

Supplementary Data File 1

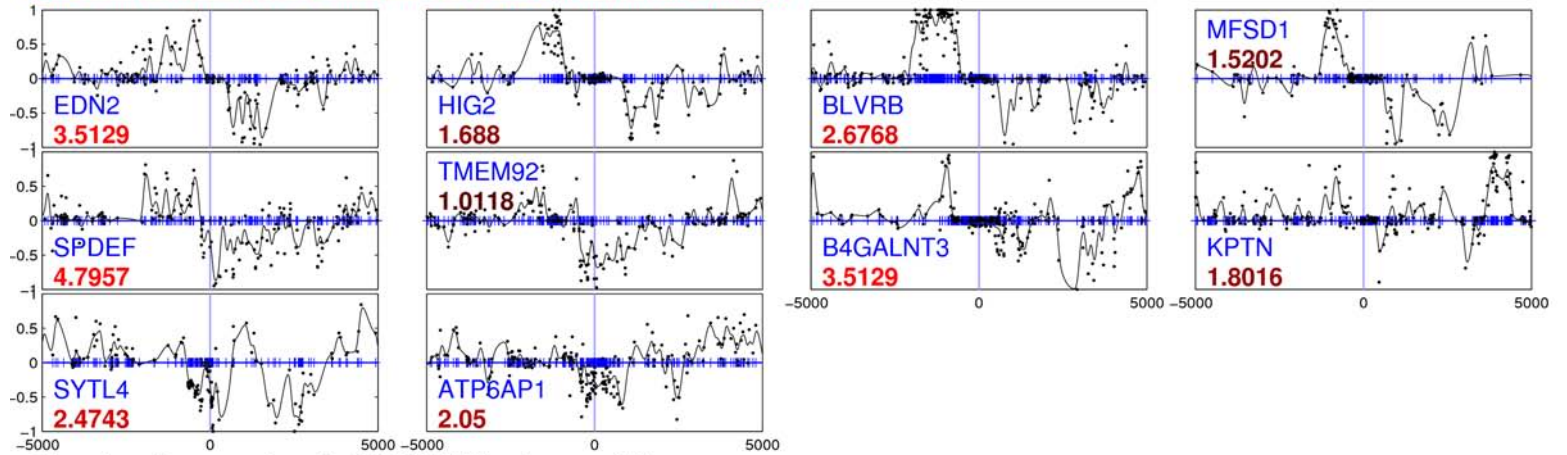
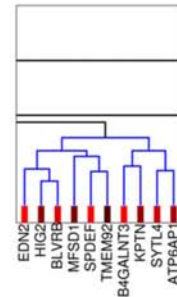
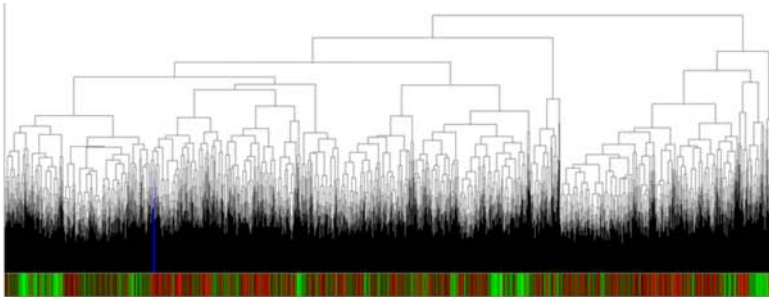
Complete clustering results for HMEC-HCC1954 WGBS data

The following pages contain all significant clusters identified in this dataset. The upper left panel on each page shows the full dendrogram. Methylation signatures are shown for each gene in the cluster marked in blue on the dendrogram. Expression values are plotted on a heat scale below the dendrogram (red is upregulated, green is downregulated). The upper right panel on each page is the section of the dendrogram with the identified cluster. The lower panel shows the individual methylation signatures for each gene in the cluster. For each signature, the y-axis represents the methylation difference score, ranging from -1 to 1. The x-axis denotes distance from the TSS, which is indicated by the vertical blue line at the center of each box. Blue tick marks indicate all CpG locations. Black dots represent all experimentally measured methylation difference scores. The black curve is the final signature used for clustering. Values in green and red denote the \log_2 fold expression change: red for upregulated and green for downregulated.

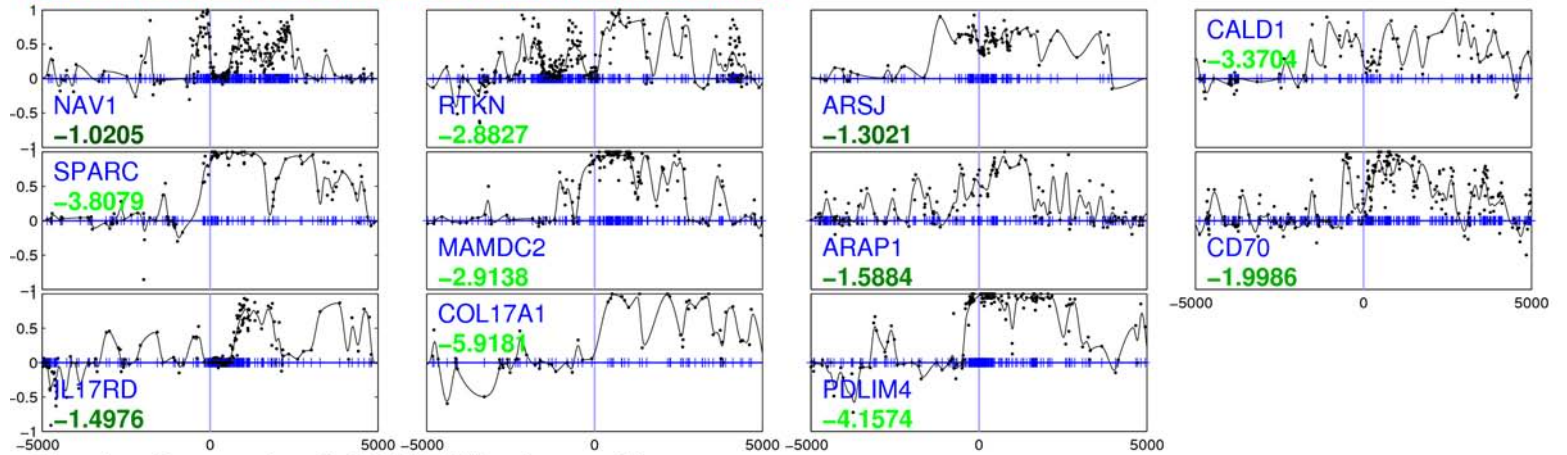
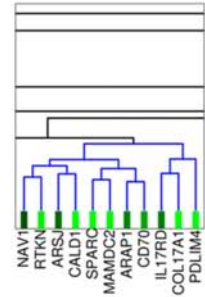
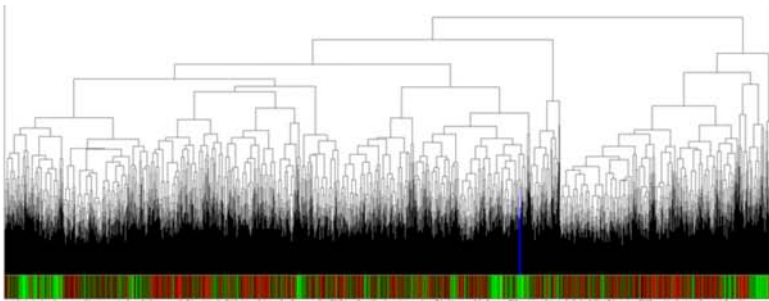
Example Pattern Clusters

See Figure 3 in main text for pattern descriptions

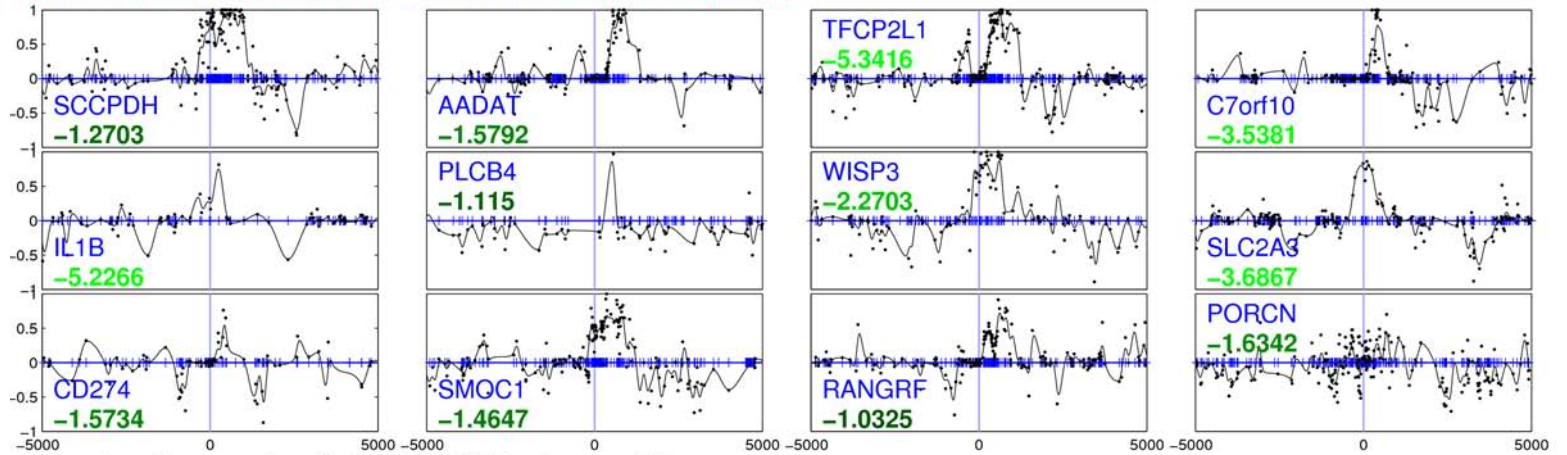
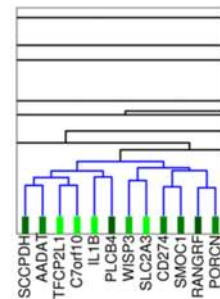
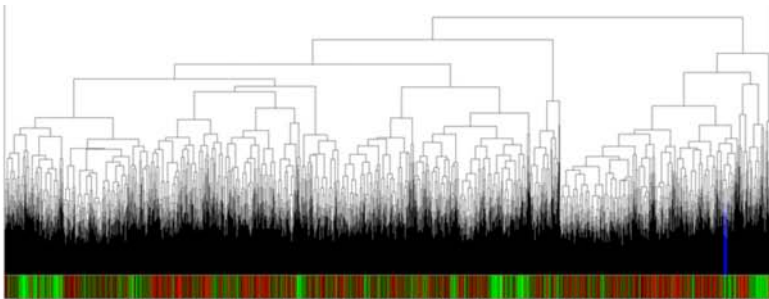
TSS1	Clusters 5,7
TSS2	Clusters 2,3,6,10,11
TSS2i	Cluster 14
PROX1i	Clusters 16, 25
PROX2	Clusters 9, 13, 15, 17
PROX3i	Cluster s 1, 4, 8, 12



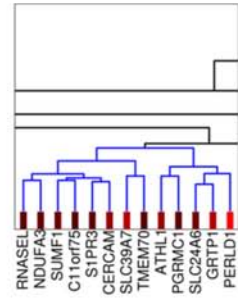
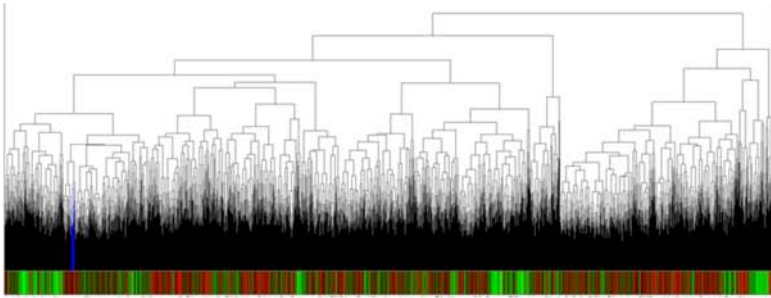
Cluster 1, pval = 0.0093613, size = 10



