TableS4: Gene ontology (GO) enrichment analysis of the possible downstream target genes.

Ontology	Term	P value	Count
BP	urogenital system development	6.63E-07	15
BP	renal system development	4.92E-06	13
BP	sodium ion transport	8.08E-06	11
BP	axis elongation	1.03E-05	5
BP	positive regulation of sodium ion transmembrane transporter activity	1.33E-05	4
BP	kidney development	1.51E-05	12
BP	regulation of ion transmembrane transport	1.63E-05	16
BP	potassium ion transport	1.99E-05	11
BP	branch elongation of an epithelium	3.43E-05	4
BP	regulation of ion transmembrane transporter activity	4.15E-05	11
CC	postsynaptic membrane	3.90E-05	12
CC	glutamatergic synapse	8.18E-05	12
CC	basolateral plasma membrane	0.00016225	9
CC	postsynaptic specialization	0.00033442	11
CC	main axon	0.00037308	5
CC	synaptic membrane	0.0005765	12
CC	postsynaptic density	0.00074735	10
CC	asymmetric synapse	0.00082071	10
CC	neuron to neuron synapse	0.00133803	10
CC	neuron projection membrane	0.00174714	4
MF	monovalent inorganic cation transmembrane transporter activity	8.44E-05	13
MF	metal ion transmembrane transporter activity	0.00032279	13
MF	ion gated channel activity	0.00039418	11
MF	gated channel activity	0.00049261	11
MF	Rac GTPase binding	0.00052762	5
MF	sodium ion transmembrane transporter activity	0.00059662	7