Supplemental Table 4. Array-revealed Average Gene Expression Values for Members of Various Molecular Pathways

Number of Genes in Pathway	Average (No Omentectomy; 6 vs. 0 Mo)	Average (Yes Omentectomy; 6 vs. 0 Mo)	Average (No Omentectomy; 12 vs. 0 Mo)	Average (Yes Omentectomy; 12 vs. 0 Mo)	Pathway Number	Pathway
137	9.14E-01	6.97E-01	7.59E-01	5.90E-01	86	Metabolic pathways
43	9.20E-01	1.07E+00	8.42E-01	8.58E-01	105	Cytokine-cytokine receptor interaction
42	1.05E+00	1.04E+00	8.84E-01	8.17E-01	102	MAPK signaling pathway
38	8.89E-01	1.02E+00	7.71E-01	7.92E-01	106	Chemokine signaling pathway
36	8.99E-01	7.61E-01	8.78E-01	4.48E-01	93	Spliceosome
30	1.01E+00	1.04E+00	8.46E-01	6.78E-01	109	Cell cycle
29	9.83E-01	8.91E-01	7.71E-01	5.96E-01	131	Focal adhesion
29	1.12E+00	7.21E-01	8.07E-01	5.76E-01	118	Phagosome
27	6.54E-01	8.19E-01	9.37E-01	8.10E-01	88	Ribosome
27	8.18E-01	6.45E-01	6.88E-01	4.45E-01	115	Protein processing in endoplasmic reticulum
26	1.02E+00	9.04E-01	8.51E-01	5.26E-01	112	Ubiquitin mediated proteolysis
26	8.36E-01	5.49E-01	8.07E-01	4.90E-01	157	Olfactory transduction
25	8.93E-01	1.20E+00	7.78E-01	9.39E-01	144	Jak-STAT signaling pathway
24	9.62E-01	9.08E-01	6.10E-01	4.67E-01	117	Endocytosis
24	1.09E+00	8.91E-01	9.23E-01	6.10E-01	124	Wnt signaling pathway
24	8.55E-01	8.13E-01	6.58E-01	5.04E-01	160	Regulation of actin cytoskeleton
24	9.86E-01	7.11E-01	7.76E-01	5.69E-01	104	Calcium signaling pathway
22	8.33E-01	6.23E-01	5.48E-01	5.41E-01	190	Toxoplasmosis
21	9.58E-01	1.18E+00	8.80E-01	9.91E-01	140	Toll-like receptor signaling pathway
20	1.01E+00	1.07E+00	6.96E-01	7.26E-01	161	Insulin signaling pathway
20	8.59E-01	1.00E+00	7.24E-01	8.32E-01	191	Amoebiasis
20	6.18E-01	7.68E-01	8.63E-01	7.26E-01	178	Parkinson's disease
20	8.36E-01	7.22E-01	9.30E-01	6.61E-01	177	Alzheimer's disease
20	8.02E-01	6.40E-01	9.49E-01	5.70E-01	16	Oxidative phosphorylation
19	1.24E+00	1.15E+00	9.73E-01	7.86E-01	128	TGF-beta signaling pathway
19	7.88E-01	7.85E-01	8.57E-01	7.47E-01	180	Huntington's disease
19	9.64E-01	7.75E-01	9.79E-01	5.14E-01	110	Oocyte meiosis
19	8.83E-01	7.69E-01	7.36E-01	5.49E-01	17	Purine metabolism
19	8.45E-01	7.31E-01	6.83E-01	4.37E-01	135	Tight junction
19	9.66E-01	7.18E-01	7.45E-01	5.82E-01	175	Pancreatic secretion
19	1.13E+00	7.17E-01	8.89E-01	4.41E-01	123	Vascular smooth muscle contraction
18	7.13E-01	8.21E-01	4.81E-01	5.85E-01	151	Leukocyte transendothelial migration
18	8.53E-01	7.33E-01	6.91E-01	5.18E-01	155	Neurotrophin signaling pathway
18	9.09E-01	5.87E-01	8.15E-01	4.06E-01	108	Neuroactive ligand-receptor interaction
17	1.15E+00	1.64E+00	1.08E+00	1.37E+00	188	Chagas disease
17	9.31E-01	8.29E-01	7.33E-01	5.54E-01	184	Epithelial cell signaling in Helicobacter pylori infection
17	9.02E-01	7.05E-01	7.09E-01	5.47E-01	107	Phosphatidylinositol signaling system
17	7.78E-01	5.49E-01	7.84E-01	4.91E-01	209	Systemic lupus erythematosus