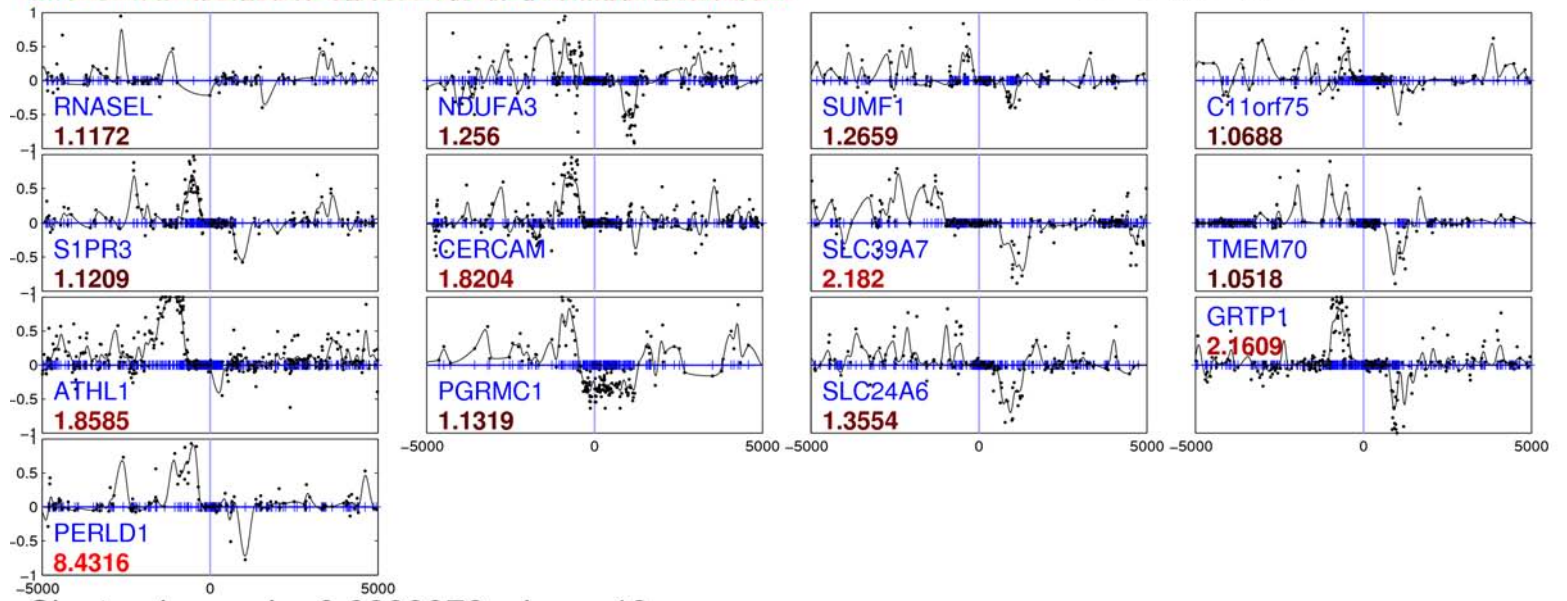
Cluster 2, pval = 0.0014724, size = 11



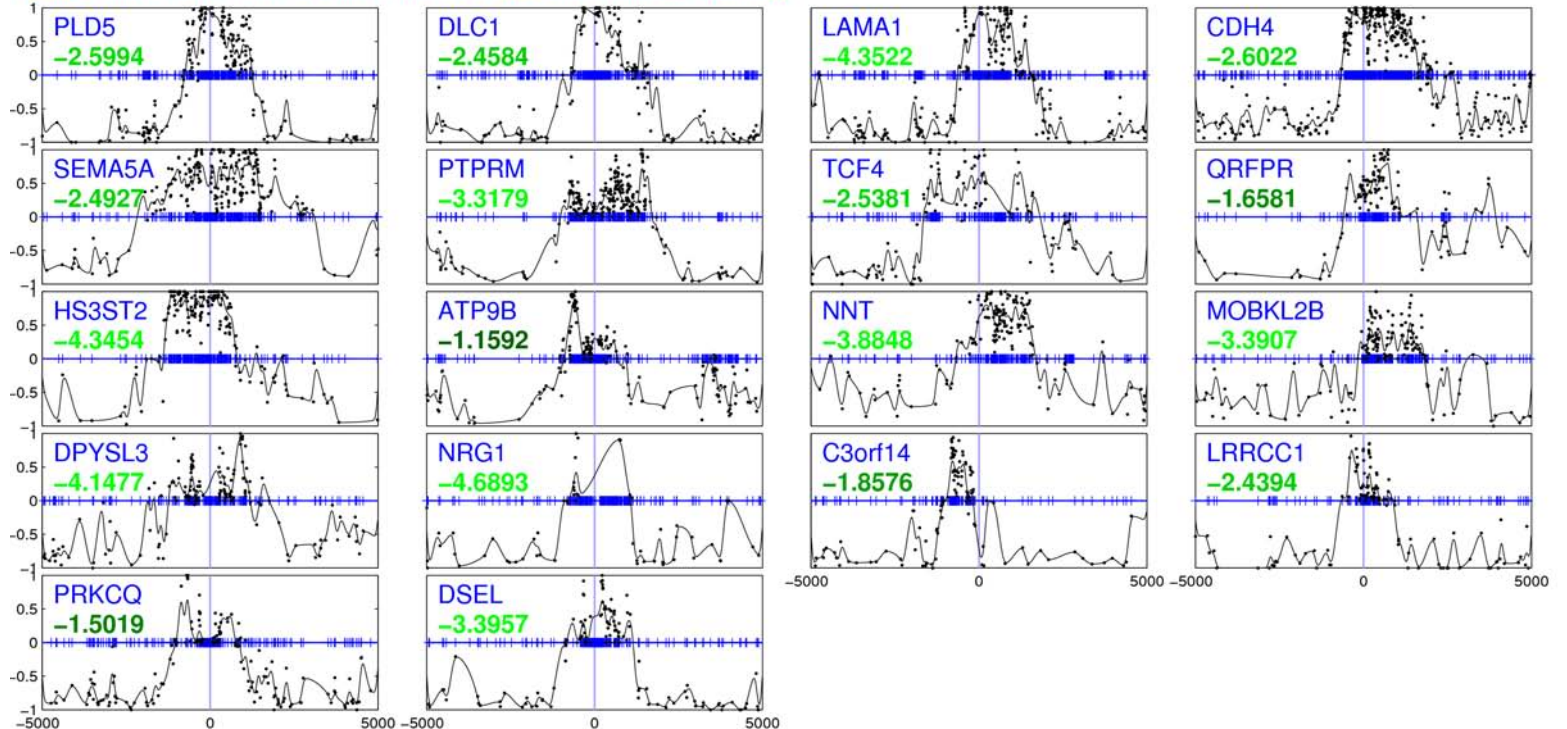
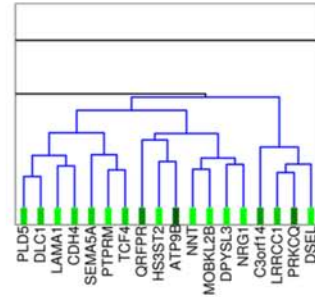
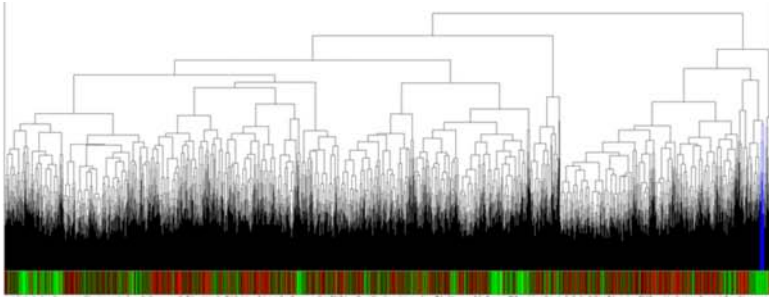
Cluster 3, pval = 0.00063357, size = 12



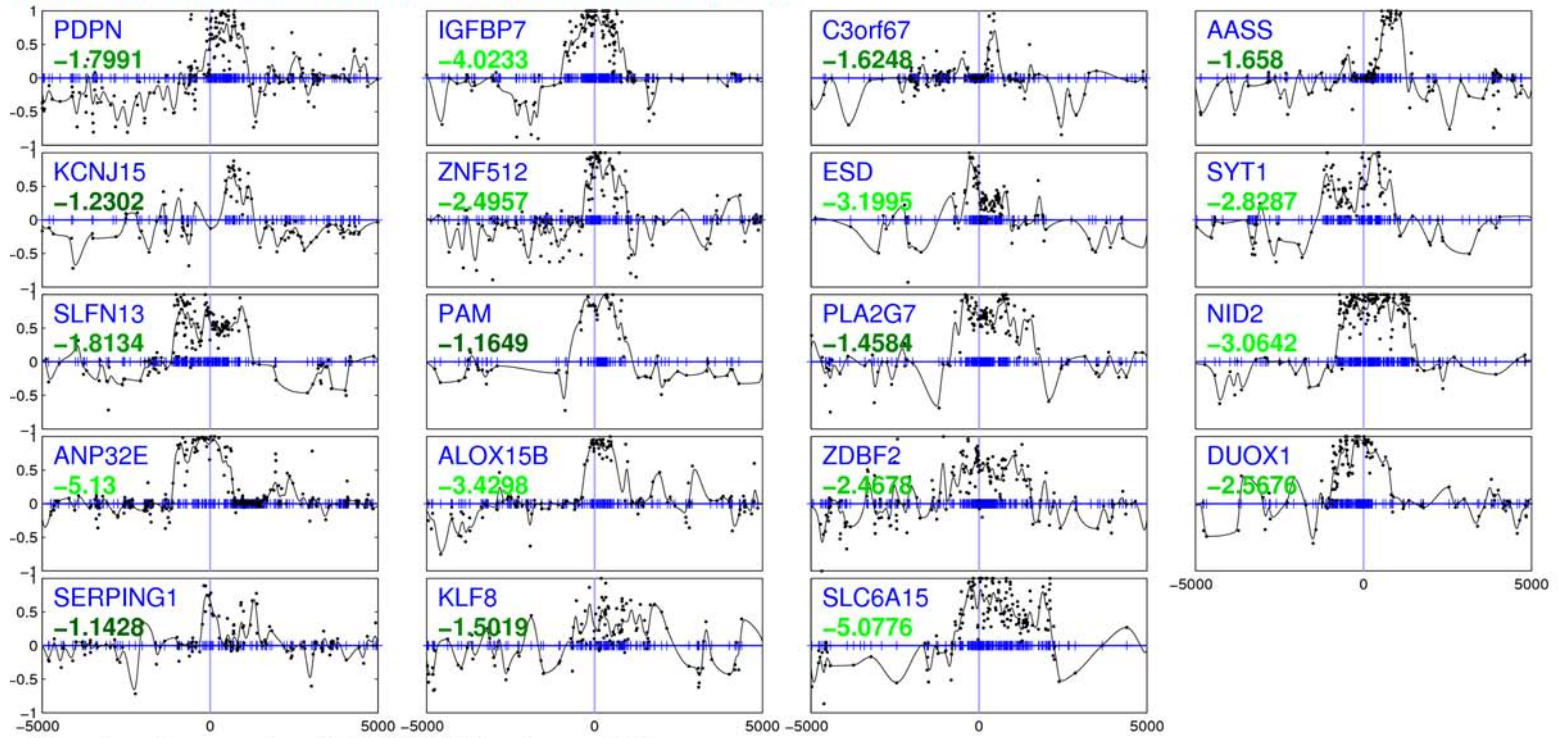
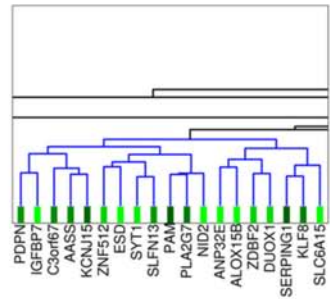
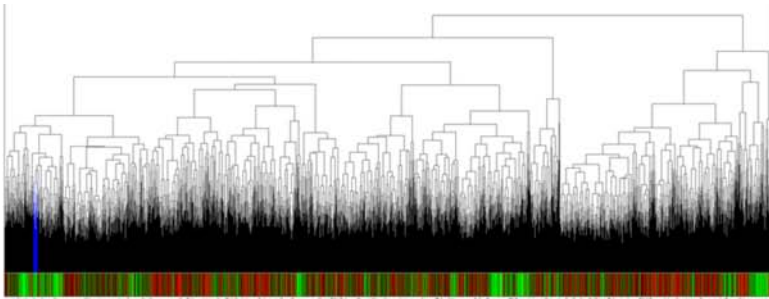
RNASEL
 NDUFA3
 SUMF1
 C11orf75
 S1PR3
 CERCAM
 SLC39A7
 TMEM70
 ATHL1
 PGRMC1
 SLC24A6
 GRTP1
 PERLD1



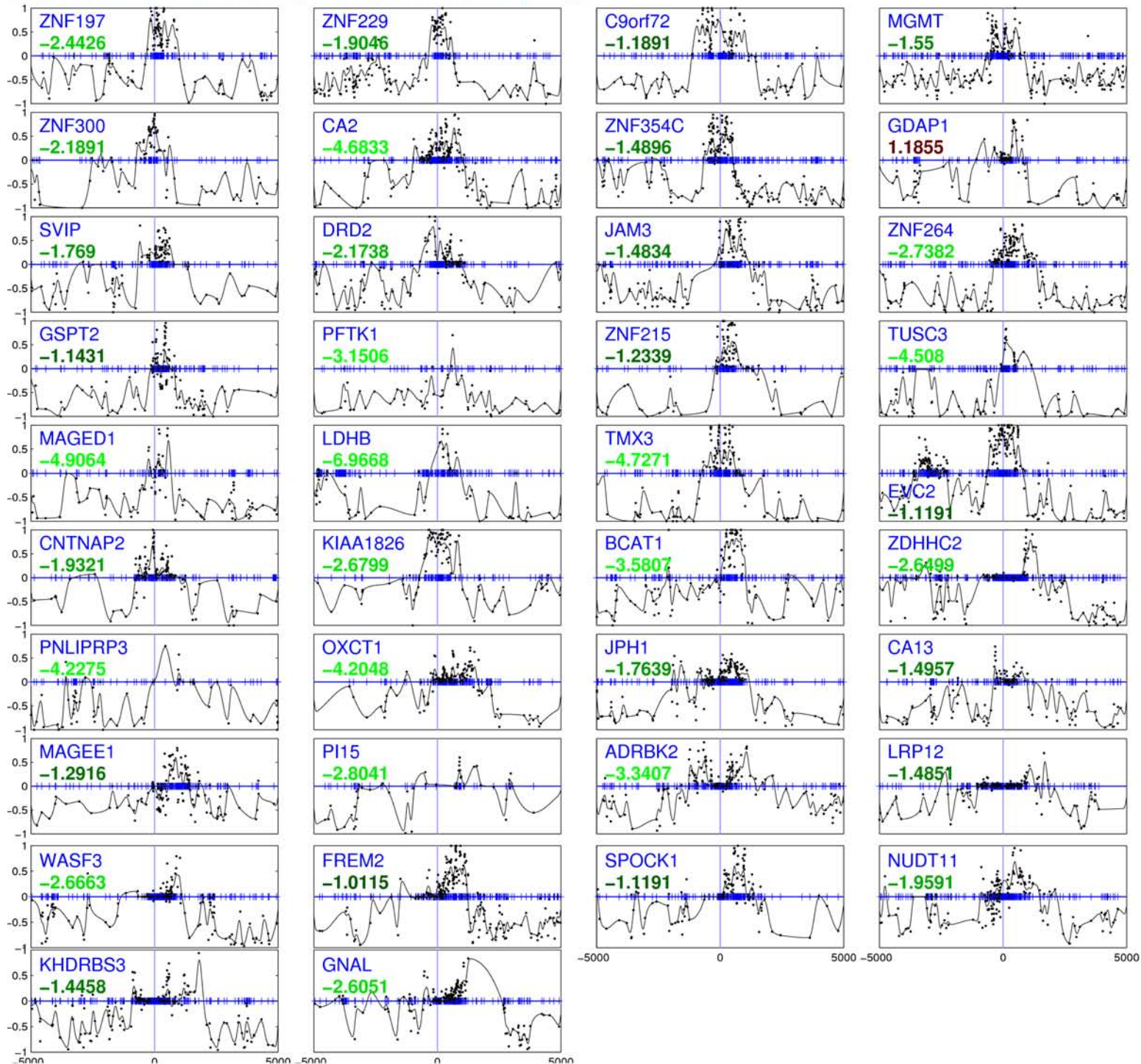
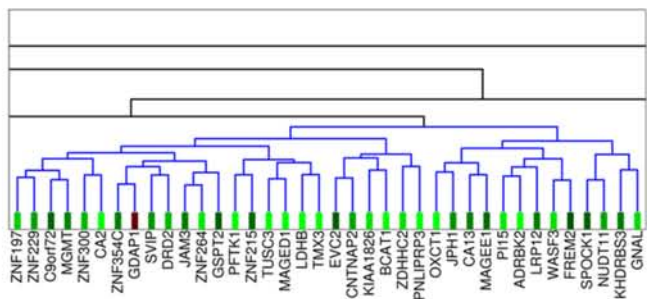
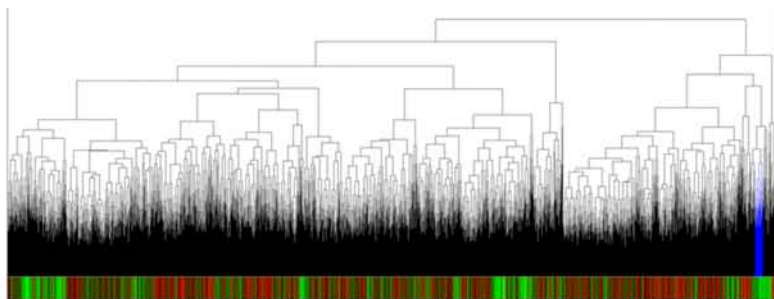
Cluster 4, pval = 0.0099378, size = 13



