

Supplemental Materials

Table S1. The most significant regulated genes by 8-OHD (100 μ M) in K562 cells.

ID	Symbol	log ₂ FC	p Value	q Value
4017	<i>LOXL2</i>	7.54	2.26E-05	5.02E-03
2051	<i>EPHB6</i>	5.16	7.95E-05	6.12E-03
885	<i>CCK</i>	4.89	3.77E-06	3.78E-03
6281	<i>S100A10</i>	4.89	1.76E-04	7.72E-03
3866	<i>KRT15</i>	4.88	2.63E-05	5.26E-03
1294	<i>COL7A1</i>	4.83	3.83E-04	9.43E-03
2669	<i>GEM</i>	4.58	1.11E-04	6.82E-03
1191	<i>CLU</i>	4.45	6.57E-07	2.77E-03
221476	<i>PI16</i>	4.45	1.47E-06	2.77E-03
5054	<i>SERPINE1</i>	4.38	2.40E-05	5.15E-03
9610	<i>RIN1</i>	4.31	3.48E-05	5.32E-03
3566	<i>IL4R</i>	4.31	4.98E-04	1.06E-02
3604	<i>TNFRSF9</i>	4.15	3.24E-04	9.02E-03
10381	<i>TUBB3</i>	4.12	3.92E-05	5.34E-03
5329	<i>PLAUR</i>	4.11	9.85E-04	1.32E-02
969	<i>CD69</i>	-3.82	1.02E-04	6.56E-03
6941	<i>TCF19</i>	-3.85	1.40E-05	4.50E-03
492307	<i>C8orf22</i>	-3.91	6.81E-04	1.15E-02
55274	<i>PHF10</i>	-4.03	2.10E-04	7.99E-03
7923	<i>HSD17B8</i>	-4.07	1.39E-03	1.51E-02
6296	<i>ACSM3</i>	-4.07	5.43E-04	1.08E-02
138311	<i>FAM69B</i>	-4.10	1.85E-04	7.80E-03
55808	<i>ST6GALNAC1</i>	-4.21	1.41E-04	7.26E-03
462	<i>SERPINC1</i>	-4.26	1.87E-04	7.80E-03
159989	<i>CCDC67</i>	-4.47	2.29E-04	8.02E-03
1572	<i>CYP2F1</i>	-4.65	3.50E-05	5.32E-03
445	<i>ASS1</i>	-4.73	4.02E-06	3.78E-03
138255	<i>C9orf135</i>	-4.73	7.93E-04	1.21E-02
83729	<i>INHBE</i>	-4.94	1.18E-05	4.35E-03
57520	<i>HECW2</i>	-6.01	8.33E-04	1.22E-02

Table S2. Overrepresented gene sets in DAVID GO BP DIRECT annotations database obtained from comparisons in gene expression profiles between 100 μ M 8-OHD treatment vs. vehicle control ($p < 0.05$ and minimal number of genes per group ≥ 30).

Term	Count	%	p value
GO:0007264~small GTPase mediated signal transduction	58	1.83	2.81E-03
GO:0006914~autophagy	35	1.10	3.81E-03
GO:0006366~transcription from RNA polymerase II promoter	107	3.37	4.26E-03
GO:0045944~positive regulation of transcription from RNA polymerase II promoter	189	5.95	6.43E-03
GO:0006468~protein phosphorylation	95	2.99	7.27E-03
GO:0006357~regulation of transcription from RNA polymerase II promoter	92	2.90	7.94E-03
GO:0007568~aging	40	1.26	8.53E-03
GO:0008360~regulation of cell shape	35	1.10	8.83E-03
GO:0045893~positive regulation of transcription, DNA-templated	105	3.31	9.12E-03
GO:0006461~protein complex assembly	30	0.95	9.87E-03
GO:0042127~regulation of cell proliferation	43	1.35	1.32E-02
GO:0006886~intracellular protein transport	52	1.64	1.77E-02
GO:0051607~defense response to virus	38	1.20	2.29E-02
GO:0060271~cilium morphogenesis	32	1.01	2.84E-02
GO:0006351~transcription, DNA-templated	348	10.96	2.92E-02
GO:0006397~mRNA processing	40	1.26	3.06E-02
GO:0051092~positive regulation of NF-kappaB transcription factor activity	31	0.98	3.49E-02
GO:0042981~regulation of apoptotic process	46	1.45	3.50E-02
GO:0042493~response to drug	62	1.95	4.28E-02
GO:0008283~cell proliferation	73	2.30	4.42E-02
GO:0001525~angiogenesis	47	1.48	4.78E-02

