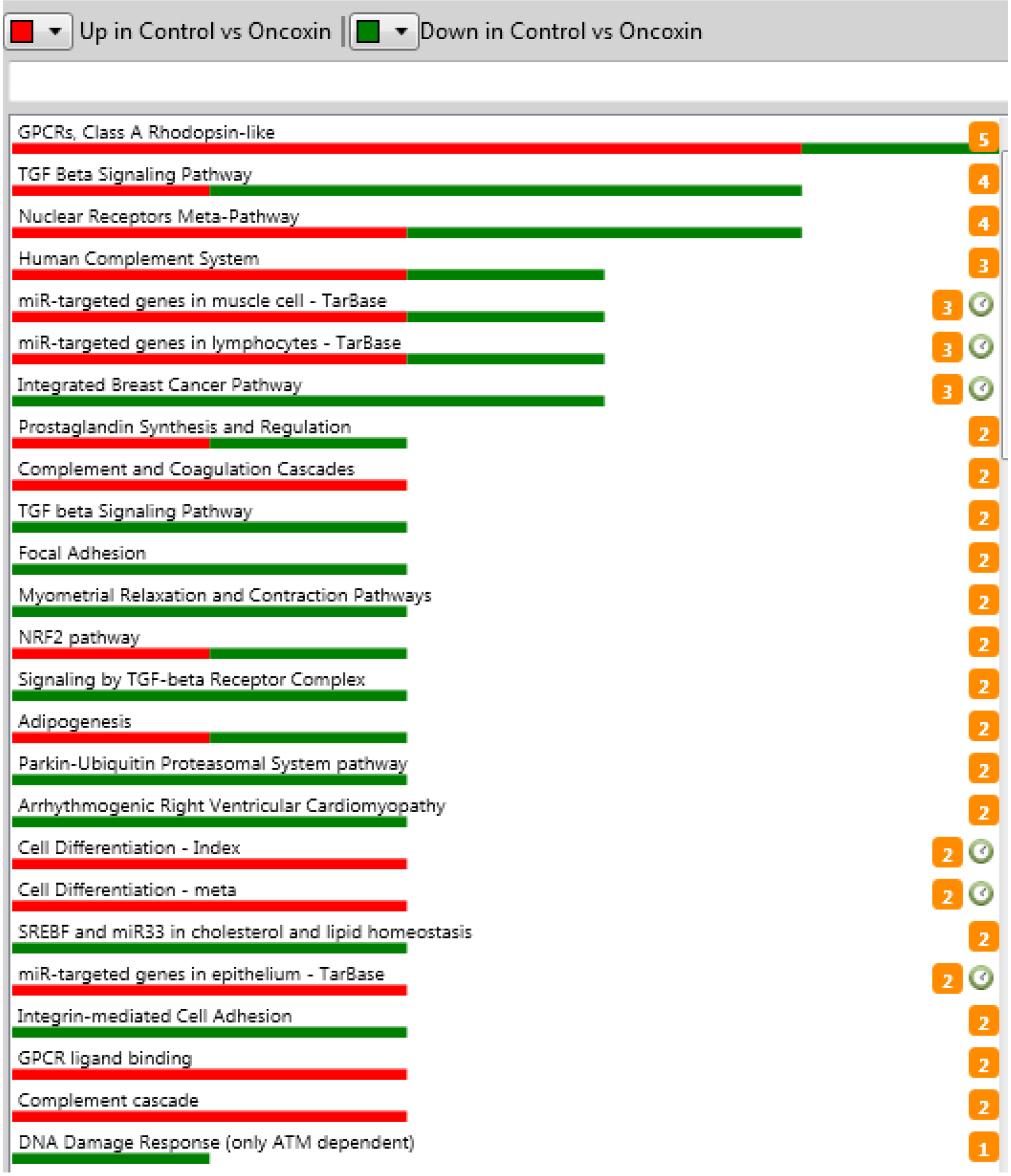
SUPPLEMENTARY TABLE AND FIGURE

Supplementary Table S1: In vivo effect of OOS on gene expression profiles. The gene expression profile of three control tumors was compared to that of three tumors treated with 100 µl of OOS. A list with those genes whose expression changed above 1.5 times with the treatment is shown in the table.