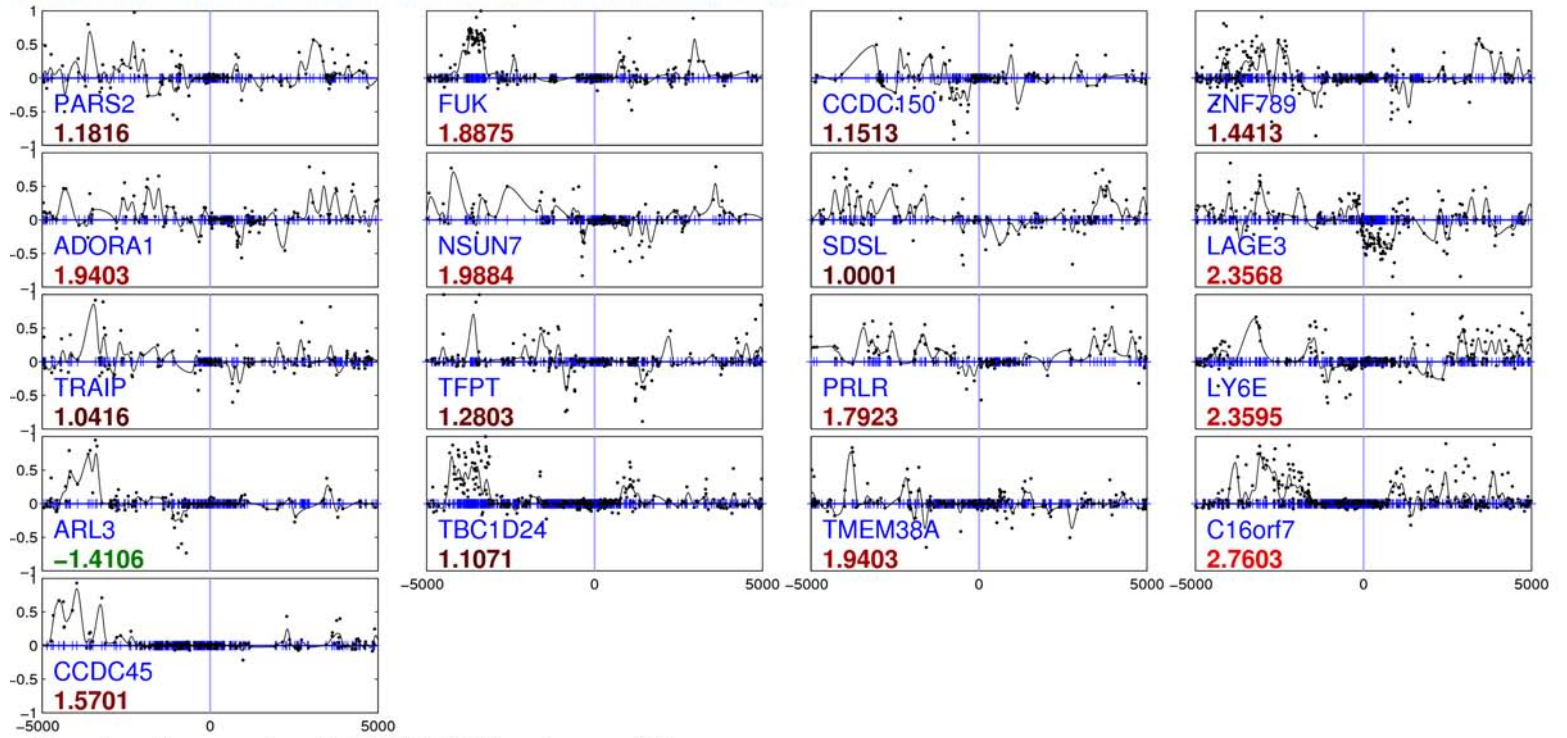
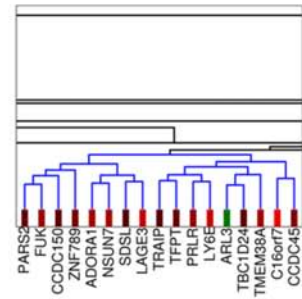
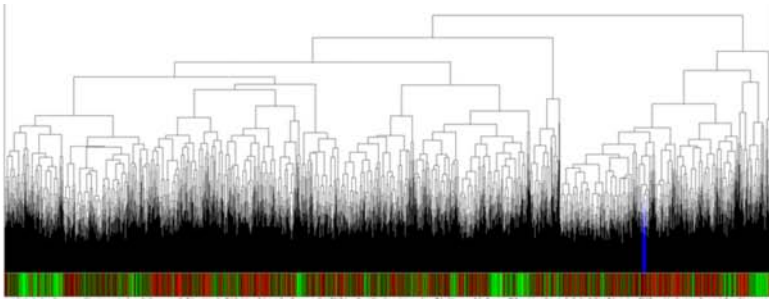
Cluster 5, pval = 0.00040535, size = 18



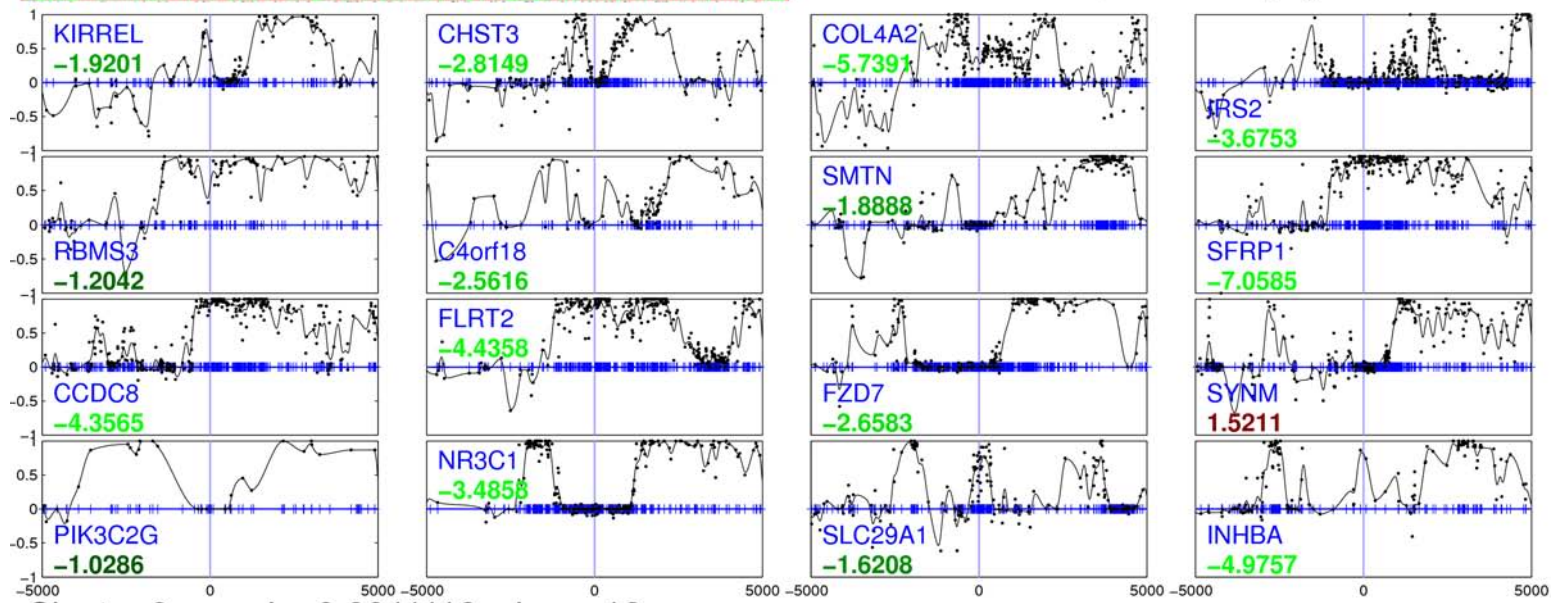
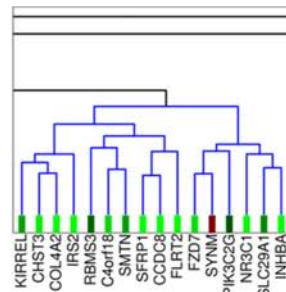
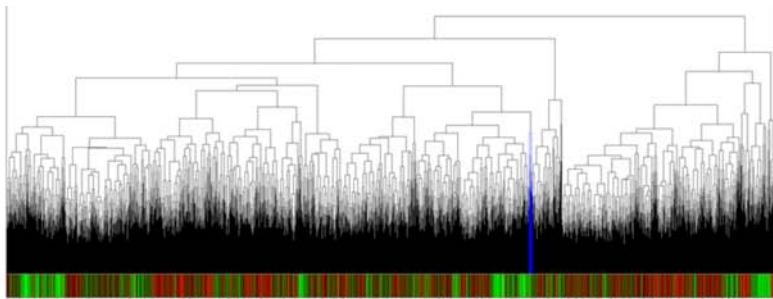
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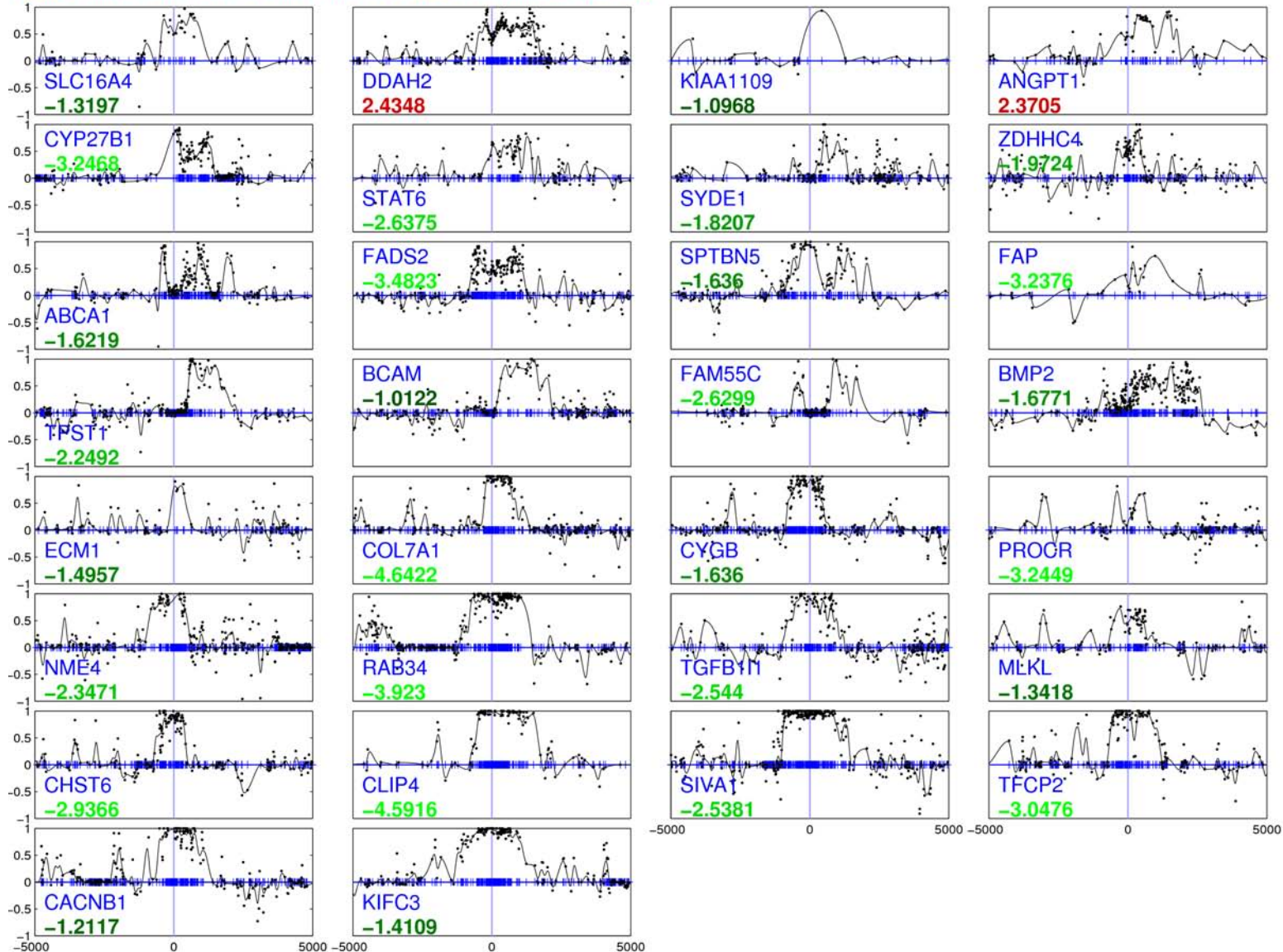
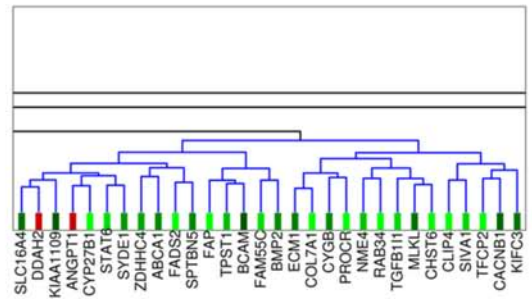
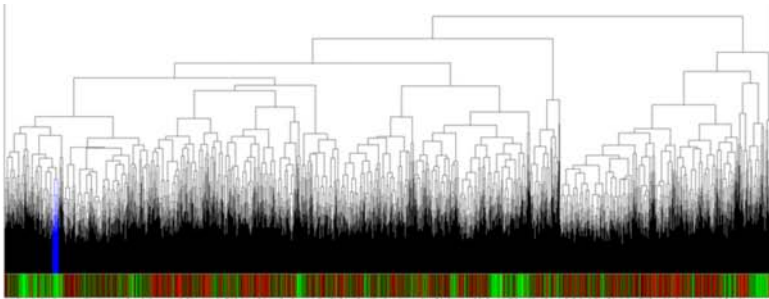
Cluster 7, pval = 9.8829e-06, size = 38