16	1.01E+00	9.96E-01	8.22E-01	5.38E-01	89	RNA degradation
16	1.05E+00	9.14E-01	7.64E-01	5.83E-01	129	Axon guidance
16	1.10E+00	8.44E-01	7.67E-01	6.57E-01	173	Salivary secretion
16	8.73E-01	7.83E-01	7.85E-01	6.71E-01	133	Cell adhesion molecules (CAMs)
16	1.00E+00	7.17E-01	8.60E-01	5.44E-01	162	GnRH signaling pathway
16	9.75E-01	6.75E-01	8.64E-01	4.24E-01	163	Progesterone-mediated oocyte maturation
15	1.10E+00	1.70E+00	1.09E+00	1.69E+00	189	Malaria
15	1.17E+00	1.58E+00	1.06E+00	1.32E+00	141	NOD-like receptor signaling pathway
15	1.15E+00	1.14E+00	9.53E-01	9.78E-01	213	Hypertrophic cardiomyopathy (HCM)
15	1.01E+00	1.07E+00	8.10E-01	8.19E-01	103	ErbB signaling pathway
15	9.86E-01	9.38E-01	9.20E-01	7.29E-01	147	T cell receptor signaling pathway
15	8.68E-01	8.62E-01	7.59E-01	7.30E-01	96	PPAR signaling pathway
15	8.38E-01	6.76E-01	8.95E-01	5.02E-01	119	Peroxisome
15	9.53E-01	6.55E-01	8.99E-01	6.00E-01	81	Aminoacyl-tRNA biosynthesis
15	8.74E-01	6.46E-01	5.78E-01	4.95E-01	150	Fc gamma R-mediated phagocytosis
14	9.94E-01	1.38E+00	7.73E-01	1.08E+00	111	p53 signaling pathway
14	9.74E-01	8.72E-01	8.50E-01	7.32E-01	174	Gastric acid secretion
14	9.14E-01	8.56E-01	6.31E-01	5.65E-01	214	Arrhythmogenic right ventricular cardiomyopathy (ARVC)
14	1.02E+00	8.14E-01	8.49E-01	6.64E-01	215	Dilated cardiomyopathy
14	8.53E-01	7.73E-01	7.78E-01	6.14E-01	146	Natural killer cell mediated cytotoxicity
14	9.47E-01	7.47E-01	7.98E-01	7.29E-01	116	Lysosome

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Number of Genes in Pathway	Average (No Omentectomy; 6 vs. 0 Mo)	Average (Yes Omentectomy; 6 vs. 0 Mo)	Average (No Omentectomy; 12 vs. 0 Mo)	Average (Yes Omentectomy; 12 vs. 0 Mo)	Pathway Number	Pathway
14	9.78E-01	7.26E-01	8.47E-01	4.73E-01	164	Melanogenesis
13	1.19E+00	1.09E+00	9.69E-01	7.07E-01	132	ECM-receptor interaction
13	1.01E+00	8.89E-01	8.71E-01	8.39E-01	187	Leishmaniasis
13	7.48E-01	8.12E-01	7.23E-01	5.75E-01	194	Renal cell carcinoma
12	7.92E-01	1.02E+00	8.38E-01	9.49E-01	122	Cardiac muscle contraction
12	1.04E+00	9.51E-01	9.34E-01	7.27E-01	148	B cell receptor signaling pathway
12	9.02E-01	8.57E-01	7.57E-01	6.59E-01	19	Pyrimidine metabolism
12	7.83E-01	8.52E-01	7.44E-01	5.33E-01	98	Nucleotide excision repair
12	9.57E-01	8.44E-01	8.04E-01	6.22E-01	197	Glioma
12	9.54E-01	7.59E-01	7.55E-01	4.29E-01	198	Prostate cancer
12	9.74E-01	7.44E-01	7.10E-01	5.29E-01	52	Inositol phosphate metabolism
12	8.41E-01	6.62E-01	9.50E-01	4.67E-01	216	Viral myocarditis
12	8.87E-01	6.18E-01	5.93E-01	4.68E-01	149	Fc epsilon RI signaling pathway
12	1.12E+00	6.15E-01	8.82E-01	5.69E-01	54	Glycerophospholipid metabolism
12	1.12E+00	5.93E-01	7.24E-01	3.99E-01	156	Long-term depression
12	9.55E-01	5.63E-01	8.00E-01	4.35E-01	183	Vibrio cholerae infection
12	1.11E+00	4.04E-01	1.02E+00	3.71E-01	138	Antigen processing and presentation
11	9.20E-01	1.16E+00	6.36E-01	8.49E-01	166	Type II diabetes mellitus