Table S3. The KEGG pathways associated with 100 μ M 8-OHD treatment in K562 cells

KEGG Pathway	gene count	%	<i>p</i> Value
hsa01100:Metabolic pathways	261	8.223	4.82E-07
hsa00760:Nicotinate and nicotinamide metabolism	15	0.473	6.55E-05
hsa04142:Lysosome	37	1.166	1.67E-04
hsa03018:RNA degradation	24	0.756	2.27E-03
hsa05231:Choline metabolism in cancer	29	0.914	2.77E-03
hsa04146:Peroxisome	25	0.788	2.97E-03
hsa05202:Transcriptional misregulation in cancer	42	1.323	4.20E-03
hsa01230:Biosynthesis of amino acids	22	0.693	4.72E-03
hsa05211:Renal cell carcinoma	20	0.630	8.16E-03
hsa01200:Carbon metabolism	29	0.914	1.43E-02
hsa01130:Biosynthesis of antibiotics	48	1.512	1.67E-02
hsa04950:Maturity onset diabetes of the young	10	0.315	1.87E-02
hsa05120:Epithelial cell signaling in Helicobacter pylori infection	19	0.599	2.03E-02
hsa04010:MAPK signaling pathway	55	1.733	2.24E-02
hsa04966:Collecting duct acid secretion	10	0.315	2.41E-02
hsa04152:AMPK signaling pathway	30	0.945	2.48E-02
hsa04662:B cell receptor signaling pathway	19	0.599	2.71E-02
hsa04666:Fc gamma R-mediated phagocytosis	22	0.693	2.83E-02
hsa00600:Sphingolipid metabolism	14	0.441	3.58E-02
hsa05323:Rheumatoid arthritis	22	0.693	4.52E-02
hsa05166:HTLV-I infection	53	1.670	4.93E-02

Table S4. The BioCarta pathways associated with 100 μ M 8-OHD treatment in K562 cells

BioCarta pathway	gene count	%	<i>p</i> Value
Signaling Pathway from G-Protein Families	15	0.473	1.07E-03
Signaling of Hepatocyte Growth Factor Receptor	15	0.473	2.07E-03
NFAT and Hypertrophy of the heart (Transcription in the broken heart)	19	0.599	3.77E-03
Fc Epsilon Receptor I Signaling in Mast Cells	15	0.473	4.91E-03
TPO Signaling Pathway	11	0.347	5.09E-03
PDGF Signaling Pathway	12	0.378	5.69E-03
Mechanism of Gene Regulation by Peroxisome Proliferators via PPAR α (alpha)	18	0.567	6.06E-03
IGF-1 Signaling Pathway	10	0.315	6.28E-03
T Cell Receptor Signaling Pathway	16	0.504	6.34E-03
MAPKinase Signaling Pathway	26	0.819	6.61E-03
The IGF-1 Receptor and Longevity	8	0.252	9.19E-03
BCR Signaling Pathway	13	0.410	1.05E-02
Effects of calcineurin in Keratinocyte Differentiation	9	0.284	1.12E-02
Inhibition of Cellular Proliferation by Gleevec	10	0.315	1.25E-02
EGF Signaling Pathway	11	0.347	1.33E-02
IL-2 Receptor Beta Chain in T cell Activation	14	0.441	1.33E-02
Insulin Signaling Pathway	9	0.284	2.18E-02
Control of skeletal myogenesis by HDAC & calcium/calmodulin-dependent kinase (CaMK)	11	0.347	2.26E-02
METS affect on Macrophage Differentiation	8	0.252	2.80E-02
Role of Erk5 in Neuronal Survival	8	0.252	2.80E-02
Regulation of BAD phosphorylation	10	0.315	2.93E-02
B Cell Survival Pathway	7	0.221	3.60E-02
Corticosteroids and cardioprotection	8	0.252	3.78E-02
CXCR4 Signaling Pathway	9	0.284	4.85E-02
Nerve growth factor pathway (NGF)	8	0.252	4.96E-02

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Figure S2. MetaCore process network map showing apoptosis/anti-apoptosis mediated by external signals via MAPK and JAK/STAT in response to 8-OHD. DEGs are denoted with a circle (red=upregulation, blue =downregulation).