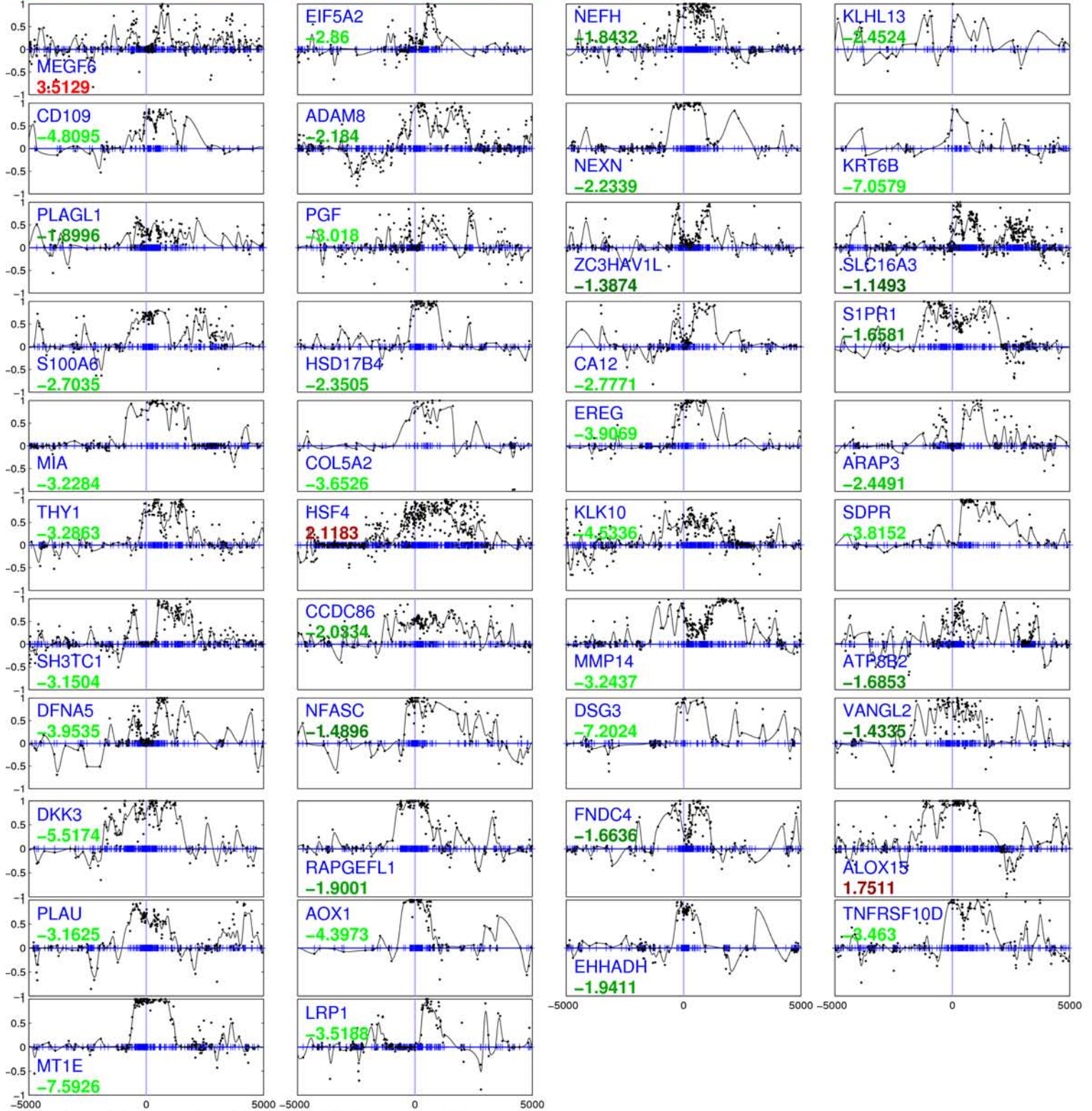
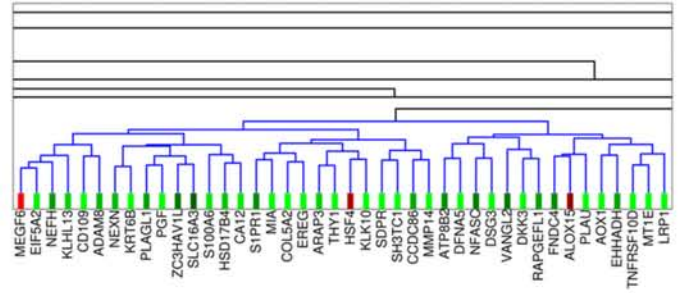
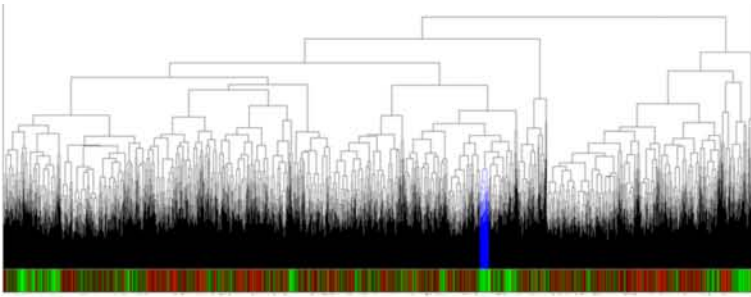
Cluster 8, pval = 0.00098184, size = 17



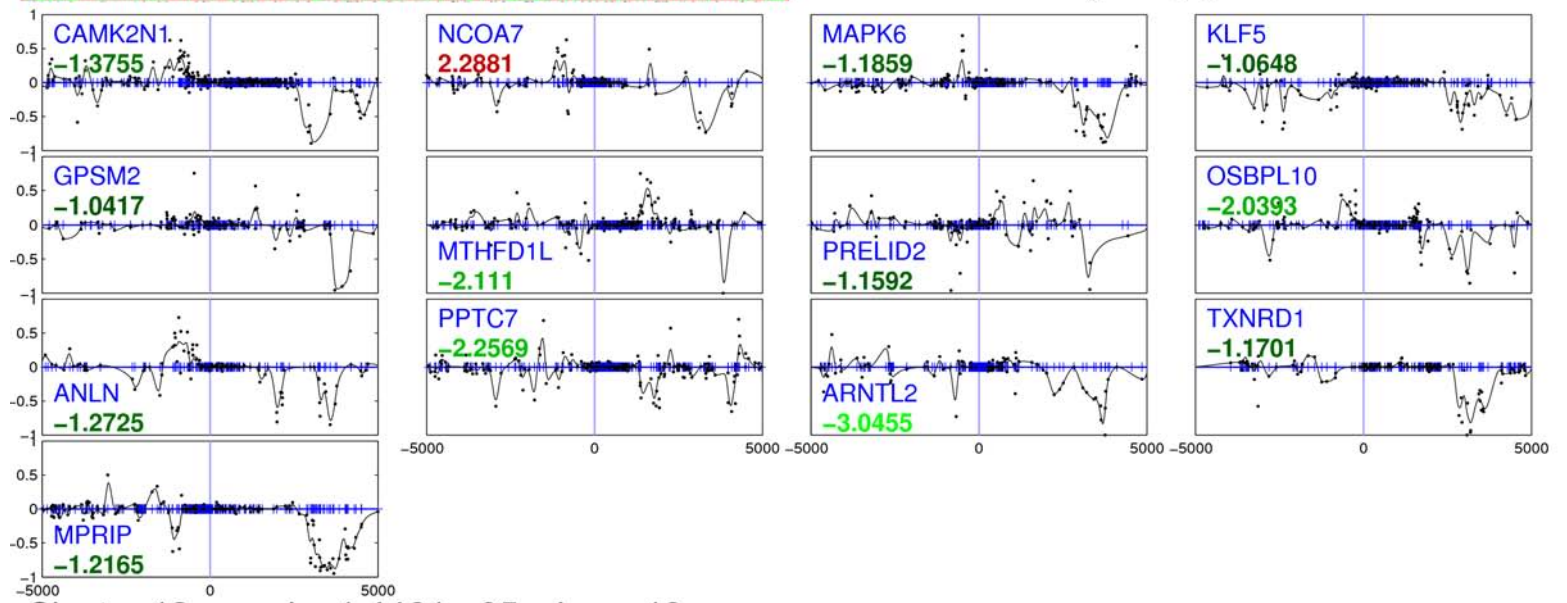
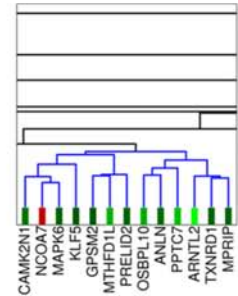
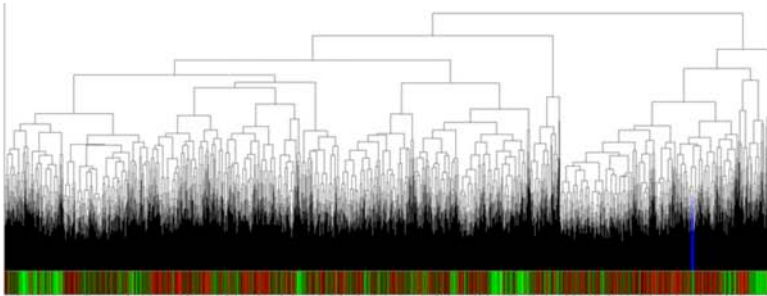
Cluster 9, pval = 0.0011116, size = 16



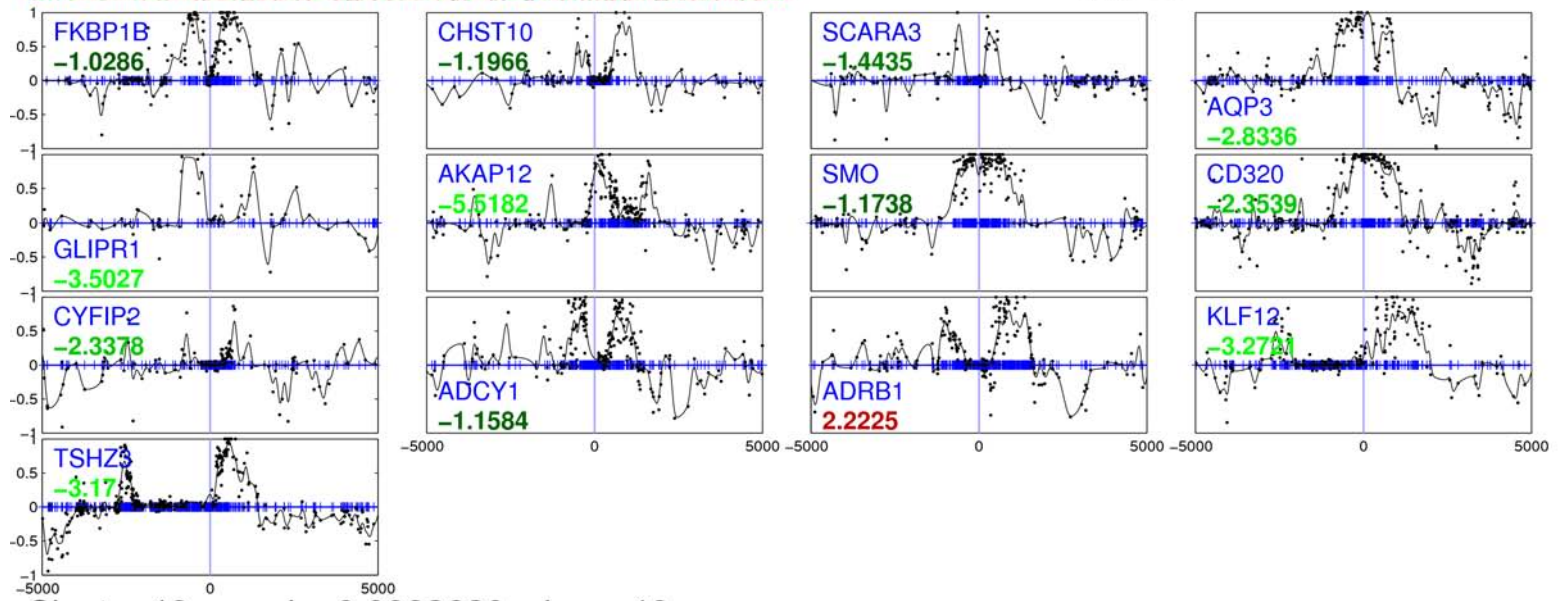
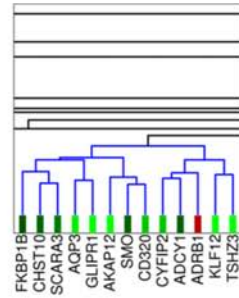
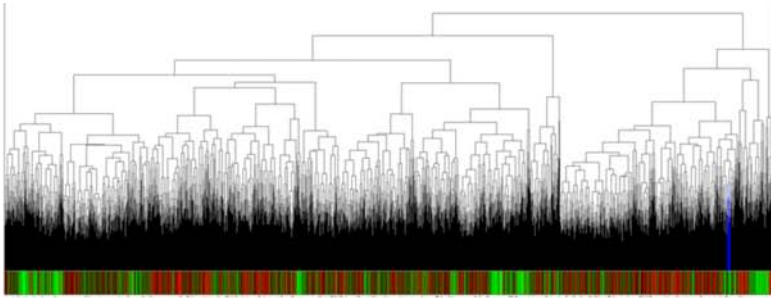
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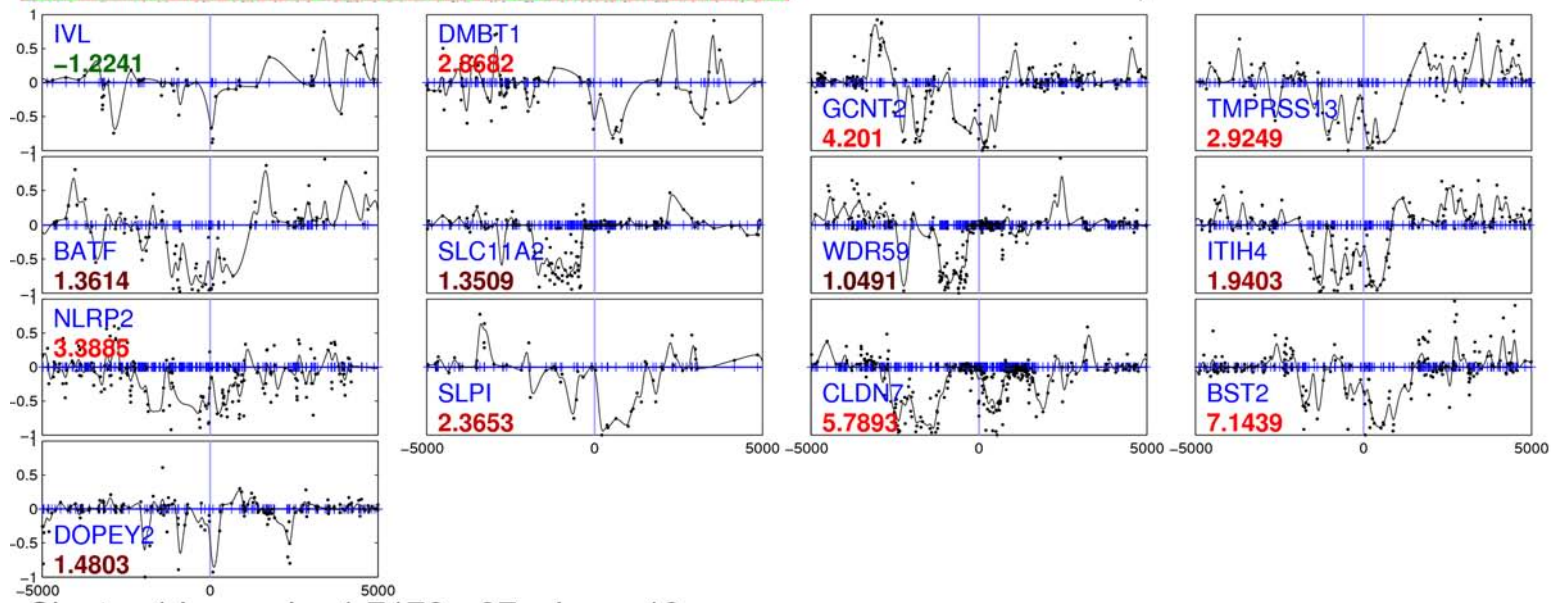
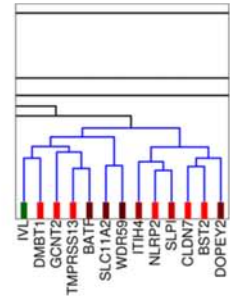
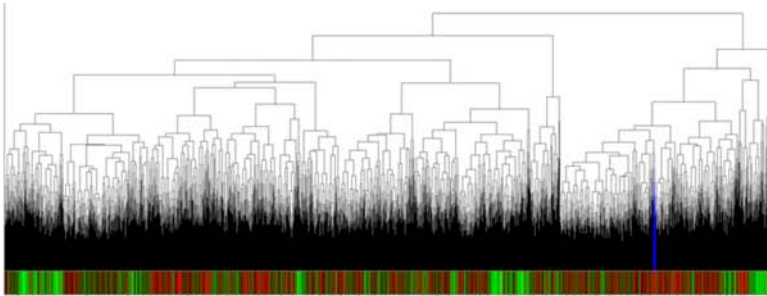
Cluster 11, pval = 0.0062485, size = 42