11	8.74E-01	1.09E+00	8.93E-01	1.11E+00	145	Hematopoietic cell lineage
11	9.68E-01	1.05E+00	6.99E-01	6.81E-01	186	Shigellosis
11	8.84E-01	9.20E-01	6.49E-01	6.44E-01	204	Acute myeloid leukemia
11	1.07E+00	8.55E-01	8.49E-01	4.38E-01	136	Gap junction
11	7.55E-01	7.89E-01	6.00E-01	2.83E-01	134	Adherens junction
11	8.81E-01	7.44E-01	6.45E-01	3.83E-01	195	Pancreatic cancer
11	7.94E-01	6.93E-01	6.42E-01	6.32E-01	130	VEGF signaling pathway
11	7.34E-01	5.14E-01	9.64E-01	5.10E-01	94	Proteasome
10	1.14E+00	1.13E+00	8.39E-01	9.08E-01	165	Adipocytokine signaling pathway
10	8.47E-01	1.13E+00	7.29E-01	1.04E+00	137	Complement and coagulation cascades
10	9.65E-01	1.05E+00	7.84E-01	7.78E-01	203	Chronic myeloid leukemia
10	5.95E-01	8.38E-01	4.96E-01	7.29E-01	121	Apoptosis
10	9.15E-01	8.04E-01	7.19E-01	4.59E-01	142	RIG-I-like receptor signaling pathway
9	1.19E+00	1.46E+00	1.15E+00	1.18E+00	193	Colorectal cancer
9	1.11E+00	6.94E-01	9.44E-01	4.68E-01	154	Long-term potentiation
9	8.31E-01	8.45E-01	6.20E-01	5.28E-01	201	Melanoma
9	8.25E-01	7.49E-01	6.29E-01	5.75E-01	169	Aldosterone-regulated sodium reabsorption
9	6.99E-01	8.96E-01	7.35E-01	8.47E-01	205	Small cell lung cancer
8	1.06E+00	8.96E-01	7.96E-01	7.39E-01	83	Drug metabolism - cytochrome P450
8	9.91E-01	8.99E-01	7.68E-01	4.61E-01	87	ABC transporters
8	8.93E-01	8.57E-01	6.23E-01	4.76E-01	185	Pathogenic Escherichia coli infection
8	8.76E-01	6.89E-01	6.82E-01	4.63E-01	120	mTOR signaling pathway
8	8.53E-01	7.08E-01	6.34E-01	4.06E-01	206	Non-small cell lung cancer
8	8.50E-01	8.40E-01	6.78E-01	6.88E-01	39	Glutathione metabolism
8	8.45E-01	6.90E-01	8.27E-01	5.21E-01	91	Basal transcription factors
8	8.35E-01	1.19E+00	5.06E-01	7.76E-01	182	Bacterial invasion of epithelial cells
8	8.13E-01	4.51E-01	7.39E-01	4.88E-01	56	Arachidonic acid metabolism
8	7.41E-01	5.90E-01	6.69E-01	4.16E-01	41	N-Glycan biosynthesis
8	6.61E-01	1.10E+00	4.22E-01	8.29E-01	176	Carbohydrate digestion and absorption
7	1.22E+00	6.50E-01	9.09E-01	7.44E-01	27	Arginine and proline metabolism
7	1.06E+00	1.04E+00	7.12E-01	5.85E-01	5	Fructose and mannose metabolism
7	9.99E-01	1.27E+00	9.49E-01	1.14E+00	143	Cytosolic DNA-sensing pathway
7	9.74E-01	1.14E+00	6.11E-01	8.45E-01	71	Nicotinate and nicotinamide metabolism
7	8.87E-01	1.18E+00	6.56E-01	7.80E-01	196	Endometrial cancer
7	8.87E-01	7.79E-01	8.61E-01	8.13E-01	82	Metabolism of xenobiotics by cytochrome P450
7	8.62E-01	8.86E-01	4.18E-01	6.29E-01	40	Starch and sucrose metabolism
7	8.21E-01	5.72E-01	5.44E-01	5.45E-01	200	Basal cell carcinoma
7	7.71E-01	9.63E-01	7.45E-01	5.94E-01	113	SNARE interactions in vesicular transport
7	7.27E-01	1.00E+00	5.18E-01	5.35E-01	45	Amino sugar and nucleotide sugar metabolism
6	1.28E+00	1.90E+00	9.61E-01	1.73E+00	202	Bladder cancer
6	1.21E+00	6.18E-01	1.19E+00	4.30E-01	2	Citrate cycle (TCA cycle)

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6	1.19E+00	6.51E-01	9.14E-01	5.93E-01	10	Fatty acid metabolism
