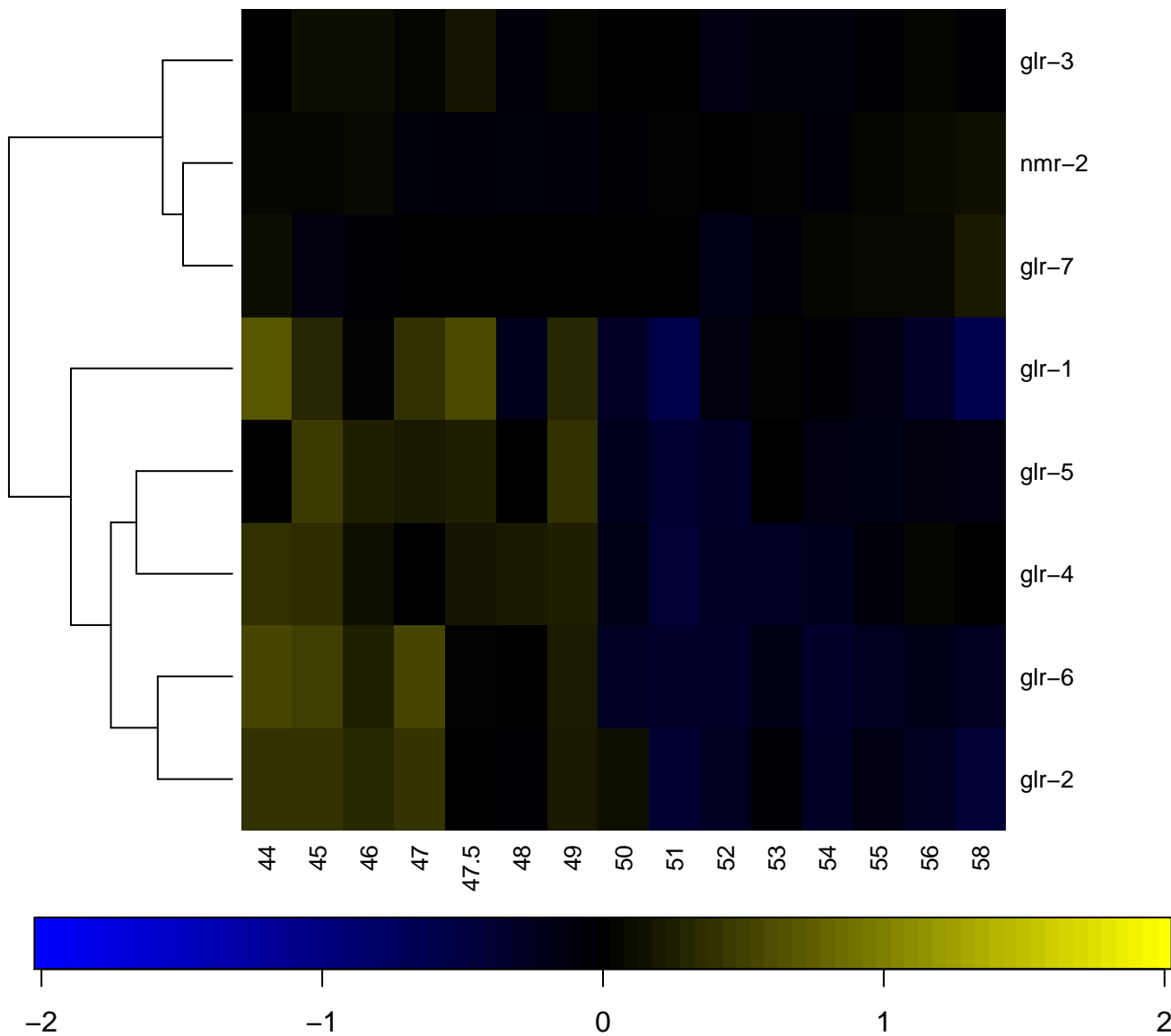
Glucose/ribitol dehydrogenase



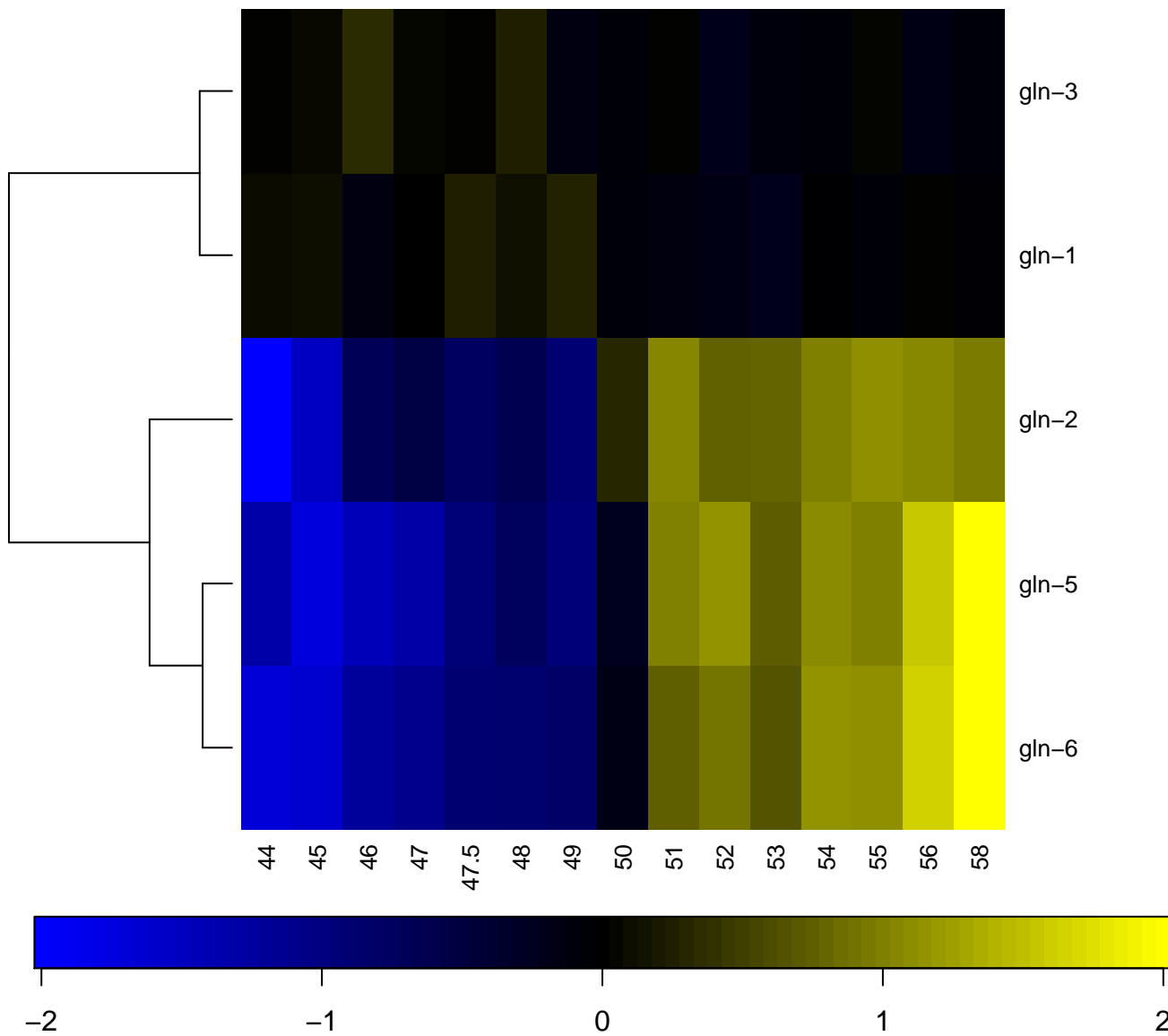
Glutamate receptor-related



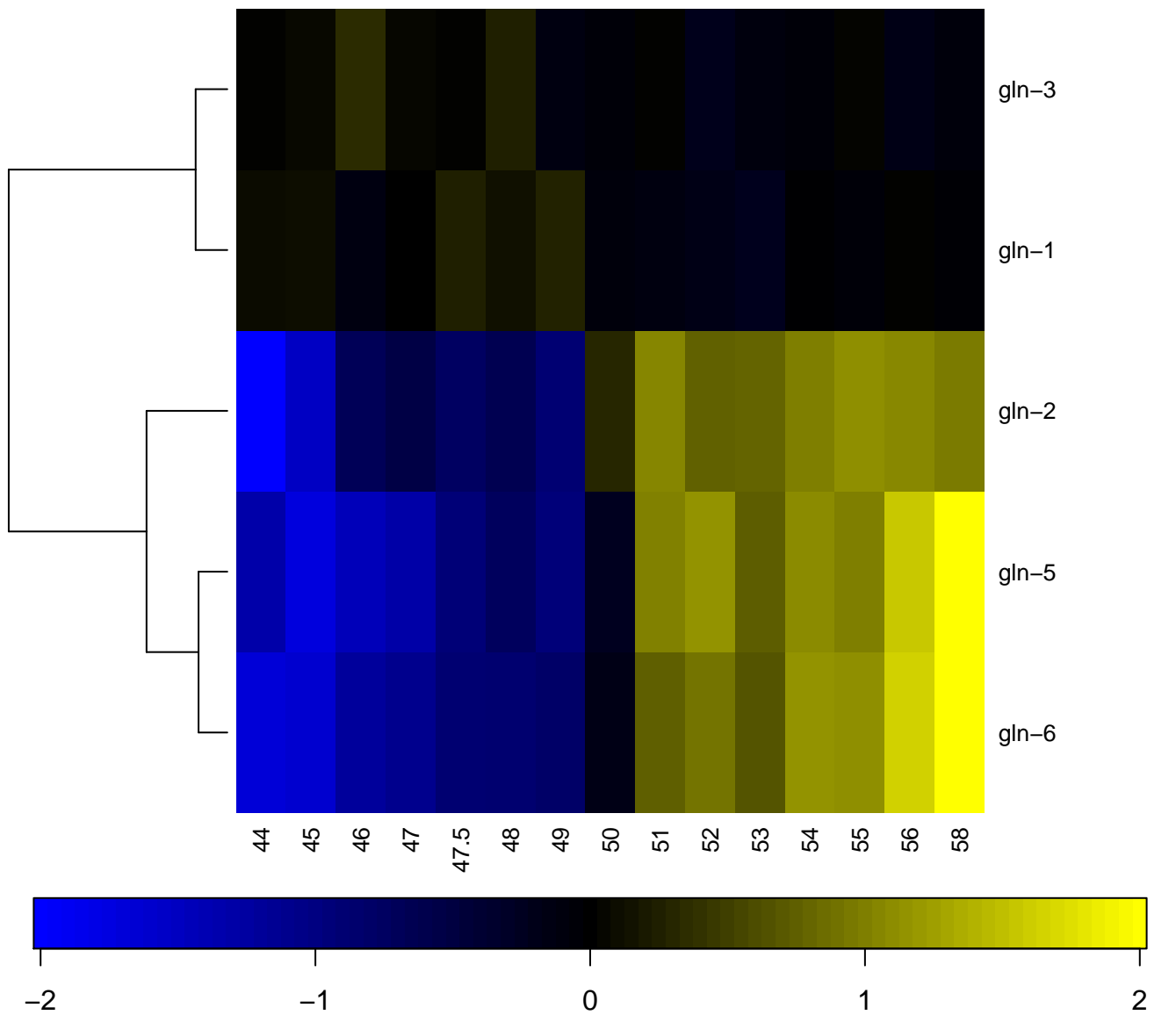
Glutamate receptor, L-glutamate/glycine-binding



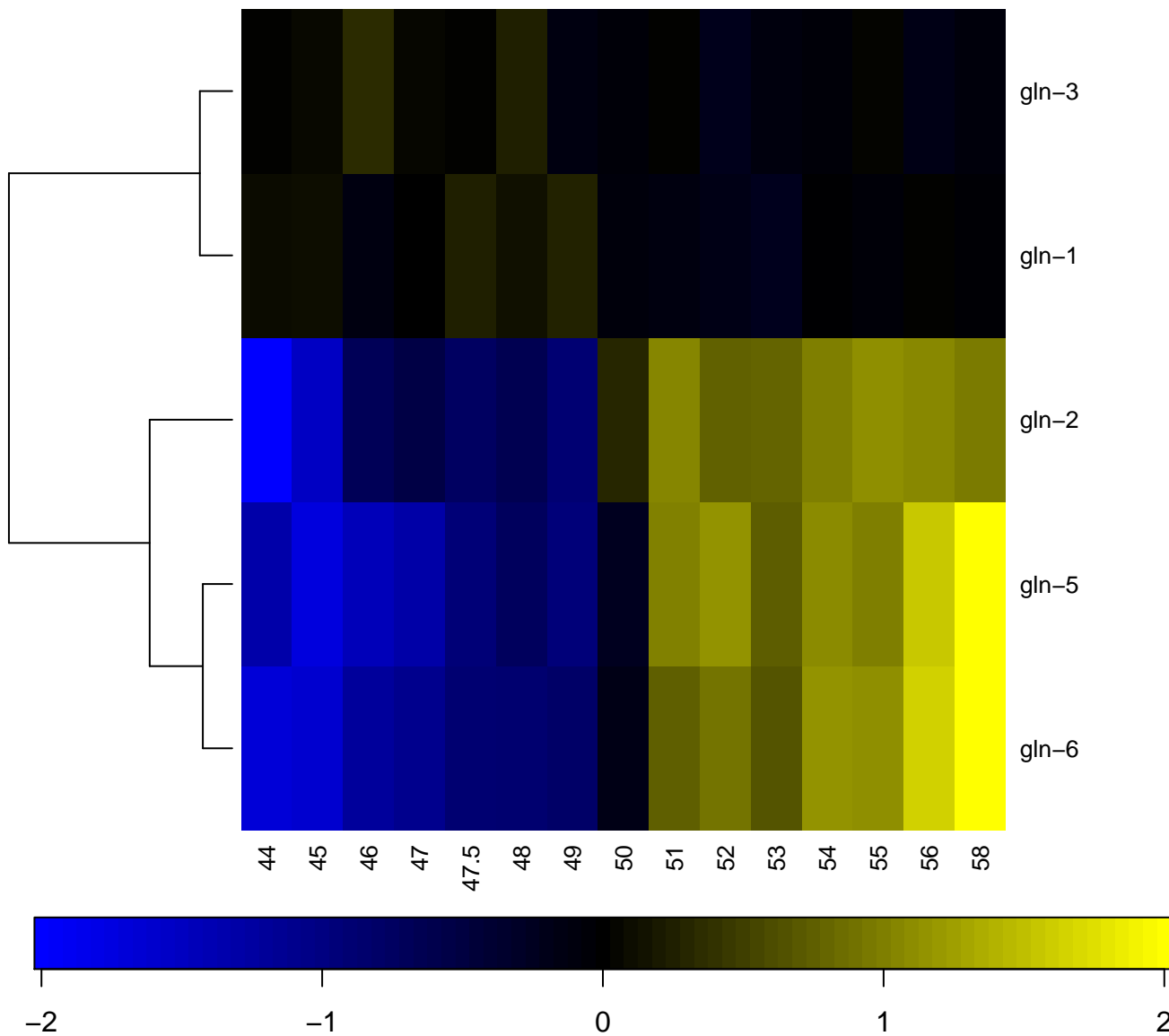
Glutamine synthetase, beta-Grasp



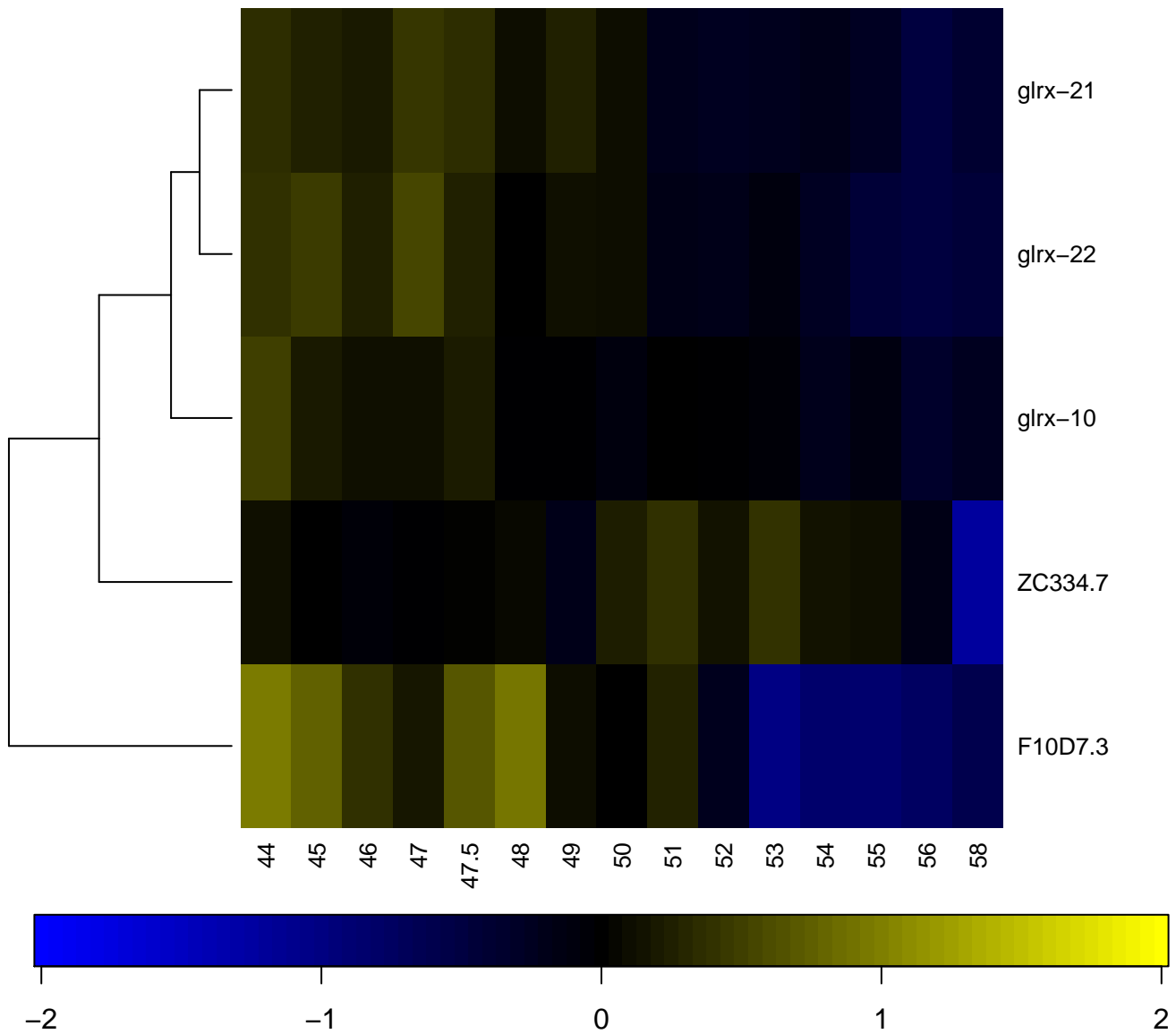
Glutamine synthetase, beta-Grasp domain



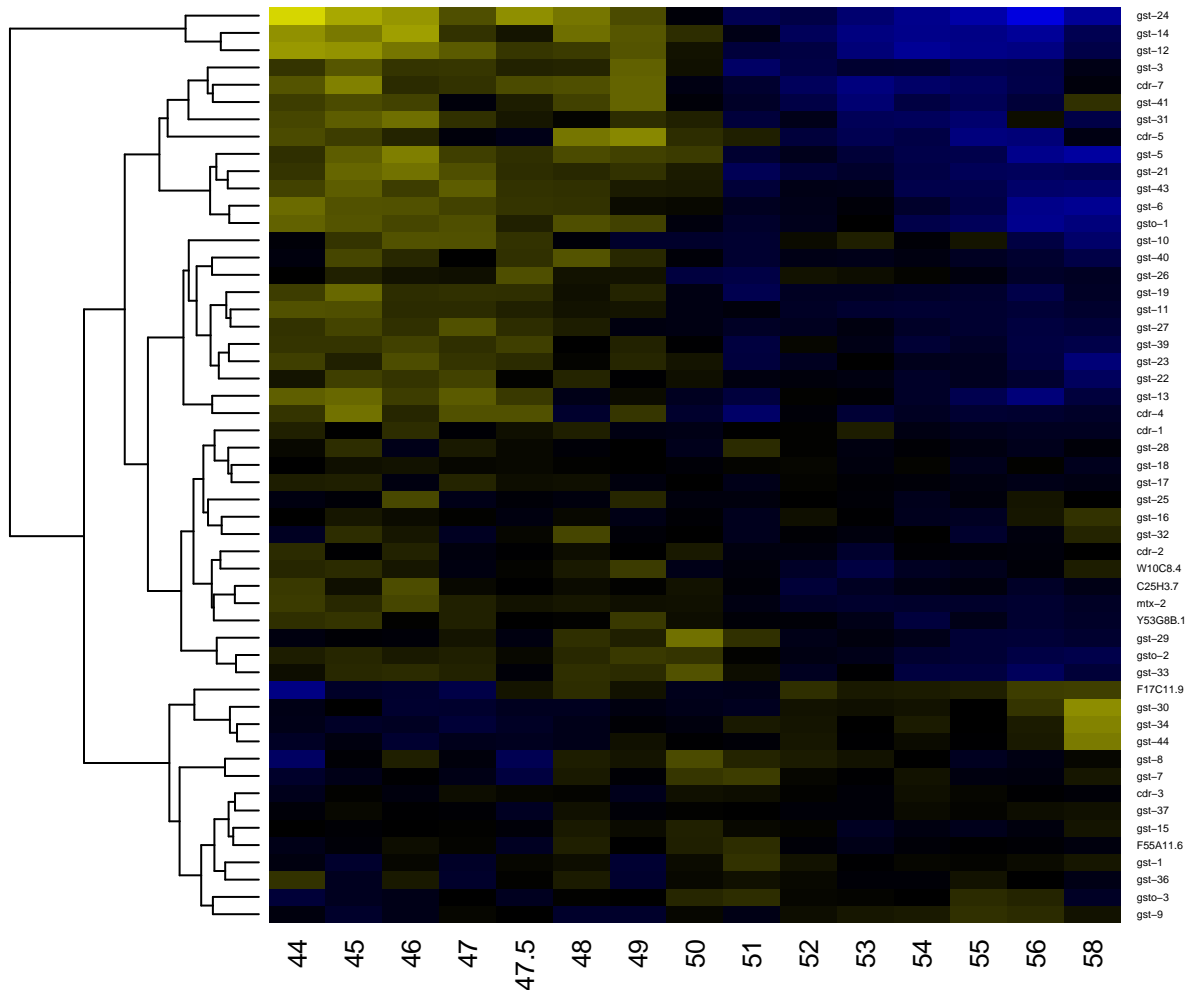
Glutamine synthetase, catalytic domain



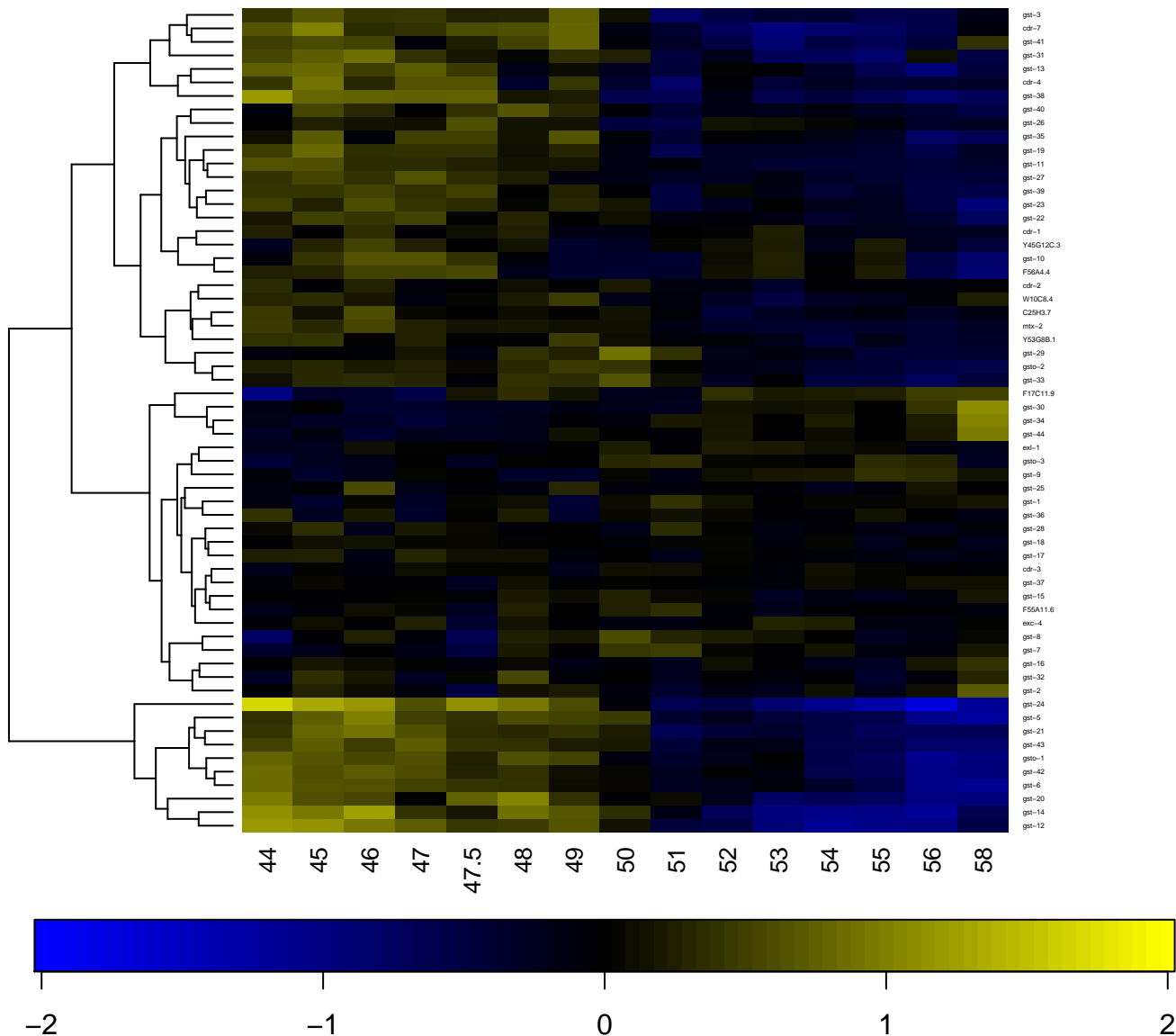
Glutaredoxin subgroup



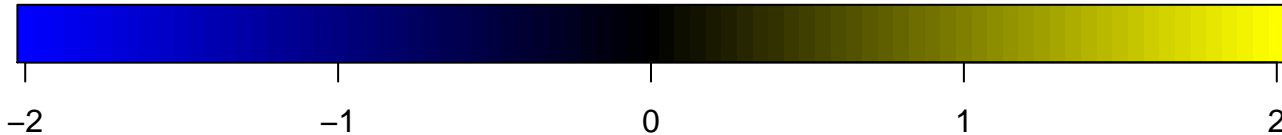
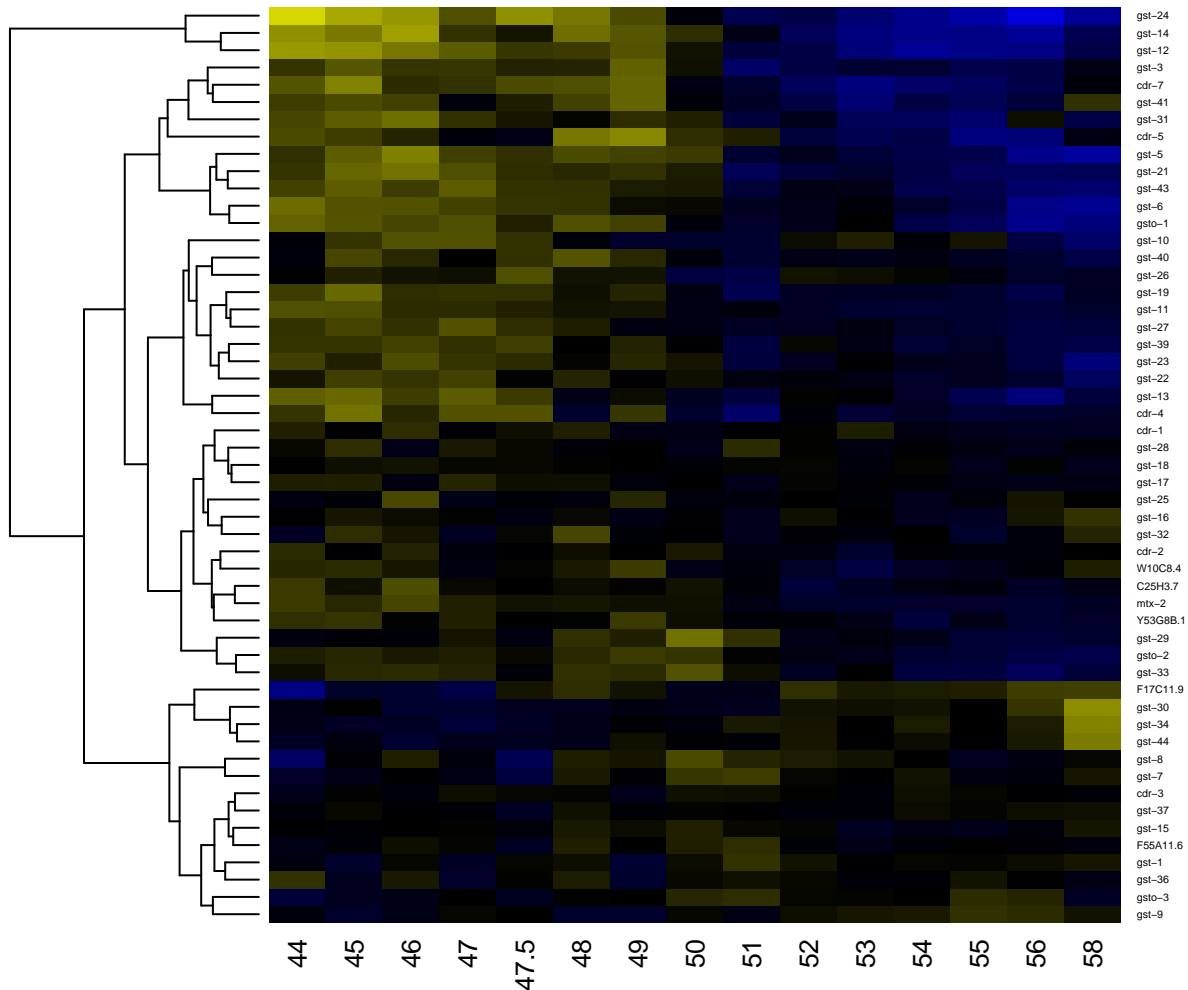
Glutathione S-transferase, C-terminal



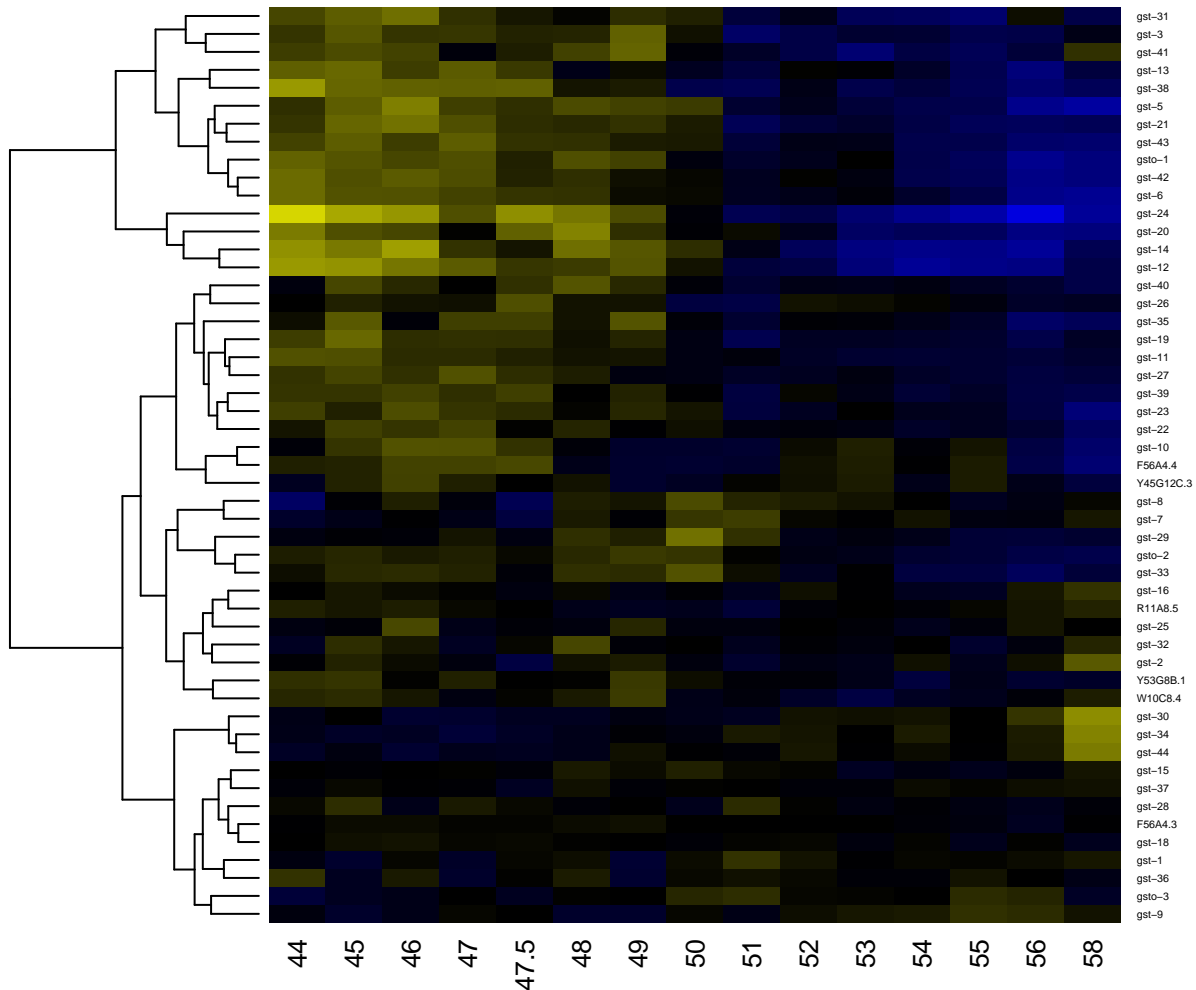
Glutathione S-transferase, C-terminal-like



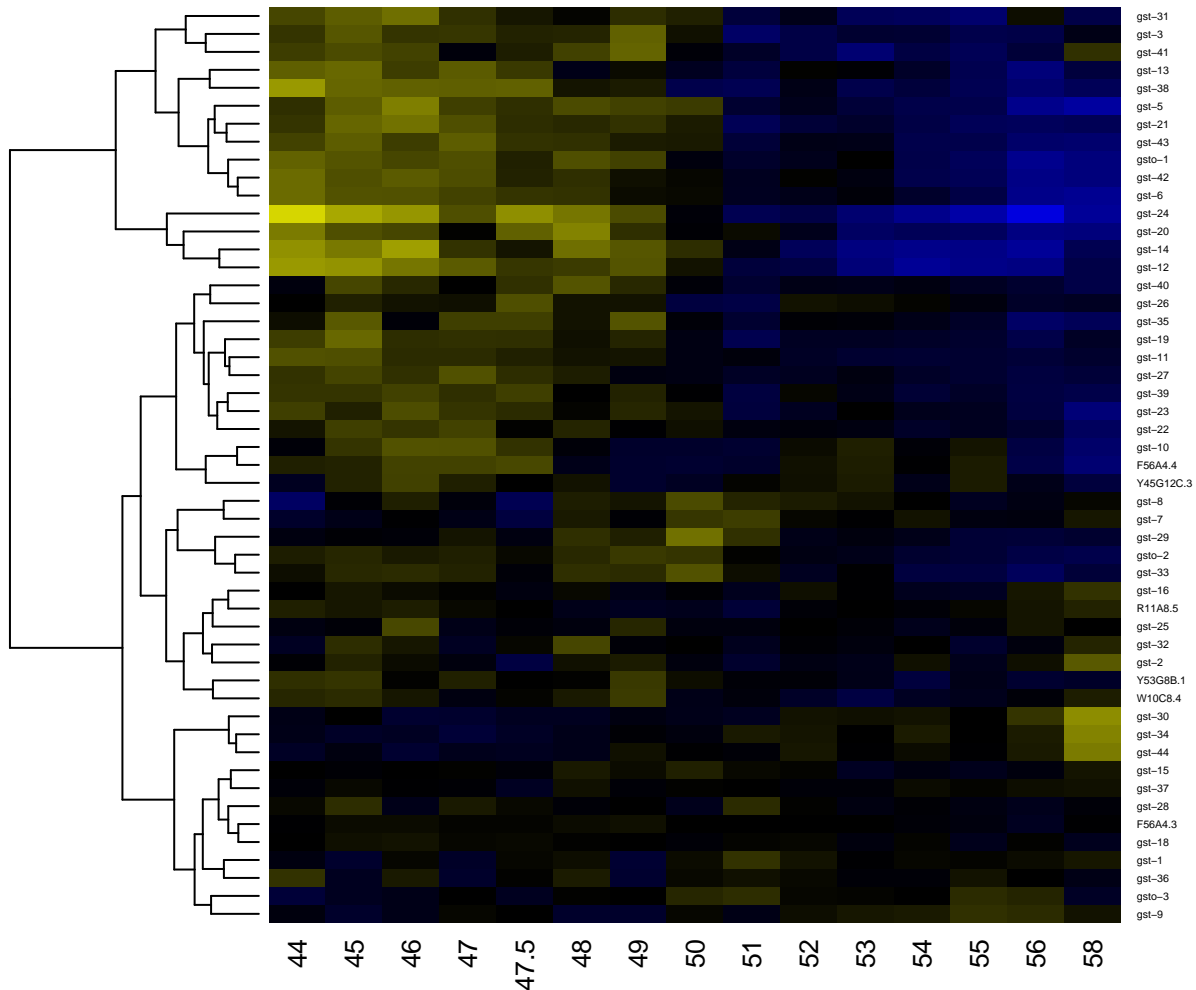
Glutathione S-transferase, C-terminal domain



Glutathione S-transferase, N-terminal



Glutathione S-transferase, N-terminal domain



-2

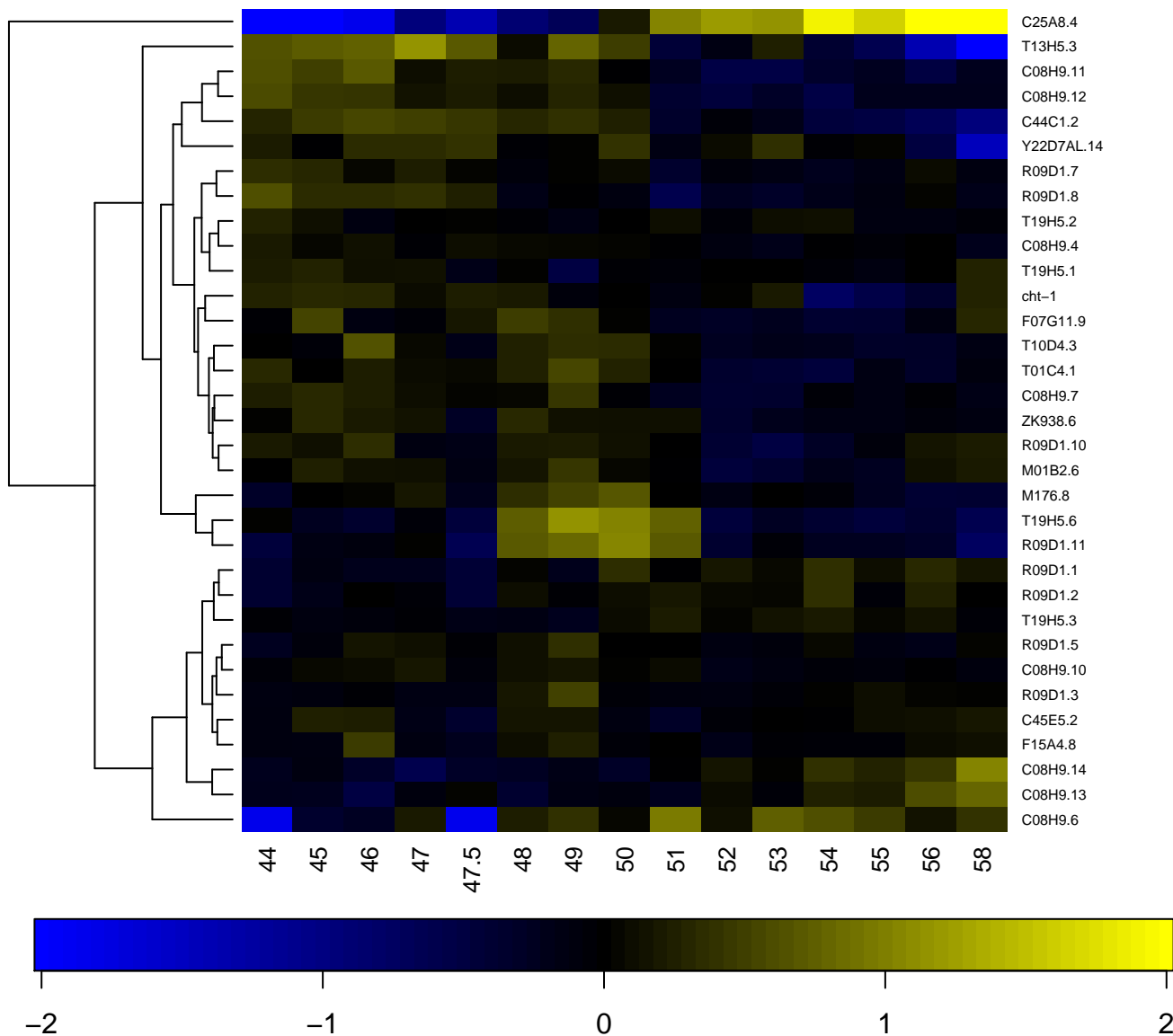
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0

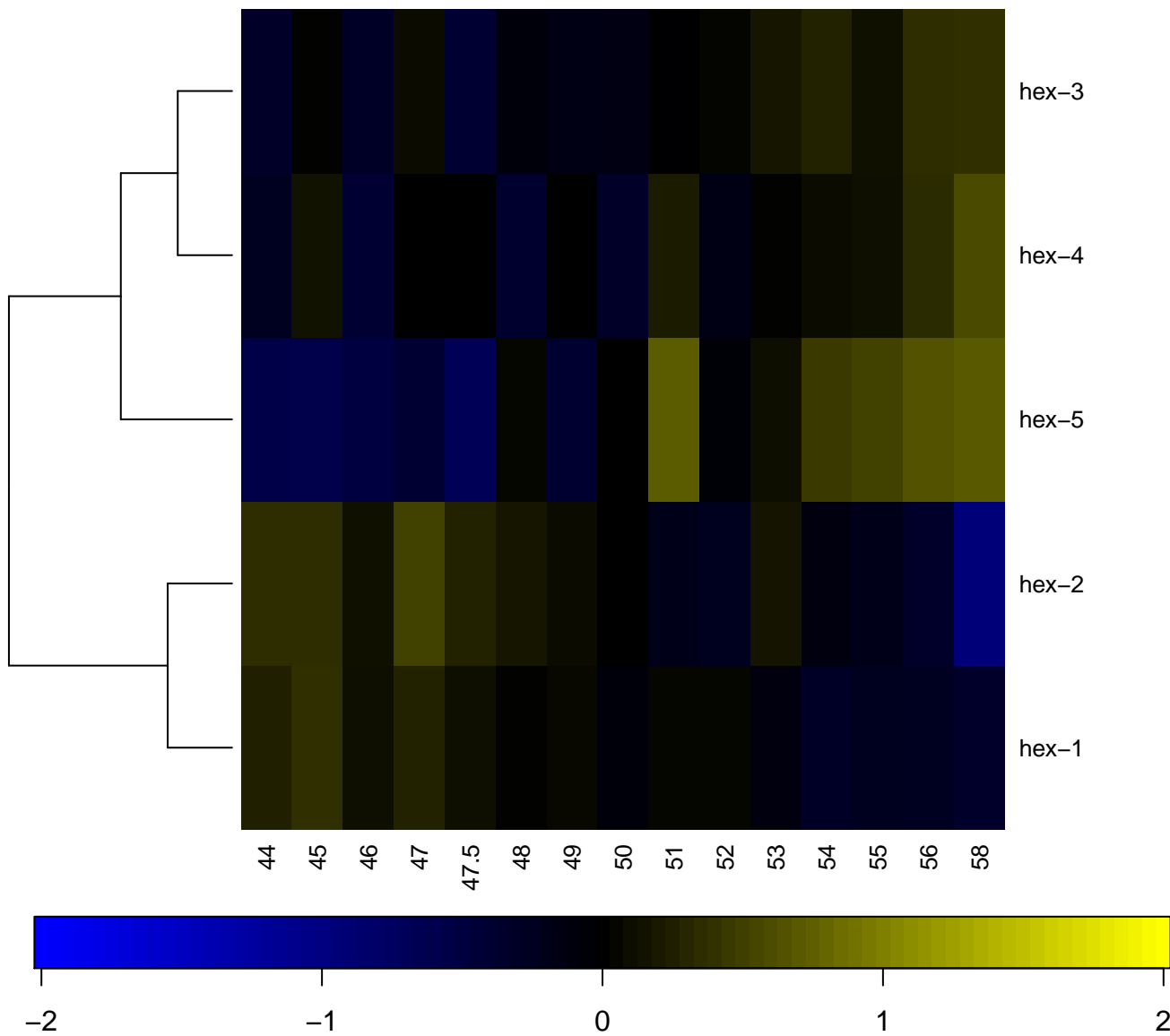
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2

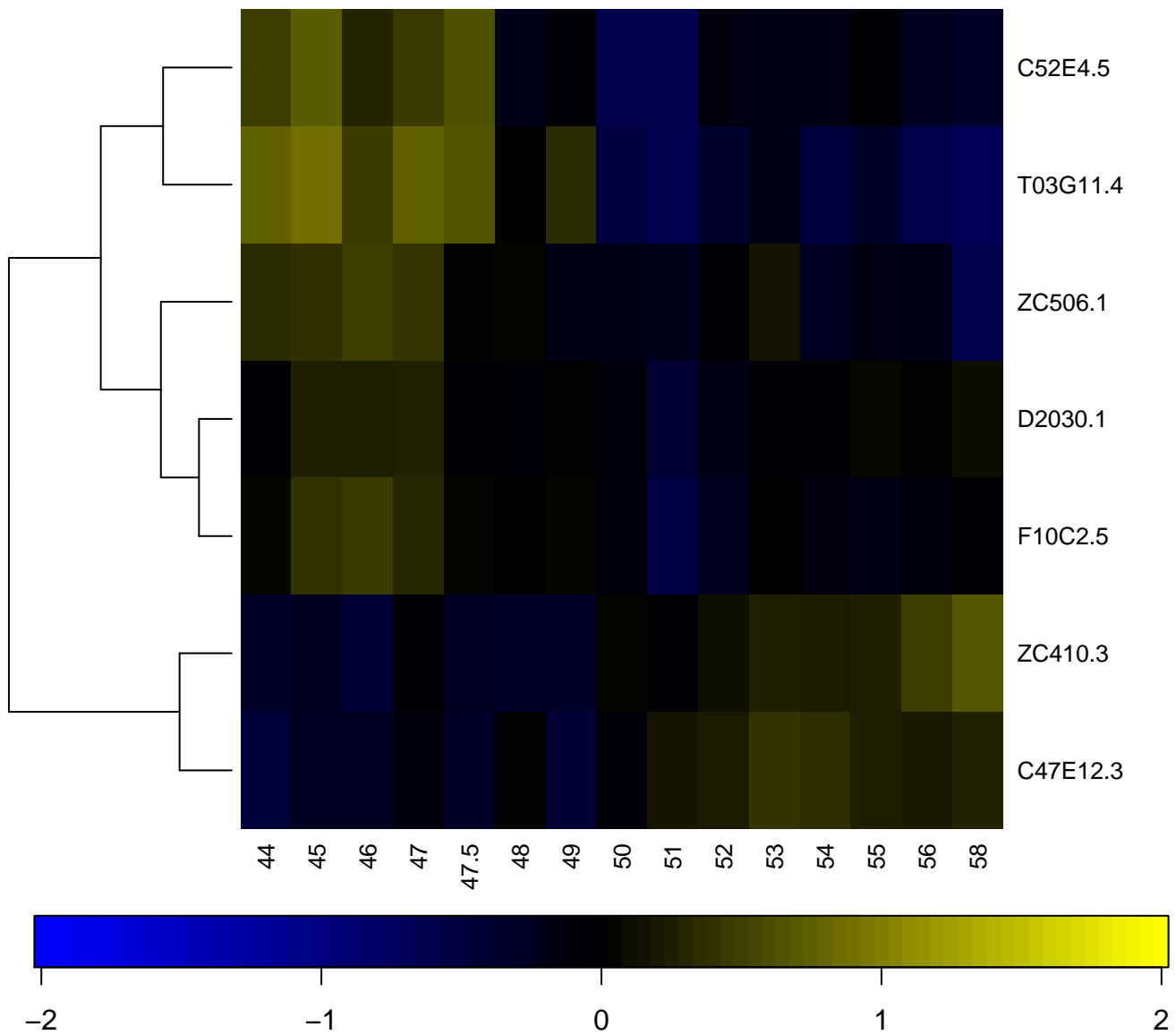
Glycoside hydrolase, family 18, catalytic domain



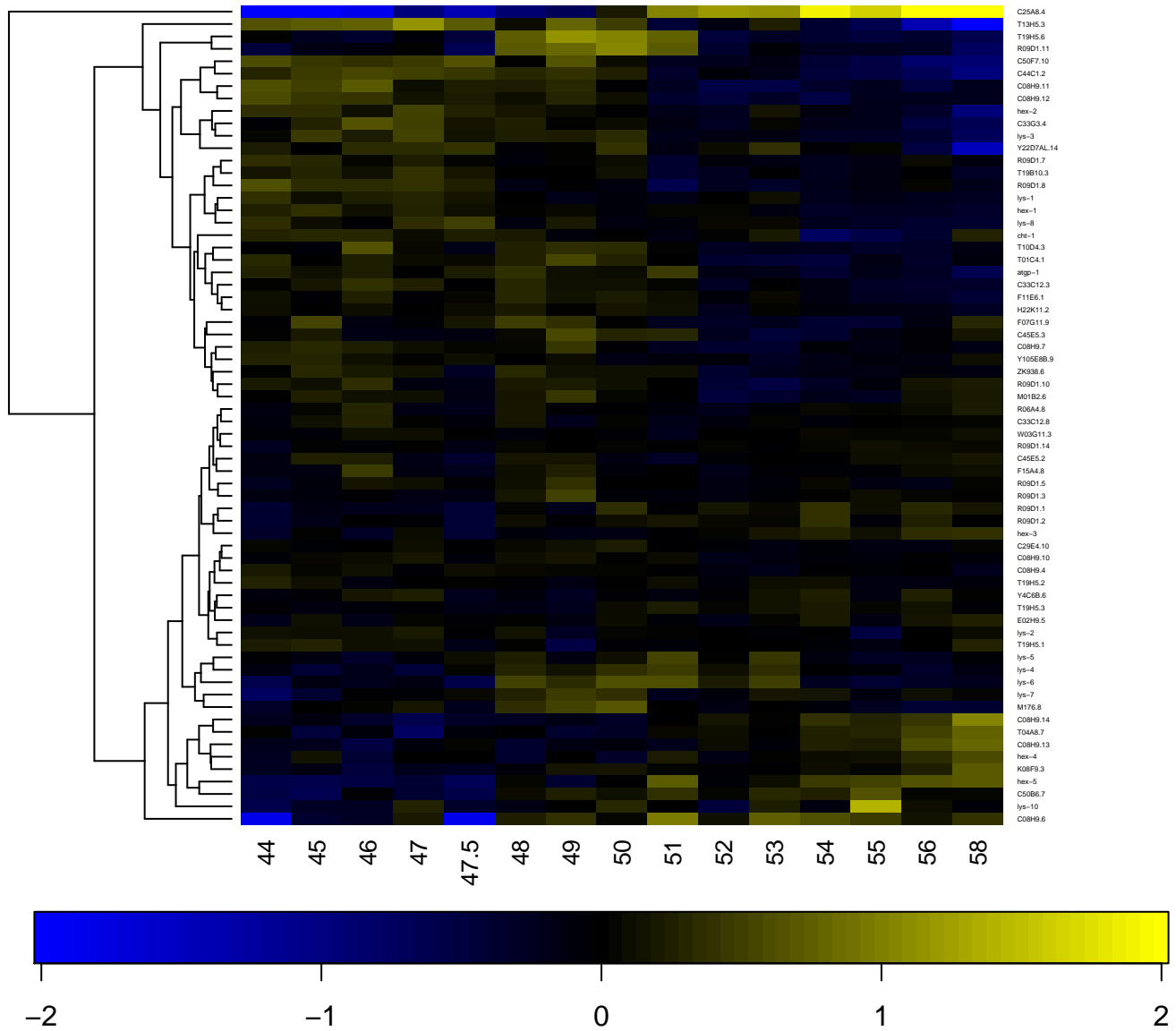
Glycoside hydrolase, family 20, catalytic core



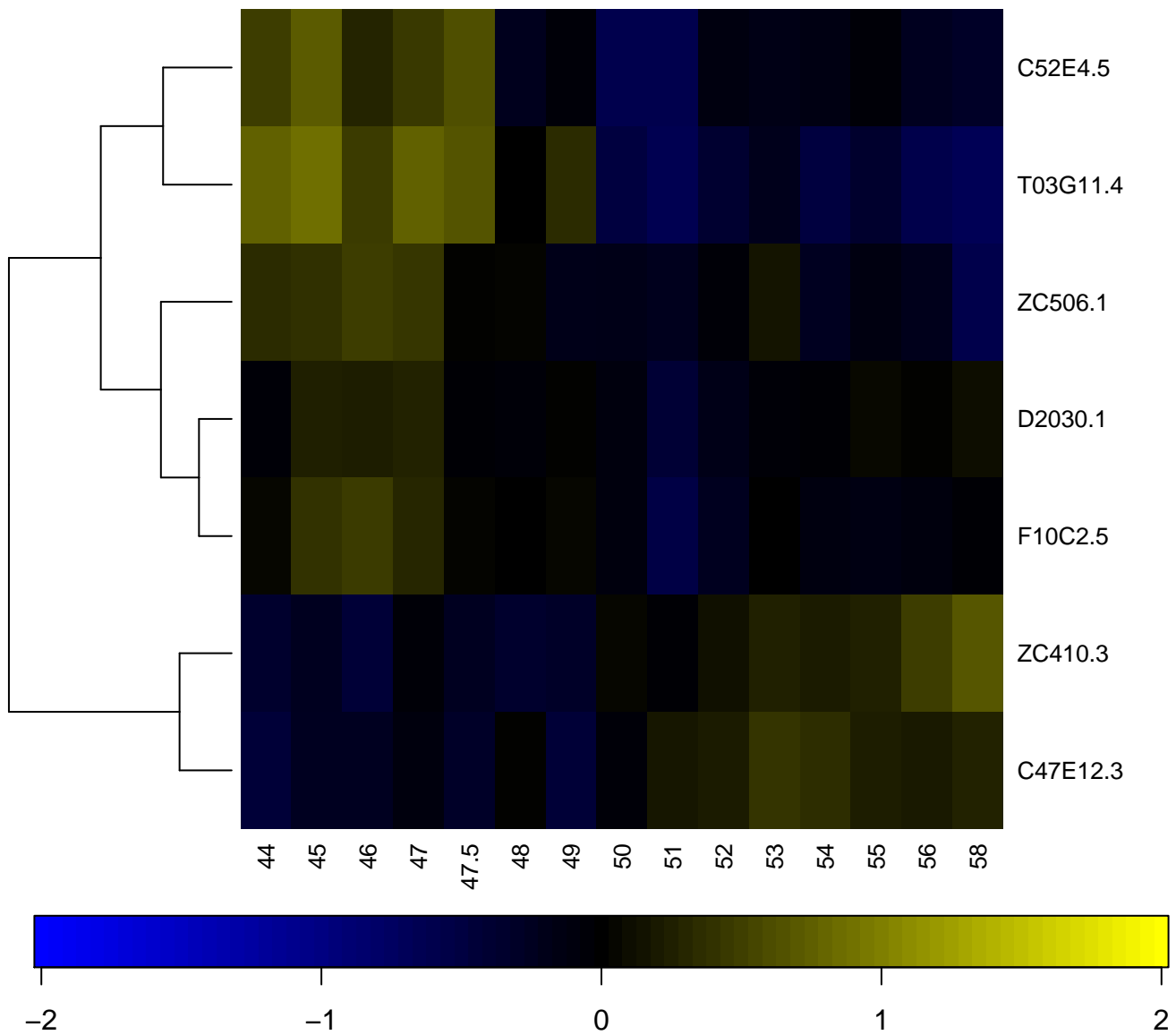
Glycoside hydrolase, family 47



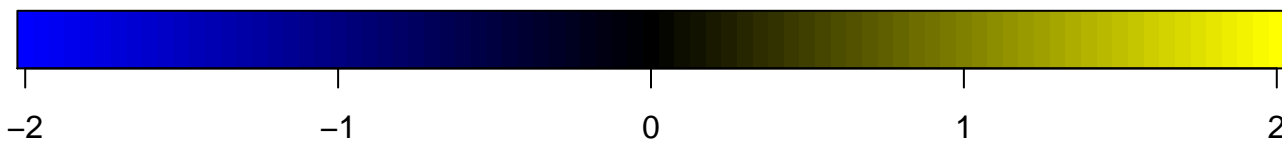
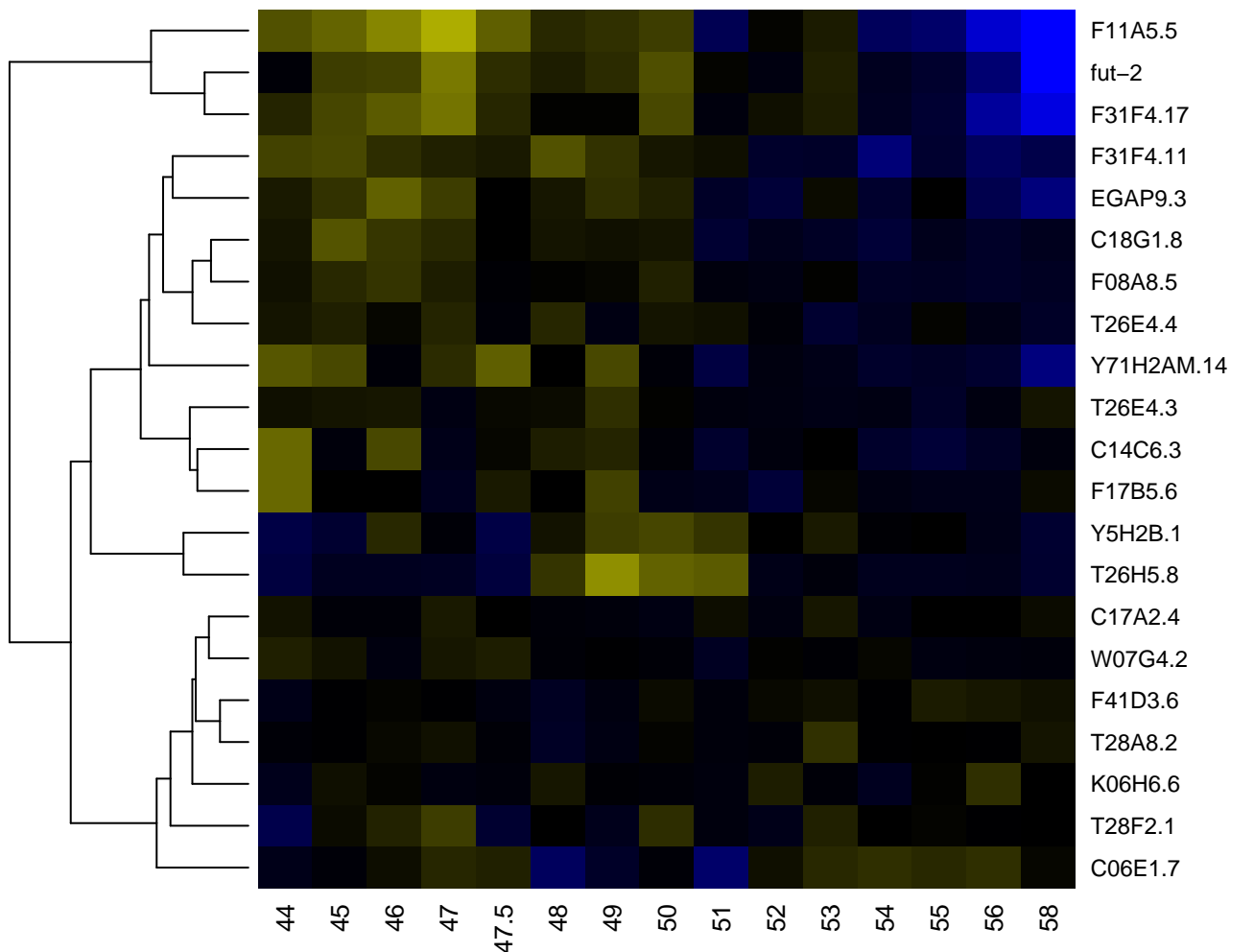
Glycoside hydrolase, subgroup, catalytic core



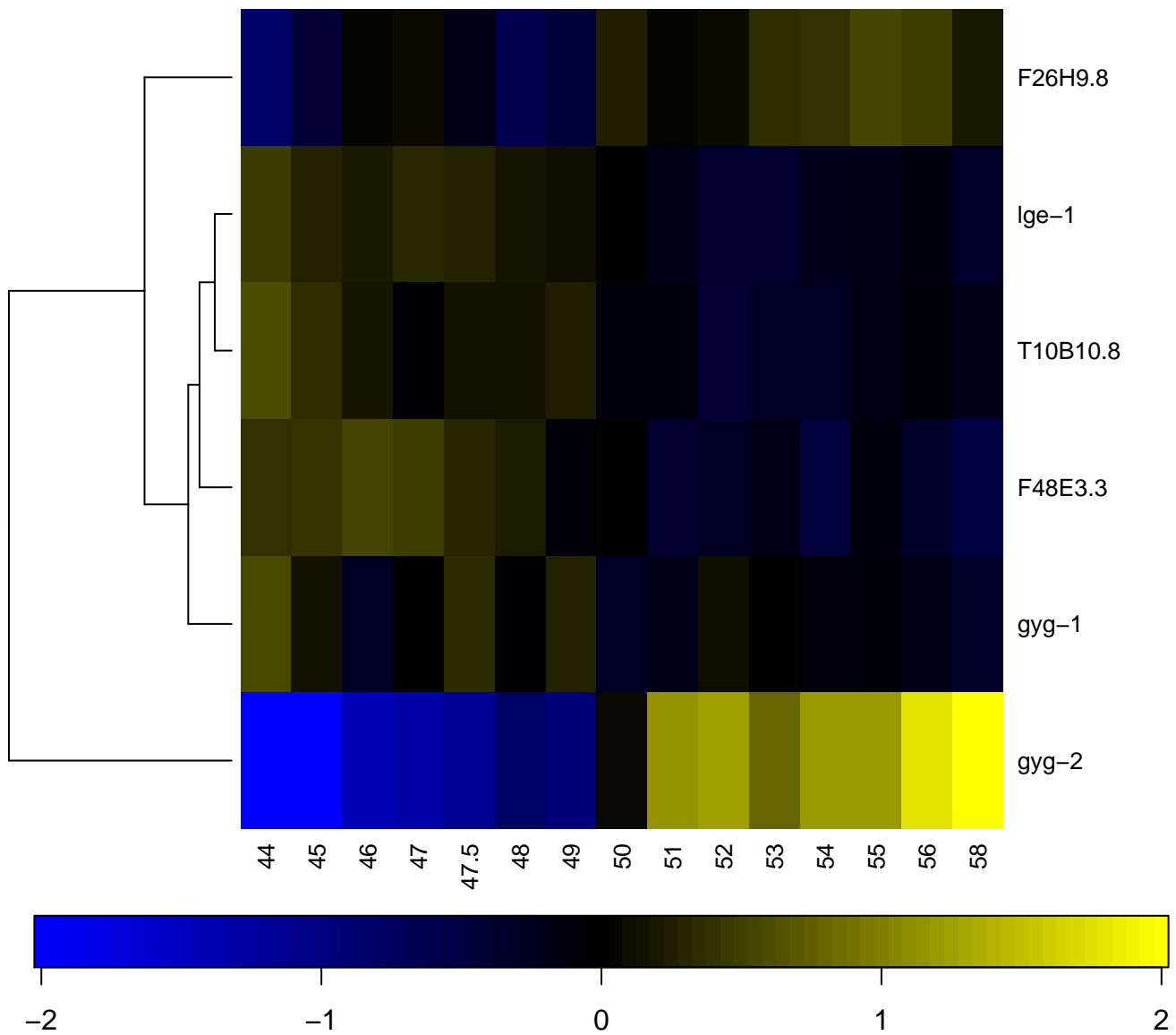
Glycosyl hydrolase family 47



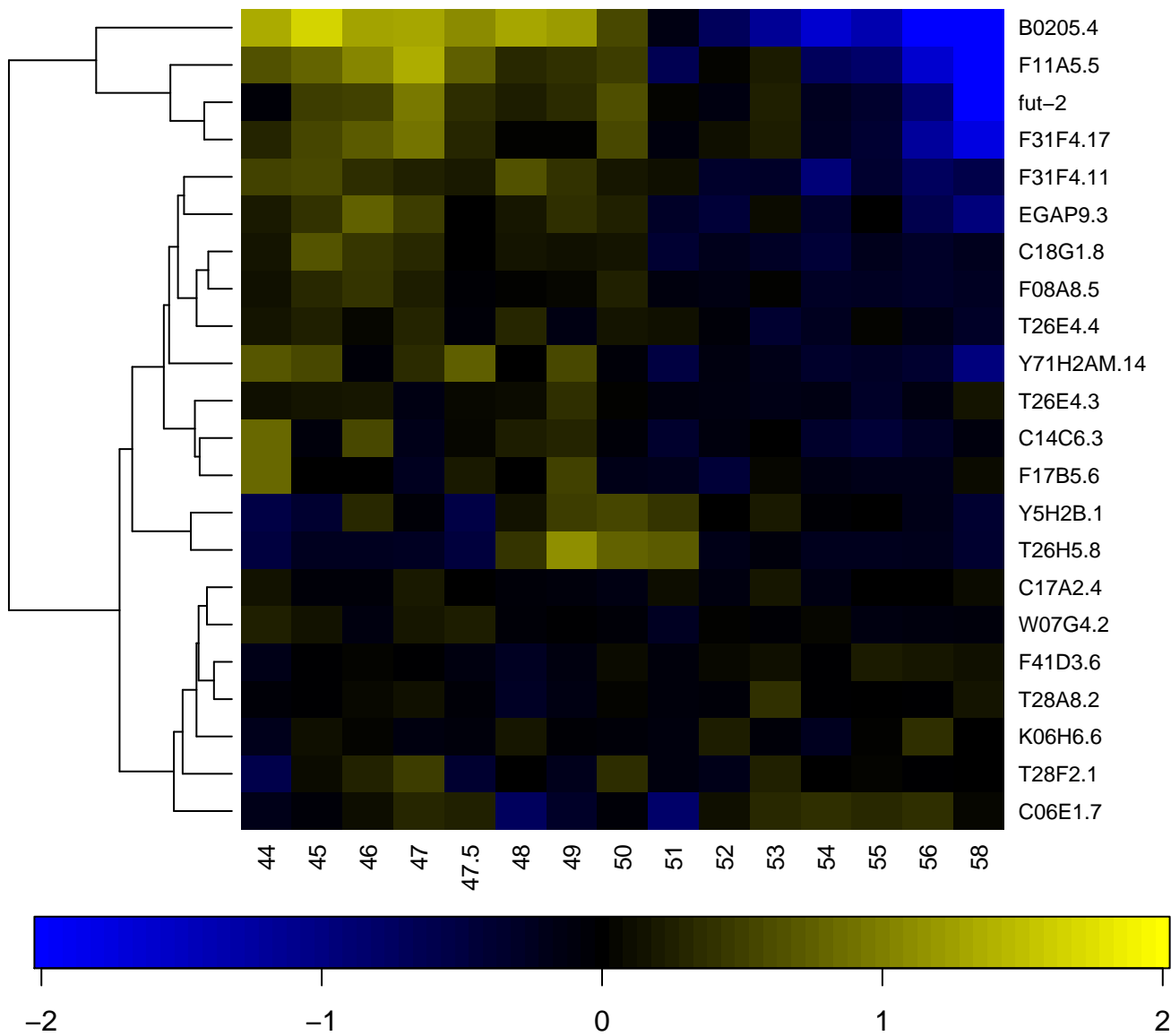
Glycosyl transferase family 11



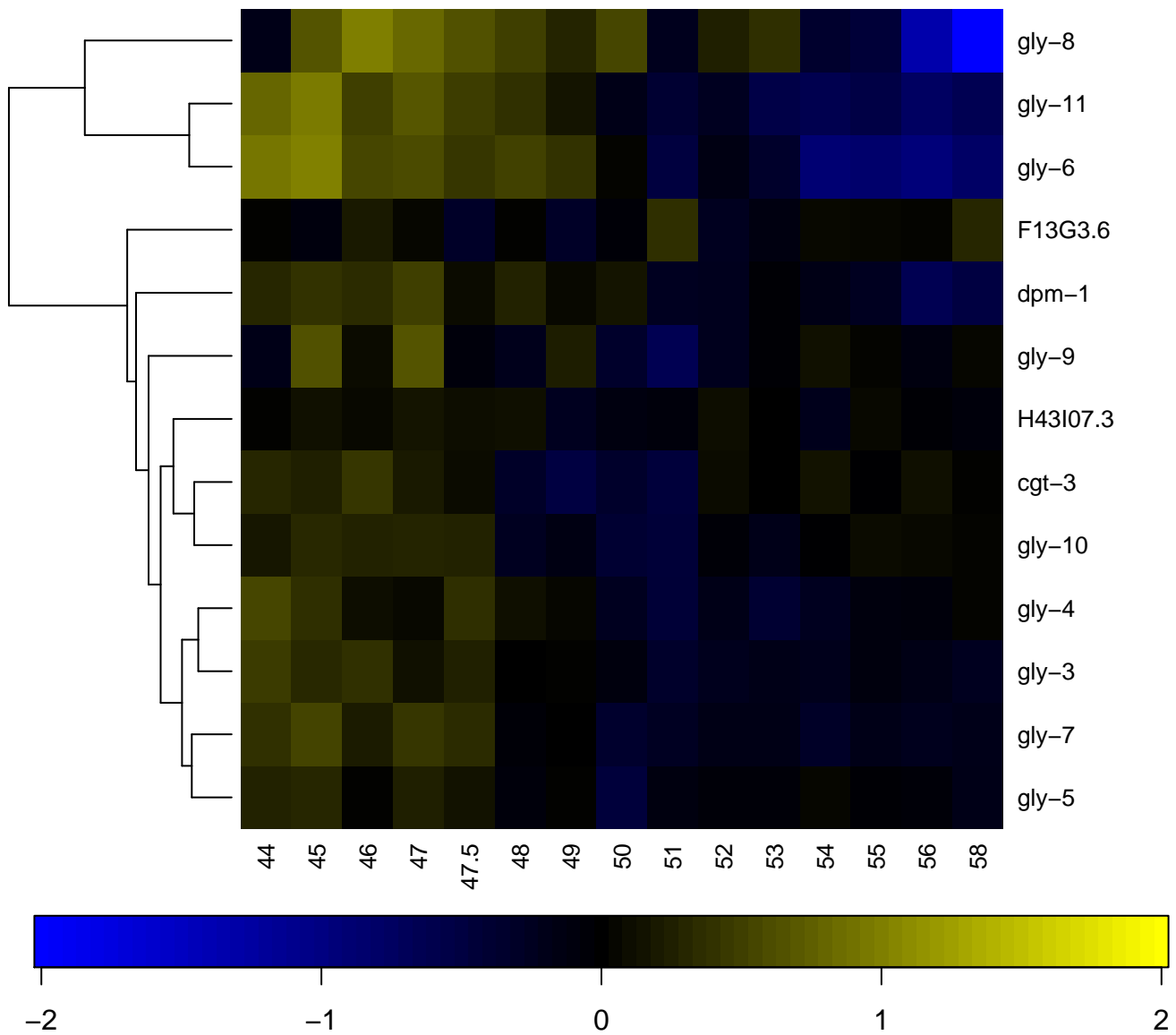
Glycosyl transferase family 8



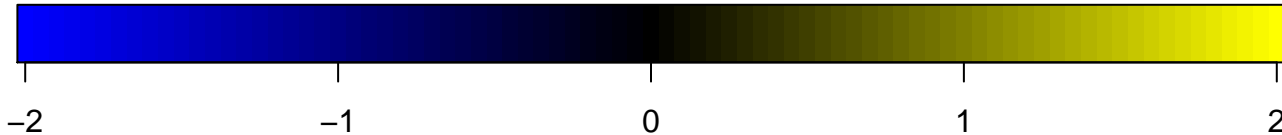
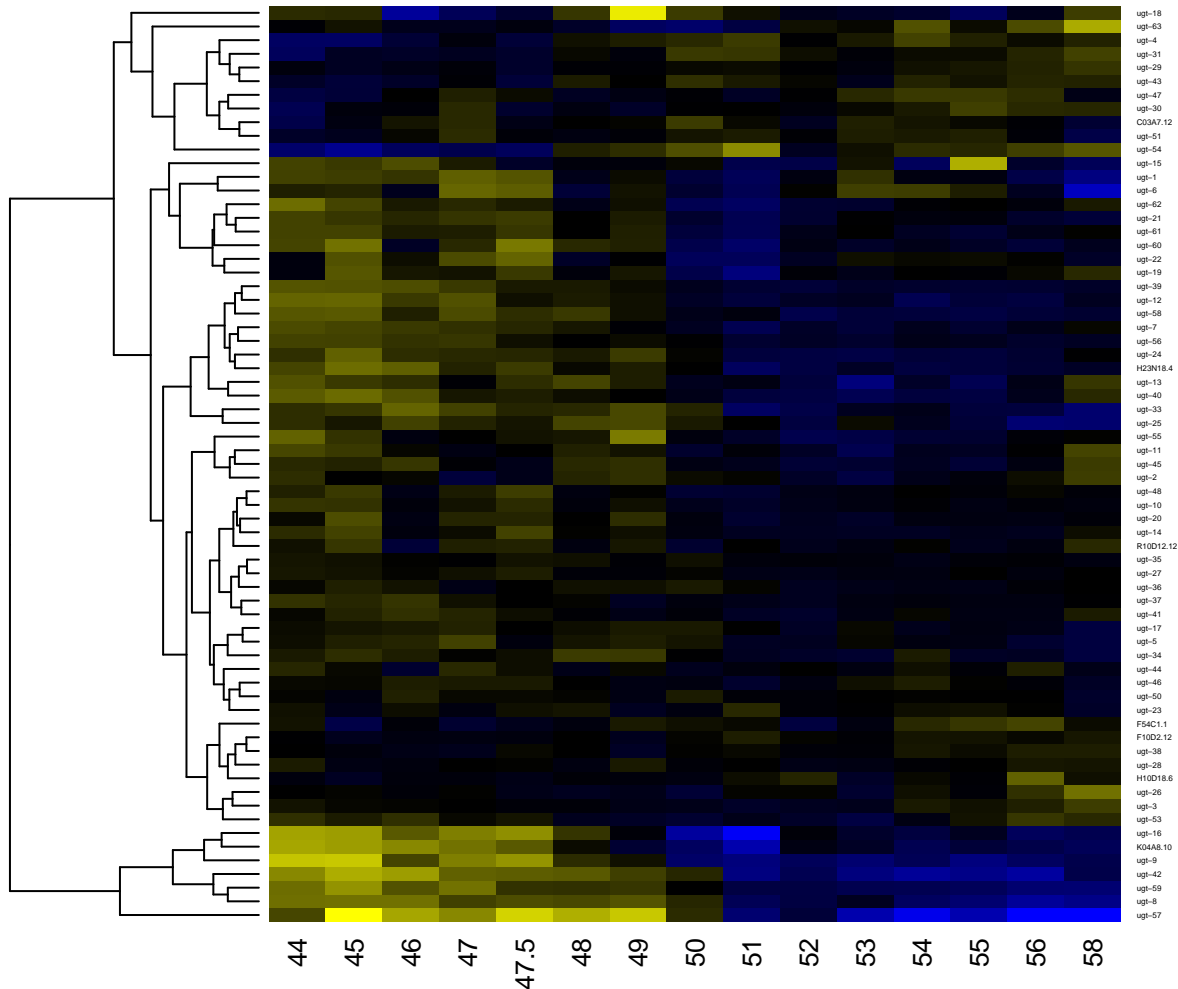
Glycosyl transferase, family 11



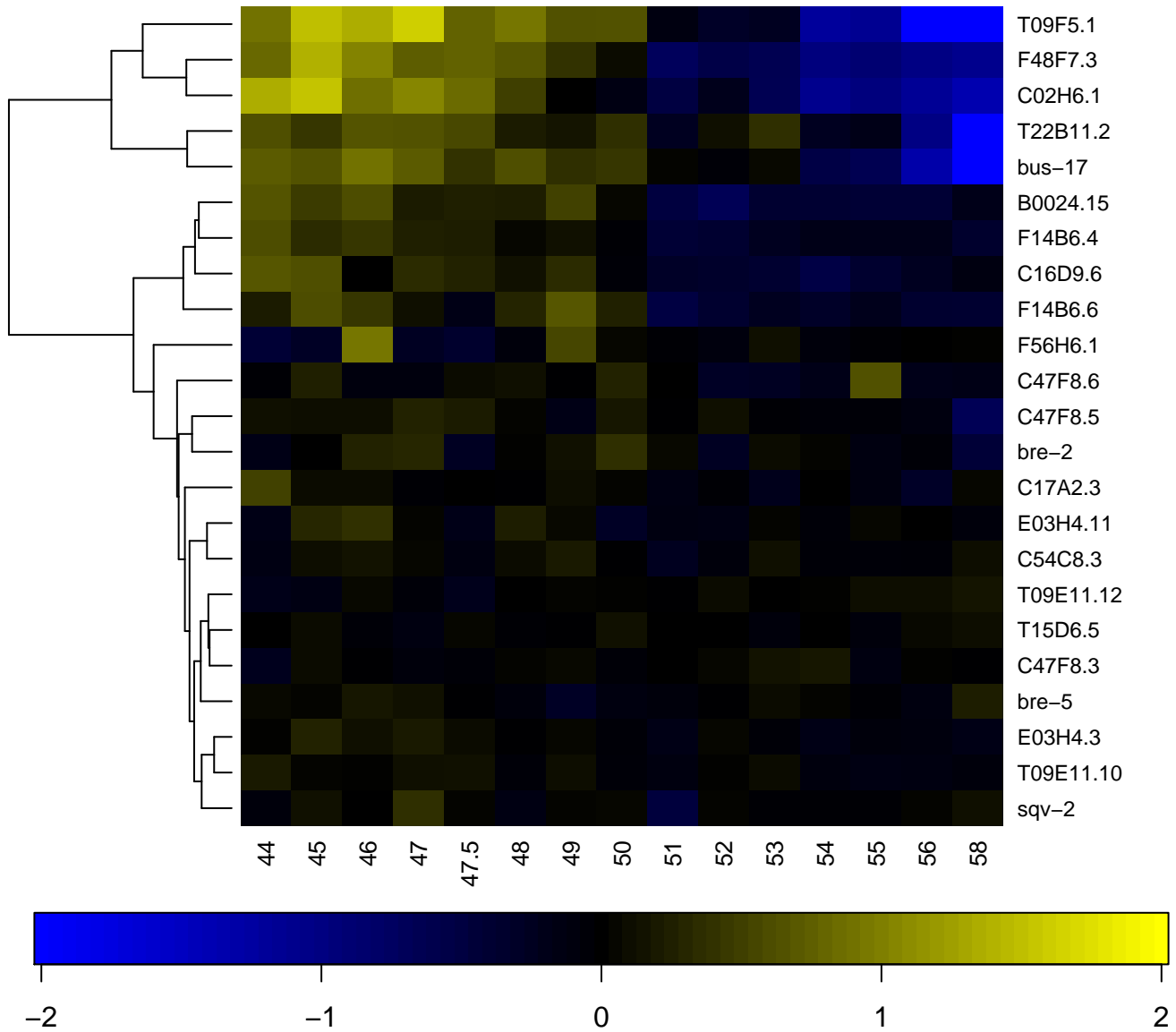
Glycosyl transferase, family 2



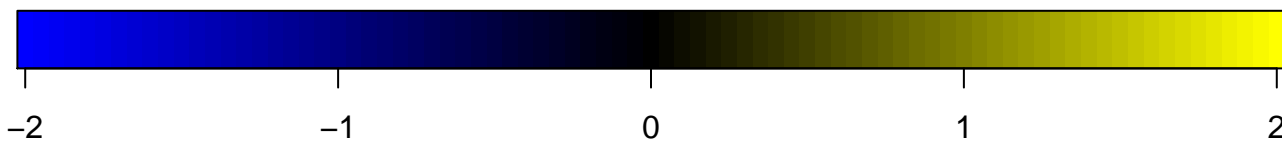
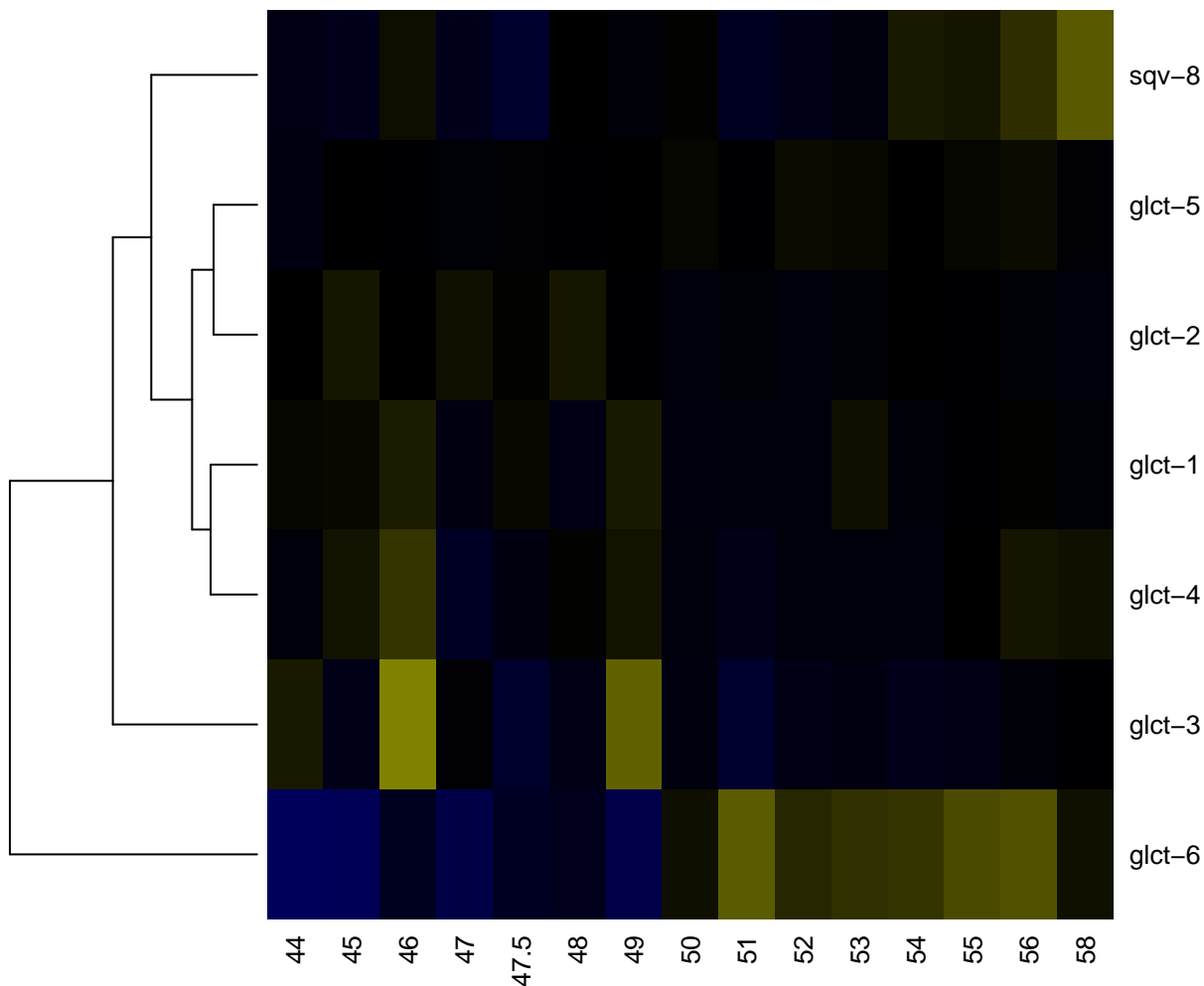
Glycosyl transferase, family 28, C-terminal



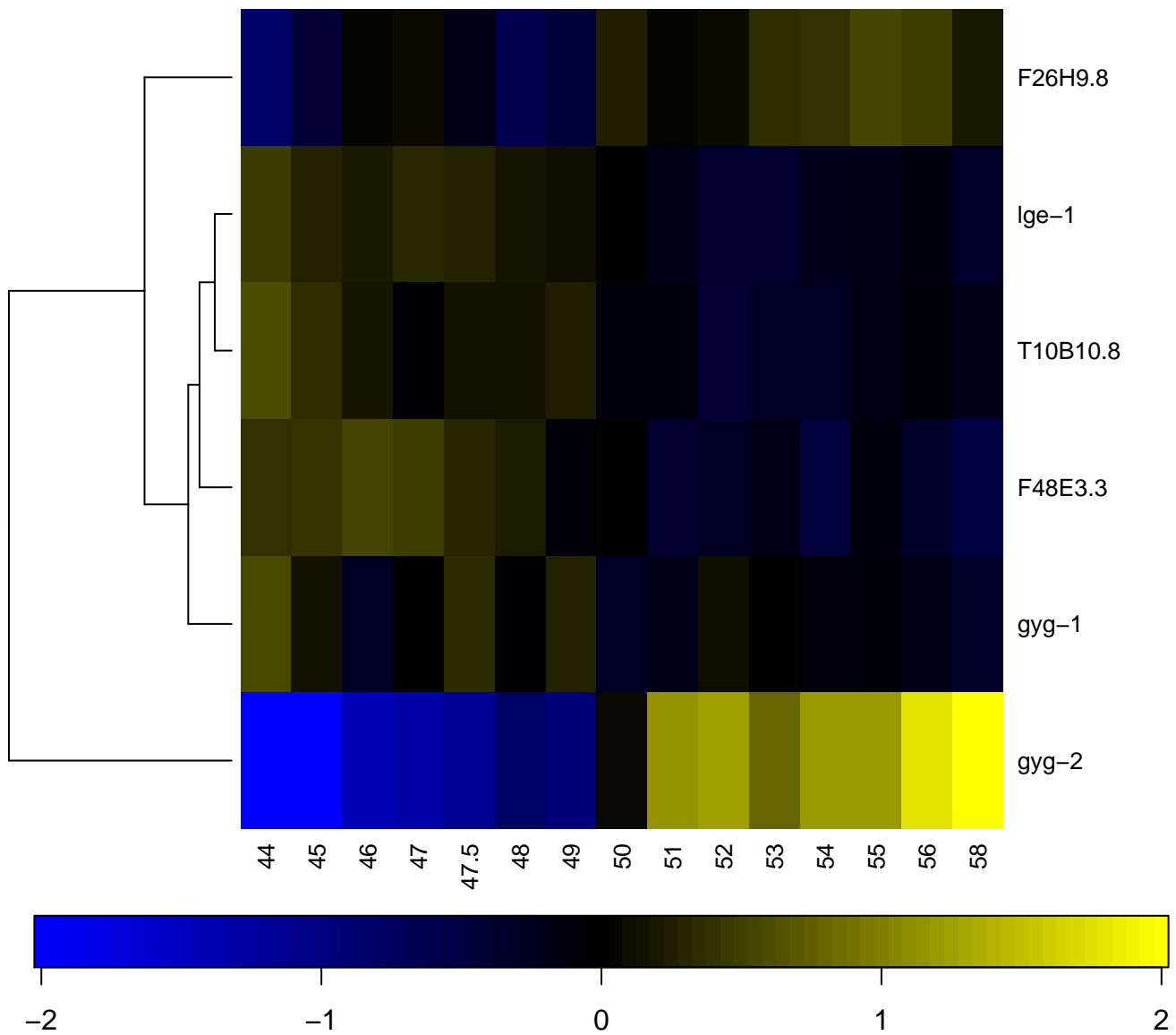
Glycosyl transferase, family 31



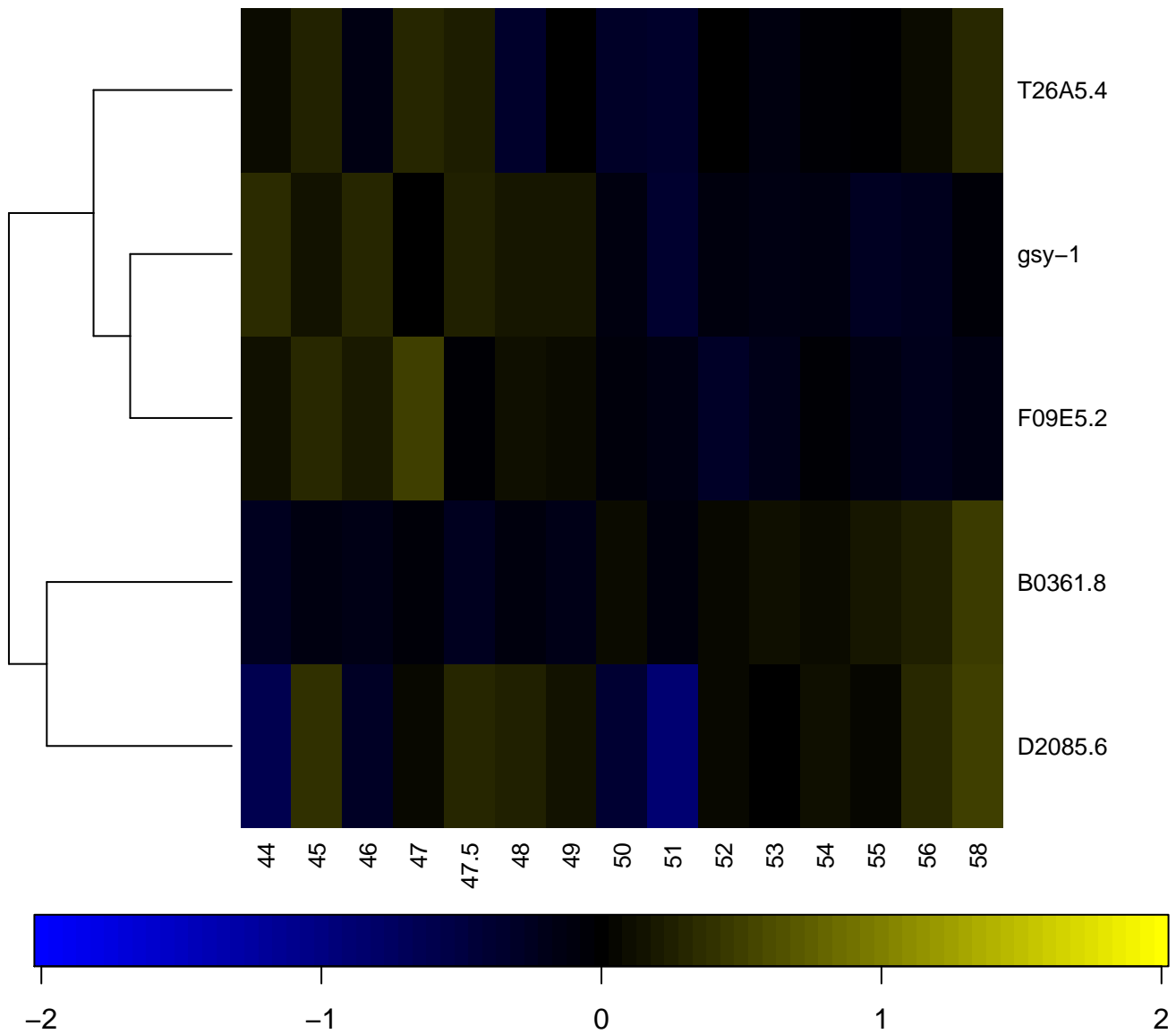
Glycosyl transferase, family 43



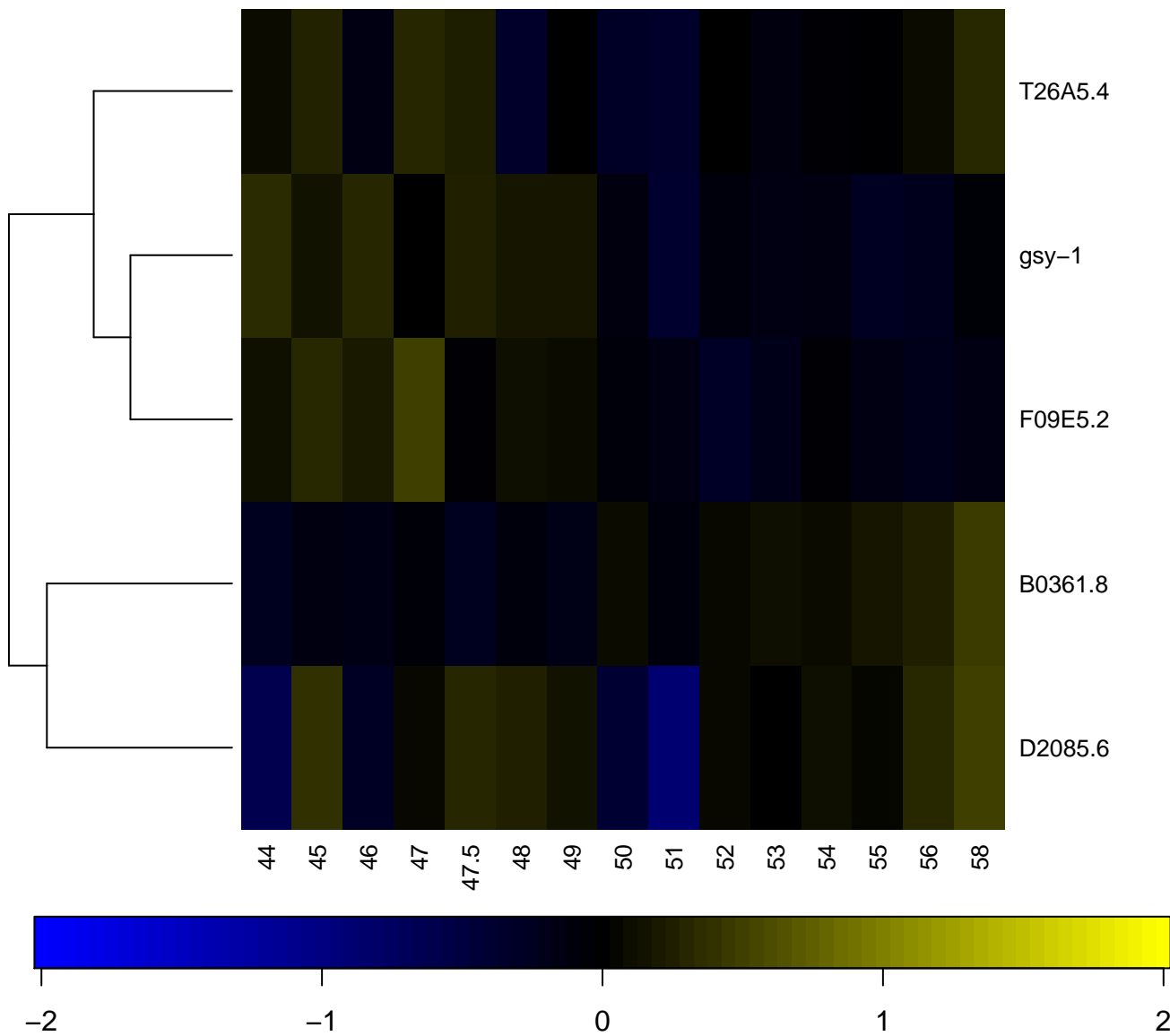
Glycosyl transferase, family 8



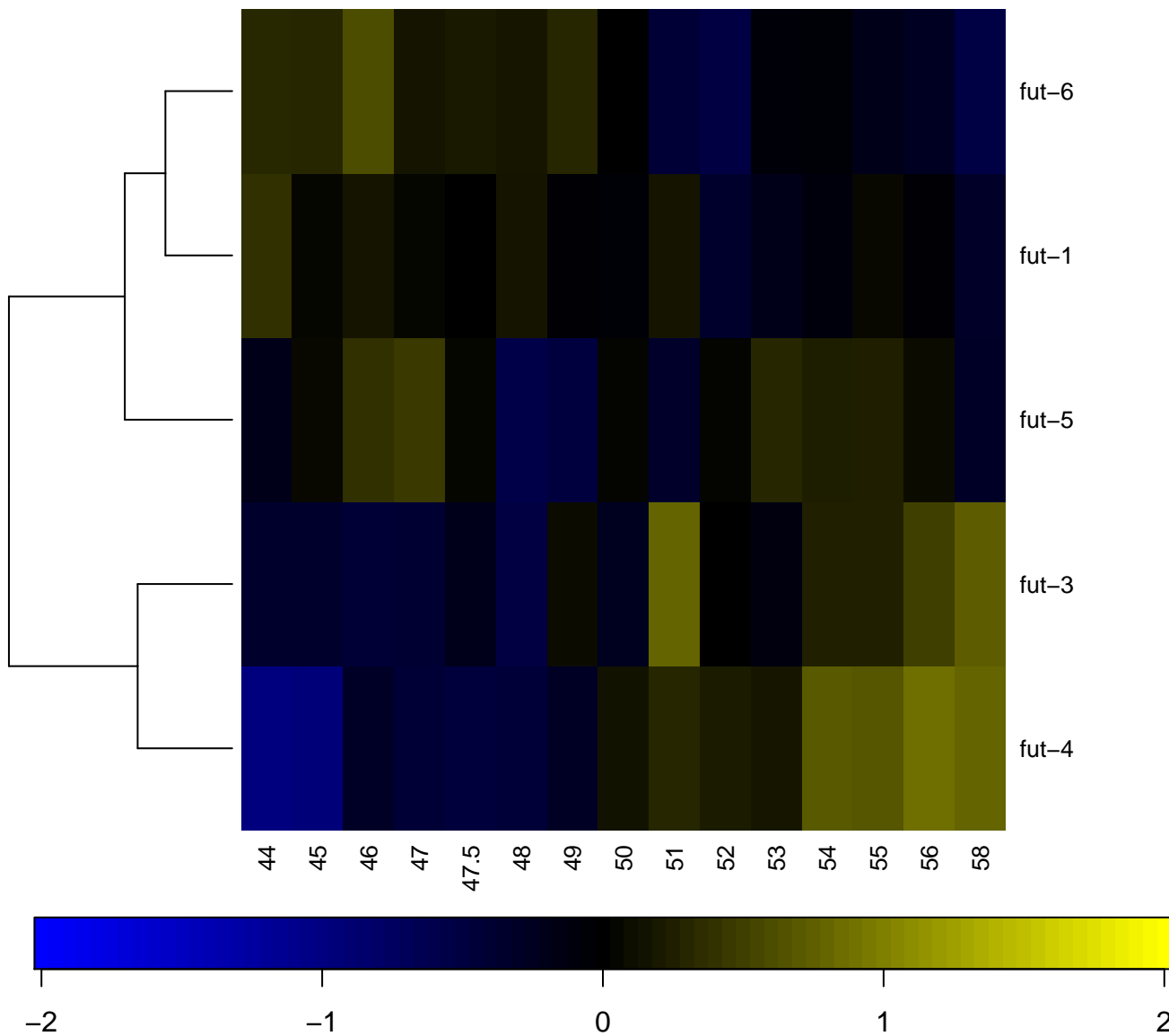
Glycosyl transferase, group 1



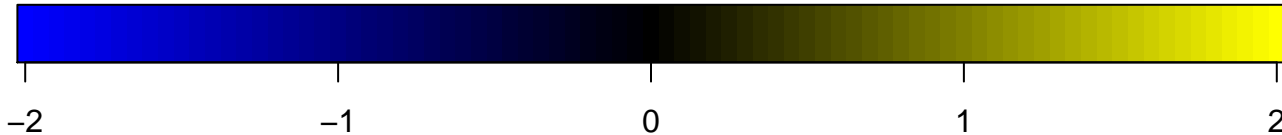
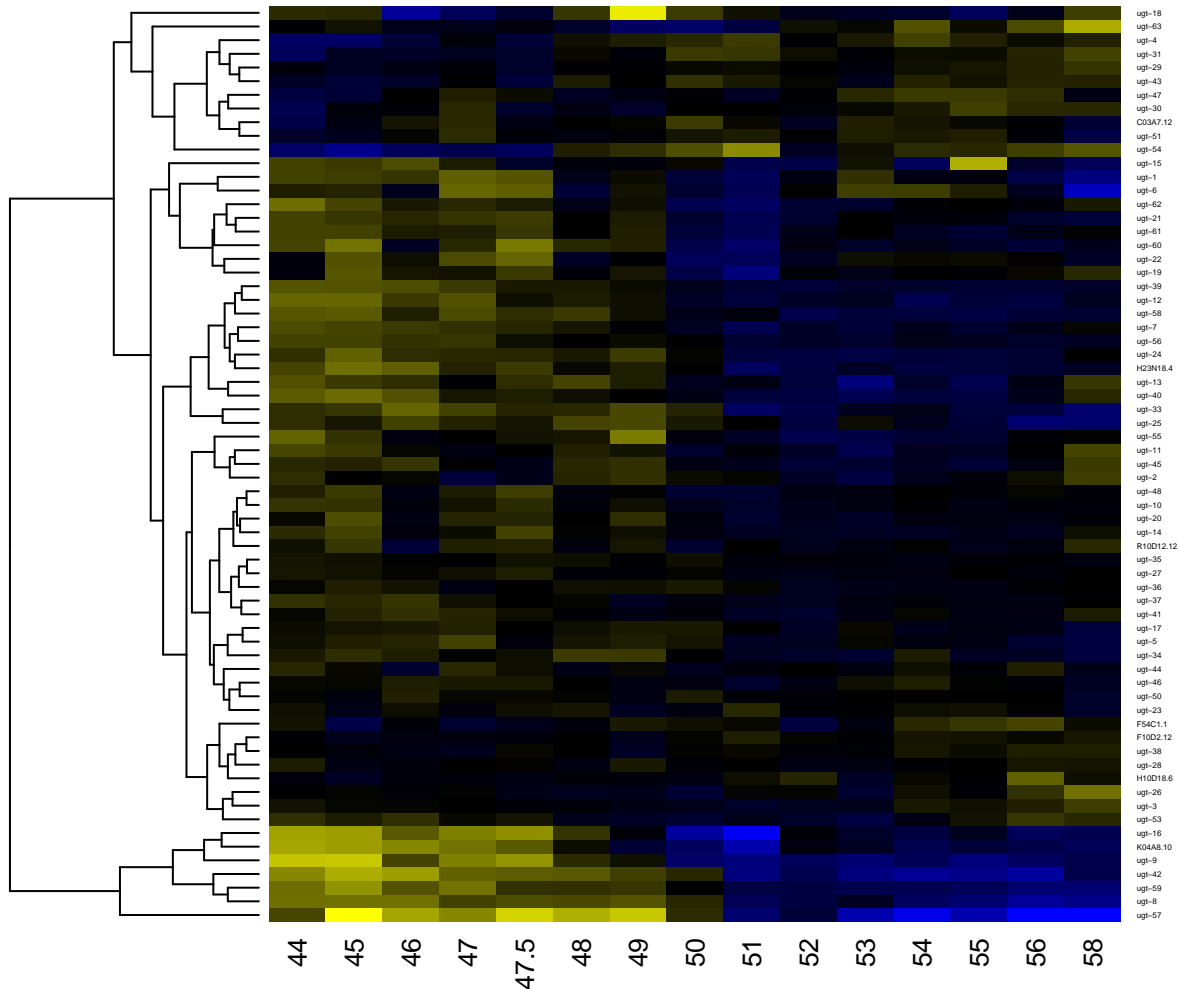
Glycosyl transferases group 1



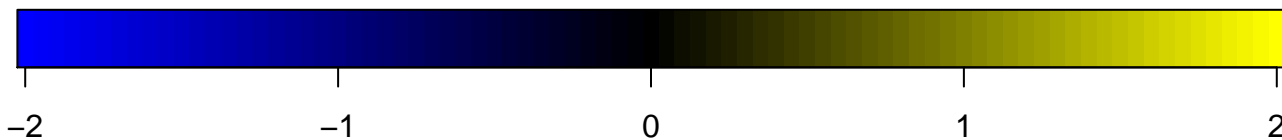
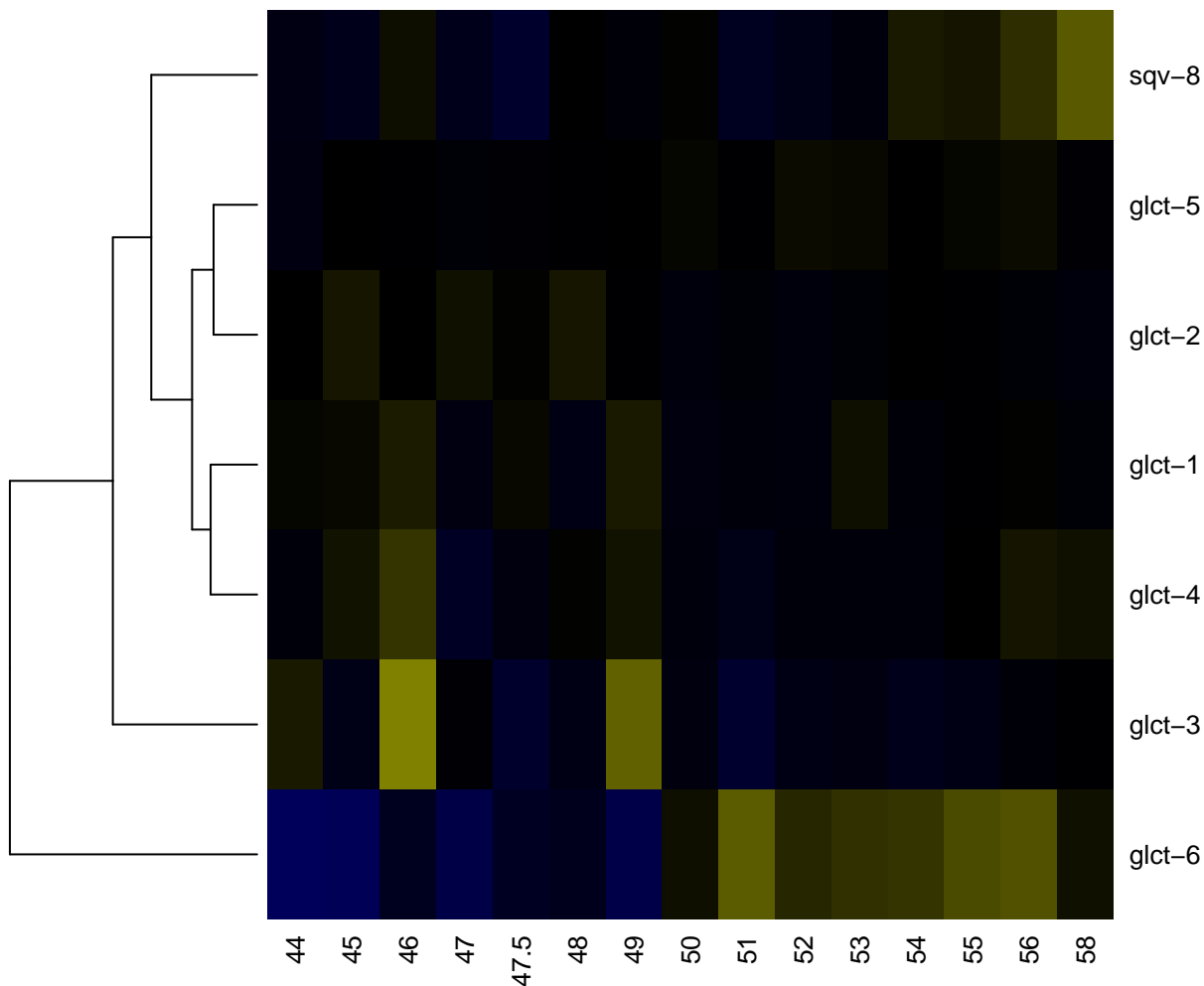
Glycosyltransferase family 10 (fucosyltransferase)



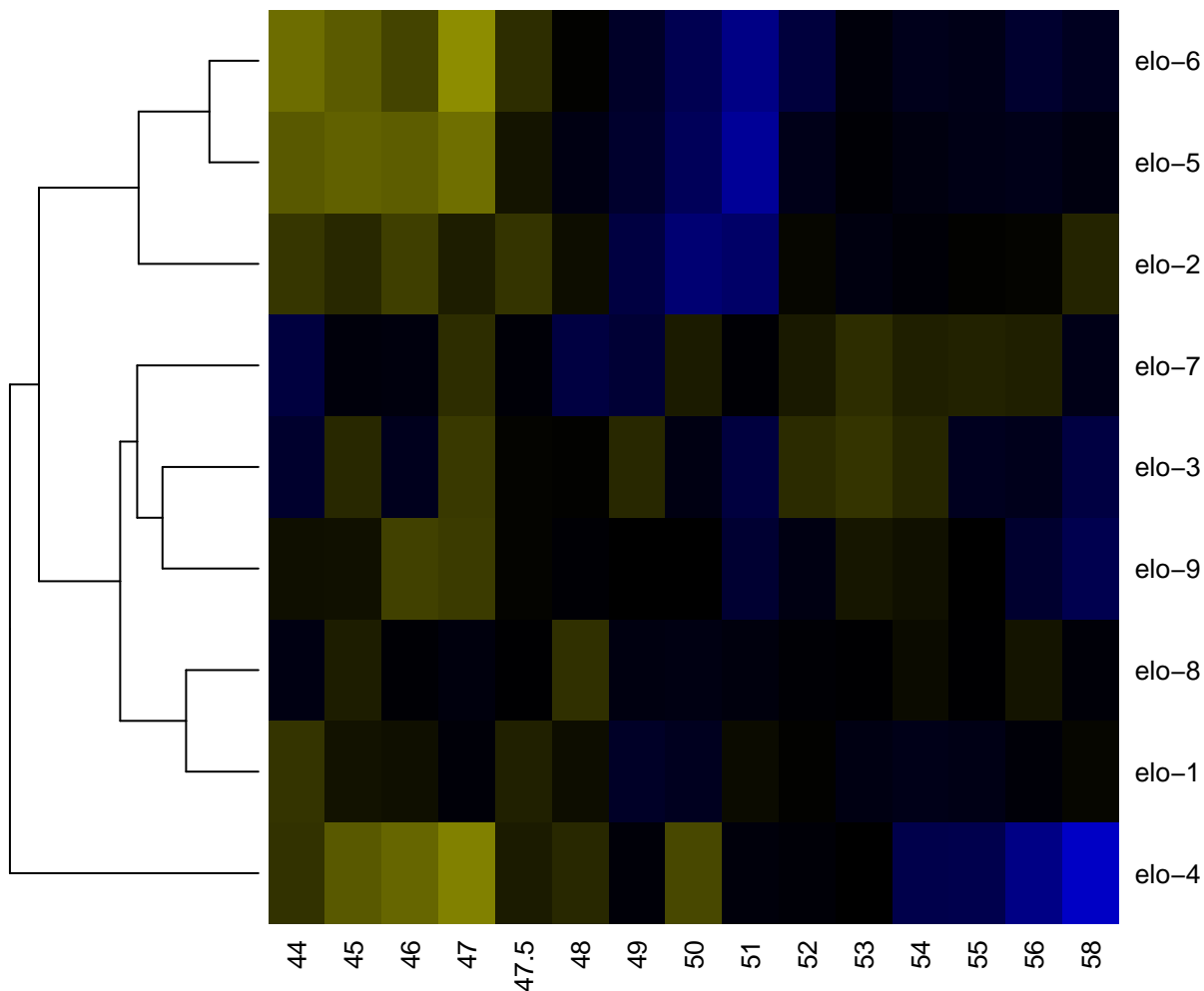
Glycosyltransferase family 28 C-terminal domain



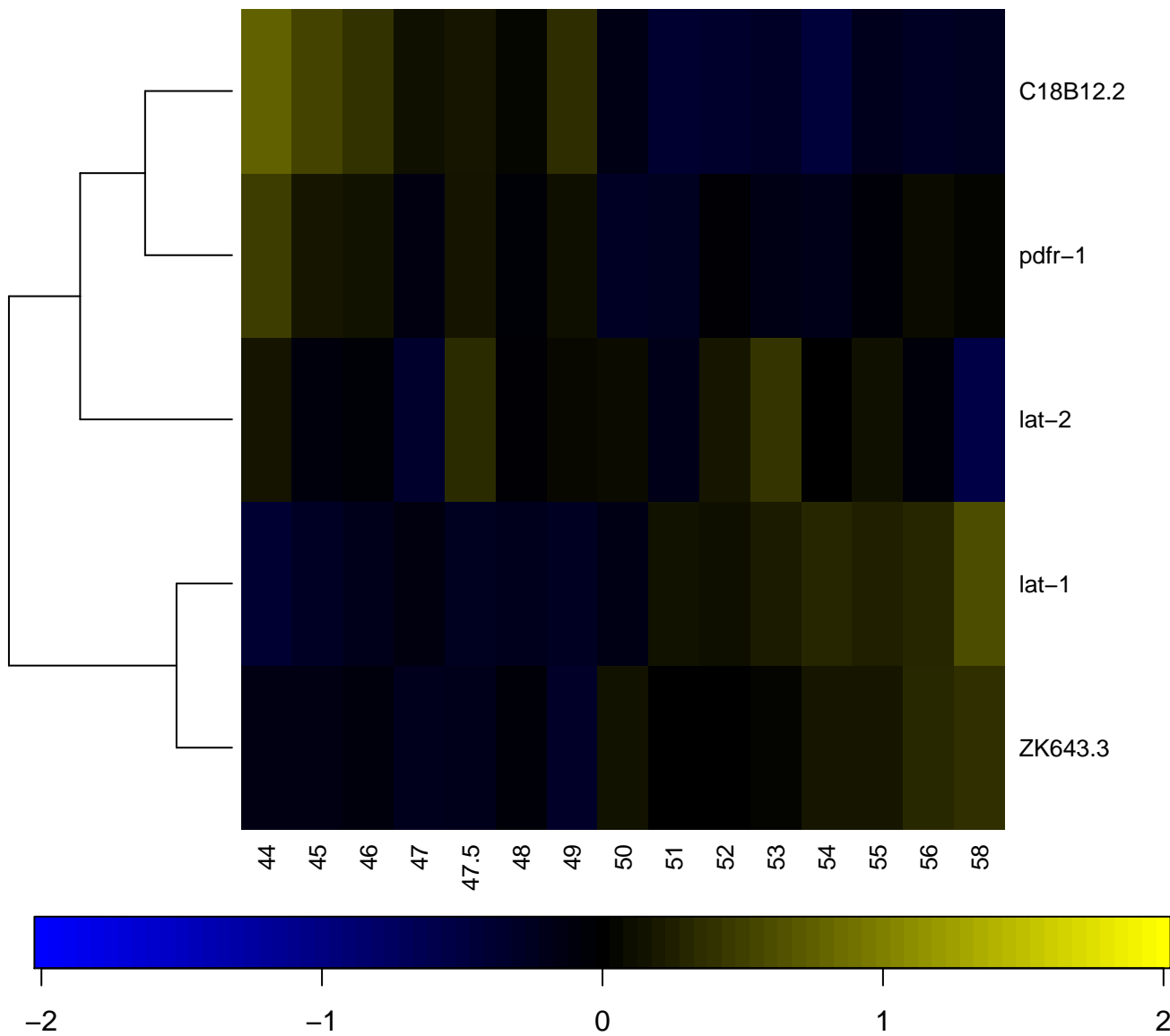
Glycosyltransferase family 43



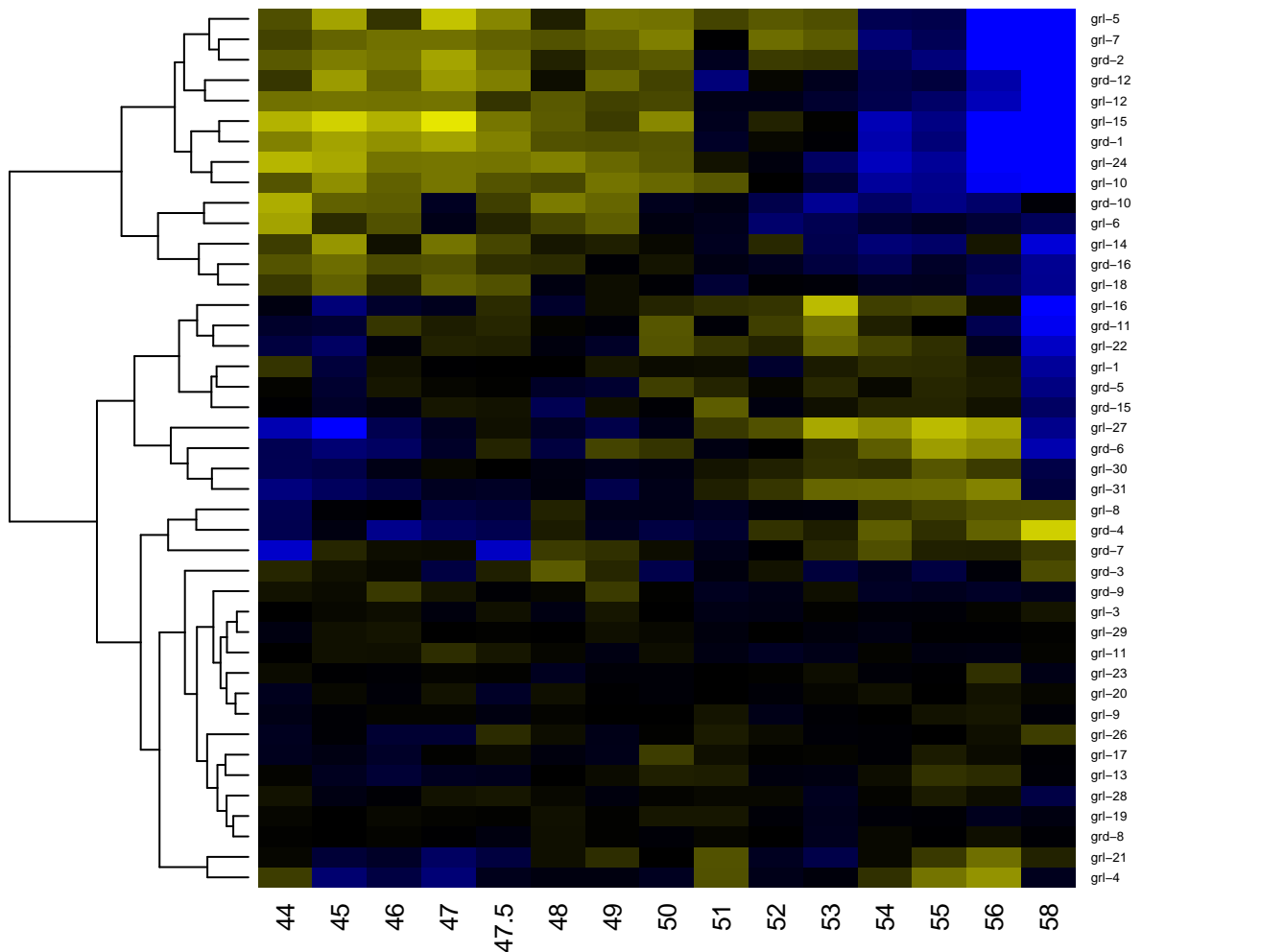
GNS1/SUR4 family



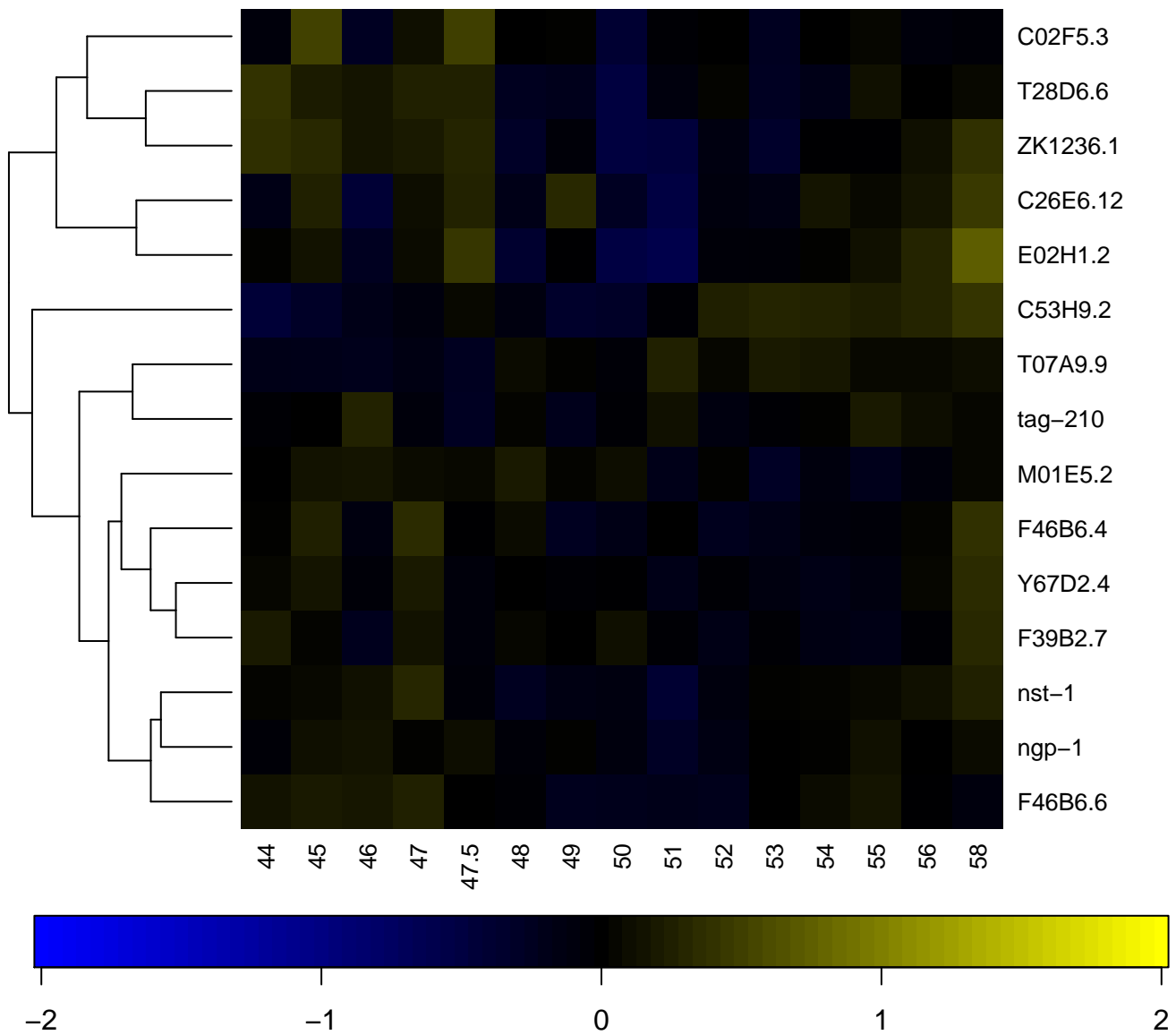
GPCR, family 2, extracellular hormone receptor domain



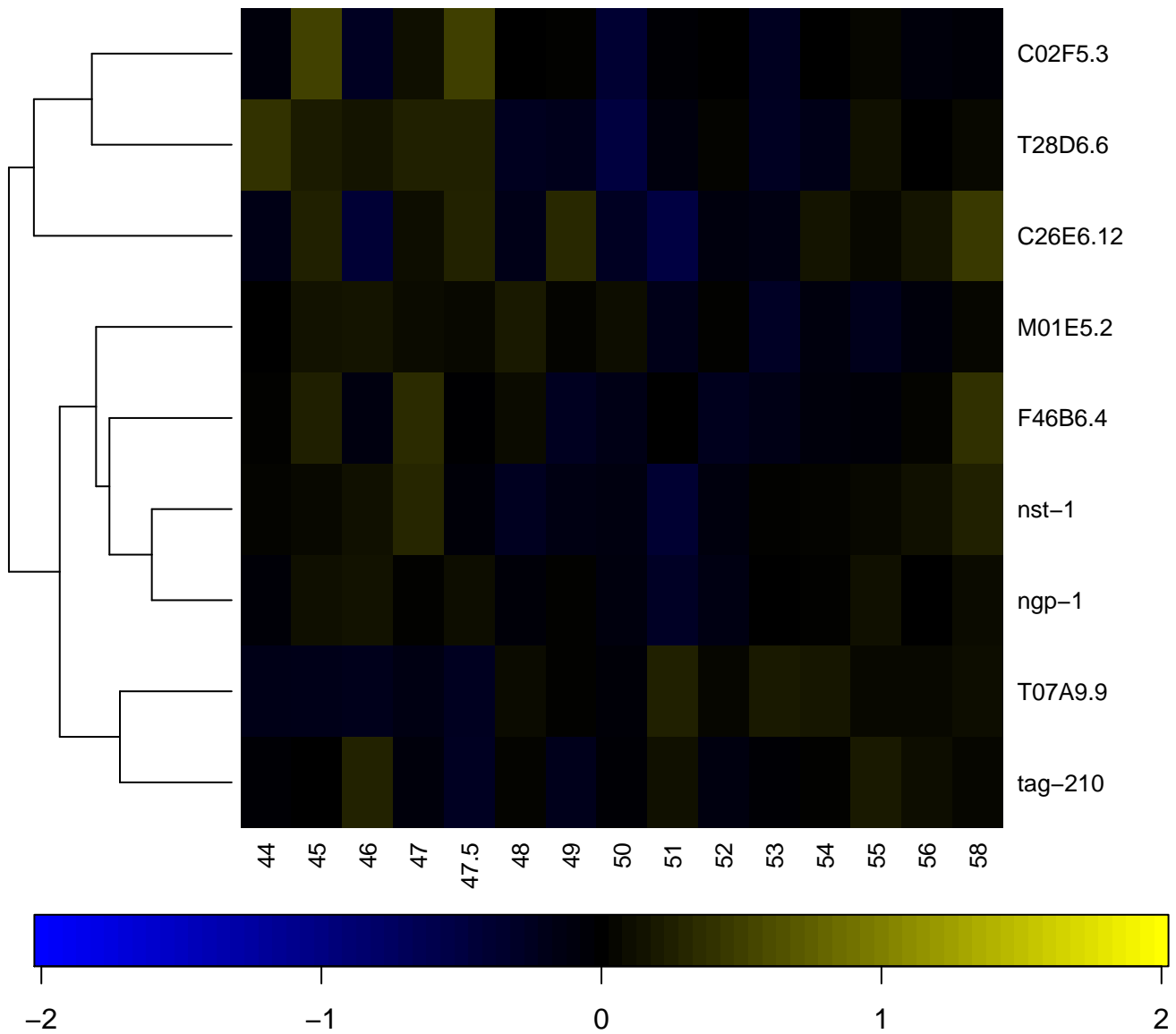
Ground-like domain



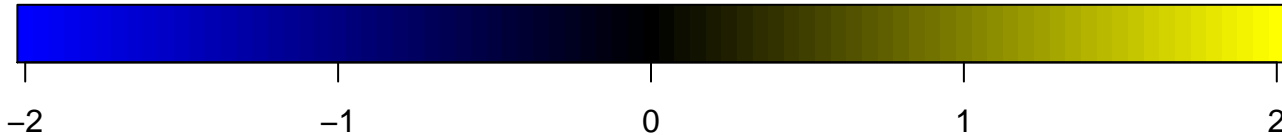
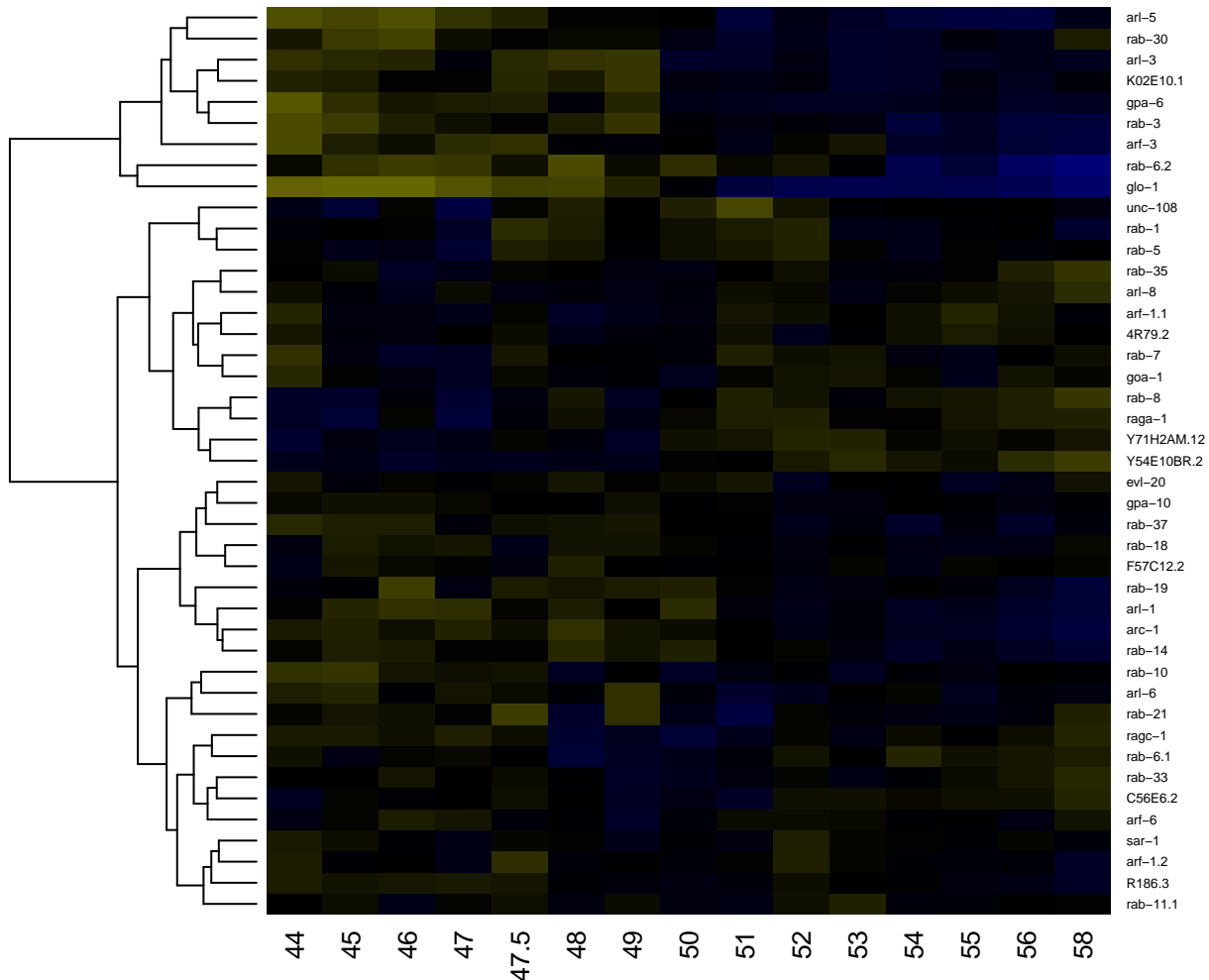
GTP-binding protein, HSR1-related



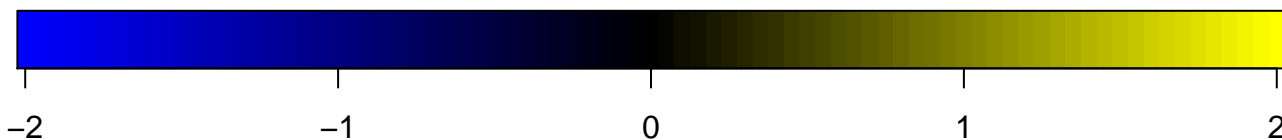
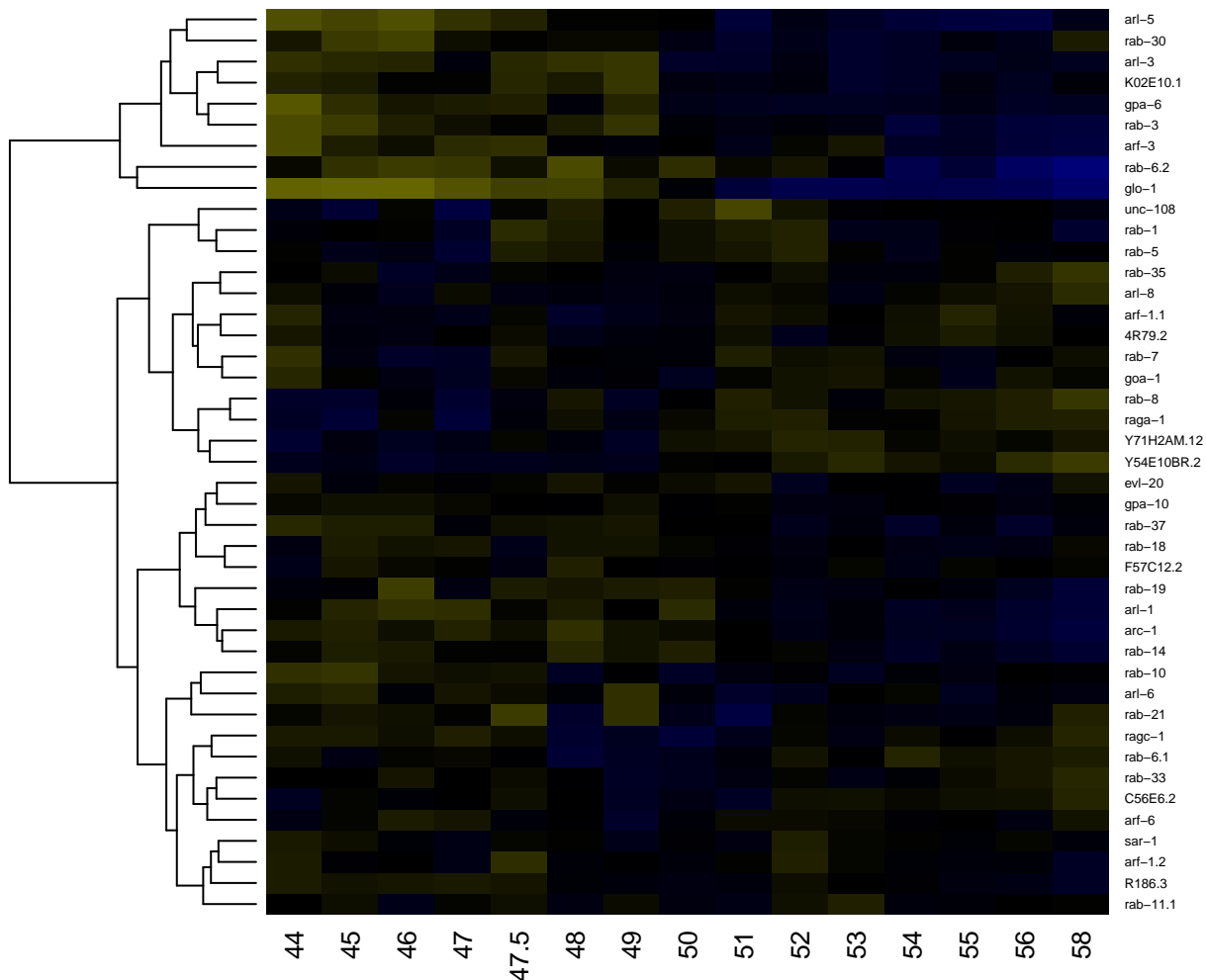
GTP1/OBG



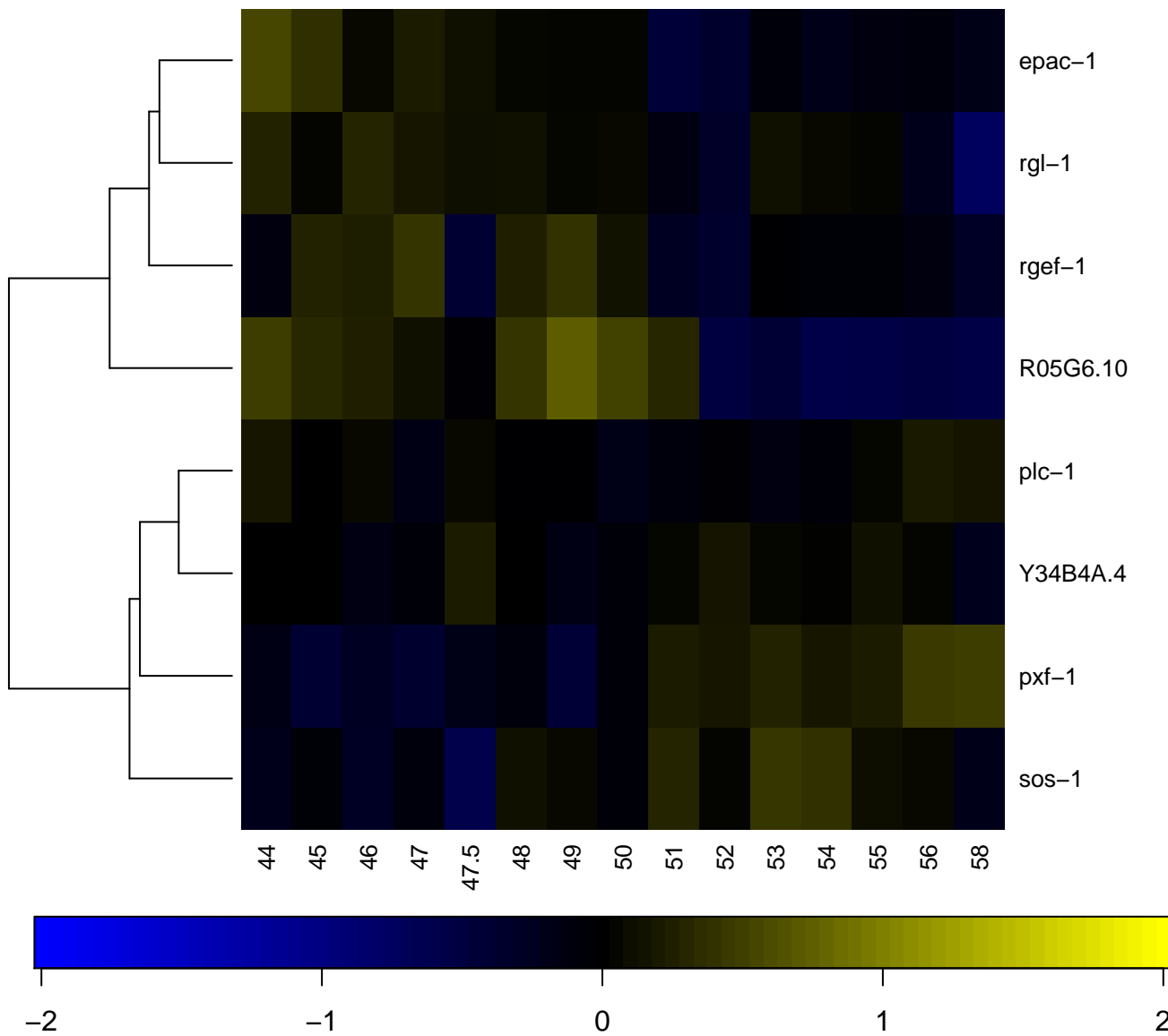
Gtr1/RagA G protein



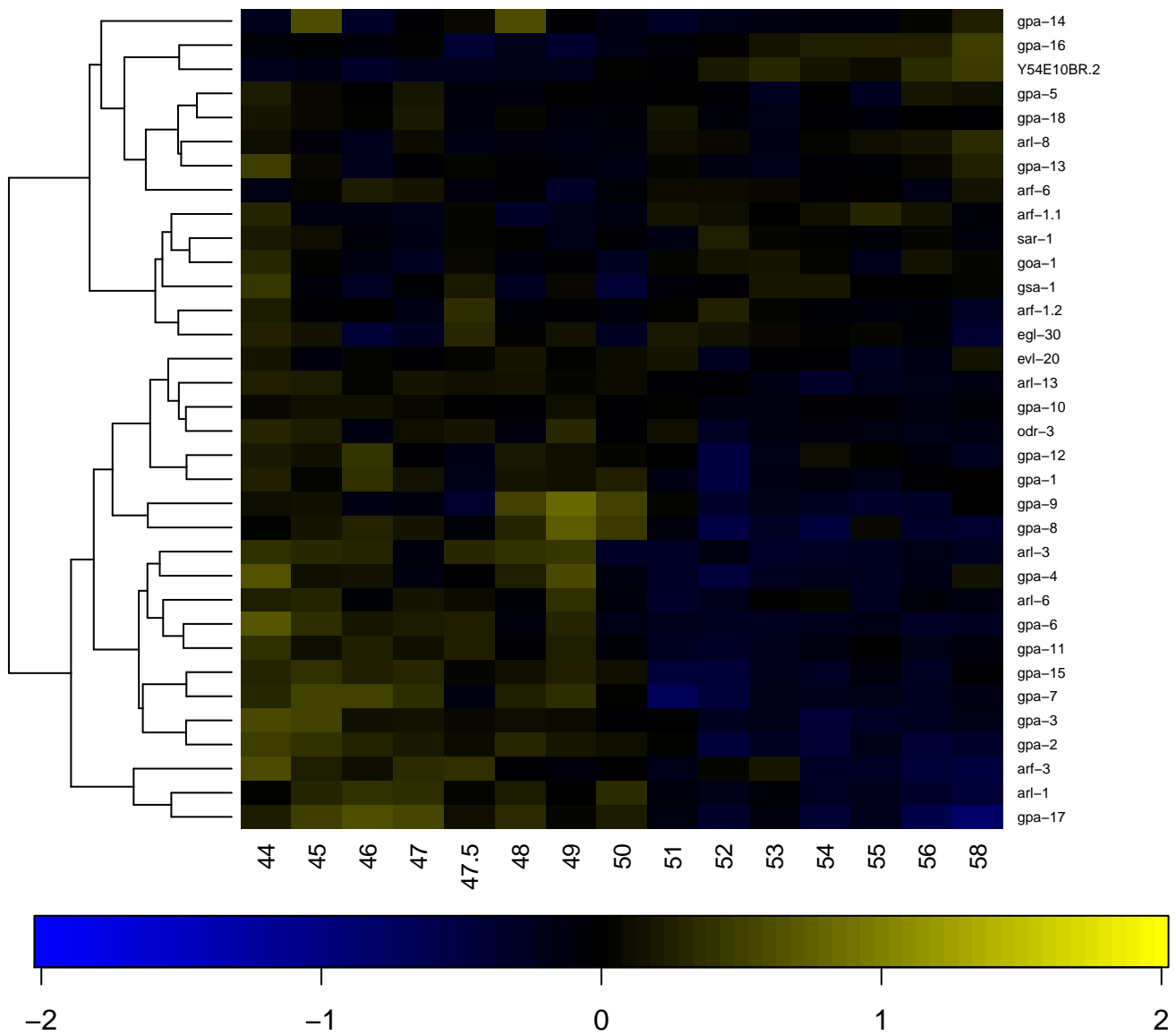
Gtr1/RagA G protein conserved region



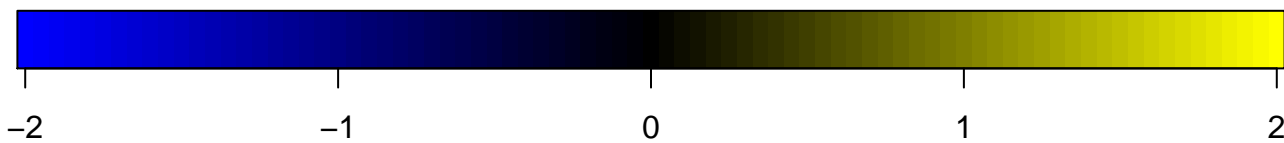
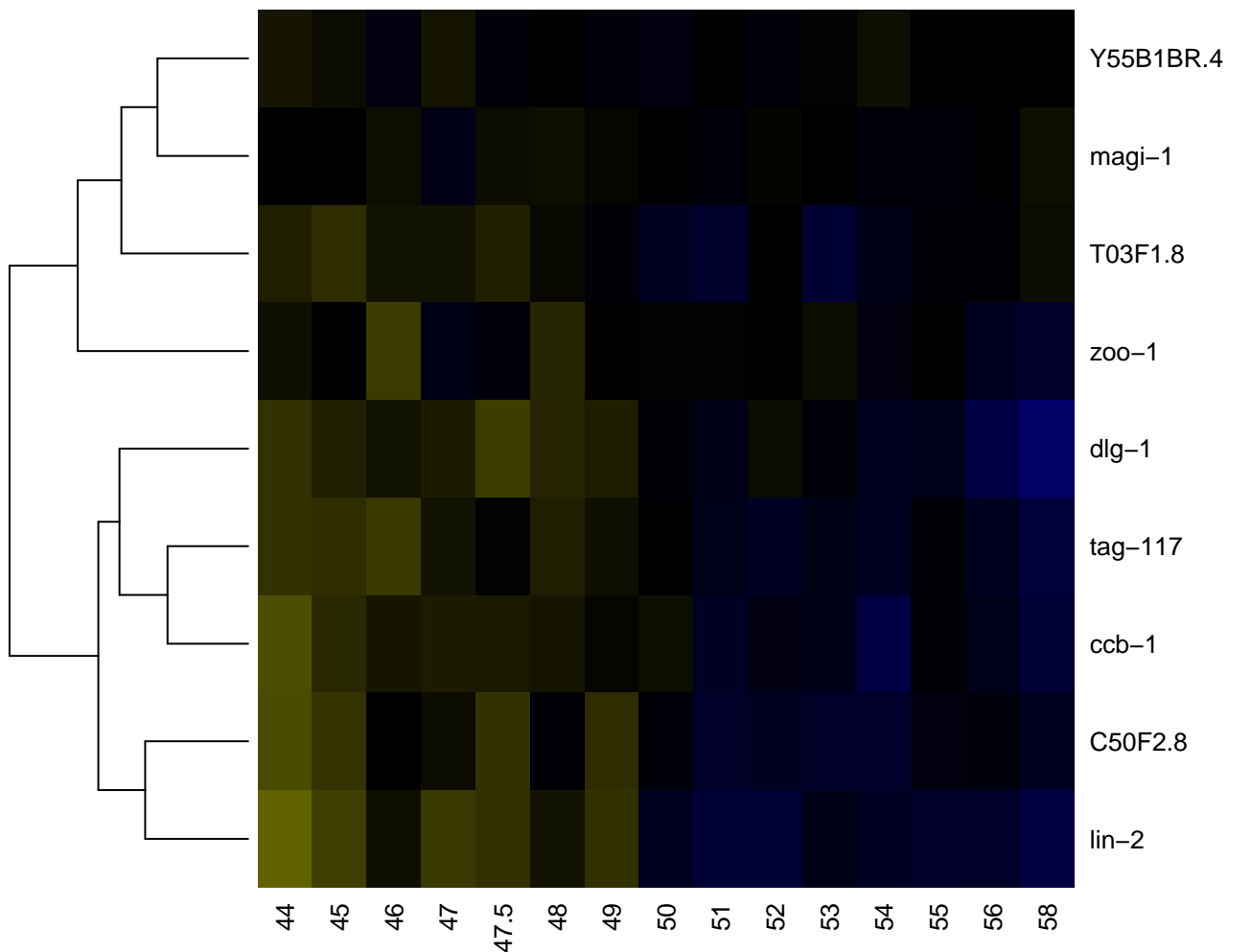
Guanine–nucleotide dissociation stimulator CDC25



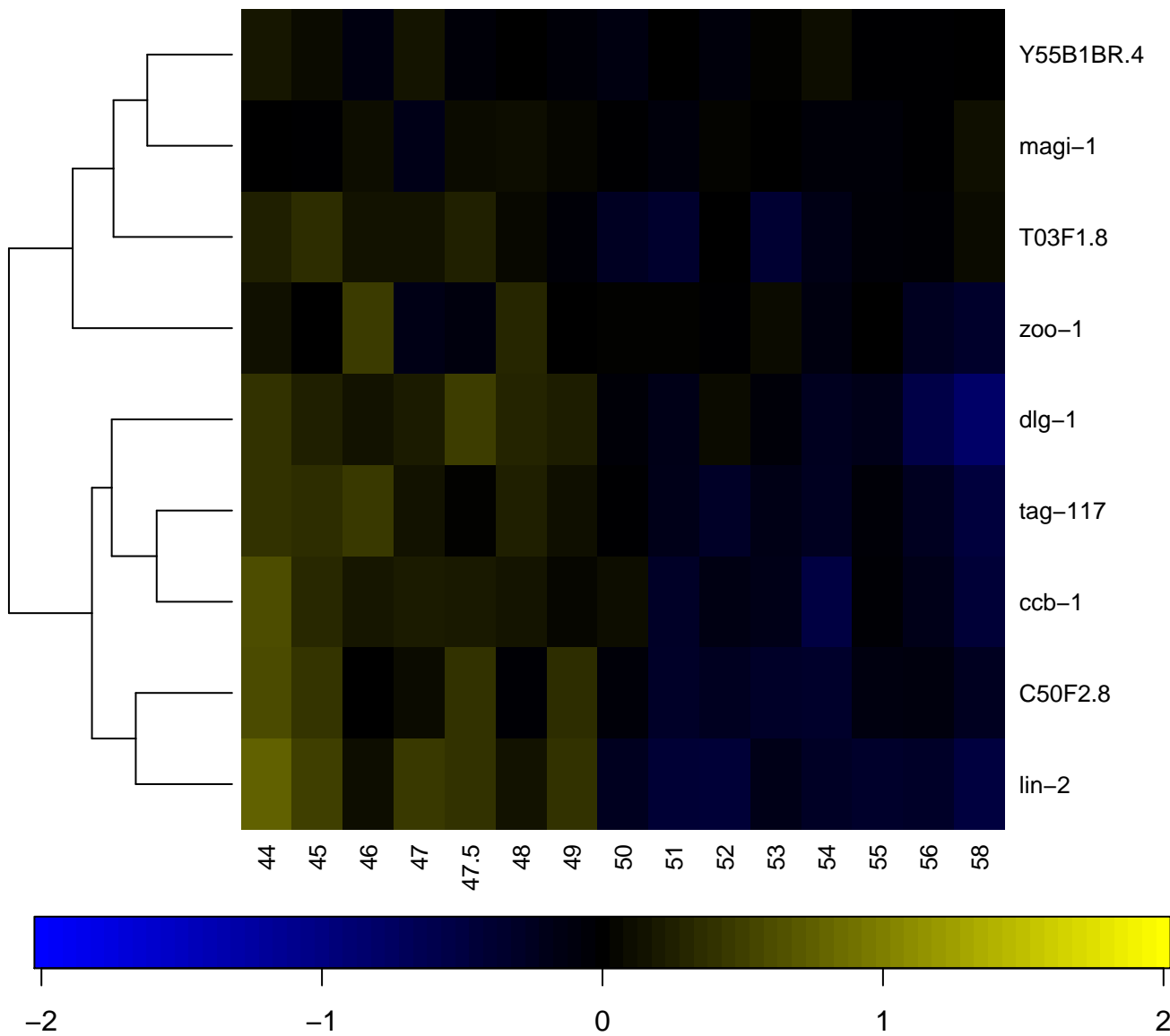
Guanine nucleotide binding protein (G-protein), alpha subu



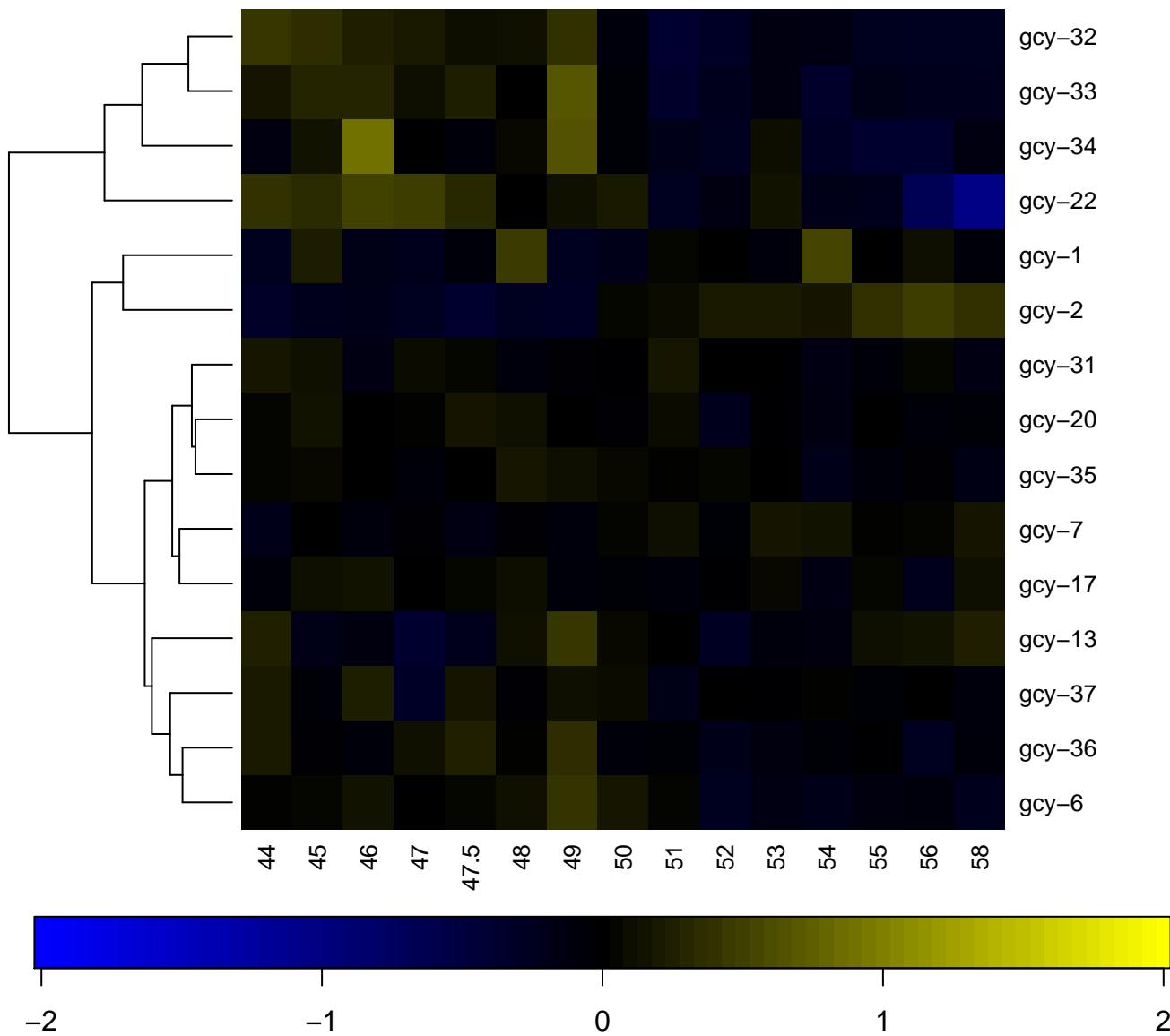
Guanylate kinase



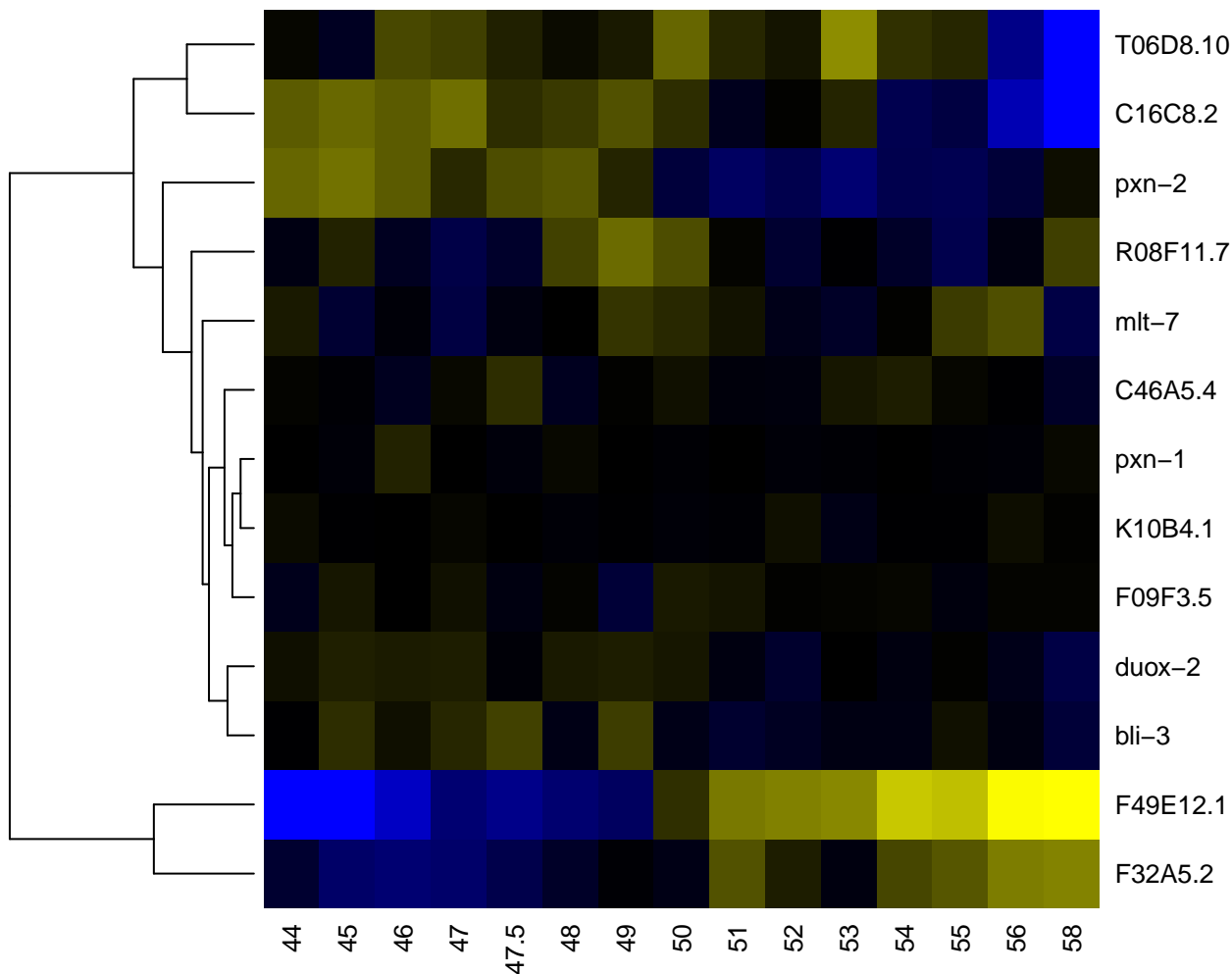
Guanylate kinase/L-type calcium channel



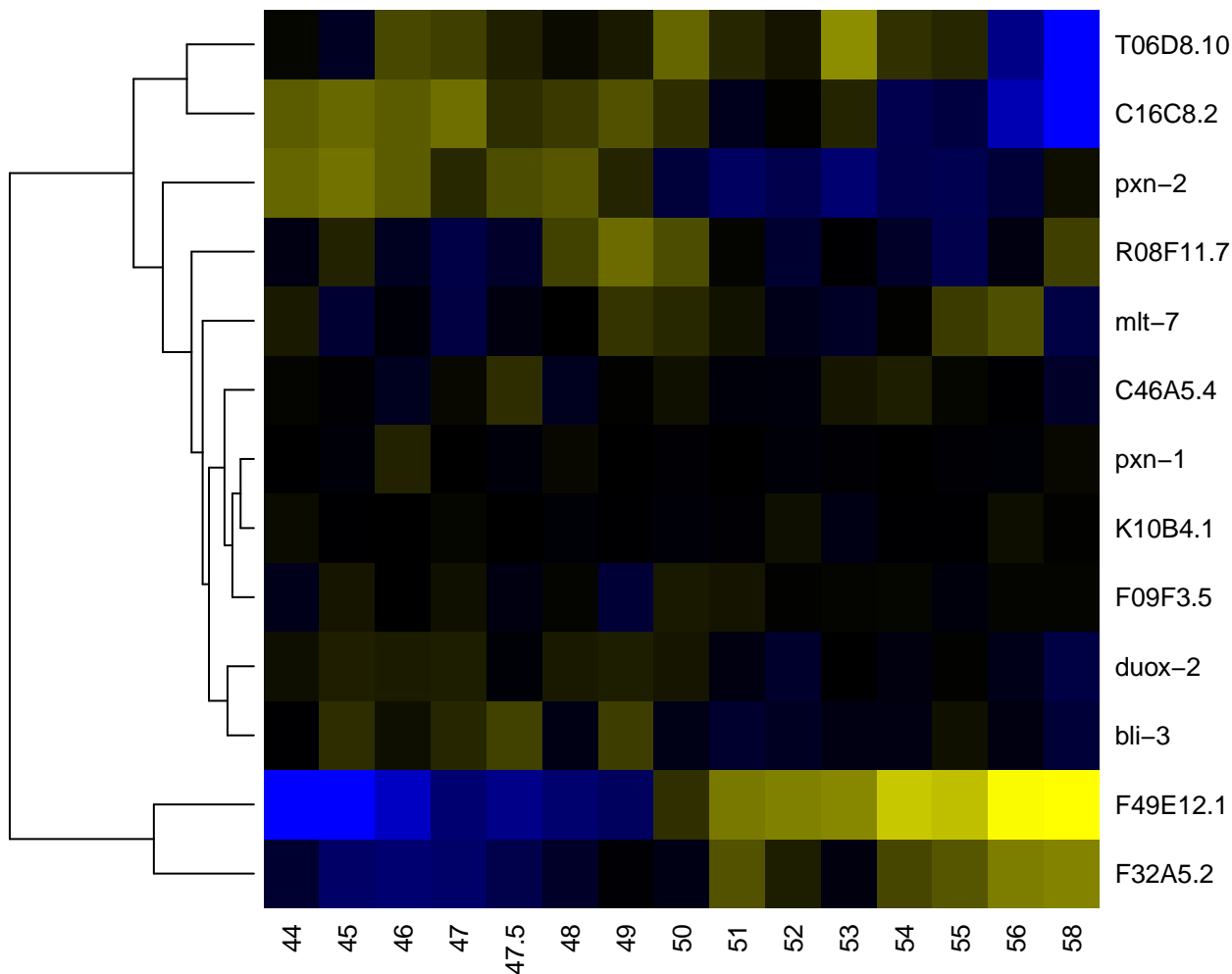
Haem NO binding associated



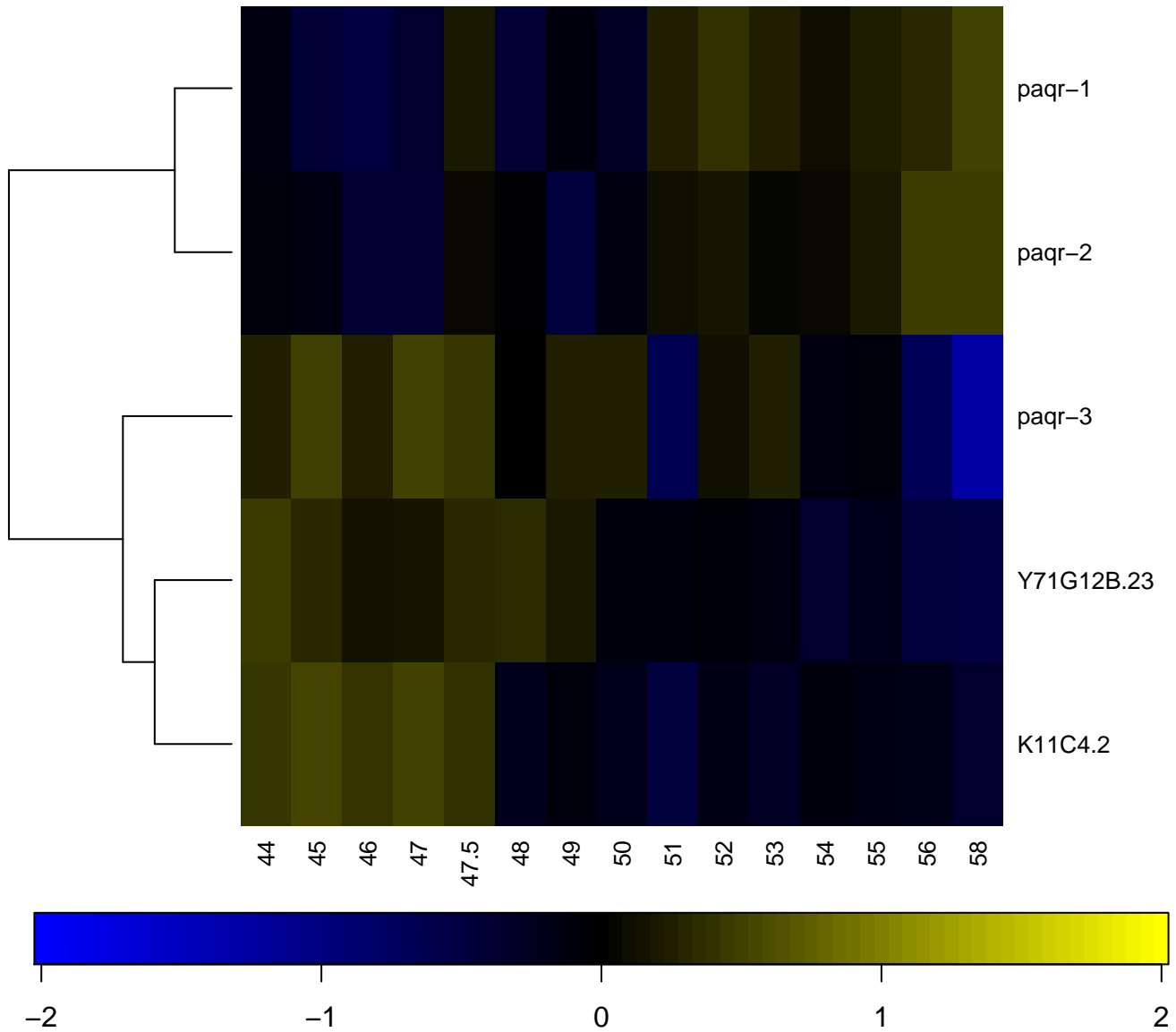
Haem peroxidase, animal



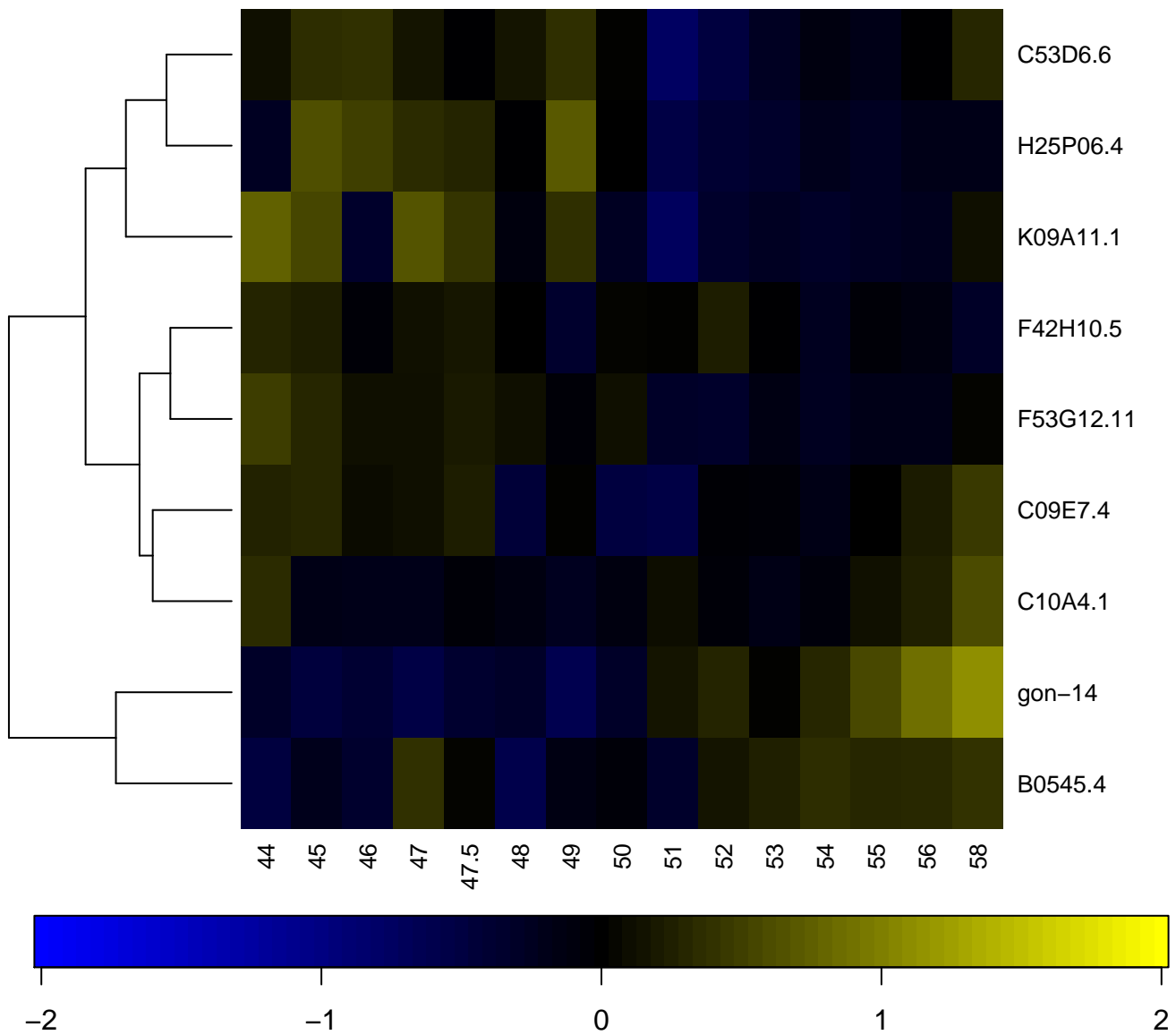
Haem peroxidase, animal, subgroup



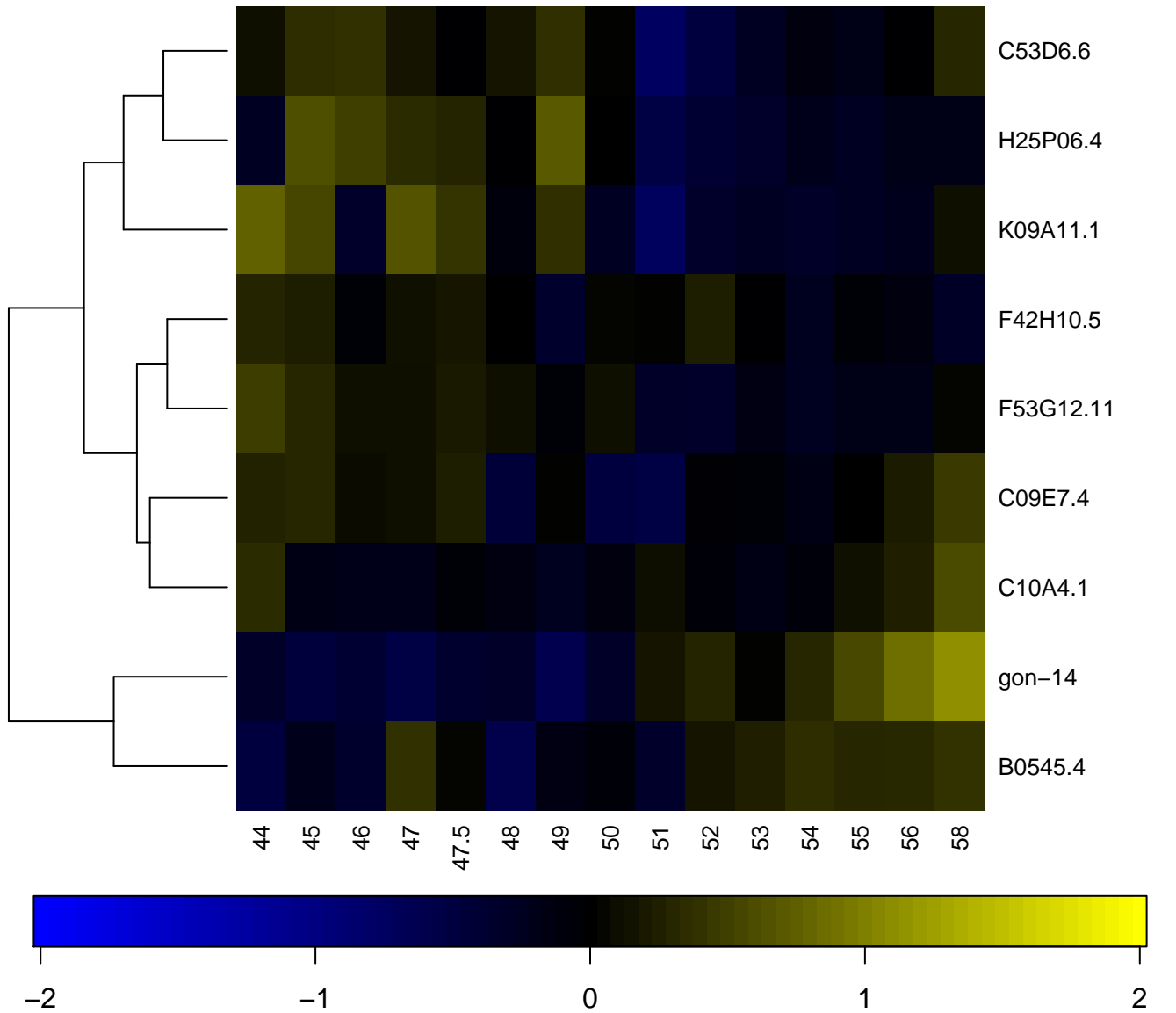
Haemolysin-III related



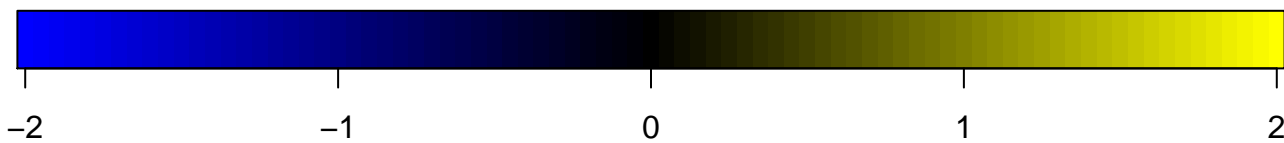
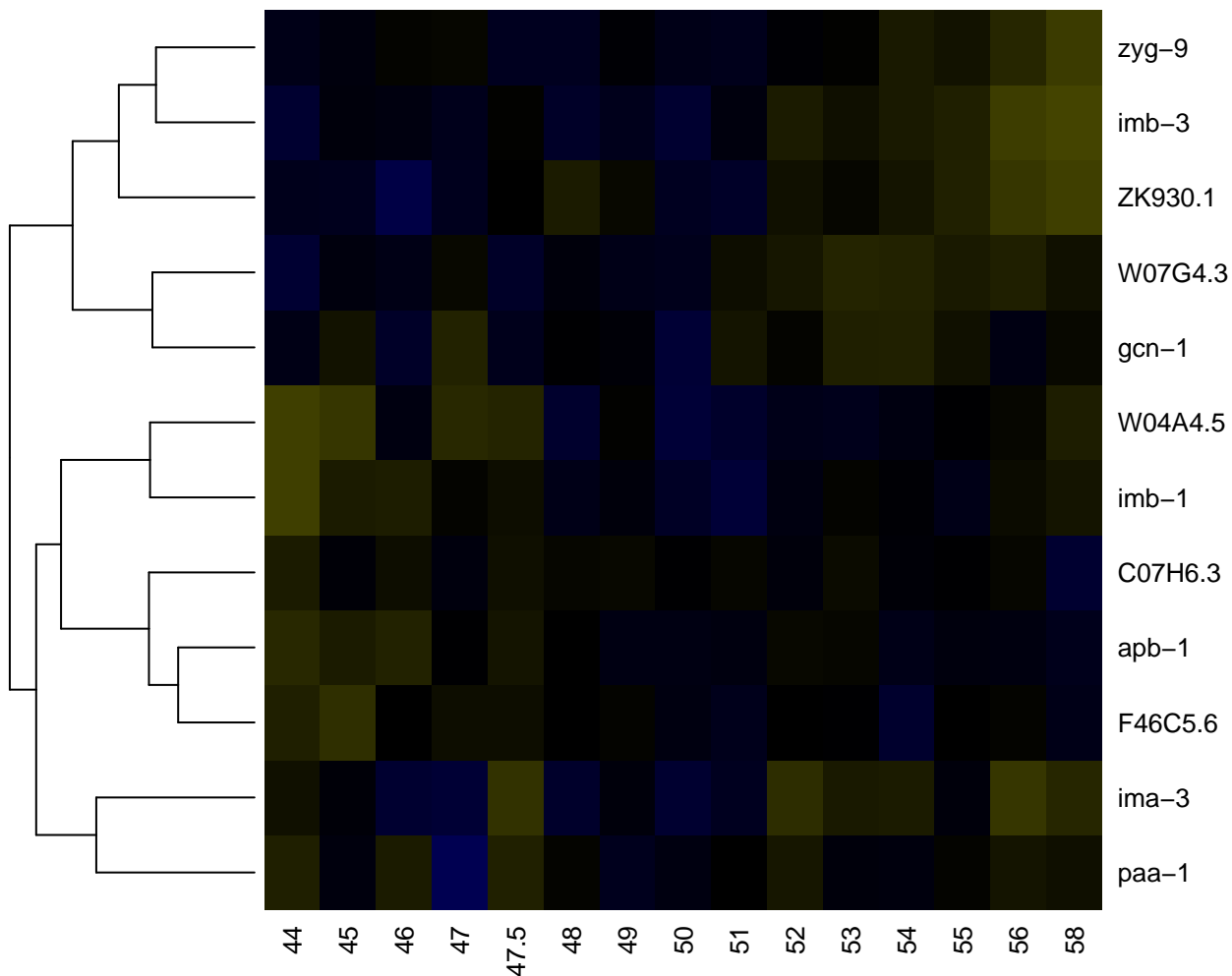
HAT dimerisation



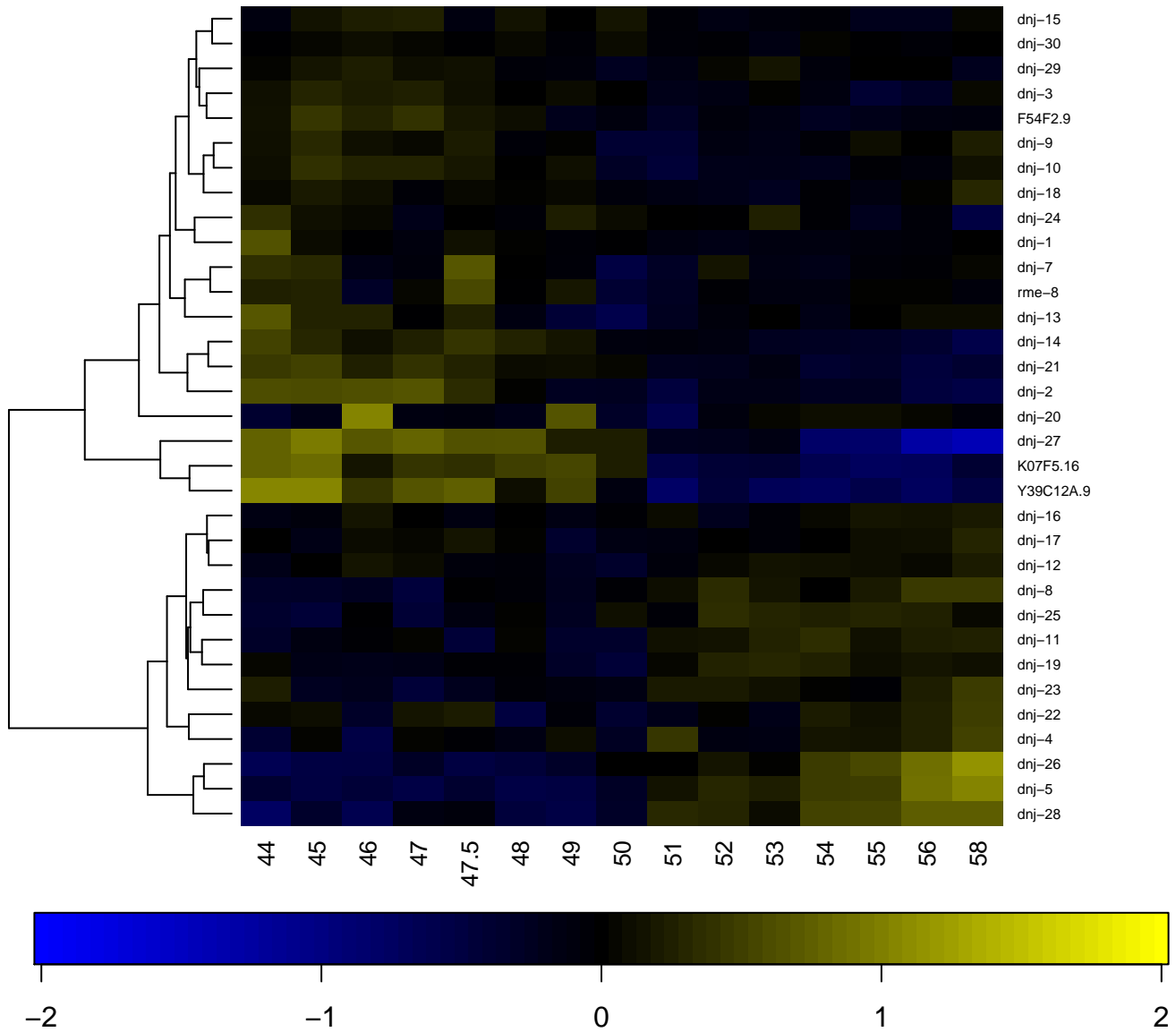
hAT family dimerisation domain



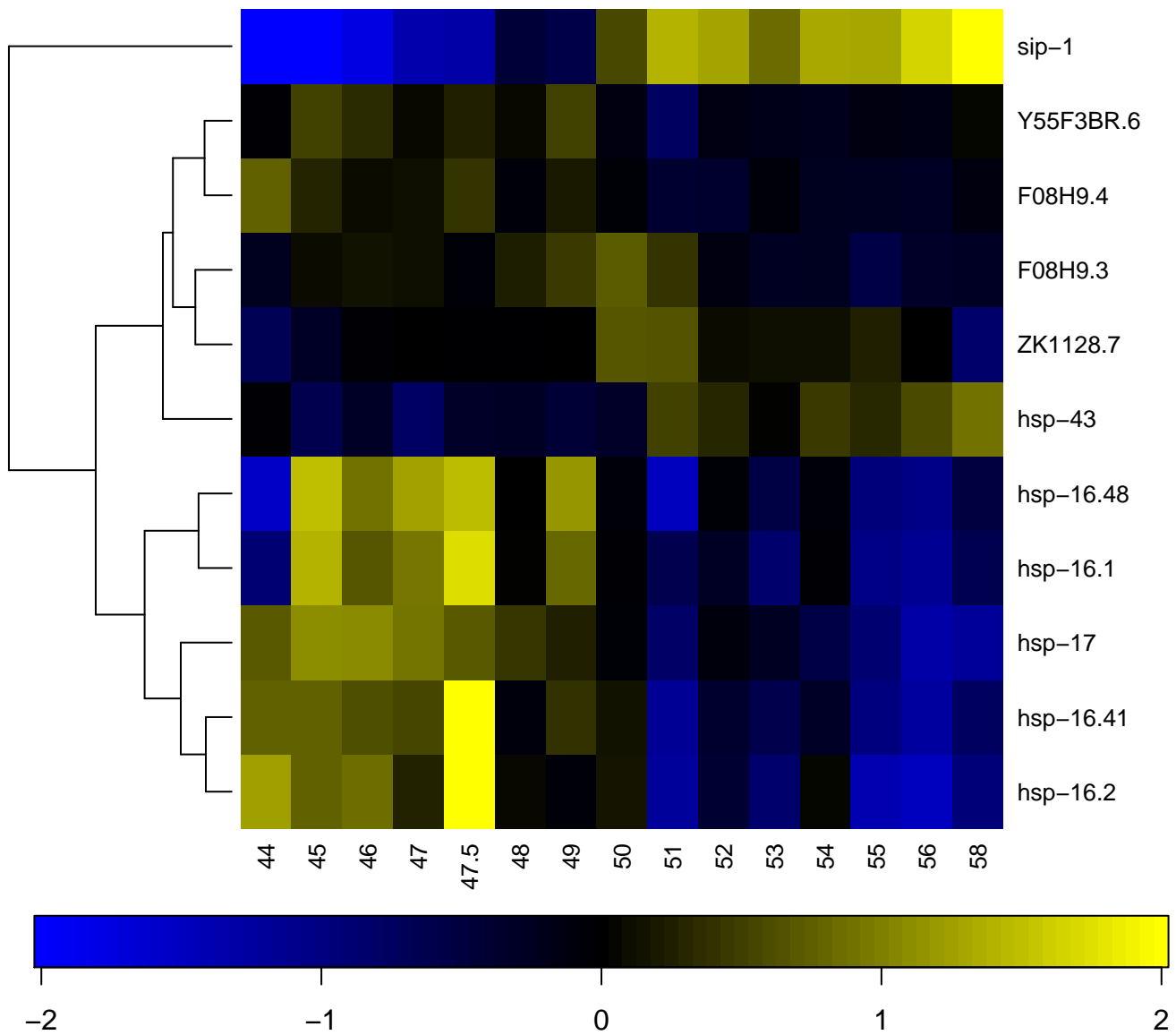
HEAT repeat



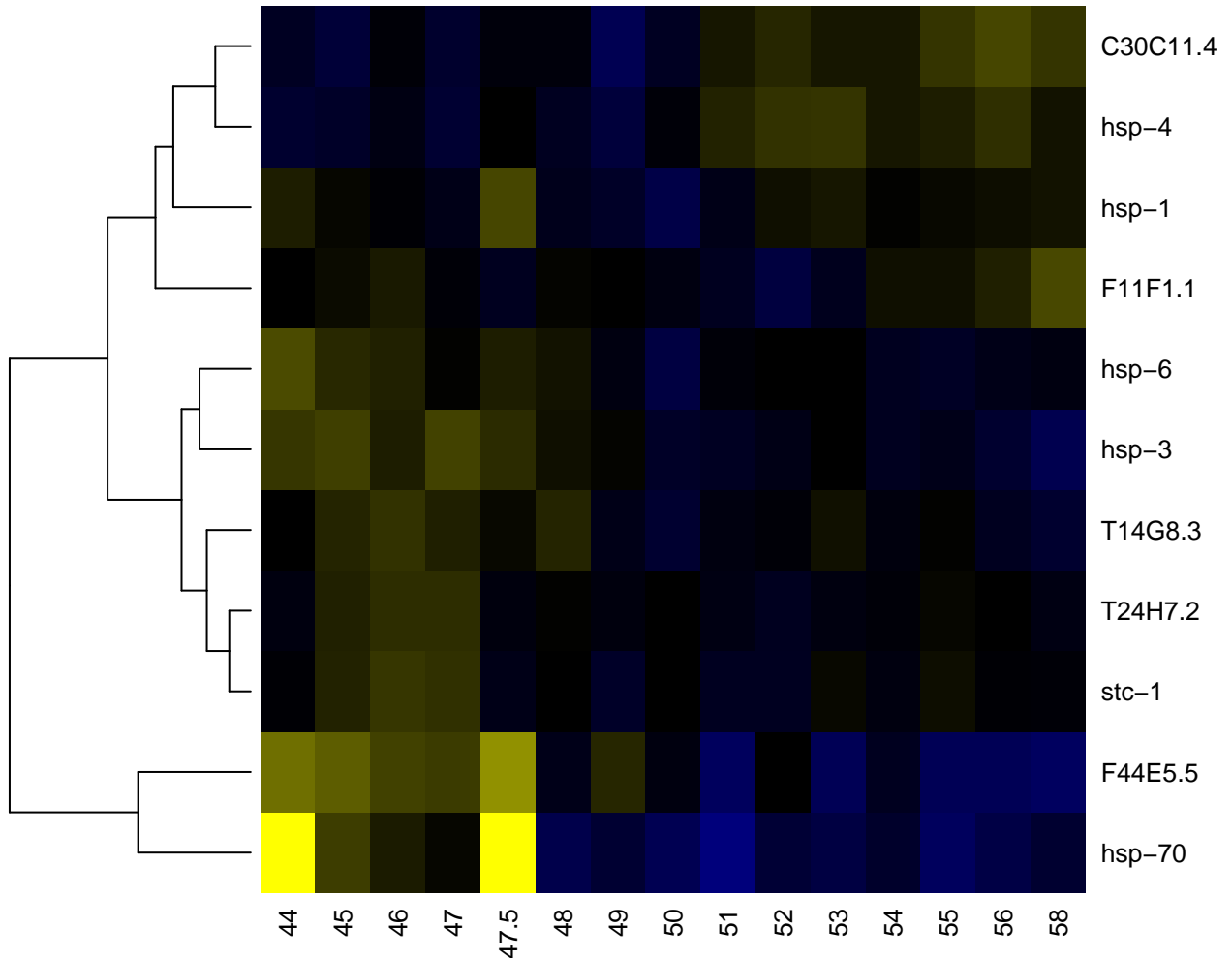
Heat shock protein DnaJ, N-terminal



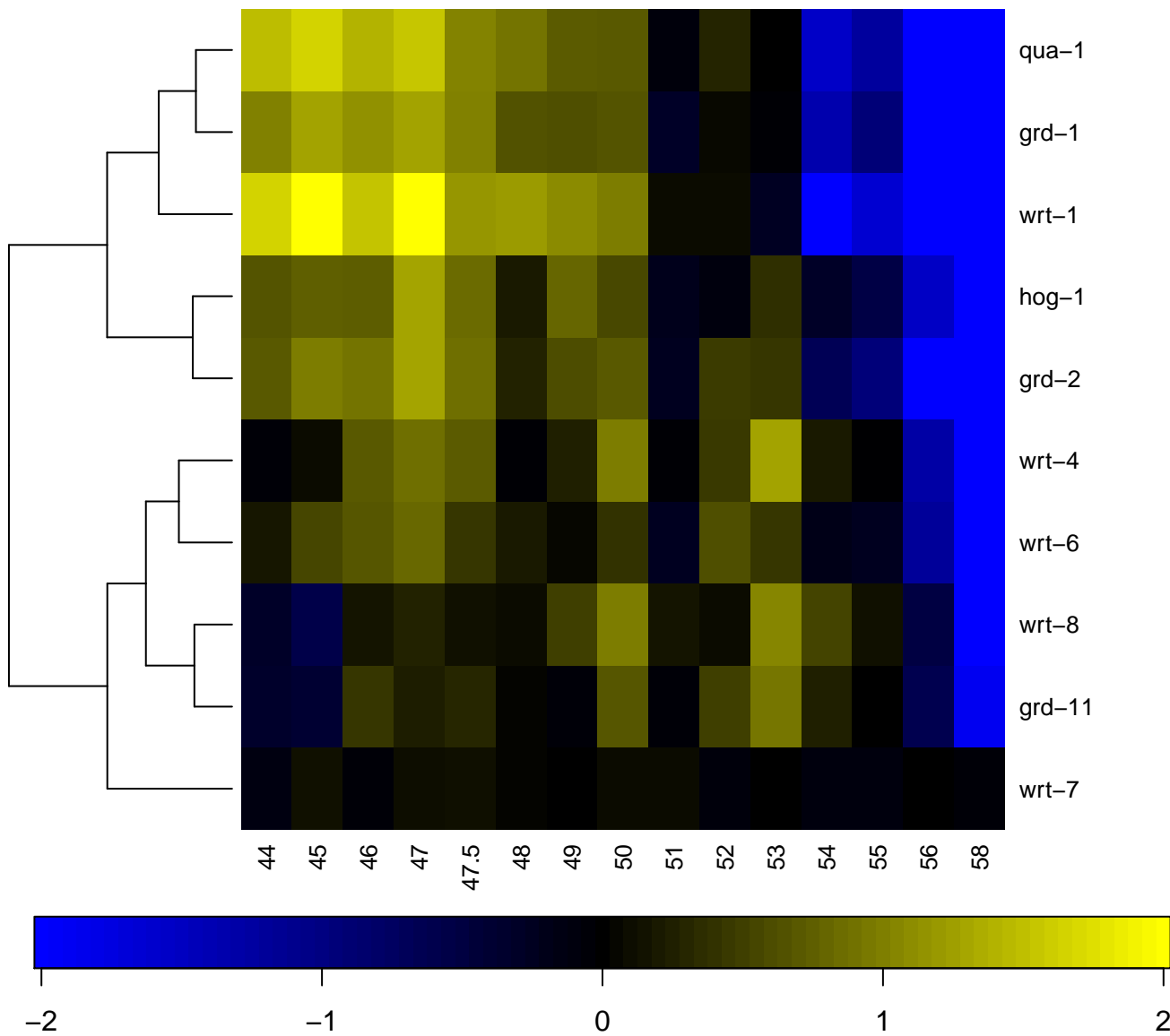
Heat shock protein Hsp20



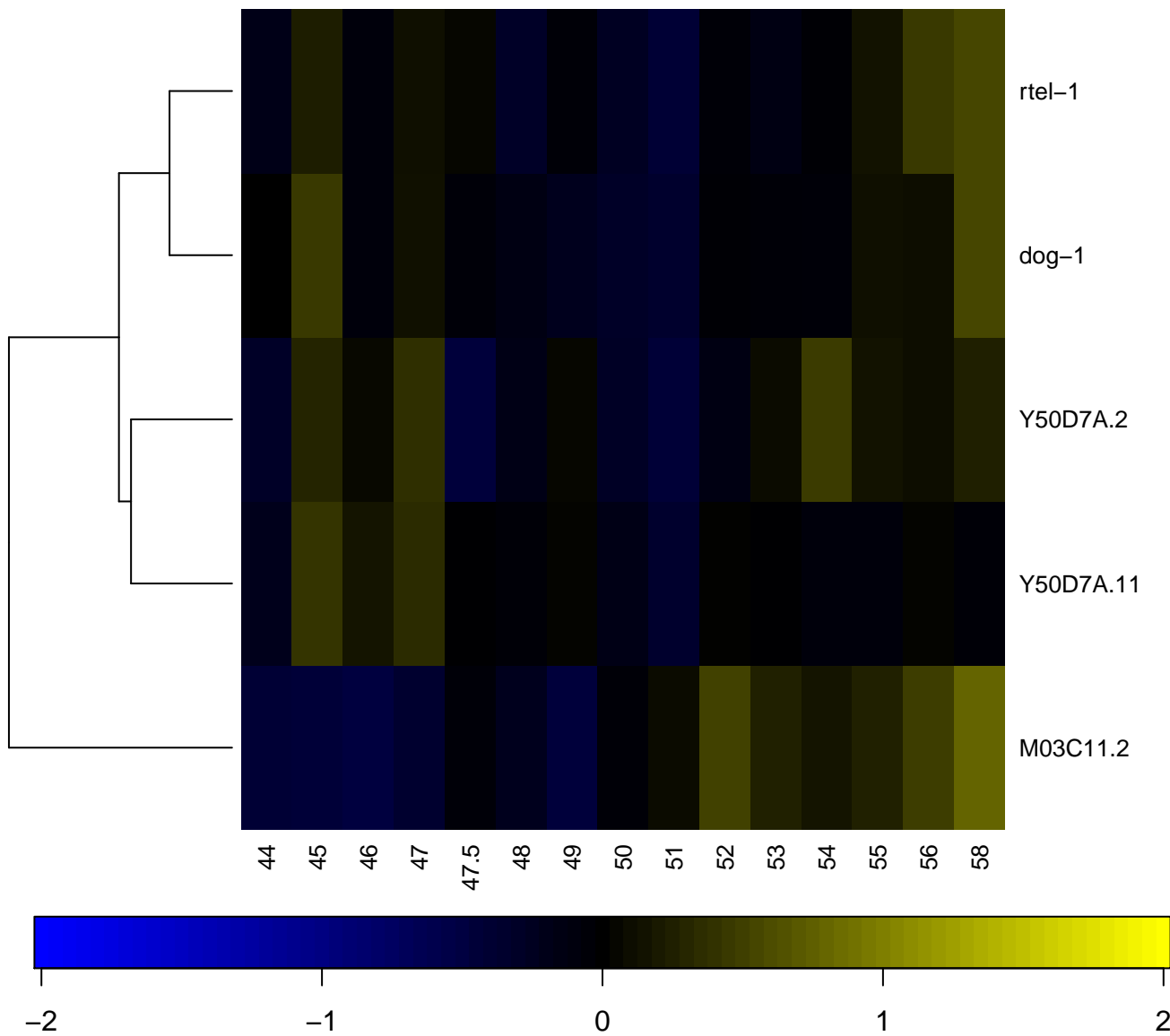
Heat shock protein Hsp70



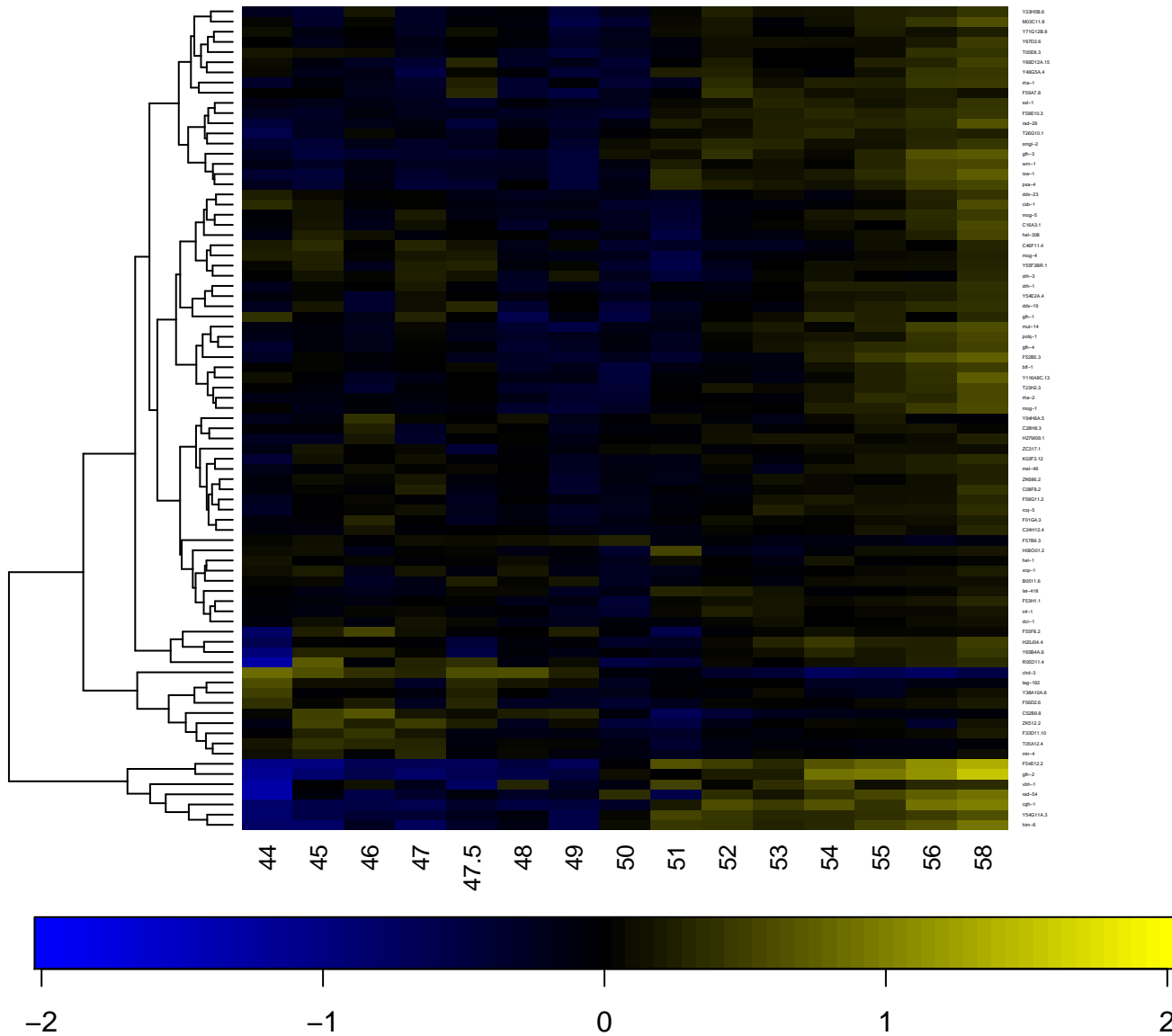
Hedgehog/intein hint domain, C-terminal



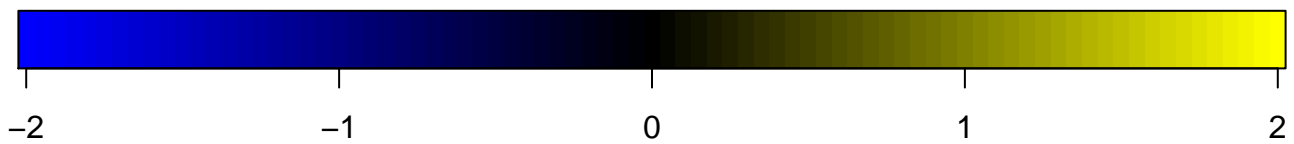
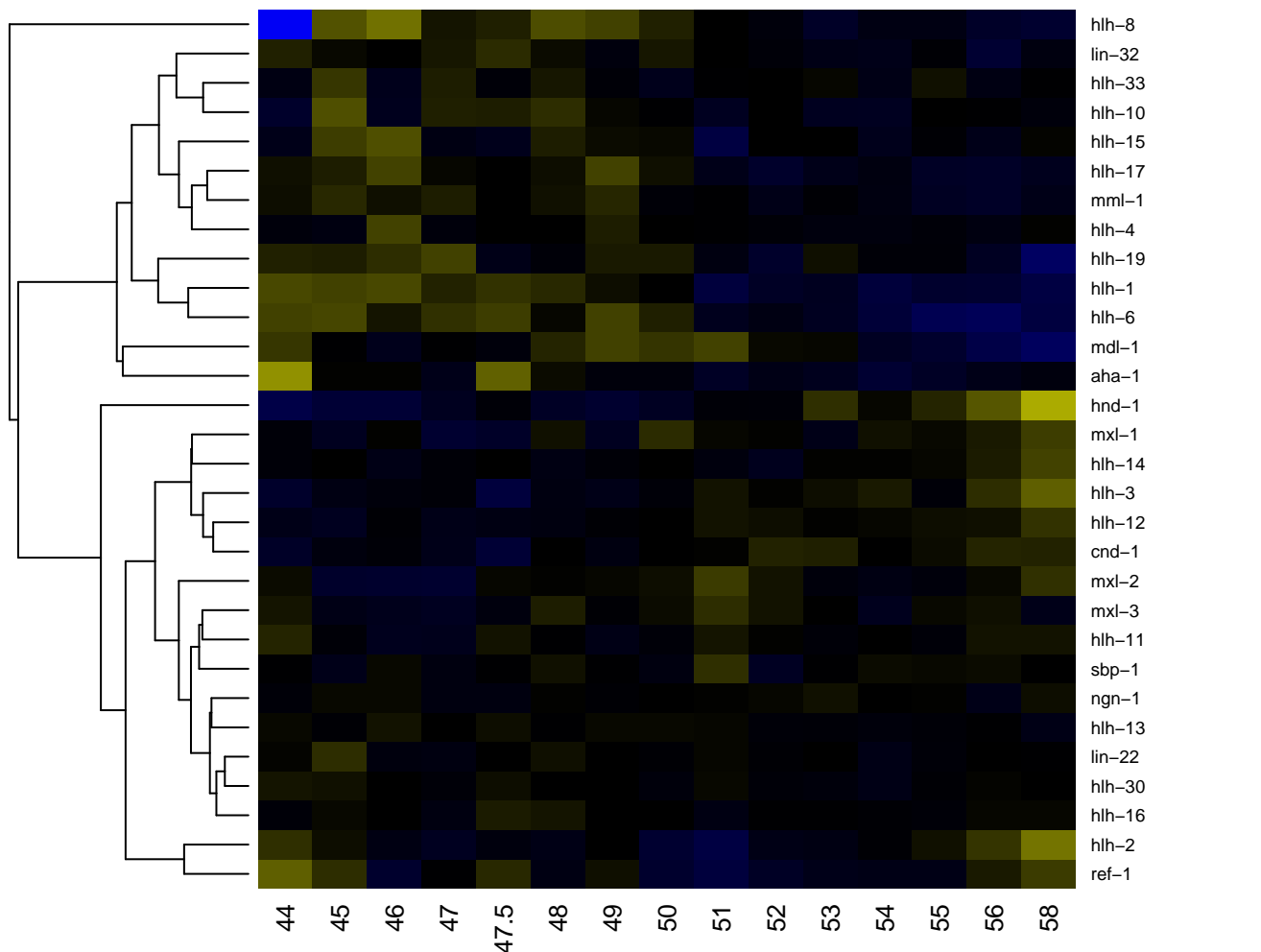
Helicase-like, DEXD box c2 type



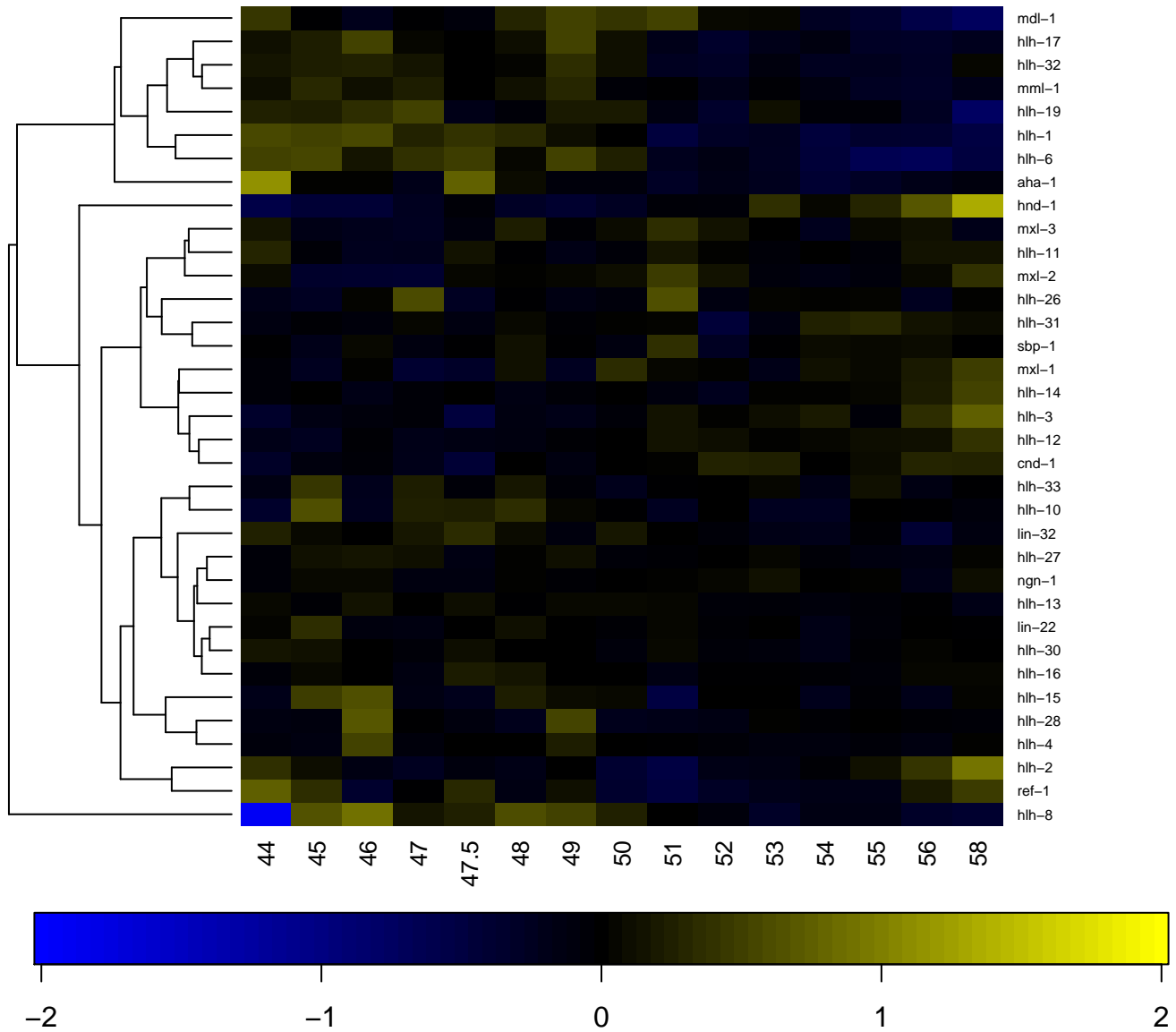
Helicase conserved C-terminal domain



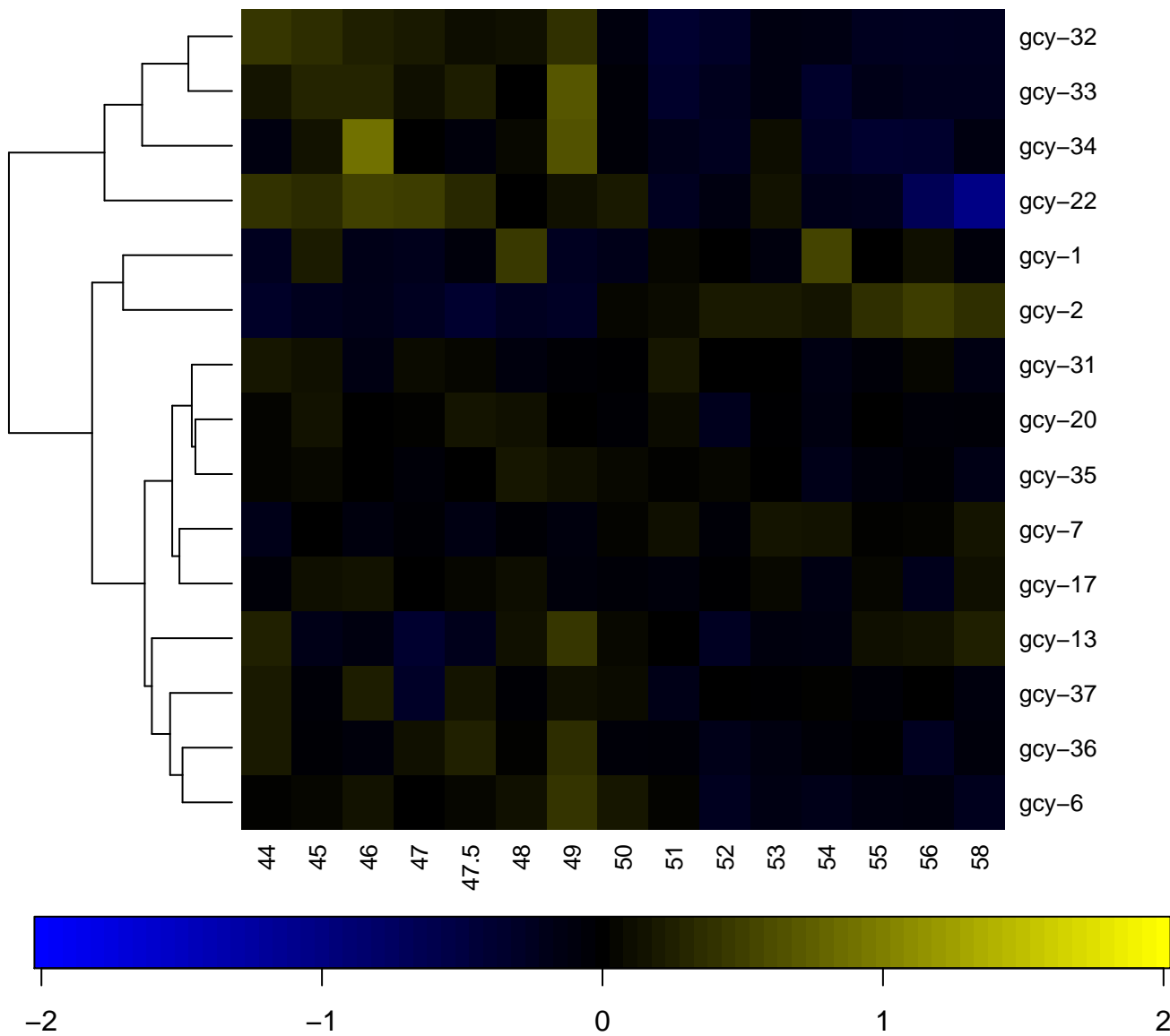
Helix-loop-helix DNA-binding



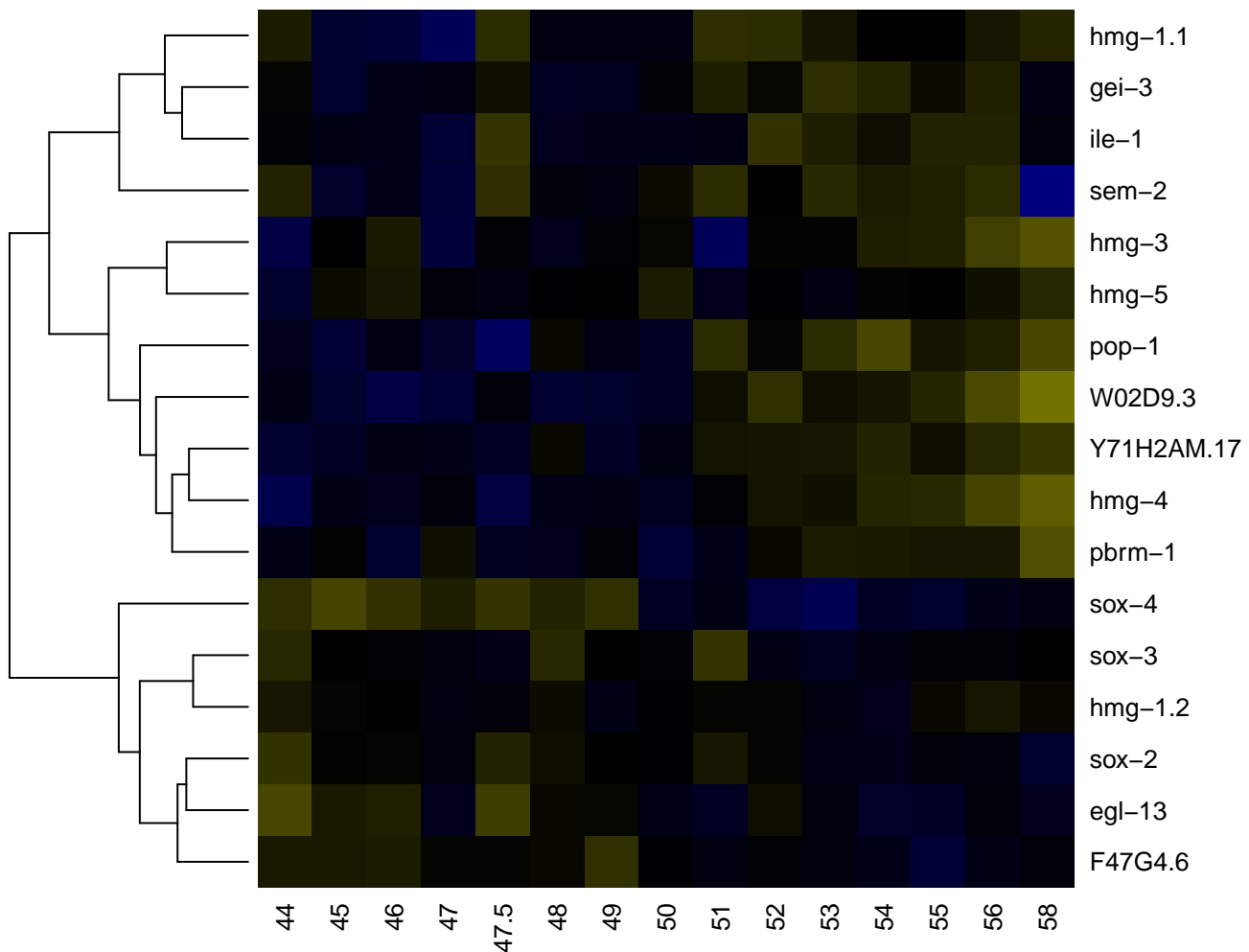
Helix-loop-helix DNA-binding domain



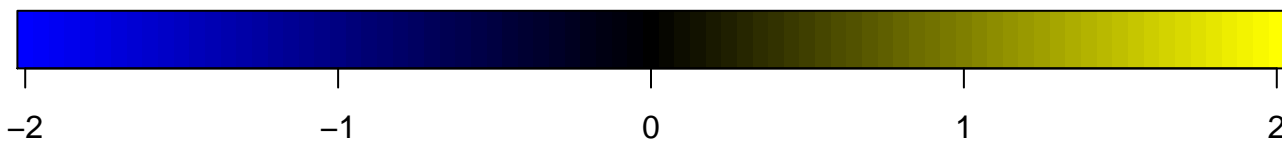
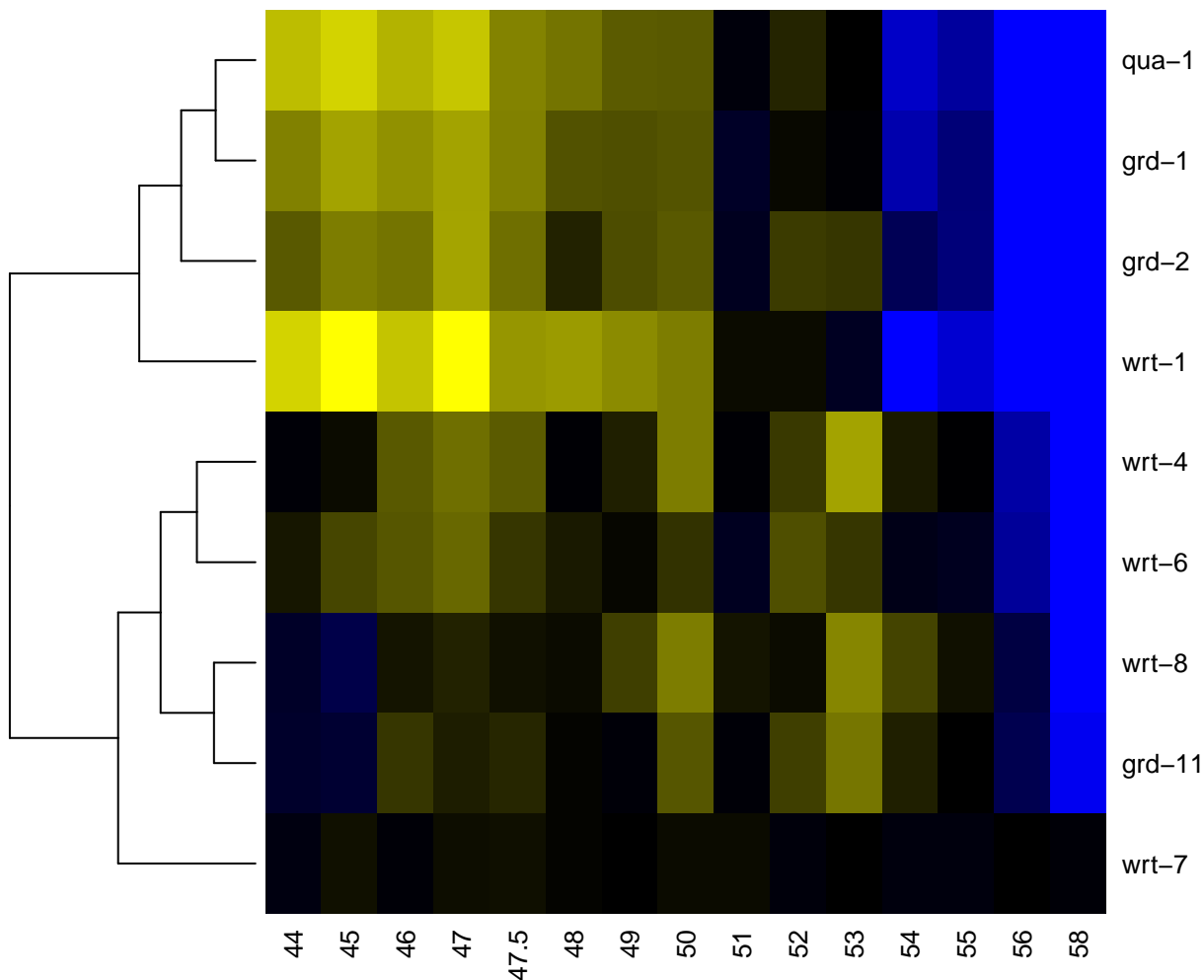
Heme NO binding associated



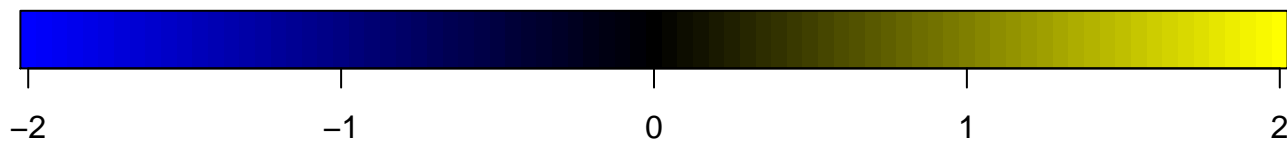
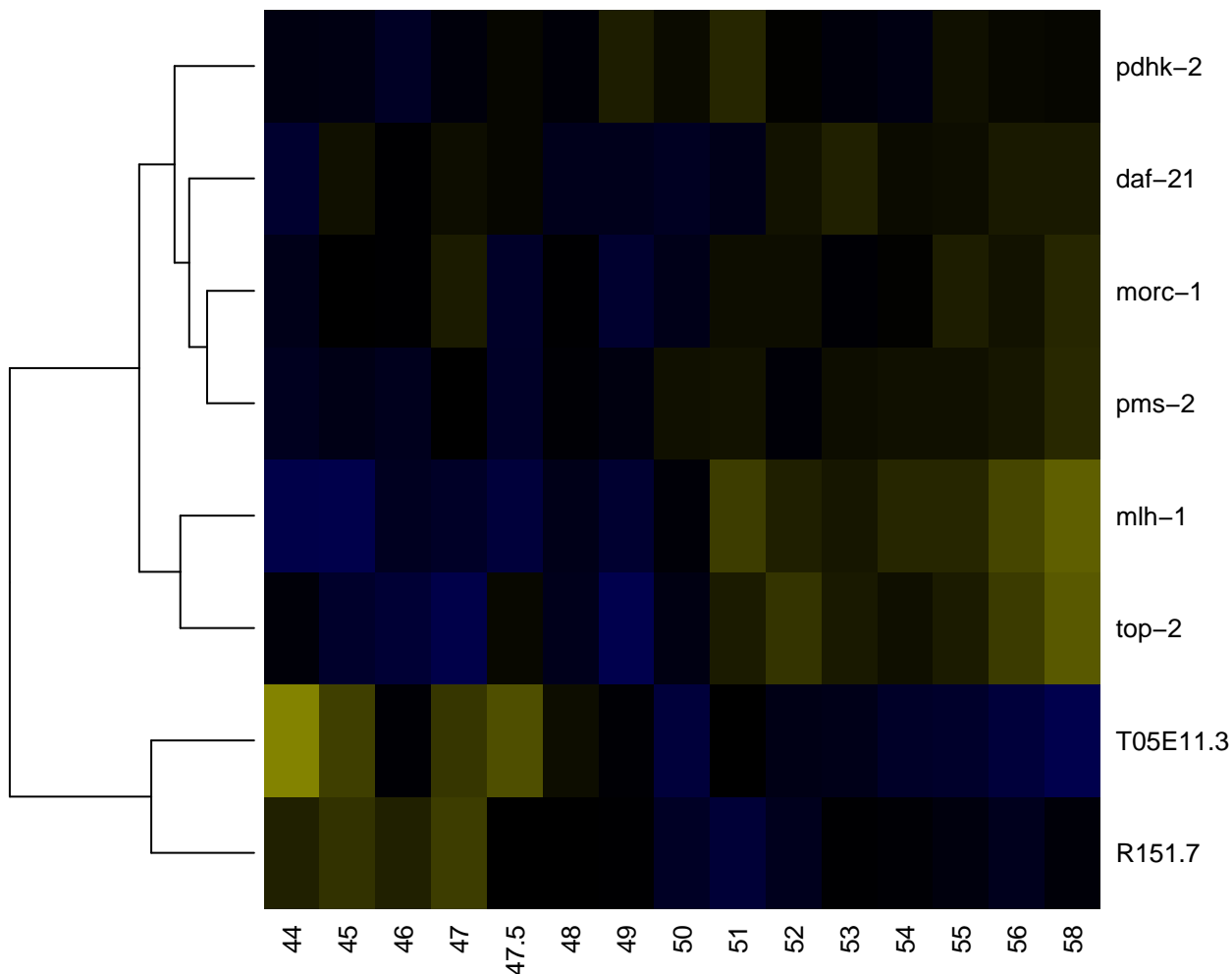
High mobility group, HMG1/HMG2



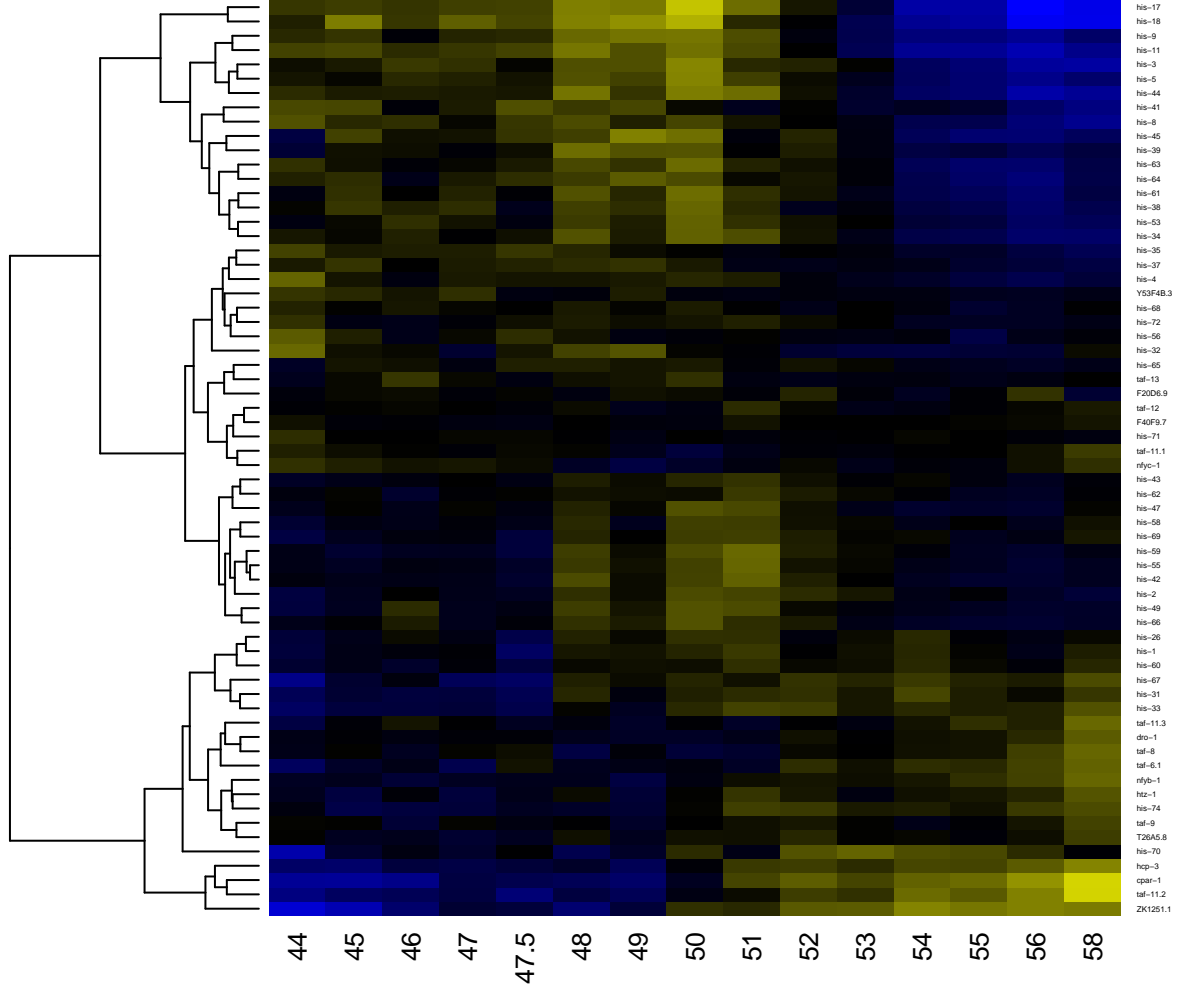
Hint module



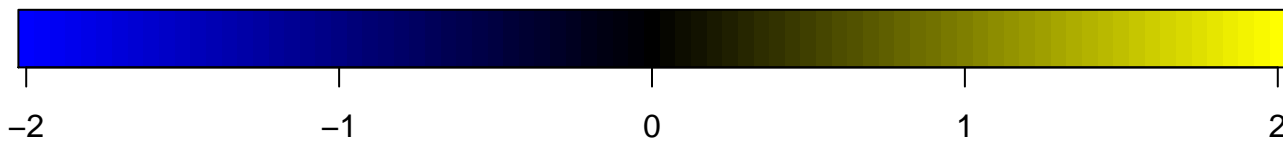
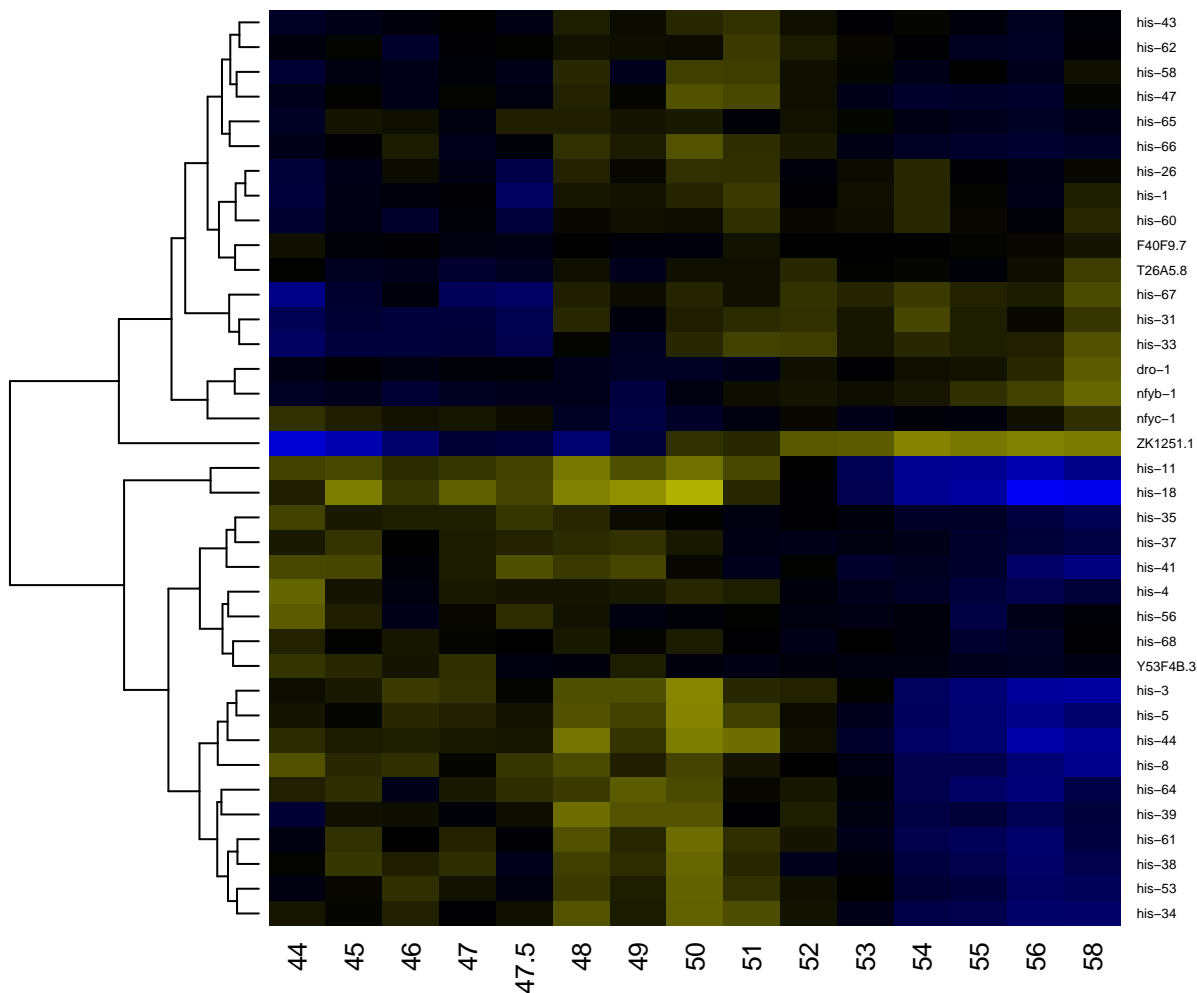
Histidine kinase-, DNA gyrase B-, and HSP90-like ATPase



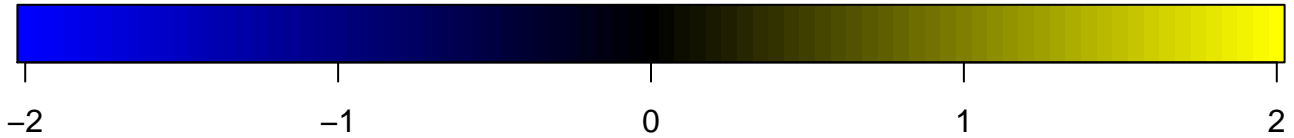
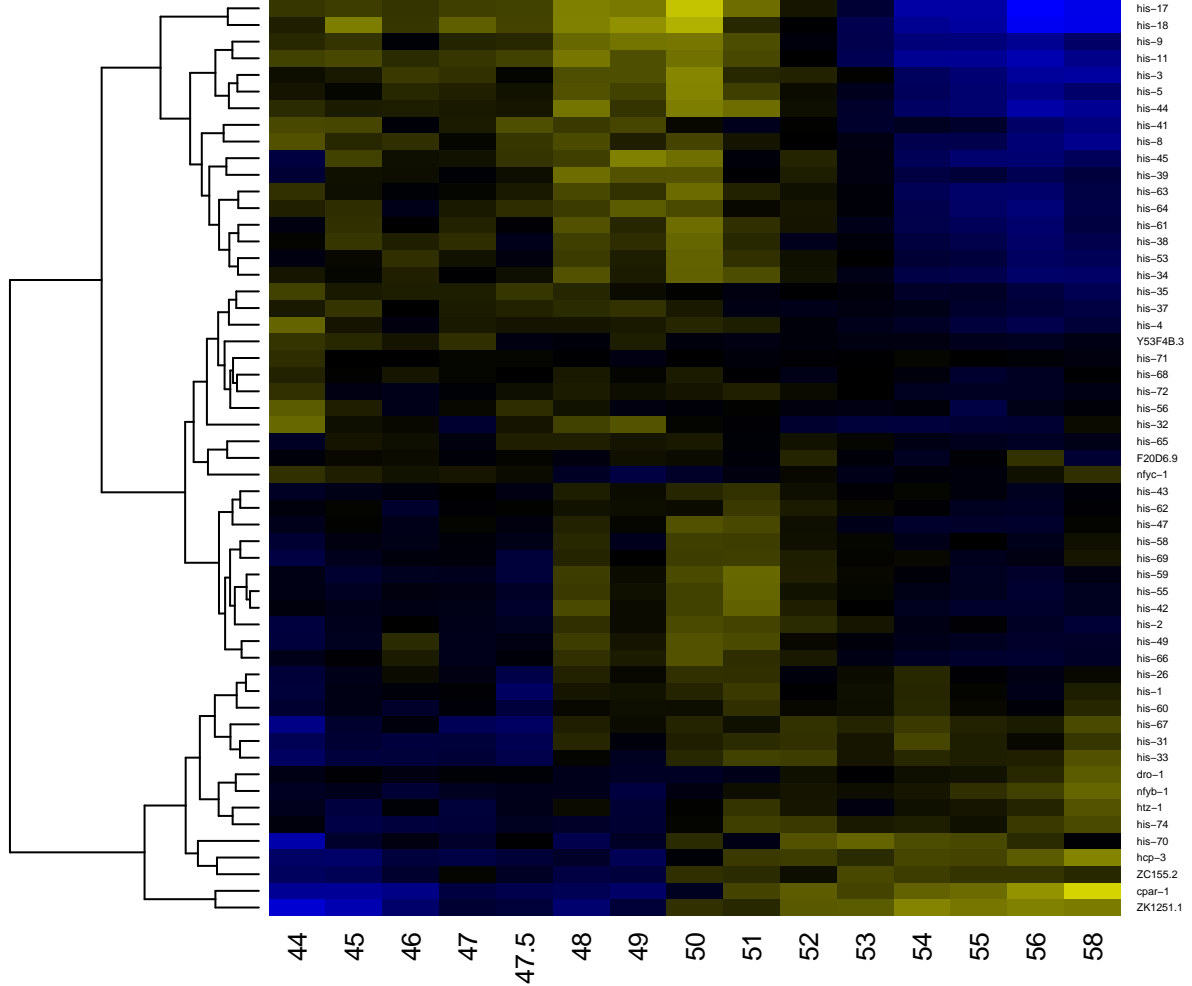
Histone-fold



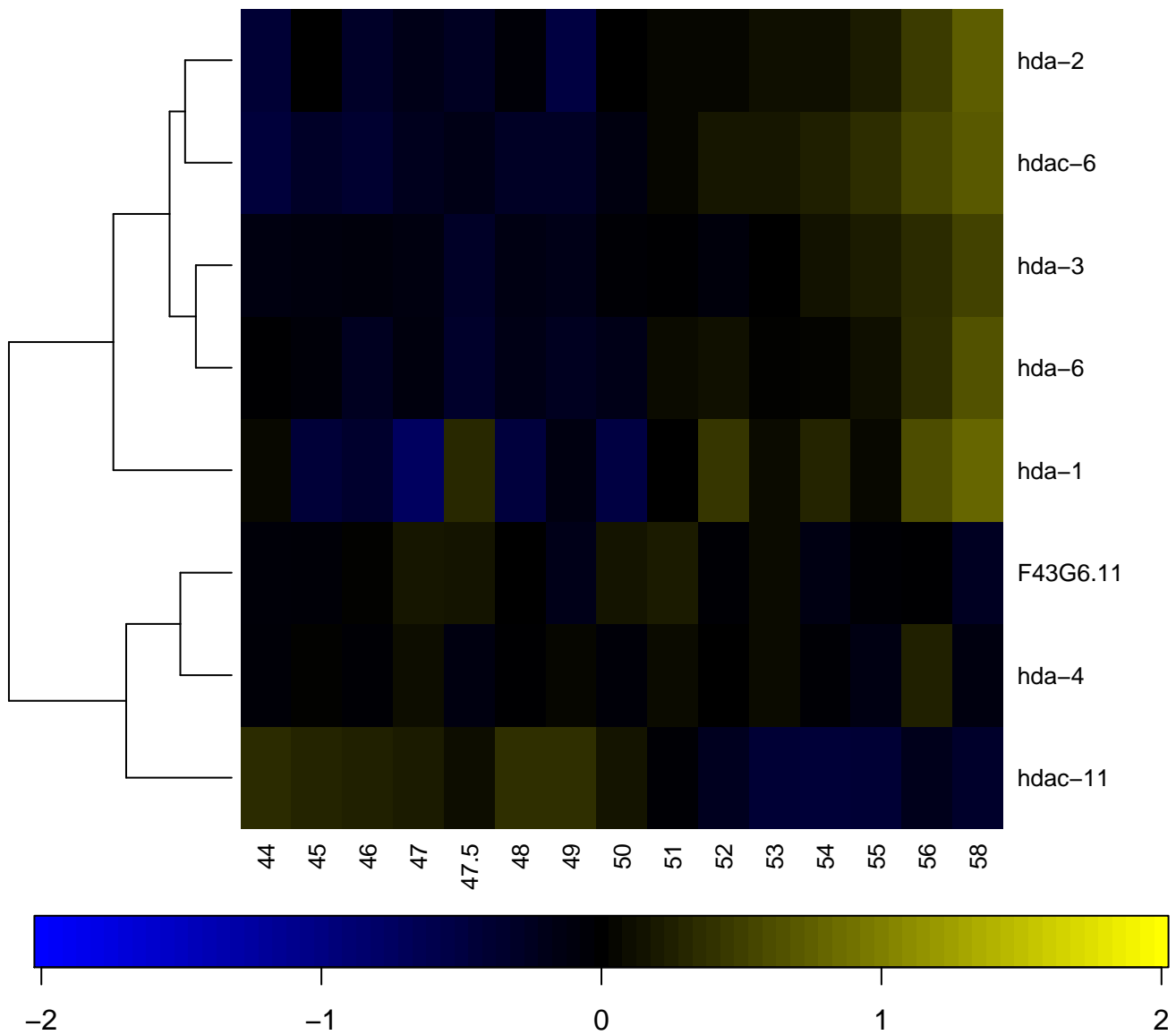
stone-like transcription factor (CBF/NF-Y) and archaeal his



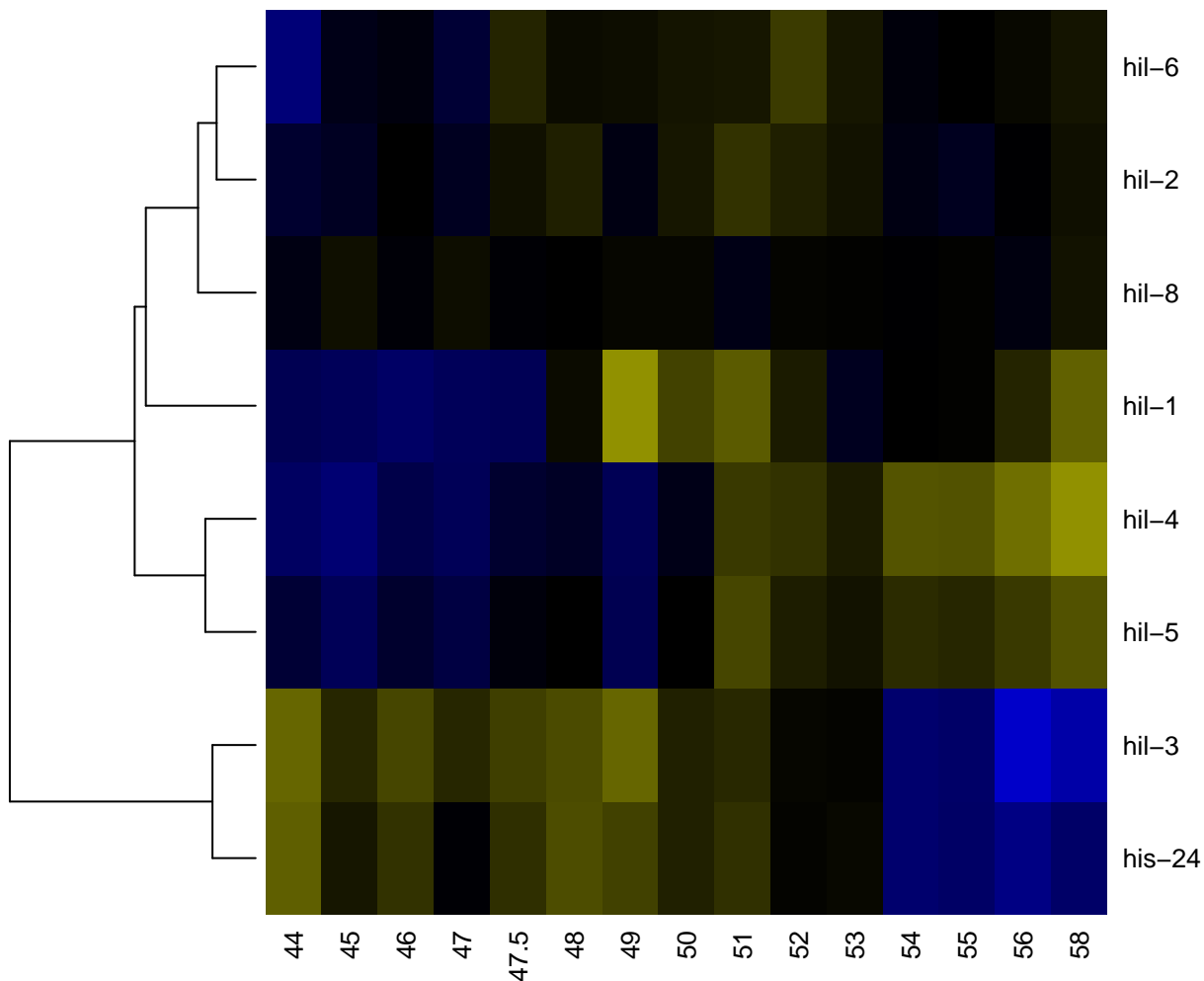
Histone core



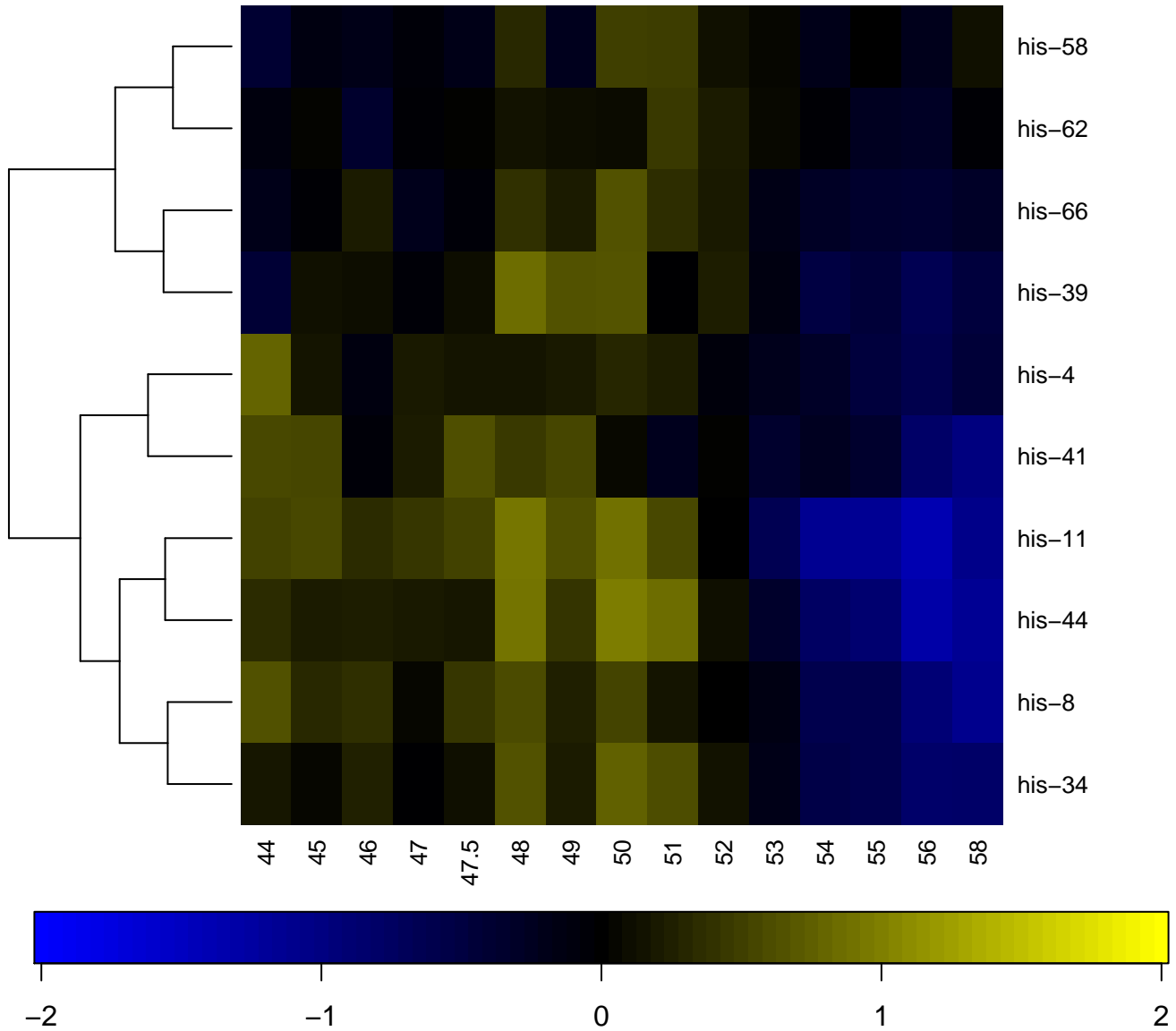
Histone deacetylase superfamily



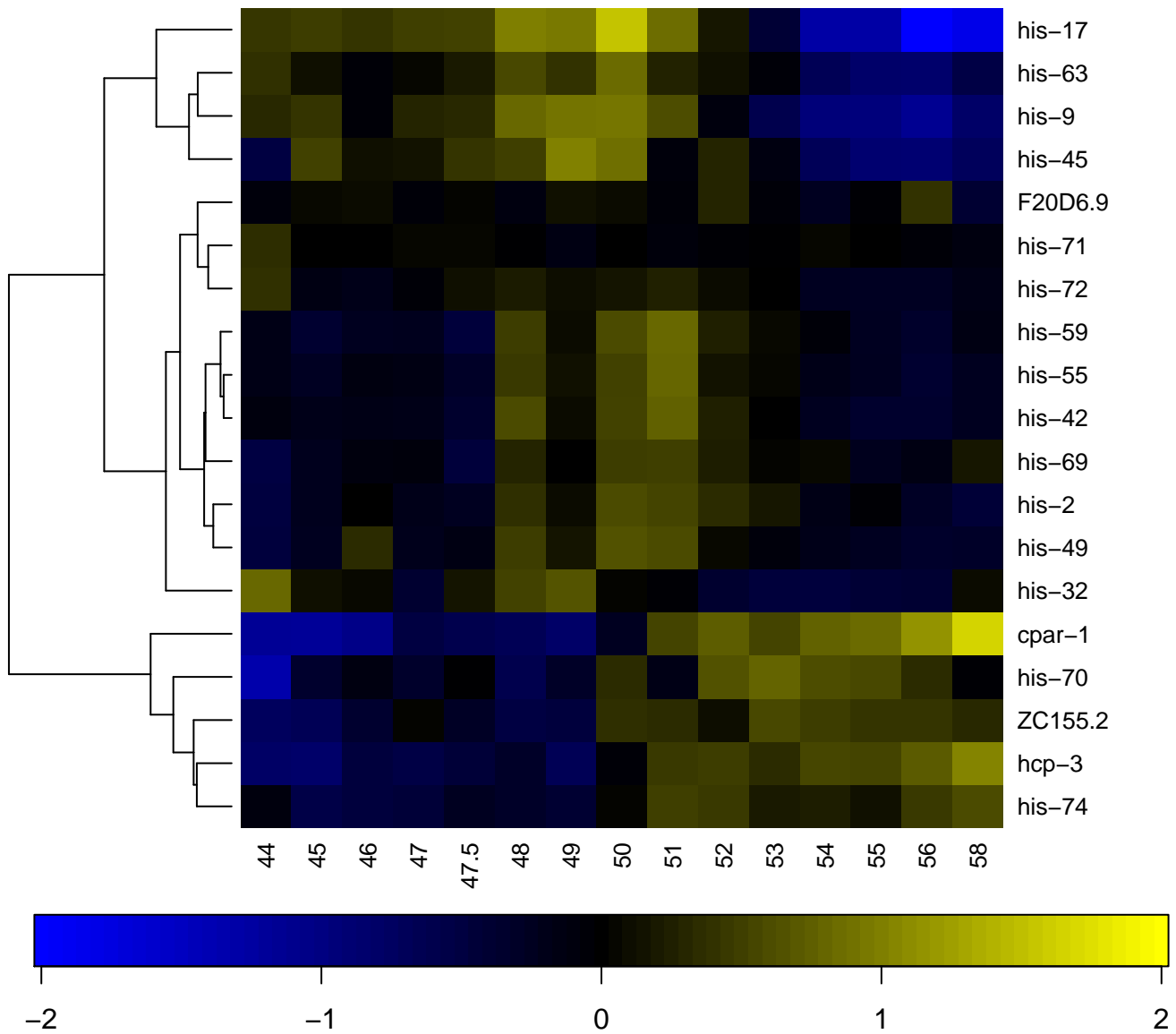
Histone H1/H5



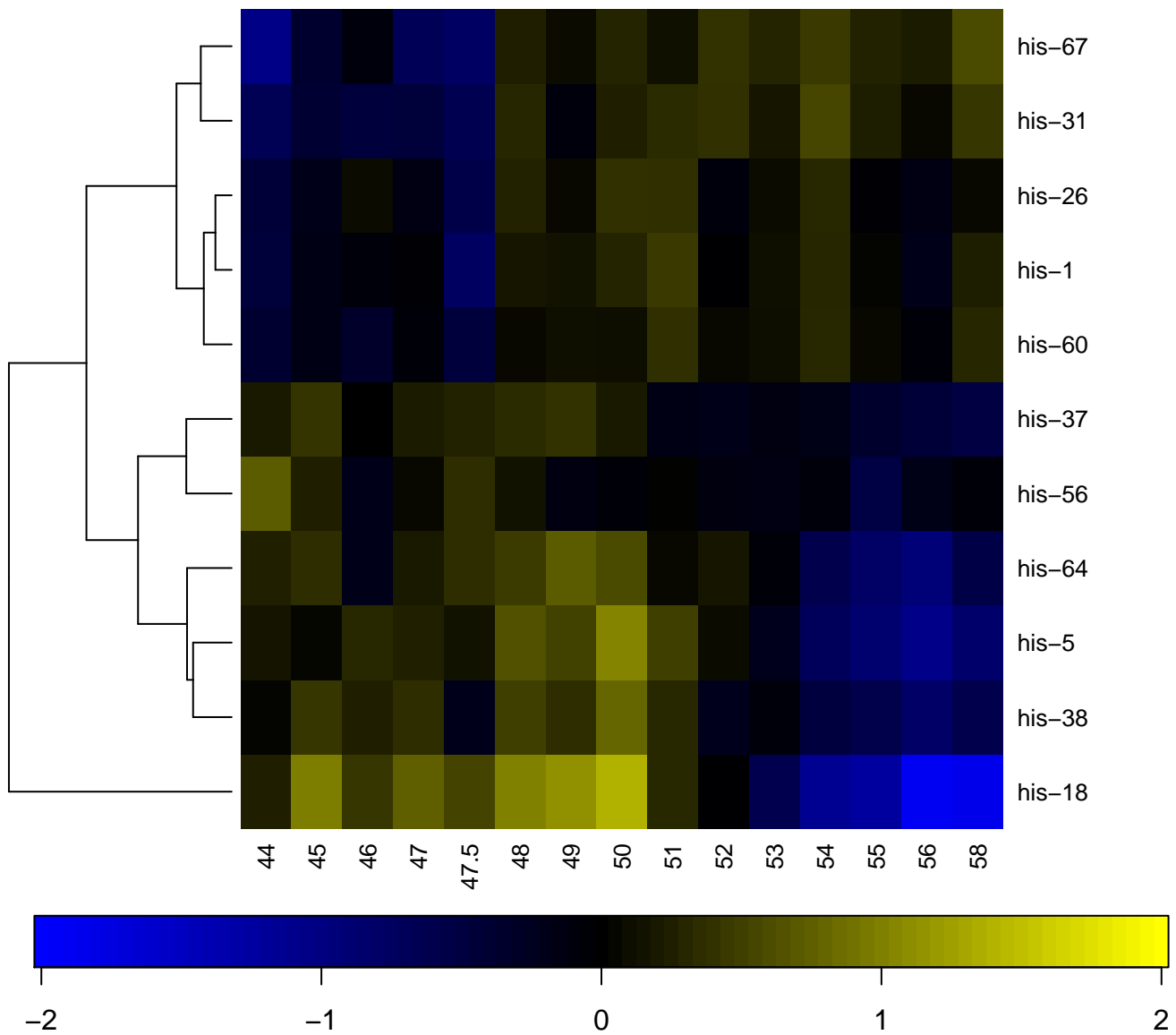
Histone H2B



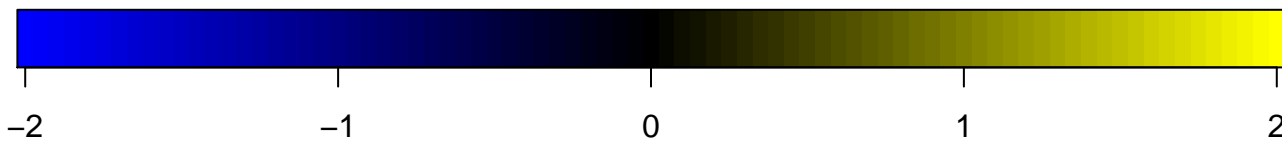
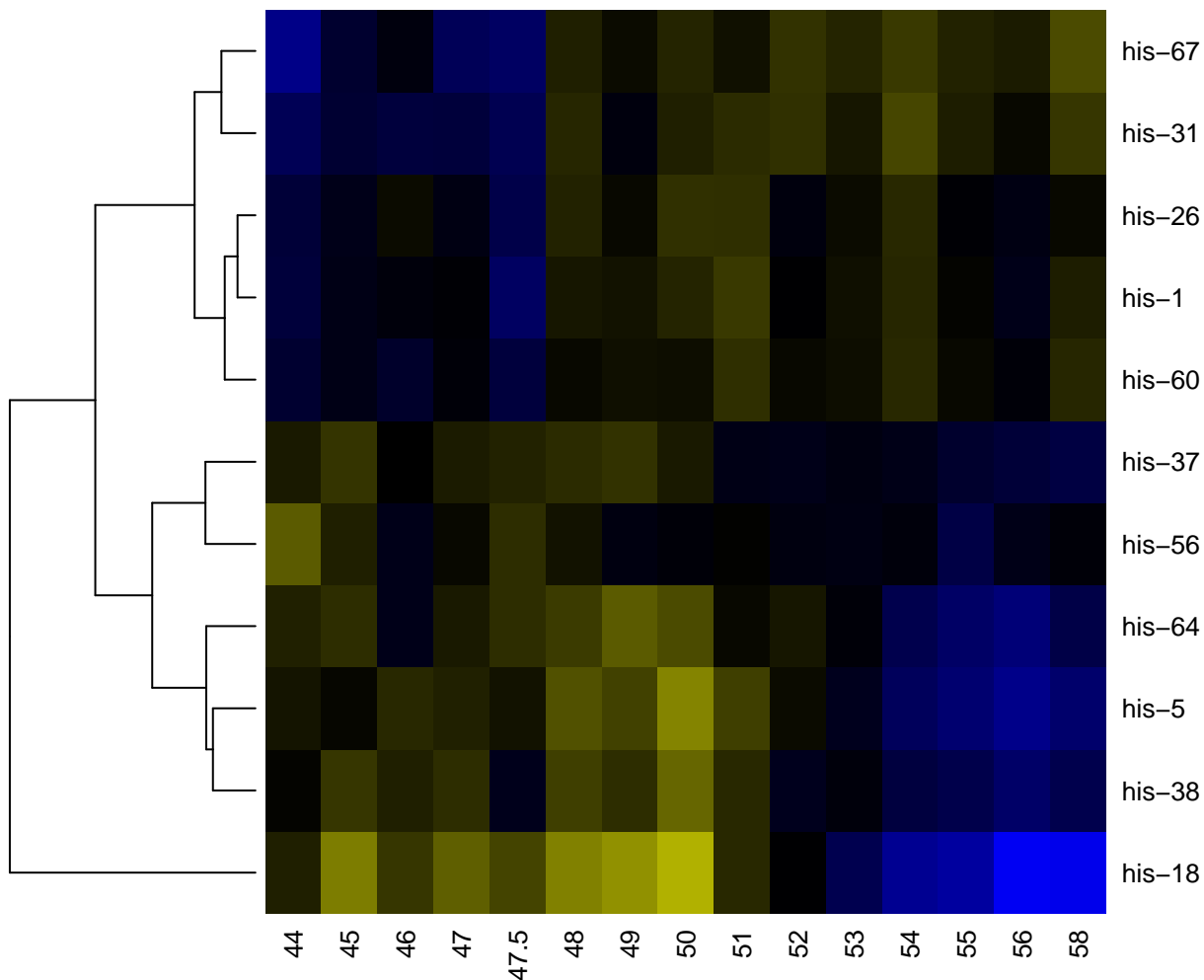
Histone H3



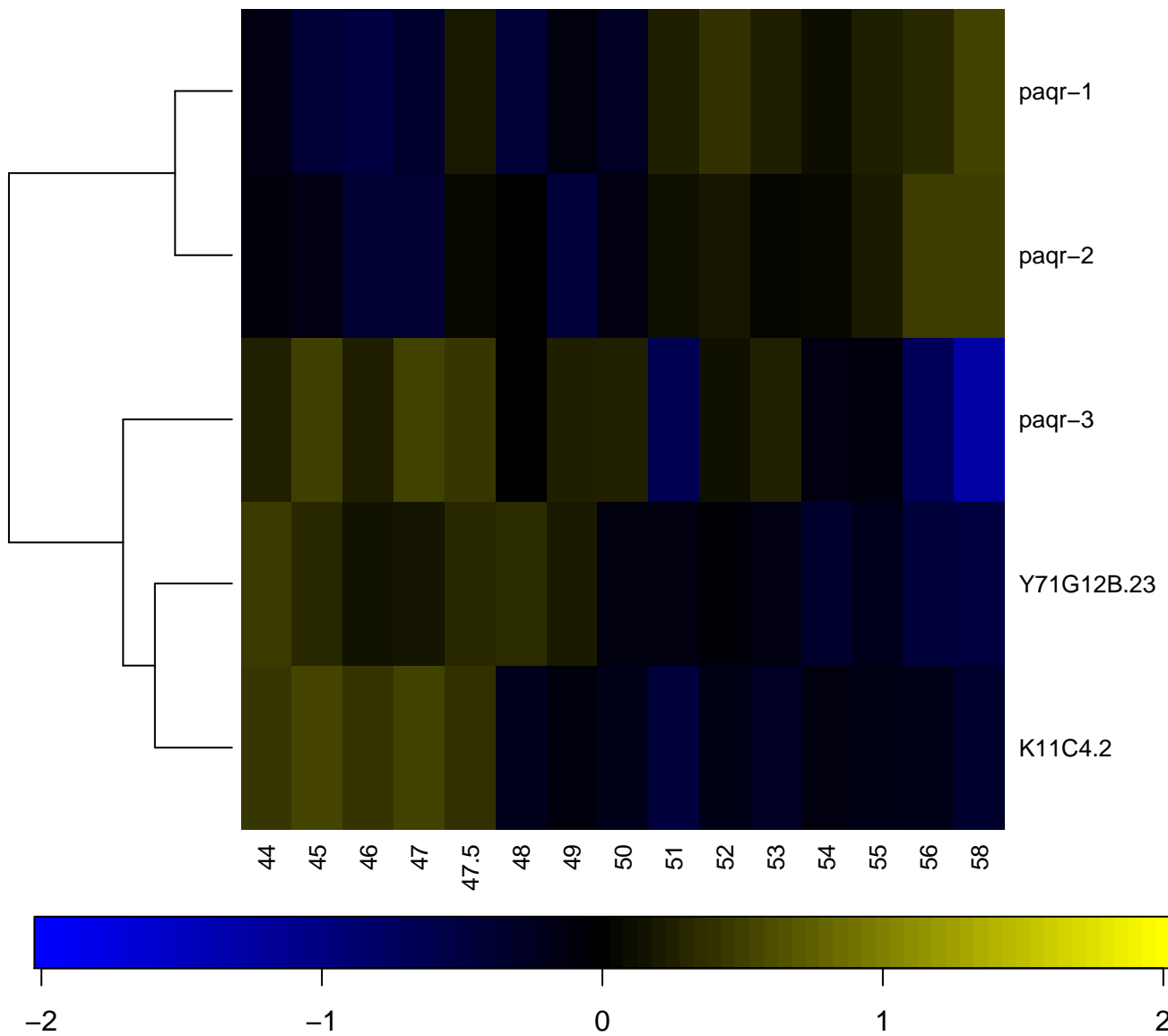
Histone H4



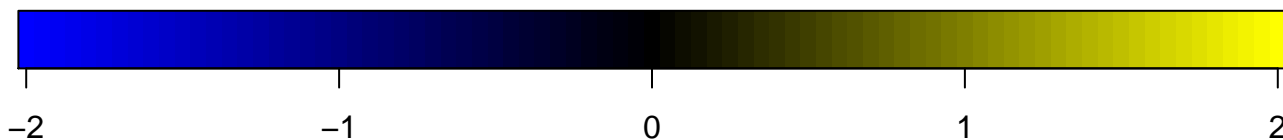
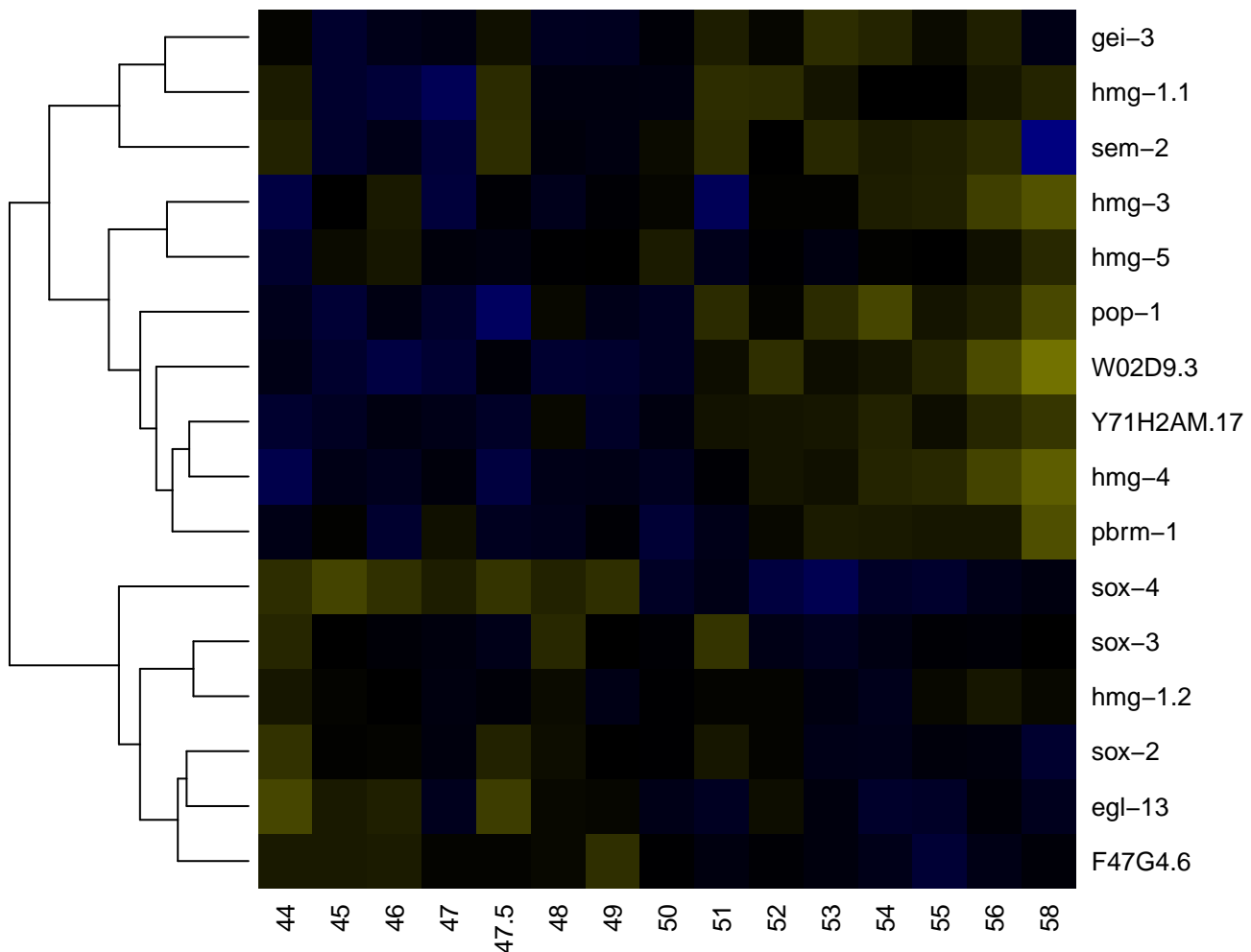
Histone H4, conserved site



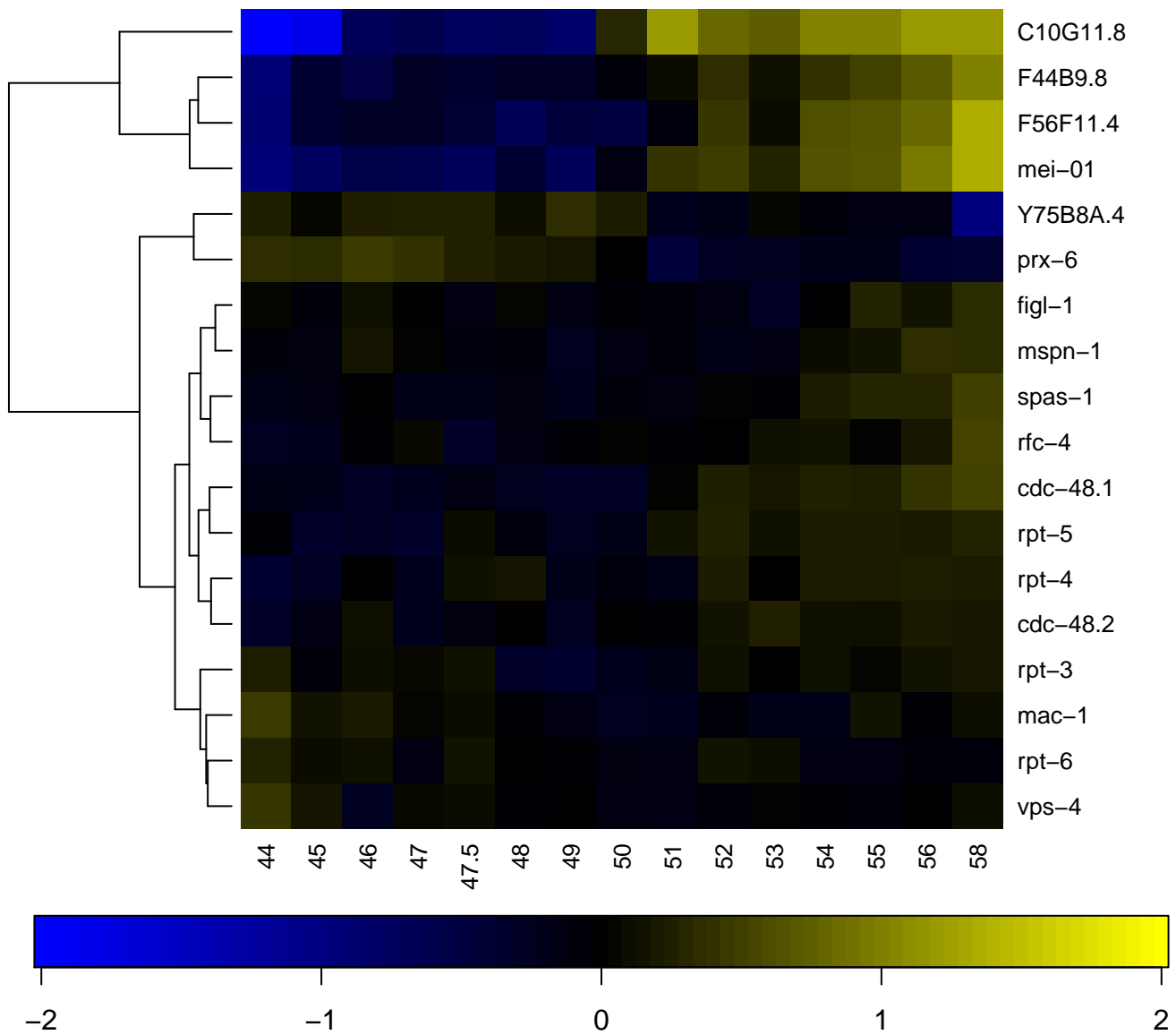
Hly-III related



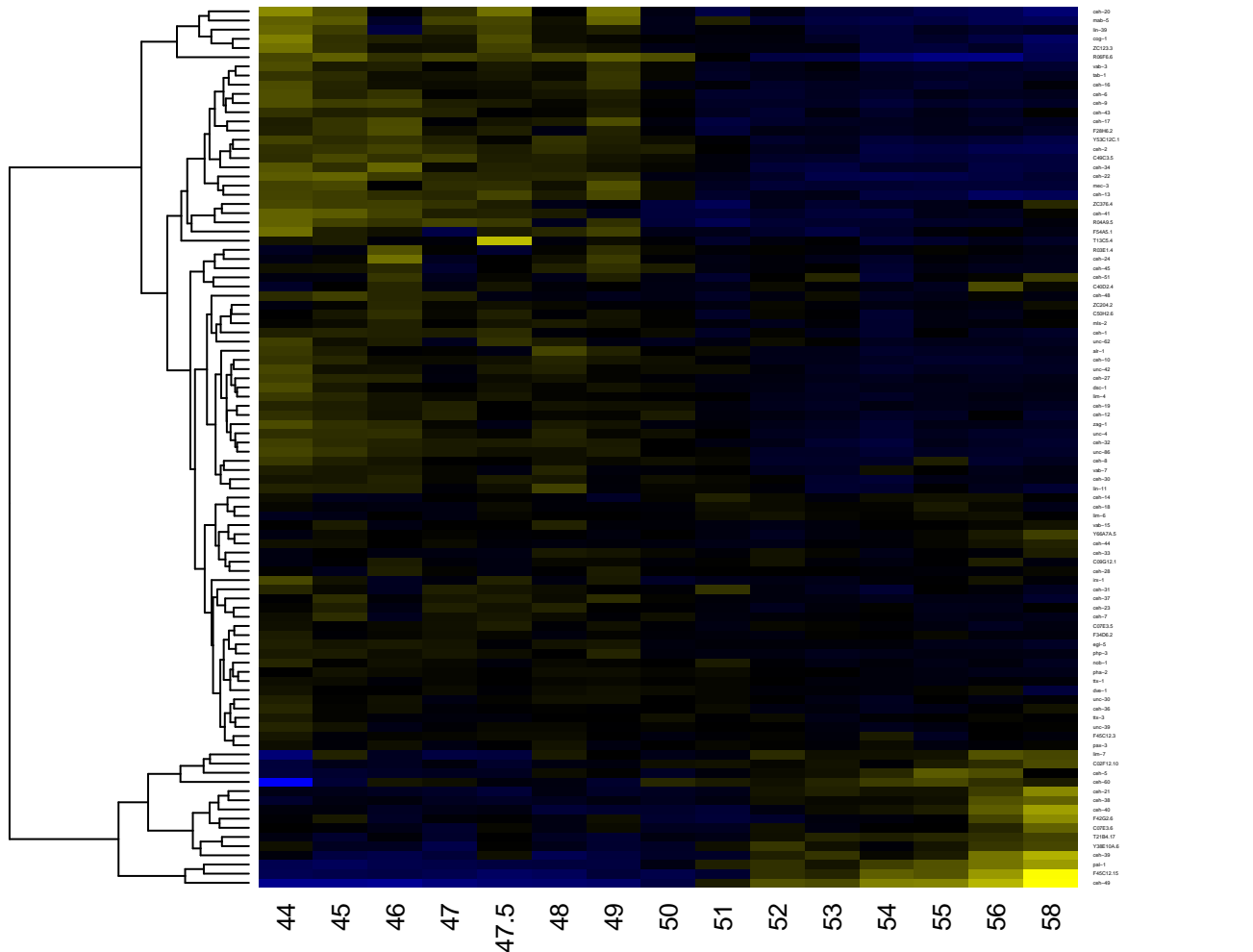
HMG (high mobility group) box



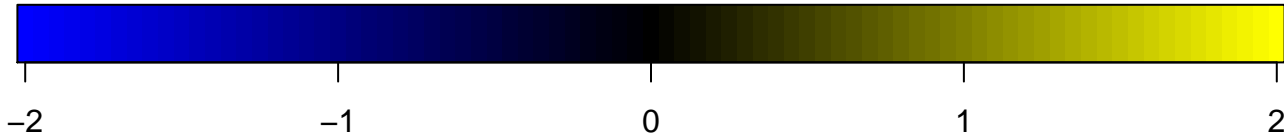
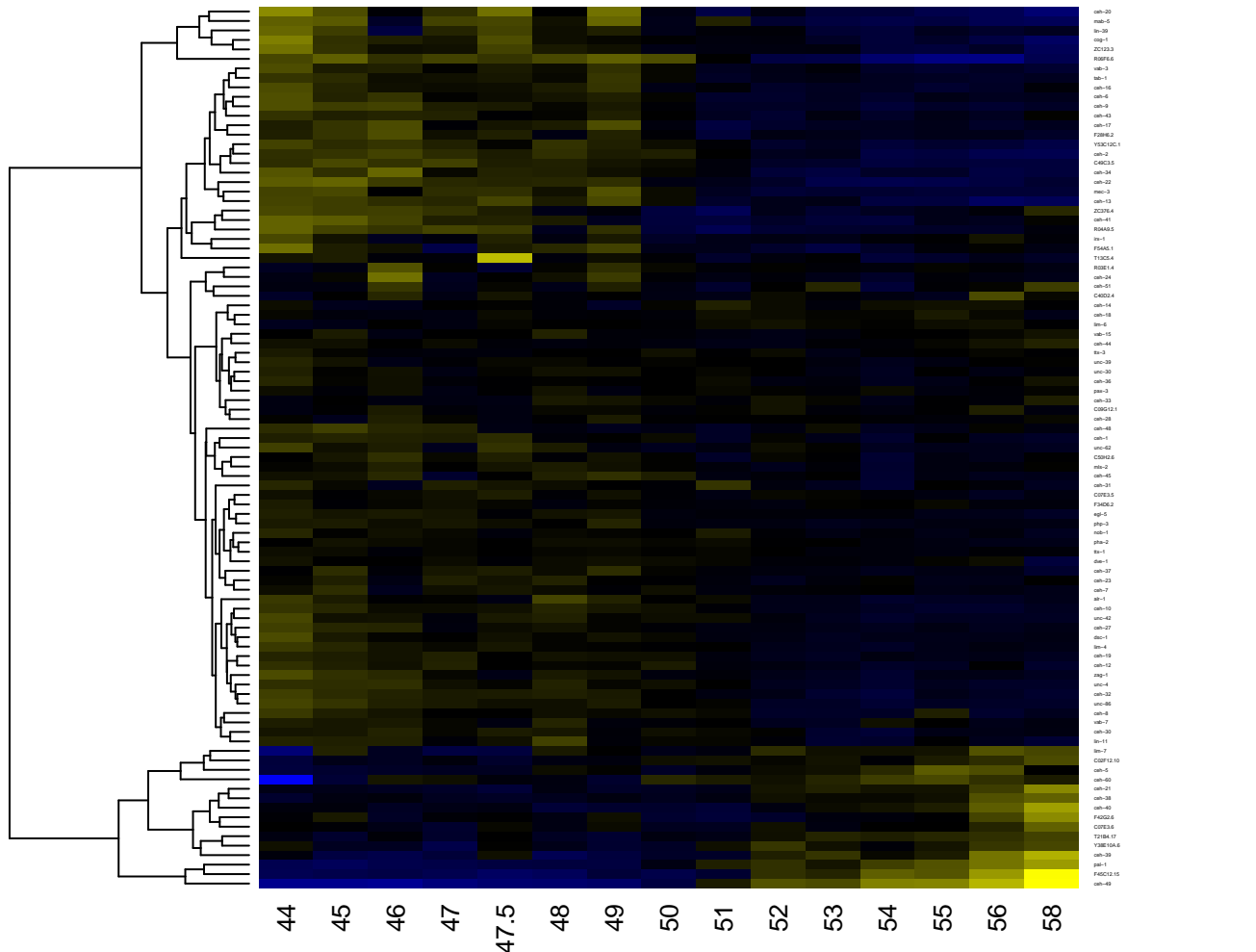
Holliday junction DNA helicase ruvB N-terminus



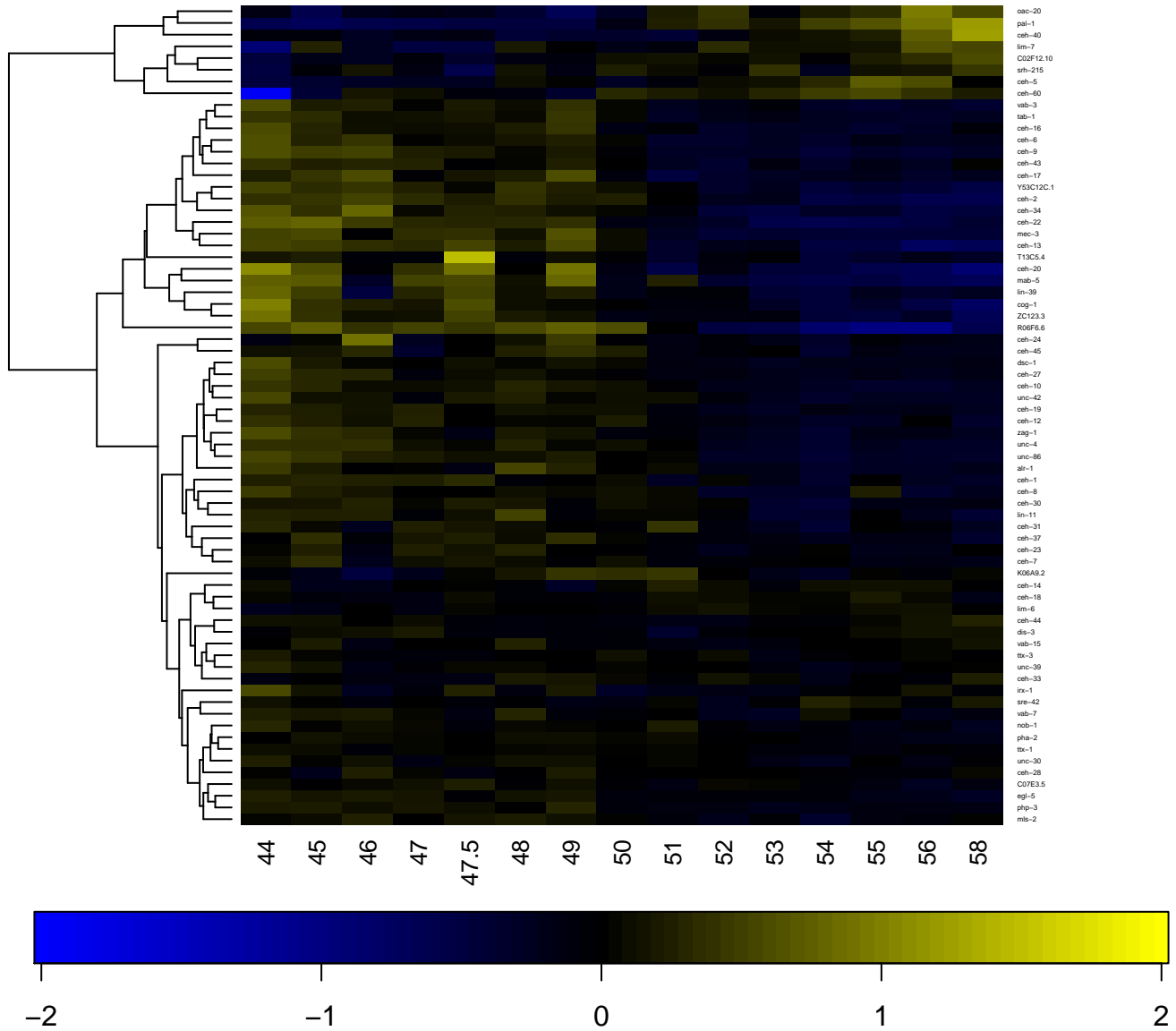
Homeobox



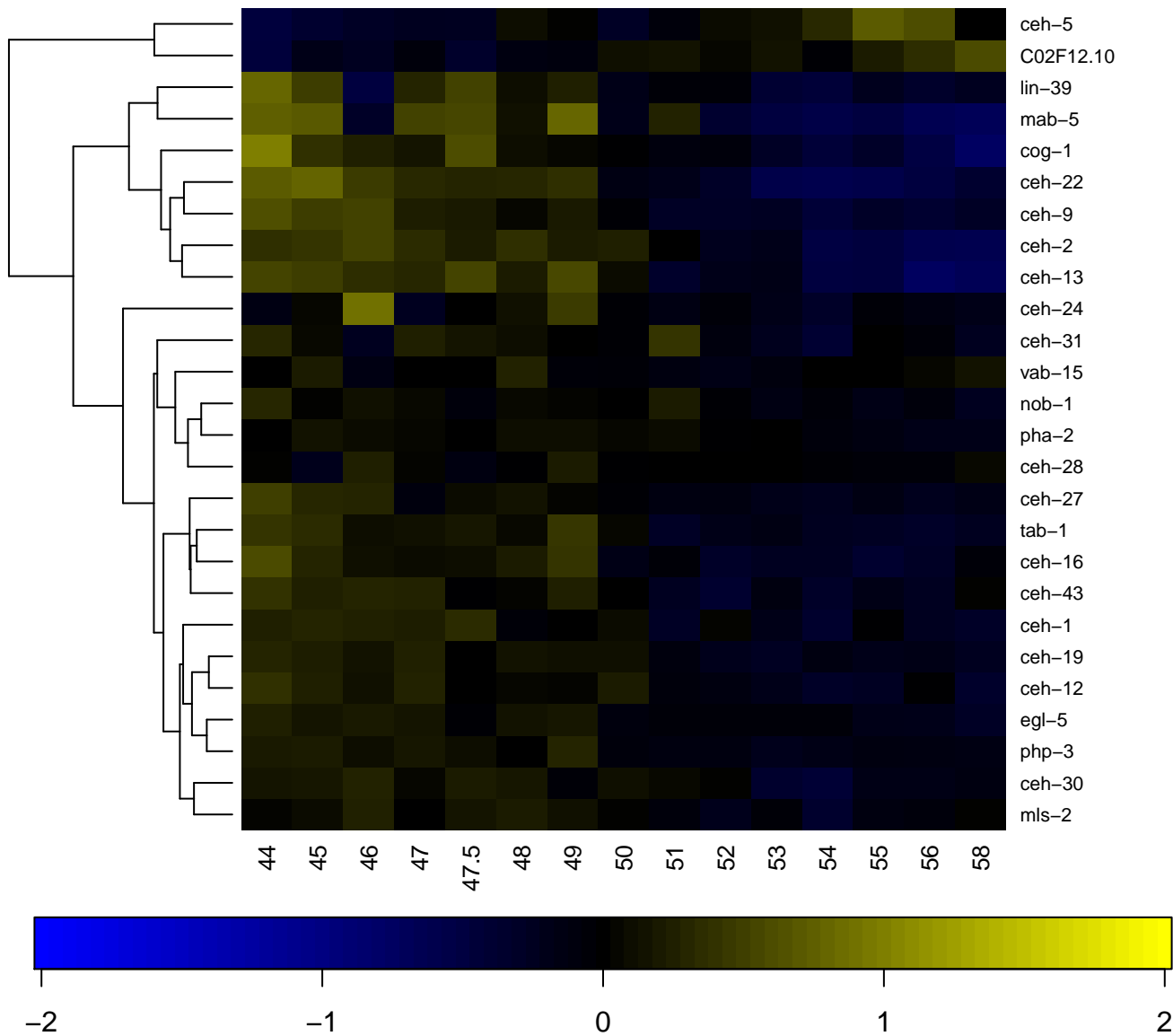
Homeobox domain



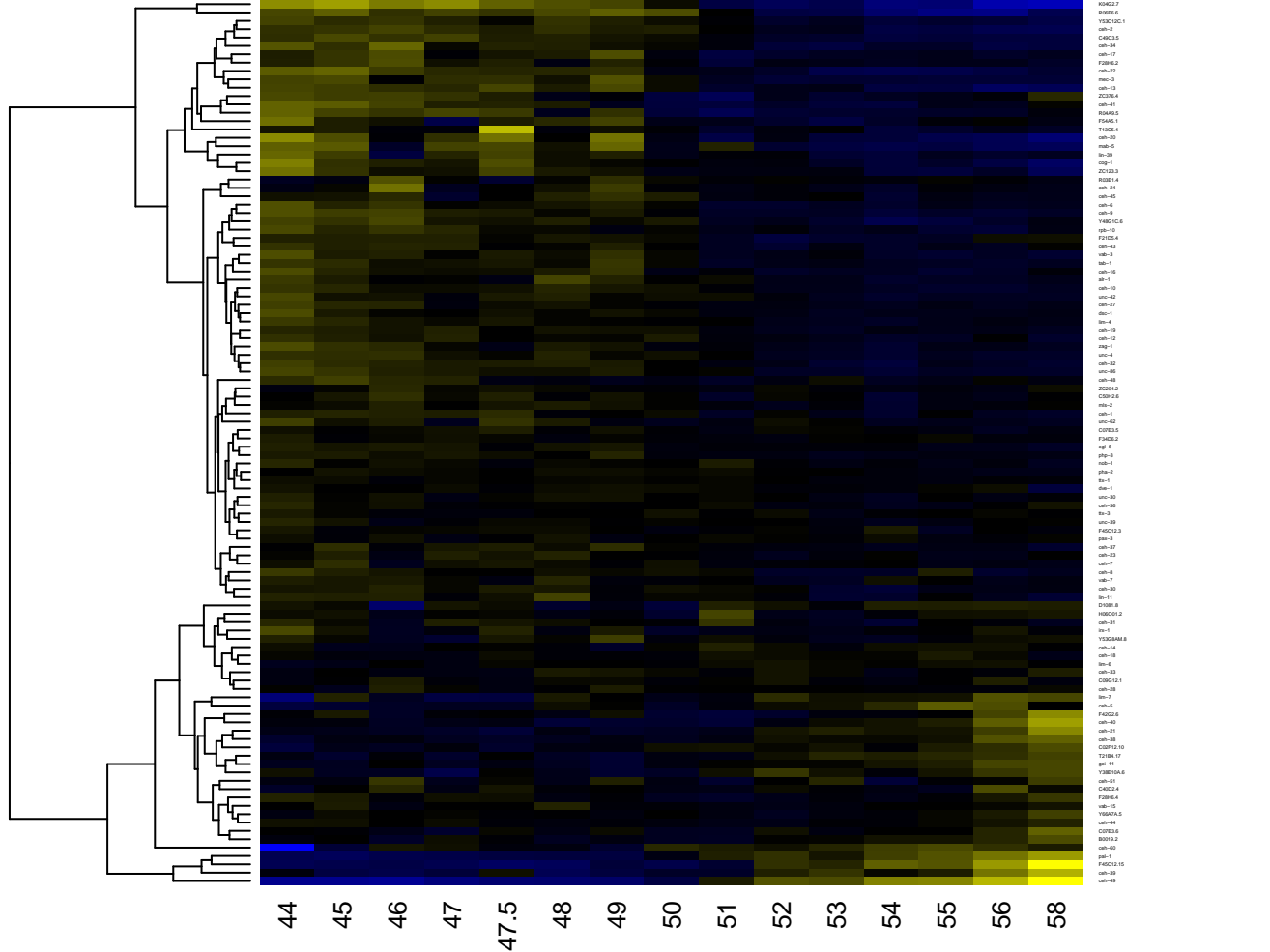
Homeobox, conserved site



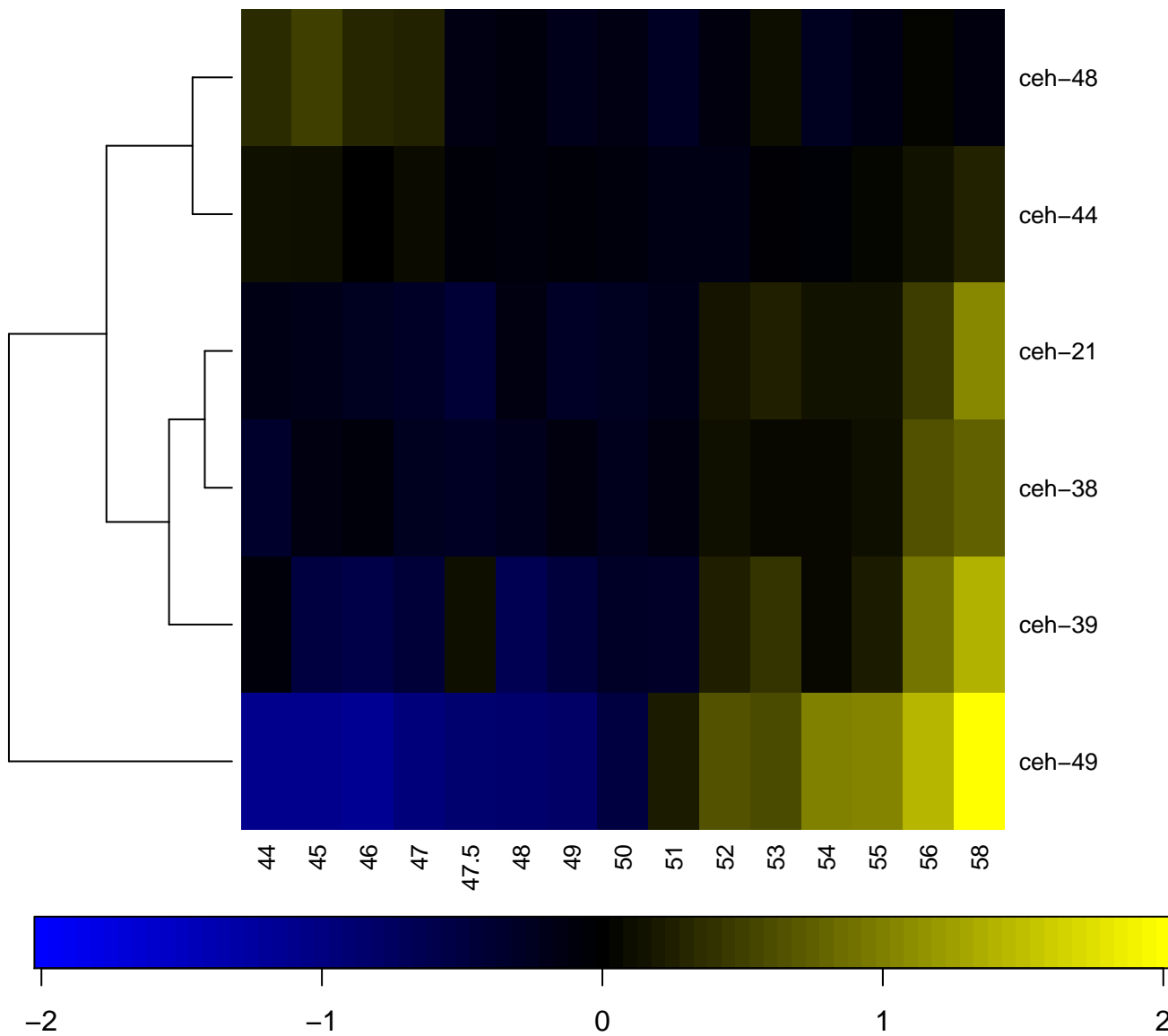
Homeobox, region



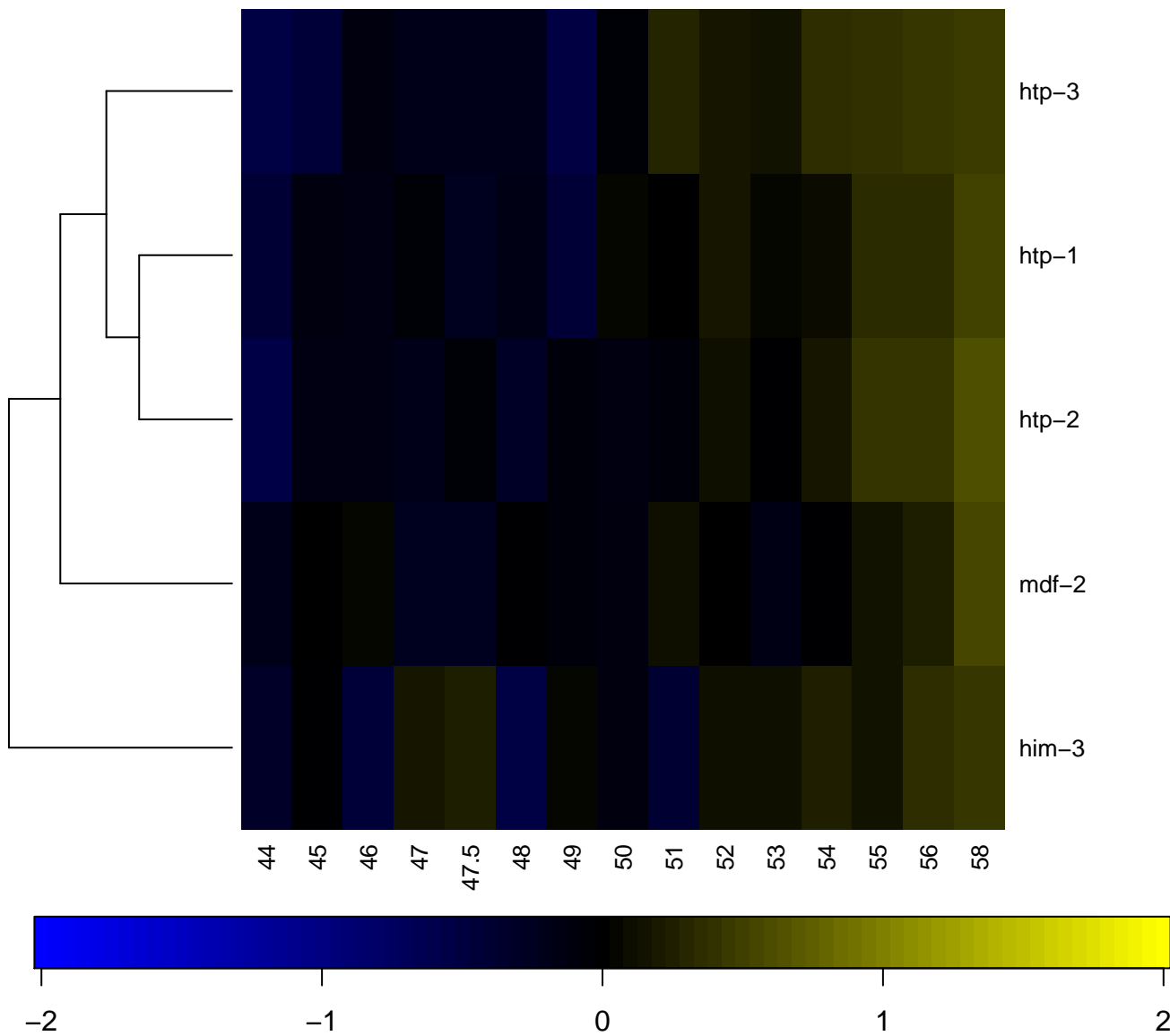
Homeodomain-related



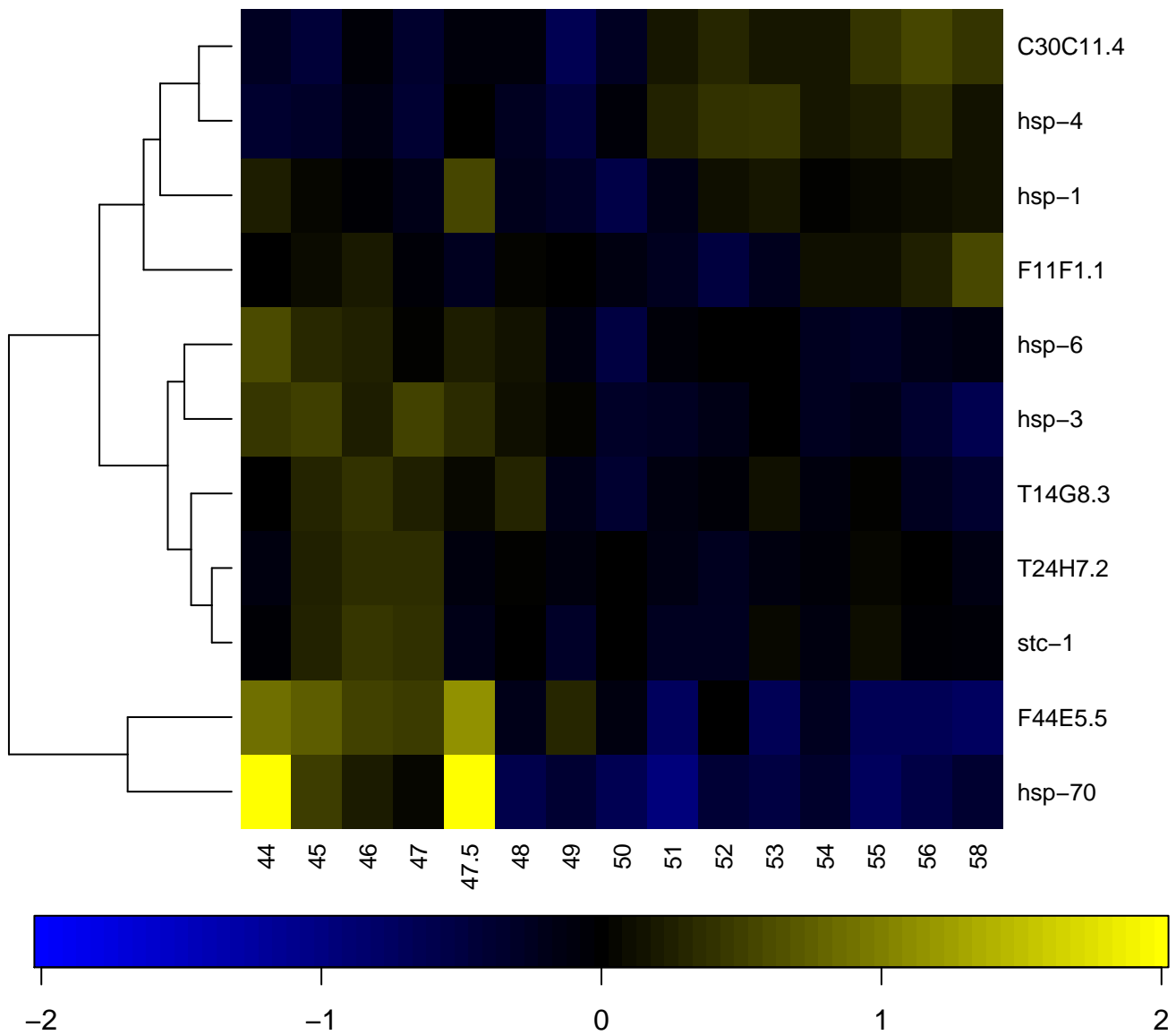
Homeodomain protein CUT



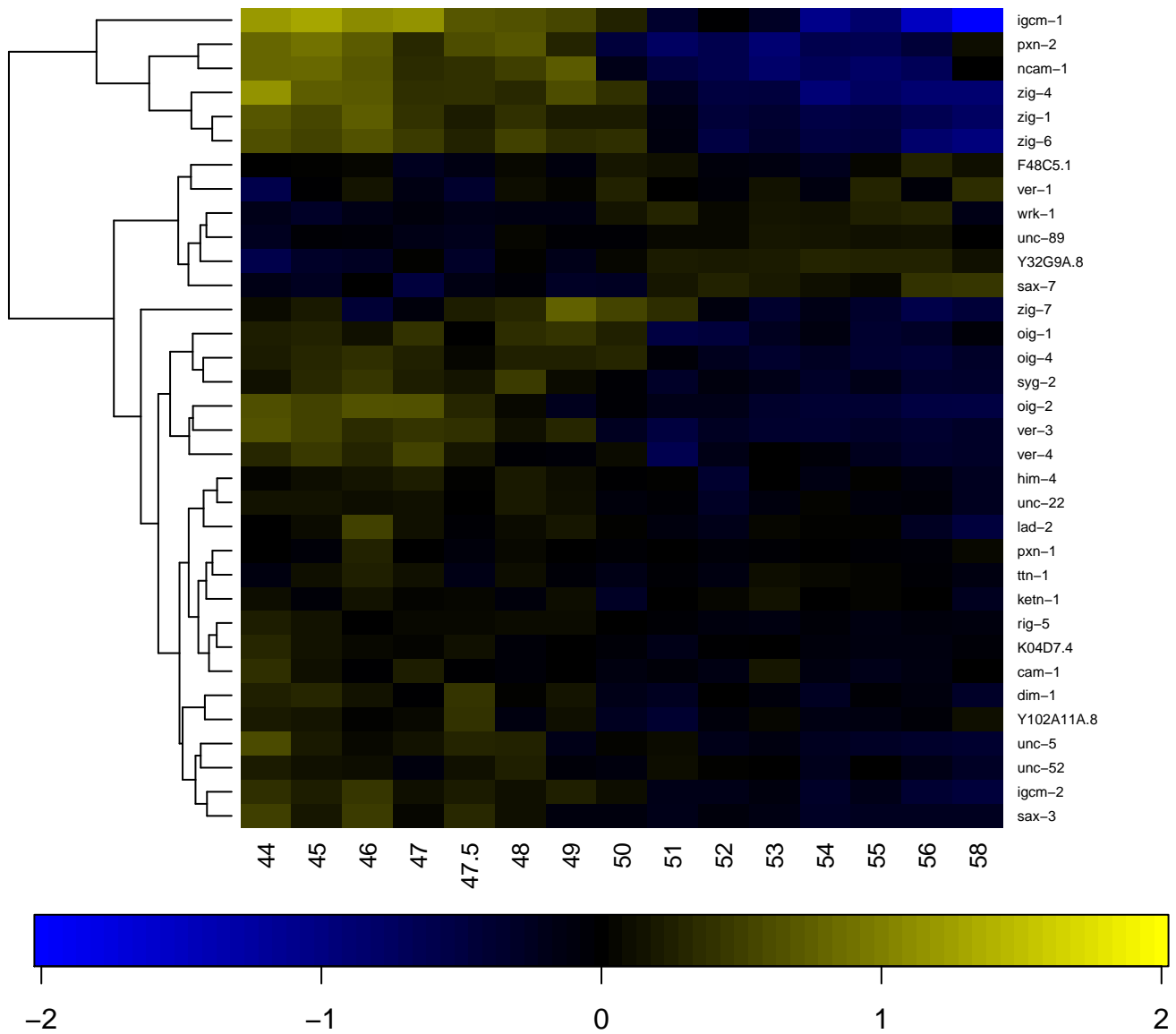
HORMA domain



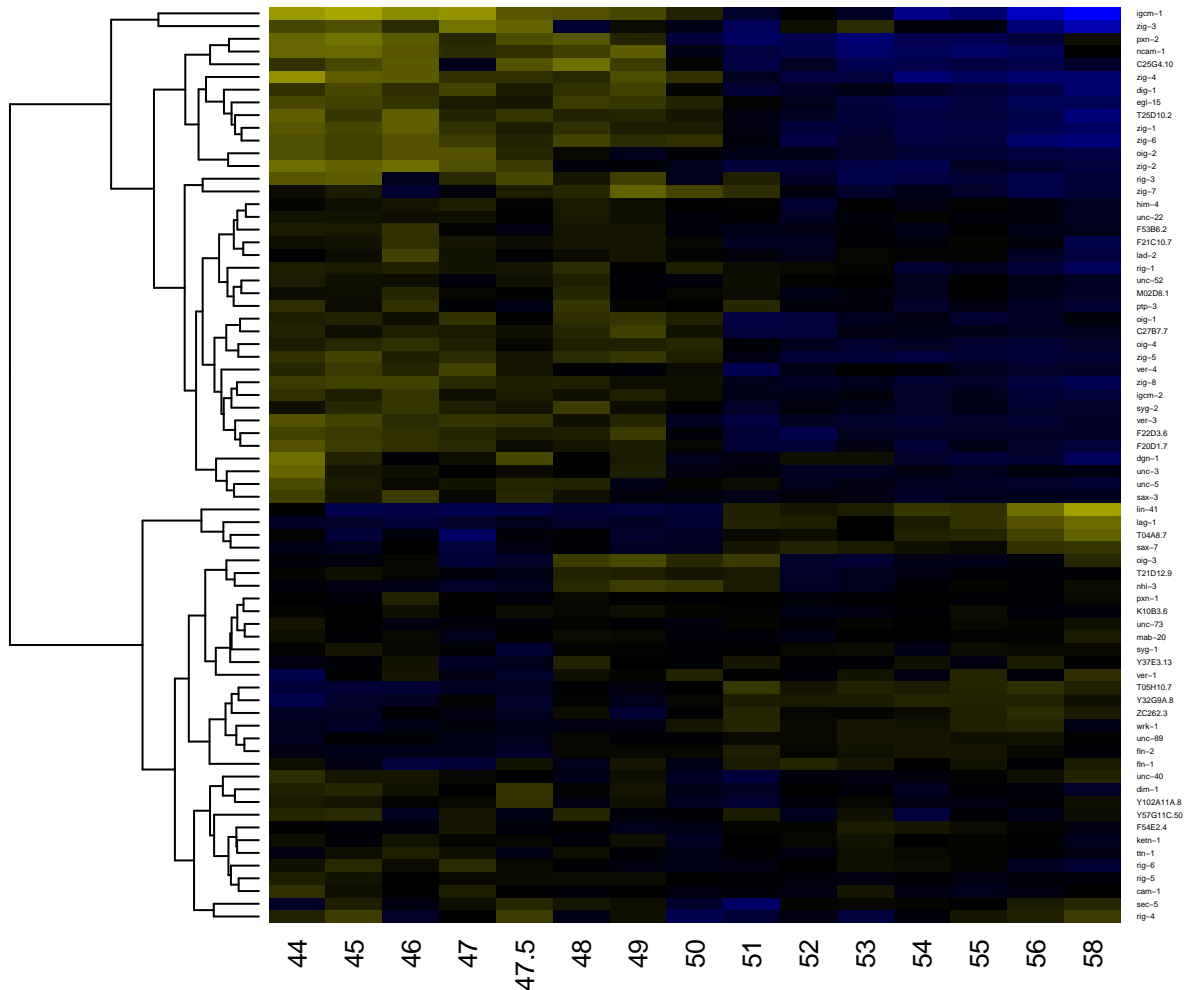
Hsp70 protein



Immunoglobulin



Immunoglobulin-like fold



-2

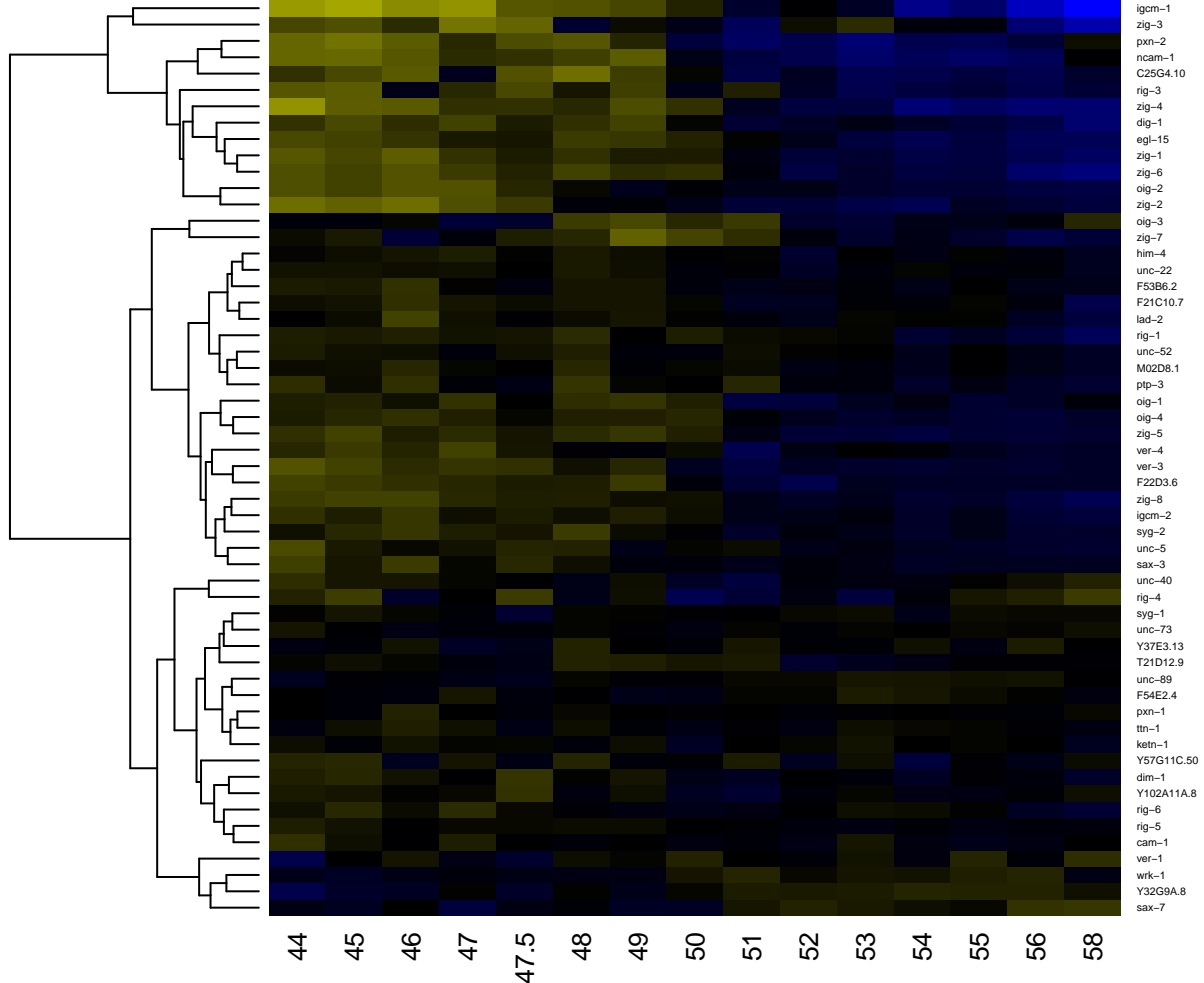
-1

0

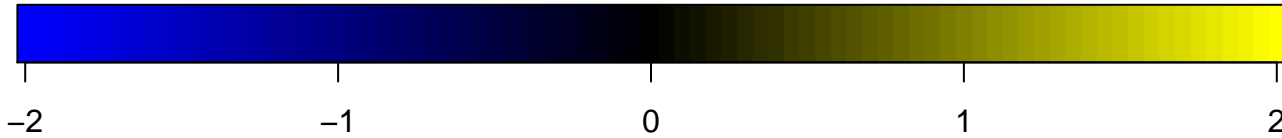
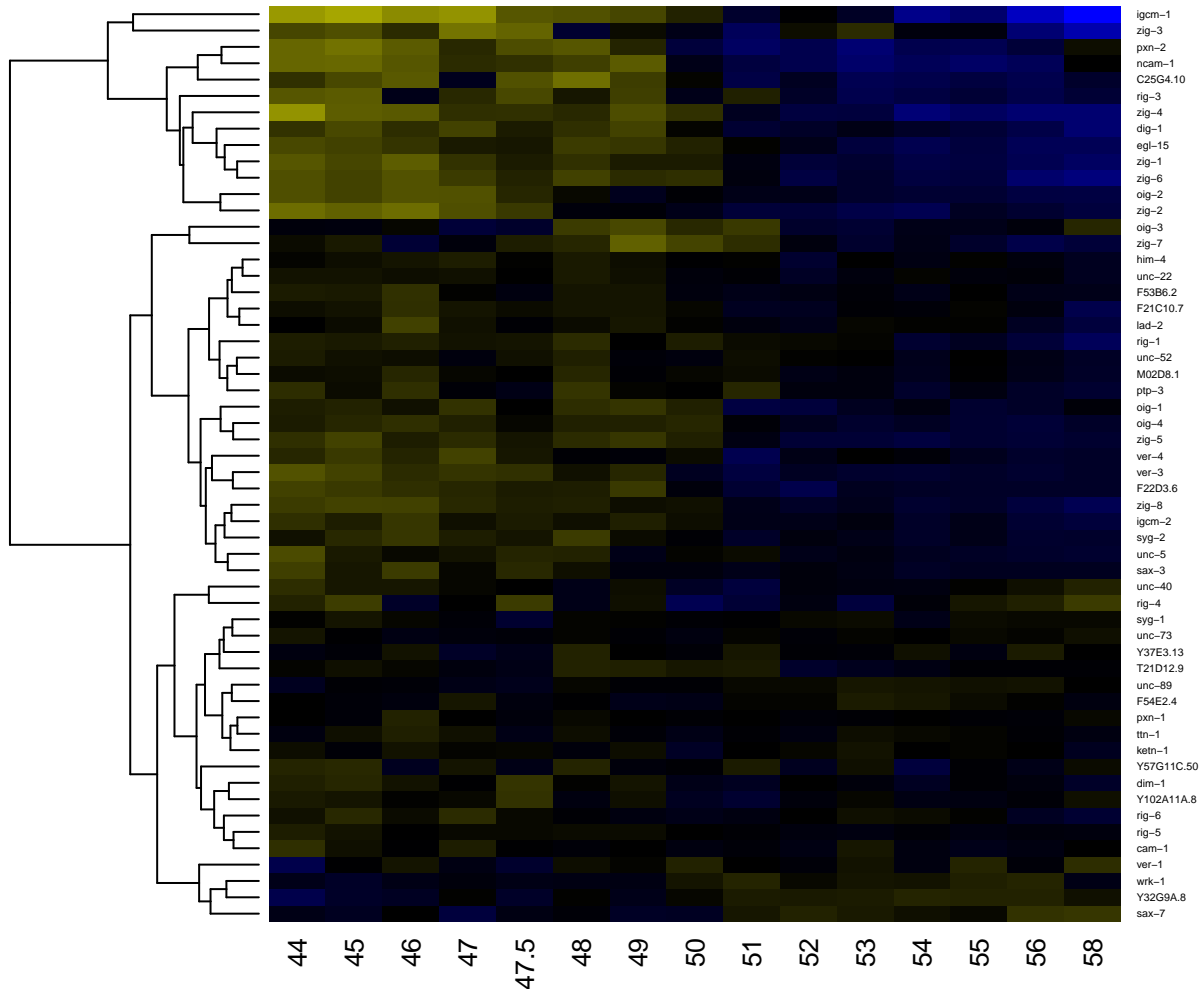
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2

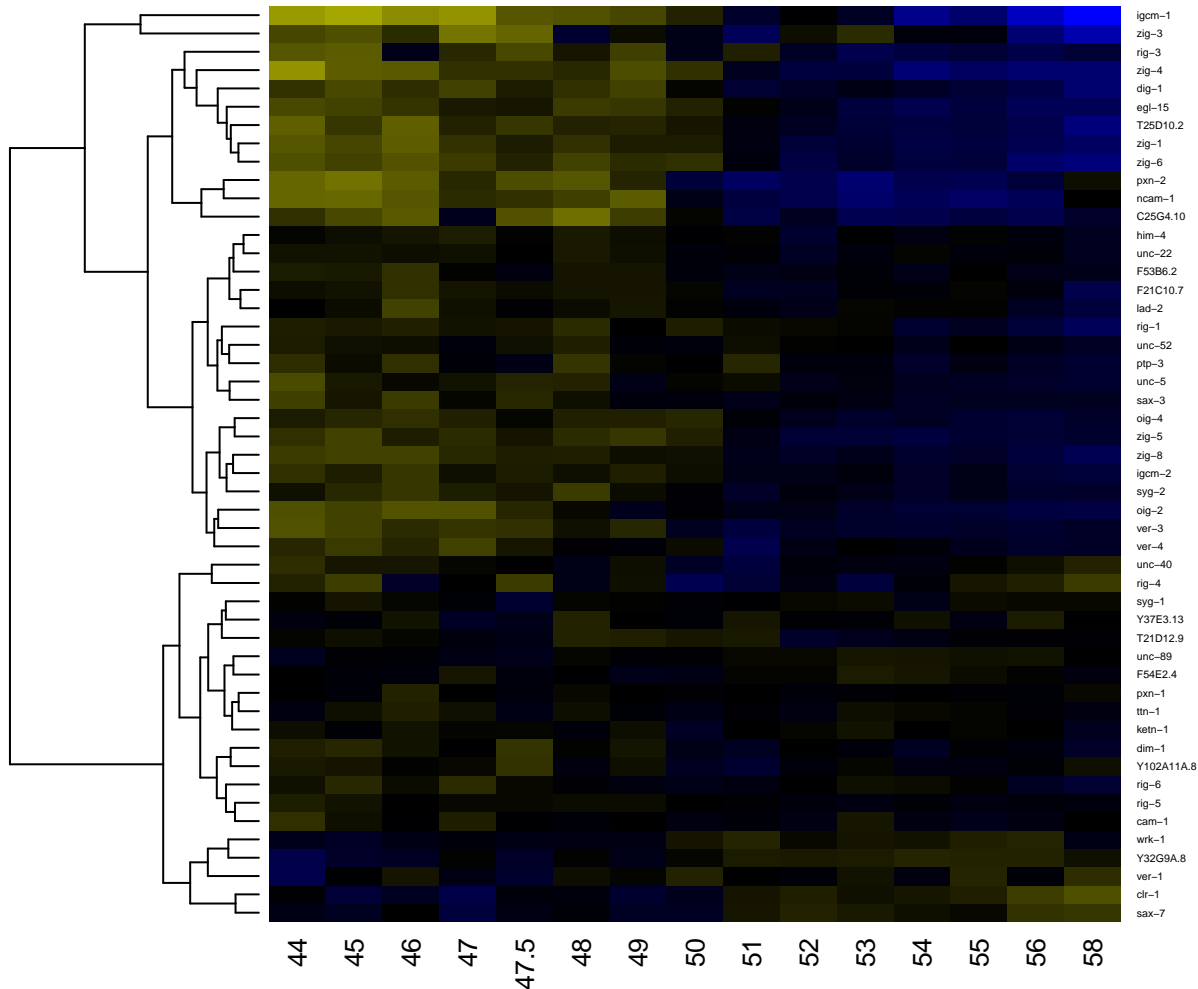
Immunoglobulin I-set



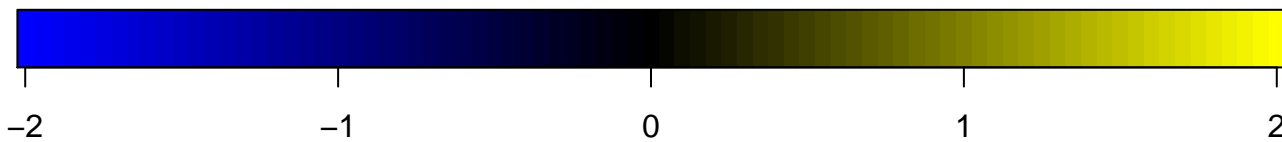
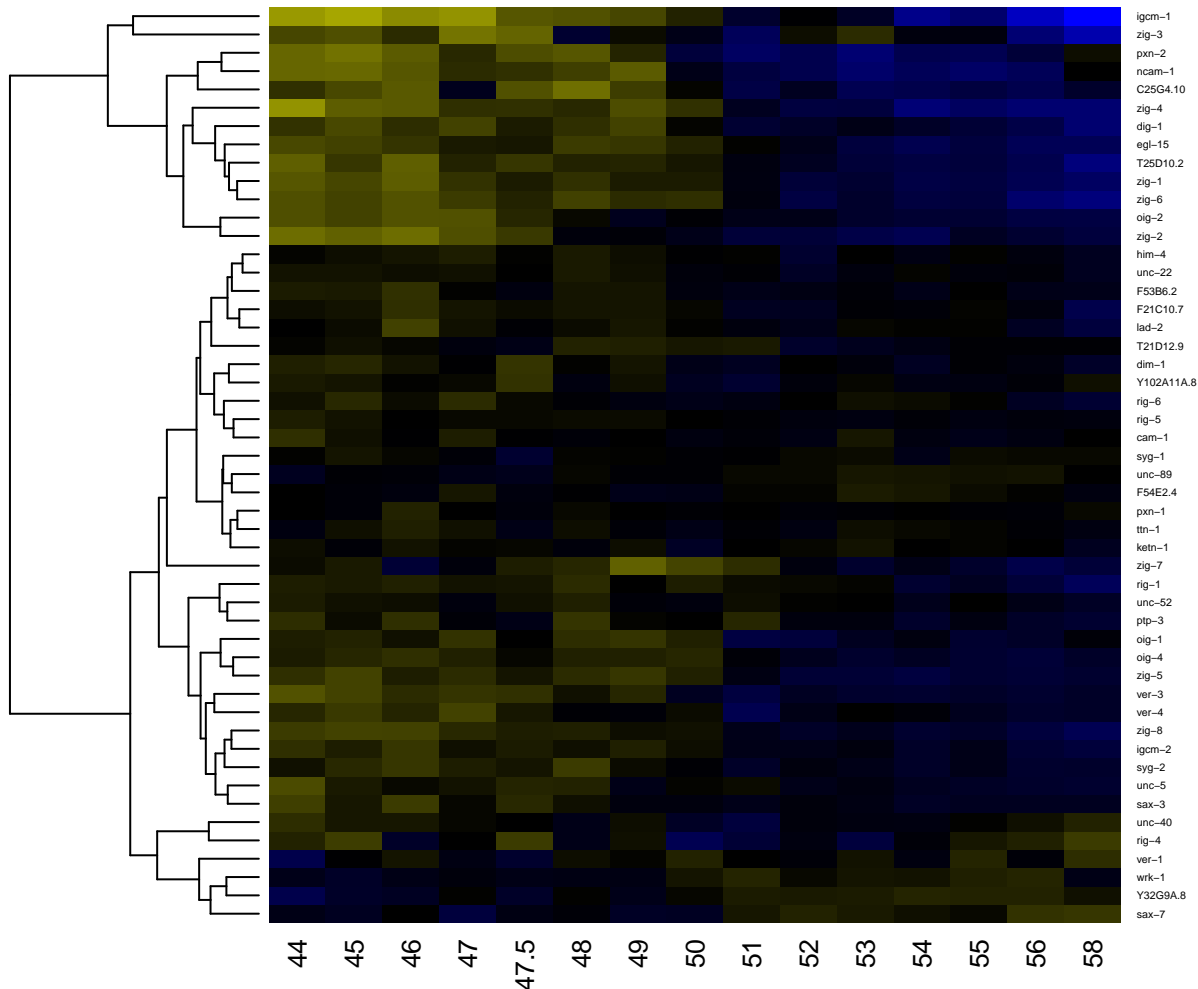
Immunoglobulin I-set domain



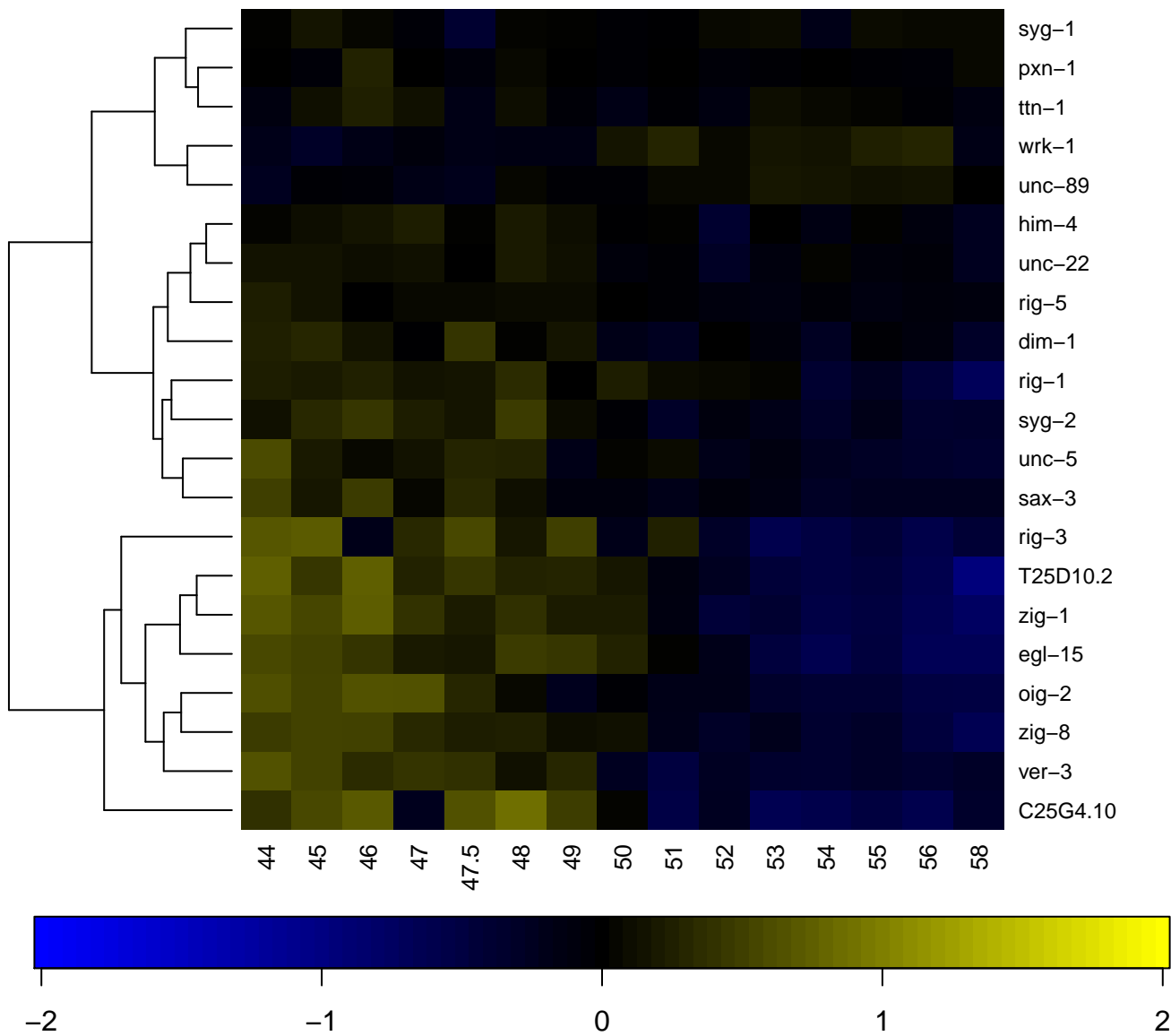
Immunoglobulin subtype



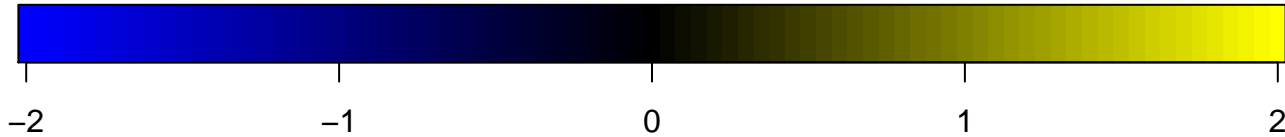
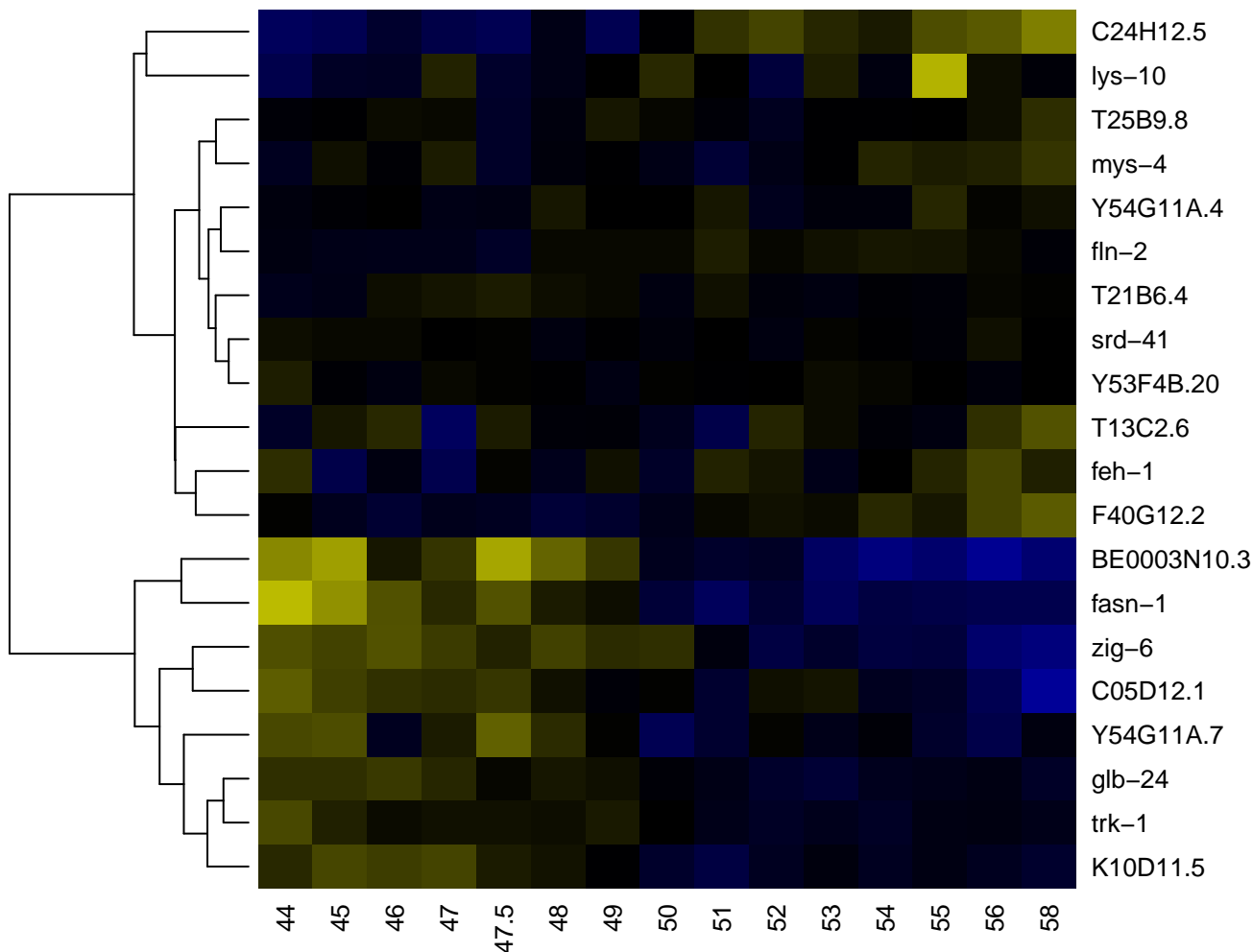
Immunoglobulin subtype 2



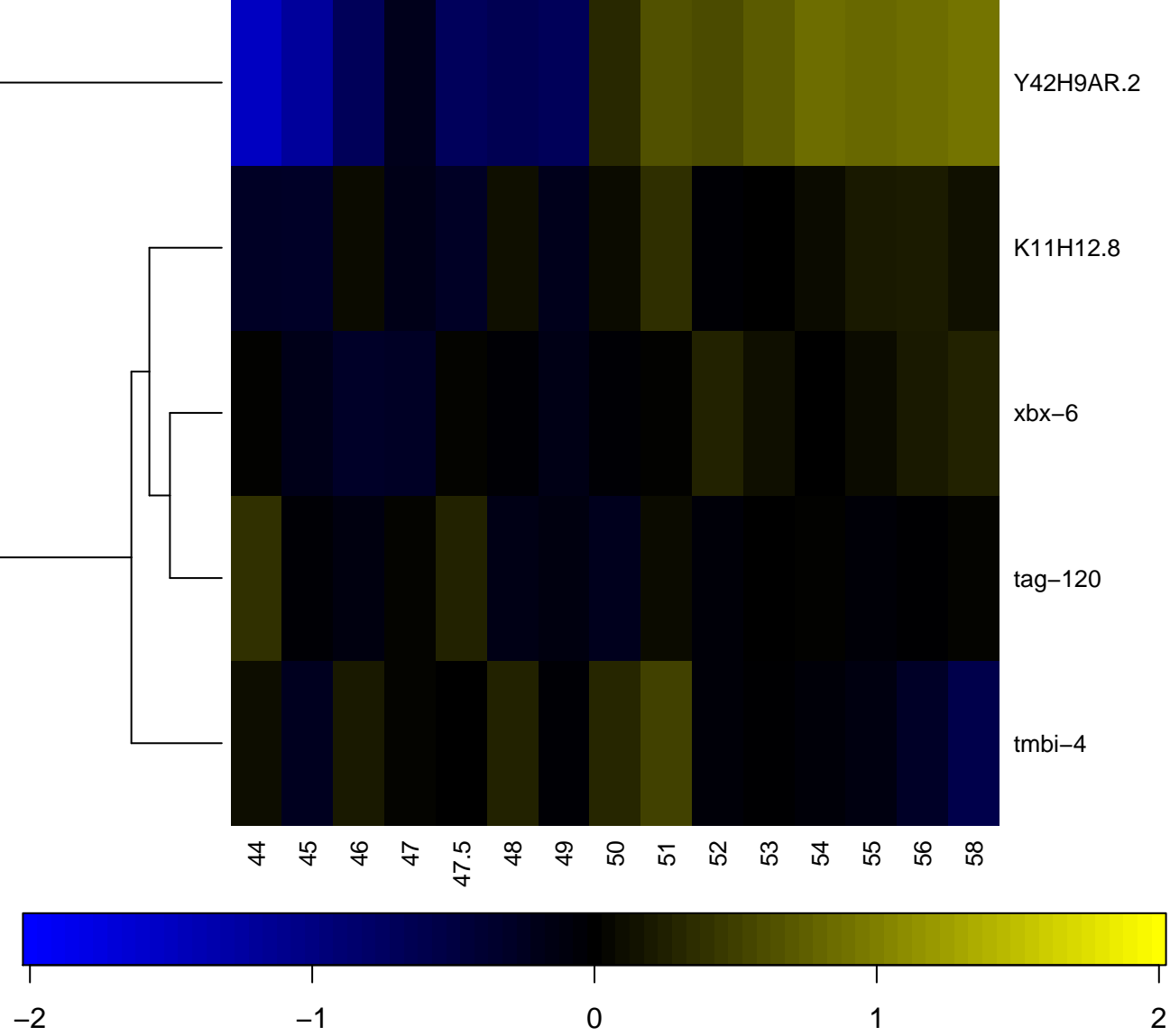
Immunoglobulin V-set



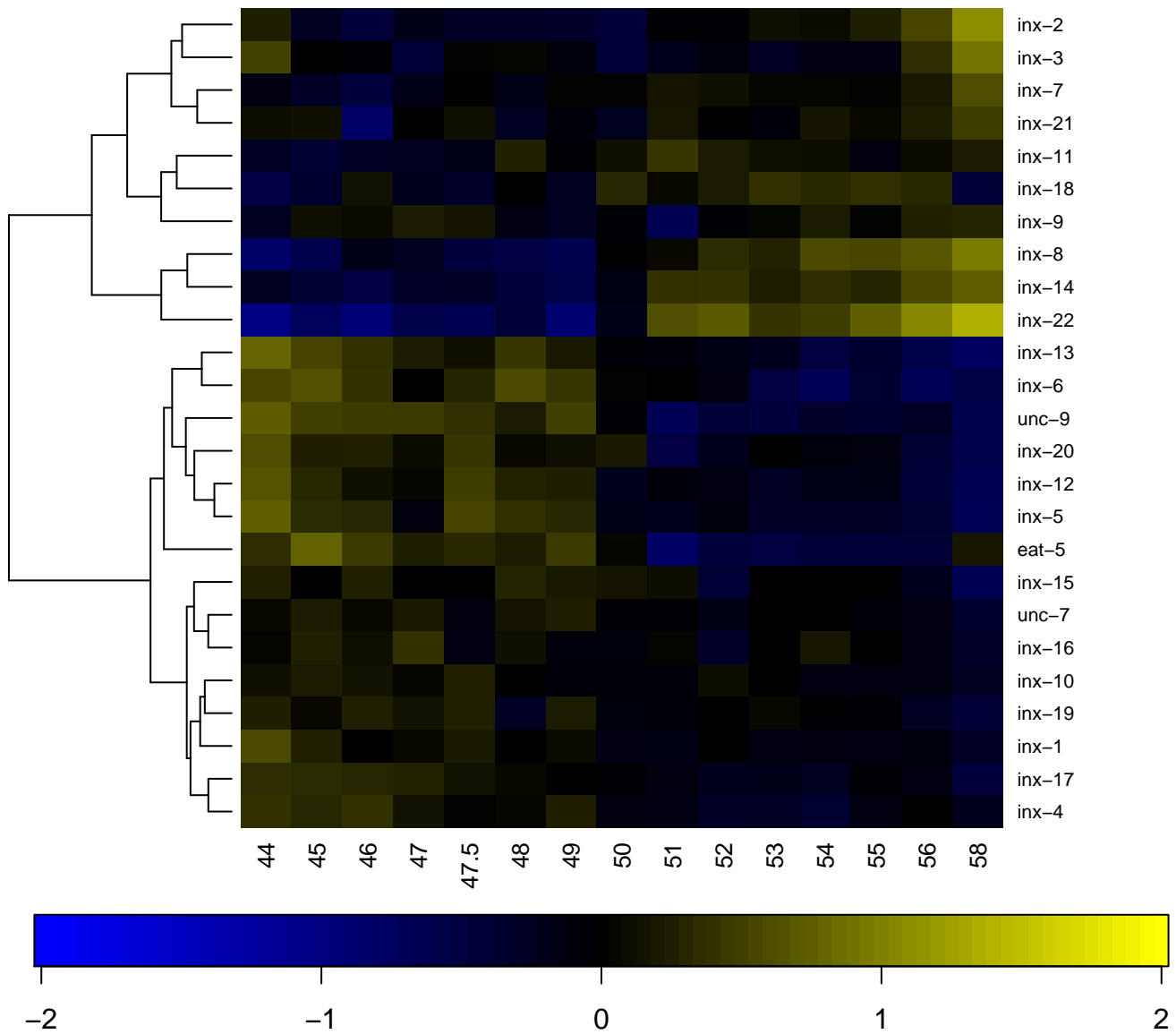
immunoglobulin/major histocompatibility complex, conserved



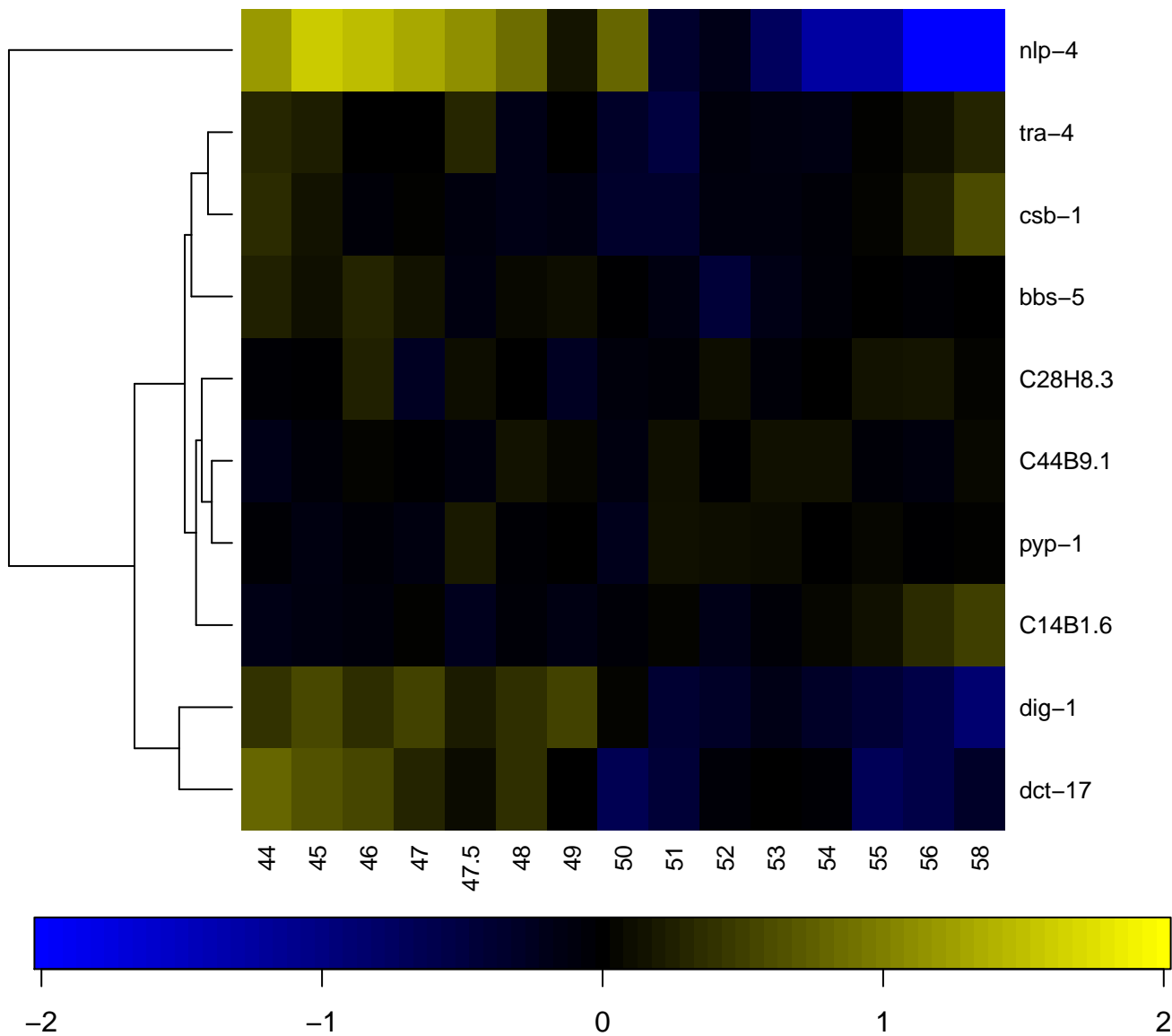
Inhibitor of apoptosis-promoting Bax1 related



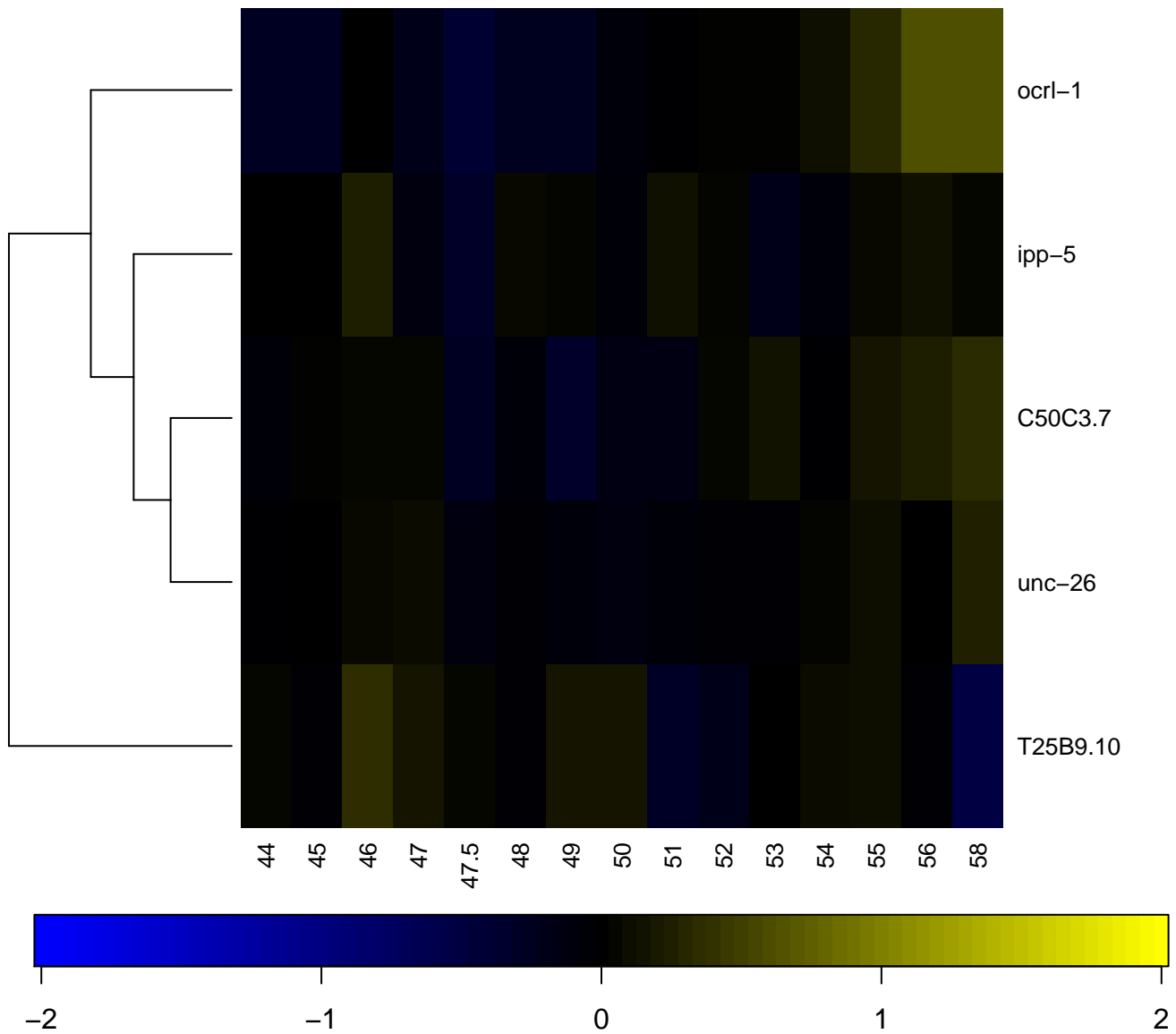
Innexin



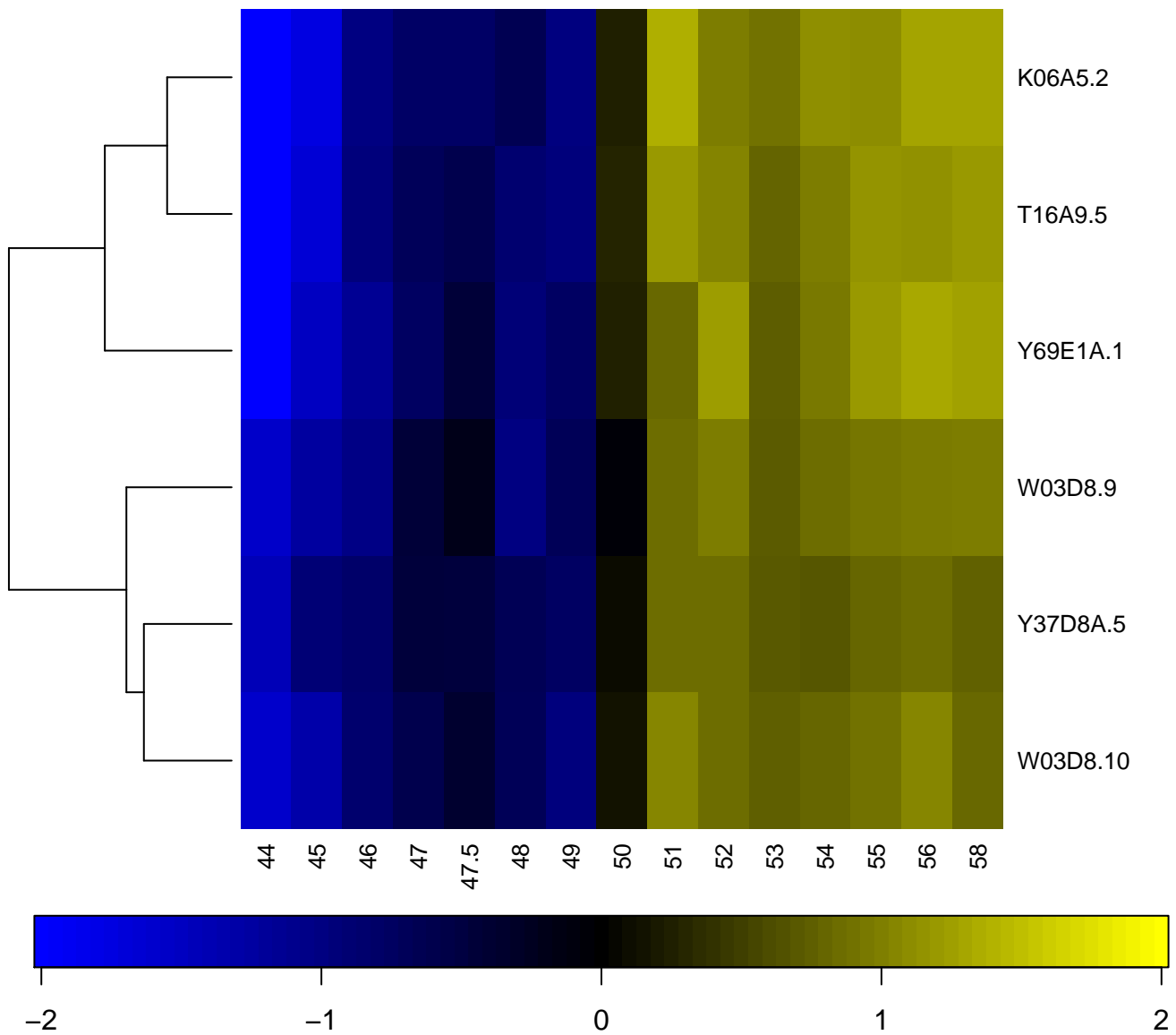
Inorganic pyrophosphatase



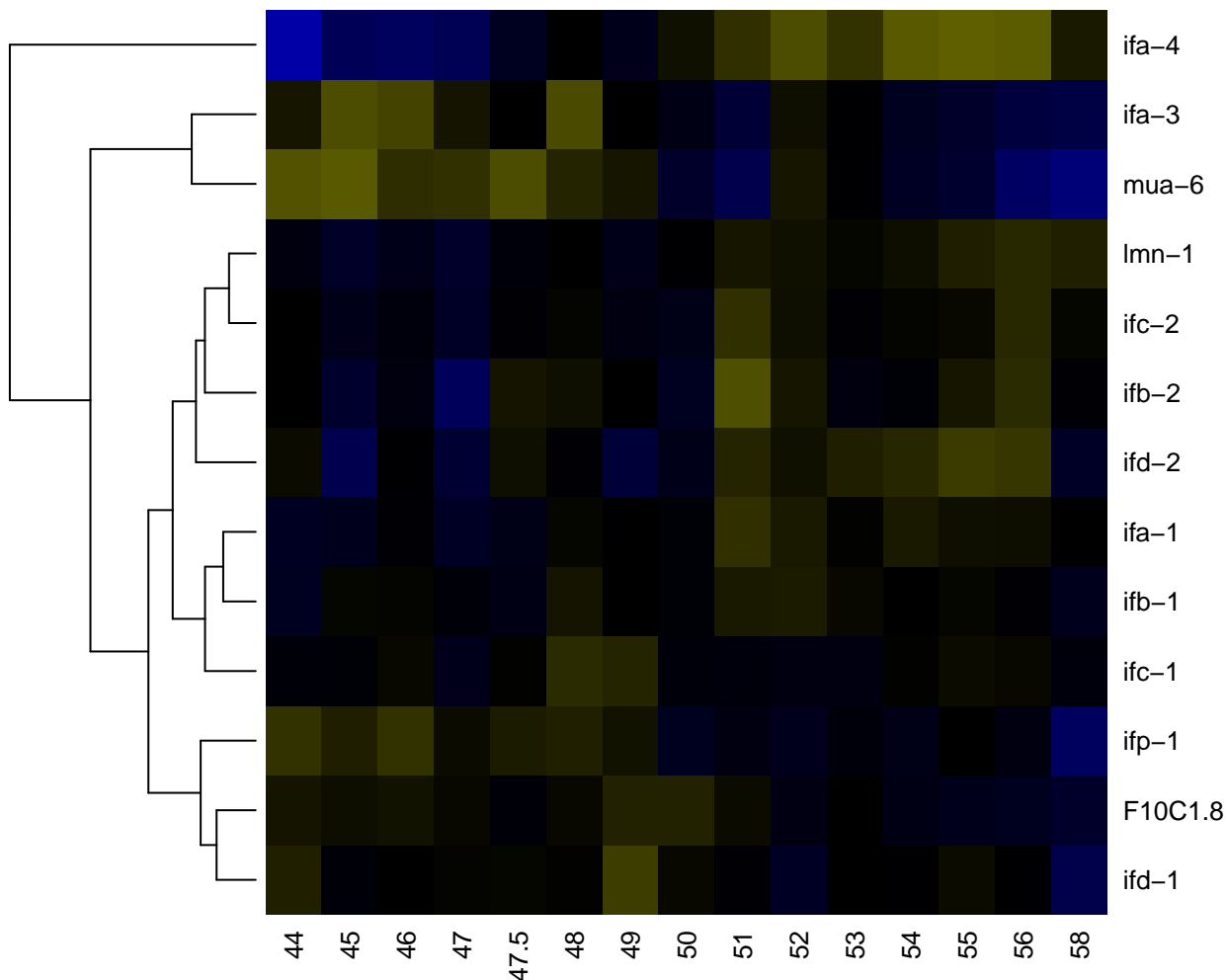
Inositol polyphosphate related phosphatase



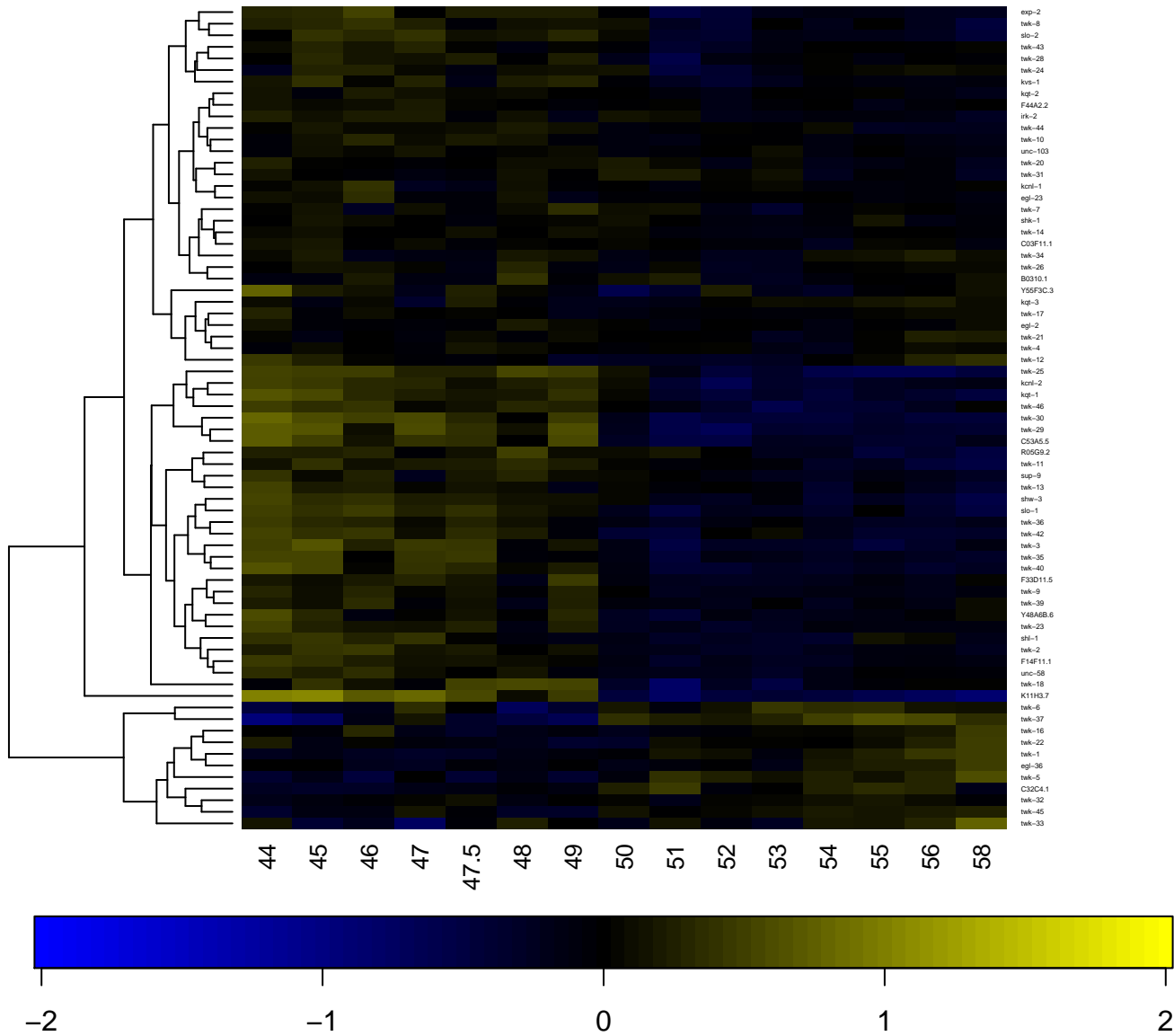
Interactor of ZYG-11



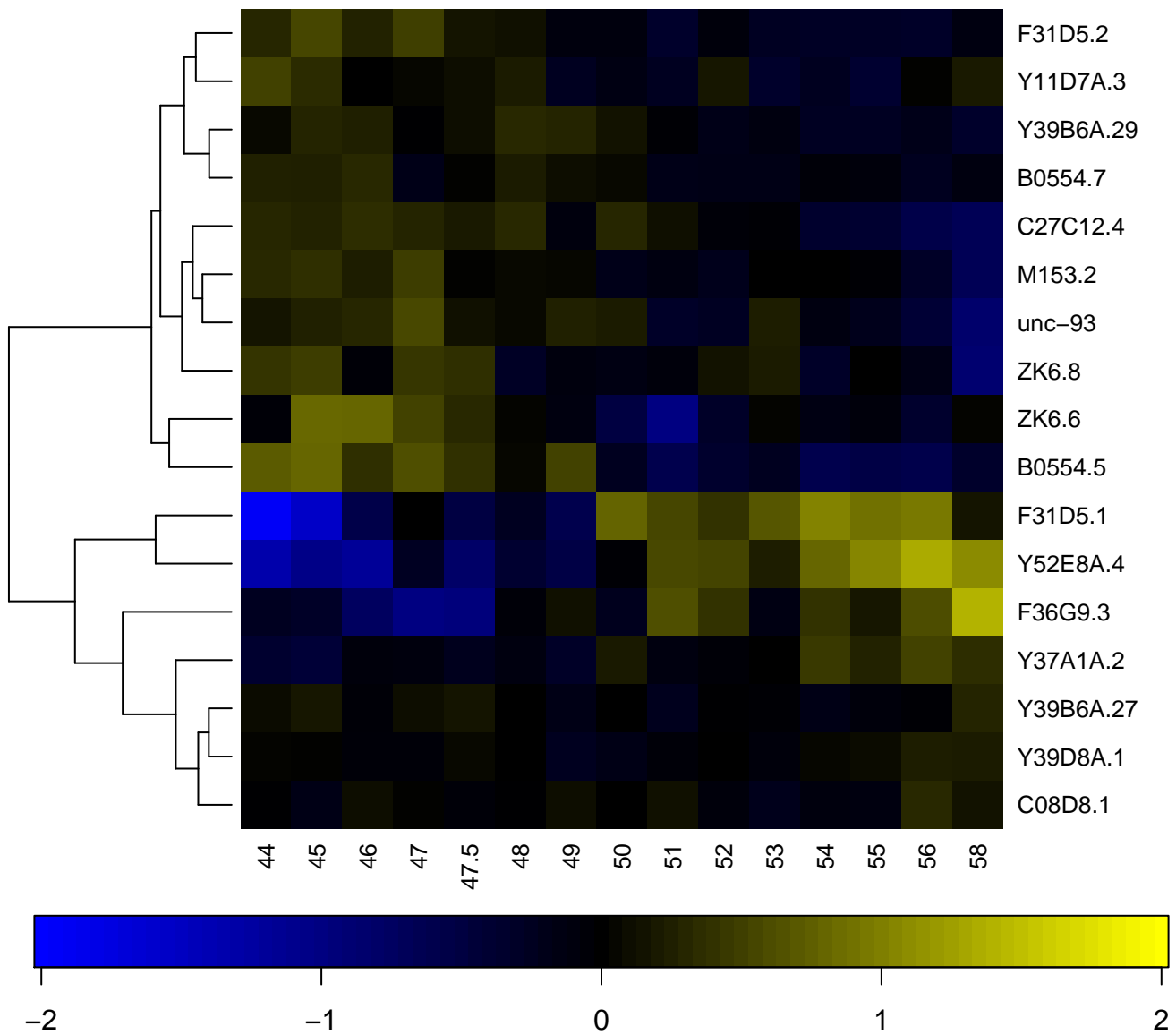
Intermediate filament protein



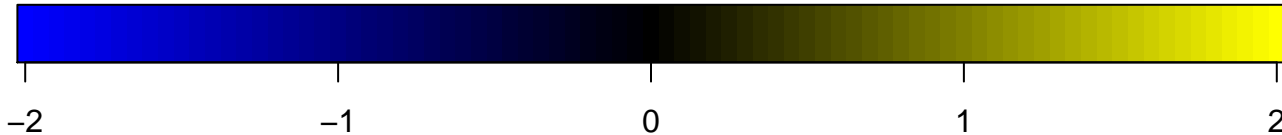
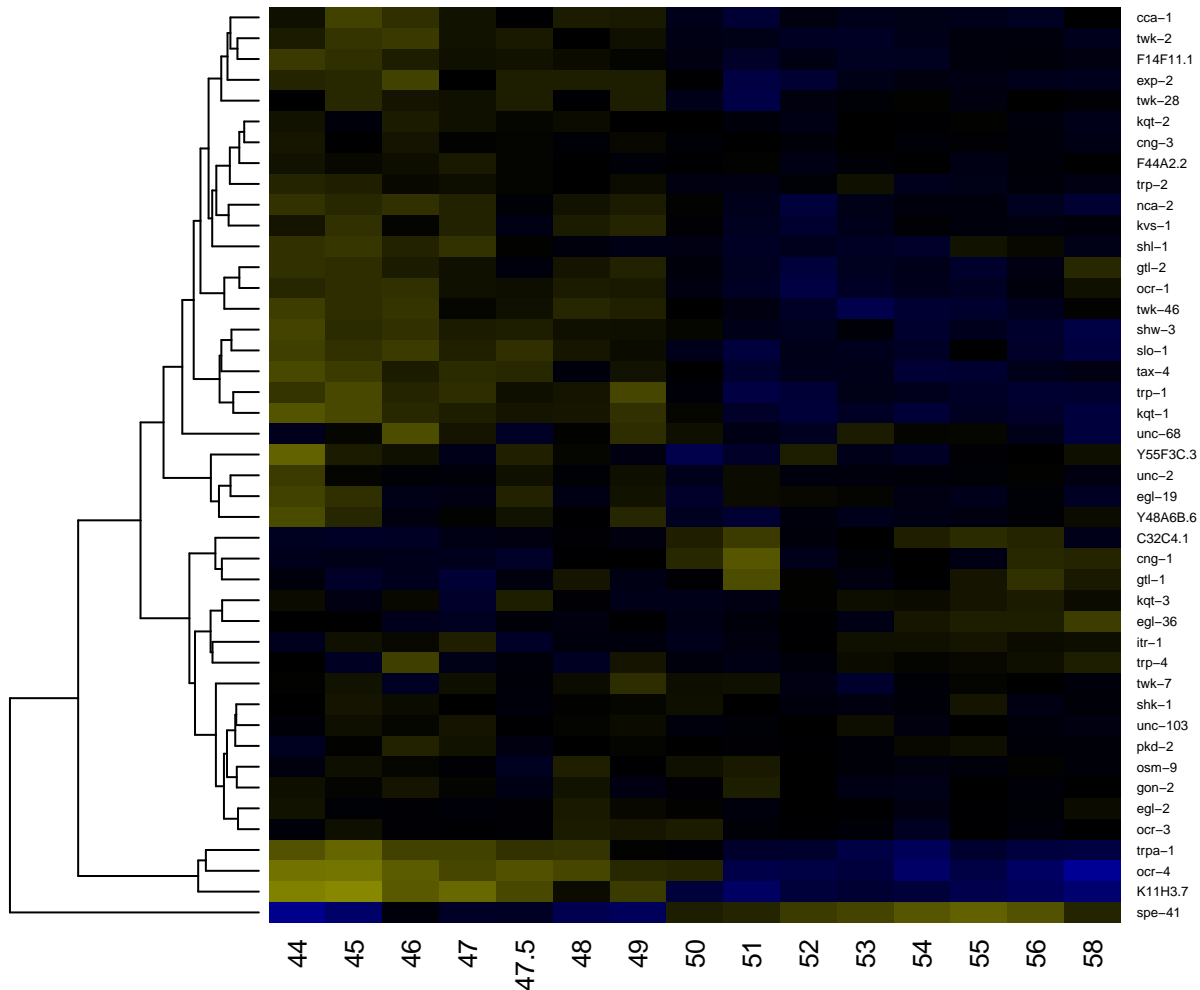
Ion channel



