

Modulation of acyl-carnitines, the broad mechanism behind *Wolbachia*-mediated inhibition of medically important flaviviruses in *Aedes aegypti*.

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SI Appendix

Dataset 1. Complete set of median-normalized LCMS data. Names of individual metabolites are listed on top and median normalized raw data is shown. Each sheet includes data from each experimental combination (i.e. *wMel/ZIKV African*, *wMel/ZIKV Asian* and *wMel/DENV-1*).

Dataset 2. Table of significantly modulated metabolites (p-value <0.05). Two-way ANOVA analysis was performed on each set of experimental data from *wMel/ZIKV African*, *wMel/ZIKV Asian* and *wMel/DENV-1* experiments. Both p-values and BH-adjusted p-values are shown.

Fig. S1. Confirmation of the presence of *Wolbachia* in *Aag2.wMel*, but not *Aag2.TET* cells.

(A) Bar chart displaying *wMel* density in *Aag2.wMel* and *Aag2.TET* cells. *Wolbachia* density in cells was determined by comparing the relative abundance of *Wolbachia TM513* gene to that of the single-copy mosquito *rps17* gene using qPCR. *Aag2.wMel* cells had *Wolbachia* density of about 35 and *Aag2.TET* cells had none. All conditions were performed in triplicates; error bars represent SEM. (B) Western blot identifying presence of *Wolbachia* surface protein (WSP) in cells. A thick band correlating to *Wolbachia* surface protein was observed in *Aag2.wMel* but not *Aag2.TET* cells. (C) Visualization of *wMel* in *Aag2* cells using a fluorescent in situ hybridisation (FISH) assay. *wMel* was labelled with Rhodamine/ROX (Red) and cells were visualized by a DAPI (blue) stain. *wMel* (Red dots) was seen in *Aag2.wMel* but not *Aag2.TET* cells.

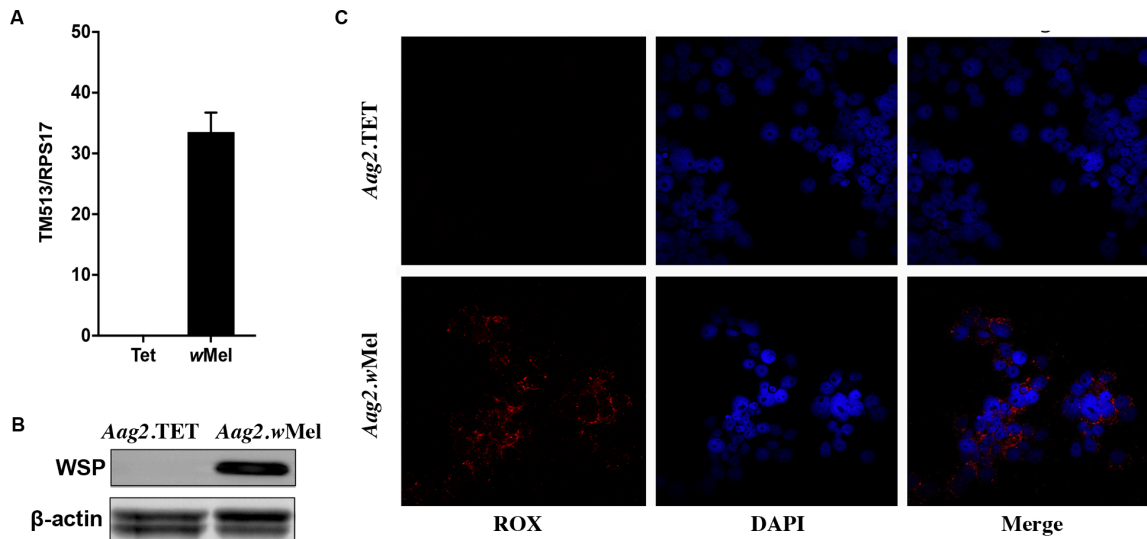


Fig. S2. Effects of the presence of *Wolbachia* strain *wMel* on ZIKV and DENV replication in *Ae. aegypti* cell culture. *Aag2.wMel* (*wMel*) and *Aag2.TET* (*Tet*) cells were infected with ZIKV and DENV-1 at a multiplicity of infection (MOI) of 5 and levels of virus were measured at 24, 48, and 72 h.p.i. (A, D) Plaque assay was performed in BHK-21 cells to quantify the levels of infectious virus produced; A: ZIKV; D: DENV (B, E) Viral genome replication was analyzed by qRT-PCR and relative expression of virus against *rps17*, a mosquito housekeeping gene is shown. Virus-specific primers targeting the NS5 region were used to identify infection; B: ZIKV; E: DENV (C, F) Levels of virus protein were measured by western blotting using virus-specific antibodies against the NS1 protein (ZIKV) (C) and the envelope protein (DENV) (F). β -actin is used as a loading control. N=2 experiments were conducted in triplicates independently of each other to generate data. Data are represented as mean \pm SEM; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$; n.s. : Not significant, two-tailed Student's *t*-test.

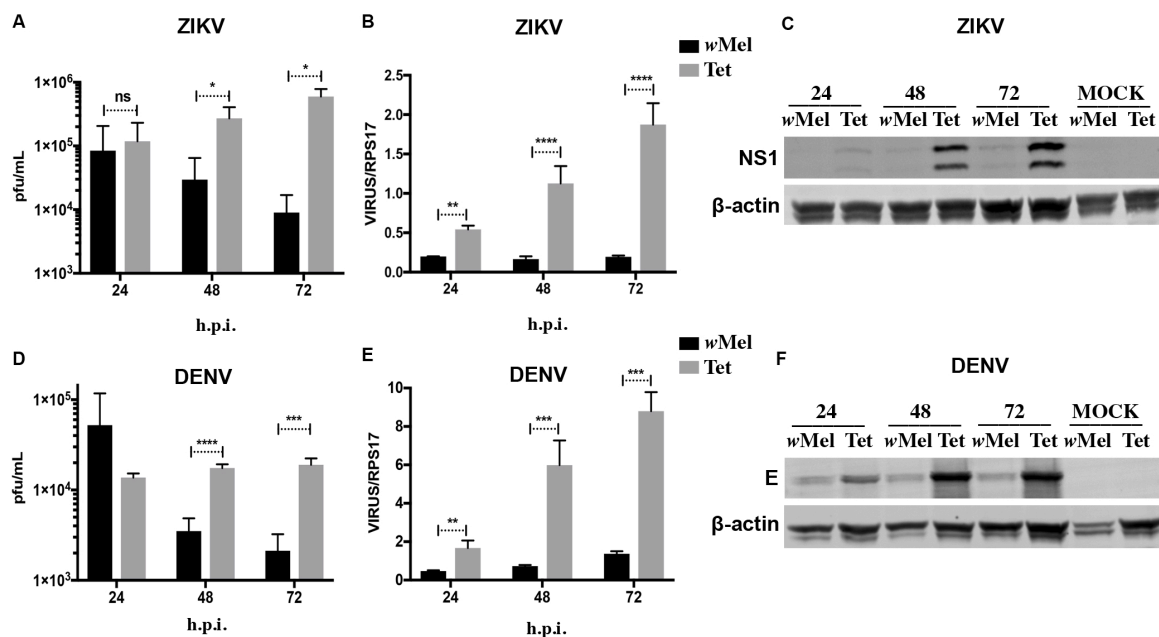
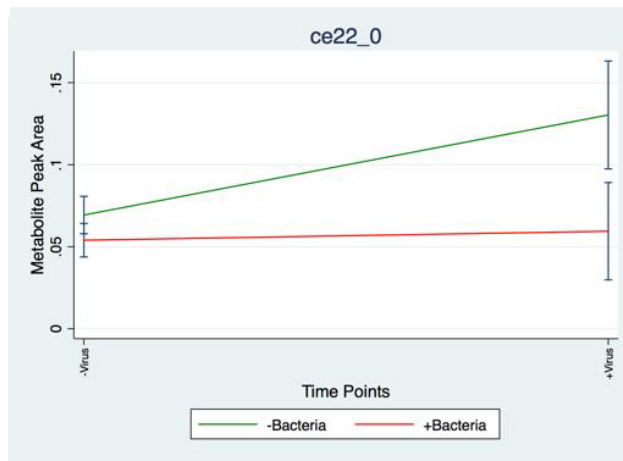
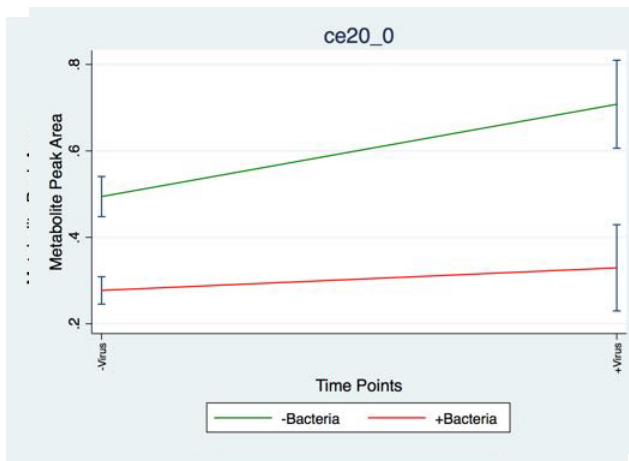
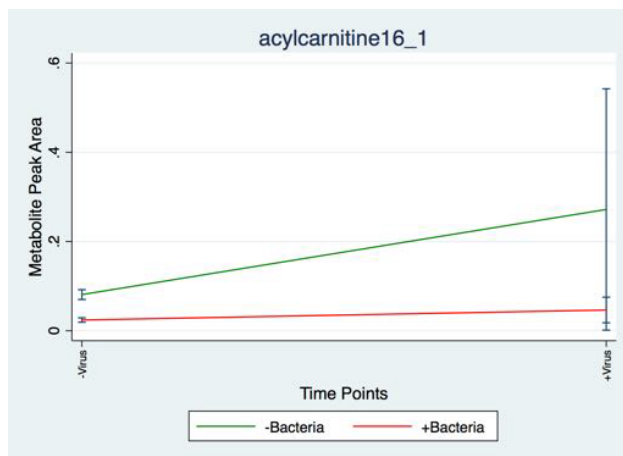
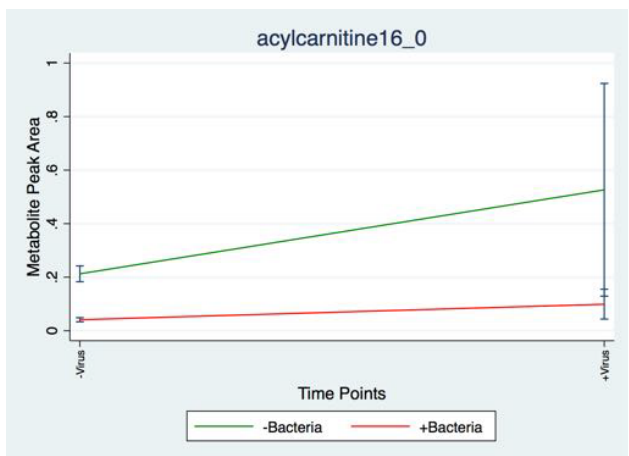
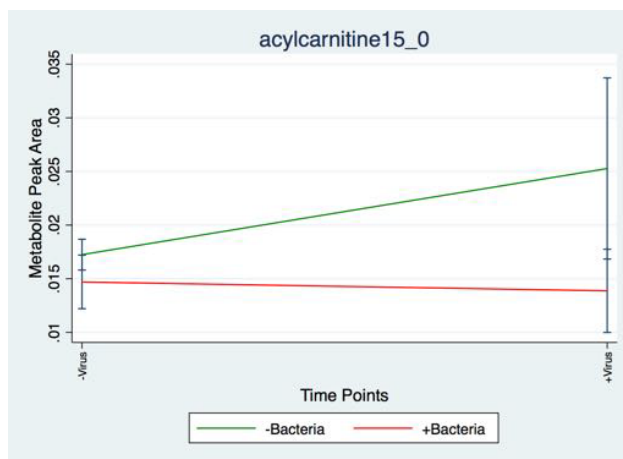
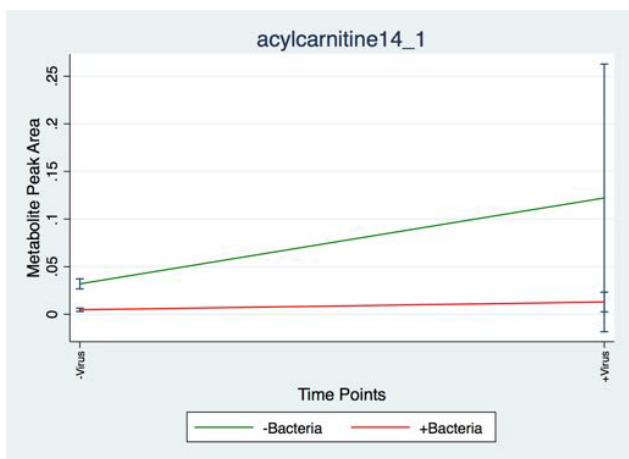
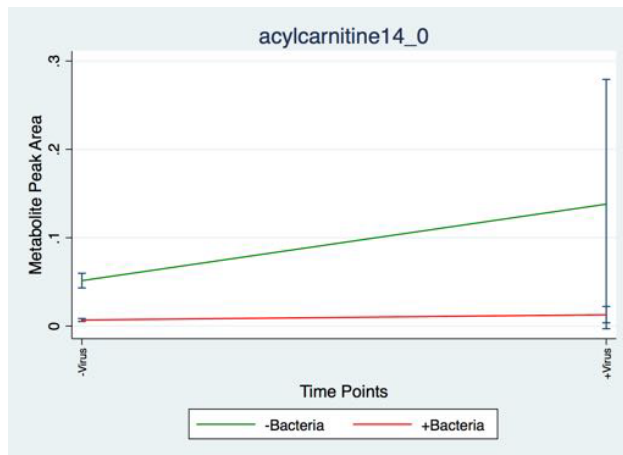
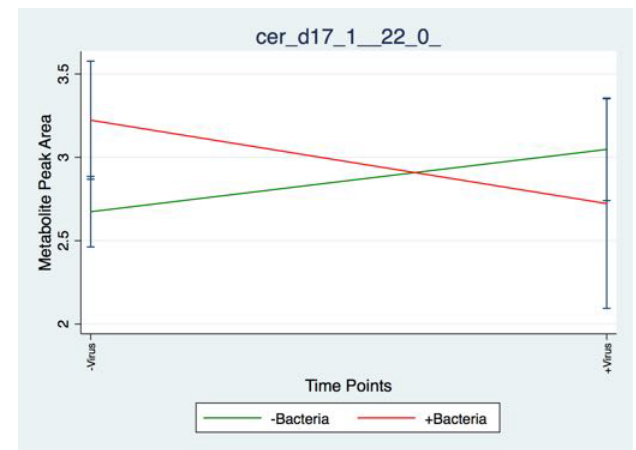
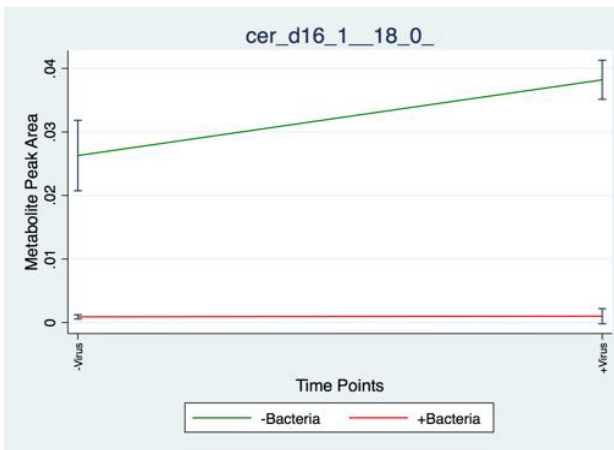
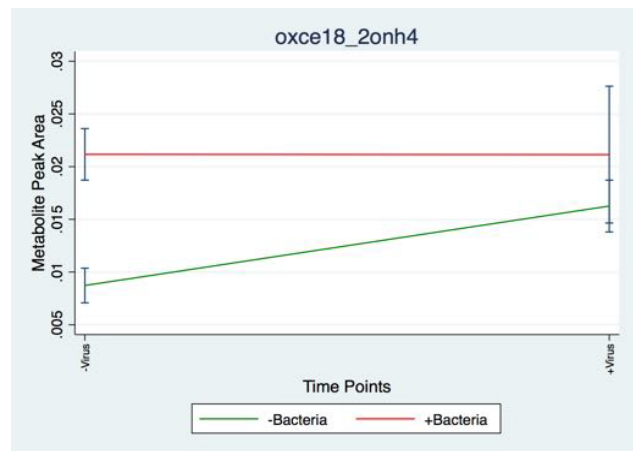
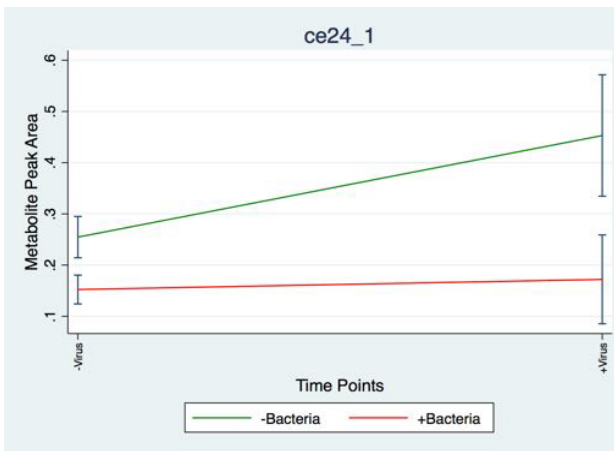
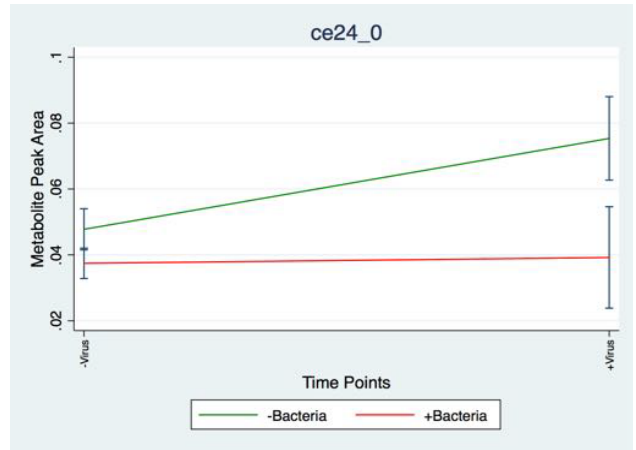
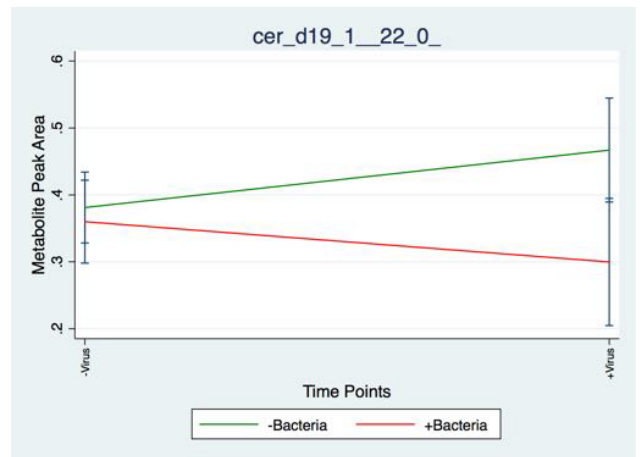
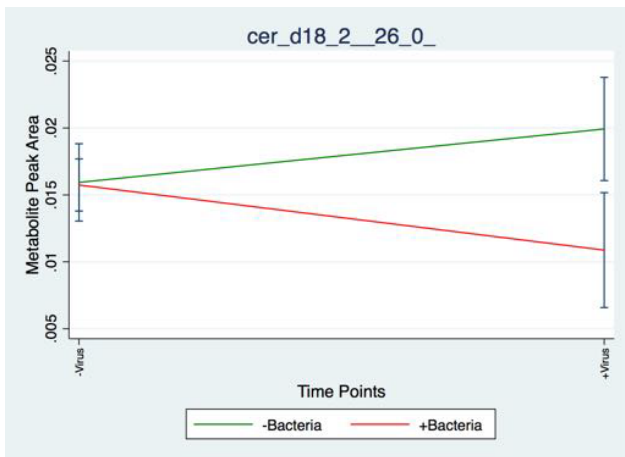
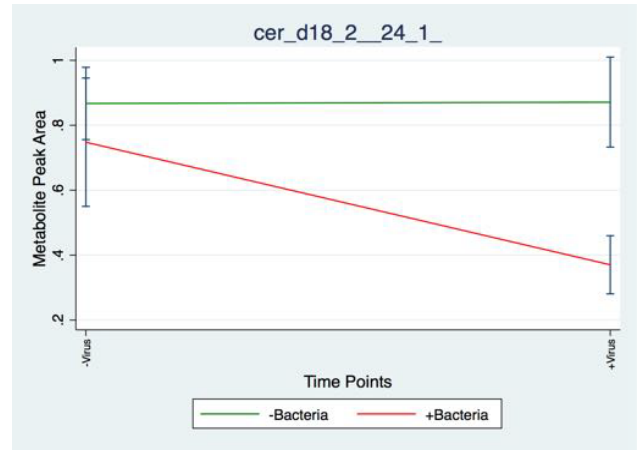


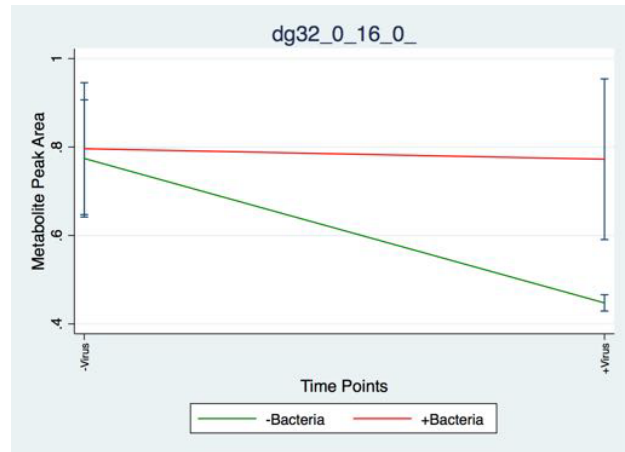
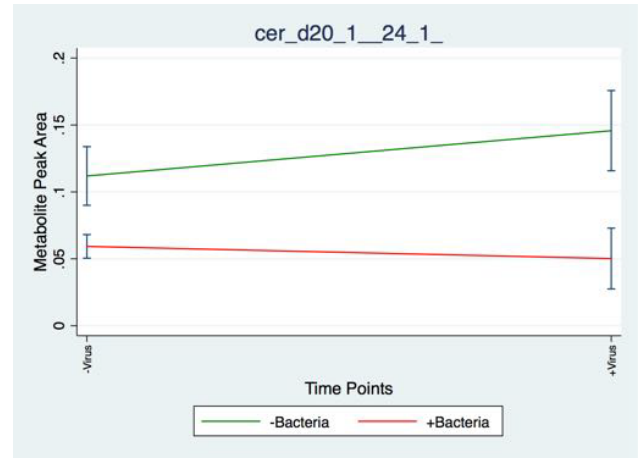
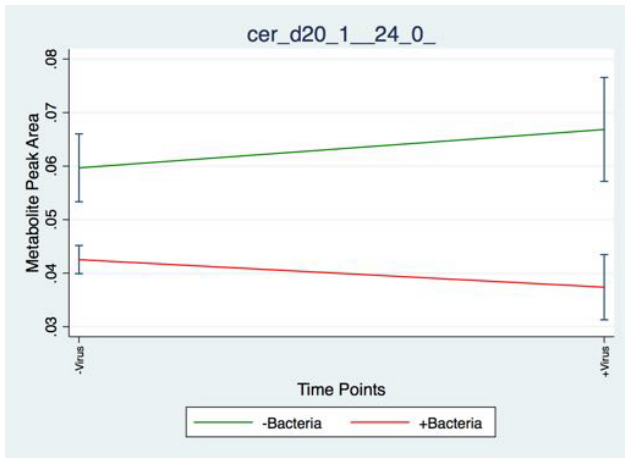
Fig. S3. Two-way ANOVA plots from LCMS analysis. Each metabolite was normalised to the median of the sample, as shown in Dataset 1. The interaction between bacteria and virus (i.e. all four data sets: bacteria +/- and virus +/-) were analysed using a two-way ANOVA test. The two-way ANOVA plot for each significantly modulated metabolite is displayed. Briefly, the red line and green line depict the presence and absence of *w*Mel respectively. The endpoints on the x-axis depict absence of virus and virus infection. The plots, thus, simultaneously demonstrate the pattern of behaviour for each metabolite in the presence of *w*Mel only, virus only and in the presence of both *w*Mel and virus. Hence, three sets of data can be interpreted from each plot. Names of each metabolite are shown above the plots and “_” represents “:”. i.e. dg32_0_16_0_ is DG 32:0 16:0.