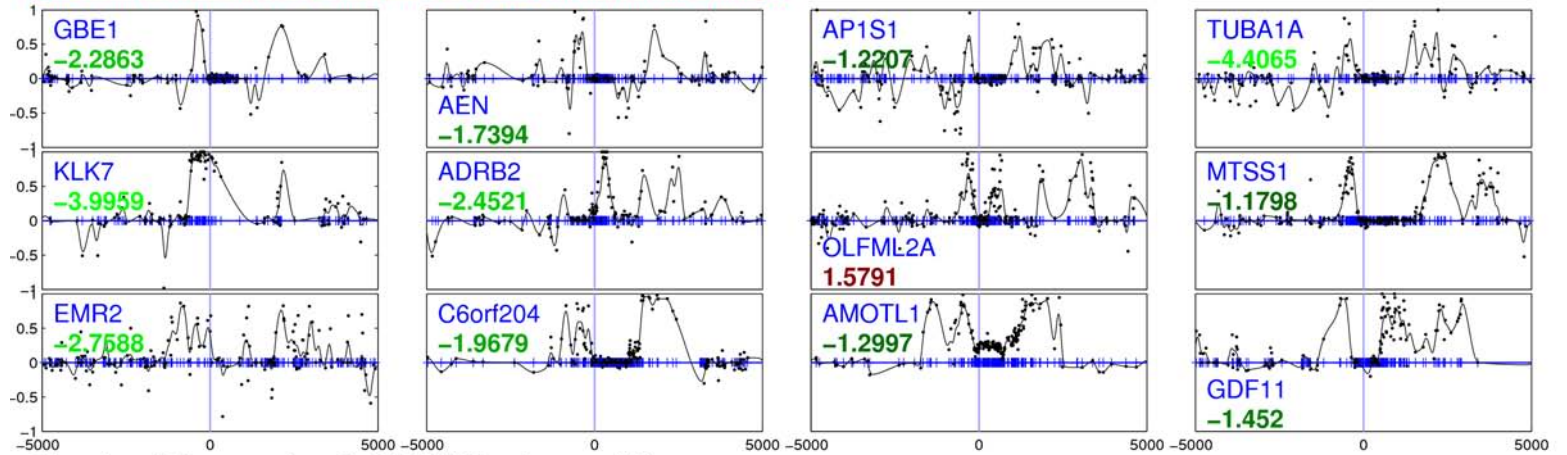
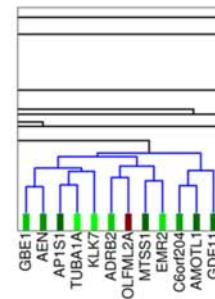
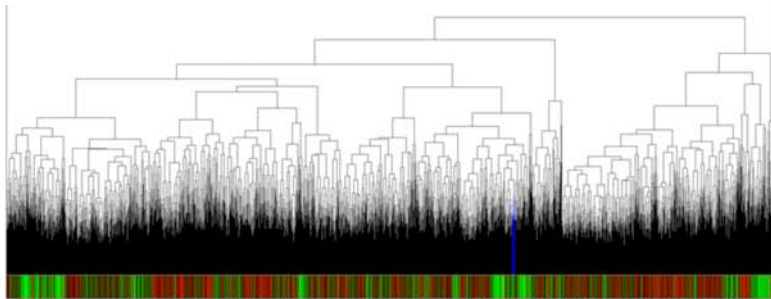
Cluster 12, pval = 1.4461e-05, size = 13



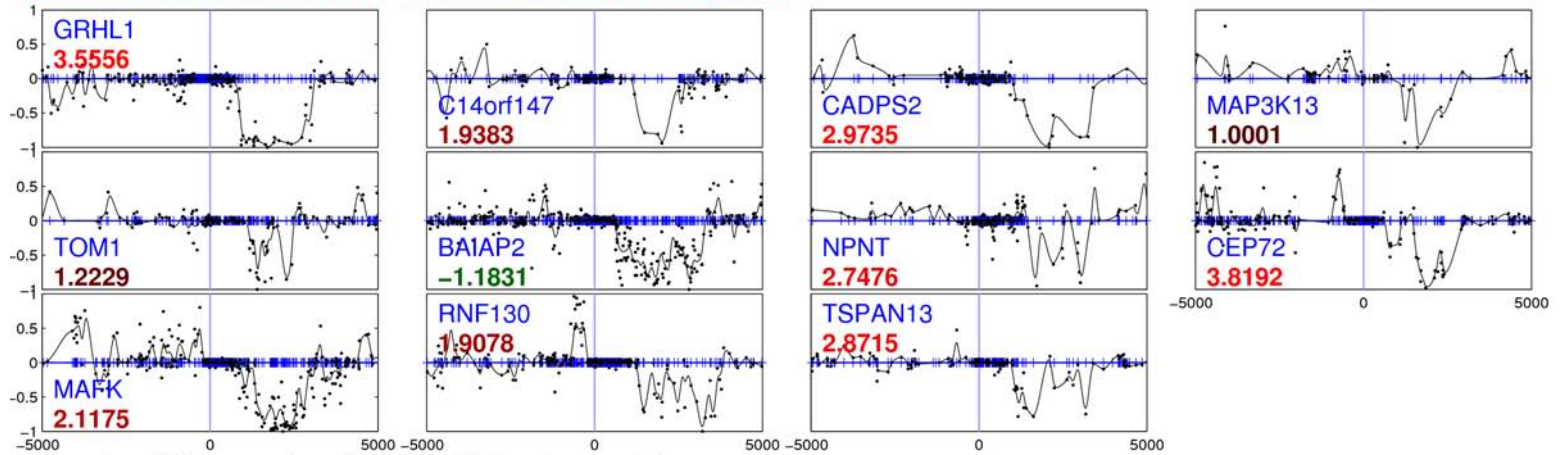
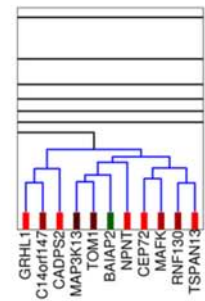
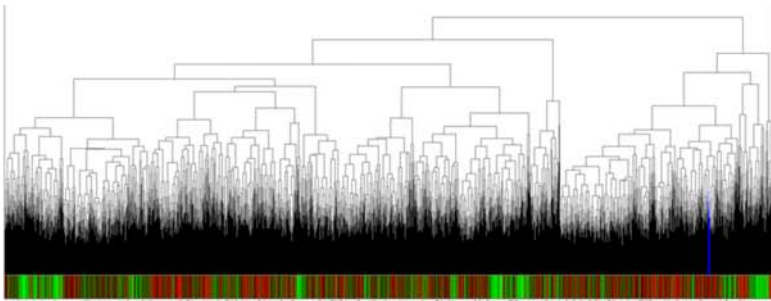
Cluster 13, pval = 0.0082623, size = 13



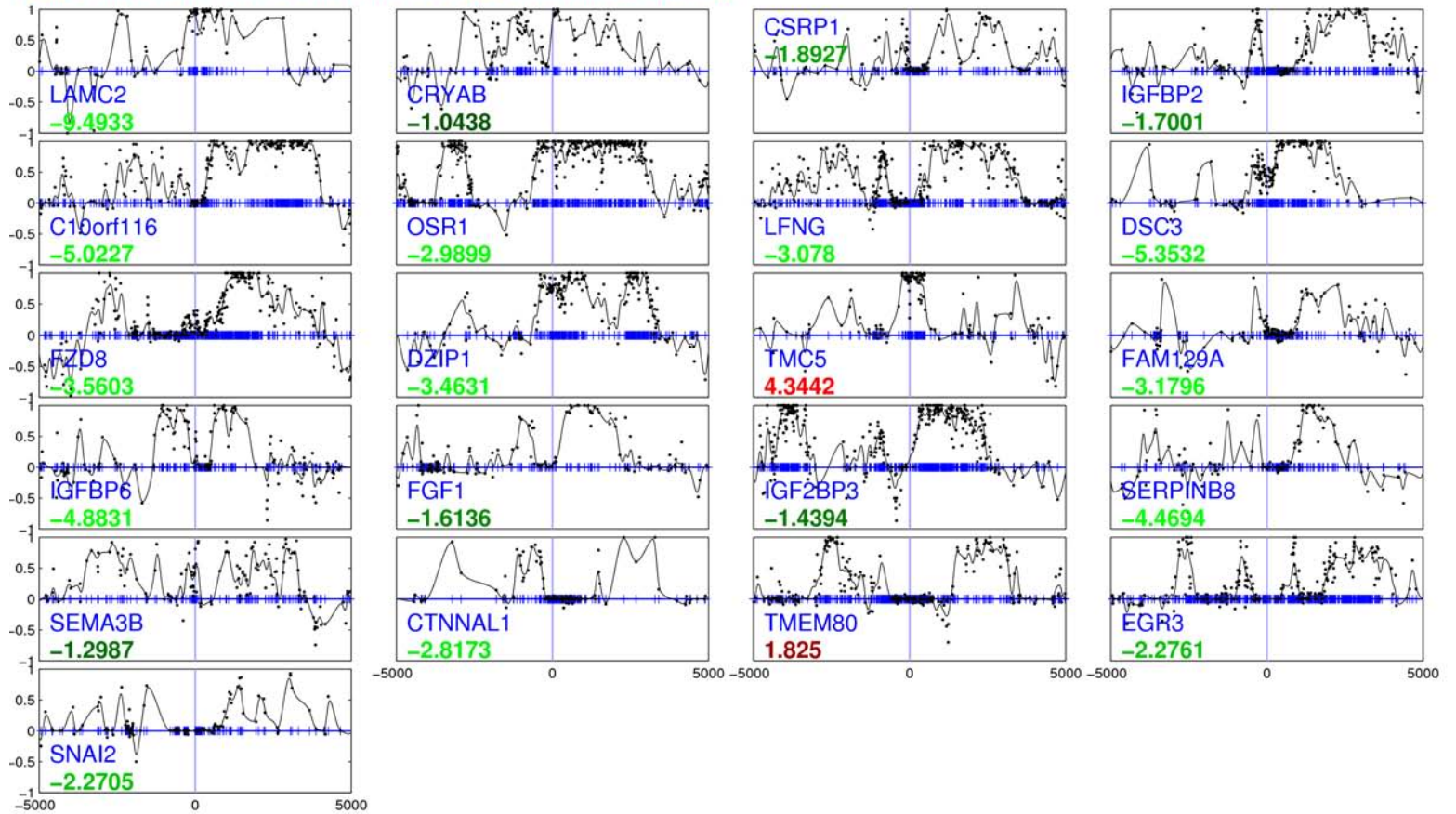
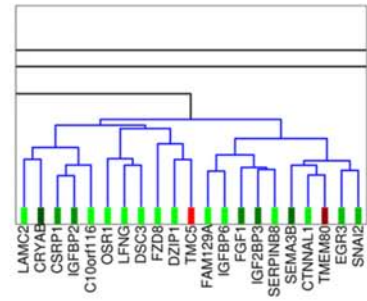
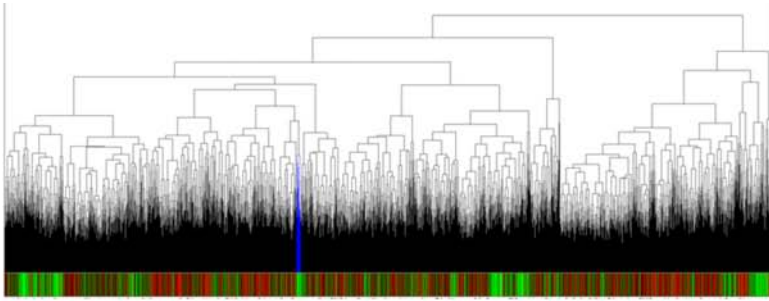
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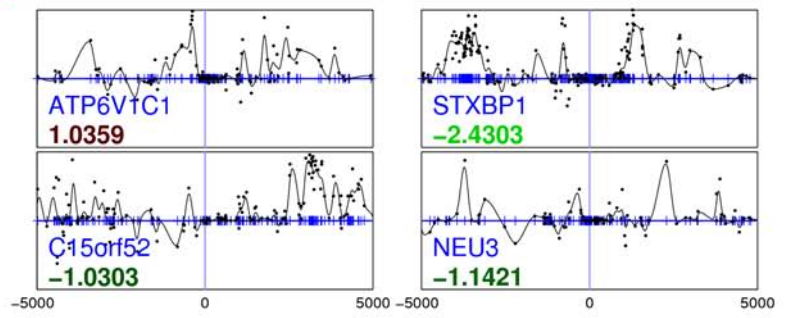
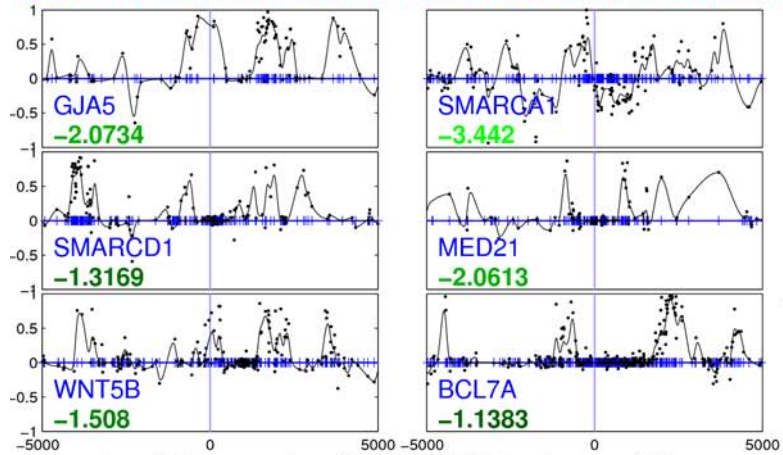
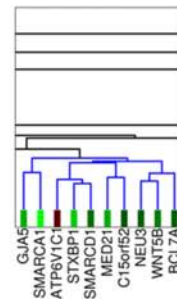
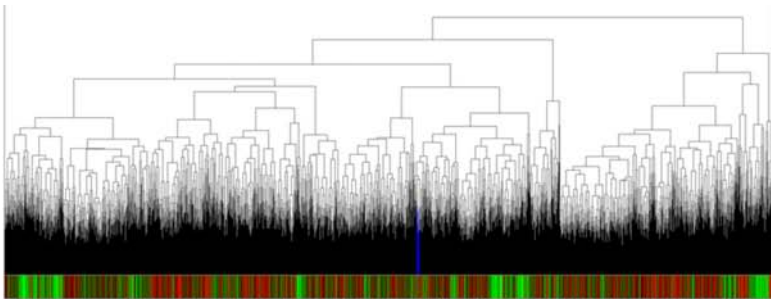
Cluster 15, pval = 0.010638, size = 12