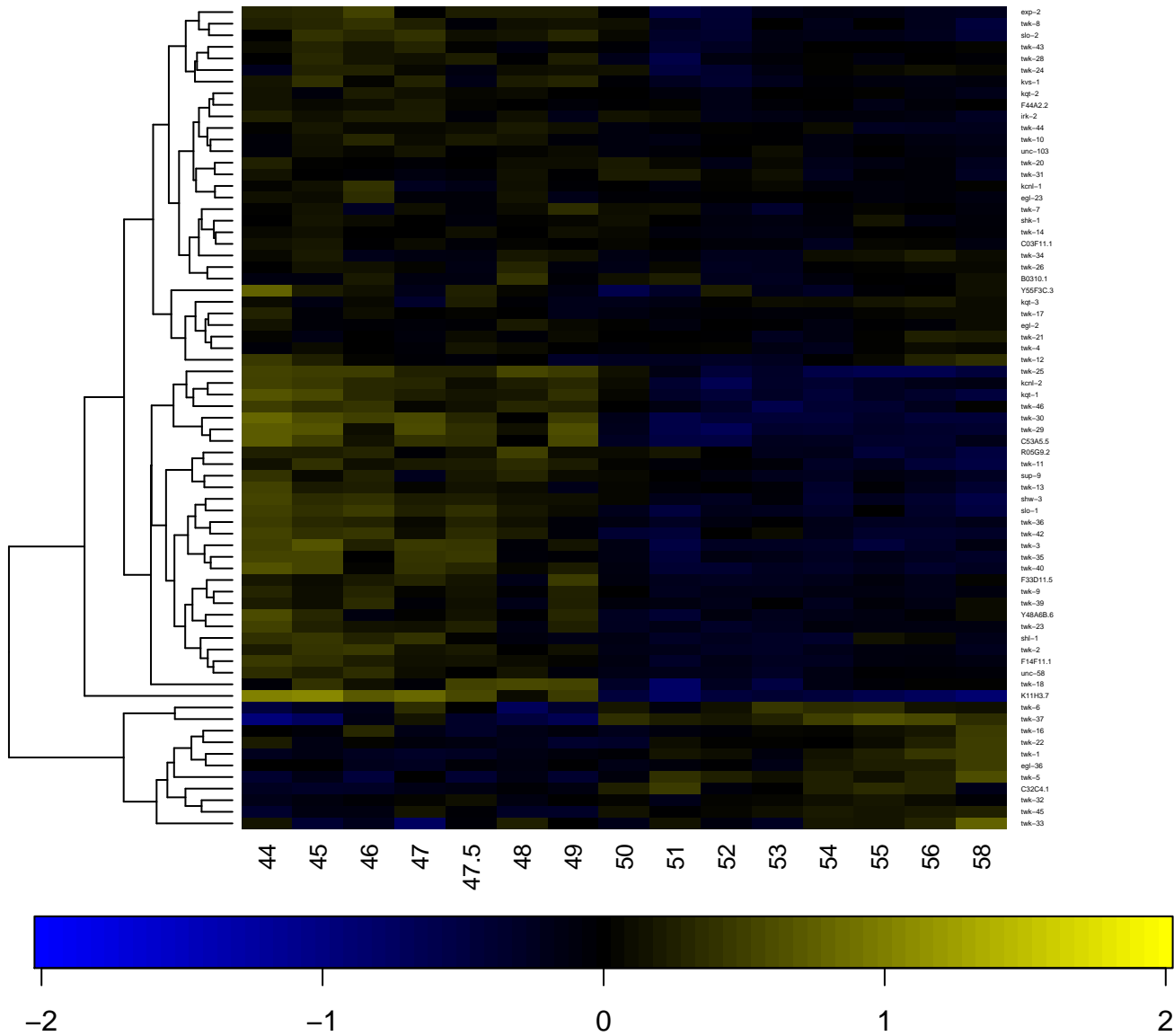
Ion channel regulatory protein, UNC-93



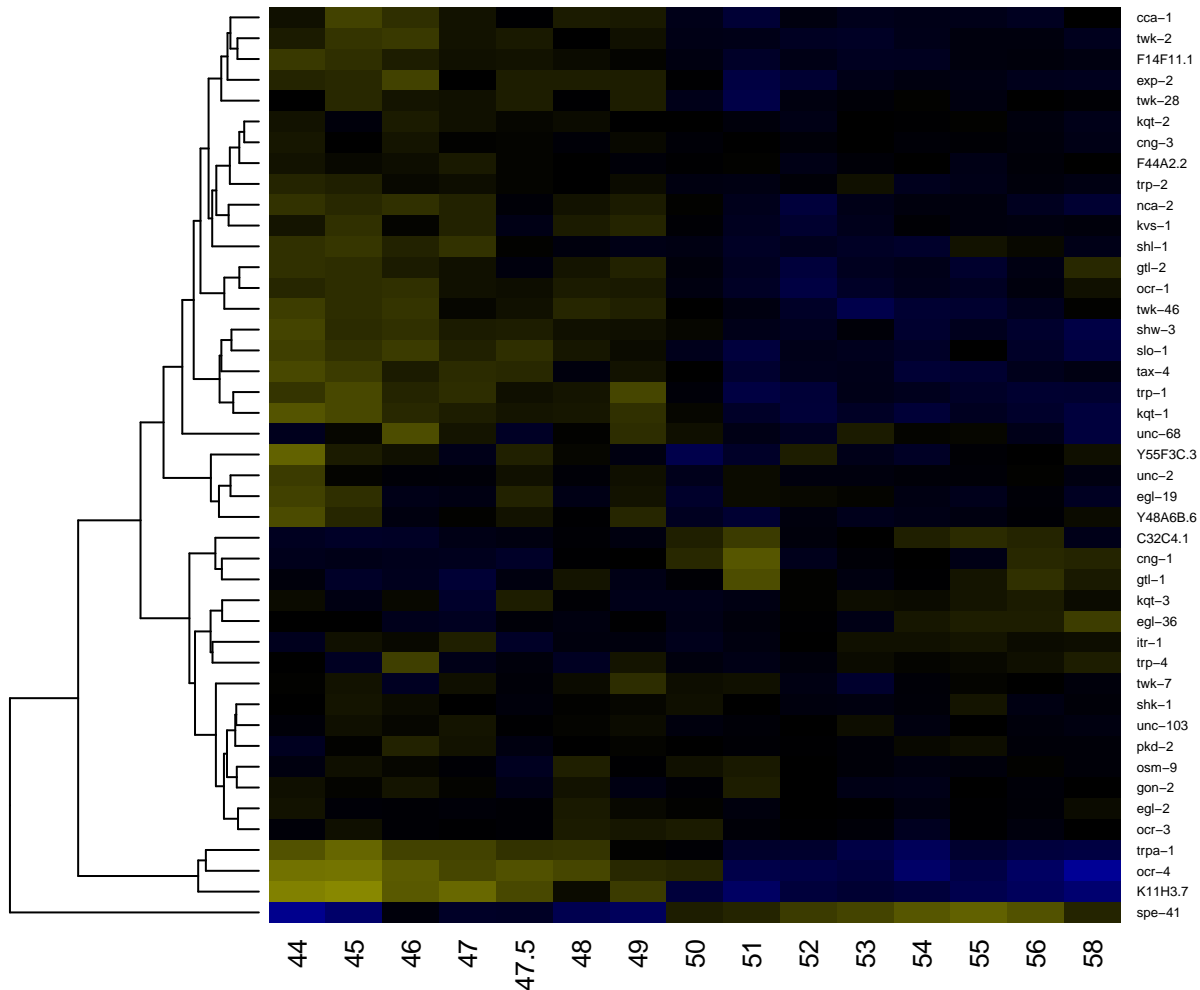
Ion transport



Ion transport 2



Ion transport protein



-2

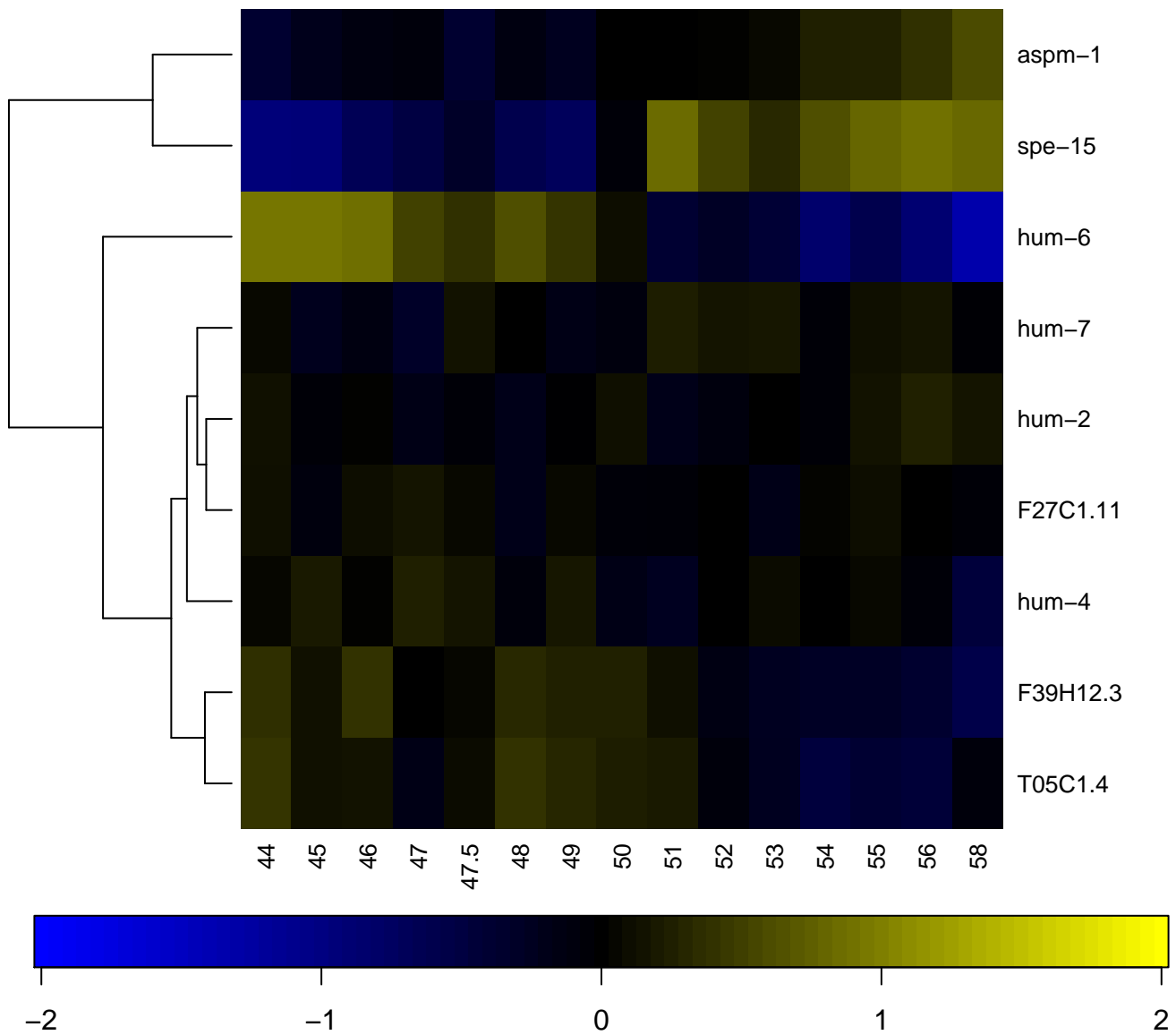
-1

0

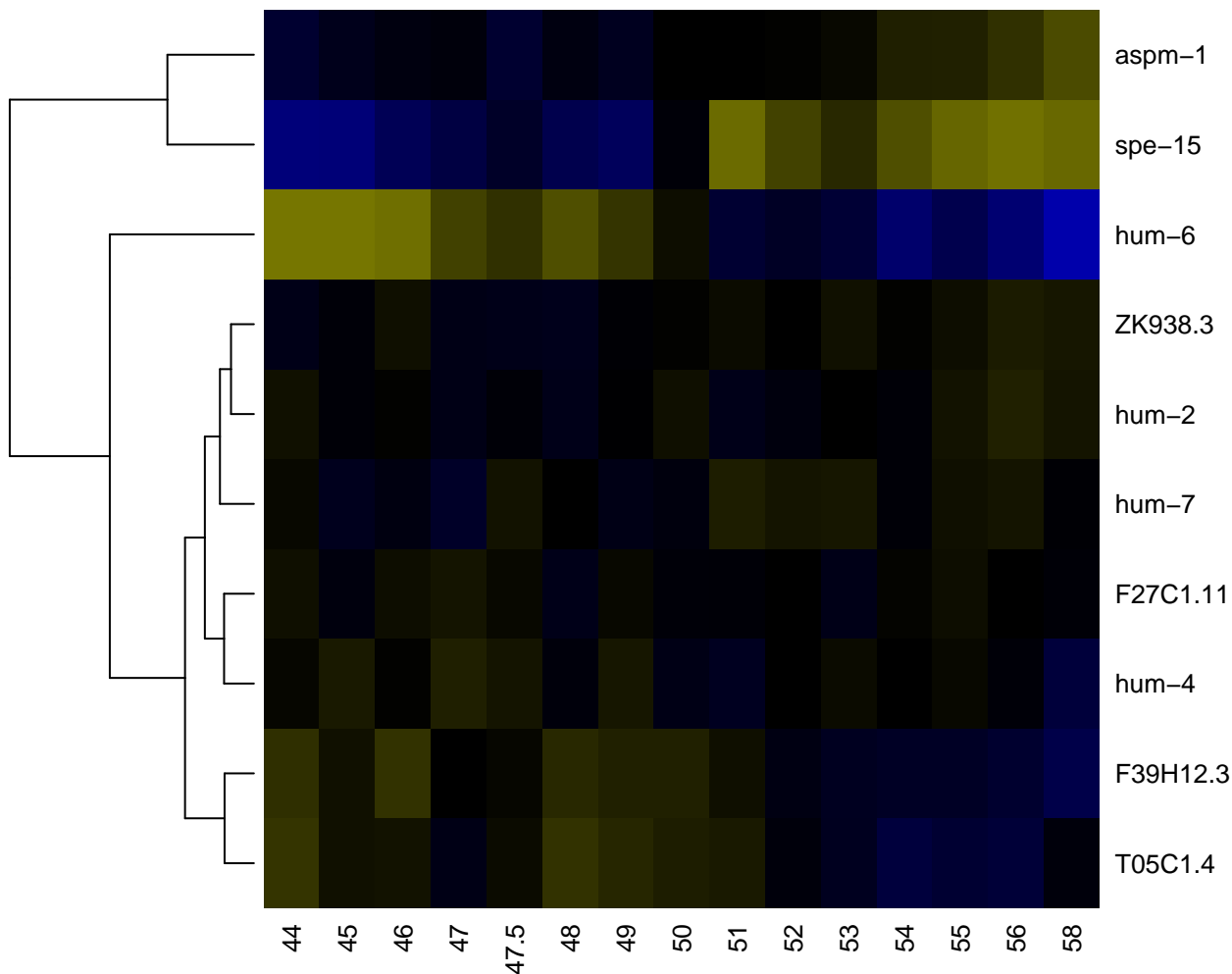
1

2

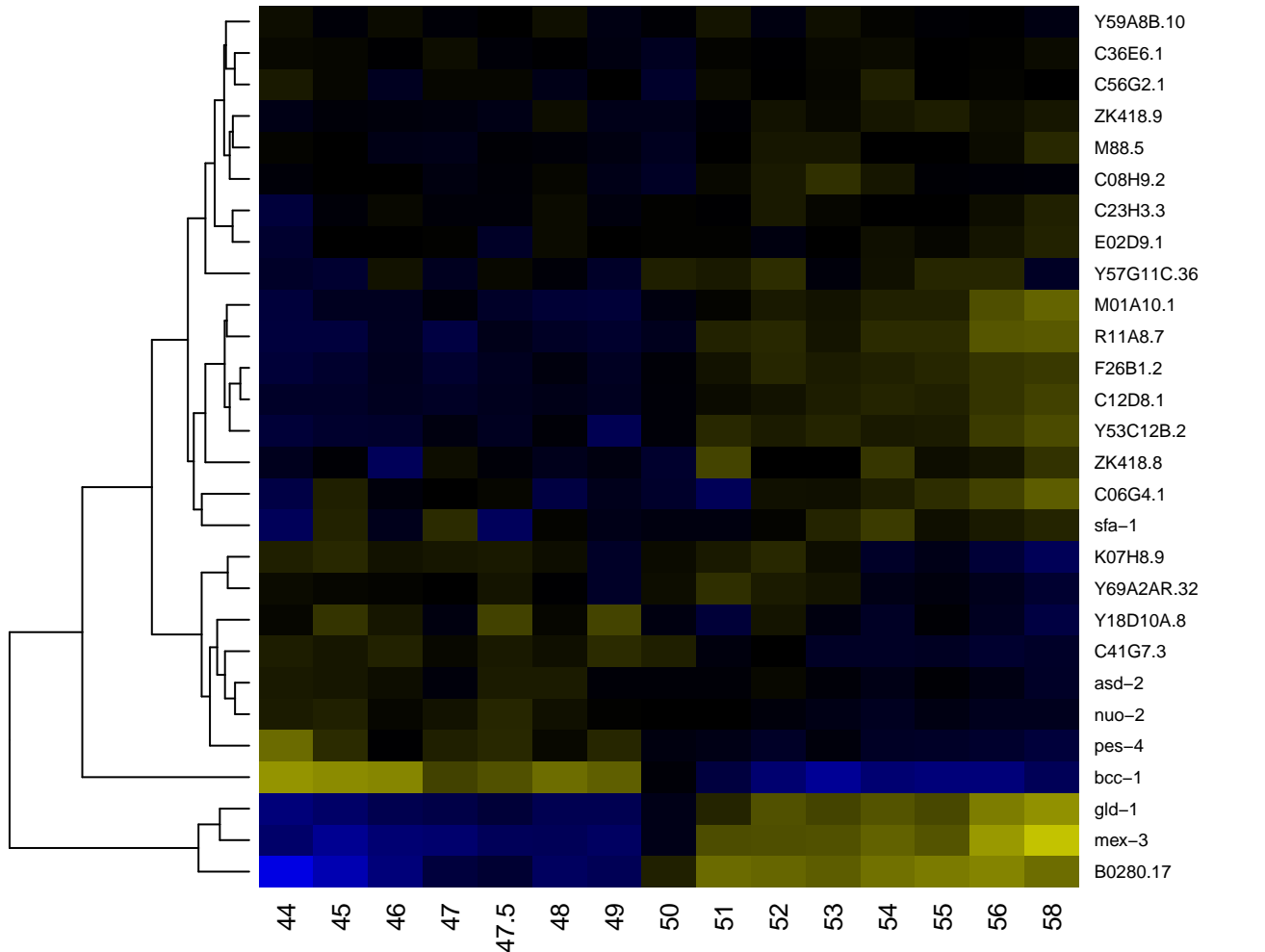
IQ calmodulin-binding motif



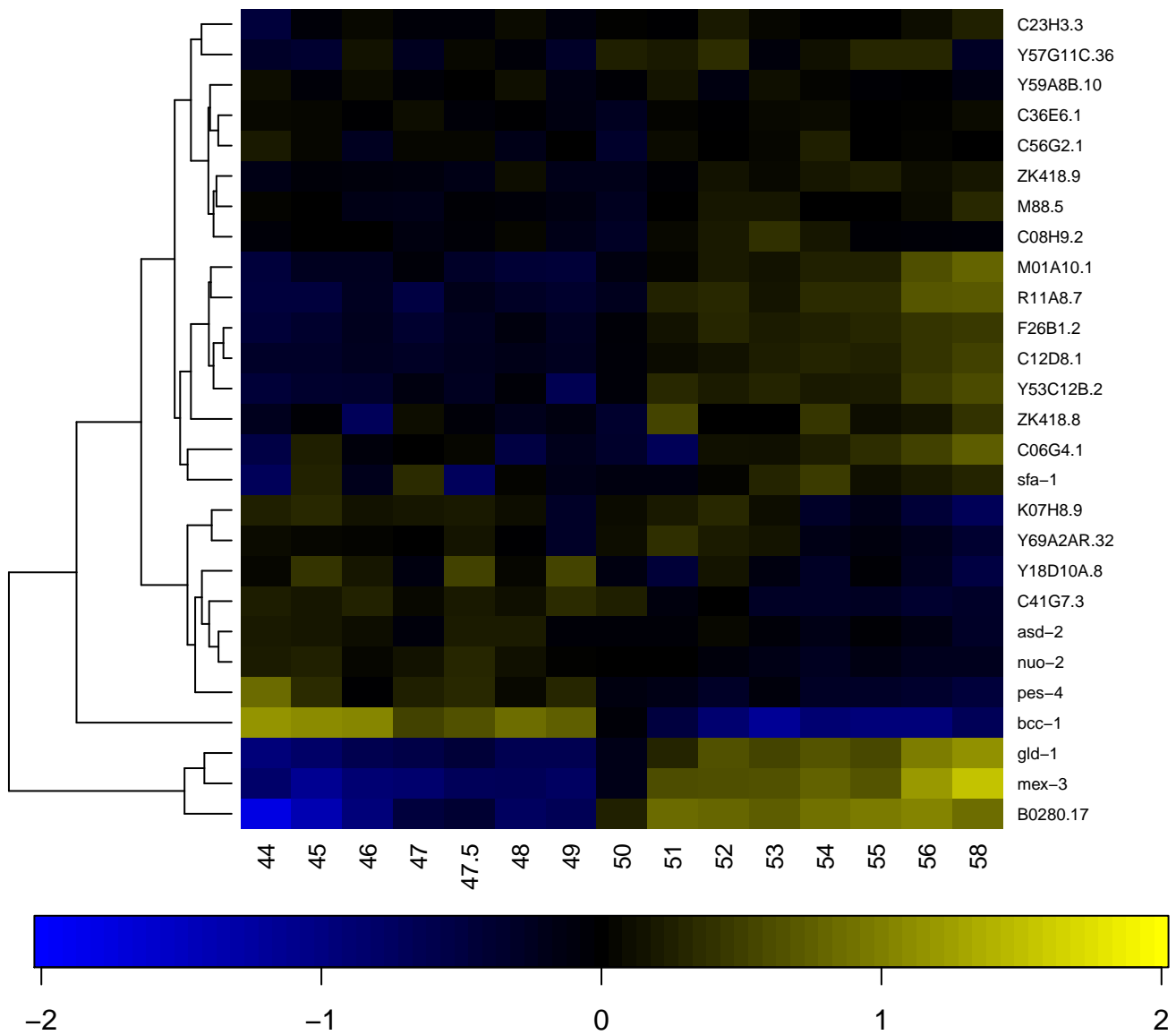
IQ motif, EF-hand binding site



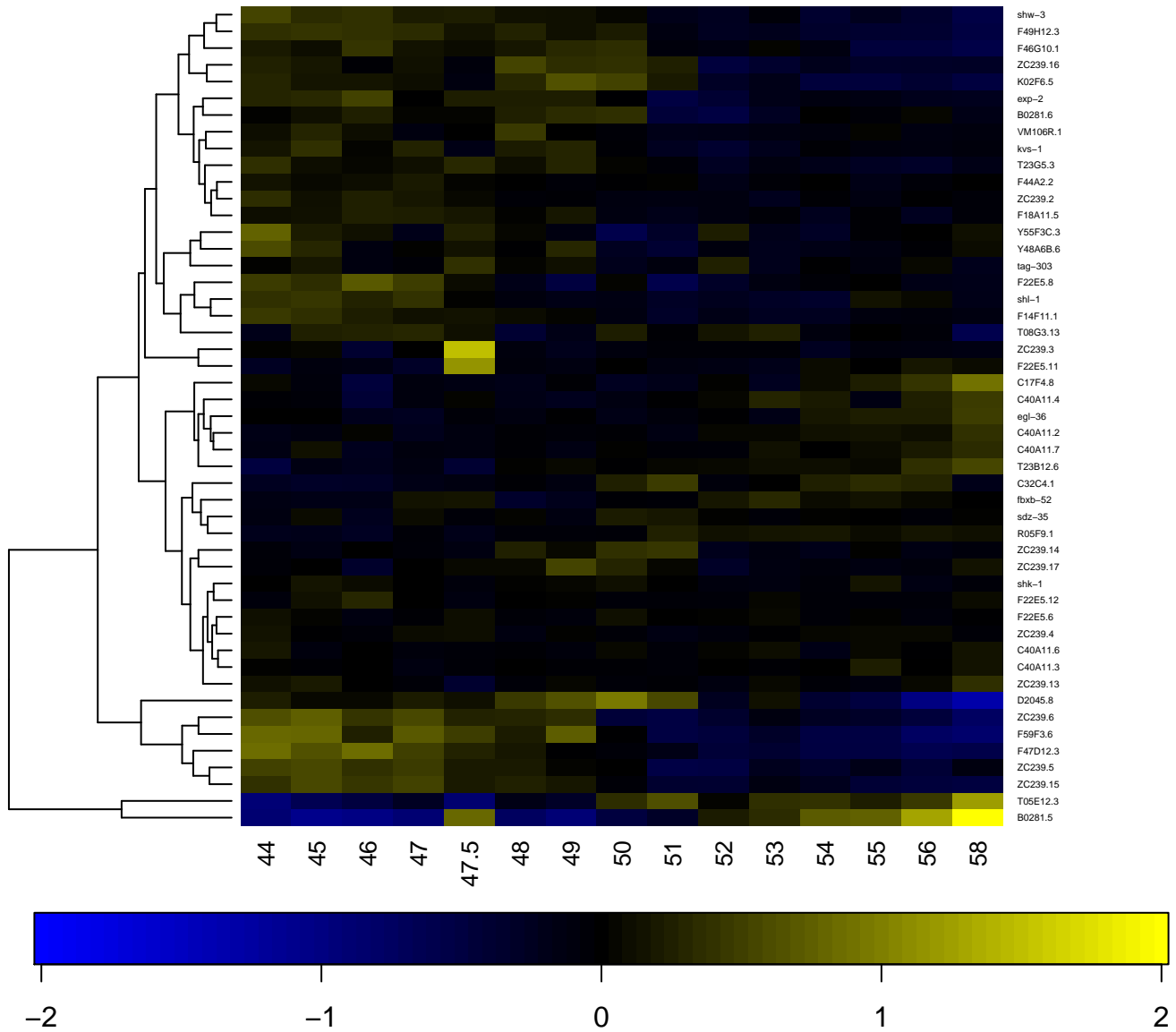
K Homology



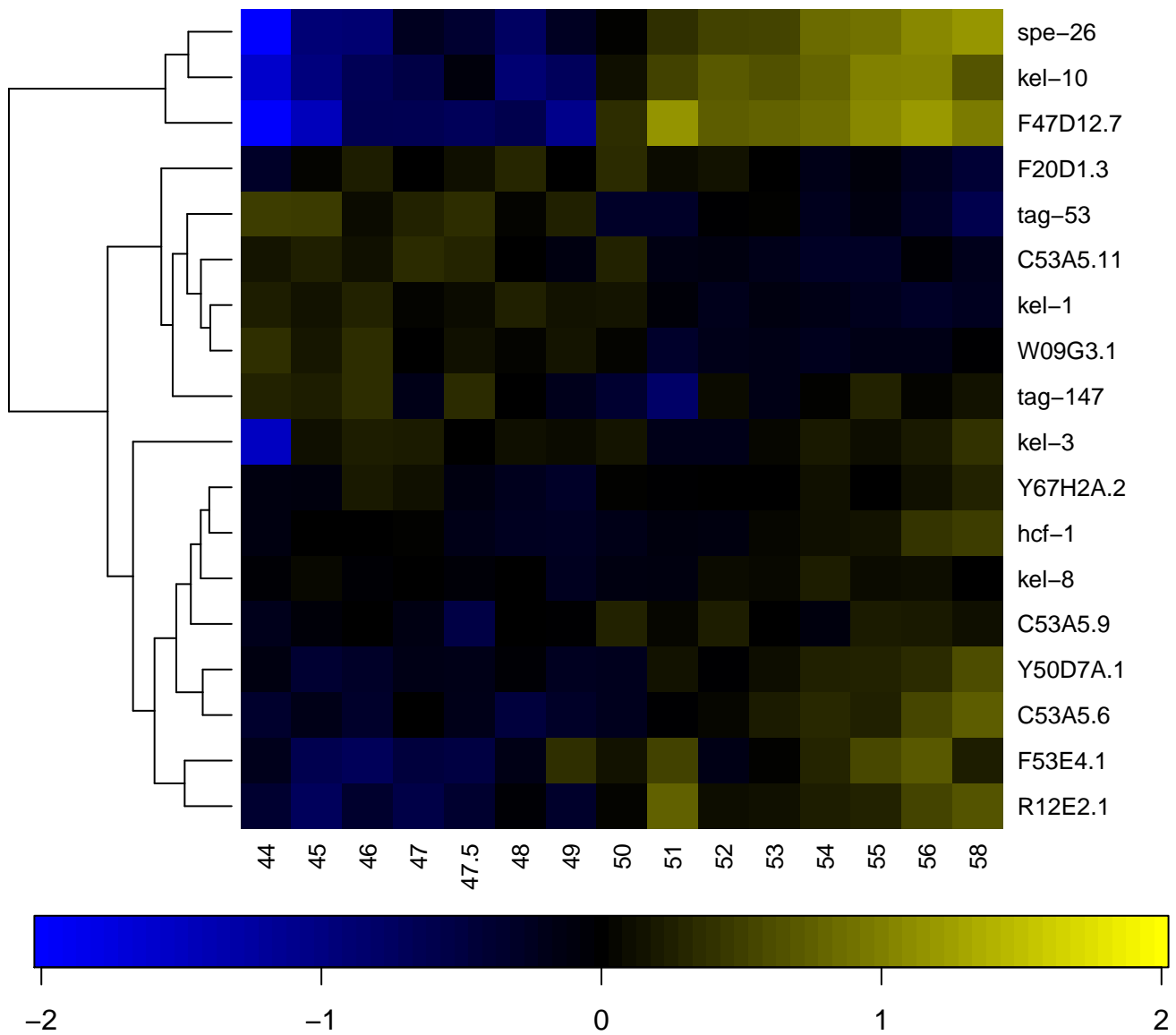
K Homology, type 1, subgroup



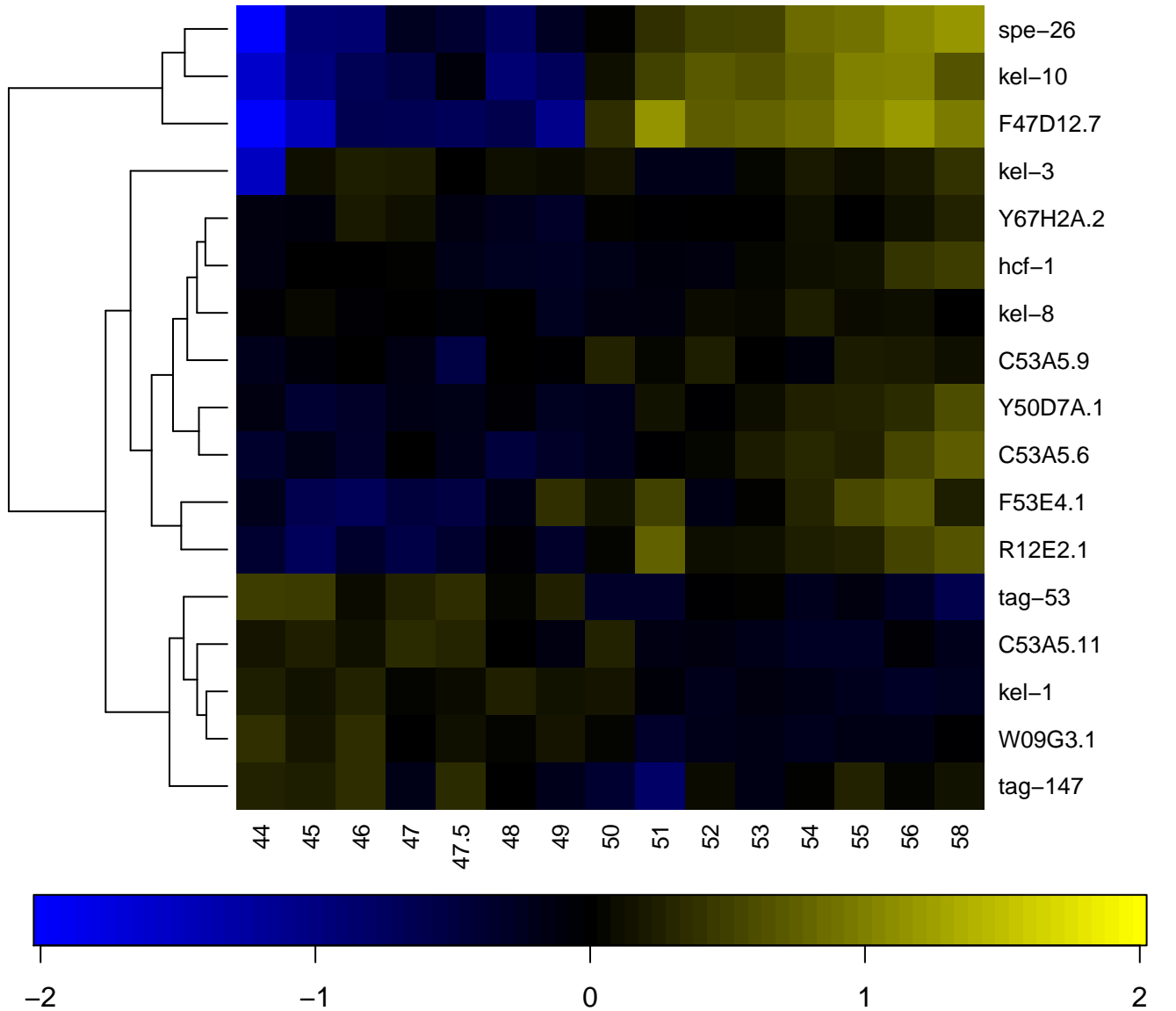
K⁺ channel tetramerisation domain



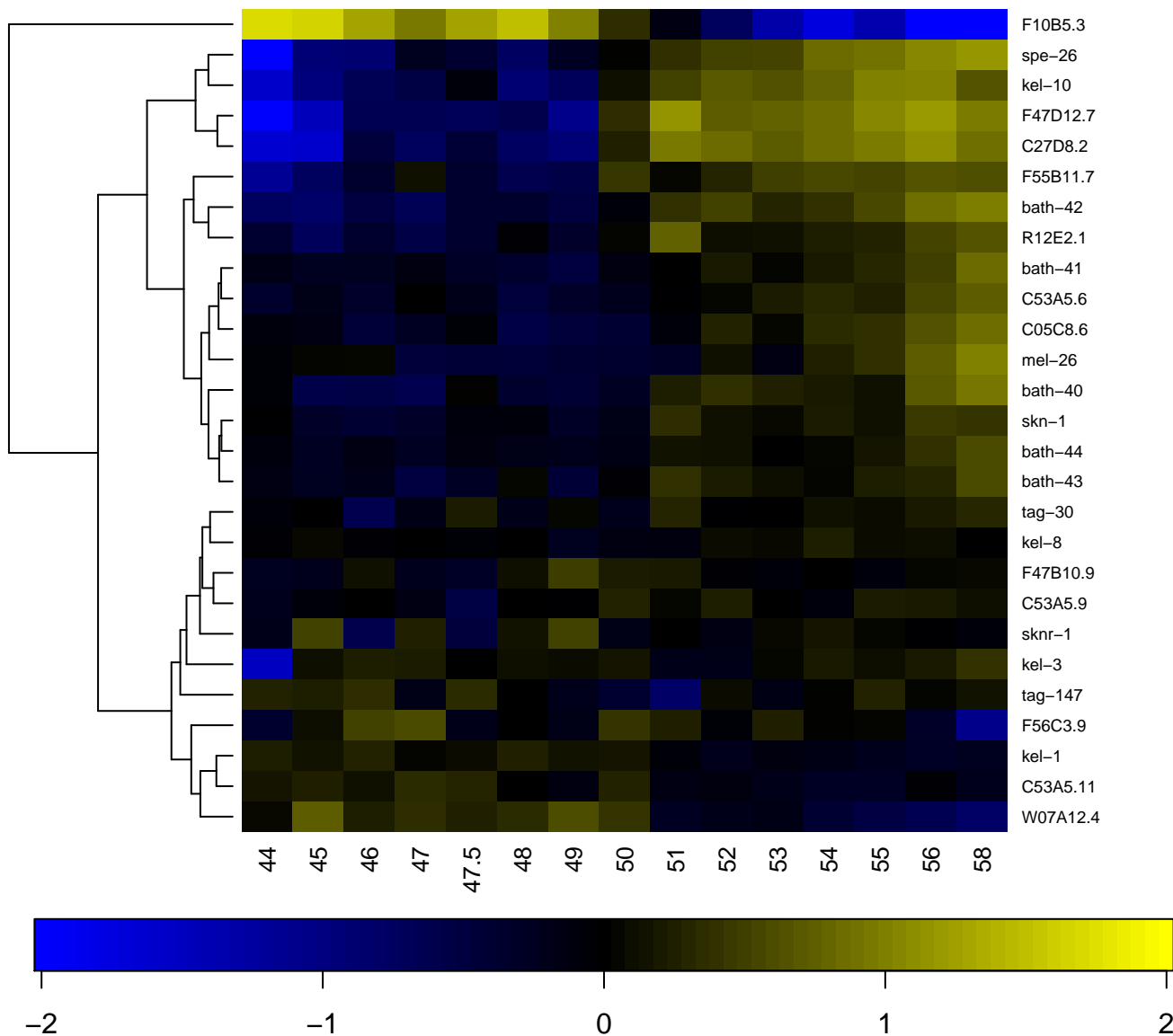
Kelch-type beta propeller



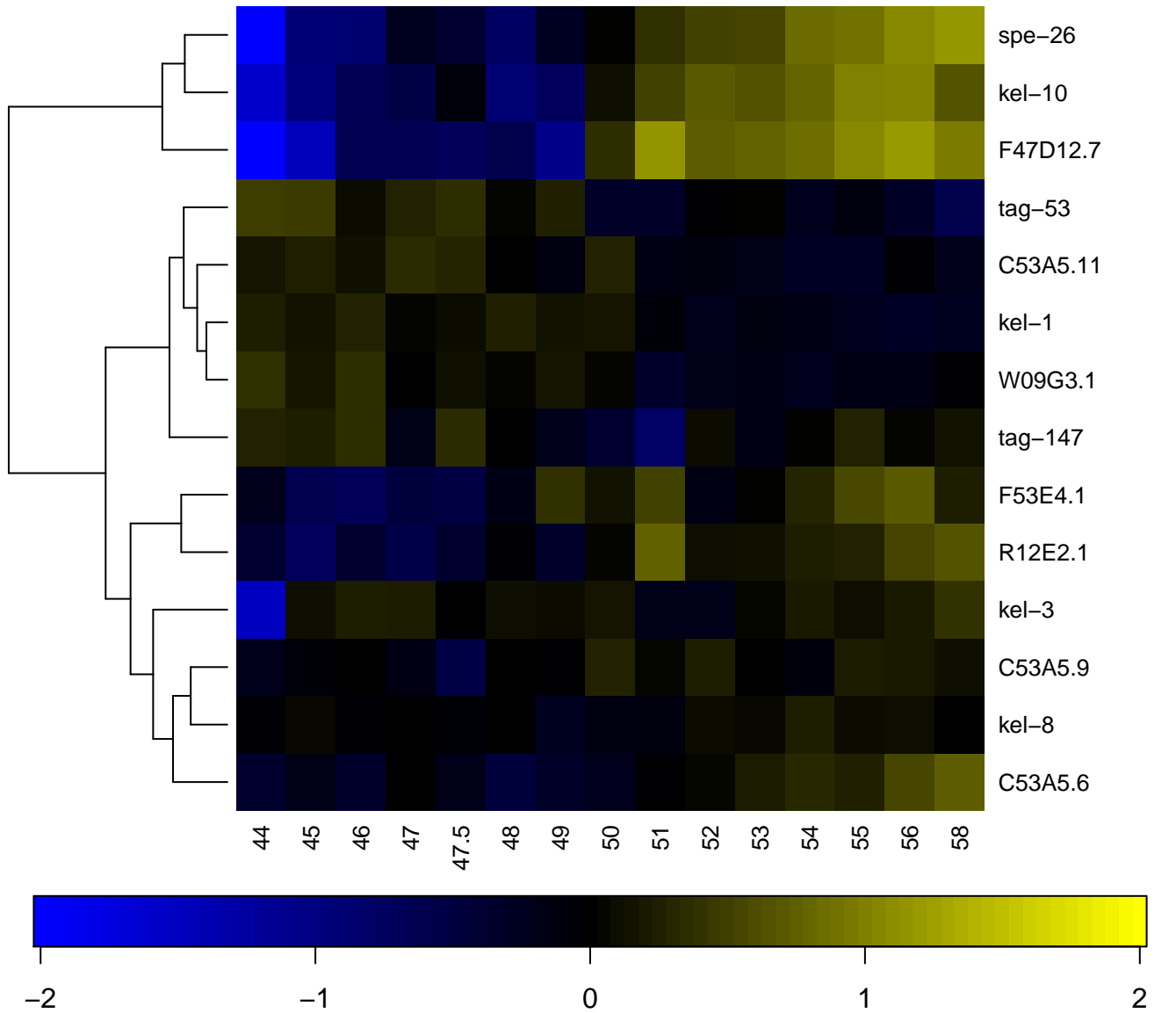
Kelch motif



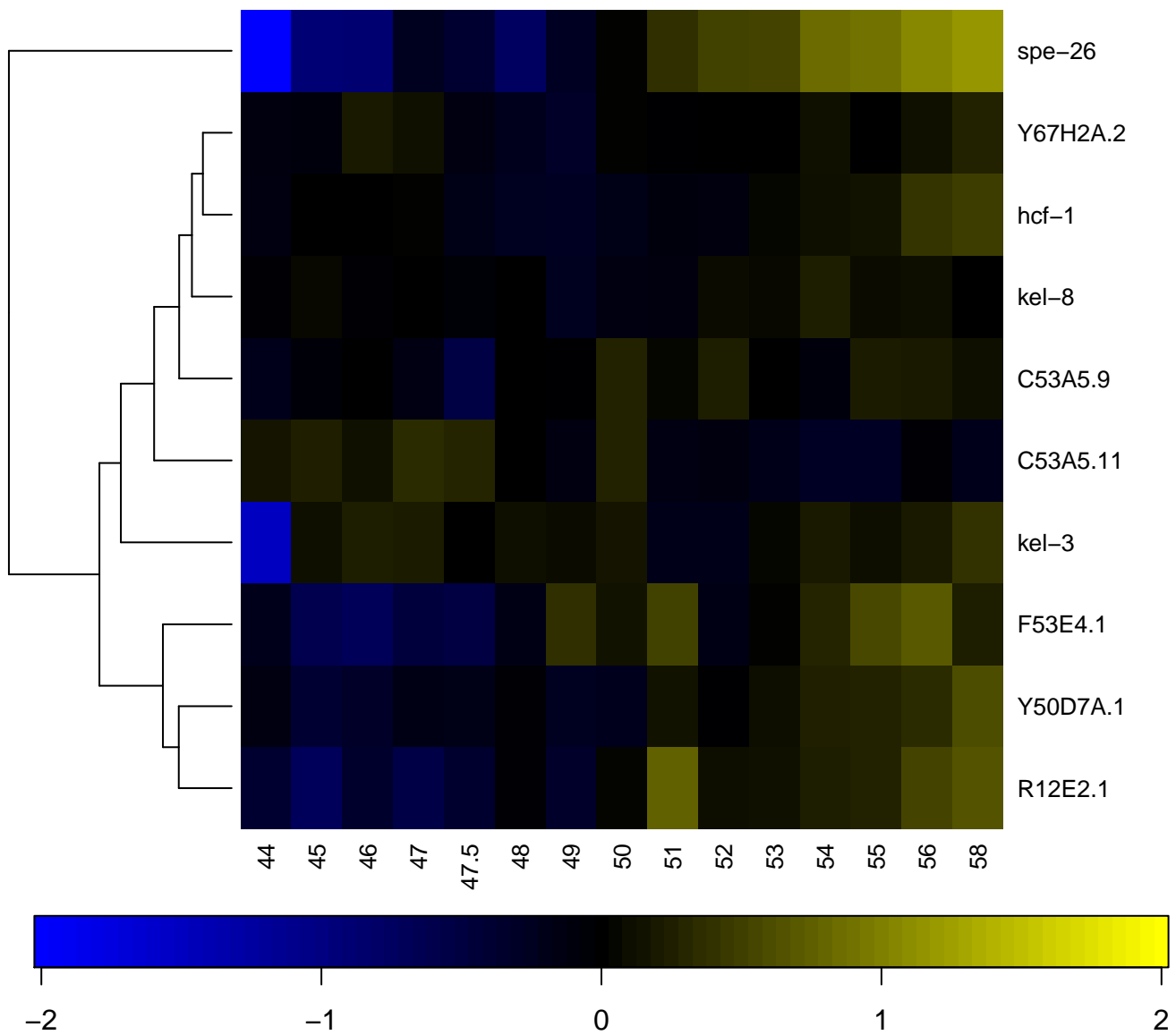
Kelch related



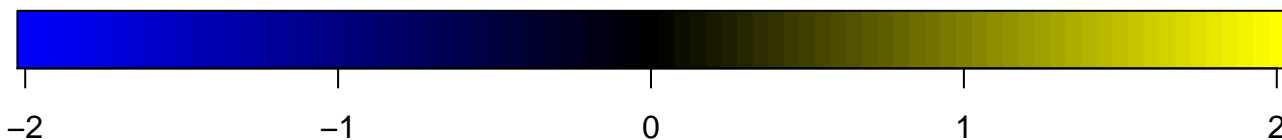
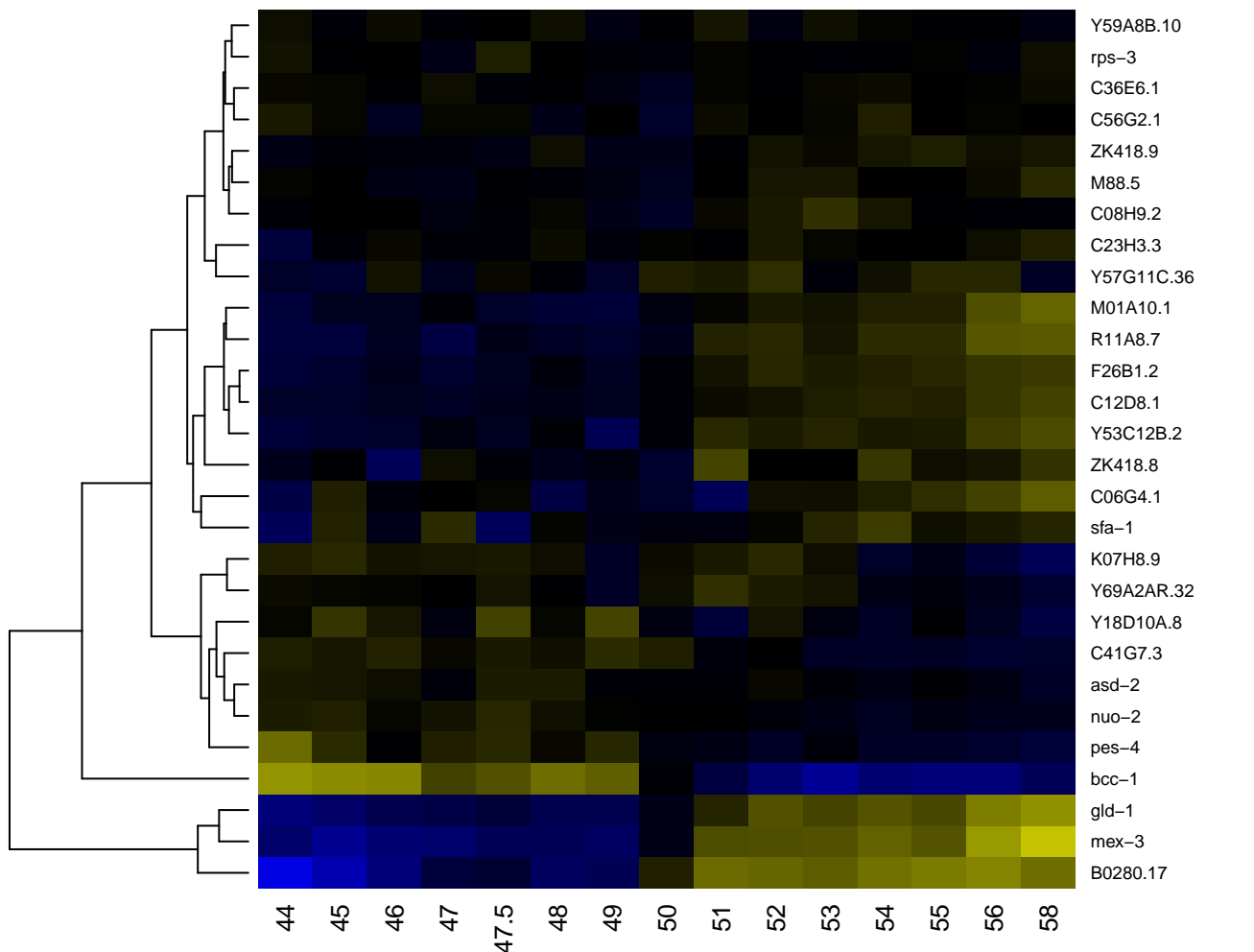
Kelch repeat type 1



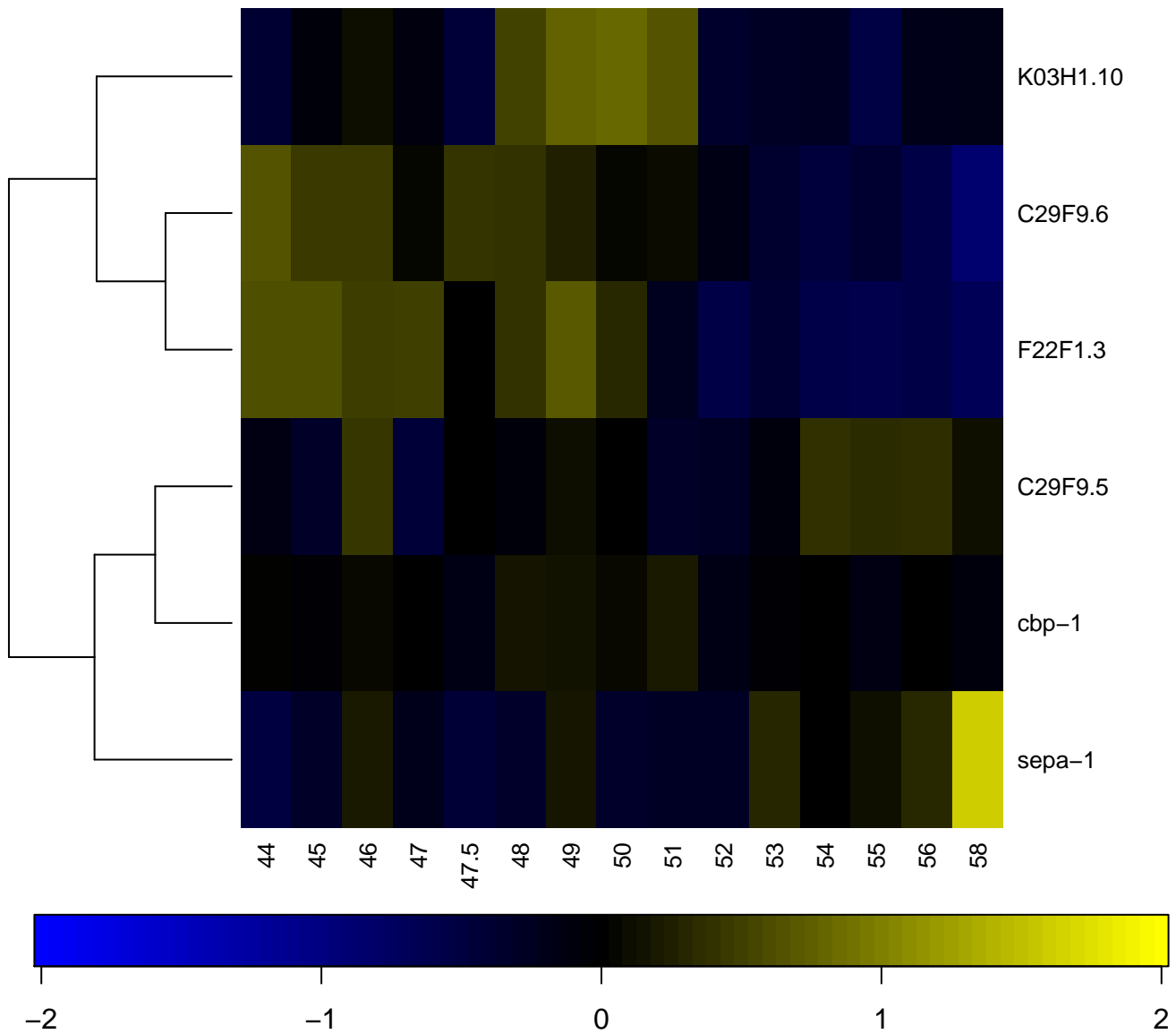
Kelch repeat type 2



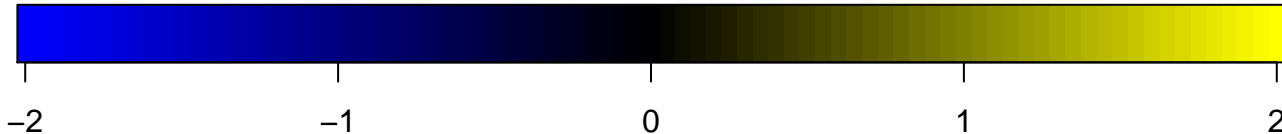
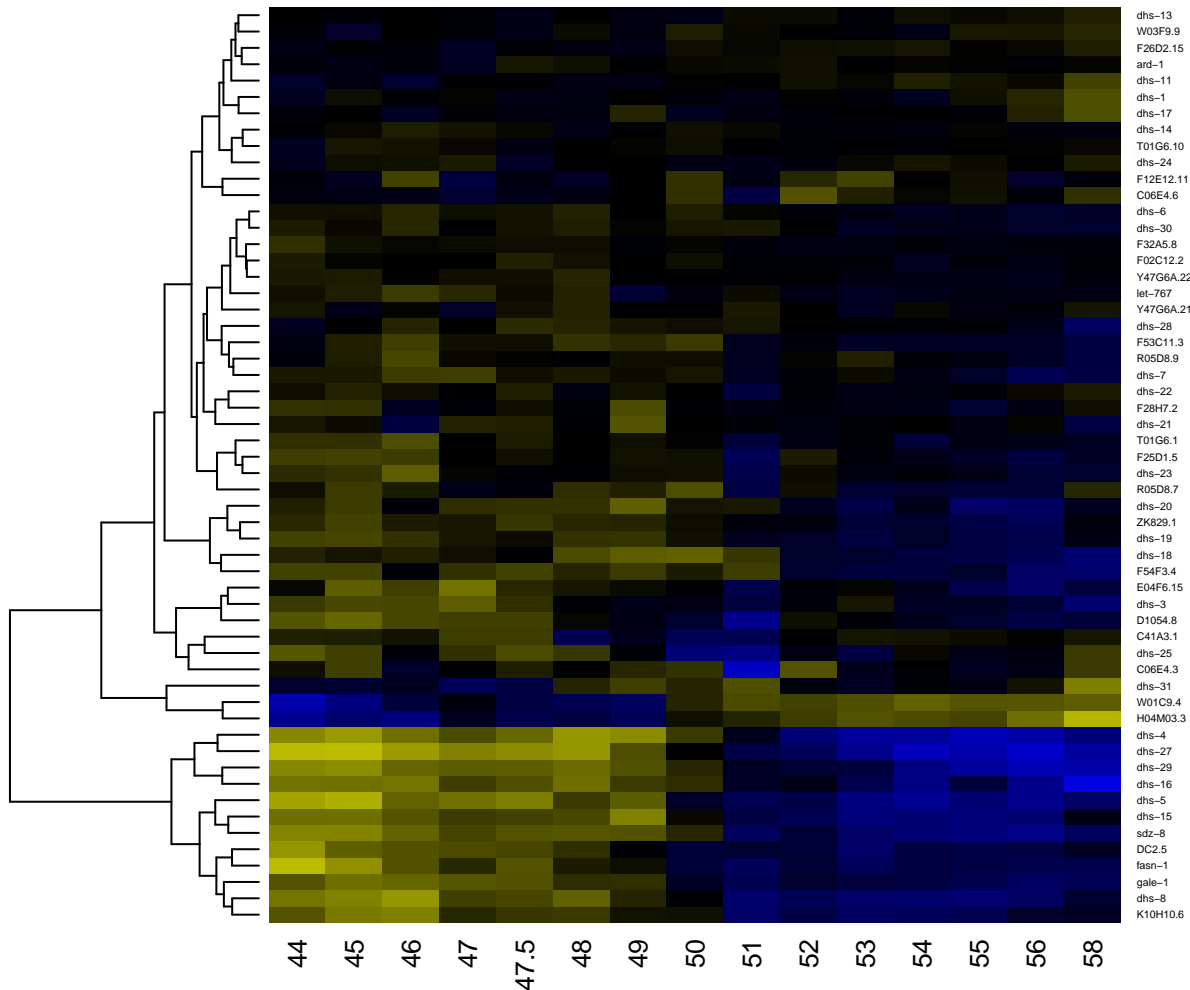
KH domain



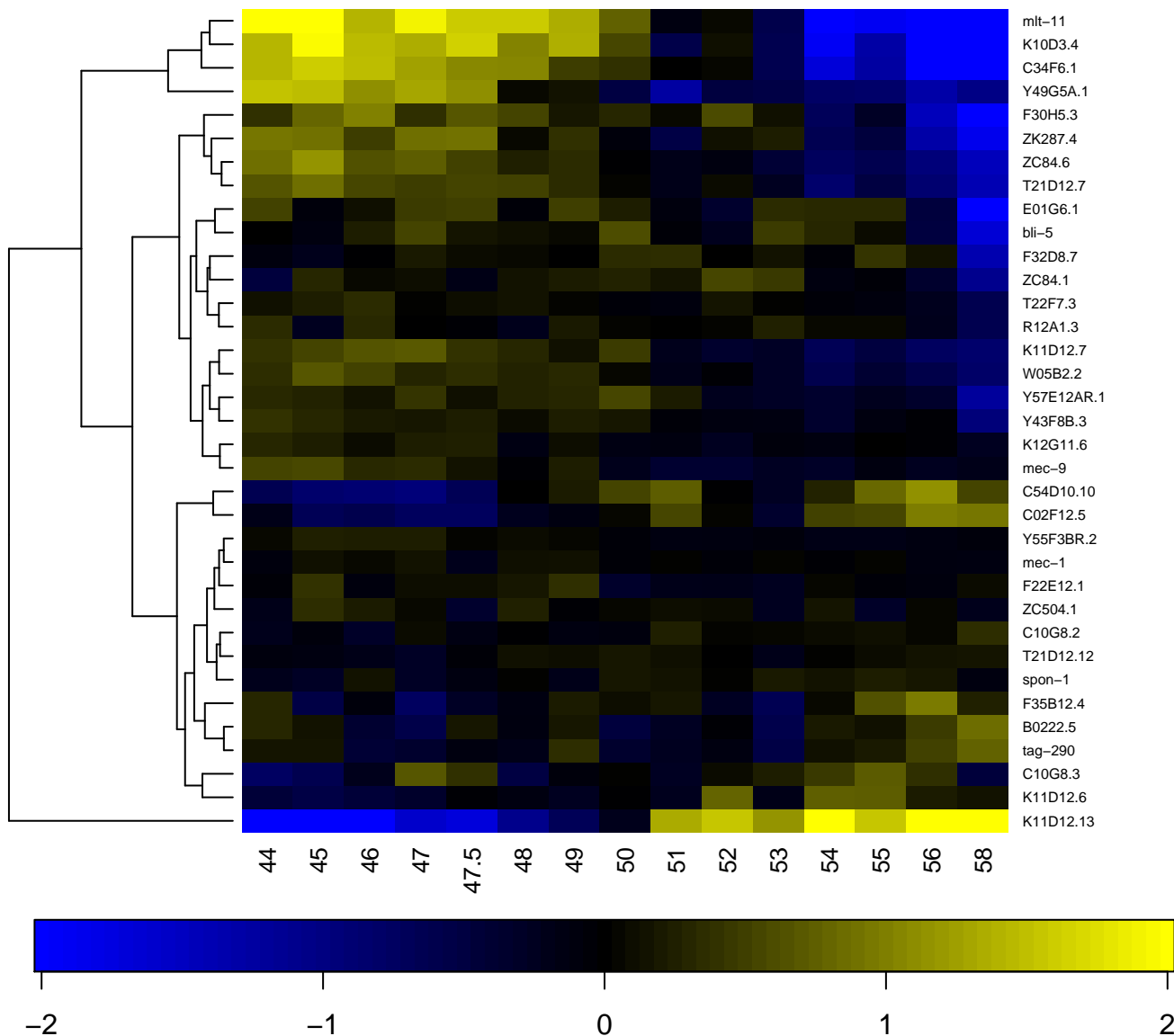
KIX domain



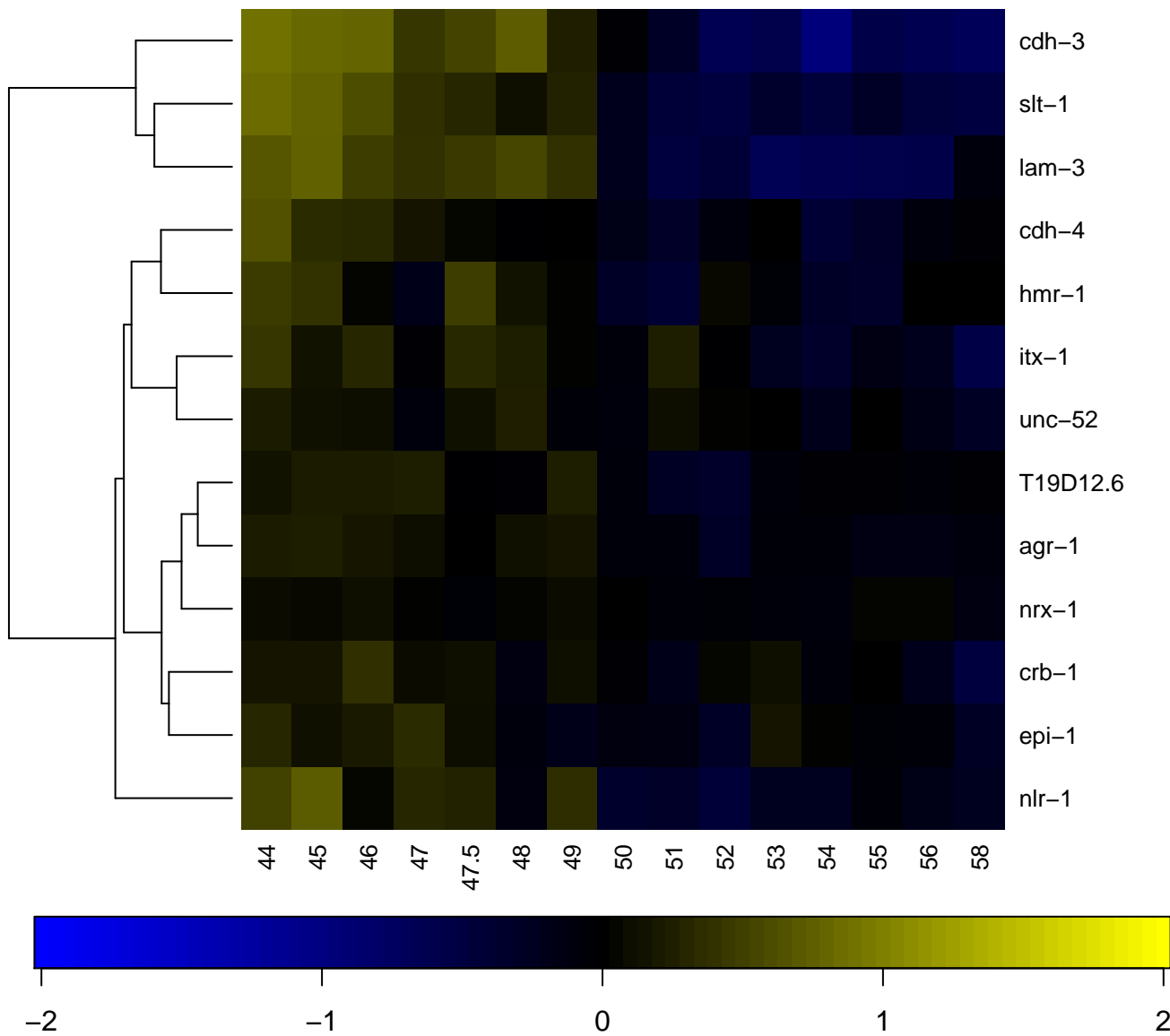
KR domain



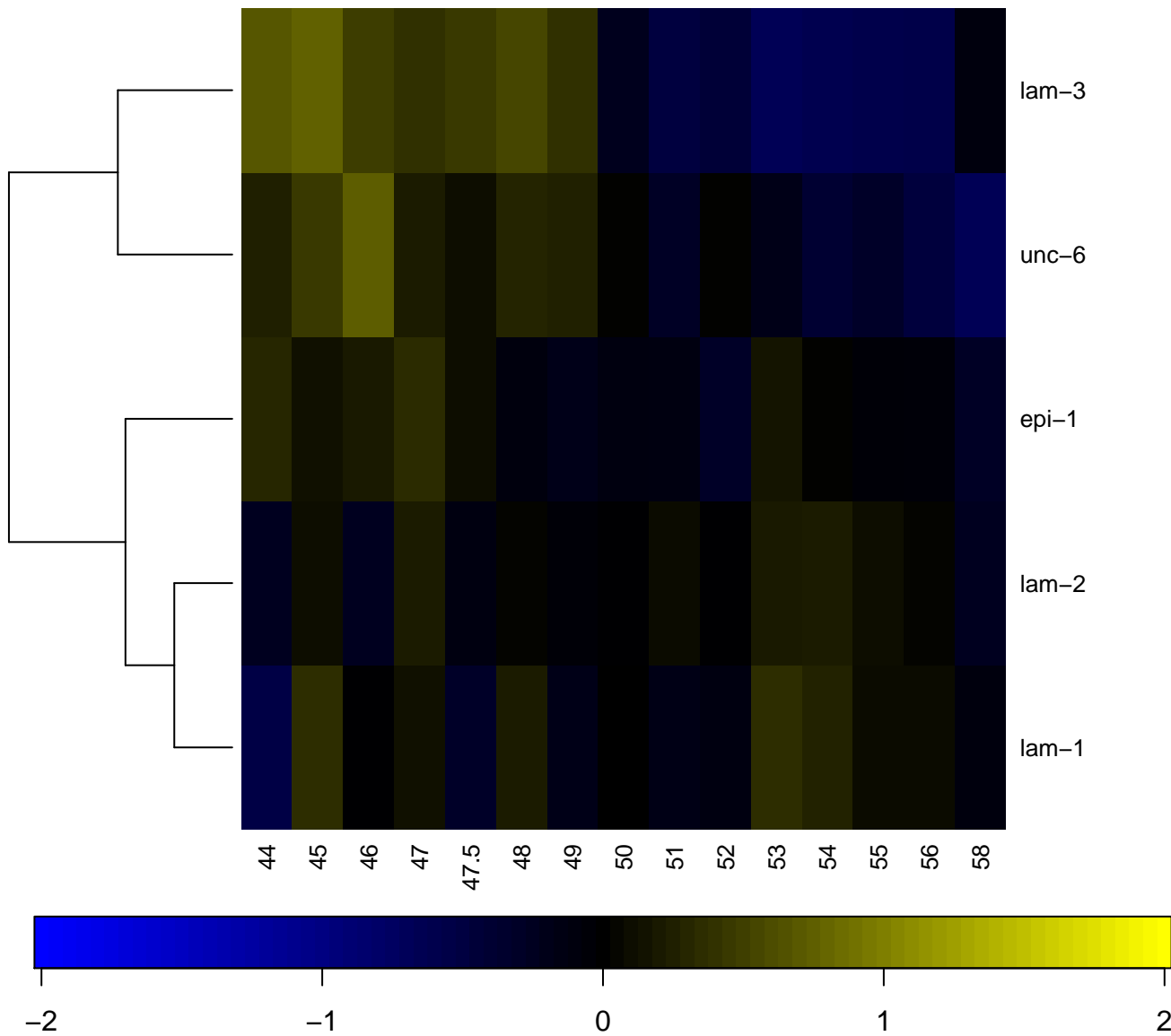
Kunitz/Bovine pancreatic trypsin inhibitor domain



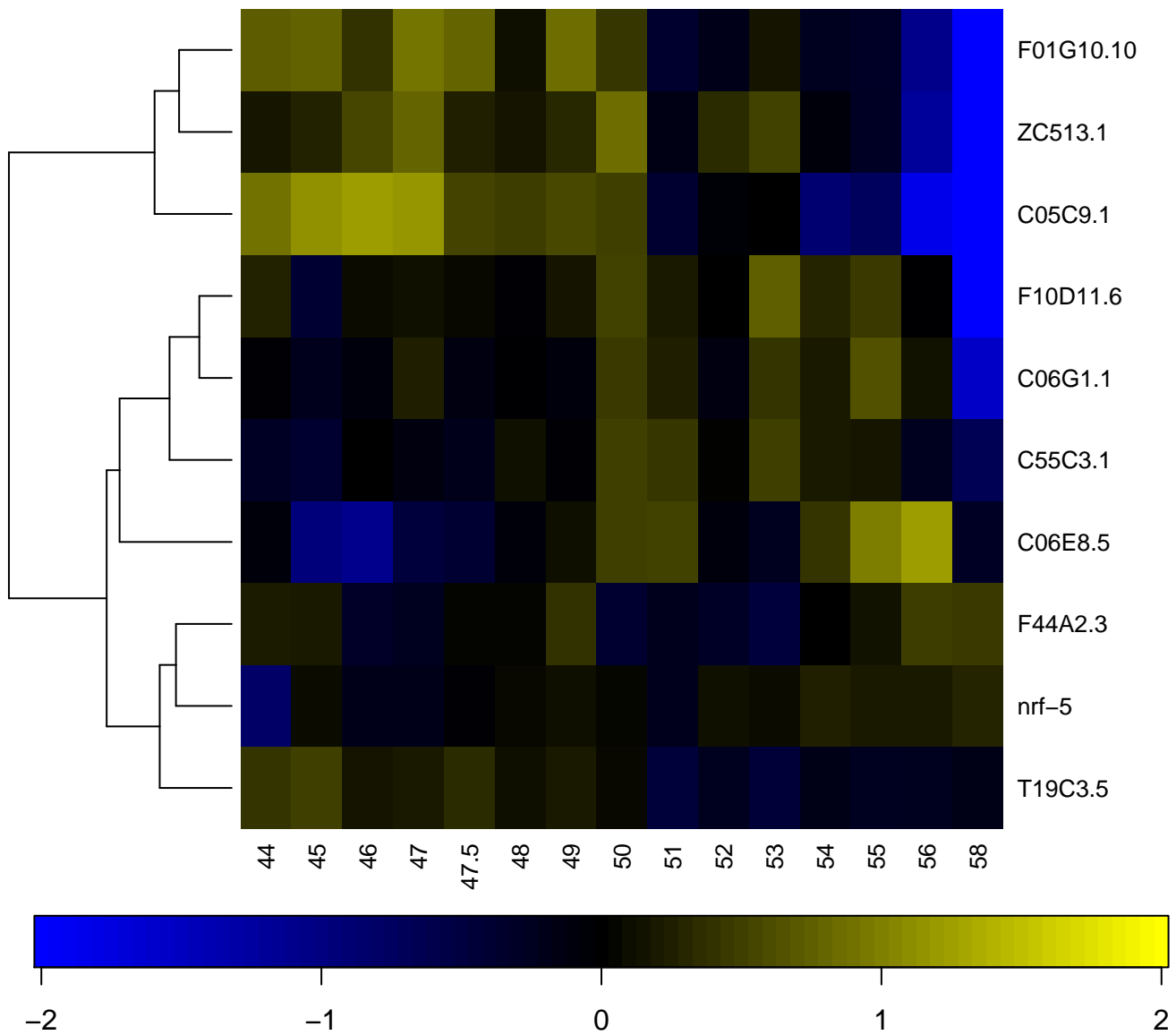
Laminin G, subdomain 2



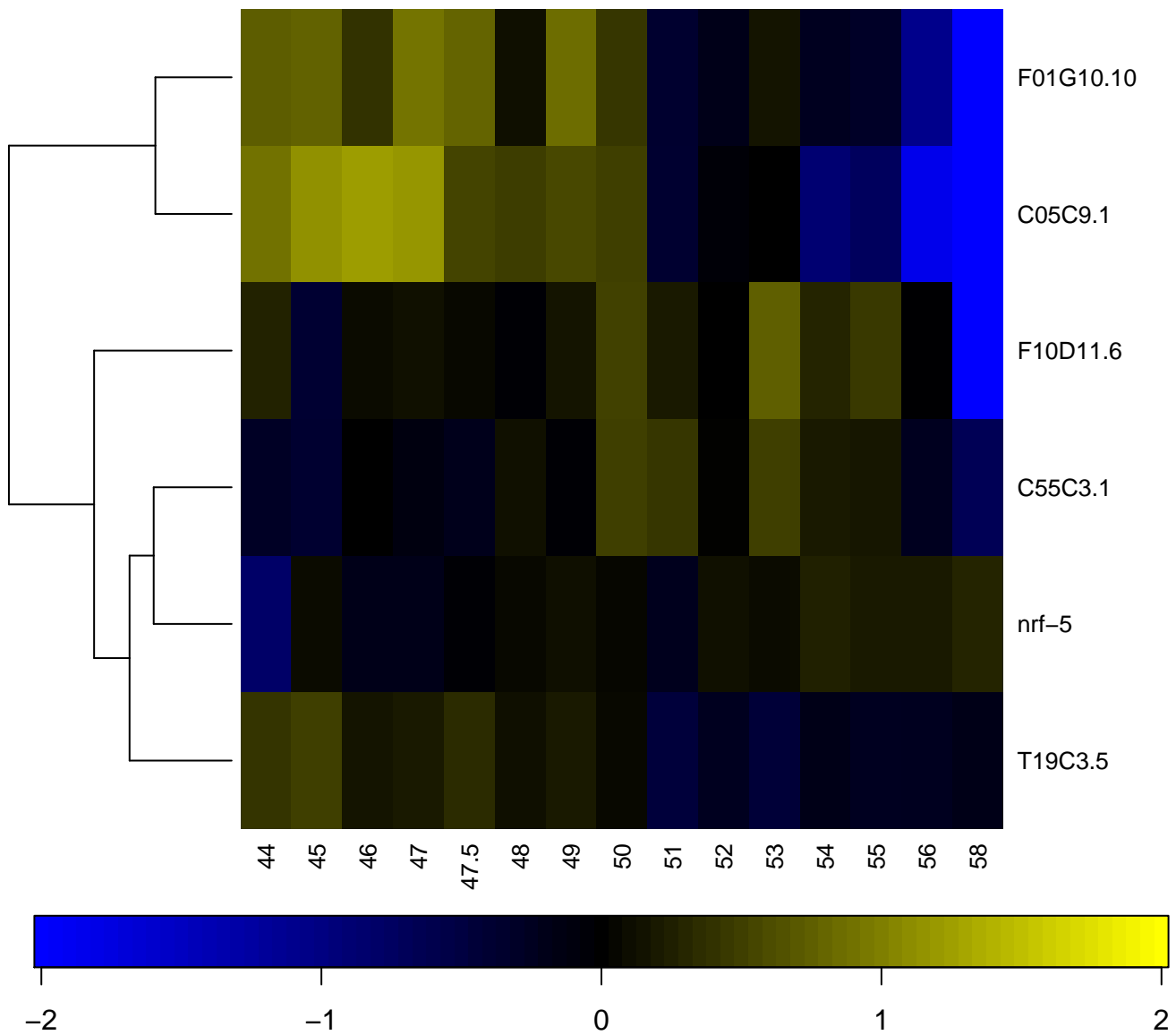
Laminin N-terminal (Domain VI)



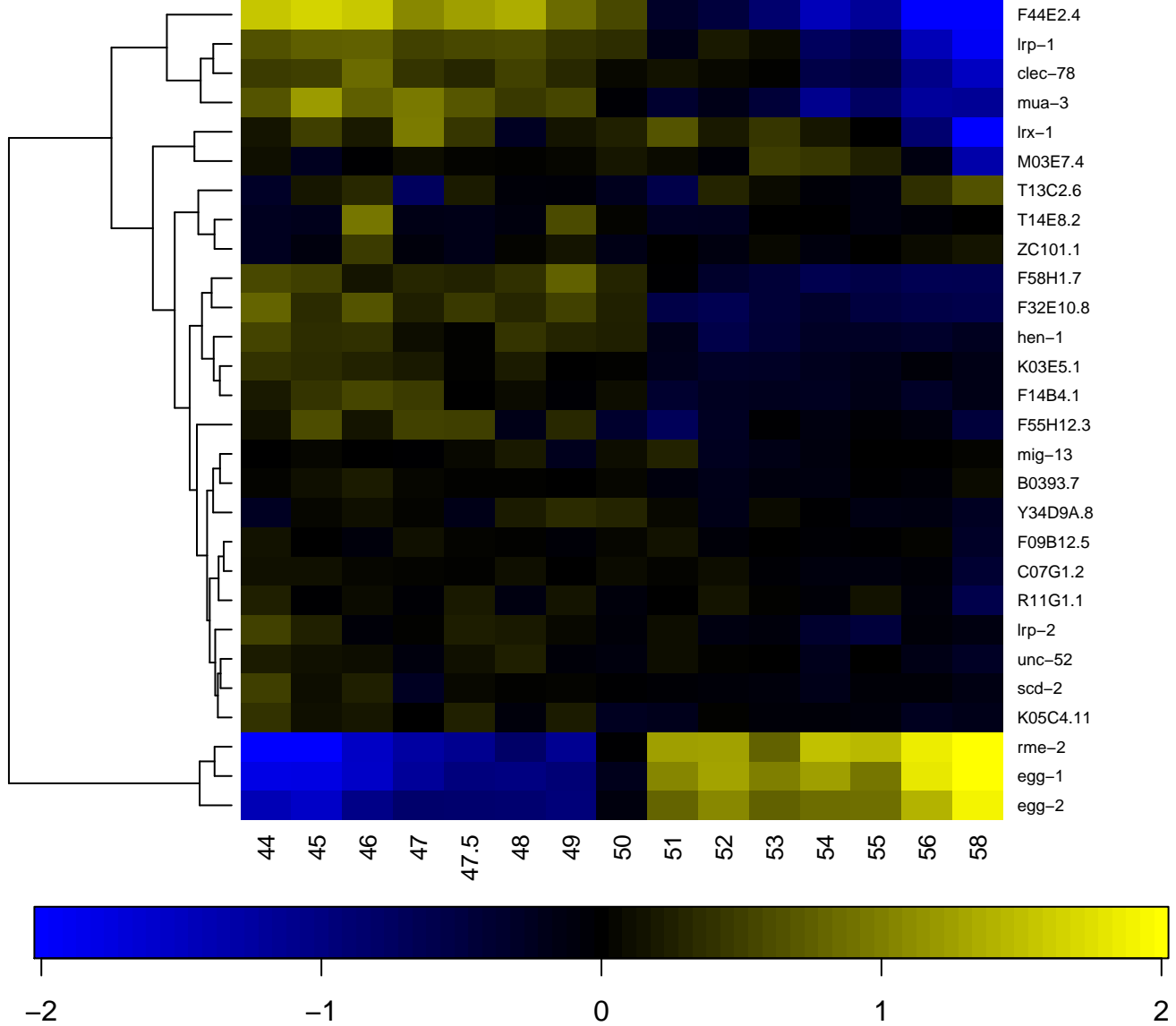
LBP / BPI / CETP family, C-terminal domain



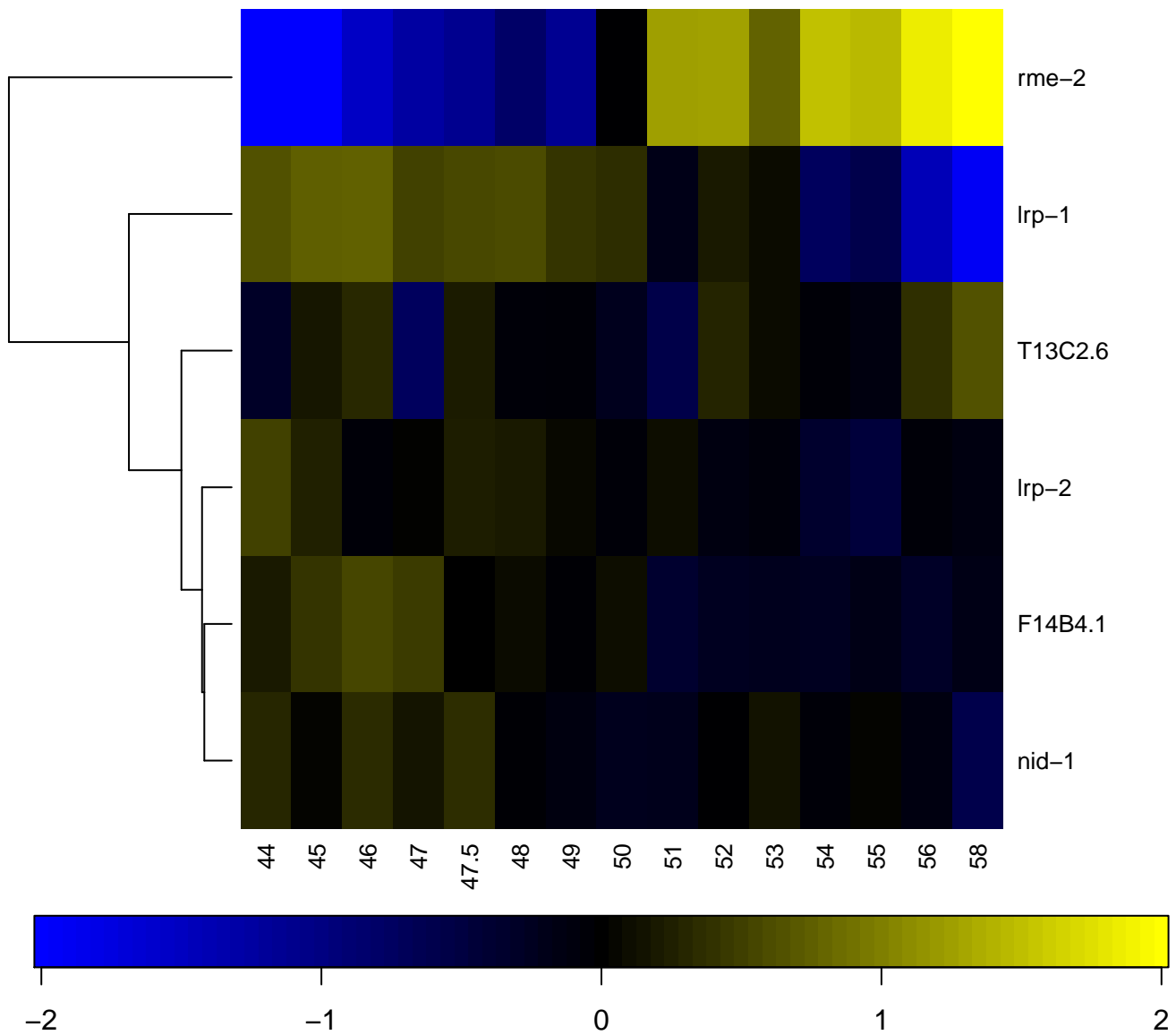
LBP / BPI / CETP family, N-terminal domain



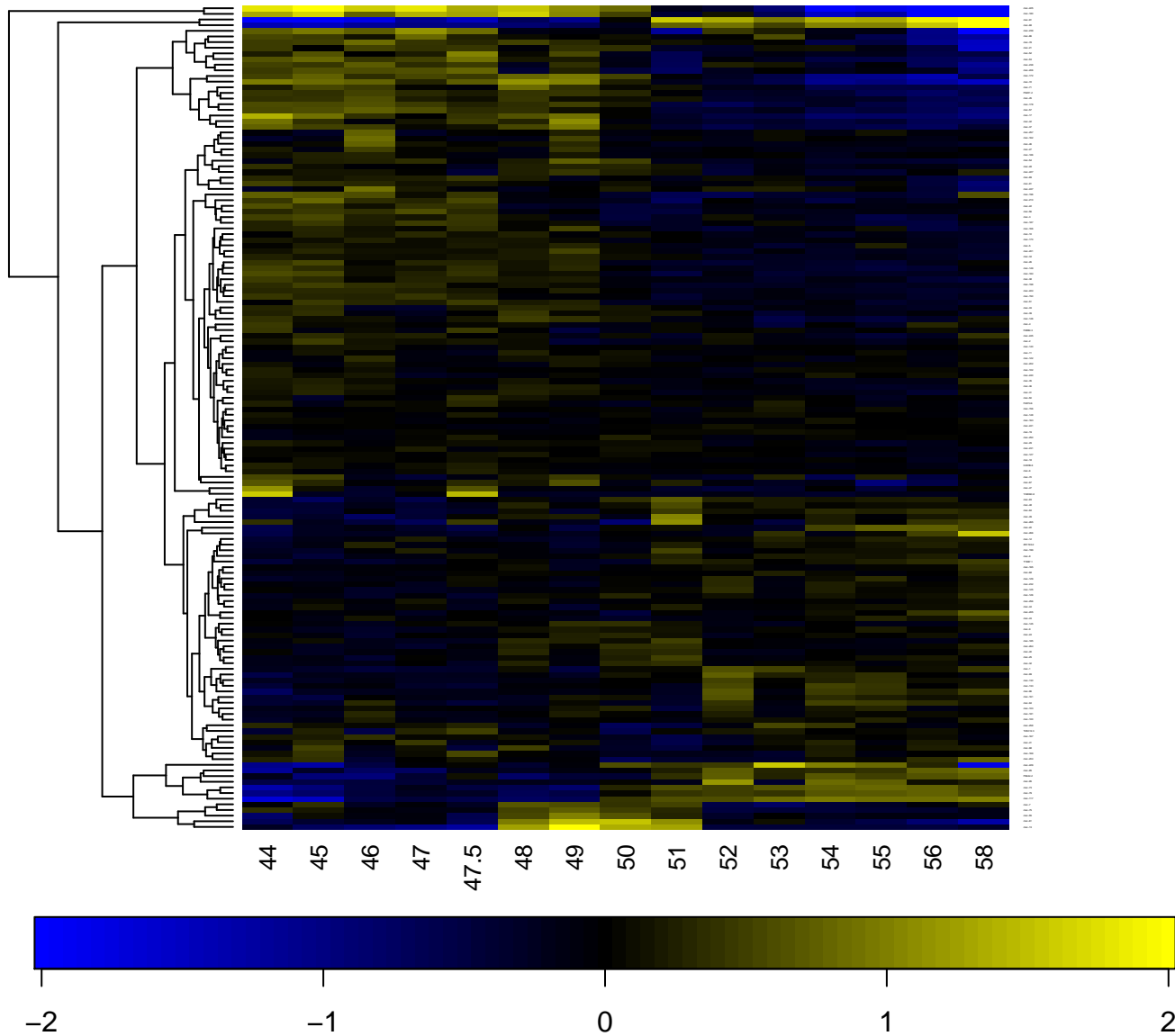
LDLR class A repeat



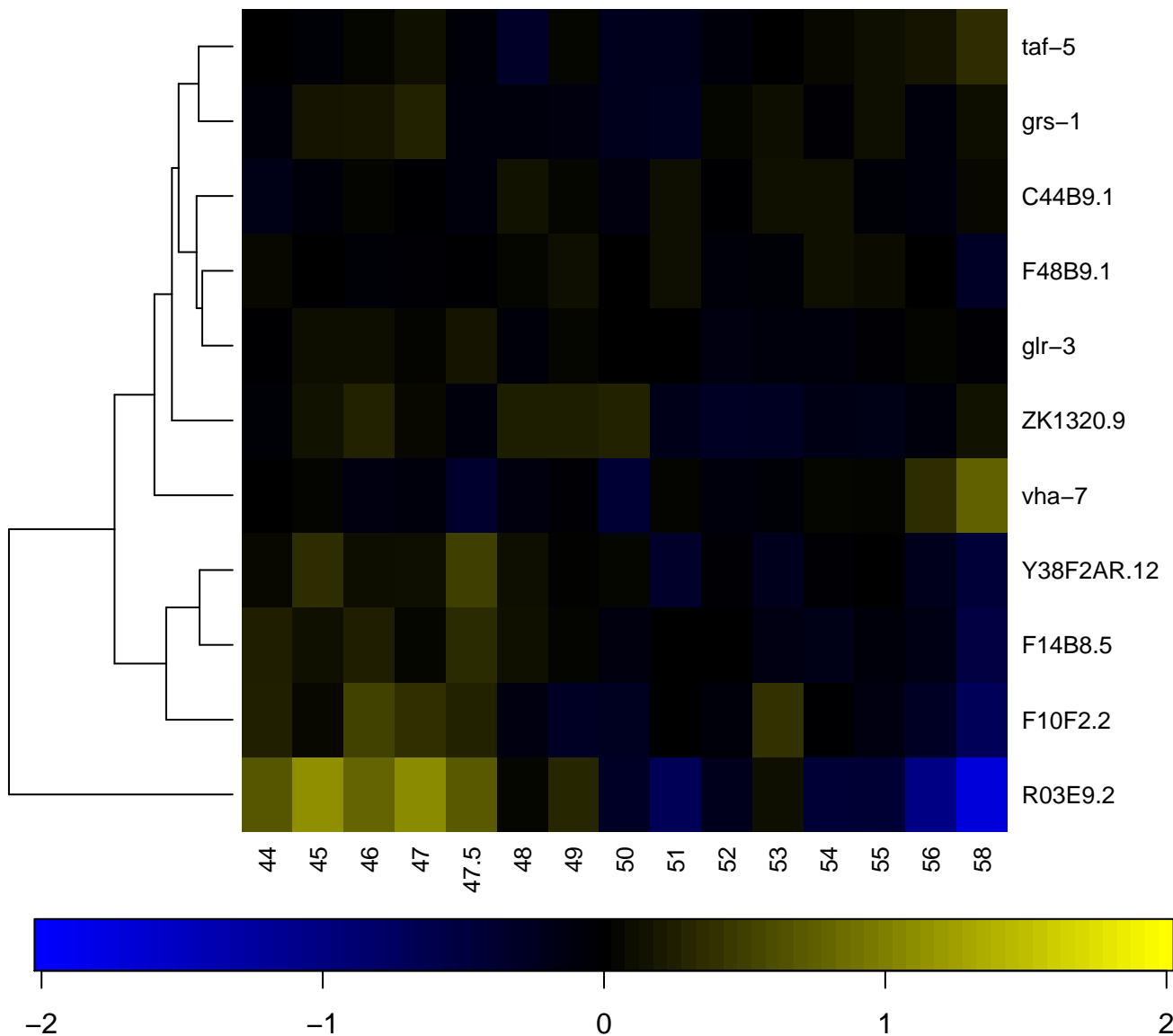
LDLR class B repeat



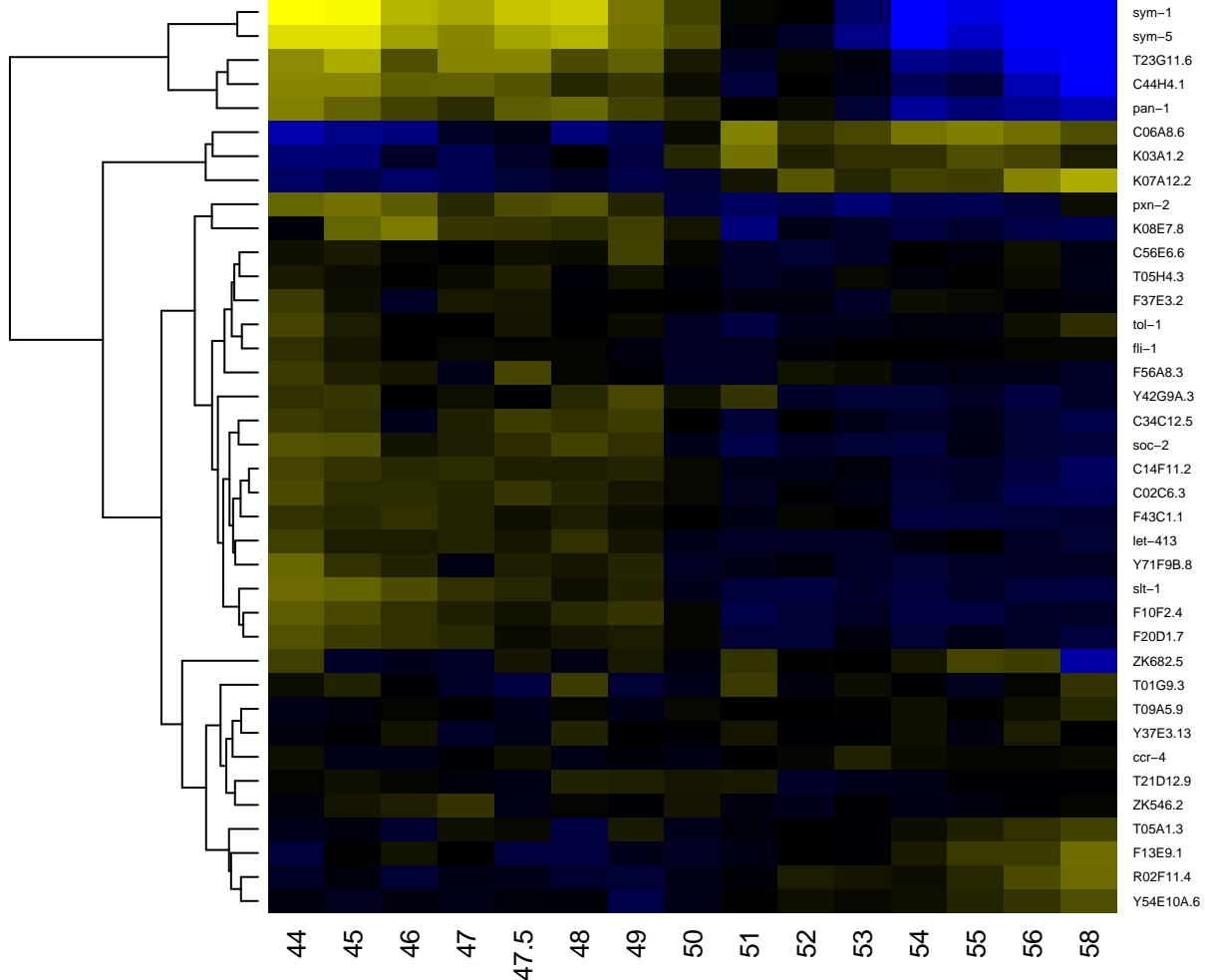
Lectin C-type domain



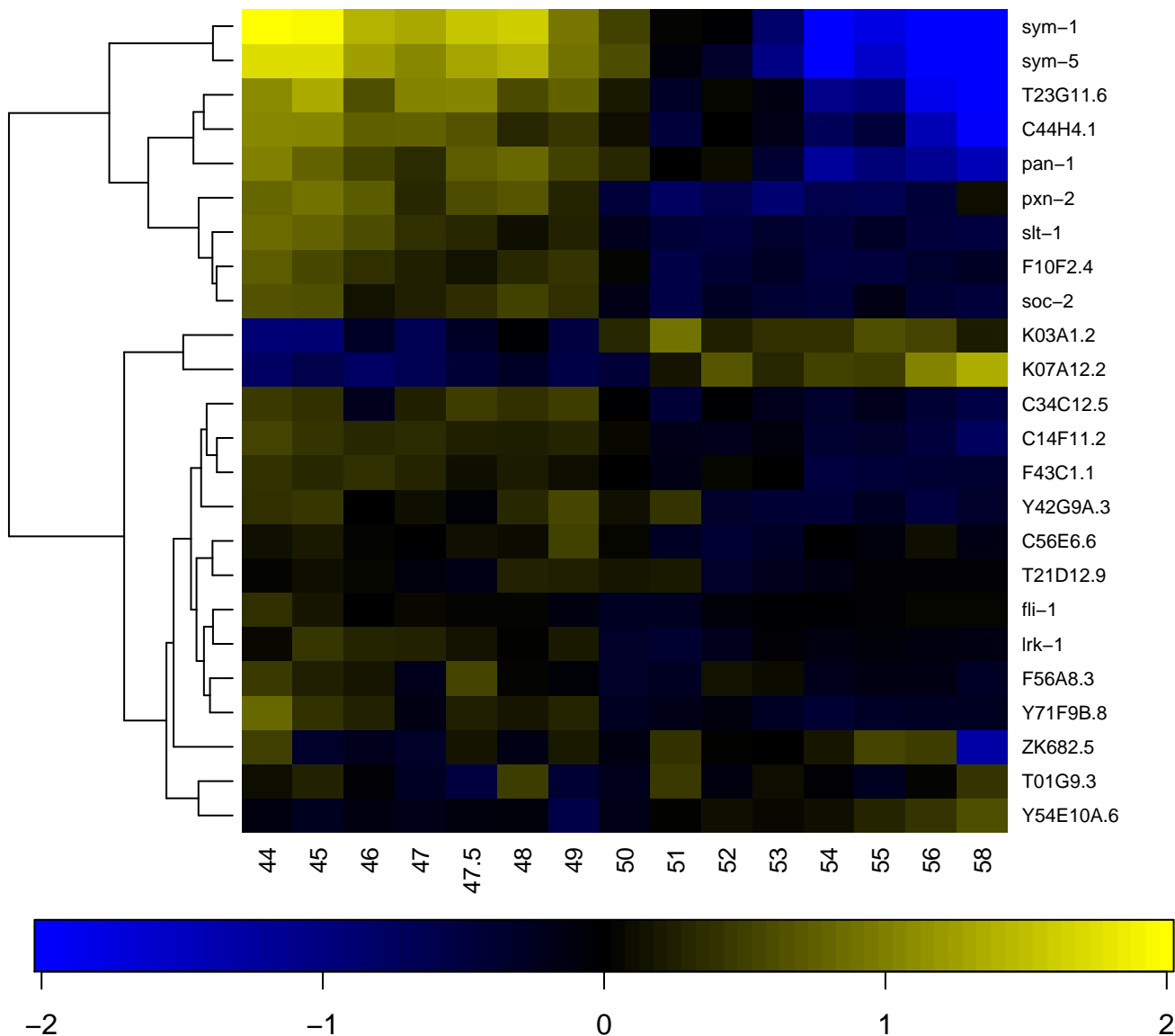
Legume lectin, beta chain, Mn/Ca-binding site



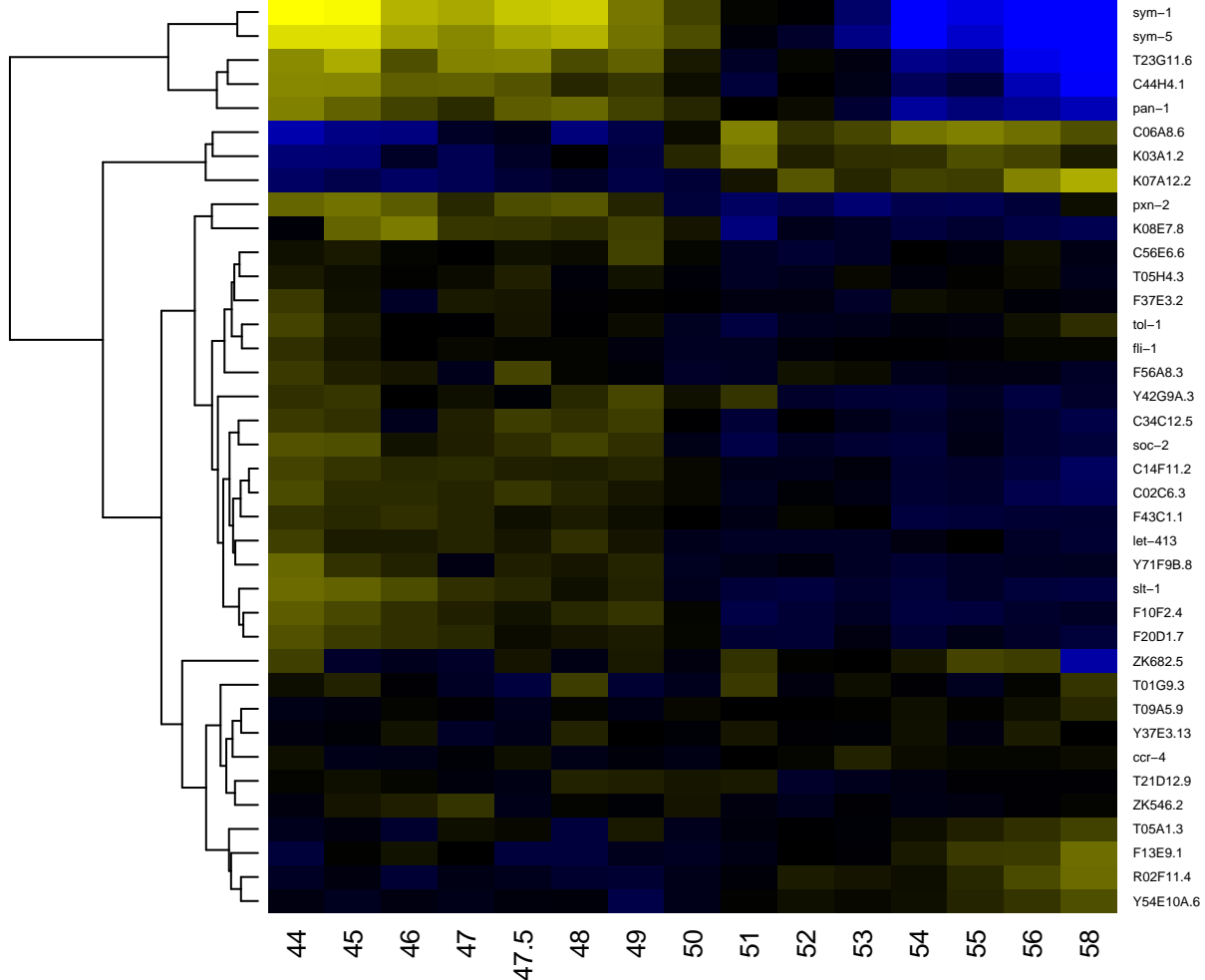
Leucine-rich repeat



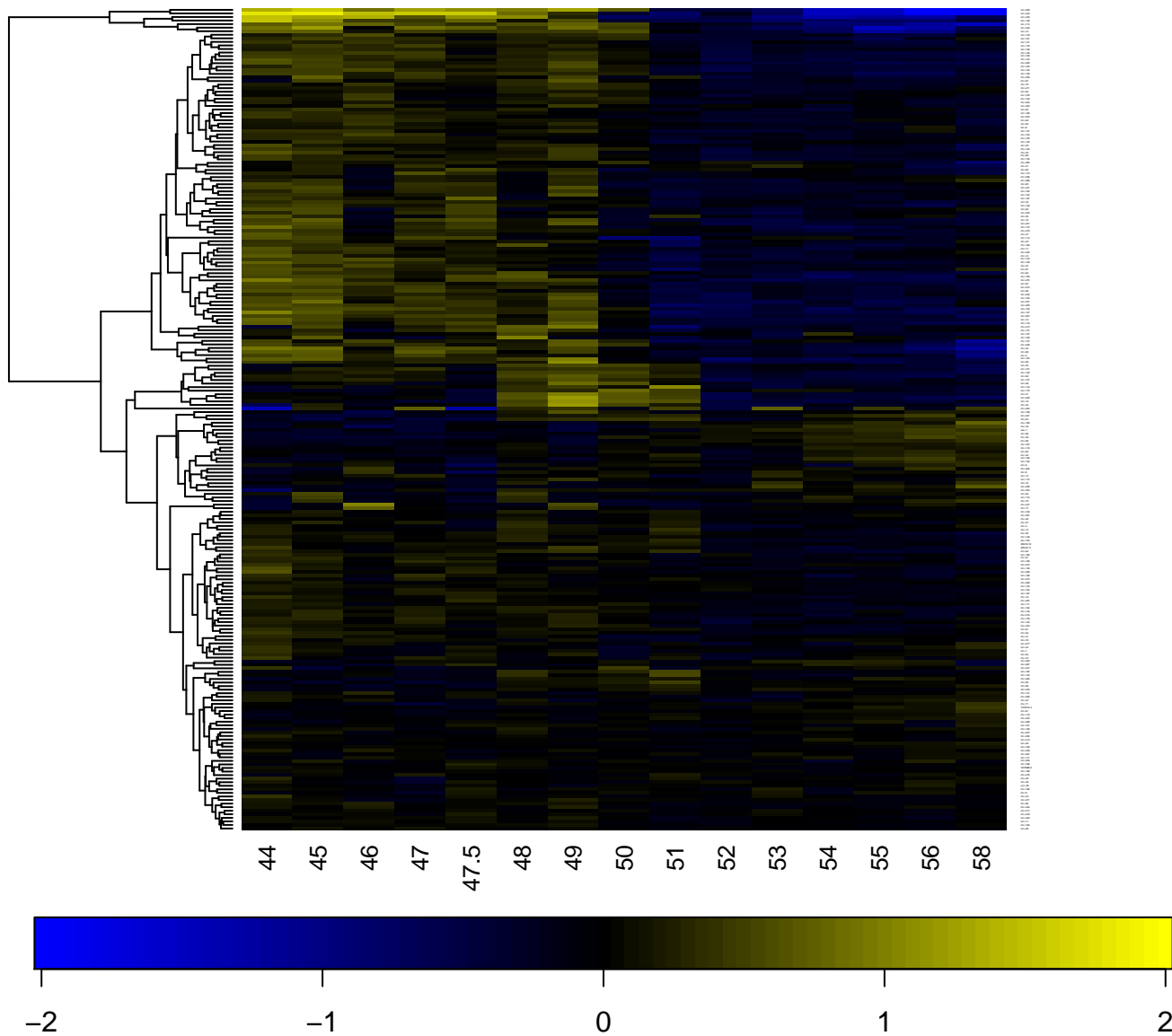
Leucine-rich repeat, typical subtype



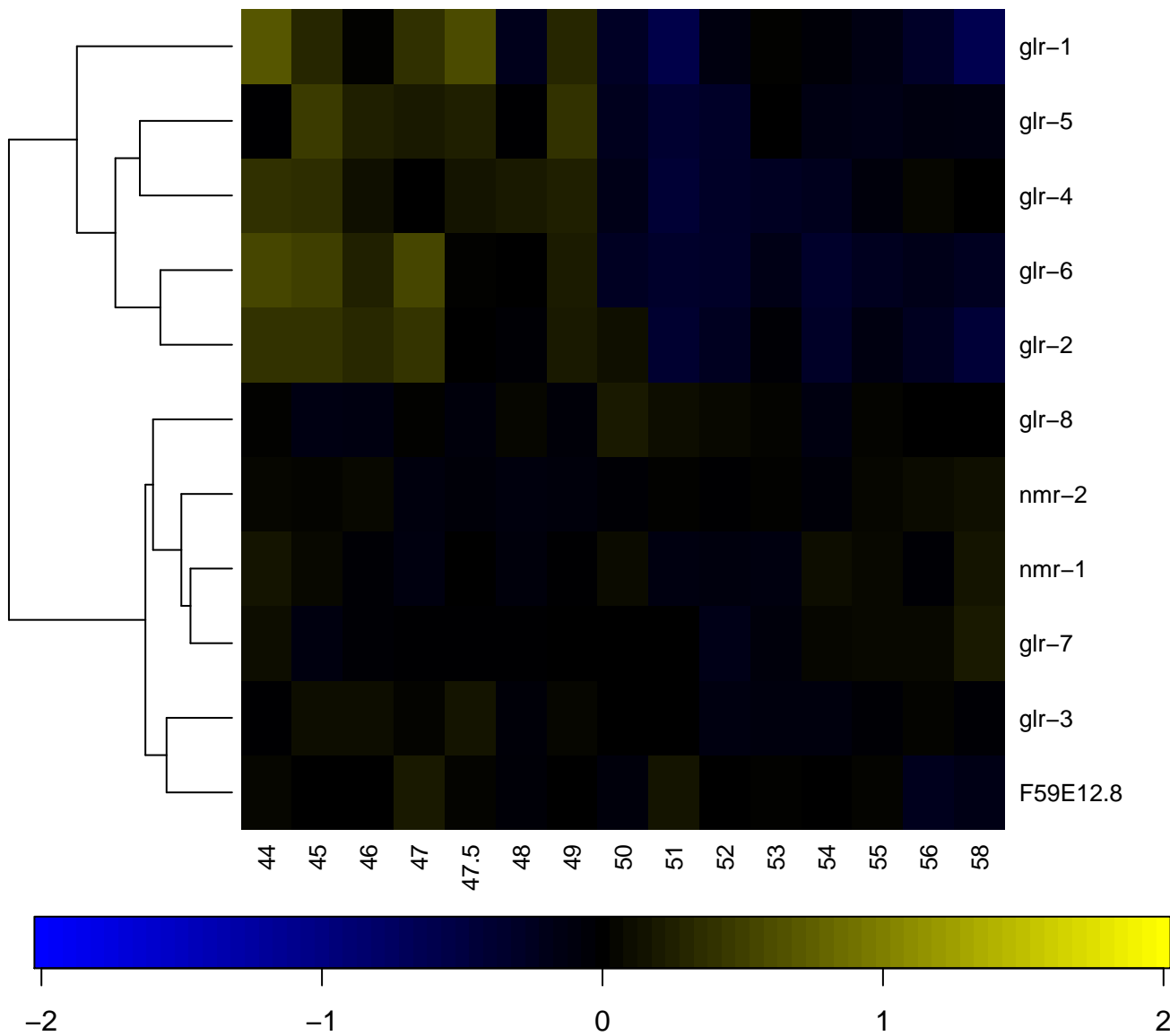
Leucine Rich Repeat



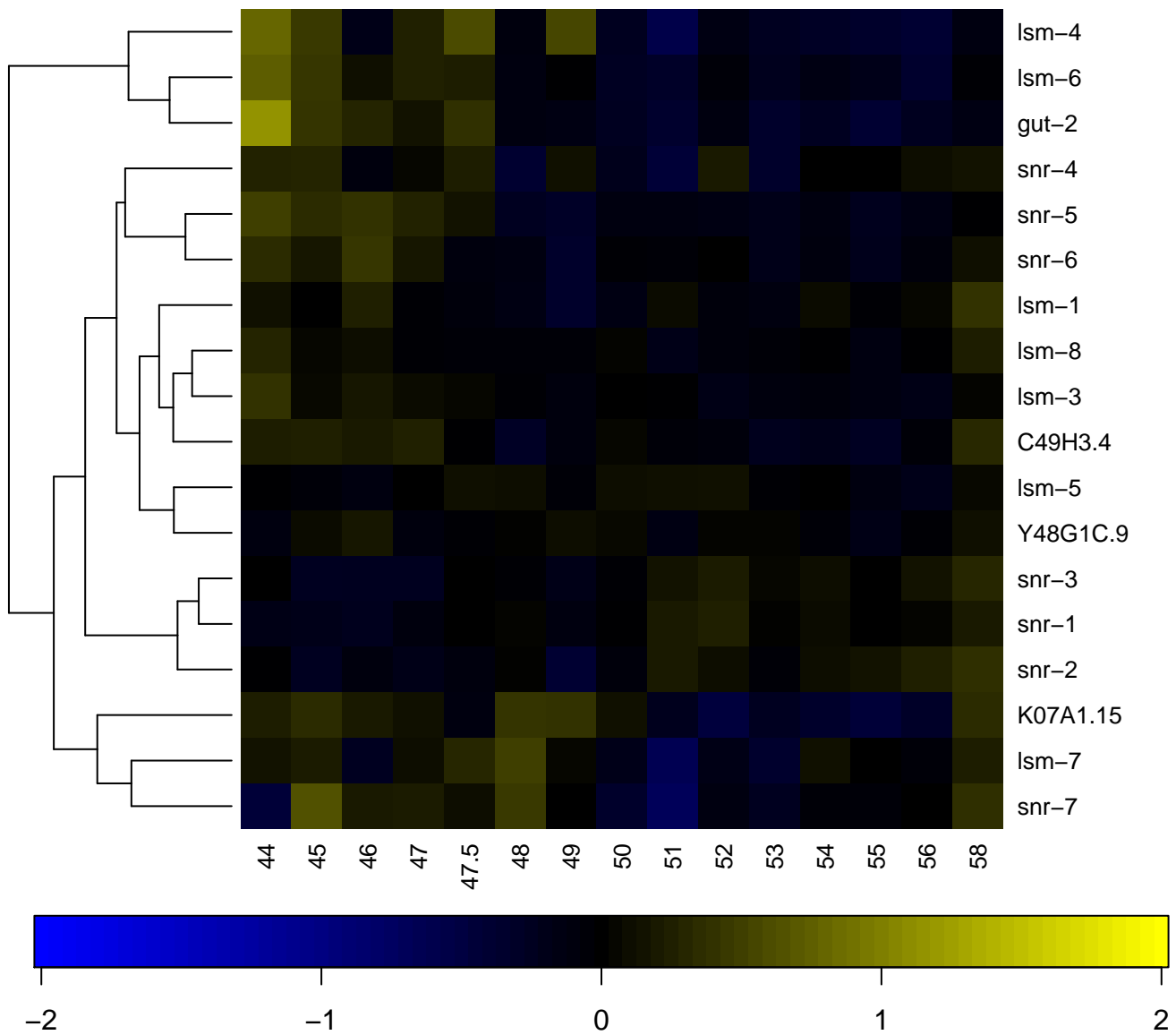
Ligand-binding domain of nuclear hormone receptor



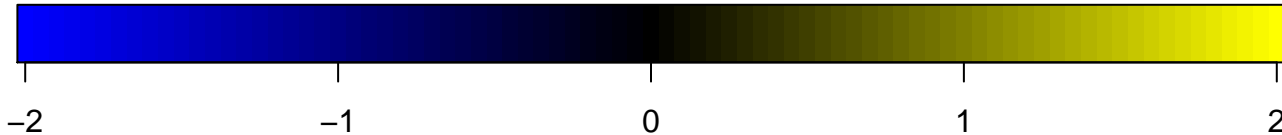
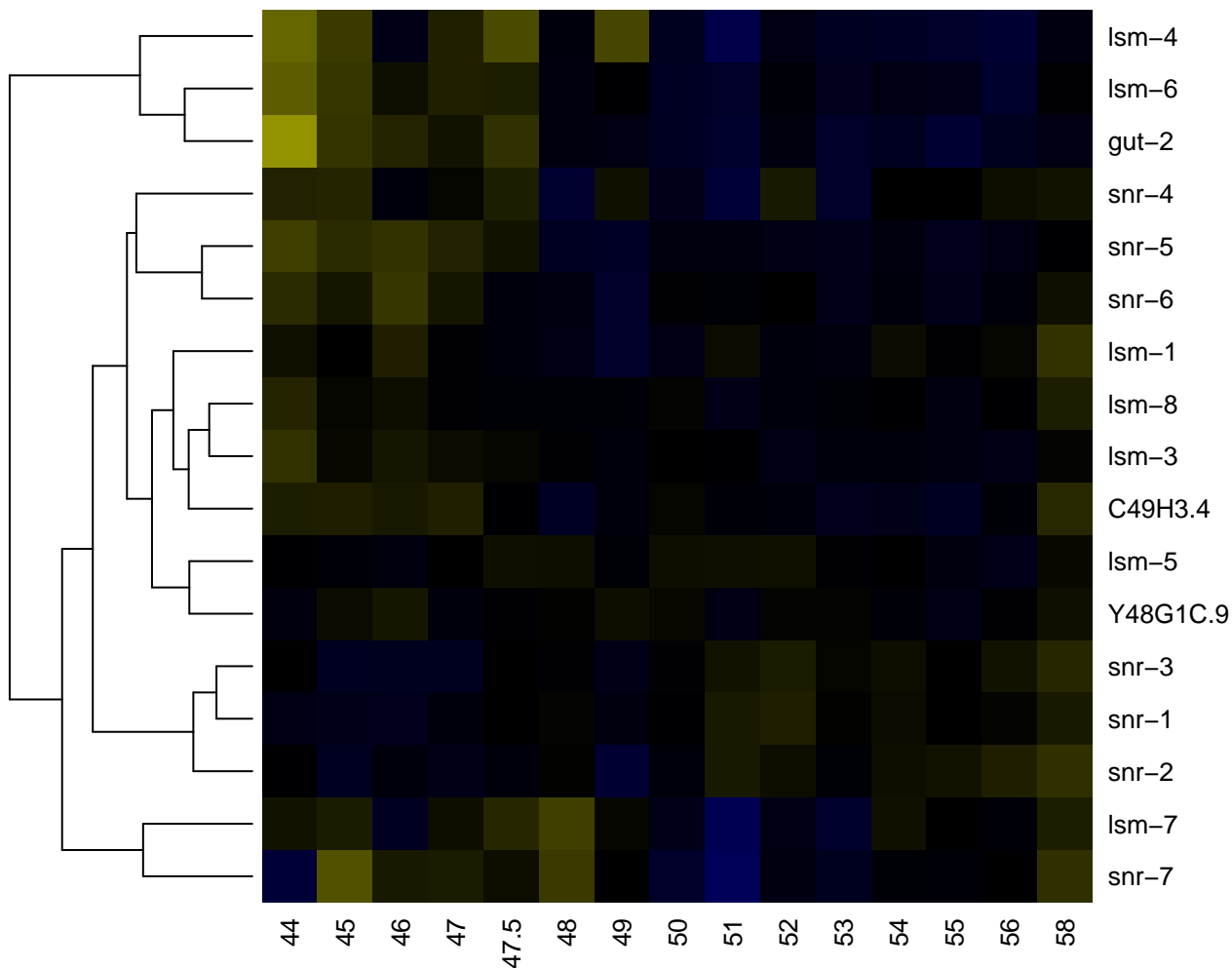
Ligand-gated ion channel



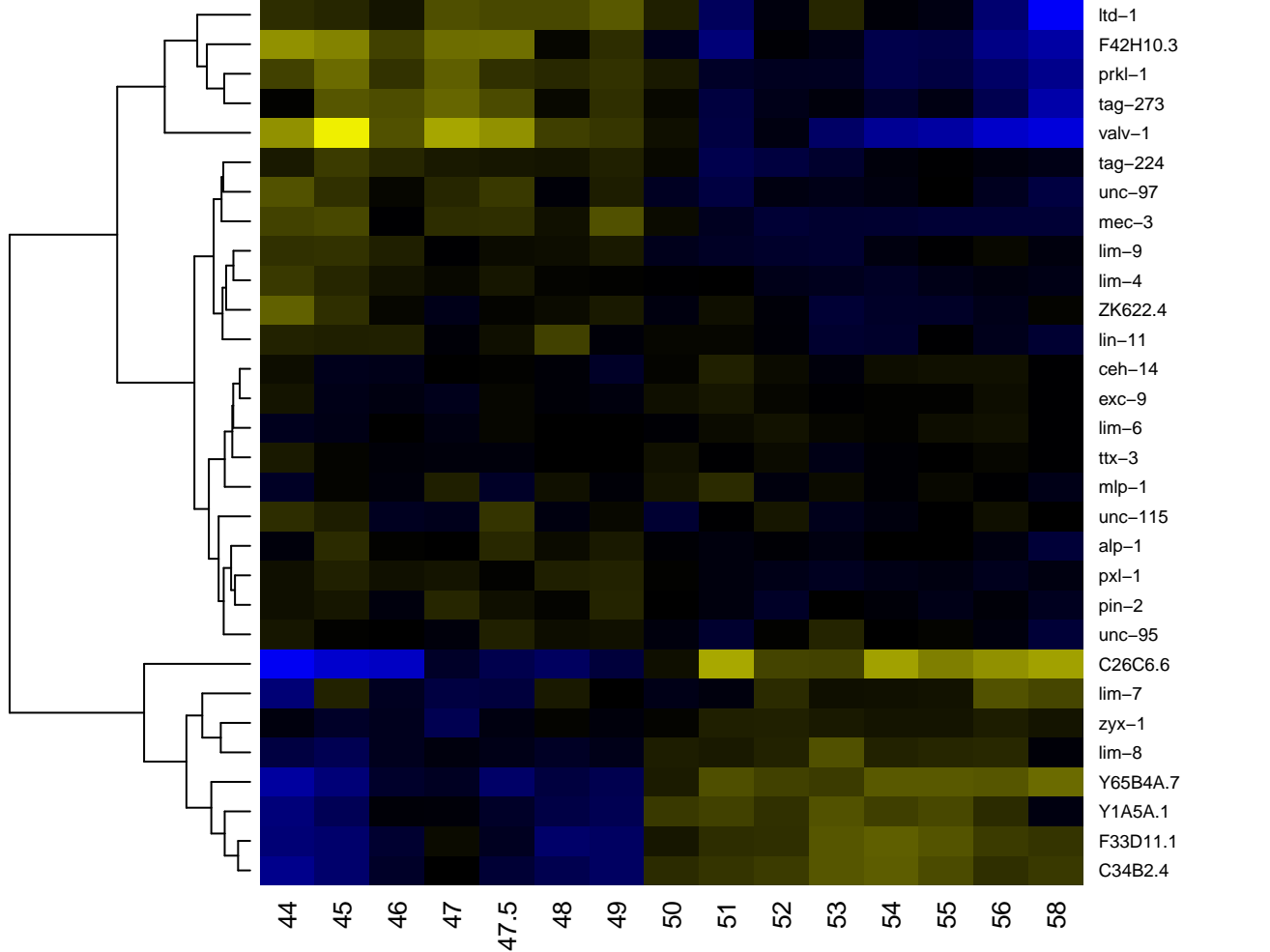
Like-Sm ribonucleoprotein (LSM) domain



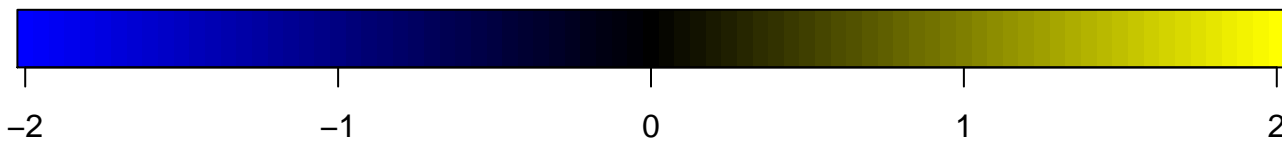
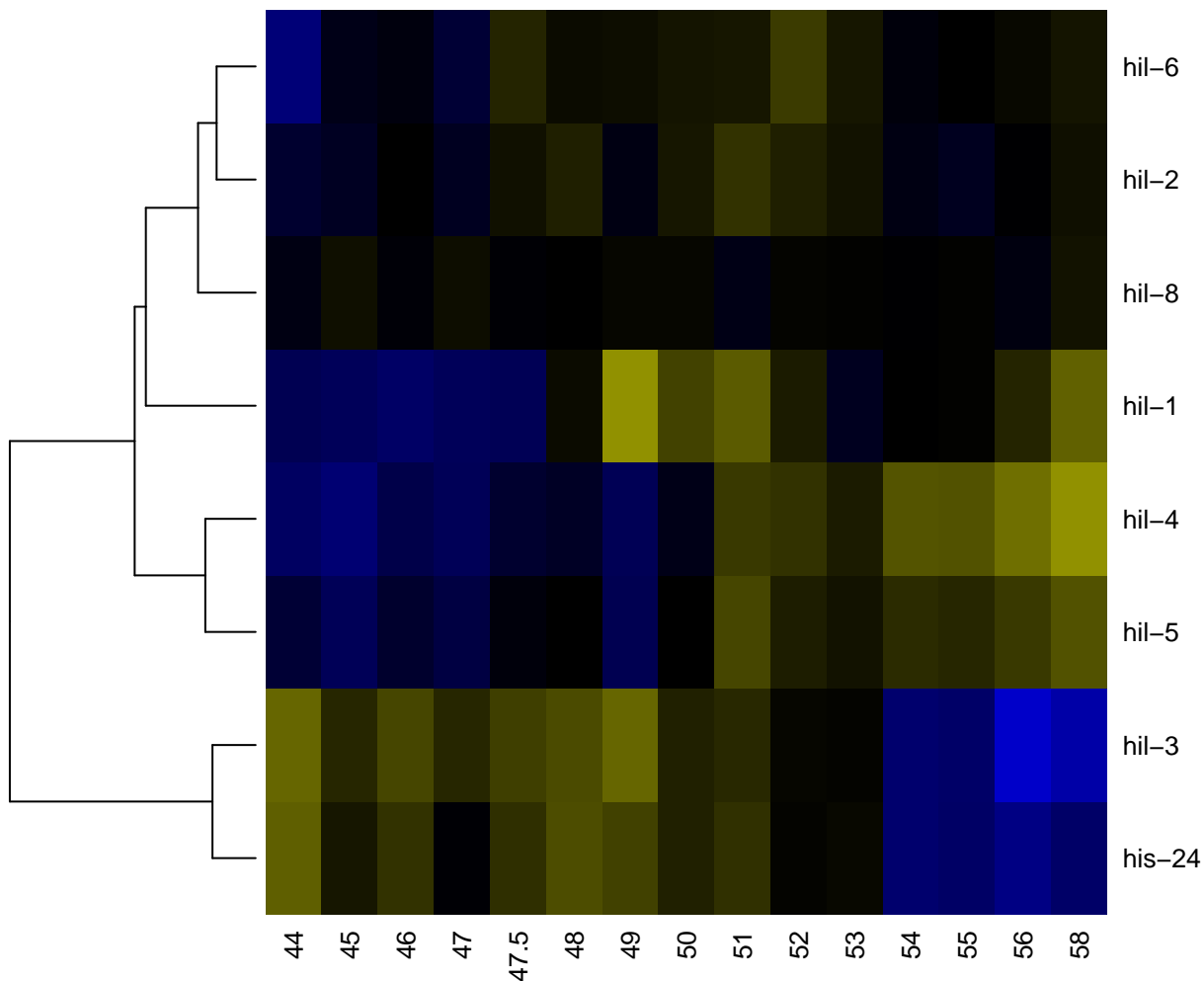
e-Sm ribonucleoprotein (LSM) domain, eukaryotic/archaea-



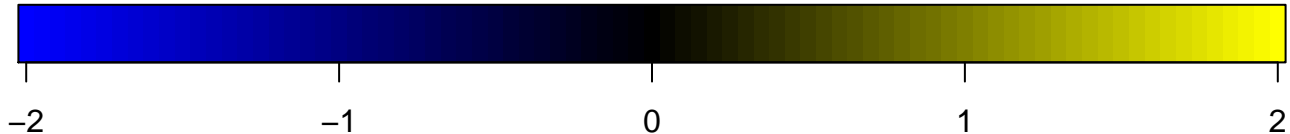
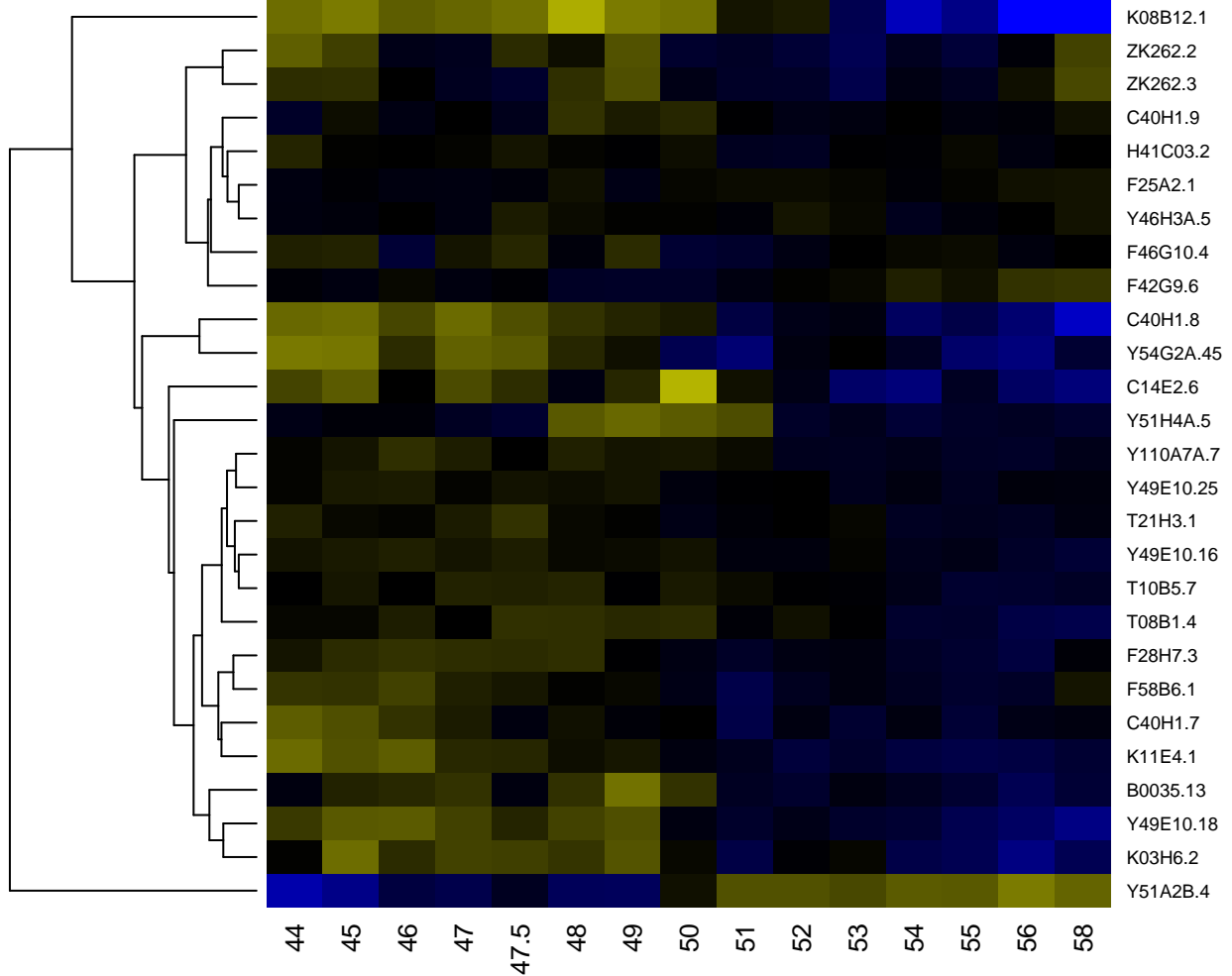
LIM domain



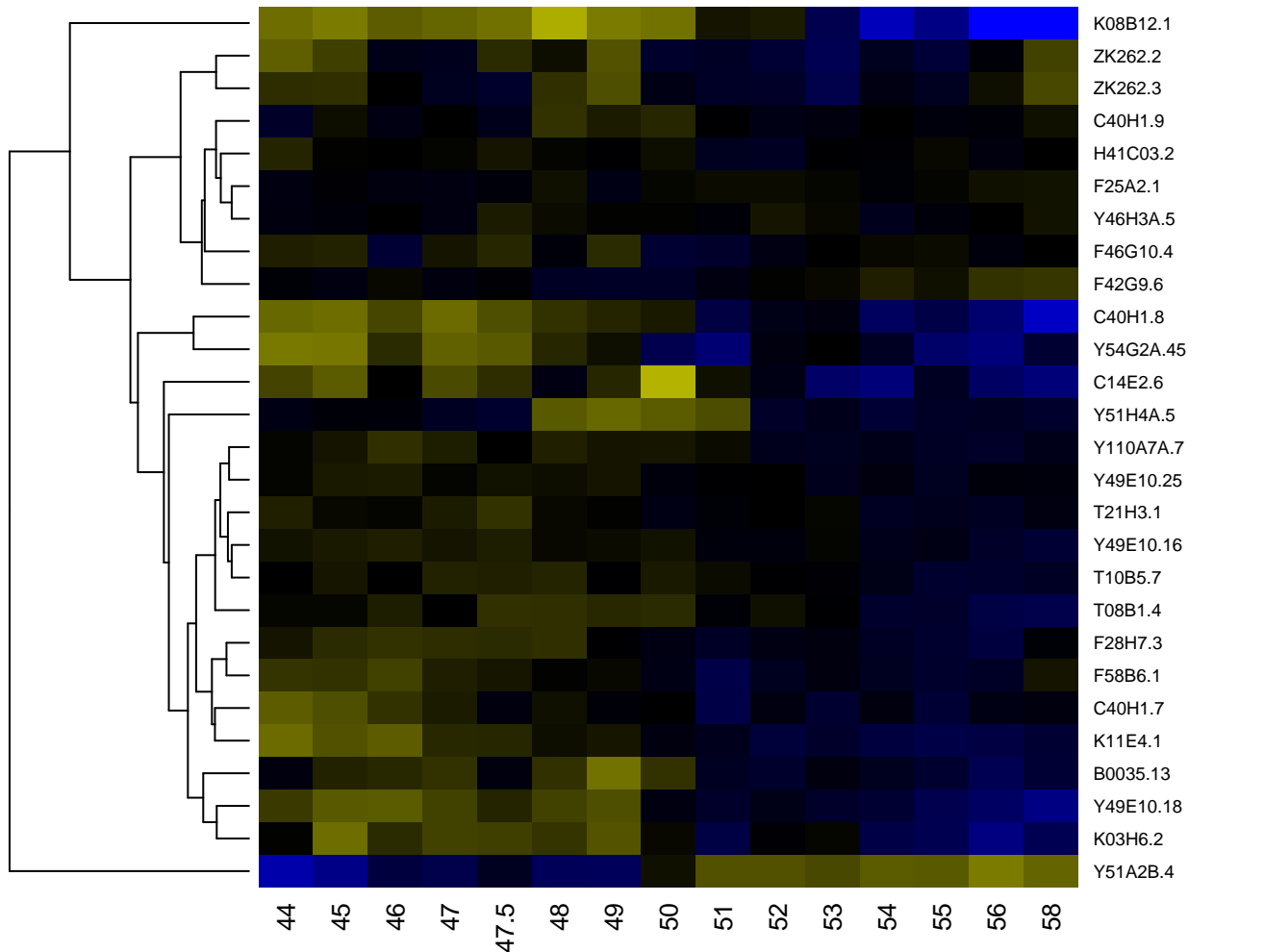
linker histone H1 and H5 family



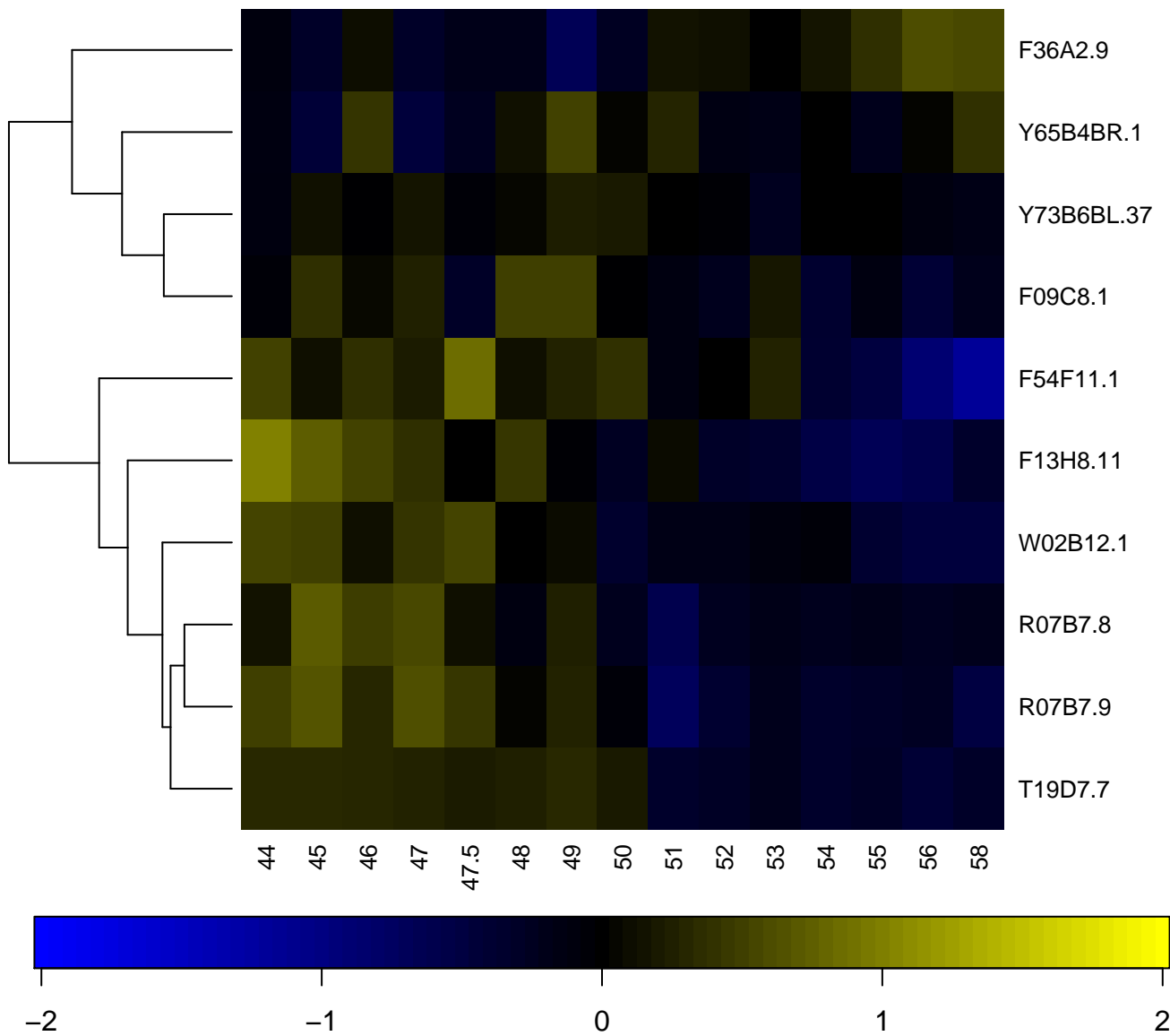
Lipase (class 3)



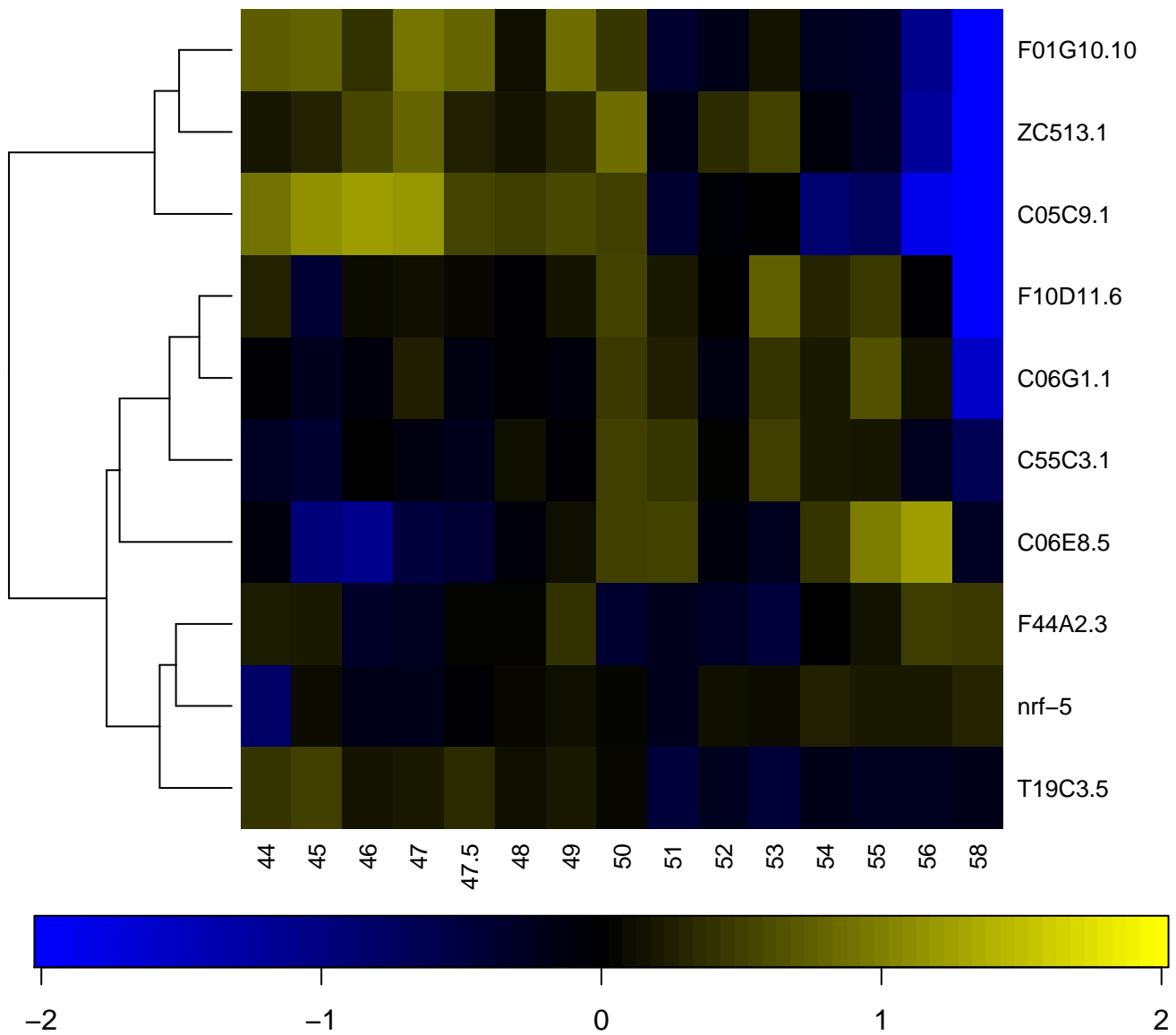
Lipase, class 3



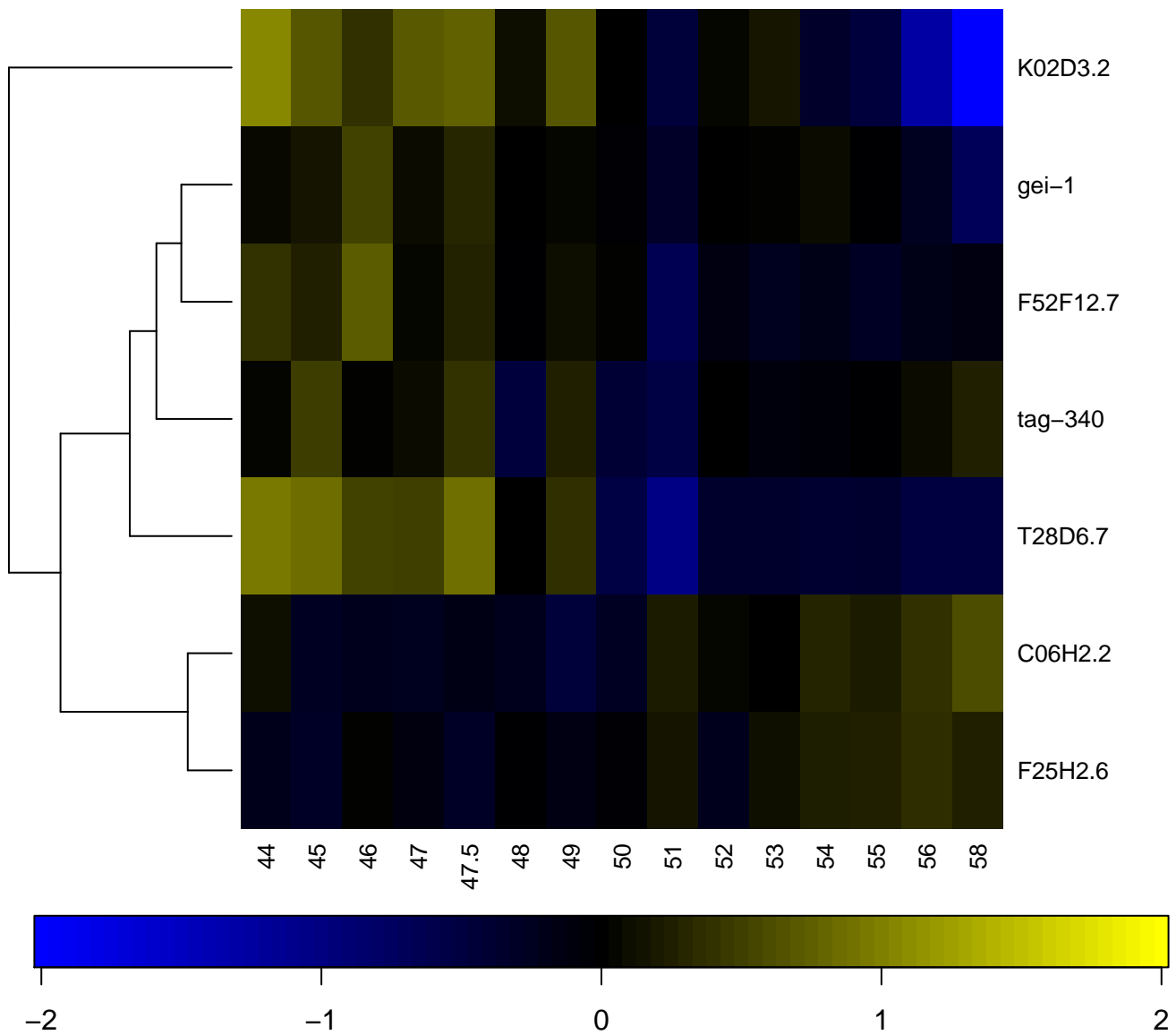
Lipase, GDSL



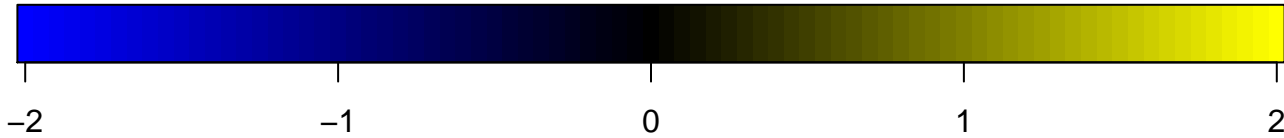
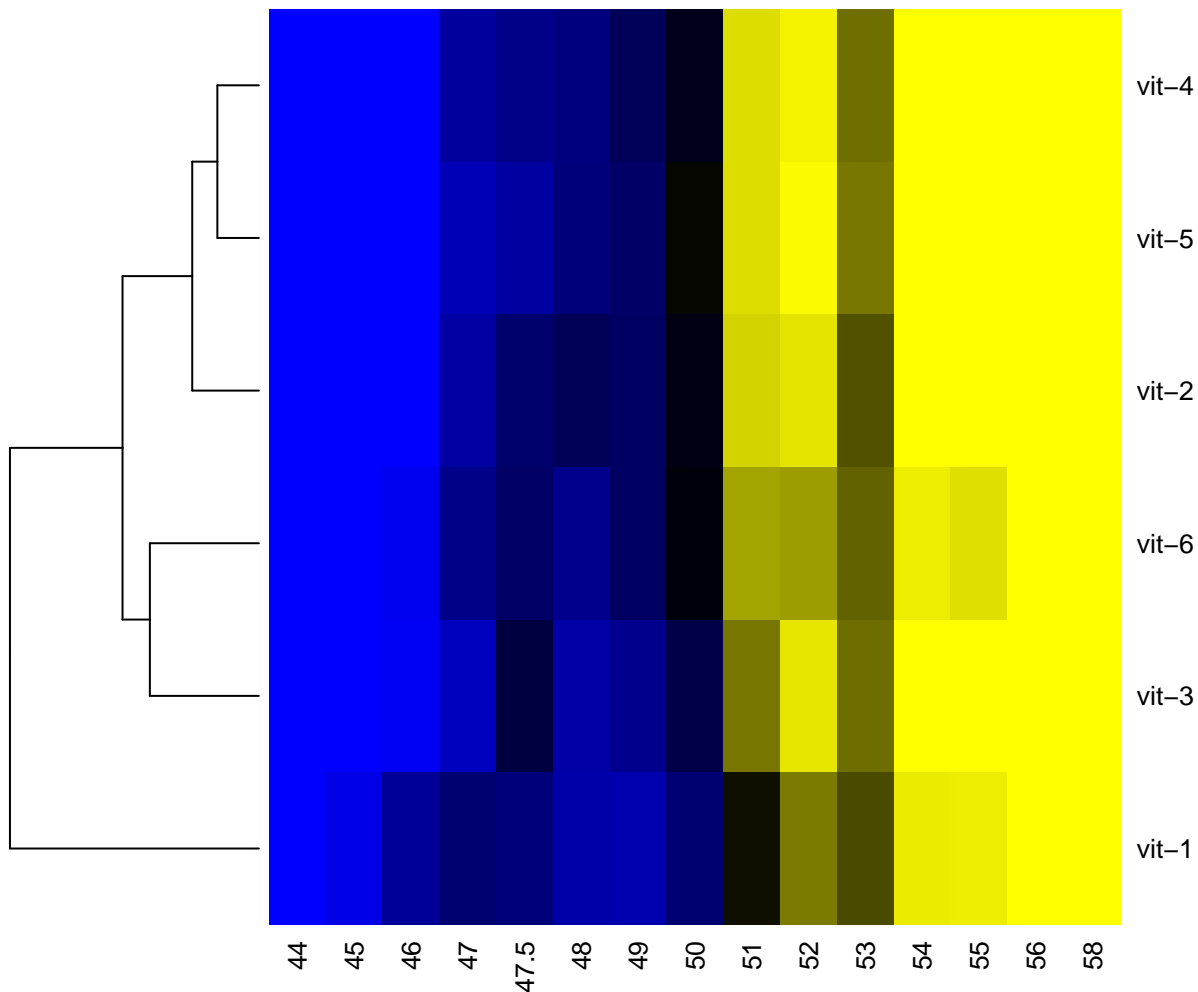
Lipid-binding serum glycoprotein, C-terminal



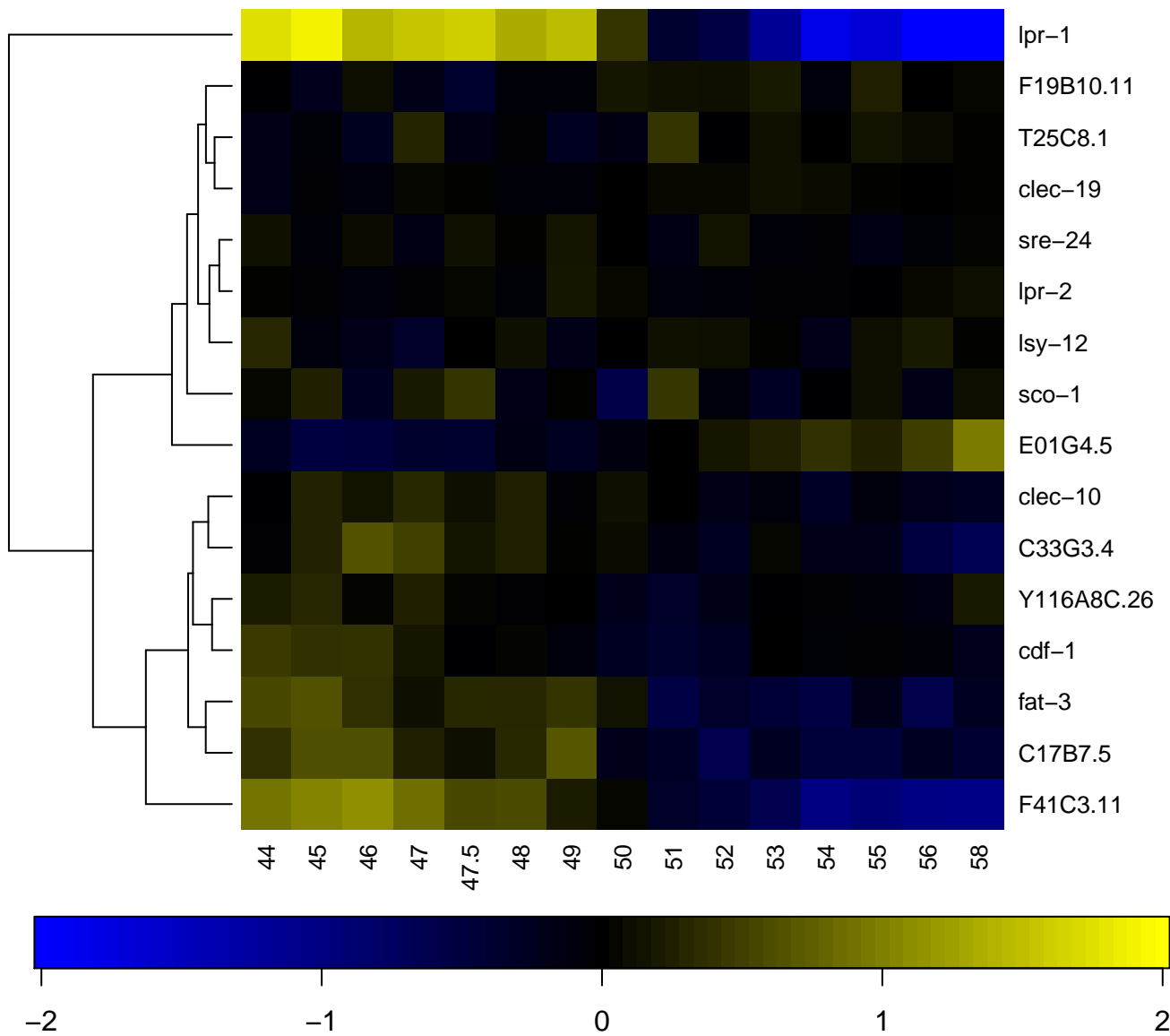
Lipid-binding START



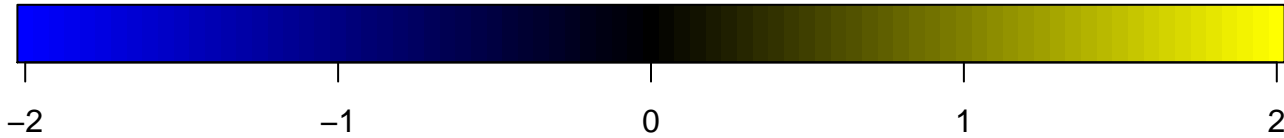
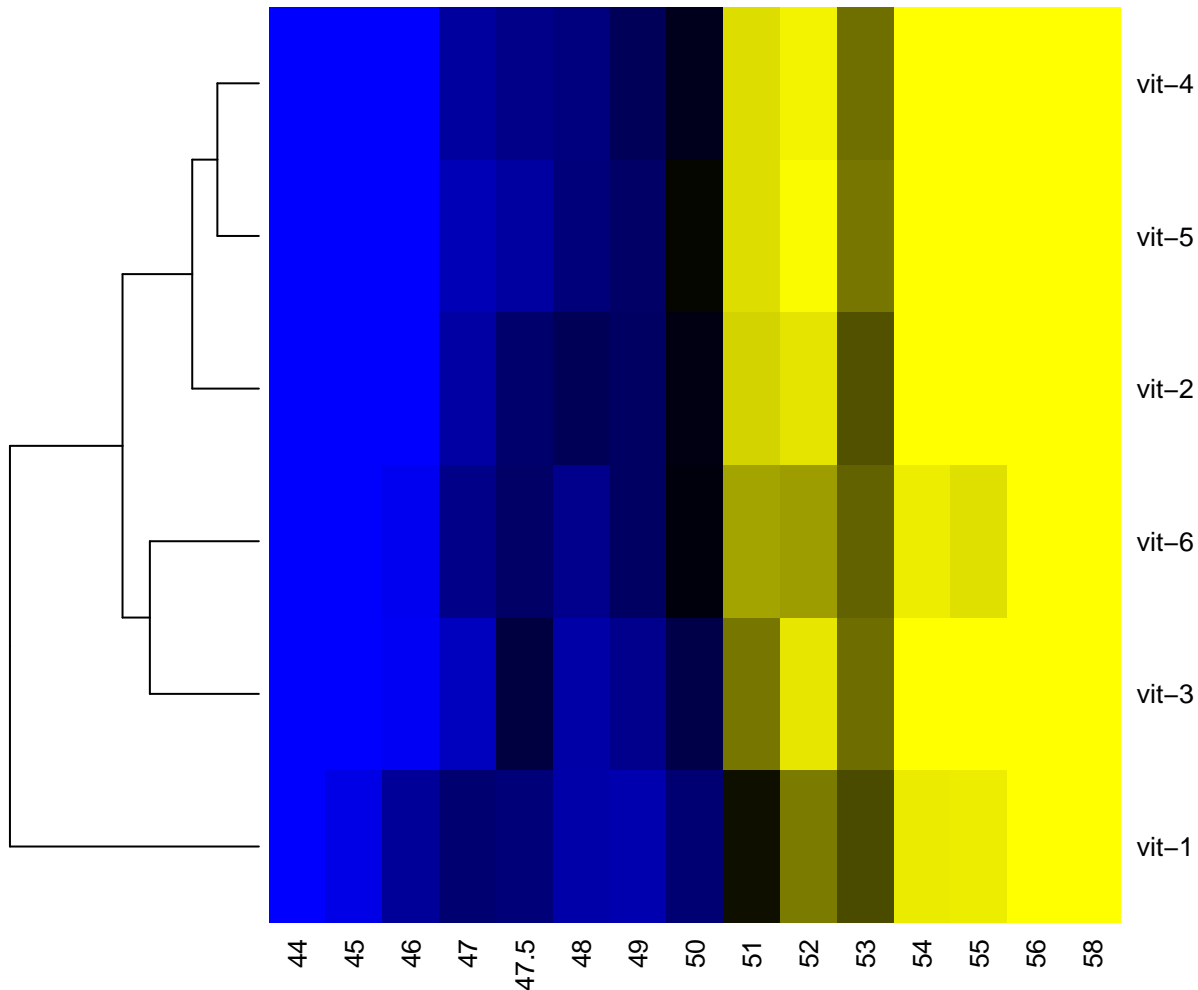
Lipid transport protein, N-terminal



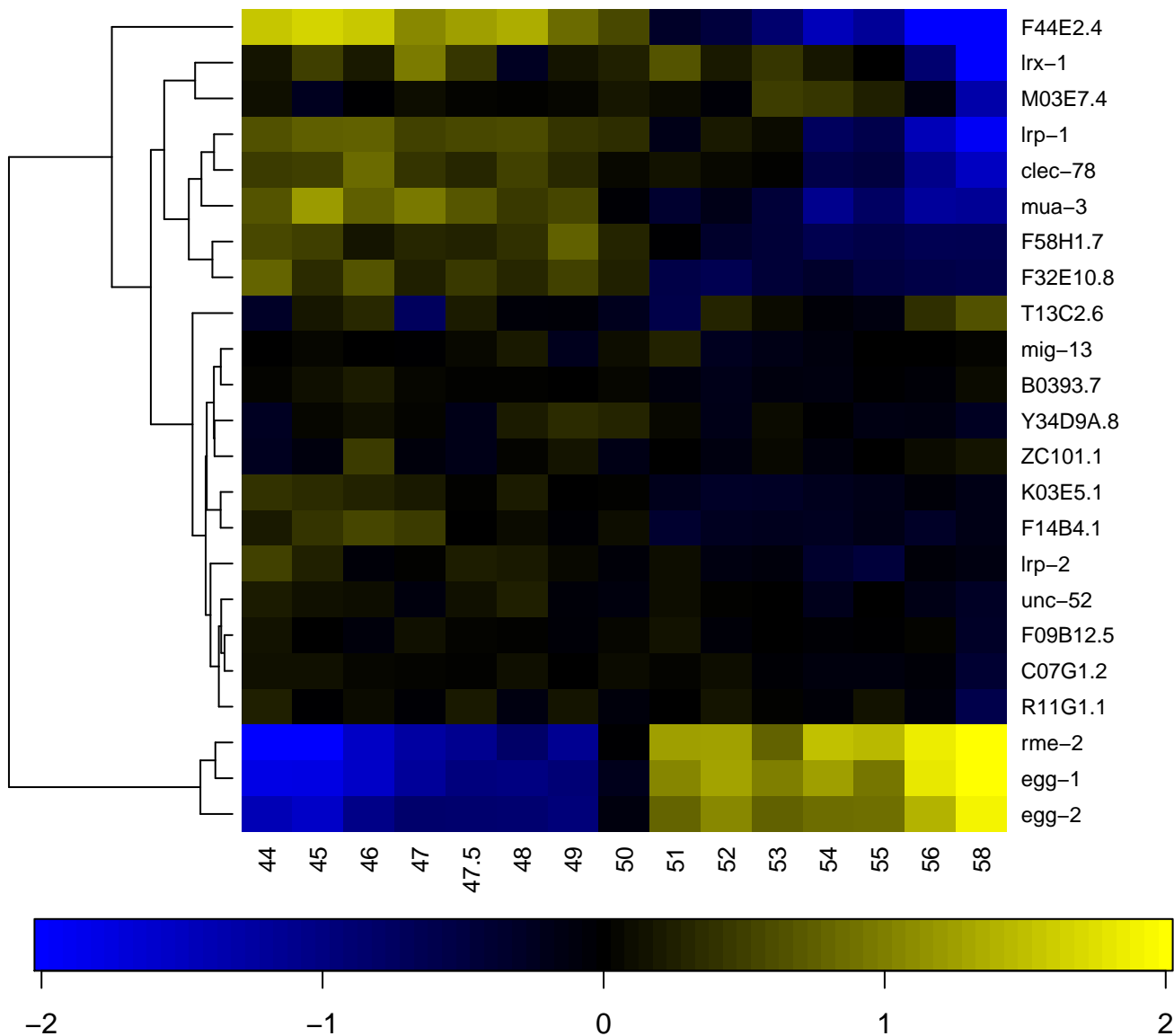
Lipocalin conserved site



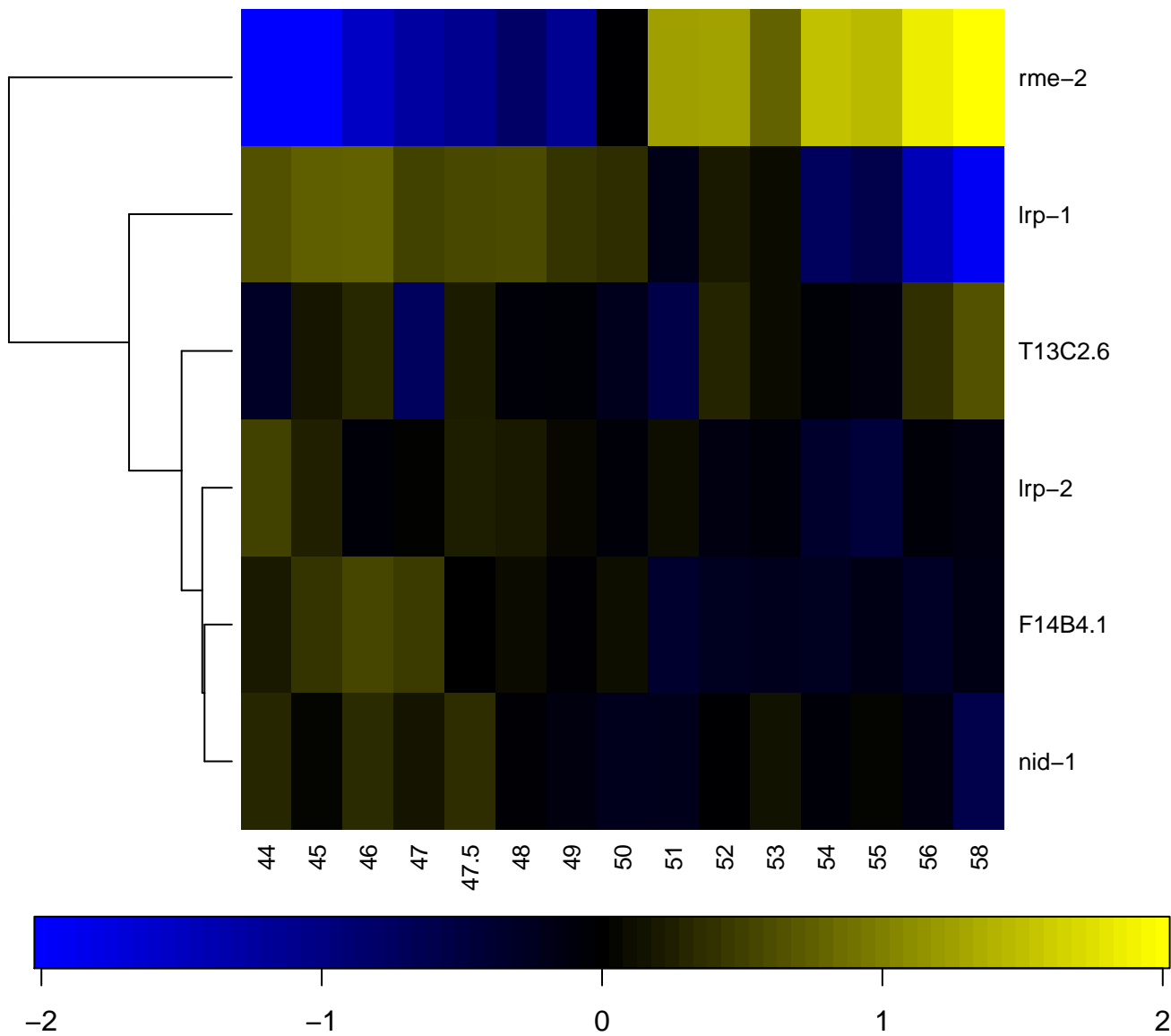
Lipoprotein amino terminal region



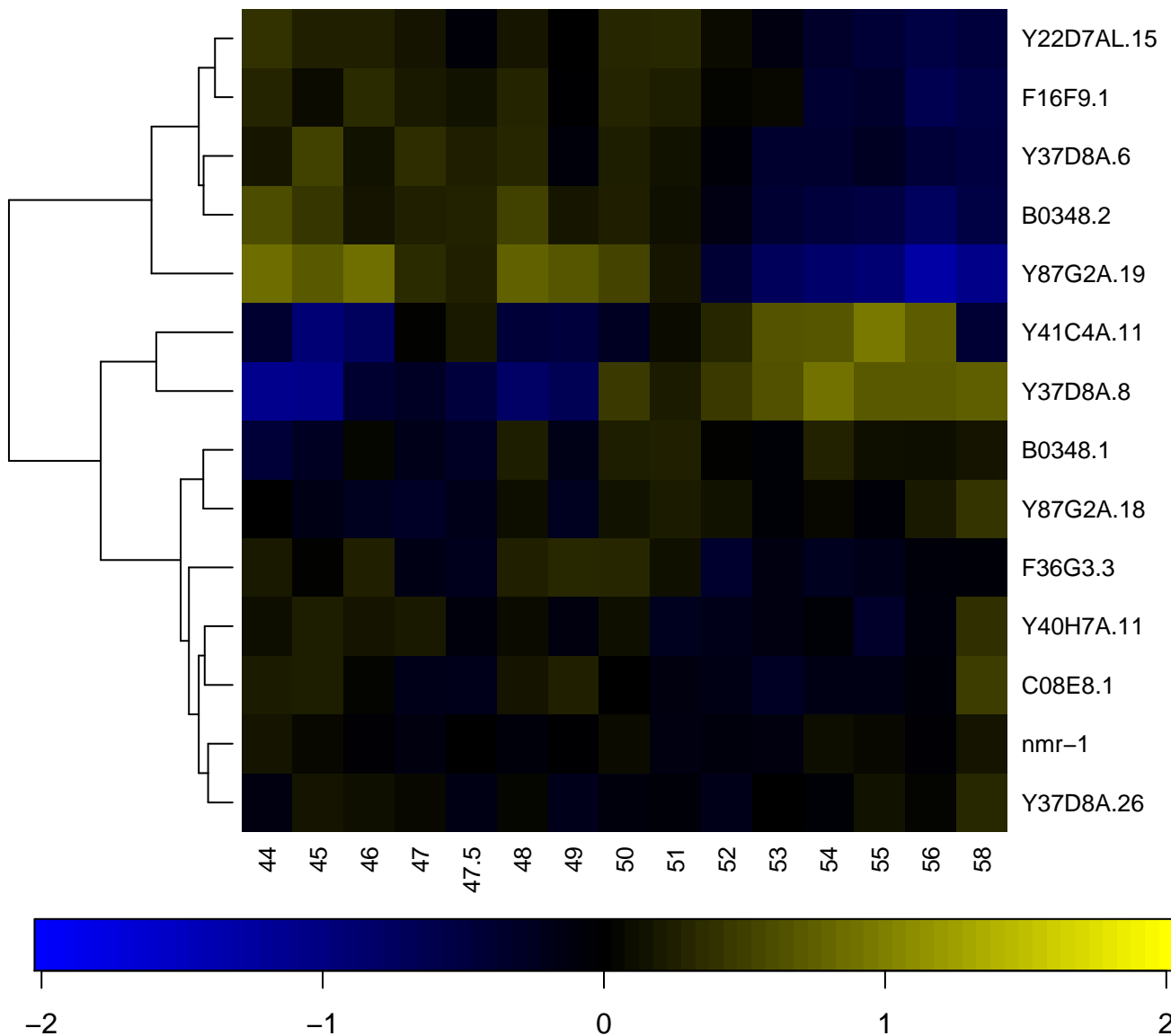
Low-density lipoprotein receptor domain class A



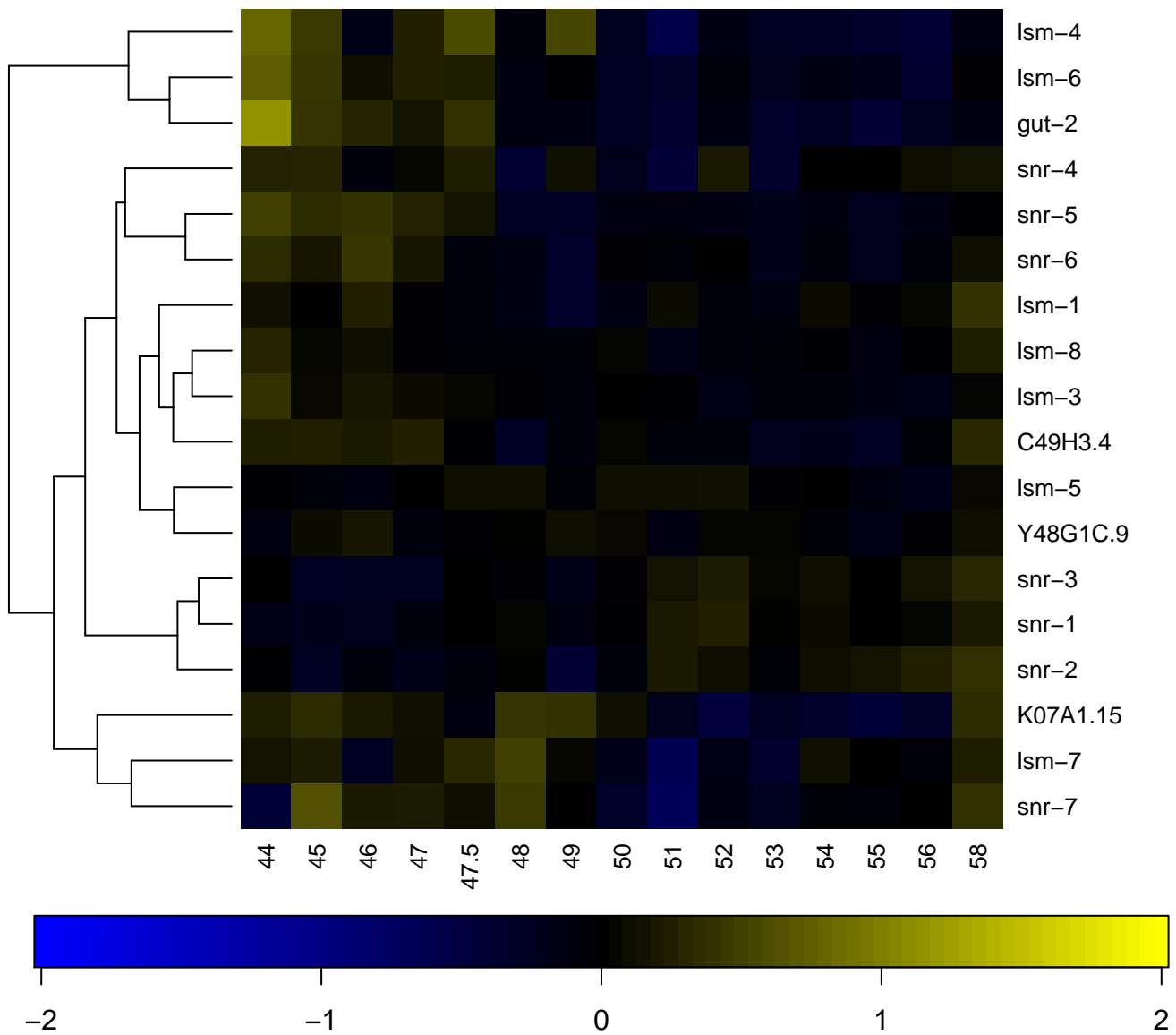
Low-density lipoprotein receptor repeat class B



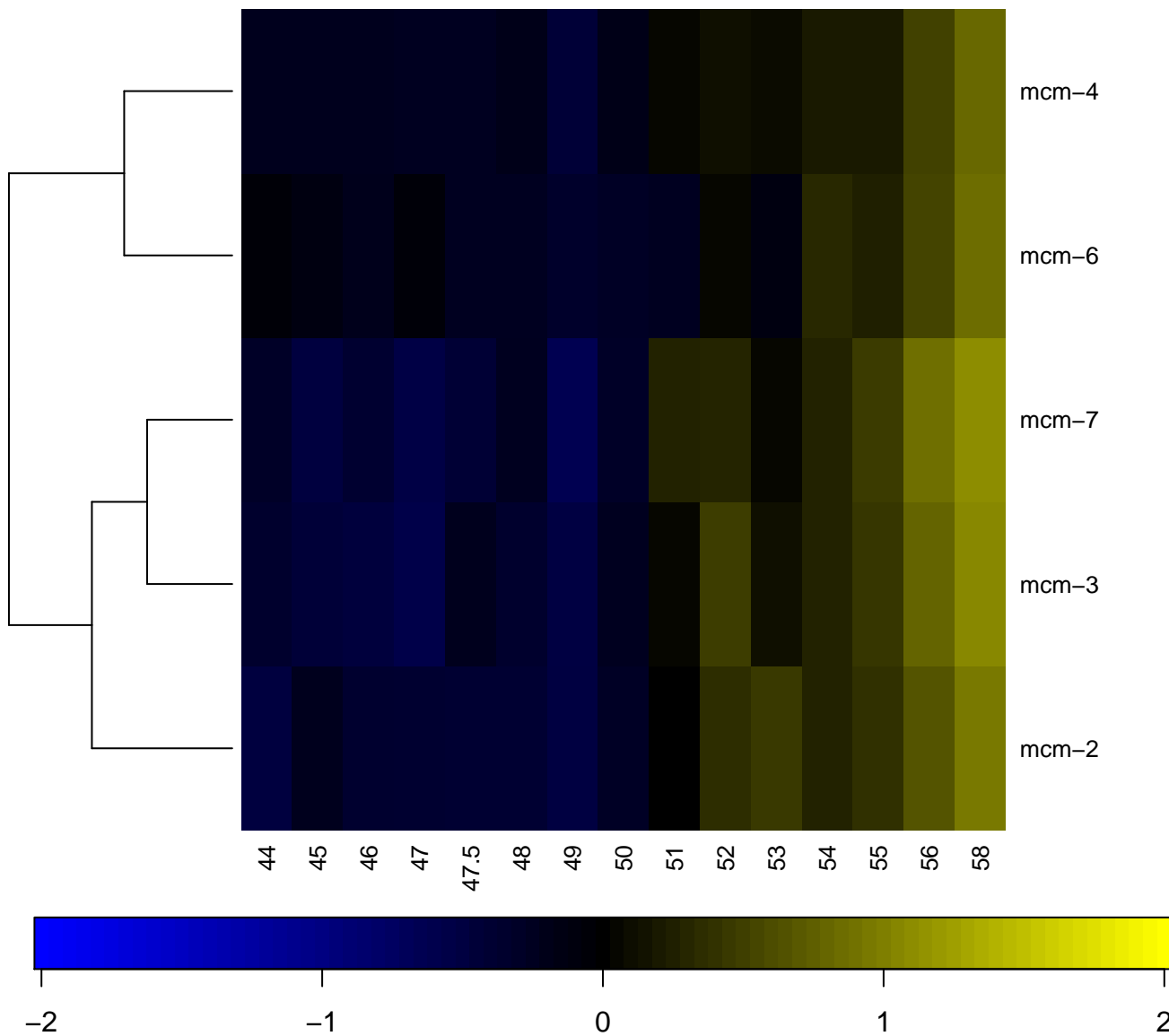
LPS-induced tumor necrosis factor alpha factor



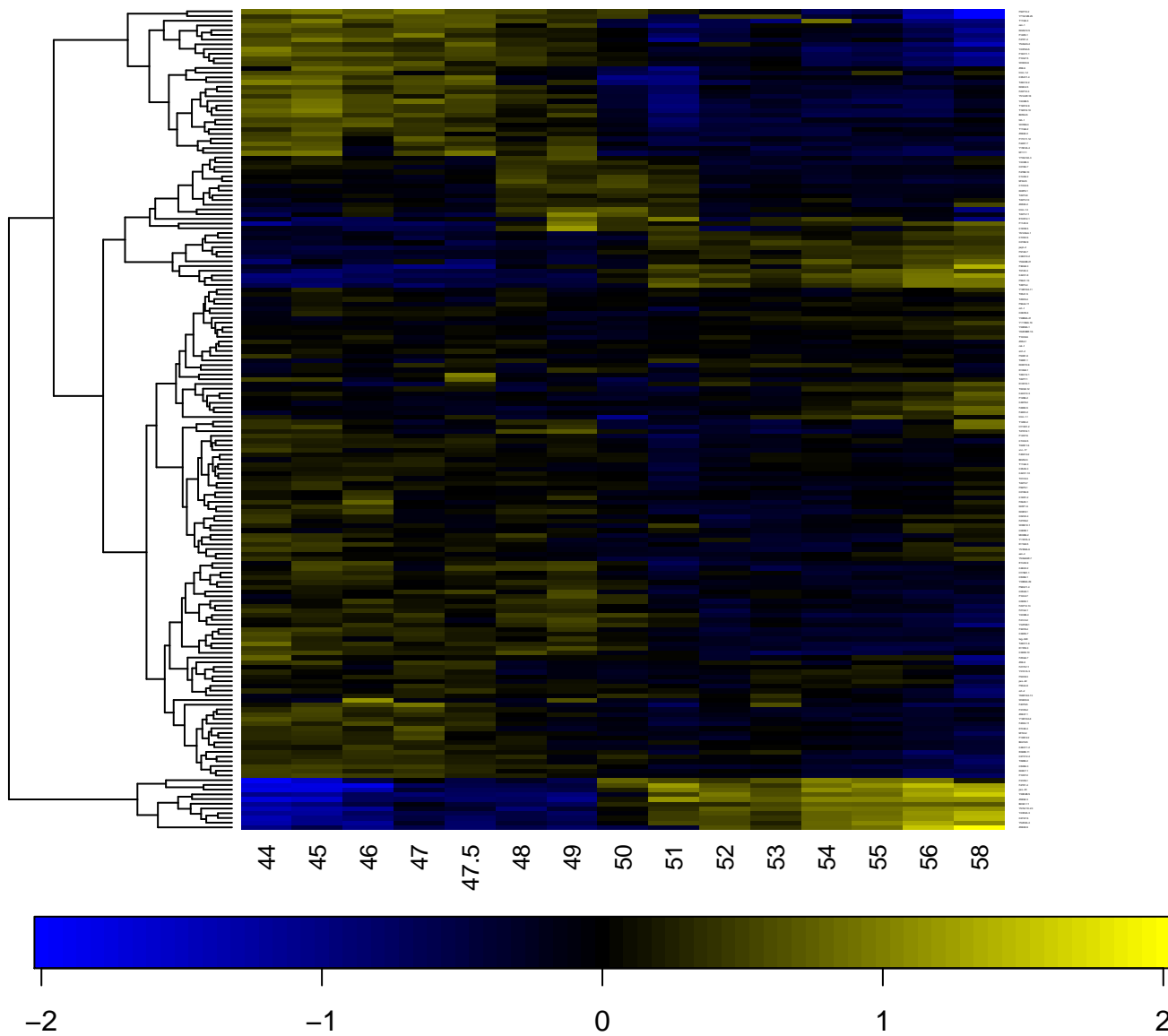
LSM domain



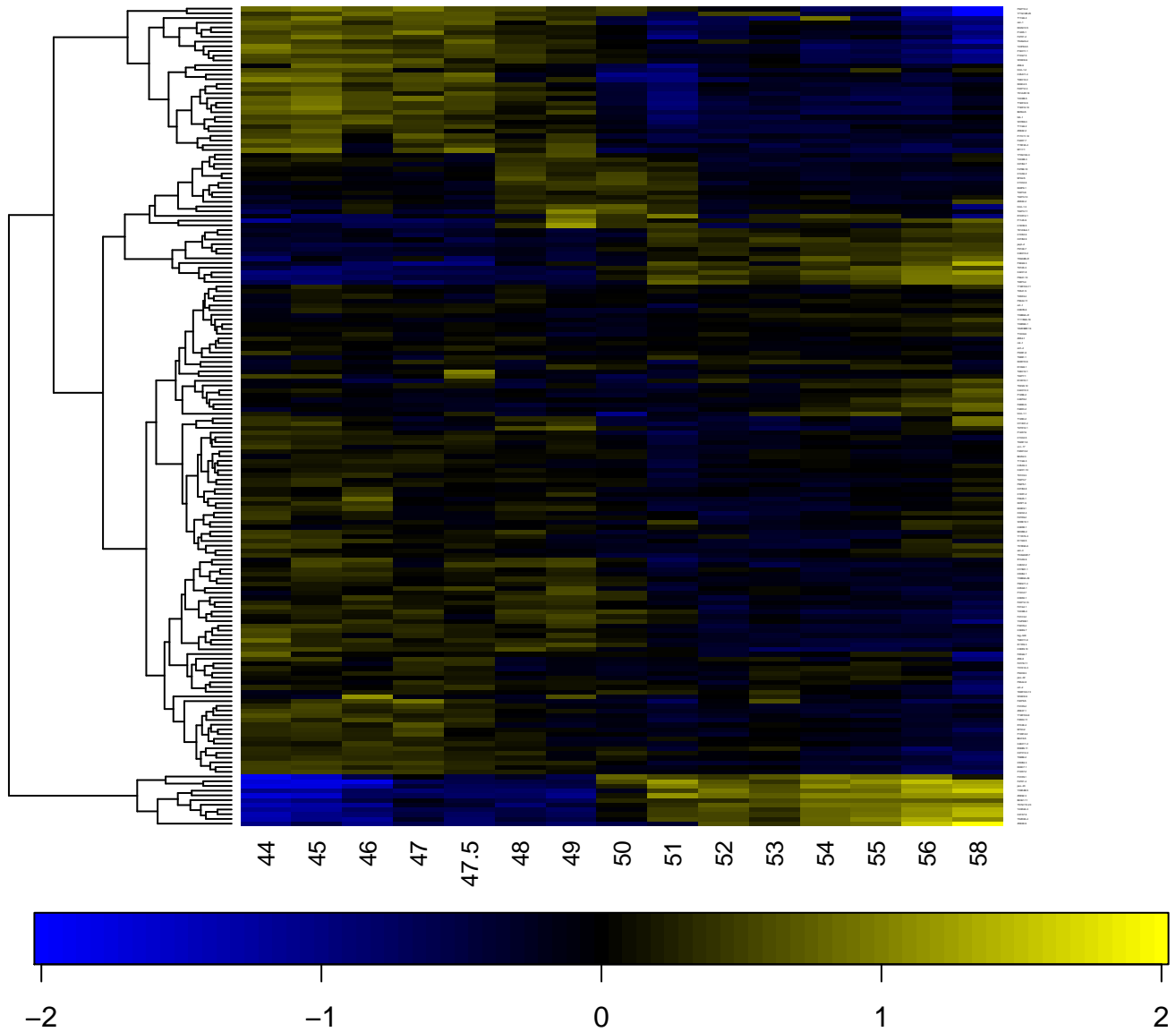
Magnesium chelatase, subunit ChII



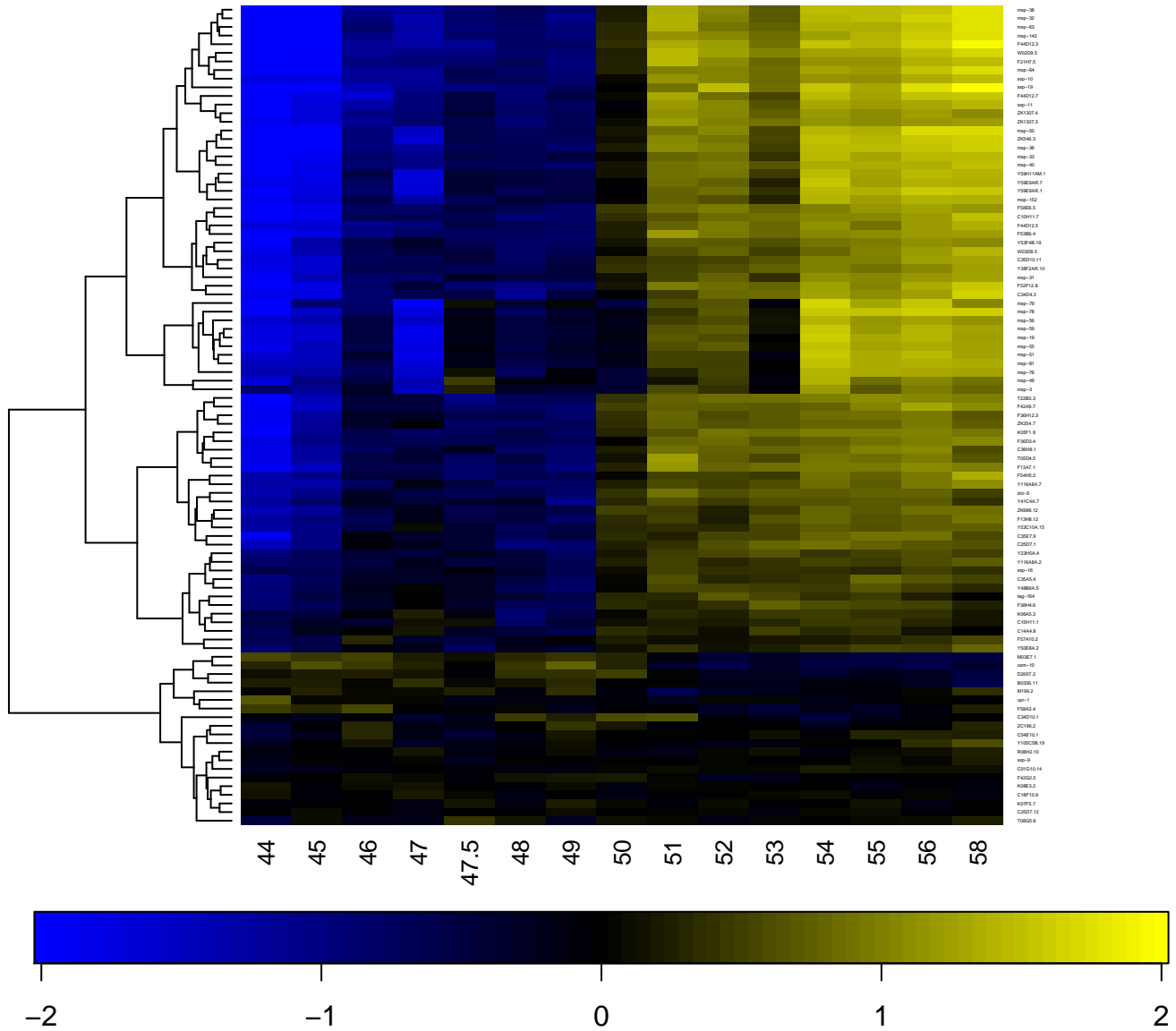
Major Facilitator Superfamily



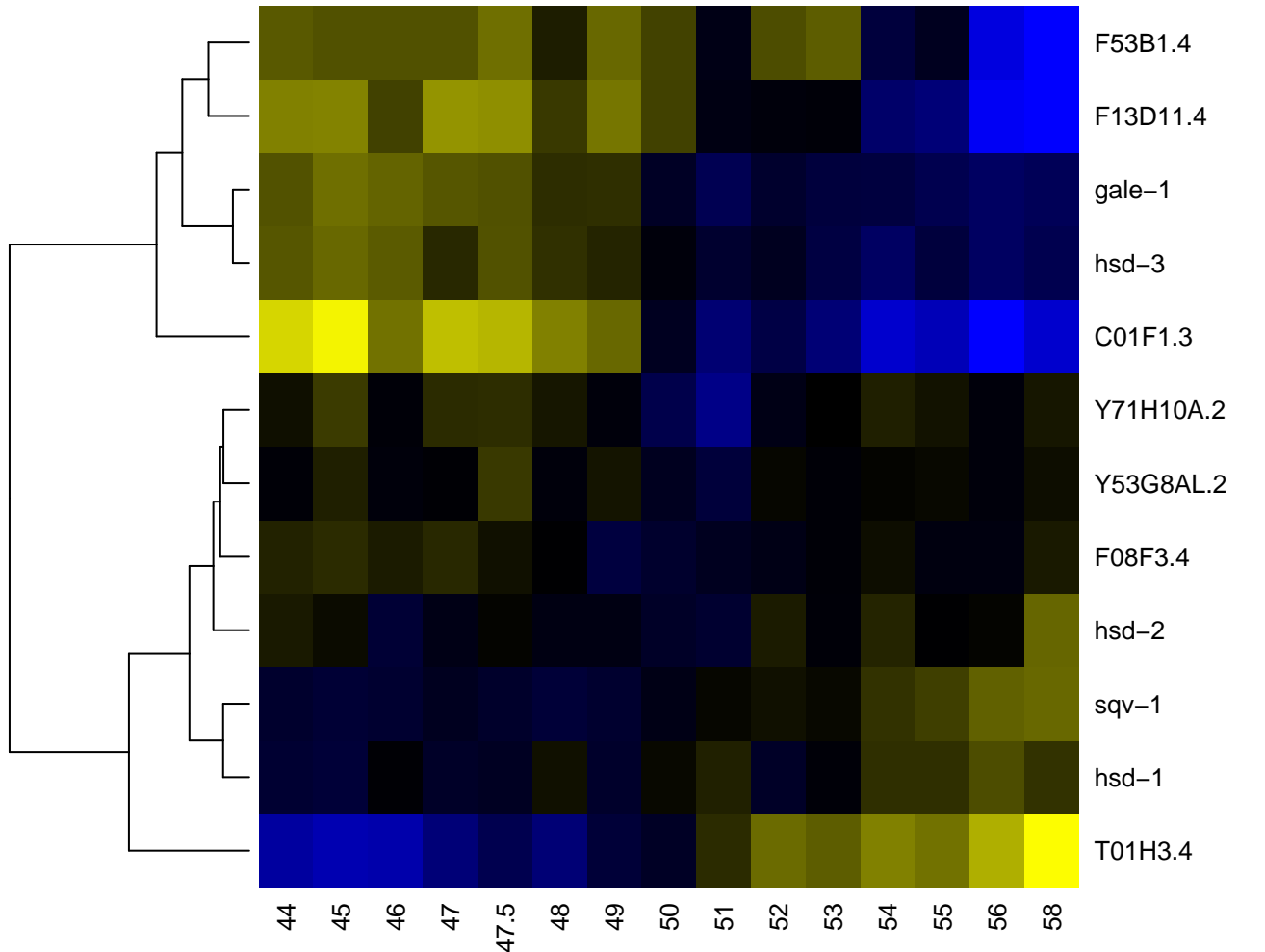
Major facilitator superfamily MFS-1



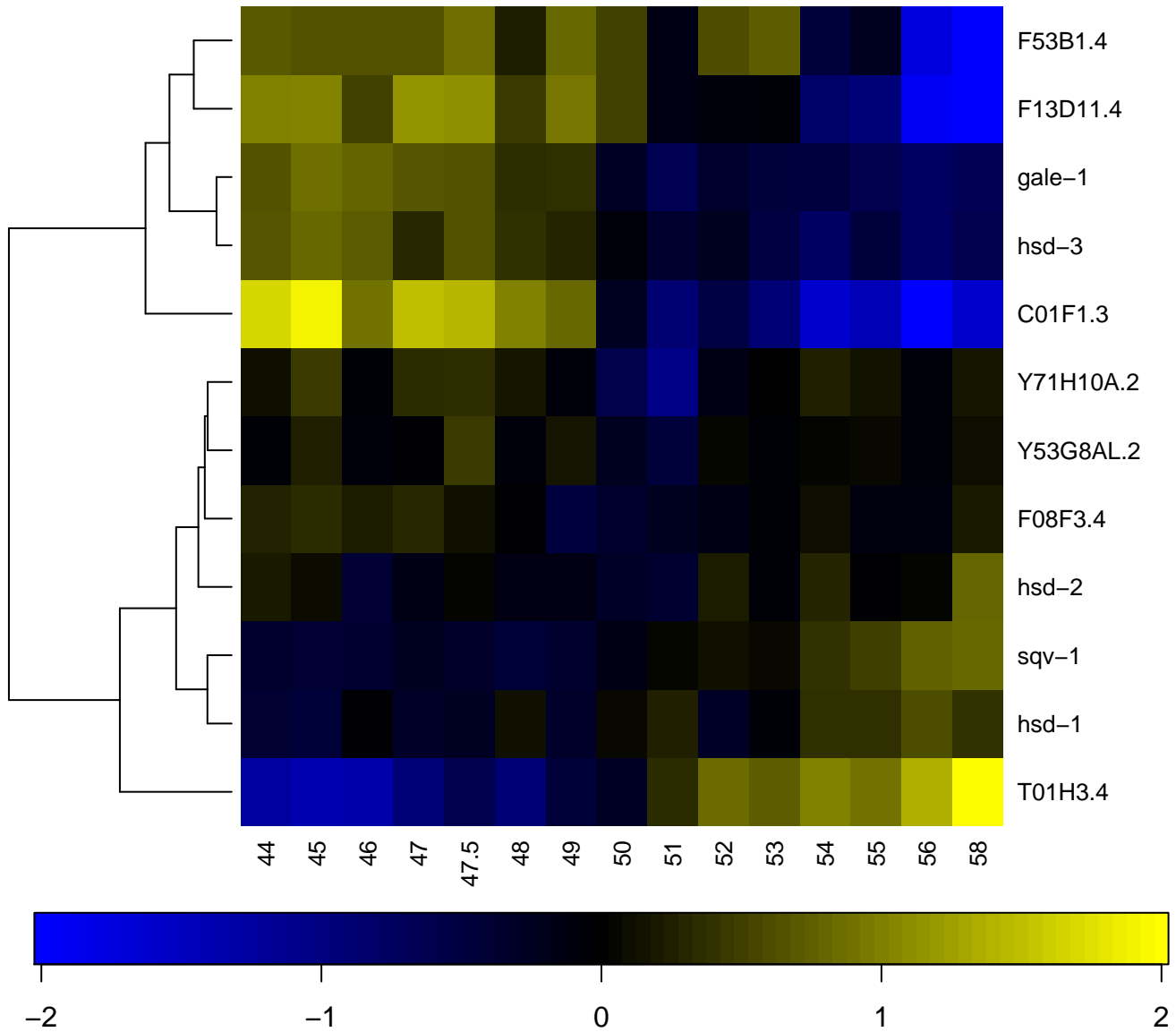
Major sperm protein



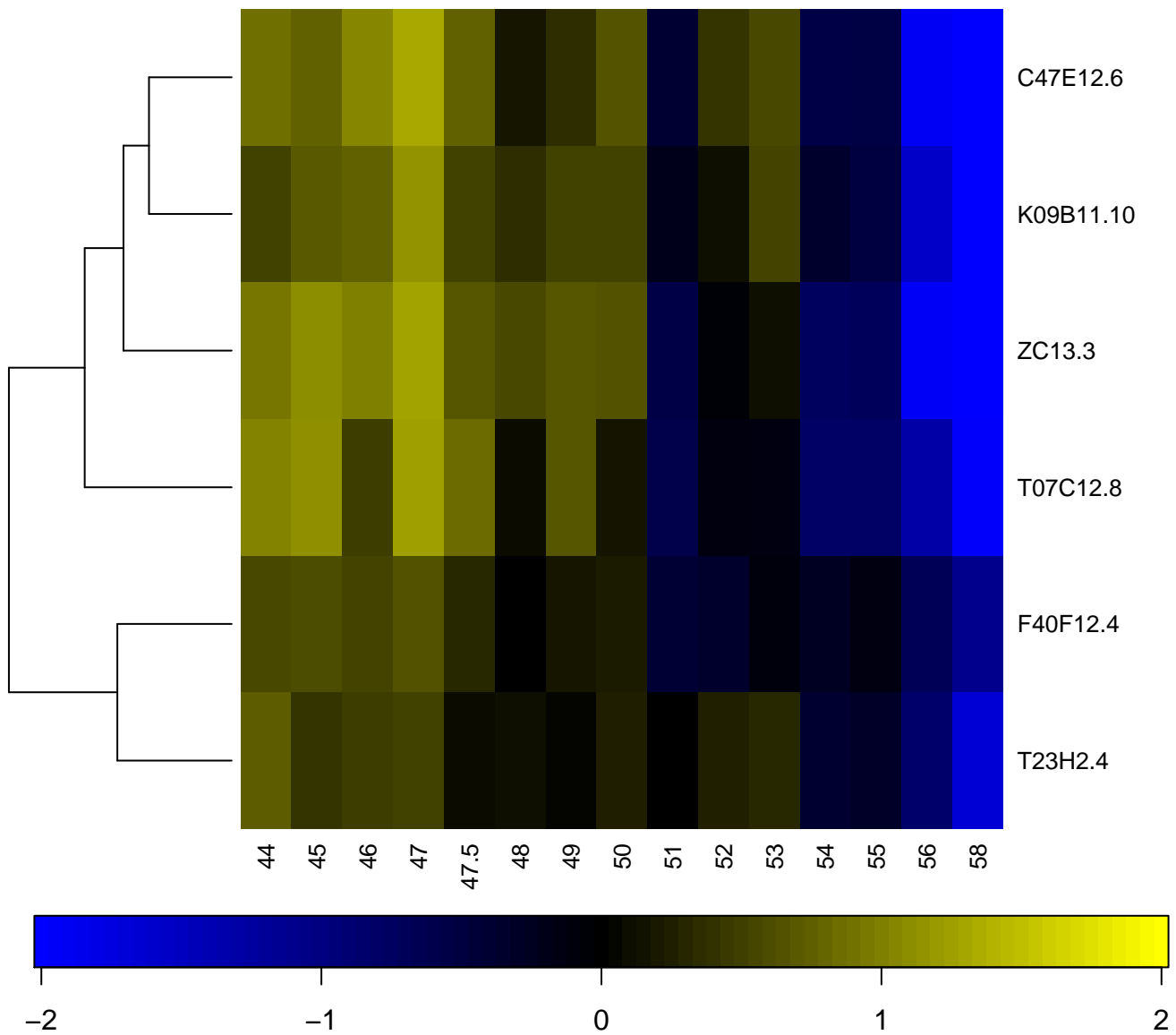
Male sterility protein



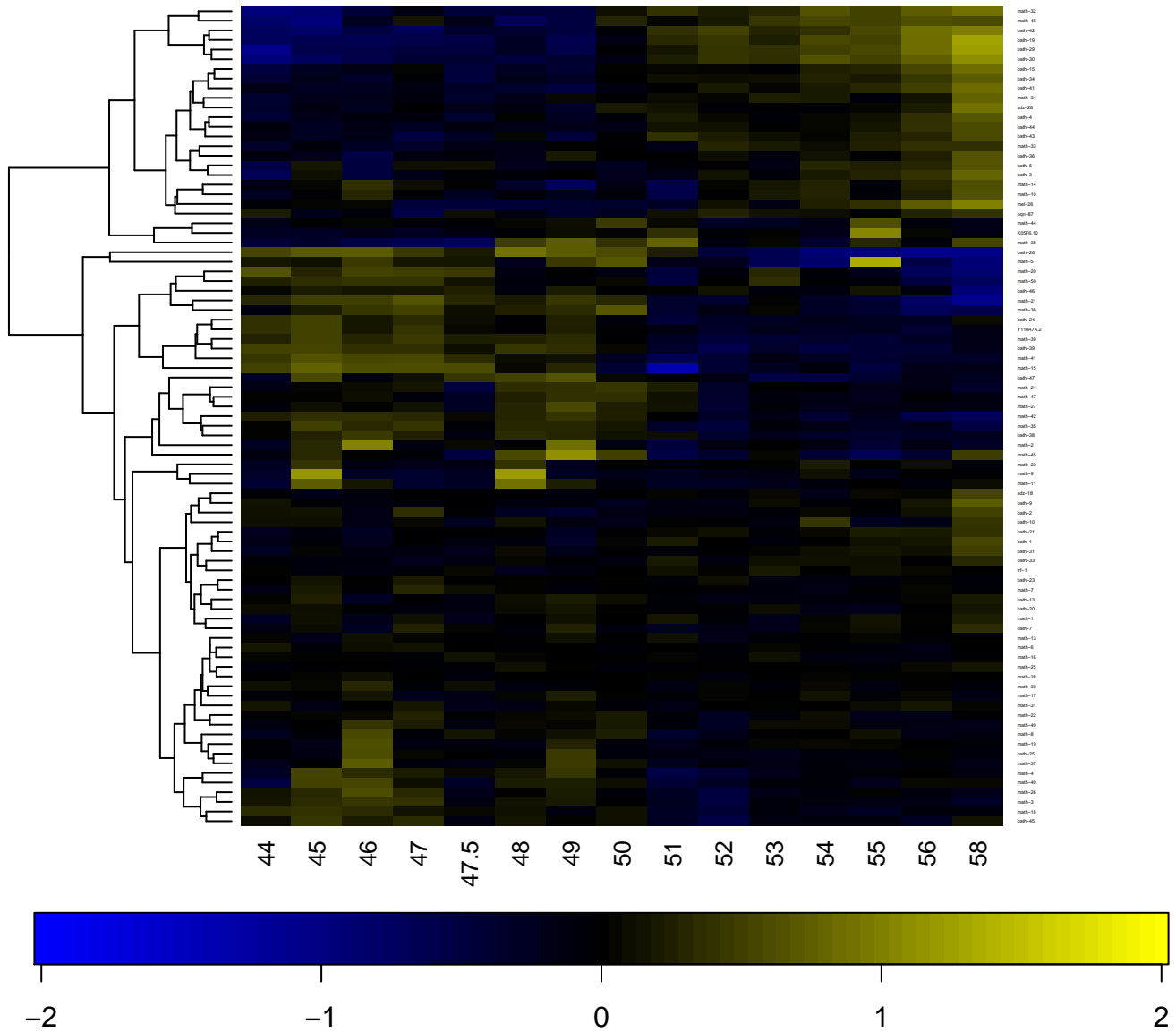
Male sterility, NAD-binding



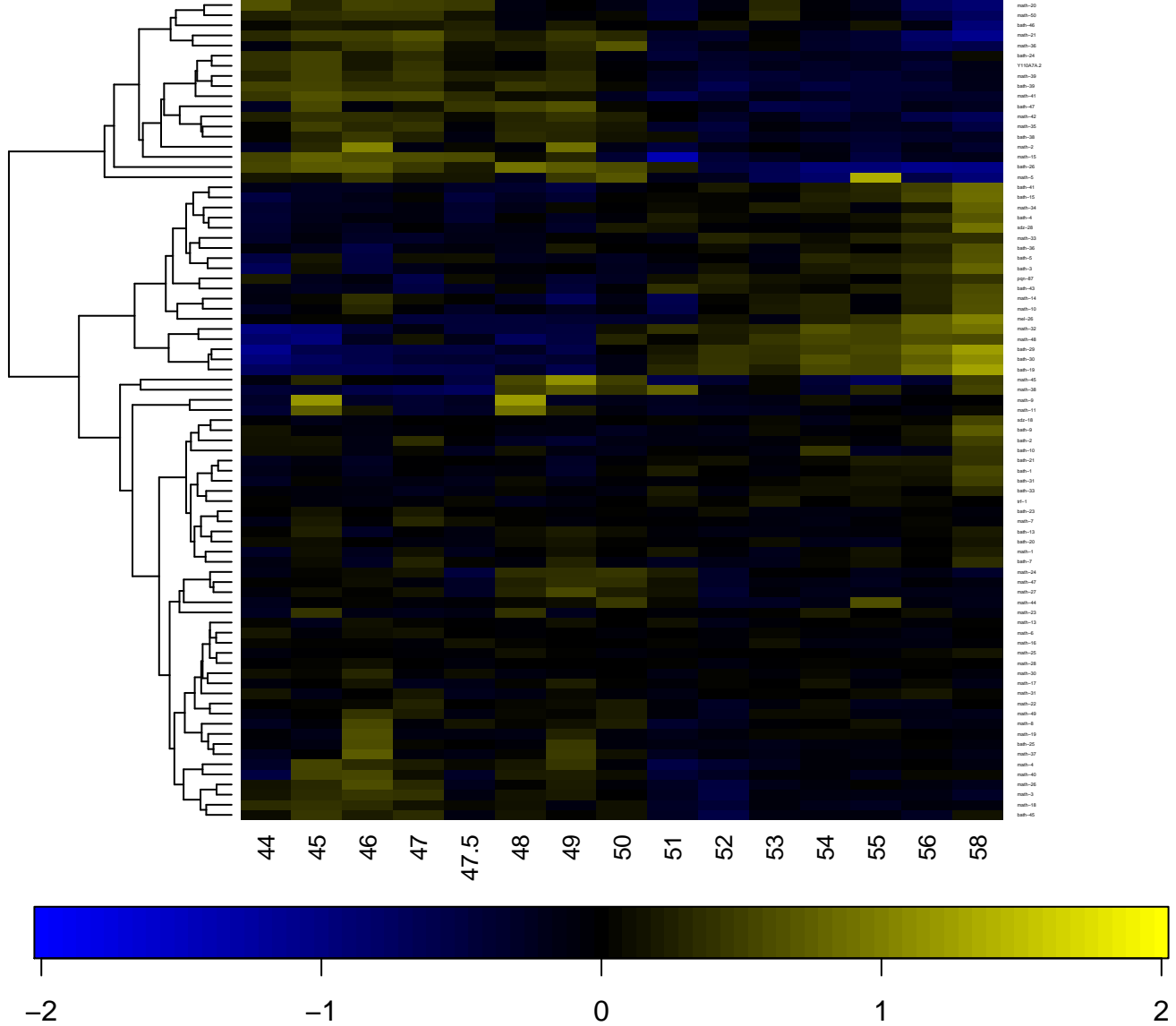
MAM



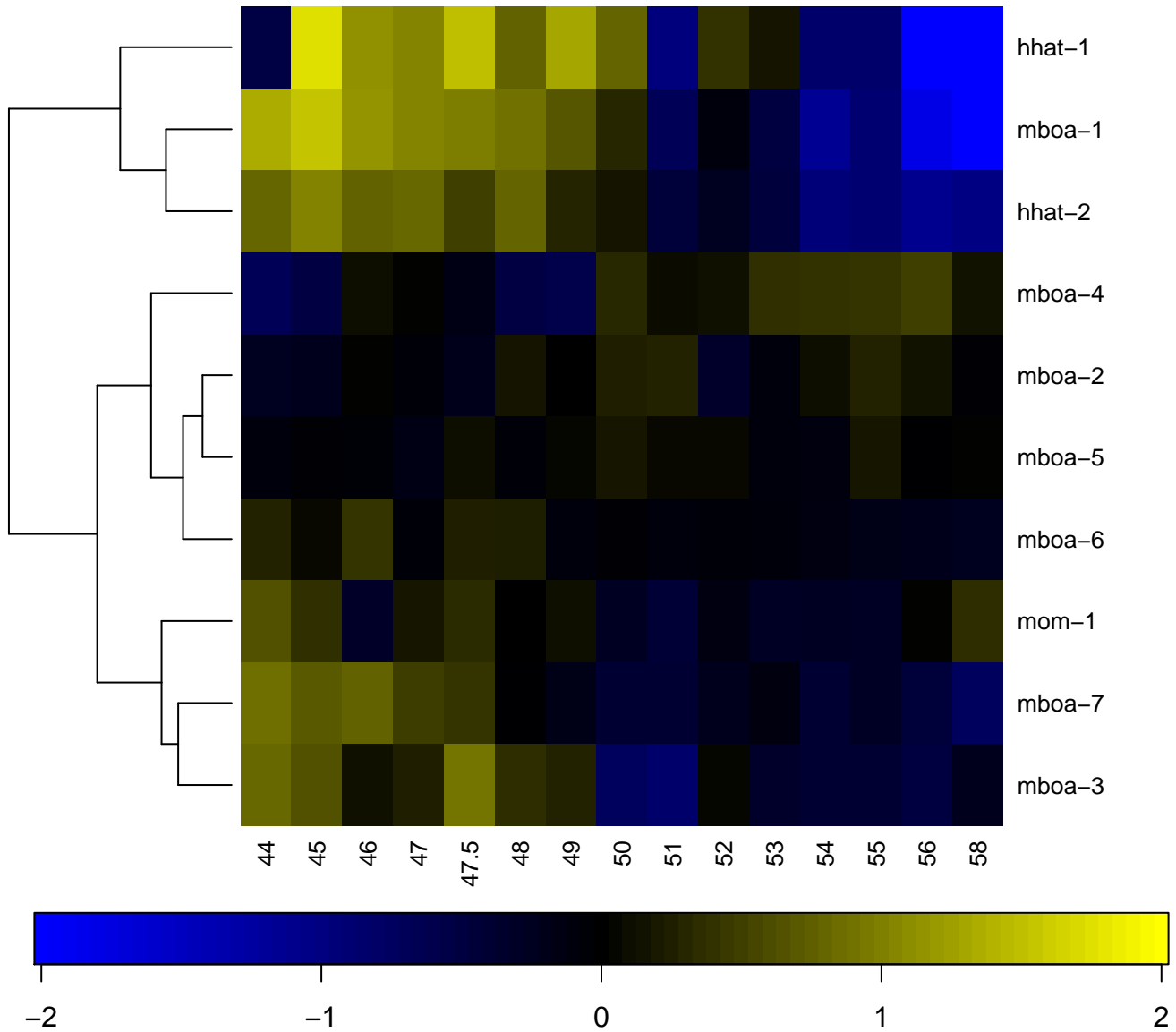
MATH



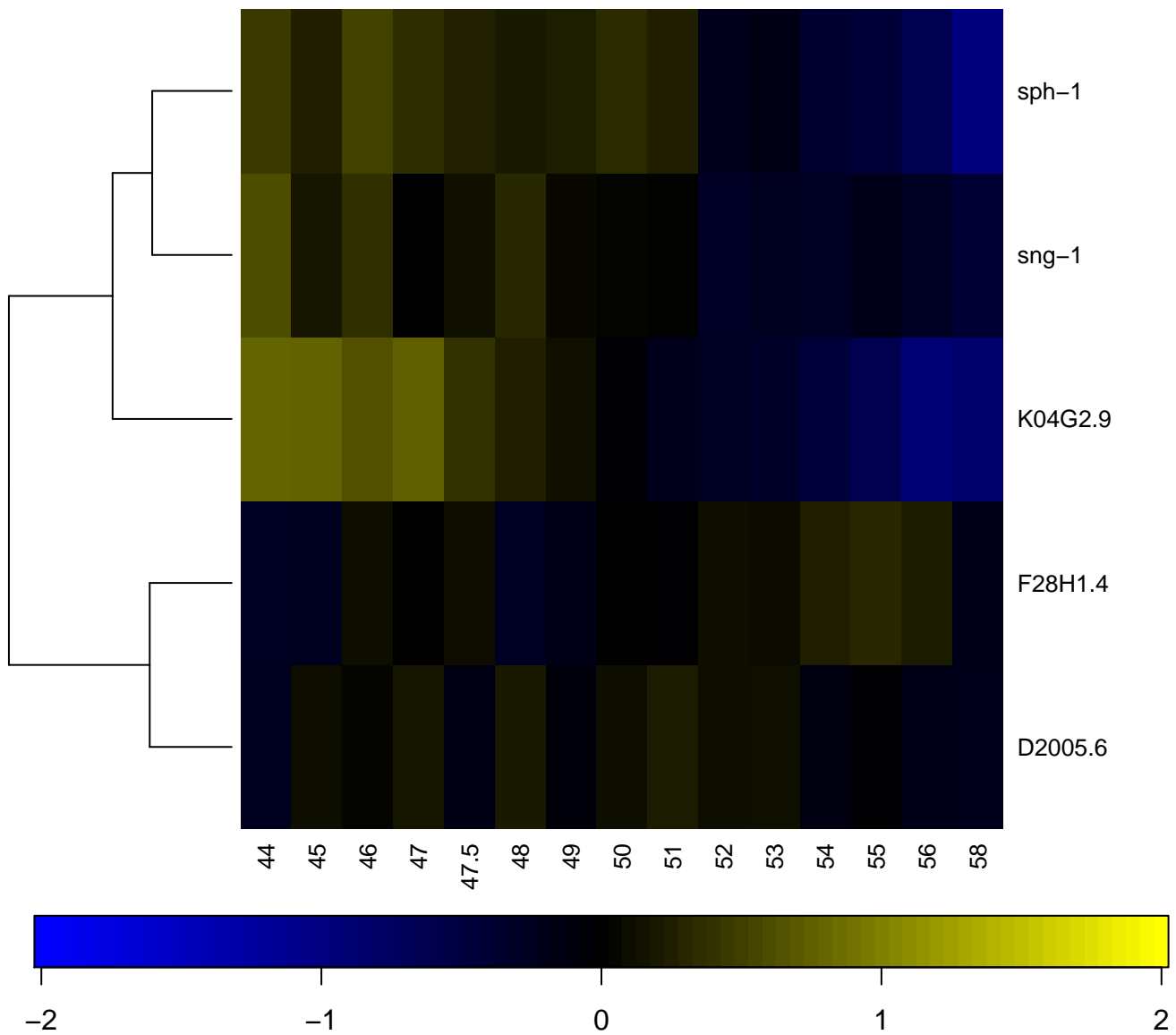
MATH domain



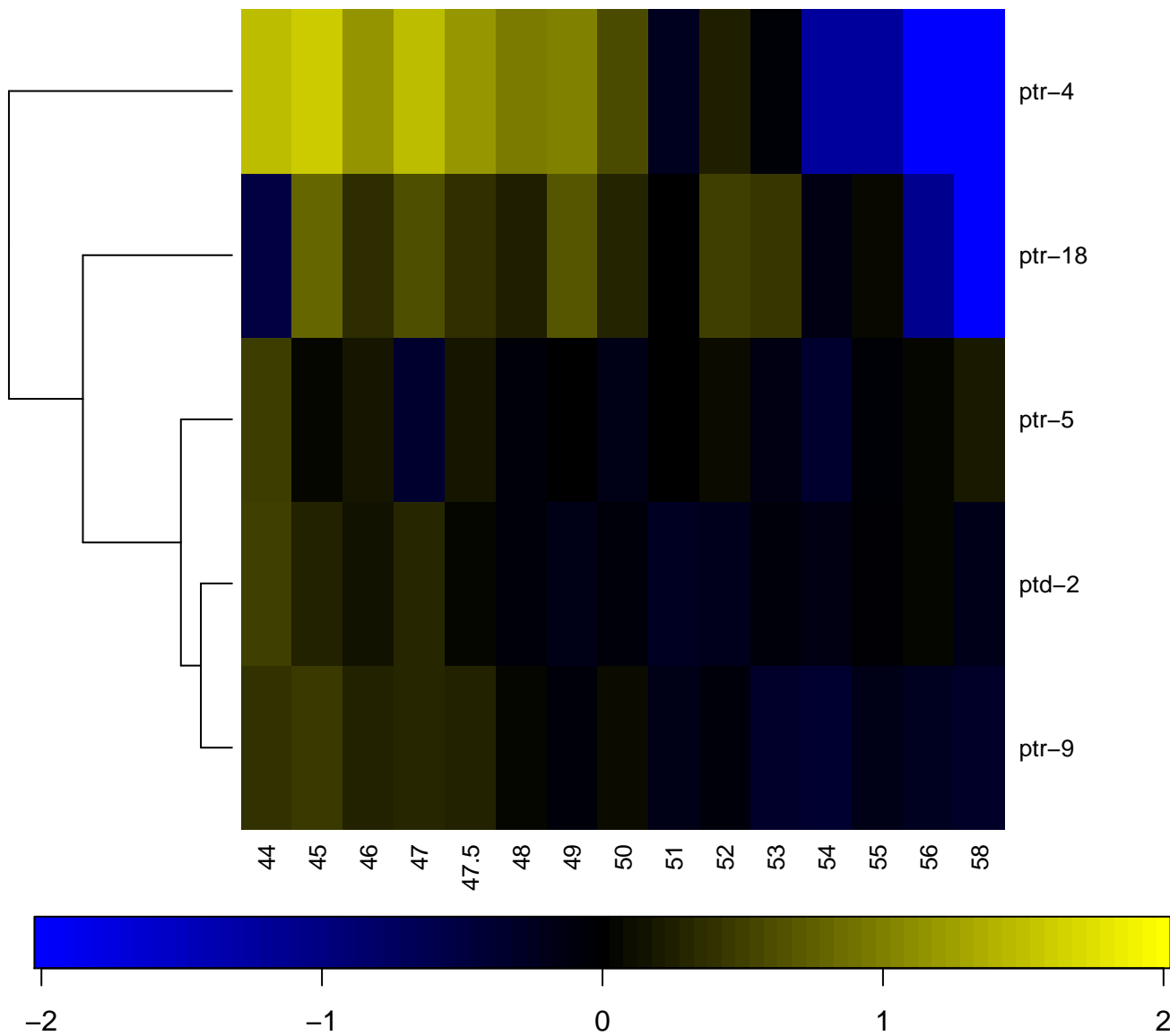
MBOAT family



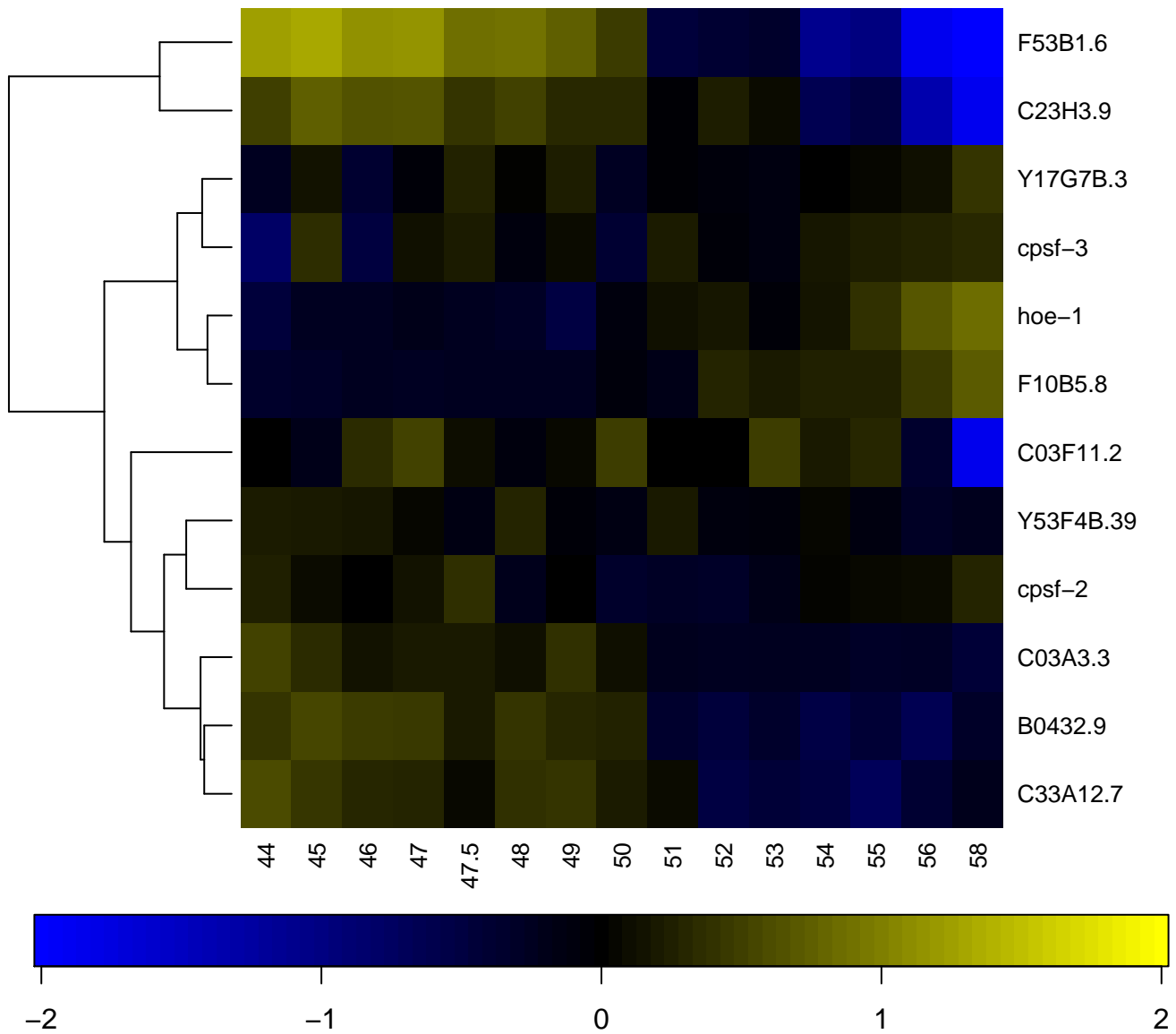
Membrane-associated domain



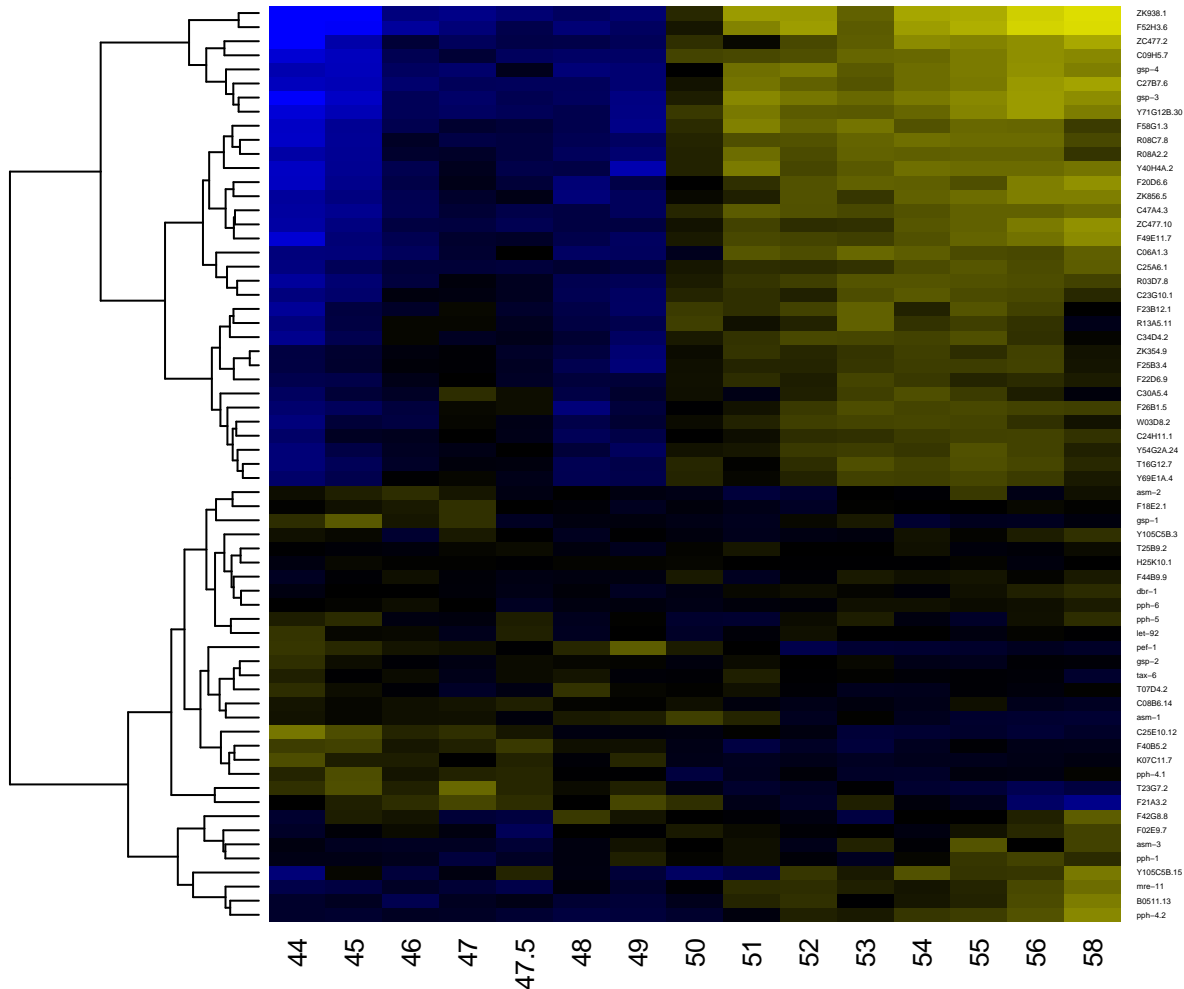
Membrane transport protein MMPL type



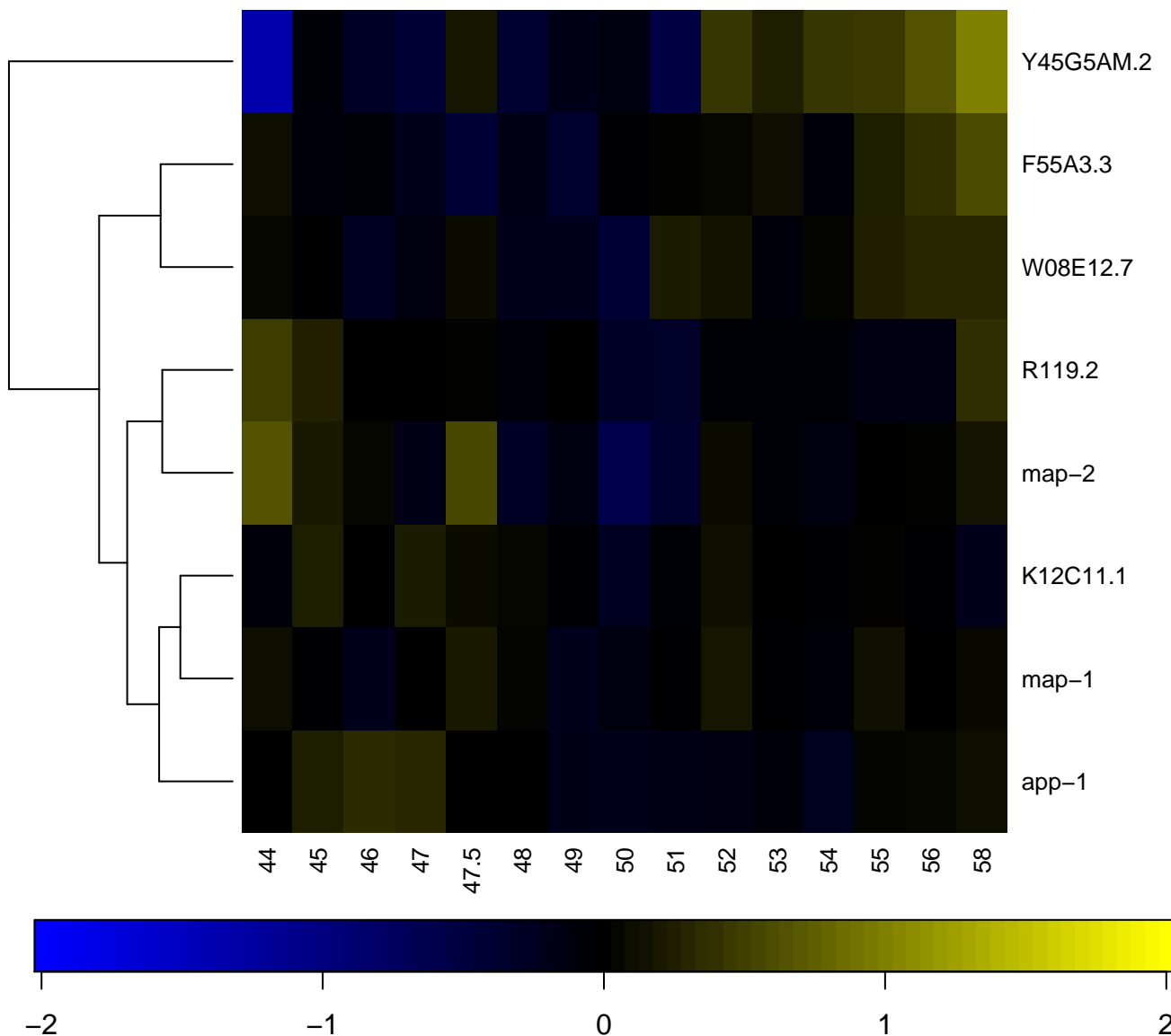
Metallo-beta-lactamase superfamily



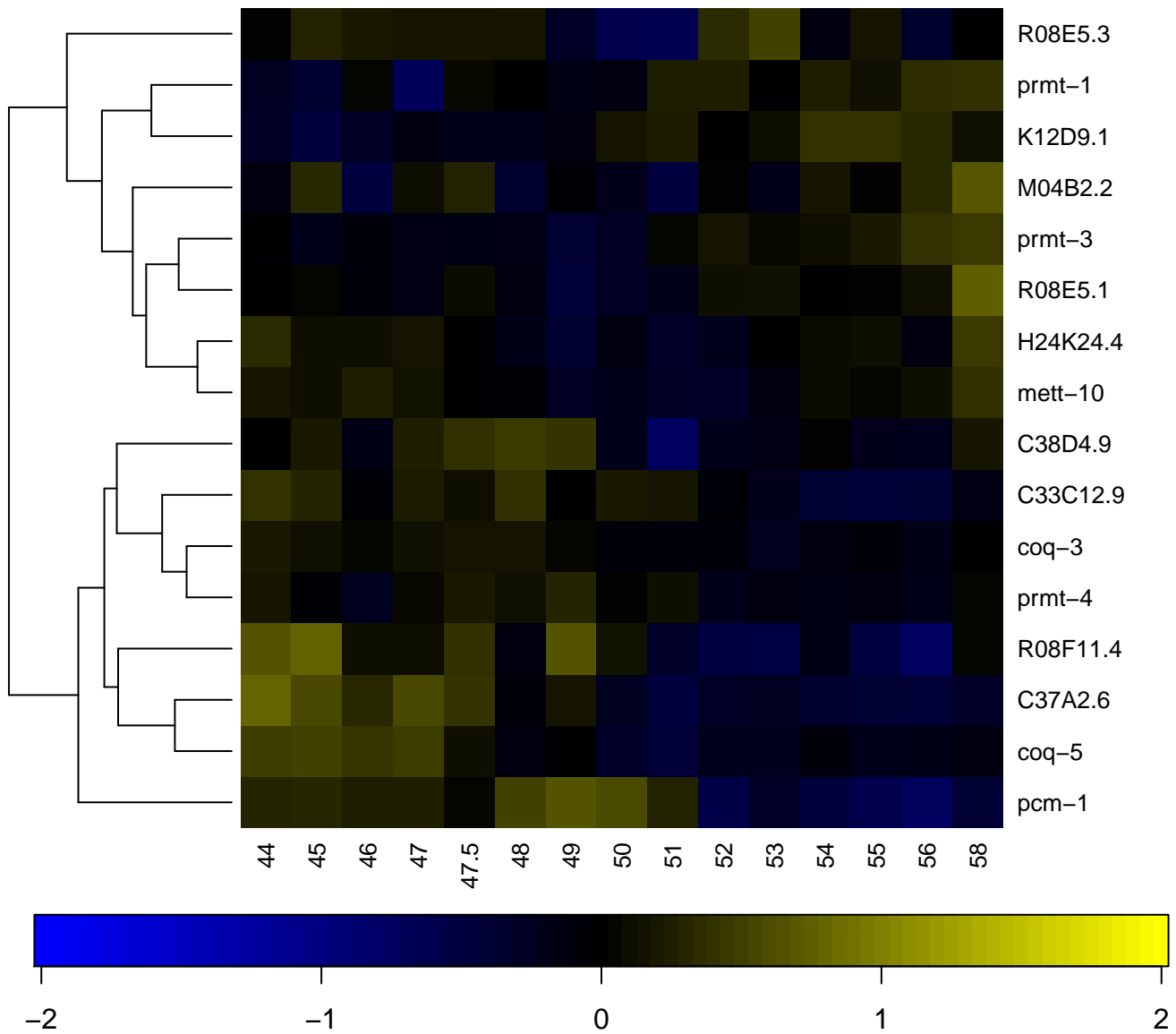
Metallo-dependent phosphatase



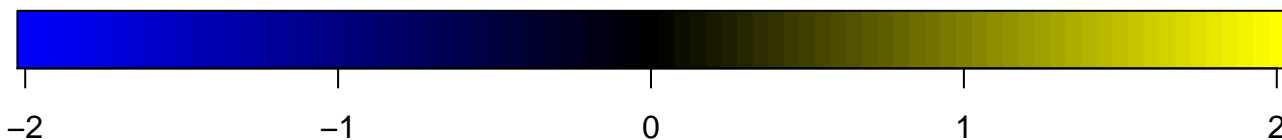
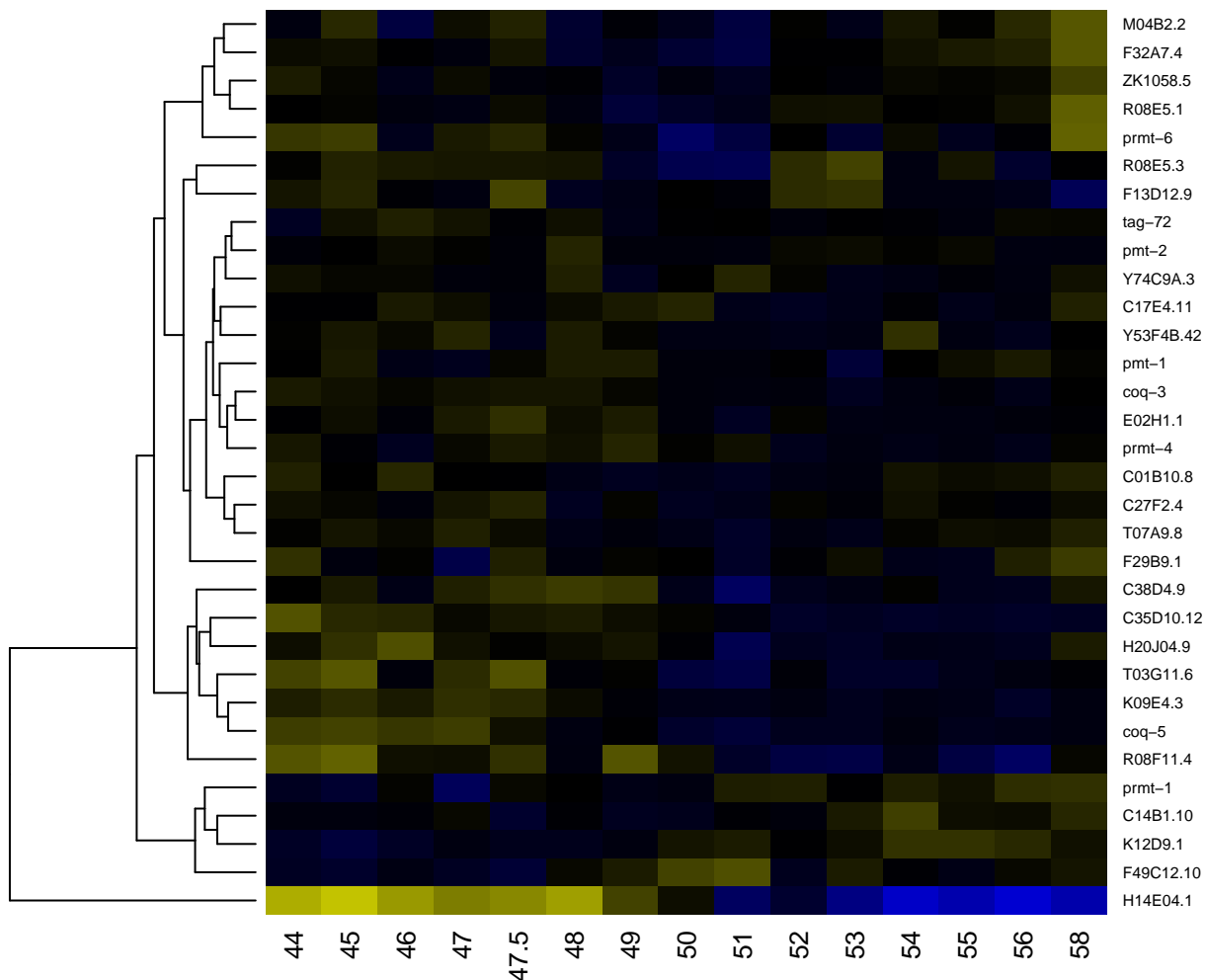
Metallopeptidase family M24



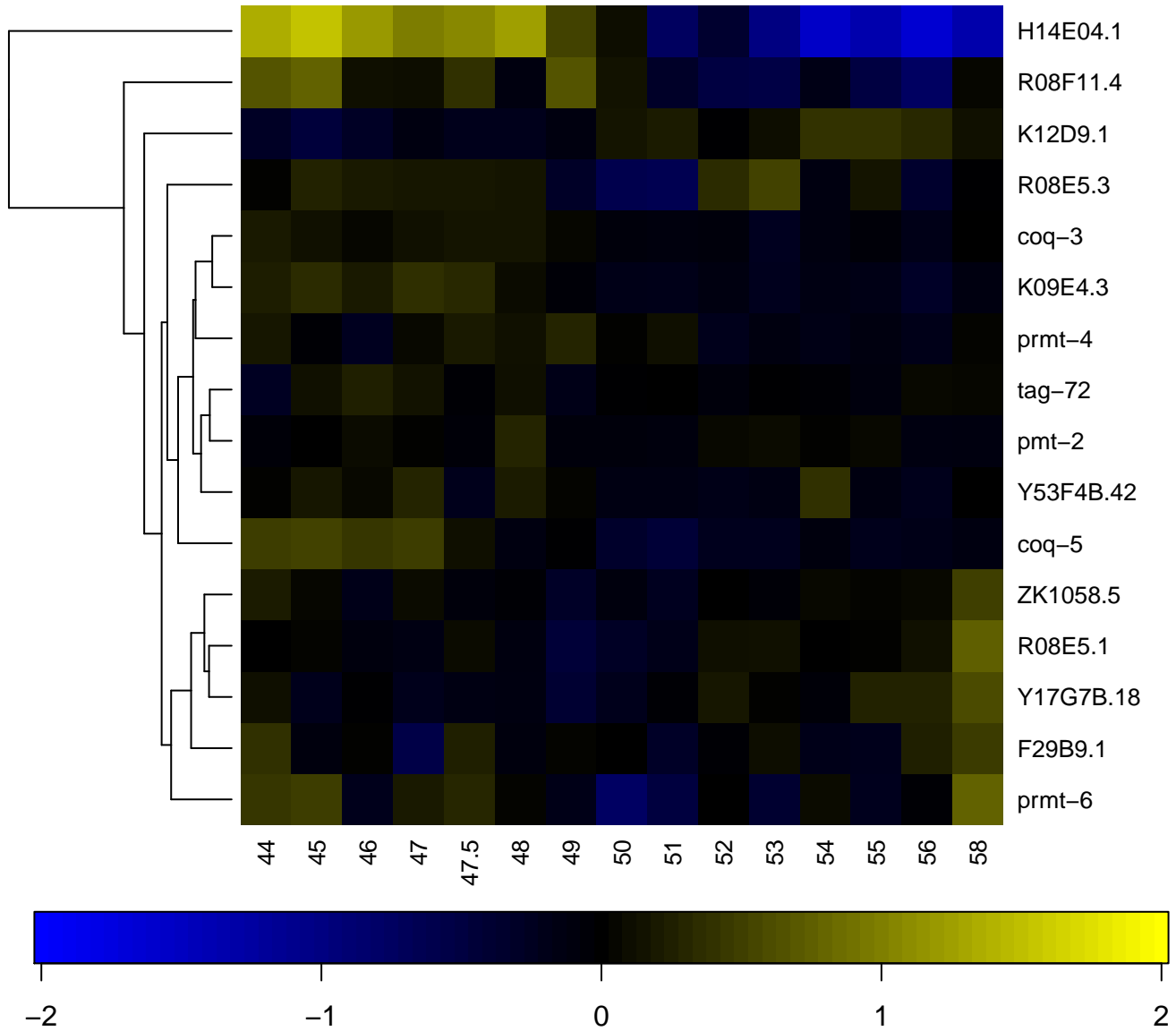
Methyltransferase small domain



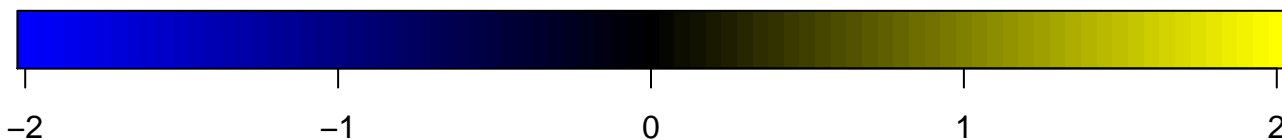
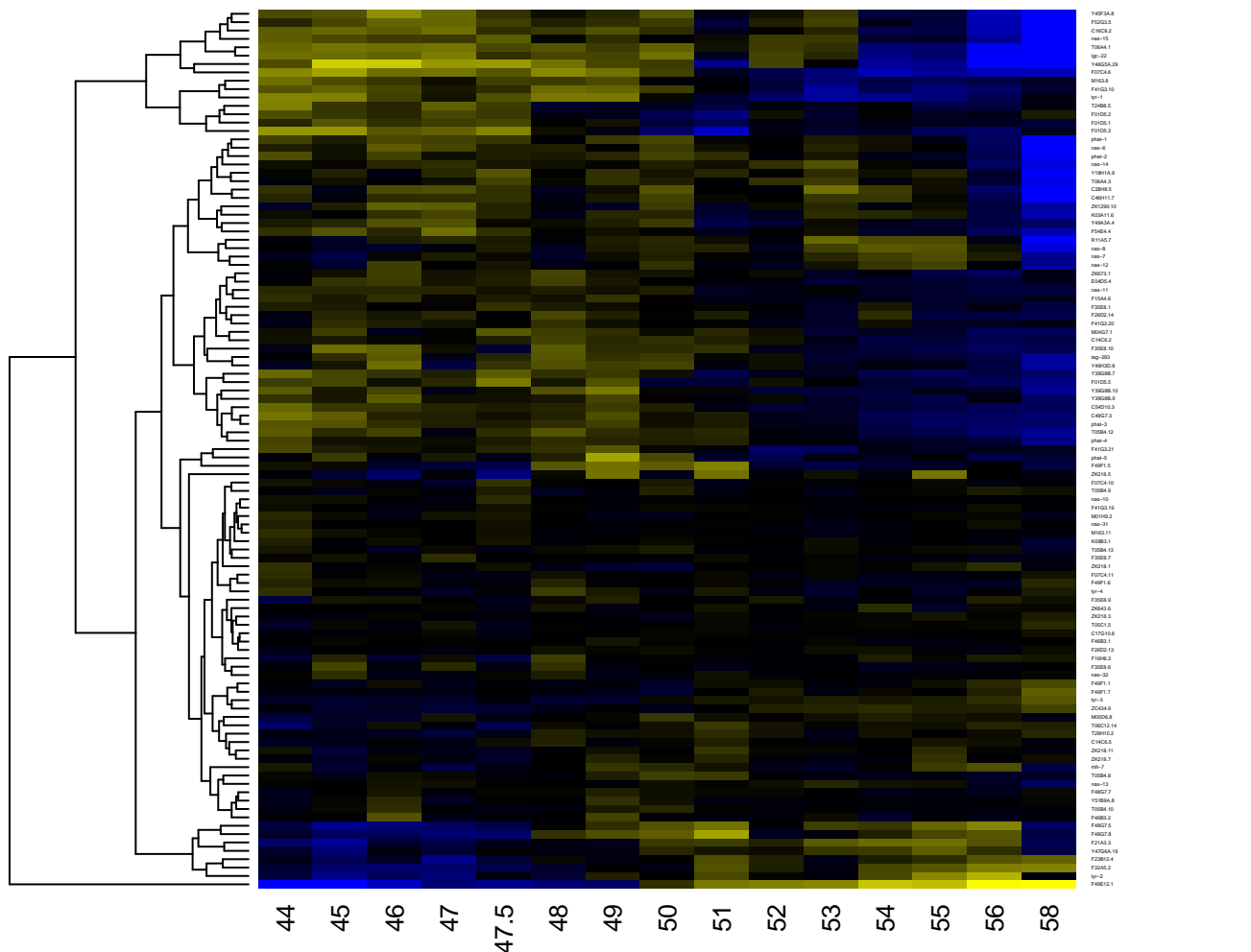
Methyltransferase type 11



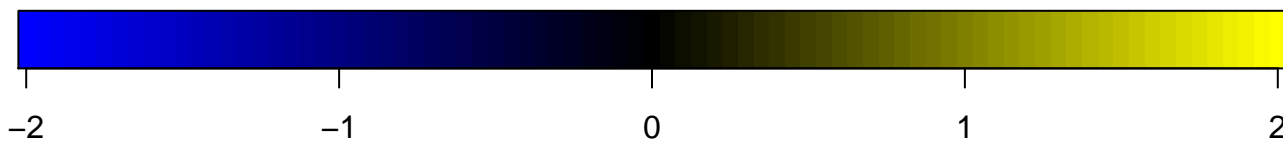
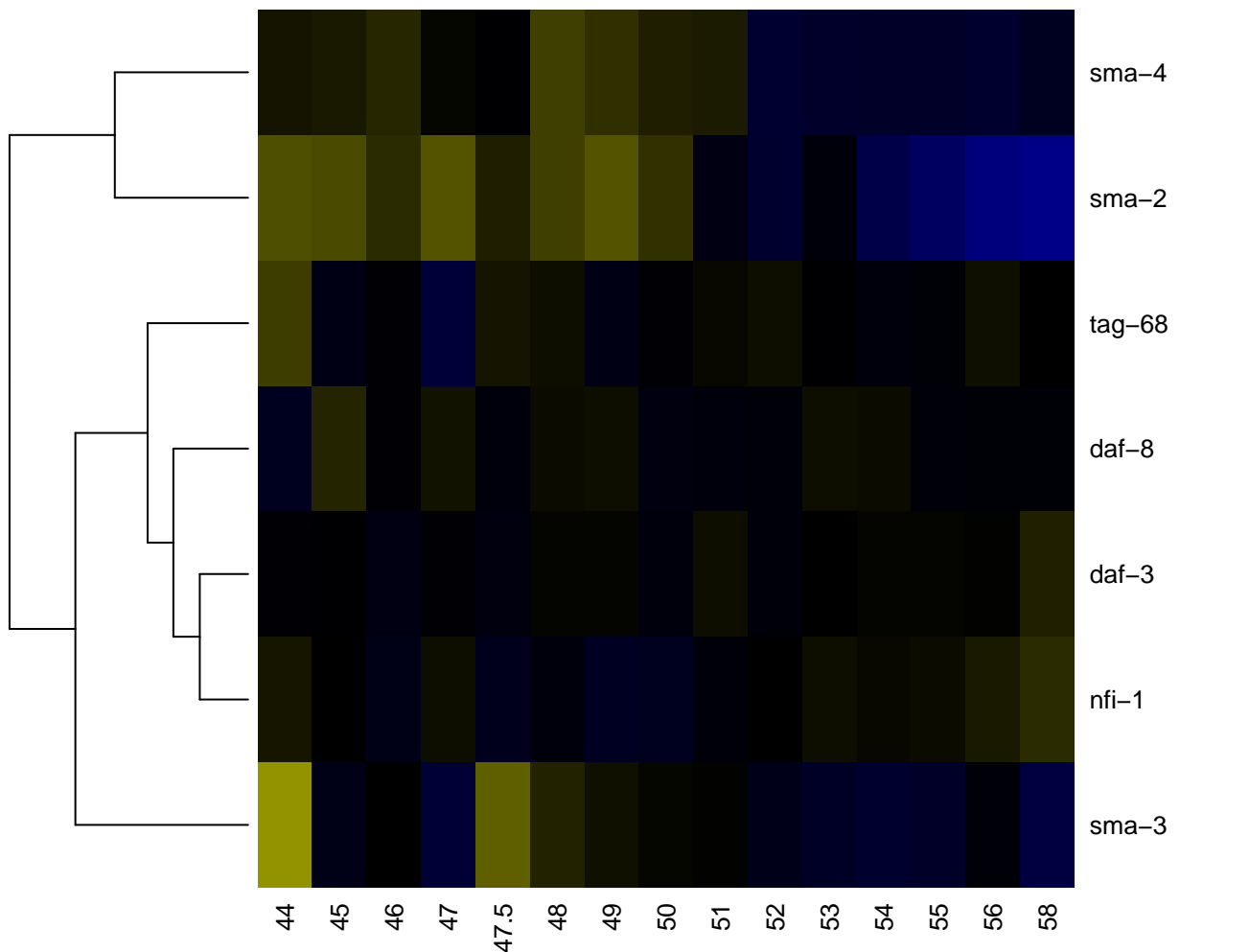
Methyltransferase type 12



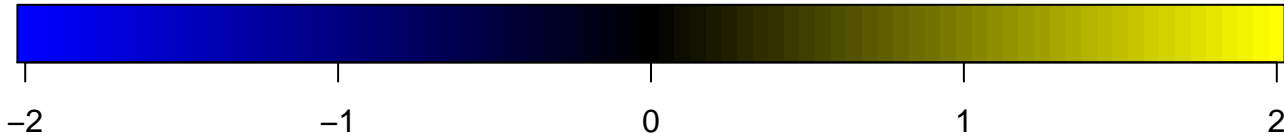
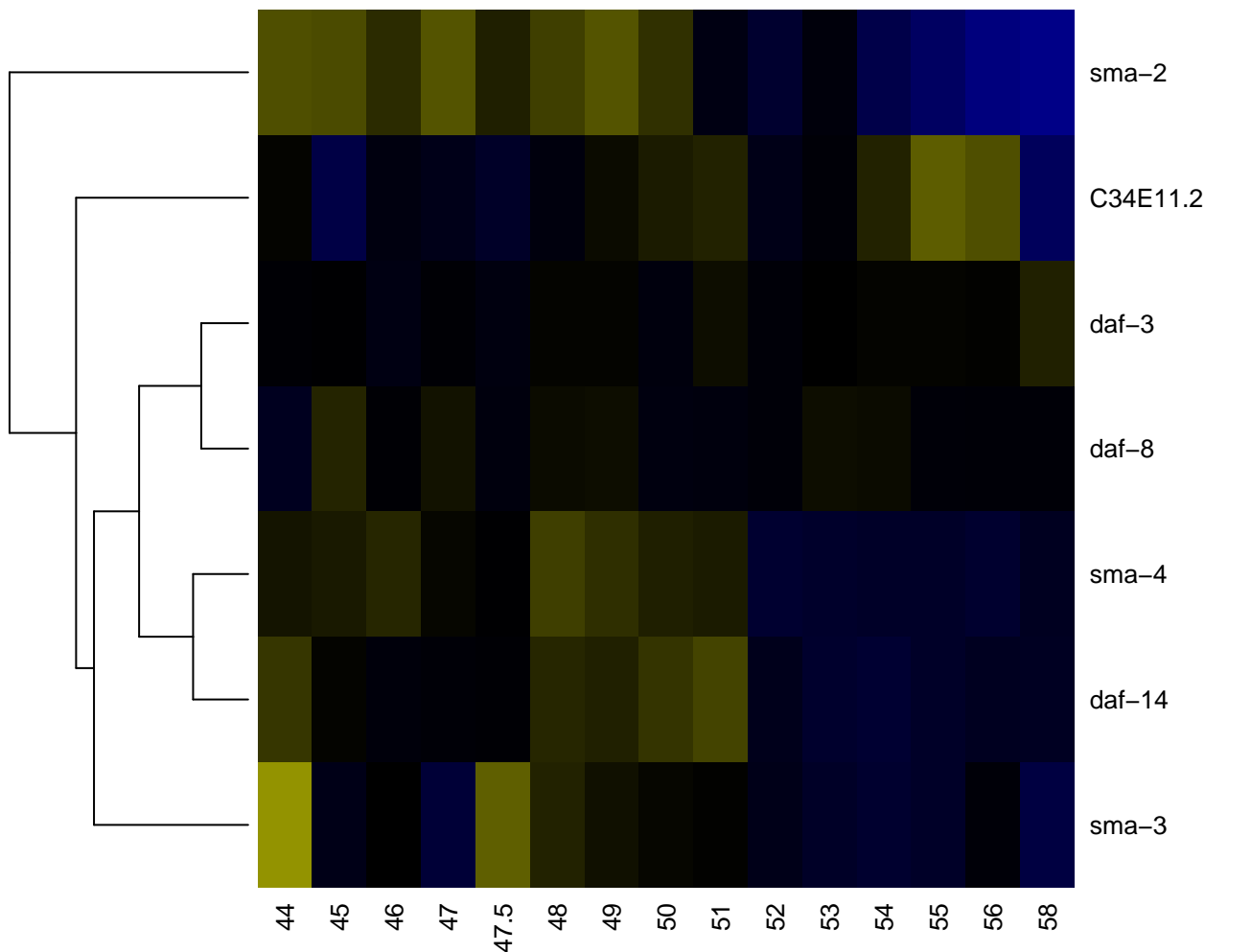
Metridin-like ShK toxin



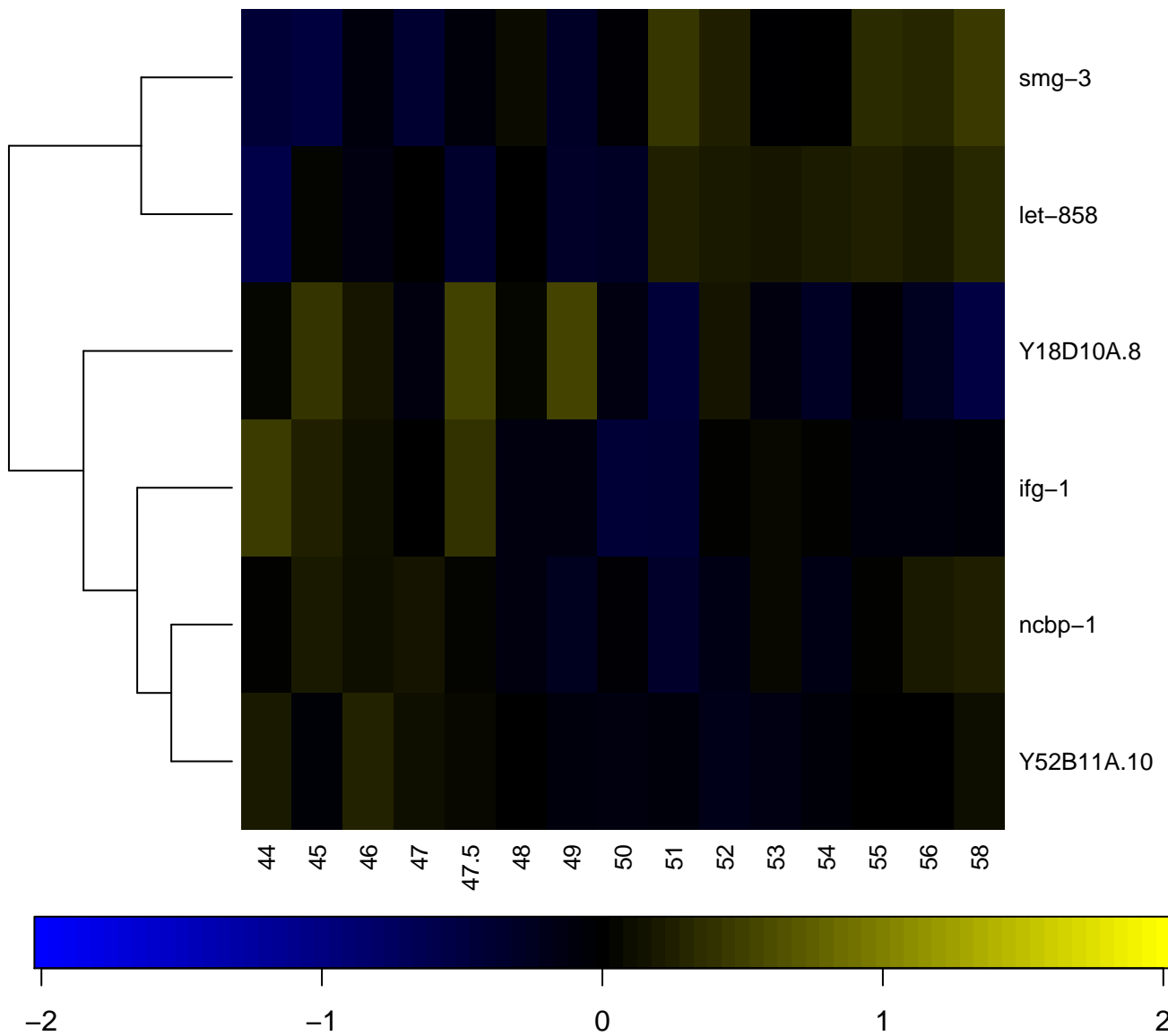
MH1 domain



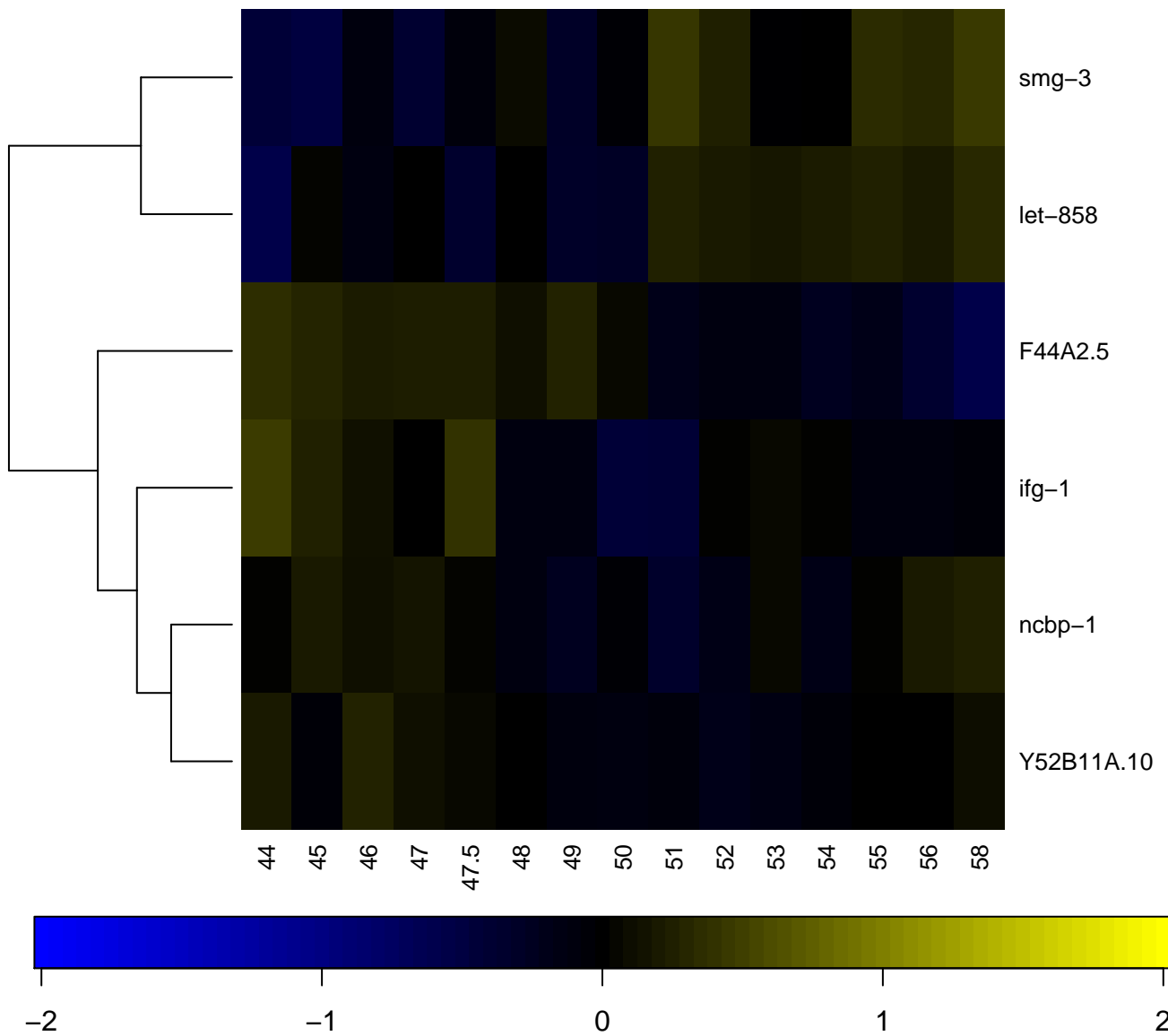
MH2 domain



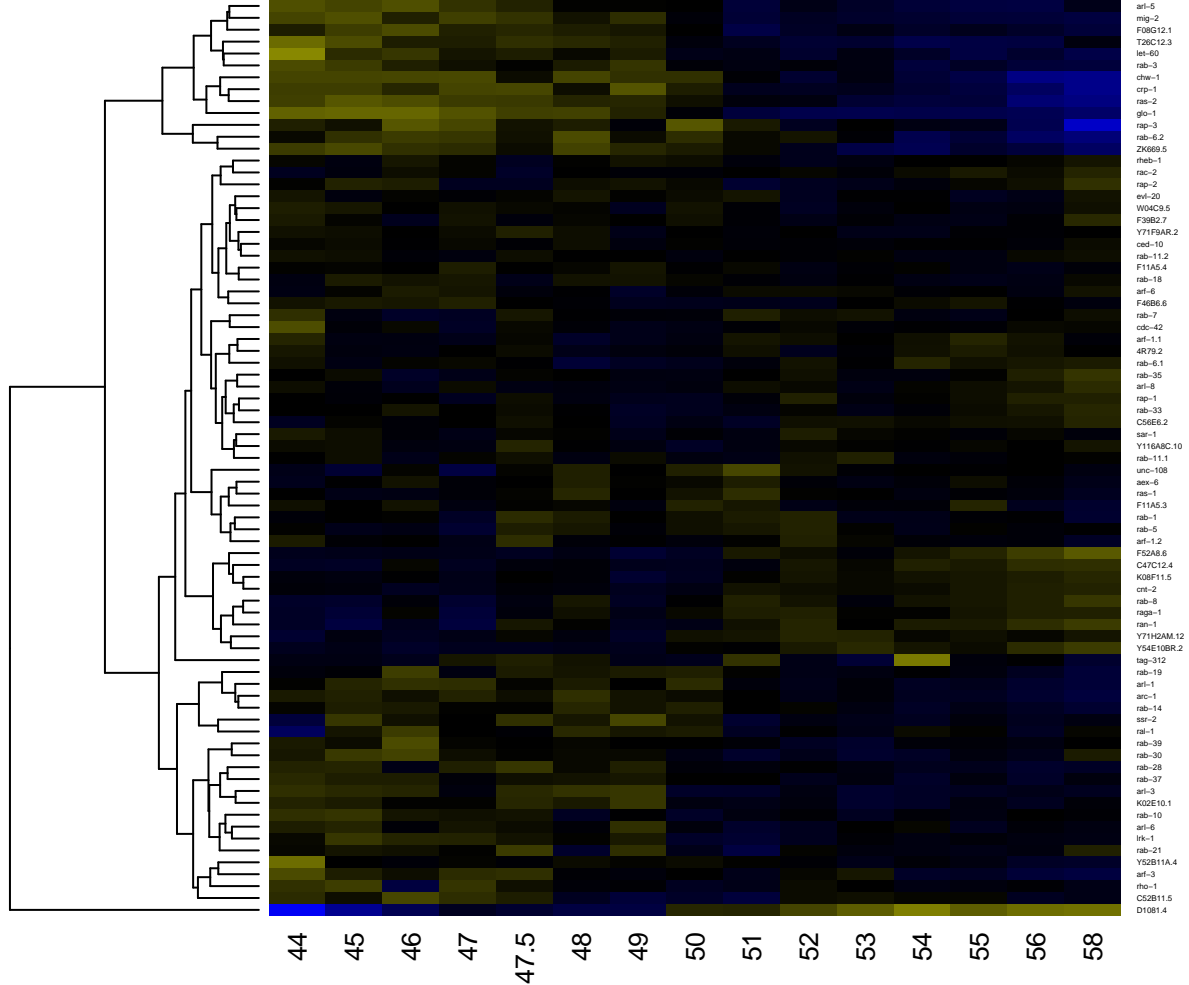
MIF4-like, type 1/2/3



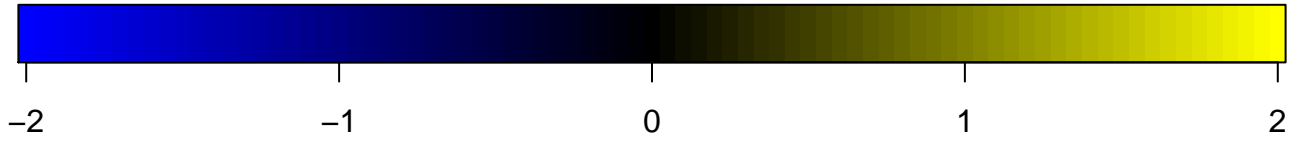
MIF4G-like, type 3



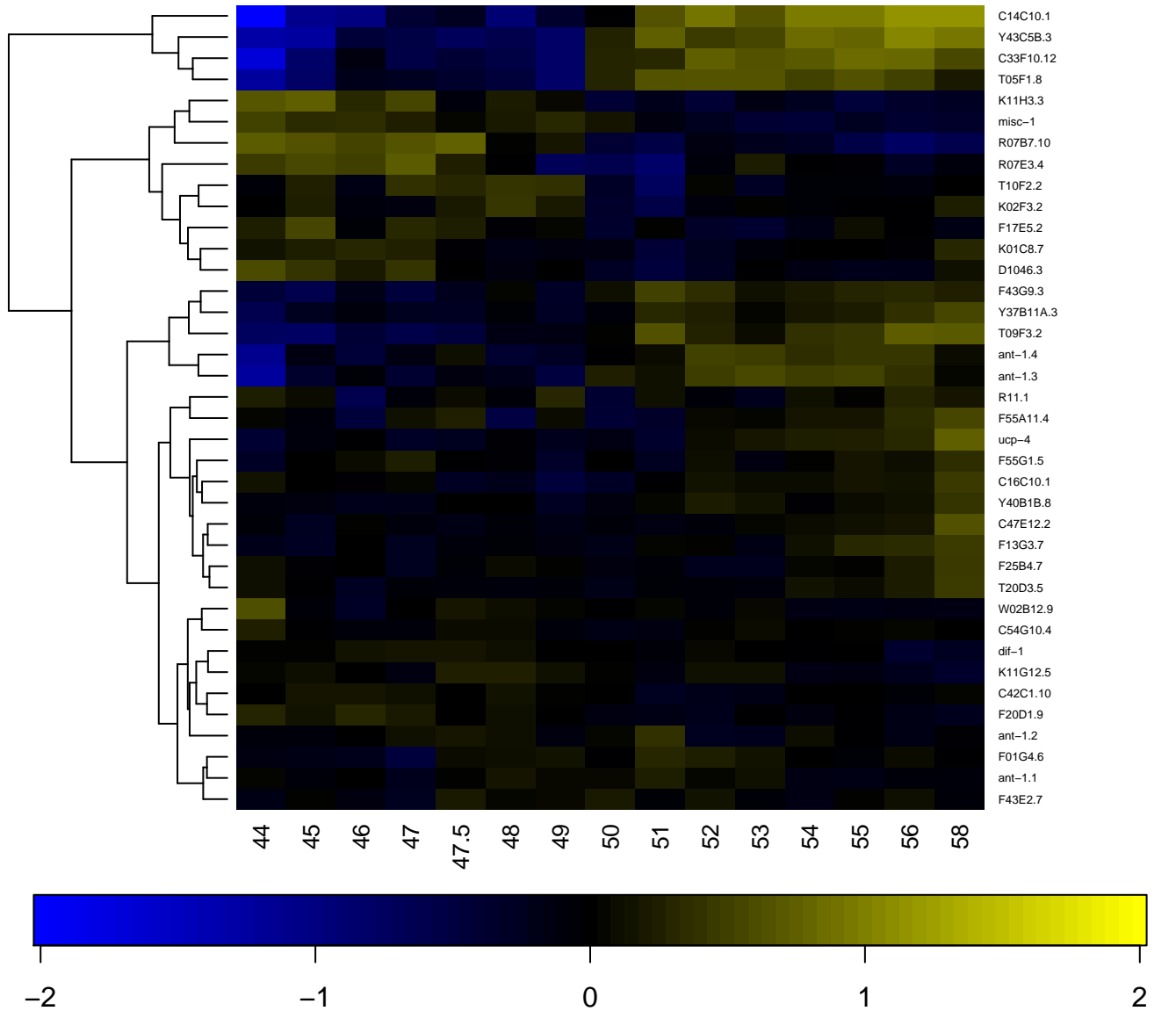
Miro-like protein



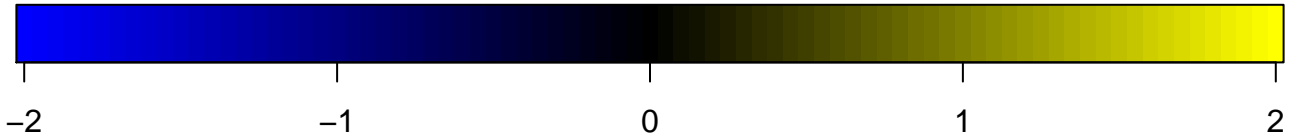
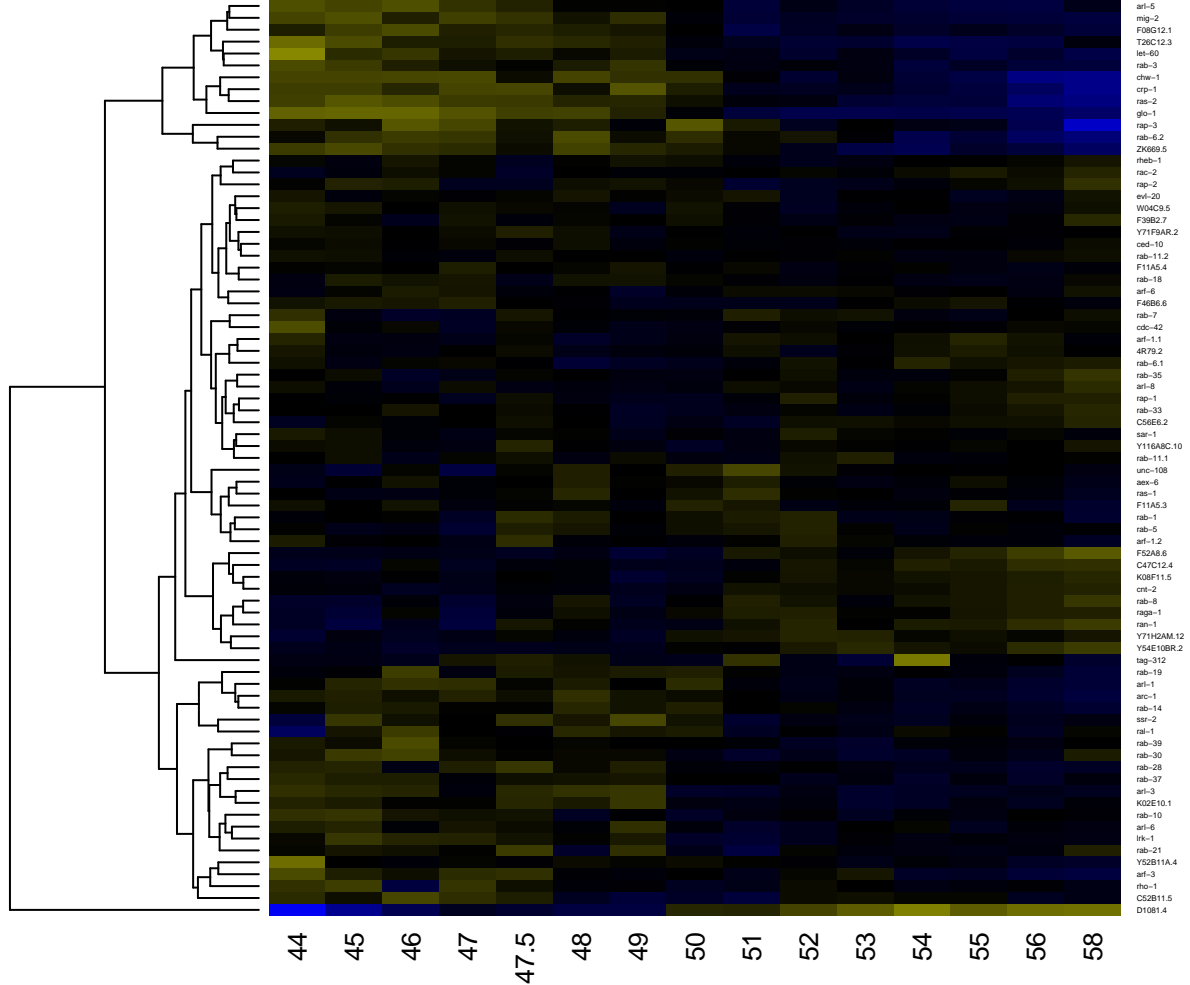
- arl-5
- mig-2
- F08G12.1
- T26C12.3
- let-60
- rab-3
- chw-1
- crp-1
- ras-2
- glo-1
- rap-3
- rab-6.2
- ZK689.5
- rheb-1
- rac-2
- rap-2
- evl-20
- W04C9.5
- F39B2.7
- Y71F9AR.2
- ced-10
- rab-11.2
- F11A5.4
- rab-18
- arf-6
- F46B6.6
- rab-7
- osb-42
- arf-1.1
- 4R79.2
- rab-6.1
- rab-35
- arl-8
- rap-1
- rab-33
- C56E2.2
- sar-1
- Y116ABC.10
- rab-11.1
- unc-108
- axx-6
- ras-1
- F11A5.3
- rab-1
- rab-5
- arf-1.2
- F52A8.6
- C47C12.4
- K08F11.5
- crn-2
- rab-8
- rggs-1
- ran-1
- Y71H2AM.12
- Y54E10BR.2
- tag-312
- rab-19
- arf-1
- arc-1
- rab-14
- sar-2
- ral-1
- rab-39
- rab-30
- rab-28
- rab-37
- arf-3
- K02E10.1
- rab-10
- arf-6
- tk-1
- rab-21
- Y52B11A.4
- arf-3
- rho-1
- C52B11.5
- D10B1.4



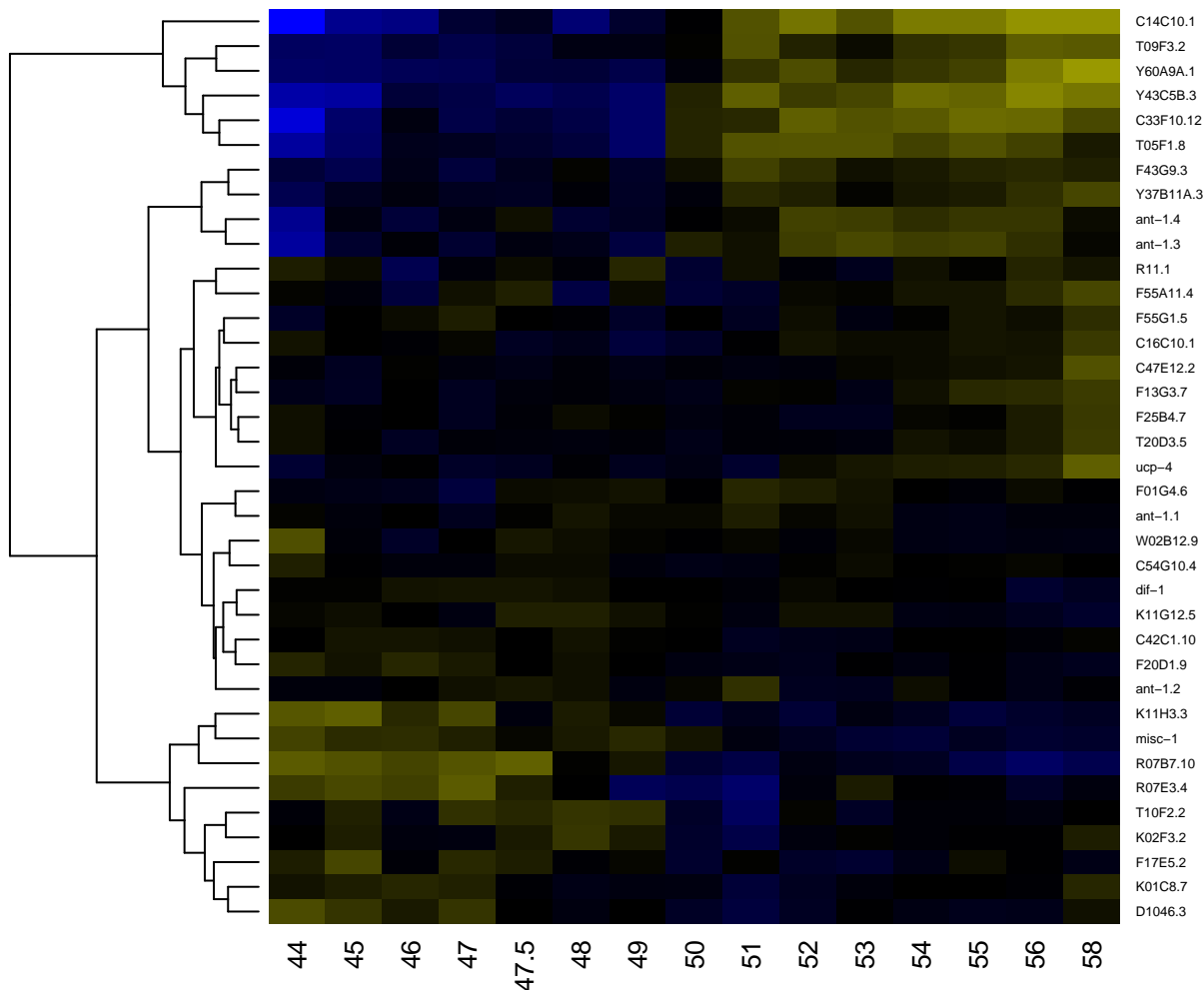
Mitochondrial carrier protein



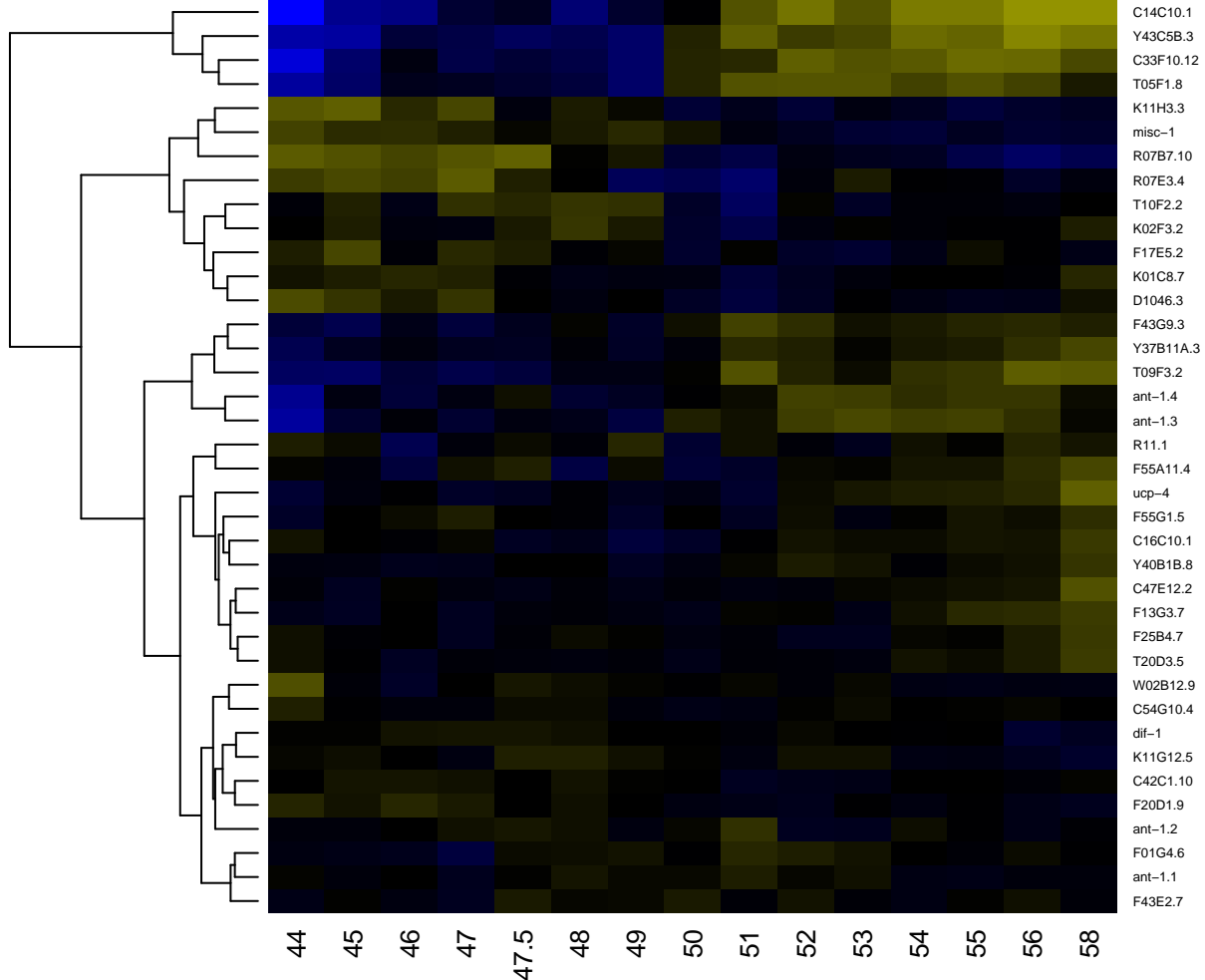
Mitochondrial Rho-like



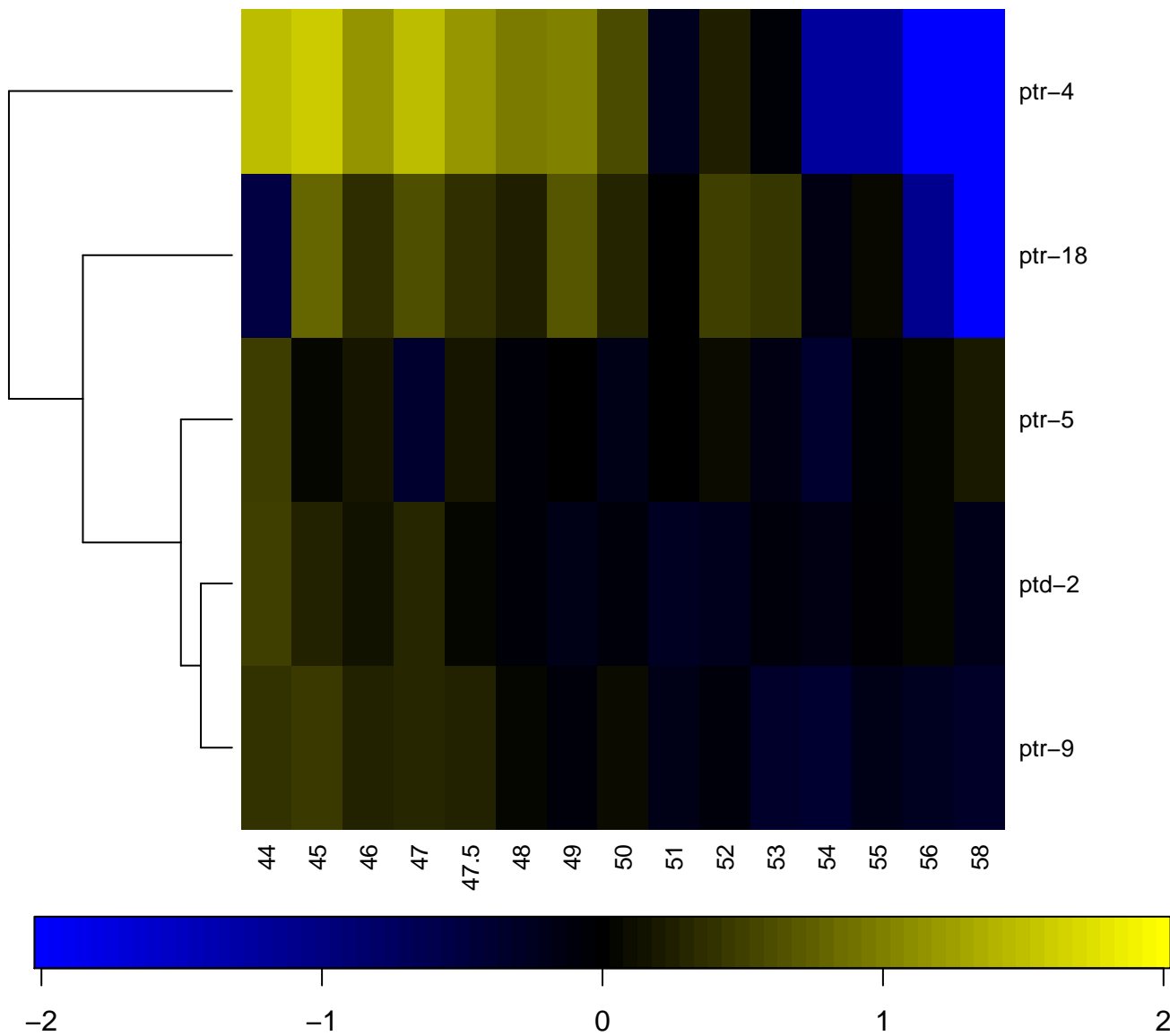
Mitochondrial substrate carrier



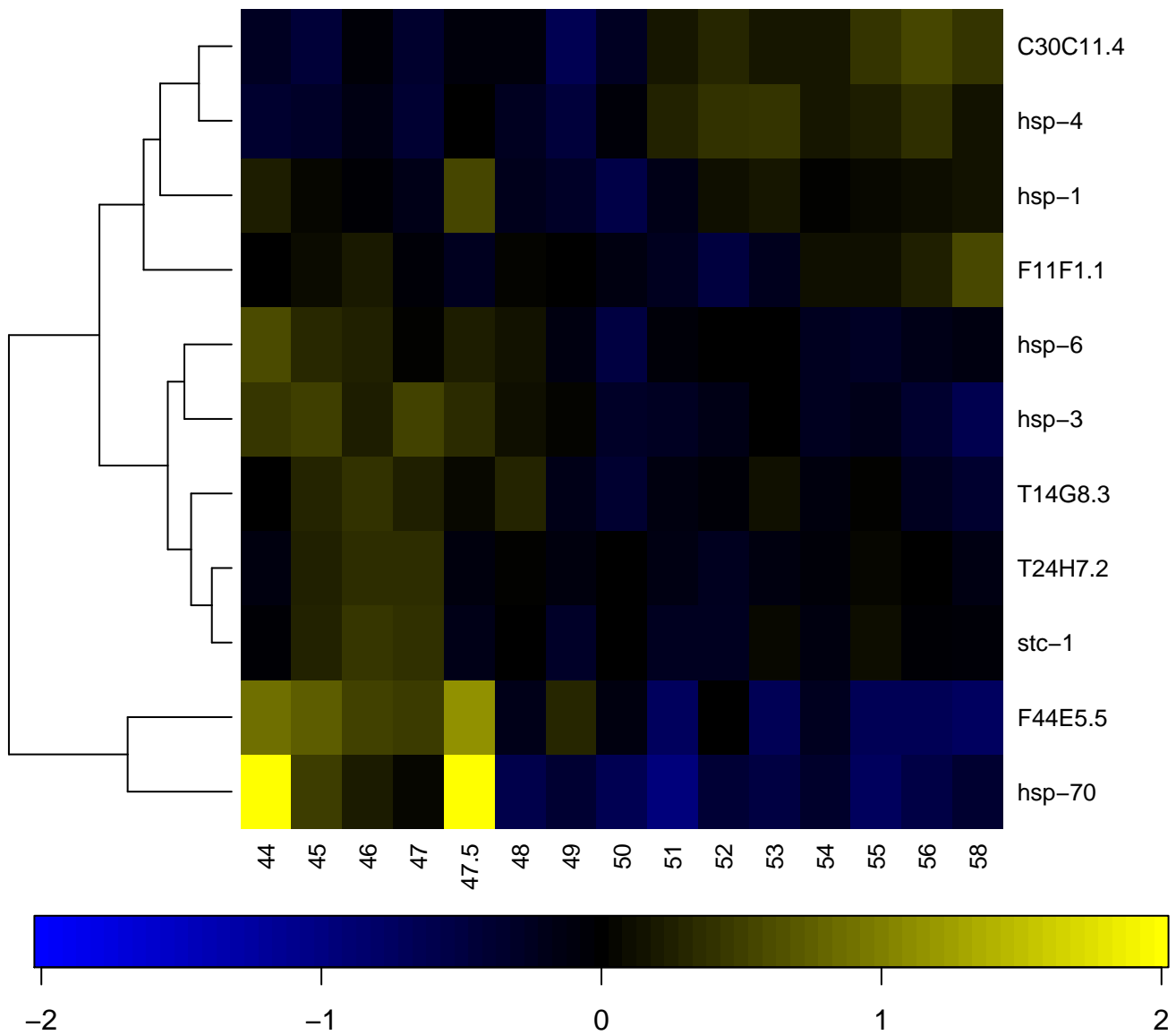
Mitochondrial substrate/solute carrier



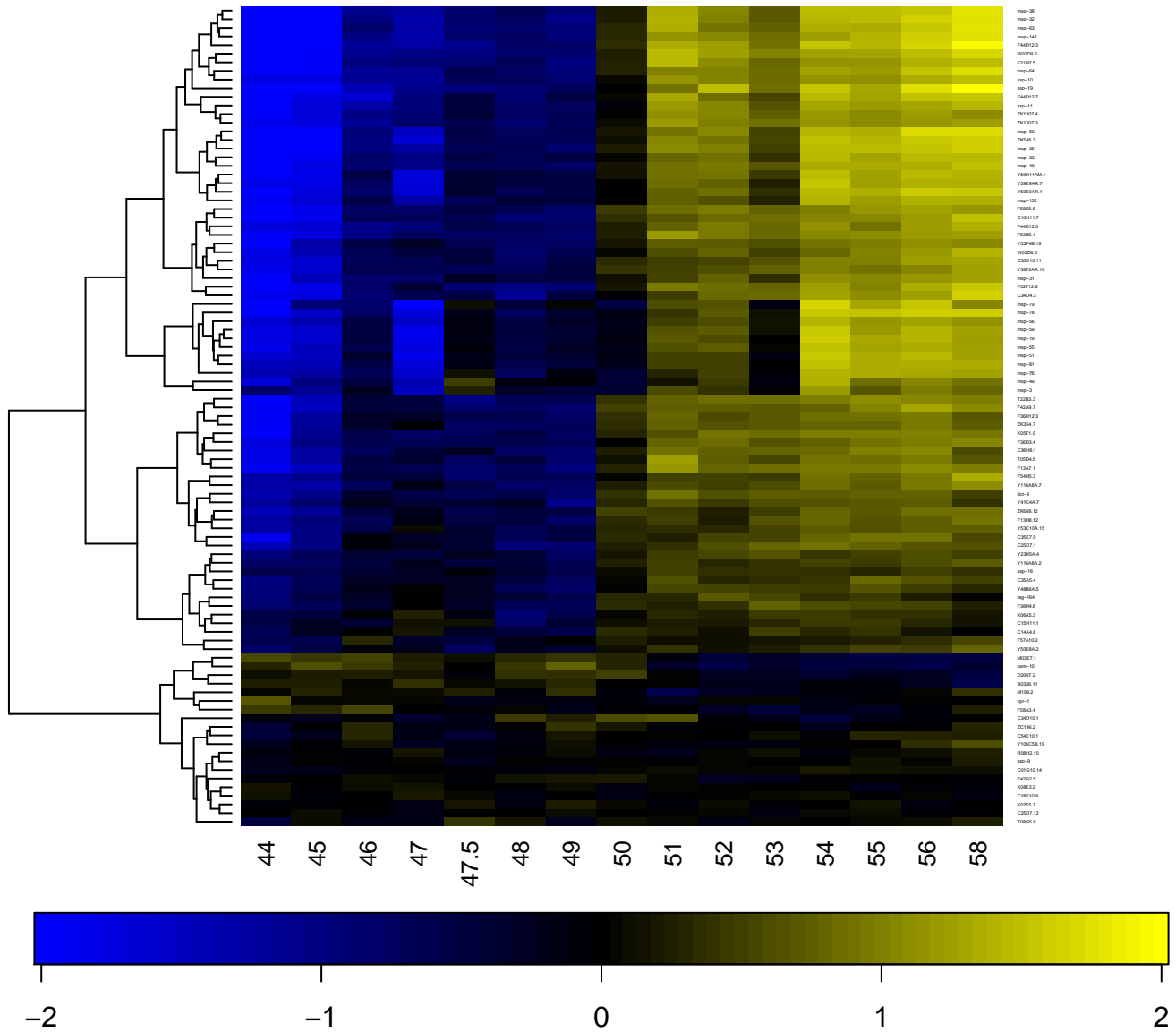
MMPL family



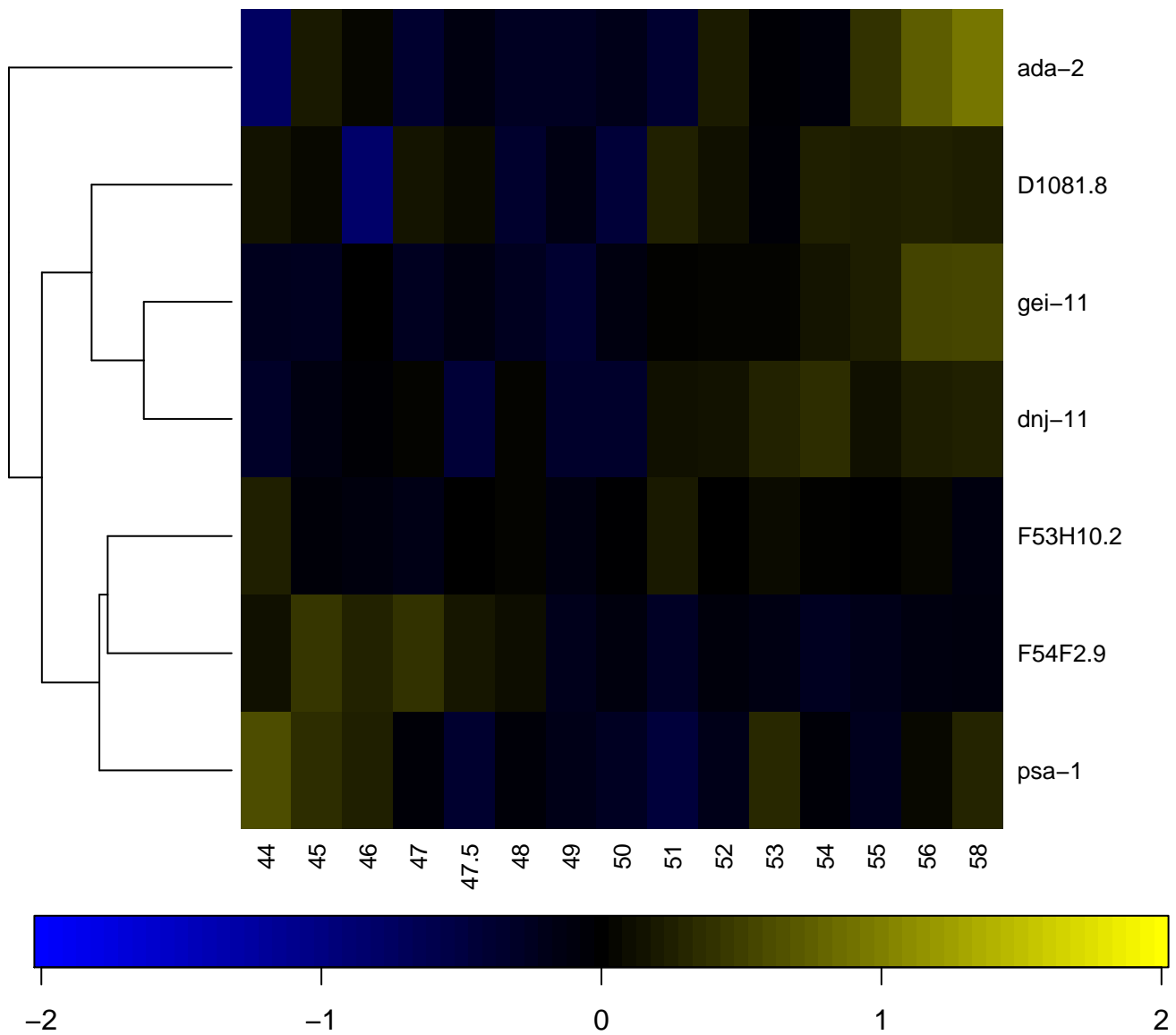
MreB/Mbl protein



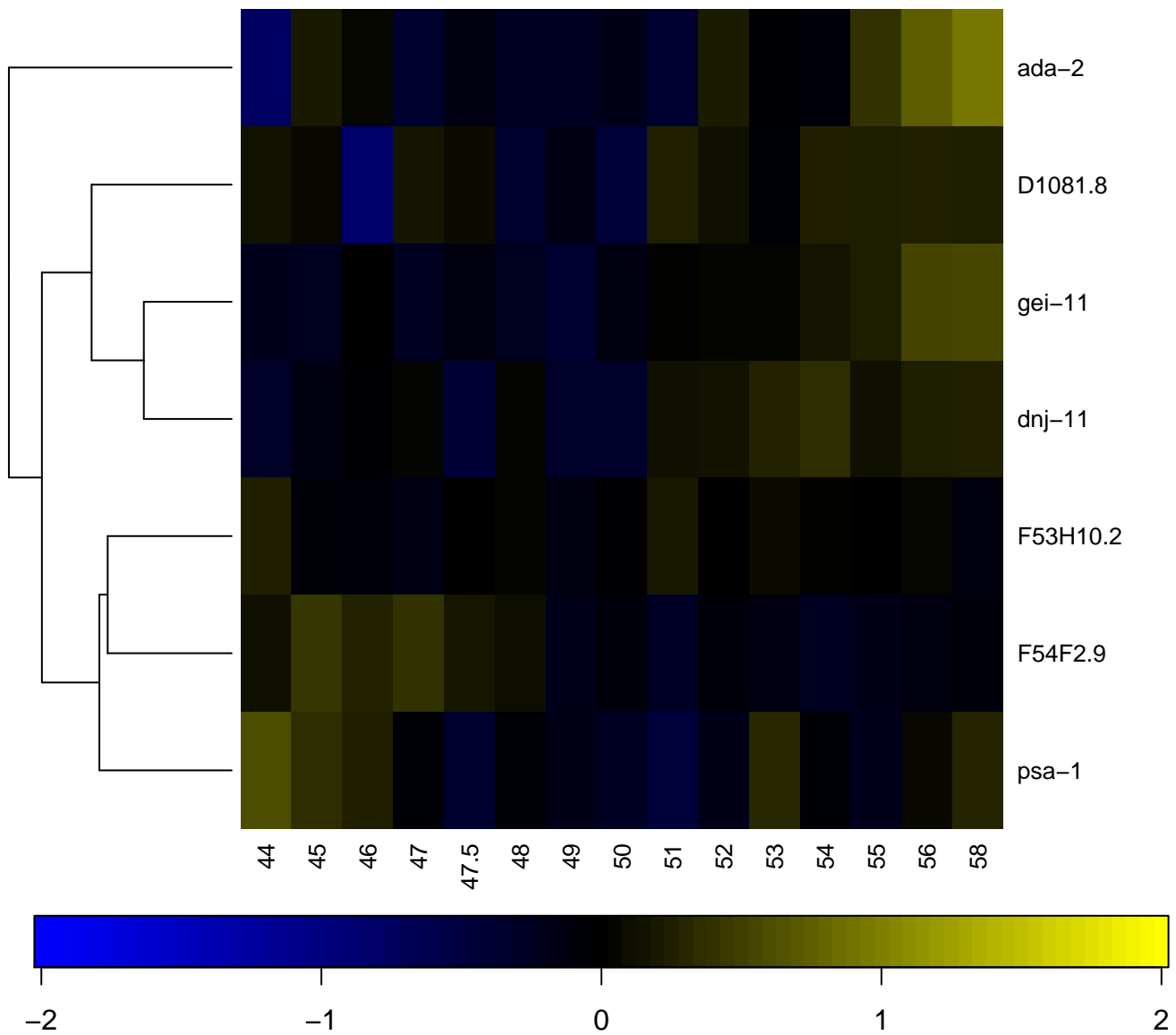
MSP (Major sperm protein) domain



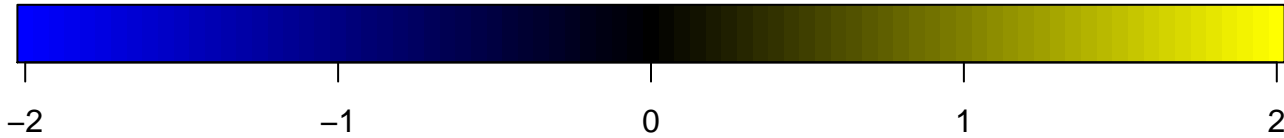
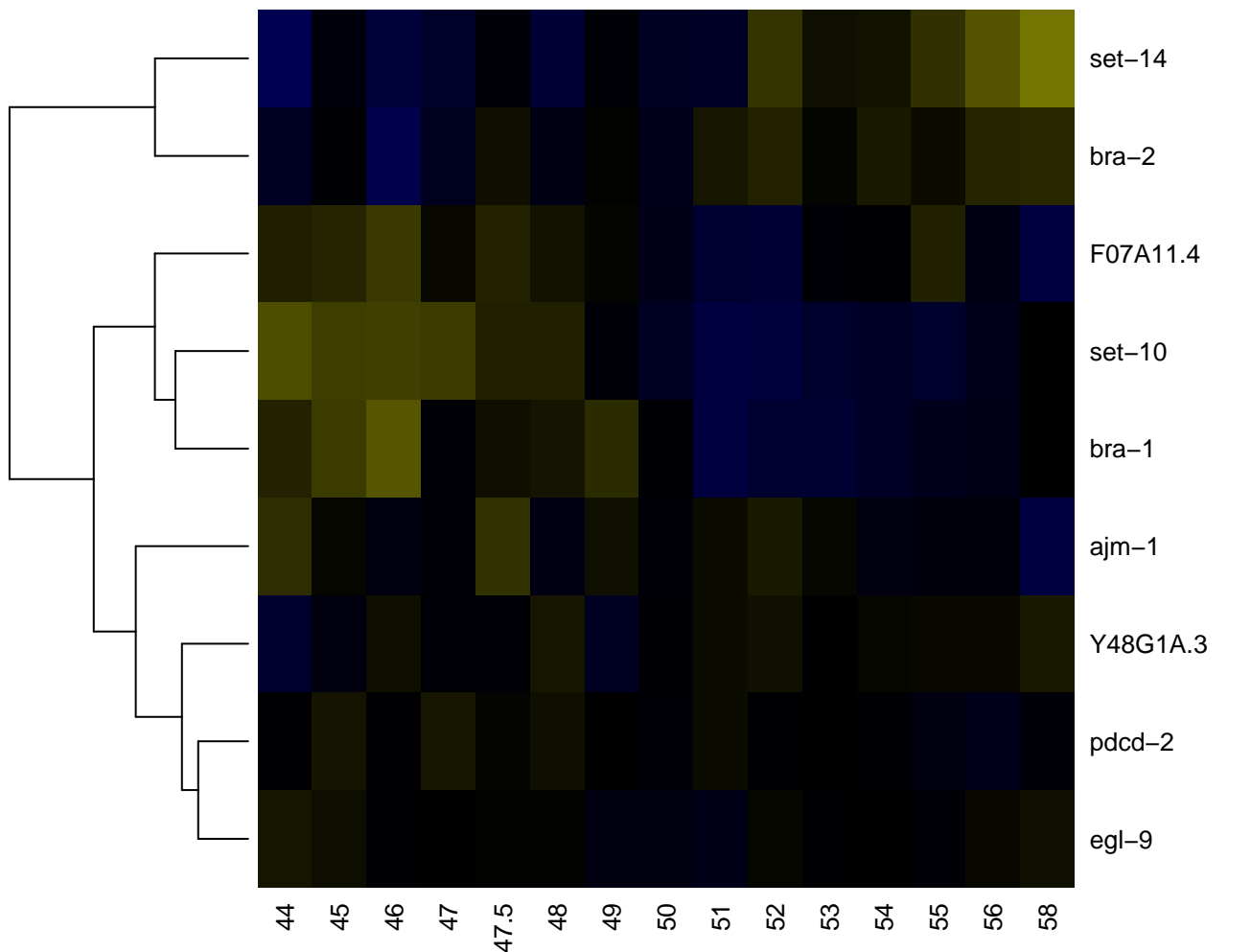
Myb-like DNA-binding domain



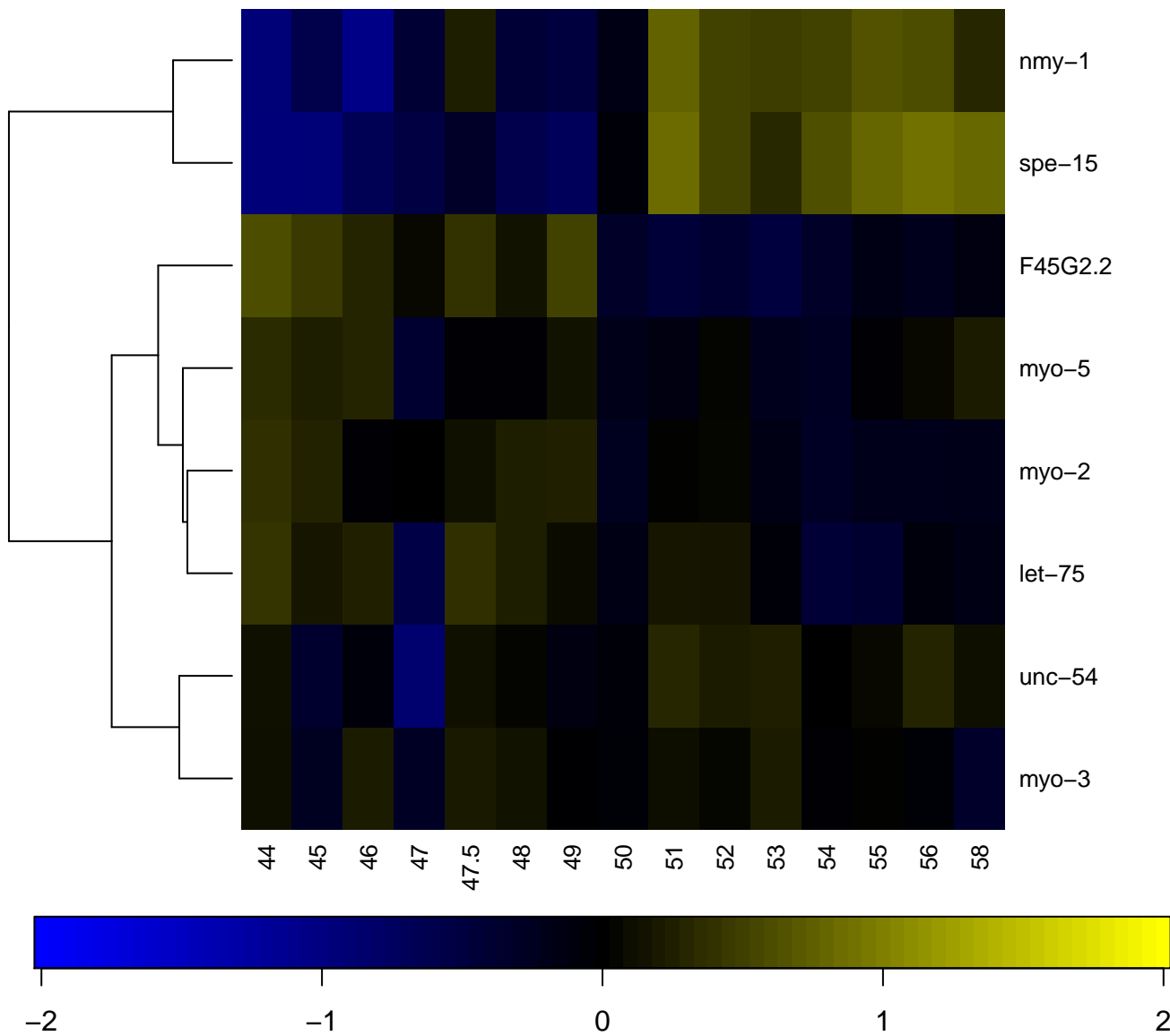
Myb, DNA-binding



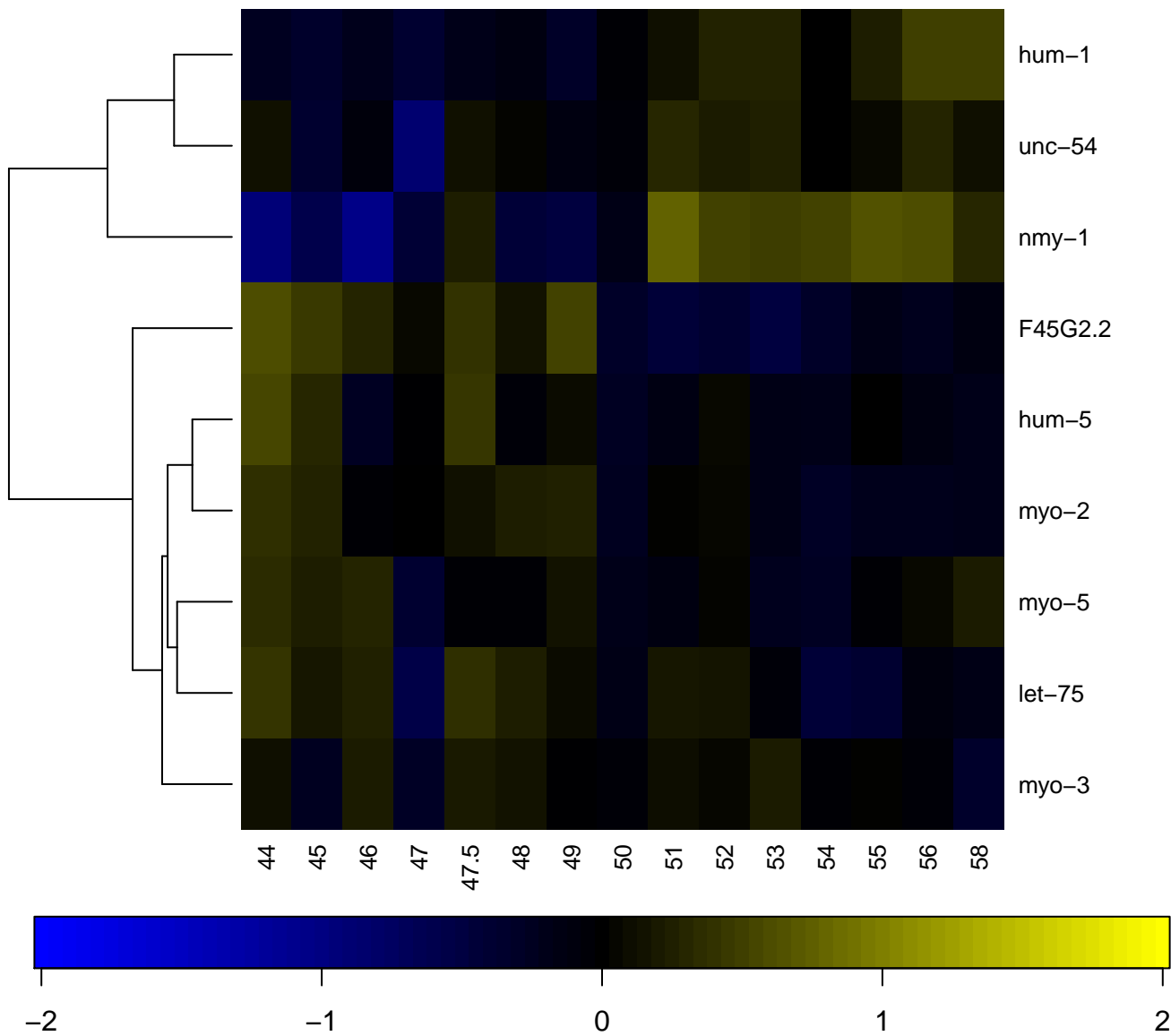
MYND finger



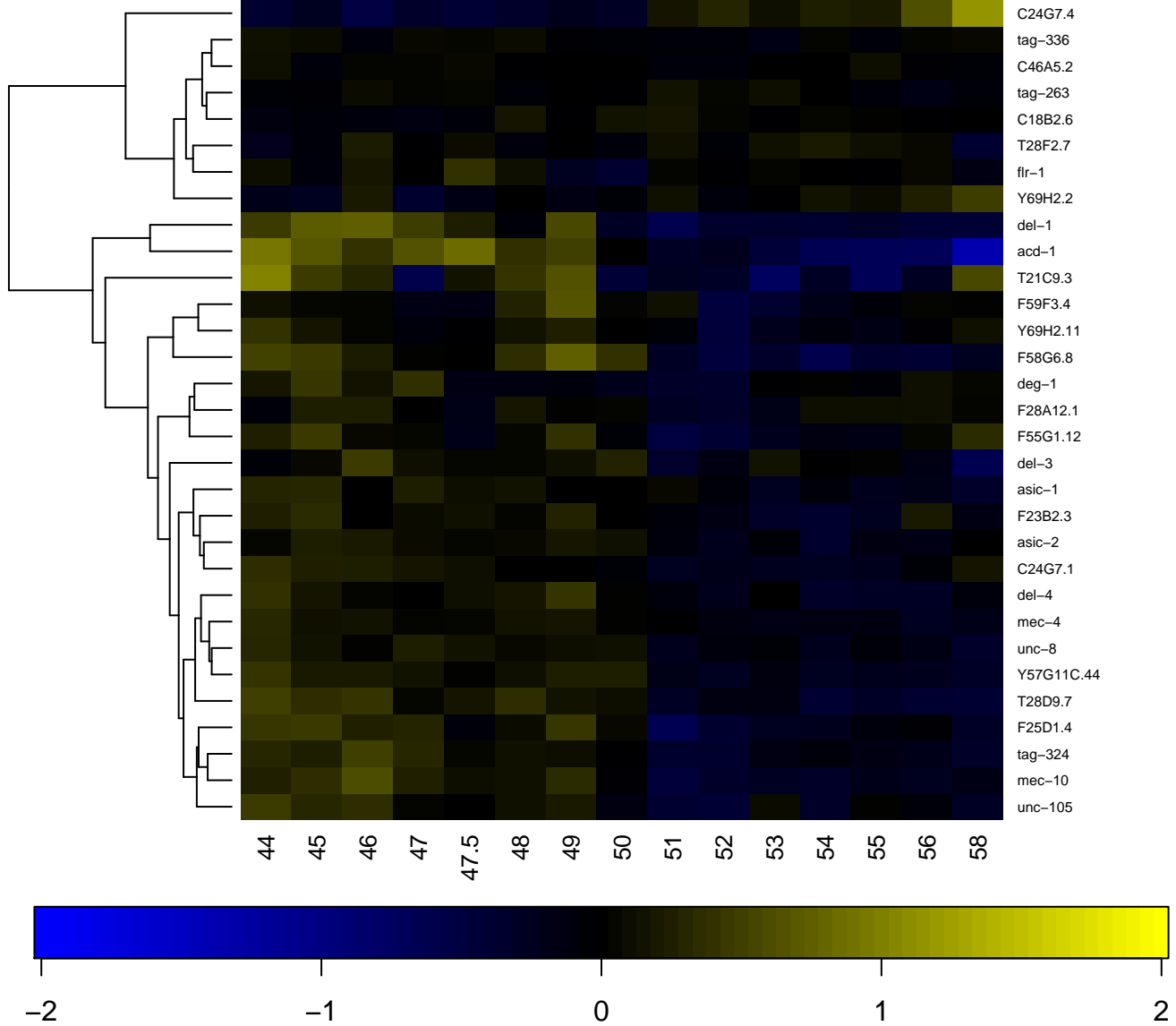
Myosin N-terminal SH3-like domain



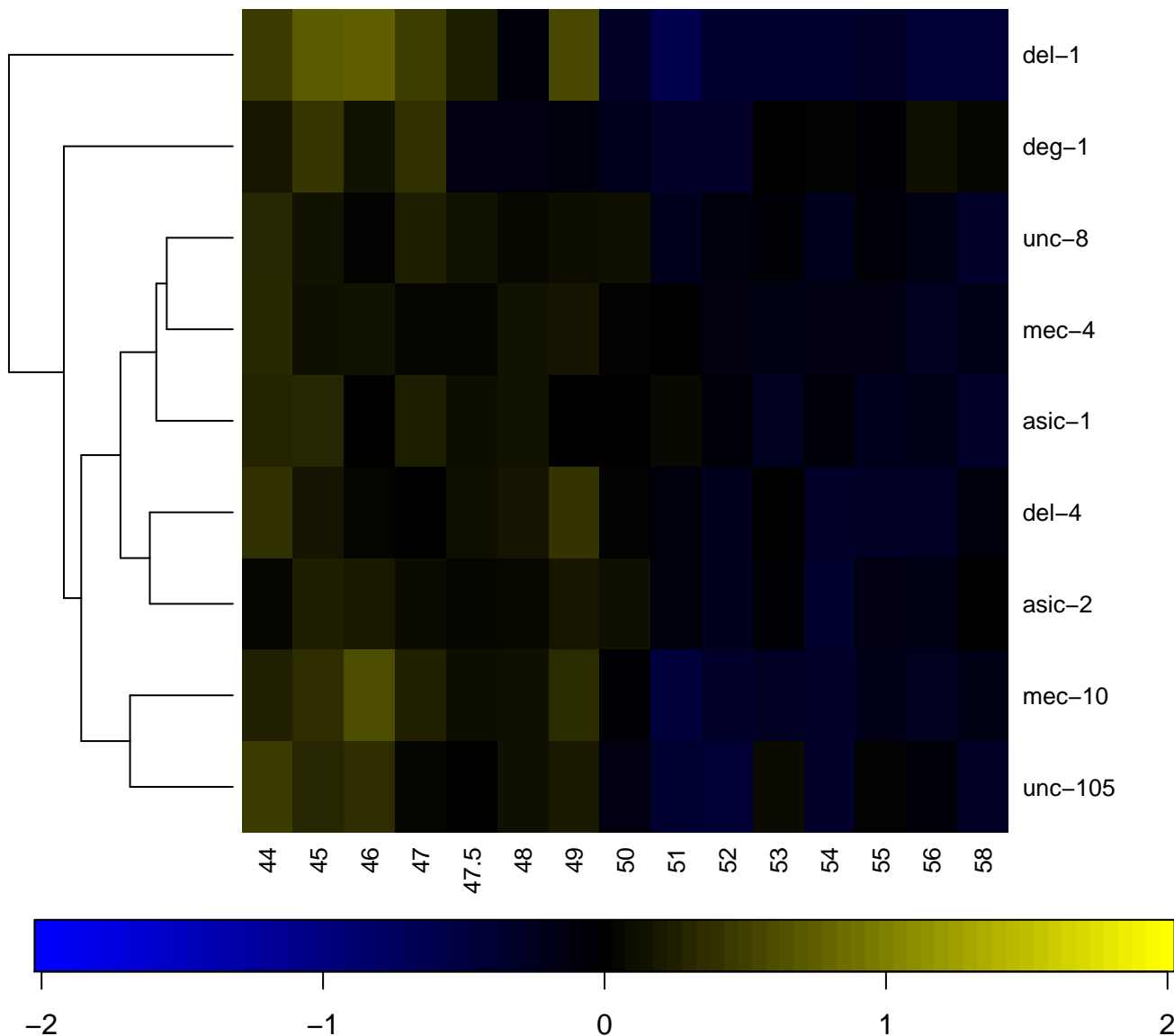
Myosin tail



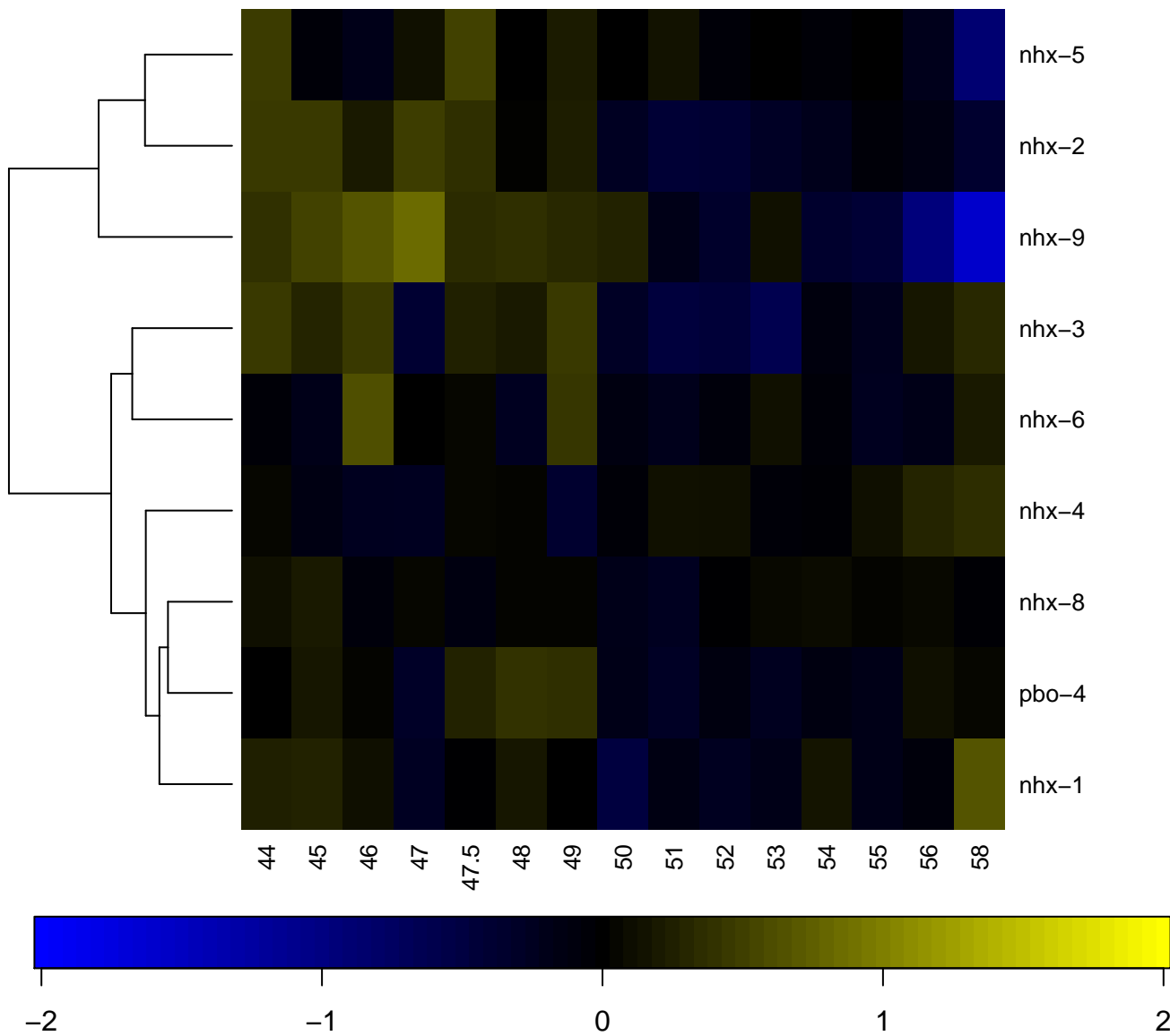
Na⁺ channel, amiloride-sensitive



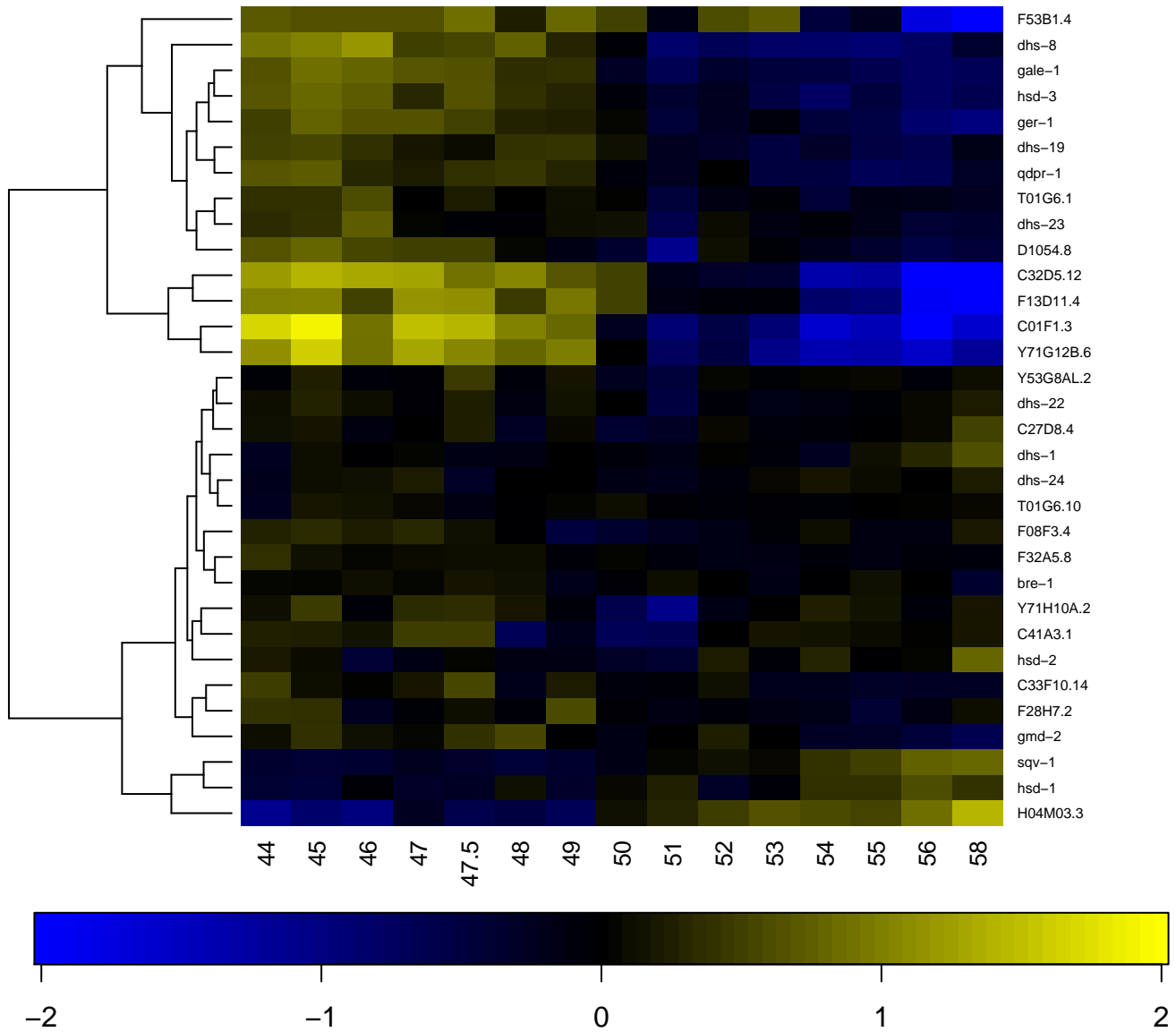
Na⁺ channel, amiloride-sensitive, conserved site



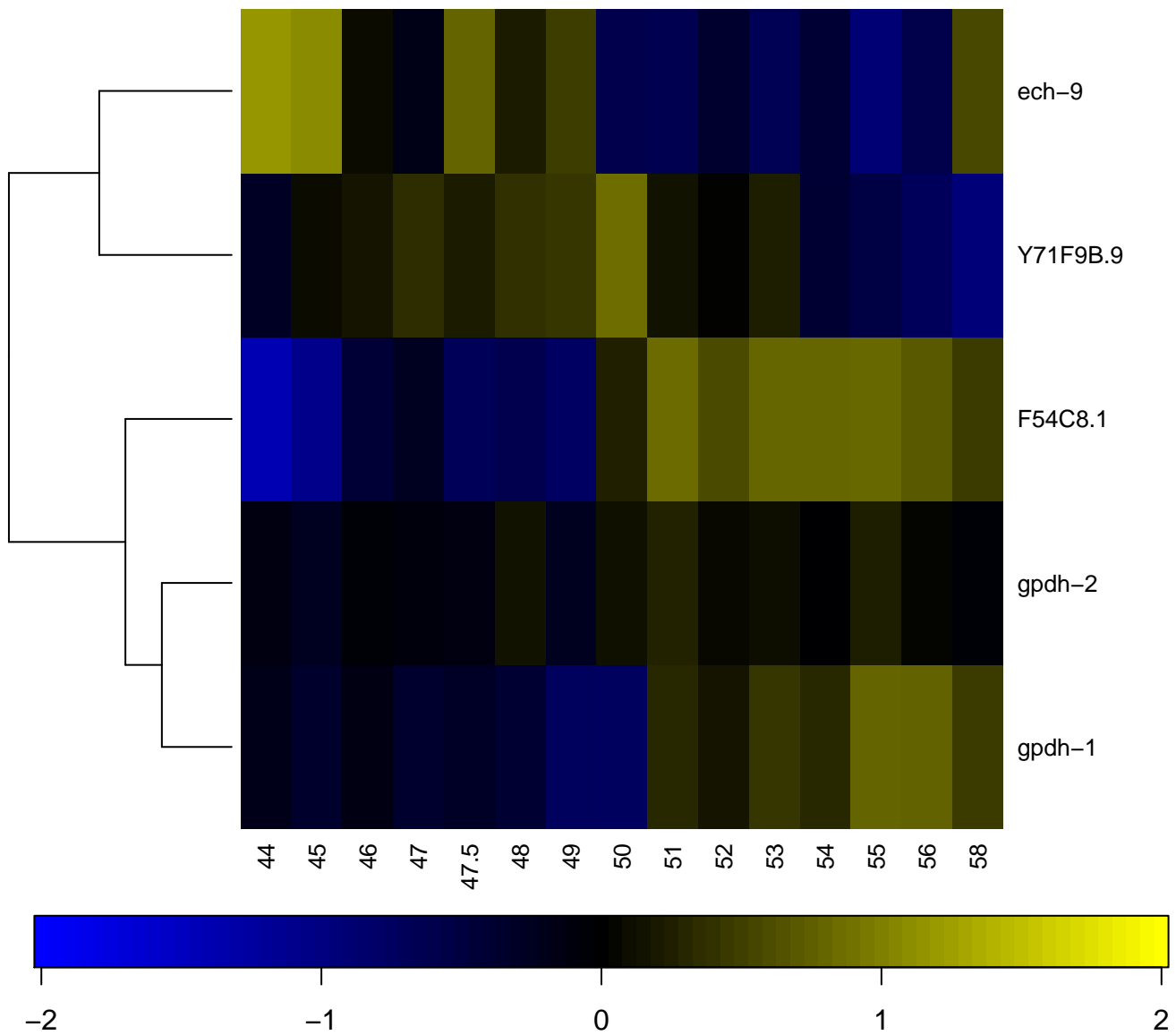
Na⁺/H⁺ exchanger



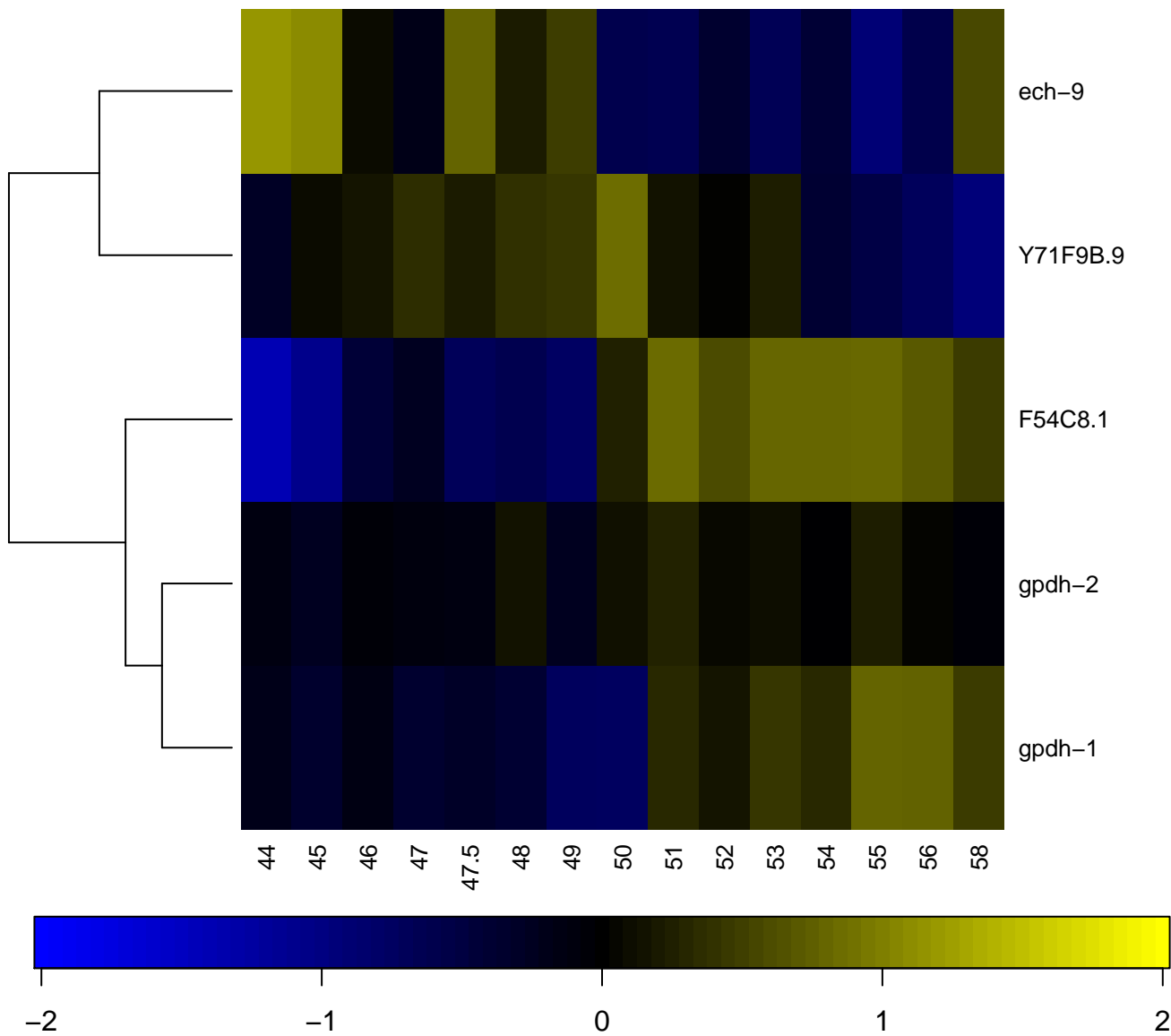
NAD-dependent epimerase/dehydratase



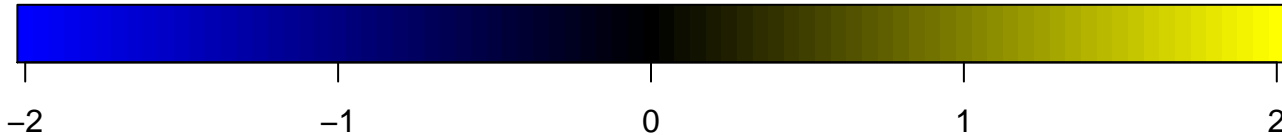
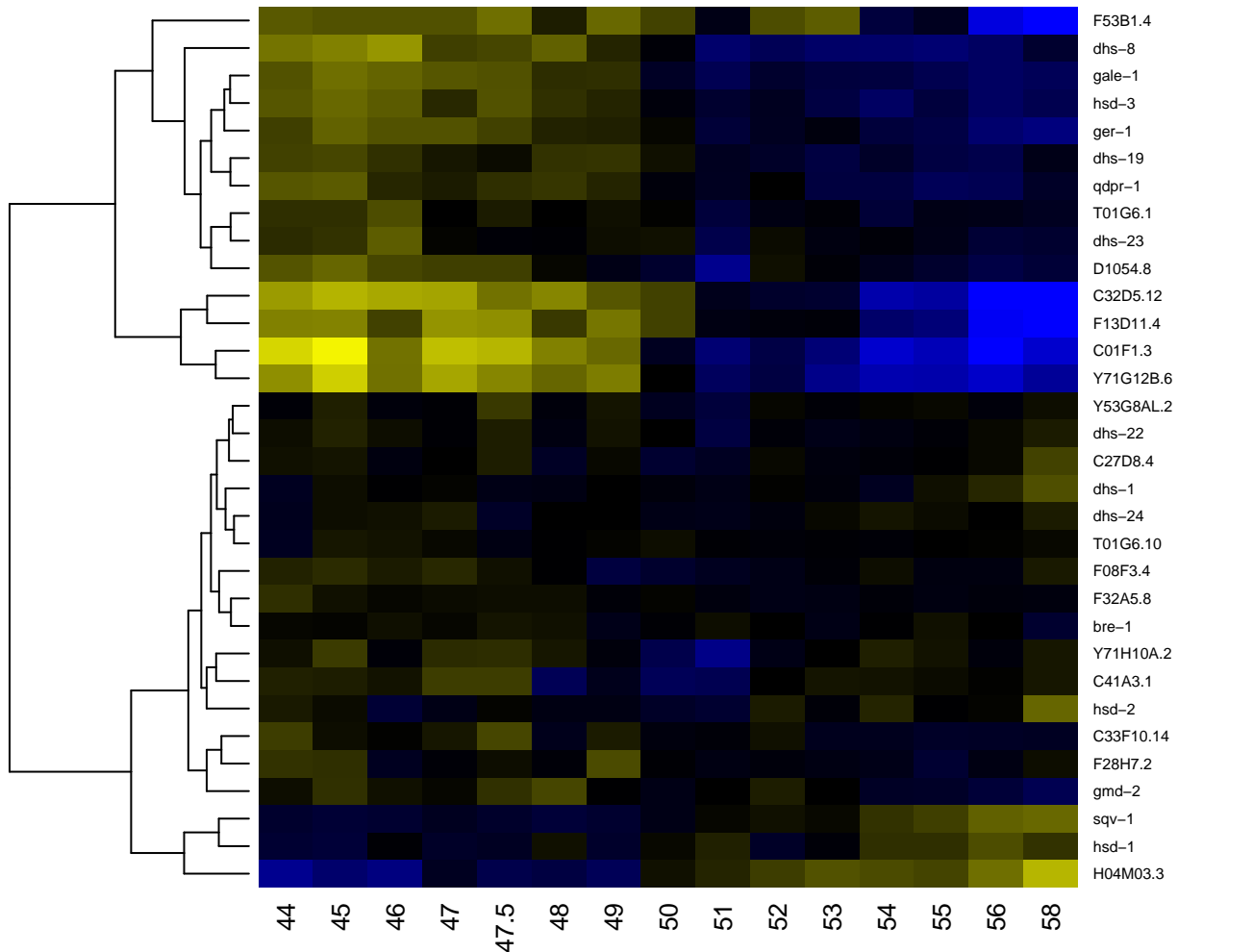
D-dependent glycerol-3-phosphate dehydrogenase N-term



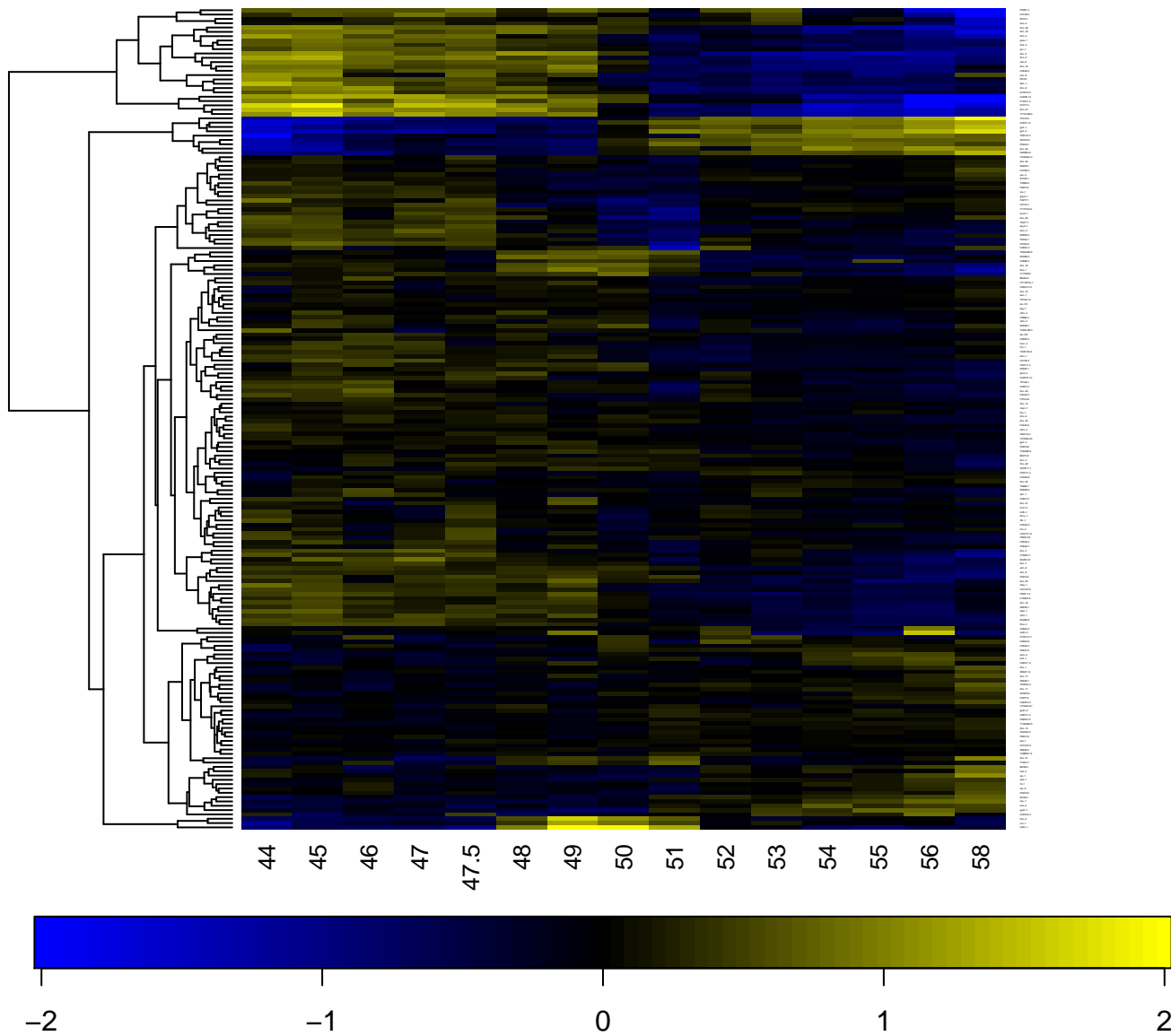
D-dependent glycerol-3-phosphate dehydrogenase, N-term



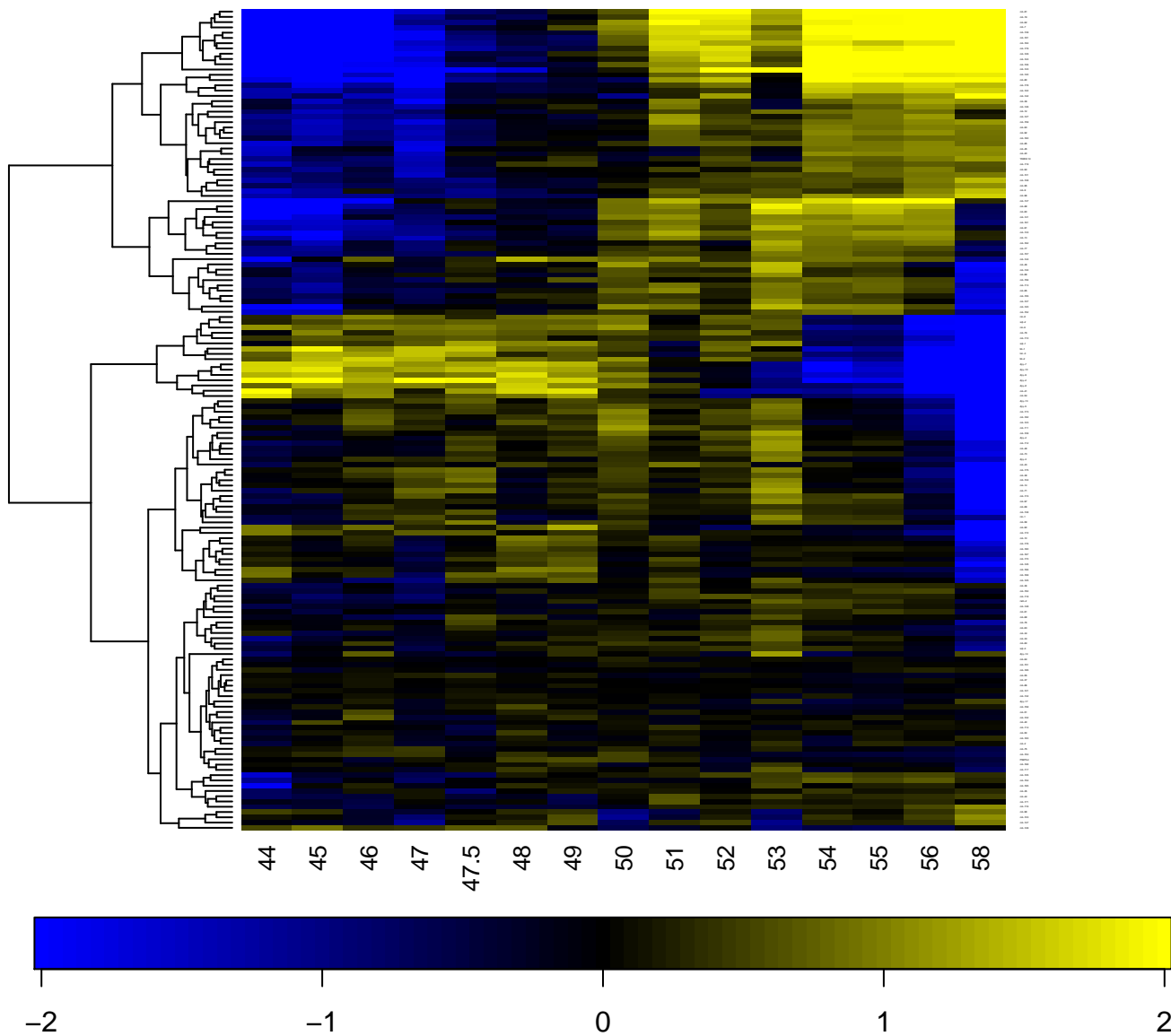
NAD dependent epimerase/dehydratase family



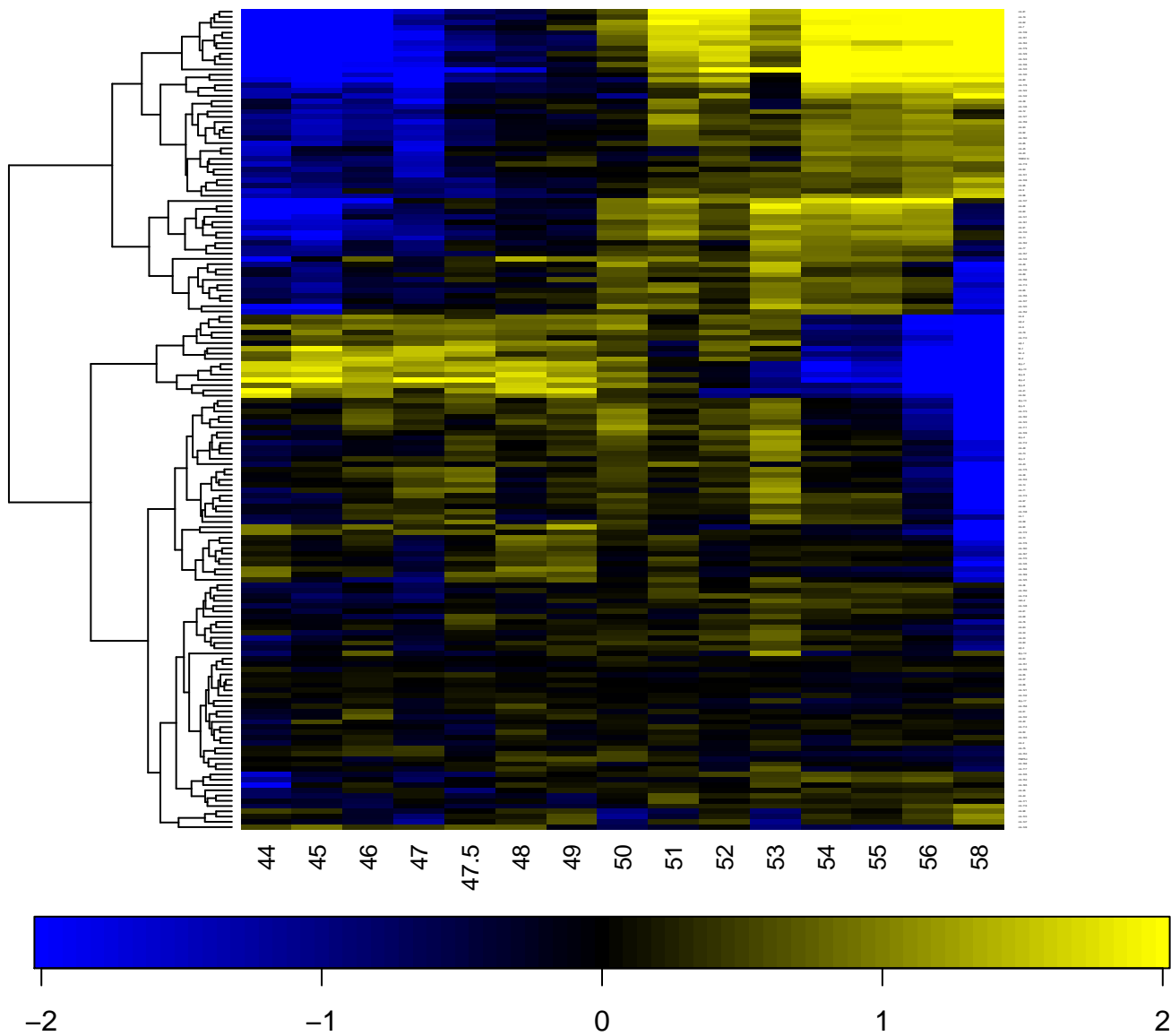
NAD(P)-binding domain



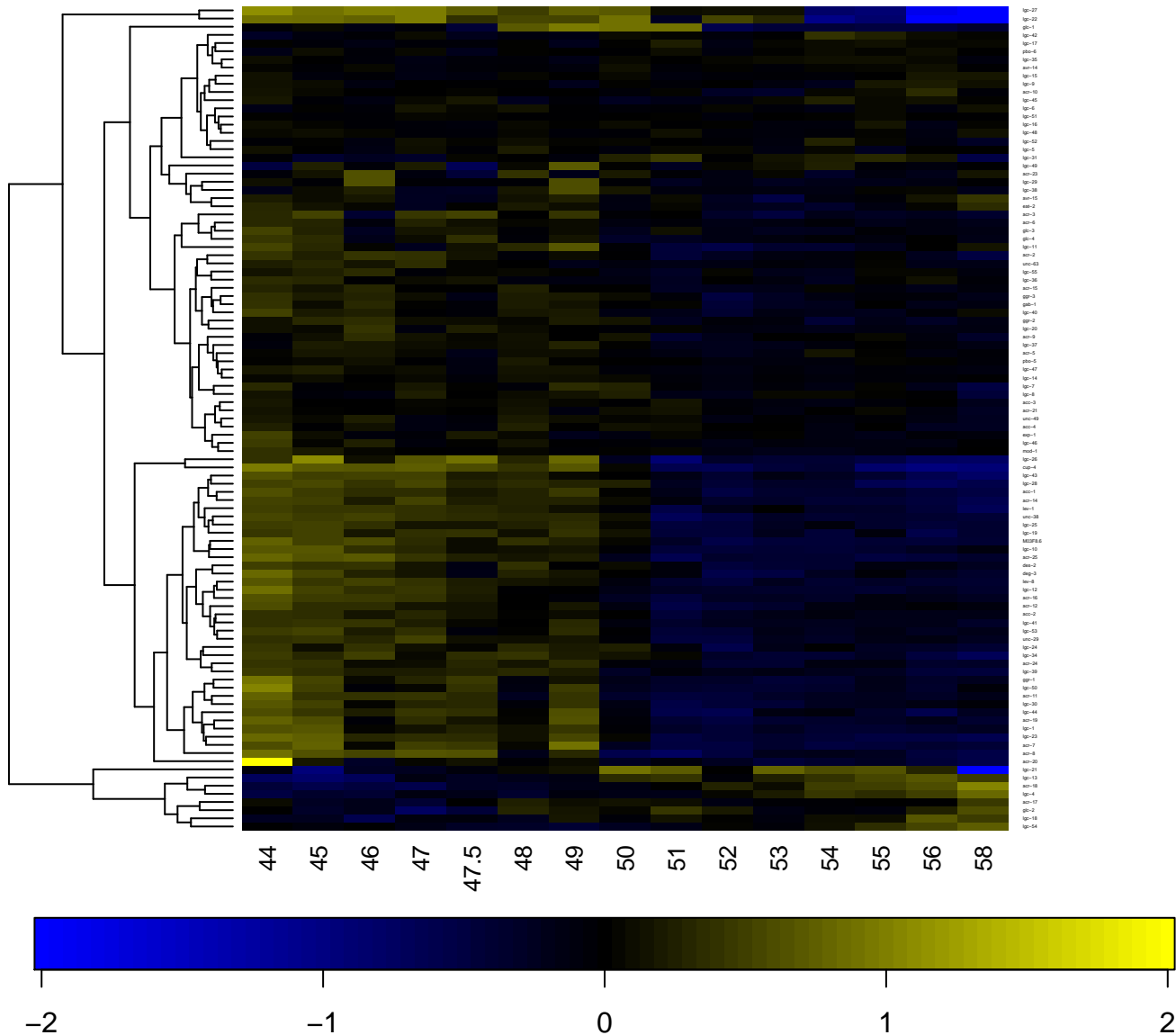
Nematode cuticle collagen N-terminal domain



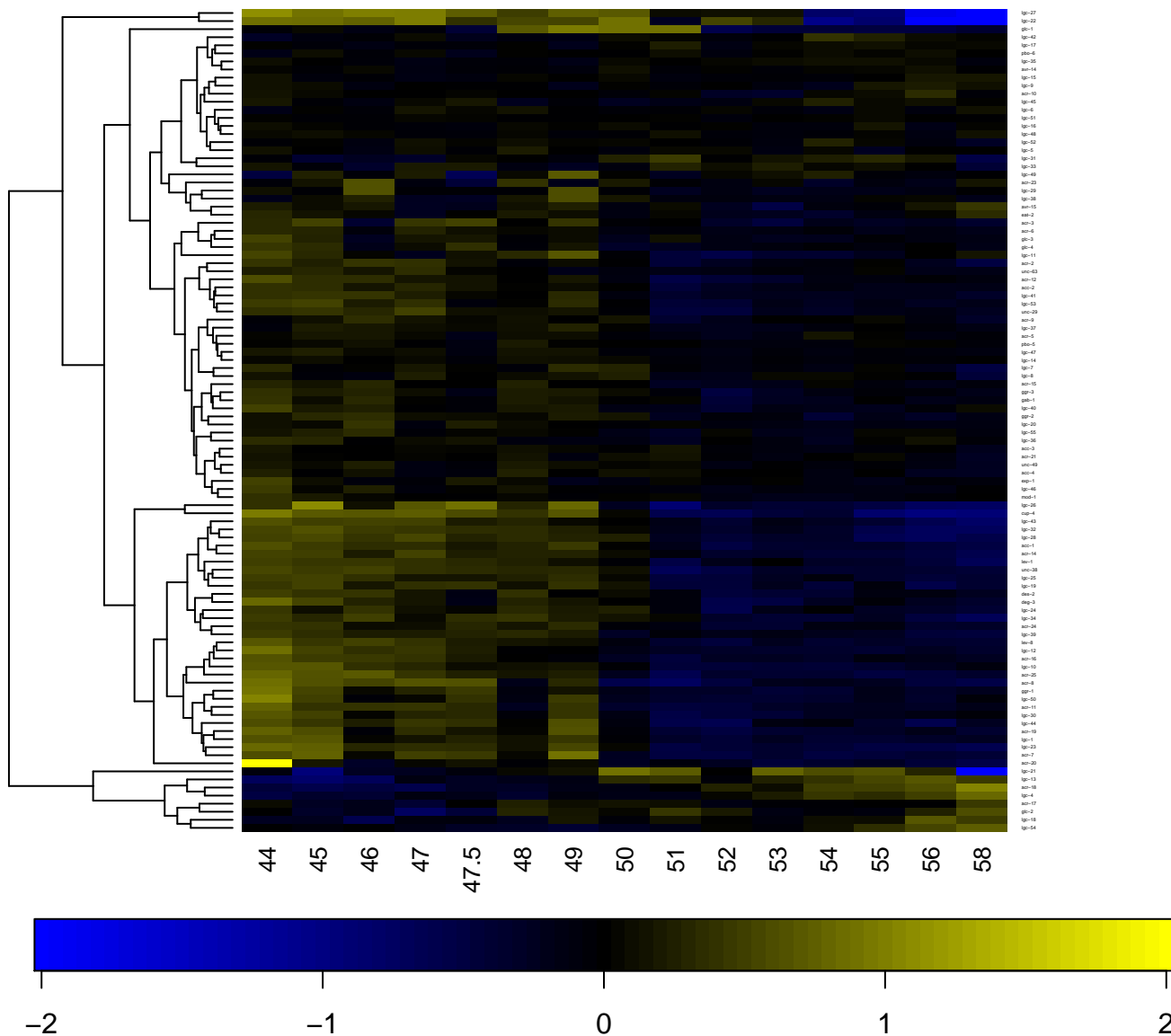
Nematode cuticle collagen, N-terminal



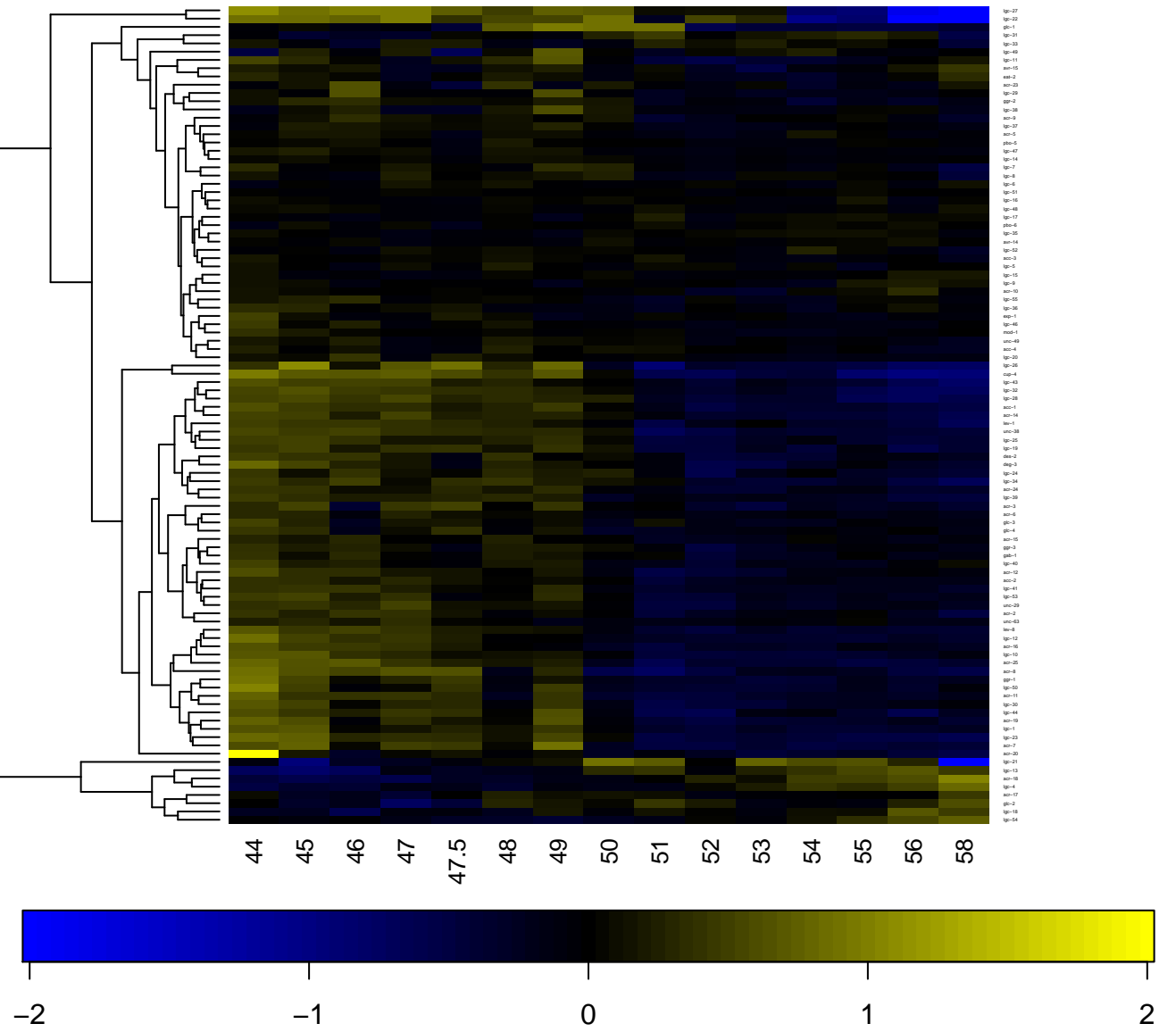
Neurotransmitter-gated ion-channel



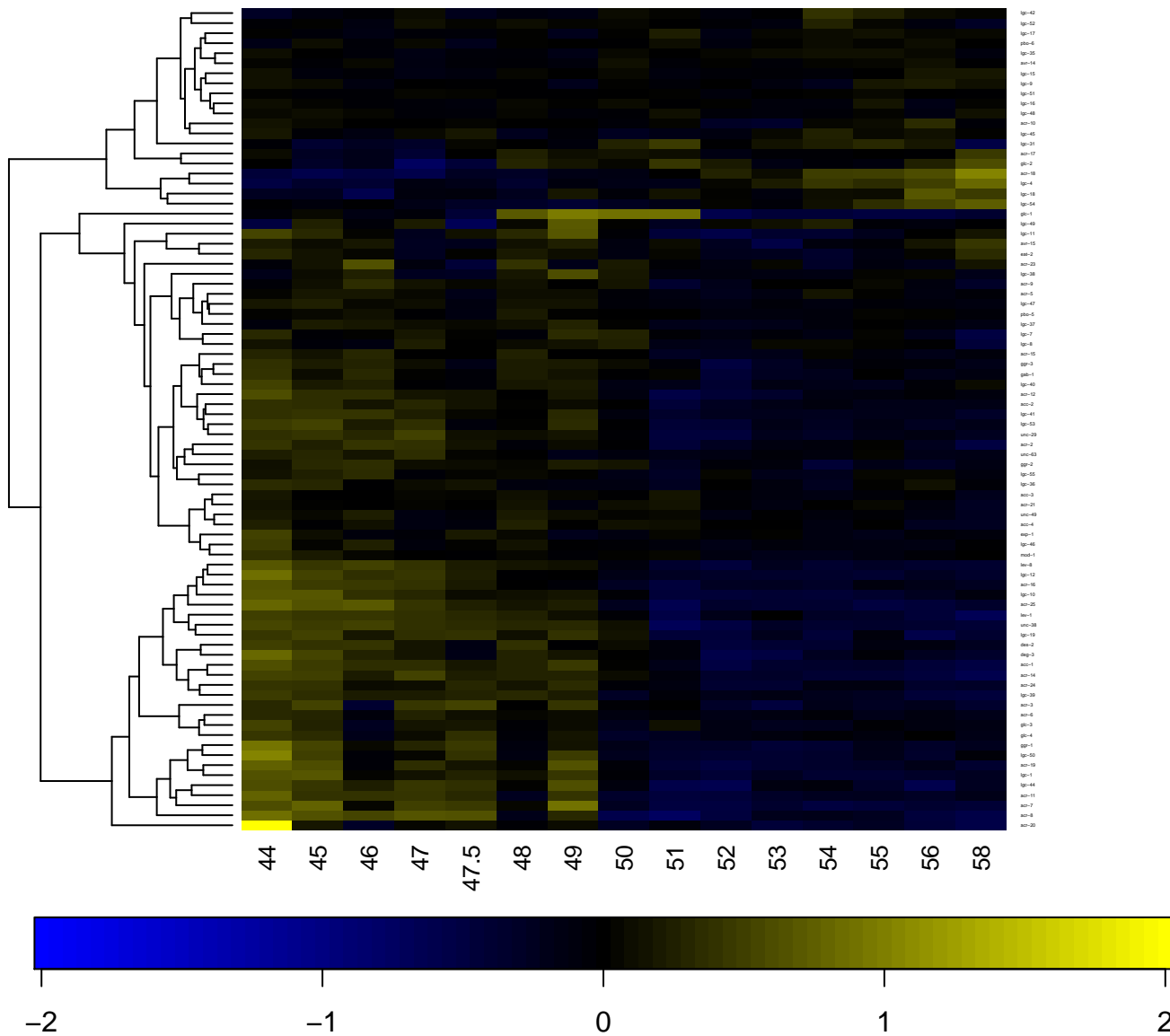
Neurotransmitter-gated ion-channel ligand-binding



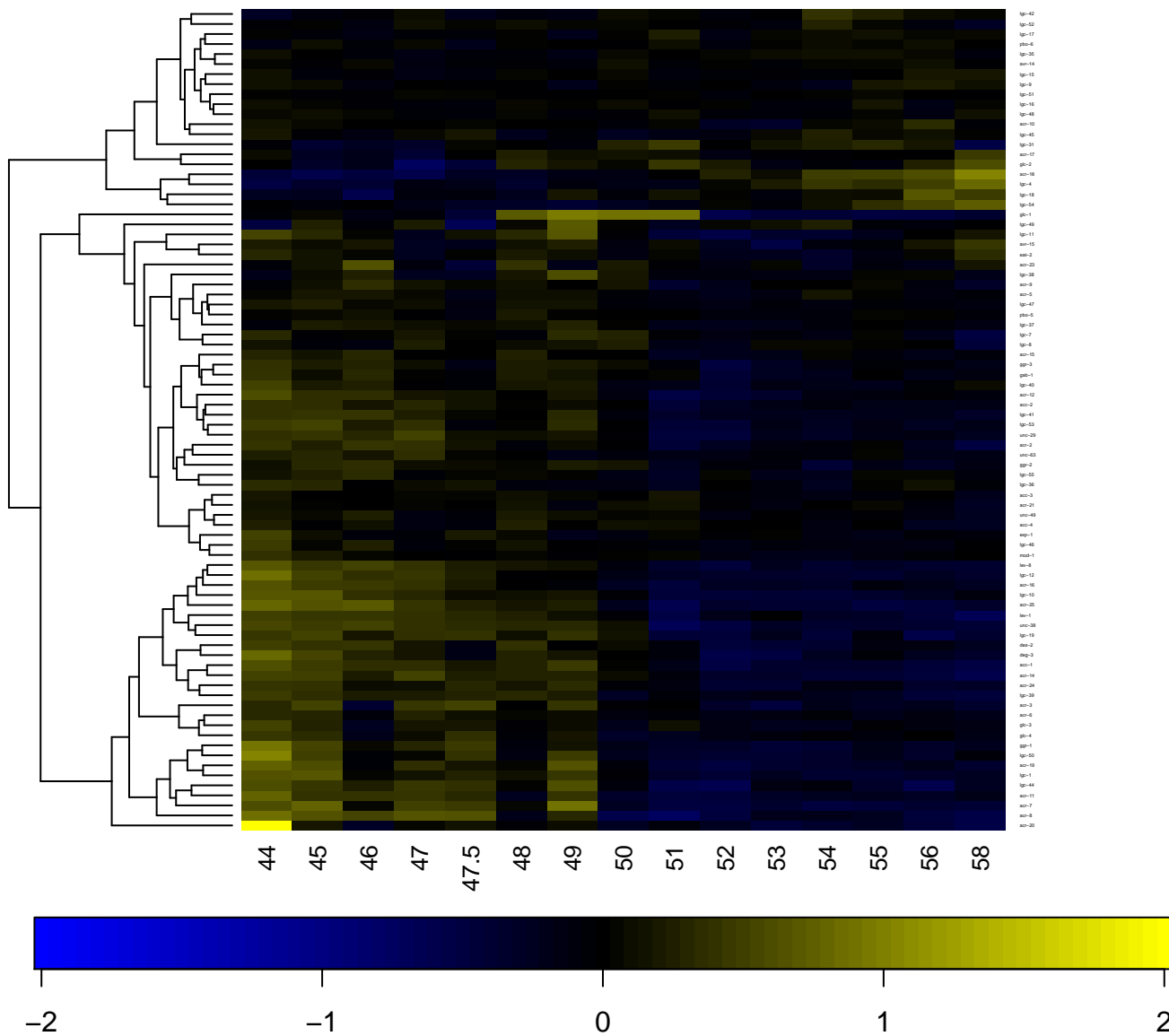
Neurotransmitter-gated ion-channel ligand binding domain



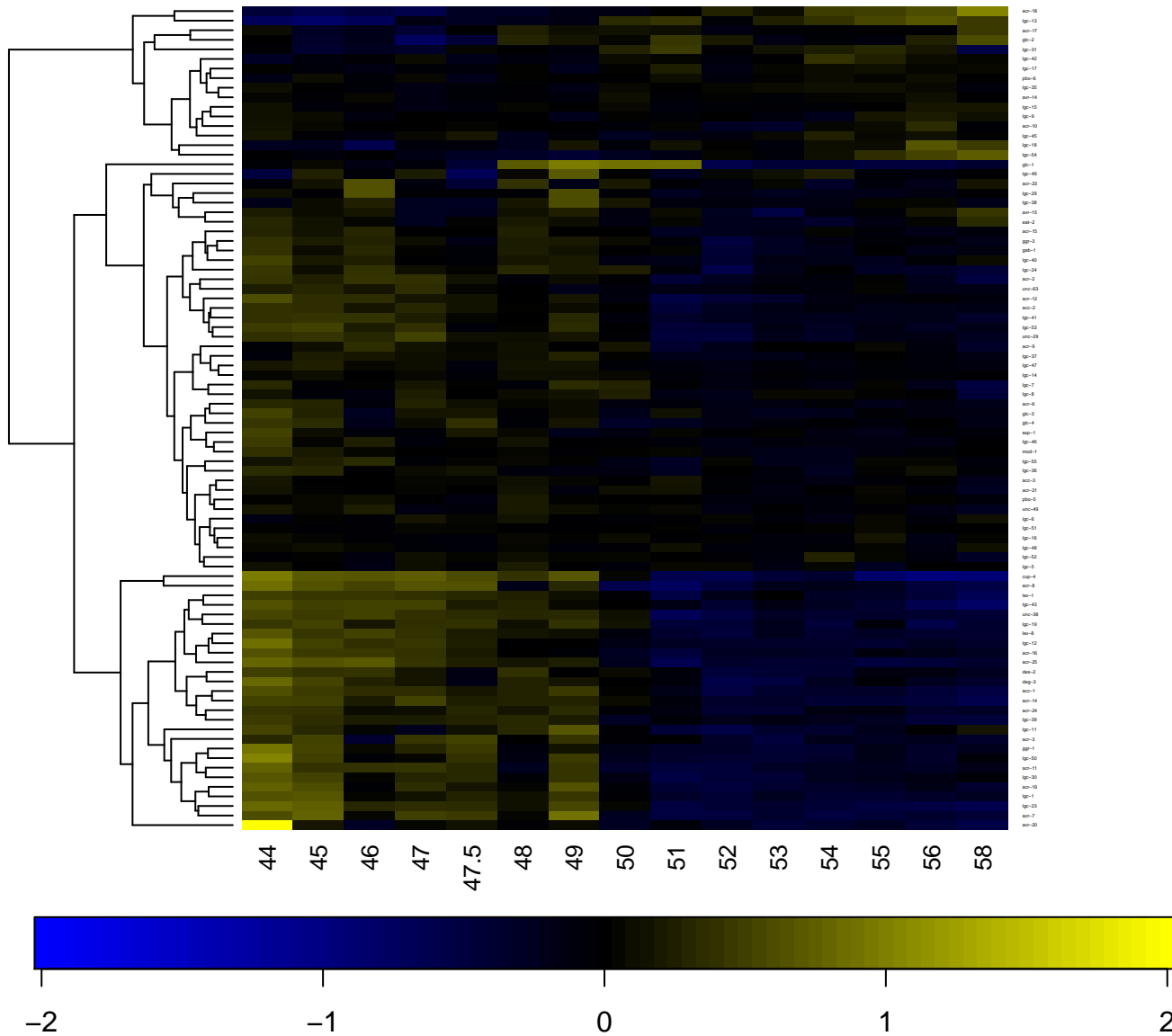
Neurotransmitter-gated ion-channel transmembrane domain



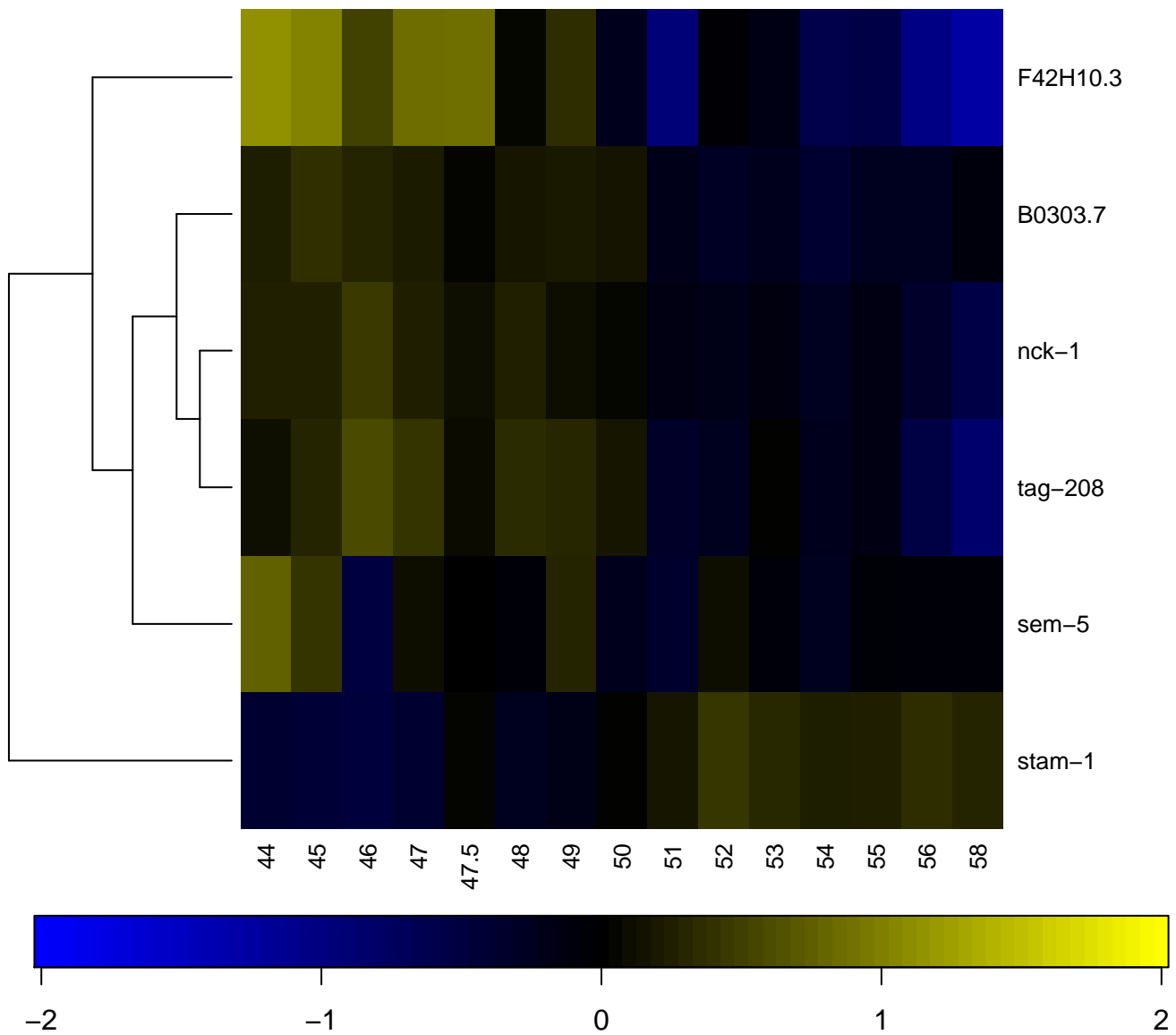
Neurotransmitter-gated ion-channel transmembrane region



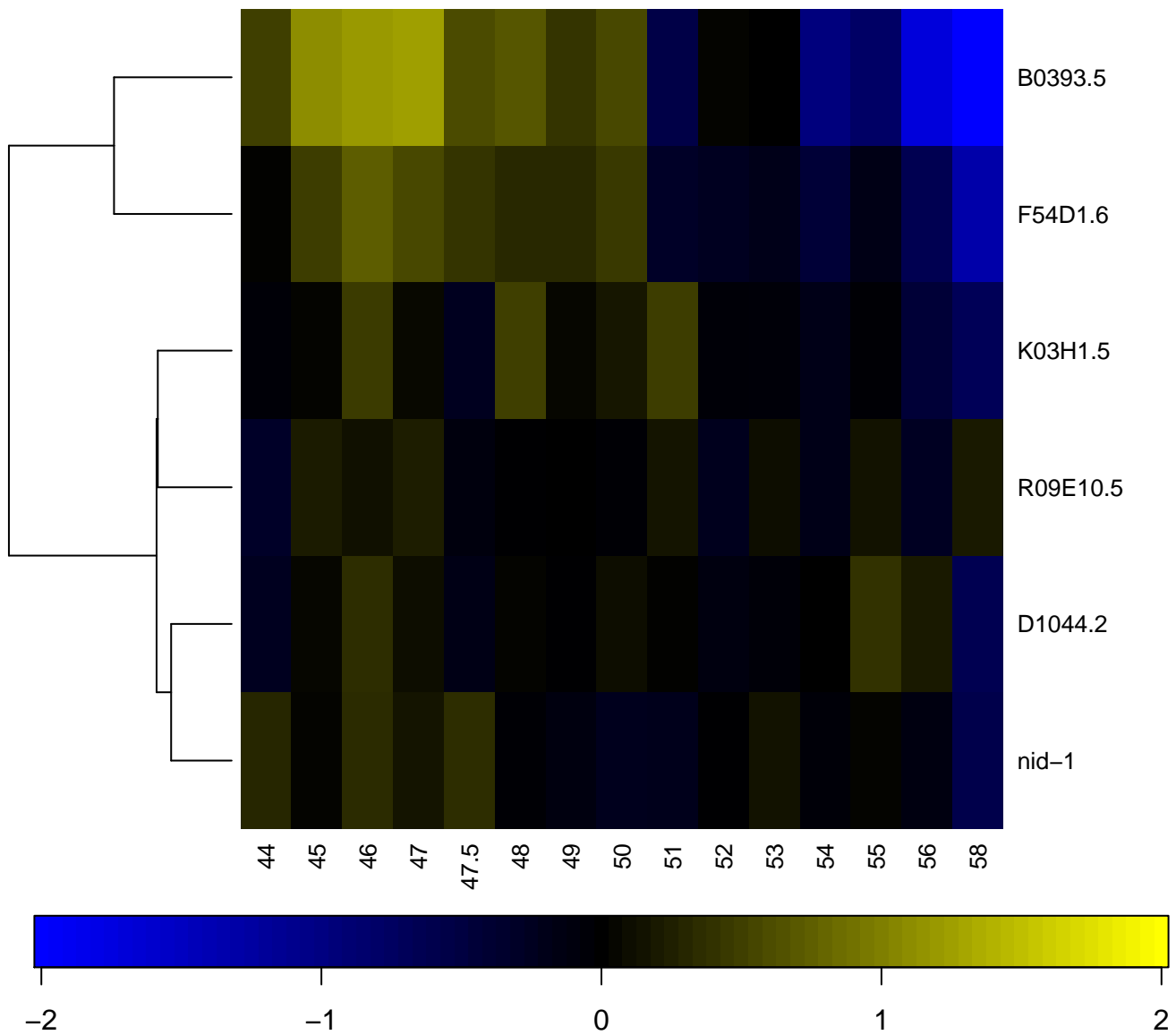
Neurotransmitter-gated ion-channel, conserved site



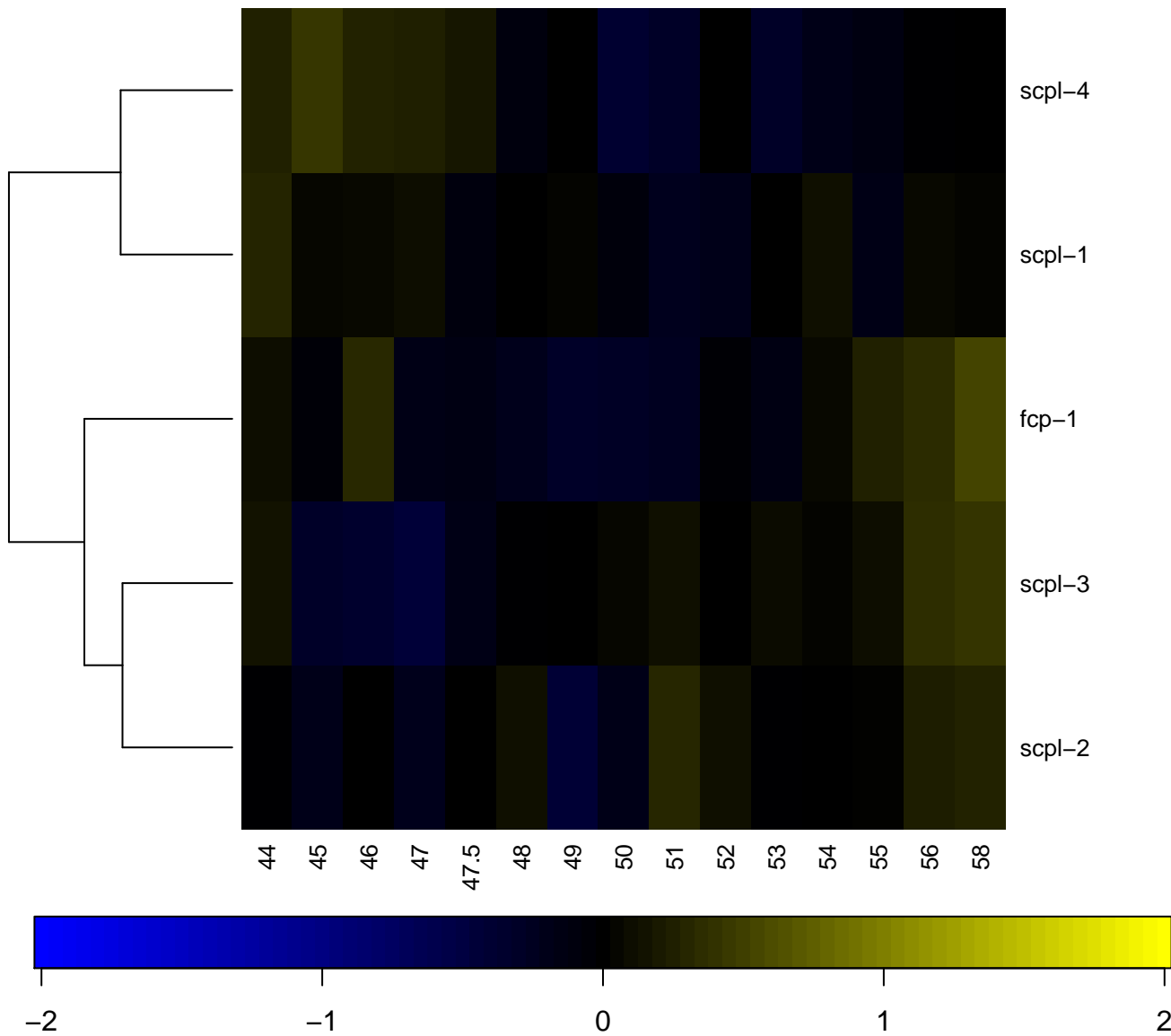
Neutrophil cytosol factor 2 p67phox



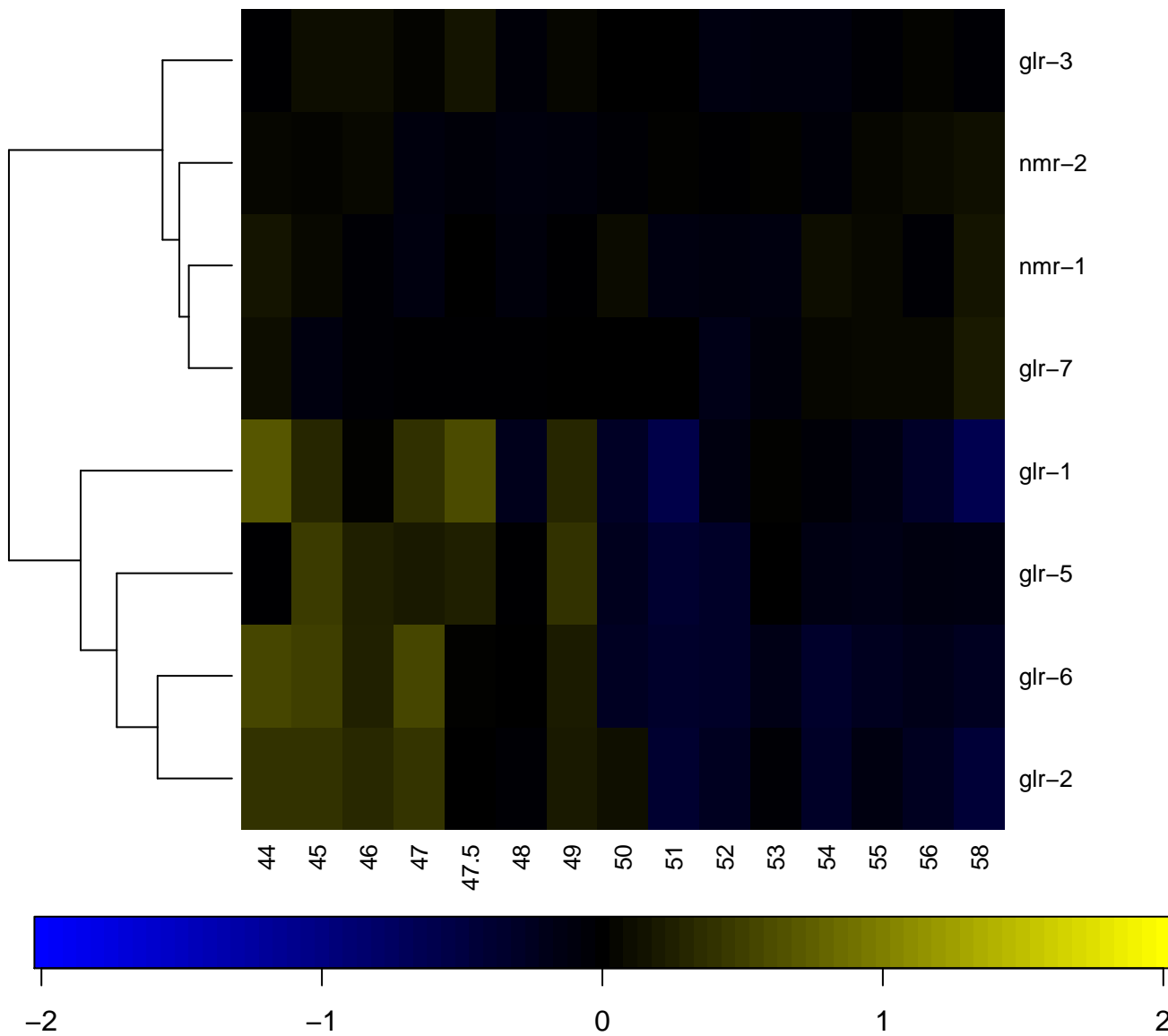
Nidogen, extracellular domain



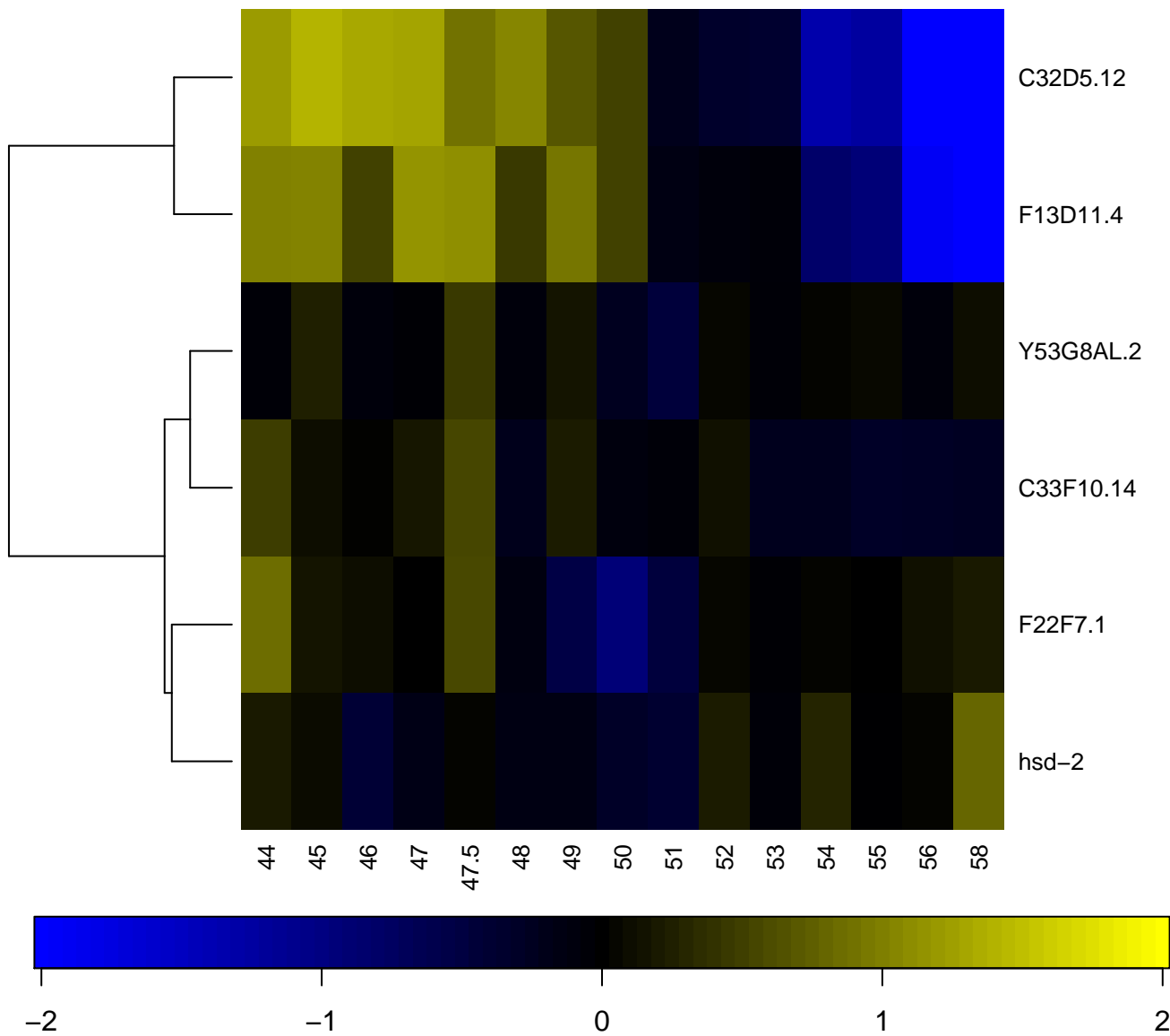
NLI interacting factor



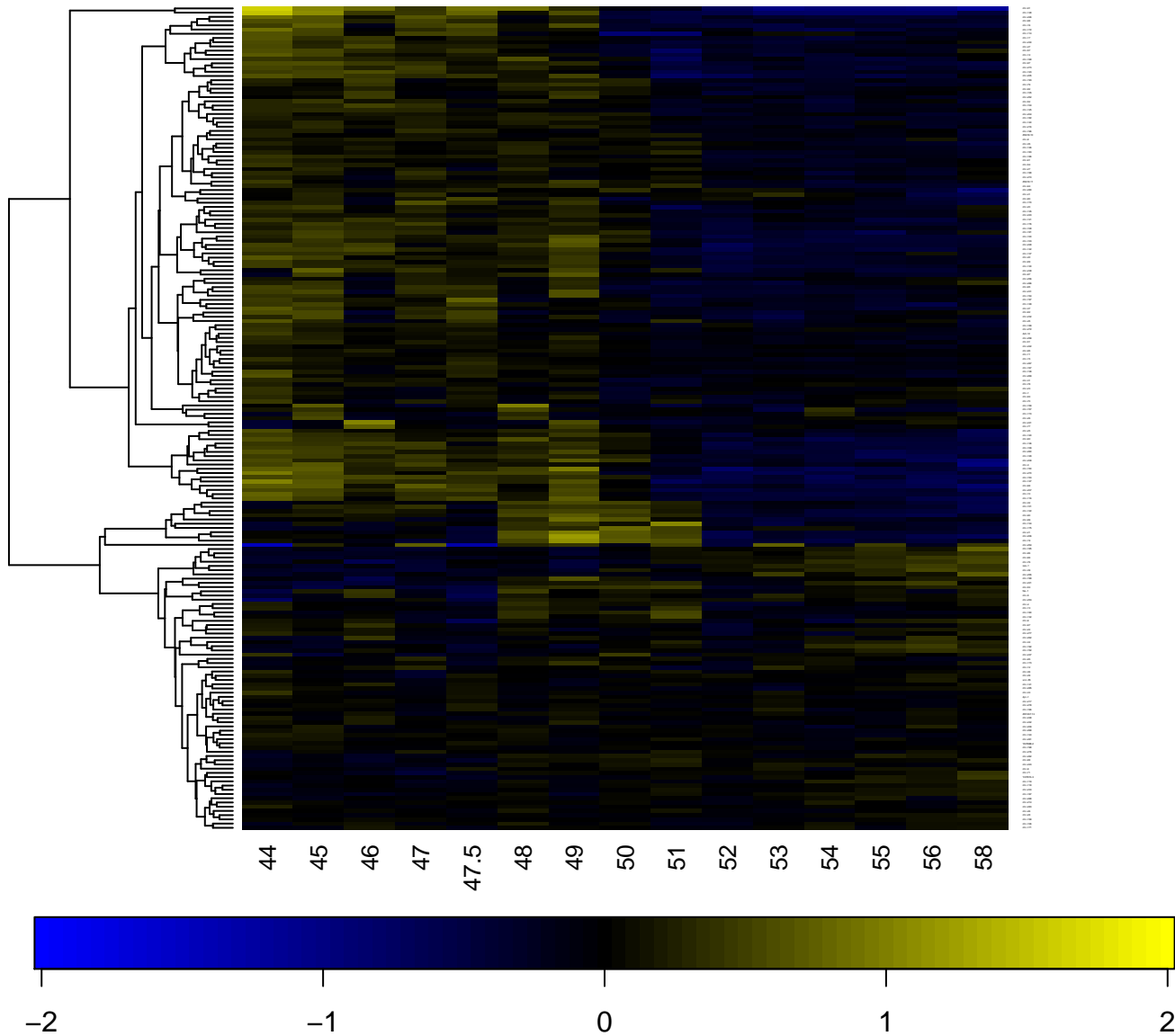
NMDA receptor



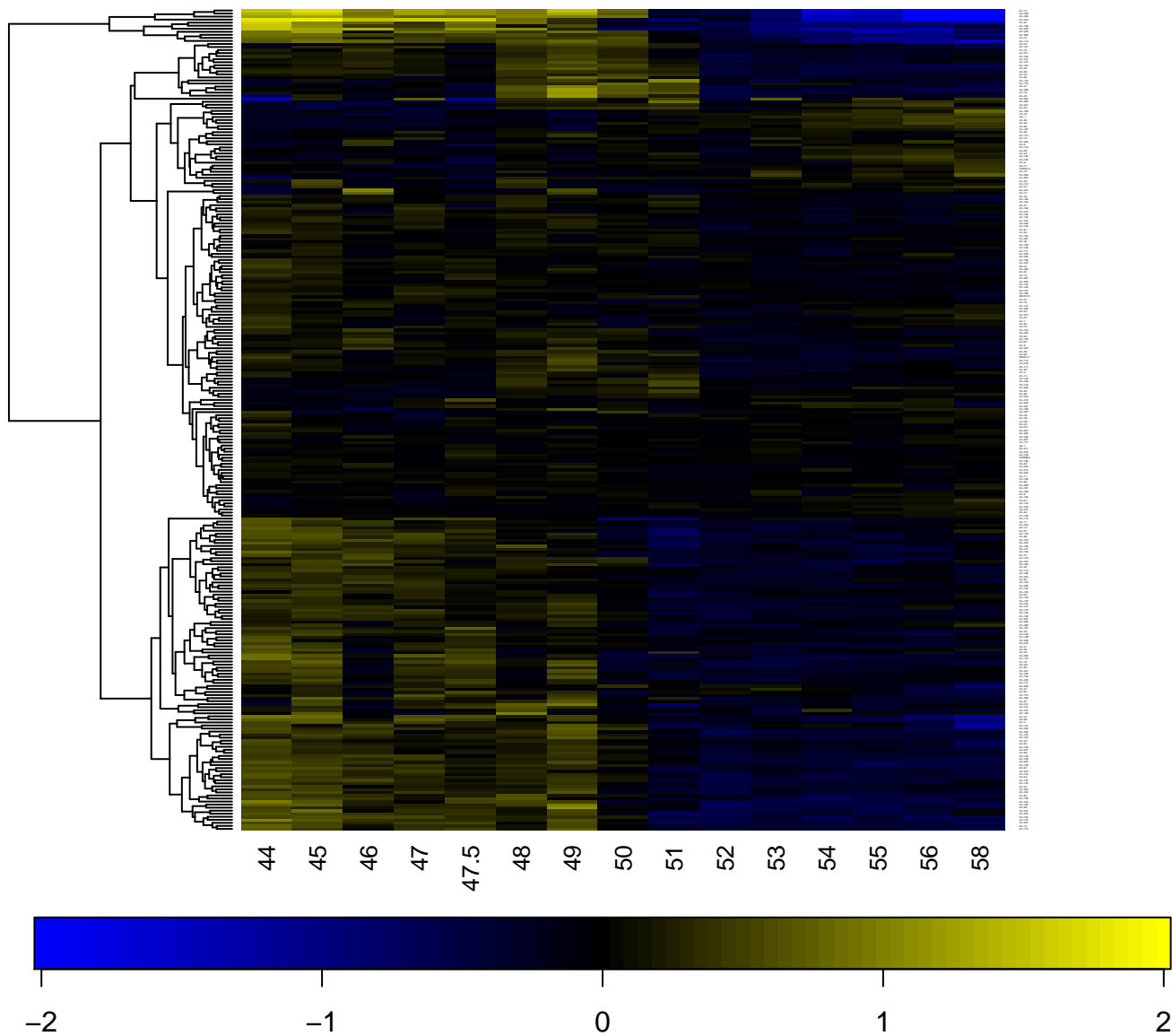
NmrA-like family



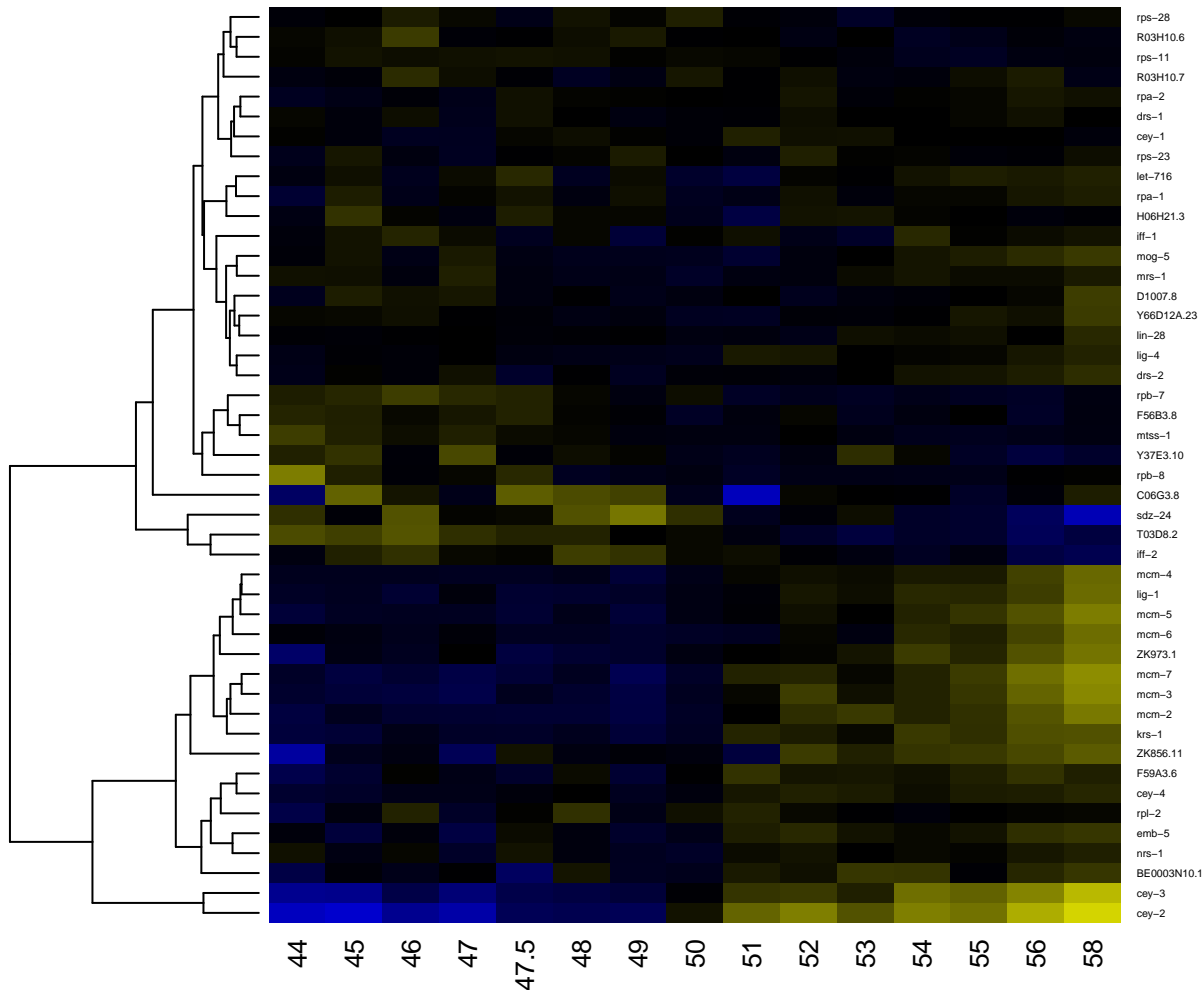
Nuclear hormone receptor, ligand-binding



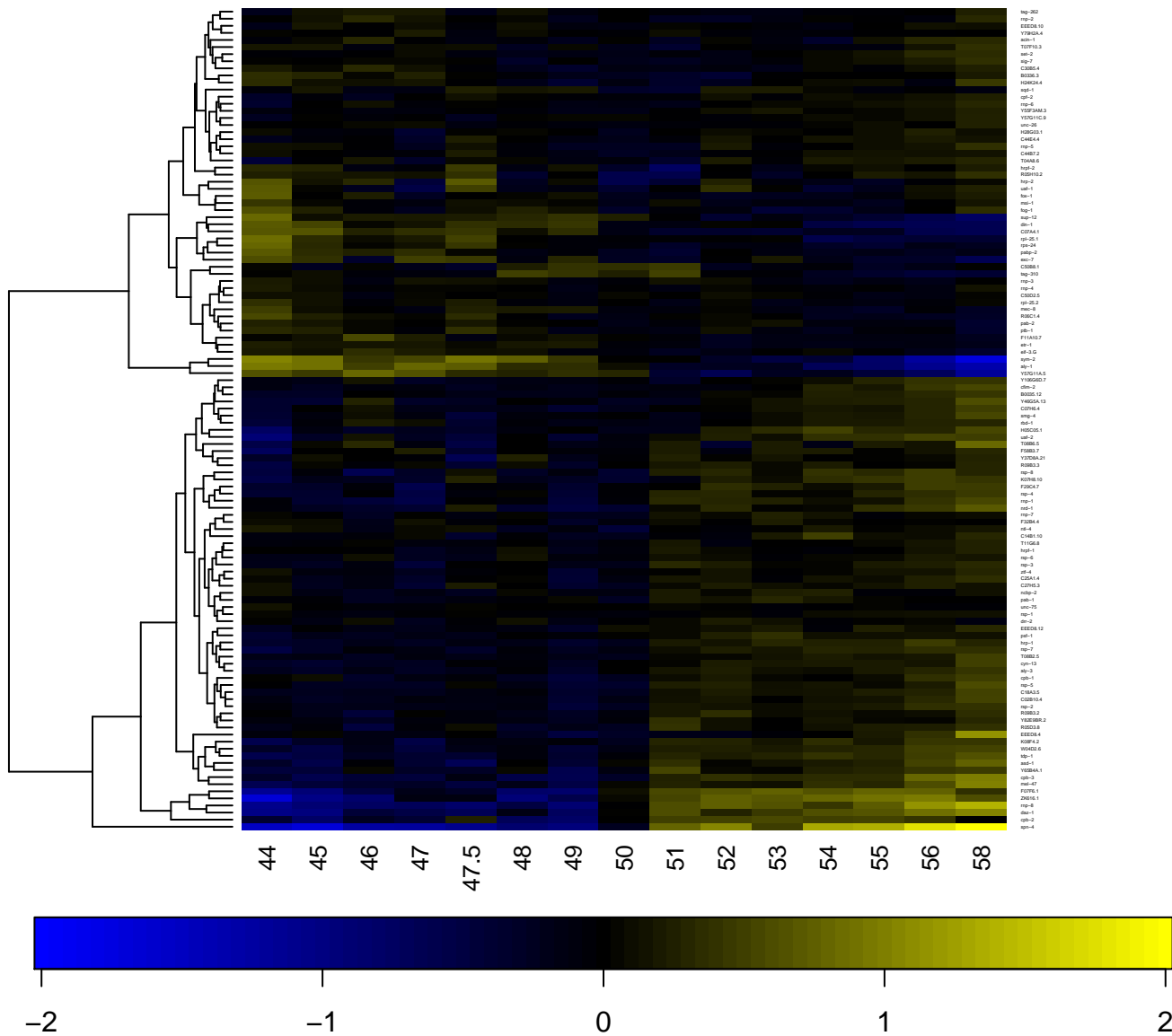
Nuclear hormone receptor, ligand-binding, core