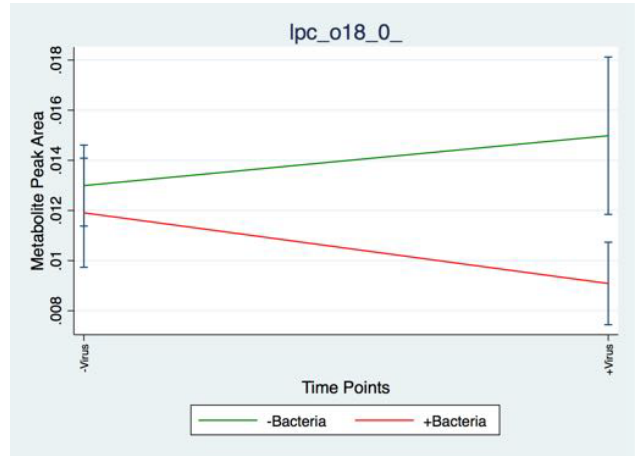
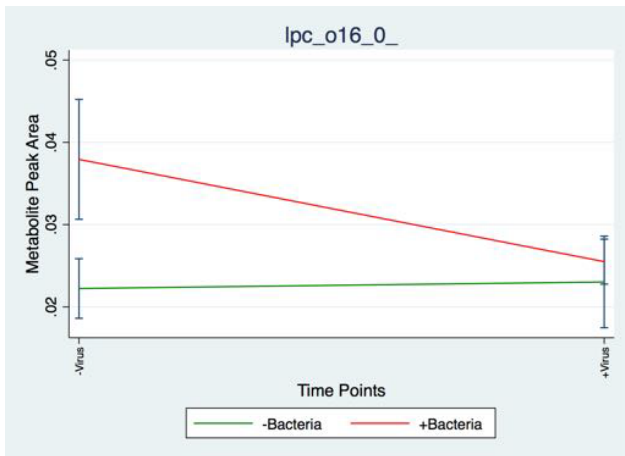
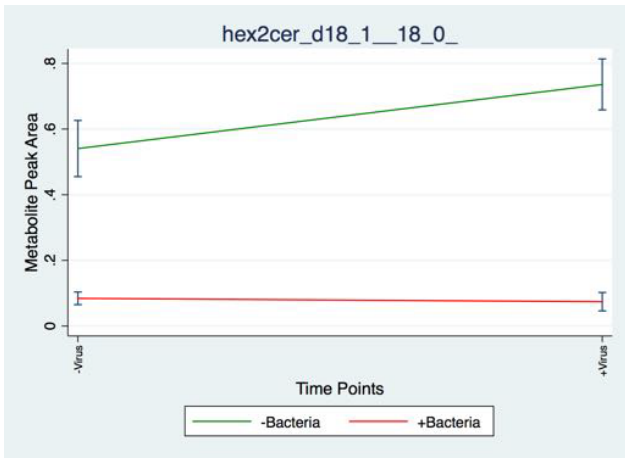
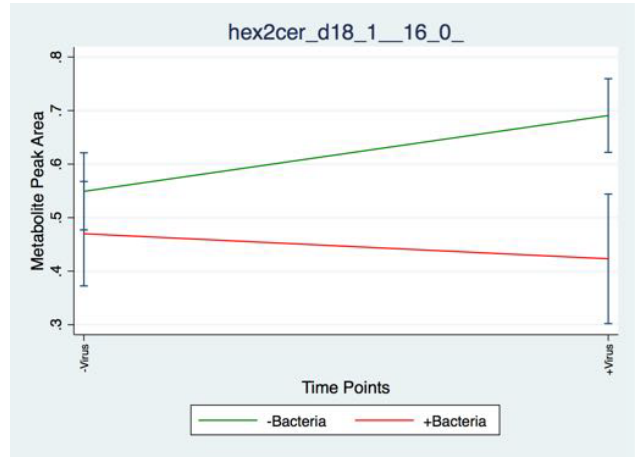
Two-way ANOVA plots – DENV-1

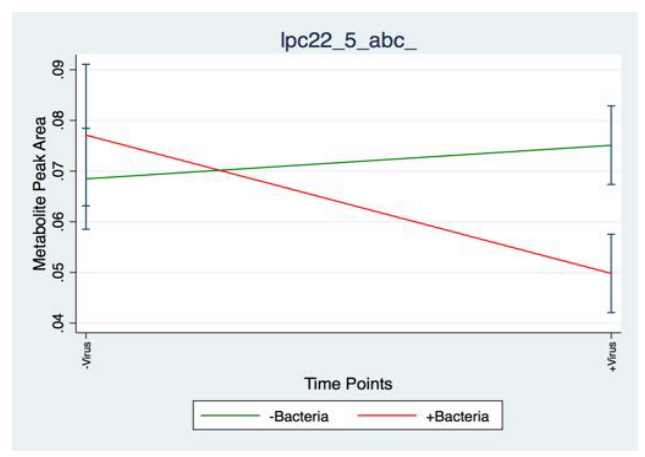
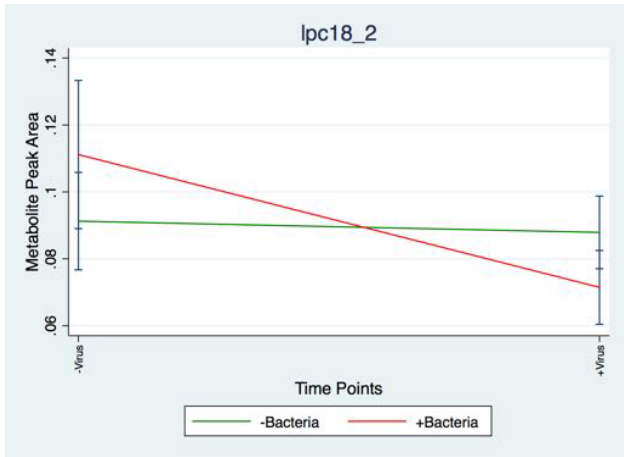
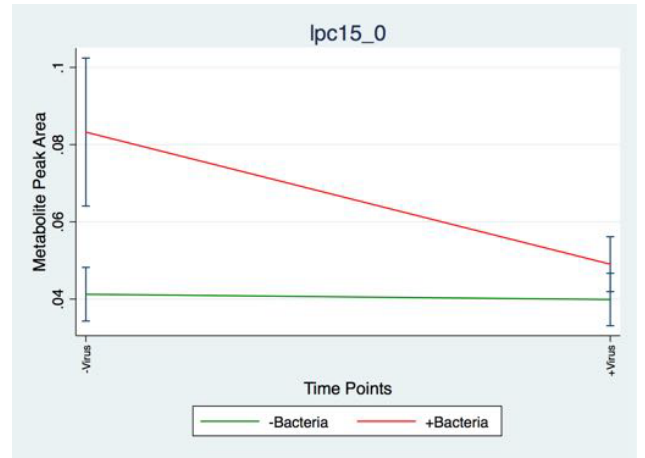
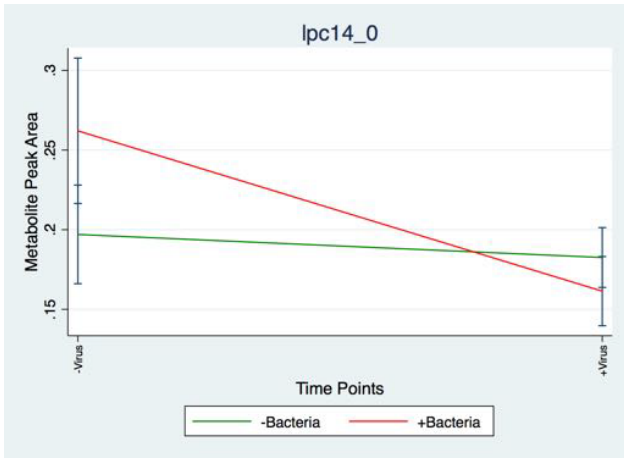
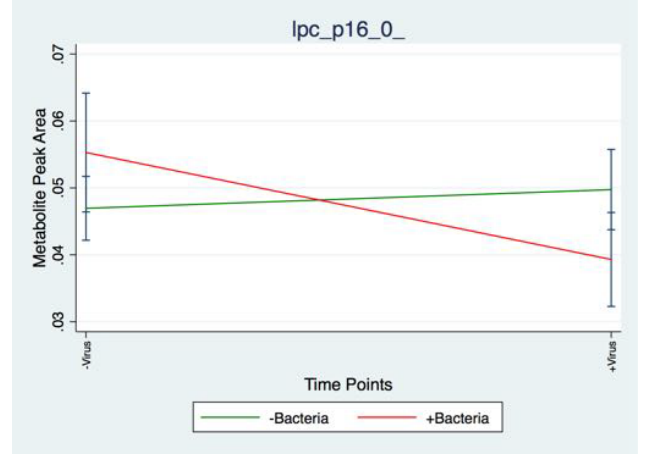
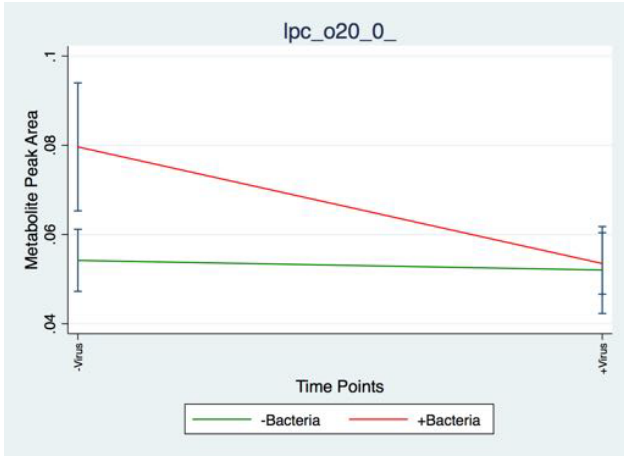


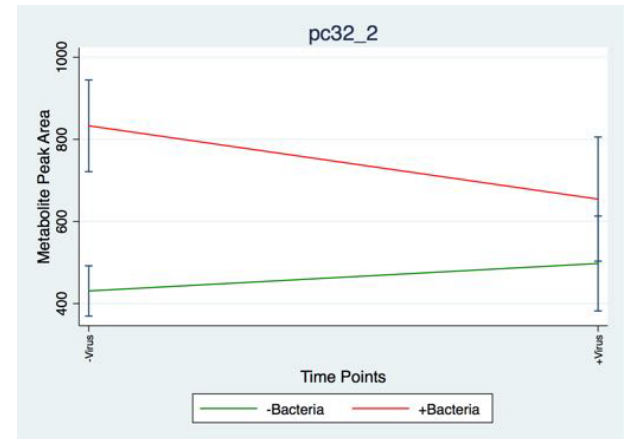
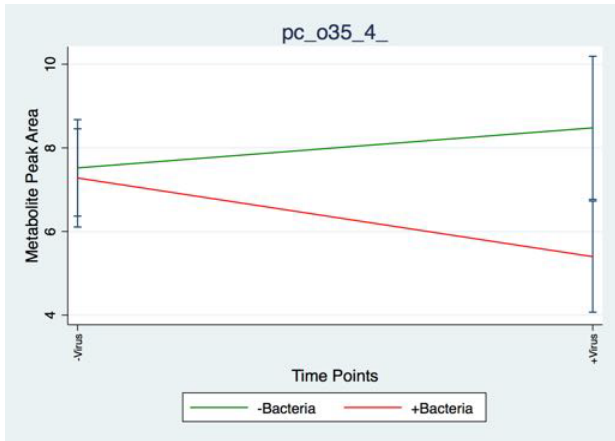
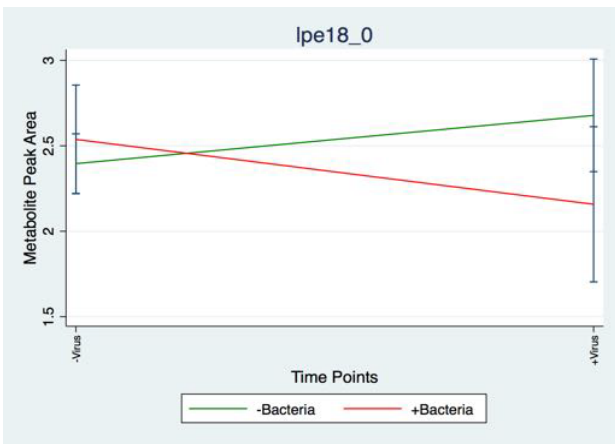


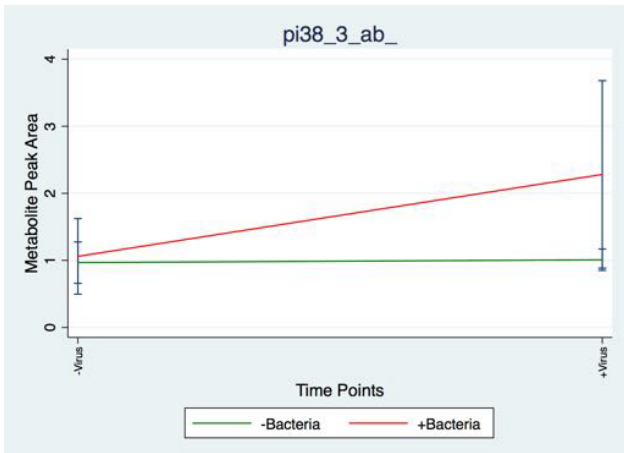
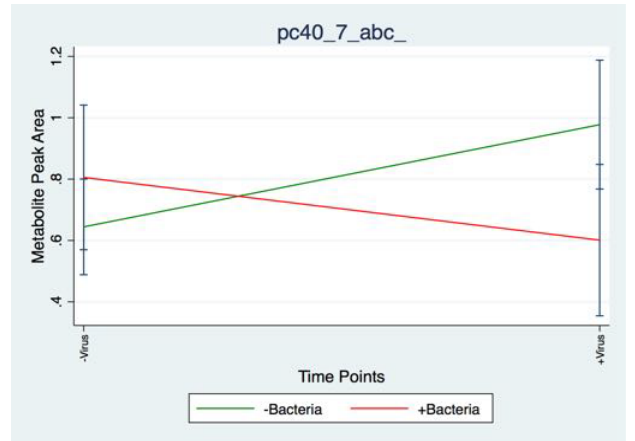
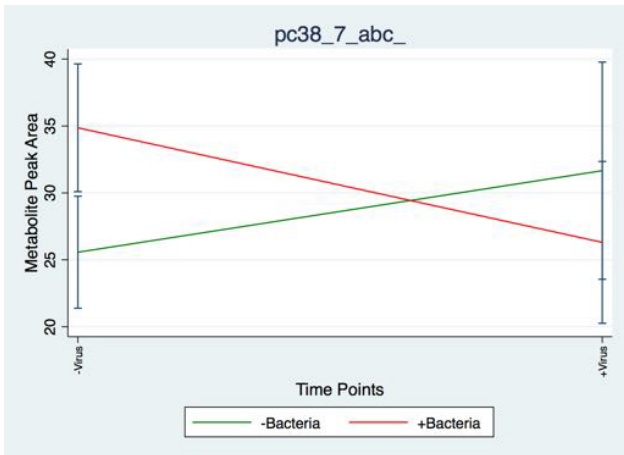
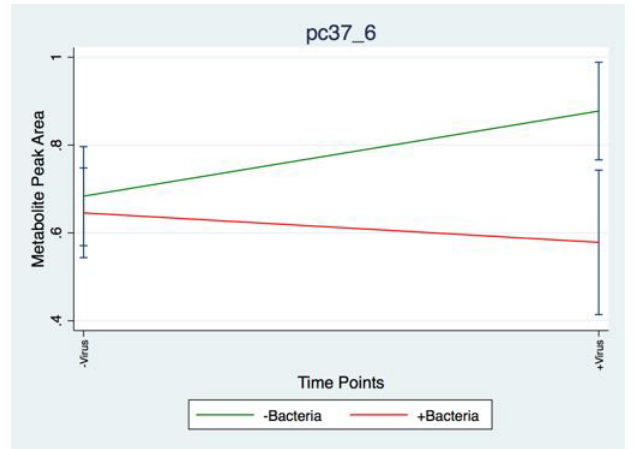
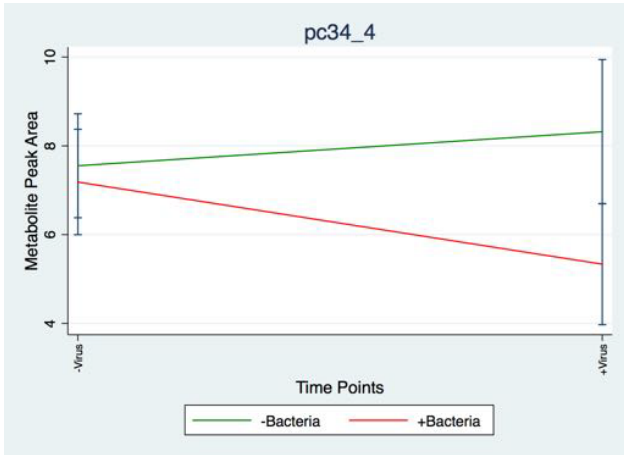




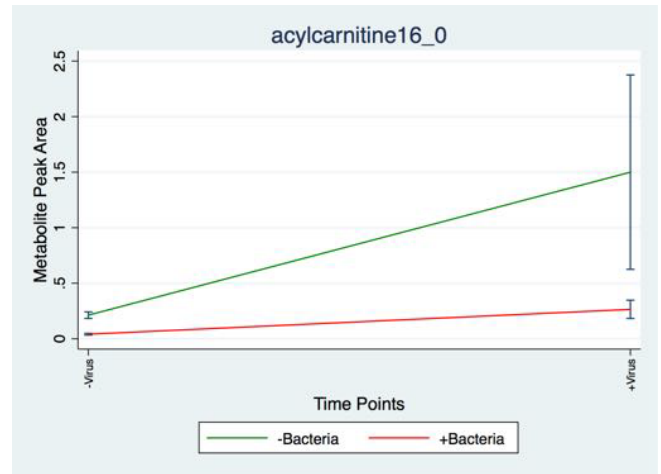
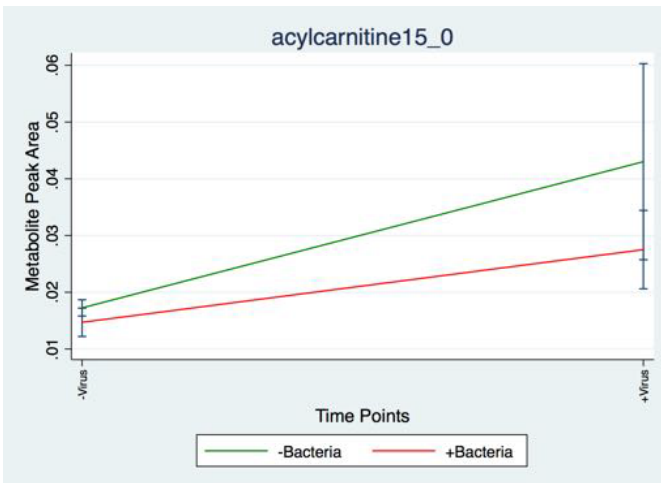
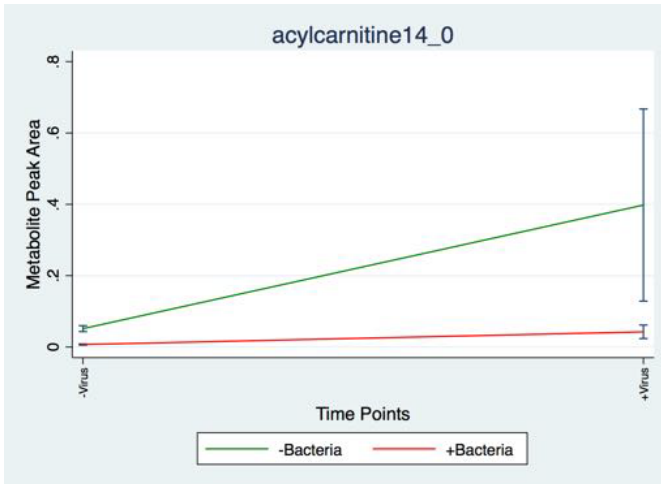


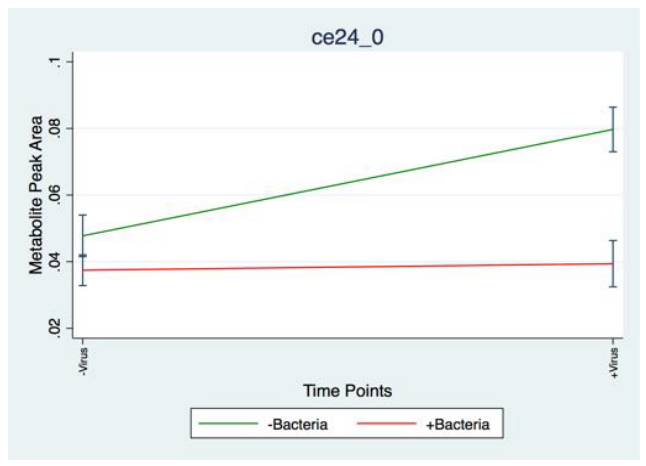
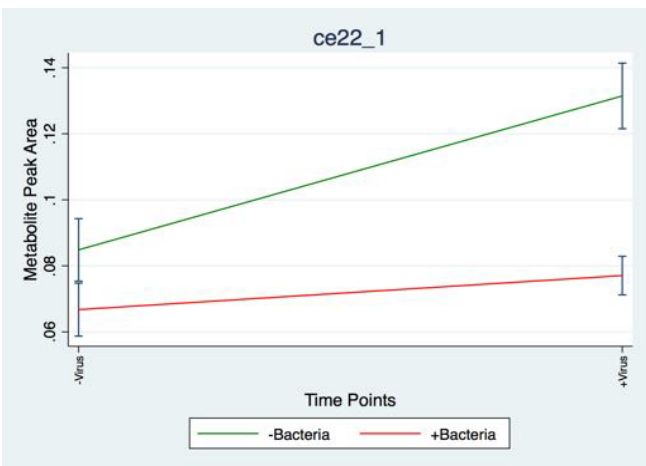
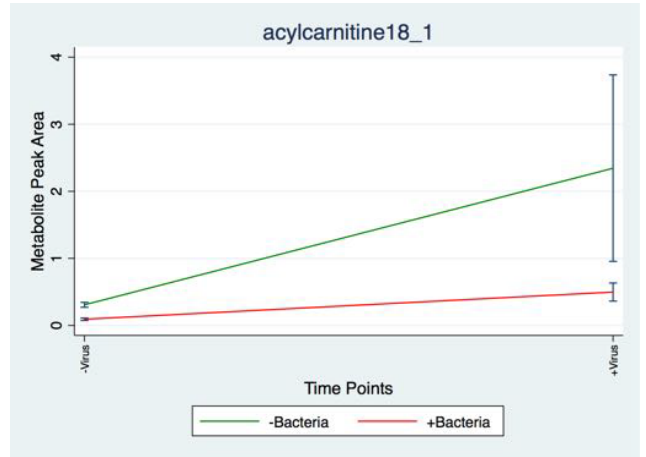
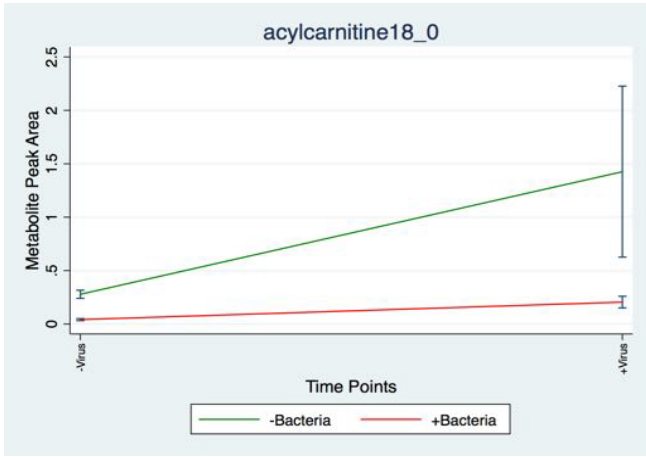