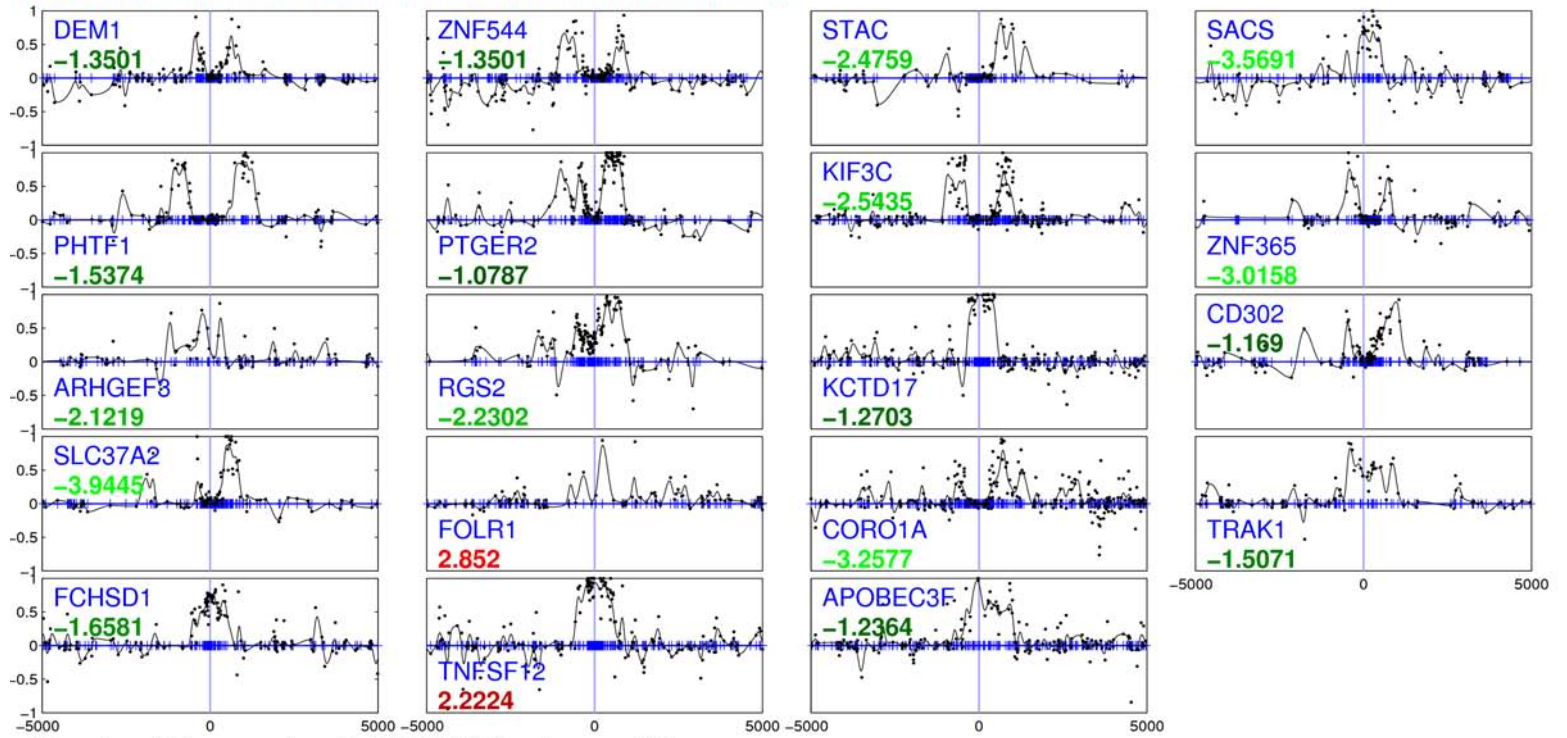
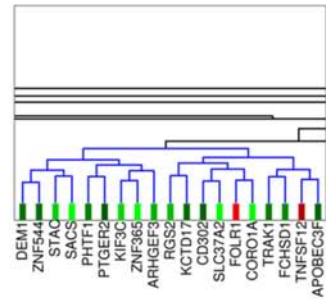
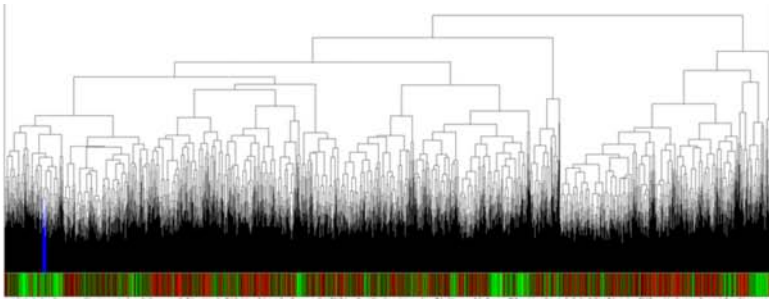
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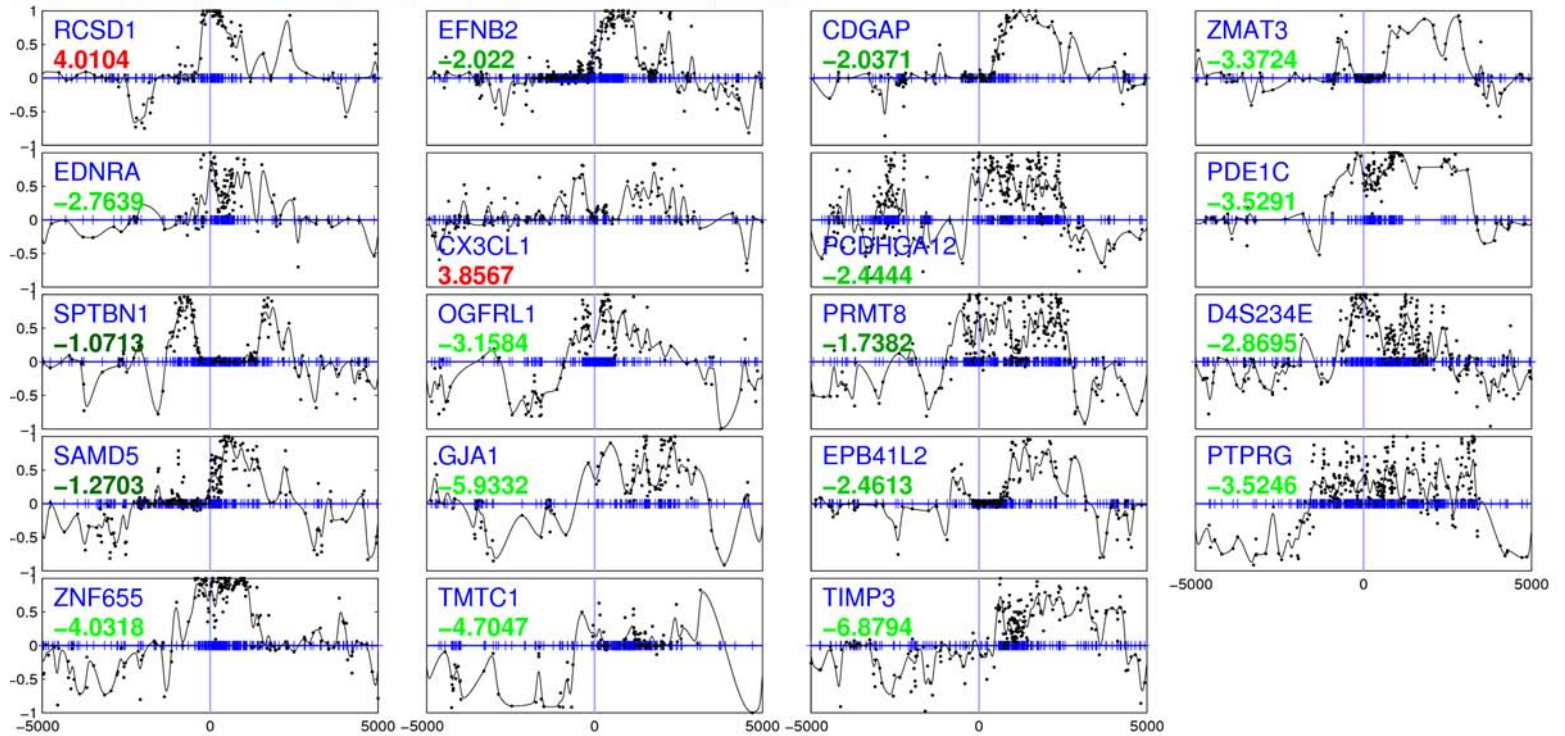
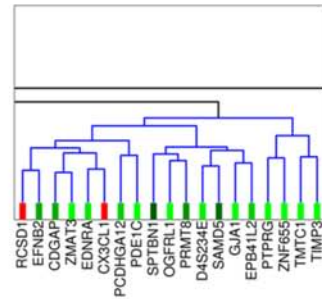
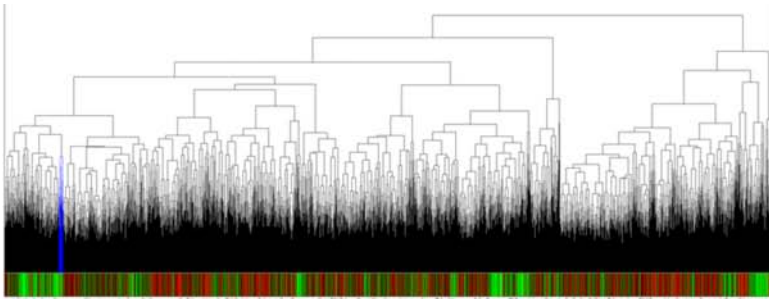
Cluster 17, pval = 0.00070033, size = 21



