Table S5. Full Analysis: TRBE motifs over-represented in IMCD-specific genes versus non-IMCD-specific genes

Genomatix TRBE (Name)		BioBase TRBE	f_{IMCD}	f_{PT}	Ratio	p
AP2	(Activator protein 2)	V$AP2_Q6	4.33	3.33	1.30	***
CREB	(cAMP-responsive element binding proteins)	V$CREBATF_Q6	0.82	0.64	1.29	***
ETS	(Human and murine ETS1 factors)	V$CETS1P54_03	6.29	5.93	1.06	*
RXR	(RXR heterodimer binding sites)	V$VDR_Q3	5.64	4.95	1.14	***
SRF	(Serum response element binding factor)	V$SRF_Q6	0.07	0.03	2.02	*

Genomatix TRBE (Name)		BioBase TRBE	f_{IMCD}	f_{mTAL}	Ratio	p
ETS	(Human and murine ETS1 factors)	V$ETS_Q6	3.65	3.16	1.16	***
FKHD	(Fork head domain factors)	V$HNF3B_01	1.94	1.68	1.16	*
GATA	(GATA binding factors)	V$GATA4_Q3	3.75	3.36	1.11	*
HOX	(homeobox binding factor)	V$NCX_01	8.67	8.02	1.08	*

Genomatix TRBE (Name)		BioBase TRBE	f_{IMCD}	f_{Common}	Ratio	p
AP2	(Activator protein 1)	V$AP2_Q6	4.33	2.66	1.63	***
CREB	(cAMP-responsive element binding proteins)	V$TAXCREB_01	1.05	0.89	1.18	***
ETS	(Human and murine ETS1 factors)	V$ETS_Q6	3.65	3.46	1.06	*
RXR	(RXR heterodimer binding sites)	V$VDR_Q3	5.64	3.68	1.53	***

BioBase ExPlain software suite was used to locate TRBE motifs in 379 IMCD-specific transcripts (signal above median and no signal in mTAL or PT), 155 unique mTAL transcripts (signal above median and no signal in IMCD or PT), 301 unique PT transcripts (signal above median and no signal in IMCD or mTAL), and 379 common transcripts common to all three tubule segments. Significant overrepresentation of TRBE motifs in IMCD-specific transcripts versus in mTAL-specific, PT-specific, or common transcripts was tested. f_{IMCD}, f_{mTAL}, f_{PT}, and f_{common}: frequency of TRBE motif in IMCD, mTAL, PT, and common transcripts. Significance: *, p<0.05; **, p<0.01; ***, p<0.005.