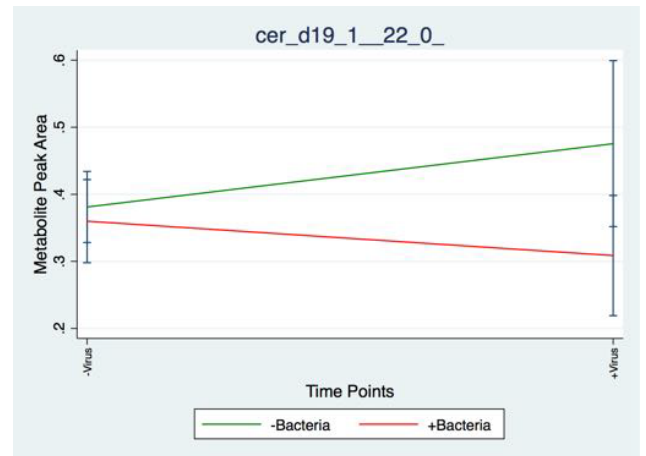
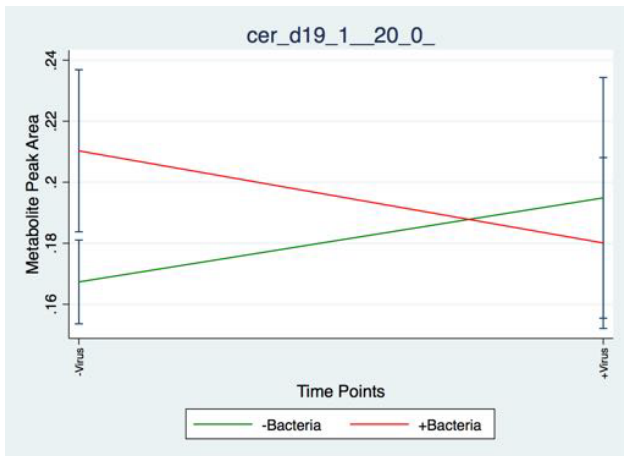
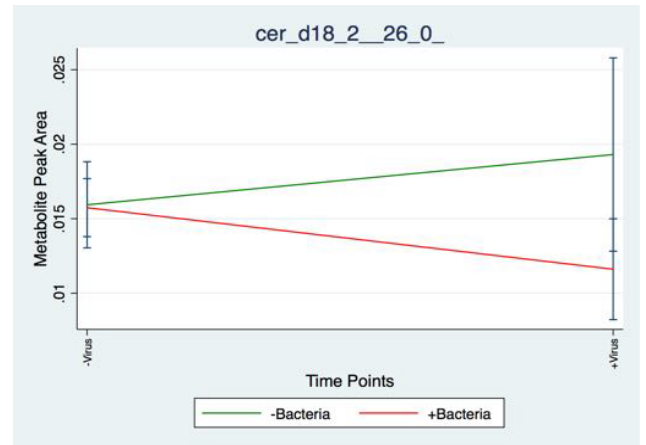
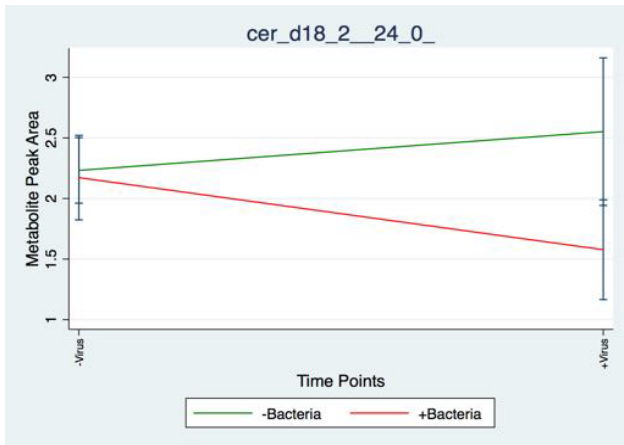


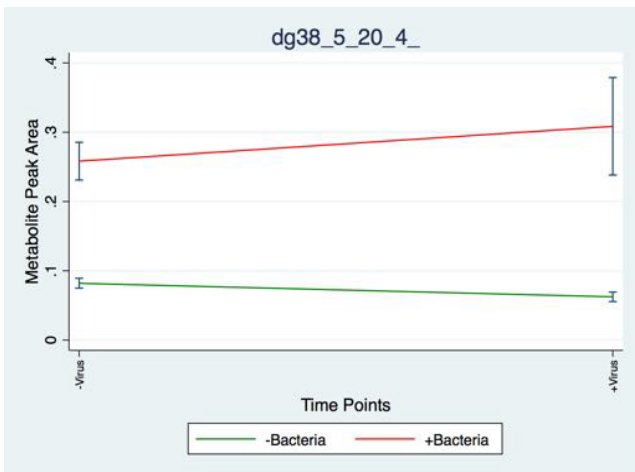
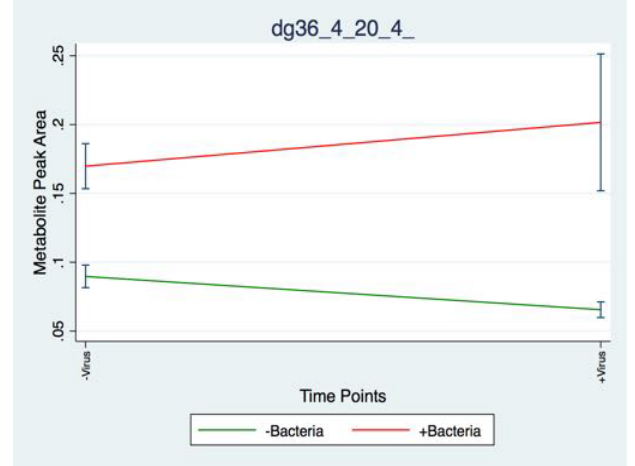


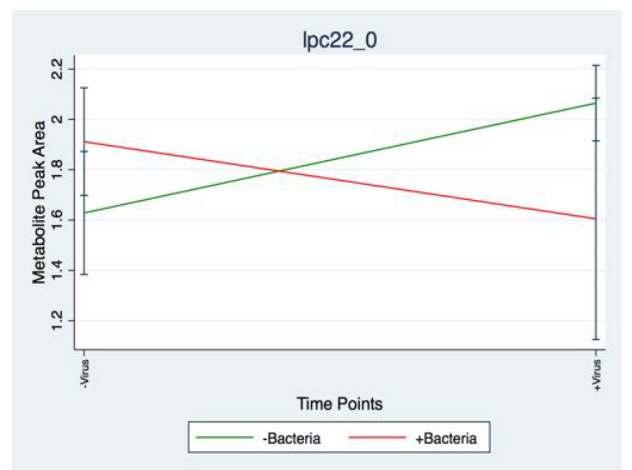
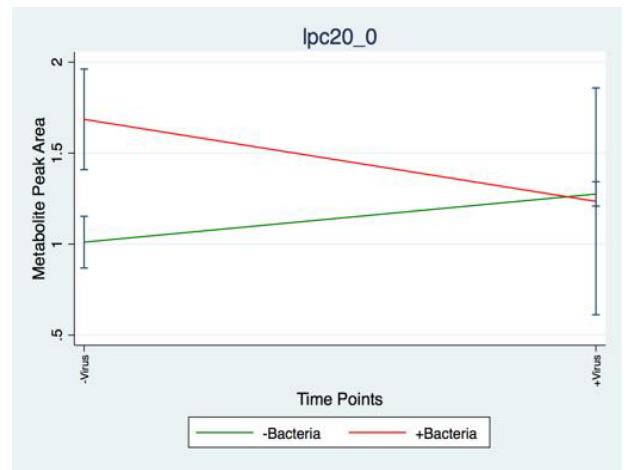
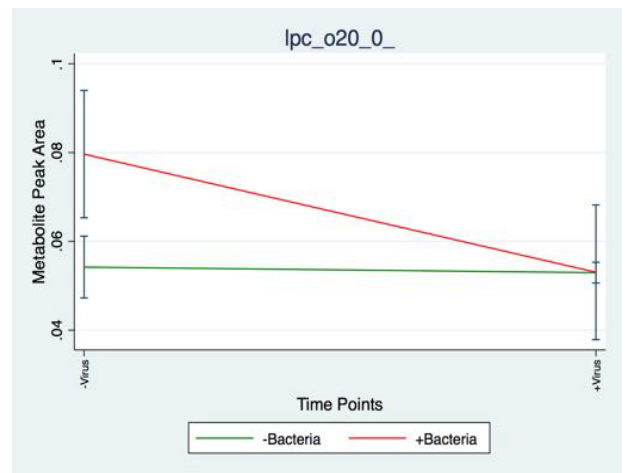
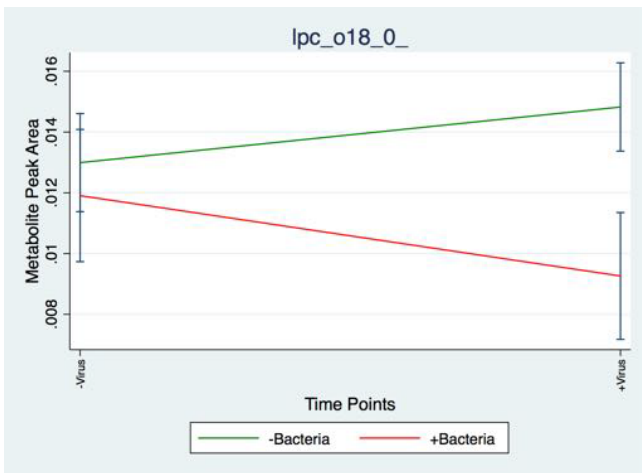
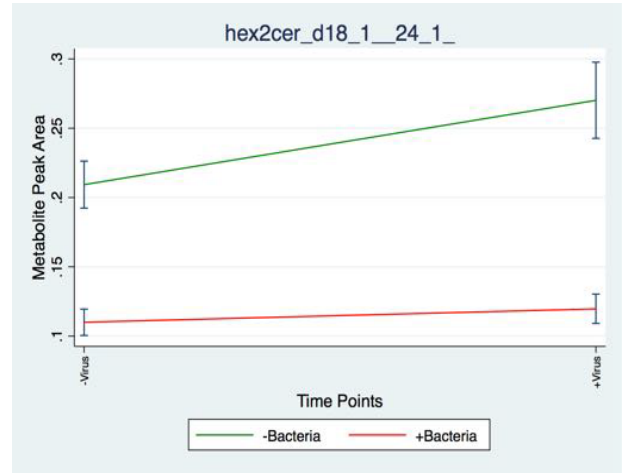
Two-way ANOVA plots – ZIKV Asian

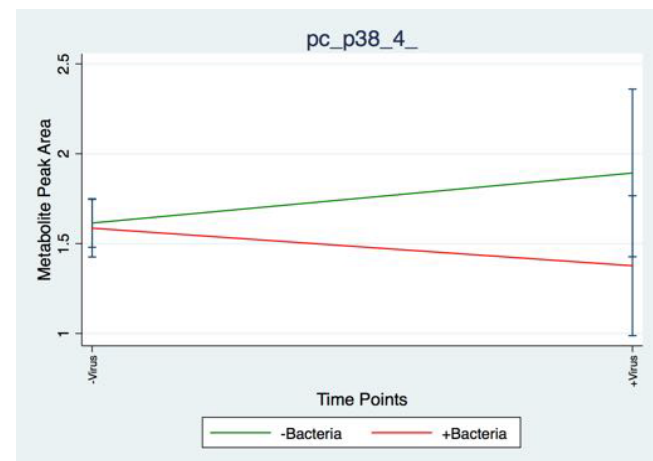
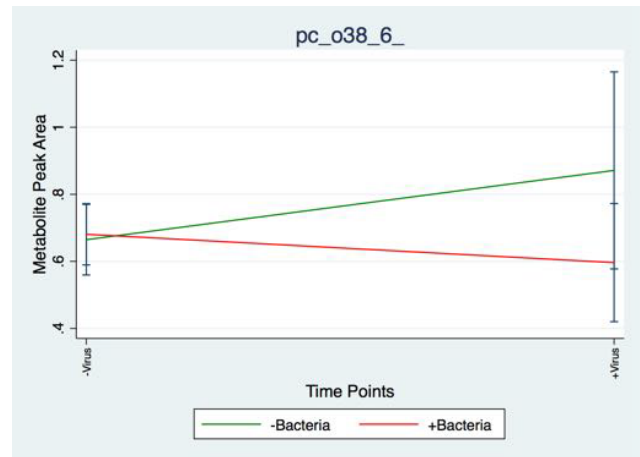
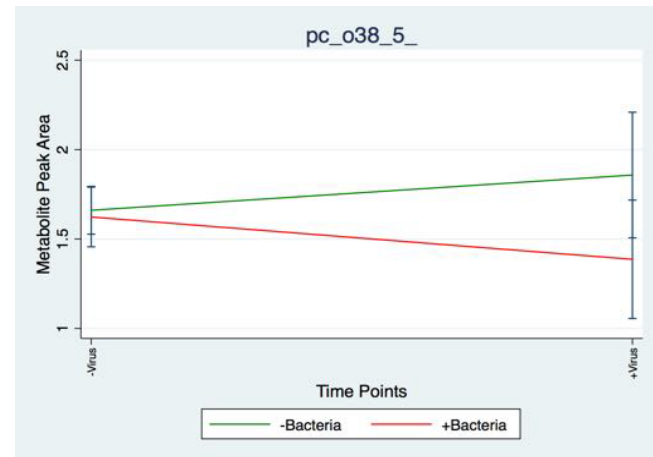
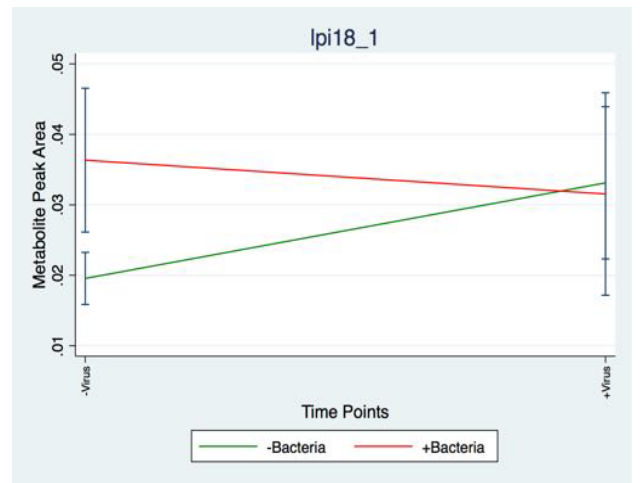


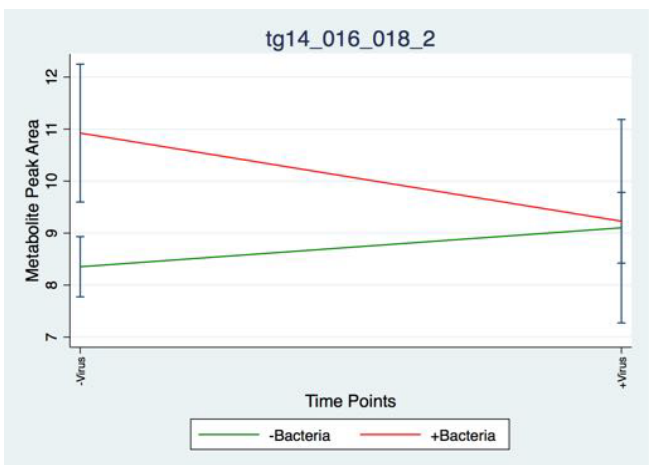
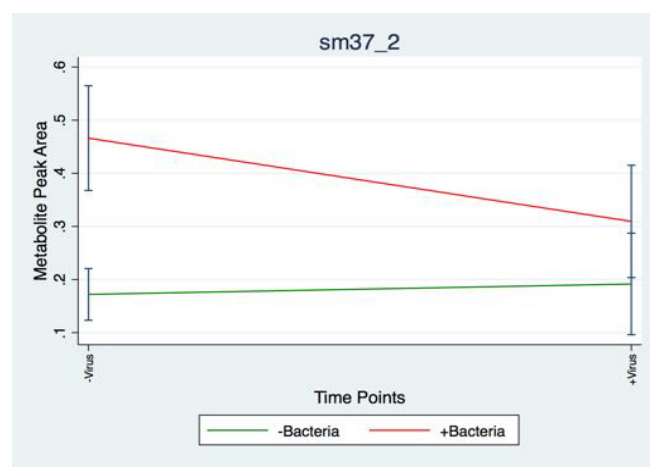
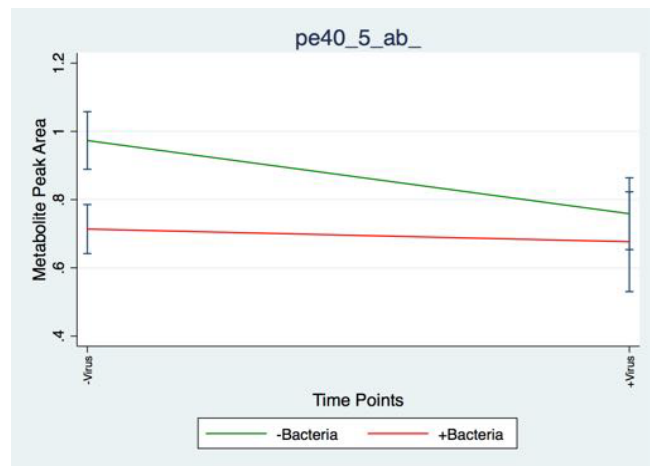
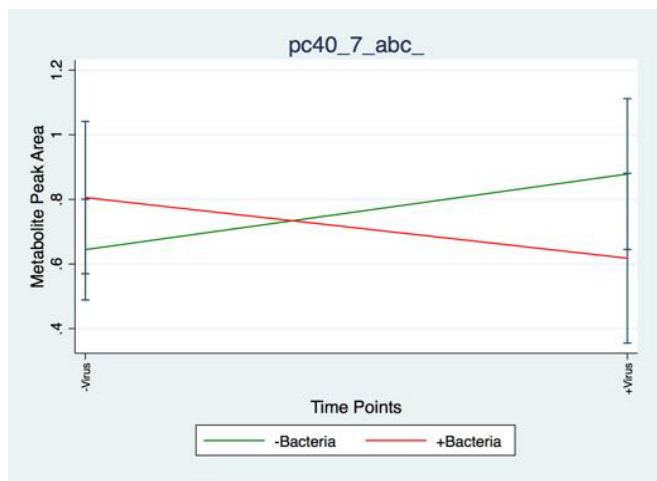
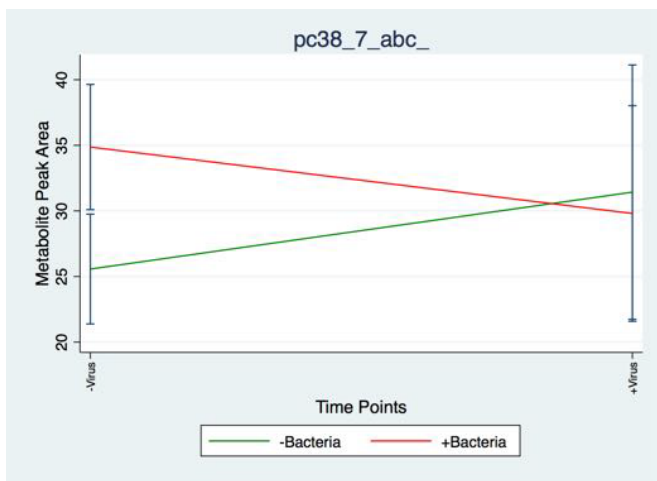


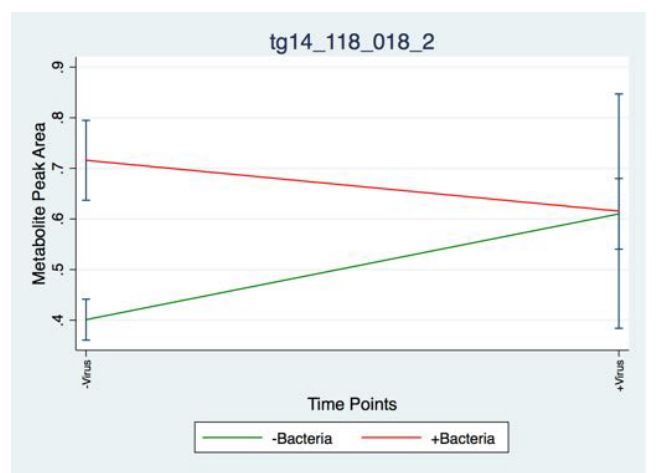




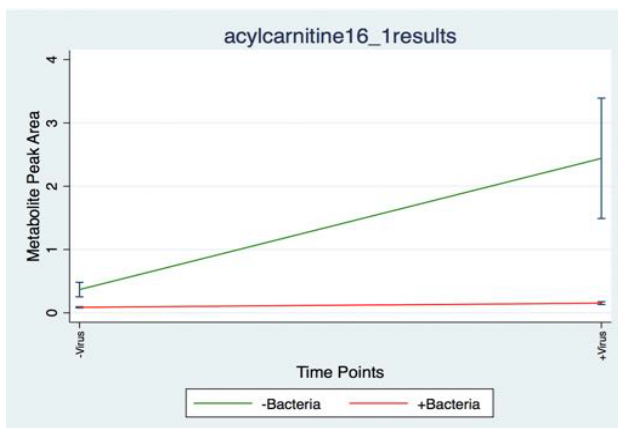
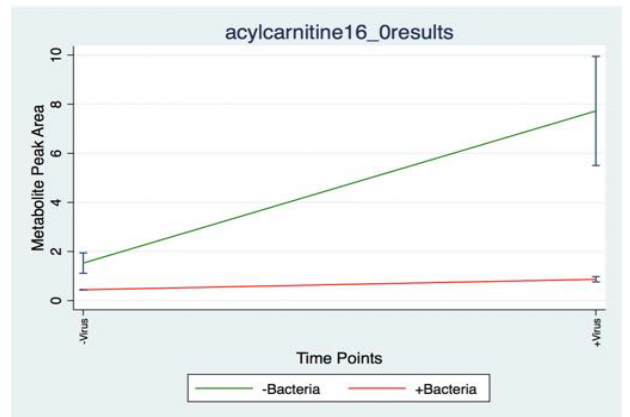
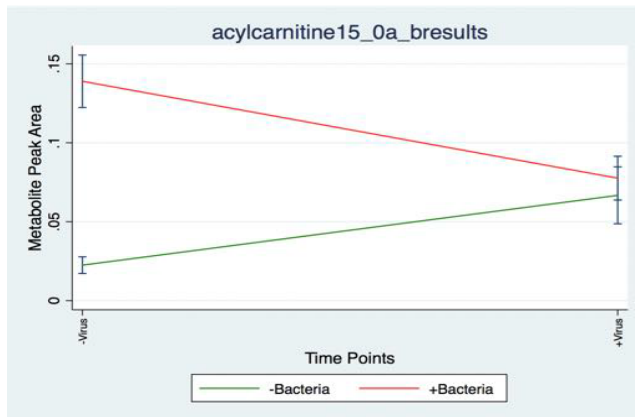
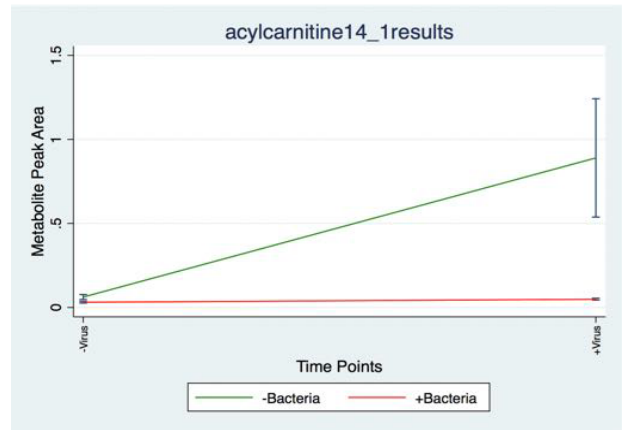
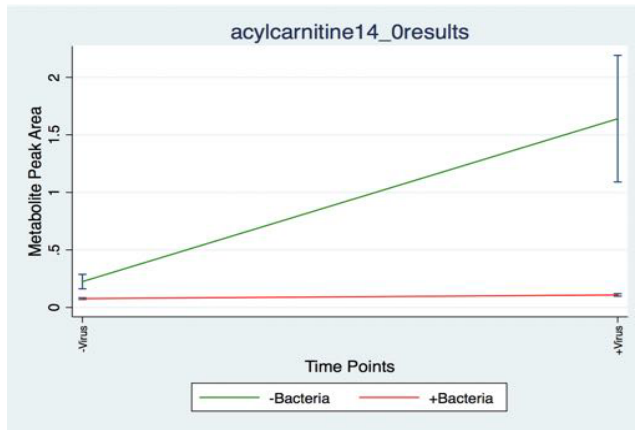
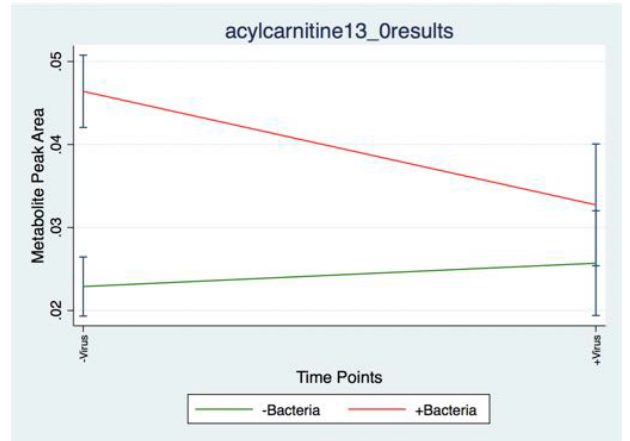