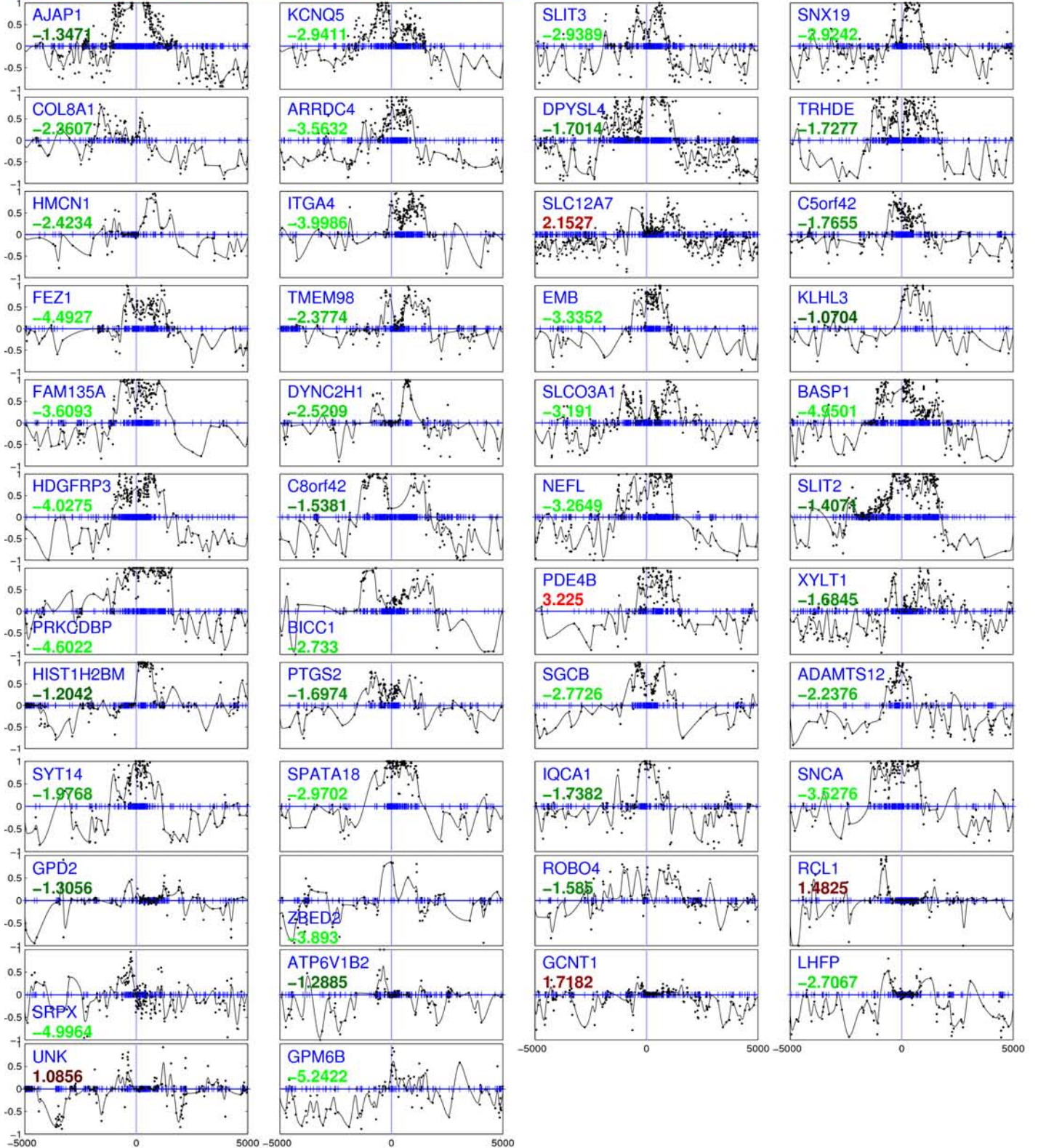
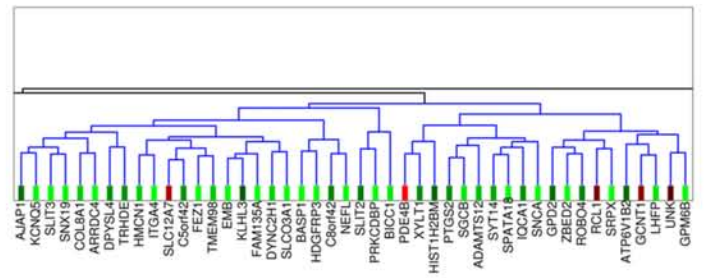
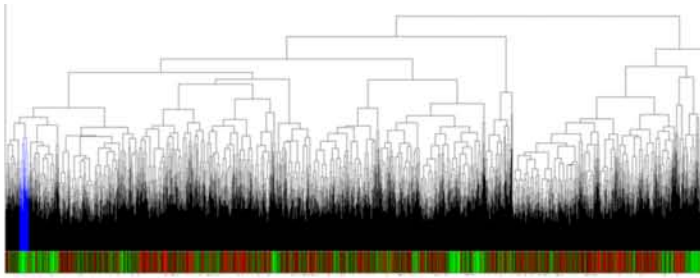
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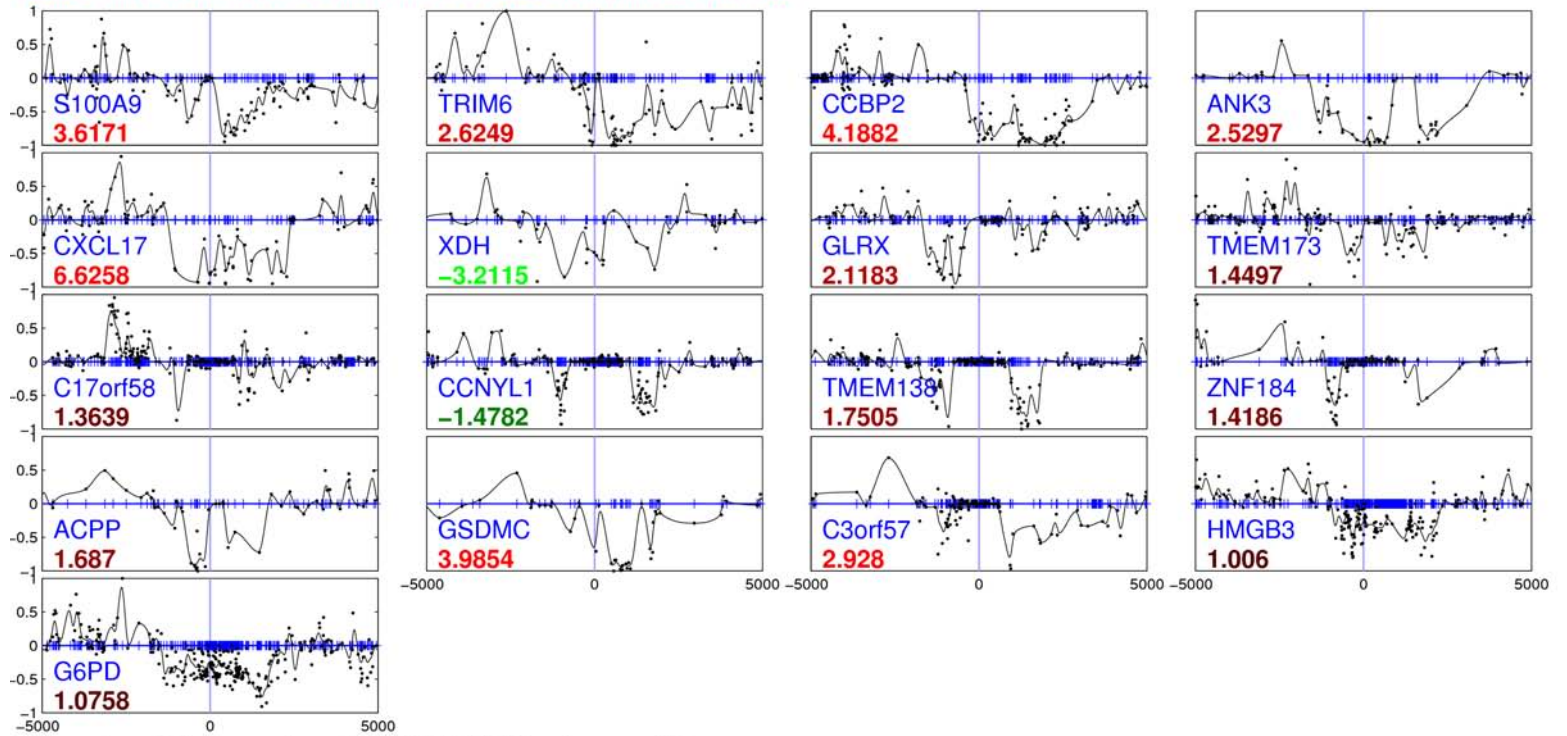
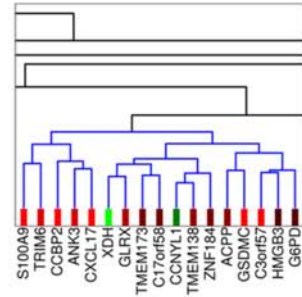
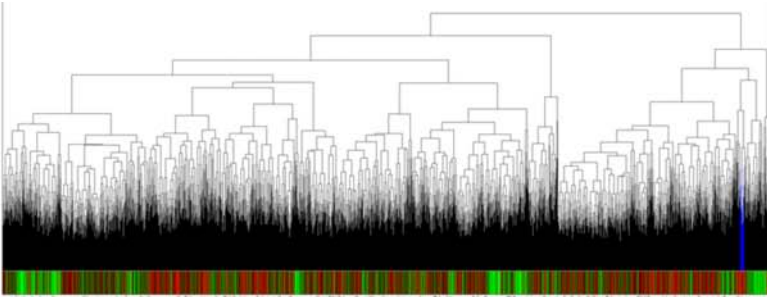
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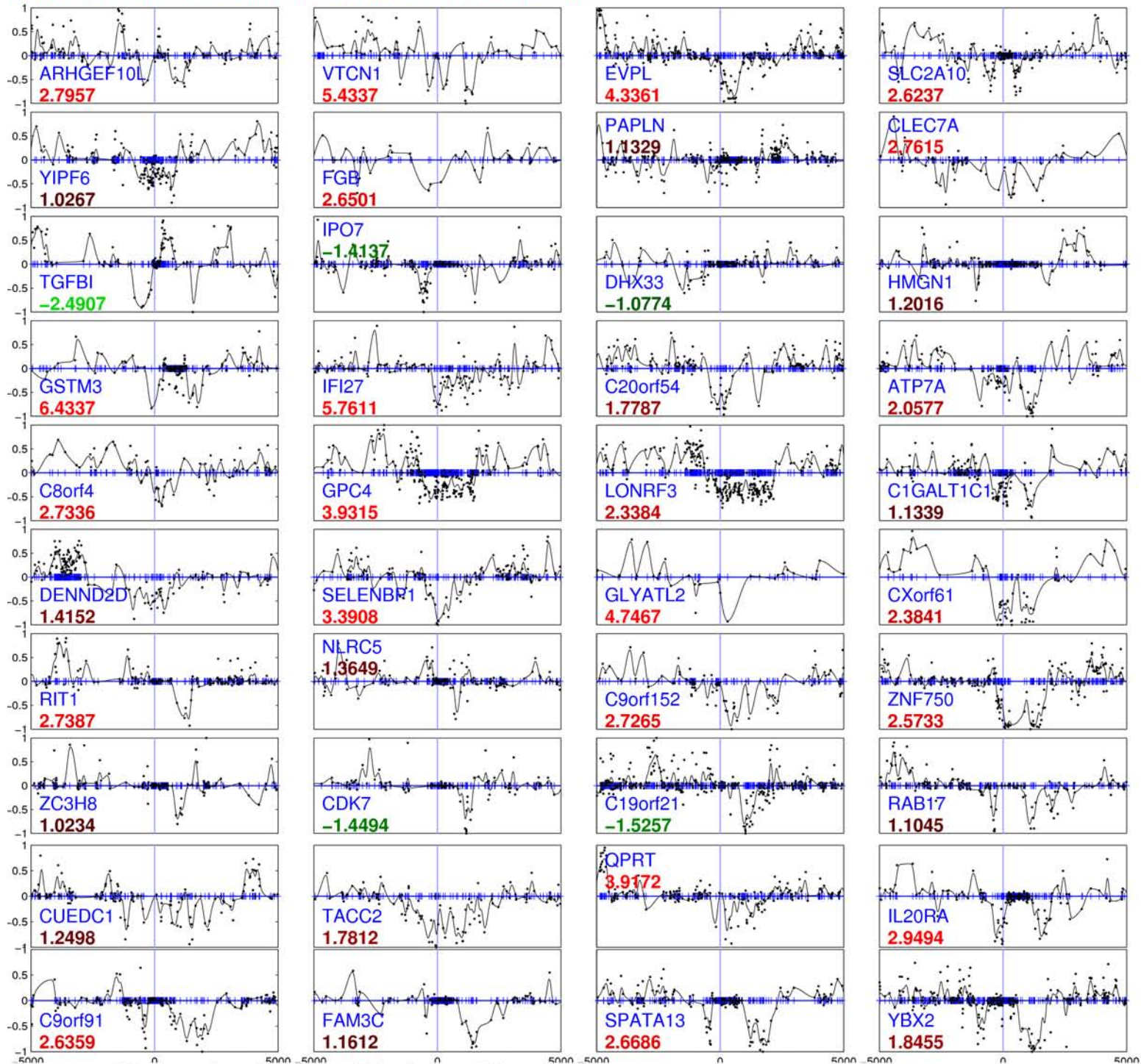
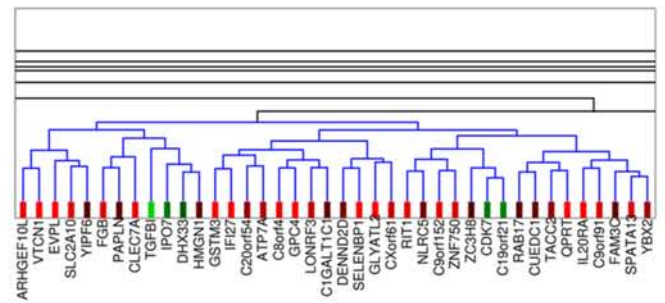
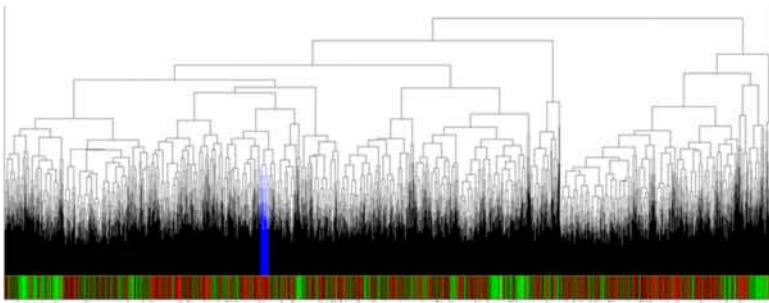
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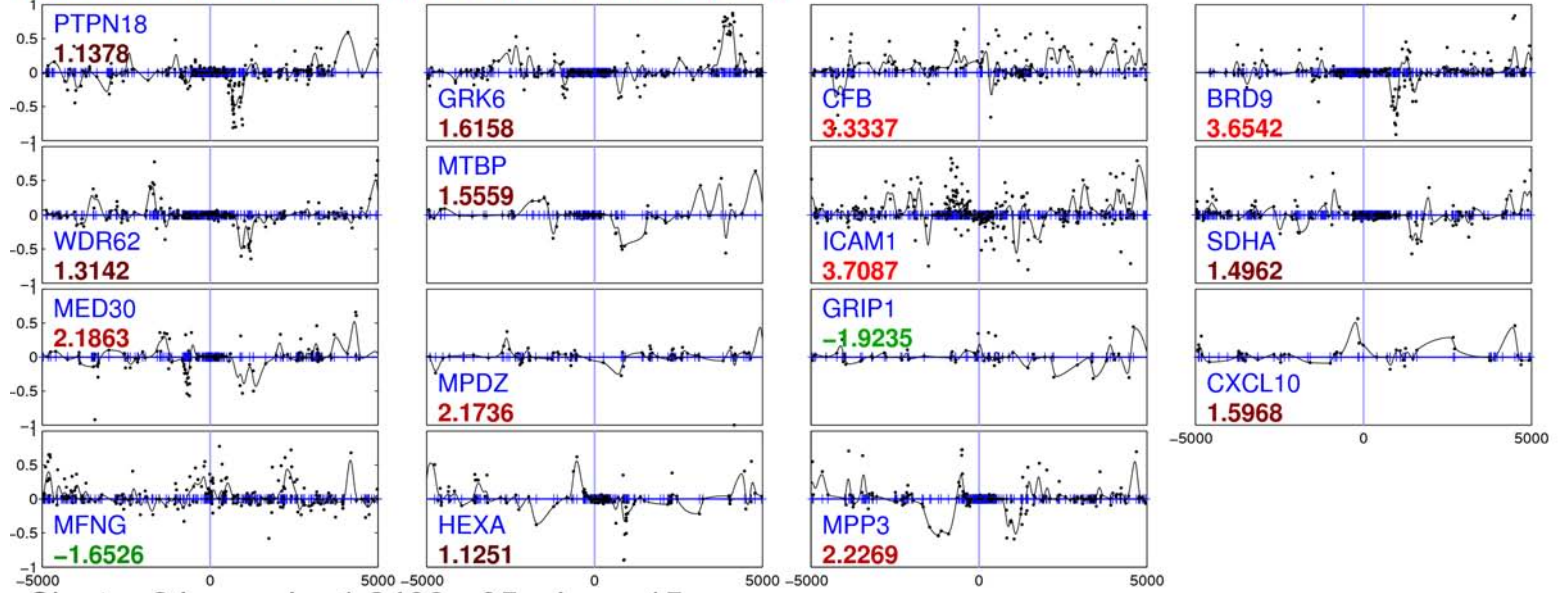
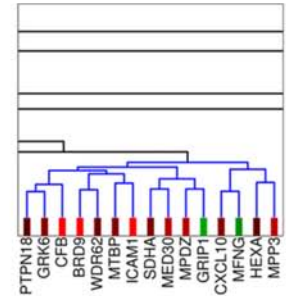
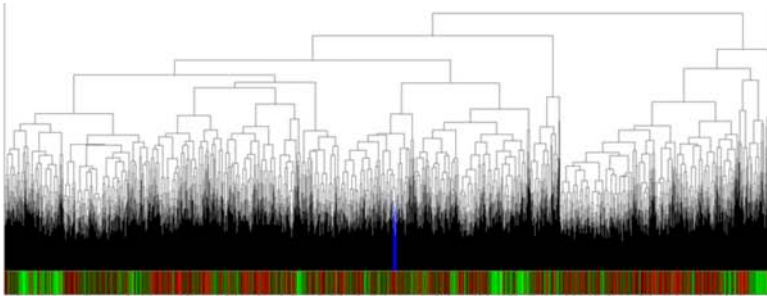
Cluster 21, pval = 0.0028159, size = 46



