ID	Score	Focus Molecules	Top Functions
1	61	32	Energy Production, Small Molecule Biochemistry, Genetic Disorder
2	55	30	Molecular Transport, Small Molecule Biochemistry, Cellular Function and Maintenance
3	44	26	Cellular Compromise, Cellular Assembly and Organization, Cellular Function and Maintenance
4	39	24	Cell-To-Cell Signaling and Interaction, Nervous System Development and Function, Cellular Assembly and Organization
5	33	21	Genetic Disorder, Neurological Disease, Metabolic Disease
6	23	17	Cellular Assembly and Organization, RNA Post-Transcriptional Modification, Protein Synthesis
7	19	14	Cellular Development, DNA Replication, Recombination, and Repair, Nucleic Acid Metabolism
8	19	14	Gene Expression, Genetic Disorder, Metabolic Disease
9	17	13	Carbohydrate Metabolism, Molecular Transport, Small Molecule Biochemistry
10	16	13	RNA Post-Transcriptional Modification, Cell Death, Post-Translational Modification
11	15	12	RNA Post-Transcriptional Modification, Cellular Function and Maintenance, Carbohydrate Metabolism
12	15	12	Carbohydrate Metabolism, Nucleic Acid Metabolism, Small Molecule Biochemistry
13	15	12	Genetic Disorder, Hepatic System Disease, Liver Cholestasis
14	14	11	Gene Expression, Lipid Metabolism, Molecular Transport
15	12	10	Cell Signaling, Infection Mechanism, Cell Death
16	2	1	Genetic Disorder
17	2	1	Genetic Disorder, Metabolic Disease, Lipid Metabolism
18	2	1	Molecular Transport, Protein Trafficking
19	2	1	Lipid Metabolism, Nucleic Acid Metabolism, Small Molecule Biochemistry
20	2	1	Cell Morphology, Cancer, Reproductive System Disease
21	2	1	Cancer, Cellular Development, Skeletal and Muscular System Development and Function
22	2	1	Genetic Disorder, Neurological Disease, Small Molecule Biochemistry
23	2	1	Lipid Metabolism, Small Molecule Biochemistry
24	1	1	Cancer, Genetic Disorder, Hepatic System Disease
25	1	1	DNA Replication, Recombination, and Repair, Cellular Compromise, Cell Death

Table 4. The rank list of the metabolic networks which encompass differentially expressed genes between ROP-Os/+ and C57-Os/+. Genes from the SAGE kidney libraries, which met the 2-fold difference in expression level cut-off between ROP-Os/+ and C57-Os/+ were assigned biological functions using the Ingenuity Pathways Knowledge Base. A right-tailed Fisher's exact test was used to calculate a p-value describing the probability that each biological function assigned to that network is due to chance alone. Networks were ranked according to the combinatorial p-value of differentially expressed genes represented in the network. Corresponding network diagrams are shown as supplemental figures S3-S14.