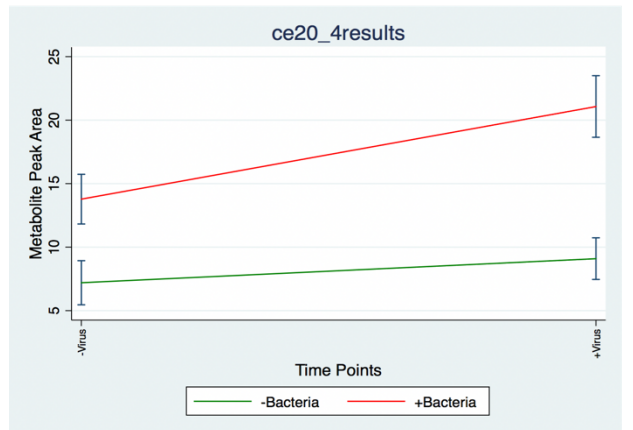
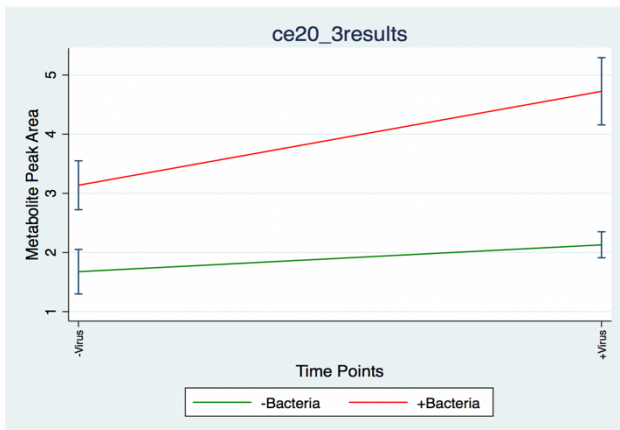
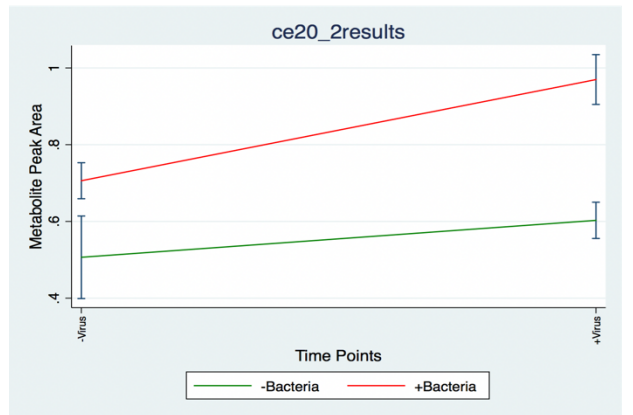
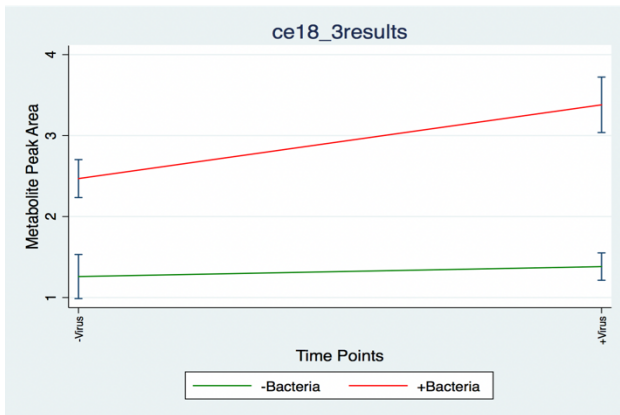
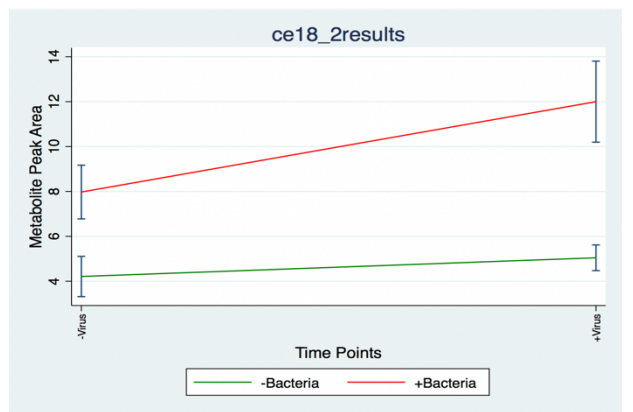
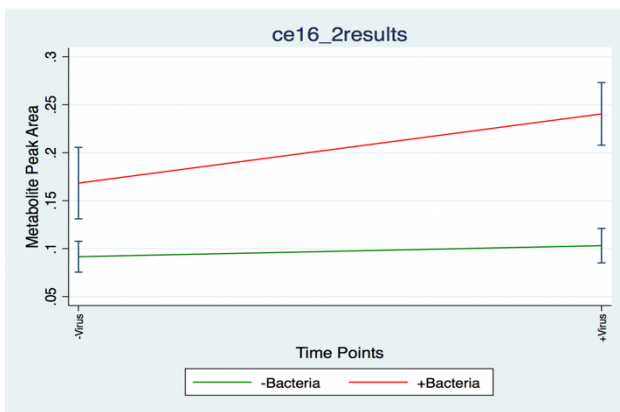
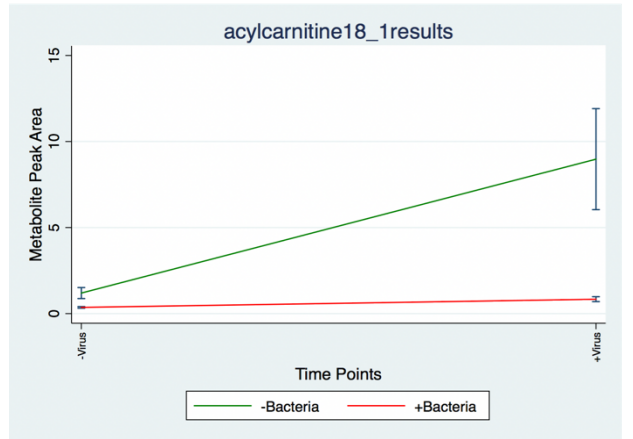
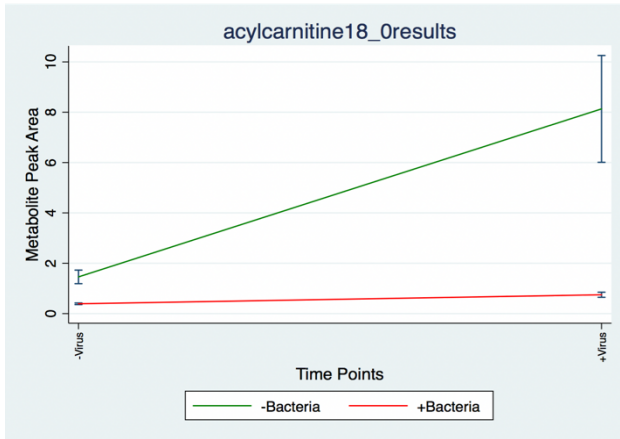


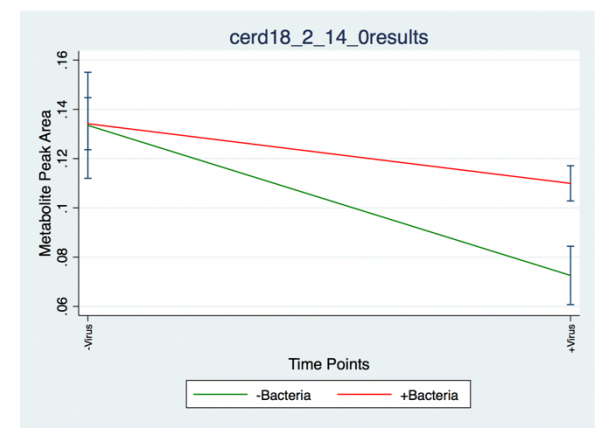
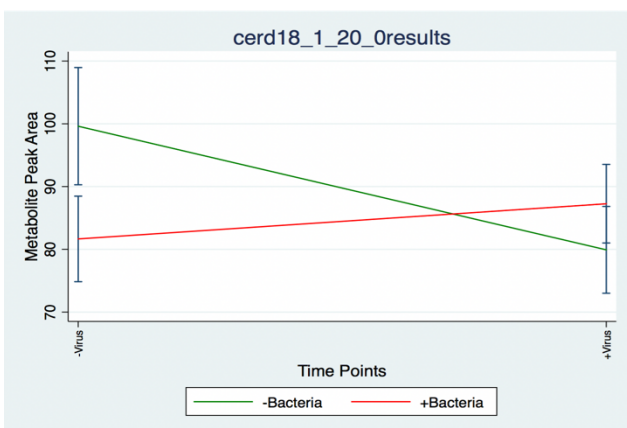
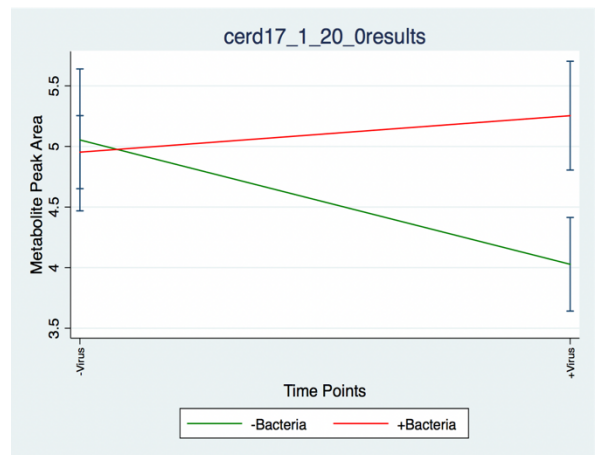
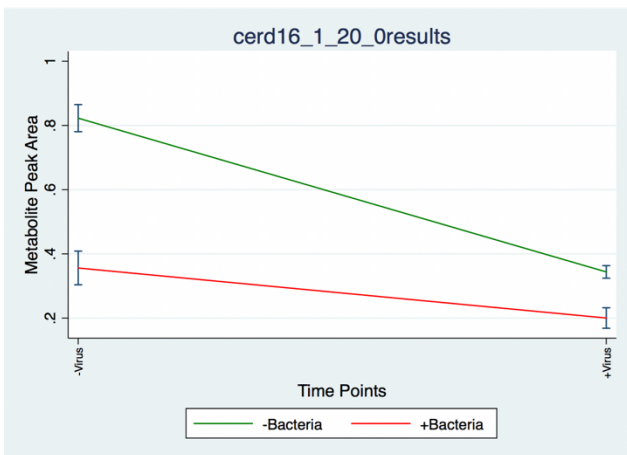
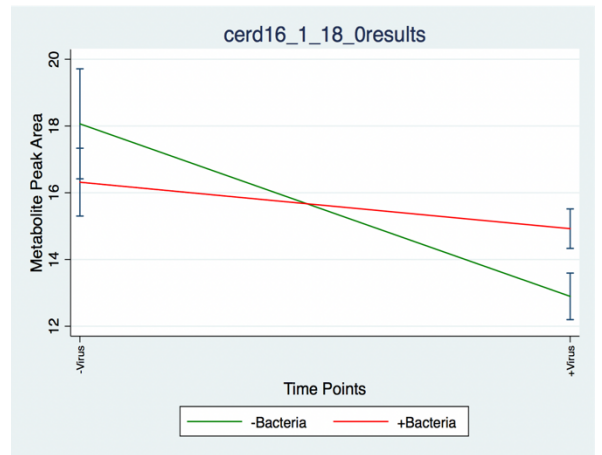
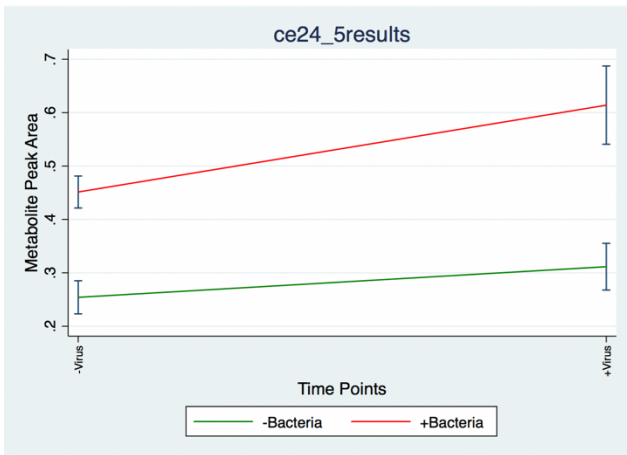
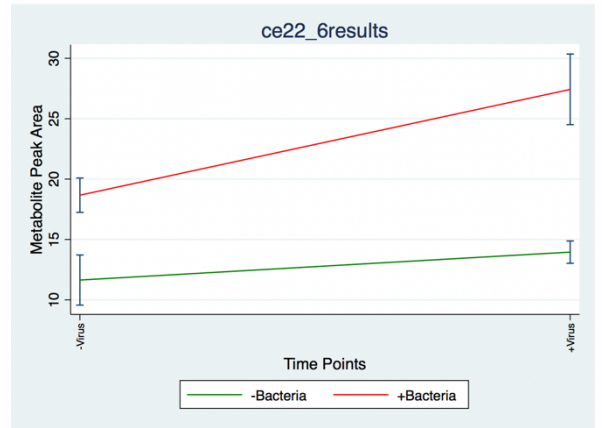
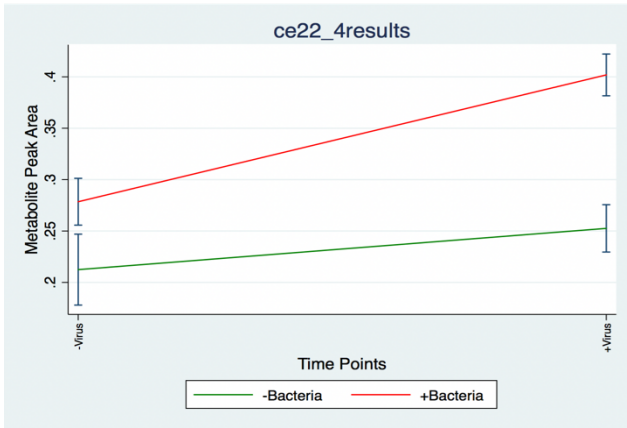


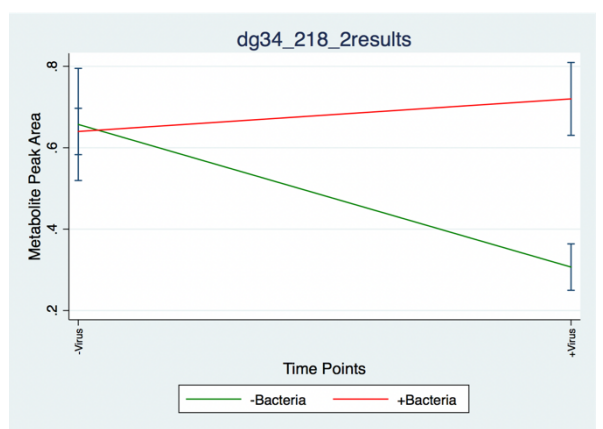
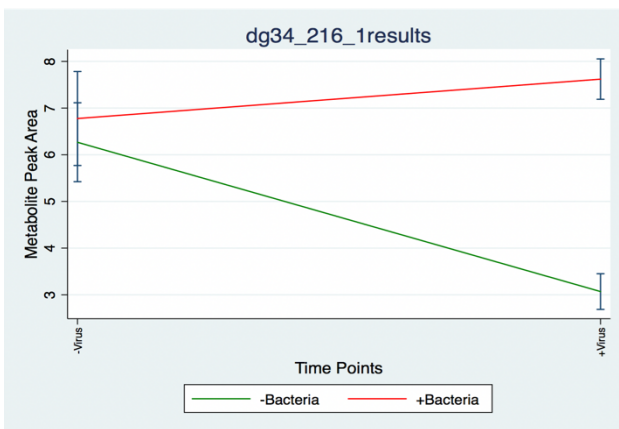
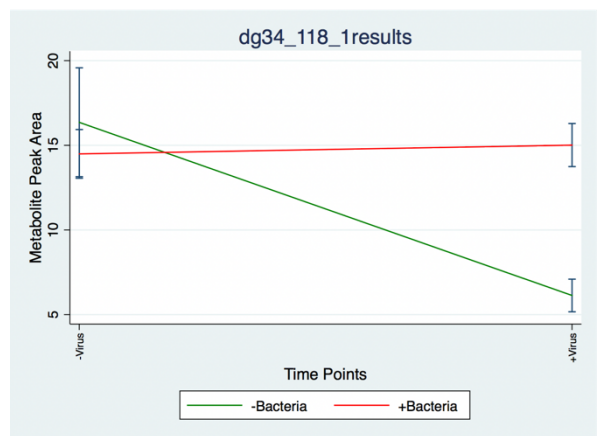
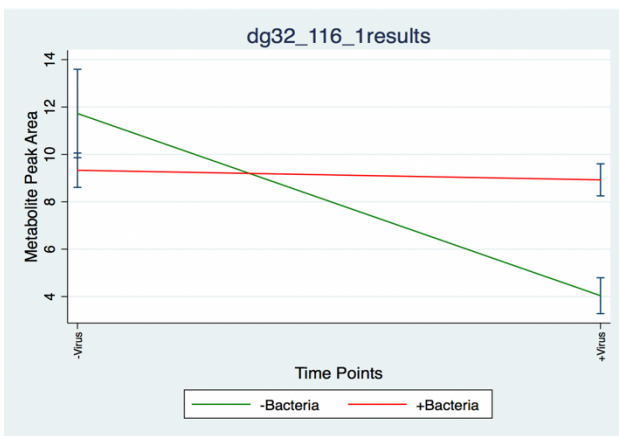
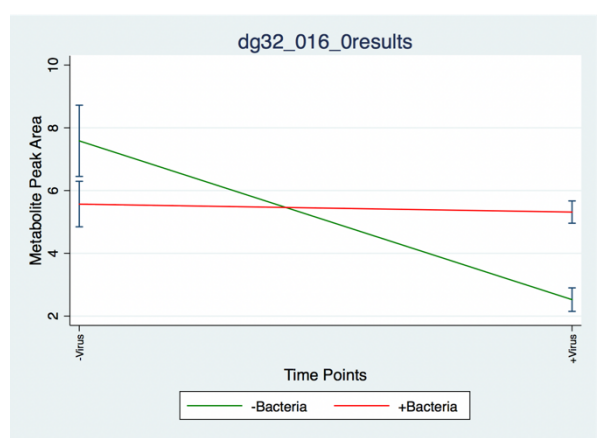
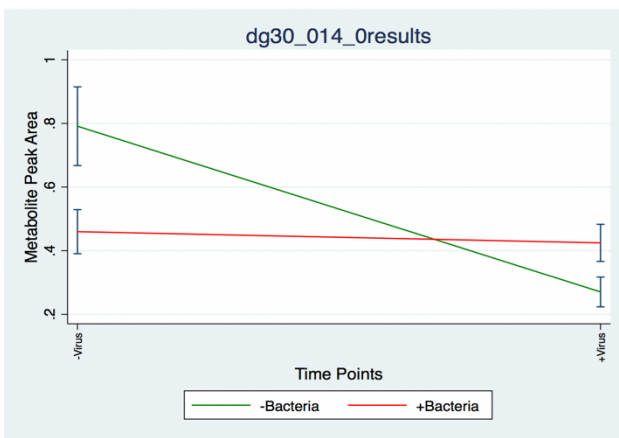
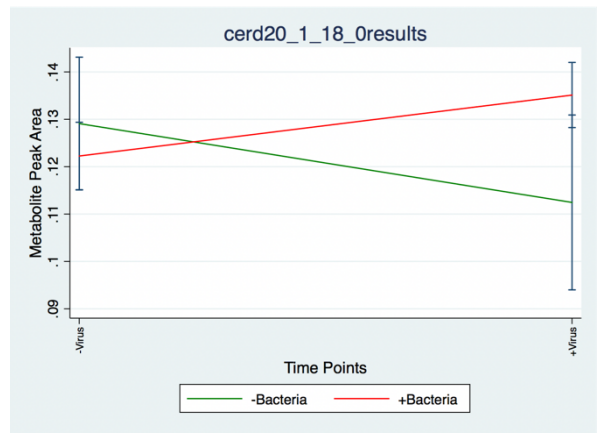
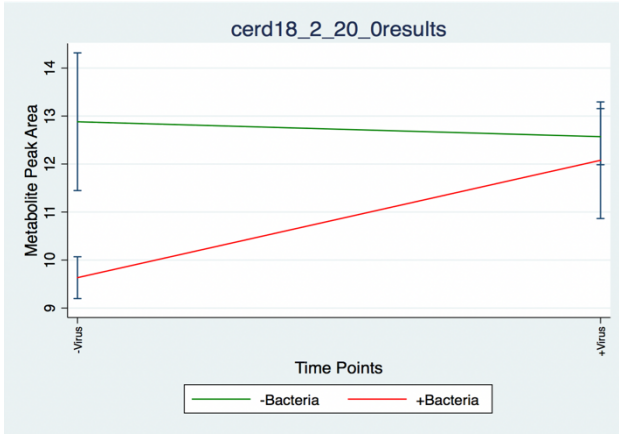


