Supplementary material for Takahashi *et al*. (August 7, 2001) *Proc. Natl. Acad. Sci. USA*, 10.1073/pnas.171209998

Table 3. Commonly down-regulated genes in clear cell renal cell carcinoma (RCC)

GenBank accession no.	Down-regulated gene	Average fold	% of RCC
R89067	Kininogen	27.2	100
T53220	Fatty acid-binding protein 1, liver	22.8	95.8
AA682293	Phenylalanine hydroxylase	20.4	96.0
AA705692	ESTs	18.0	100
AA954947	Epidermal growth factor (β-urogastone)	15.0	100
H72098	Aldolase B, fructose-biphosphate	13.6	100
AA411988	ESTs	13.3	100
T73187	Plasminogen	12.0	100
T51617	Solute carrier family 22, member 3	11.8	96.4
AA777384	ESTs	11.0	96.2
H53340	Metallothionein 1G	10.0	100
AA844930	Glycoprotein 2 (zymogen granule membrane)	9.6	100
AA101792	Phosphatidylinositol glycan, class F	9.4	96.6
AA858026	Protein C inhibitor (plasminogen activator inhibitor III)	9.4	100
H18950	ESTs, highly similar to hepatocyte nuclear factor 4 γ	9.2	100
AA405769	Phosphoenolpyruvate carboxykinase 1 (soluble)	8.9	96.6
AA040387	X-prolyl aminopeptidase 2, membrane-bound	8.8	96.4
H77766	Metallothionein 1H	8.4	96.6
W16424	ESTs	8.4	92.6
H88329	Calbindin 1 (28 kD)	8.1	100
N62179	Methylmalonate-semialdehyde dehydrogenase	7.9	100
AA775872	Glypican 3	7.9	100
AA457718	*Homo sapiens* mRNA; cDNA DKEZp564B076	7.8	95.7
R24266	Growth factor receptor-bound protein	7.1	80.8
R54778	Collagen, type XVI, α 1	7.1	100
AA702640	Dopa decarboxylase	7.0	96.3
N55459	RNA helicase-related protein	6.9	96.6
AA664180	Glutathione peroxidase 3	6.6	92.9
R10382	Protein C inhibitor (plasminogen activator inhibitor III)	6.4	92.6
AA227594	Mal, T-cell differentiation protein	6.3	100
H68509	UDP glycosyltransferase 2 family, polypeptide B10	6.1	95.5
AA676466	Argininosuccinate sythetase	6.1	96.4

H96140	Acyl-coenzyme A dehydrogenase, short/branched chain	6.0	96.0
H11346	Aldehyde dehydrogenase 4	6.0	92.9
AA862999	Calcium-sensing receptor	6.0	100
AA497001	ESTs, Weakly similar to BcDNA.GH02901	6.0	96.3
AA449780	EST	5.9	88.9
H11369	Aldehyde dehydrogenase 4	5.8	88.9
AA704995	Putative glycine-*N*-acyltrasferase	5.6	92.9
T94781	Potassium inwardly rectifying channel, subfamily J	5.6	92.9
N89673	ESTs	5.6	92.6
H37880	ESTs, moderately similar to ALU SUBFAMILY SP	5.6	96.3
AA663884	Synaptosomal-associated protein, 25 kD	5.5	95.7
R25818	Aldehyde dehydrogenase 9	5.5	100
AA700604	Sorbitol dehydrogenase	5.4	92.6
W95082	Hydroxysteroid (11-β) dehydrogenase 2	5.4	96.6
AA677655	Klotho	5.4	92.3
N80129	Metallothionein 1L	5.3	86.2
AA402915	Aminoacylase 1	5.3	96.3
AA863424	Dipeptidase 1 (renal)	5.2	93.1
H72722	ESTs, highly similar to Metallotheionein-1B	5.2	86.2
N78083	Glycine dehydrogenase	5.1	96.4
R06601	ESTs, moderately similar to Metallothionein-II	5.1	82.8
AA131240	ESTs	5.0	92.0
AA485965	Succinate-CoA ligase, GDP-forming, α subunit	4.9	92.9
AA196287	ESTs, weakly similar to alternative spliced product using exon 13A	4.9	96.6
R61229	Glycine amidinotrasferase (L-arginine: glycine amidinotrasferase)	4.8	82.8
AA872383	Metallothionein 1E (functional)	4.8	82.8
N23898	G protein-coupled receptor kinase 2 (*Drosophila*)-like	4.8	92.9
AA699427	Fructose-biphosphatase 1	4.7	93.1
T68892	Secreted frizzled-related protein 1	4.7	96.2
AA873355	ATPase, Na+/K+ transporting, α 1 polypeptide	4.7	100
AI000188	UDP glycosyltrasferase 2 family, polypeptide B7	4.6	85.7
AA459197	Sodium channel, nonvoltage-gated 1 α	4.6	89.7
AA460298	Methylmalonate-semialdehyde dehydrogenase	4.4	91.7
W86431	Protein C inhibitor (plasminogen activator inhibitor III)	4.4	100

T65482	L-3-hydroxyacyl-coenzyme A dehydrogenase, short chain	4.4	96.2
AA457374	DKFZP586B0319	4.3	91.7
R33037	ESTs	4.3	92.0
AA437099	ESTs	4.3	85.2
W01011	SA (rat hypertension-associated) homolog	4.2	89.7
R16596	EST, moderately similar to Cd-7 metallothionein-2	4.1	86.2
AA863449	Oviductal glycoprotein 1, 120 kD	4.0	92.9
N53031	UDP glycosyltrasferase 2 family, polypeptide B4	4.0	86.2
AA458884	S100 calcium-binding protein A2	4.0	92.9
AA608575	Propionyl coenzyme A carboxylase, α polypeptide	3.8	89.7
H18608	Solute carrier family 22 (organic anion transporter), member 8	3.6	89.3

Seventy-seven genes or expressed sequence tags (ESTs) that are at least 3-fold down-regulated in at least 75% of RCC (*n* = 29). Average fold reflect average ratios of all nonflagged spots. Percentage of RCC is the fraction of tumors that had at least 2-fold down-regulation.