Supplementary Data.

Supplemental Table 1. Selected parameters of STAR alignment and abundance quantification. See below.

Supplemental Figure 1. Mode calculations for Raloxifene and Resorcinol. See below.

Supplemental file 1 – Raloxifene EC_{20} vs CC_{20} DEGs using a 1.5-fold change cutoff and a padj (q) < 0.05.

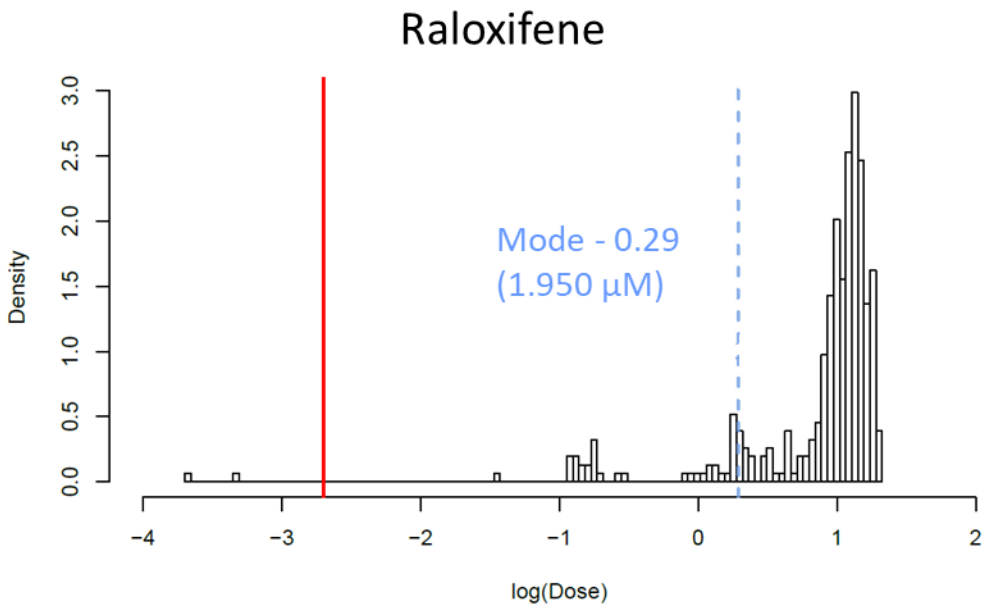
Supplemental file 2 – Resorcinol EC_{20} vs CC_{20} DEGs using a 1.5-fold change cutoff and a padj (q) < 0.05.

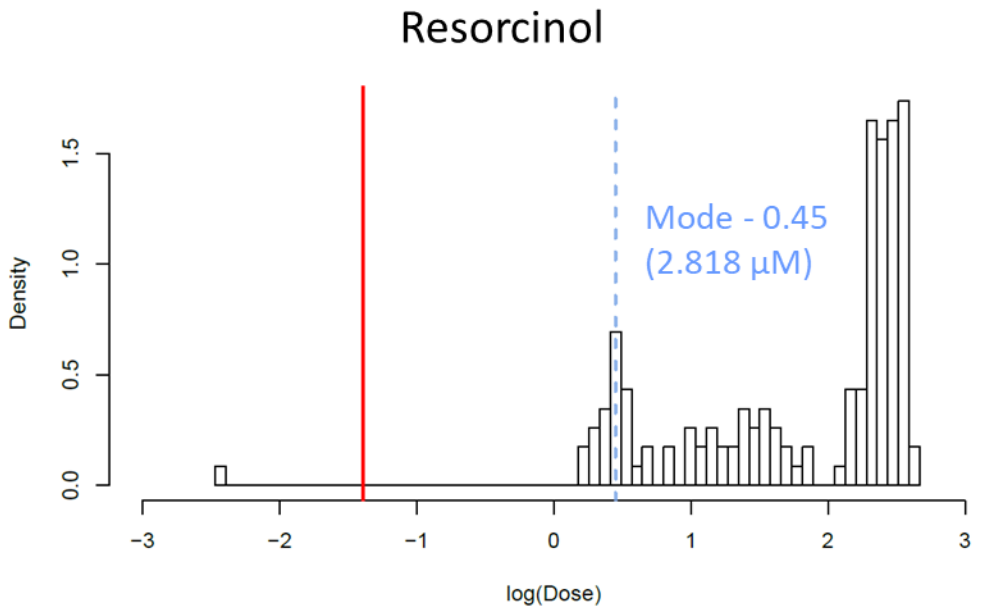
Supplemental file 3 – gProfiler result files for Raloxifene using DEGs with Fold Change > 1.5 and q < 0.05.

Supplemental file 4 – gProfiler result files for Resorcinol using DEGs with Fold Change > 1.5 and q < 0.05.

	Raloxifene	Resorcinol
	Avg	Avg
Number of input reads	14707017	15547133
UNIQUE READS:		
Uniquely mapped reads number	12169325	12872796
Uniquely mapped reads %	82.77	83.11
Average mapped length	123.48	123.48
Number of splices: Total	4118938	4595125
Number of splices: Annotated (sjdb)	4045838	4505657
Mismatch rate per base, %	0.46	0.50
Deletion rate per base	0.00	0.00
Deletion average length	2.47	2.53
Insertion rate per base	0.00	0.00
Insertion average length	2.06	2.13
MULTI-MAPPING READS:		
Number of reads mapped to multiple loci	2028176	2112342
% of reads mapped to multiple loci	13.76	13.29
UNMAPPED READS:		
% of reads unmapped: too many mismatches	0.00	0.00
% of reads unmapped: too short	2.88	2.87
% of reads unmapped: other	0.29	0.39
CHIMERIC READS:	0.00	0.00

Supplemental Table 1. Selected parameters of STAR alignment and abundance quantification.





Supplemental Figure 1. Histograms of mode values obtained from BMDExpress. Light blue hashed line indicates the first calculated mode, as well as the corresponding concentration.