

Obeticholic acid ameliorates Valproic acid-induced Hepatic Steatosis and Oxidative Stress

Zhibo Gai, Evelin Krajnc, Sophia Samodelov, Michele Visentin, Gerd A. Kullak-Ublick

Supplementary Table 1.

Gene	TaqMan Assay ID
hHPRT	Hs99999909_m1
Actin, beta	Mm00607939_s1
mShp	Mm00442278_m1
mOstbeta	Mm00619242_m1
mGsta2	Mm03019257_g1
mGpx1	Mm00656767_g1
mGpx2	Mm00850074_g1
mGpx6	Mm00513979_m1
hGPX1	Hs00829989_gH
hGCLM	Hs00157694_m1
hNQO1	Hs00168547_m1
hSOD2	Hs00167309_m1
mCyp2c39	Mm04207909_g1
mCyp2c44	Mm01197188_m1
mAcot1	Mm01622471_s1
mPparg	Mm01184322_m1

Supplementary R Script

EdgeR Bioconductor: Comparison of OCA + VPA over VPA

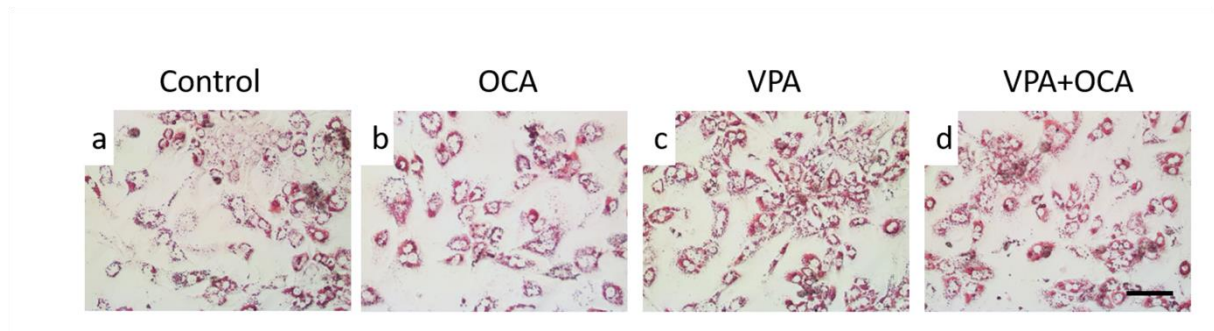
```
## R version 3.5.0 (2018-04-23)
## Platform: x86_64-pc-linux-gnu (64-bit)
## Running under: Debian GNU/Linux 8 (jessie)
##
## Matrix products: default
## BLAS: /usr/lib/libblas/libblas.so.3.0
## LAPACK: /usr/lib/lapack/liblapack.so.3.0
##
## locale:
## [1] LC_CTYPE=en_US.UTF-8          LC_NUMERIC=C
## [3] LC_TIME=en_US.UTF-8           LC_COLLATE=en_US.UTF-8
## [5] LC_MONETARY=en_US.UTF-8       LC_MESSAGES=en_US.UTF-8
## [7] LC_PAPER=en_US.UTF-8          LC_NAME=en_US.UTF-8
## [9] LC_ADDRESS=en_US.UTF-8        LC_TELEPHONE=en_US.UTF-8
## [11] LC_MEASUREMENT=en_US.UTF-8    LC_IDENTIFICATION=en_US.UTF-8
##
## attached base packages:
## [1] tools      stats4      parallel    stats      graphics  grDevices  utils
## [8] datasets  methods    base
##
## other attached packages:
## [1] clusterProfiler_3.8.1          ReporteRs_0.8.6
## [3] ReporteRsjars_0.0.4            GO.db_3.6.0
## [5] annotate_1.58.0                XML_3.98-1.16
## [7] GOstats_2.46.0                 graph_1.58.0
## [9] Category_2.46.0                AnnotationDbi_1.42.1
## [11] gplots_3.0.1                   bindrcpp_0.2.2
## [13] ggrepel_0.8.0                  plotly_4.8.0
## [15] ggplot2_3.0.0                  htmltools_0.3.6
## [17] DT_0.4                          htmlwidgets_1.2
## [19] webshot_0.5.0                  kableExtra_0.9.0
## [21] knitr_1.20                      edgeR_3.22.3
## [23] limma_3.36.5                   Matrix_1.2-14
## [25] SummarizedExperiment_1.10.1    DelayedArray_0.6.6
## [27] BiocParallel_1.14.2            matrixStats_0.54.0
## [29] Biobase_2.40.0                 ezRun_1.3.1
## [31] GenomicRanges_1.32.7           GenomeInfoDb_1.16.0
## [33] Biostrings_2.48.0              XVector_0.20.0
## [35] IRanges_2.14.12                S4Vectors_0.18.3
## [37] BiocGenerics_0.26.0            data.table_1.11.6
##
## loaded via a namespace (and not attached):
## [1] uuid_0.1-2                      backports_1.1.2
## [3] fastmatch_1.1-0                 igraph_1.2.2
## [5] plyr_1.8.4                      lazyeval_0.2.1
## [7] GSEABase_1.42.0                 splines_3.5.0
## [9] crosstalk_1.0.0                 digest_0.6.17
## [11] GOSemSim_2.6.2                  viridis_0.5.1
## [13] gdata_2.18.0                    magrittr_1.5
## [15] memoise_1.1.0                   readr_1.1.1
## [17] R.utils_2.7.0                   officer_0.3.2
## [19] enrichplot_1.0.2                prettyunits_1.0.2
## [21] colorspace_1.3-2                blob_1.1.1
## [23] rvest_0.3.2                     BiasedUrn_1.07
## [25] dplyr_0.7.6                     crayon_1.3.4
## [27] RCurl_1.95-4.11                 jsonlite_1.5
```