6	1.12E+00	7.92E-01	8.20E-01	4.05E-01	170	Vasopressin-regulated water reabsorption
6	1.04E+00	7.63E-01	9.80E-01	7.59E-01	29	Tyrosine metabolism
6	9.87E-01	8.30E-01	9.36E-01	7.60E-01	153	Circadian rhythm - mammal
6	9.04E-01	7.86E-01	5.98E-01	6.78E-01	127	Hedgehog signaling pathway
6	8.17E-01	6.79E-01	8.13E-01	7.31E-01	97	Base excision repair
6	7.38E-01	9.61E-01	7.44E-01	6.01E-01	95	Protein export
6	7.04E-01	8.84E-01	7.33E-01	7.48E-01	92	DNA replication
5	1.34E+00	1.12E+00	1.49E+00	1.20E+00	211	Graft-versus-host disease
5	1.14E+00	6.73E-01	9.46E-01	5.31E-01	23	Valine, leucine and isoleucine degradation
5	1.14E+00	1.10E+00	9.20E-01	8.76E-01	199	Thyroid cancer
5	1.14E+00	1.19E+00	1.37E+00	1.14E+00	152	Intestinal immune network for IgA production
5	1.07E+00	3.07E-01	5.44E-01	3.98E-01	84	Drug metabolism - other enzymes
5	1.04E+00	4.30E-01	8.74E-01	4.87E-01	15	Steroid hormone biosynthesis
5	1.01E+00	9.74E-01	8.23E-01	9.34E-01	20	Alanine, aspartate and glutamate metabolism
5	9.92E-01	6.71E-01	8.52E-01	5.92E-01	55	Ether lipid metabolism
5	9.59E-01	6.14E-01	4.03E-01	7.53E-01	76	Retinol metabolism
5	8.82E-01	4.16E-01	6.08E-01	4.41E-01	172	Collecting duct acid secretion
5	7.86E-01	9.34E-01	5.04E-01	4.55E-01	158	Taste transduction
5	5.25E-01	9.15E-01	3.50E-01	9.09E-01	53	Glycosylphosphatidylinositol(GPI)-anchor biosynthesis
4	1.39E+00	2.88E+00	1.61E+00	2.70E+00	181	Prion diseases
4	1.30E+00	8.40E-01	1.01E+00	6.89E-01	28	Histidine metabolism
4	9.89E-01	6.39E-01	9.83E-01	4.63E-01	65	Propanoate metabolism
4	8.80E-01	4.29E-01	5.91E-01	8.34E-01	77	Porphyrin and chlorophyll metabolism
4	8.76E-01	5.19E-01	9.75E-01	9.51E-01	21	Glycine, serine and threonine metabolism
4	8.53E-01	5.64E-01	7.66E-01	6.23E-01	58	alpha-Linolenic acid metabolism
4	8.46E-01	1.52E-01	1.10E+00	1.23E-01	208	Autoimmune thyroid disease
4	8.37E-01	2.93E-01	7.30E-01	2.18E-01	212	Primary immunodeficiency
4	8.26E-01	4.10E-01	6.13E-01	3.83E-01	179	Amyotrophic lateral sclerosis (ALS)
4	7.67E-01	9.83E-01	7.29E-01	4.86E-01	100	Homologous recombination
4	7.63E-01	4.30E-01	4.94E-01	4.57E-01	51	Glycerolipid metabolism
4	4.89E-01	9.76E-01	2.69E-01	3.40E-01	101	Non-homologous end-joining
4	4.63E-01	9.41E-01	4.84E-01	9.43E-01	60	Glycosphingolipid biosynthesis - lacto and neolacto series
3	1.53E+00	1.30E+00	1.37E+00	9.49E-01	3	Pentose phosphate pathway
3	1.34E+00	6.06E-01	1.11E+00	2.55E-01	31	Tryptophan metabolism
3	1.22E+00	6.99E-01	1.06E+00	8.23E-01	30	Phenylalanine metabolism
3	1.19E+00	8.49E-01	7.50E-01	4.44E-01	114	Regulation of autophagy
3	1.09E+00	9.88E-01	8.43E-01	9.23E-01	4	Pentose and glucuronate interconversions
3	1.08E+00	5.84E-01	9.26E-01	6.48E-01	22	Cysteine and methionine metabolism
3	1.05E+00	1.36E+00	9.64E-01	7.87E-01	1	Glycolysis / Gluconeogenesis
3	1.02E+00	7.54E-01	8.32E-01	6.52E-01	24	Valine, leucine and isoleucine biosynthesis
3	9.77E-01	1.59E-01	8.58E-01	3.91E-01	64	Glyoxylate and dicarboxylate metabolism
