

Webtable 4

The number of matrices found using the program MATCH and the TRANSFAC Professional Database (Release 7.4) in the set of 62 upstream sequences of genes differentially regulated between the glomeruli and tubulointerstitial samples. Different cutoff values for the core similarity and the matrix similarity were used in the analysis.

Core Similarity	Matrix Similarity	No. total matrices	No. unique matrices
0.999	0.999	124	38
0.990	0.990	220	68
0.975	0.975	427	115
0.962	0.962	770	154
0.950	0.950	1275	178