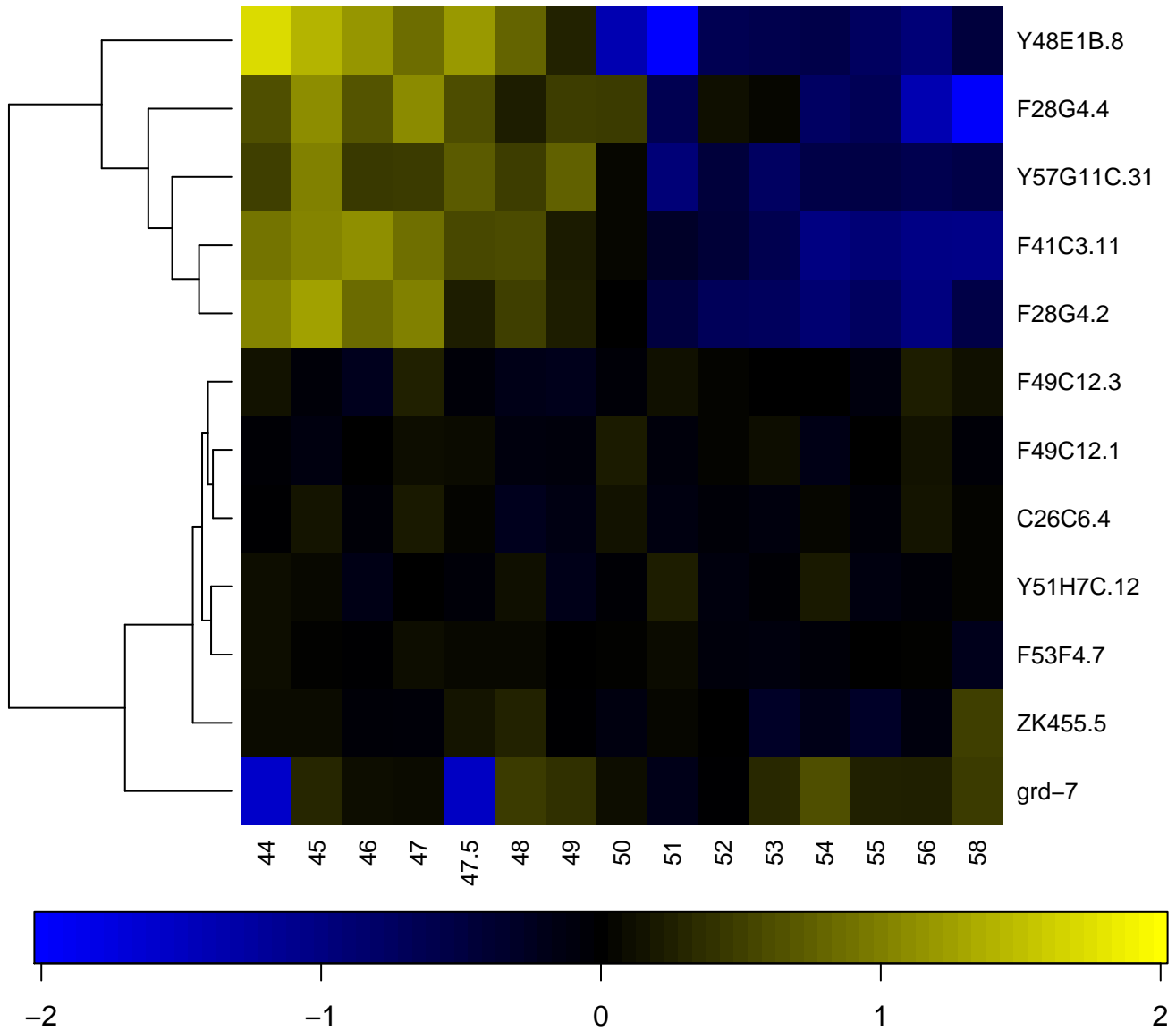
Nucleic acid-binding, OB-fold



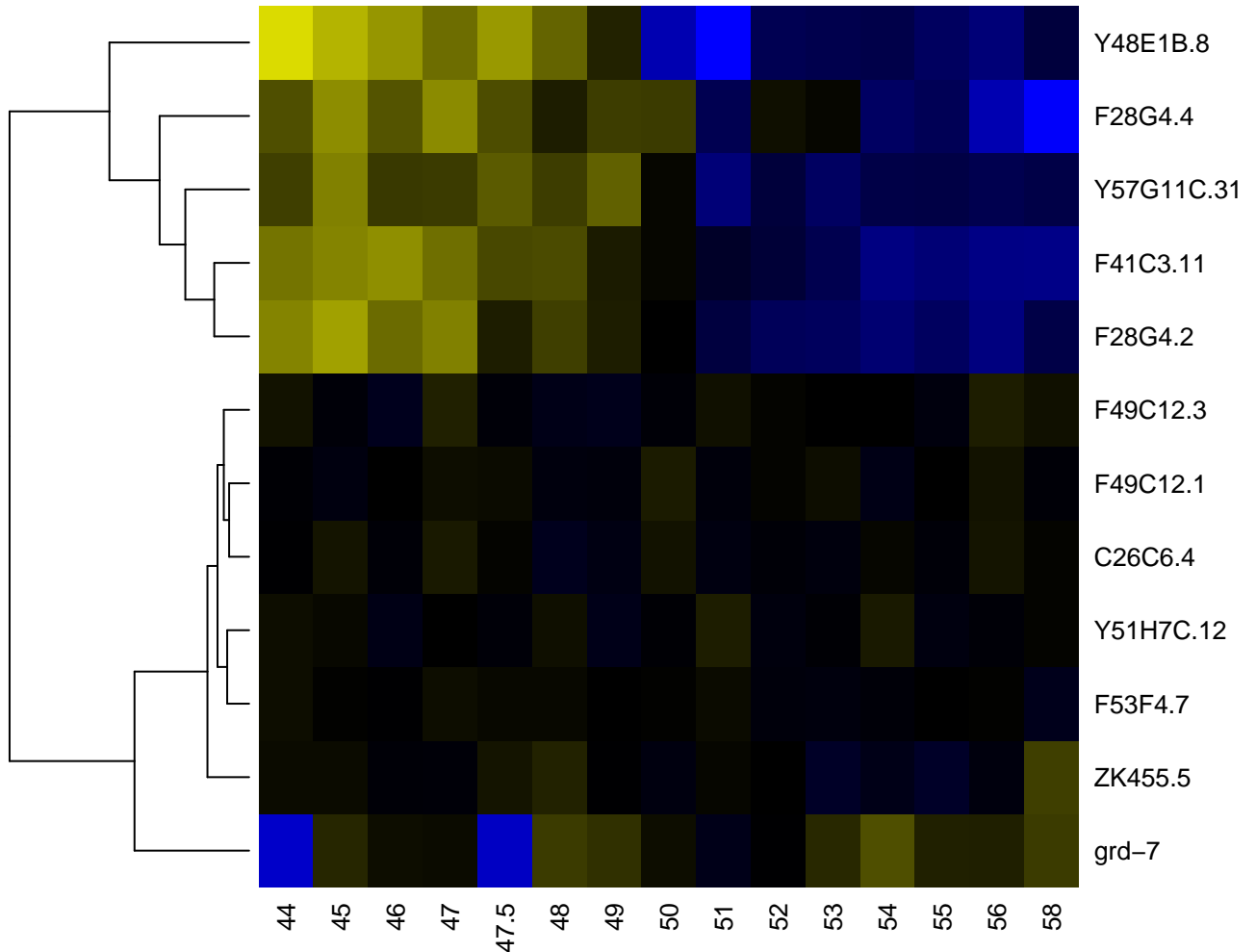
Nucleotide-binding, alpha-beta plait



Nucleotide-diphospho-sugar transferase



Nucleotide-diphospho-sugar transferase, predicted



-2

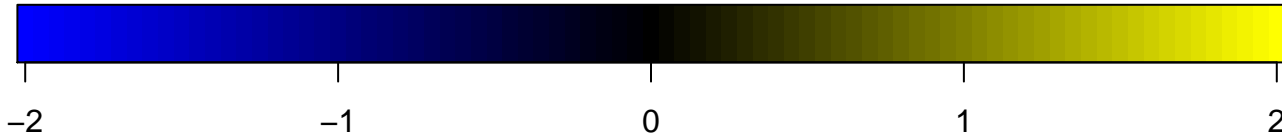
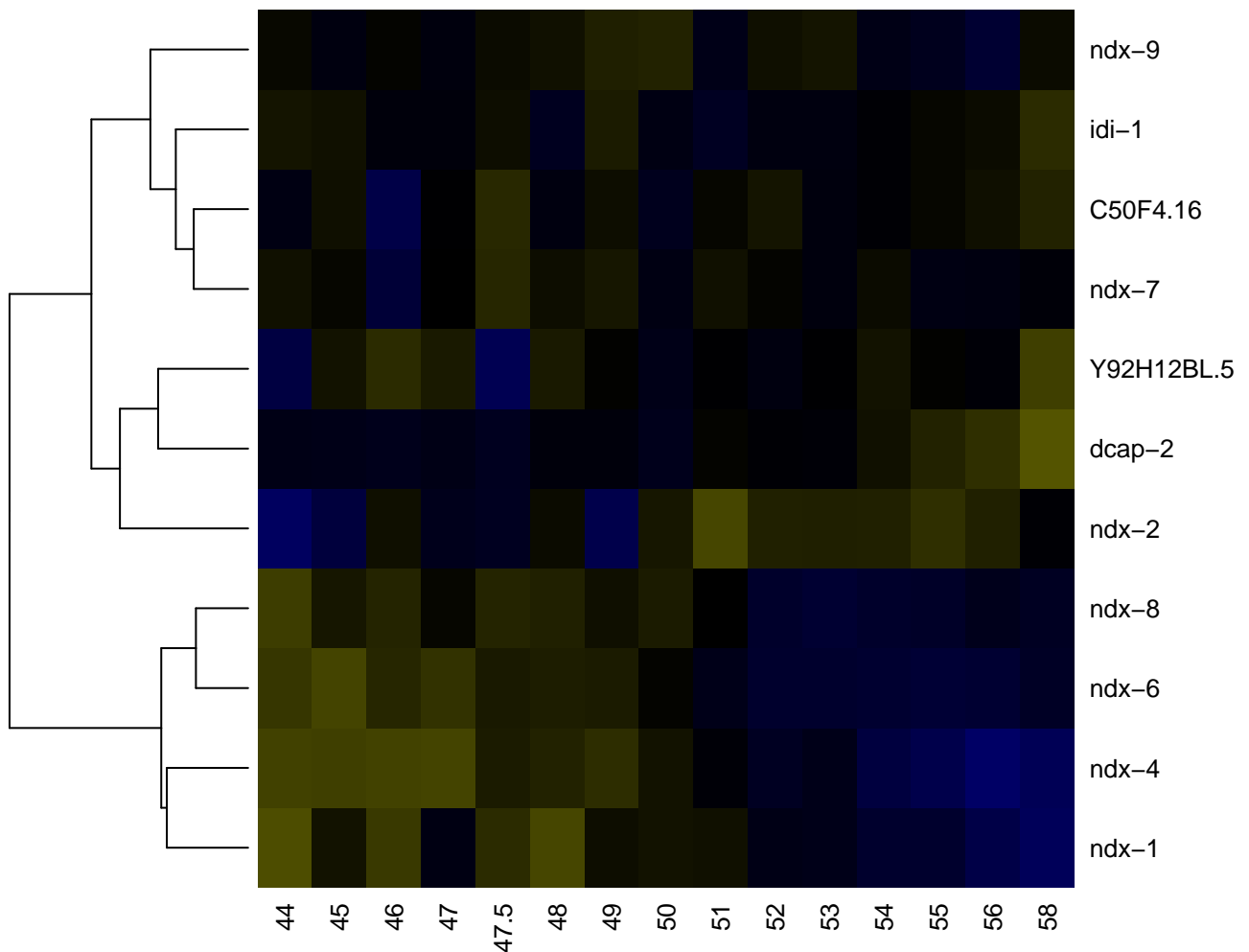
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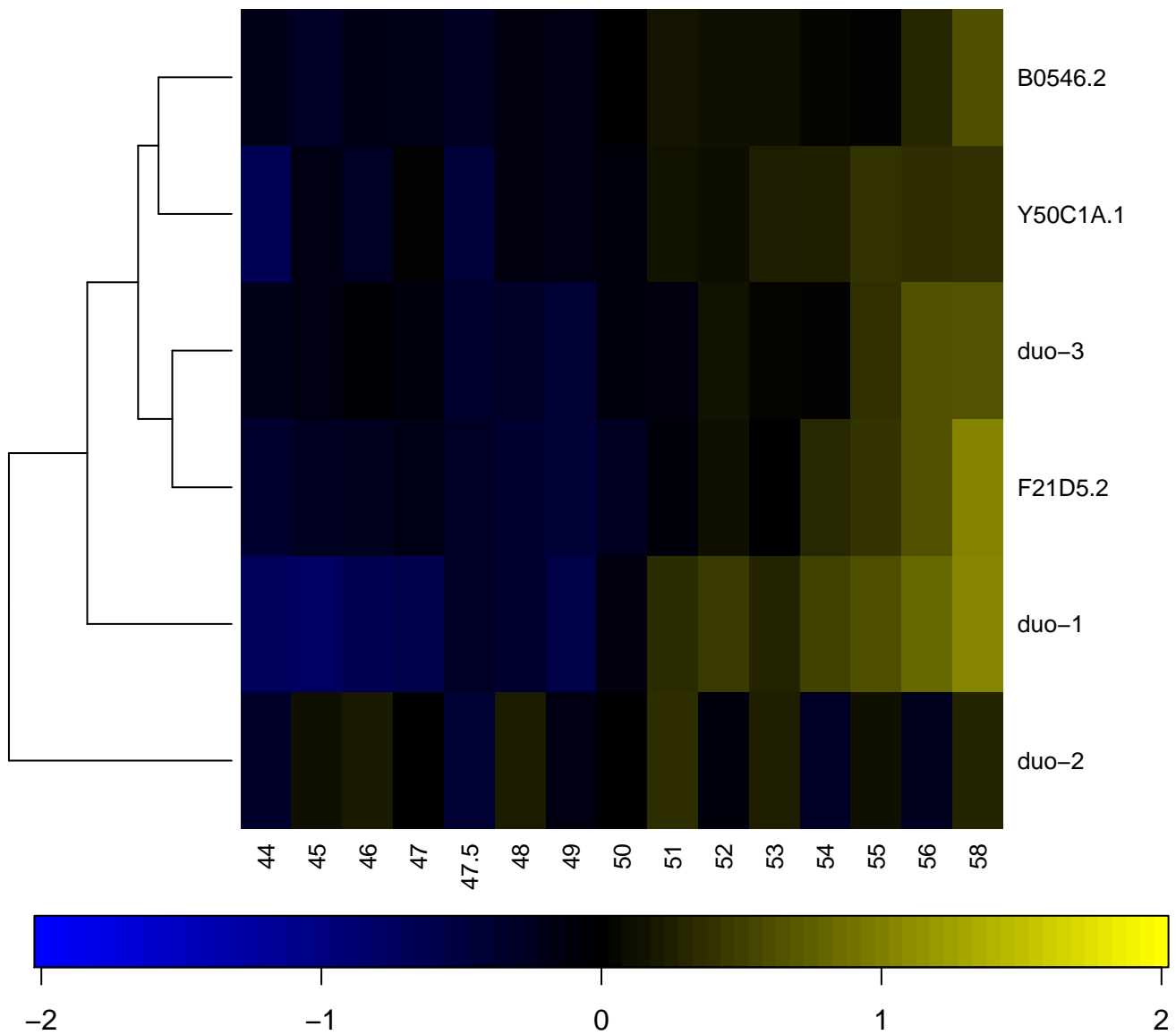
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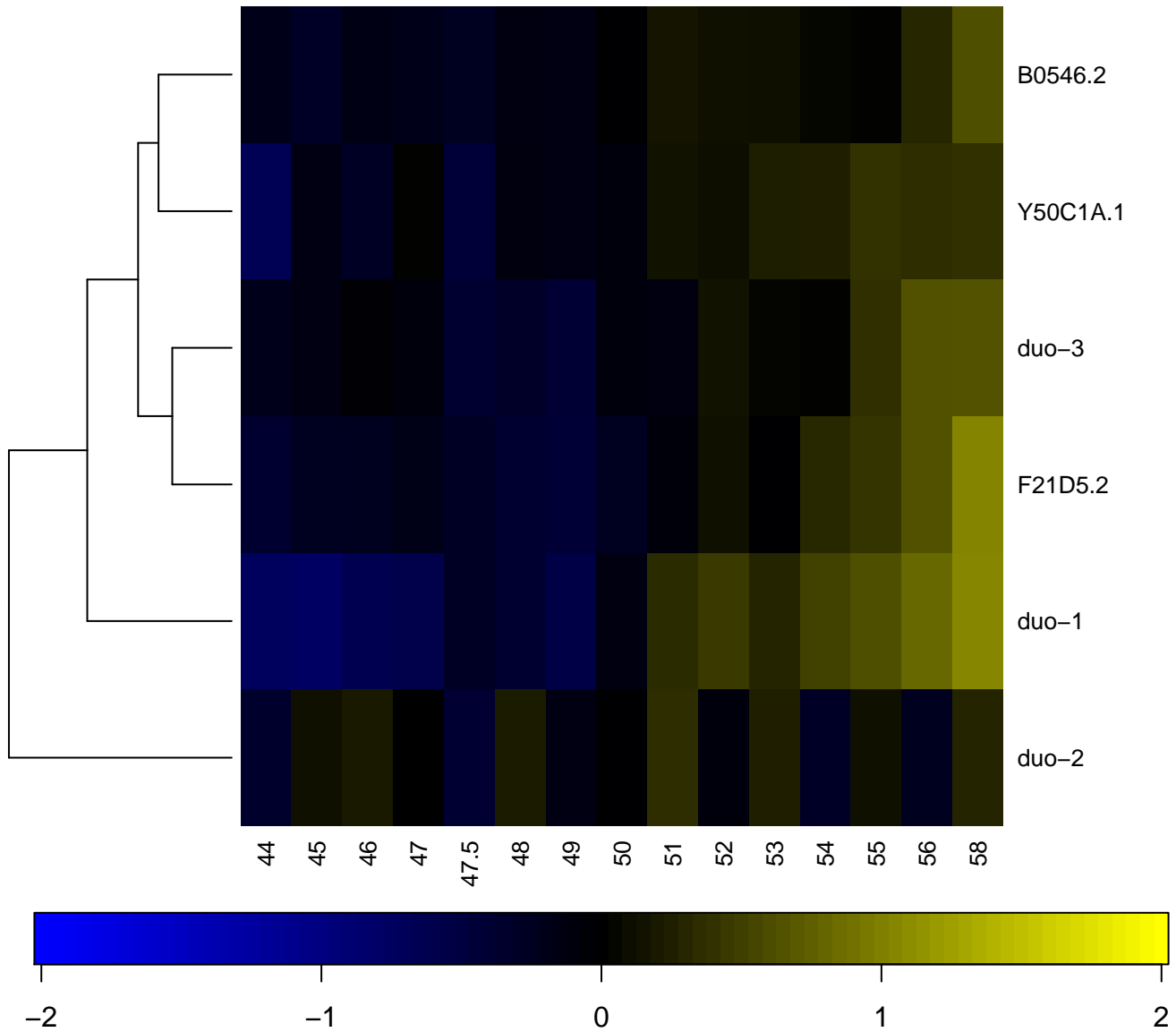
NUDIX domain



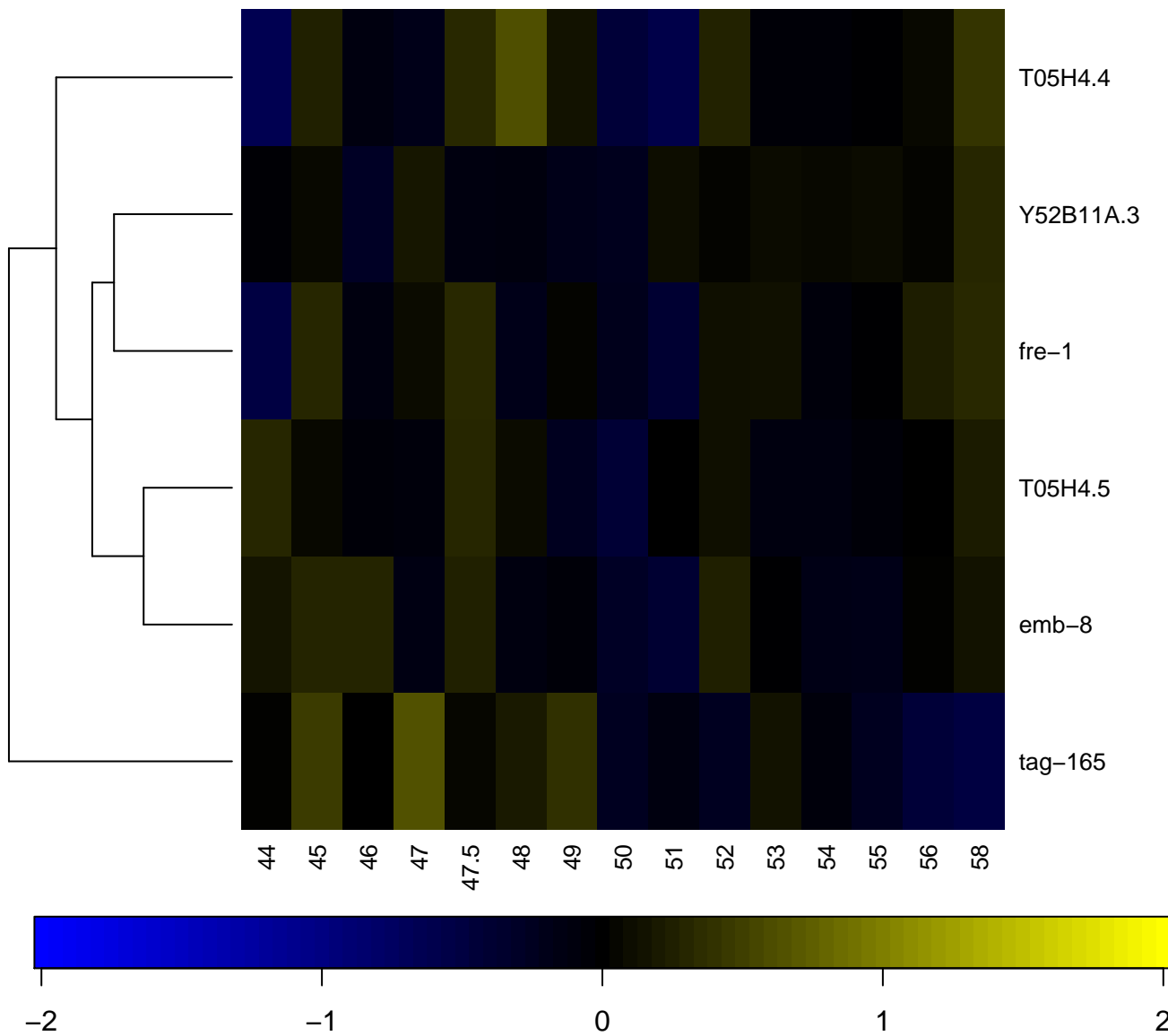
OTU-like cysteine protease



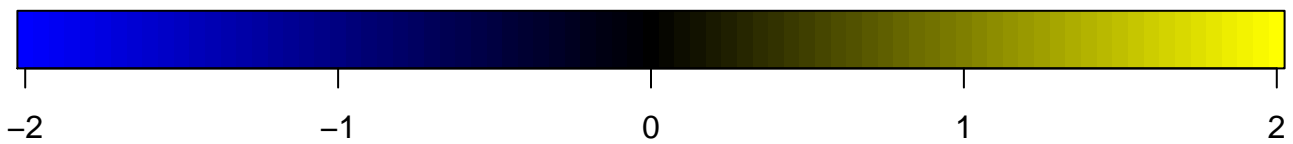
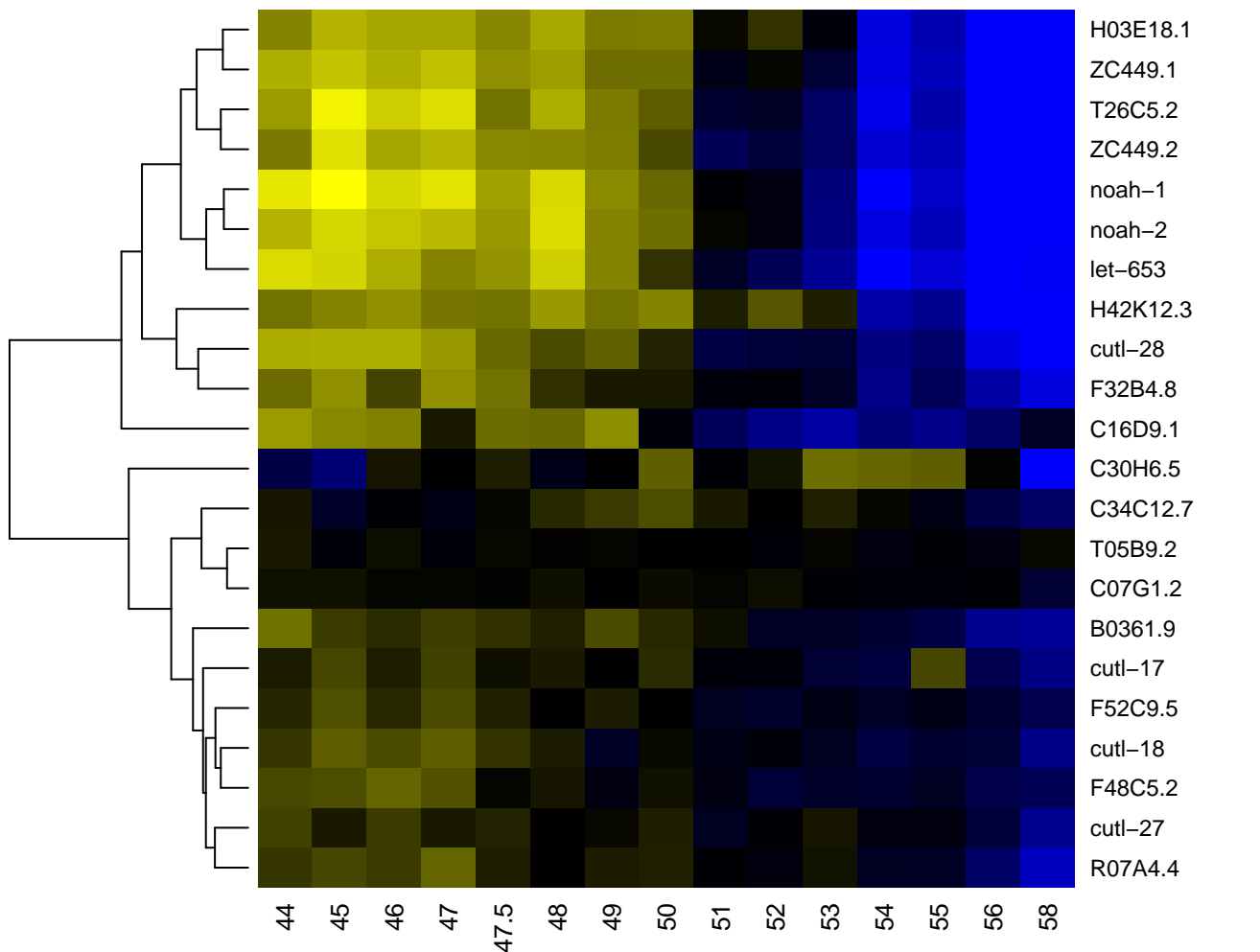
Ovarian tumour, otubain



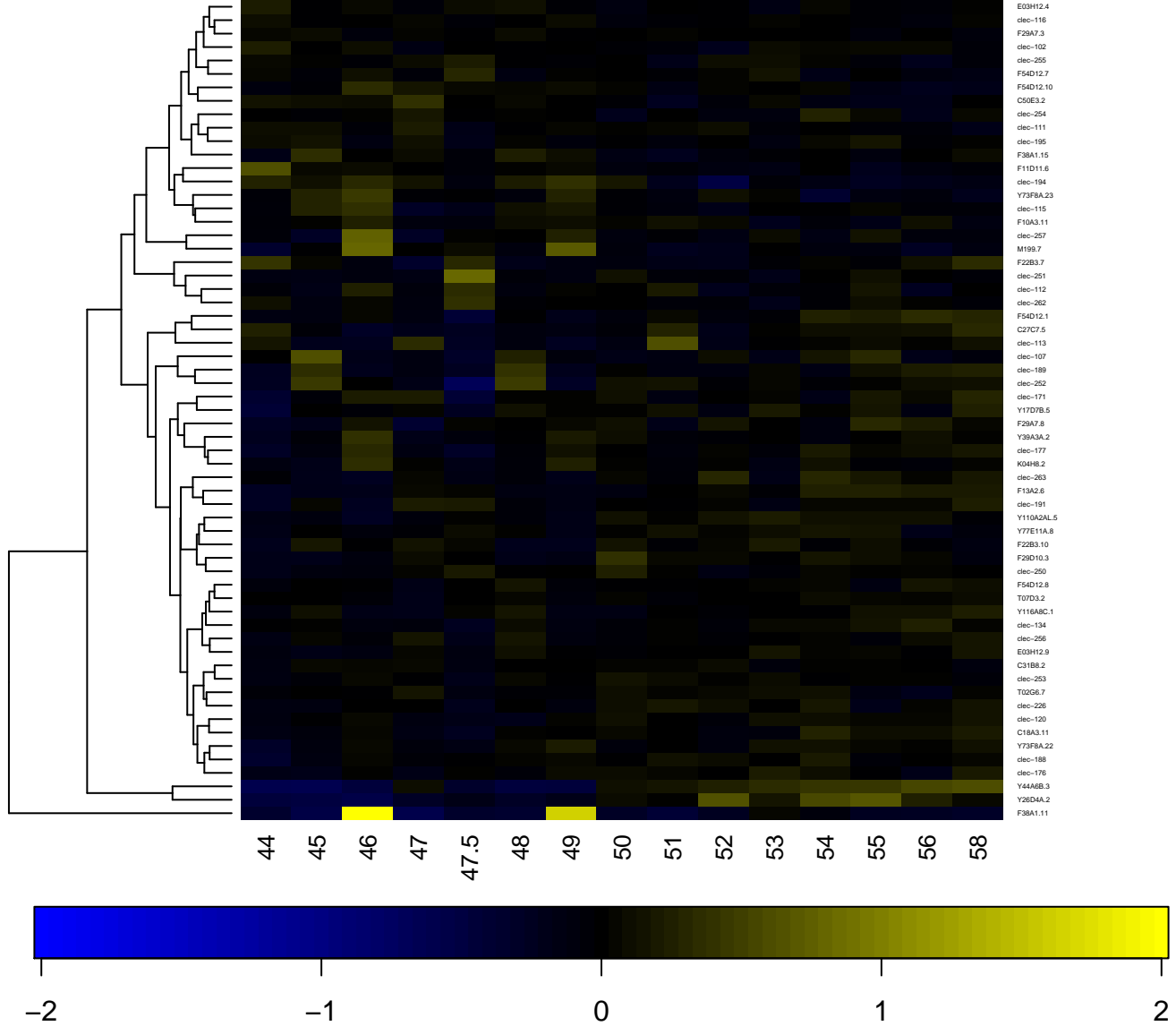
Oxidoreductase FAD/NAD(P)-binding



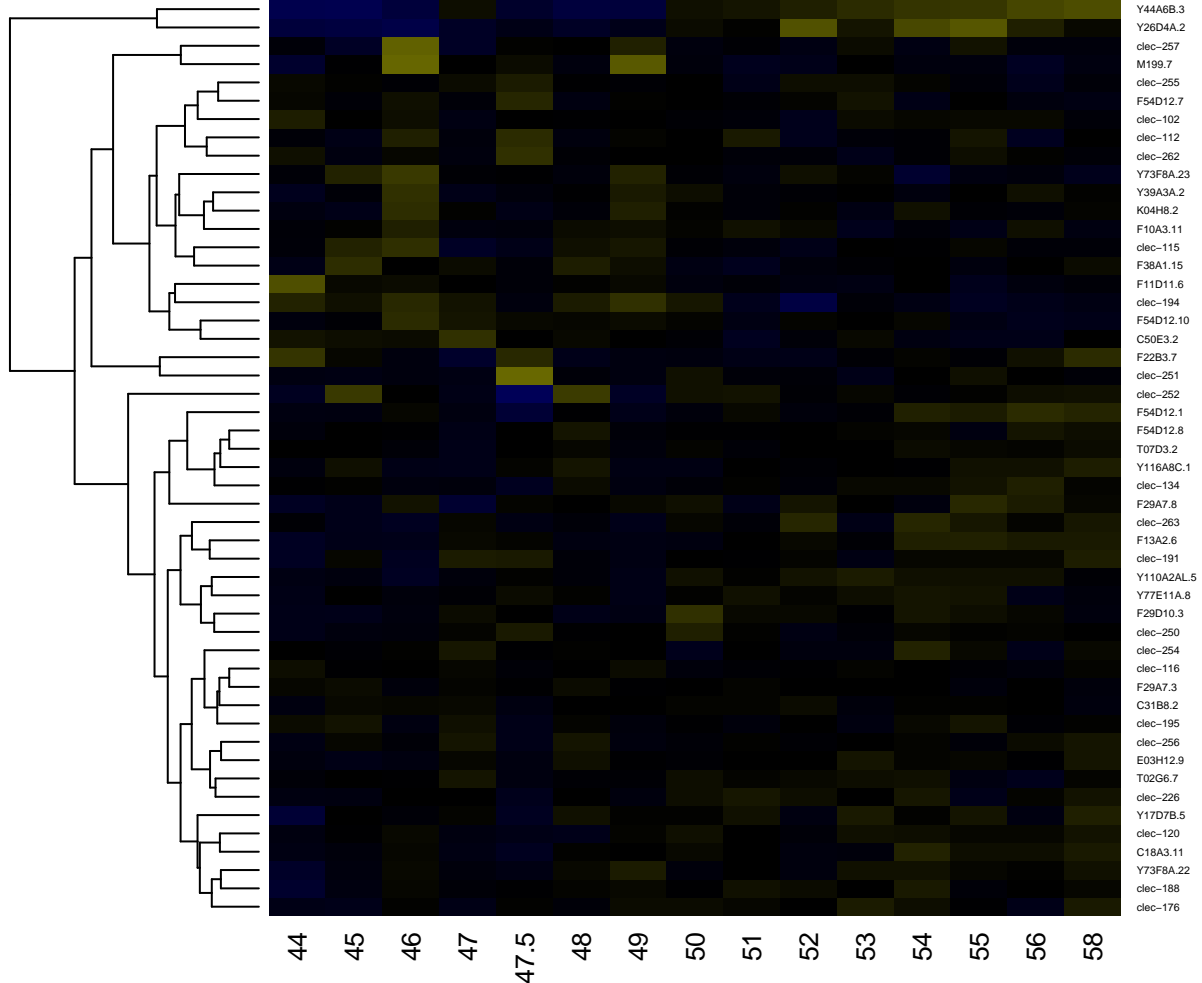
PAN-1 domain



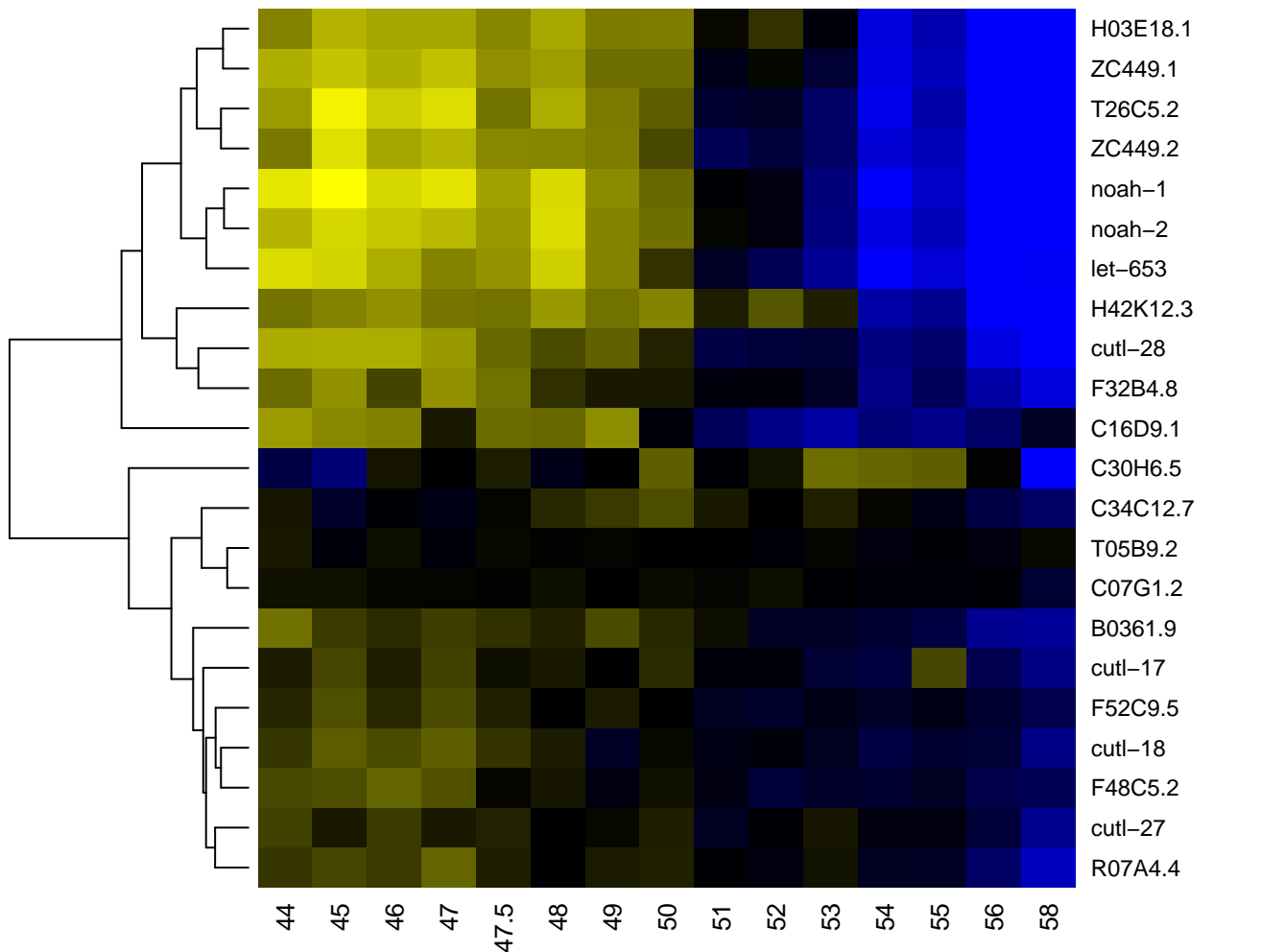
PAN-3 domain



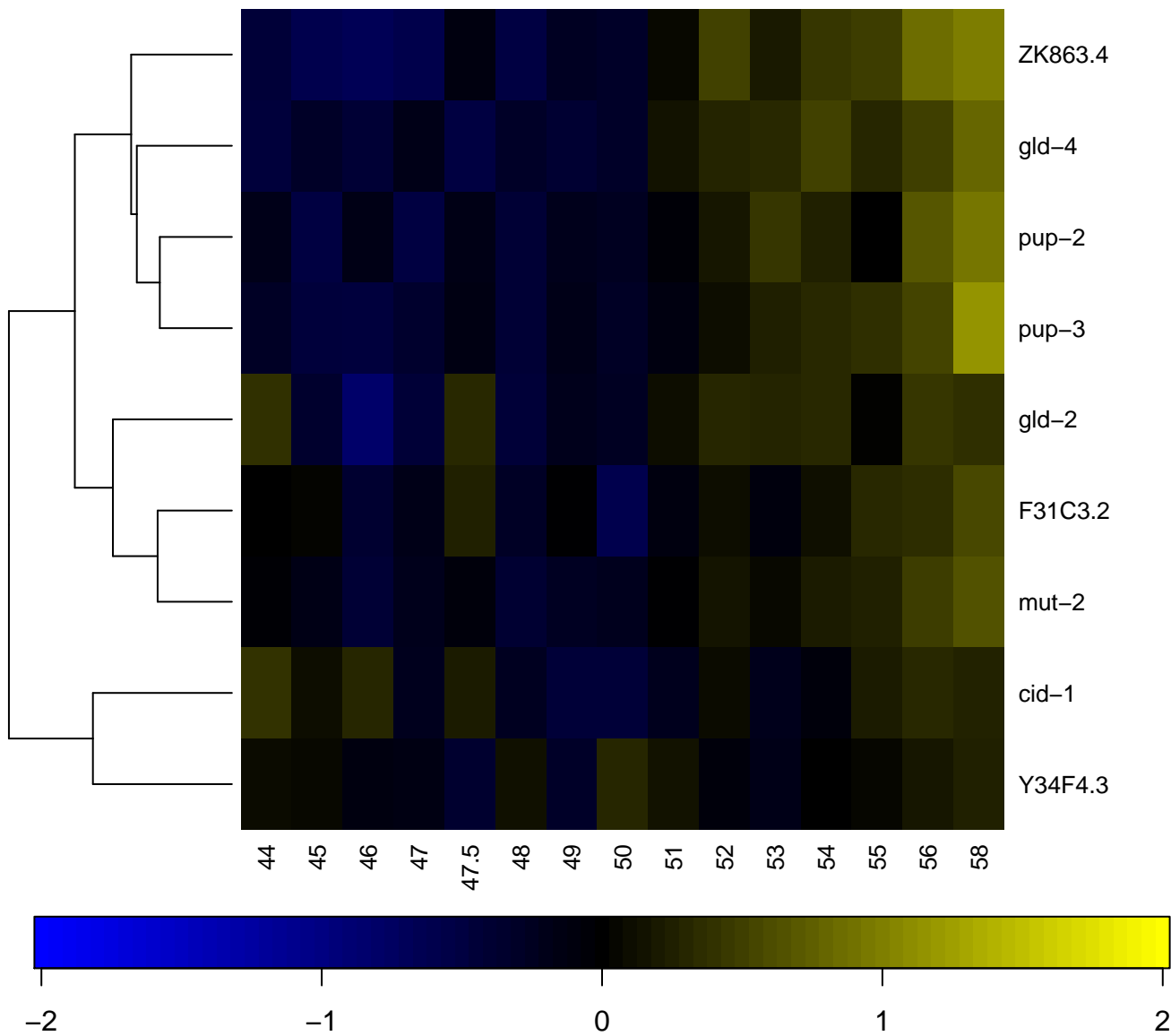
PAN-like domain



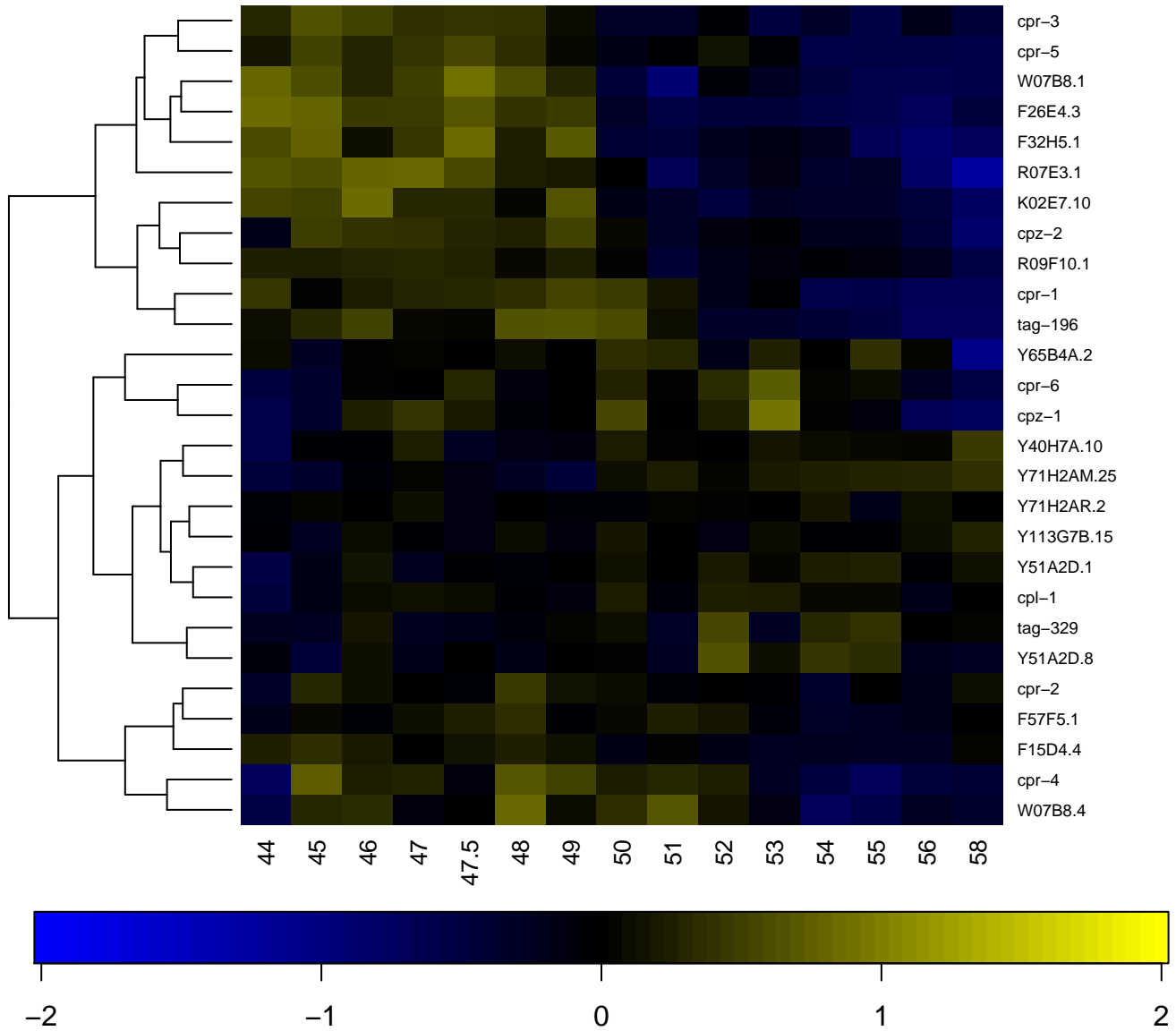
PAN domain



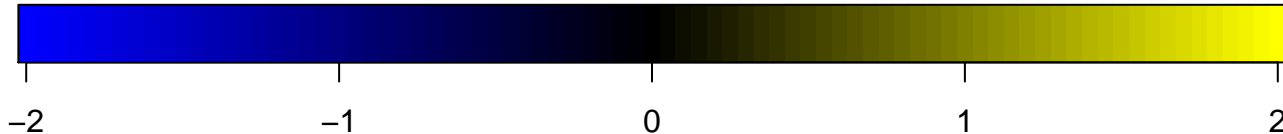
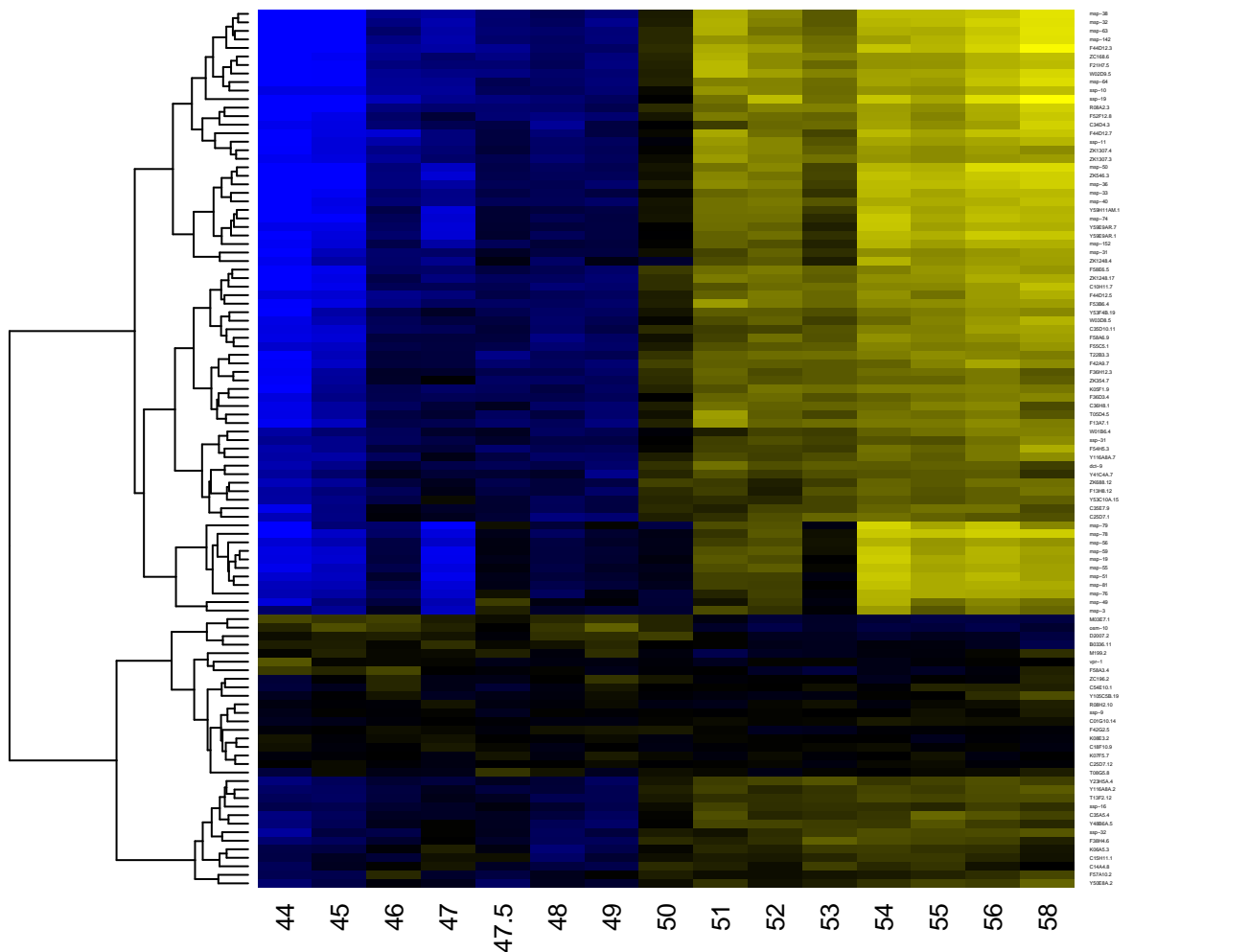
PAP/25A-associated



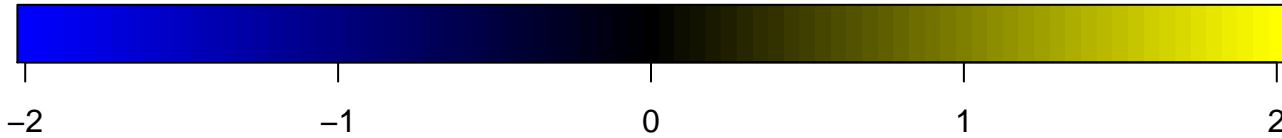
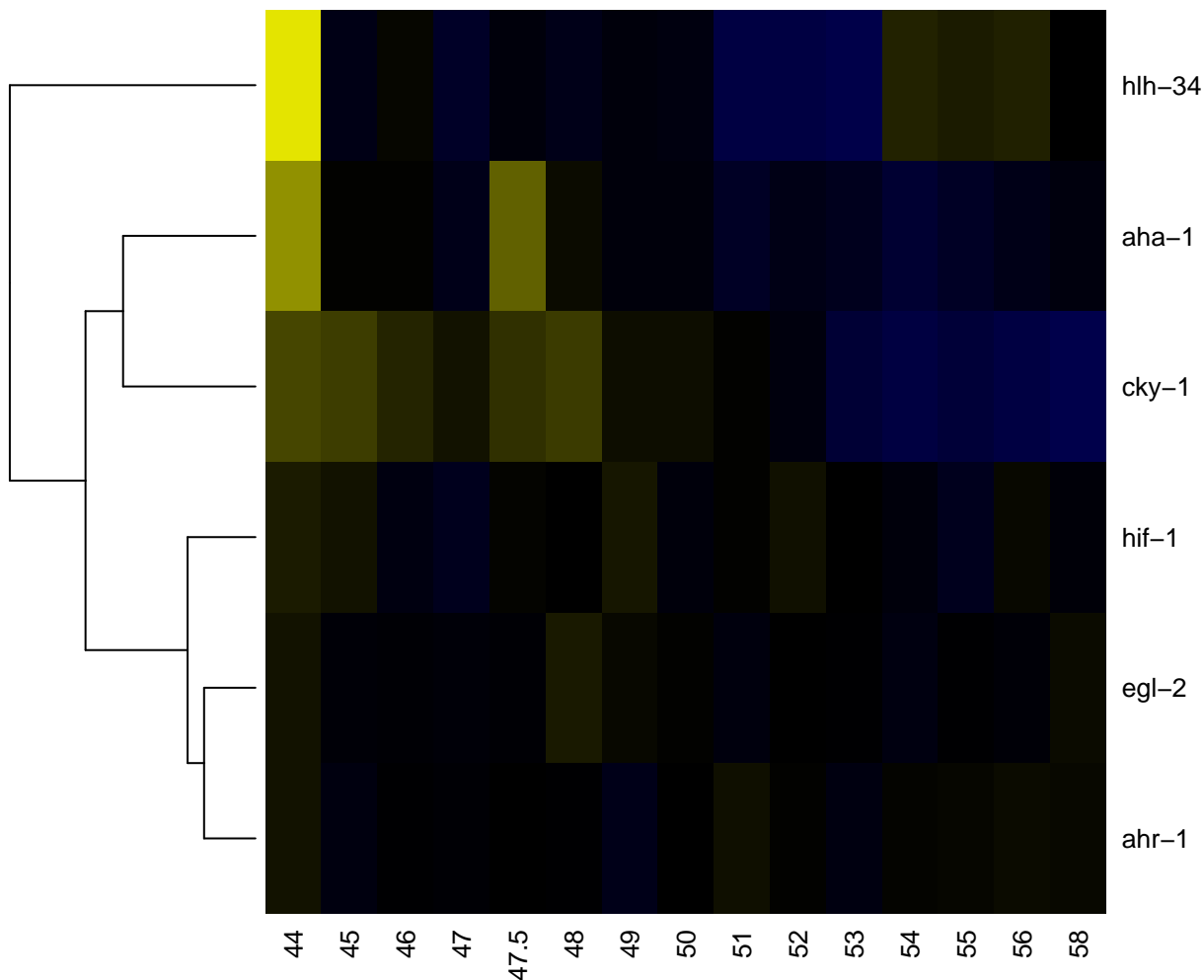
Papain family cysteine protease



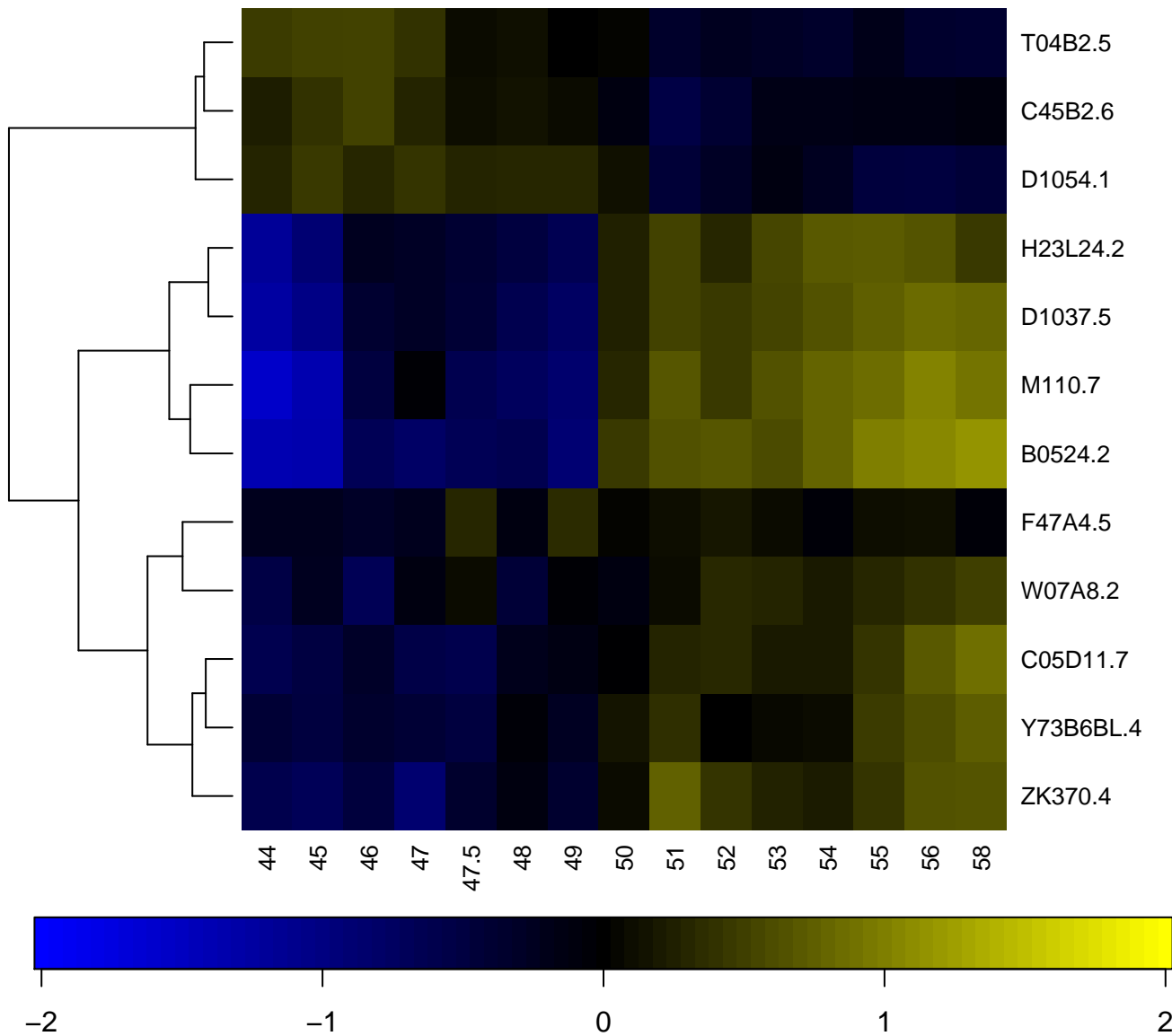
PapD-like



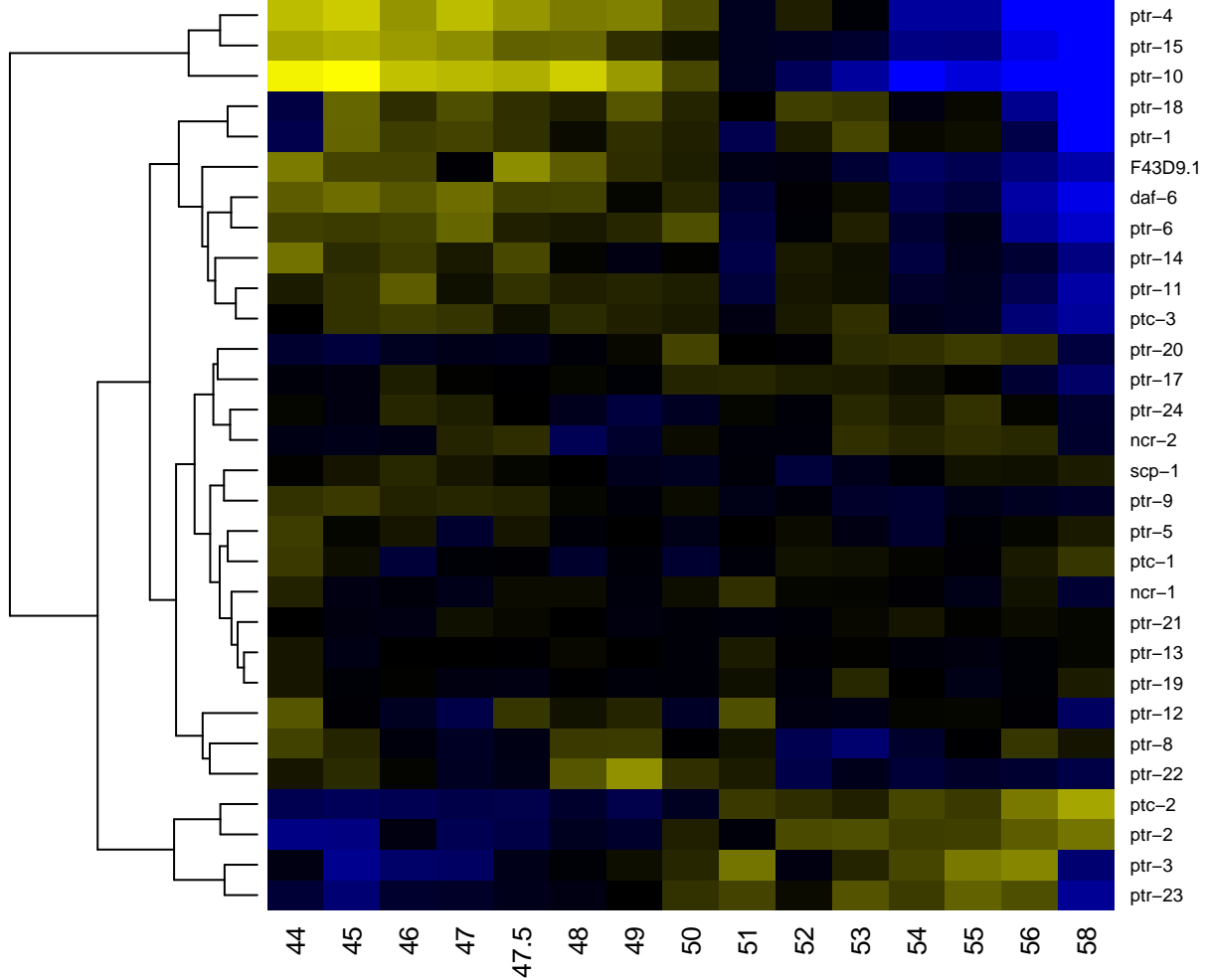
PAS fold



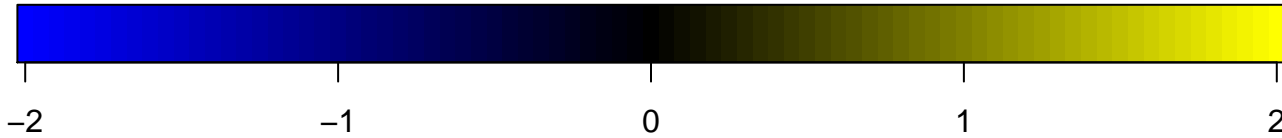
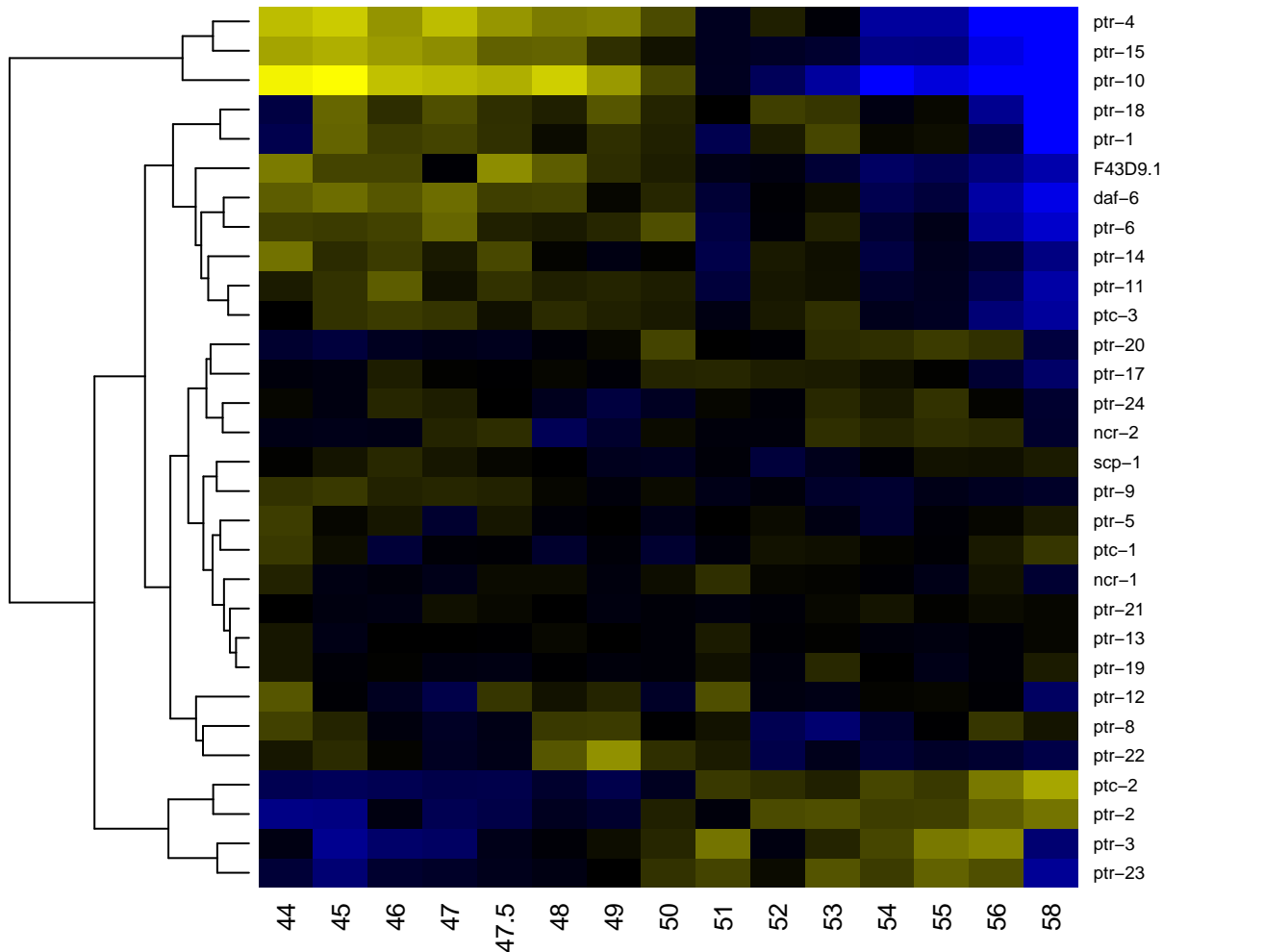
Patatin/Phospholipase A2-related



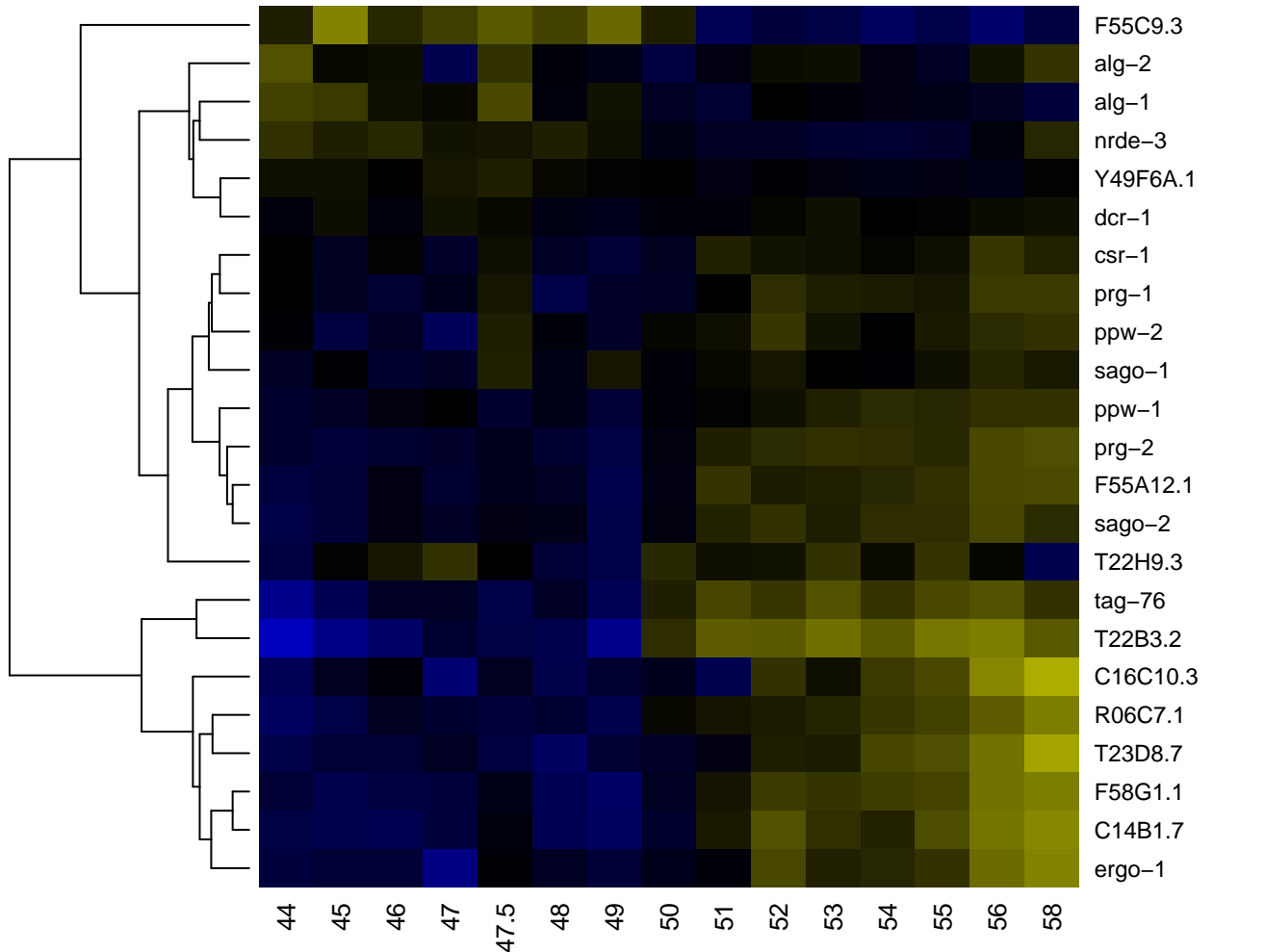
Patched



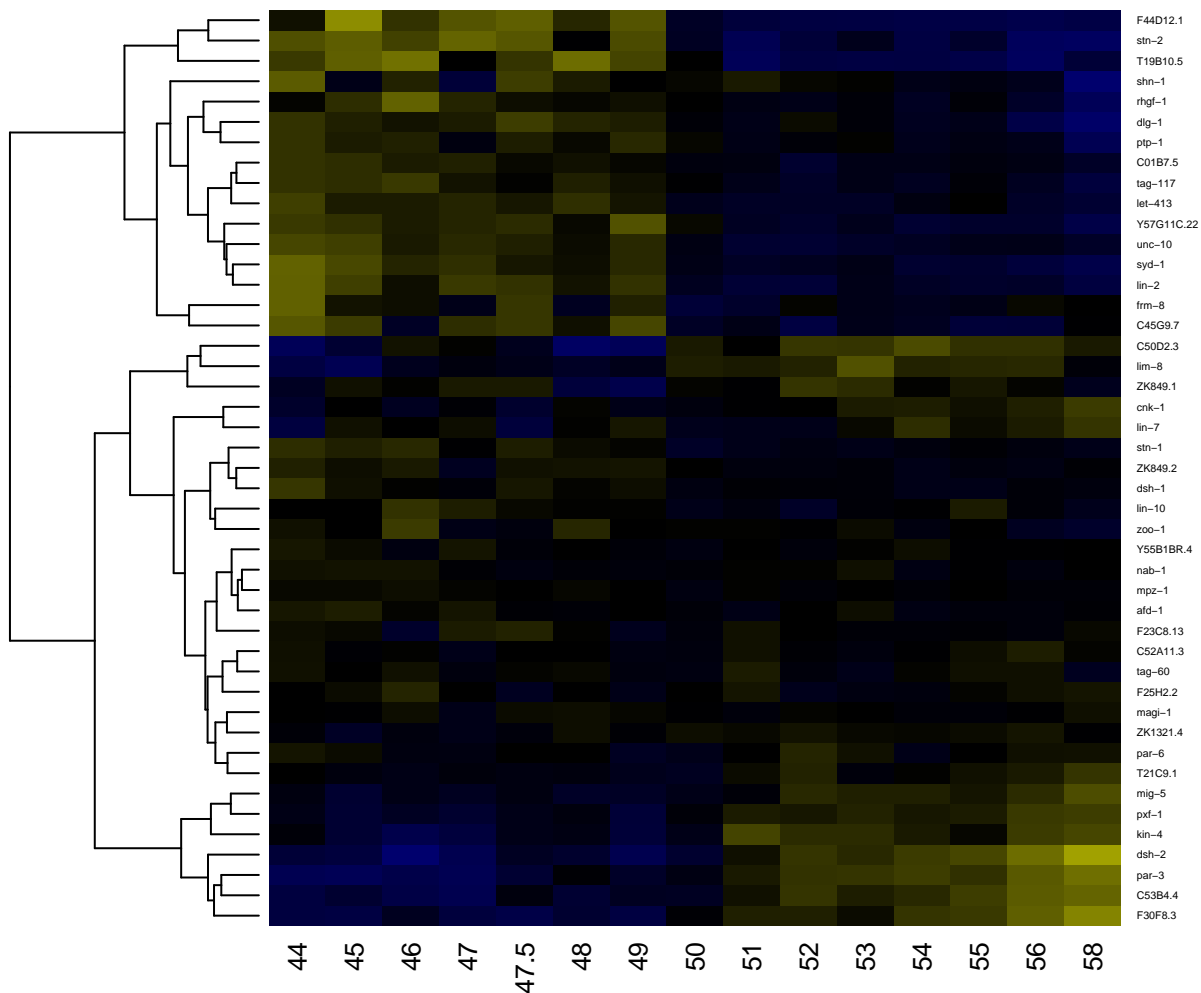
Patched family



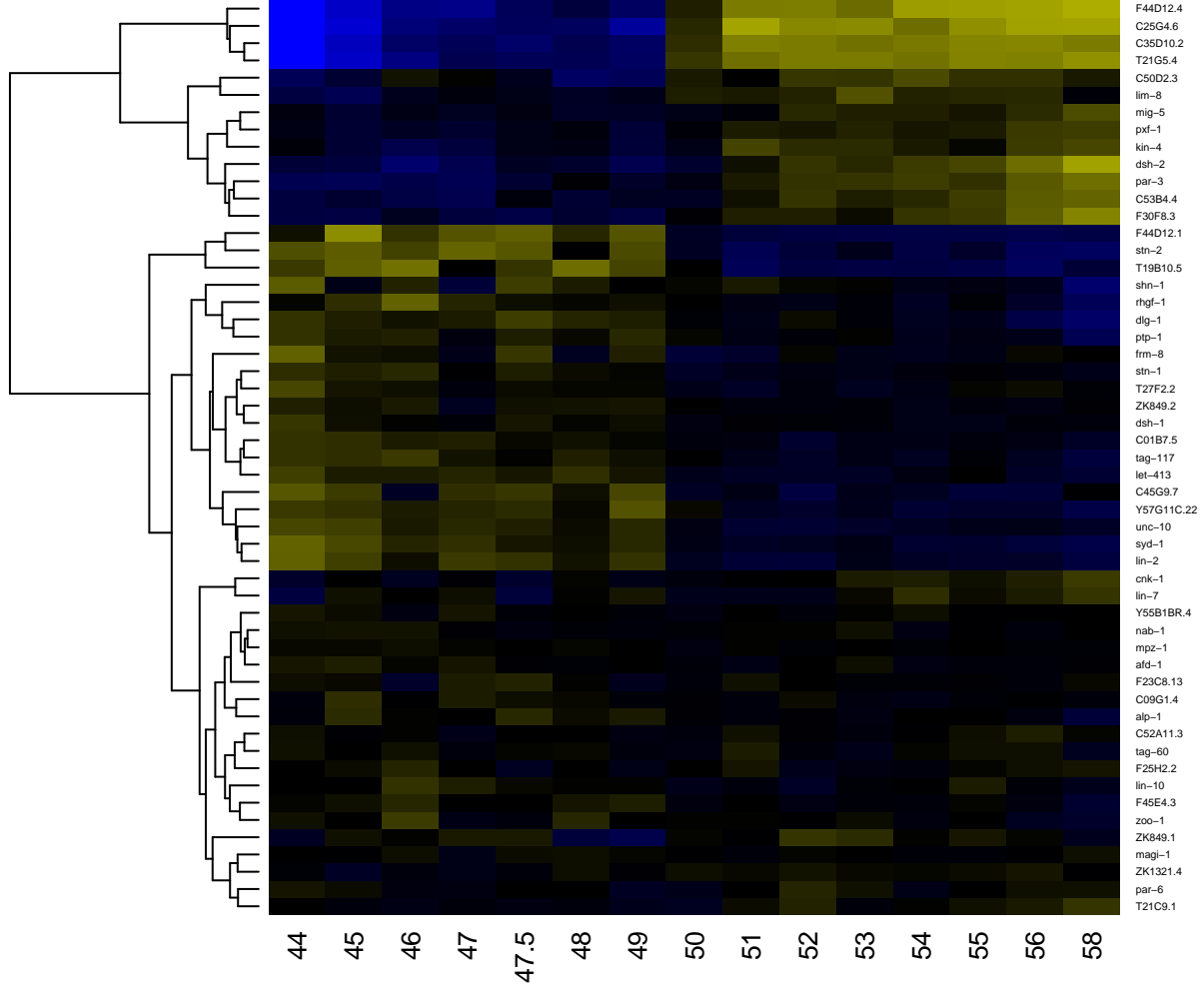
PAZ domain



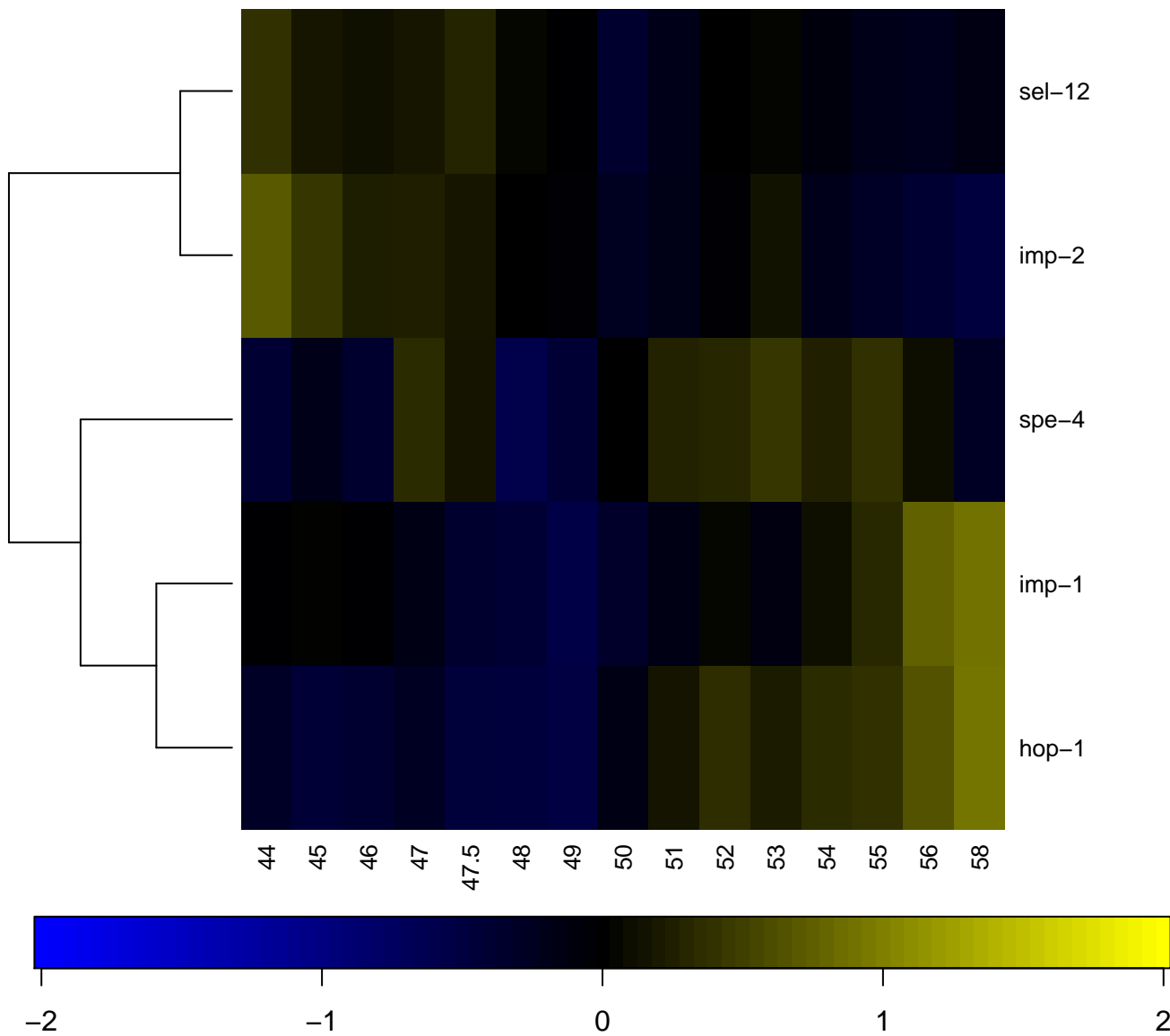
PDZ domain (Also known as DHR or GLGF)



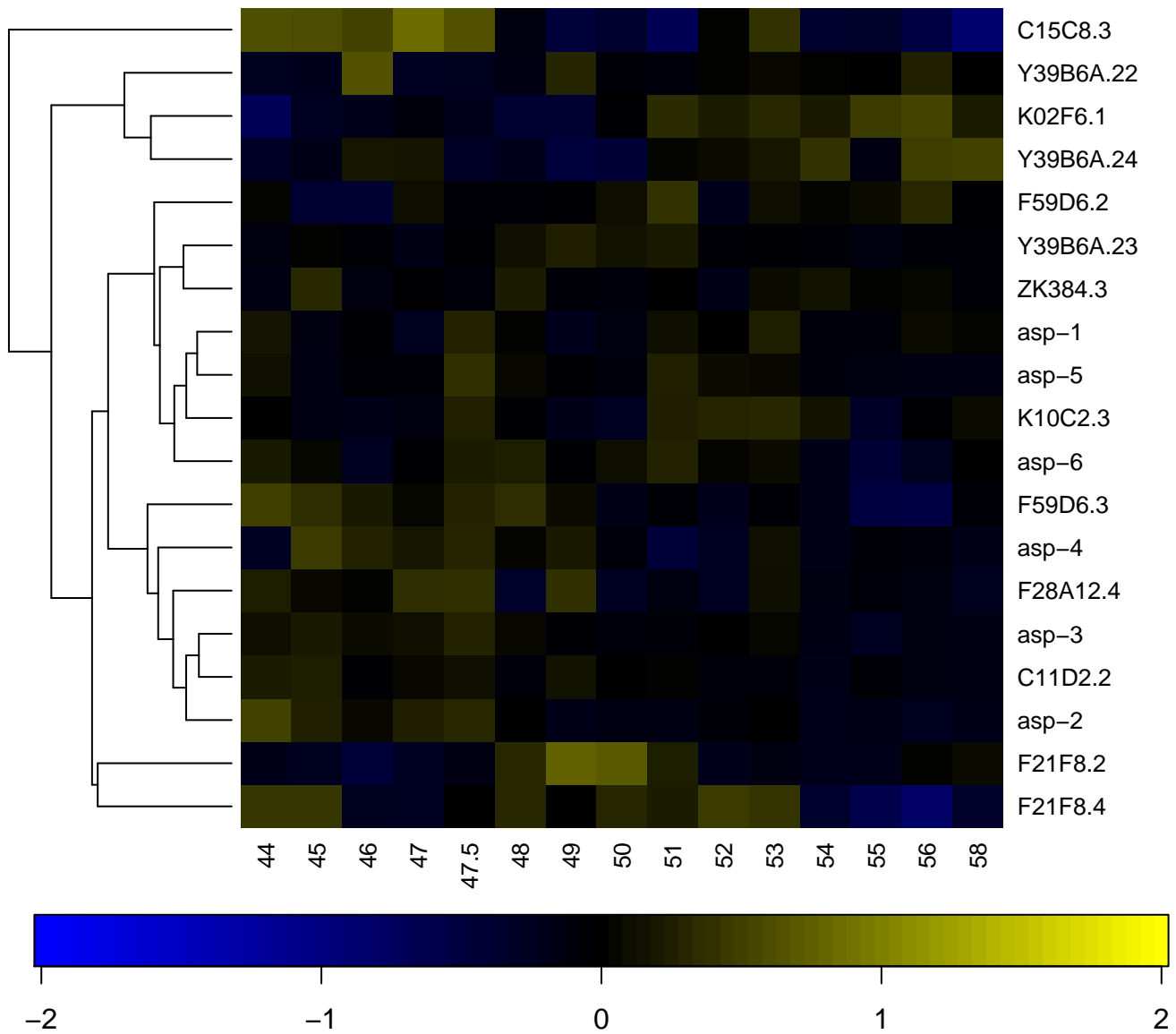
PDZ/DHR/GLGF



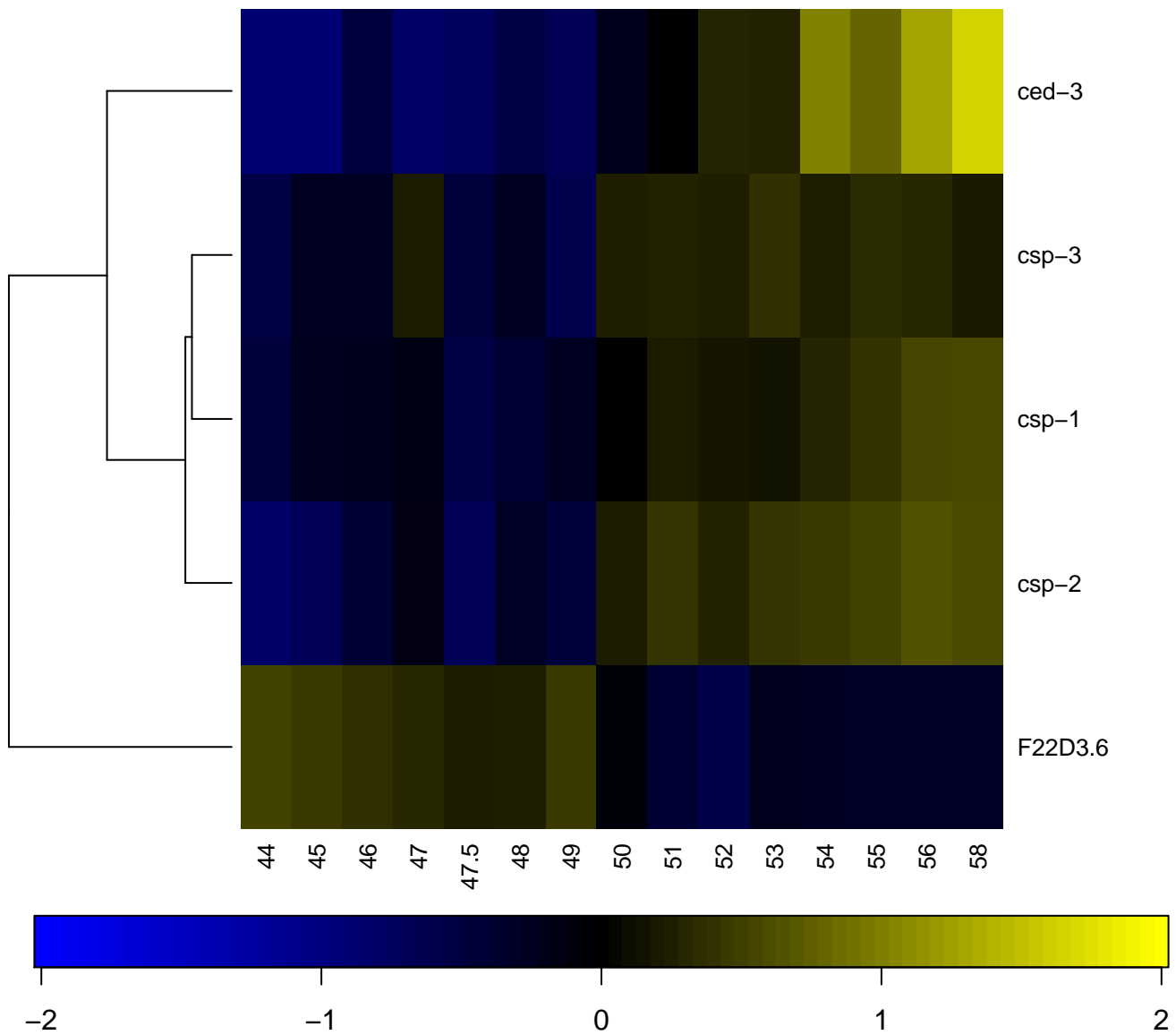
Peptidase A22, presenilin signal peptide



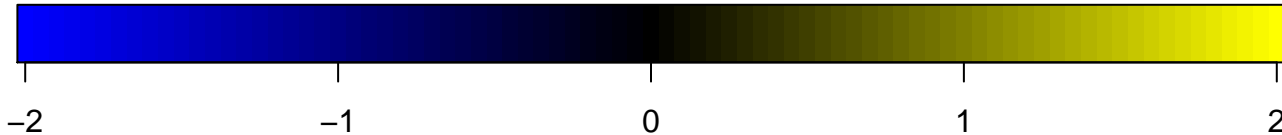
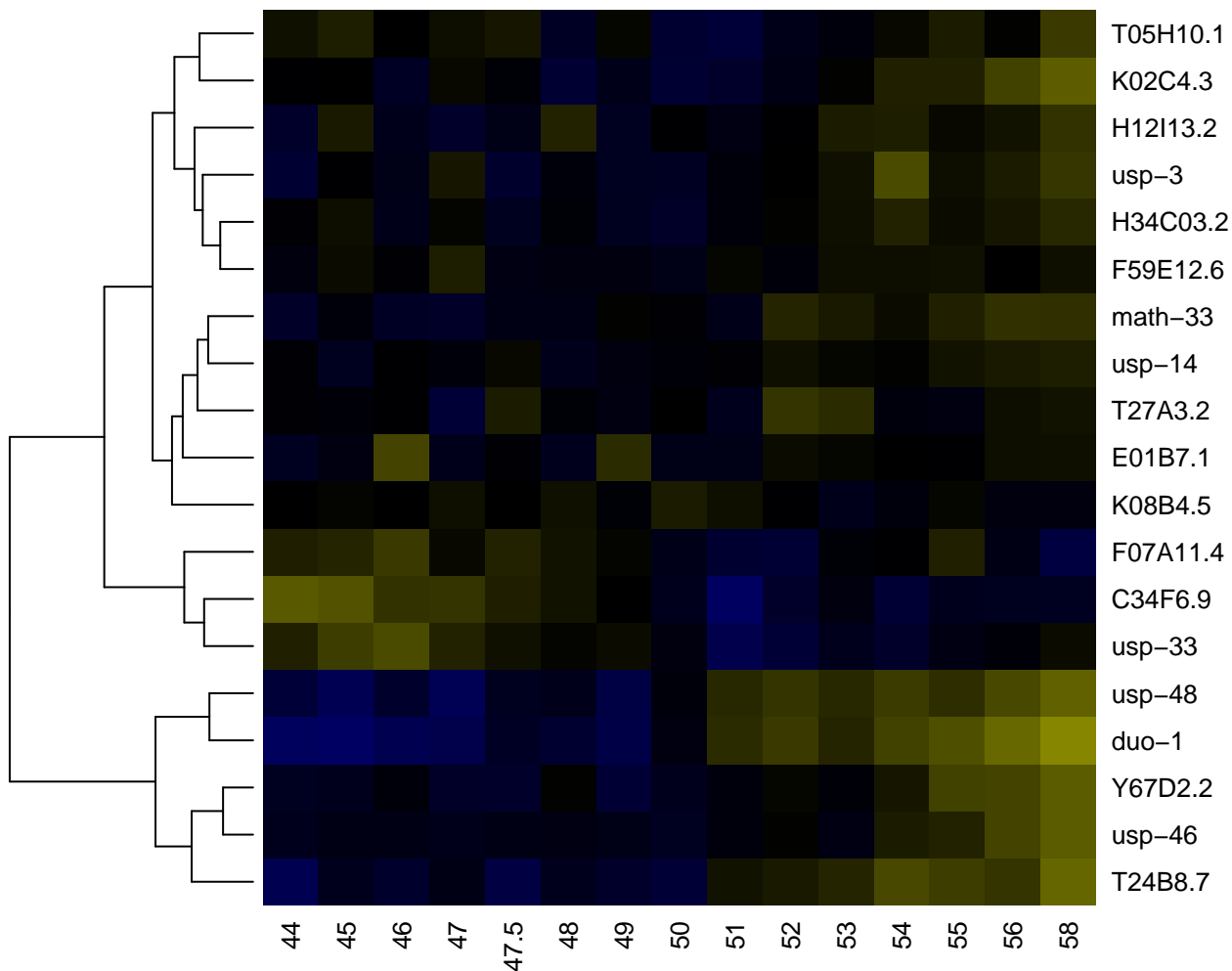
Peptidase aspartic, catalytic



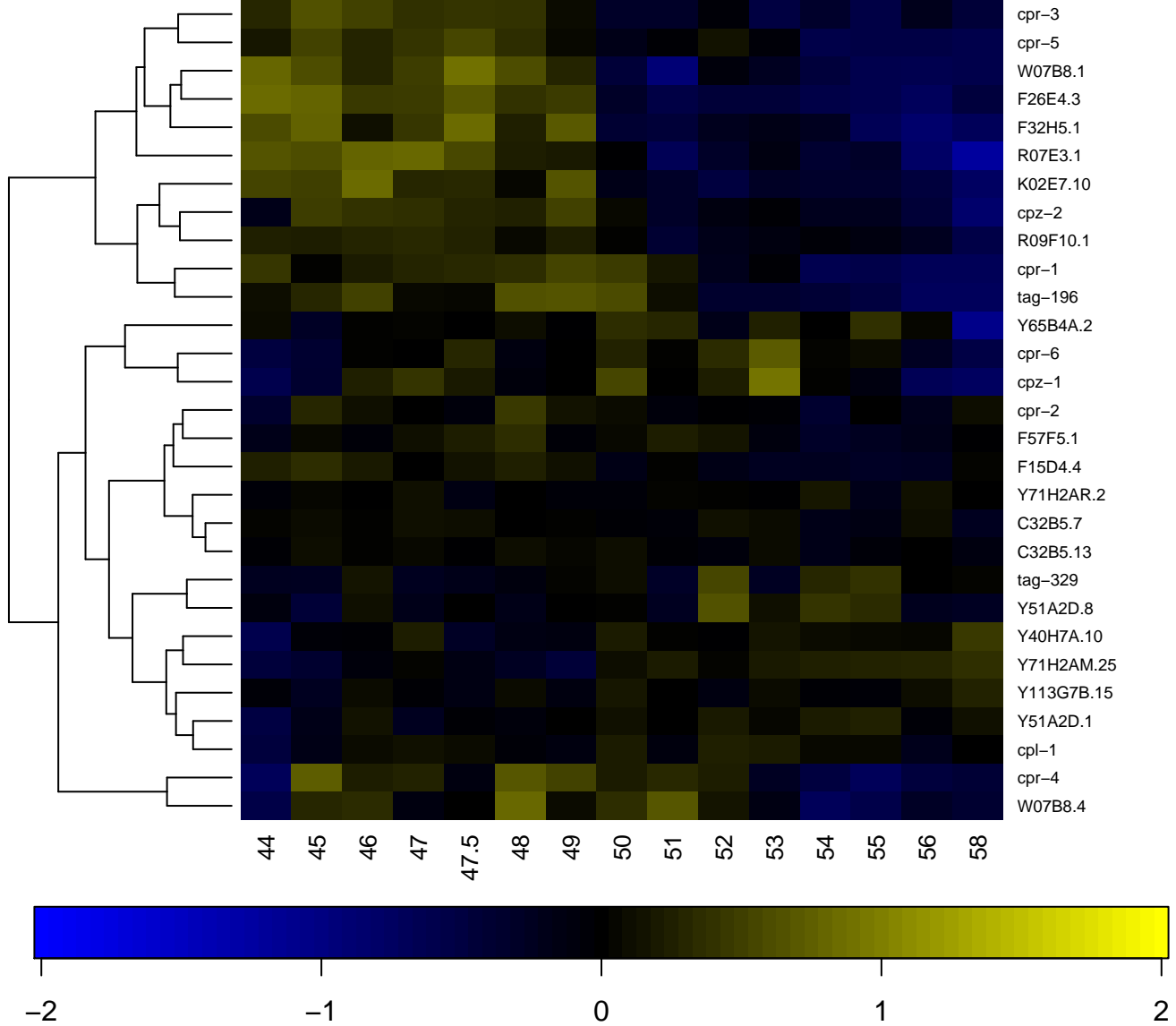
Peptidase C14, caspase catalytic



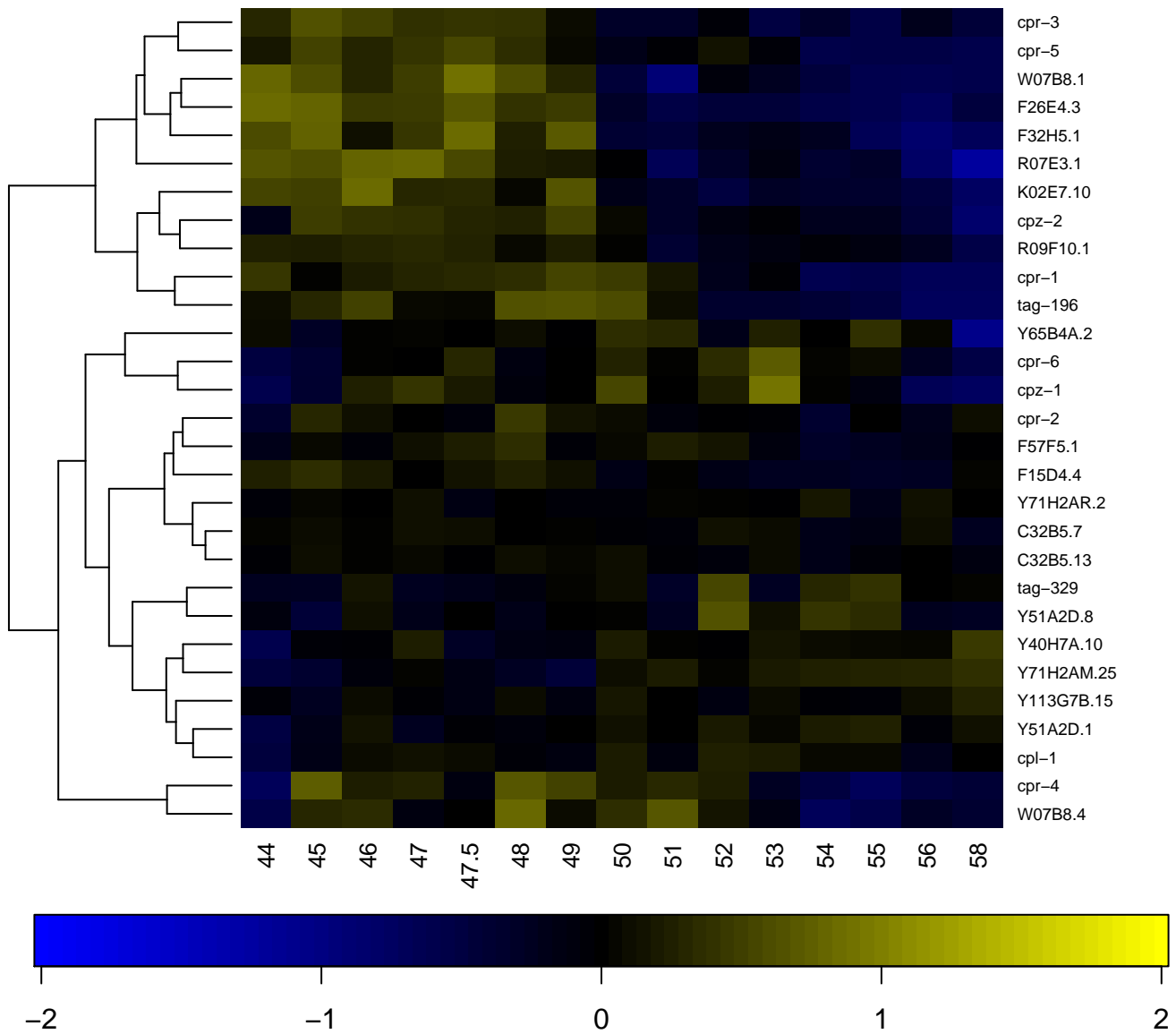
dase C19, ubiquitin carboxyl-terminal hydrolase 2, conserv



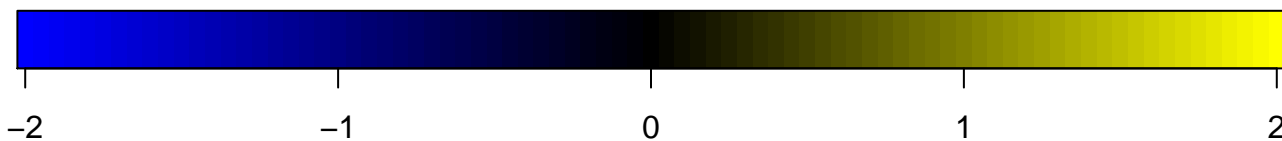
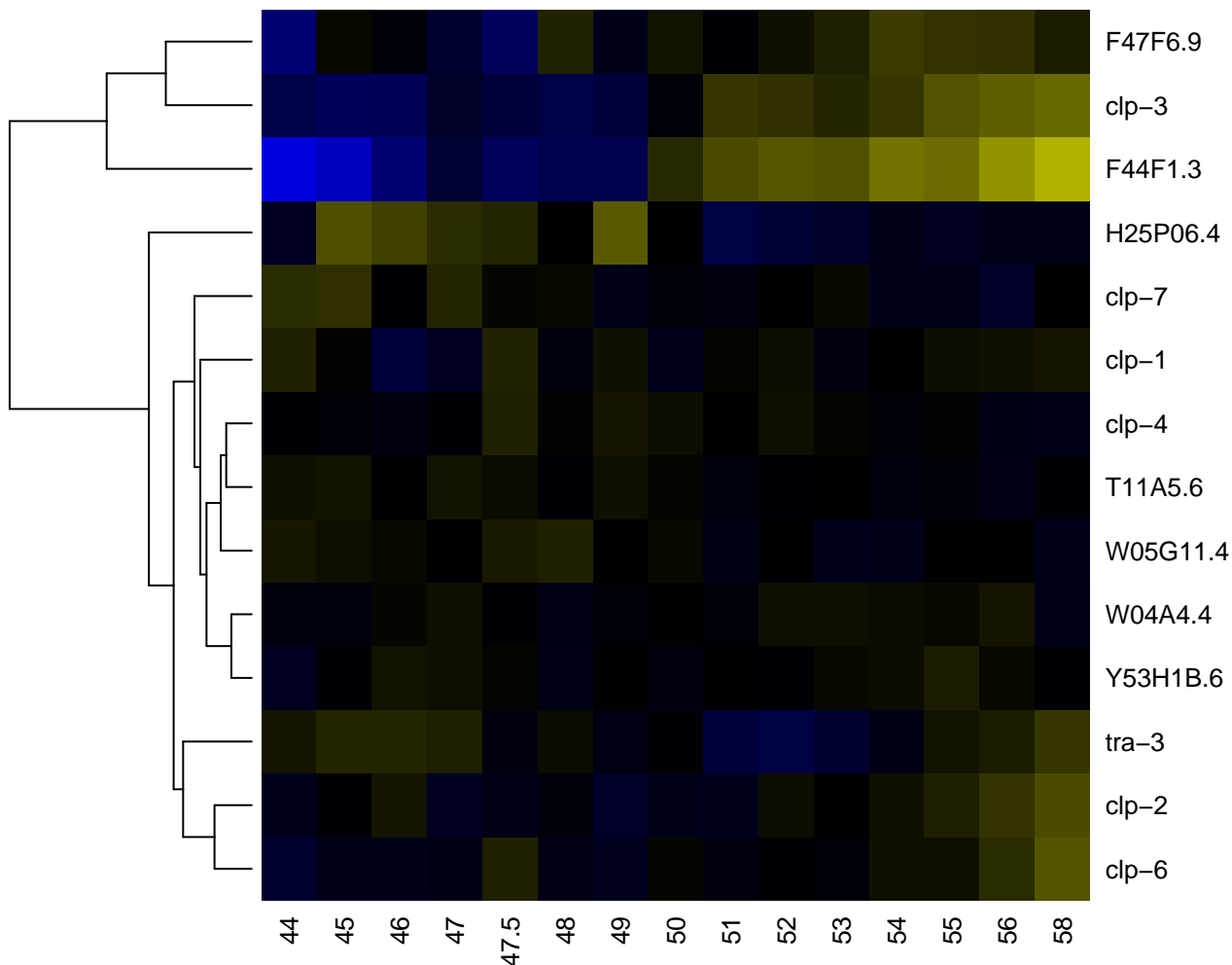
Peptidase C1A, papain



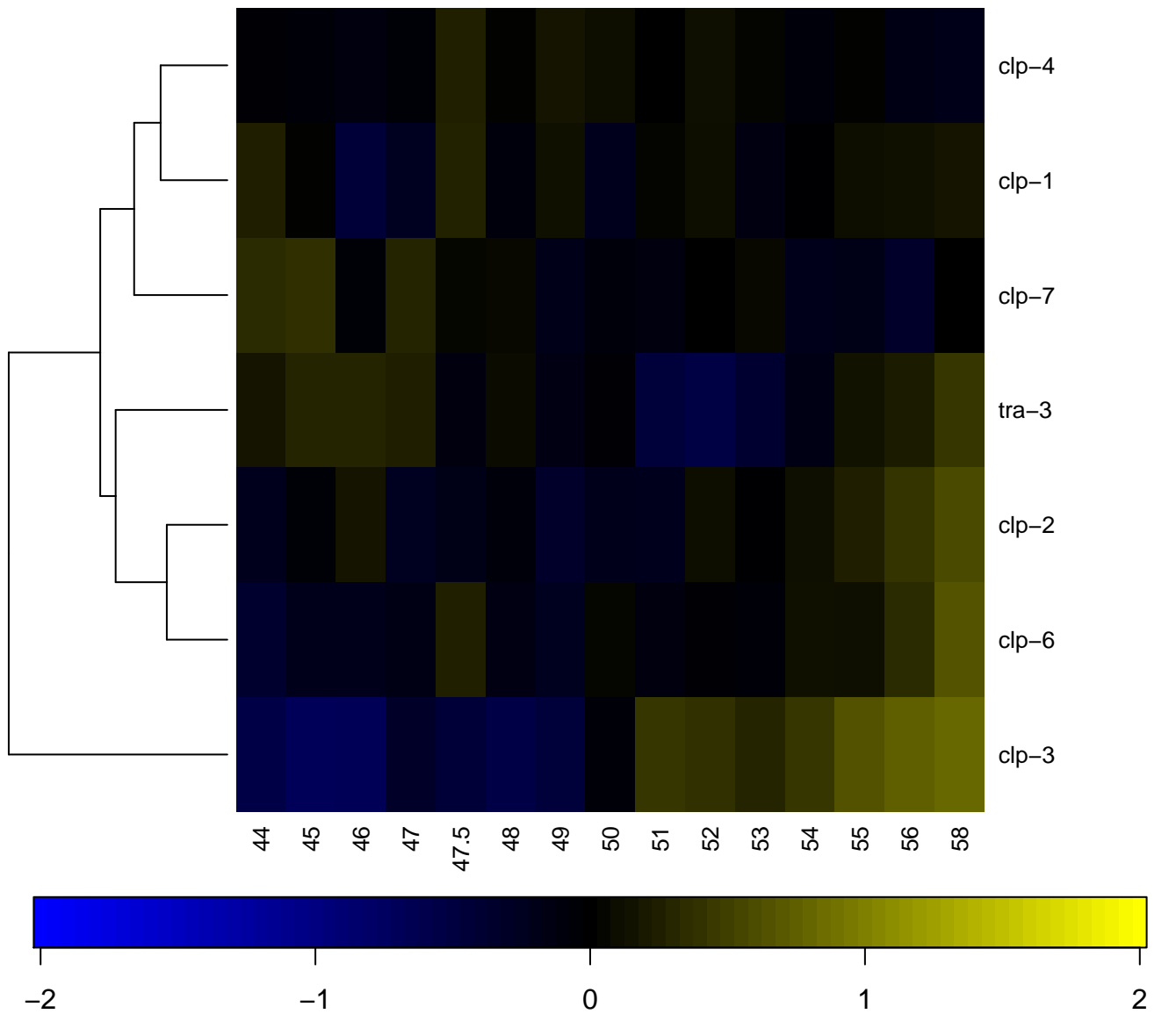
Peptidase C1A, papain C-terminal



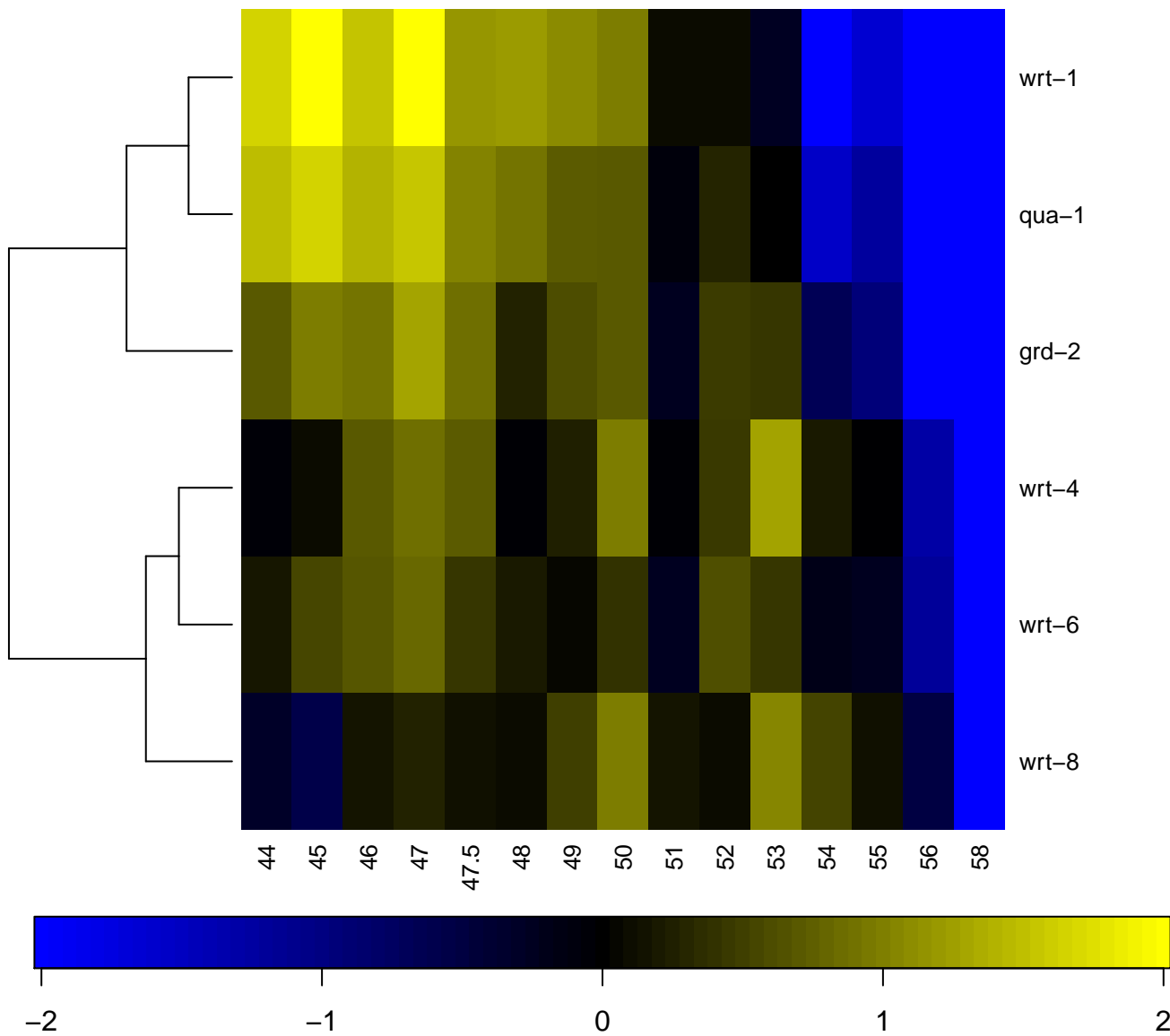
Peptidase C2, calpain family



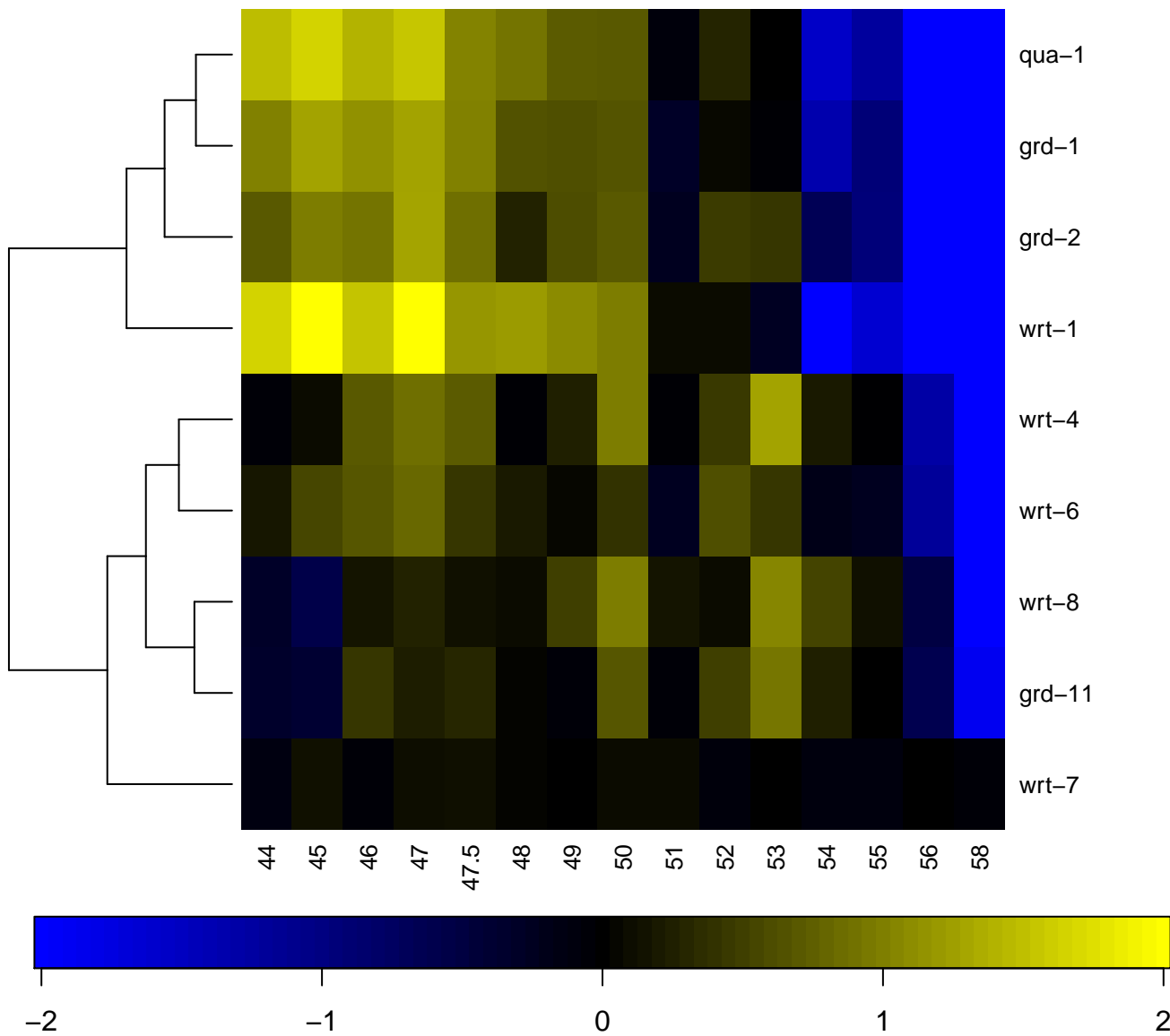
Peptidase C2, calpain, large subunit, domain III



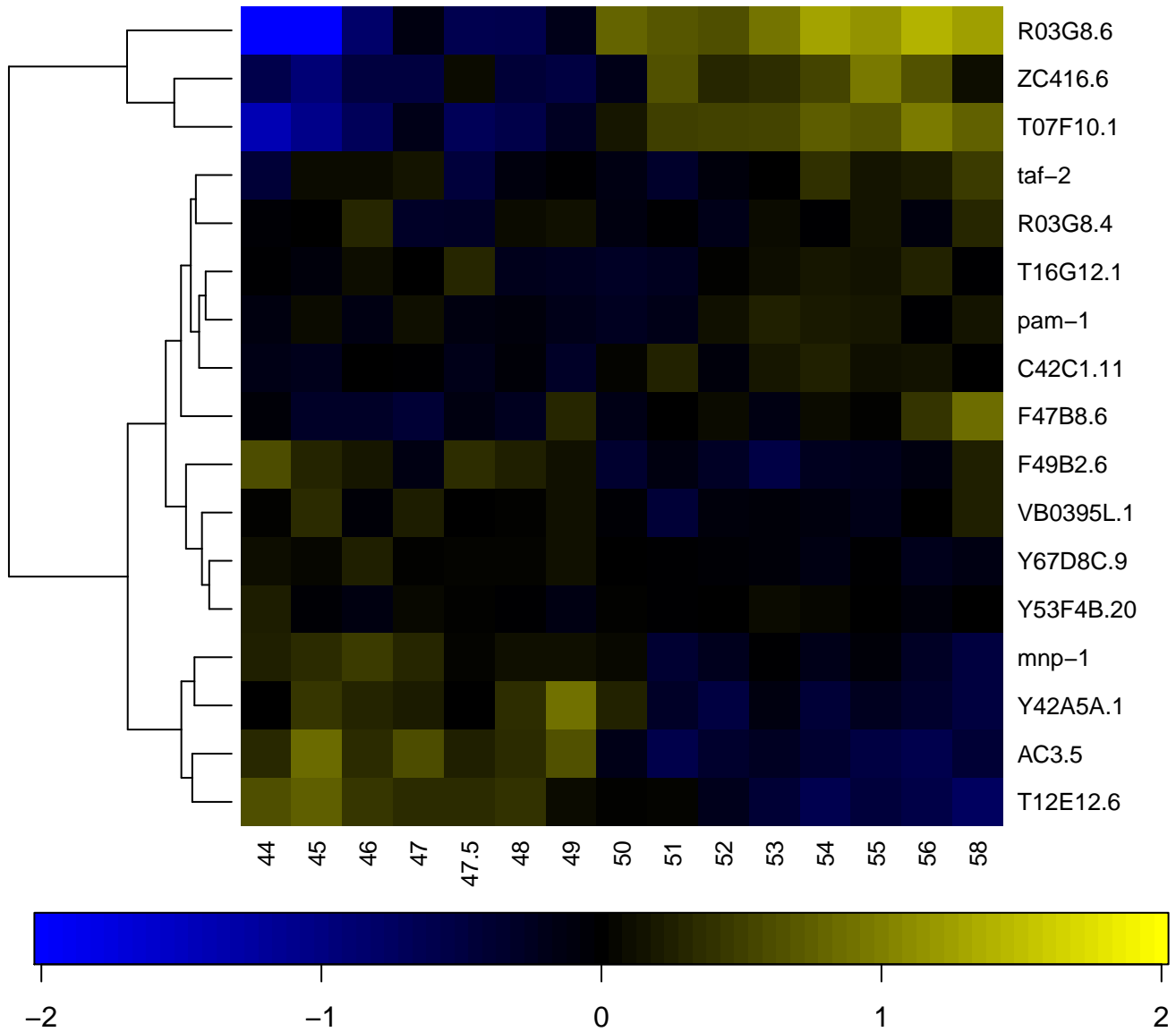
Peptidase C46, hedgehog protein



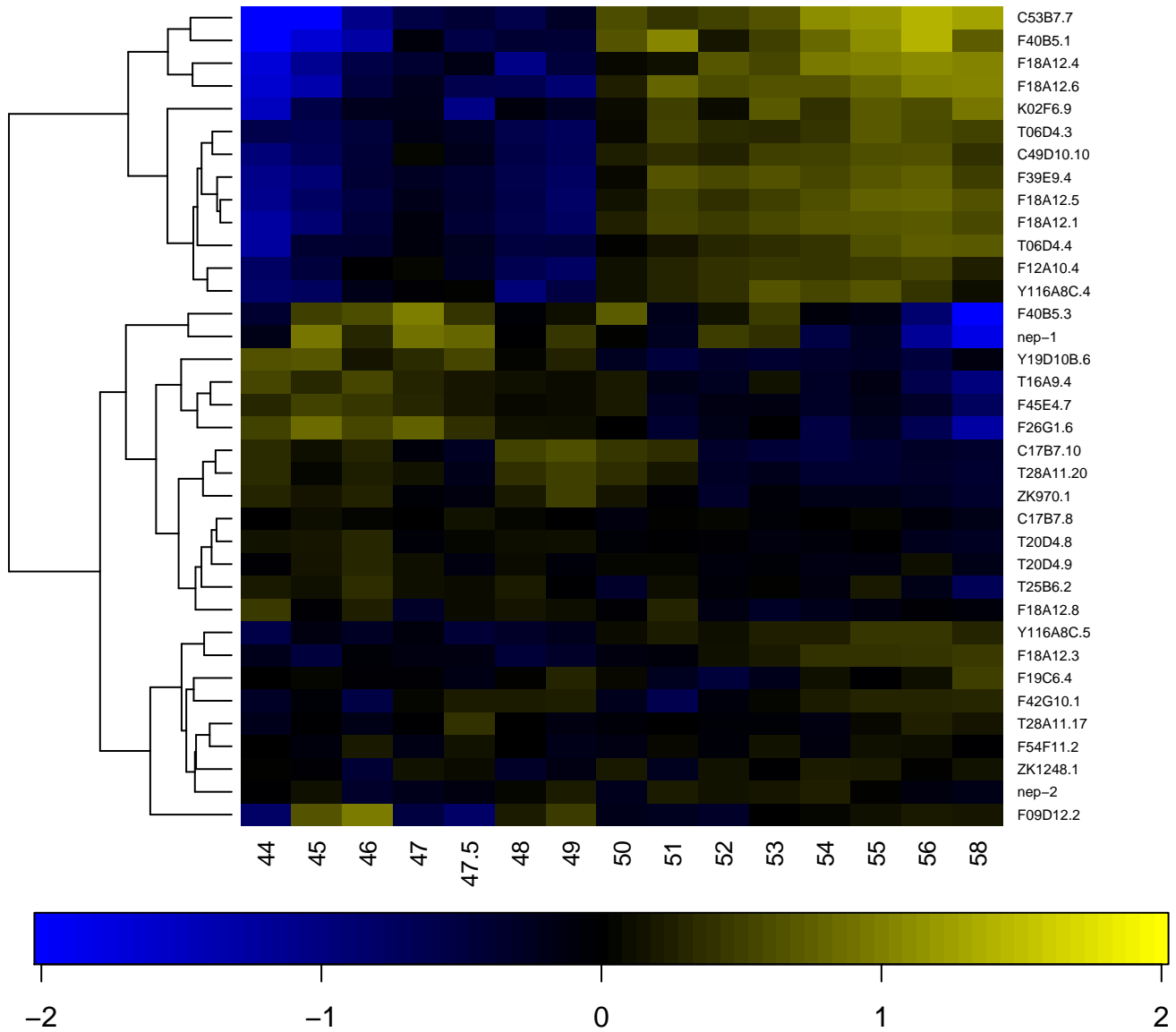
Peptidase C46, hedgehog protein, hint region



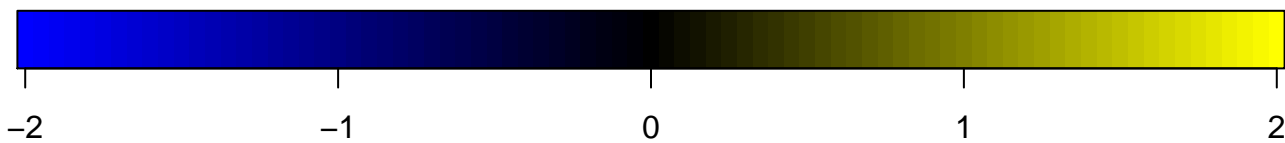
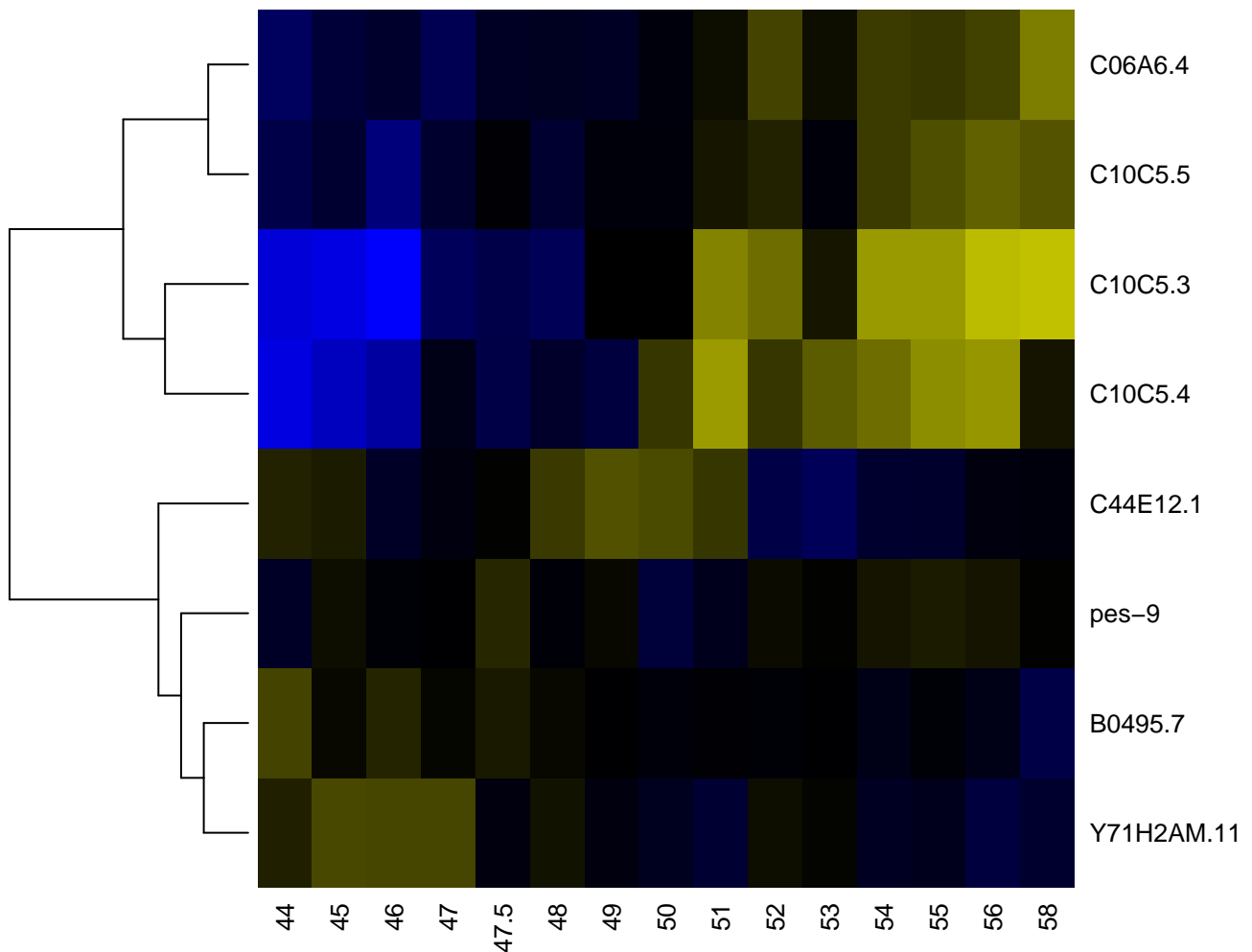
Peptidase family M1



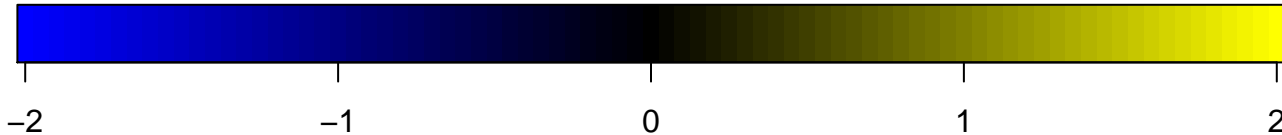
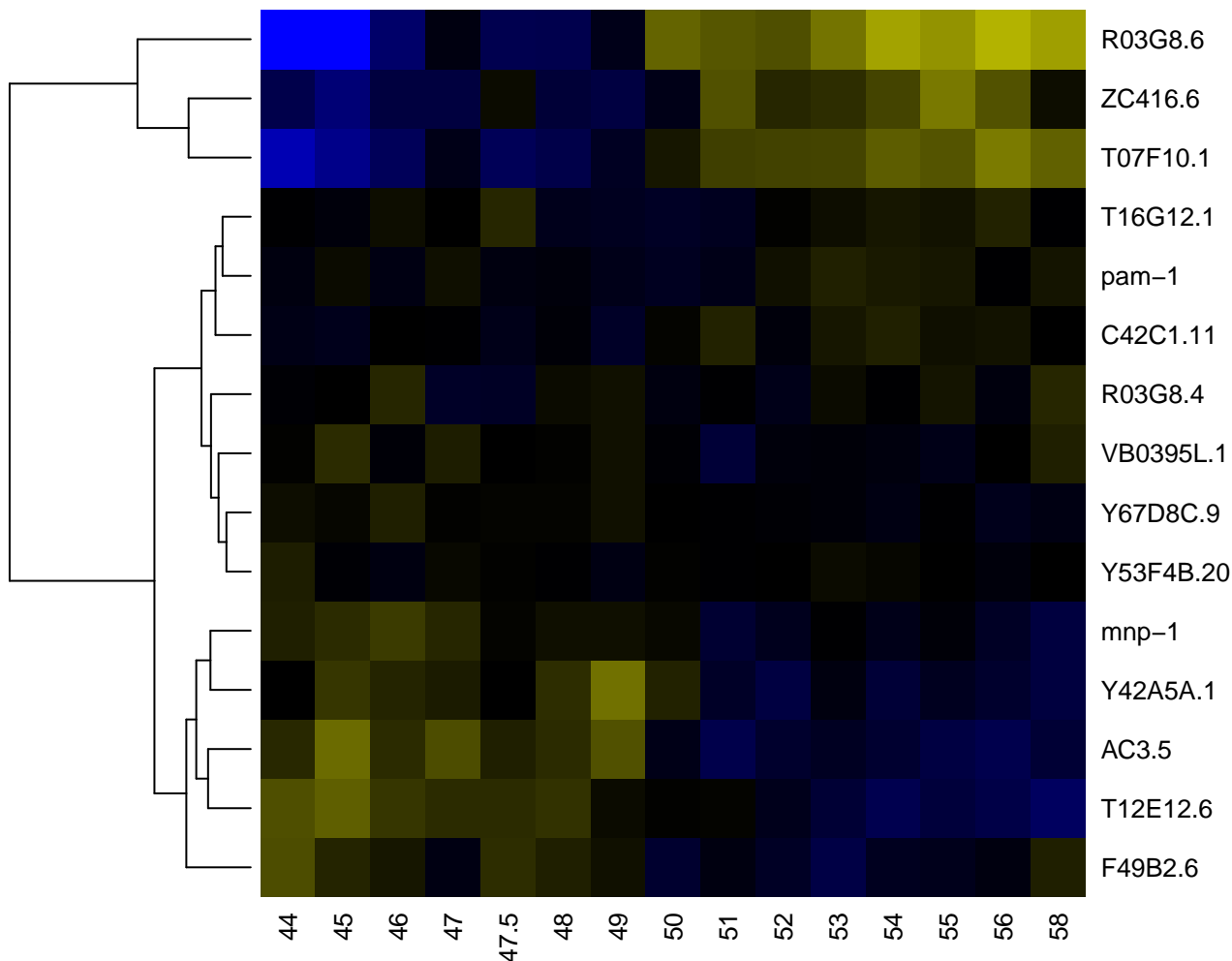
Peptidase family M13



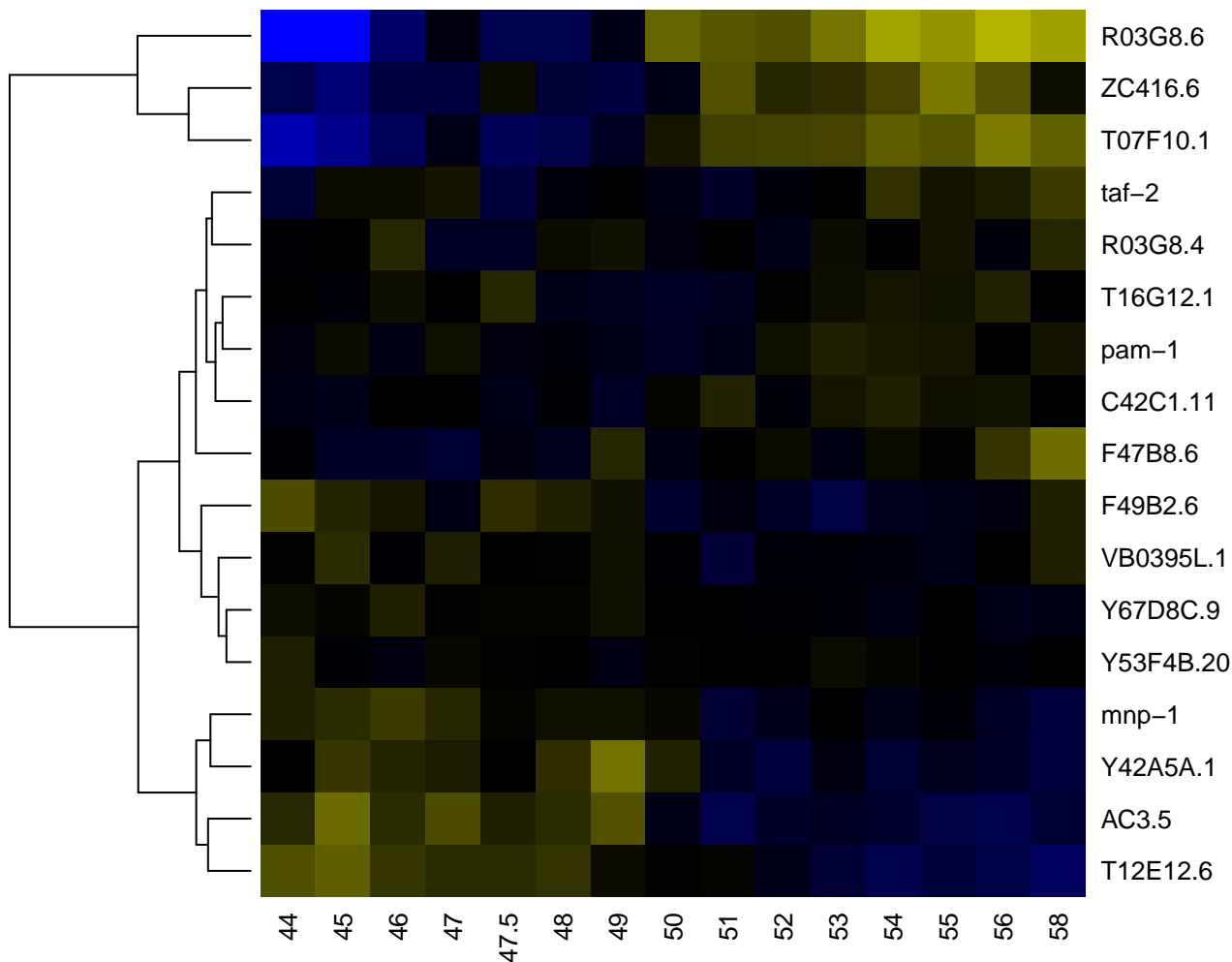
Peptidase family M20/M25/M40



Peptidase M1, membrane alanine aminopeptidase



Peptidase M1, membrane alanine aminopeptidase, N-termin



-2

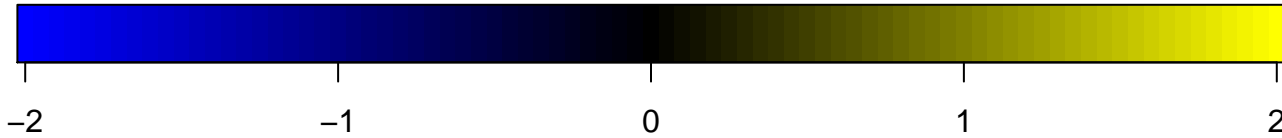
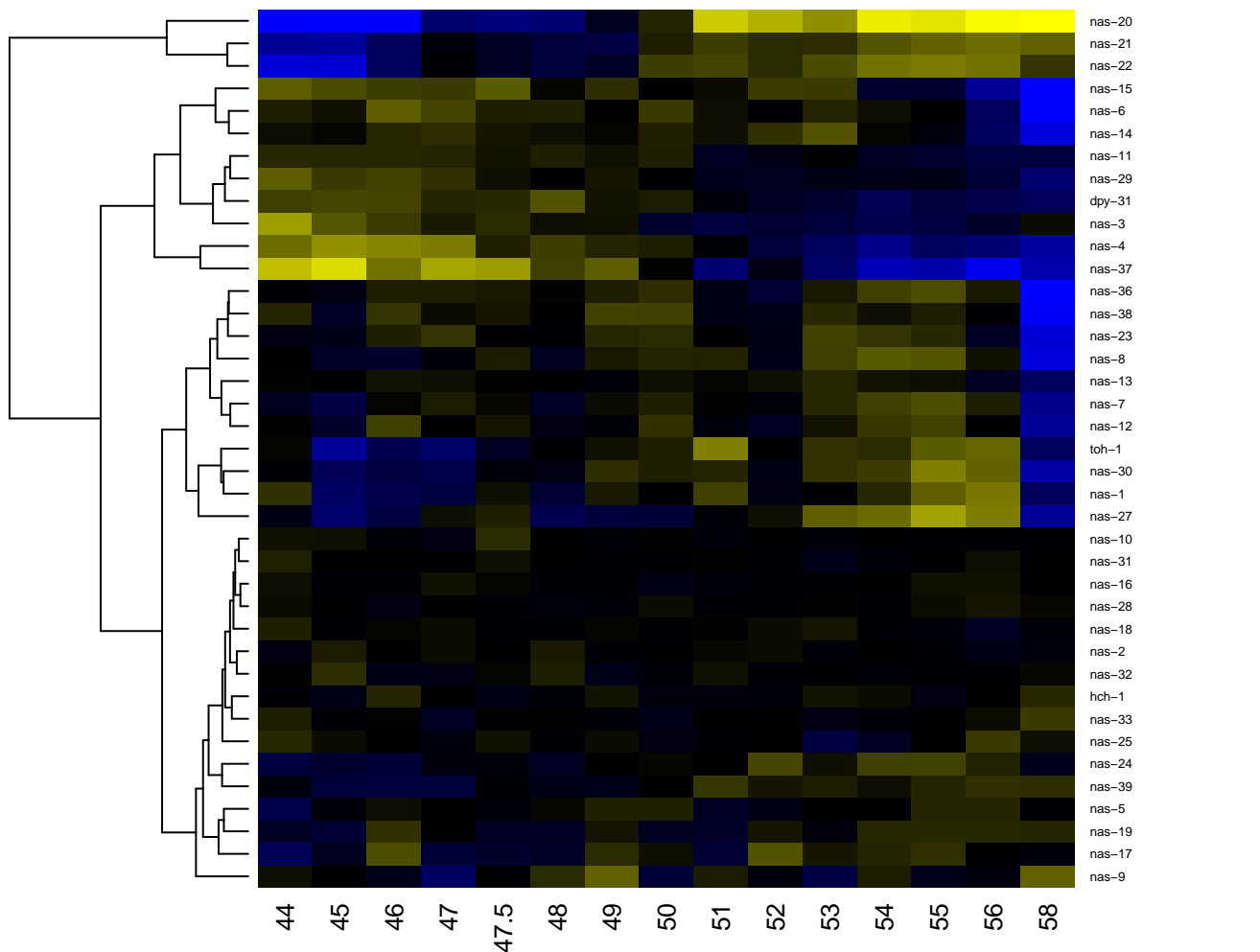
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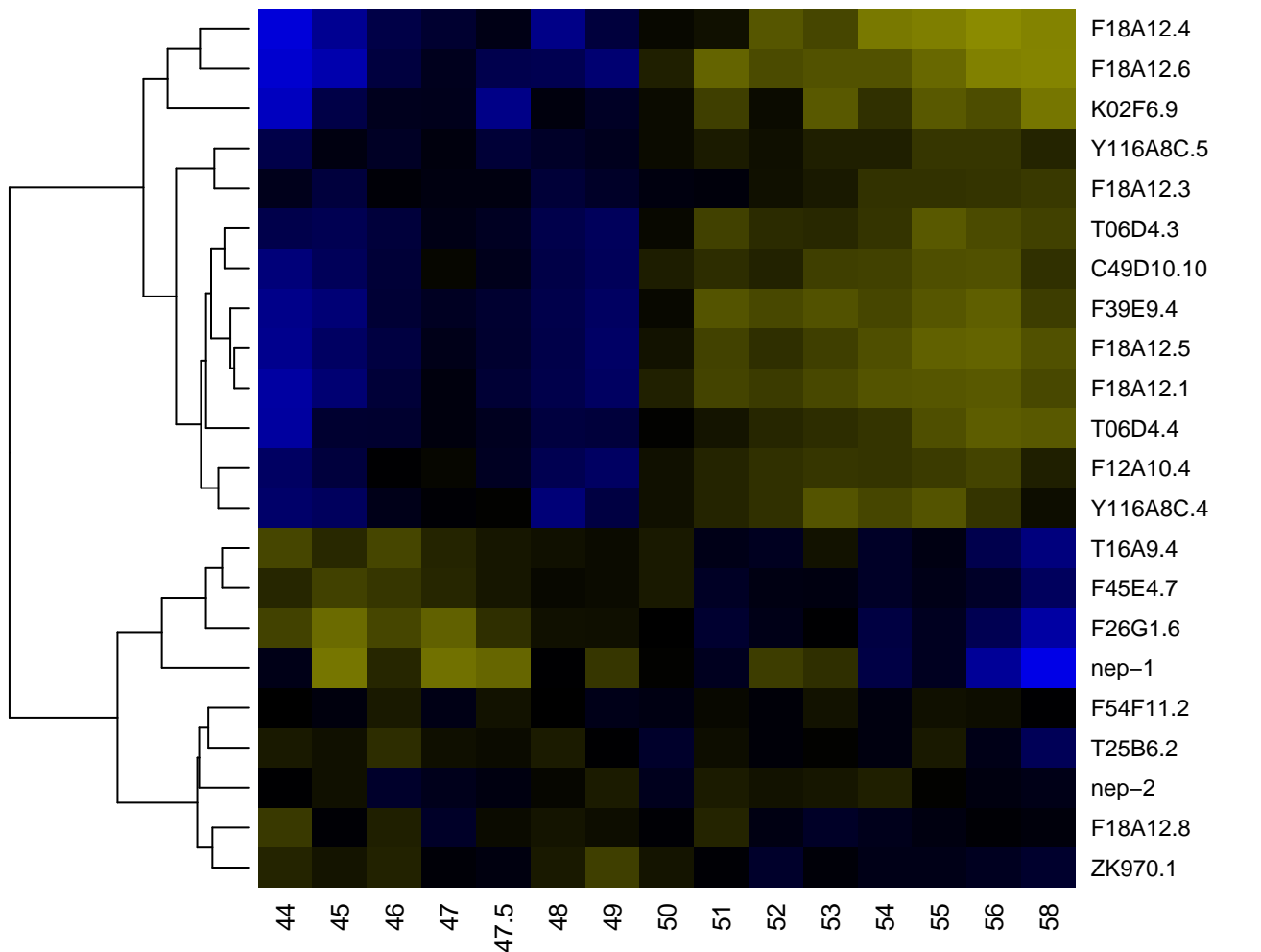
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2

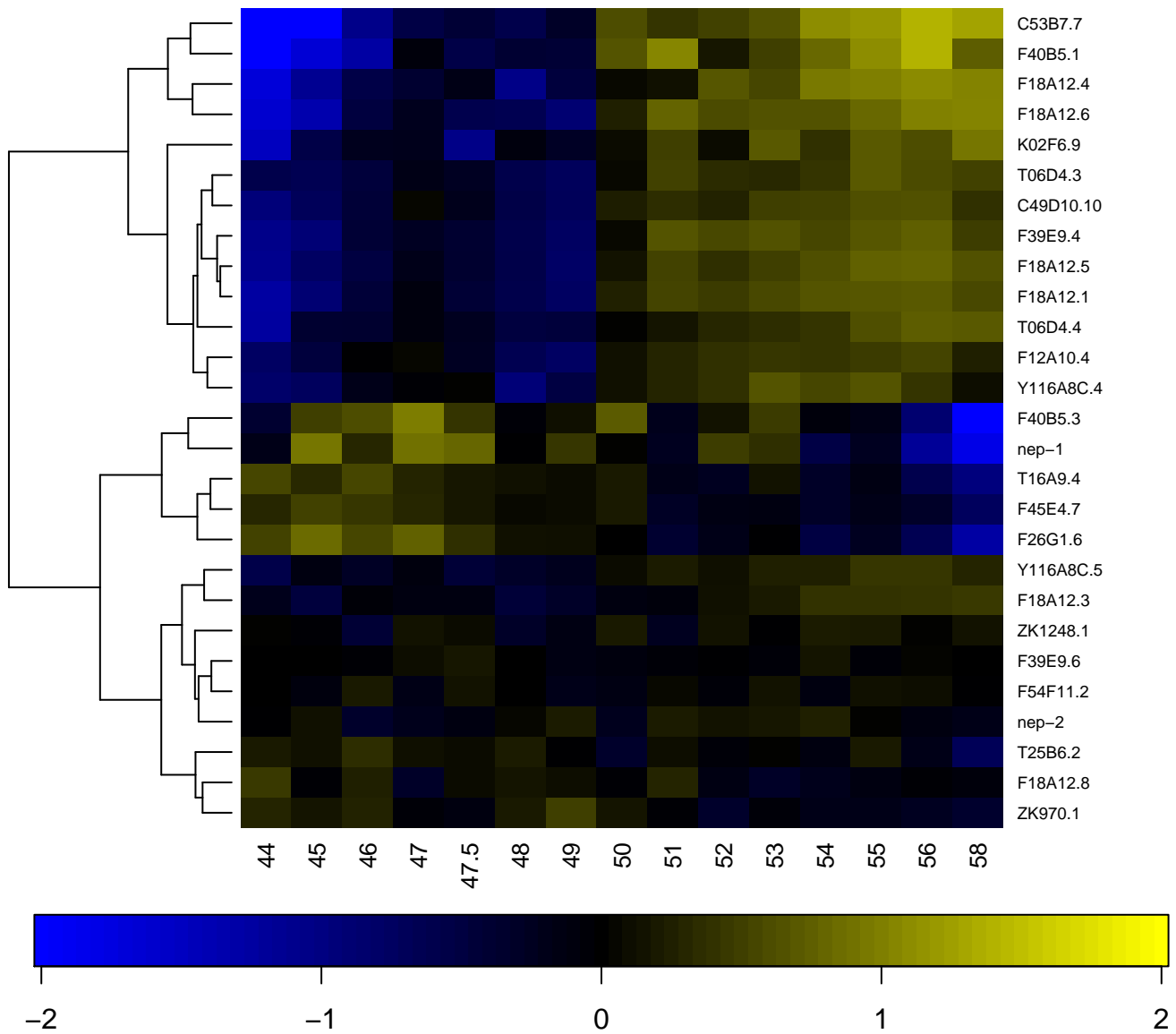
Peptidase M12A, astacin



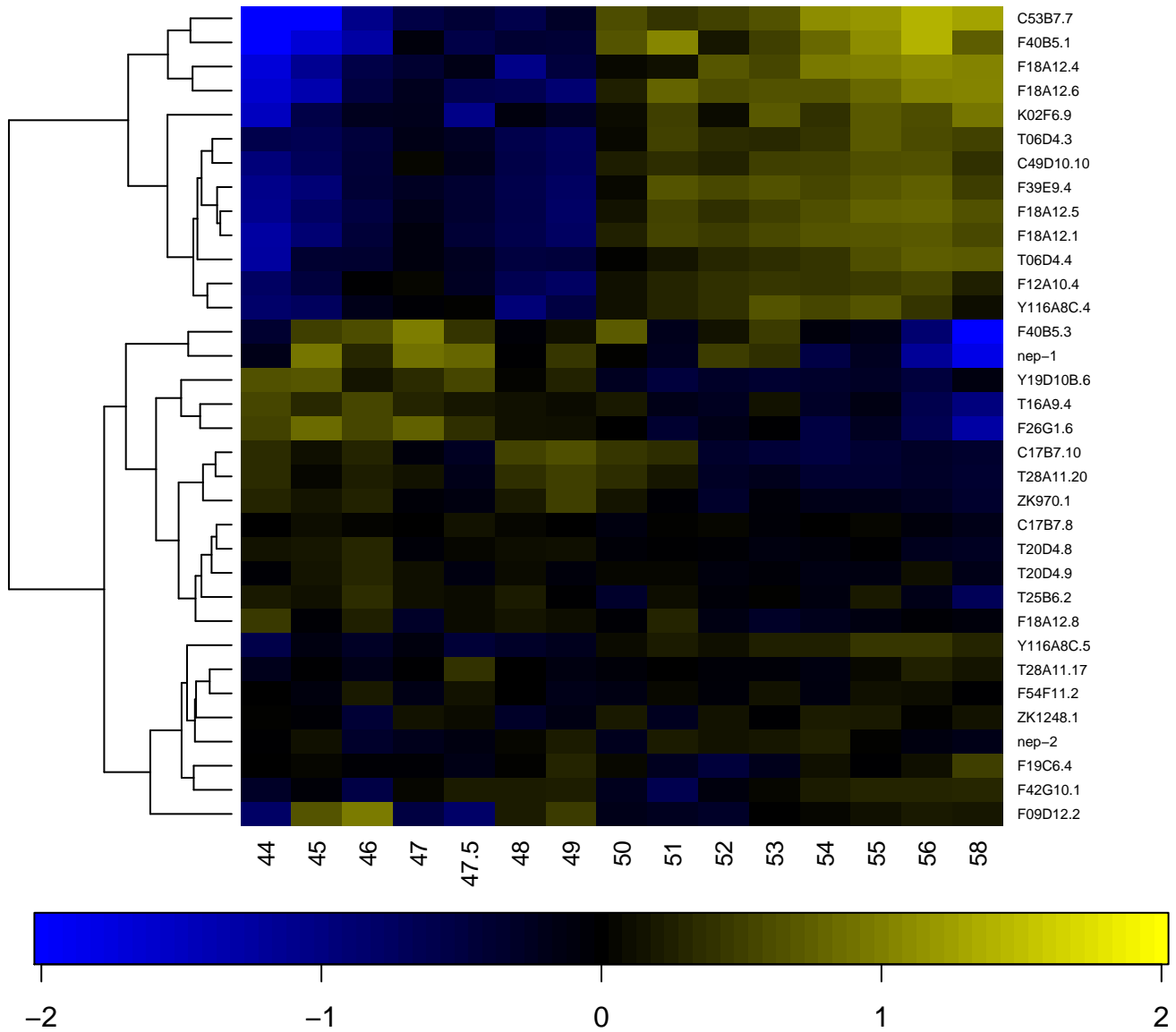
Peptidase M13



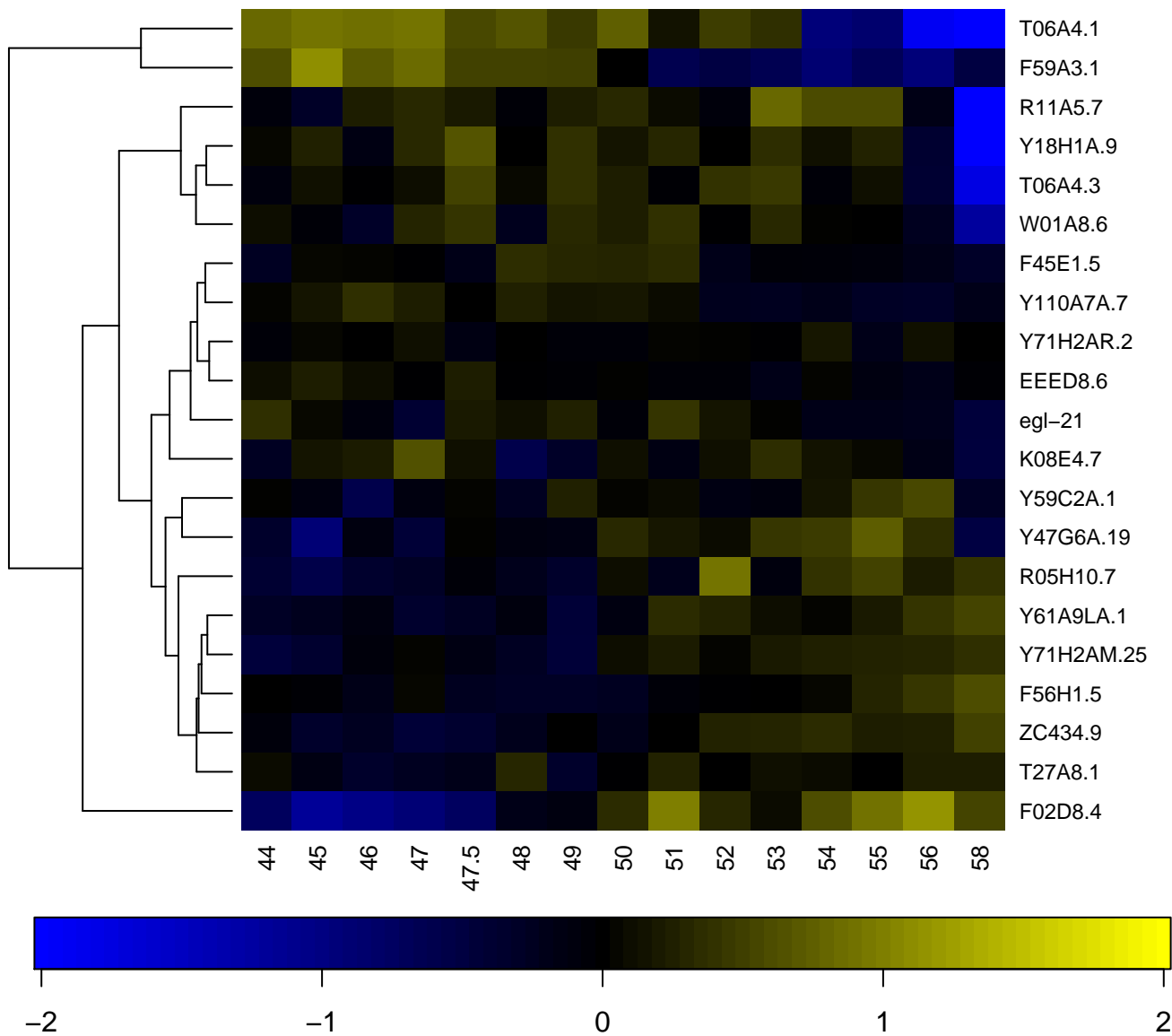
Peptidase M13, neprilysin



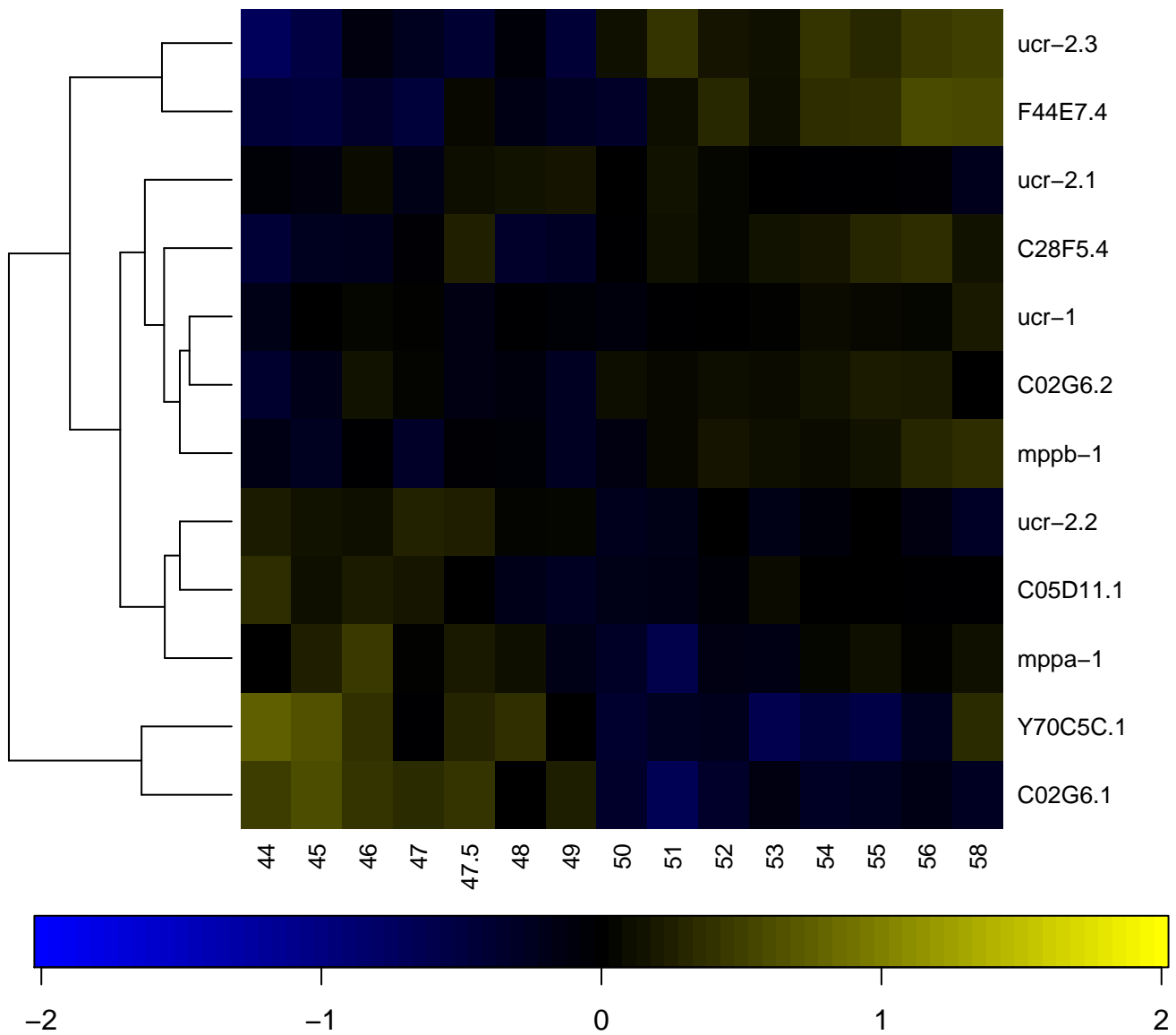
Peptidase M13, neprilysin, C-terminal



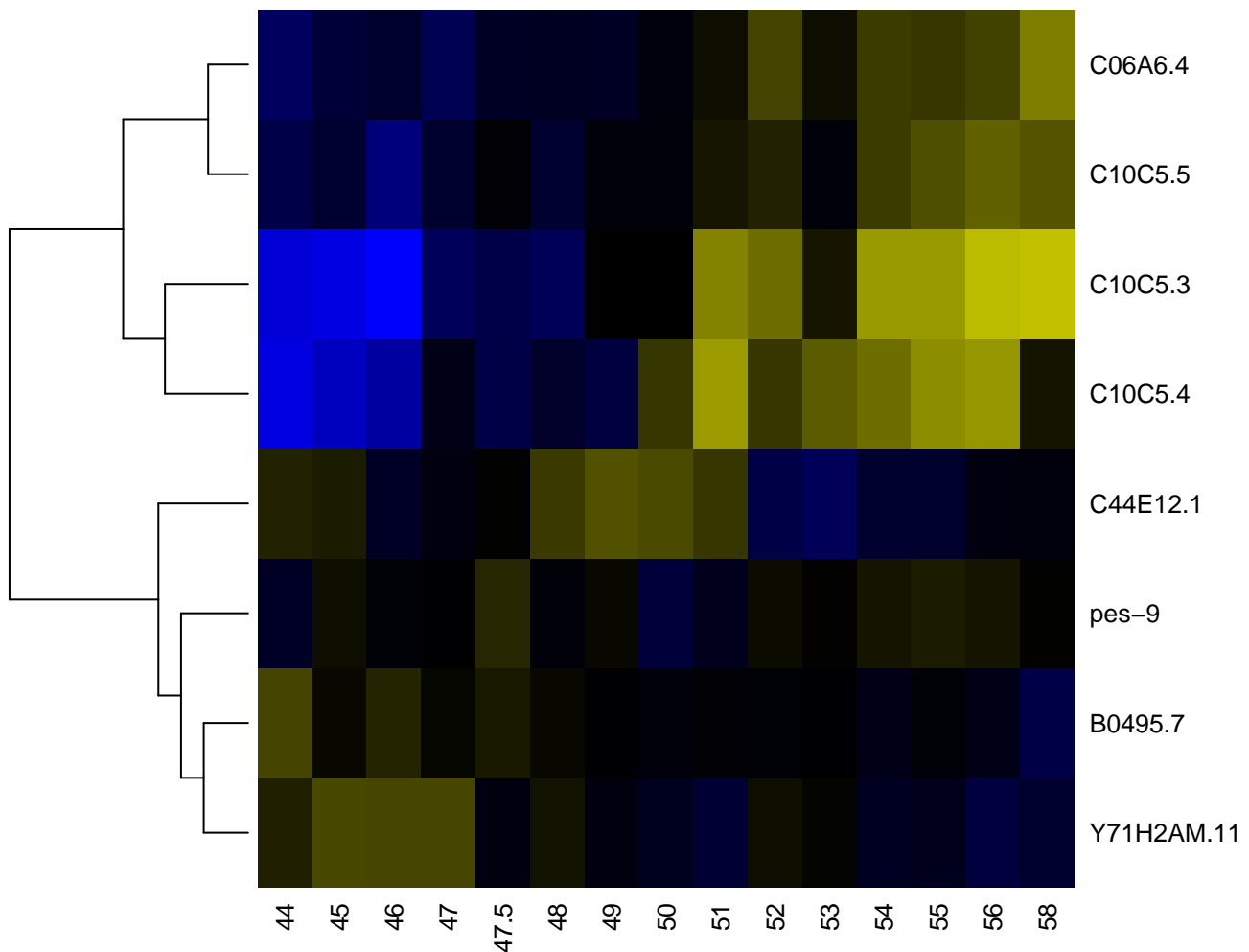
Peptidase M14, carboxypeptidase A



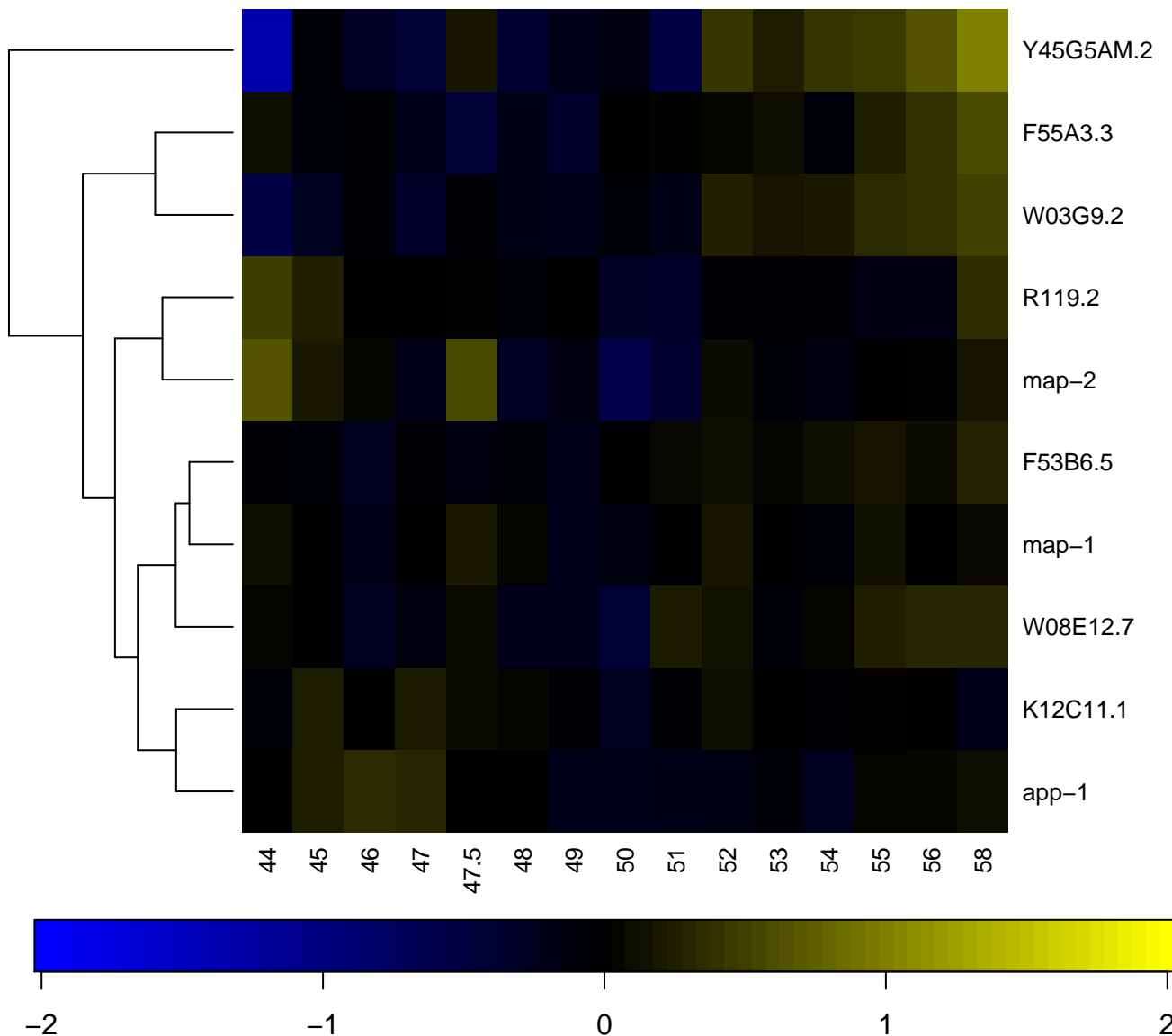
Peptidase M16 inactive domain



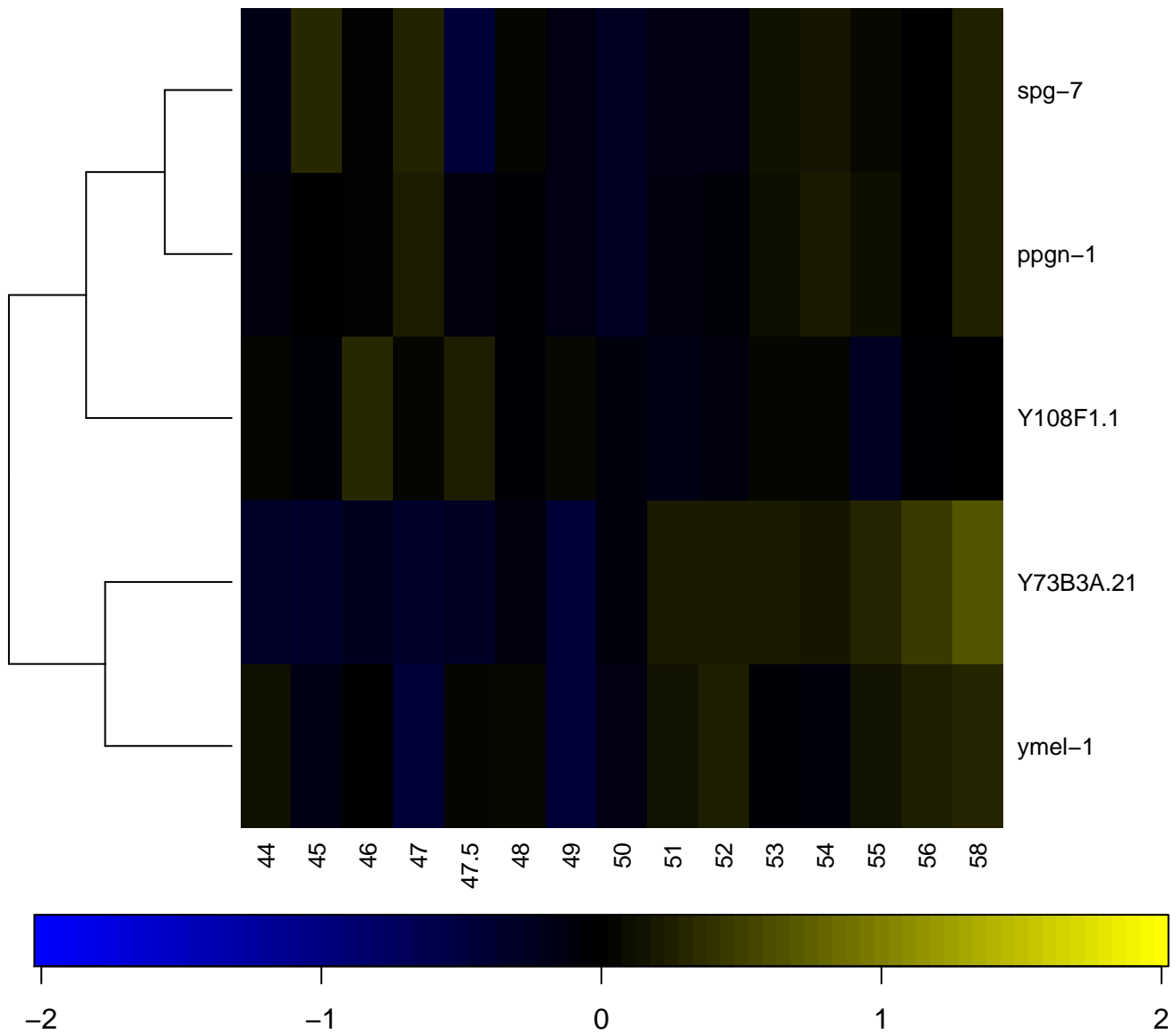
Peptidase M20



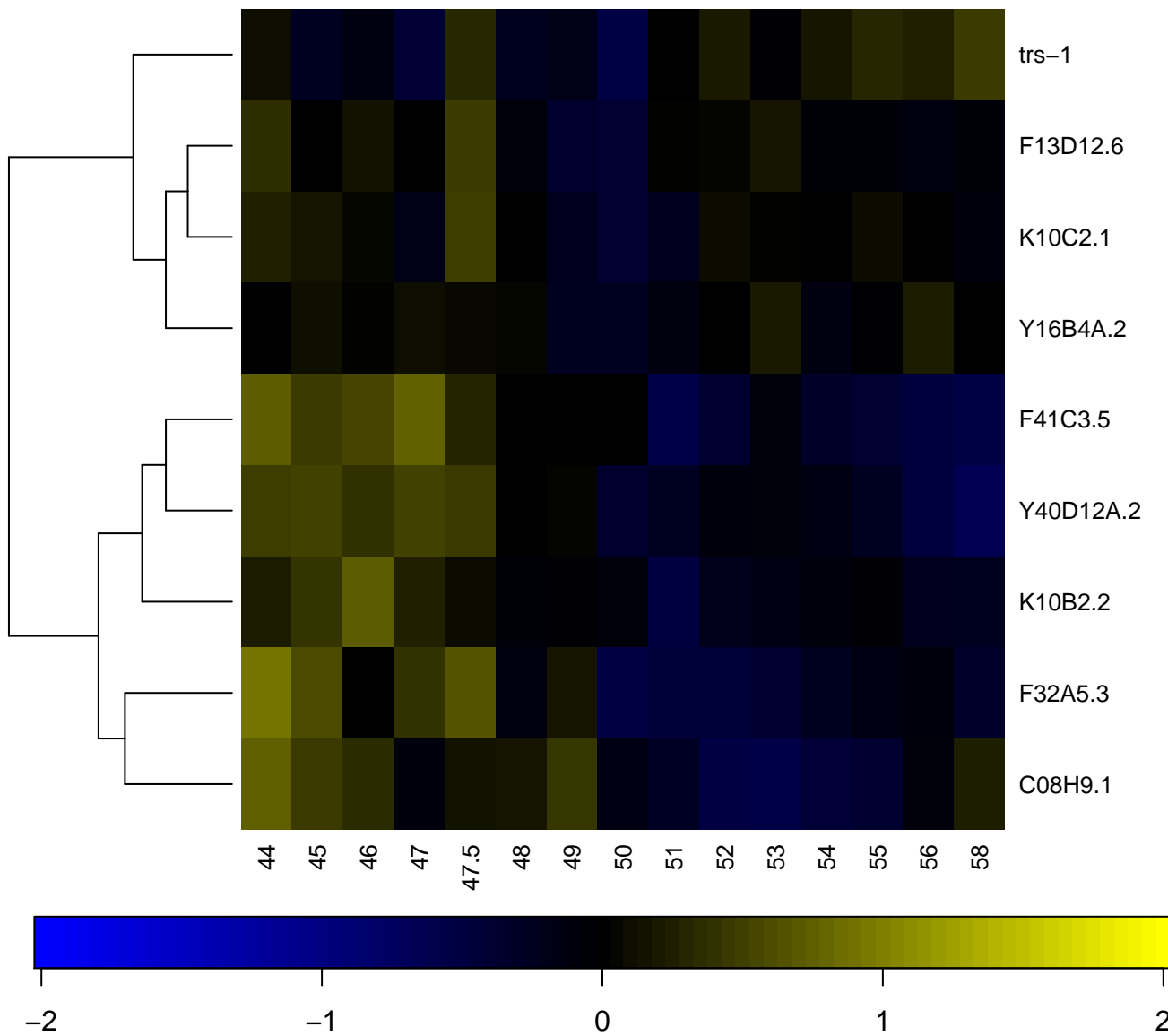
Peptidase M24, structural domain



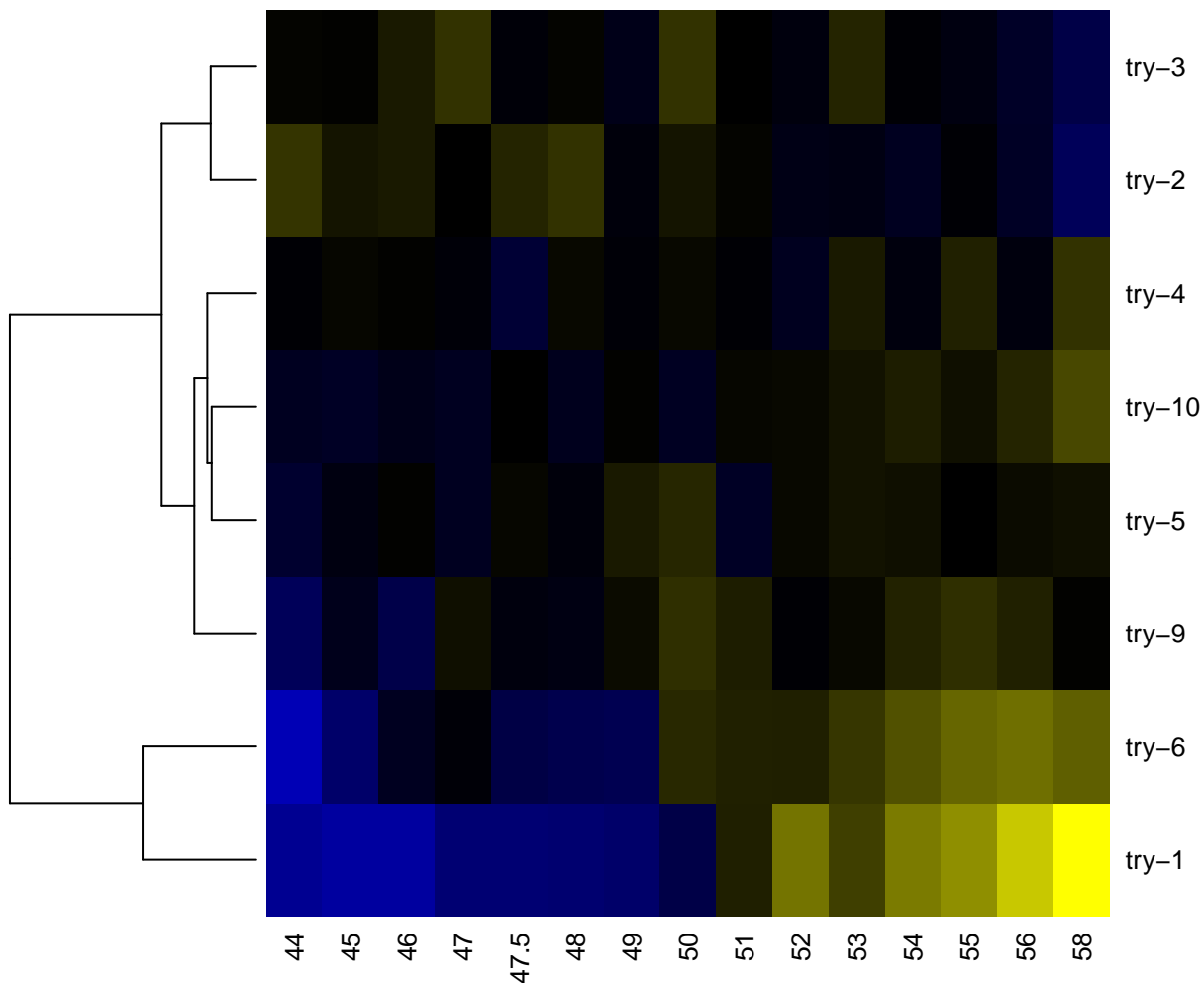
Peptidase M41



Peptidase S10, serine carboxypeptidase, active site



Peptidase S1A, chymotrypsin



-2

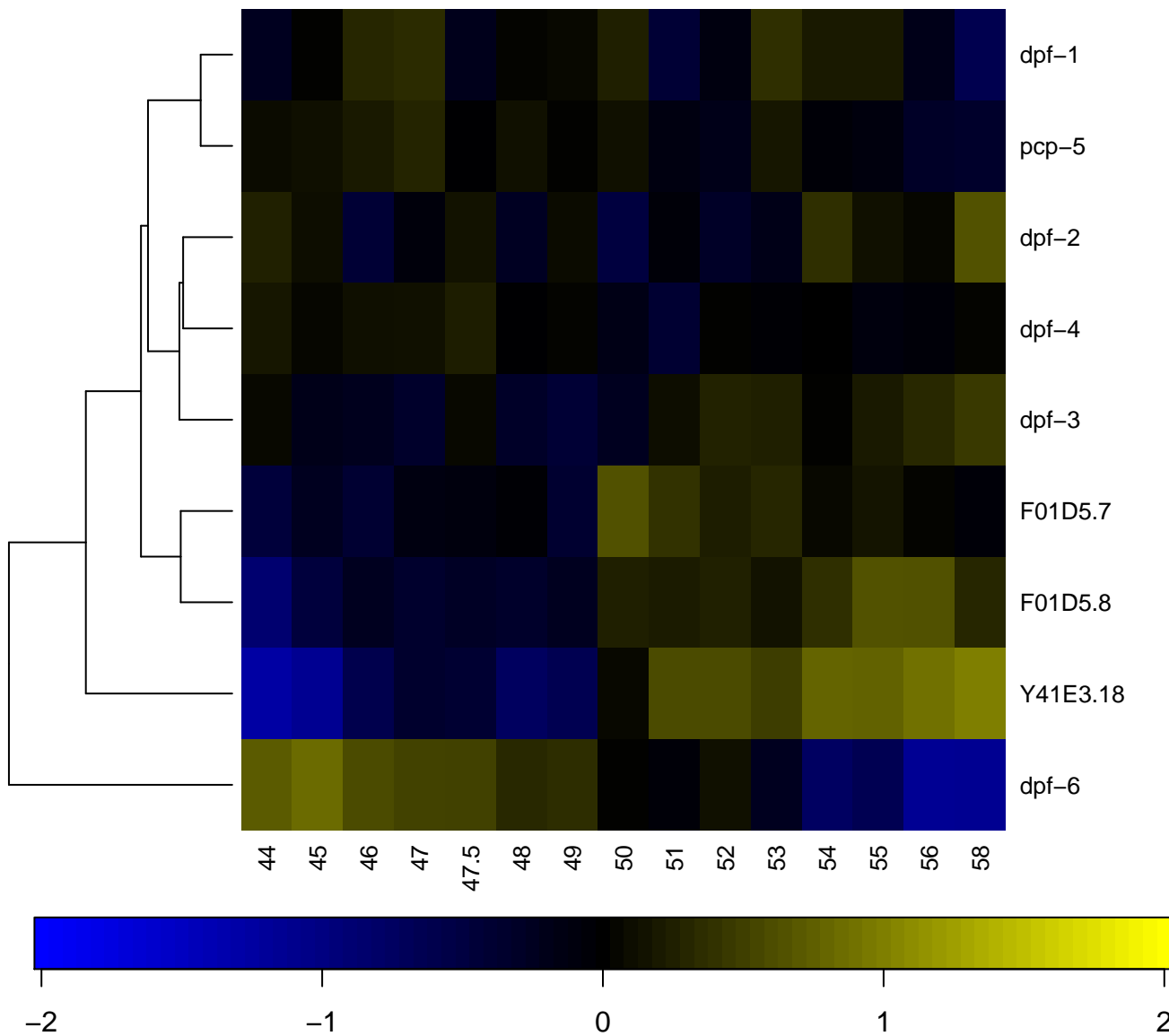
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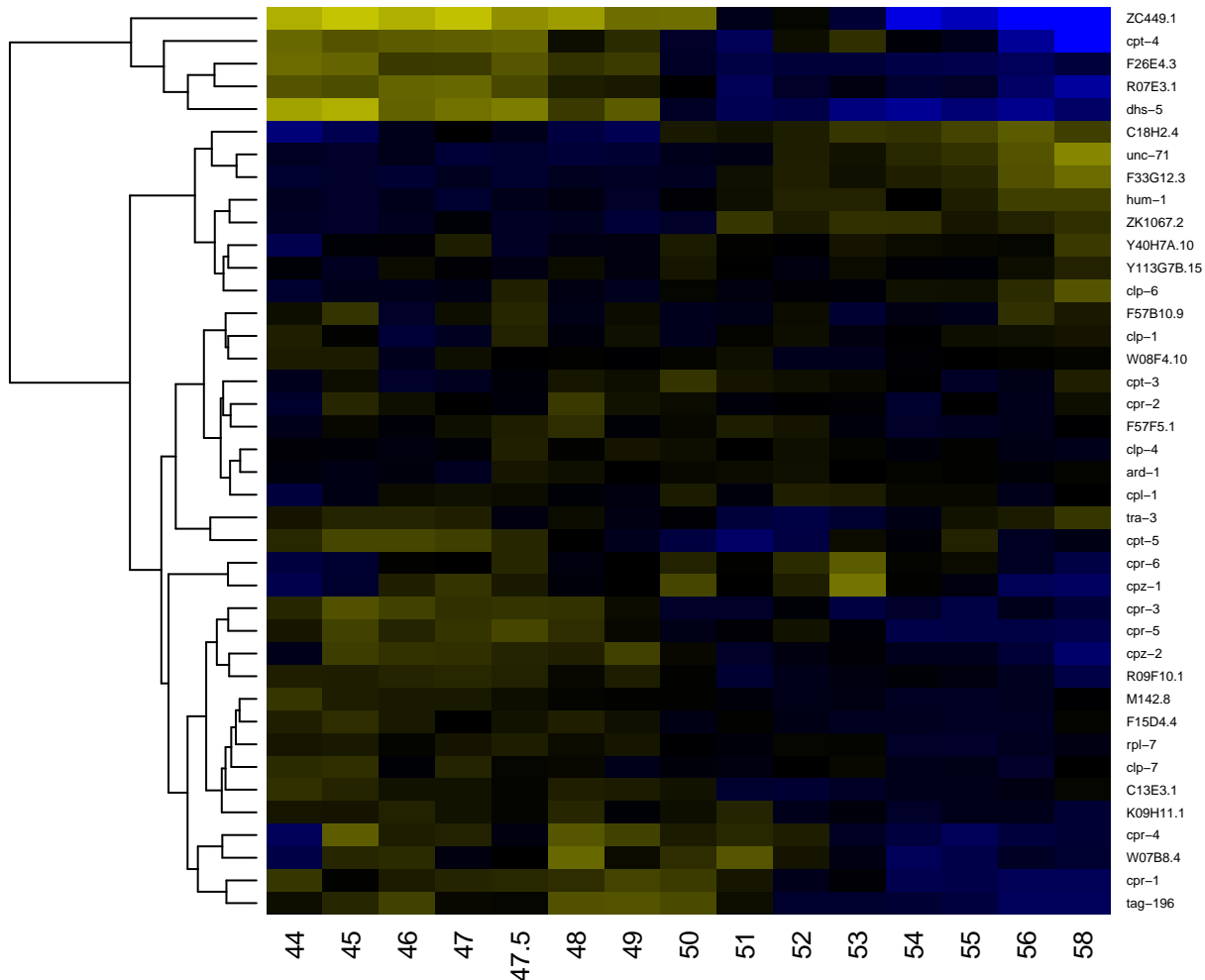
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Peptidase S9, prolyl oligopeptidase, catalytic domain



Peptidase, cysteine peptidase active site



-2

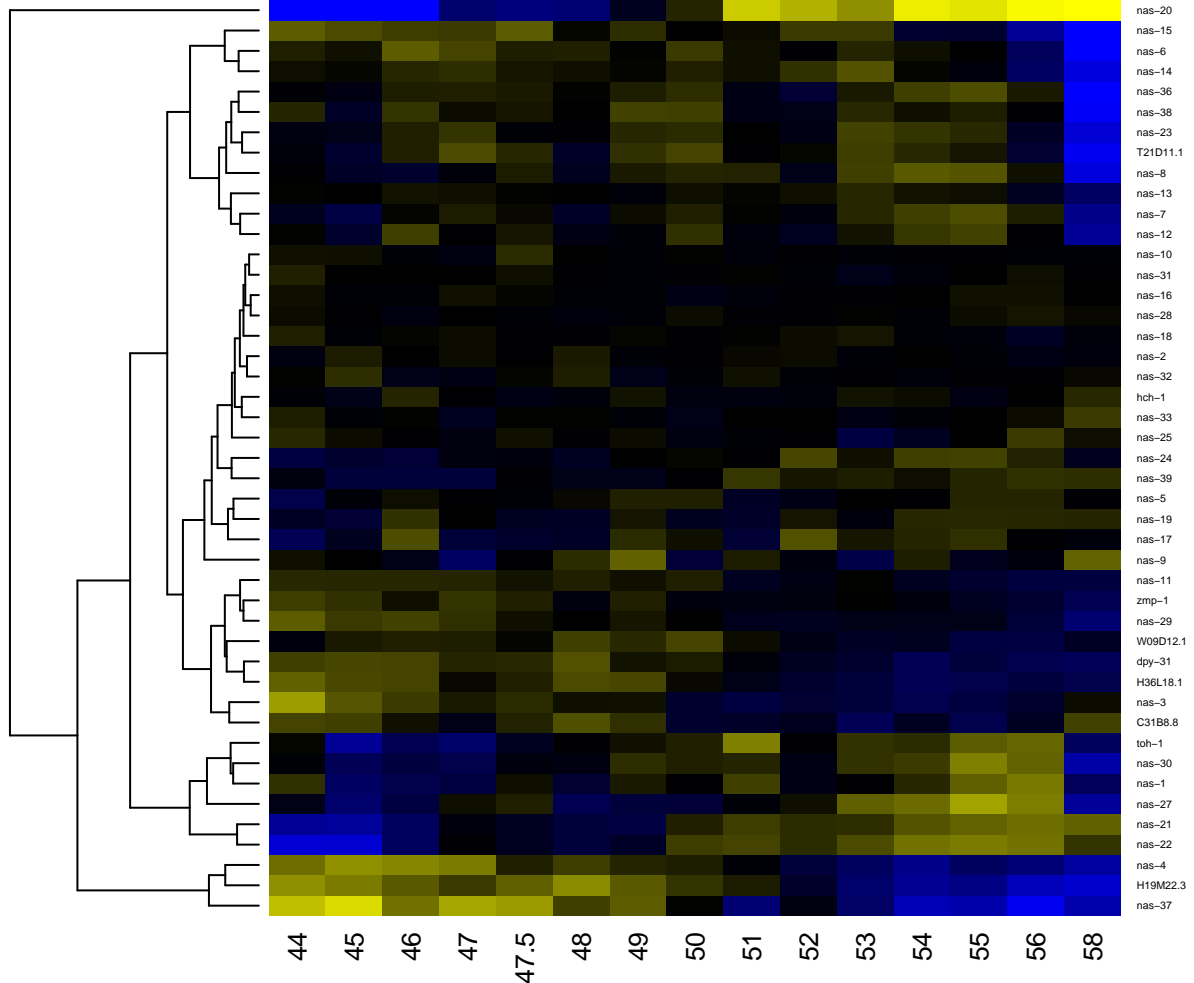
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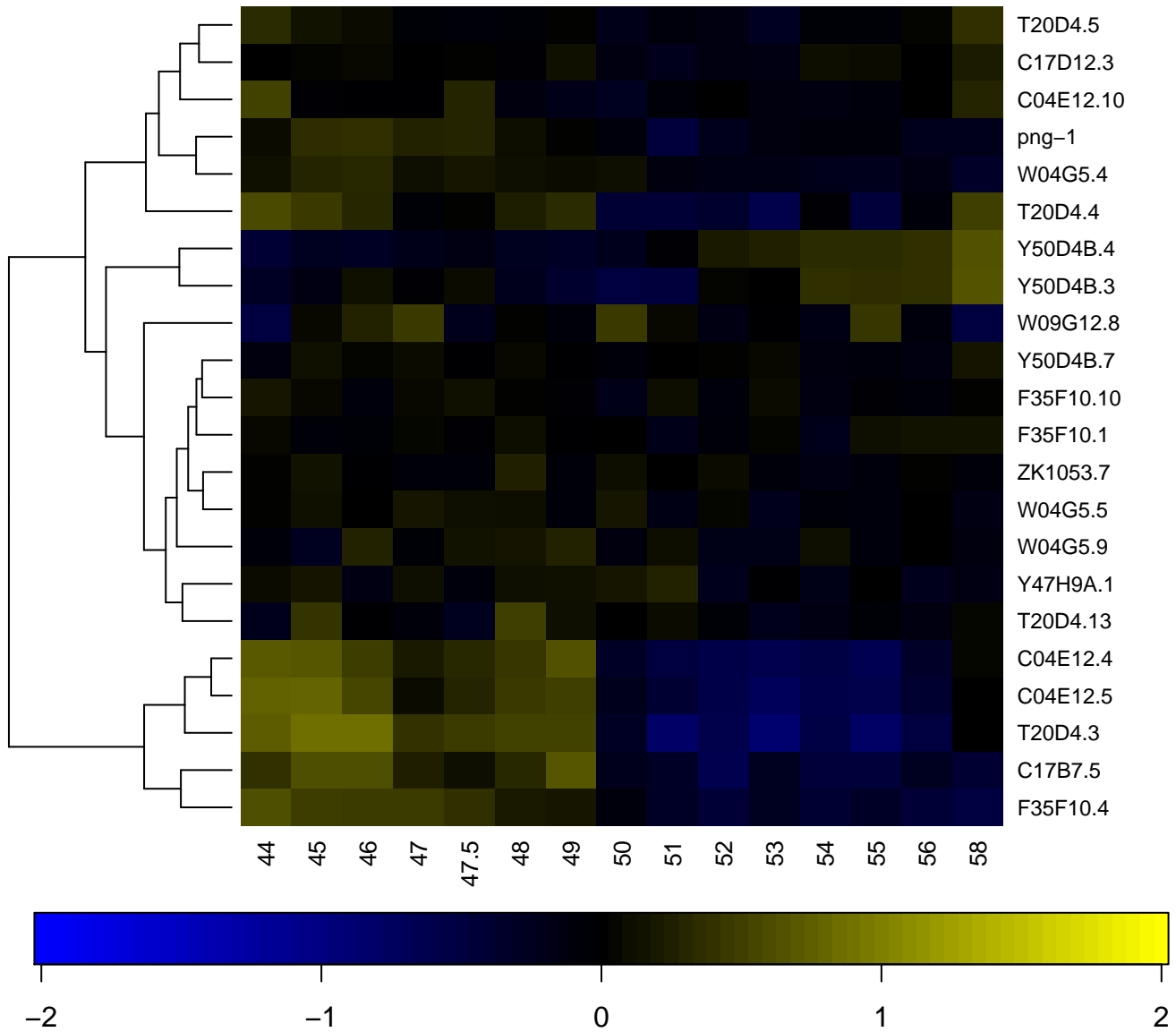
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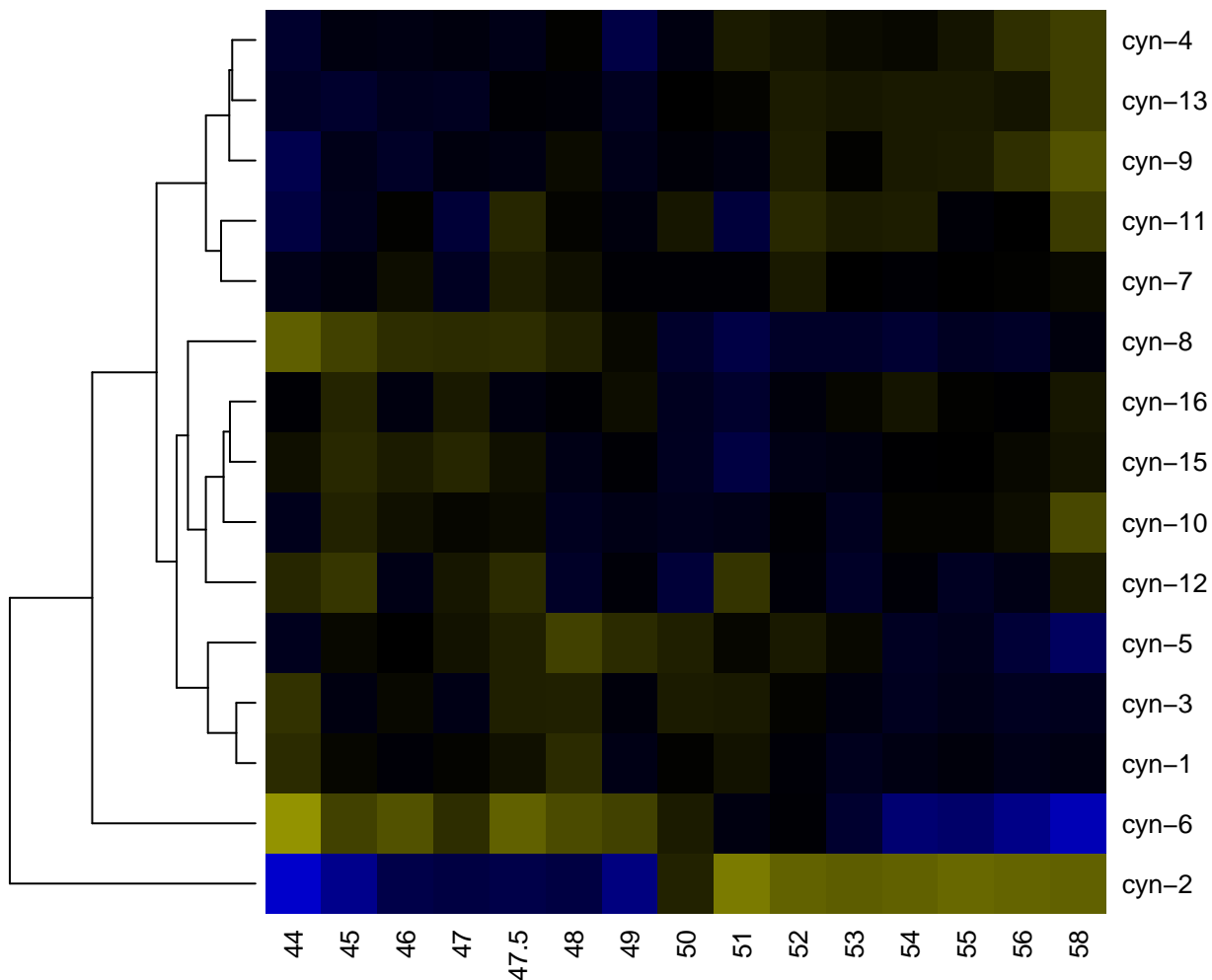
Peptidase, metallopeptidase



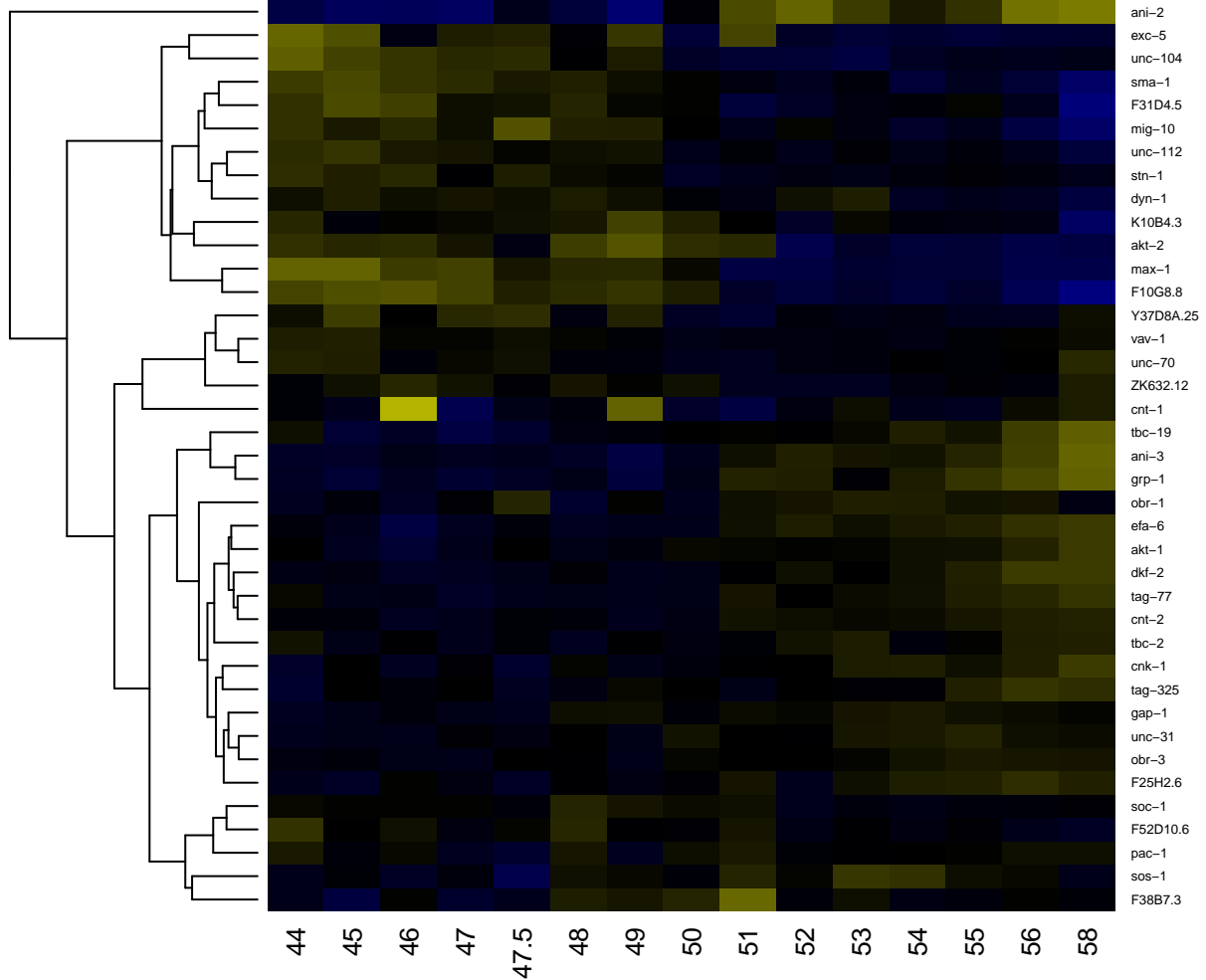
Peptide N glycanase, PAW domain



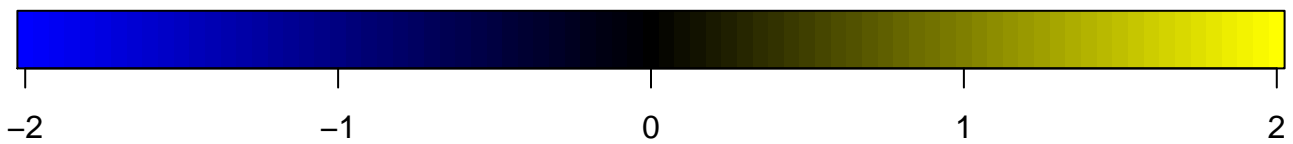
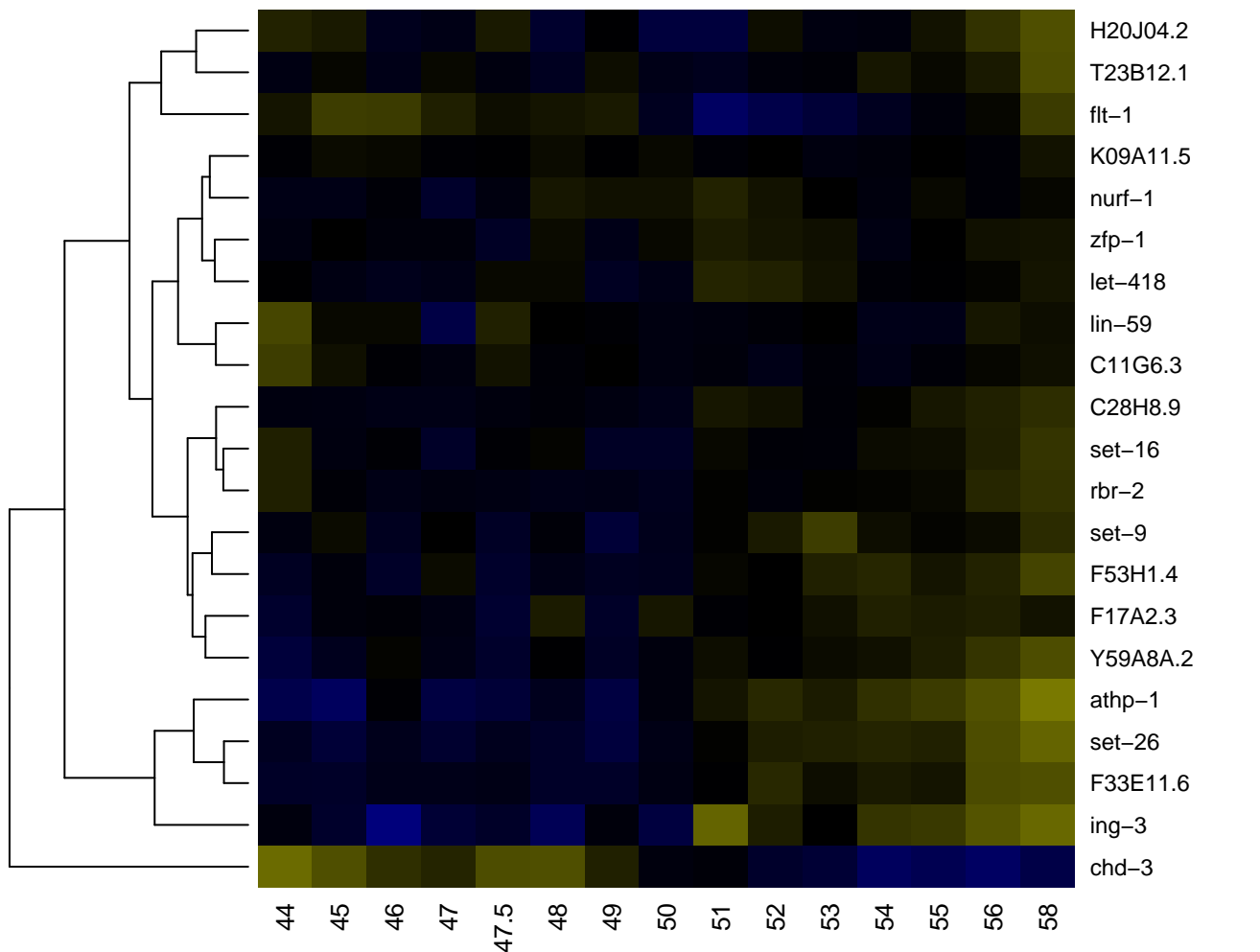
cidyl-prolyl cis-trans isomerase, cyclophilin-type, conserved



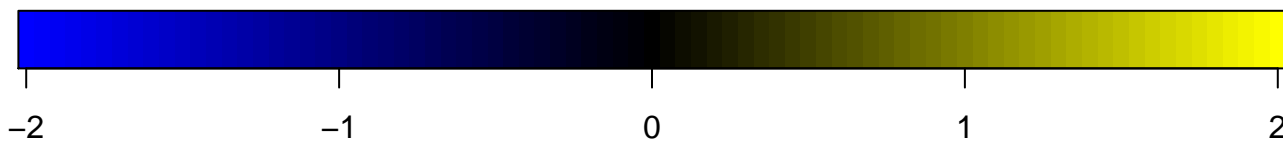
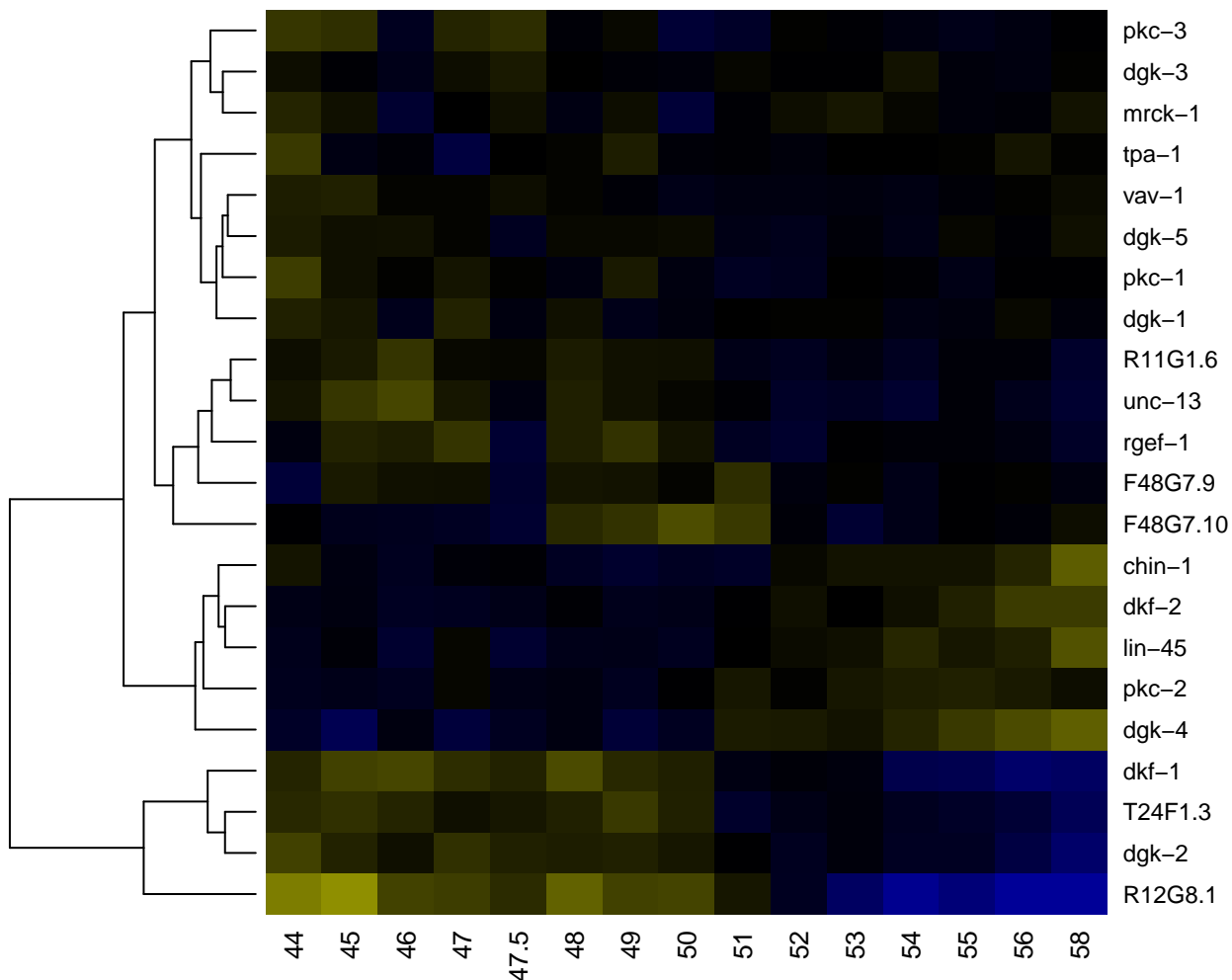
PH domain



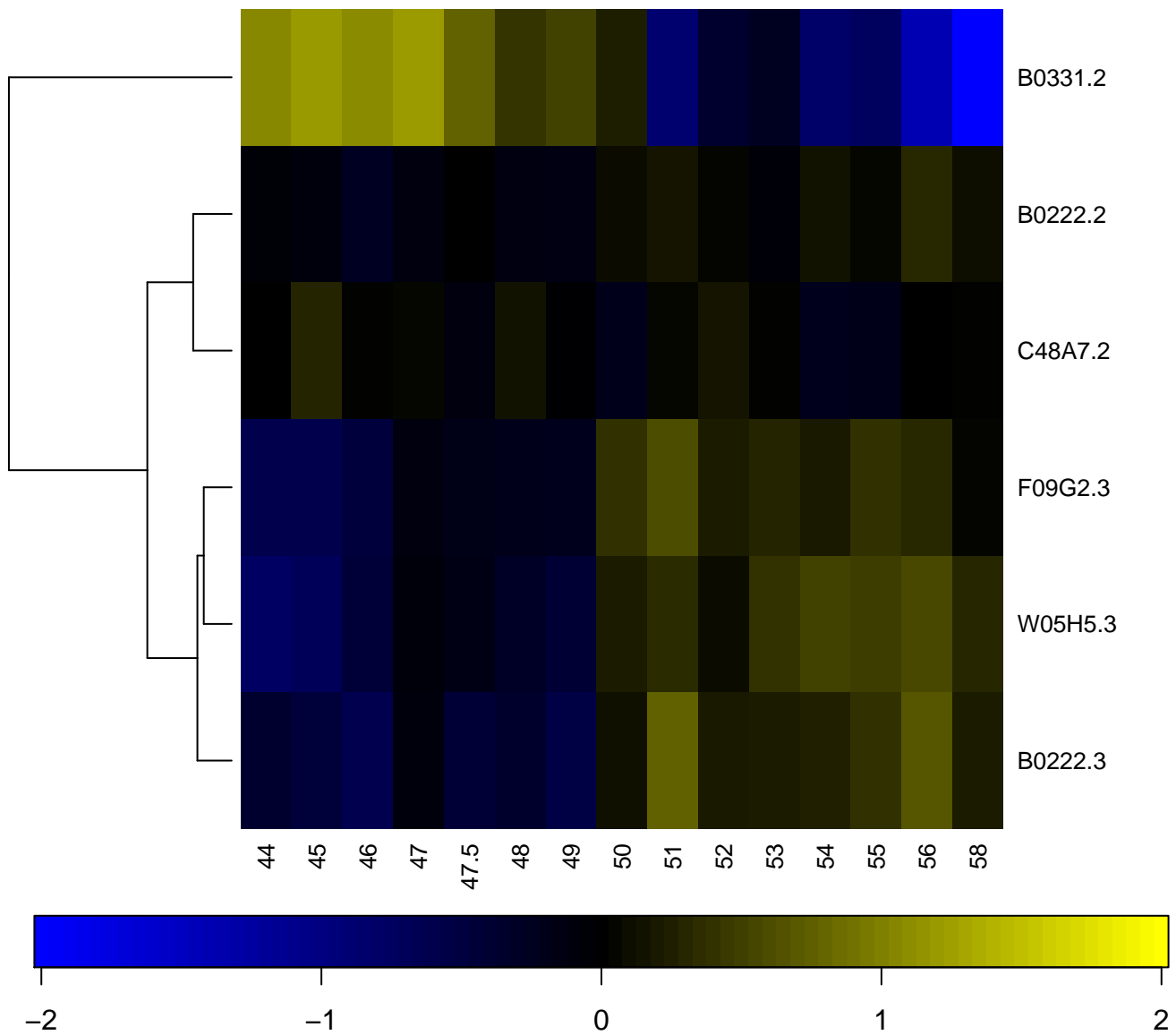
PHD-finger



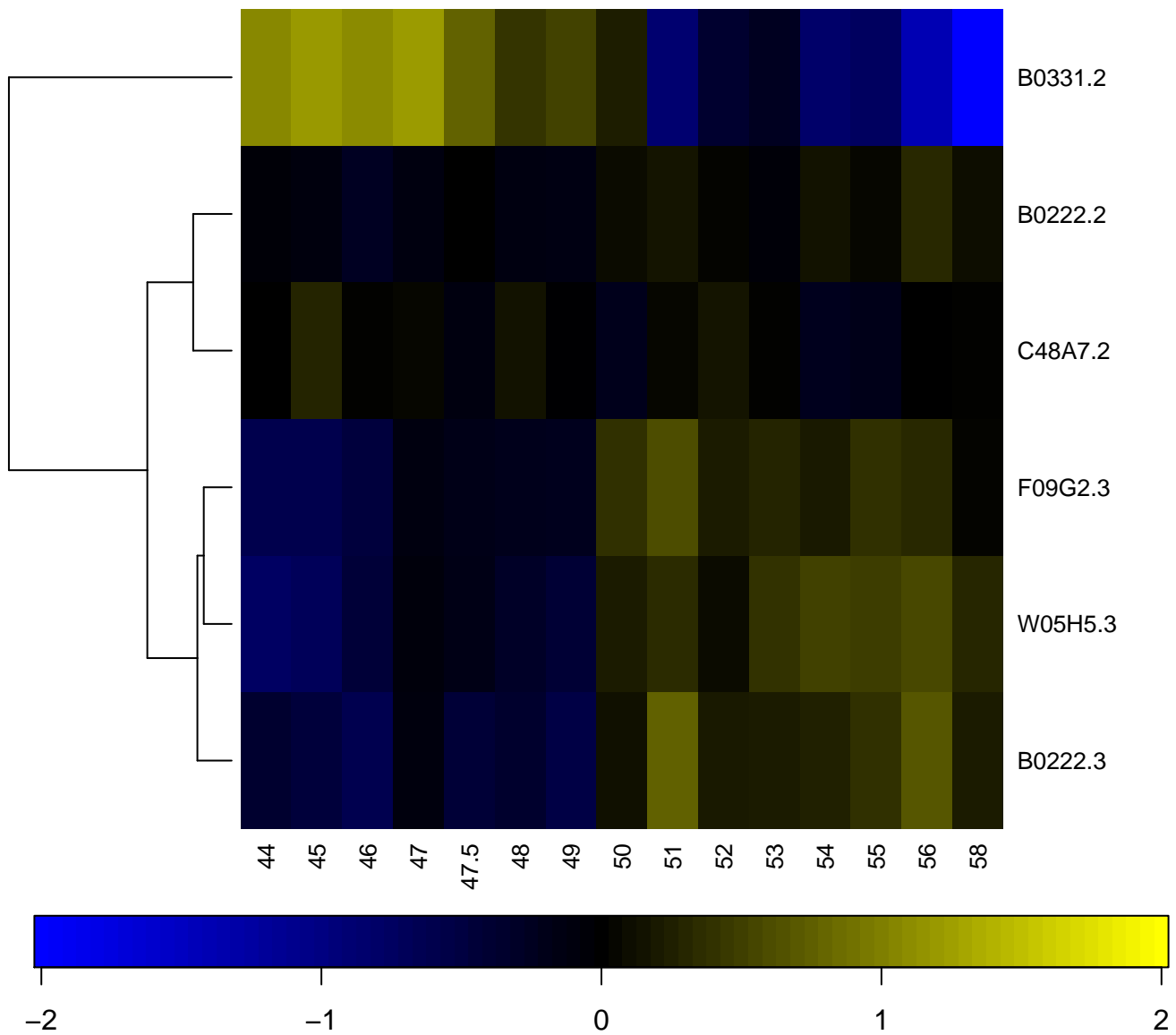
Phorbol esters/diacylglycerol binding domain (C1 domain)



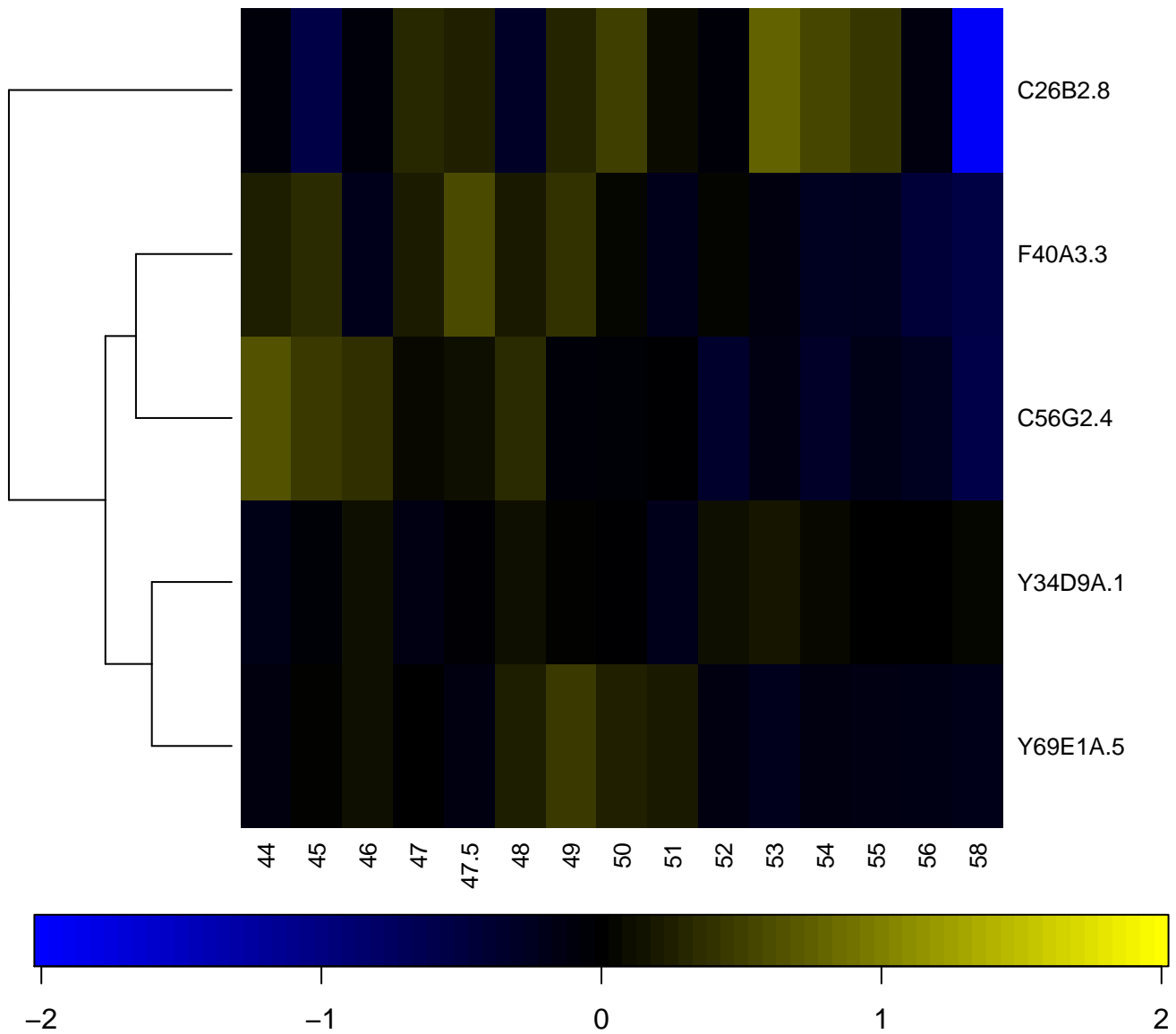
Phosphate transporter



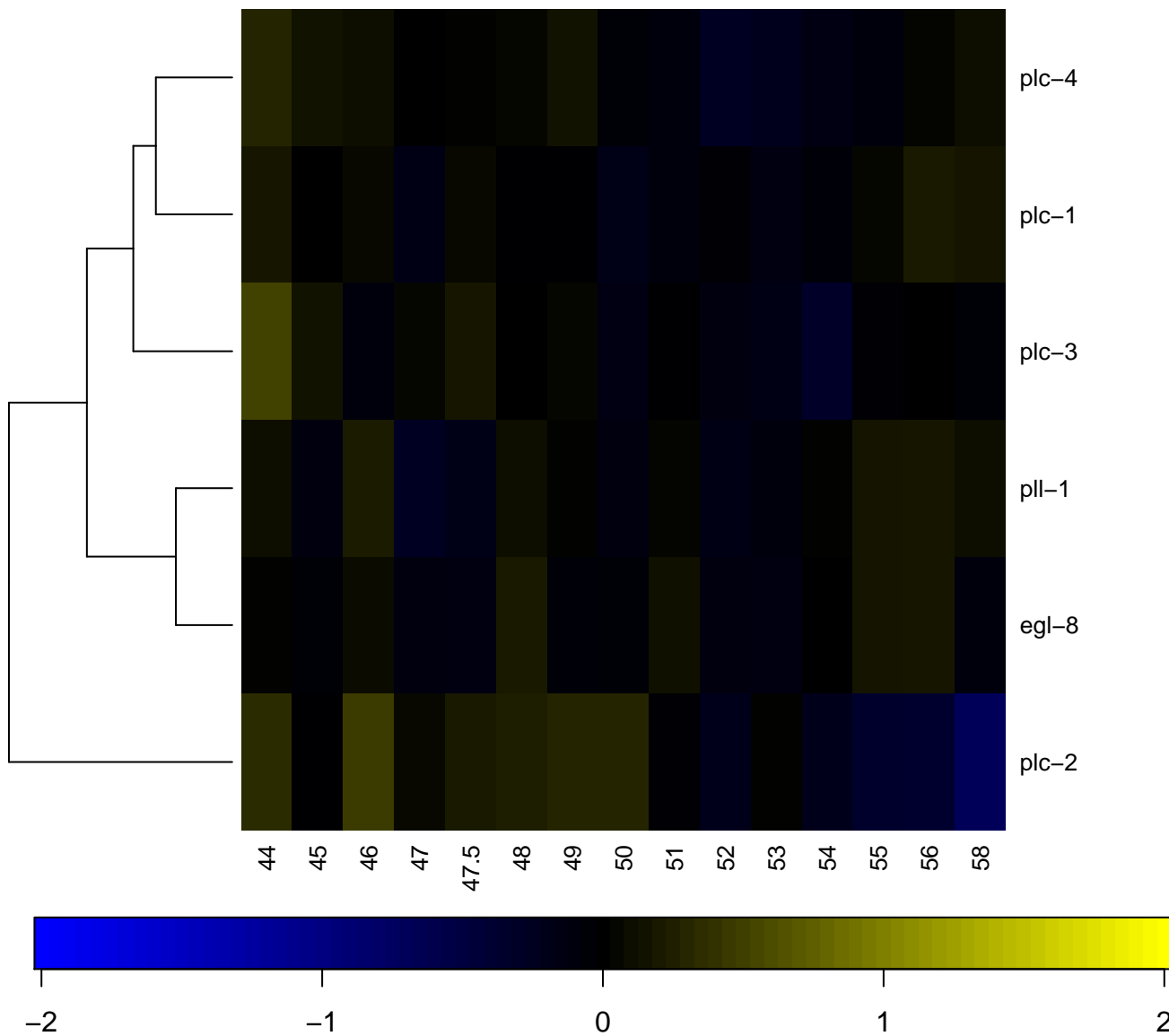
Phosphate transporter family



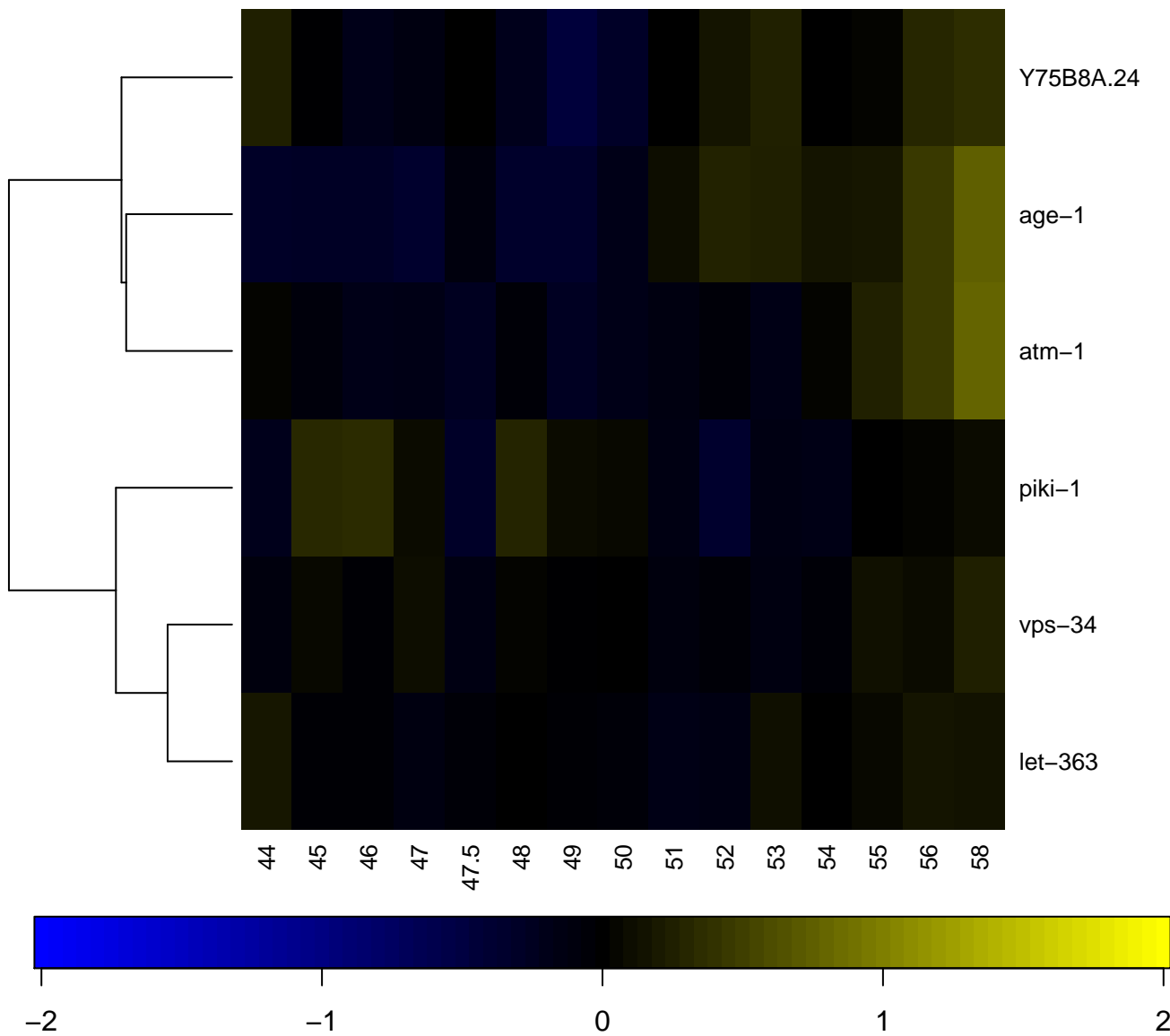
Phosphatidylethanolamine-binding protein PEBP



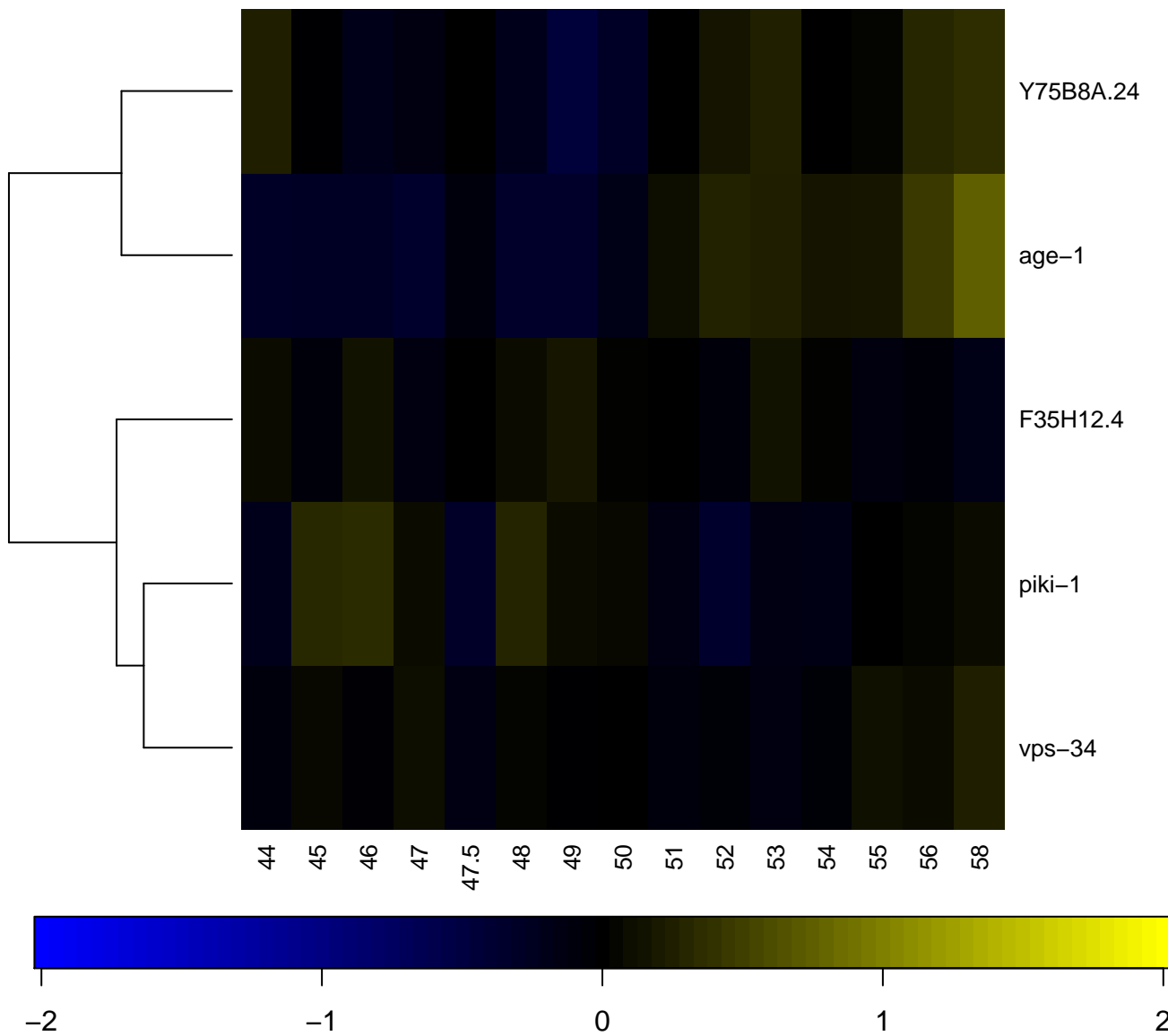
Phosphatidylinositol-specific phospholipase C, X domain



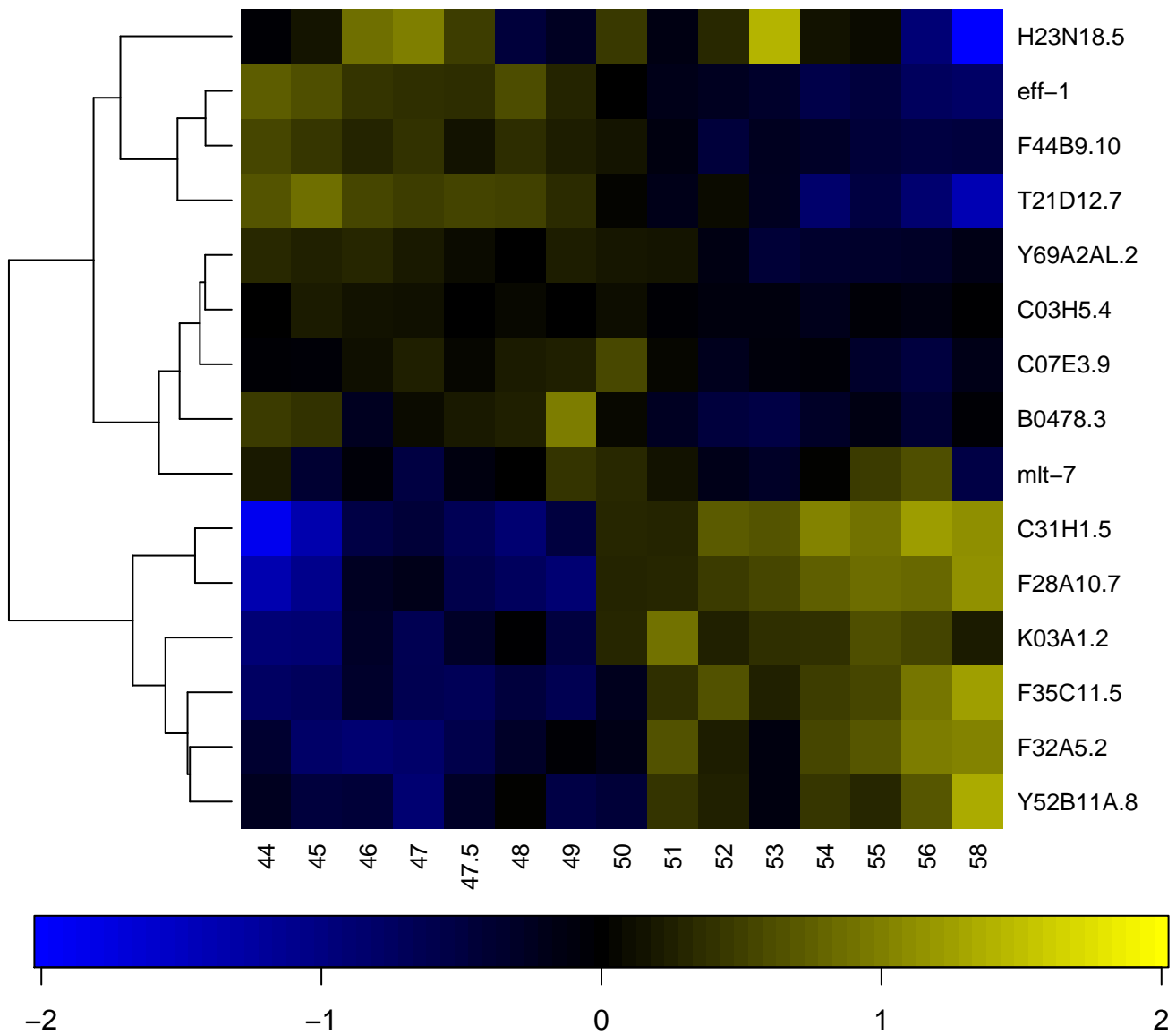
Phosphatidylinositol 3/4-kinase, conserved site



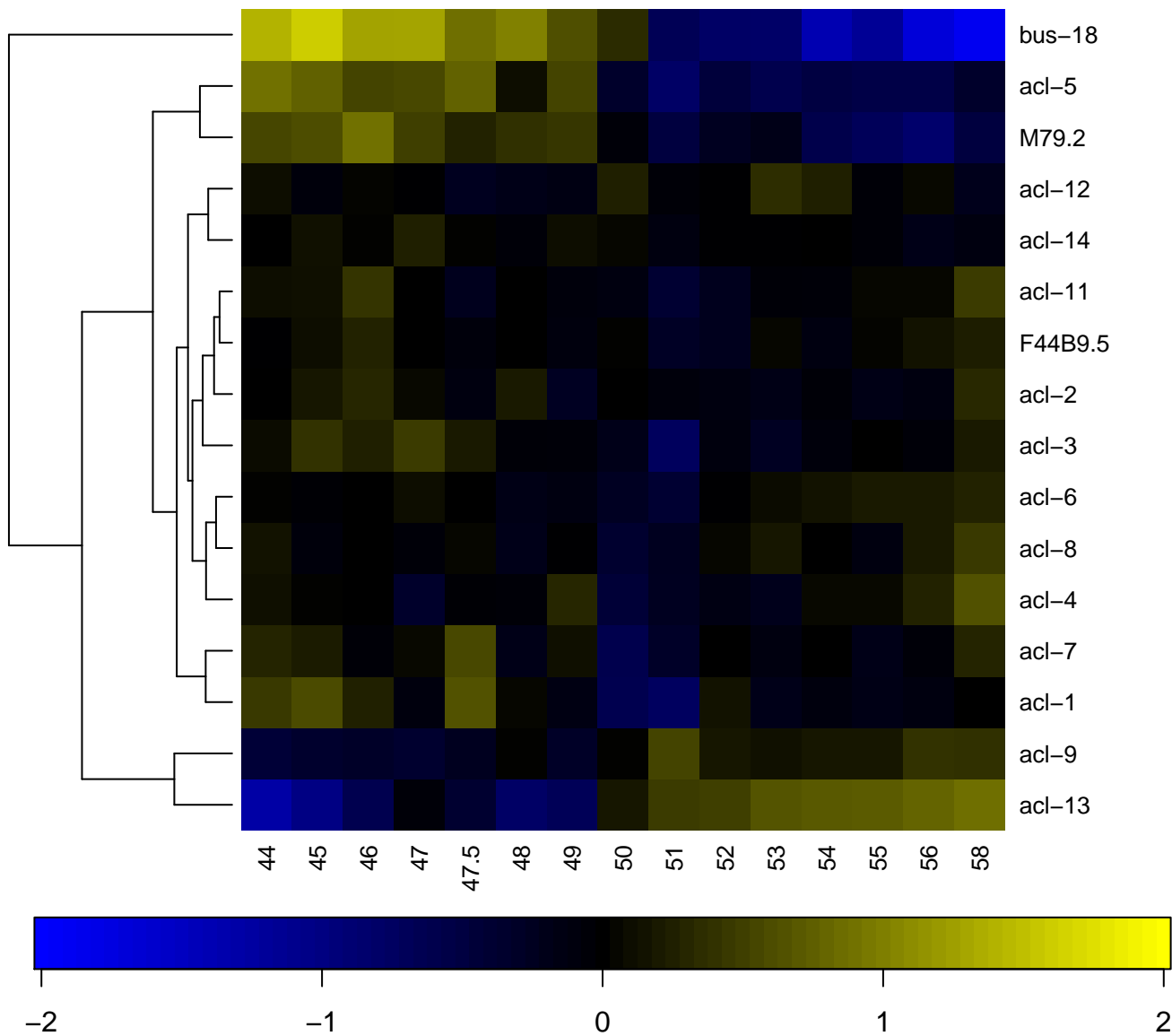
Phosphatidylinositol Kinase



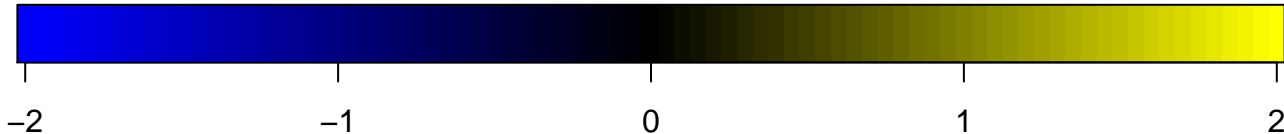
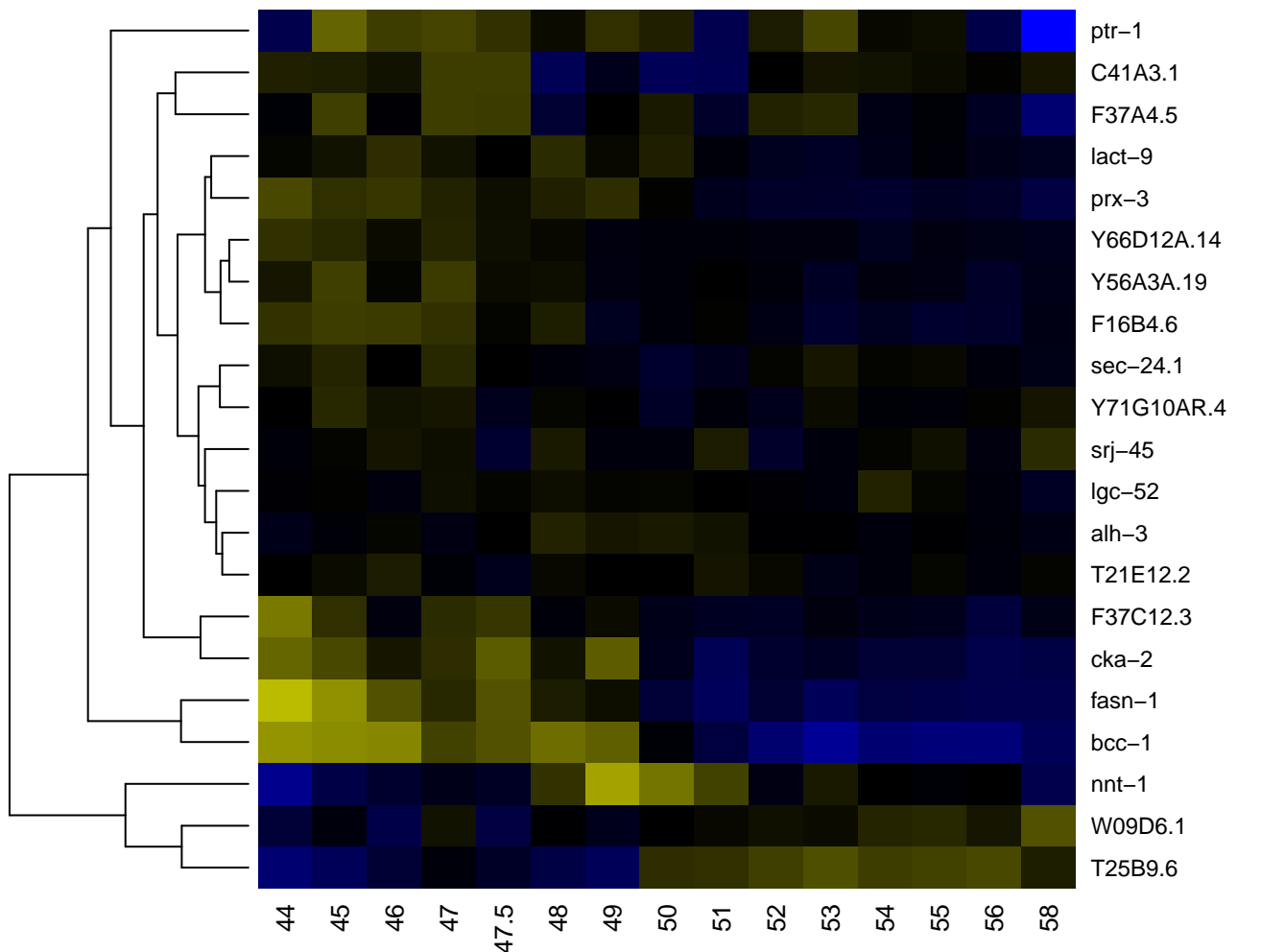
Phospholipase A2, active site



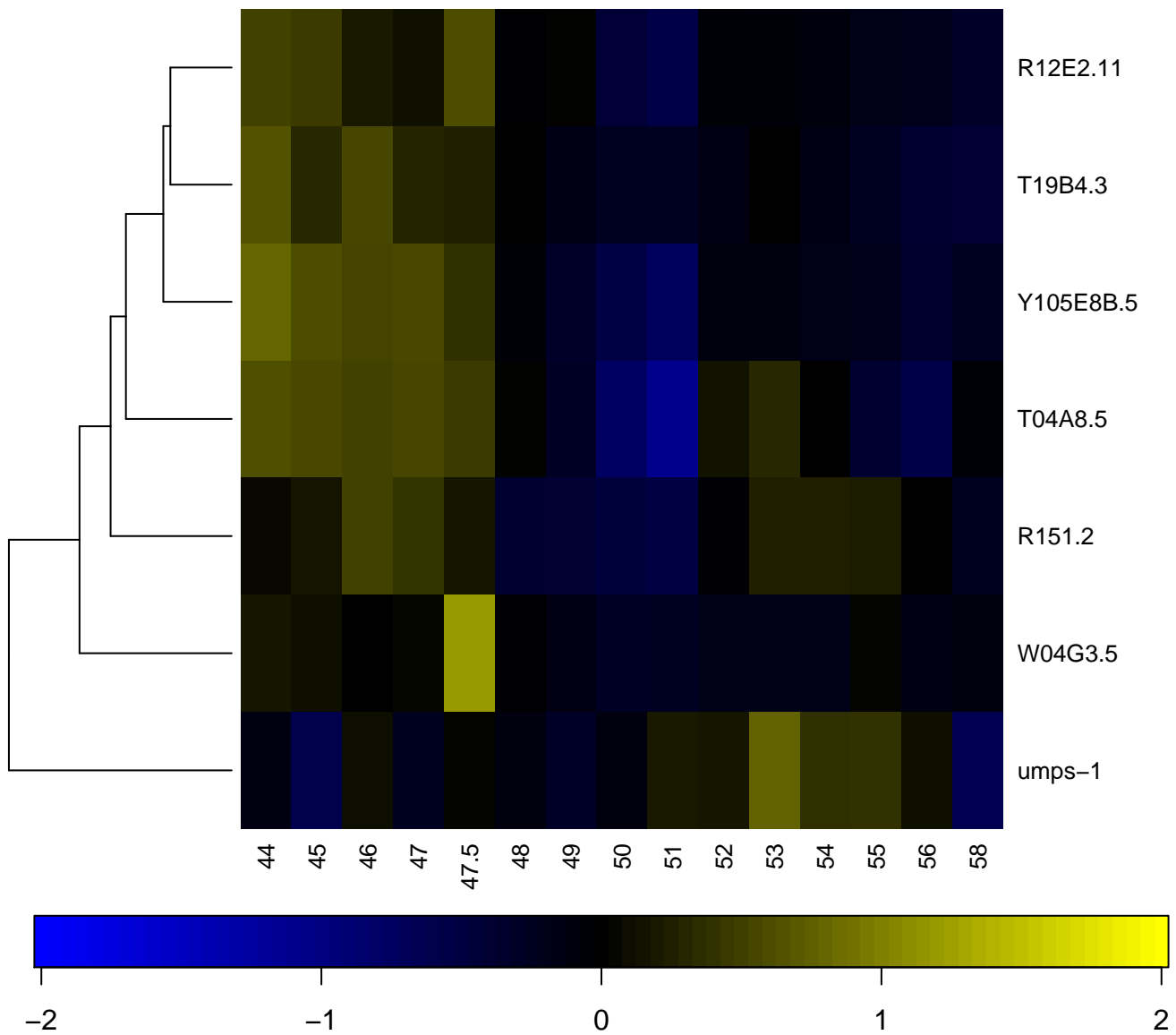
Phospholipid/glycerol acyltransferase



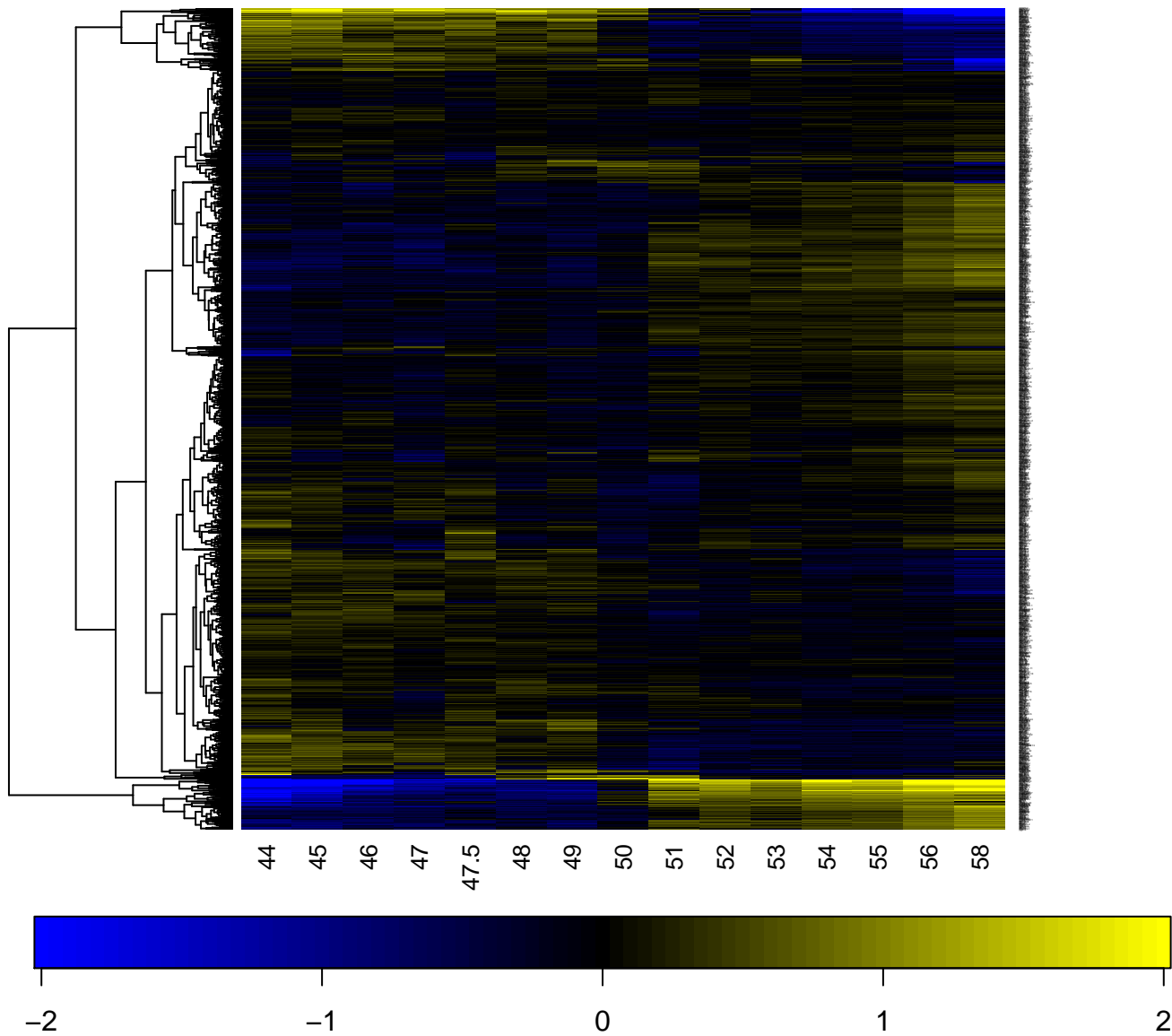
Phosphopantetheine attachment site



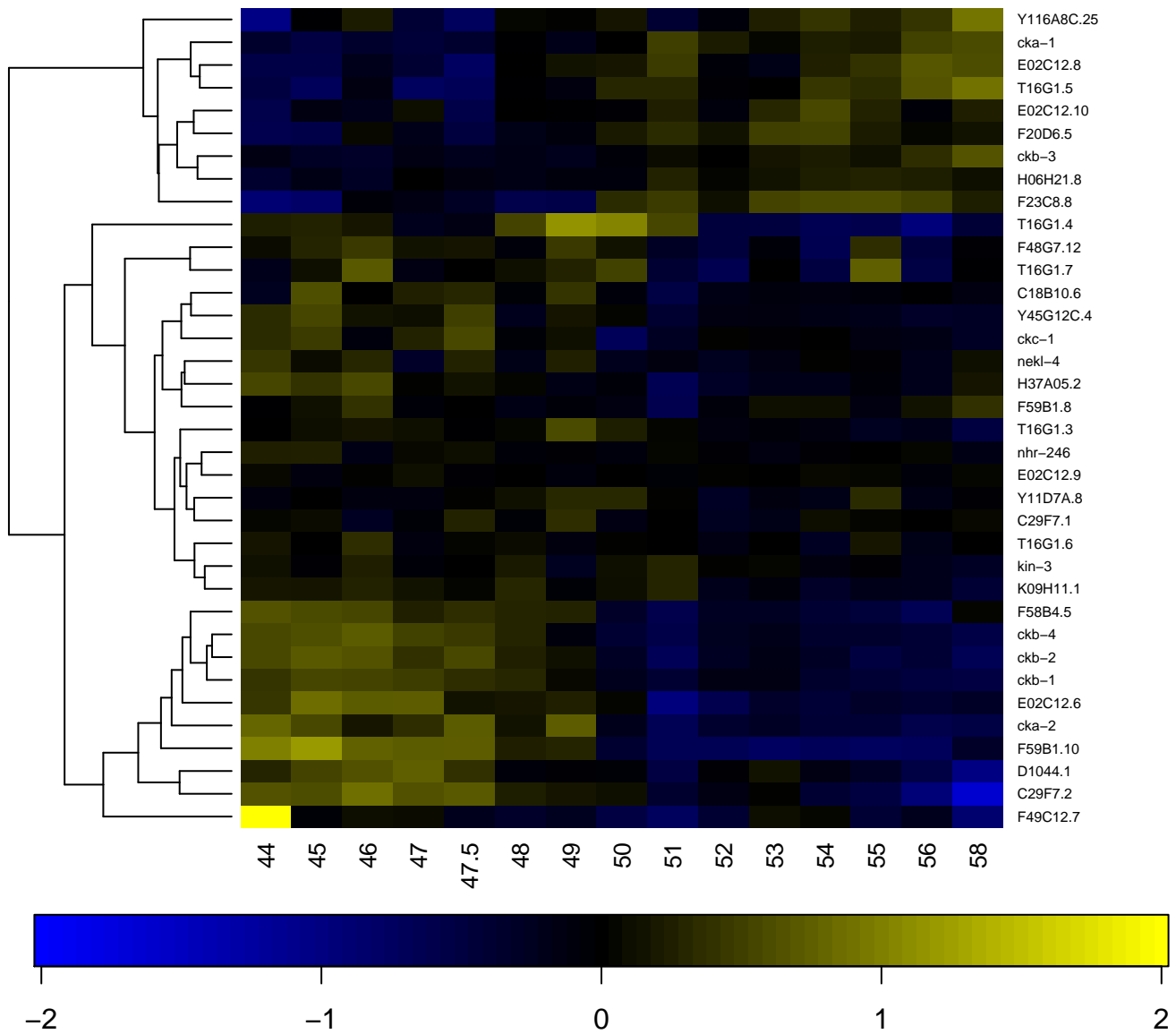
Phosphoribosyl transferase domain



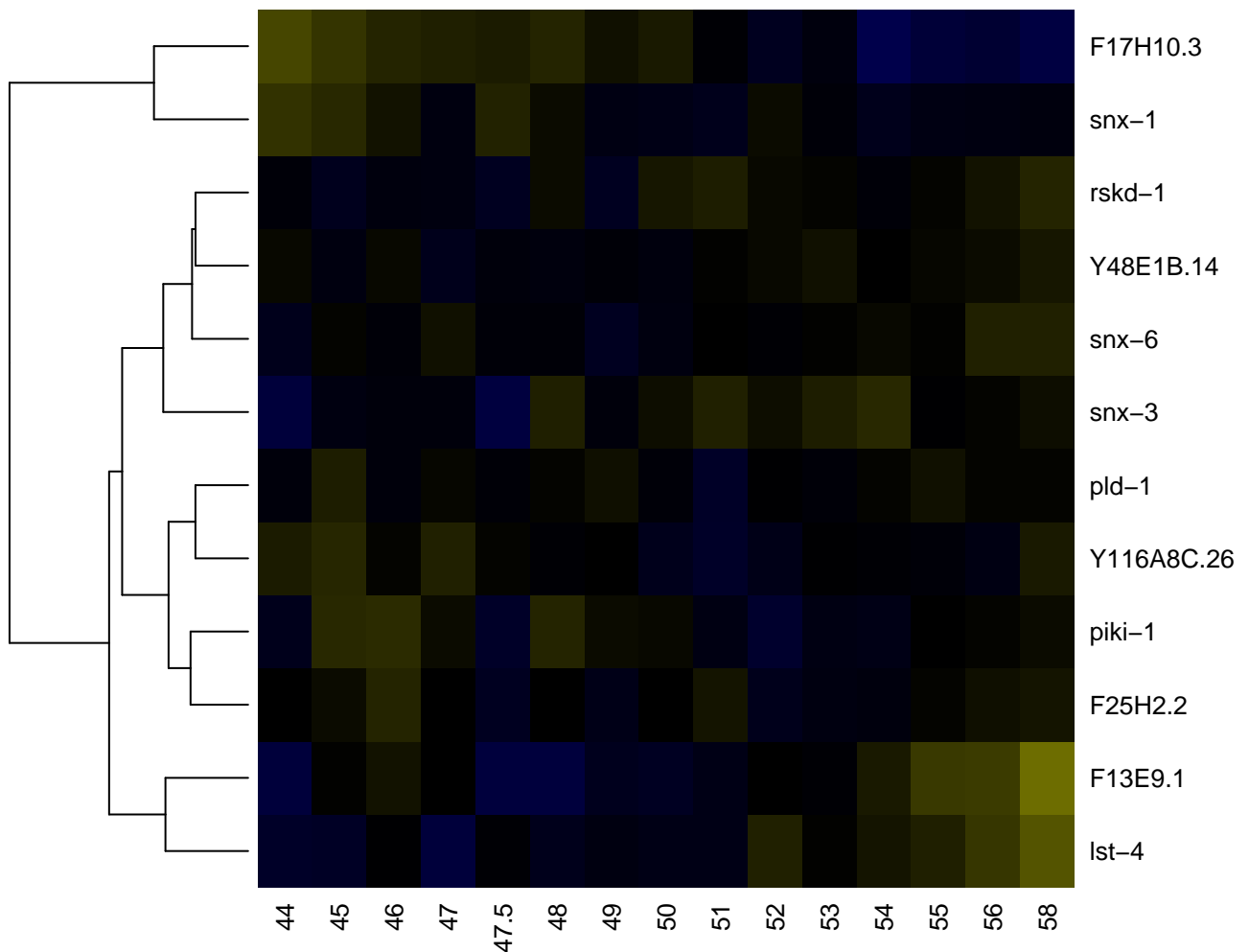
Phosphorylation site



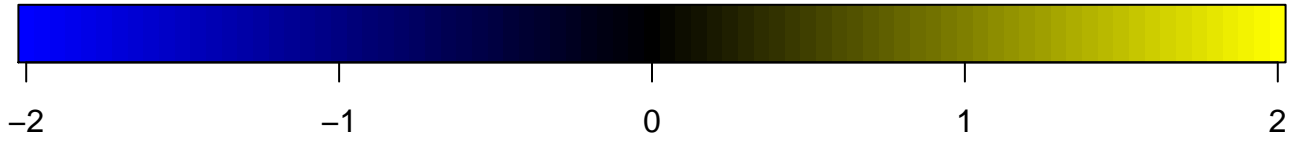
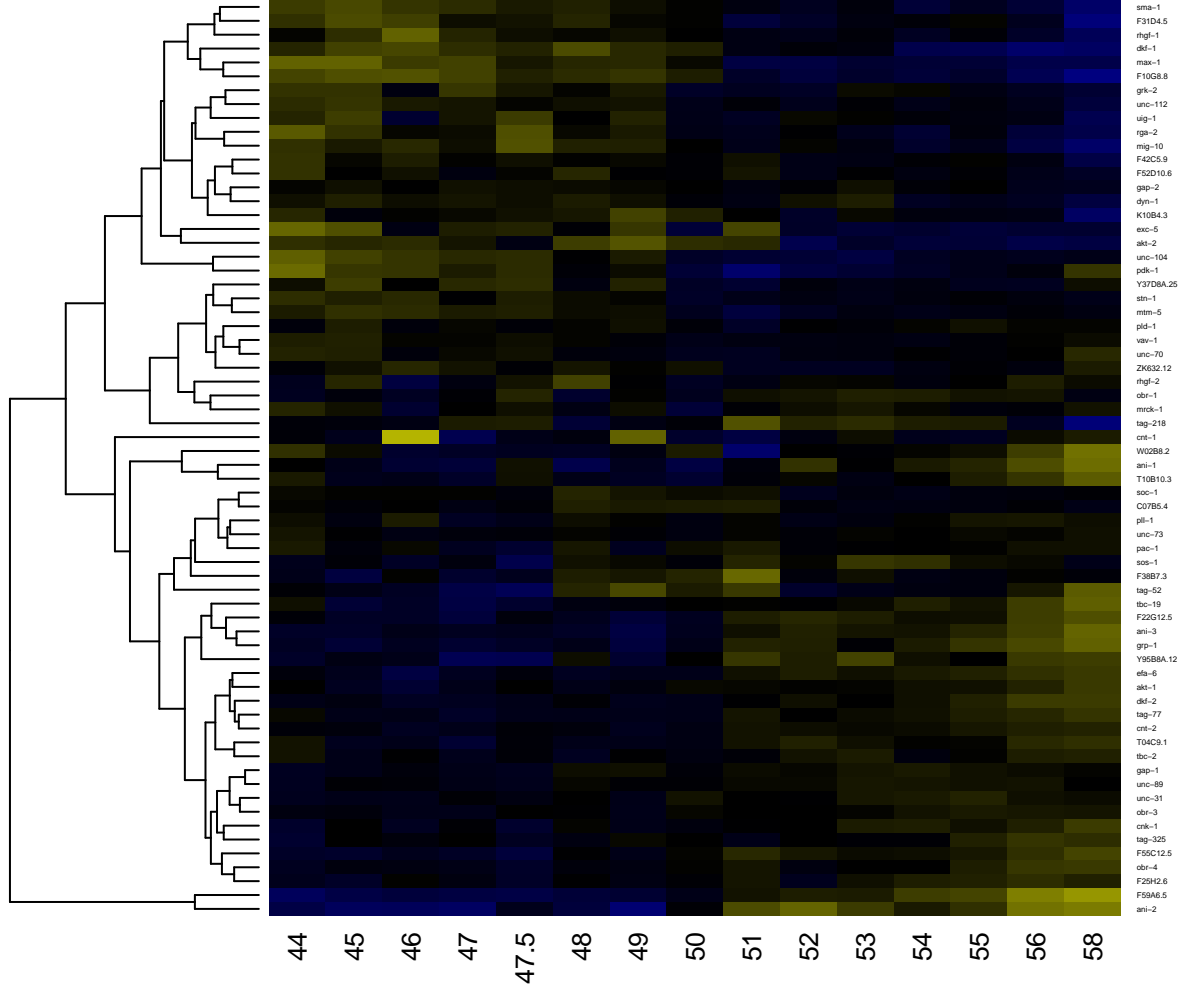
Phosphotransferase enzyme family



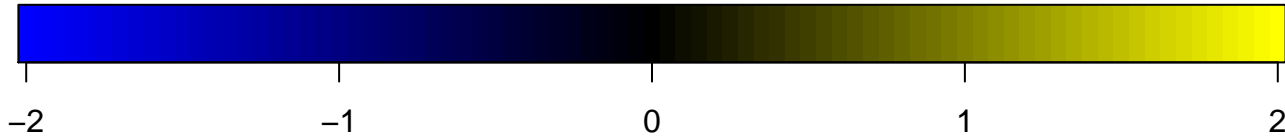
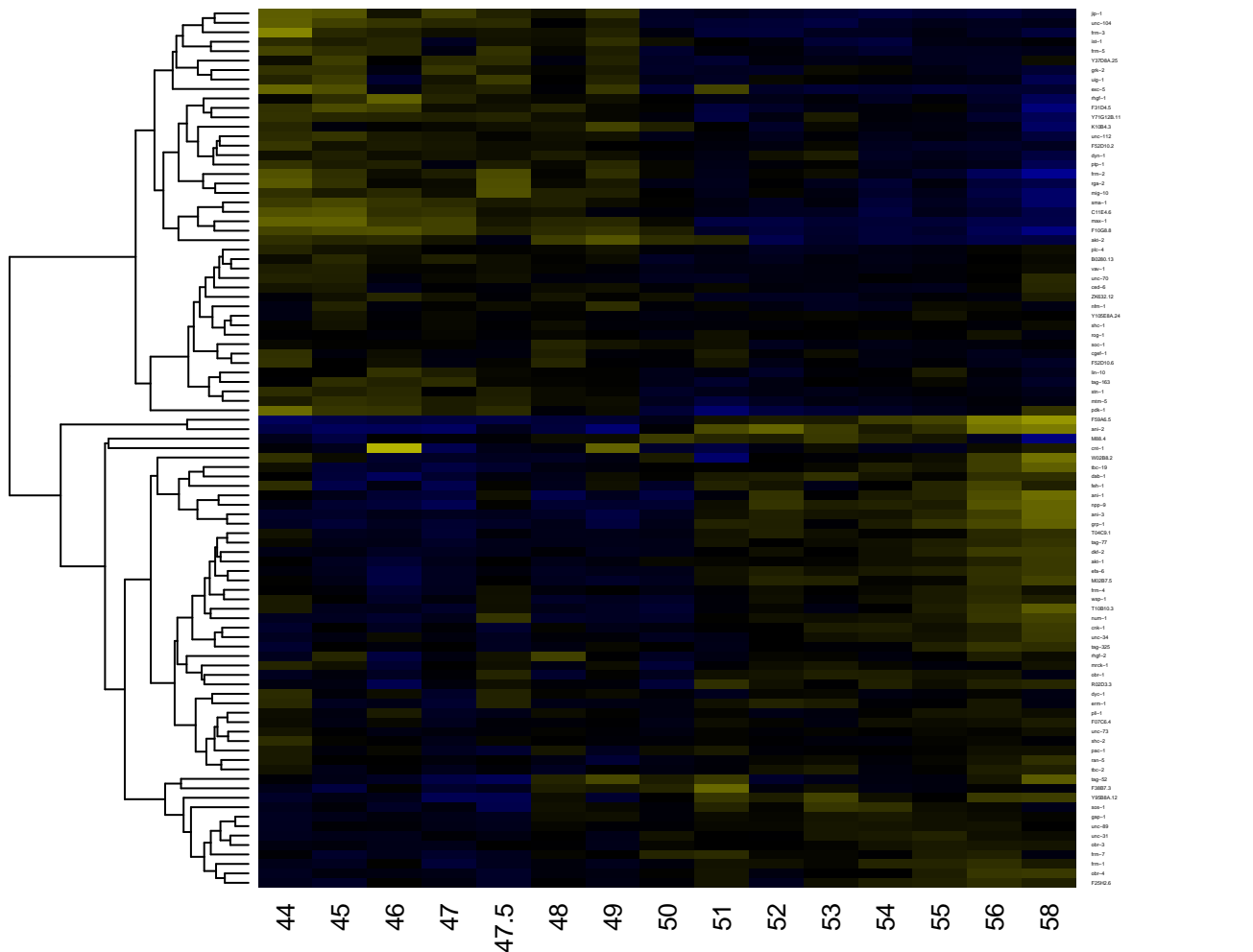
Phox-like



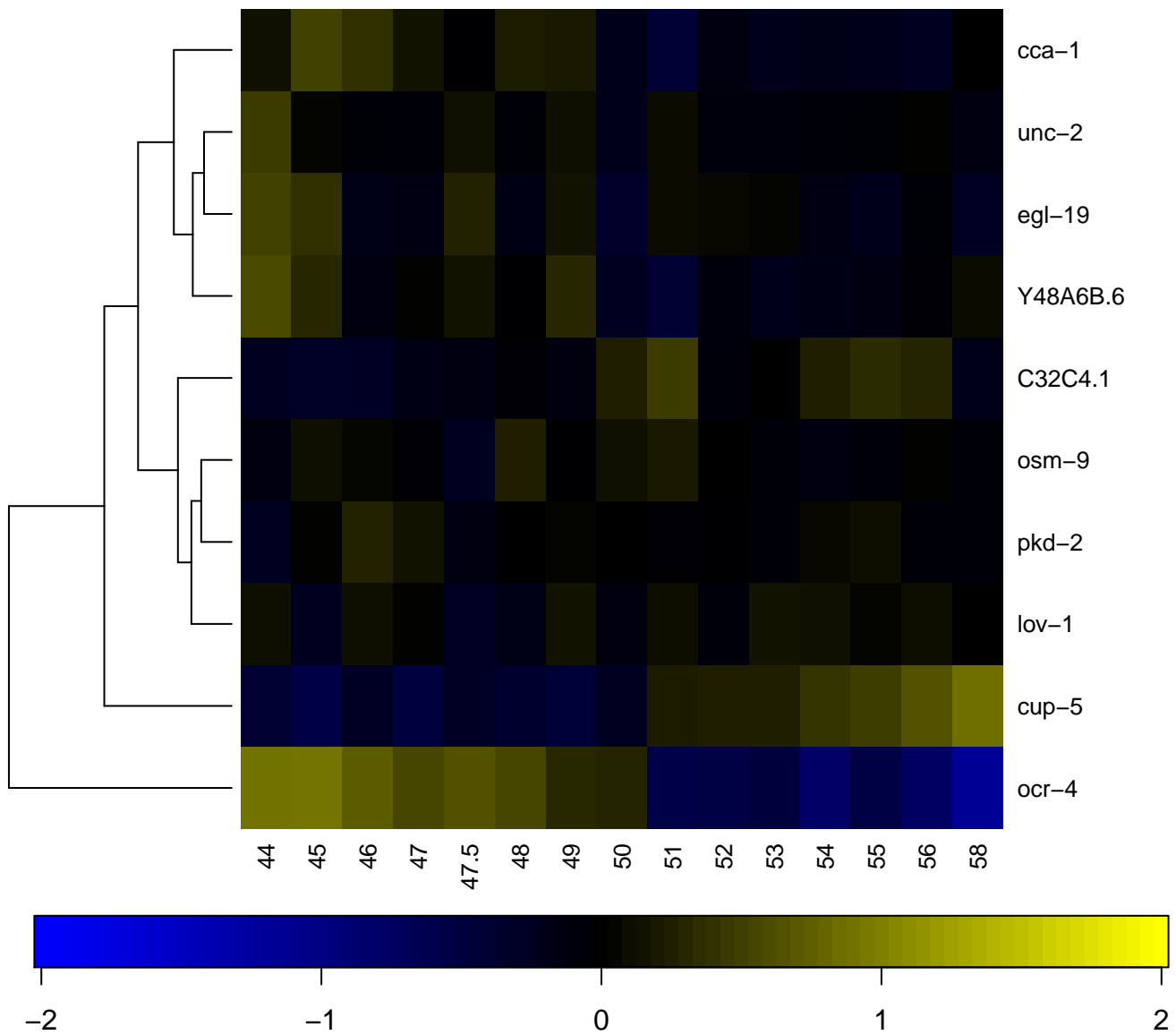
Pleckstrin homology



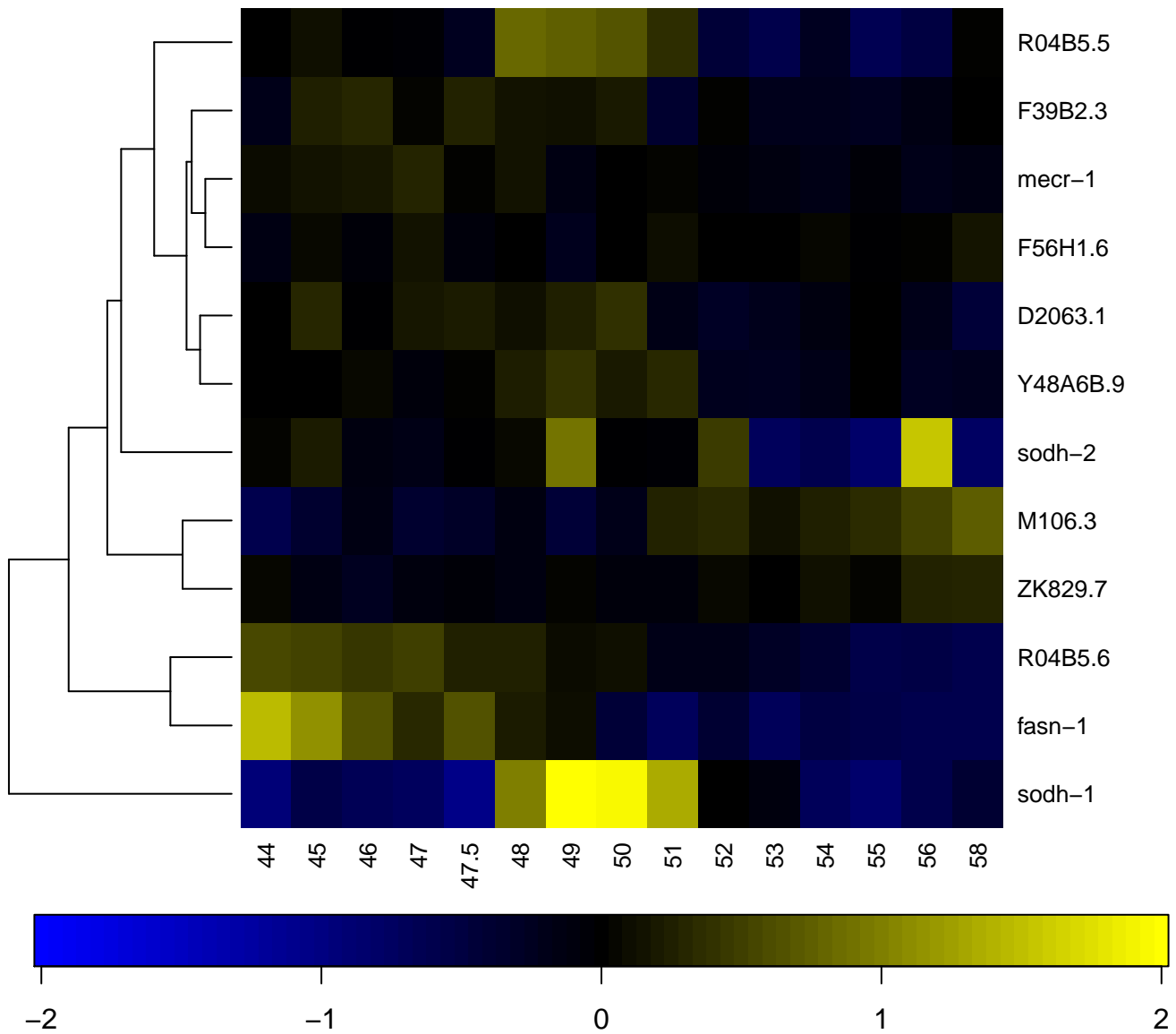
Pleckstrin homology-type



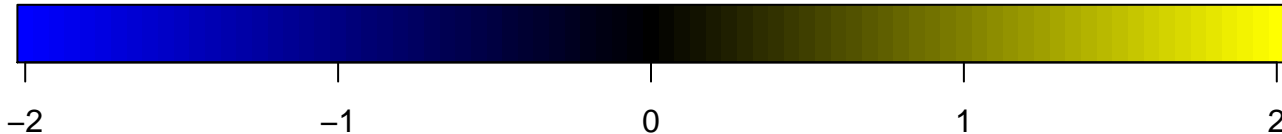
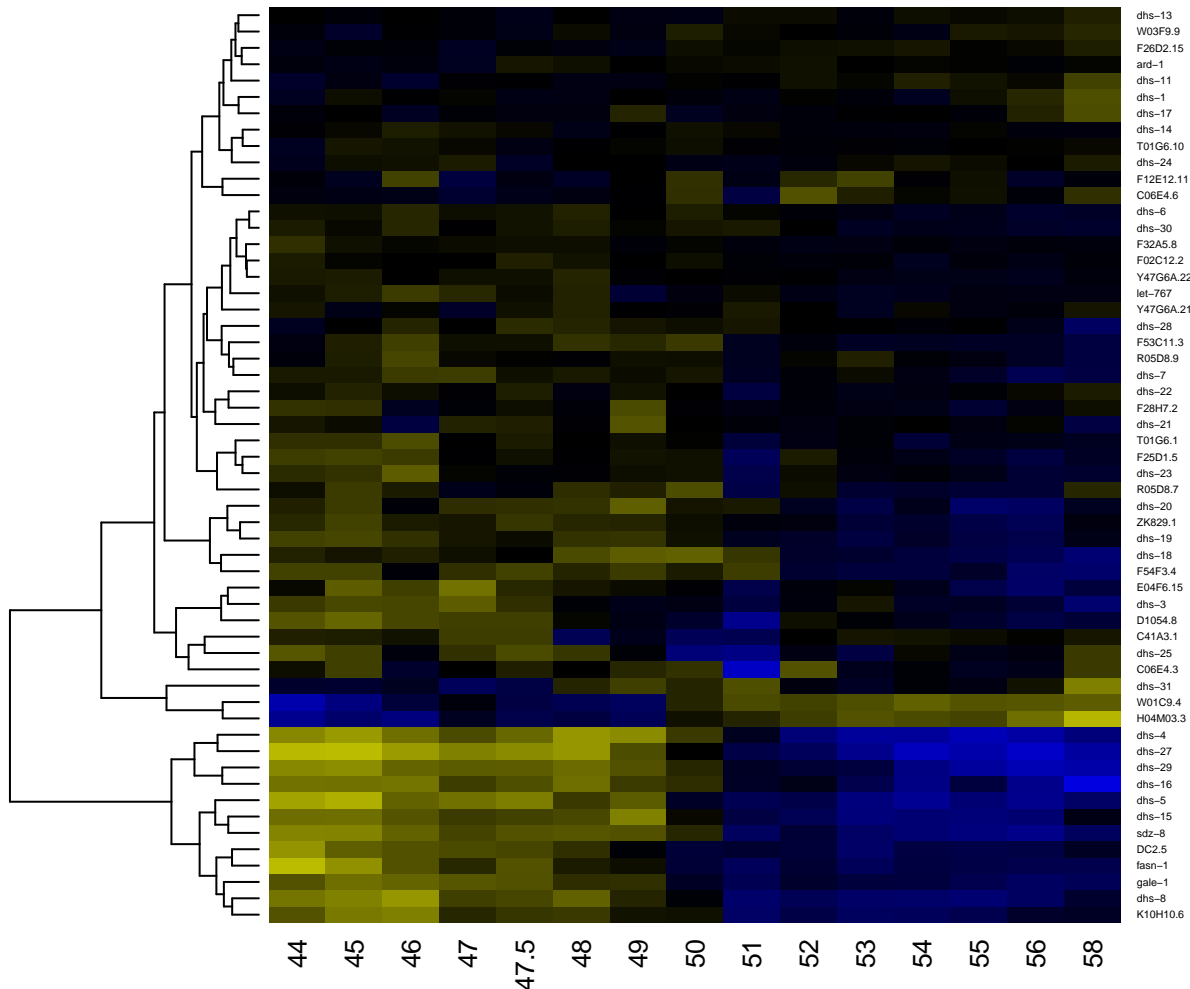
Polycystin cation channel



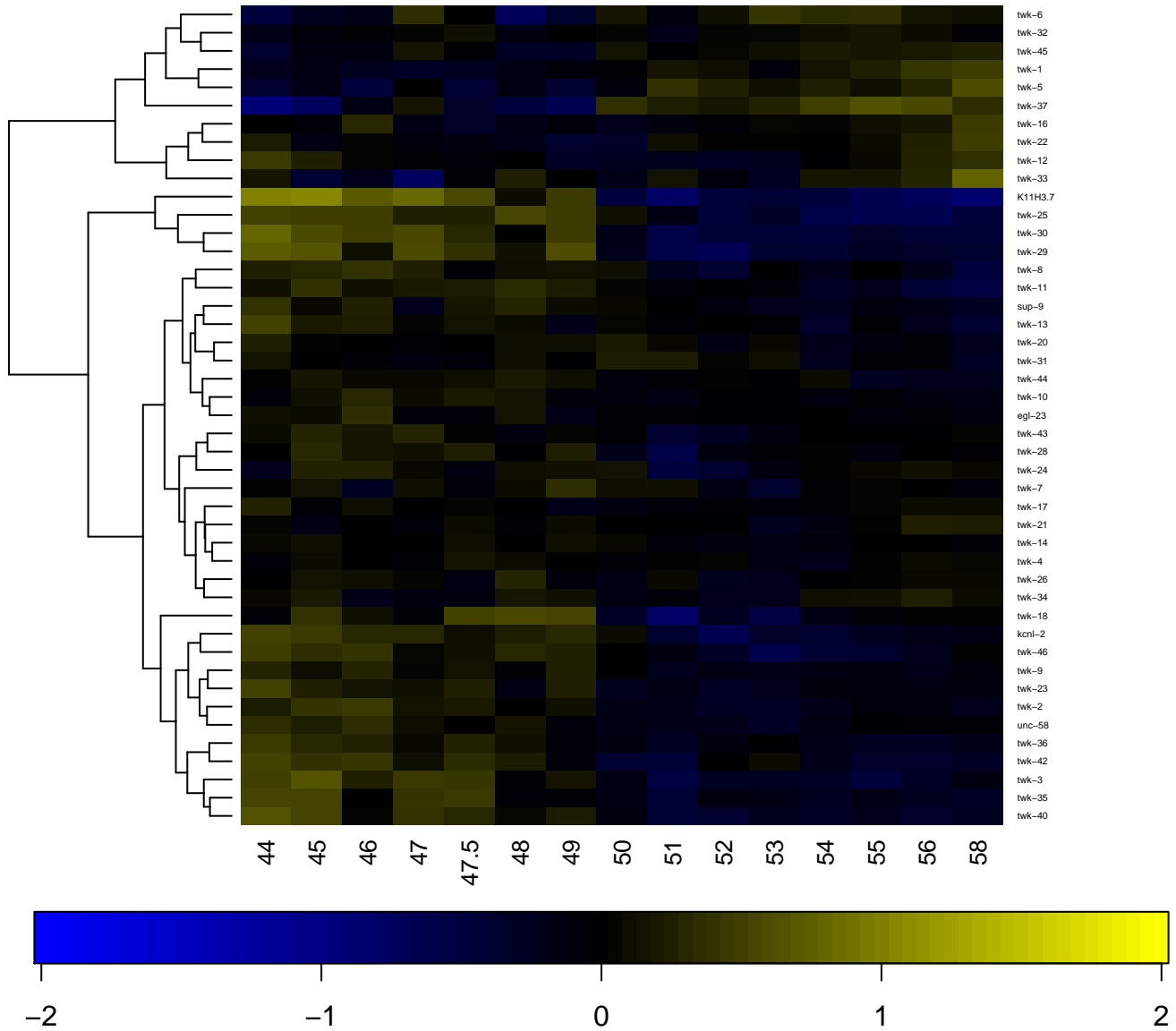
Polyketide synthase, enoylreductase



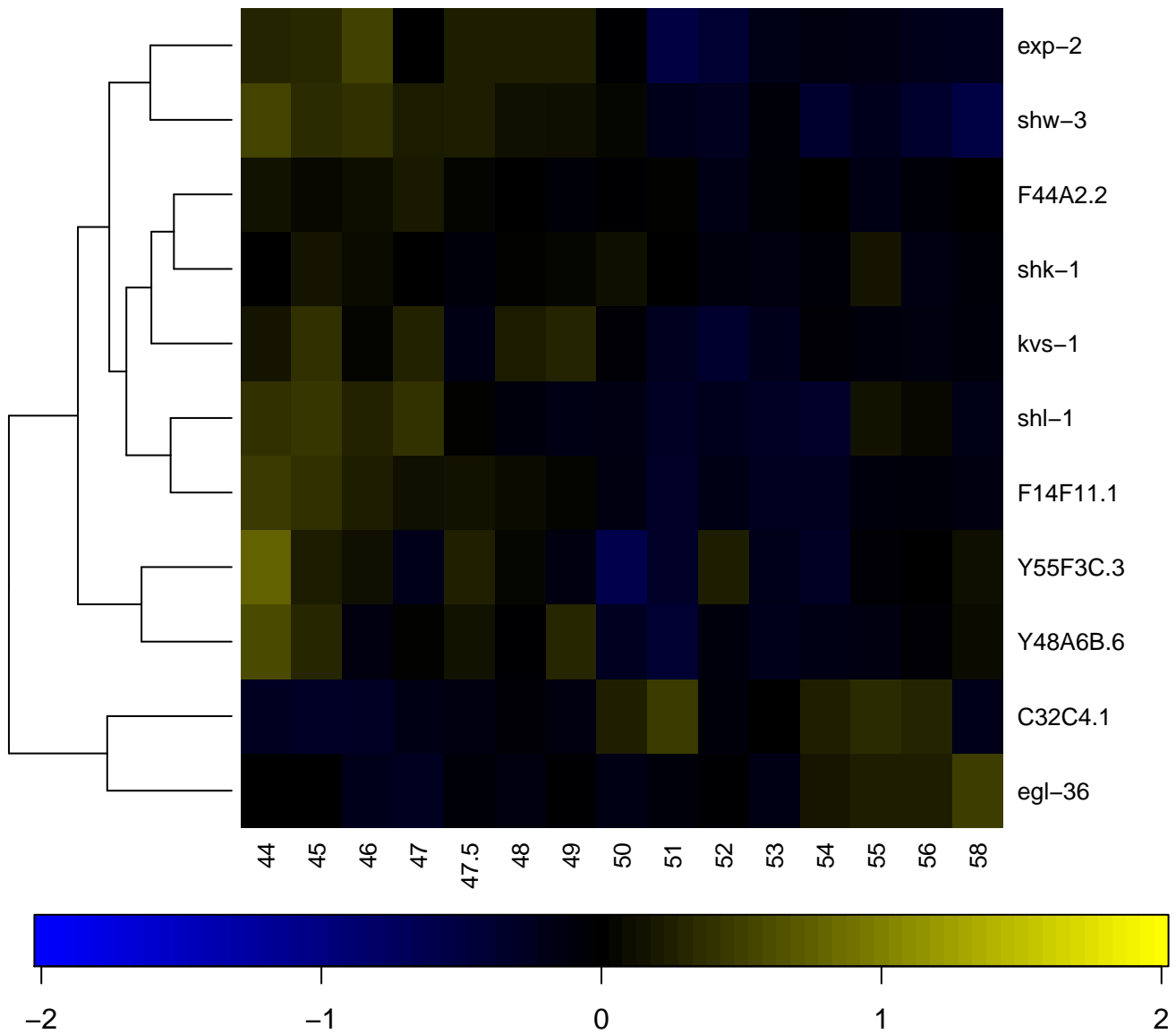
Polyketide synthase, KR



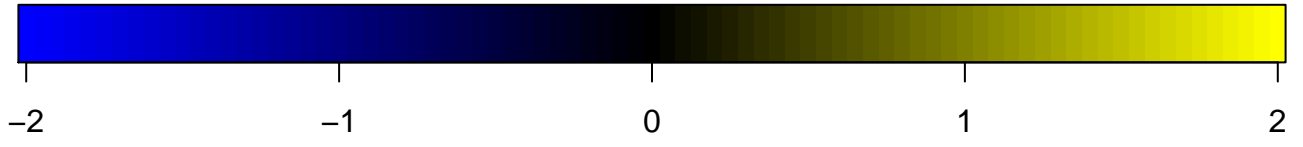
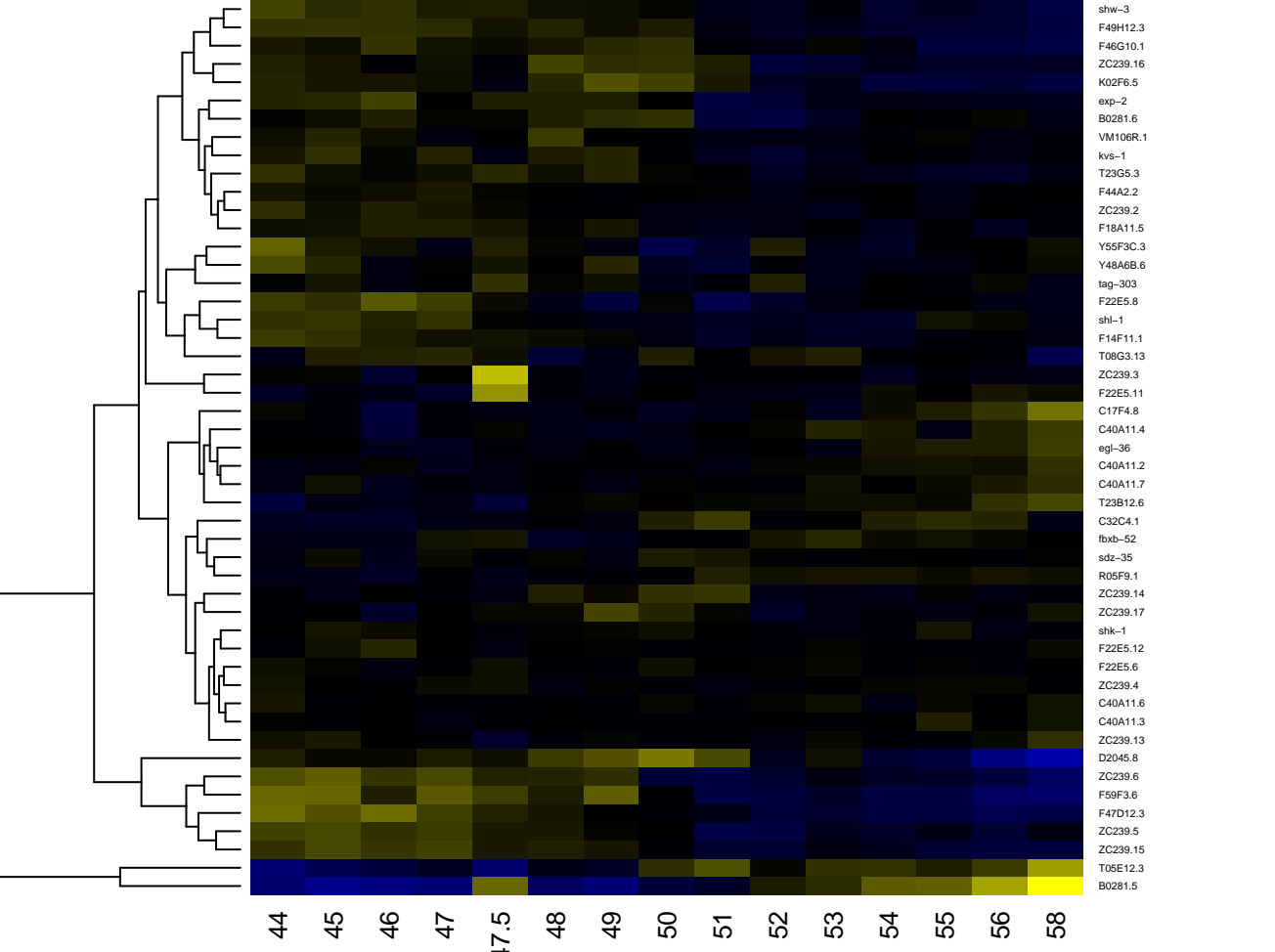
Potassium channel, two pore-domain



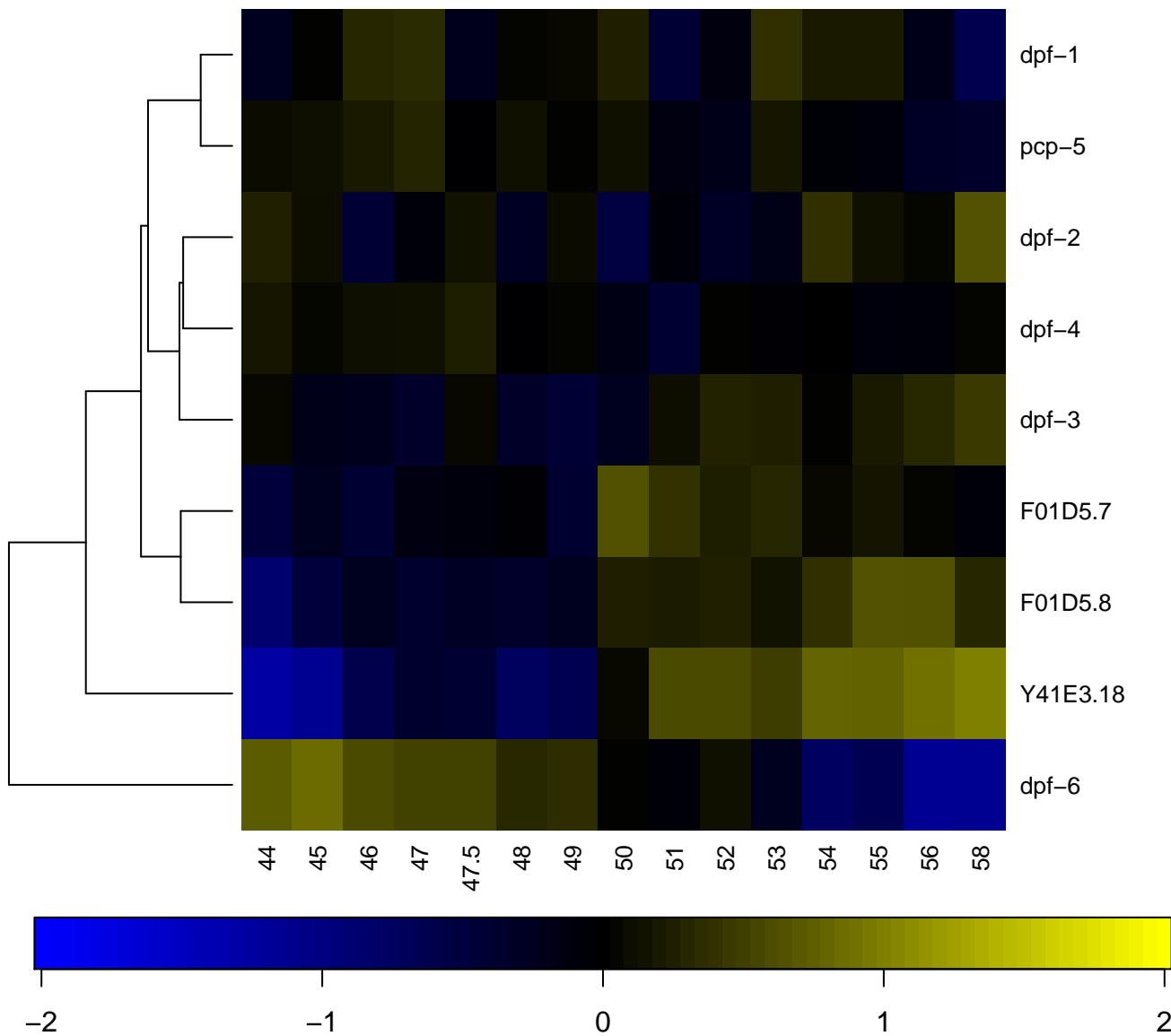
Potassium channel, voltage dependent, Kv



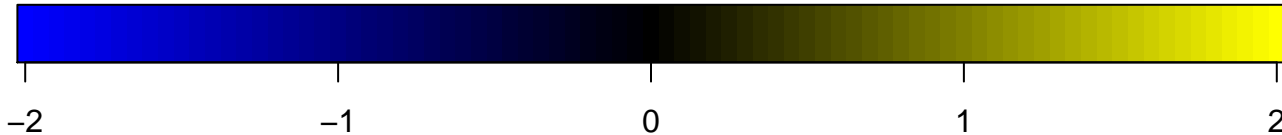
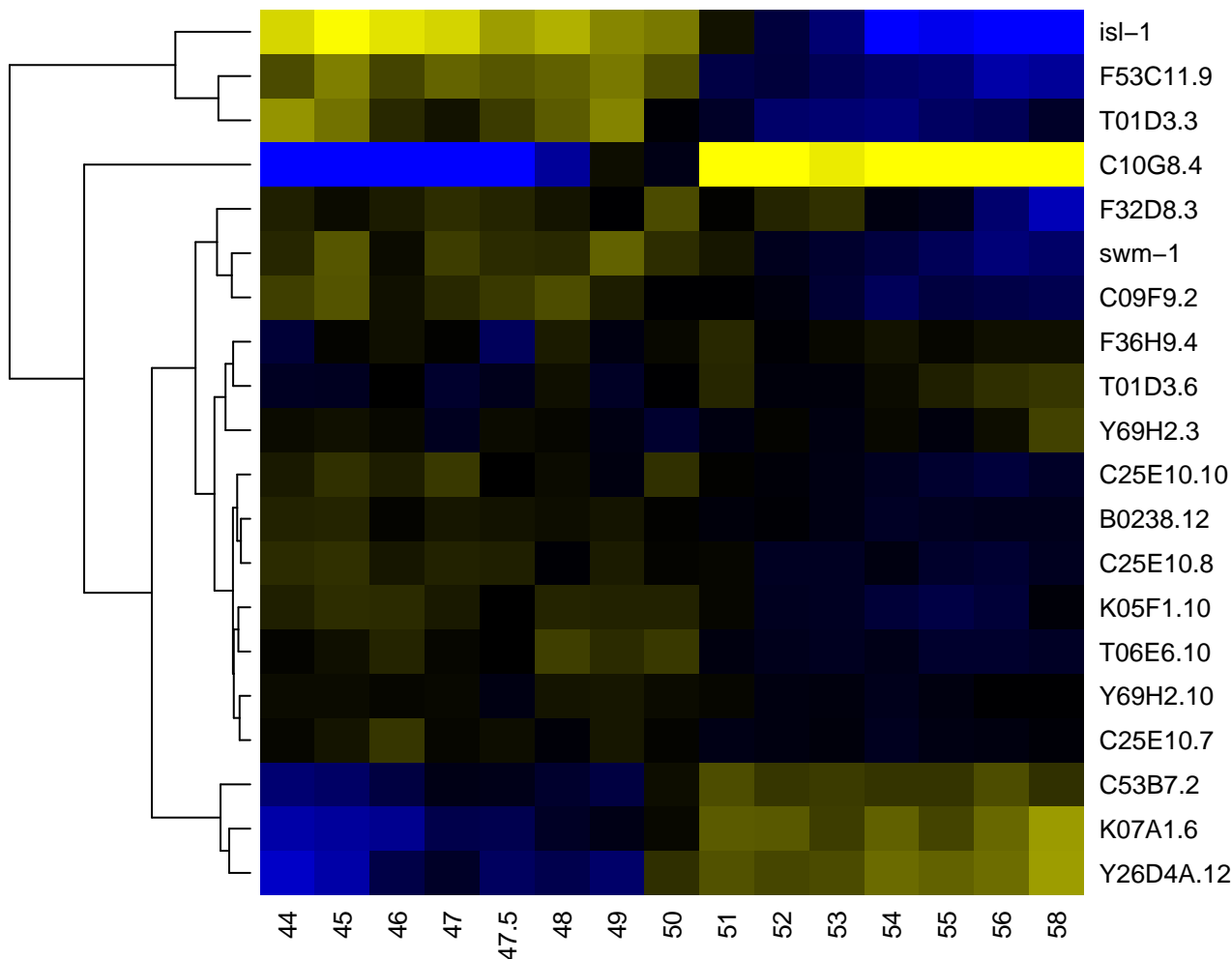
Potassium channel, voltage dependent, Kv, tetramerisatio



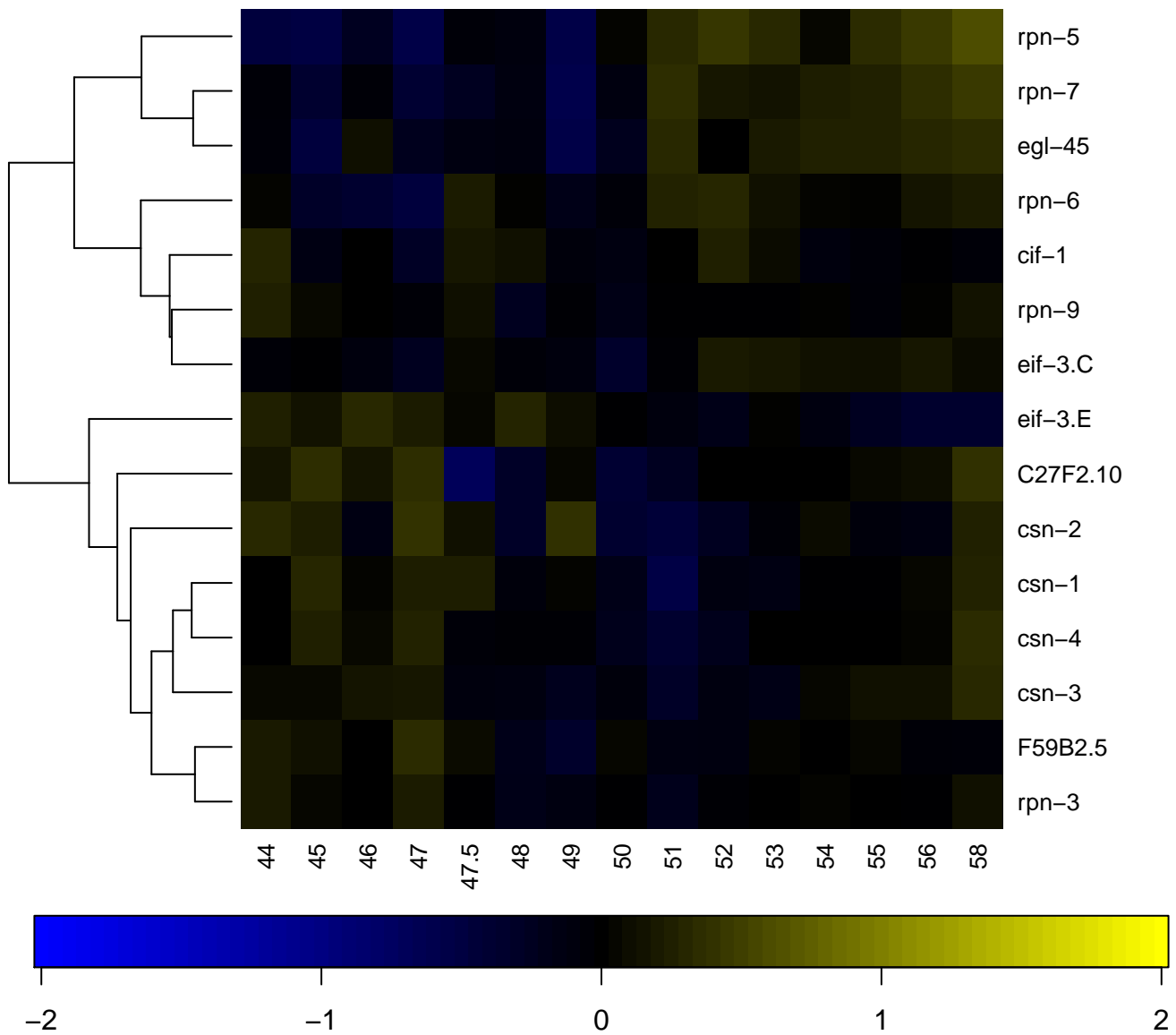
Prolyl oligopeptidase family



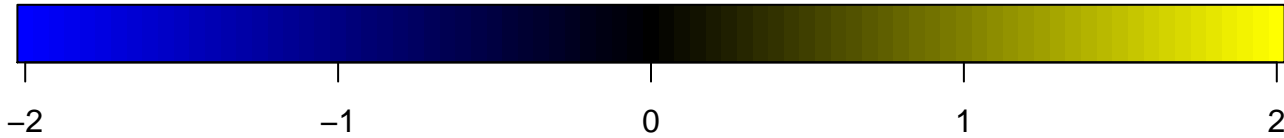
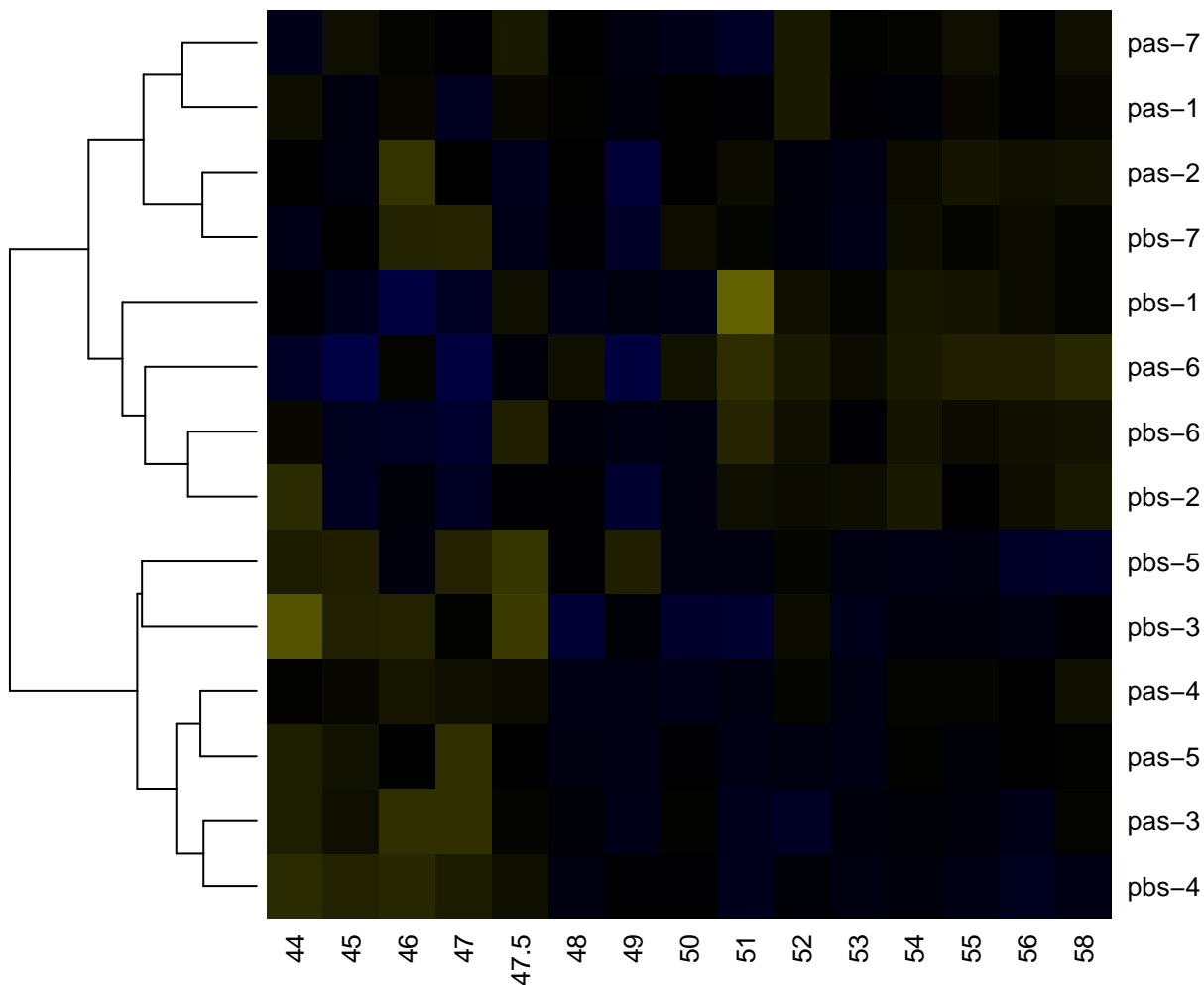
Protease inhibitor I8, cysteine-rich trypsin inhibitor-like



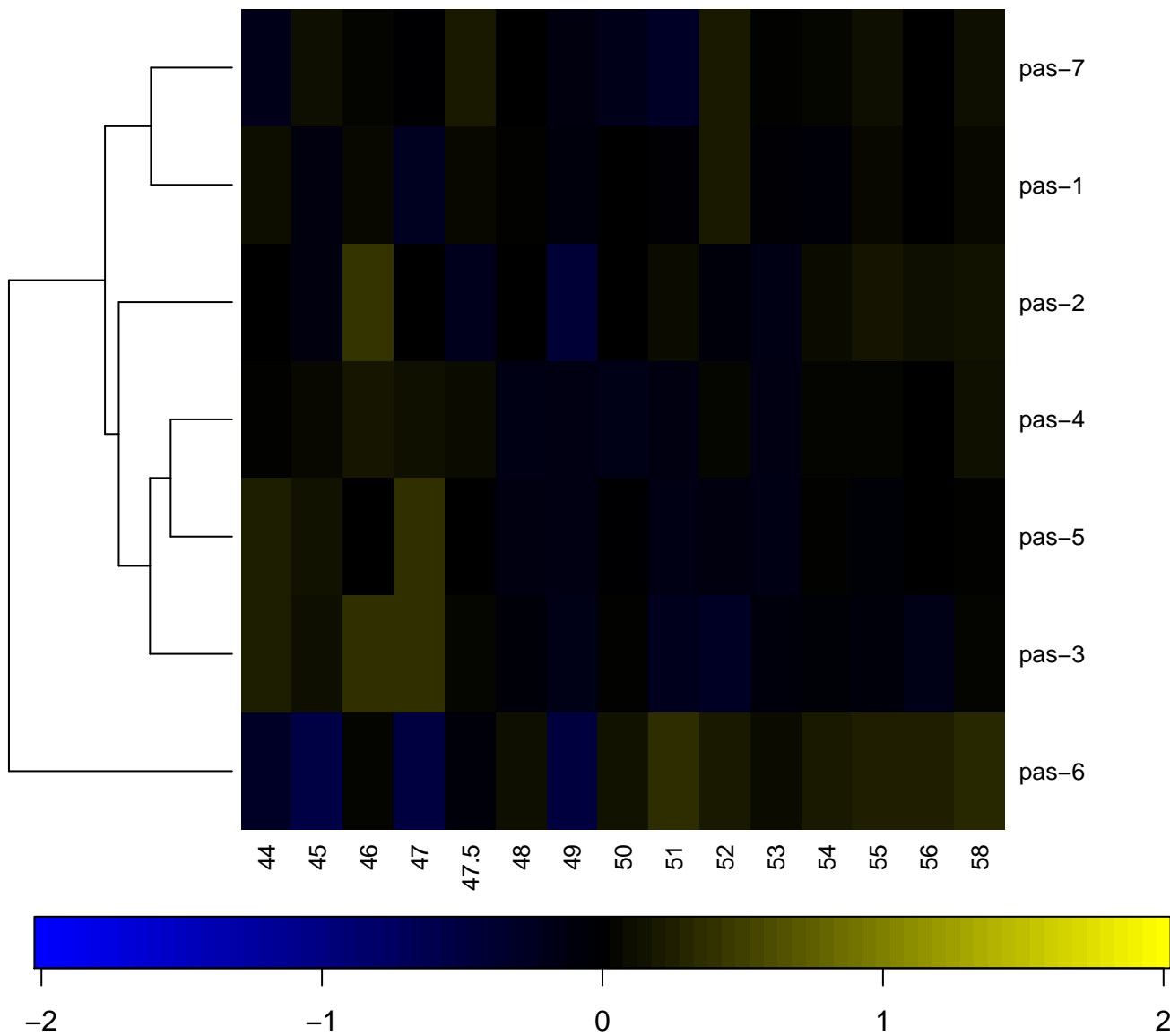
Proteasome component (PCI) domain



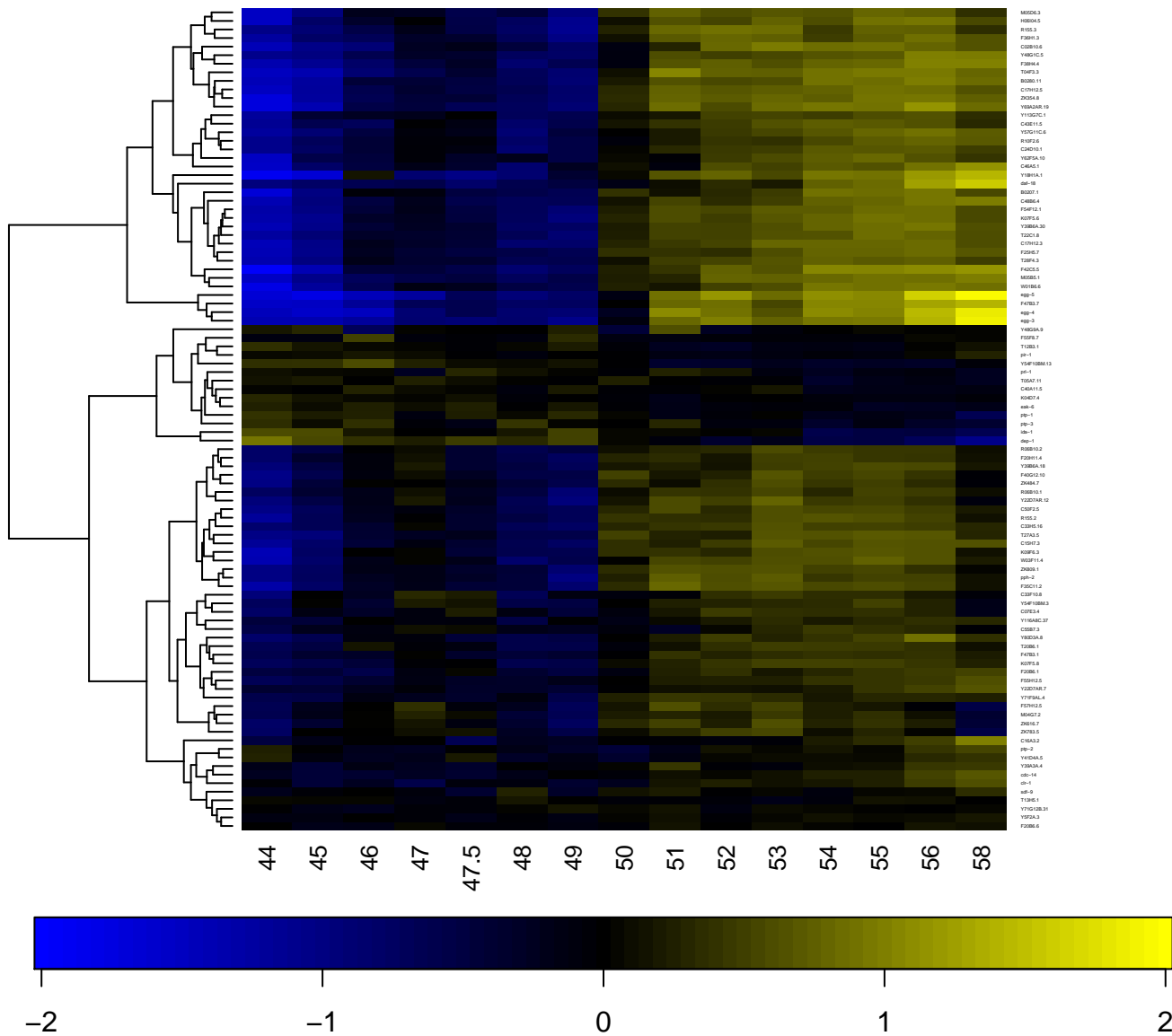
Proteasome subunit



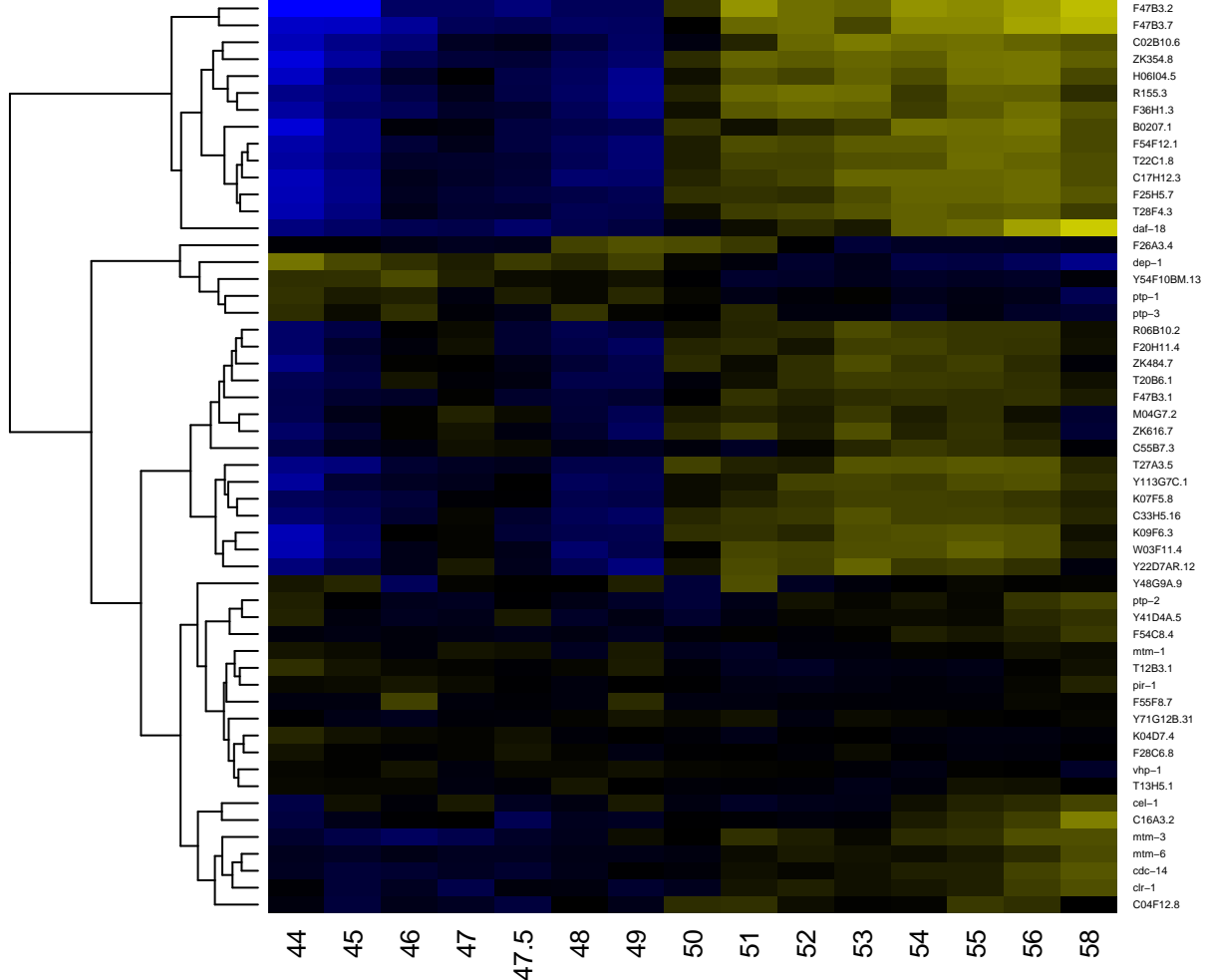
Proteasome subunit A N-terminal signature



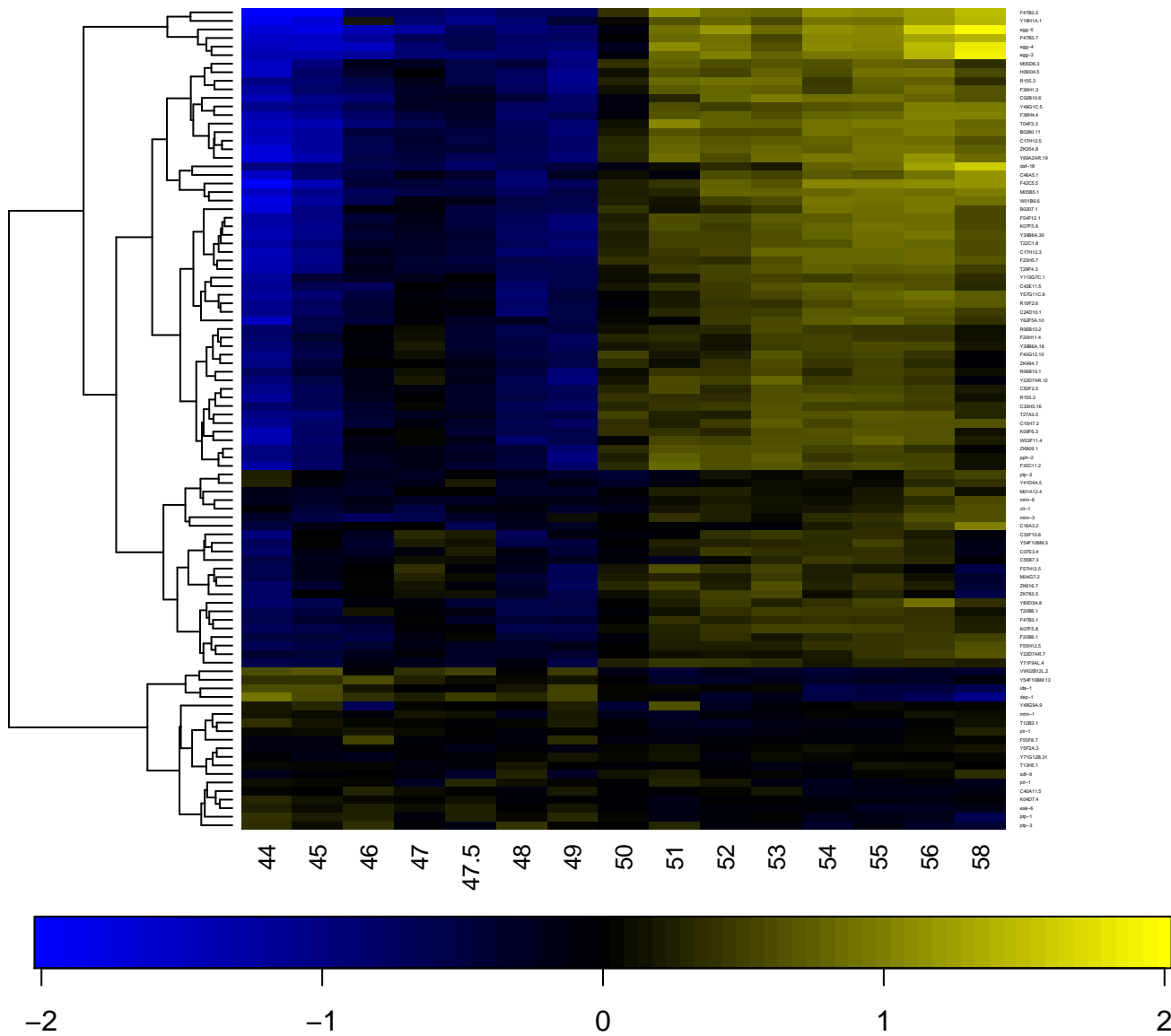
Protein-tyrosine phosphatase



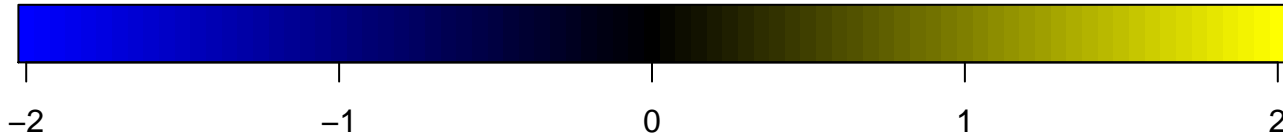
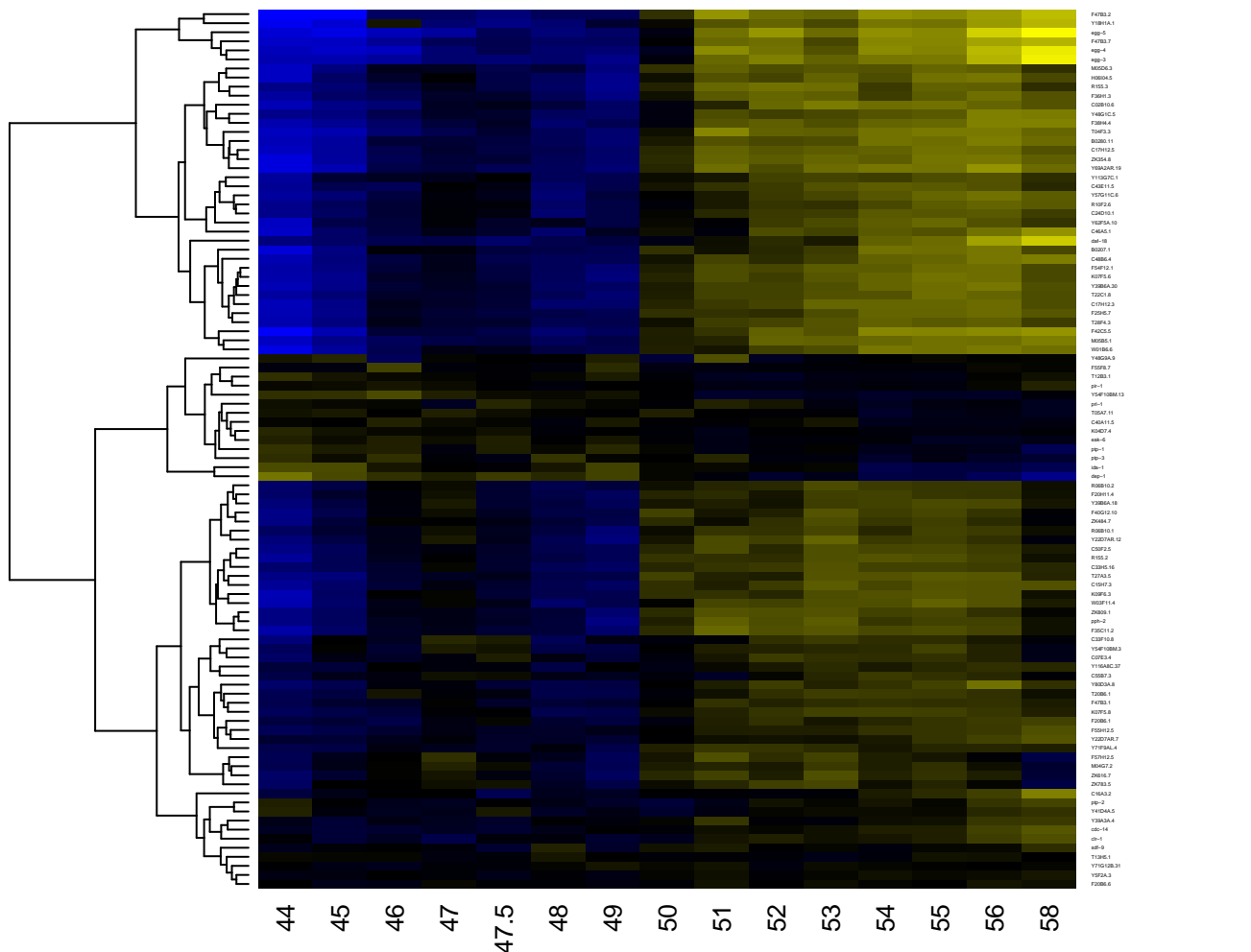
Protein-tyrosine phosphatase, active site



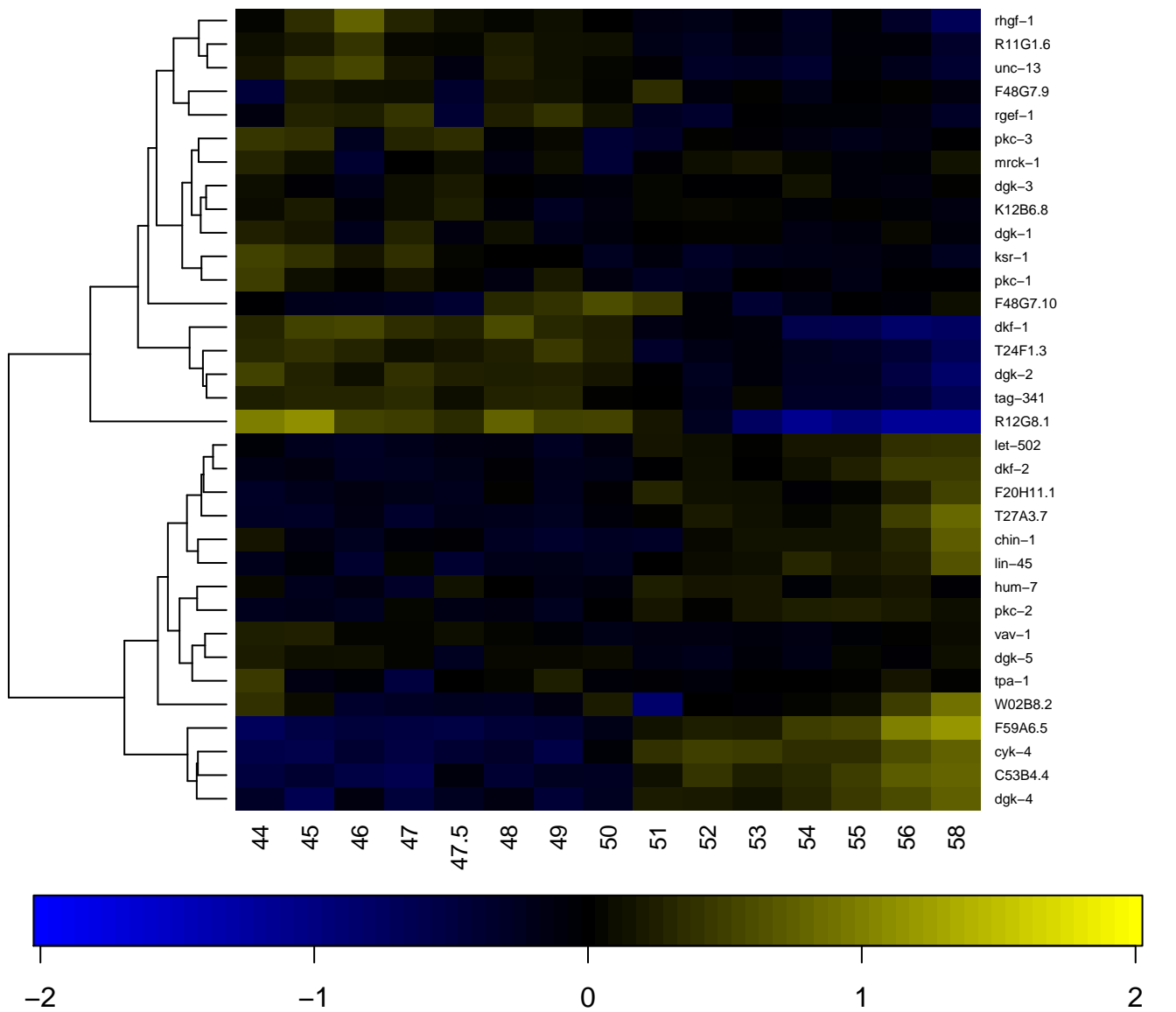
Protein-tyrosine phosphatase, catalytic



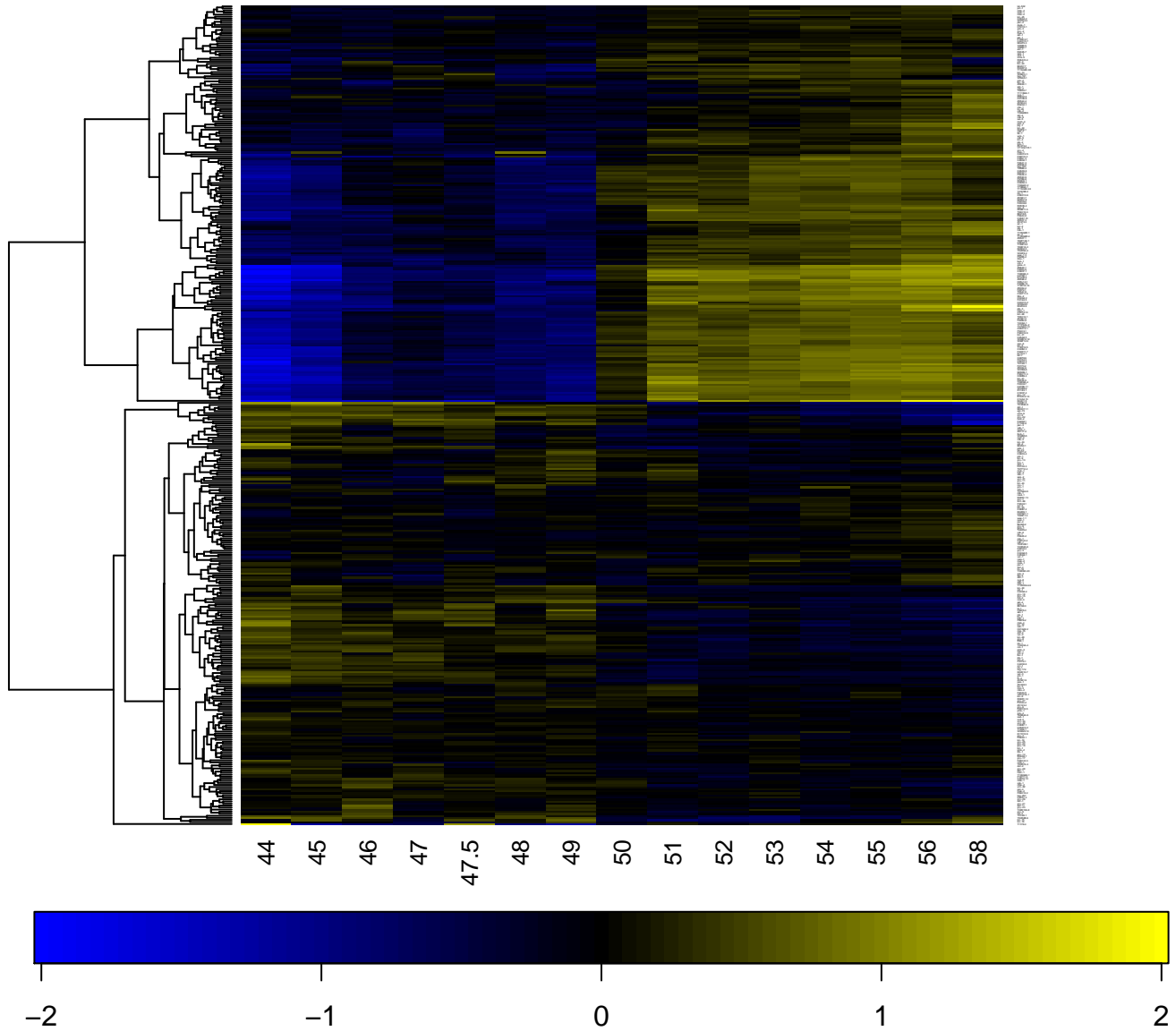
Protein-tyrosine phosphatase, receptor/non-receptor type



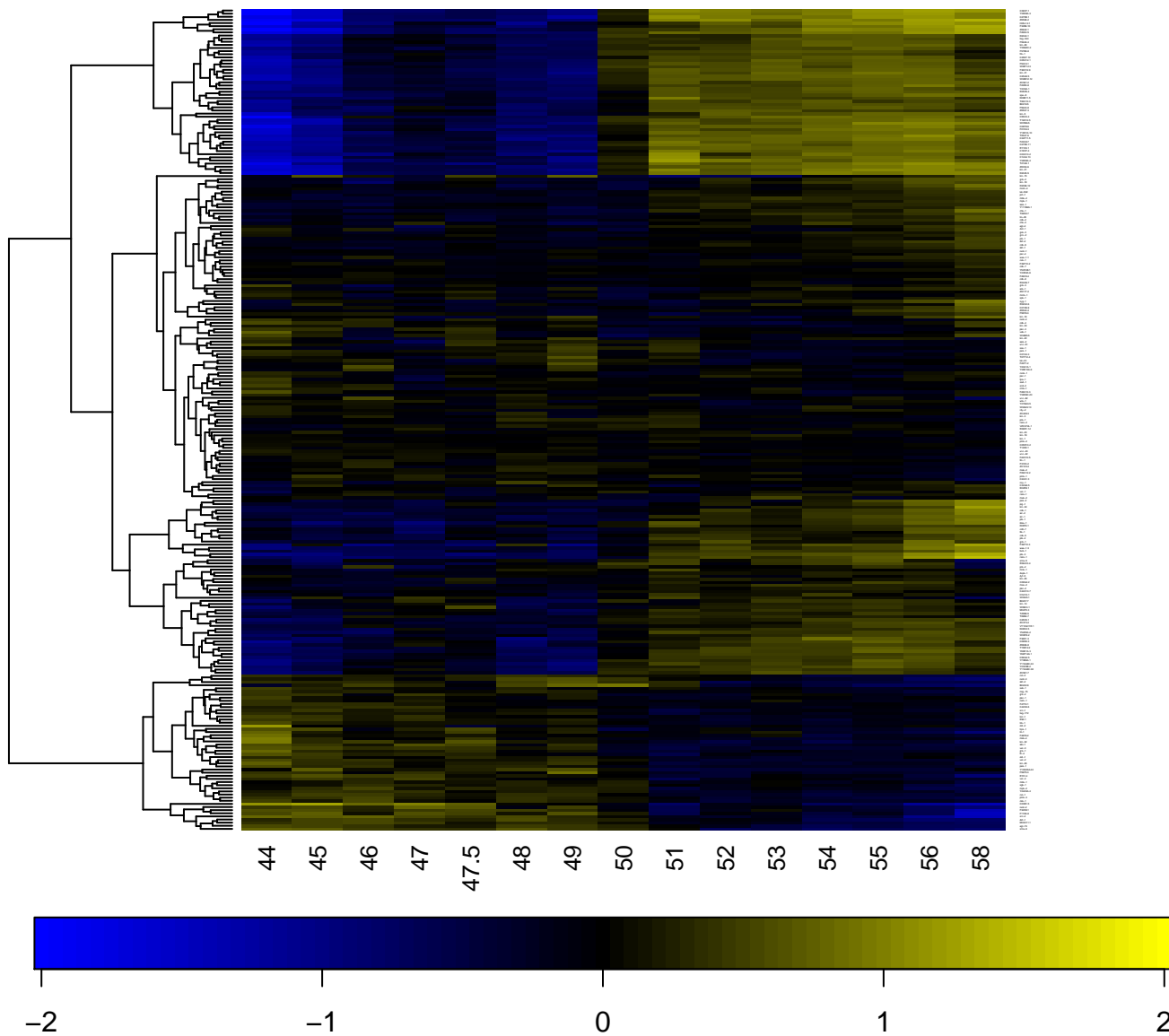
Protein kinase C-like, phorbol ester/diacylglycerol binding



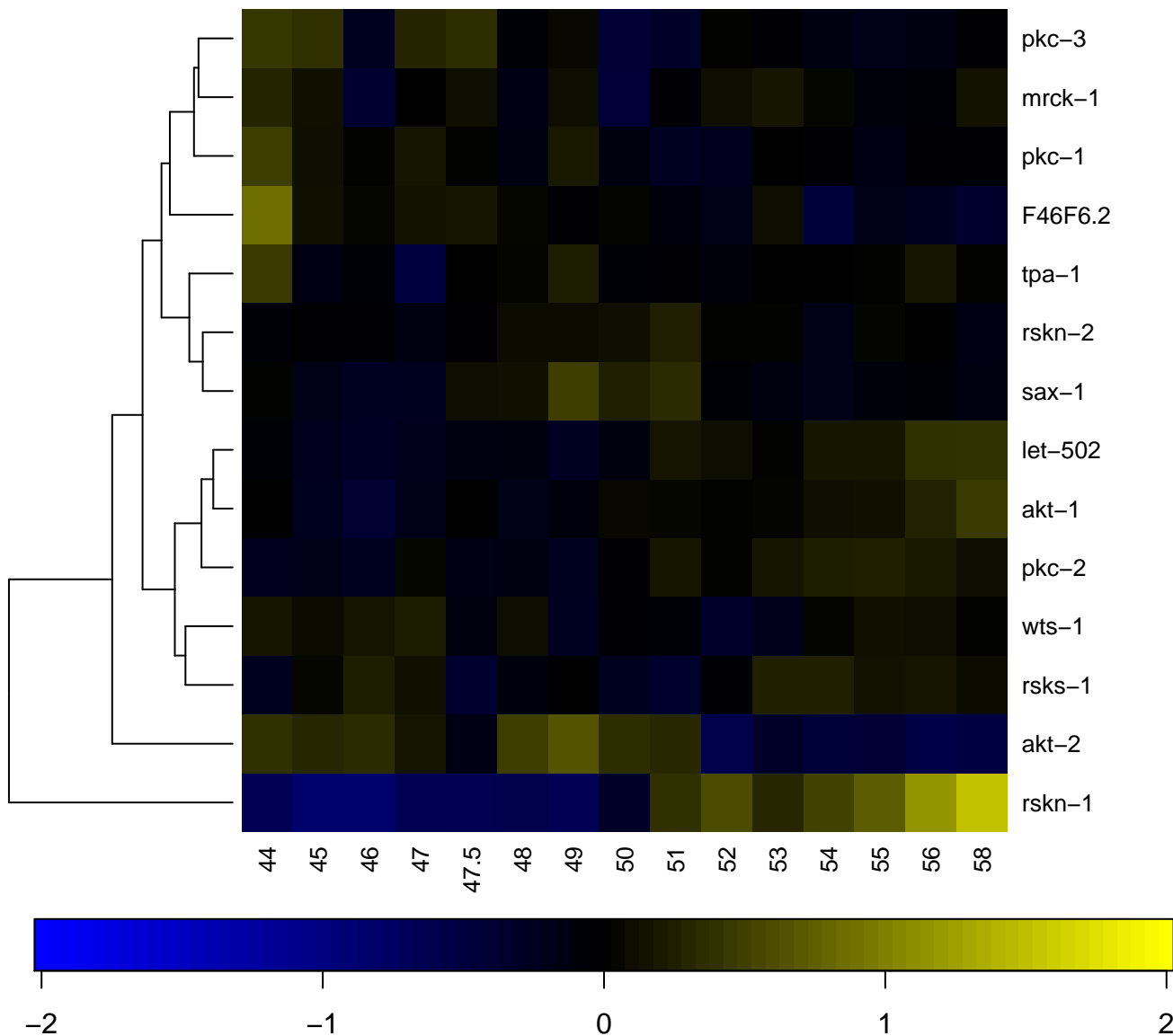
Protein kinase domain



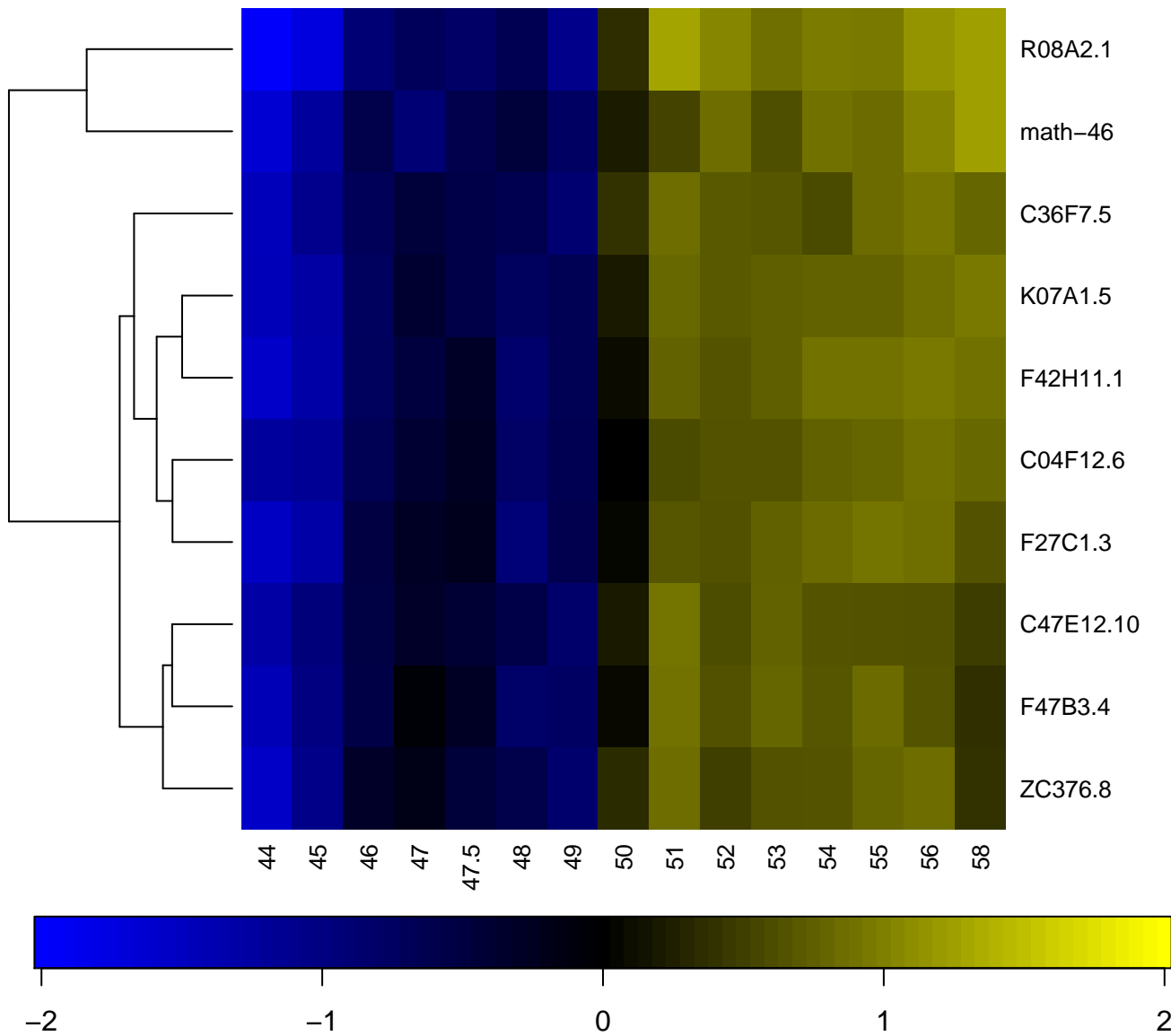
Protein kinase, ATP binding site



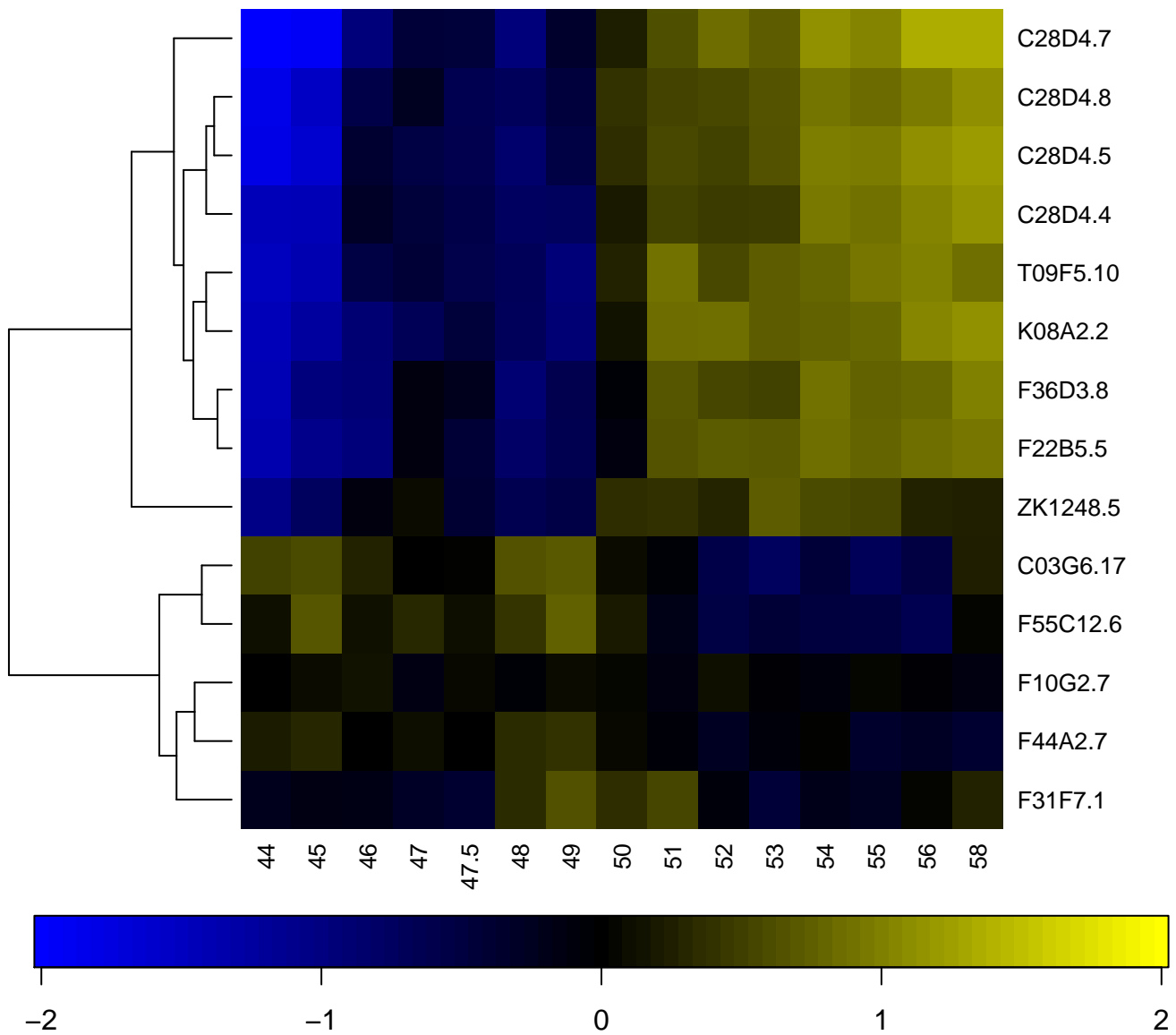
Protein kinase, C-terminal



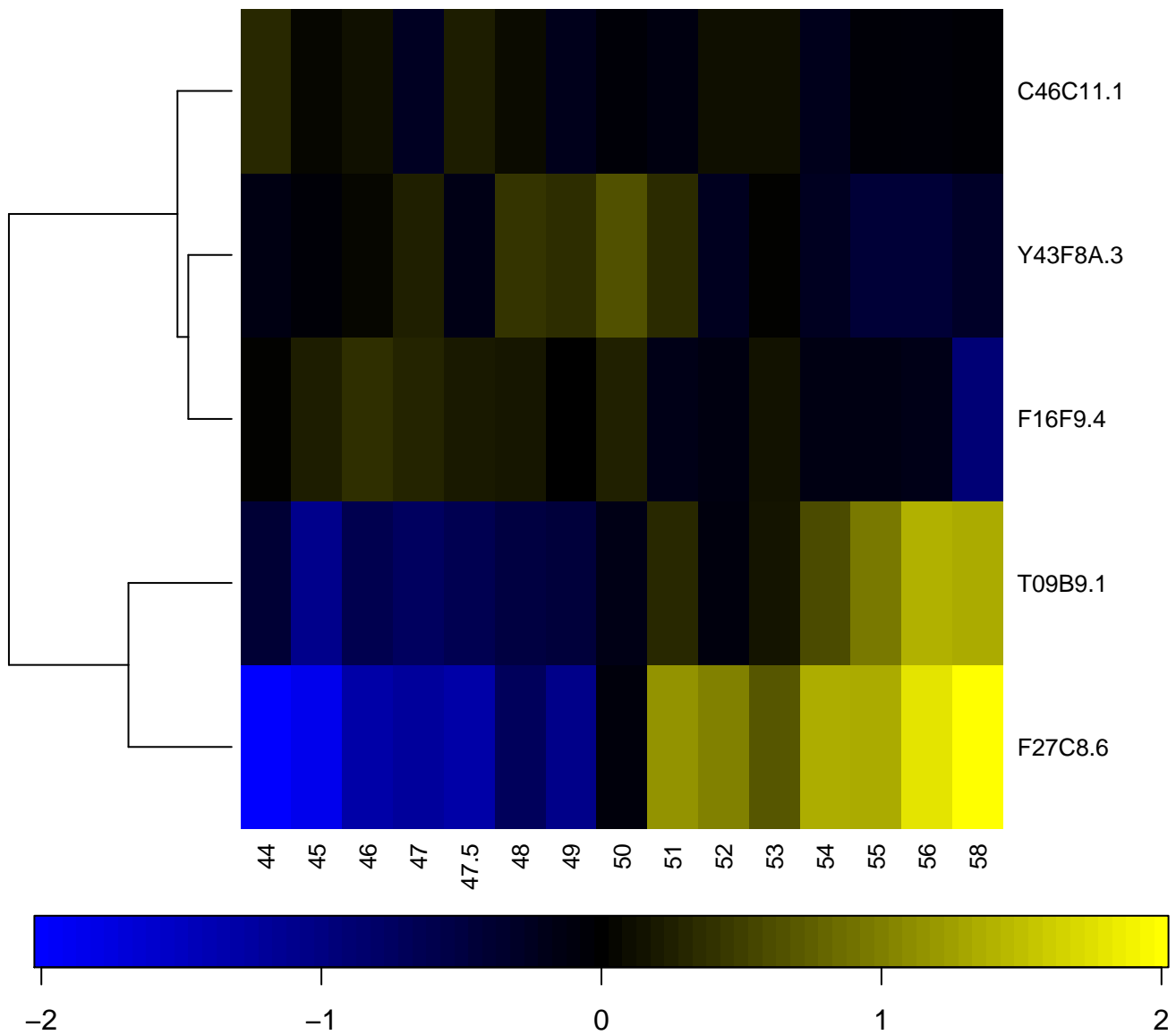
Protein of unknown function



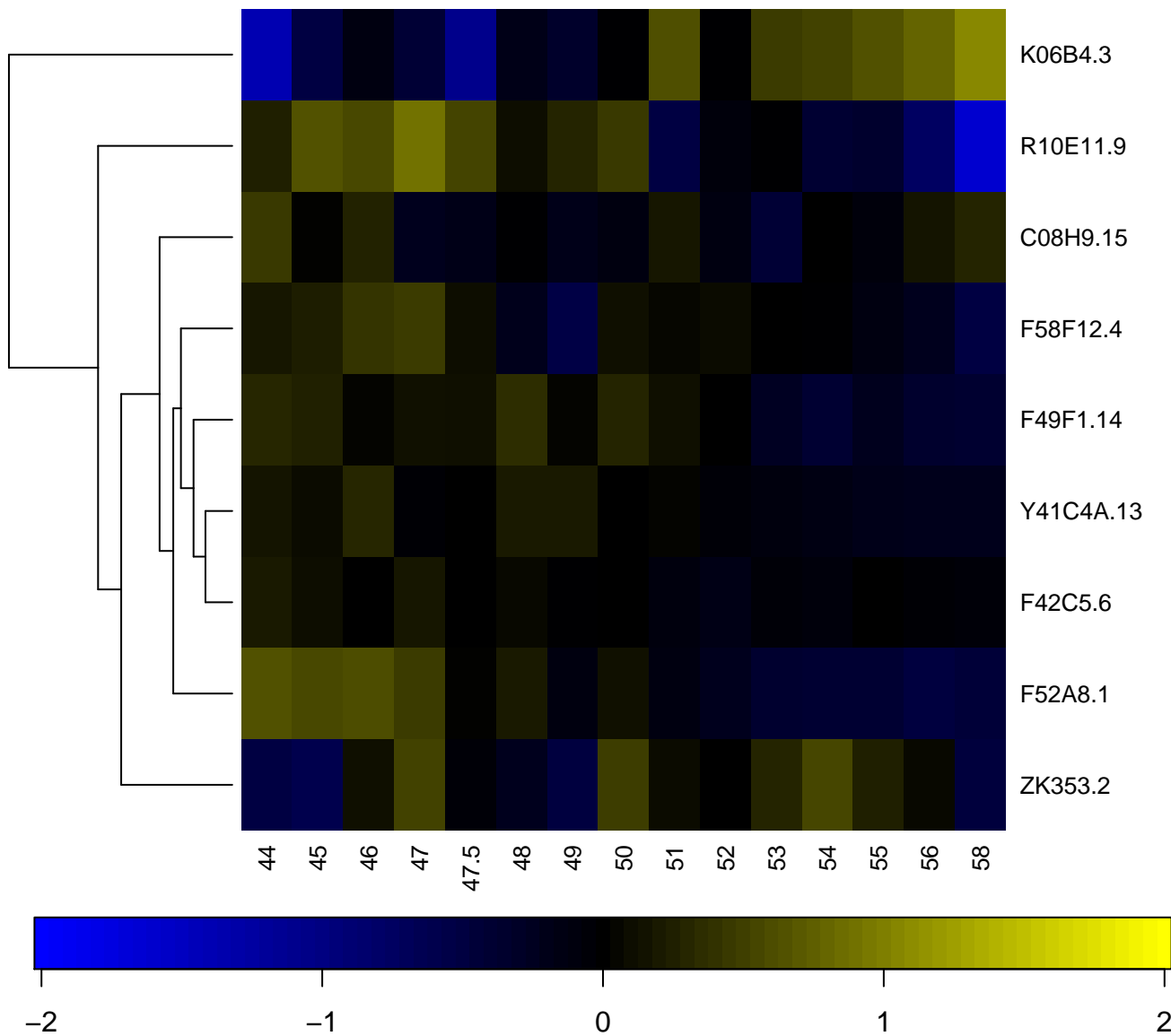
Protein of unknown function (DUF1248)



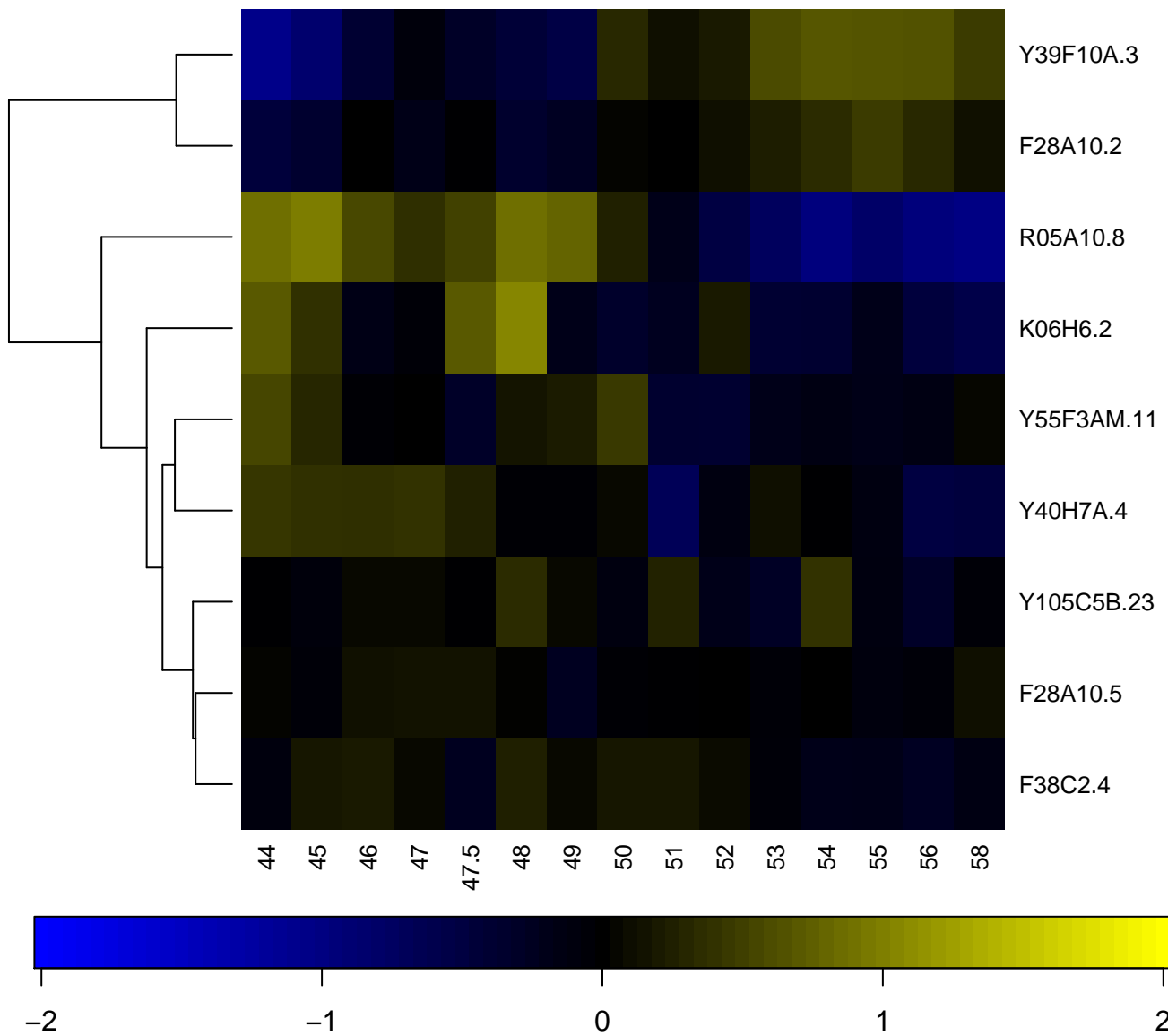
Protein of unknown function (DUF2424)



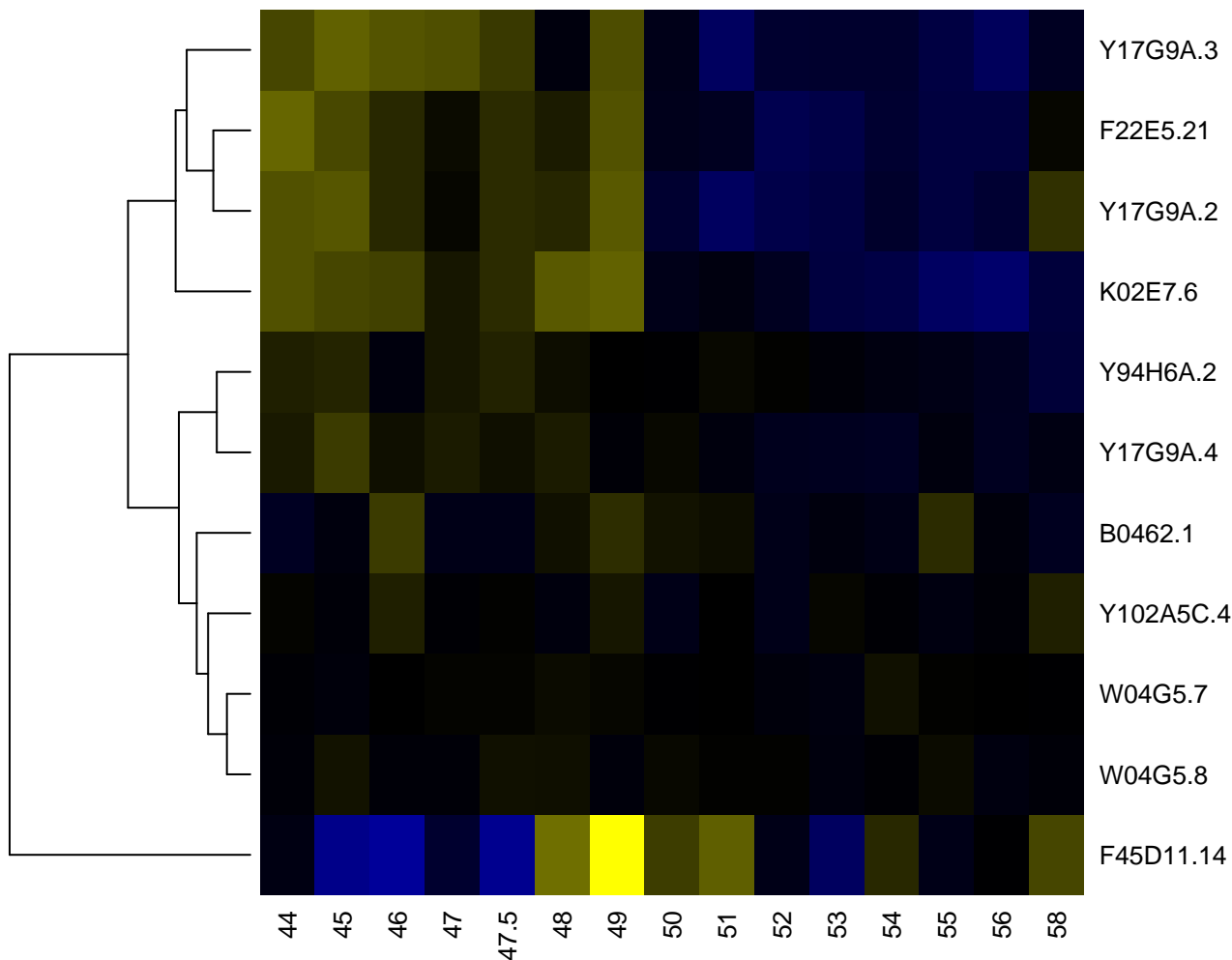
Protein of unknown function (DUF2650)



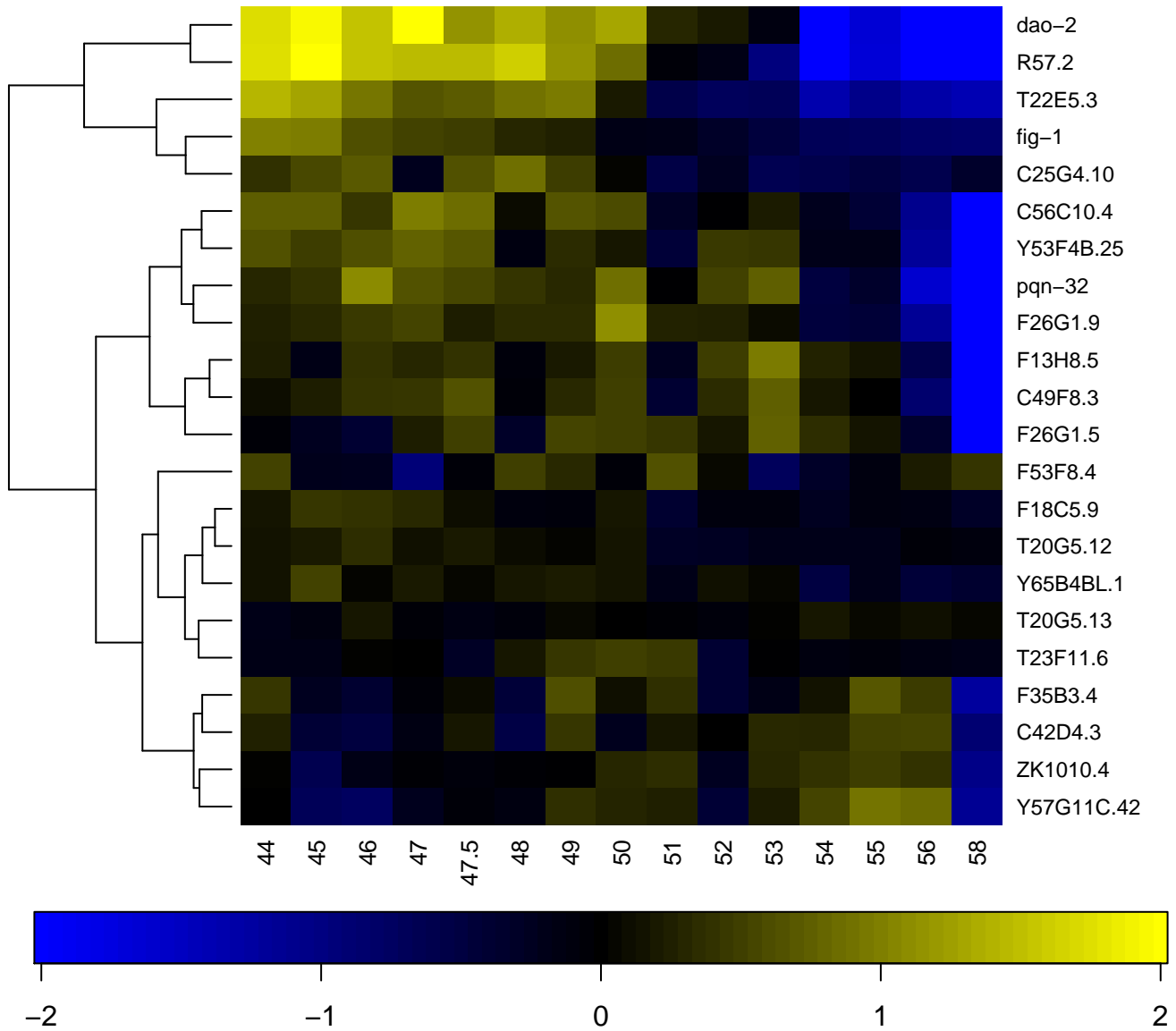
Protein of unknown function (DUF672)



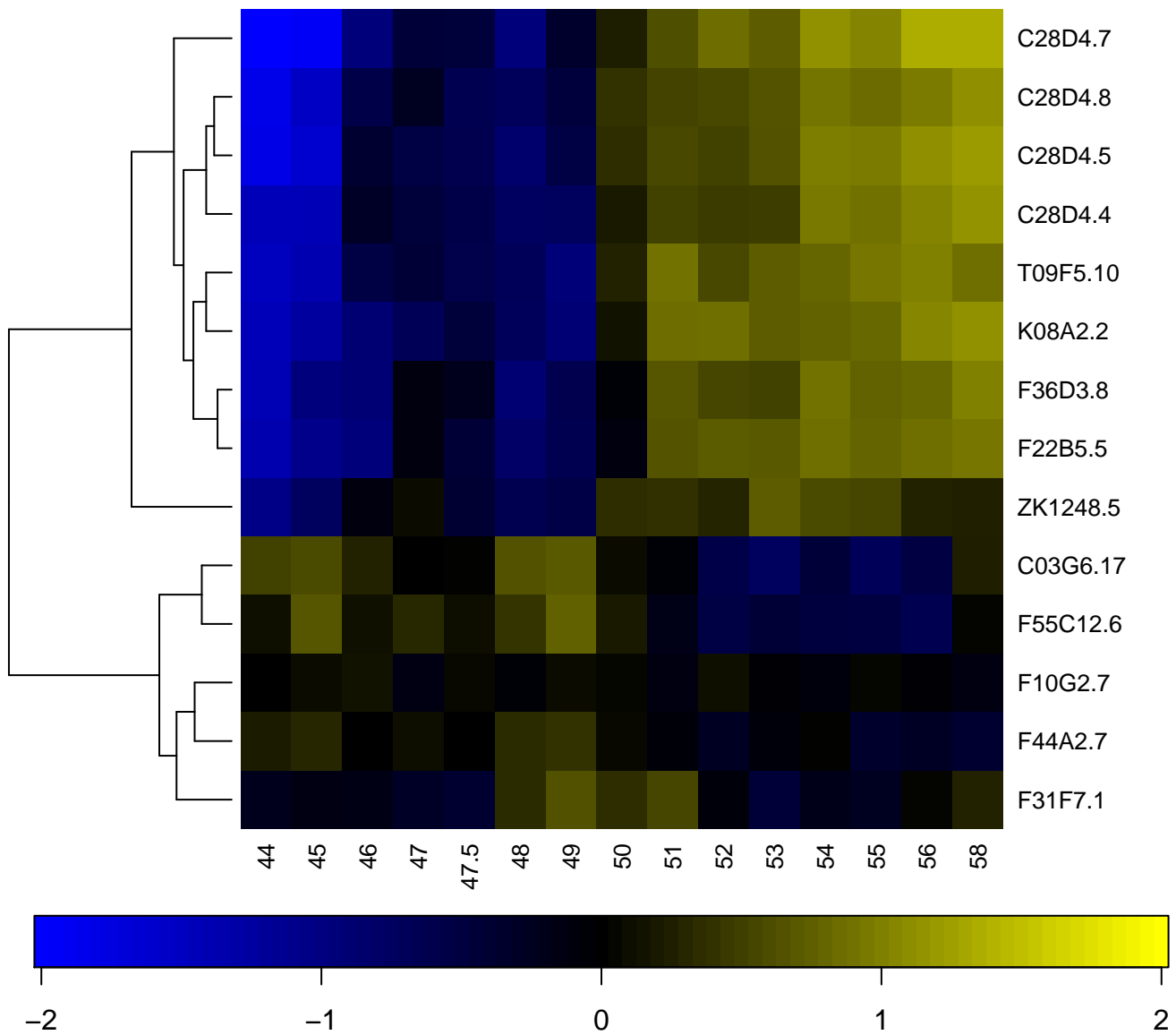
Protein of unknown function (DUF684)



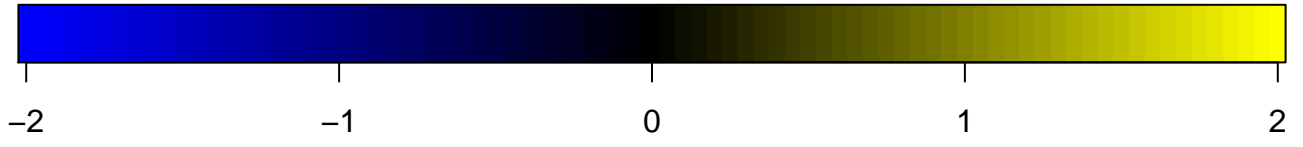
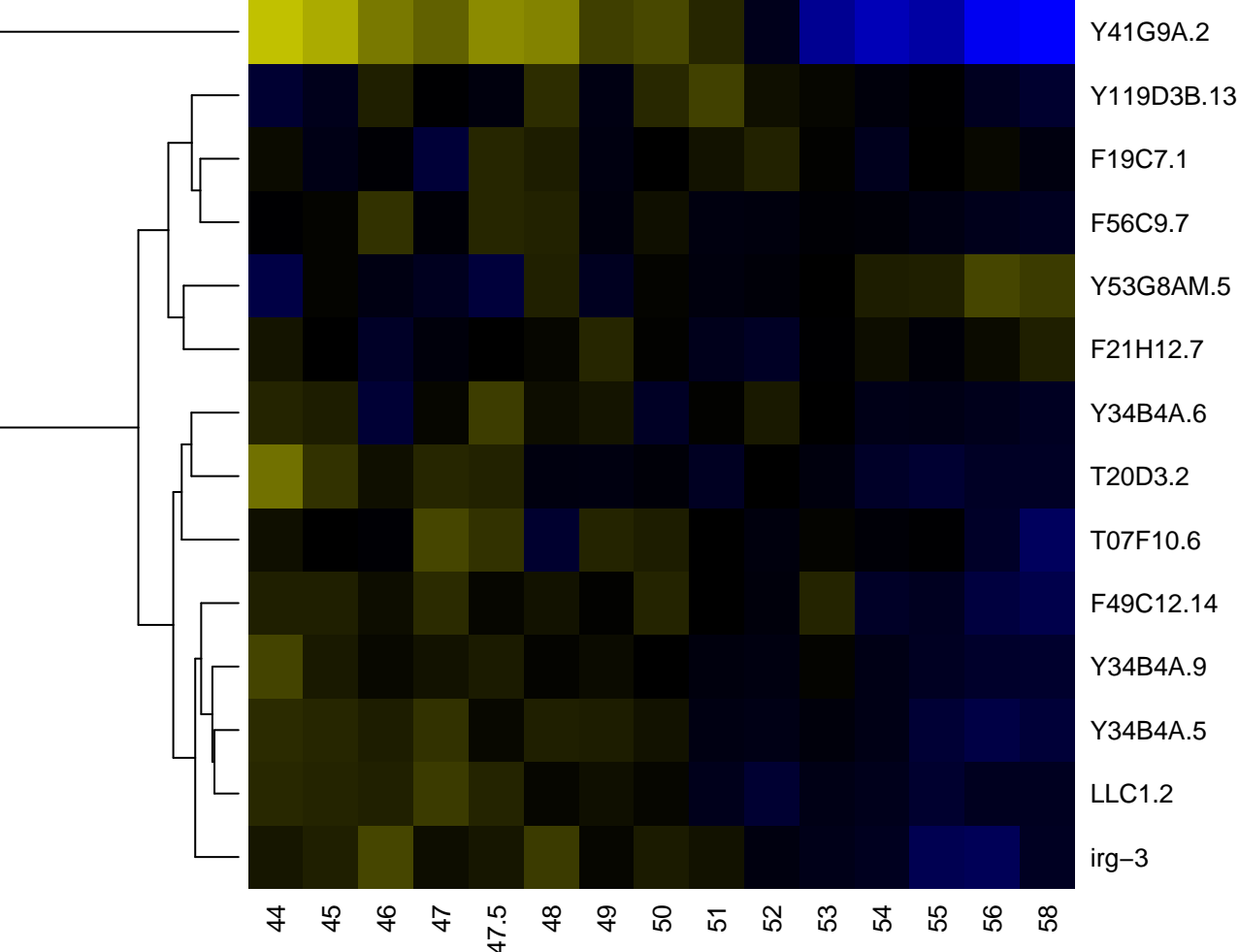
Protein of unknown function DB



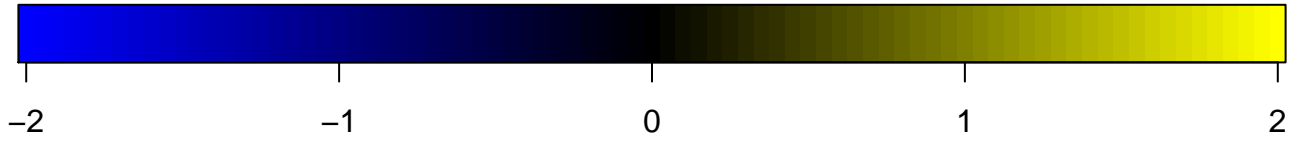
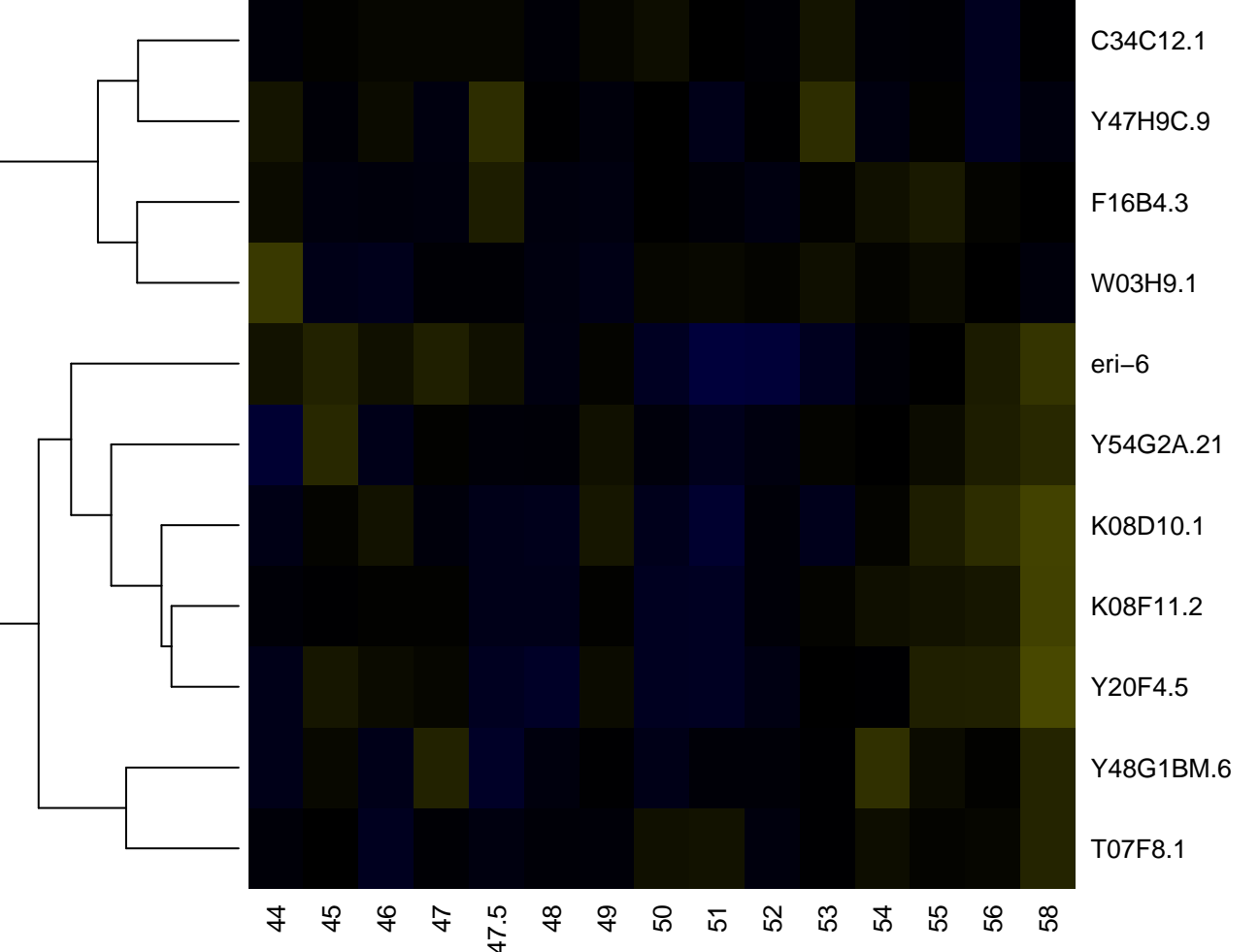
Protein of unknown function DUF1248



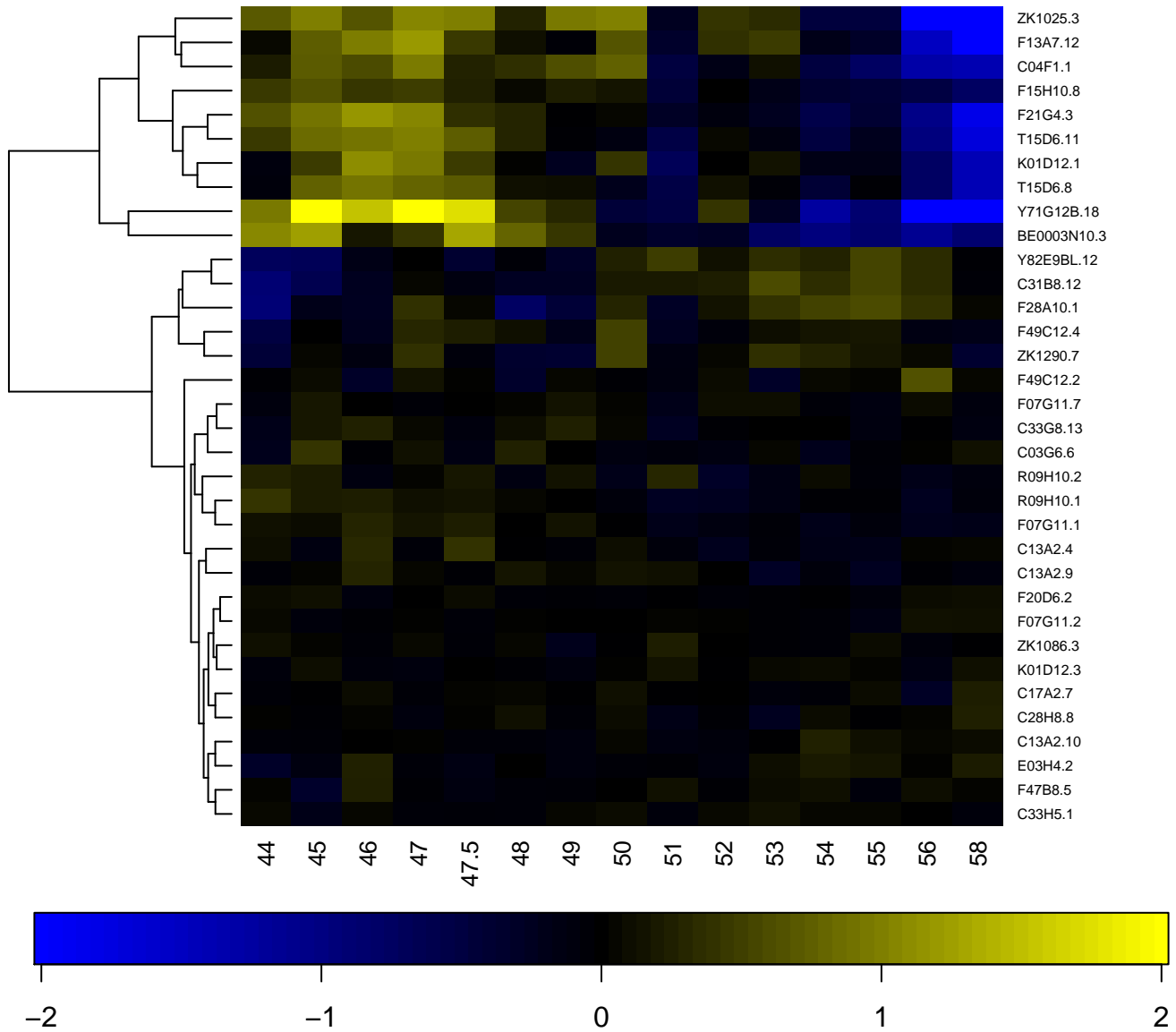
Protein of unknown function DUF1261



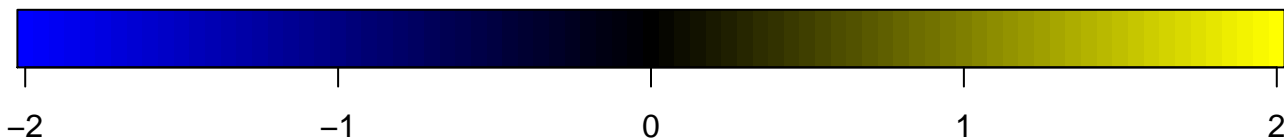
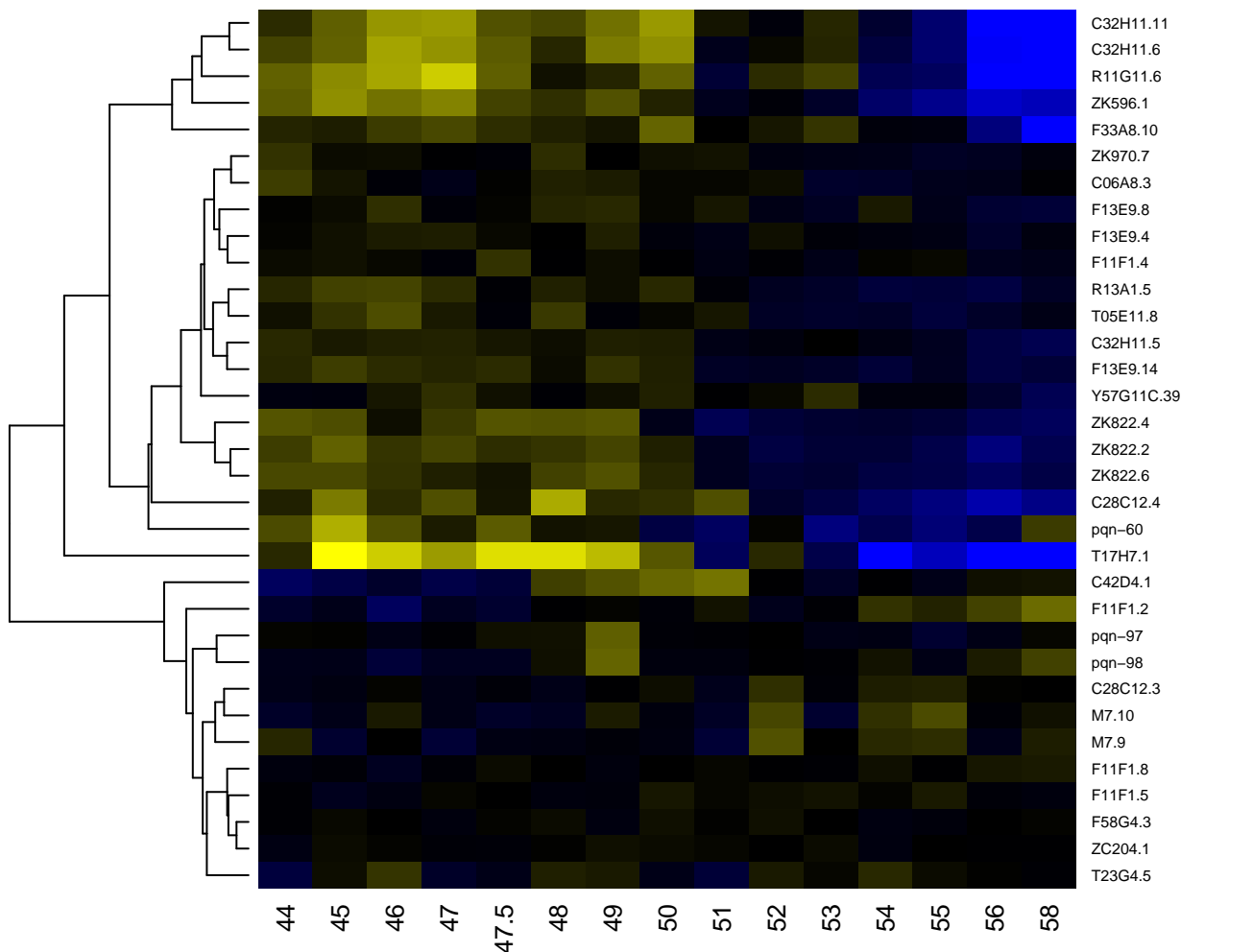
Protein of unknown function DUF1280



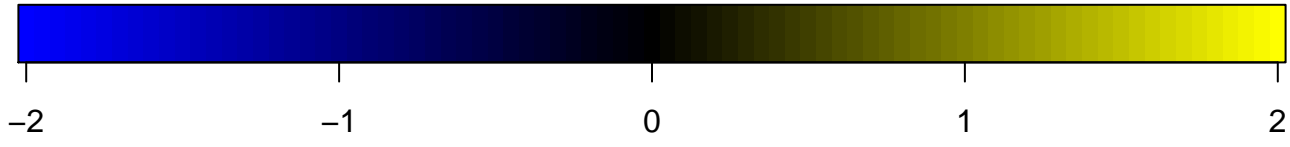
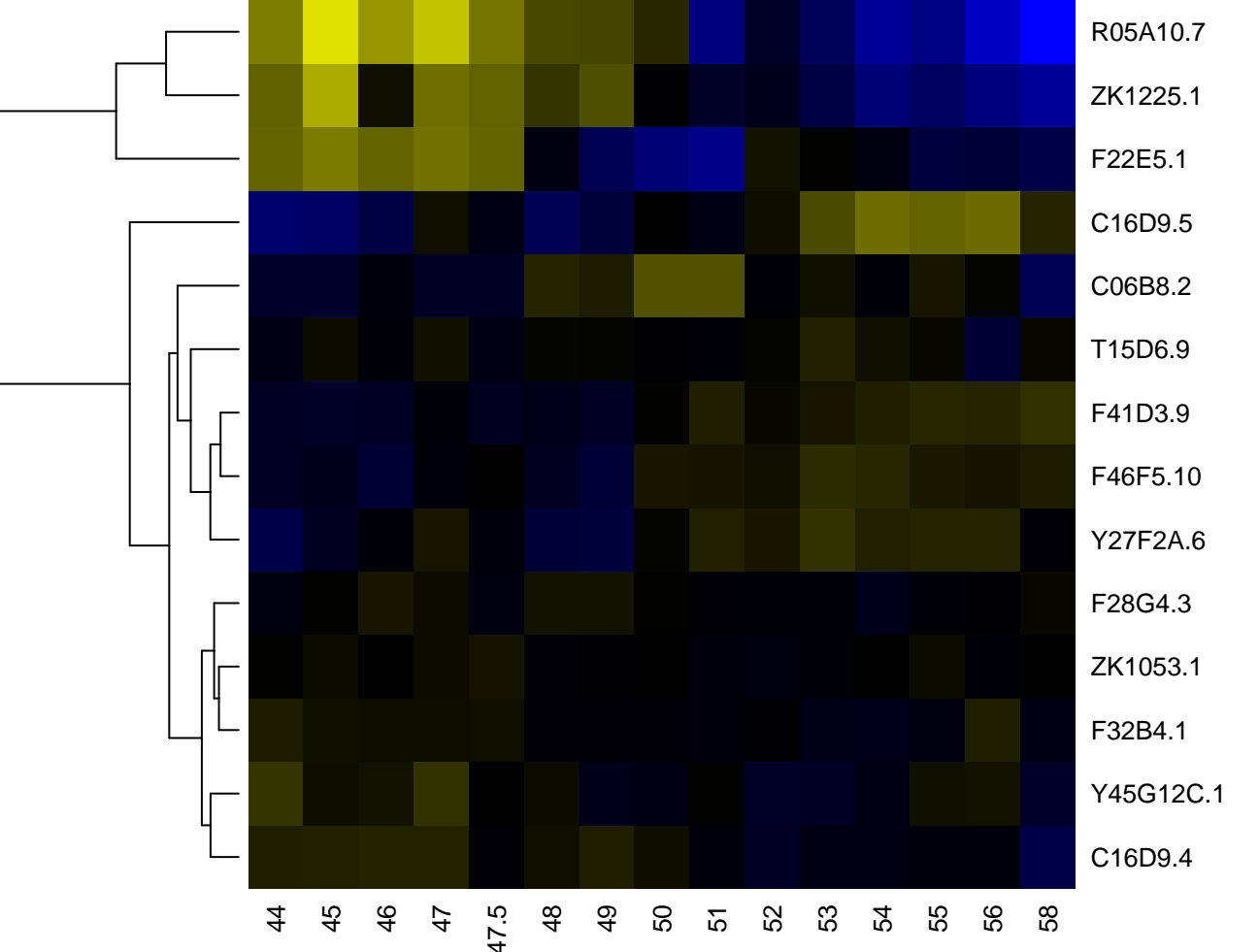
Protein of unknown function DUF13



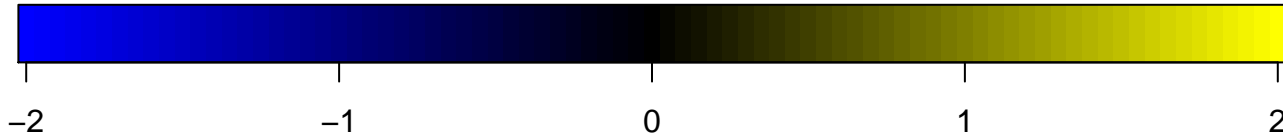
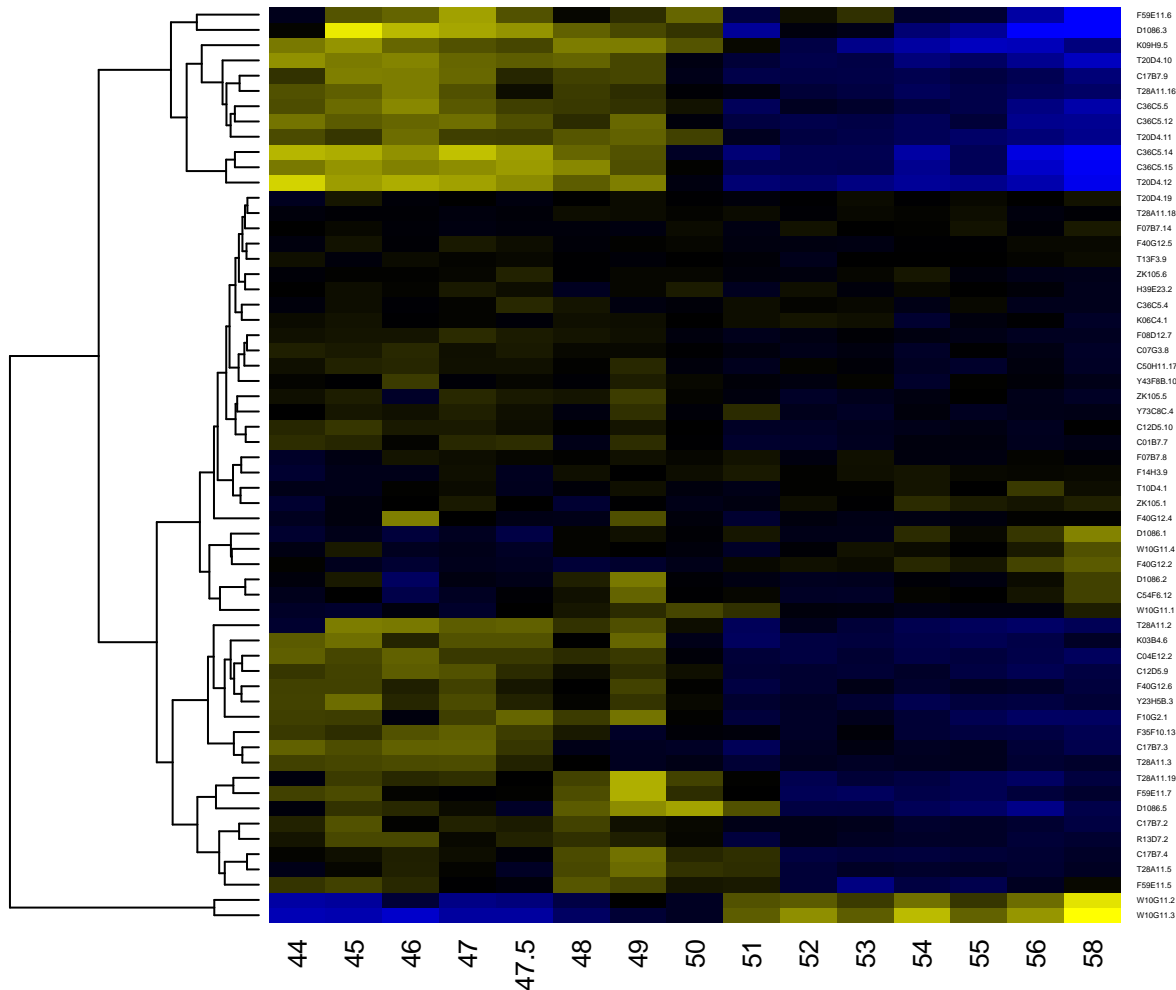
Protein of unknown function DUF148



