Measurement of expression levels in different tissues

Data set and parameter settings:

Seven cDNA microarray-experiments (two-channel – obtained internally (not publicly available) – manuscript in preparation) were performed to characterise 4595 expression patterns in 7 tissues (mouse). A common reference pool was used for each of the experiments (green channel). The red channel corresponds to a RNA pool obtained from one of 7 tissues:

- Experiment 1: Brain
- Experiment 2: Heart
- Experiment 3: Kidney
- Experiment 4: Liver
- Experiment 5: Lung
- Experiment 6: Skeletal muscle
- Experiment 7: Testis

The intention of this experimental setup was to detect groups of tissue-specific genes (mostly upregulated genes in one or two tissues).

The data set itself contains 4595 expression vectors with 7 values/ratios (red channel/green channel) (E = 7). A fraction of the expression ratios is missing (approximately 3.5%).
We used Adap_Cluster to cluster these gene expression vectors. We used the following parameter settings: S = 0.8 and MIN_NR_GENES = 5. Note that we did not use the default value 0.95 for S (In this data set there are almost no clusters containing expression vectors that reach the default significance level. This is caused by the rather low dimensionality (E = 7) of the data (too few experiments), giving a larger overlap between a cluster and the background). Except normalisation, no other preprocessing steps were performed.

Results:

Adap_Cluster identified 33 clusters. See the accompanying figures.
Note that a considerable number of clusters are tissue-specific (i.e., they contain genes differentially expressed in one or two tissues), reflecting the aims of the experimental setup. An overview of the most important tissue-specific clusters is given in the table below:

Table:

Cluster number	Tissue-specificity
1	Lung
2	Heart Skeletal muscle
3	Brain
4	Kidney
5	Kidney Lung
6	Heart Lung
7	Testis
8	Liver
10	Kidney Liver
20	Heart Skeletal muscle
30	Heart Skeletal muscle