The renal distal convoluted tubule (DCT) is important for the renal control of ion homeostasis and blood pressure. Although several DCT-specific ion transporting proteins have been identified, only little is yet known about the molecular mechanisms that regulate DCT function. We hypothesized that gene products that are specifically expressed in the DCT might be of particular importance for the control of DCT cell function. Here, we used Complex Object Parametric Analysis and Sorting (COPAS) to isolate DCTs in large scale for the identification of a DCT transcriptome. A renal tubule suspension was obtained from transgenic mice expressing EGFP specifically in the DCT. The tubules were then separated by COPAS in three fractions (i.e. all tubules, EGFP-positive DCTs and EGFP-negative non-DCT tubules). Real-time PCR and Western blot analysis confirmed the significant enrichment and derichment of known DCT-specific marker molecules in the EGFP-positive and EGFP-negative samples, respectively. Subsequent microarray analysis (Agilent) revealed about 400 genes that are being more than 20-fold enriched in EGFP-positive tubules compared with EGFP-negative tubules. Aside from the known DCT-specific gene-products parvalbumin, NCC and TRPM6, many novel DCT enriched gene products were identified. Among them, Slc16a7 (MCT2) and its accessory protein GP70 (embigin) sticked out. Immunohistochemistry confirmed the significant expression of these two gene products in the DCT. Thus, transcriptomic analysis of COPAS-sorted renal tubules allows the identification of novel DCT-enriched gene products and may provide a pool of novel candidate genes for DCT-specific functions and diseases.