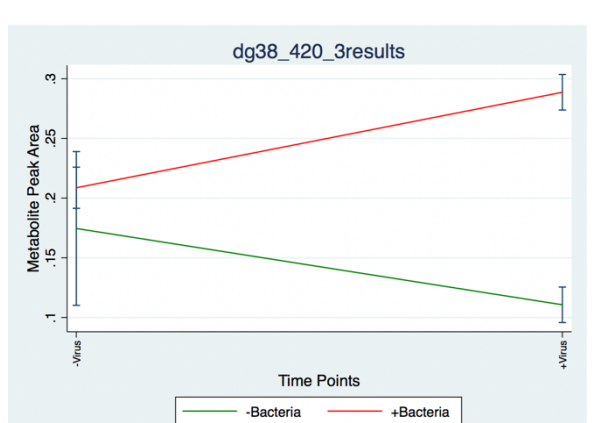
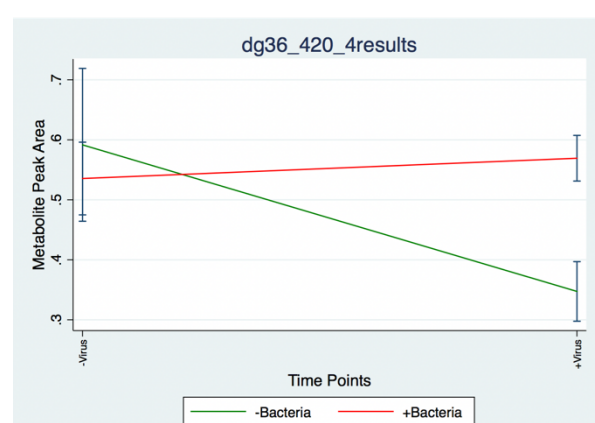
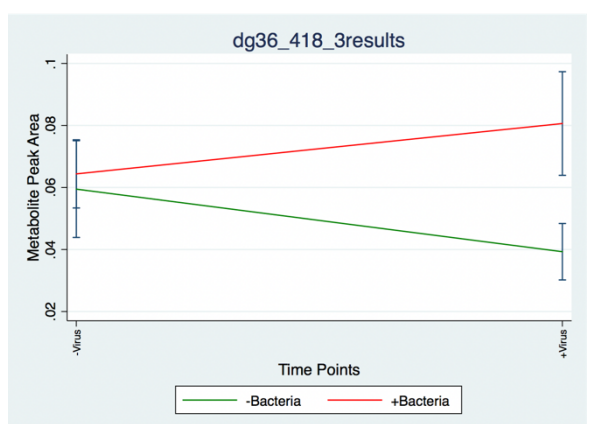
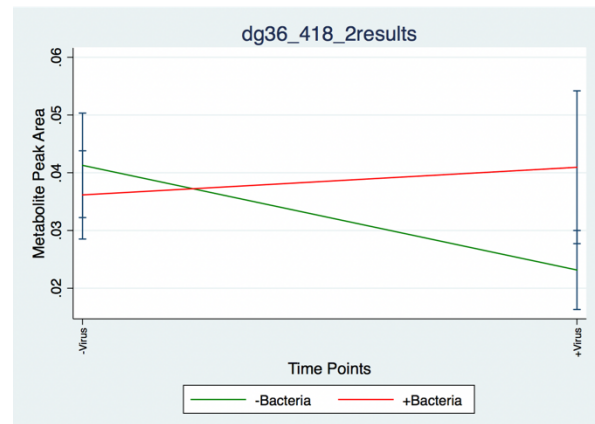
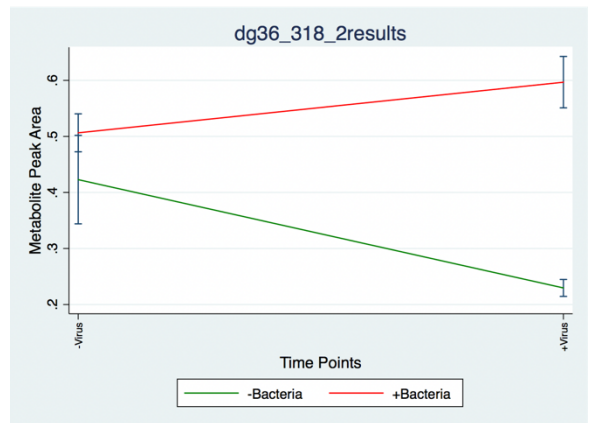
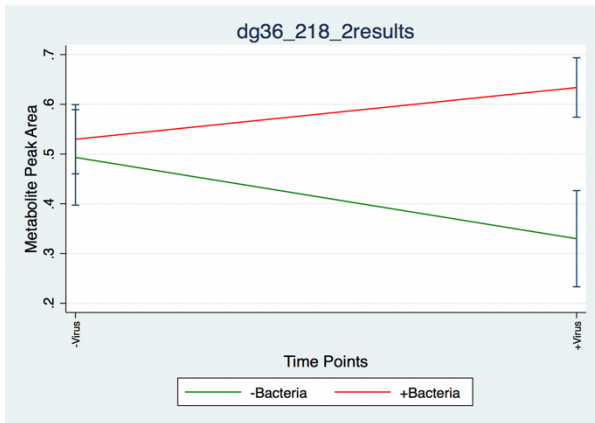
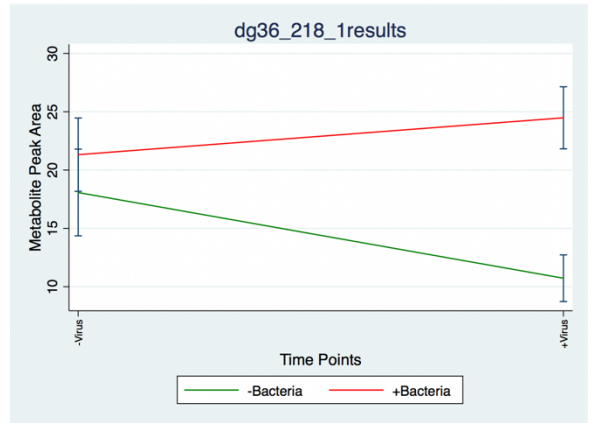
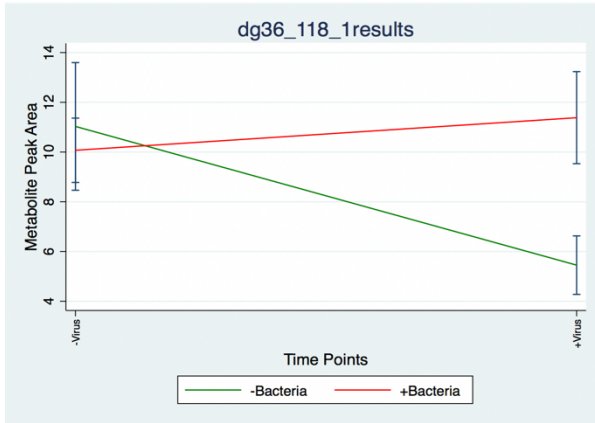
Two-way ANOVA plots – ZIKV African

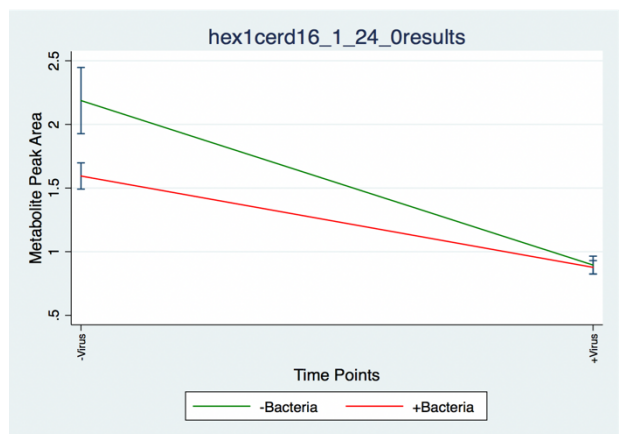
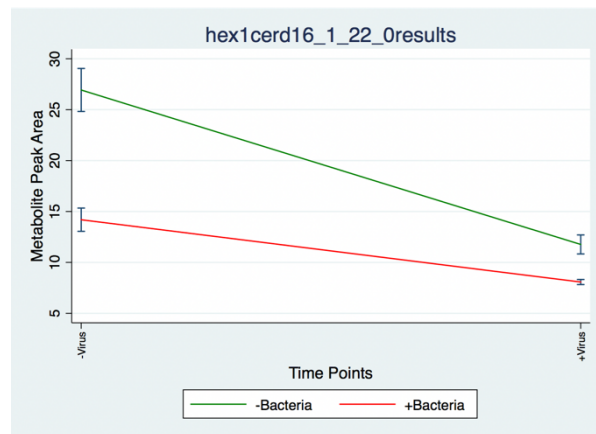
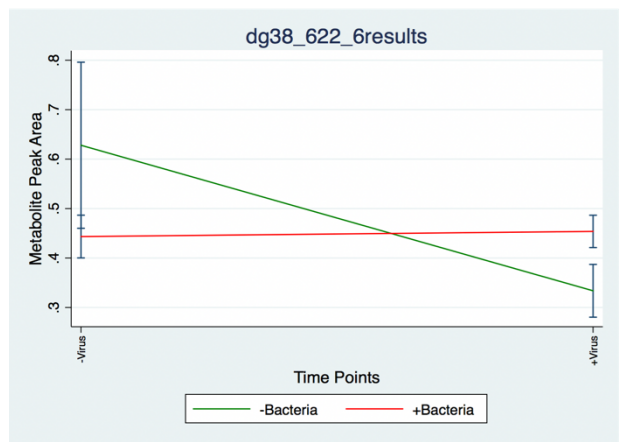
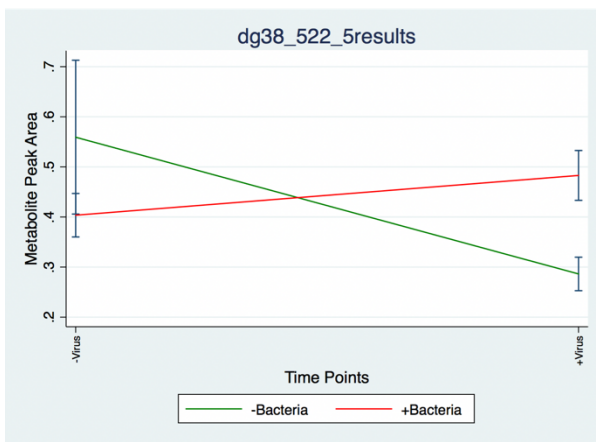
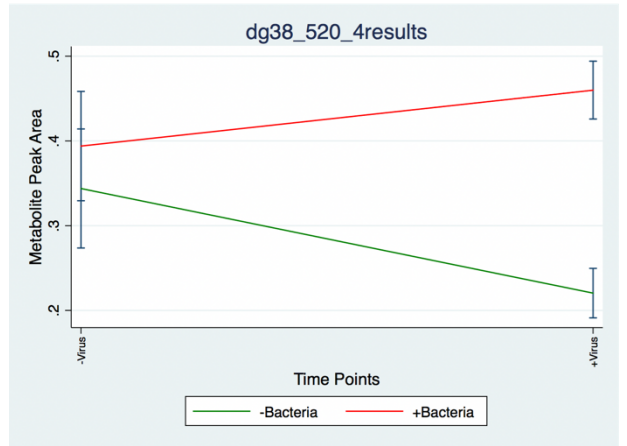


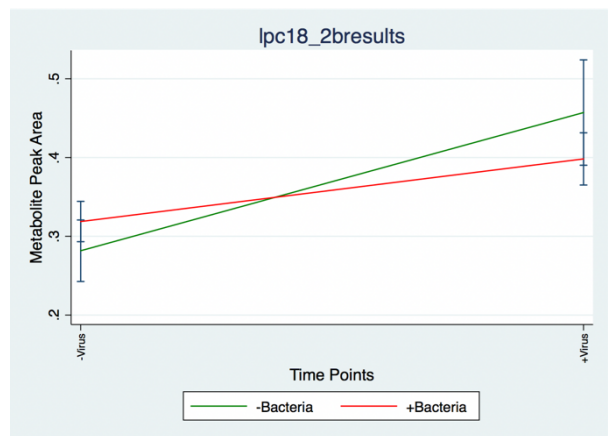
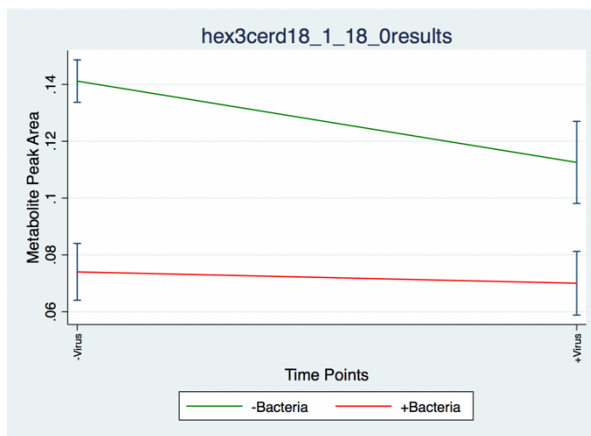
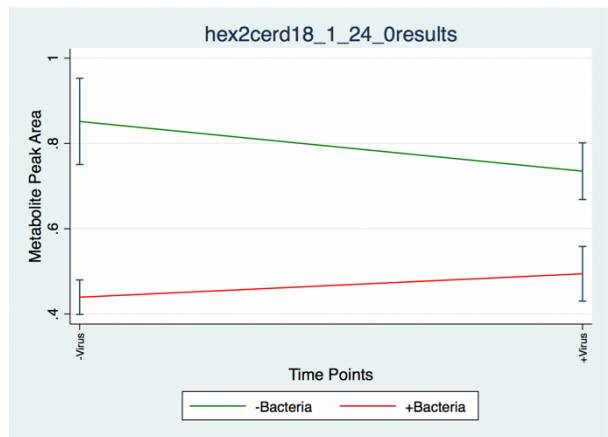
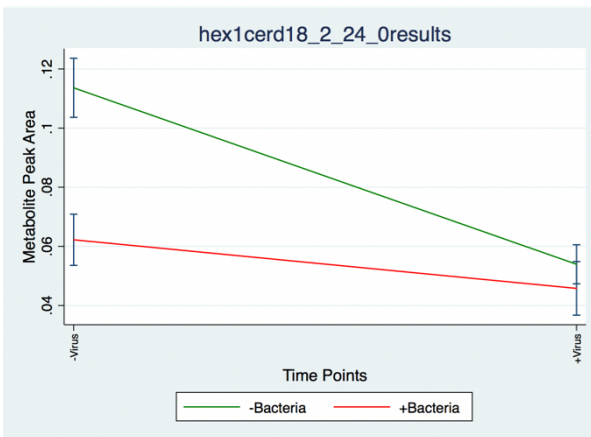
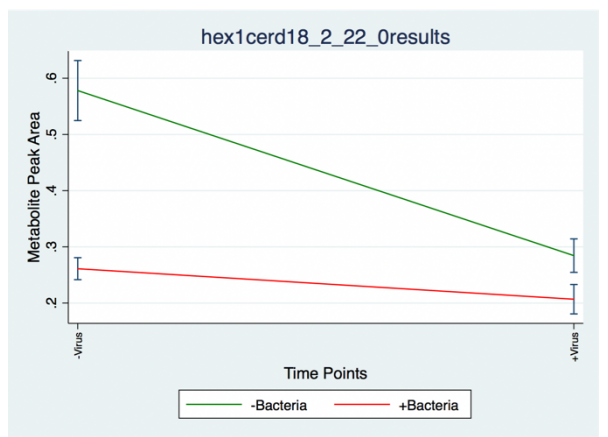
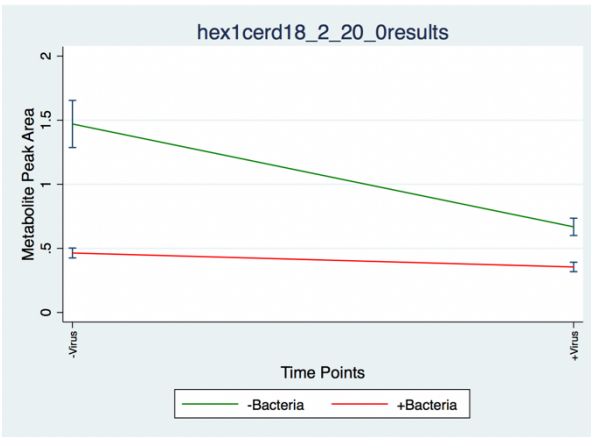


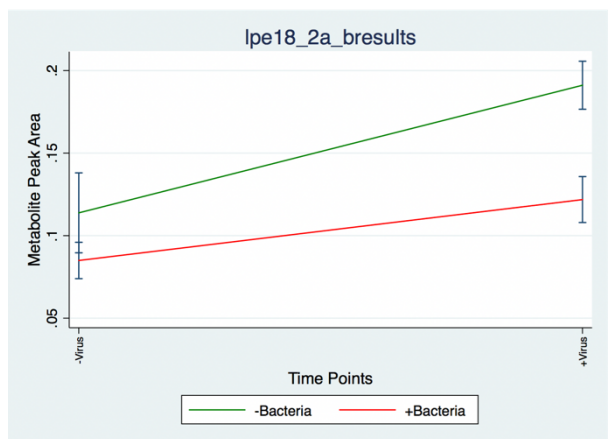
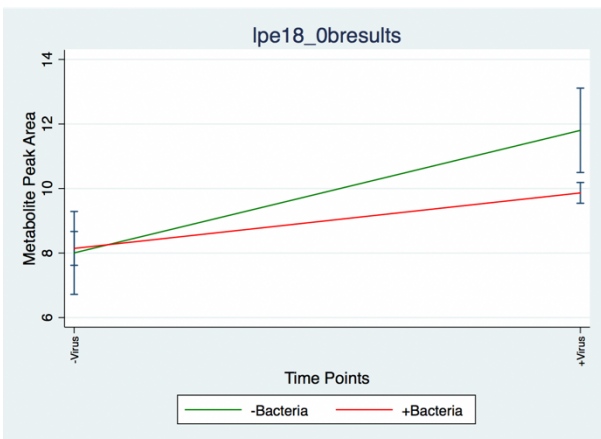
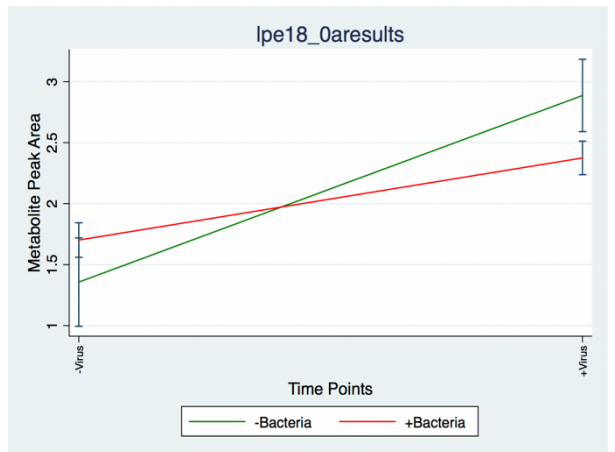
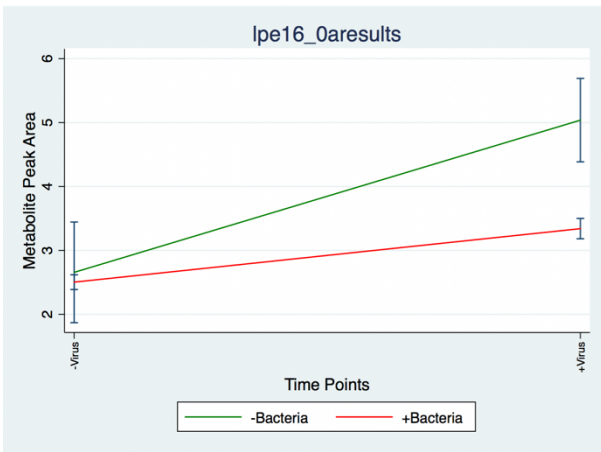
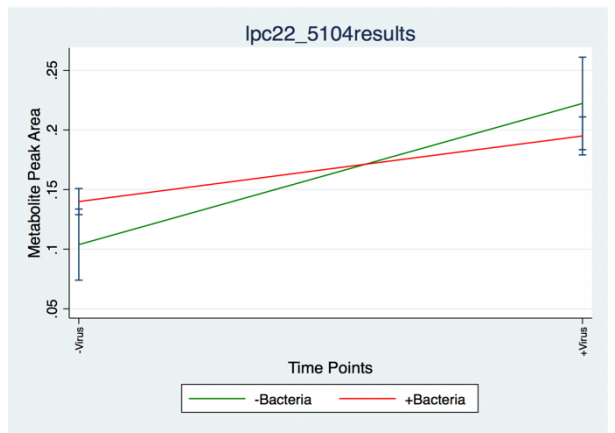
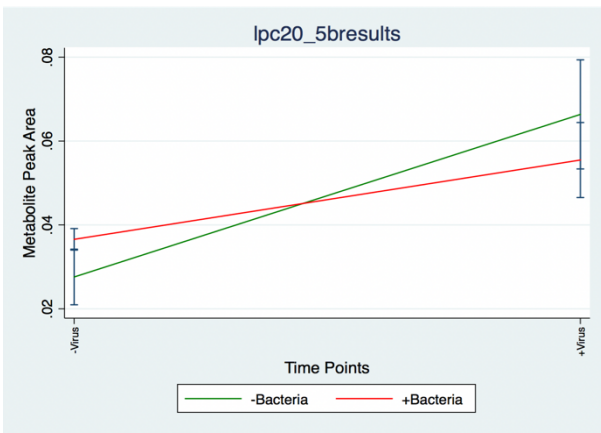
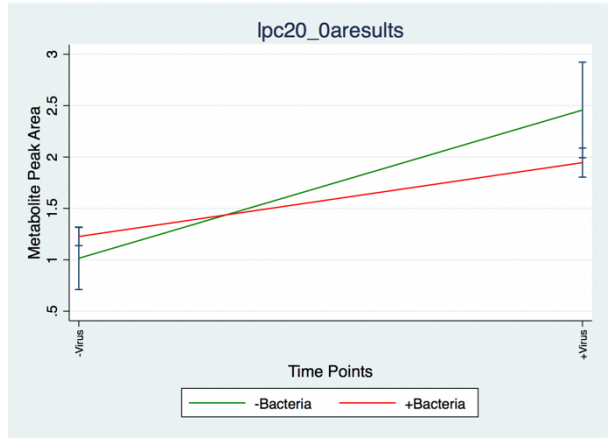
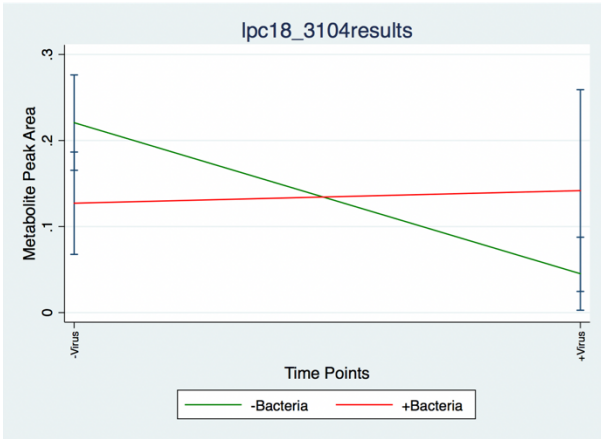


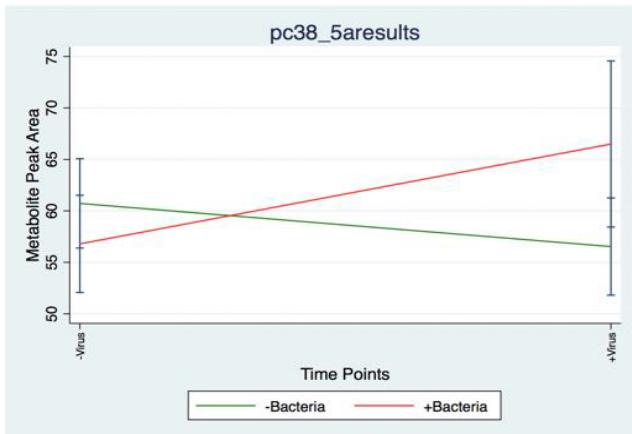
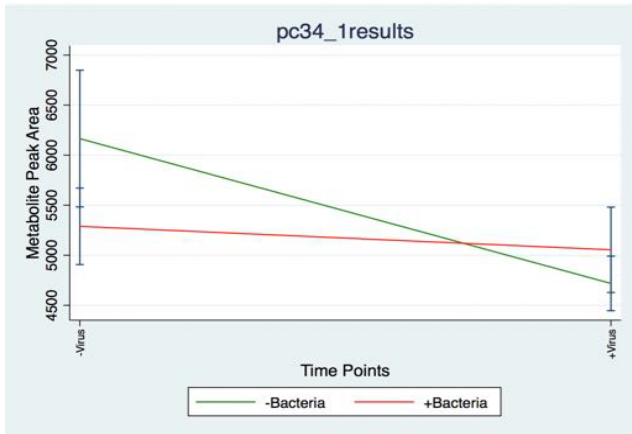
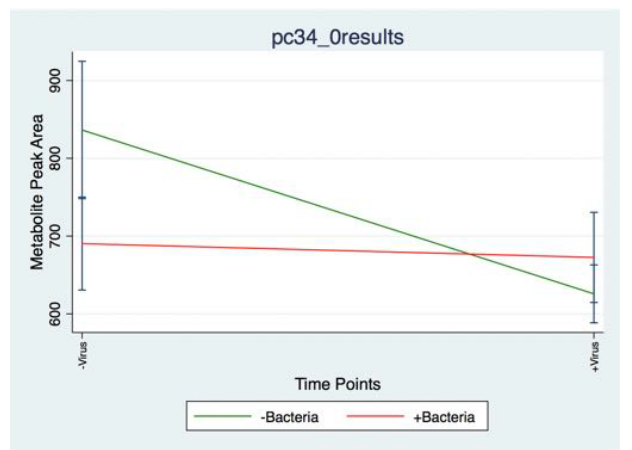
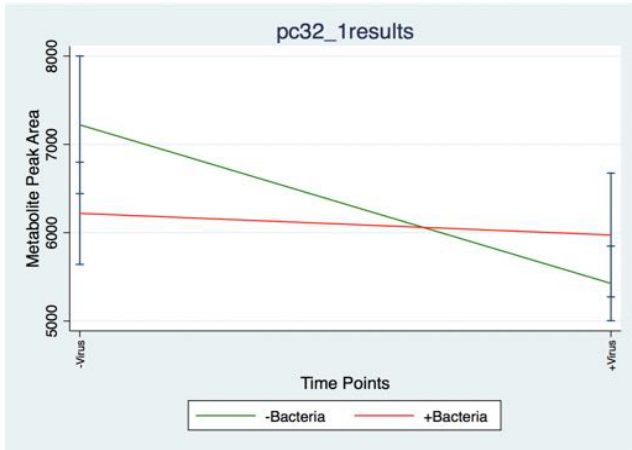
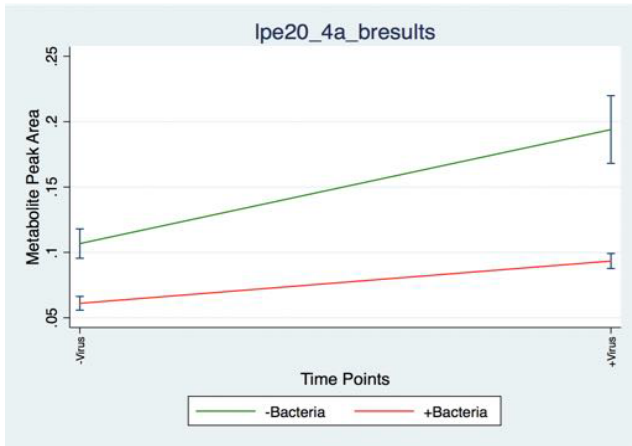




