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Nephrogenesis profiling

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Kidney organogenesis is a complex process involving mesenchymal-epithelial transformation, branch morphogenesis and terminal differentiation. In the May 8 [Proceedings of the National Academy of Sciences](#), Stuart *et al.* describe a microarray analysis of 8,740 rat genes during kidney development (*Proc Natl Acad Sci USA* 2001, **98**:5649-5654). The authors developed data-analysis software for data equalization, statistical-significance testing and data mining. About 10% of genes were found to vary significantly during nephrogenesis. These genes could be divided into five clear groups that differ in gene function, tissue distribution and embryonic expression. The five groups show distinct temporal expression patterns: early development (Group 1), mid-embryogenesis (Group 2), neonatal period (Group 3), throughout development (Group 4) and adult kidney (Group 5). Moreover, each group is characterized by an abundance of genes with similar functions: protein translation and DNA replication (Group 1), extracellular matrix (Group 2), retrotransposons (Group 3), energy metabolism and transport (Group 4), and transporters, detoxification enzymes and oxidative stress genes (Group 5). These results form the basis for a continuously updated [developmental database](#) for nephrogenesis.

References

1. Branching morphogenesis during kidney development.
2. *Proceedings of the National Academy of Sciences*, [<http://www.pnas.org>]
3. Kidney development gene expression database, [<http://organogenesis.ucsd.edu>]