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## [29] genefilter_1.62.0      bindr_0.1.1
## [31] survival_2.42-6       glue_1.3.0
## [33] rvg_0.1.9             gtable_0.2.0
## [35] zlibbioc_1.26.0       UpSetR_1.3.3
## [37] Rgraphviz_2.24.0     scales_1.0.0
## [39] DOSE_3.6.1            DBI_1.0.0
## [41] Rcpp_0.12.18          viridisLite_0.3.0
## [43] xtable_1.8-3          progress_1.2.0
## [45] units_0.6-1          bit_1.1-14
## [47] AnnotationForge_1.22.2 httr_1.3.1
## [49] fgsea_1.6.0           pkgconfig_2.0.2
## [51] rJava_0.9-10          R.methodsS3_1.7.1
## [53] locfit_1.5-9.1       labeling_0.3
## [55] reshape2_1.4.3       tidyselect_0.2.4
## [57] rlang_0.2.2          later_0.7.5
## [59] munsell_0.5.0        RSQLite_2.1.1
## [61] ggridges_0.5.0       evaluate_0.11
## [63] stringr_1.3.1        yaml_2.2.0
## [65] bit64_0.9-7          zip_1.0.0
## [67] geneLenDataBase_1.16.0 caTools_1.17.1.1
## [69] purrr_0.2.5          gggraph_1.0.2
## [71] RBGL_1.56.0          nlme_3.1-137
## [73] mime_0.5             R.oo_1.22.0
## [75] DO.db_2.9            xml2_1.2.0
## [77] biomaRt_2.36.1       compiler_3.5.0
## [79] rstudioapi_0.7       png_0.1-7
## [81] tweenr_0.1.5         tibble_1.4.2
## [83] stringi_1.2.4        highr_0.7
## [85] GenomicFeatures_1.32.2 gdtools_0.1.7
## [87] lattice_0.20-35      pillar_1.3.0
## [89] goseq_1.32.0         cowplot_0.9.3
## [91] bitops_1.0-6         qvalue_2.12.0
## [93] httpuv_1.4.5         rtracklayer_1.40.6
## [95] R6_2.2.2             promises_1.0.1
## [97] gridExtra_2.3        KernSmooth_2.23-15
## [99] MASS_7.3-50          gtools_3.8.1
## [101] assertthat_0.2.0    rprojroot_1.3-2
## [103] withr_2.1.2          GenomicAlignments_1.16.0
## [105] Rsamtools_1.32.3    GenomeInfoDbData_1.1.0
## [107] mgcv_1.8-24          hms_0.4.2
## [109] grid_3.5.0           tidyr_0.8.1
## [111] rvcheck_0.1.0       rmarkdown_1.10
## [113] ggforce_0.1.3       shiny_1.1.0
## [115] base64enc_0.1-3

```

Supplementary Fig. 1.



Supplementary Fig. 1. Lipid accumulation *in vitro*. Oil red O staining of Huh7 cells incubated for 24h with OCA (2 μ M) followed by 24h with VPA (2 mM). Representative staining from three independent experiments. Scale bar=50 μ m.