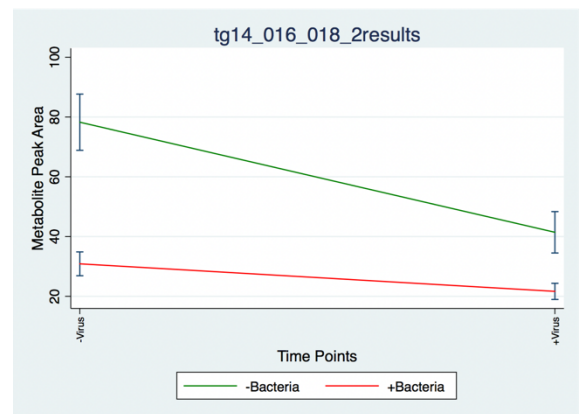
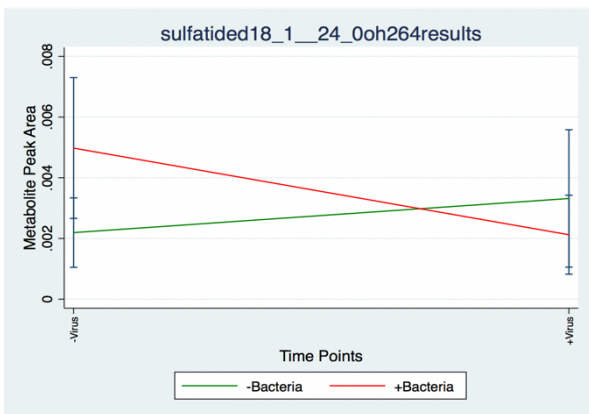
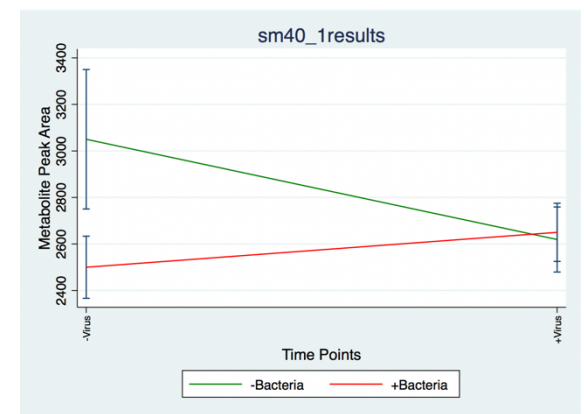
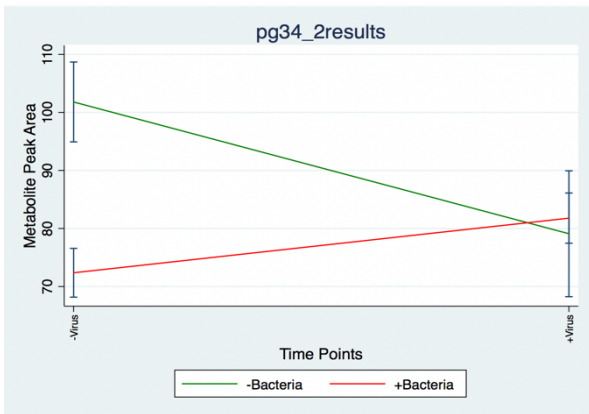
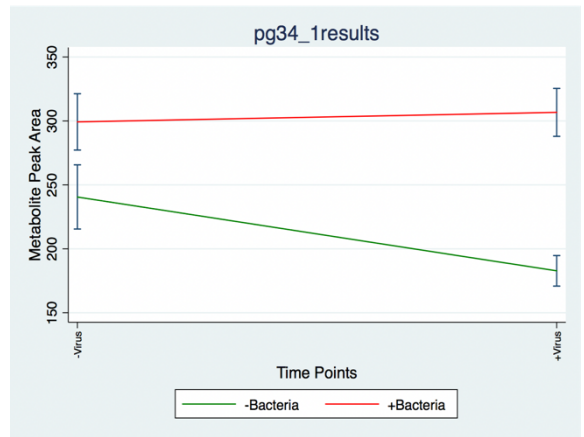


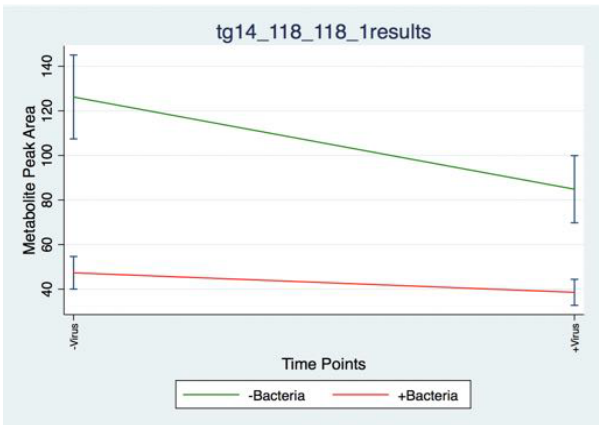
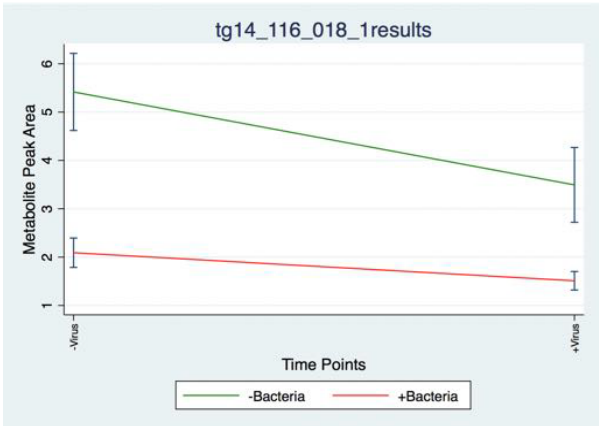
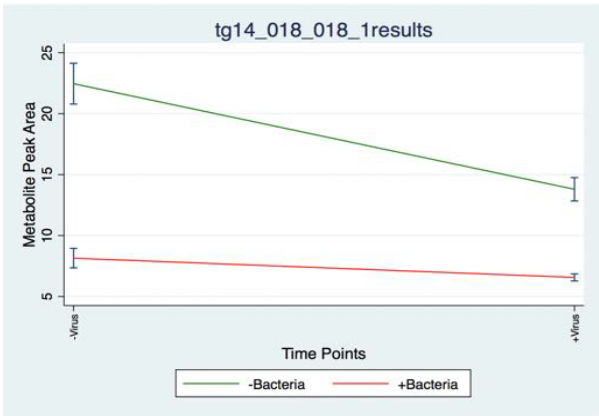


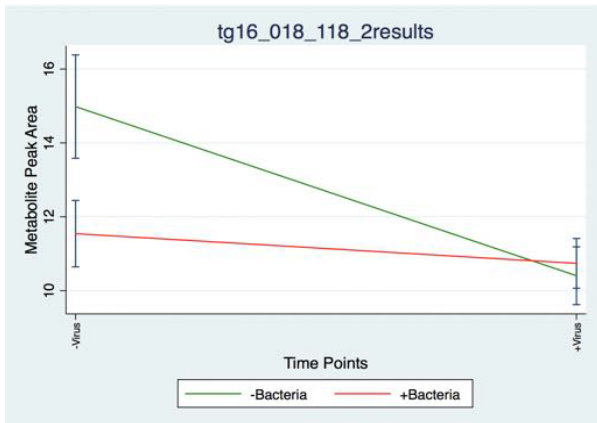
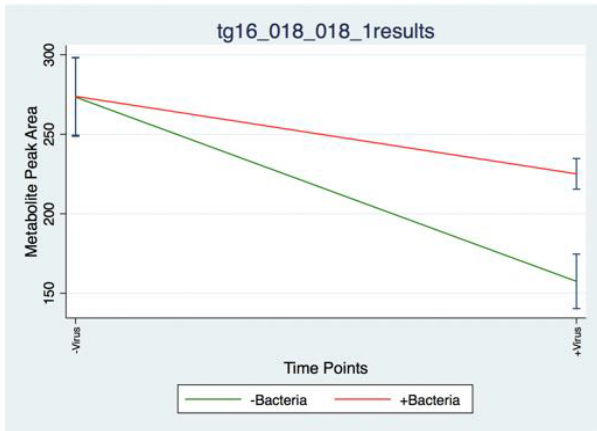


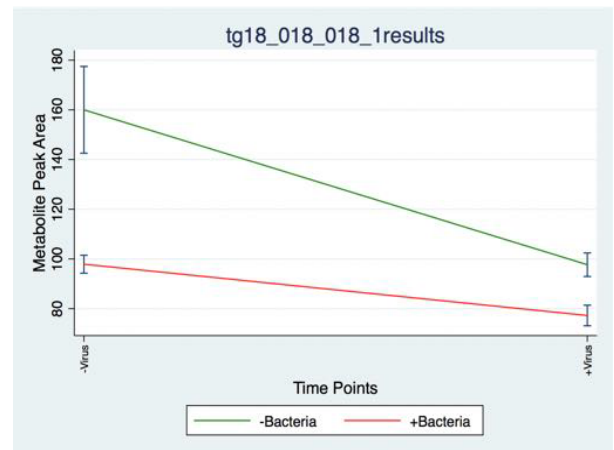
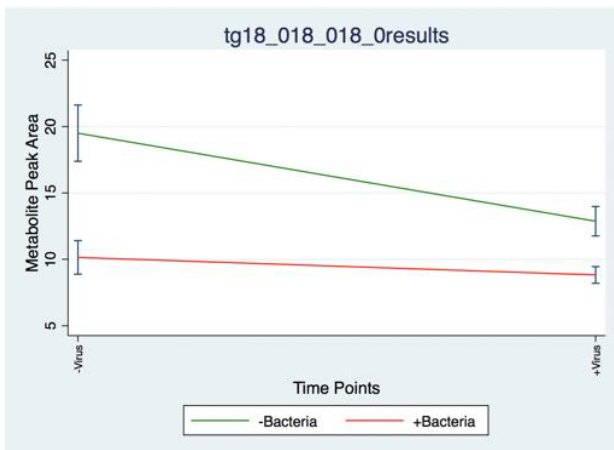


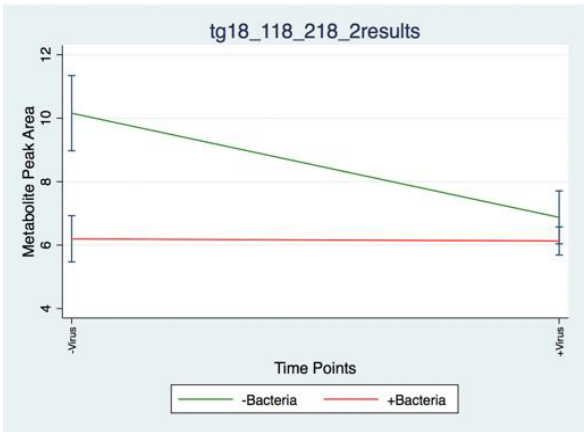
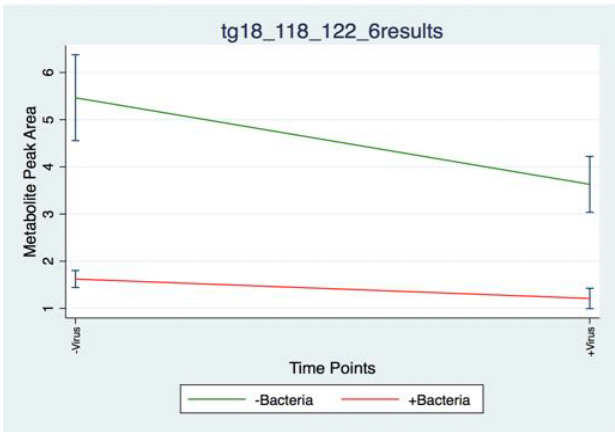
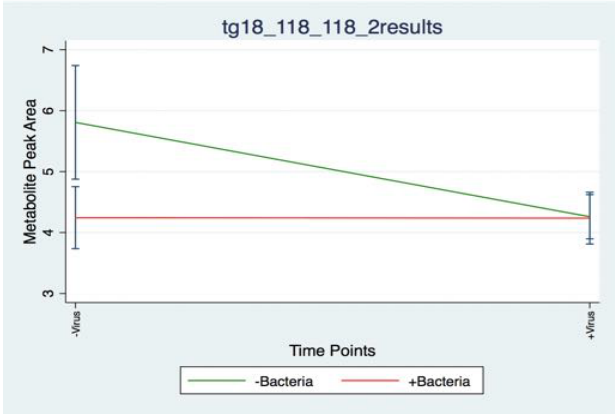
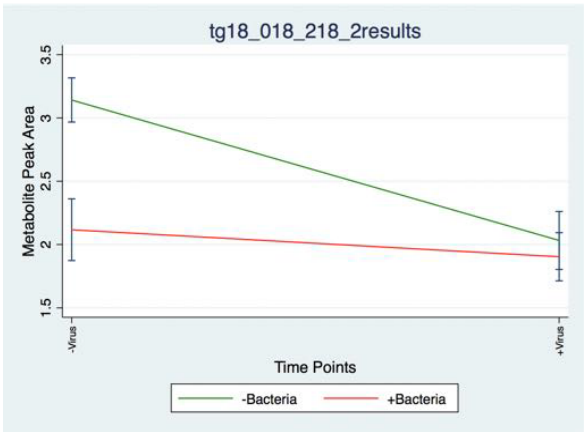












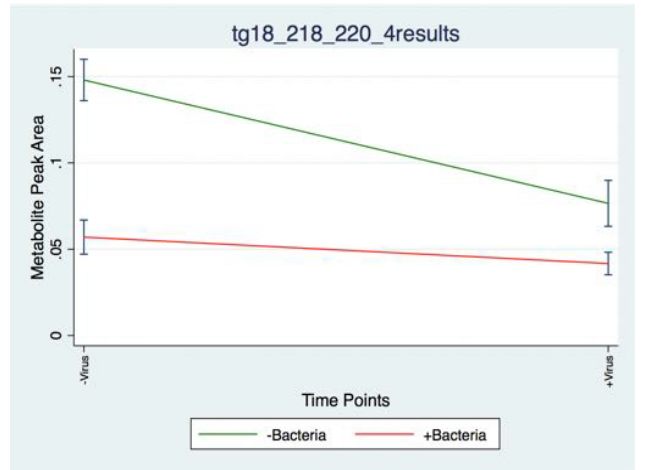
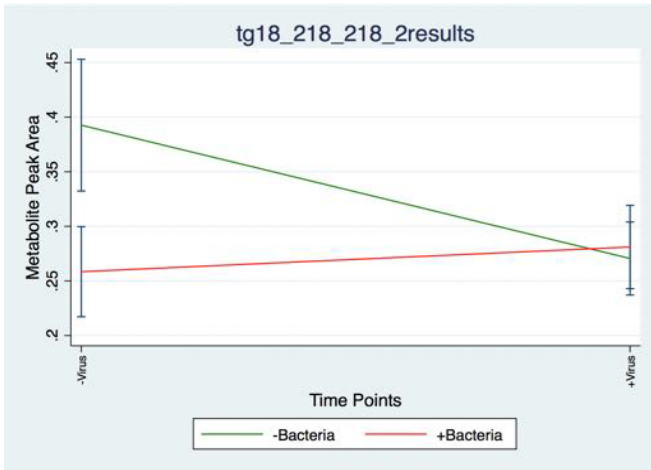


Fig. S4. Validation of etomoxir treatment. (A) Drug cytotoxicity profile of HuH7 cells after treatment with Etomoxir or the vehicle control DMSO at various concentrations over 24 H or 48 H. Cytotoxicity was measured using the CytoTox 96 Non-Radioactive Cytotoxicity Assay (Promega). LDH+ release was measured by adding the Cytotox reagent and measuring absorbance at 490nm on a plate reader (ClarioStar). Data are represented as mean \pm SEM; * $p < 0.05$; ** $p < 0.01$; *** $p < 0.001$; **** $p < 0.0001$; n.s. : Not significant, two-tailed Student's t-test. (b-c) Nile red staining of HuH7 cells after etomoxir treatment for 48 H. Cells were fixed and stained with Nile red, a dye for lipid droplets. (B) As etomoxir treatment inhibits acylcarnitines, there is an upstream accumulation of lipid droplets which can be observed in the treated cells (C) The corrected total cell fluorescence (CTCF) shows that there is significantly higher fluorescence in the etomoxir-treated cells which confirms that the treatment worked.

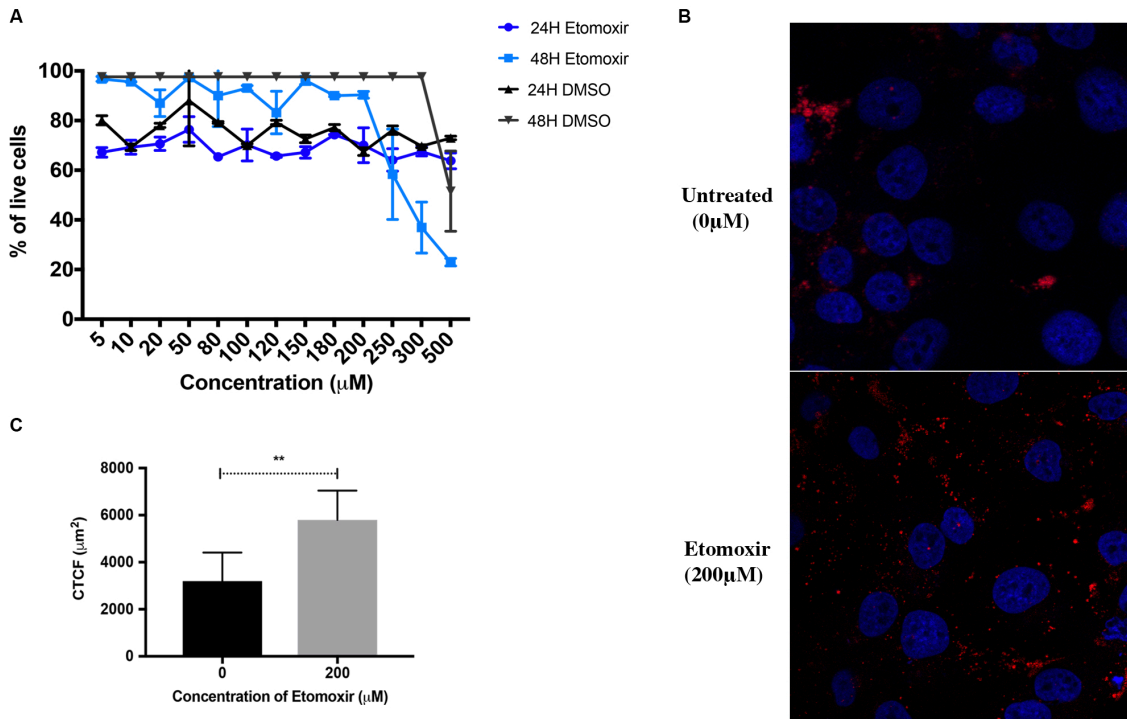
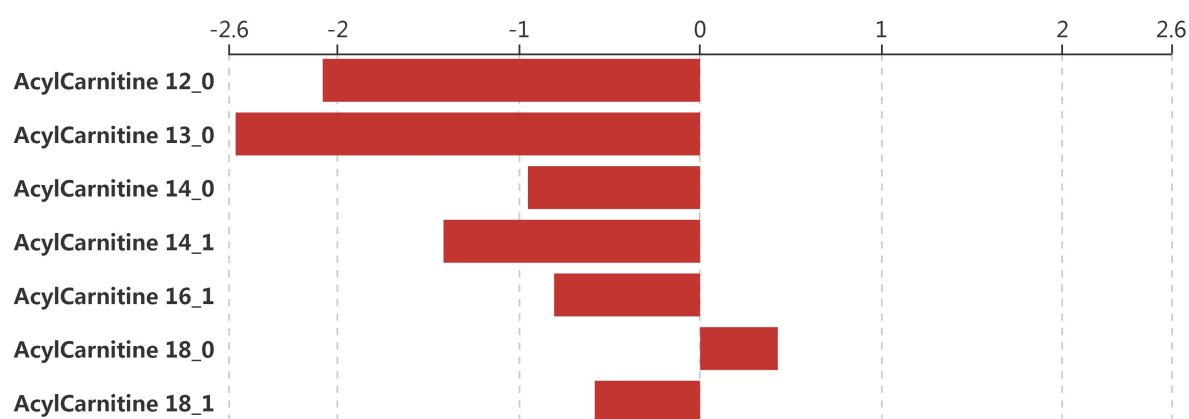
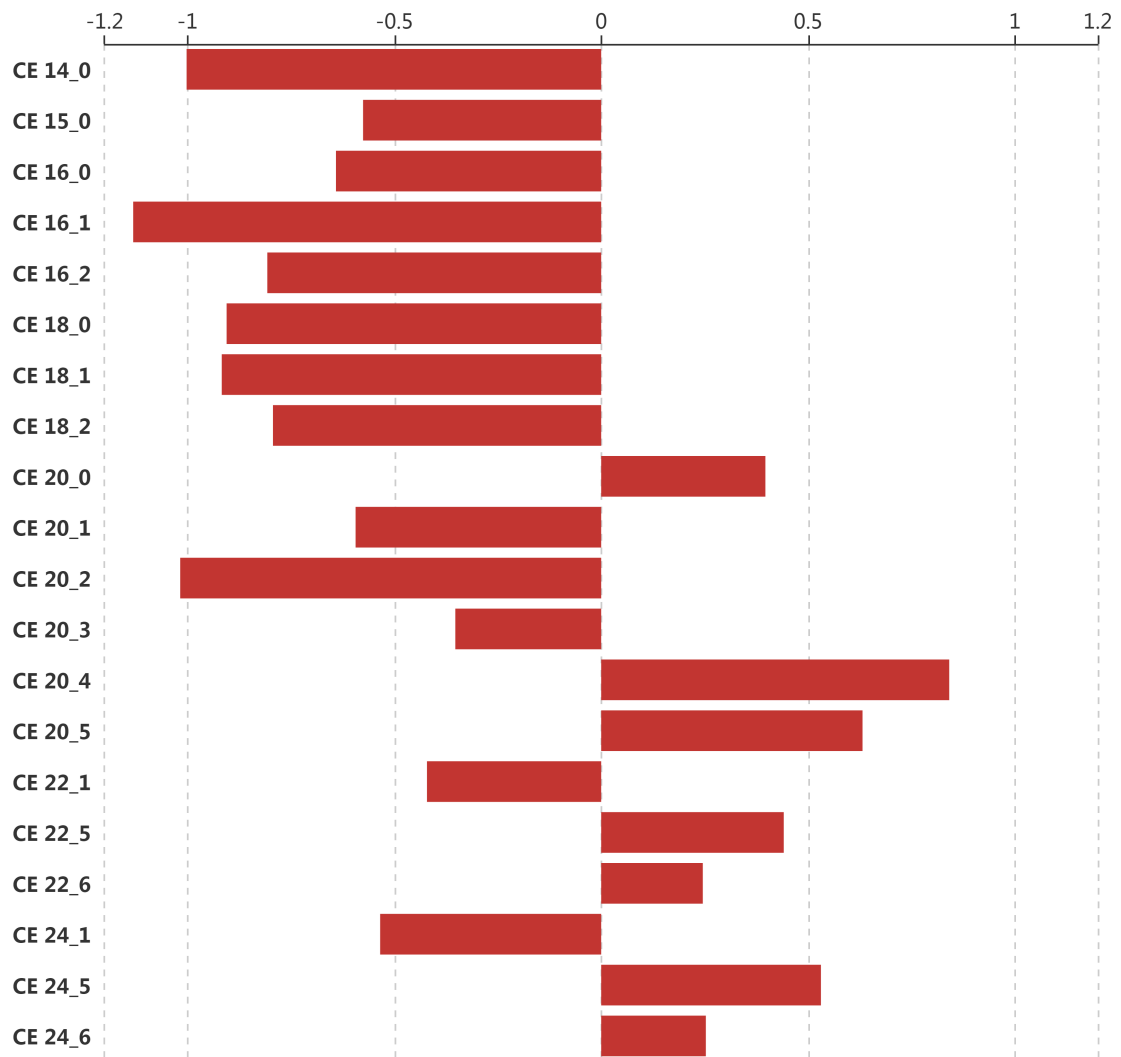


Fig. S5. LCMS results post-etomoxir treatment. Plots showing the fold changes of significantly modulated metabolites after treatment with Etomoxir. Fold changes were calculated as etomoxir-treated cells (TXT) against untreated cells (Untxt) and results were grouped according to lipid species. Briefly, HuH7 cells were treated with 200 μ M etomoxir or left untreated for 48 H after which cells were lysed for LCMS. Etomoxir treatment results in significantly changed acyl-carnitine levels as compared to untreated cells. 6 out of 7 acylcarnitines (except for acyl-carnitine 18:0) which were significantly modulated, were reduced in treated cells. There were corresponding changes in other lipid species as shown since many lipid pathways are intertwined and interrelated. It is virtually impossible to downregulate one pathway and not expect a co-related change in another. All conditions were performed in replicates of six; error bars represent SEM.