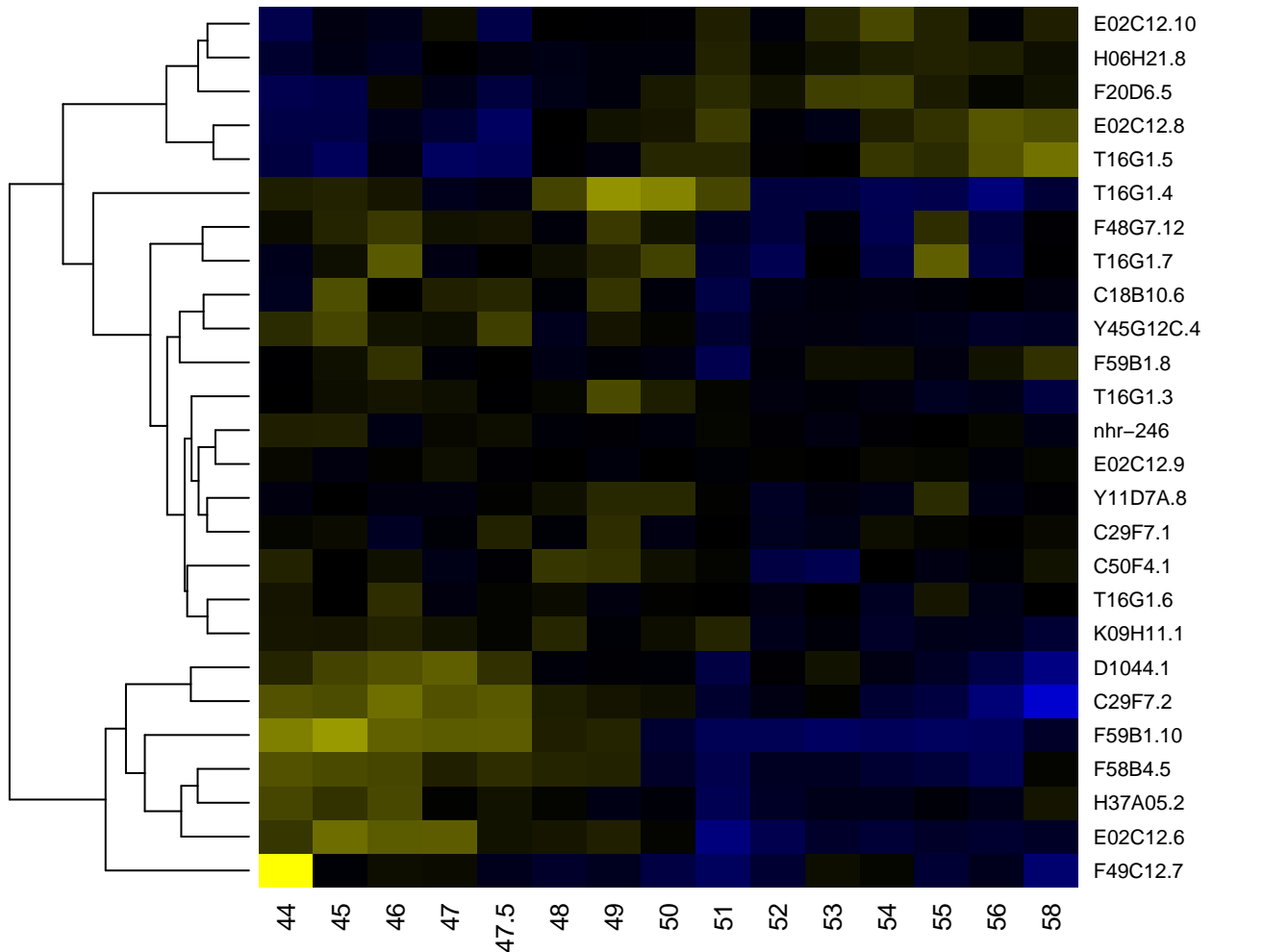
Protein of unknown function DUF1647



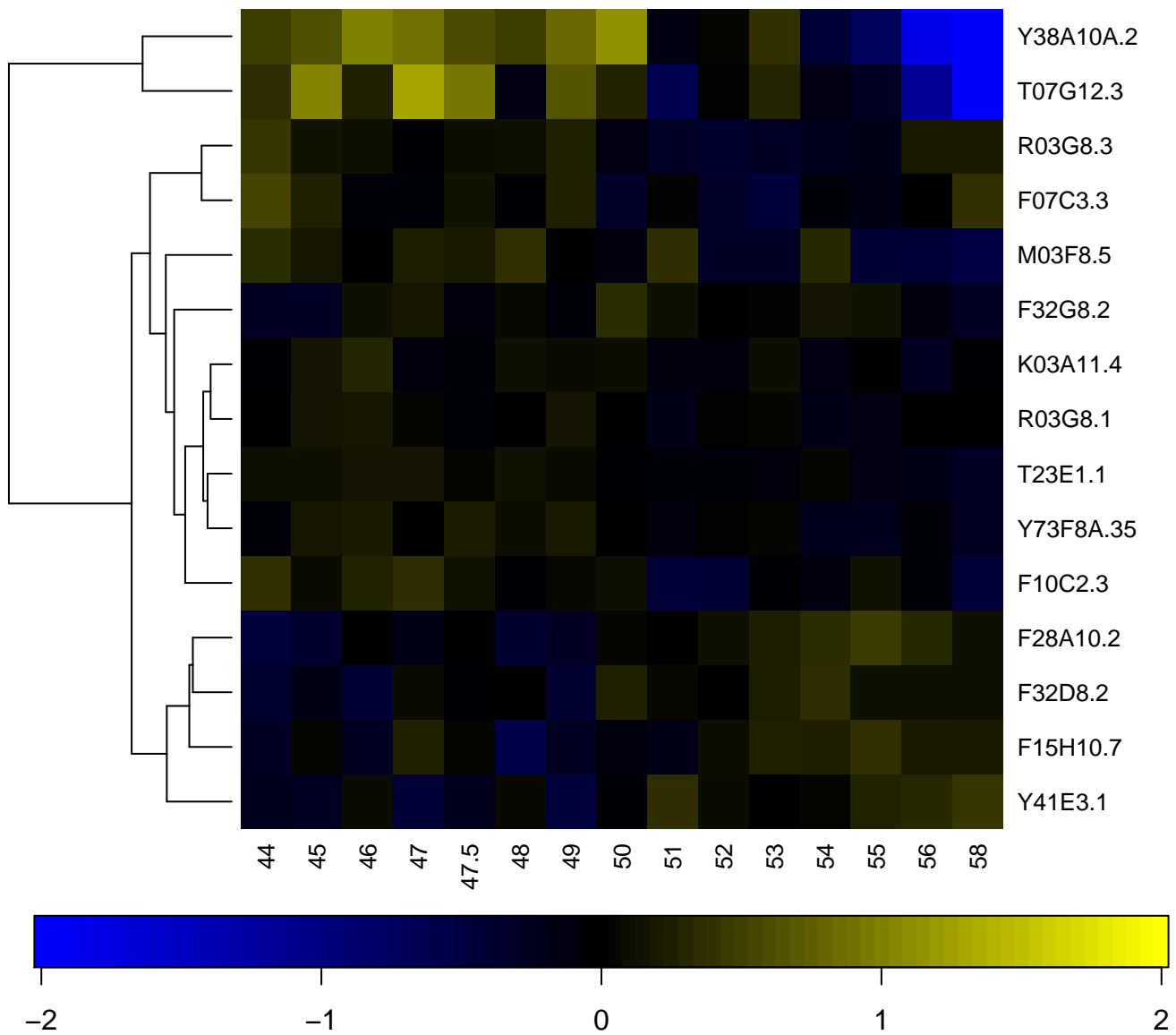
Protein of unknown function DUF19



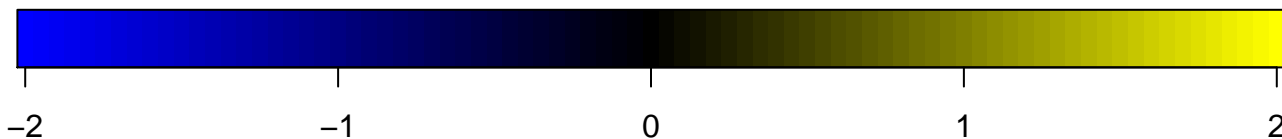
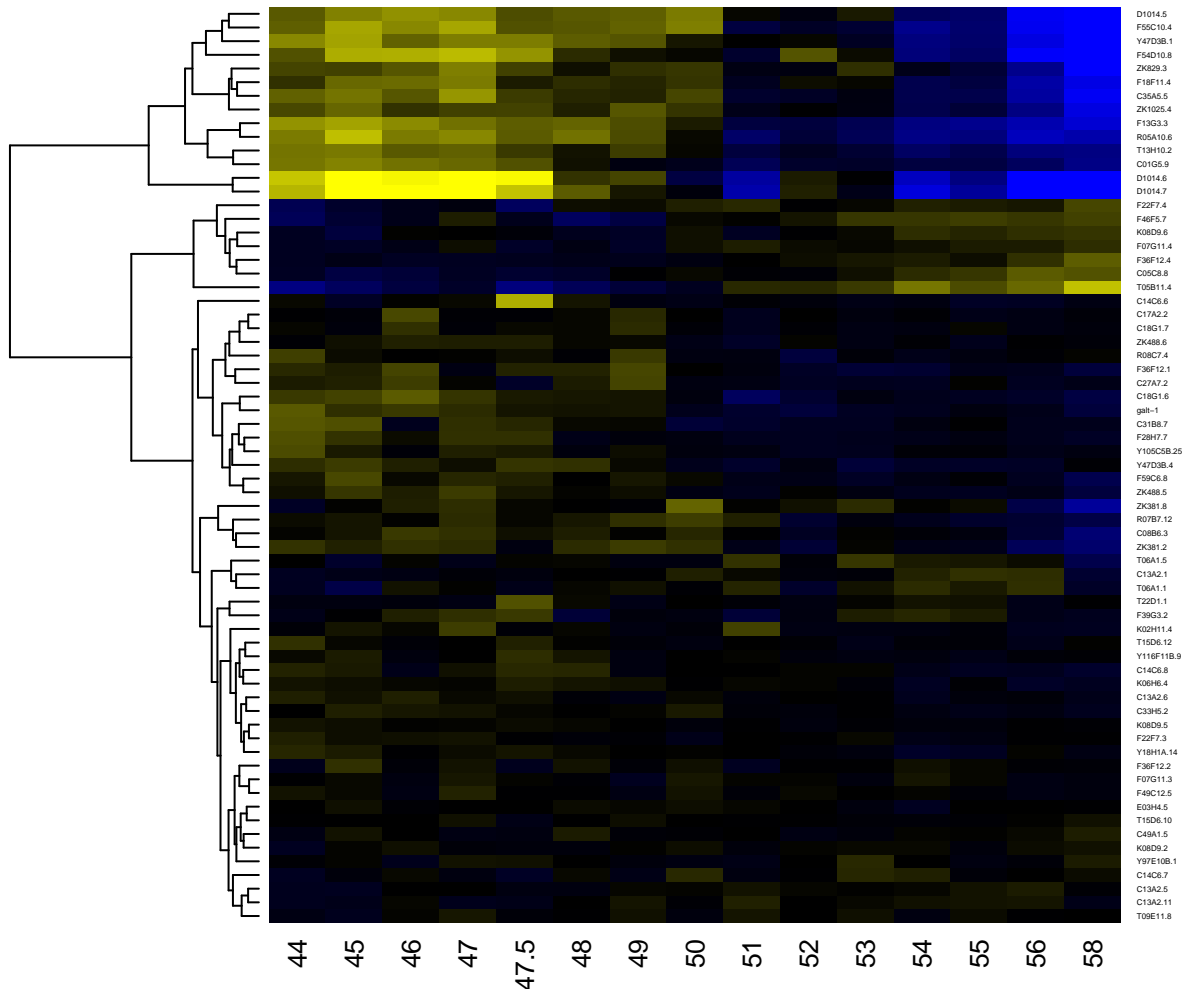
Protein of unknown function DUF227



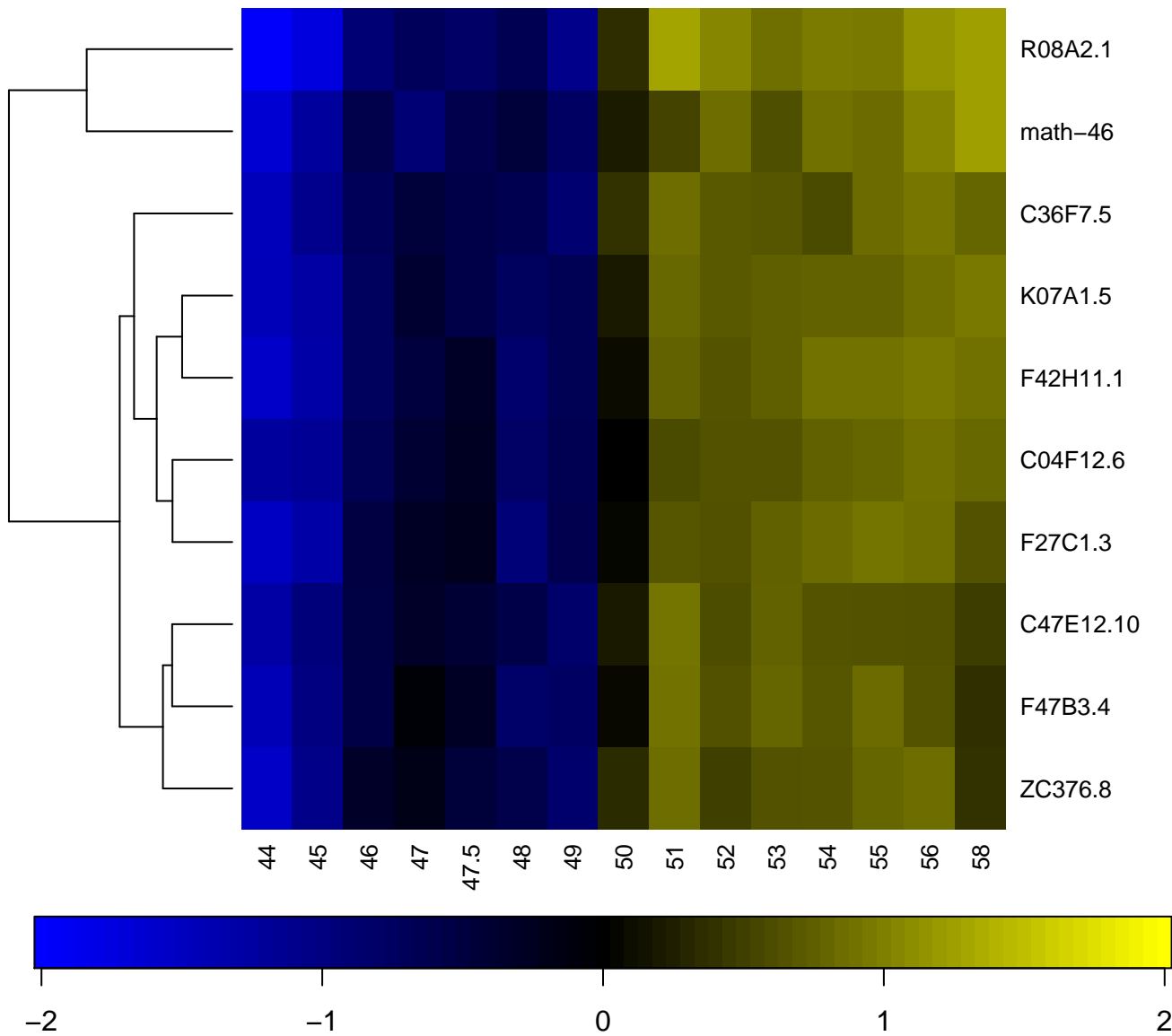
Protein of unknown function DUF229



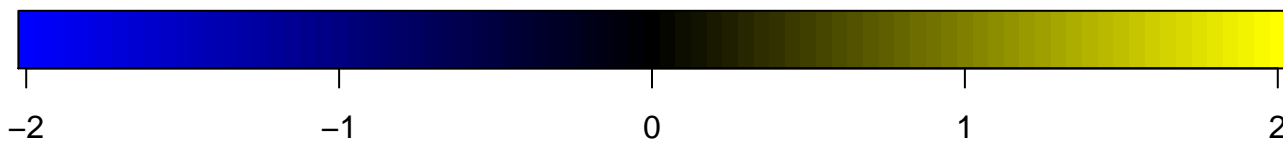
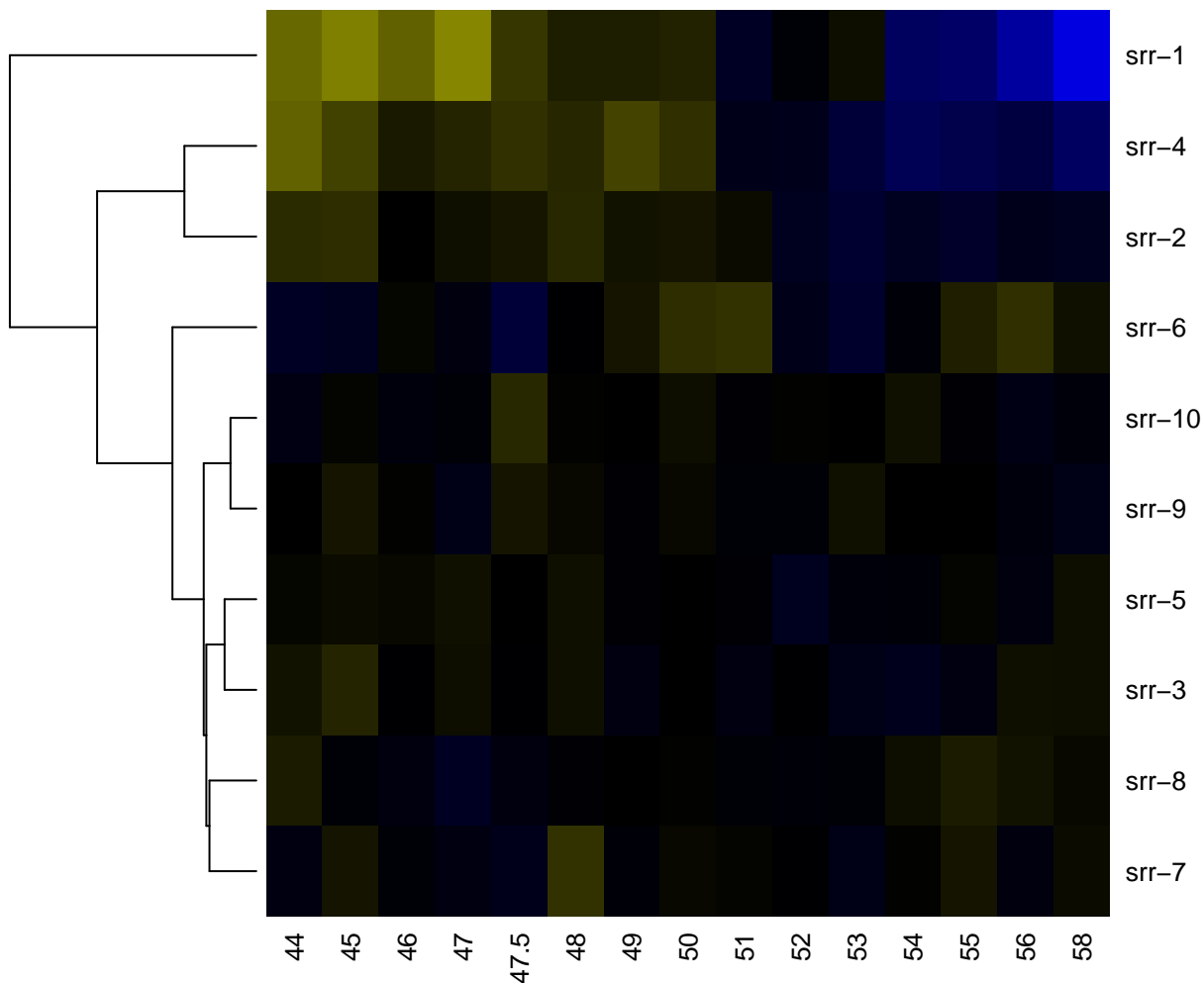
Protein of unknown function DUF23



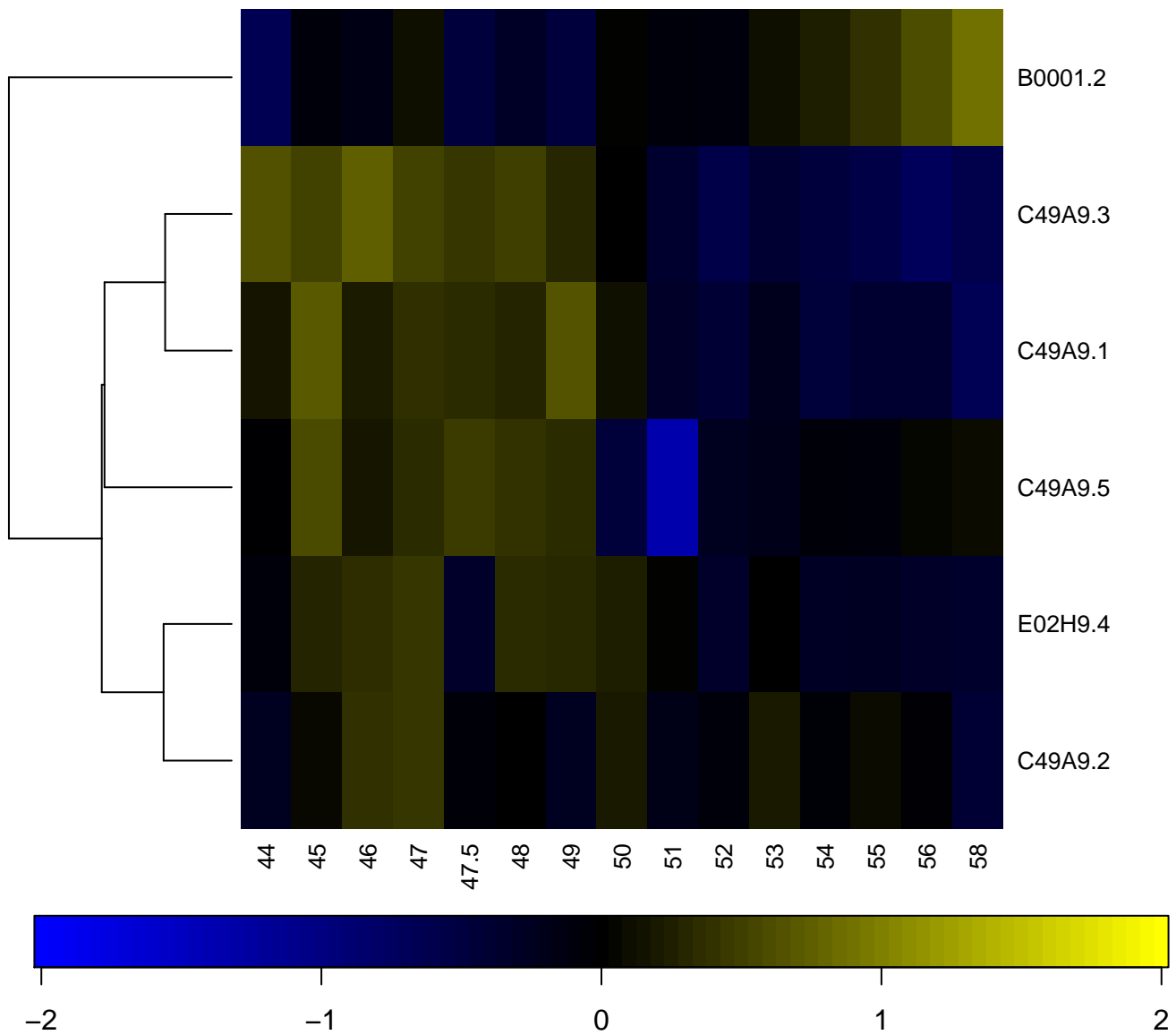
Protein of unknown function DUF236



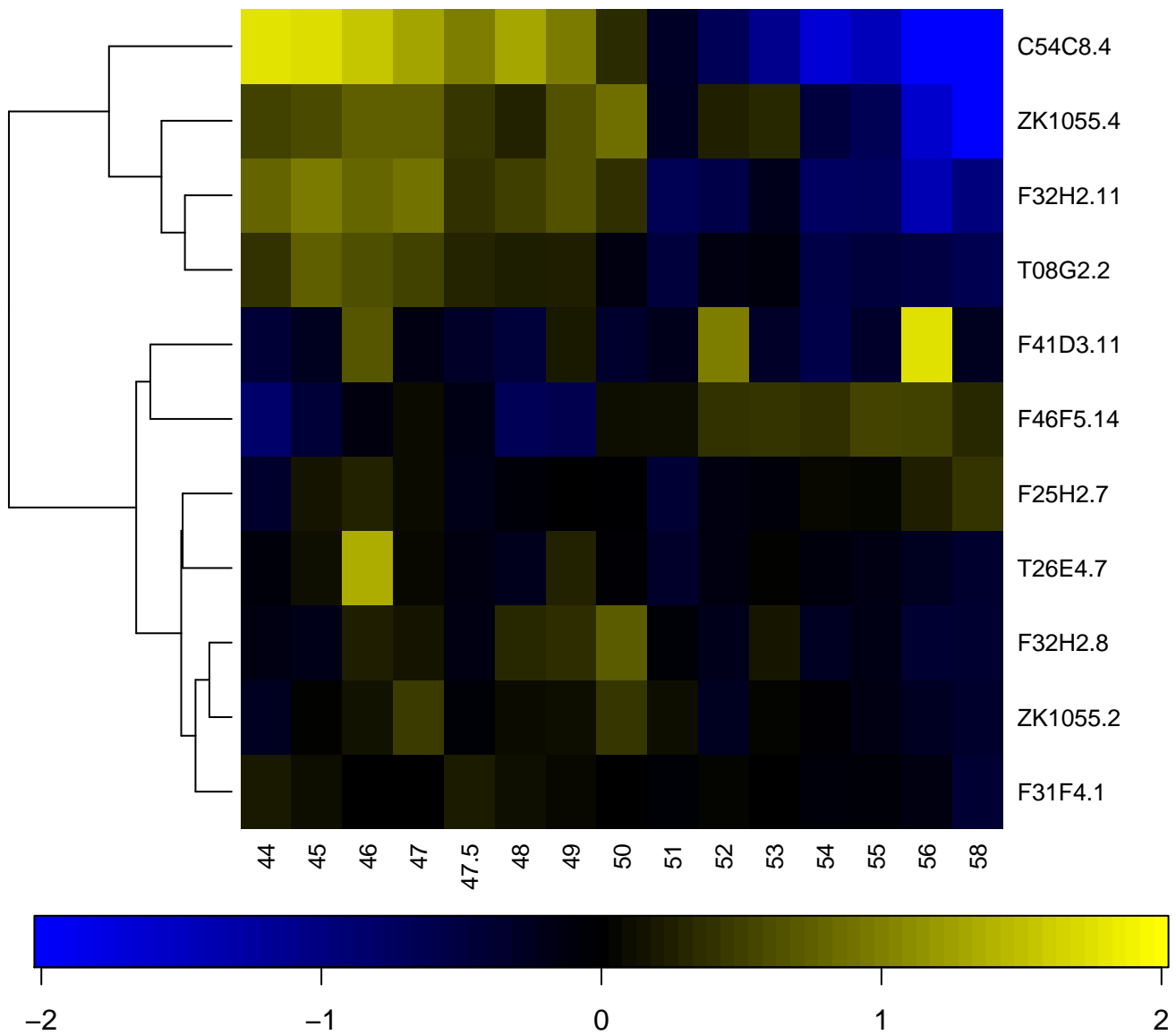
Protein of unknown function DUF267, *Caenorhabditis* speci



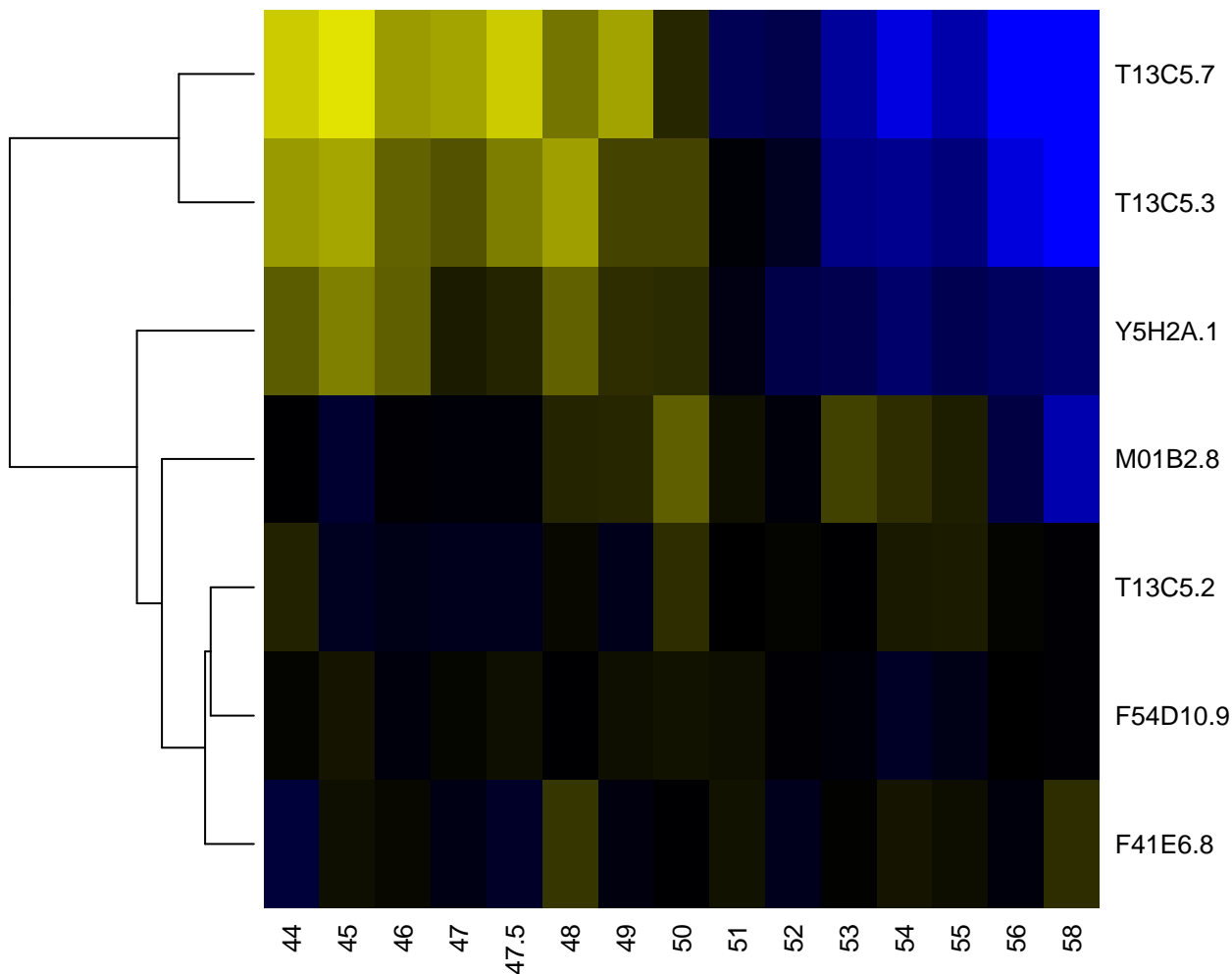
Protein of unknown function DUF272



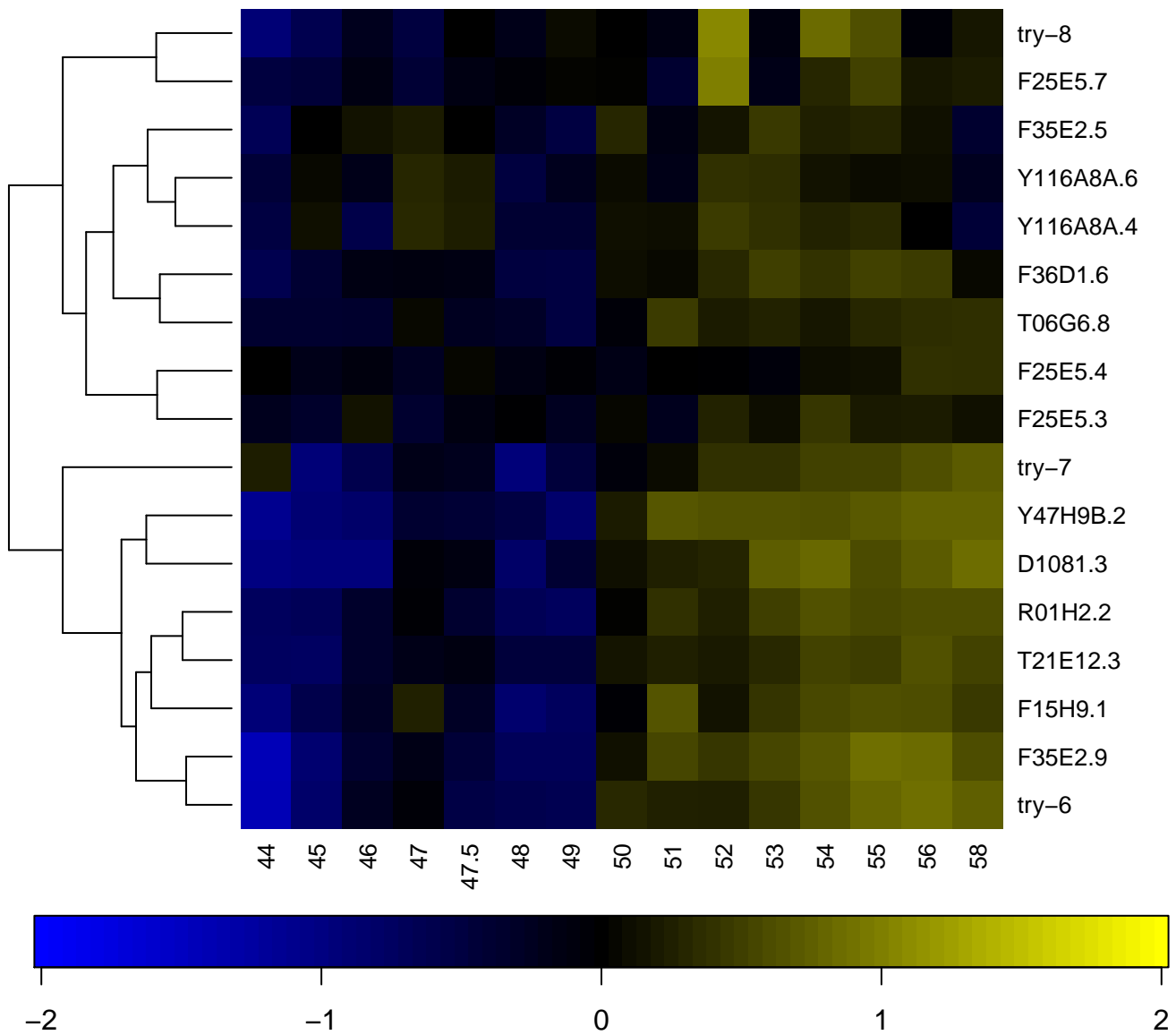
Protein of unknown function DUF273



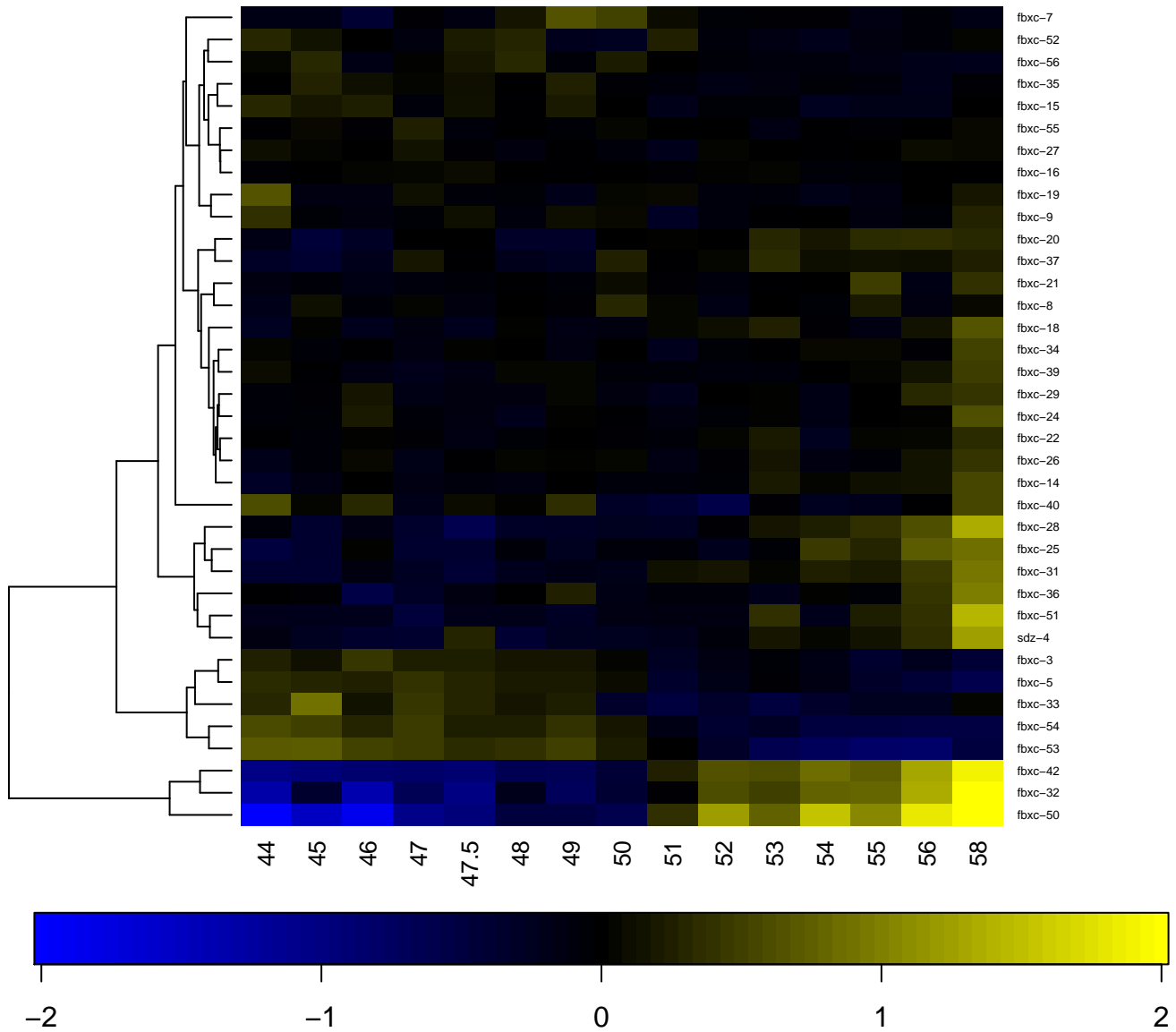
Protein of unknown function DUF282, *Caenorhabditis* speci



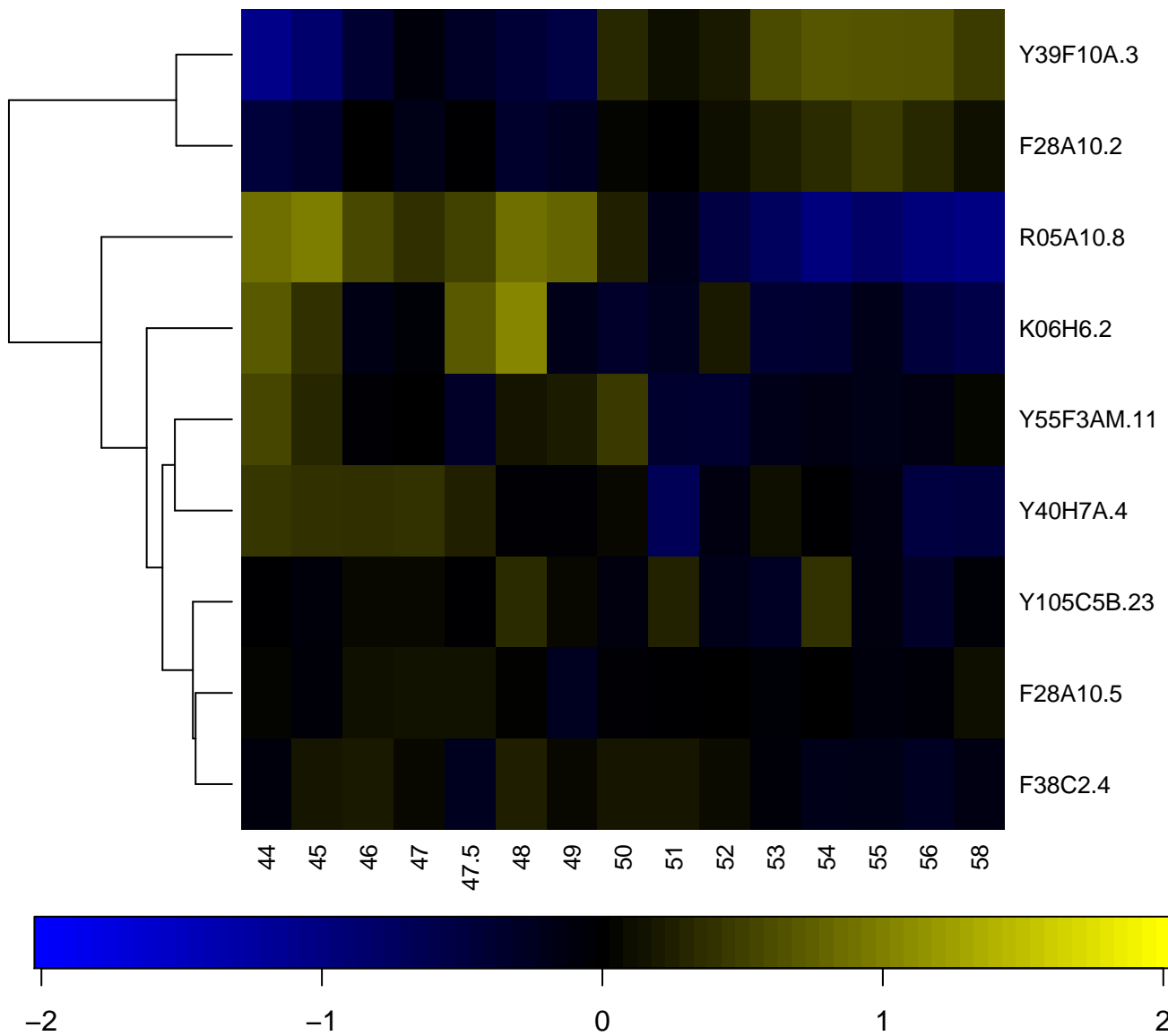
Protein of unknown function DUF316



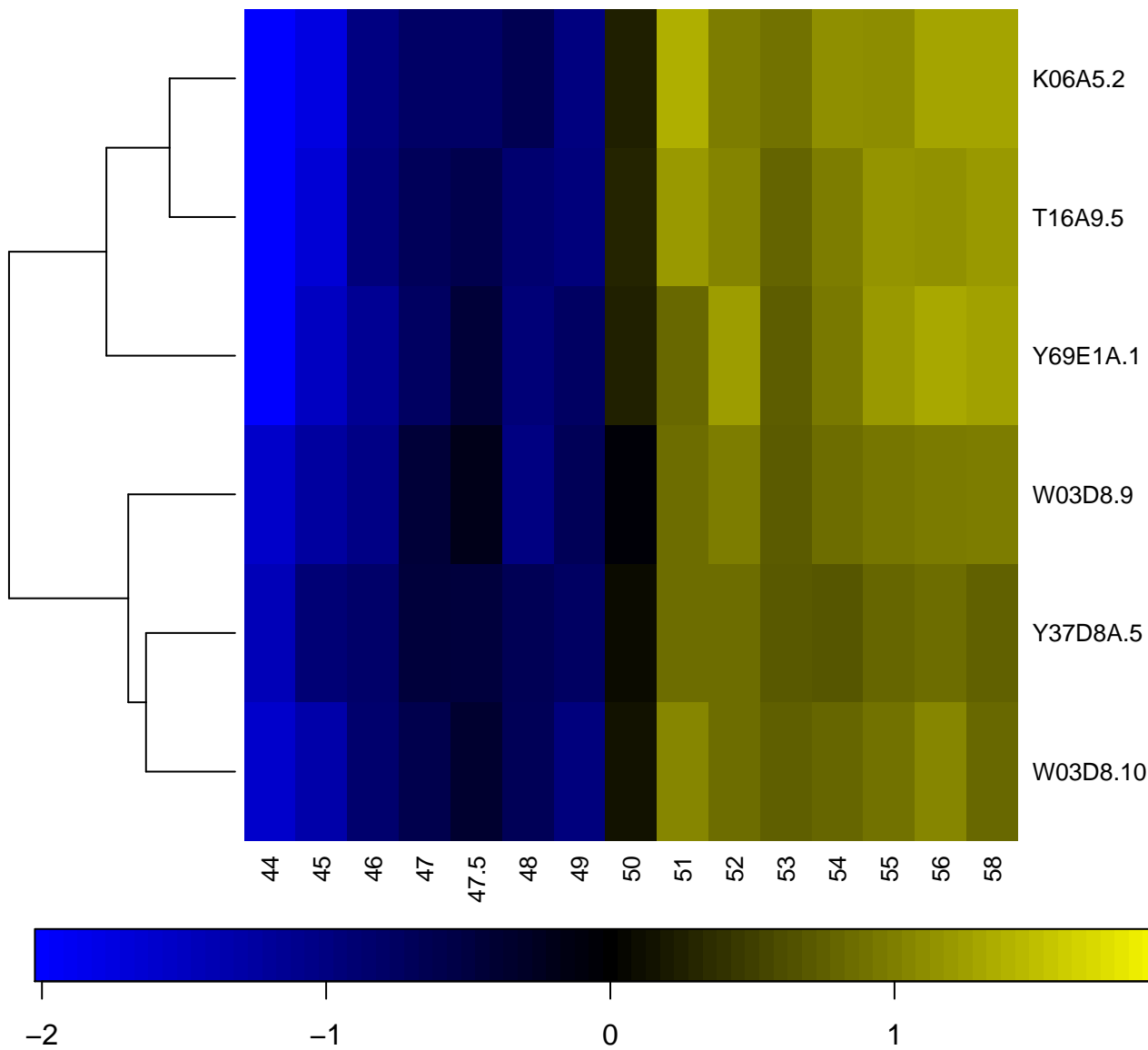
Protein of unknown function DUF3557



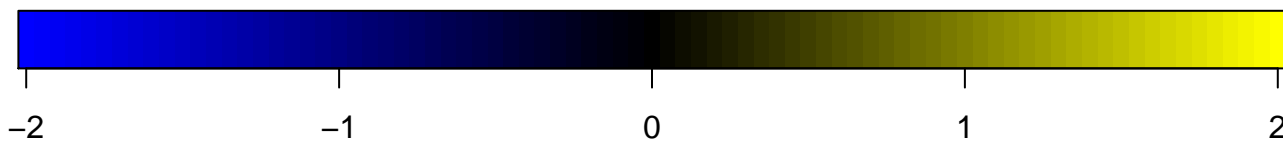
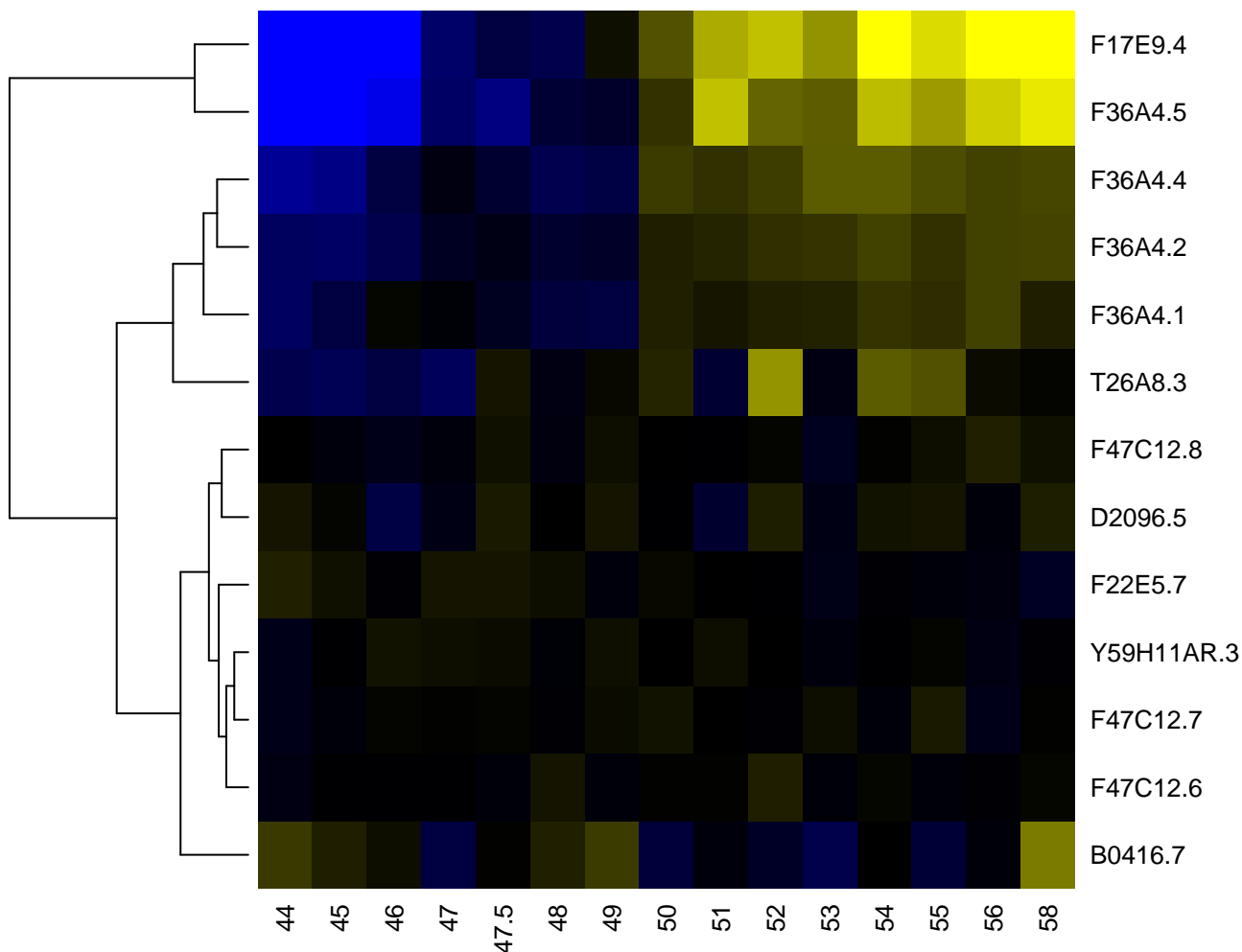
Protein of unknown function DUF672



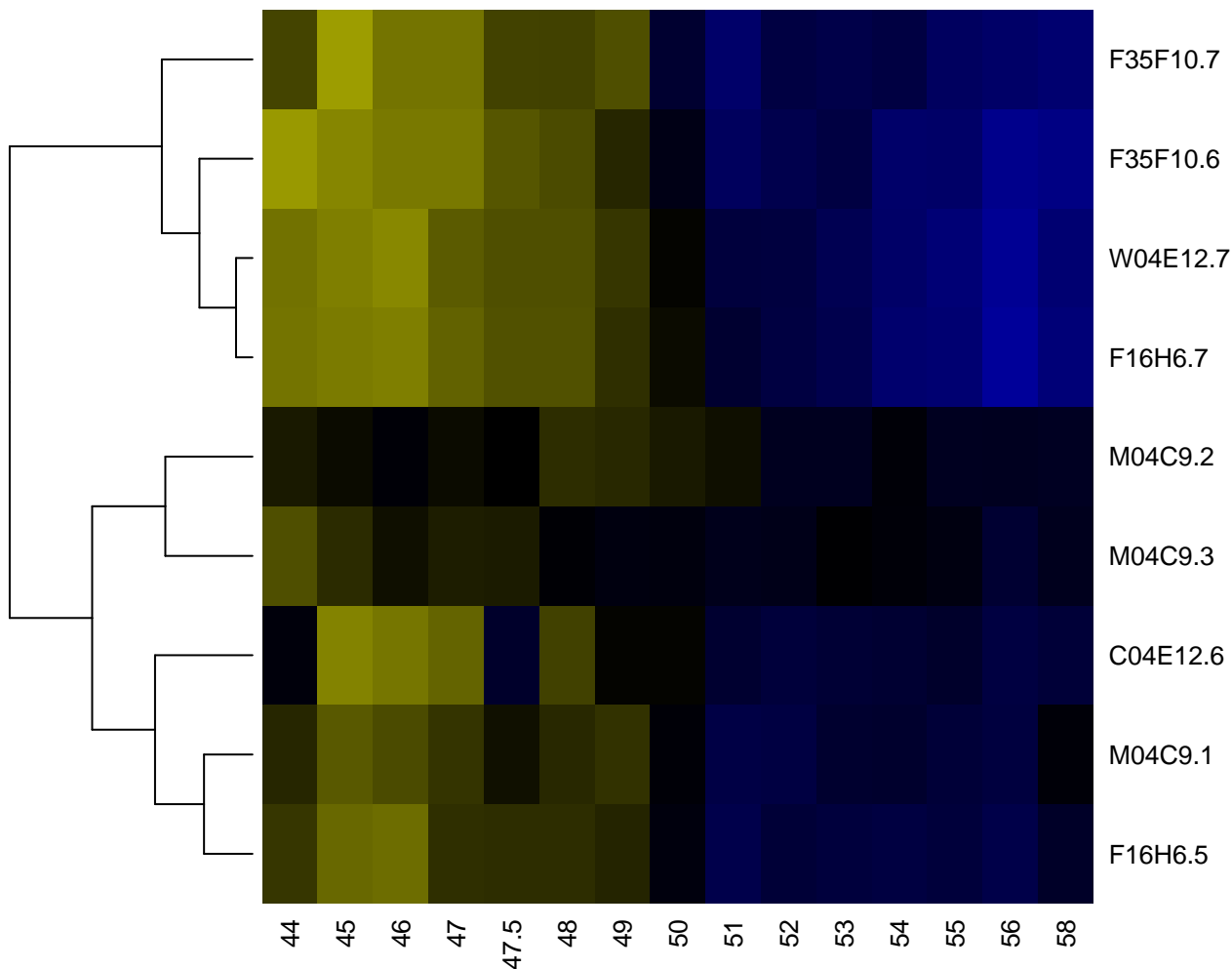
Protein of unknown function DUF856, *Caenorhabditis* speci



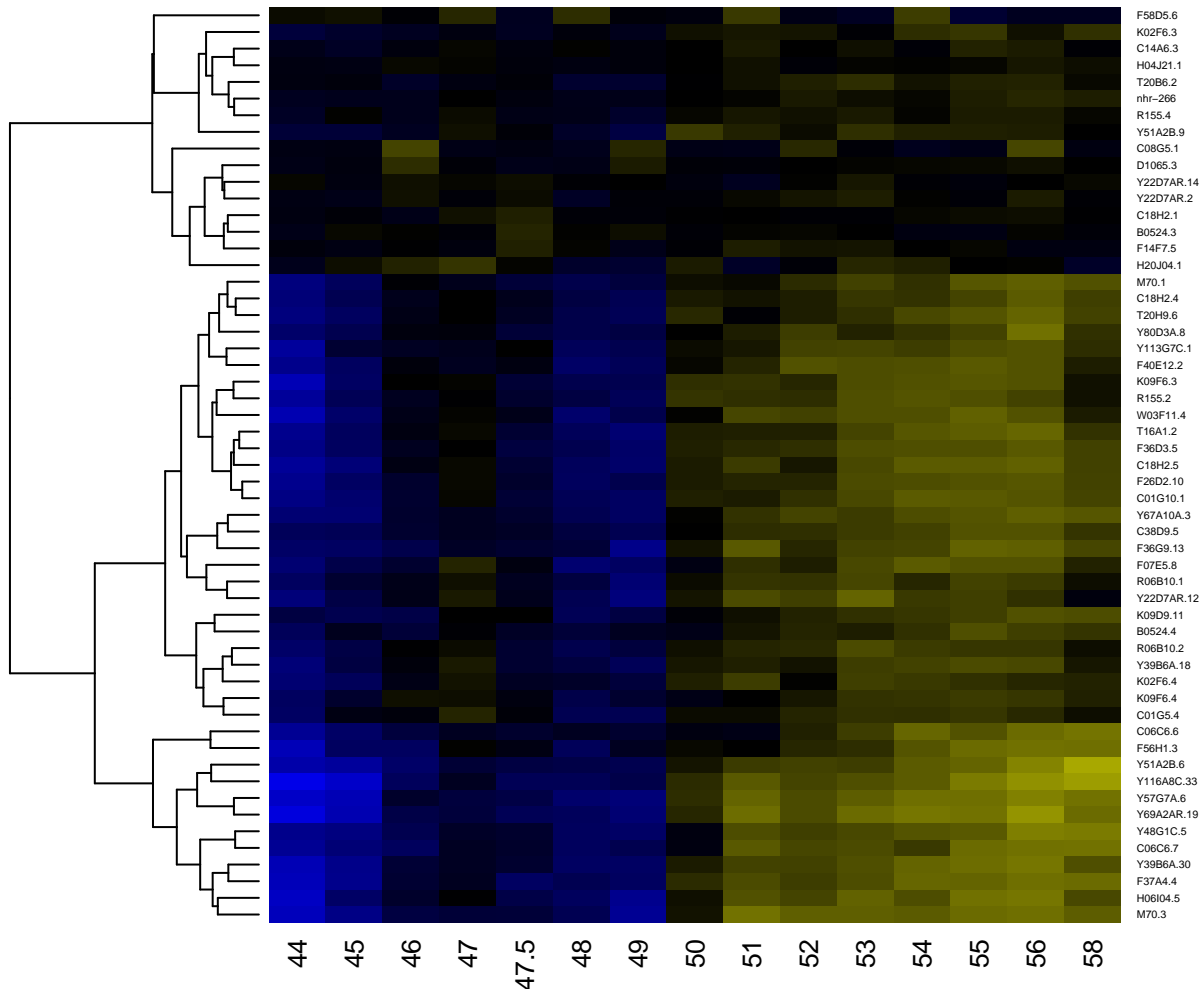
Protein of unknown function DUF870, *Caenorhabditis* speci



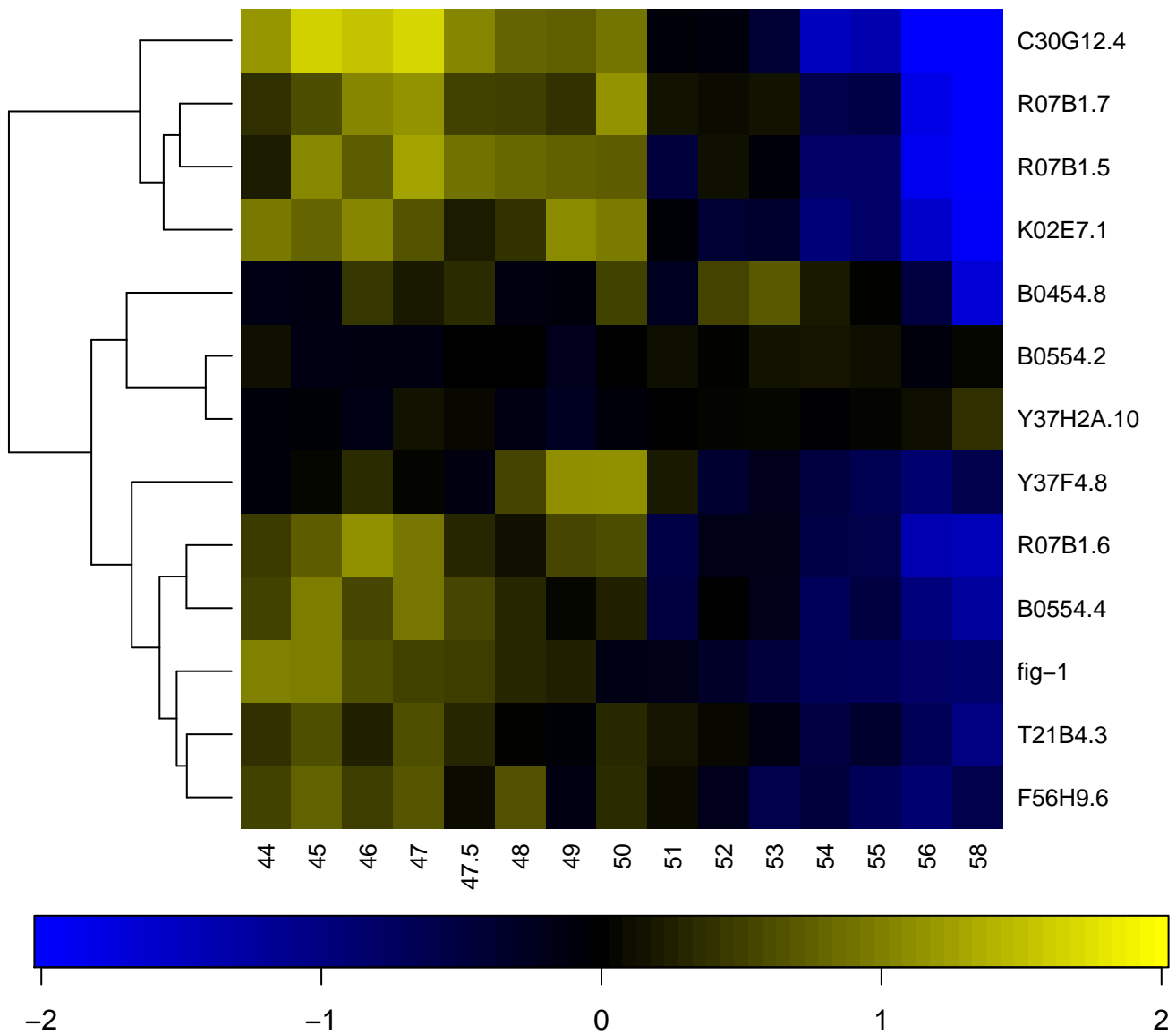
Protein of unknown function DUF976, *Caenorhabditis* speci



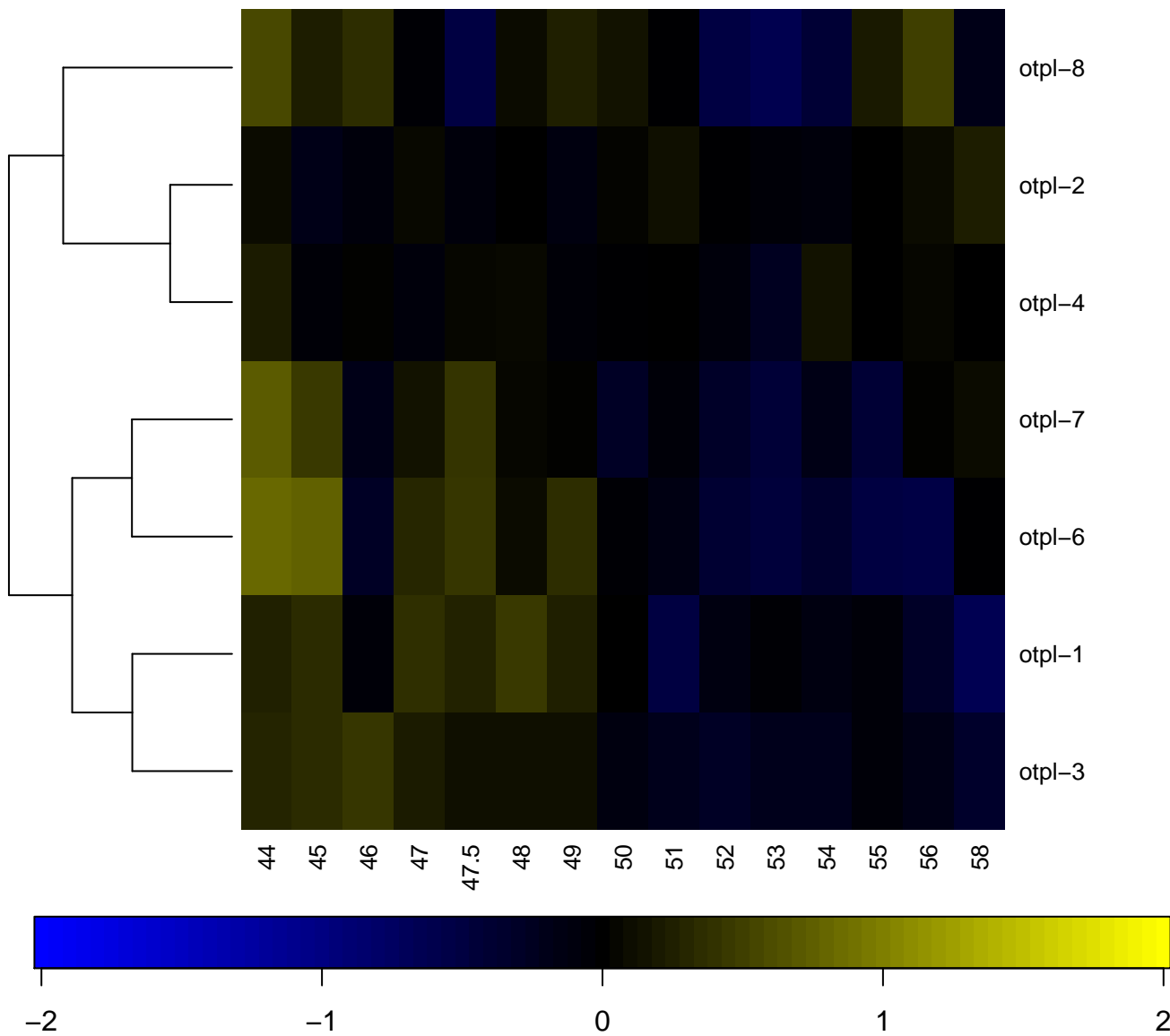
Protein of unknown function WSN



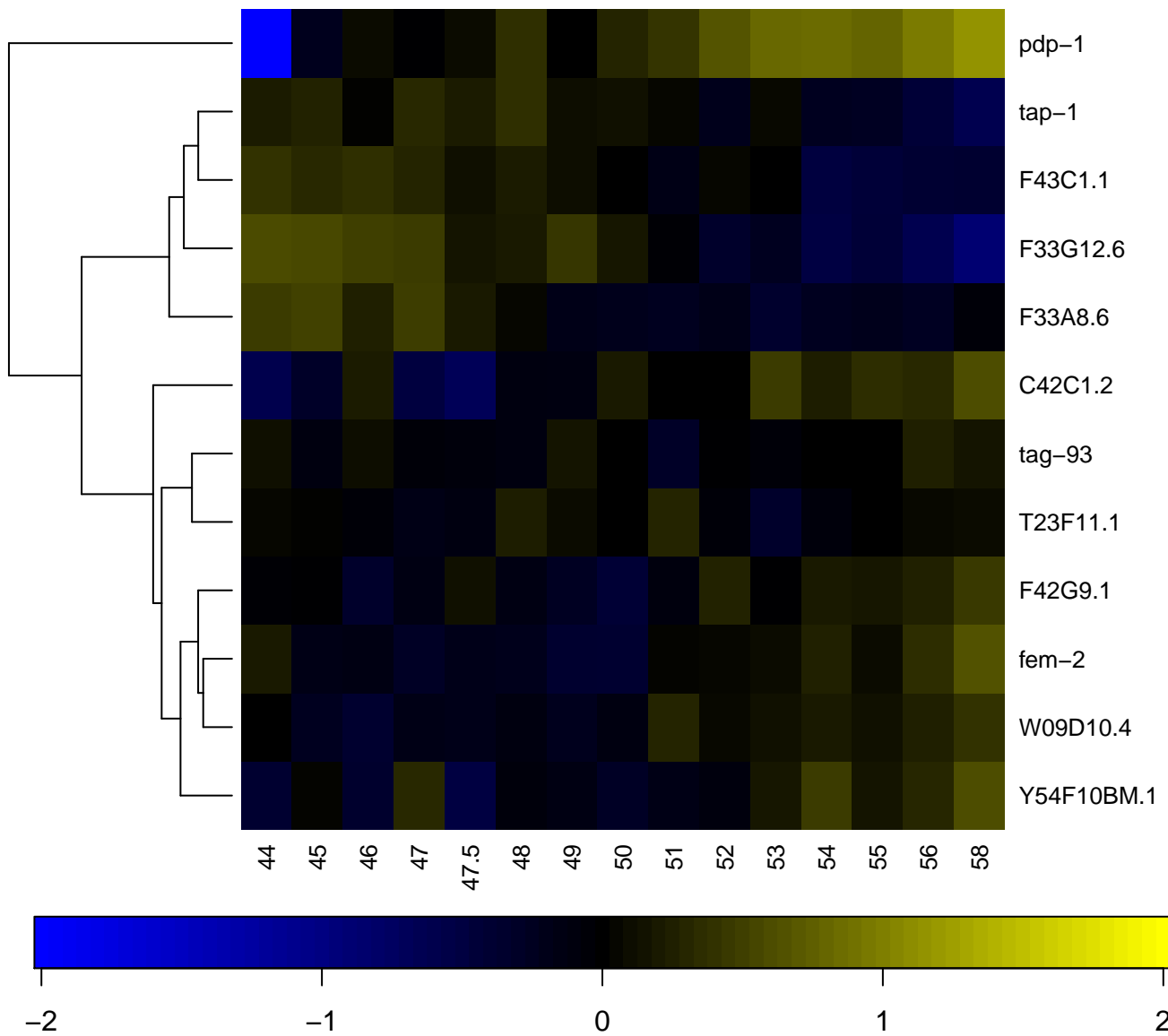
Protein of unknown function, C6 domain



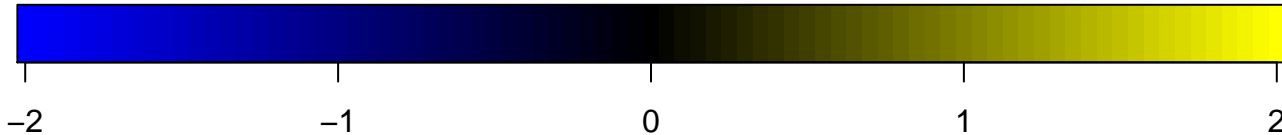
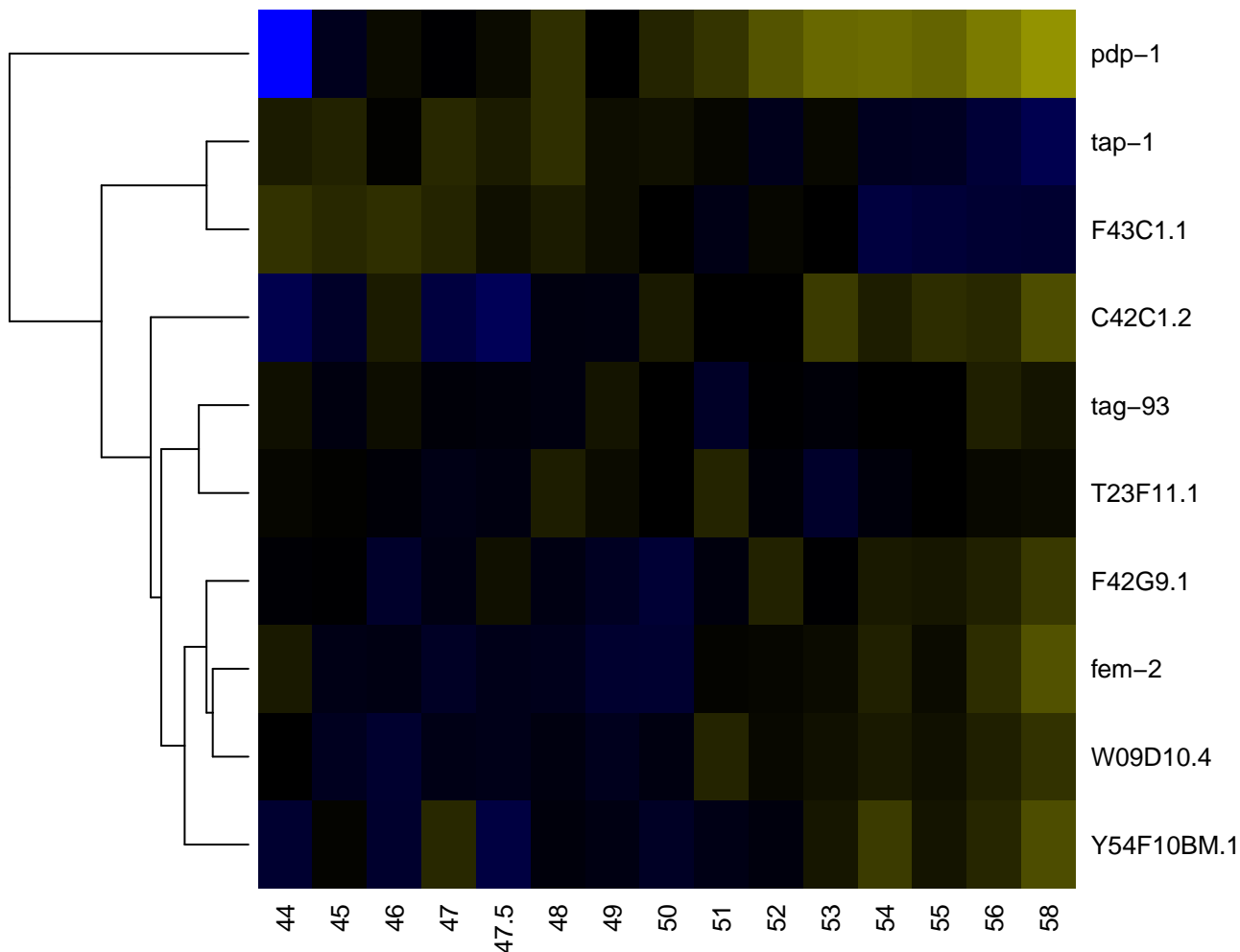
Protein of unknown function, DUF270



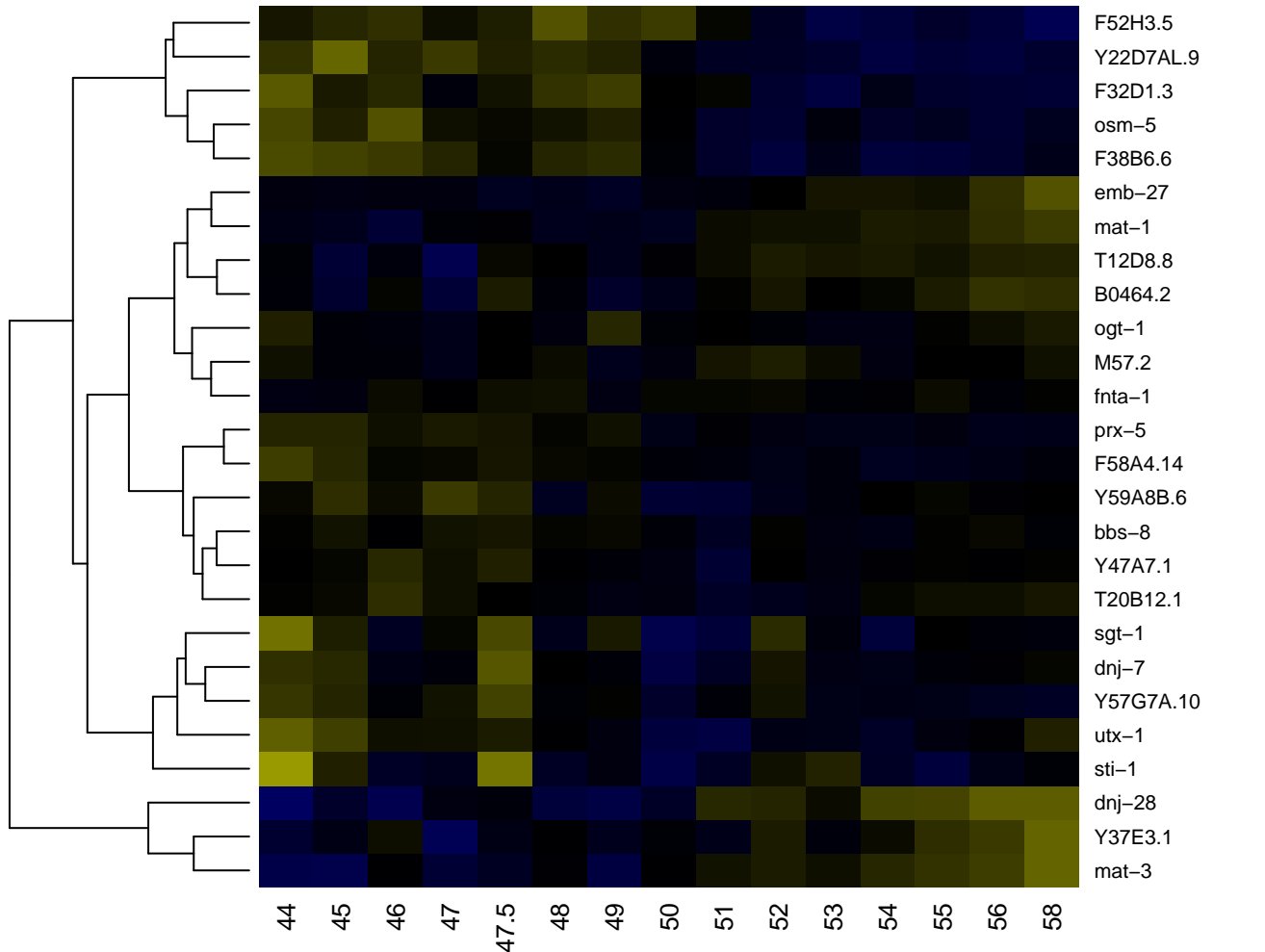
Protein phosphatase 2C-related



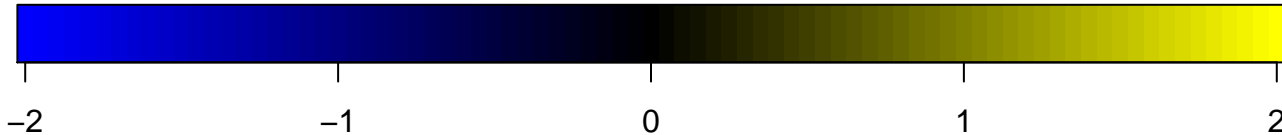
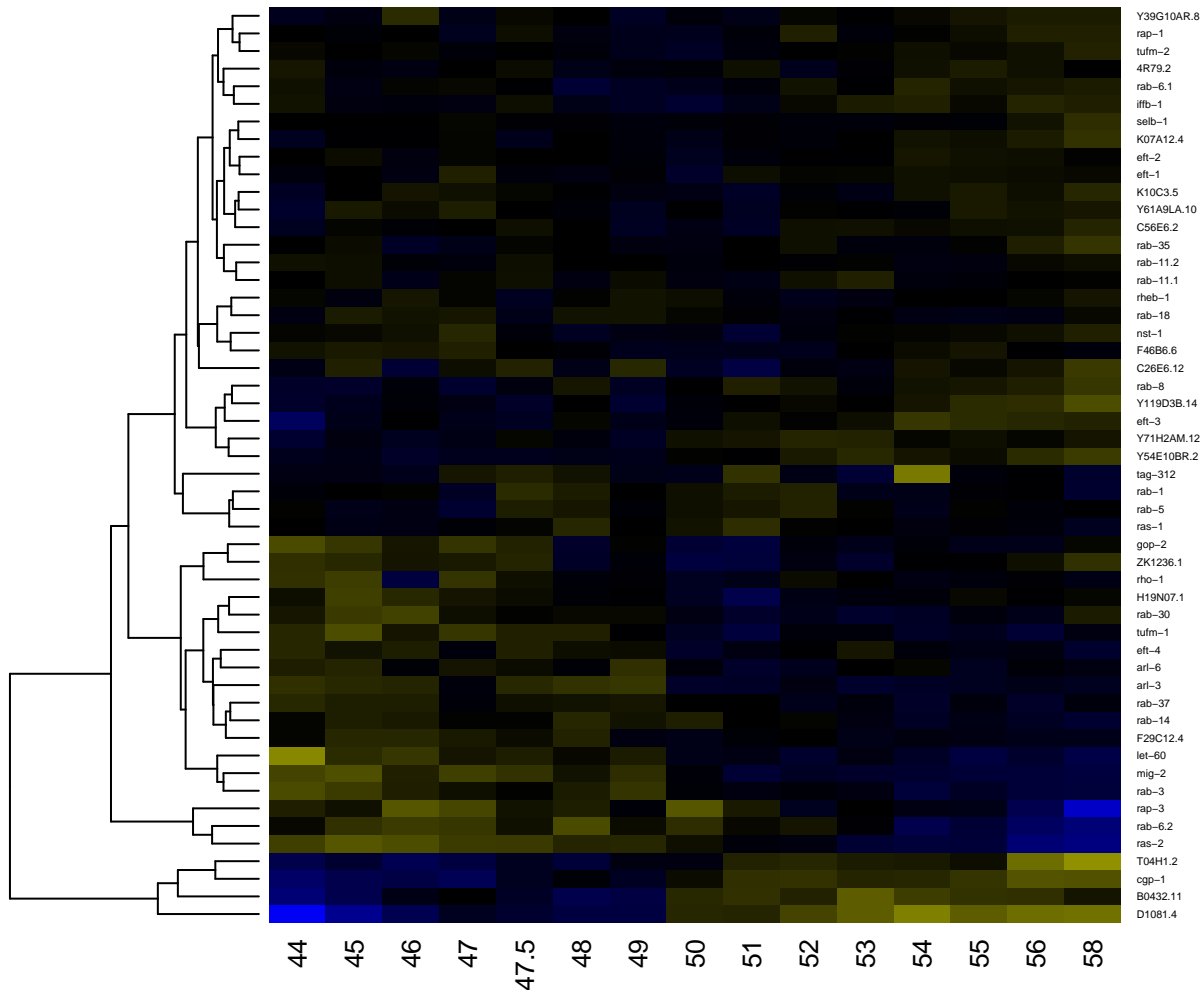
Protein phosphatase 2C, N-terminal



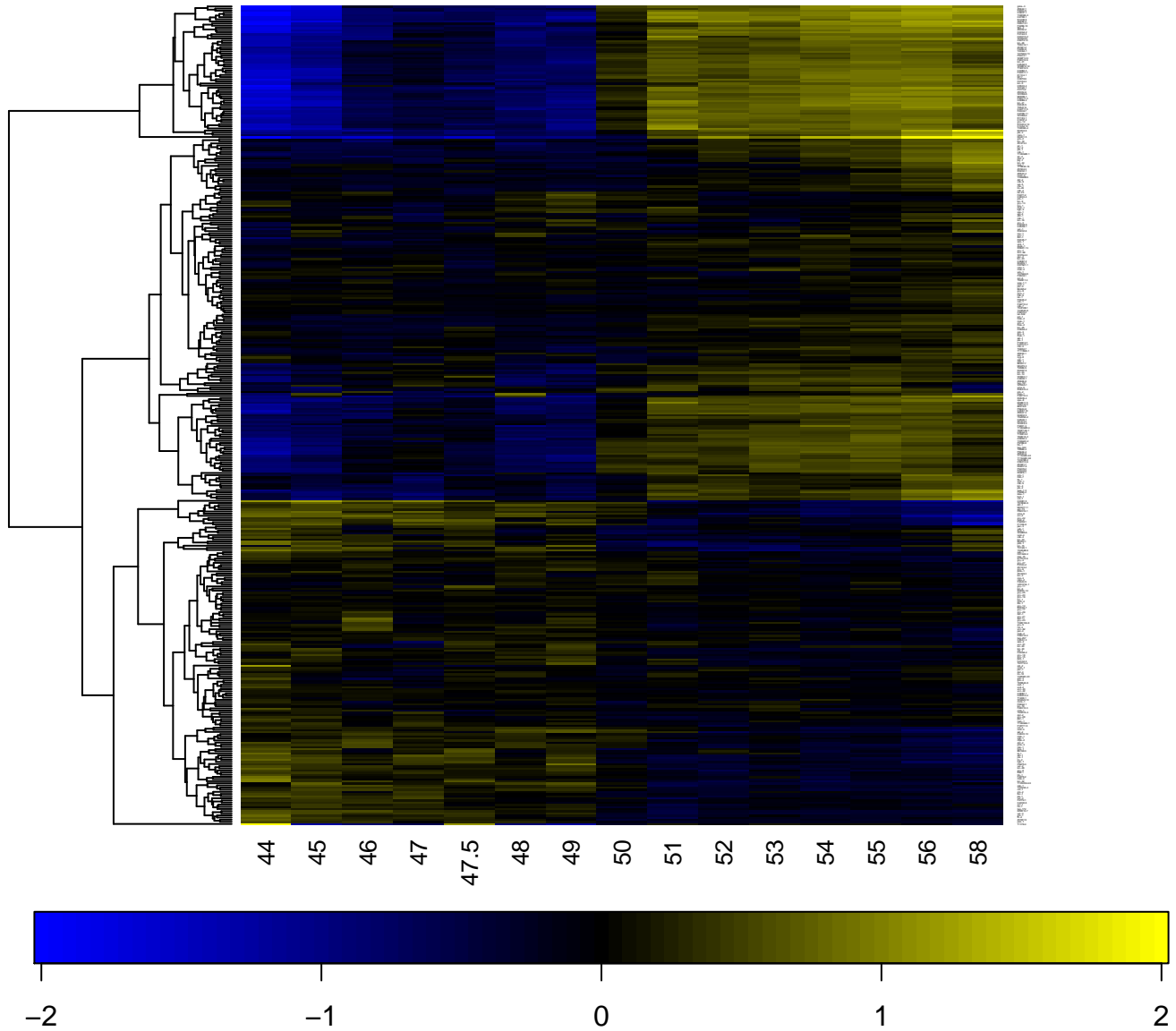
Protein prenyltransferase



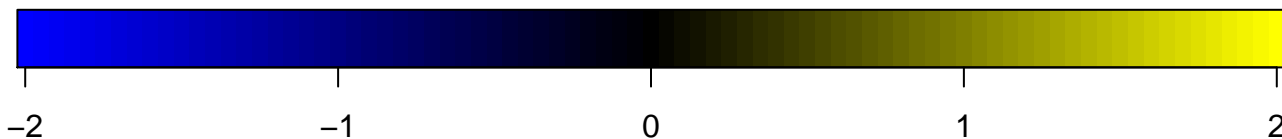
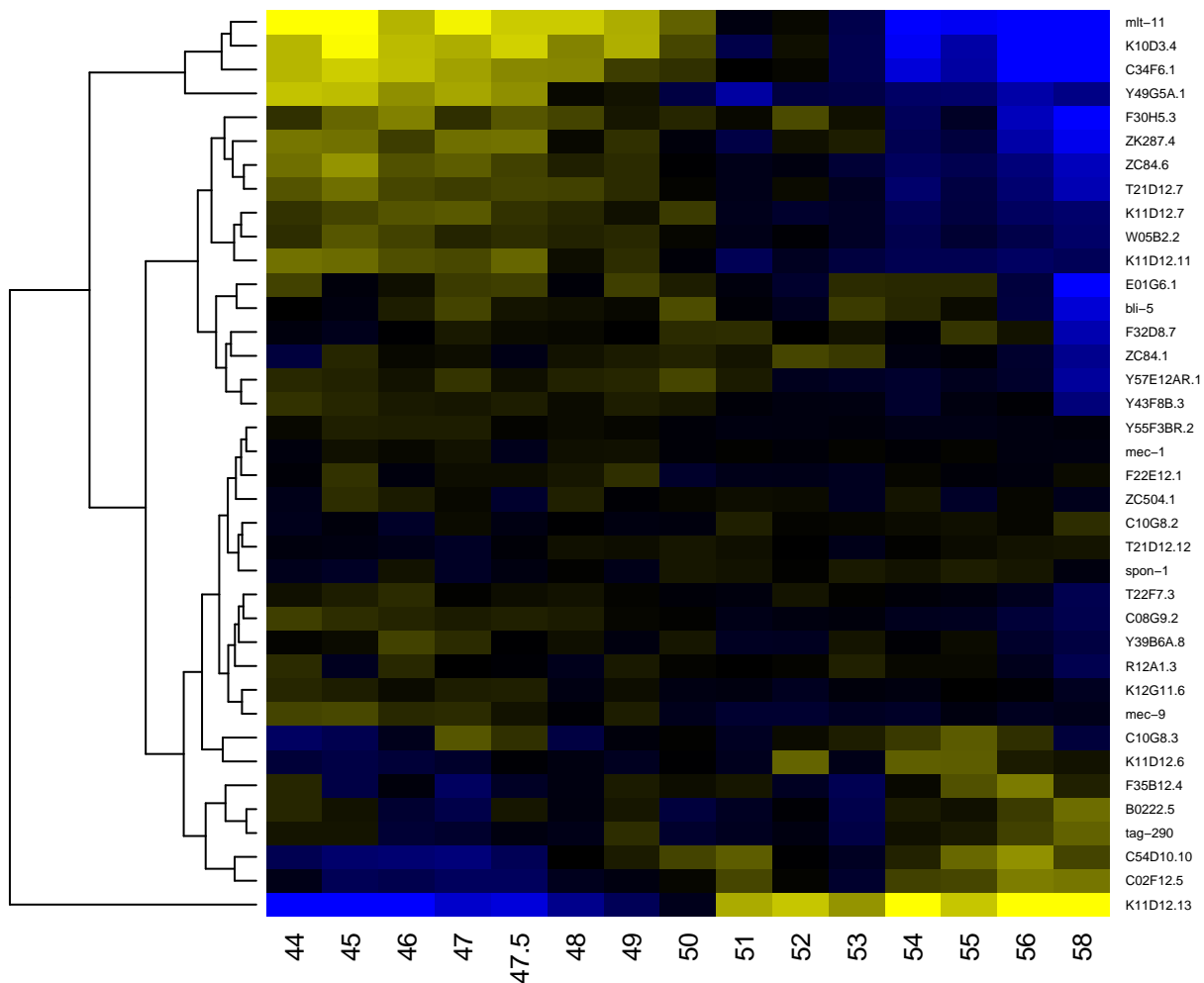
Protein synthesis factor, GTP-binding



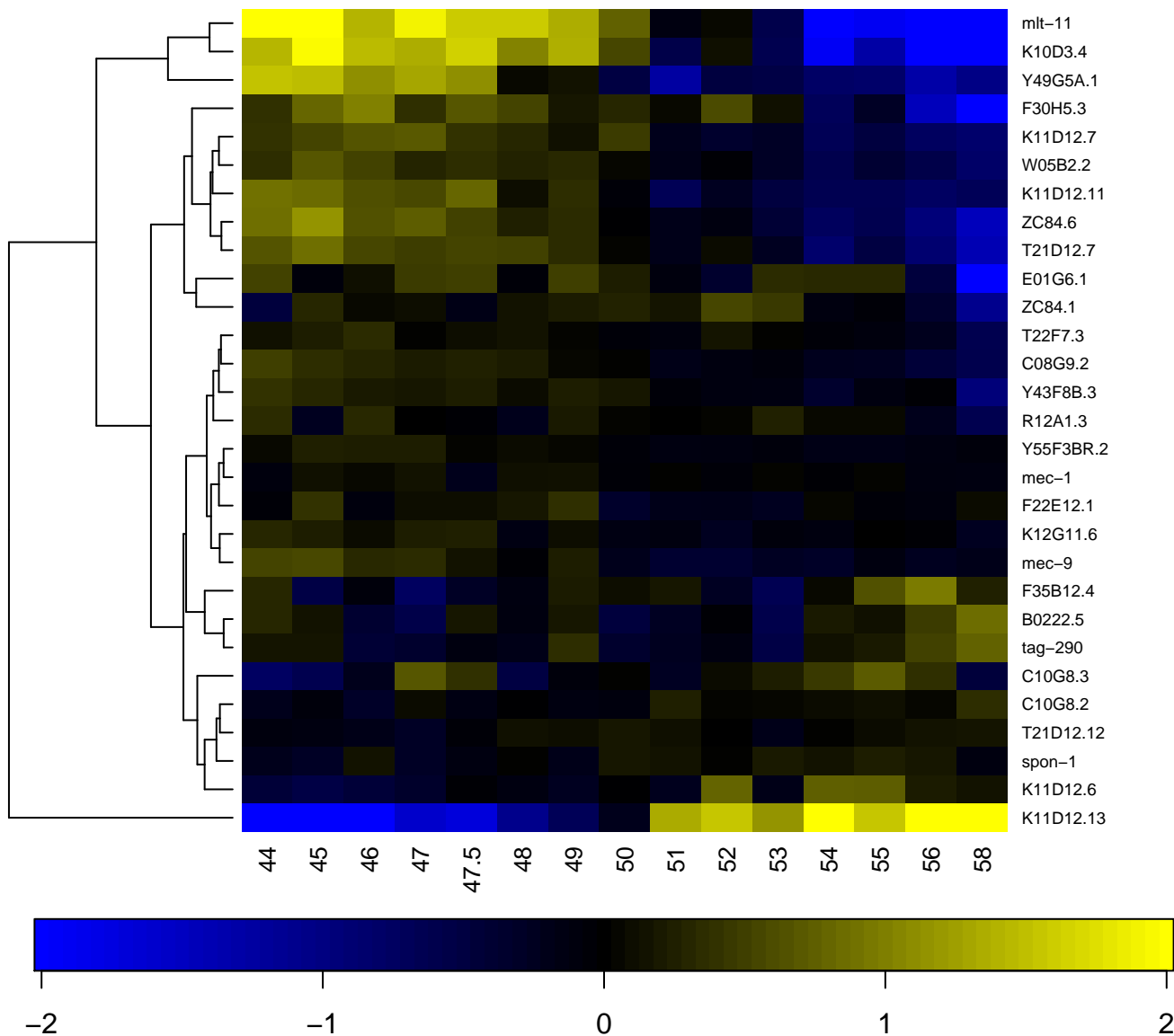
Protein tyrosine kinase



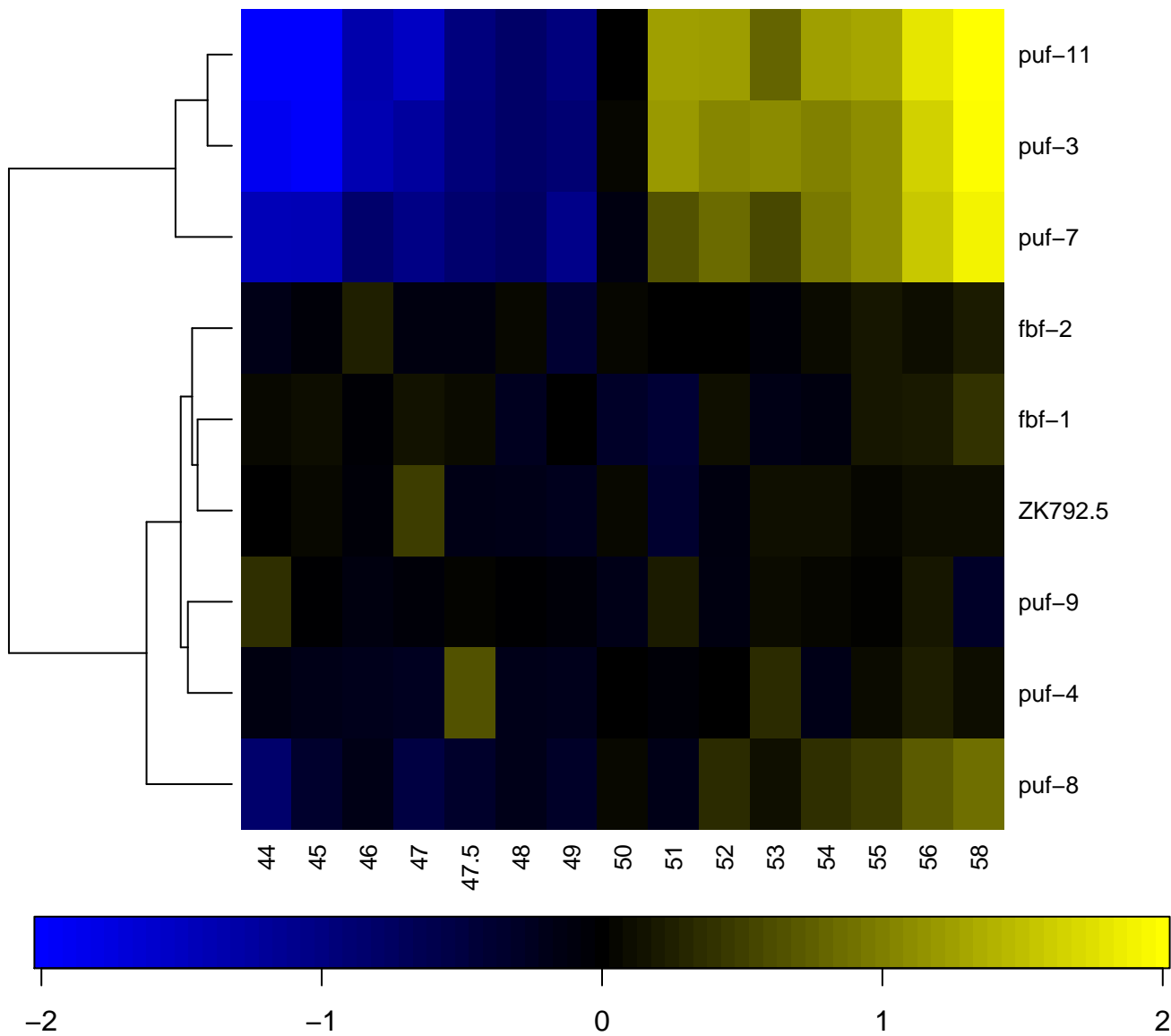
Proteinase inhibitor I2, Kunitz metazoa



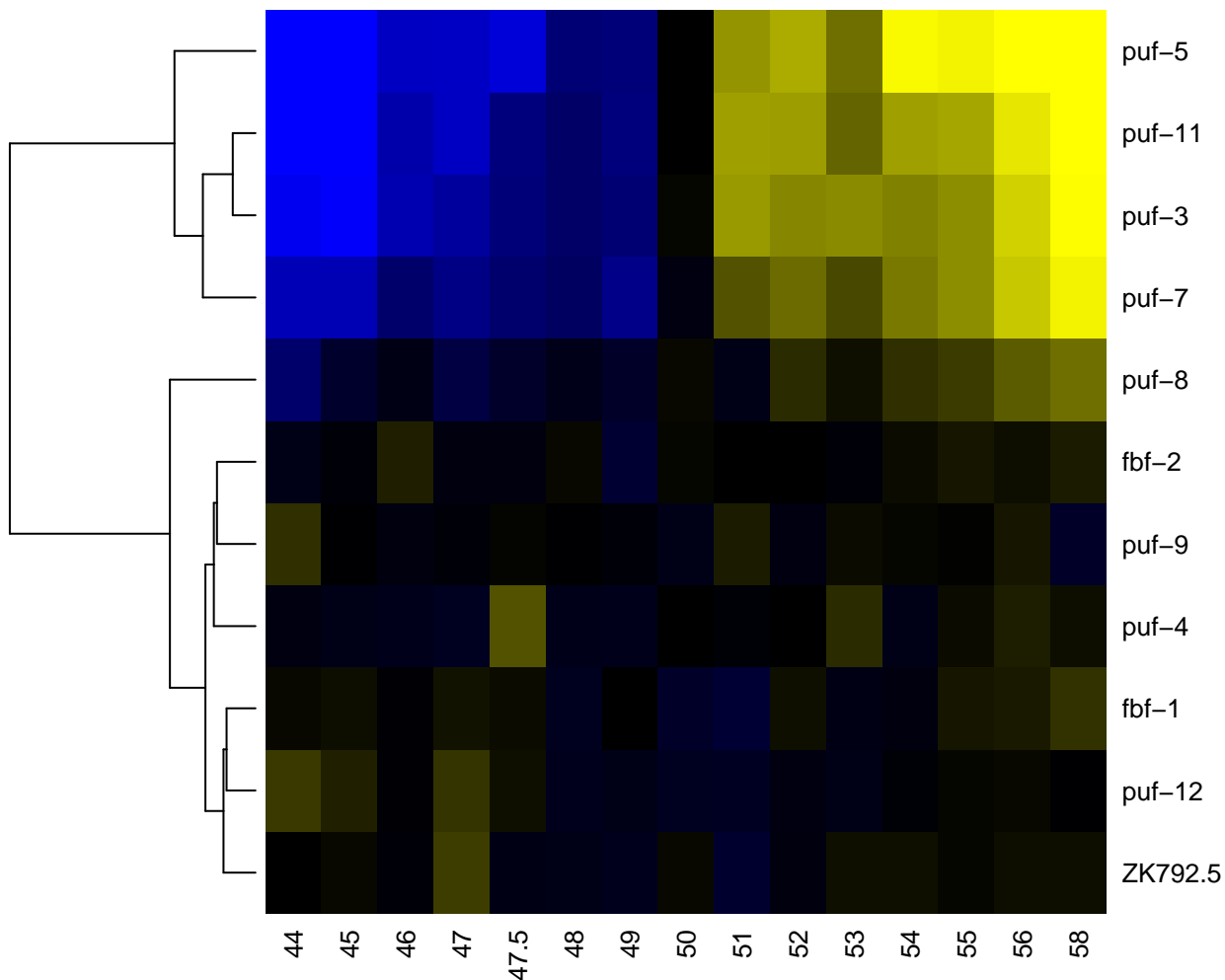
Proteinase inhibitor I2, Kunitz, conserved site



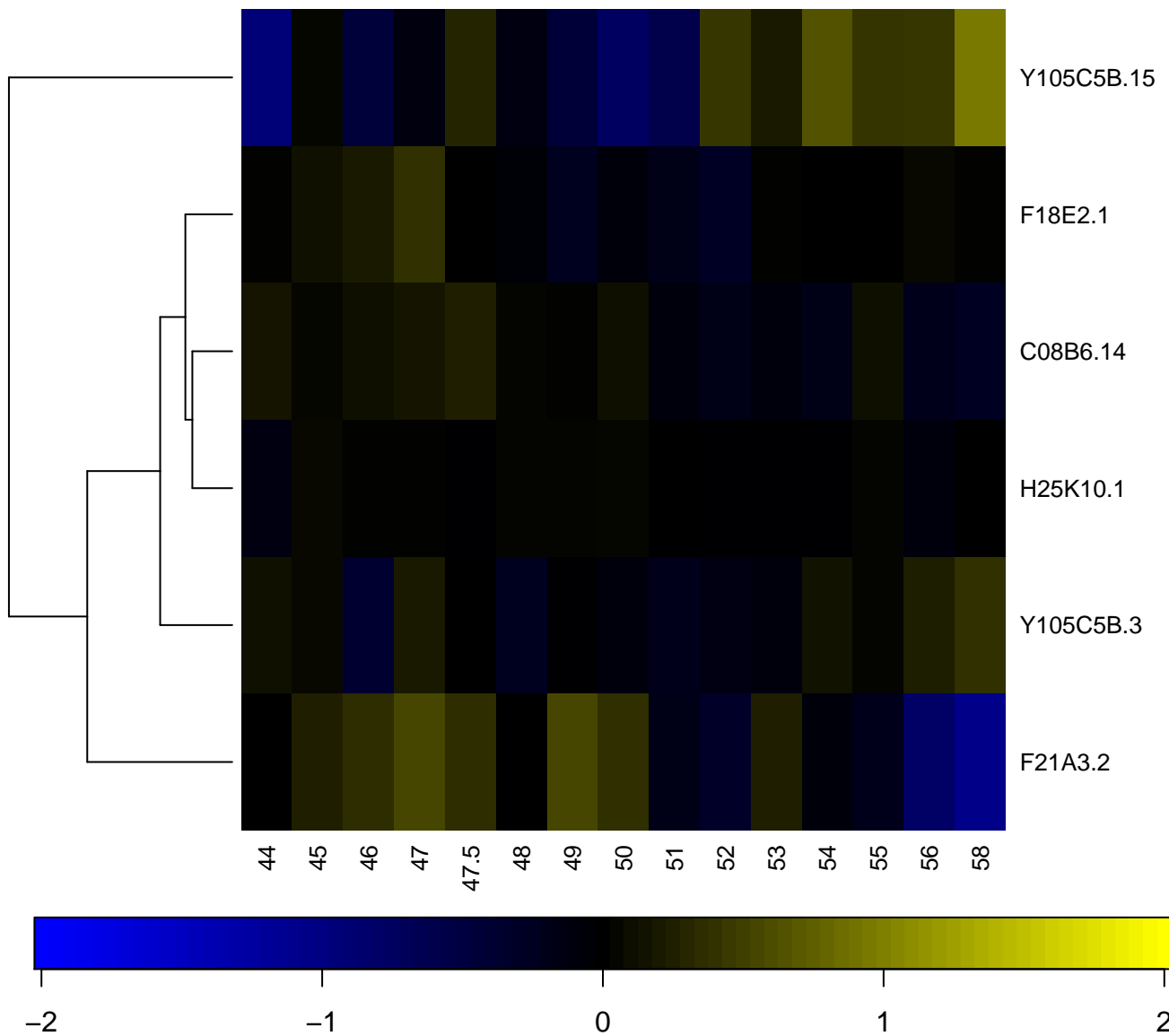
Pumilio-family RNA binding repeat



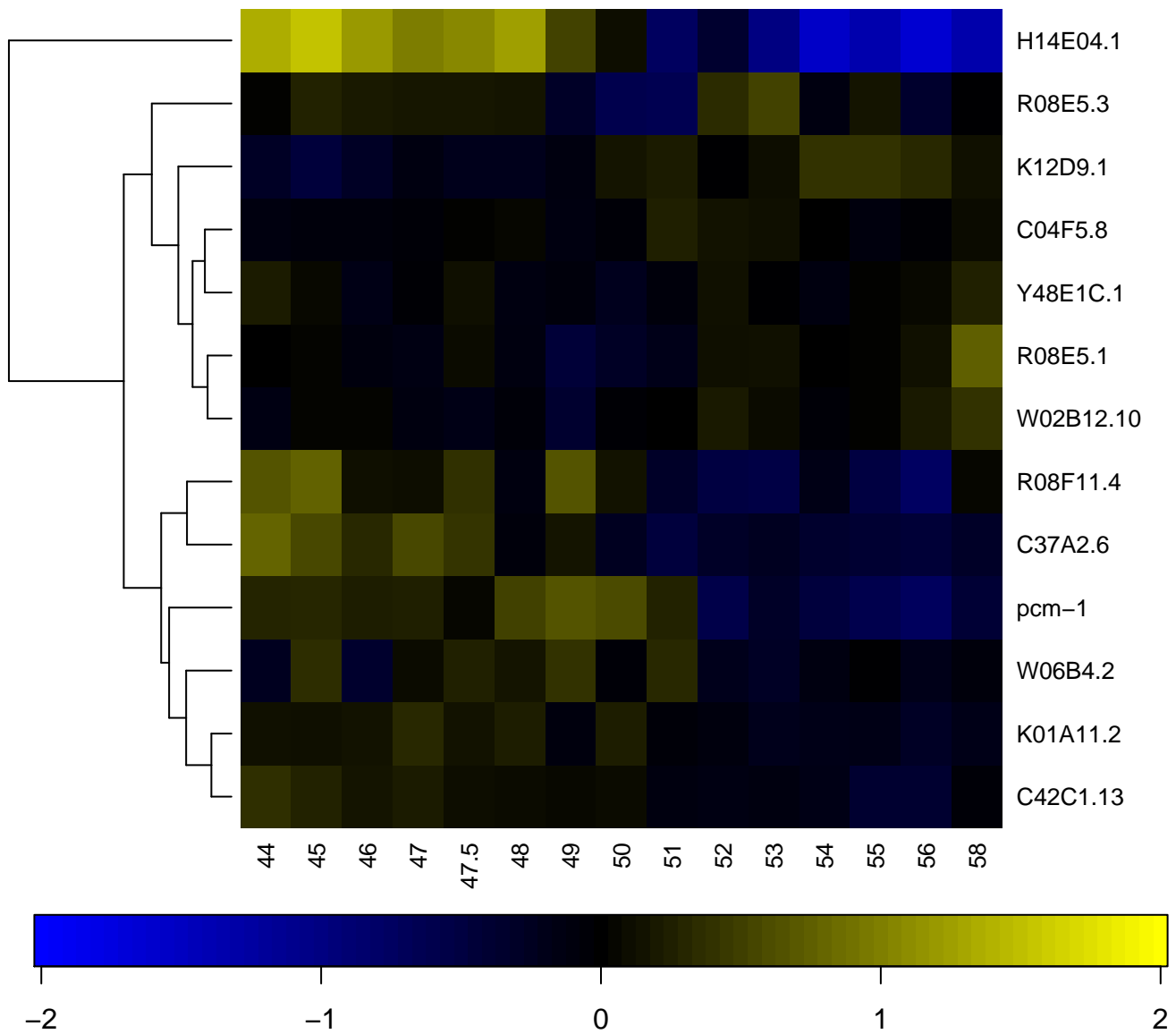
Pumilio RNA-binding repeat



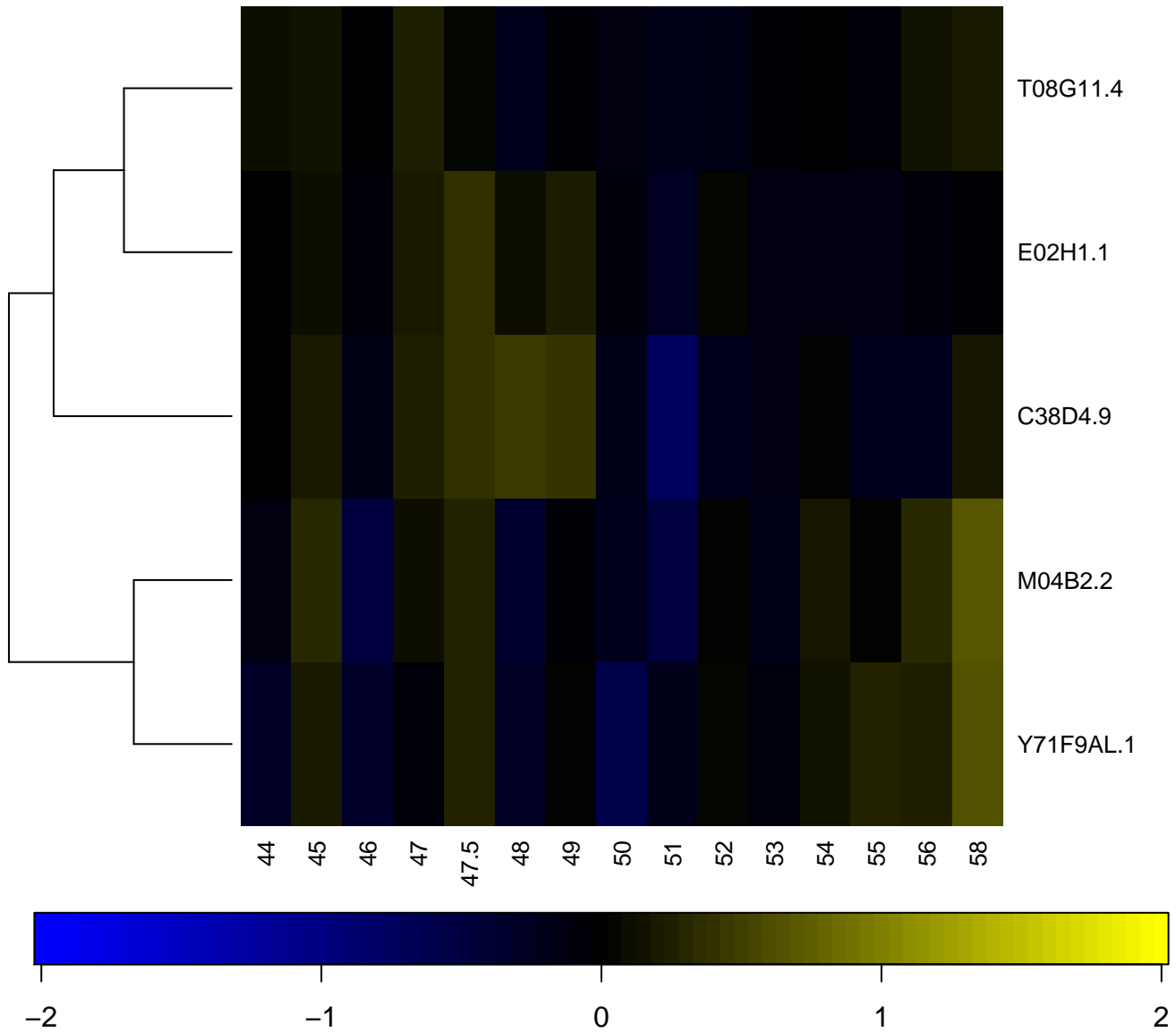
Purple acid phosphatase, N-terminal



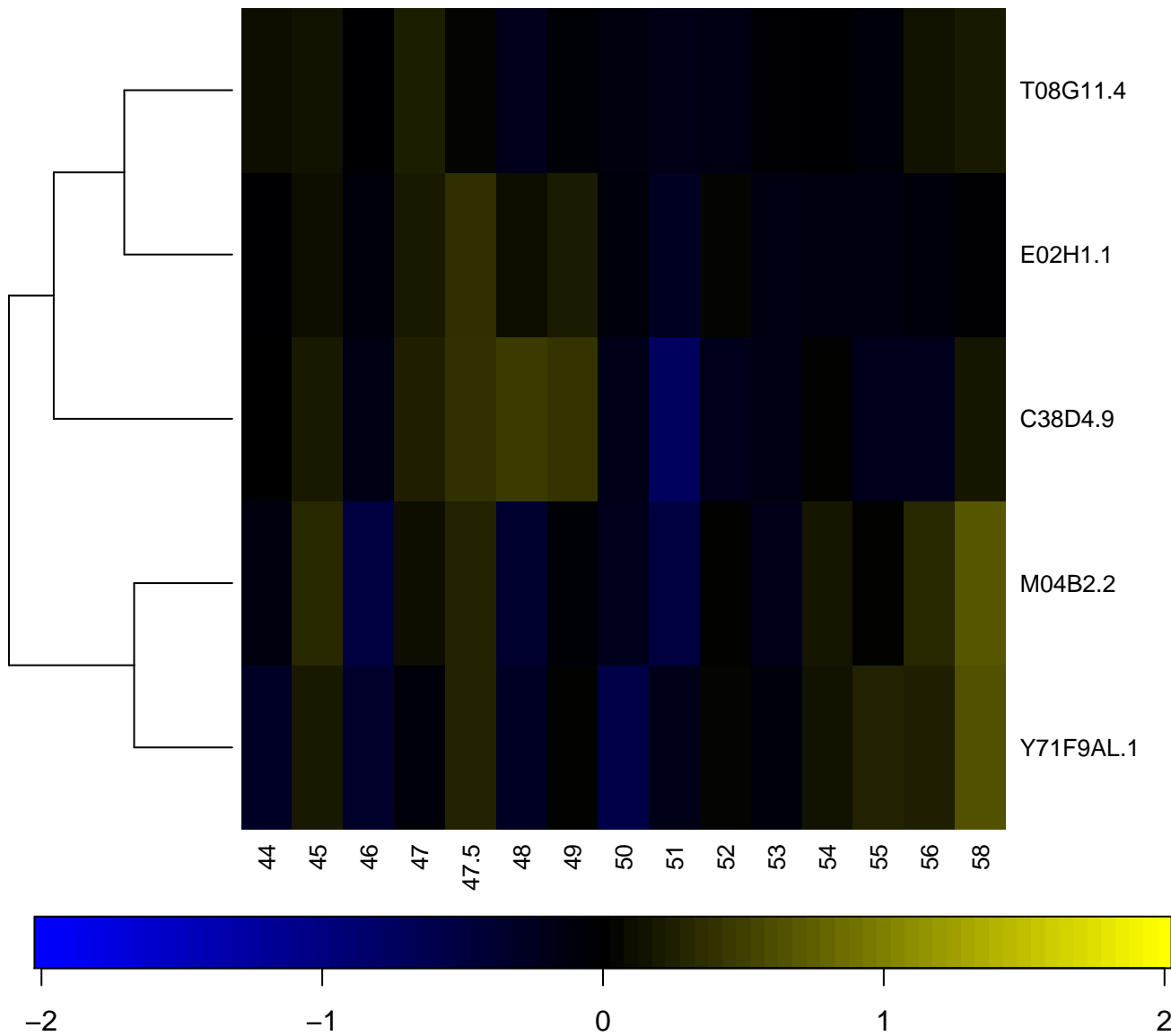
Putative methyltransferase



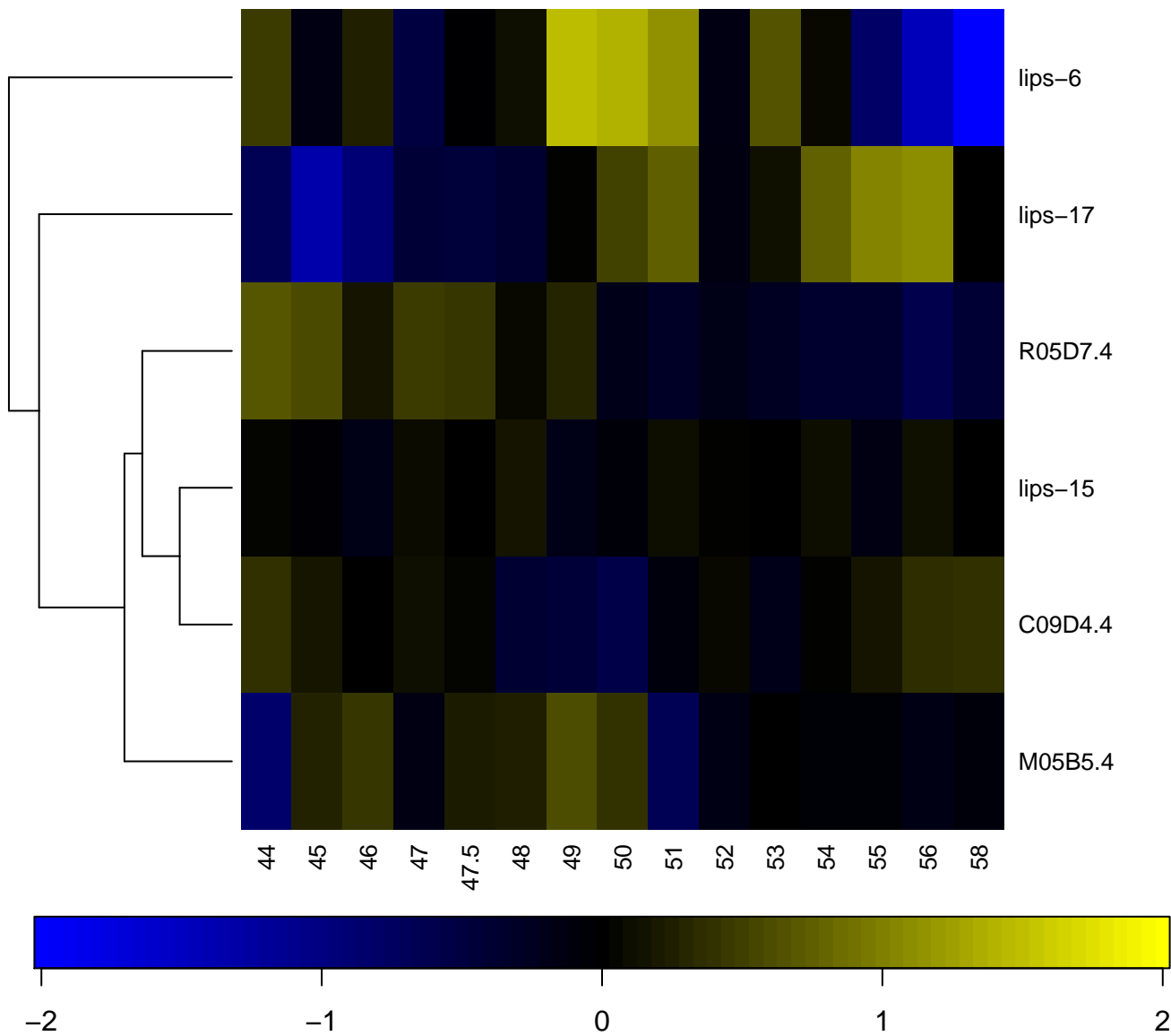
Putative RNA methylase



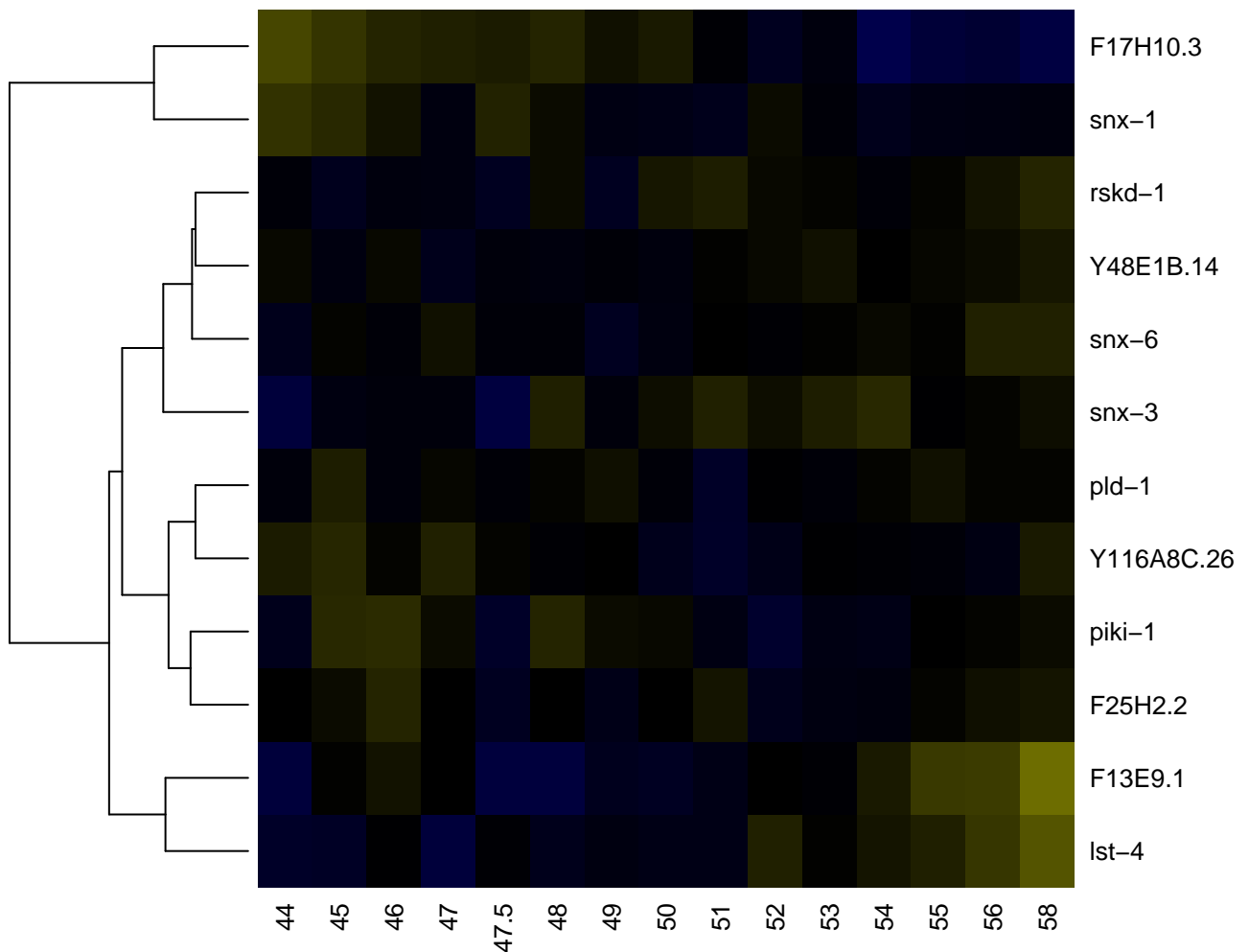
Putative RNA methylase family UPF0020



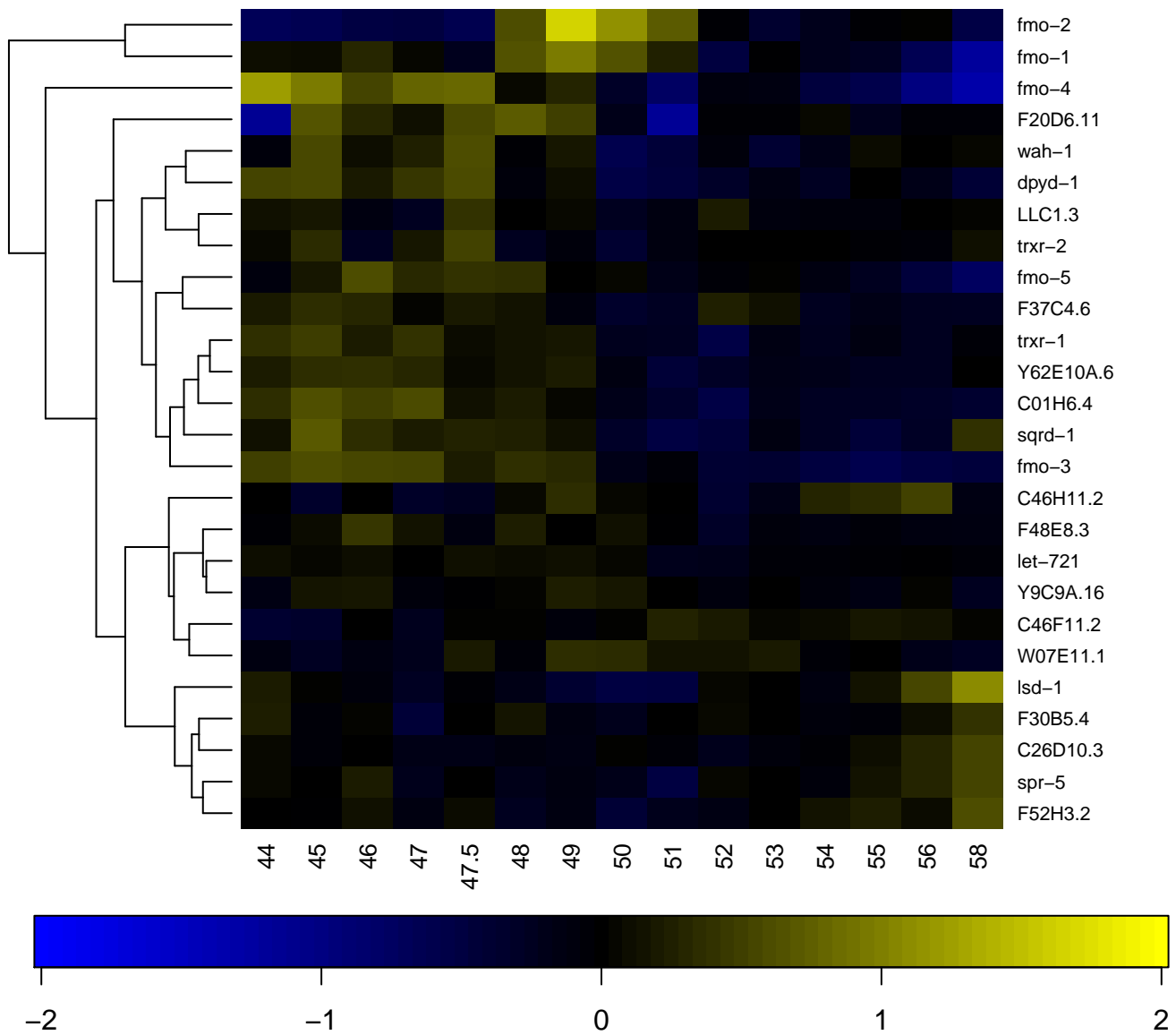
Putative serine esterase (DUF676)



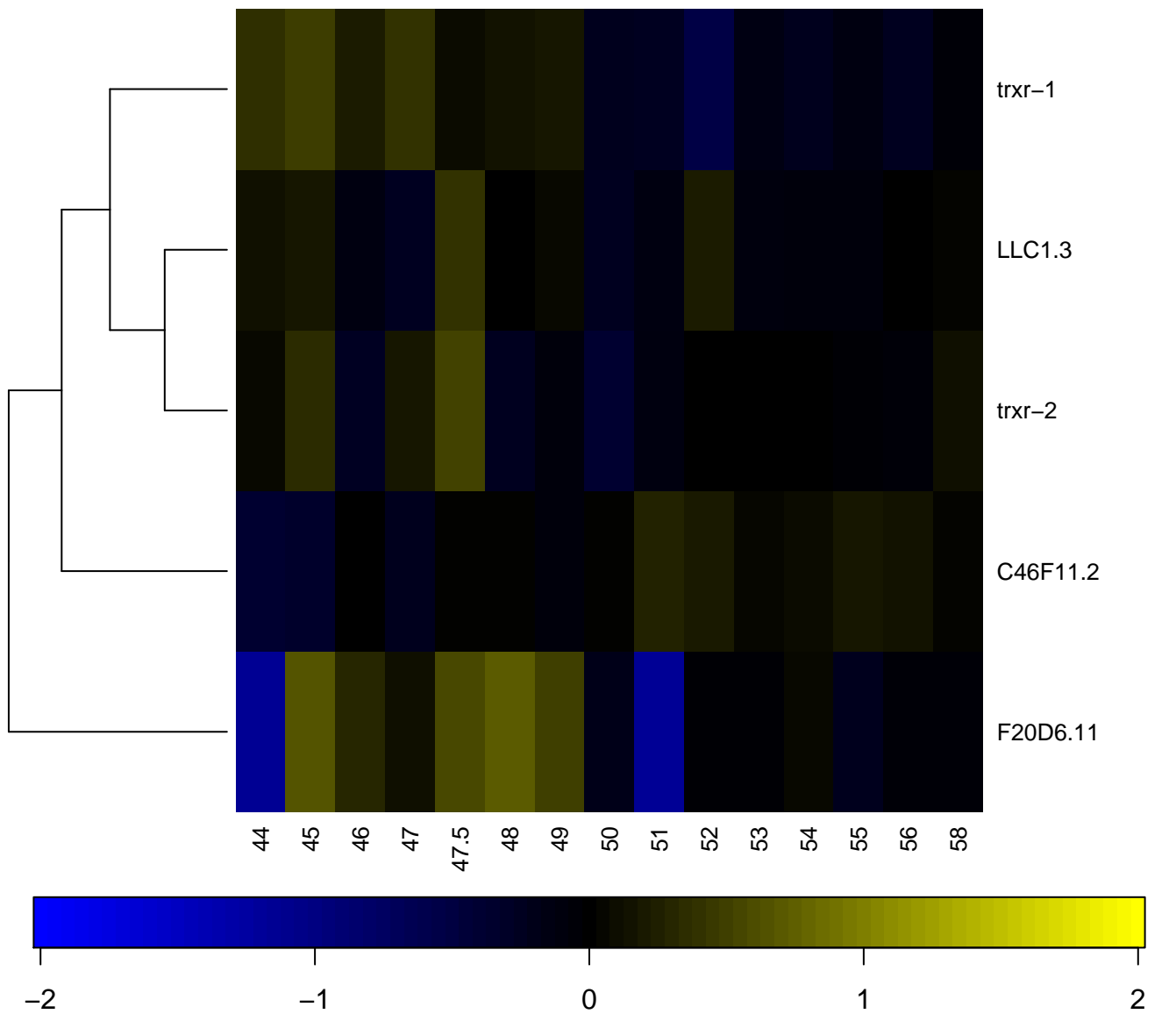
PX domain



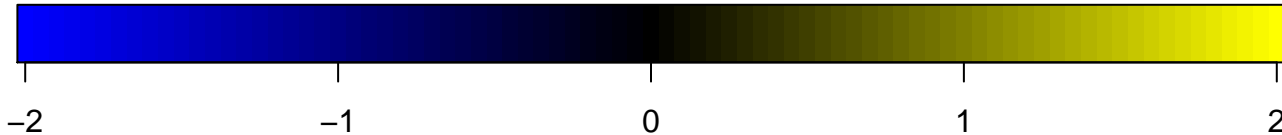
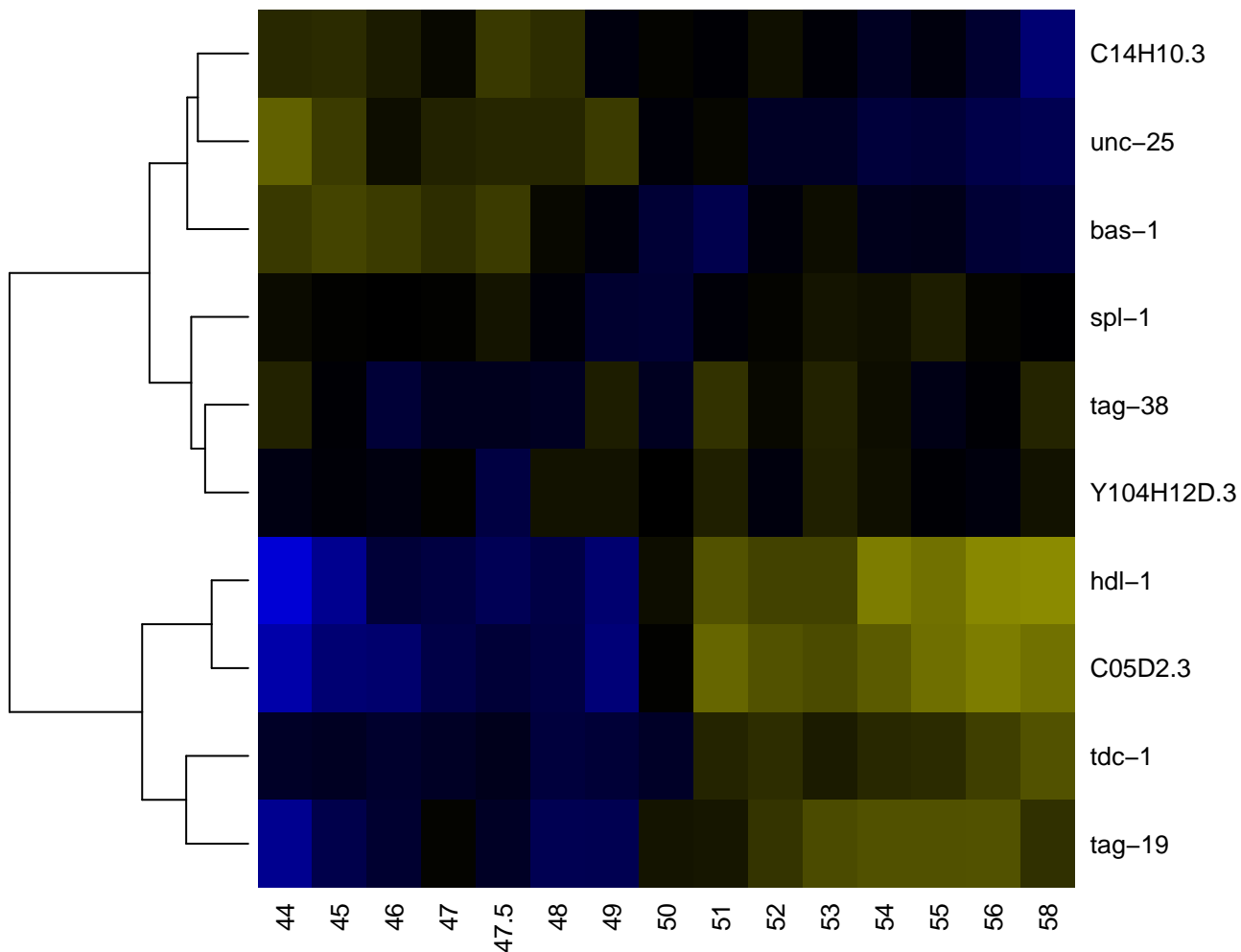
Pyridine nucleotide–disulphide oxidoreductase



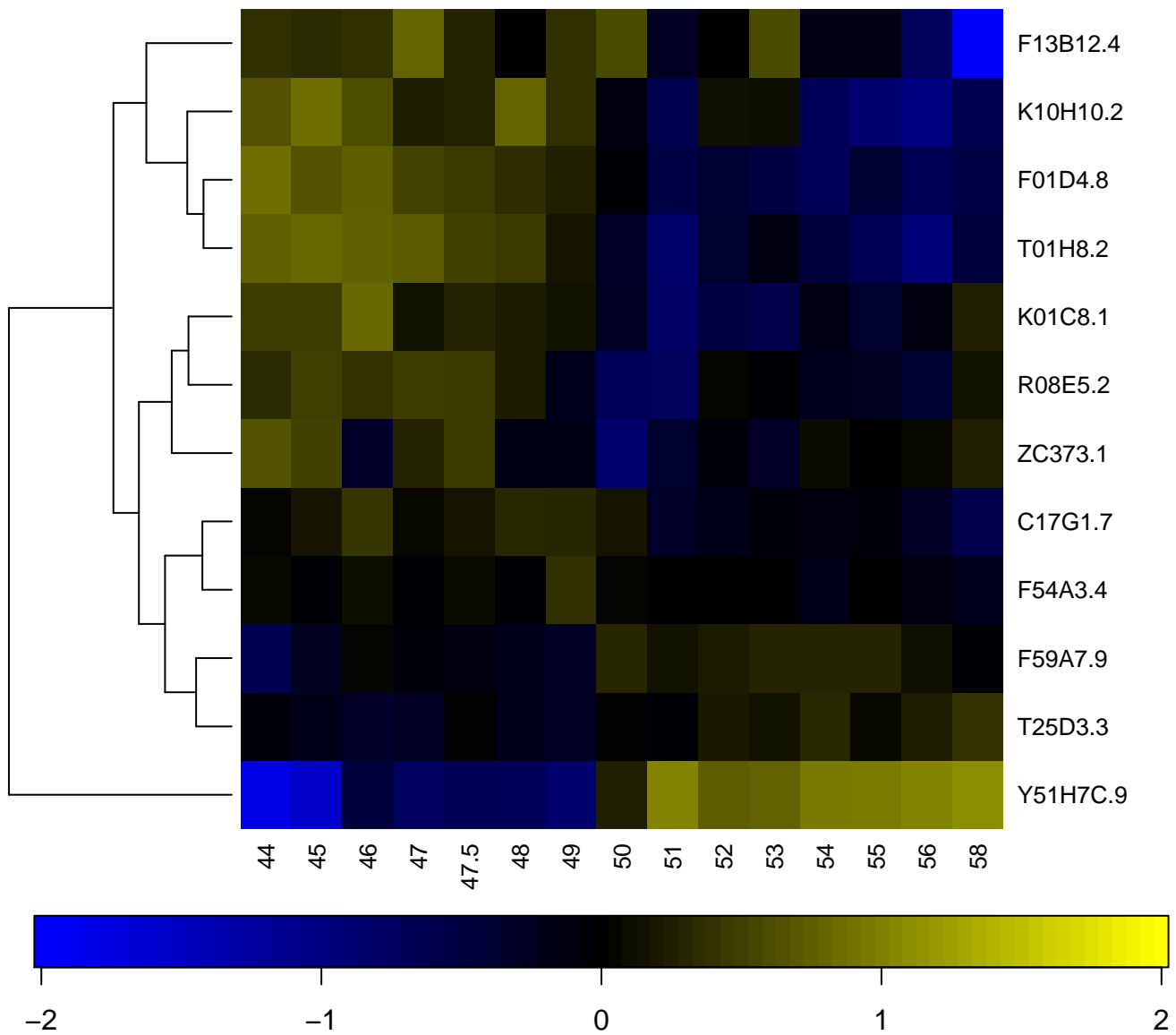
Pyridine nucleotide–disulphide oxidoreductase, dimerisation



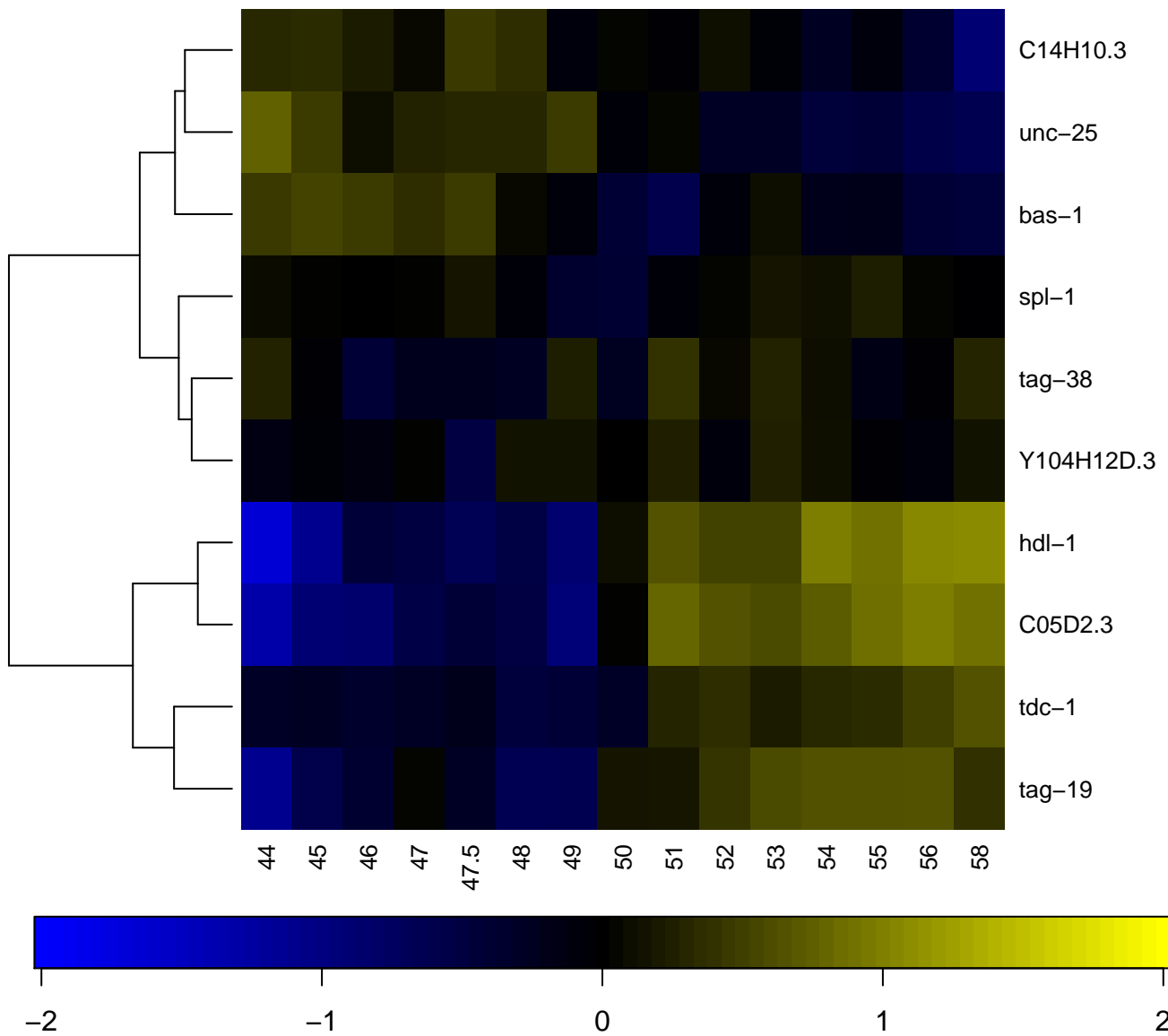
Pyridoxal-dependent decarboxylase conserved domain



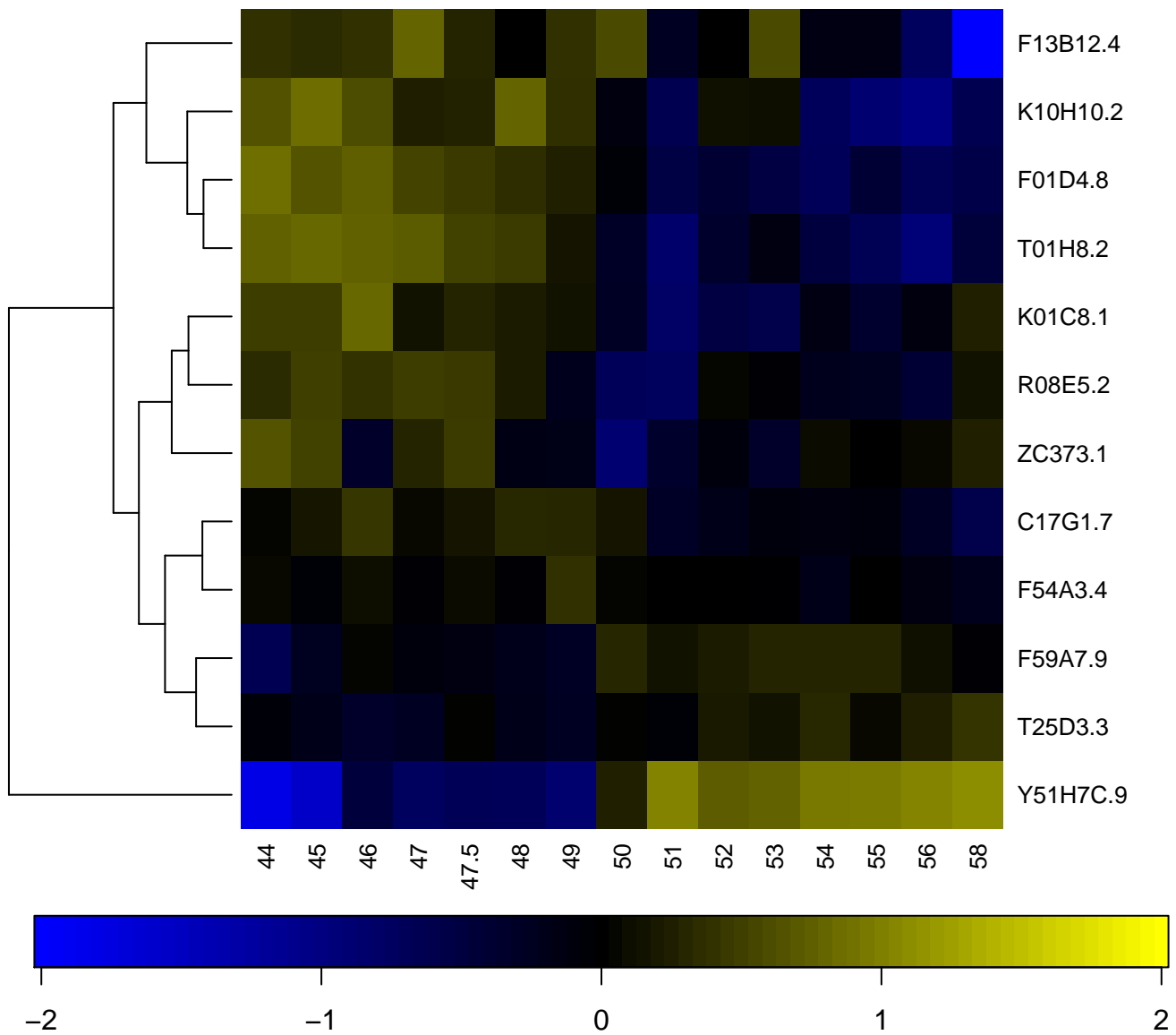
Pyridoxal-phosphate dependent enzyme



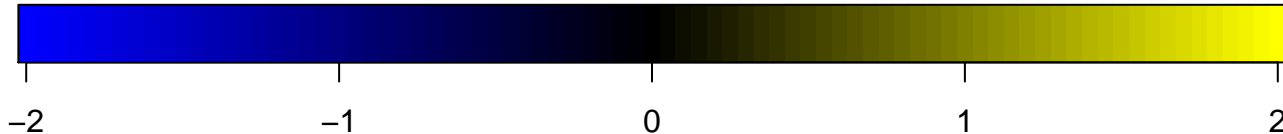
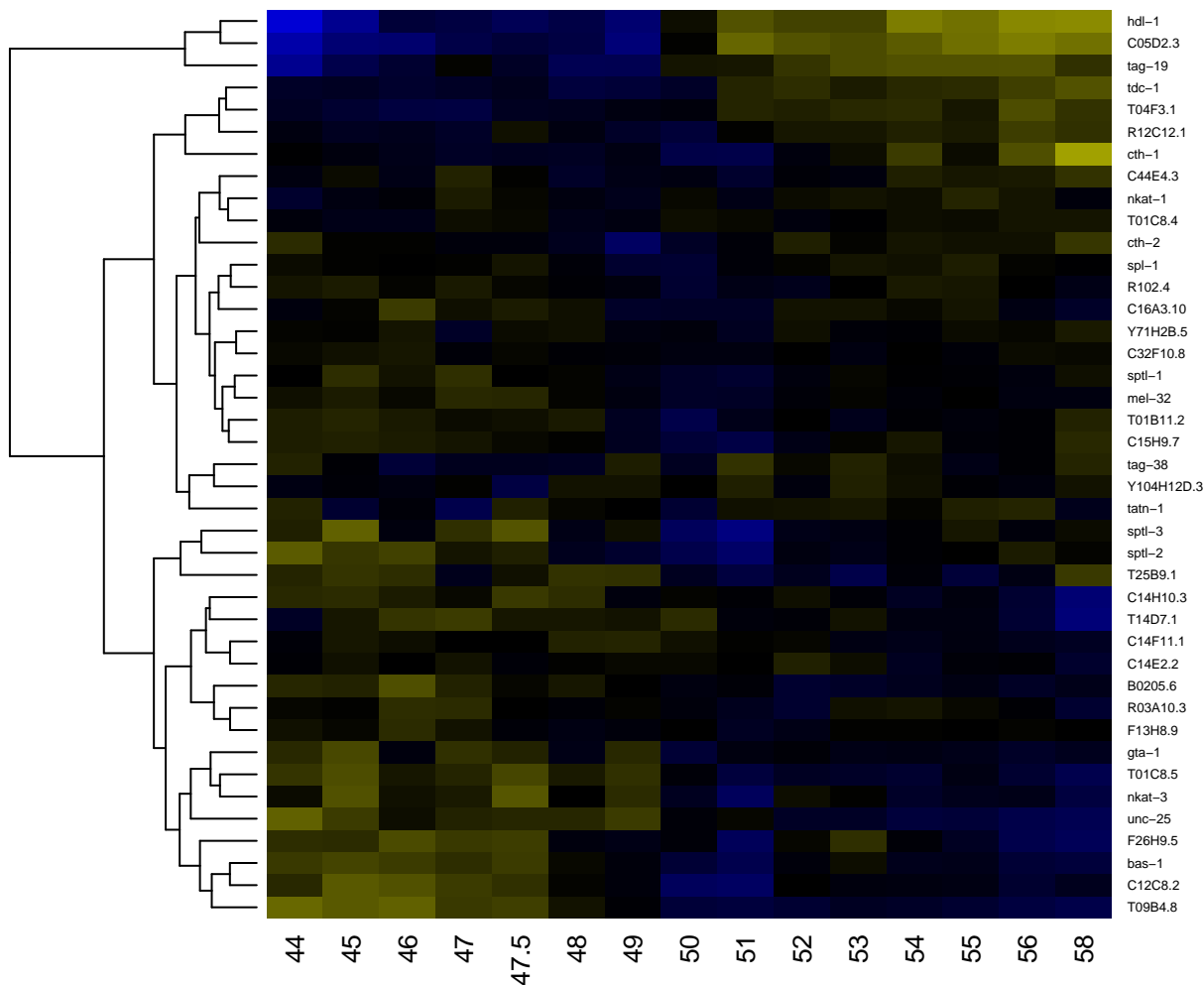
Pyridoxal phosphate-dependent decarboxylase



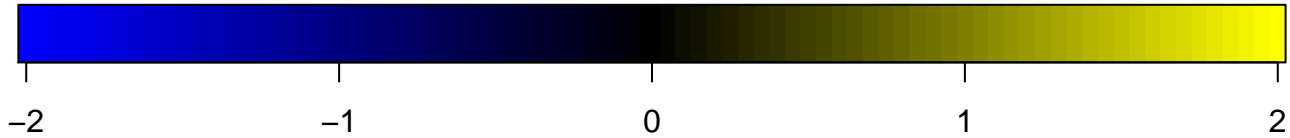
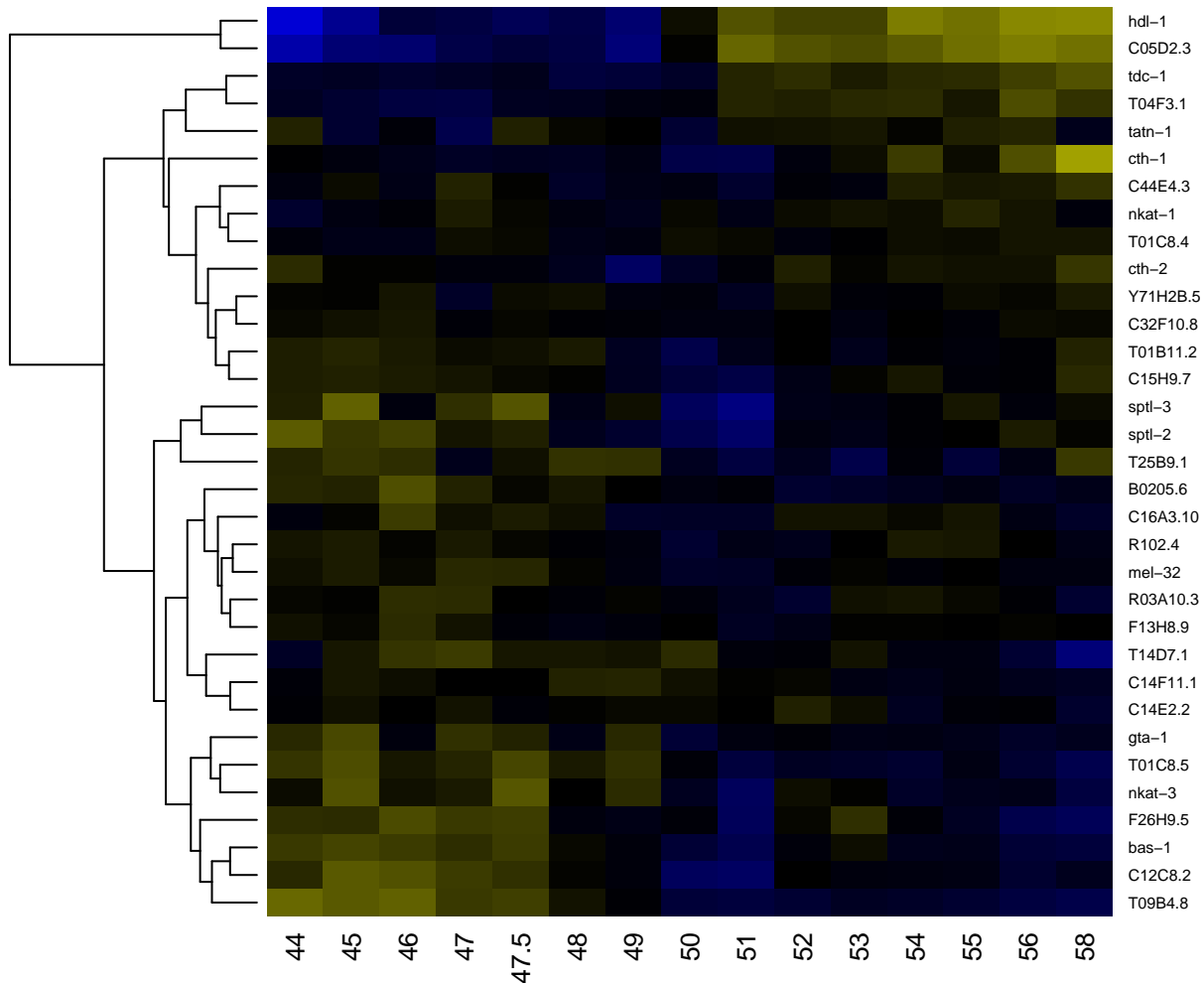
Pyridoxal phosphate-dependent enzyme, beta subunit



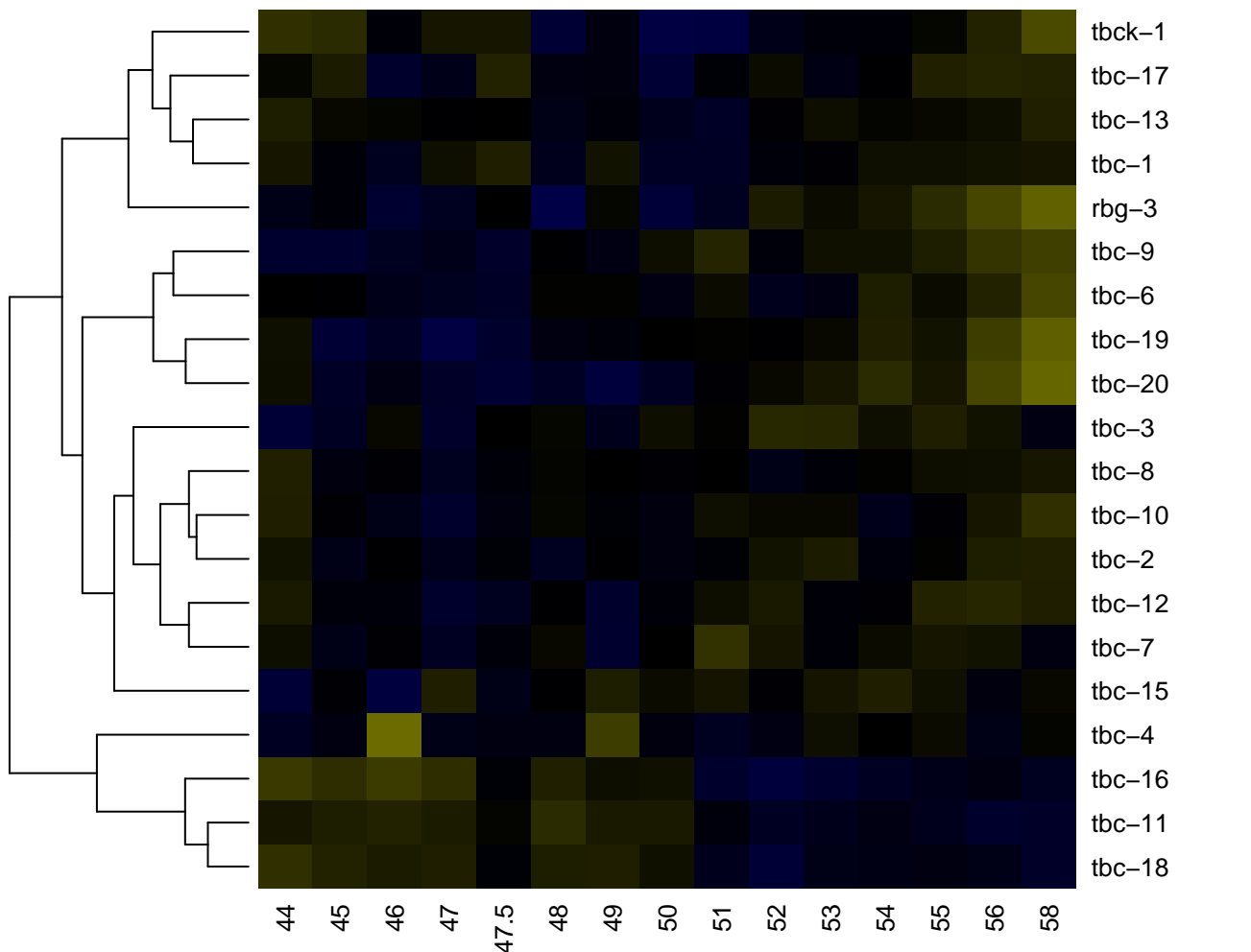
oxal phosphate-dependent transferase, major region, subd



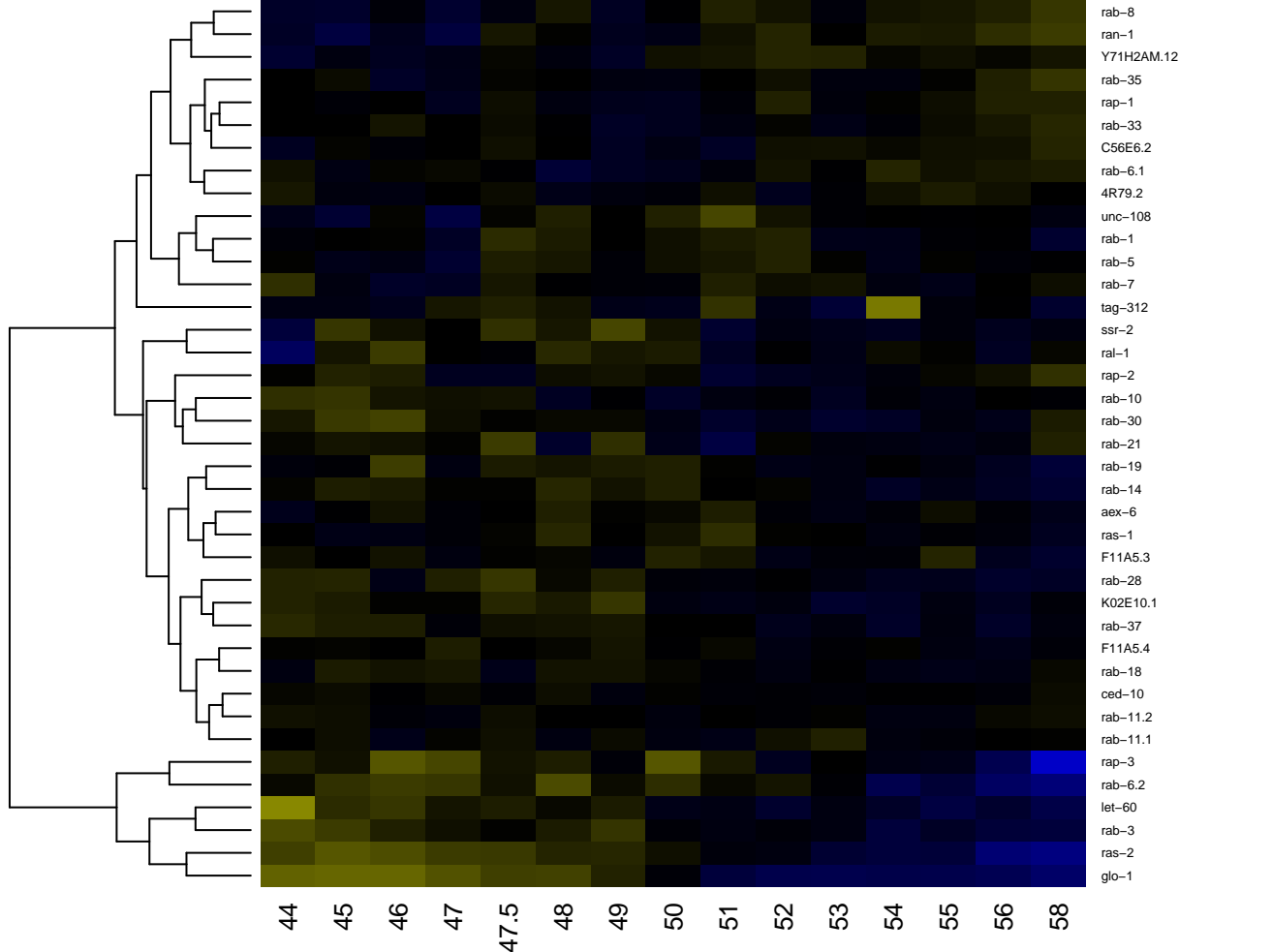
oxal phosphate-dependent transferase, major region, subd



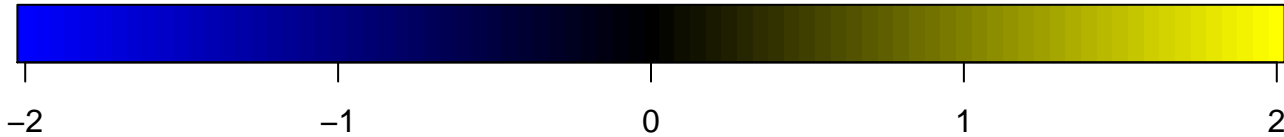
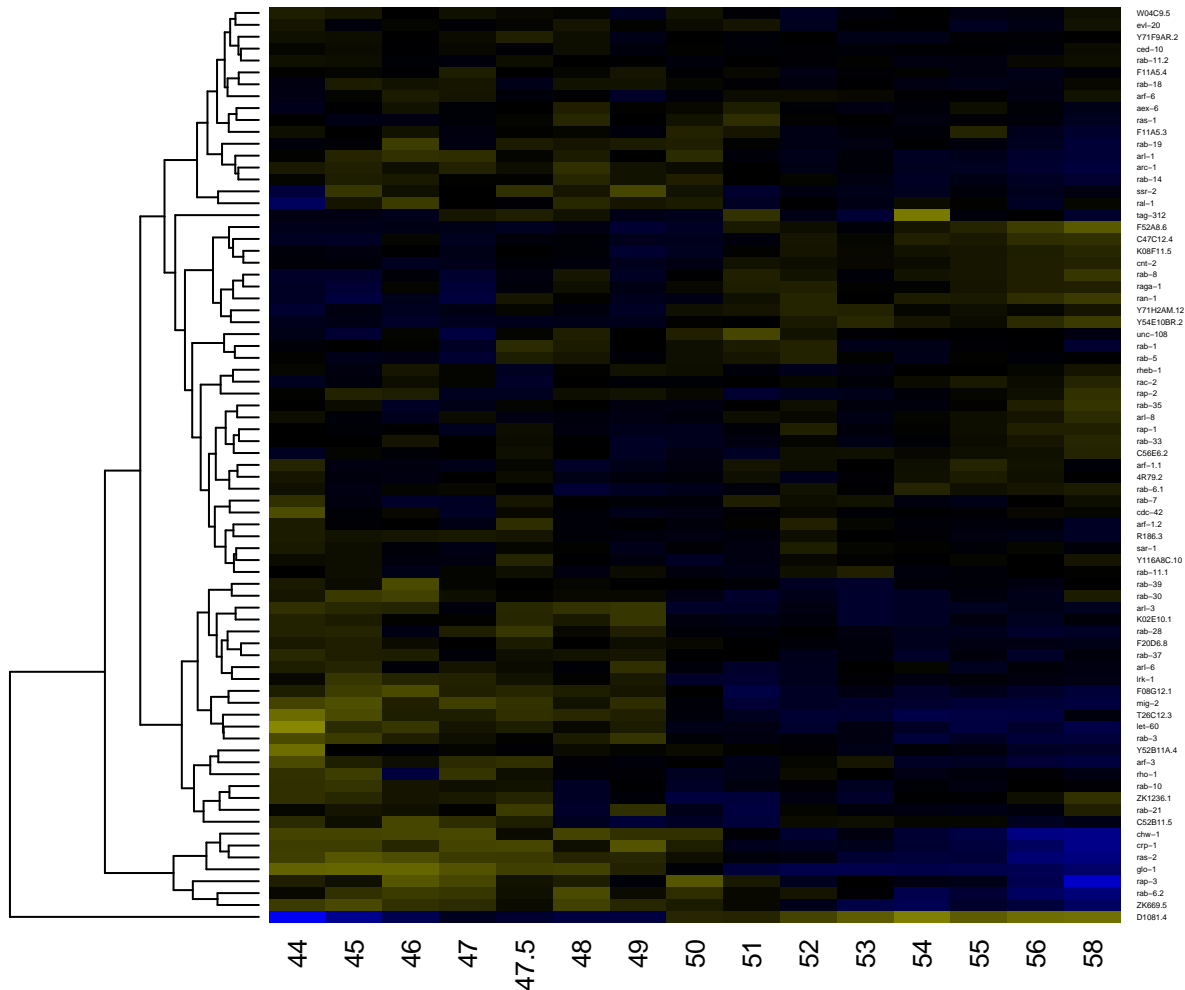
RabGAP/TBC



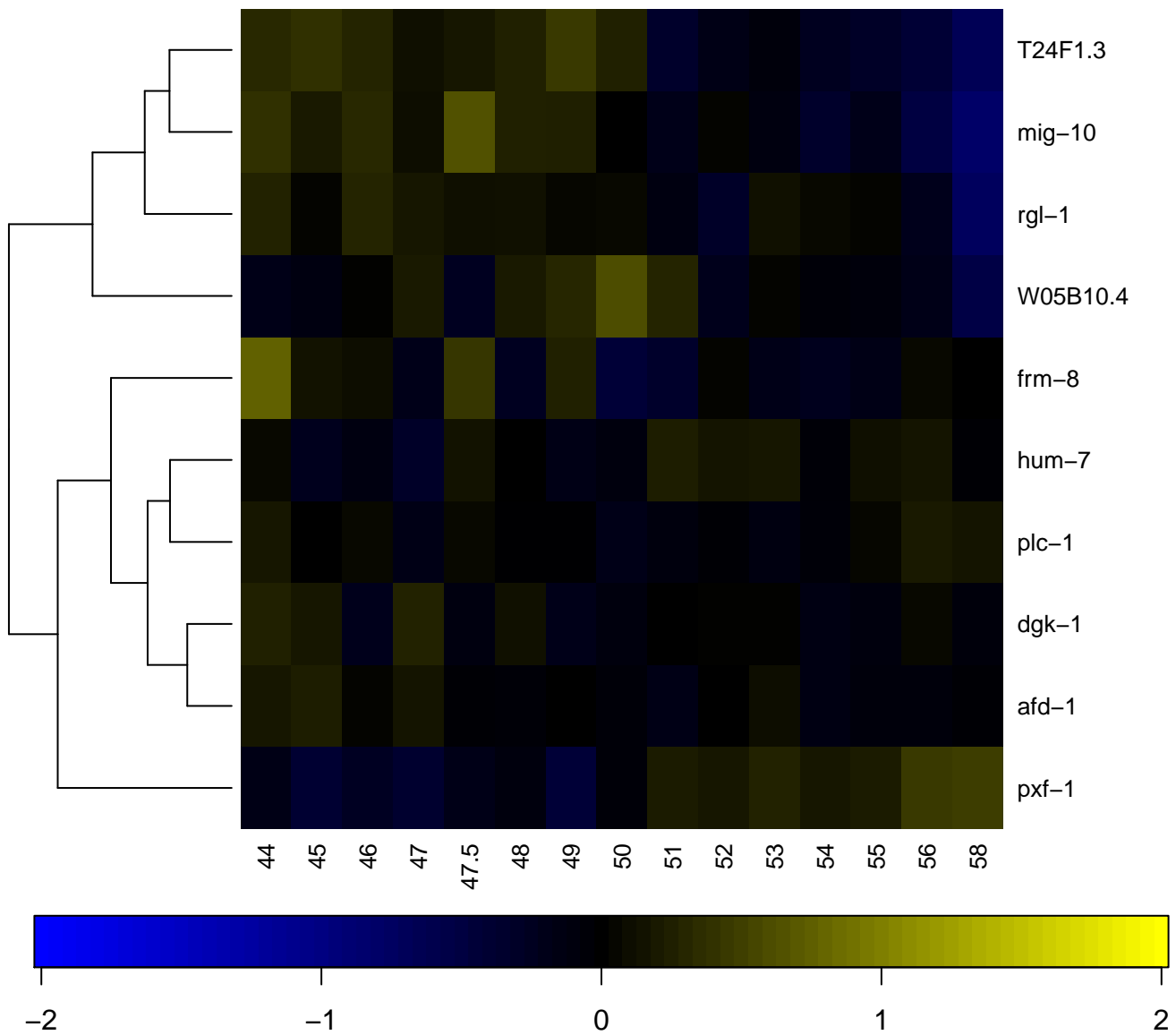
Ran GTPase



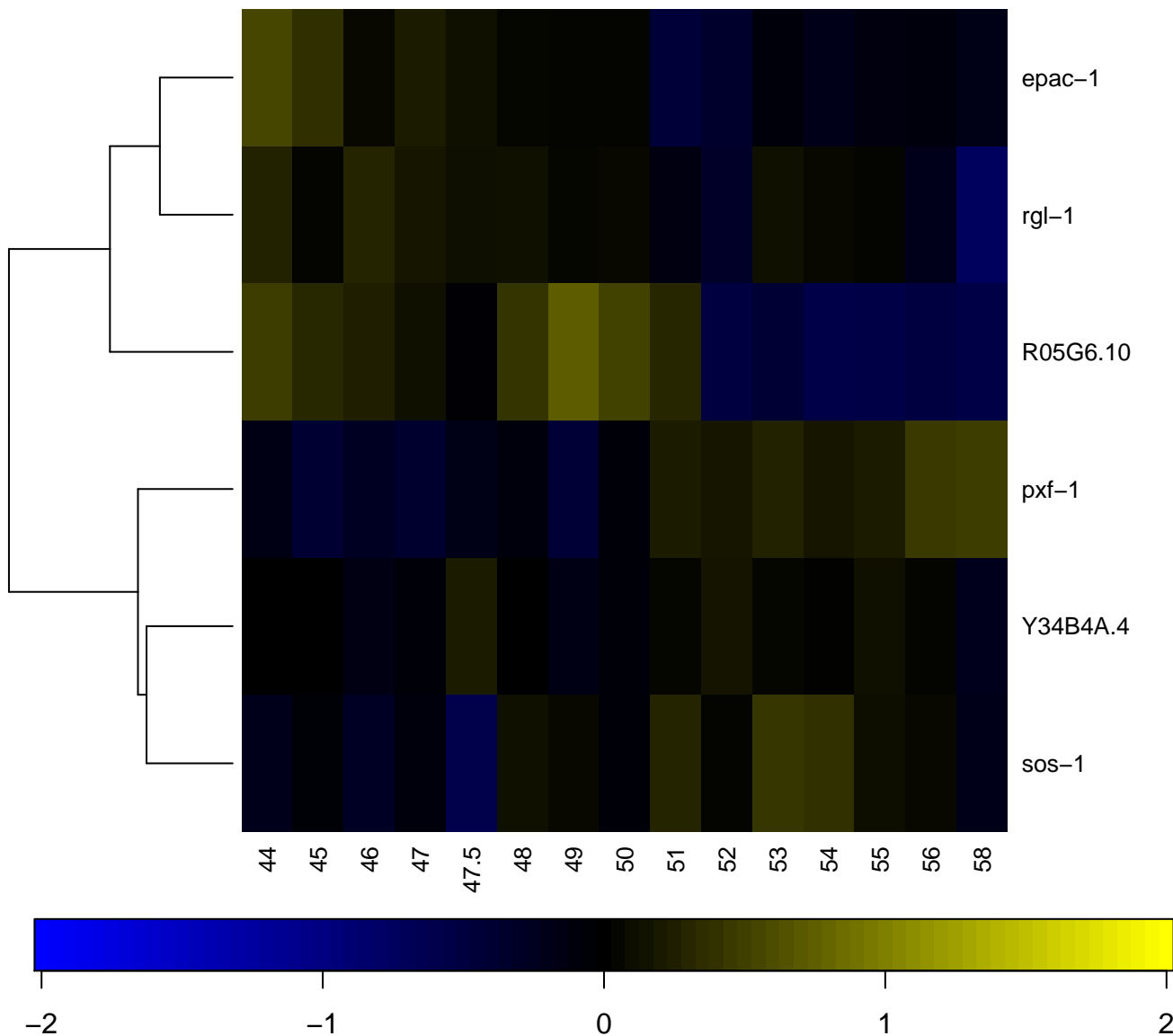
Ras



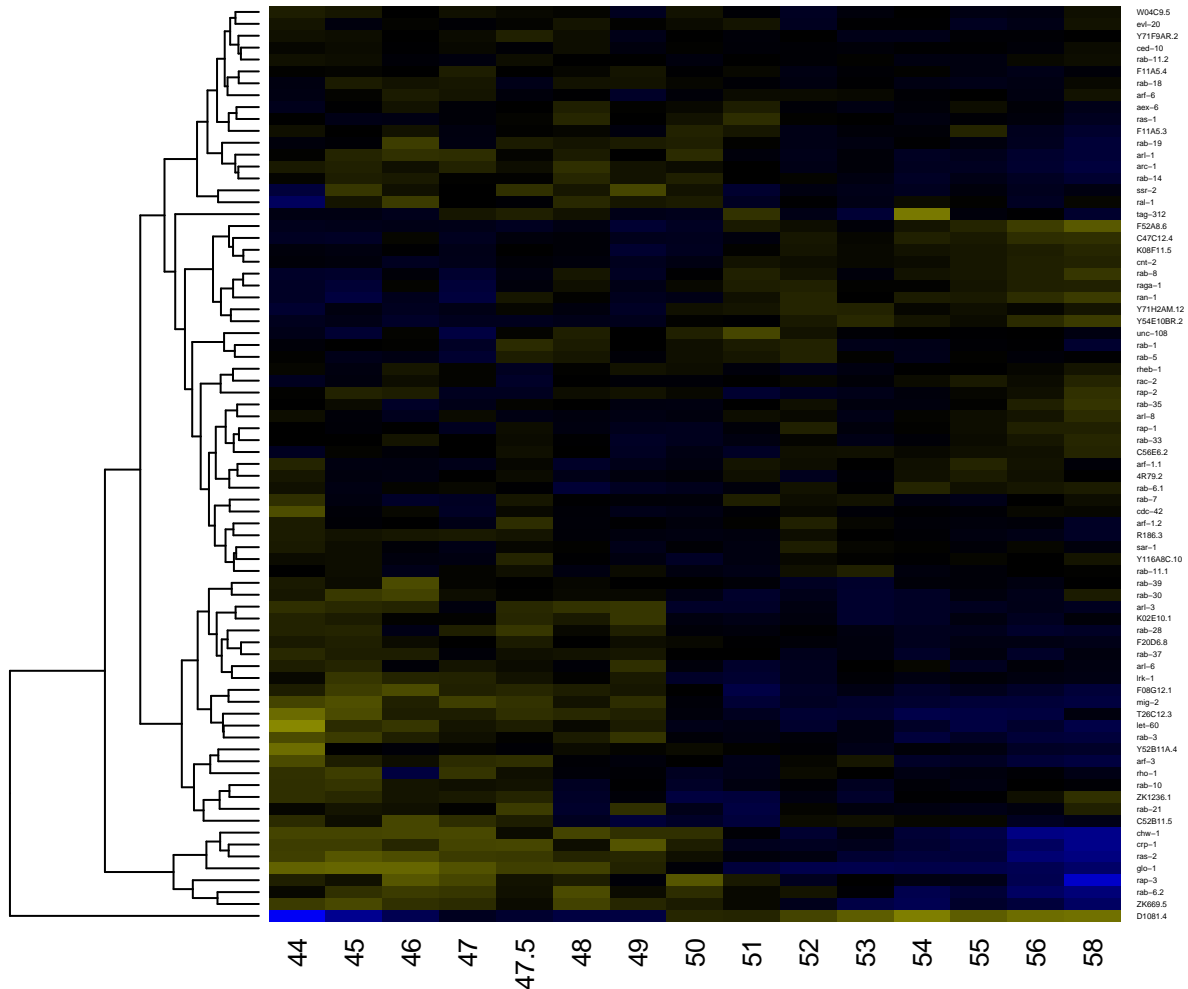
Ras-association



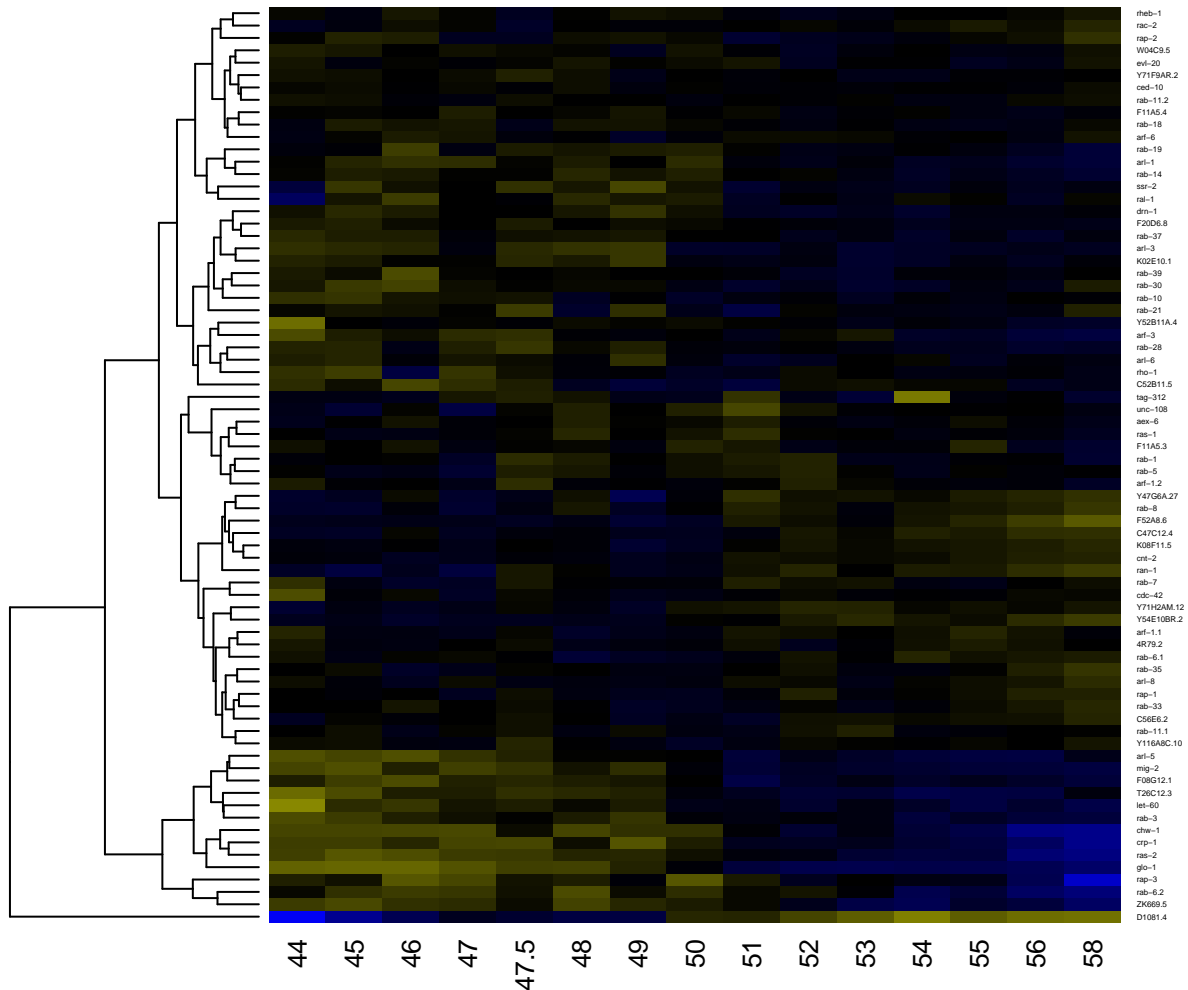
Ras-like guanine nucleotide exchange factor, N-terminal



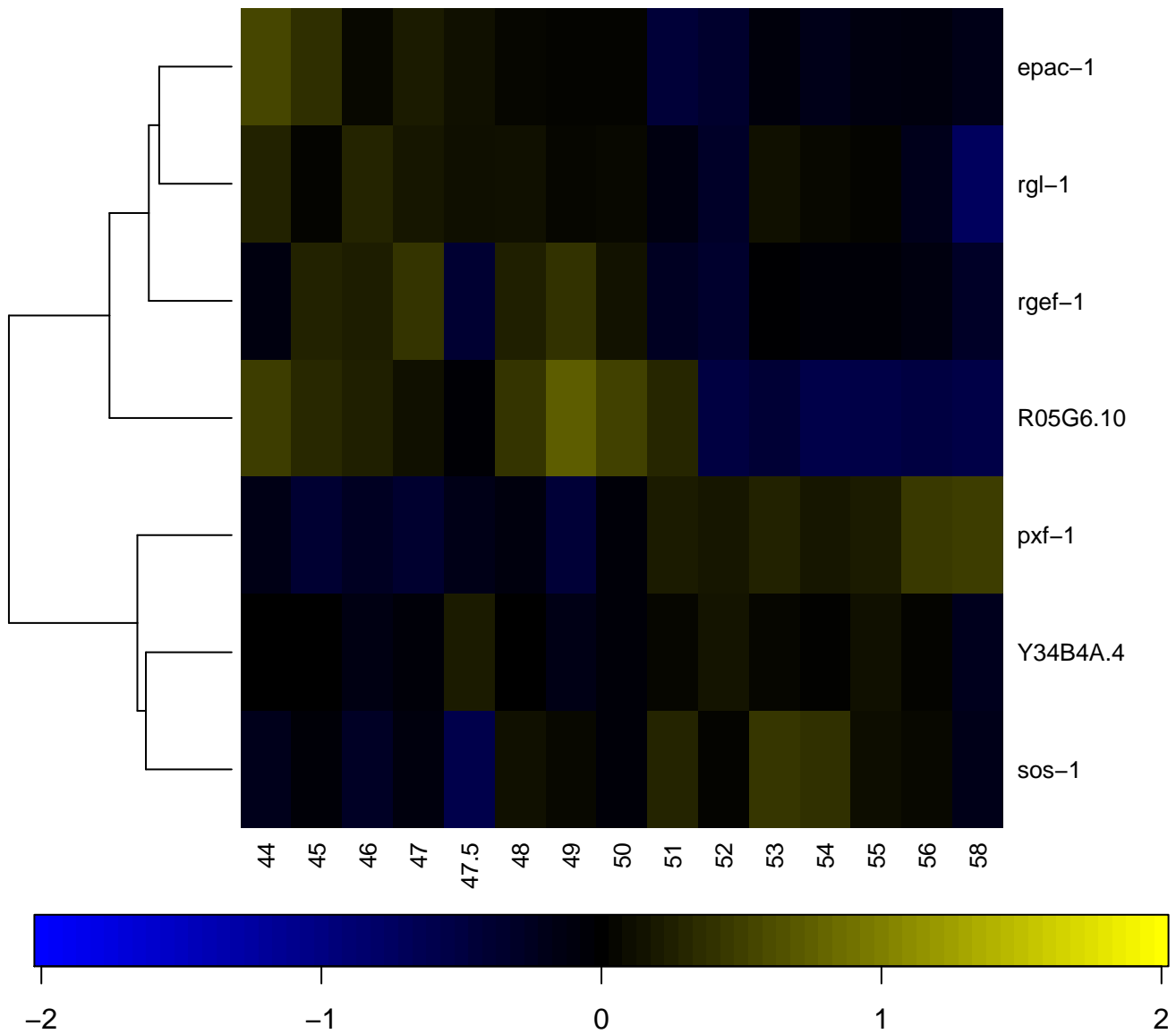
Ras family



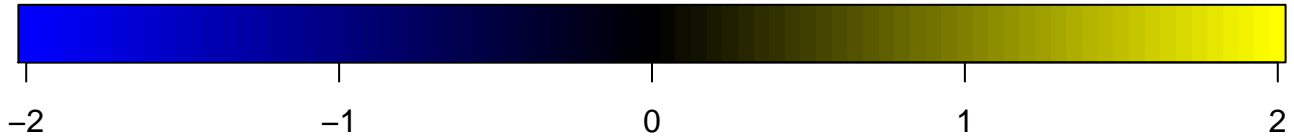
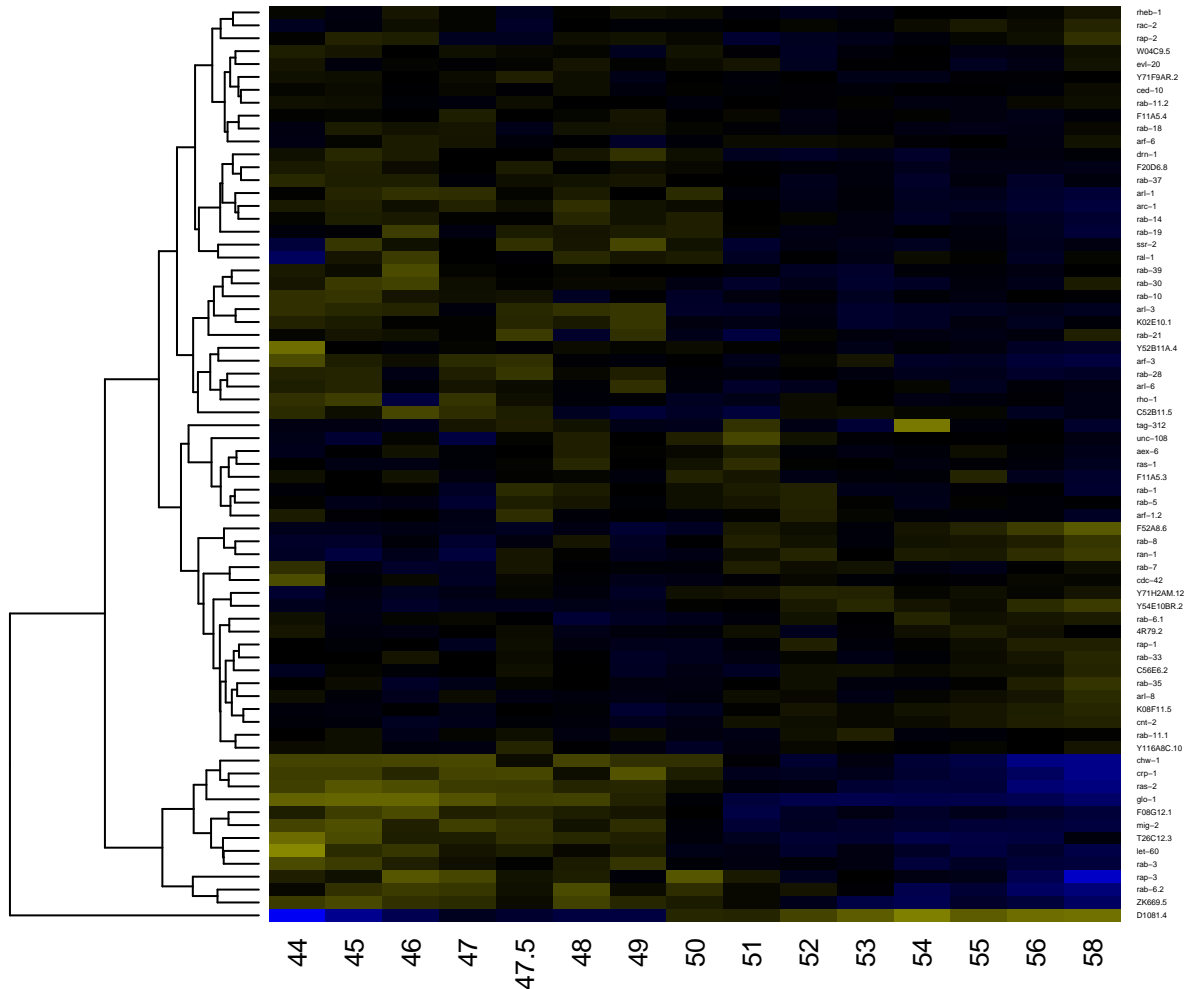
Ras GTPase



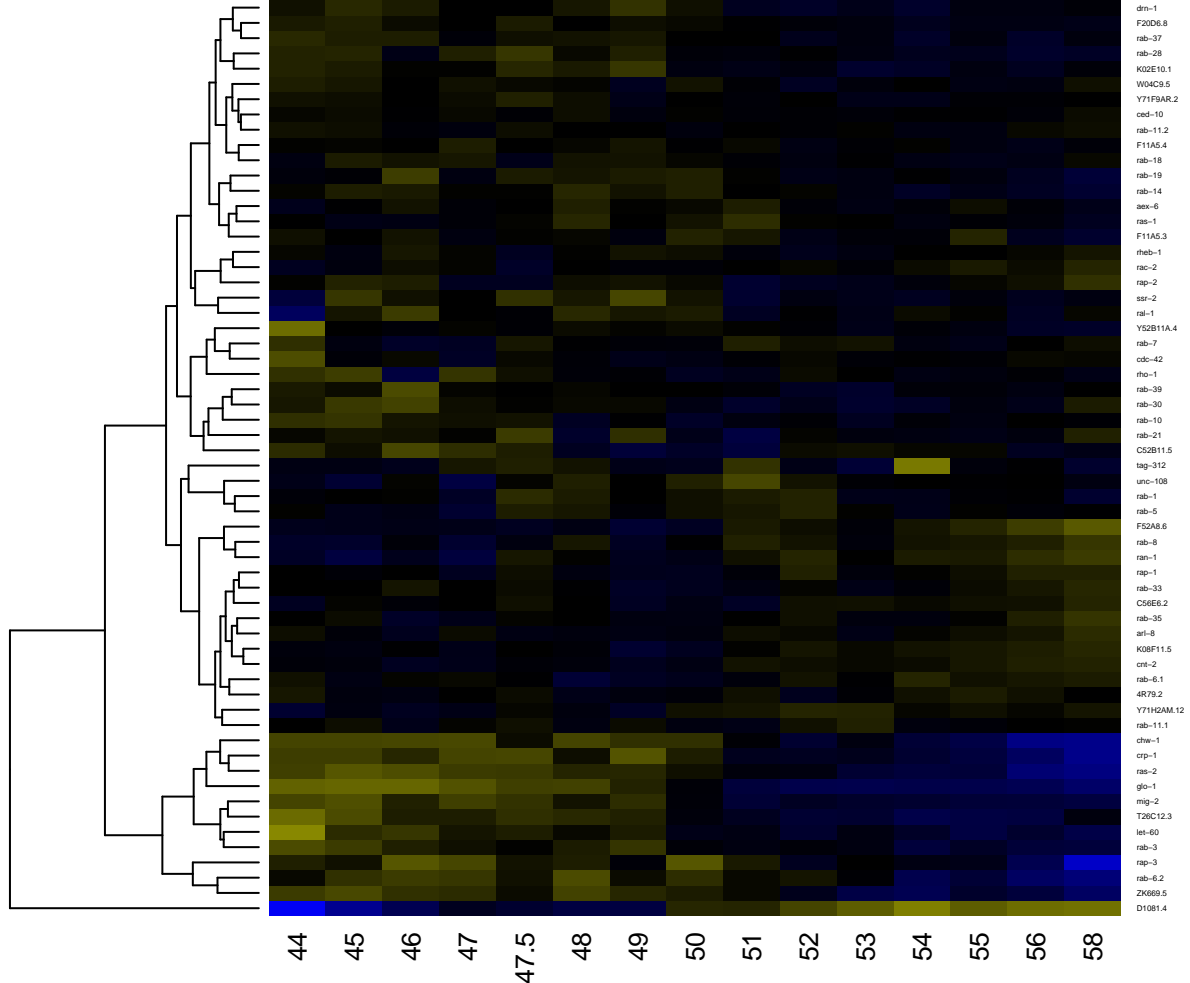
Ras guanine nucleotide exchange factor



Ras small GTPase, Rab type



Ras small GTPase, Ras type



-2

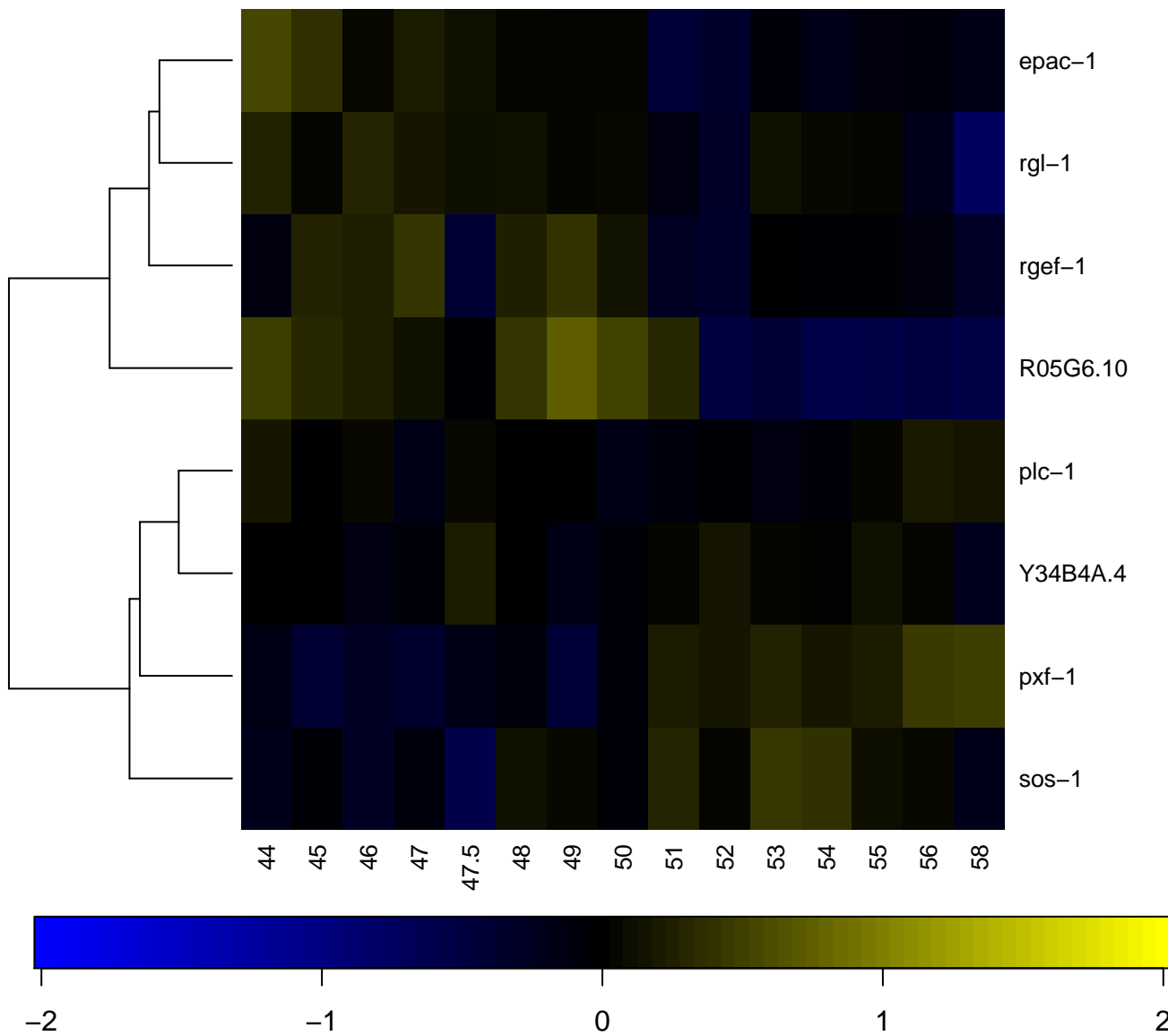
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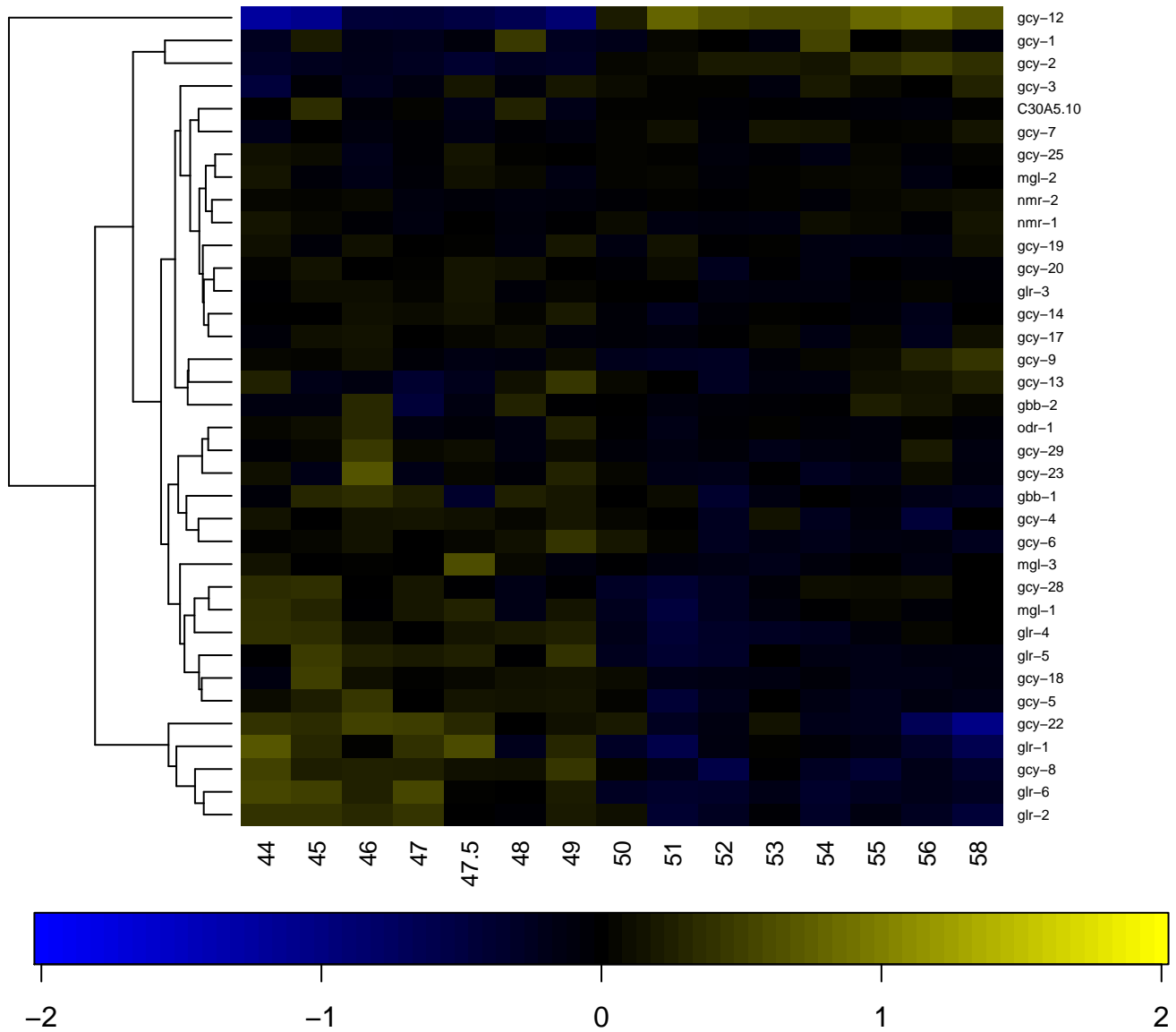
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2

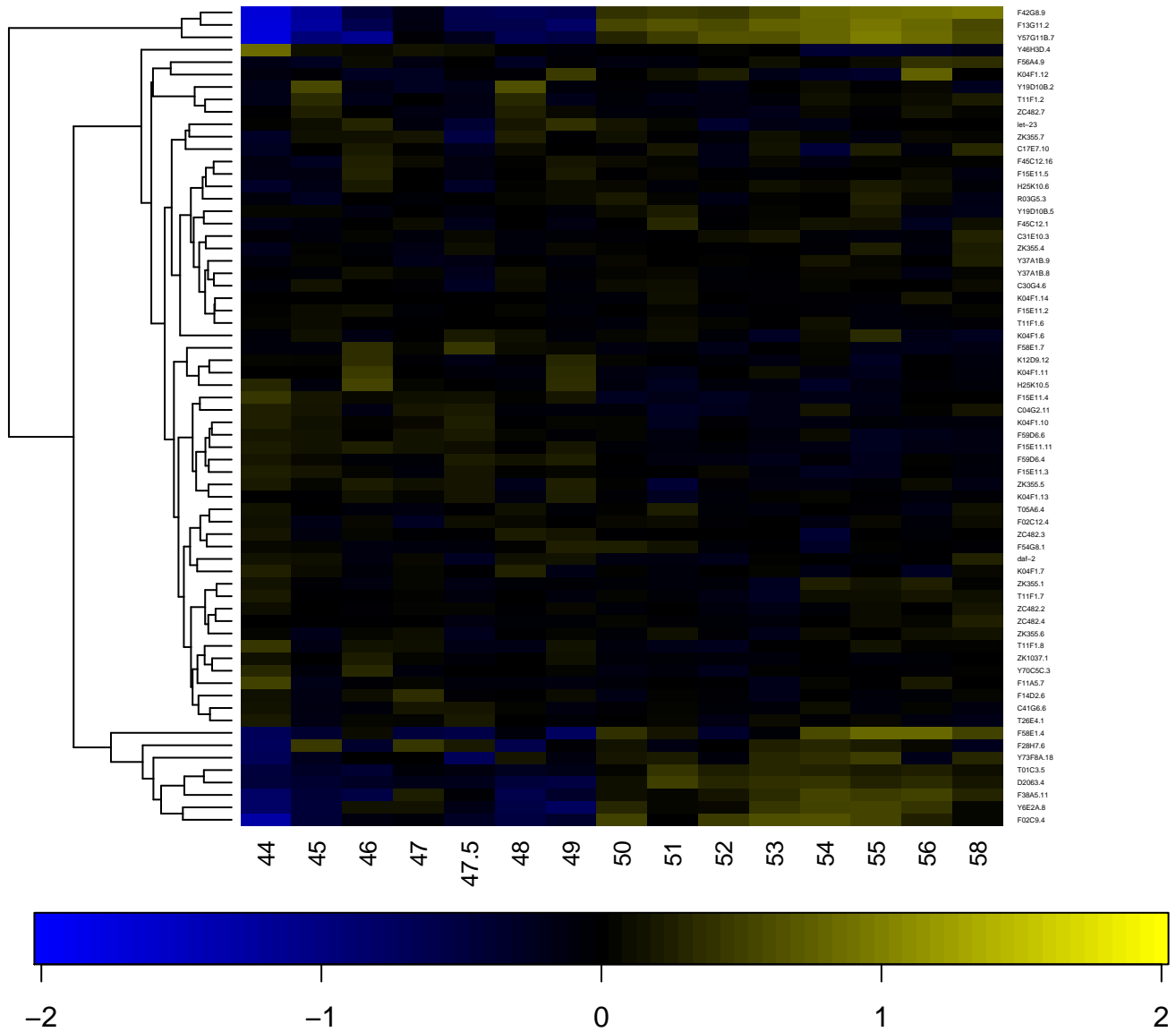
RasGEF domain



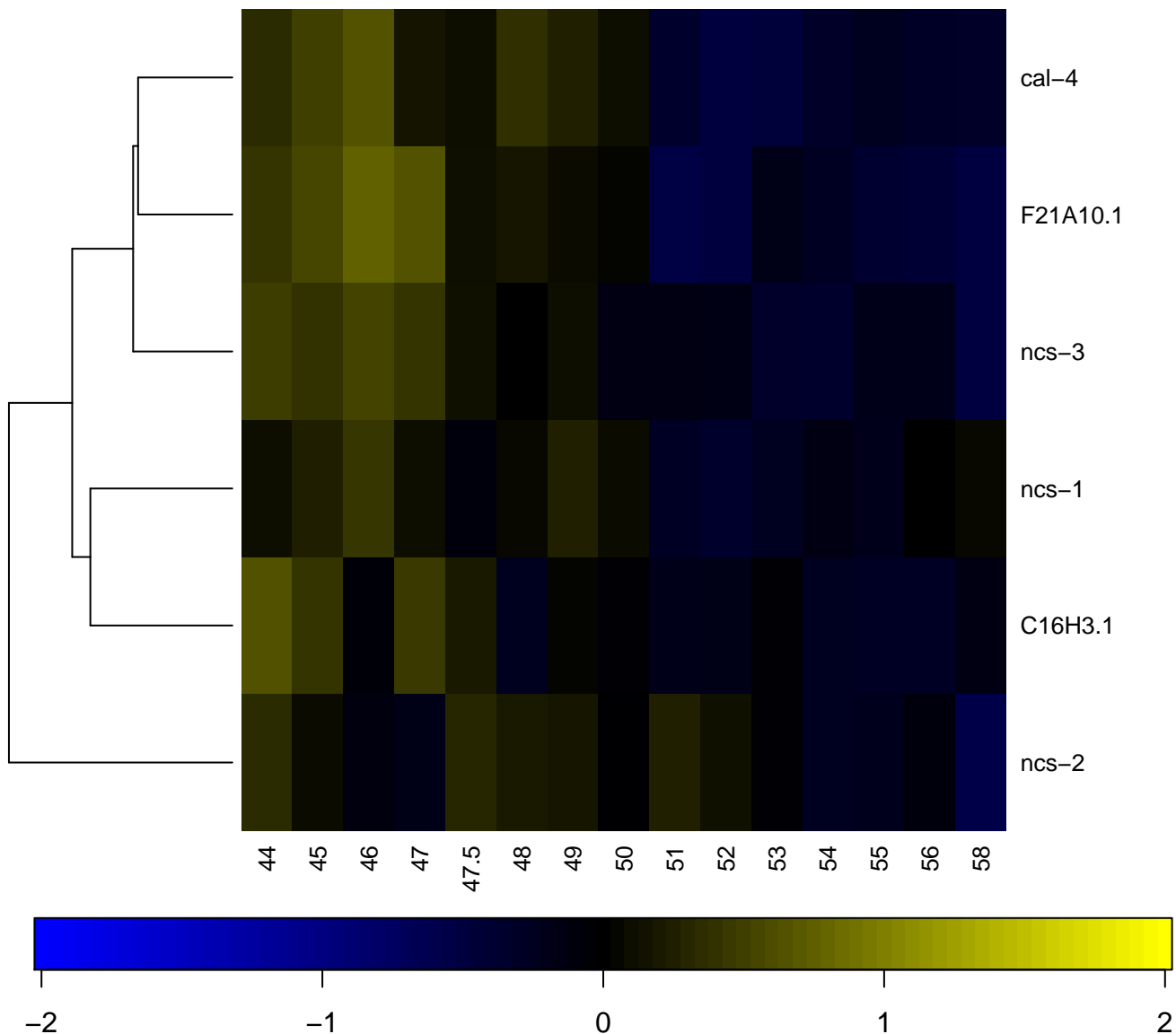
Receptor family ligand binding region



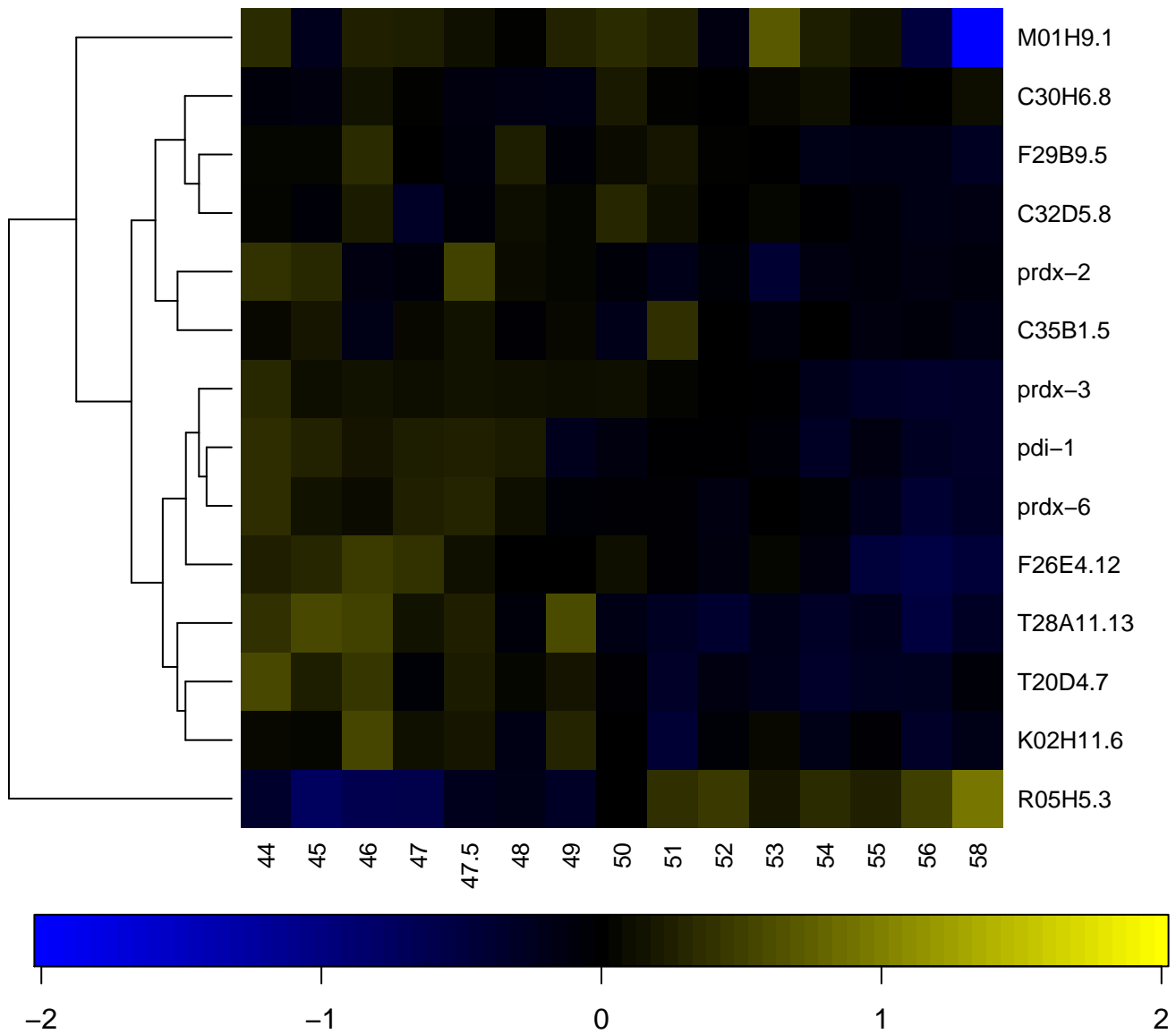
Receptor L domain



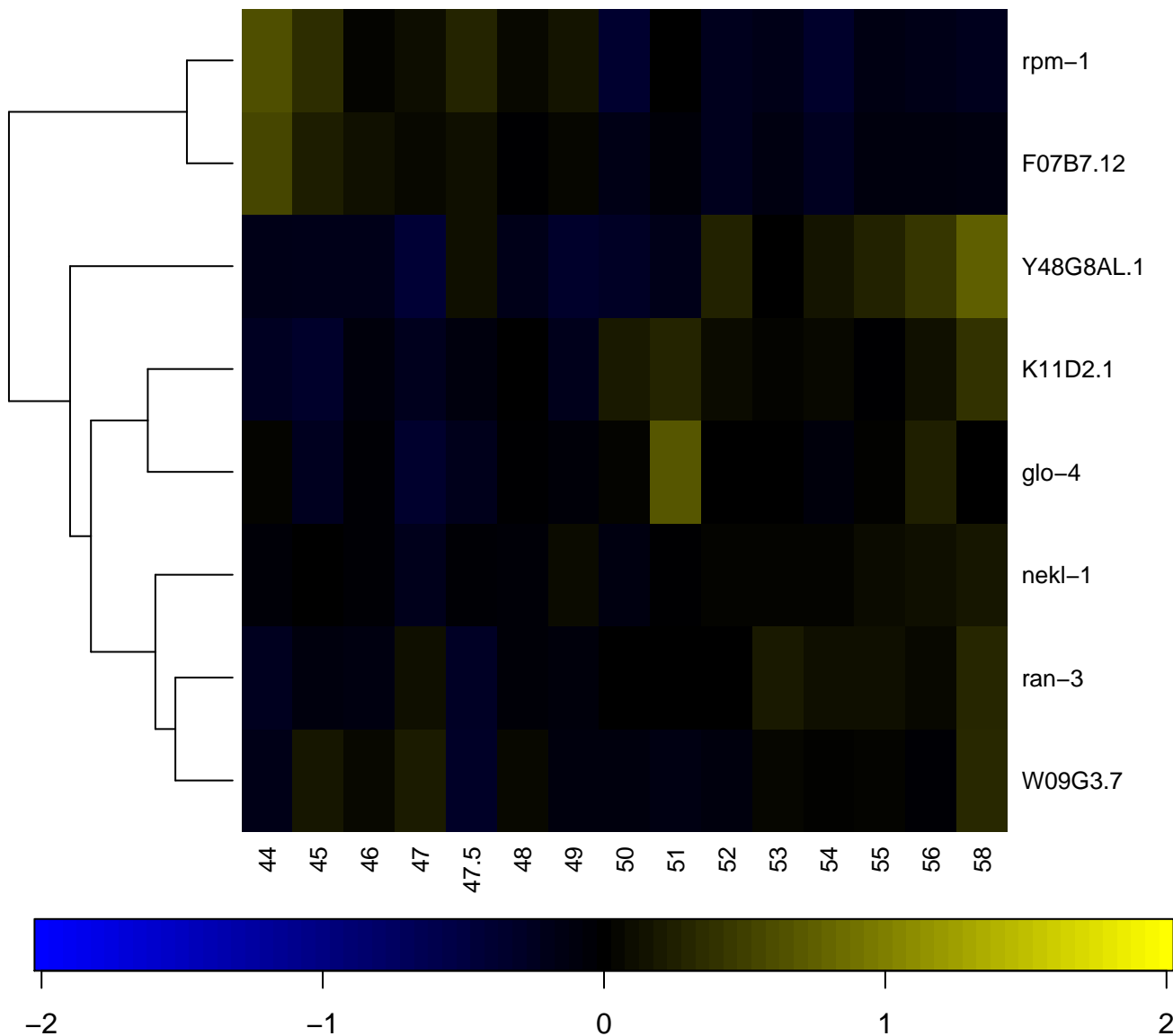
Recoverin



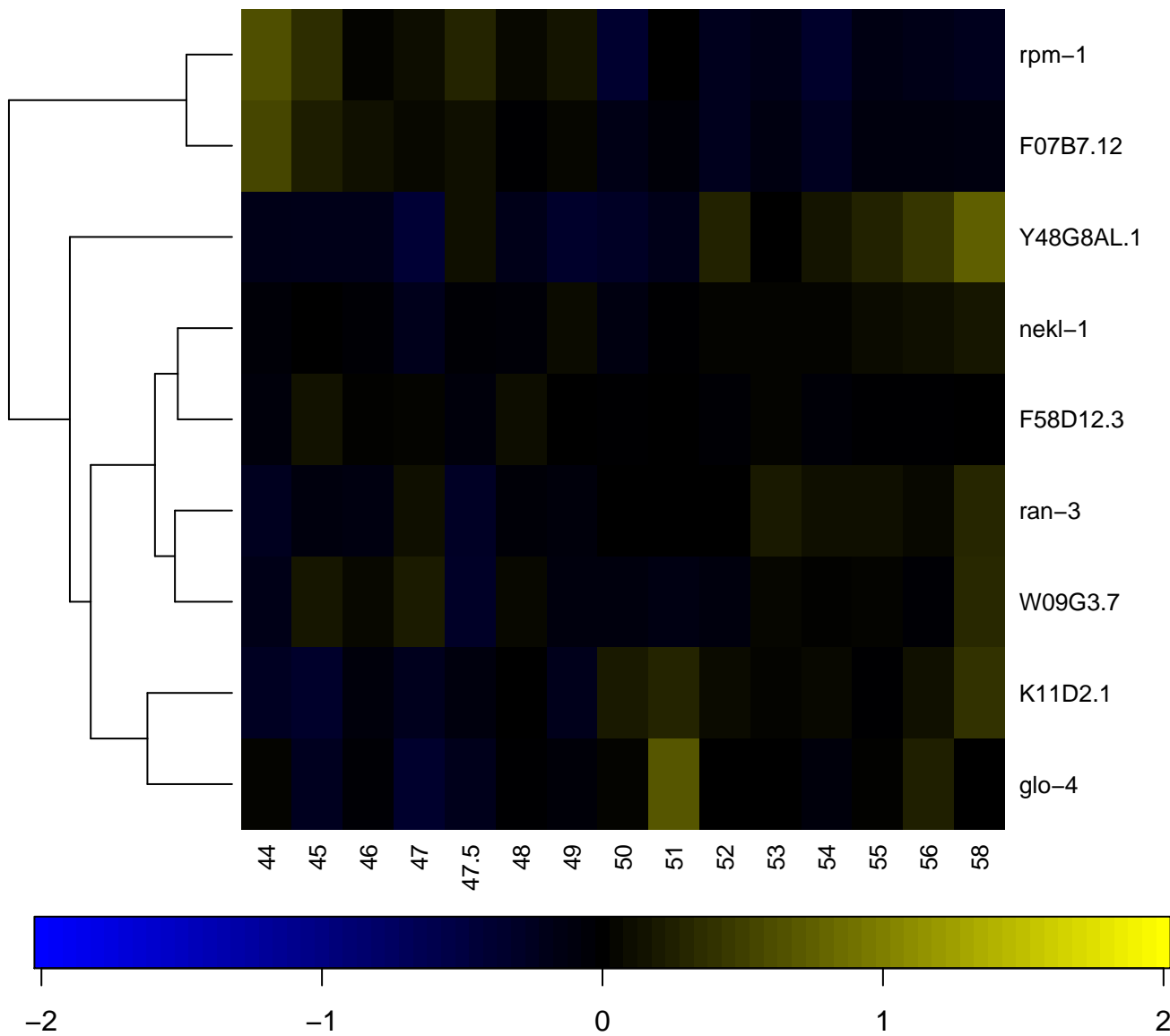
Redoxin



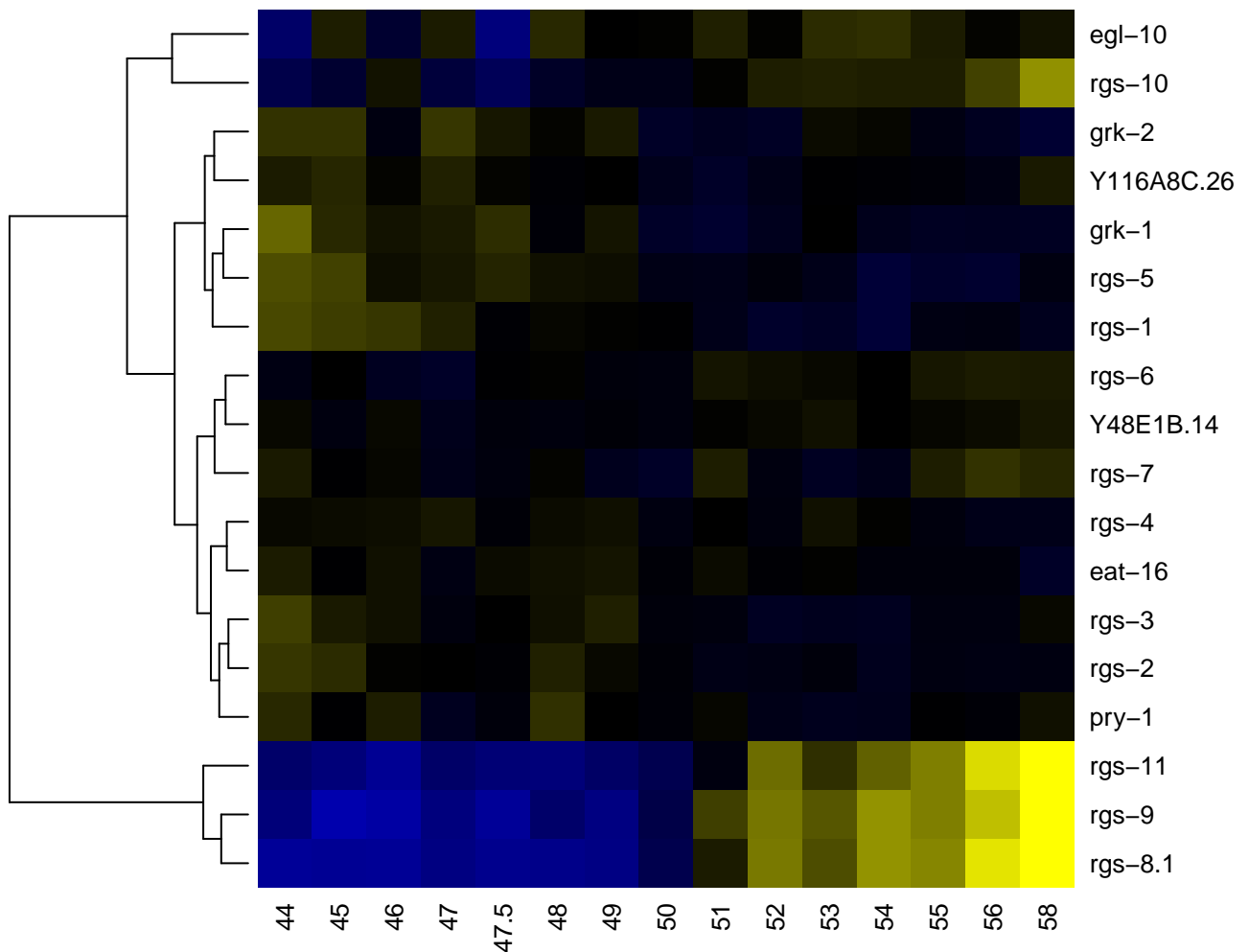
Regulator of chromosome condensation (RCC1) repeat



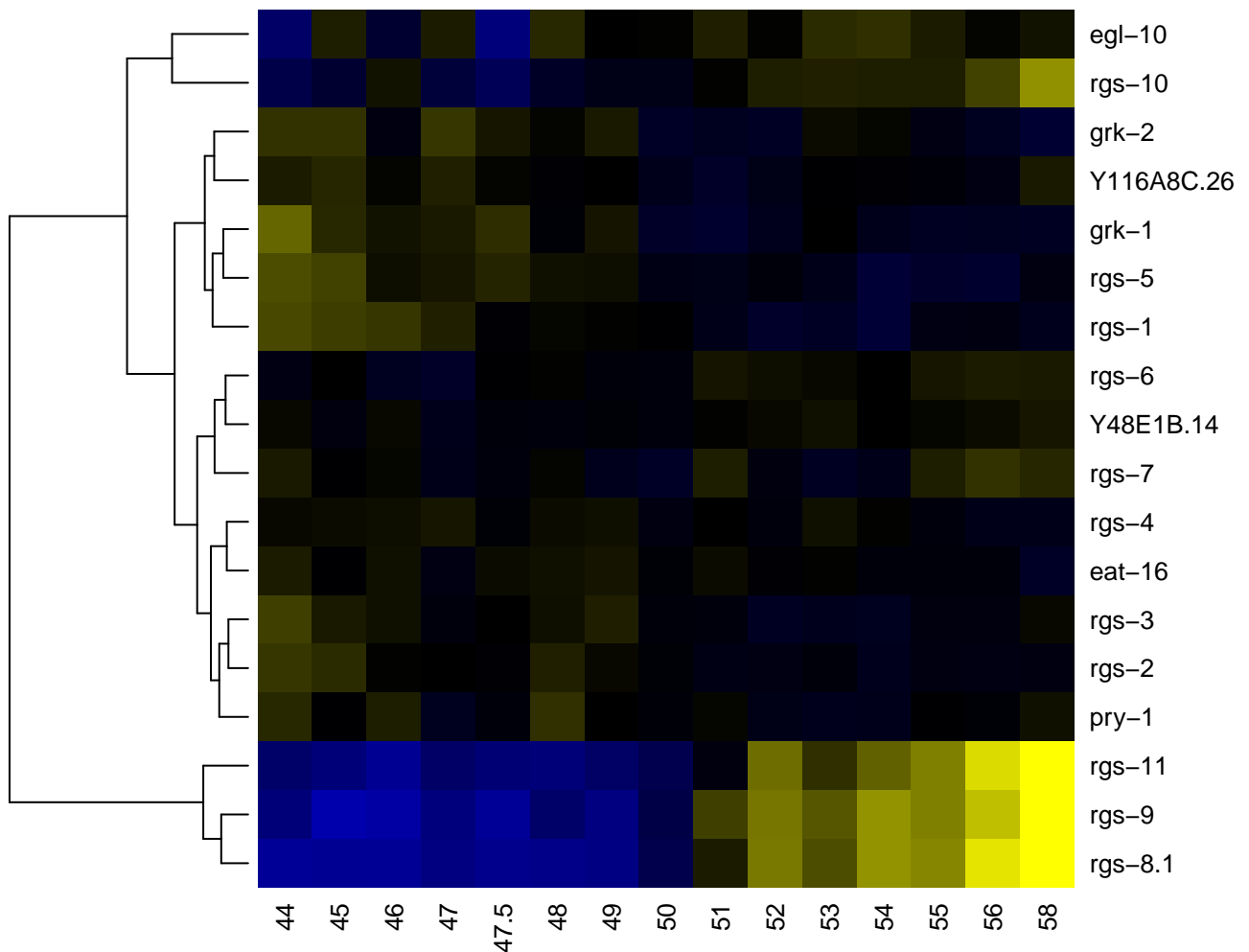
Factor of chromosome condensation/beta-lactamase-inhibitor



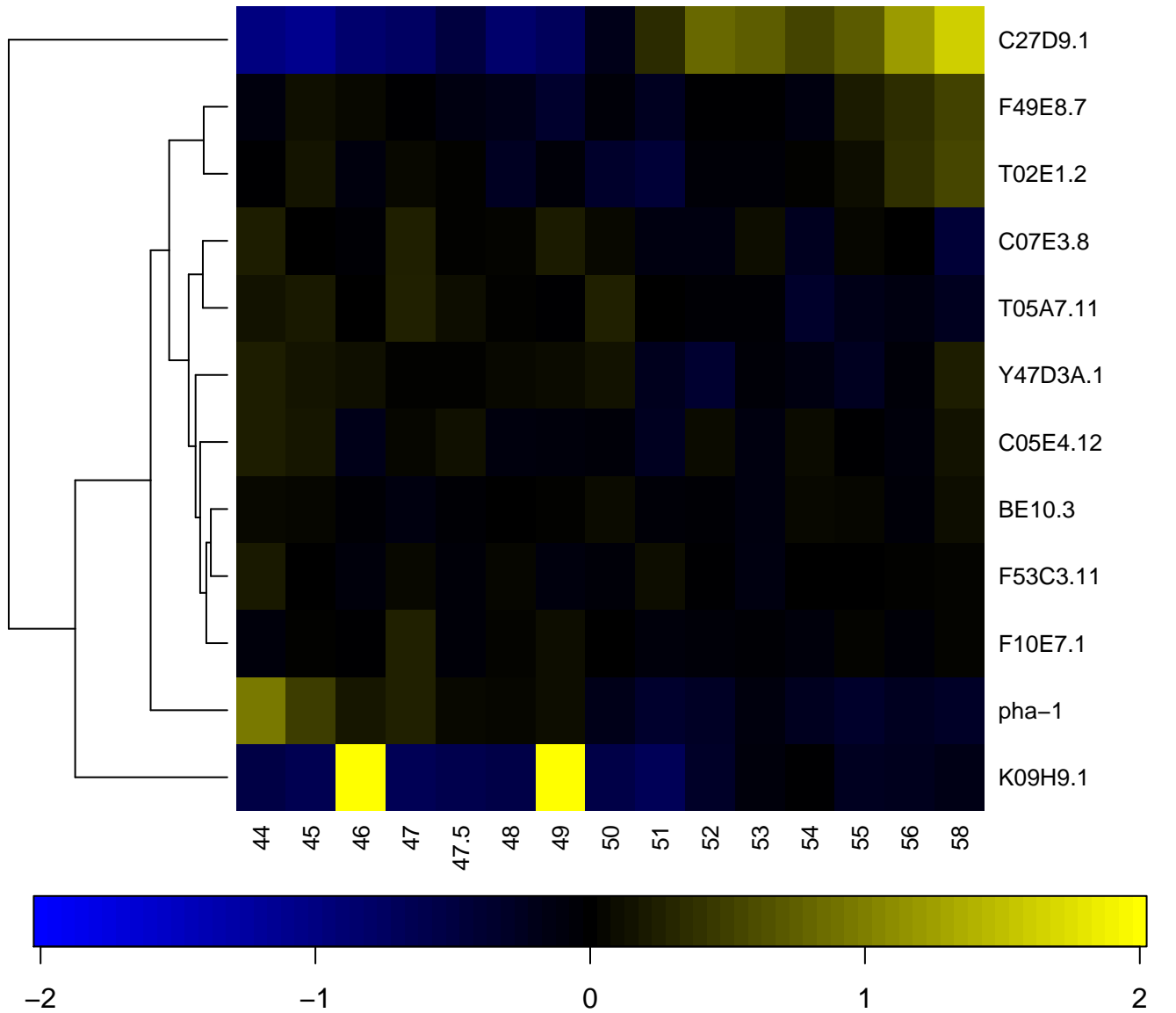
Regulator of G protein signaling domain



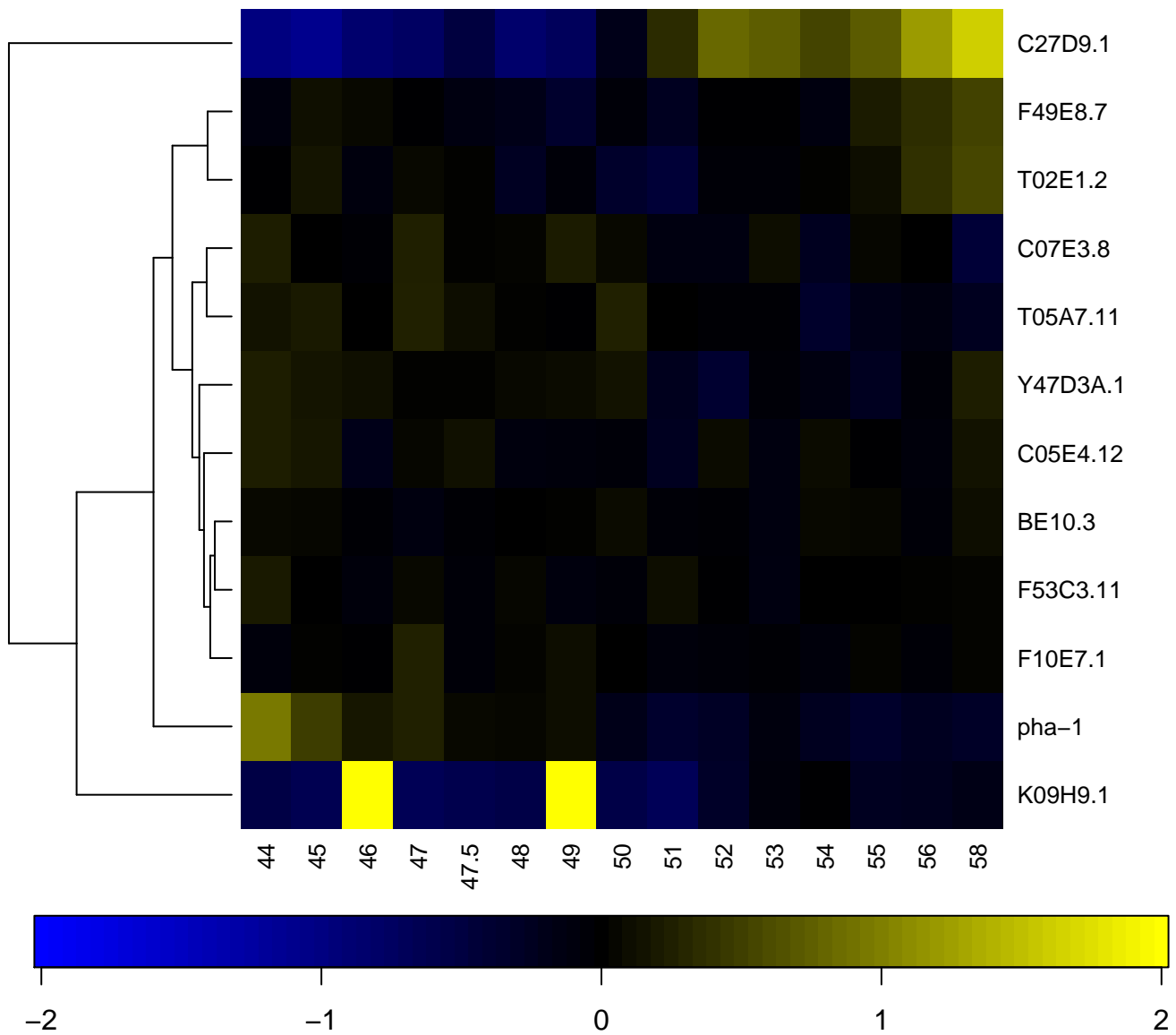
Regulator of G protein signalling



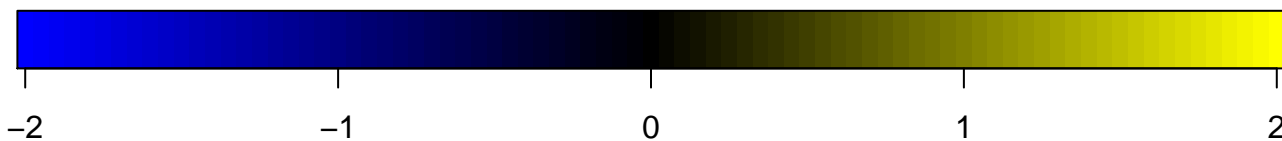
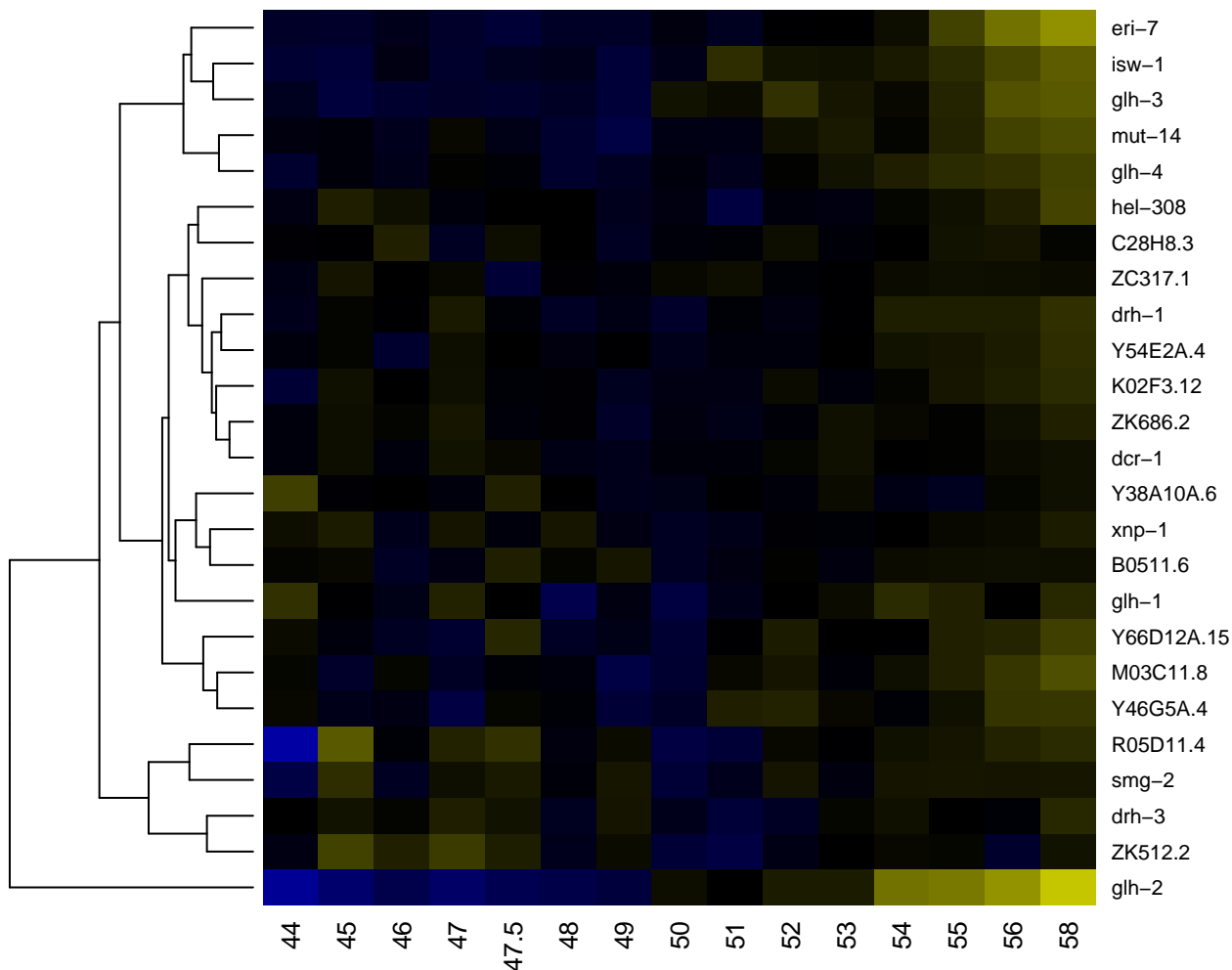
Regulator protein PHA-1



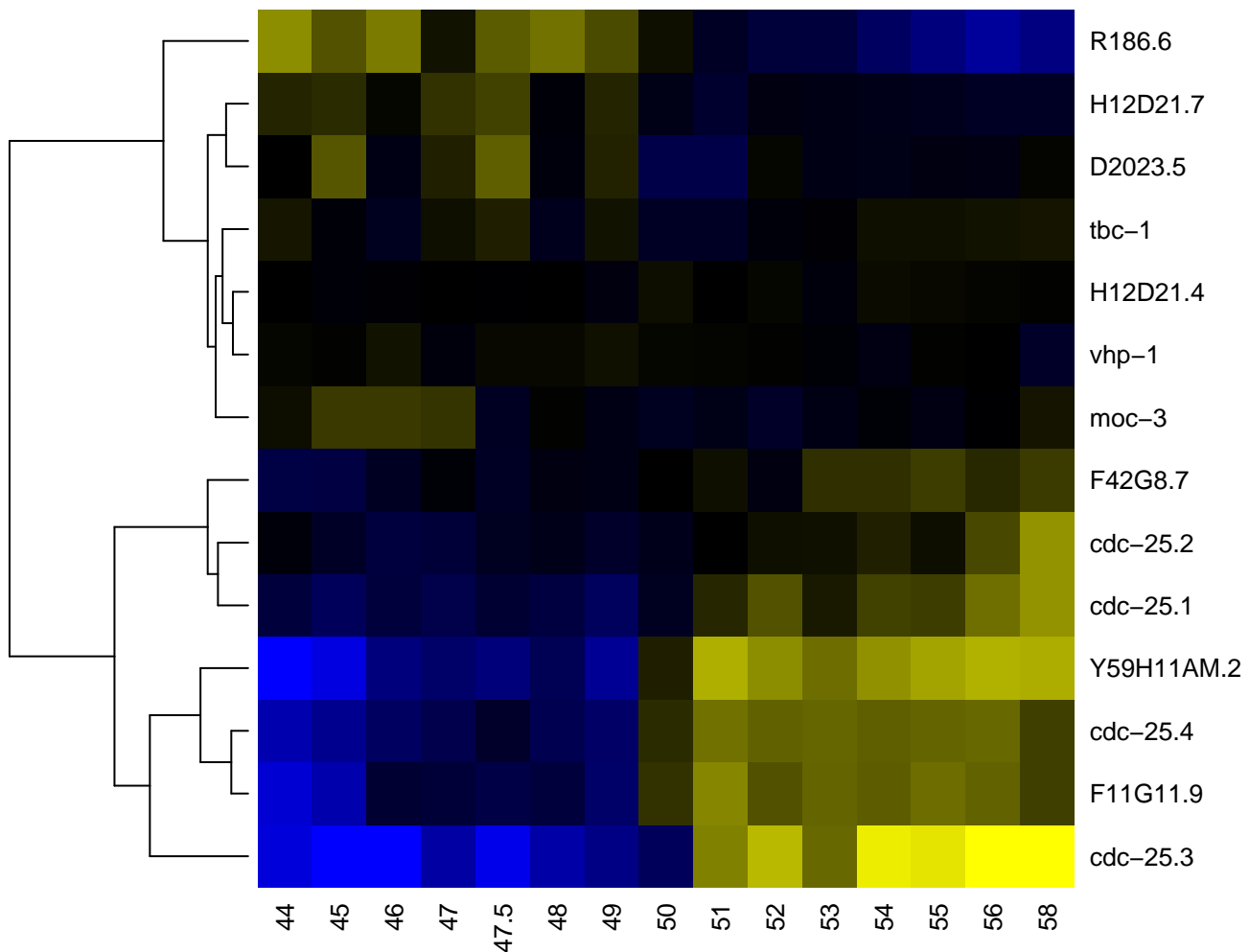
Regulator protein, PHA-1



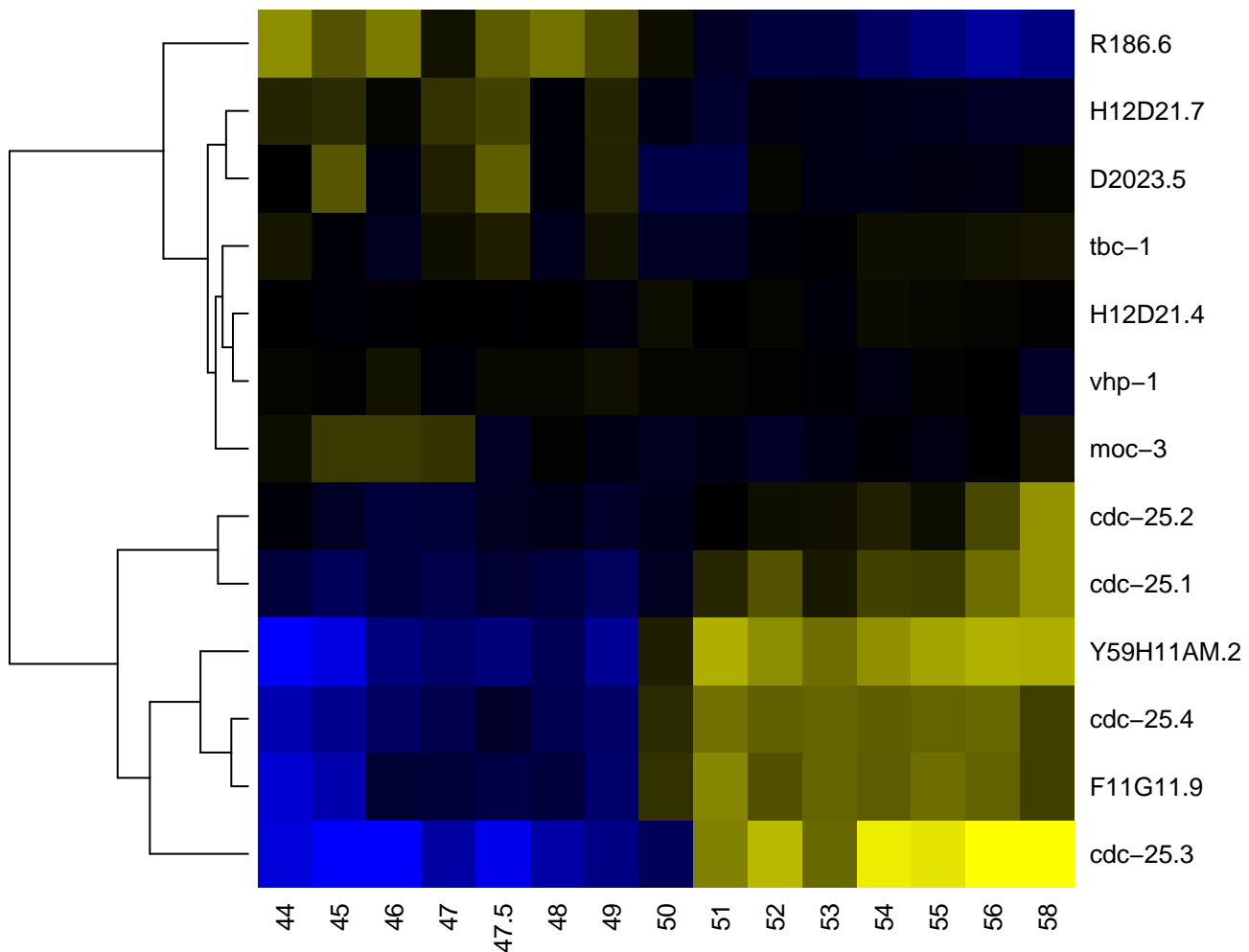
restriction endonuclease, type I, R subunit/Type III, Res subunit



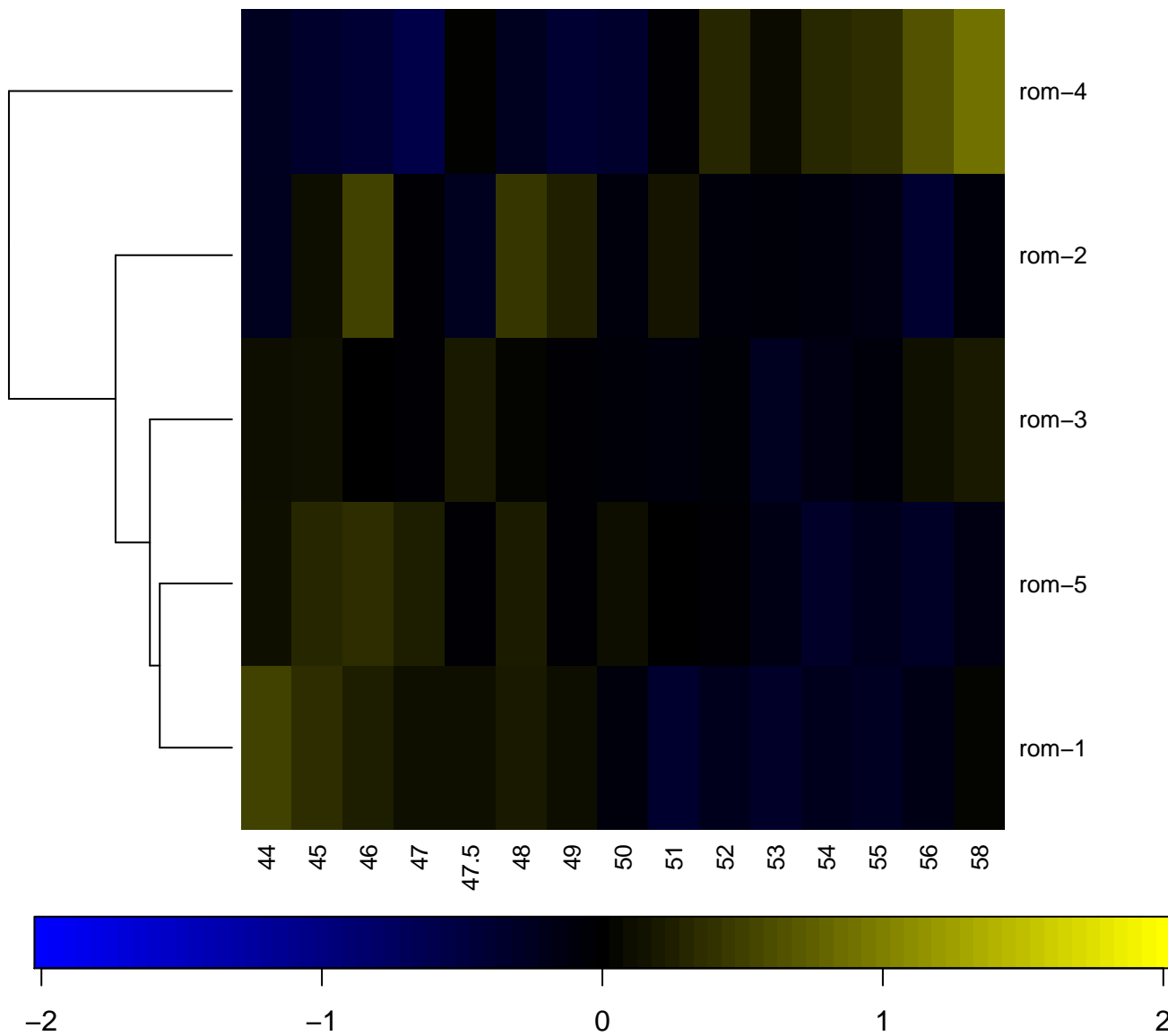
Rhodanese-like



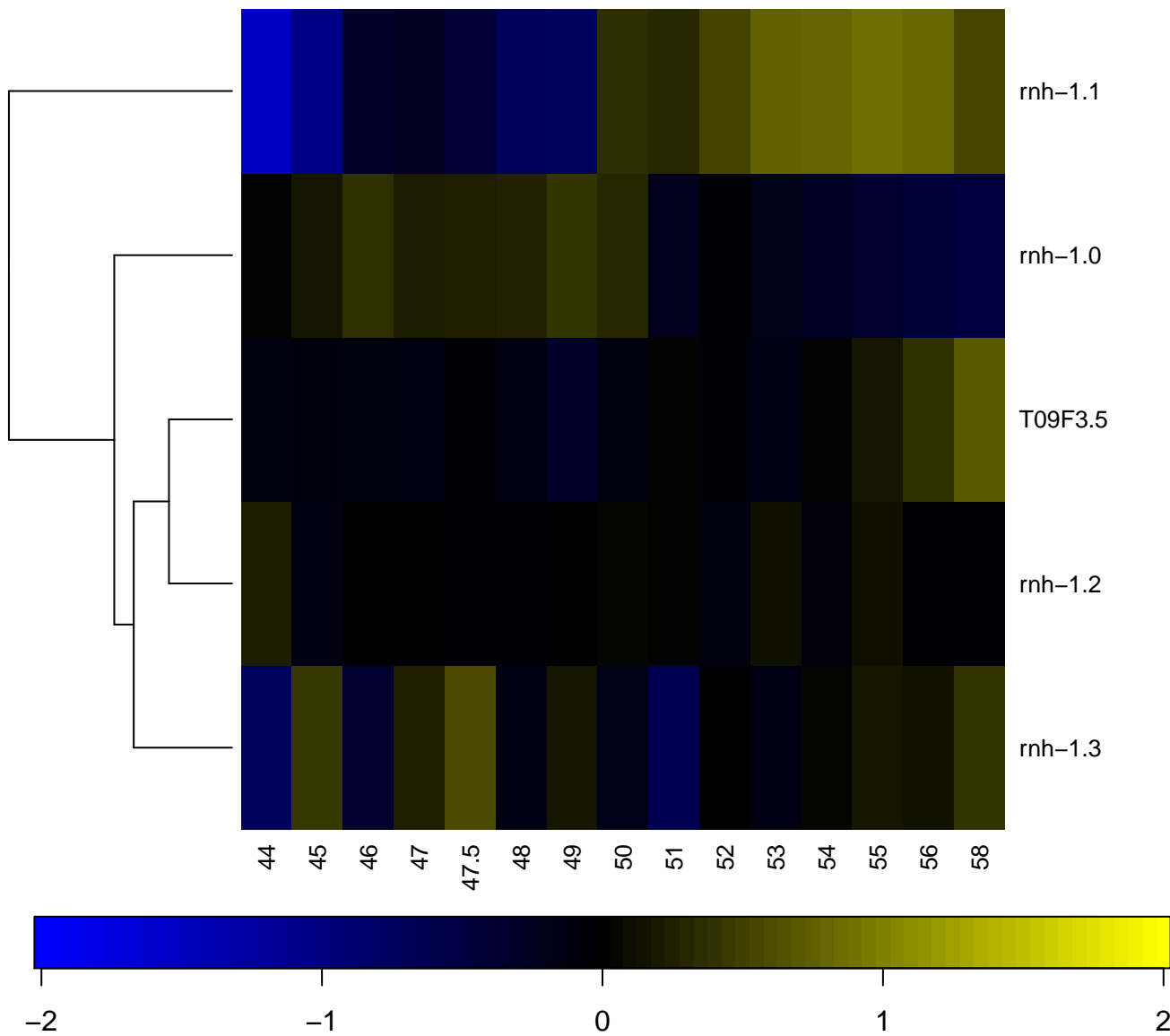
Rhodanese-like domain



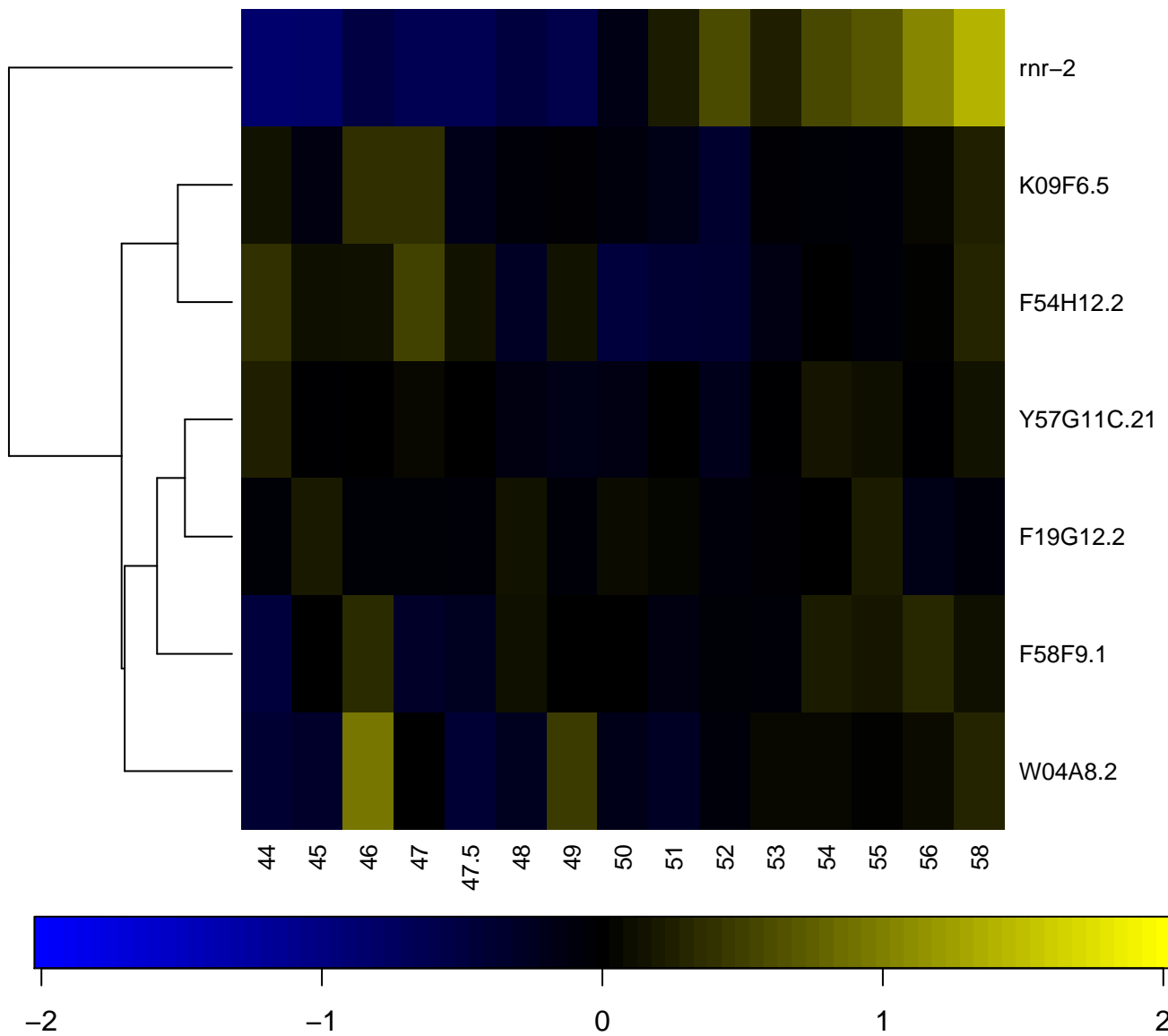
Rhomboid family



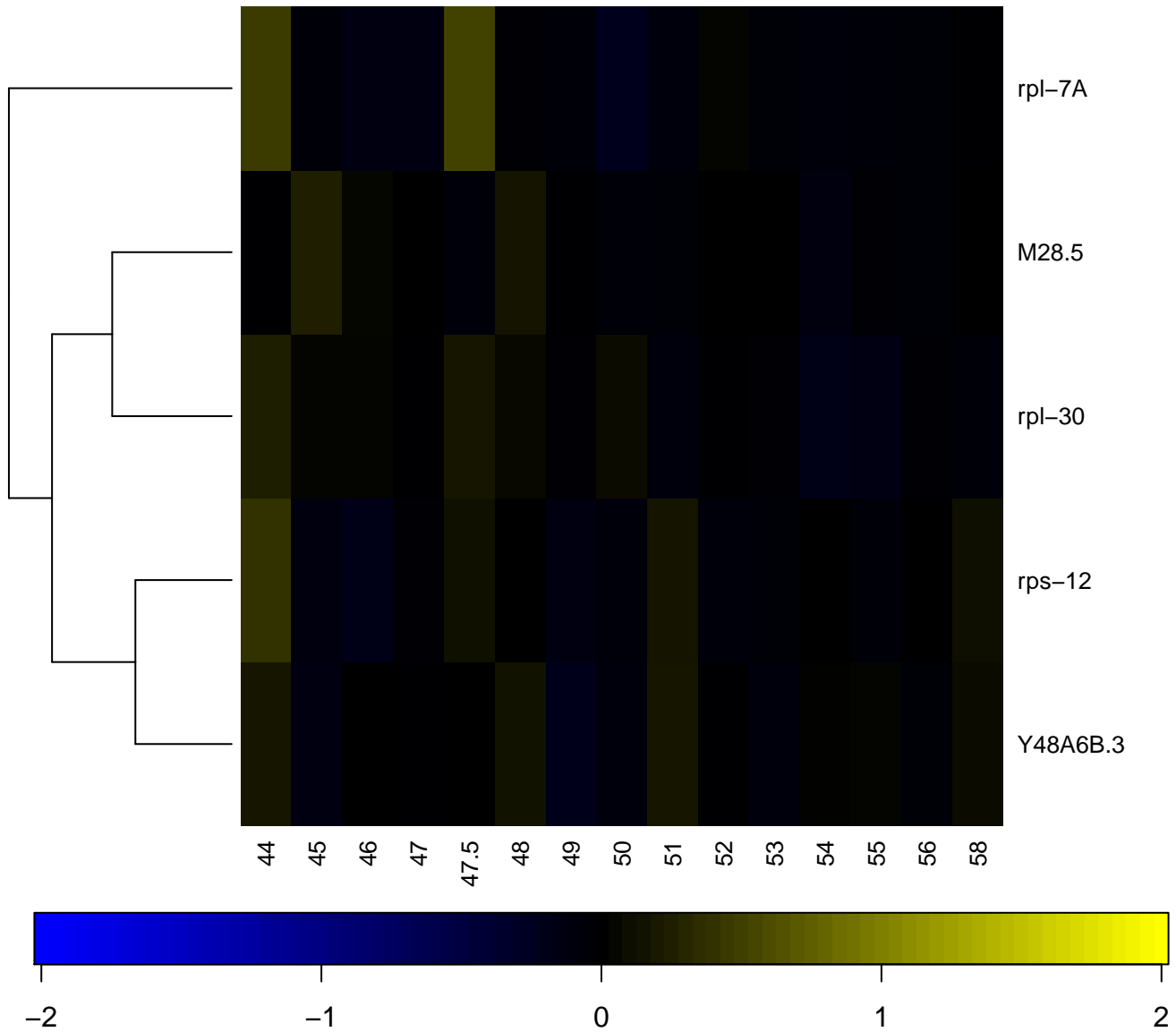
Ribonuclease H



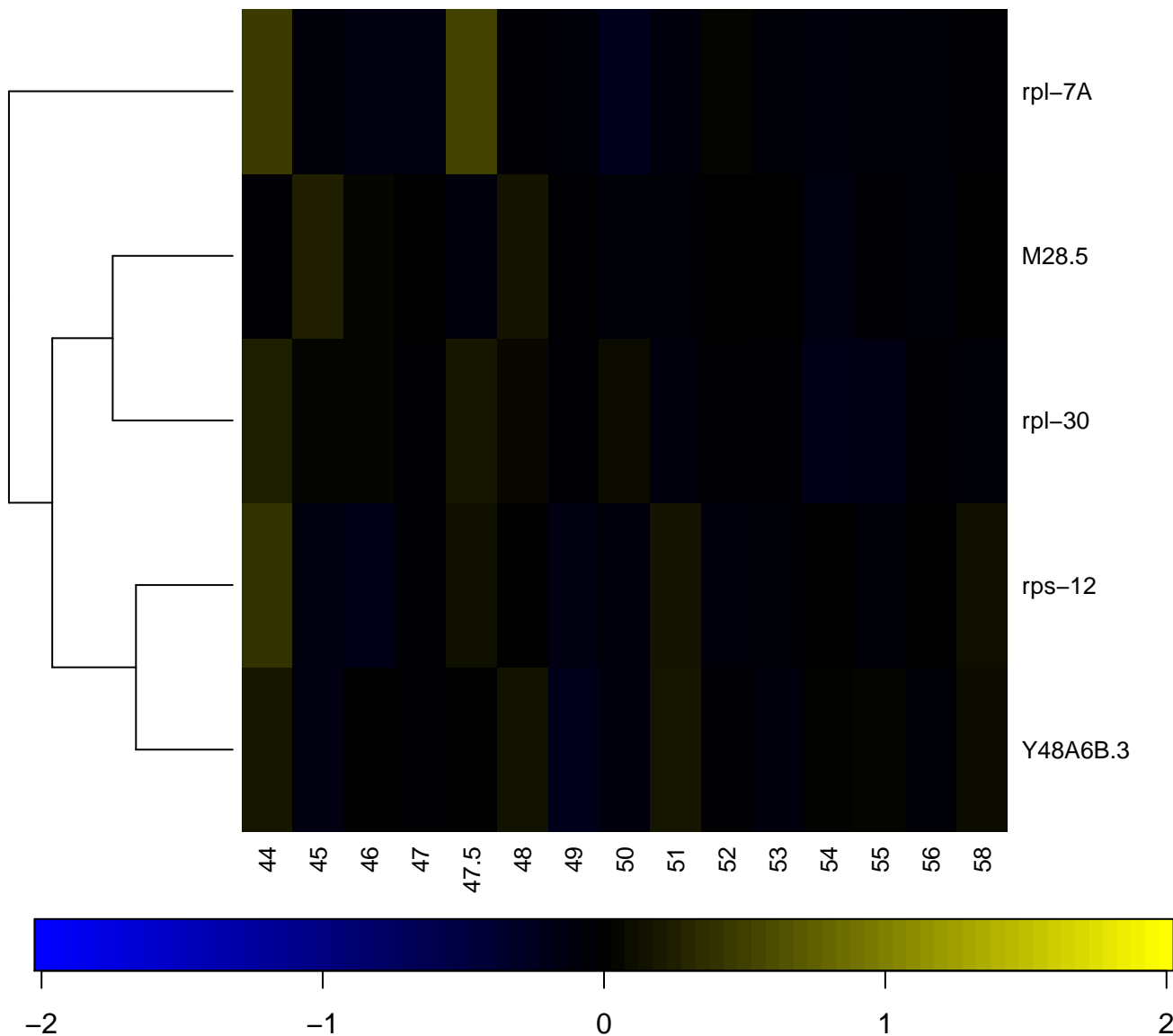
Ribonucleotide reductase



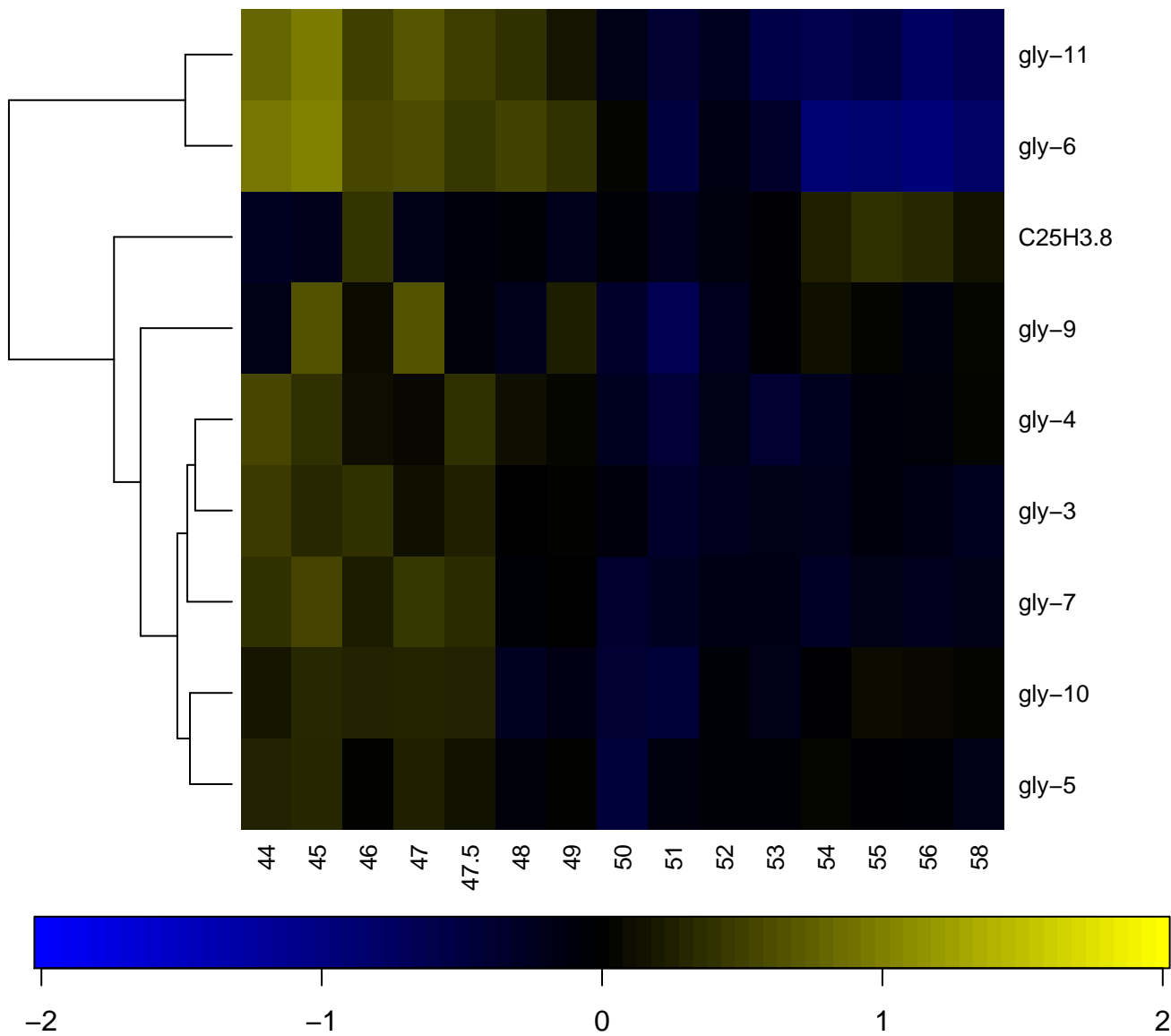
Ribosomal protein L7Ae/L30e/S12e/Gadd45



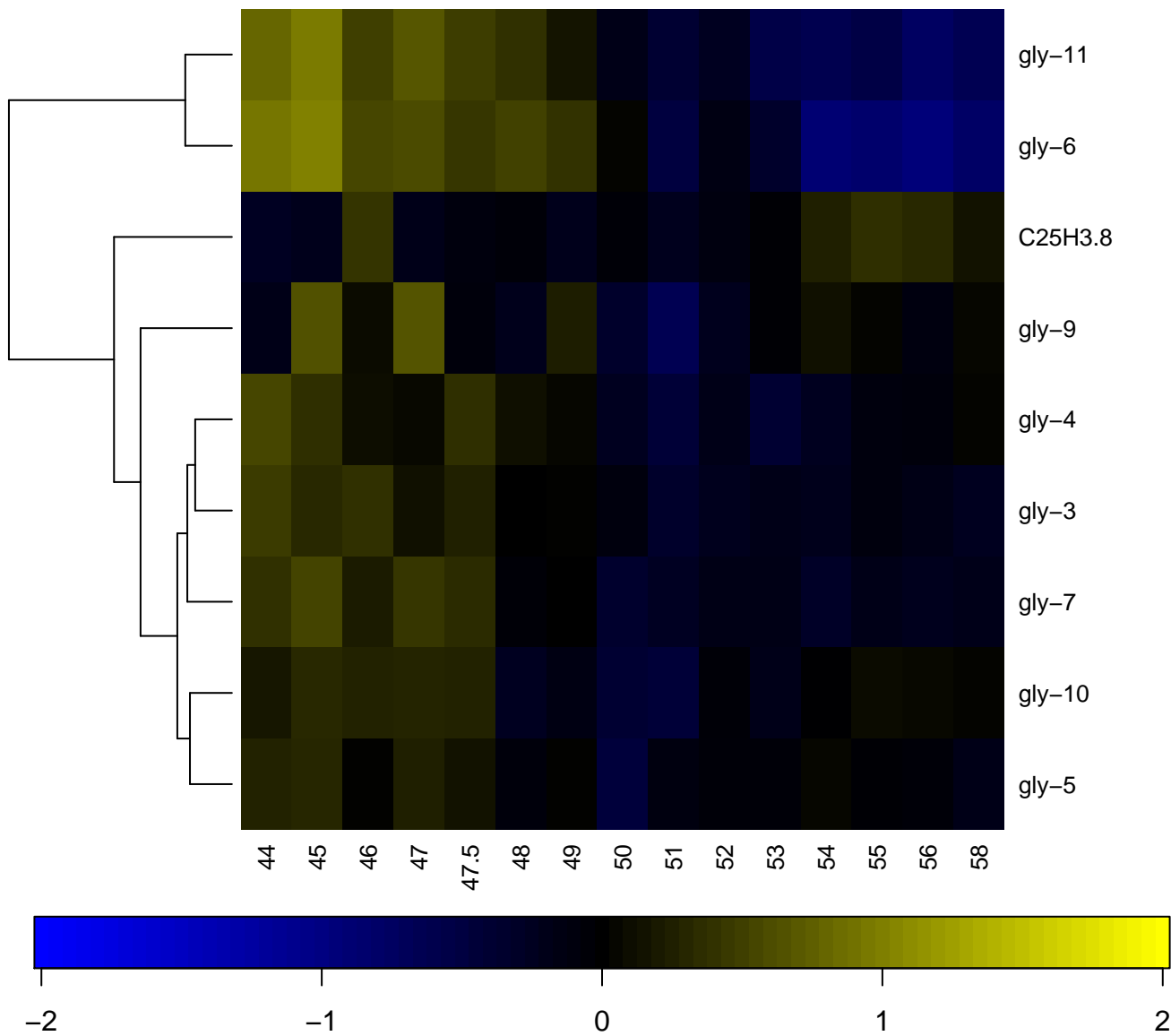
Ribosomal protein L7Ae/L30e/S12e/Gadd45 family



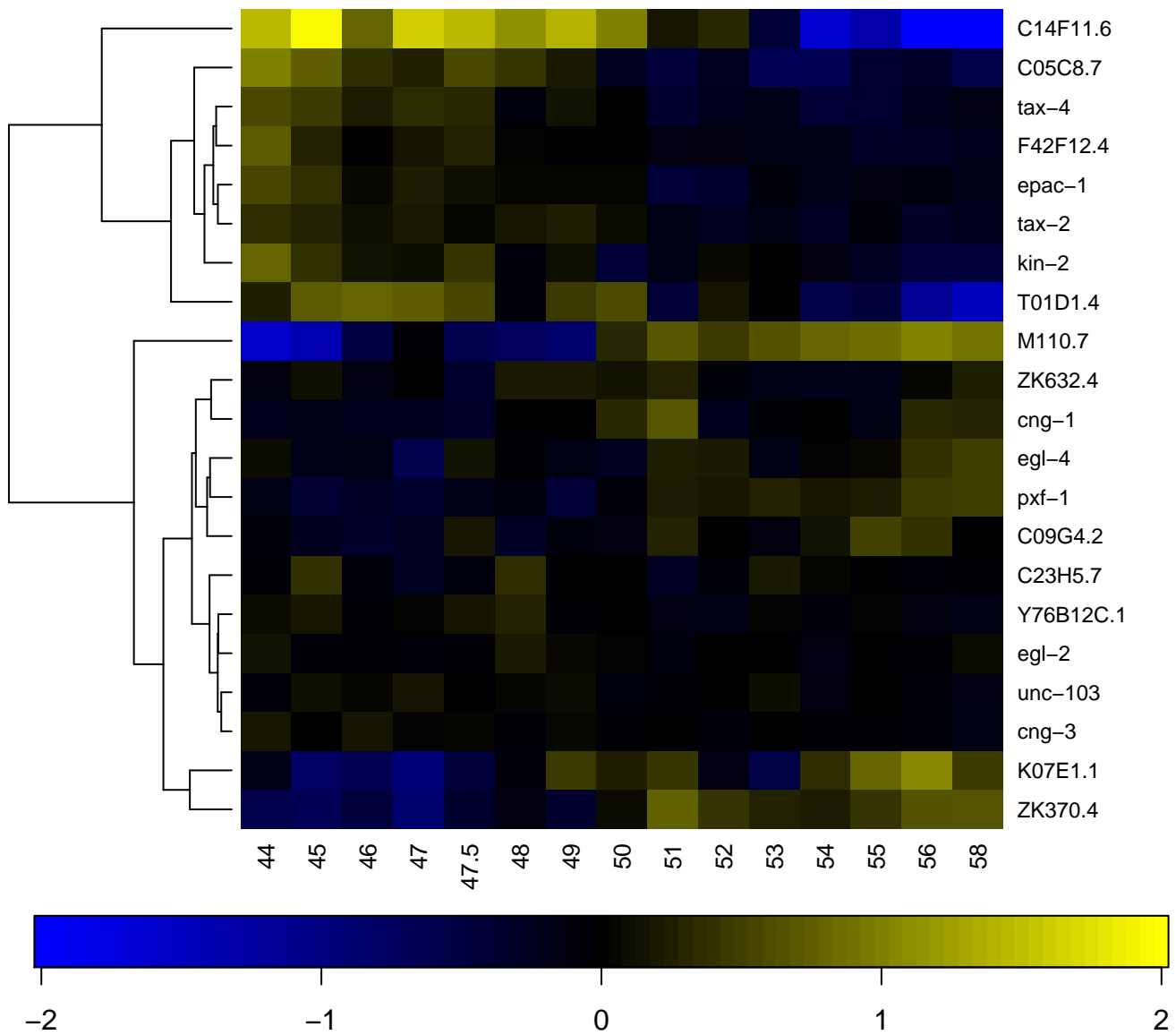
Ricin-type beta-trefoil lectin domain



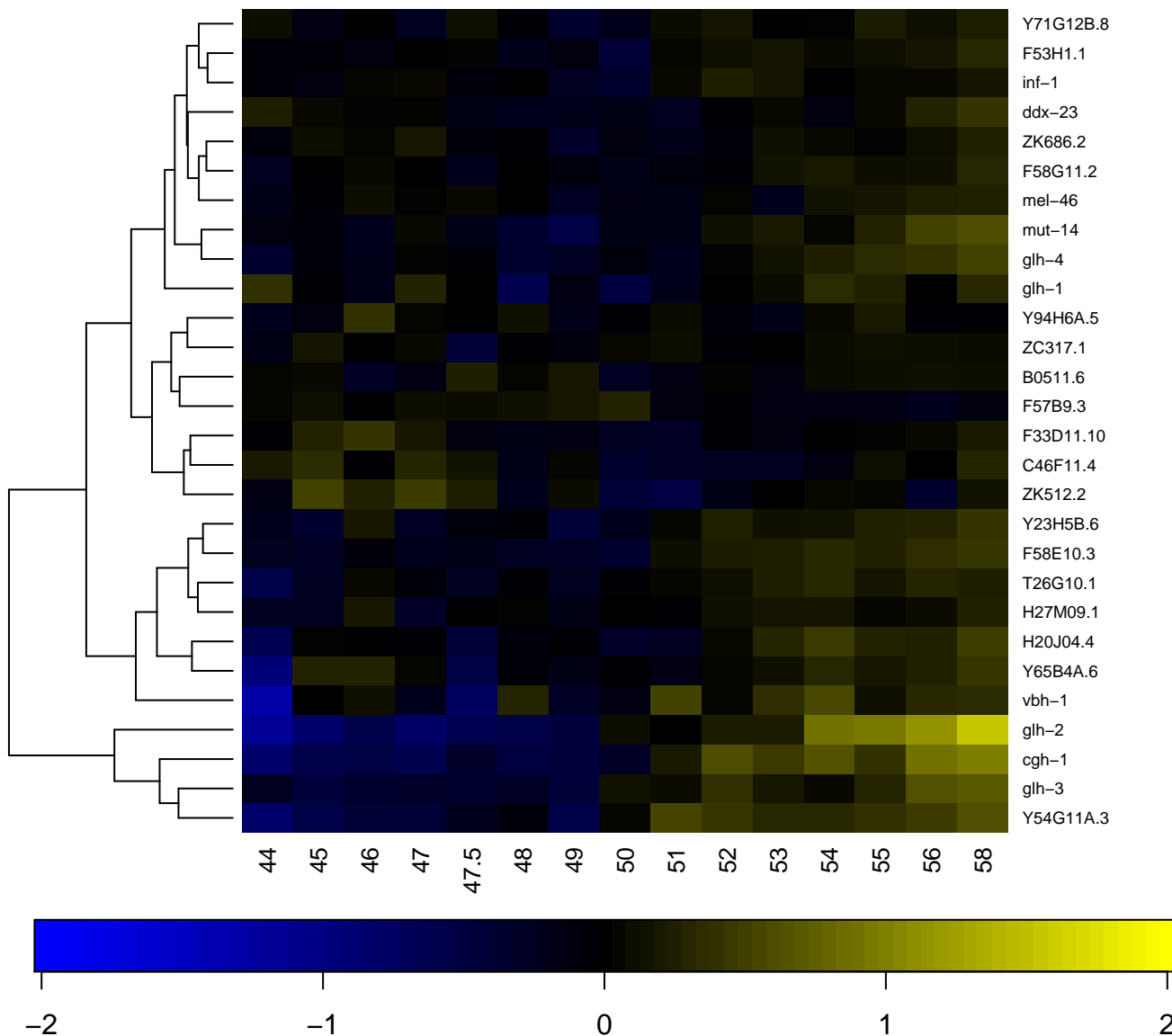
Ricin B lectin



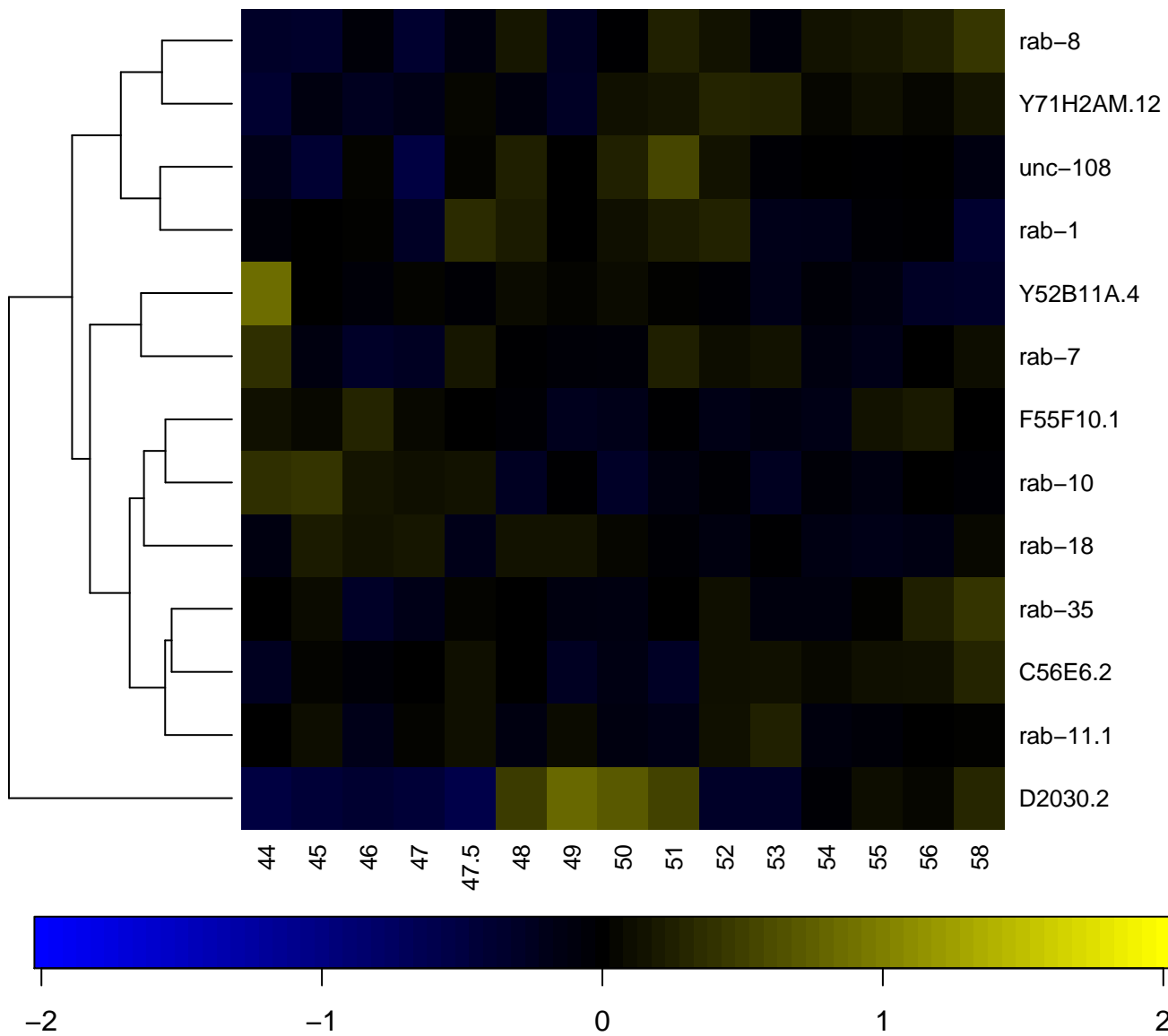
RmIC-like jelly roll fold



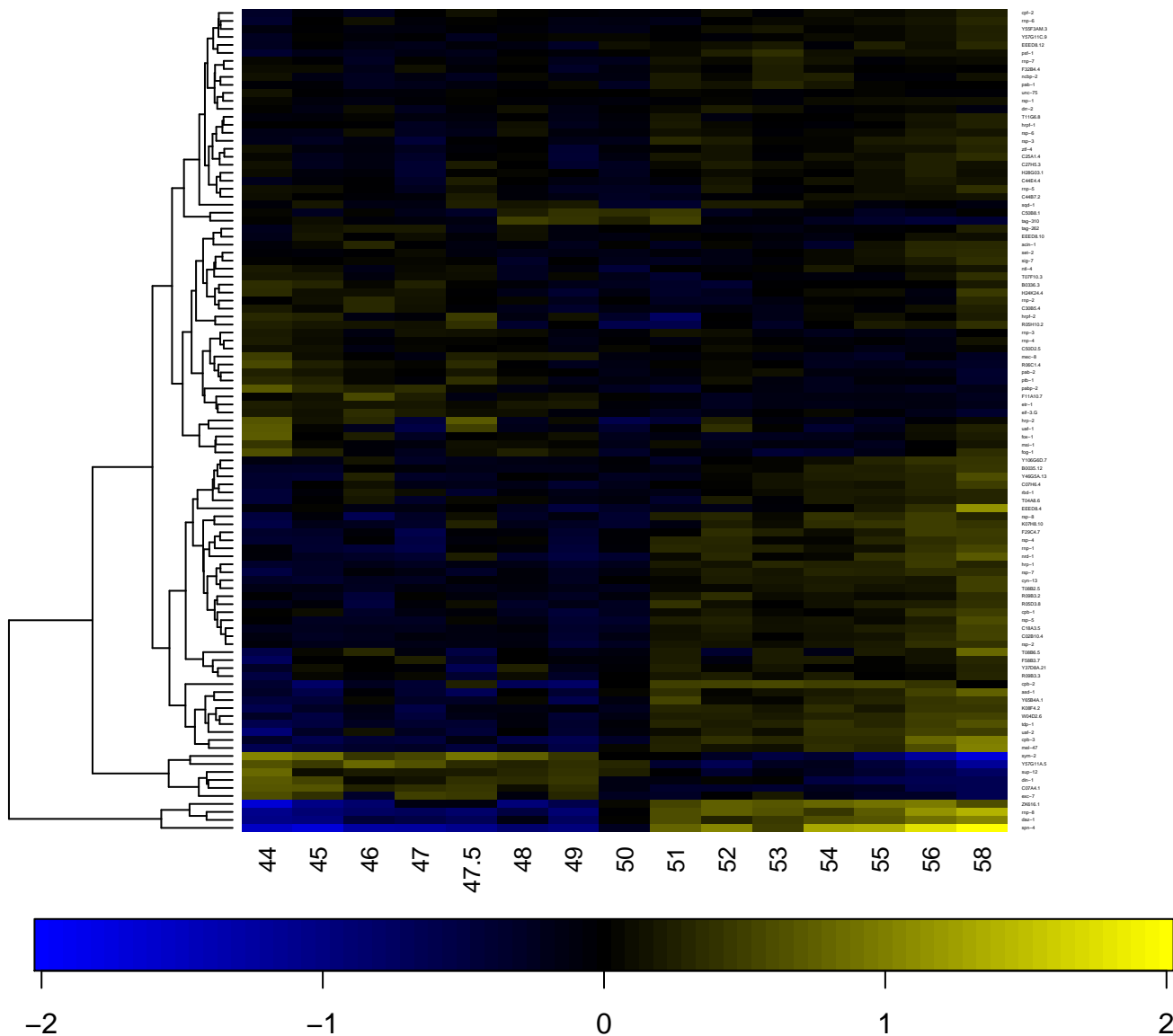
RNA helicase, ATP-dependent, DEAD-box, conserved site



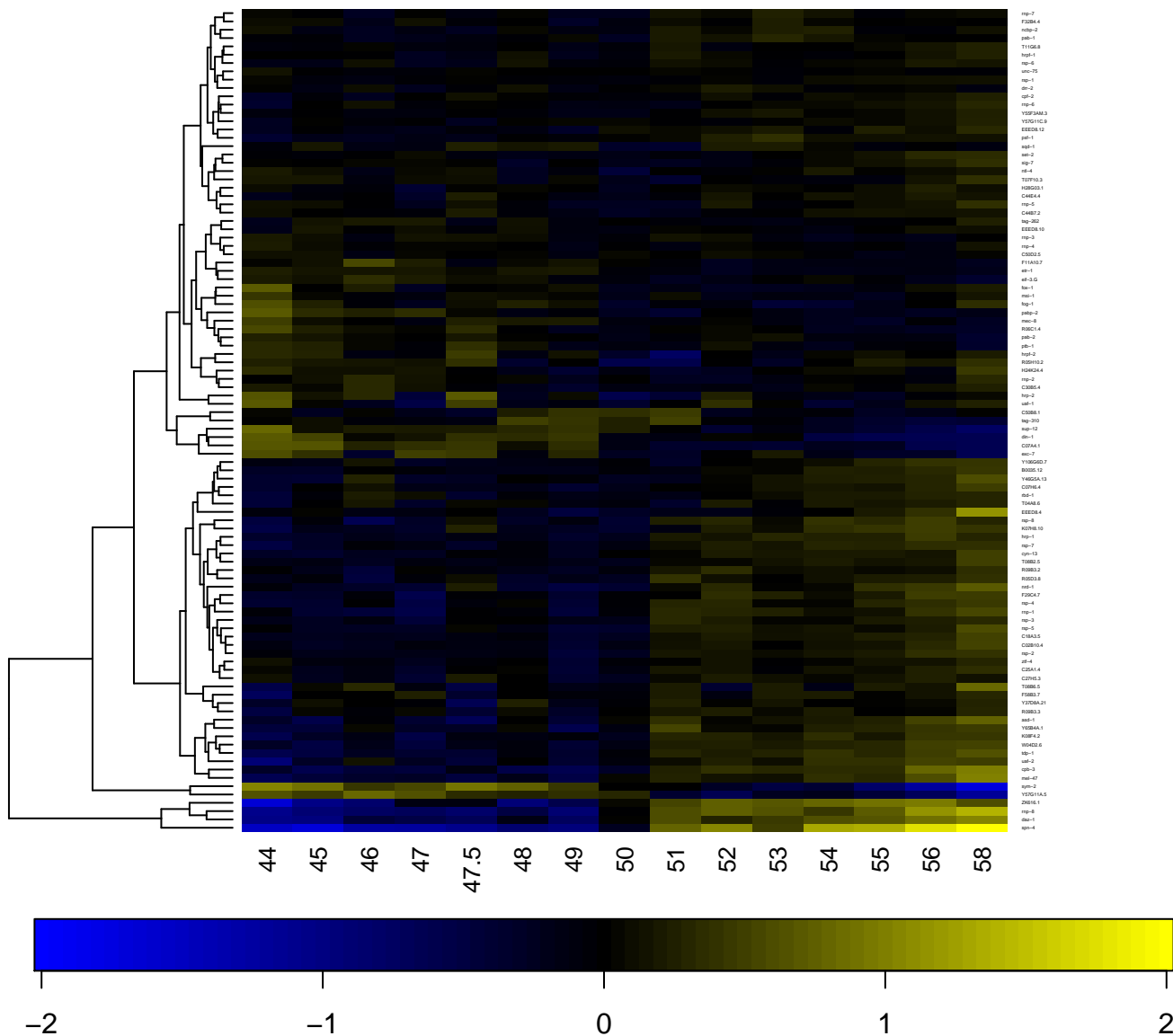
RNA polymerase sigma factor 54, interaction



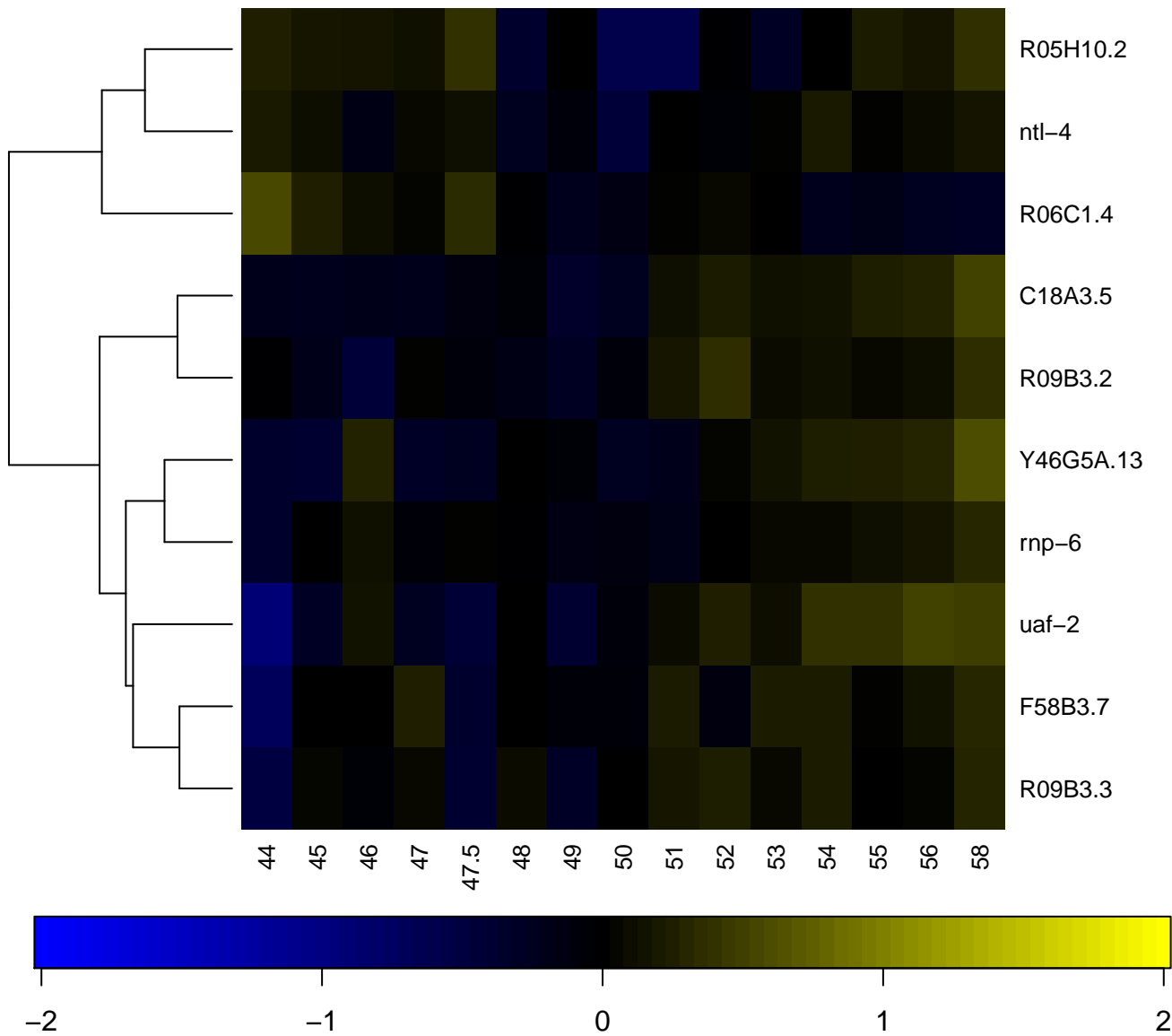
RNA recognition motif, RNP-1



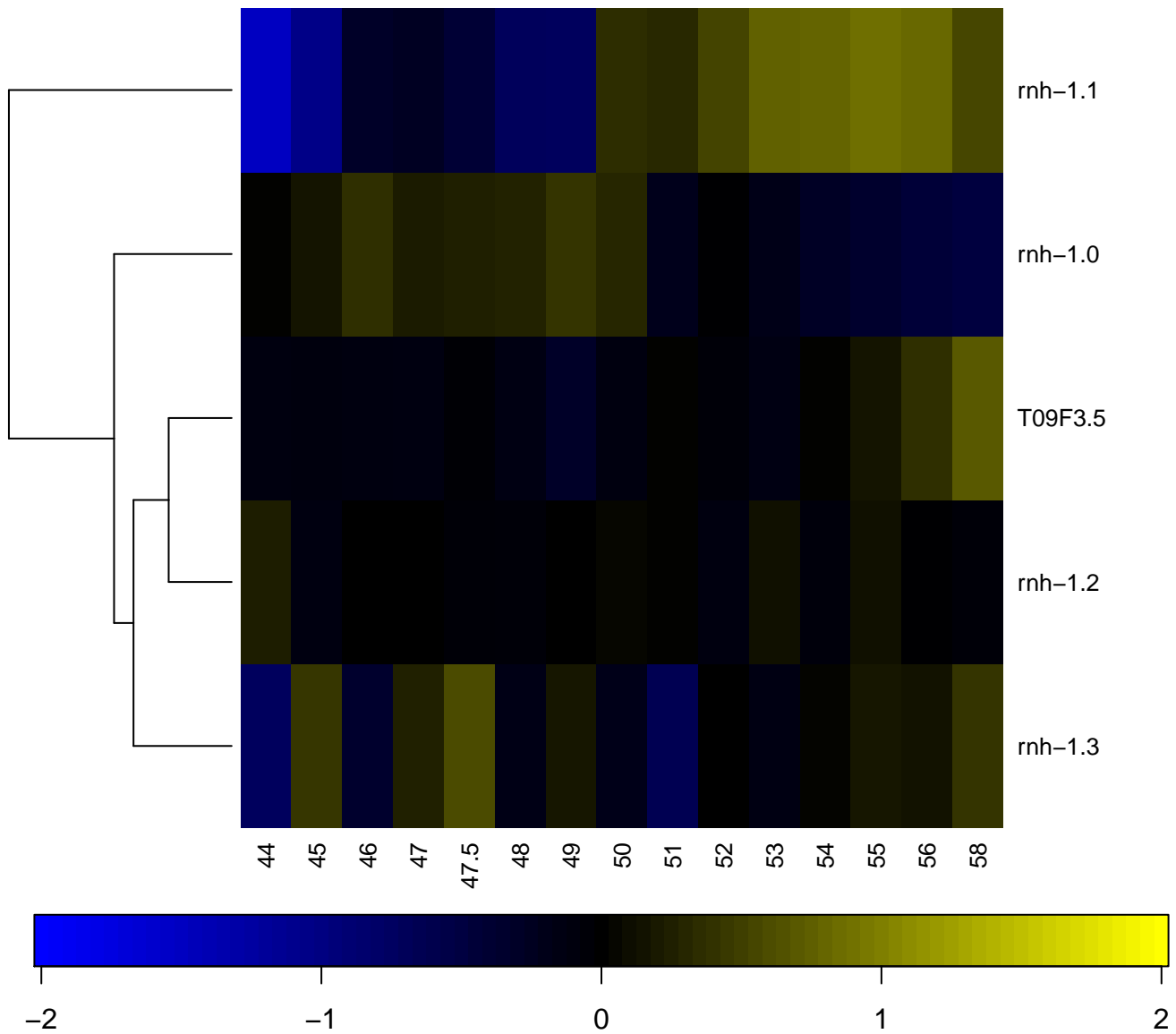
RNA recognition motif. (a.k.a. RRM, RBD, or RNP domain)



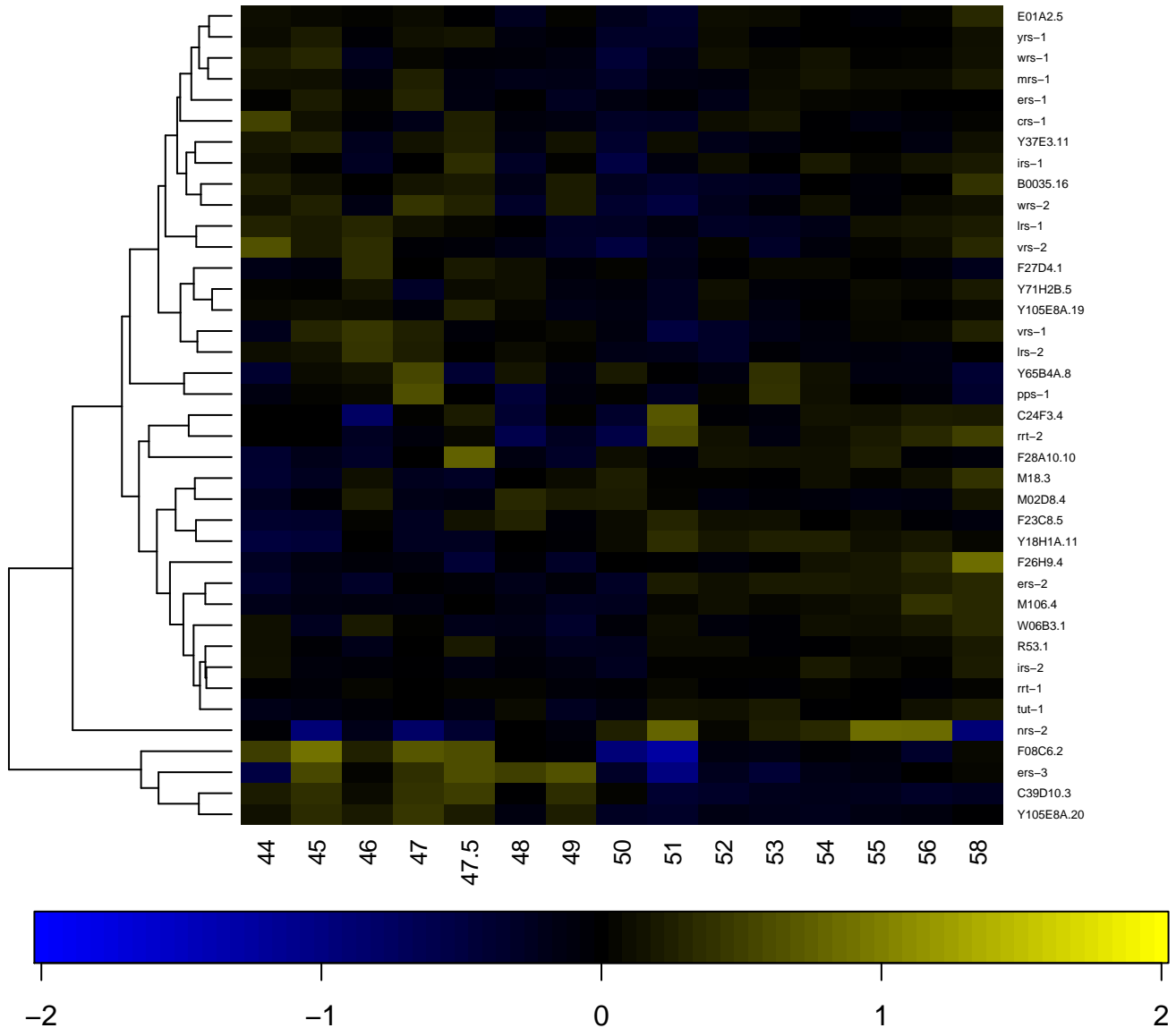
RNA recognition, domain 1



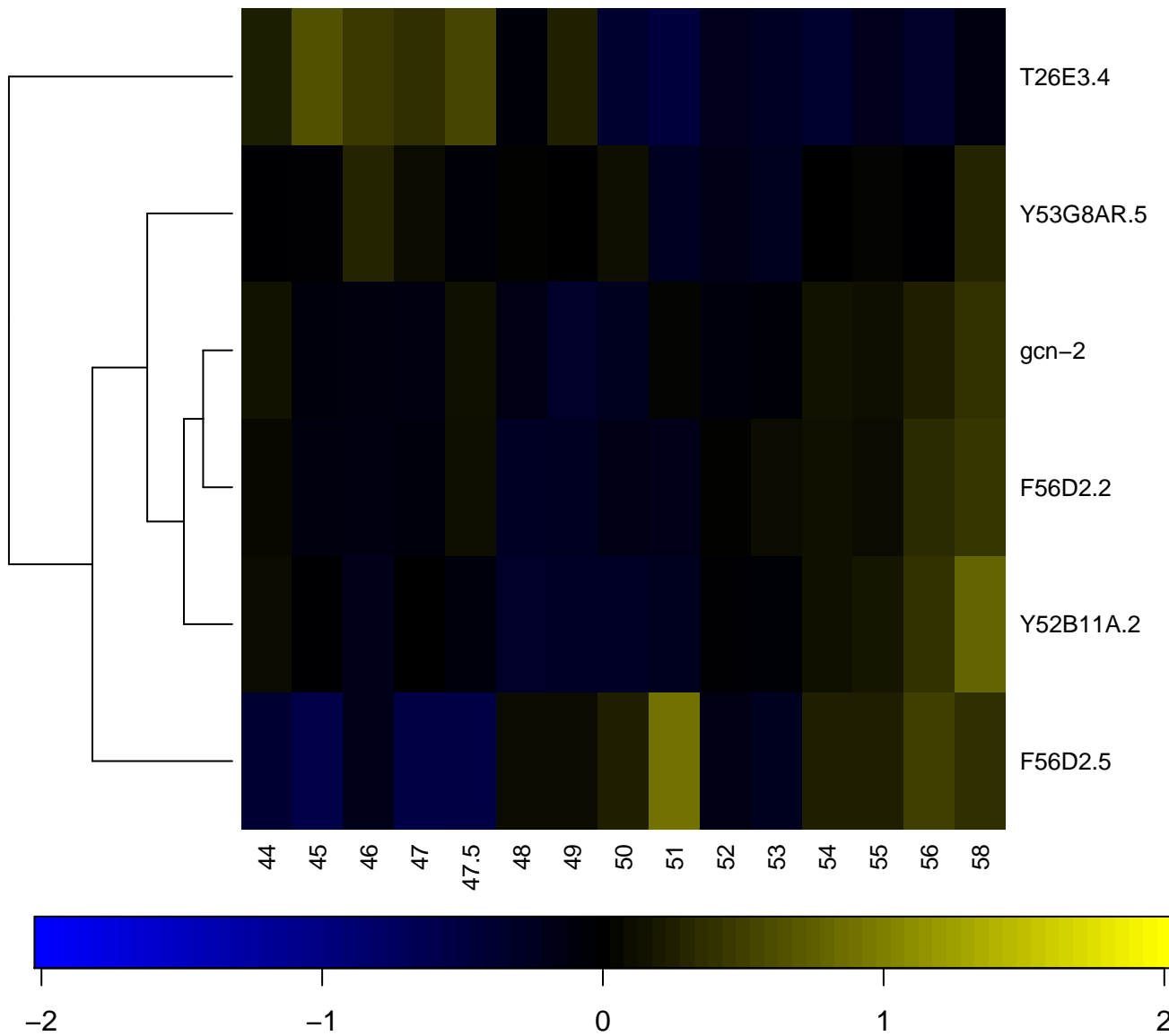
RNase H



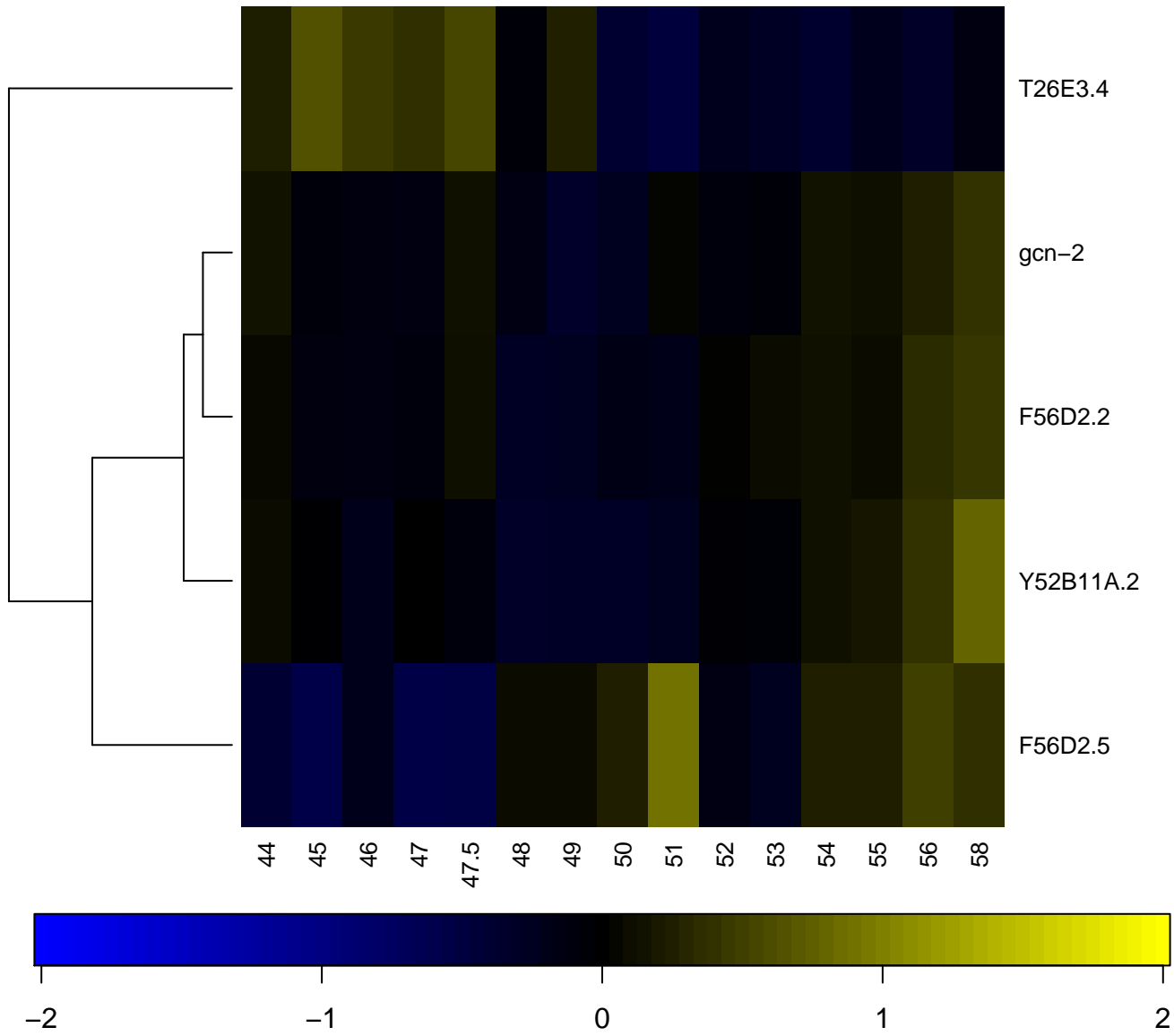
Rossmann-like alpha/beta/alpha sandwich fold



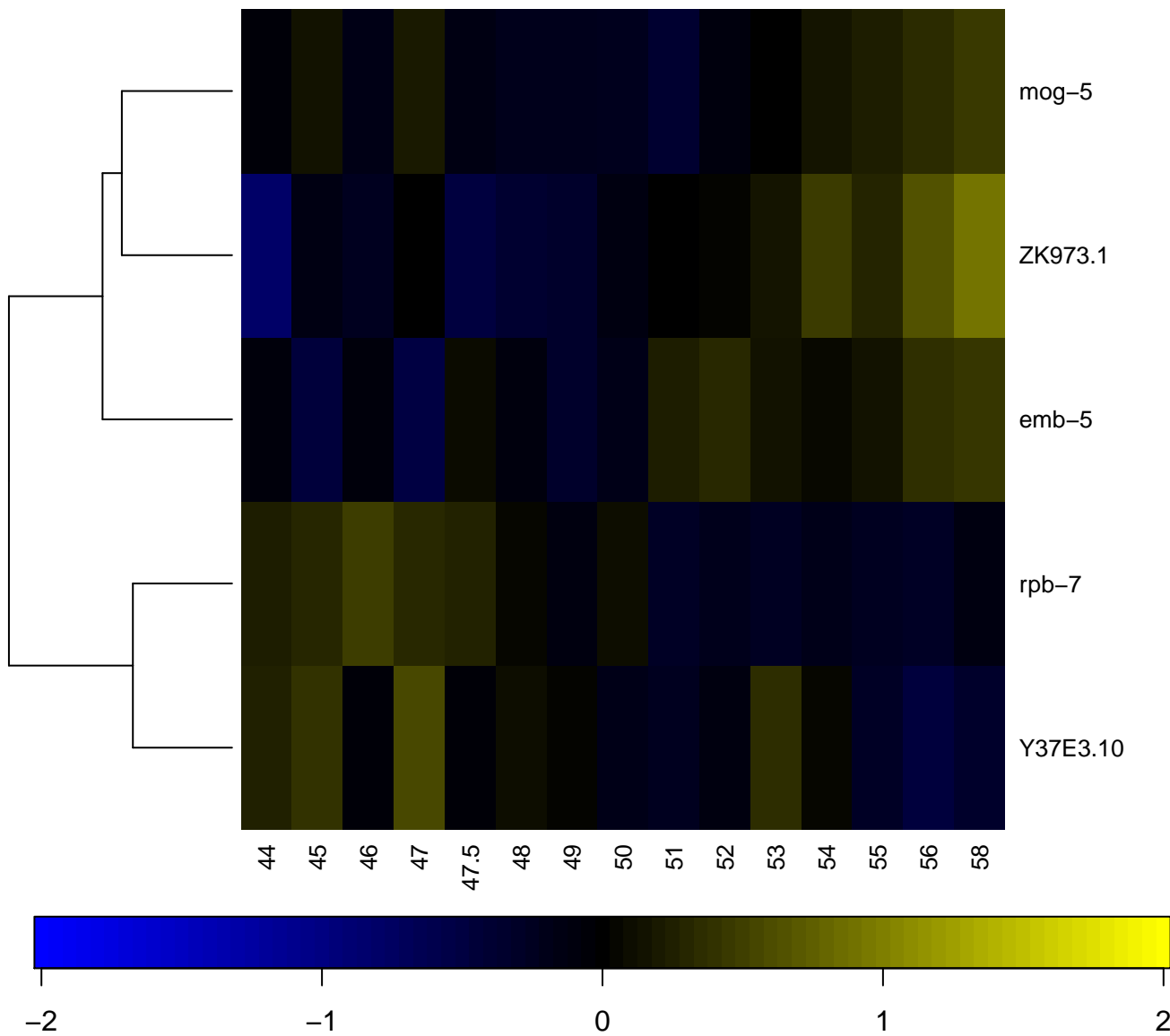
RWD



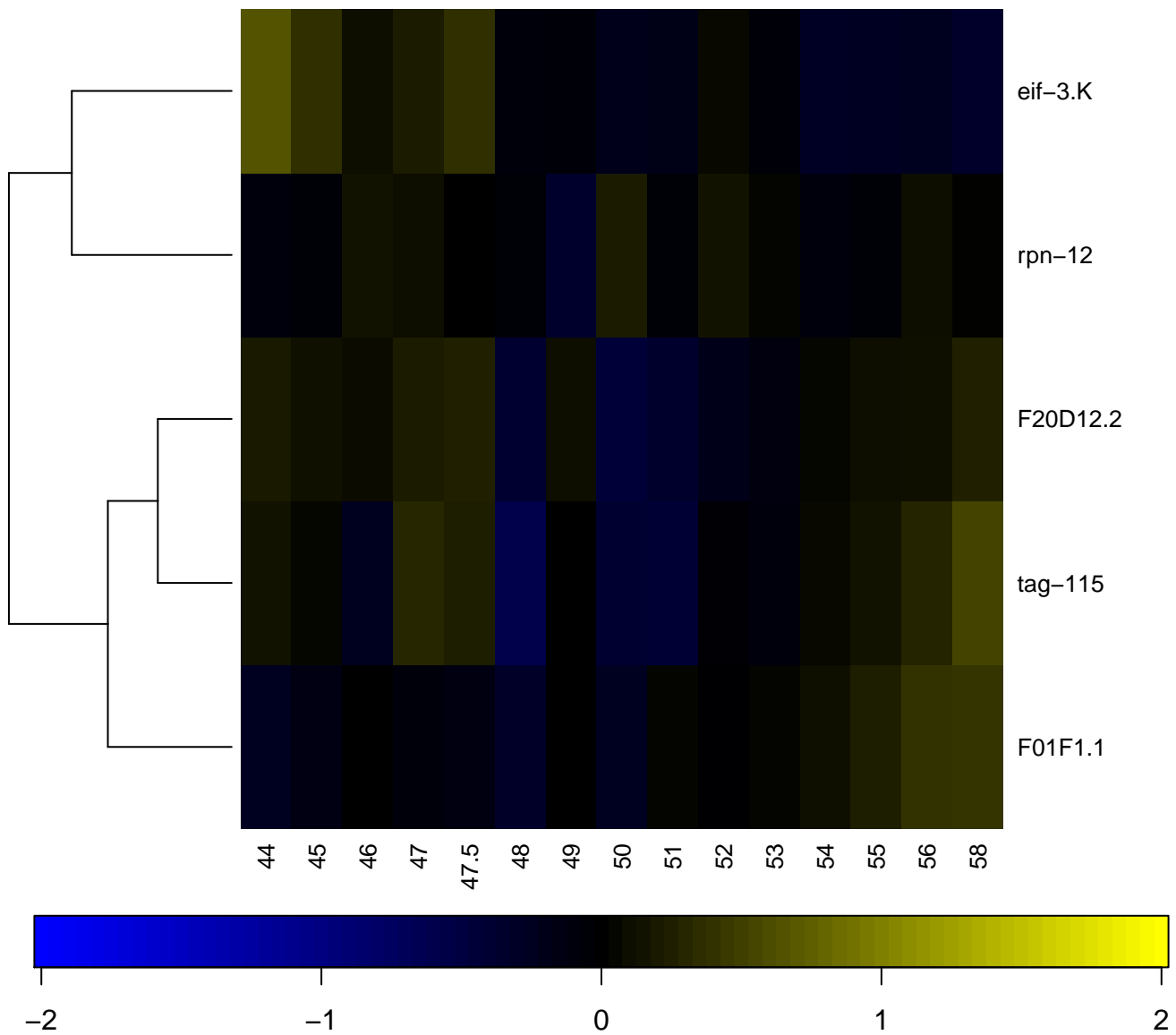
RWD domain



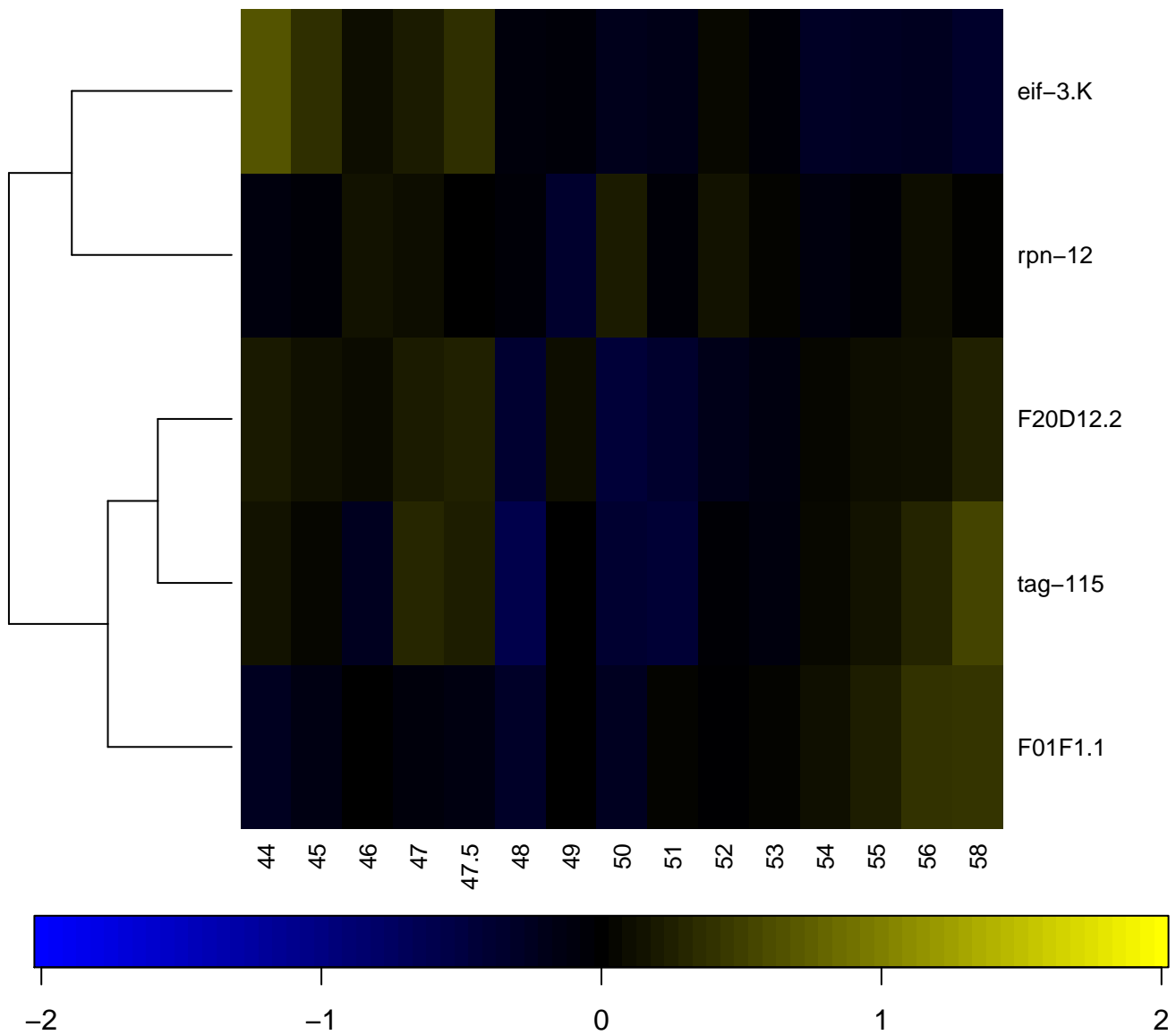
S1 RNA binding domain



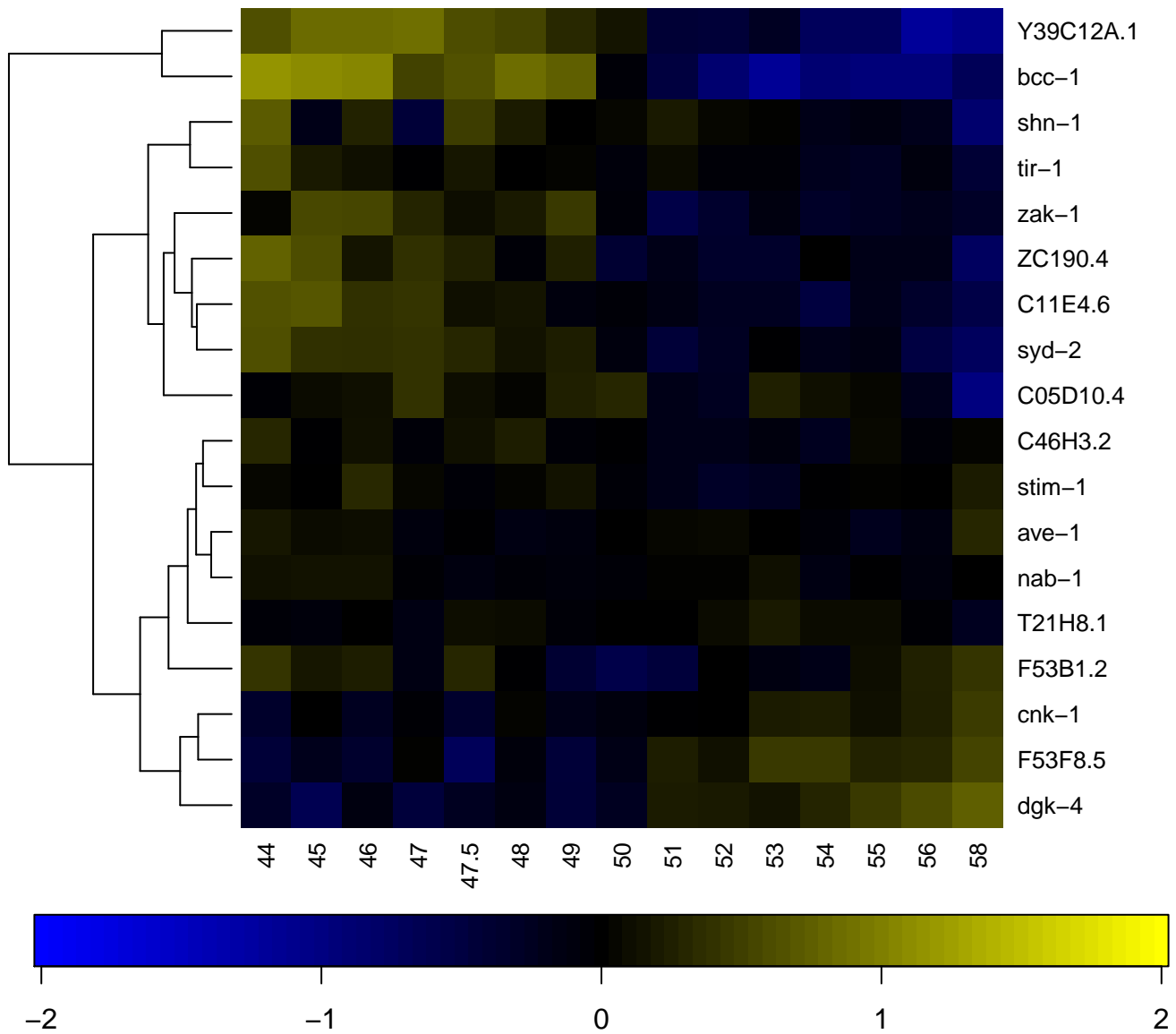
SAC3/GANP/Nin1/mts3/eIF-3 p25



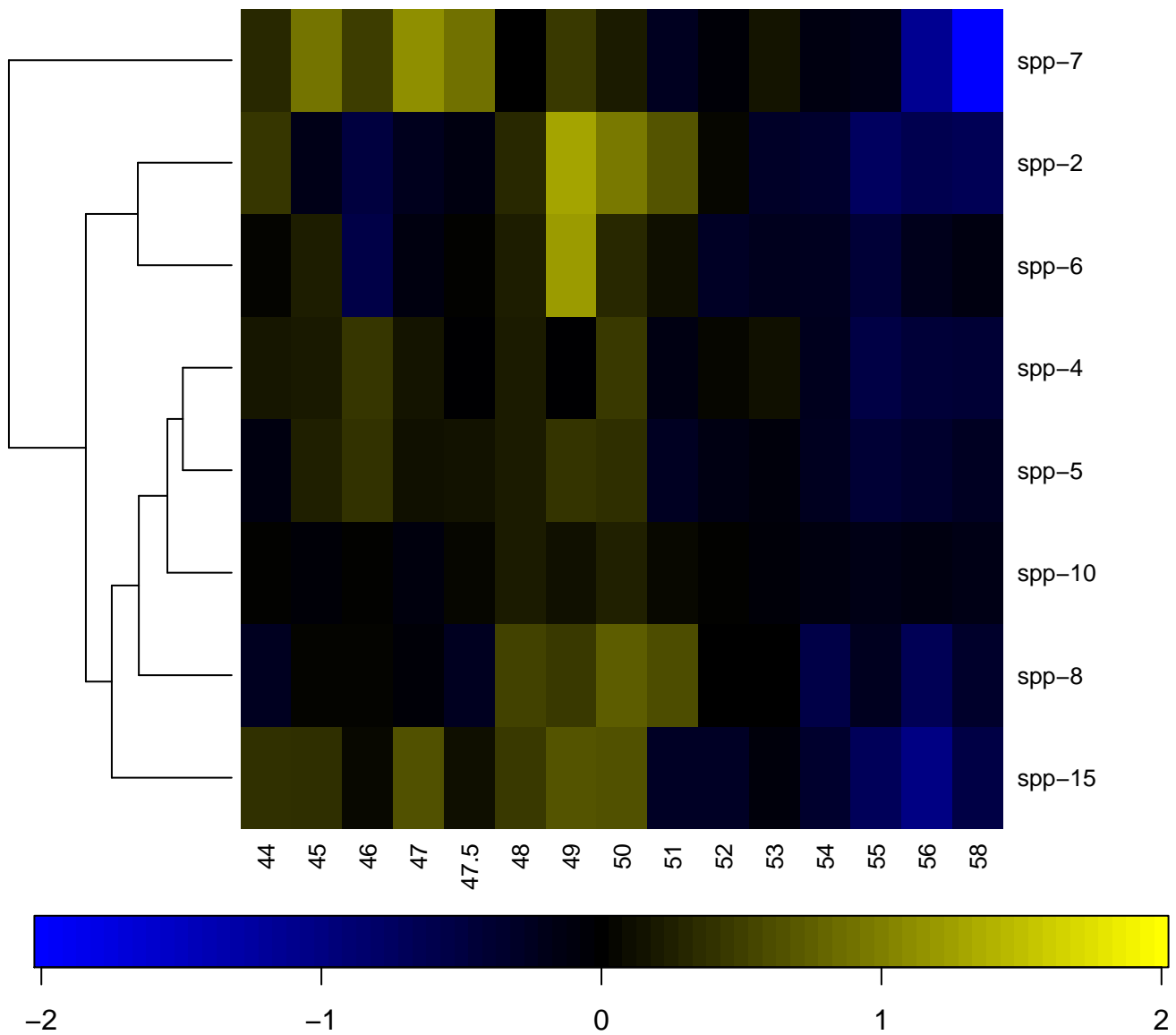
SAC3/GANP/Nin1/mts3/eIF-3 p25 family



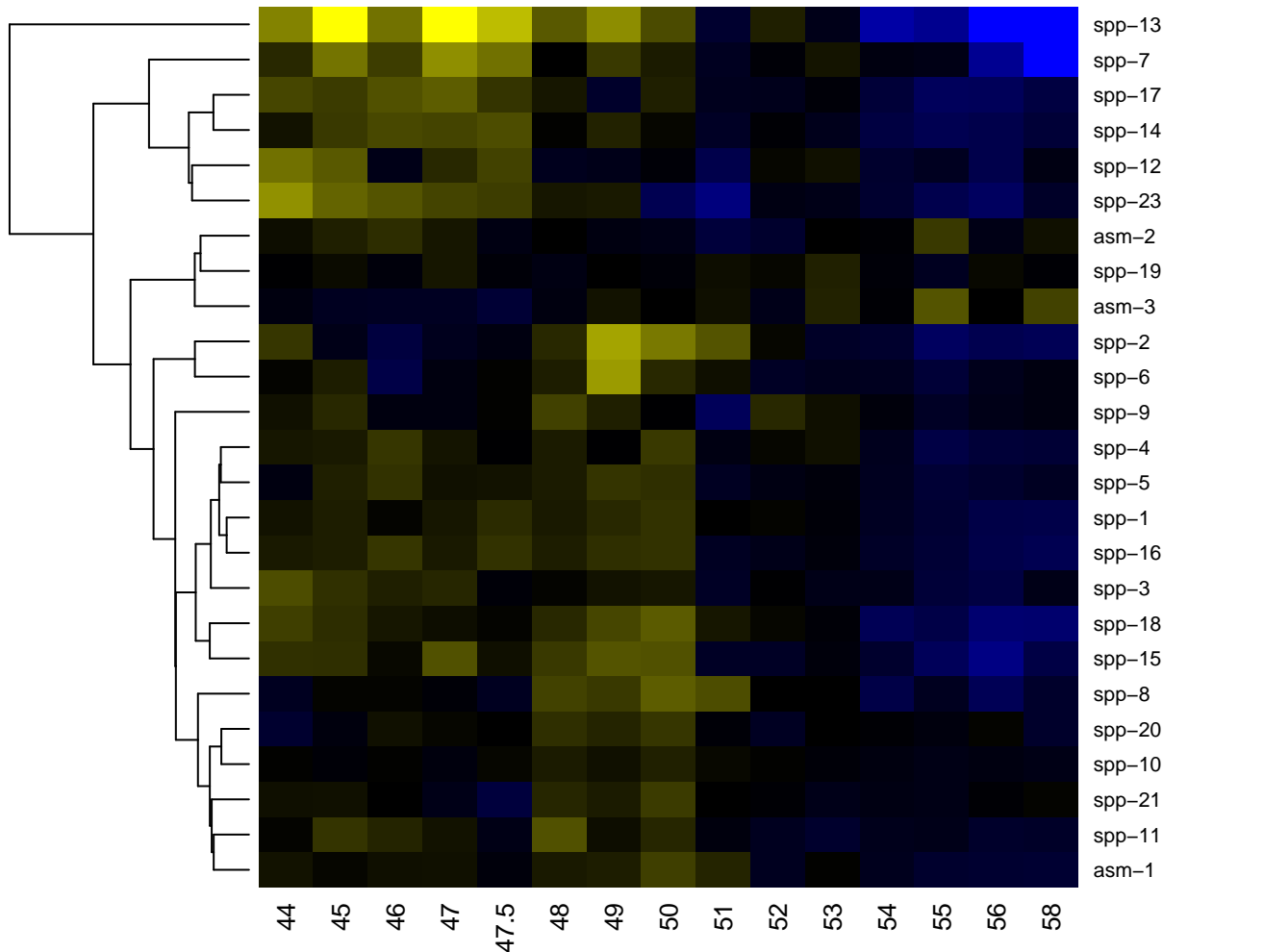
SAM domain (Sterile alpha motif)



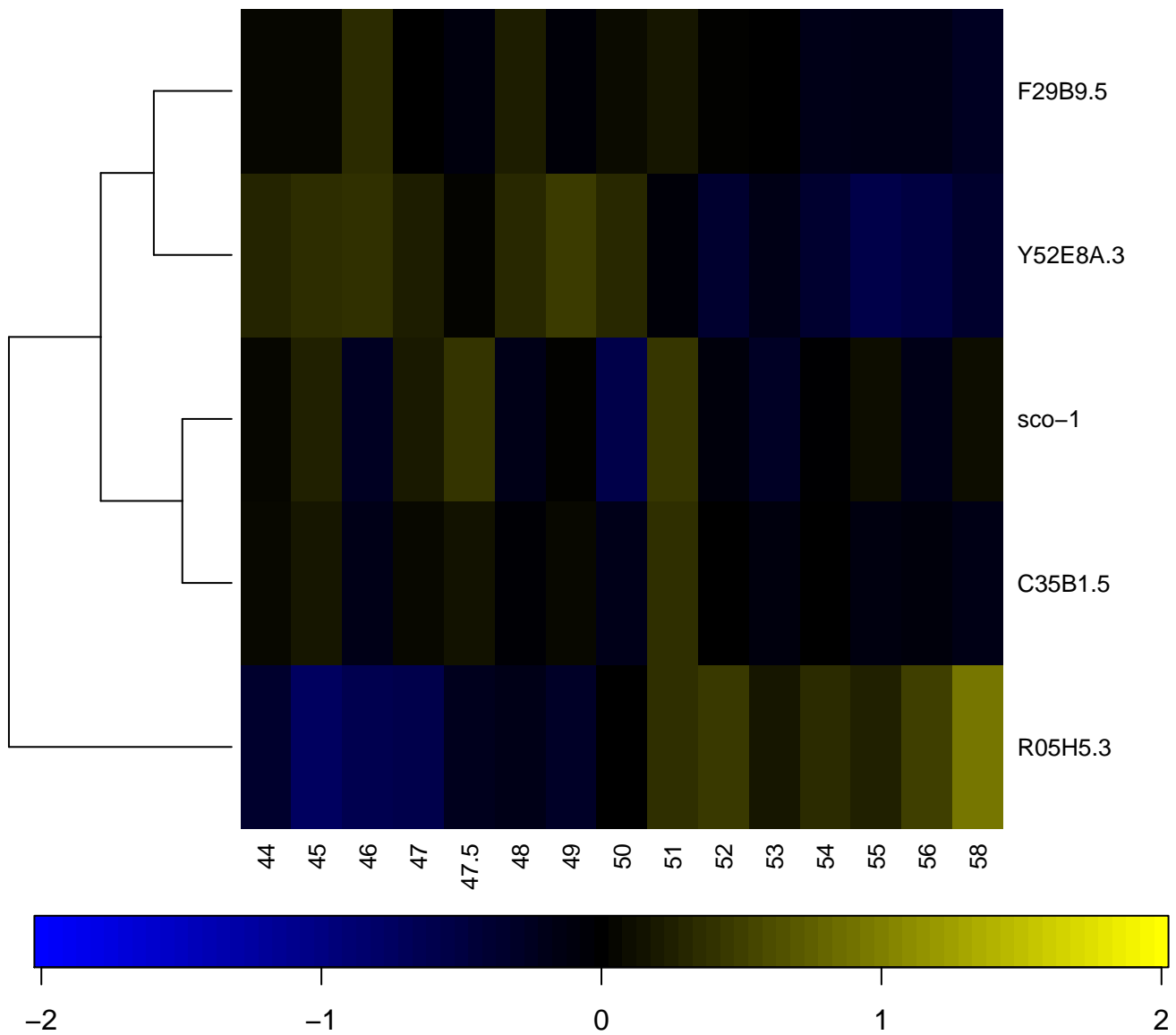
Saposin-like type B, region 2



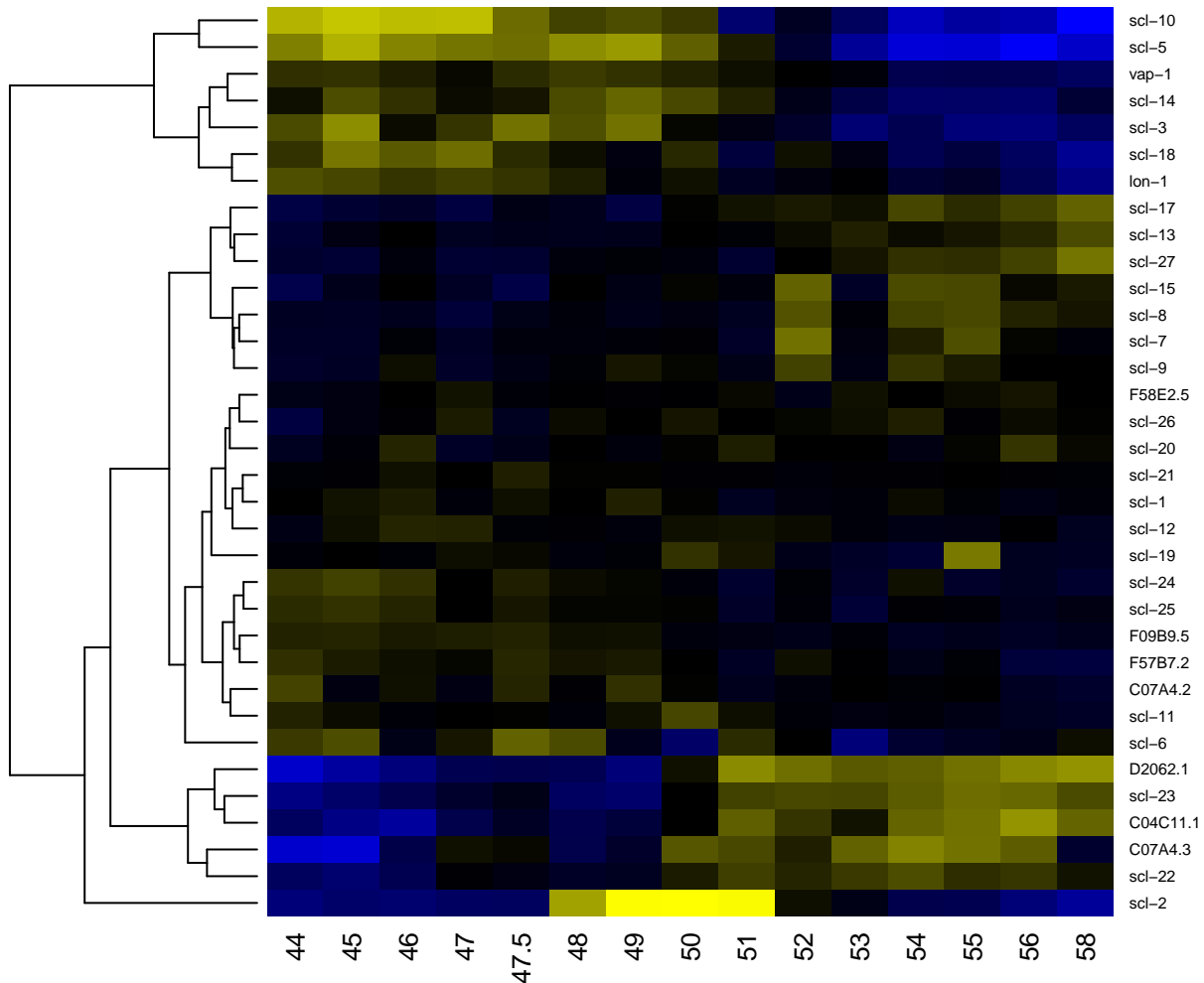
Saposin B



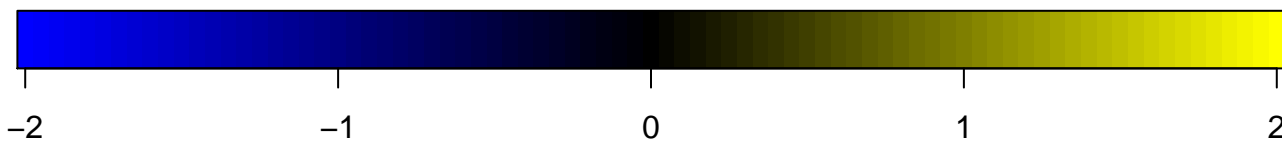
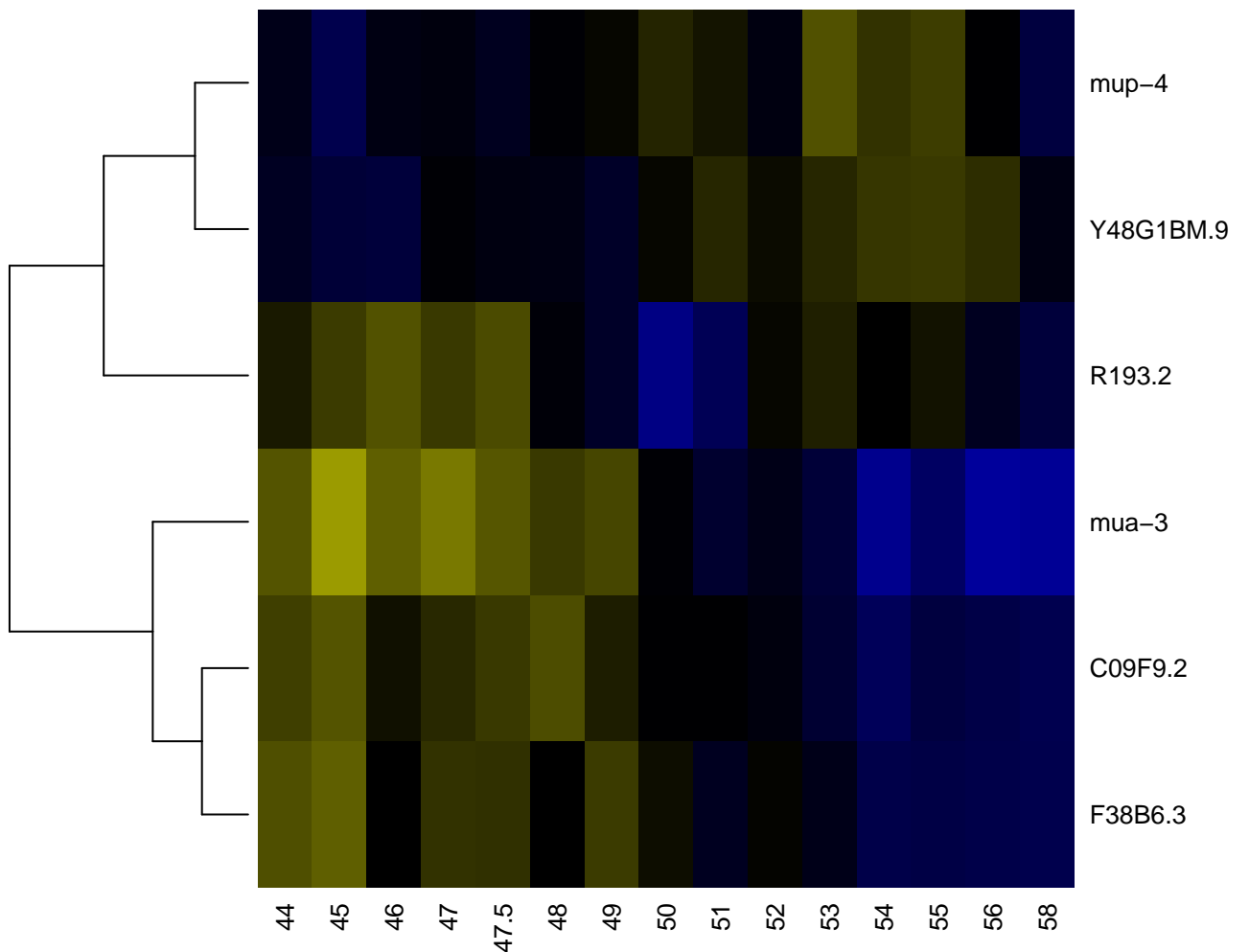
SCO1/SenC



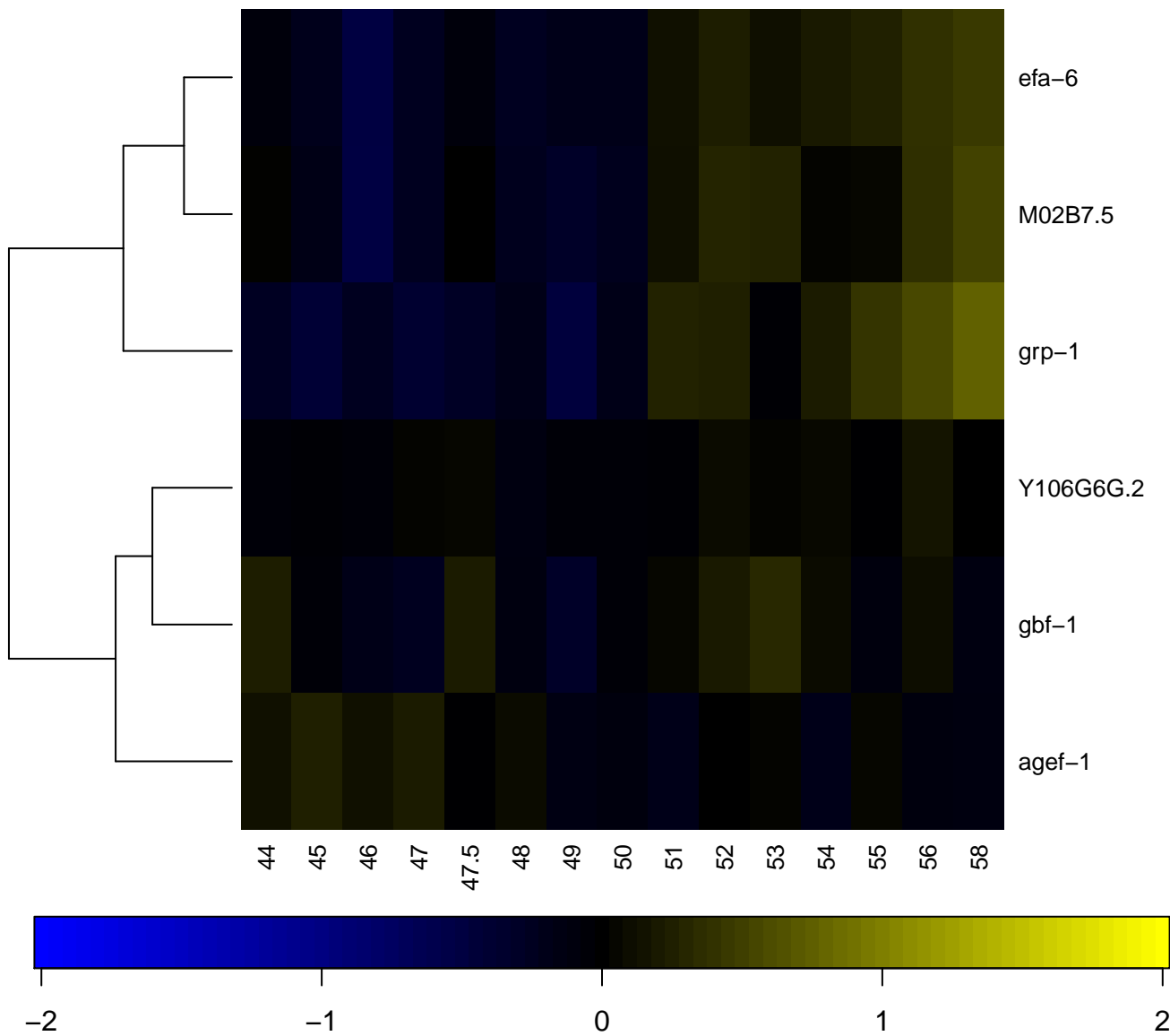
SCP-like extracellular



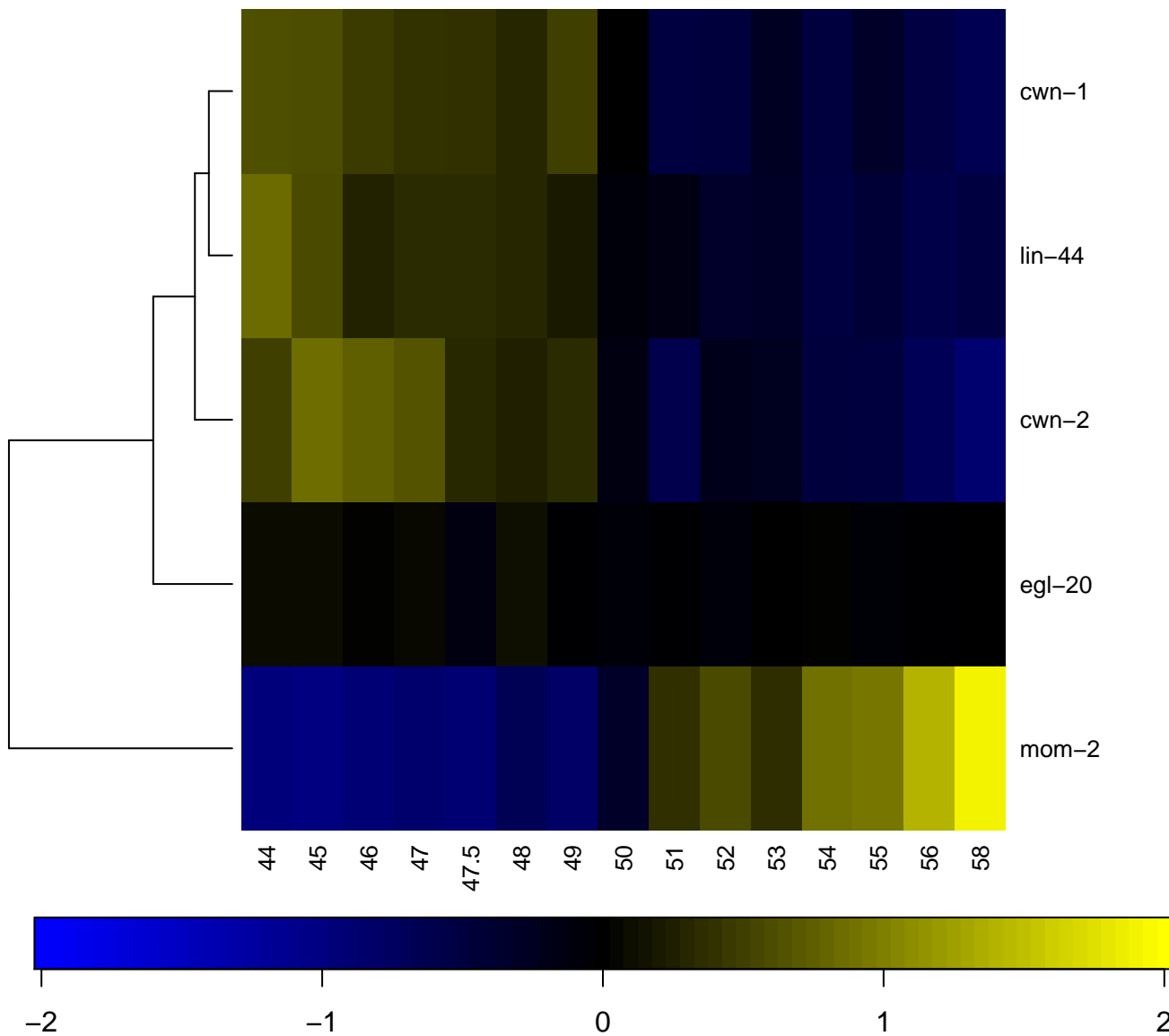
SEA



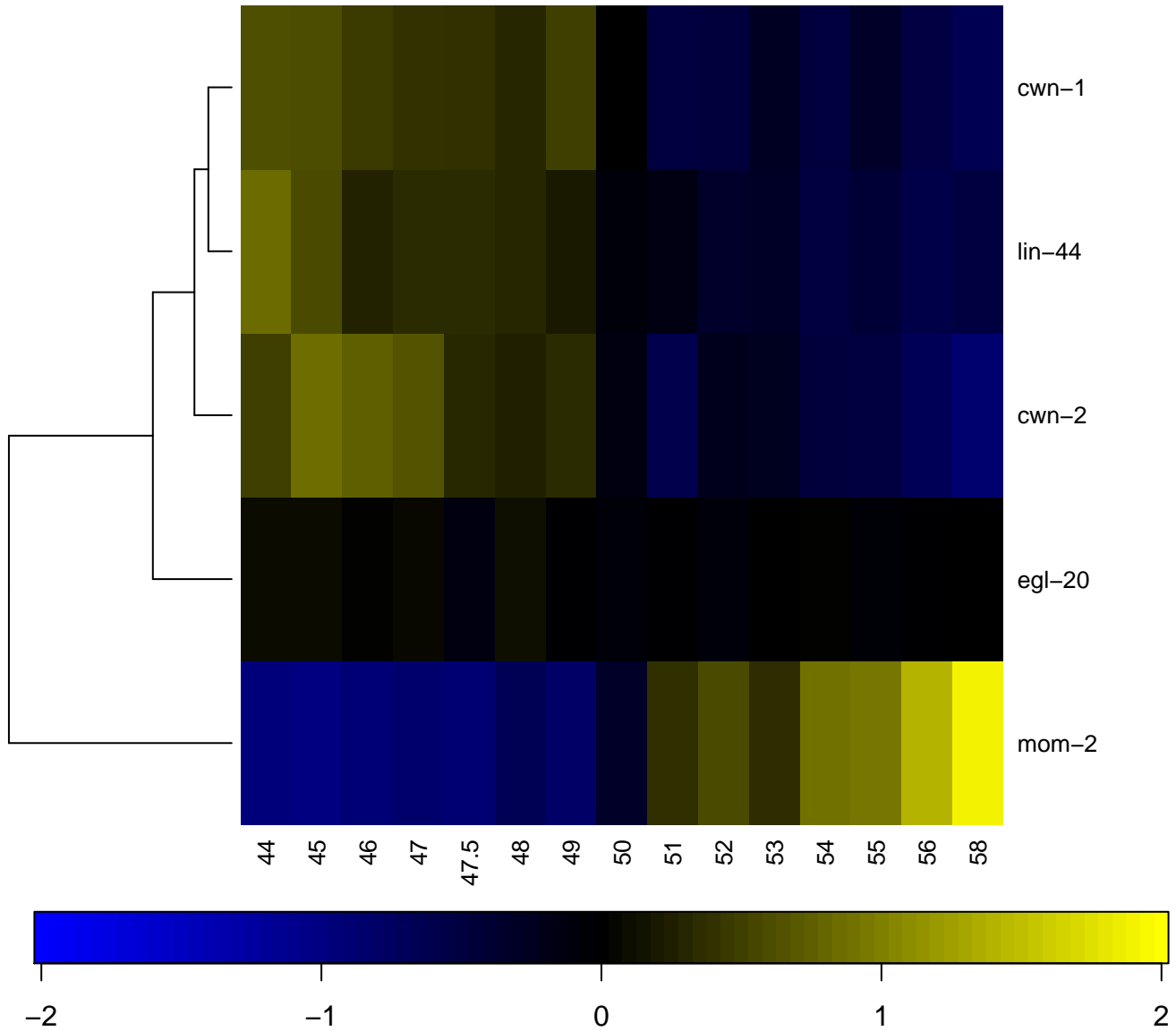
SEC7-like



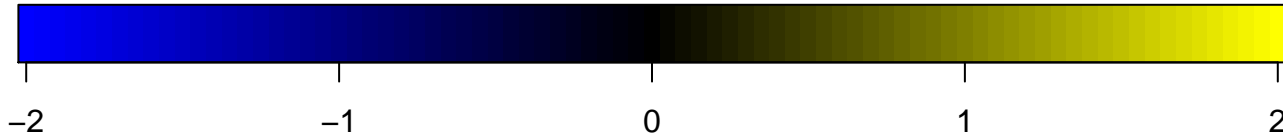
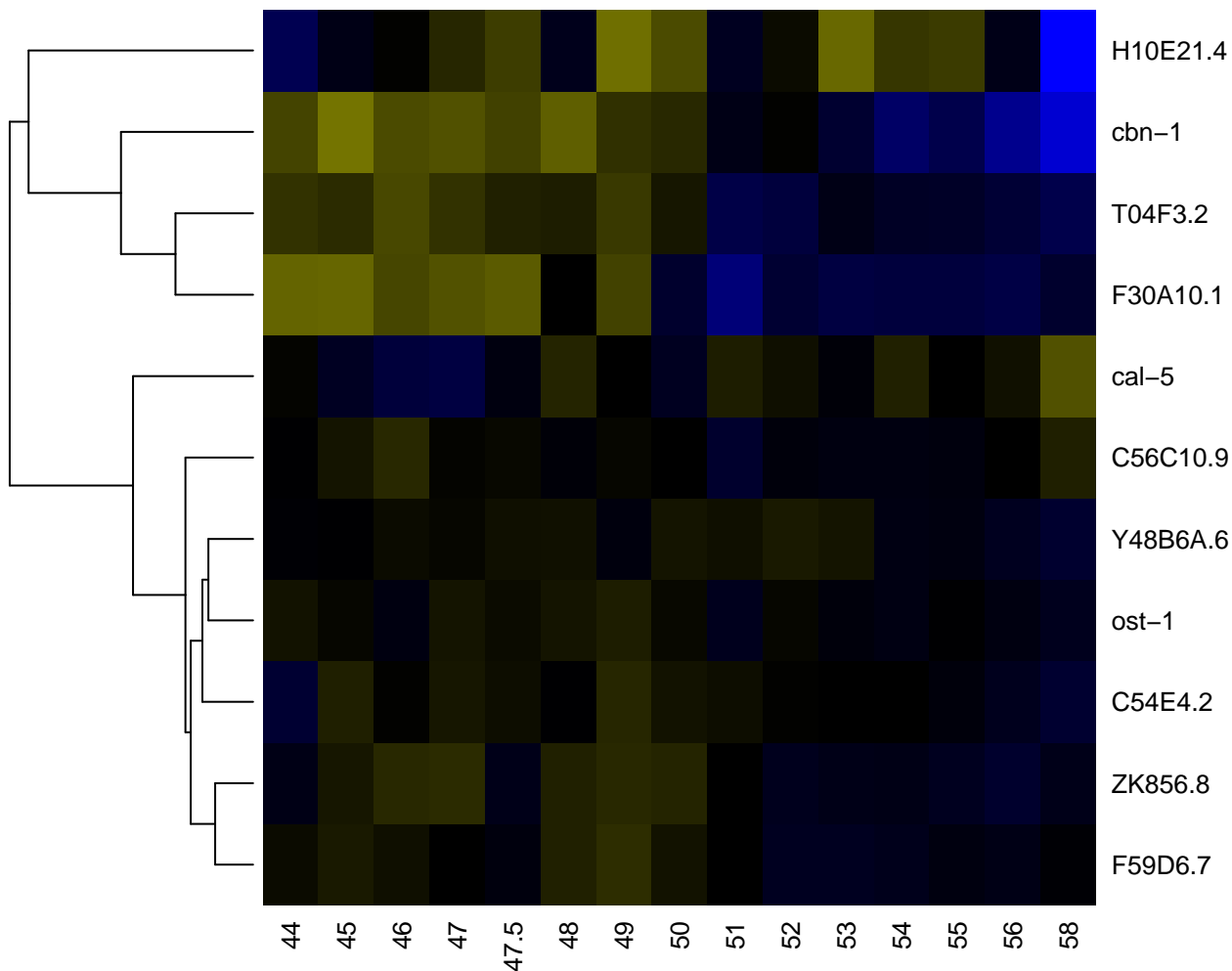
Secreted growth factor Wnt protein



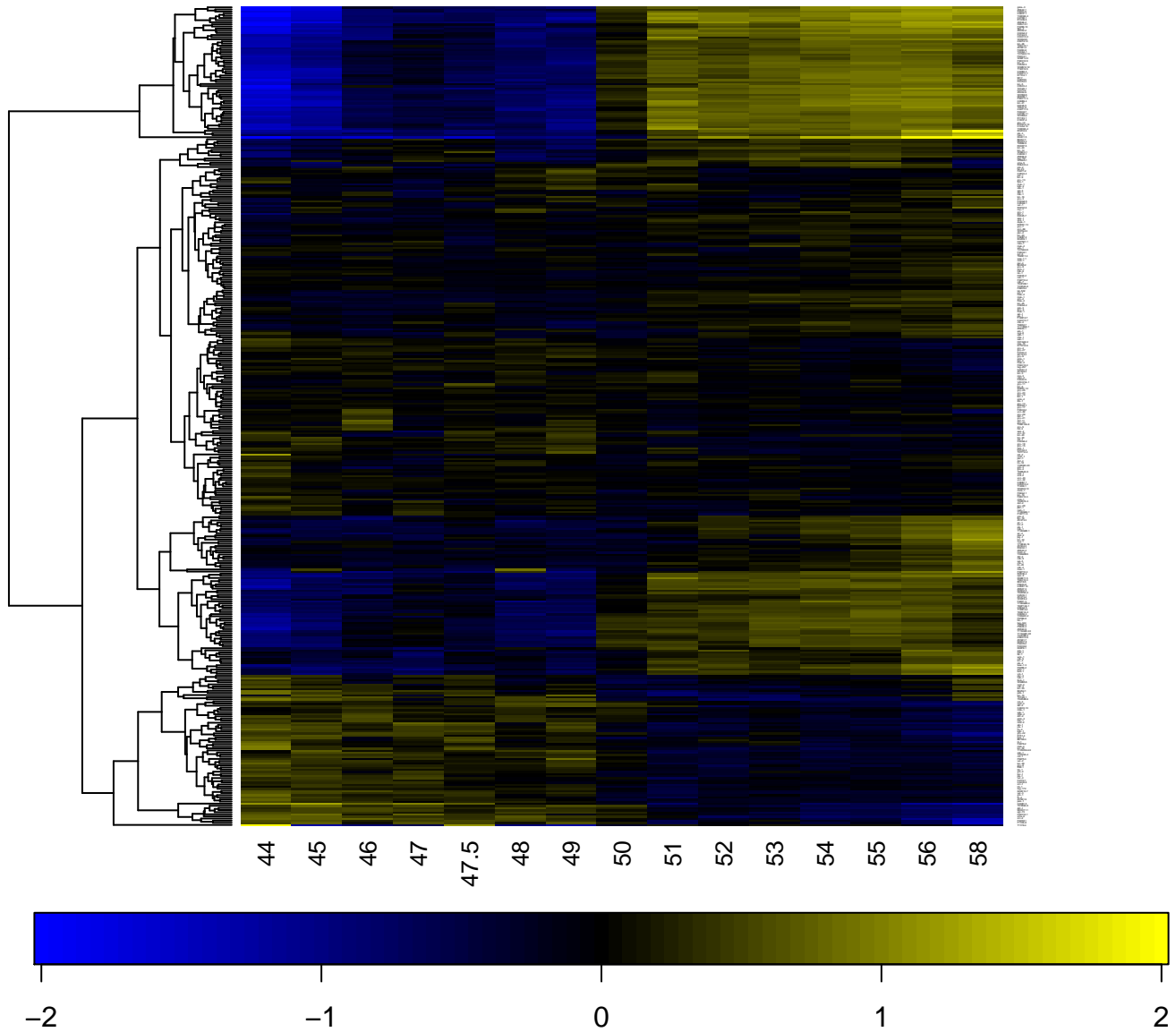
Secreted growth factor Wnt protein, conserved site



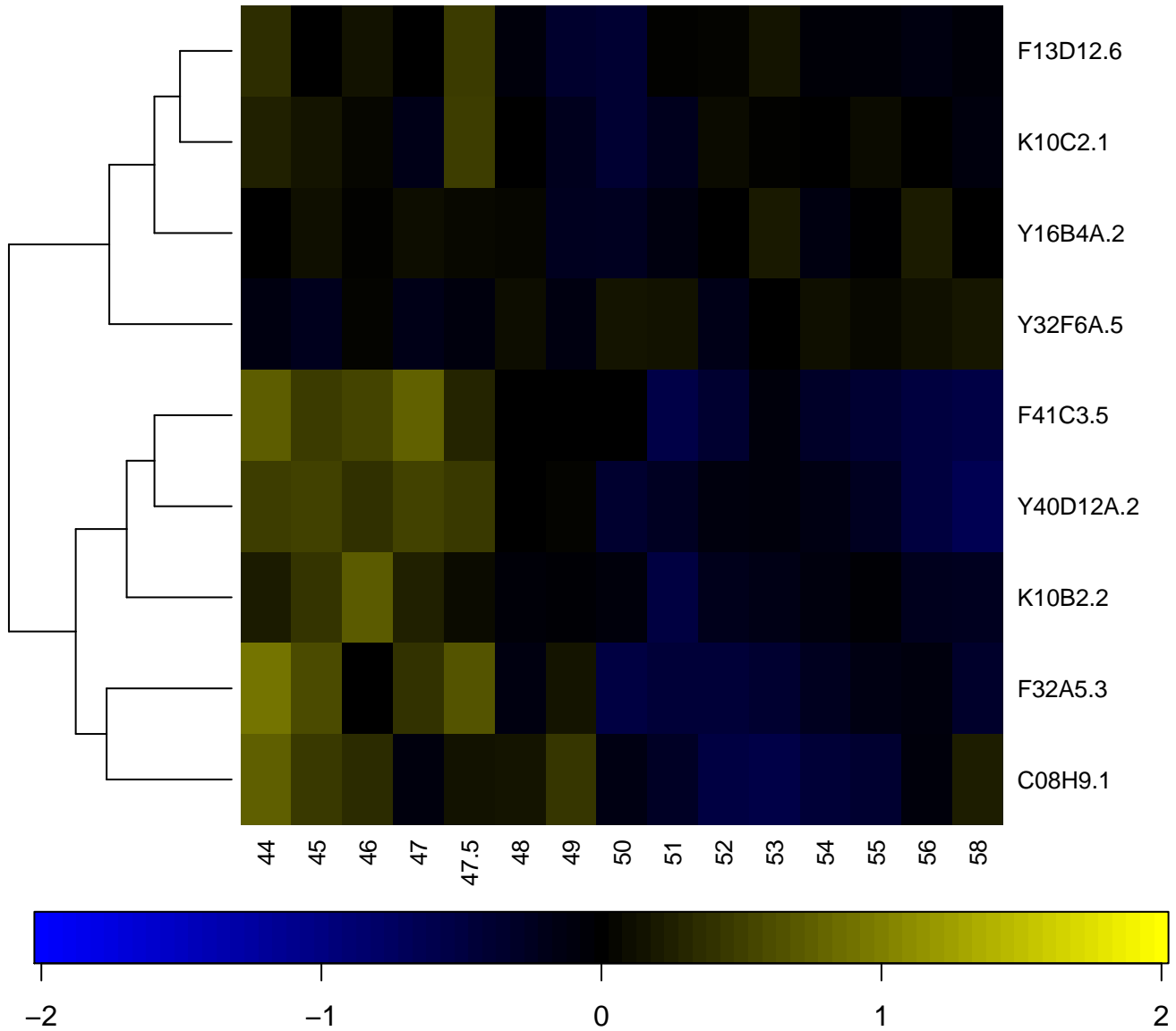
Secreted protein acidic and rich in cysteine Ca binding region



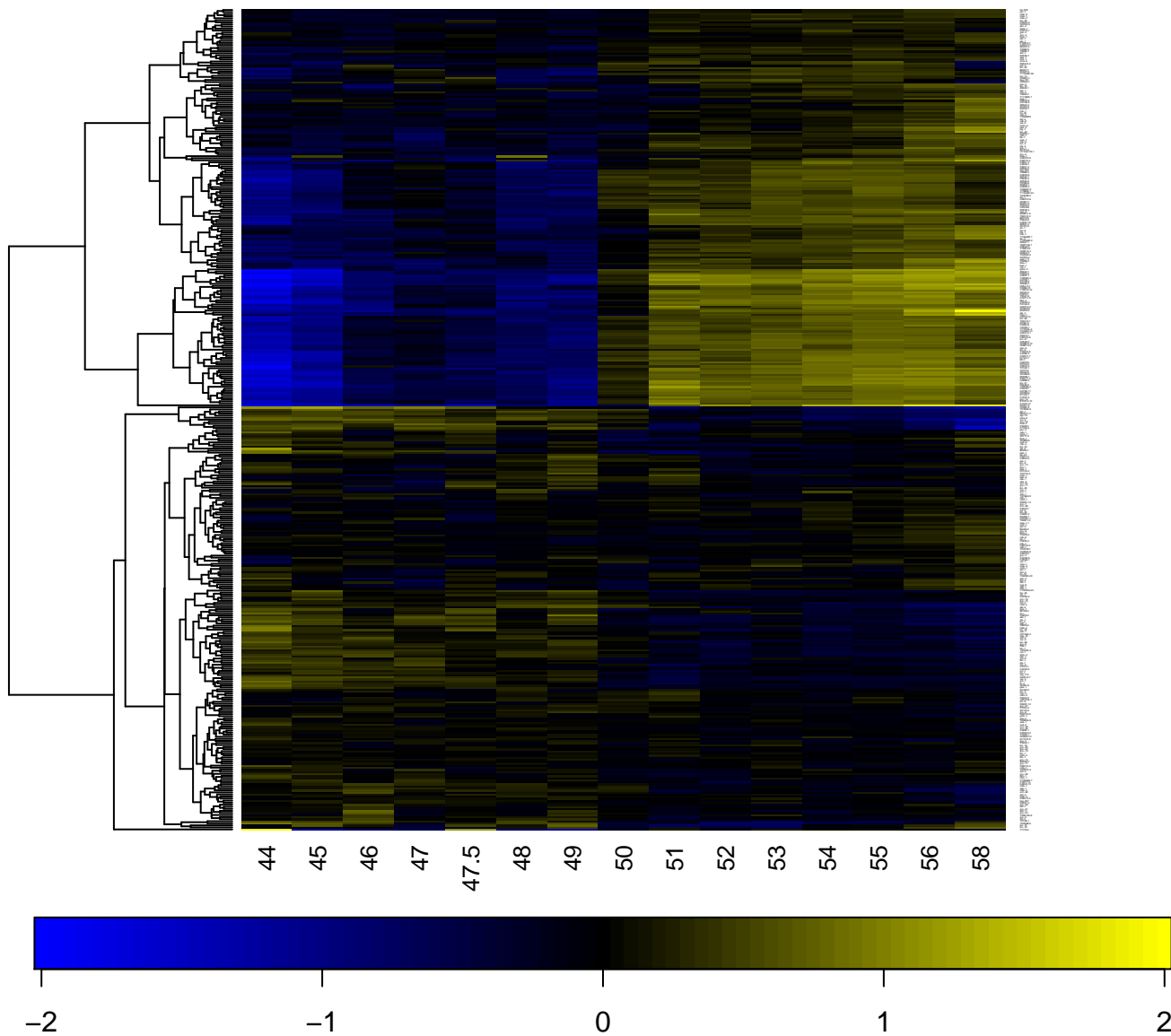
Serine–threonine/tyrosine–protein kinase



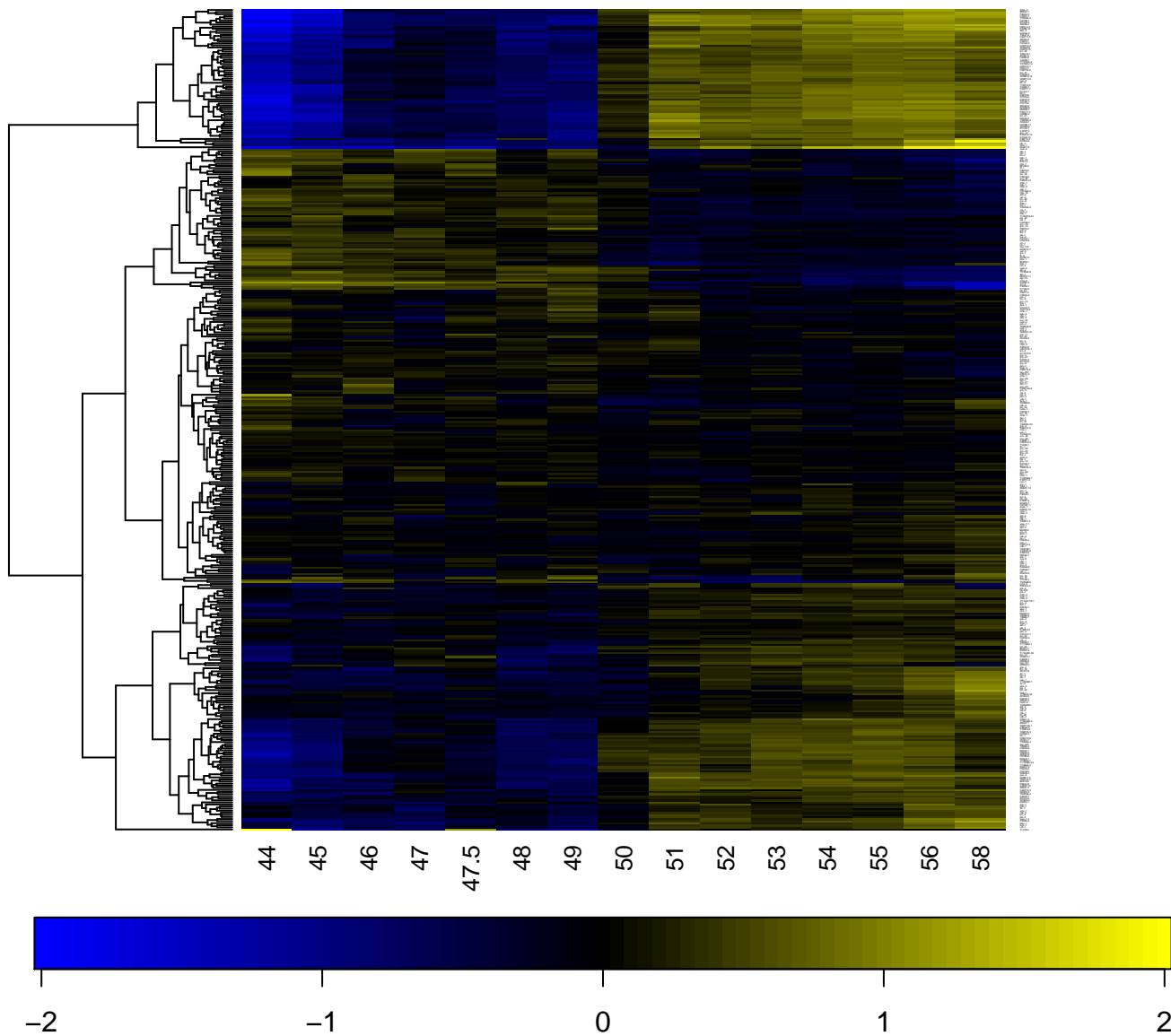
Serine carboxypeptidase



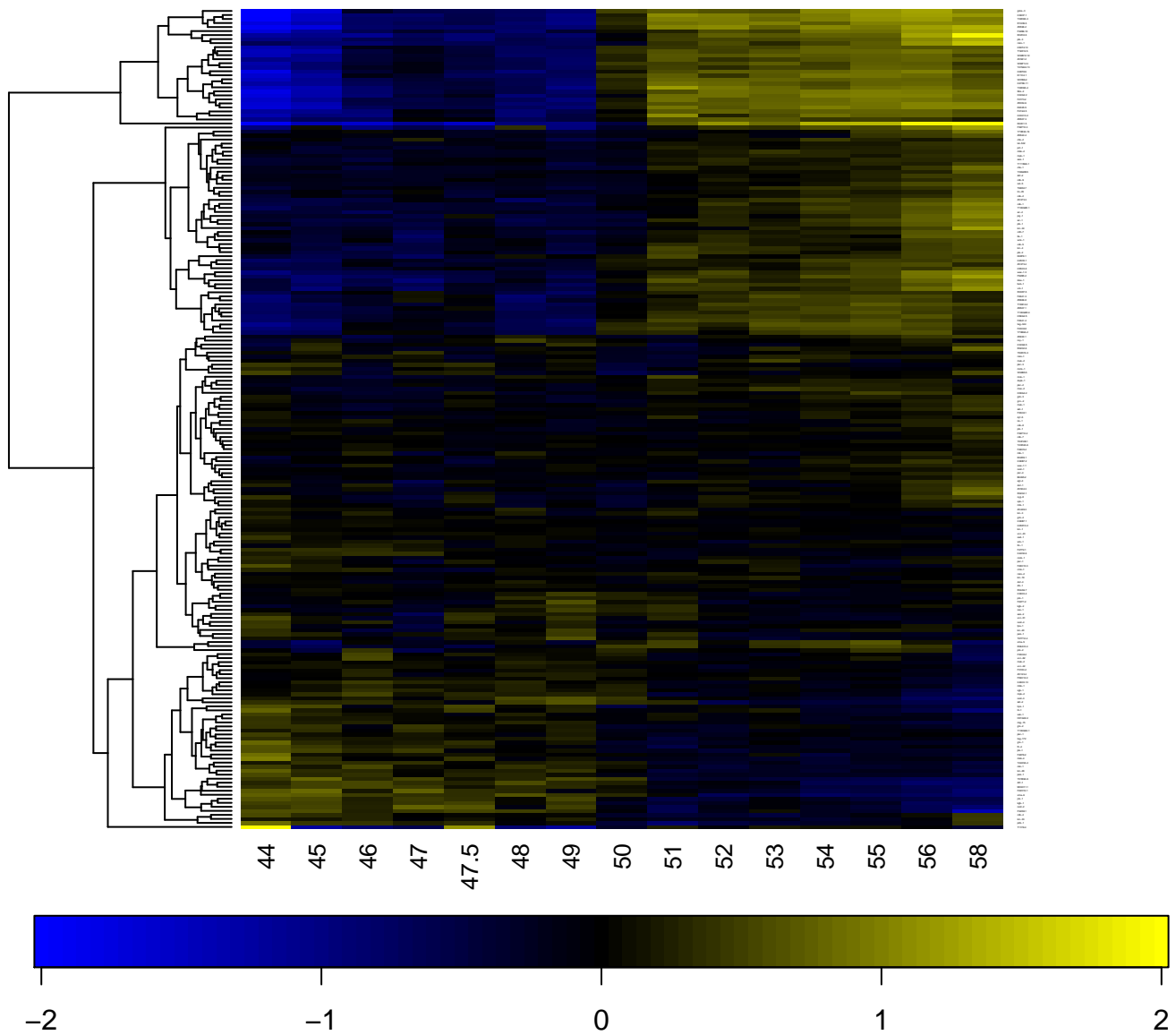
Serine/threonine-protein kinase-like domain



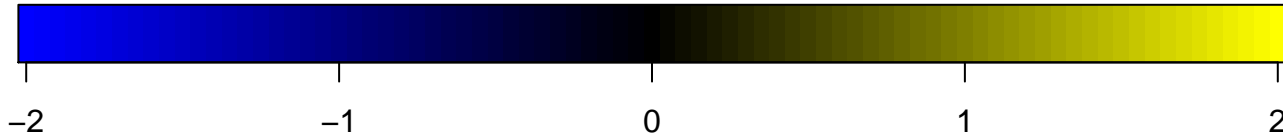
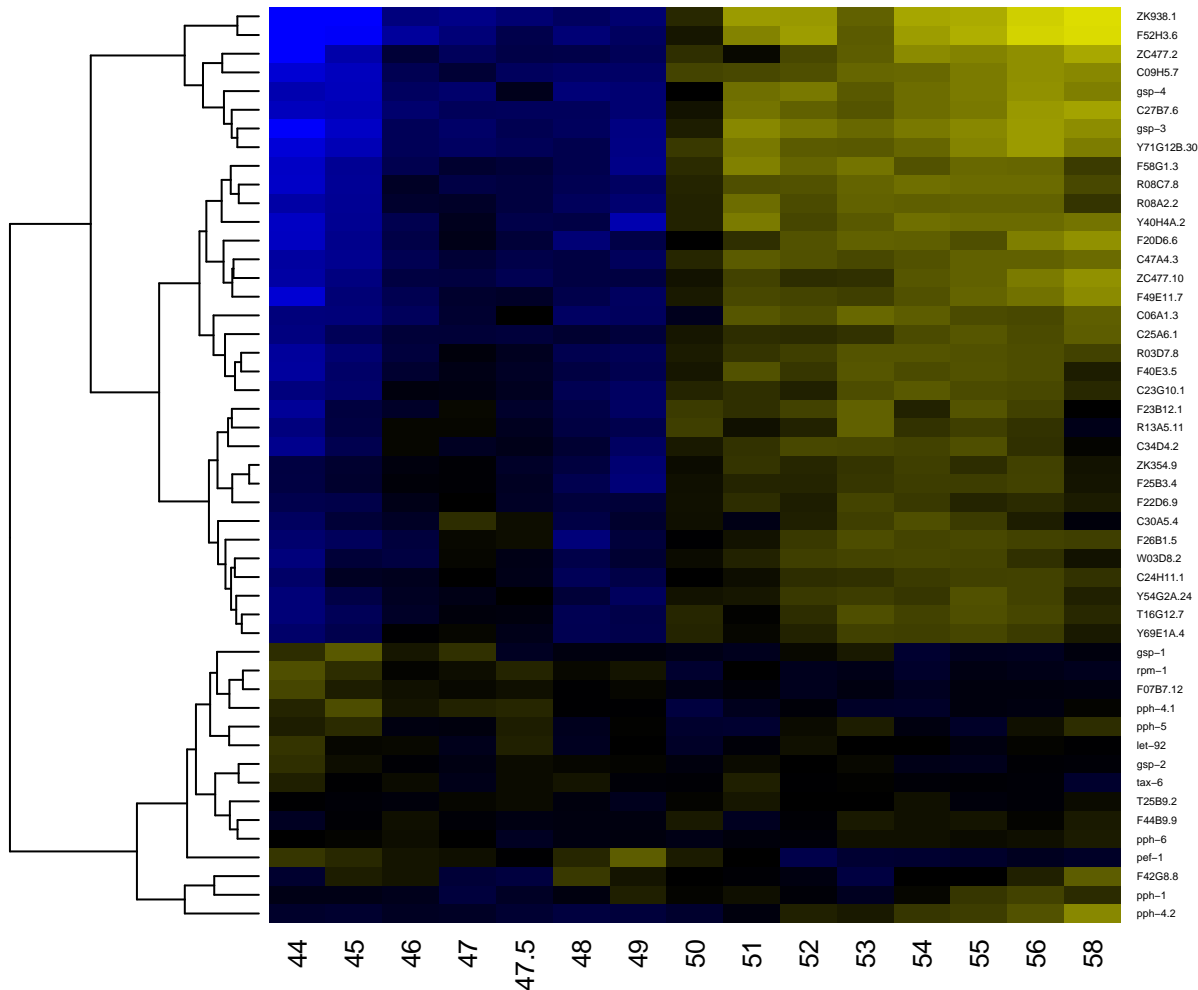
Serine/threonine-protein kinase domain



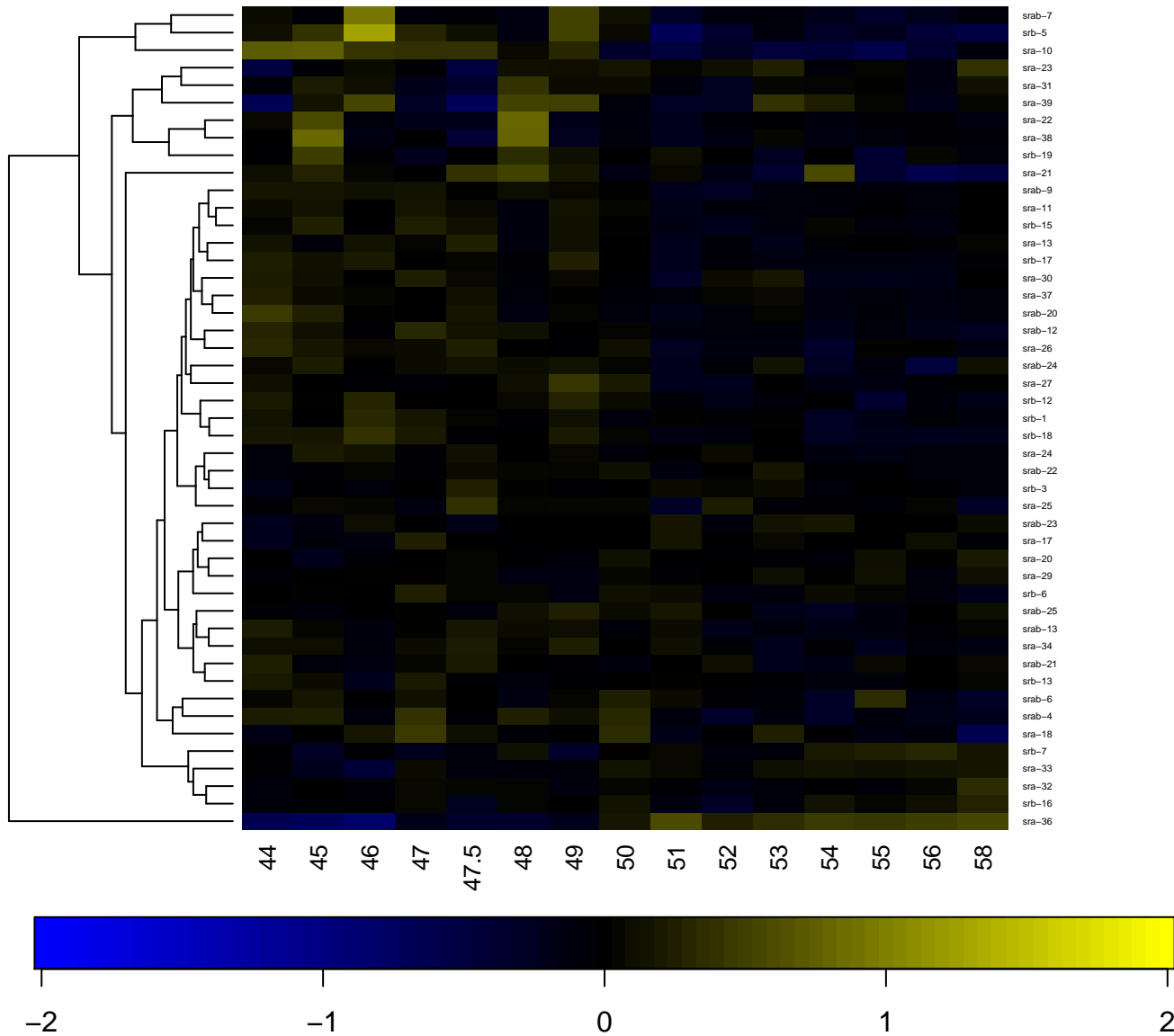
Serine/threonine-protein kinase, active site



