

Table 3. Analysis of significant TBBPA liver transcripts and pathways (1000 mg/kg)\*

<b>Ingenuity Canonical Pathways</b>	<b>-log(p-value)</b>	<b>Ratio</b>	<b>z-score</b>	<b>Molecules</b>
Interferon Signaling	8.85E00	1.94E-01	2.449	OAS1,IRF9,STAT1,IFIT3,STAT2,ISG15,MX1
Activation of IRF by Cytosolic Pattern Recognition Receptors	4.47E00	7.94E-02	1.342	IRF9,IRF7,STAT1,STAT2,ISG15
Cell Cycle: G1/S Checkpoint Regulation	3.27E00	6.25E-02	-1.000	E2F6,GSK3B,CDKN1A,HDAC4
Cyclins and Cell Cycle Regulation	2.94E00	5.13E-02	NaN	E2F6,GSK3B,CDKN1A,HDAC4
Pancreatic Adenocarcinoma Signaling	2.46E00	3.77E-02	NaN	E2F6,RALBP1,STAT1,CDKN1A
Acetyl-CoA Biosynthesis III (from Citrate)	2.23E00	1E00	NaN	ACLY
Role of JAK1, JAK2 and TYK2 in Interferon Signaling	2.06E00	8.33E-02	NaN	STAT1,STAT2
Estrogen-mediated S-phase Entry	2.06E00	8.33E-02	NaN	E2F6,CDKN1A
JAK/Stat Signaling	2.06E00	4.17E-02	NaN	STAT1,STAT2,CDKN1A

\*Analysis using ingenuity.com.