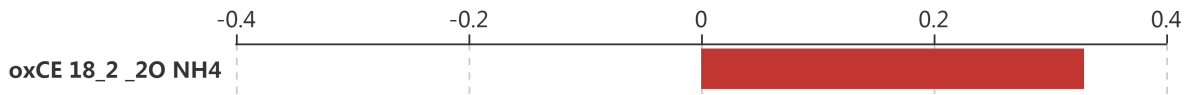
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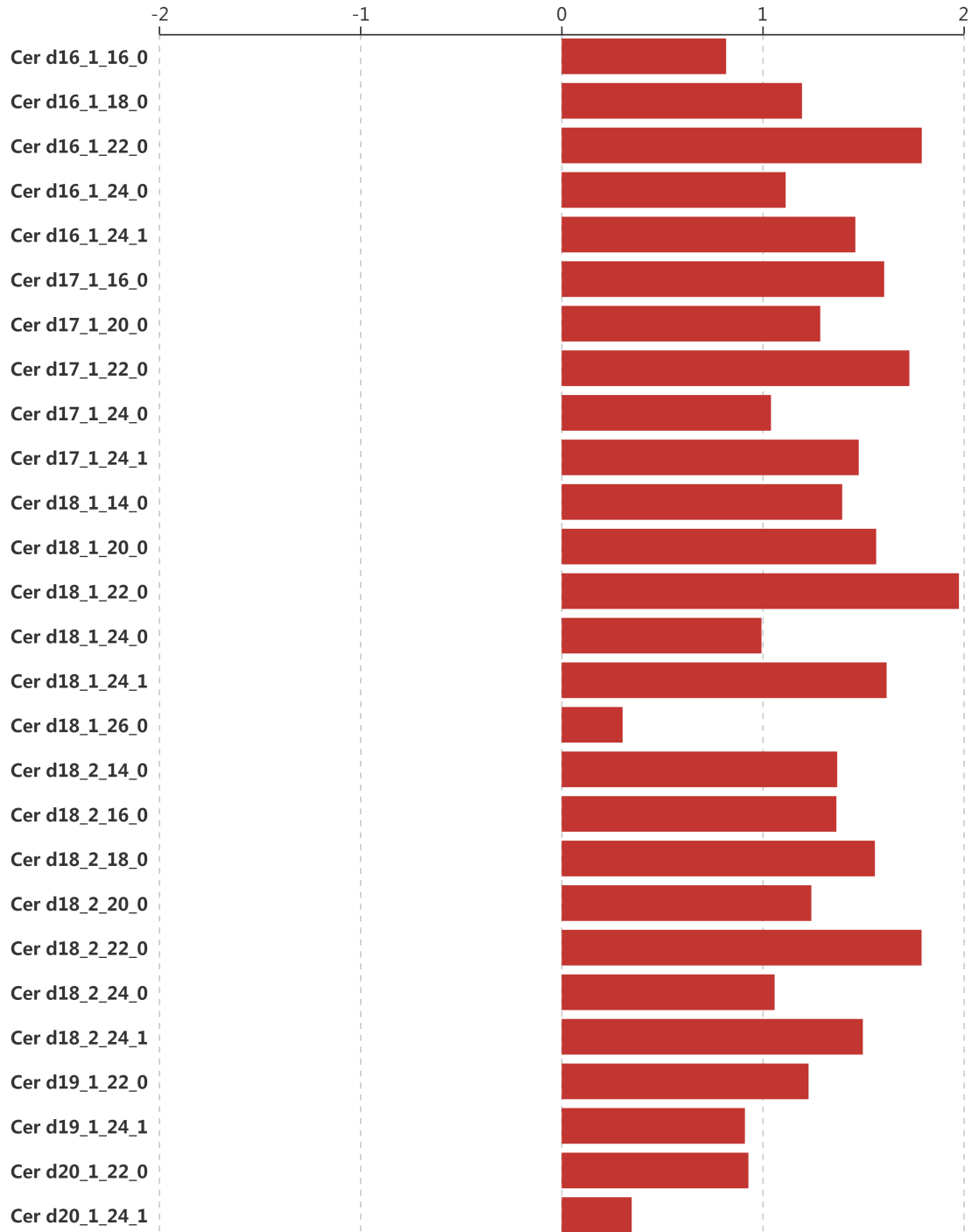
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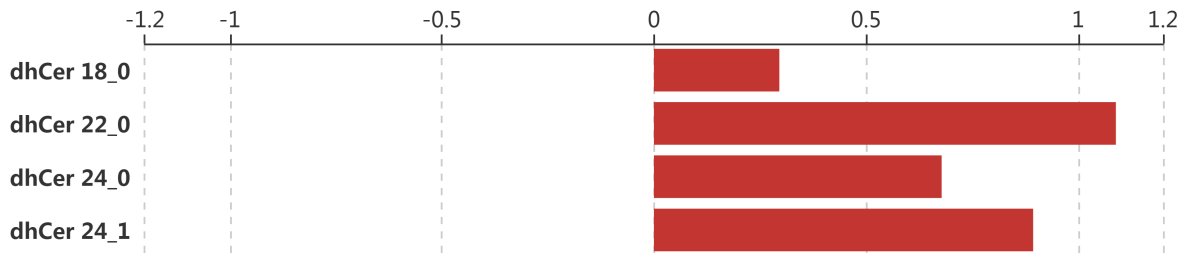
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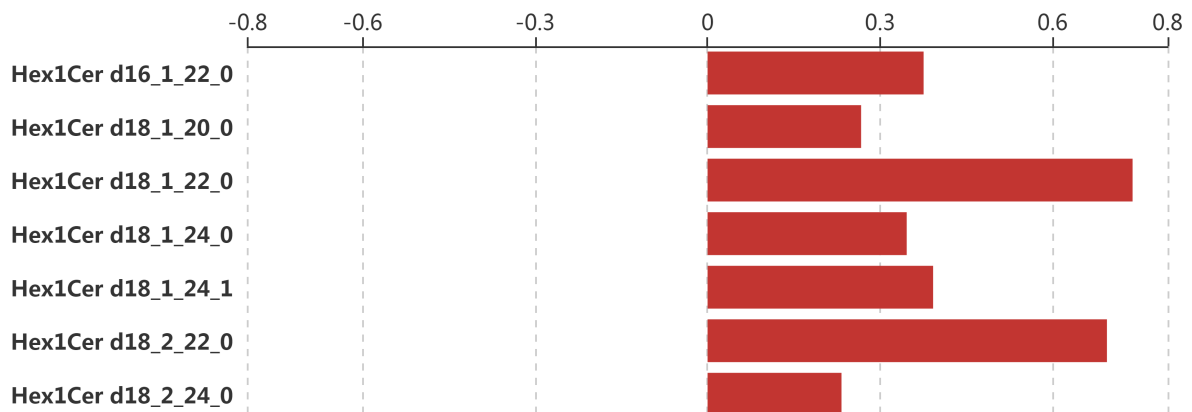
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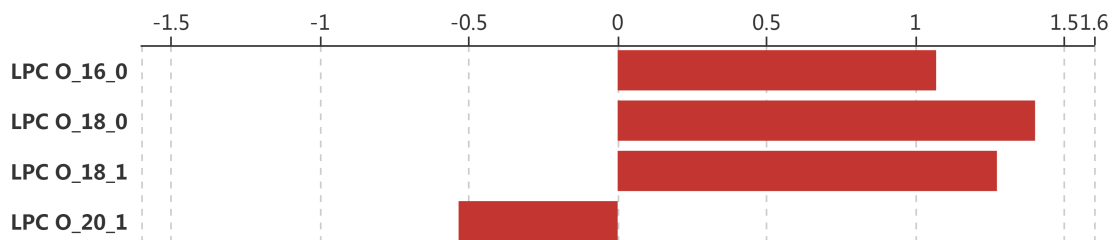
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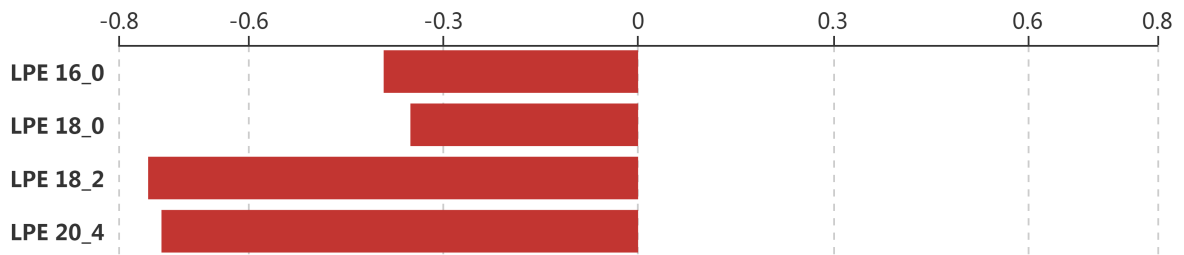
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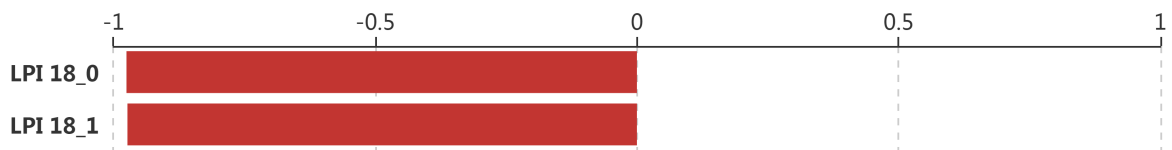
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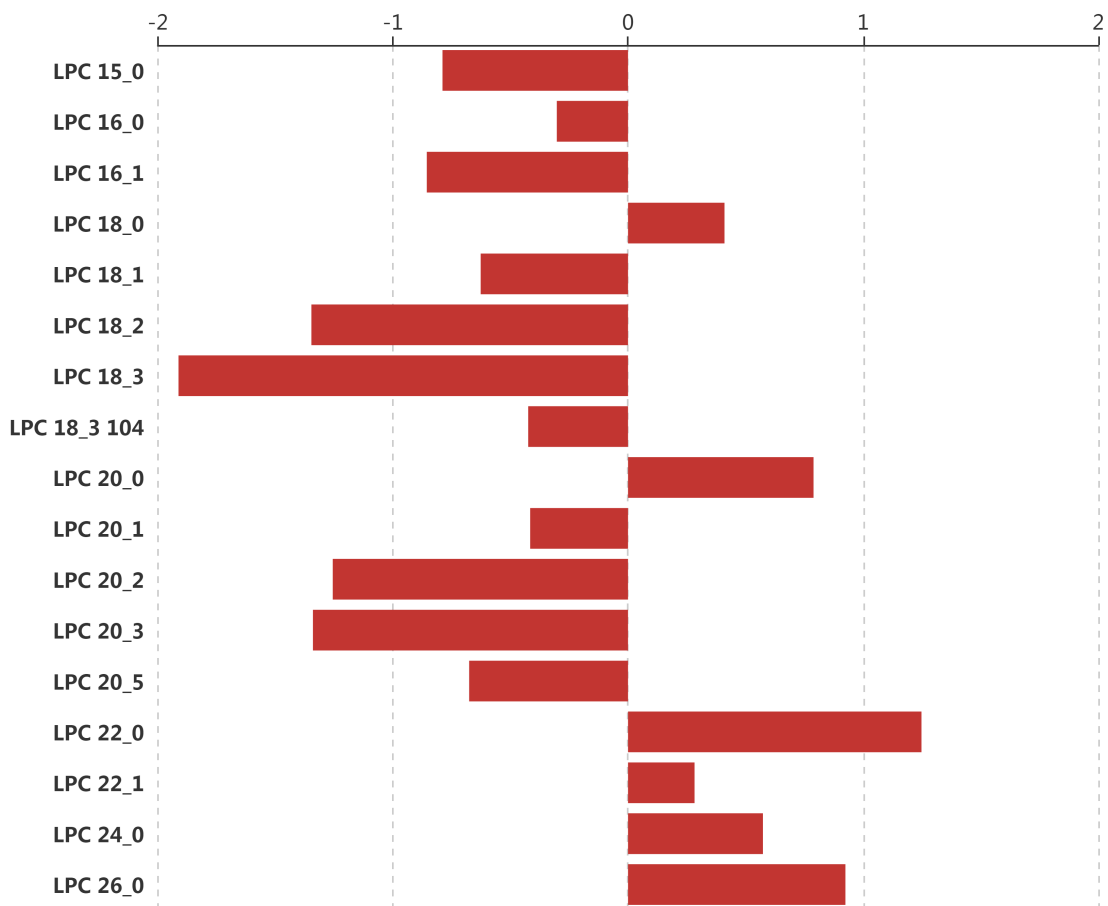
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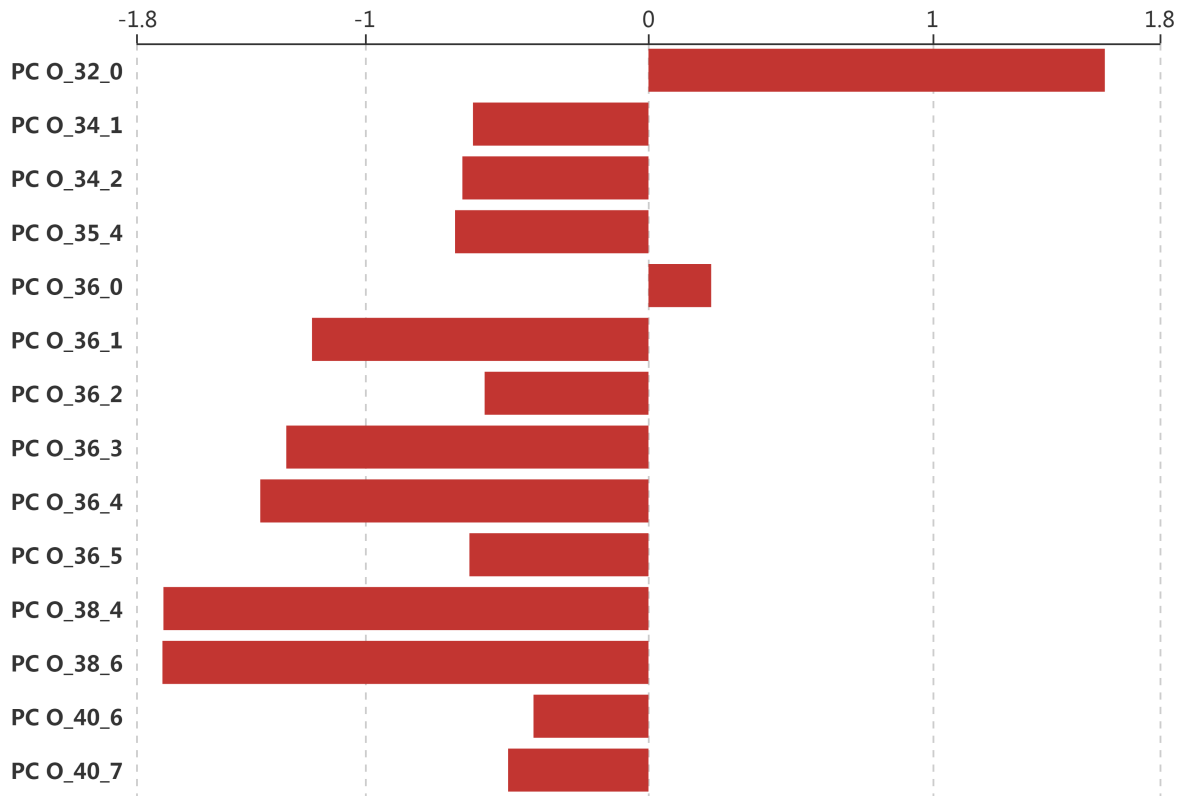
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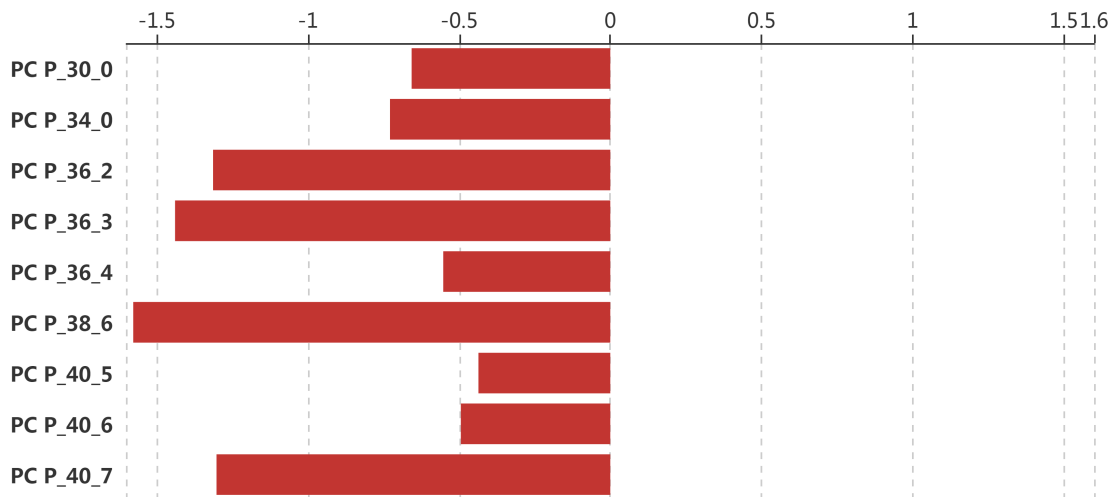
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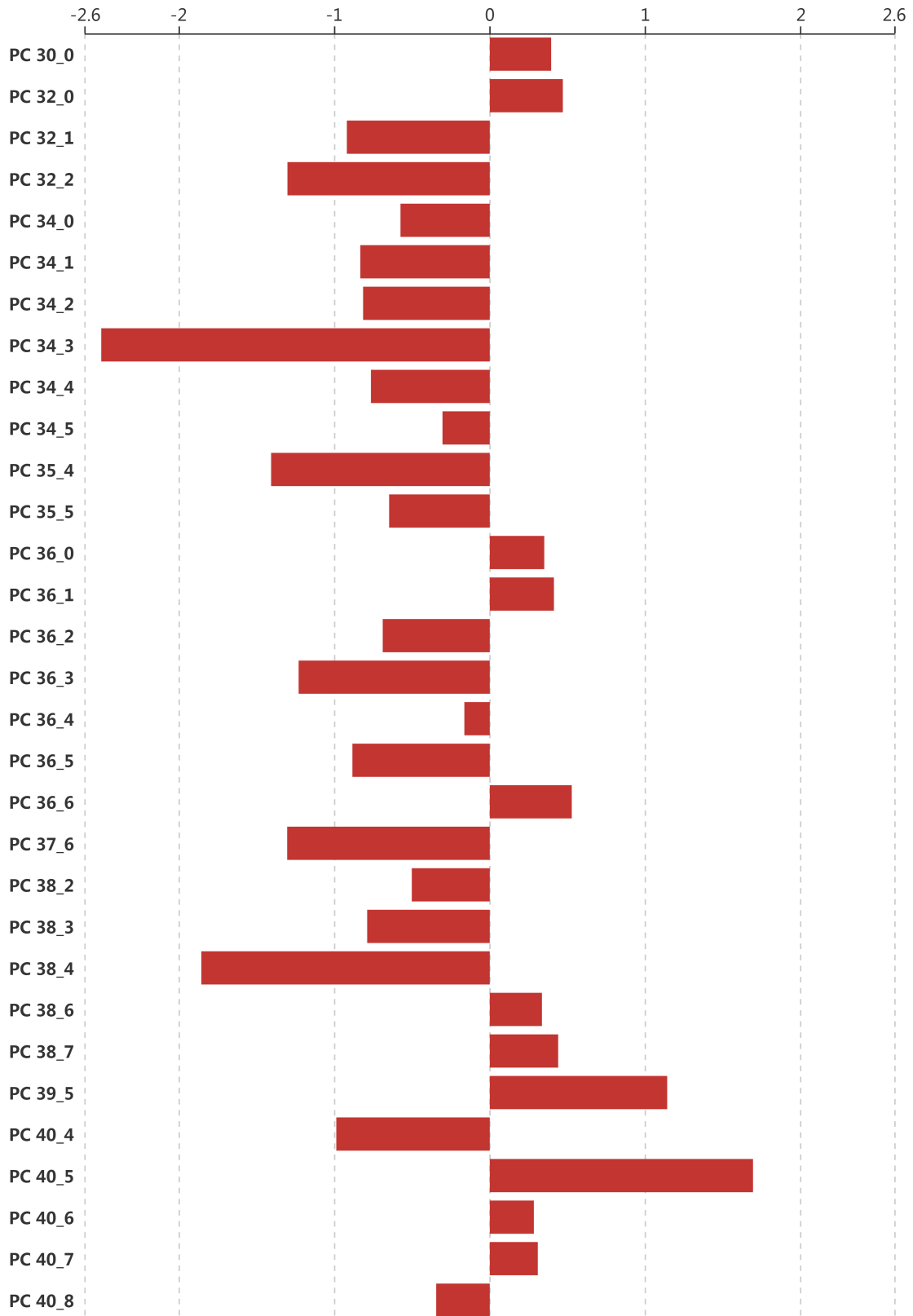
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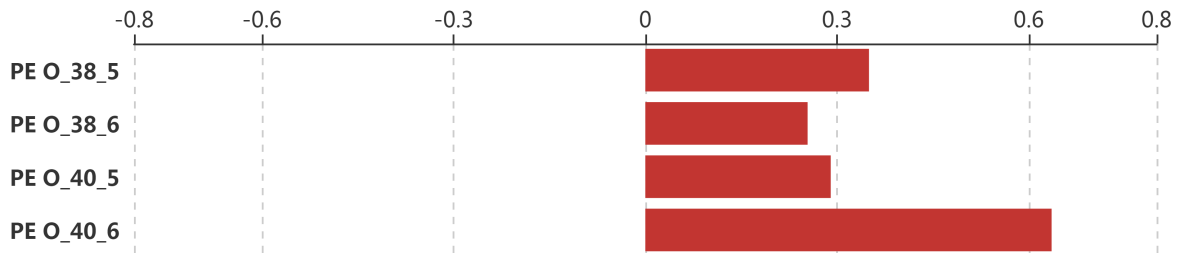
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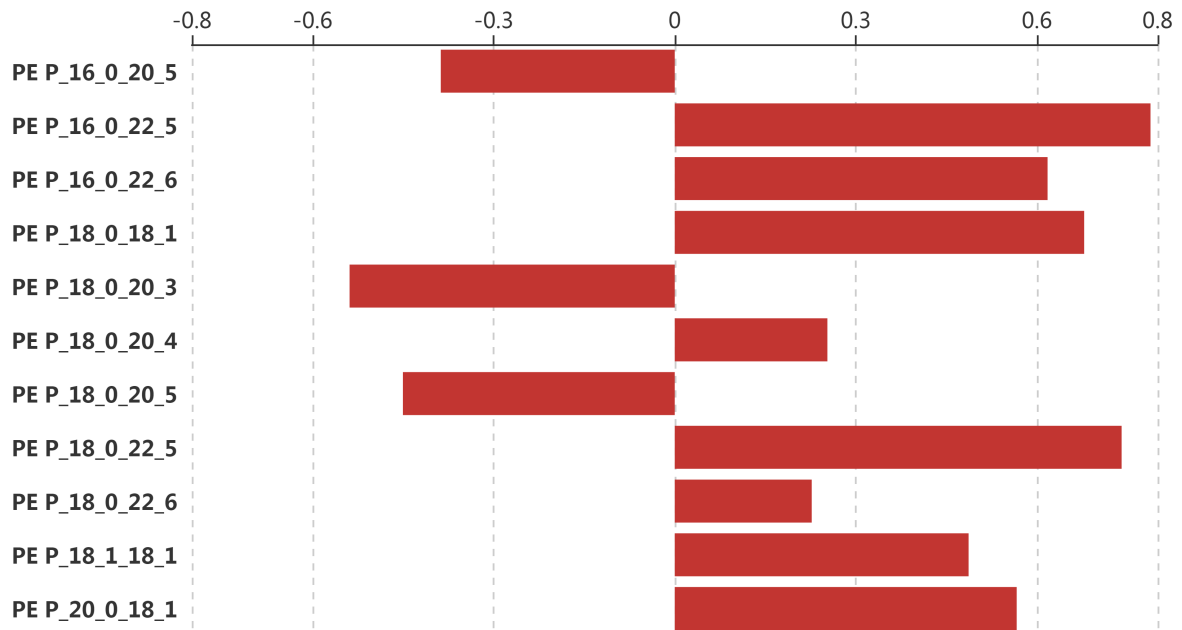
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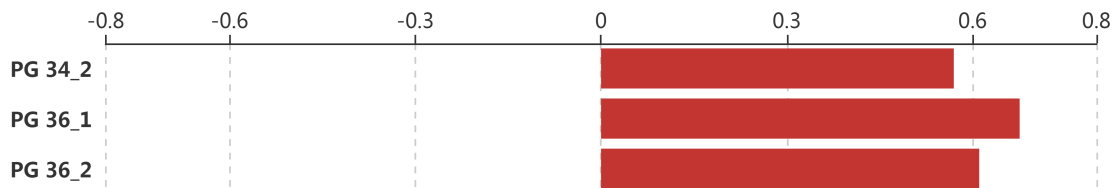
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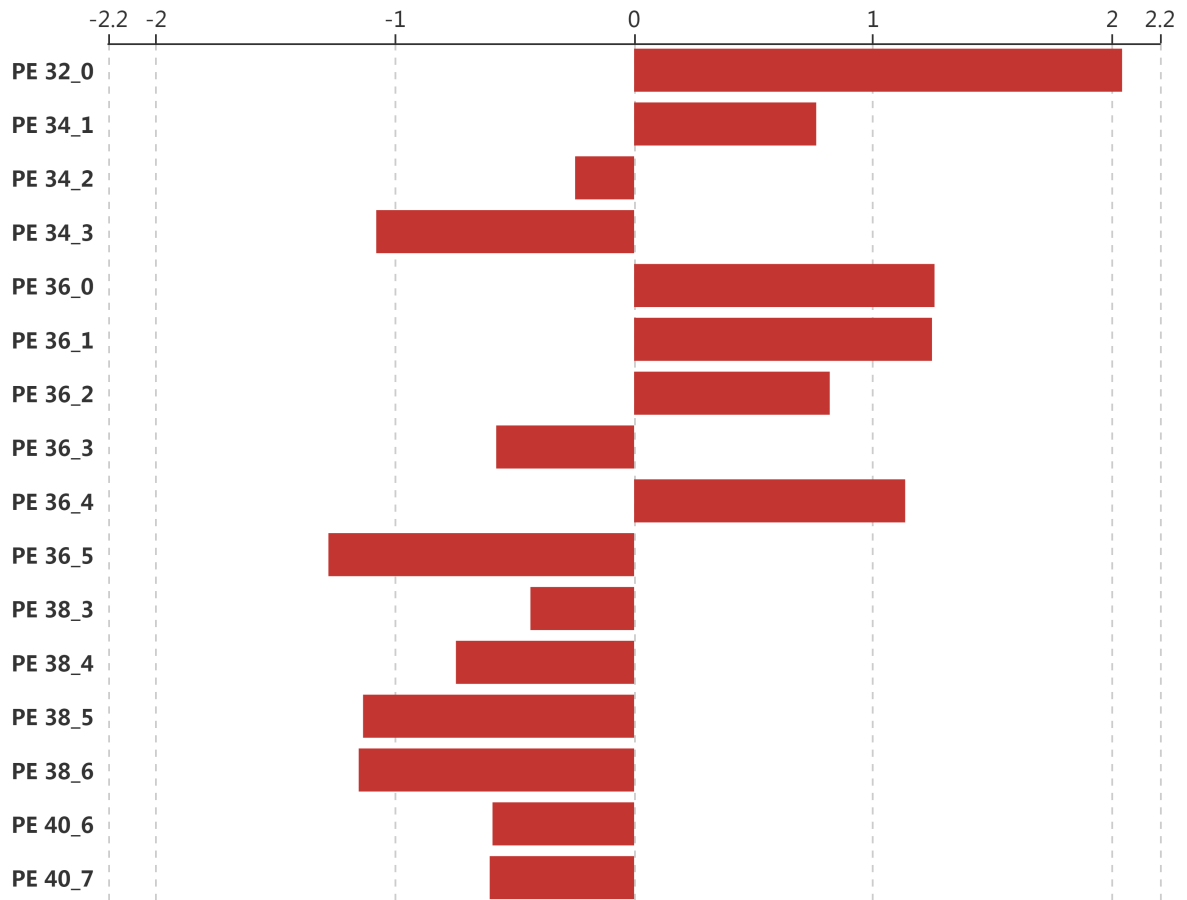
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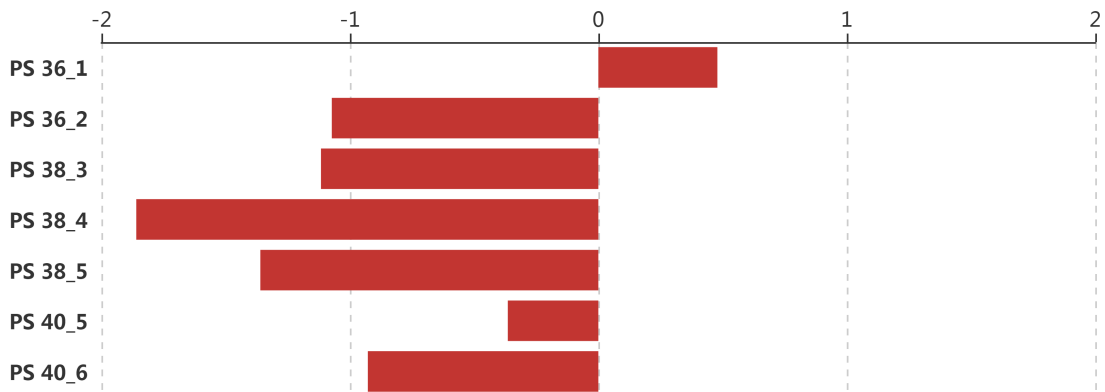
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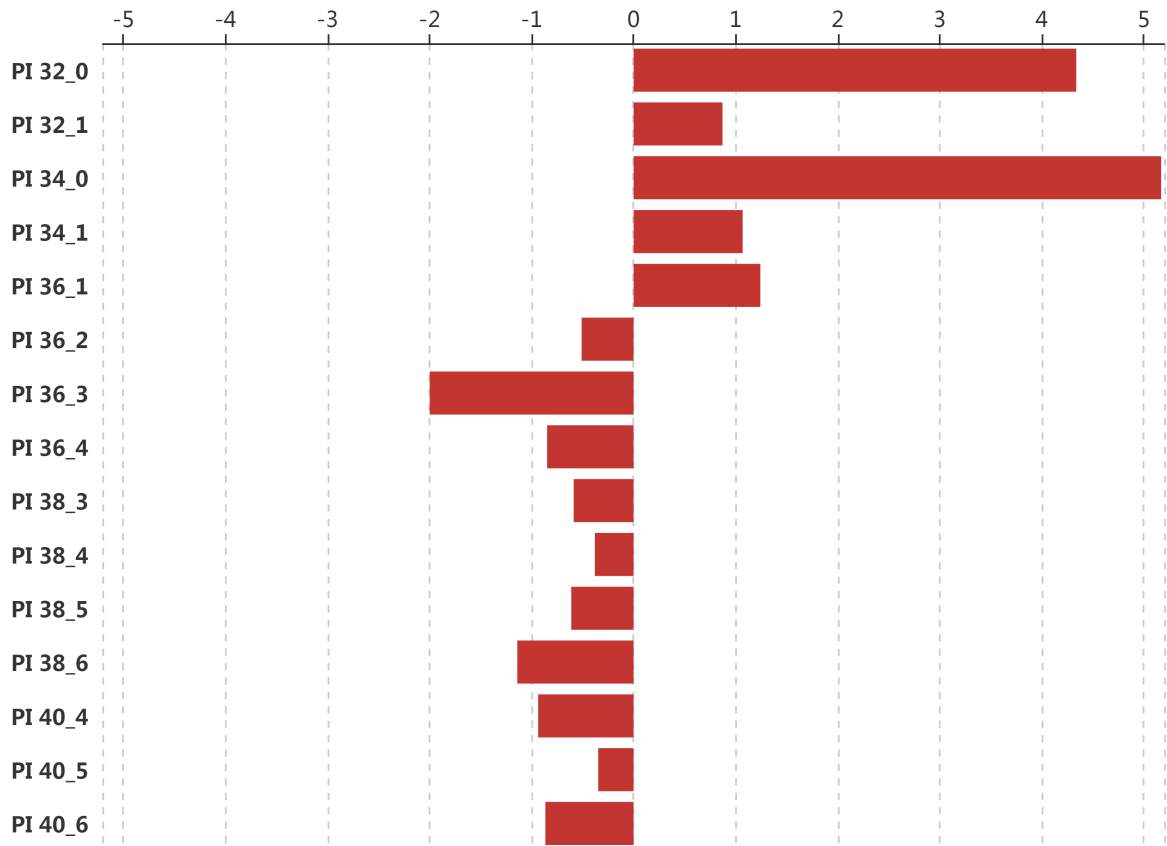
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Class Name: PS In(TXT/Untxt)