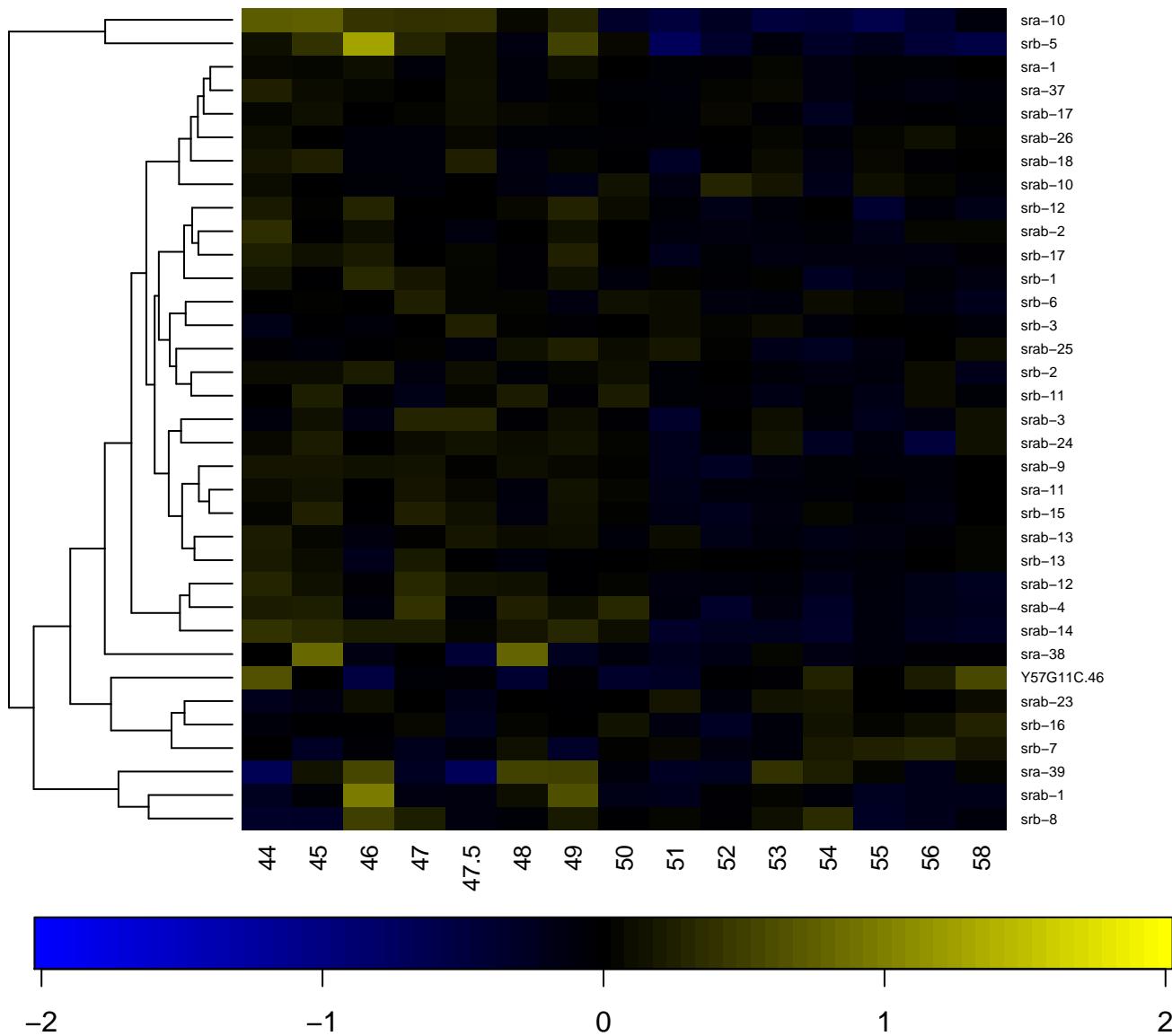
onine-specific protein phosphatase/bis(5-nucleosyl)-tetra



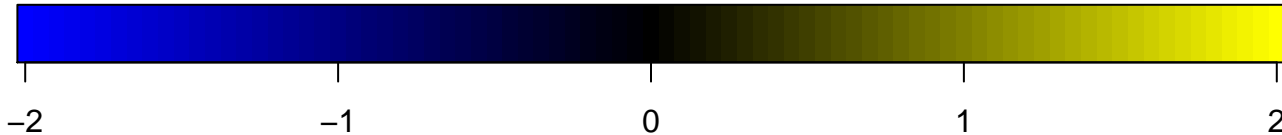
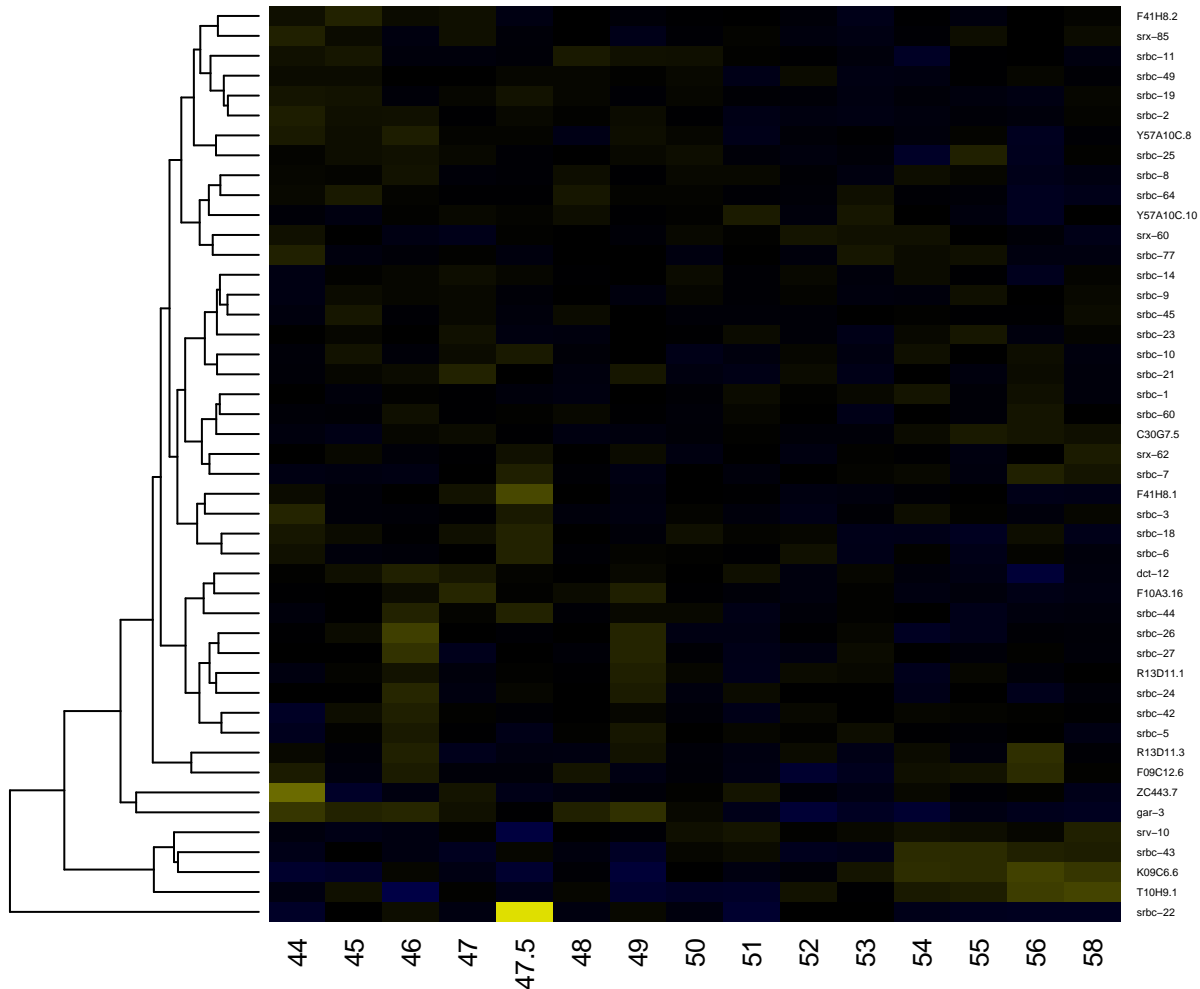
Serpentine type 7TM GPCR chemoreceptor Sra



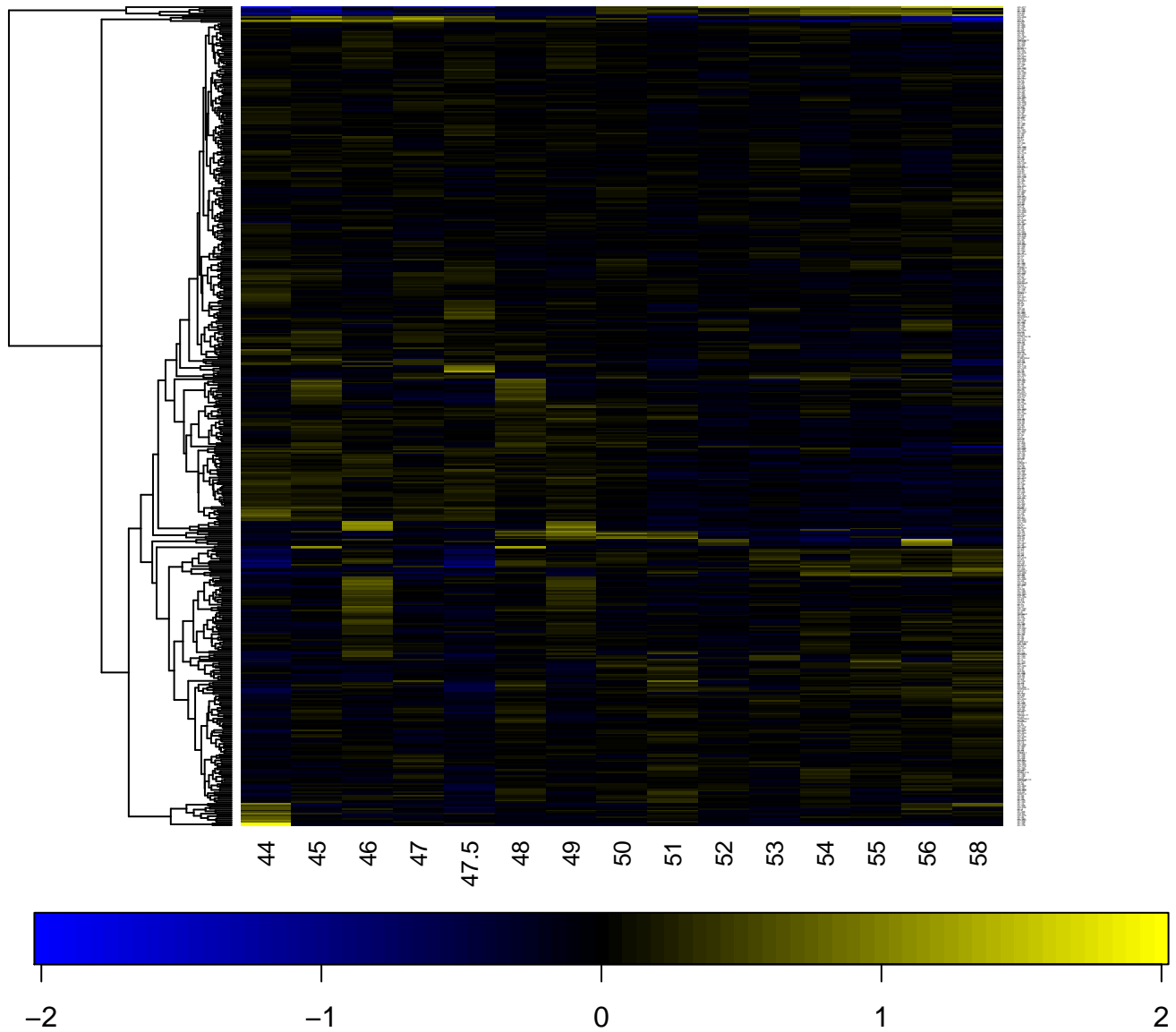
Serpentine type 7TM GPCR chemoreceptor Srb



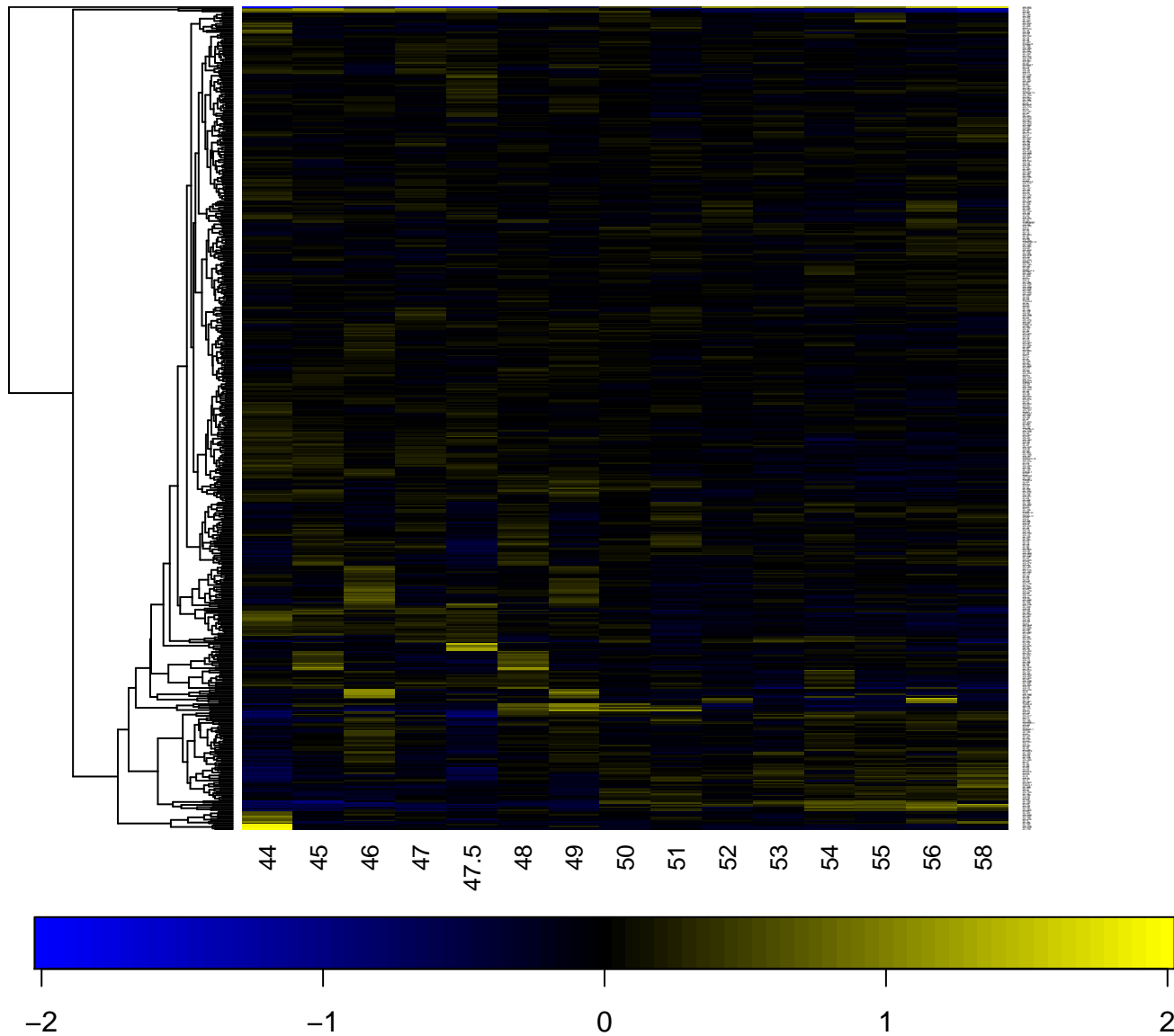
Serpentine type 7TM GPCR chemoreceptor Srbc



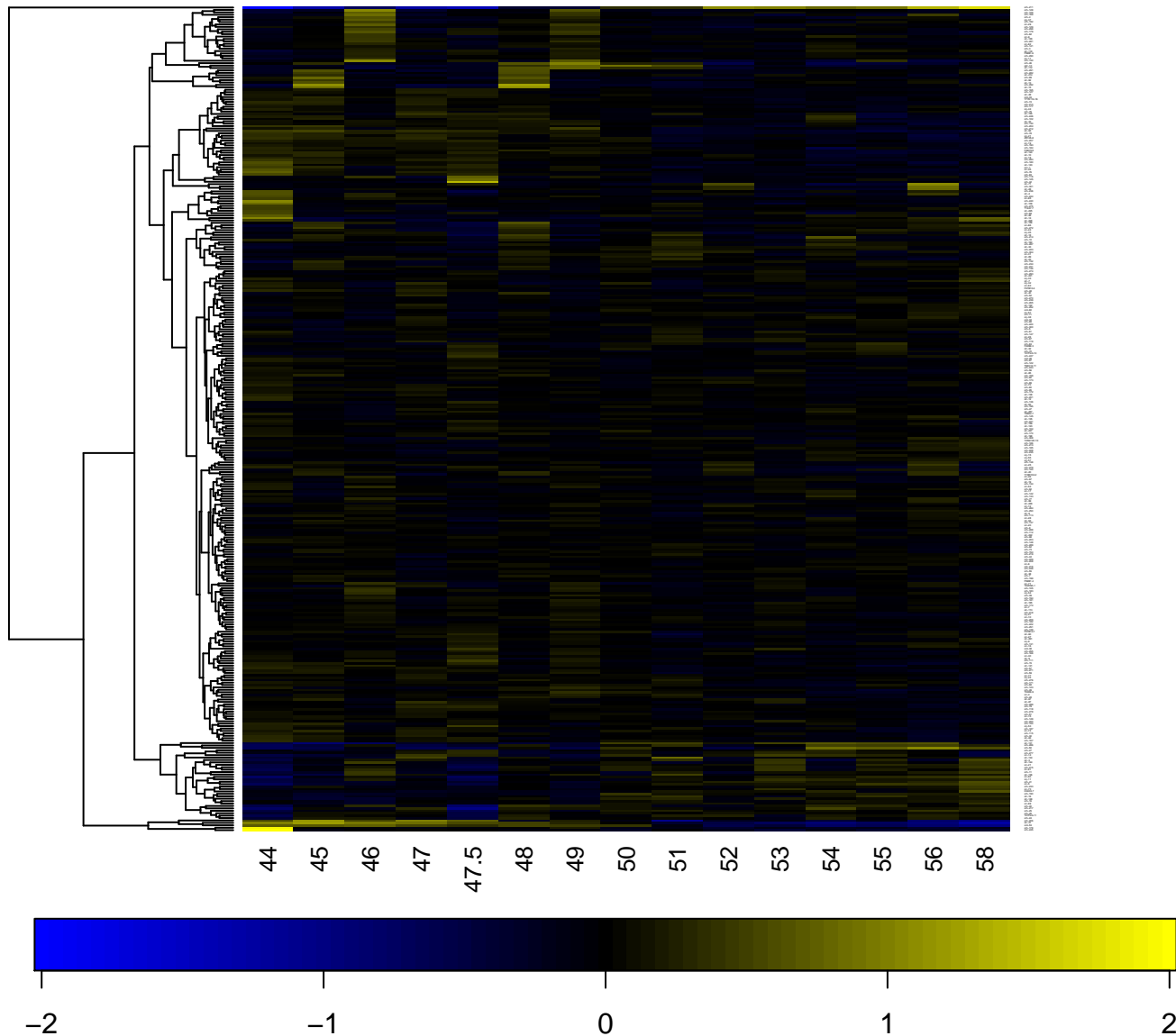
Serpentine type 7TM GPCR chemoreceptor Srd



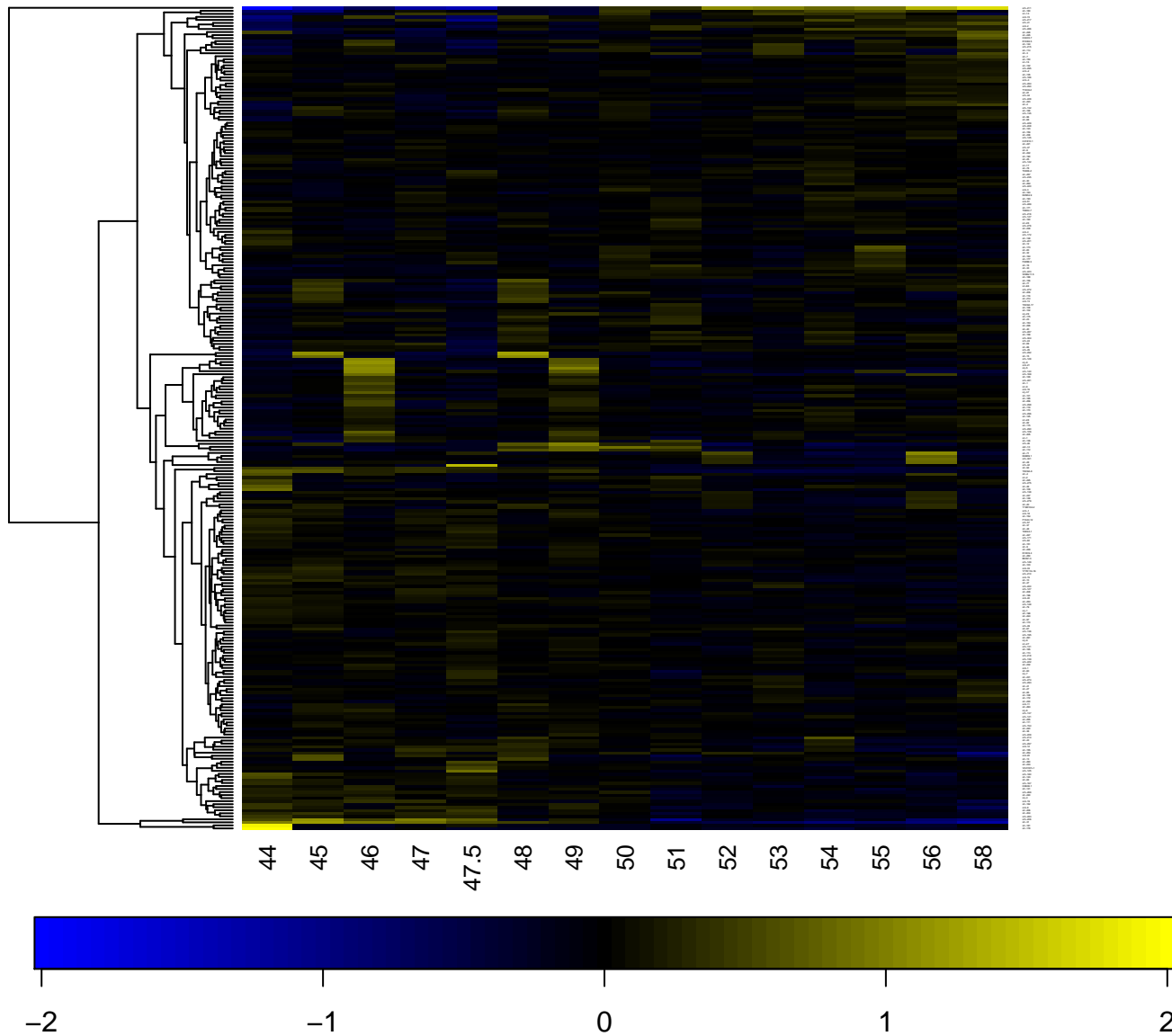
Serpentine type 7TM GPCR chemoreceptor Srh



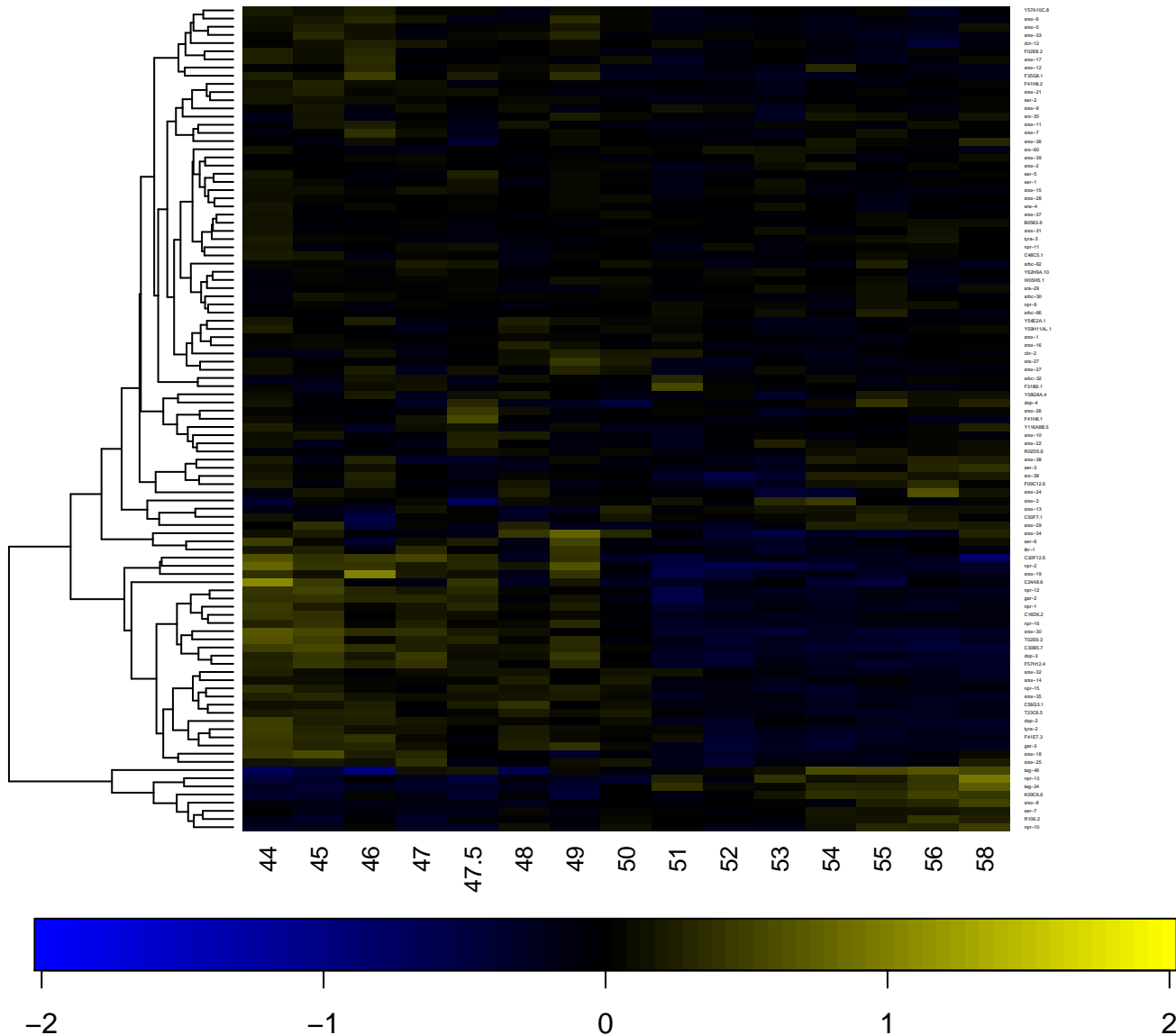
Serpentine type 7TM GPCR chemoreceptor Sri



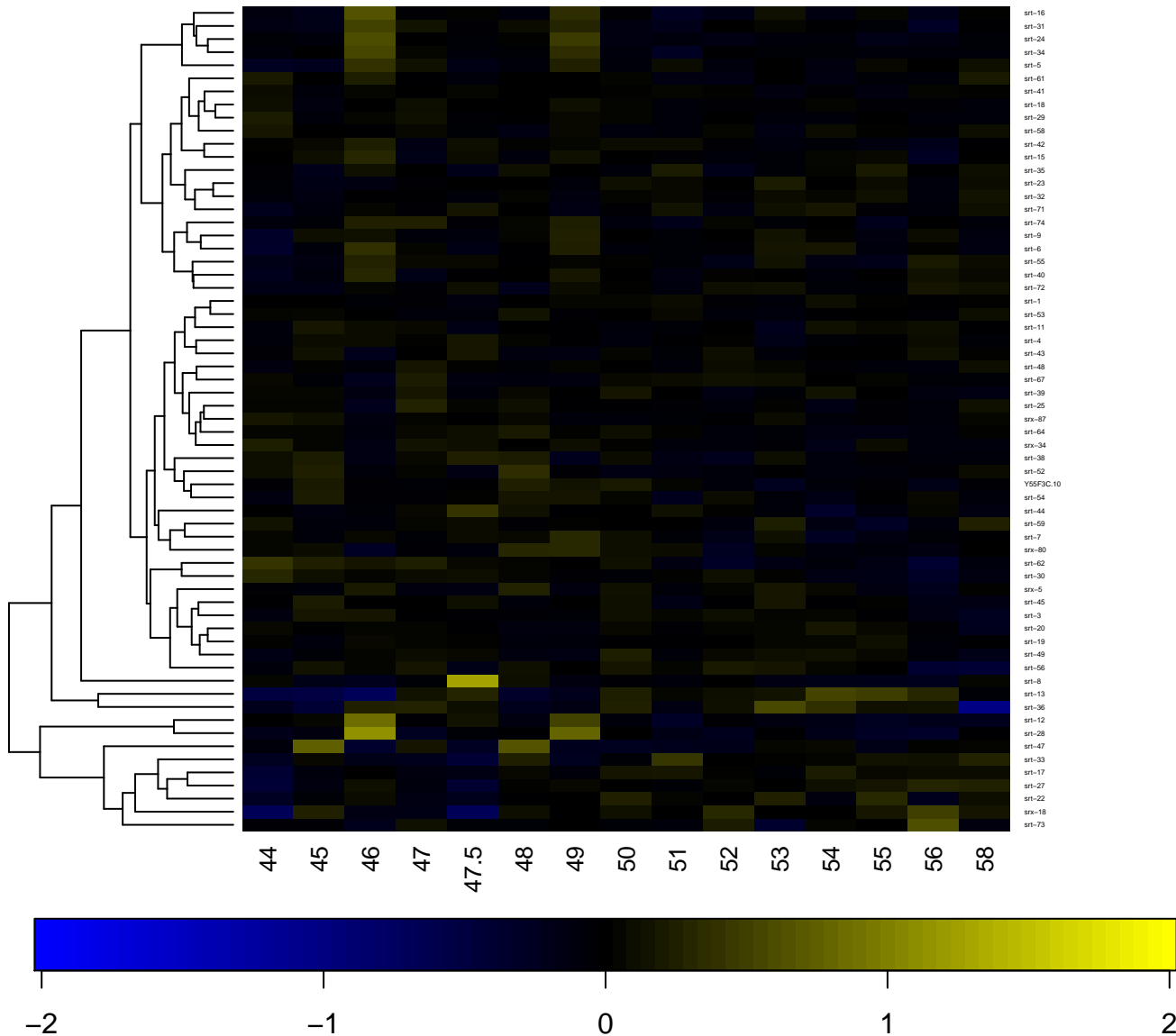
Serpentine type 7TM GPCR chemoreceptor Srj



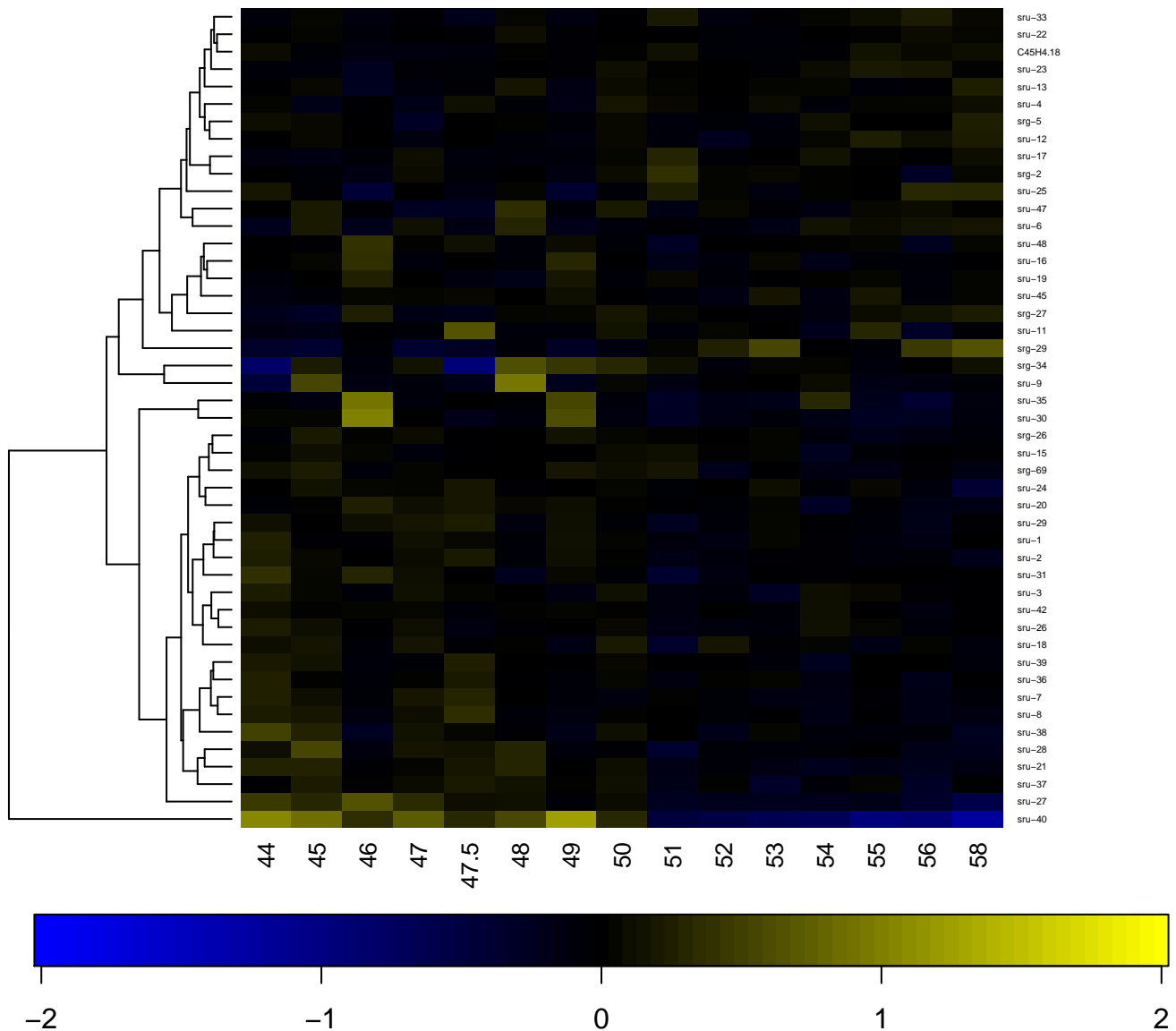
Serpentine type 7TM GPCR chemoreceptor Srsx



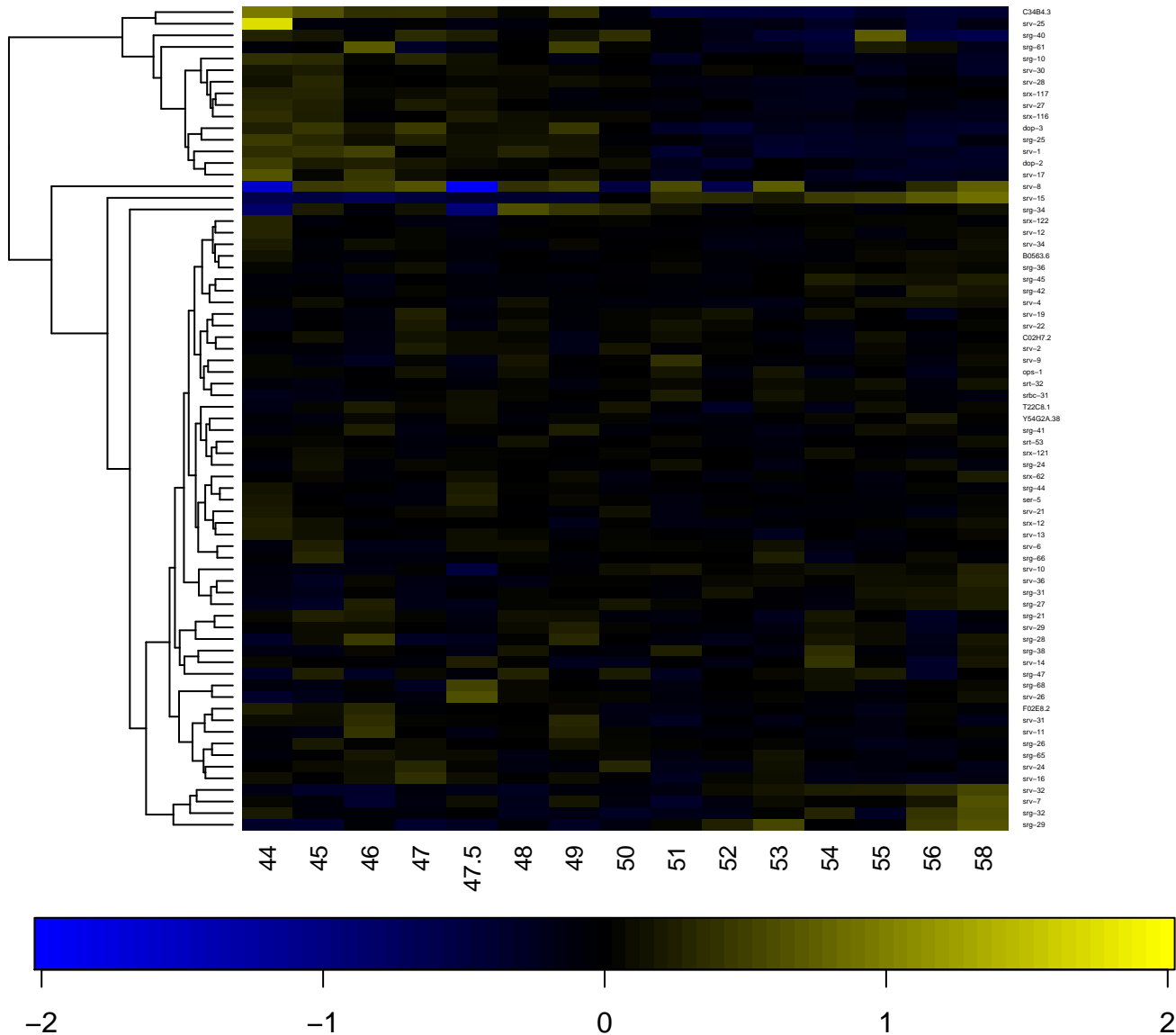
Serpentine type 7TM GPCR chemoreceptor Srt



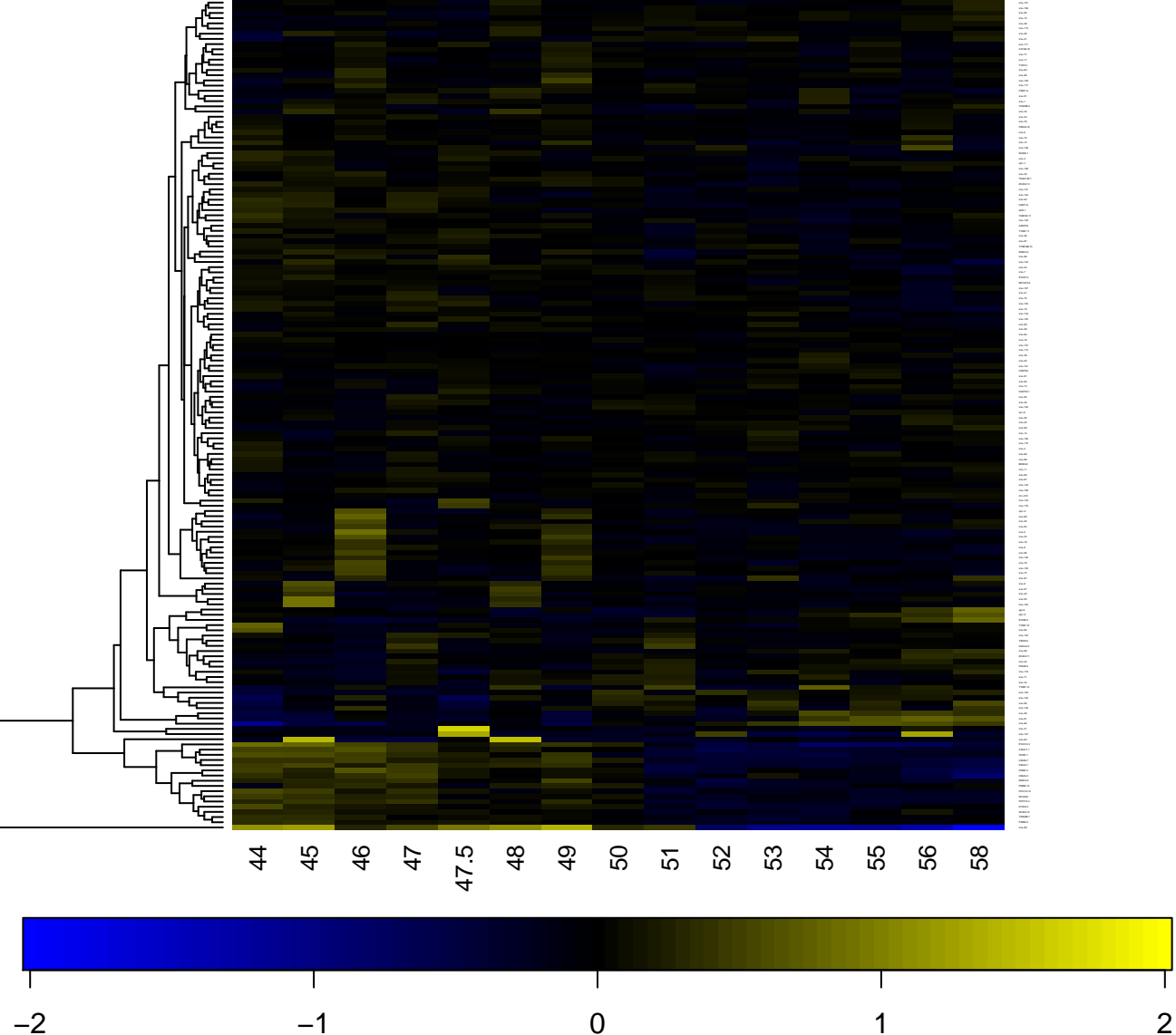
Serpentine type 7TM GPCR chemoreceptor *Sru*



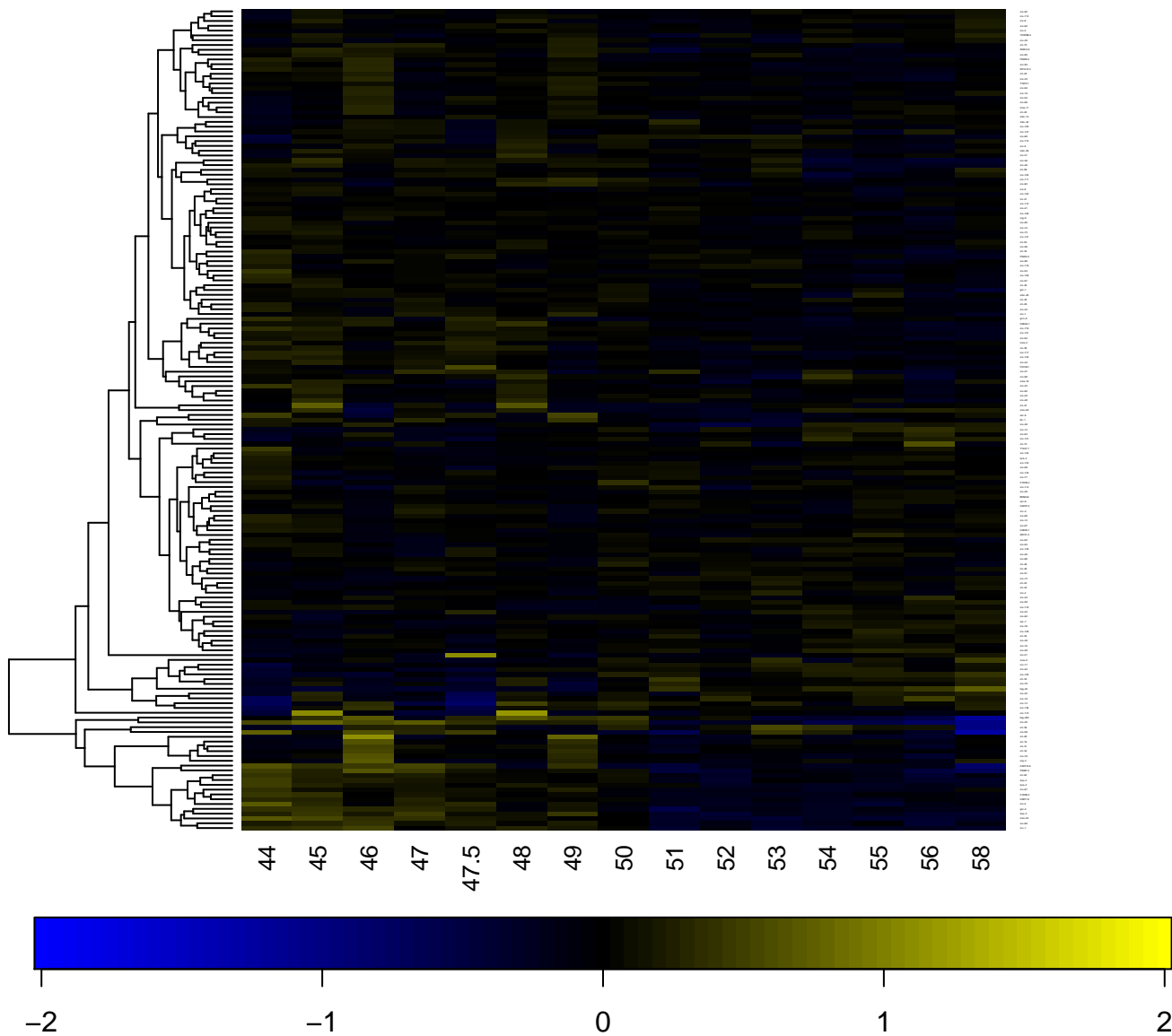
Serpentine type 7TM GPCR chemoreceptor Srv



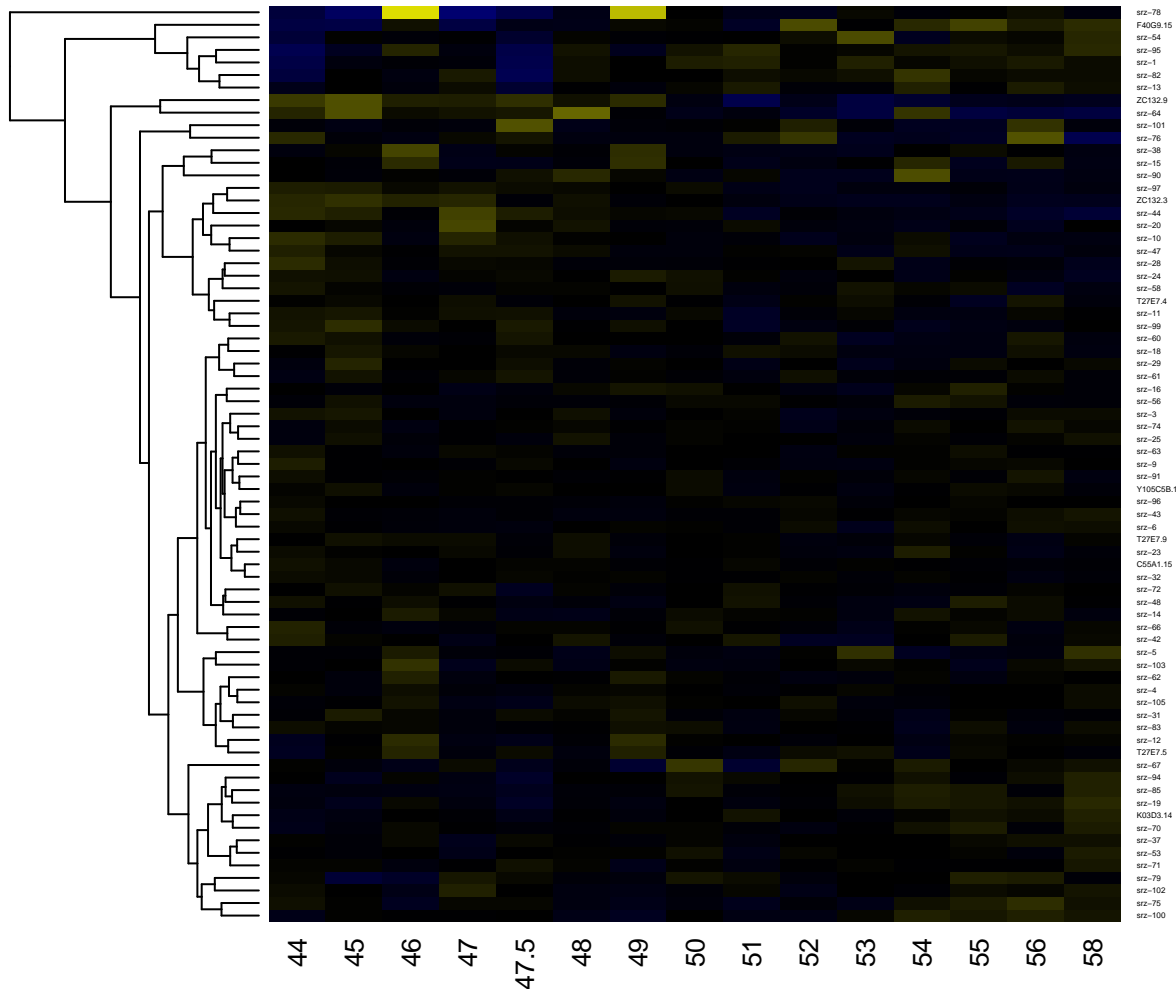
Serpentine type 7TM GPCR chemoreceptor Srw



Serpentine type 7TM GPCR chemoreceptor Srx



Serpentine type 7TM GPCR chemoreceptor Srz



-2

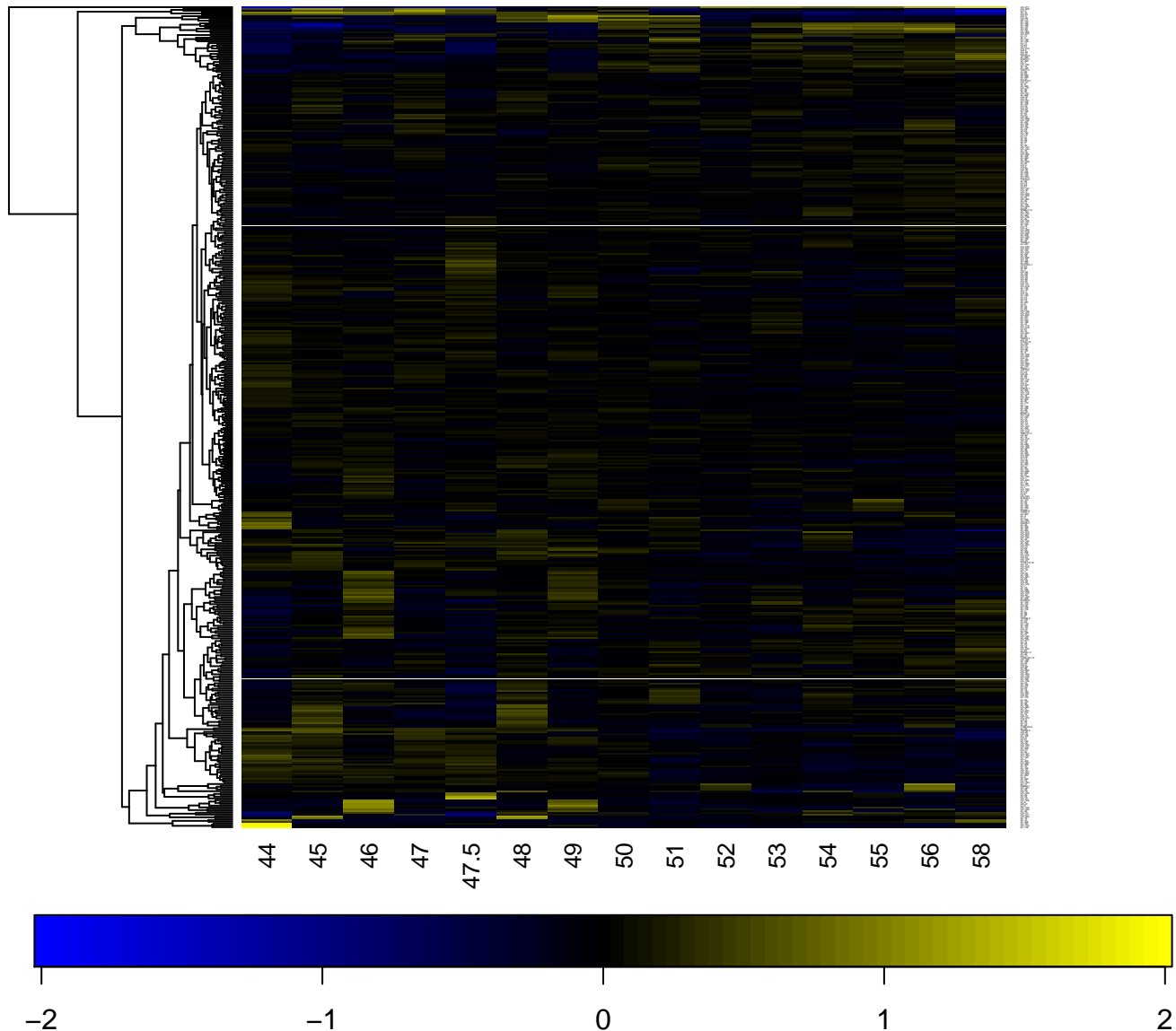
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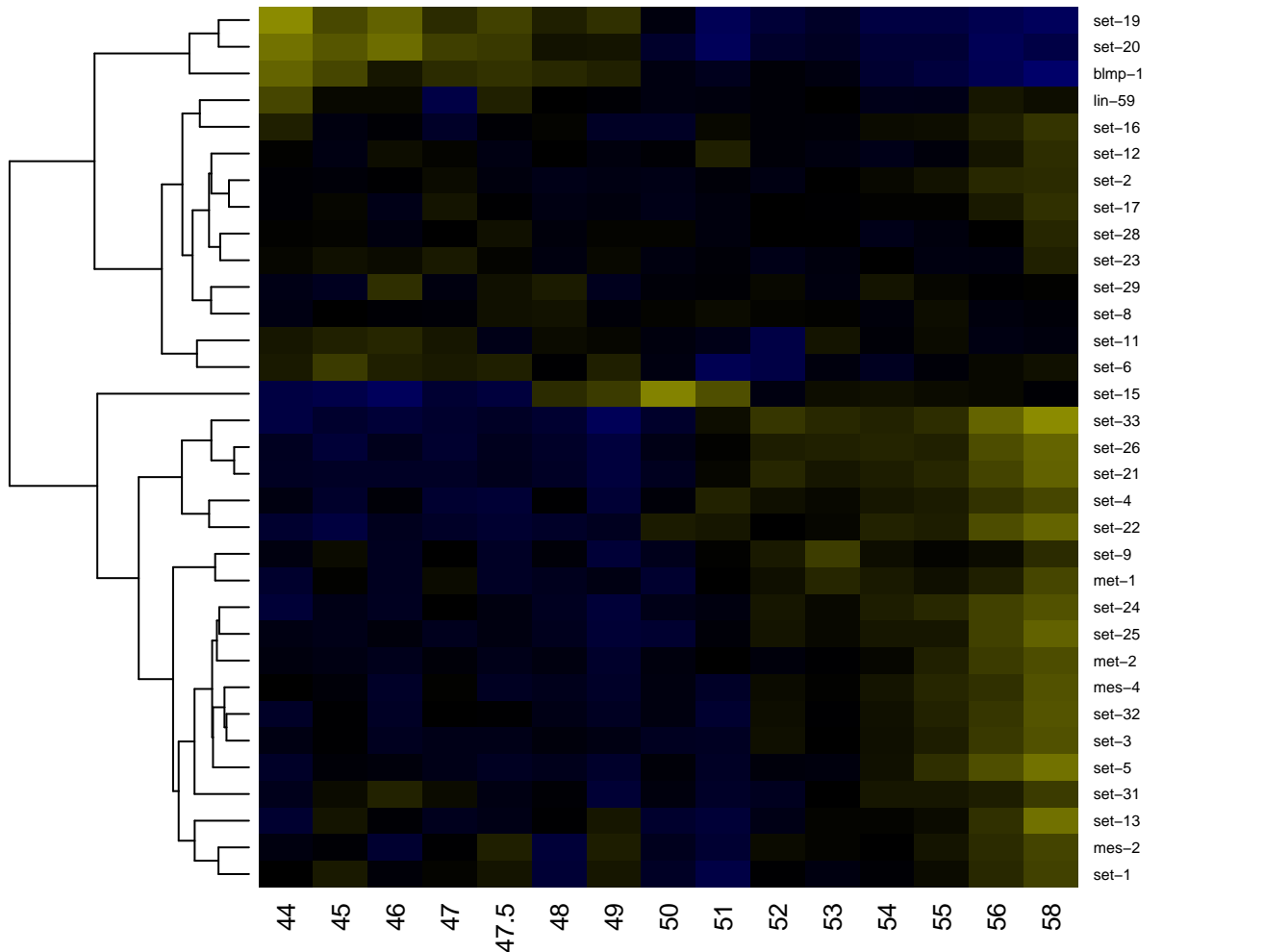
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2

Serpentine type 7TM GPCR chemoreceptor Str



SET domain



-2

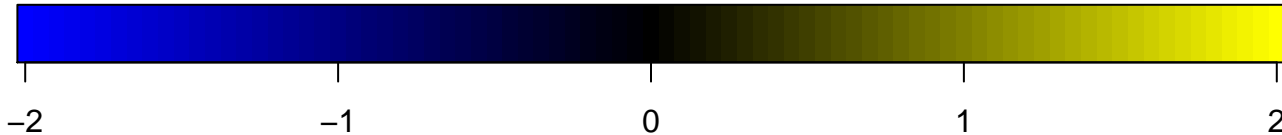
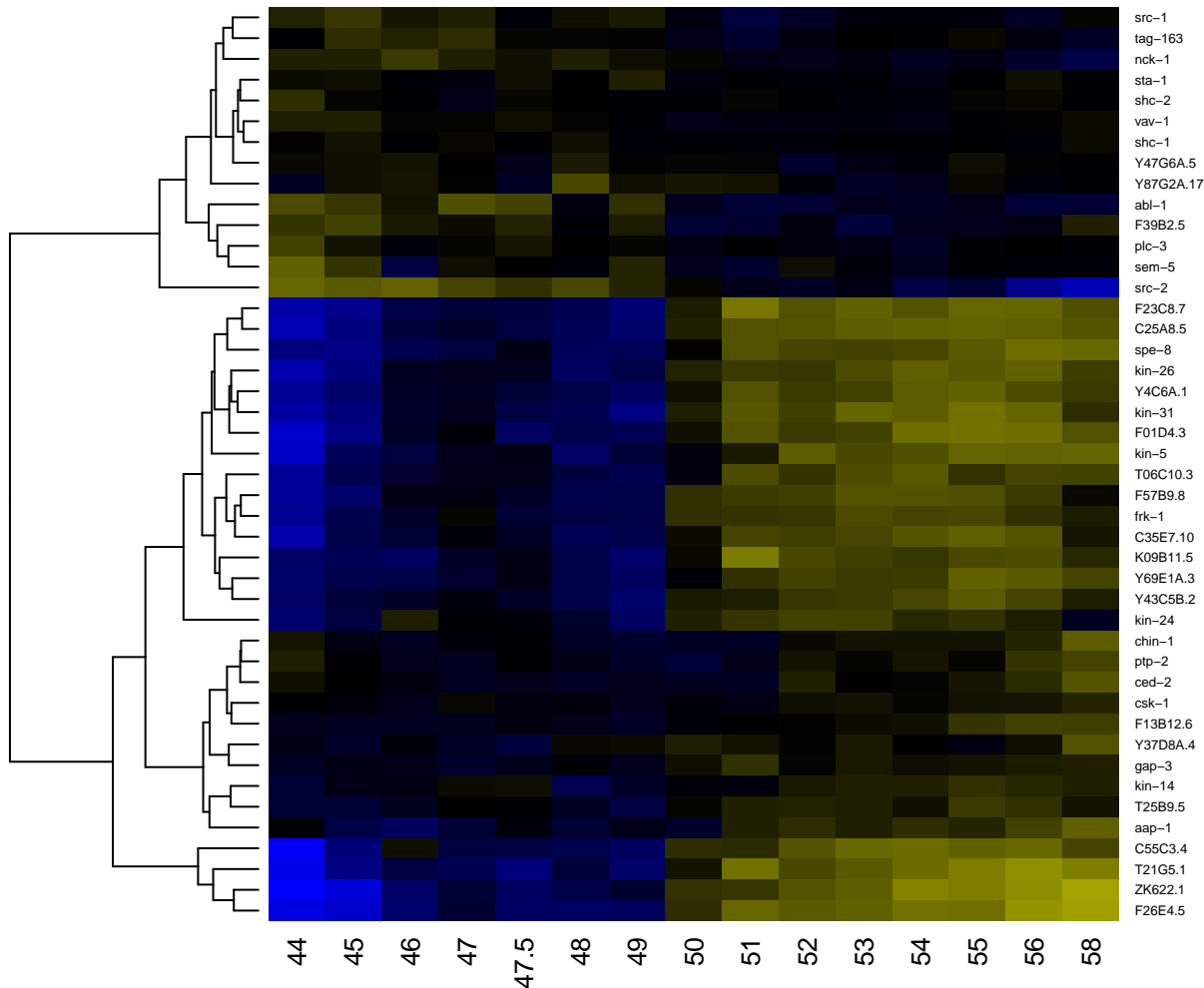
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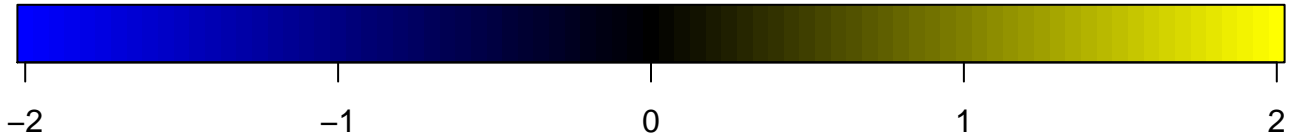
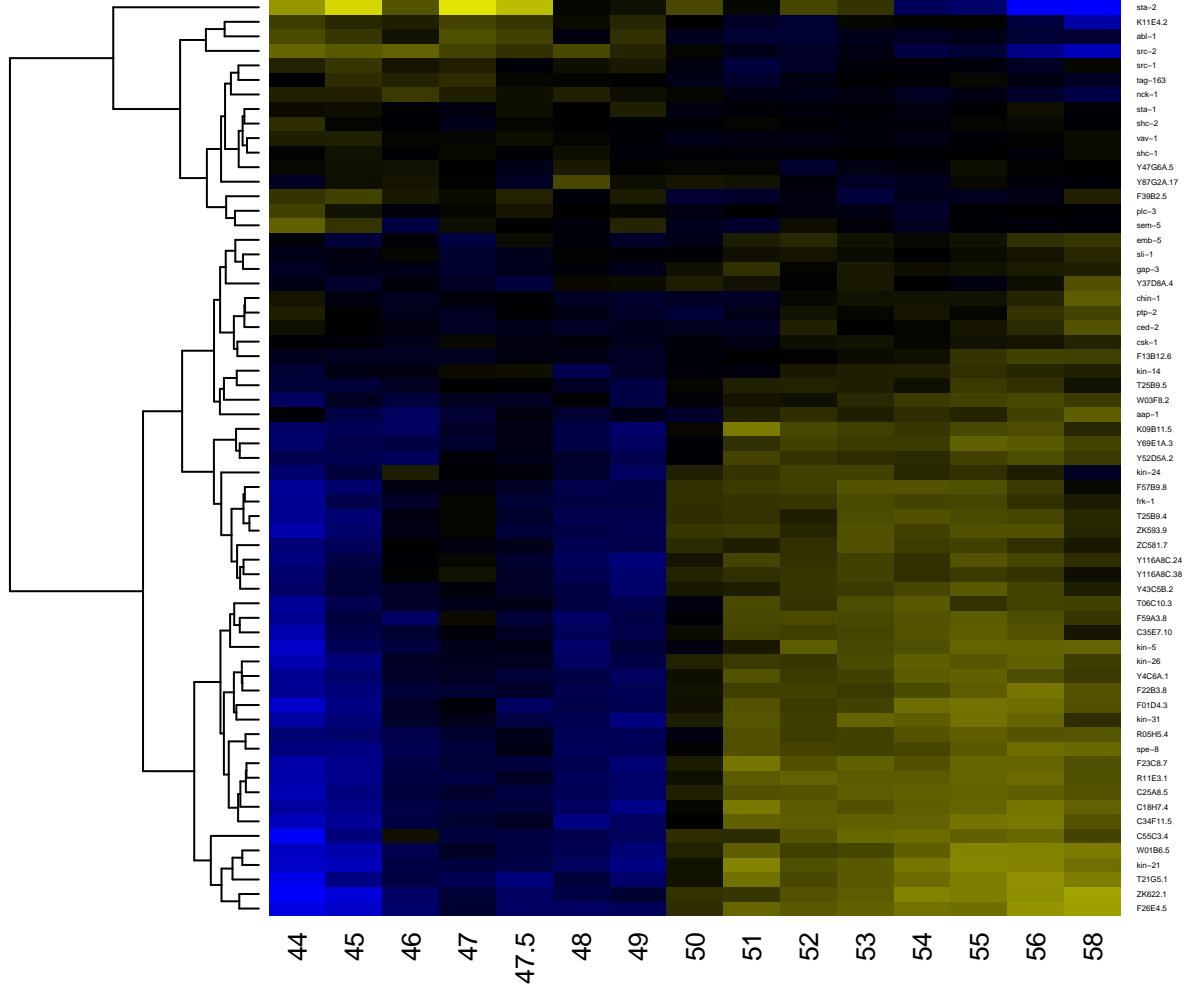
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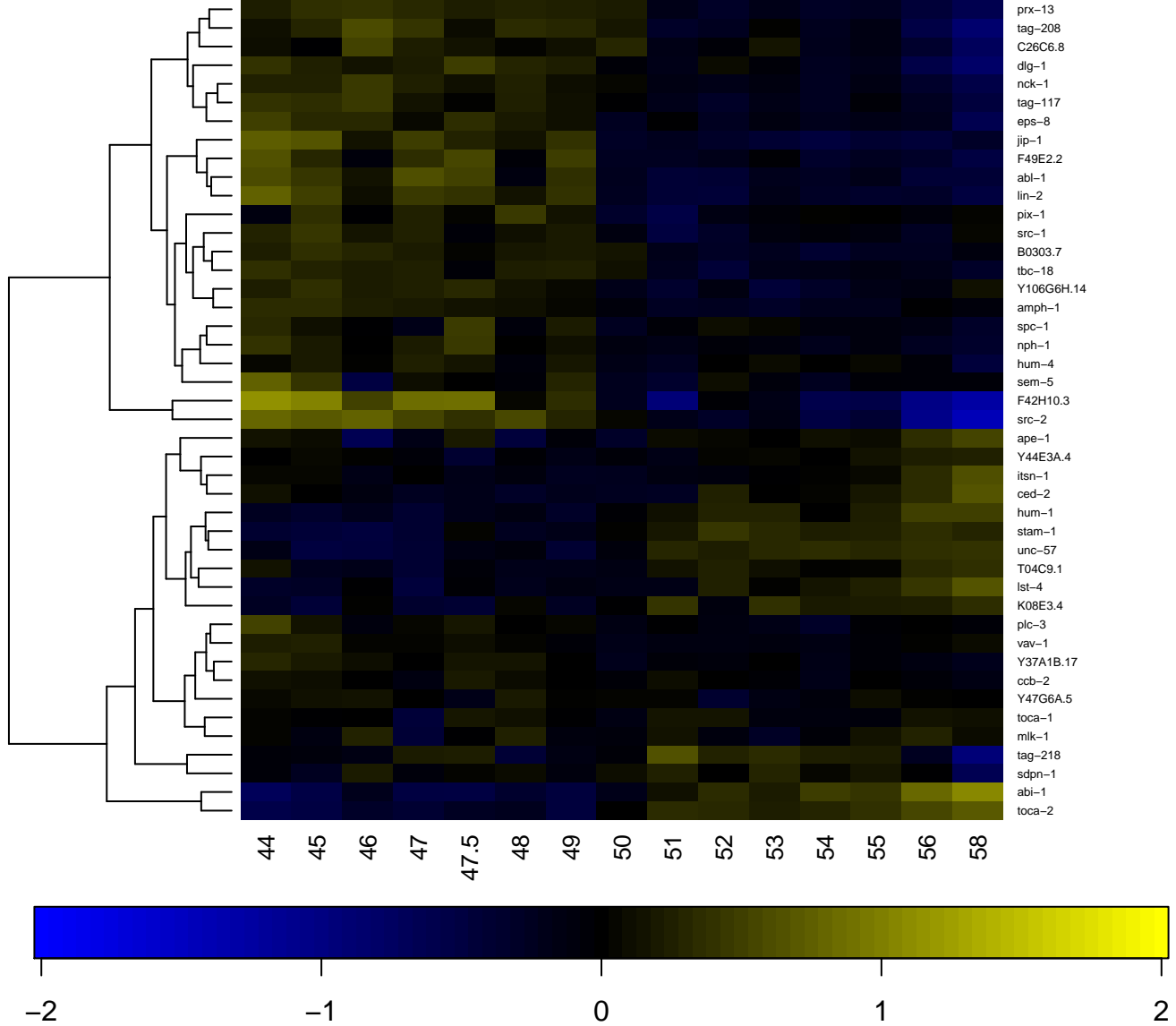
SH2 domain



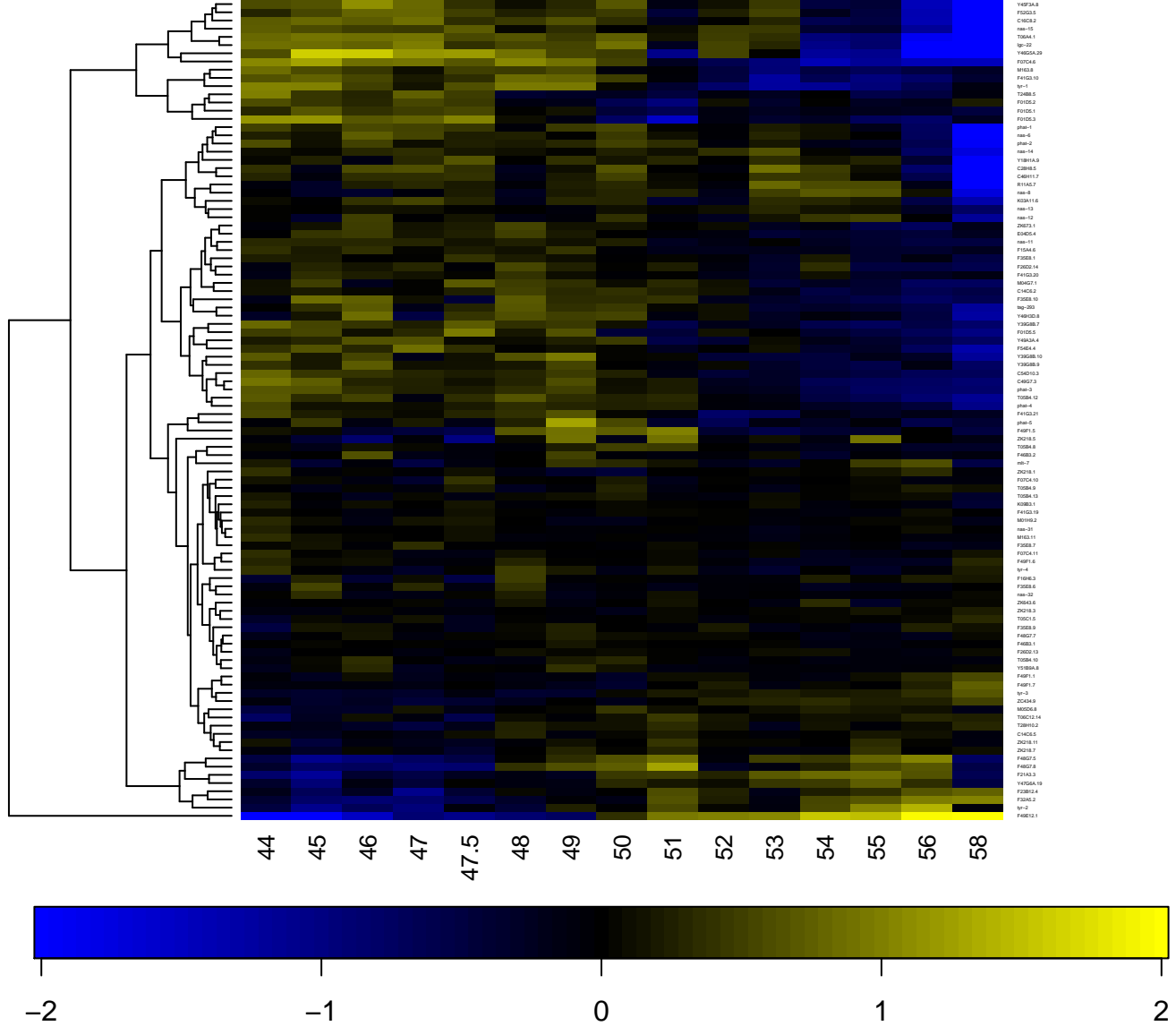
SH2 motif



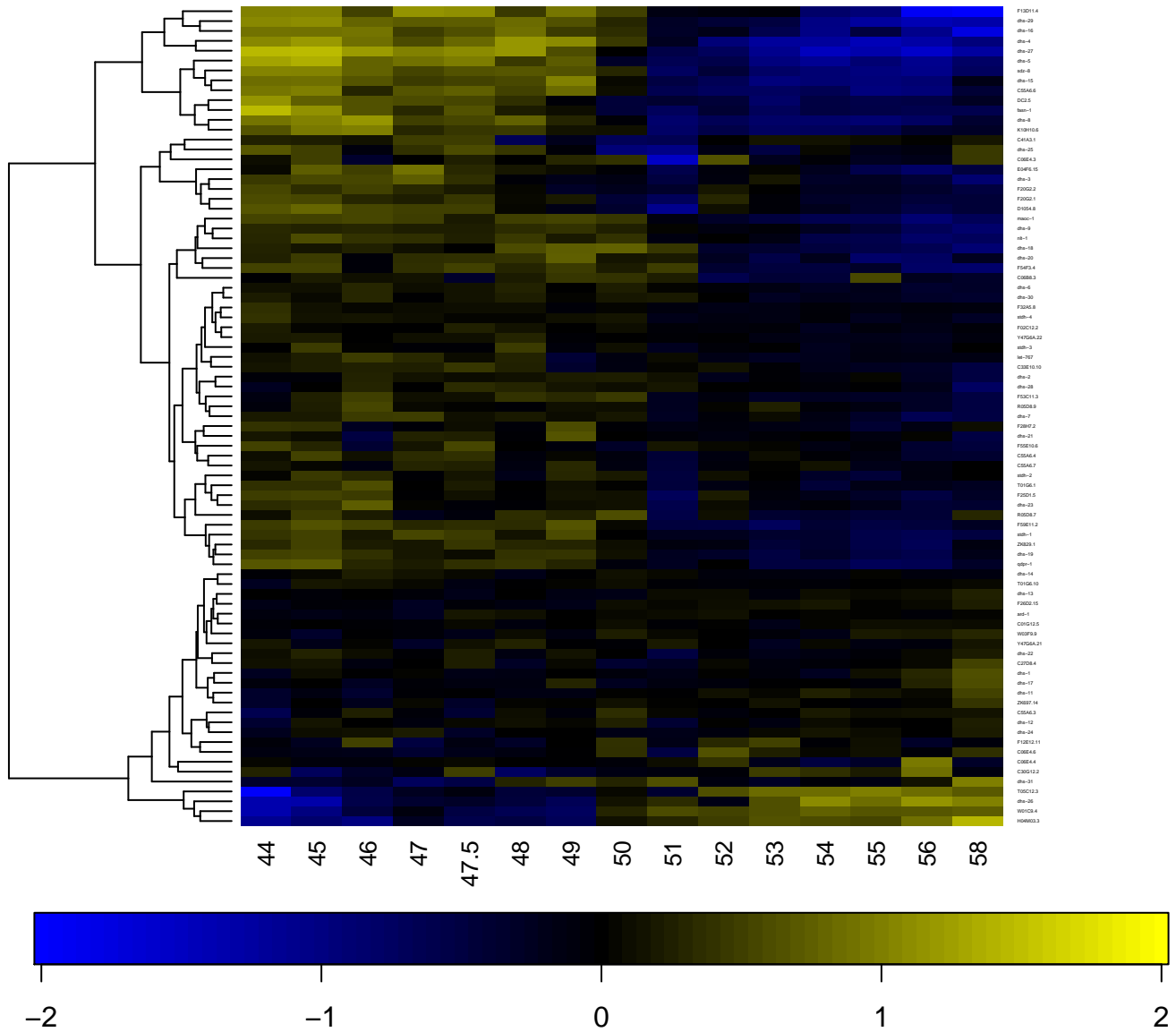
SH3 domain



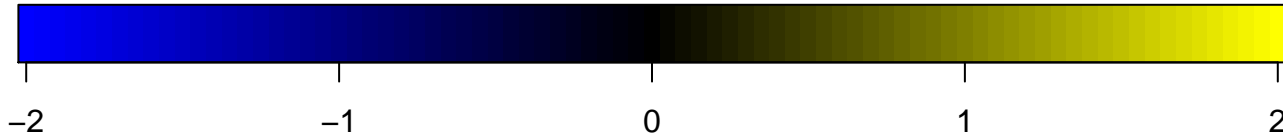
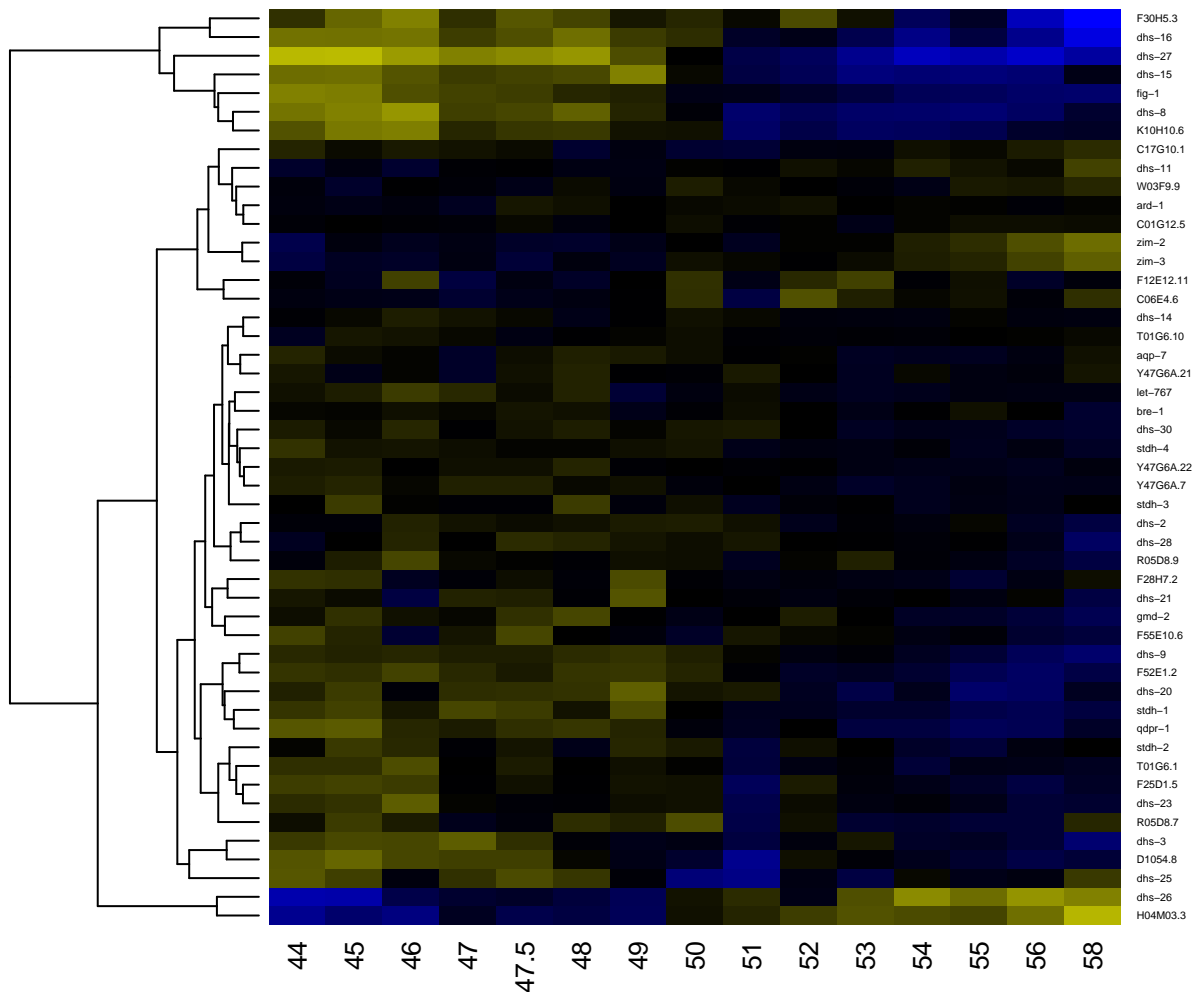
ShK domain-like



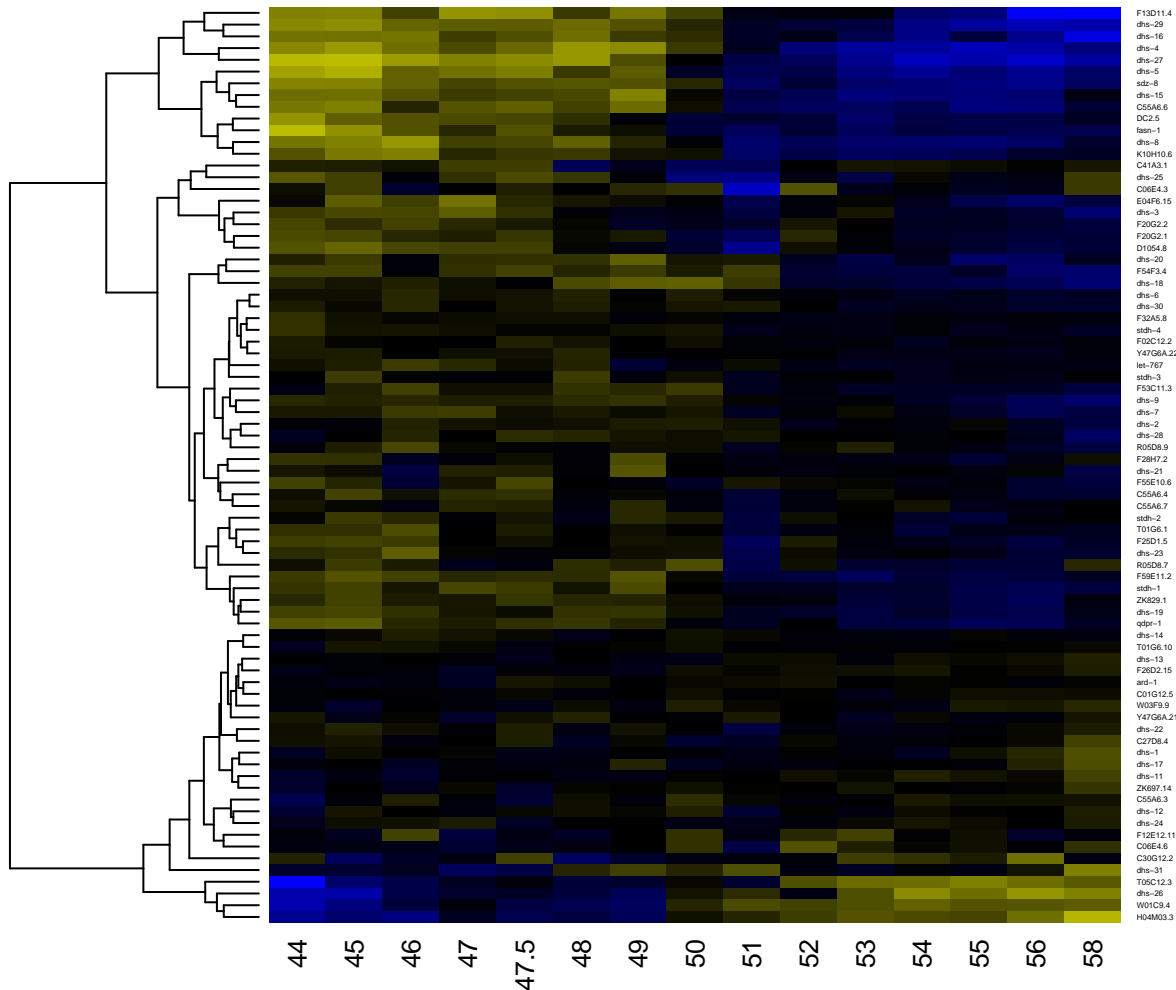
Short-chain dehydrogenase/reductase SDR



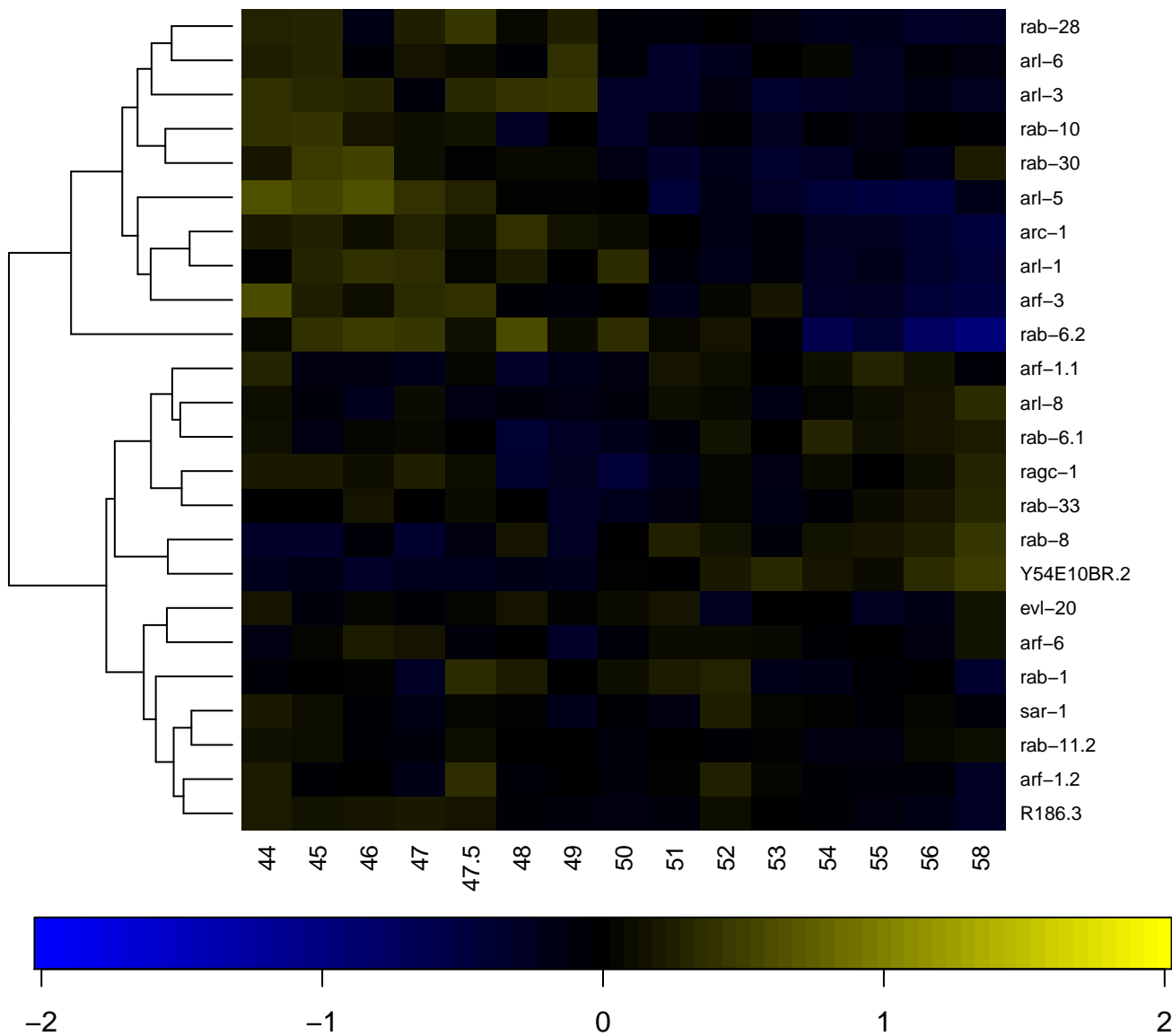
Short-chain dehydrogenase/reductase, conserved site



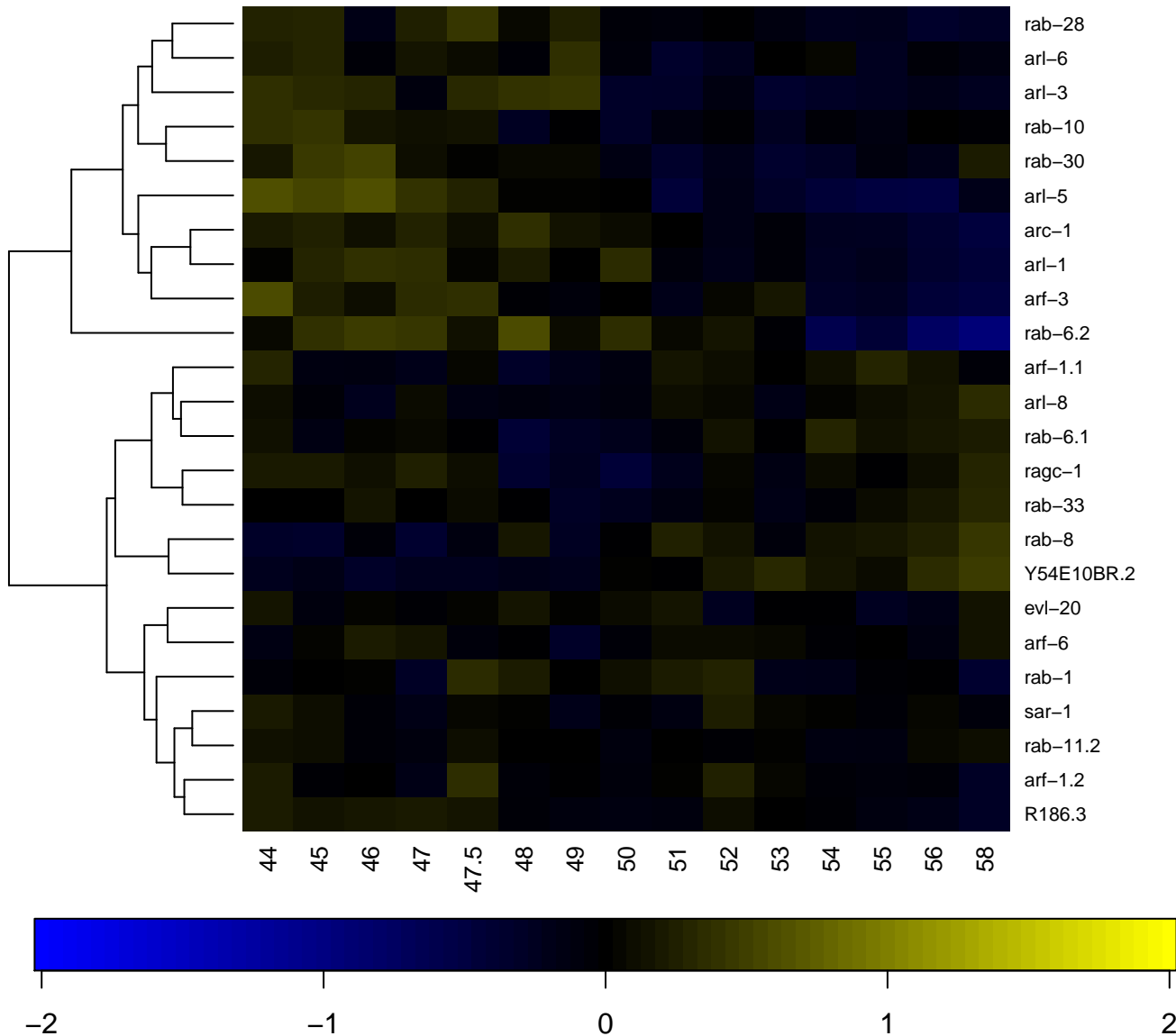
short chain dehydrogenase



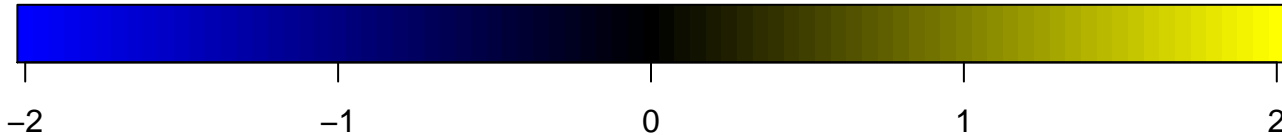
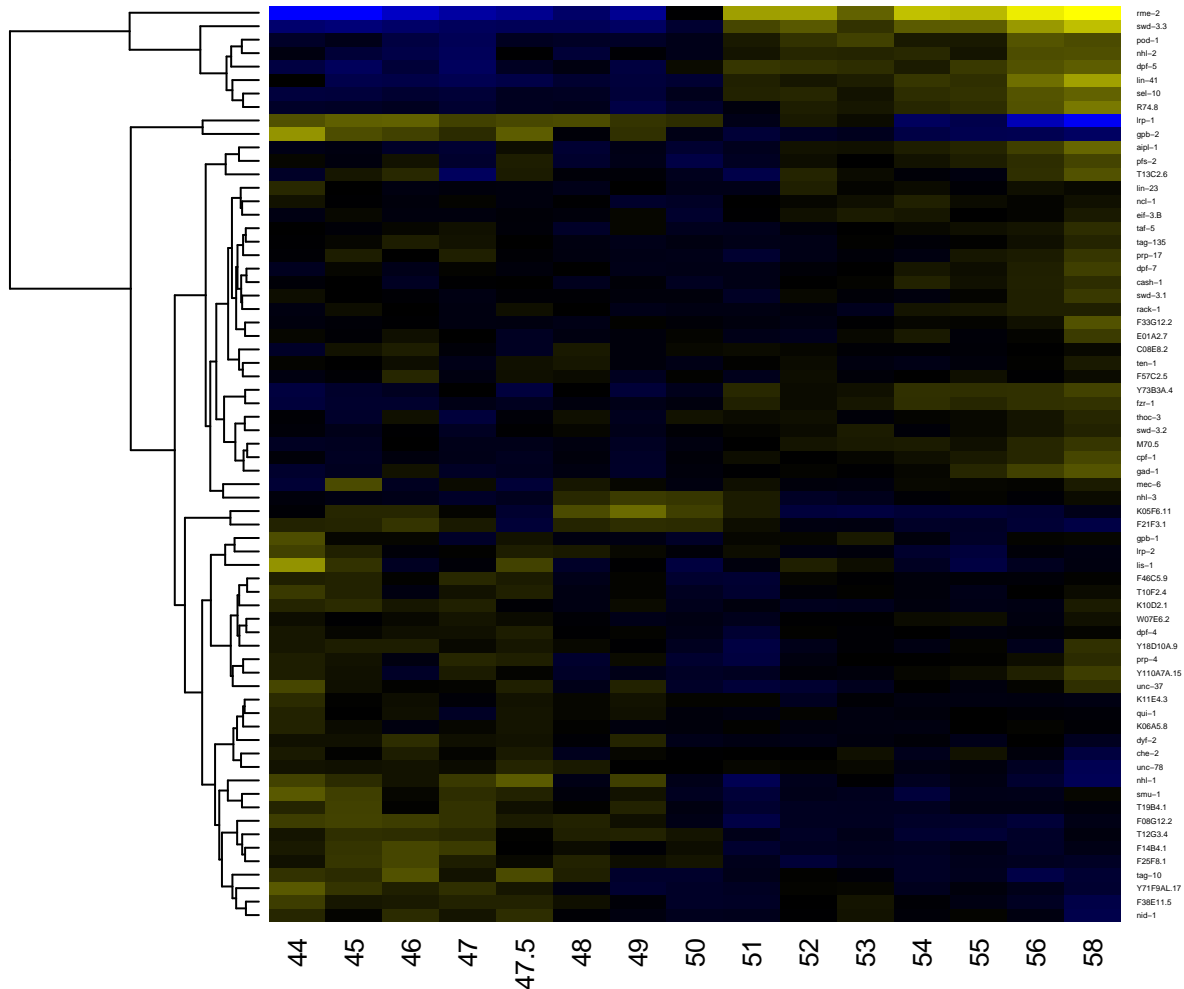
Signal recognition particle receptor beta subunit



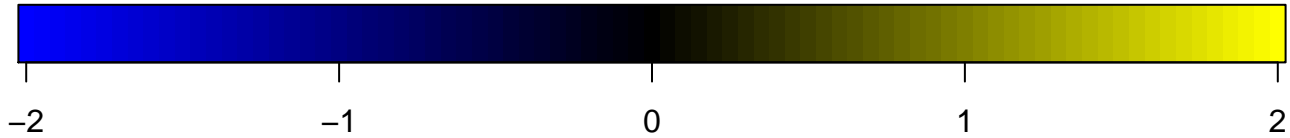
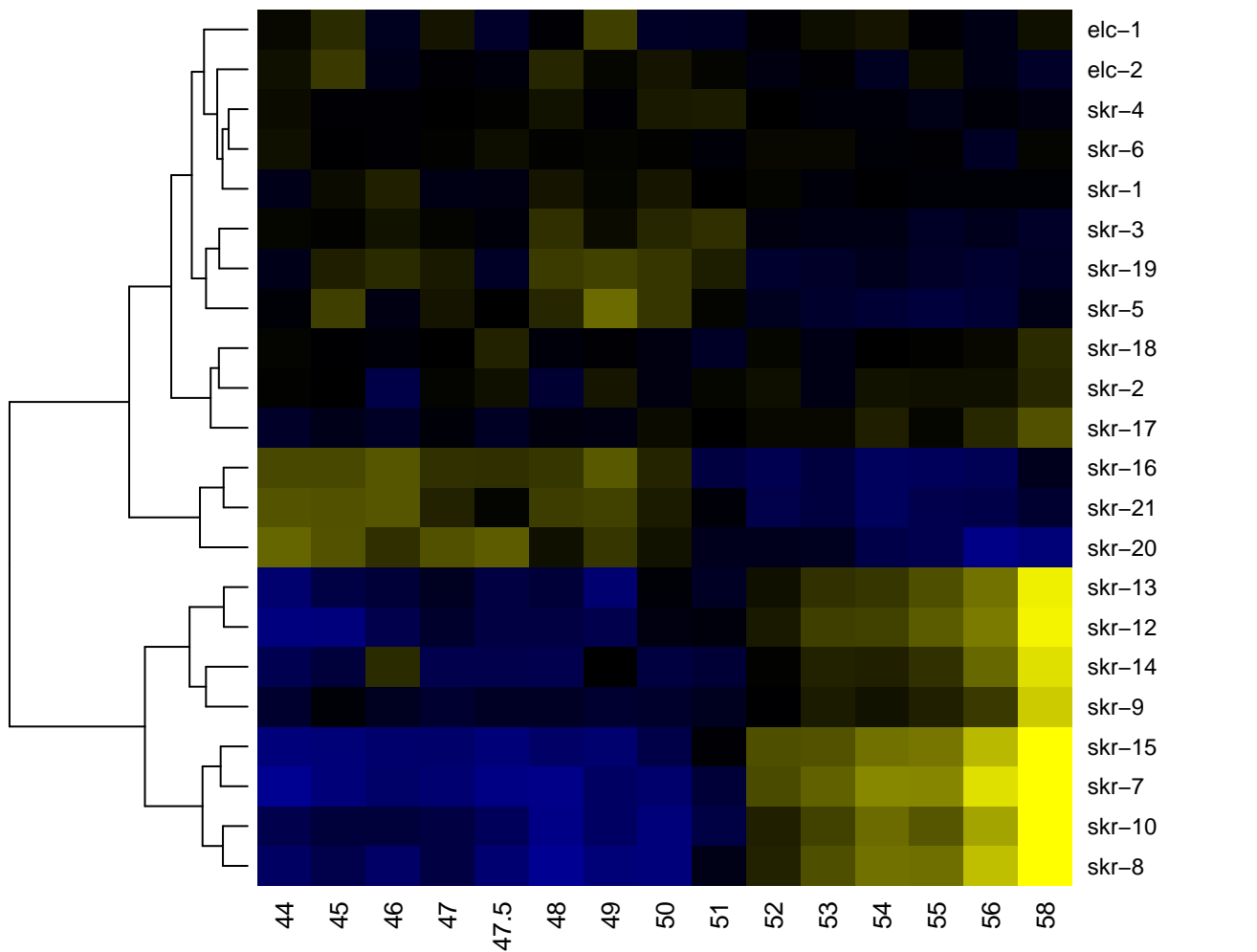
Signal recognition particle receptor, beta subunit



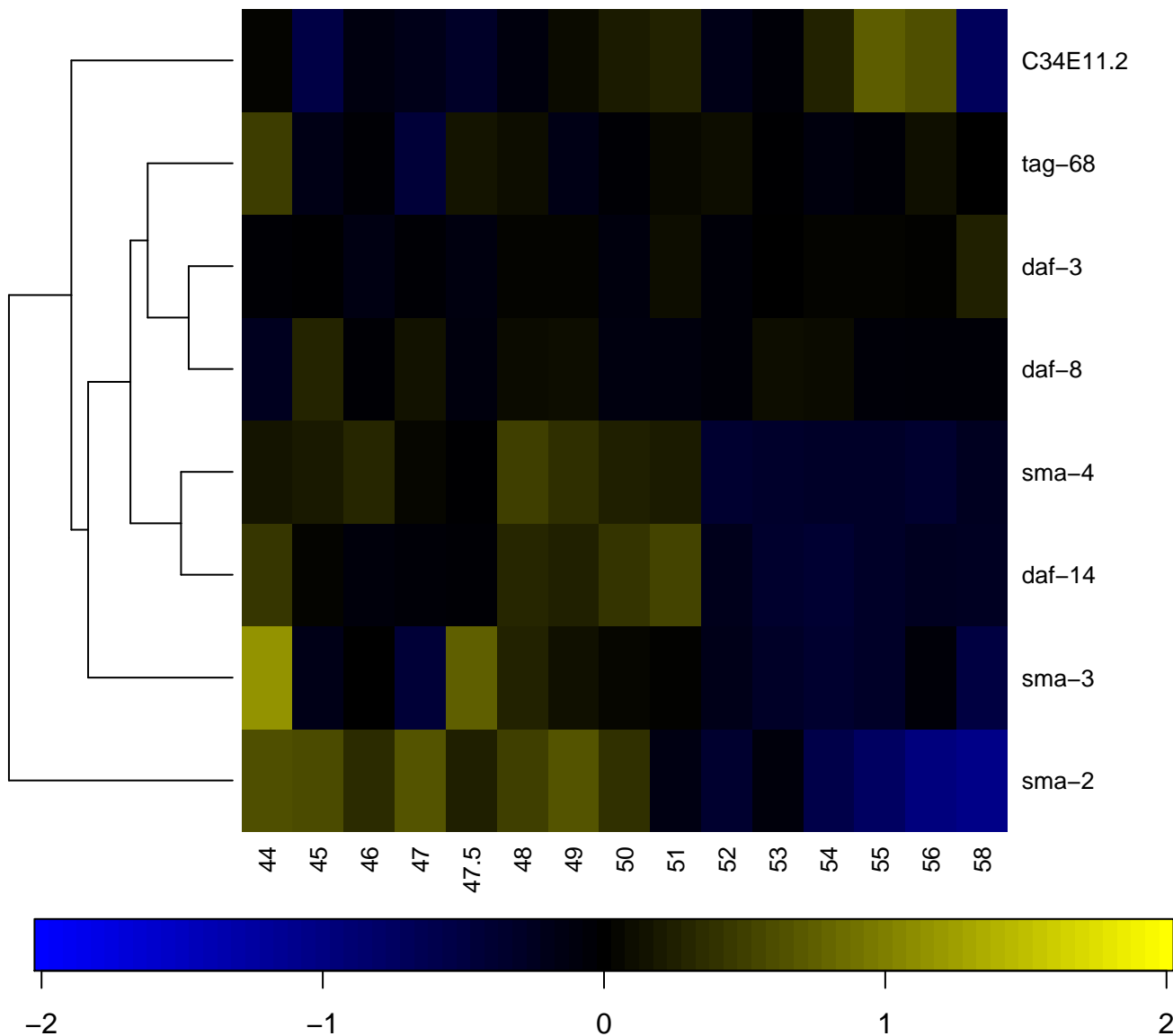
Six-bladed beta-propeller, TolB-like



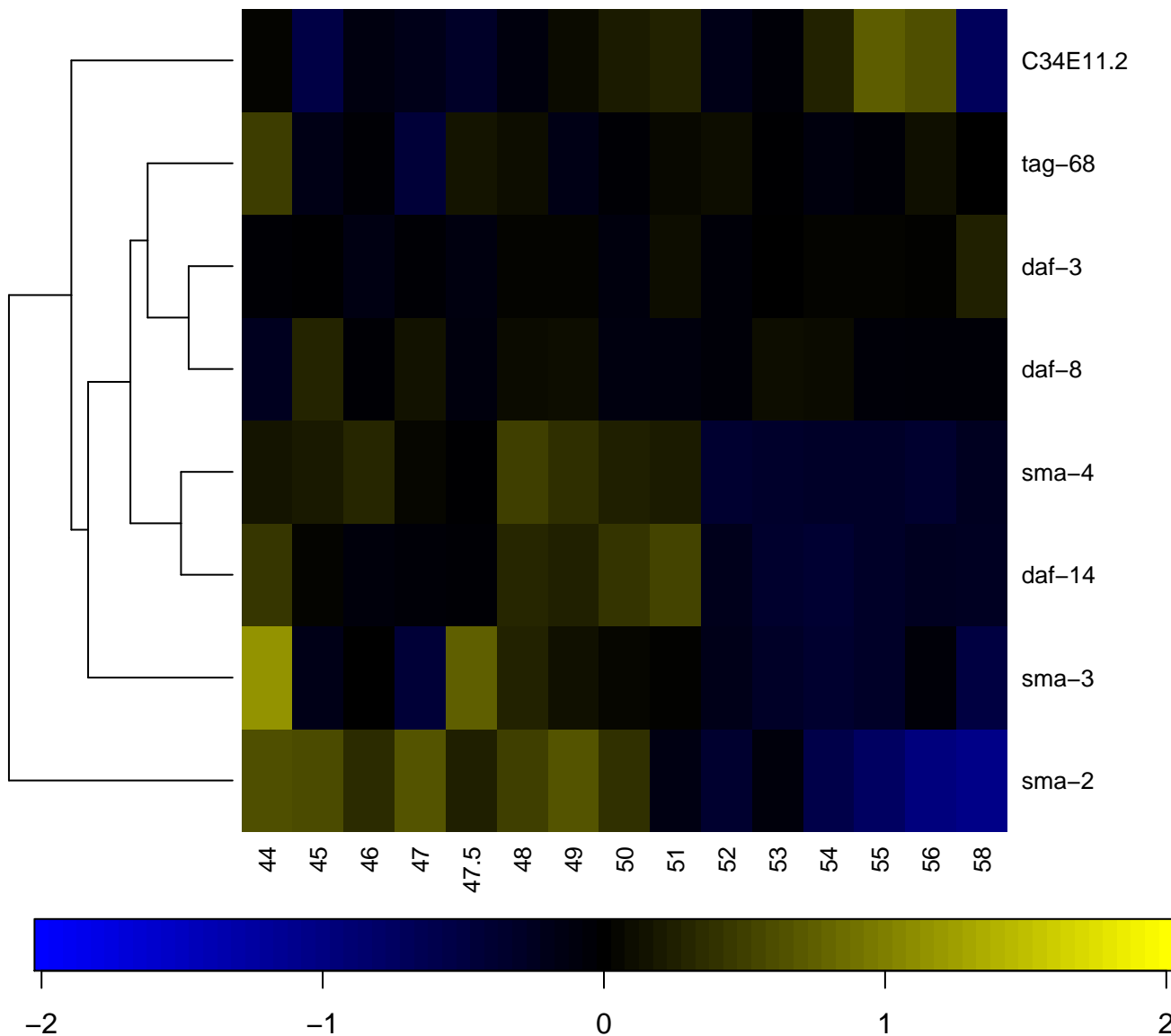
SKP1 component



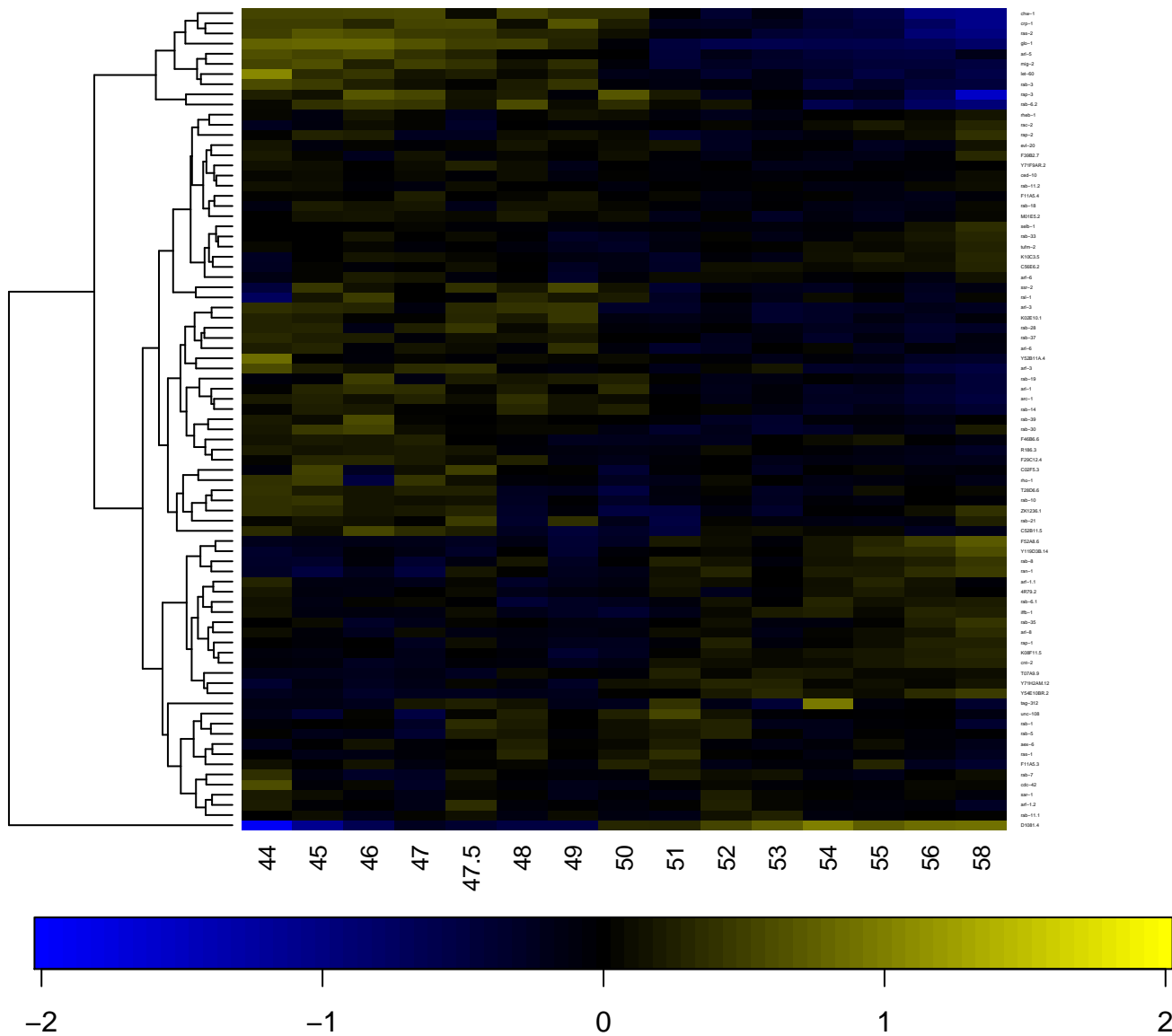
SMAD domain-like



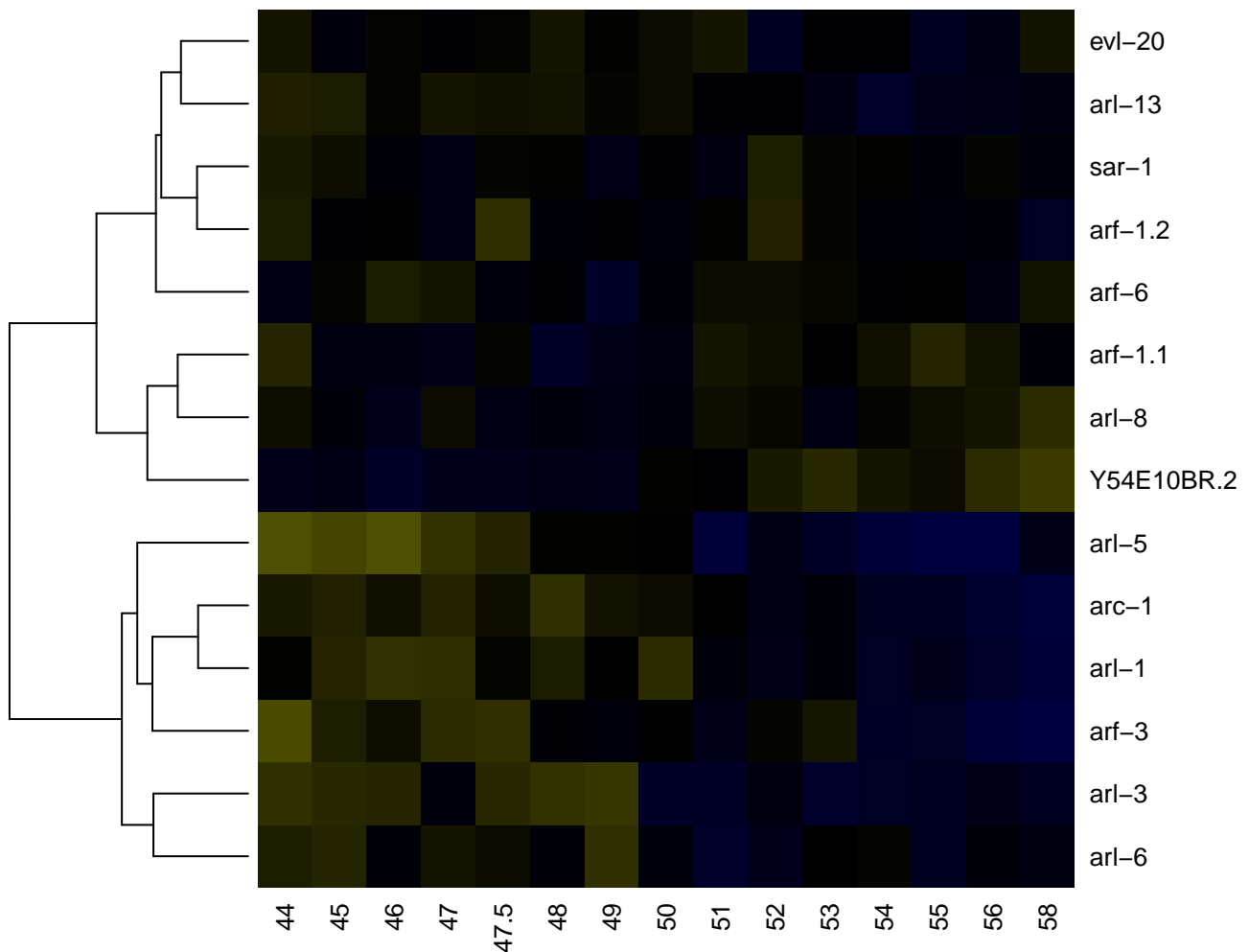
SMAD domain, Dwarfin-type



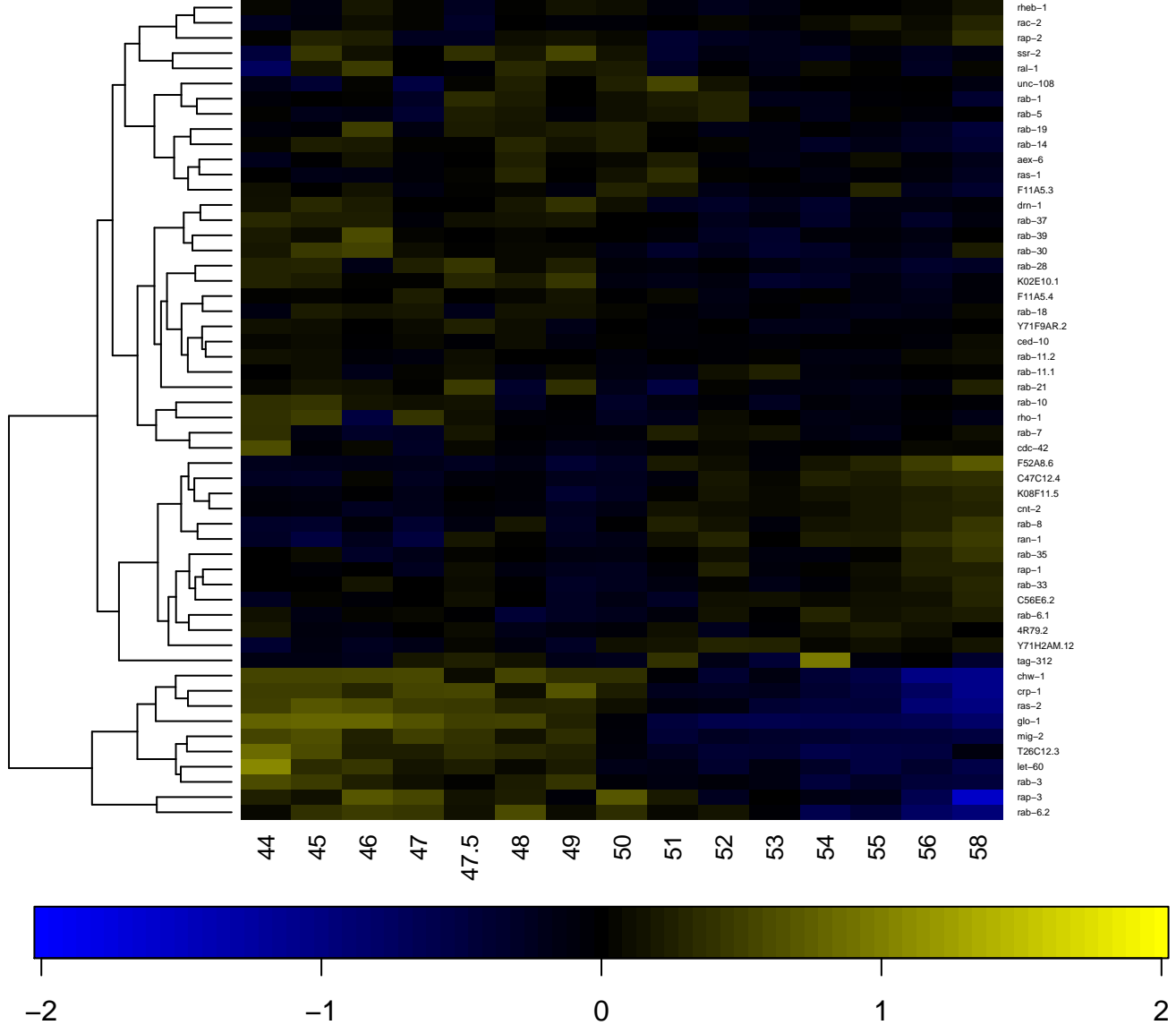
Small GTP-binding protein



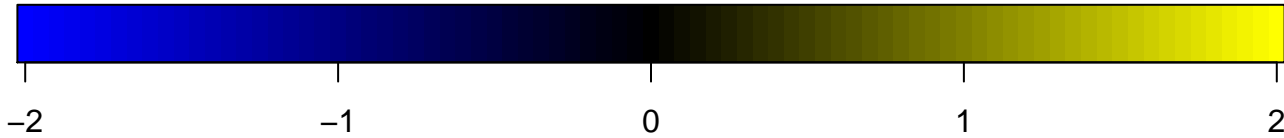
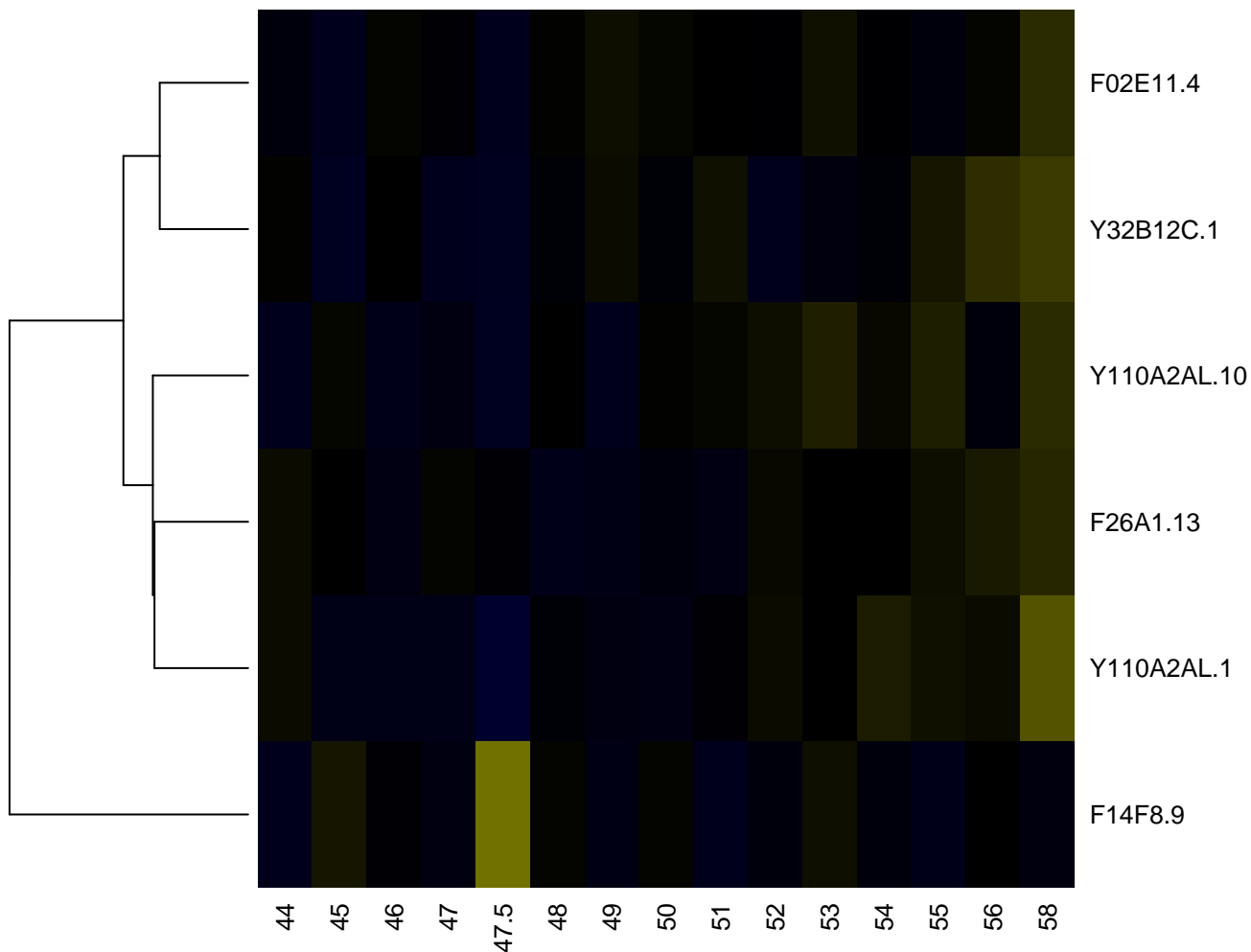
Small GTPase SAR1-type



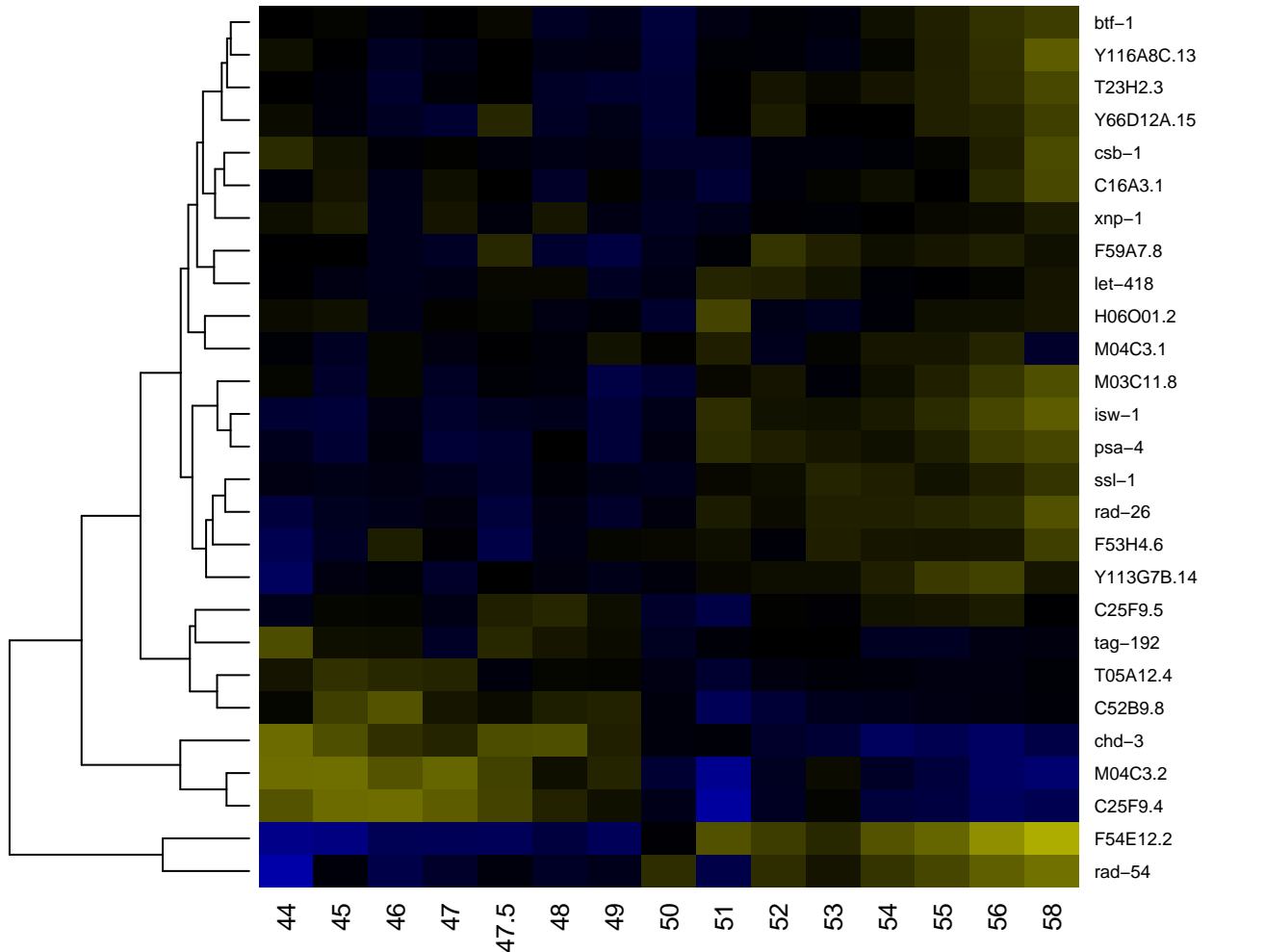
Small GTPase, Rho type



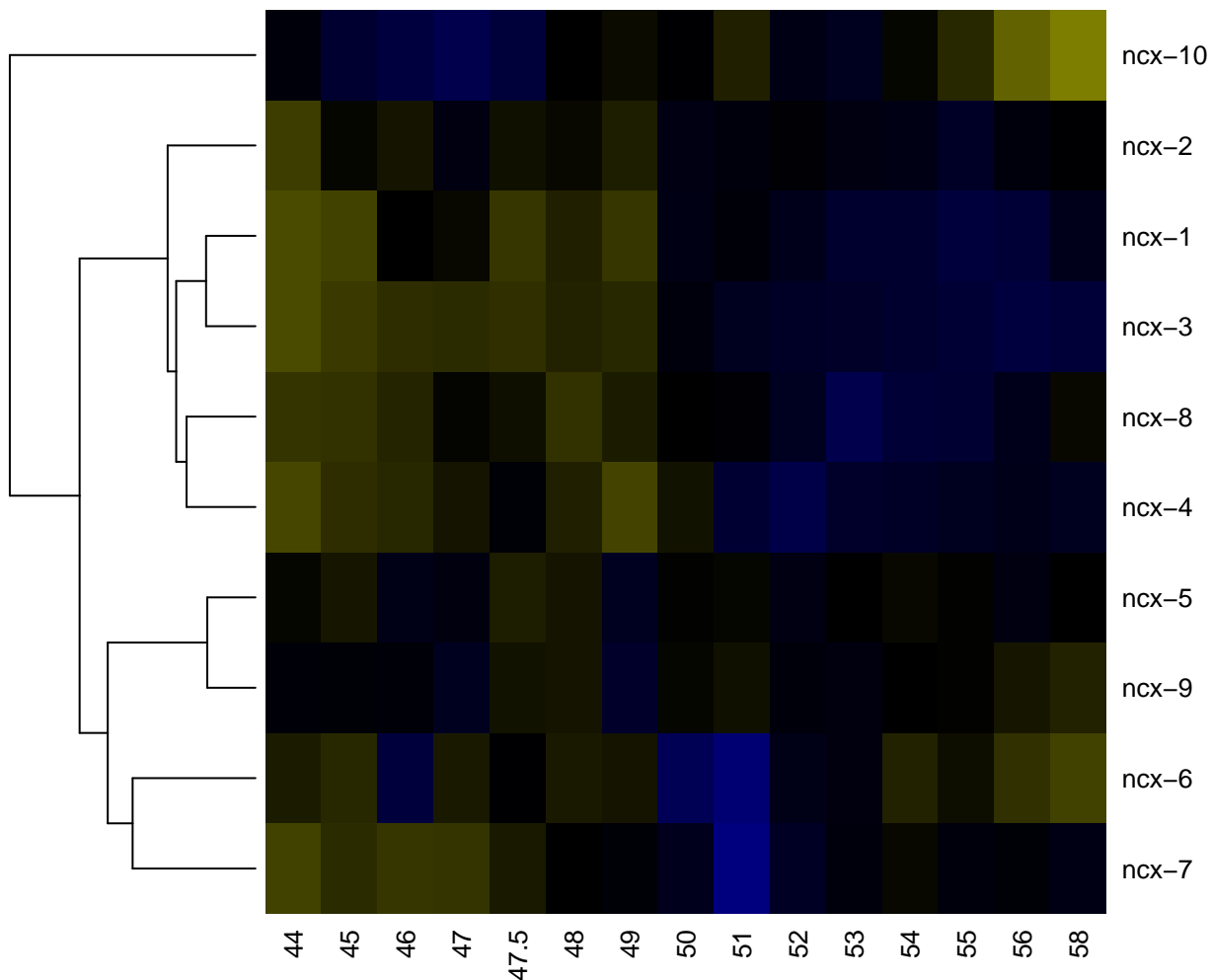
Smr protein/MutS2 C-terminal



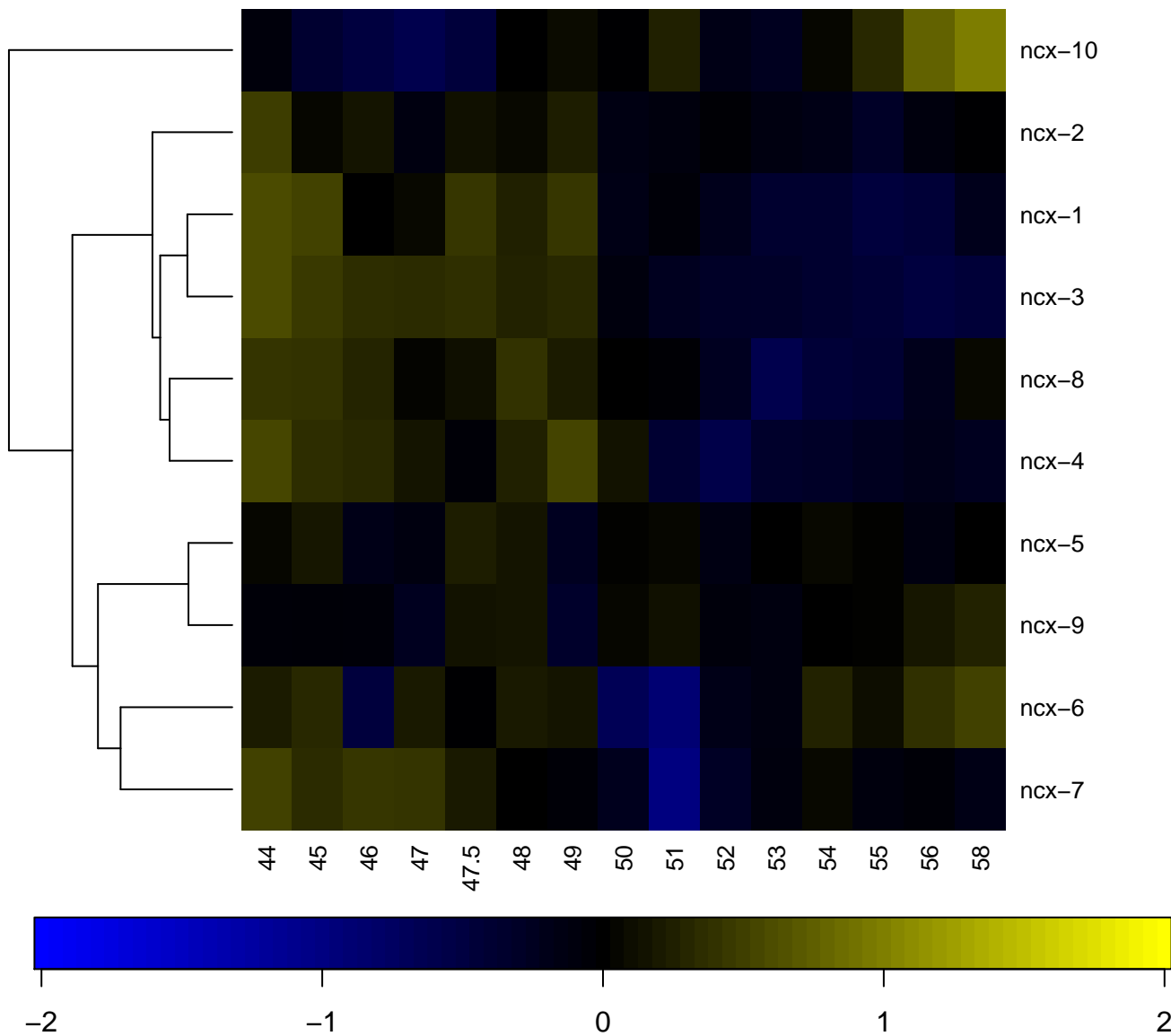
SNF2-related



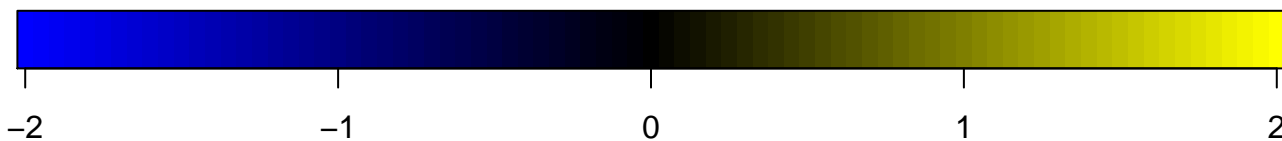
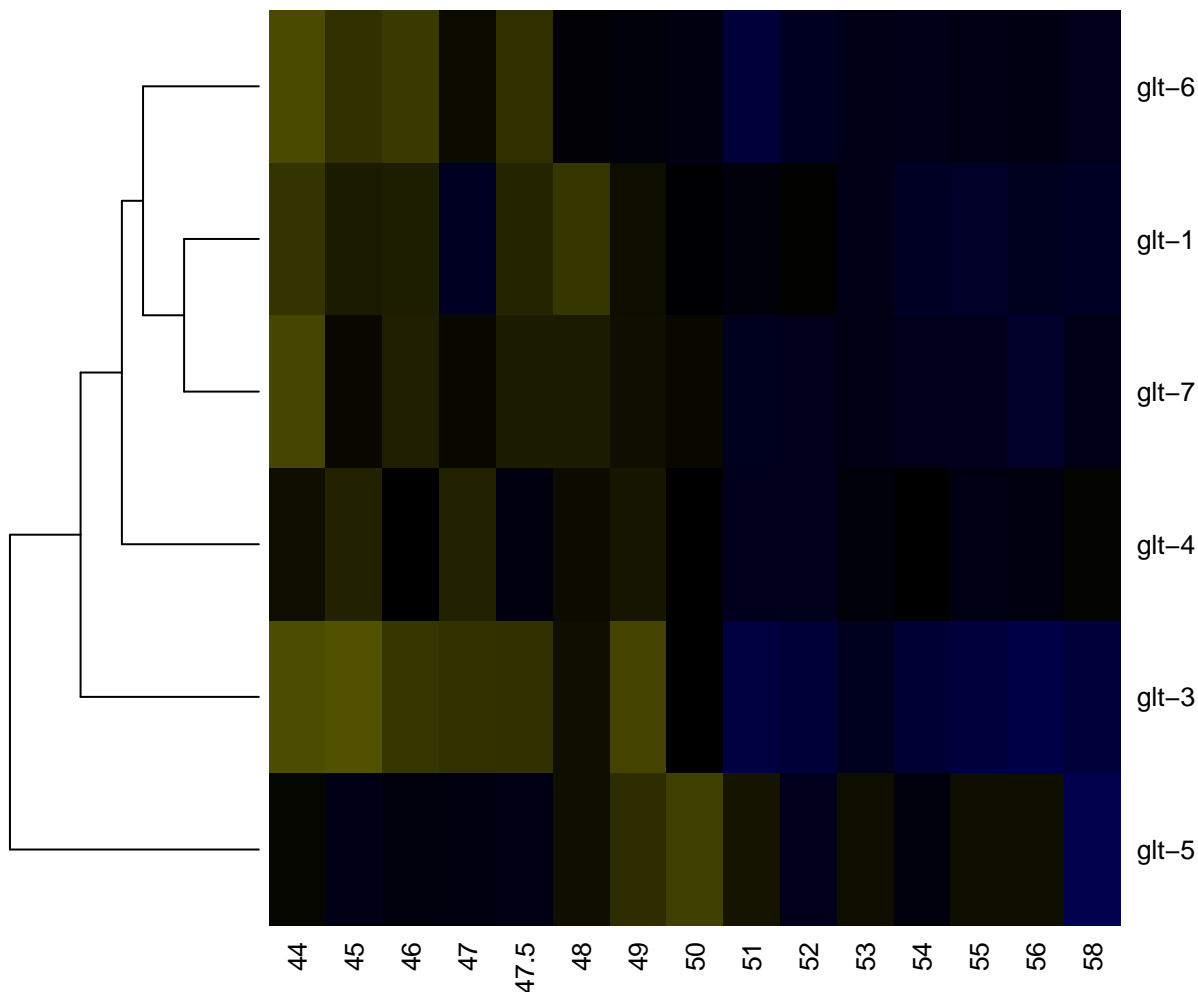
Sodium/calcium exchanger membrane region



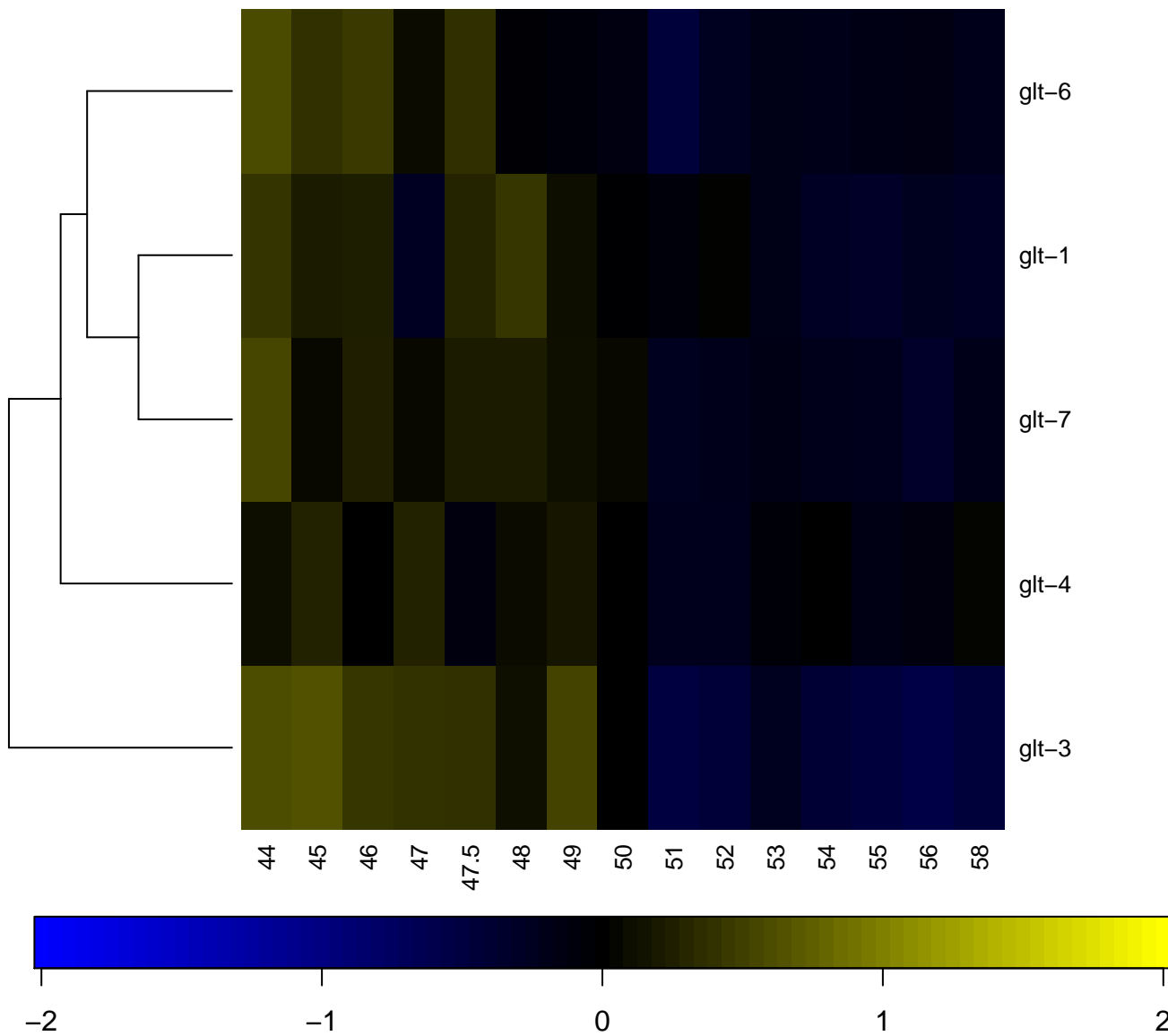
Sodium/calcium exchanger protein



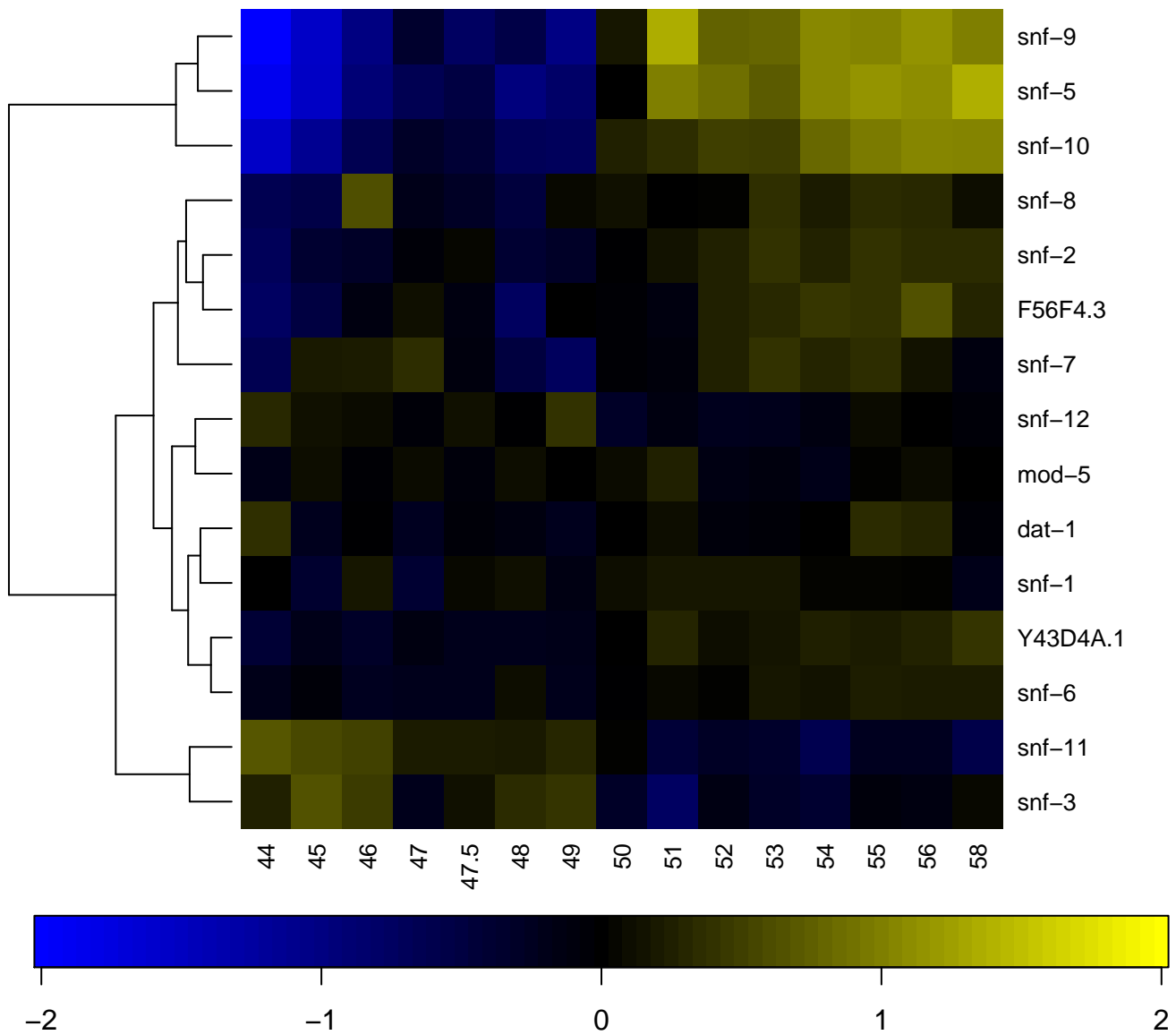
Sodium:dicarboxylate symporter family



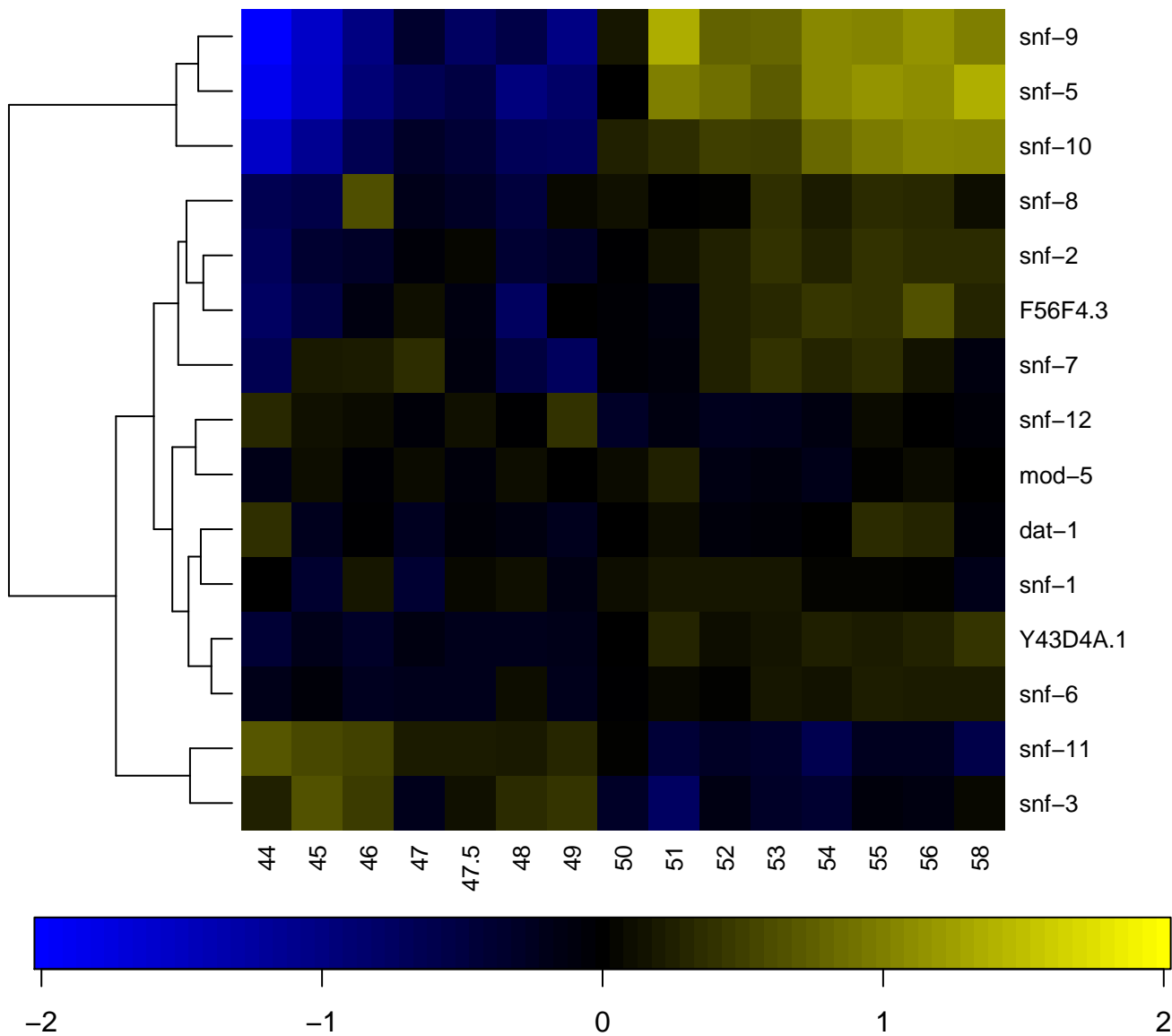
Sodium:dicarboxylate symporter, conserved site



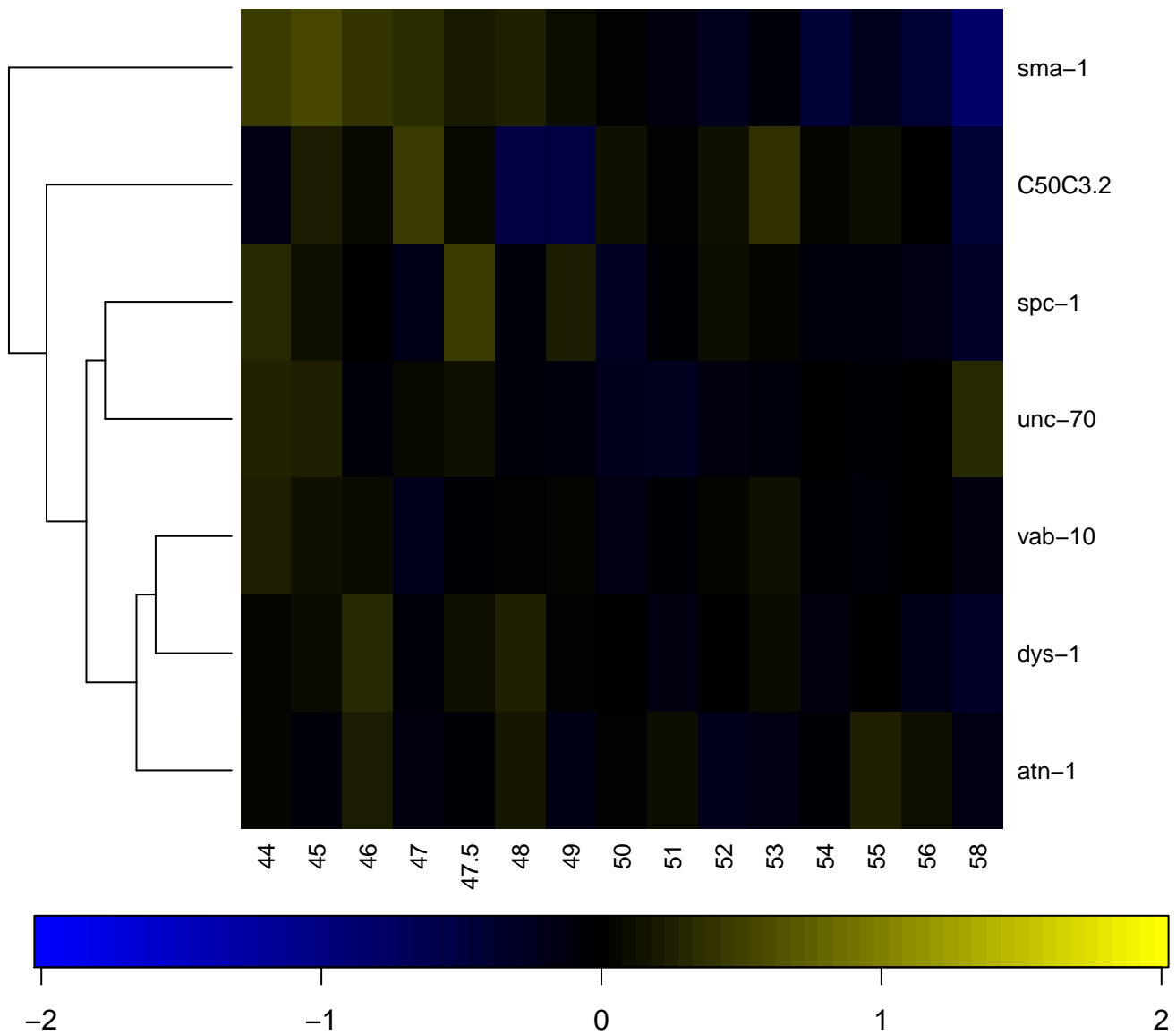
Sodium:neurotransmitter symporter



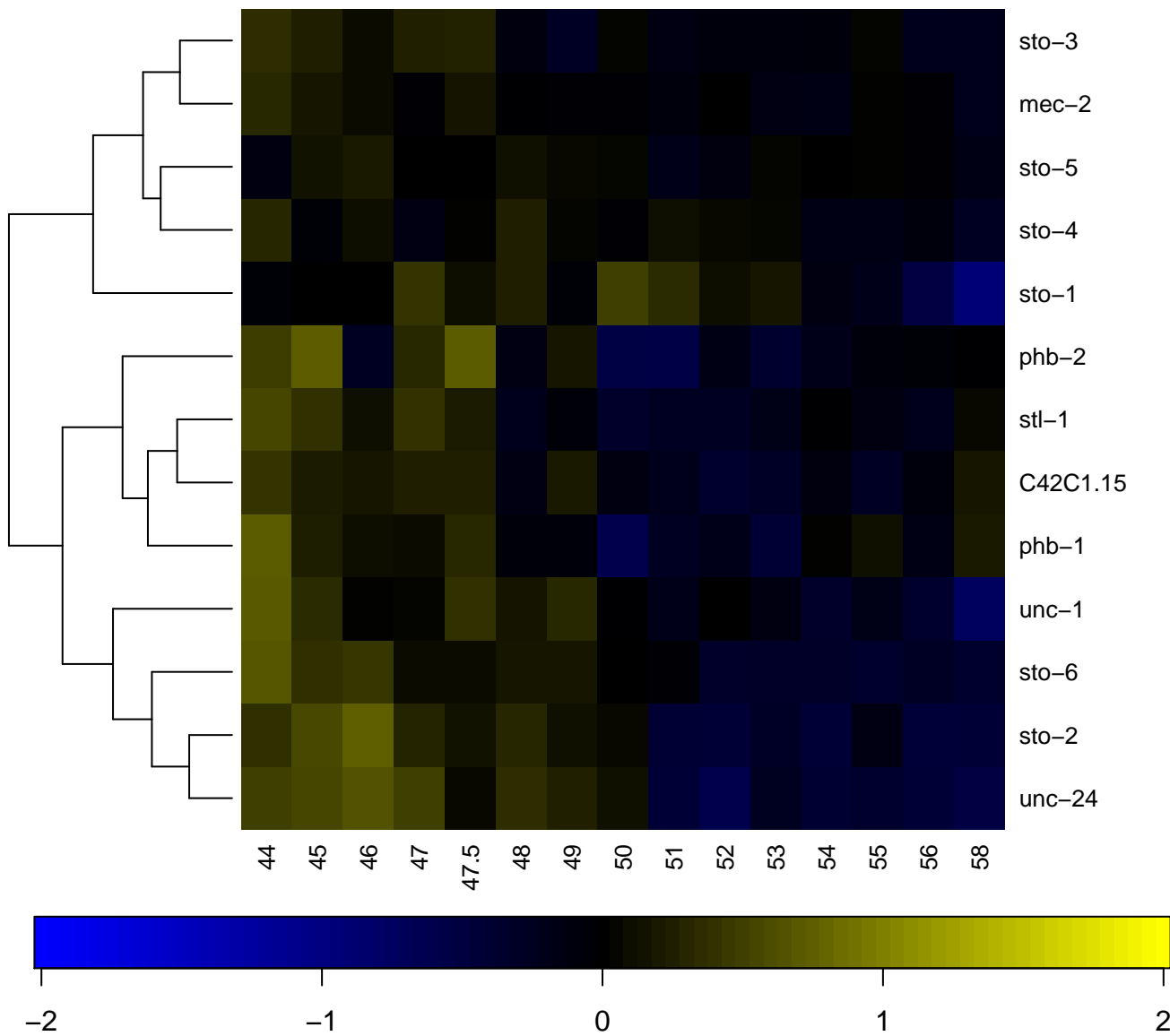
Sodium:neurotransmitter symporter family



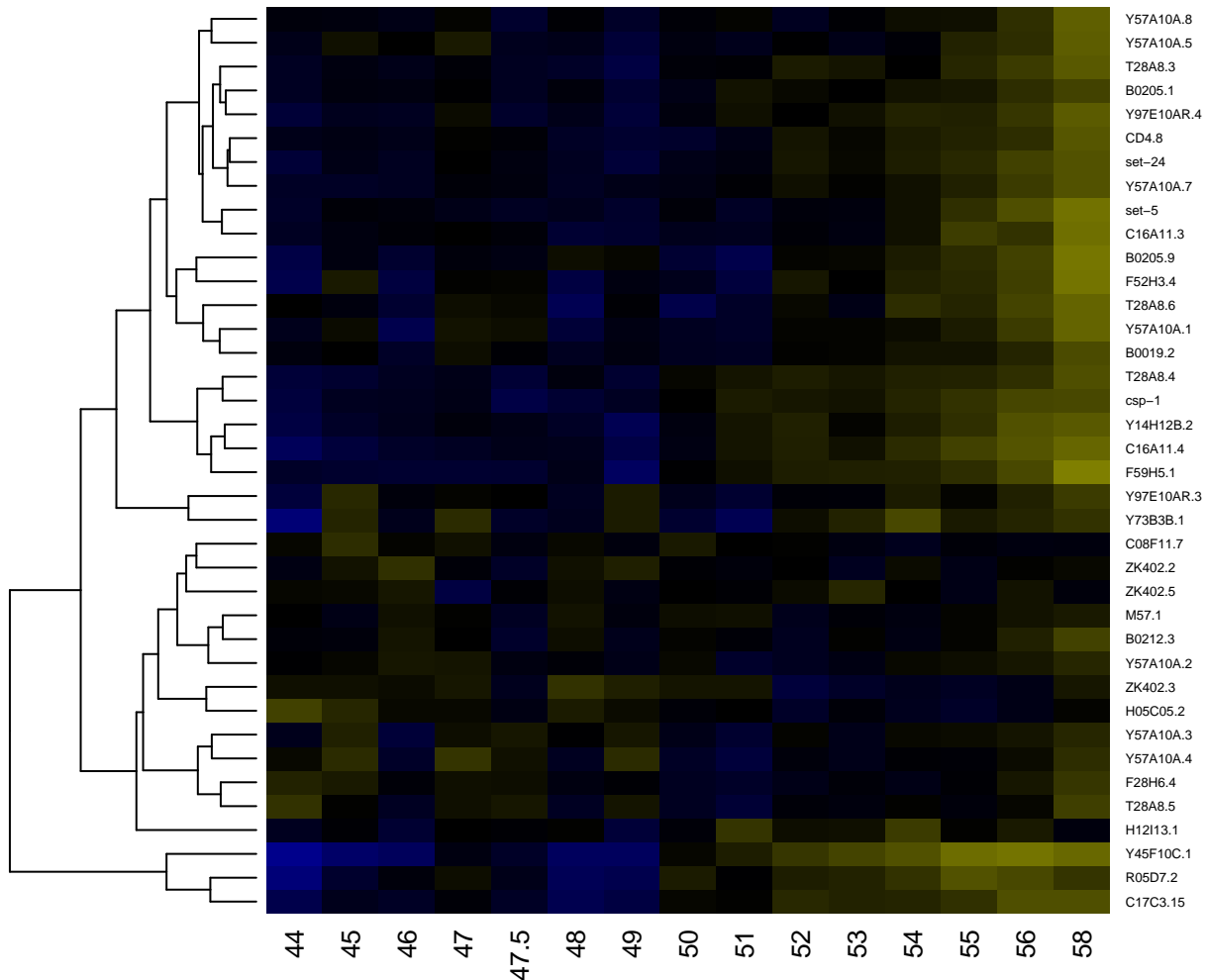
Spectrin/alpha-actinin



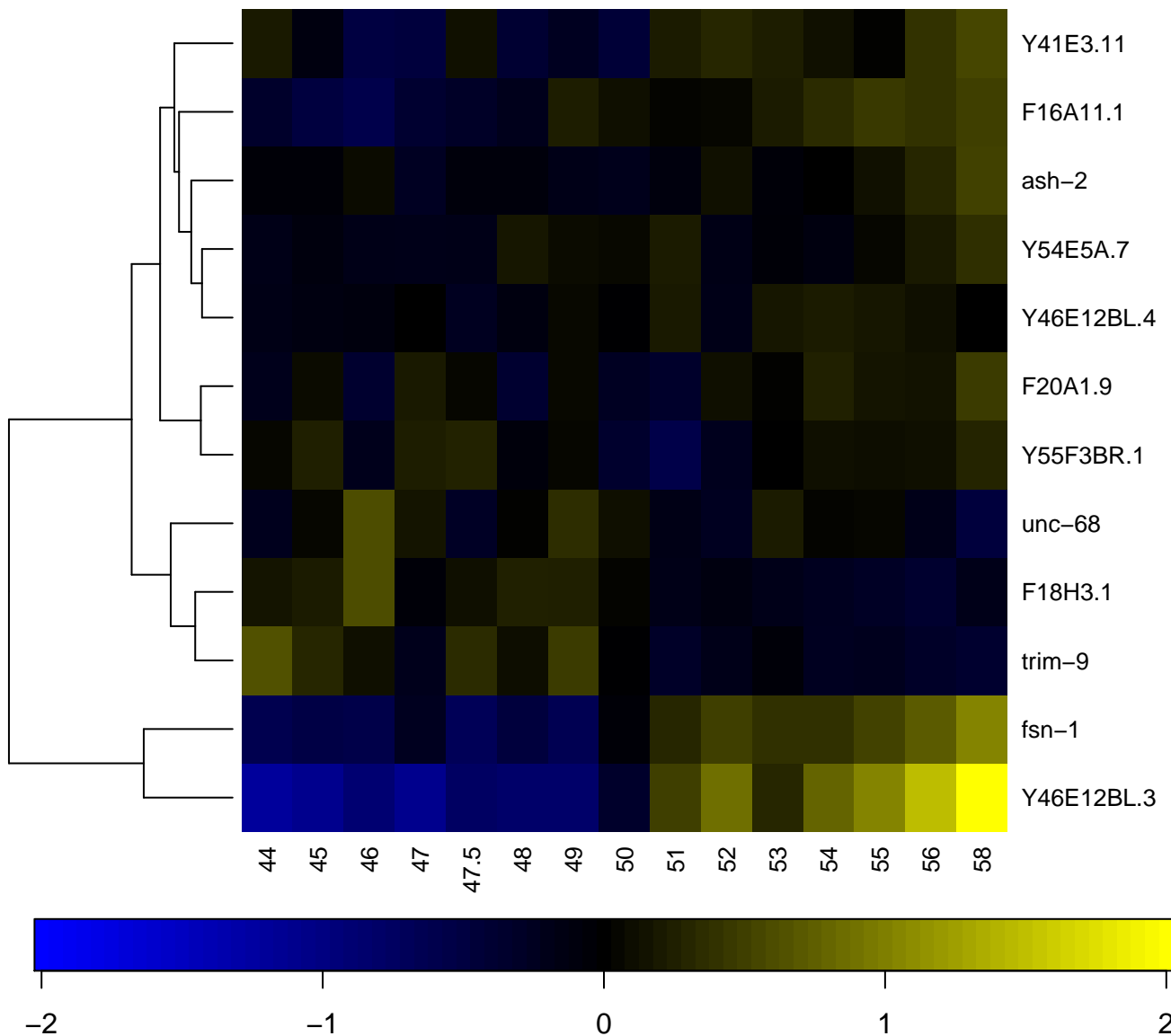
SPFH domain / Band 7 family



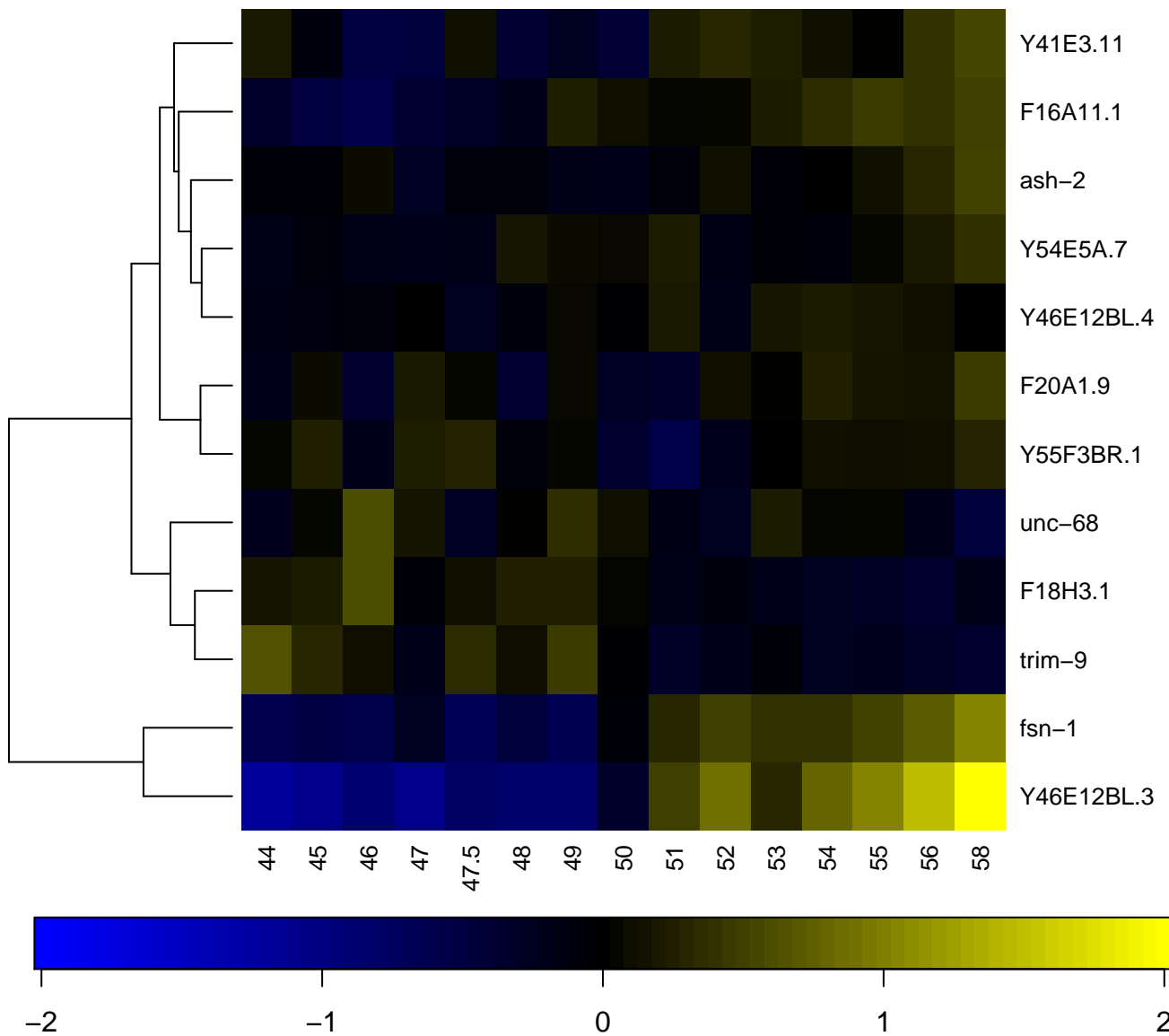
SPK



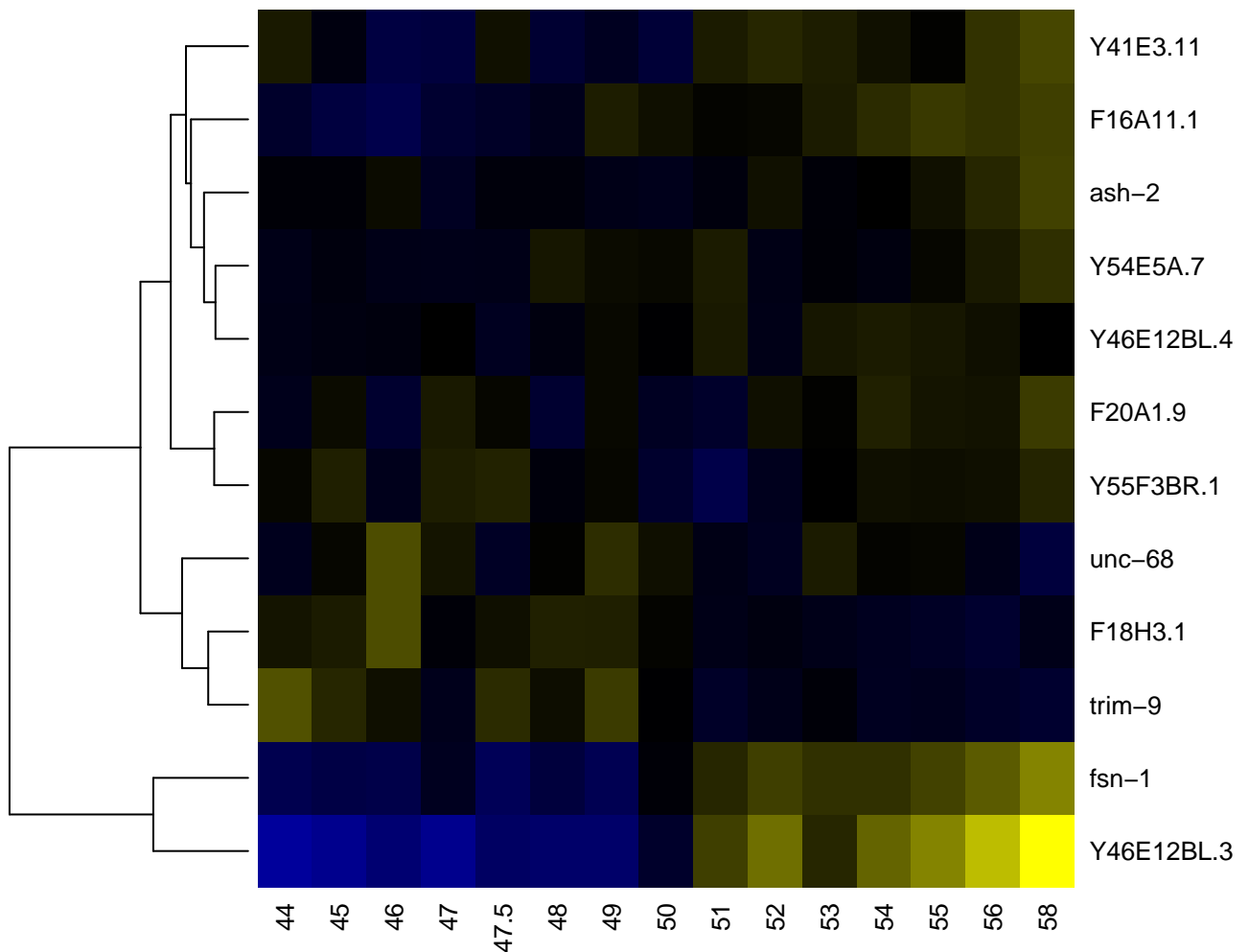
SPIa/Ryanodine receptor SPRY



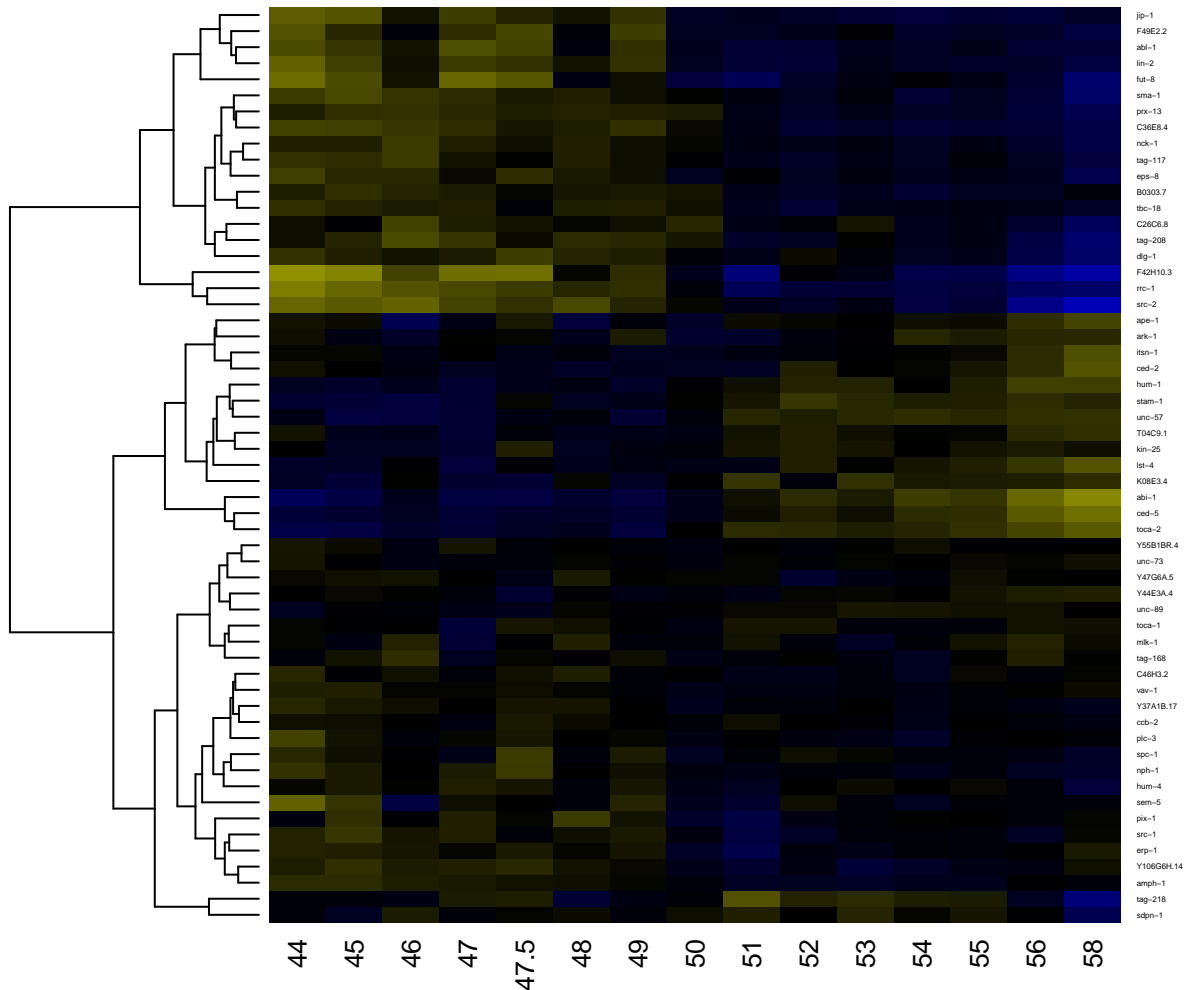
SPIa/Ryanodine receptor subgroup



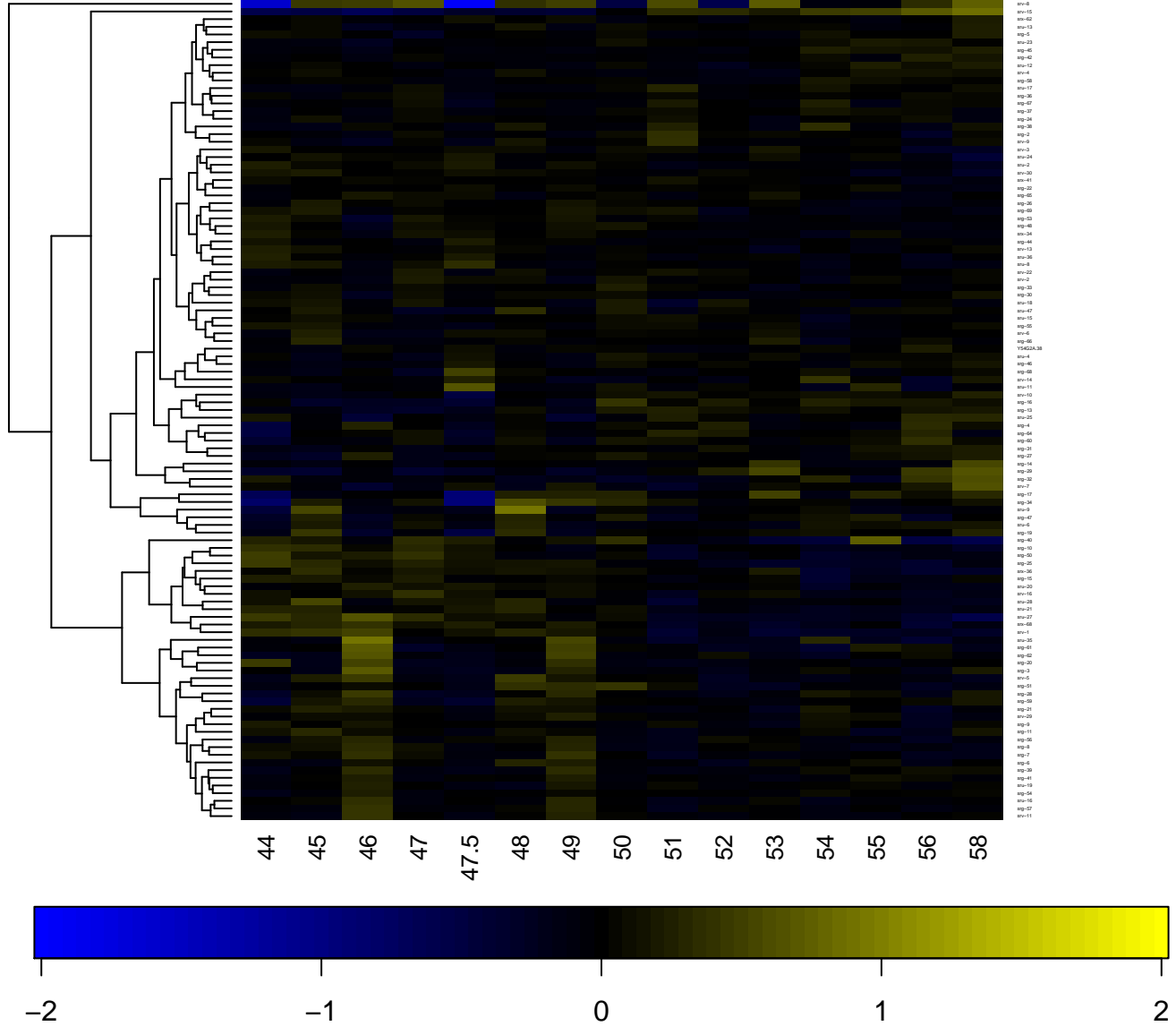
SPRY domain



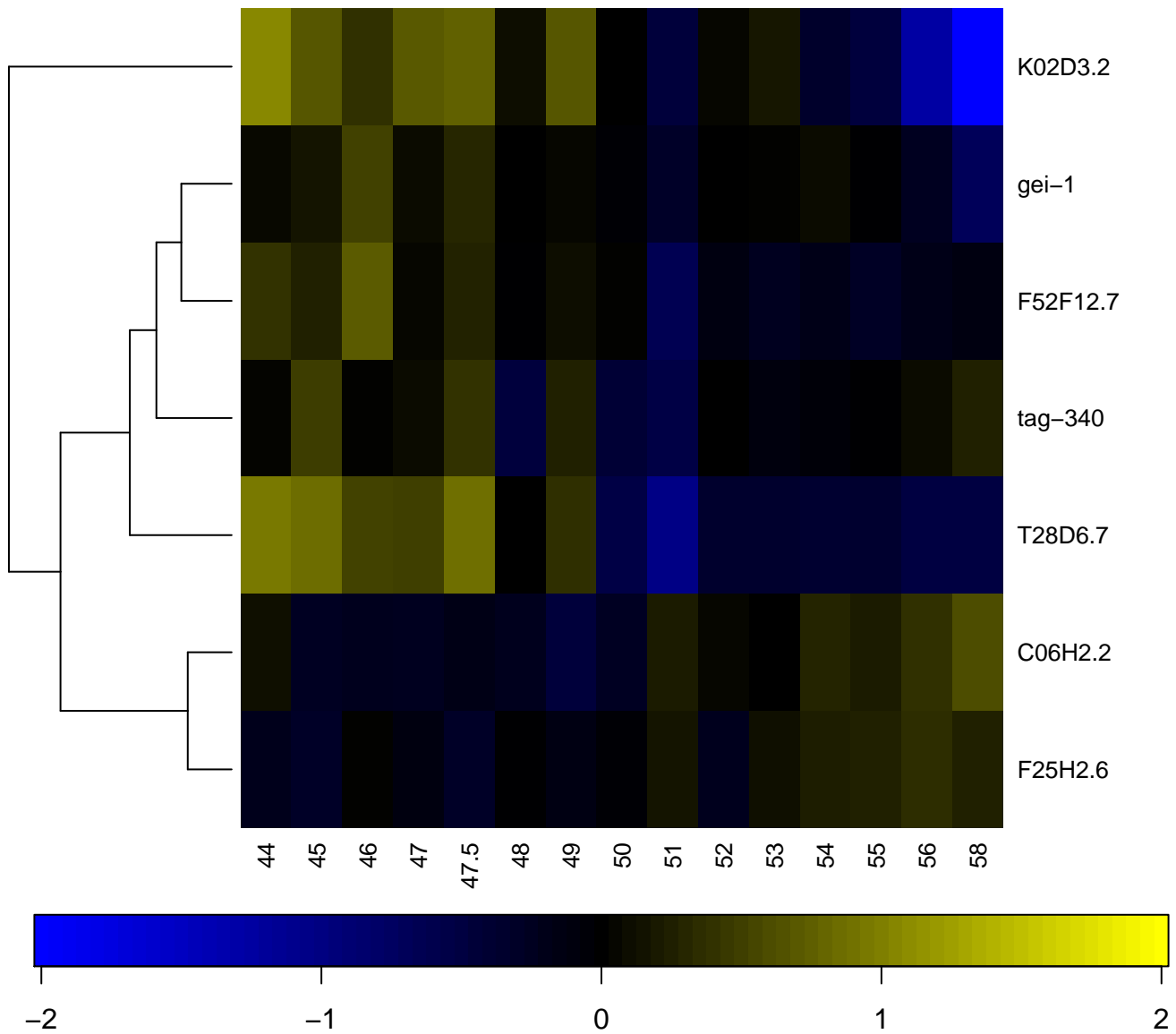
Src homology-3 domain



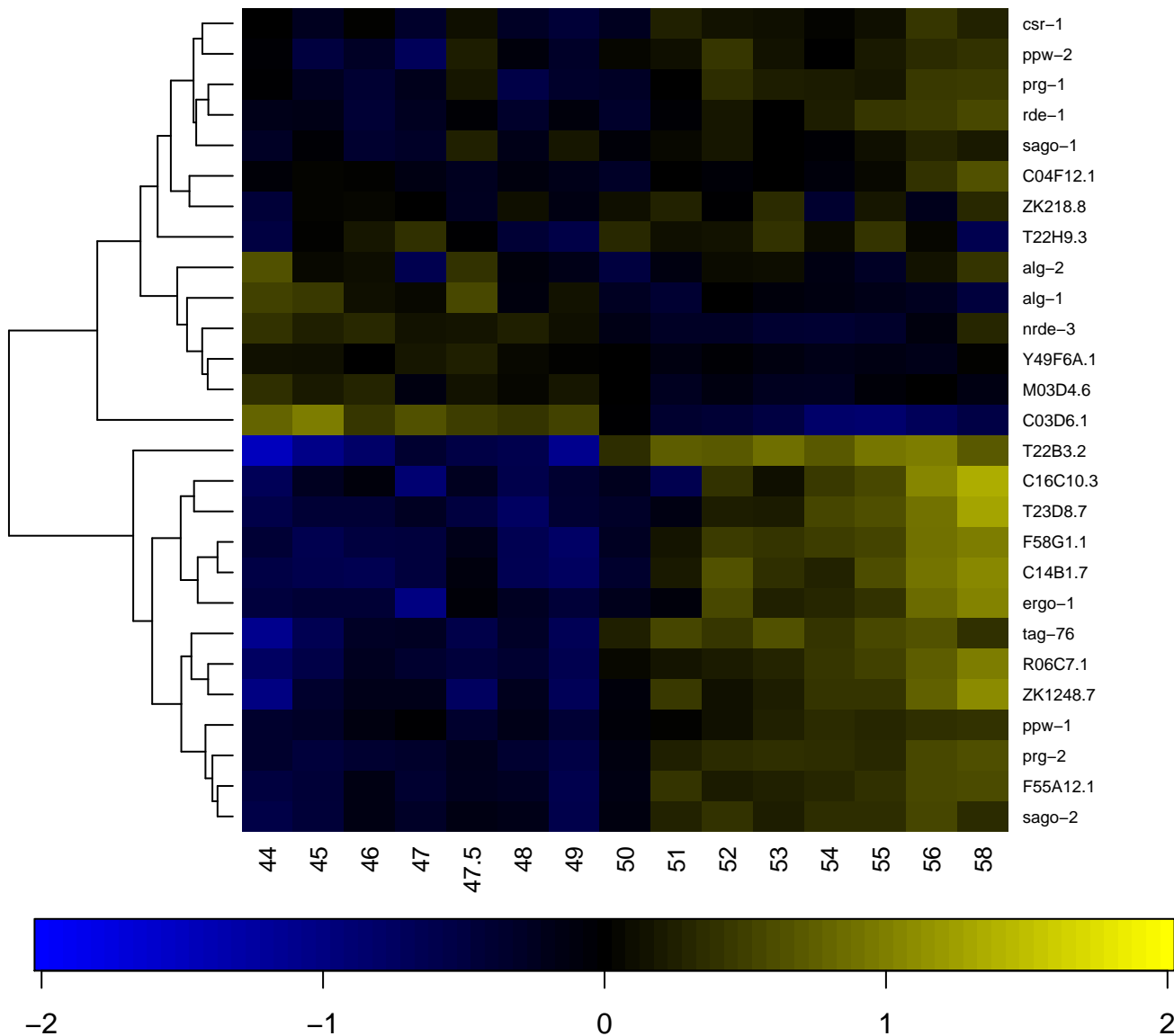
Srg family chemoreceptor



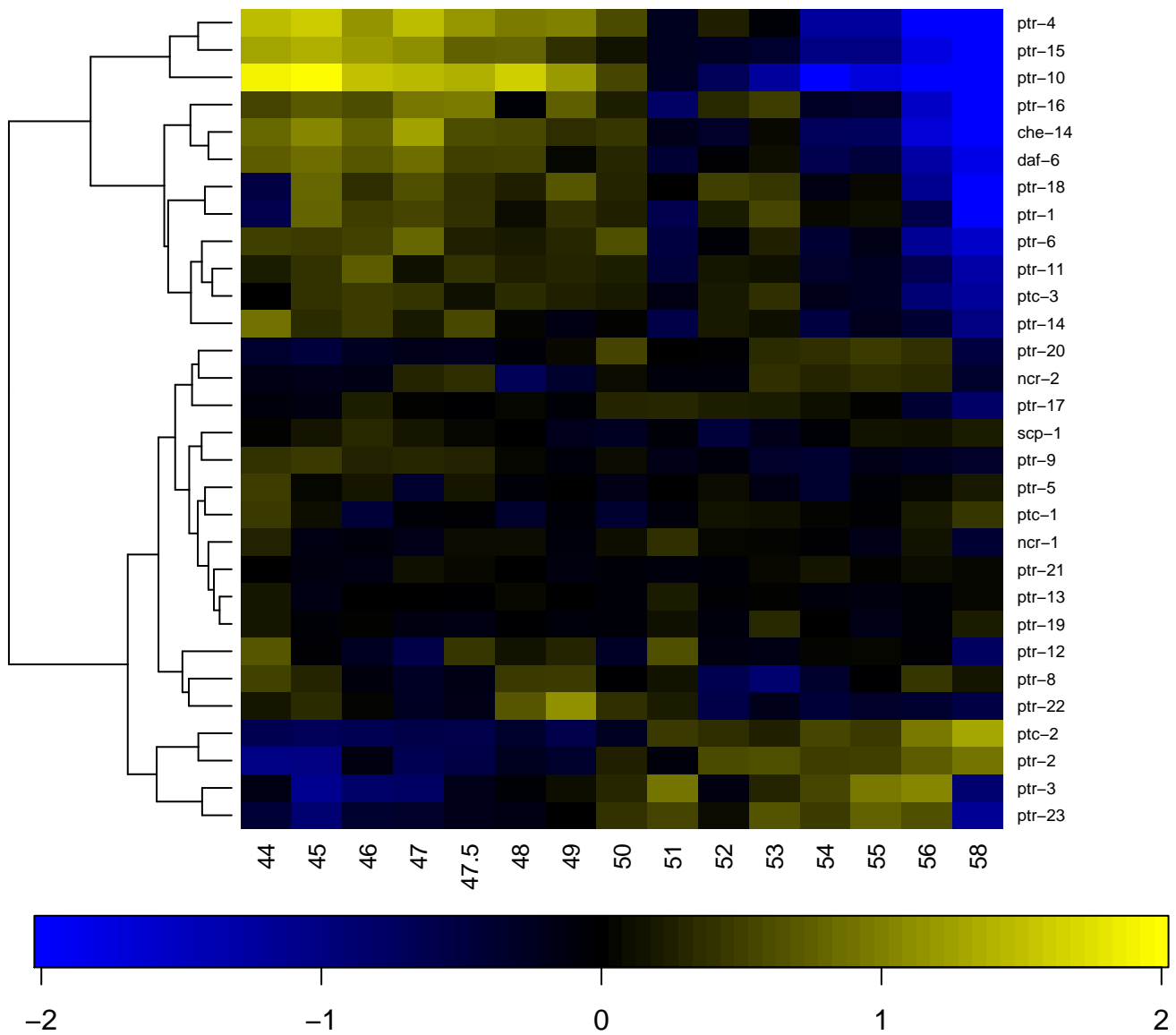
START domain



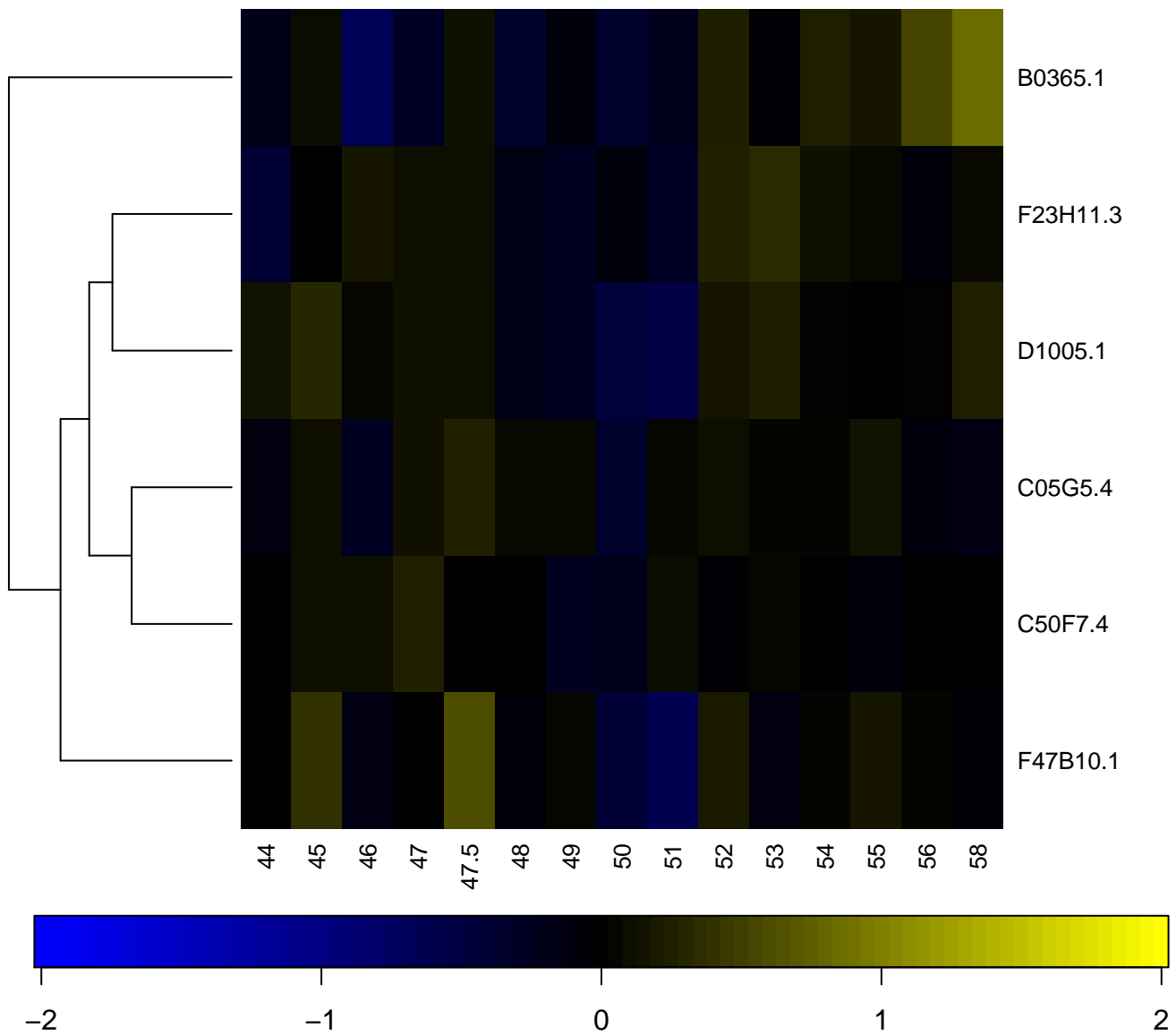
Stem cell self-renewal protein Piwi



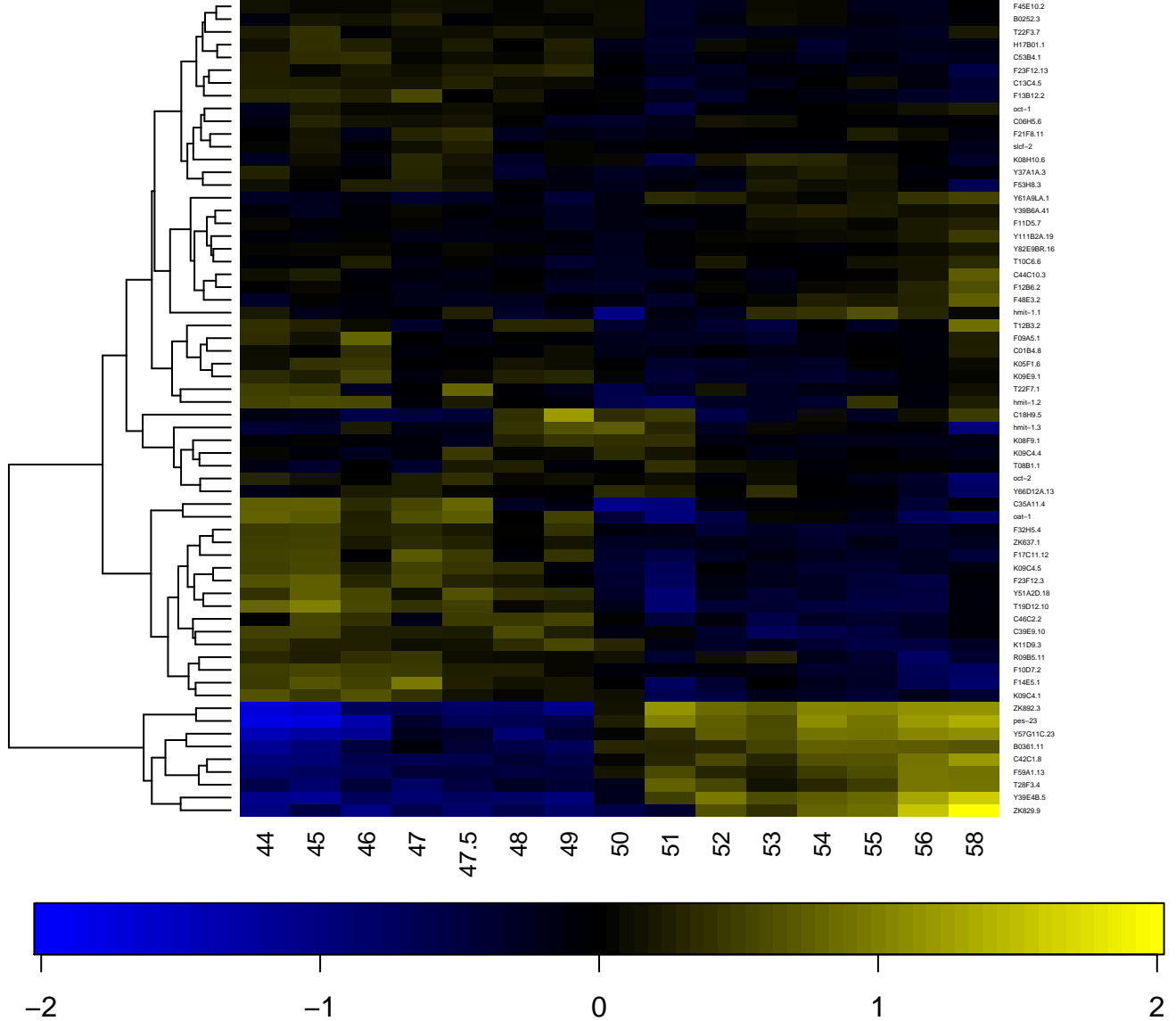
Sterol-sensing domain of SREBP cleavage-activation



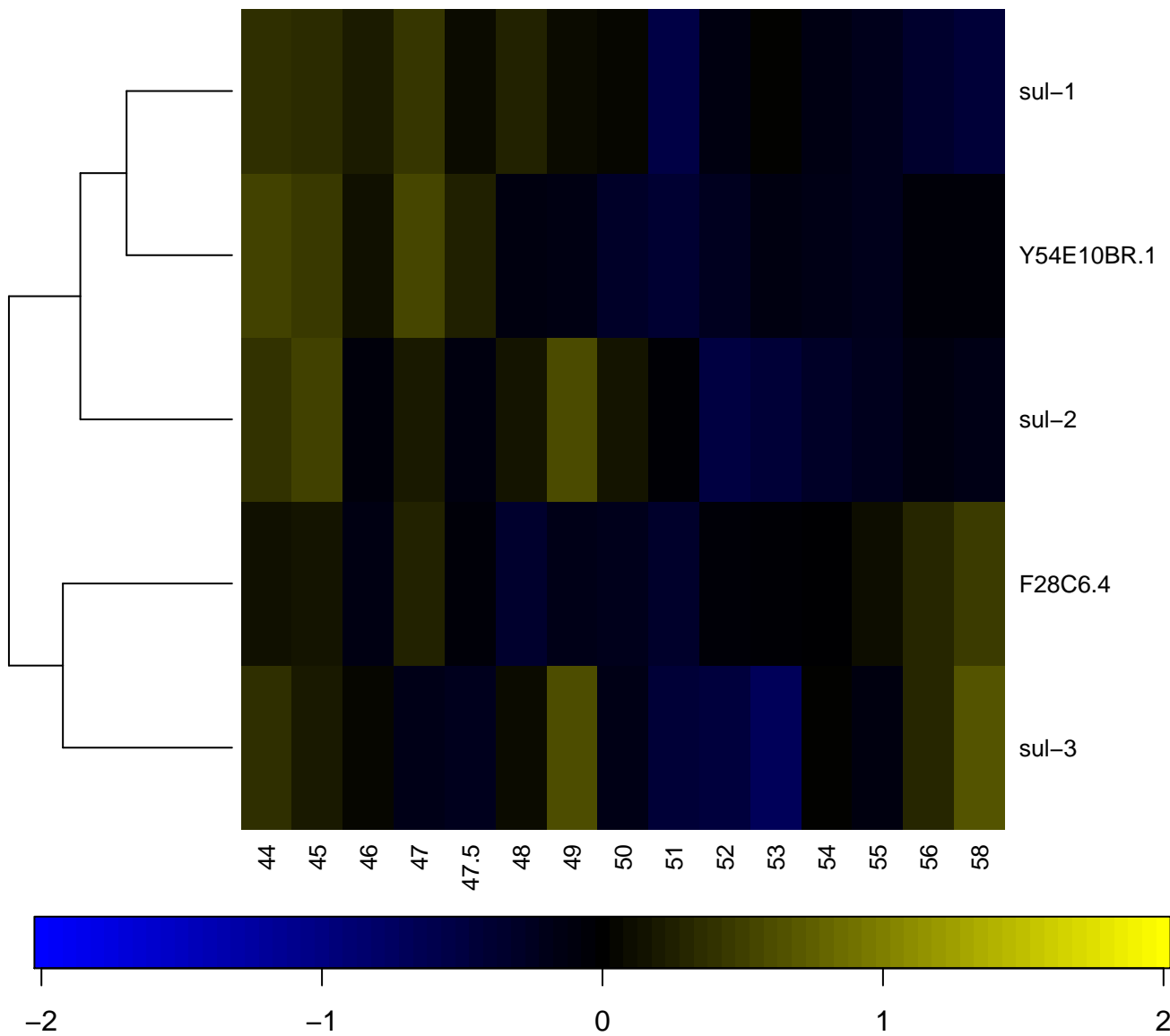
Succinyl-CoA synthetase-like



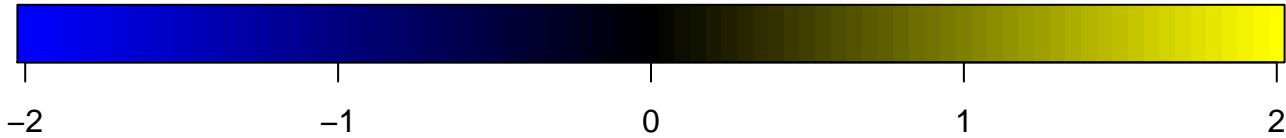
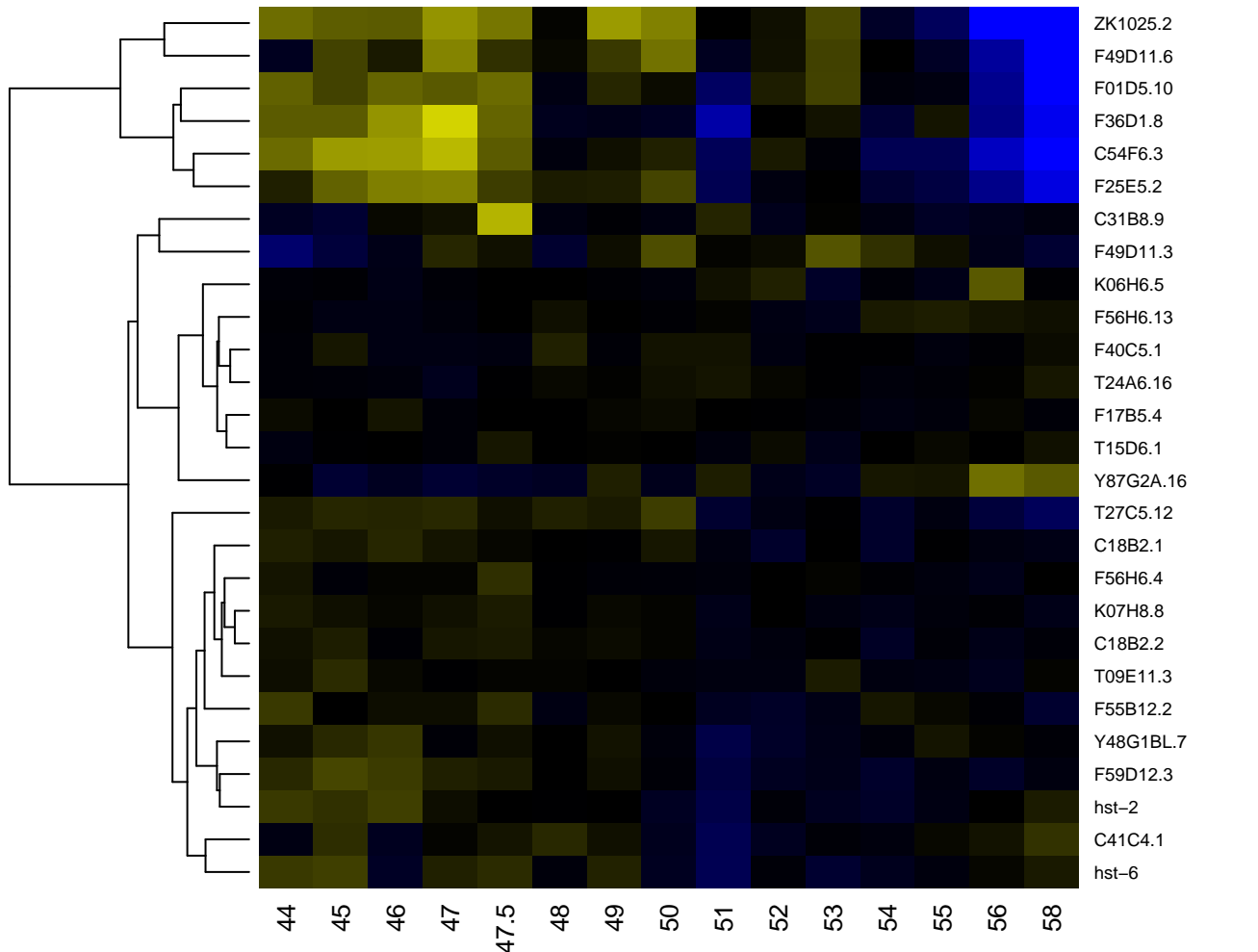
Sugar (and other) transporter



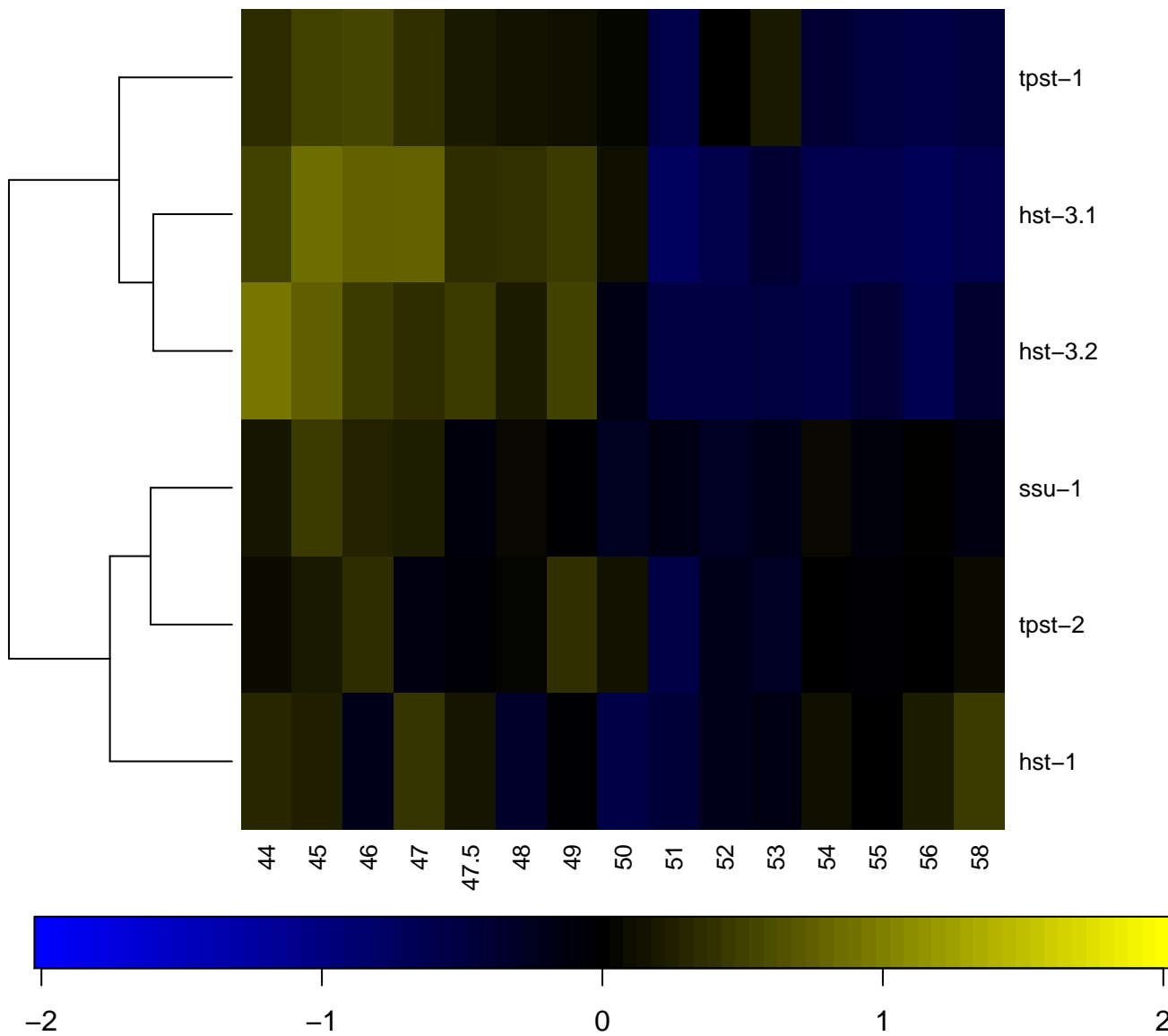
Sulfatase



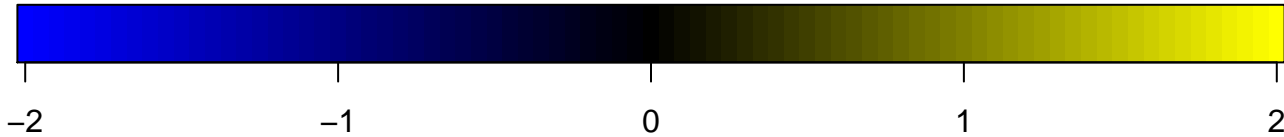
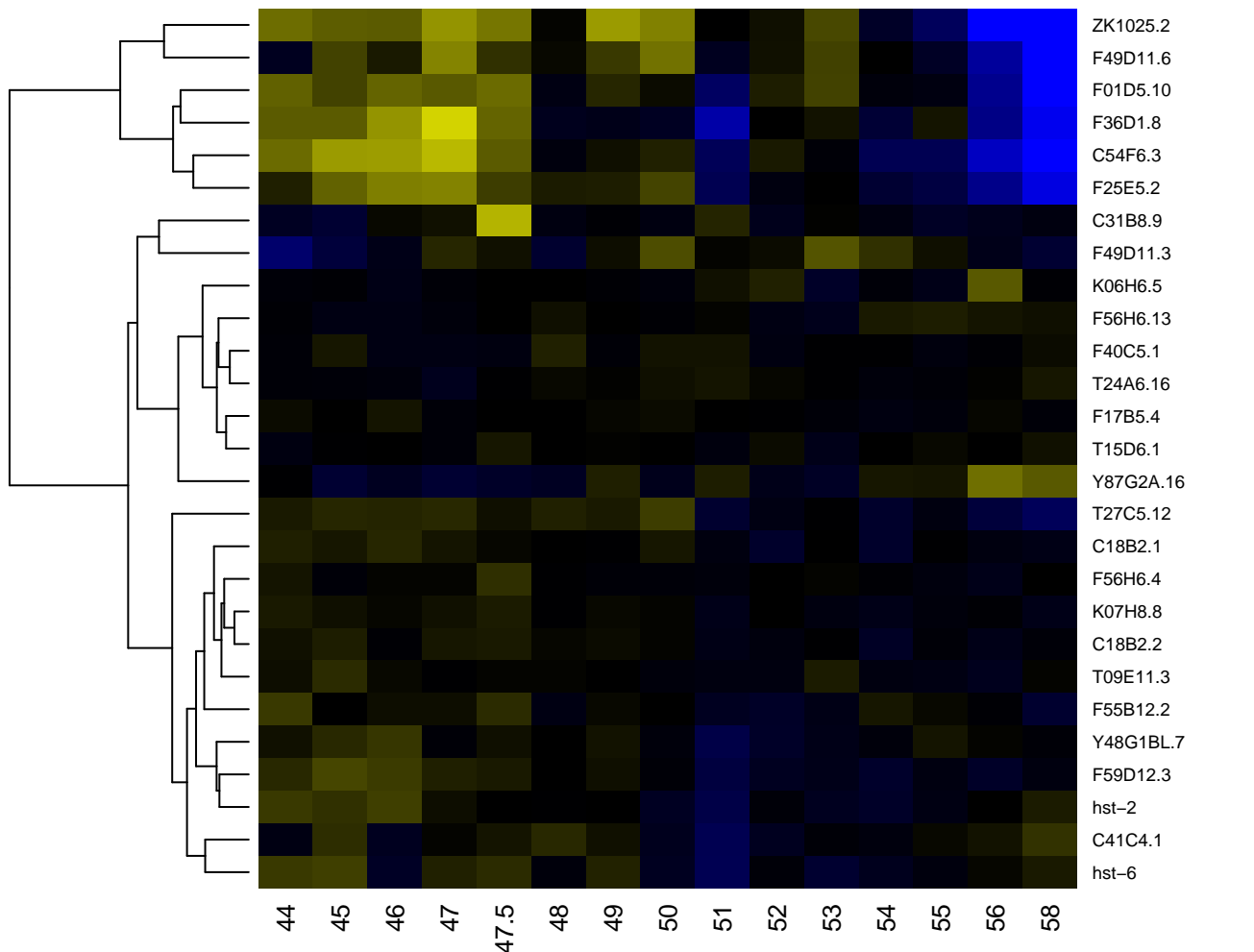
Sulfotransferase



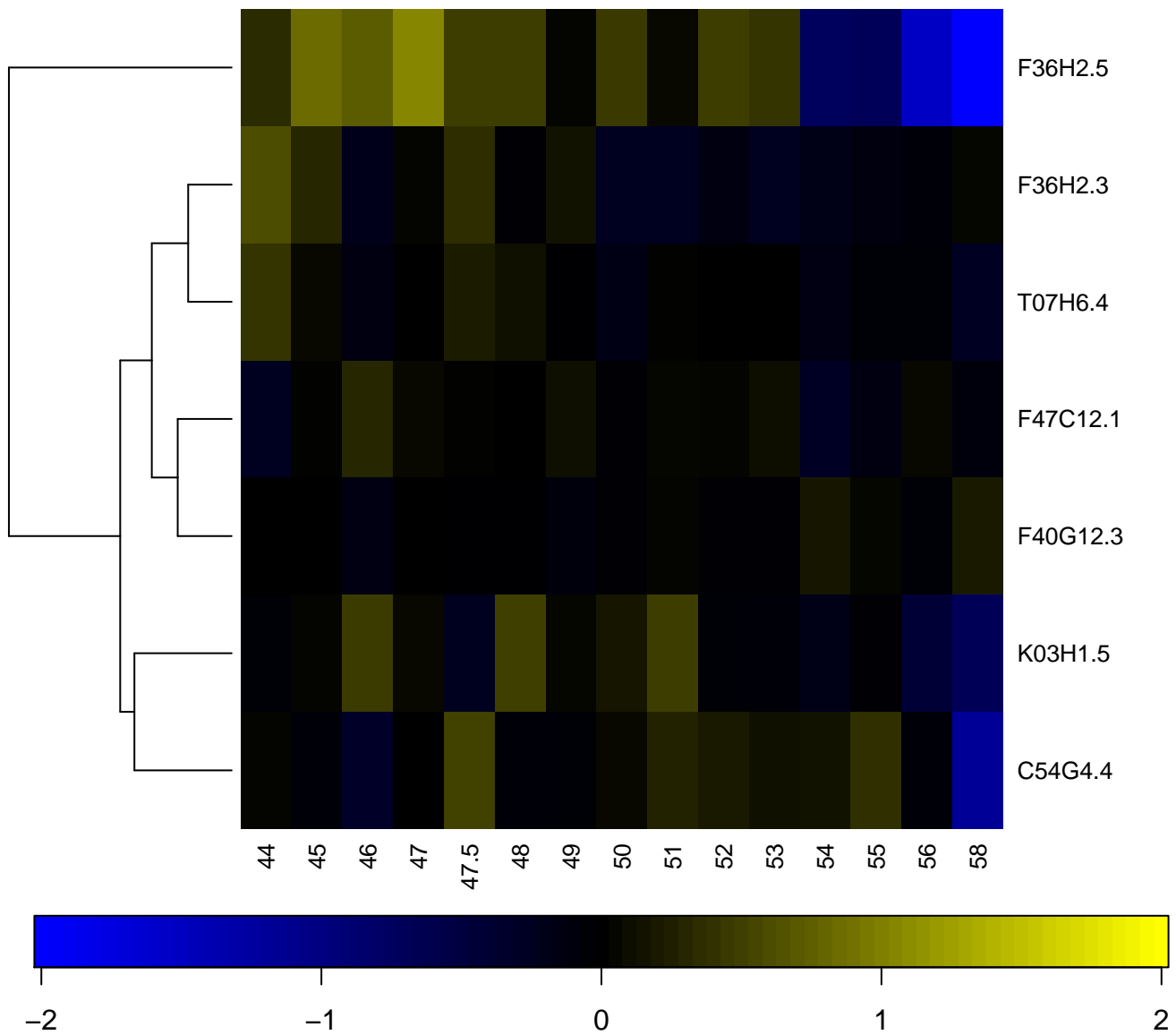
Sulfotransferase domain



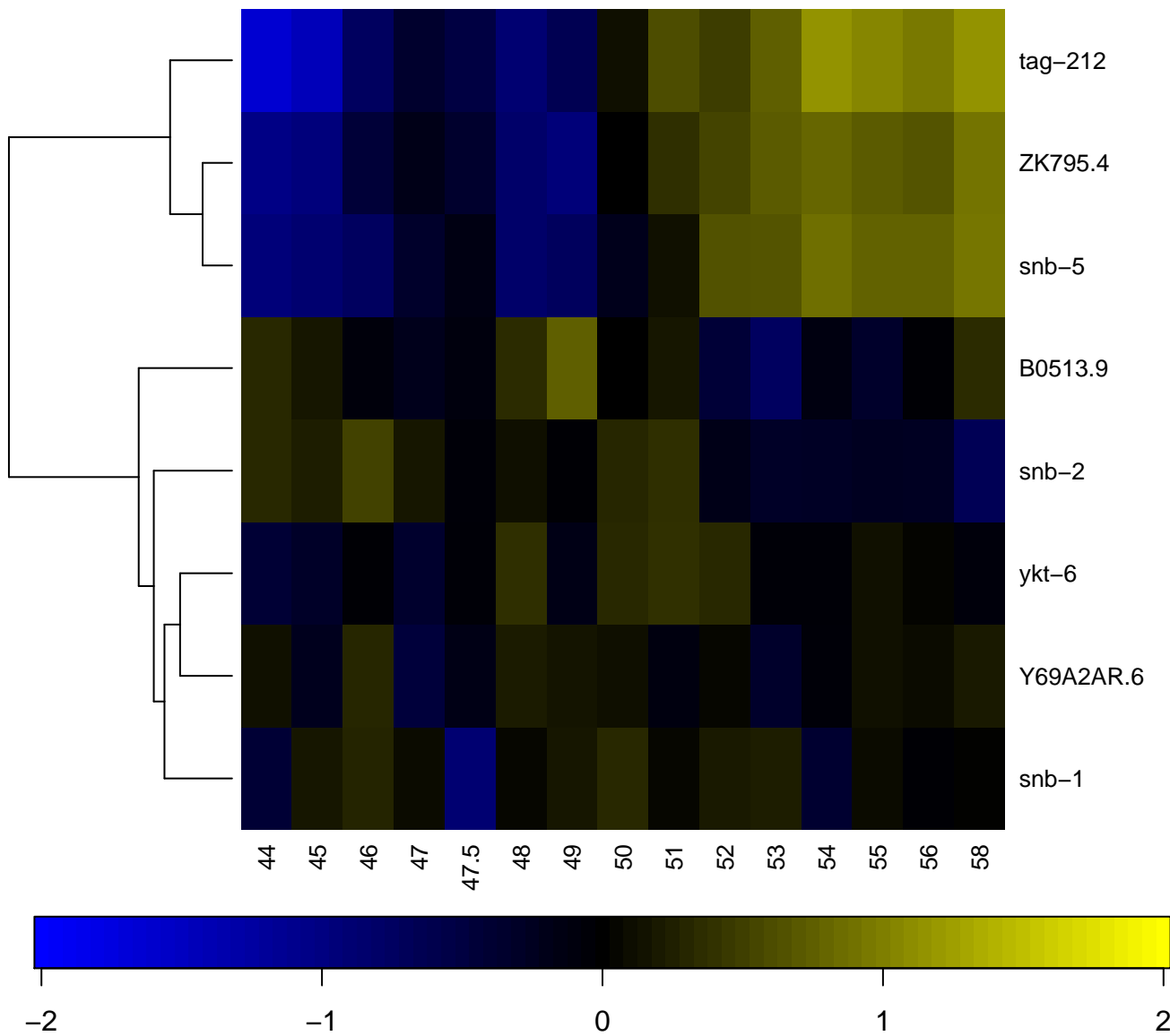
Sulfotransferase family



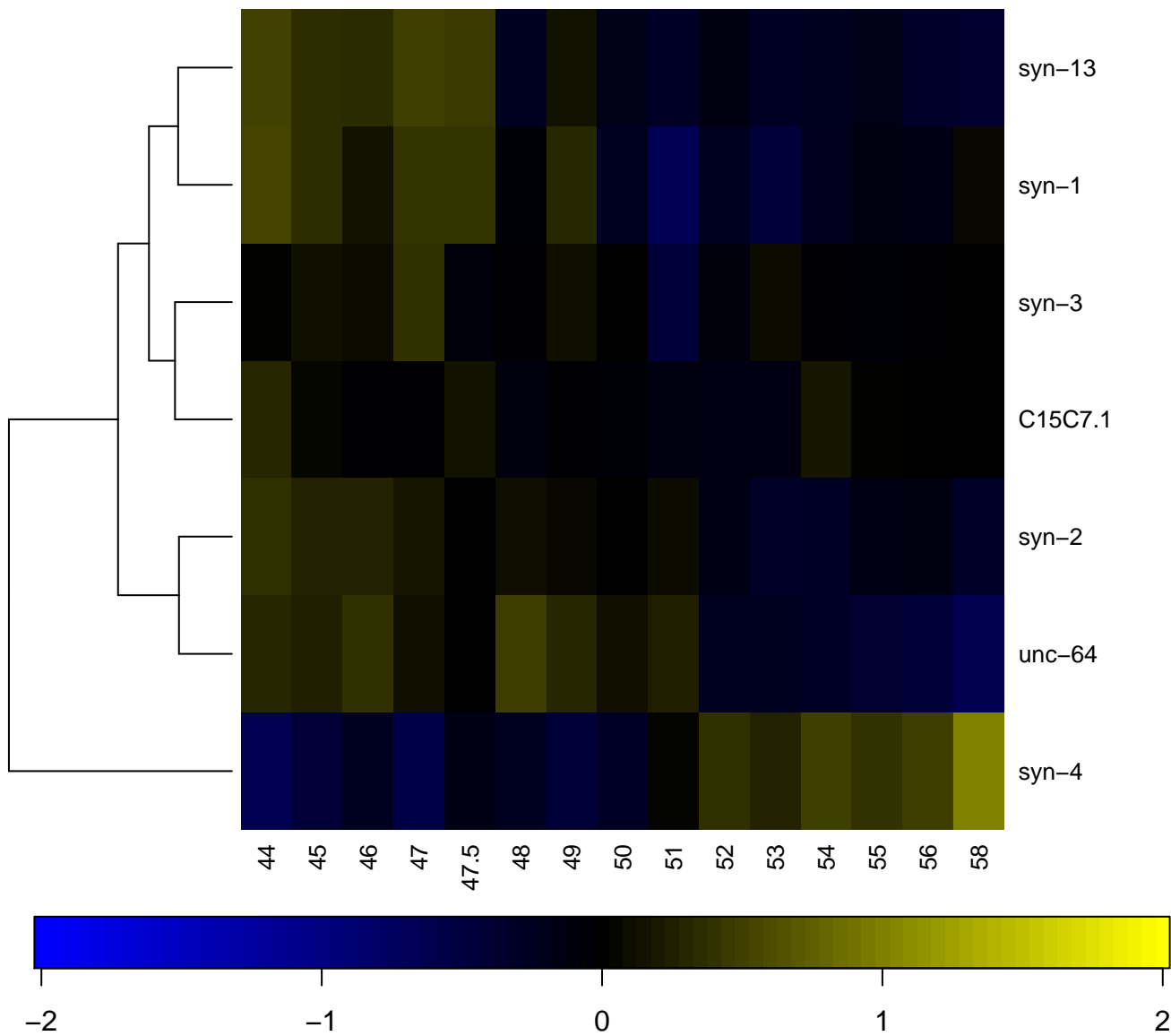
Sushi domain (SCR repeat)



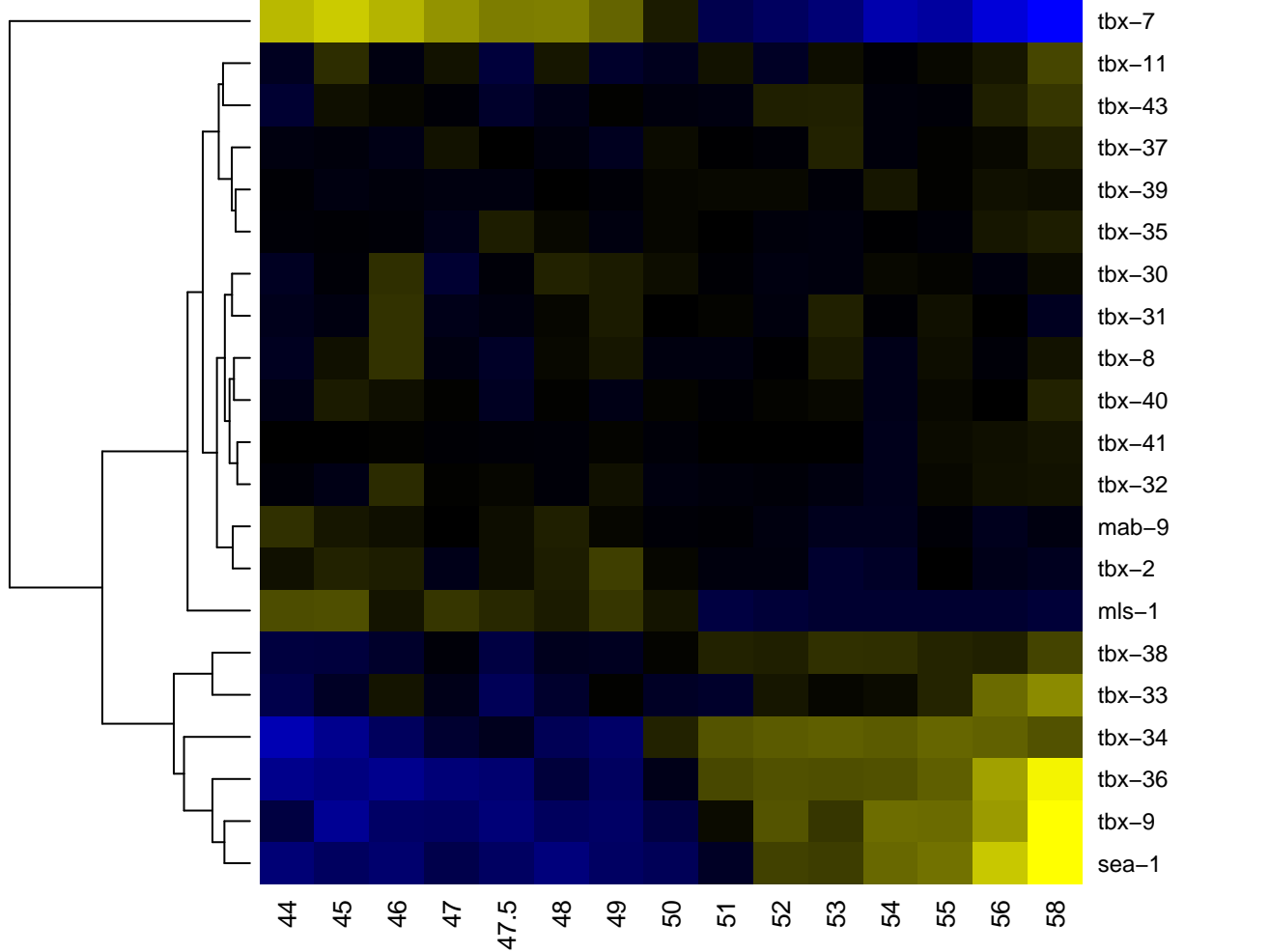
Synaptobrevin



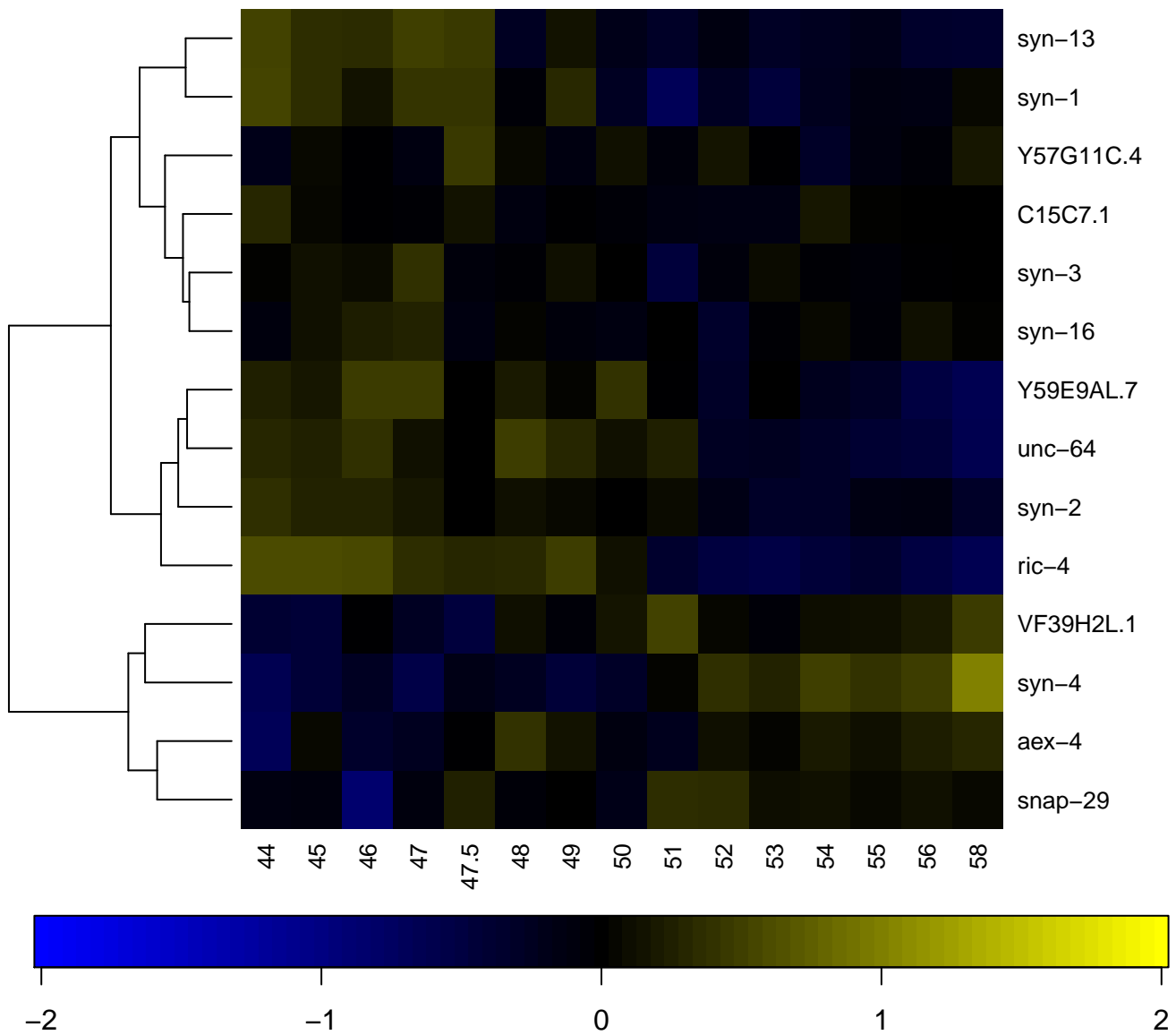
Syntaxin/epimorphin, conserved site



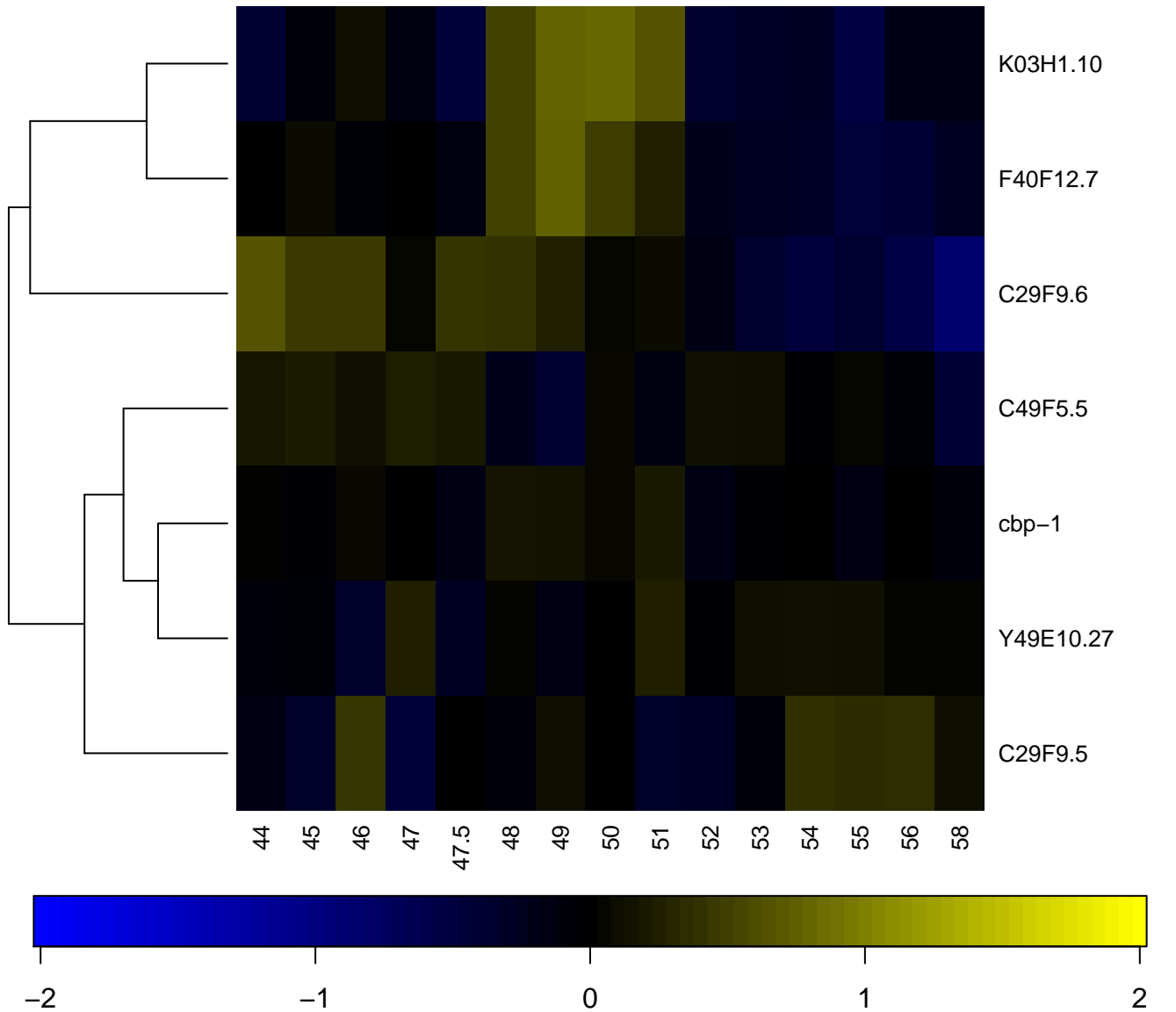
T-box



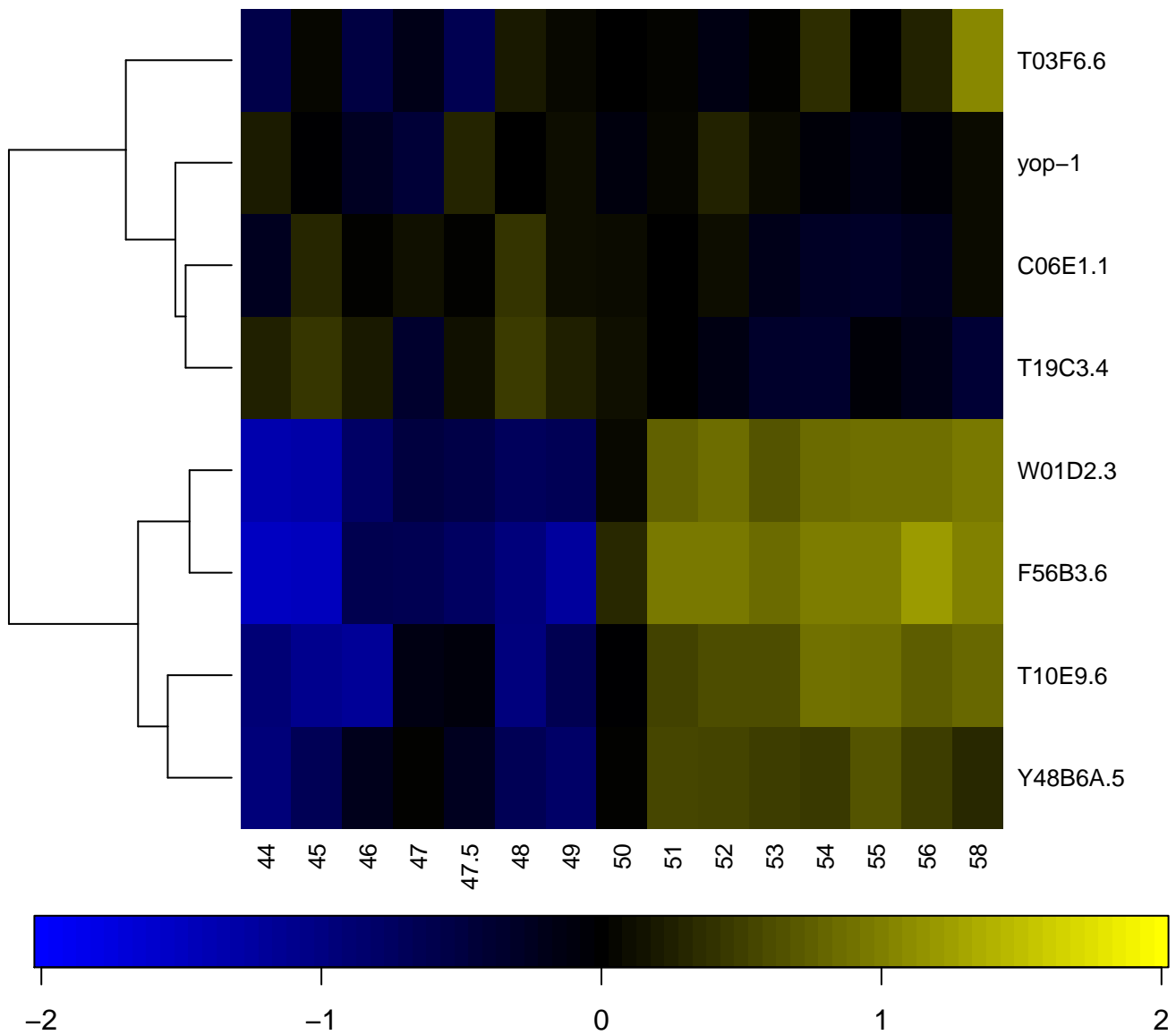
Target SNARE coiled-coil domain



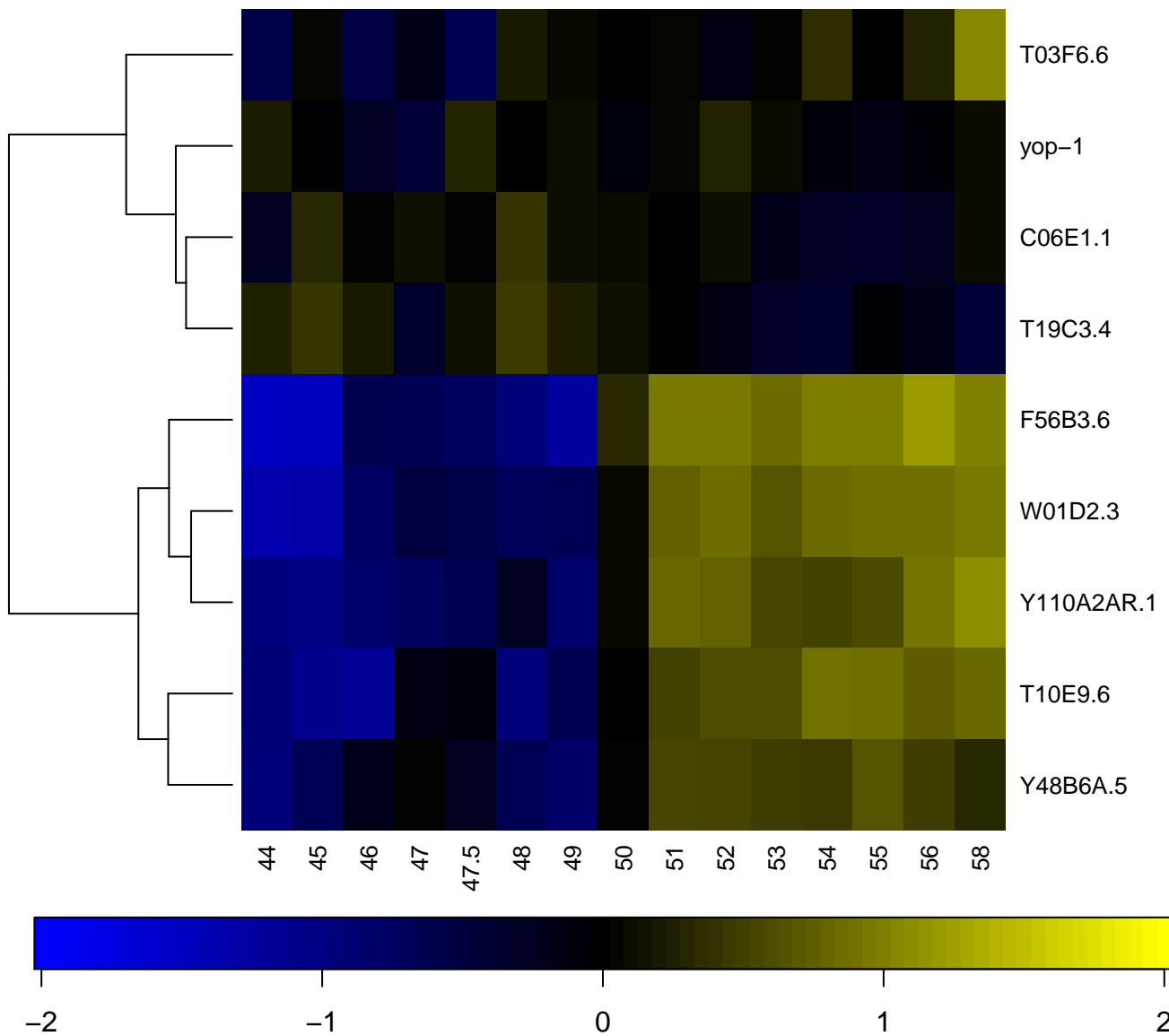
TAZ zinc finger



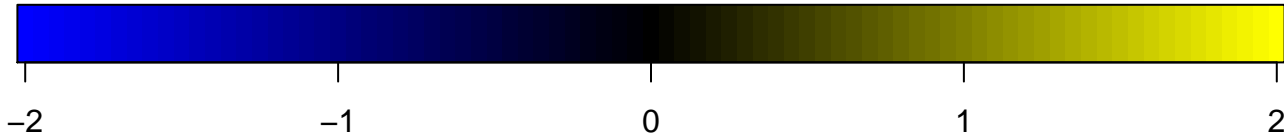
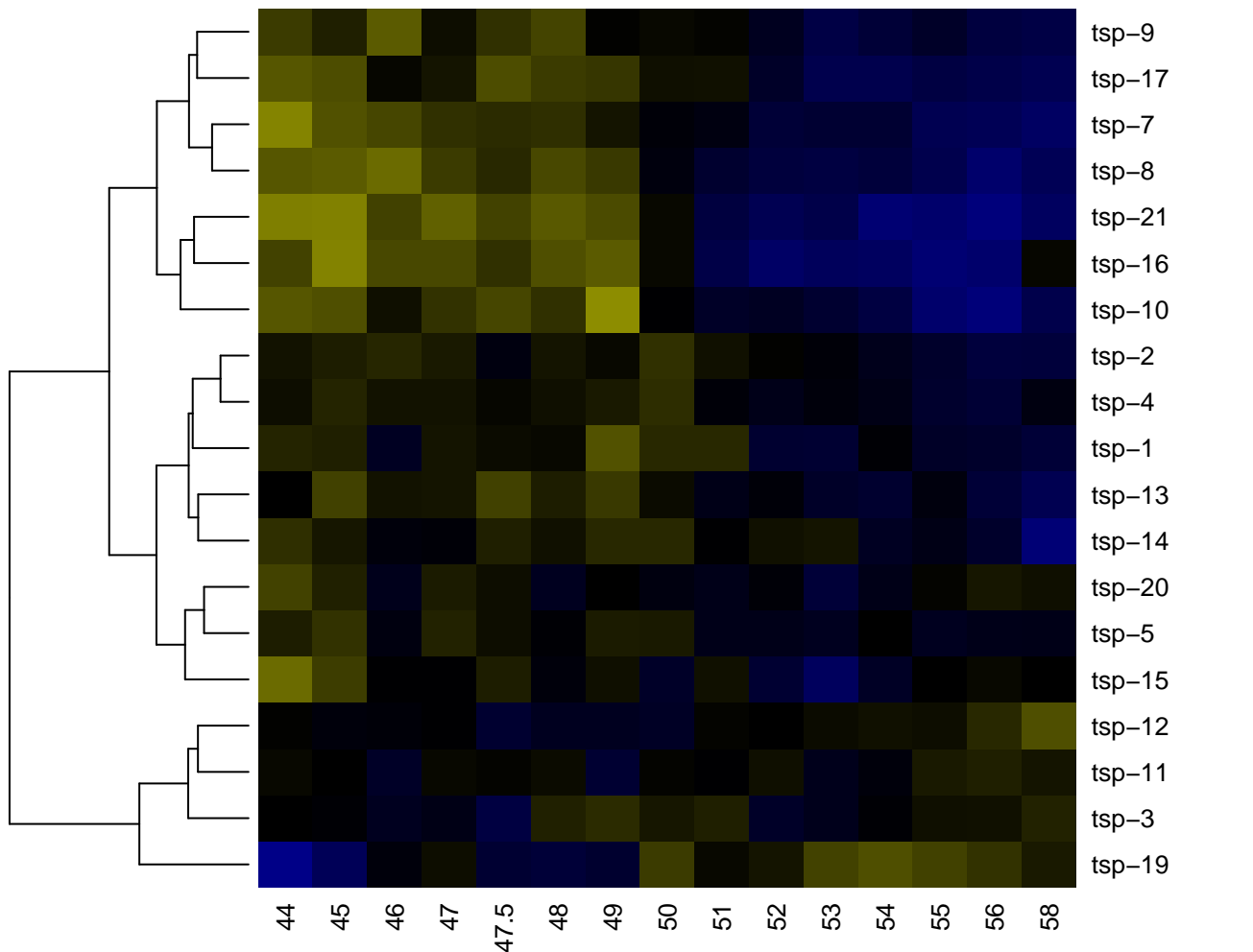
TB2/DP1, HVA22 family



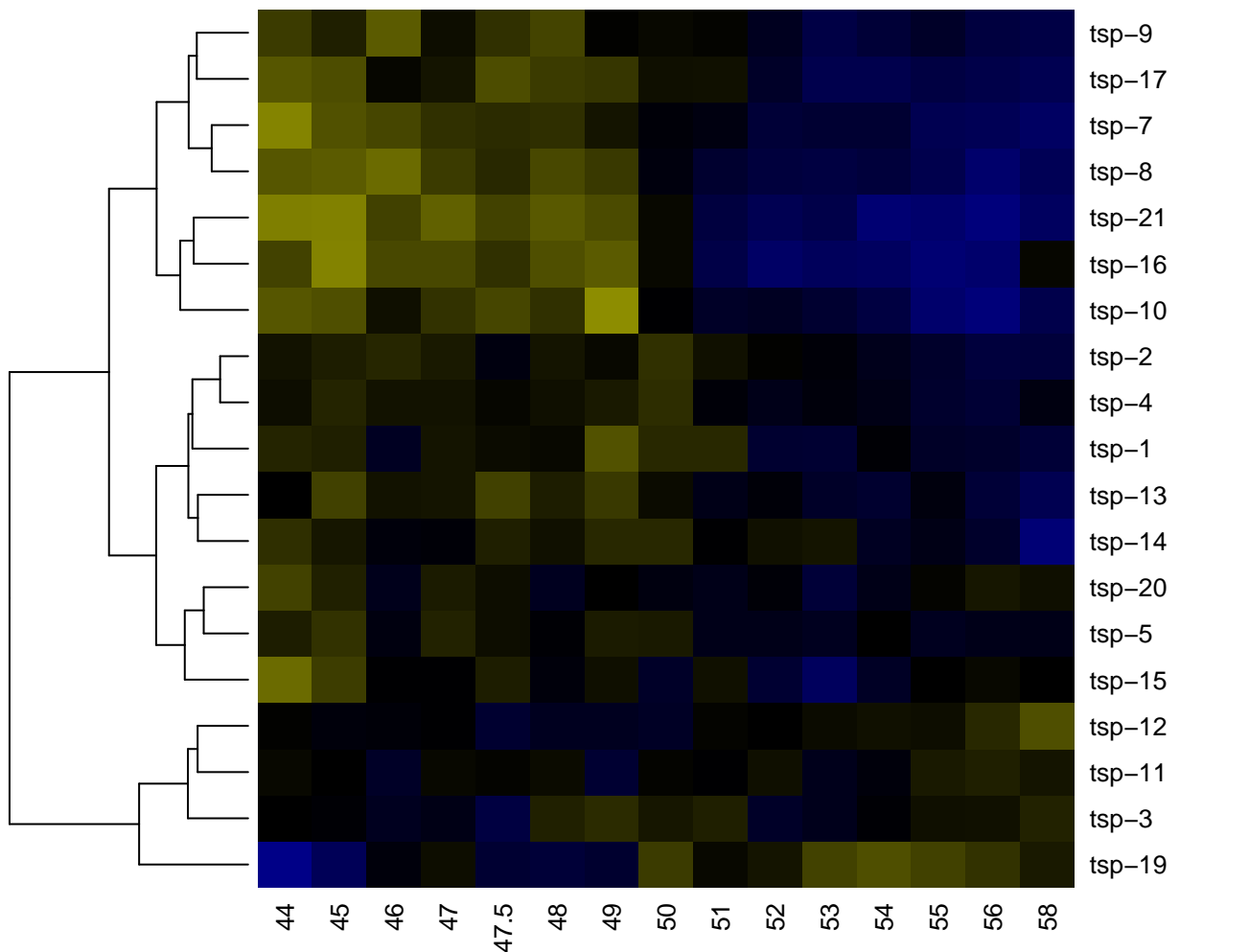
TB2/DP1/HVA22 related protein



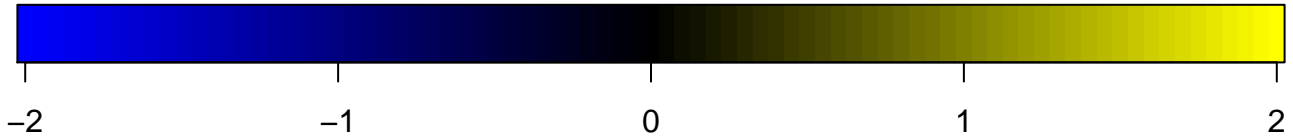
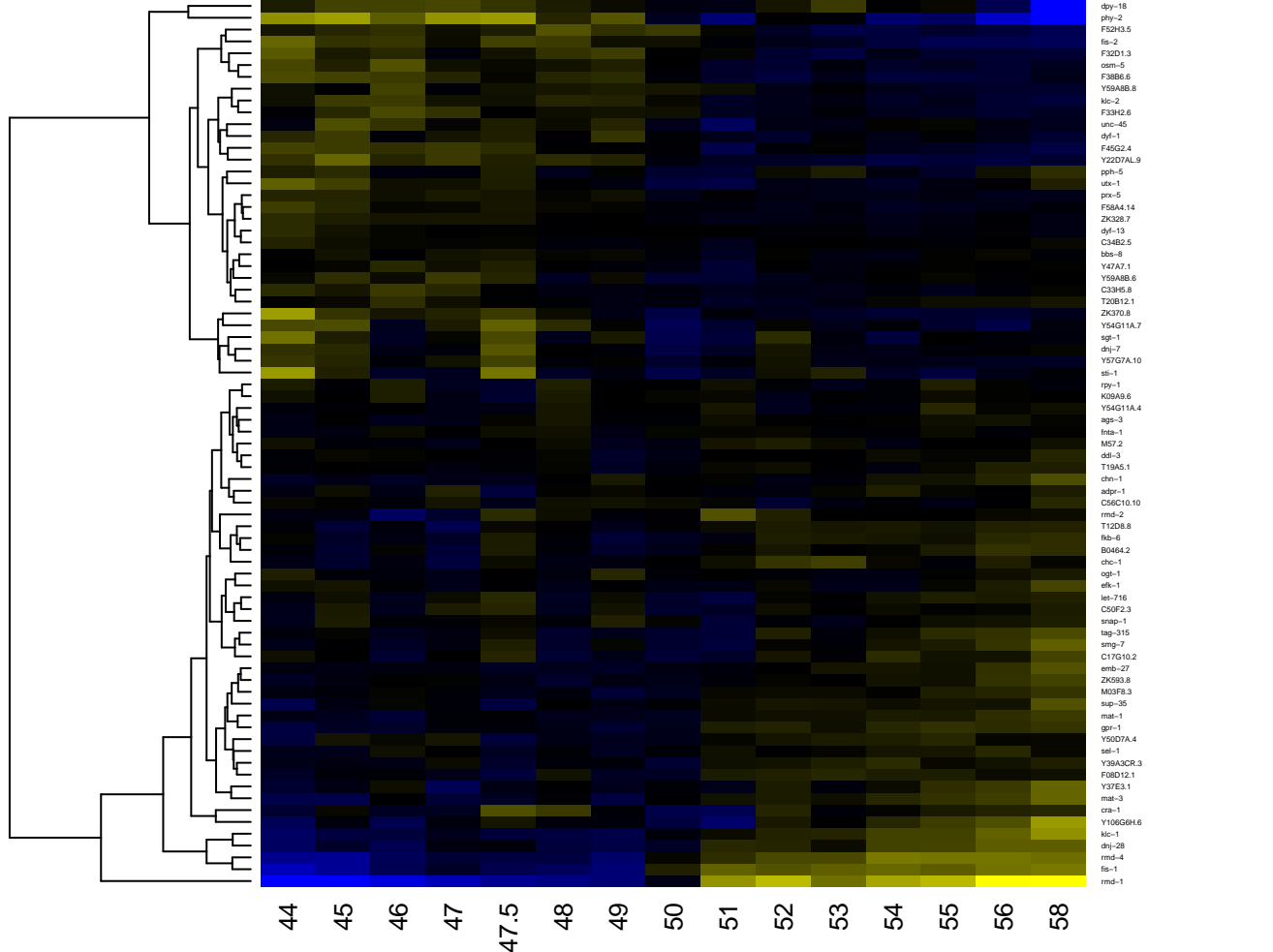
Tetraspanin



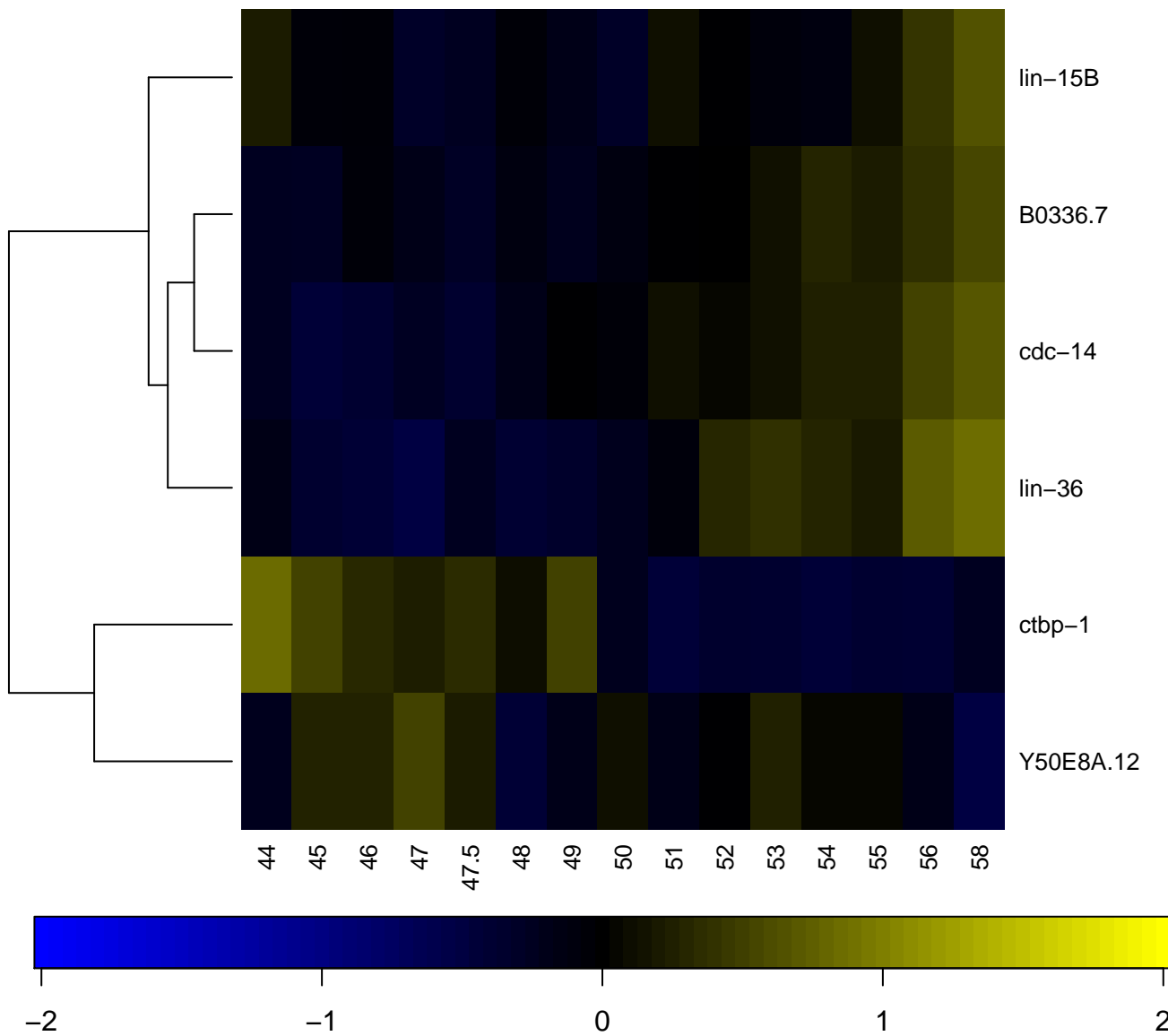
Tetraspanin family



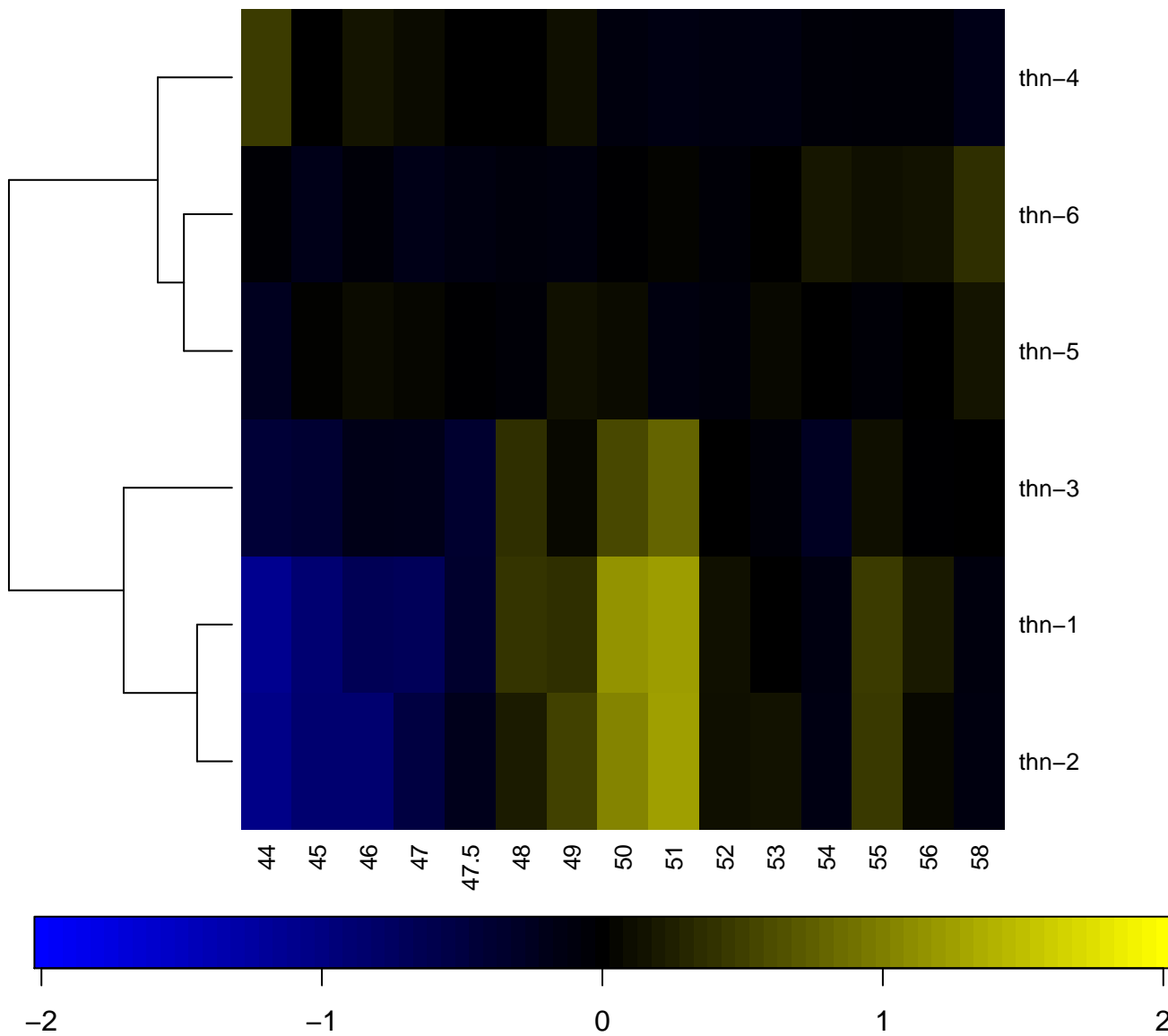
Tetratricopeptide-like helical



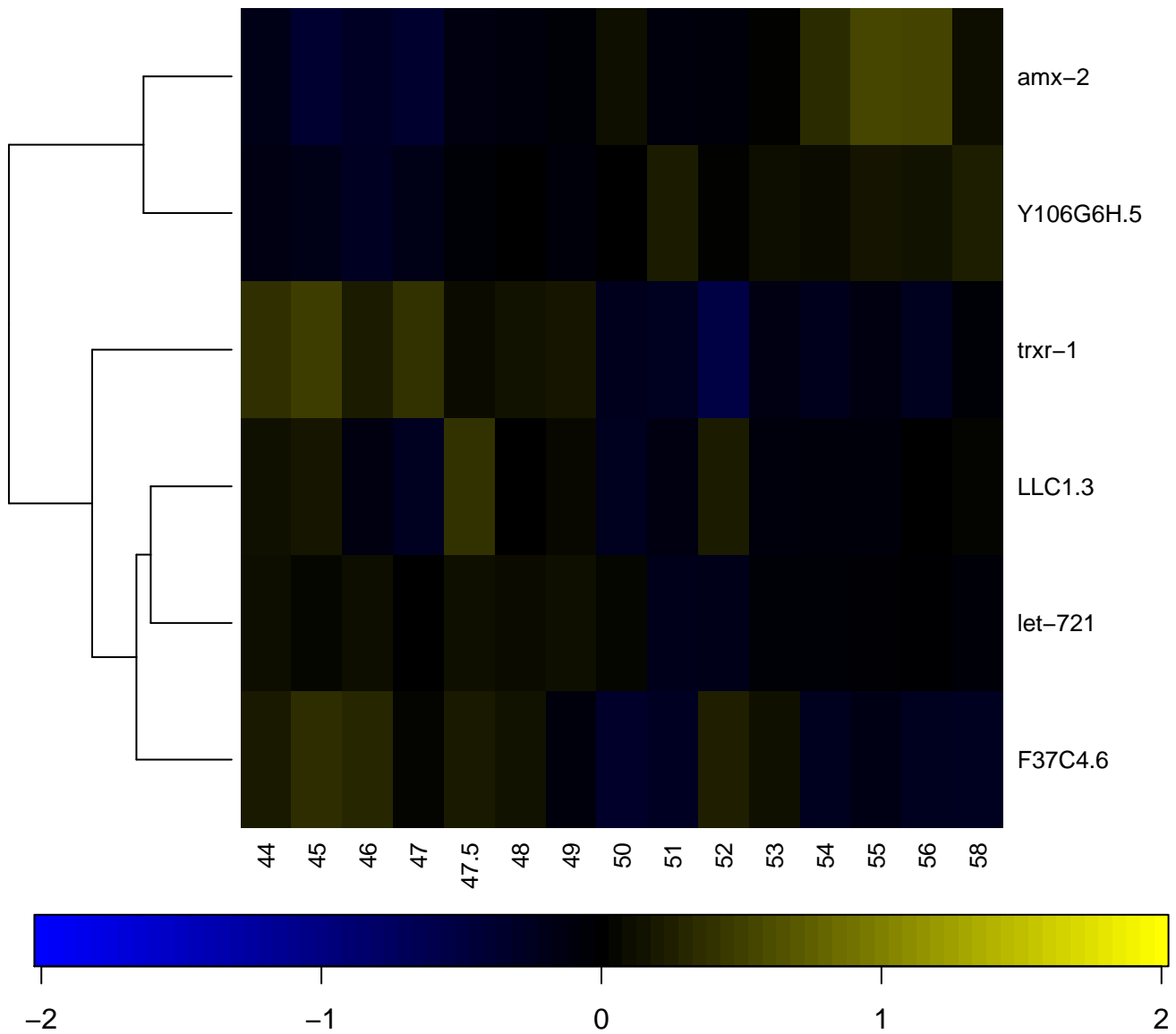
THAP domain



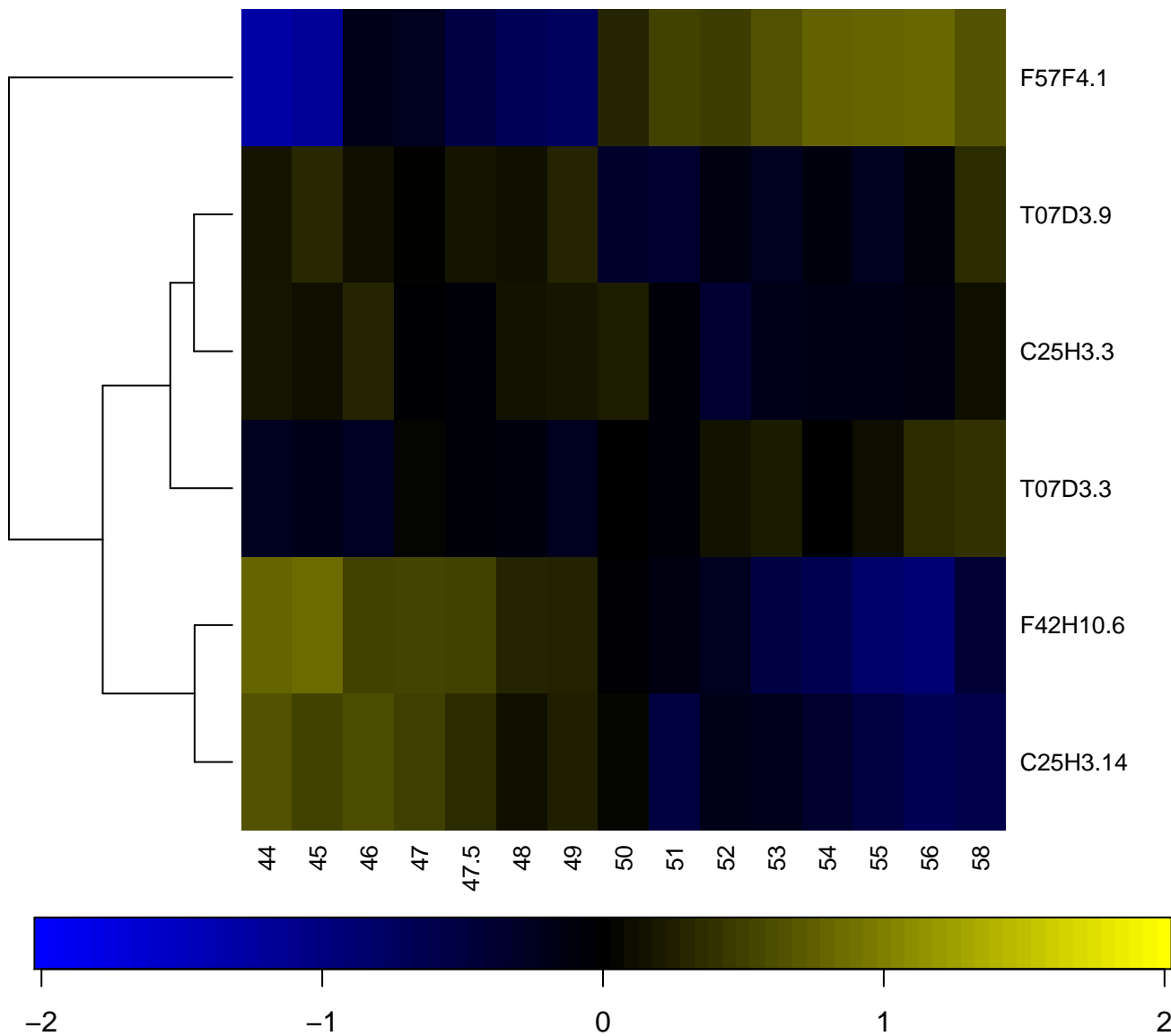
Thaumatococcus, pathogenesis-related



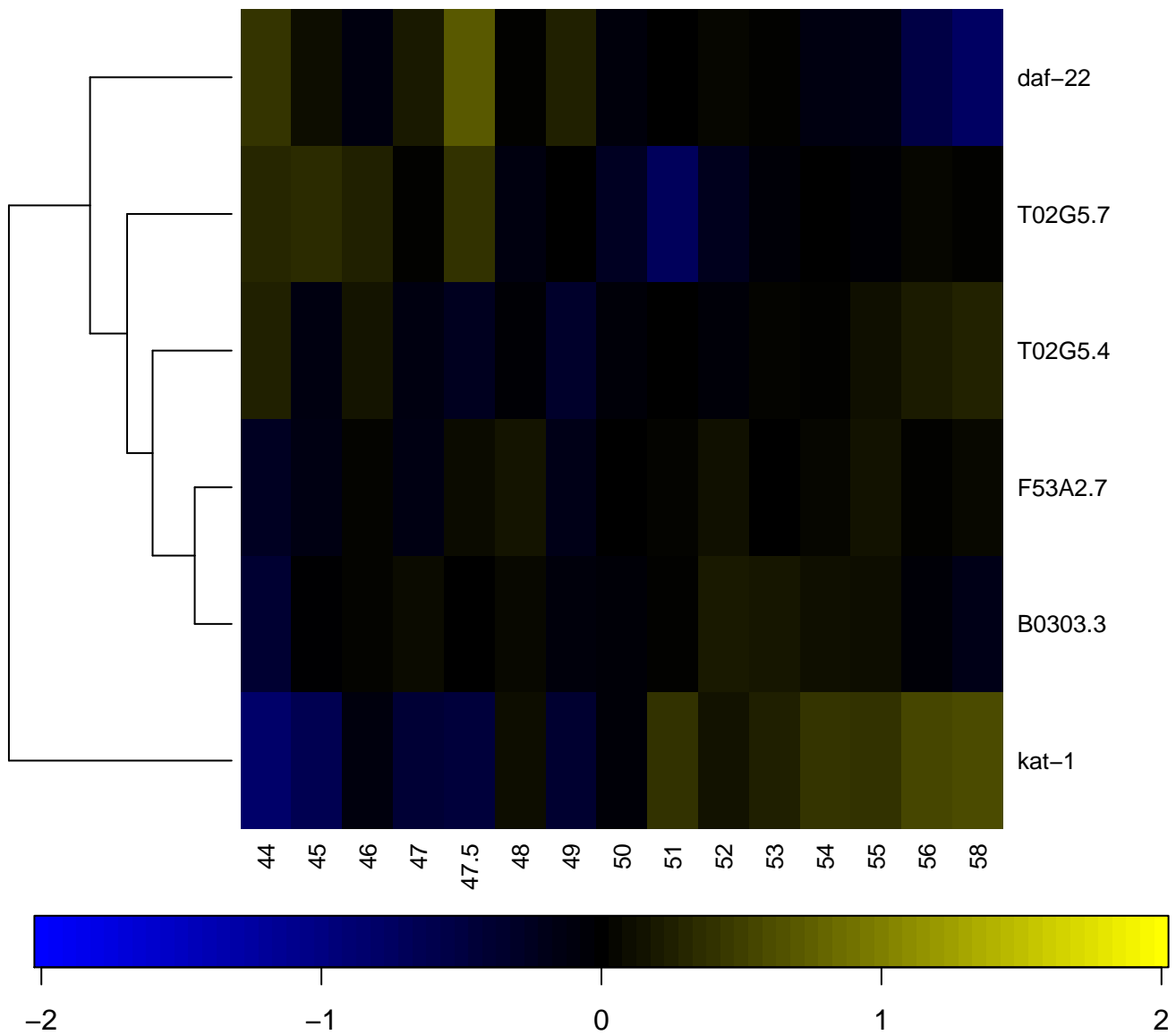
Thi4 family



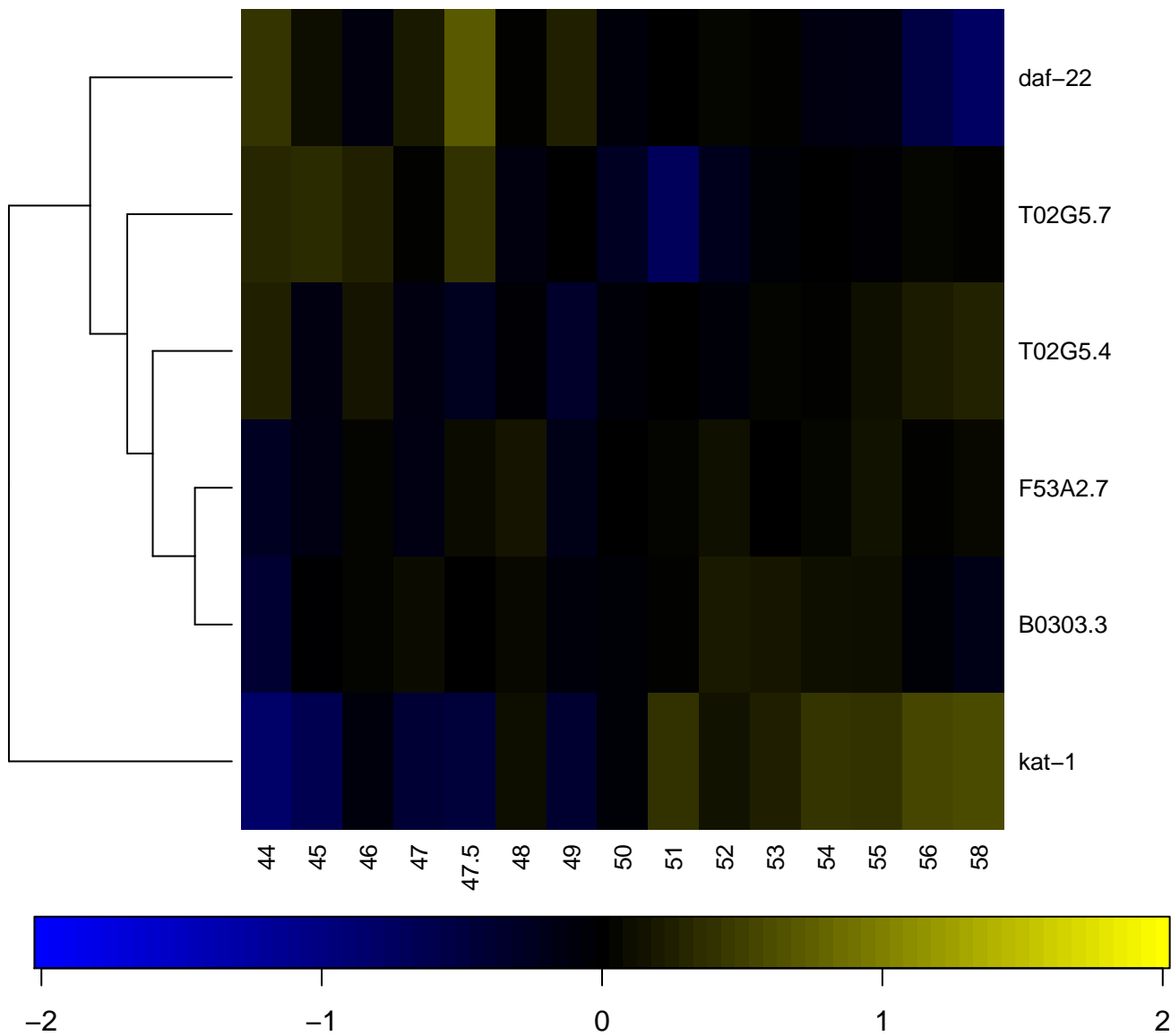
Thioesterase superfamily



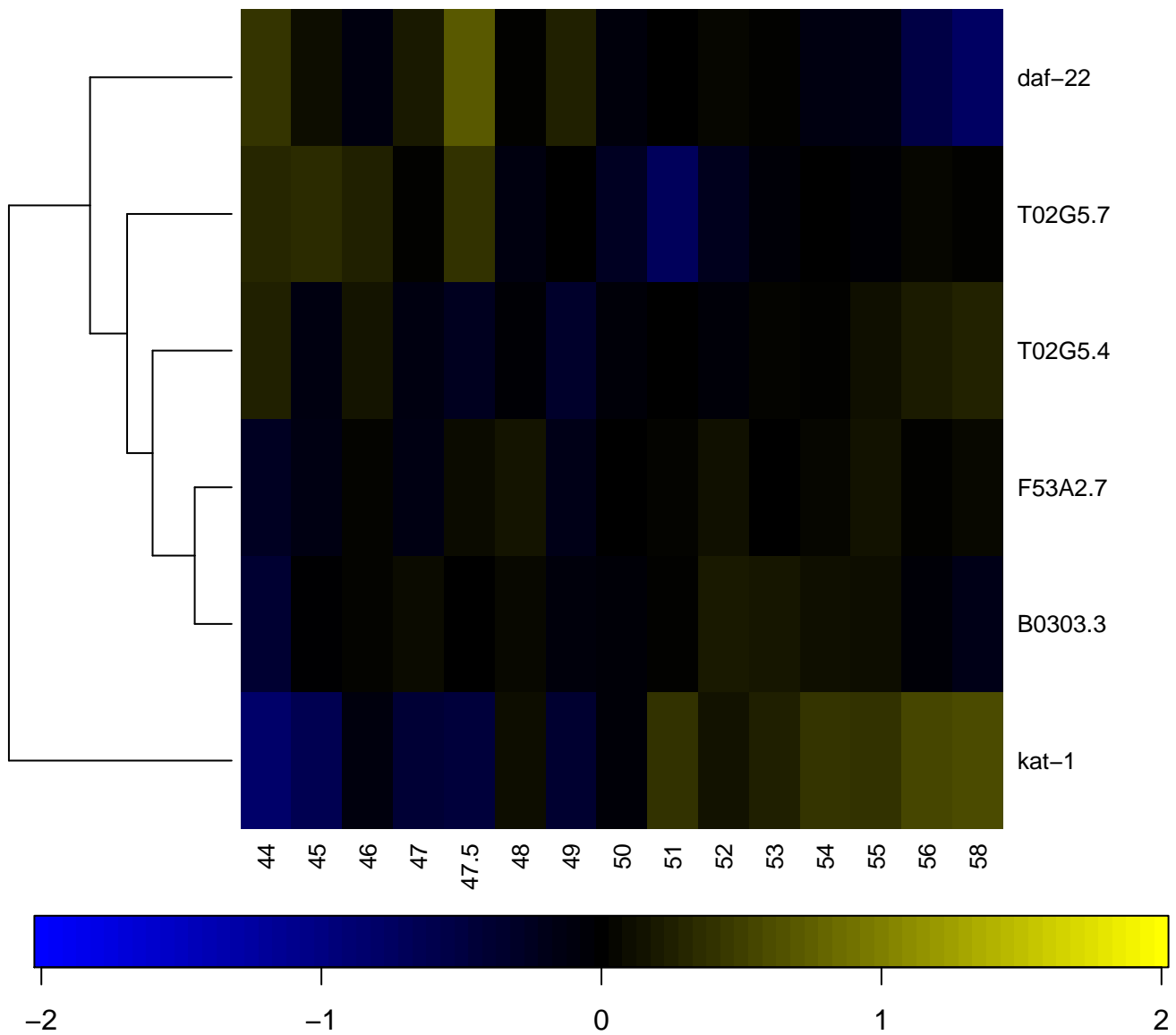
Thiolase, C-terminal



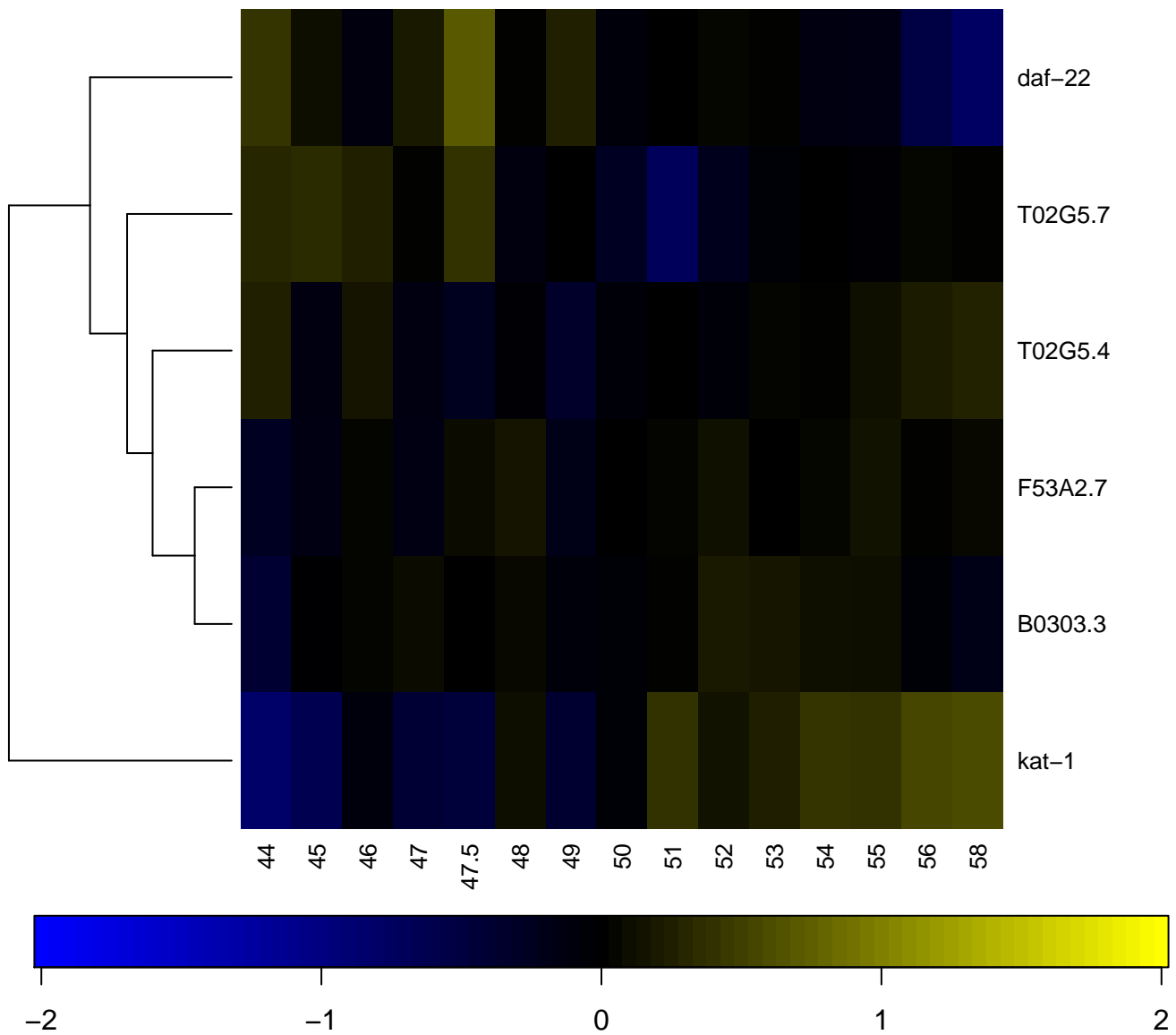
Thiolase, C-terminal domain



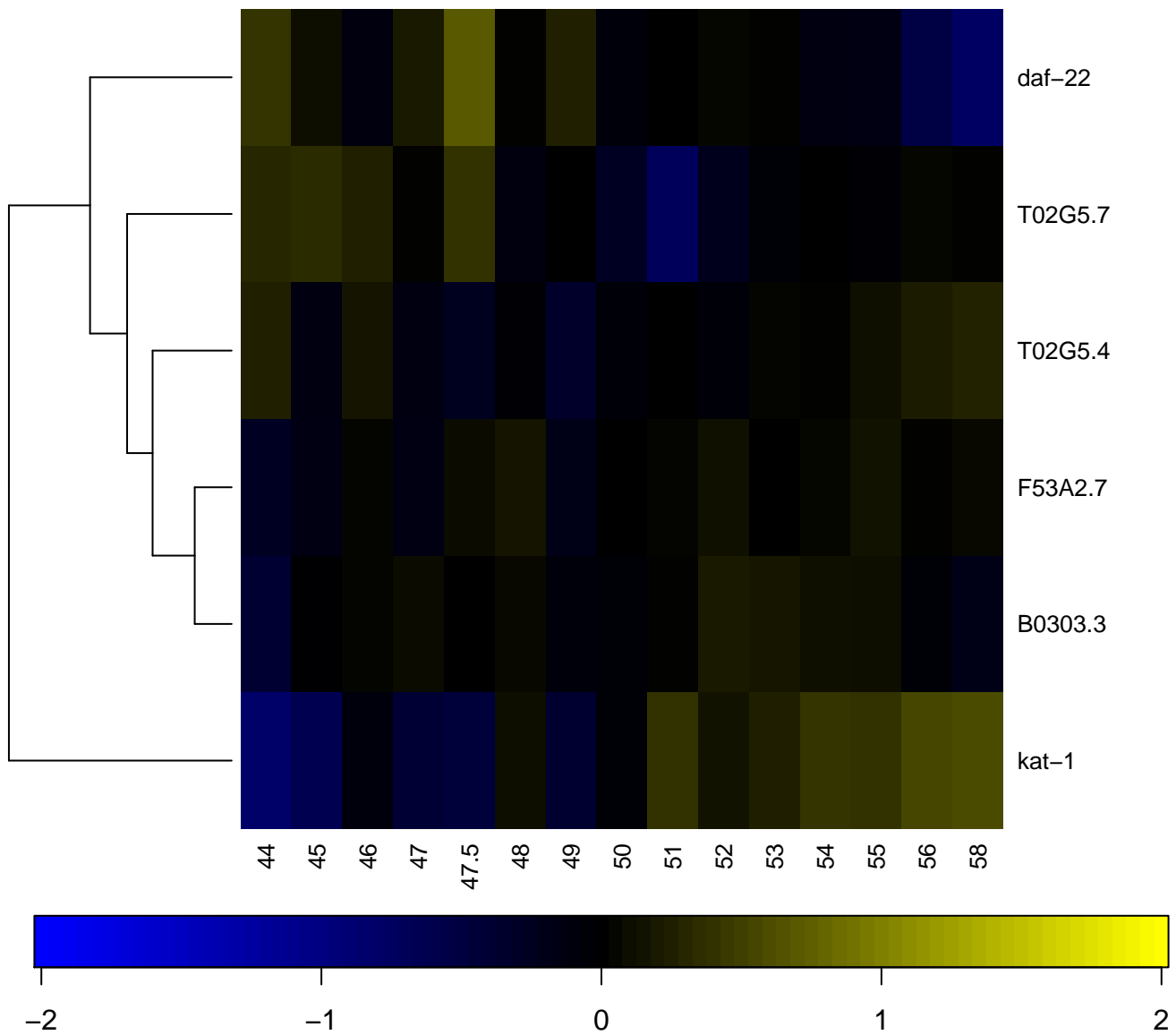
Thiolase, conserved site



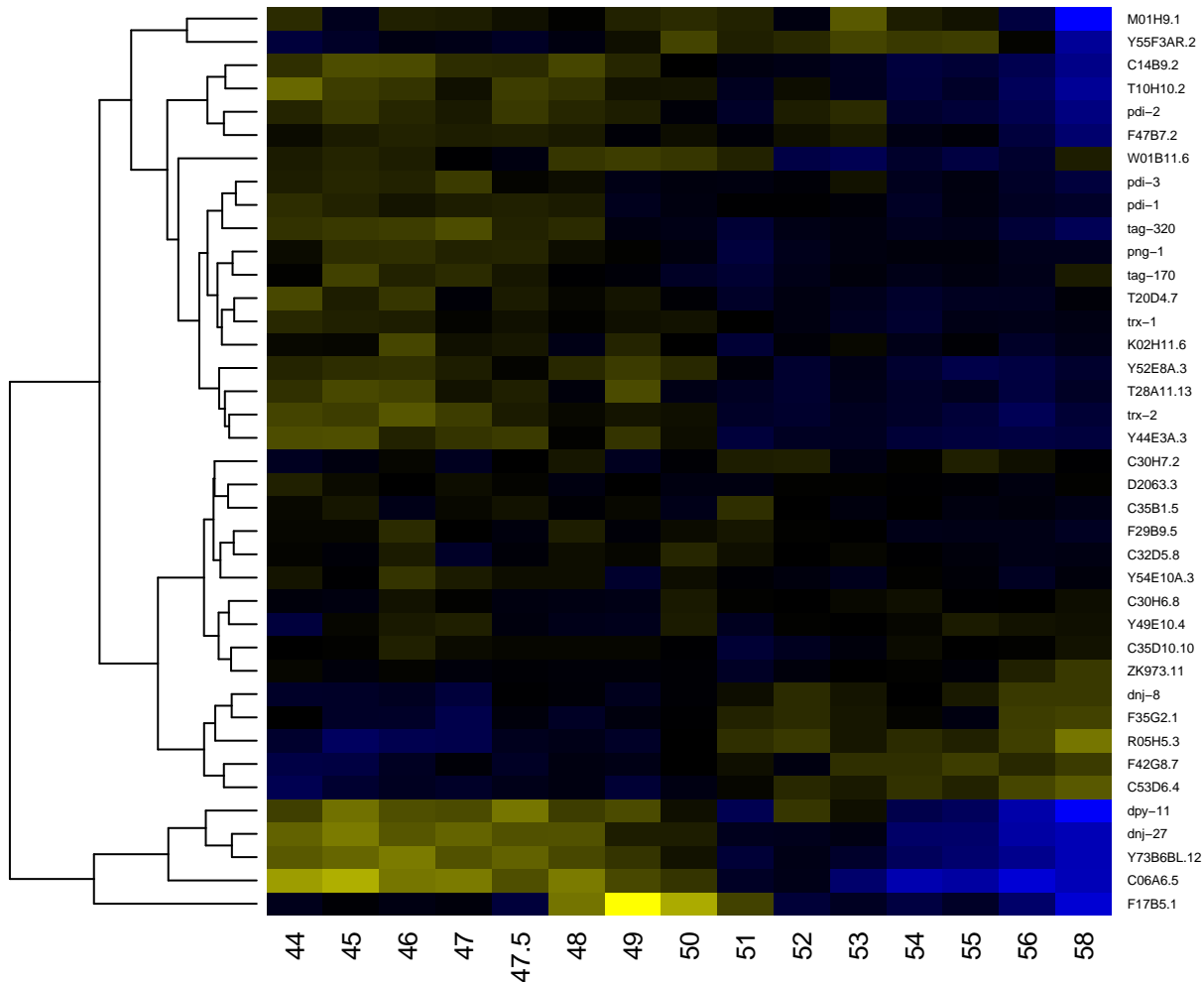
Thiolase, N-terminal



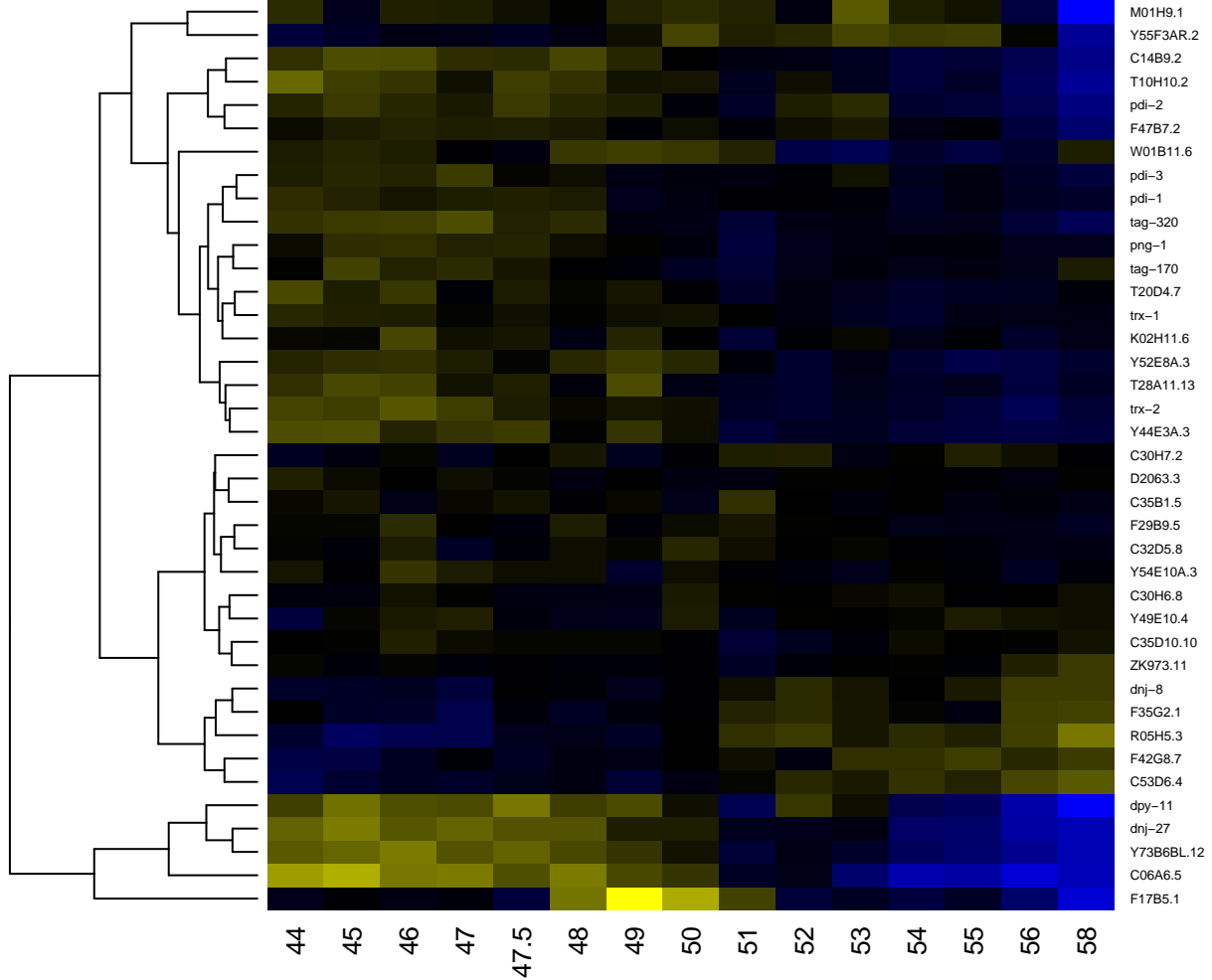
Thiolase, N-terminal domain



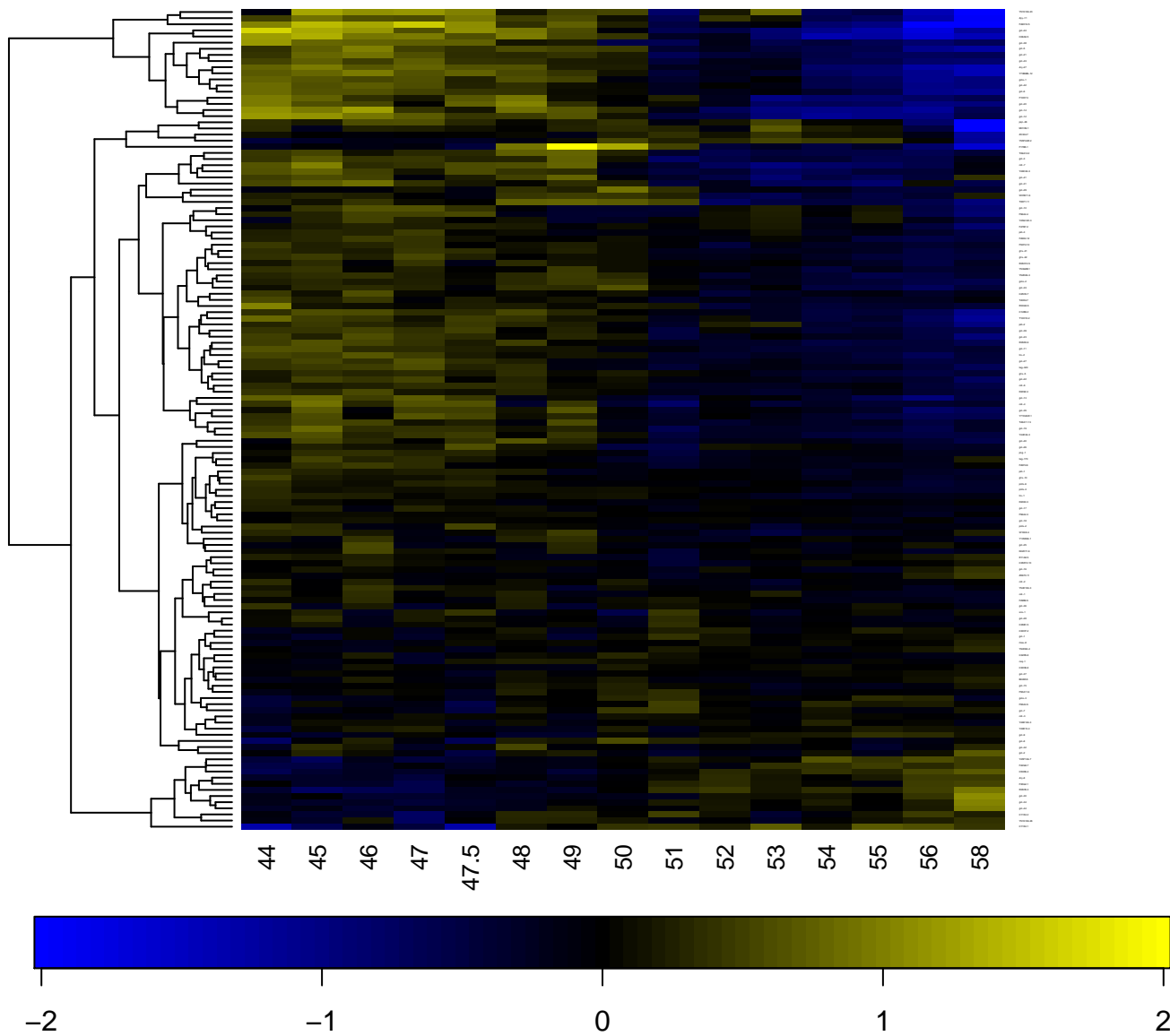
Thioredoxin



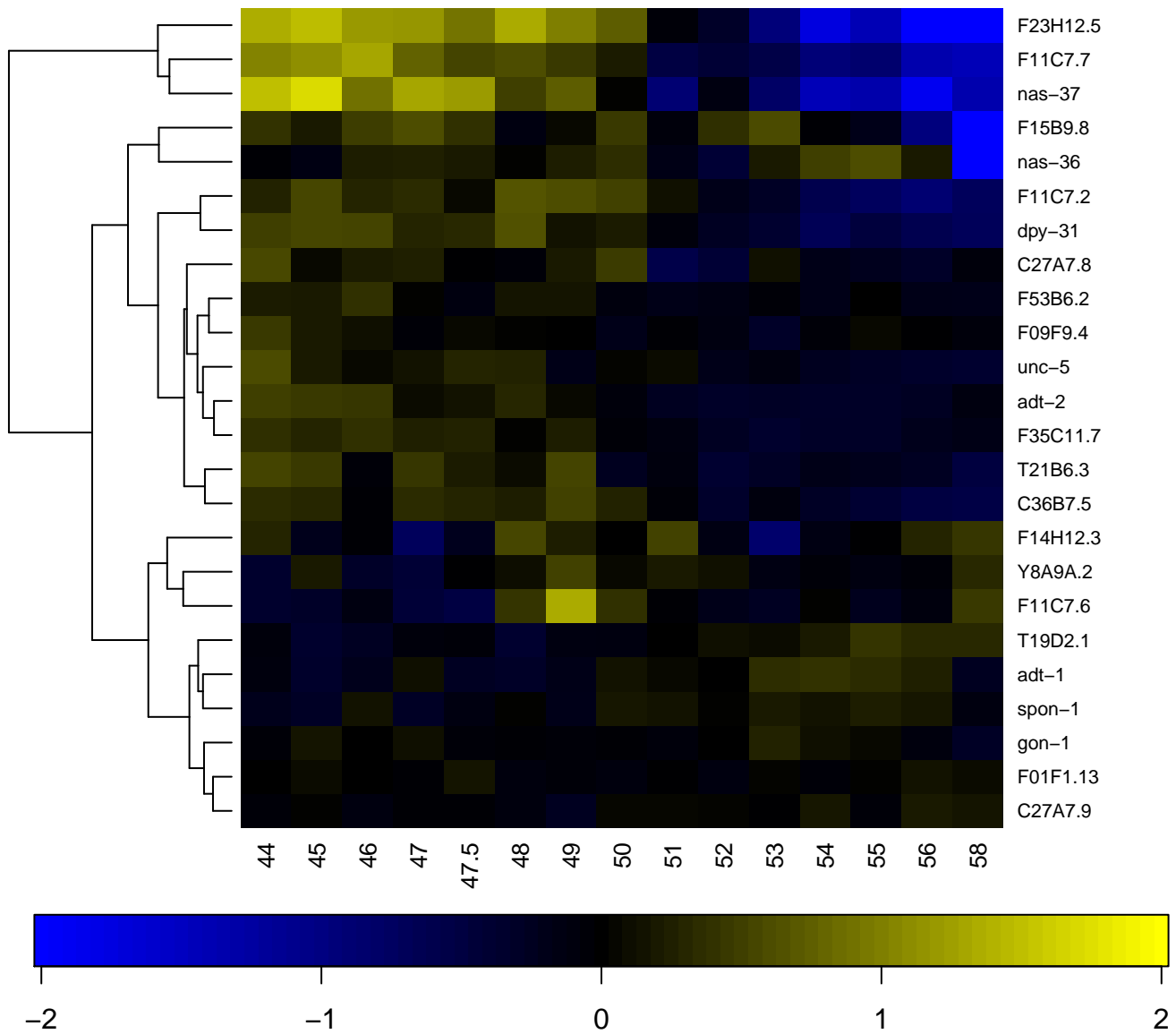
Thioredoxin domain



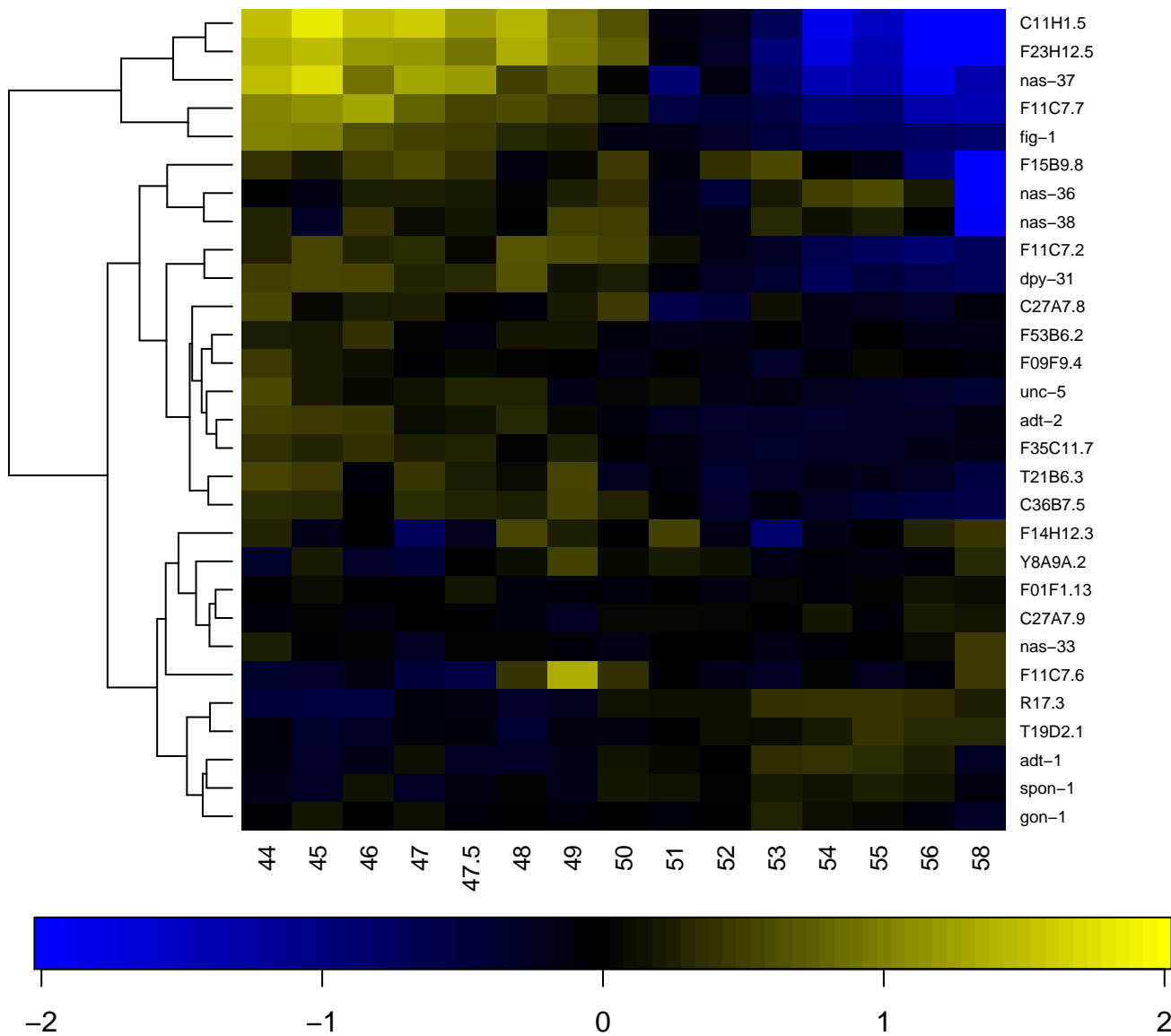
Thioredoxin fold



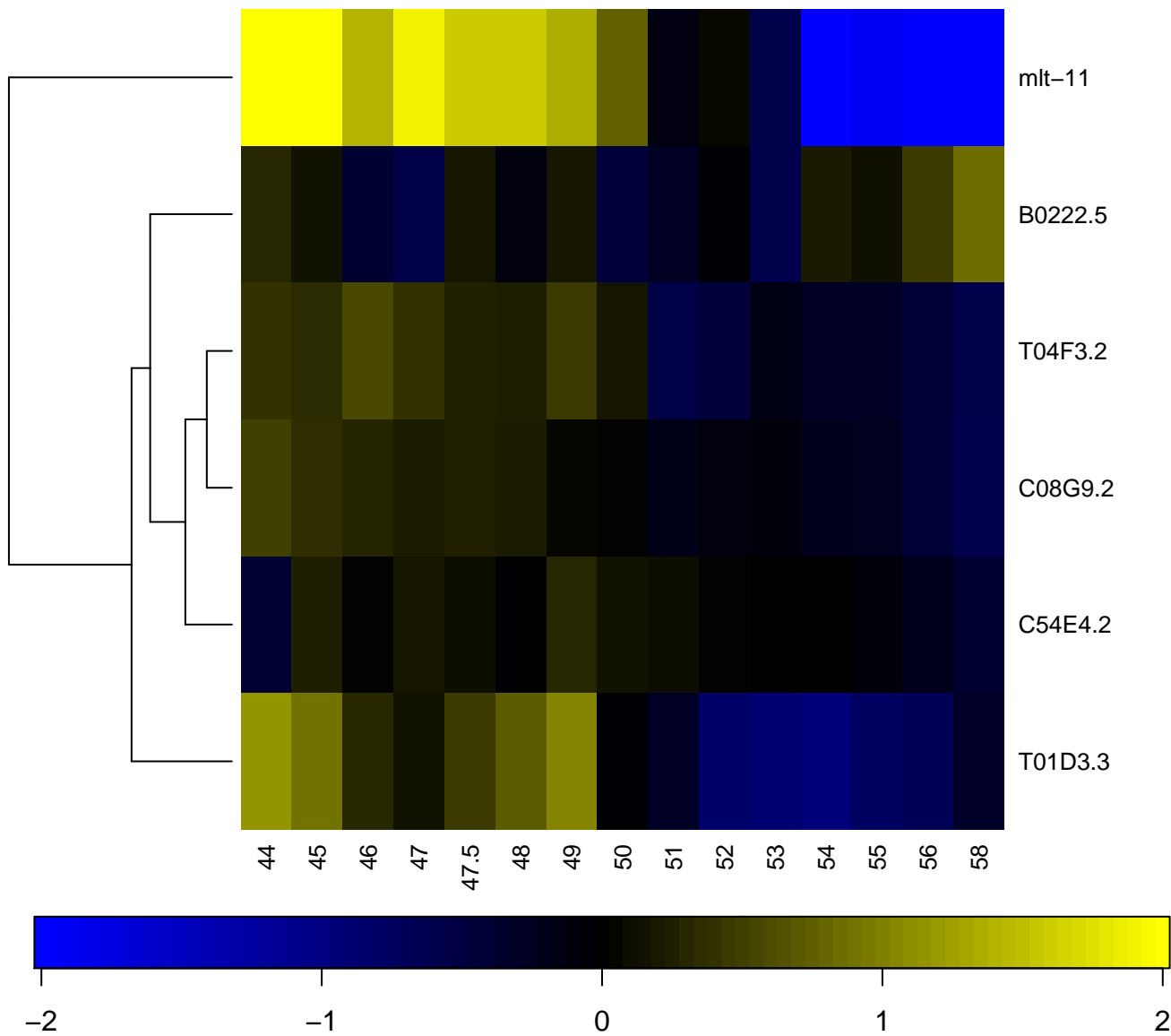
Thrombospondin type 1 domain



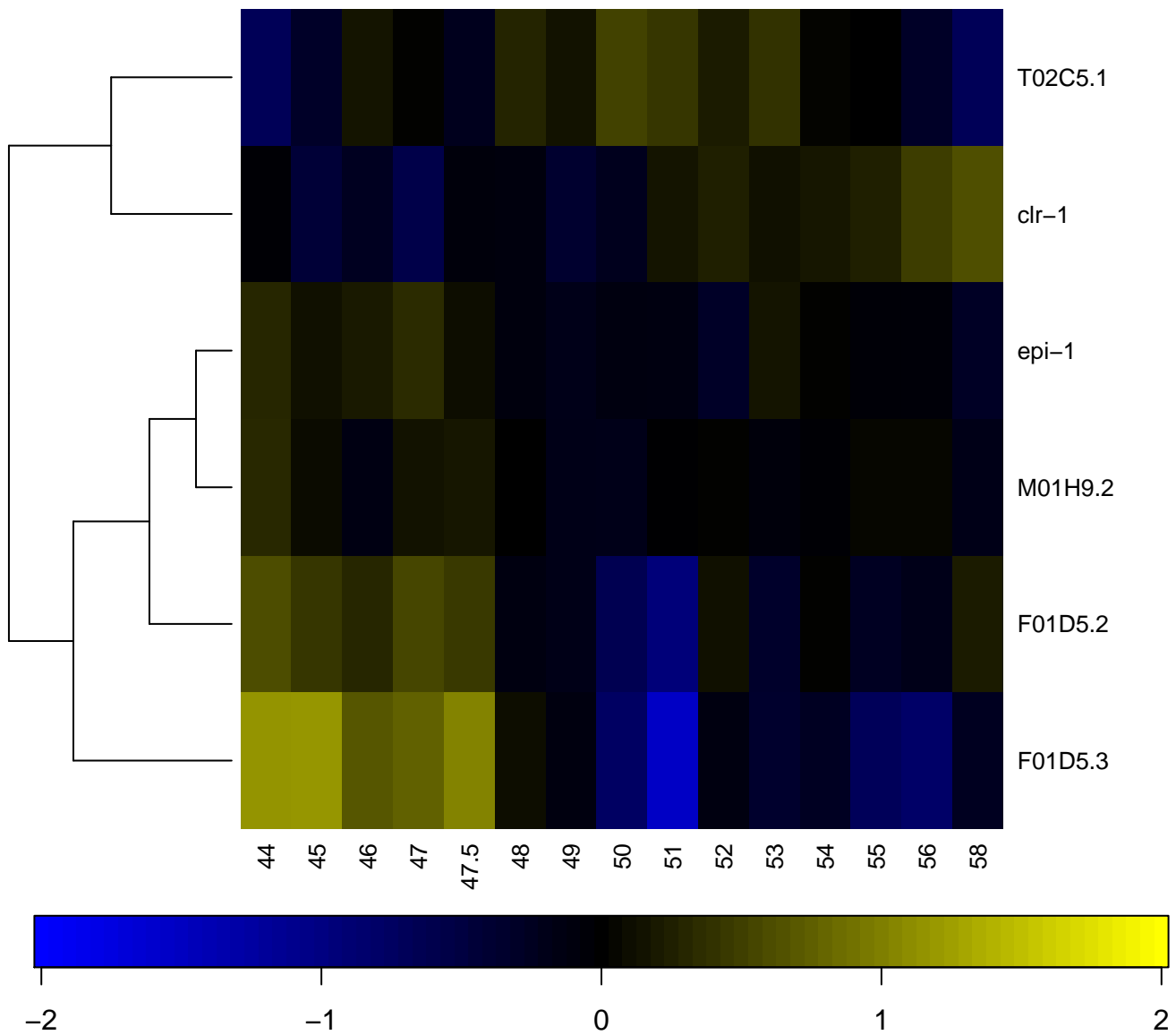
Thrombospondin, type 1 repeat



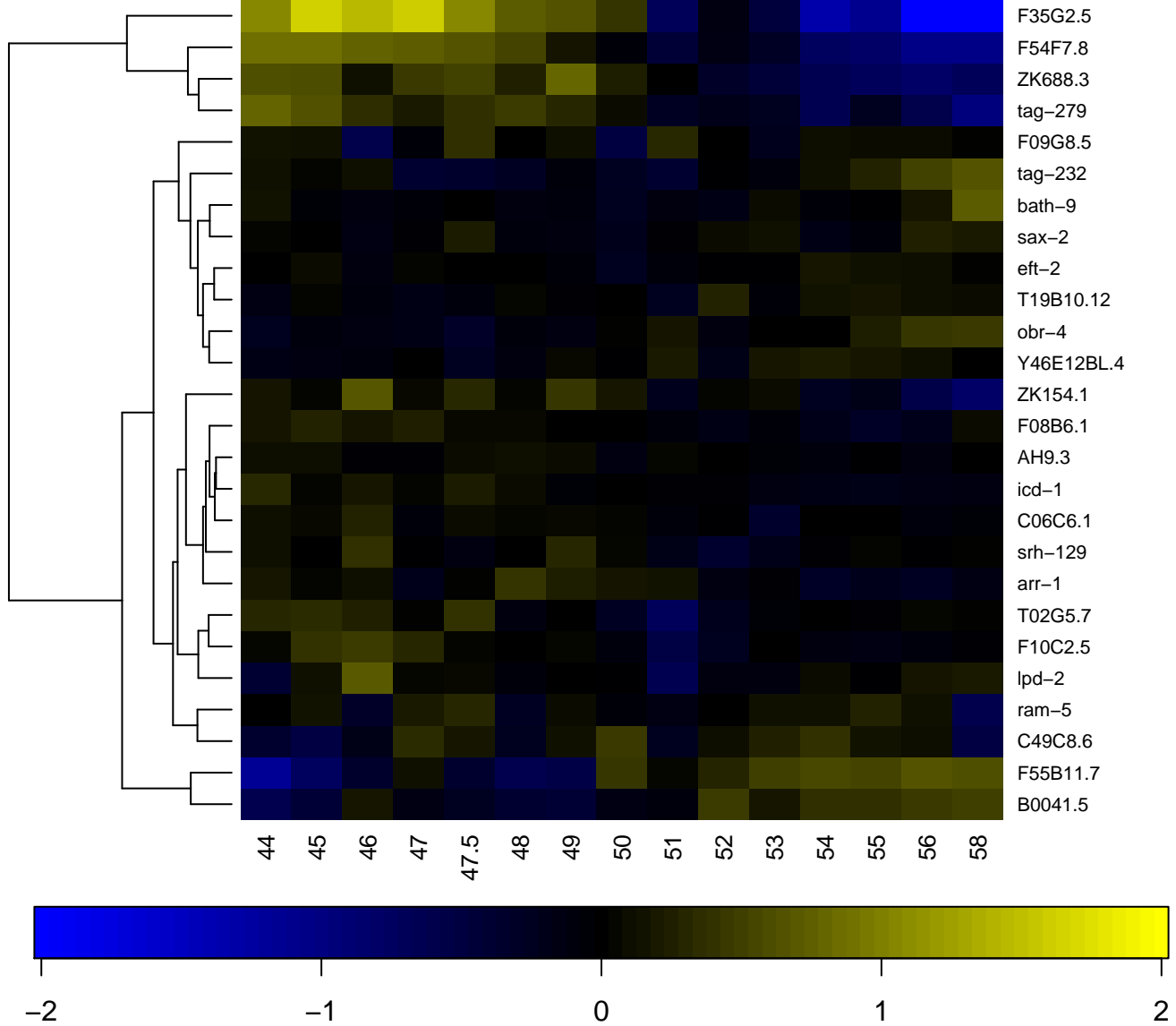
Thyroglobulin type-1



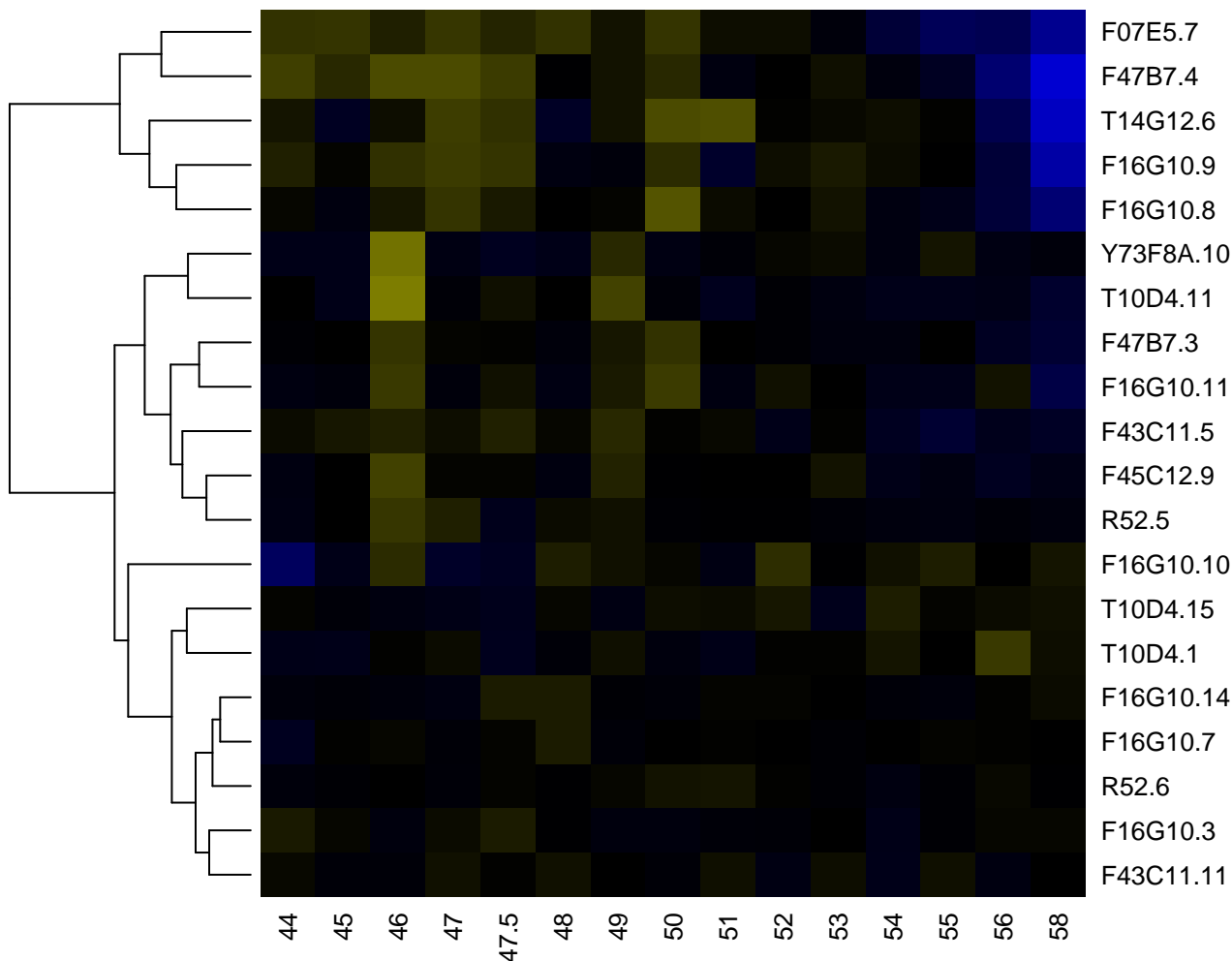
TNFR/CD27/30/40/95 cysteine-rich region



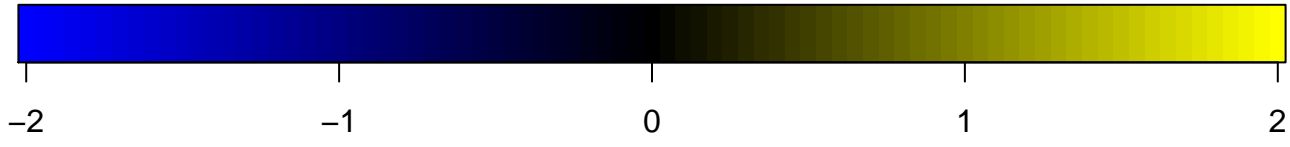
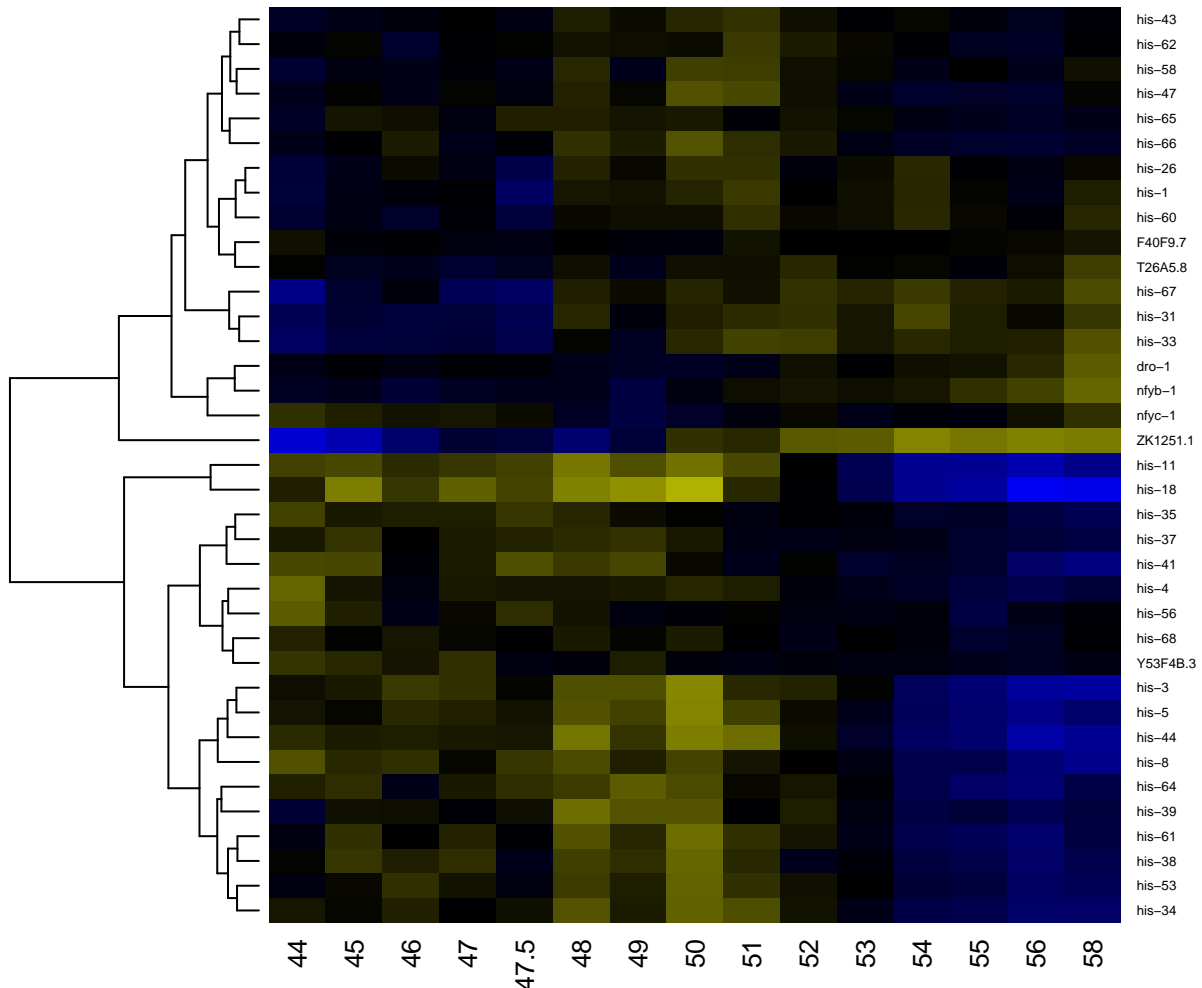
TonB box, conserved site



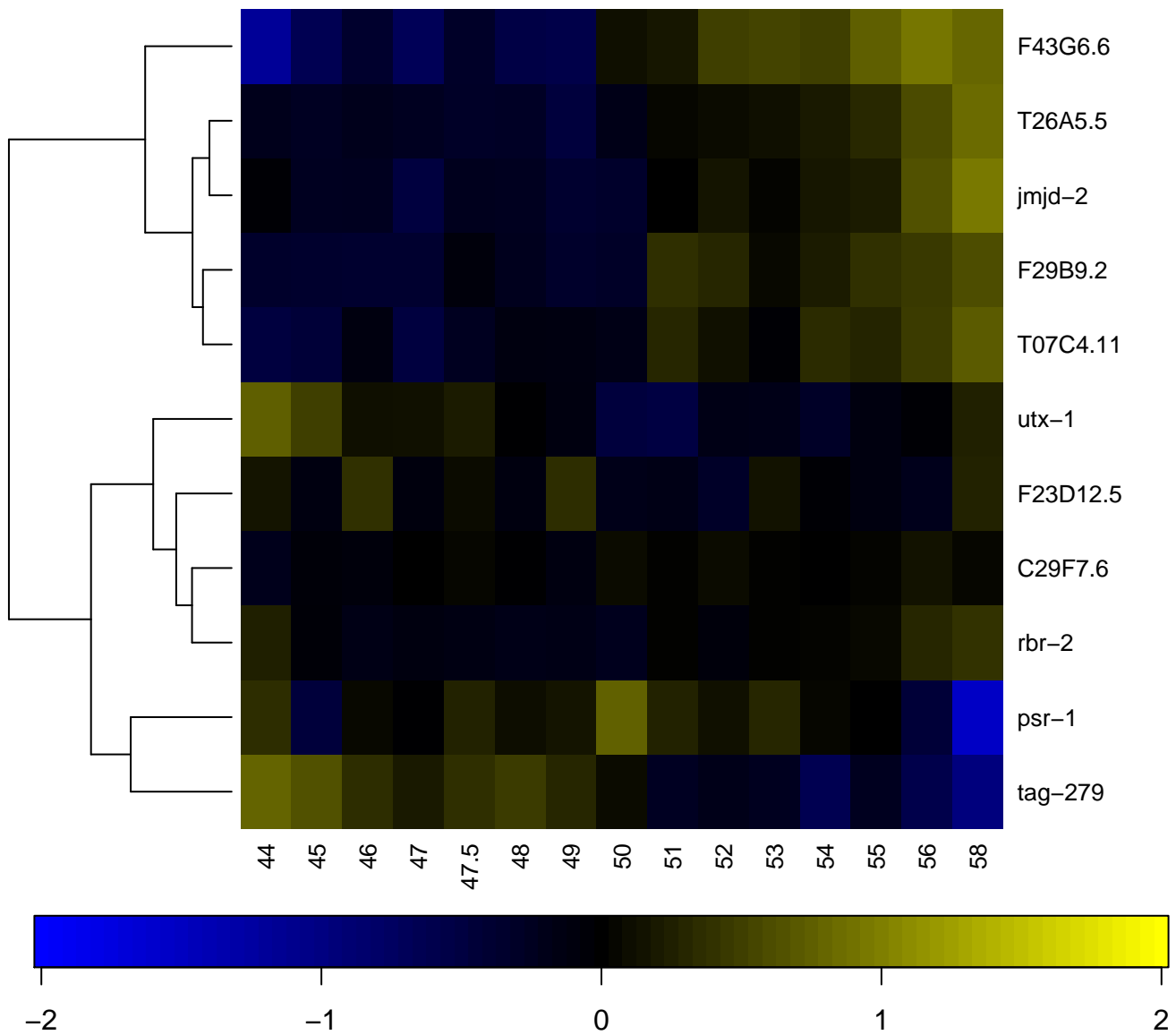
TRA-1 regulated protein R03H10.4



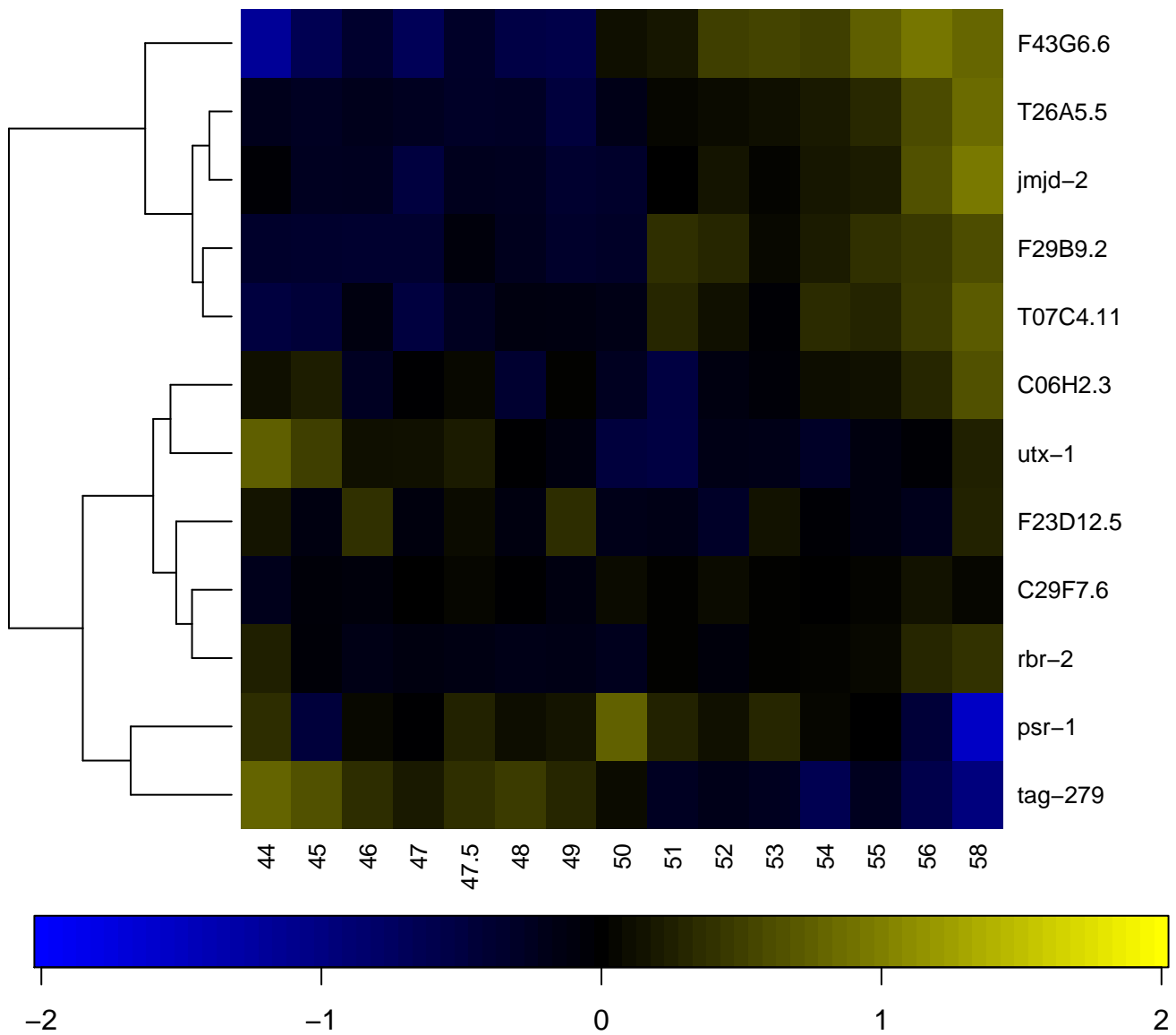
Transcription factor CBF/NF- κ B/archaeal histone



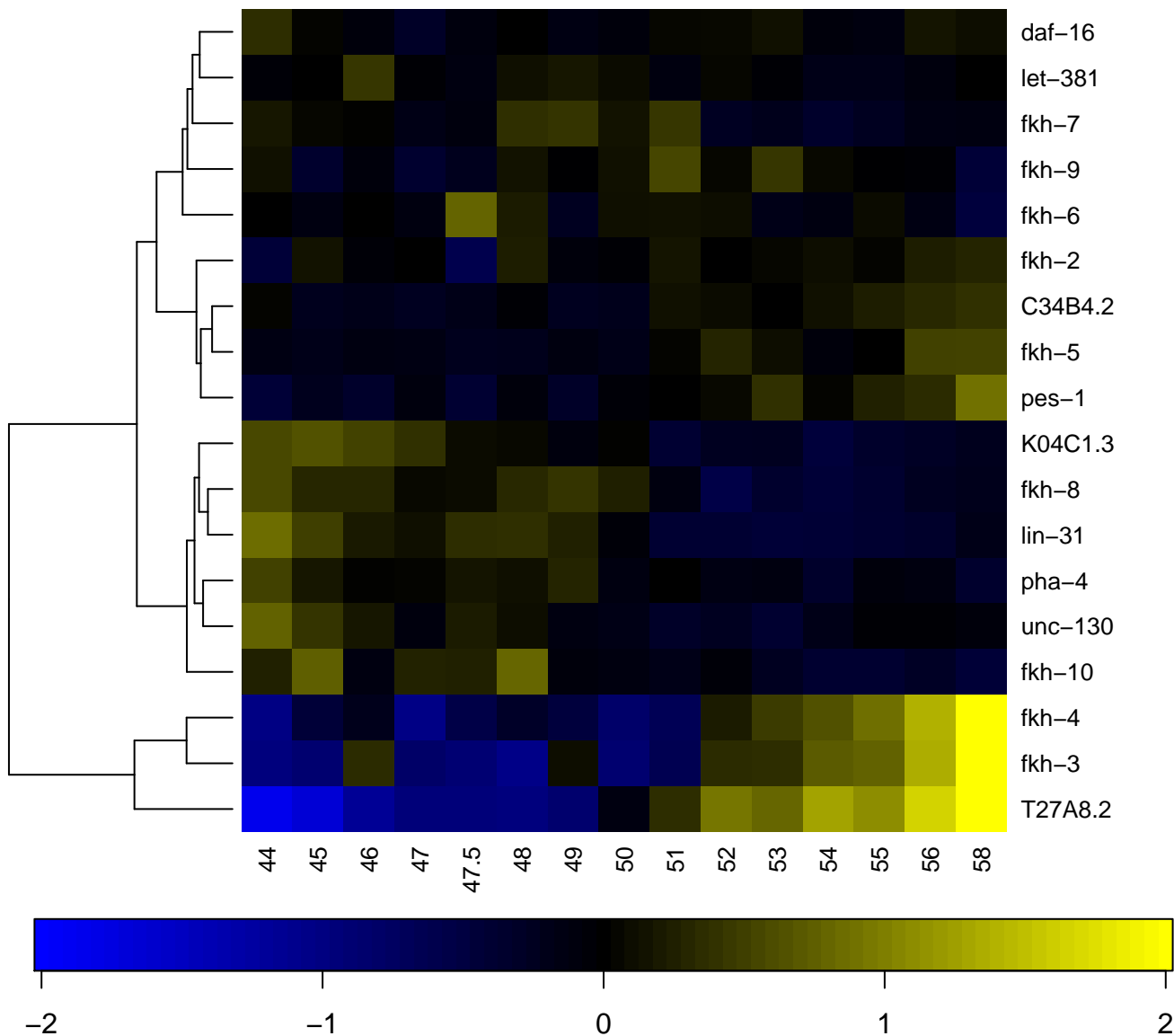
Transcription factor jumonji



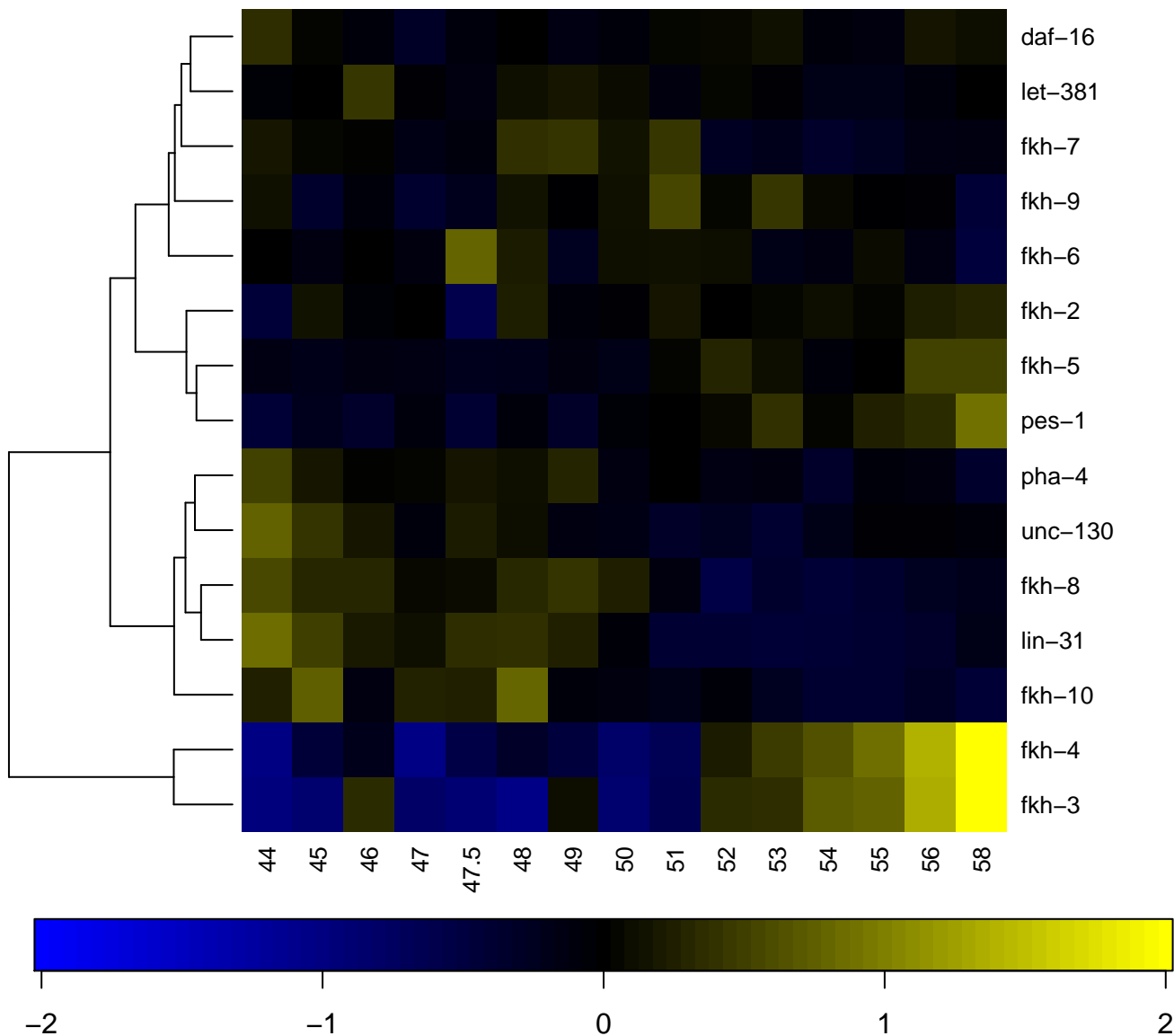
Transcription factor jumonji/aspartyl beta-hydroxylase



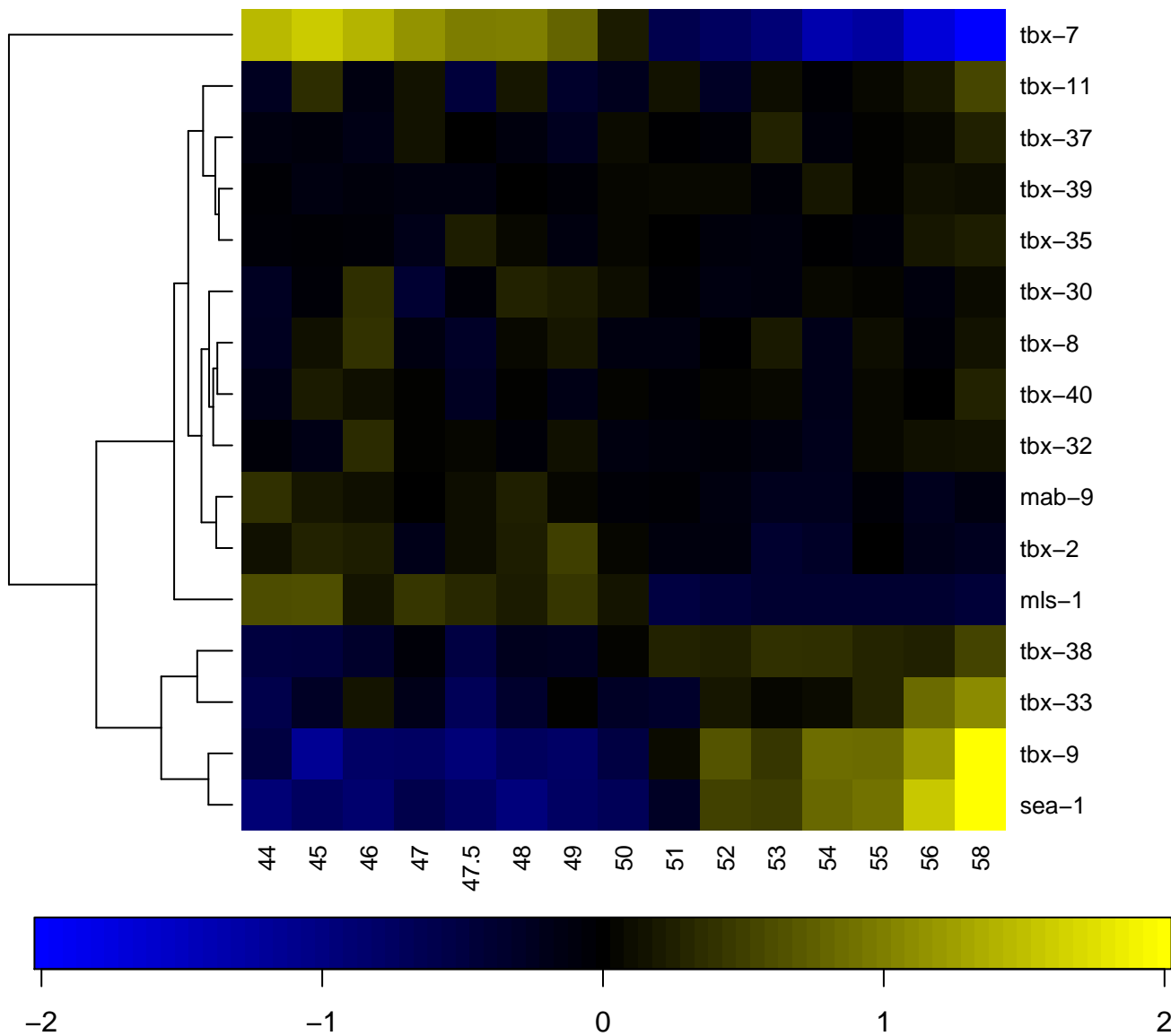
Transcription factor, fork head



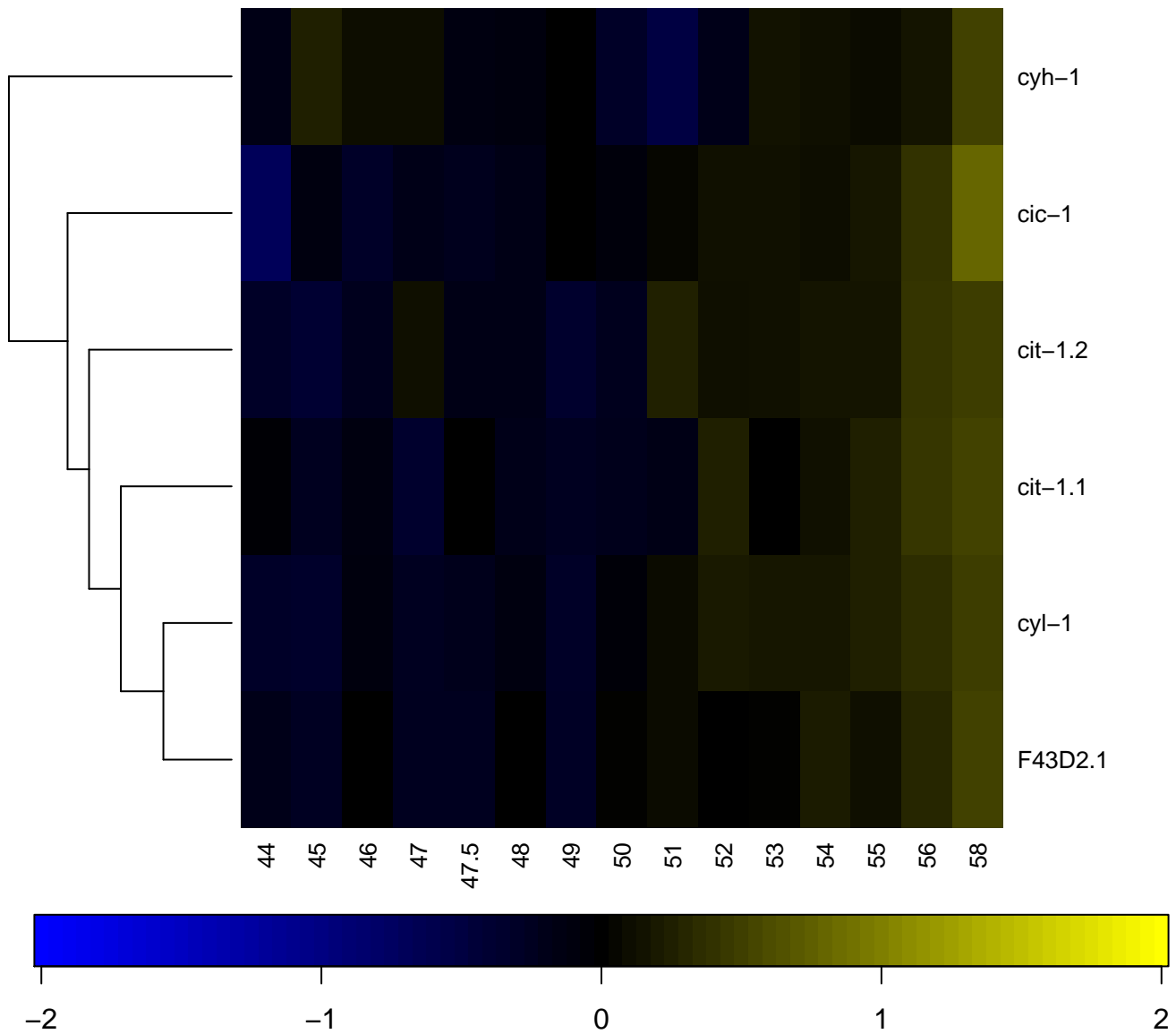
Transcription factor, fork head, conserved site



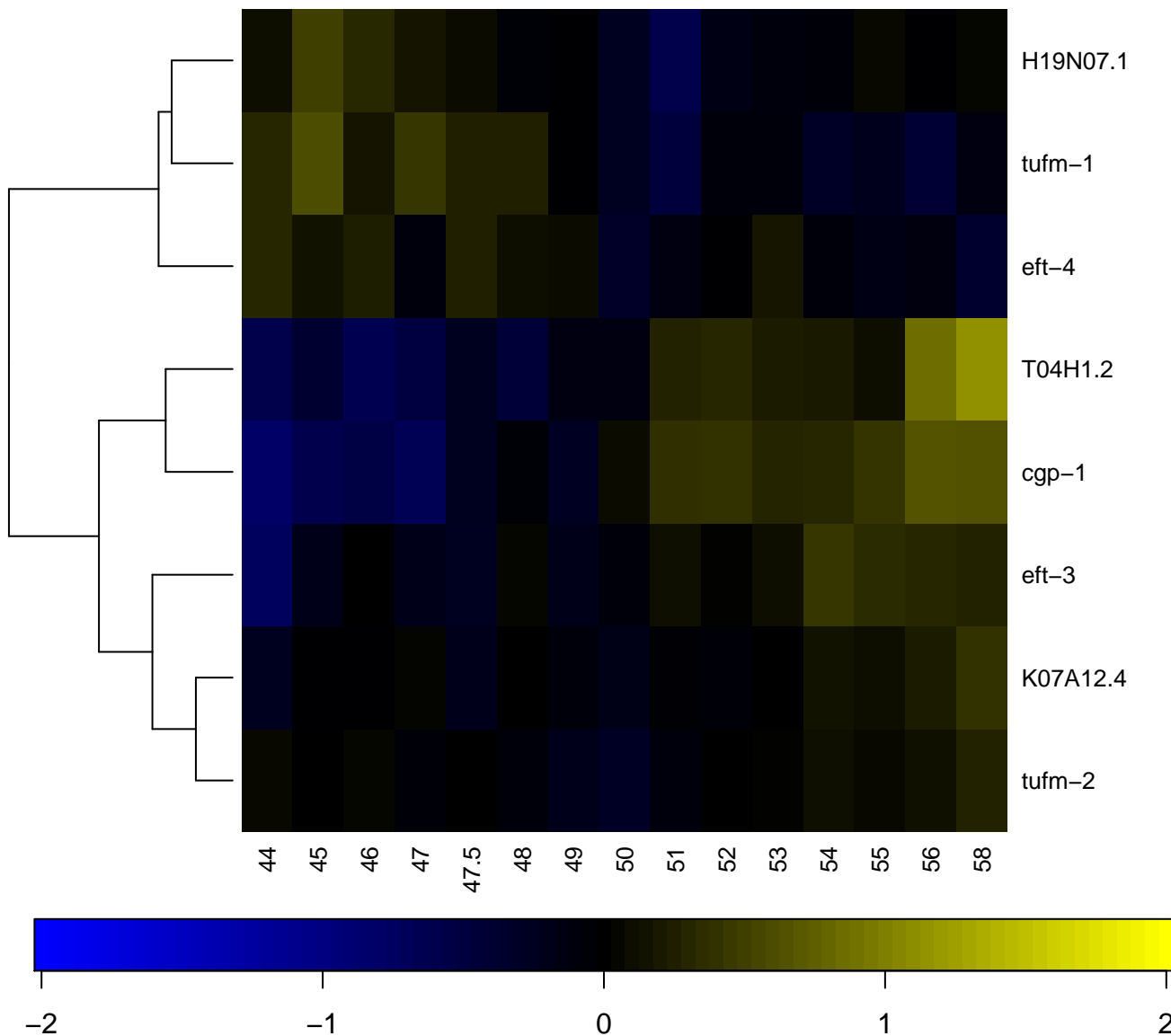
Transcription factor, T-box, conserved site



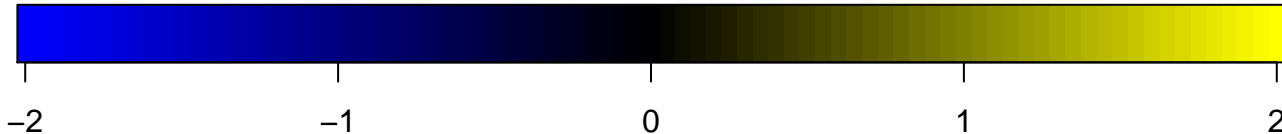
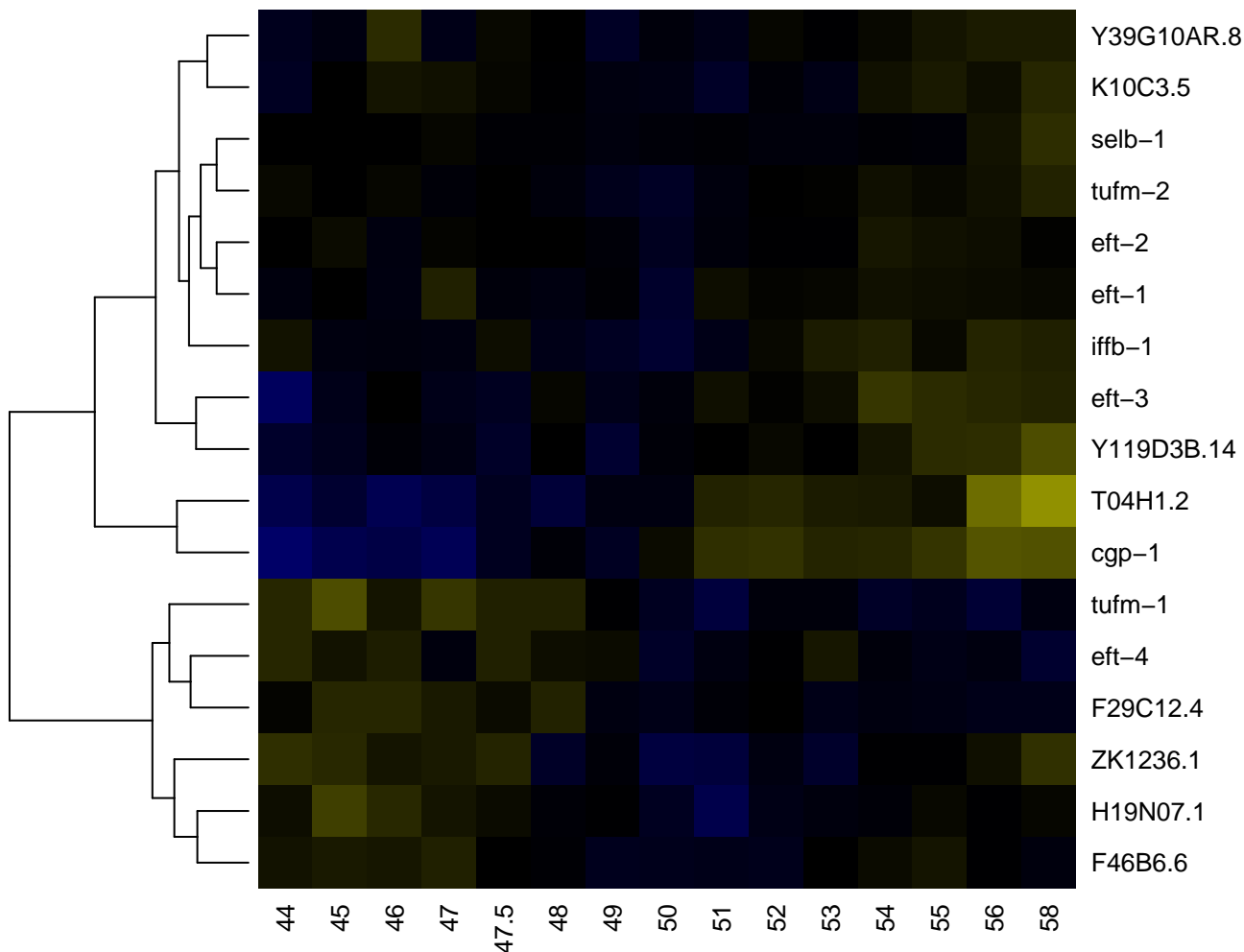
Transcription regulator cyclin



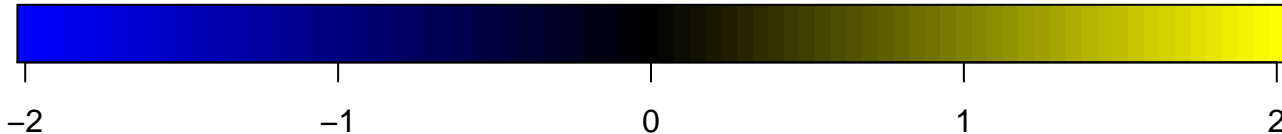
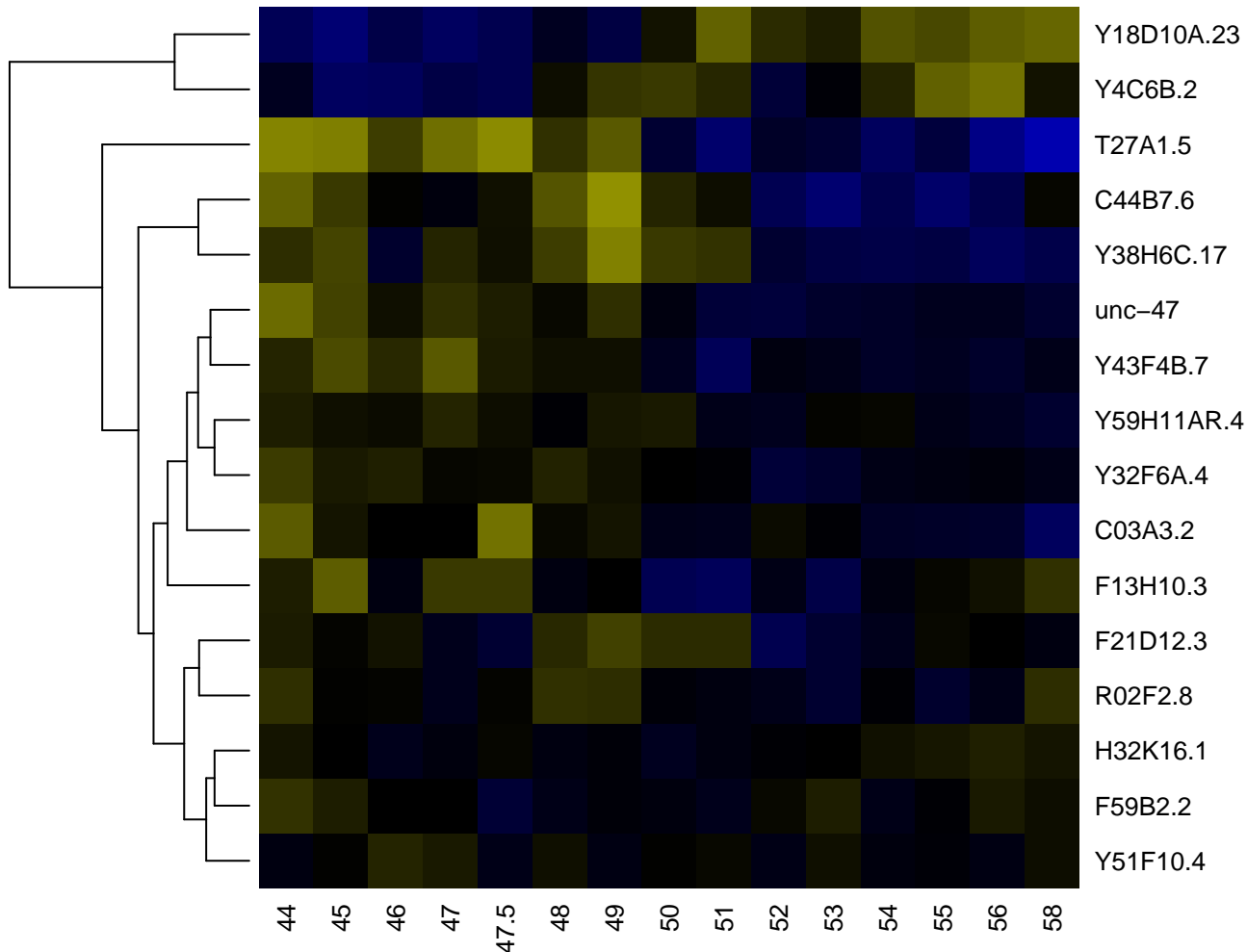
Translation elongation factor EFTu/EF1A, C-terminal



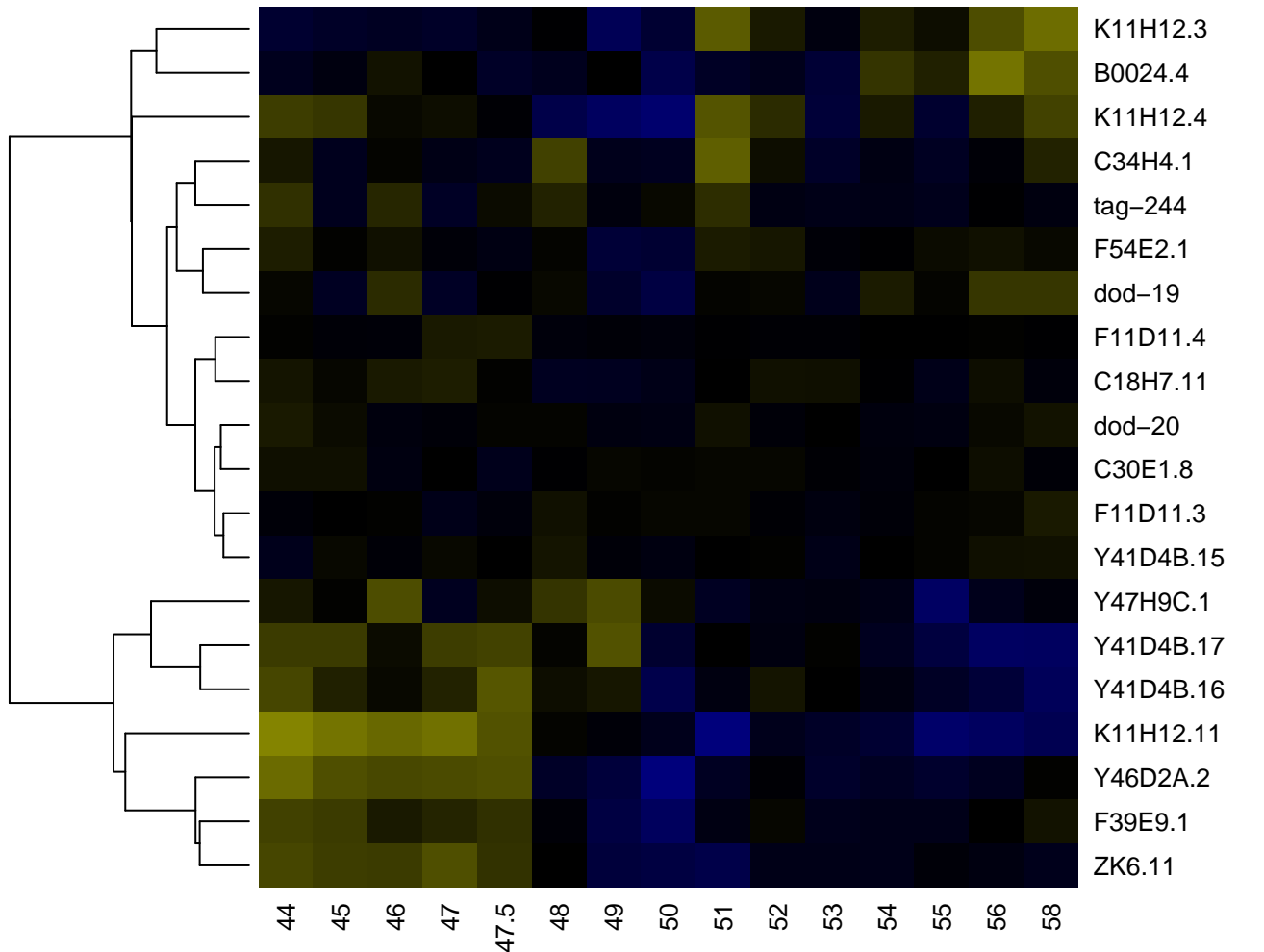
Translation elongation factor EFTu/EF1A, domain 2



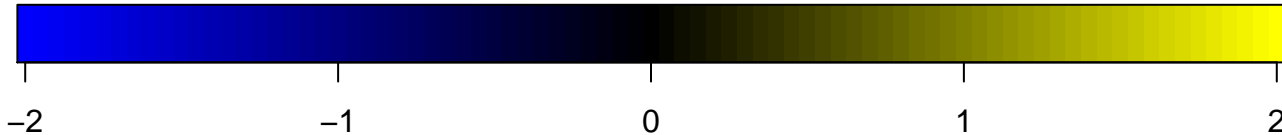
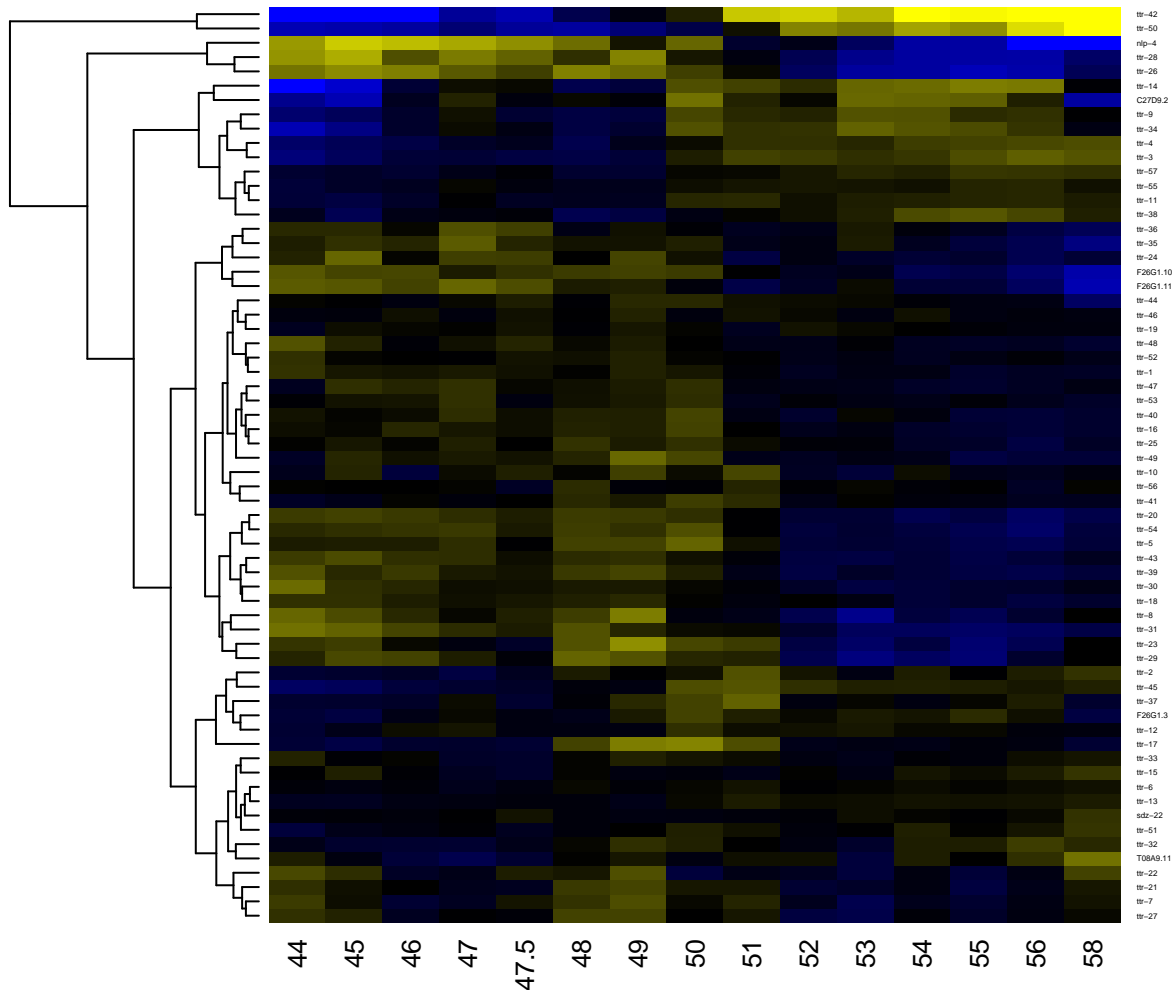
Transmembrane amino acid transporter protein



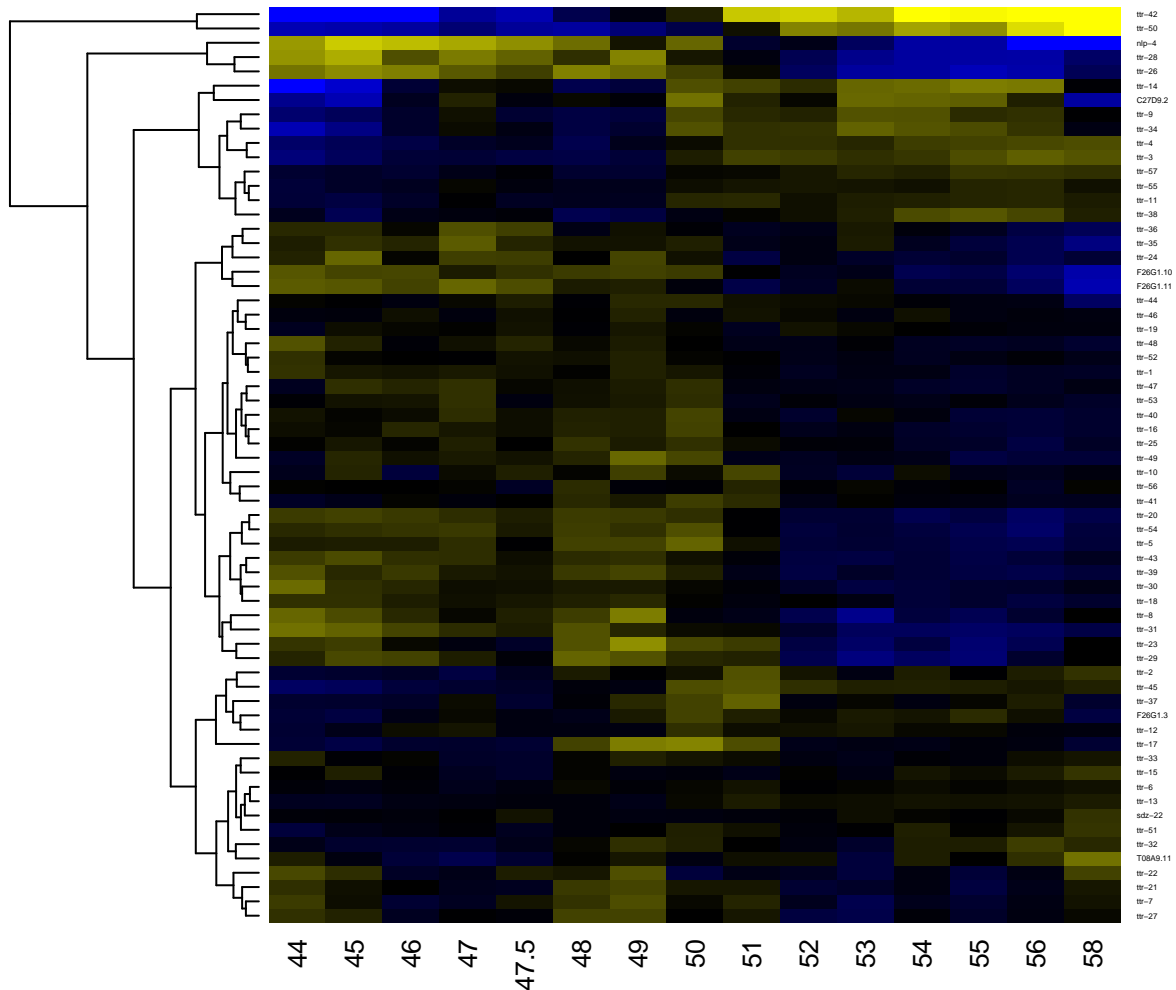
Transmembrane glycoprotein



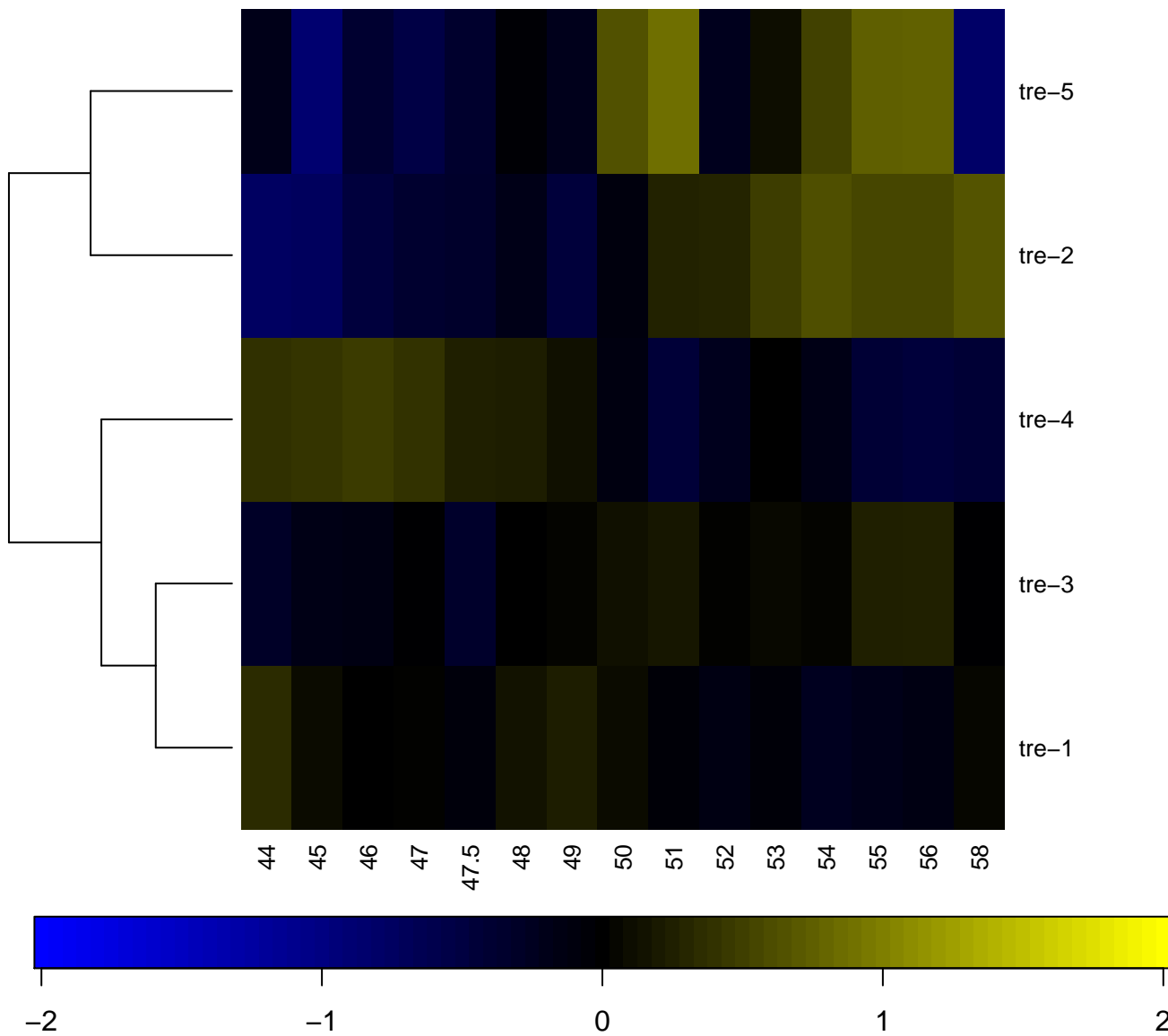
Transthyretin-like



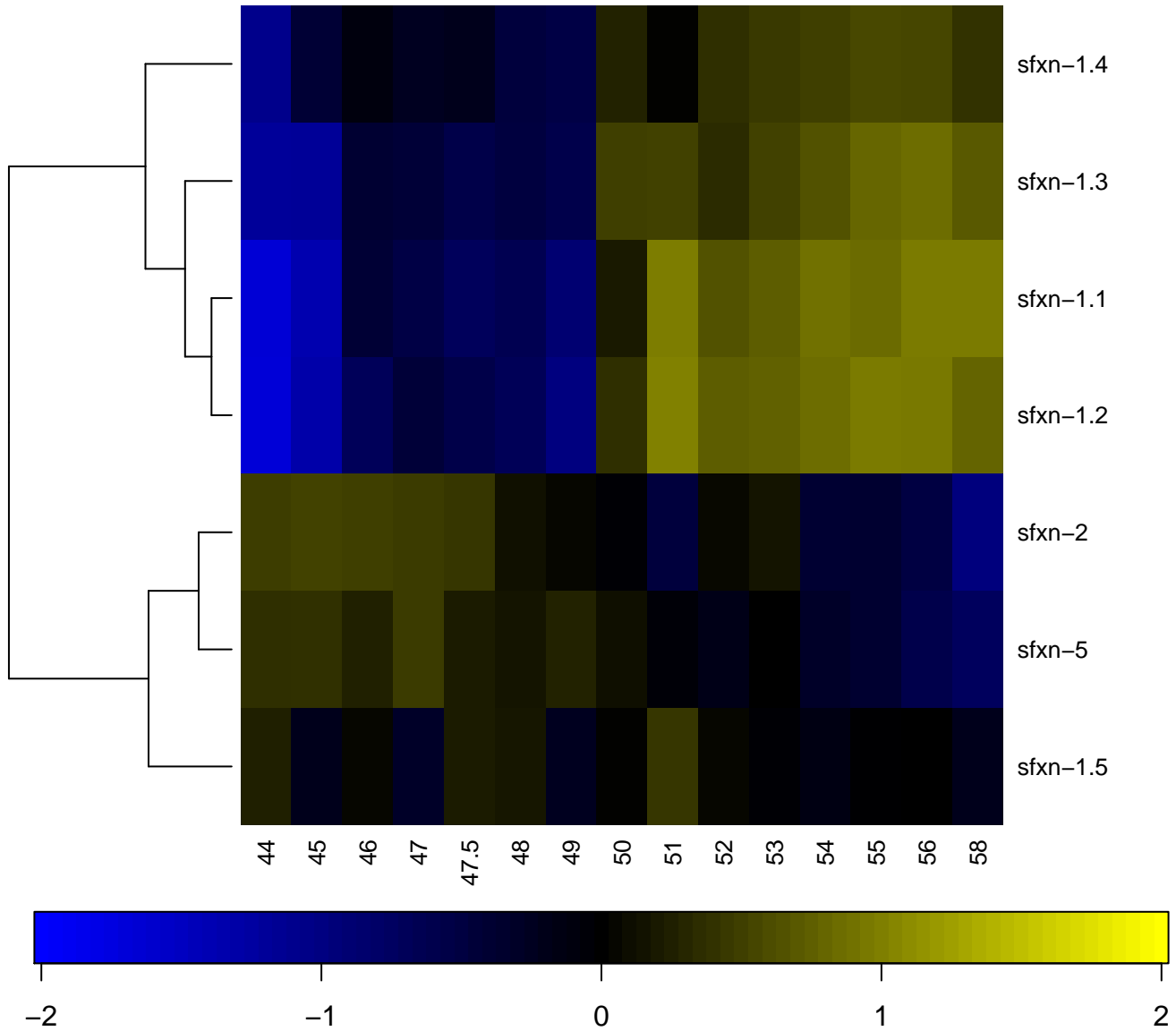
Transthyretin-like family



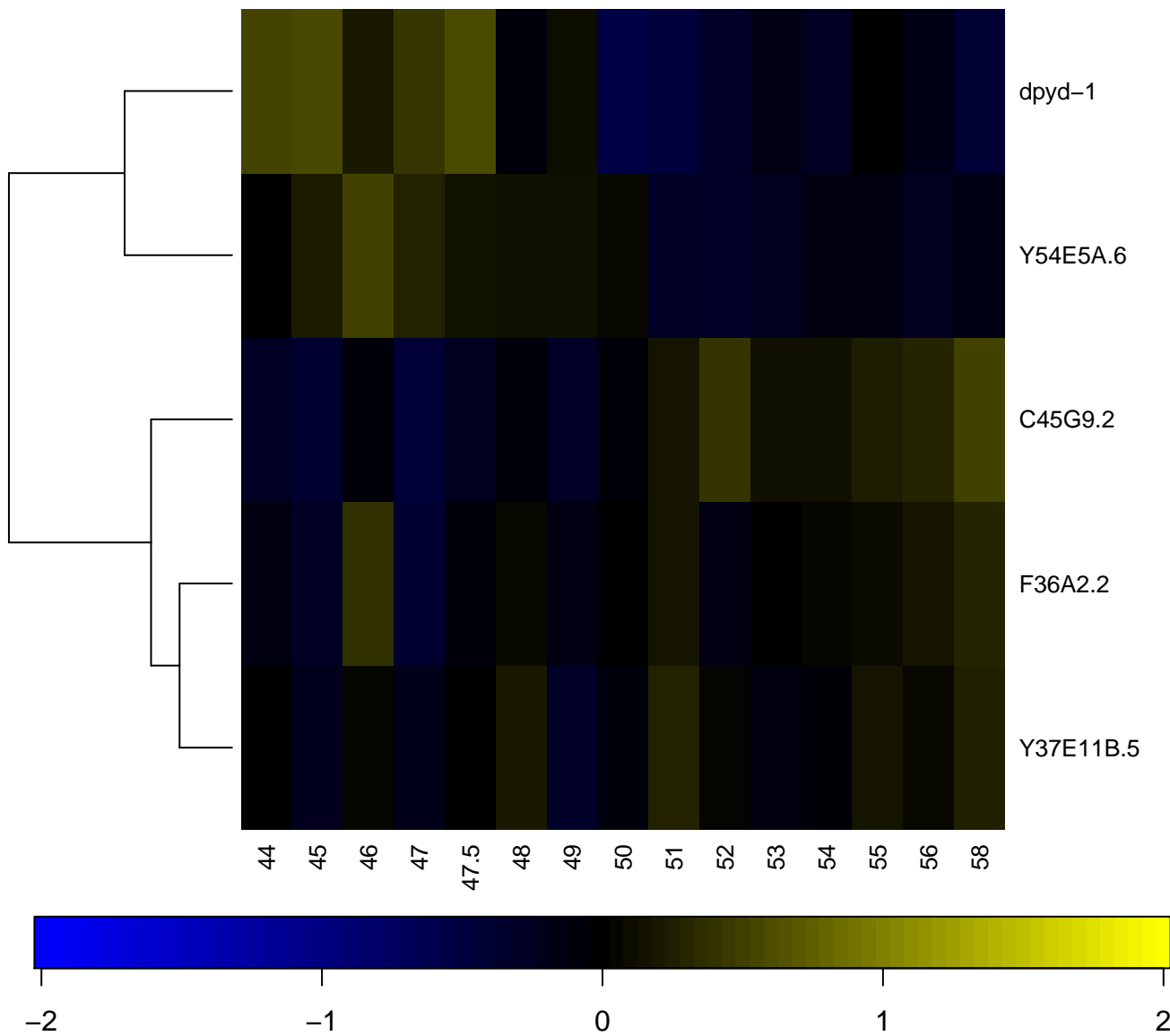
Trehalase



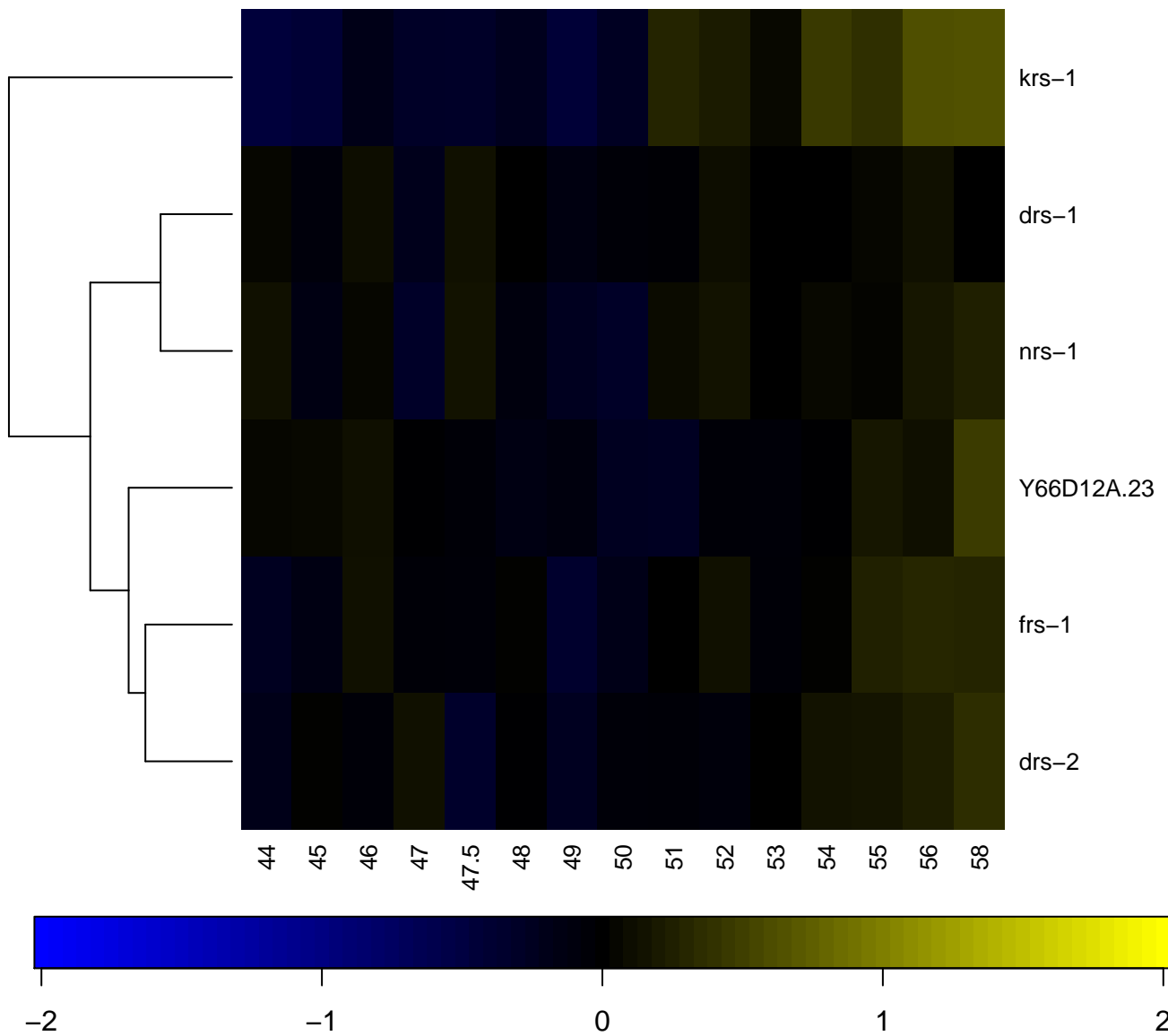
Tricarboxylate/iron carrier



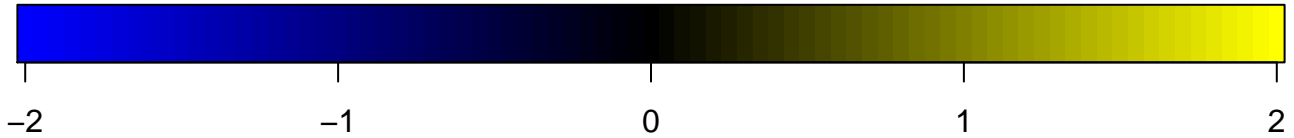
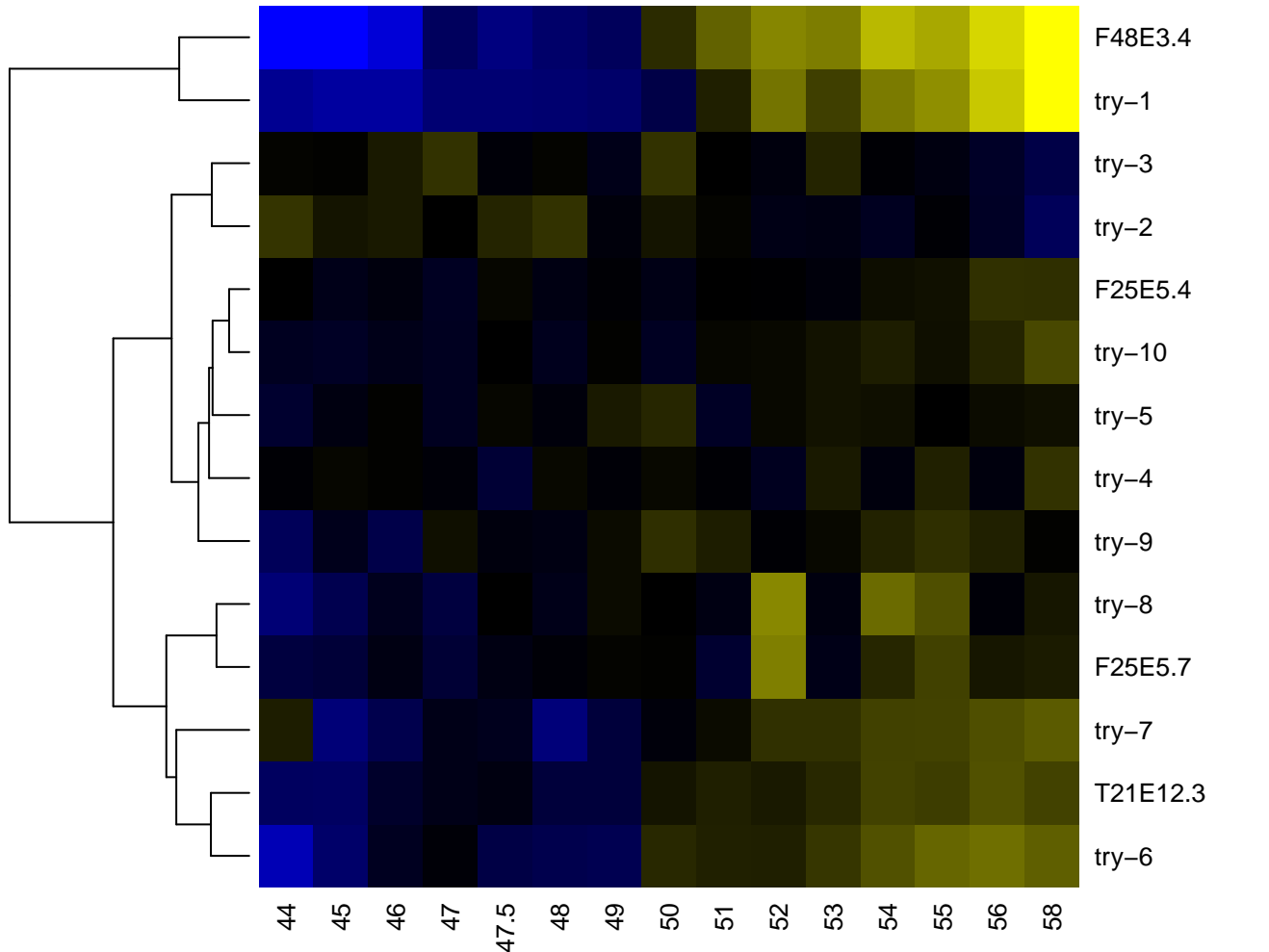
tRNA-dihydrouridine synthase



