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

Table 2. Commonly up-regulated genes in clear cell renal cell carcinoma (RCC)

GenBank accession no.	Gene name	Average fold	% of RCC
H86554	Ceruloplasmin	16.9	96.2
R00332	ESTs; highly similar to growth factor-responsive protein	14.1	96.4
T72235	Nicotinamide *N*-methyltransferase	13.5	96.6
W72051	Fatty acid-binding protein 7, brain	13.2	87.5
W70343	Lysyl oxidase	11.2	95.8
W30988	ESTs; highly similar to angiopoietin-related protein	11.1	100
H99075	ESTs	10.7	95.7
N50654	Ceruloplasmin	10.6	95.8
W93163	Tumor necrosis factor, α-induced protein 6	10.5	100
T54298	ESTs; highly similar to angiopoietin-related protein	8.1	100
AA598601	Insulin-like growth factor-binding protein 3	7.6	96.6
AA678335	Phosphodiesterase I/ nucleotide pyrophosphatase 3	7.6	84.0
AA164819	ESTs	7.1	96.3
AA485896	ESTs	6.8	96.4
N26171	ESTs	6.2	87.5
AA487787	von Willebrand factor	6.2	100
AA450189	Enolase 2, (γ, neuronal)	6.0	96.4
R62612	Fibronectin 1	5.6	93.1
H20872	Fc fragment of IgG, low-affinity IIIa, receptor for (CD16)	5.5	85.7
W72293	ESTs	5.5	93.1
AA055835	Caveolin 1, caveolae protein 22kD	5.4	92.9
AA873159	Apolipoprotein C-1	5.3	88.9
AA017544	Regulator of G-protein signaling 1	5.2	85.7
R19956	Vascular endothelial growth factor	5.1	96.4
H99816	Procollagen-lysine, 2-oxoglutarate 5-dioxygenase 2	5.1	96.4
R49597	ESTs	4.6	95.8
AA405000	*Homo sapiens* ribonuclease 6 precursor	4.5	96.2
H58873	Solute carrier family 2, member 1	4.5	93.1
T62491	Chemokine, receptor 4	4.4	89.7
AA443899	CD36 antigen-like 1	4.2	89.3
AI004331	Human MHC class II HLA-DQ-β	4.2	85.7
AA488892	ESTs, weakly similar to Gag-Pol polyprotein	4.0	85.7

Thirty-two genes or expressed sequence tags (ESTs) that are at least 3-fold up-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 up-regulation.