The CATMA project (Complete Arabidopsis Transcriptome Microarray) is coordinated by P. Hilson. The aim of this project was to provide the Arabidopsis scientific community with a generic array pertinent to address all the biological questions concerning this species.

The current version of CATMA contains 24,576 probes representing about 85% of the genes predicted by Eugène (Foissac S. et al., Nucleic Acids Res., 2003). The probes are 'Gene Sequence Tags' designed with Specific Primers & Amplicons Design Software (Thareau et al., Bioinformatics, 2003).
To the primers are then added an extension containing semi-universal sequences (16 different "forward" (one for each row of a 384-well plate) and 24 different "reverse" (one for each column of a 384-well plate) allowing each PCR product of a 384-well plate to be amplified by a different pair of primers. This technique avoids cross-contamination during the amplification.