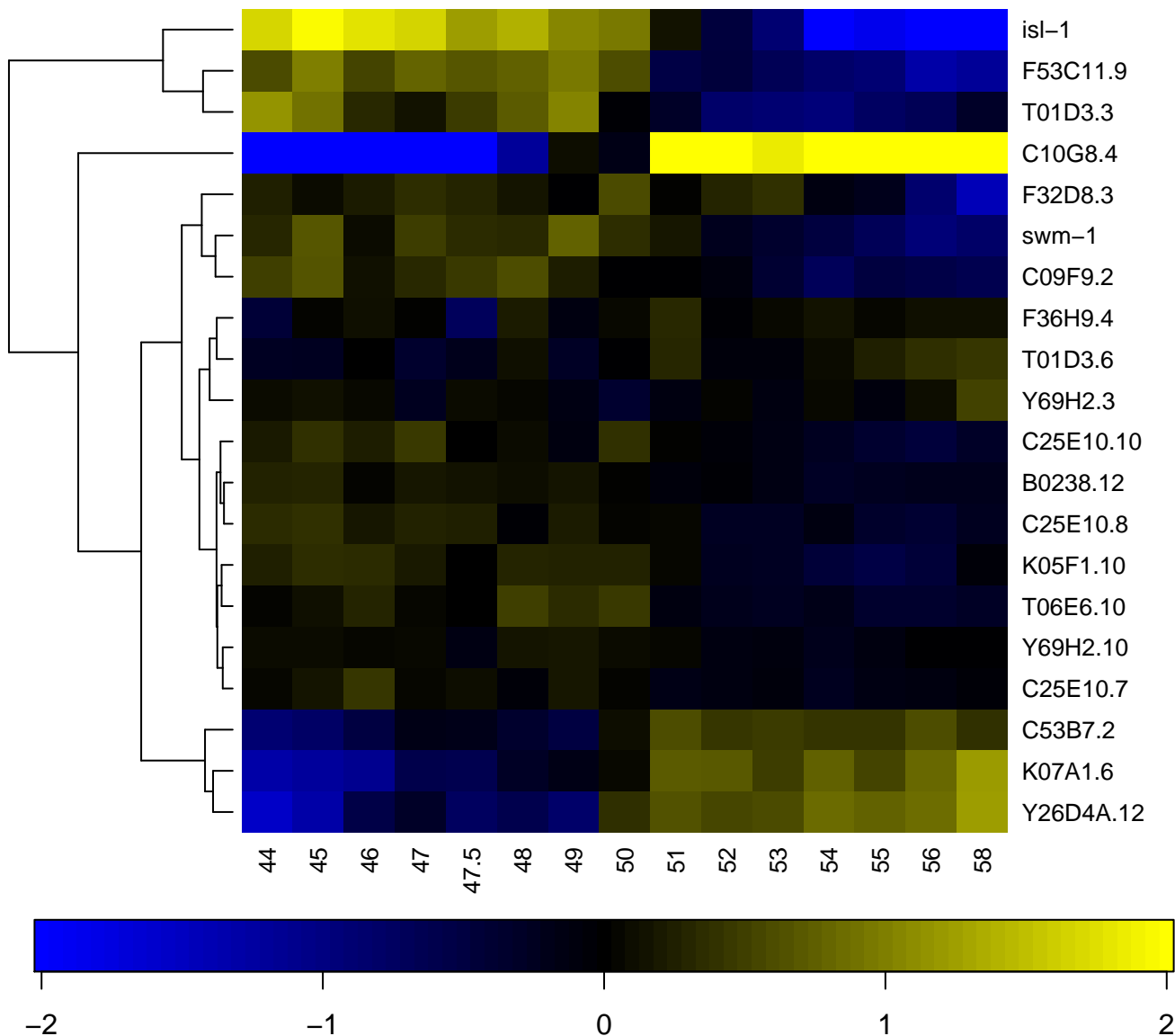
tRNA synthetases class II (D, K and N)



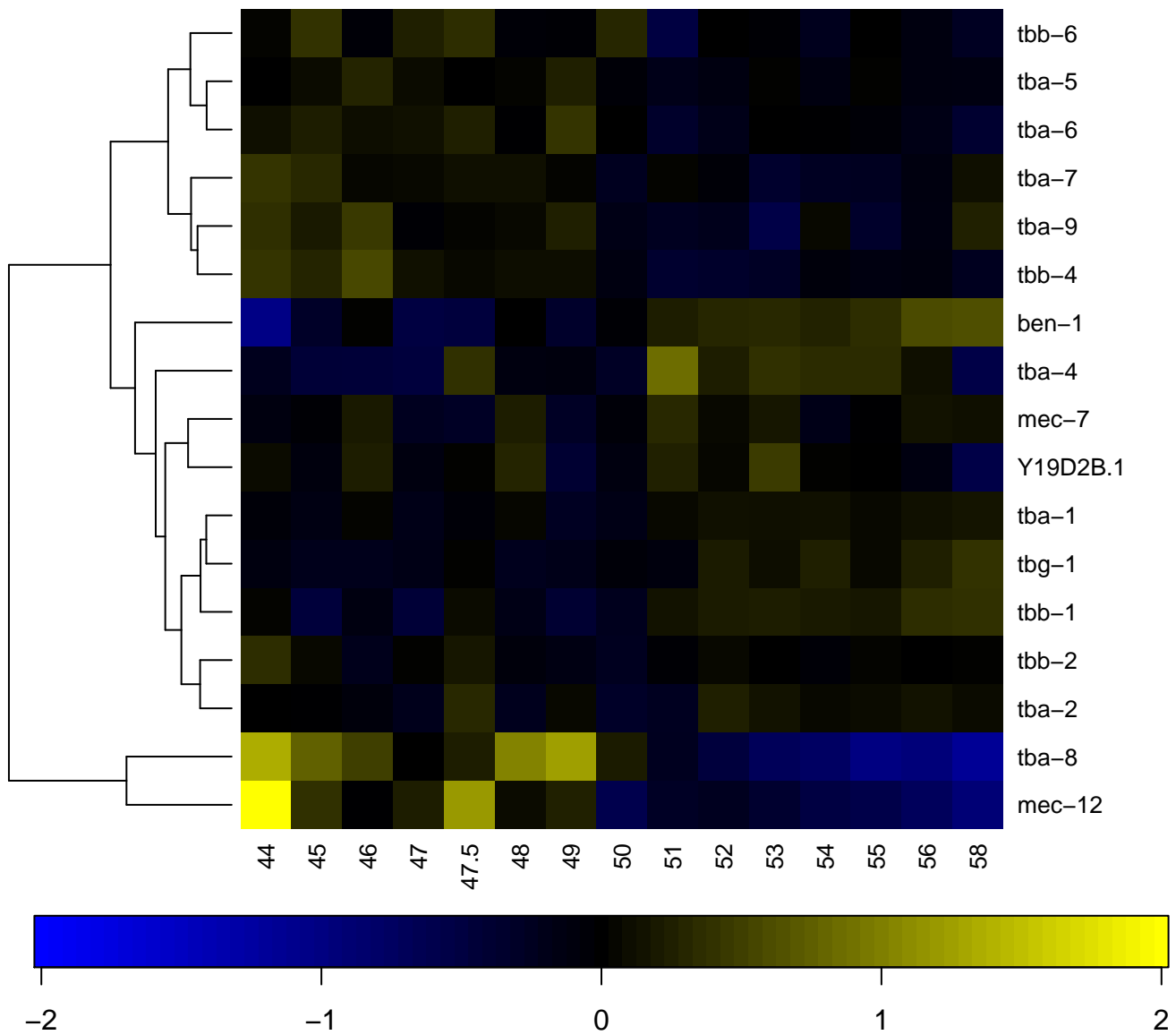
Trypsin



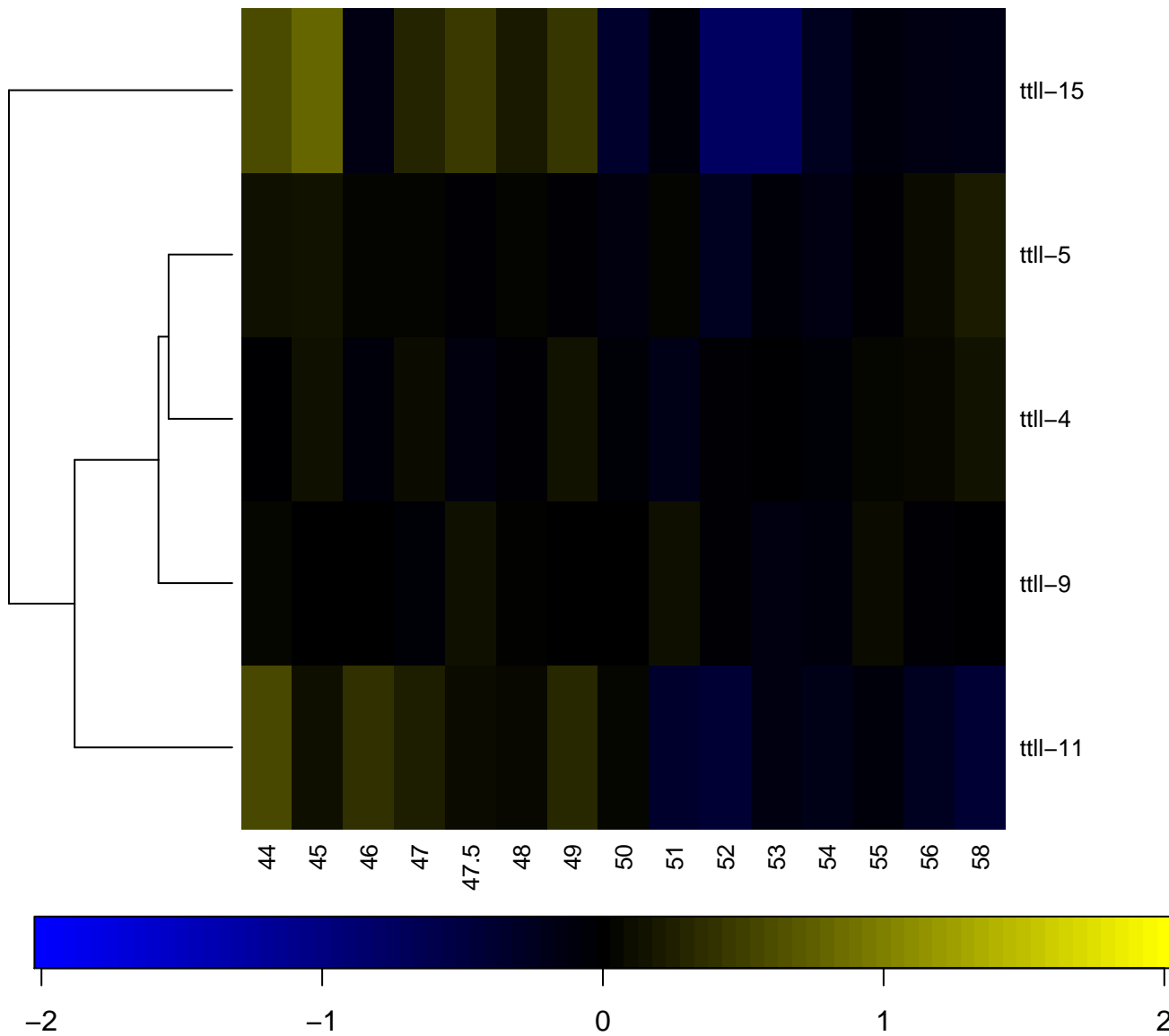
Trypsin Inhibitor like cysteine rich domain



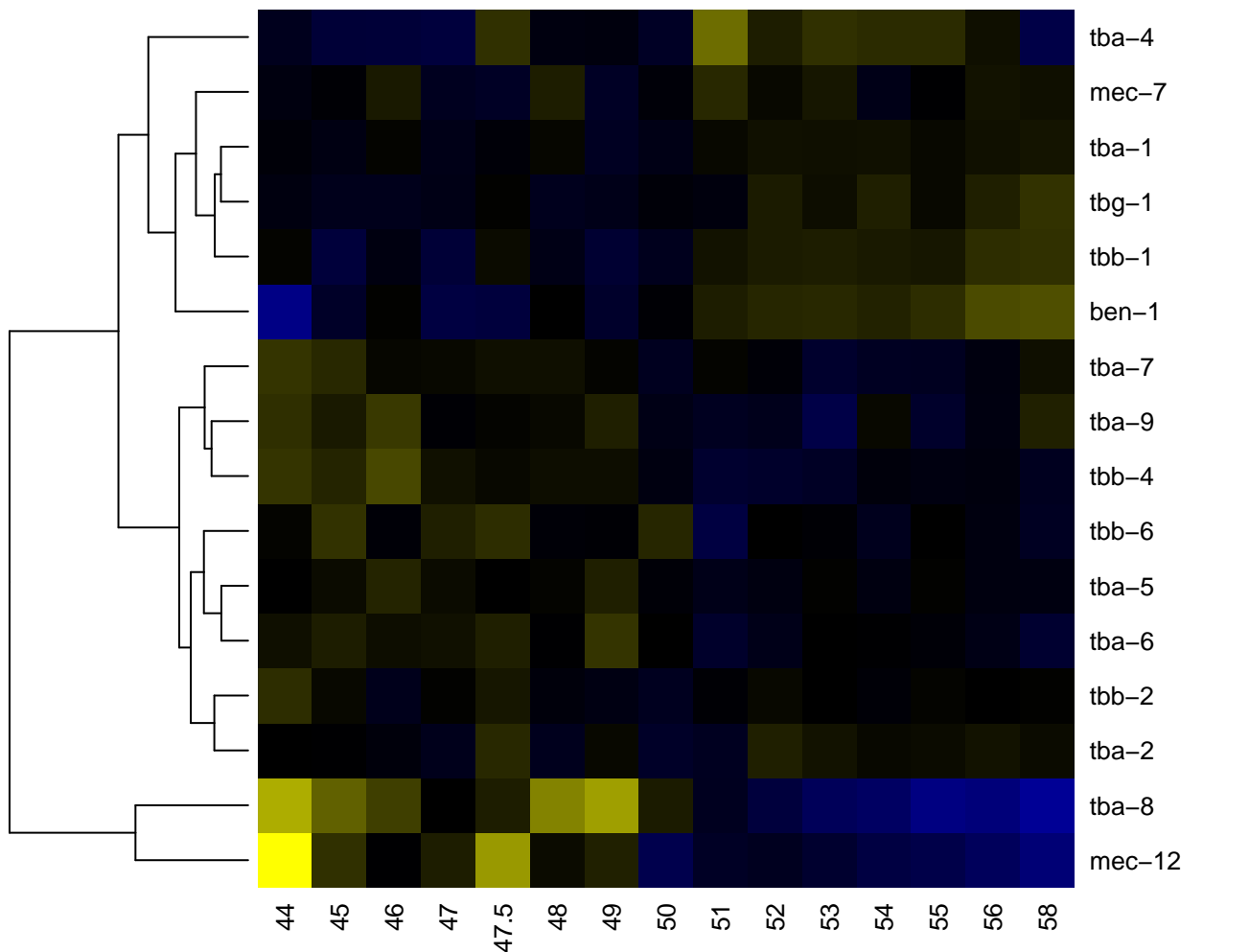
Tubulin



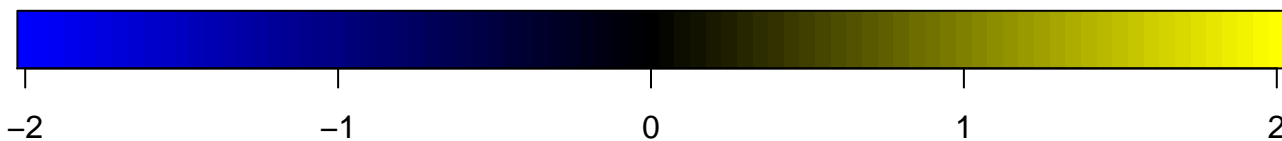
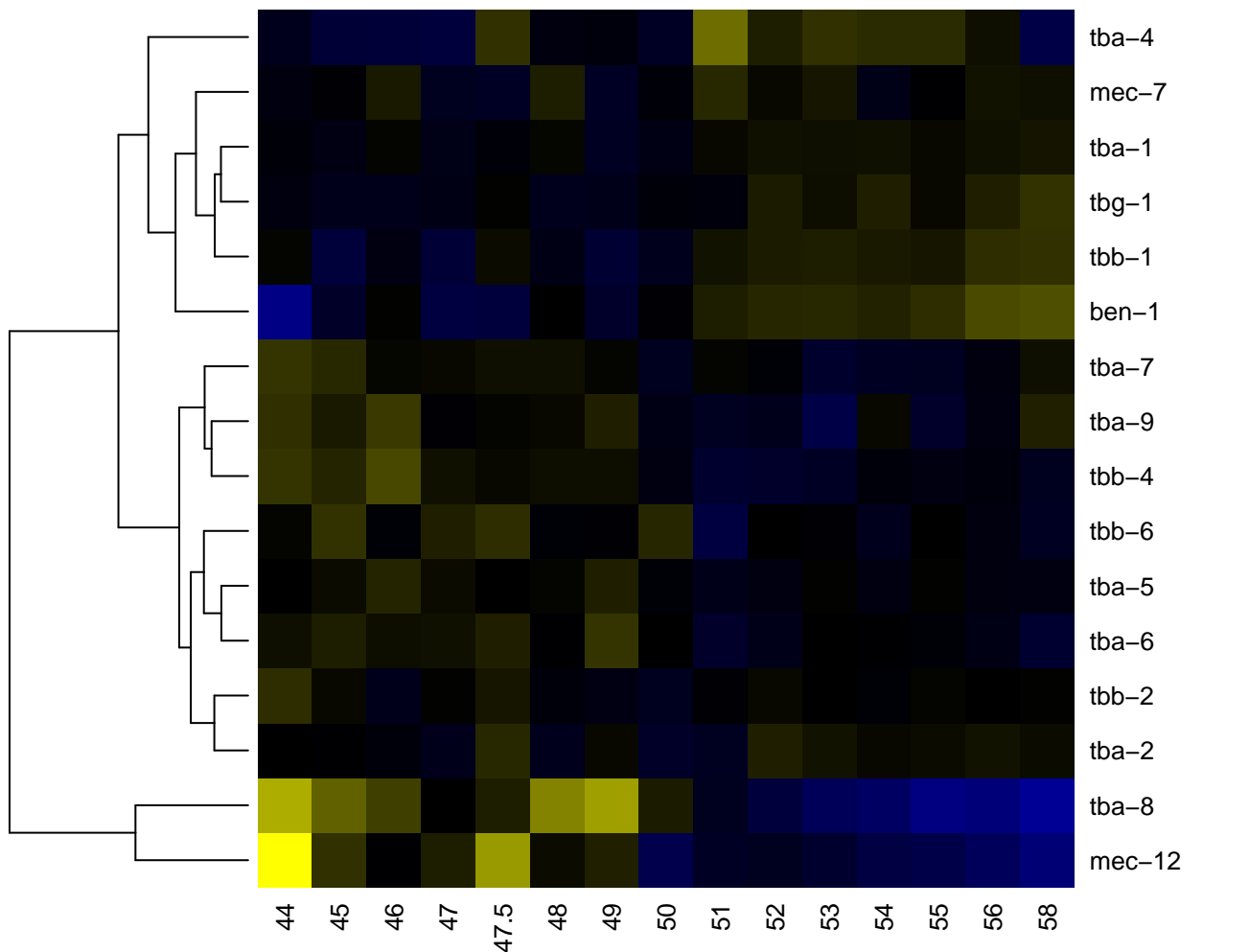
Tubulin-tyrosine ligase family



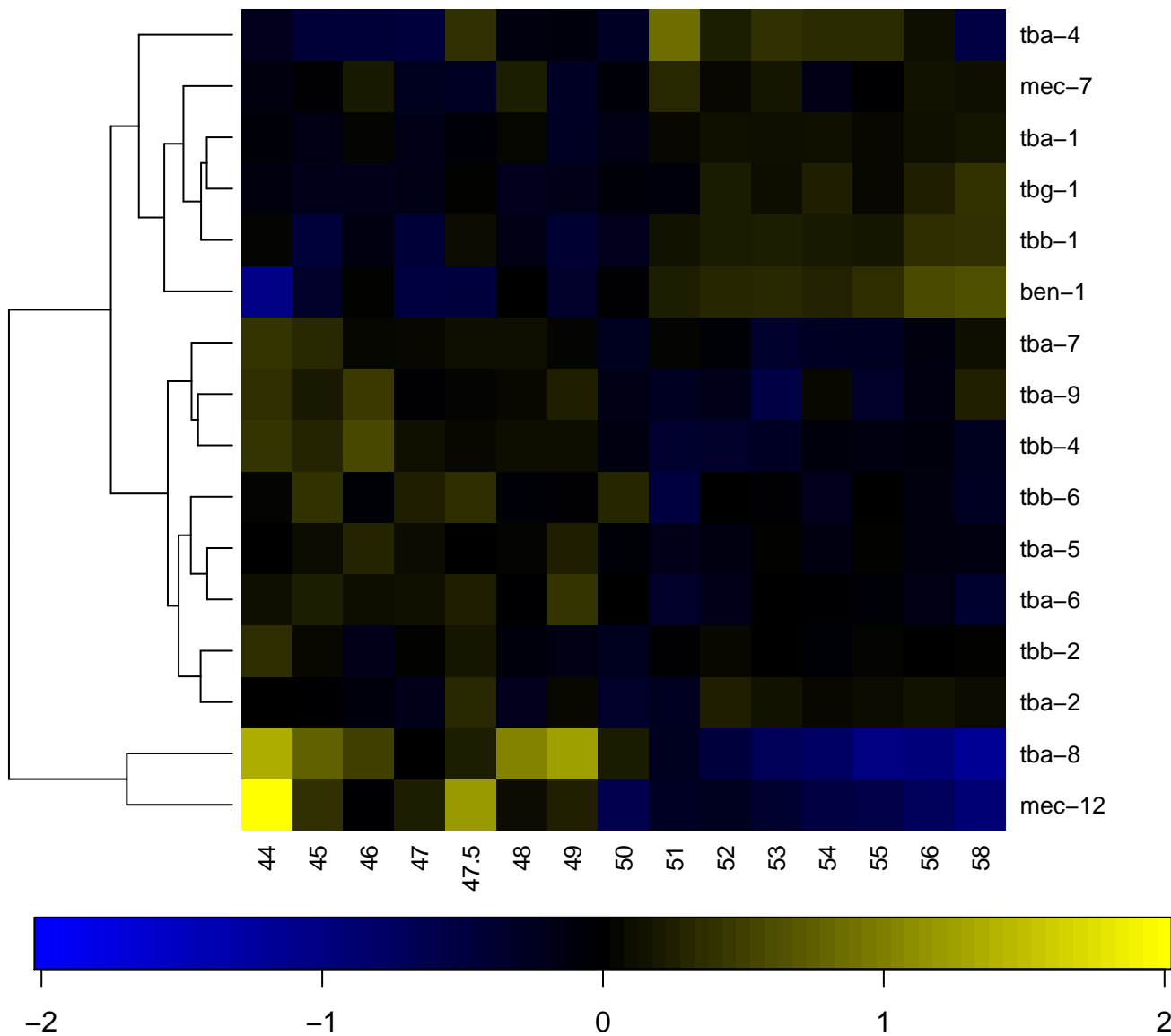
Tubulin C-terminal domain



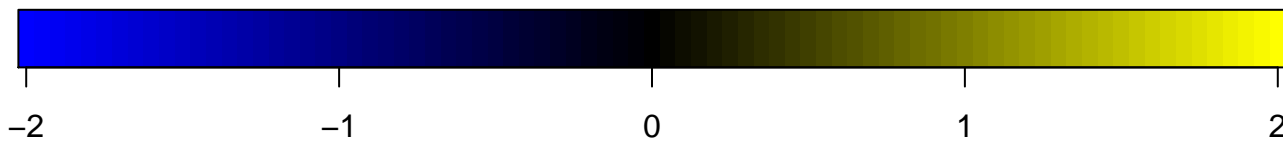
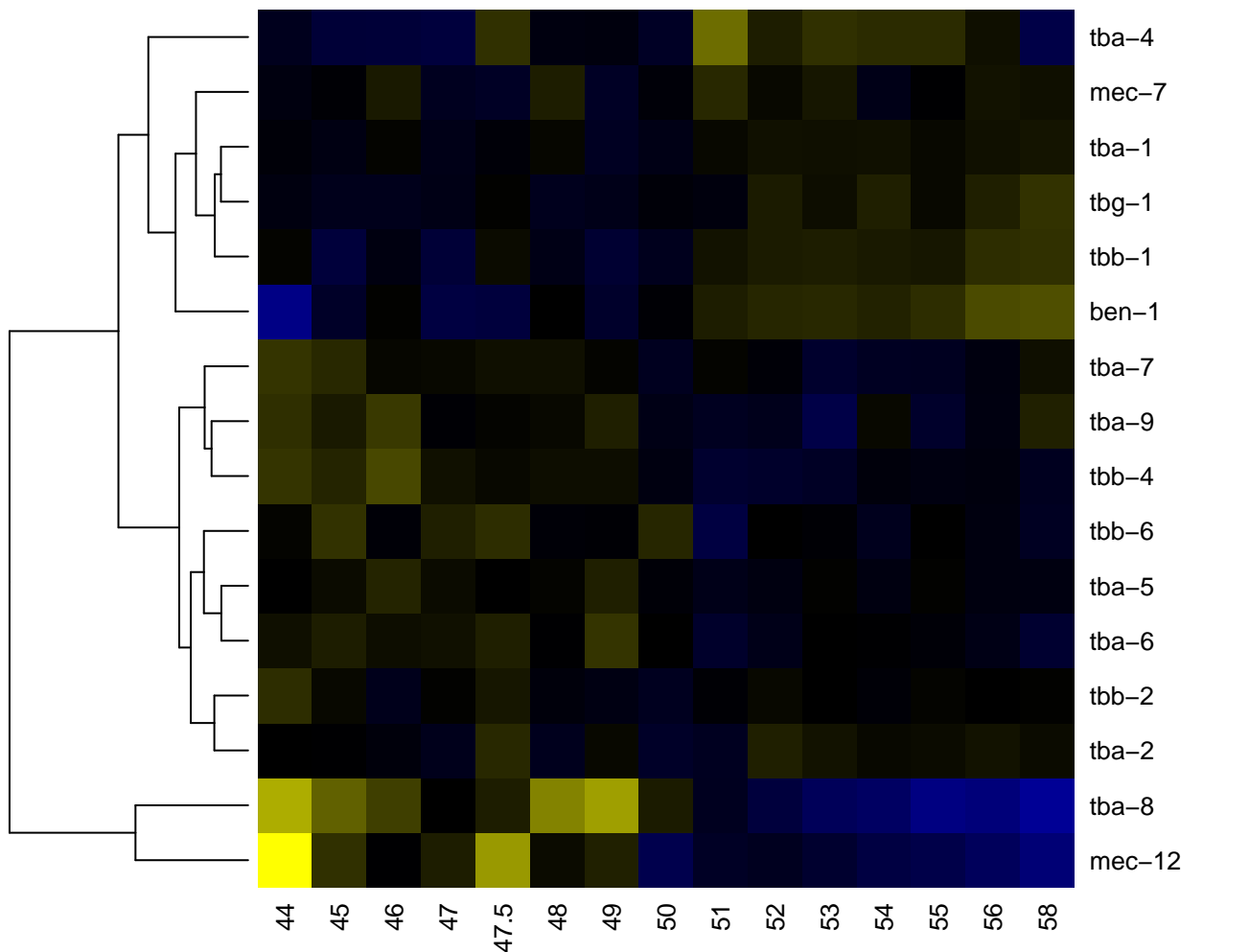
Tubulin/FtsZ family, GTPase domain



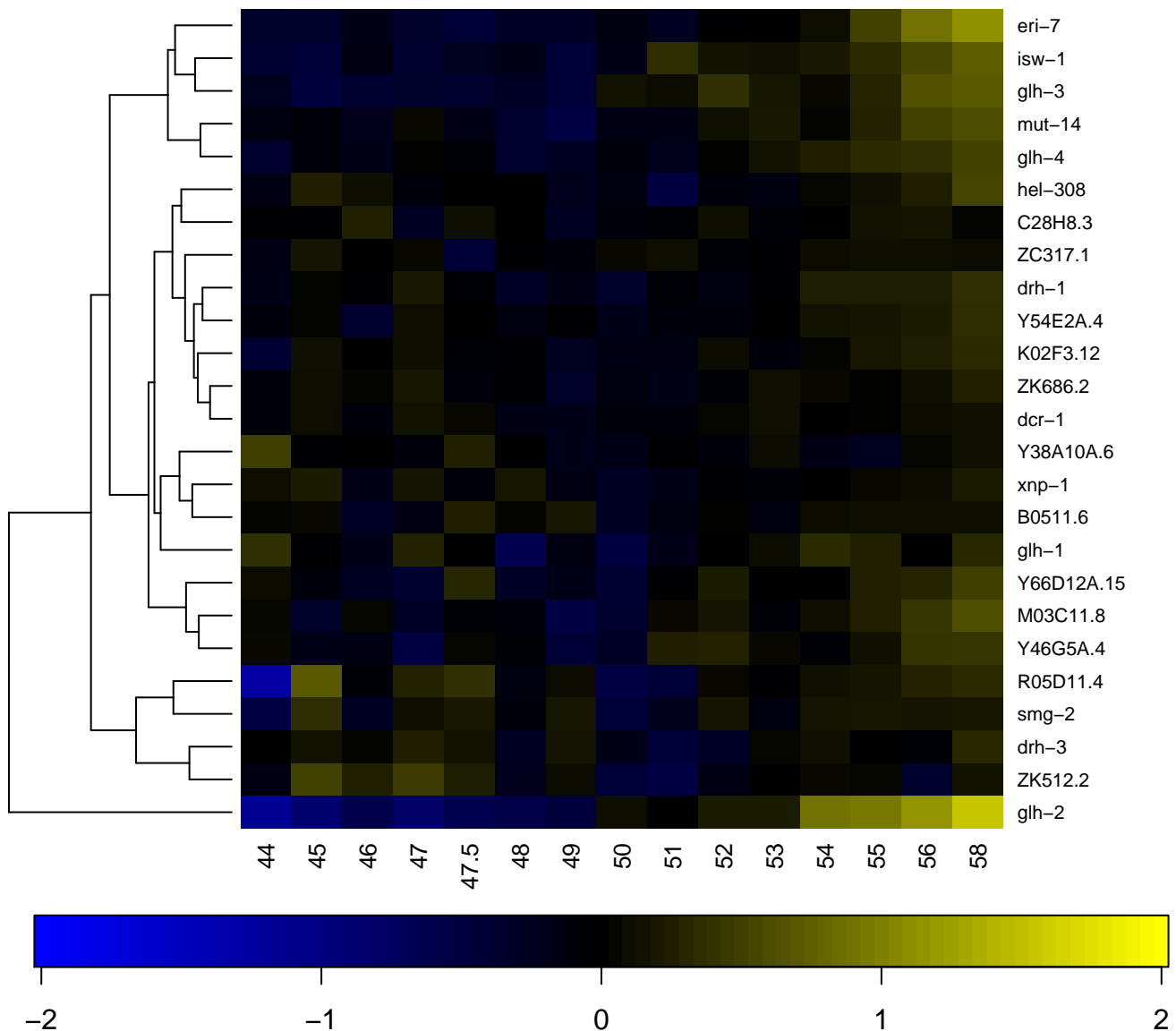
Tubulin/FtsZ, 2-layer sandwich domain



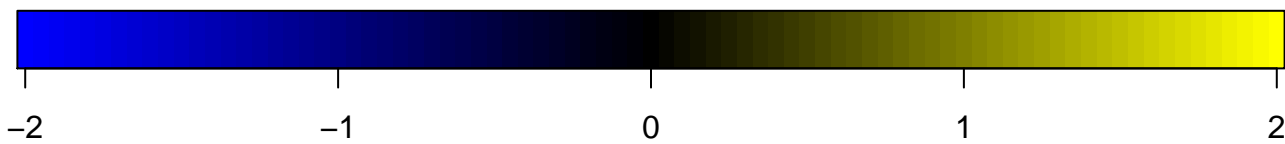
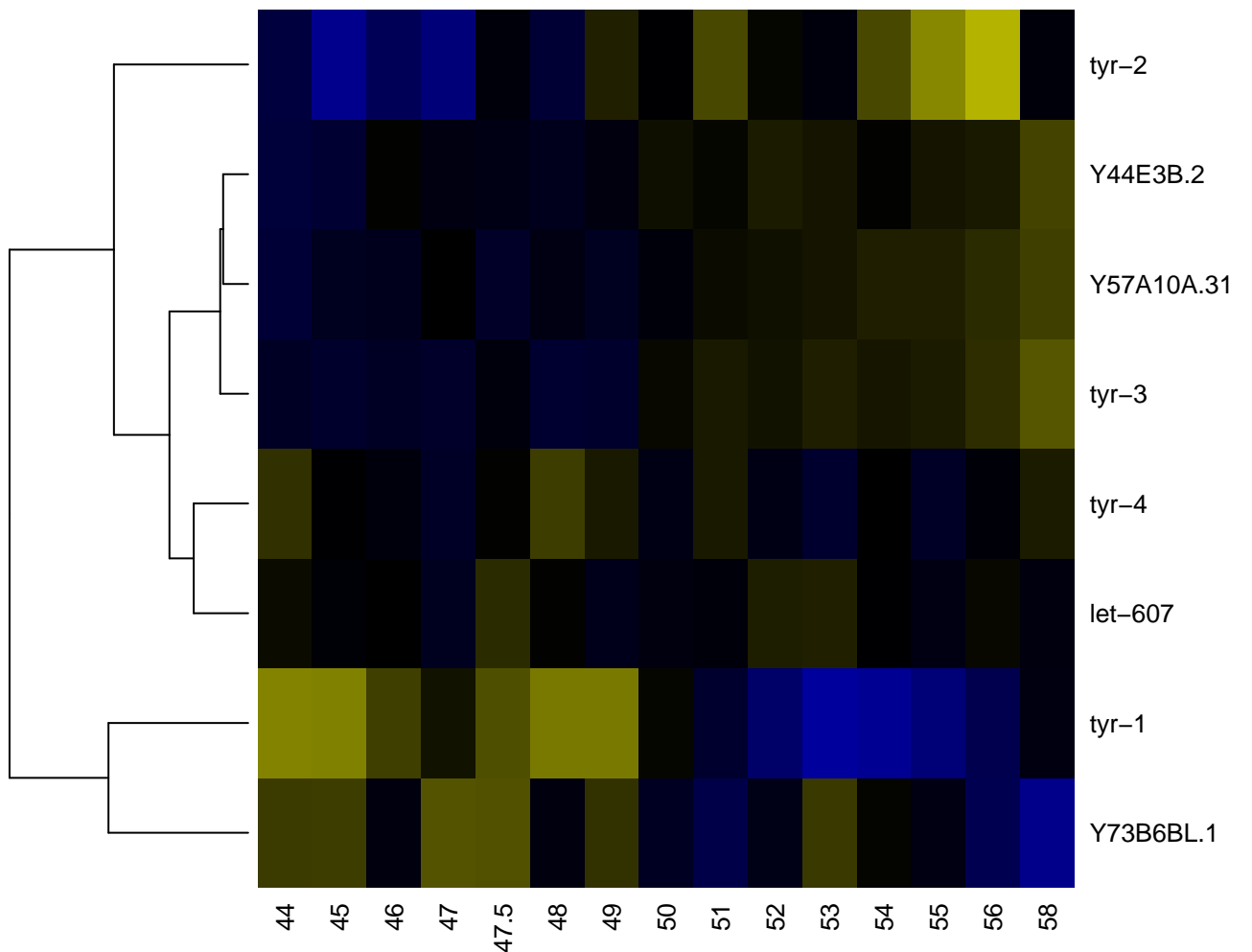
Tubulin/FtsZ, GTPase domain



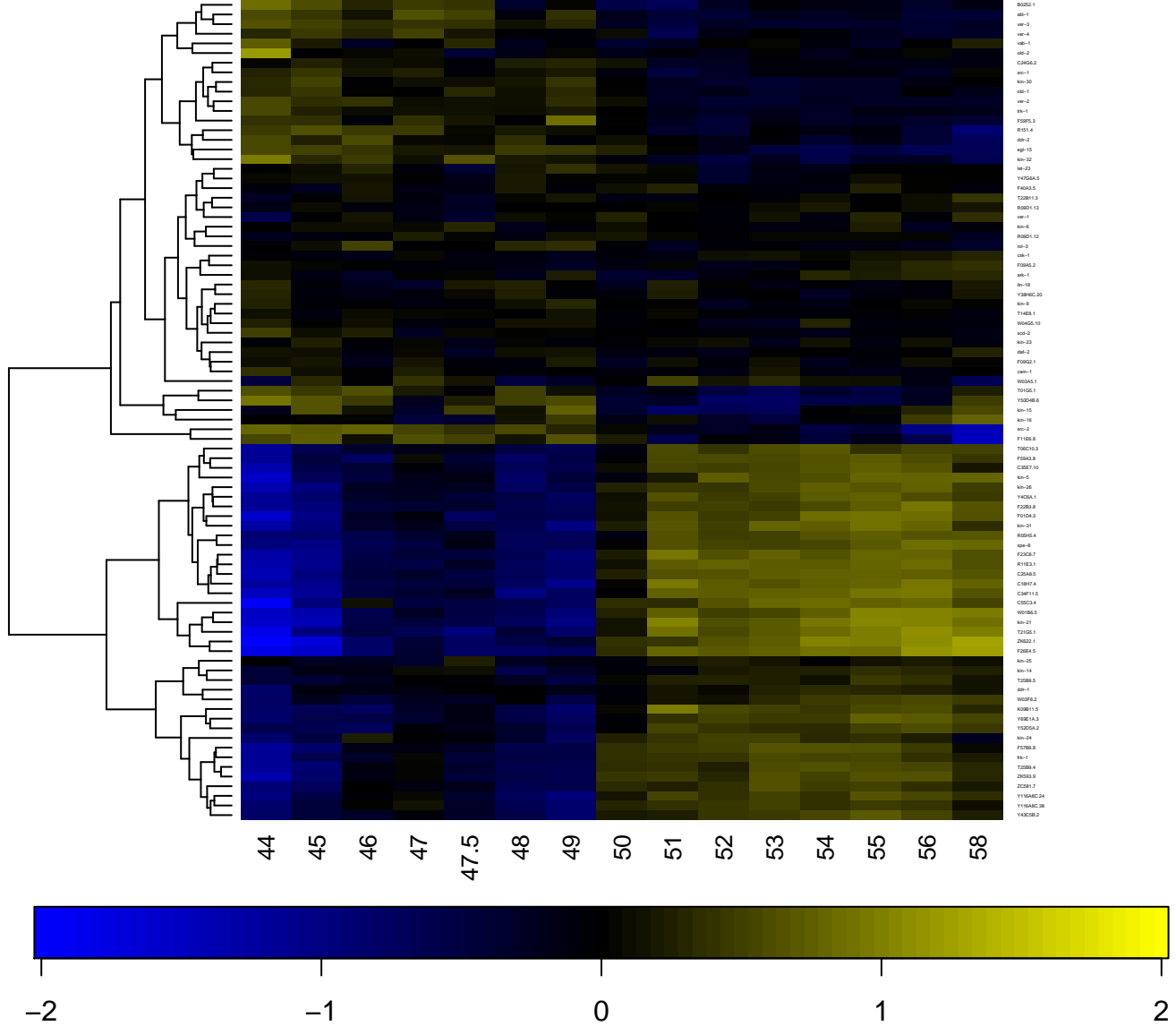
Type III restriction enzyme, res subunit



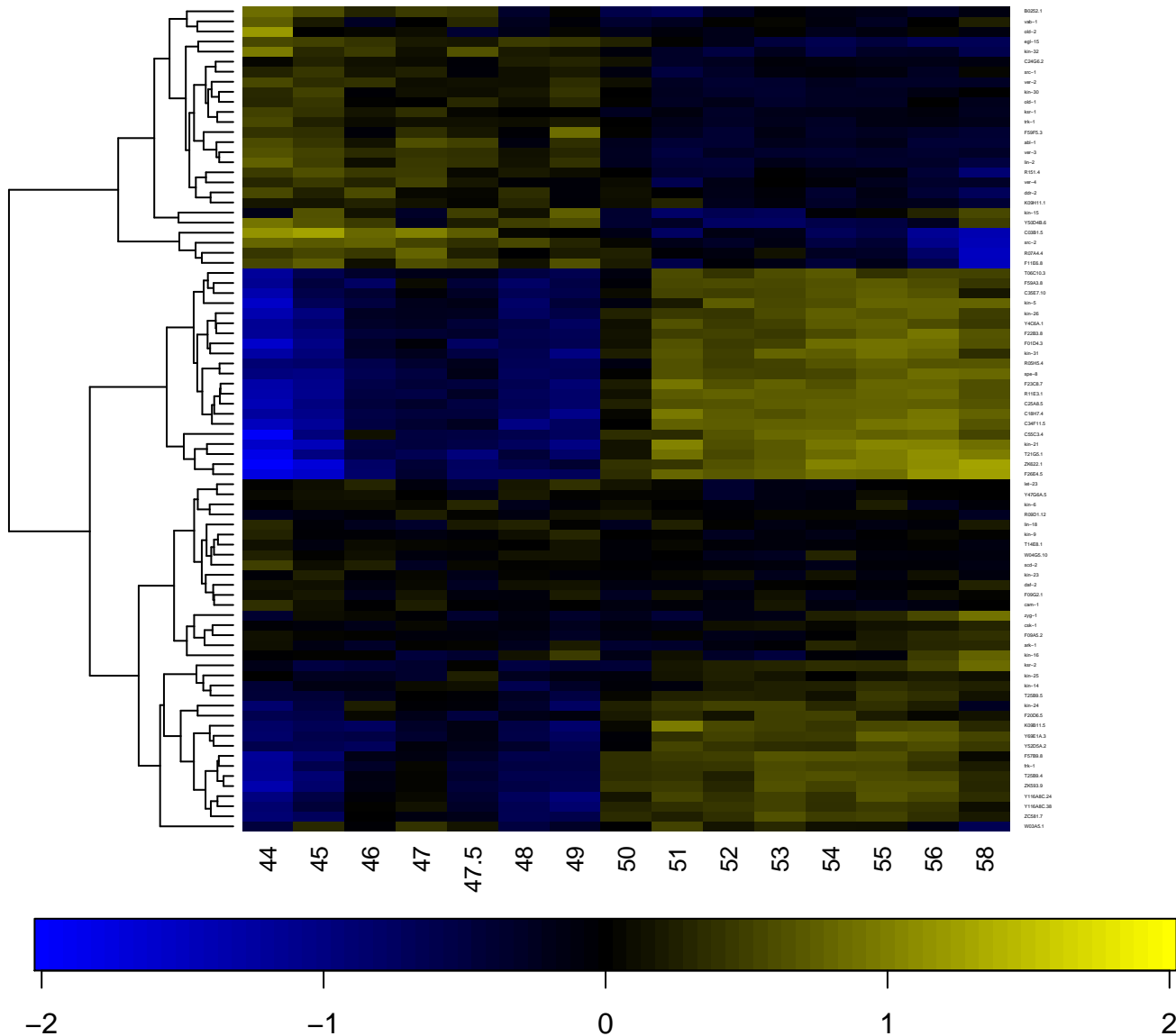
Tyrosinase



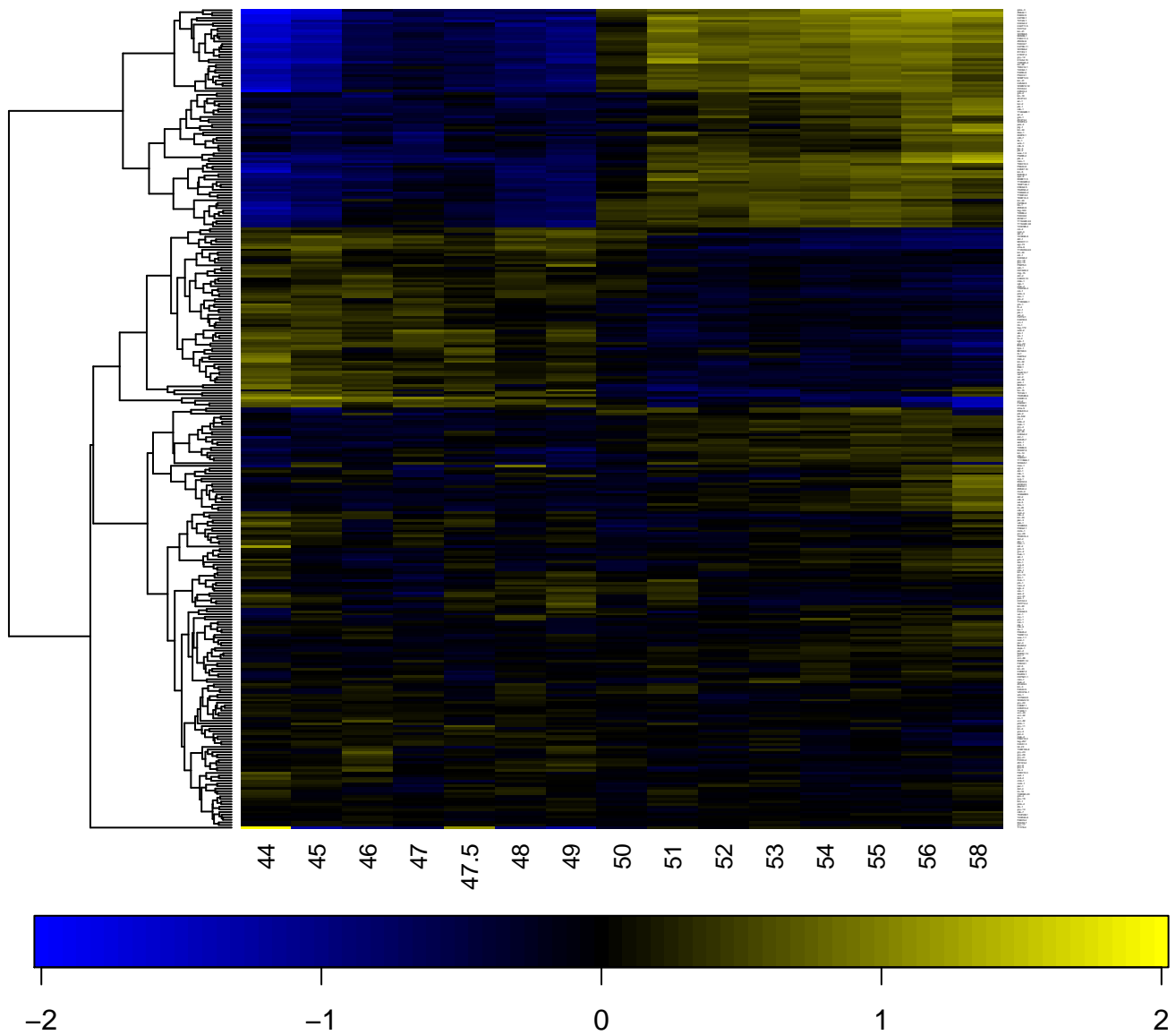
Tyrosine-protein kinase



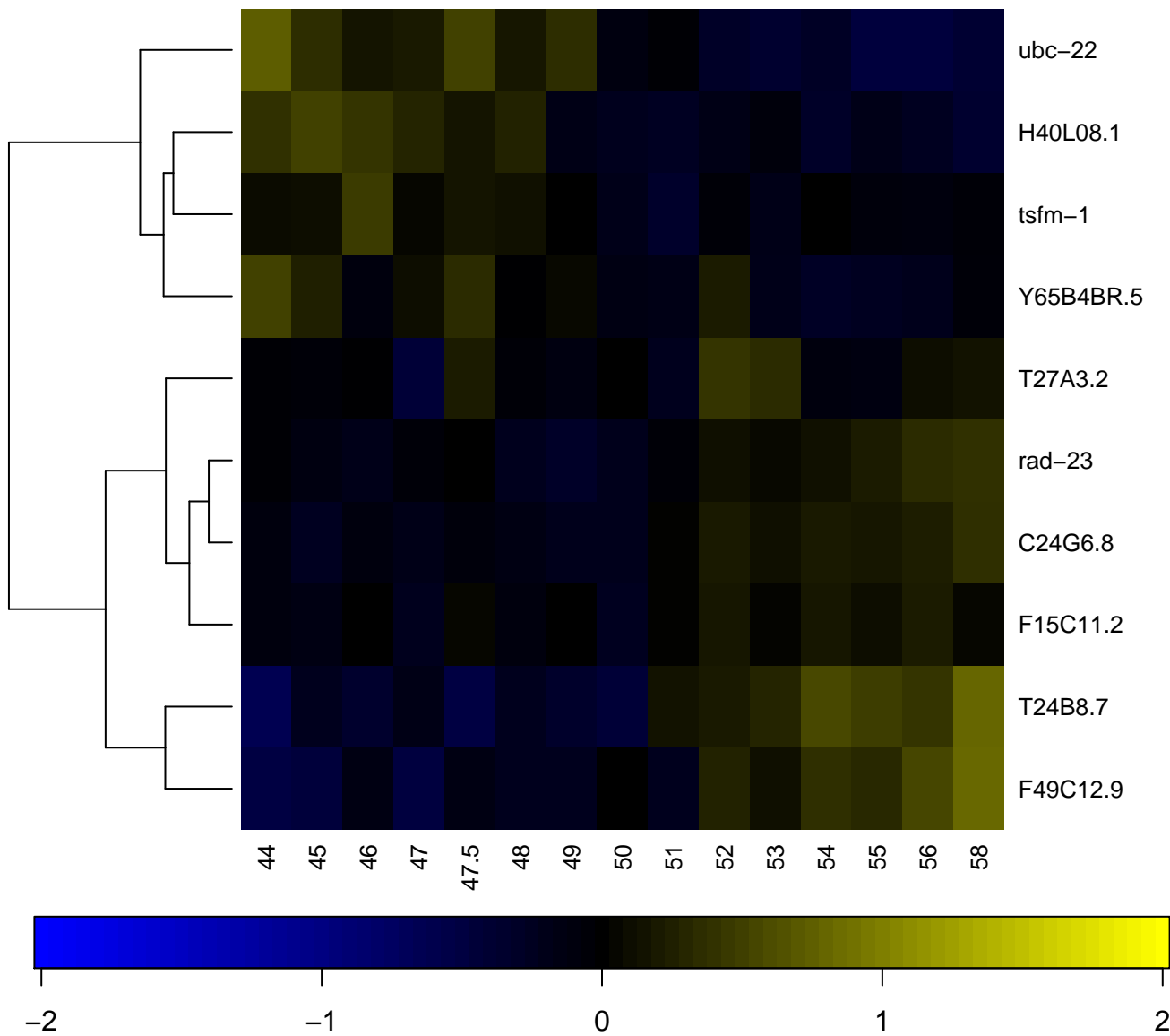
Tyrosine-protein kinase, active site



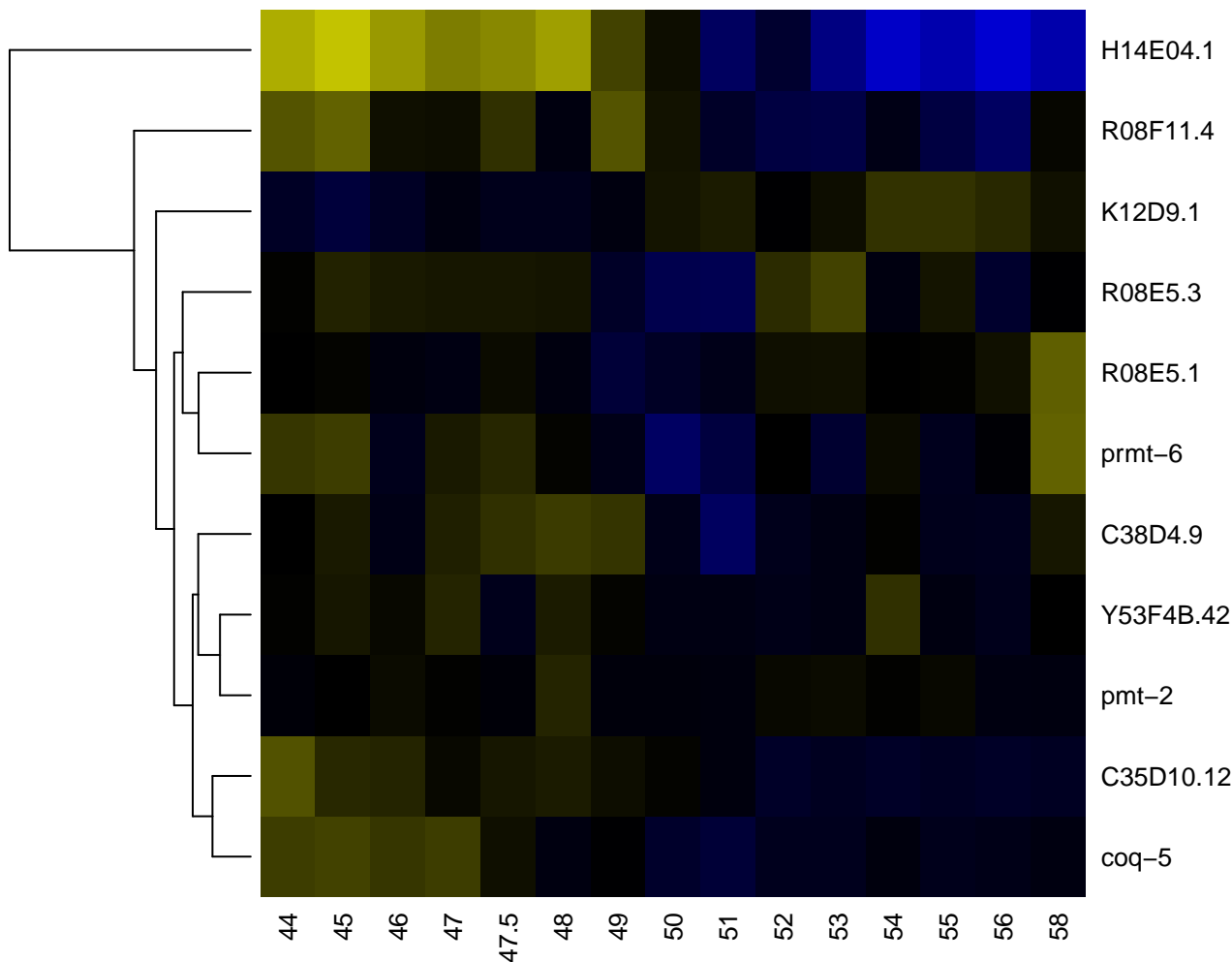
Tyrosine-protein kinase, catalytic domain



UBA/TS-N domain



UbiE/COQ5 methyltransferase



-2

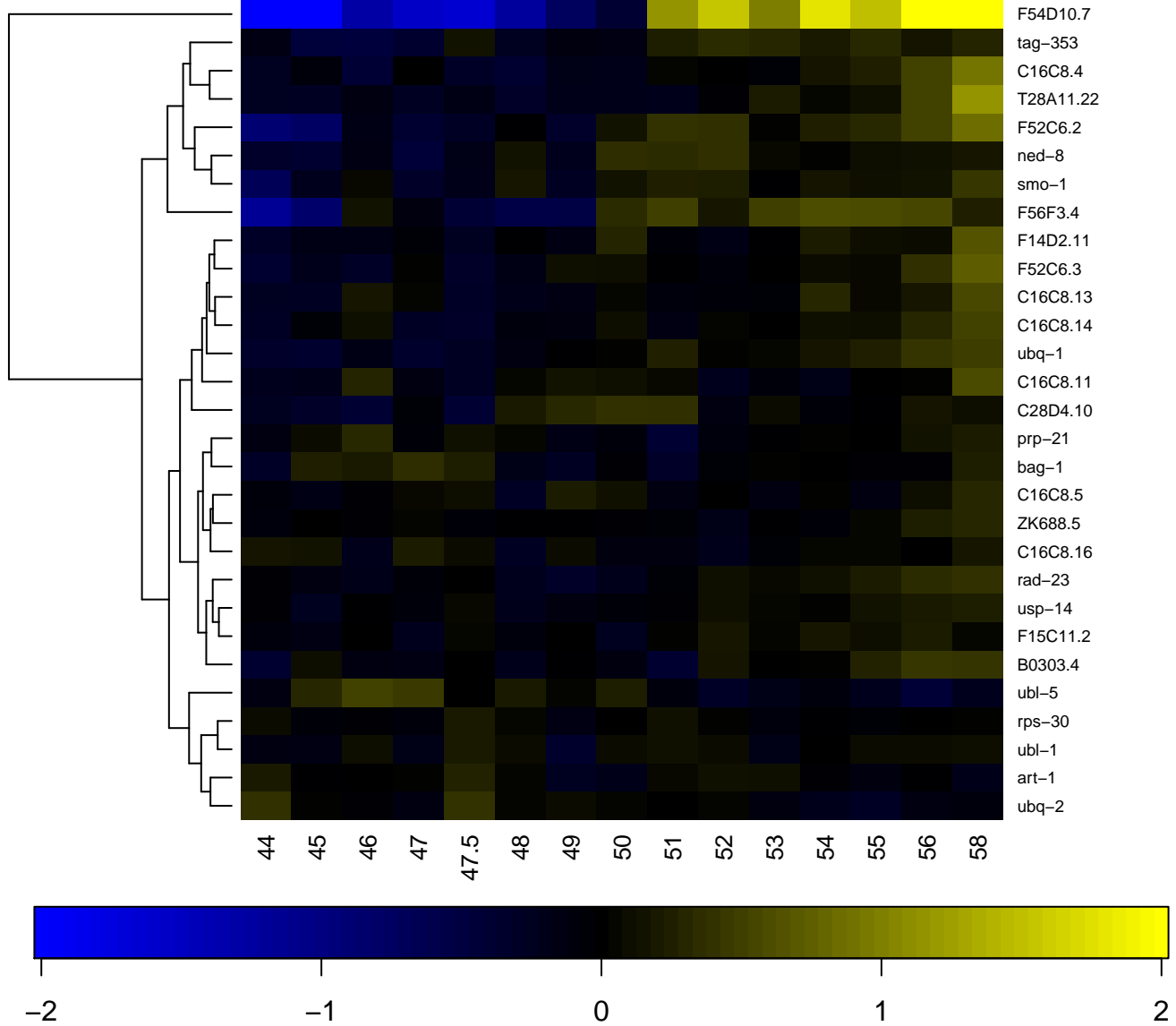
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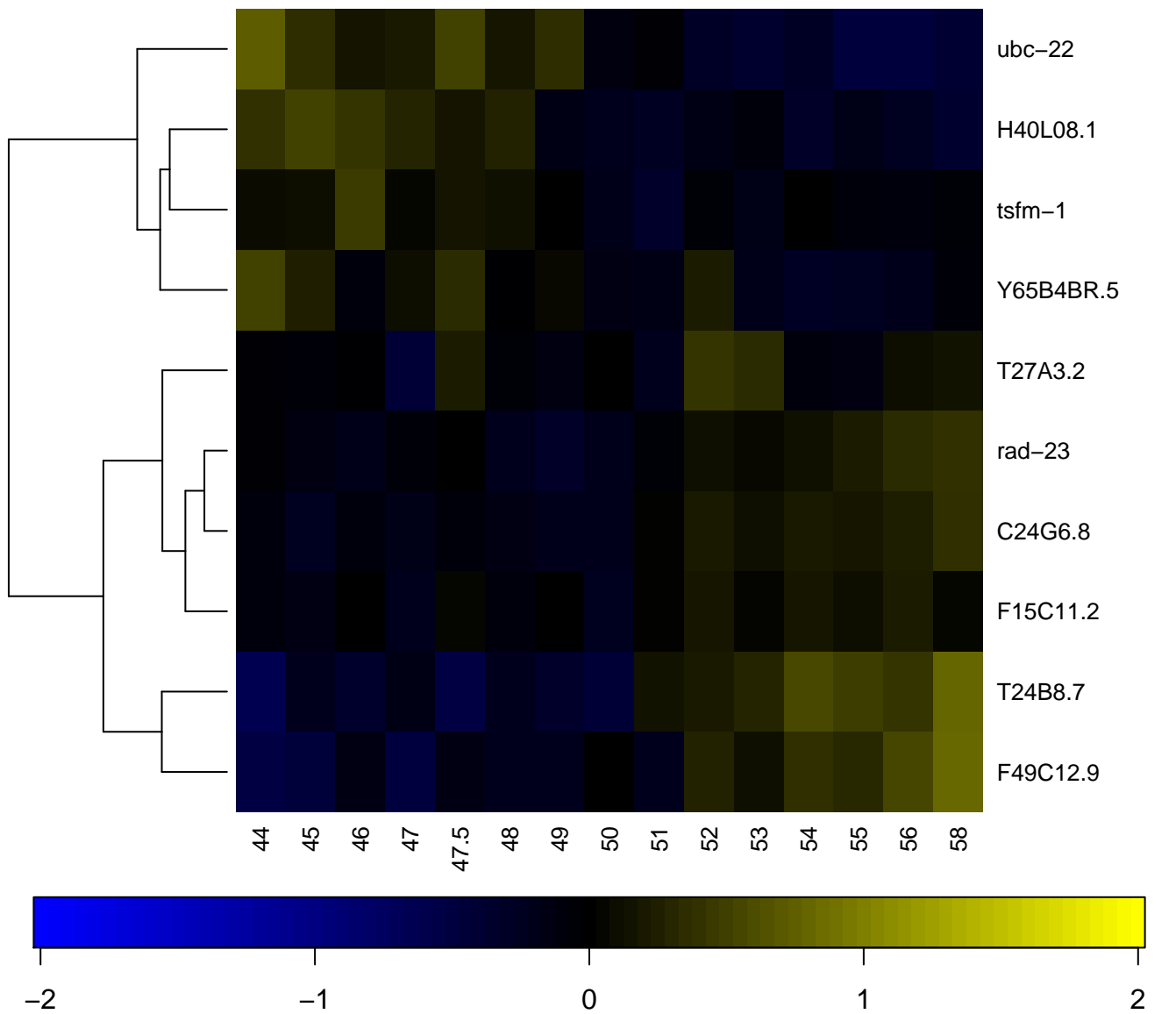
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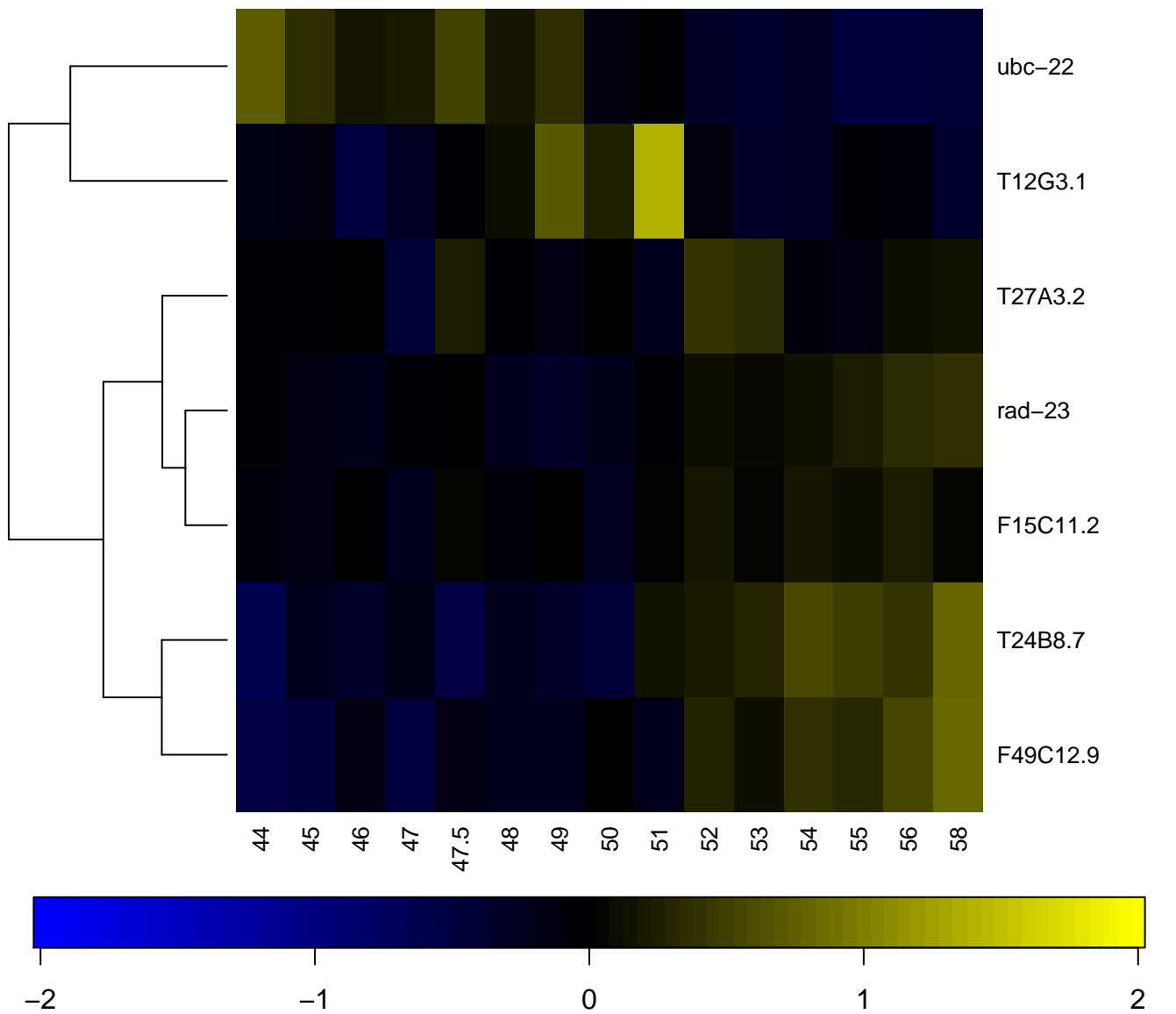
Ubiquitin



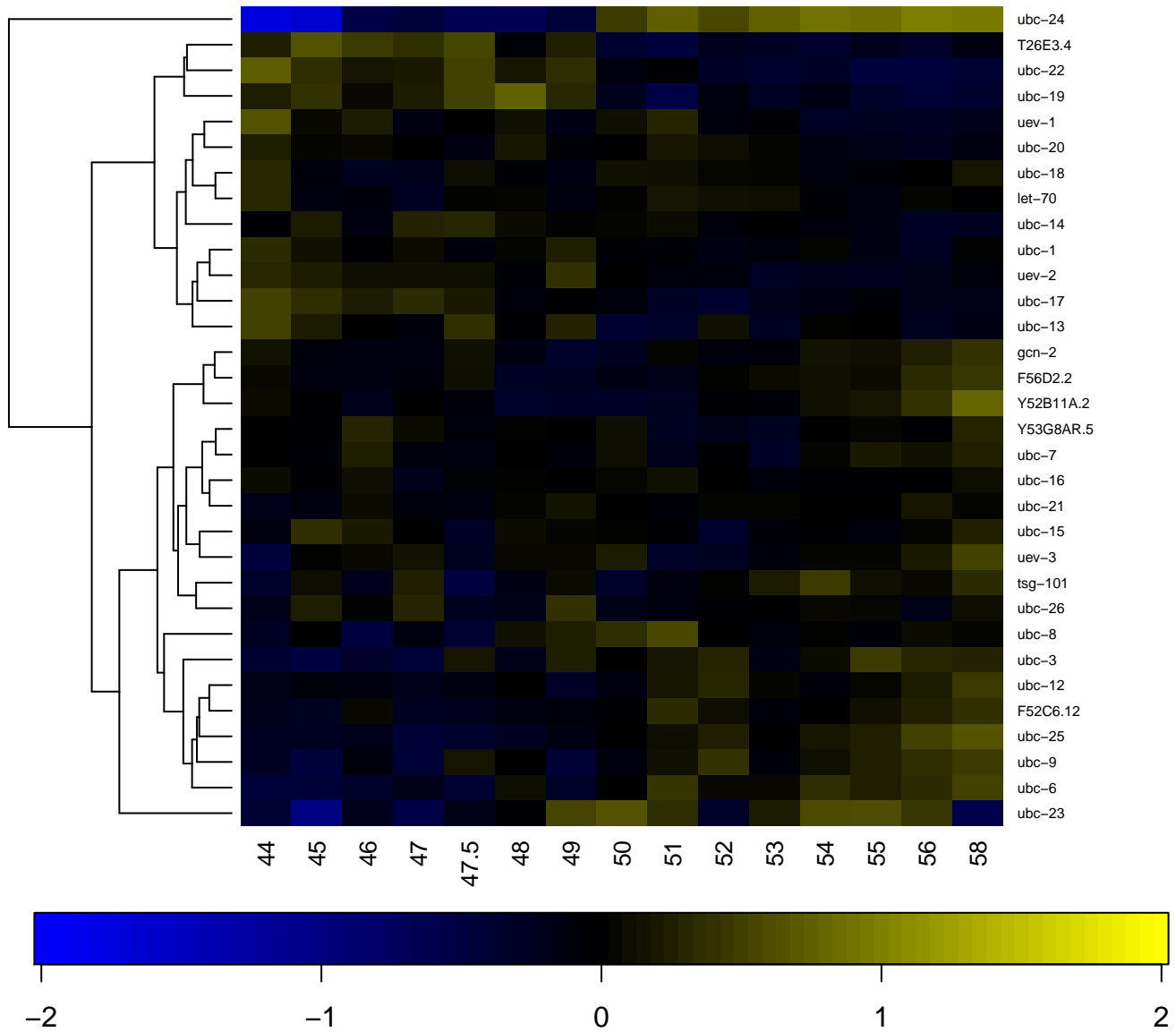
quitin-associated/translation elongation factor EF1B, N-ter



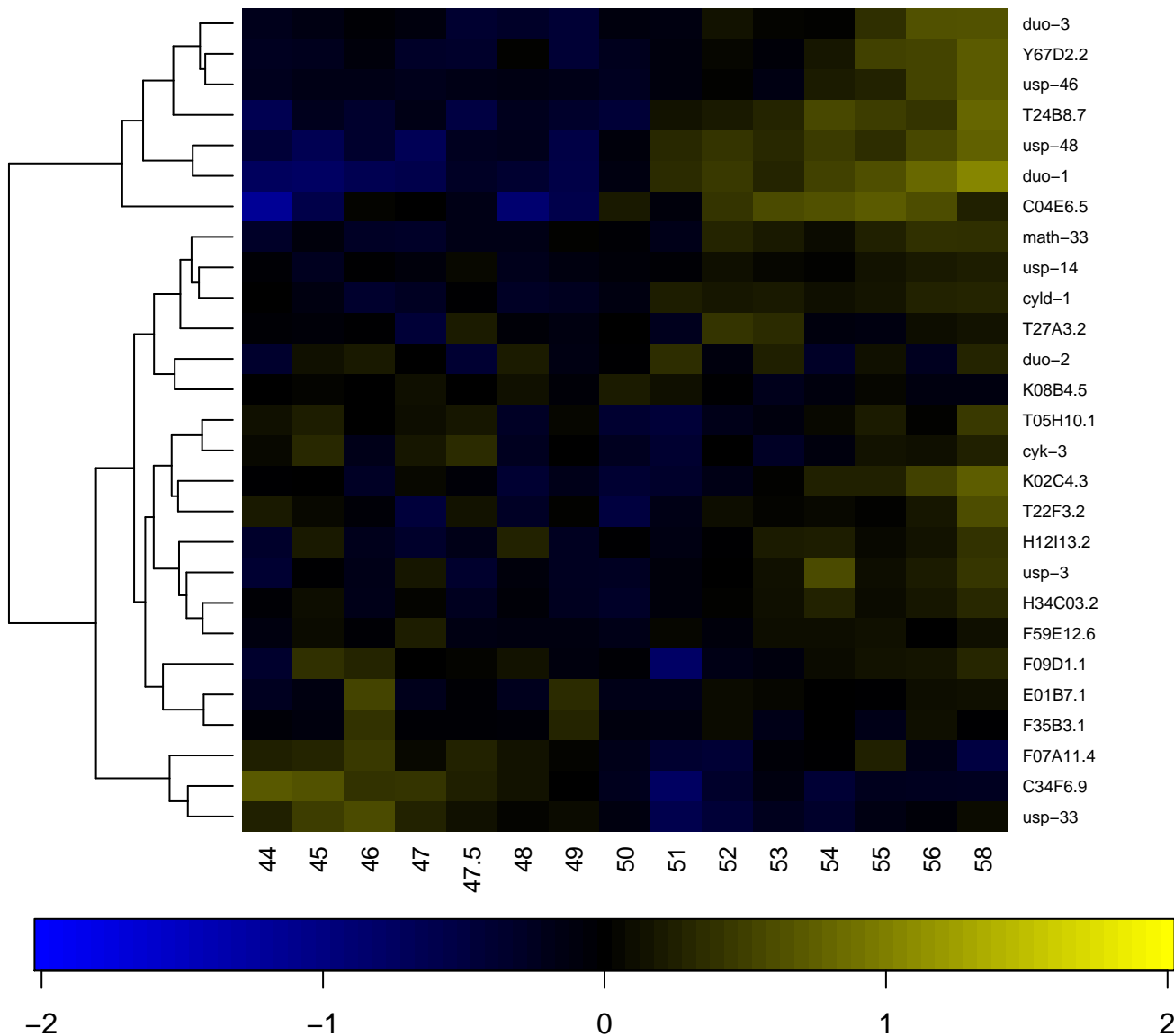
-associated/translation elongation factor EF1B, N-terminal



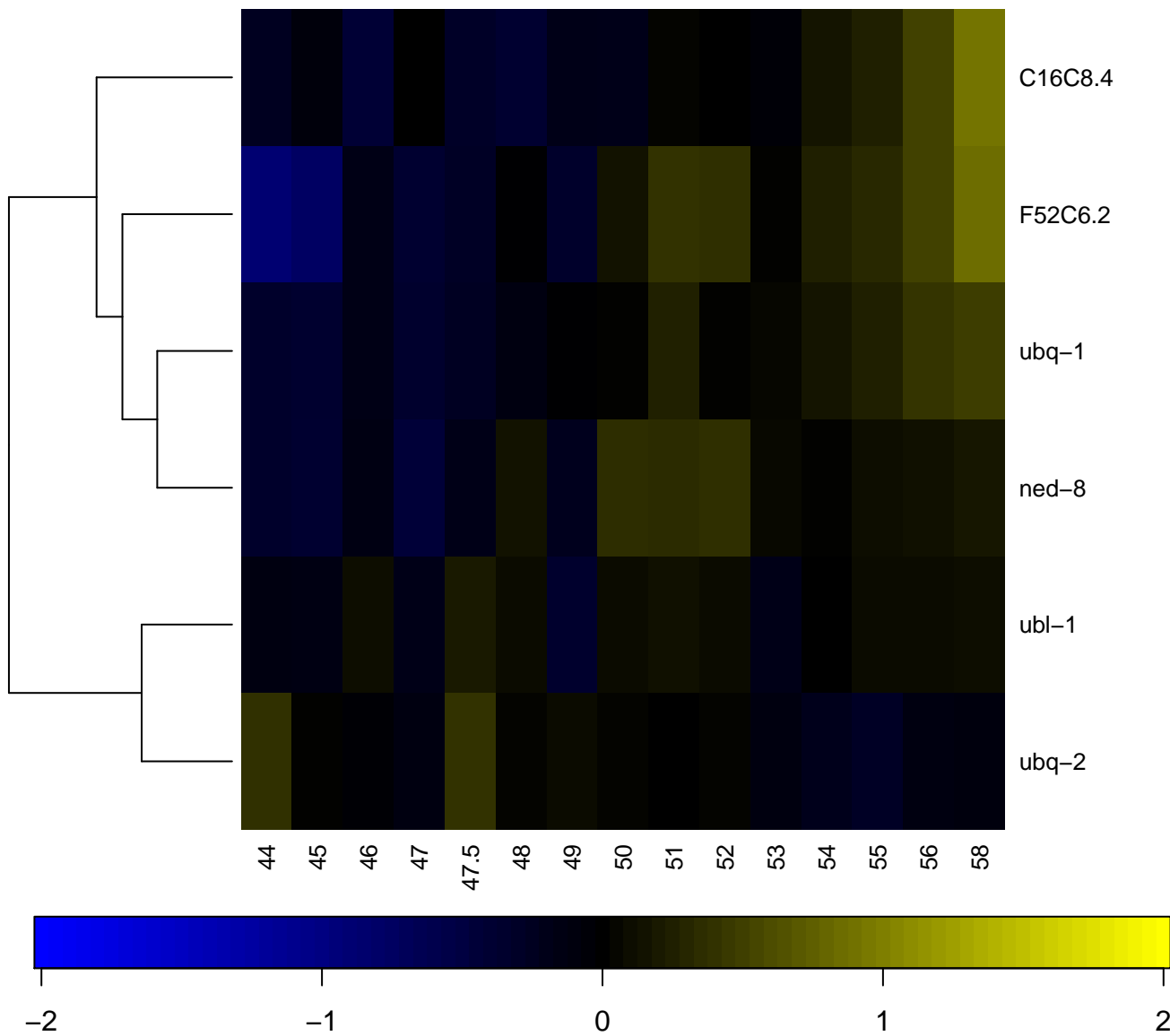
Ubiquitin-conjugating enzyme/RWD-like



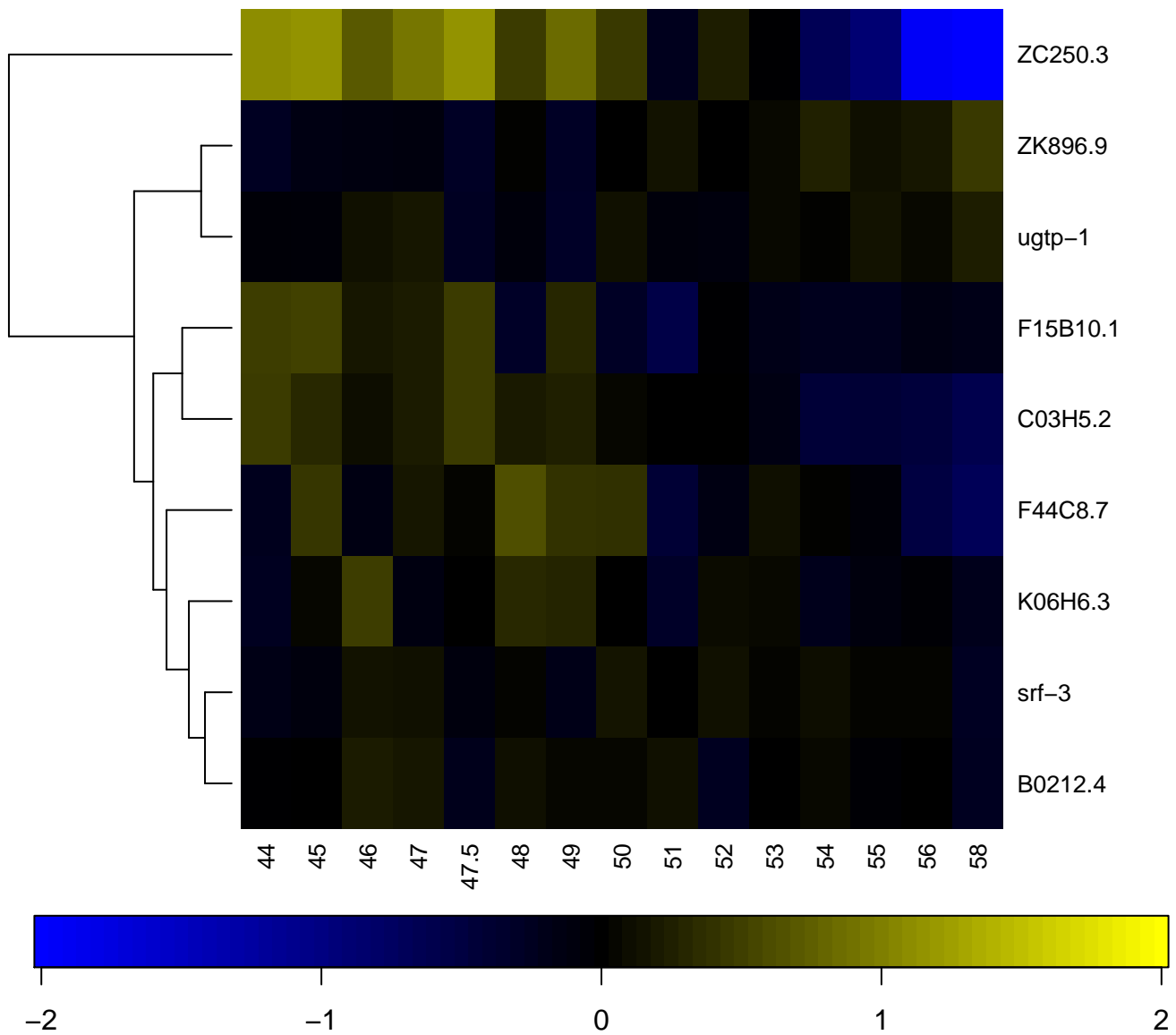
Ubiquitin carboxyl-terminal hydrolase



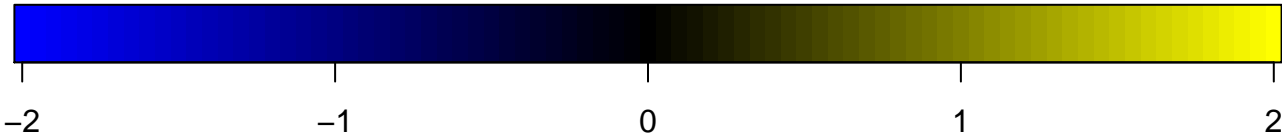
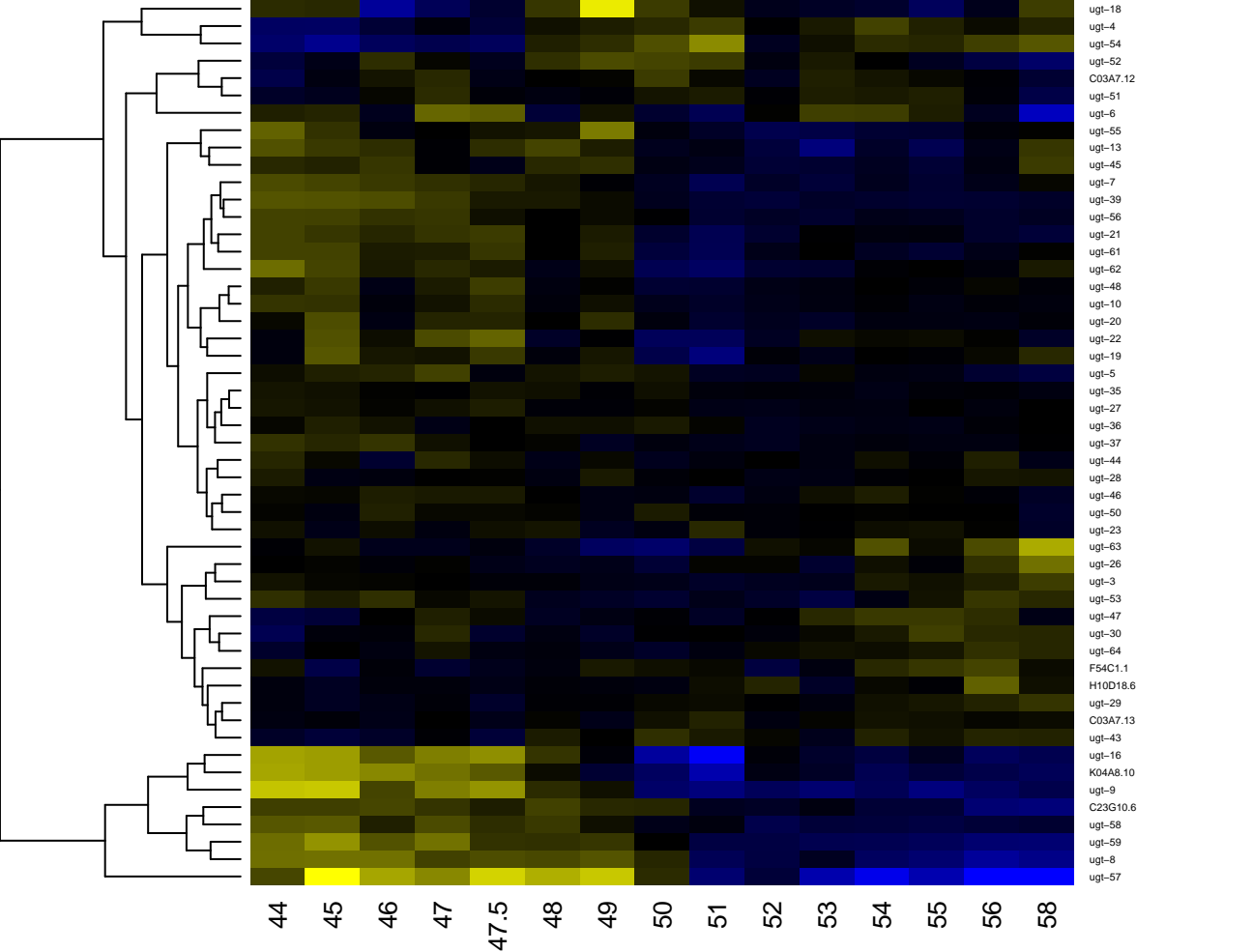
Ubiquitin subgroup



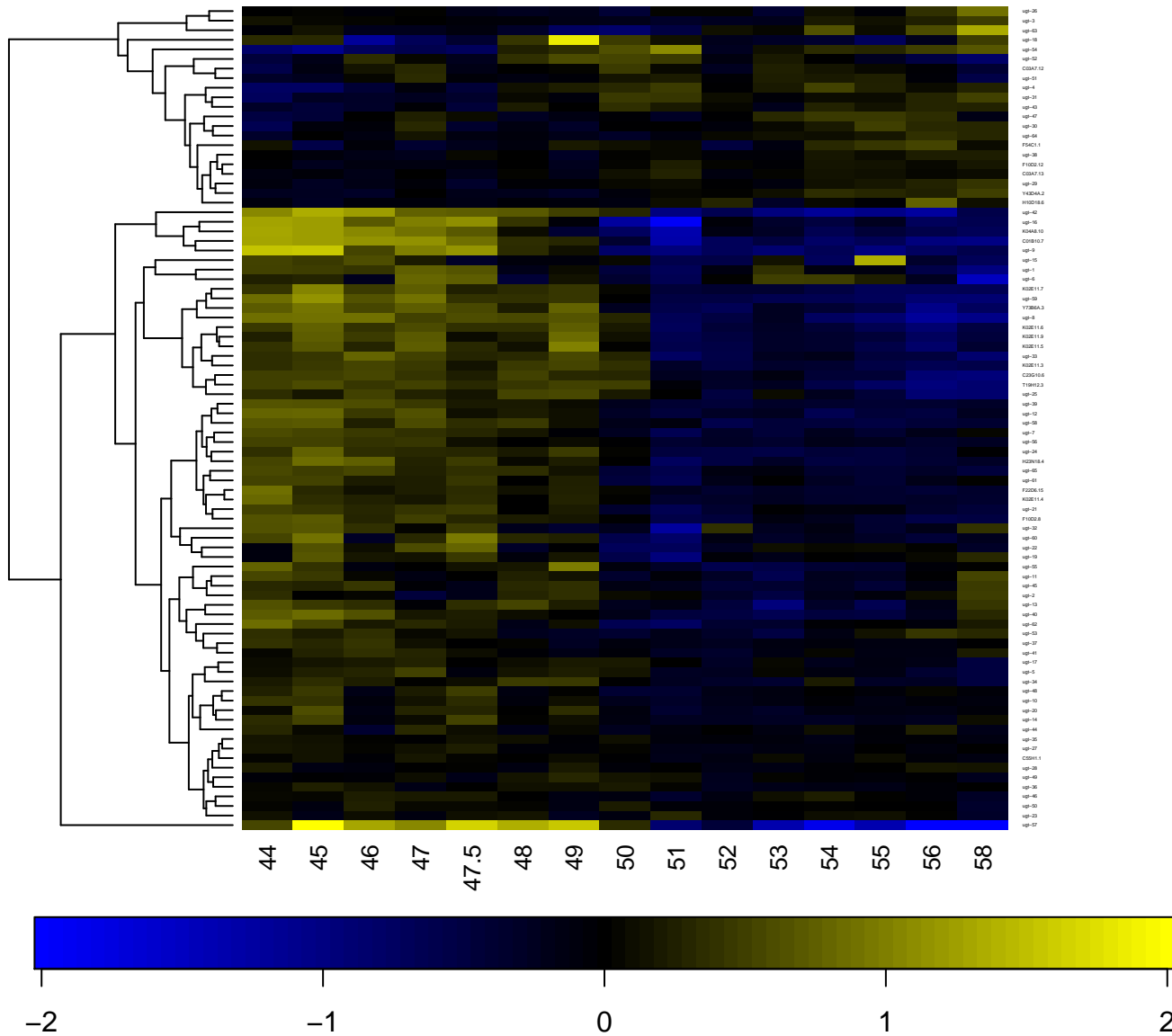
UDP-galactose transporter



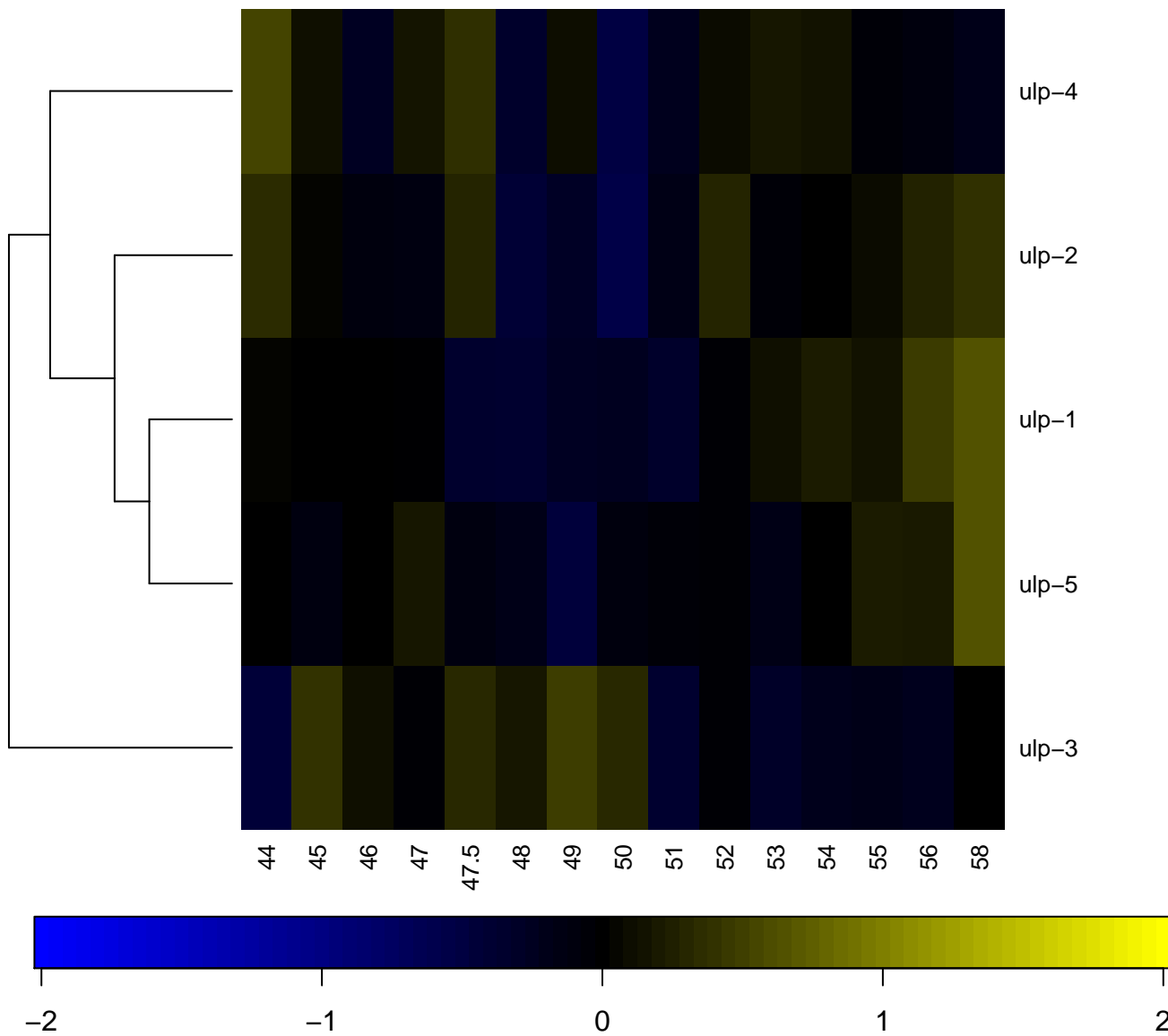
UDP-glucuronosyl and UDP-glucosyl transferase



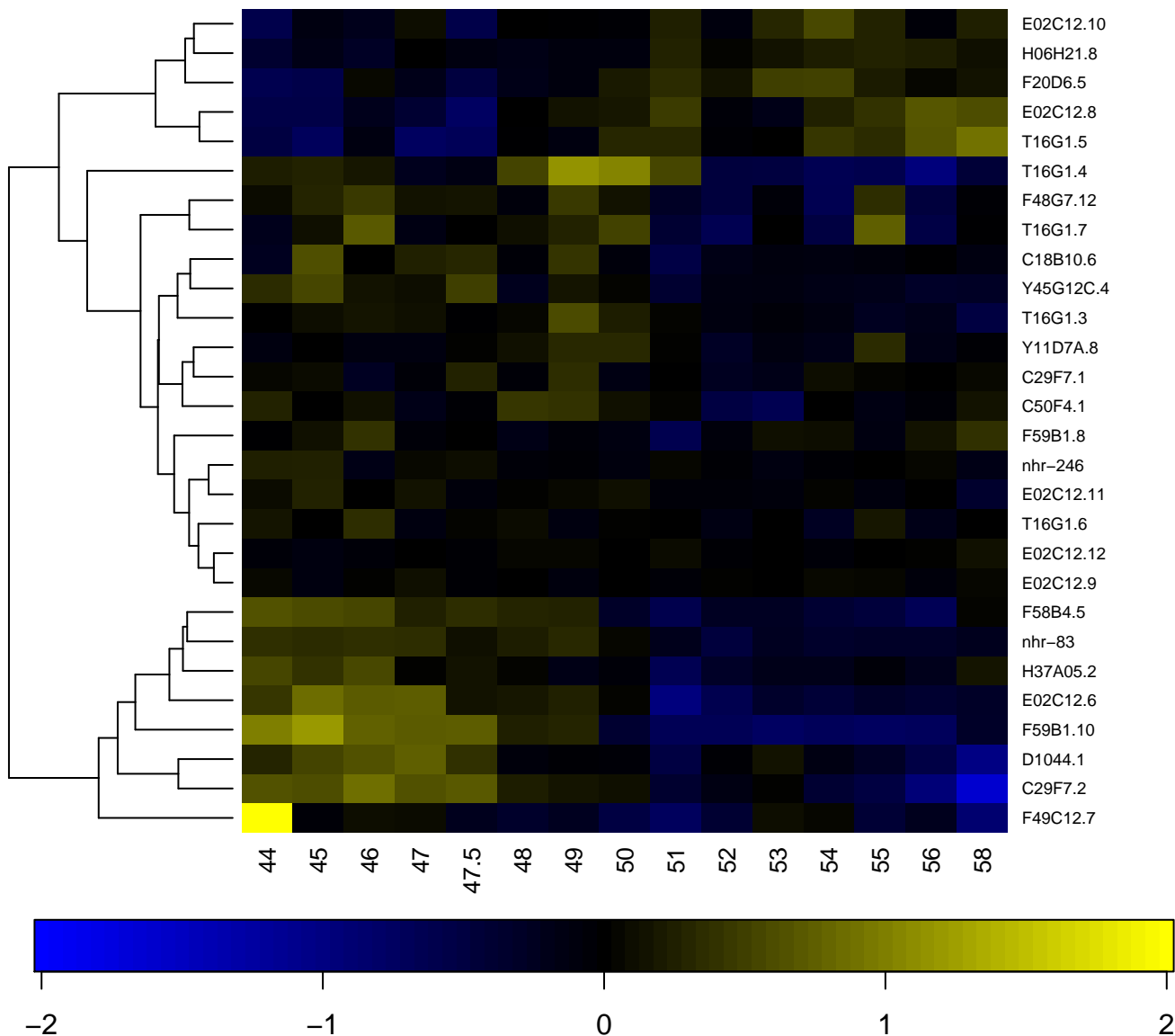
UDP-glucuronosyl/UDP-glucosyltransferase



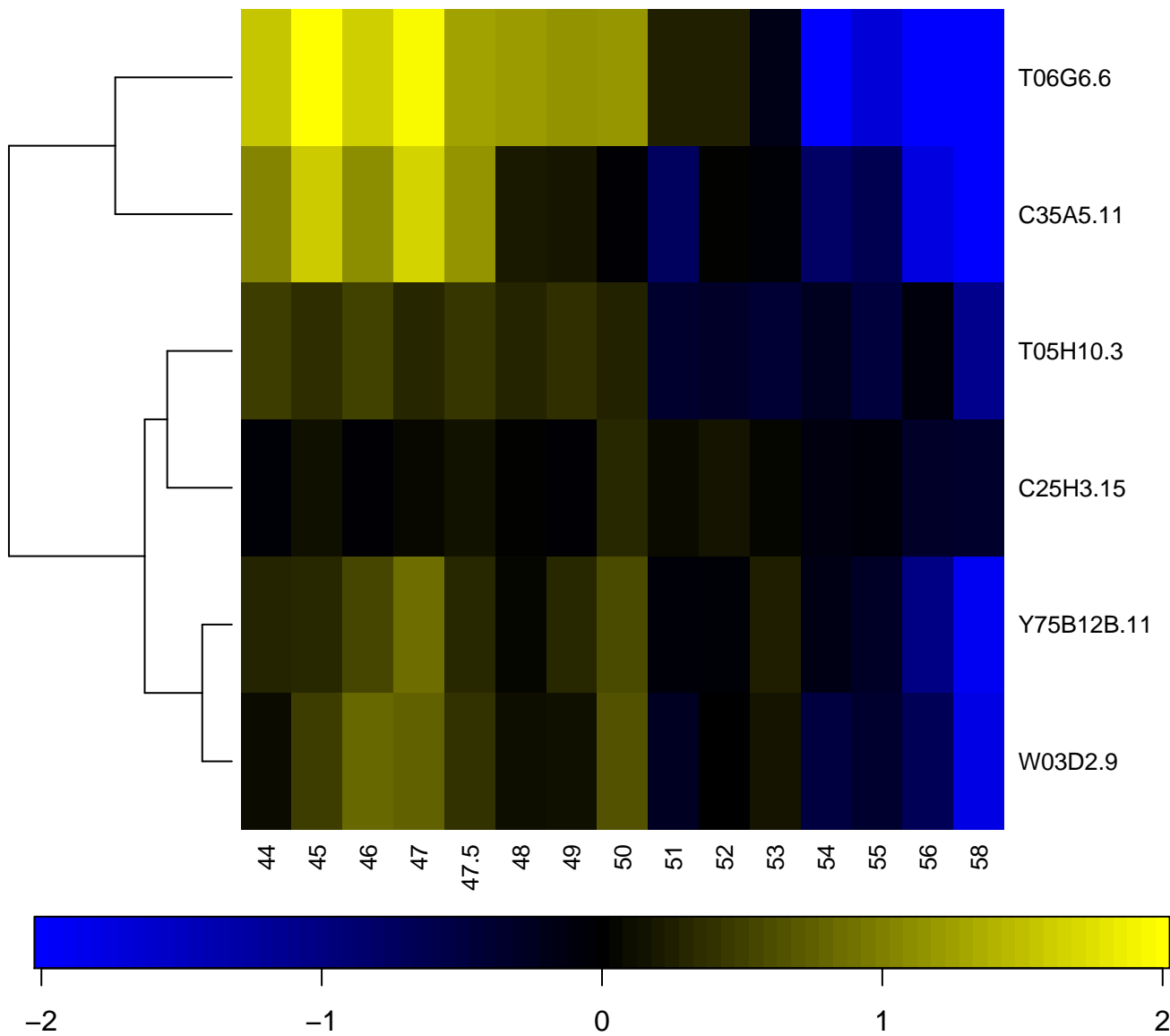
Ulp1 protease family, C-terminal catalytic domain



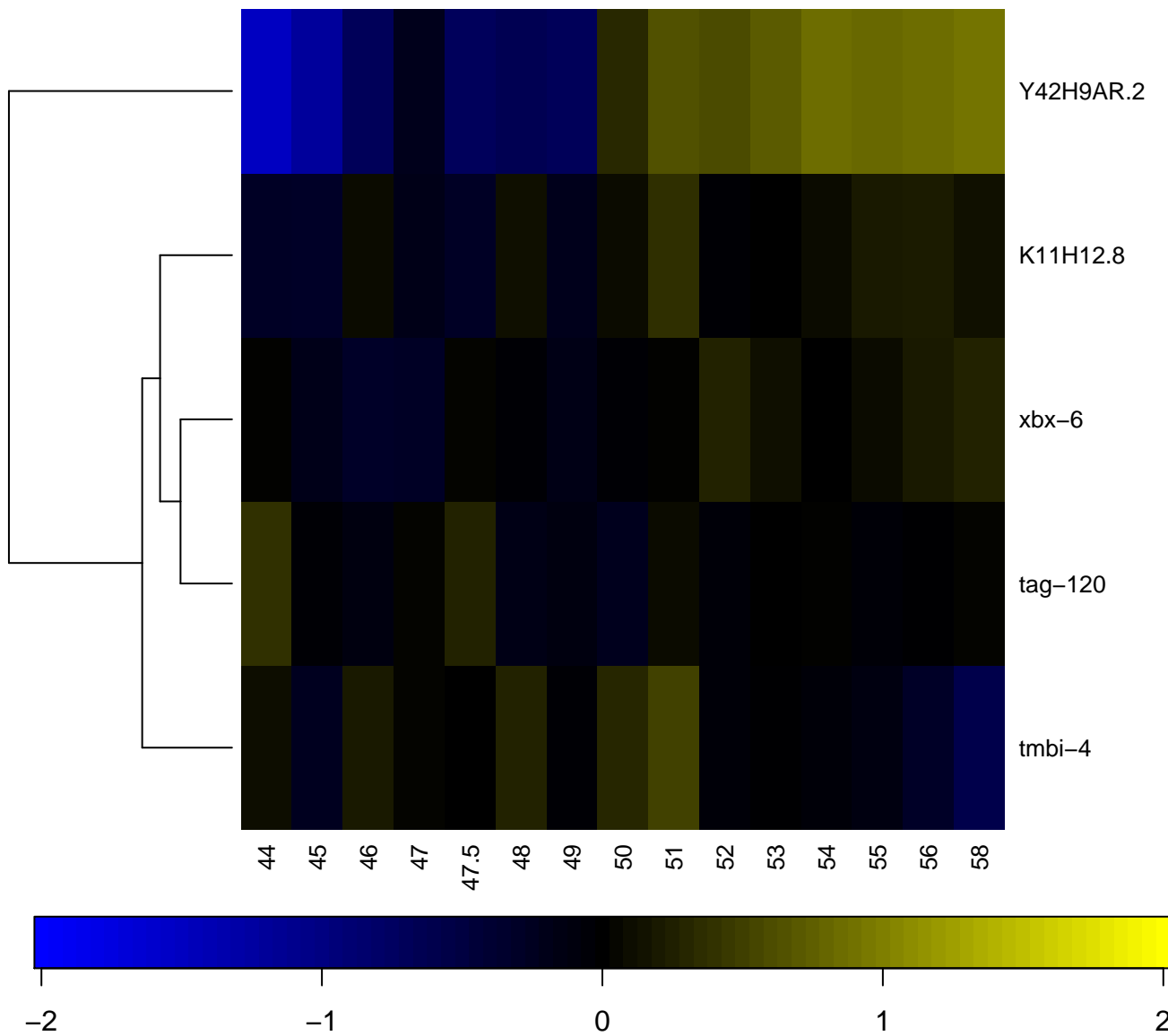
Uncharacterised kinase D1044.1



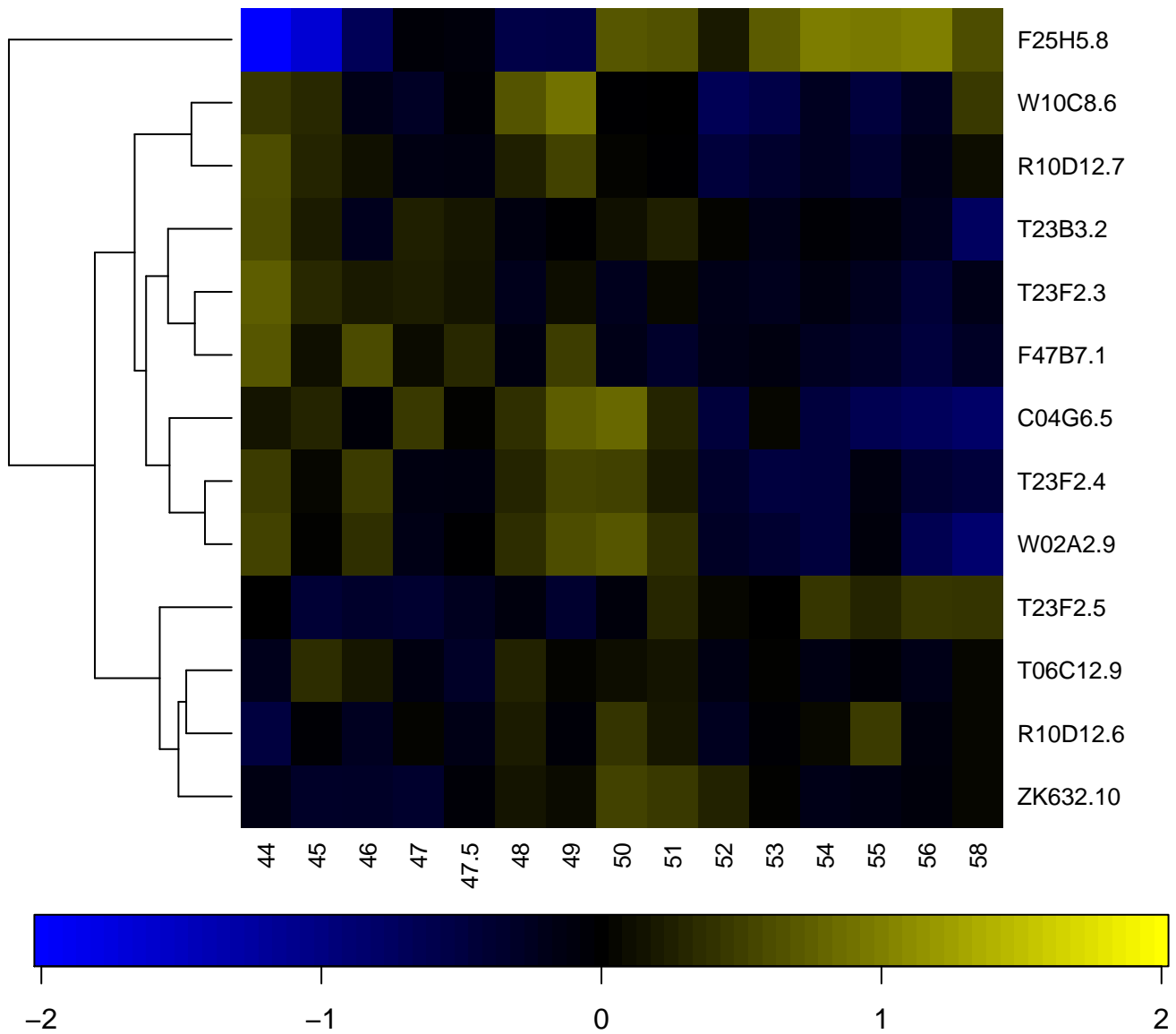
Uncharacterised protein family T05H10.3



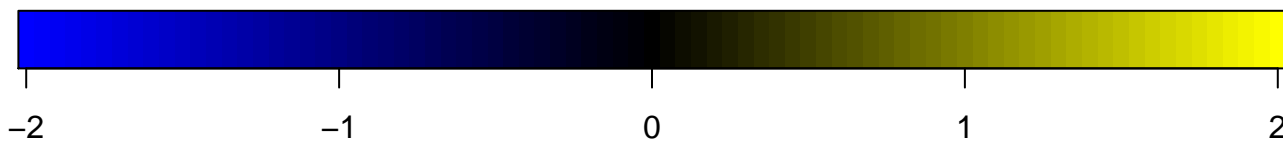
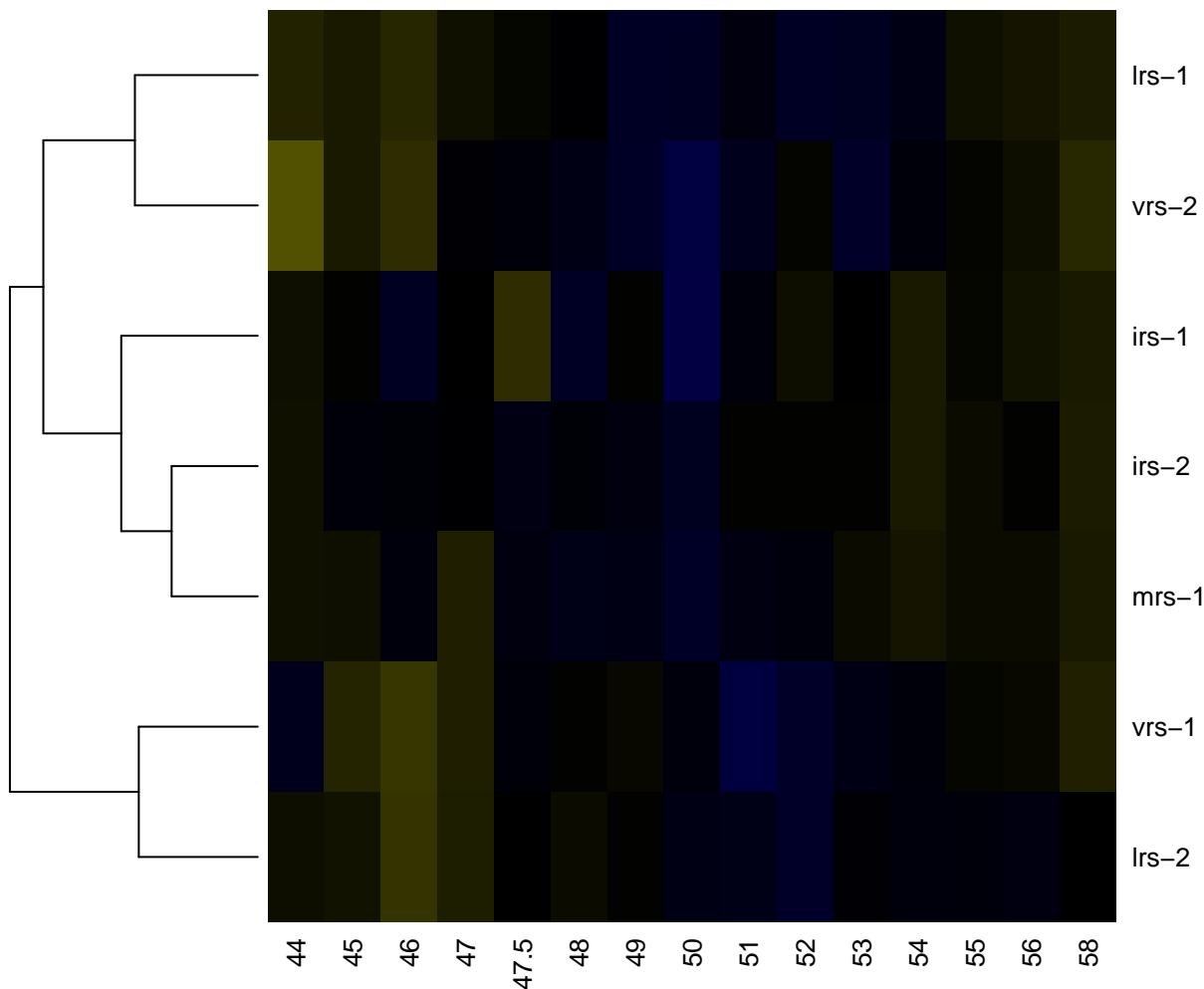
Uncharacterised protein family UPF0005



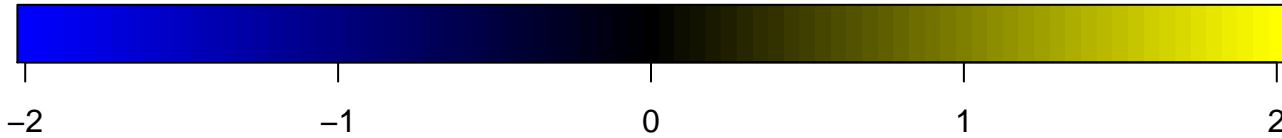
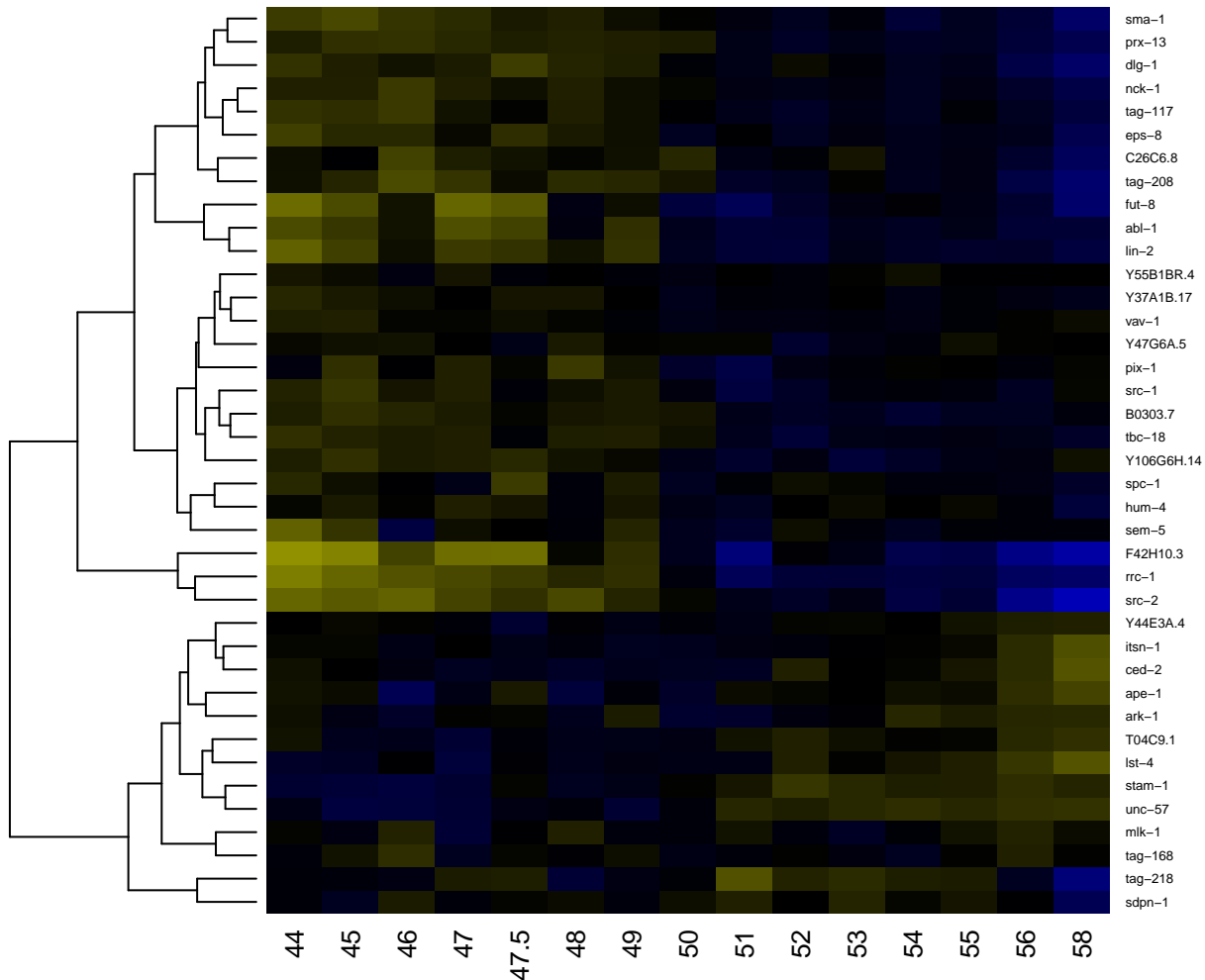
Uncharacterised protein family UPF0057



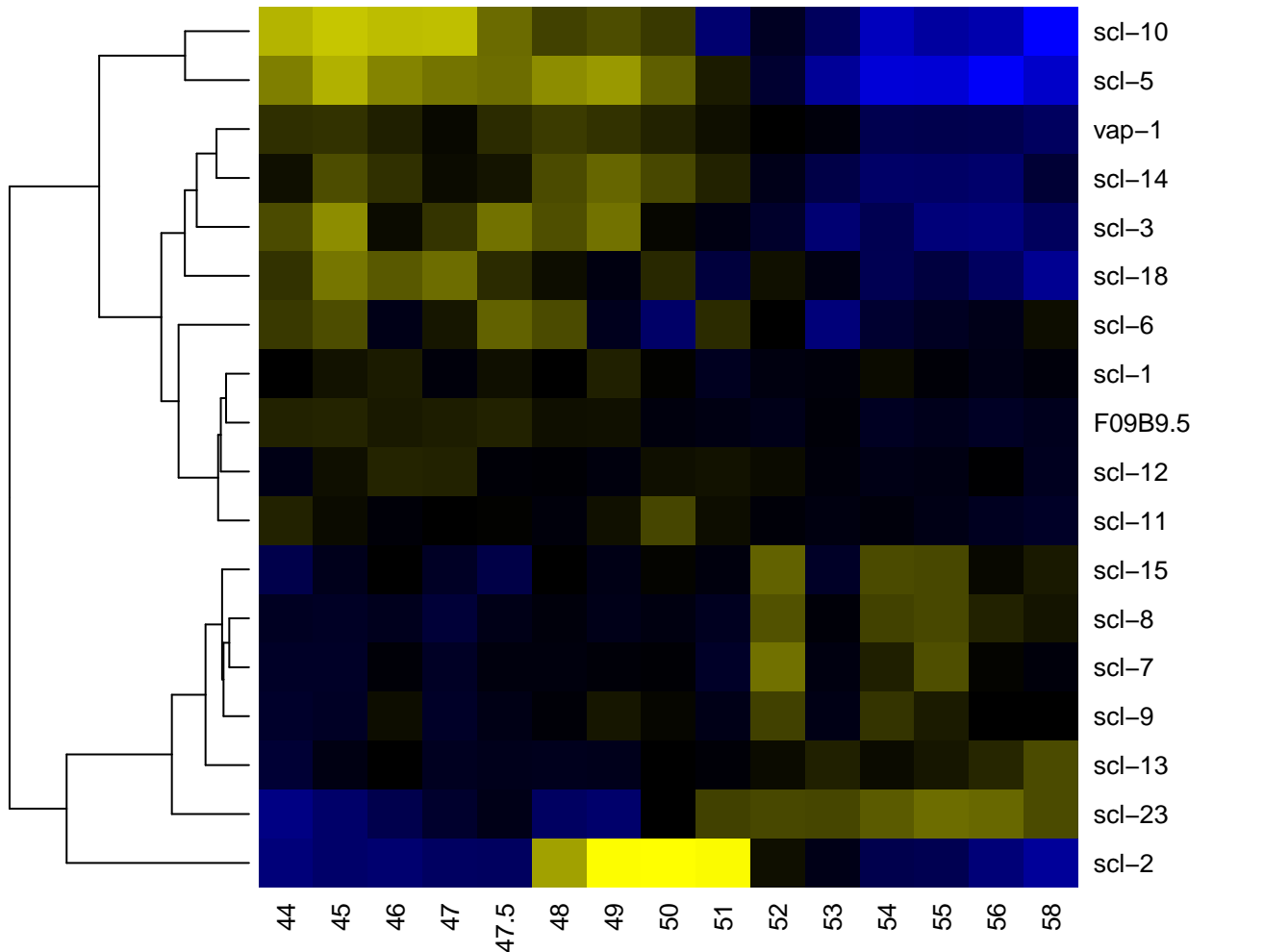
yl/Leucyl/Isoleucyl-tRNA synthetase, class I, anticodon-binding



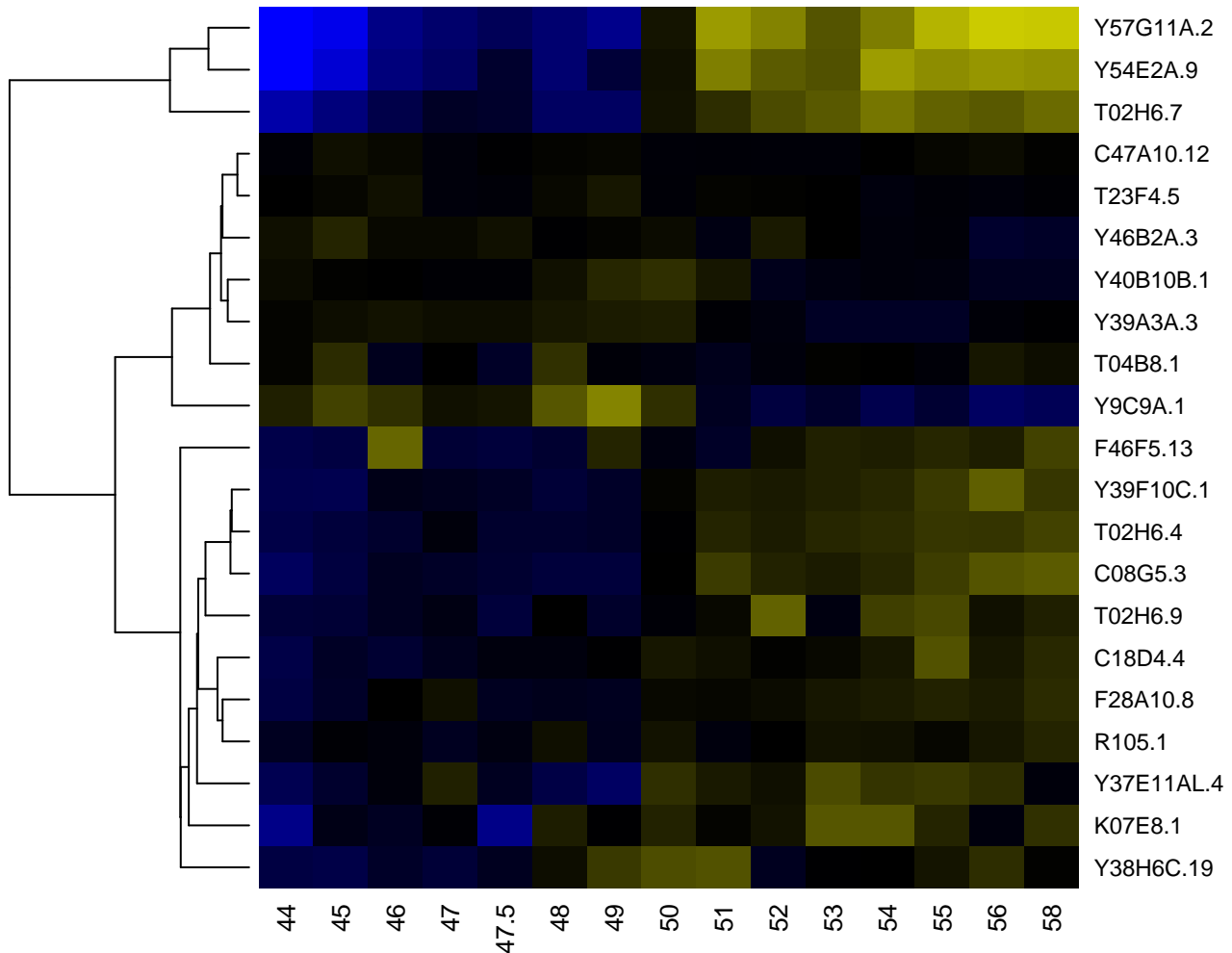
Variant SH3



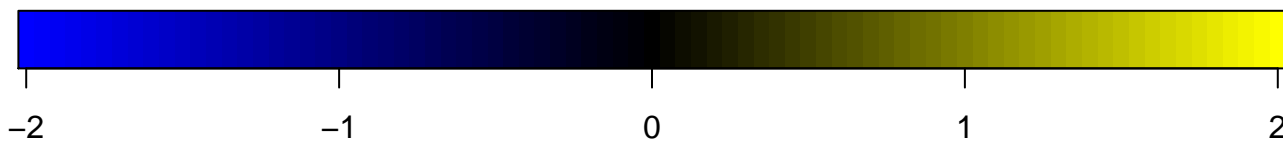
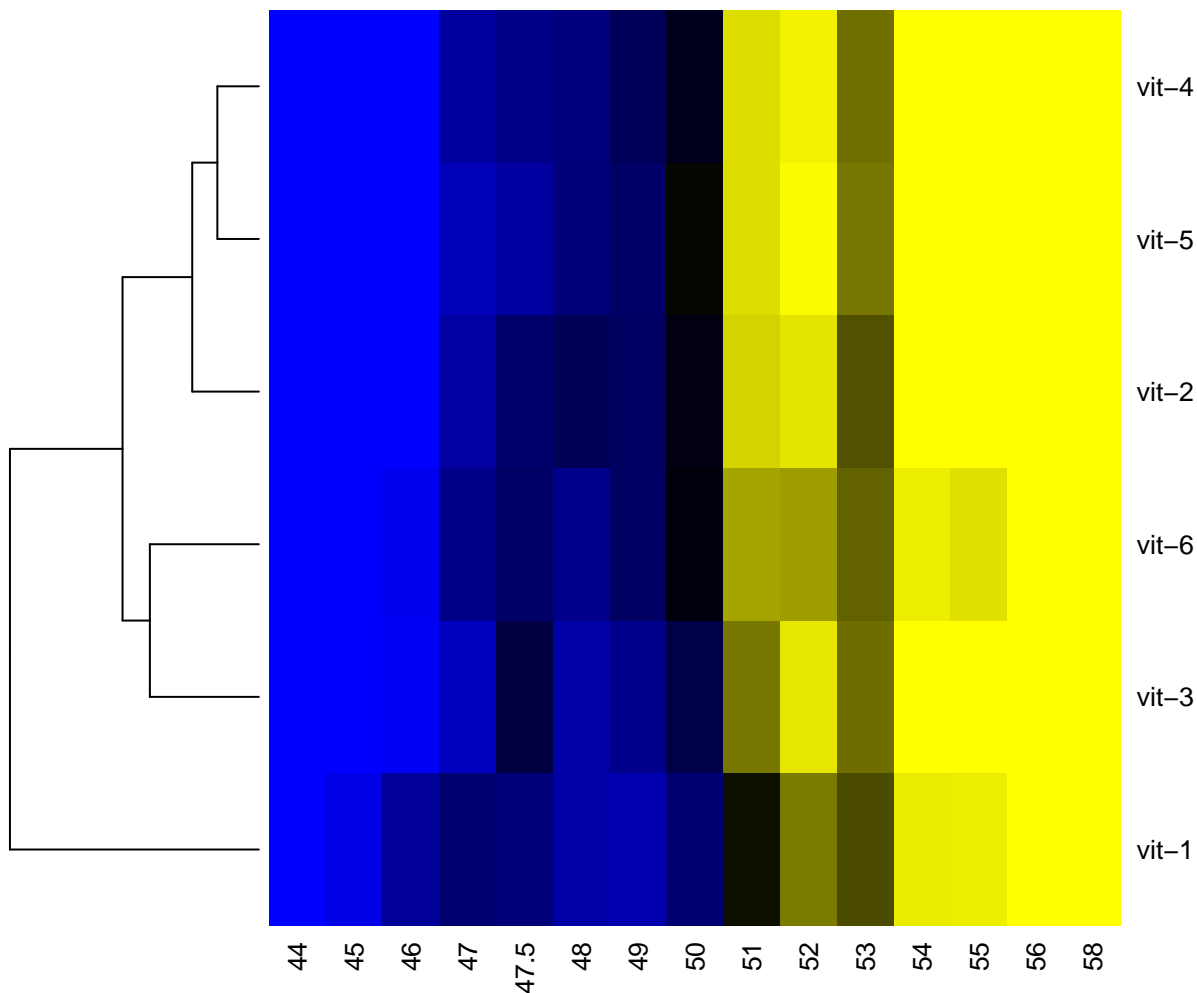
Ves allergen



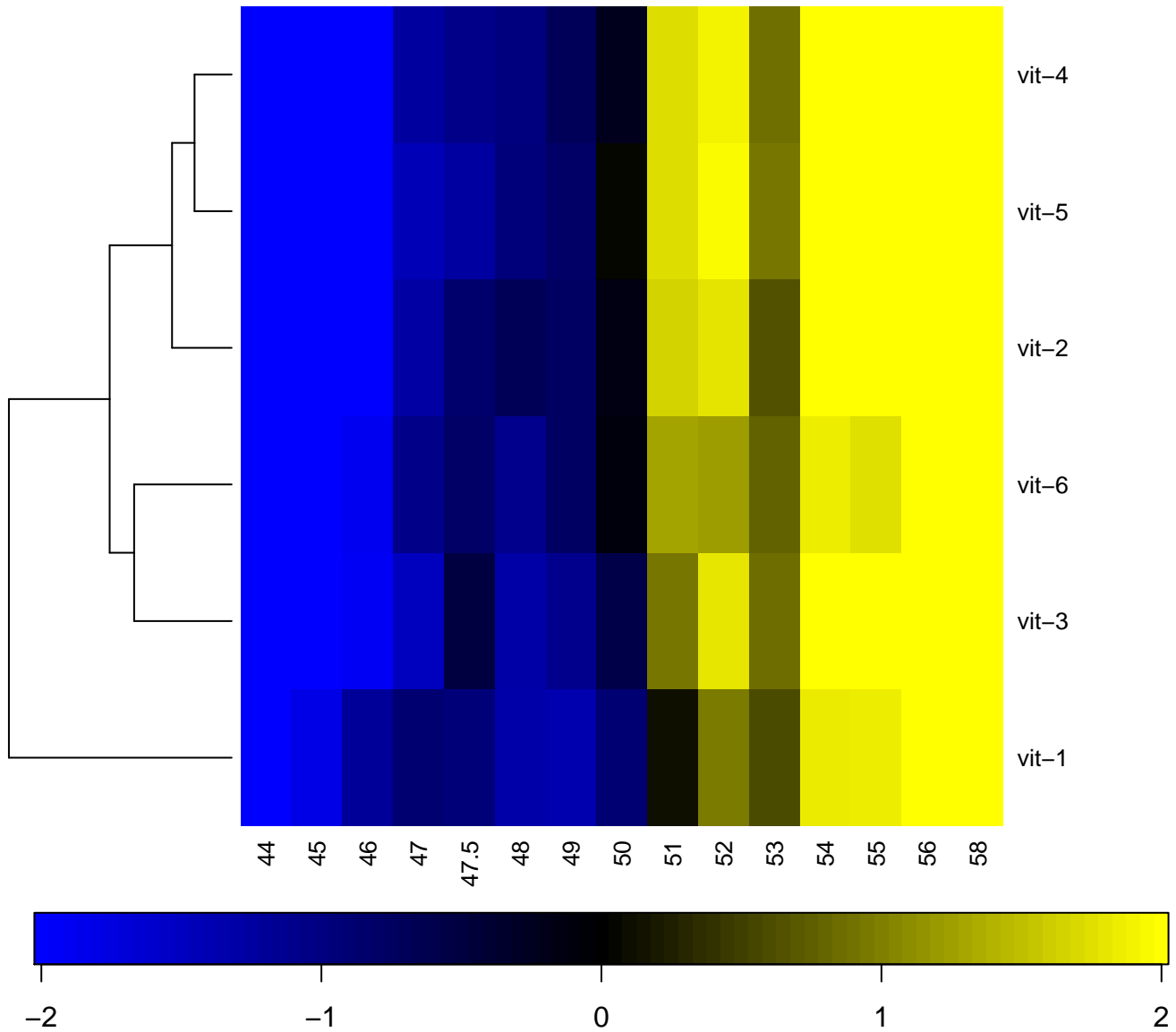
Vitelline membrane outer layer protein I (VOMI)



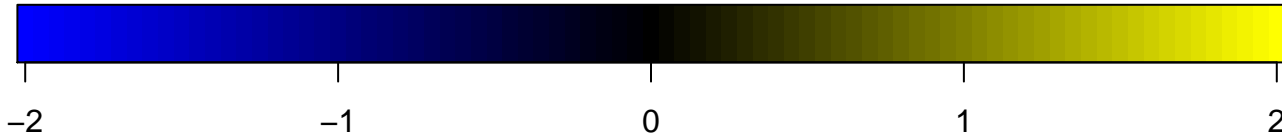
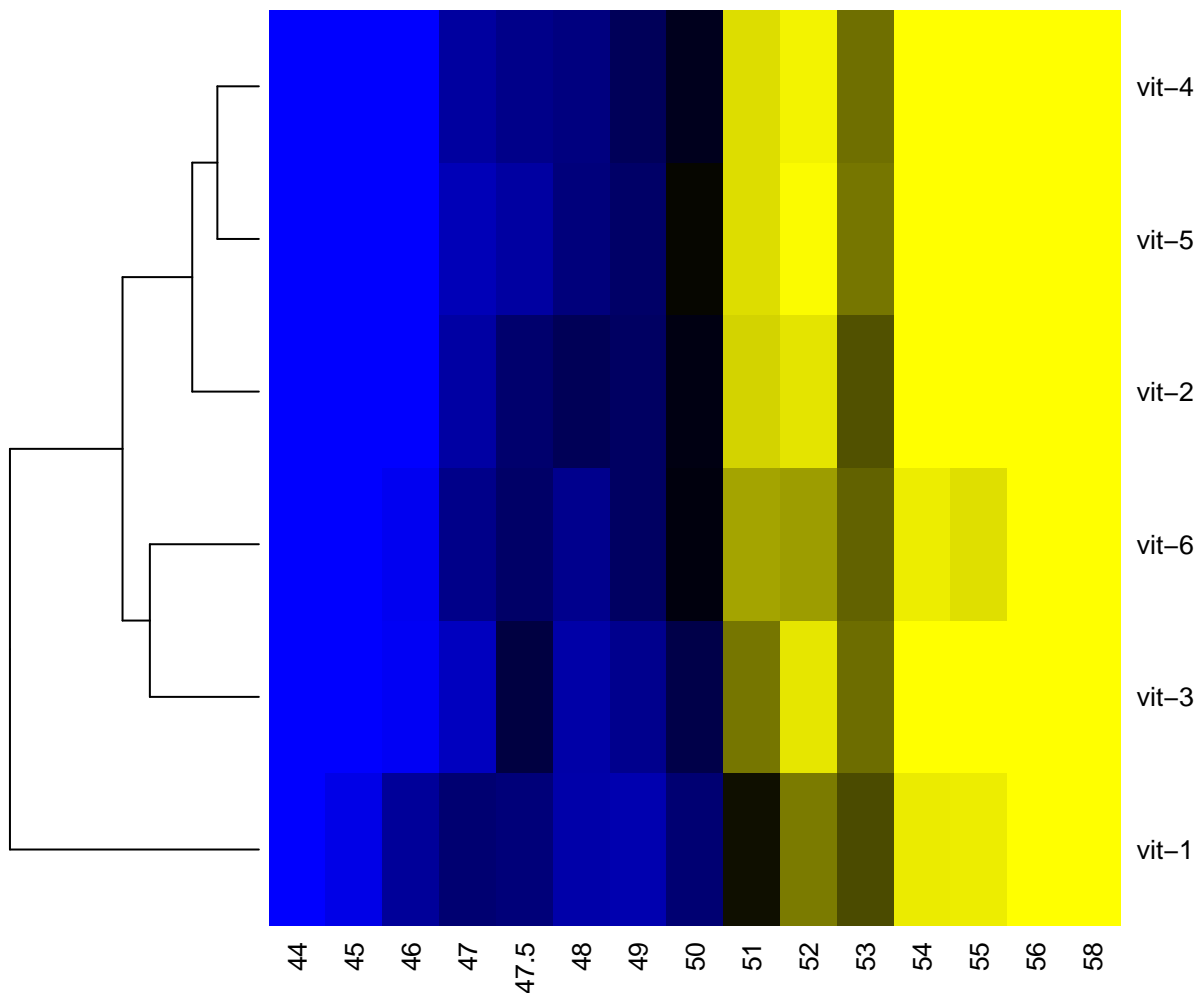
Vitellinogen, beta-sheet N-terminal



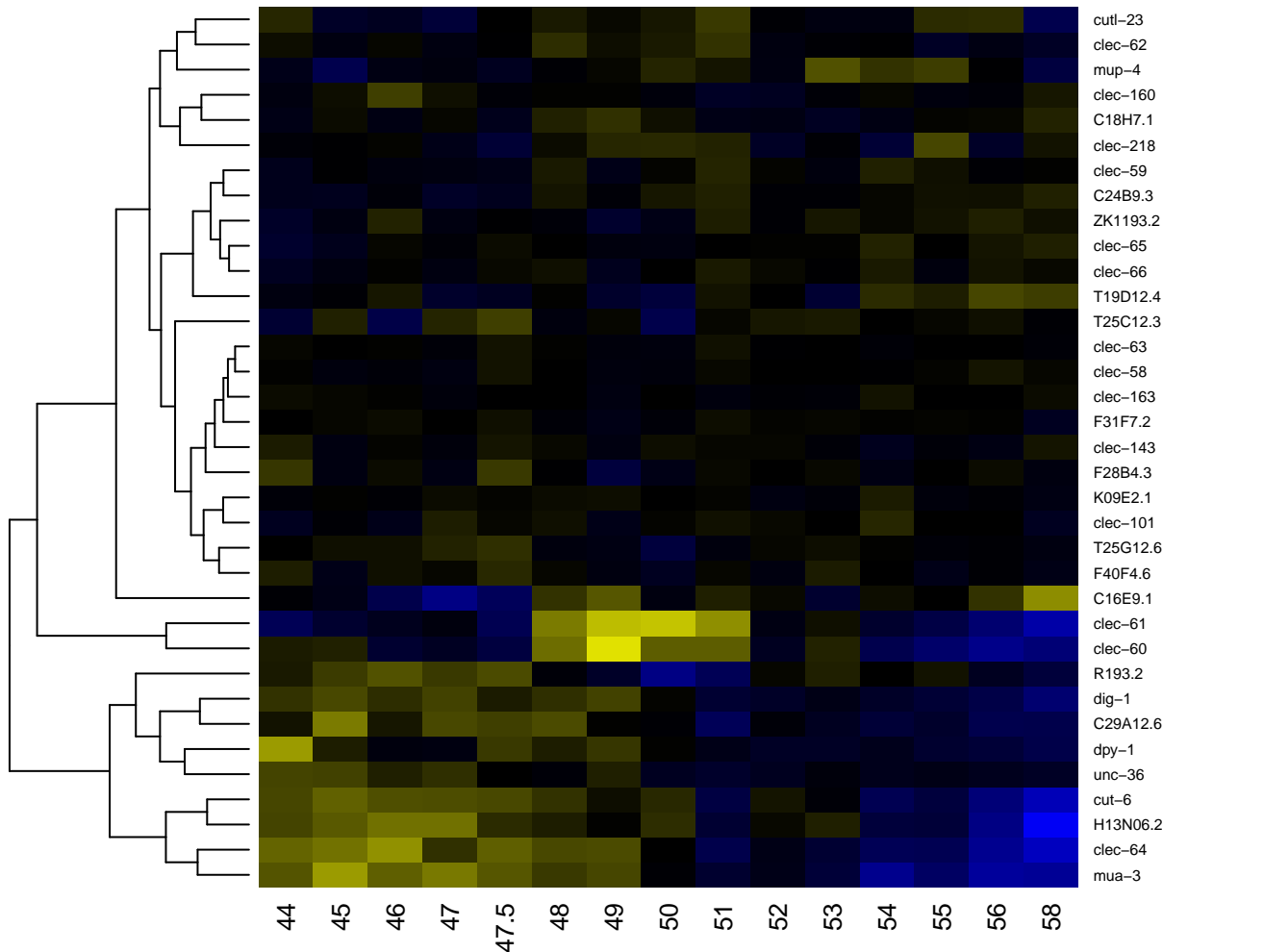
Vitellinogen, open beta-sheet



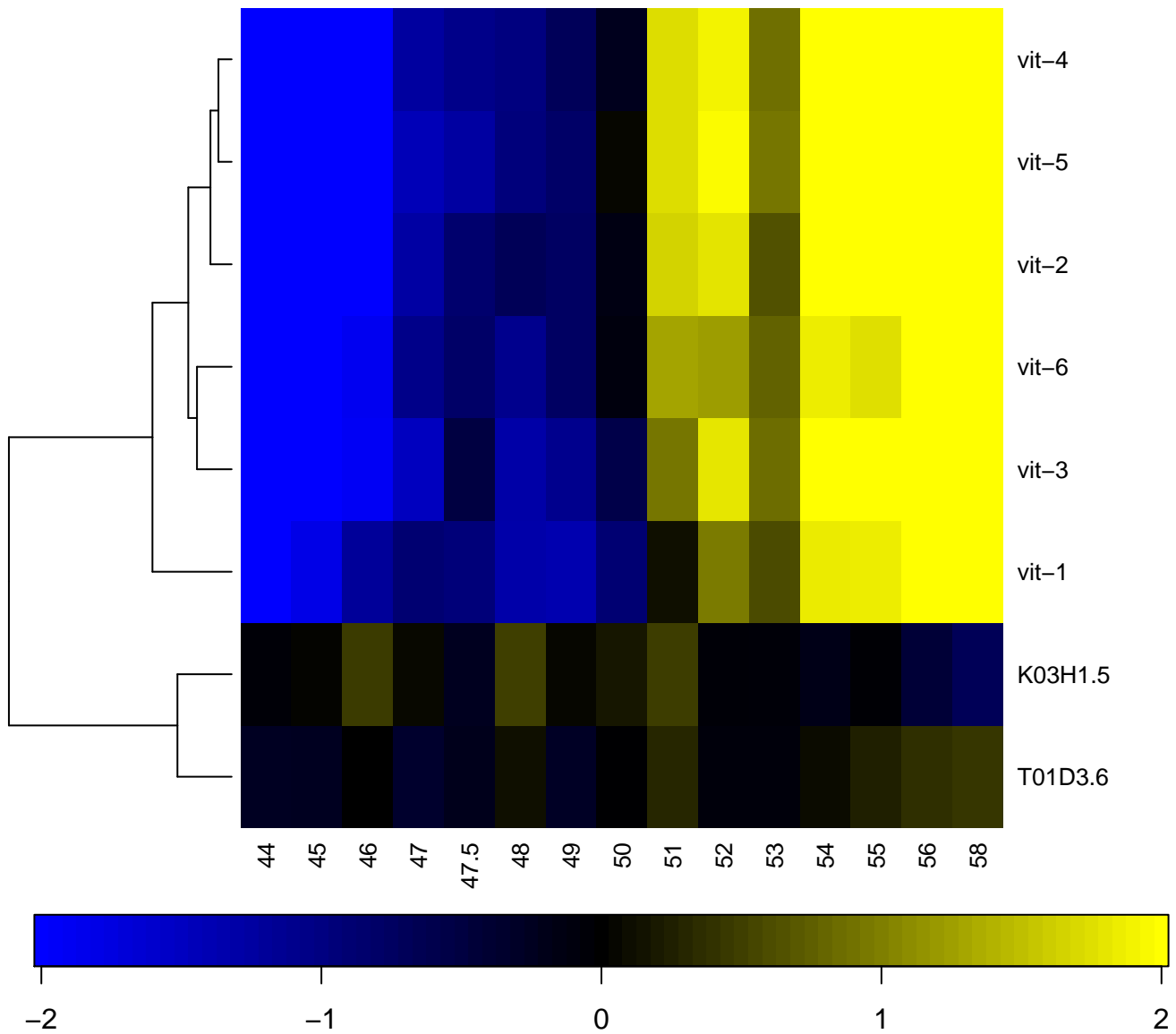
Vitellinogen, superhelical



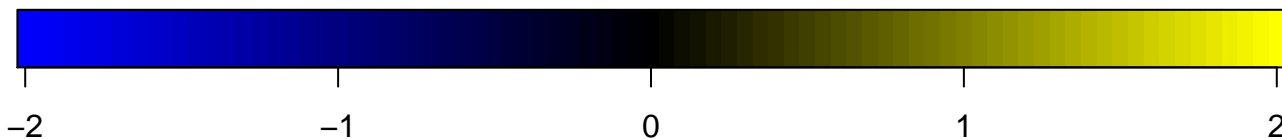
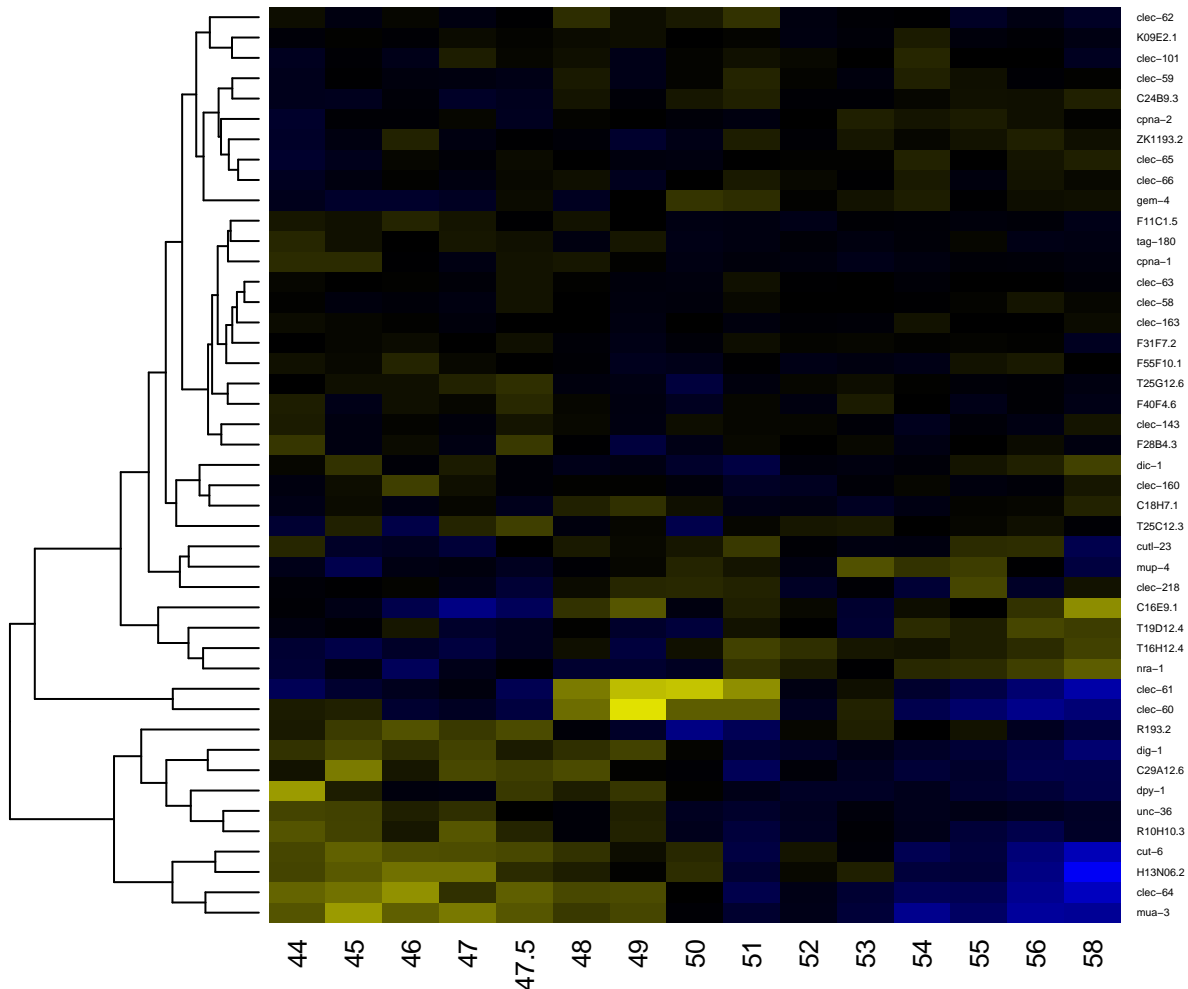
von Willebrand factor type A domain



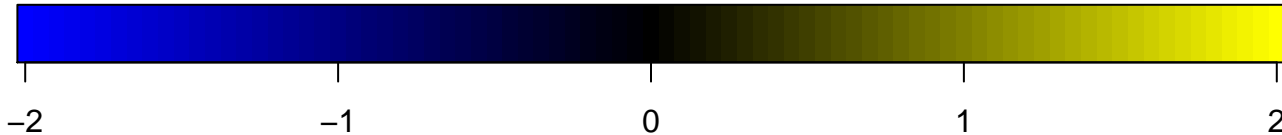
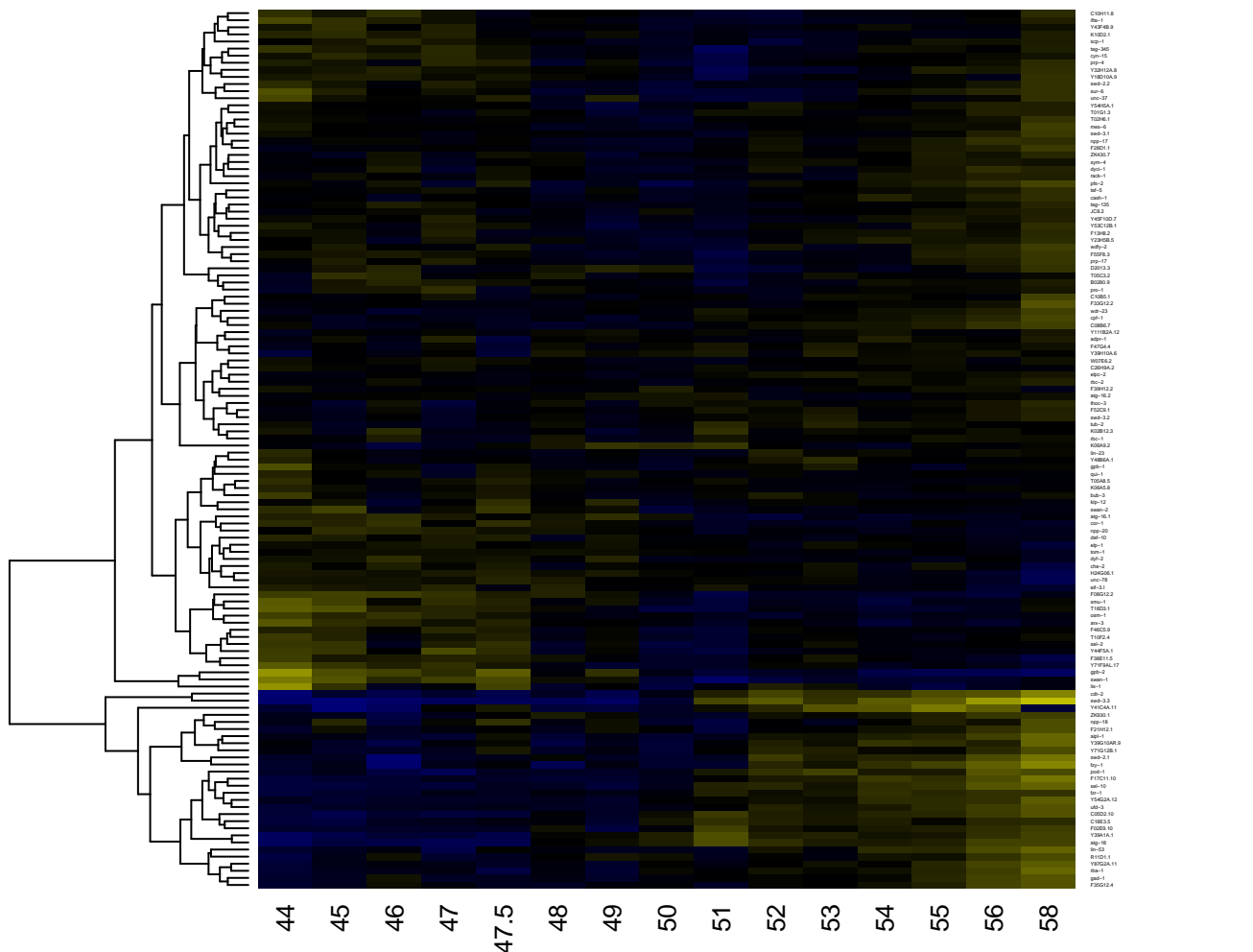
von Willebrand factor type D domain



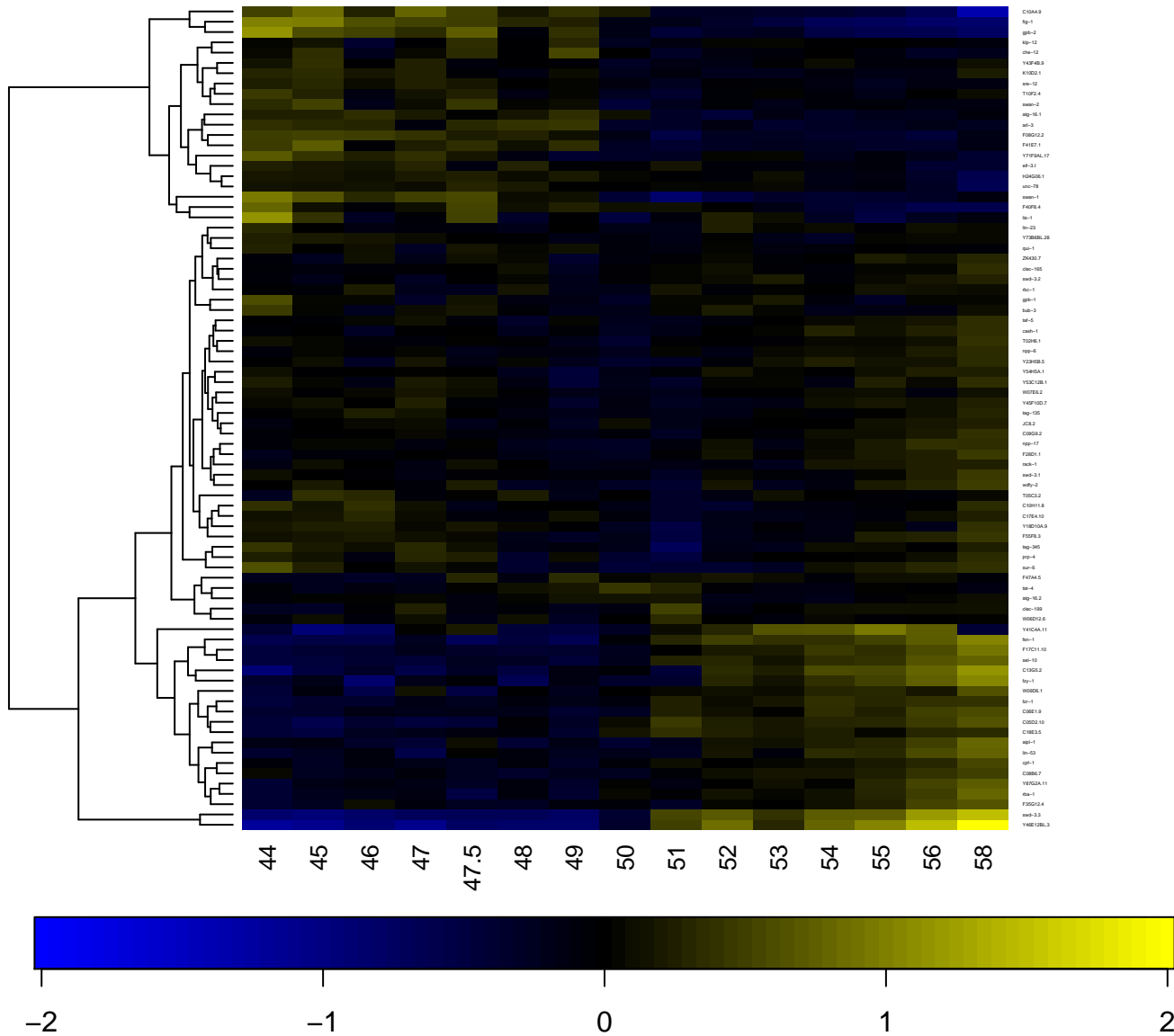
von Willebrand factor, type A



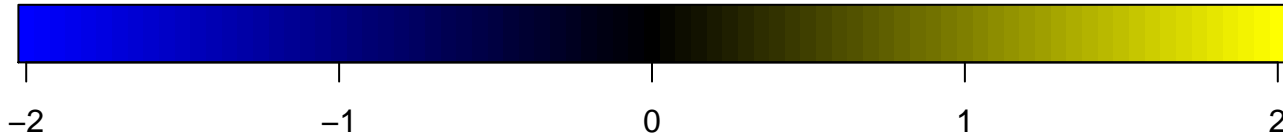
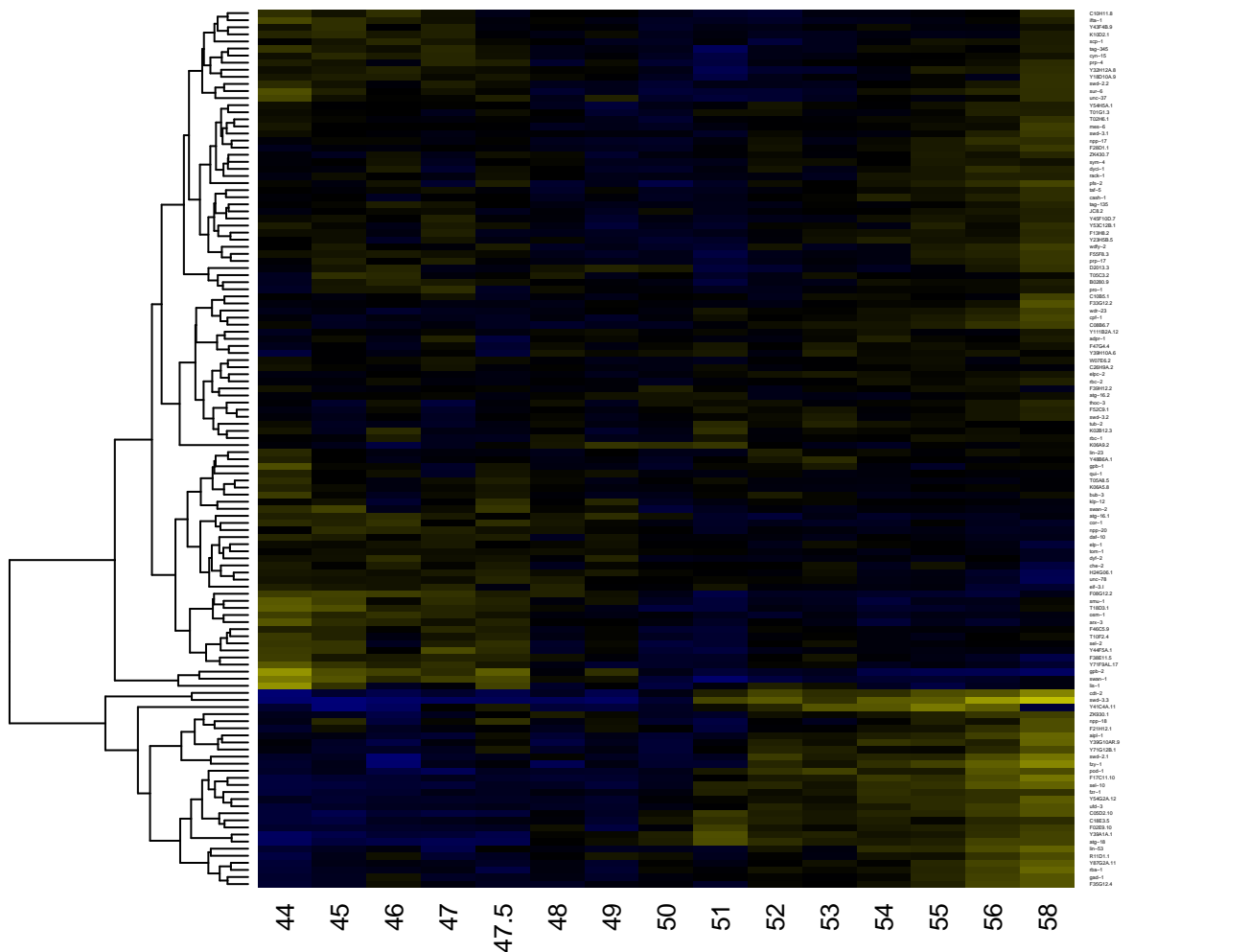
WD domain, G-beta repeat



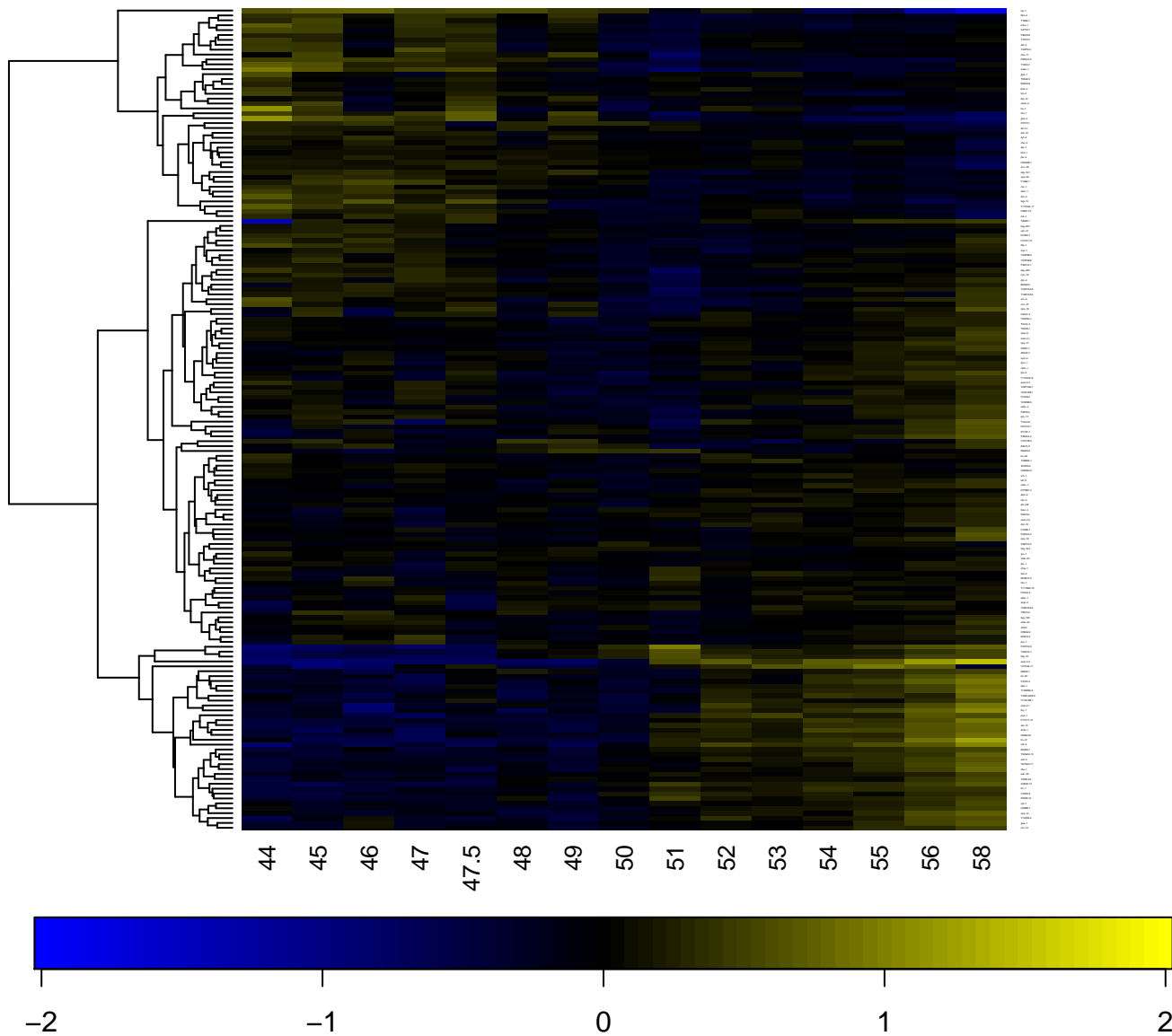
WD40 repeat, conserved site



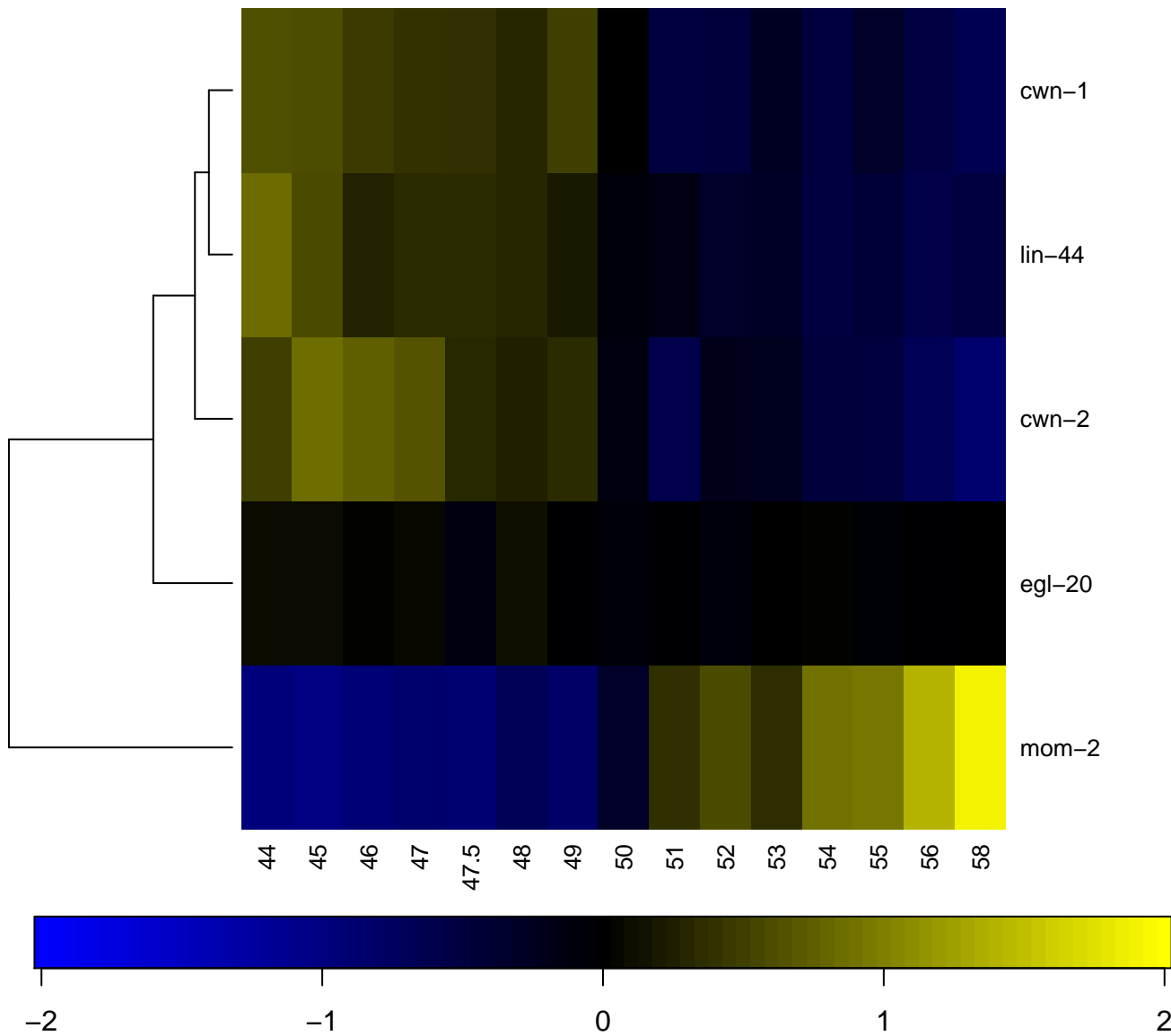
WD40 repeat, subgroup



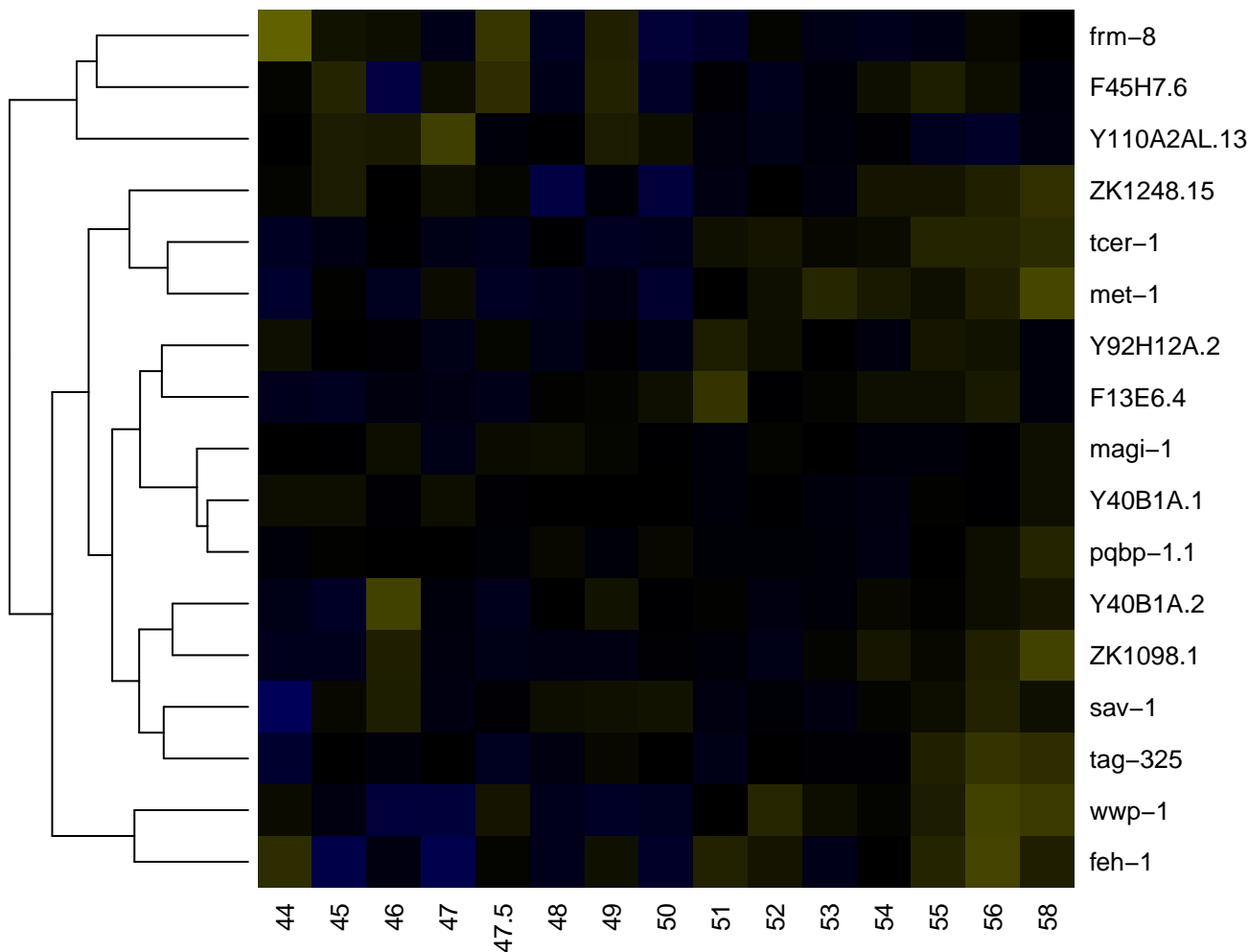
WD40/YVTN repeat-like-containing domain



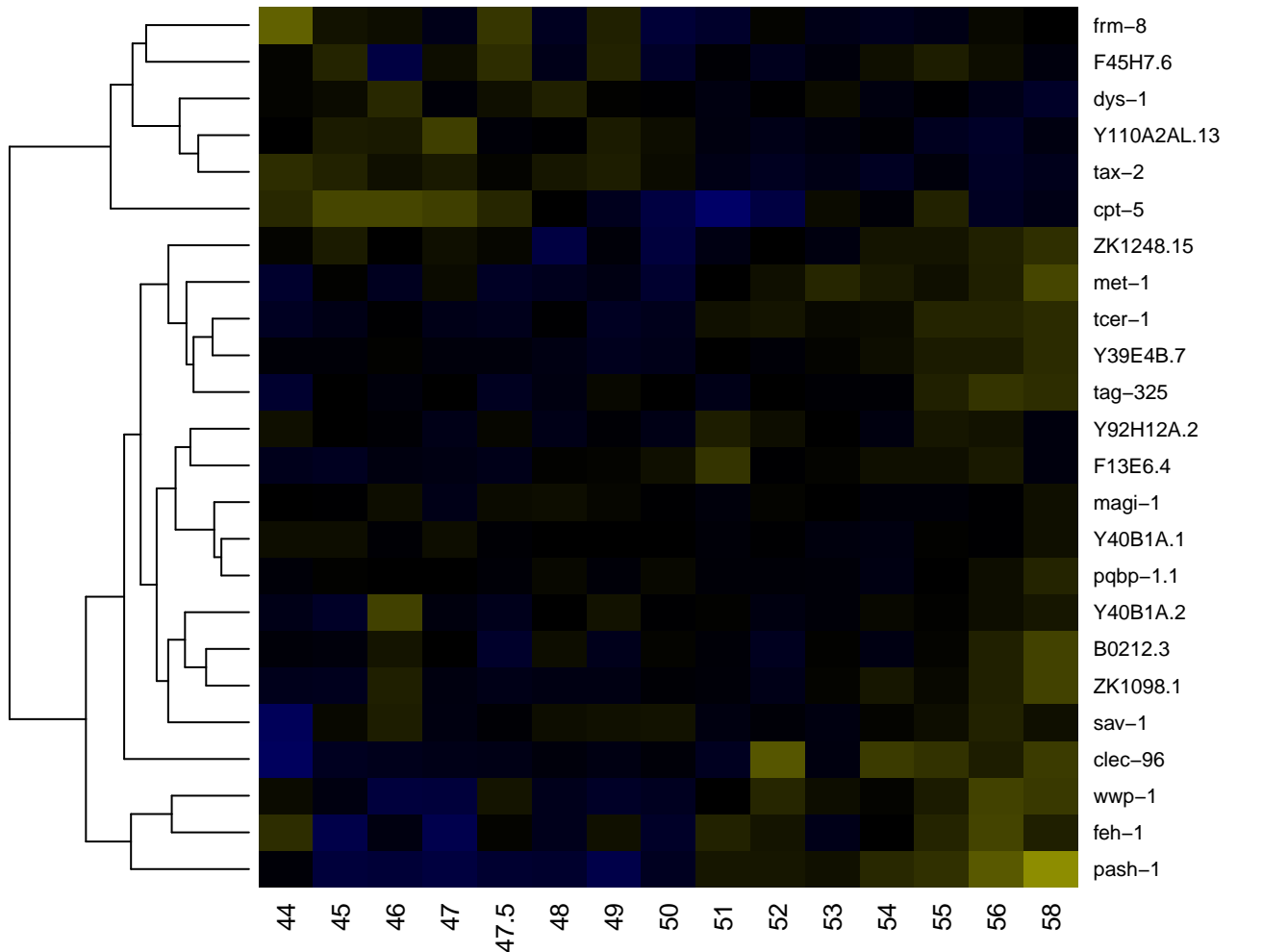
Wnt superfamily



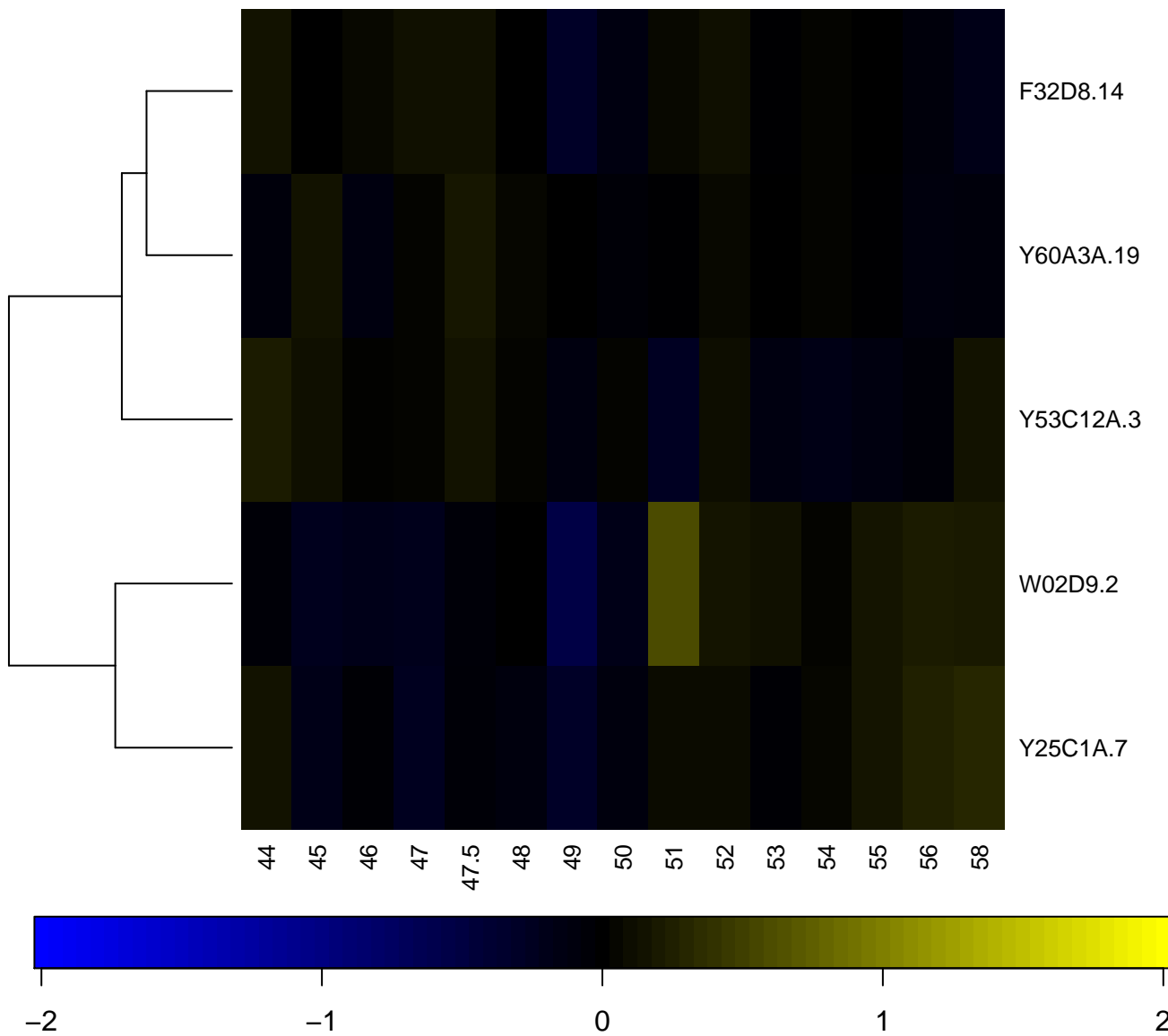
WW domain



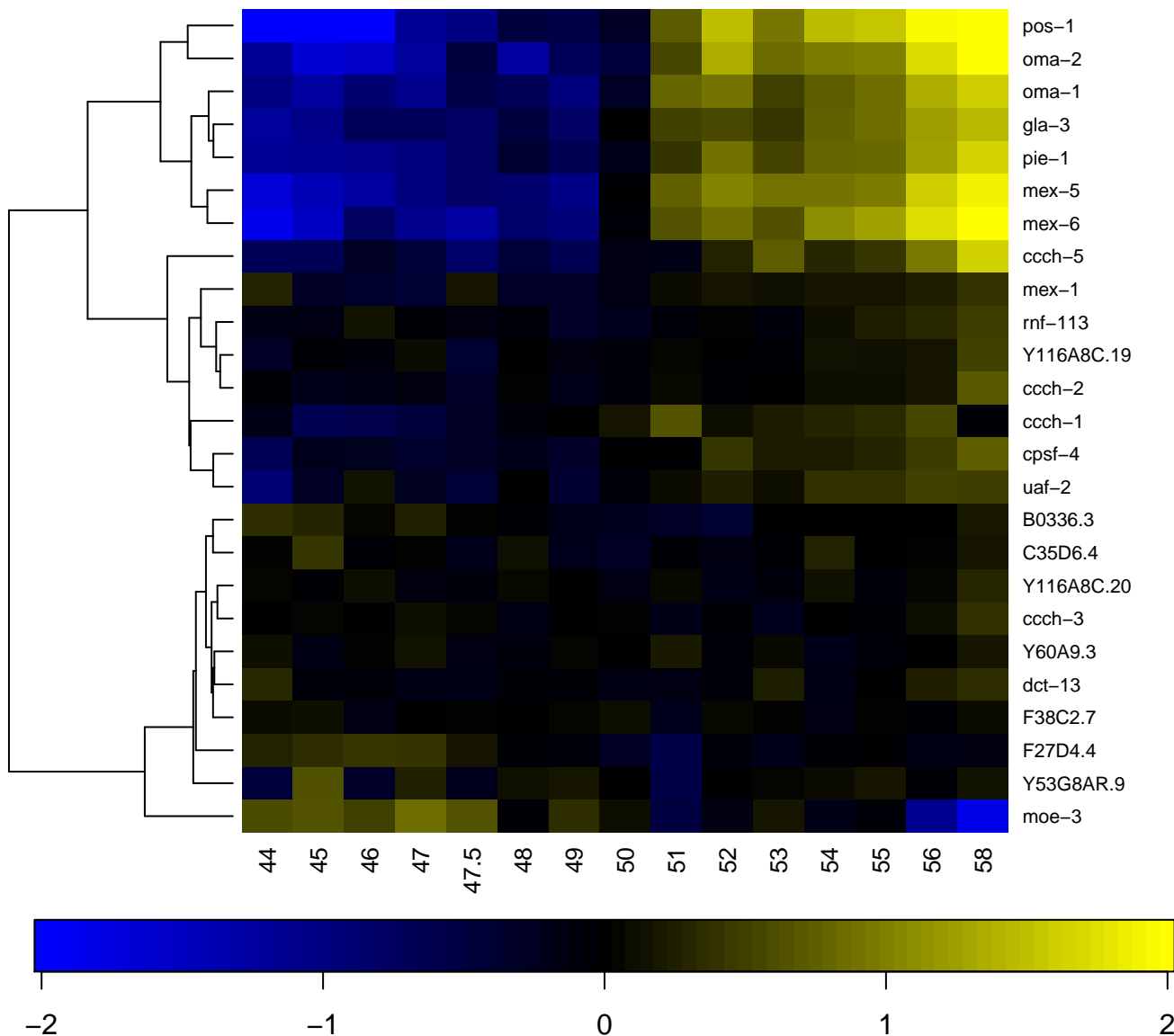
WW/Rsp5/WWP



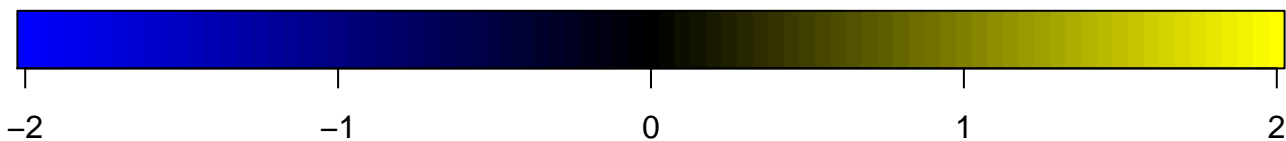
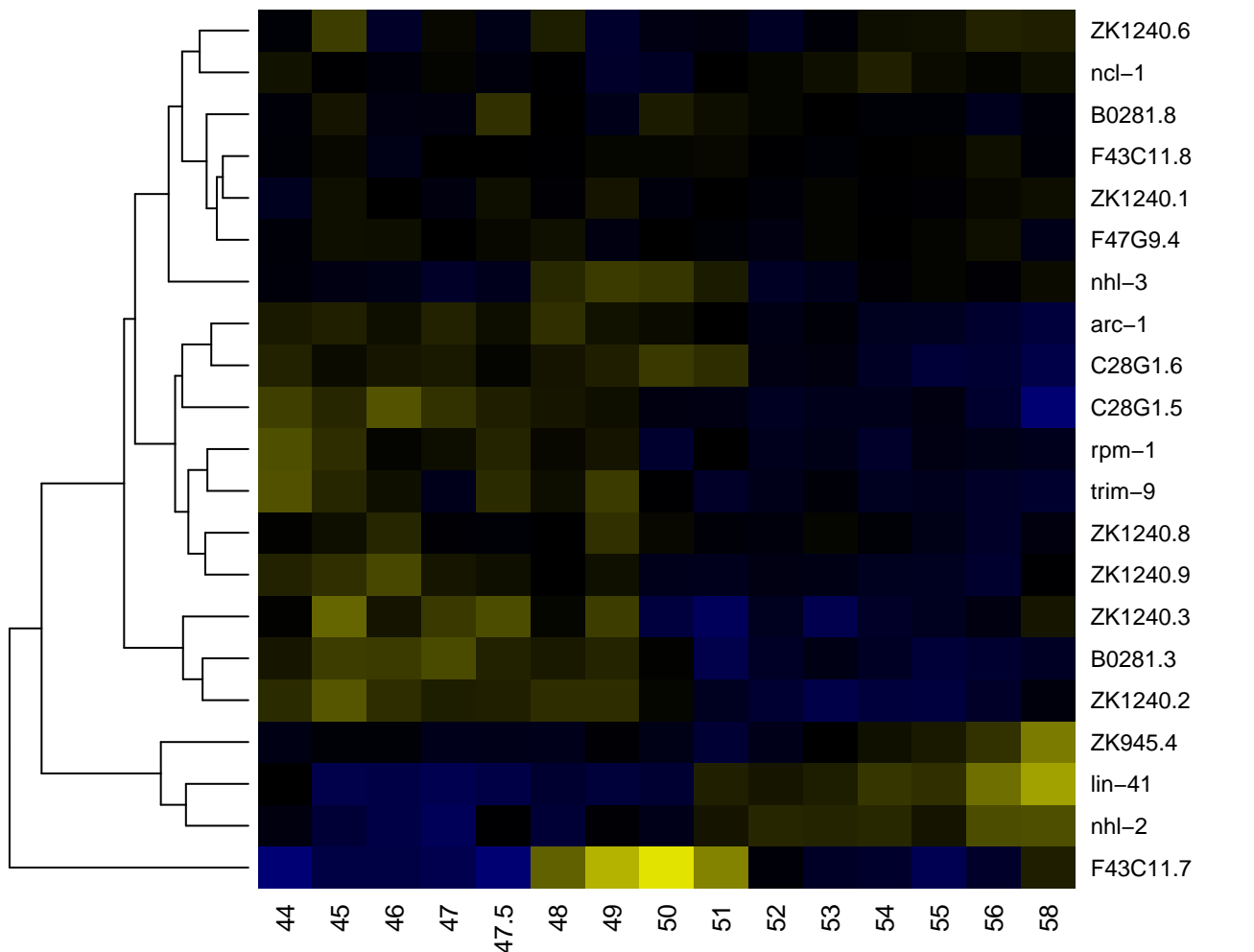
Yip1 domain



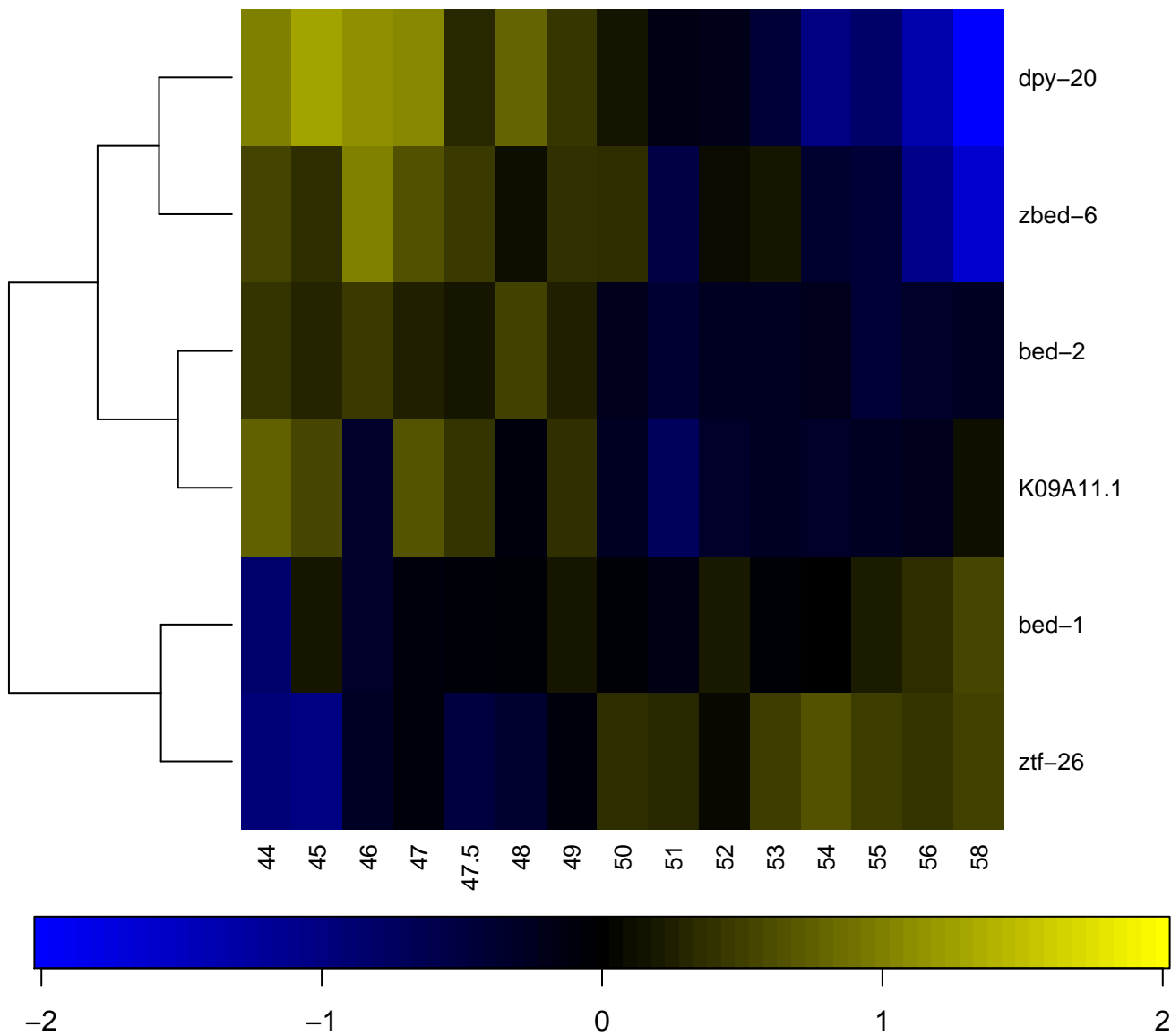
Zinc finger C-x8-C-x5-C-x3-H type (and similar)



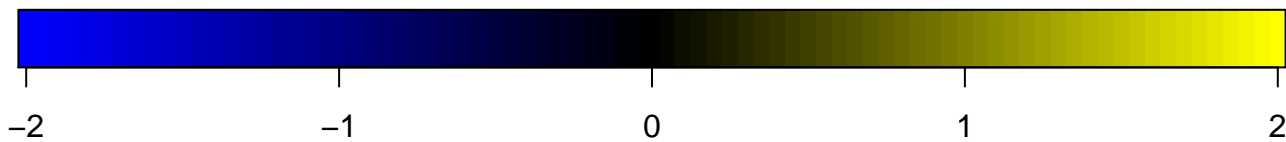
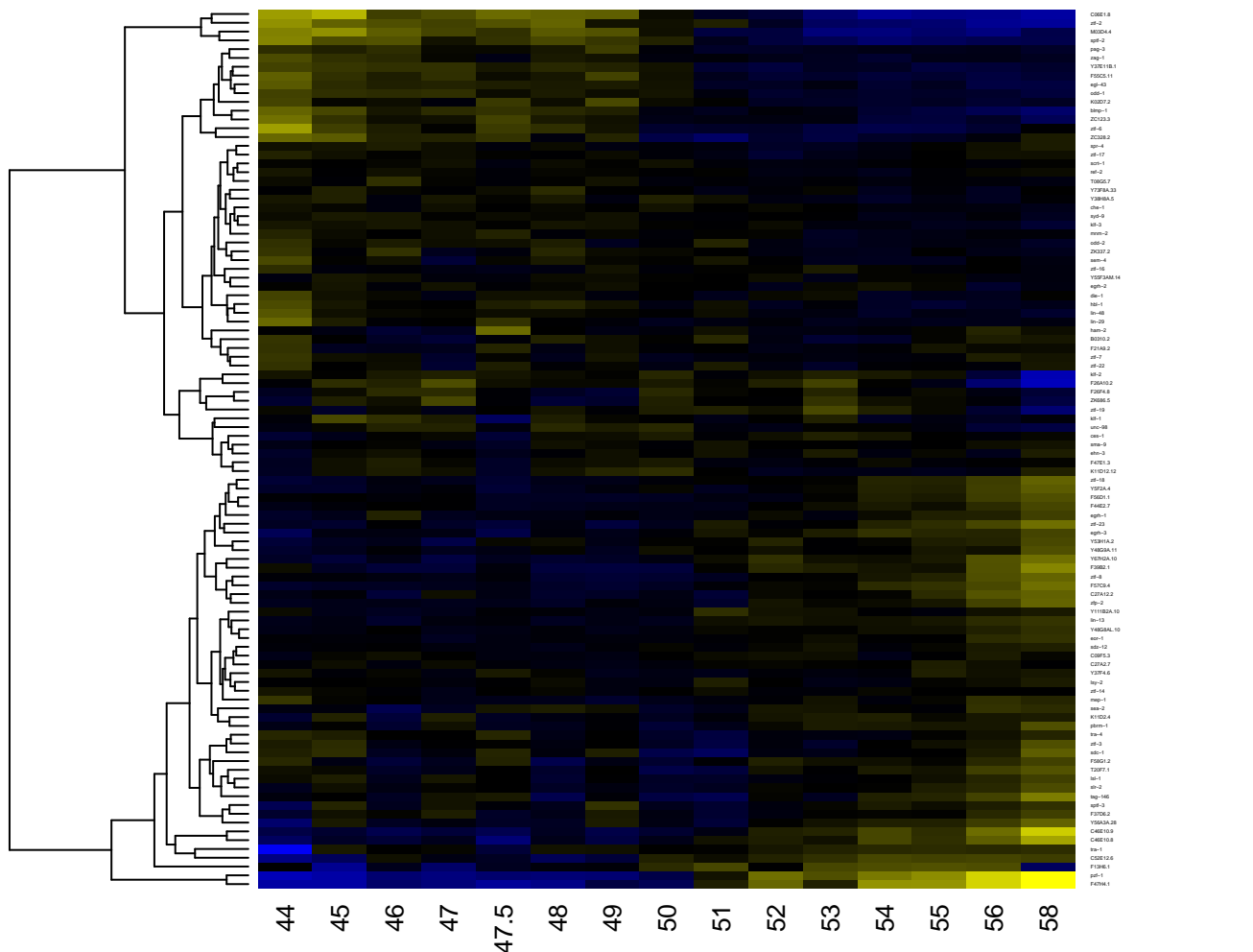
Zinc finger, B-box



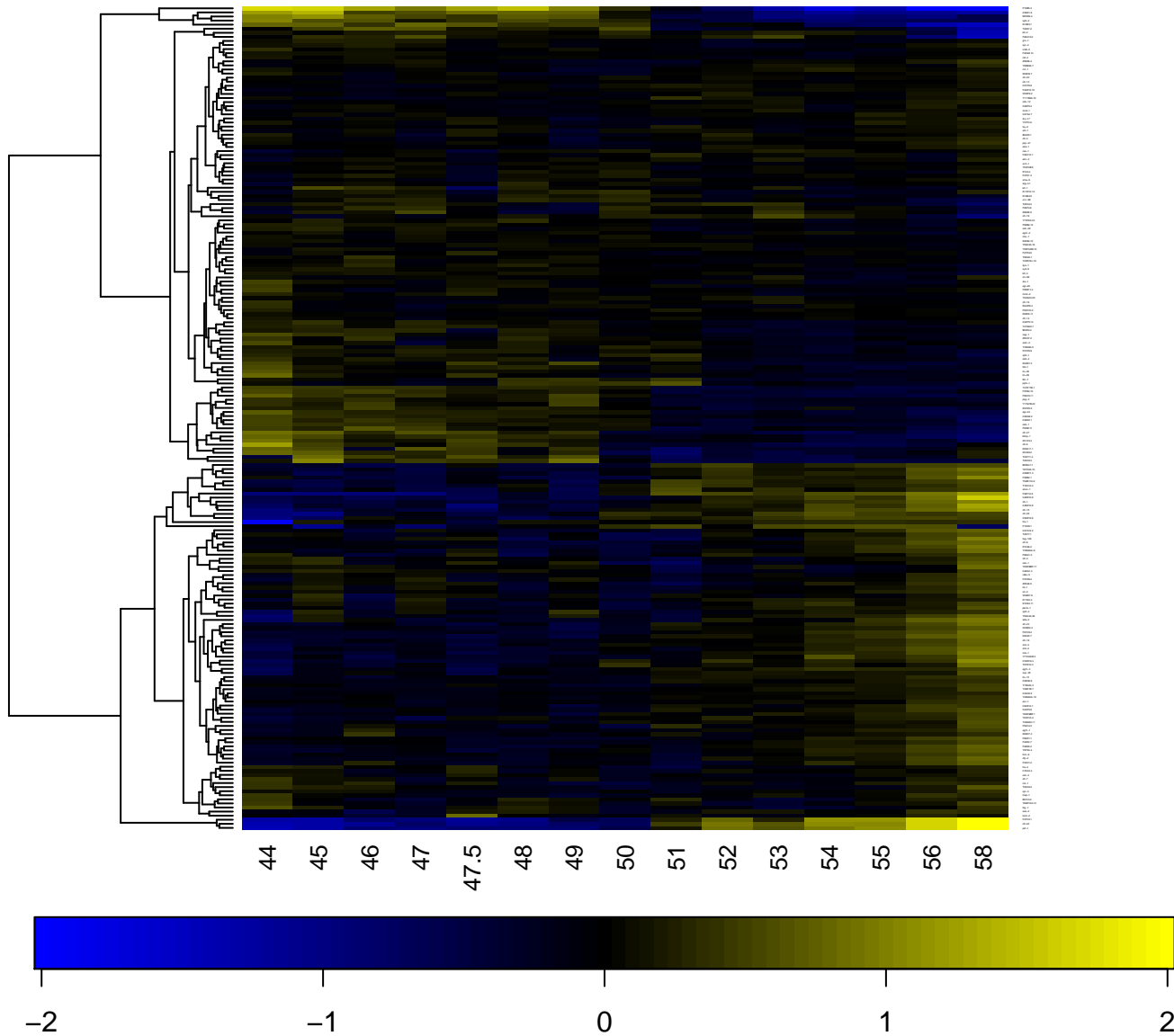
Zinc finger, BED-type predicted



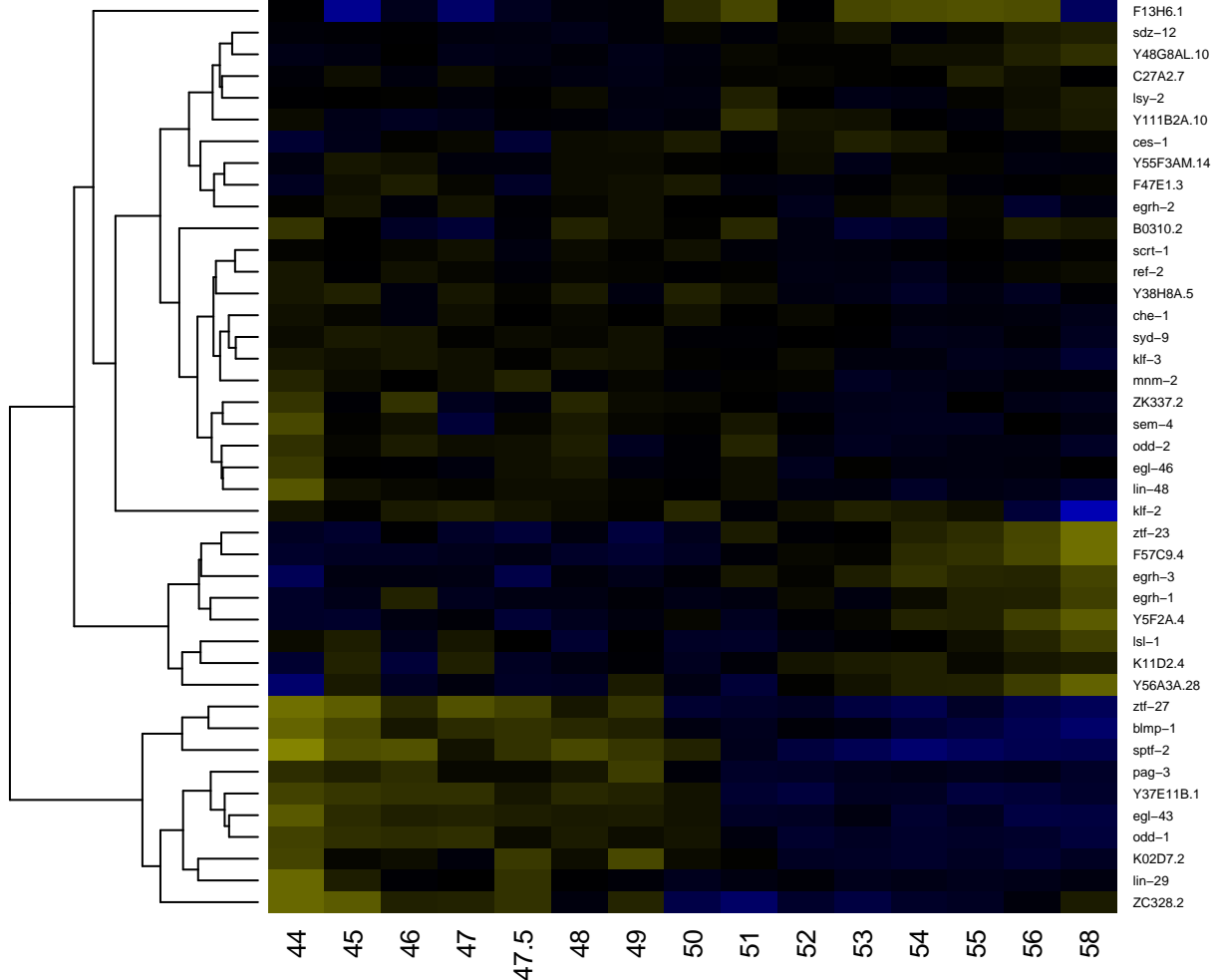
Zinc finger, C2H2-like



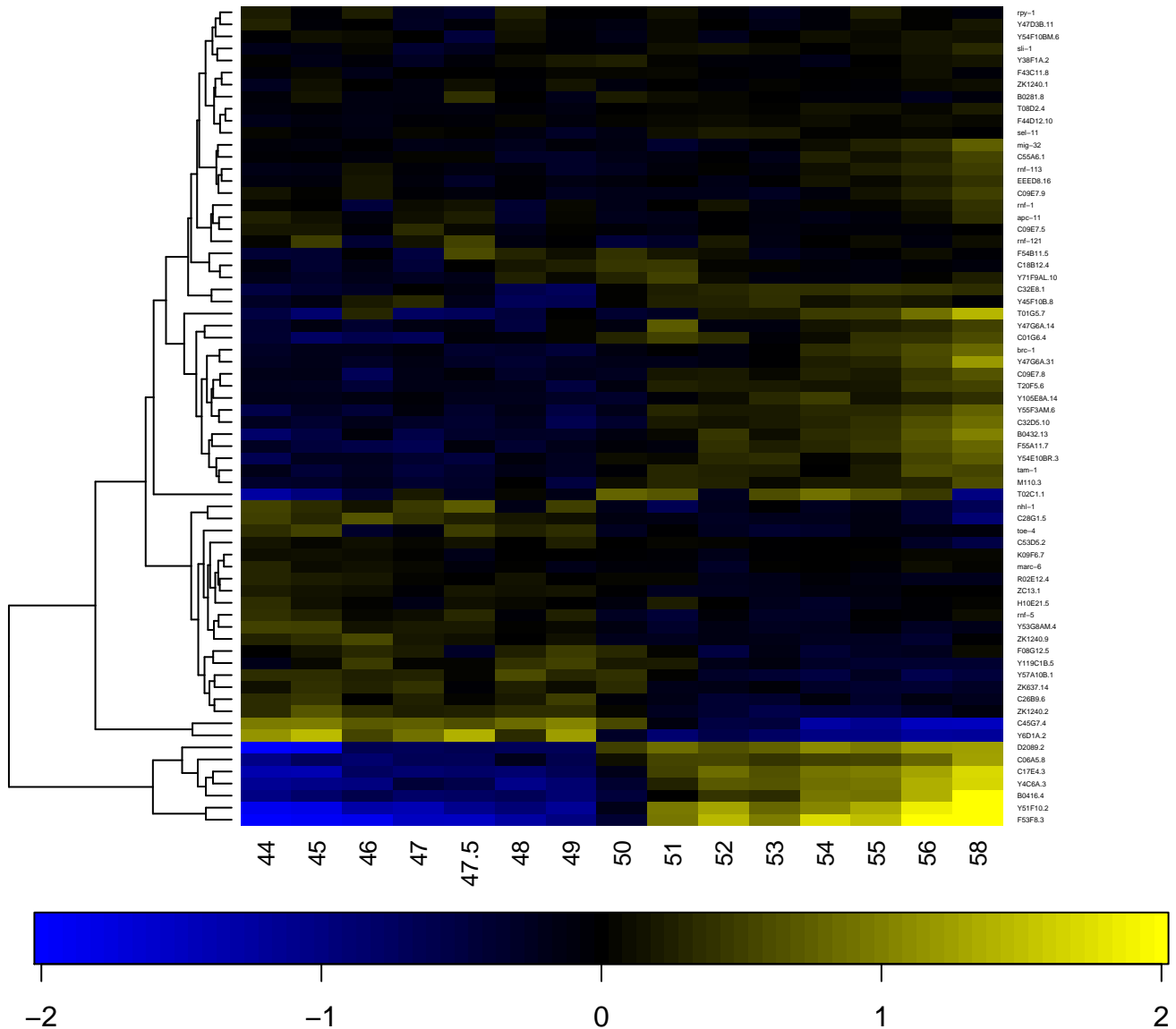
Zinc finger, C2H2-type



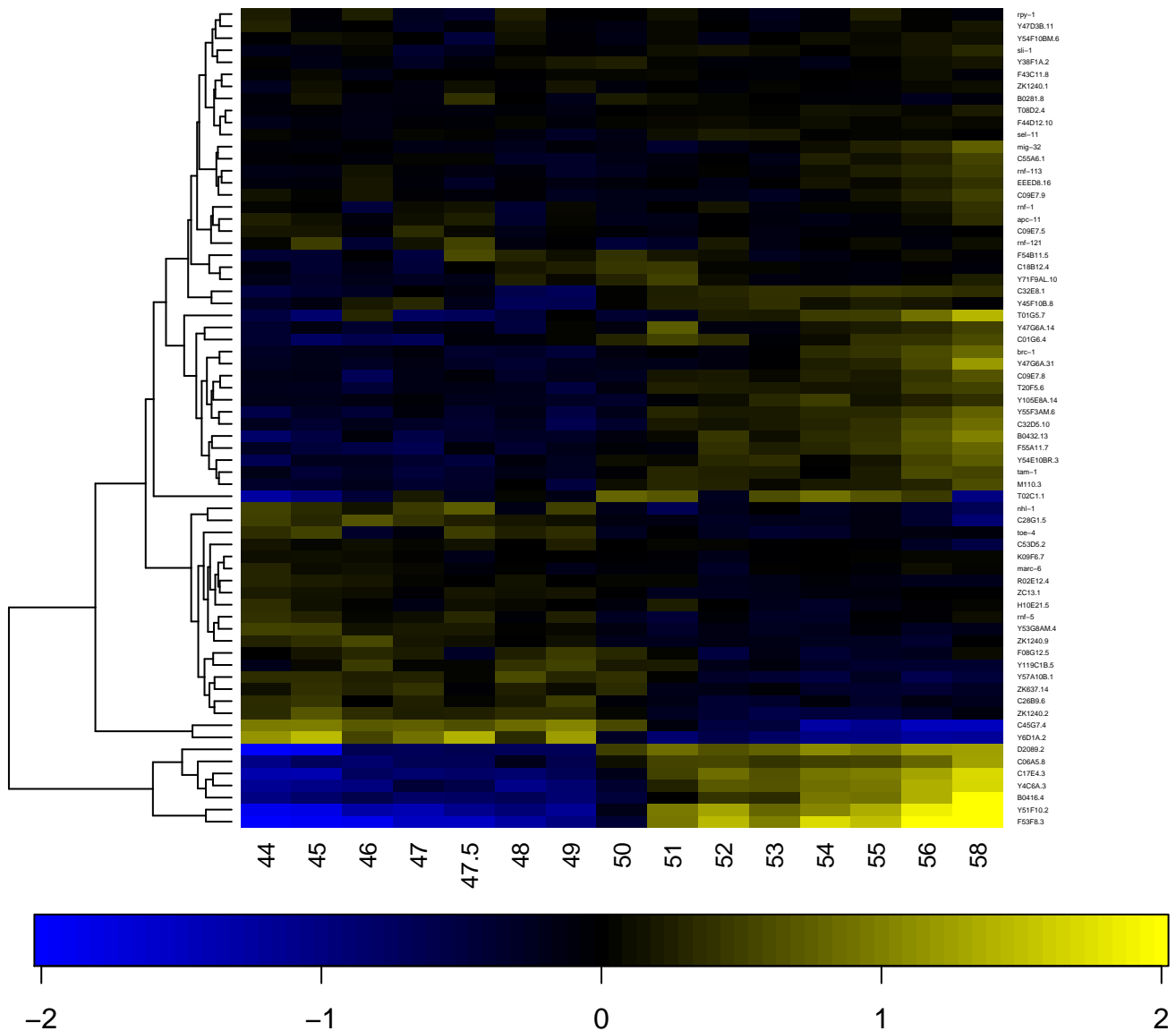
Zinc finger, C2H2 type



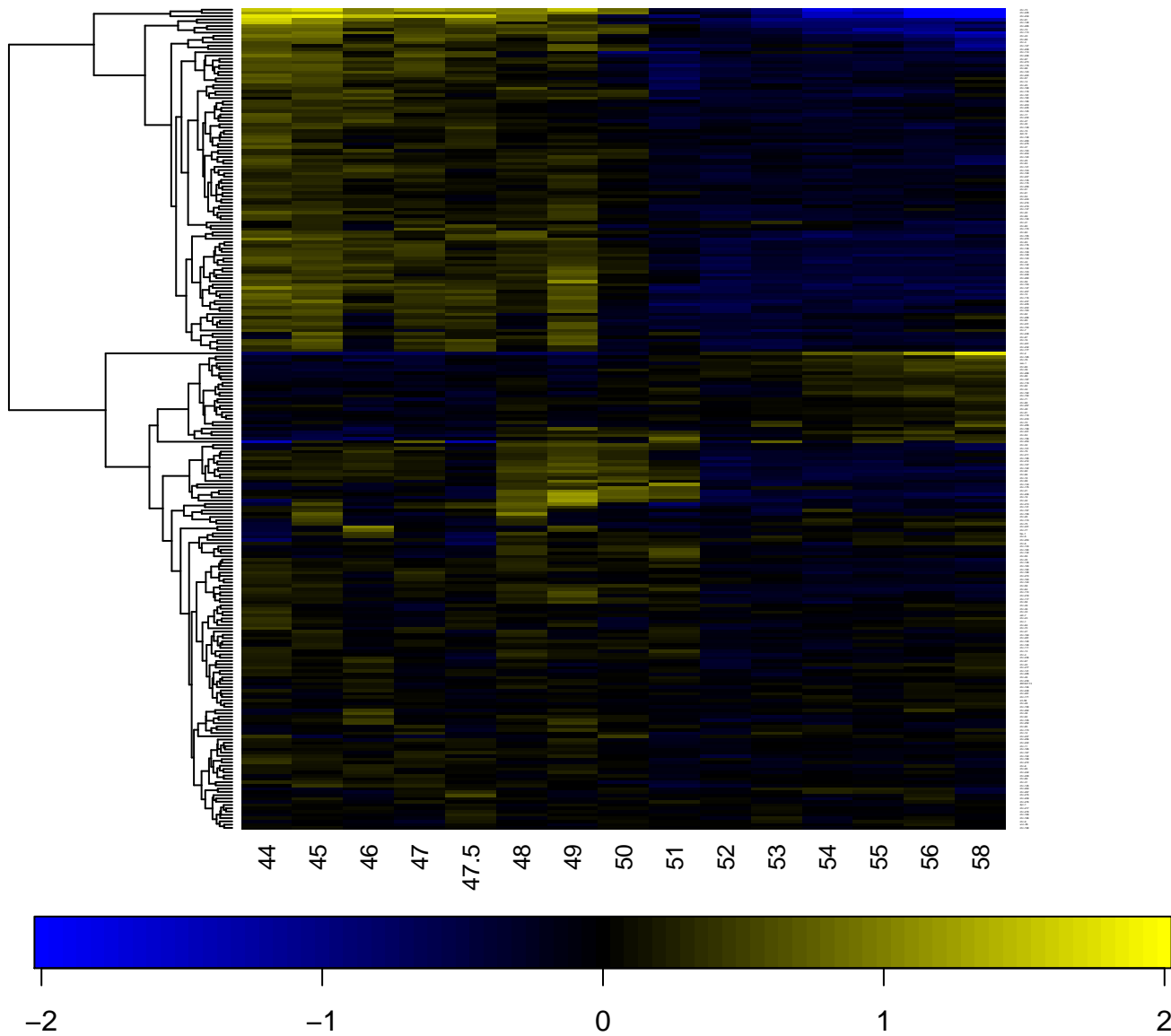
Zinc finger, C3HC4 RING-type



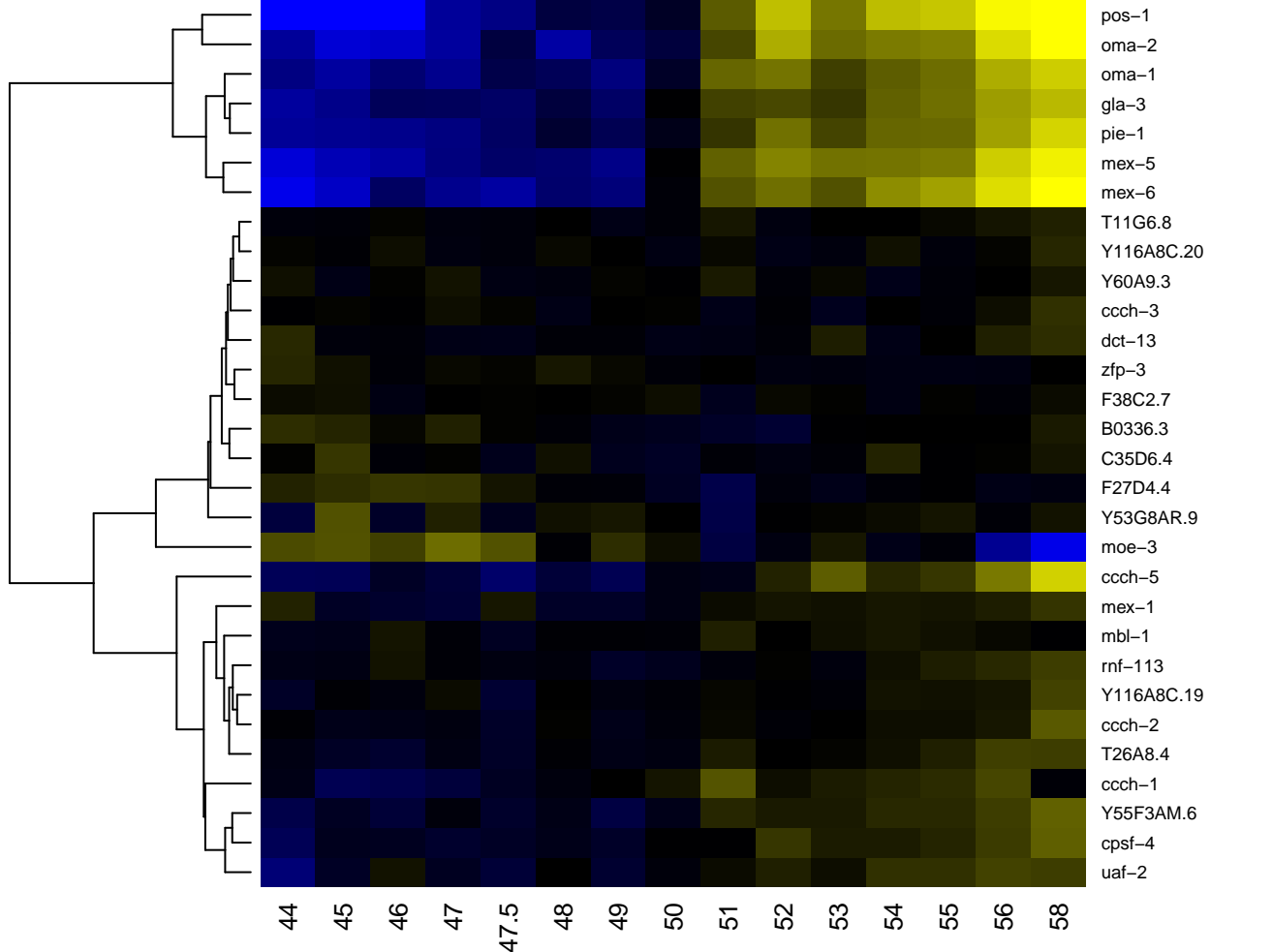
Zinc finger, C3HC4 type (RING finger)



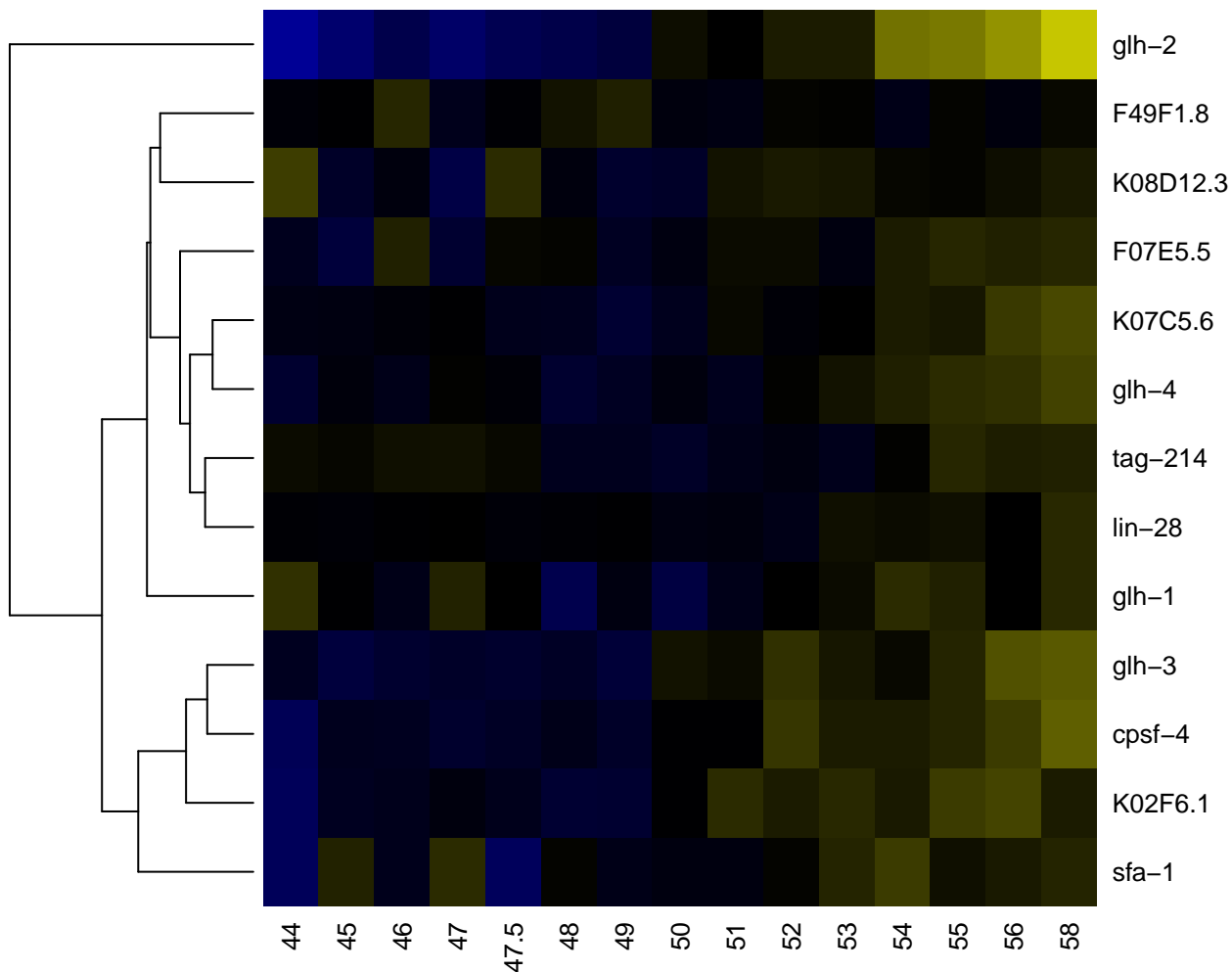
Zinc finger, C4 type (two domains)



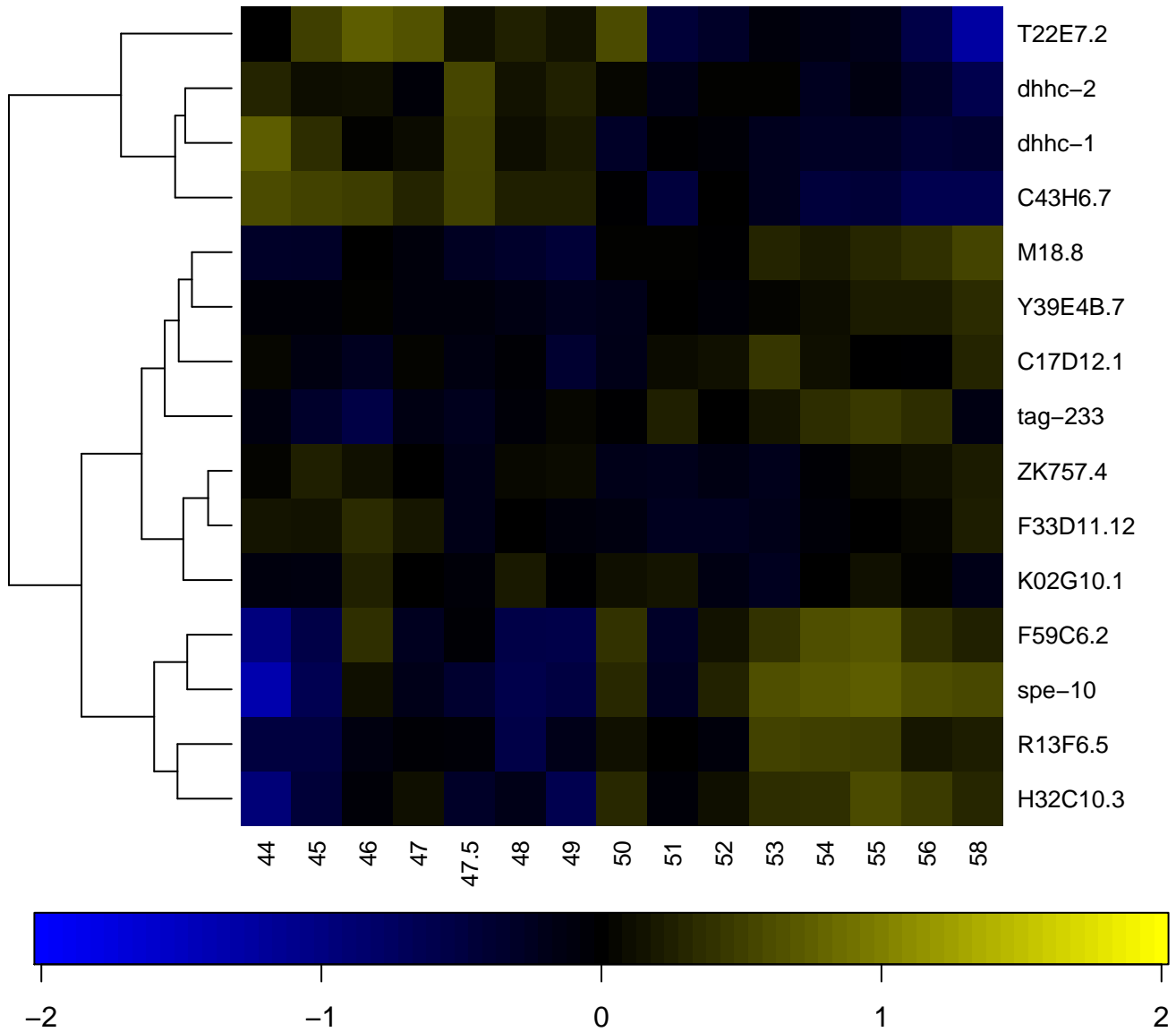
Zinc finger, CCCH-type



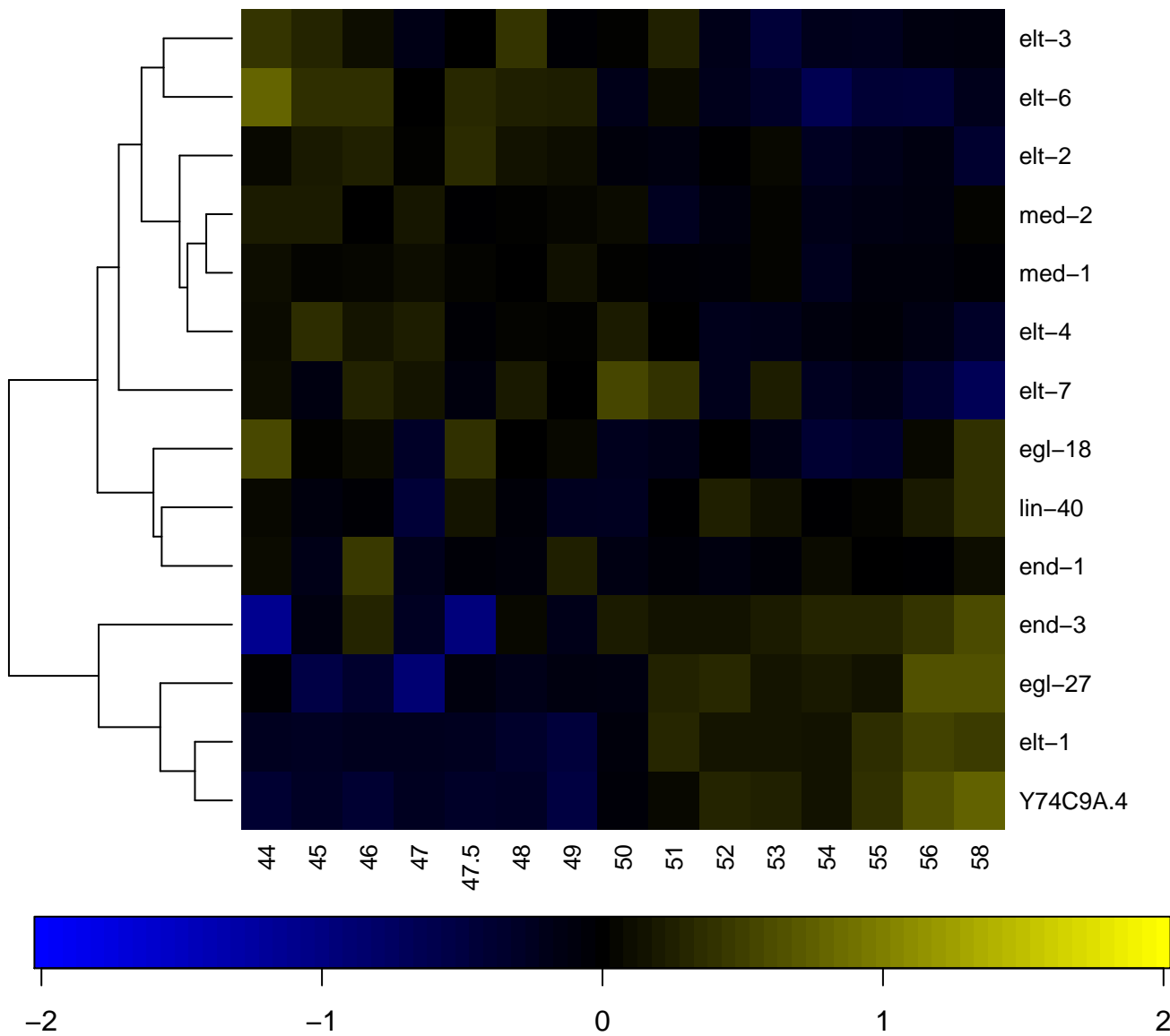
Zinc finger, CCHC retroviral-type



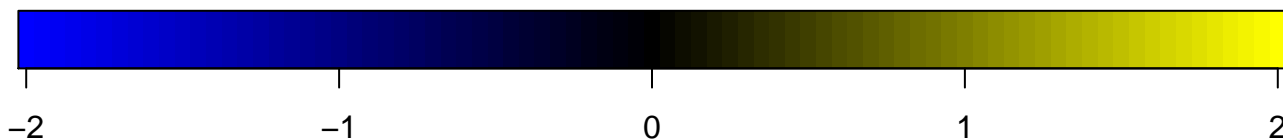
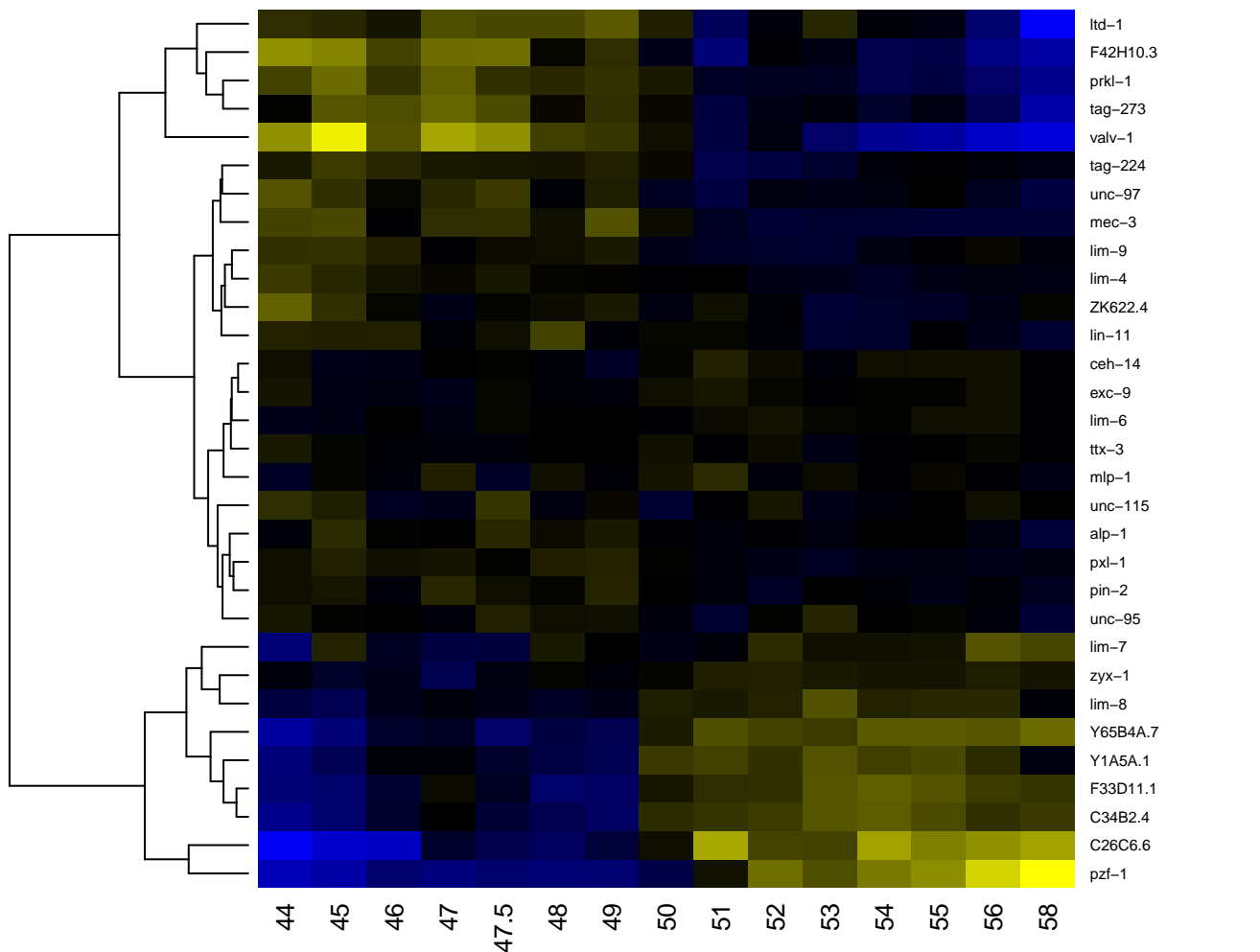
Zinc finger, DHHC-type



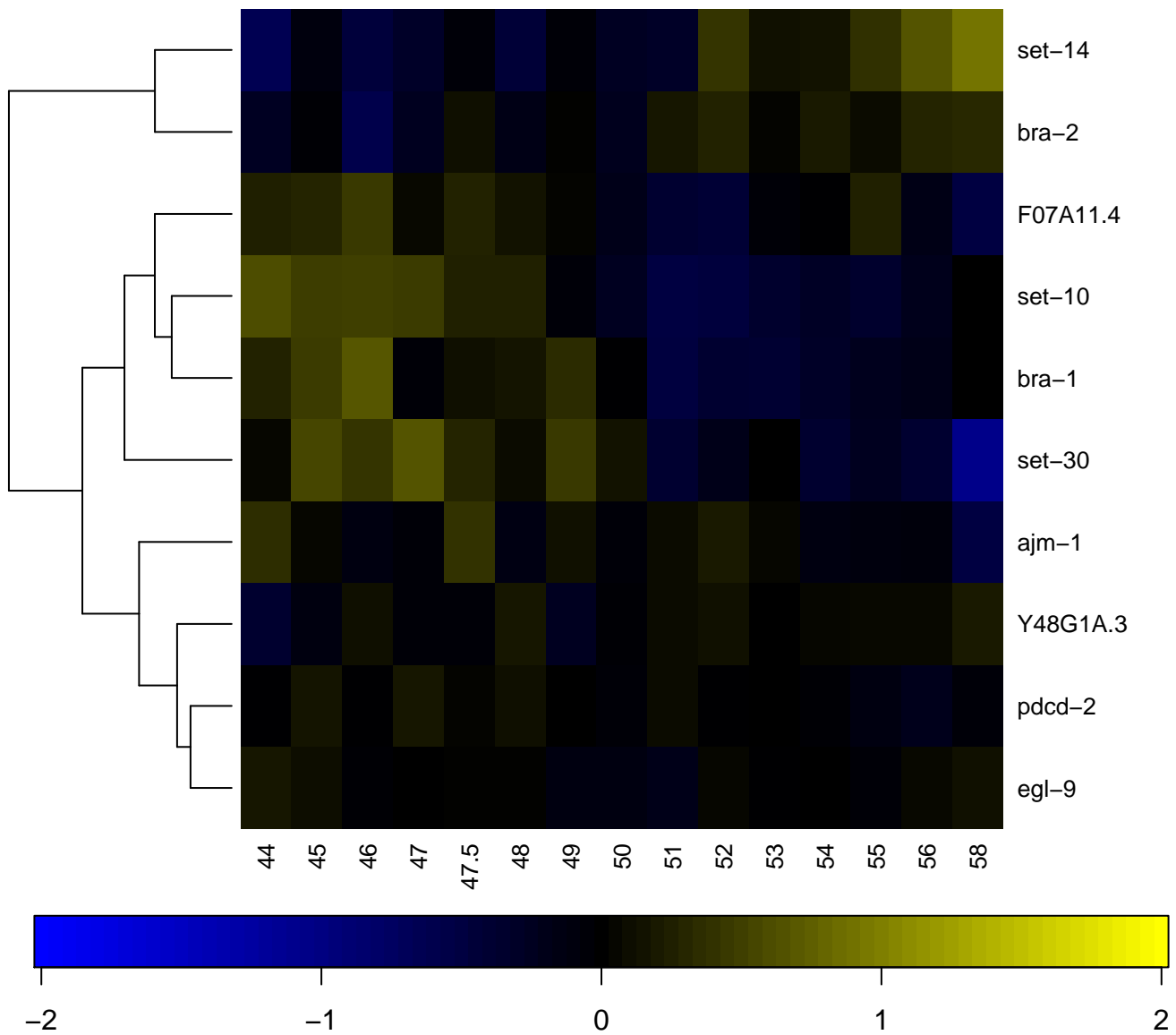
Zinc finger, GATA-type



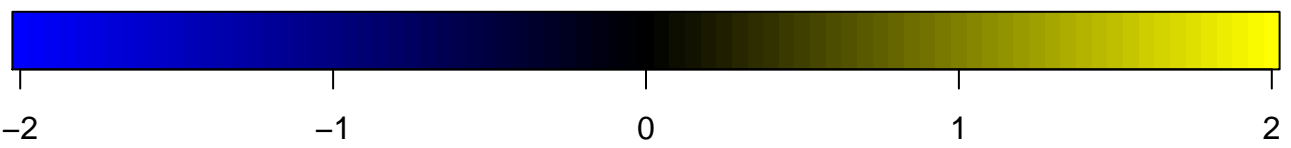
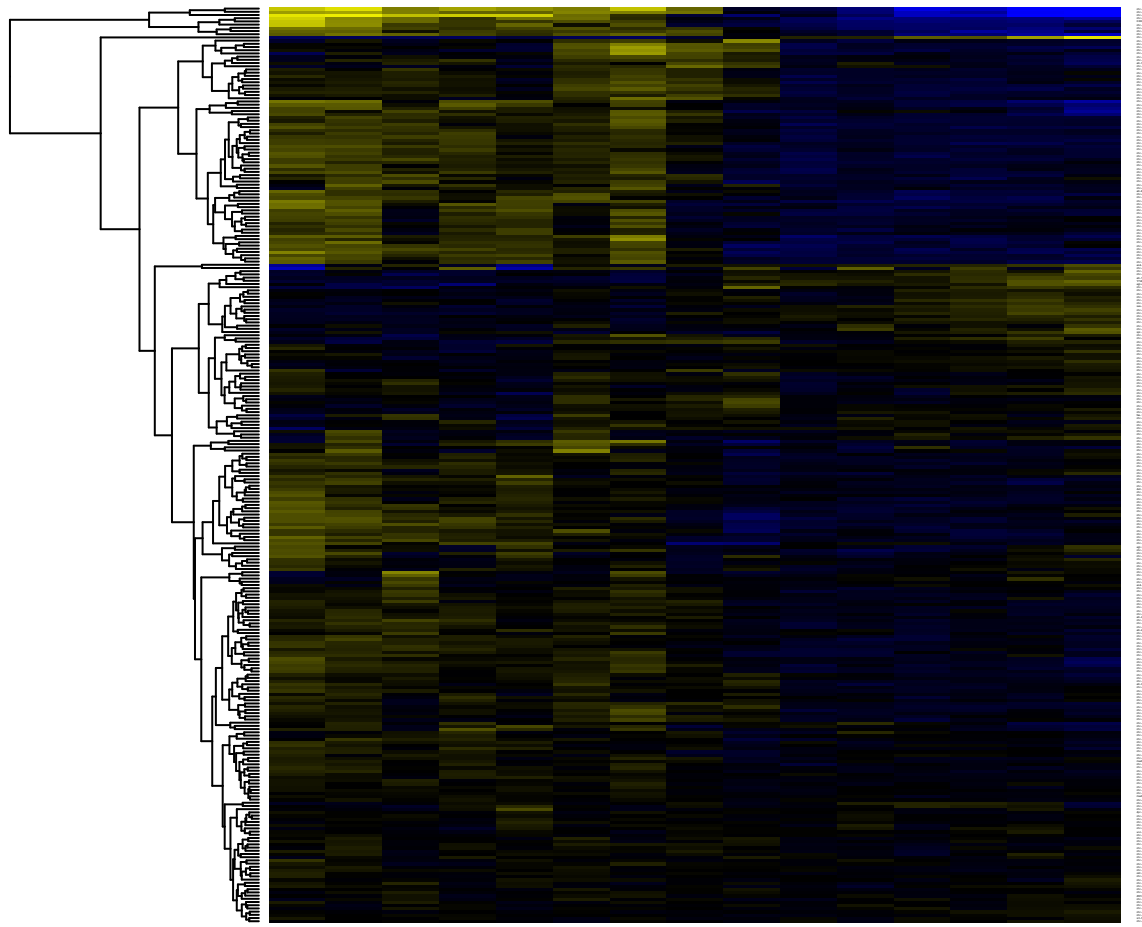
Zinc finger, LIM-type



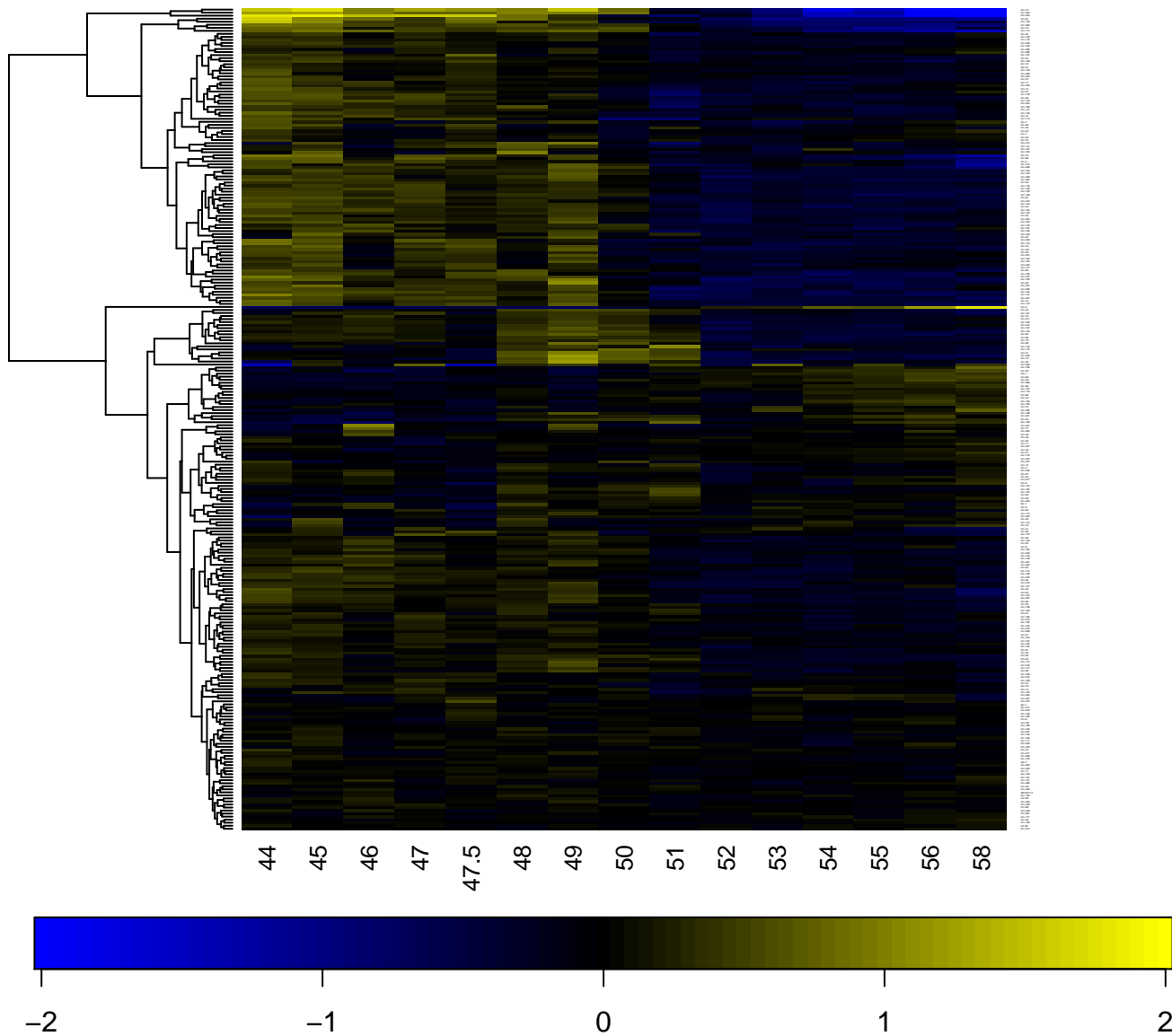
Zinc finger, MYND-type



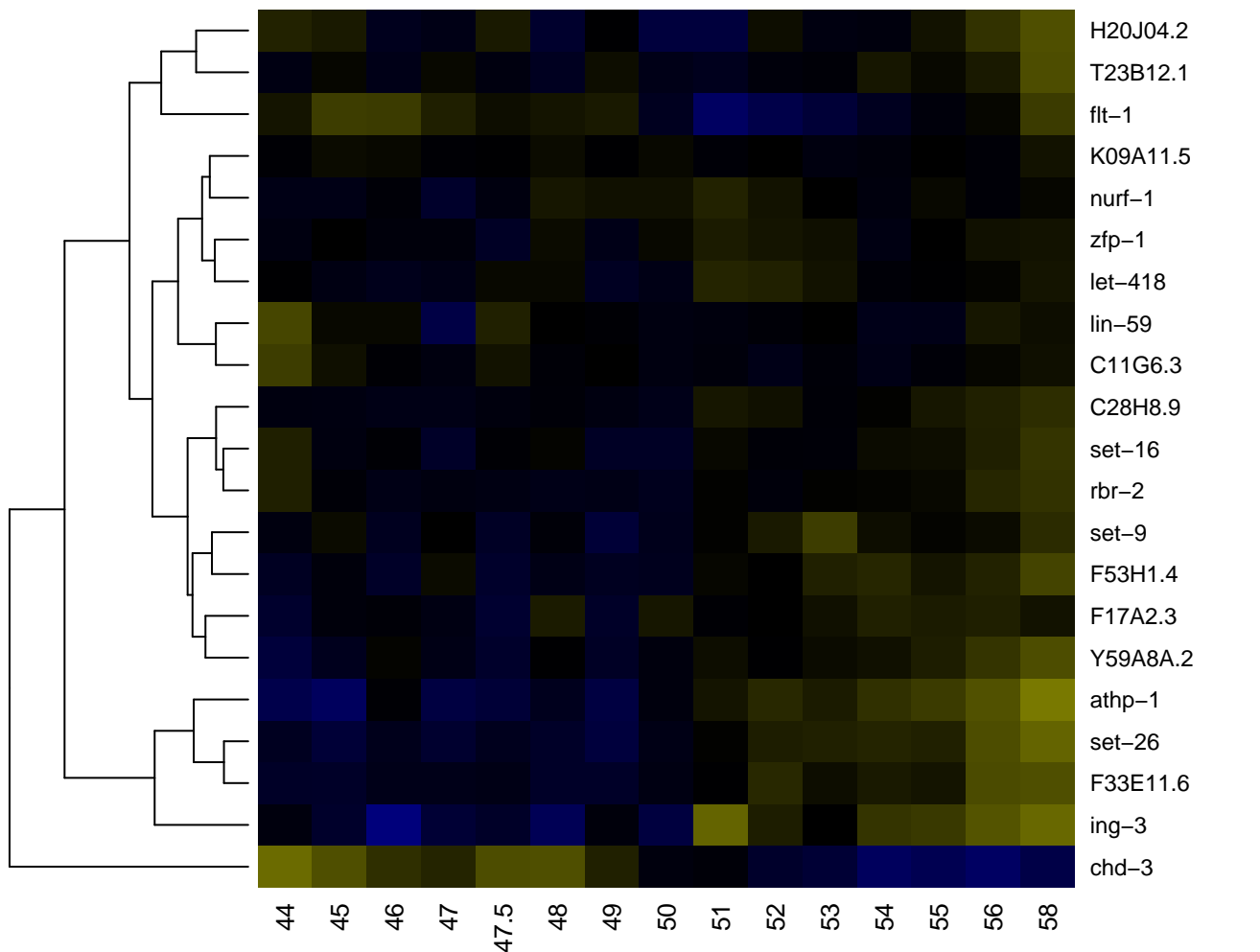
Zinc finger, NHR/GATA-type



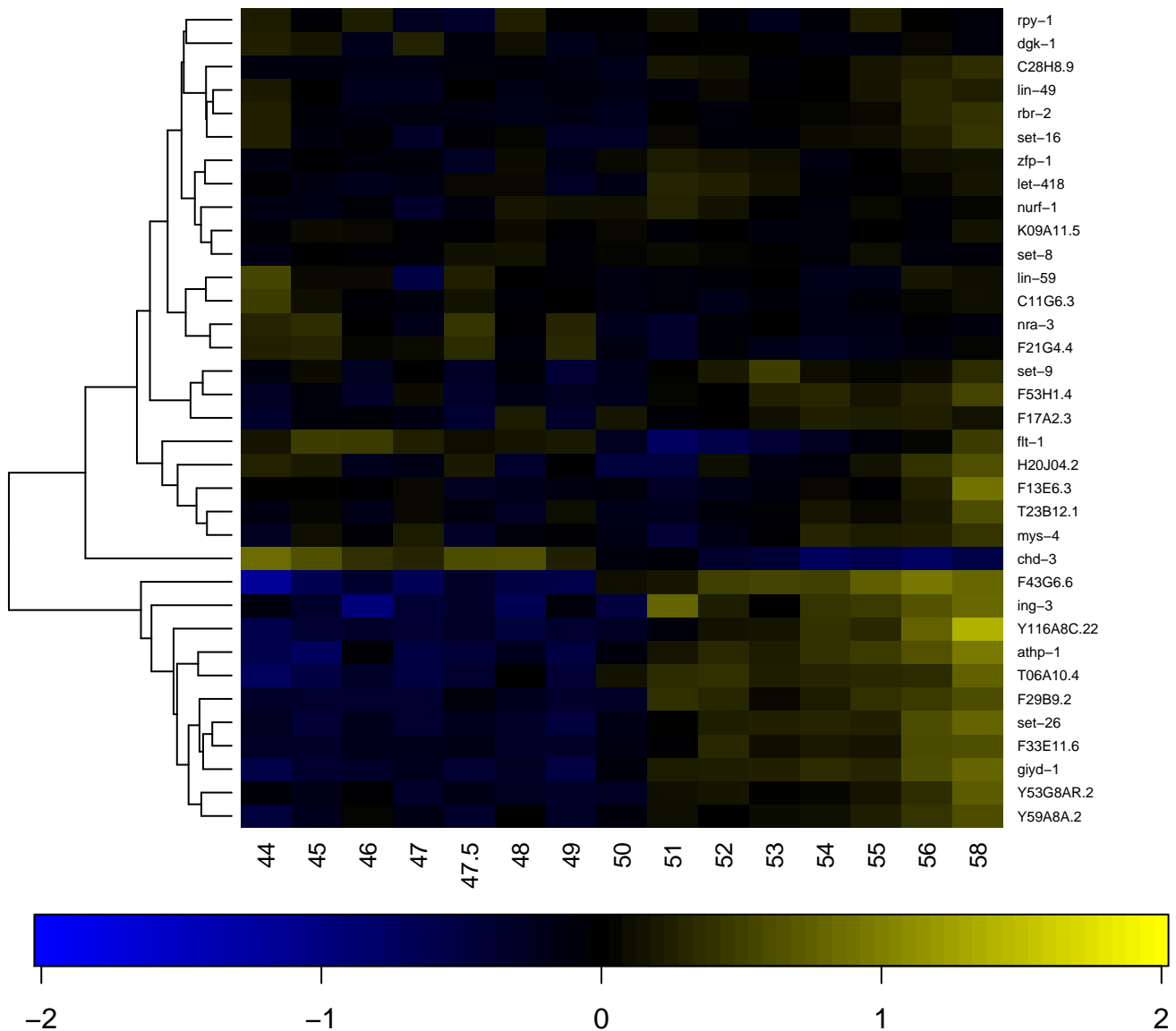
Zinc finger, nuclear hormone receptor-type



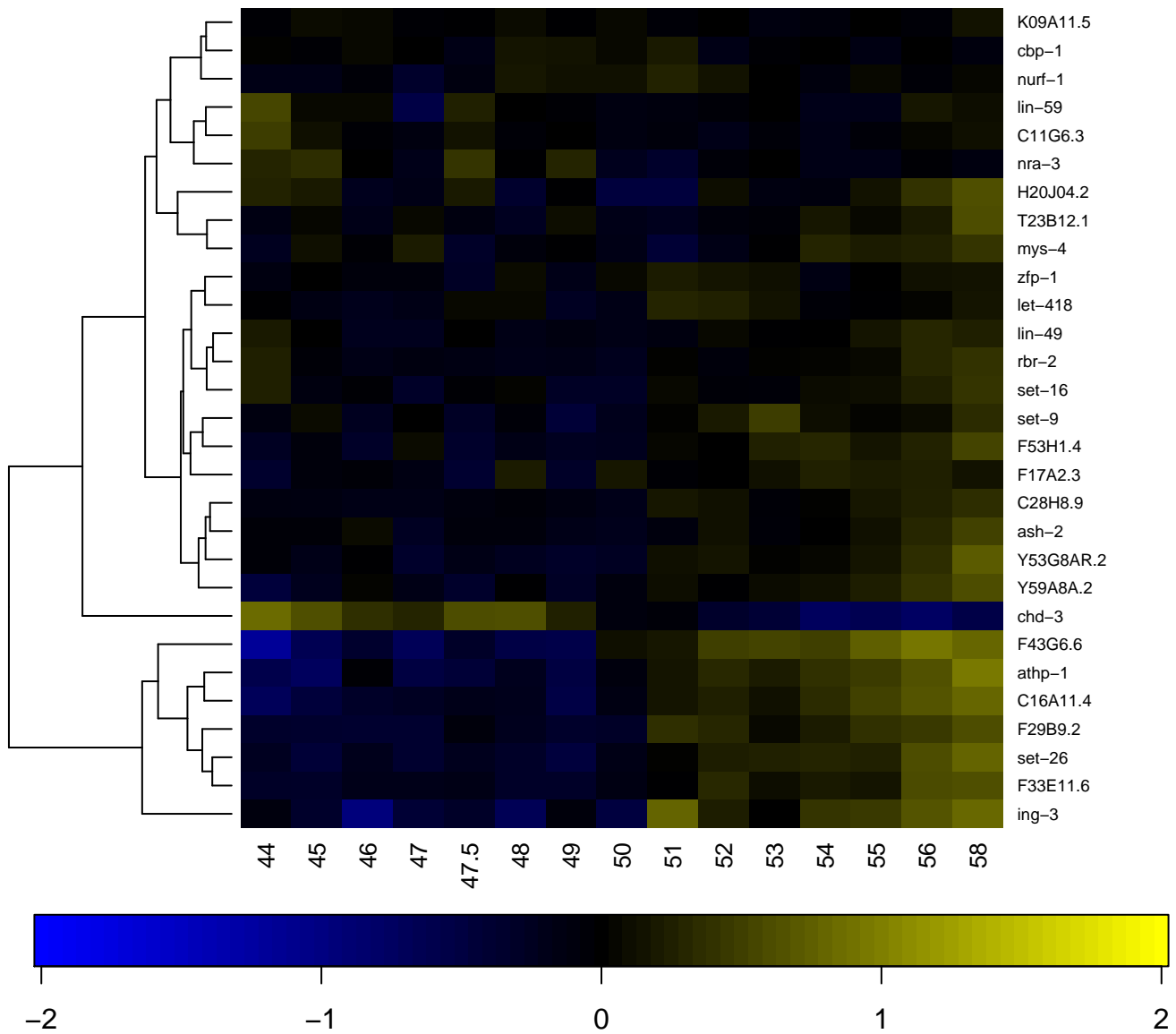
Zinc finger, PHD-finger



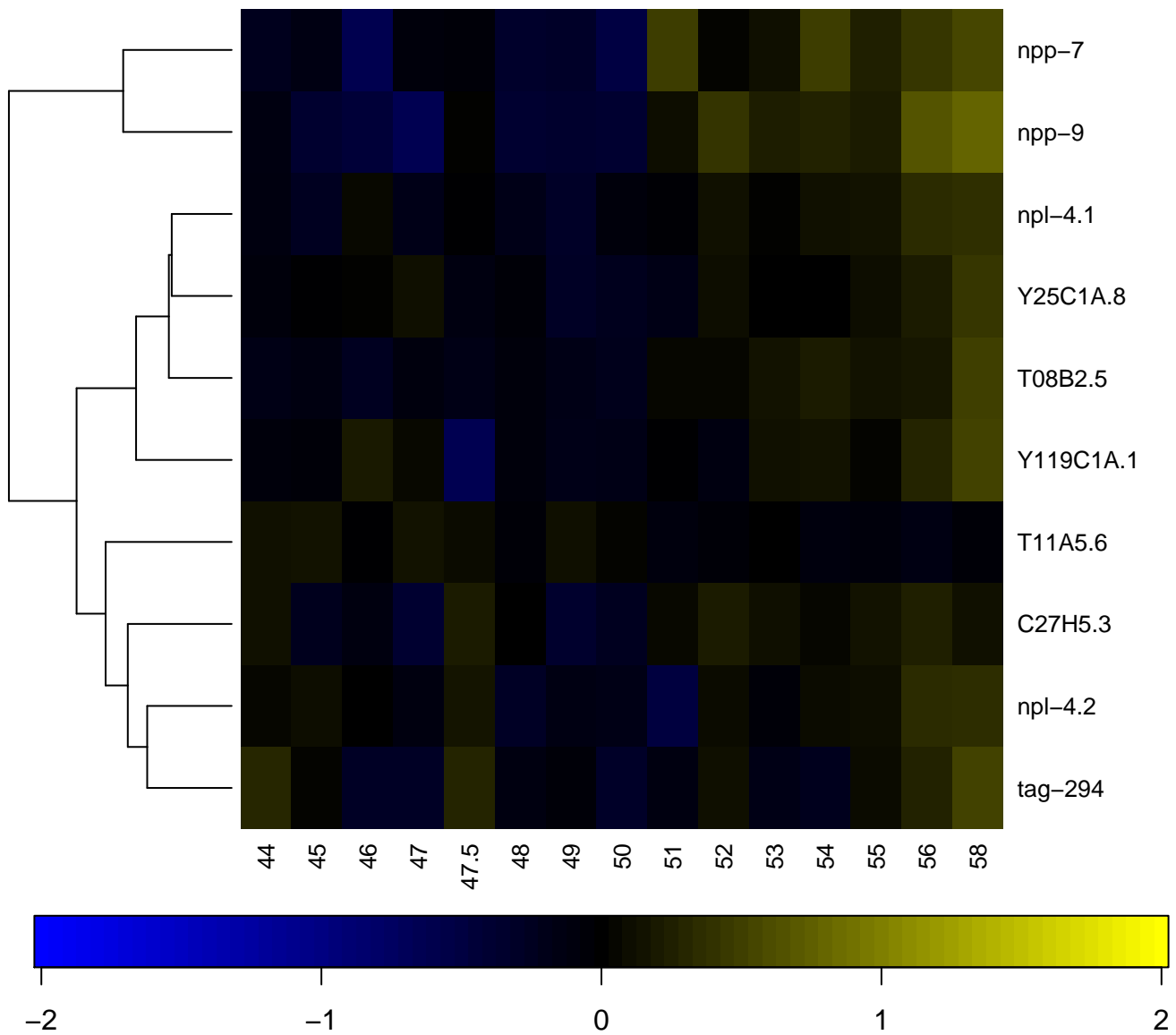
Zinc finger, PHD-type



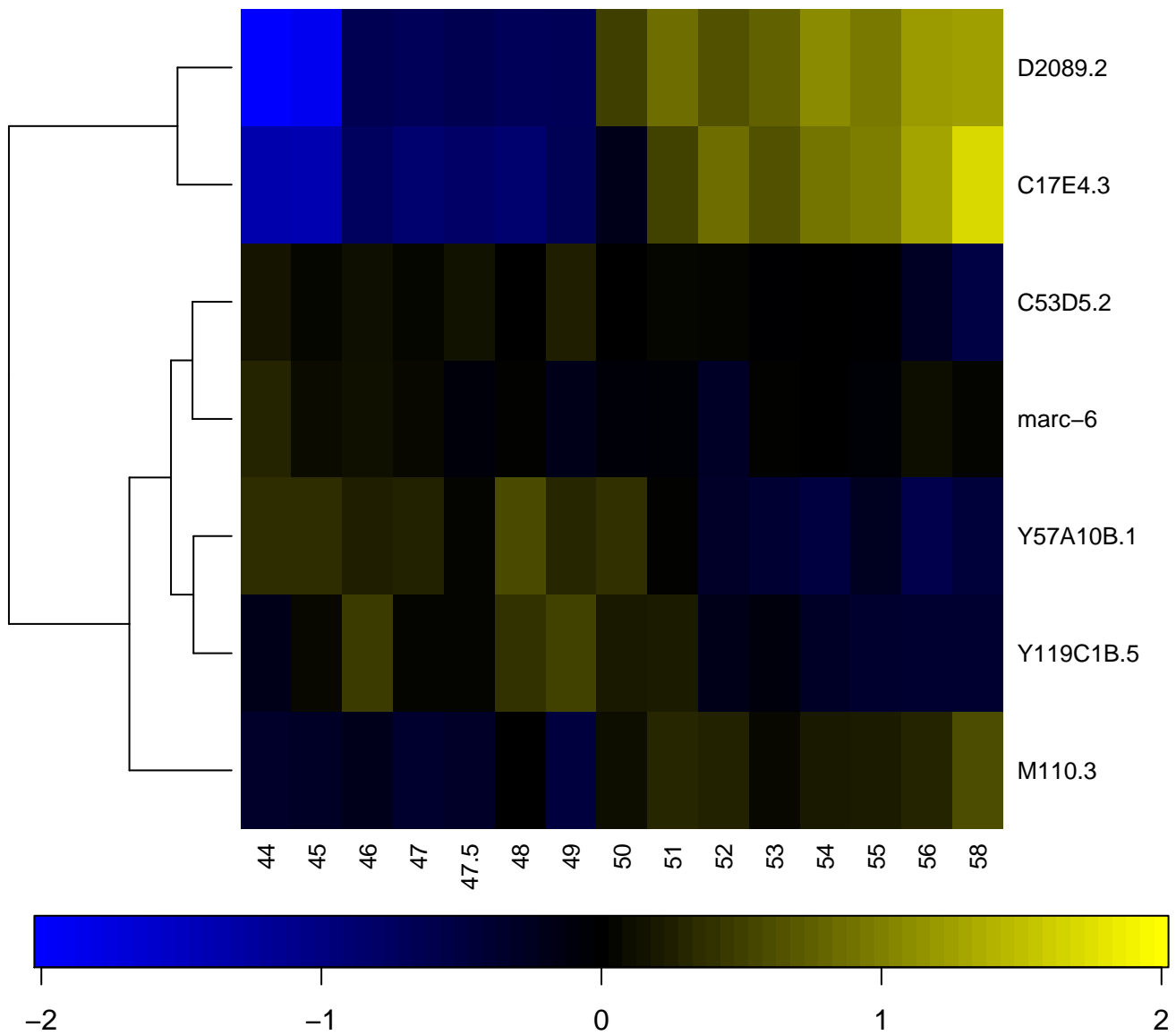
Zinc finger, PHD-type, conserved site



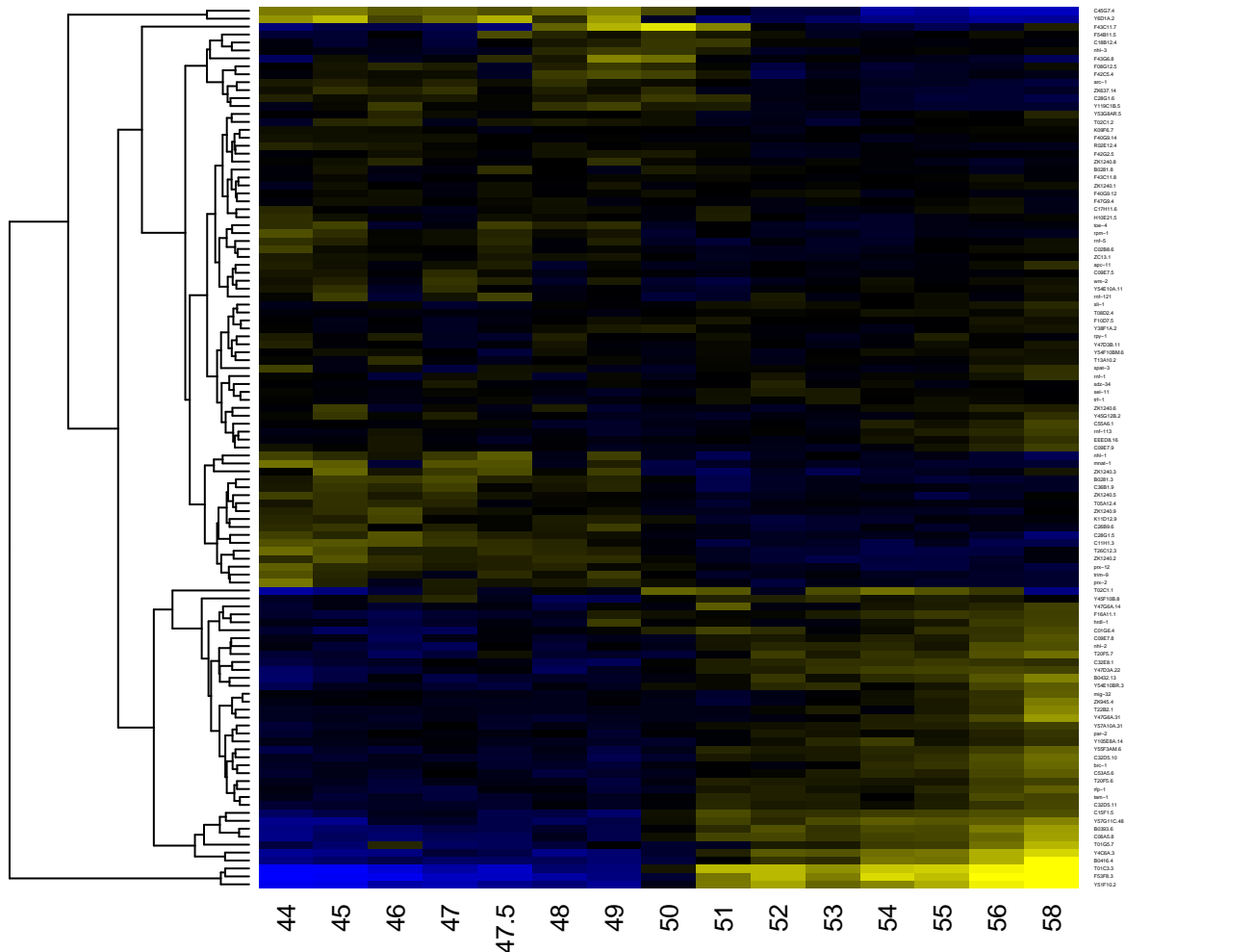
Zinc finger, RanBP2-type



Zinc finger, RING-CH-type



Zinc finger, RING-type



-2

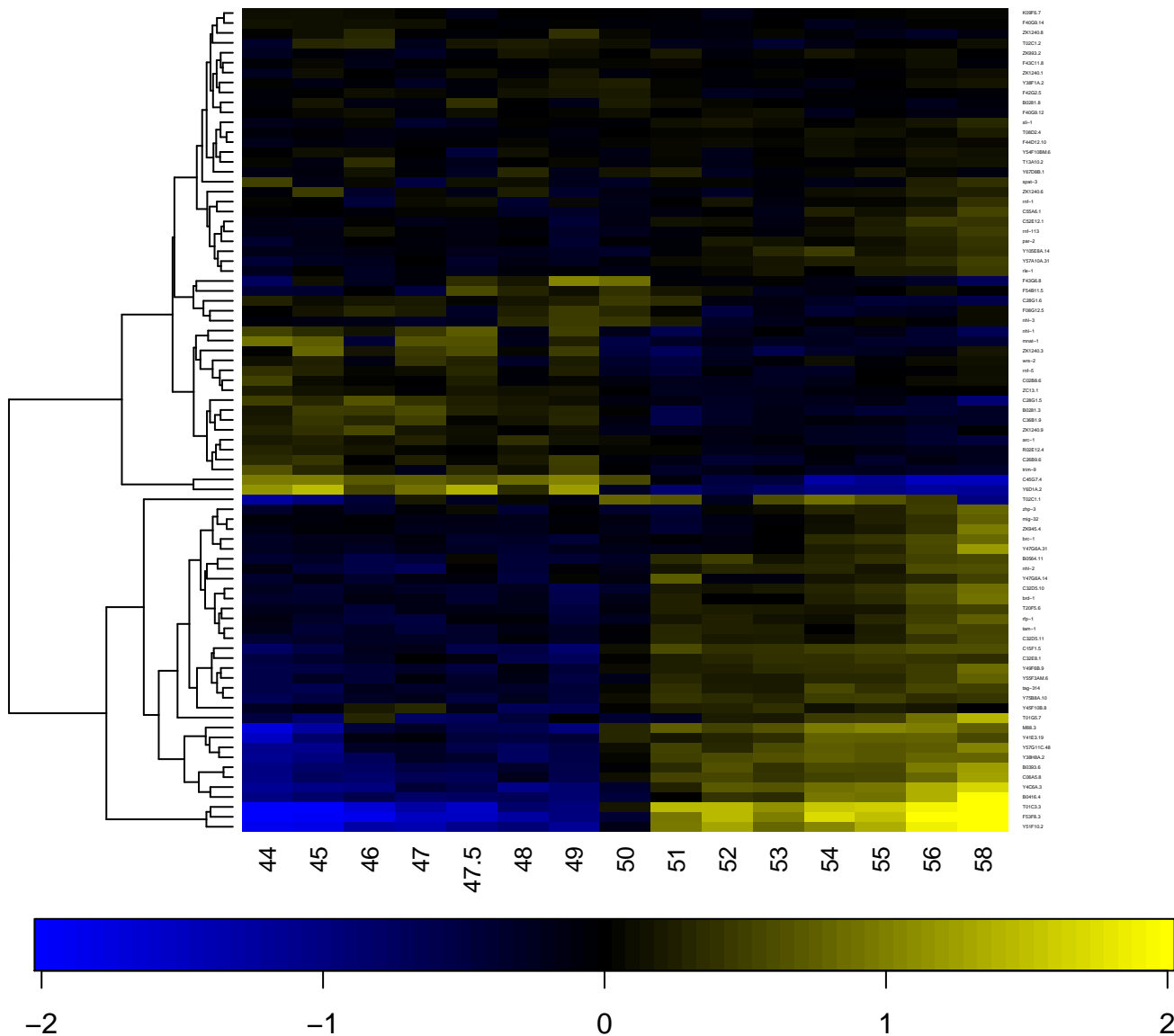
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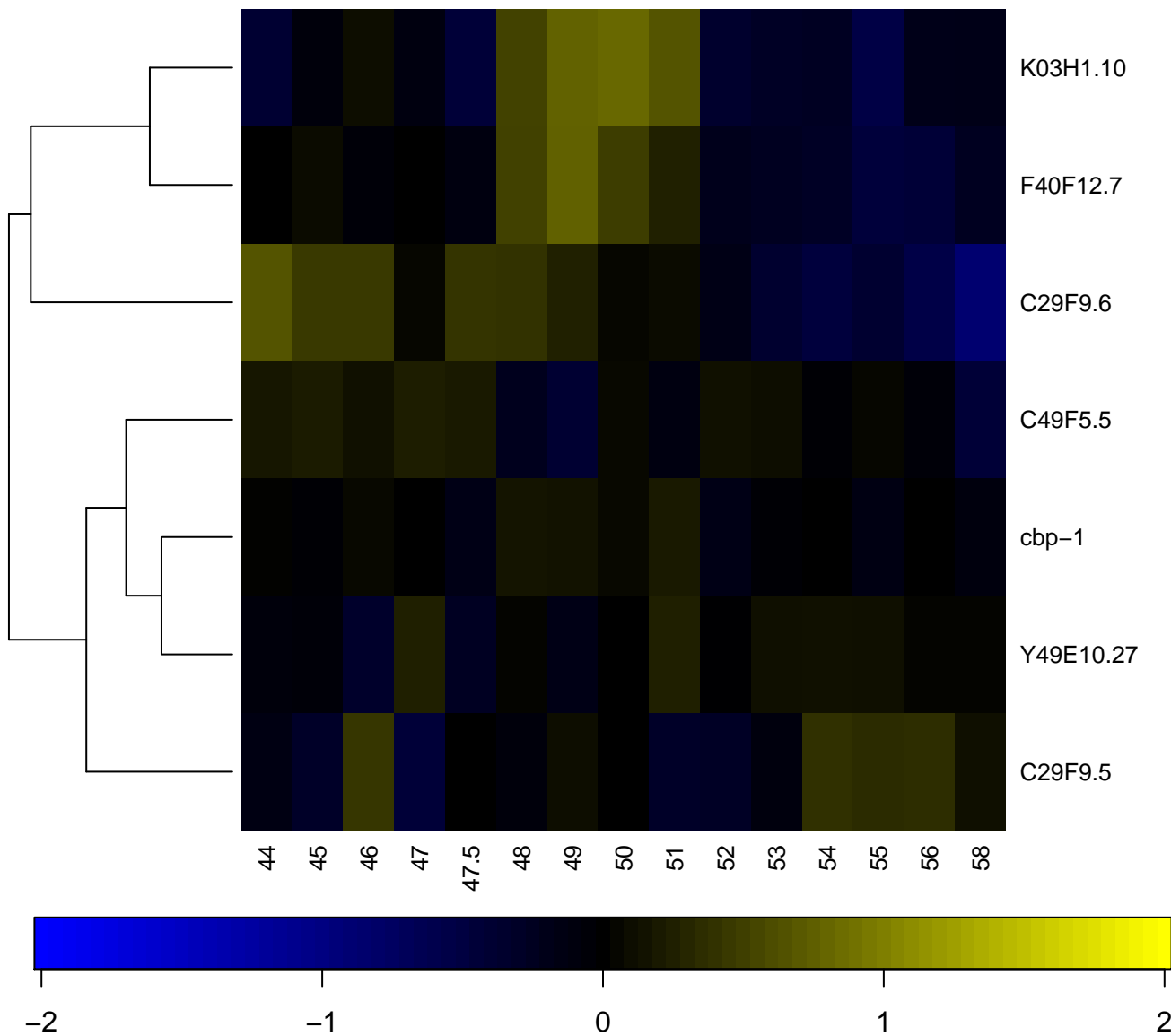
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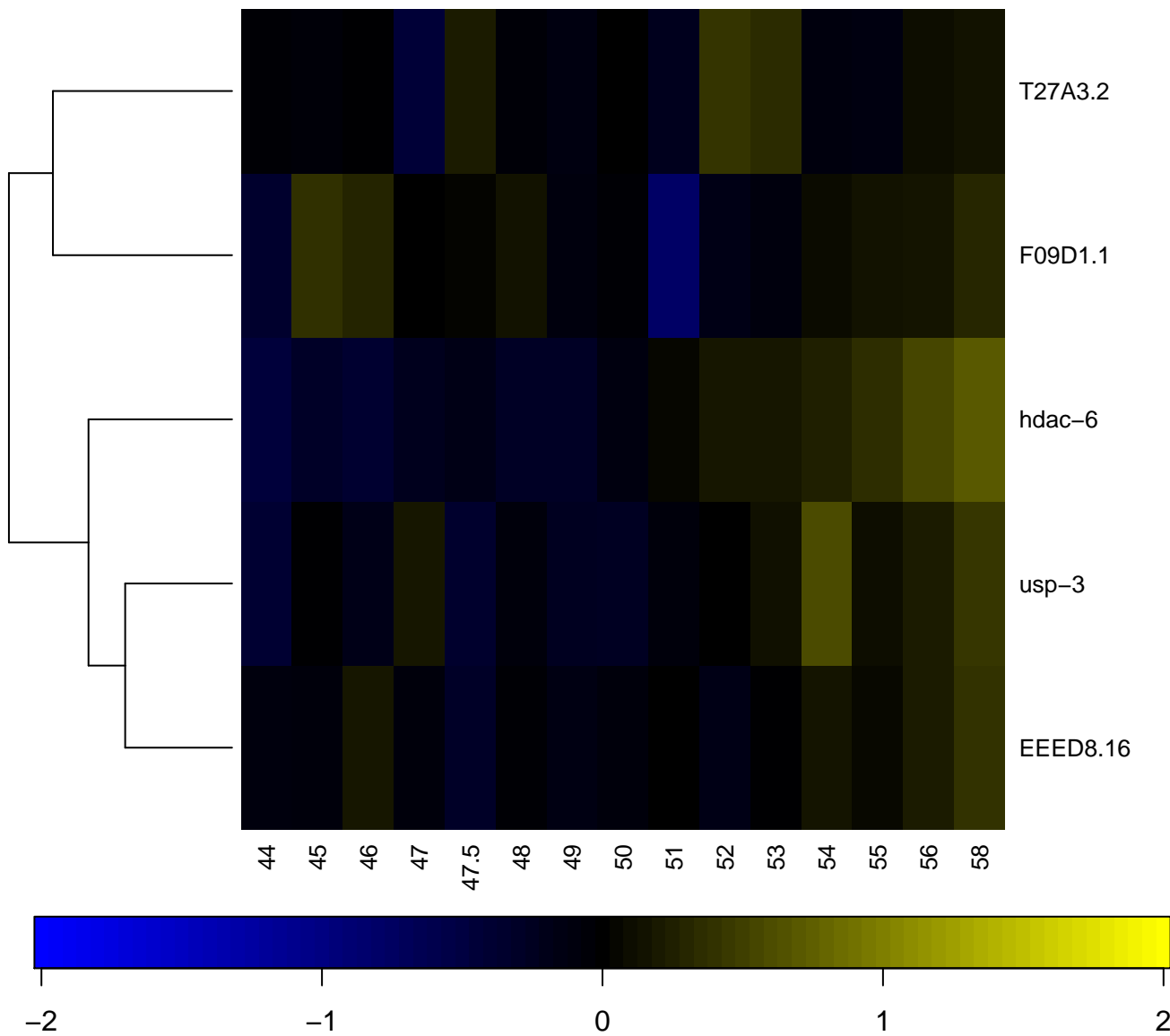
Zinc finger, RING-type, conserved site



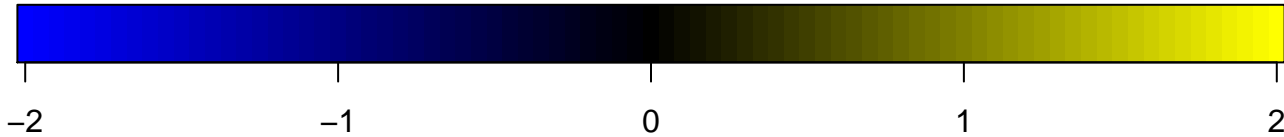
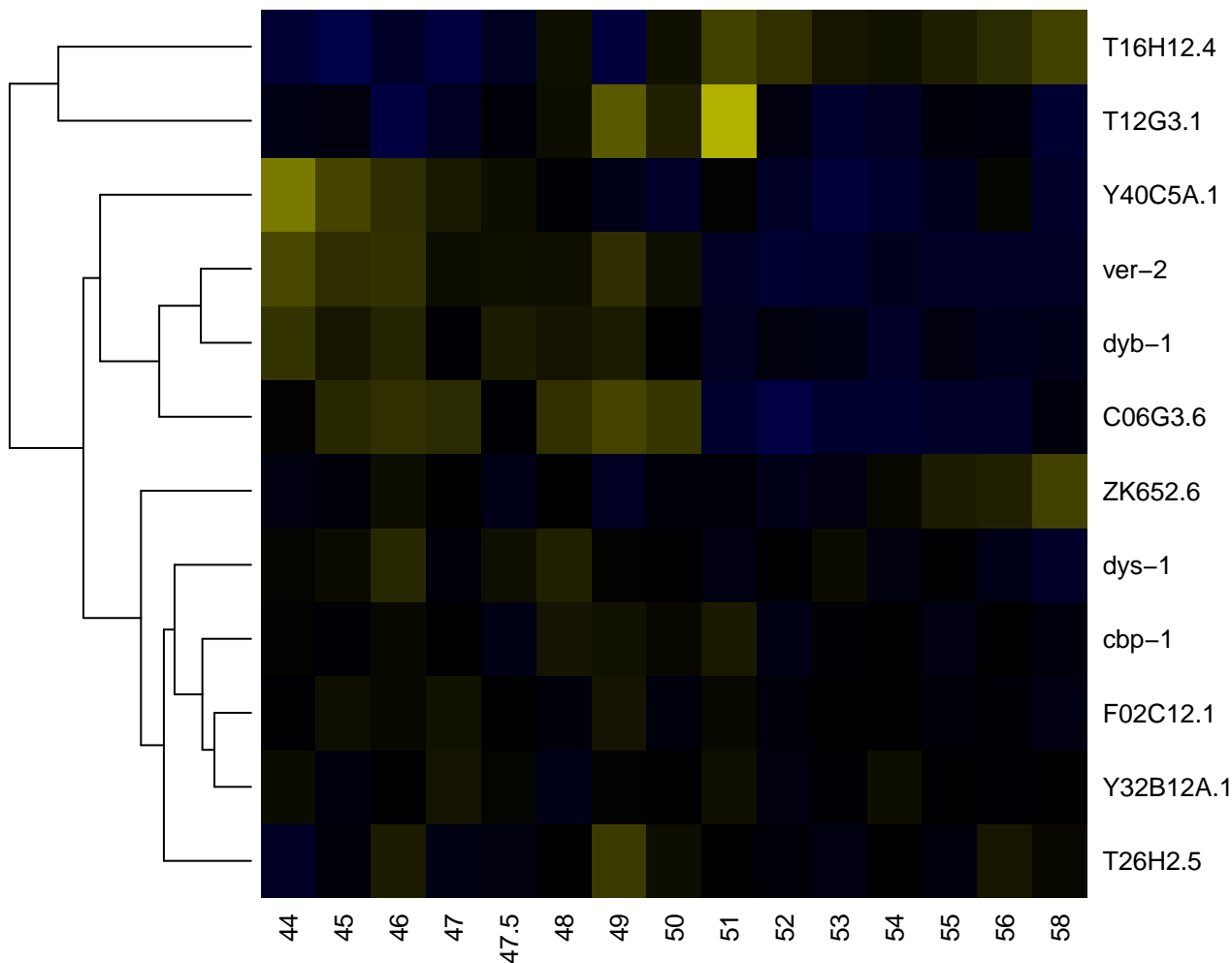
Zinc finger, TAZ-type



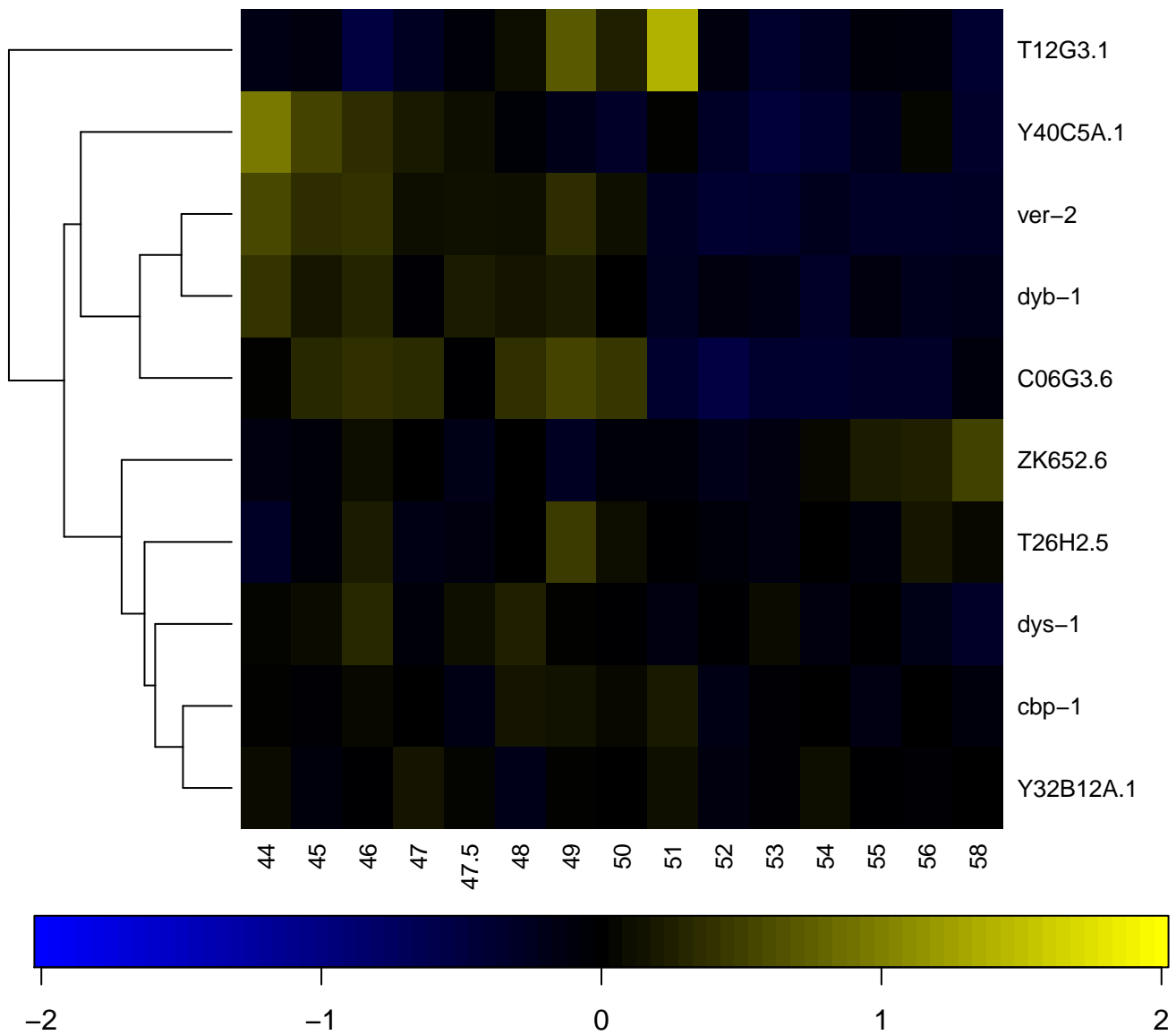
Zinc finger, UBP-type



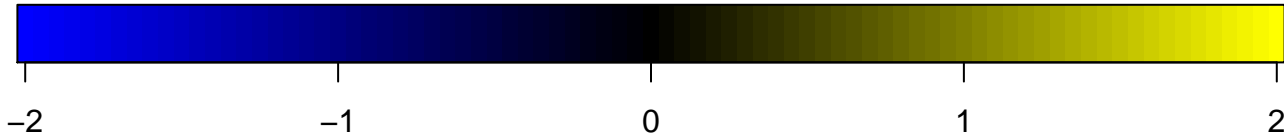
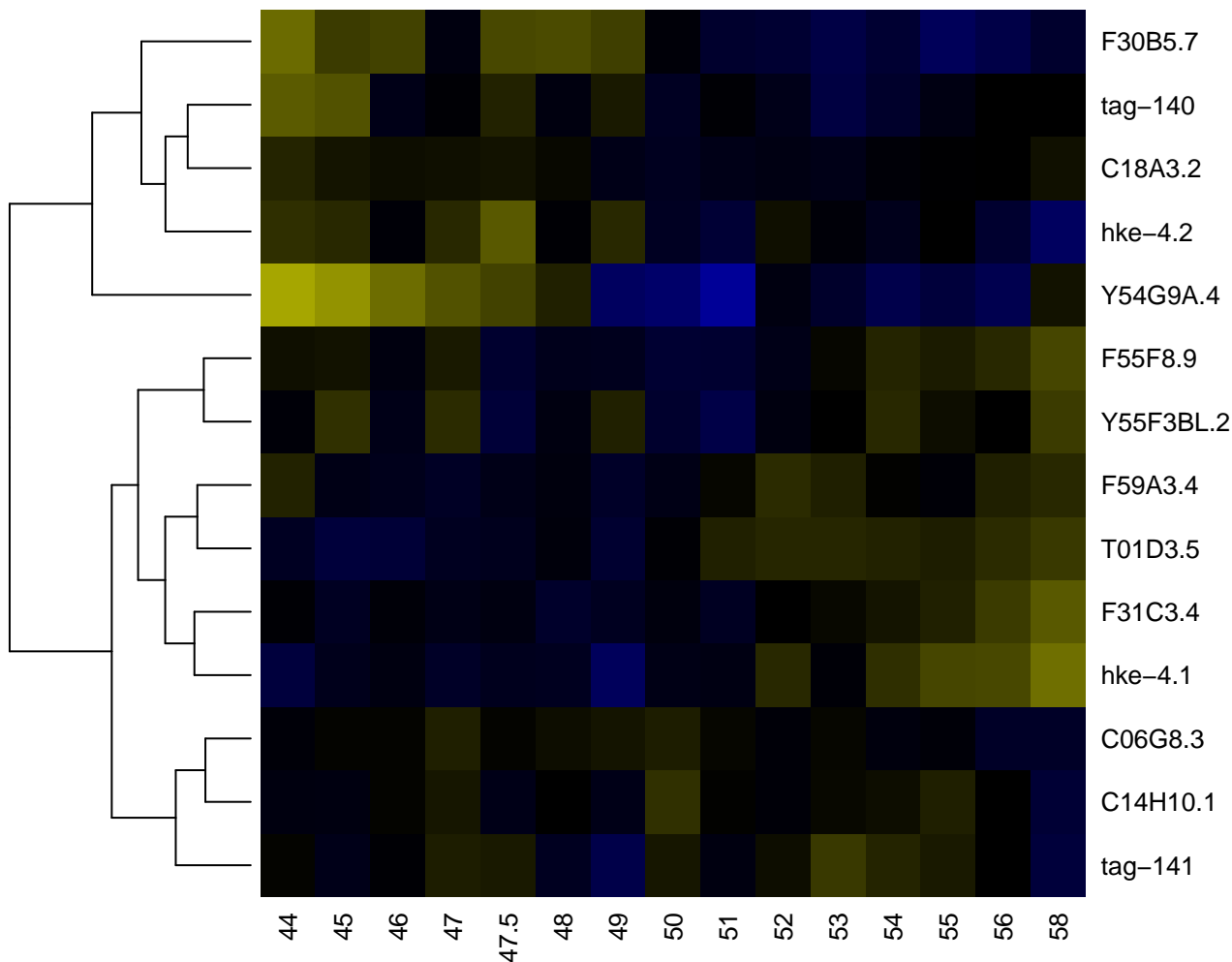
Zinc finger, ZZ-type



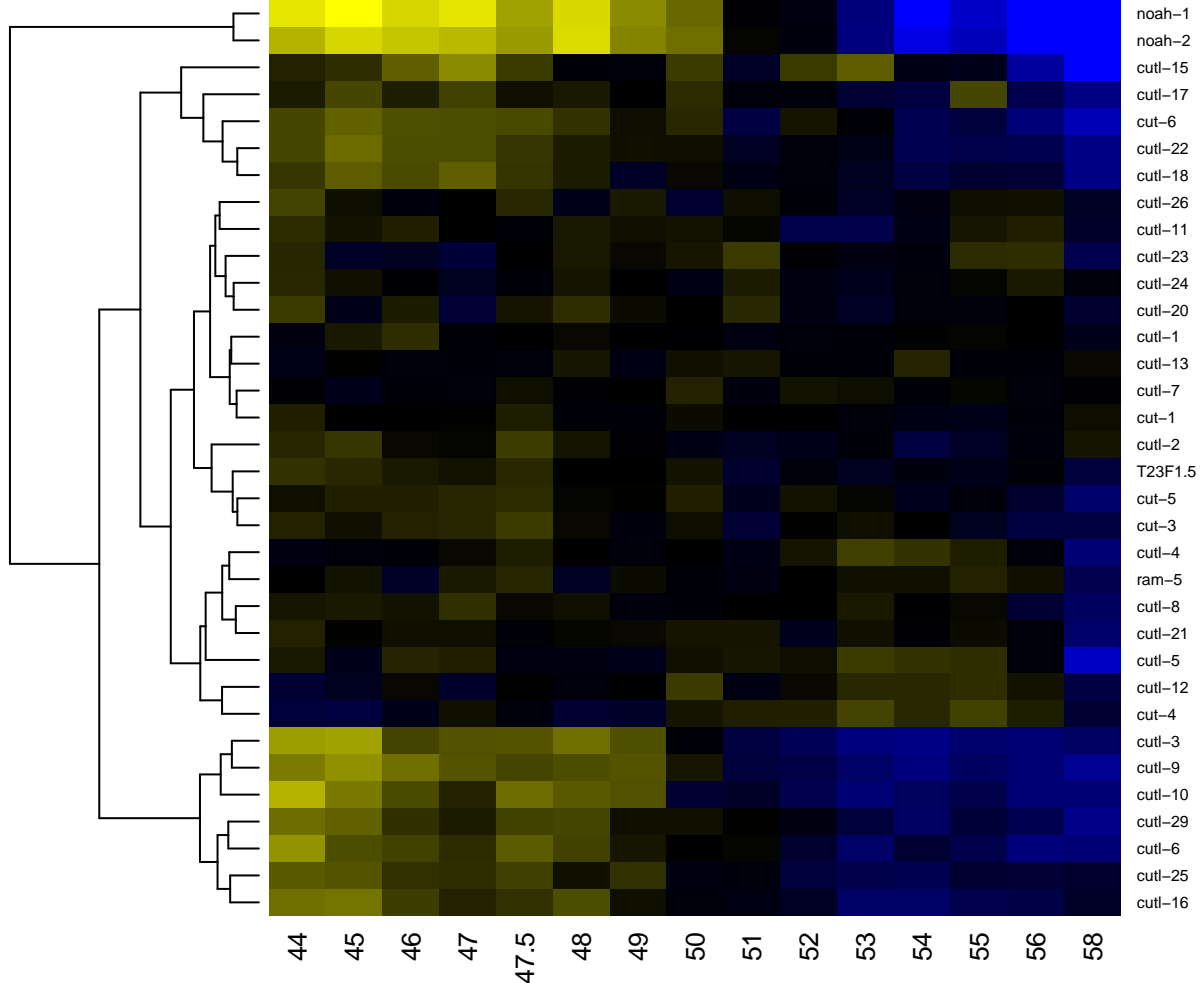
Zinc finger, ZZ type



Zinc/iron permease



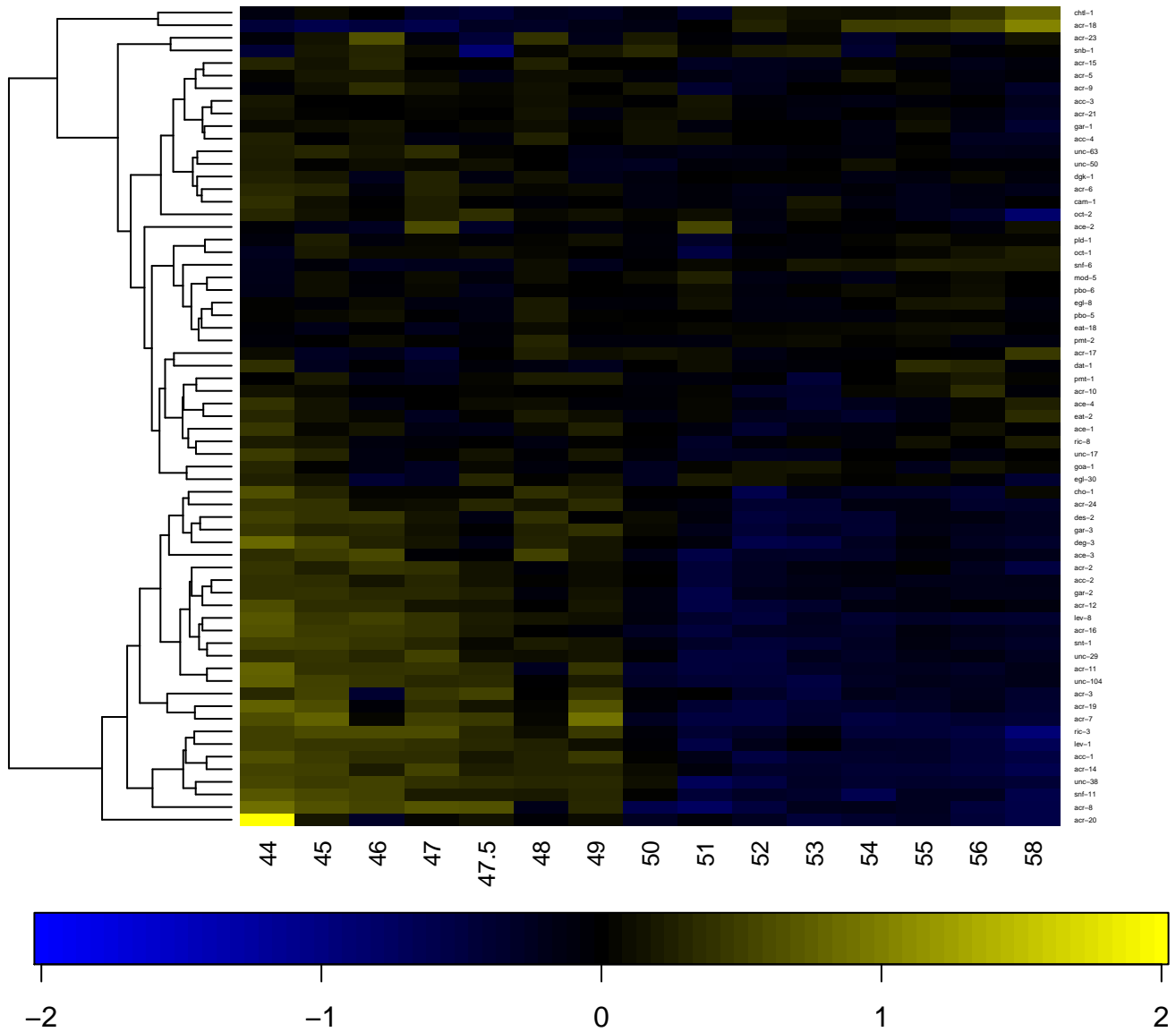
Zona pellucida-like domain



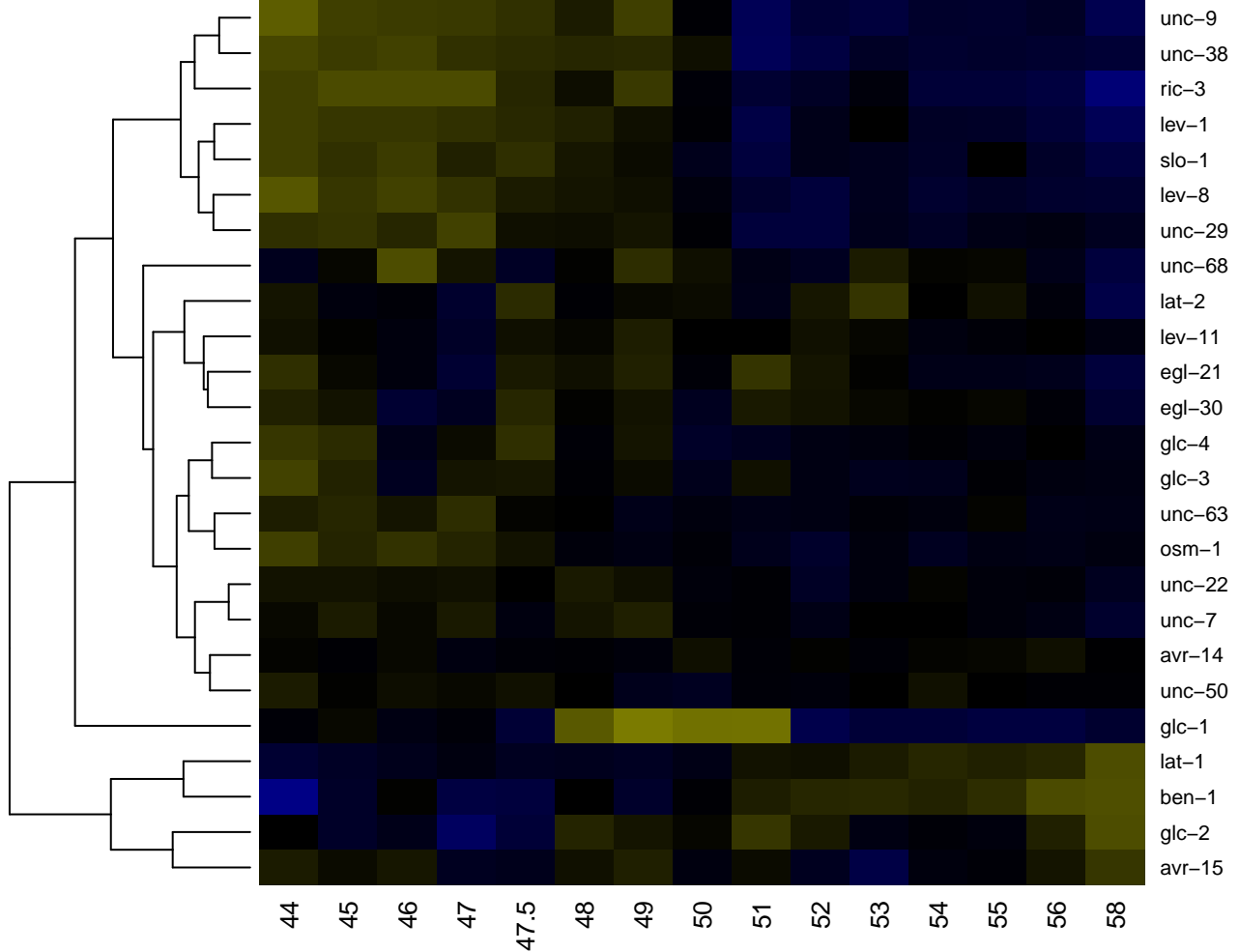
Supplementary file I | Dynamic gene expression patterns of all Wormbook Chapters.

The “heatmap” function of “R” was used to cluster genes of each individual Wormbook Chapter according to their expression pattern. Wormbook Chapter name is shown per page as figure title. The time in hours is shown on the x-axis. Gene names are shown on the y-axis. The scale bar shows the log₂ ratio with the mean for each time-point. Blue is lower than the mean and yellow is higher than the mean.

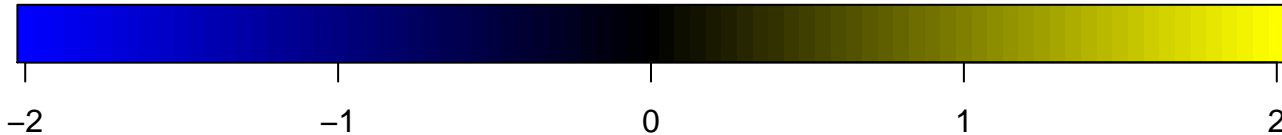
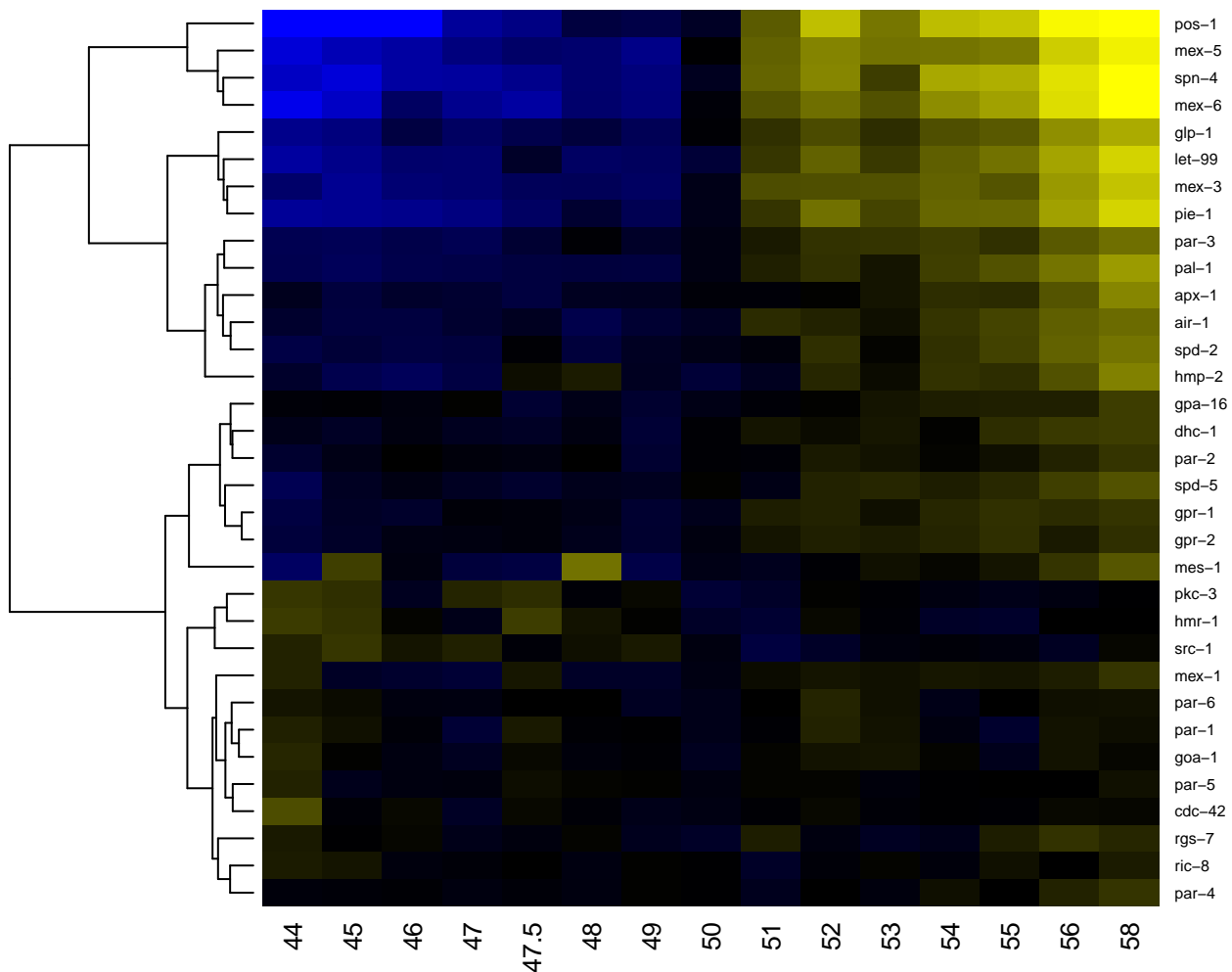
Acetylcholine



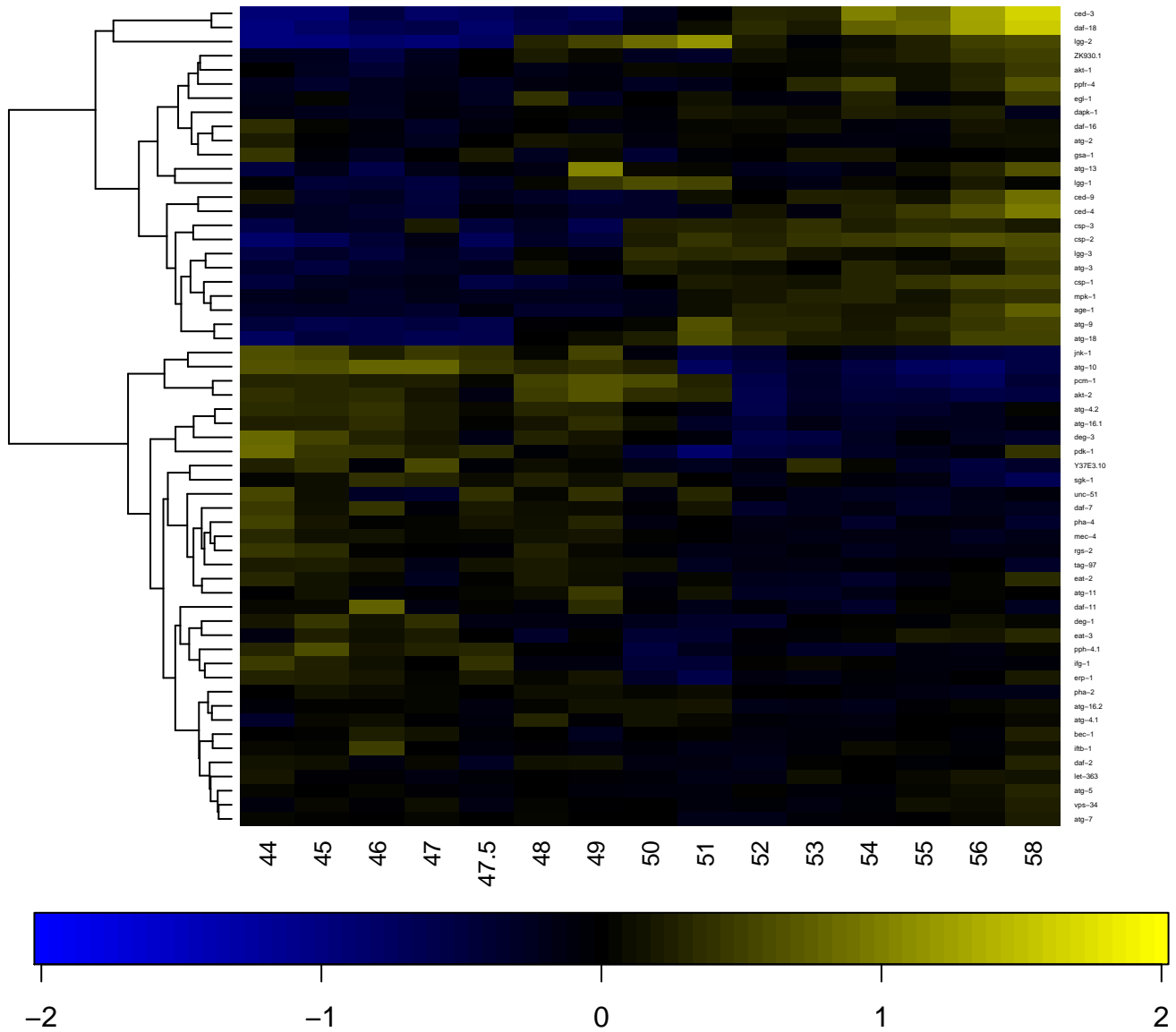
Anthelmintic drugs



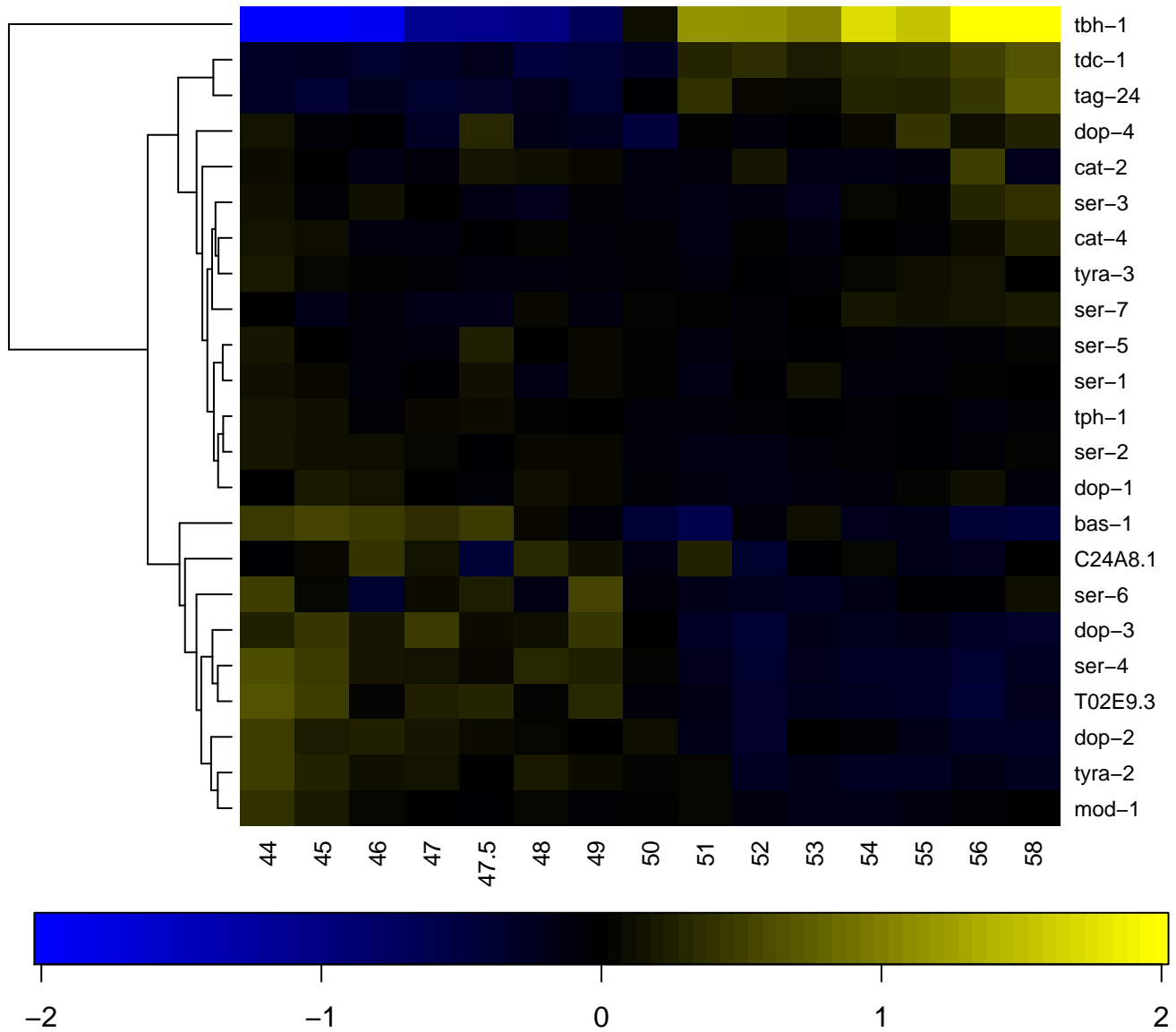
Asymmetric cell division and axis formation in the embryo



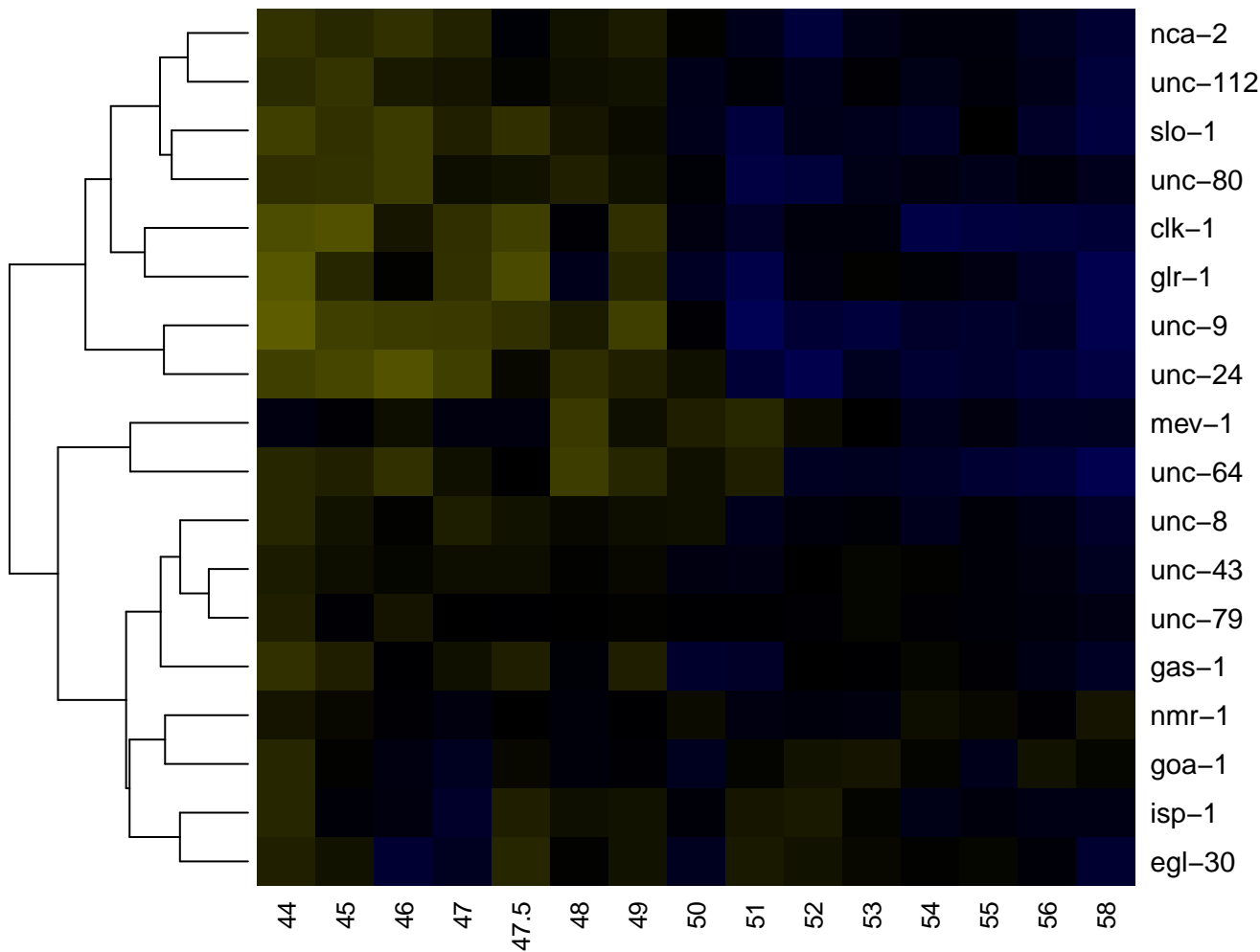
Autophagy in *C. elegans*



Biogenic amine neurotransmitters



C. elegans and volatile anesthetics



-2

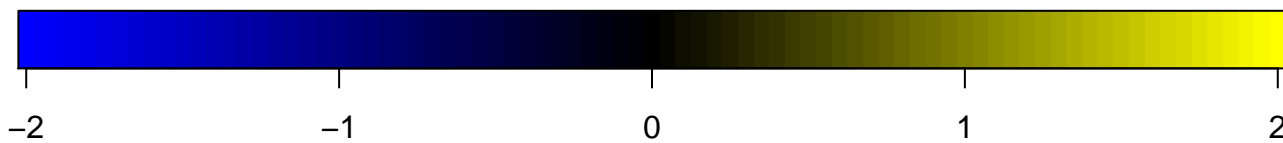
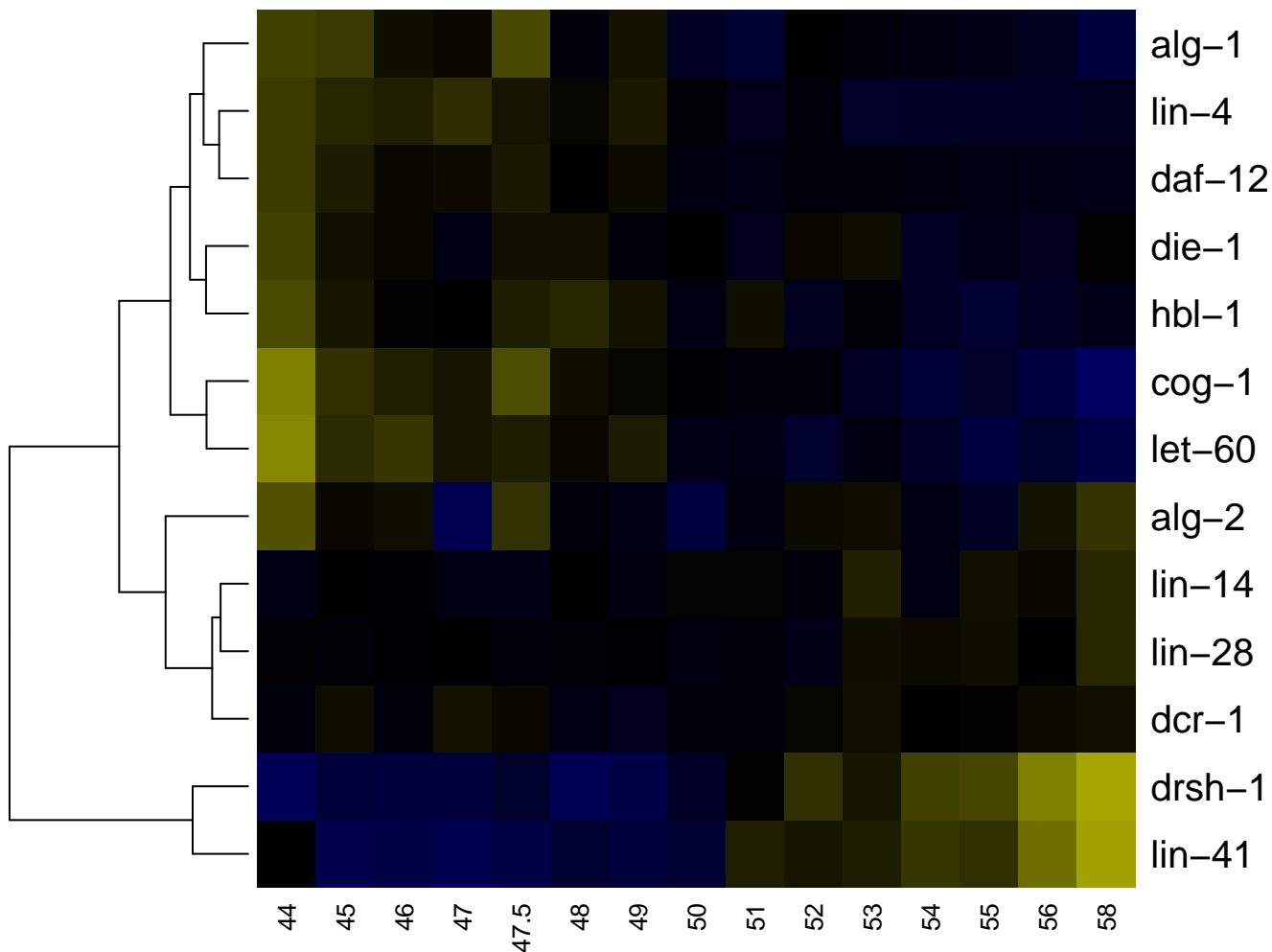
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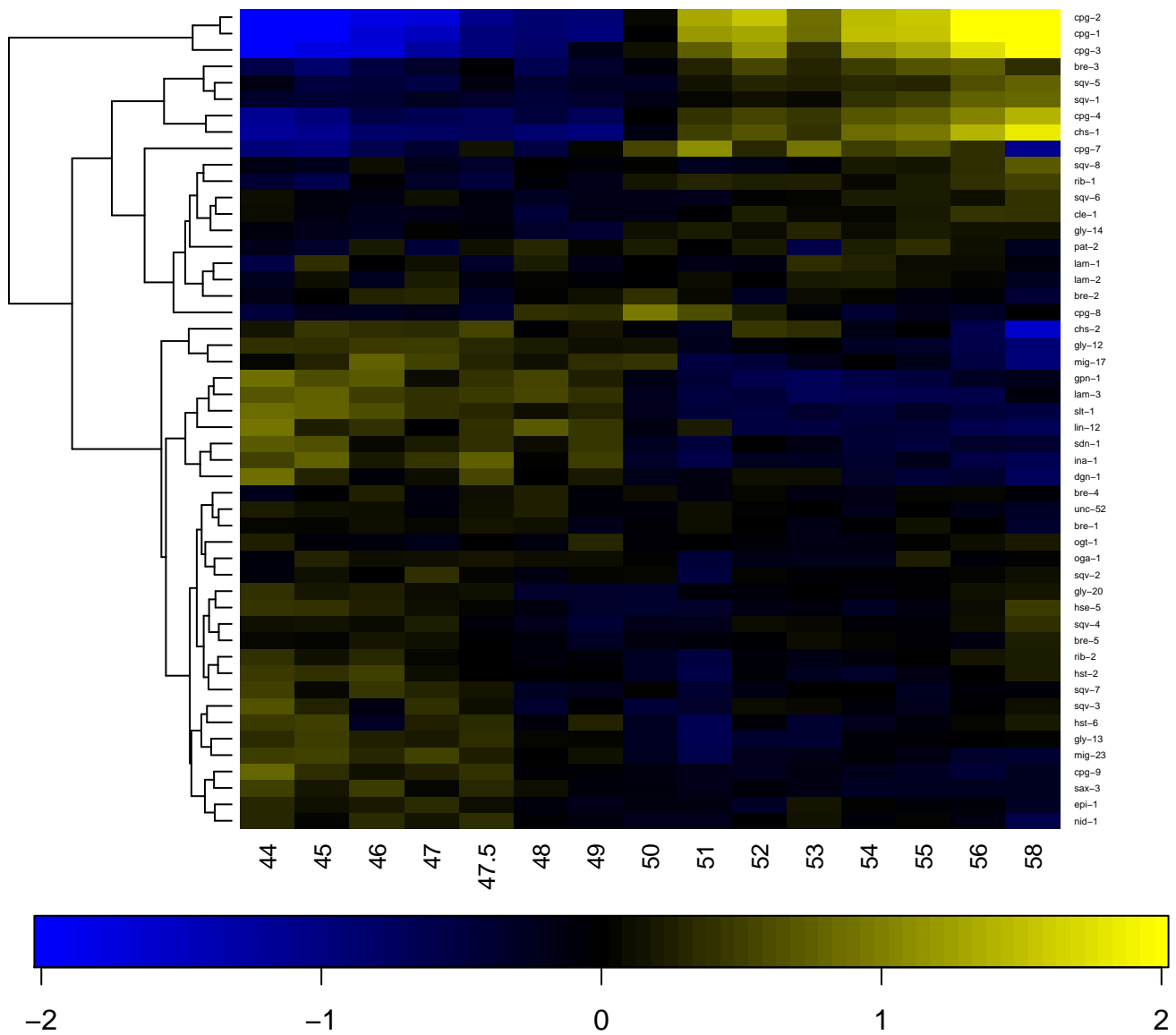
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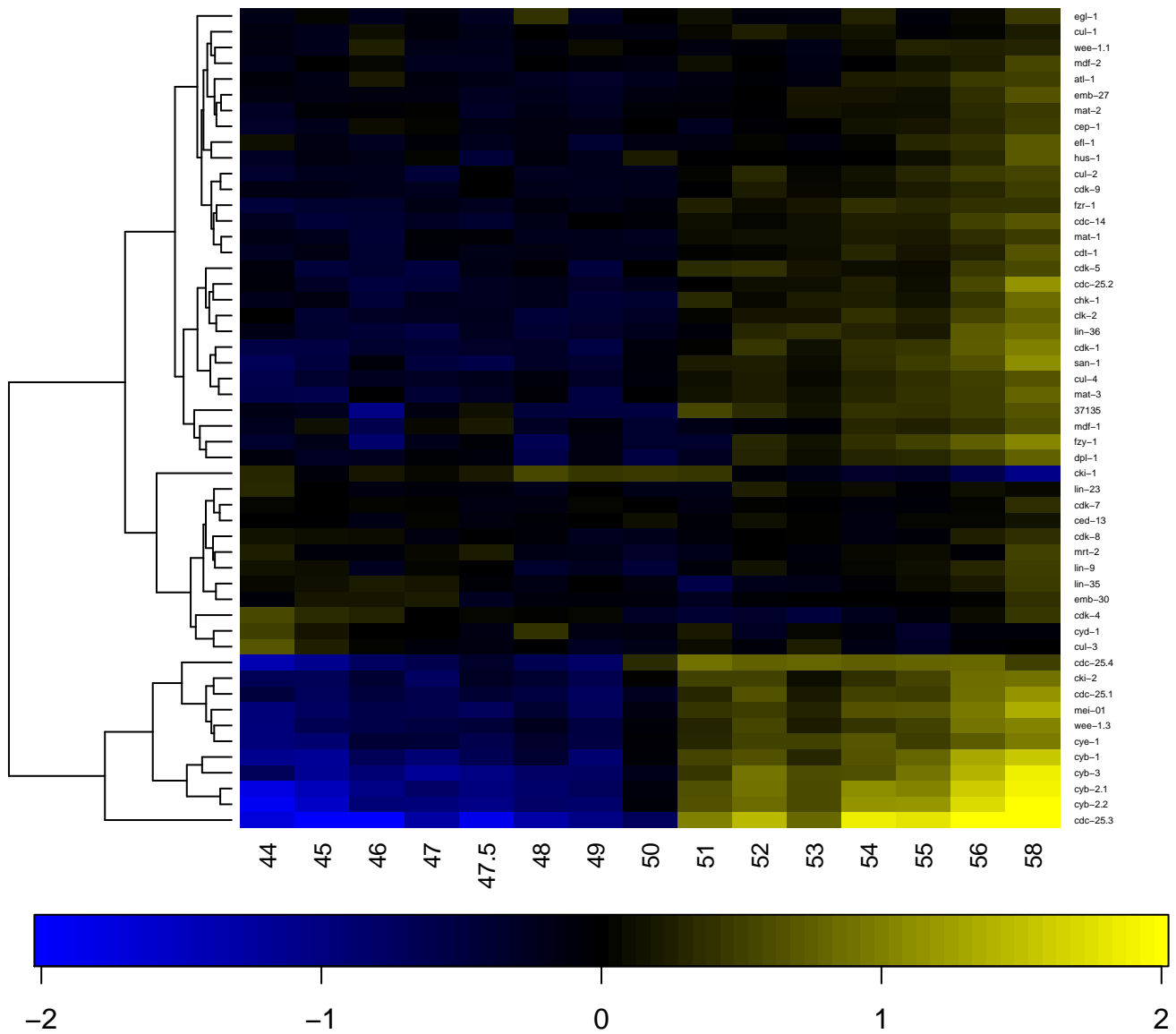
C. elegans microRNAs



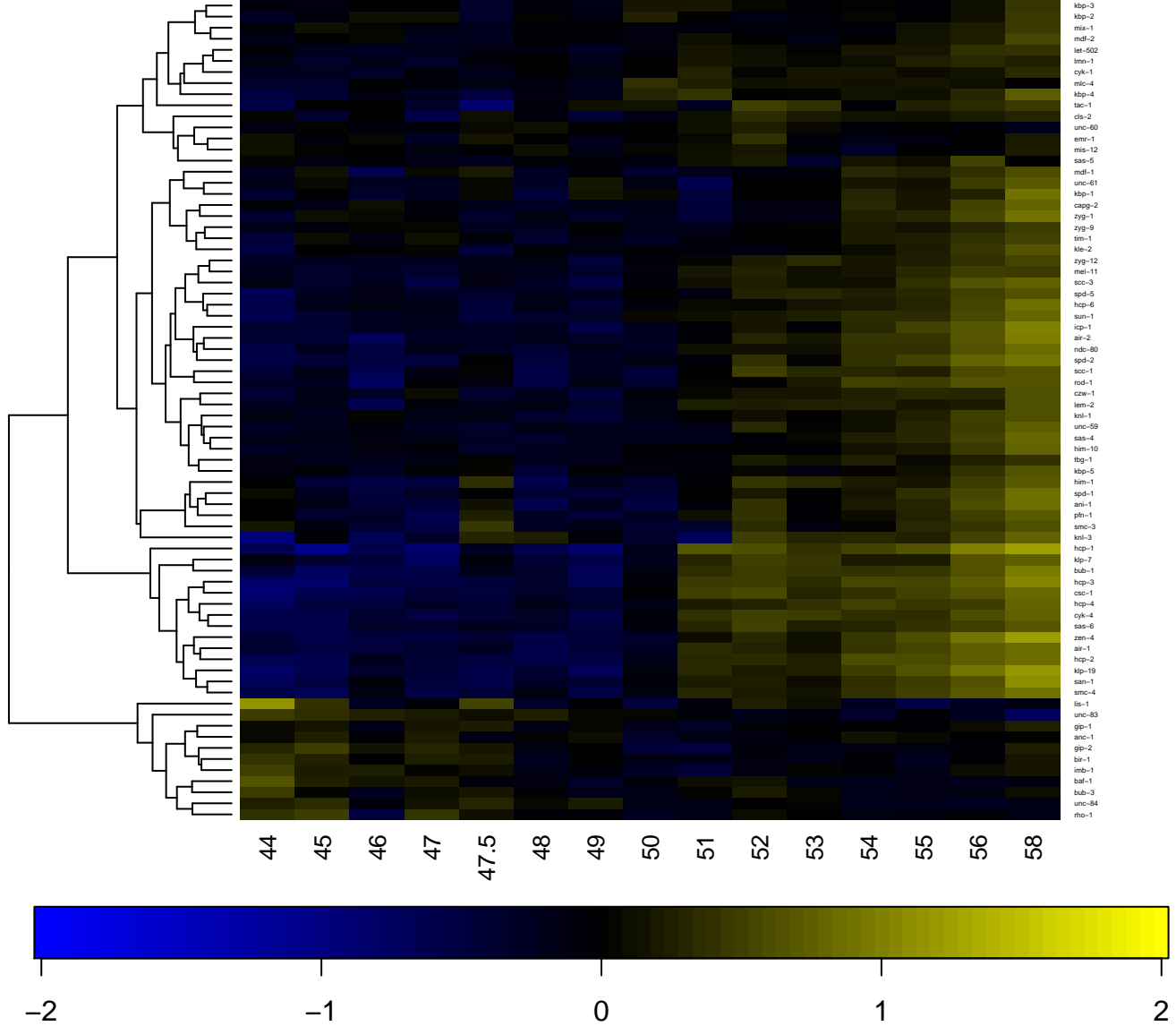
Carbohydrates and glycosylation



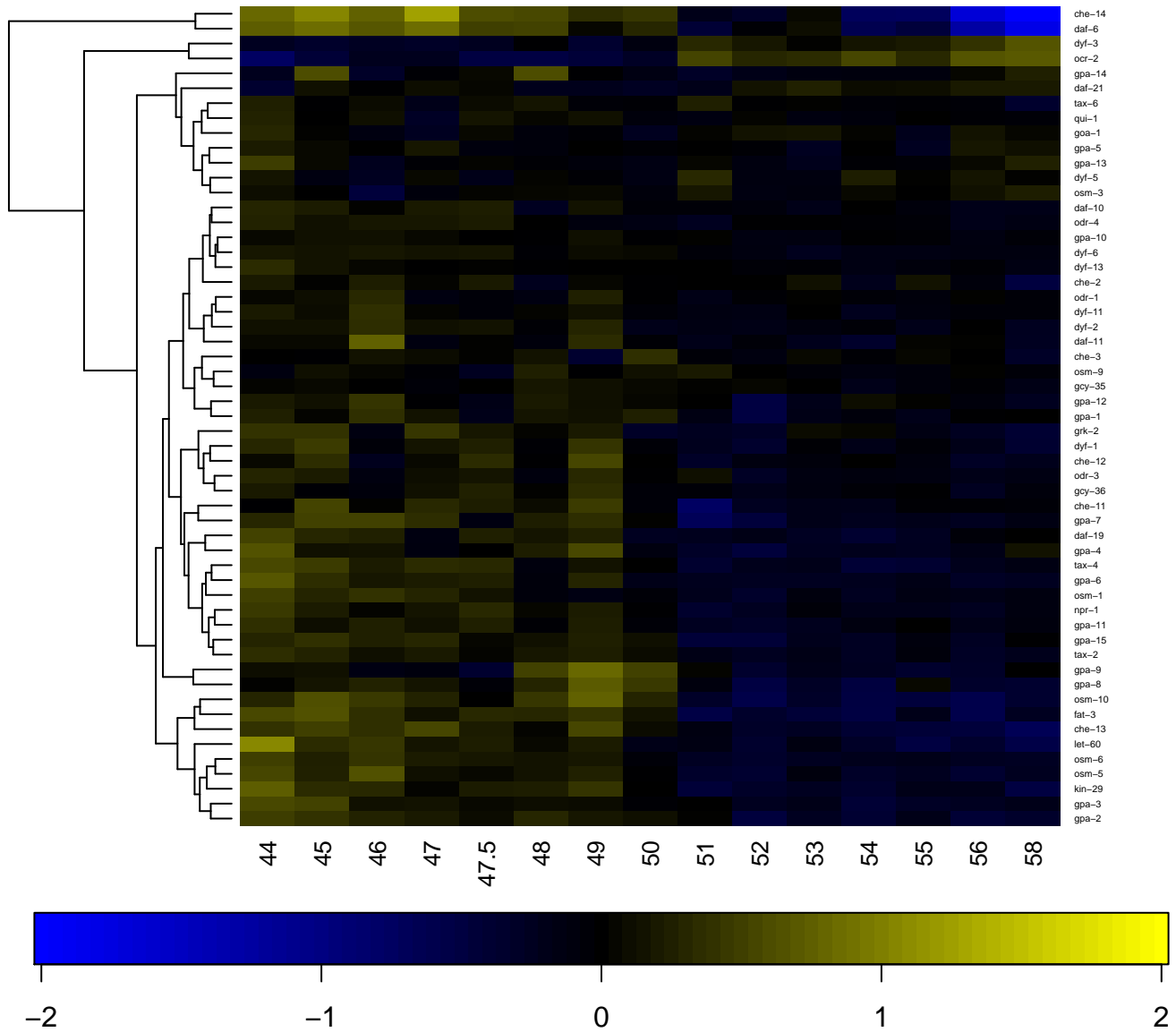
Cell-cycle regulation



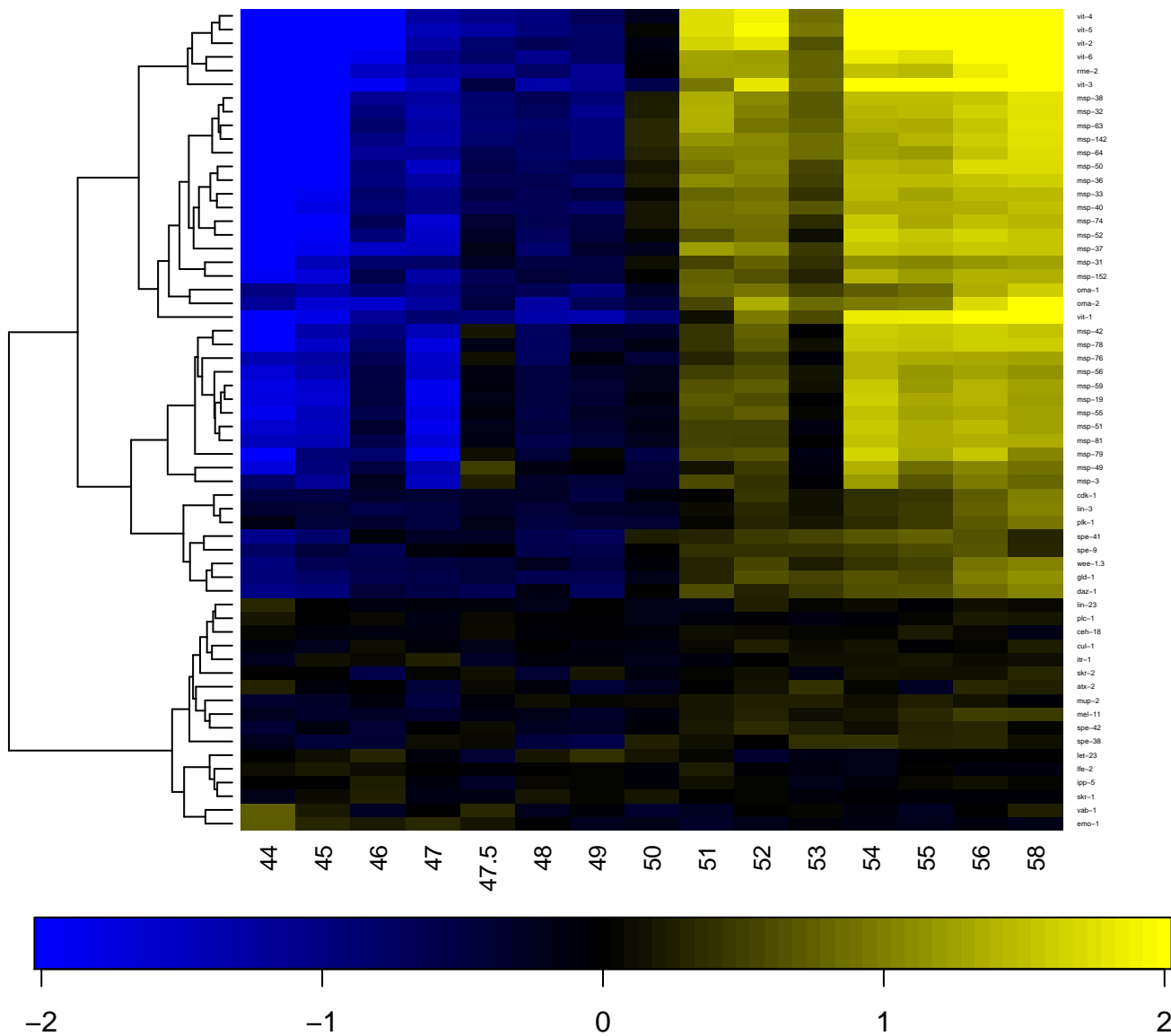
Cell division



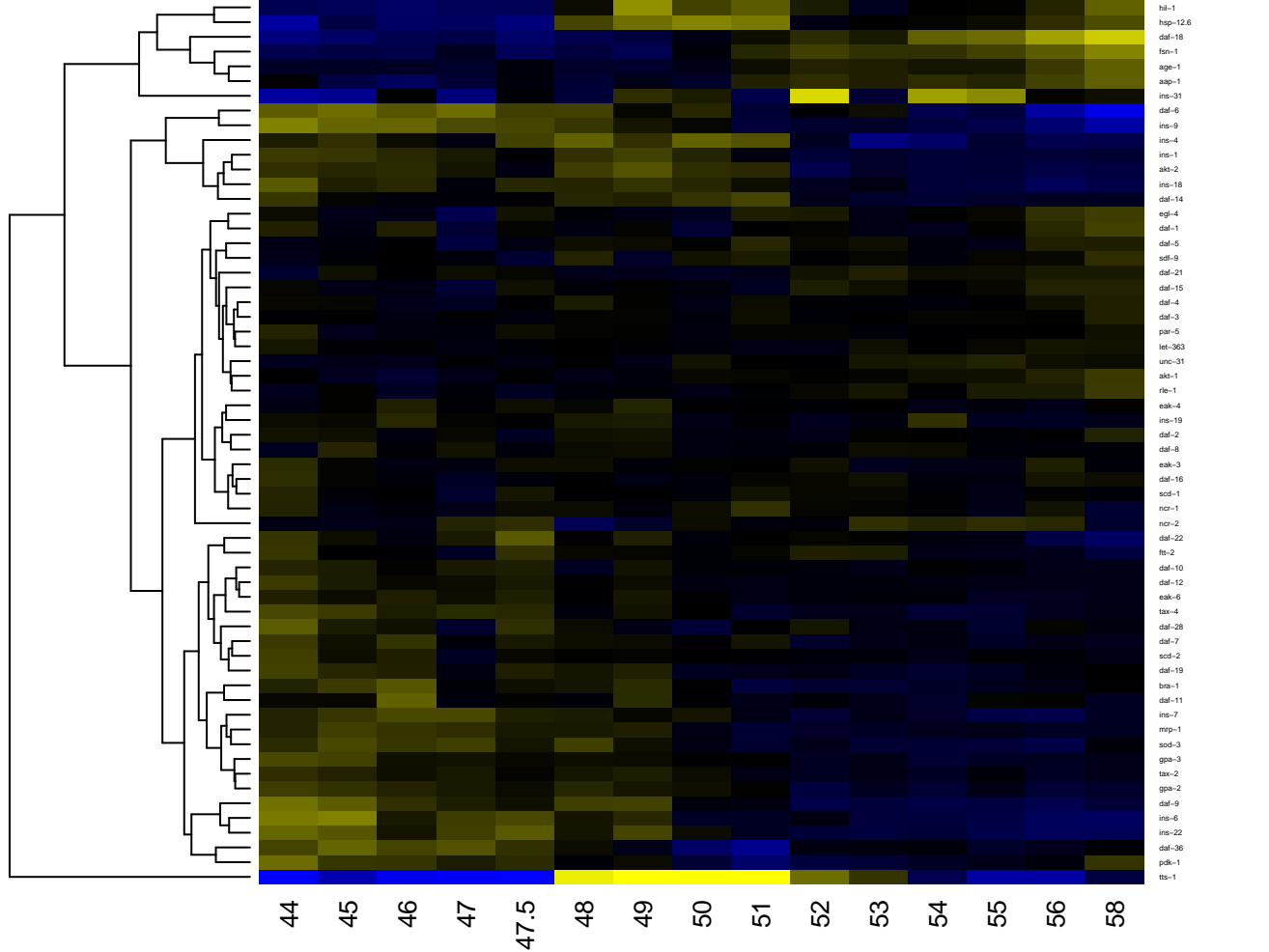
Chemosensation



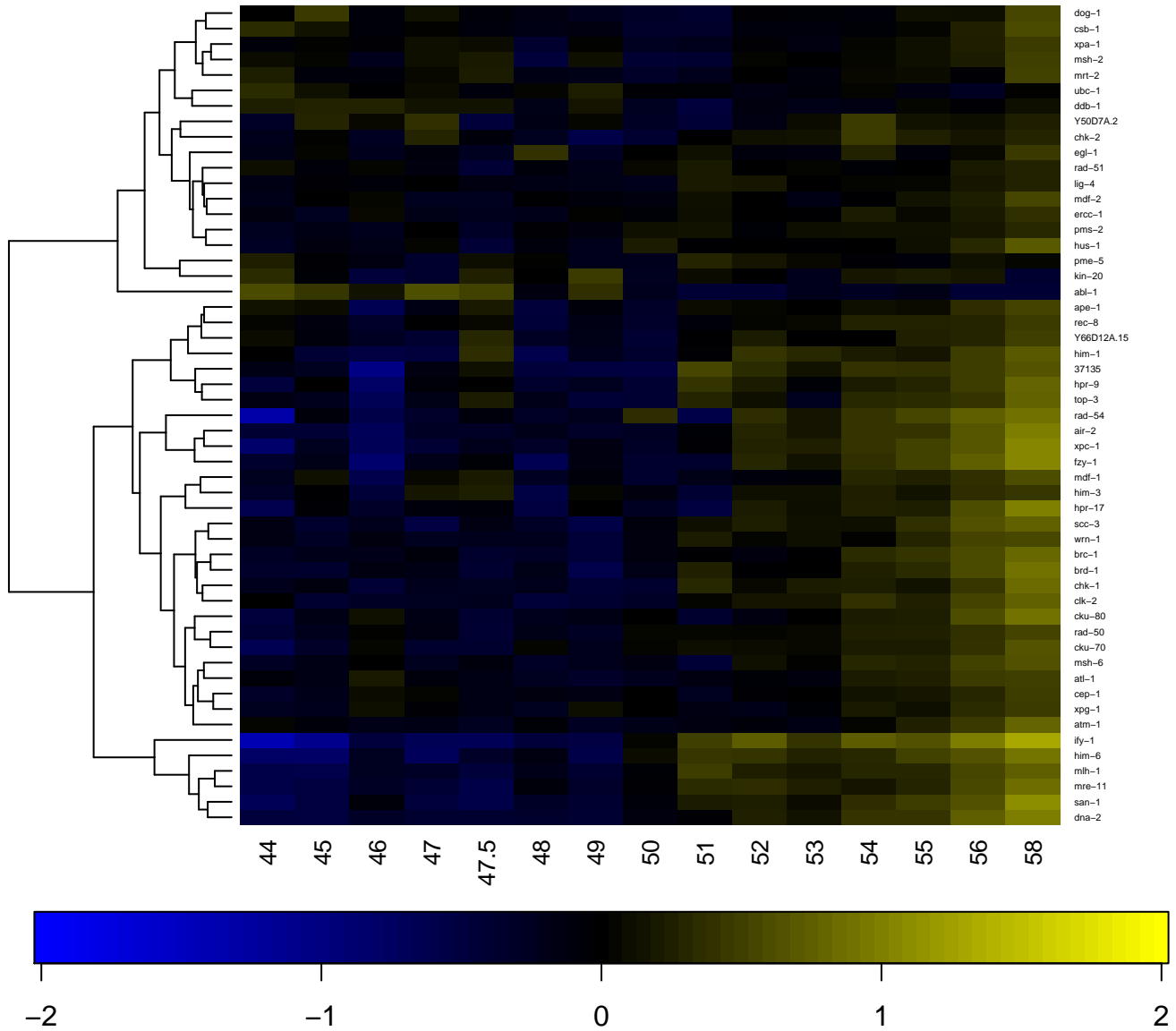
Control of oocyte meiotic maturation and fertilization



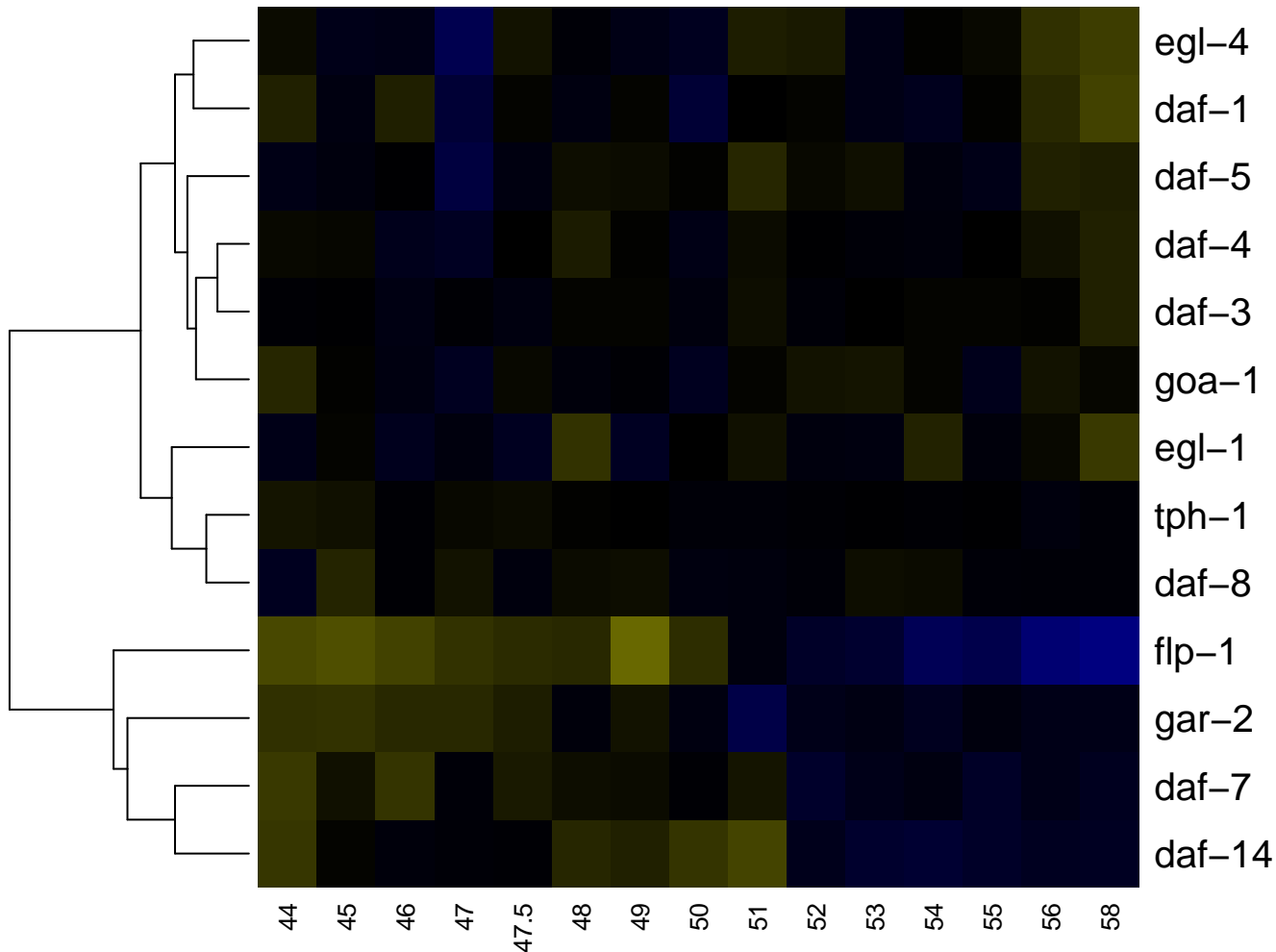
Dauer



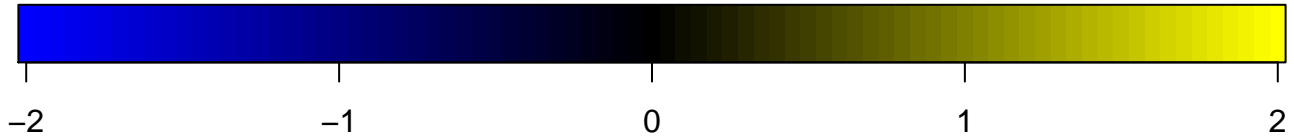
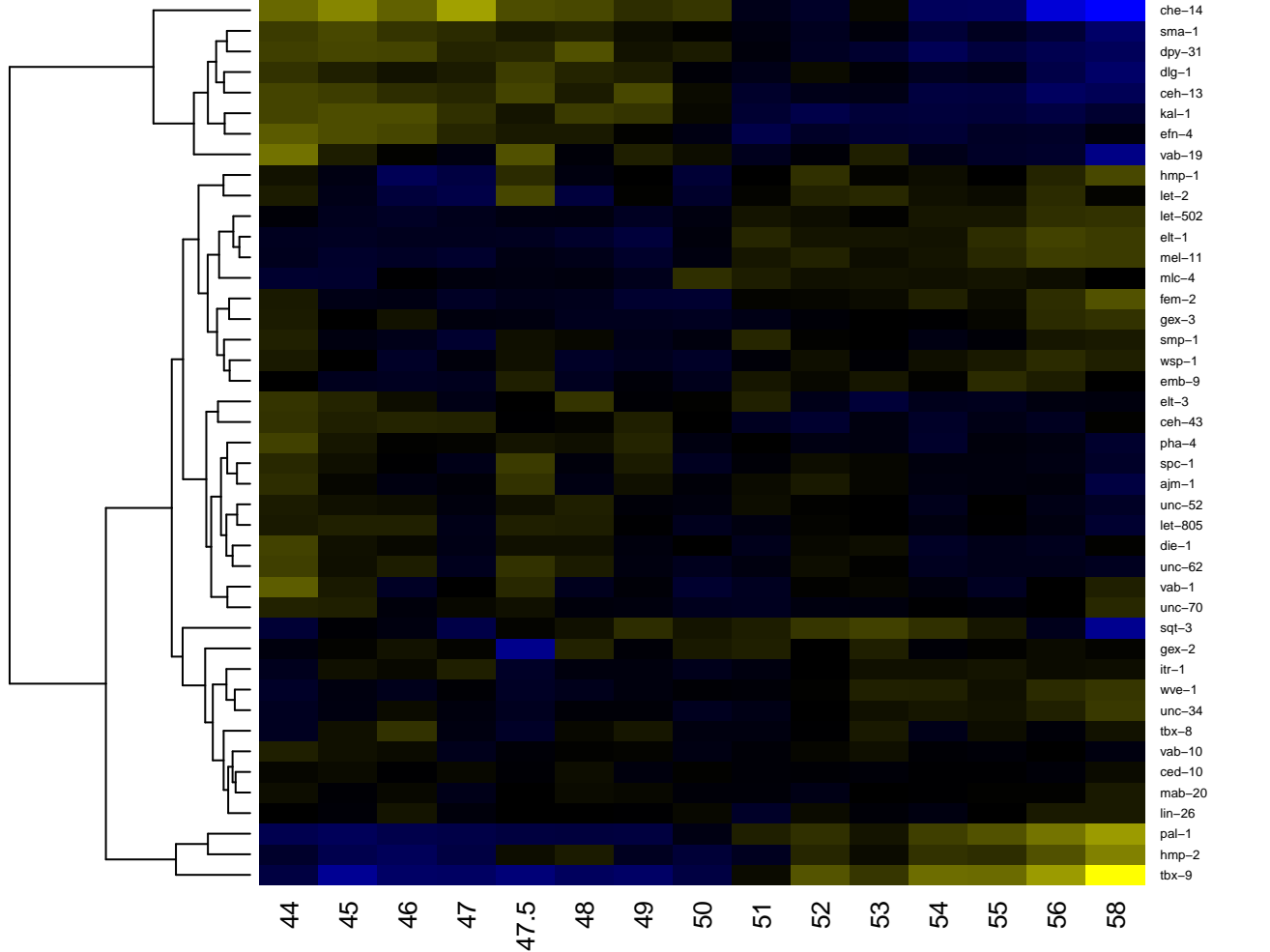
DNA repair



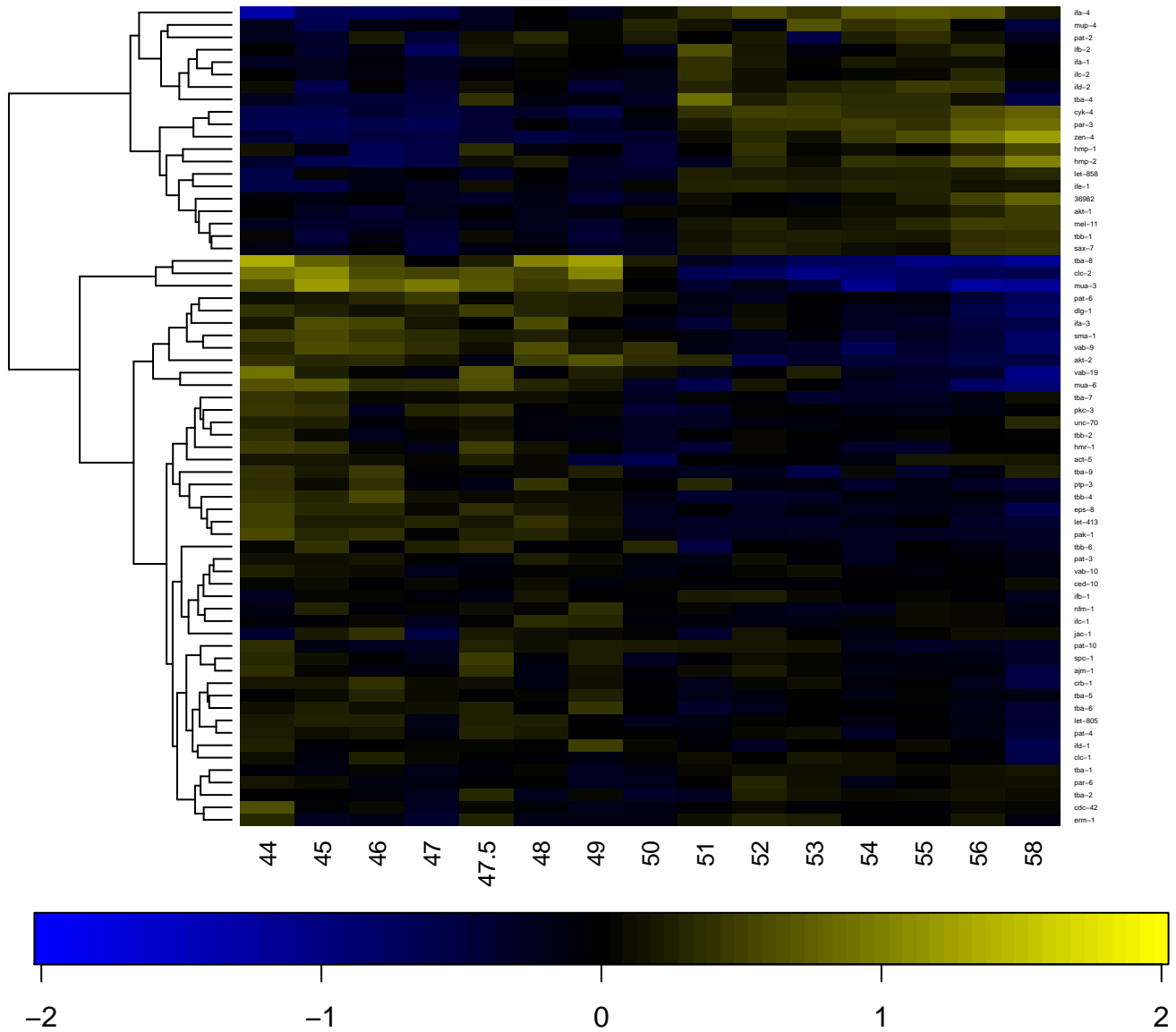
Egg-laying



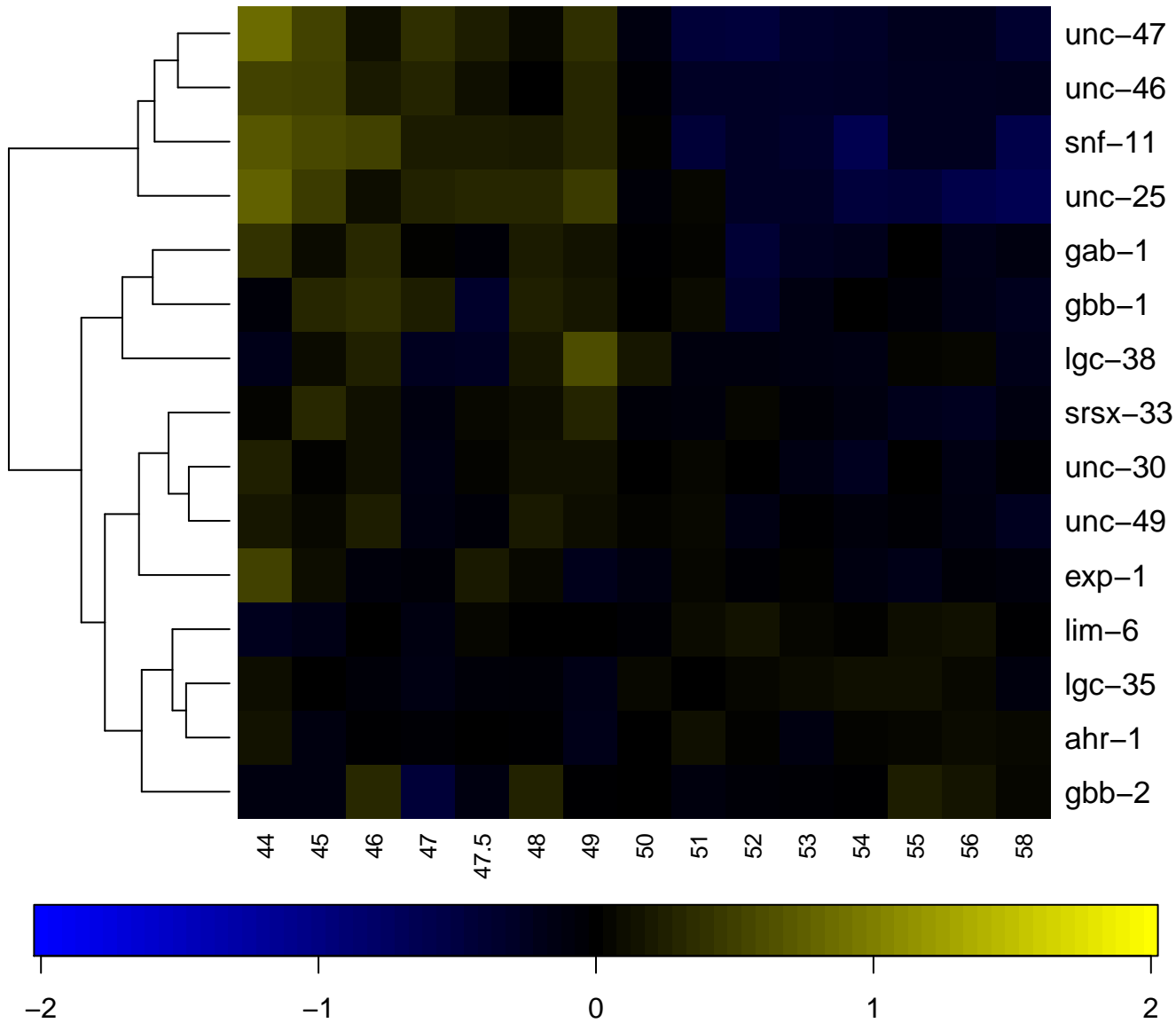
Epidermal morphogenesis



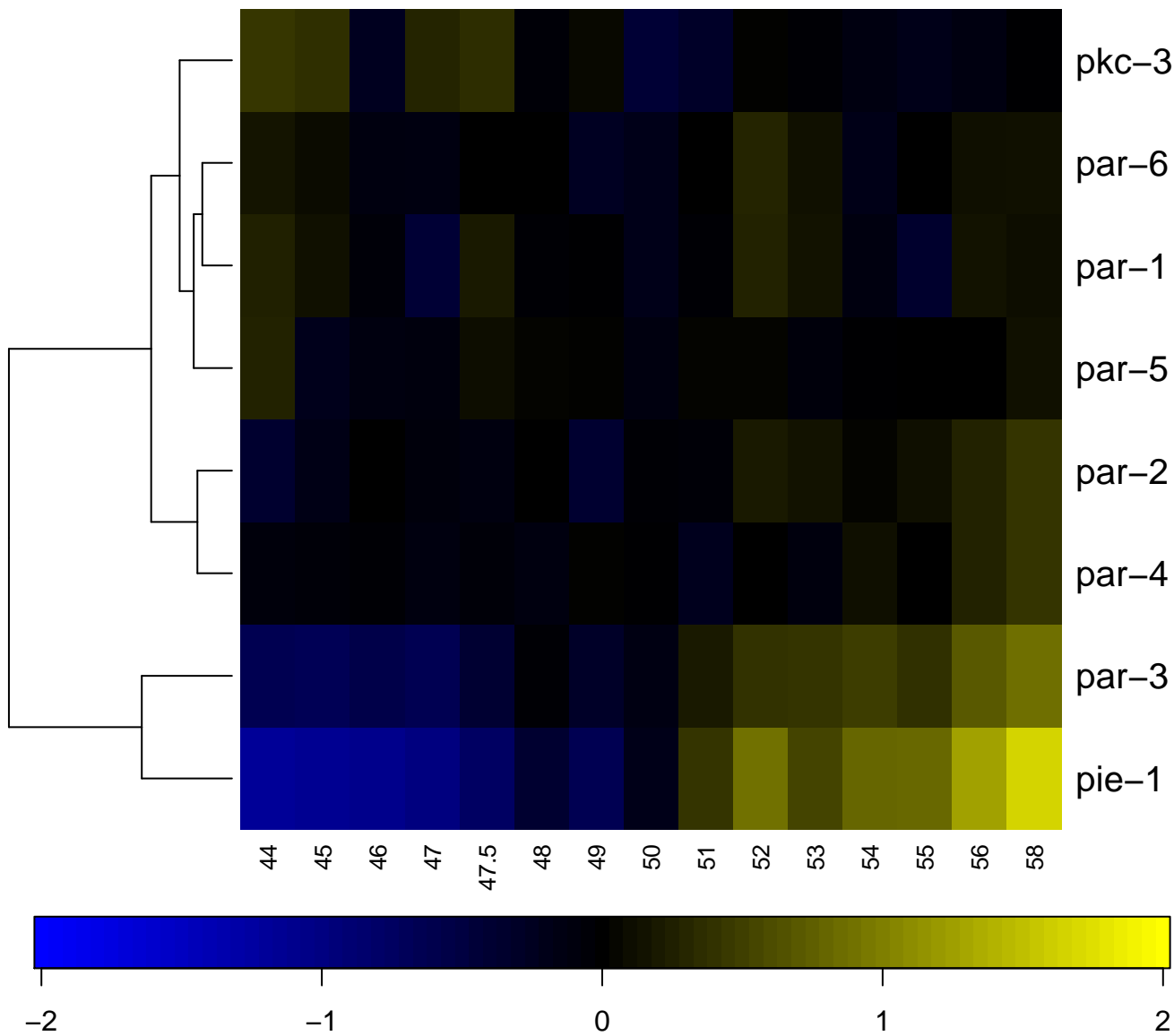
Epithelial junctions and attachments



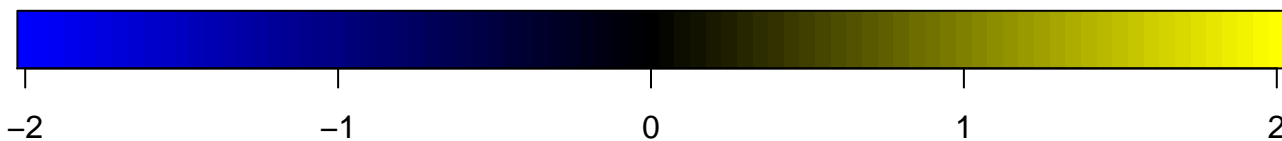
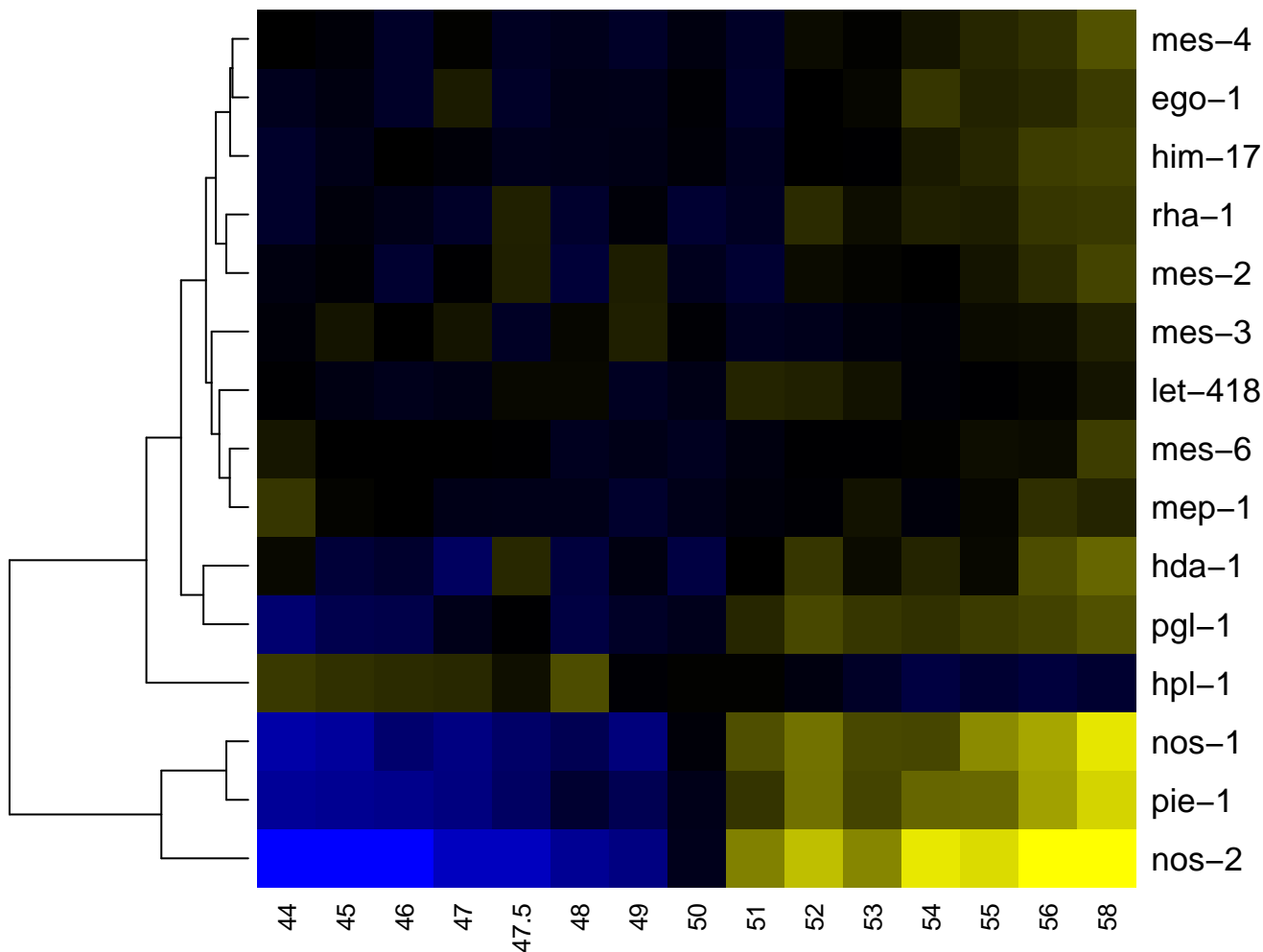
GABA



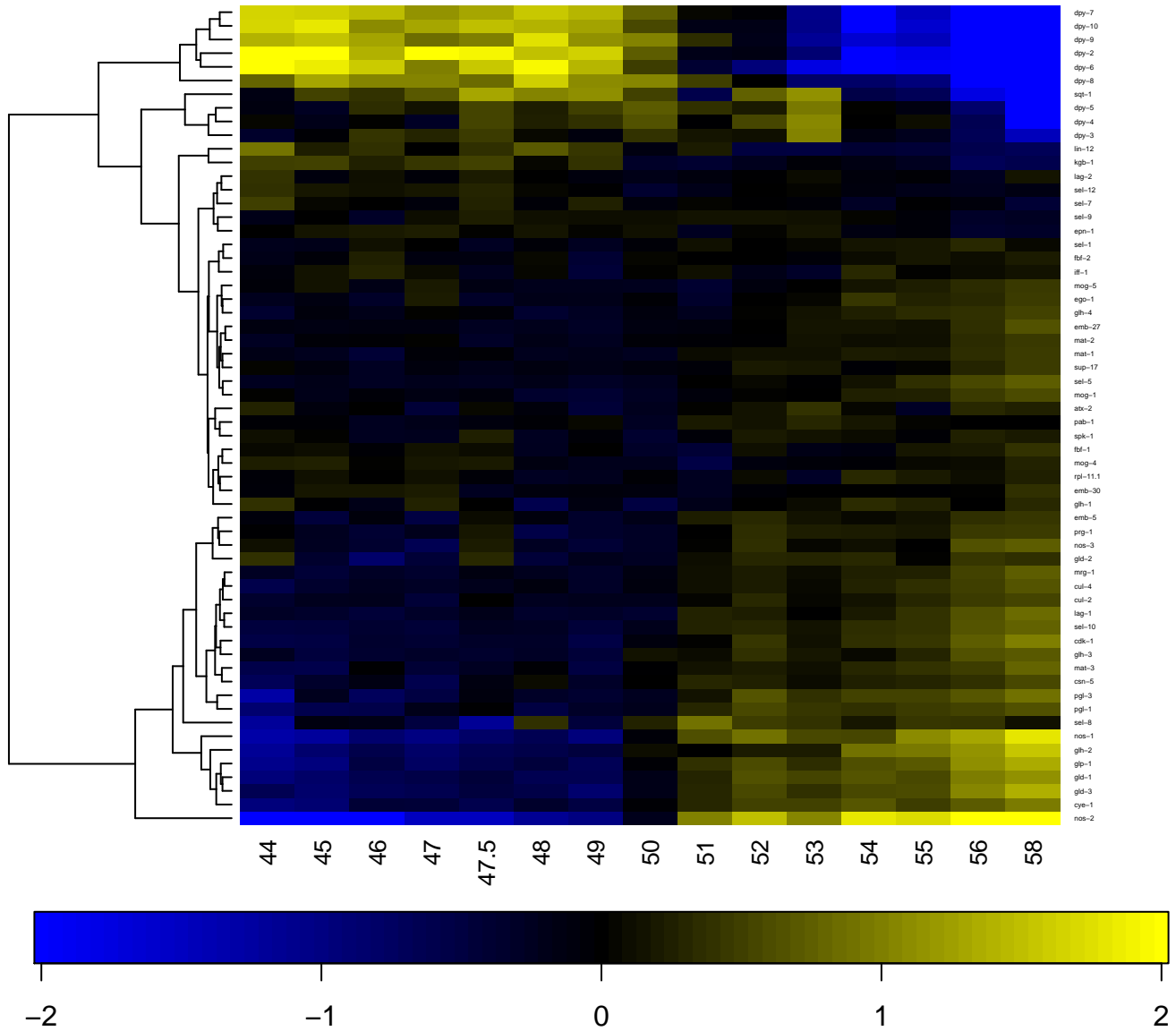
Gastrulation



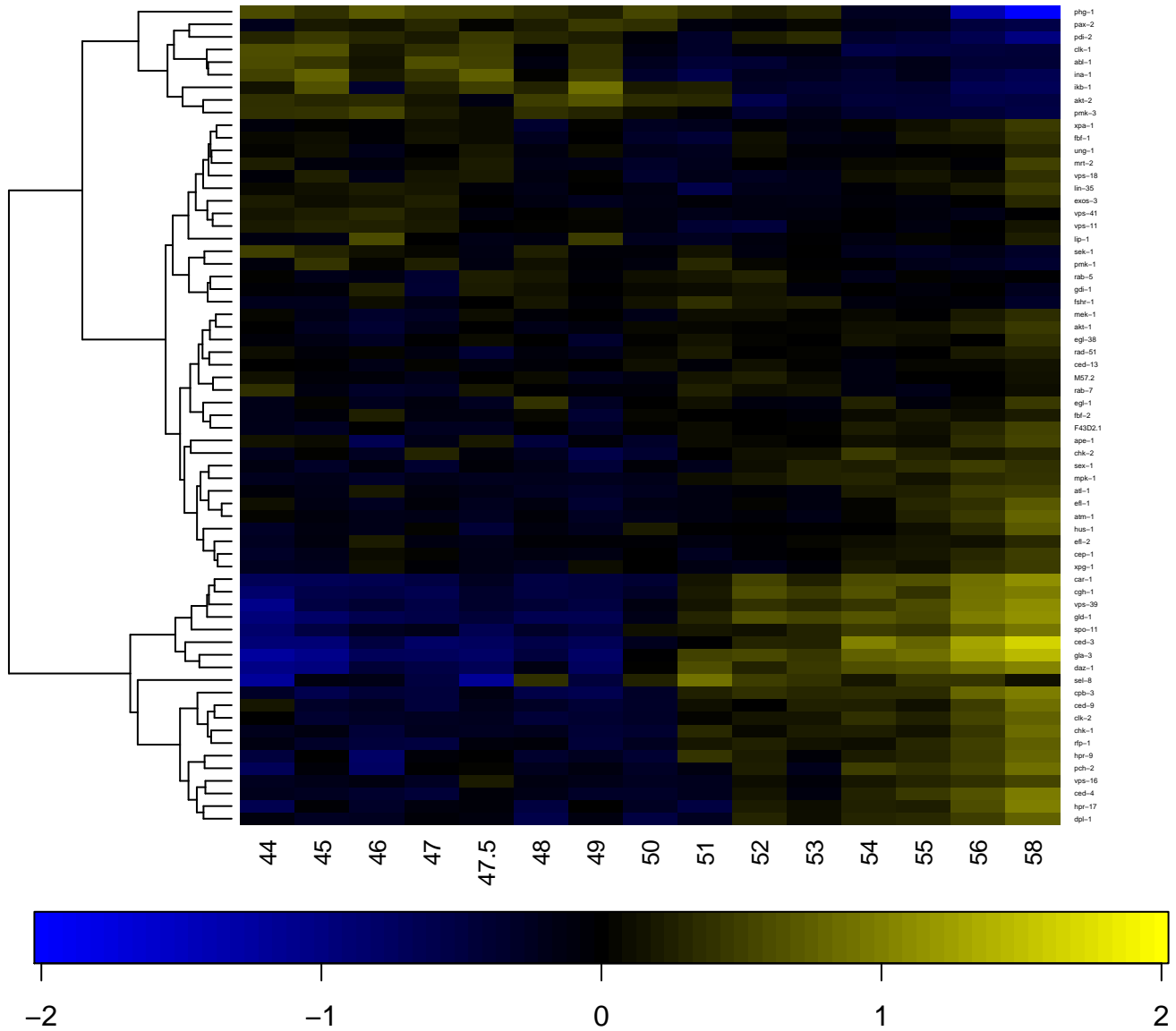
Germline chromatin



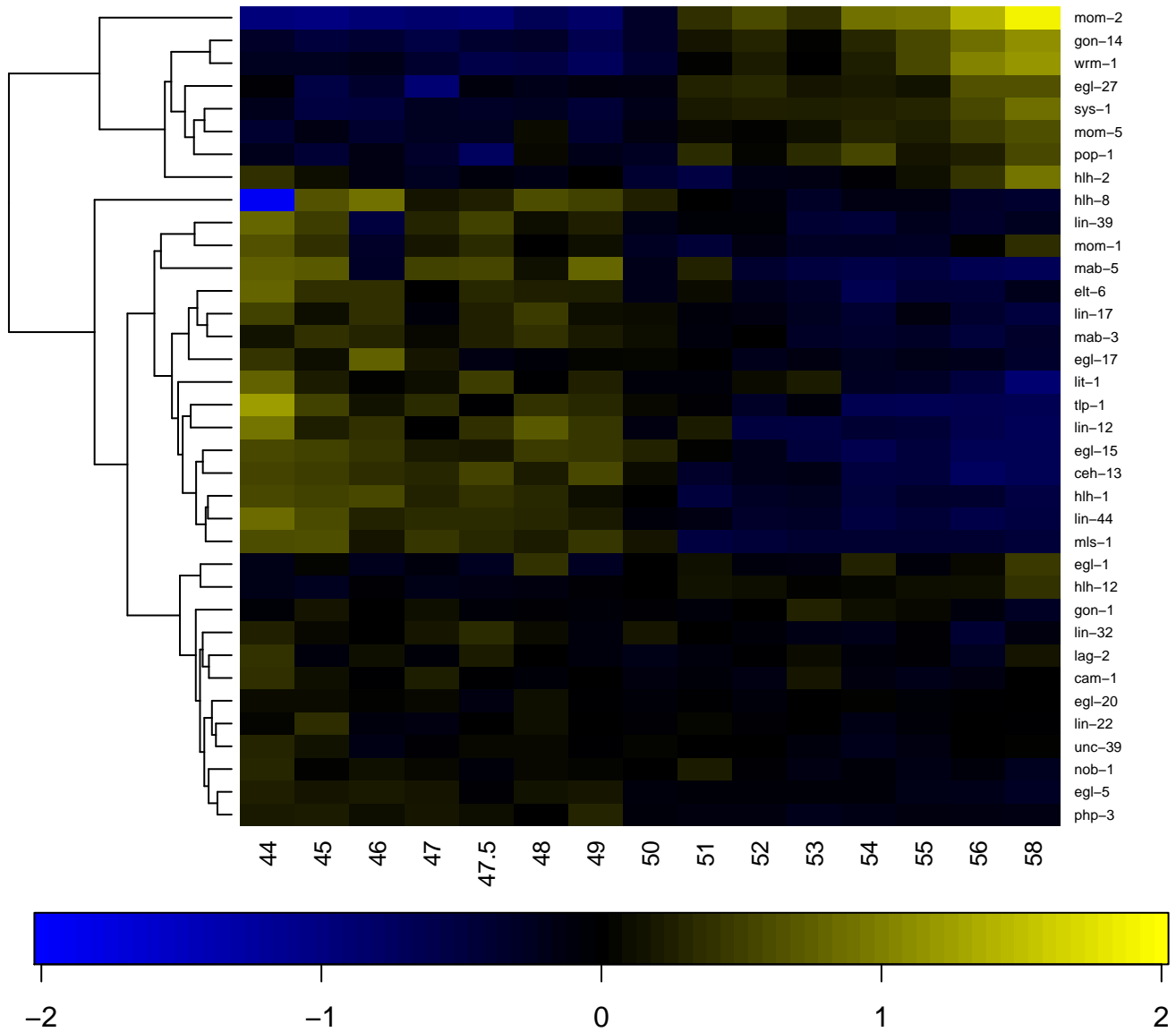
Germline proliferation and its control



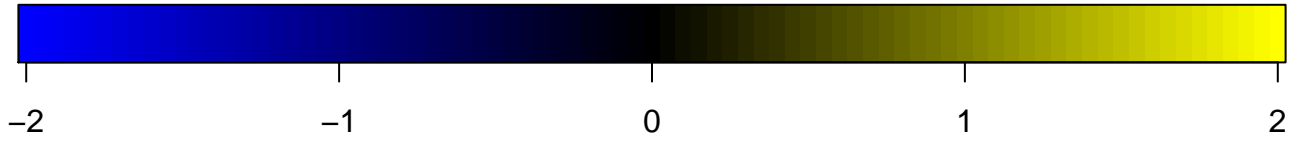
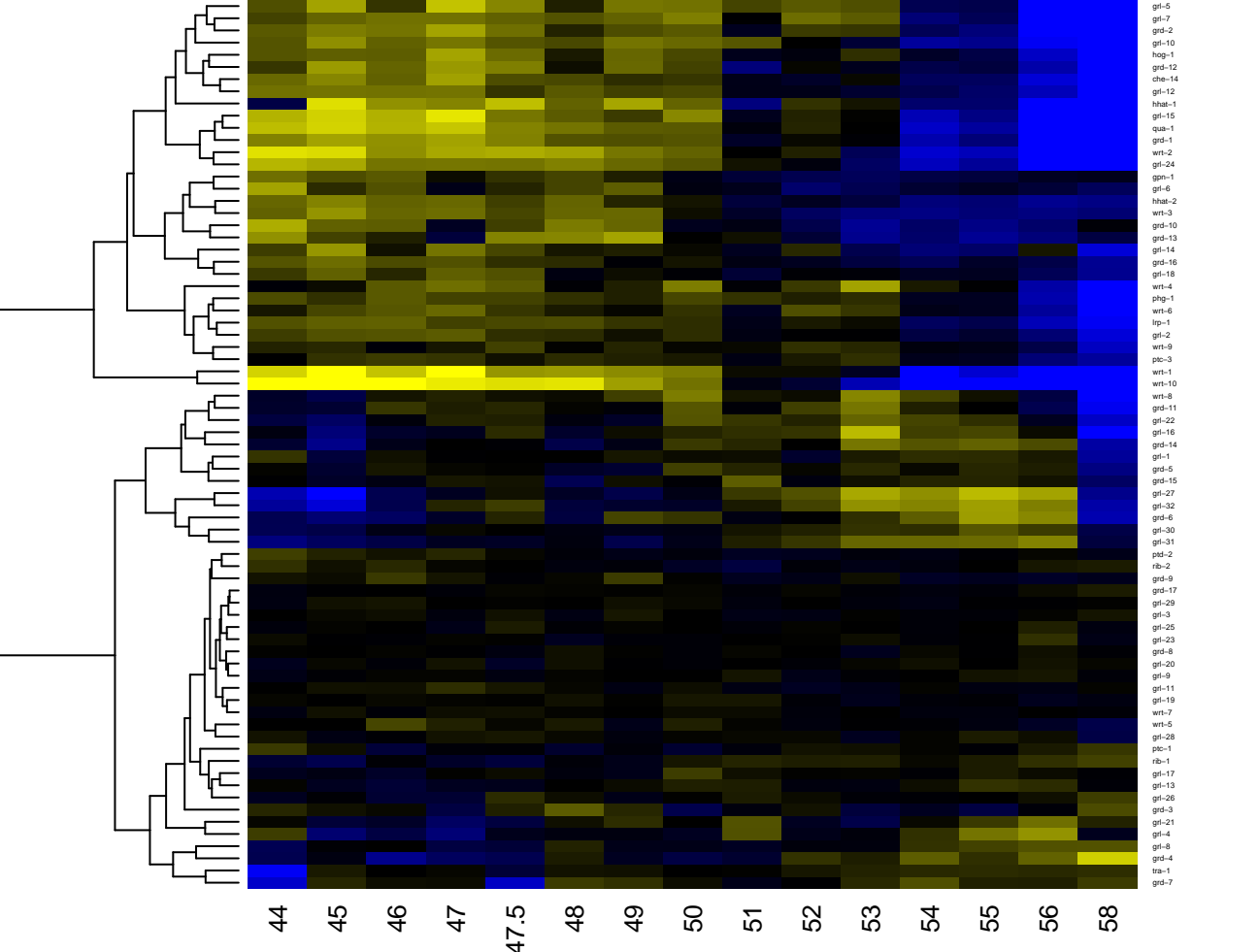
Germline survival and apoptosis



