

**S1 Fig. Manhattan and QQ plots from analyses of MetaboChip data, for each of the 22 assessed erythrocyte membrane FAs.** The dashed line in the Manhattan plots denotes the significance threshold of  $p < 4.3 \times 10^{-7}$ . P-values are calculated based on data transformed either to a standard normal or binary distribution. A) alpha-linolenic acid (18:3  $\omega$ -3), B) stearidonic acid (18:4  $\omega$ -3), C) eicosatetraenoic acid (20:4  $\omega$ -3), D) eicosapentaenoic acid (20:5  $\omega$ -3), E) docosapentaenoic acid (22:5  $\omega$ -3), F) docosahexaenoic acid (22:6  $\omega$ -3), G) linoleic acid (*cis-cis*-18:2  $\omega$ -6), H) gamma-linolenic acid (18:3  $\omega$ -6), I) dihomo-gamma-linolenic acid (20:3  $\omega$ -6), J) arachidonic acid (20:4  $\omega$ -6), K) adrenic acid (22:4  $\omega$ -6), L) docosapentaenoic acid (22:5  $\omega$ -6), M) palmitoleic acid (16:1  $\omega$ -7), N) oleic acid (18:1  $\omega$ -9), O) 11-eicosenoic acid (20:1  $\omega$ -9), P) erucic acid (22:1  $\omega$ -9), Q) nervonic acid (24:1  $\omega$ -9), R) palmitic acid (16:0), S) stearic acid (18:0), T) arachidic acid (20:0), U) behenic acid (22:0), and V) lignoceric acid (24:0). The rs11028474 variant on chromosome 11 causes the strong but spurious association signals for eicosapentaenoic acid (20:5  $\omega$ -3), docosapentaenoic acid (22:5  $\omega$ -3), docosahexaenoic acid (22:6  $\omega$ -3), and stearic acid (18:0). This variant was removed from all analyzes (see Materials and Methods section).