3	9.25E-01	5.18E-01	5.56E-01	3.04E-01	43	O-Glycan biosynthesis
3	9.09E-01	1.07E-01	1.07E+00	8.14E-02	167	Type I diabetes mellitus
3	9.09E-01	1.07E-01	1.07E+00	8.14E-02	210	Allograft rejection
3	8.98E-01	1.25E+00	9.33E-01	9.02E-01	13	Primary bile acid biosynthesis
3	8.88E-01	5.77E-01	6.73E-01	6.62E-01	57	Linoleic acid metabolism
3	8.76E-01	5.46E-01	8.13E-01	5.58E-01	33	beta-Alanine metabolism
3	8.40E-01	1.07E+00	9.49E-01	1.16E+00	79	Nitrogen metabolism
3	8.34E-01	7.38E-01	5.91E-01	5.97E-01	35	Selenoamino acid metabolism
3	8.23E-01	5.88E-01	6.63E-01	4.54E-01	26	Lysine degradation
3	8.22E-01	9.01E-01	5.44E-01	8.71E-01	168	Maturity onset diabetes of the young
3	7.88E-01	4.18E-01	8.17E-01	5.51E-01	67	One carbon pool by folate
3	7.84E-01	1.04E+00	5.48E-01	1.01E+00	171	Proximal tubule bicarbonate reclamation
3	7.81E-01	9.13E-01	5.65E-01	5.68E-01	125	Dorso-ventral axis formation
3	7.22E-01	1.13E+00	7.16E-01	7.38E-01	99	Mismatch repair
3	3.80E-01	8.50E-01	5.03E-01	7.60E-01	126	Notch signaling pathway
2	1.25E+00	7.64E-01	9.77E-01	4.51E-01	139	Renin-angiotensin system
2	1.15E+00	8.84E-01	8.31E-01	7.90E-01	90	RNA polymerase

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2	1.03E+00	1.01E+00	8.05E-01	7.59E-01	75	Folate biosynthesis
2	9.57E-01	3.77E-01	1.07E+00	3.60E-01	207	Asthma
2	8.94E-01	5.61E-01	8.80E-01	4.28E-01	62	Glycosphingolipid biosynthesis - ganglio series
2	8.94E-01	9.70E-01	6.25E-01	5.87E-01	159	Phototransduction
2	7.05E-01	9.65E-01	5.62E-01	3.13E-01	49	Glycosaminoglycan biosynthesis - keratan sulfate
2	6.83E-01	6.16E-01	1.76E-01	8.56E-01	7	Ascorbate and aldarate metabolism
2	6.06E-01	1.61E+00	9.03E-01	1.05E+00	85	Biosynthesis of unsaturated fatty acids
1	1.34E+00	5.47E-01	1.07E+00	2.52E-01	73	Biotin metabolism
1	1.19E+00	3.19E-02	5.74E-01	1.69E-01	36	Cyanoamino acid metabolism
1	1.12E+00	5.44E-01	9.68E-01	8.05E-01	32	Phenylalanine, tyrosine and tryptophan biosynthesis
1	1.01E+00	3.55E-01	2.79E-01	1.22E-02	18	Caffeine metabolism
1	1.01E+00	1.31E-01	1.14E+00	1.96E-01	11	Synthesis and degradation of ketone bodies
1	1.01E+00	1.31E-01	1.14E+00	1.96E-01	66	Butanoate metabolism
1	1.01E+00	1.31E-01	1.14E+00	1.96E-01	78	Terpenoid backbone biosynthesis
1	8.36E-01	1.68E+00	3.91E-01	6.74E-01	6	Galactose metabolism
1	8.36E-01	1.68E+00	3.91E-01	6.74E-01	46	Butirosin and neomycin biosynthesis
1	6.63E-01	8.69E-02	1.00E+00	2.89E-01	61	Glycosphingolipid biosynthesis - globo series
1	4.60E-01	7.70E-01	6.15E-01	1.19E+00	14	Ubiquinone and other terpenoid-quinone biosynthesis
1	3.83E-01	1.19E+00	1.51E-01	8.73E-01	59	Sphingolipid metabolism
1	1.96E-01	8.85E-01	6.72E-01	1.17E+00	70	Vitamin B6 metabolism
1	1.77E-01	3.31E-01	2.01E-01	1.48E+00	80	Sulfur metabolism
1	1.48E-01	5.69E-01	4.94E-02	1.08E+00	48	Glycosaminoglycan biosynthesis - chondroitin sulfate
1	1.48E-01	5.69E-01	4.94E-02	1.08E+00	50	Glycosaminoglycan biosynthesis - heparan sulfate