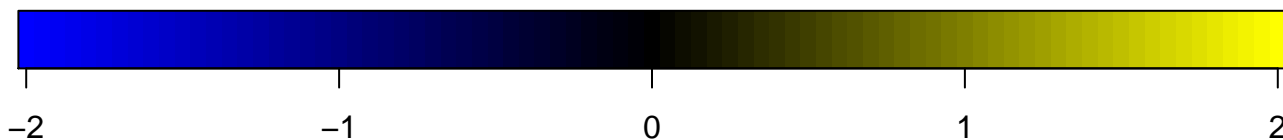
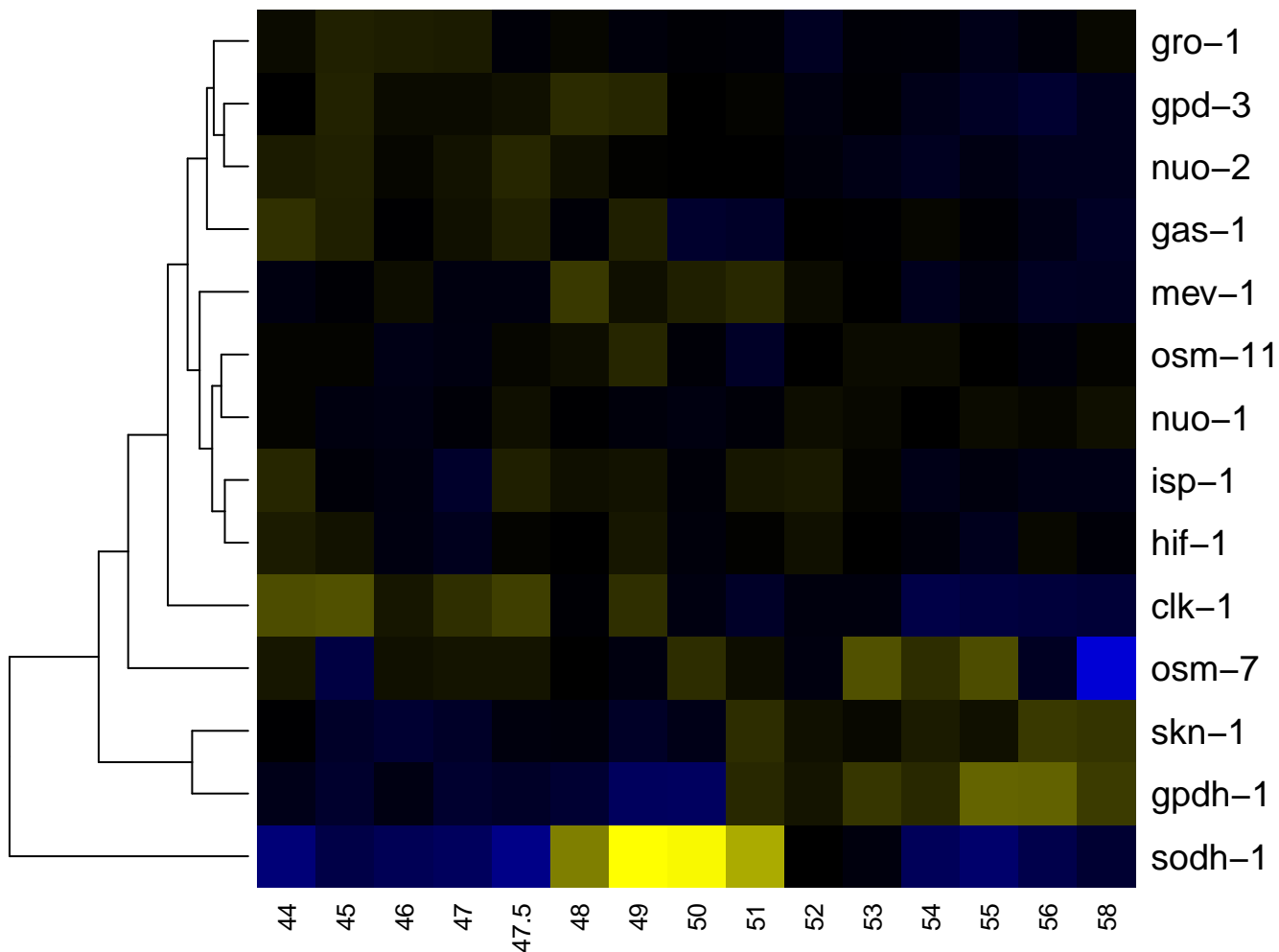
Hermaphrodite cell-fate specification



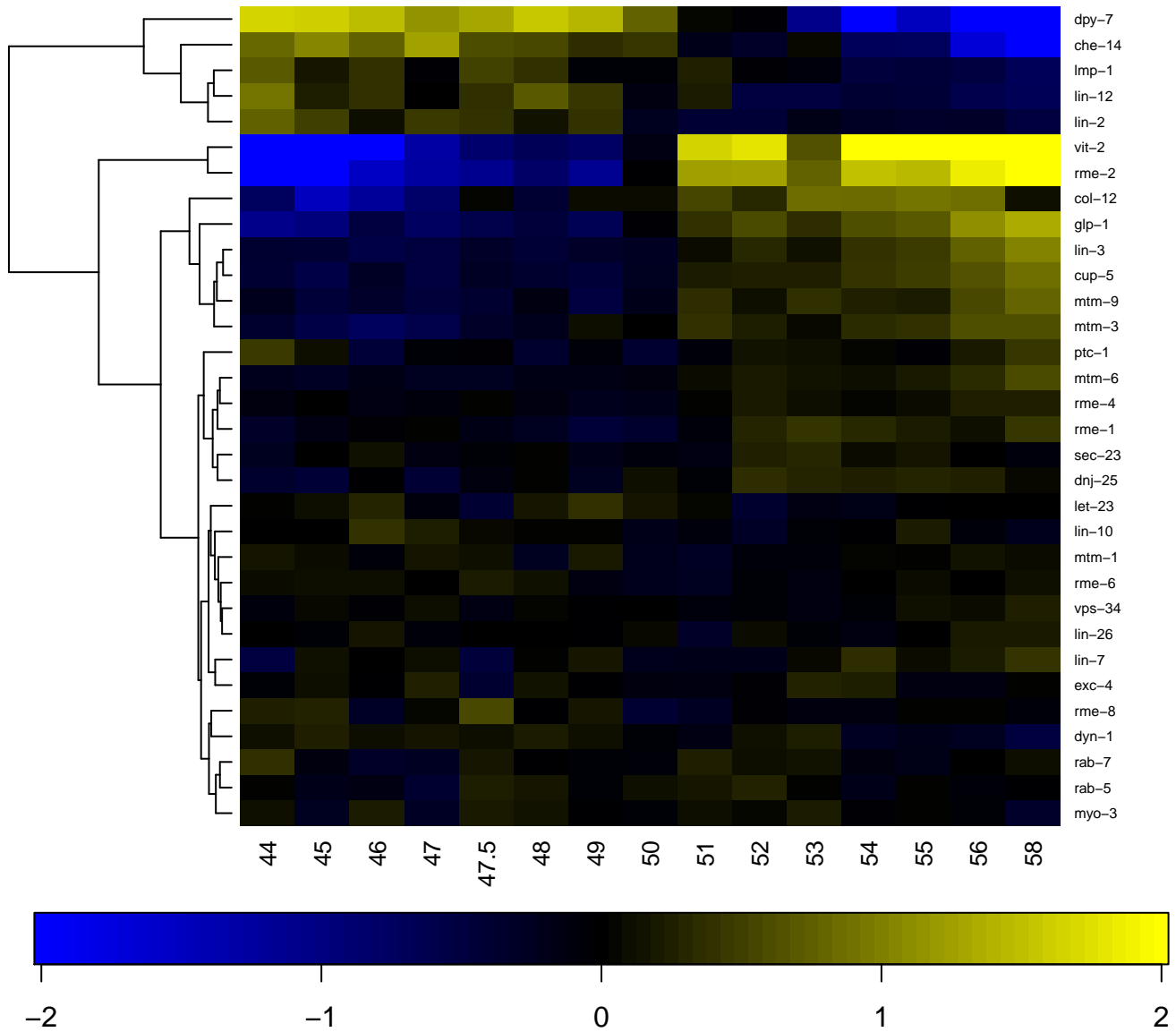
Homologs of the Hh signalling network in *C. elegans*



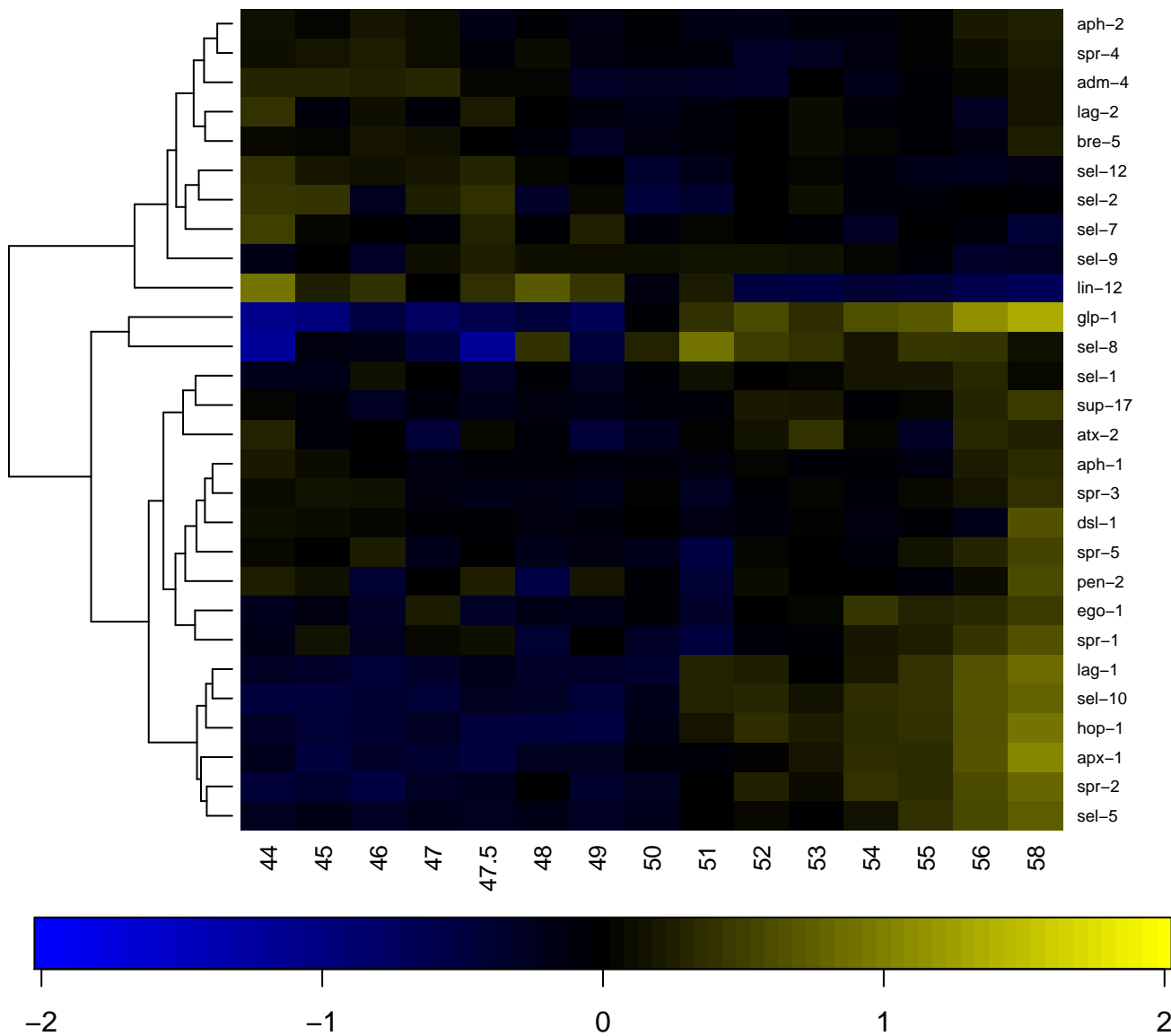
Intermediary metabolism



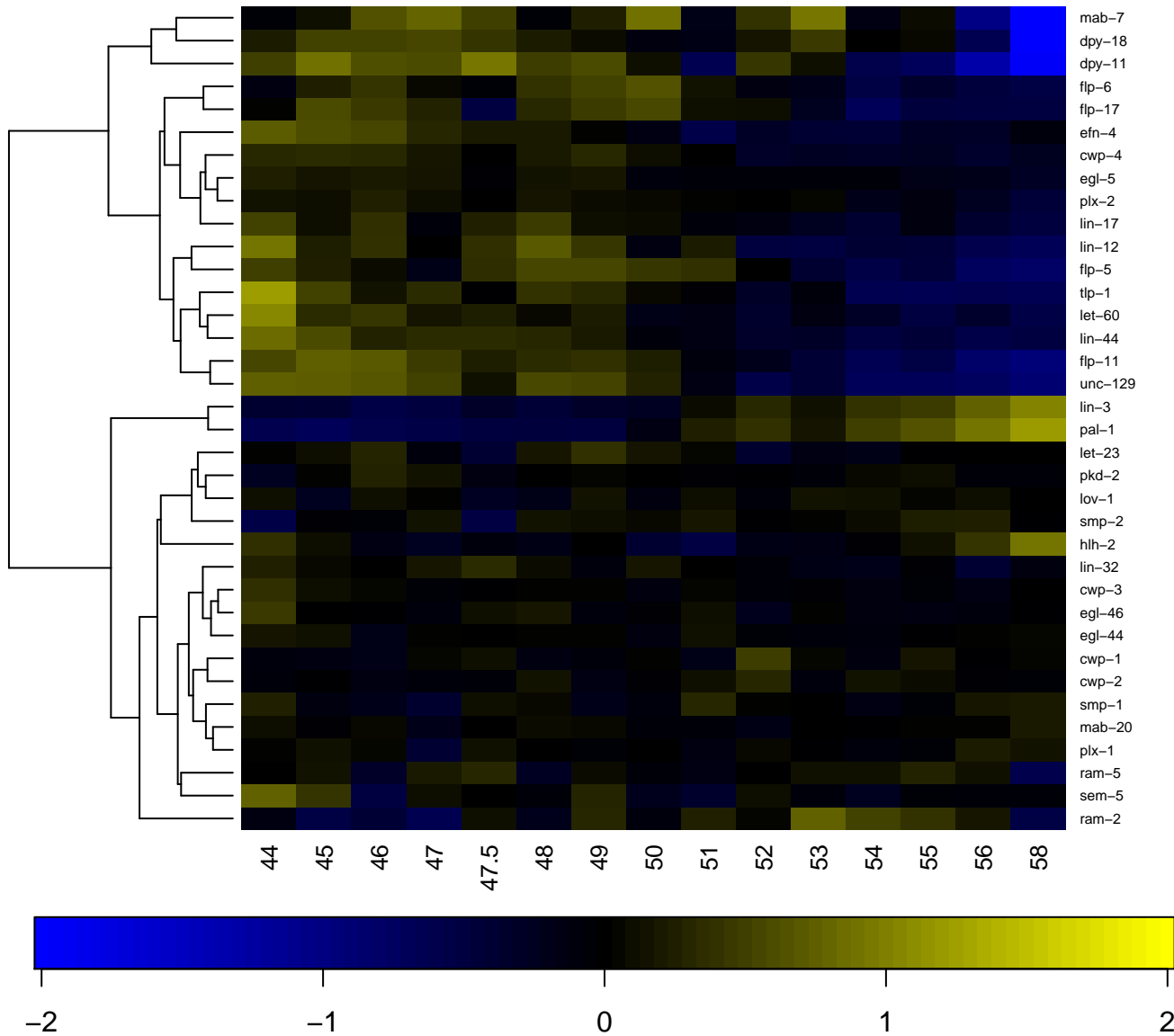
Intracellular trafficking



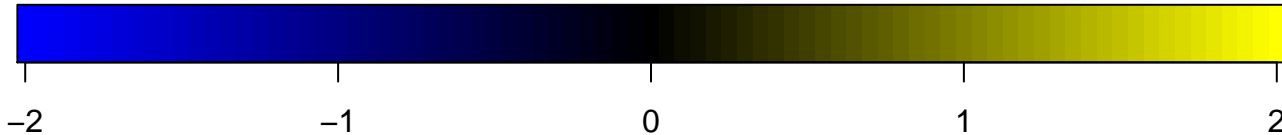
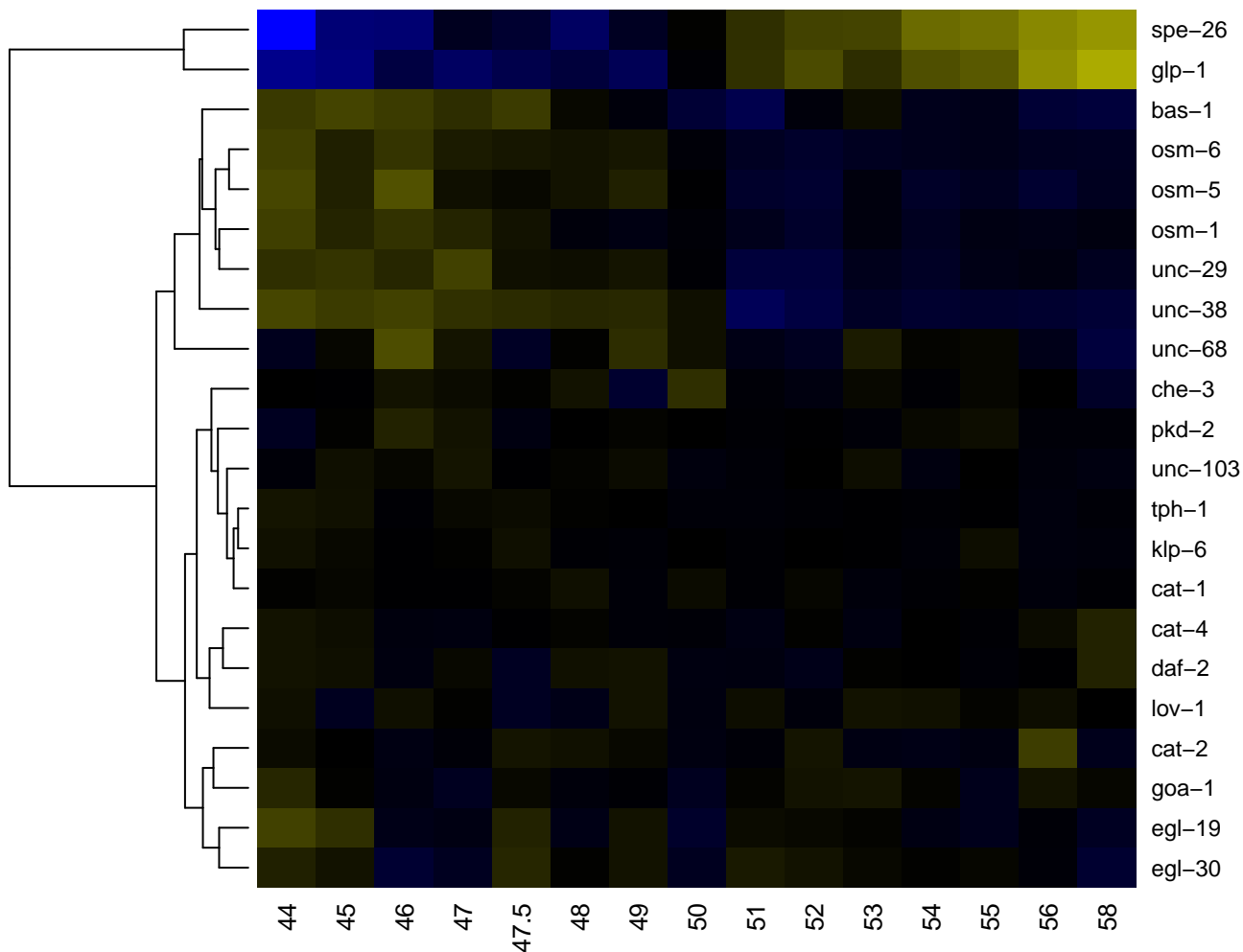
LIN-12/Notch signaling in *C. elegans*



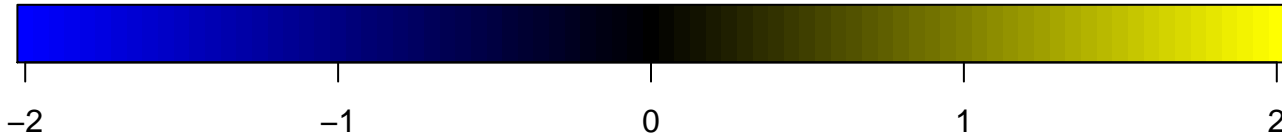
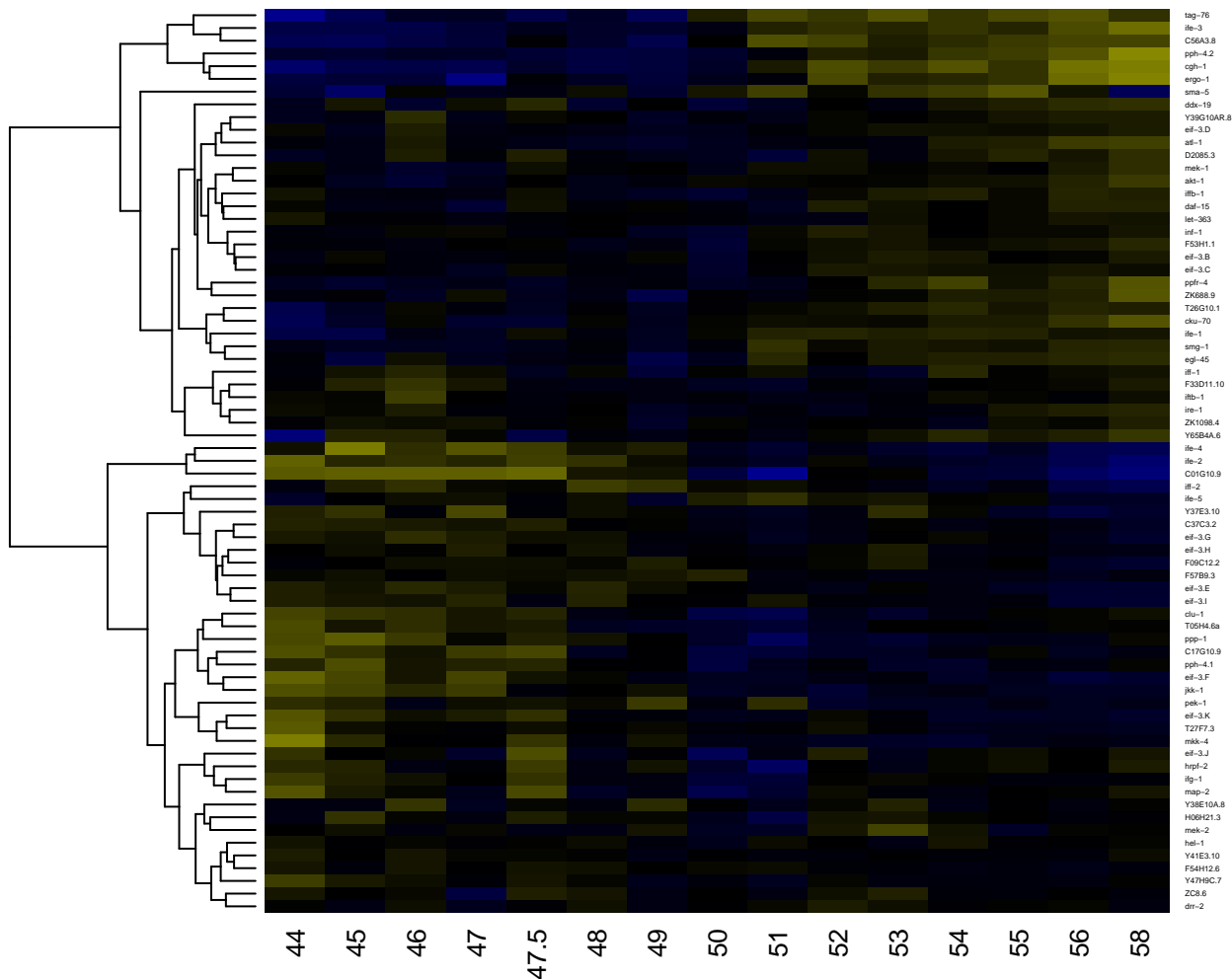
Male development



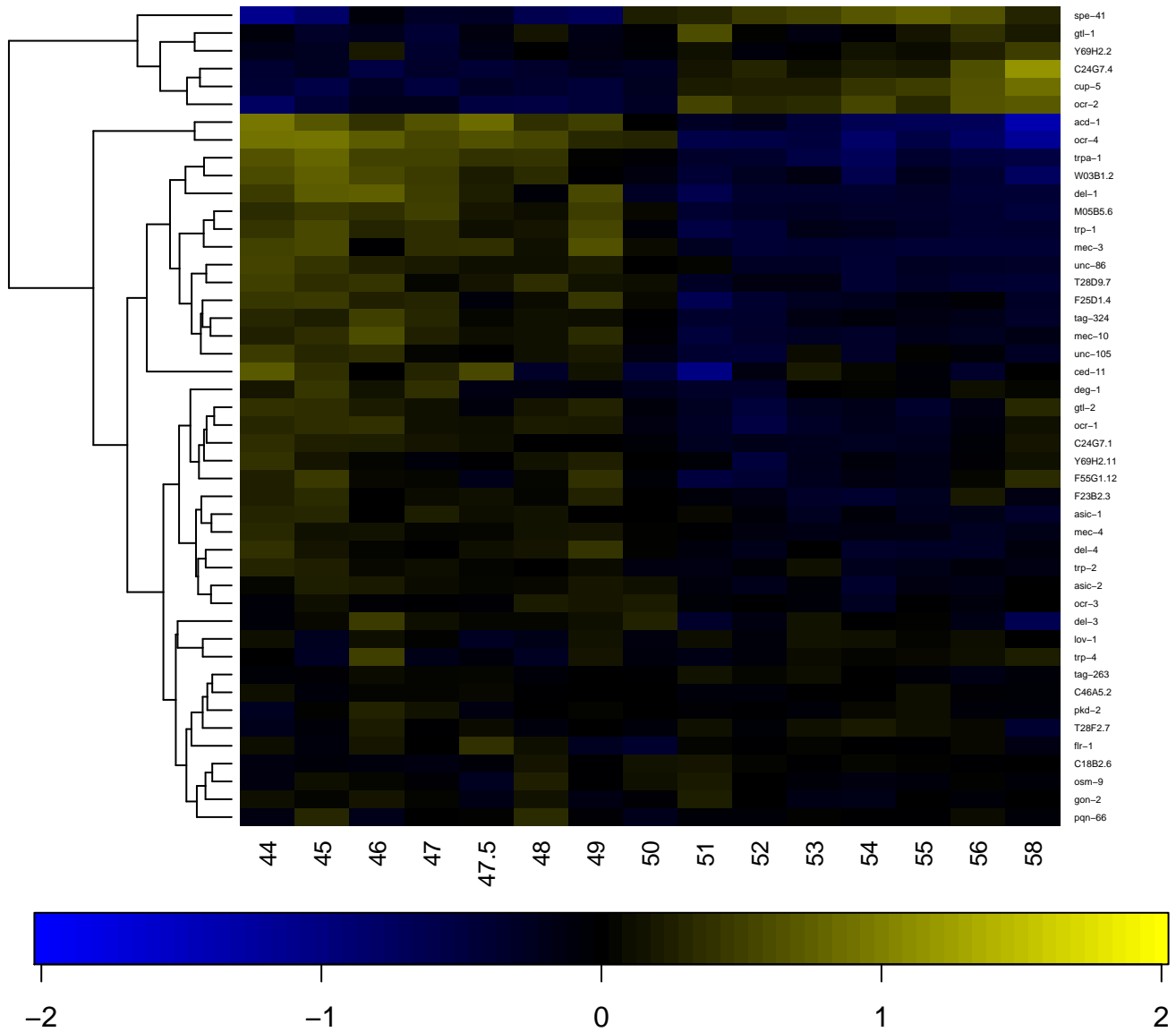
Male mating behavior



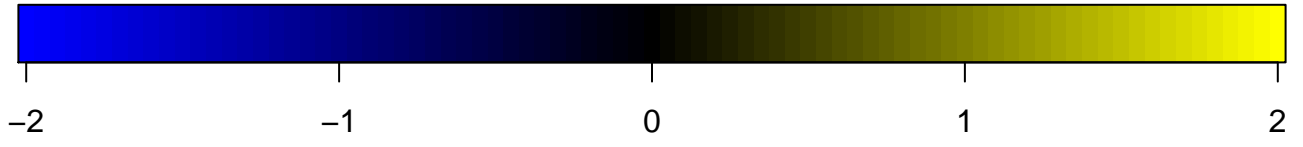
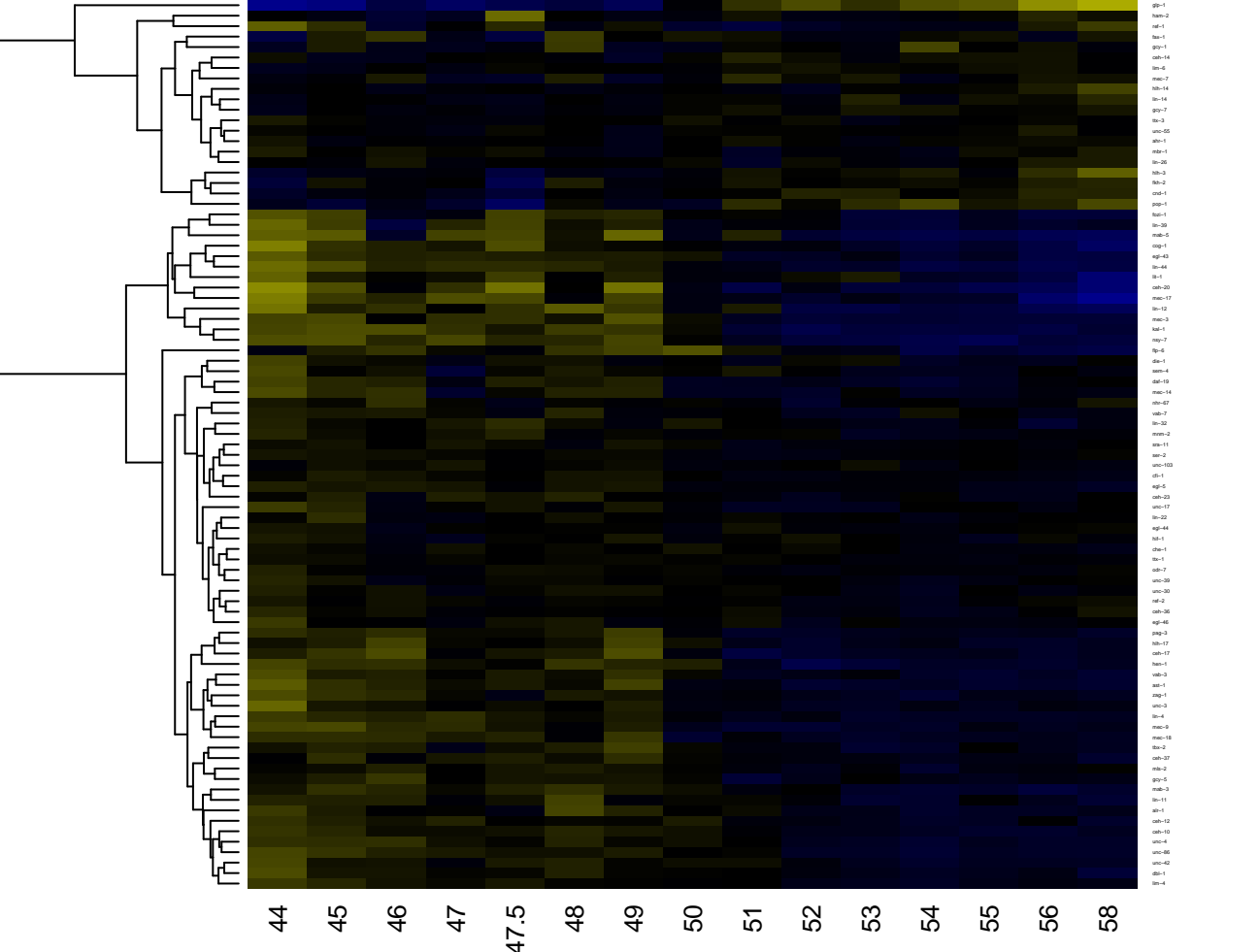
Mechanism and regulation of translation in *C. elegans*



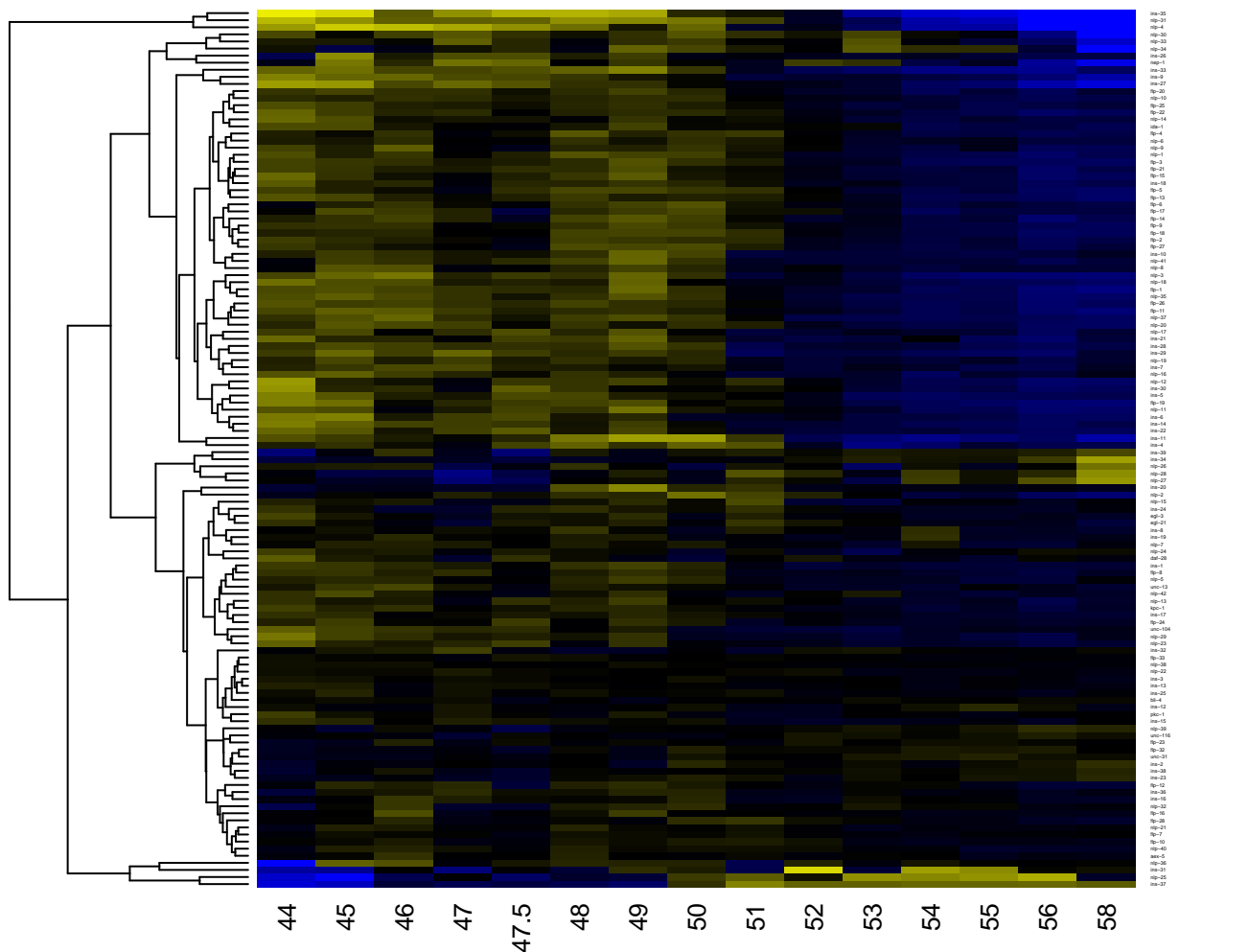
Mechanosensation



Neurogenesis



Neuropeptides



-2

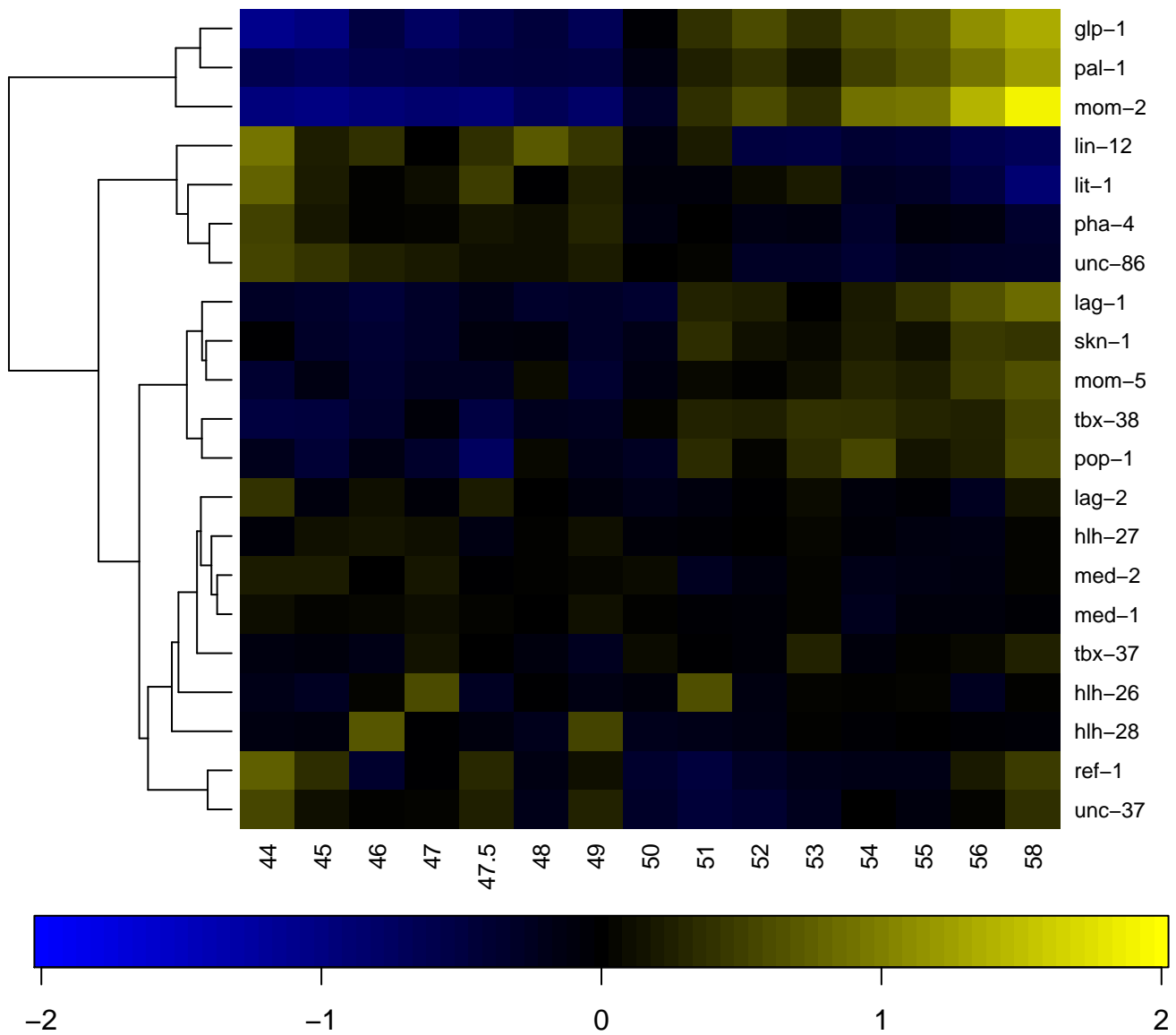
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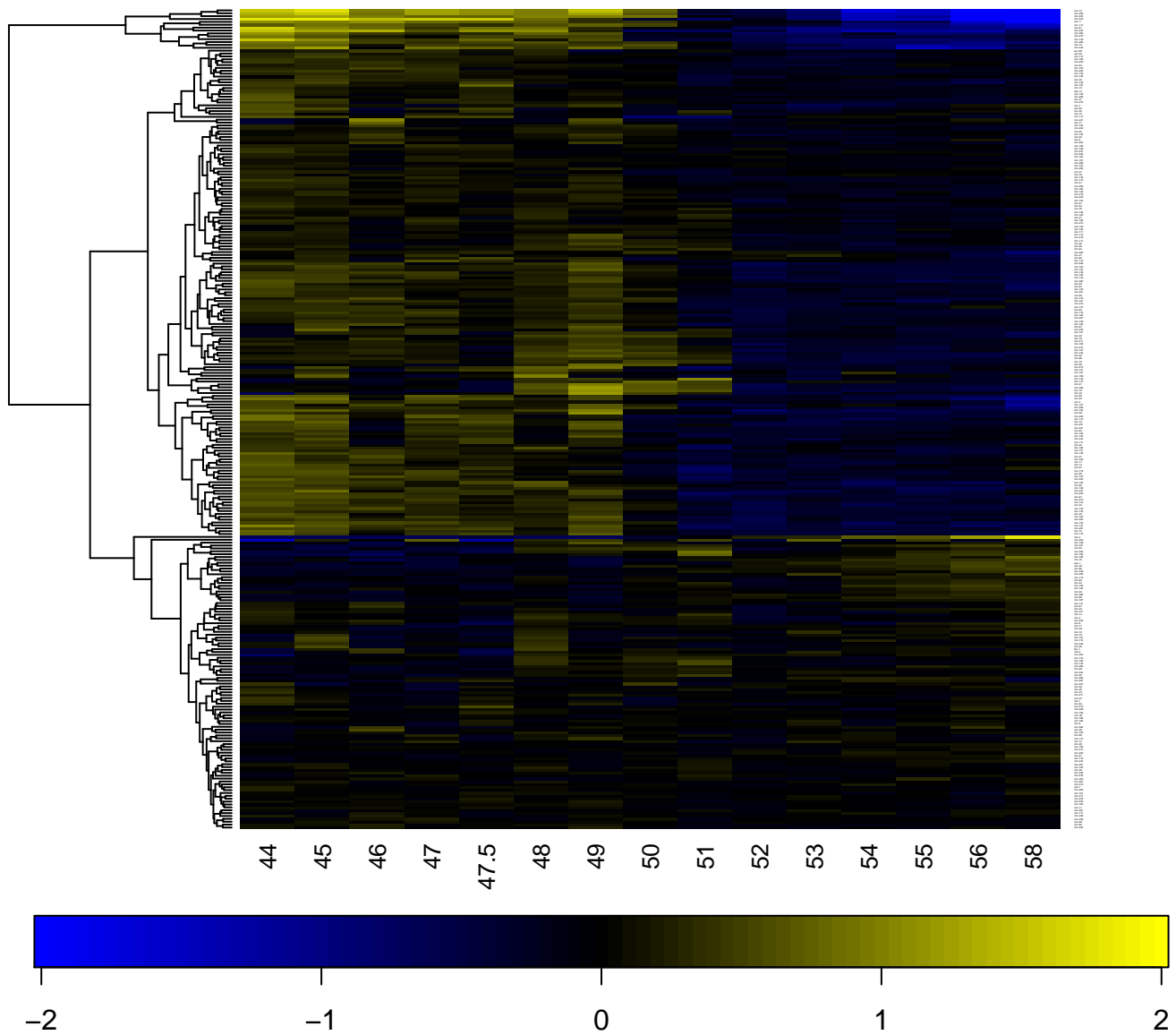
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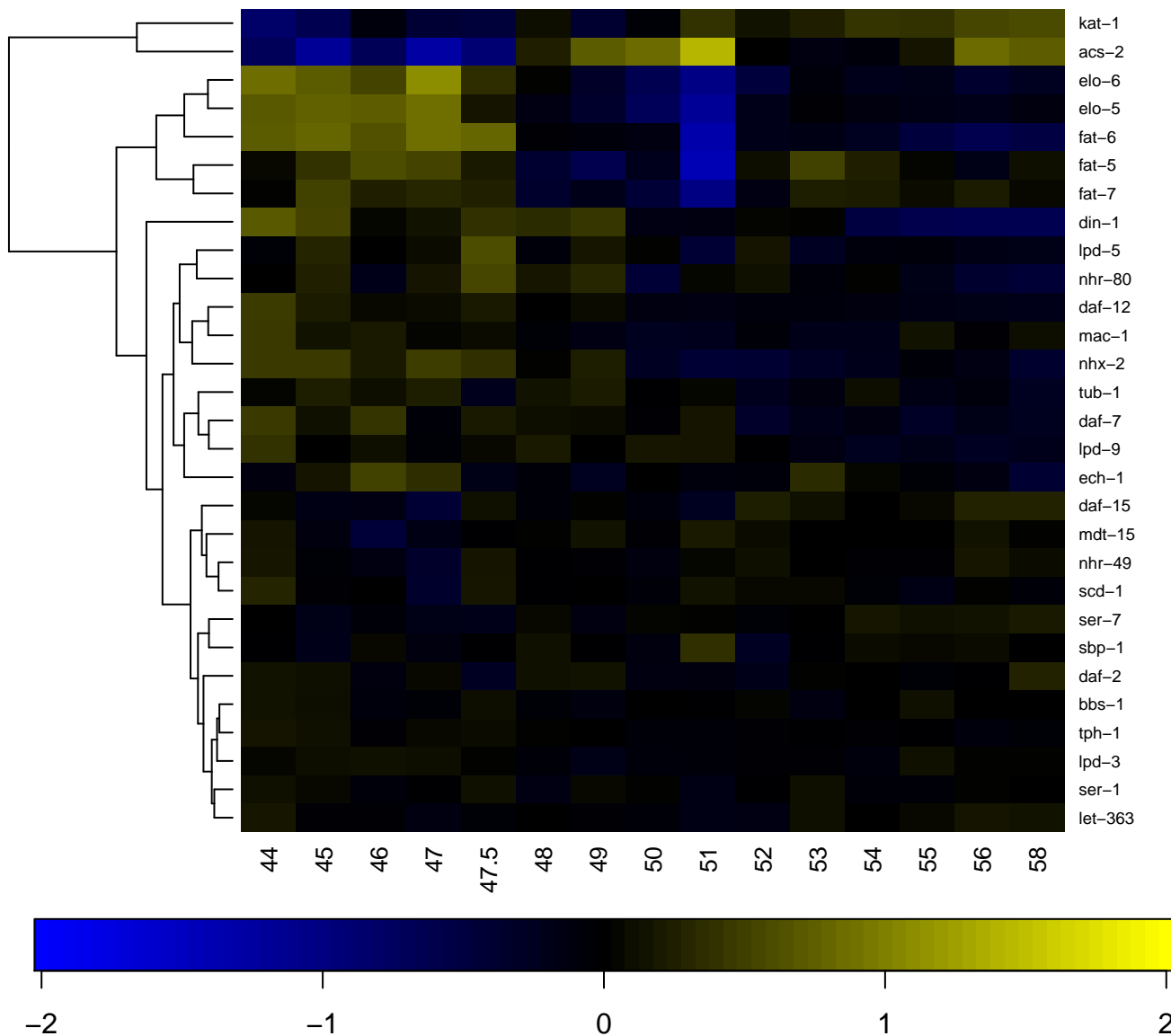
Notch signaling in the *C. elegans* embryo



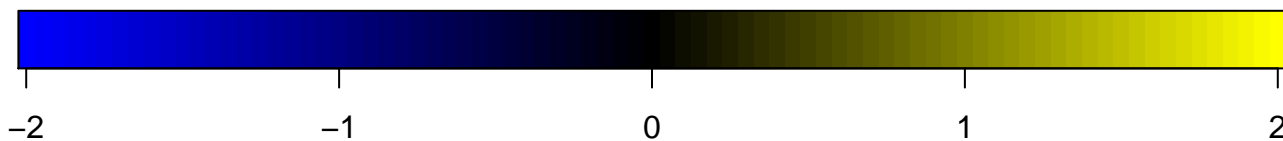
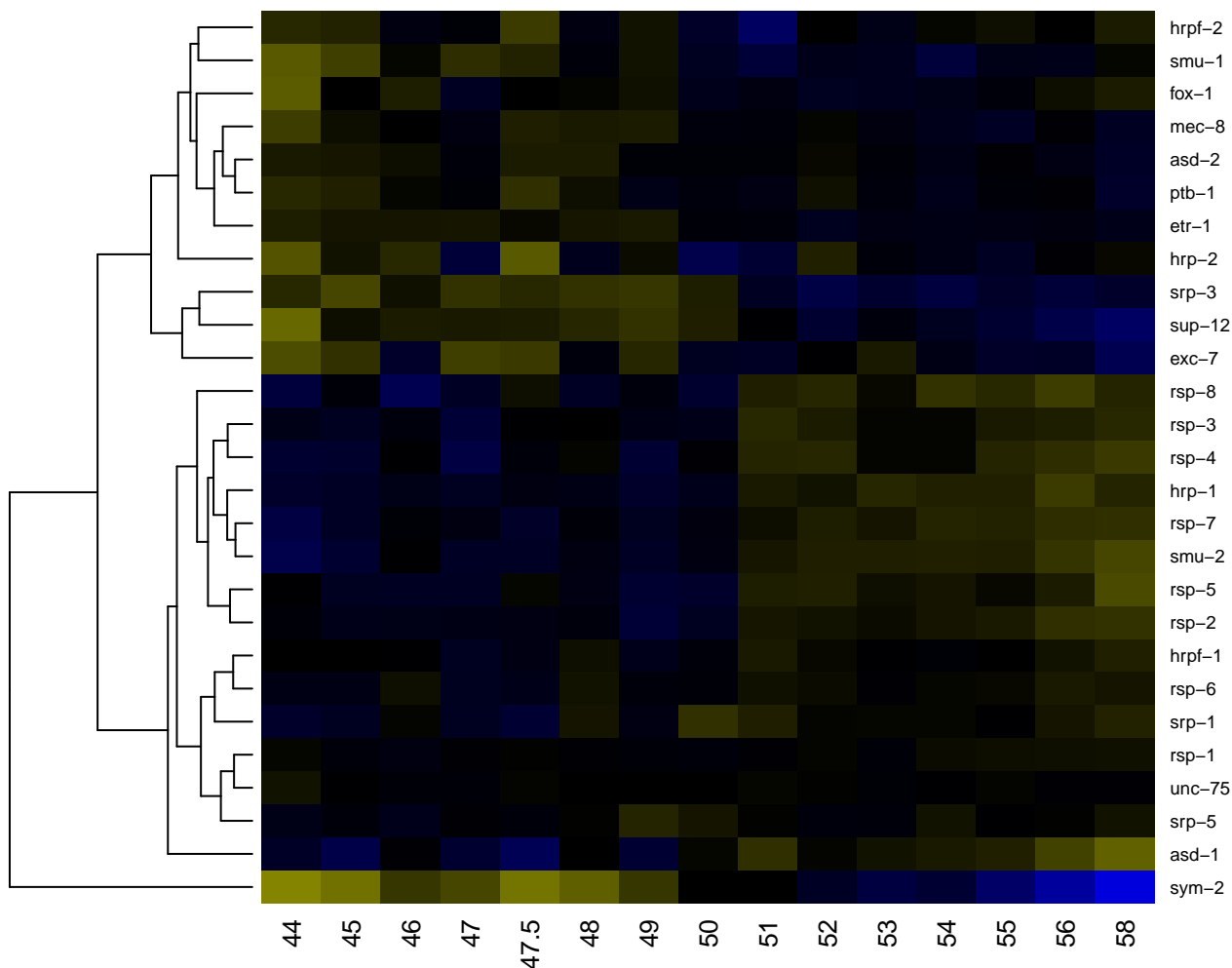
Nuclear hormone receptors in *C. elegans*



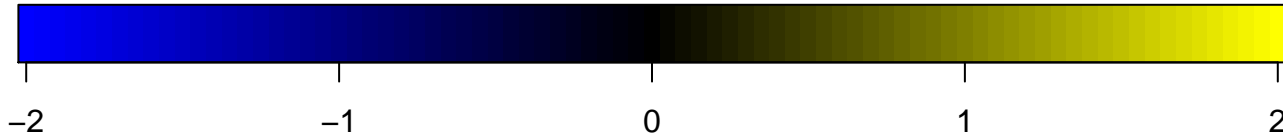
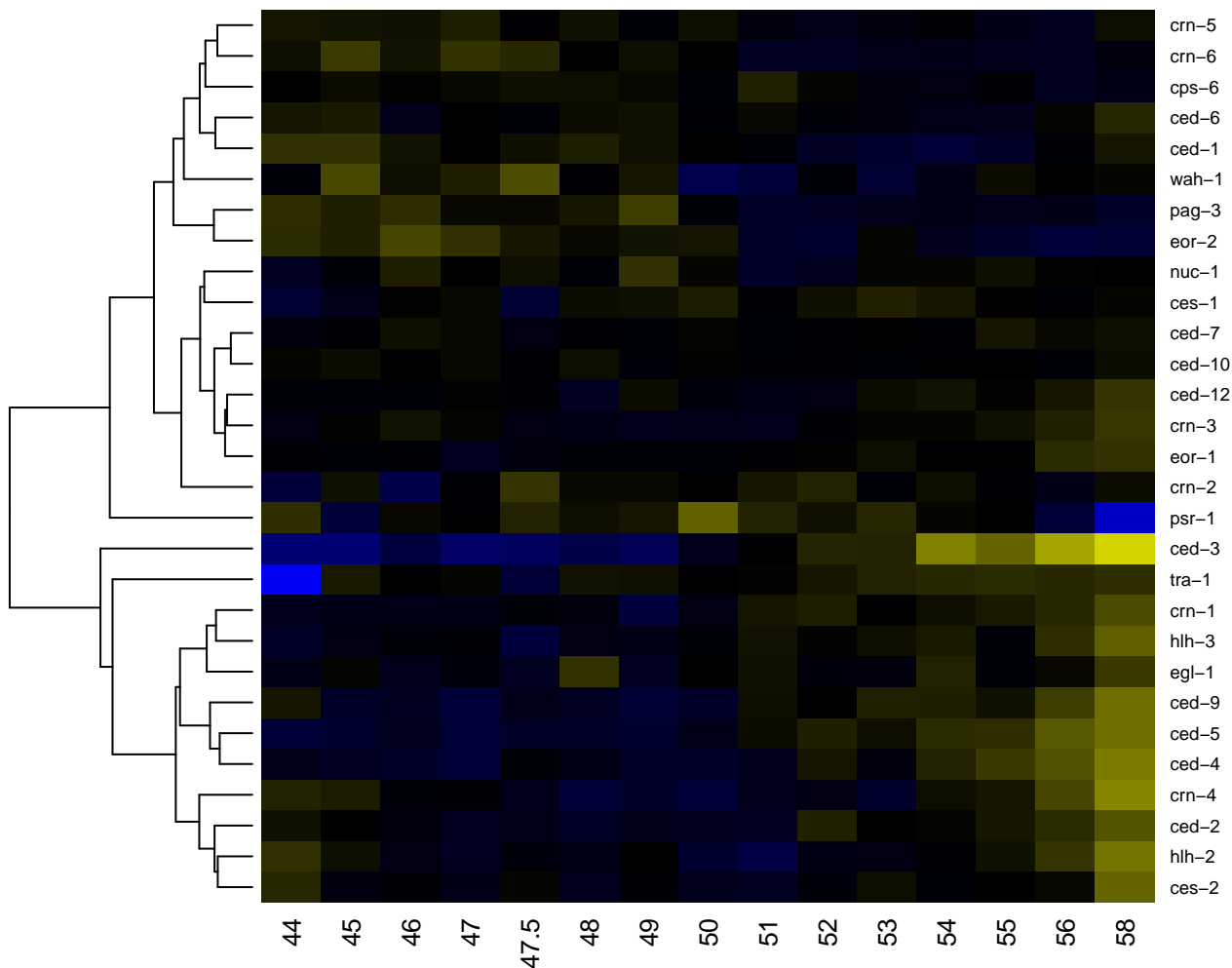
Obesity and the regulation of fat metabolism



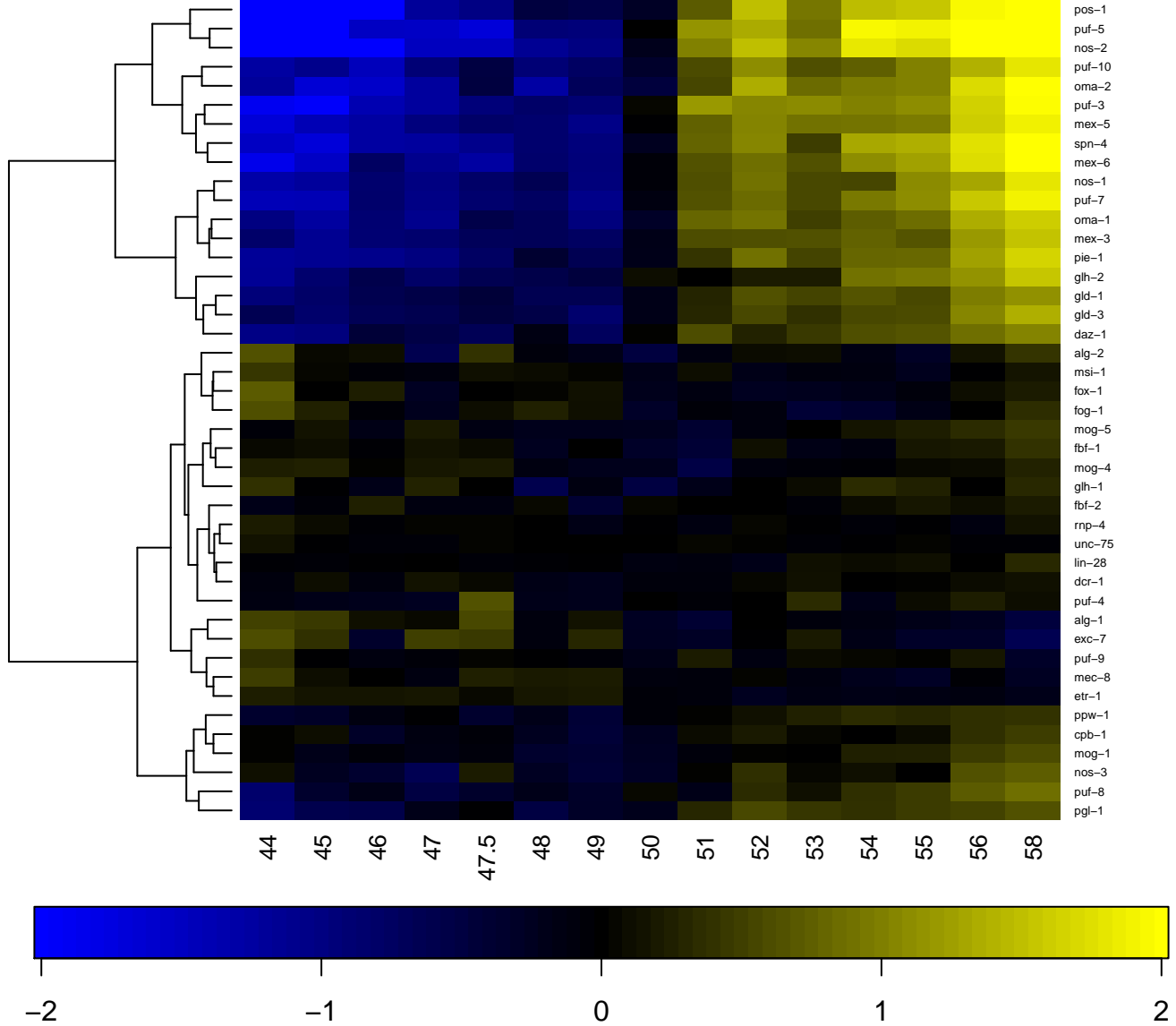
Pre-mRNA splicing and its regulation in *Caenorhabditis elegans*



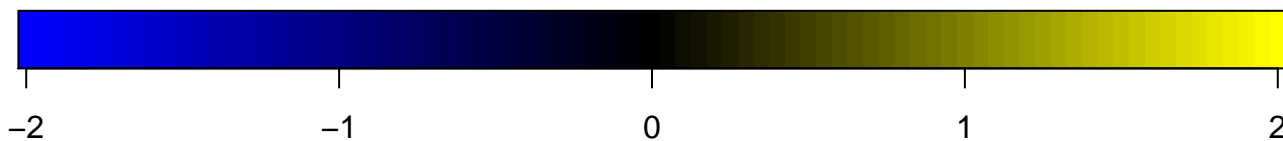
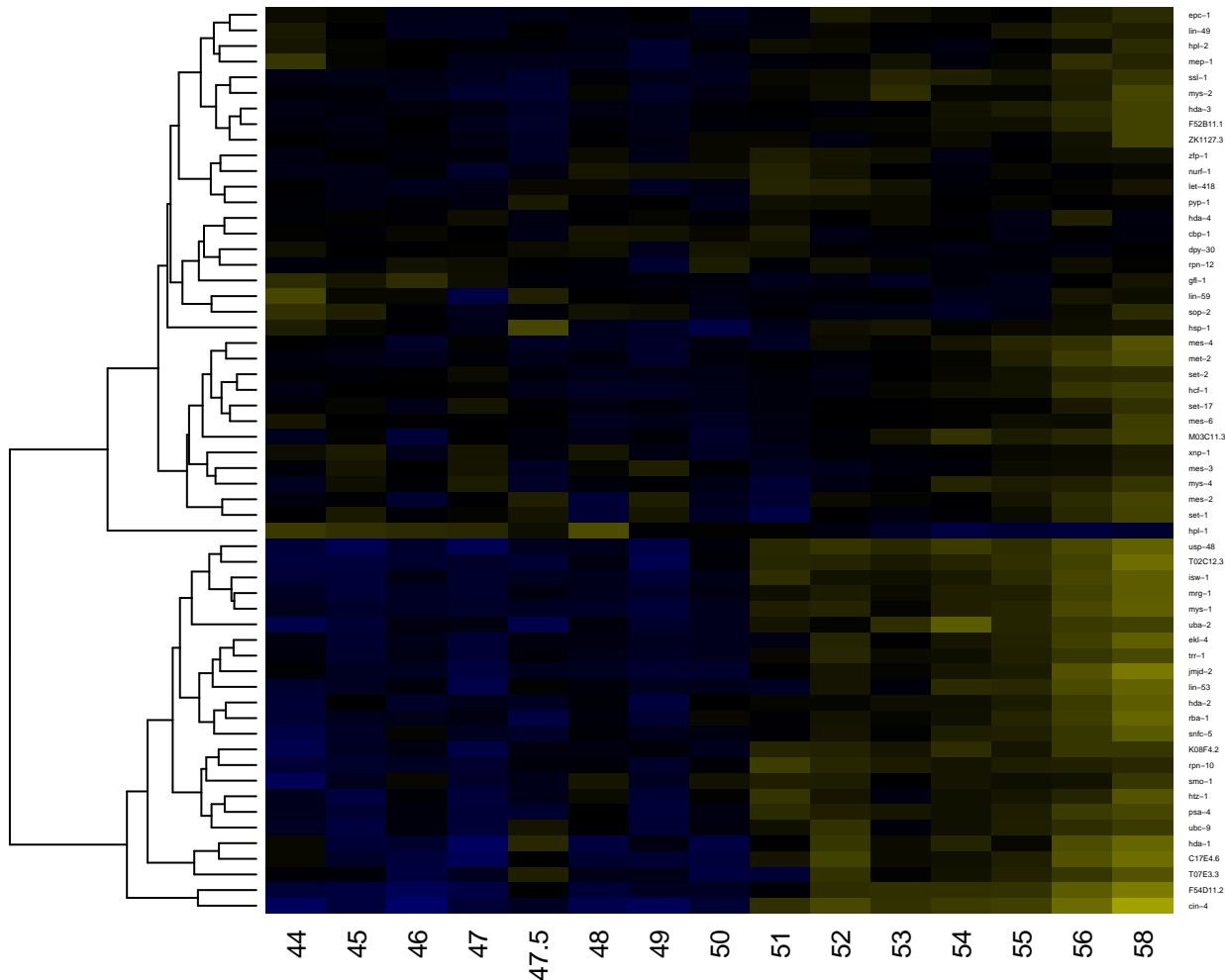
Programmed cell death



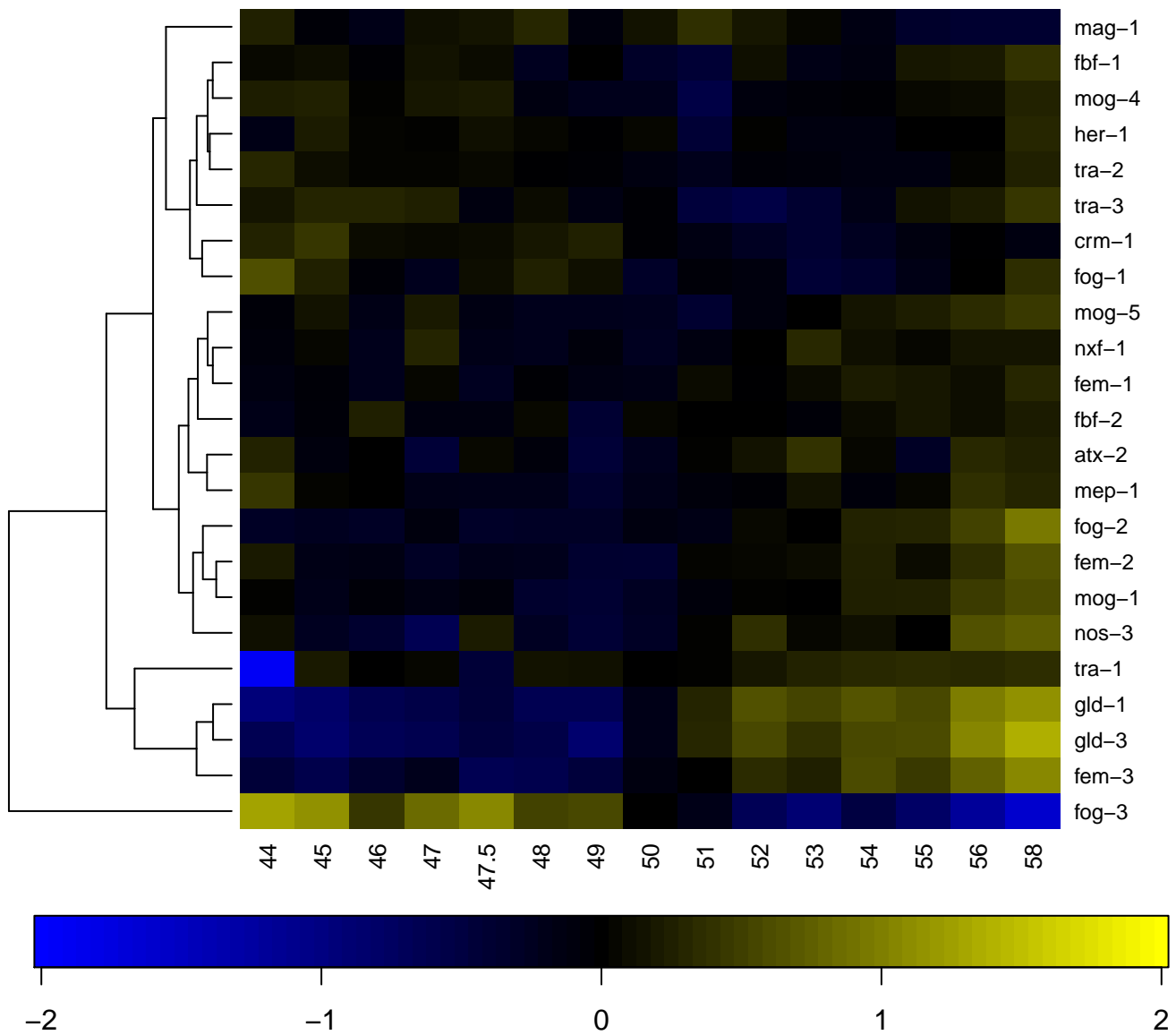
RNA-binding proteins



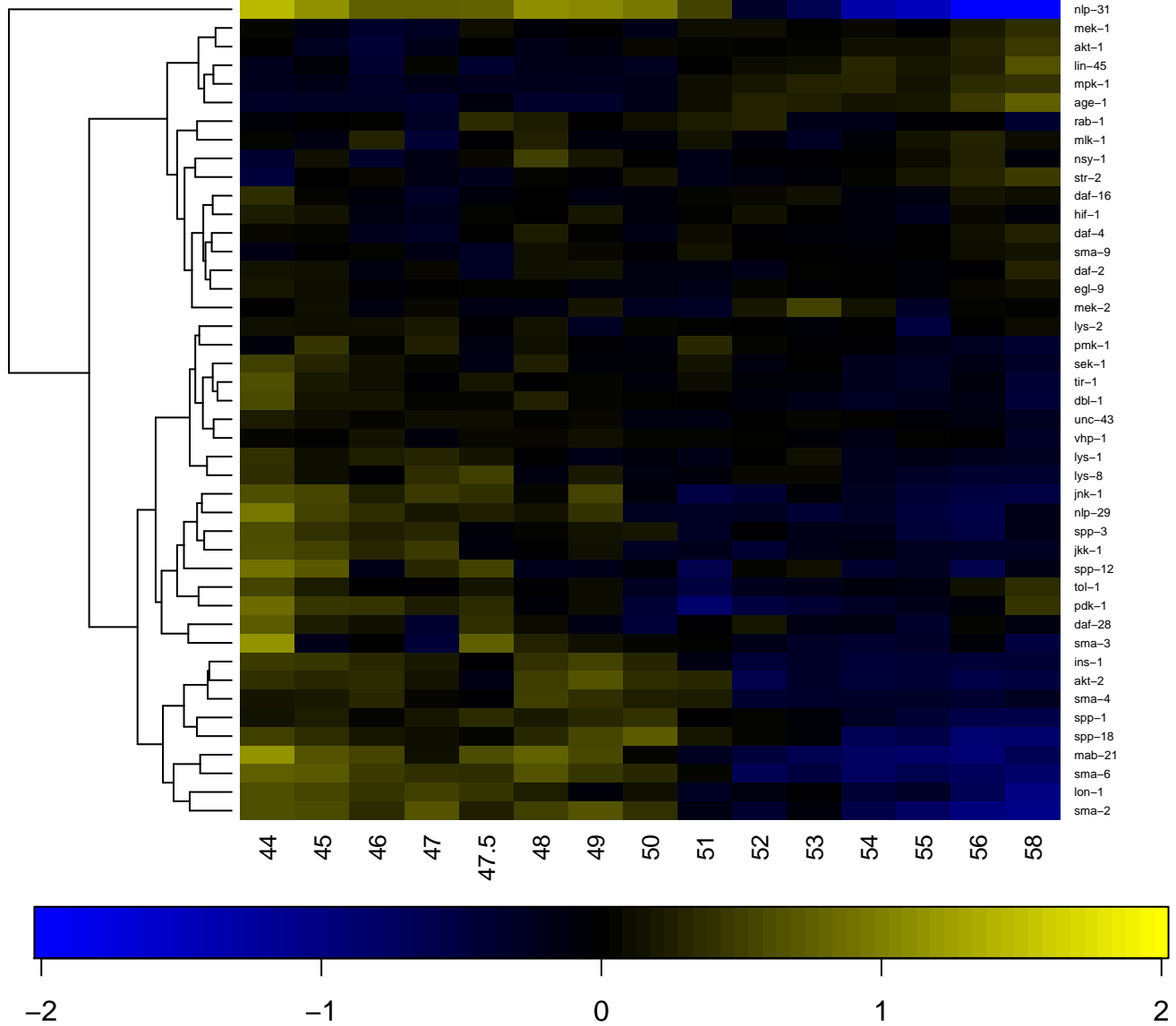
Roles of chromatin factors in *C. elegans* development



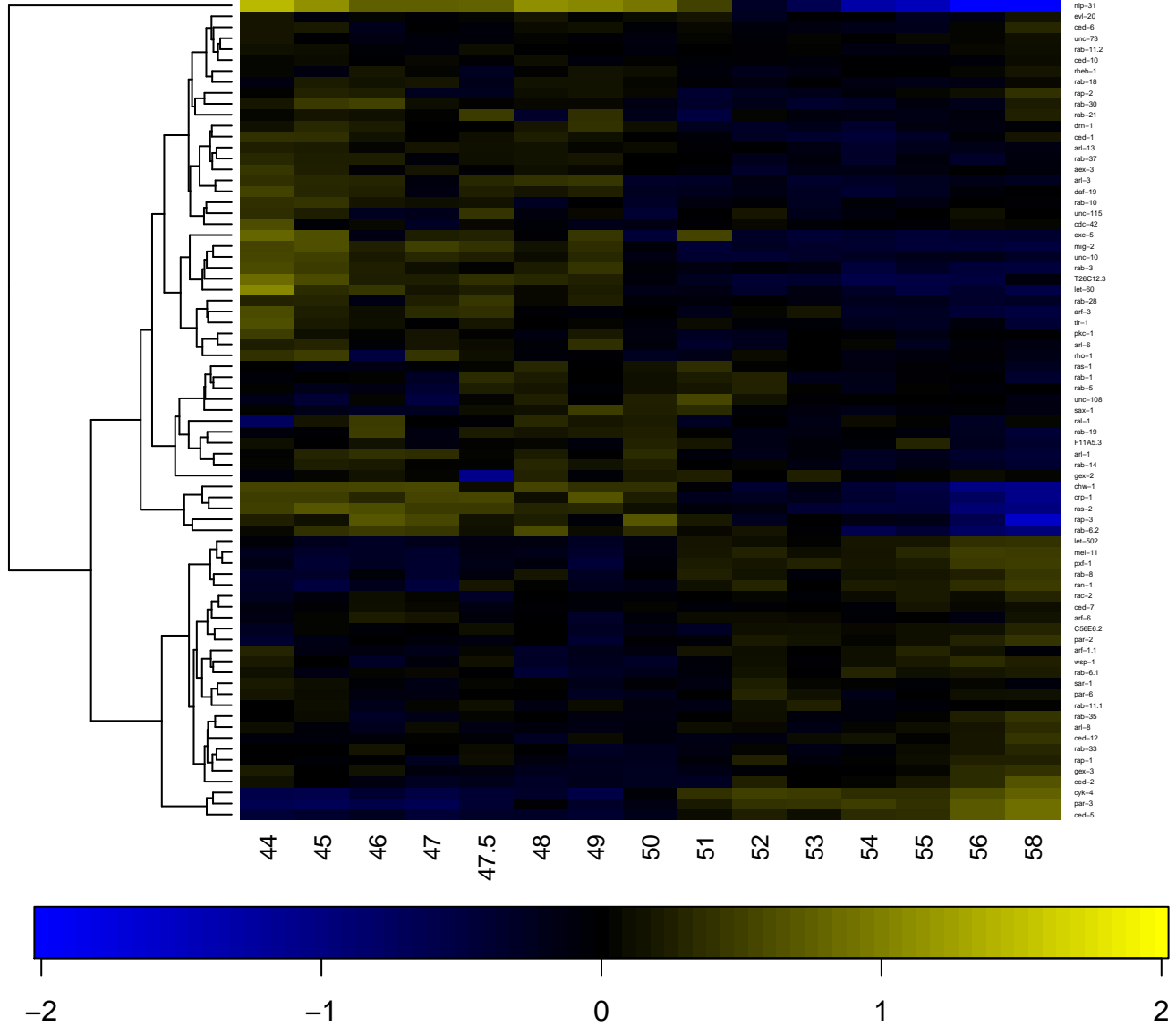
Sex determination in the germ line



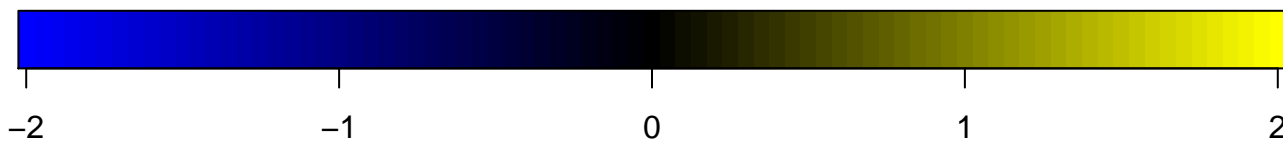
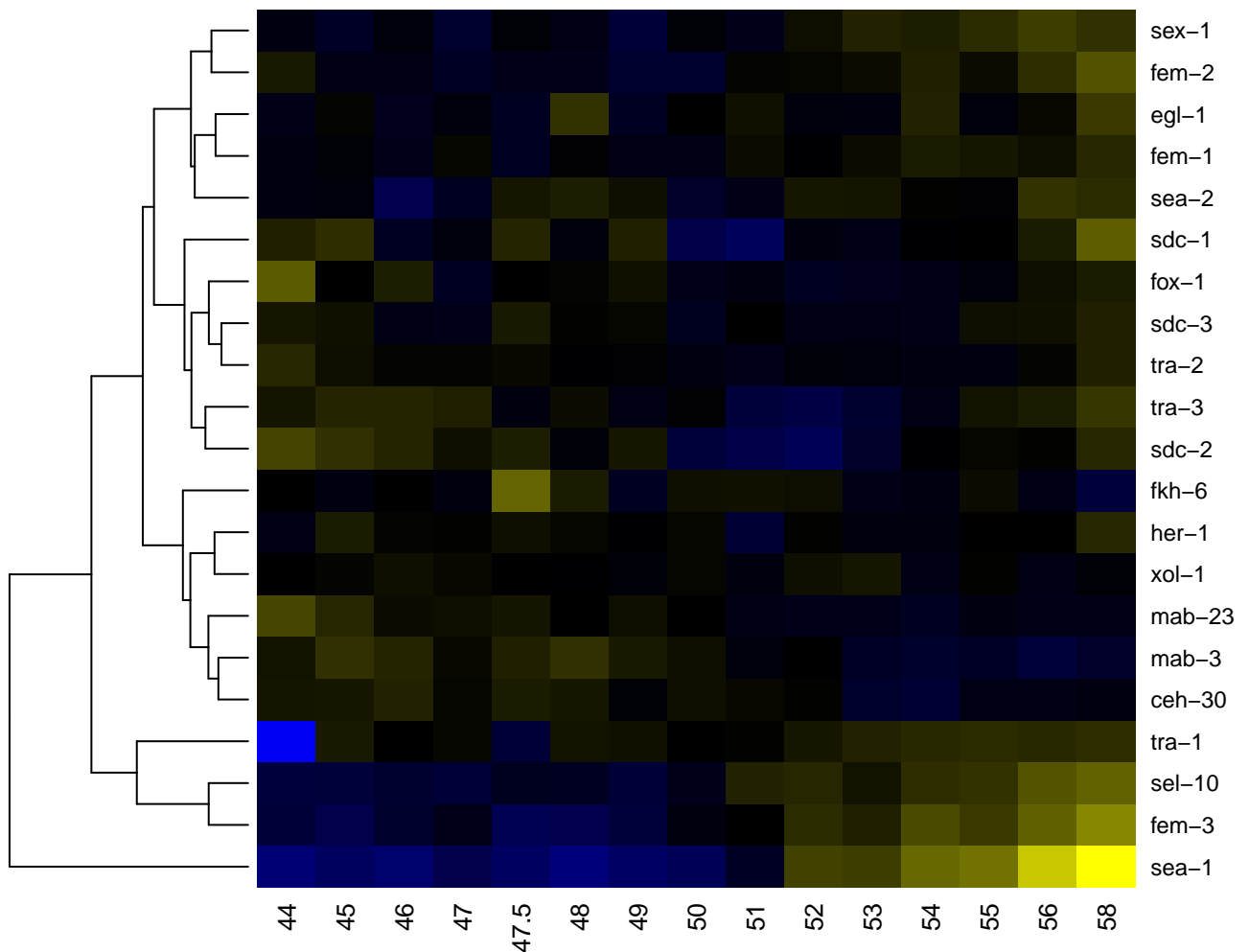
Signaling in the immune response



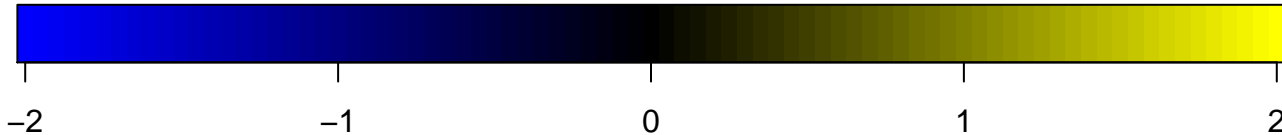
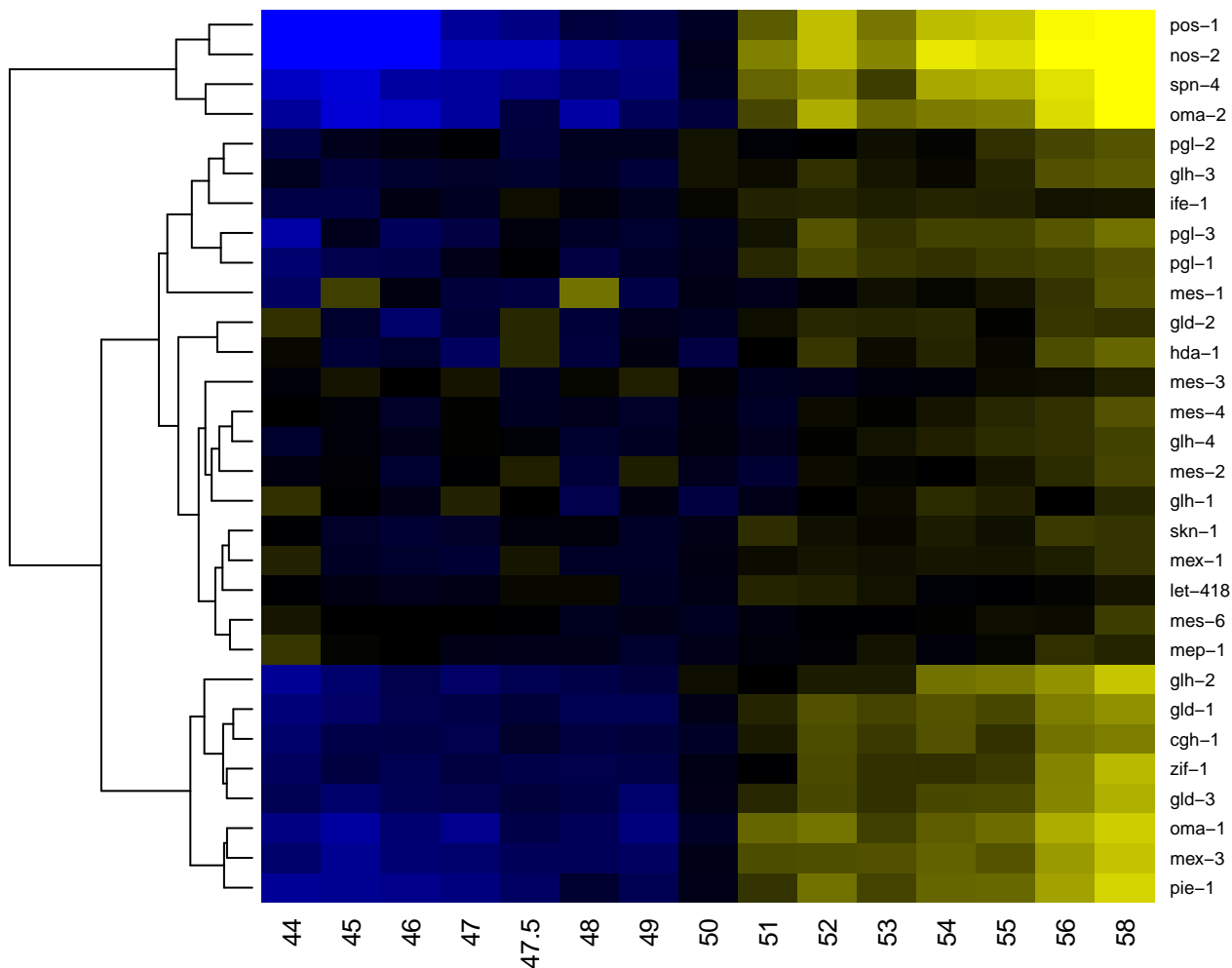
Small GTPases



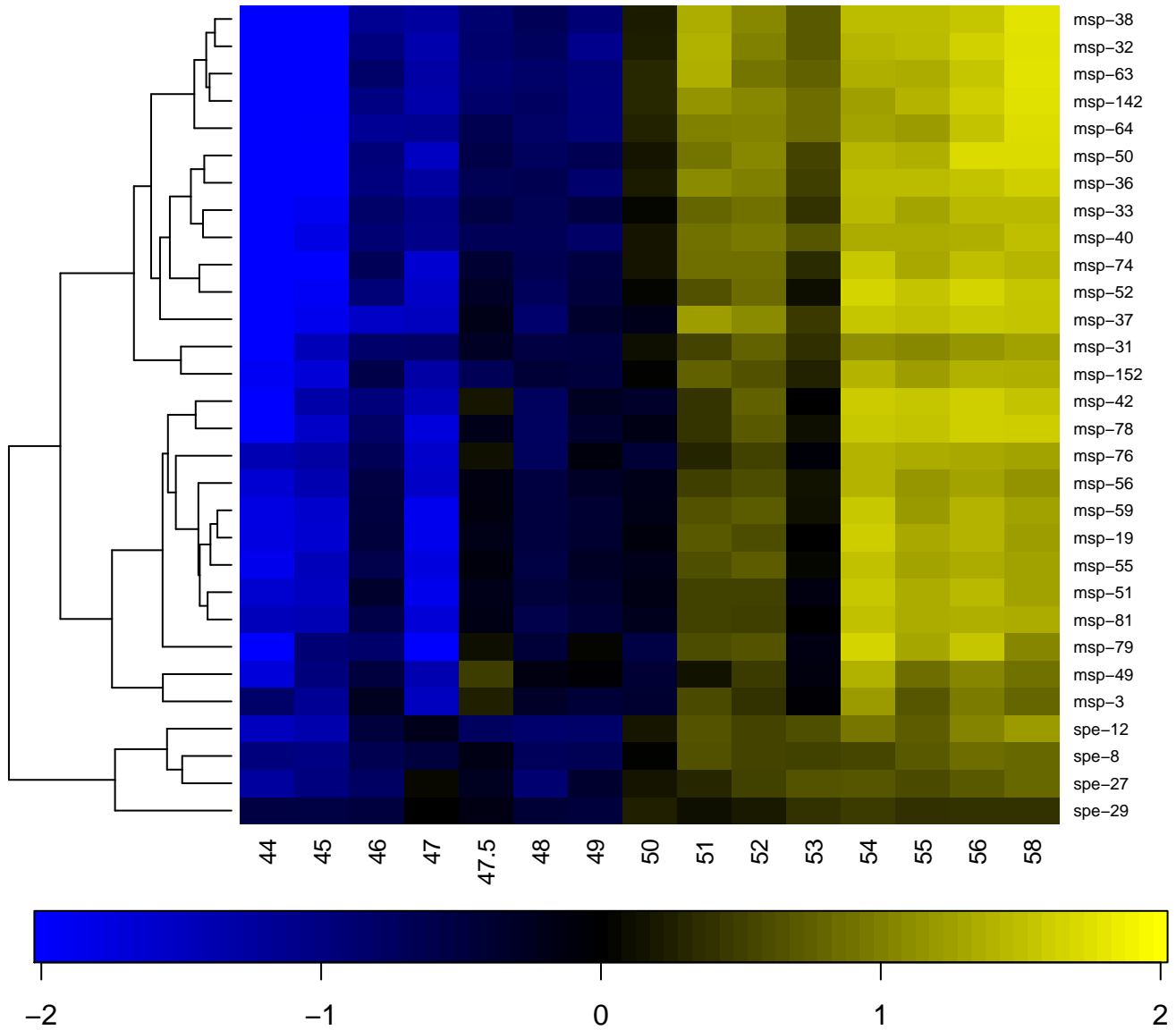
Somatic sex determination



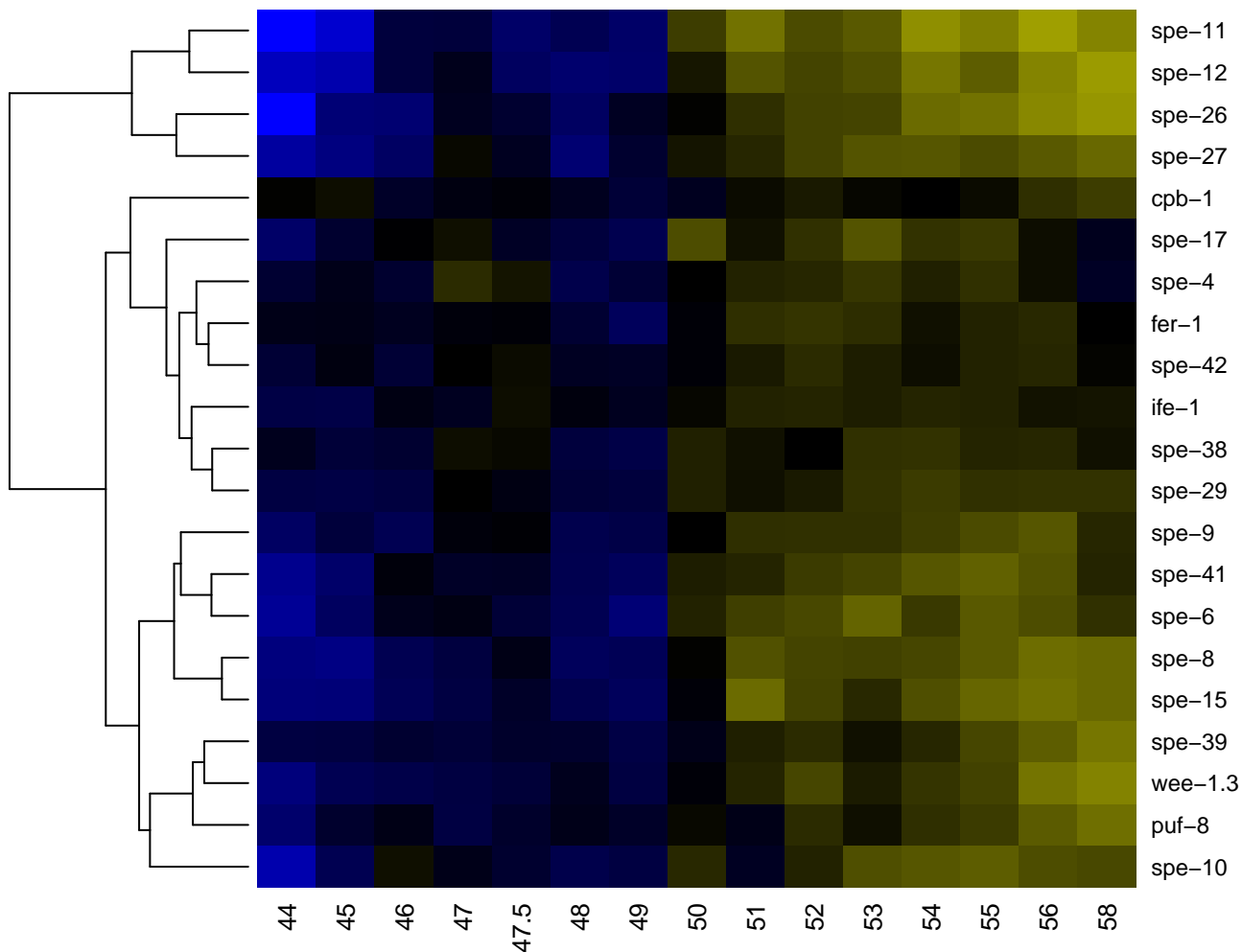
Specification of the germ line



Sperm motility and MSP



Spermatogenesis



-2

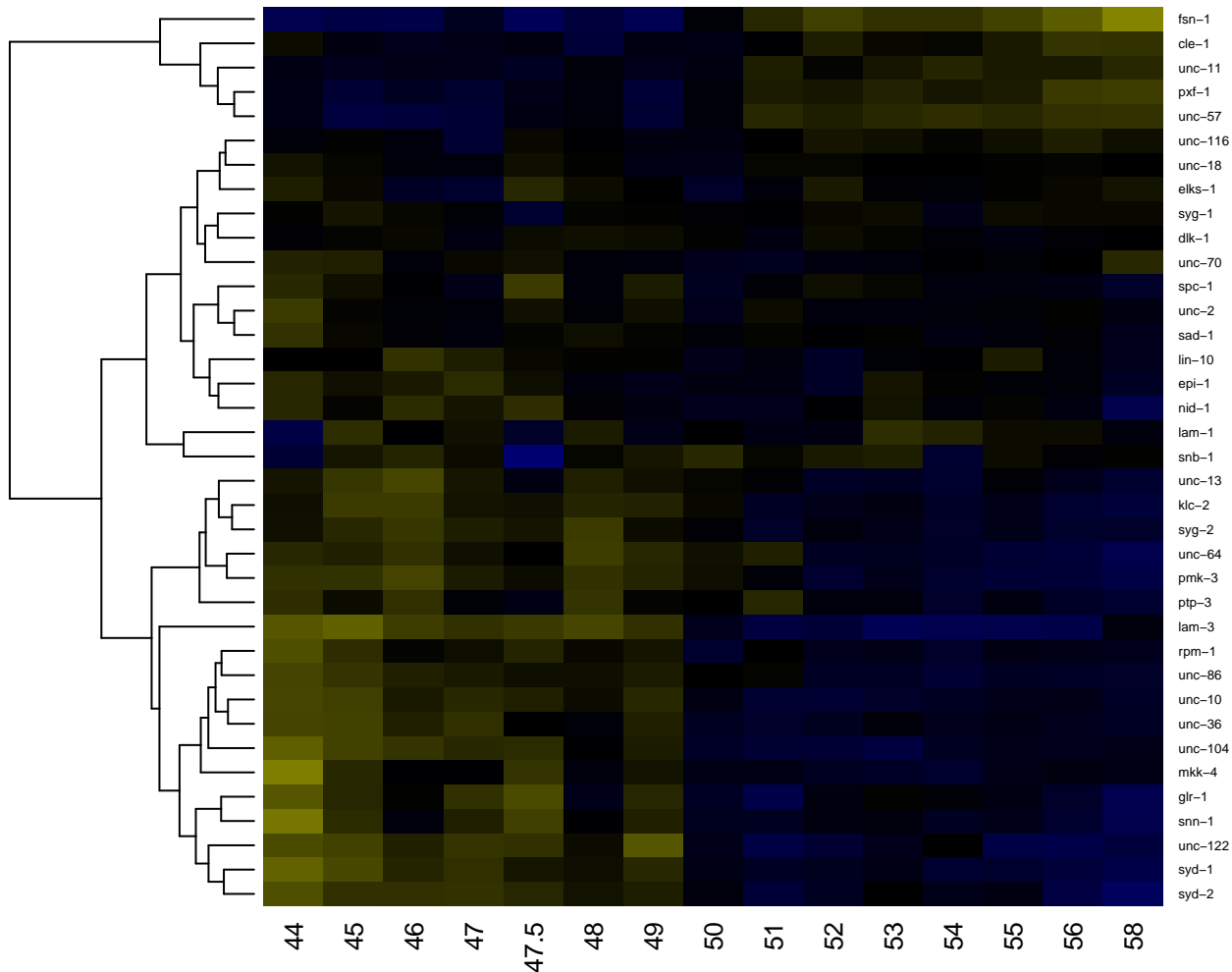
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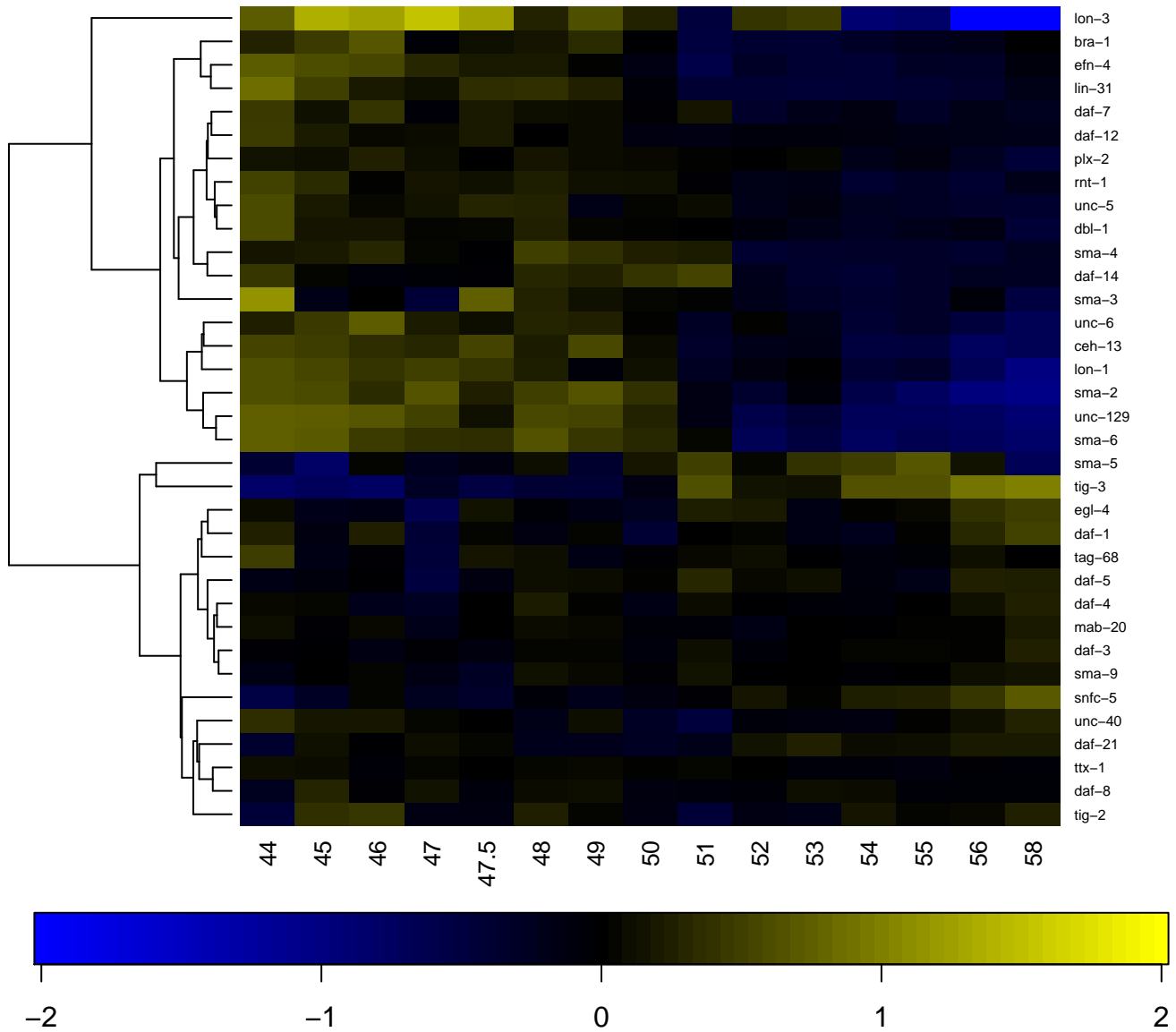
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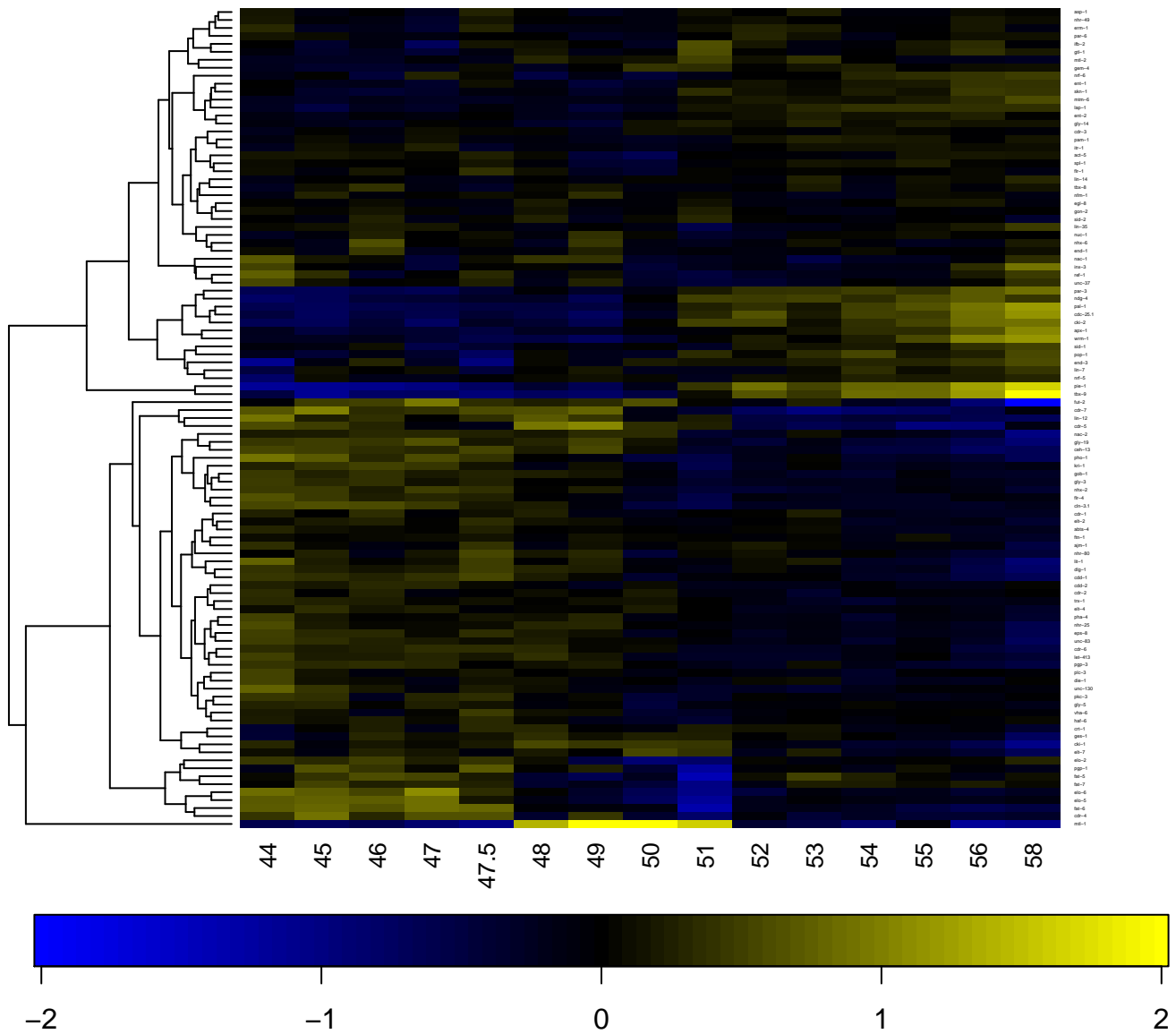
Synaptogenesis



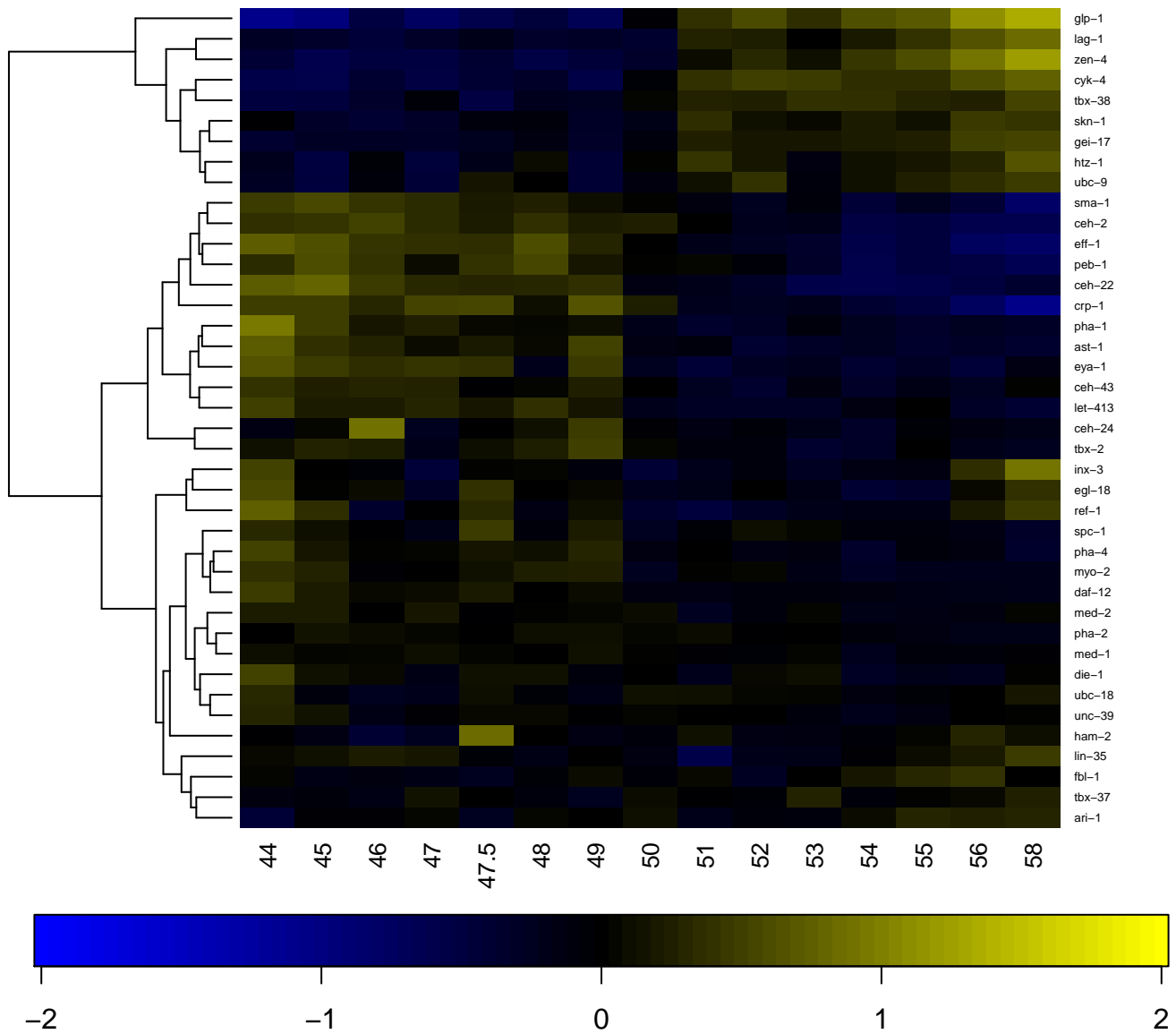
TGF-? signaling



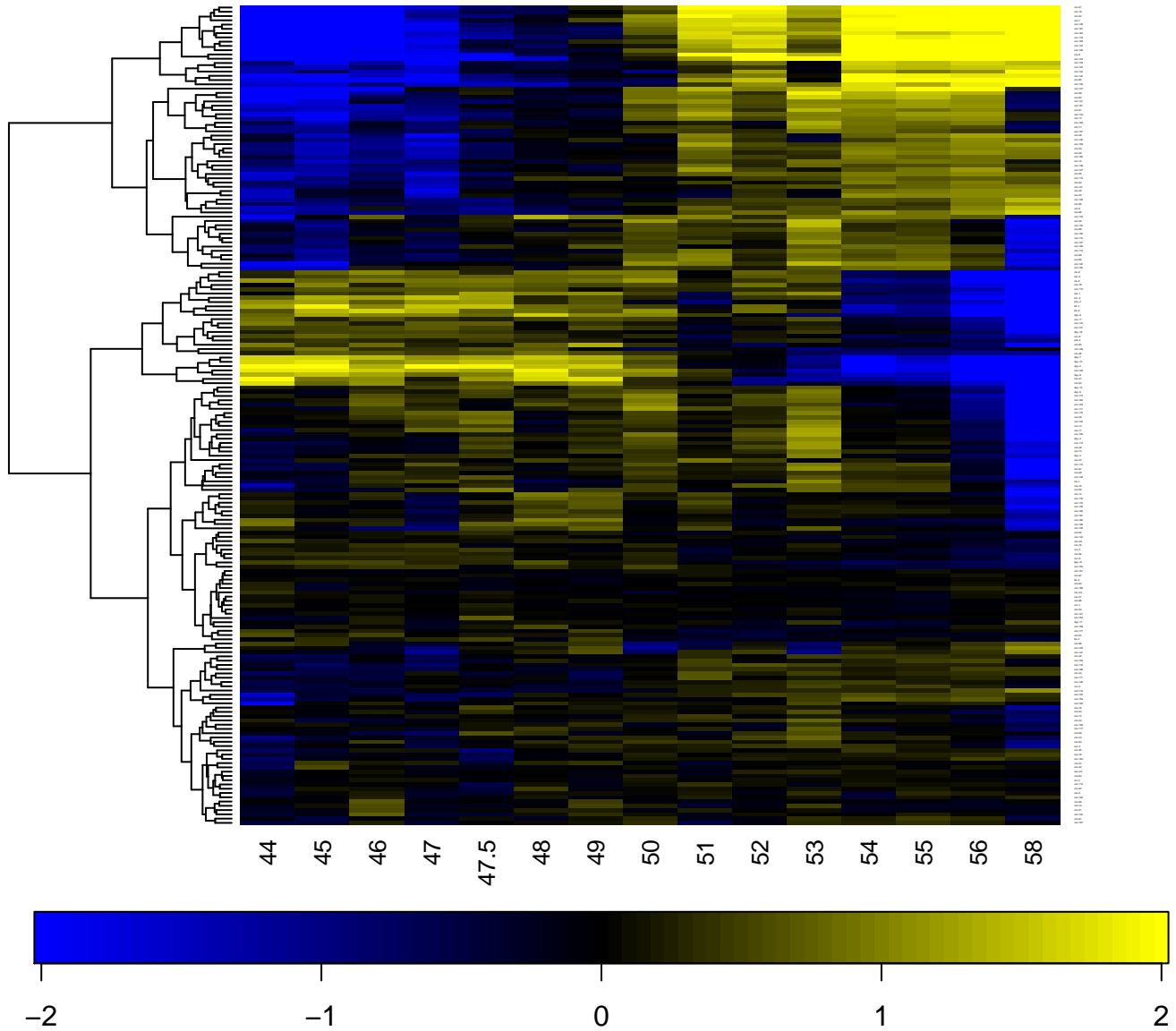
The C. elegans intestine



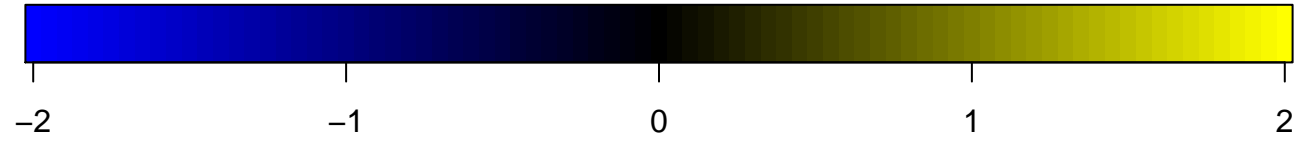
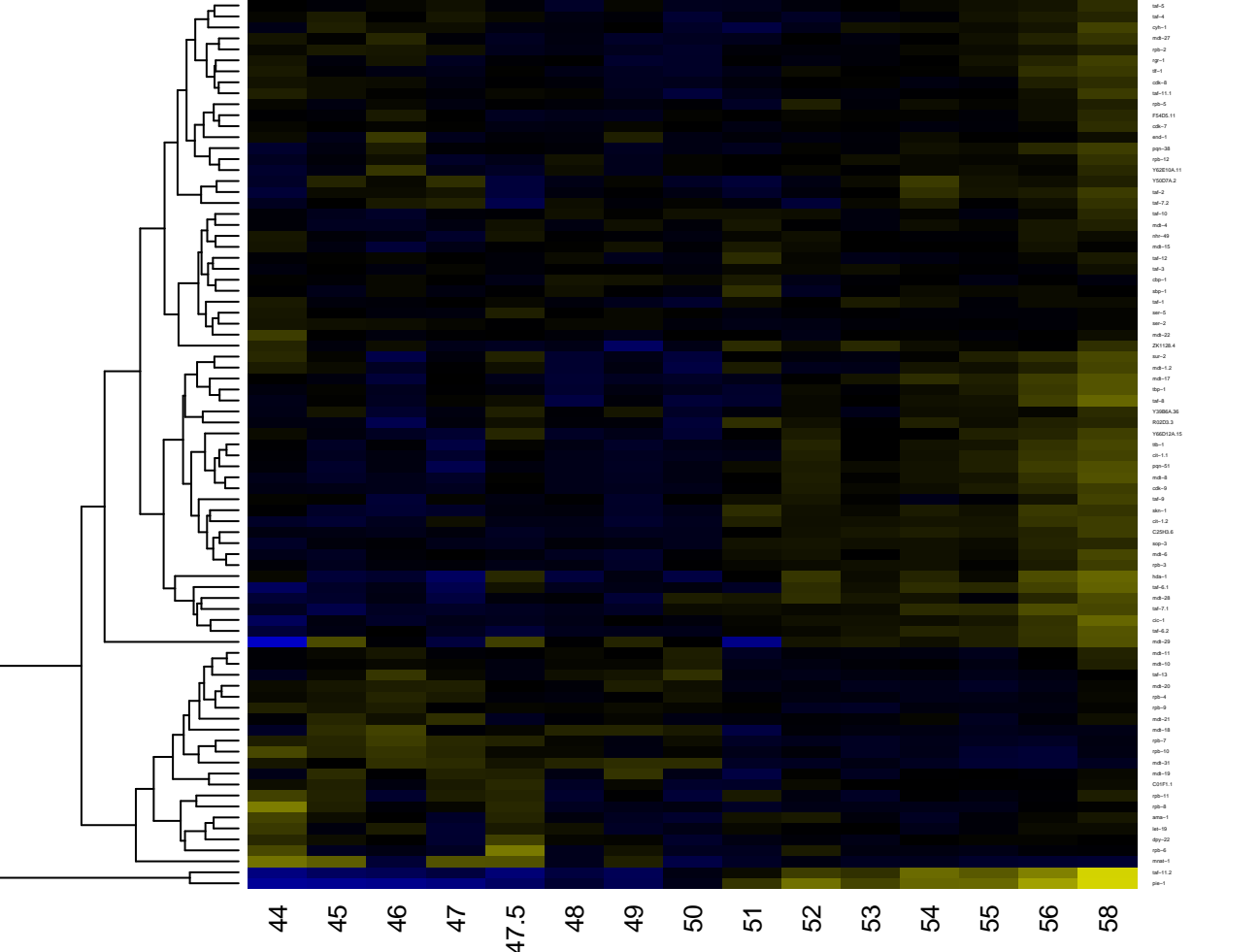
The *C. elegans* pharynx



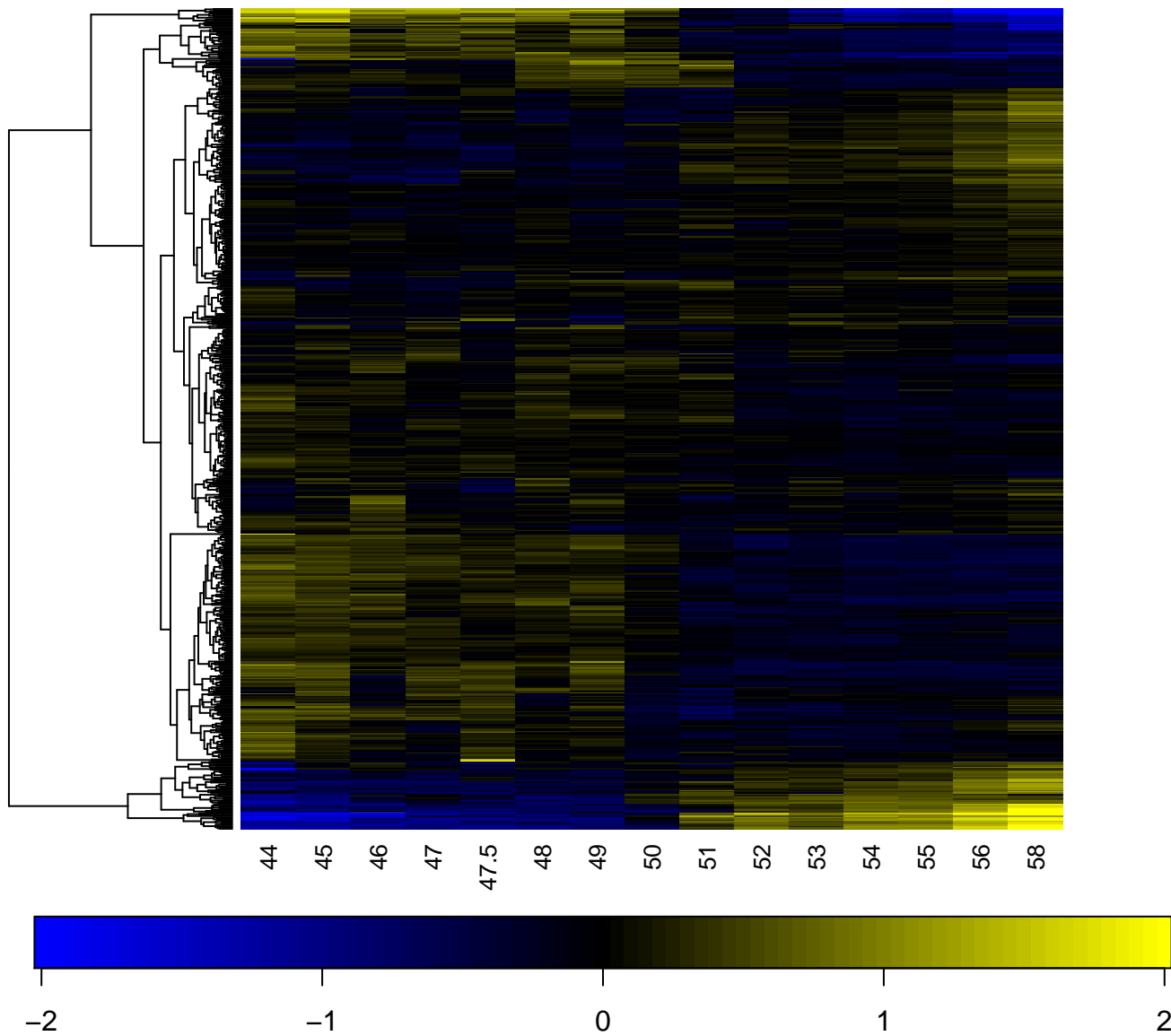
The cuticle



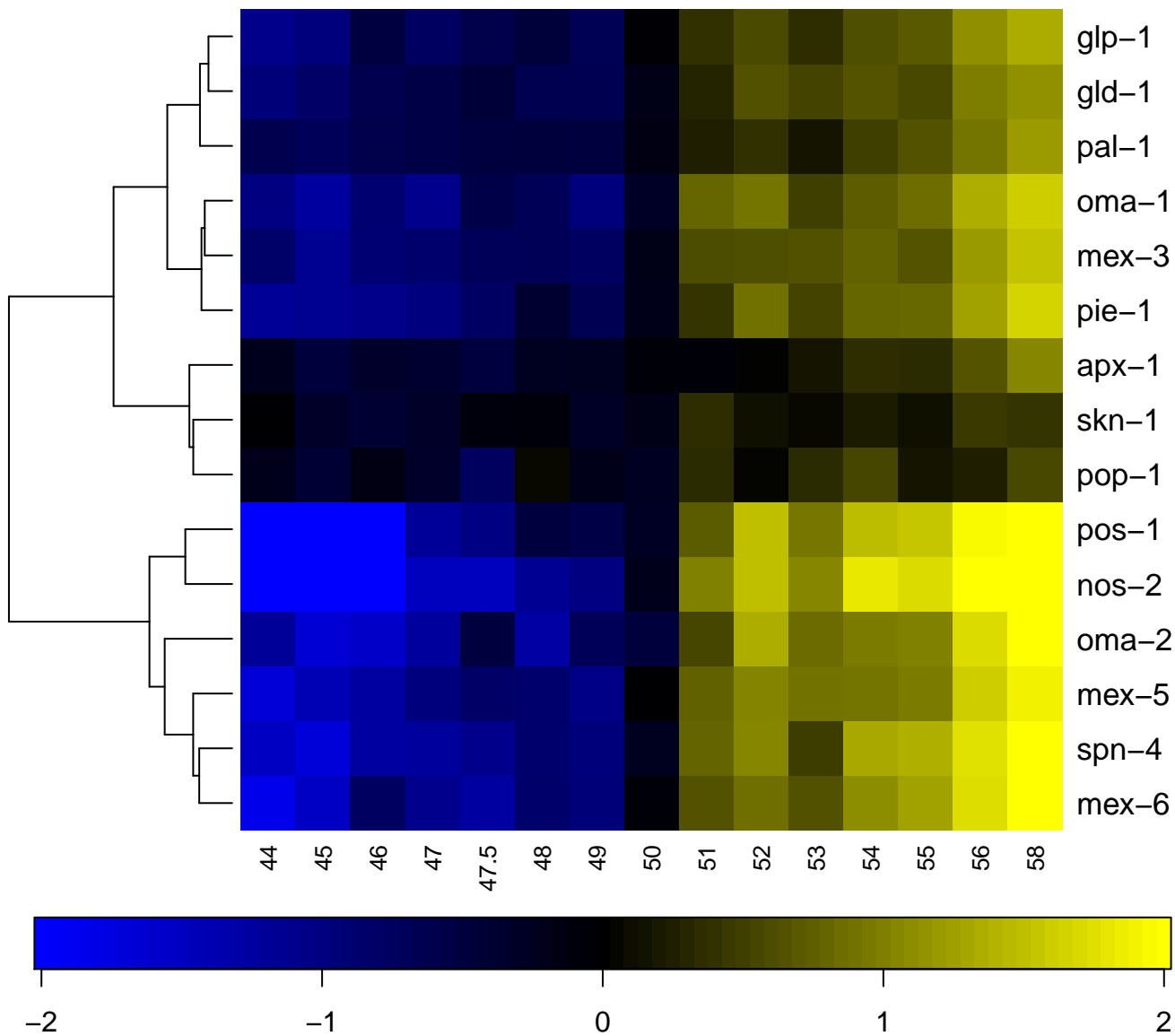
Transcription mechanisms



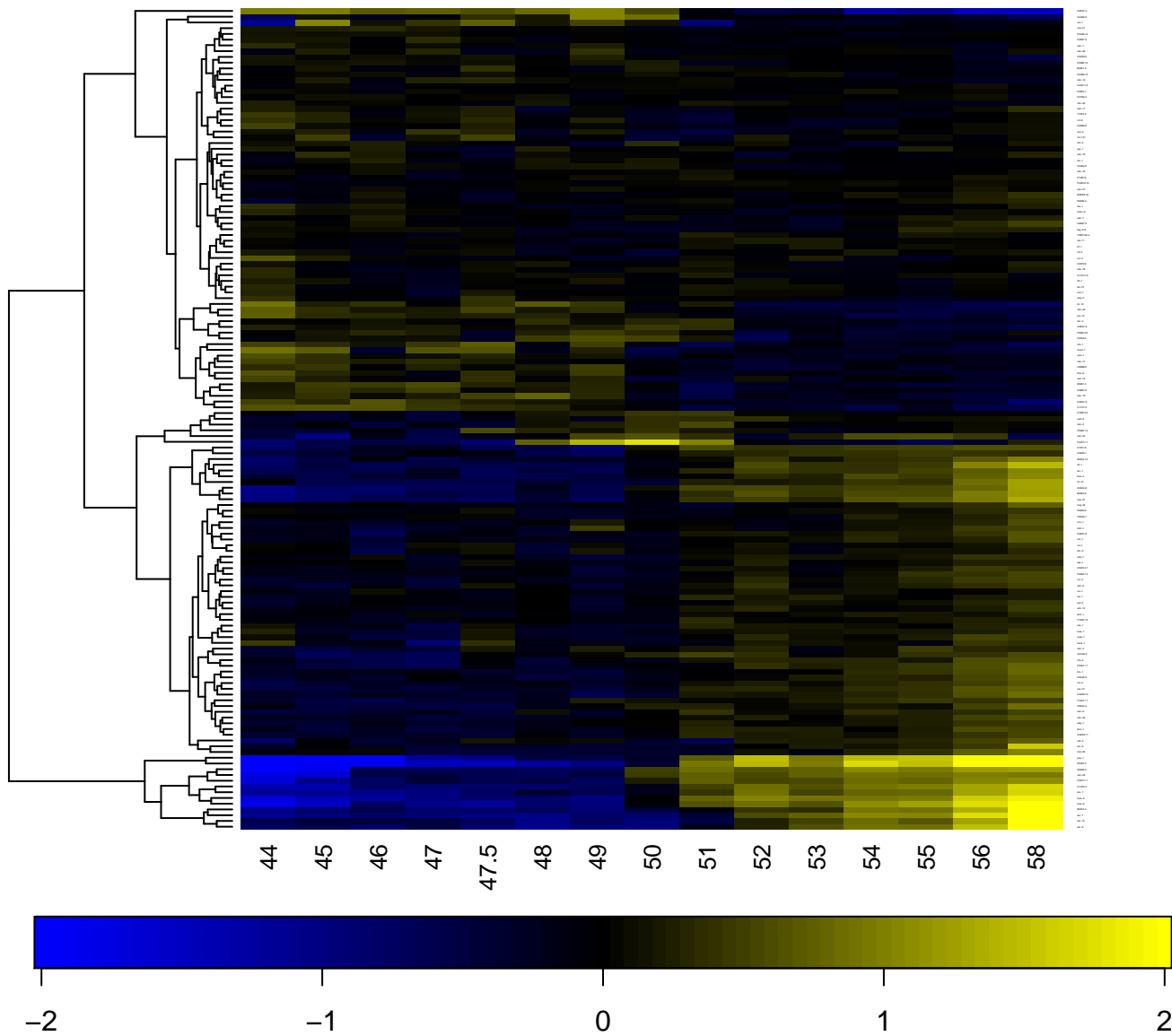
Transcriptional regulation



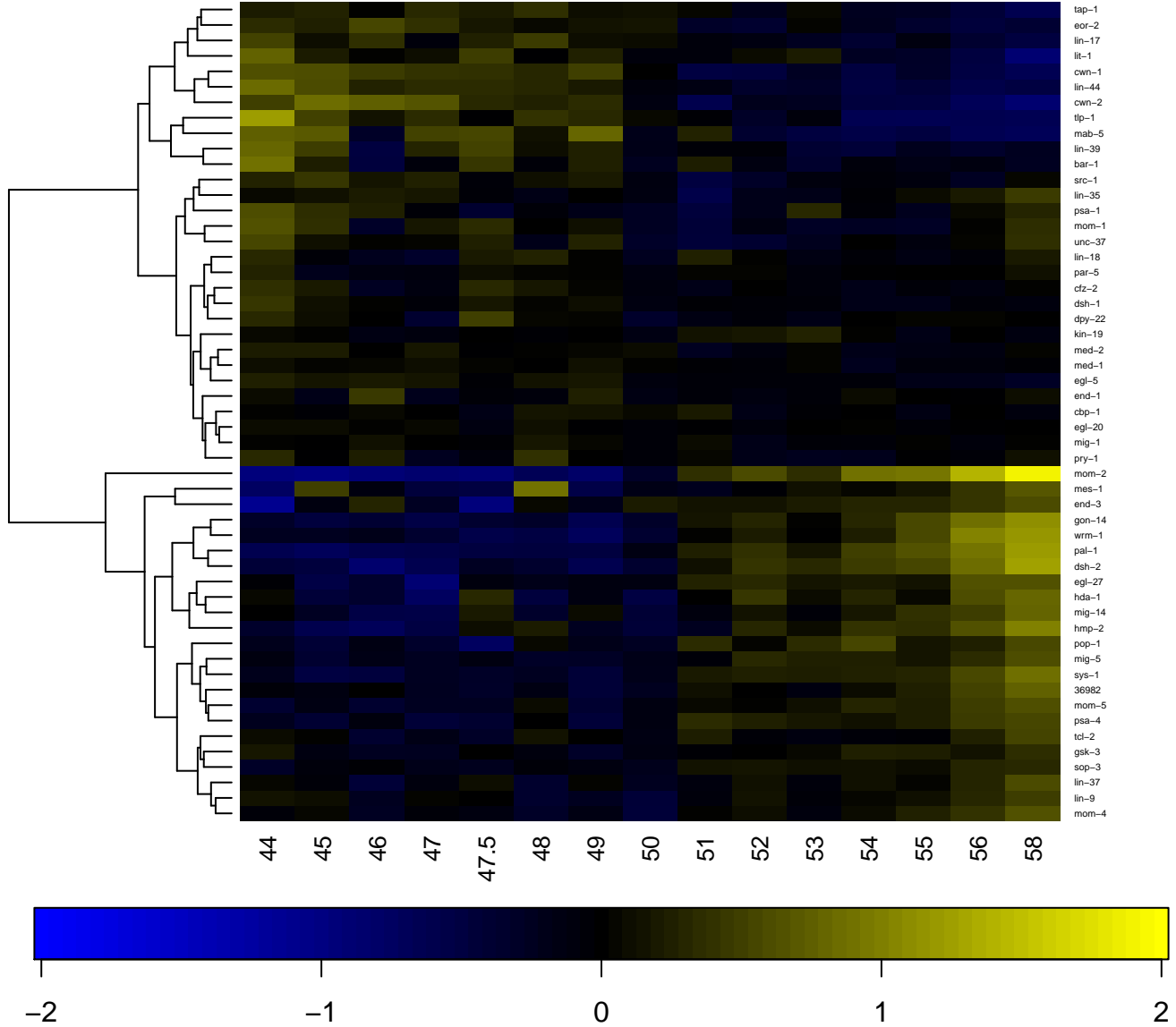
Translational control of maternal RNAs



Ubiquitin-mediated pathways in *C. elegans*



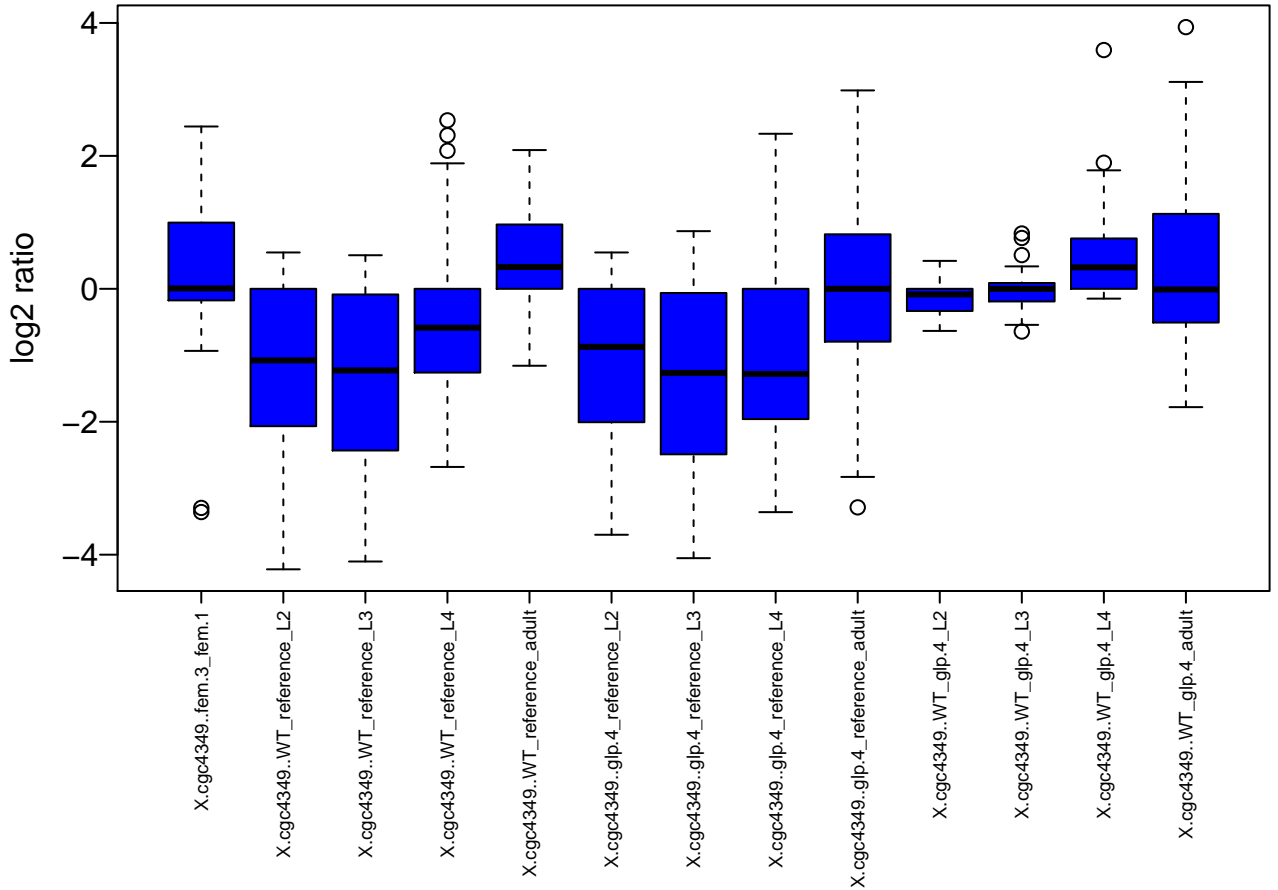
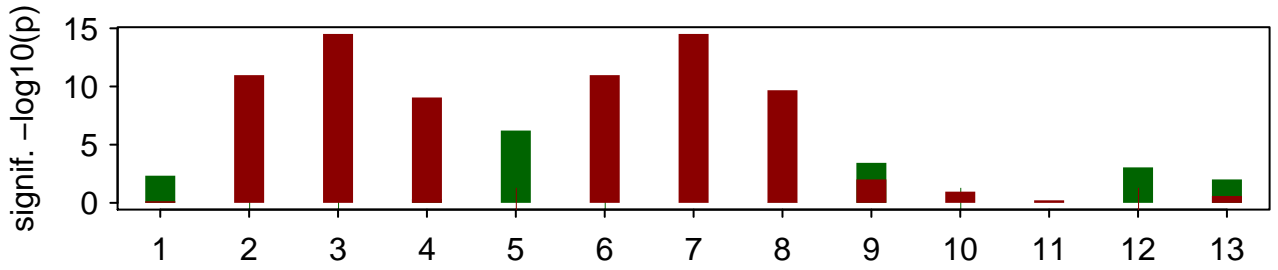
Wnt signaling



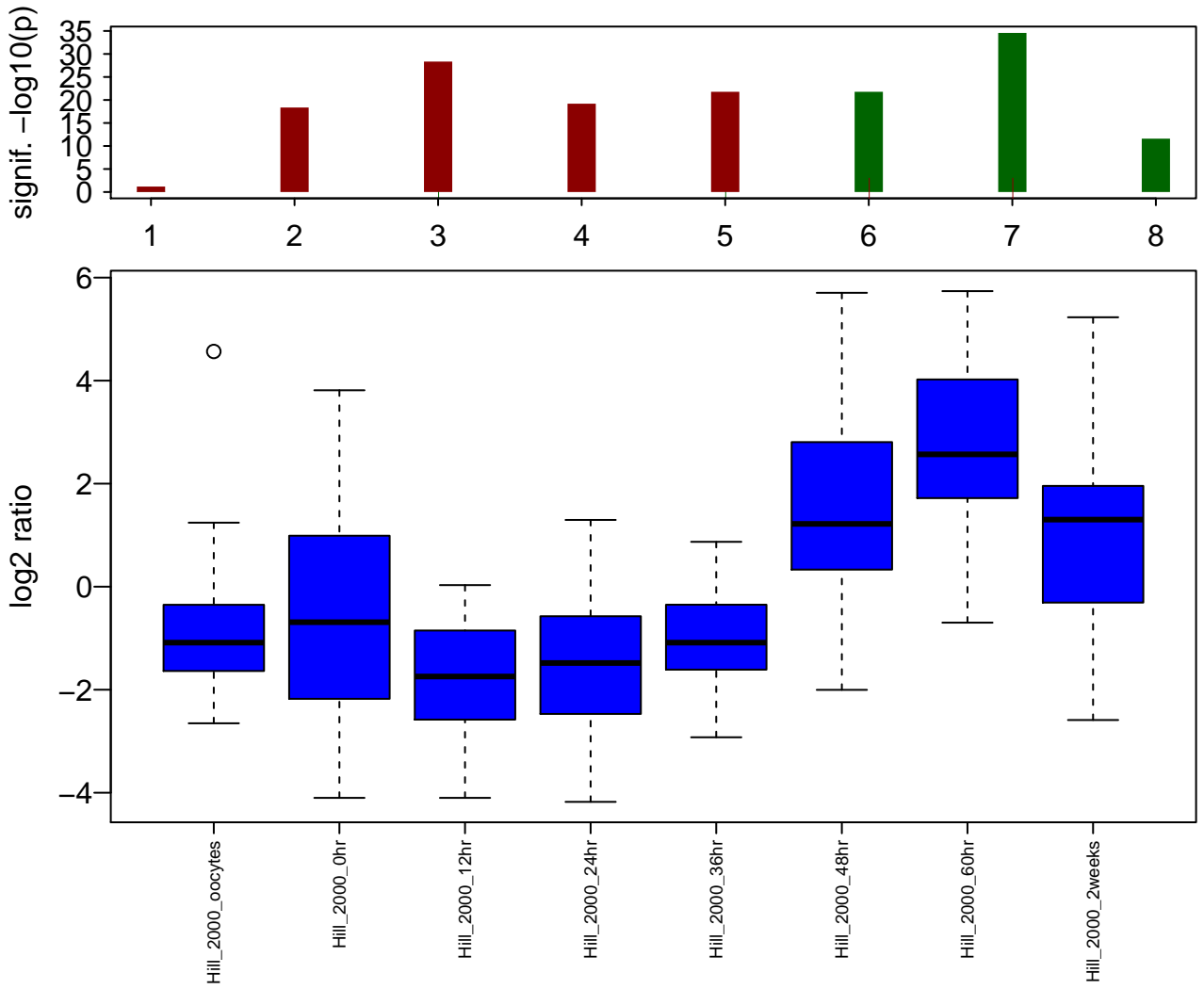
Supplementary file J | Development as a source of variation in SPELL transcript profiles.

All the sample comparisons of the micro-array experiments in the SPELL data base were tested for enrichment of developmental marker genes (cluster 1) in the top 10% up or down regulated genes. **The upper panel** shows the significance of the enrichment using a hyper-geometric test, green shows the results for the 10% most up regulated genes and red for the 10% most down regulated genes. **The lower panel** shows a box plot with the log₂ ratios of the overlapping genes developmental marker genes from cluster 1 and the 10% most up or down regulated genes. The sample names as obtained from SPELL are show on the x-axis. The publication with the original micro-array data and experimental details can be found with the Wormbase Paper ID number starting with “WBPaper” shown as page title.

