Networks illustrating the functional categories significantly enriched in the gene products represented by the probes significantly up-regulated or down-regulated (adj.P.Val <= 0.05) in the D₂ and D₃ treatment groups of the WE cohort (but not Placebo group).

Gene products represented by the significantly up- or down-regulated probes in the comparisons WE D₂ V₃ v V₁, WE D₃ V₃ v V₁ and WE P V₃ v V₁ from Fig. 2(a), and possessing ENTREZ identifiers, were subjected separately to functional enrichment analysis using compareCluster and processed in Cytoscape (see legend to Fig. 4). The complete networks for each differentially expressed group of genes are shown on pages 3 – 12.

Example of naming convention used below: cc.WE.PD2D3.down.GOBP are the down-regulated genes for each of the P, D2 and D3 categories, analysed by gene ontology enrichment using biological process categories.

Note: the images are vector graphics and you can therefore zoom in to read the different functional groups
Supplementary Data File 5 (continuation of legend)

Networks illustrating all the functional categories significantly enriched (p.adjust < 0.01) in analysis of the gene products represented by the probes significantly up- or down-regulated (adj.P.Val < 0.05) in the White European (WE) cohort treatment groups. The thickness of lines (edges) drawn to connect the nodes shown increases with increasing significance (p.adjust-values). This aimed to identify functional categories that are more extensively affected by D2, or by D3, or by both D2 and D3, than by the placebo, and took into consideration the changes occurring in the placebo treatment group during the period of the study. Network names correspond to the worksheets in the excel spreadsheet Supplementary Data File 4 summarising the comparative functional enrichment analysis results, from which these networks were constructed.

Thus:

- Names ending GOBP contain results from Gene Ontology analysis using the Biological Process sub-ontology.
- Names ending GOCC contain results from Gene Ontology analysis using the Cellular Compartment sub-ontology.
- Names ending GOMF contain results from Gene Ontology analysis using the Molecular Function sub-ontology.
- Names ending KEGG contain results from KEGG pathway analysis.
- Names ending PWAY contain results from Reactome pathway analysis.

- Names commencing cc.WE.PD2D3.down contain results from the analysis of lists of down-regulated genes from the White European D2, D3 or Placebo (P) treatment groups.

- Names commencing cc.WE.PD2D3.up contain results from the analysis of lists of up-regulated genes from the White European D2, D3 or Placebo (P) treatment groups.

- Names containing “down” = down-regulated in V3 compared to V1 in the treatment groups.

- Names containing “up” = up-regulated in V3 compared to V1 in the treatment groups.
cc.WE.PD2D3.down.GOCC
cc.WE.PD2D3.down.GOMF
Platelet activation, signaling and aggregation

Signaling by cytosolic FGFR1 fusion mutants

Neutrophil degranulation

Signal regulatory protein family interactions

Fcgamma receptor (FCGR) dependent phagocytosis

Interleukin-4 and 13 signaling

Rho GTPase cycle

CD209 (DC-SIGN) signaling

RORA activates gene expression

Integrin alphaIIb beta3 signaling

MAPK3 (ERK1) activation

Chromatin organization

Interleukin receptor SHC signaling

Chromatin modifying enzymes

Interleukin-2 family signaling

CD209 (DC-SIGN) signaling

Interleukin-3, 5 and GM-CSF signaling

Signaling by Rho GTPases

Interleukin receptor SHC signaling

Chromatin modifying enzymes

Interleukin-2 family signaling

Signaling by Interleukins

Signal regulatory protein family interactions

NOTCH1 Intracellular Domain Regulates Transcription

CD209 (DC-SIGN) signaling

Interleukin-2 family signaling

Signal regulatory protein family interactions

cc.WE.PD2D3.down.PWAY
cc.WE.PD2D3.up.GOBP
cc.WE.PD2D3.up.PWAY