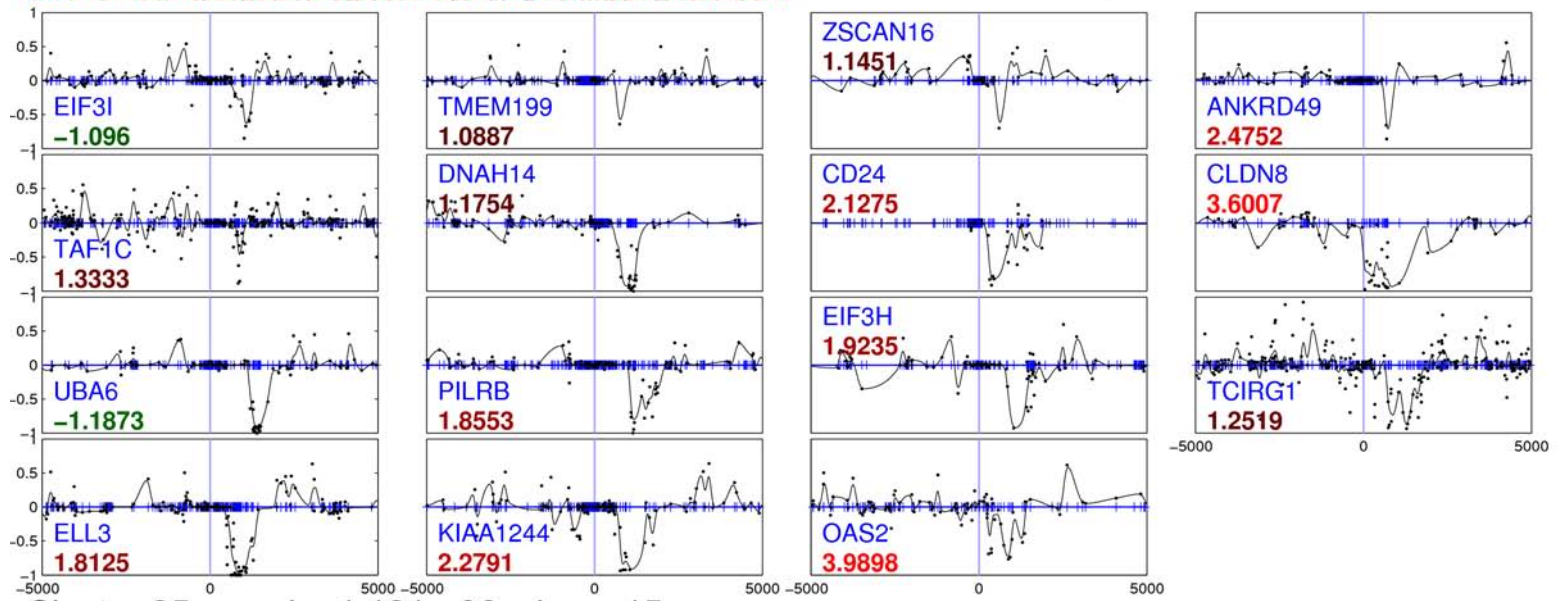
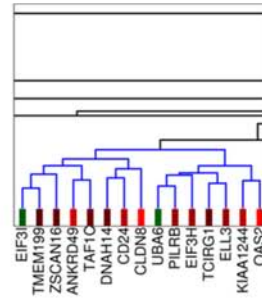
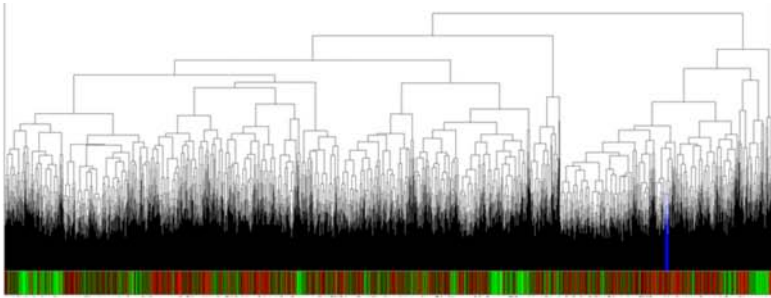
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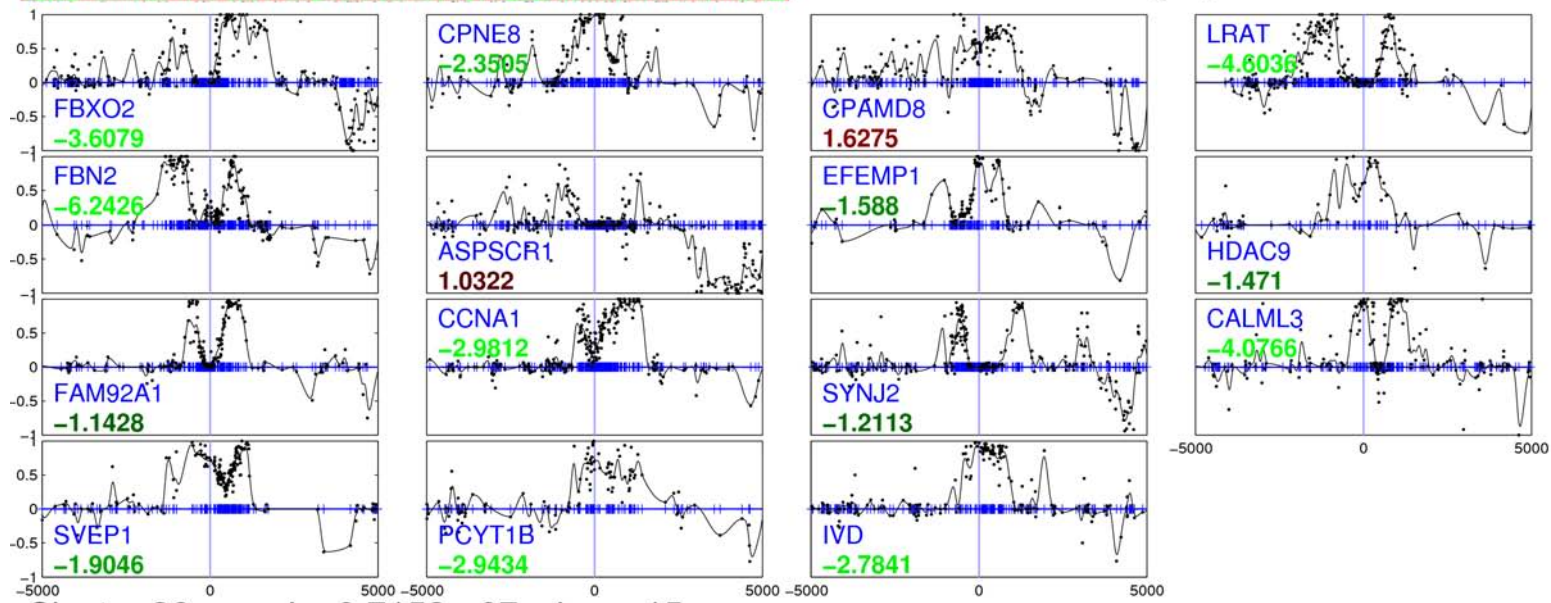
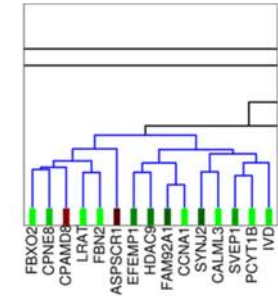
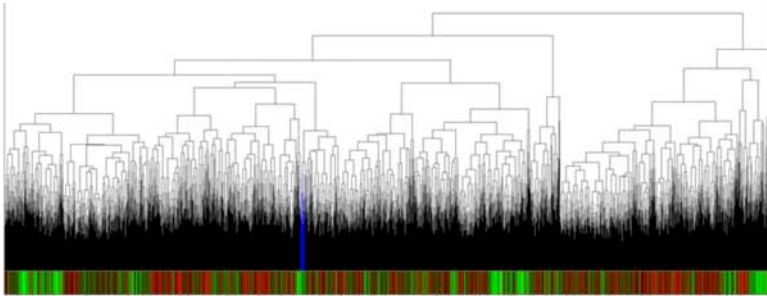
Cluster 23, pval = 4.8183e-08, size = 40



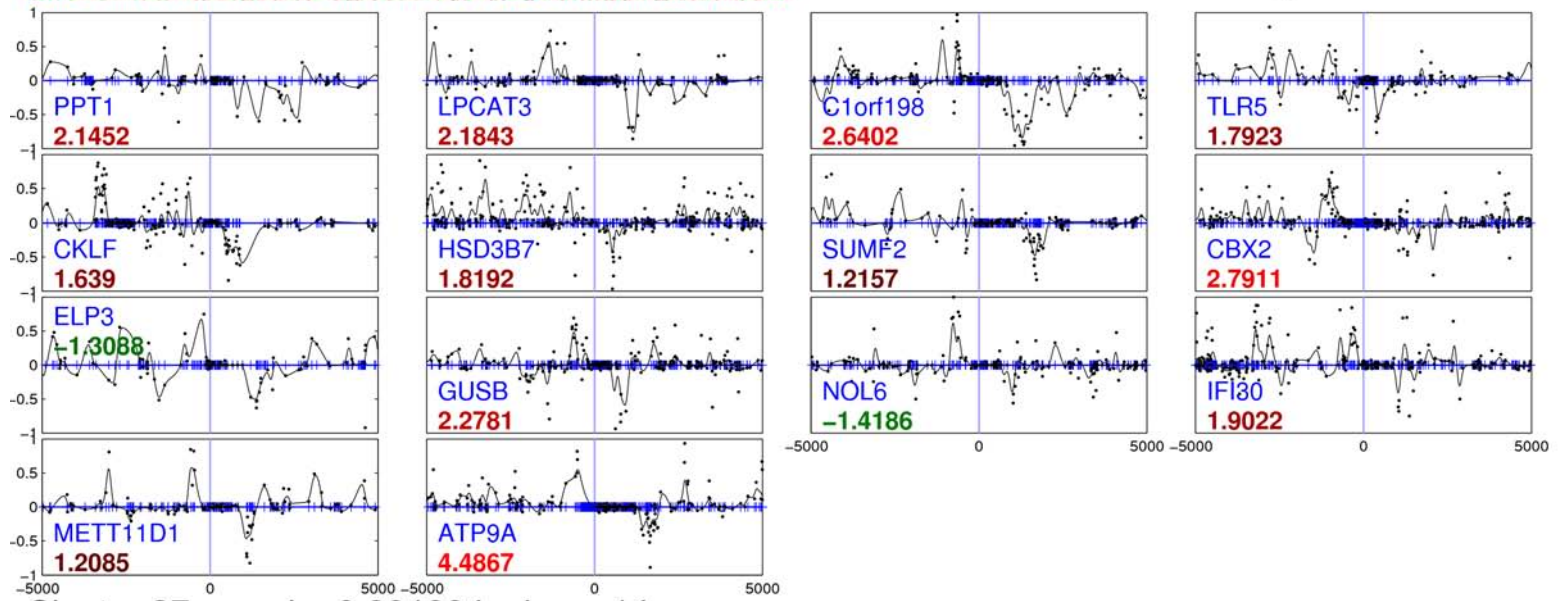
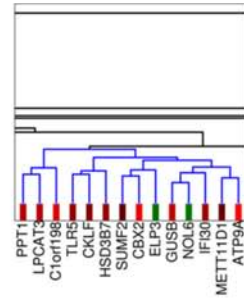
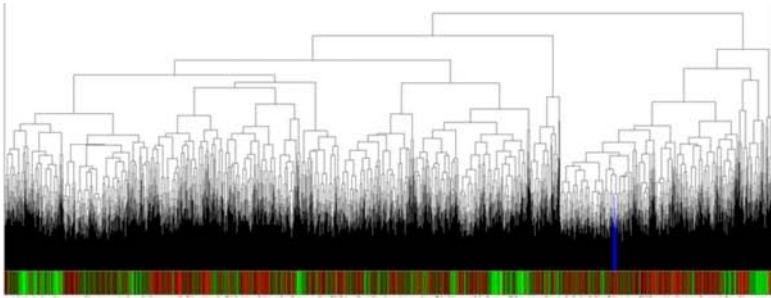
Cluster 24, pval = 1.2499e-05, size = 15



Cluster 25, pval = 1.181e-06, size = 15



Cluster 26, pval = 3.7152e-07, size = 15



Cluster 27, pval = 0.001034, size = 14