General informations and conditions

to Jean Pierre Renou (URGV)

The consumables costs (230€/hybridization, taxes not included) will be paid by the partner. The CD-rom containing the raw and analyzed data is sent to the partner. Then the transcriptome results will be integrated in the database developed at the URGV: CATdb (MIAME compliant: et al. Nat Genet. 29(4):365-7).

The CATMA microarray

Sample preparation

in-vitro

Repetitions
Procedure

Summary of the protocol:

- Checking of the total RNA (Bioanalyser Agilent and ribogreen).
- Reverse Transcription (1µg total RNA) with an oligodT-T7 promoter.
- Purification and in vitro transcription (T7 polymerase): production of 80µg of aRNA or so.
- Purification and RT (5µg of aRNA) with Cy3 or Cy5-dCTP.
- Purification, quantification of the fluorochromes, 30 pmoles of each labelled sample are used per slide.
- Prehybridization of the slides after "post-processing". Hybridization at 42°C O/N with formamide.
- Washing and drying of the slides.
- Scanning with constant PMT (photomultiplicators): the data normalization is performed at the statistical analysis step.

After the statistical analysis the gene lists contain the log2 normalized intensities per samples, the log2 normalized ratios, and the p-values (Bonferroni or FDR correction) which provide the threshold

Publication of the results

Document to be sent with the request

1 – PROJECT TITLE
2 – Name address, tel number and e-mail address of the partner
3 – Description the project (briefly)
4 – Experimental design: nb of comparisons
5 – Number of slides, samples description (organ, harvesting stage according to Boyes et al. Plant Cell 2001, treatment…)
6 – Expected date of sample shipping

When the project will commence the collaborators must fill the document (submission_collaborator.xls, downloadable from this website) describing the samples needed for database submission.