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## Erratum to: A methodology for elucidating regulatory mechanisms leading to changes in lipid profiles

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The original version of article unfortunately contained mistakes. The top portion of Fig. 1 had overlapping text and the second author name was spelled incorrectly. These mistakes are now corrected through this erratum.

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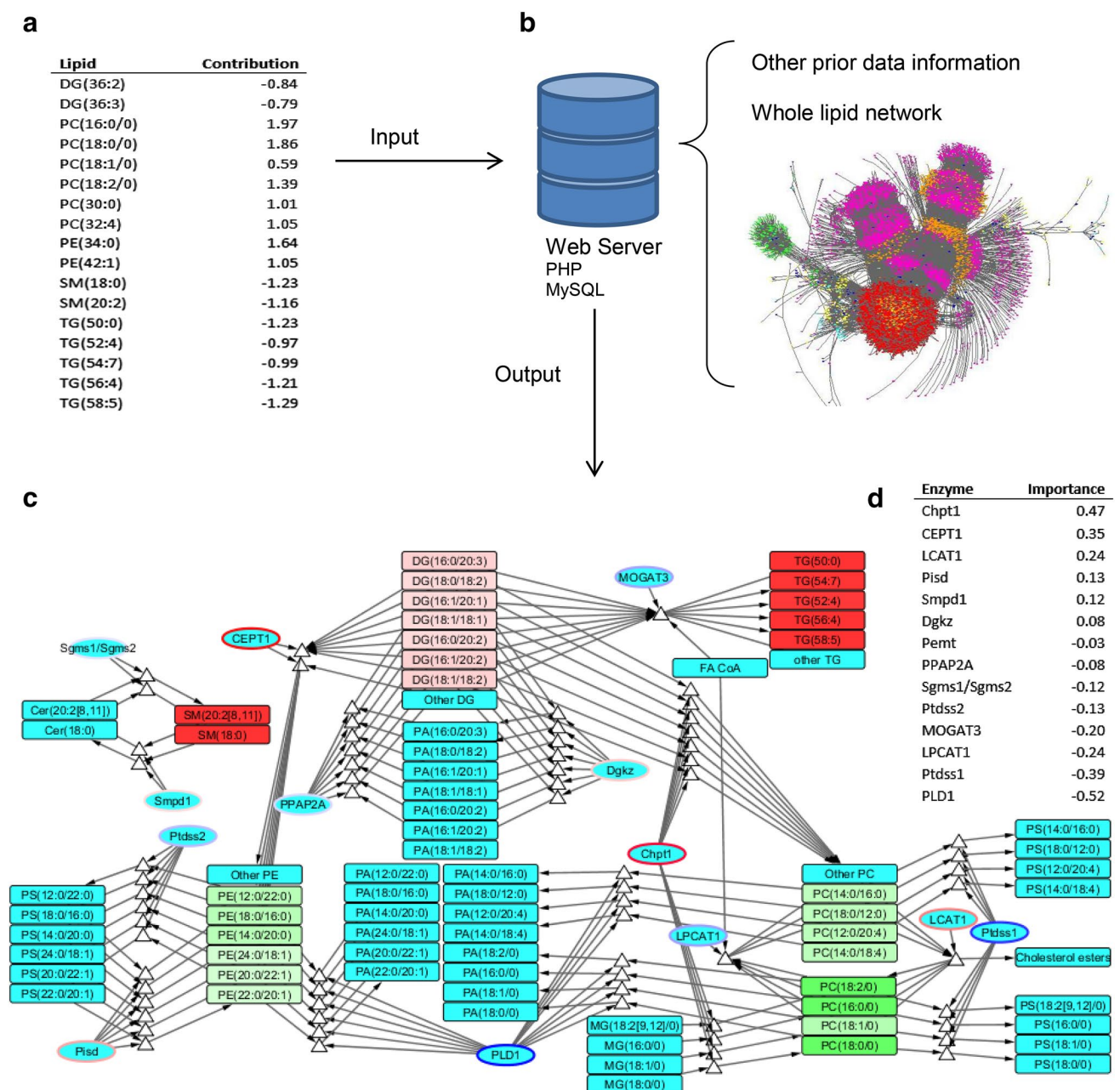
The online version of the original article can be found under  
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**Fig. 1** The Lipid network method. **a** Input list of lipids with OPLS-DA model scores. **b** Depicts the web server that contains scripts and the lipidomic network, in which node colours *green, dark blue, orange, red* and *white* respectively correspond to glycerophospholipids, sphingolipids, diglycerides, enzymes and specific reactions. **c** Derived subset of lipid metabolism linking the input perturbed metabolites; metabolite, reaction and enzyme nodes are respectively represented by *rectangles, triangles* and *ellipses*; input metabolite

nodes are respectively coloured a *brighter shade* or *green* or *red* depending on the extent to which their levels have been elevated or decreased, or *blue* if they correspond to nodes introduced during the subset retrieval; the borders of enzyme nodes are *shaded blue* or *red* respectively to depict the extent of positive or negative Relative Importance Score (the sign corresponding to the increase or decrease in enzyme activity). **d** The list of retrieved enzymes ranked by Relative Importance