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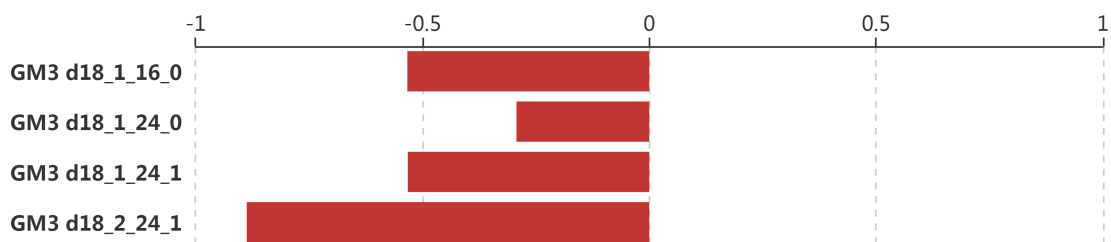
Class Name: Ubiquinone In(TXT/Untxt)



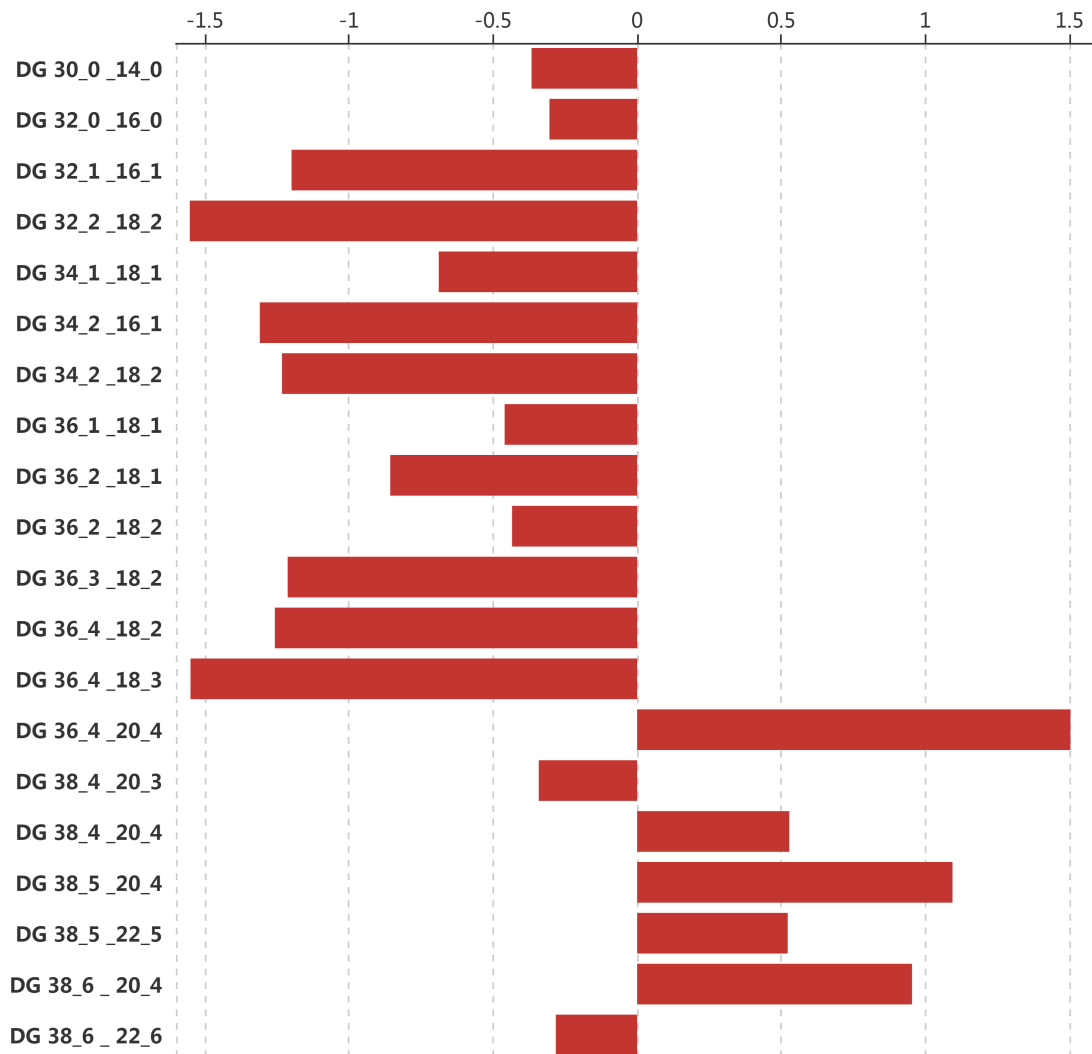
Class Name: TG-O In(TXT/Untxt)



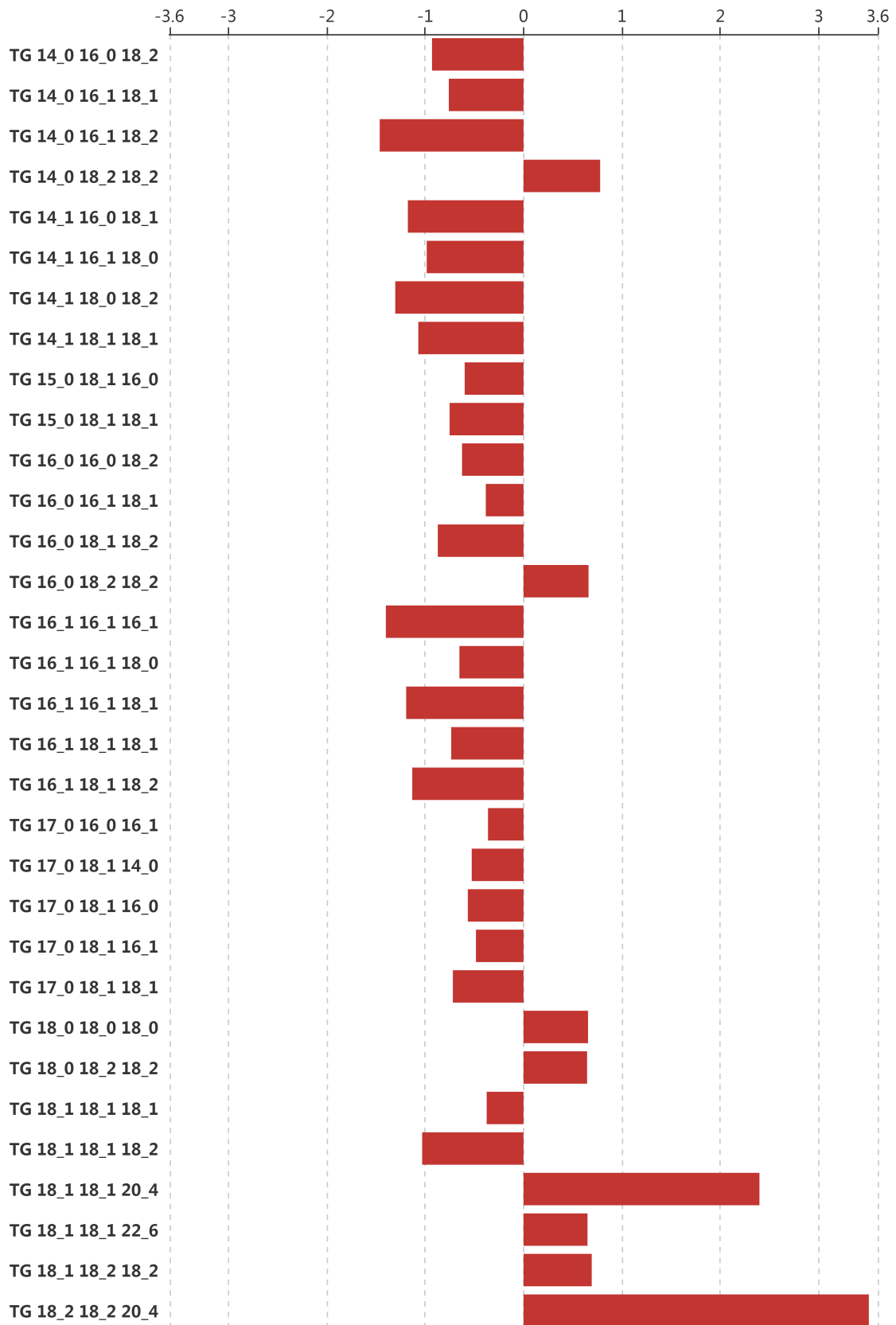
Class Name: GM3 In(TXT/Untxt)



Class Name: DG In(TXT/Untxt)



Class Name: TG In(TXT/Untxt)



Class Name: SM In(TXT/Untxt)

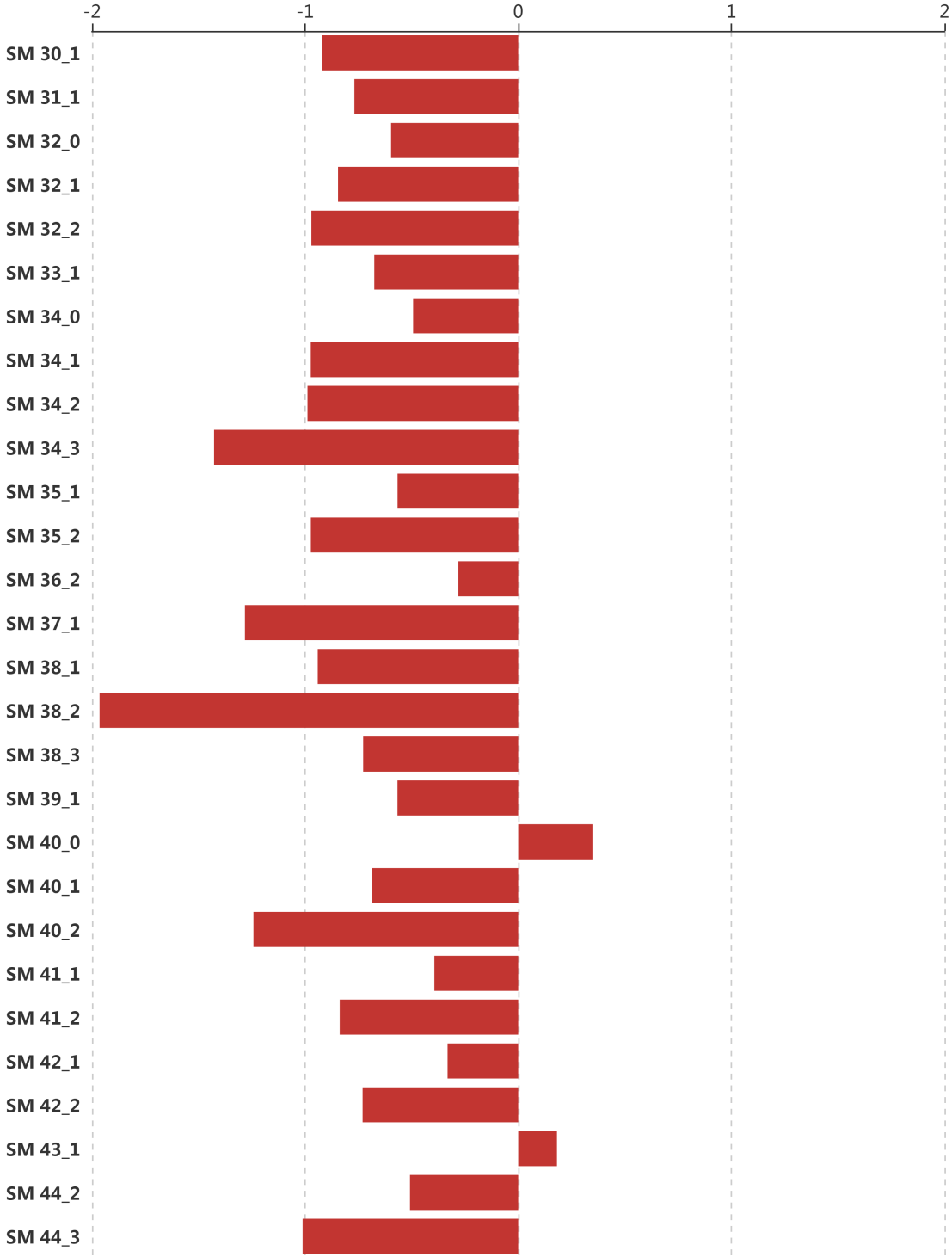


Fig. S6. Cellular ATP assay. Plots showing the cellular ATP levels of *Aag2.wMel* and *Aag2.TET* cells. Cellular ATP levels were plotted against cell counts. Blue: *Aag2.TET*; Red: *Aag2.wMel*. Replicates of four were measured; error bars represent SEM.