See Supplentary table 1



🟥 Up in Control vs Oncoxin | 🟩 Down in Control vs Oncoxin

GPCRs, Class A Rhodopsin-like	5
TGF Beta Signaling Pathway	4
Nuclear Receptors Meta-Pathway	4
Human Complement System	3
miR-targeted genes in muscle cell - TarBase	3
miR-targeted genes in lymphocytes - TarBase	3
Integrated Breast Cancer Pathway	3
Prostaglandin Synthesis and Regulation	2
Complement and Coagulation Cascades	2
TGF beta Signaling Pathway	2
Focal Adhesion	2
Myometrial Relaxation and Contraction Pathways	2
NRF2 pathway	2
Signaling by TGF-beta Receptor Complex	2
Adipogenesis	2
Parkin-Ubiquitin Proteasomal System pathway	2
Arrhythmogenic Right Ventricular Cardiomyopathy	2
Cell Differentiation - Index	2
Cell Differentiation - meta	2
SREBF and miR33 in cholesterol and lipid homeostasis	2
miR-targeted genes in epithelium - TarBase	2
Integrin-mediated Cell Adhesion	2
GPCR ligand binding	2
Complement cascade	2
DNA Damage Response (only ATM dependent)	1

(*Continued*)

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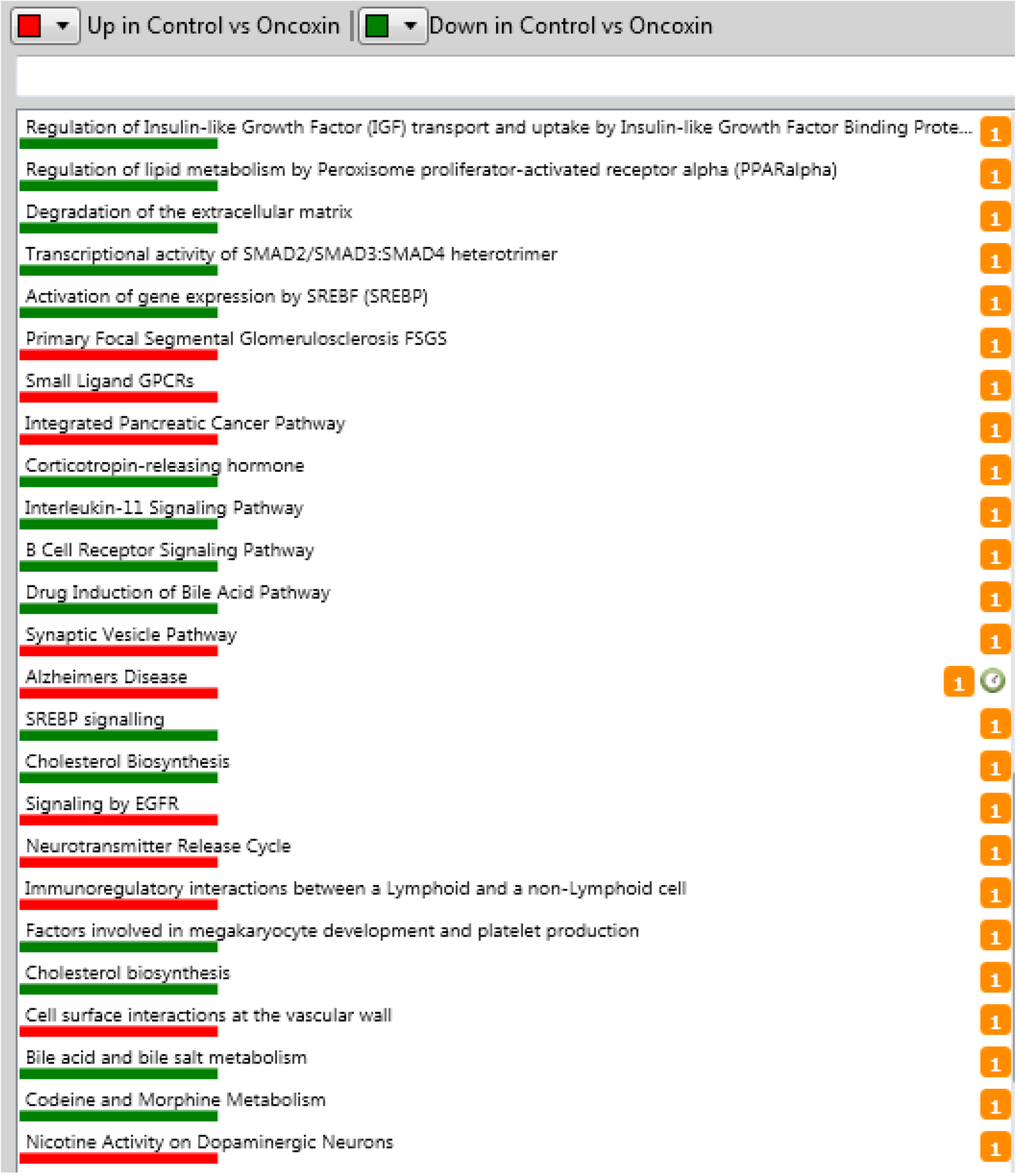
Metapathway biotransformation	🟥	1
Senescence and Autophagy in Cancer	🟩	1
Notch Signaling Pathway	🟩	1
Calcium Regulation in the Cardiac Cell	🟩	1
Endochondral Ossification	🟩	1
Wnt Signaling Pathway	🟩	1
Wnt Signaling Pathway and Pluripotency	🟩	1
Striated Muscle Contraction	🟥	1
Fatty Acid Biosynthesis	🟩	1
XBP1(S) activates chaperone genes	🟩	1
EV release from cardiac cells and their functional effects	🟩	1
Triacylglyceride Synthesis	🟩	1
Nuclear Receptors in Lipid Metabolism and Toxicity	🟩	1
Glucocorticoid Receptor Pathway	🟥	1
Vitamin D Receptor Pathway	🟩	1
Pregnane X Receptor pathway	🟩	1
Constitutive Androstane Receptor Pathway	🟩	1
Liver X Receptor Pathway	🟩	1
Apoptosis-related network due to altered Notch3 in ovarian cancer	🟩	1
Ectoderm Differentiation	🟥	1
Mesodermal Commitment Pathway	🟩	1
Dopaminergic Neurogenesis	🟥	1
Amyotrophic lateral sclerosis (ALS) SOD1 - CHMP2B MODEL	🟩	1
Hair Follicle Development: Cytodifferentiation (Part 3 of 3)	🟩	1
Mammary gland development pathway - Puberty (Stage 2 of 4)	🟩	1