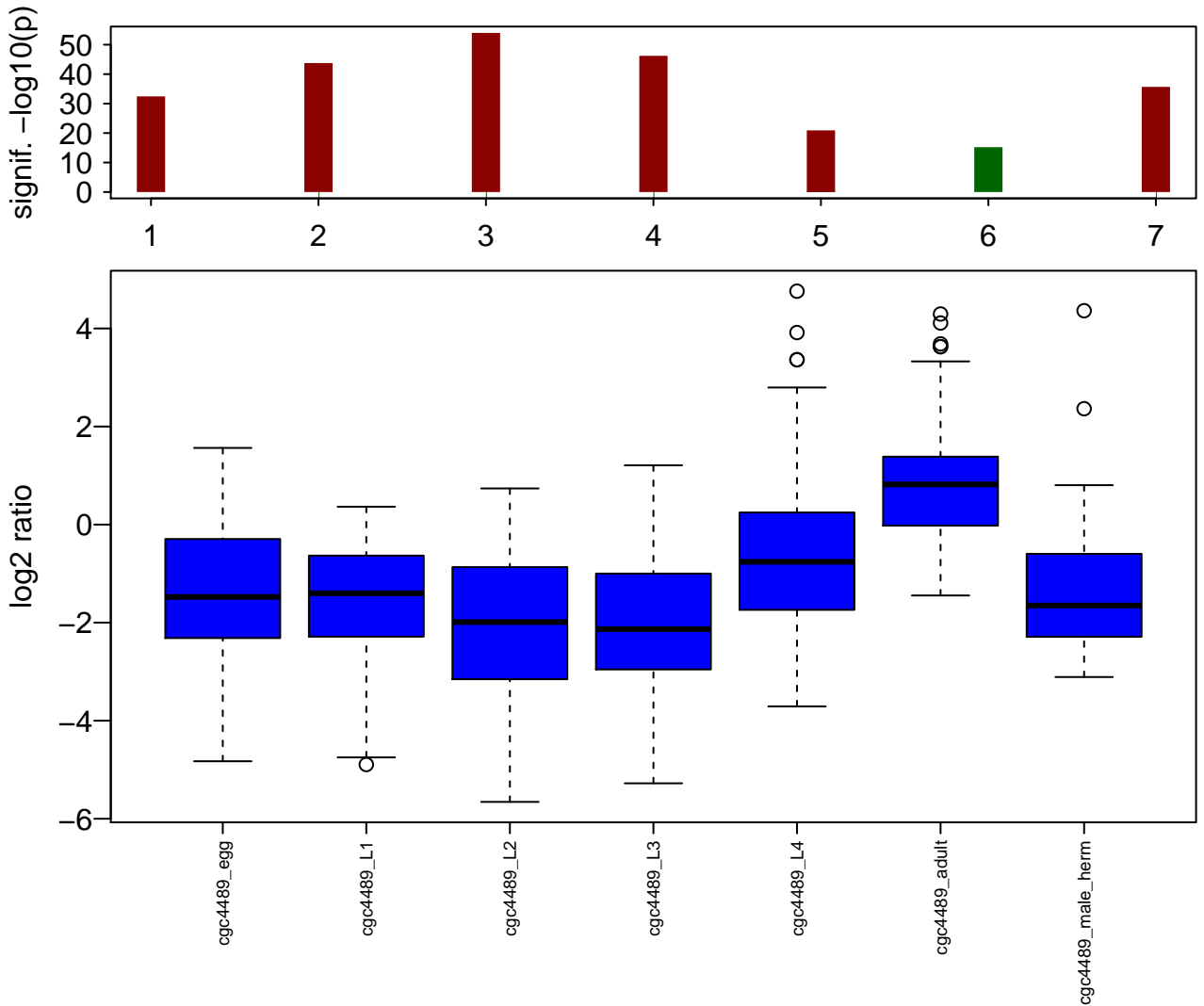
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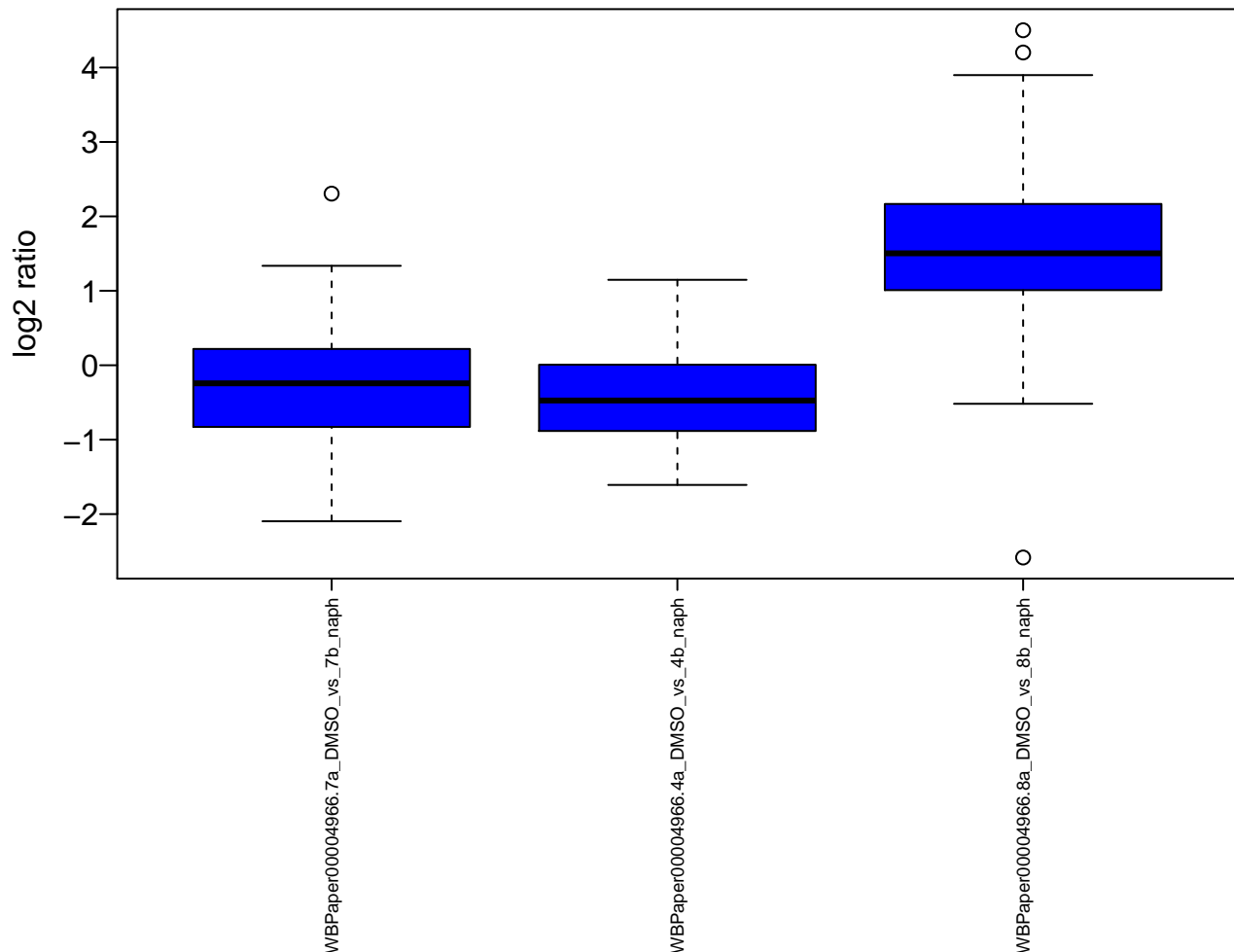
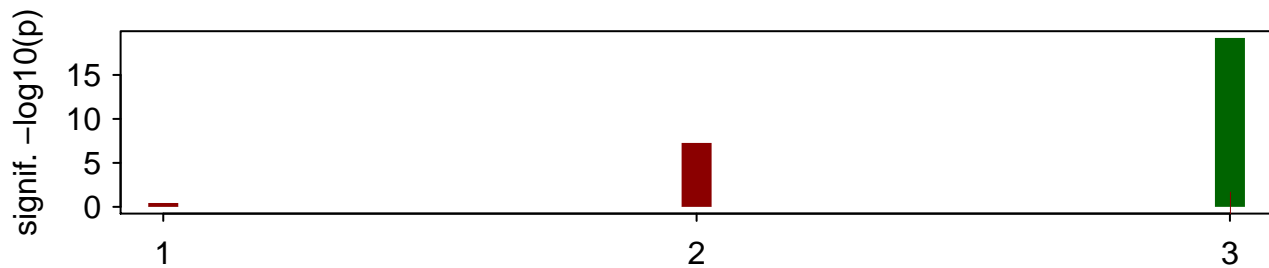
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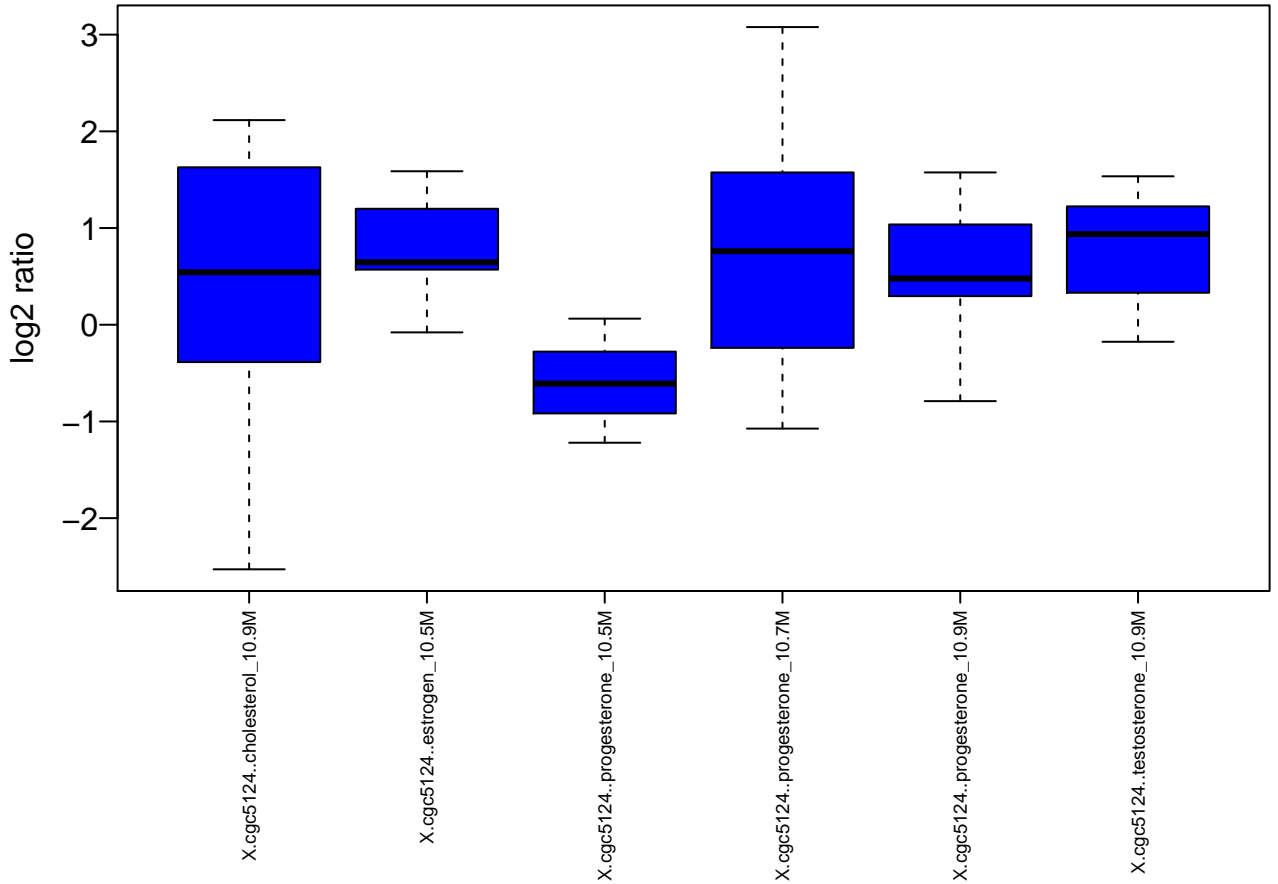
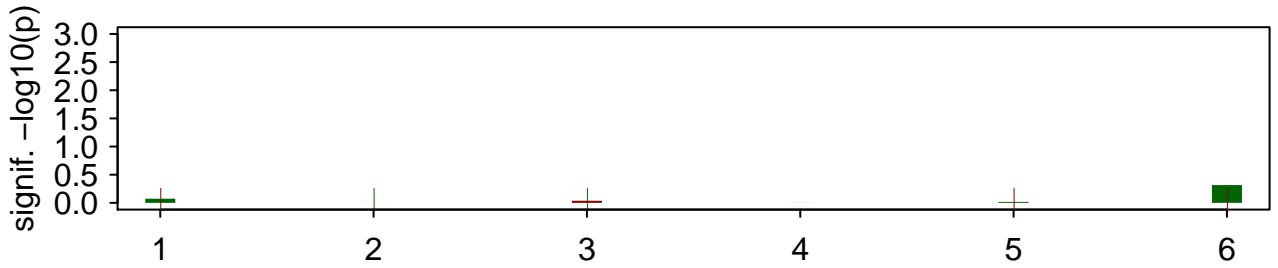
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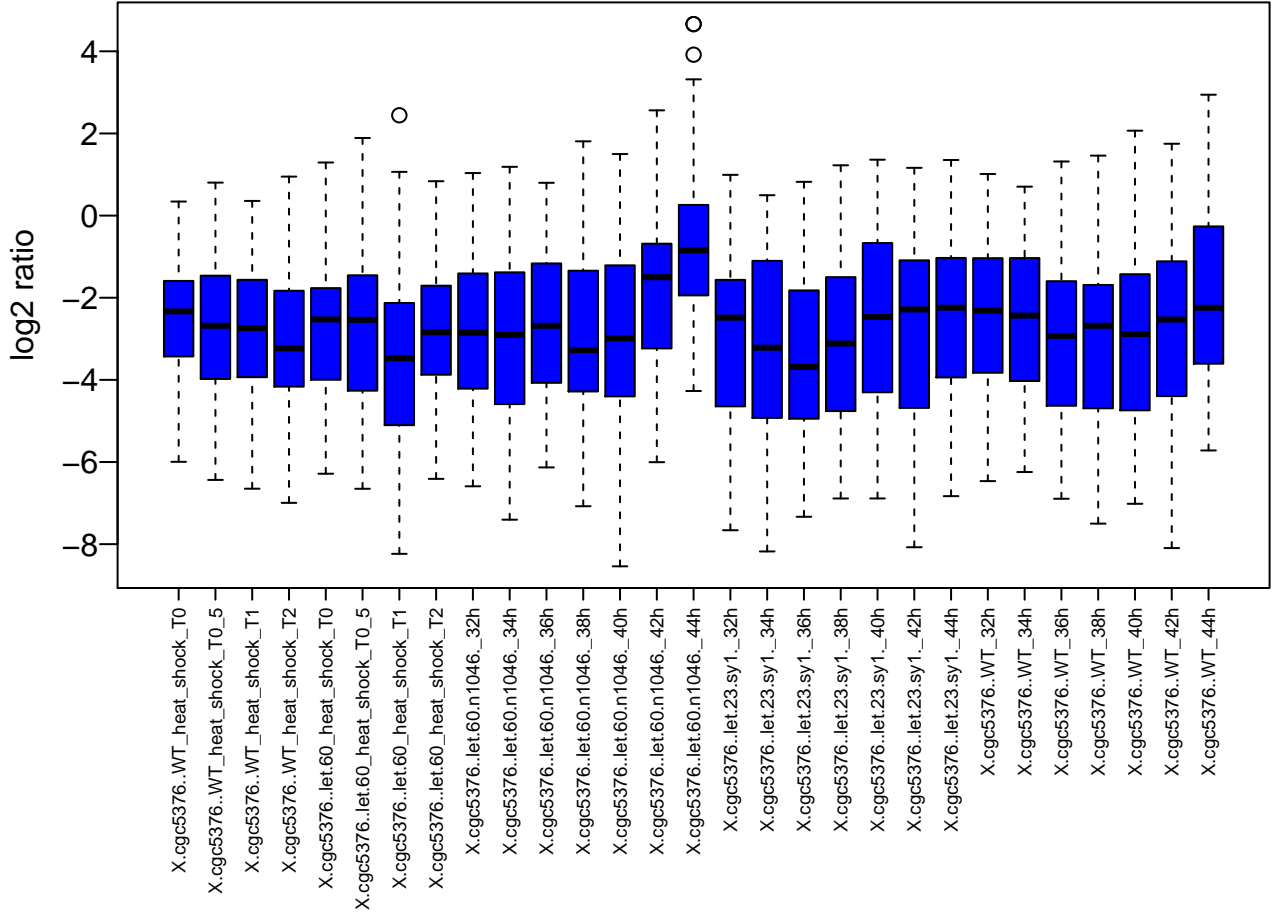
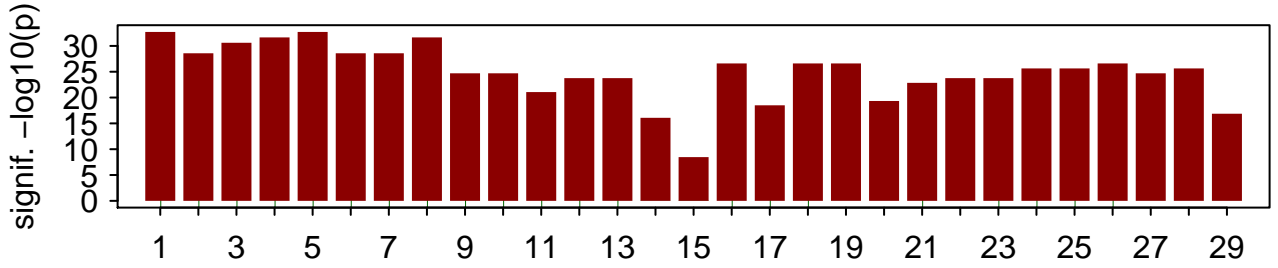
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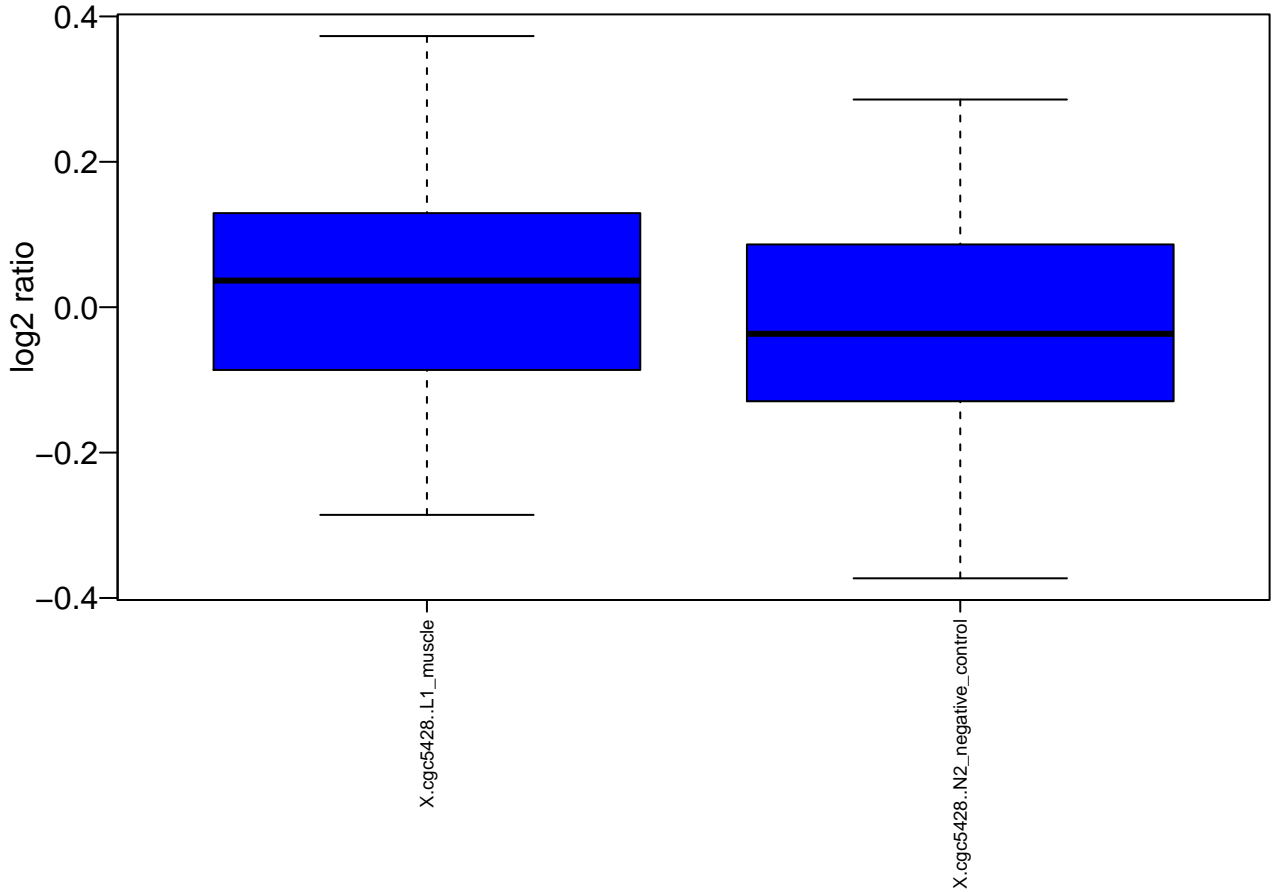
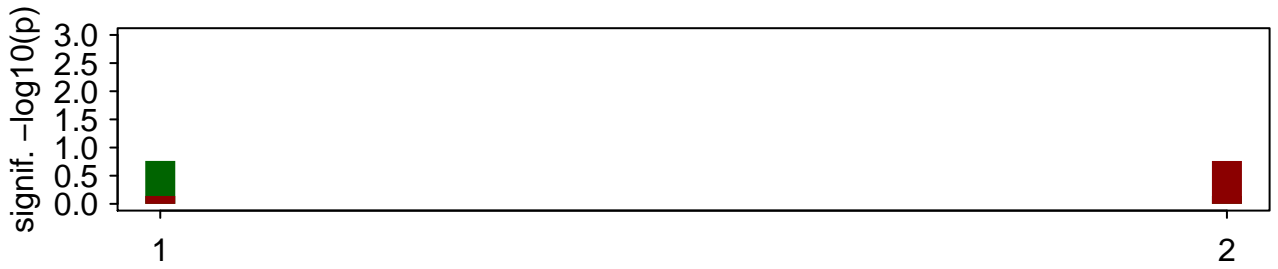
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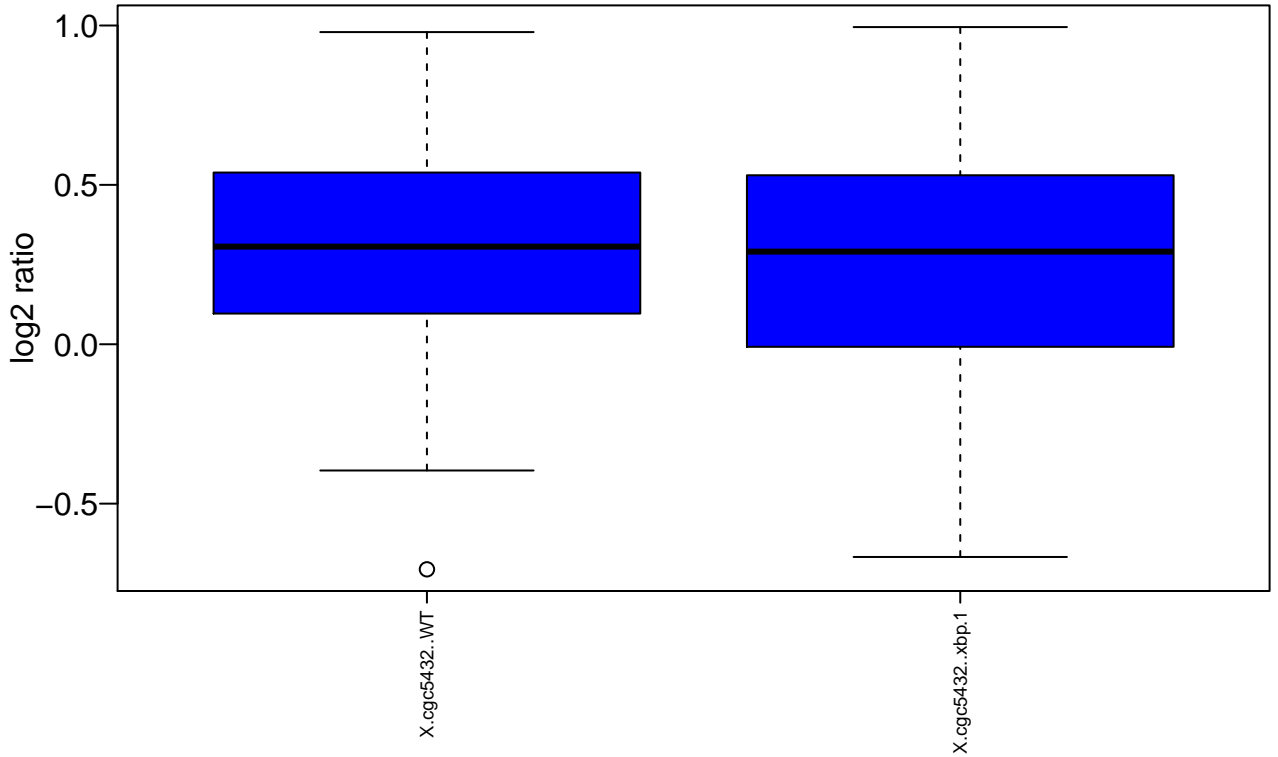
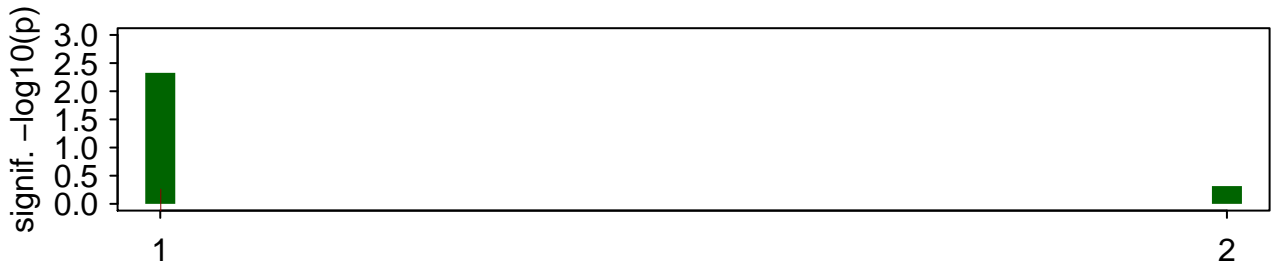
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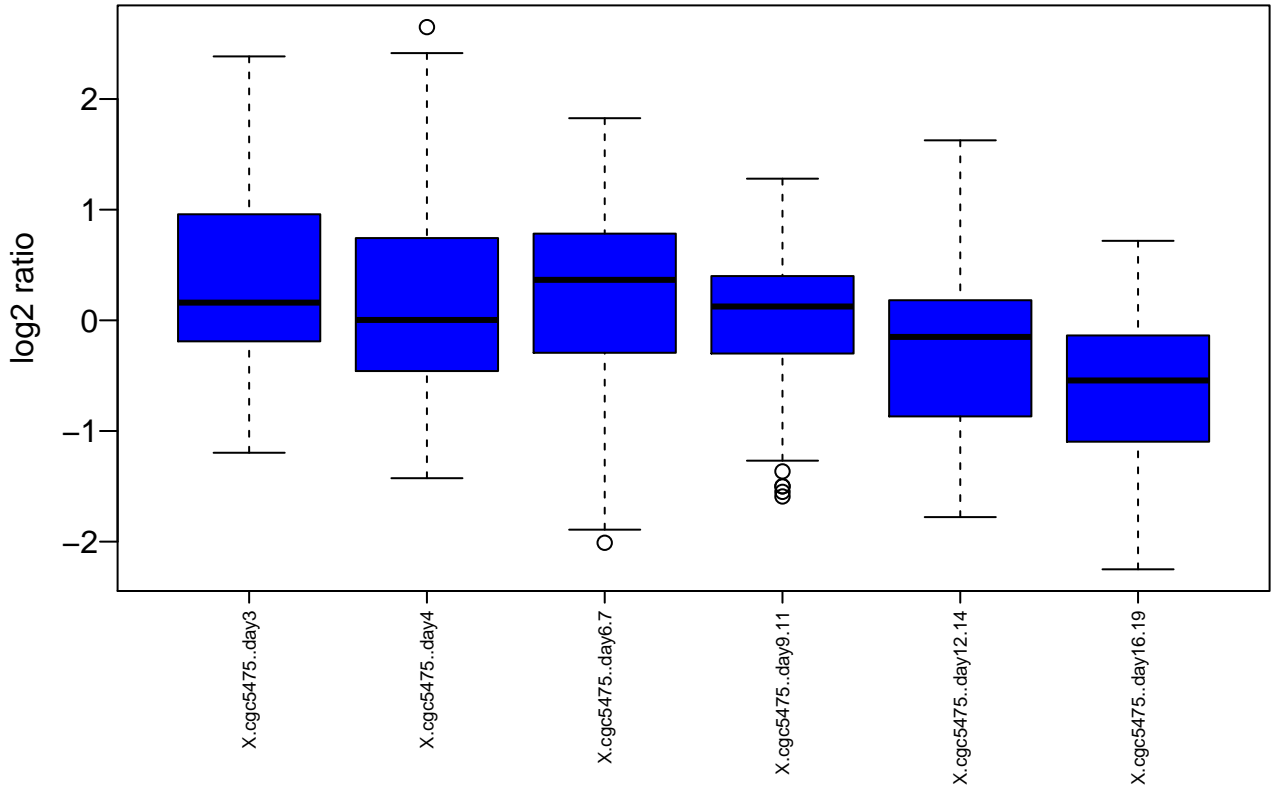
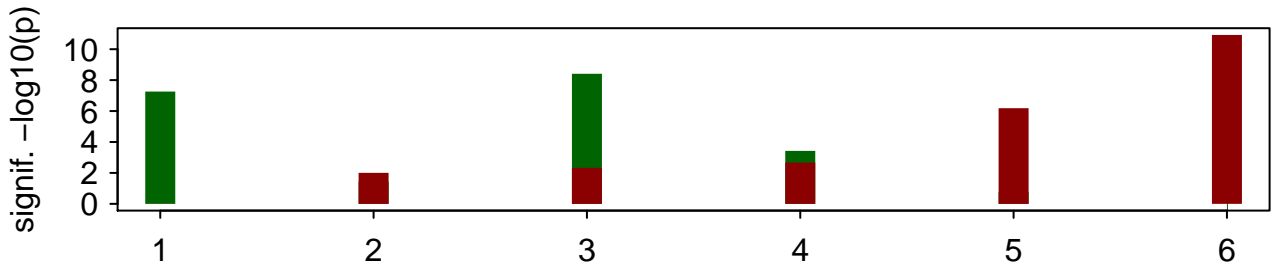
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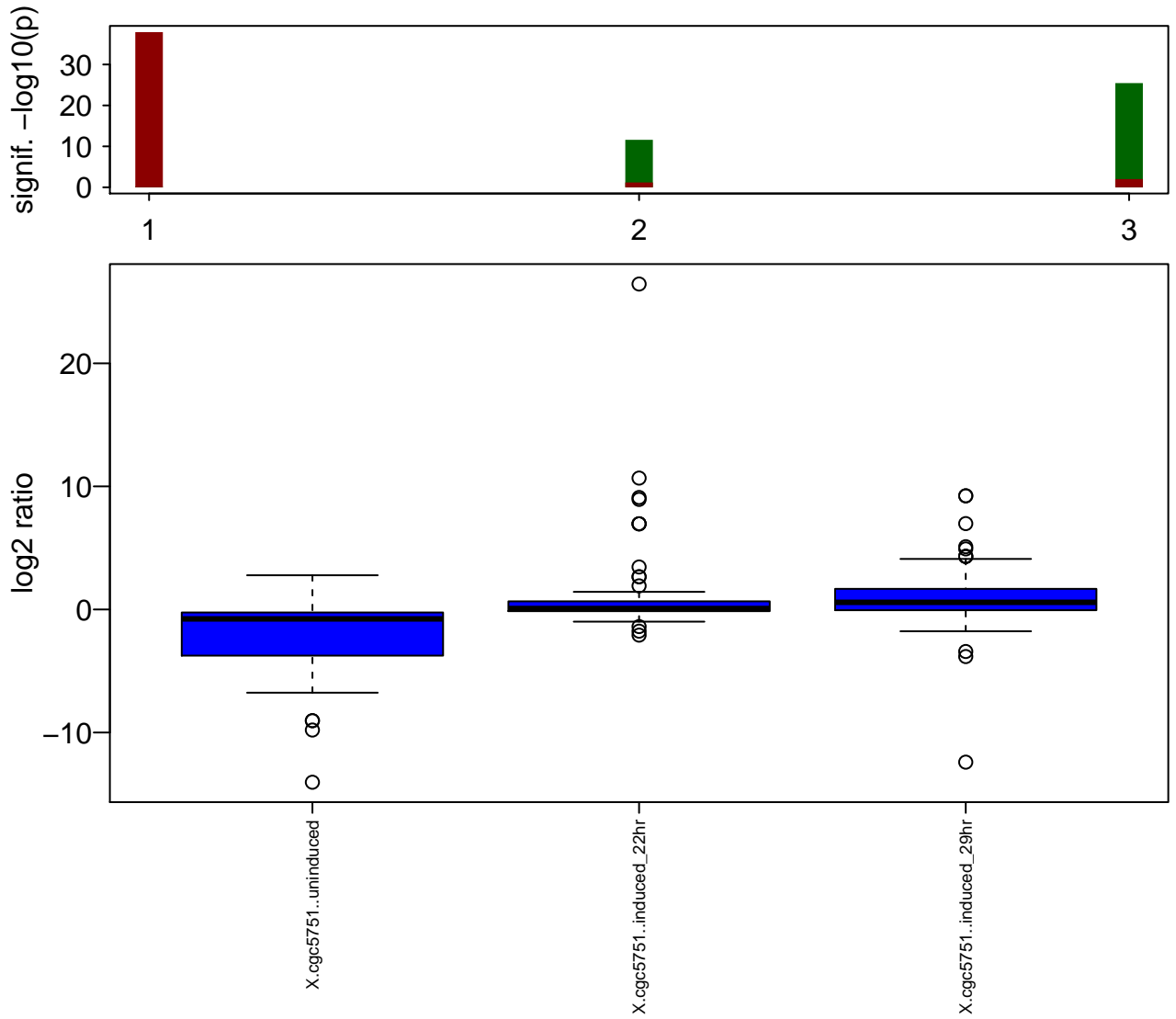
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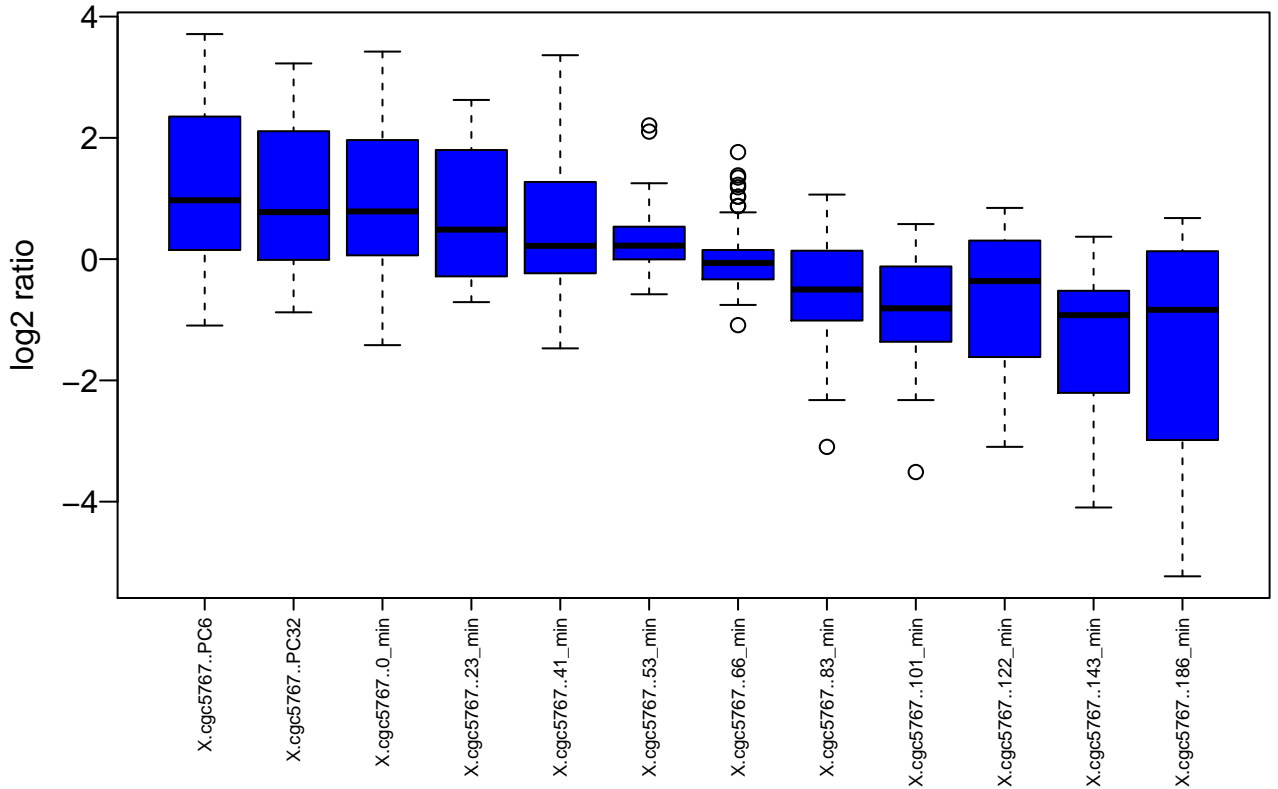
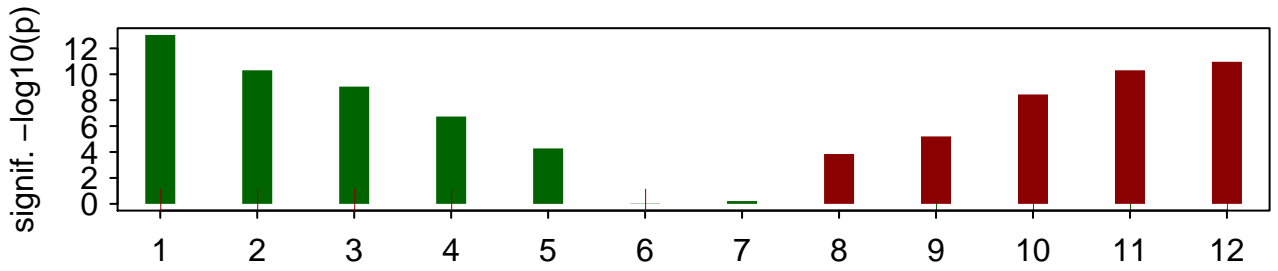
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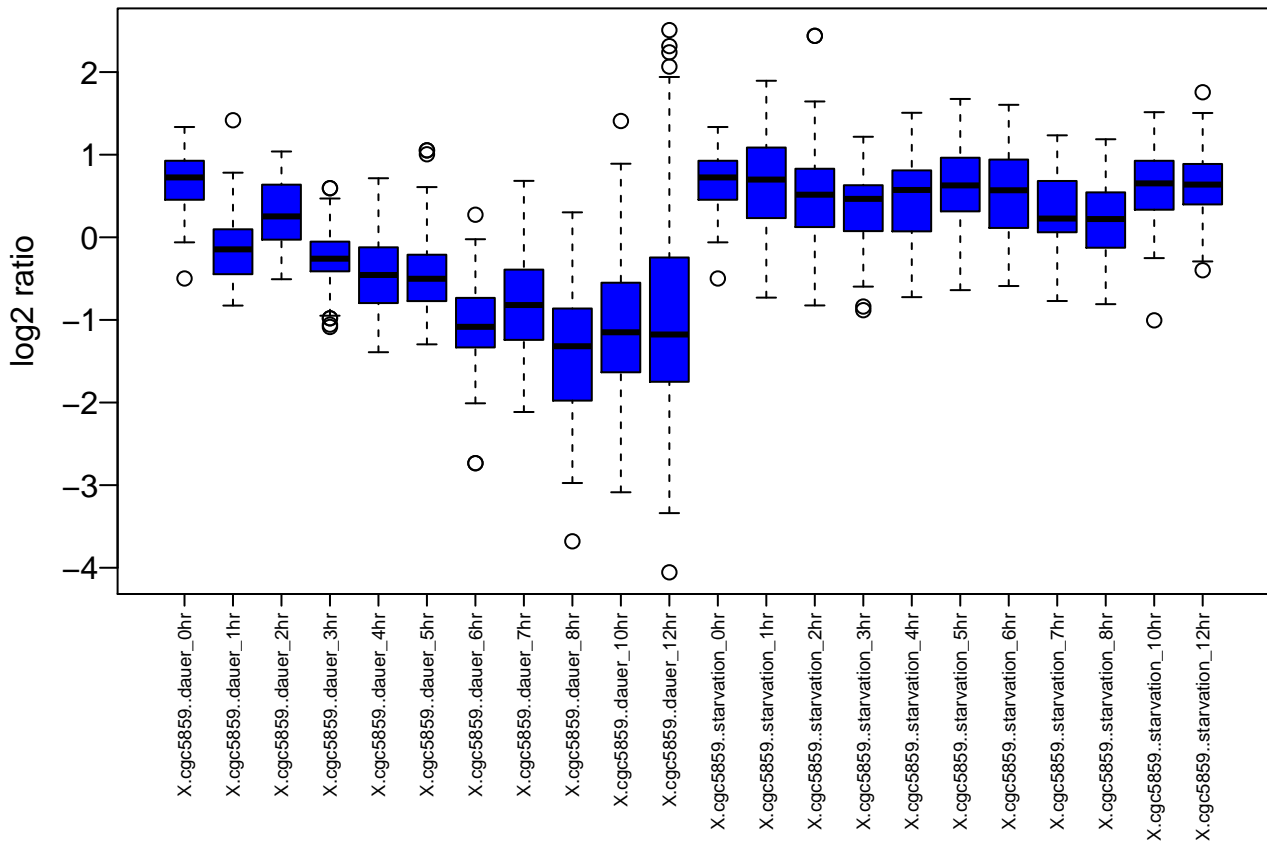
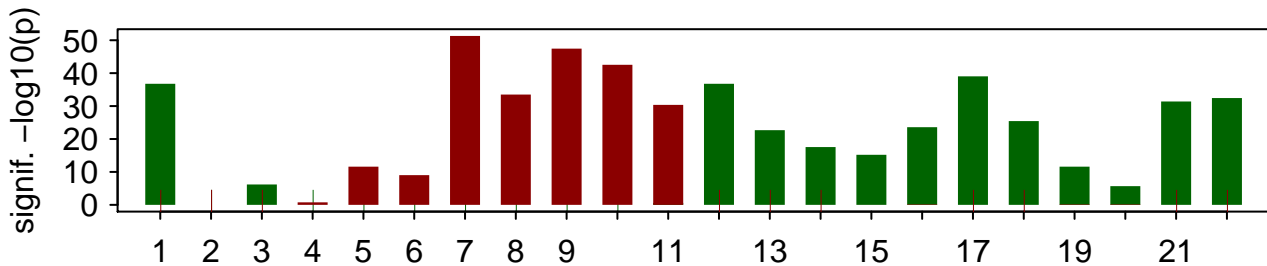
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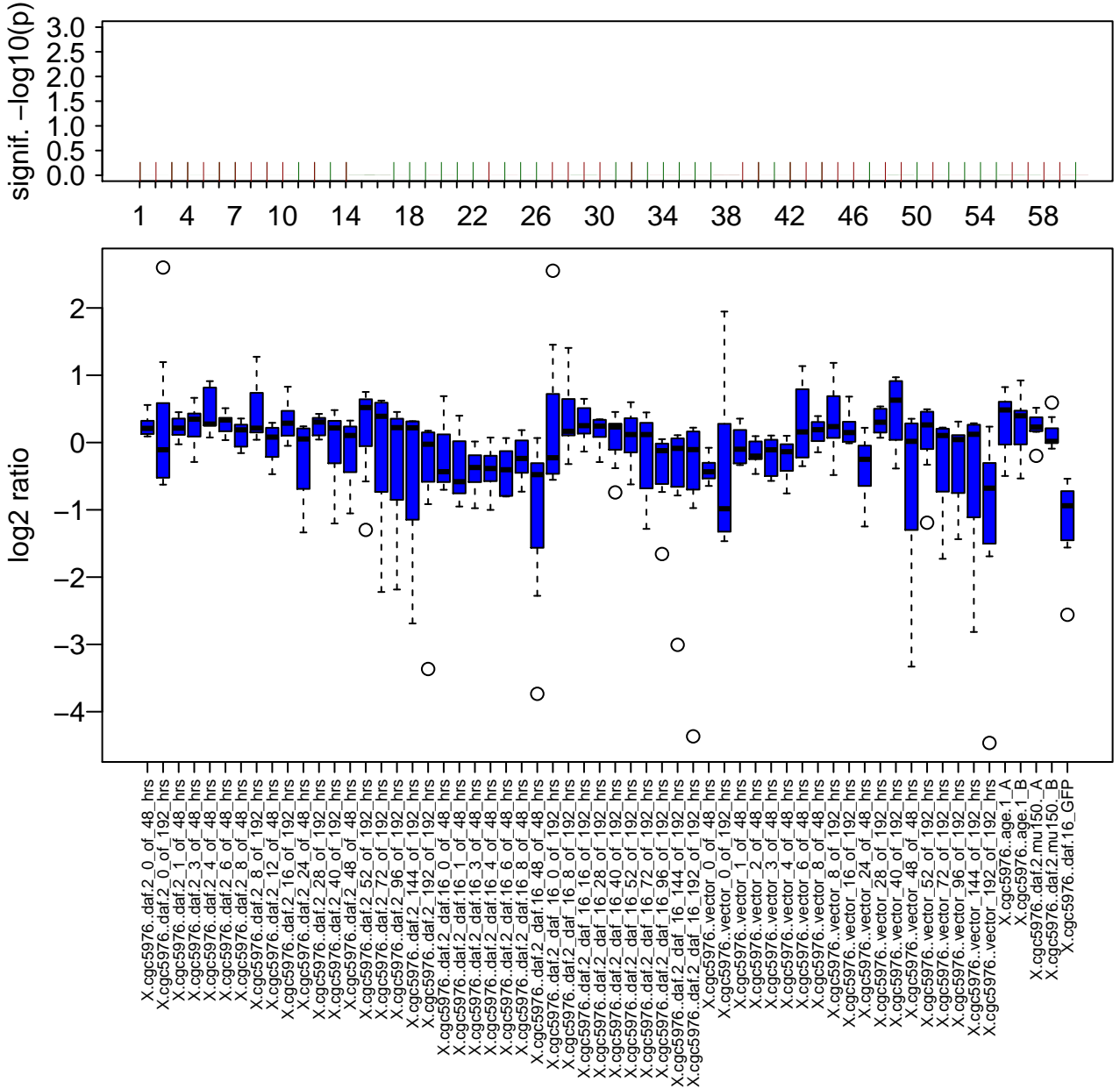
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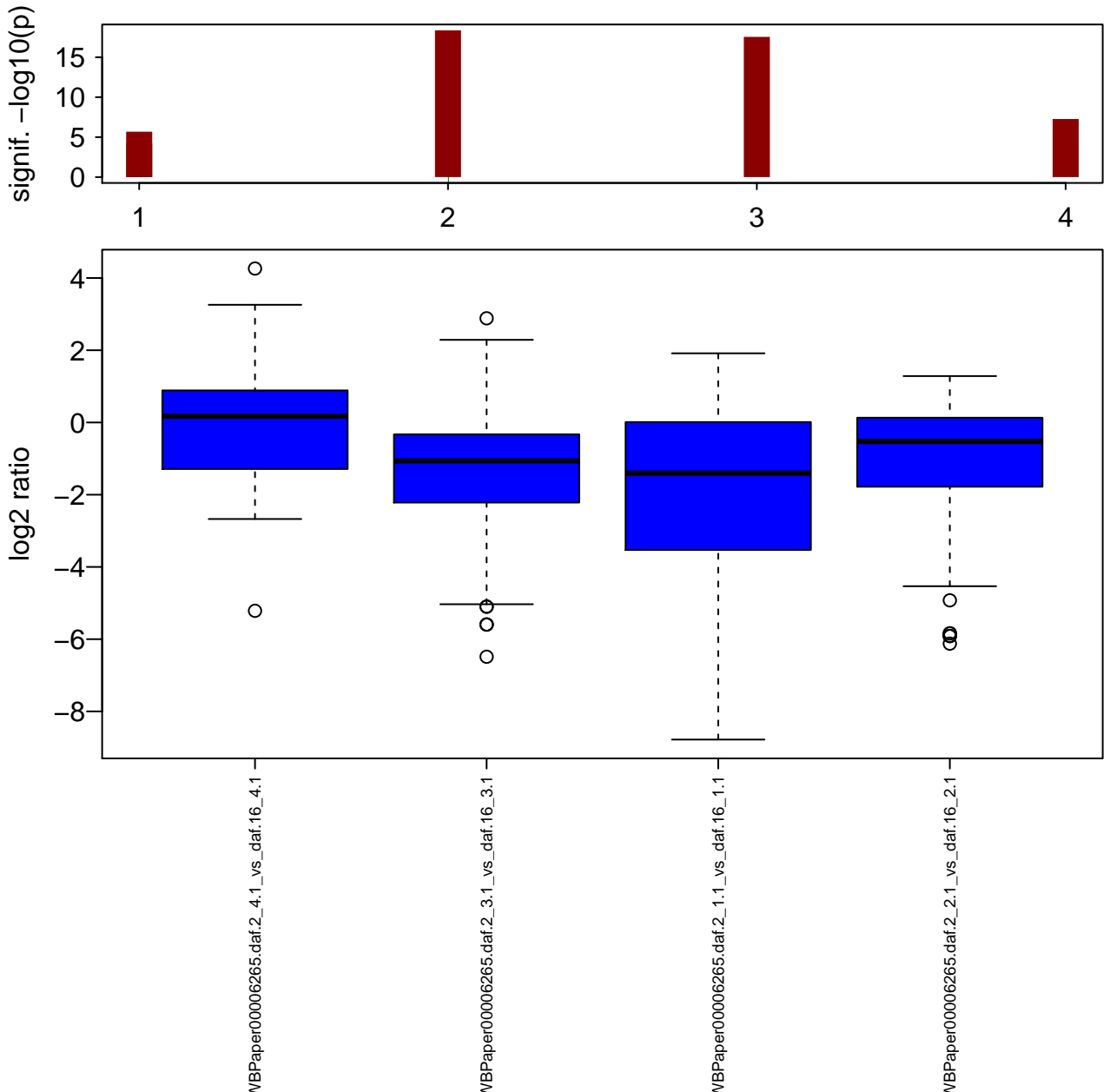
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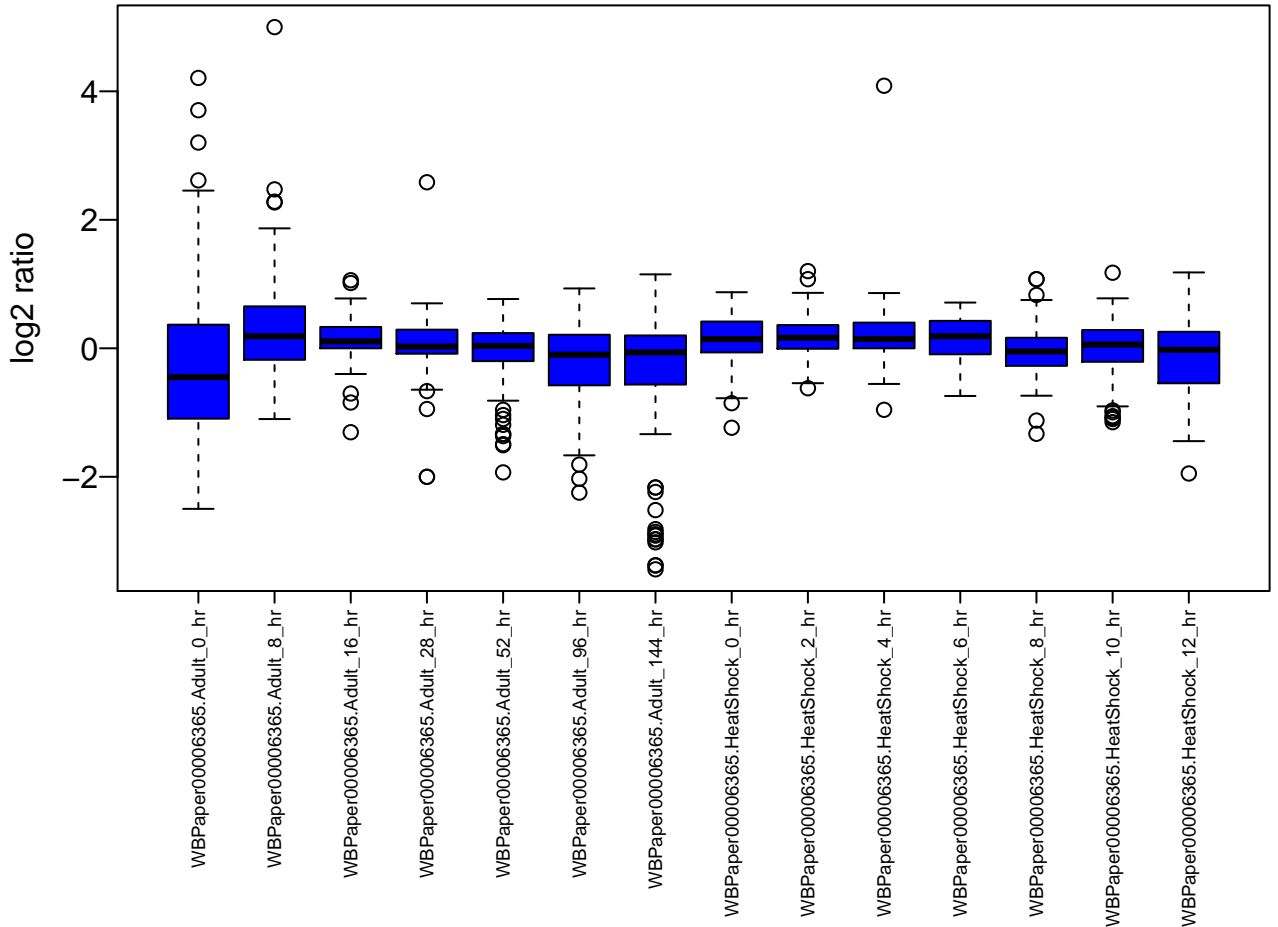
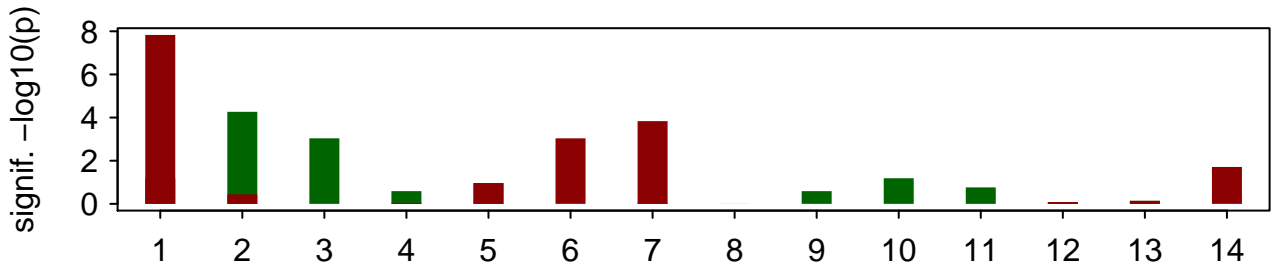
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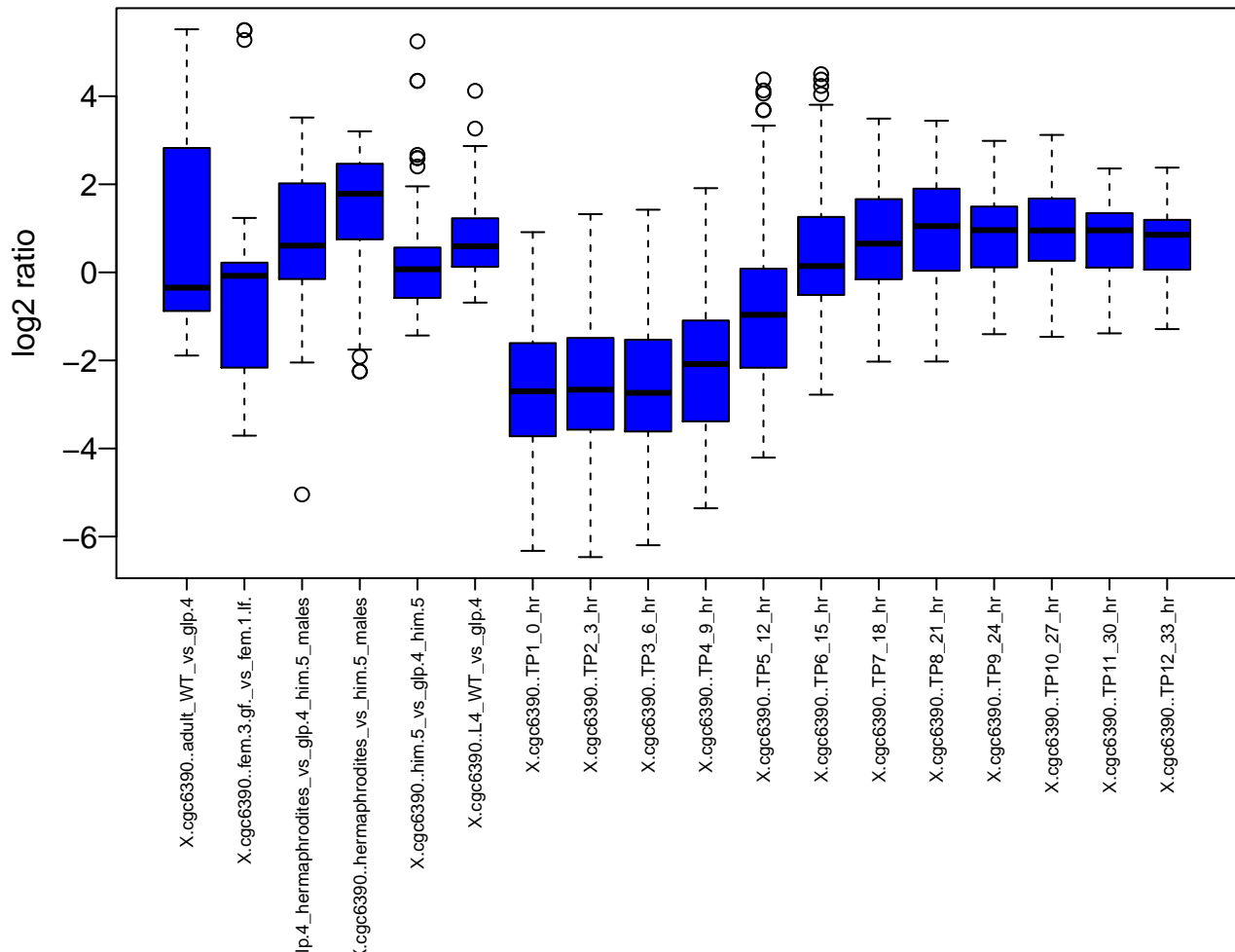
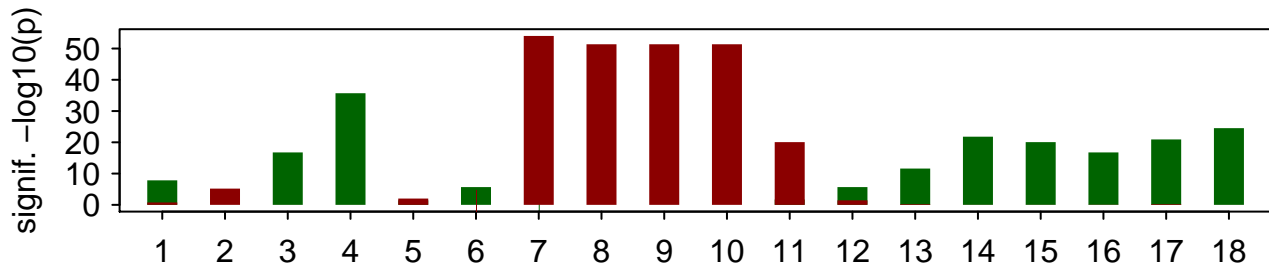
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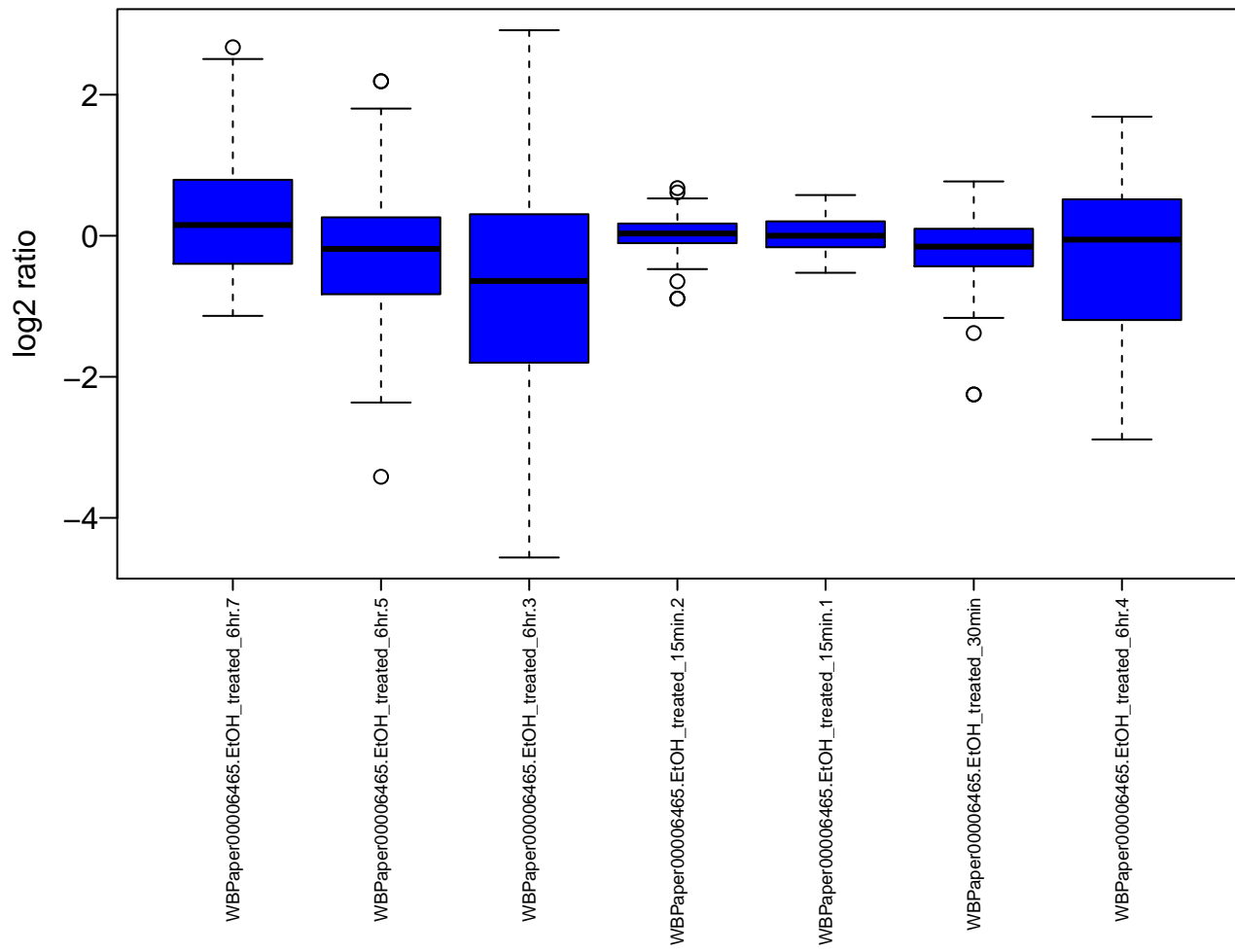
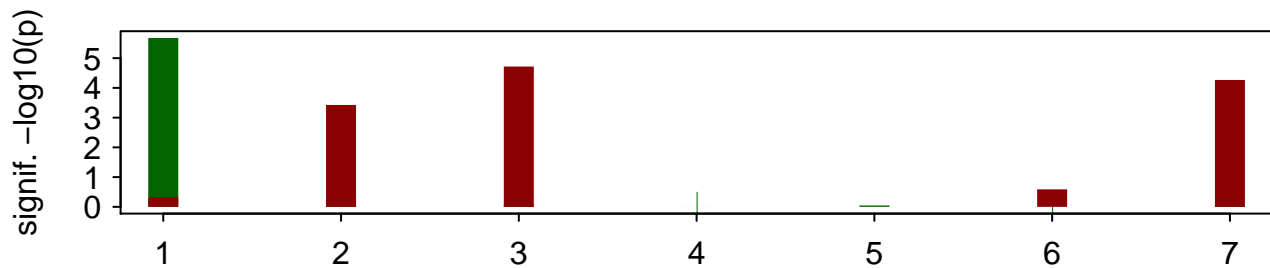
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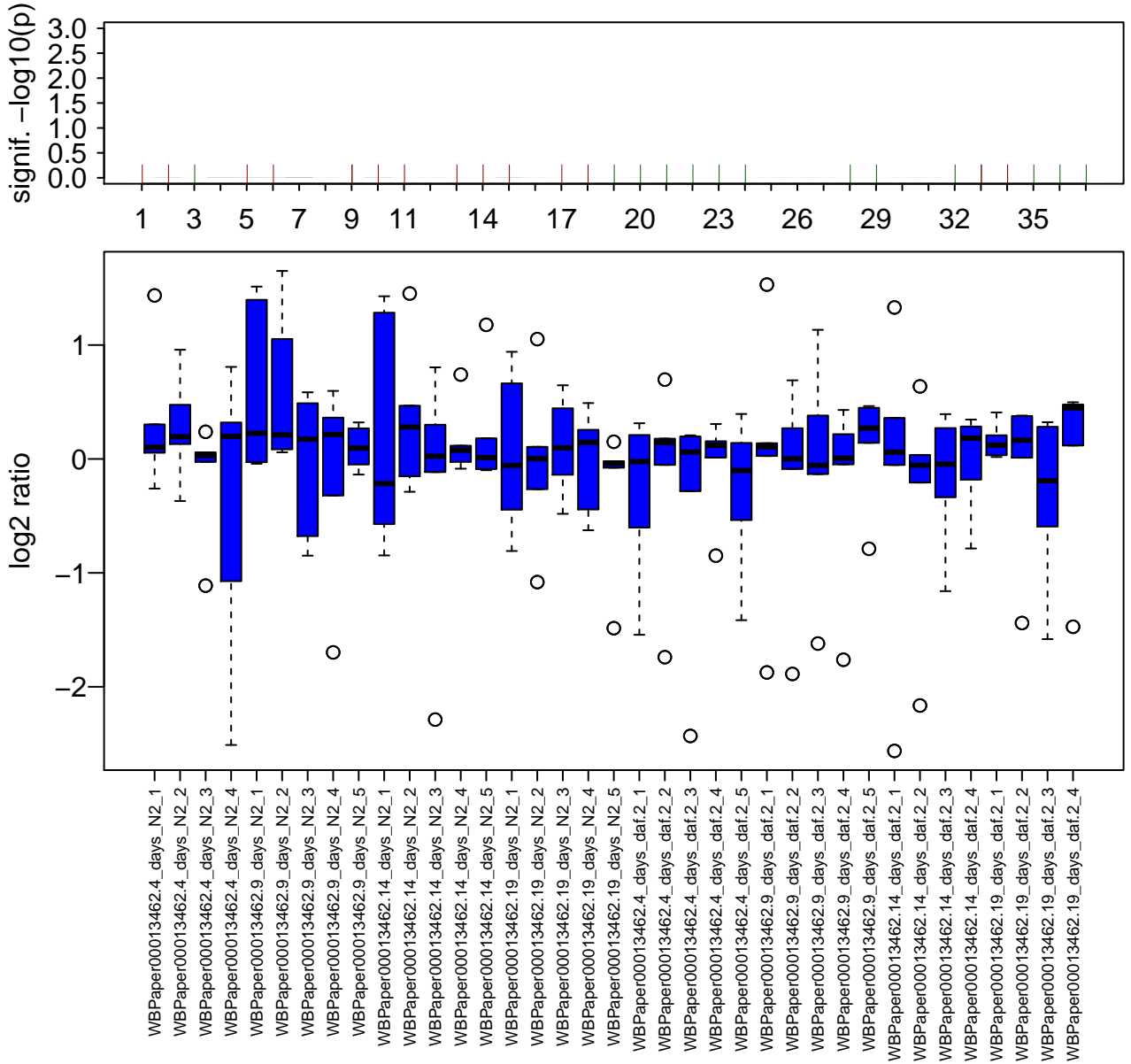
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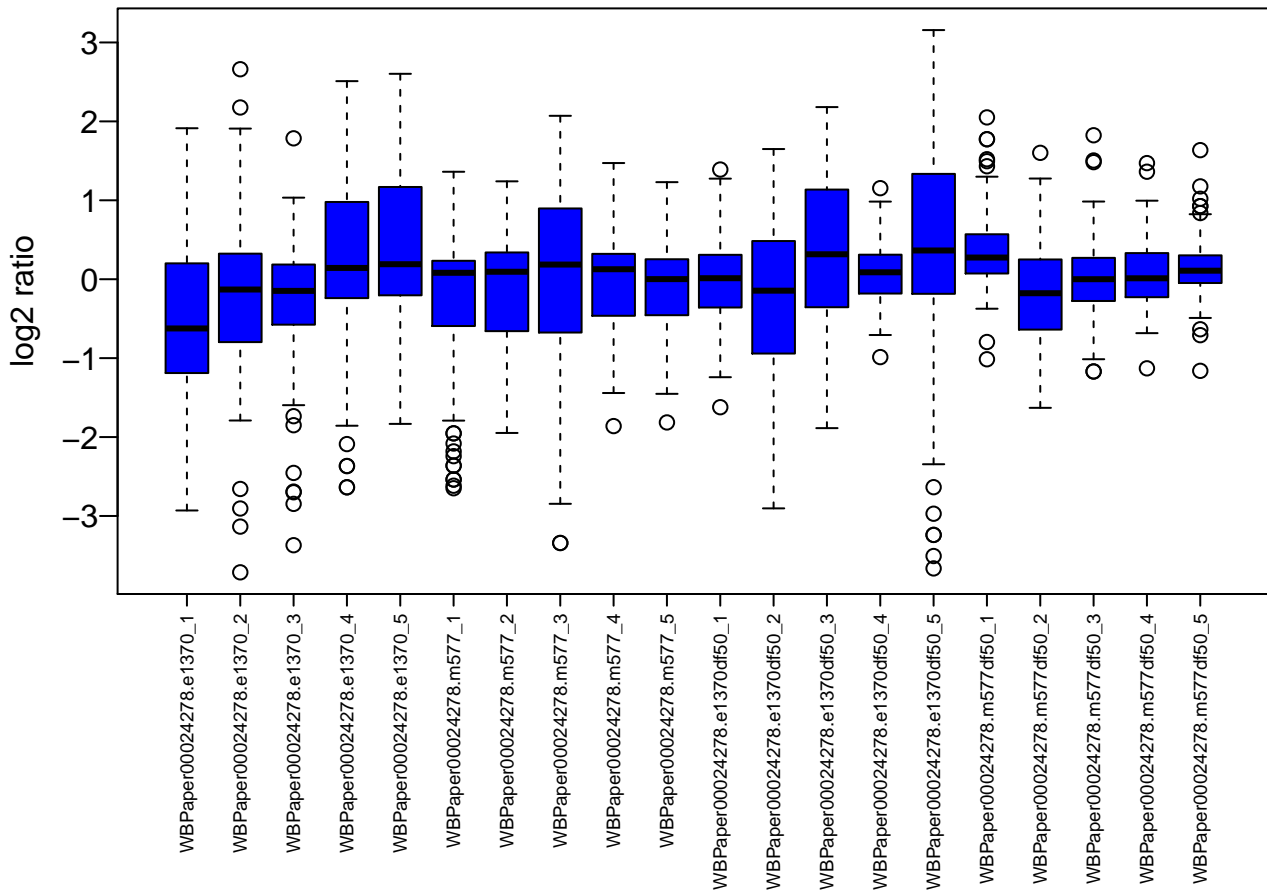
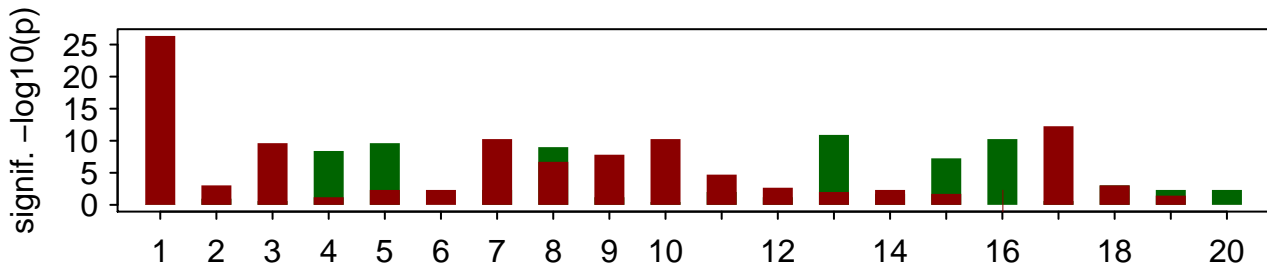
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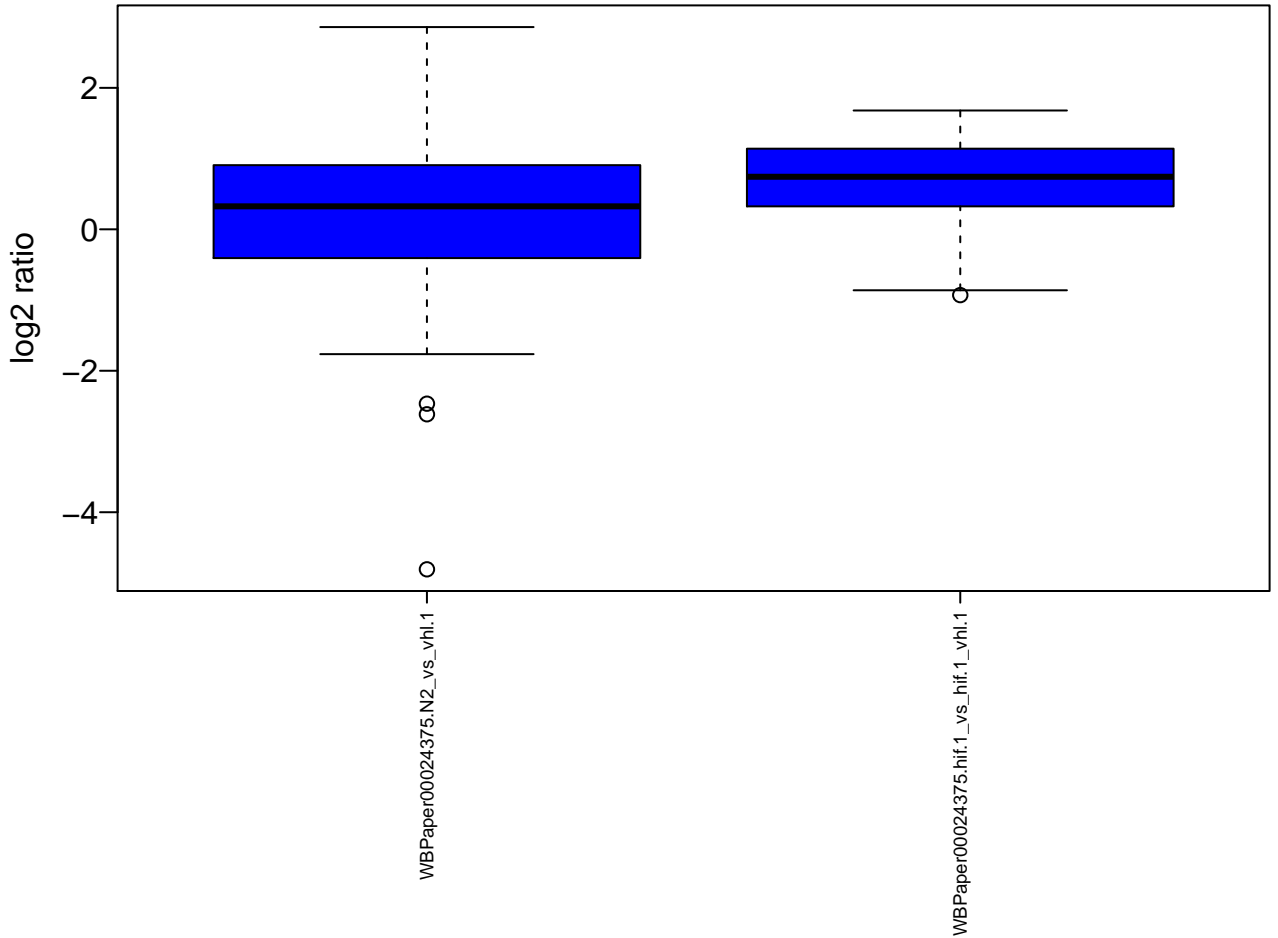
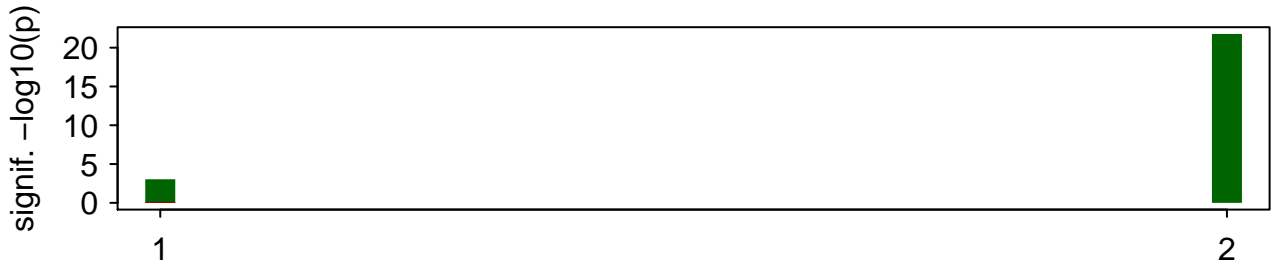
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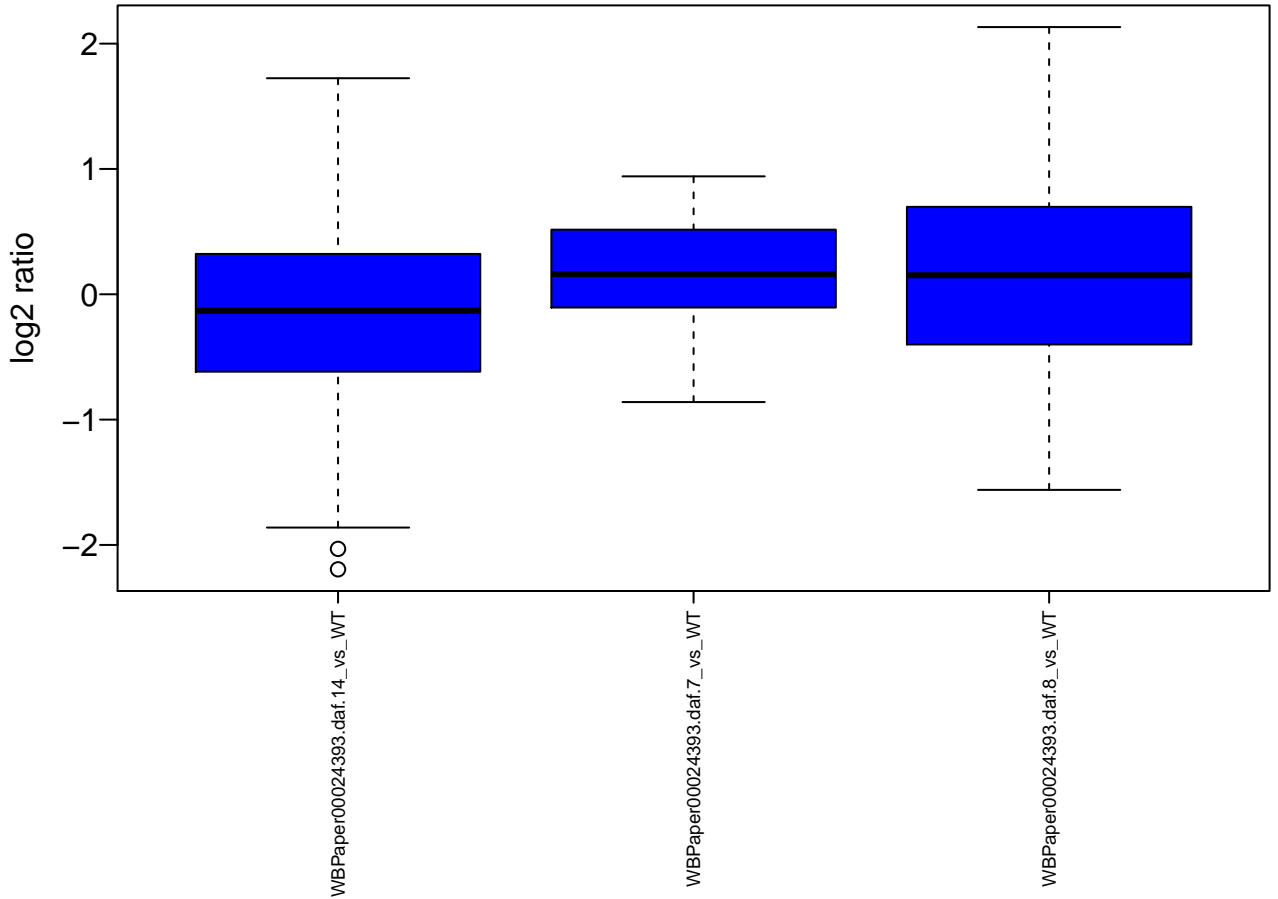
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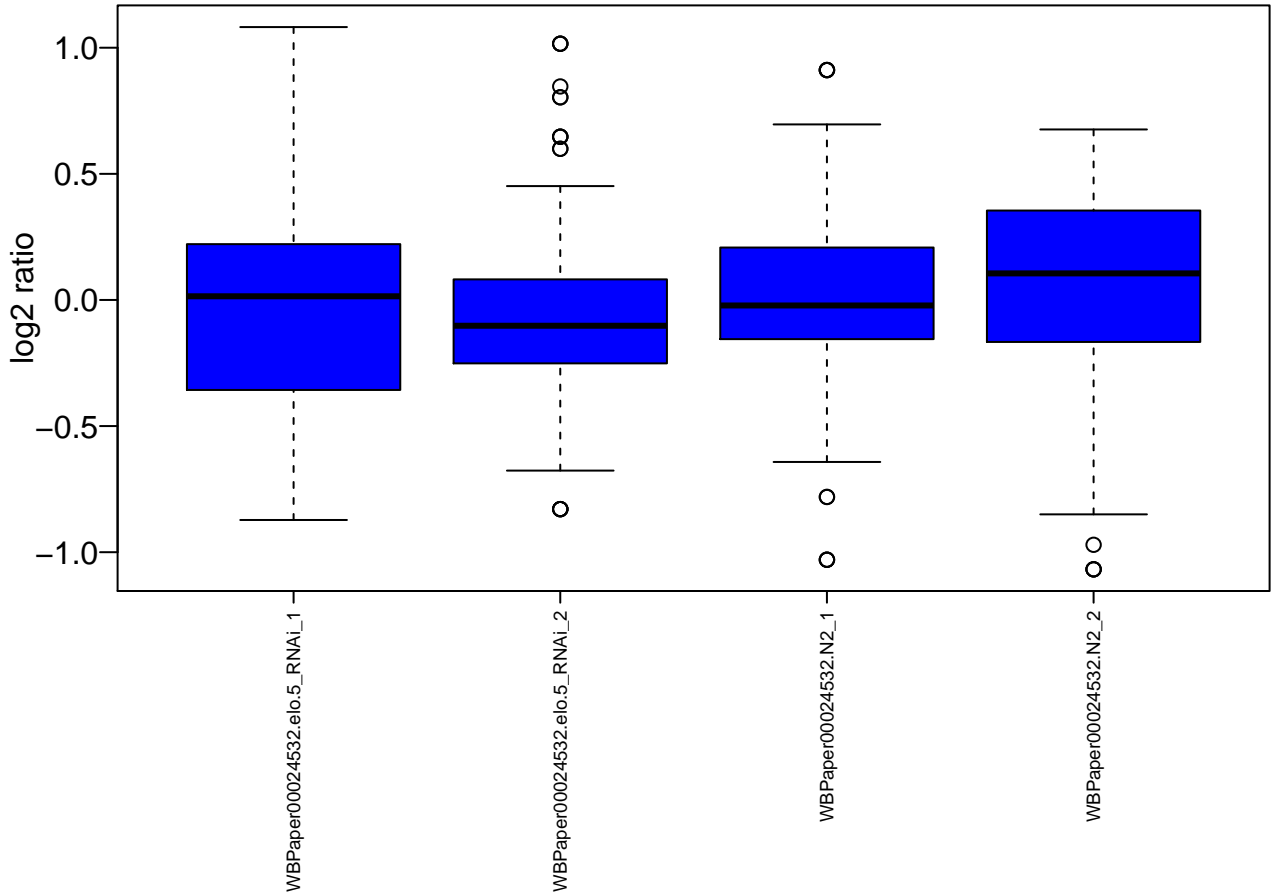
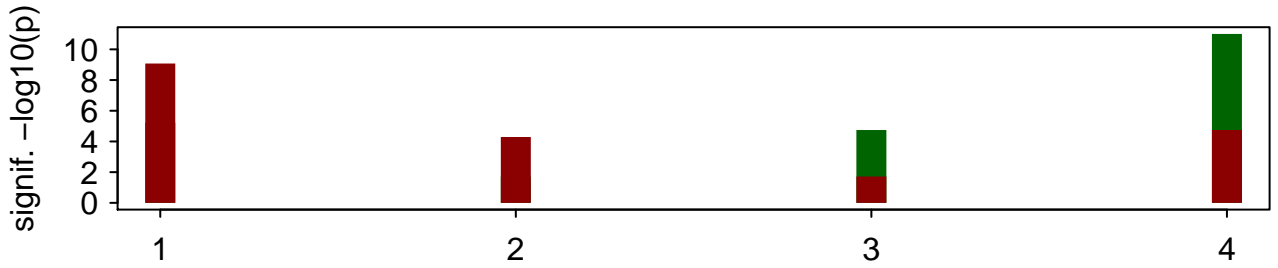
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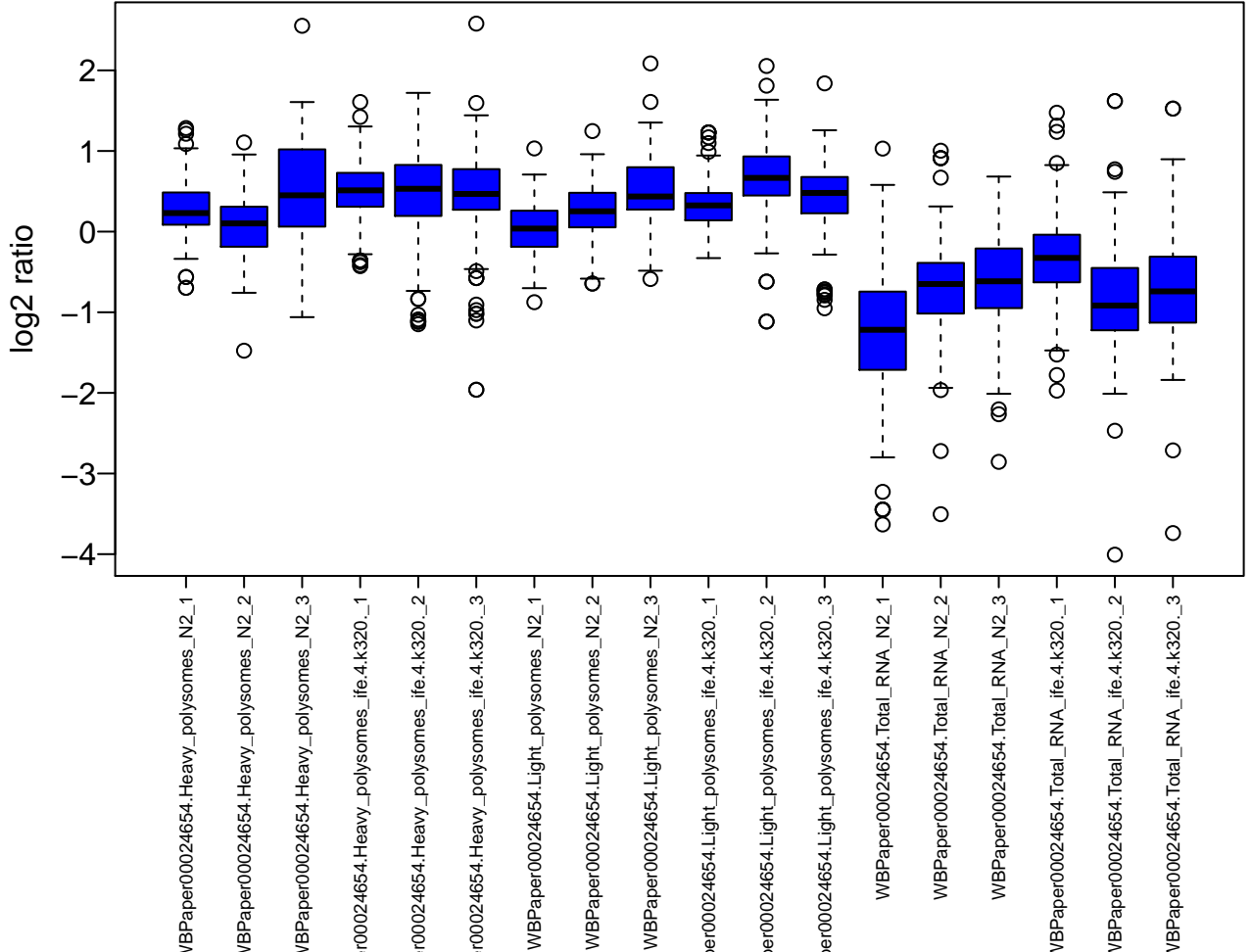
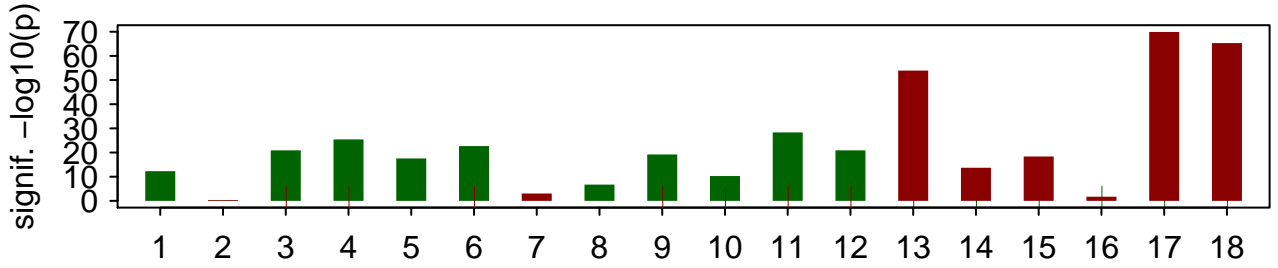
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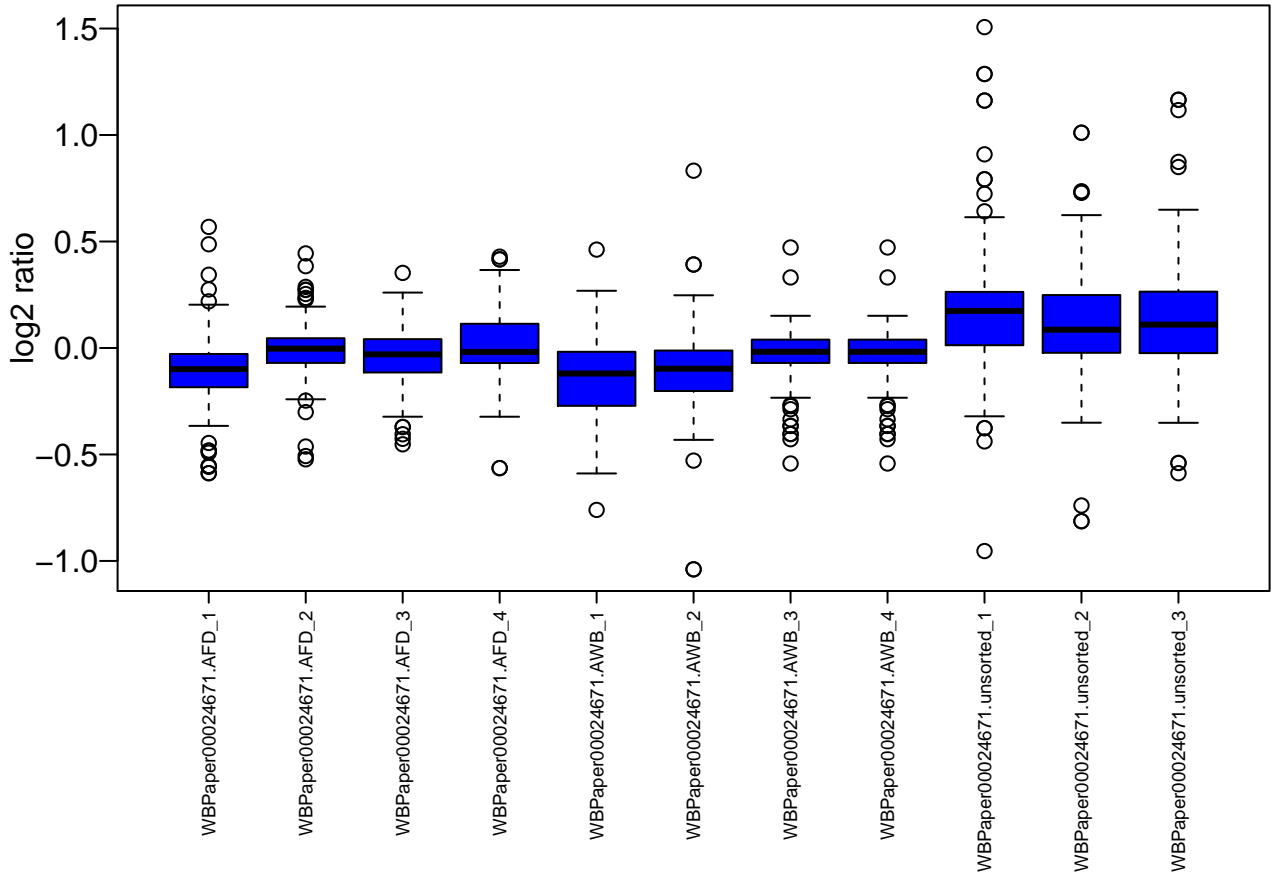
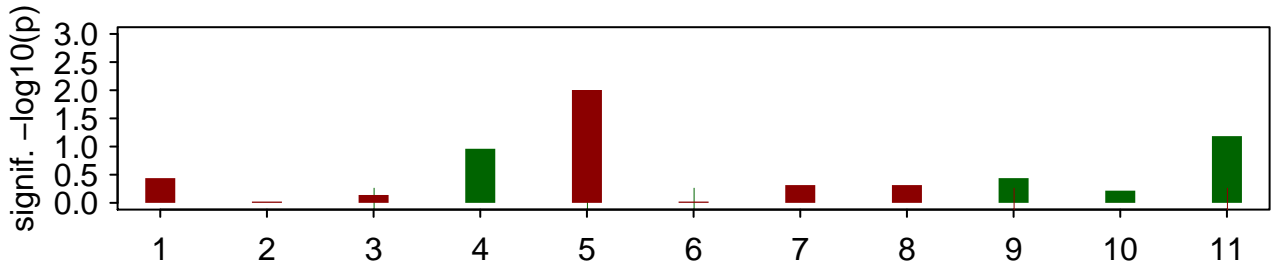
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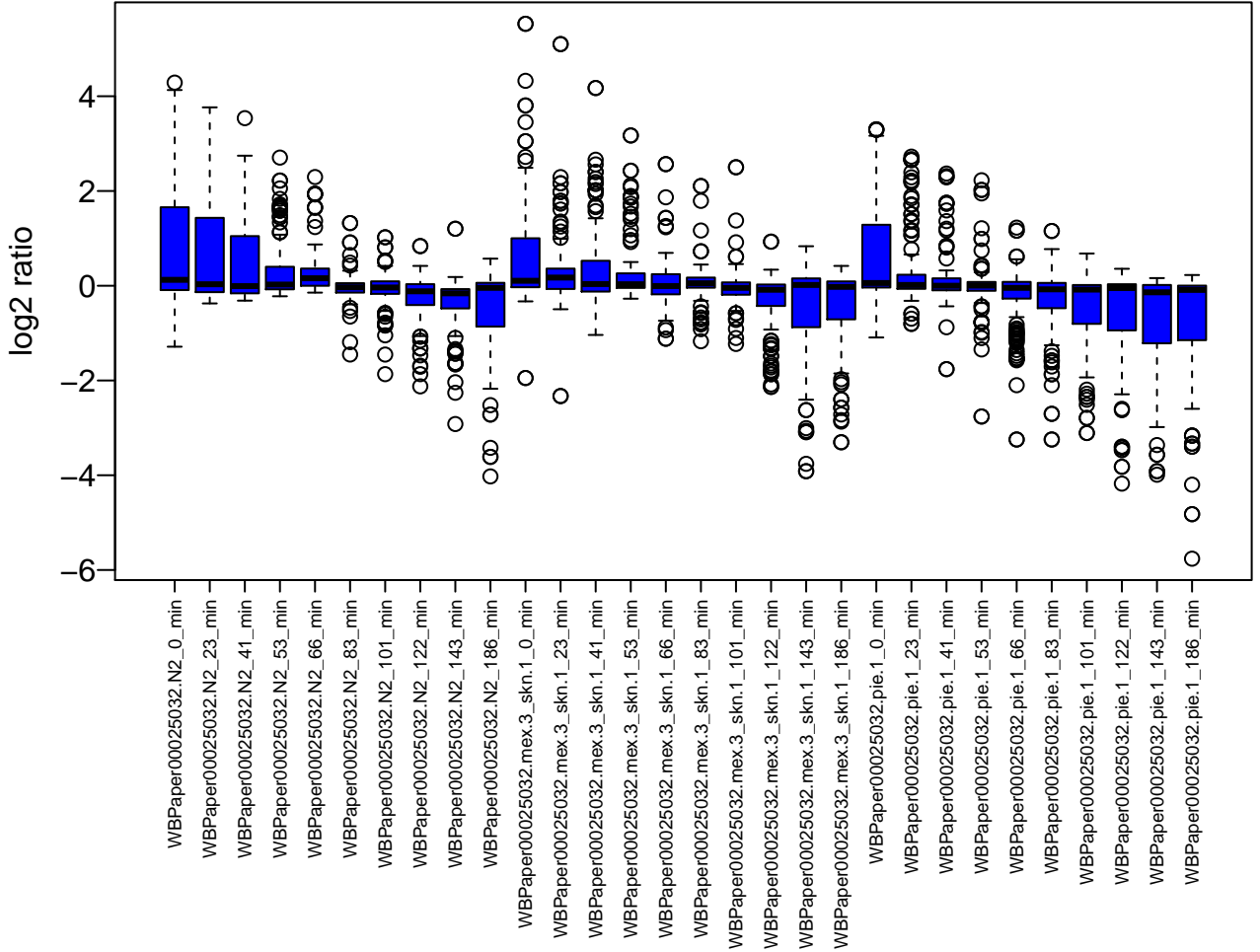
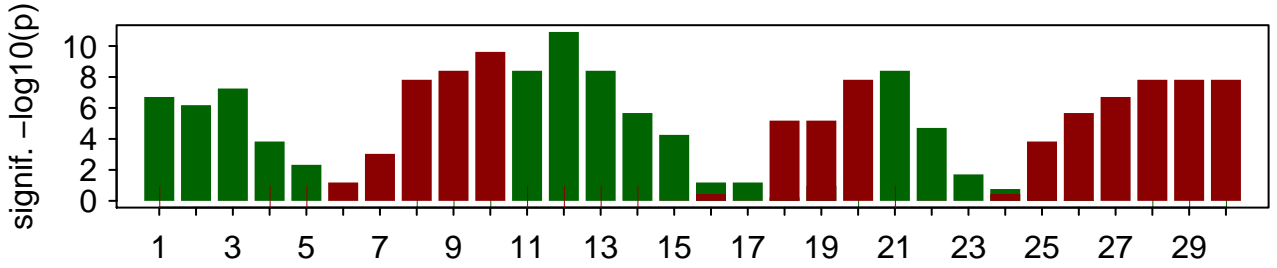
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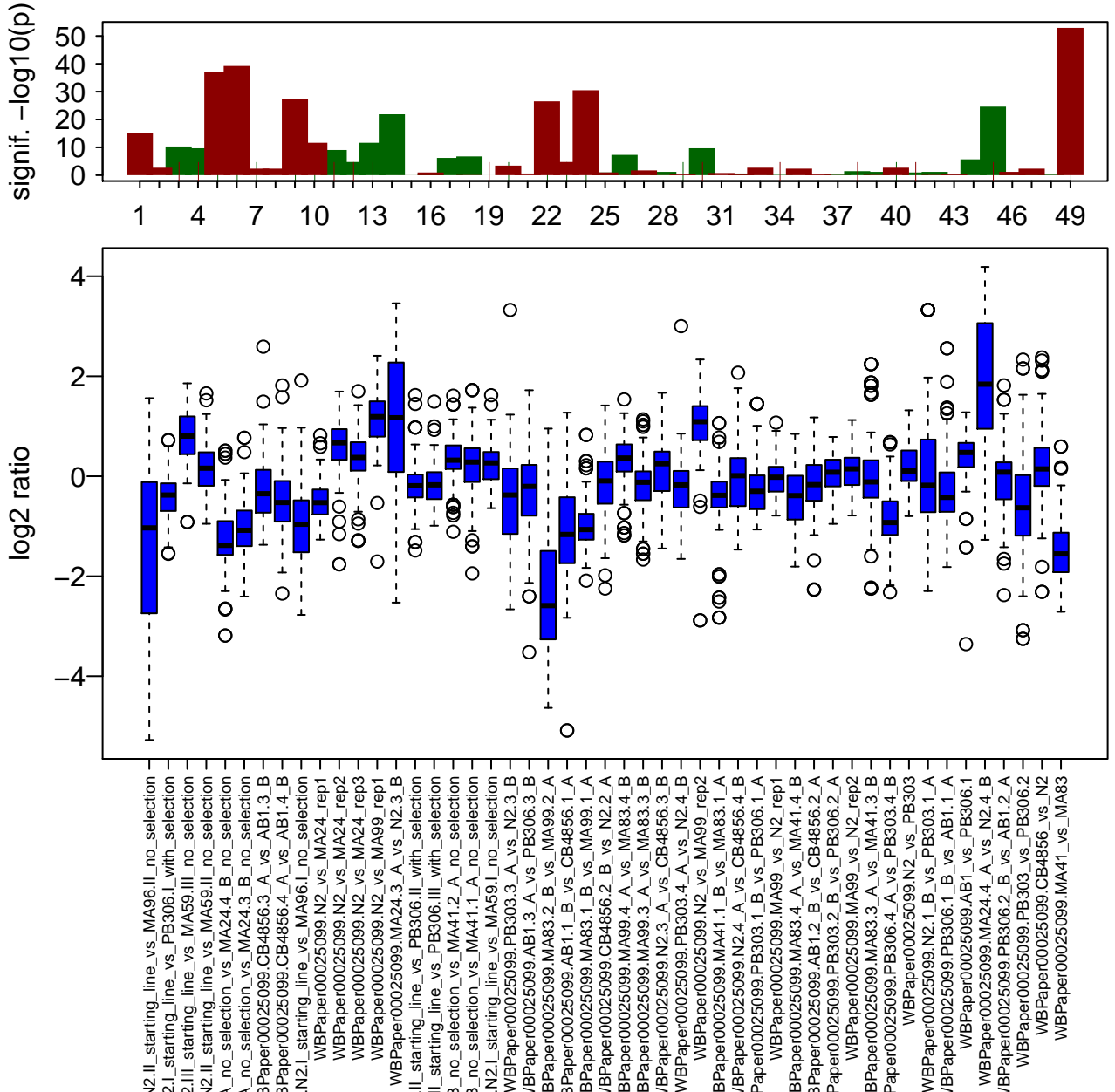
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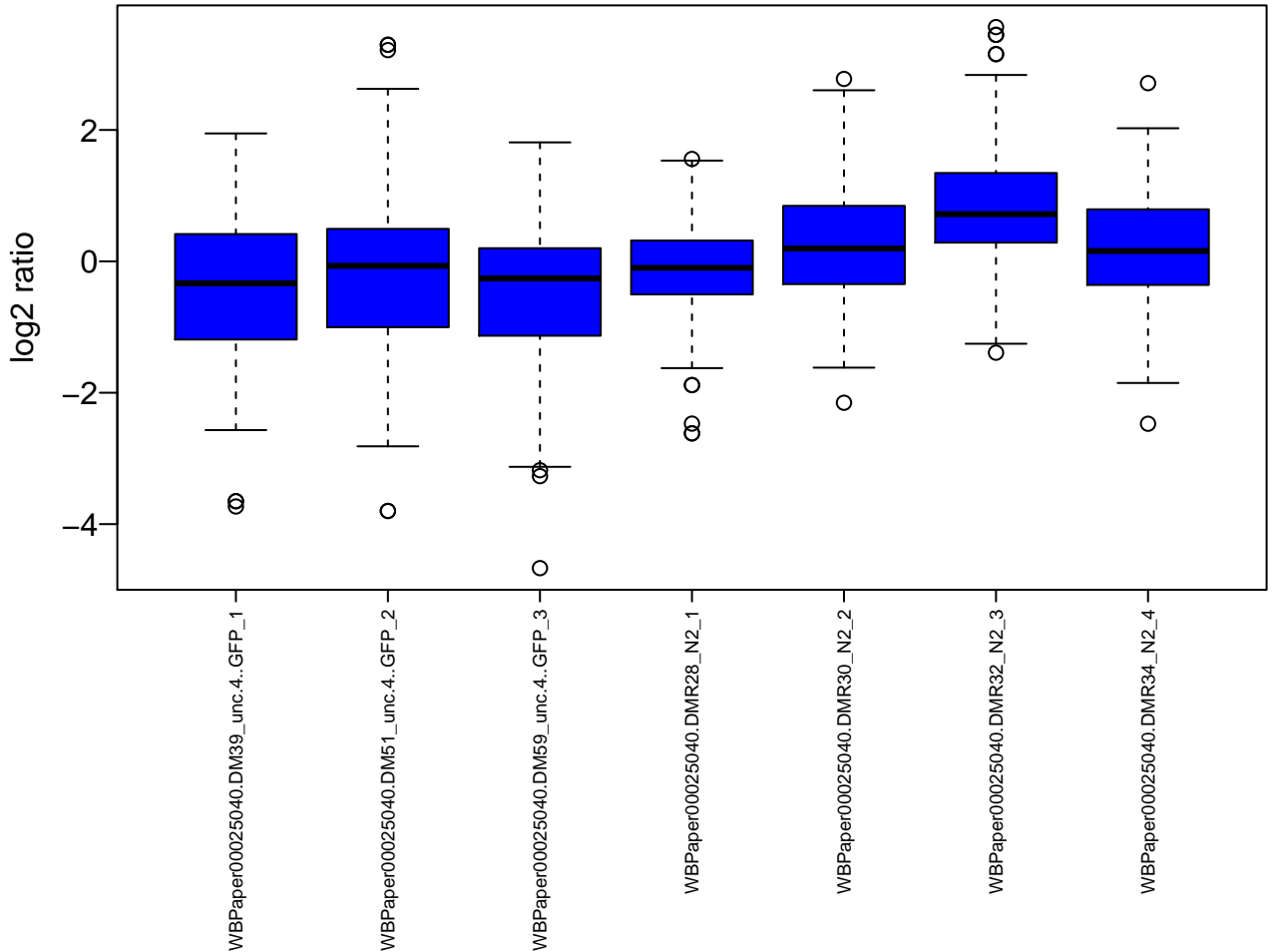
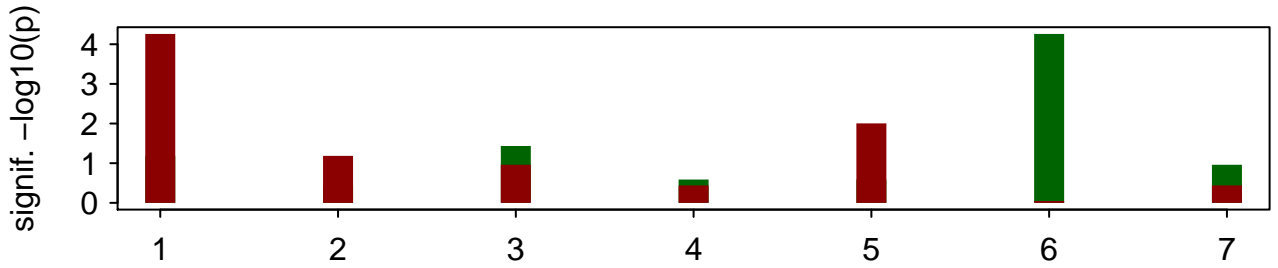
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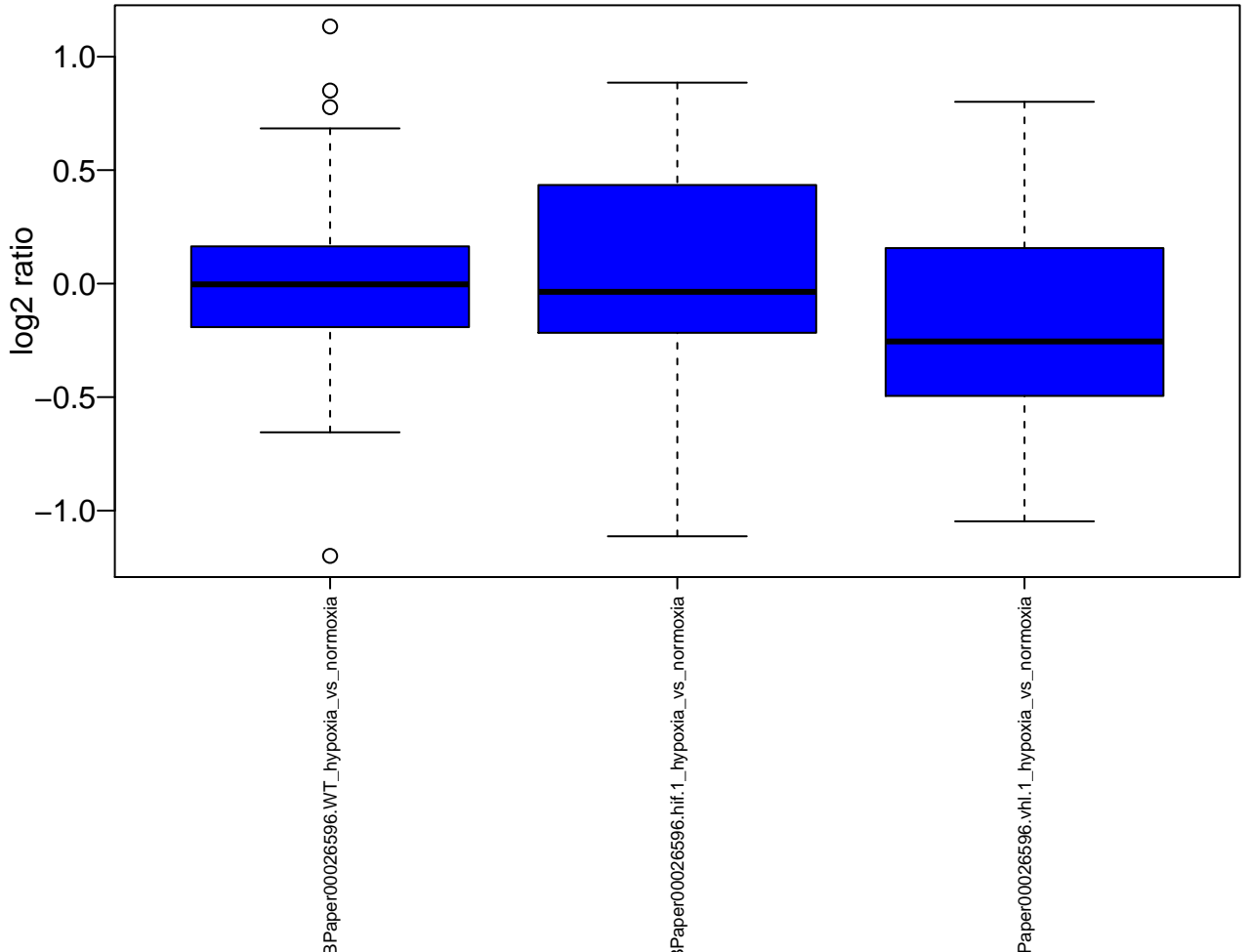
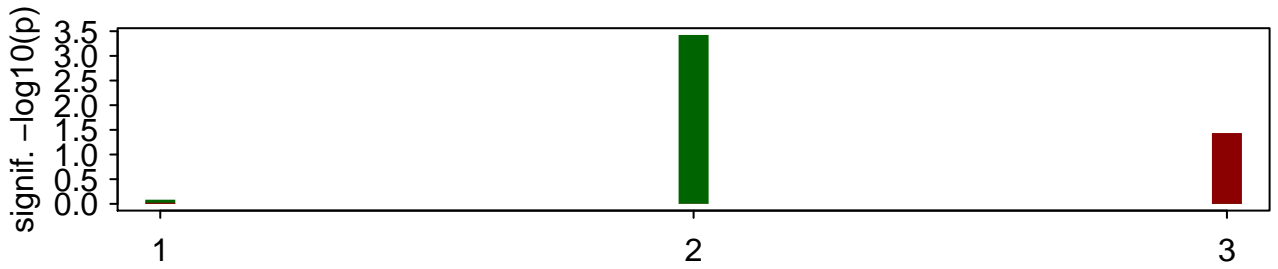
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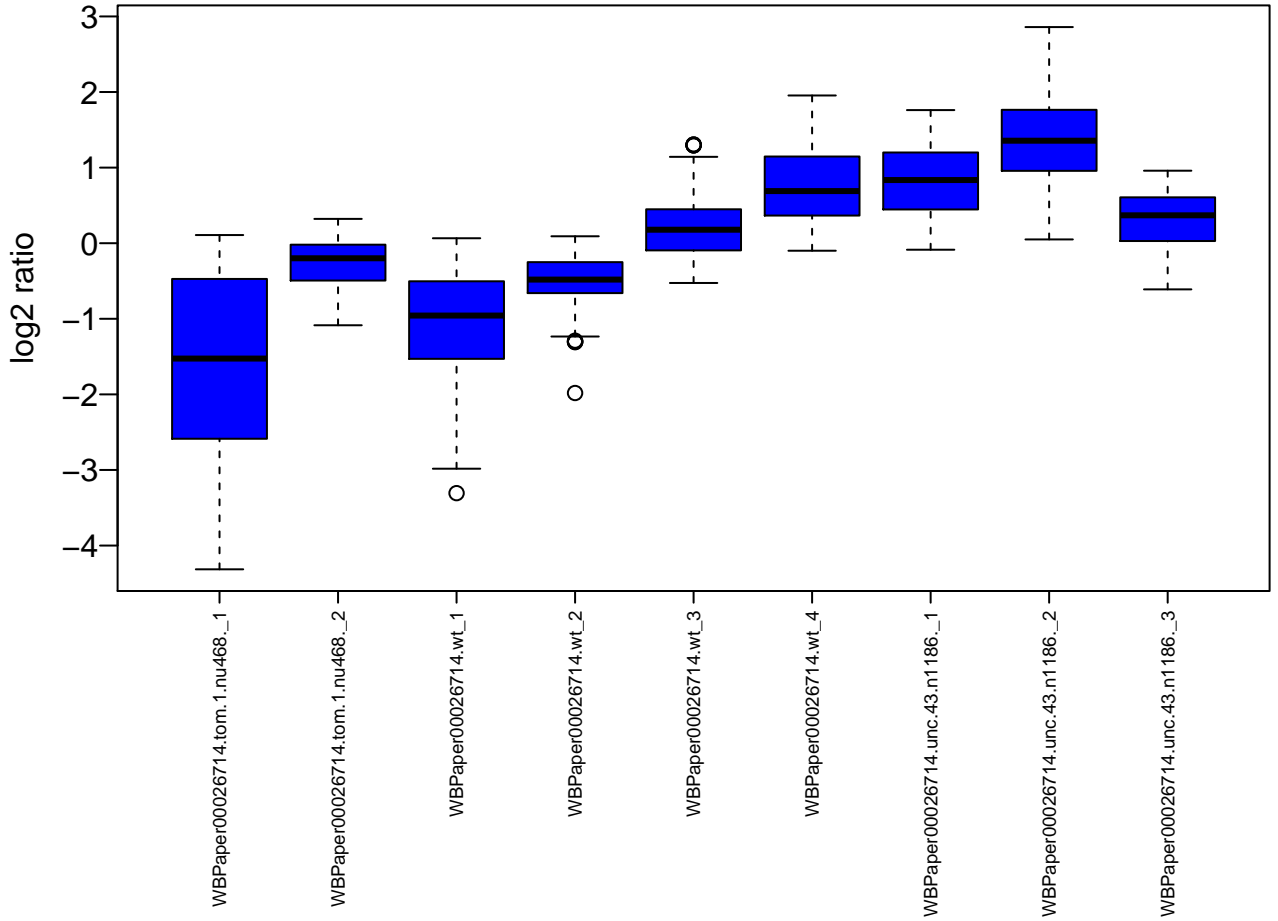
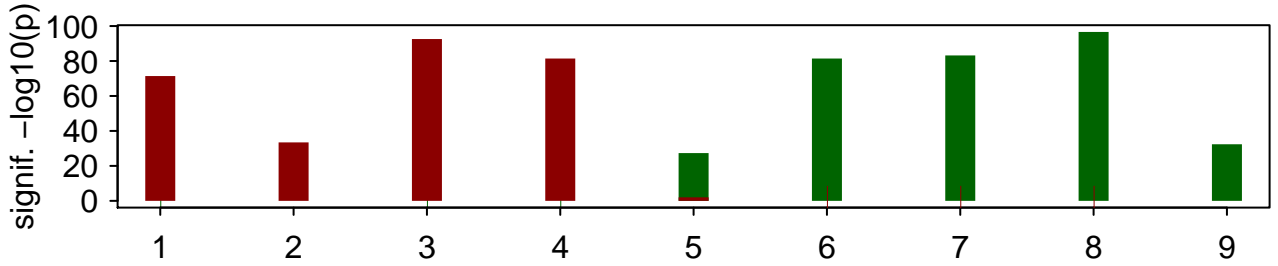
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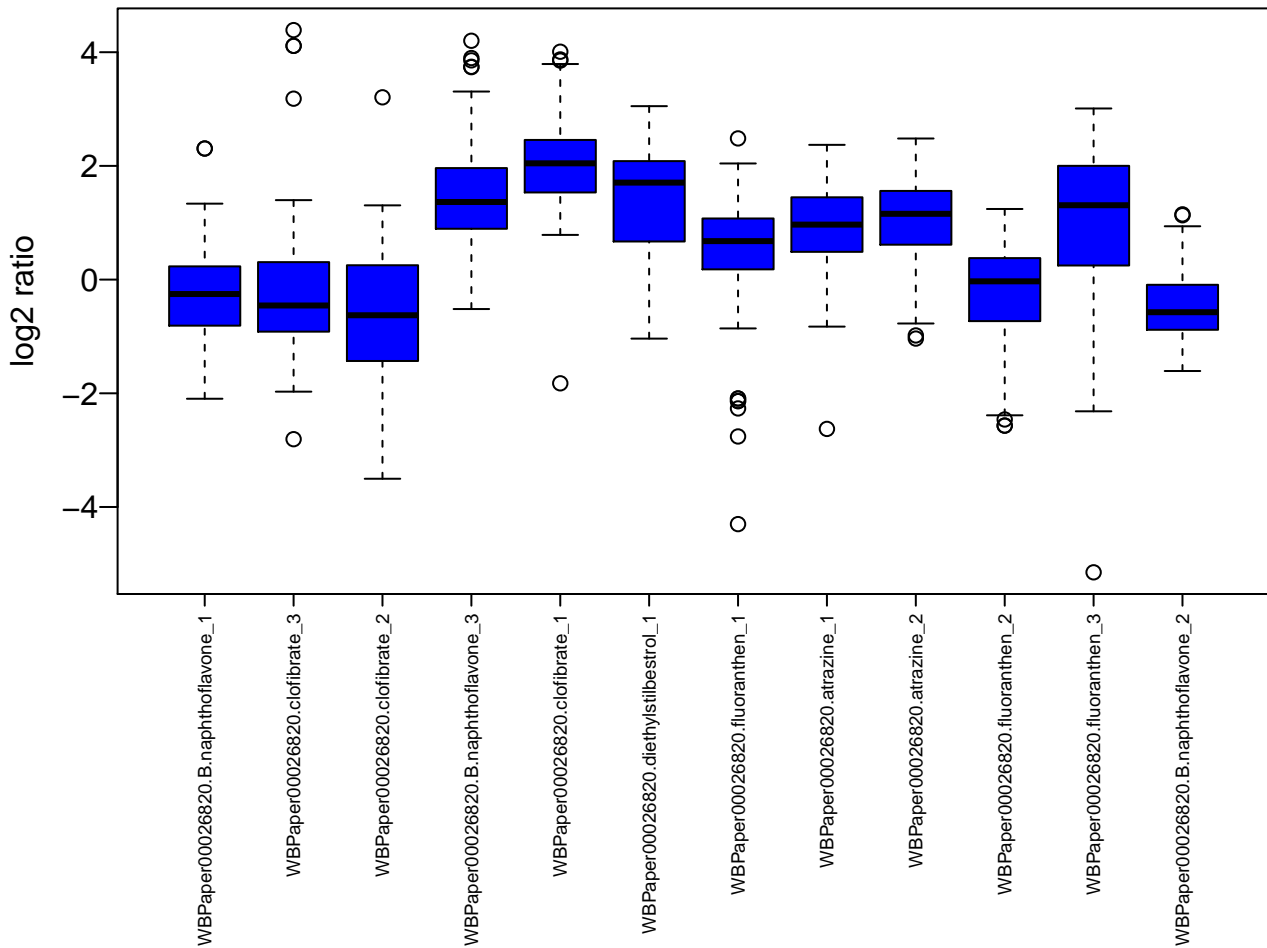
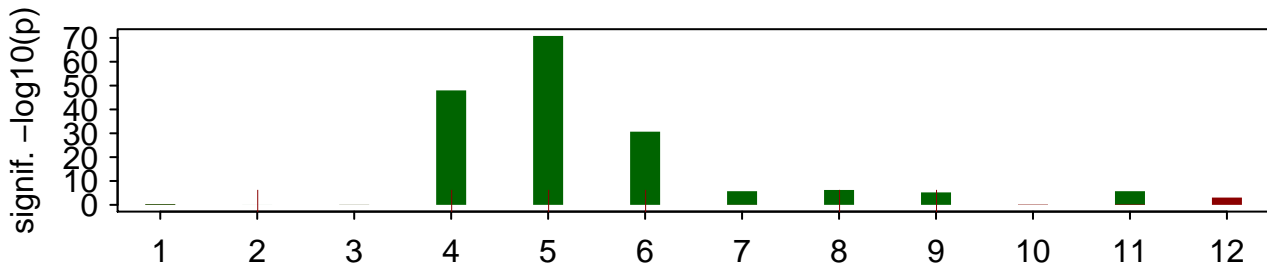
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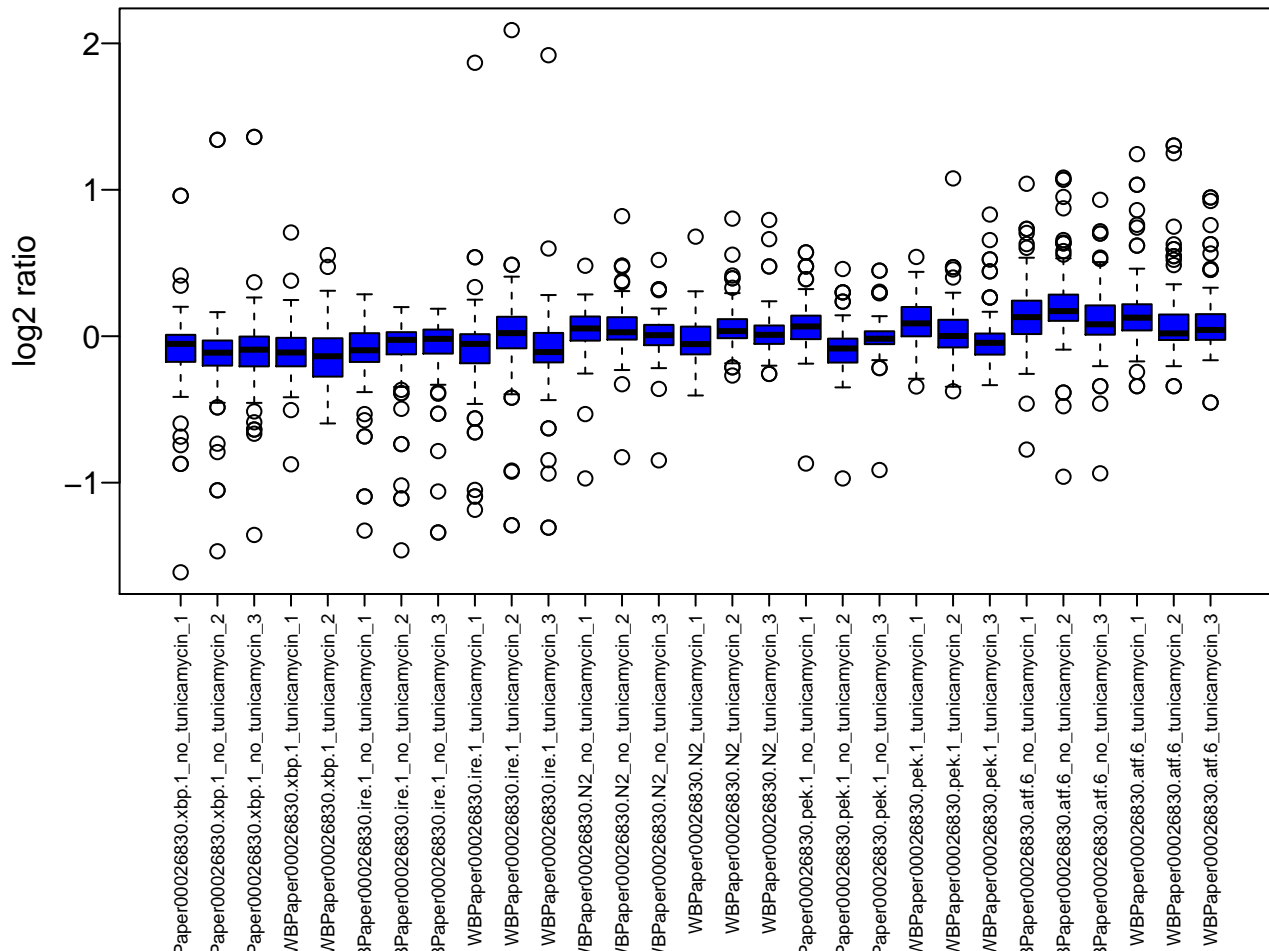
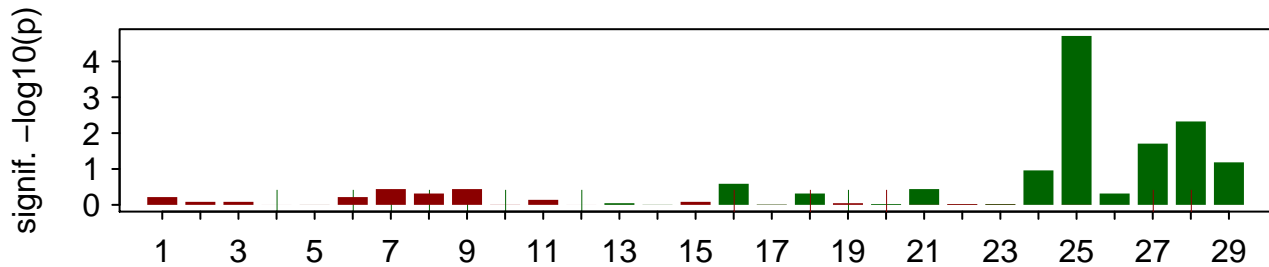
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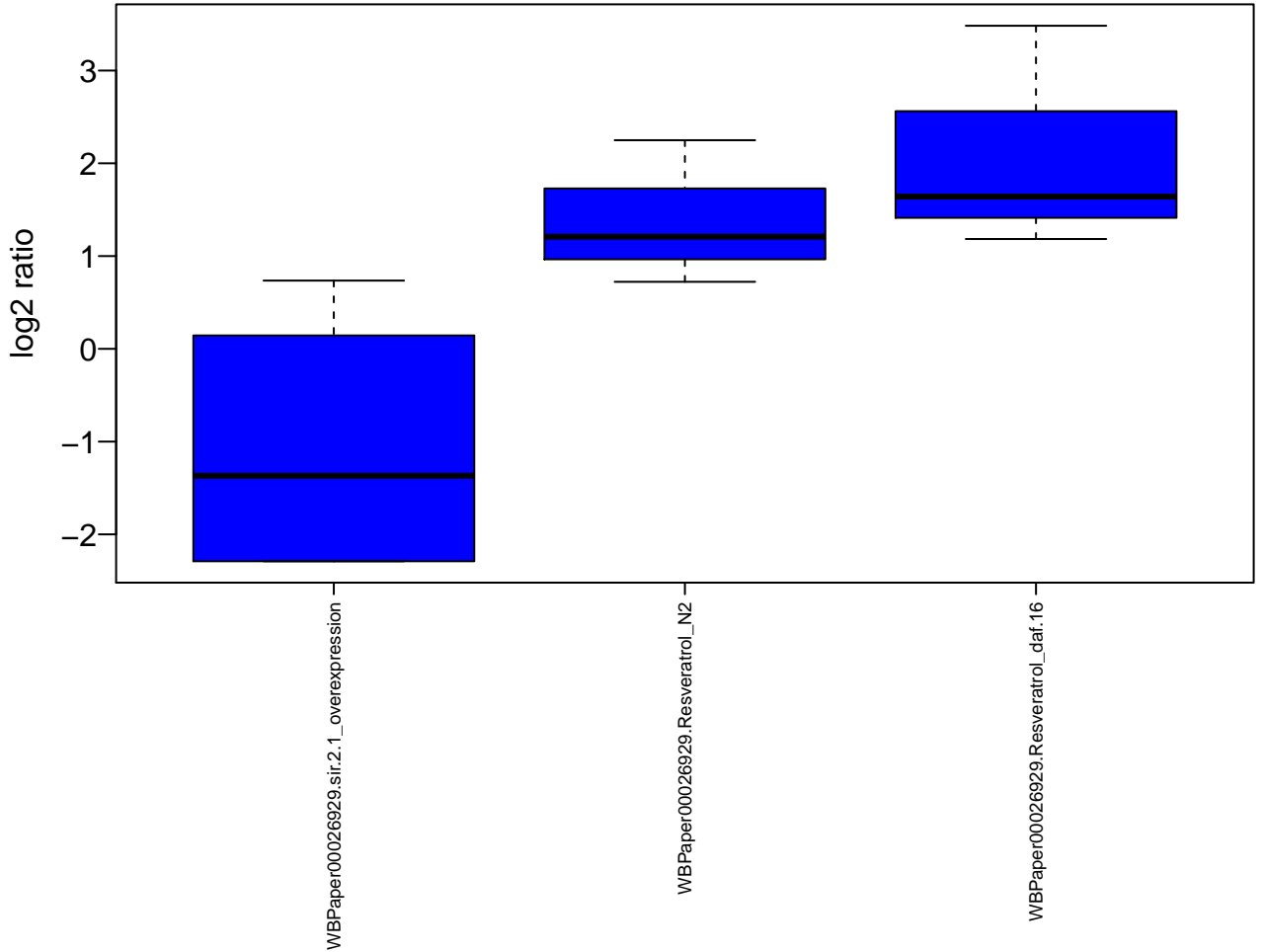
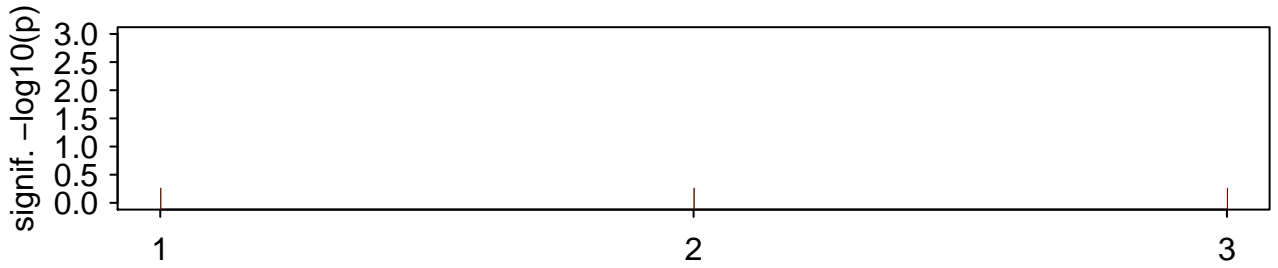
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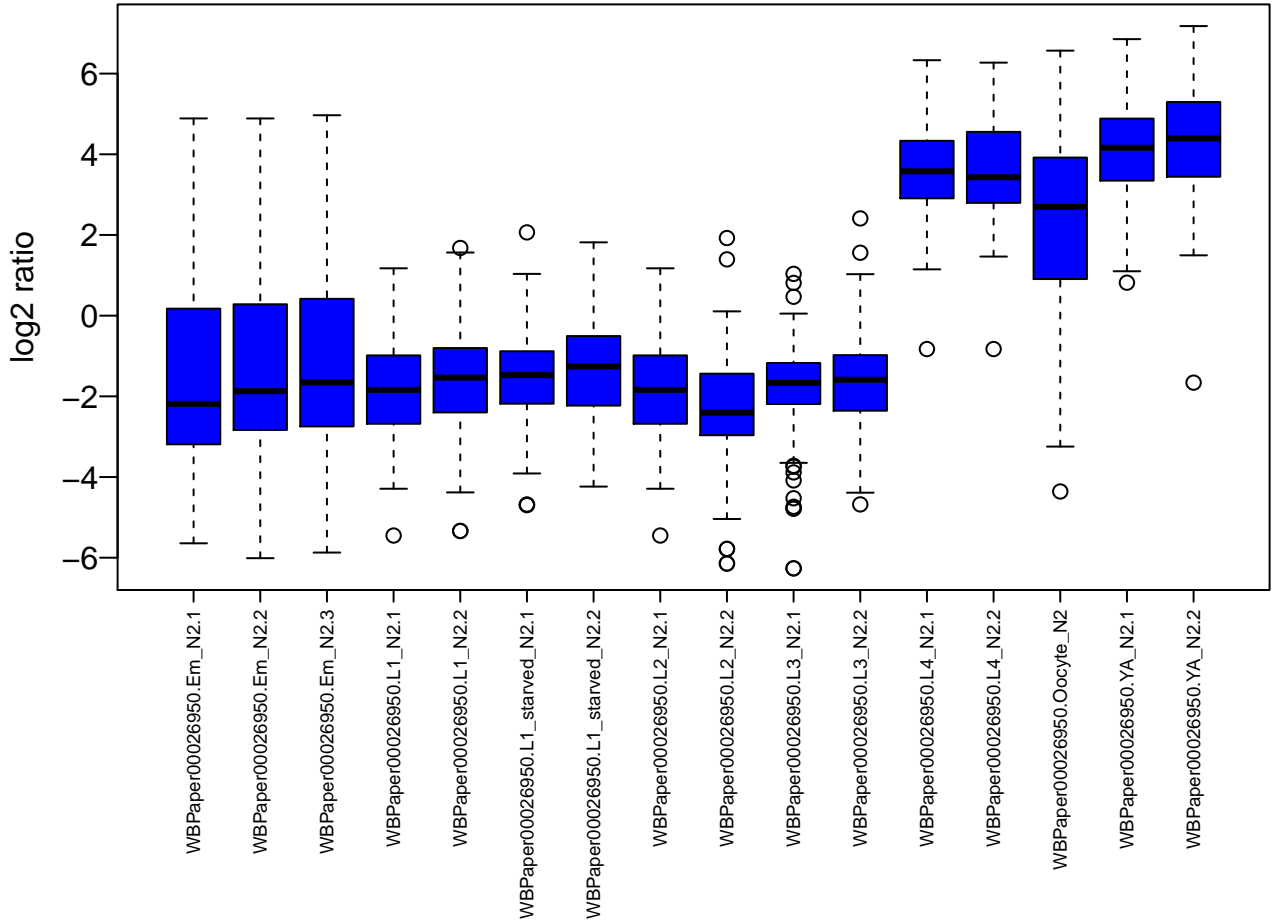
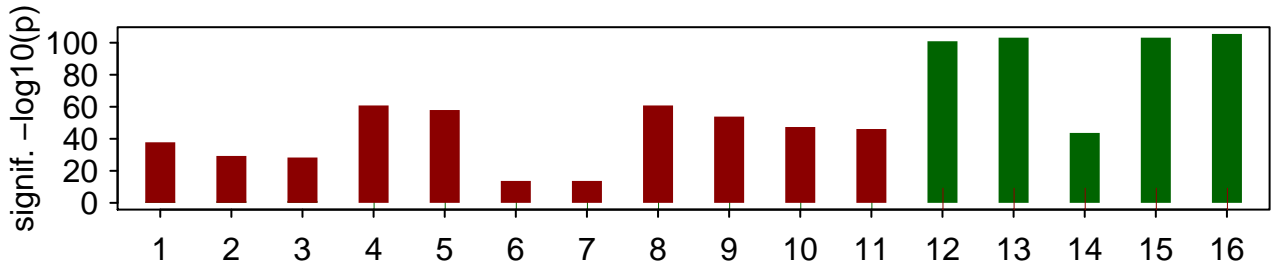
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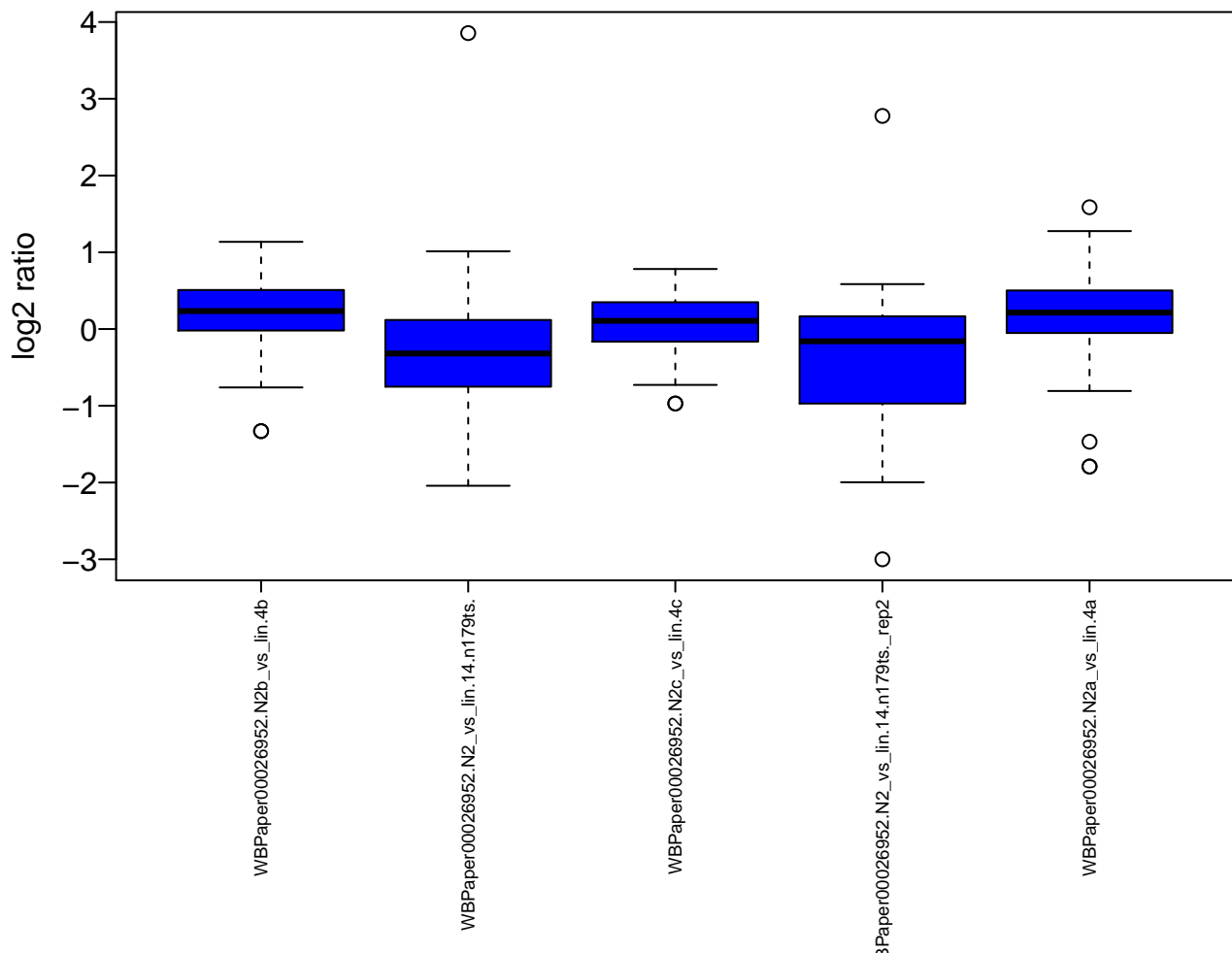
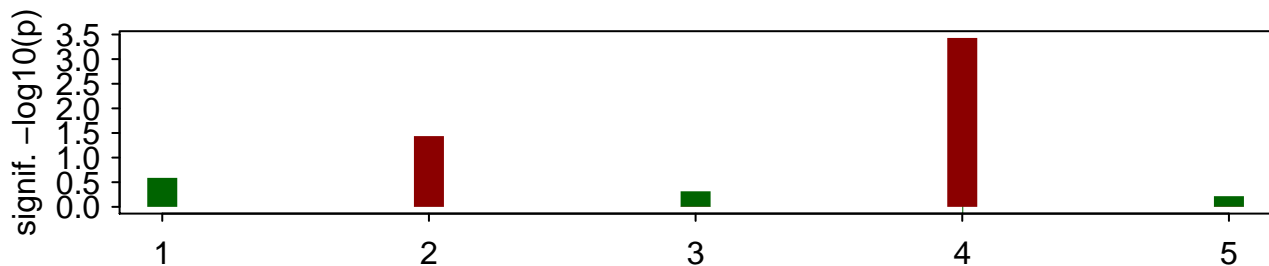
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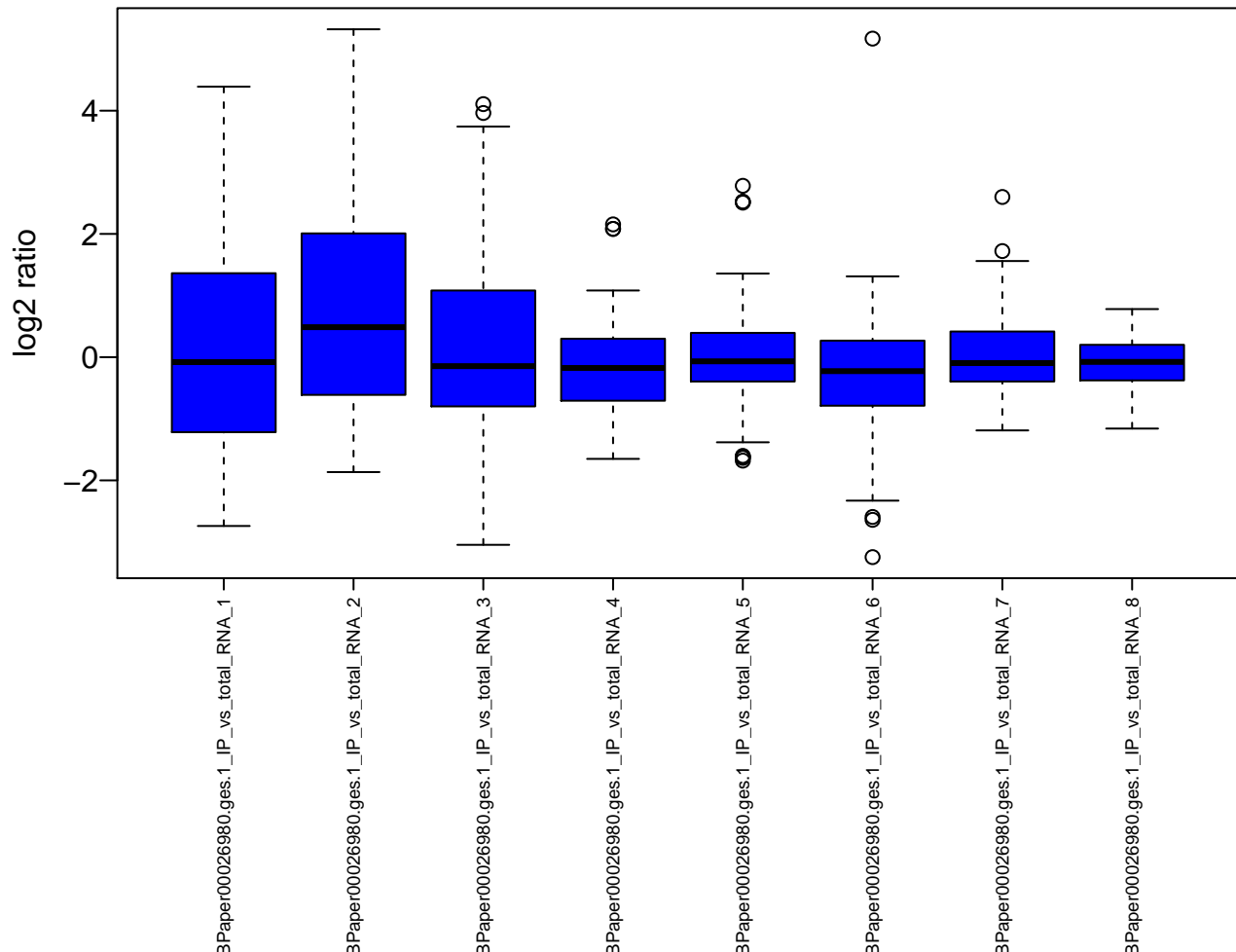
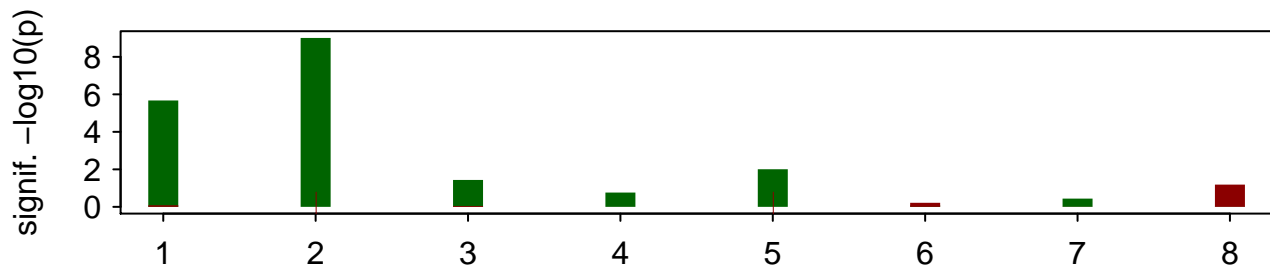
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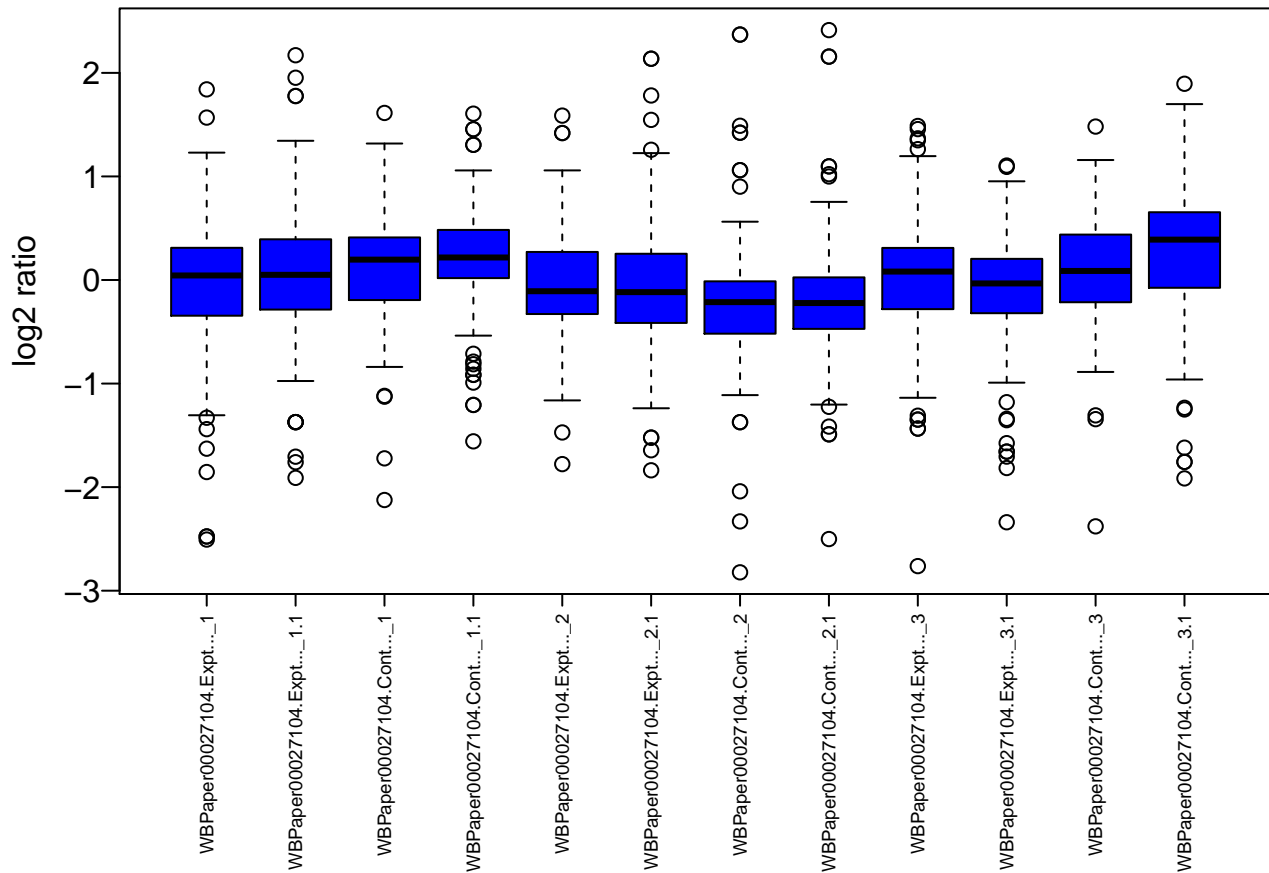
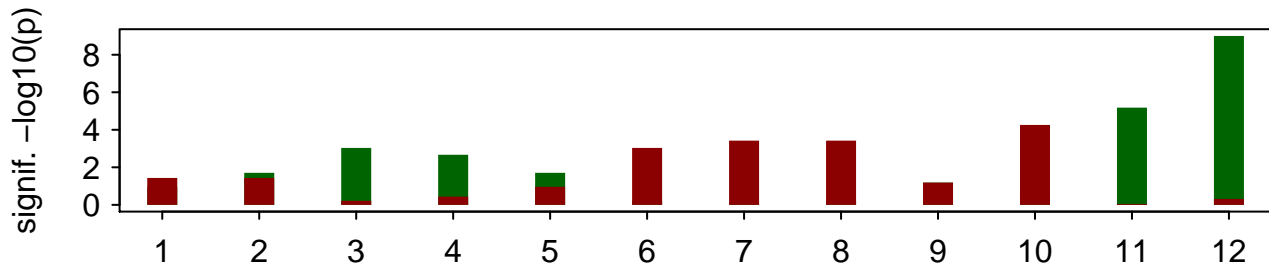
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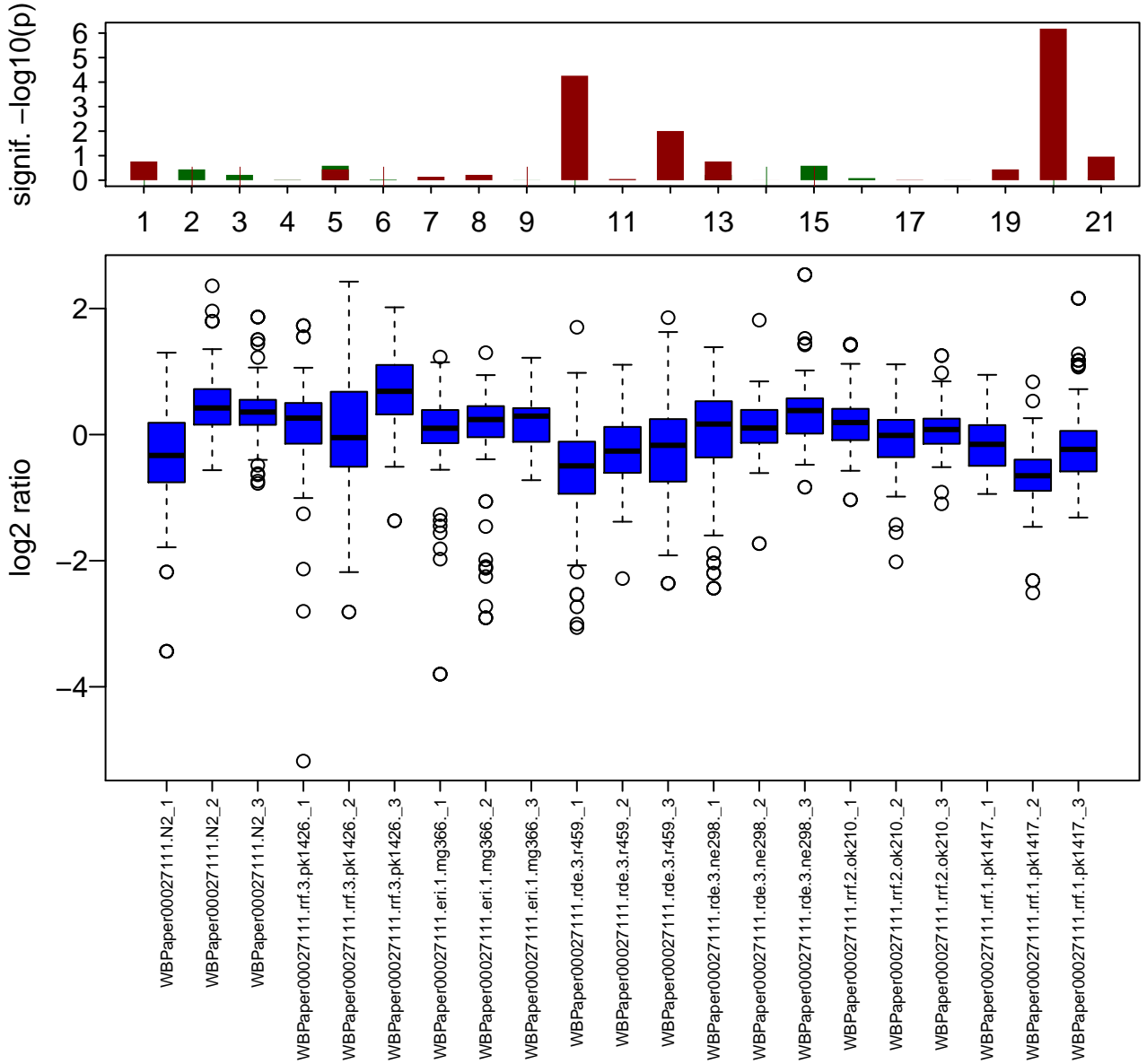
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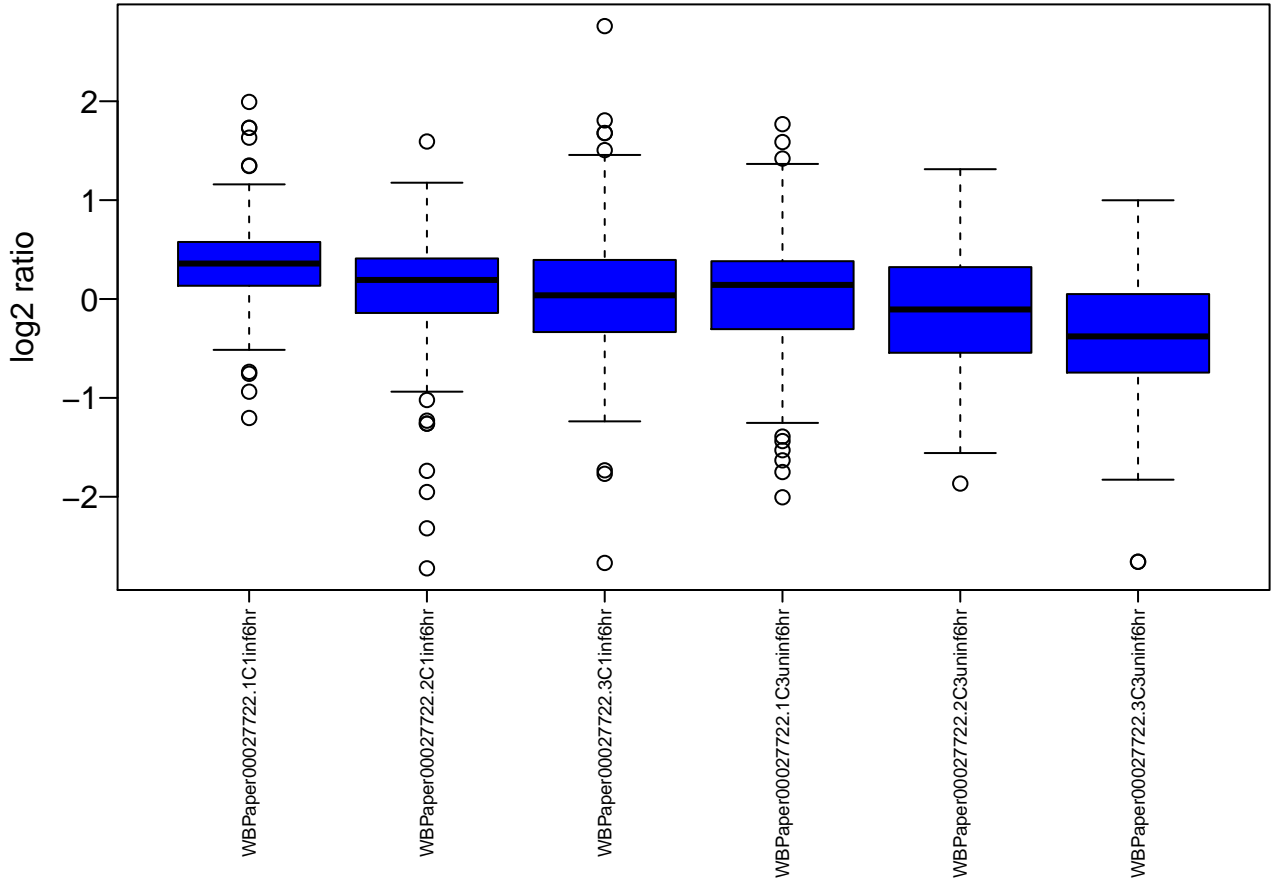
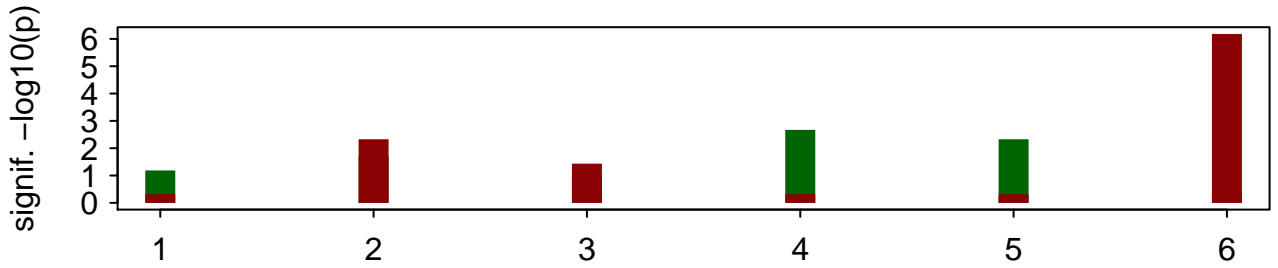
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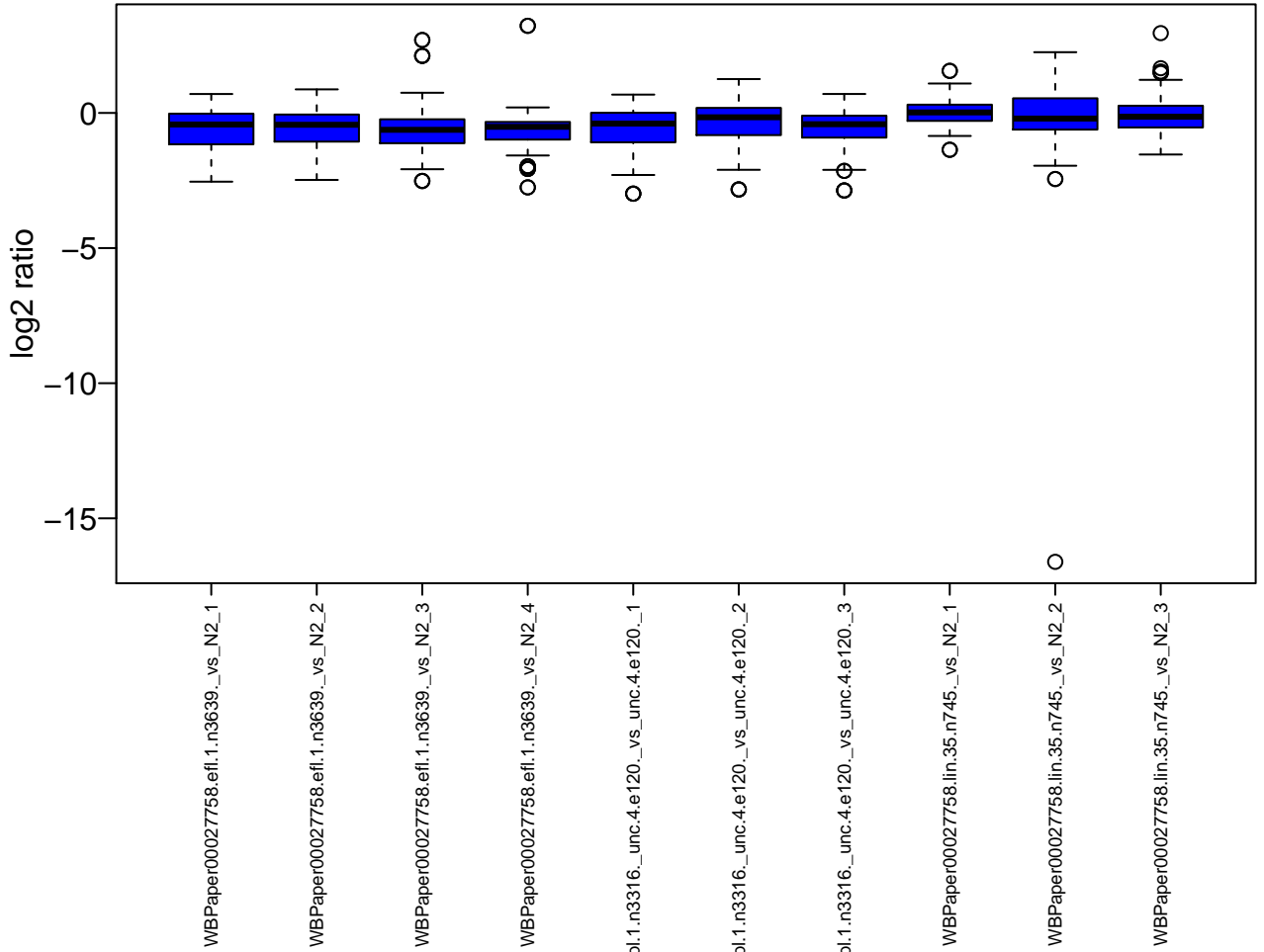
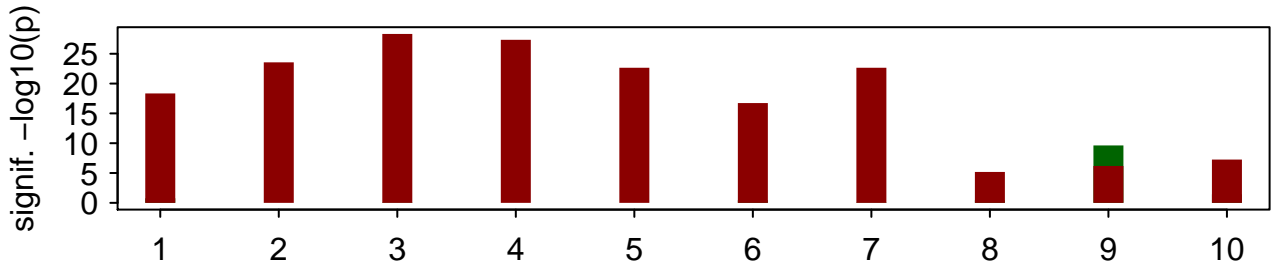
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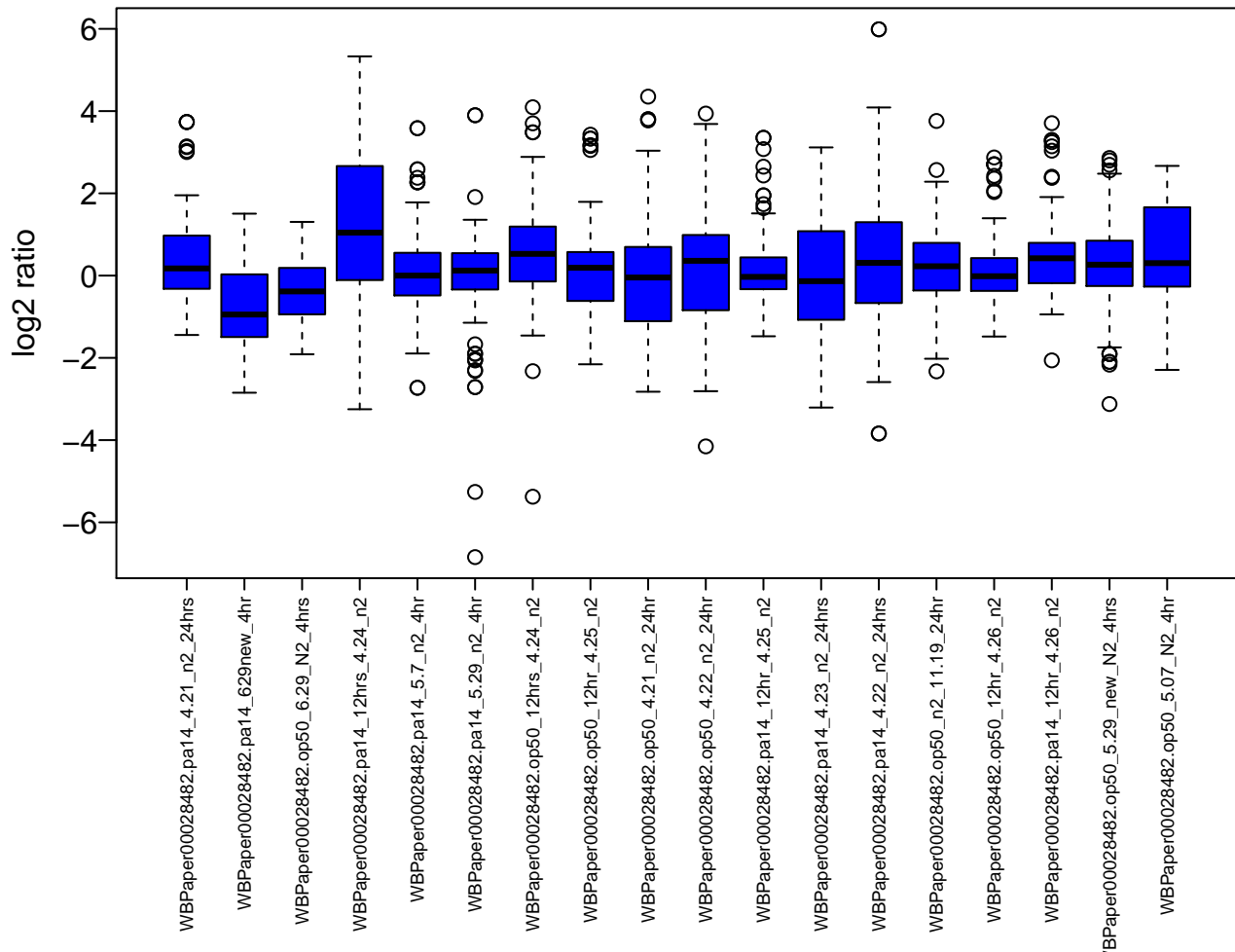
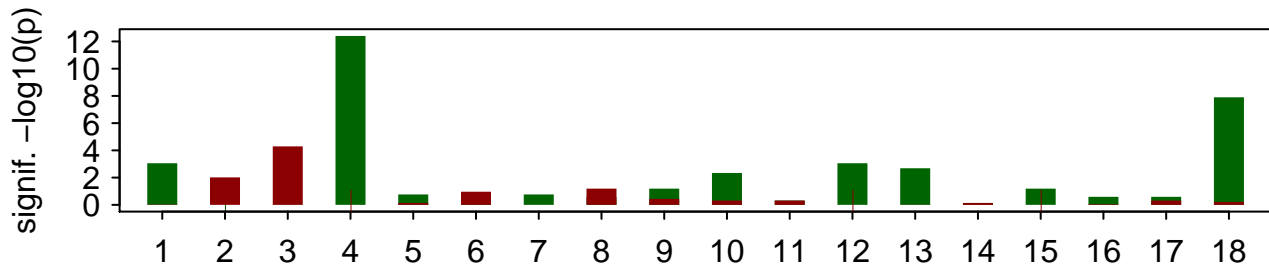
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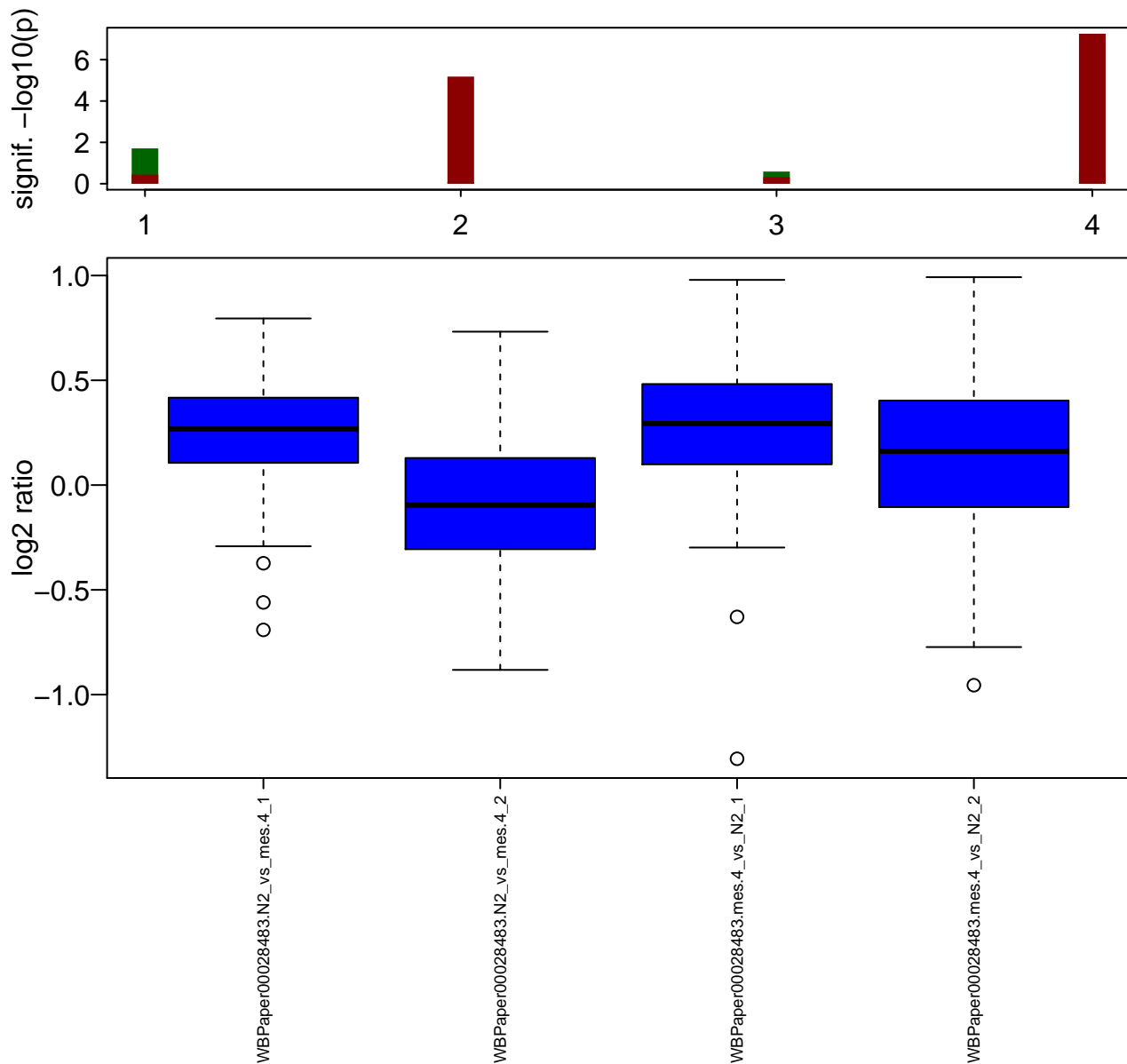
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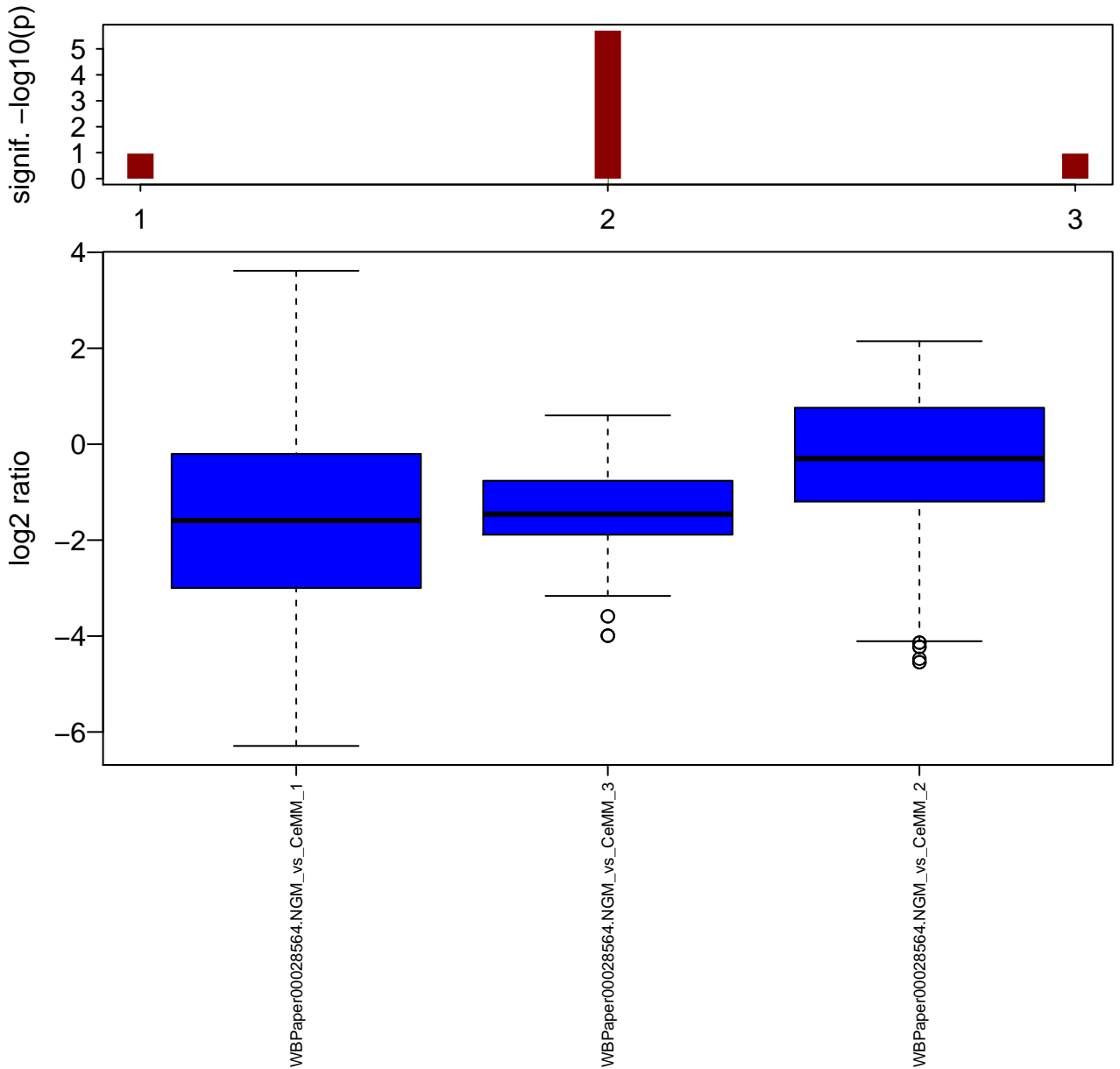
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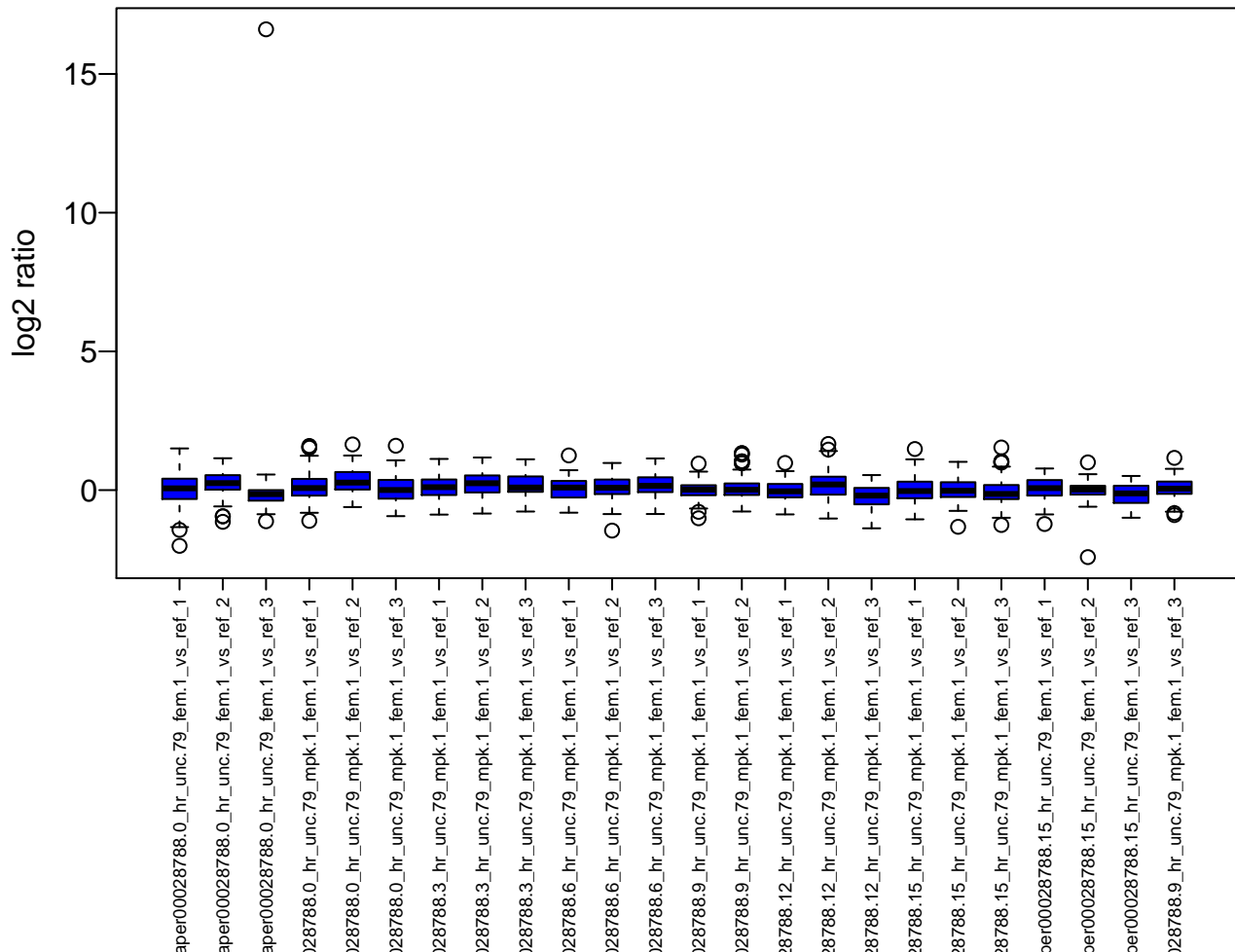
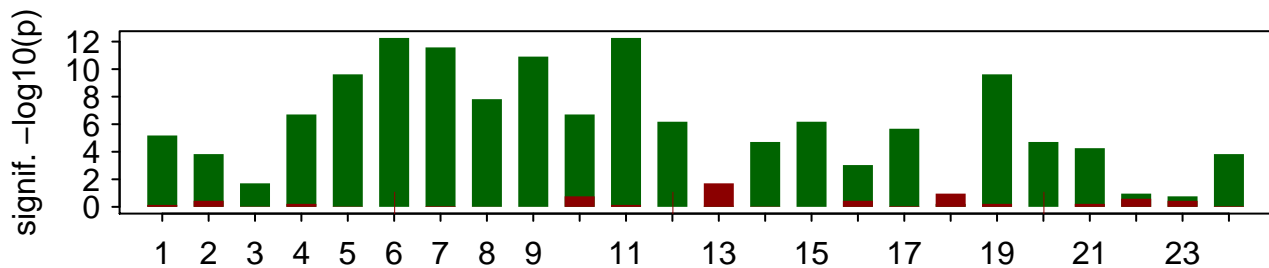
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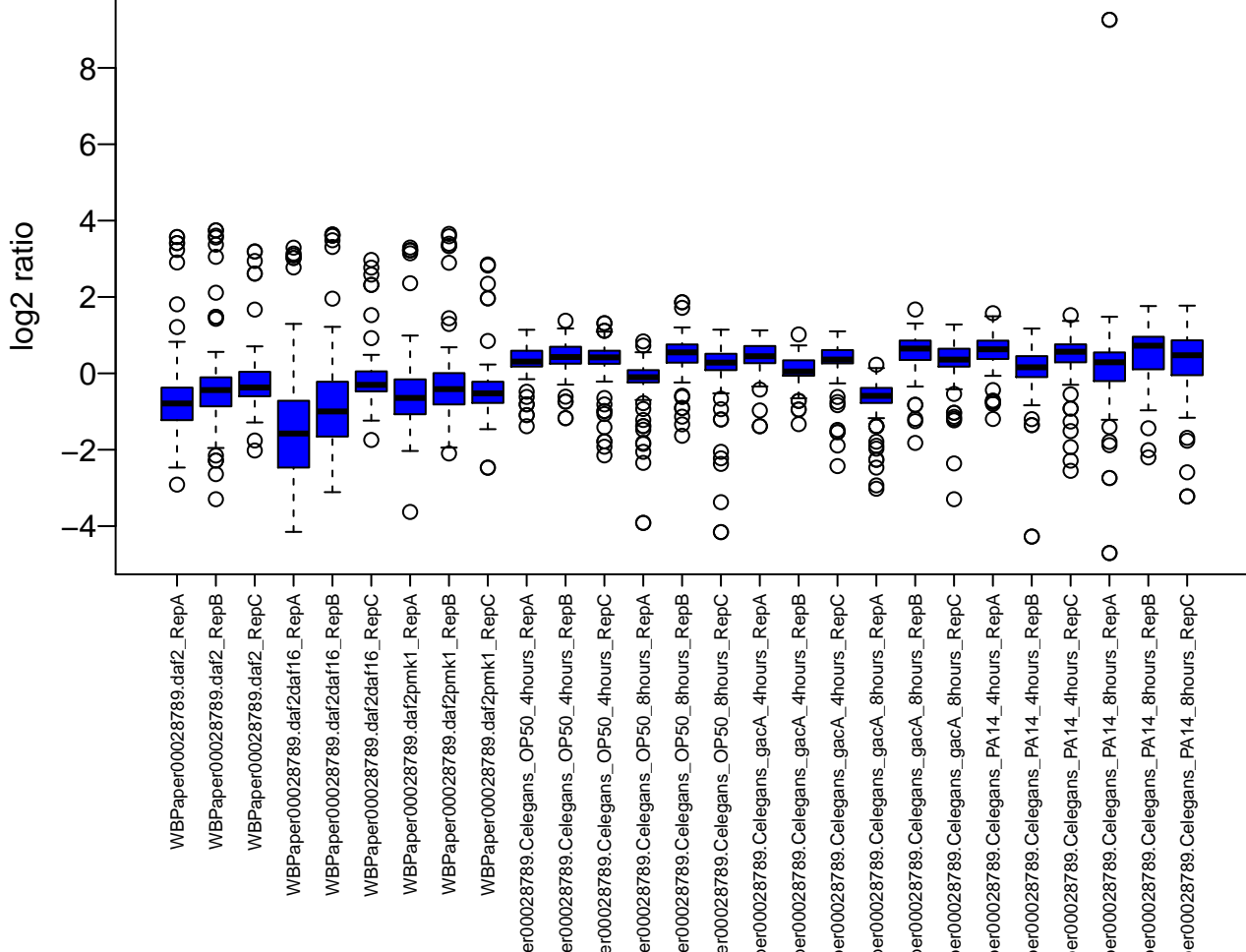
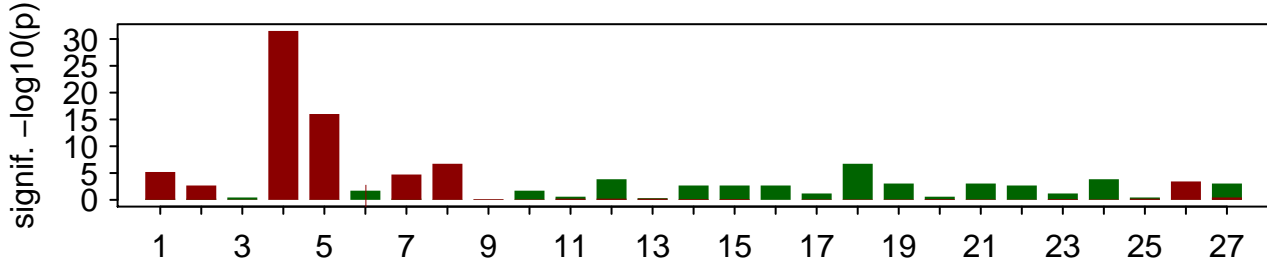
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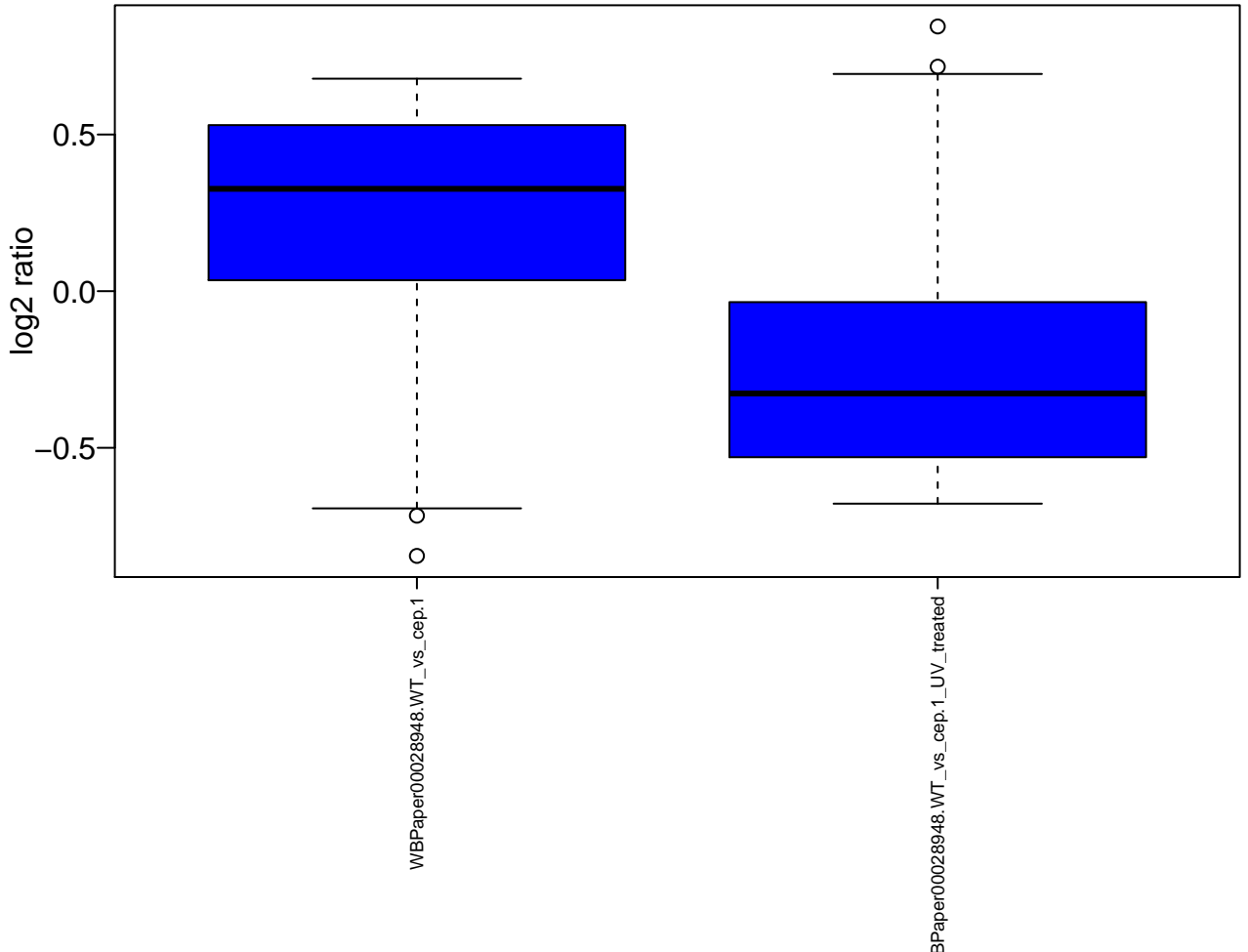
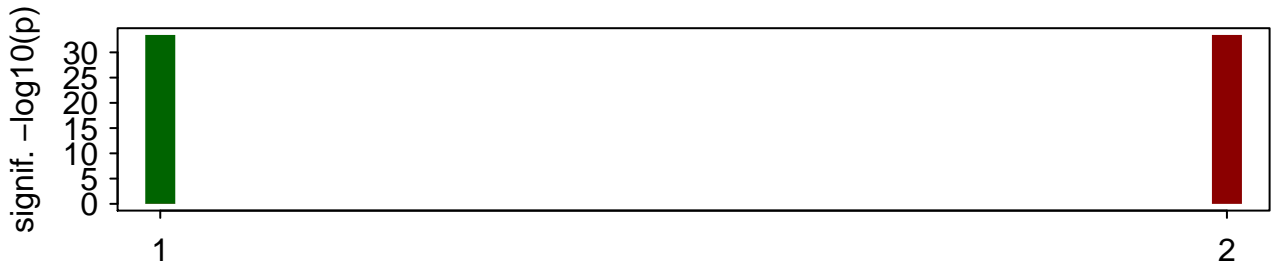
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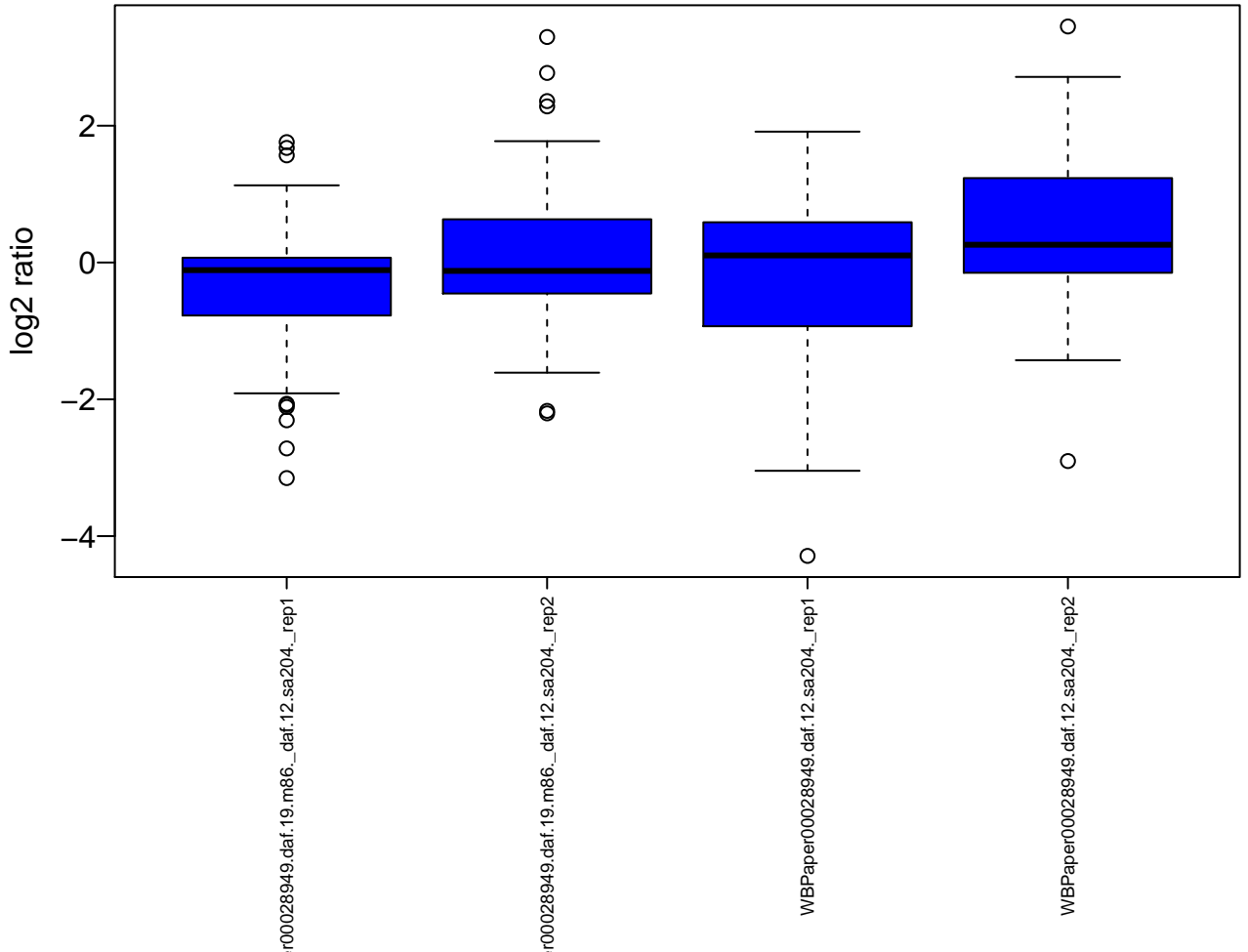
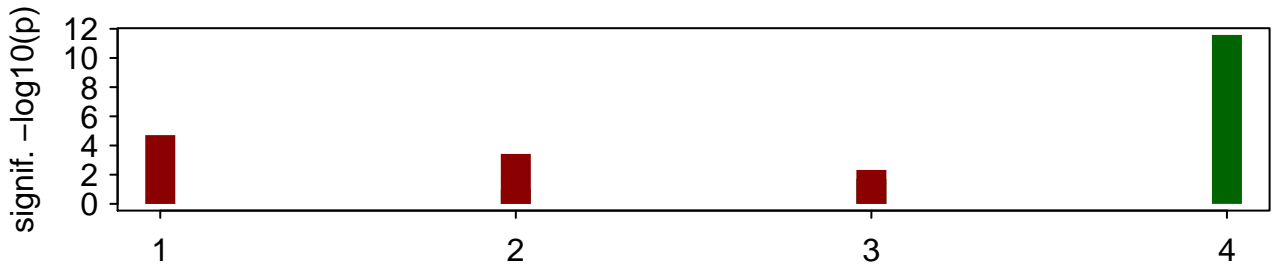
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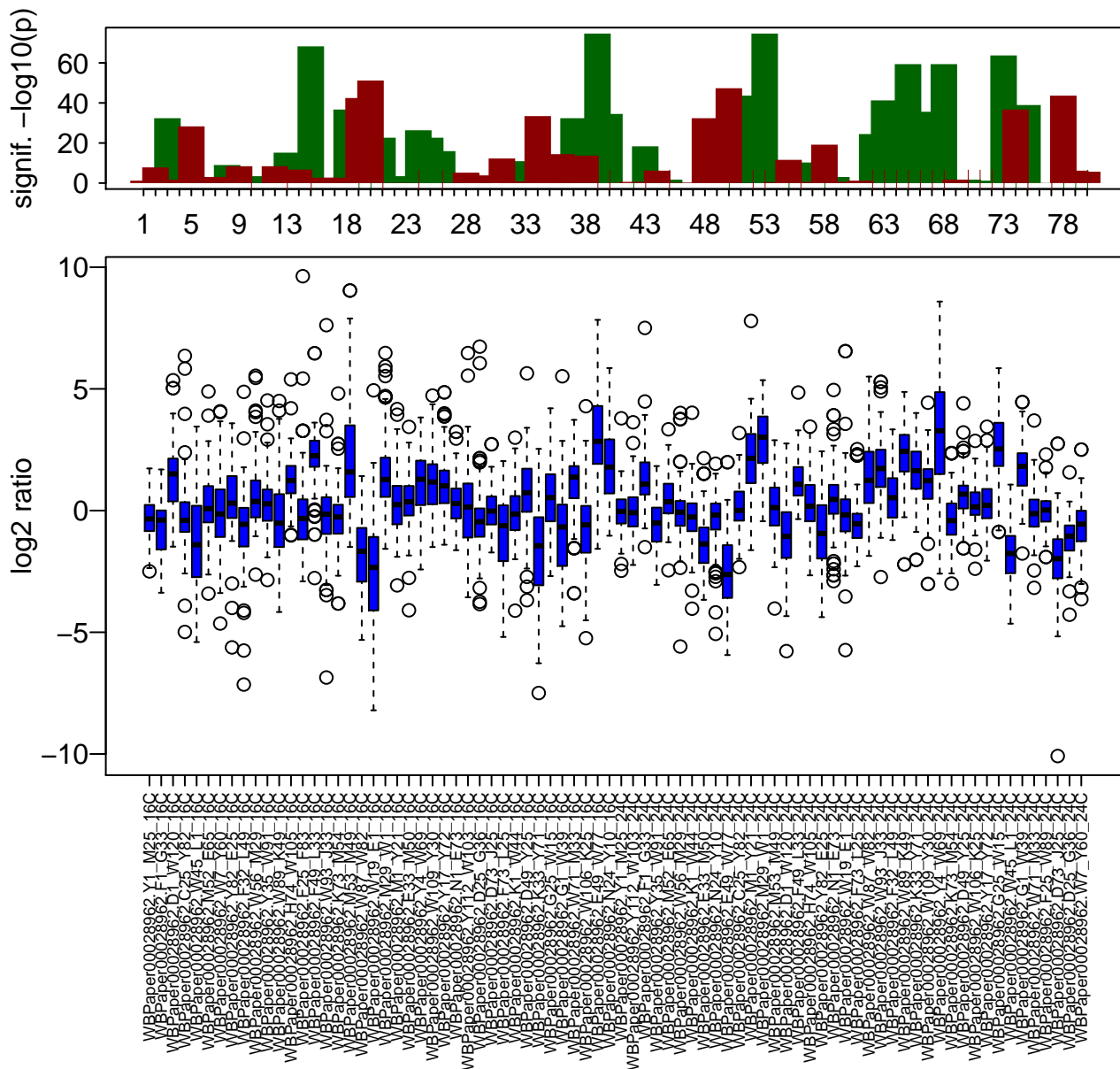
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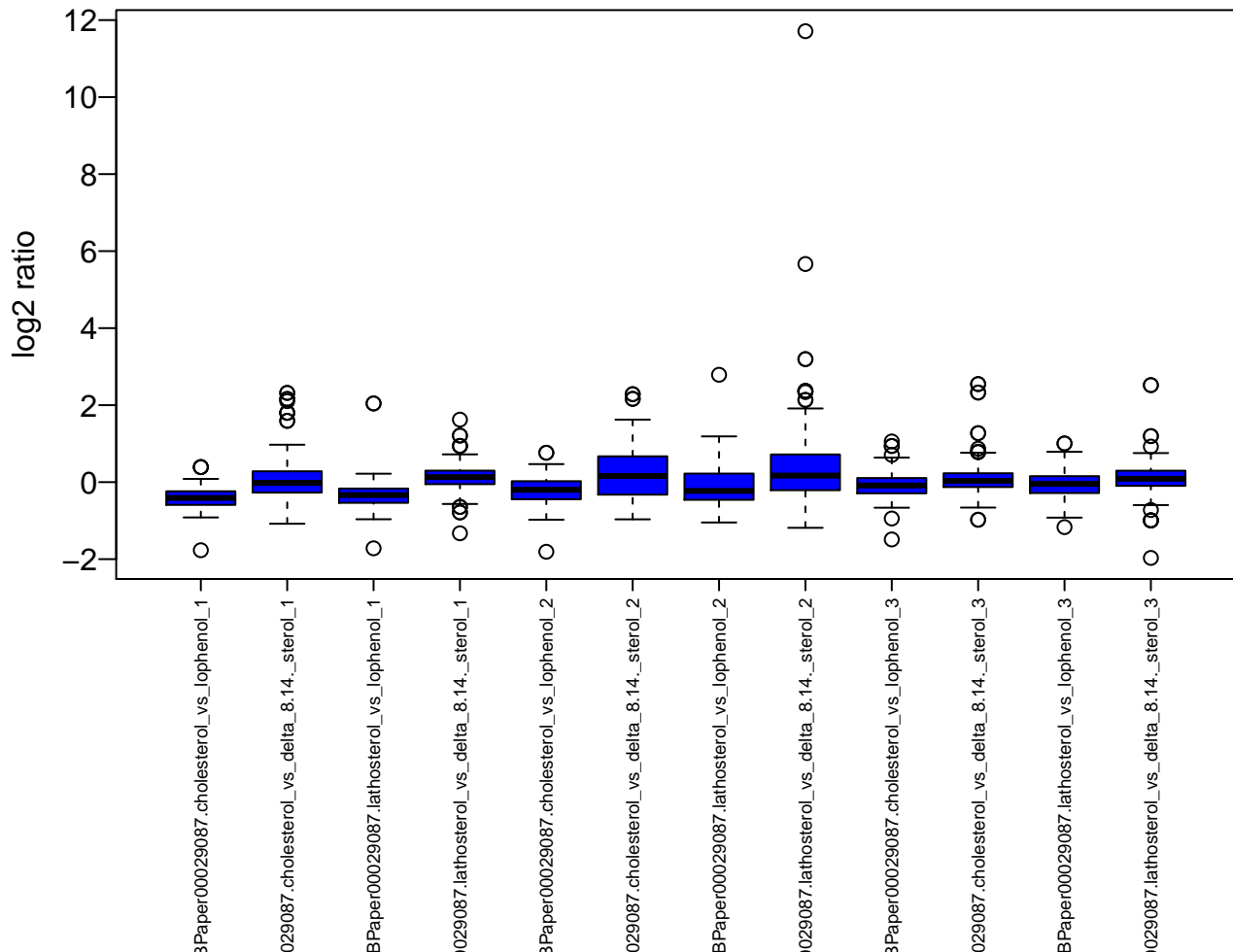
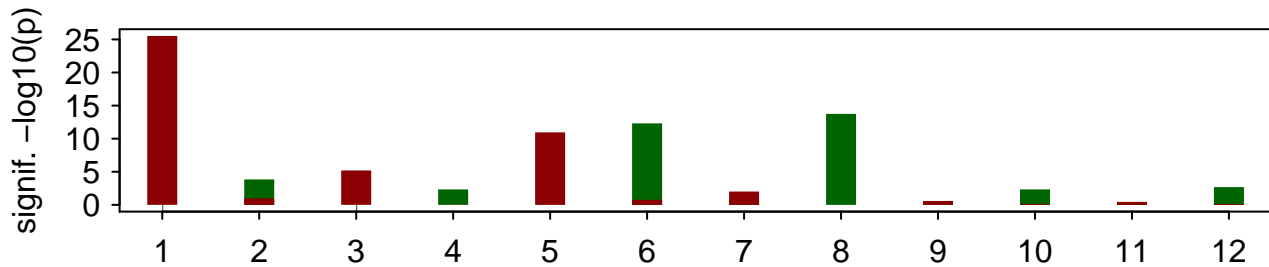
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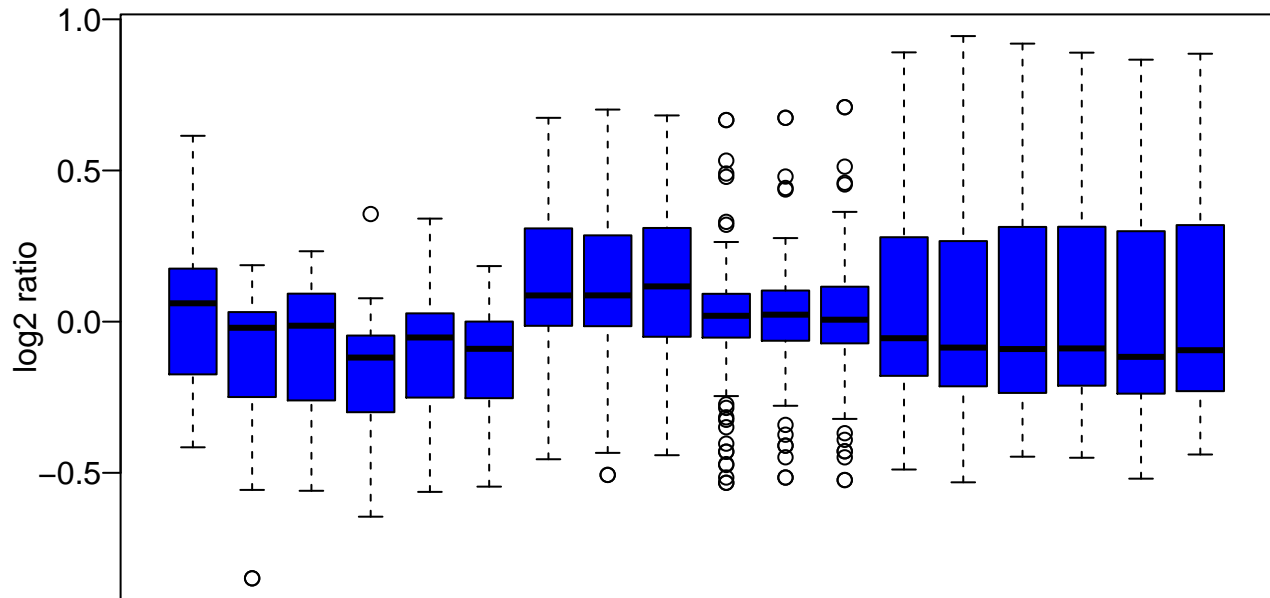
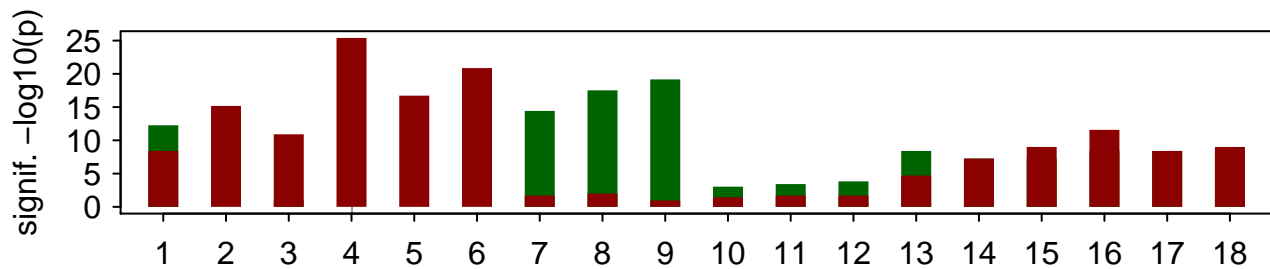
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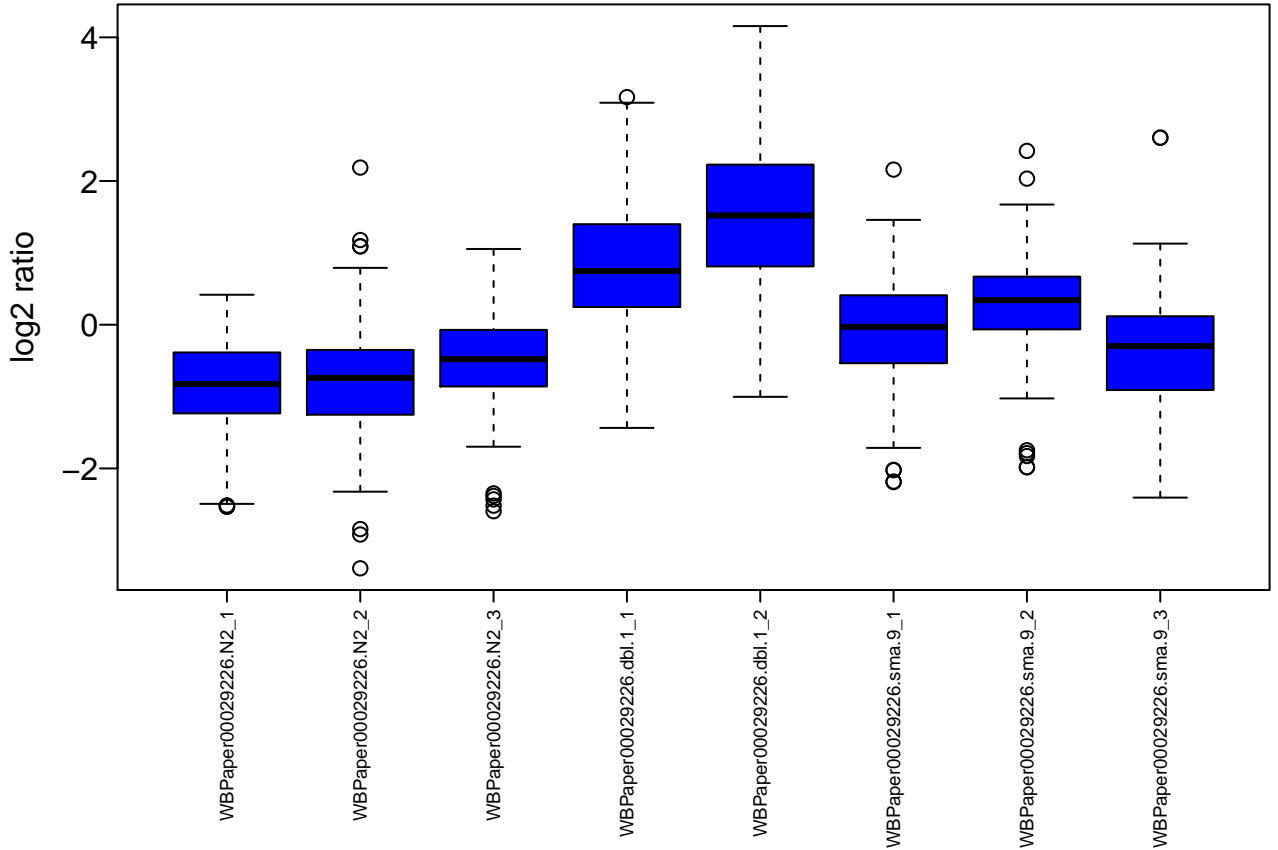
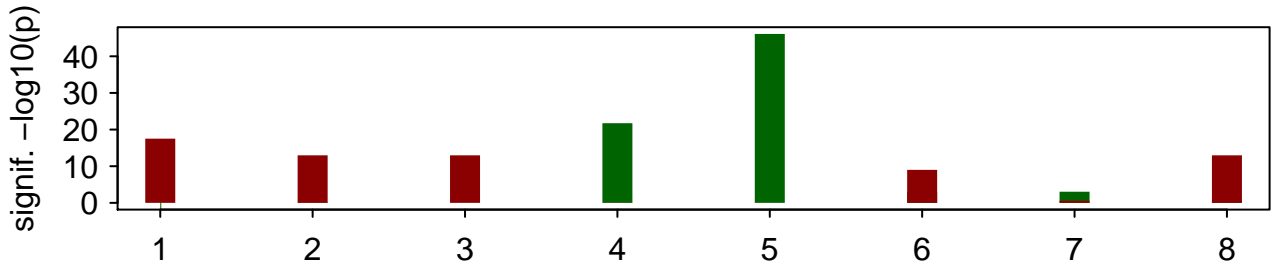
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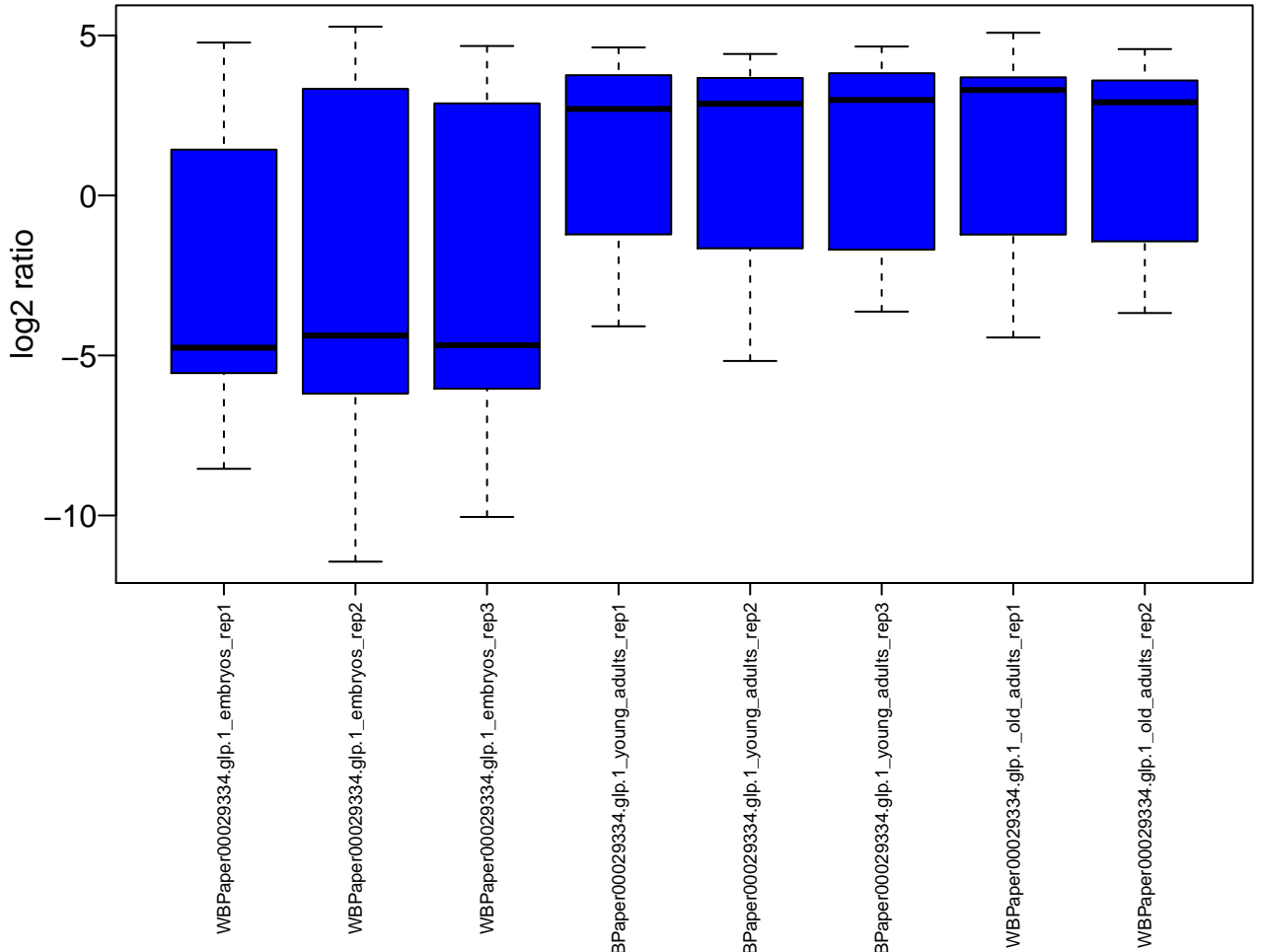
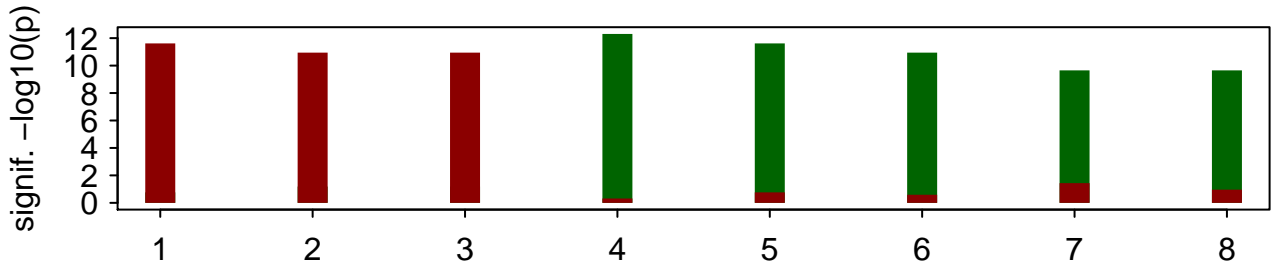
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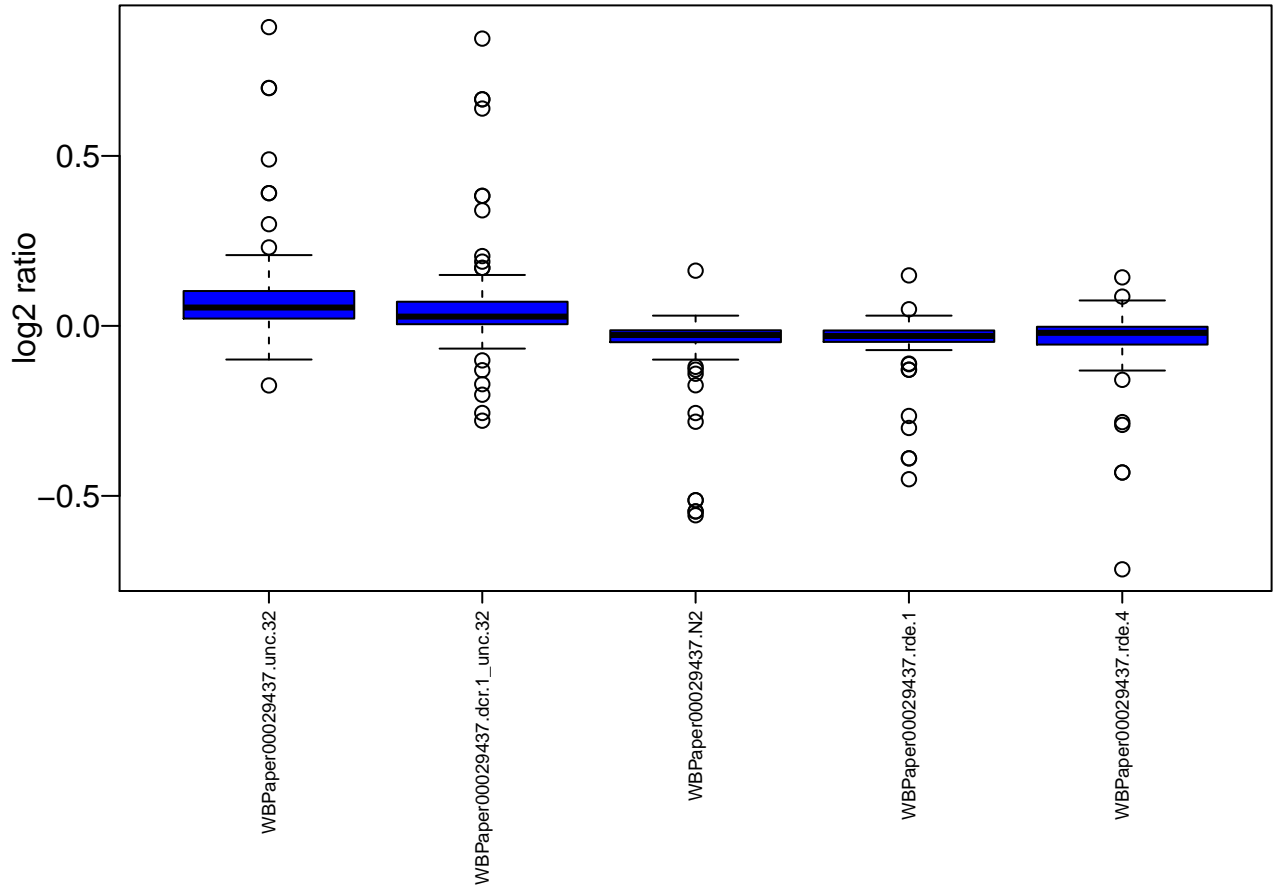
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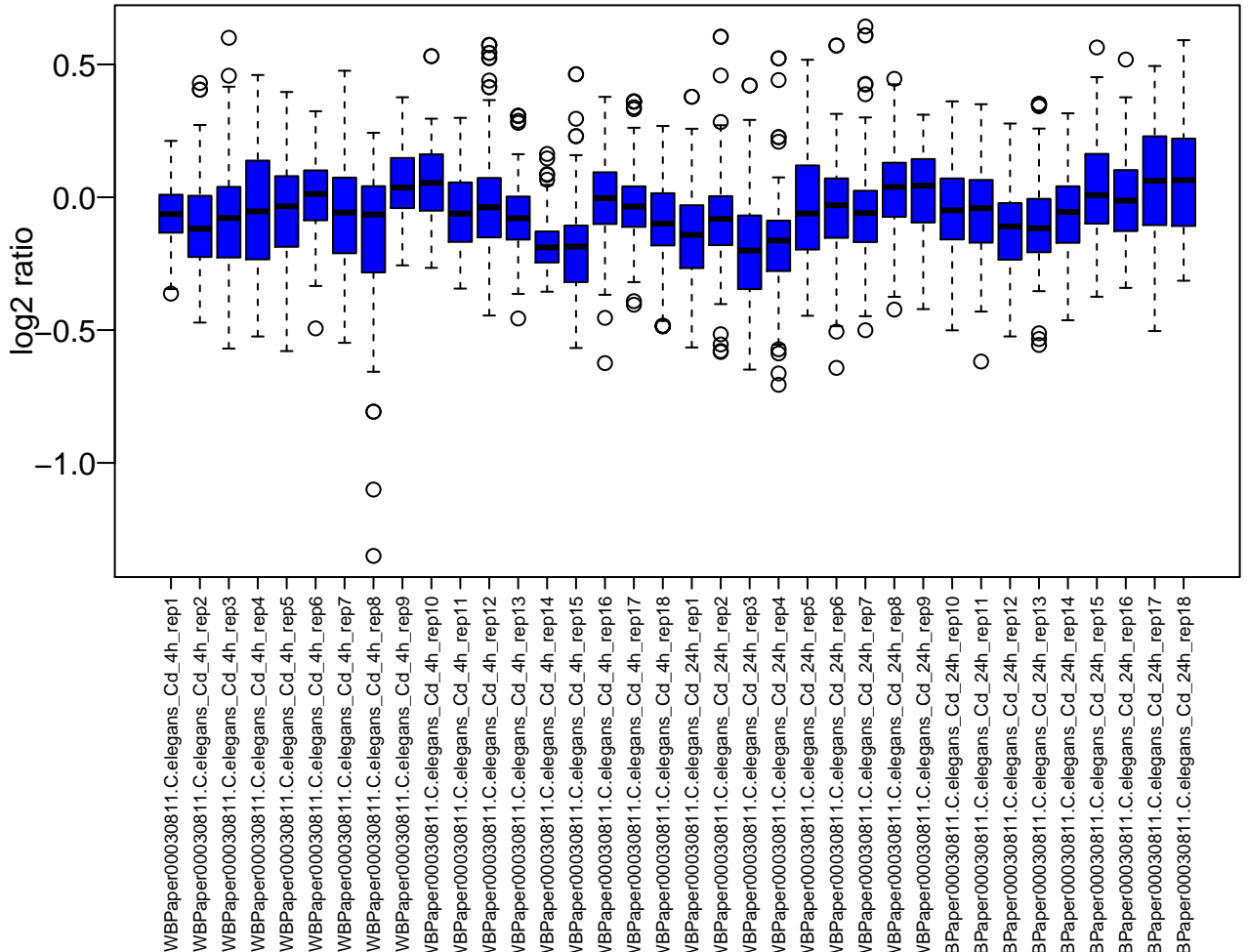
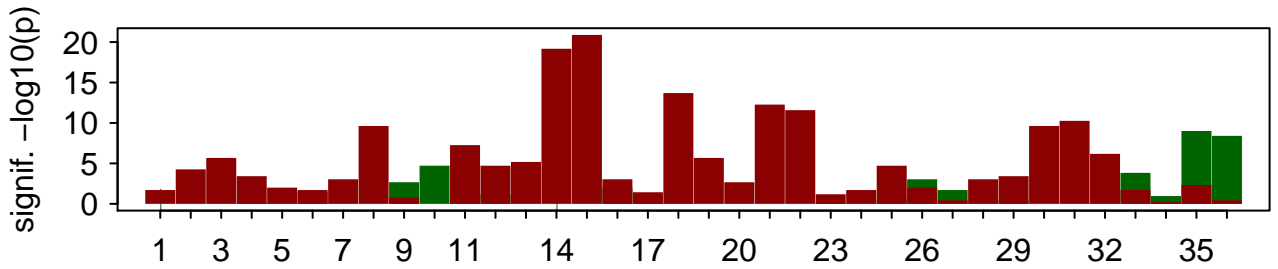
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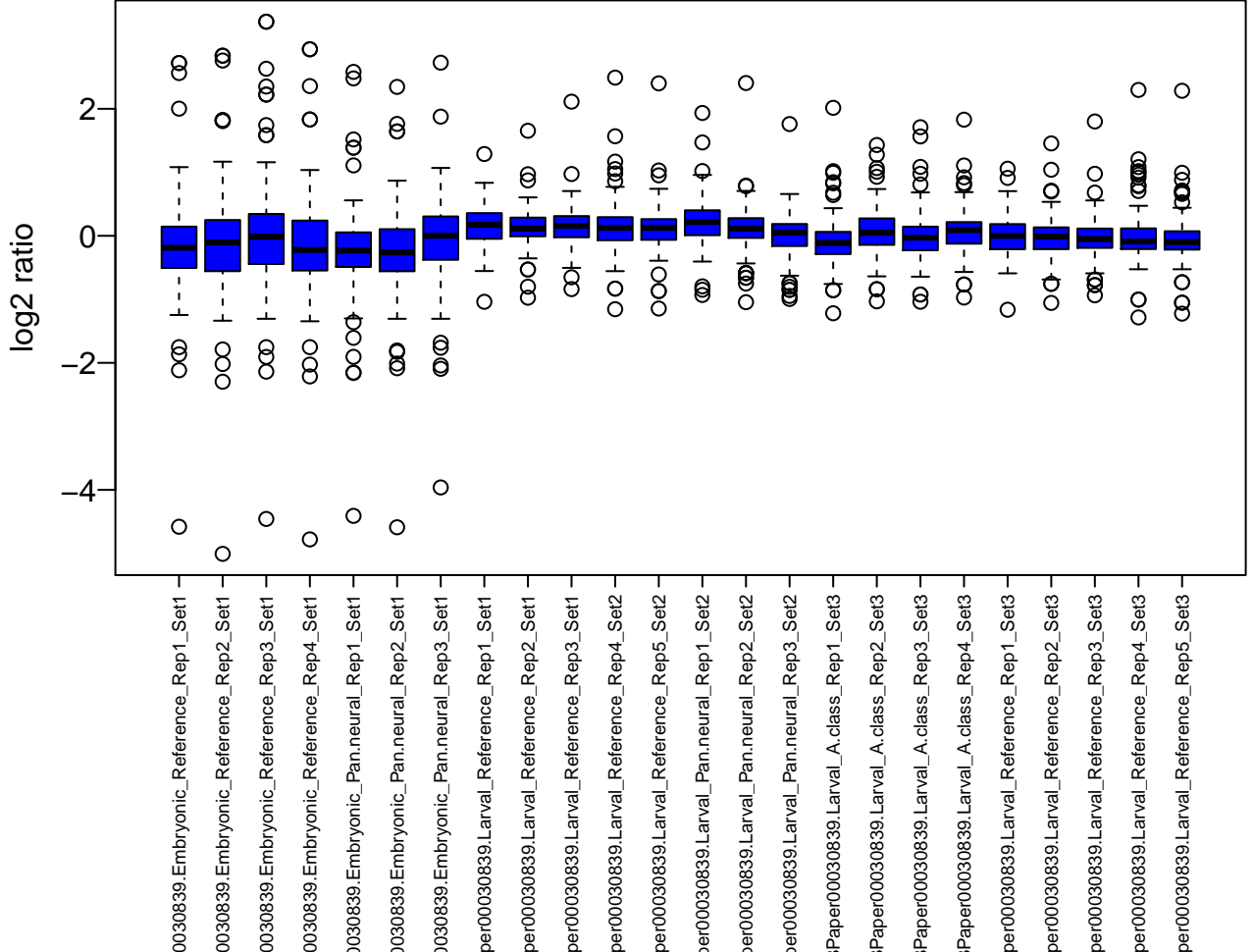
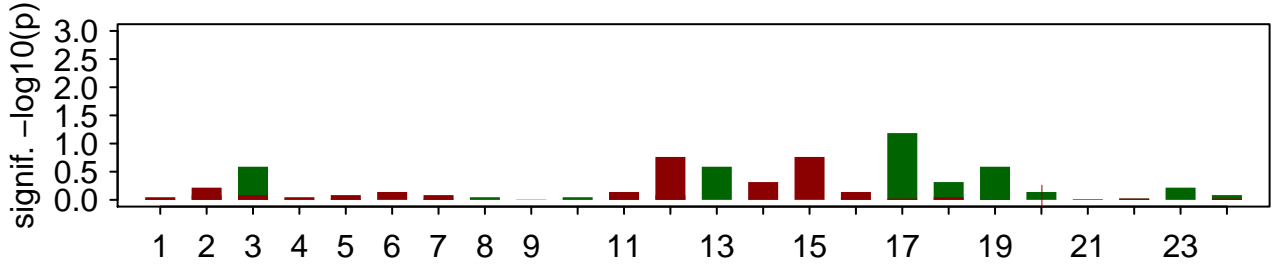
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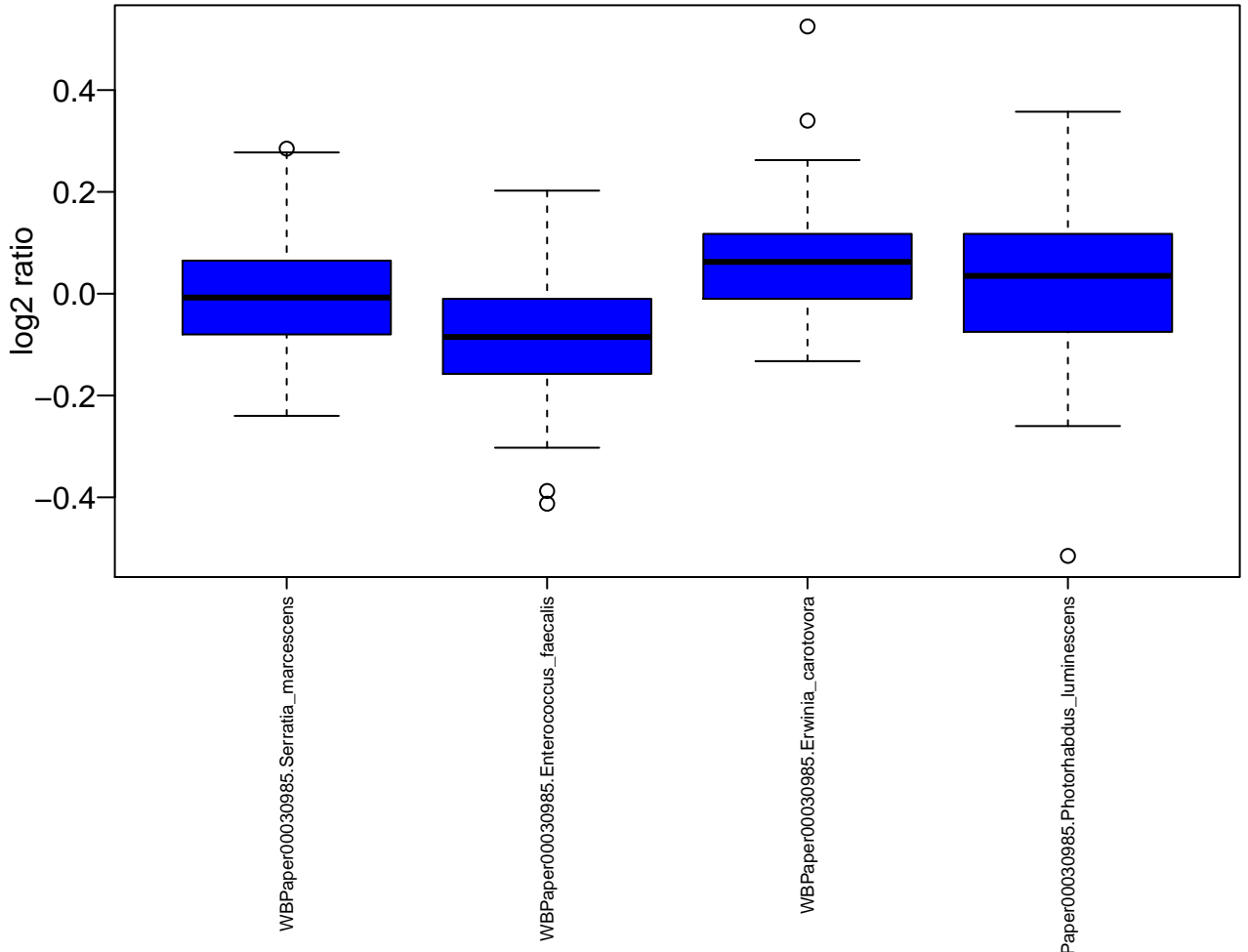
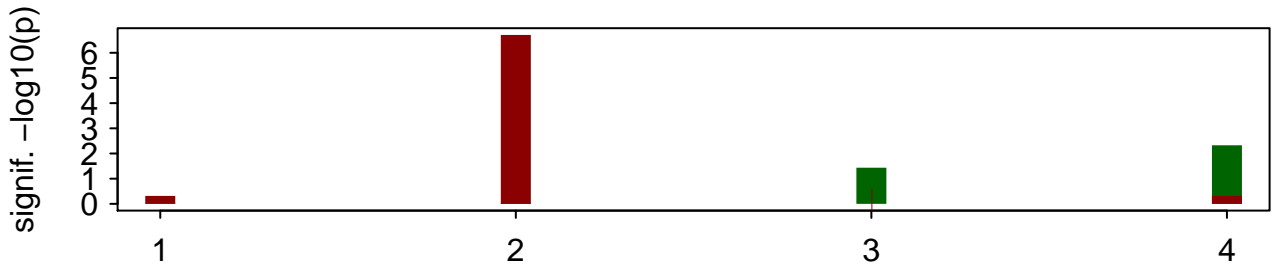
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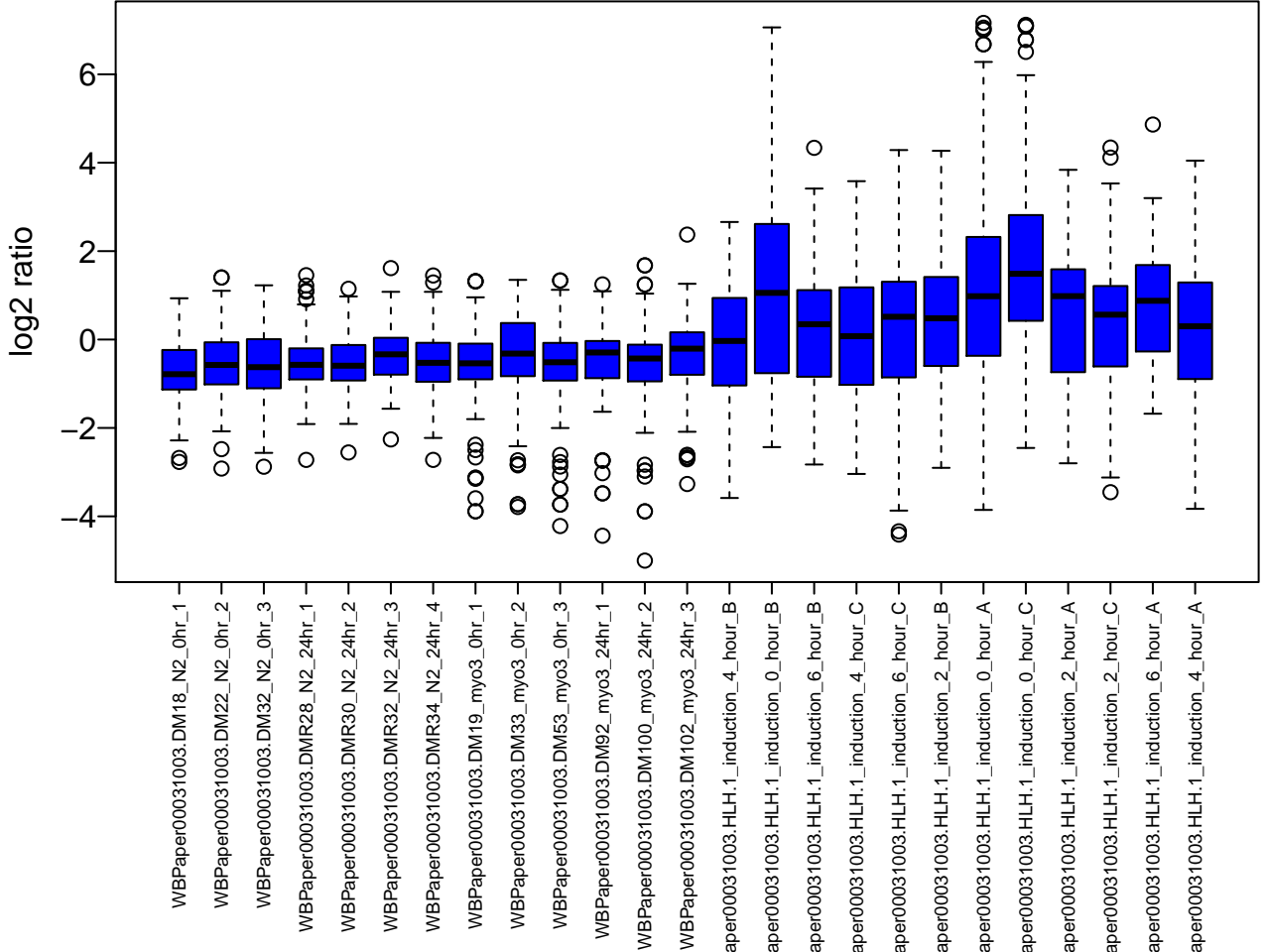
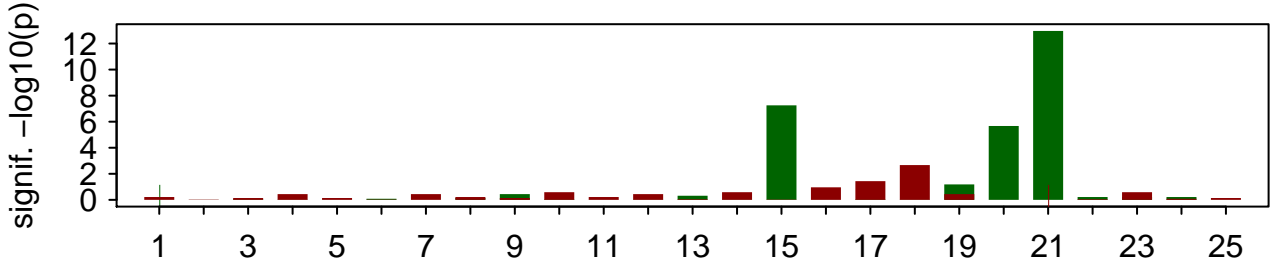
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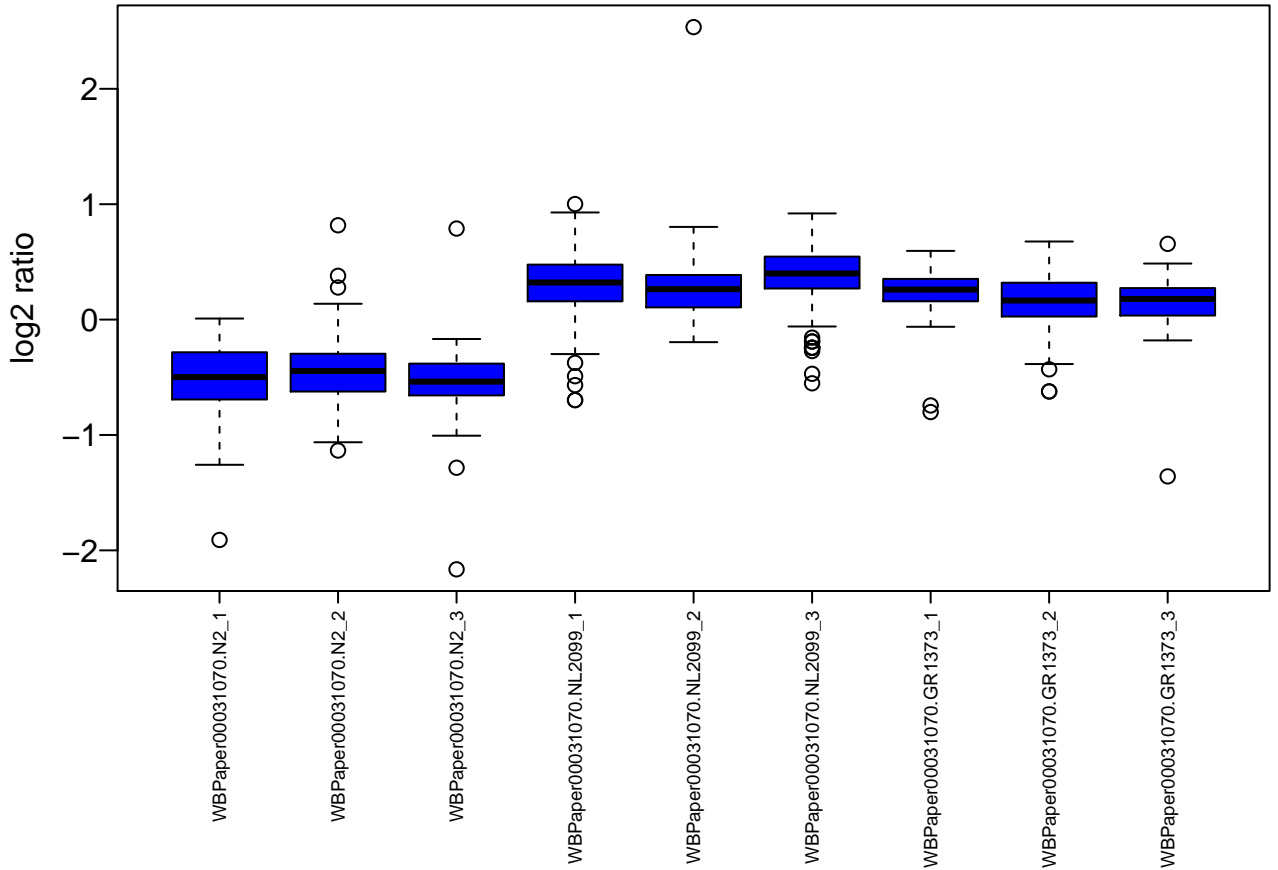
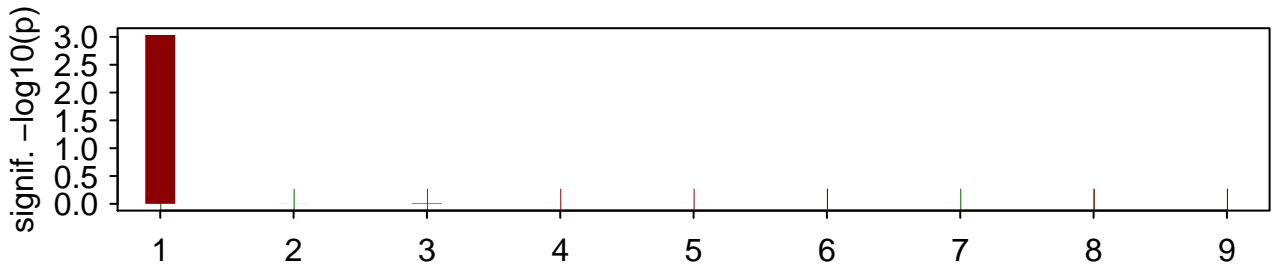
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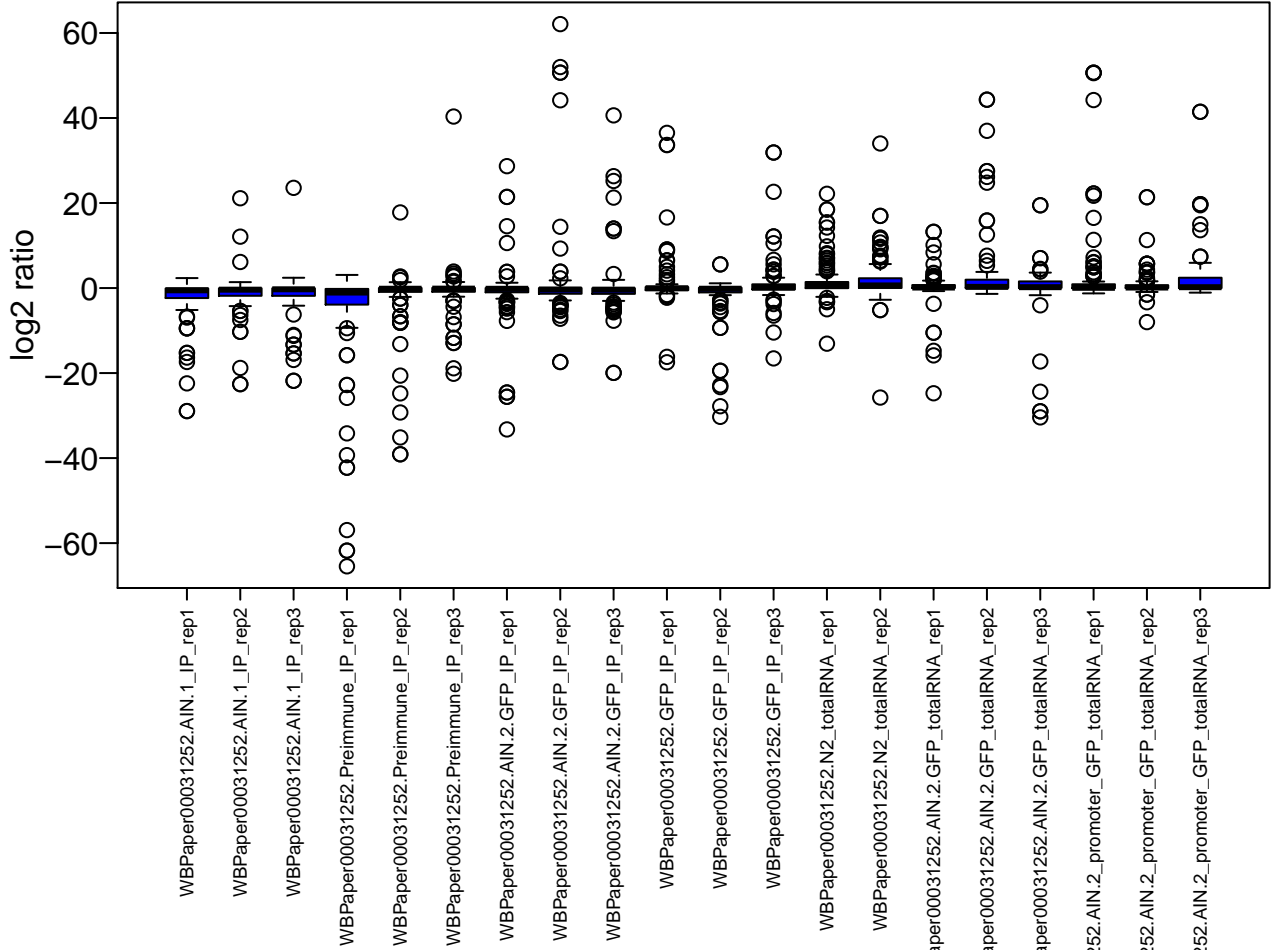
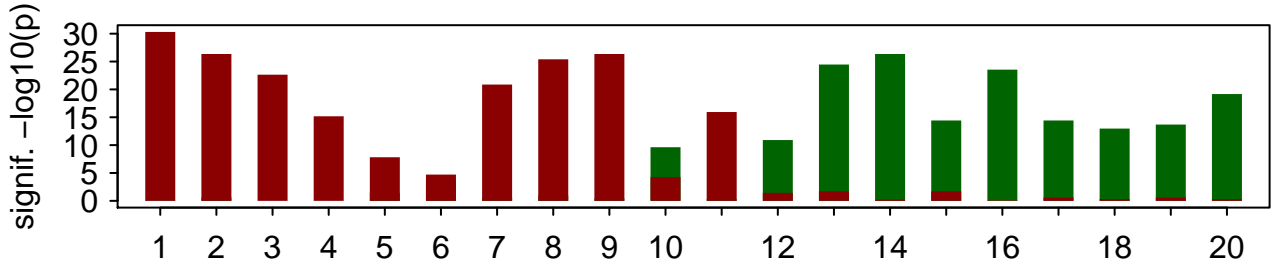
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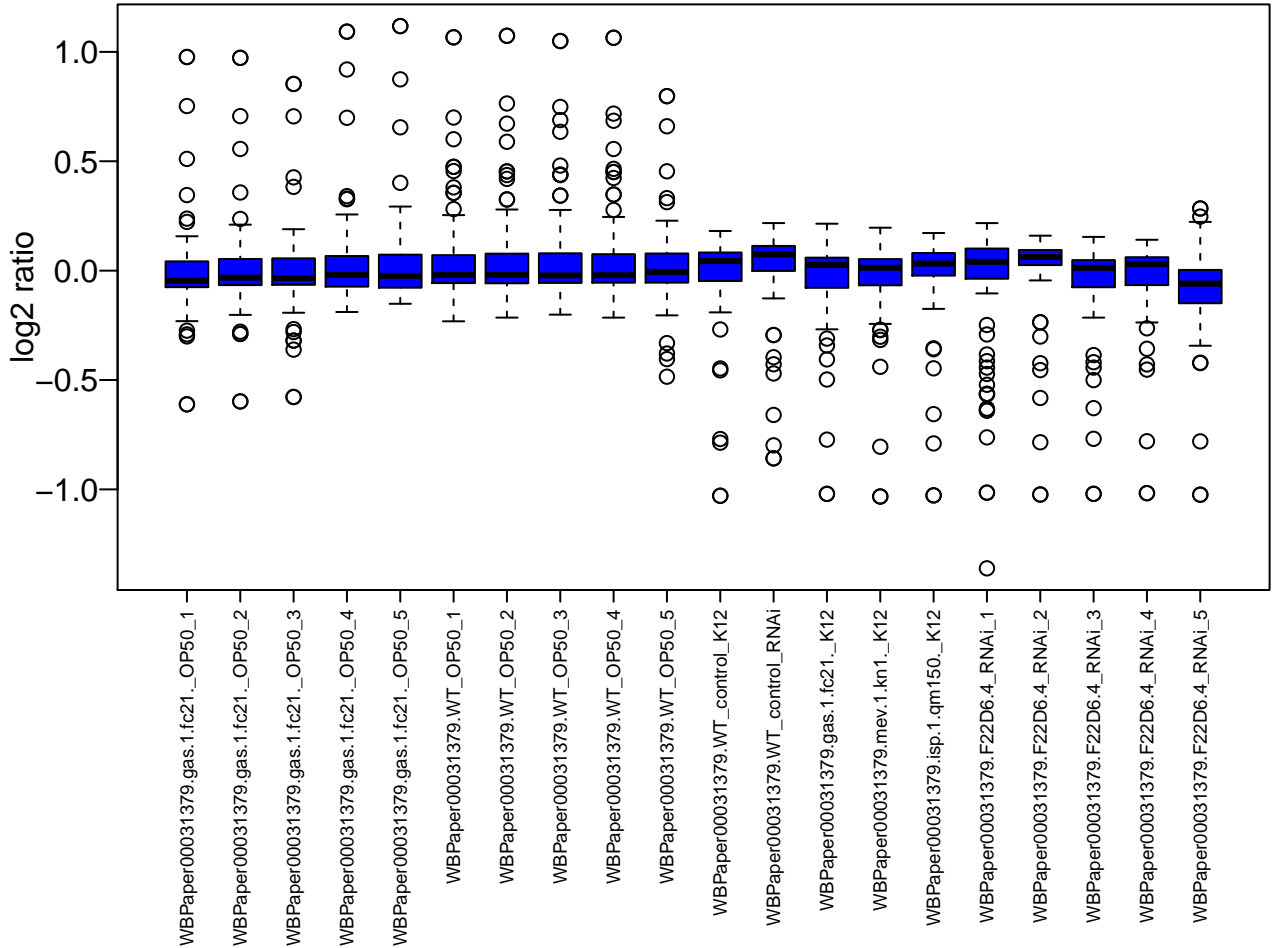
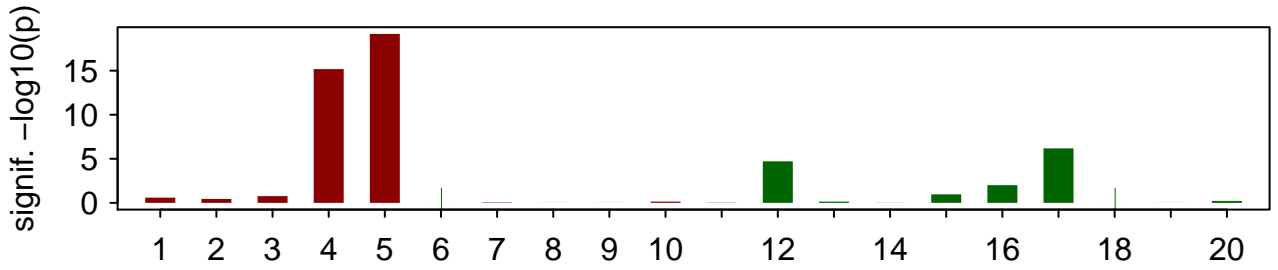
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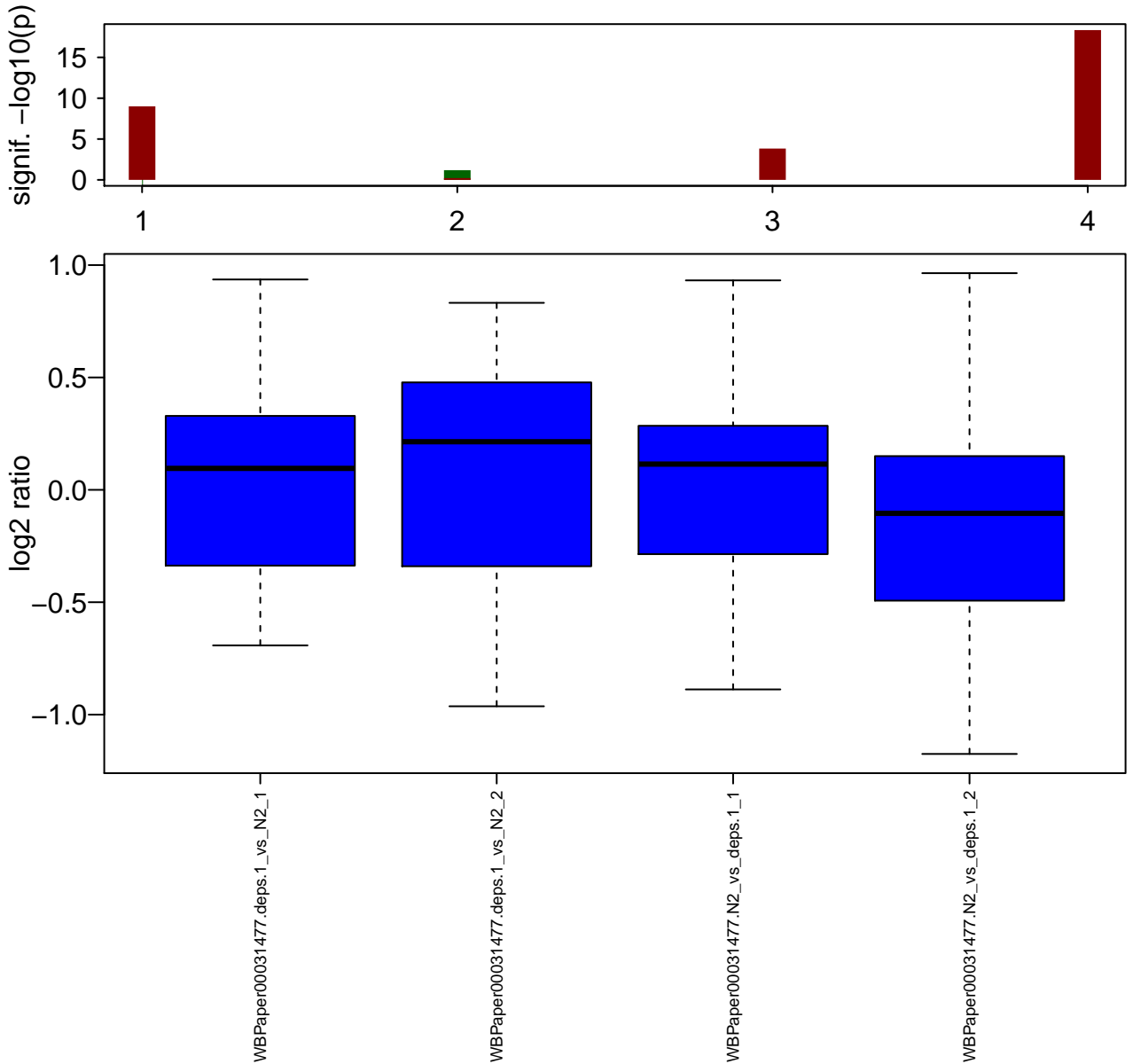
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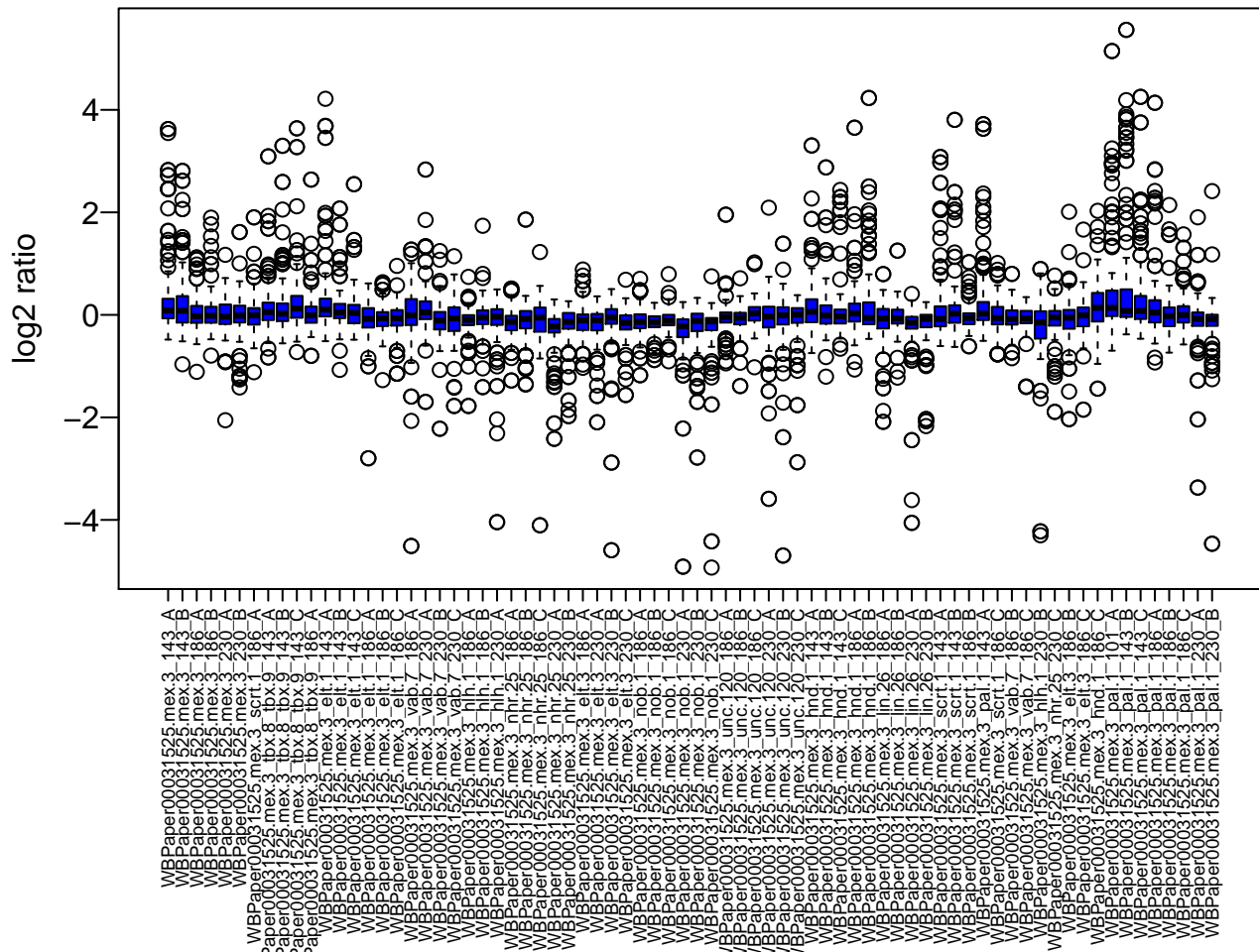
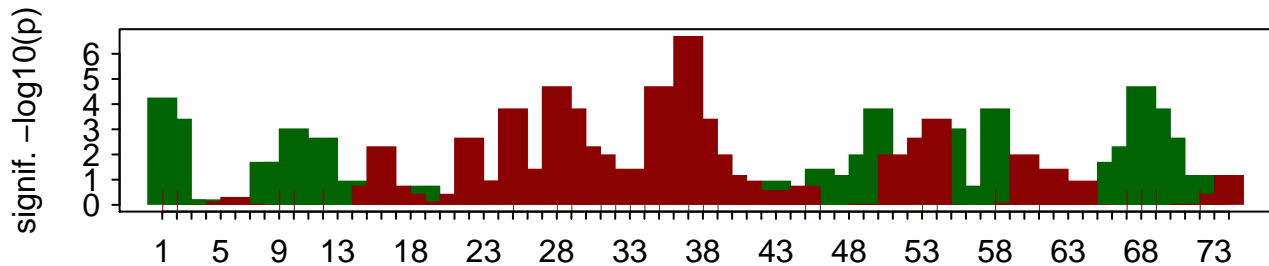
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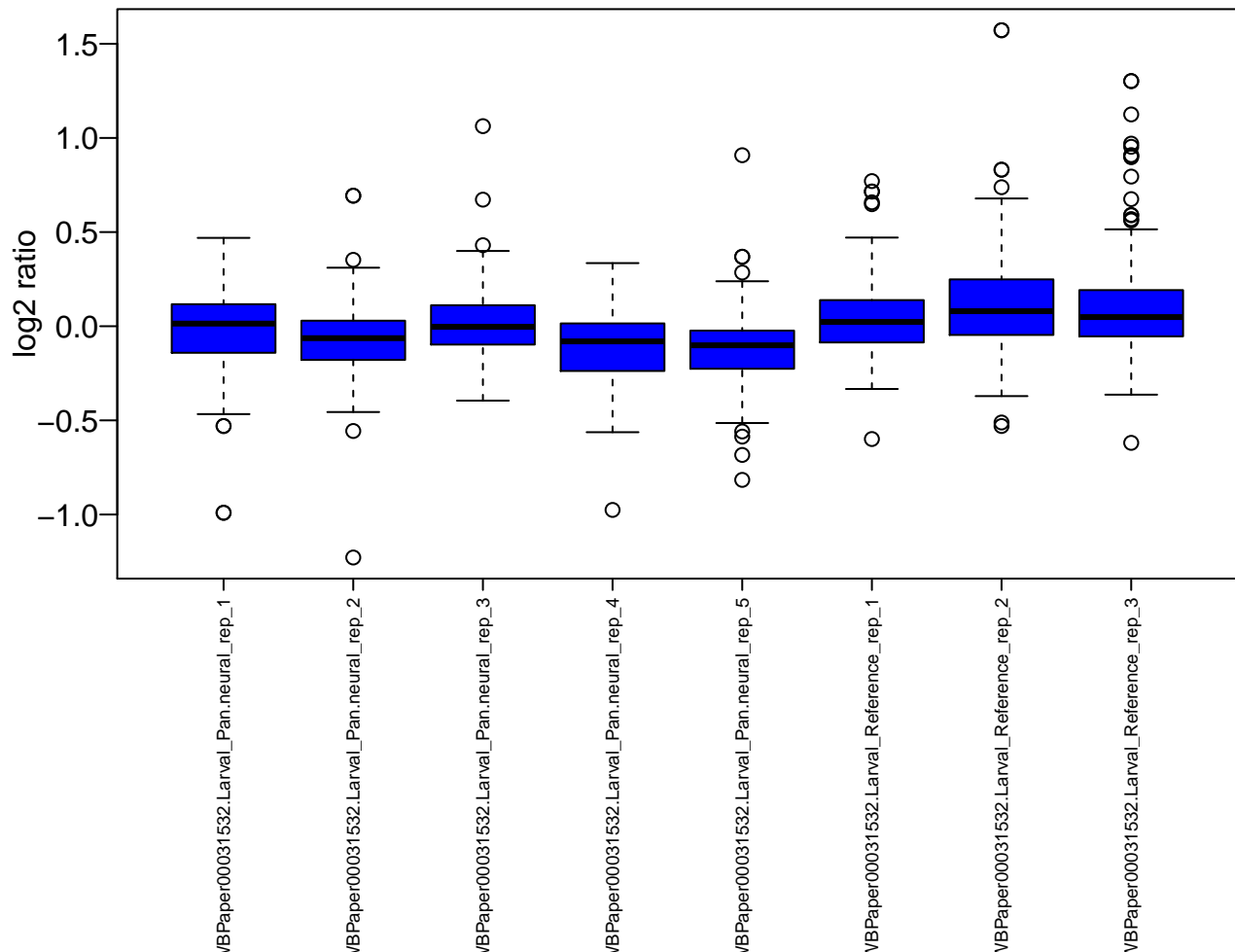
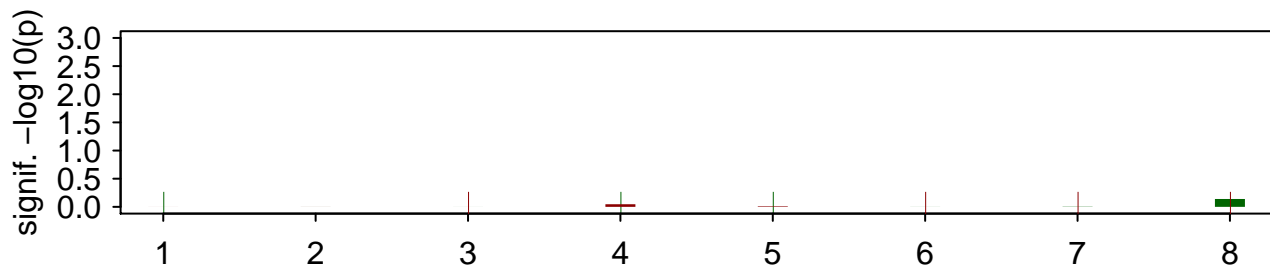
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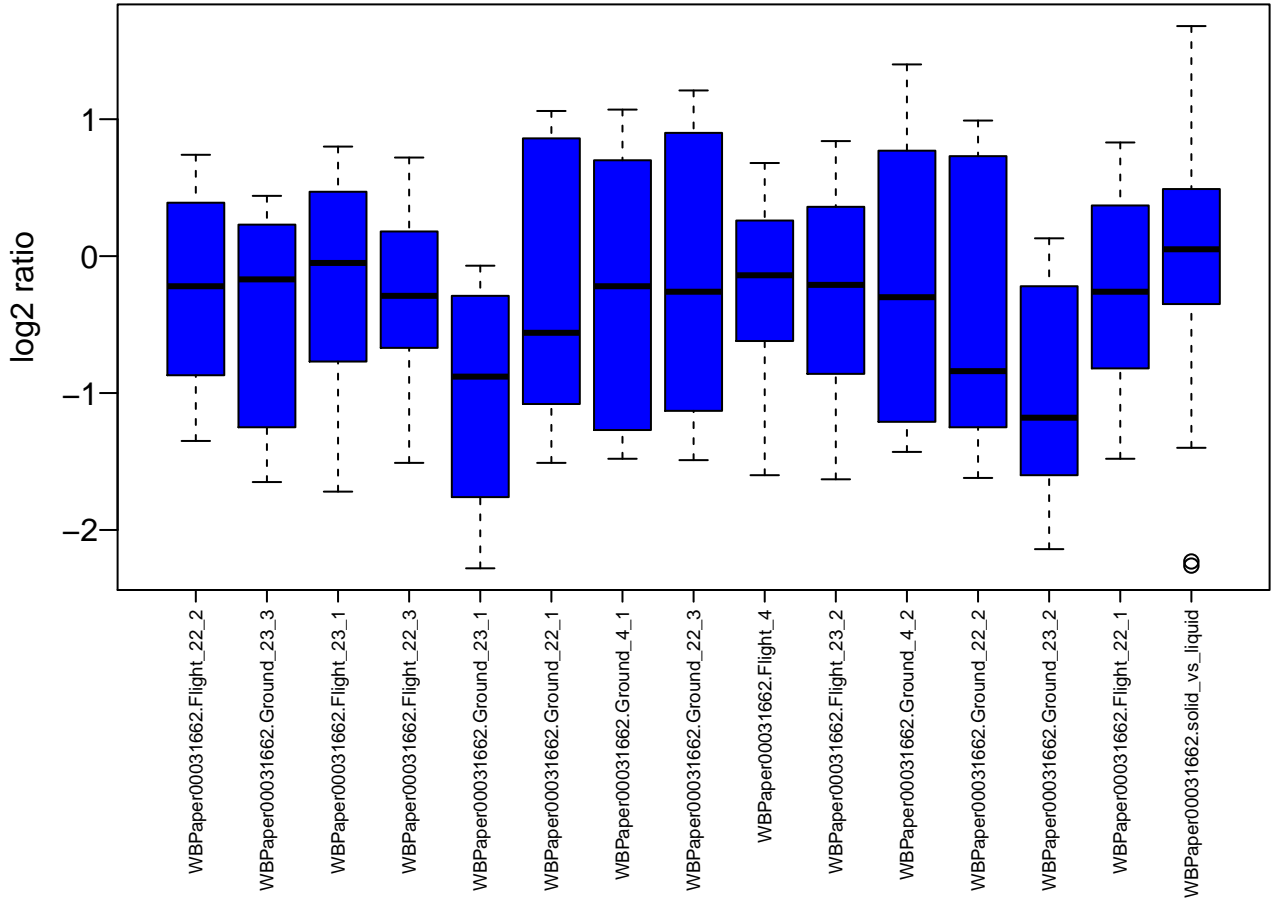
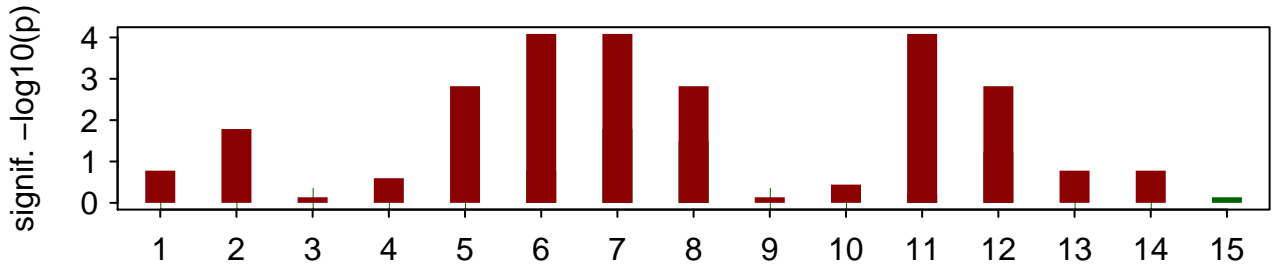
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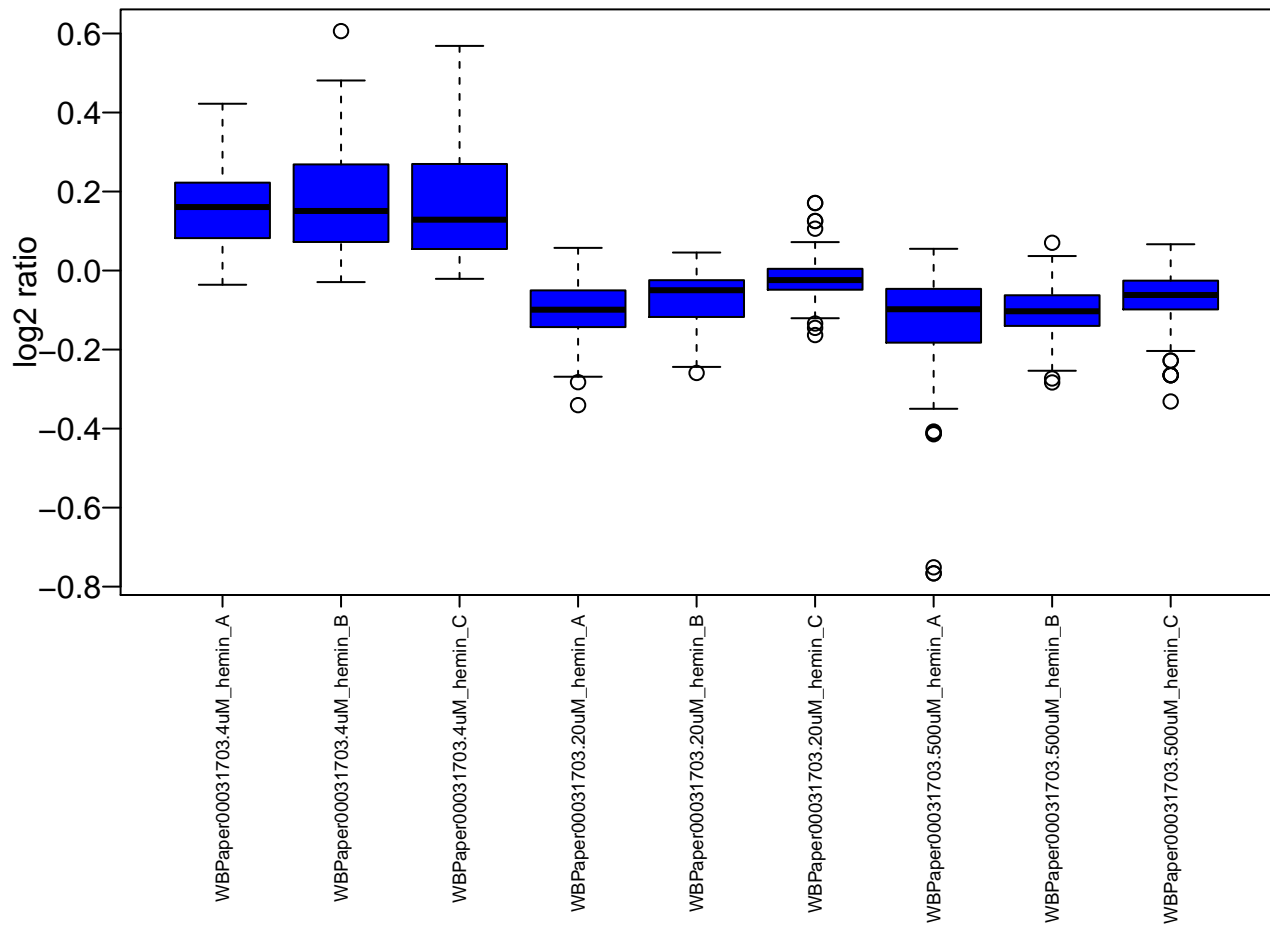
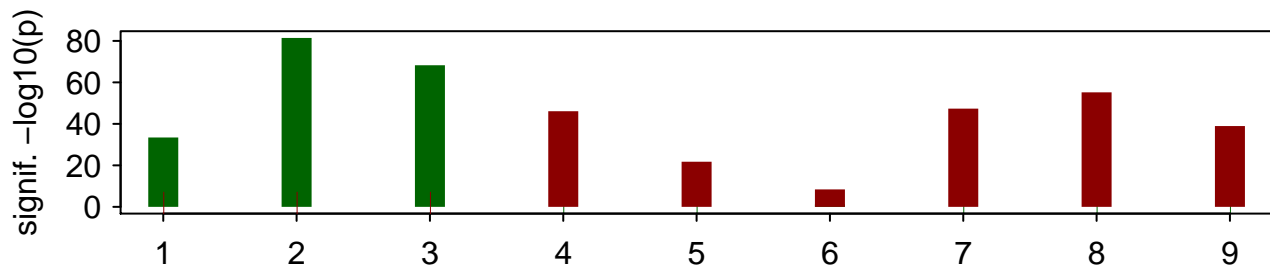
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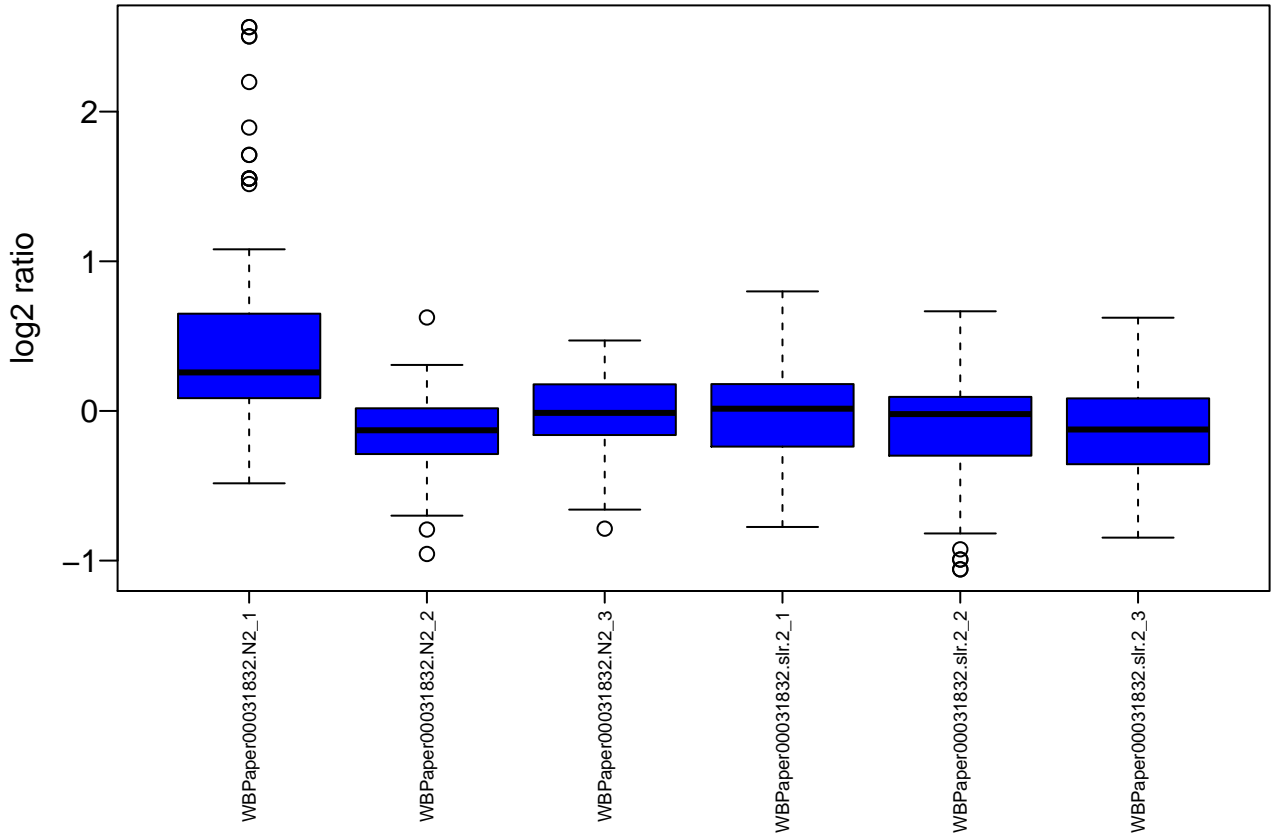
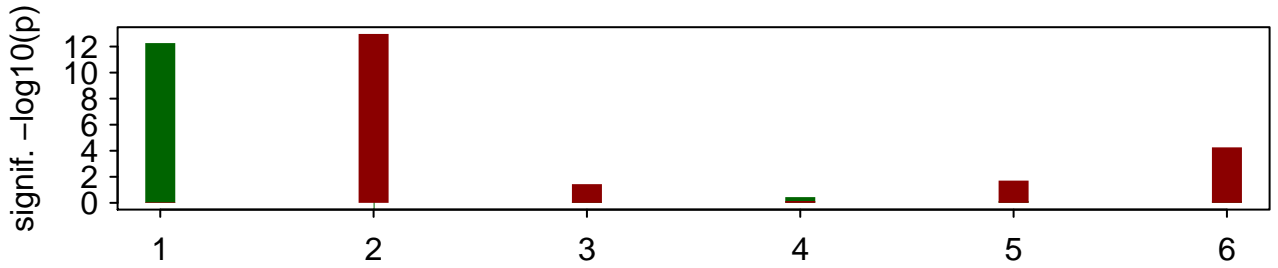
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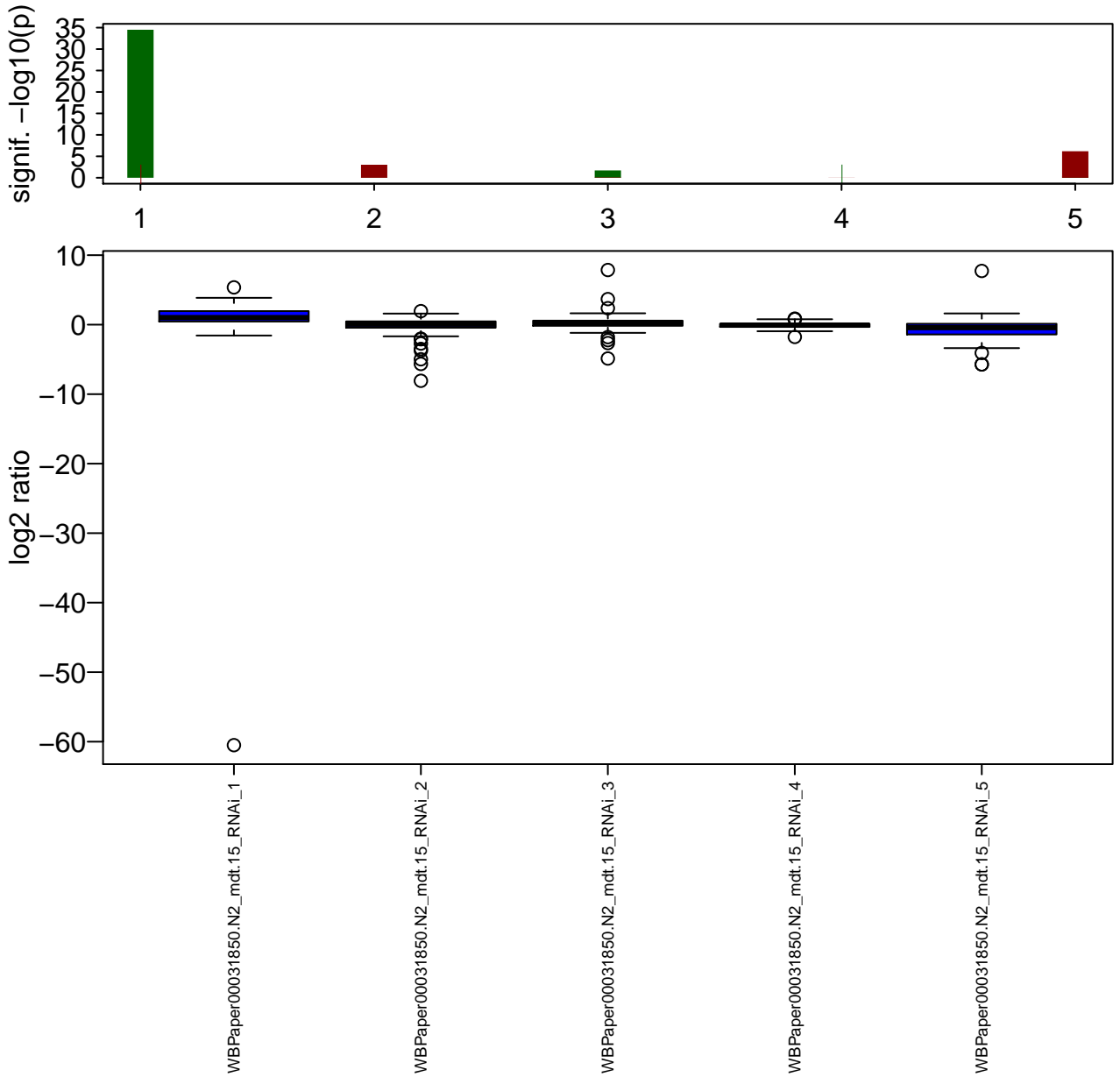
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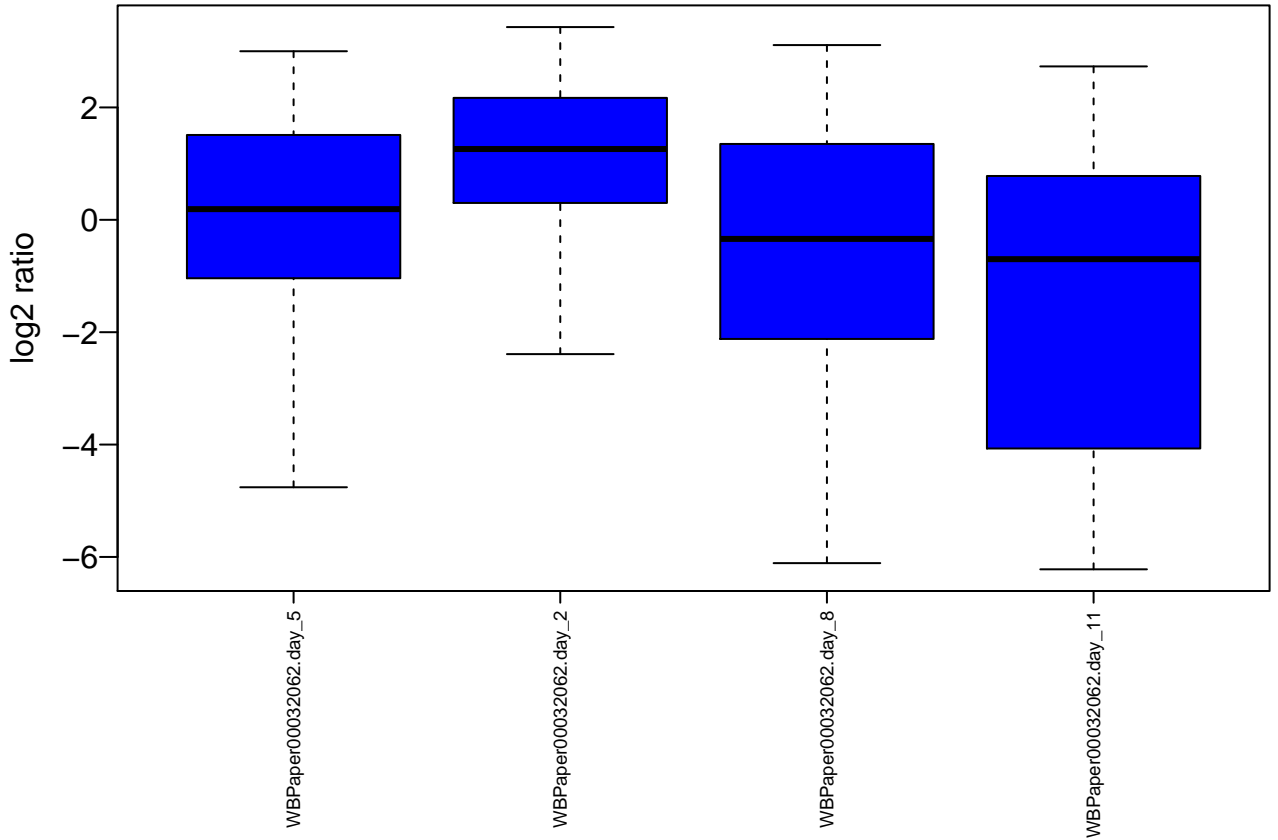
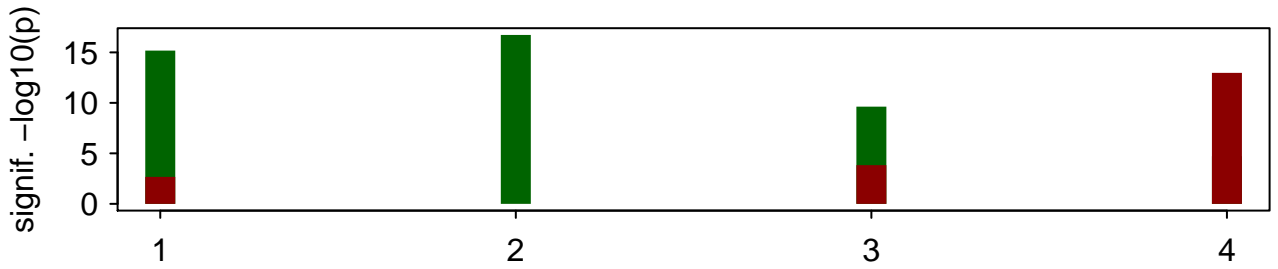
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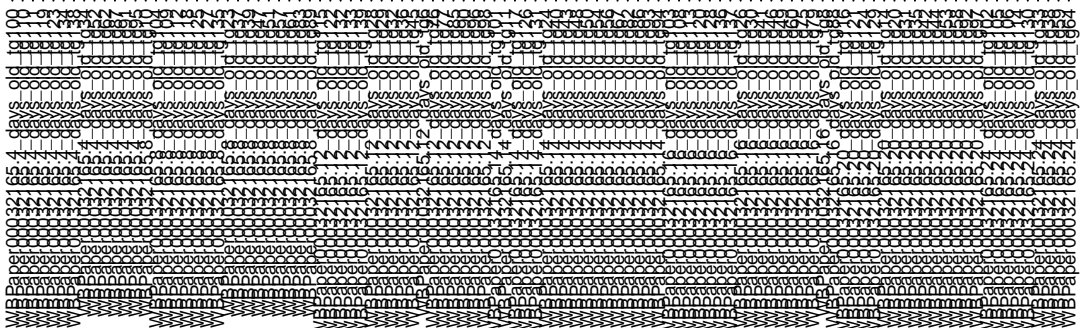
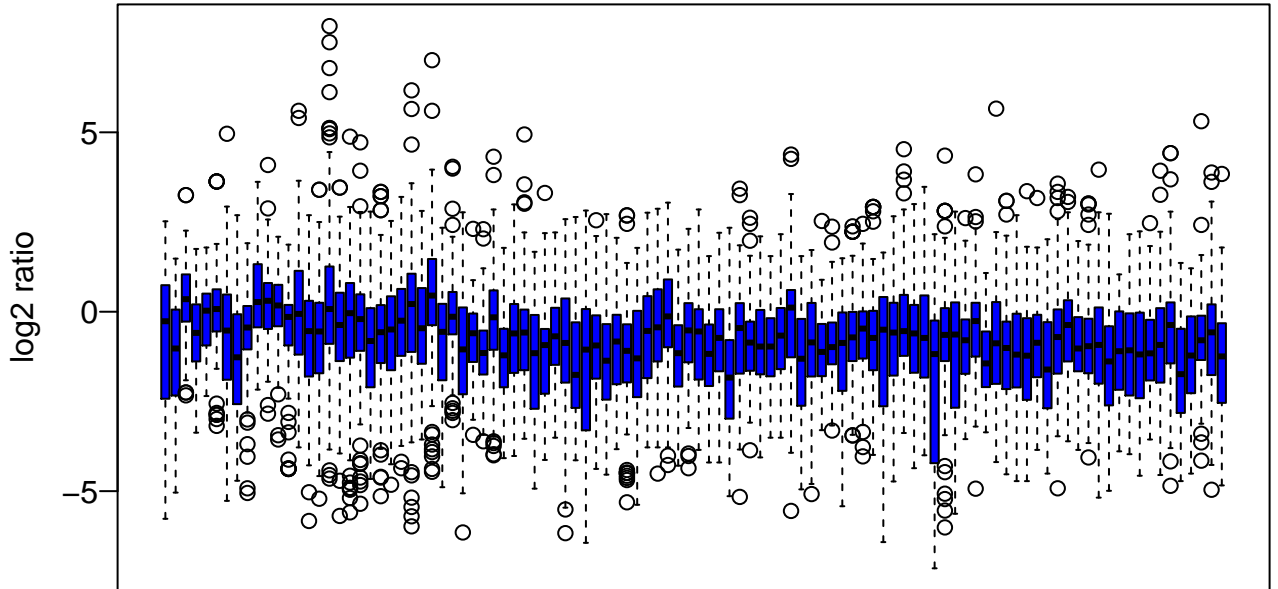
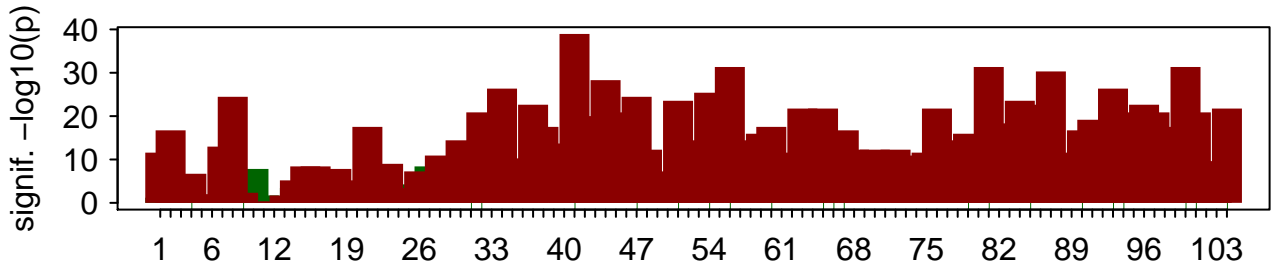
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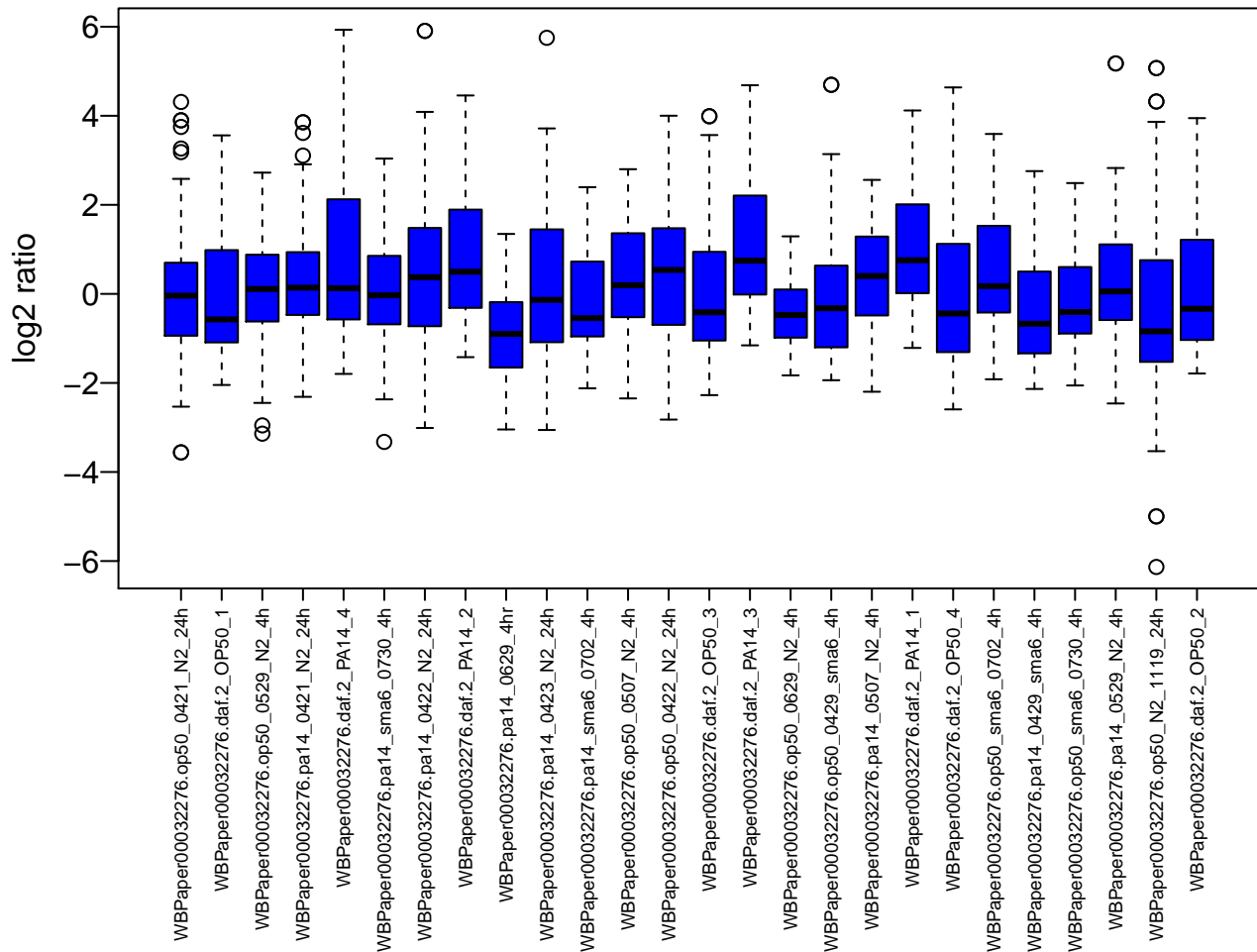
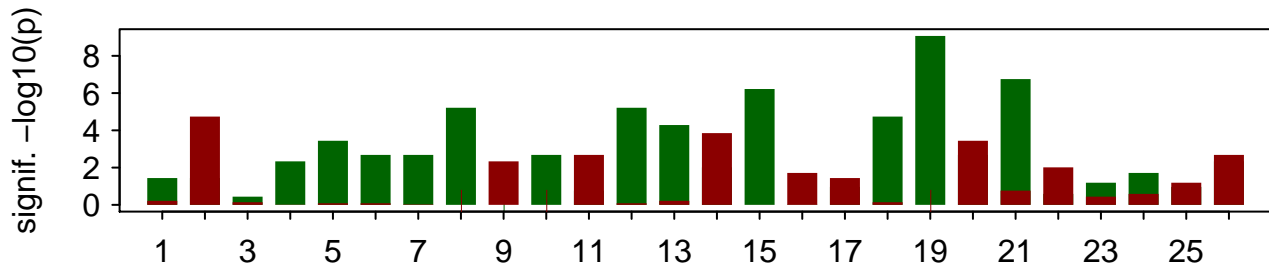
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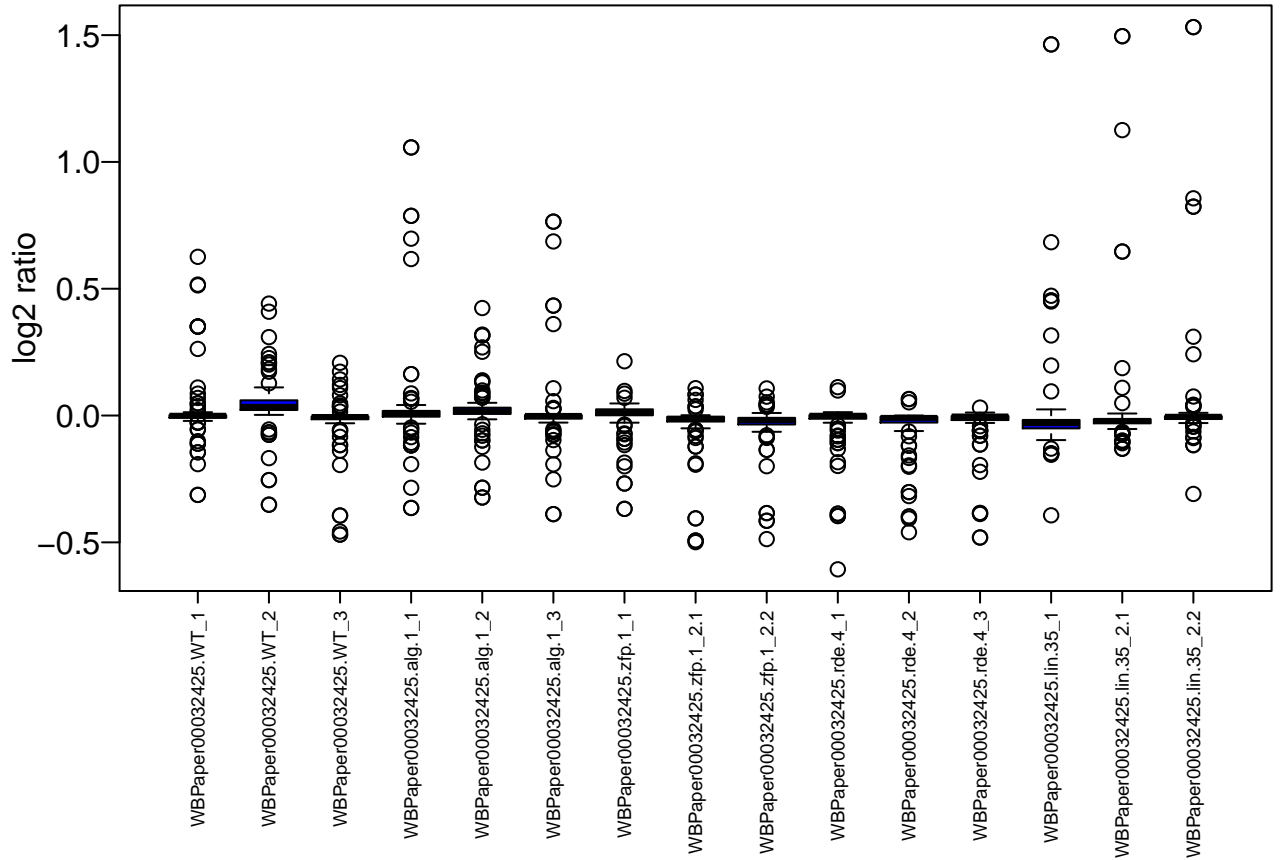
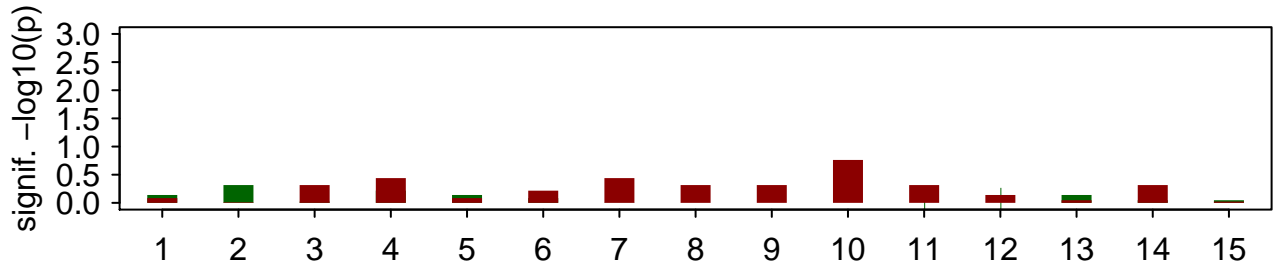
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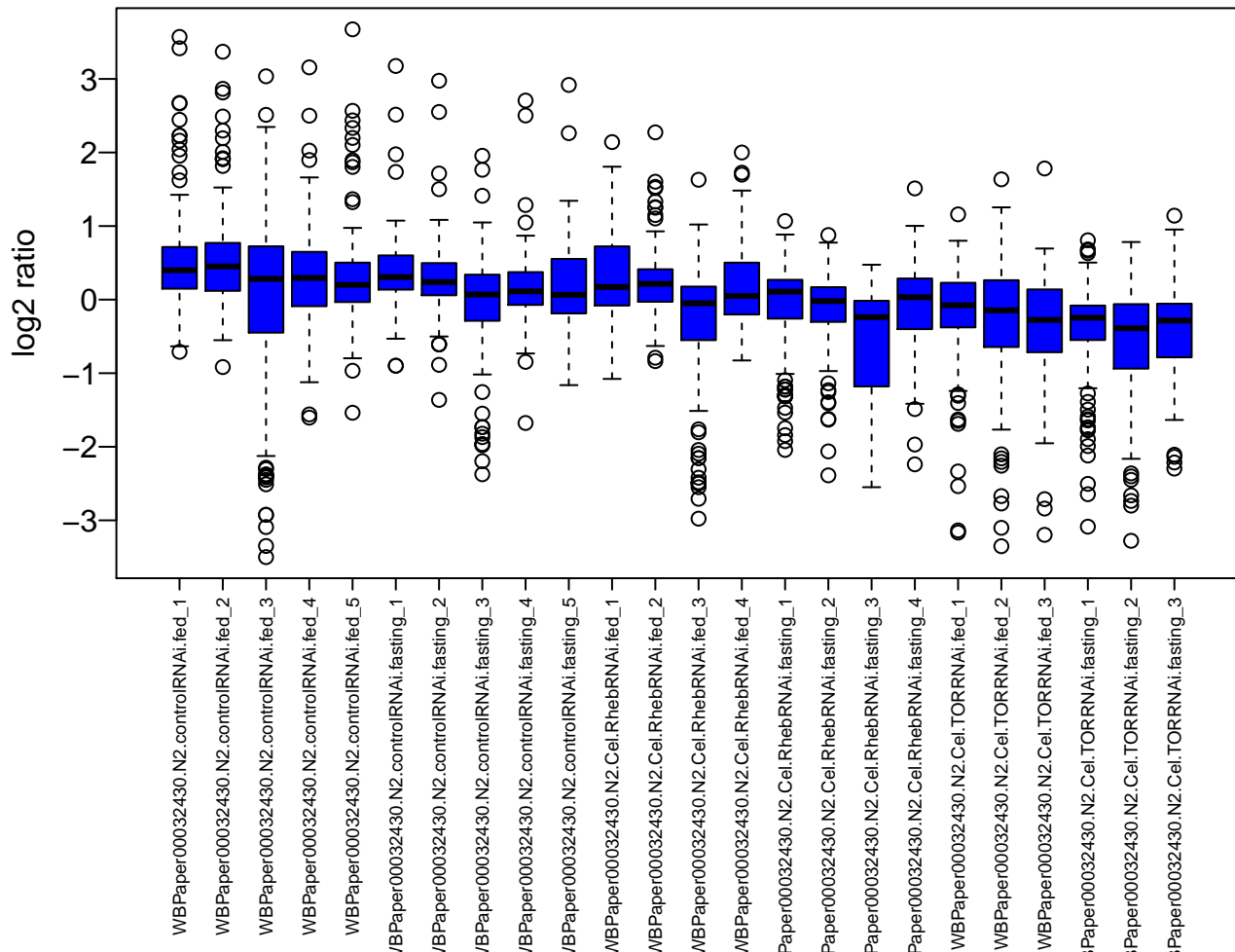
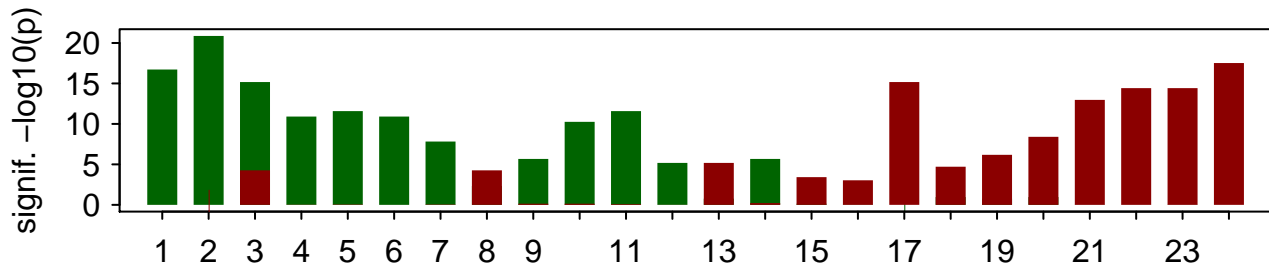
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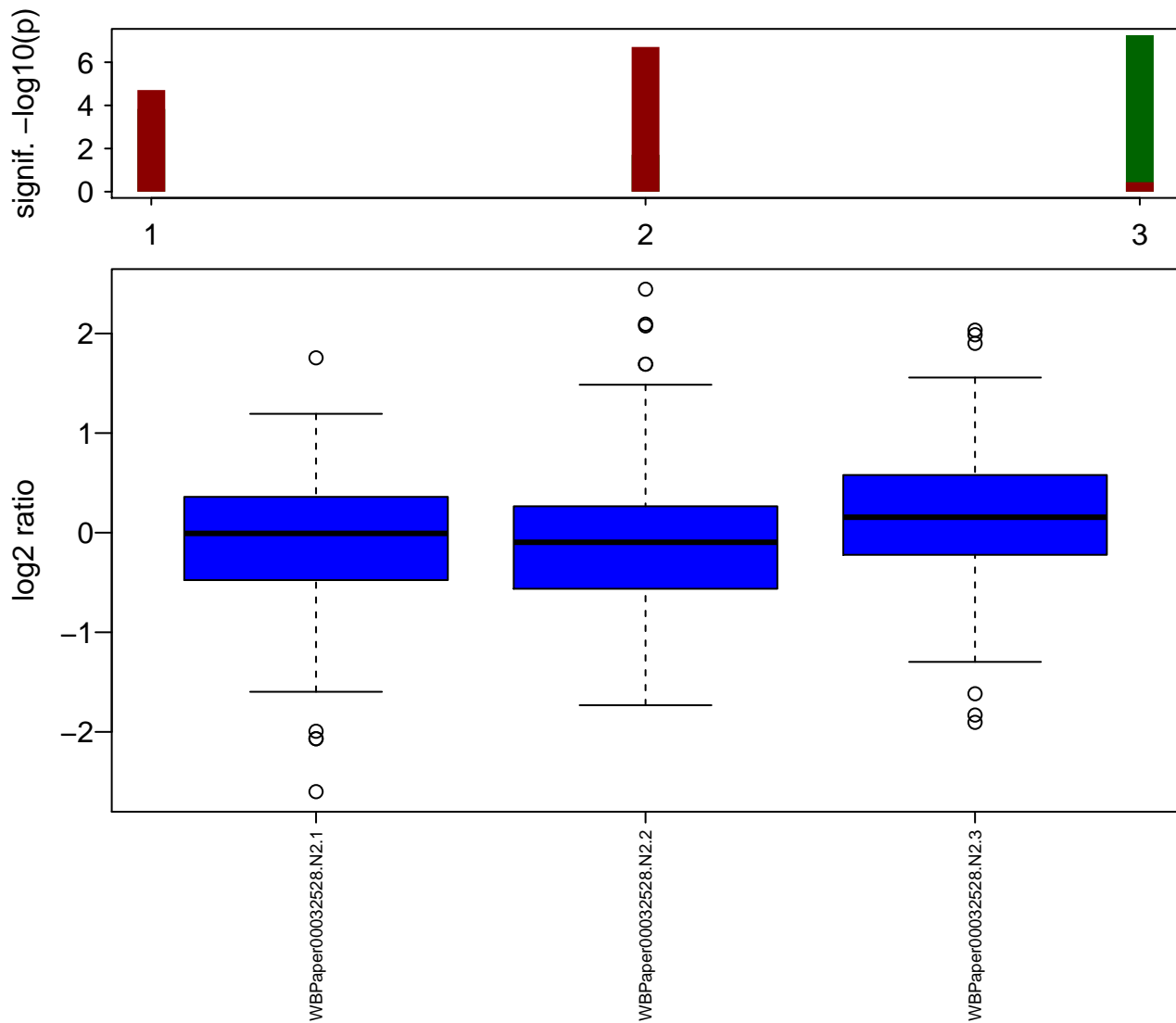
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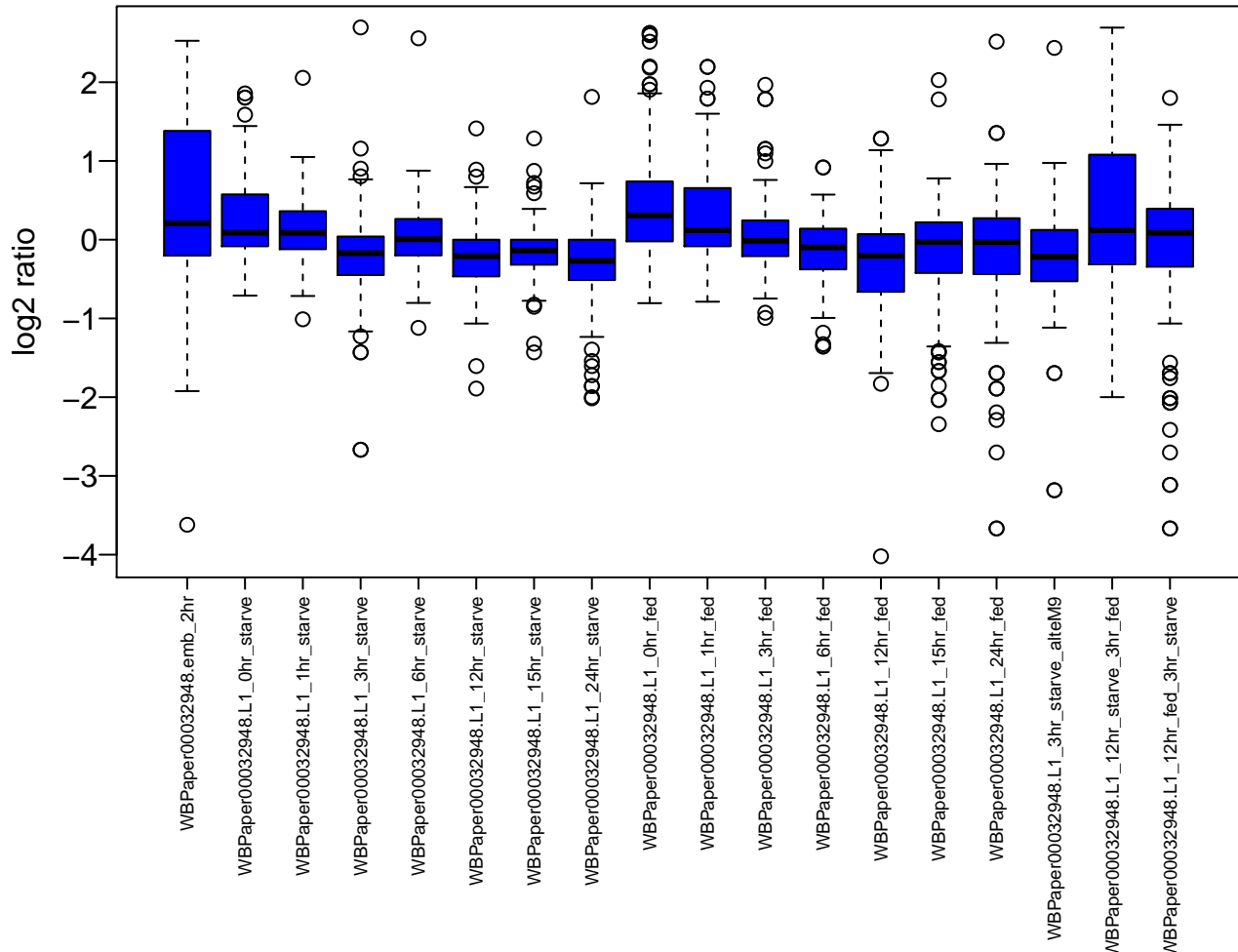
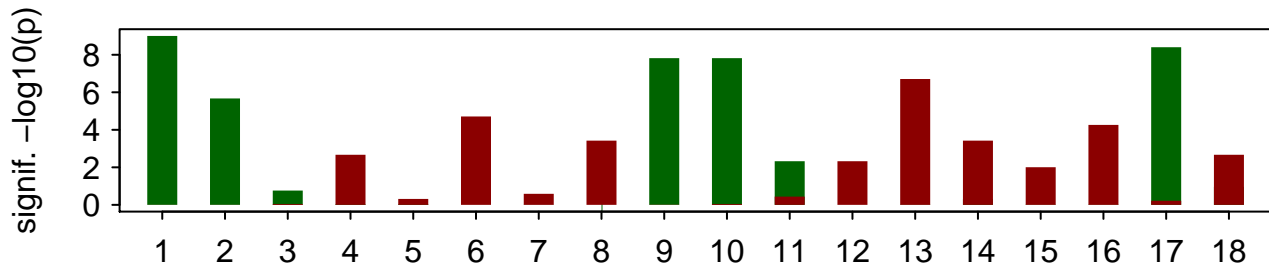
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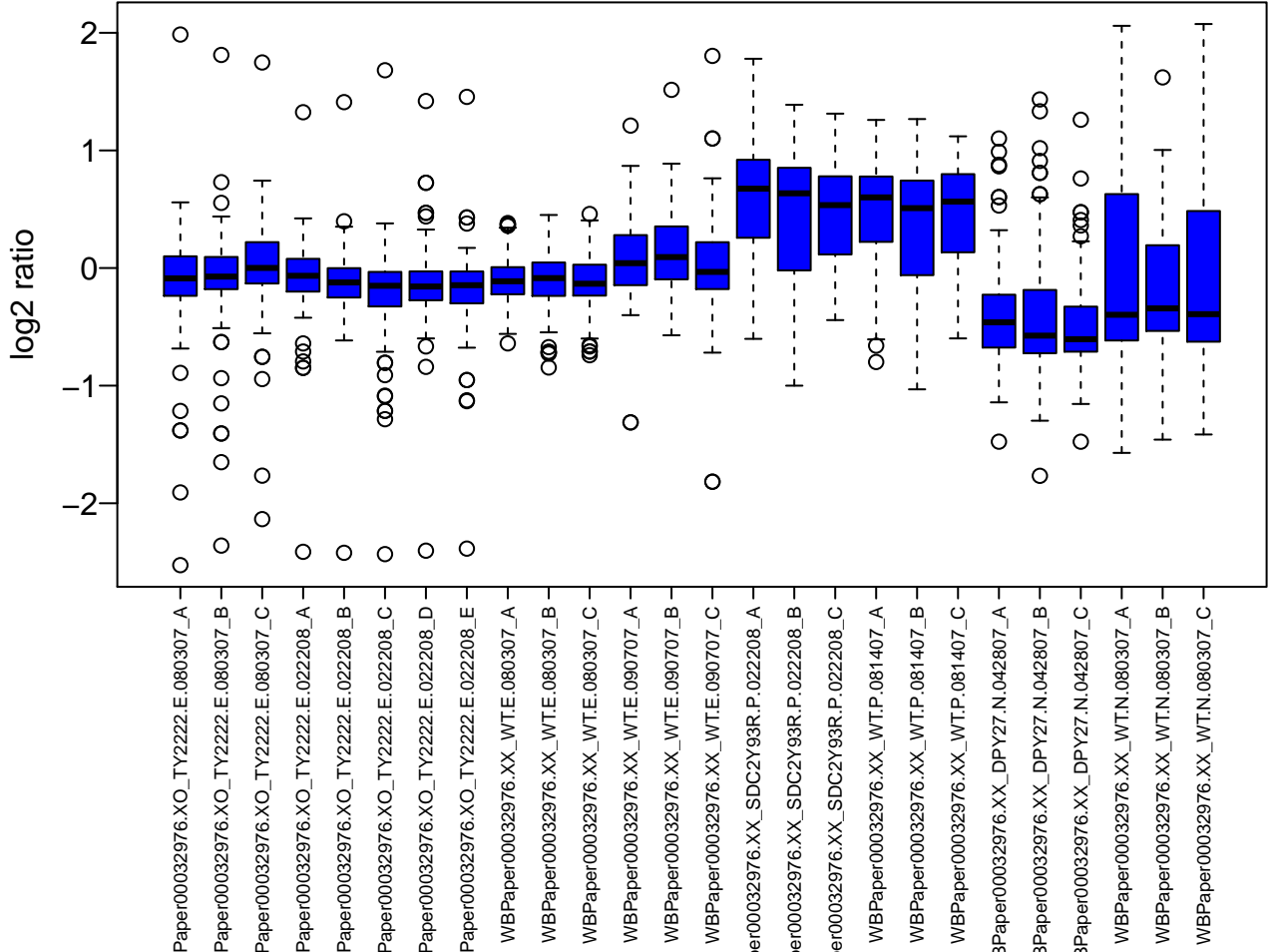
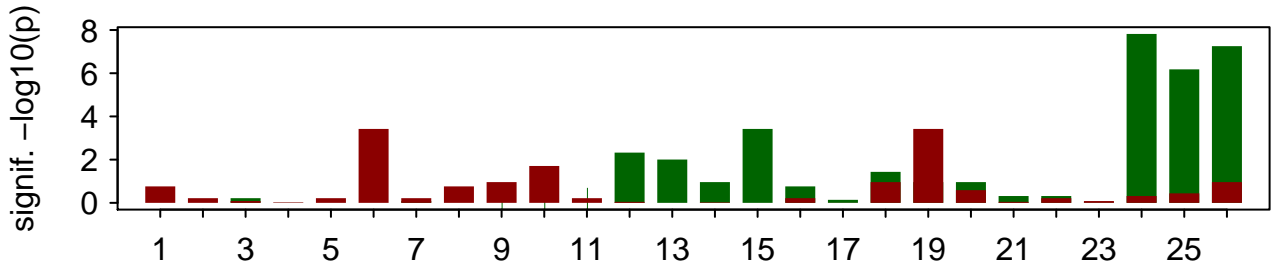
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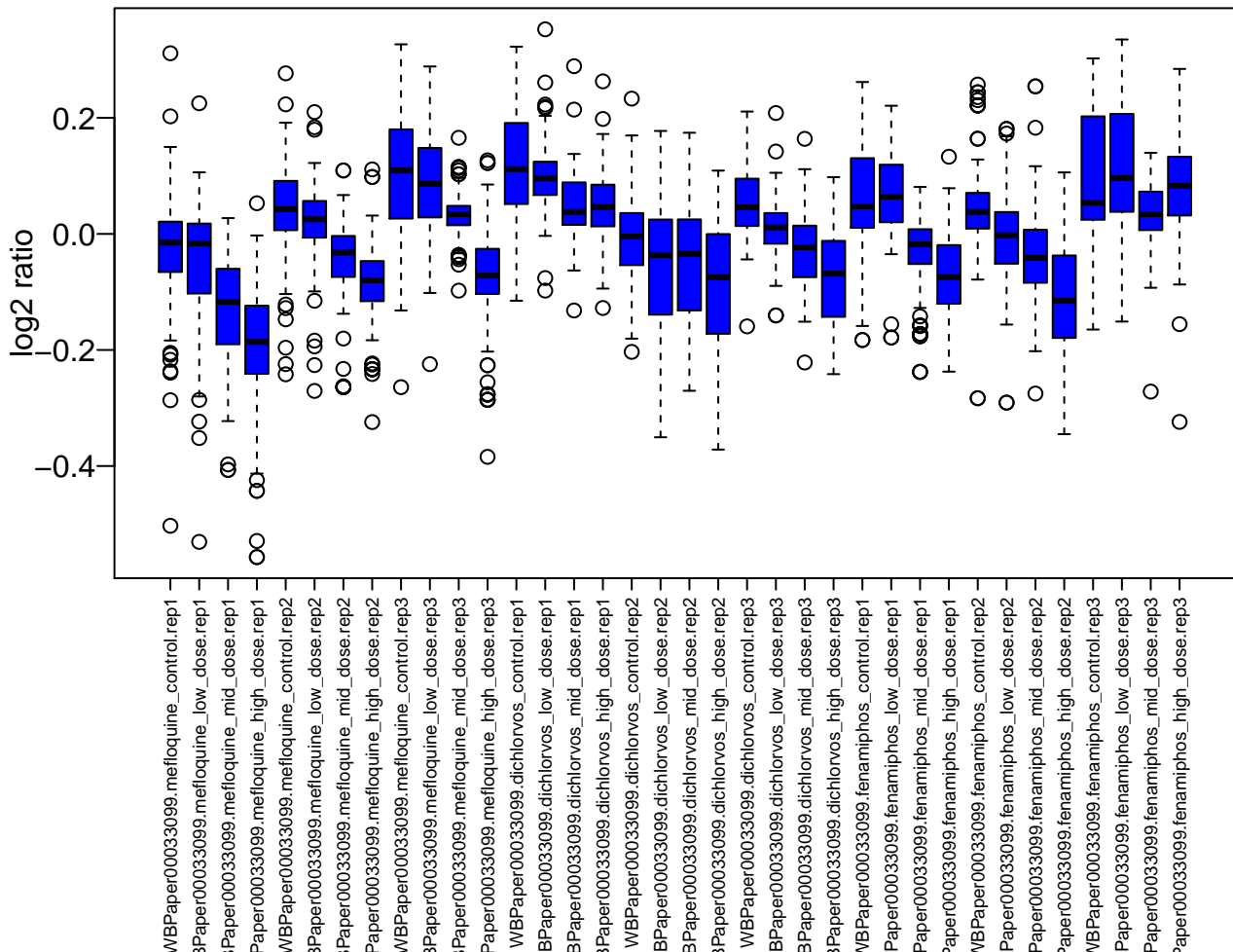
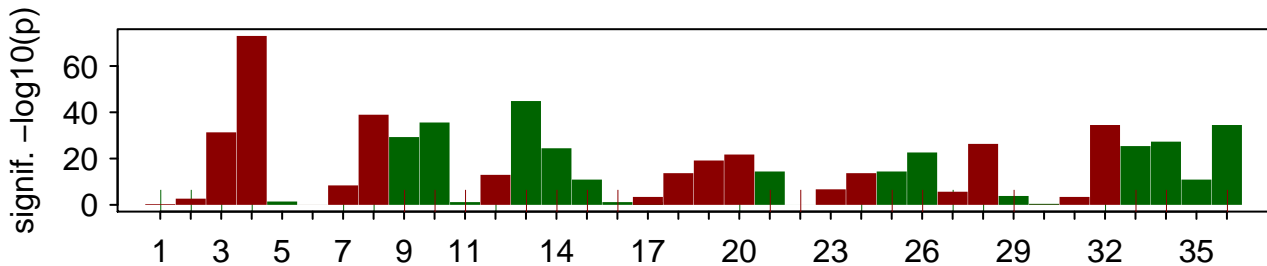
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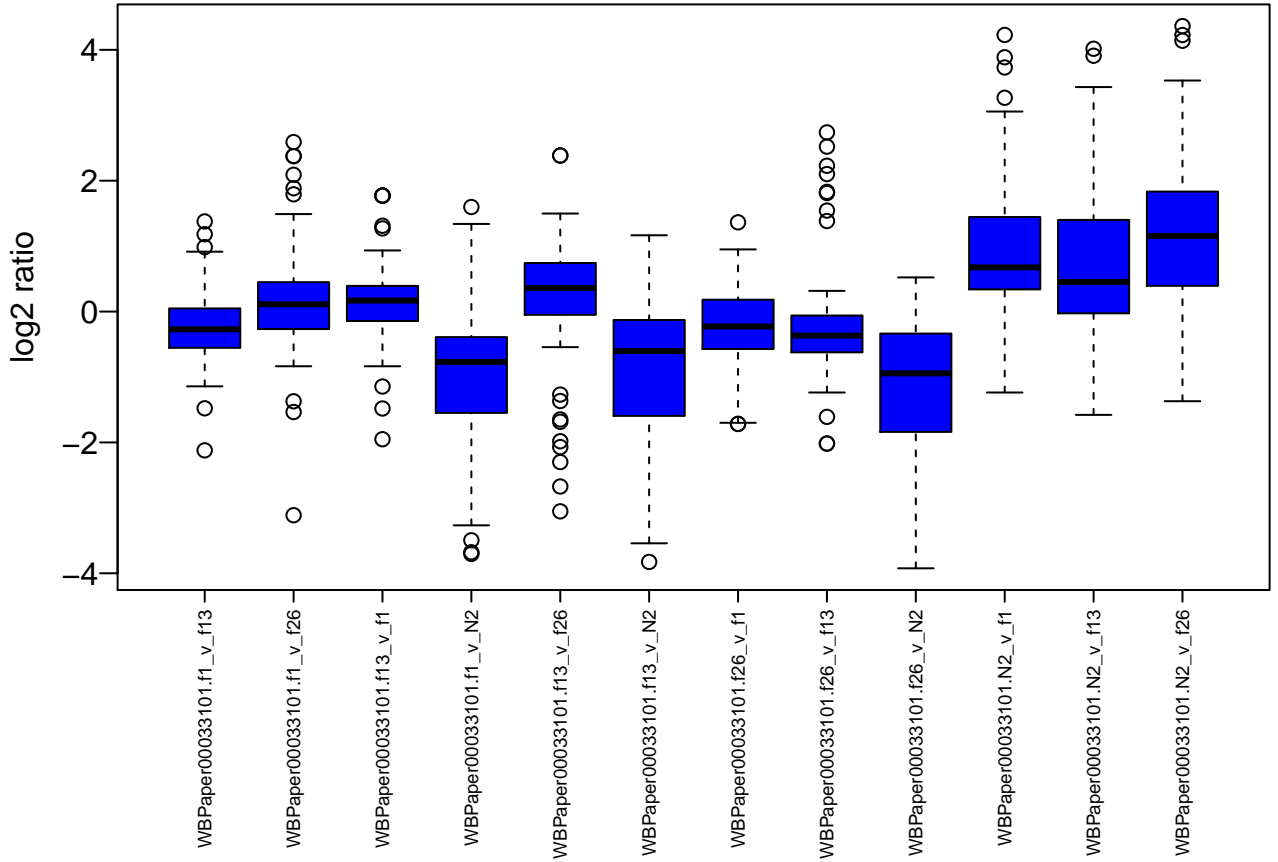
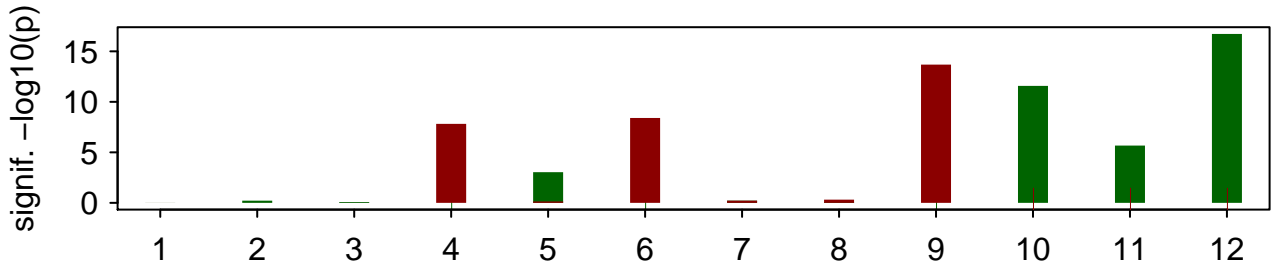
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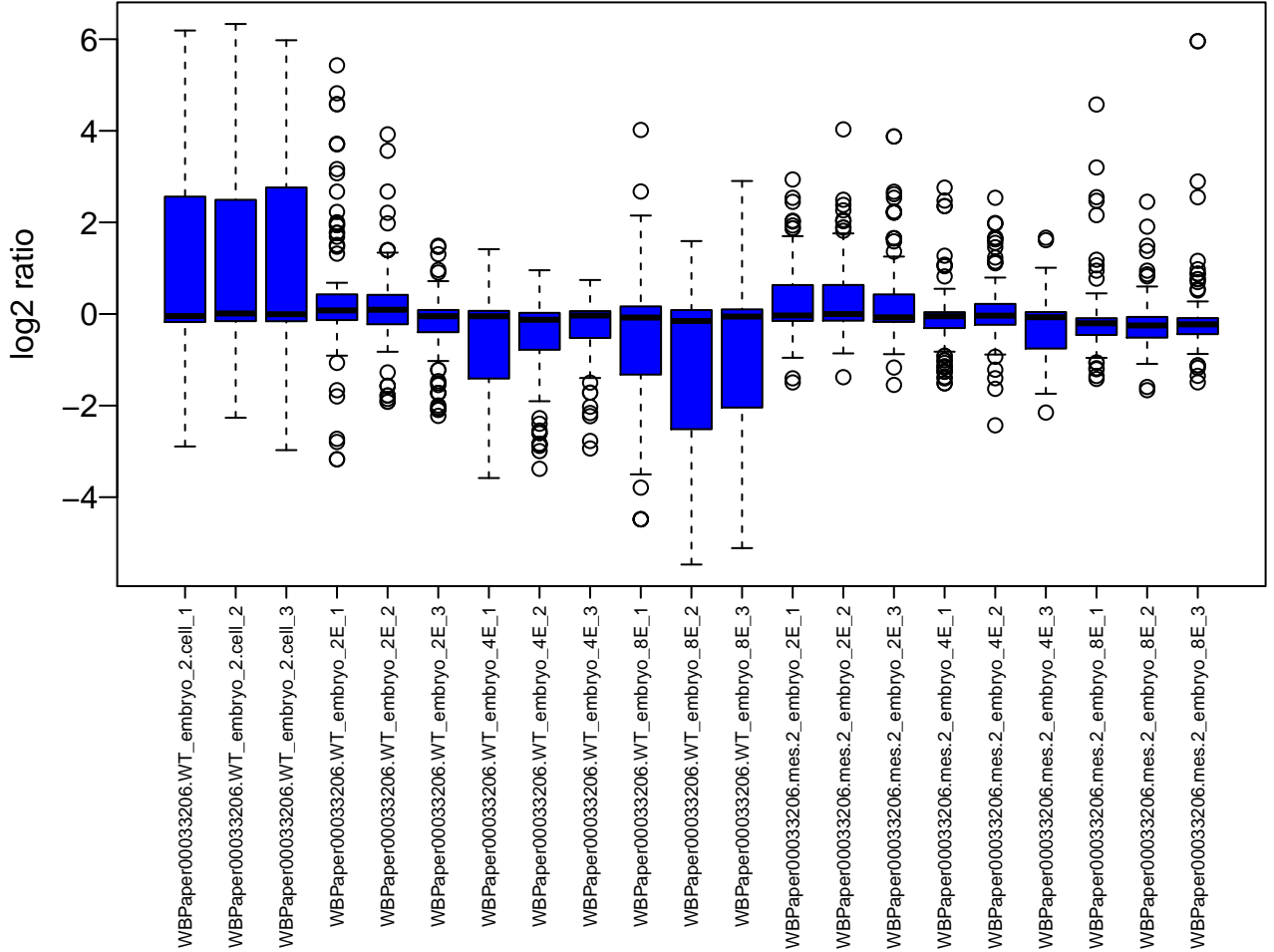
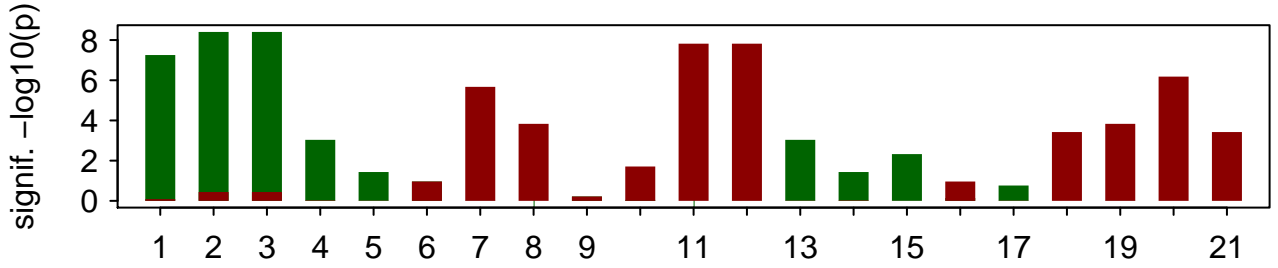
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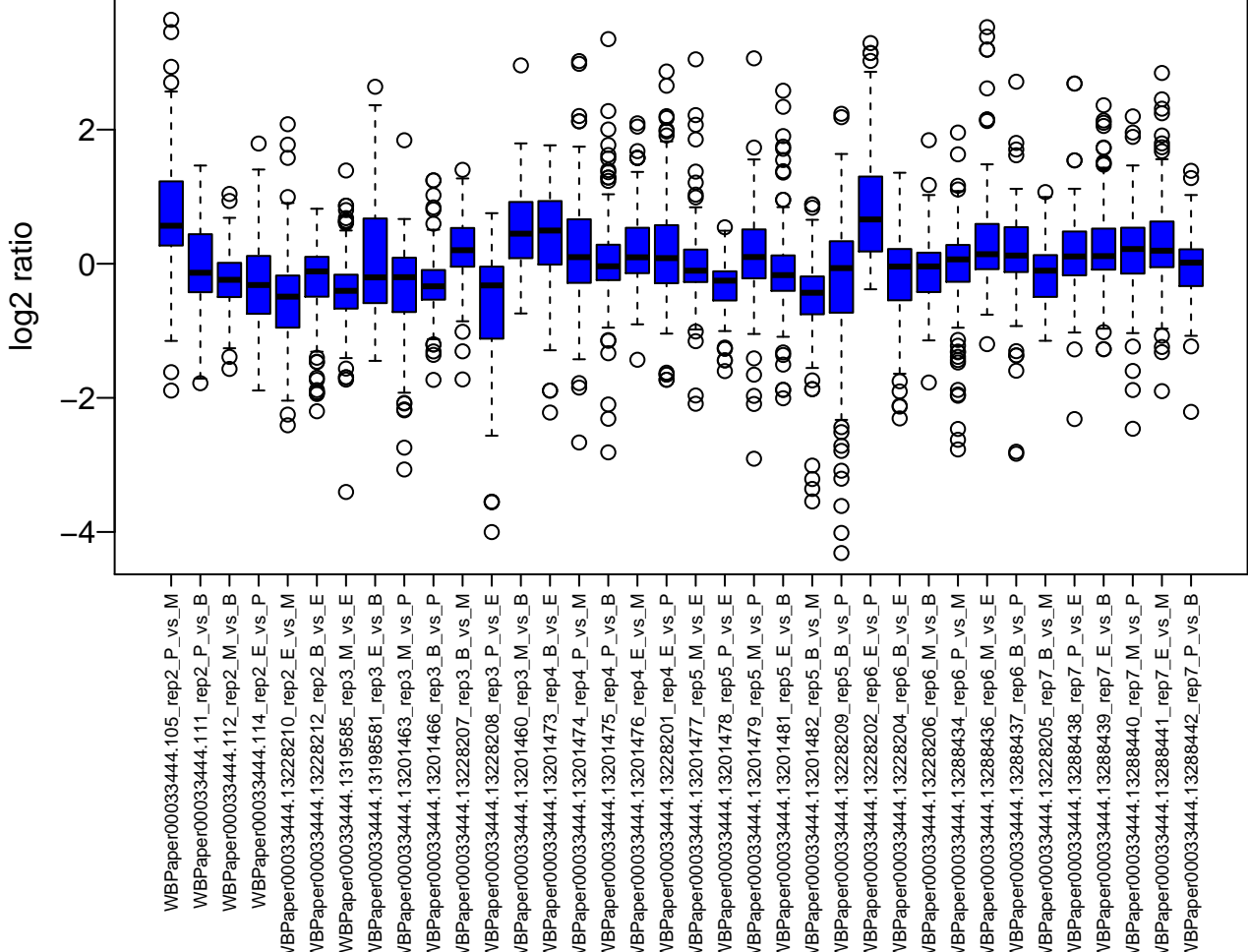
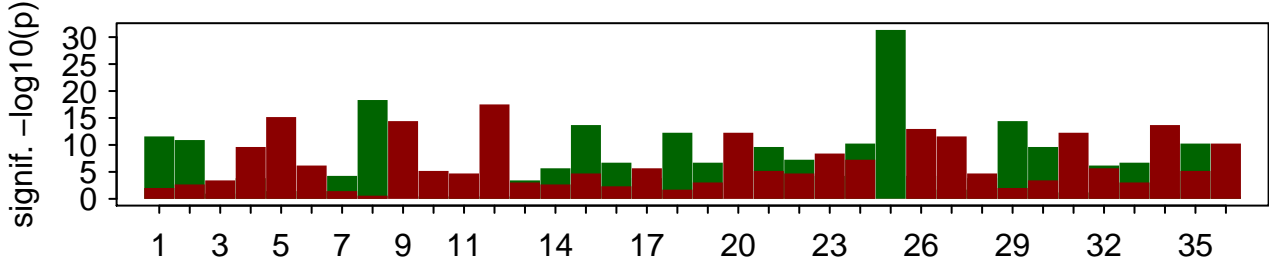
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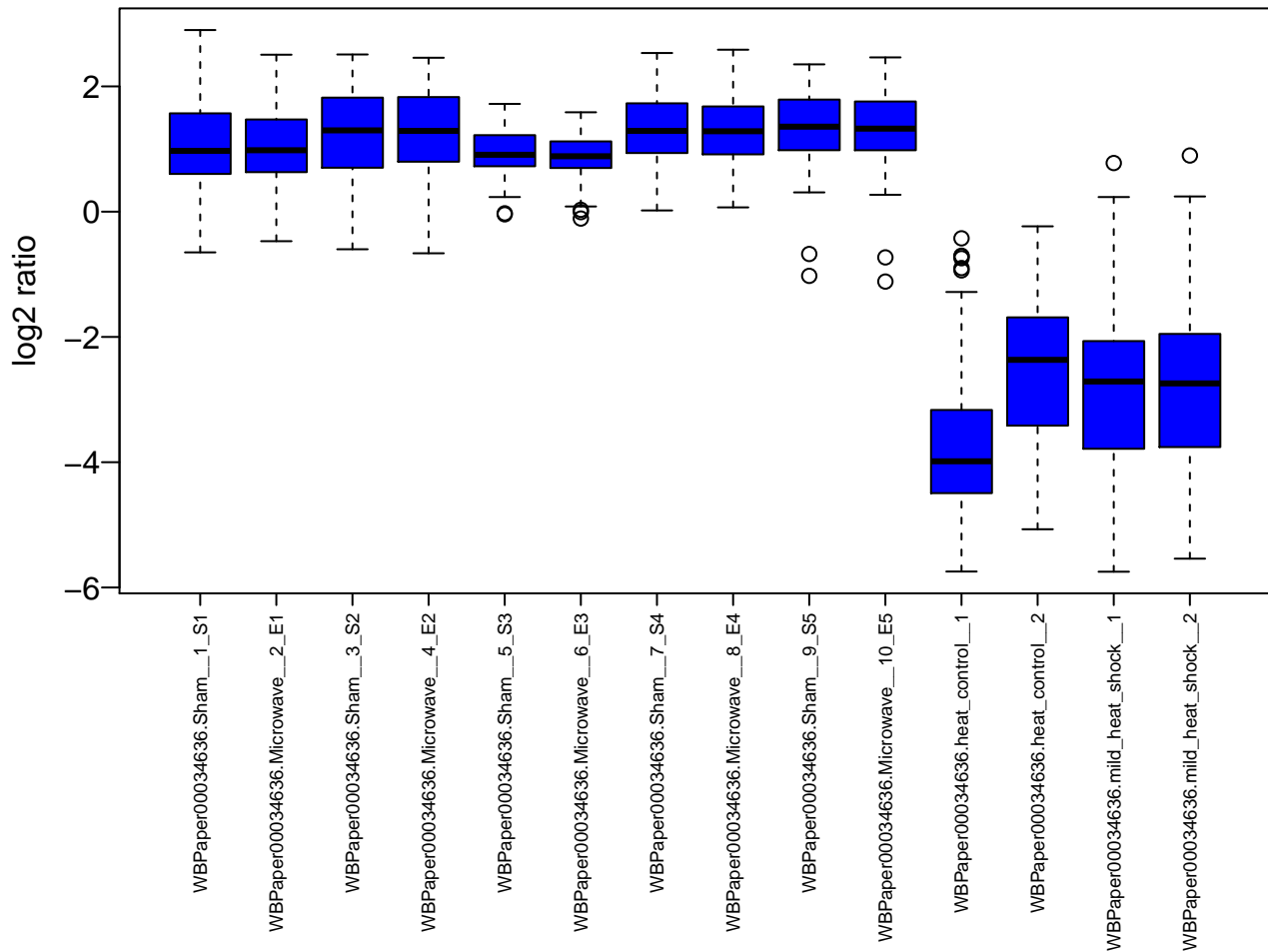
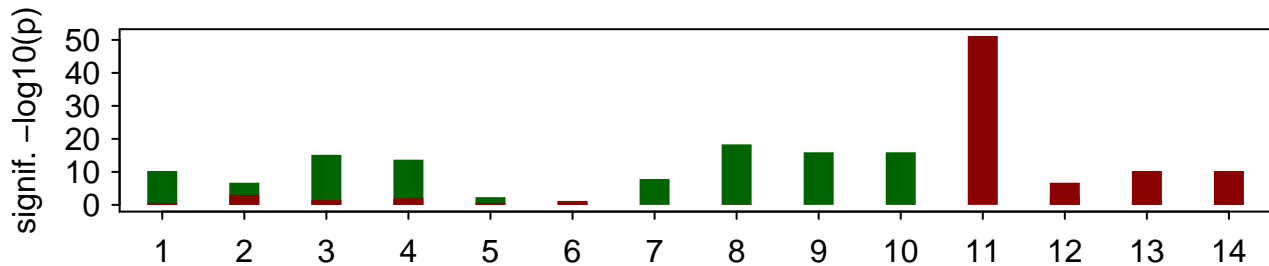
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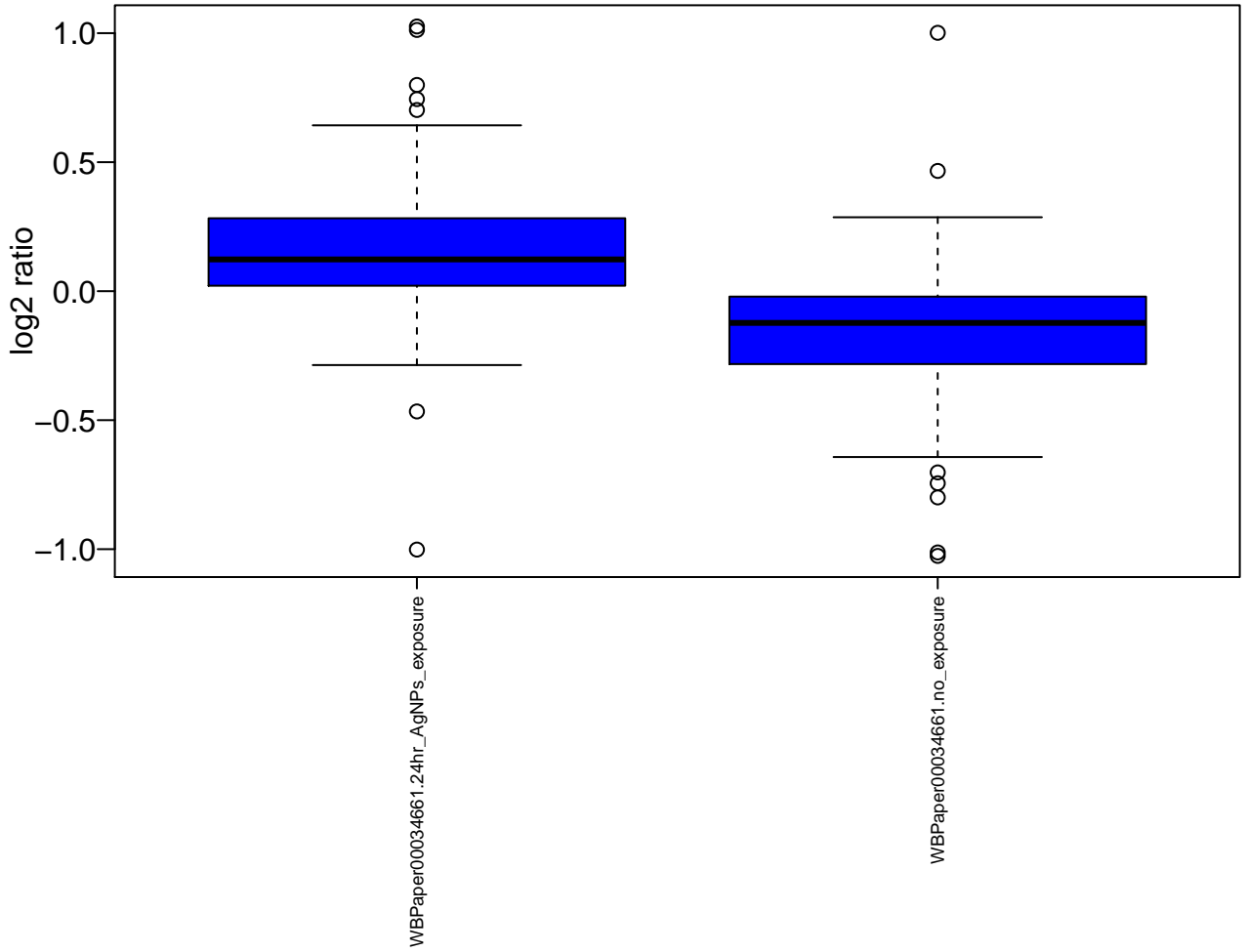
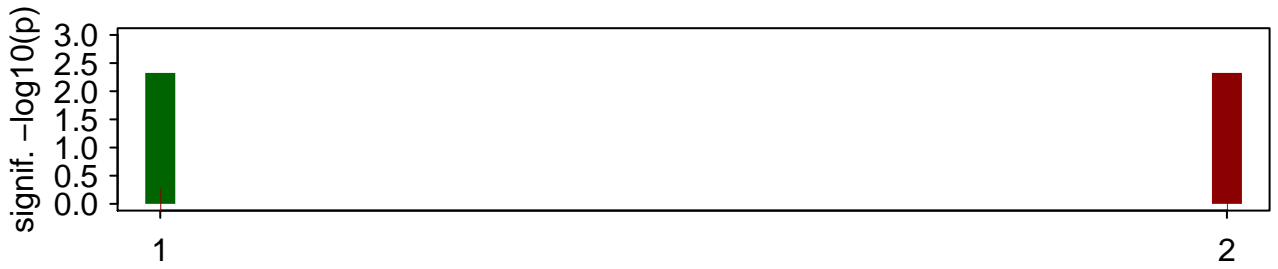
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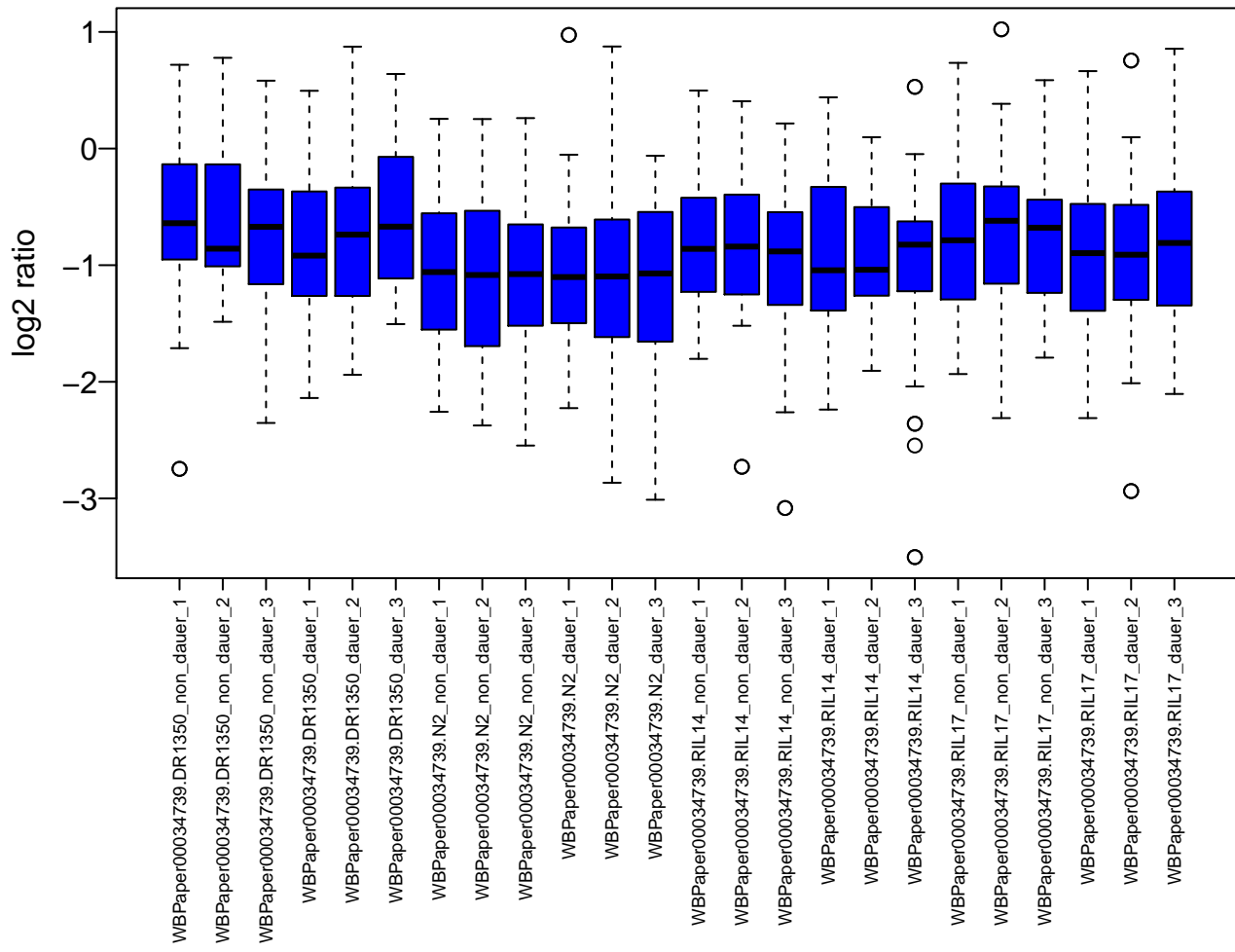
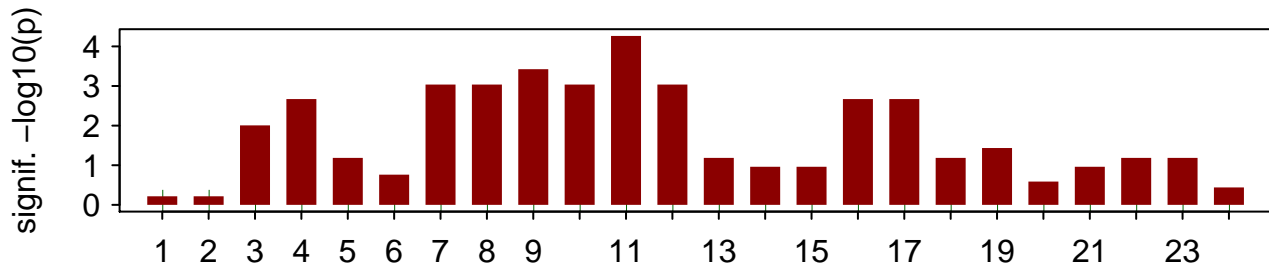
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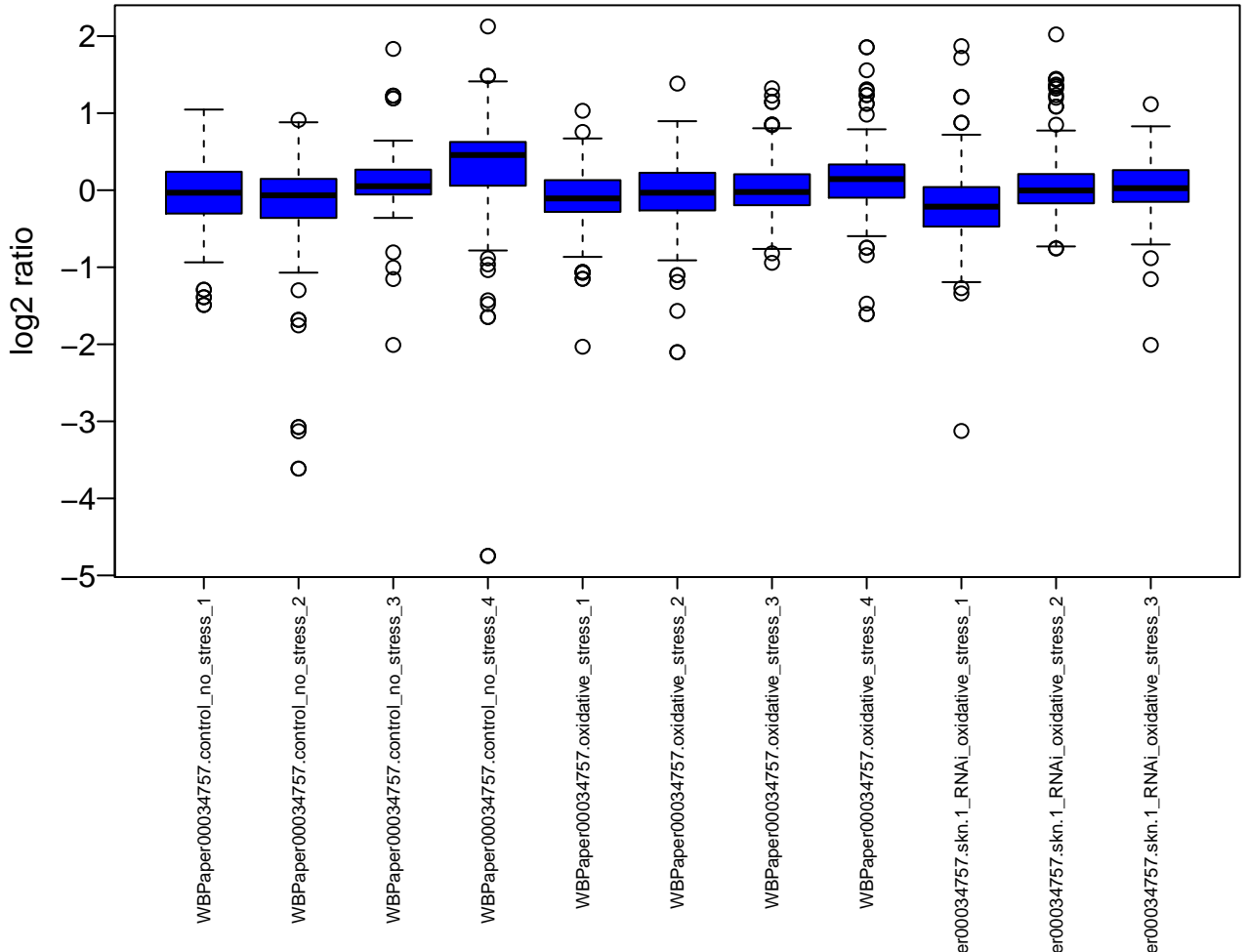
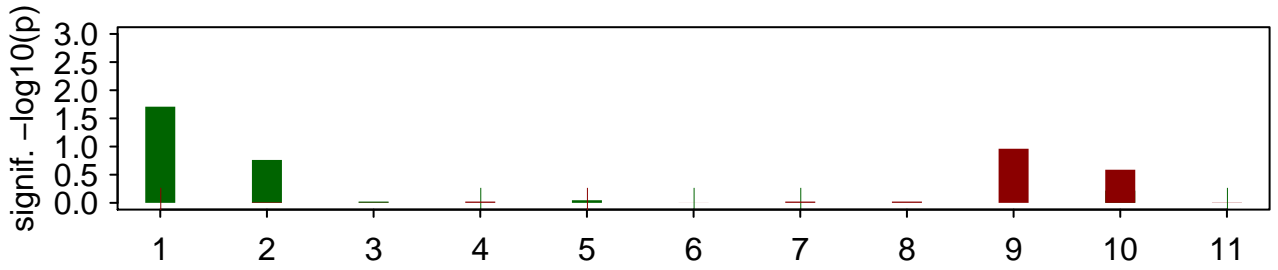
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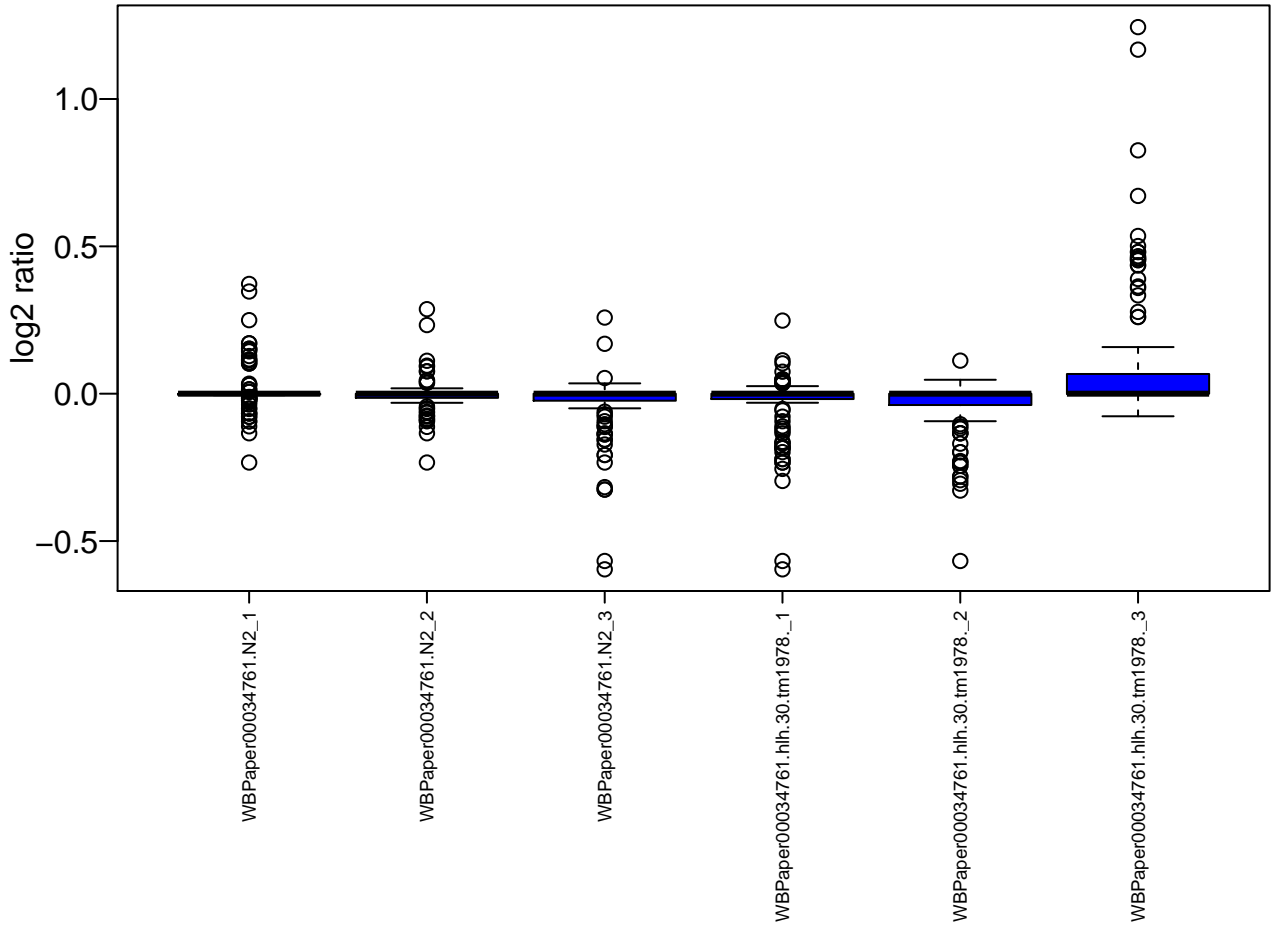
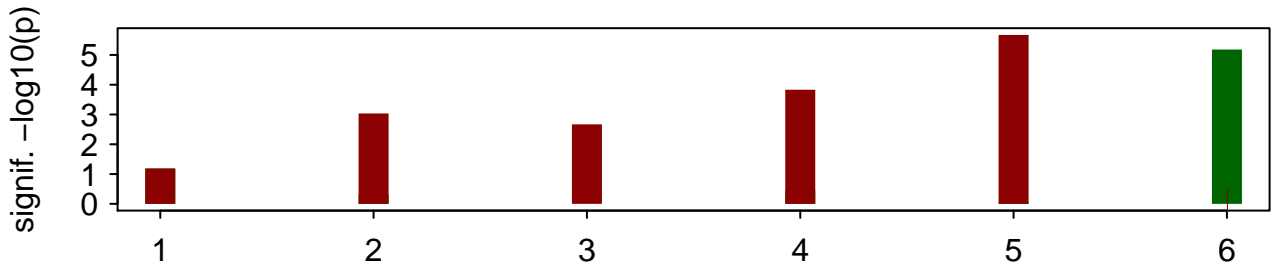
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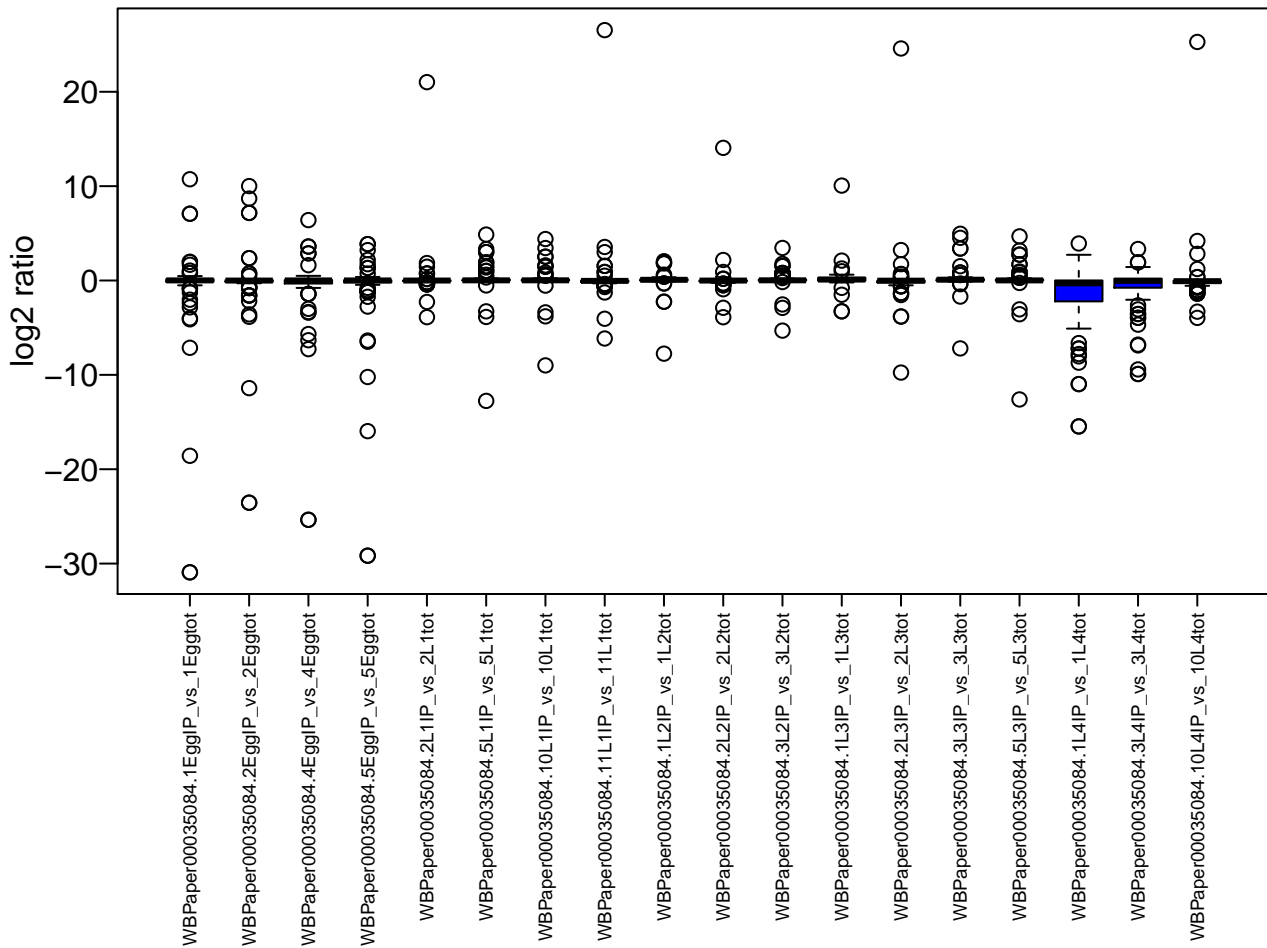
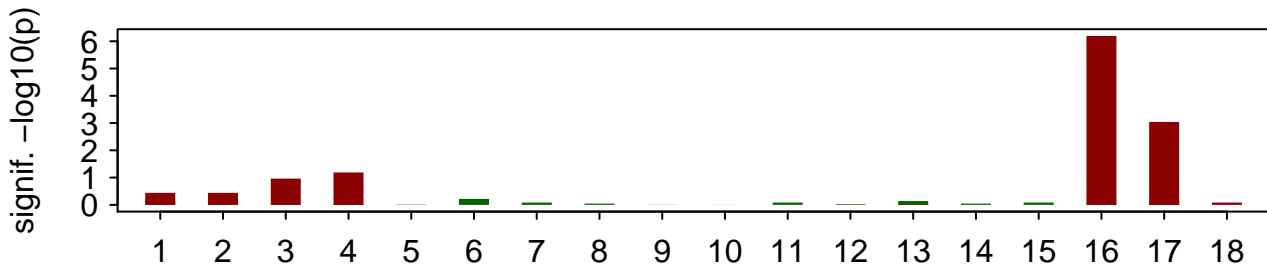
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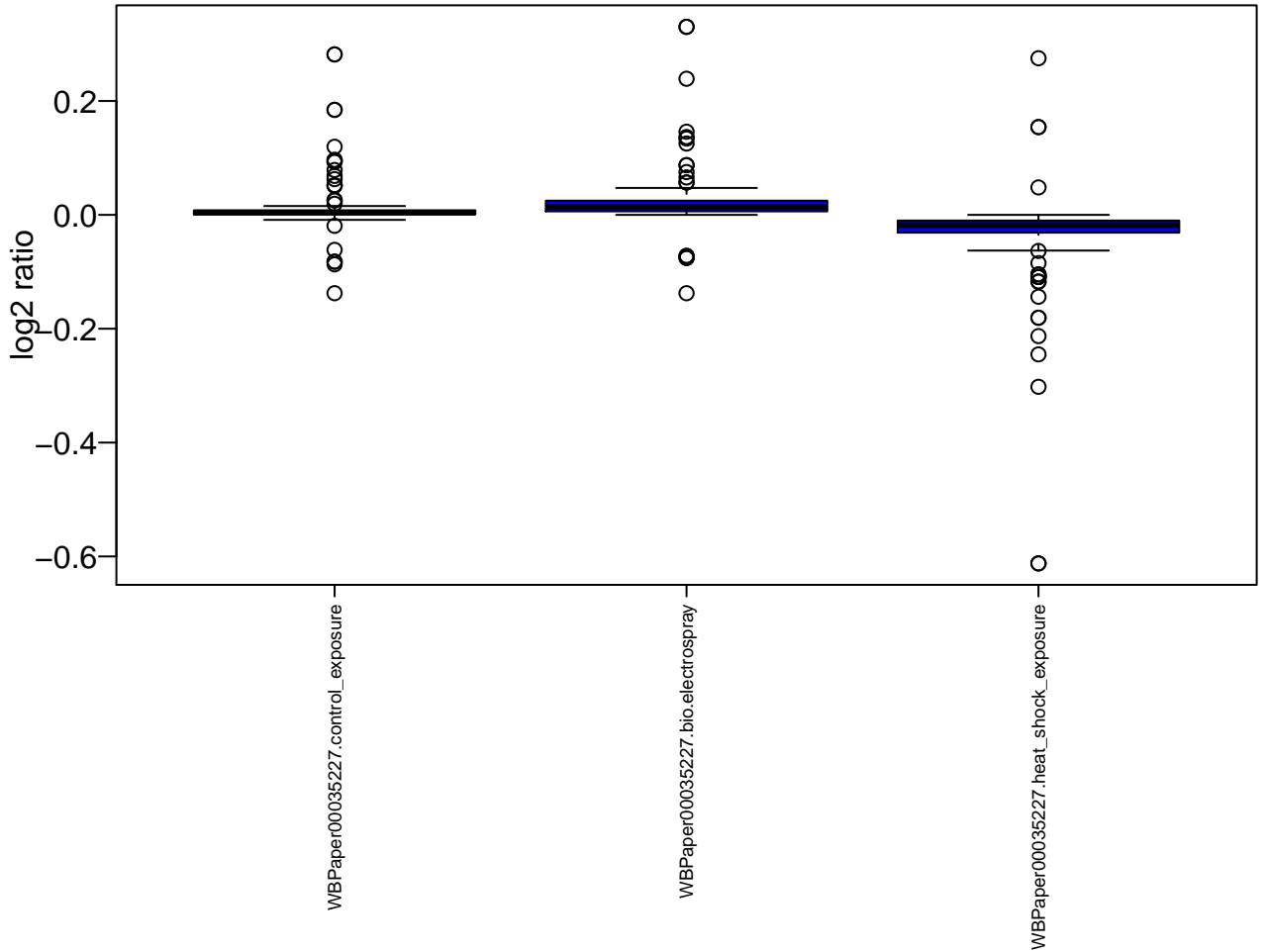
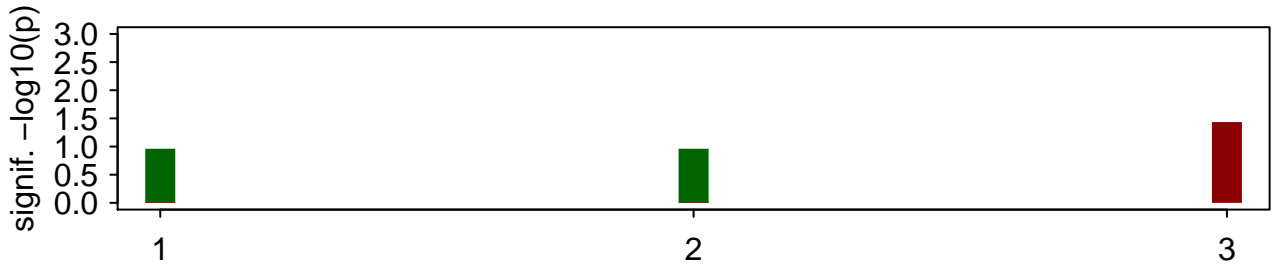
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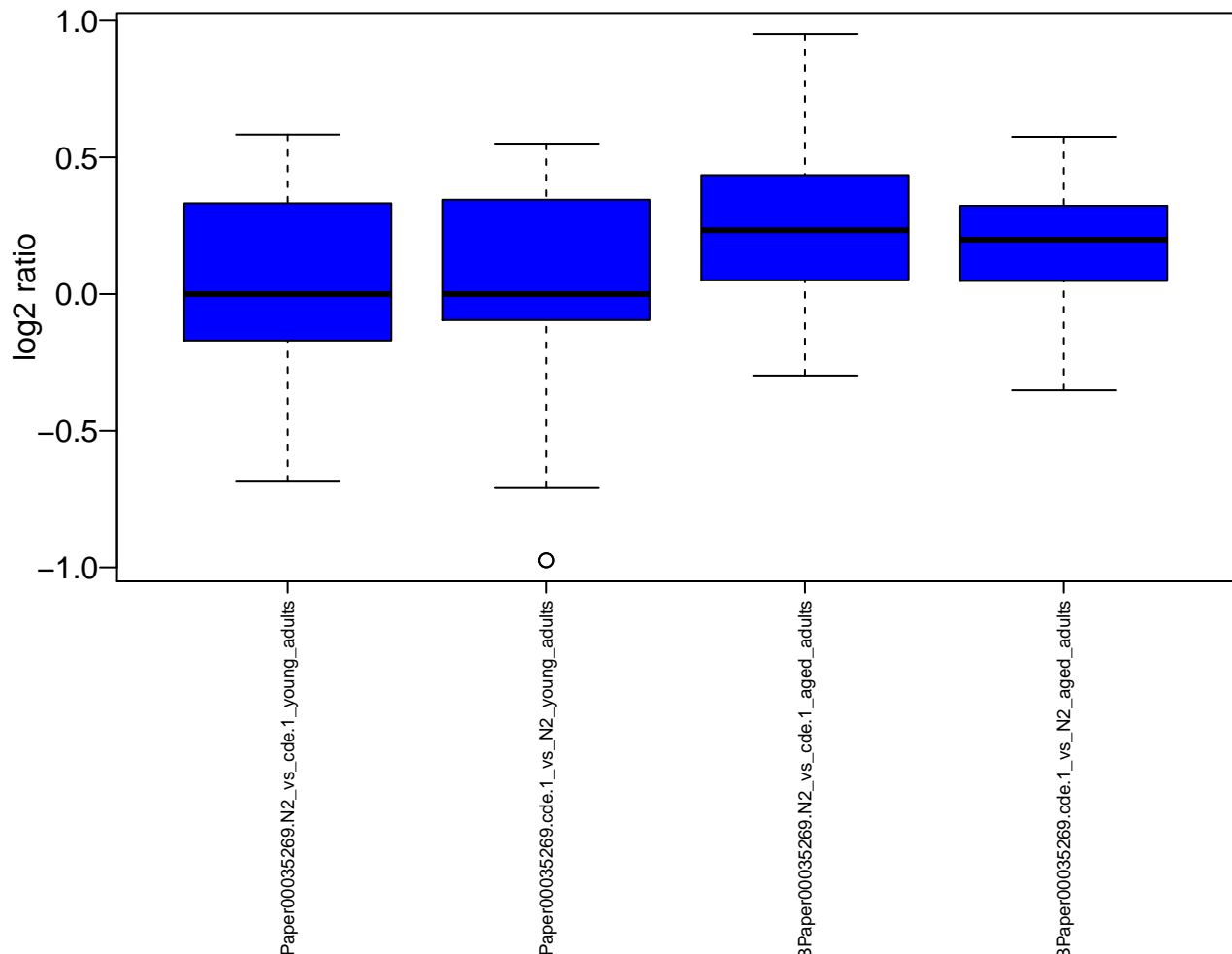
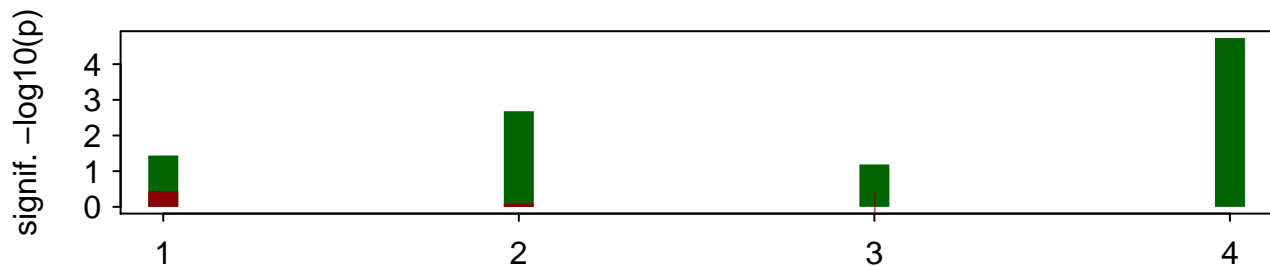
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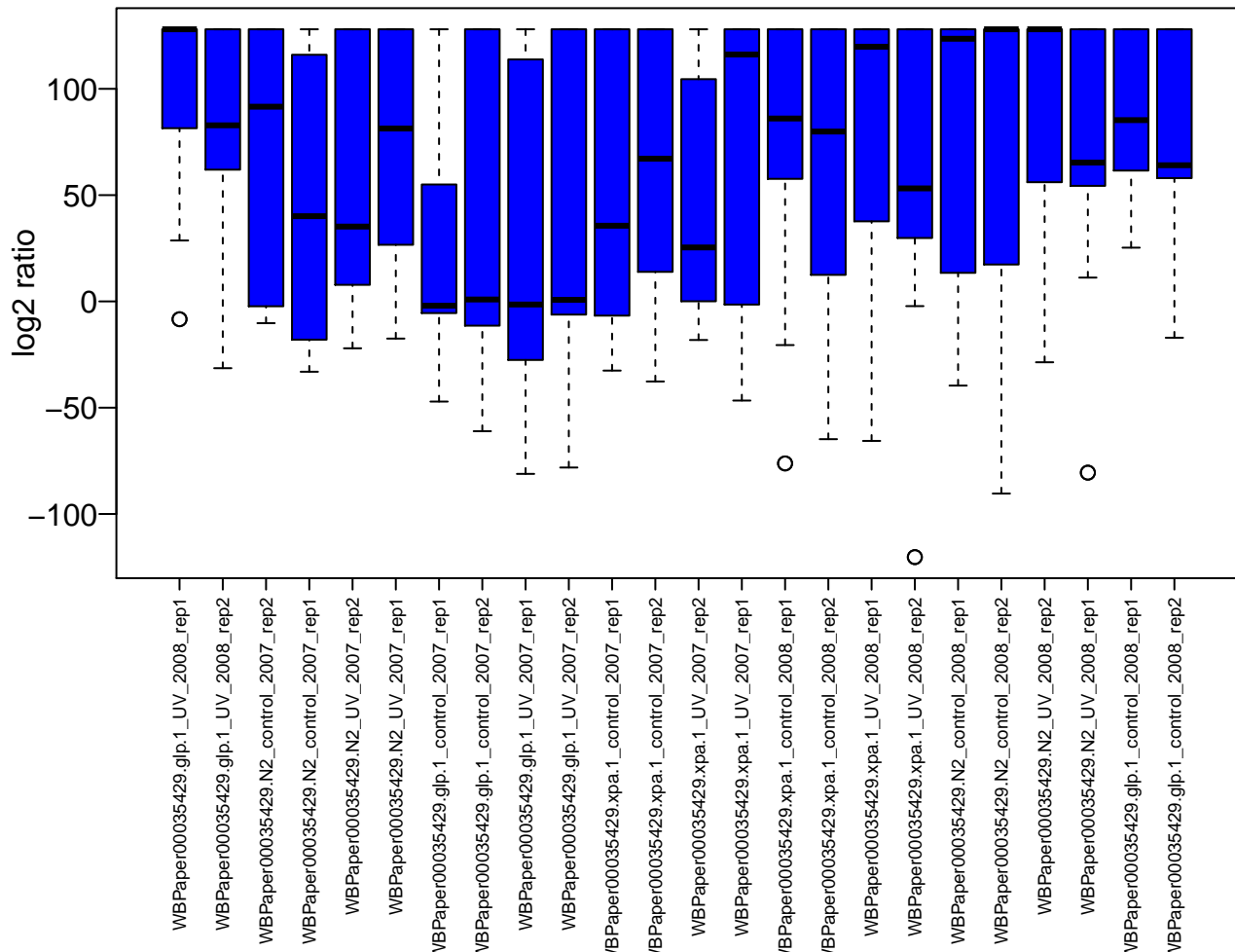
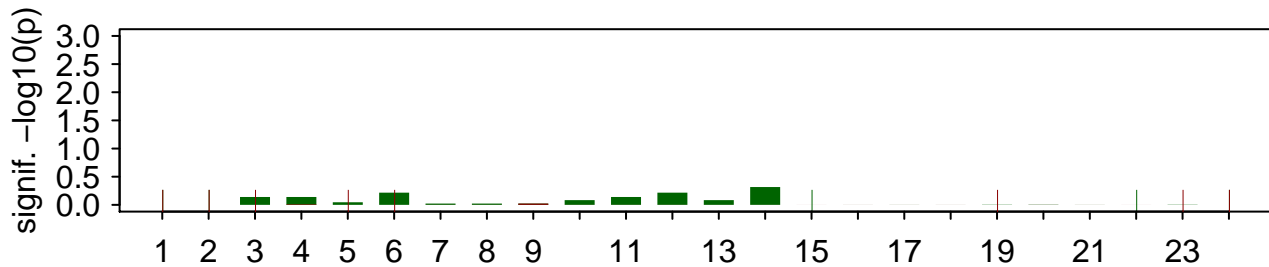
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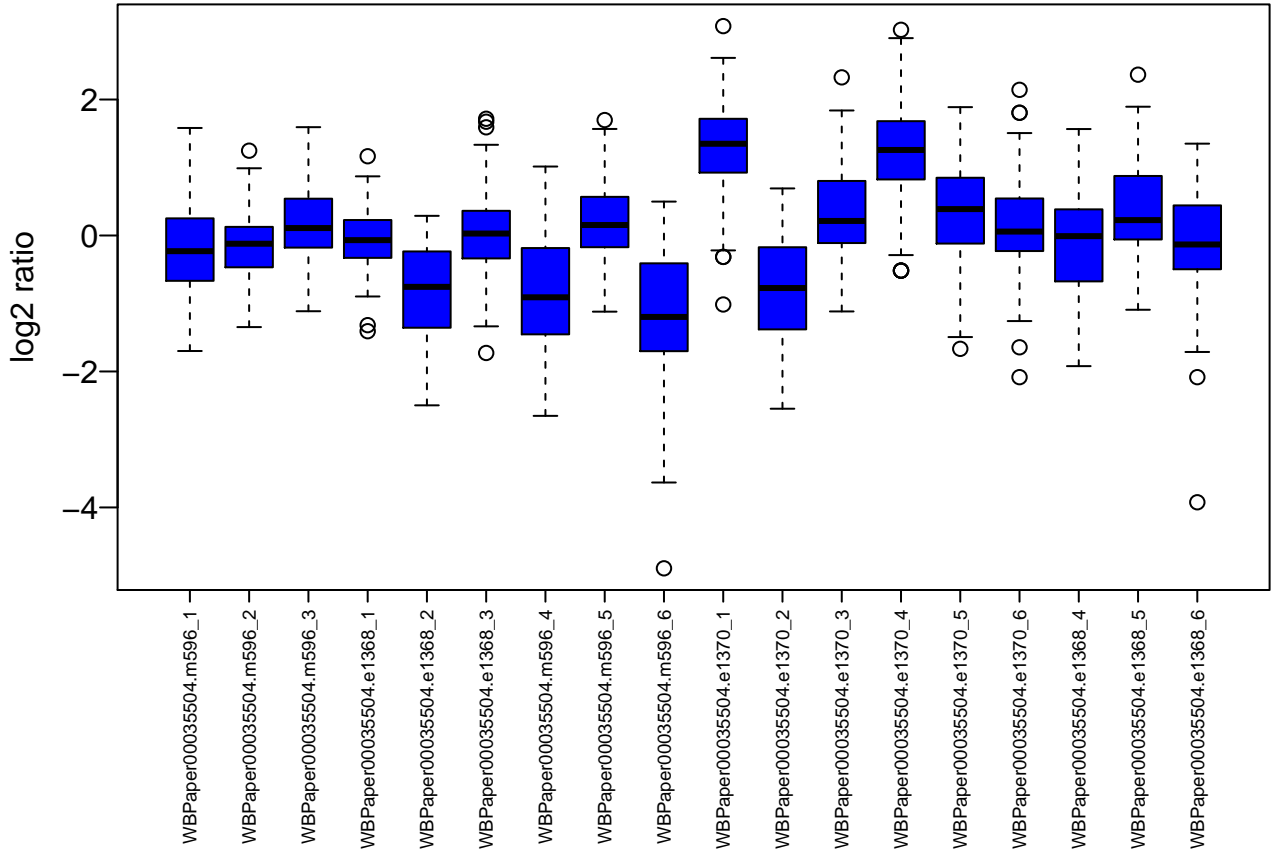
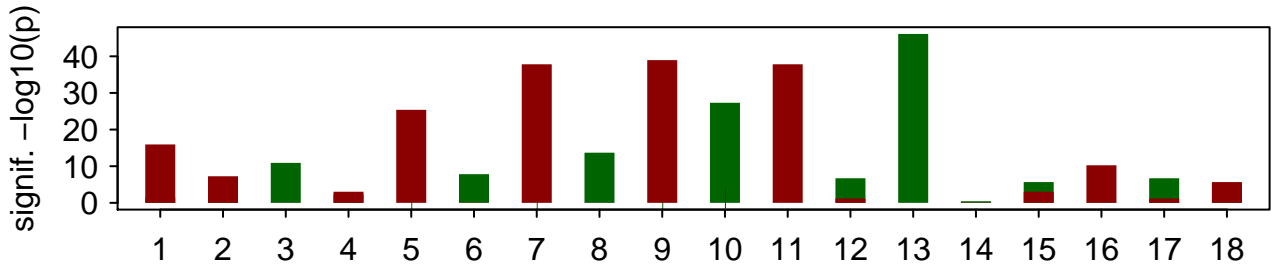
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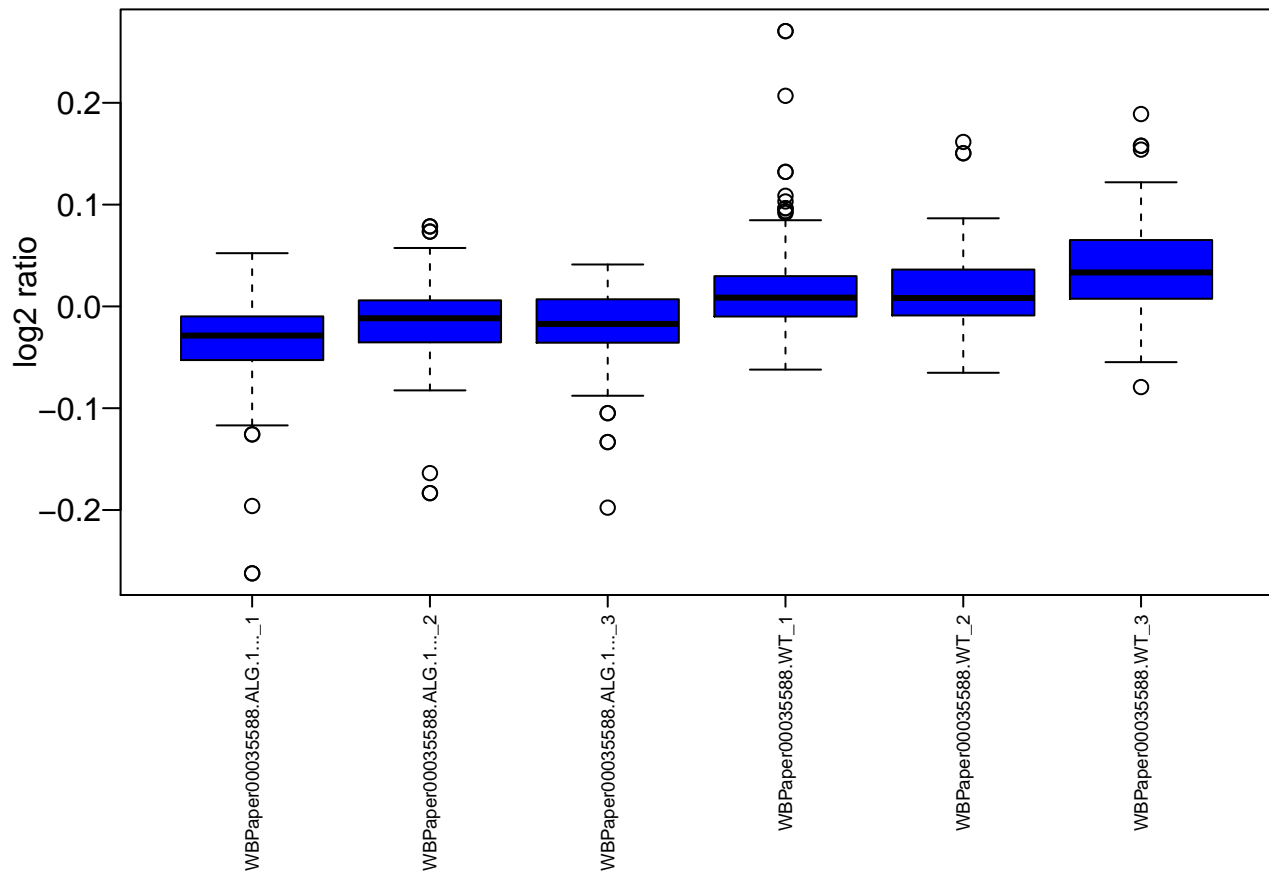
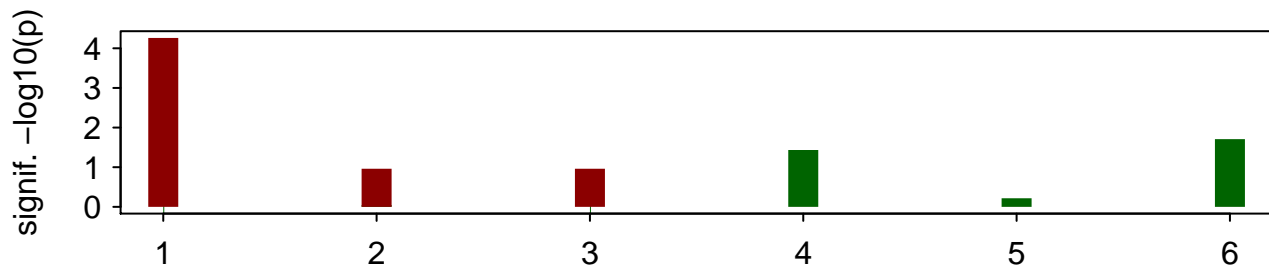
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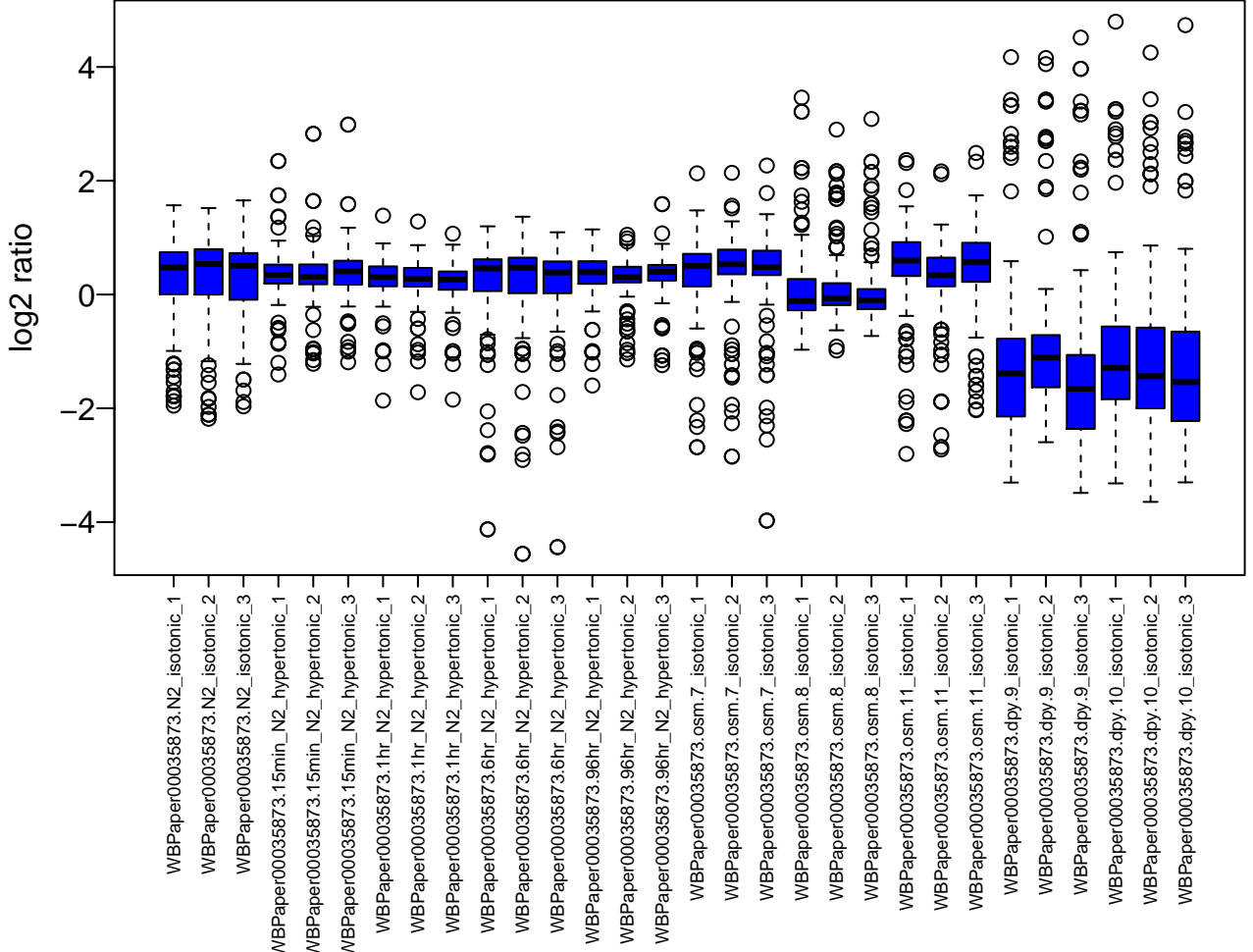
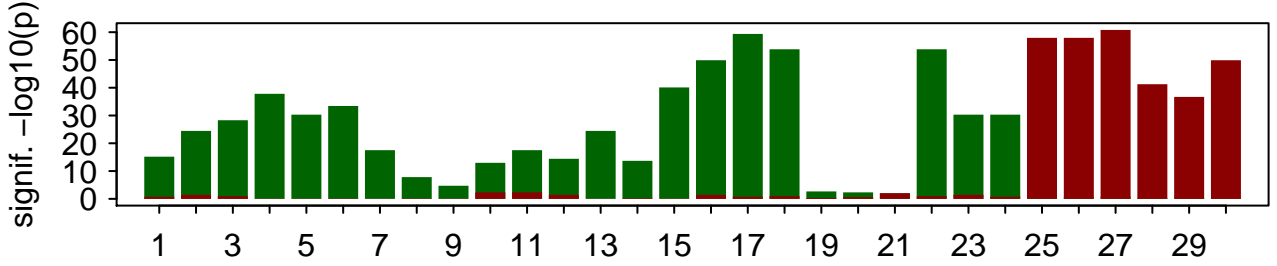
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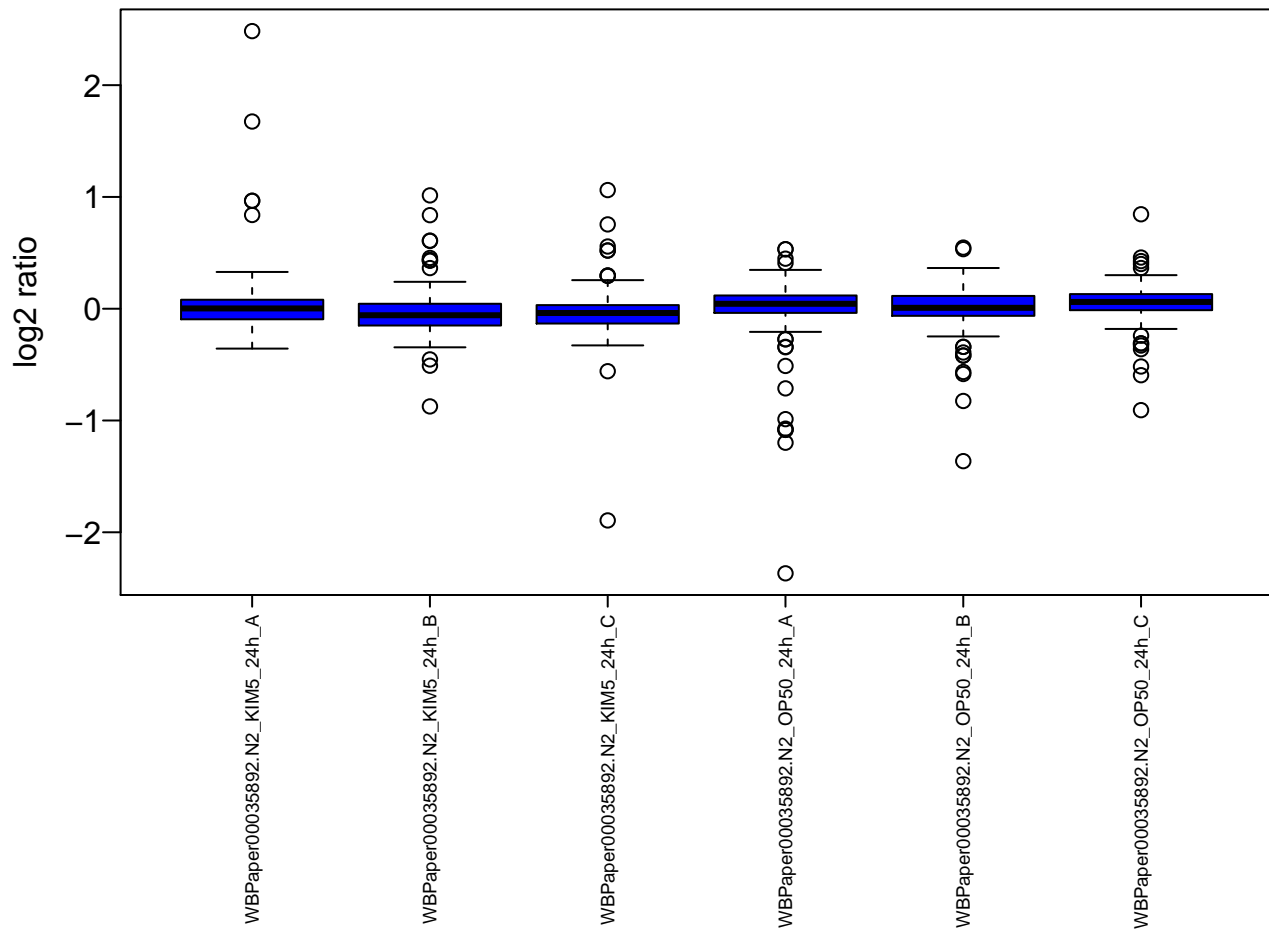
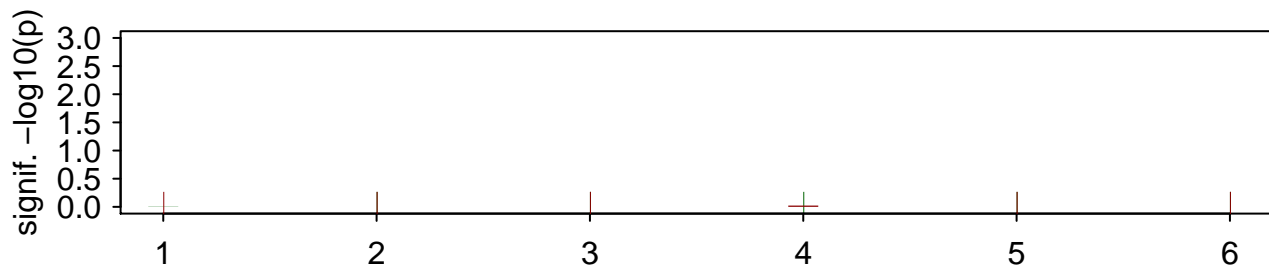
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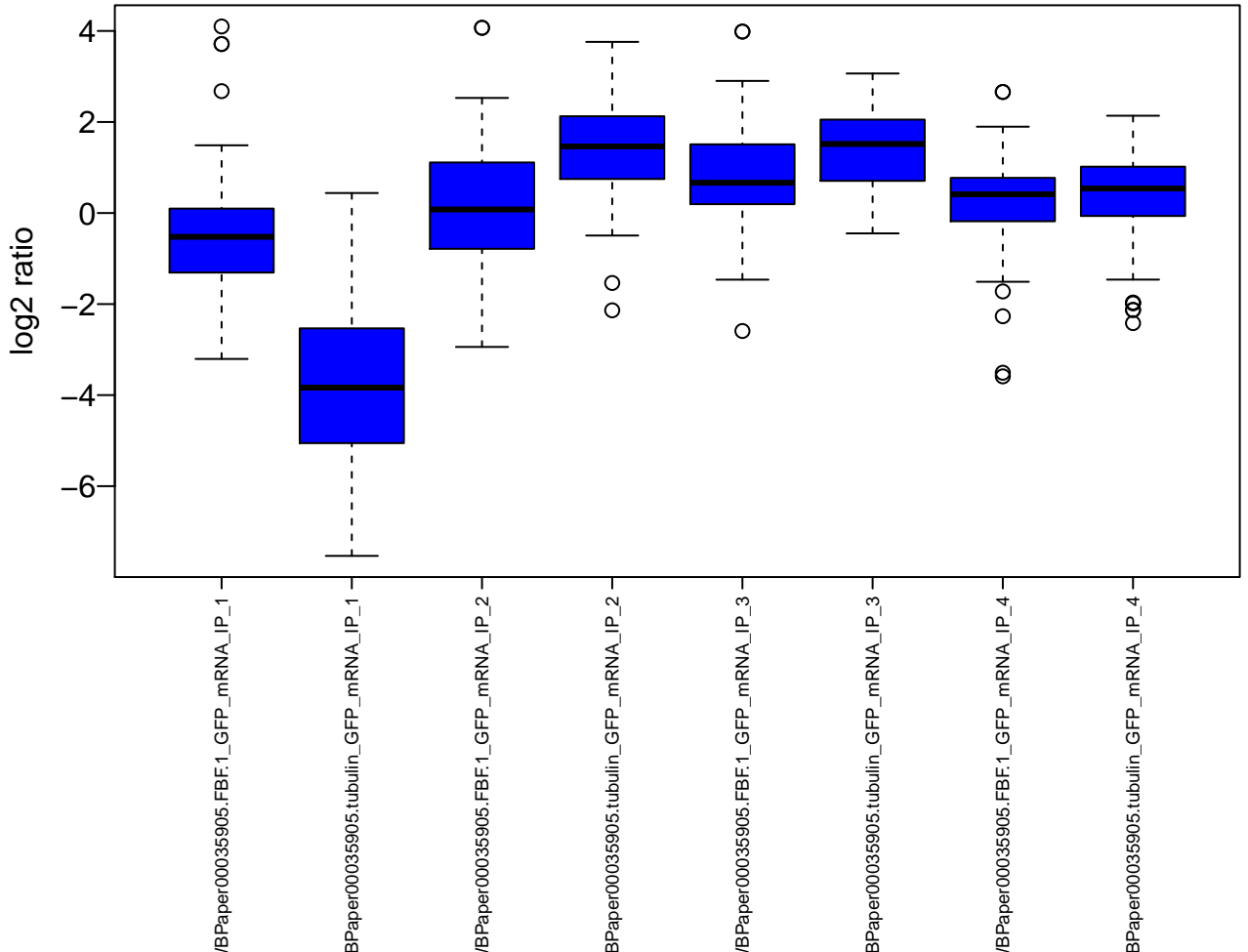
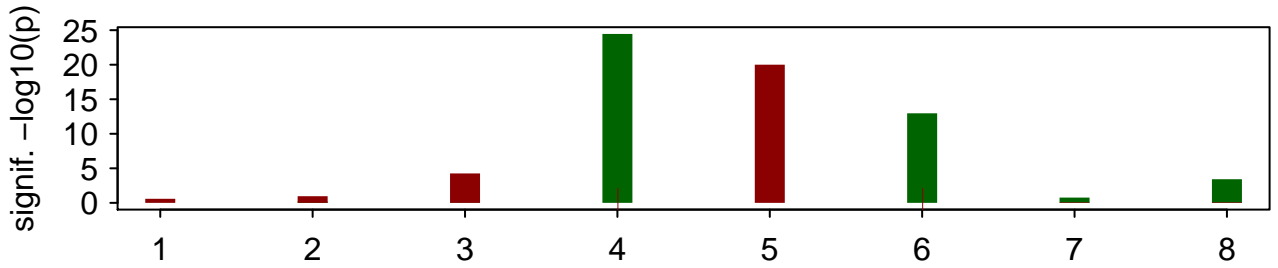
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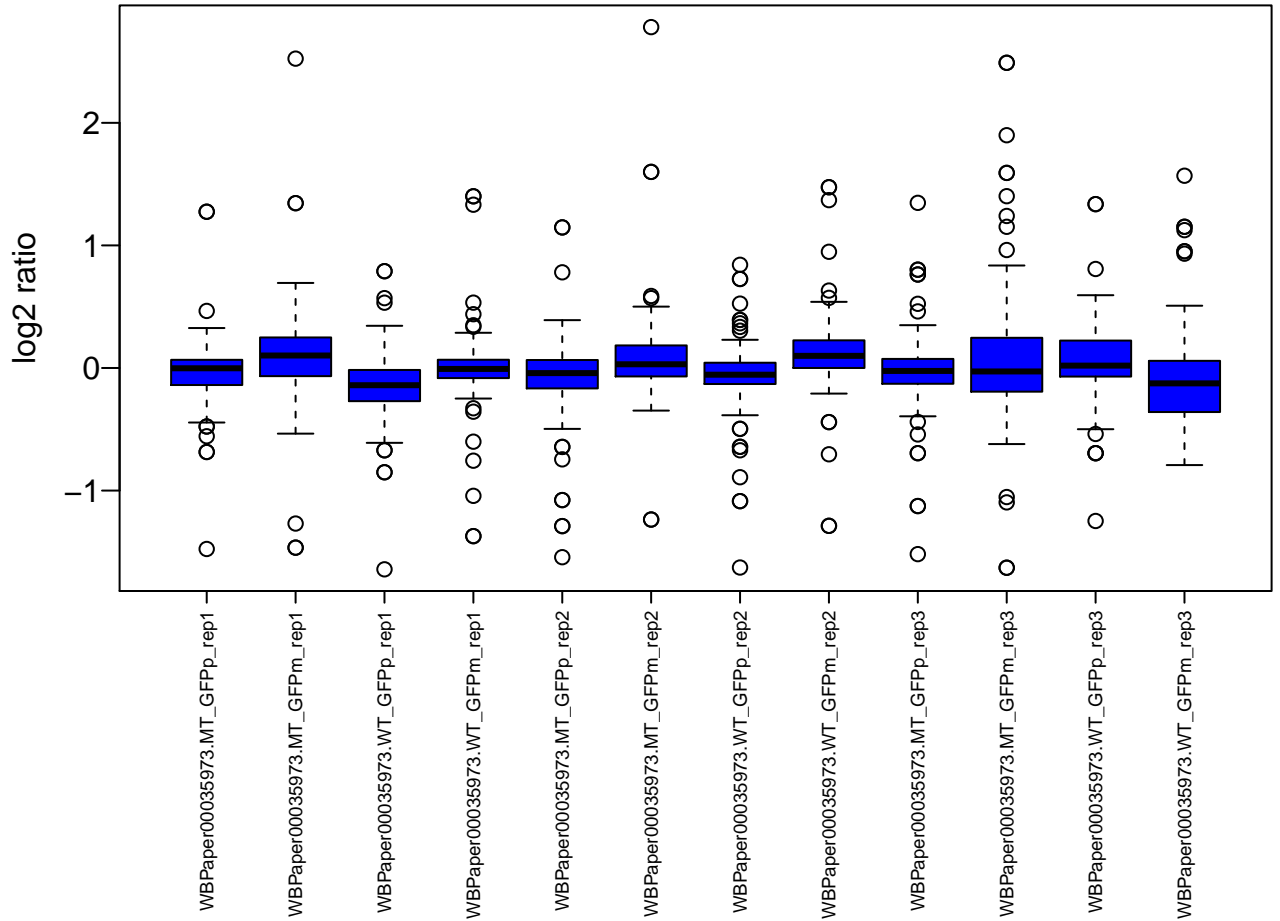
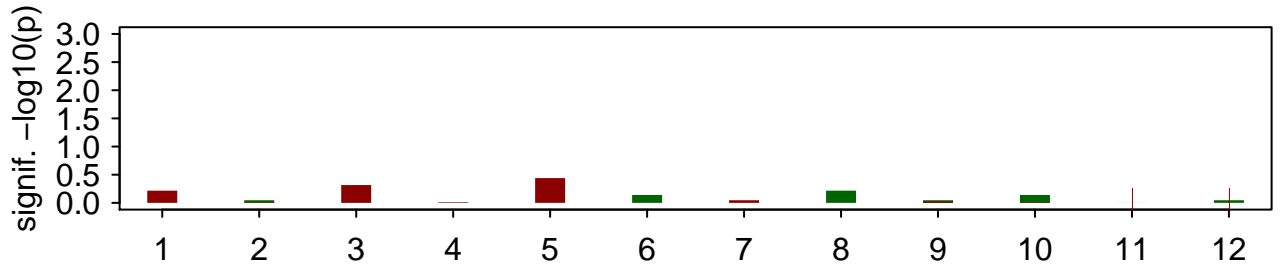
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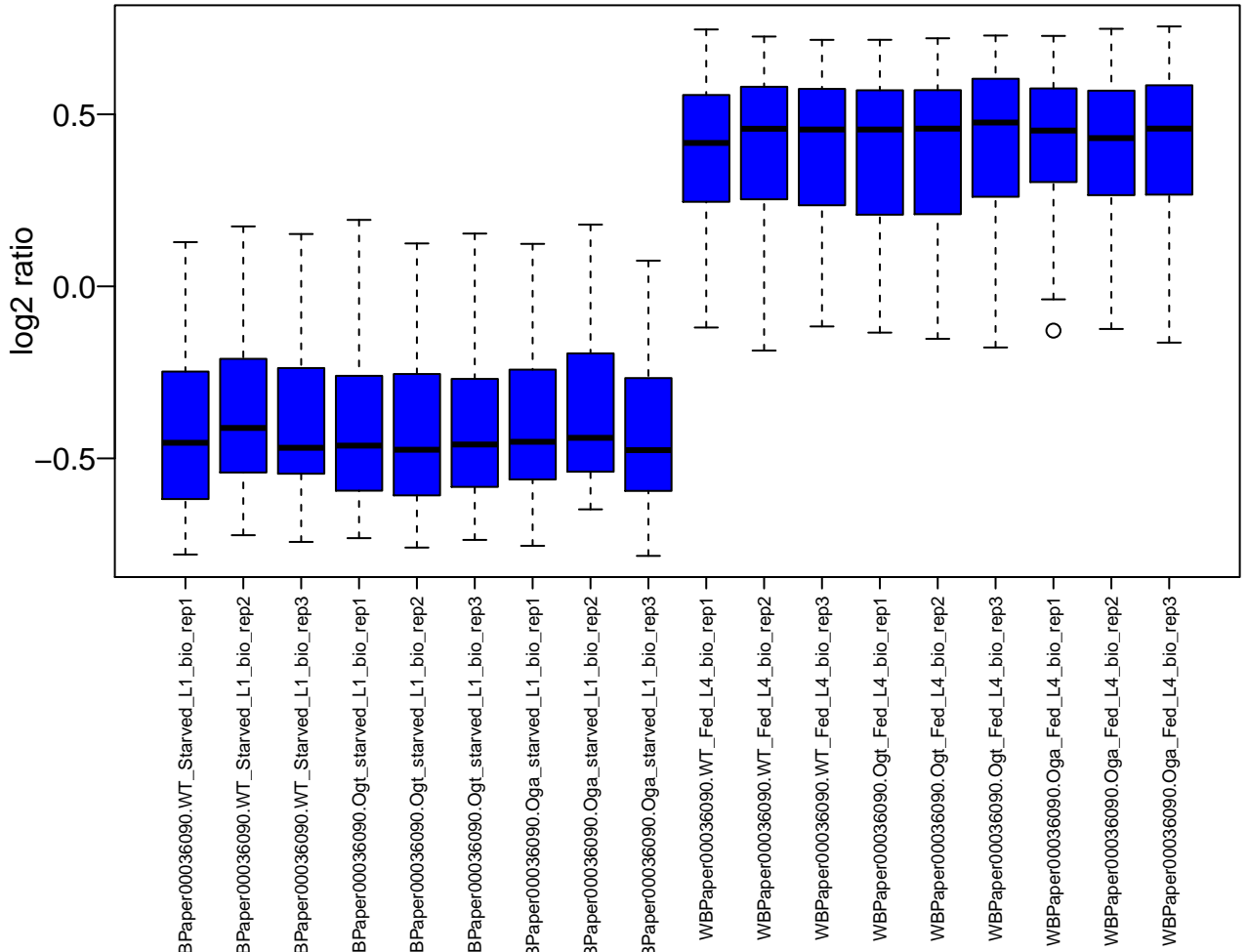
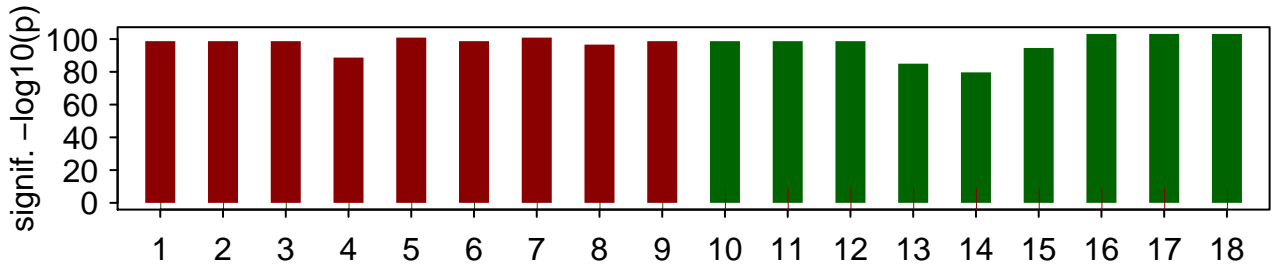
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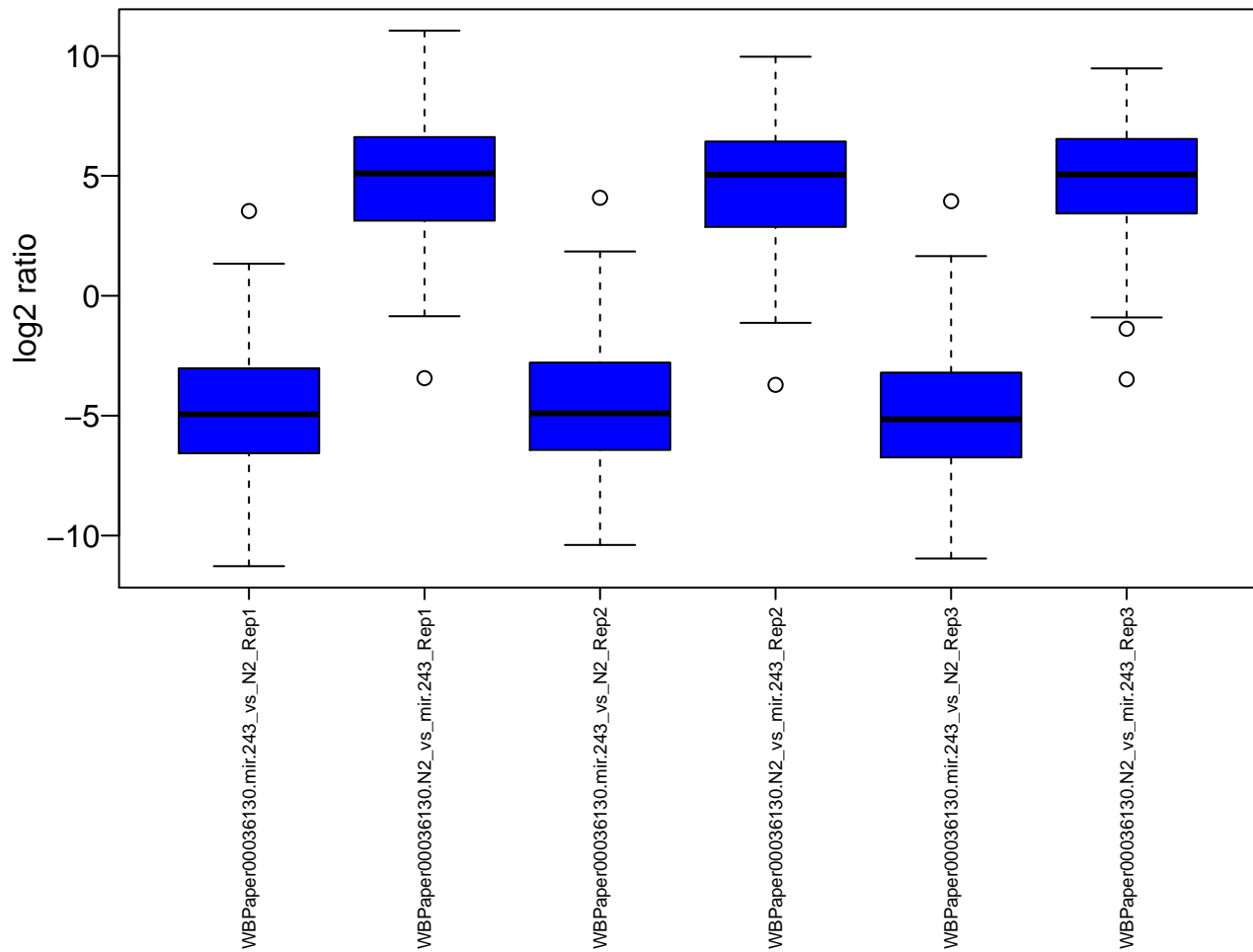
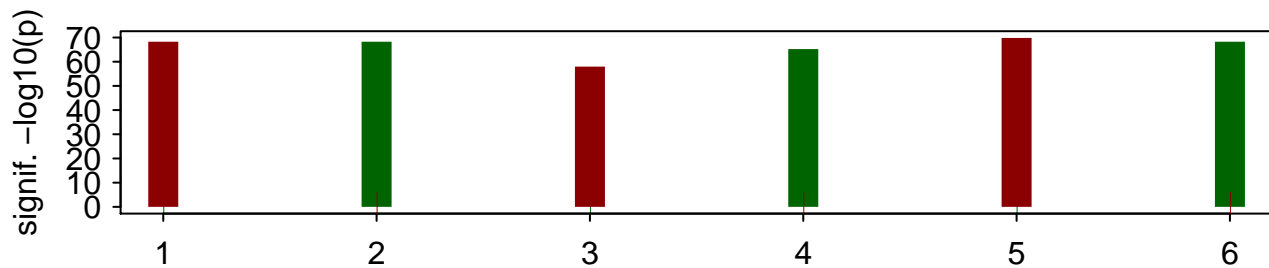
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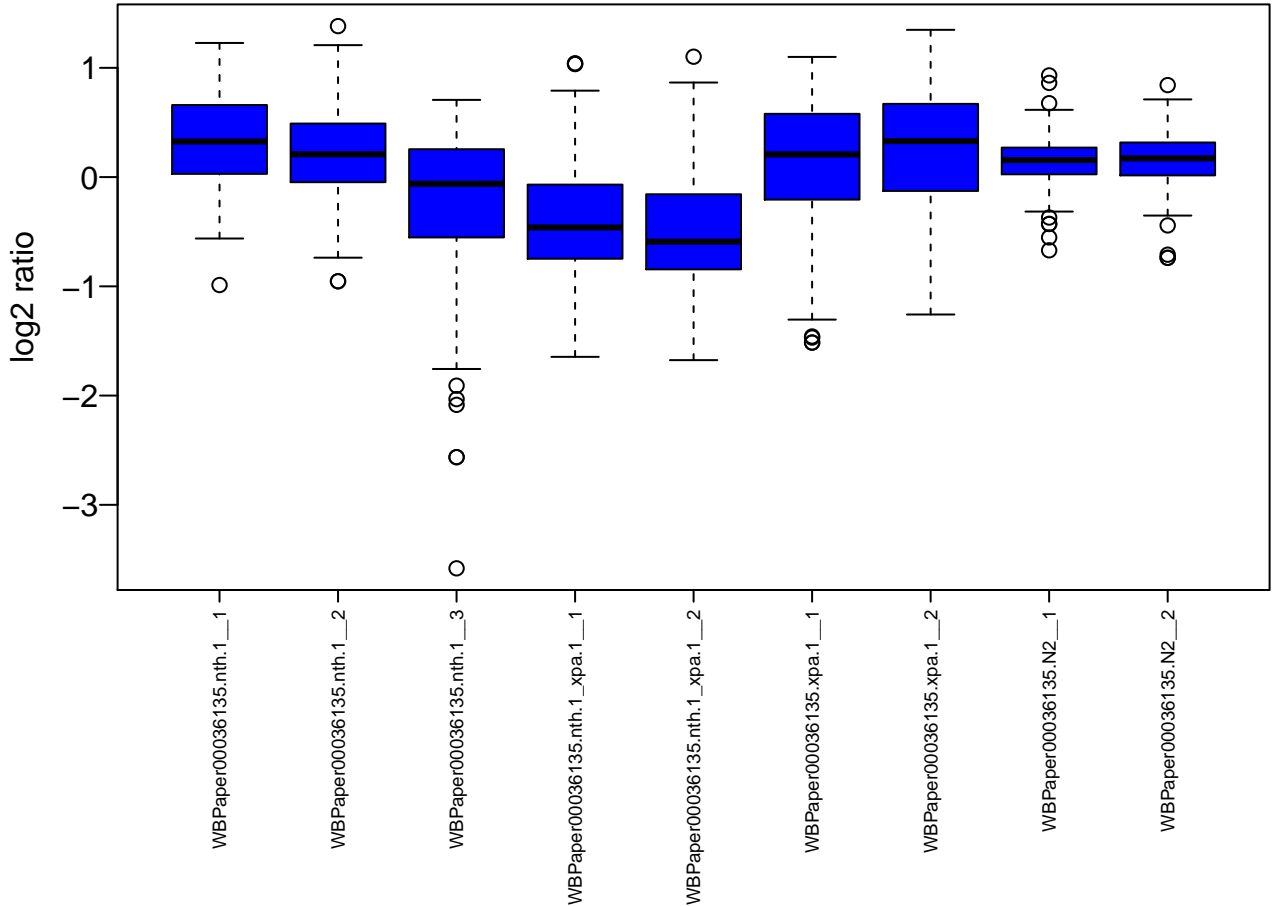
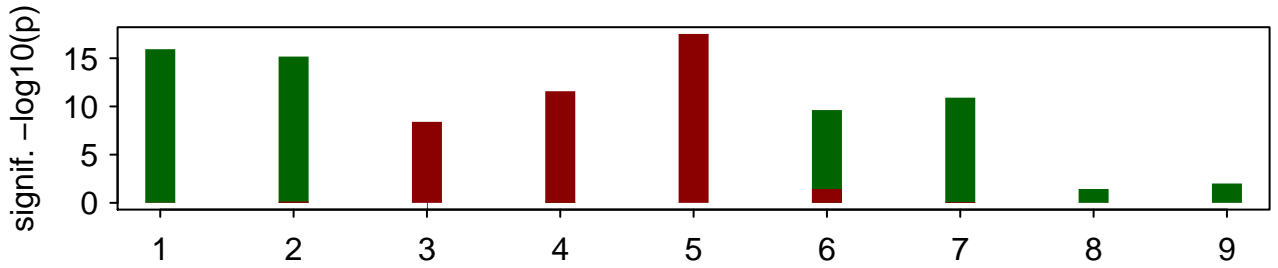
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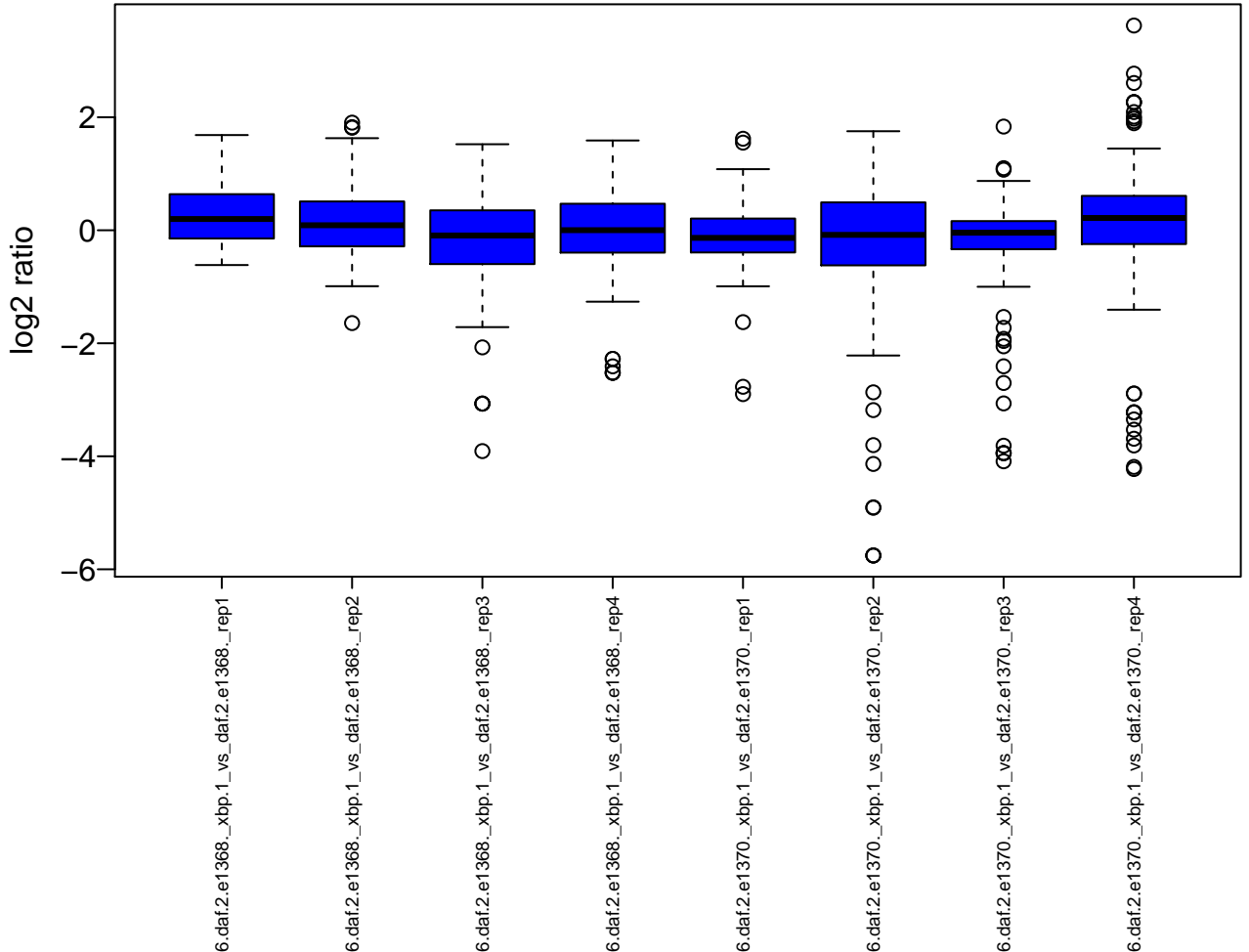
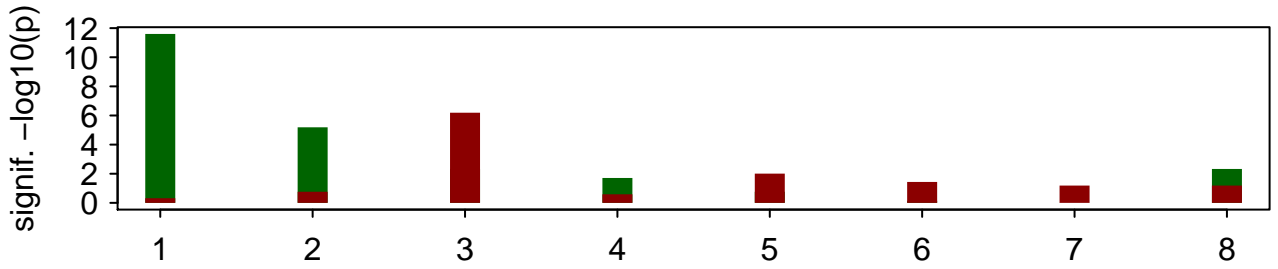
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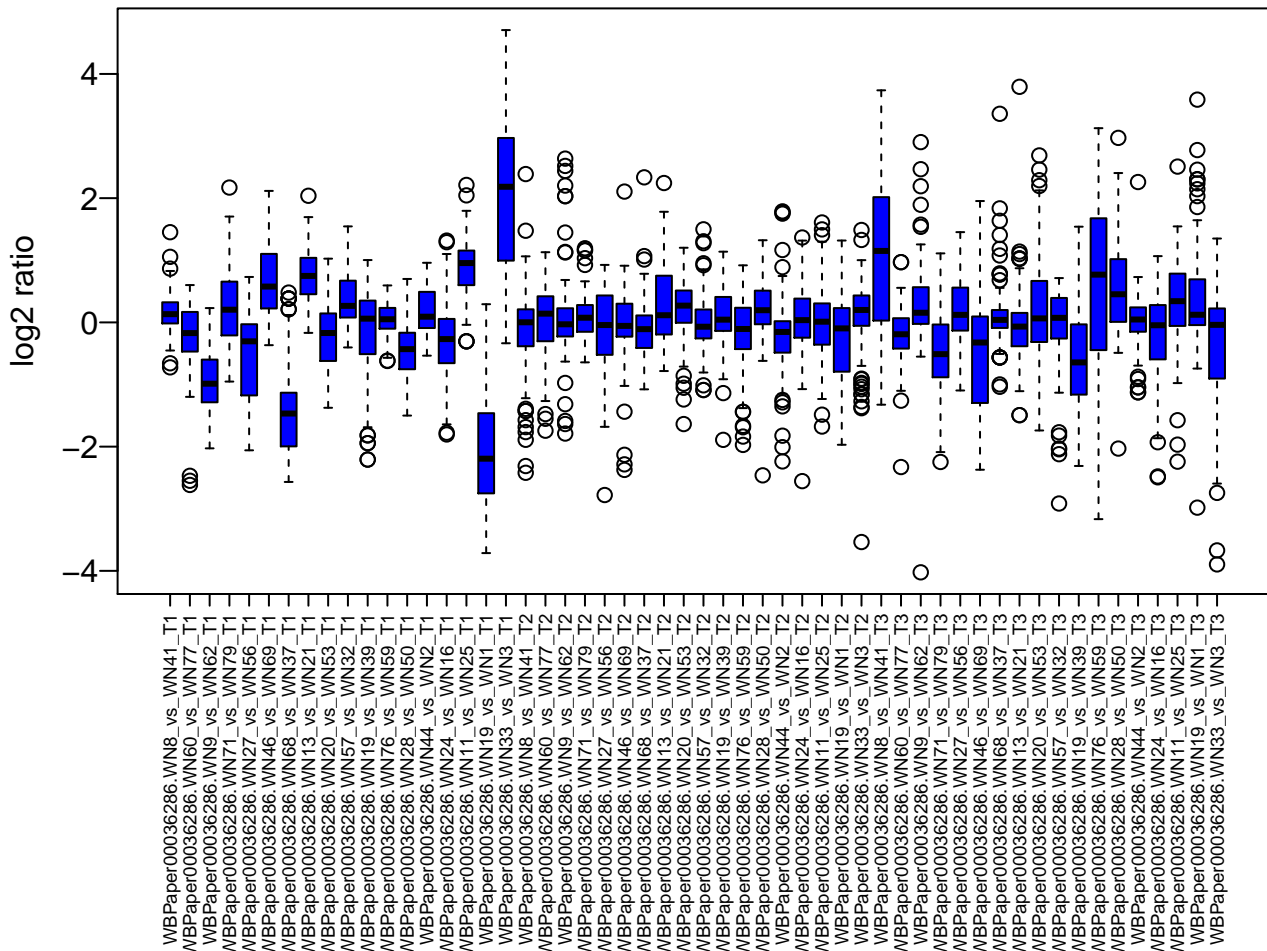
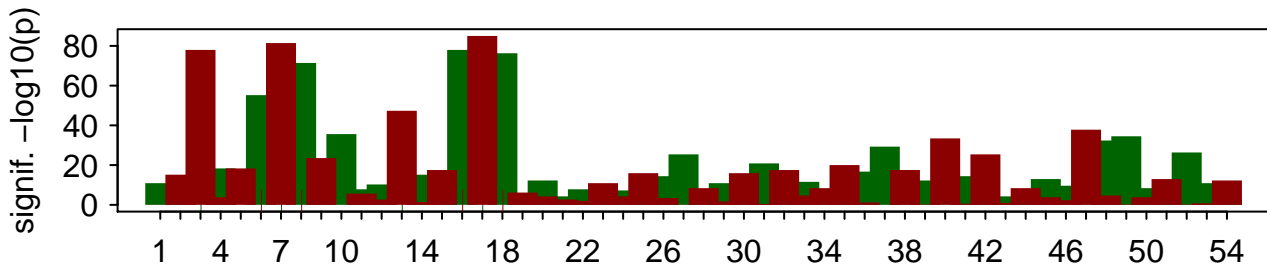
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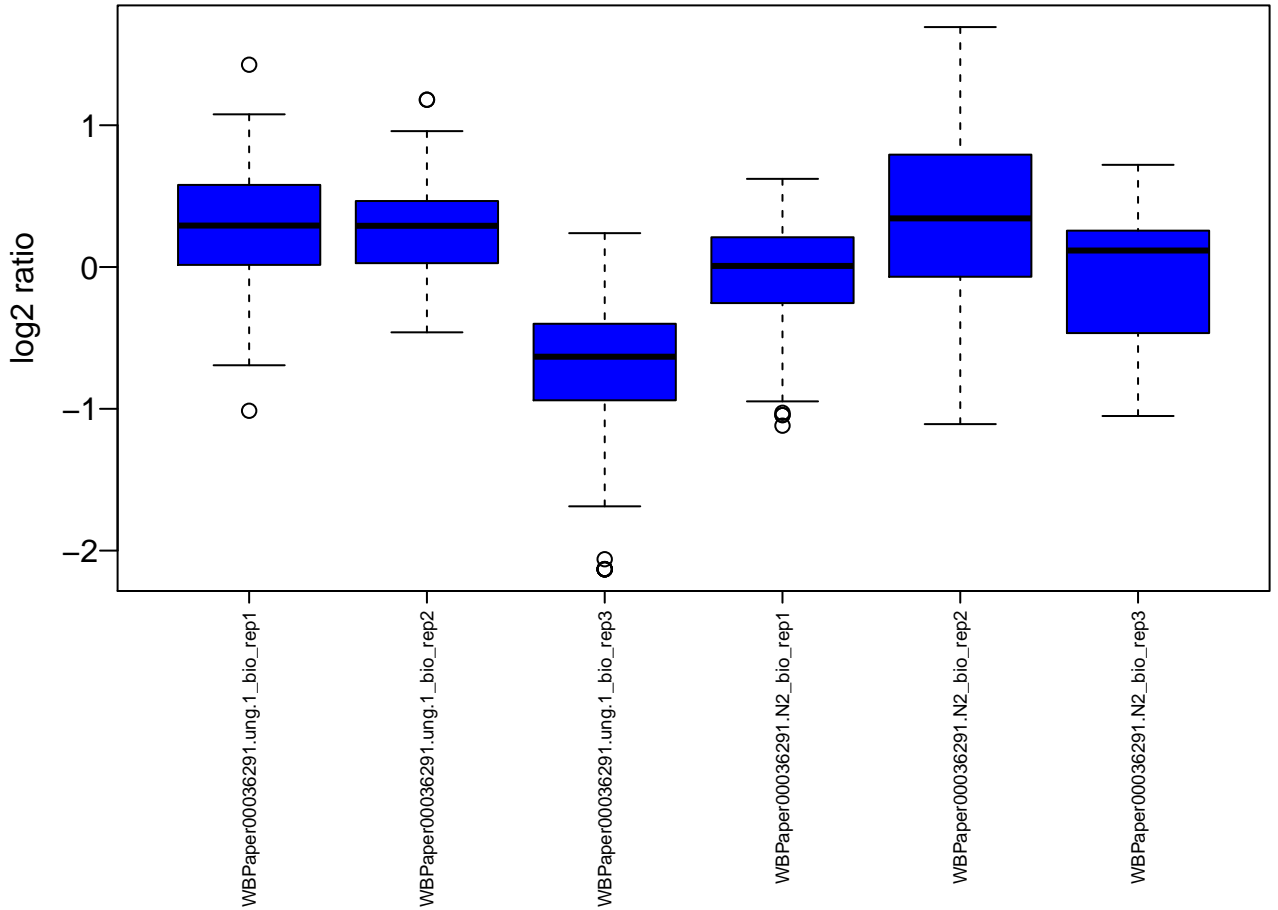
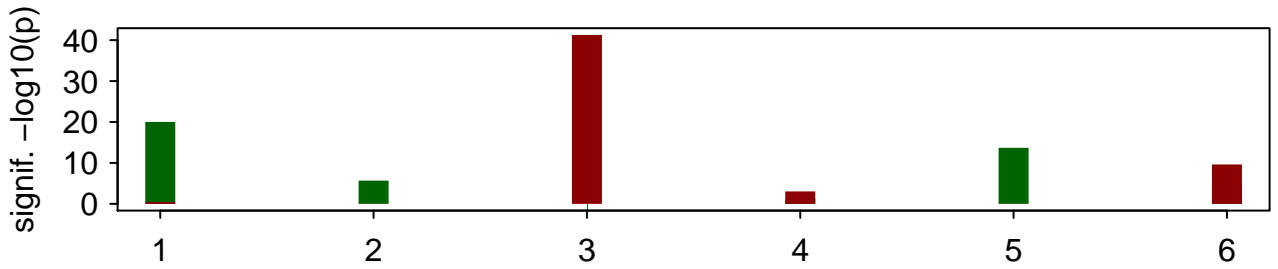
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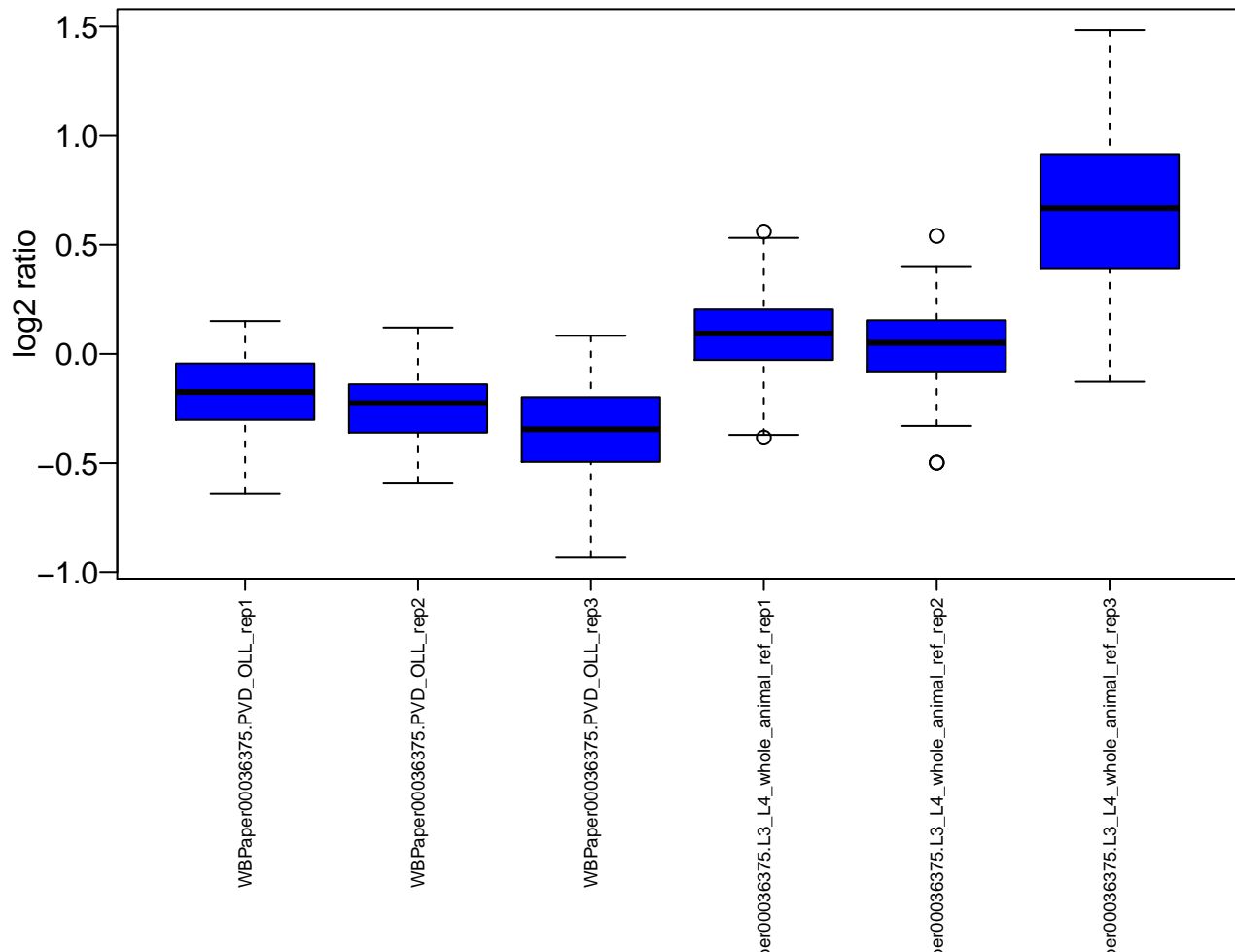
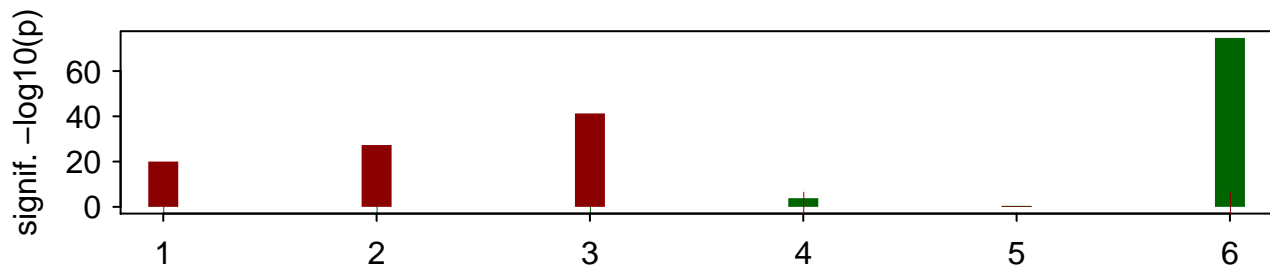
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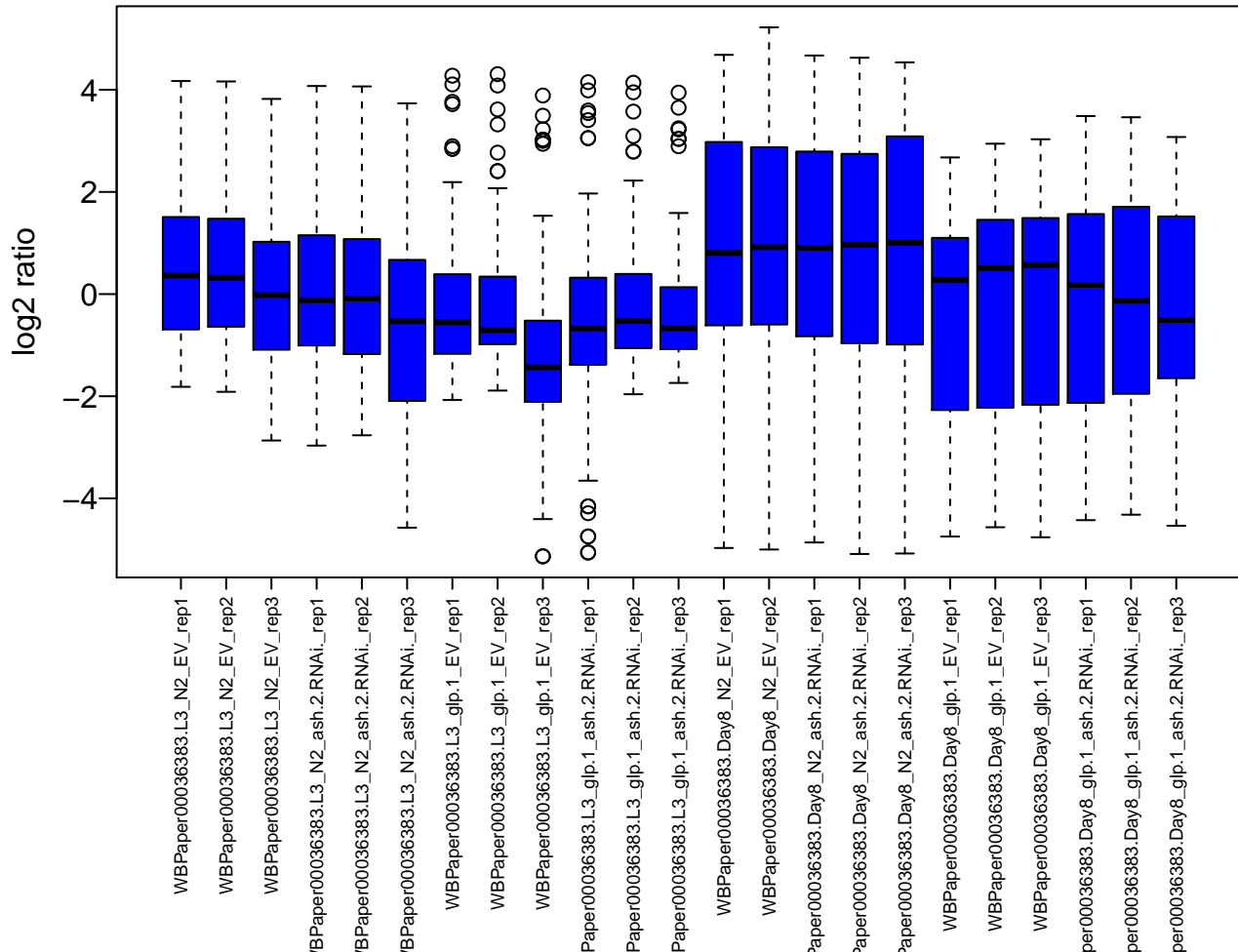
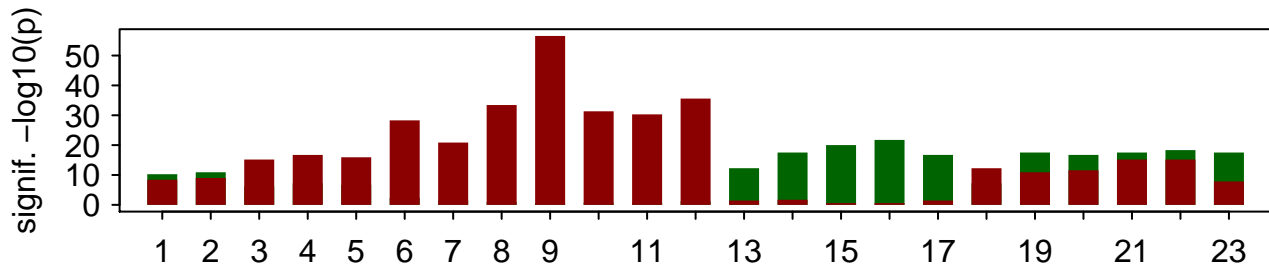
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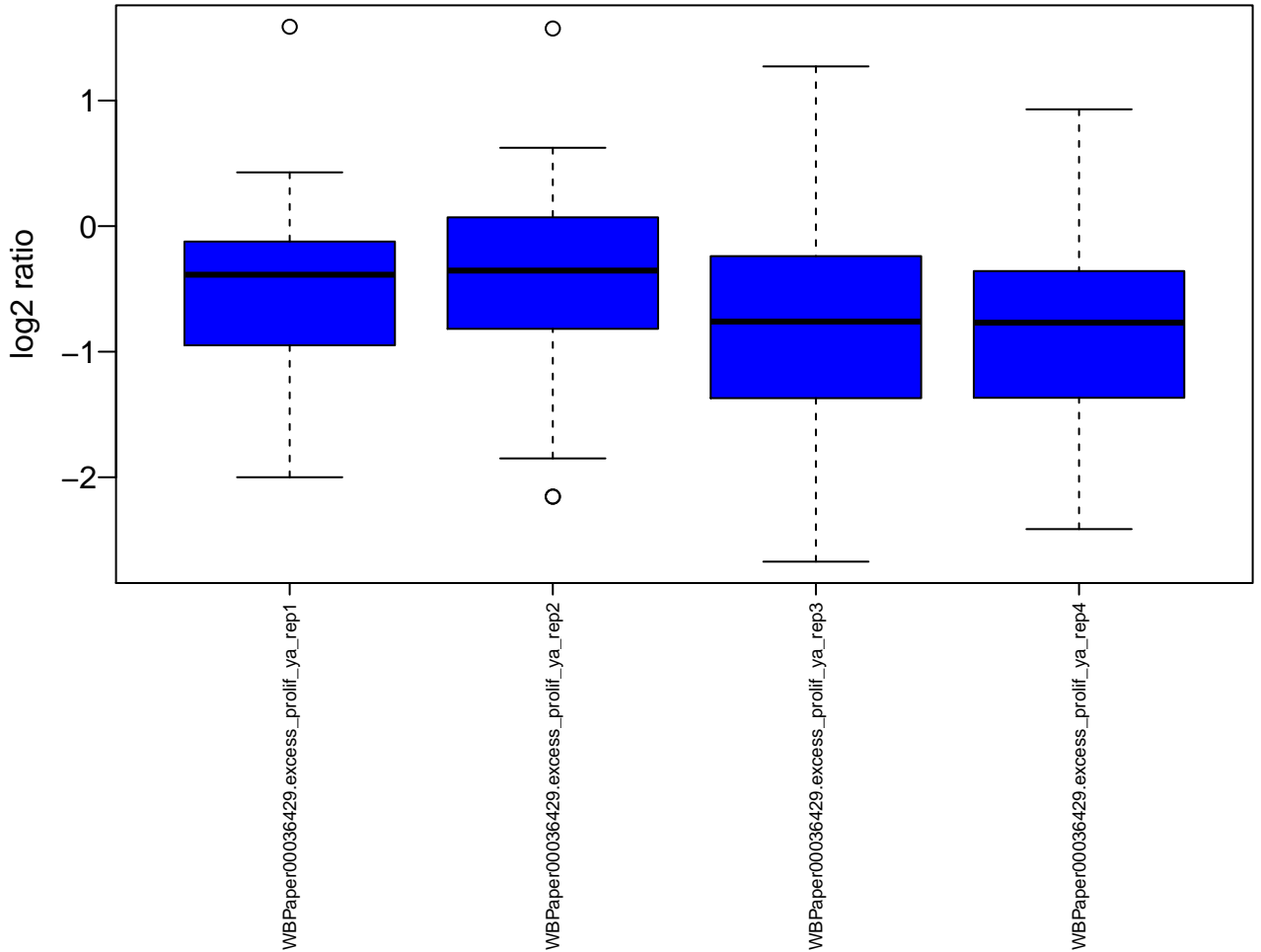
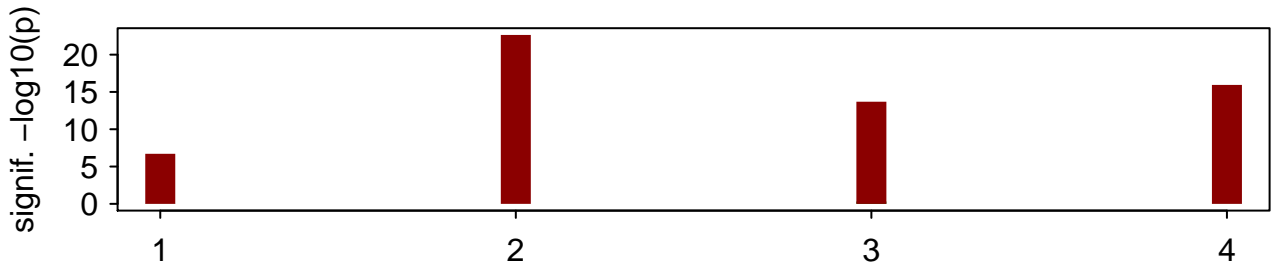
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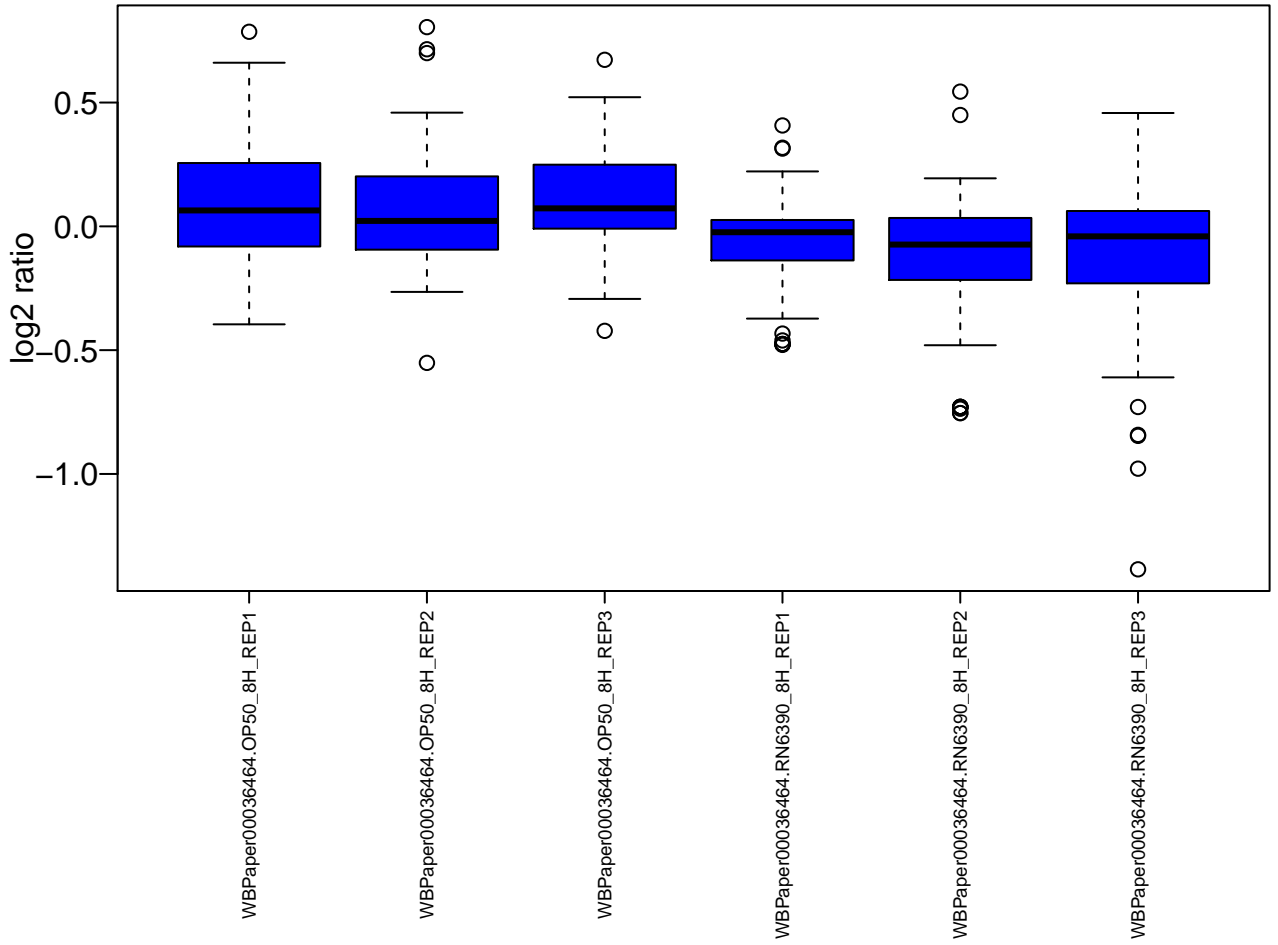
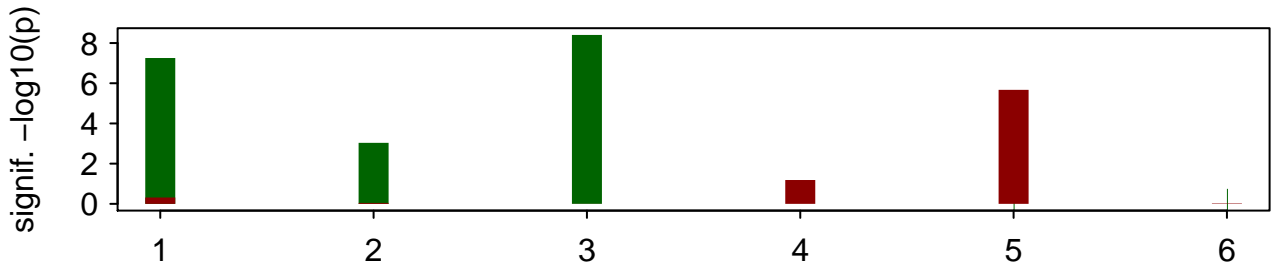
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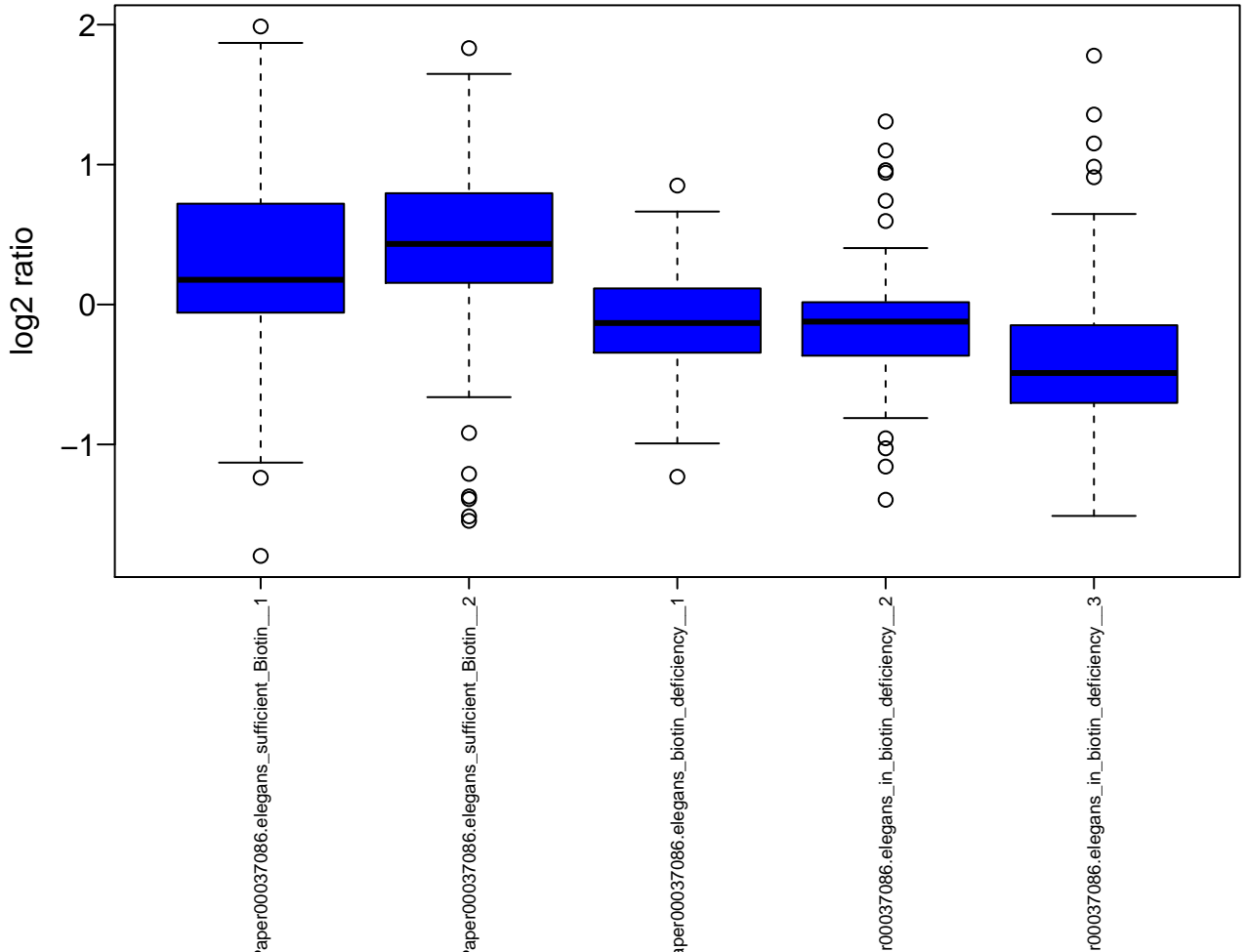
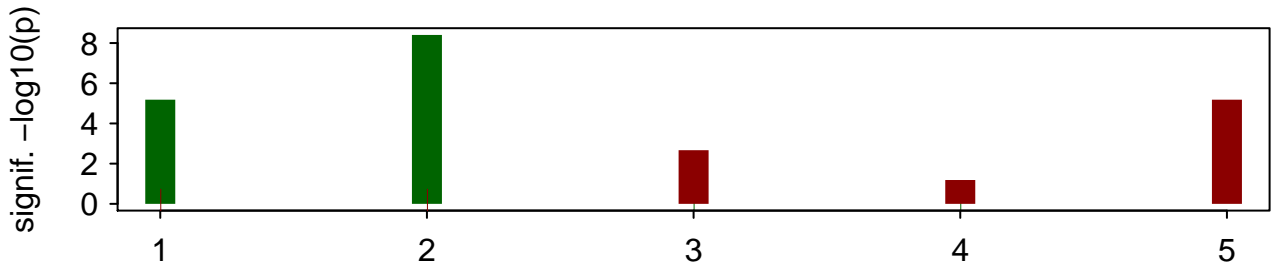
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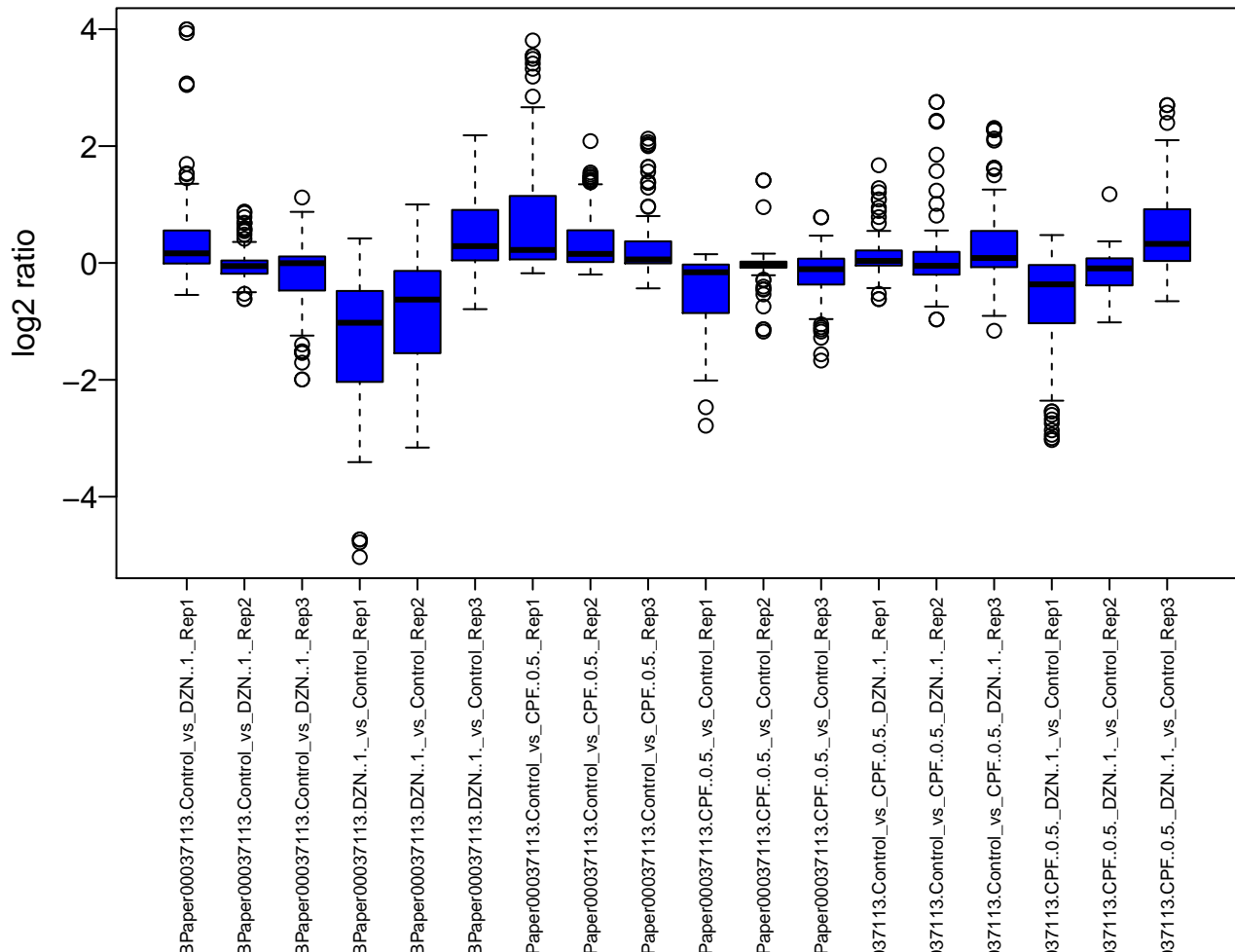
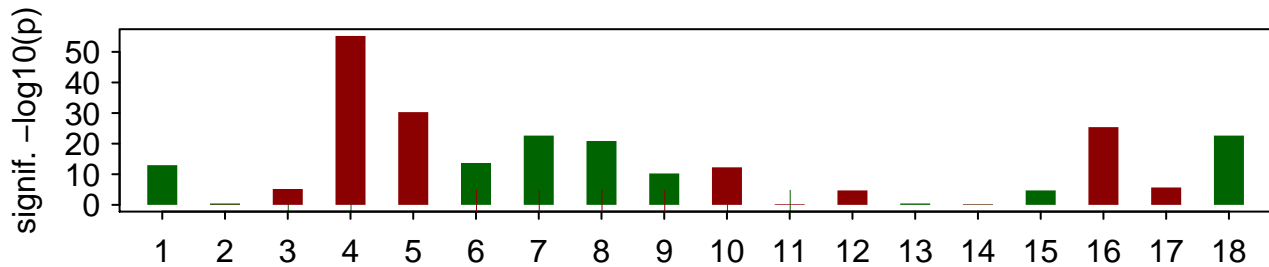
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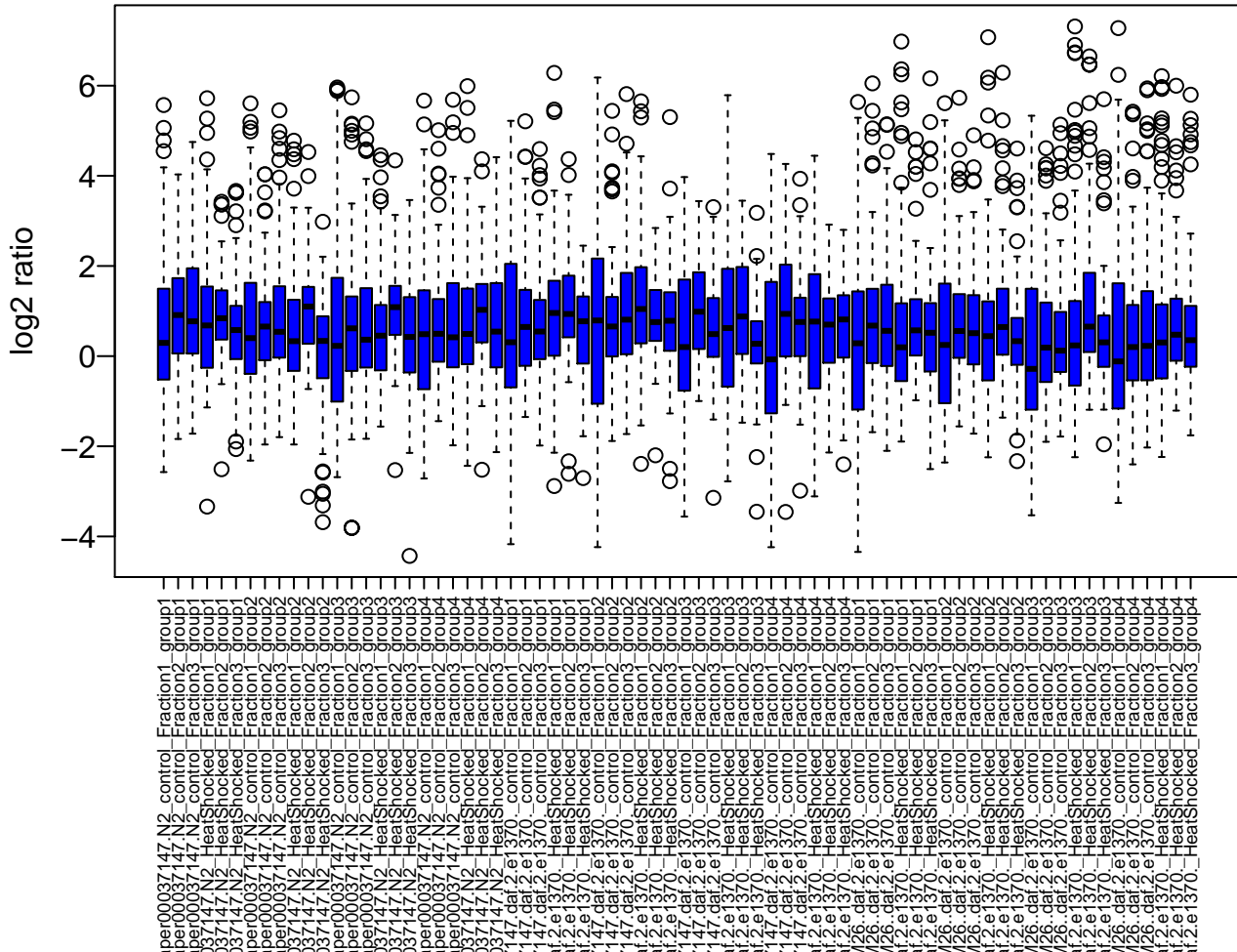
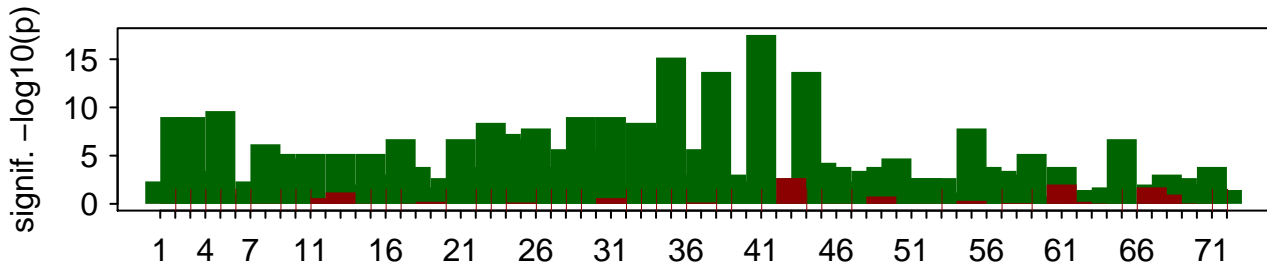
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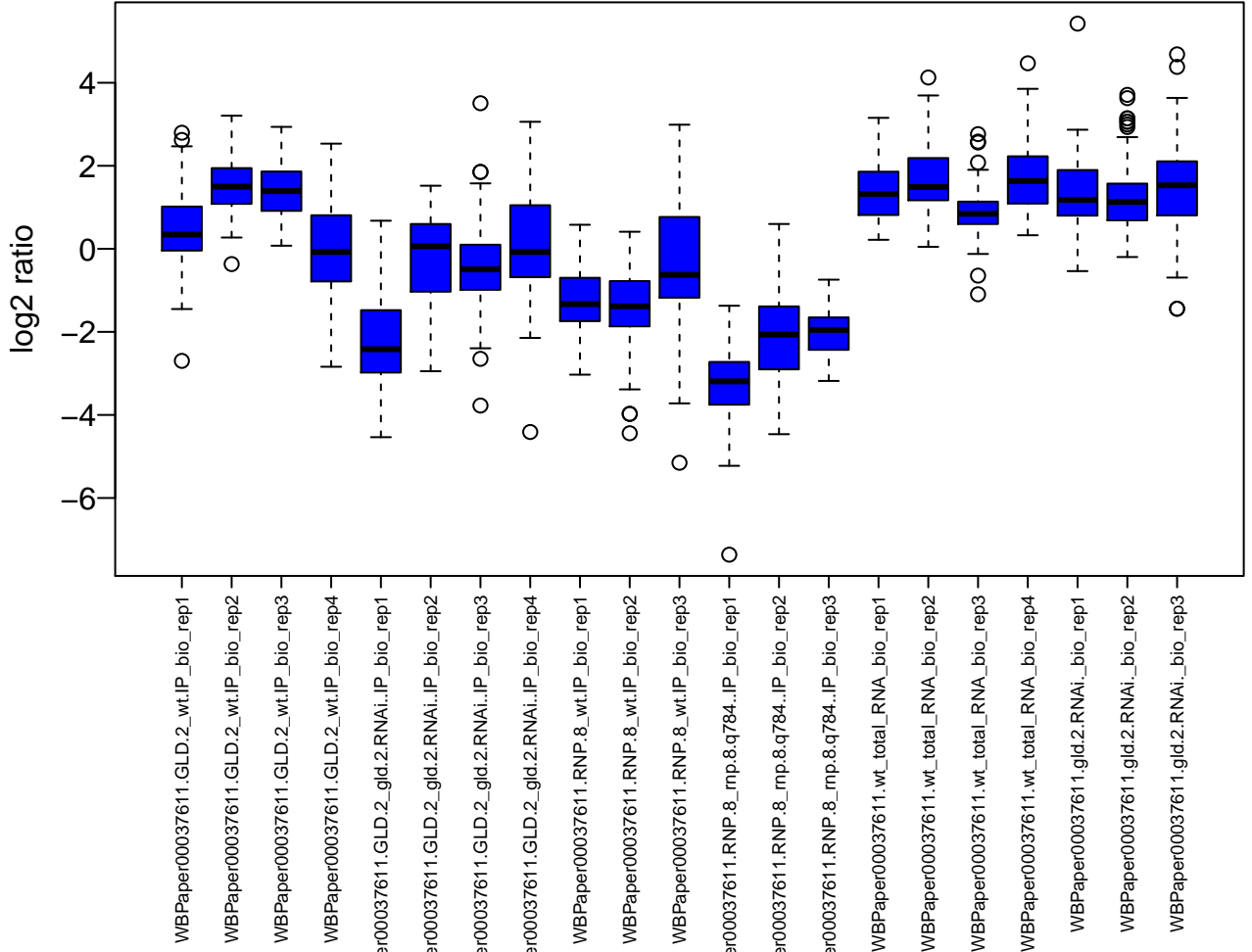
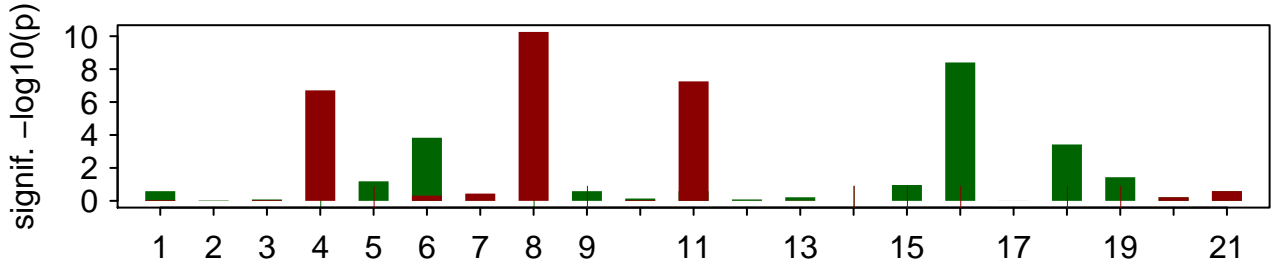
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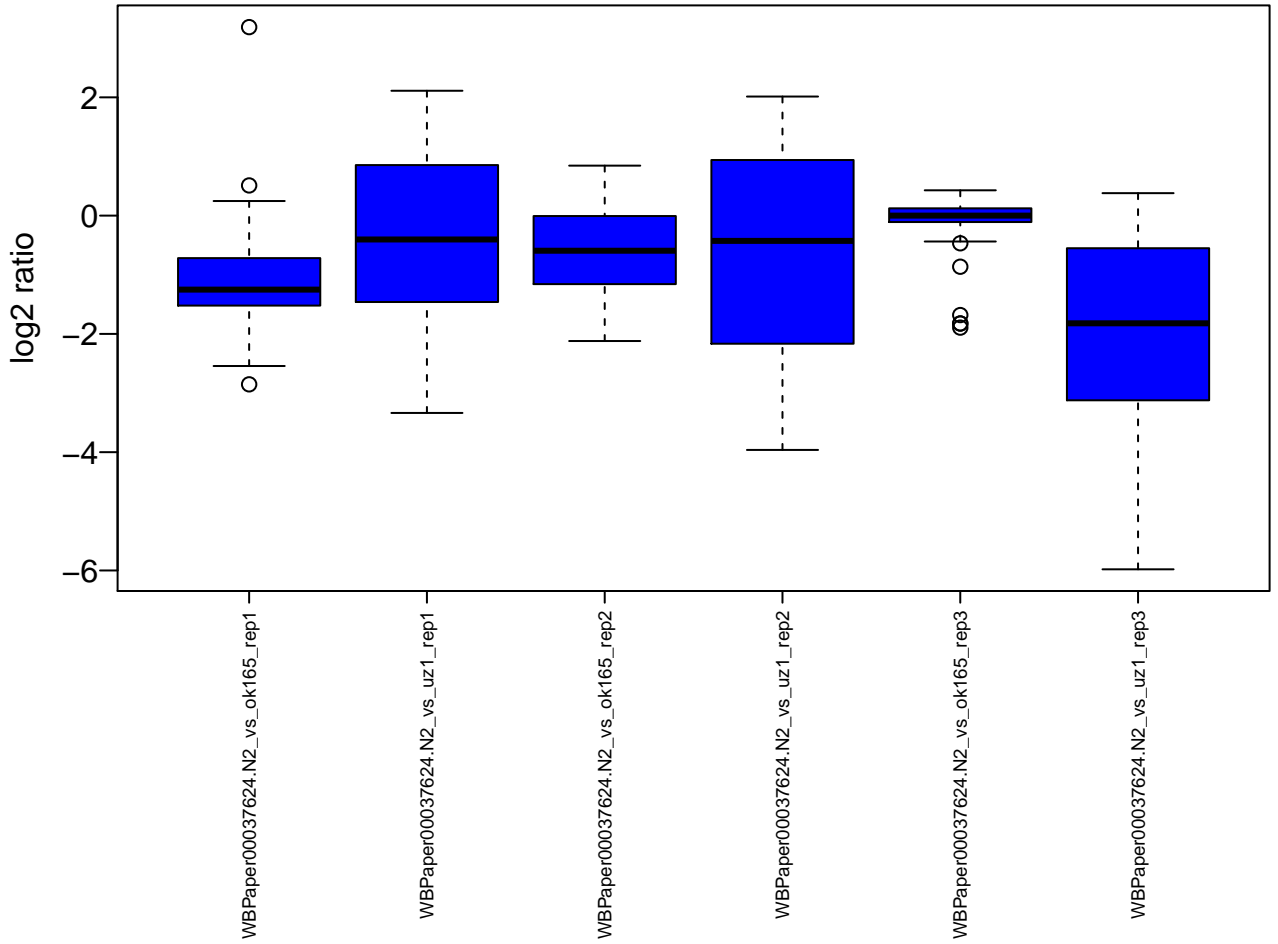
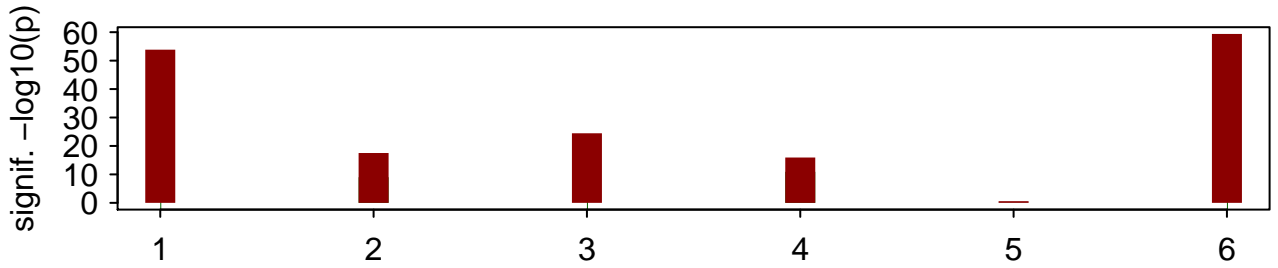
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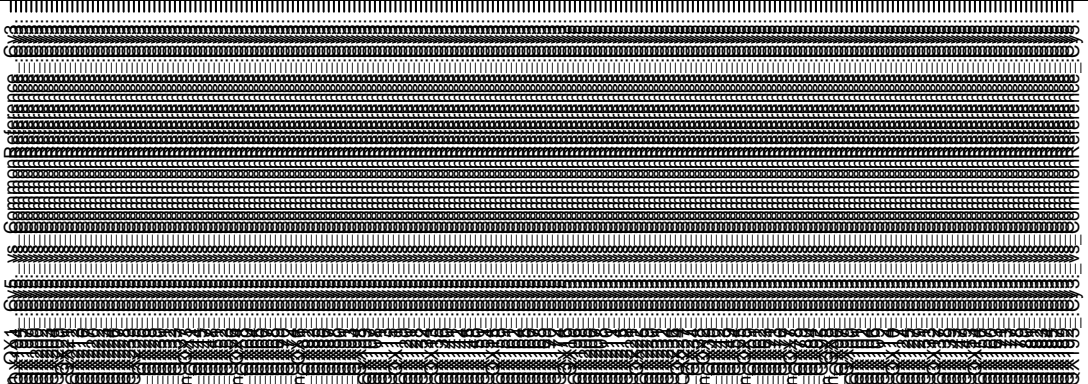
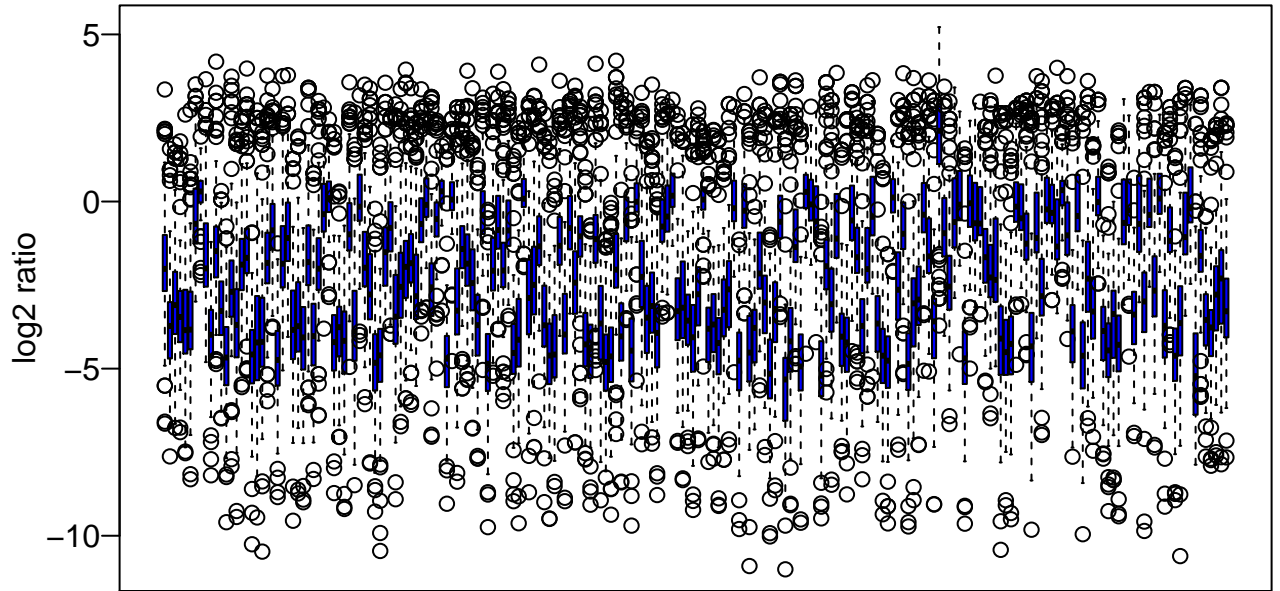
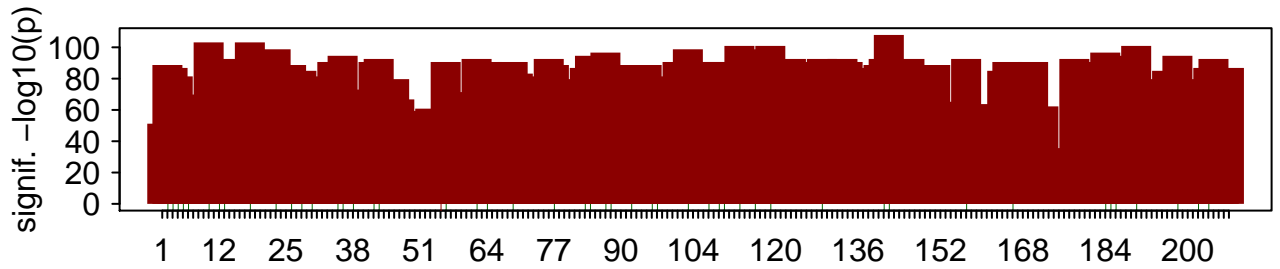
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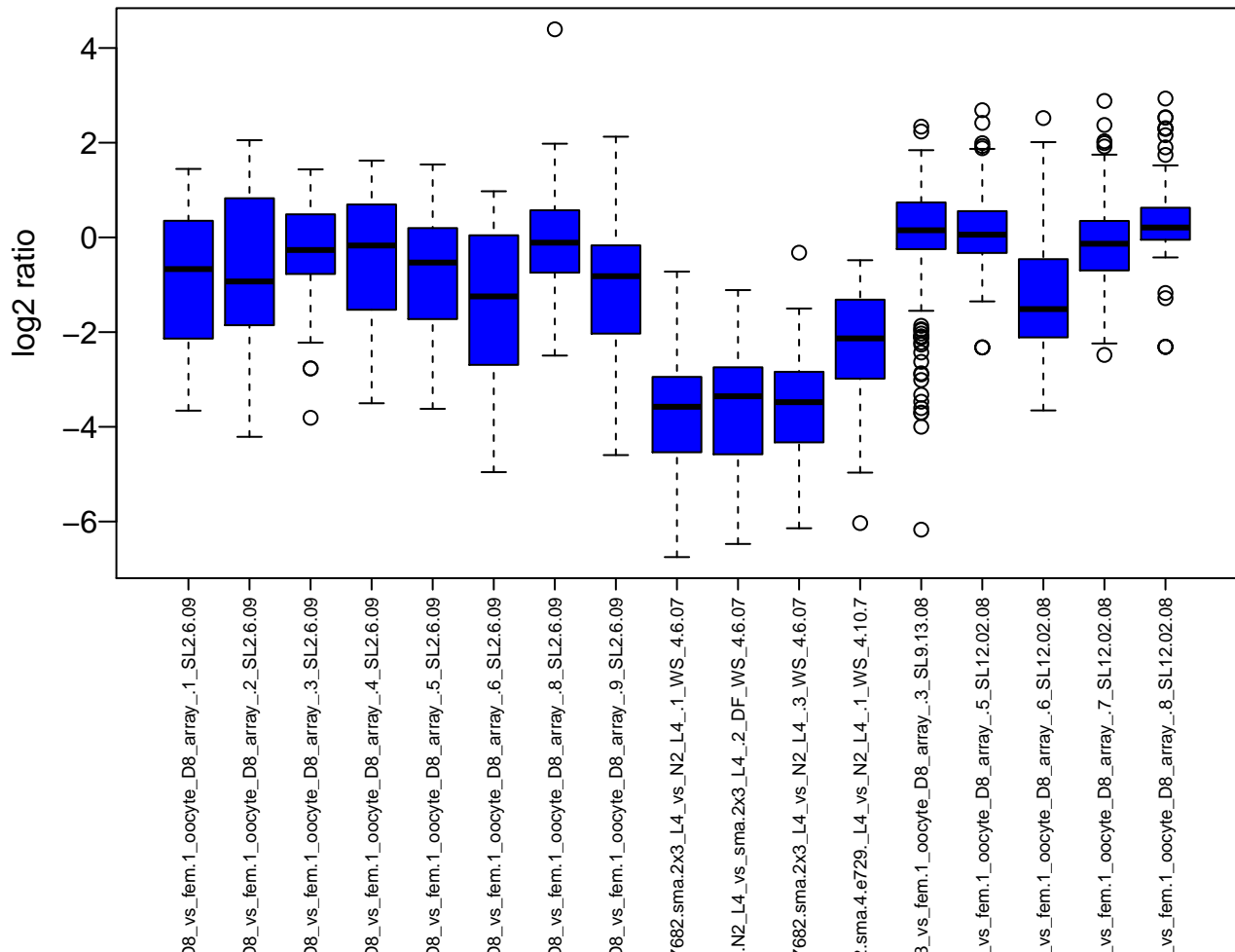
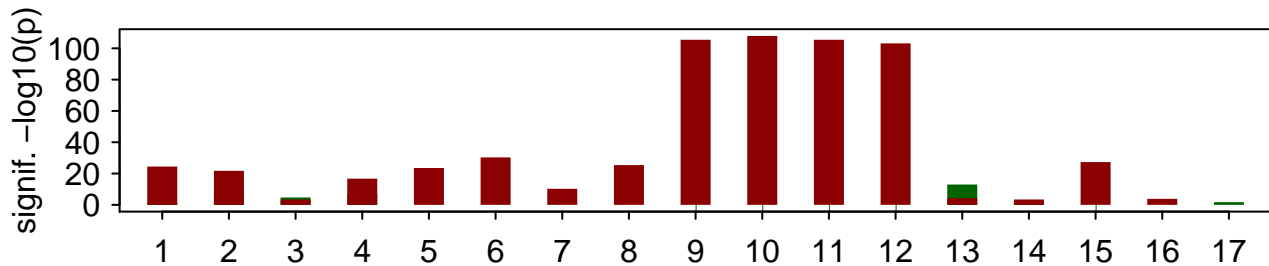
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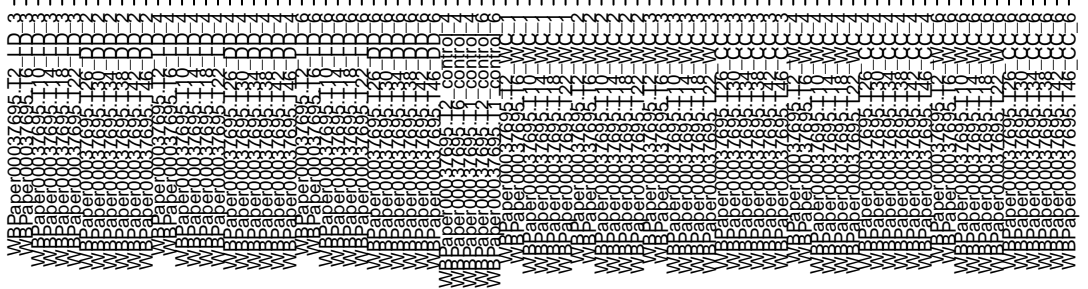
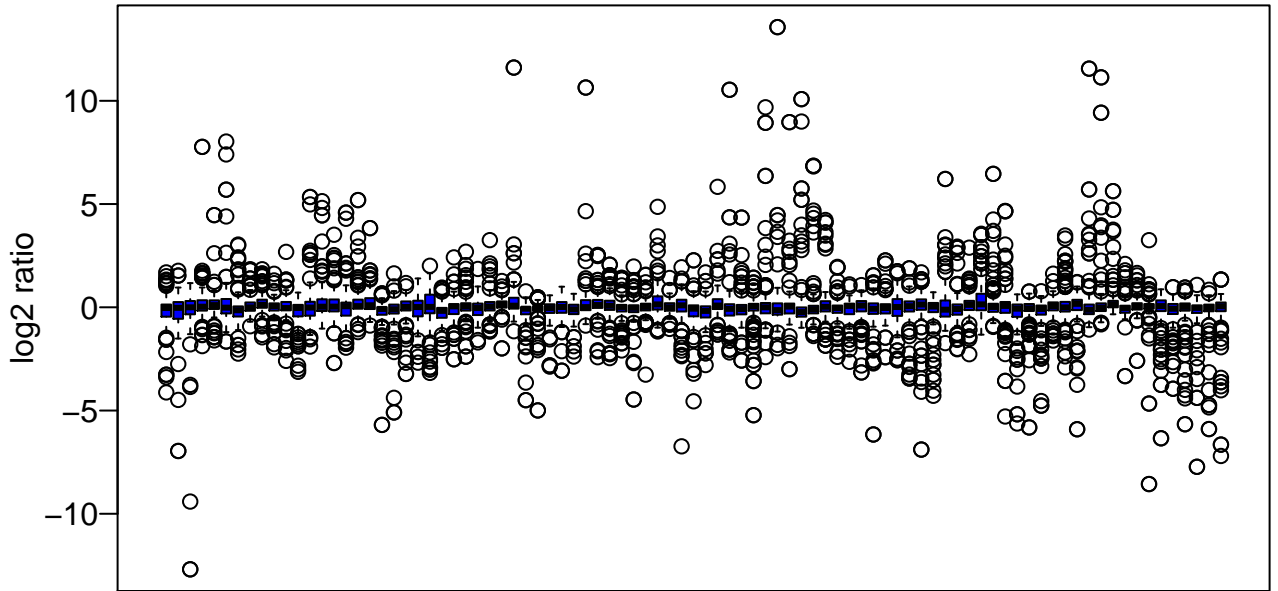
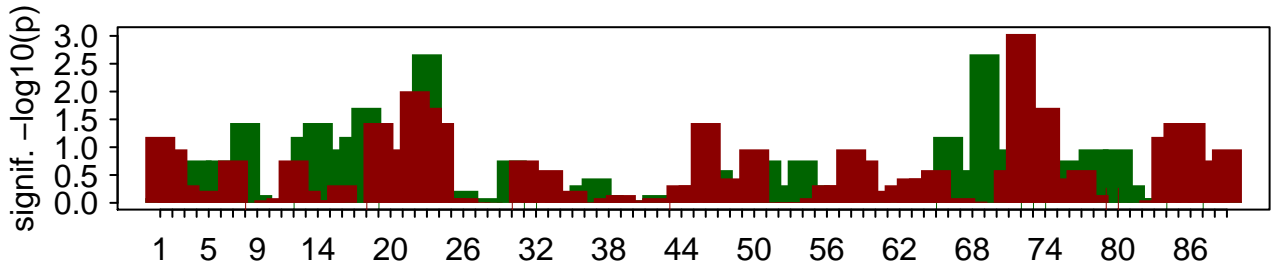
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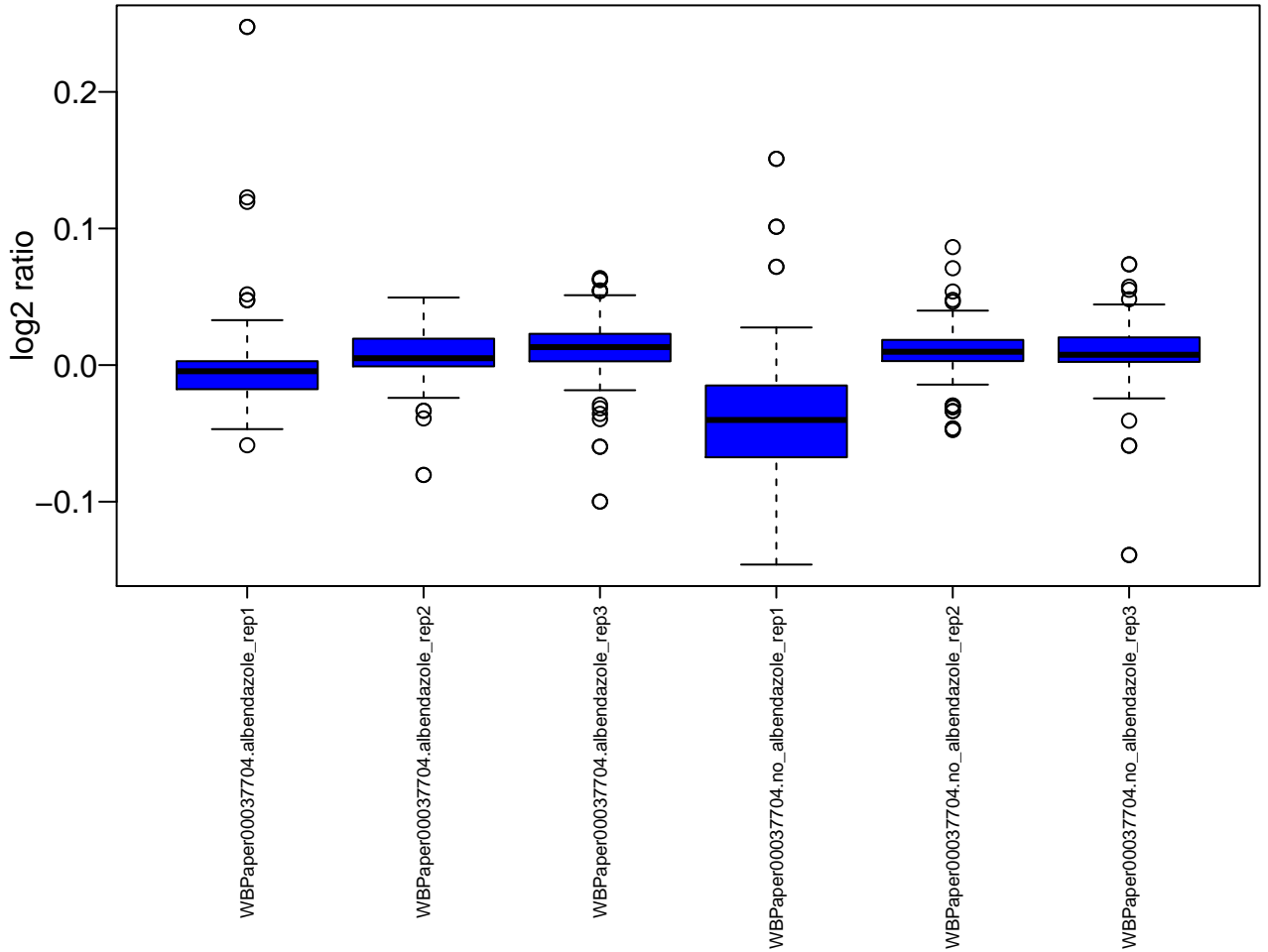
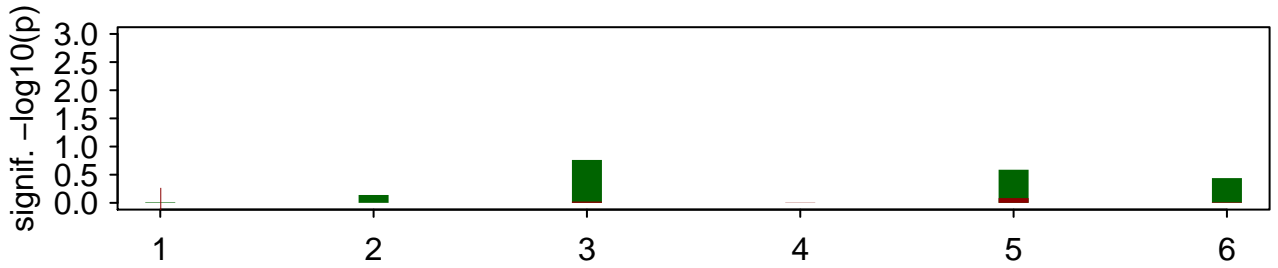
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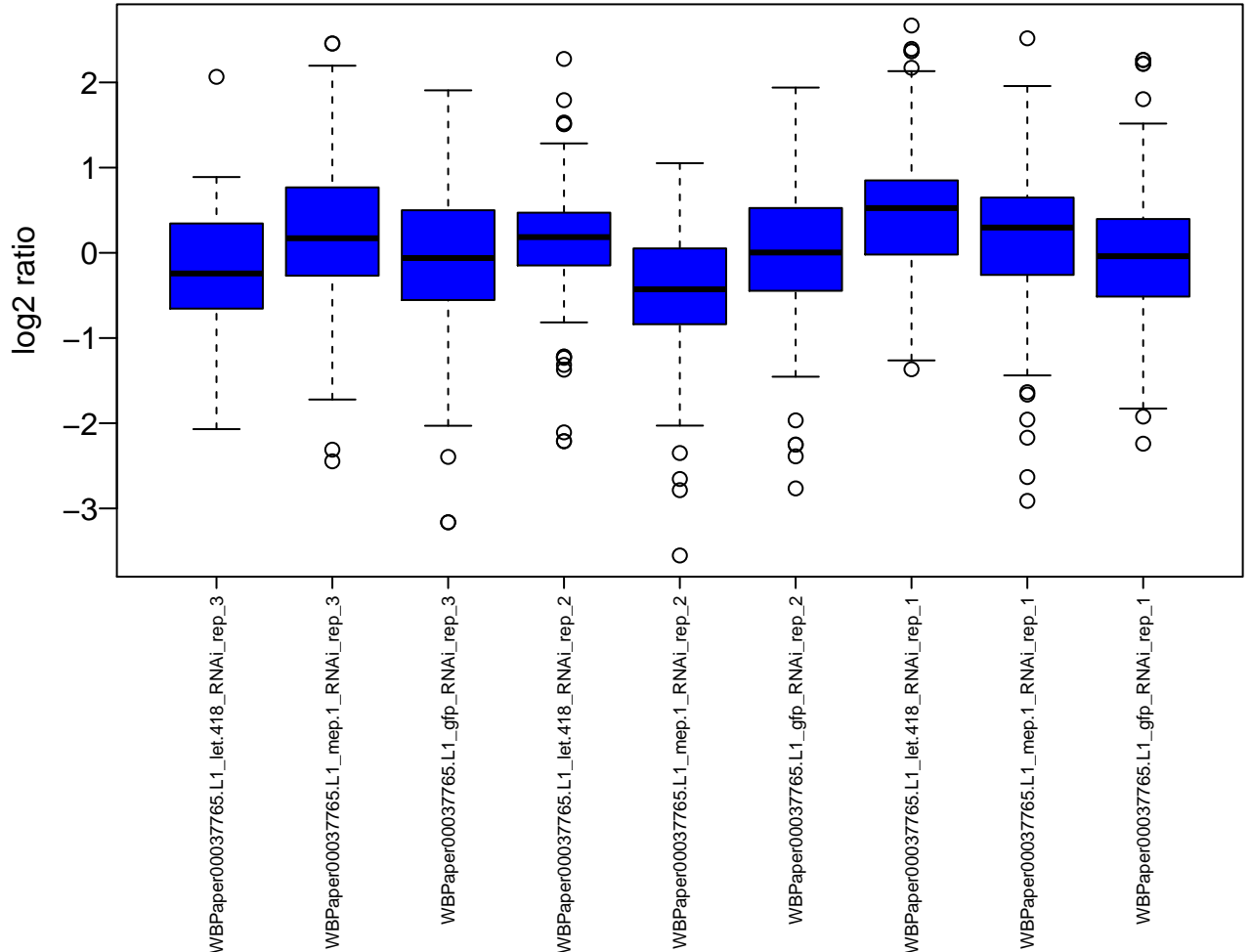
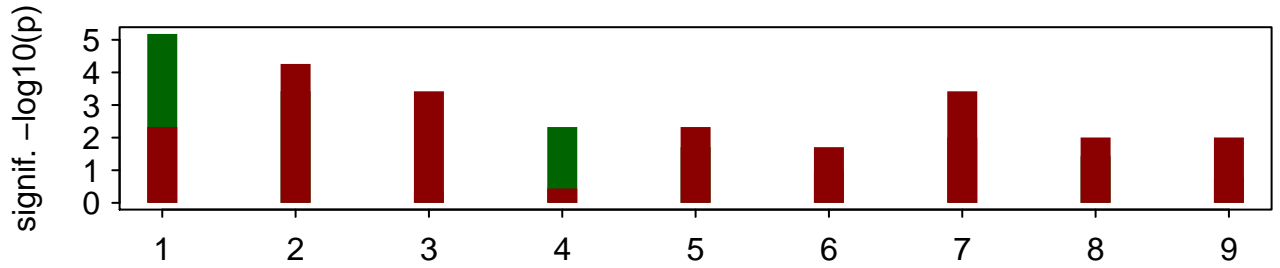
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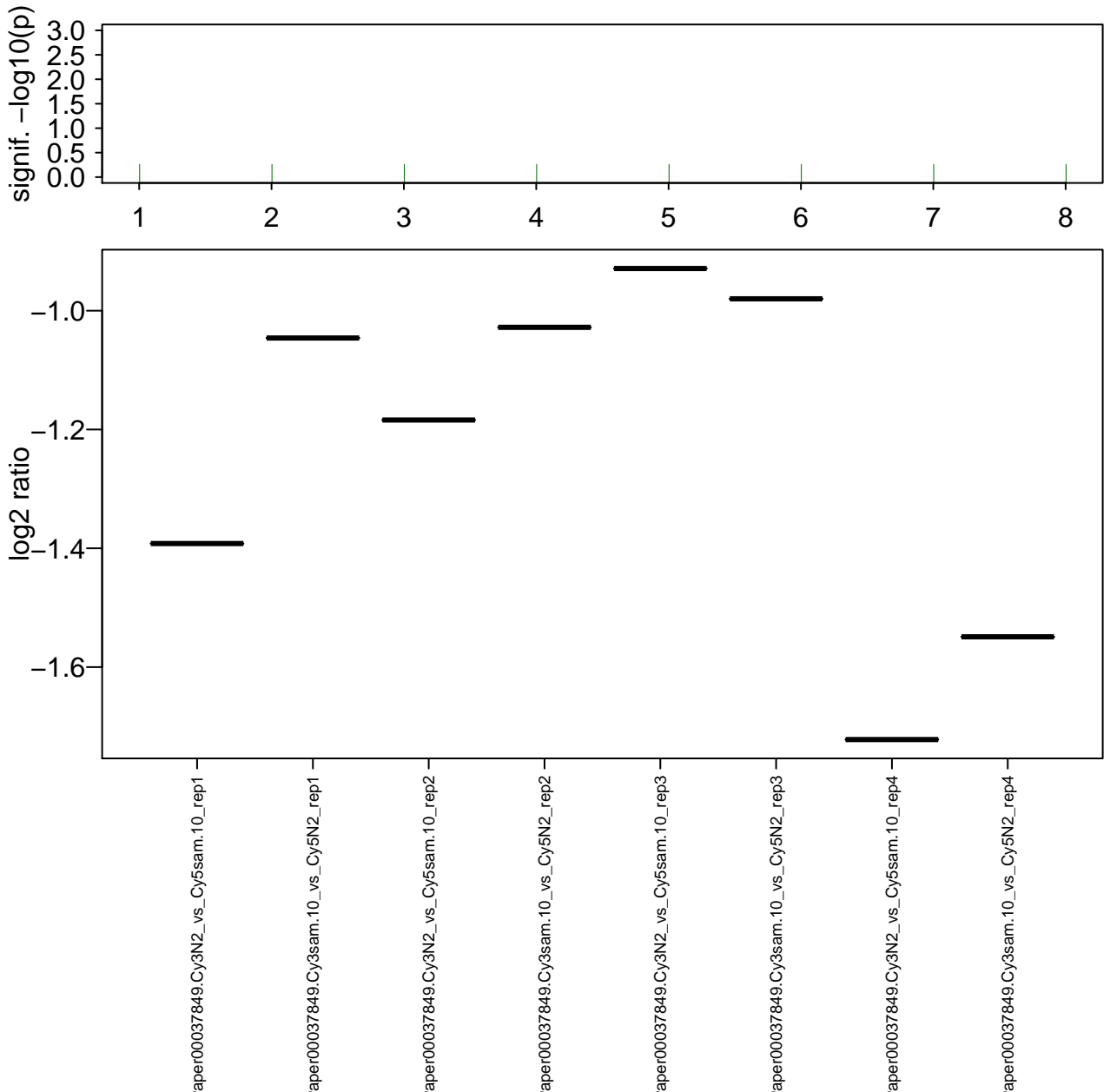
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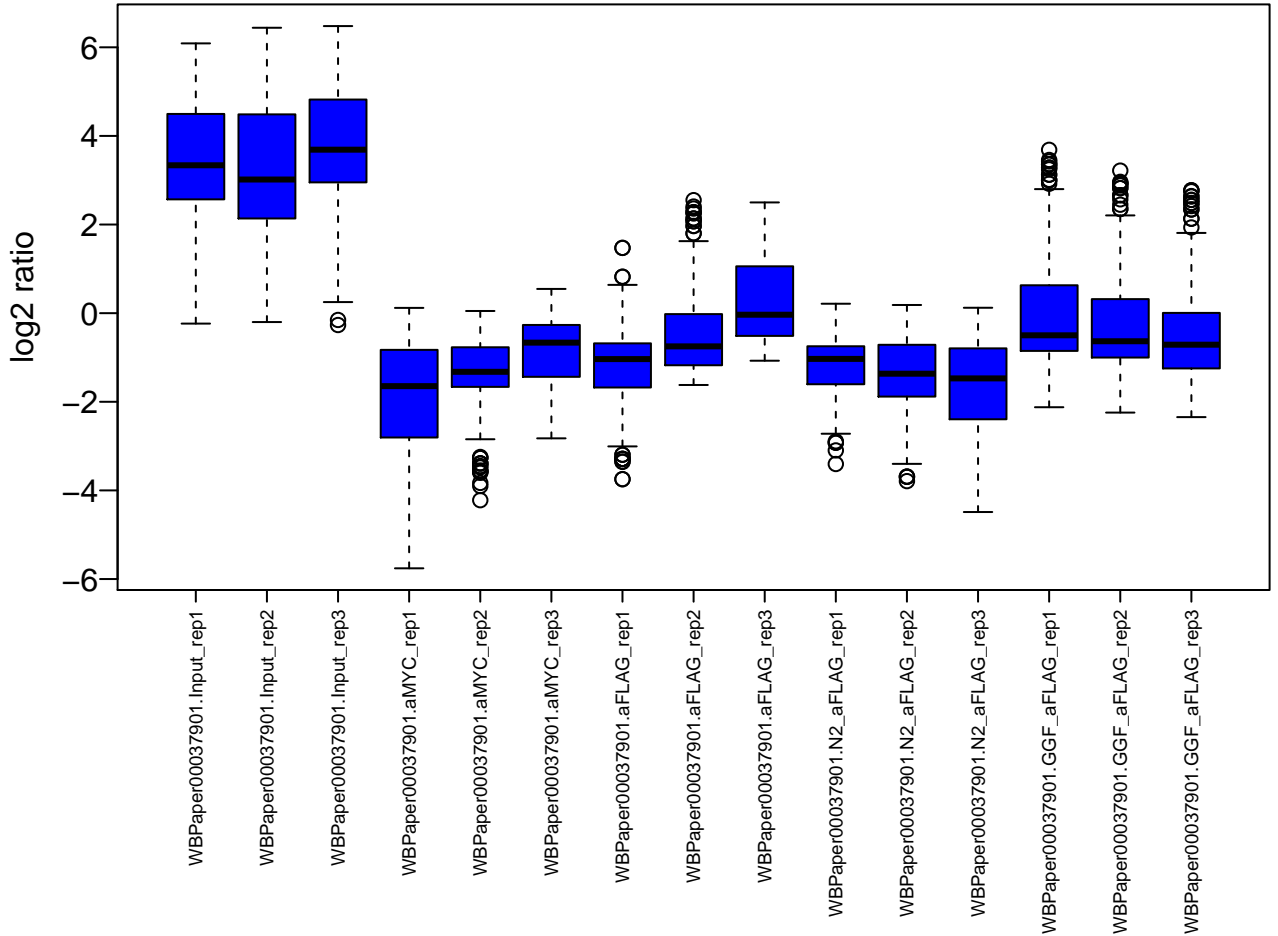
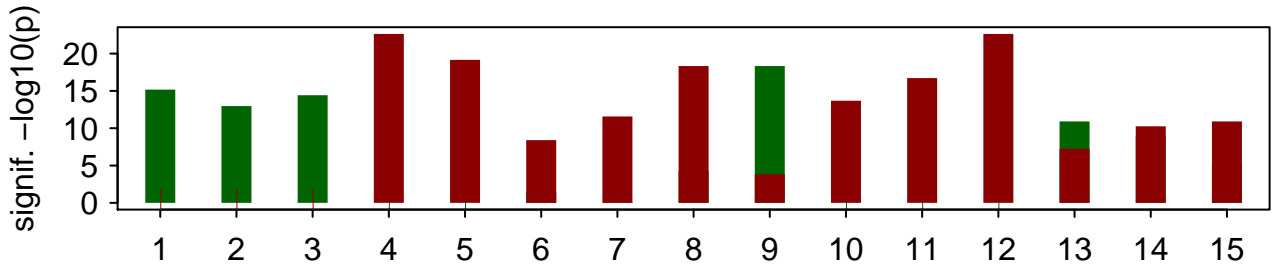
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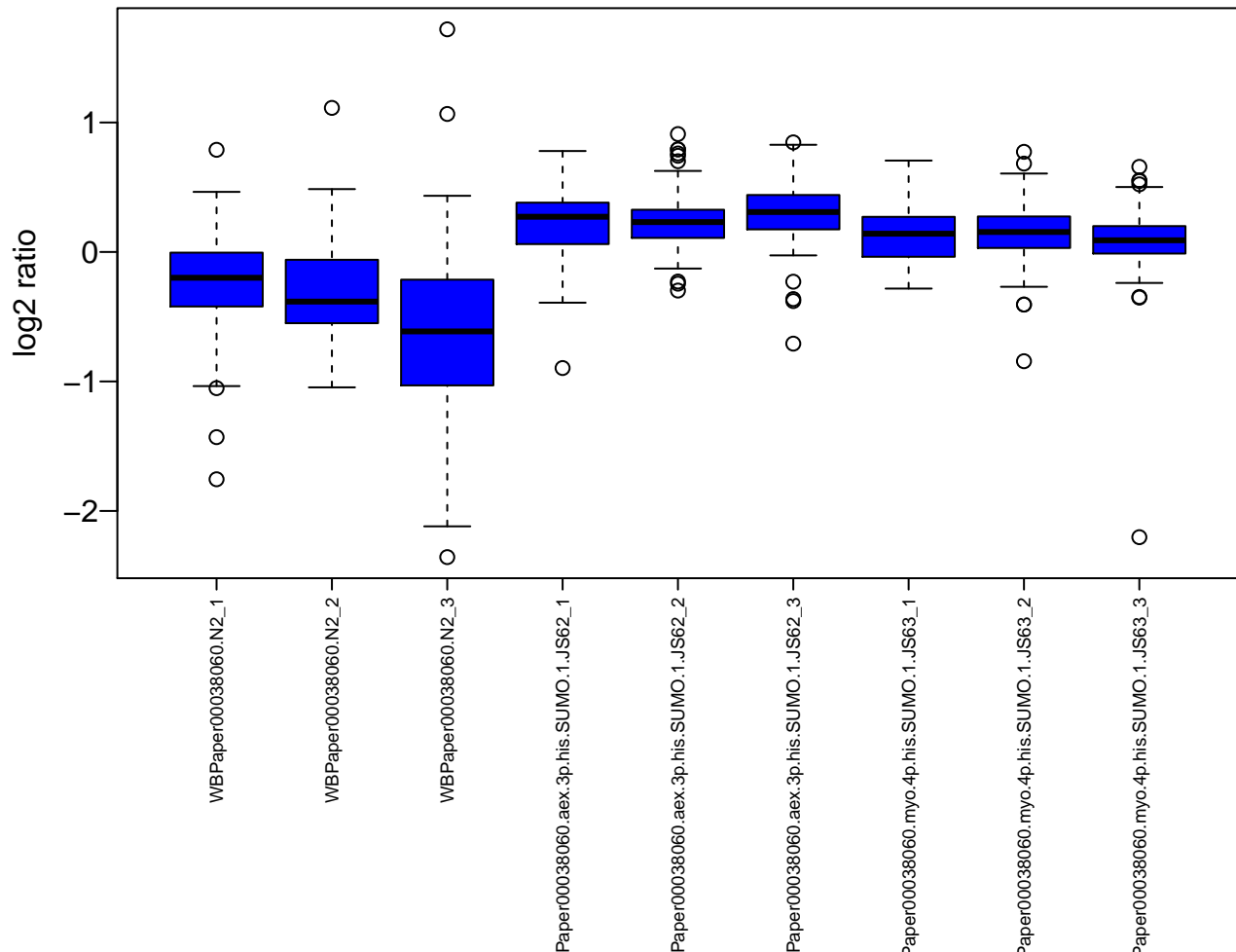
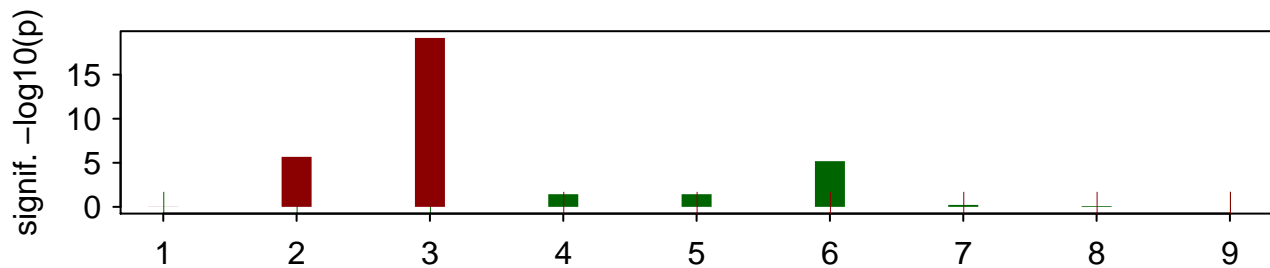
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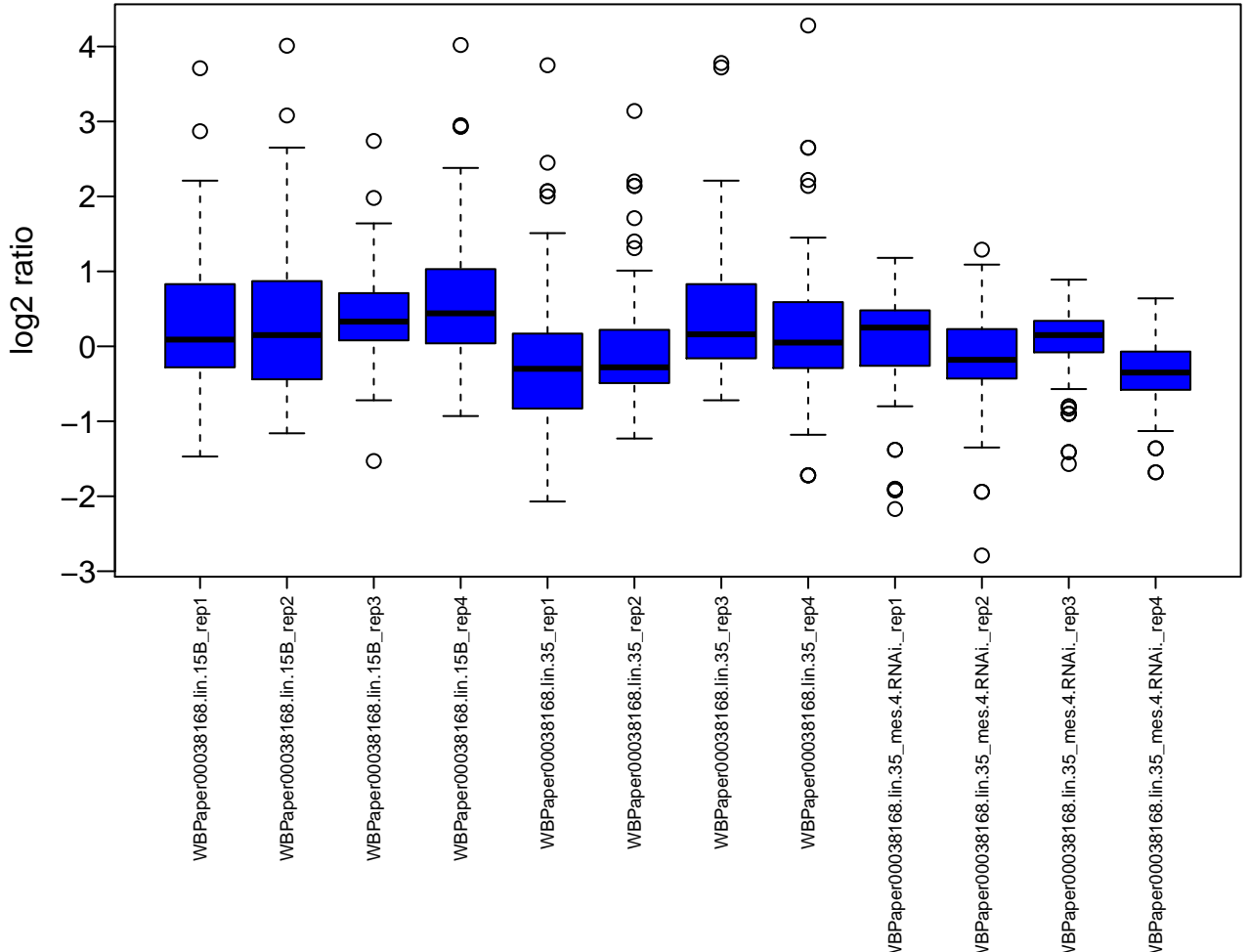
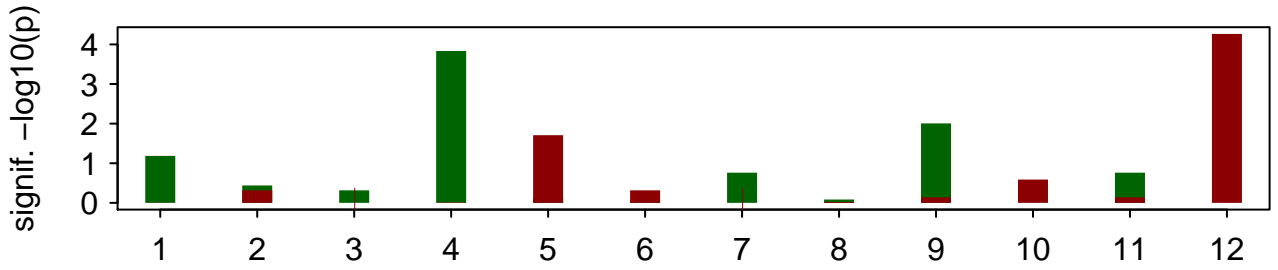
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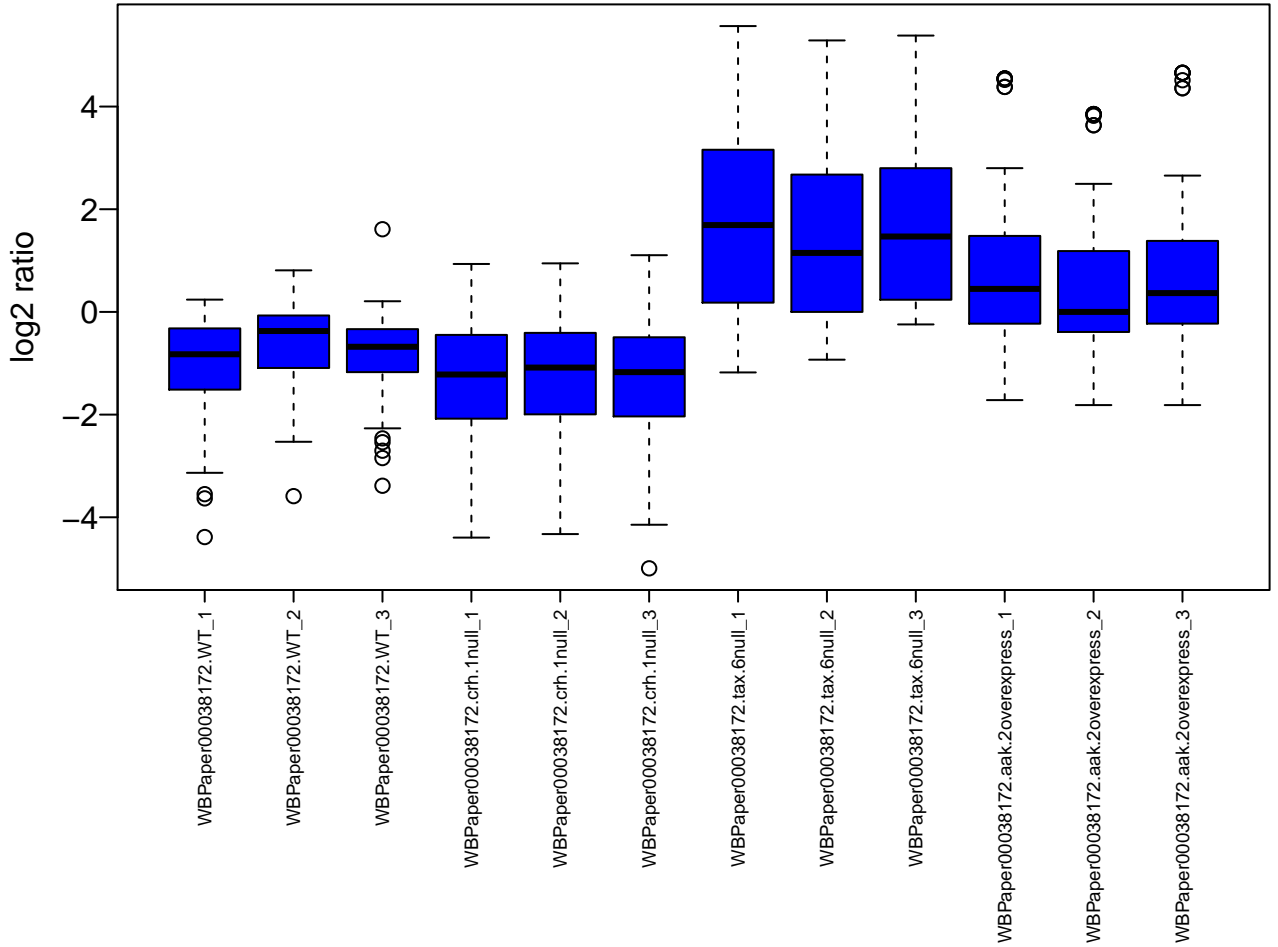
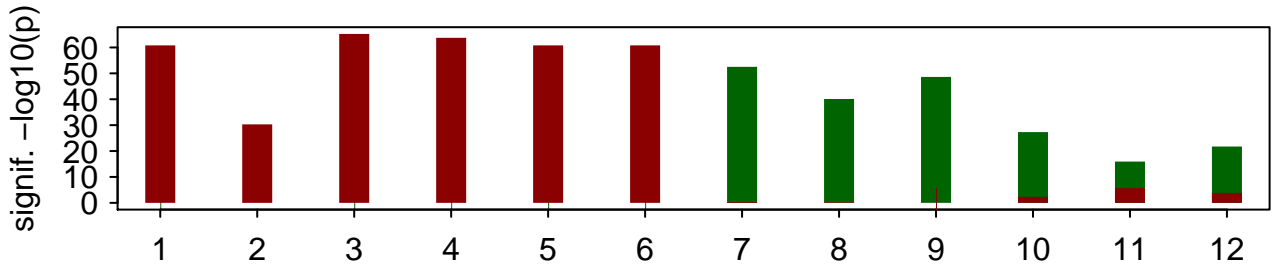
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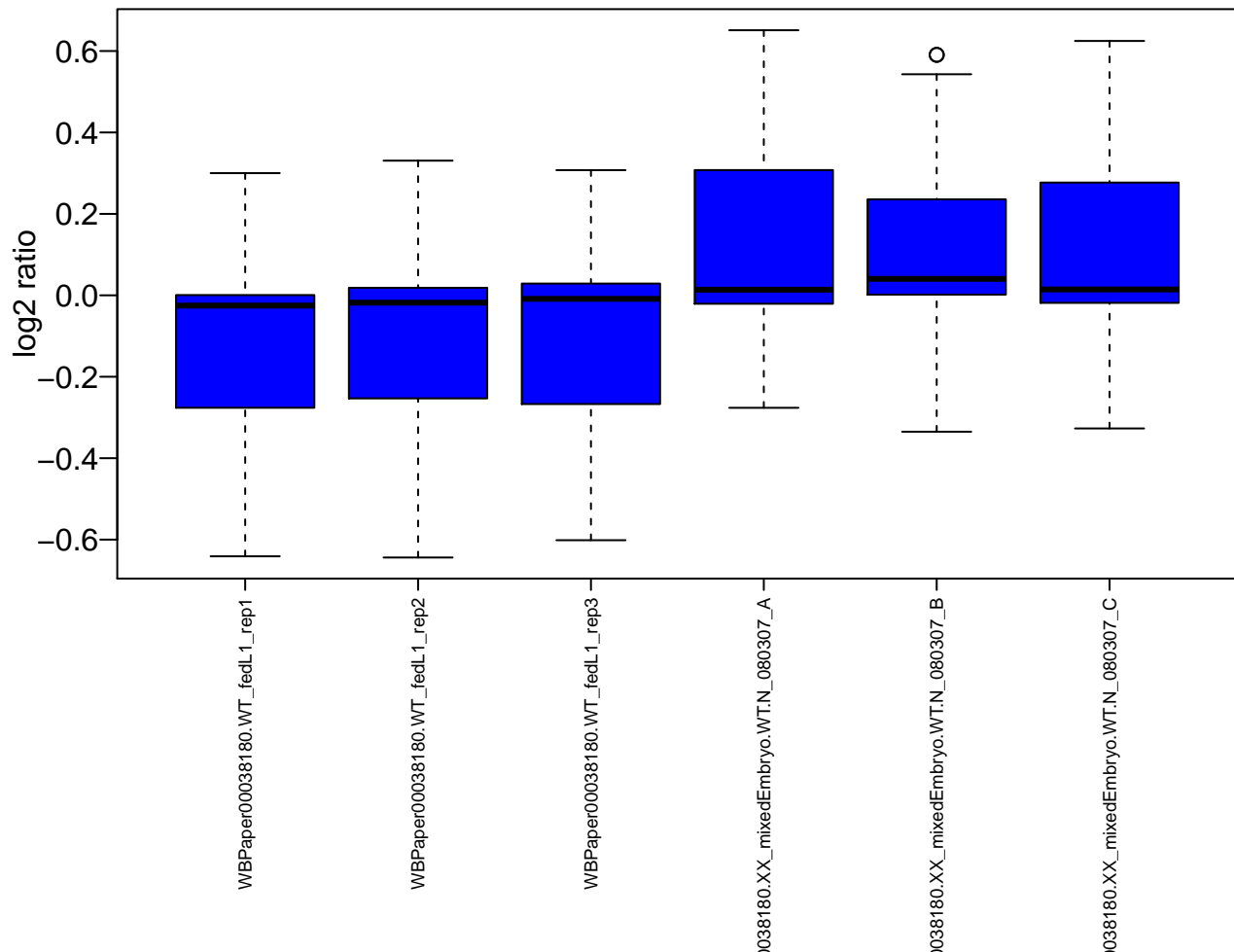
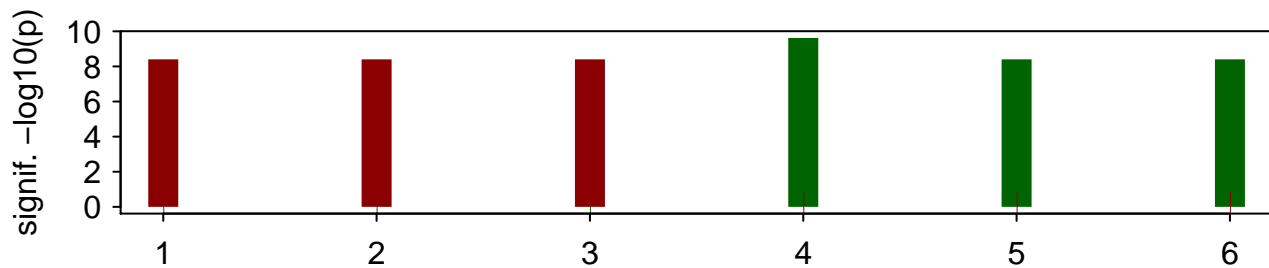
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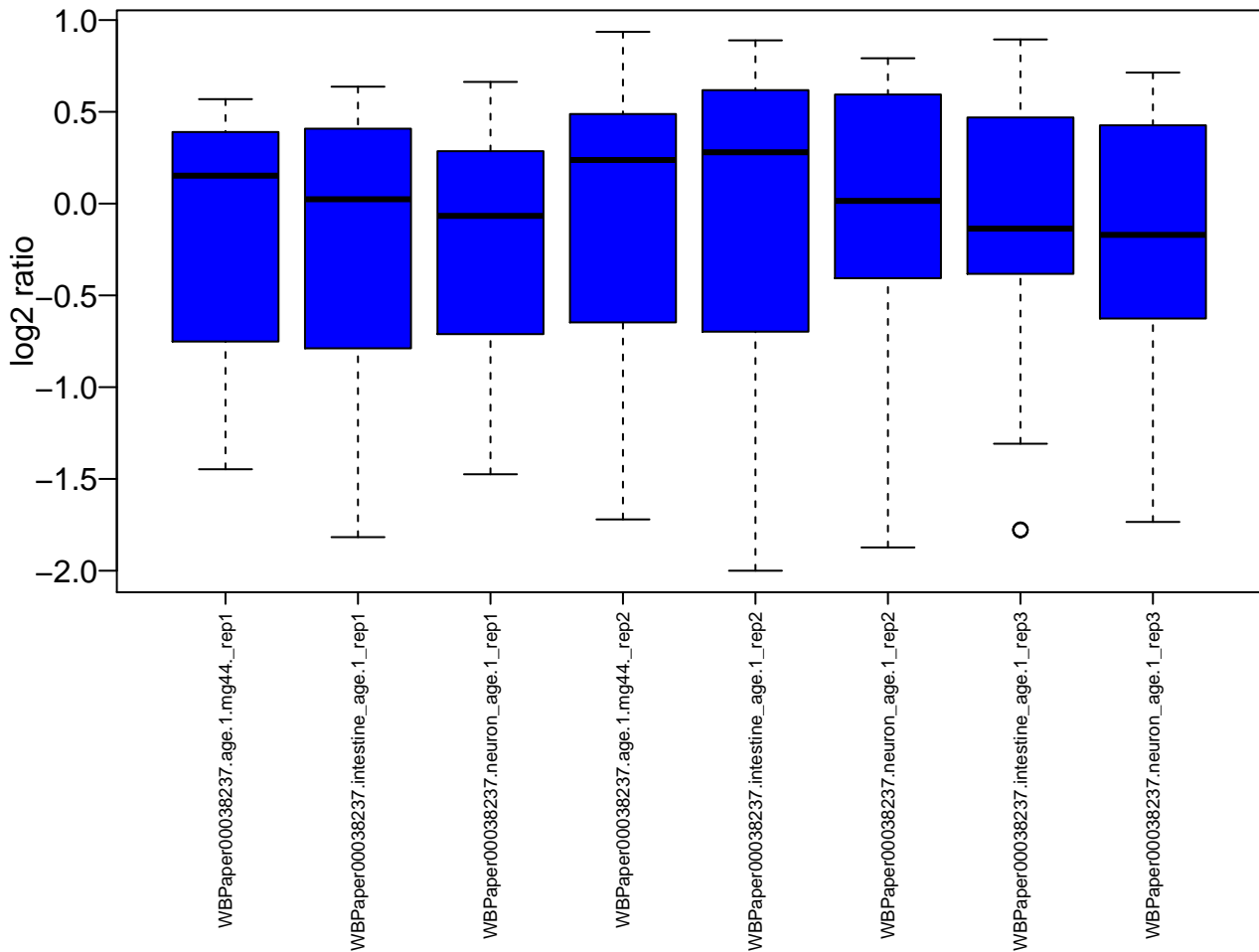
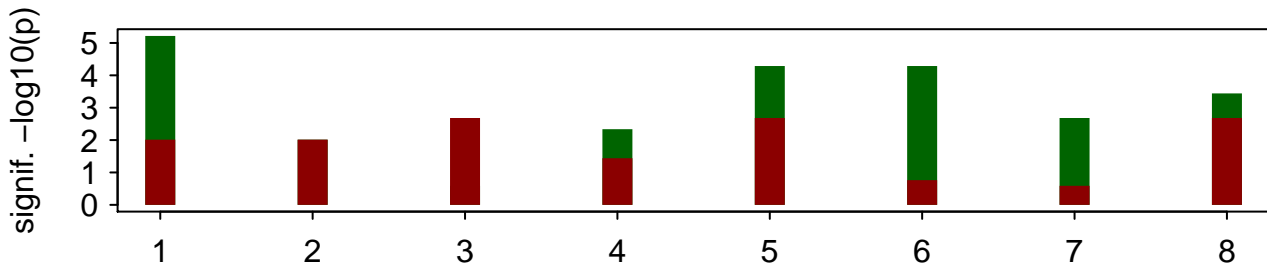
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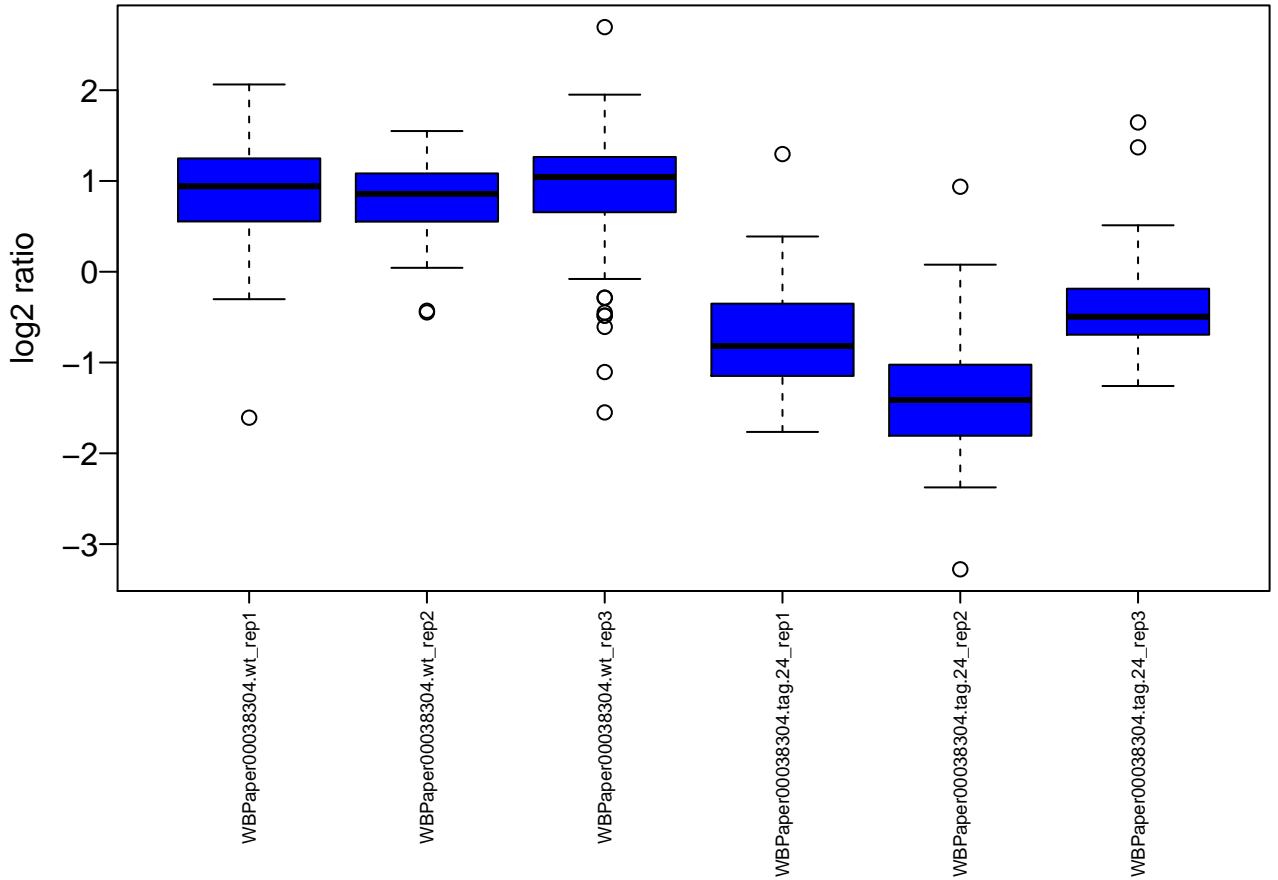
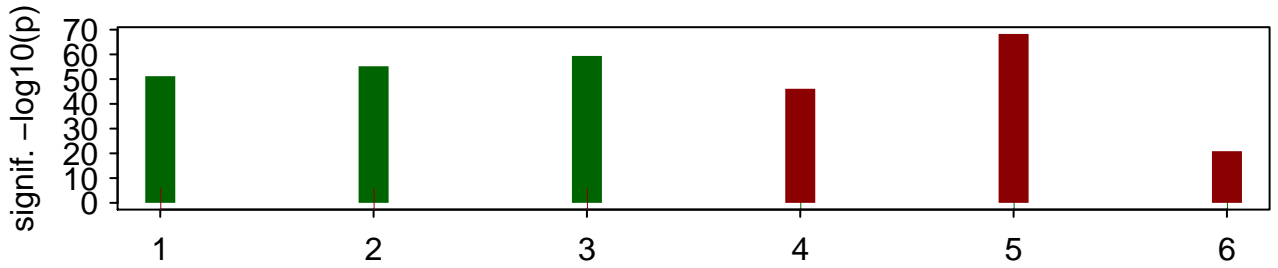
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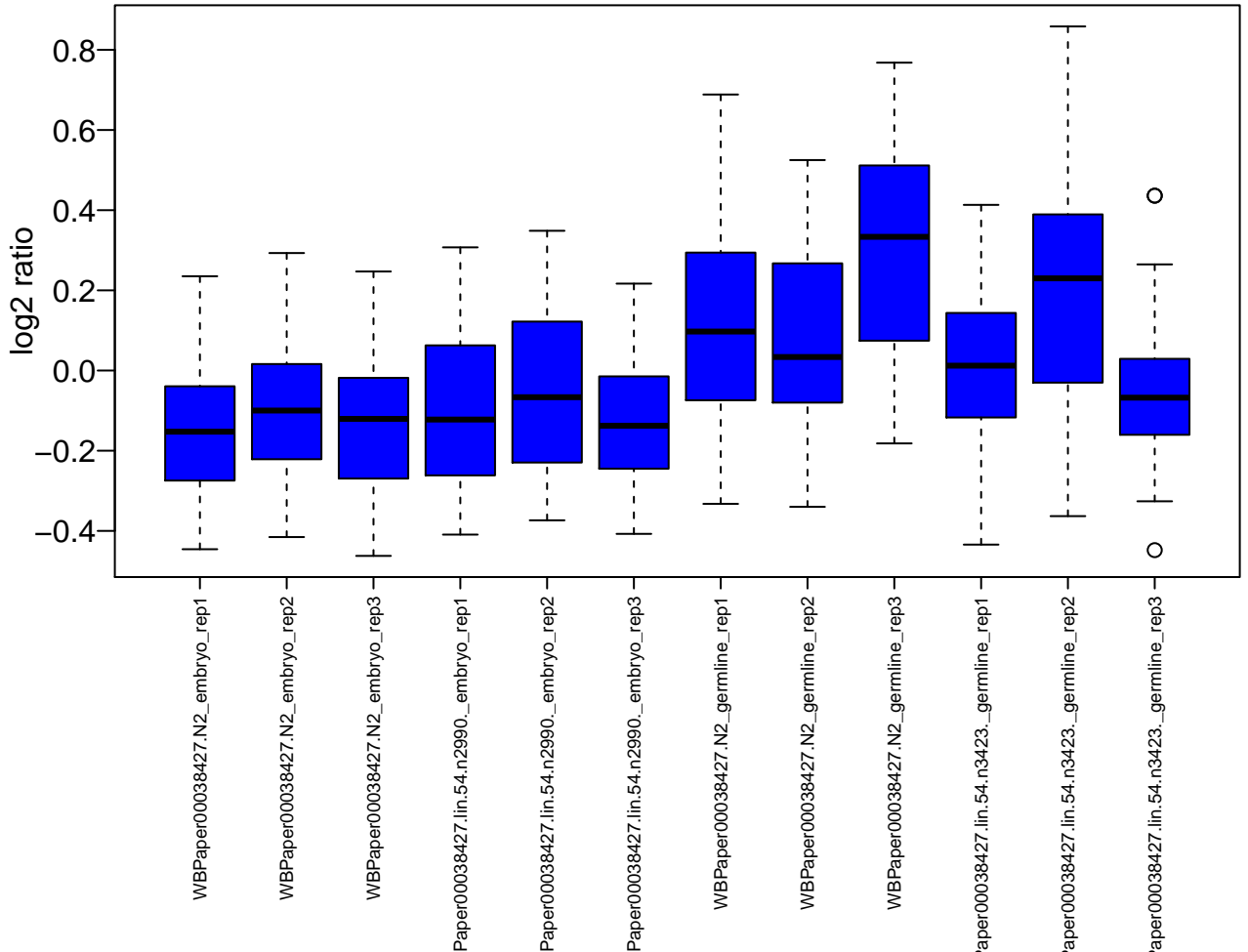
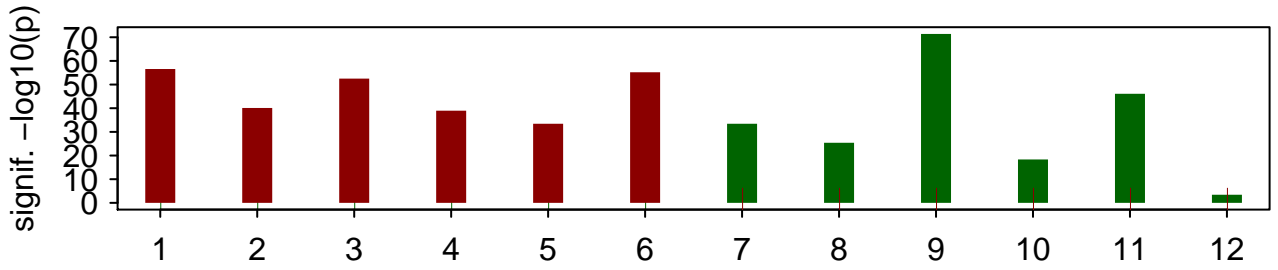
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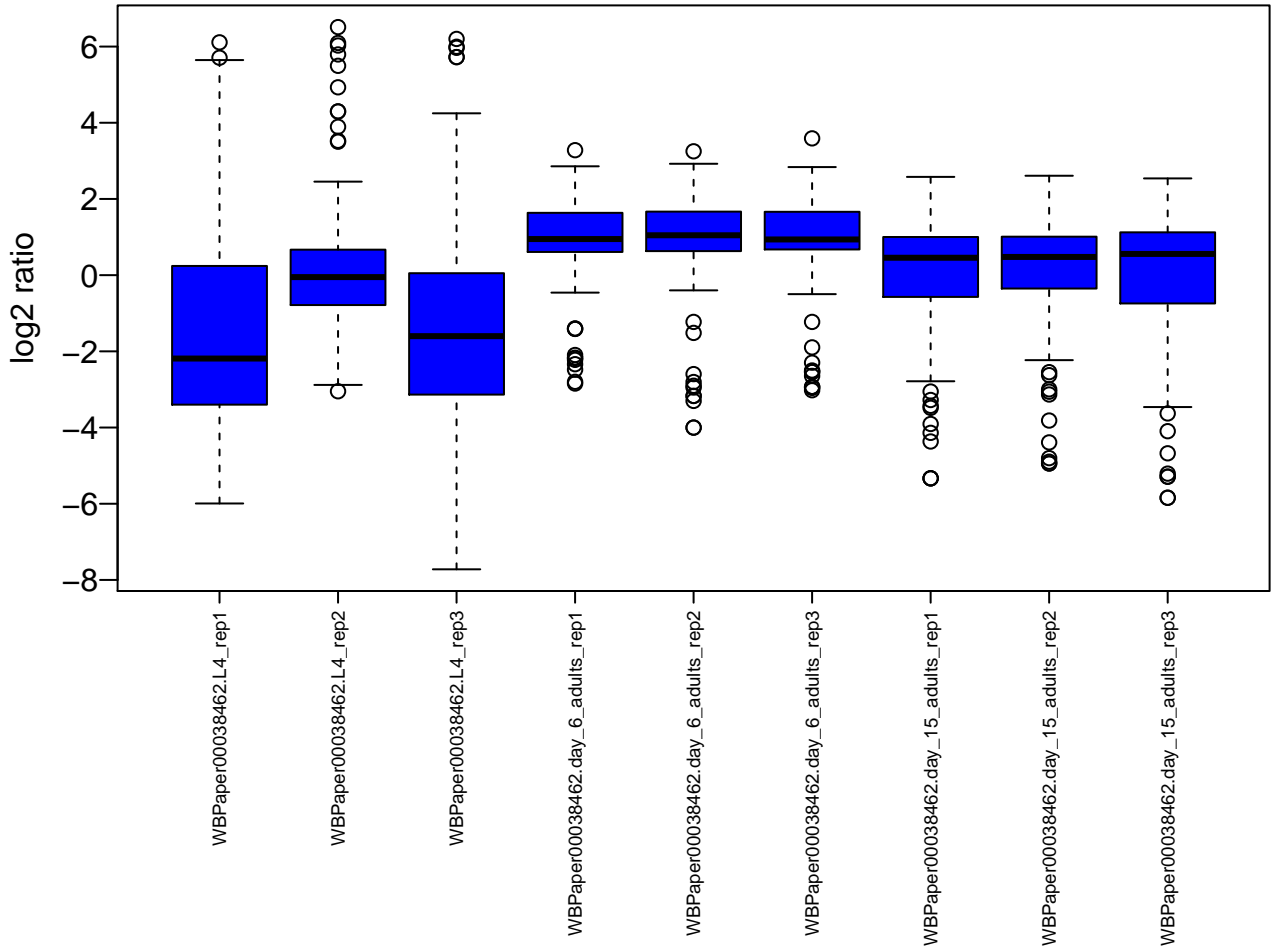
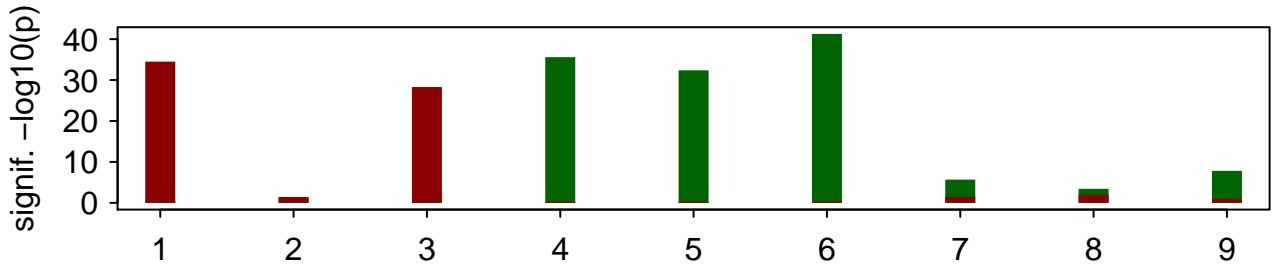
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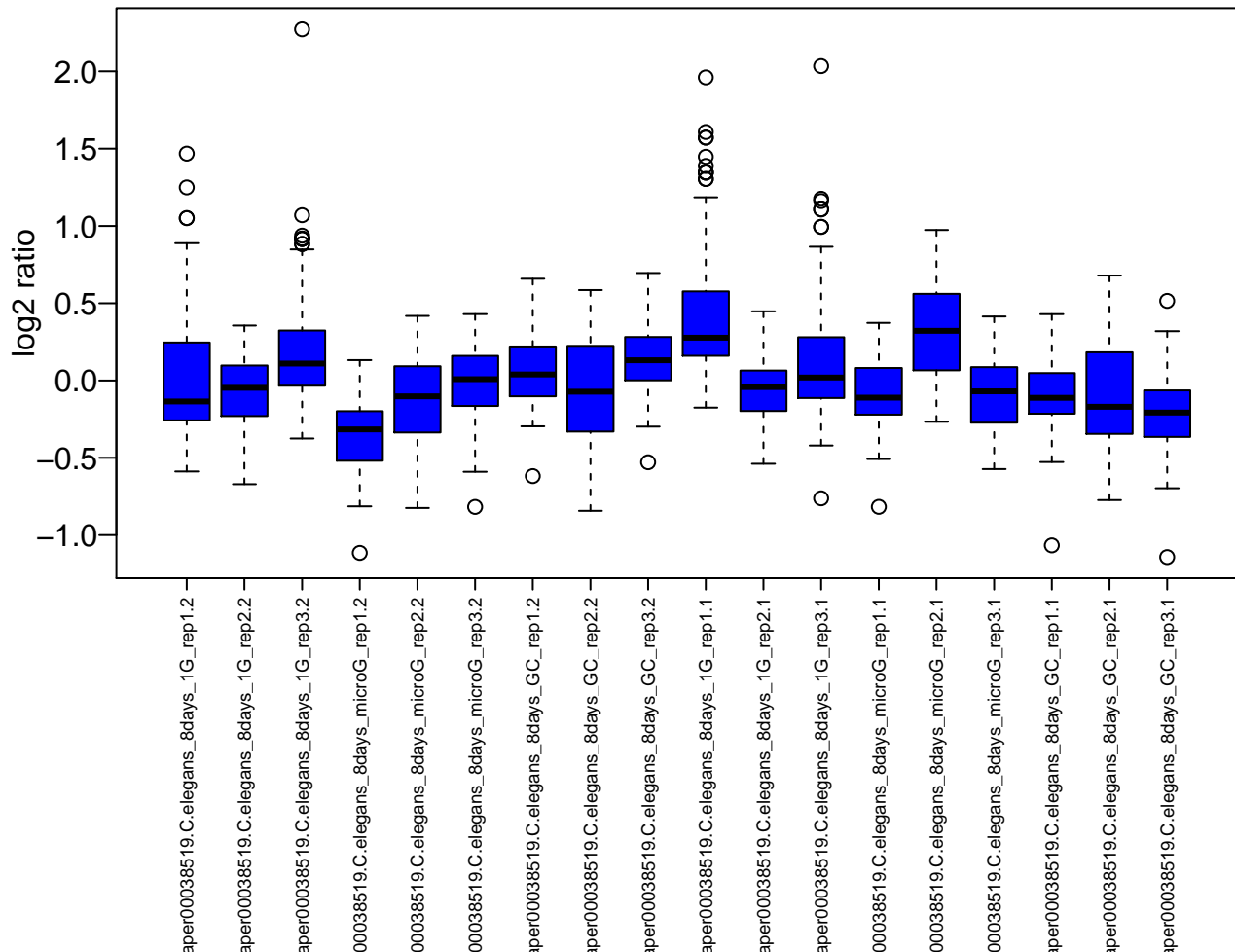
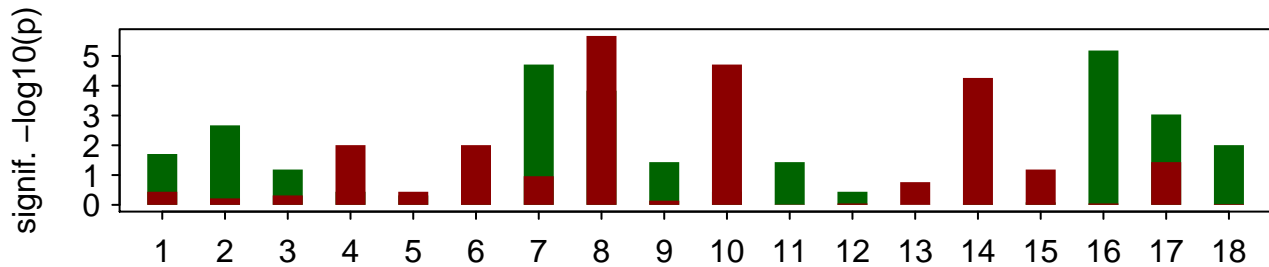
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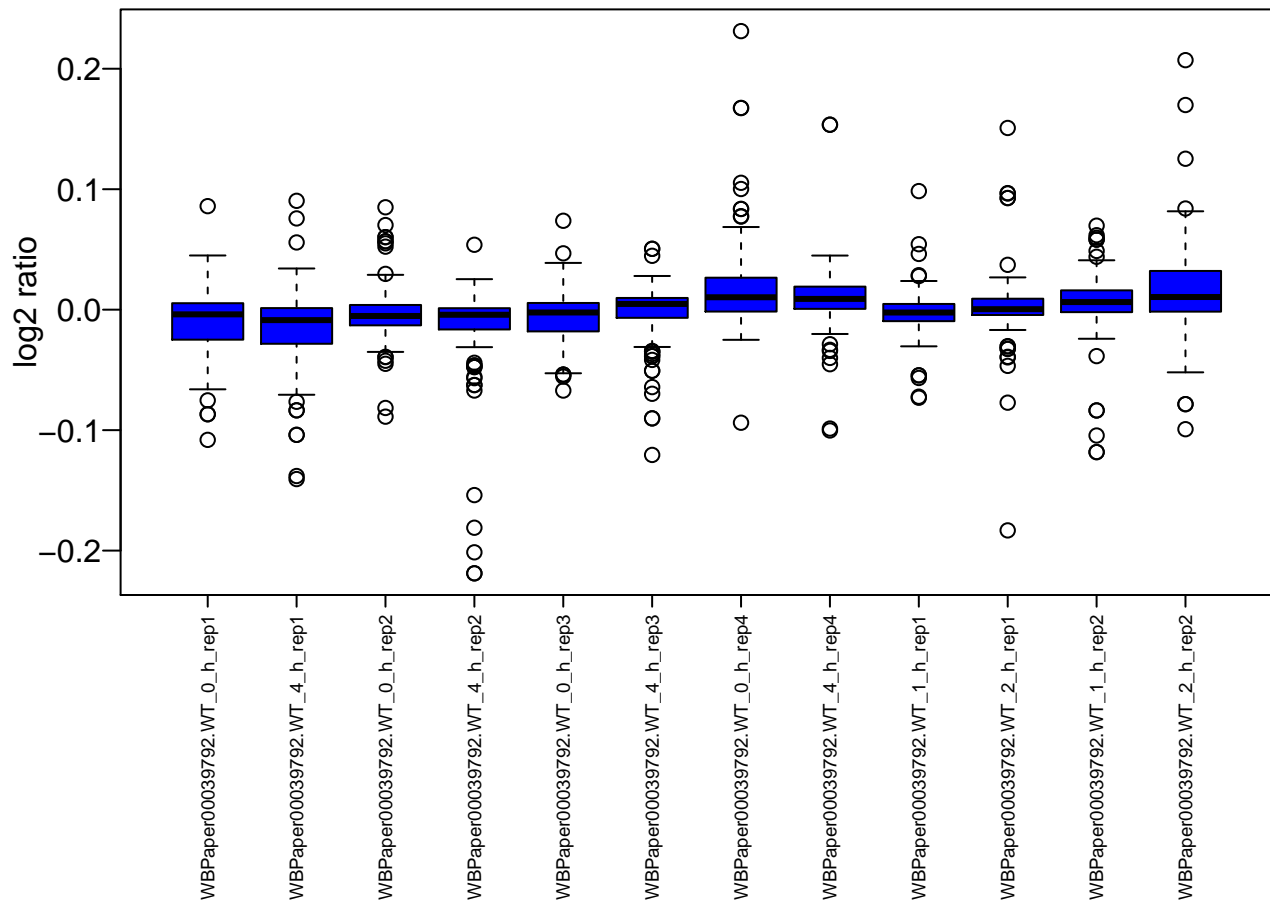
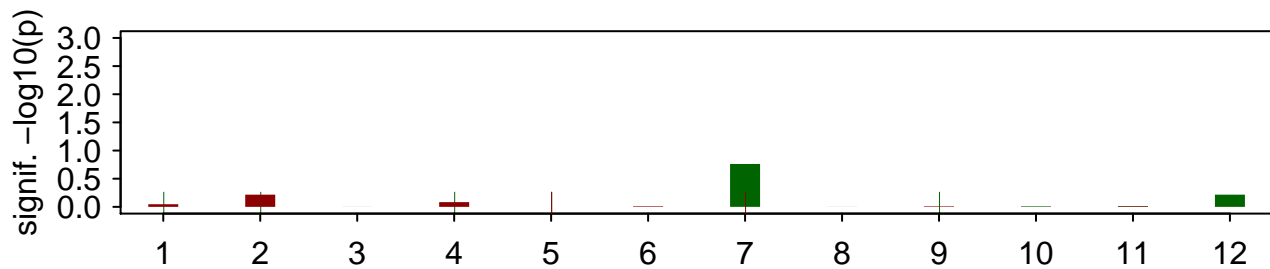
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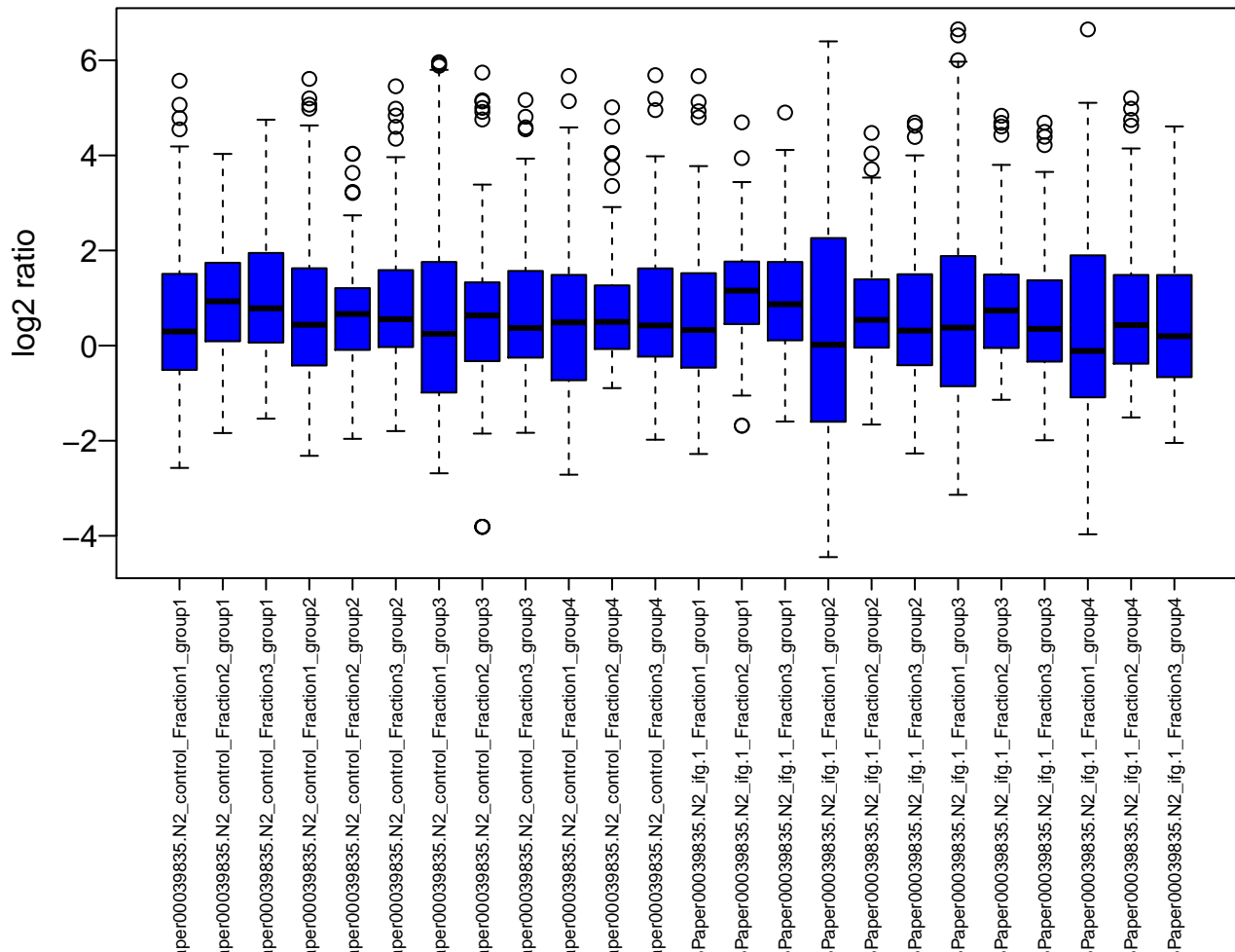
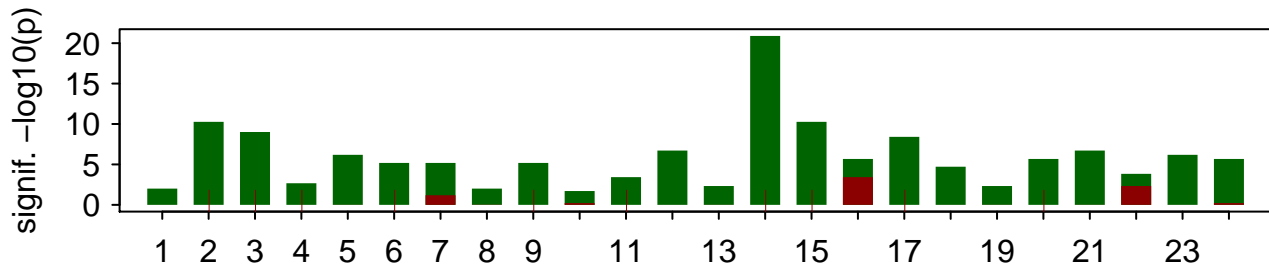
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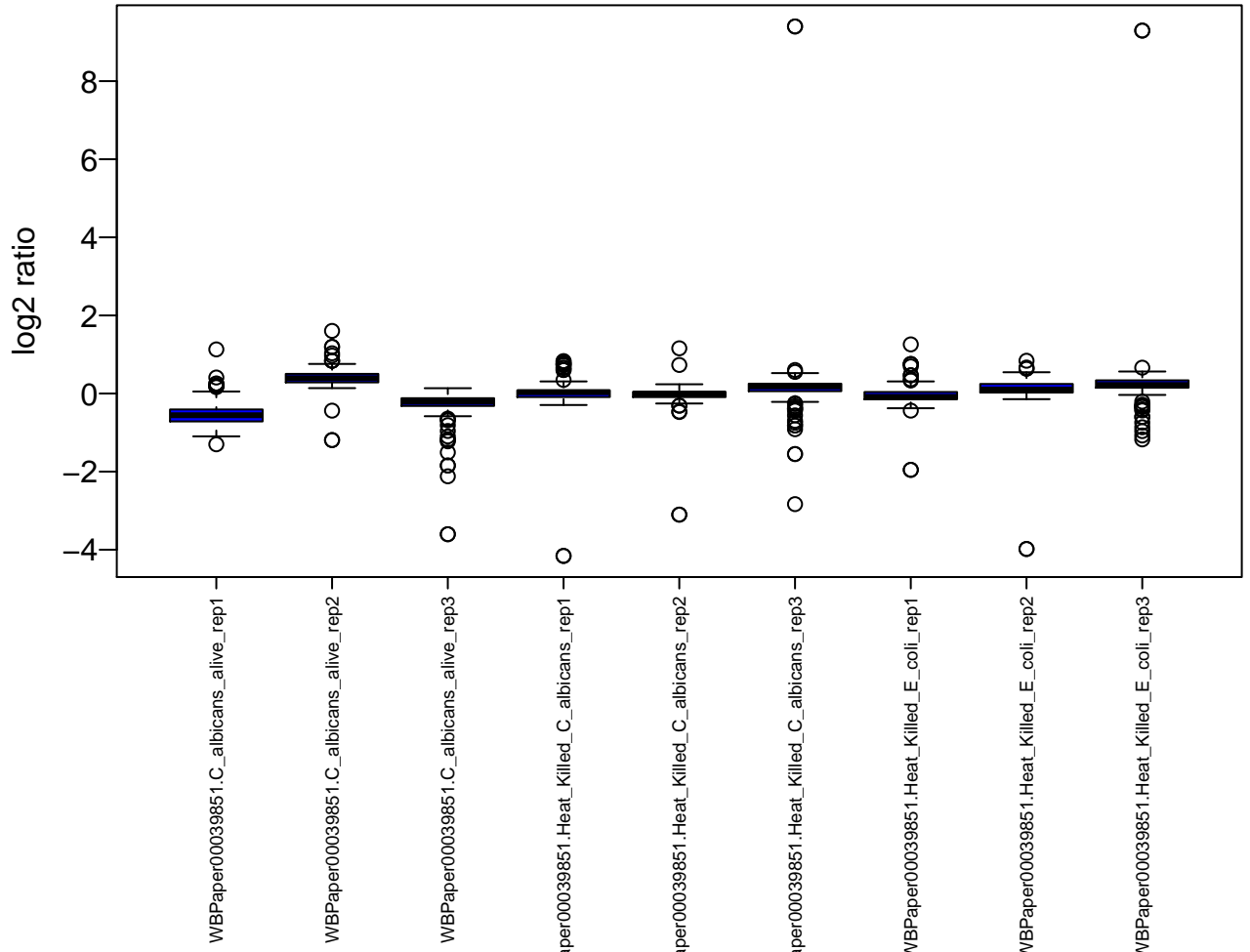
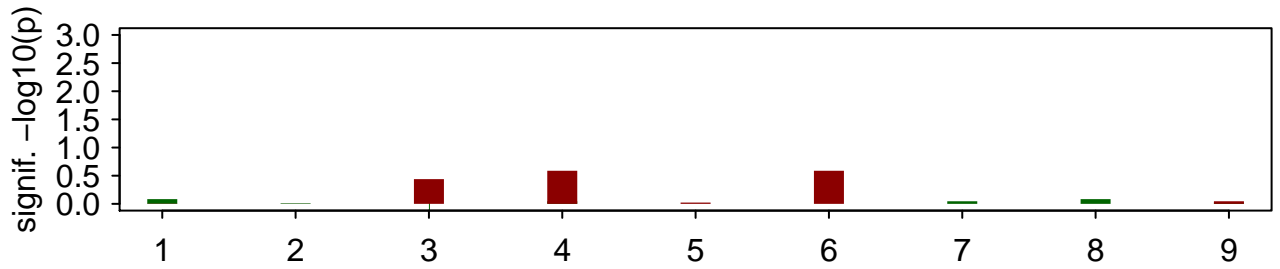
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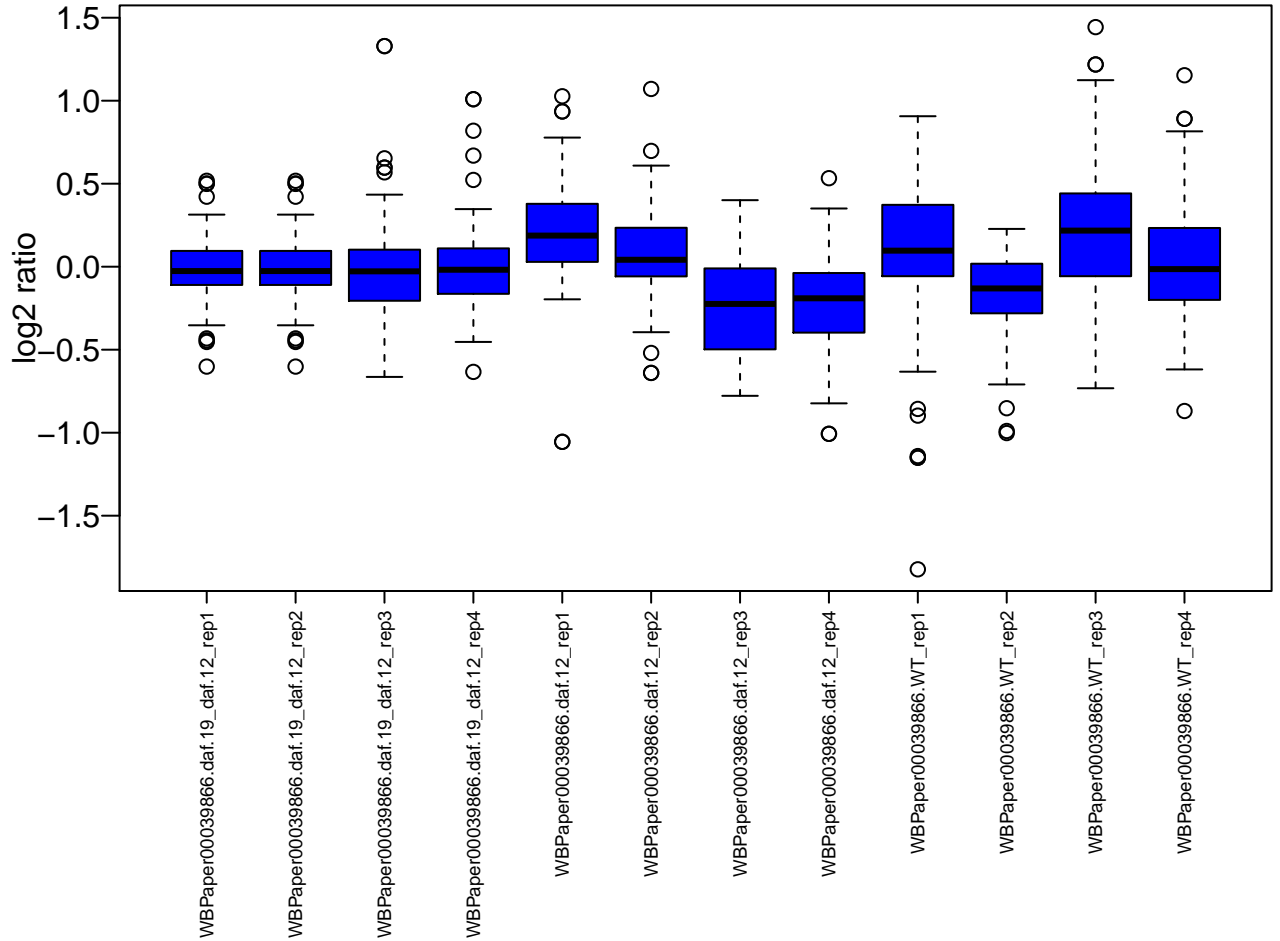
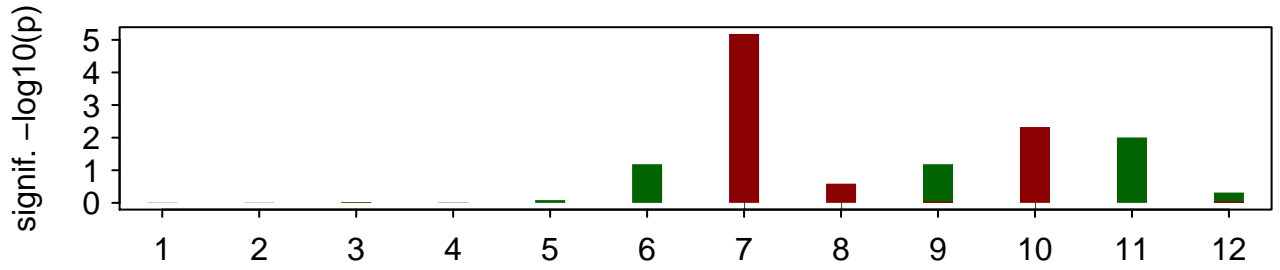
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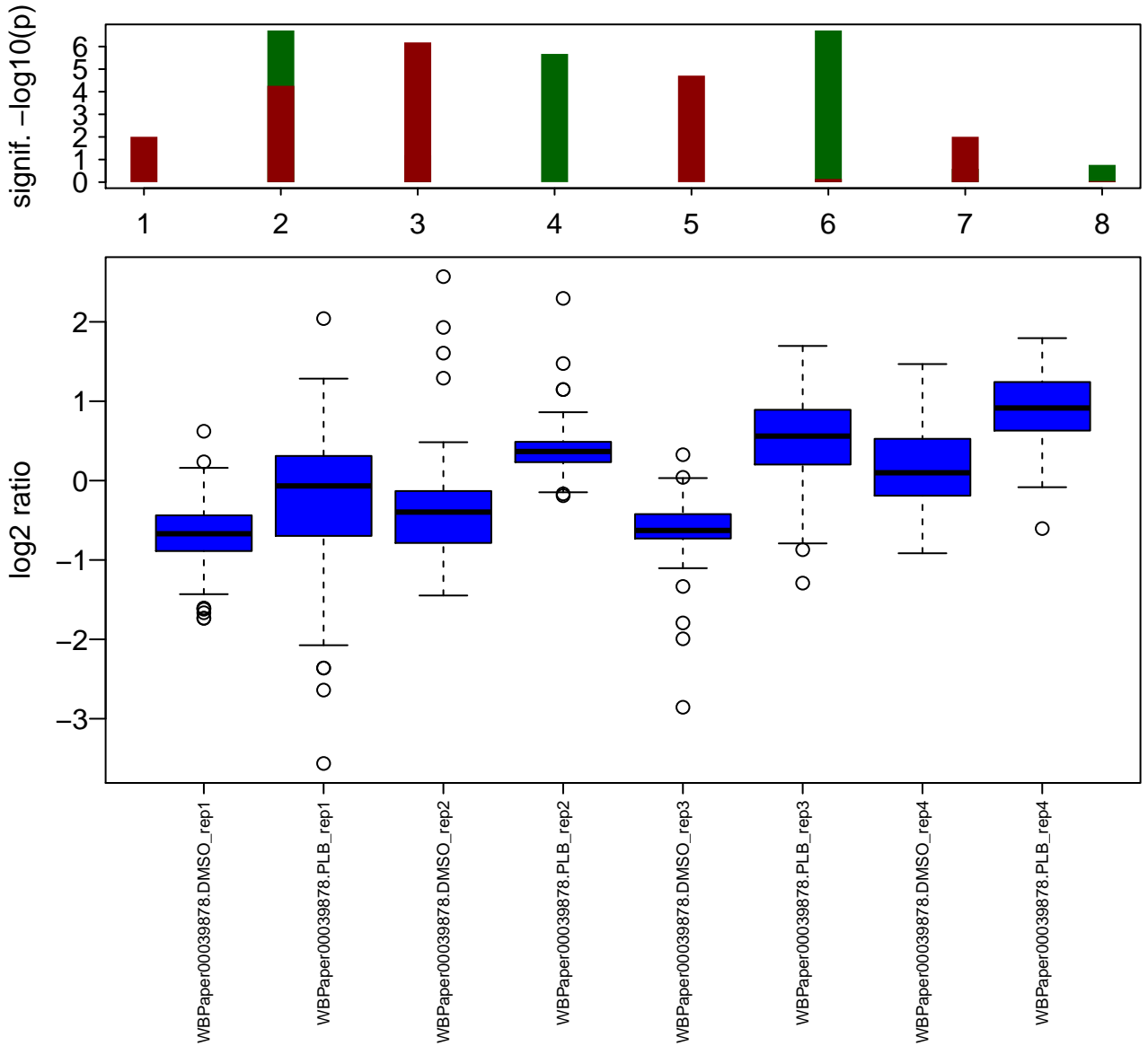
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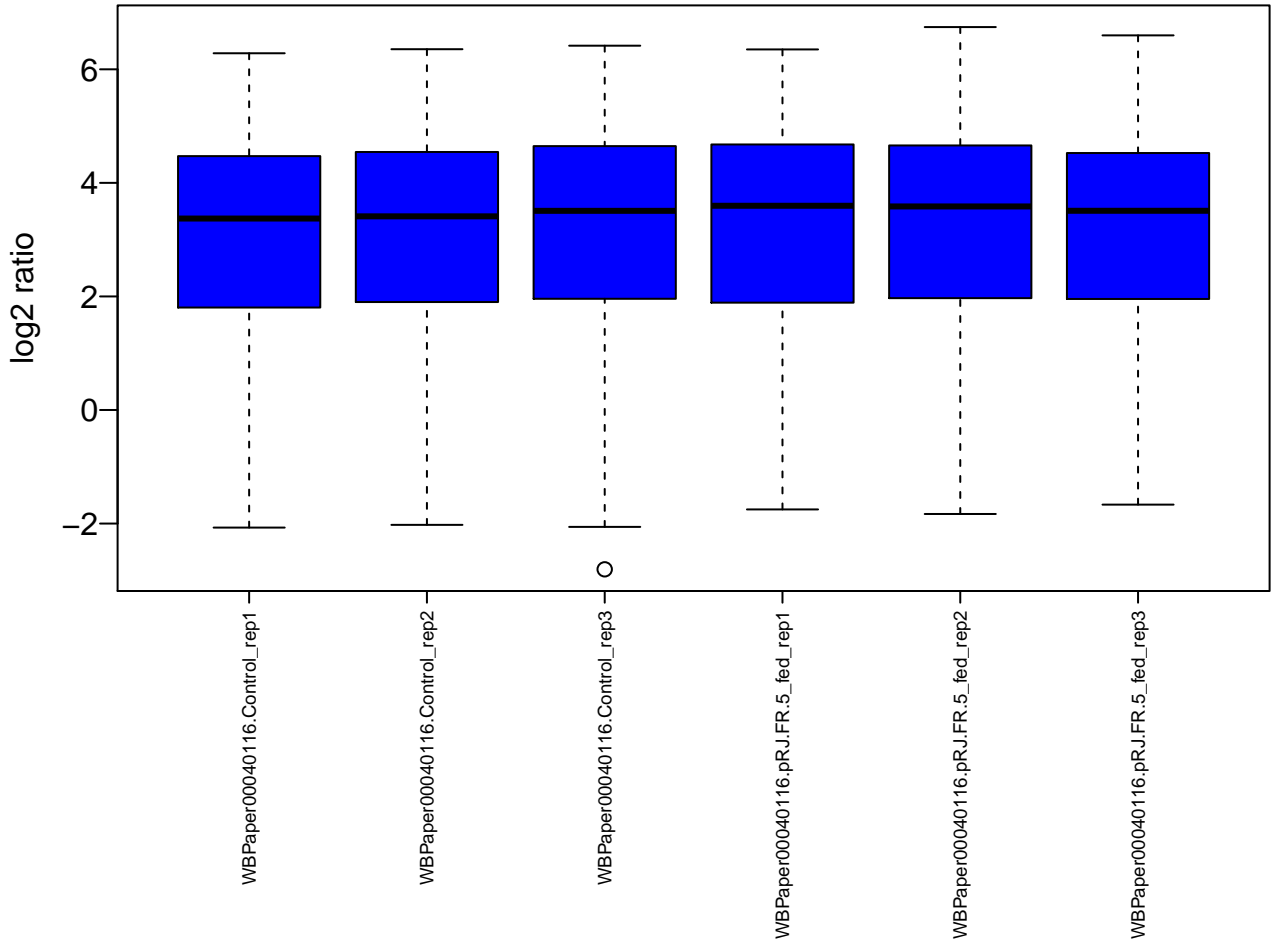
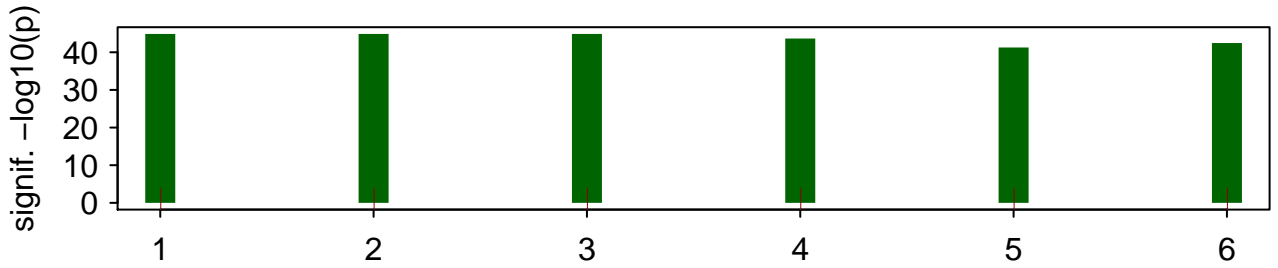
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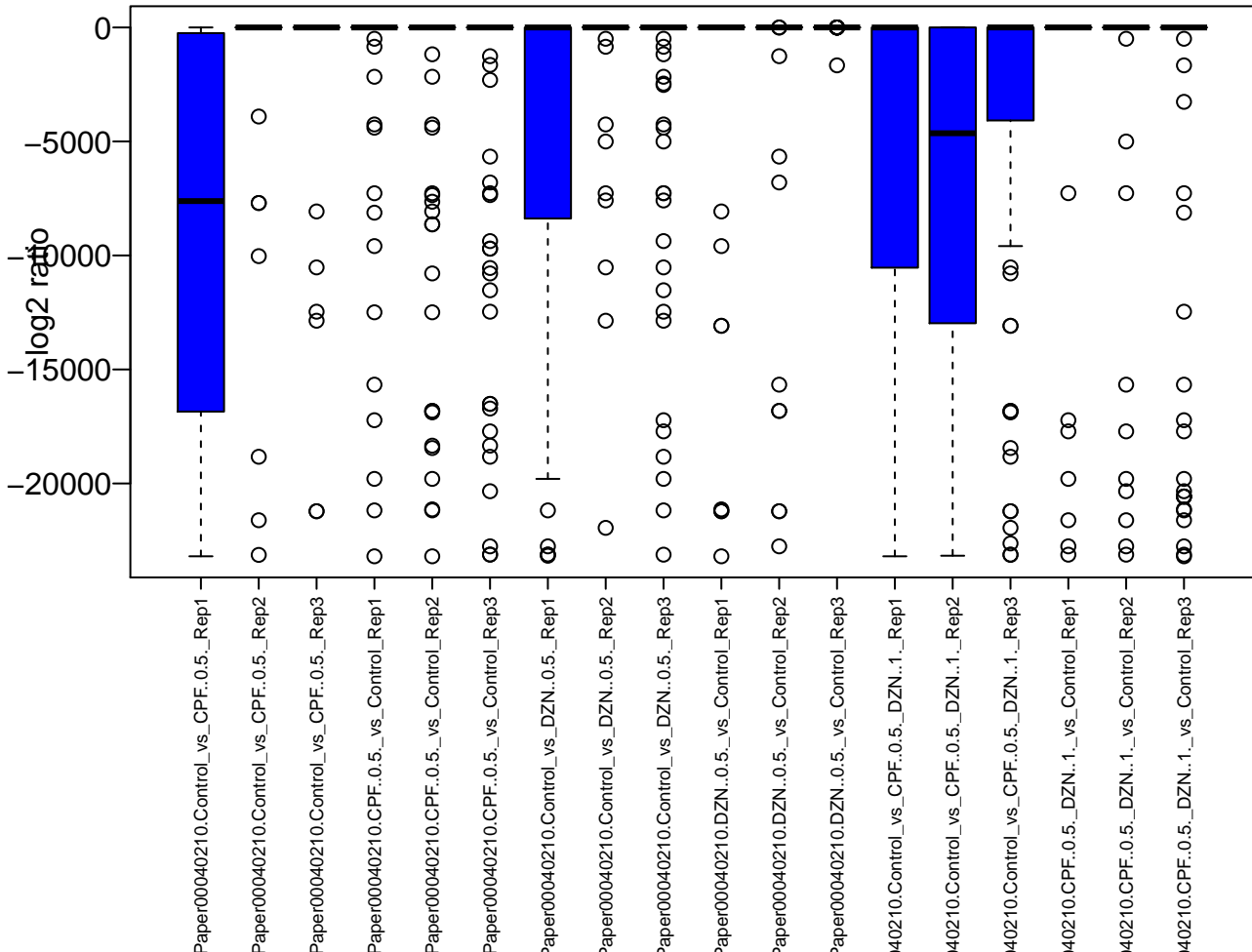
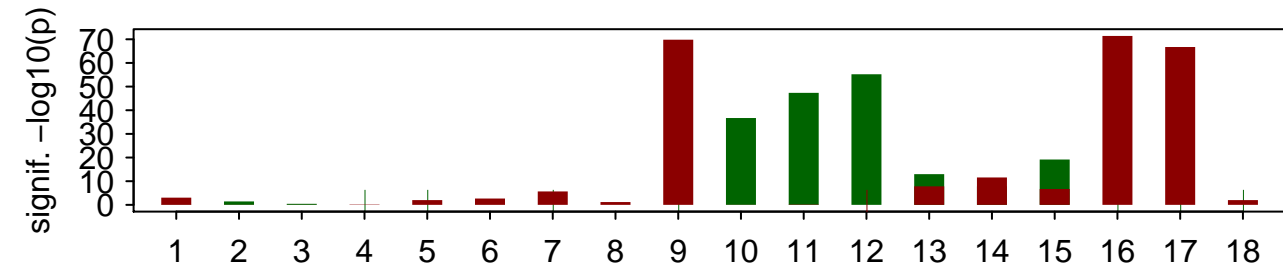
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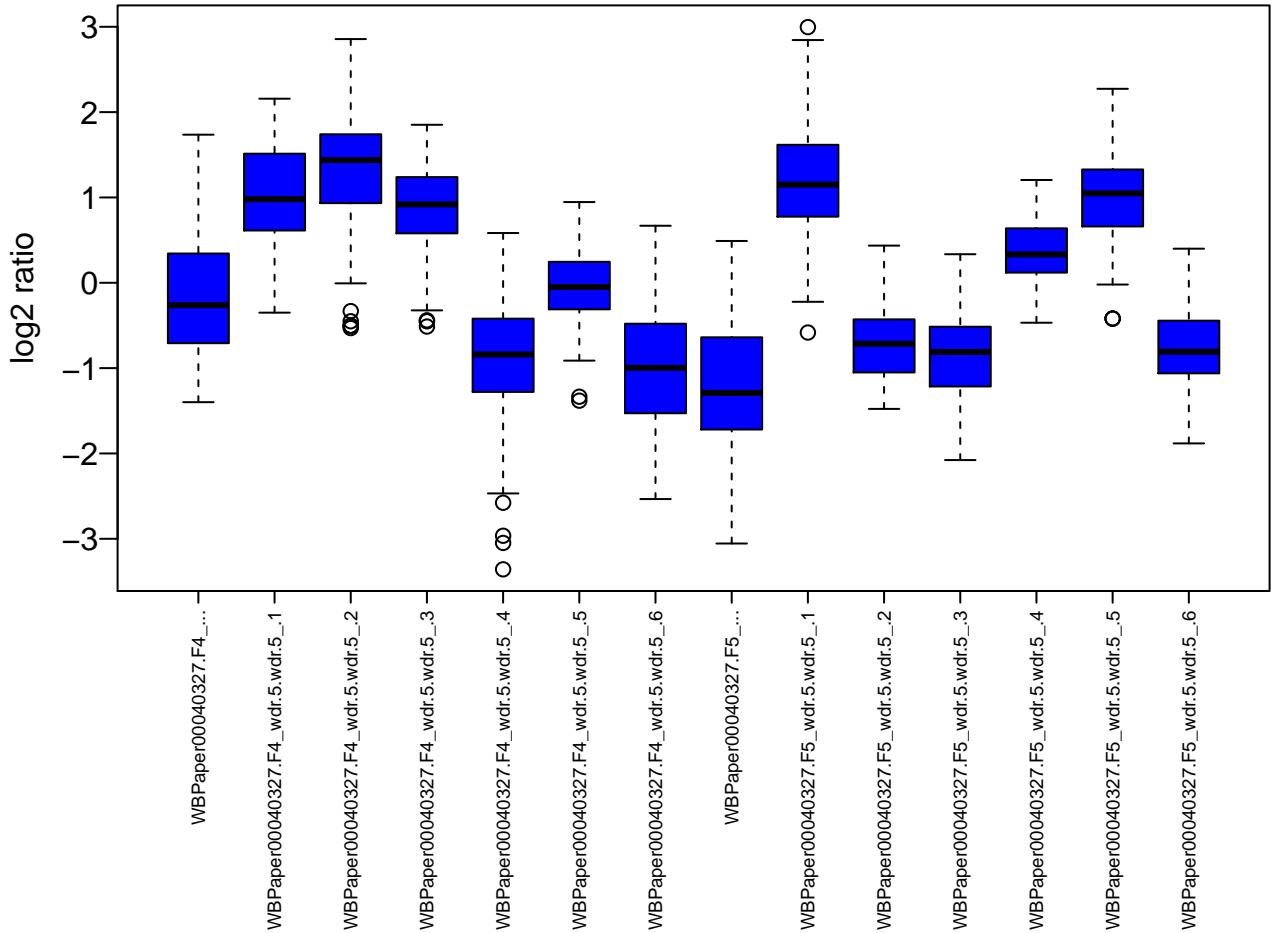
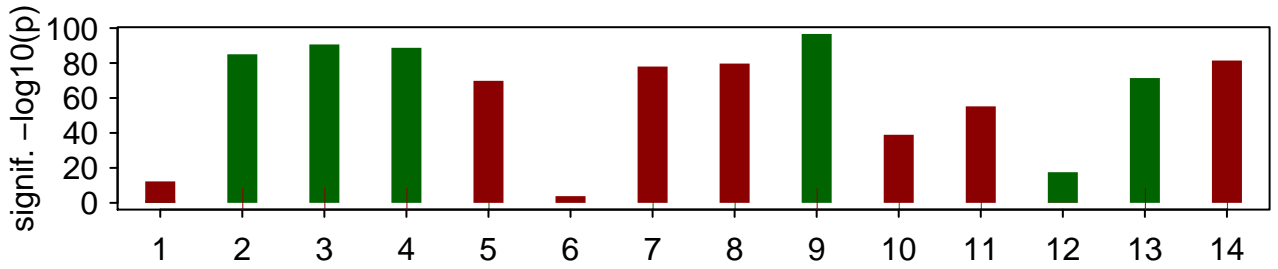
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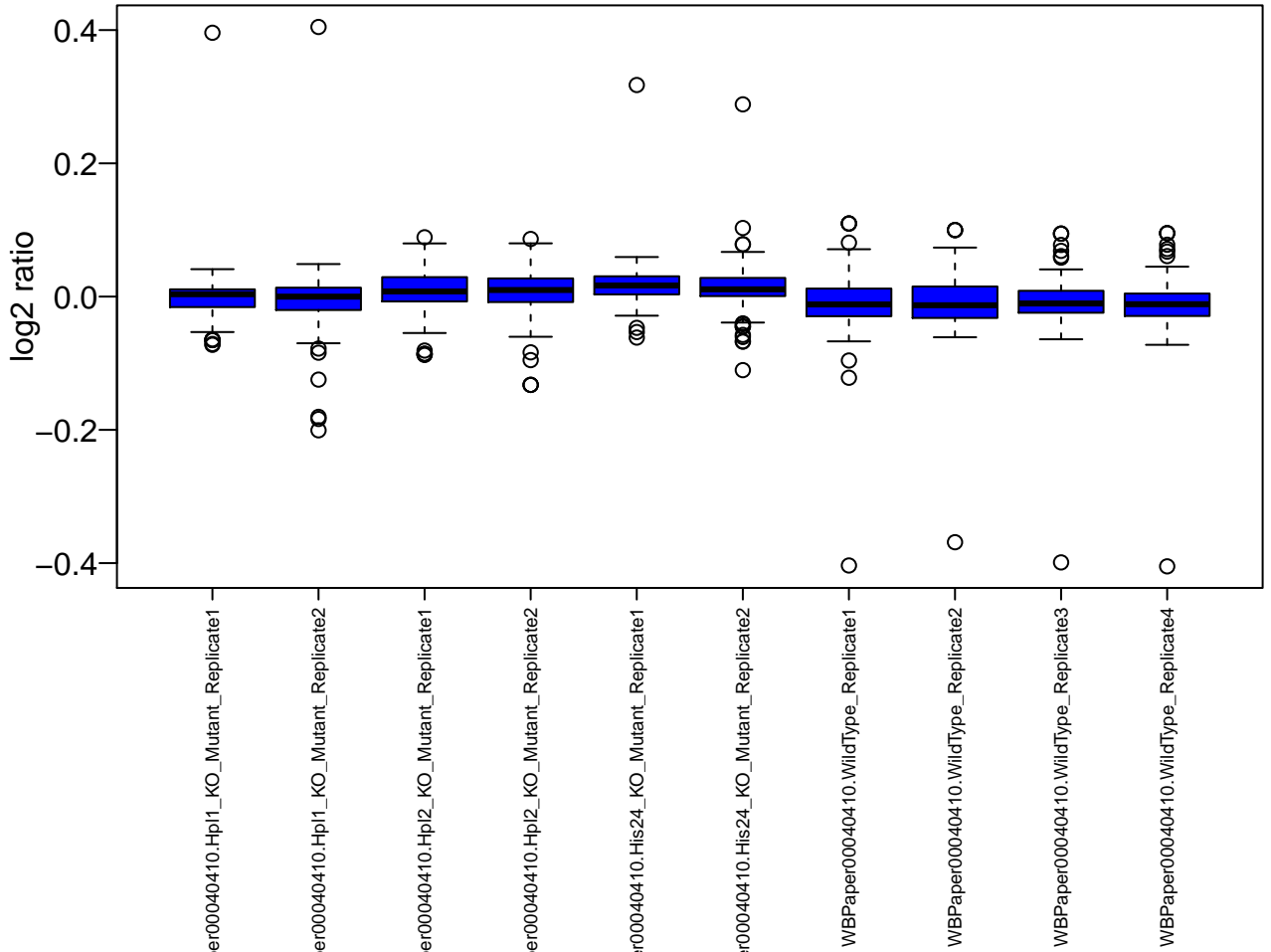
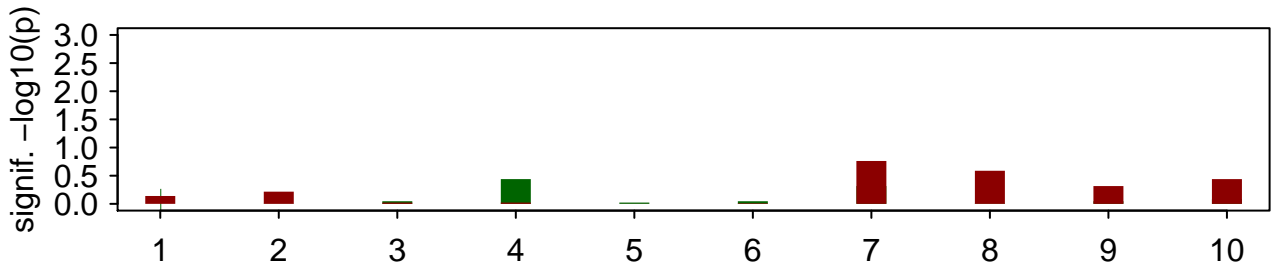
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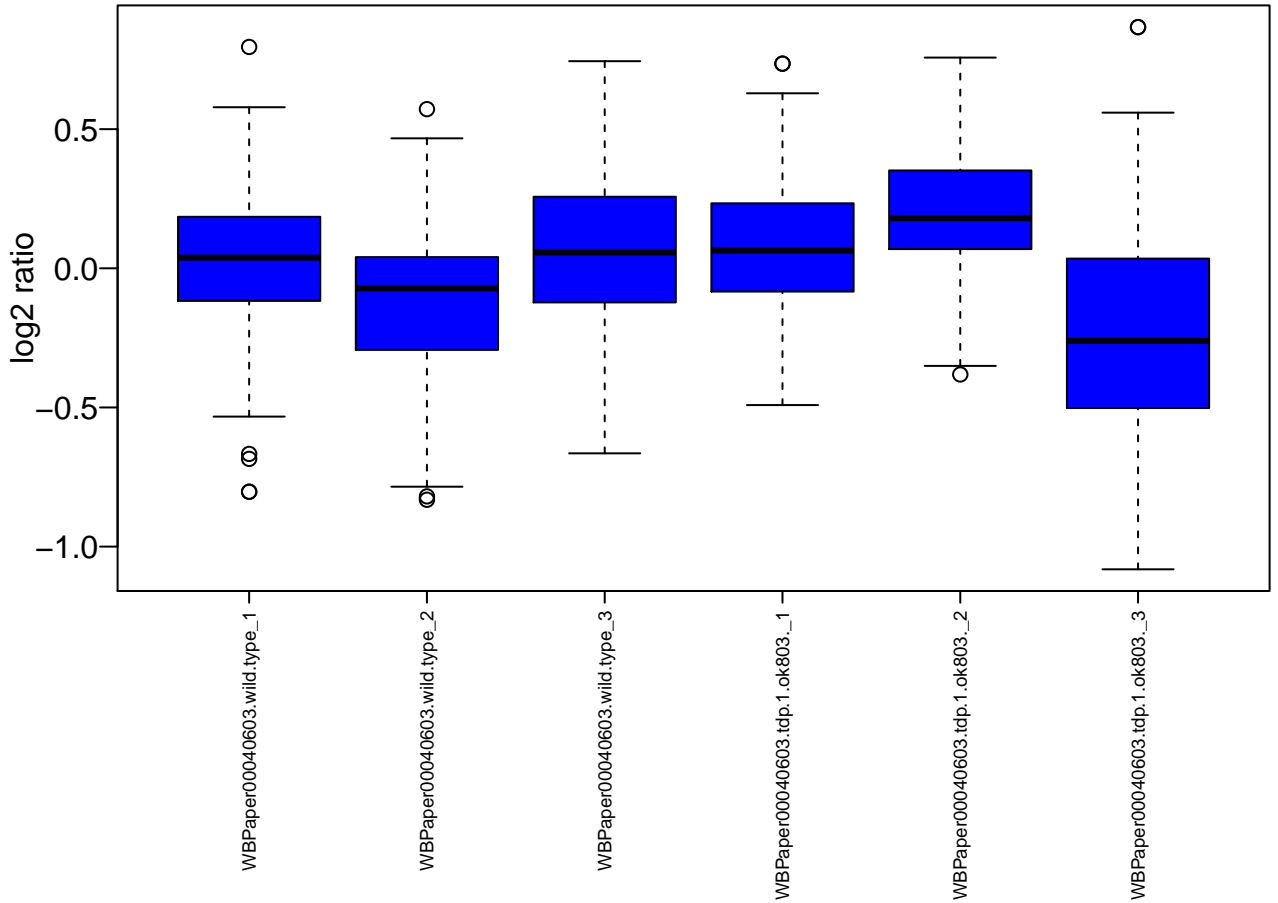
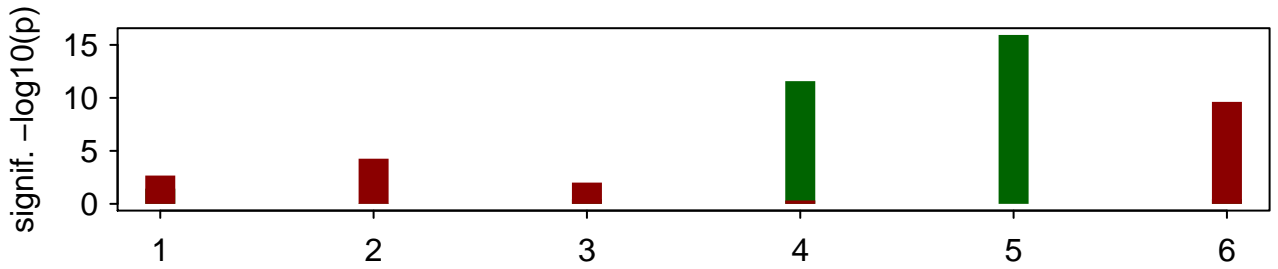
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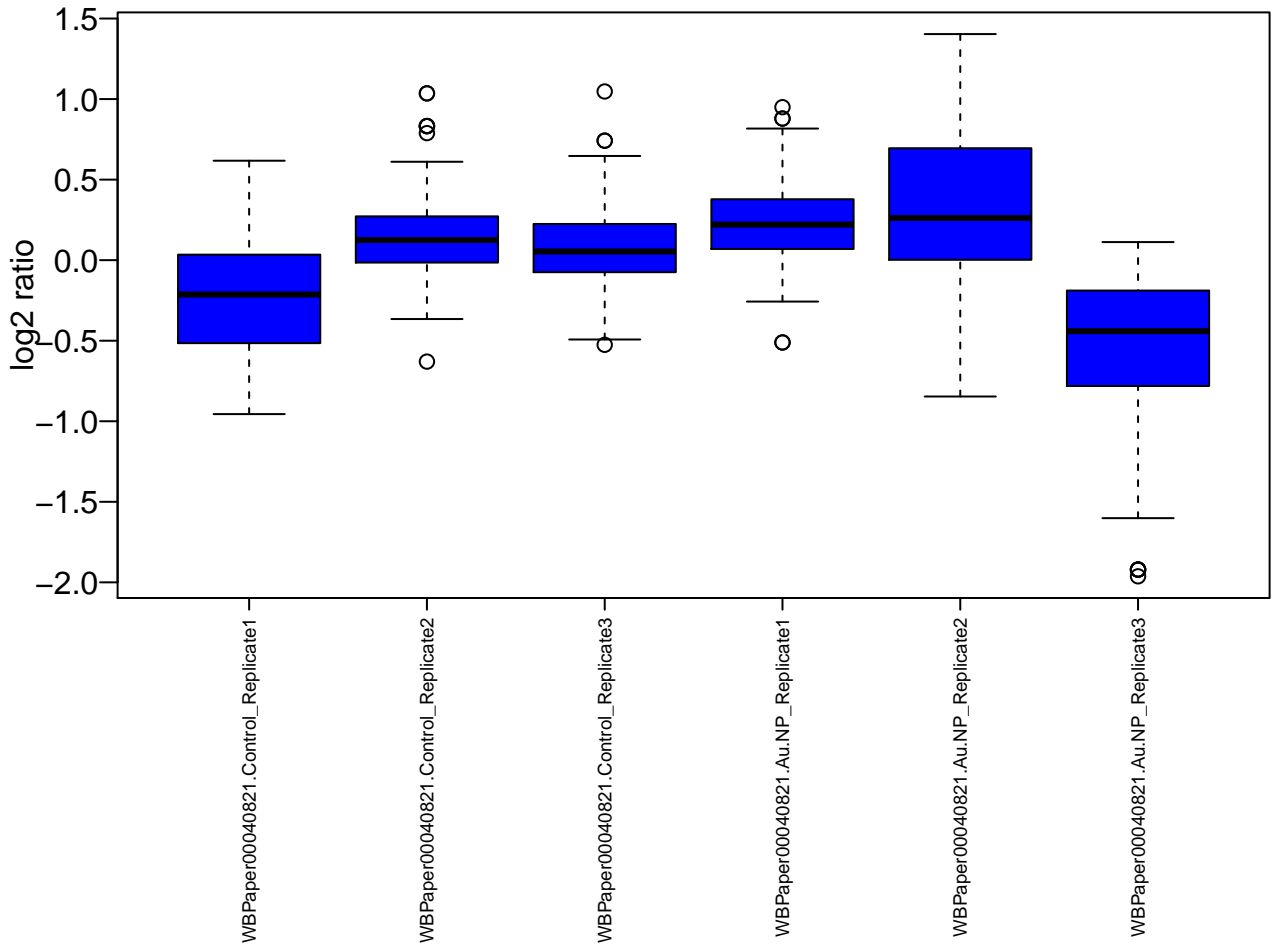
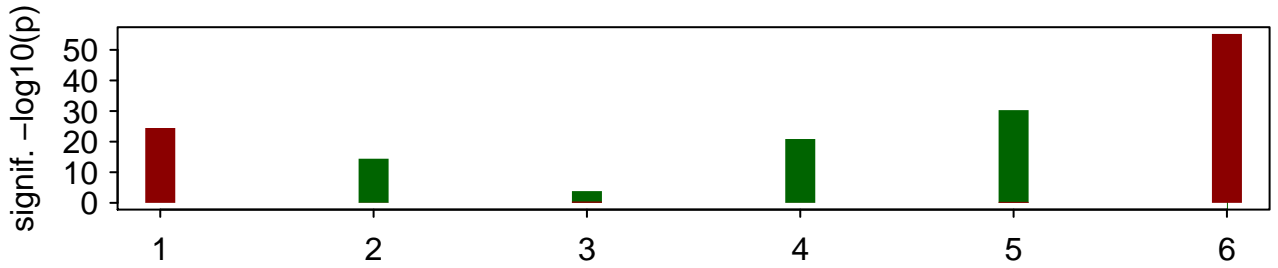
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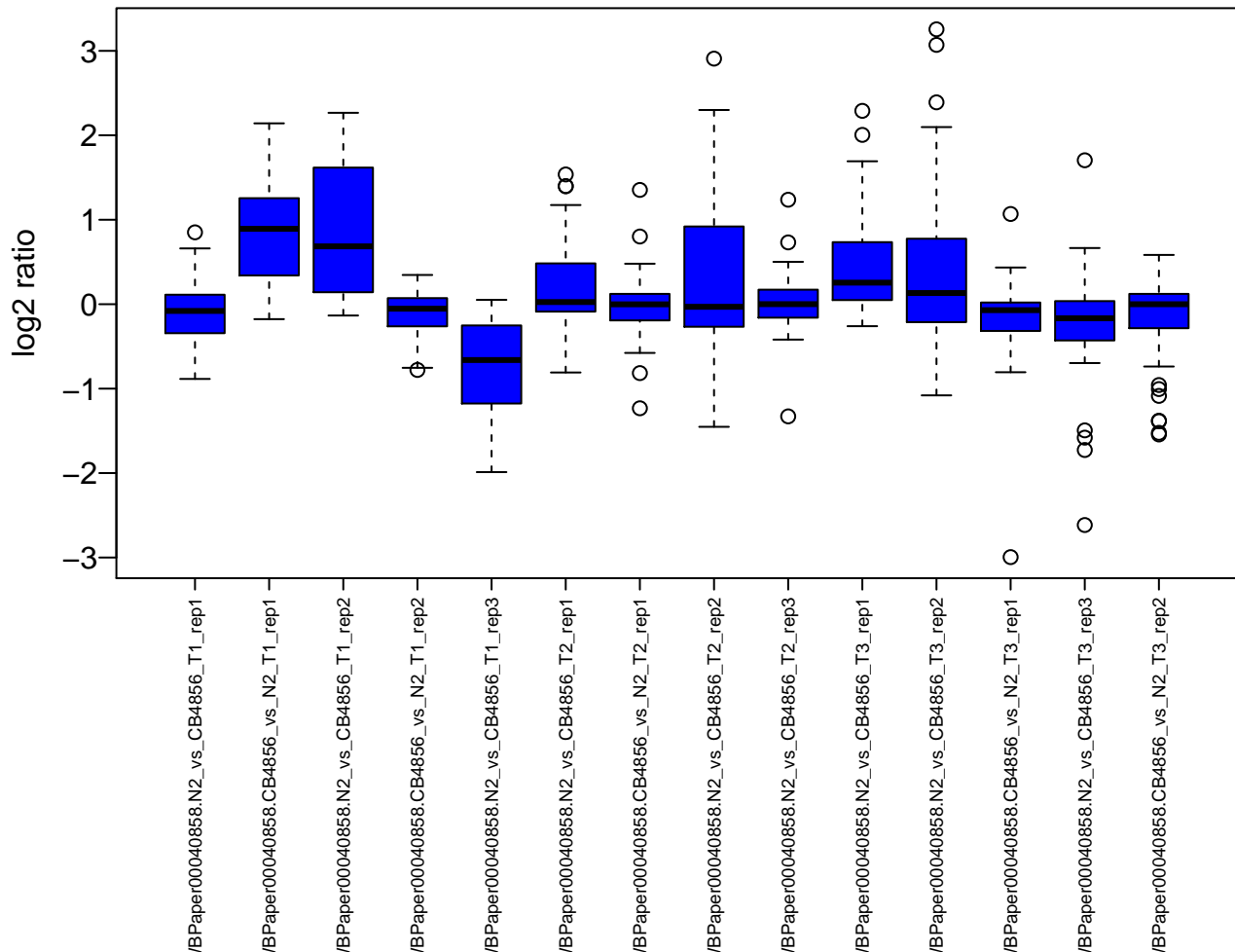
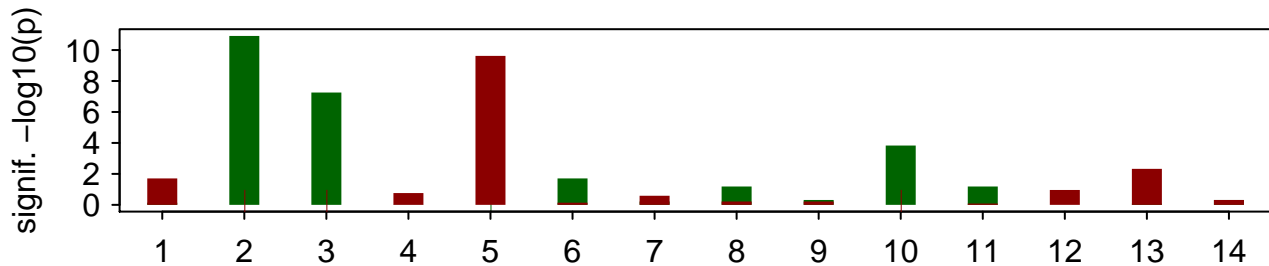
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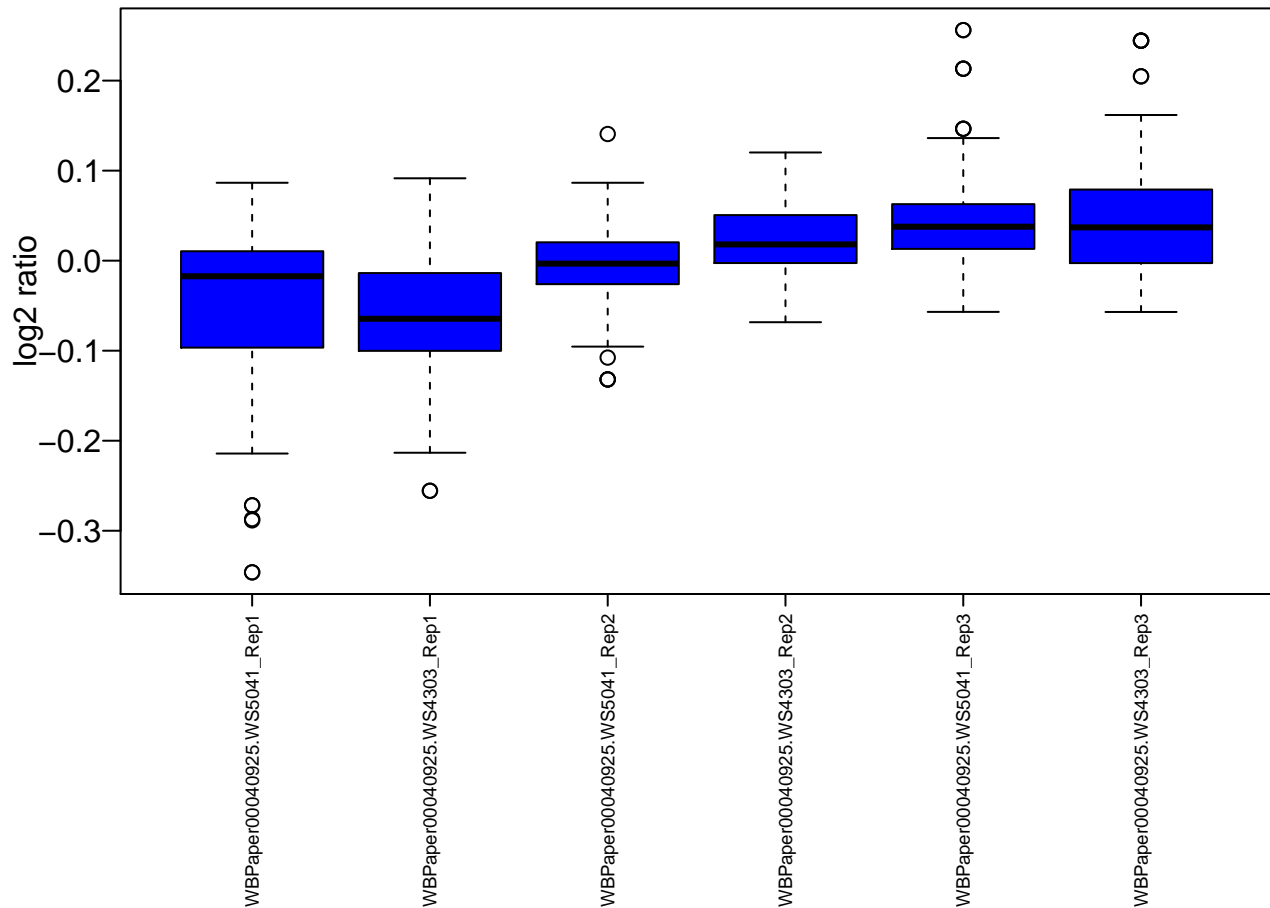
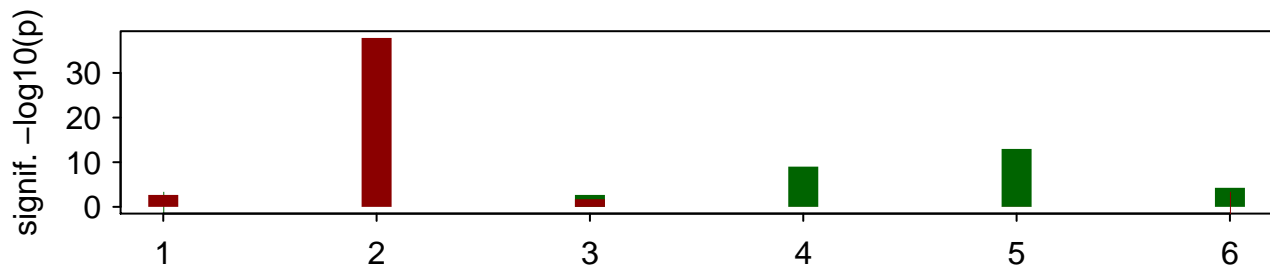
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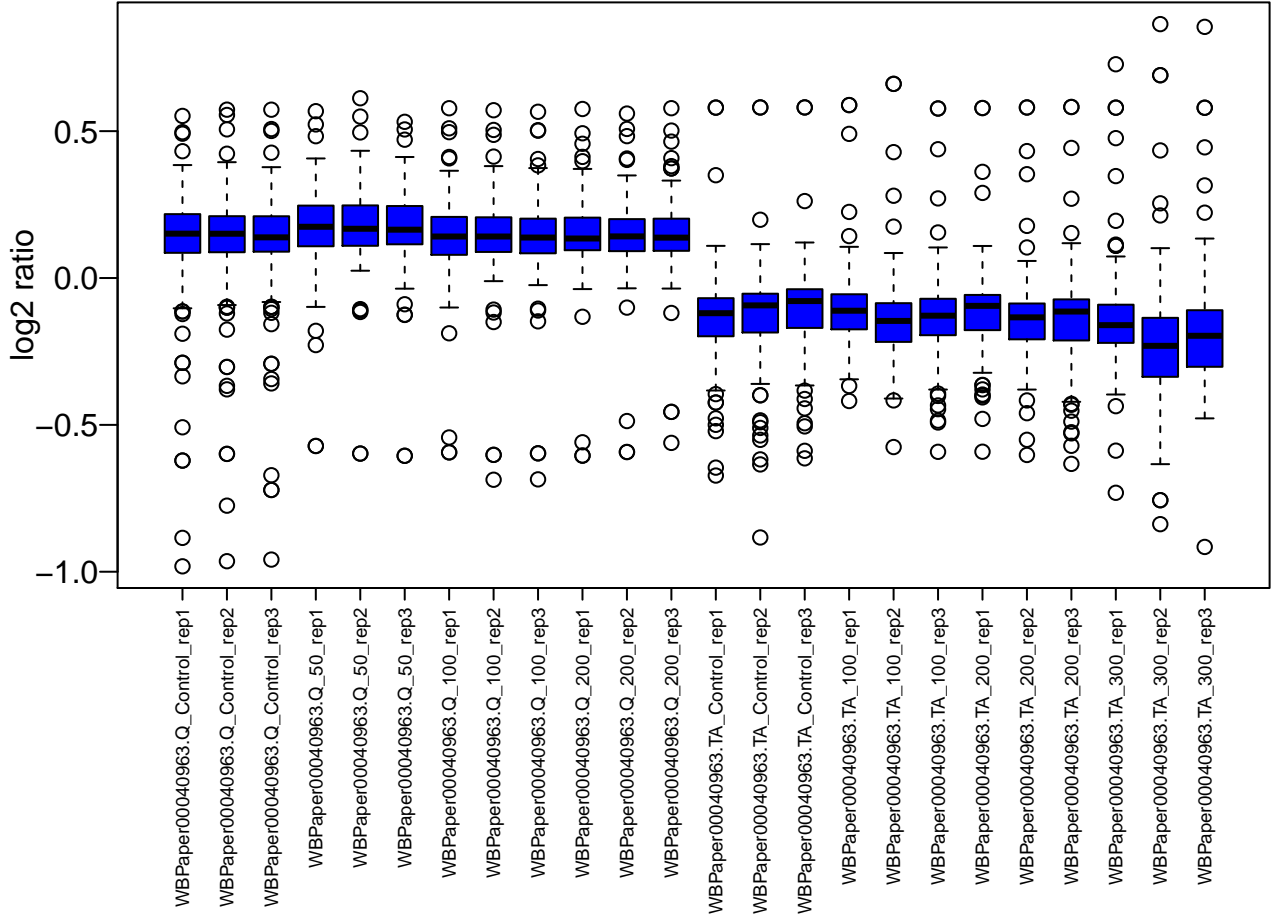
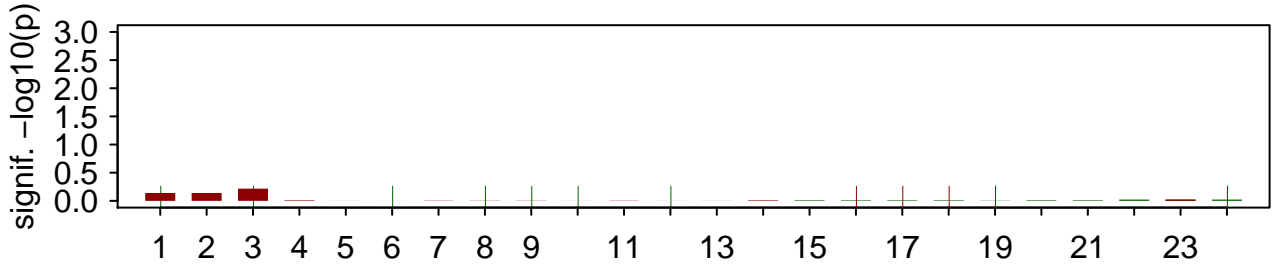
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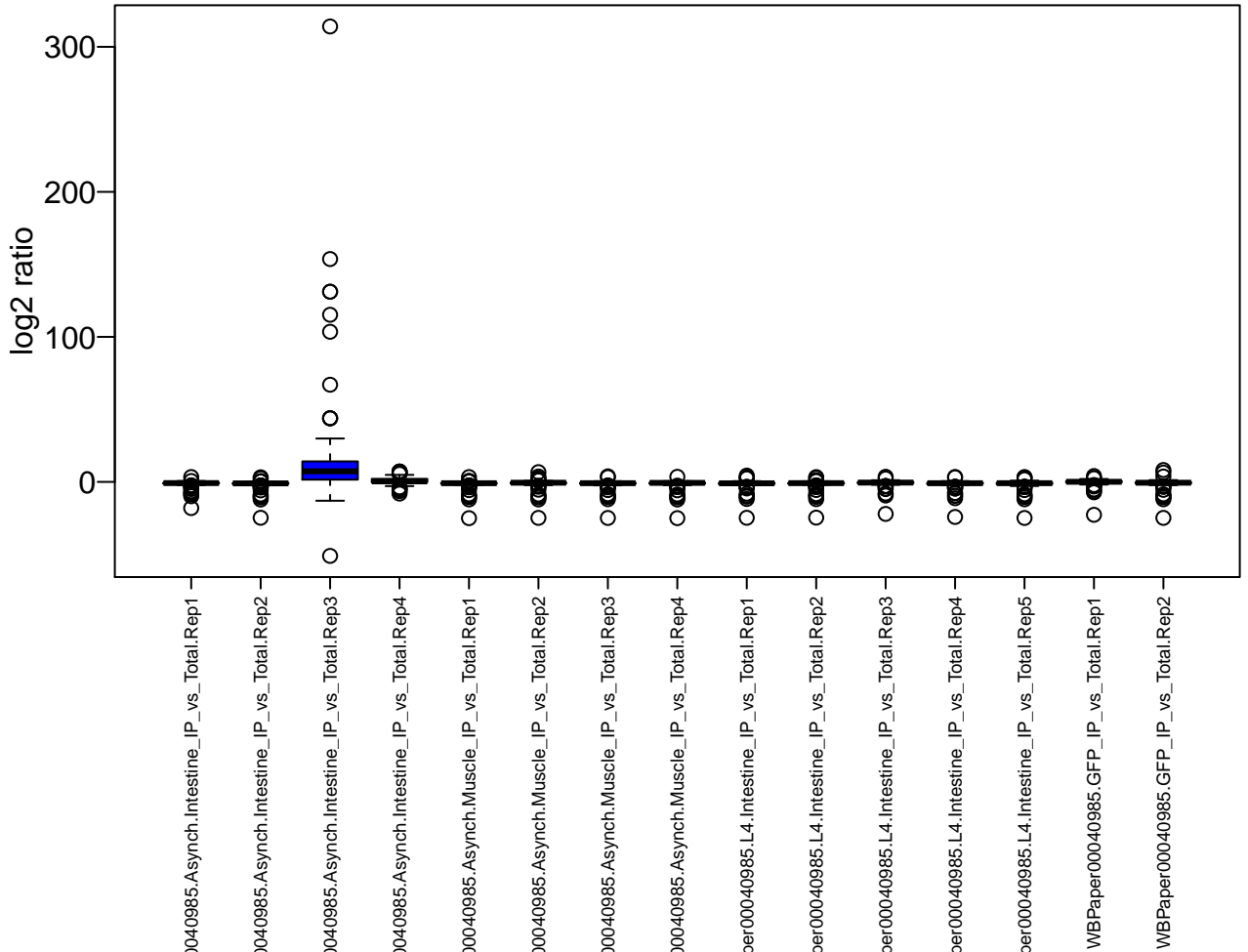
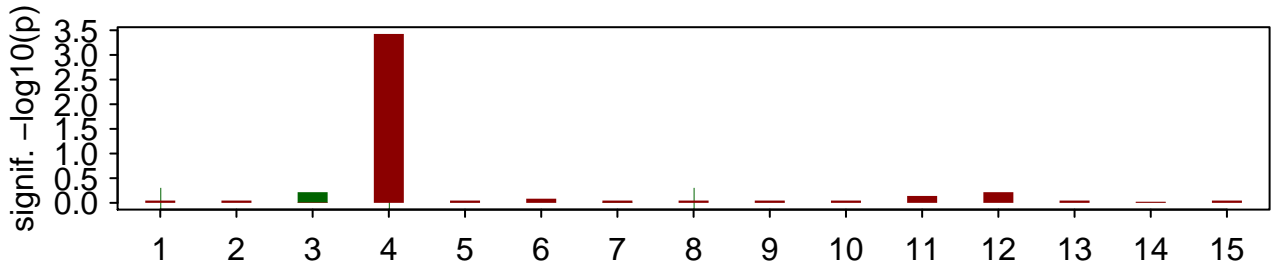
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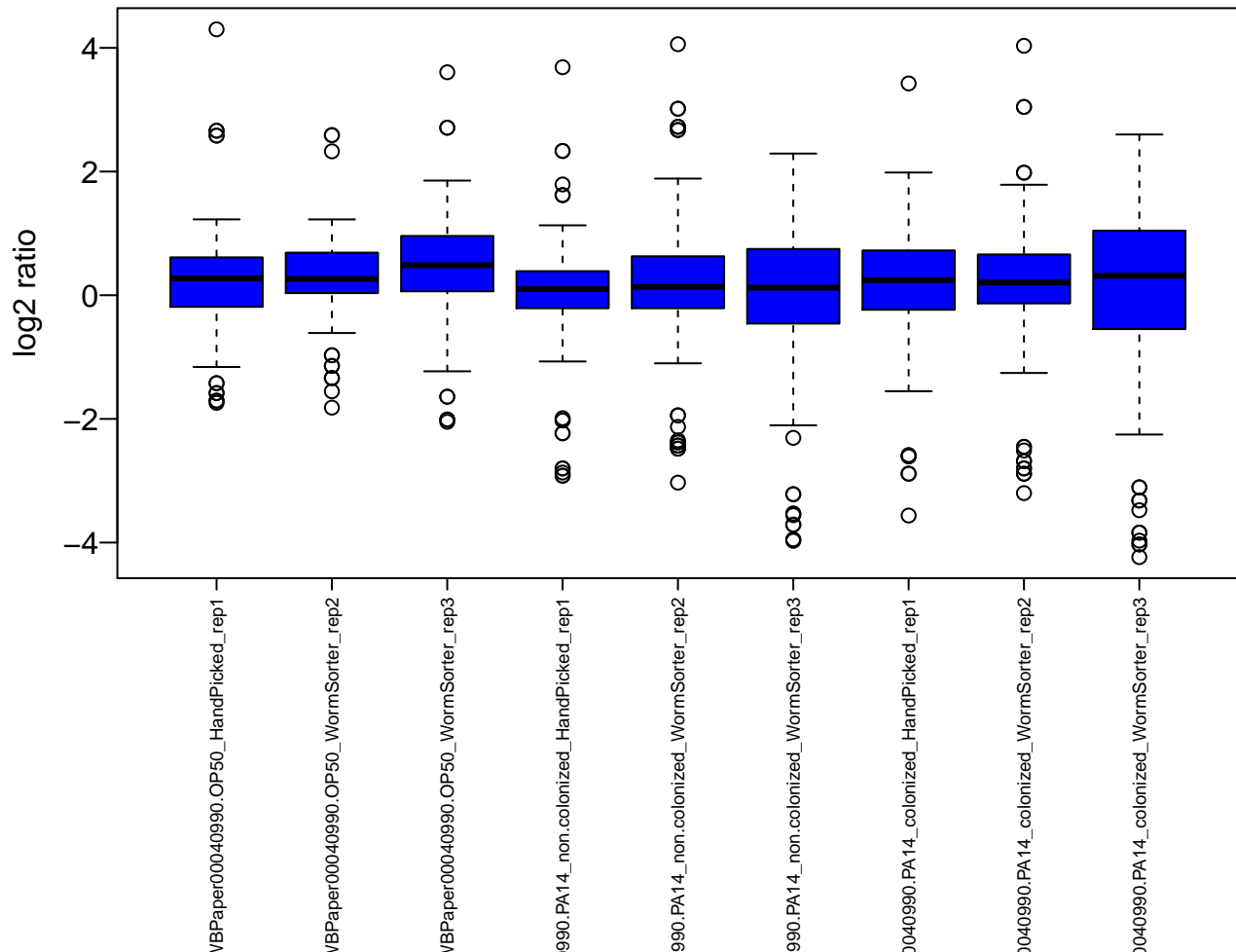
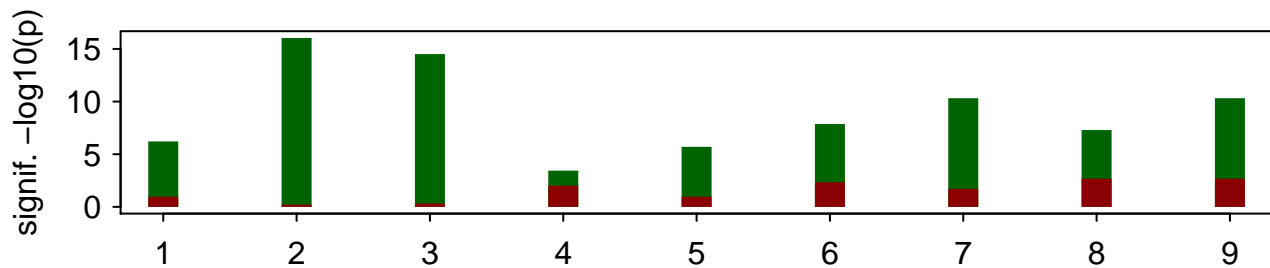
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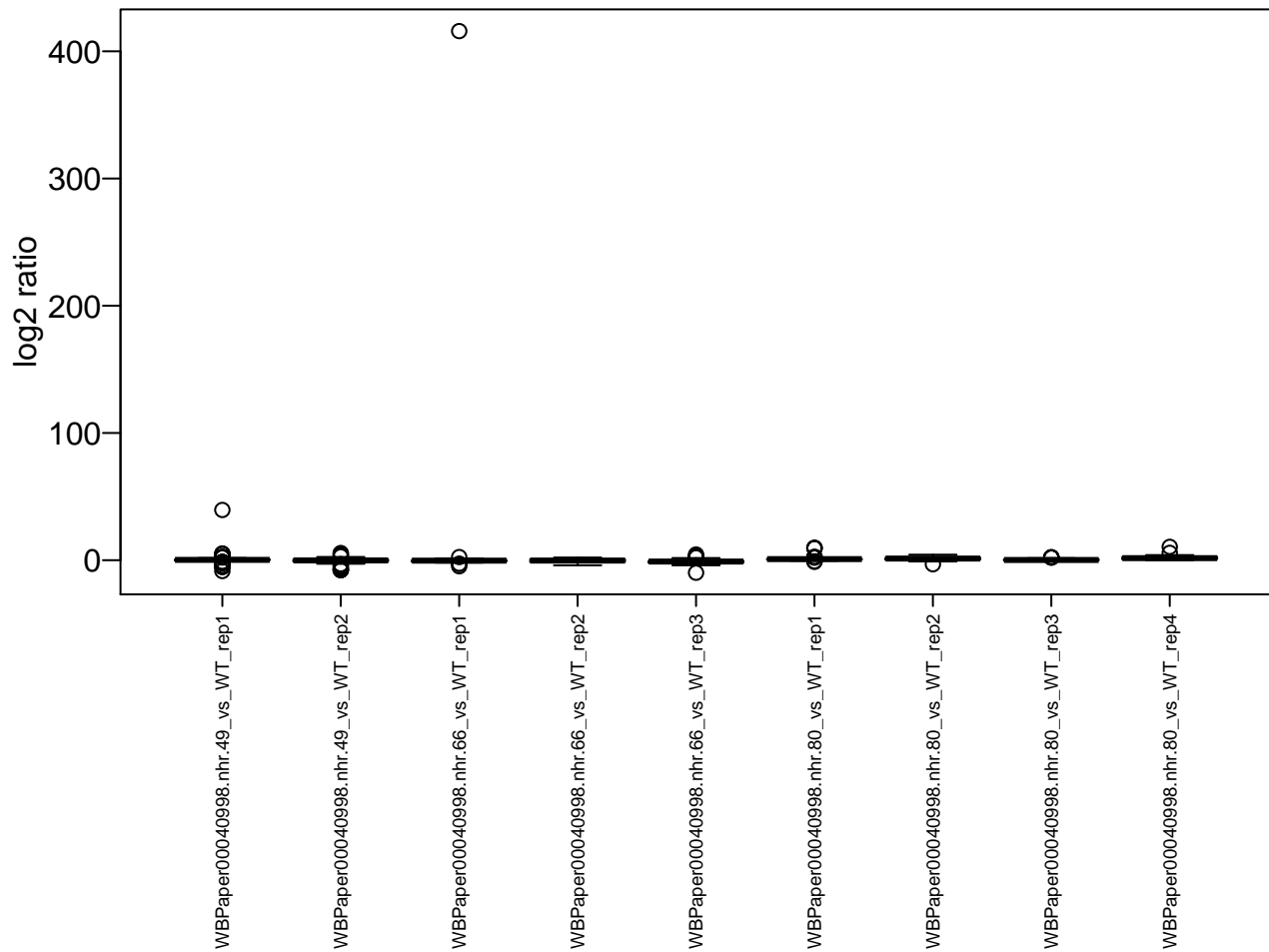
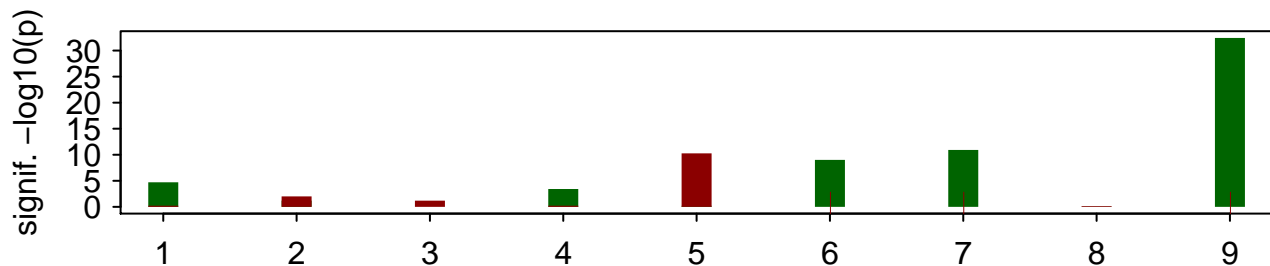
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