(*Continued*)



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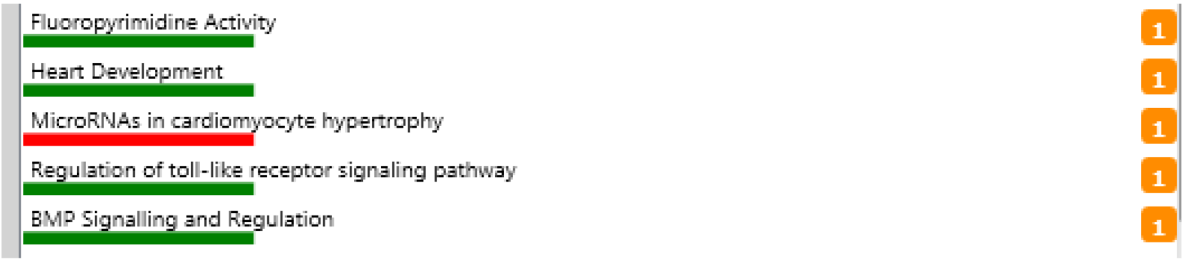
- Regulation of Insulin-like Growth Factor (IGF) transport and uptake by Insulin-like Growth Factor Binding Prote... 🟩 1
- Regulation of lipid metabolism by Peroxisome proliferator-activated receptor alpha (PPARalpha) 🟩 1
- Degradation of the extracellular matrix 🟩 1
- Transcriptional activity of SMAD2/SMAD3:SMAD4 heterotrimer 🟩 1
- Activation of gene expression by SREBF (SREBP) 🟩 1
- Primary Focal Segmental Glomerulosclerosis FSGS 🟥 1
- Small Ligand GPCRs 🟥 1
- Integrated Pancreatic Cancer Pathway 🟥 1
- Corticotropin-releasing hormone 🟩 1
- Interleukin-11 Signaling Pathway 🟩 1
- B Cell Receptor Signaling Pathway 🟩 1
- Drug Induction of Bile Acid Pathway 🟩 1
- Synaptic Vesicle Pathway 🟥 1
- Alzheimers Disease 🟥 1
- SREBP signalling 🟩 1
- Cholesterol Biosynthesis 🟩 1
- Signaling by EGFR 🟥 1
- Neurotransmitter Release Cycle 🟥 1
- Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell 🟥 1
- Factors involved in megakaryocyte development and platelet production 🟩 1
- Cholesterol biosynthesis 🟩 1
- Cell surface interactions at the vascular wall 🟥 1
- Bile acid and bile salt metabolism 🟩 1
- Codeine and Morphine Metabolism 🟩 1
- Nicotine Activity on Dopaminergic Neurons 🟥 1

(*Continued*)



Fluoropyrimidine Activity	🟩	1
Heart Development	🟩	1
MicroRNAs in cardiomyocyte hypertrophy	🟥	1
Regulation of toll-like receptor signaling pathway	🟩	1
BMP Signalling and Regulation	🟩	1

Supplementary Figure S1: Pathways in vivo deregulated after OOS treatment. Genes found to be deregulated al least 1.5 times in the Affimetrix Expression Console were analyzed with the same software to evaluate the pathways in which gene expression is altered. Below each altered pathway, genes upregulated in the control condition (red) or after OOS treatment (green), are shown. Besides, the total number of genes deregulated in a given pathway are shown in an orange box at the end of each line.