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Supporting Information for

A comprehensive transcriptome characterisation of individual Nuclear Receptor pathways in the human small intestine.

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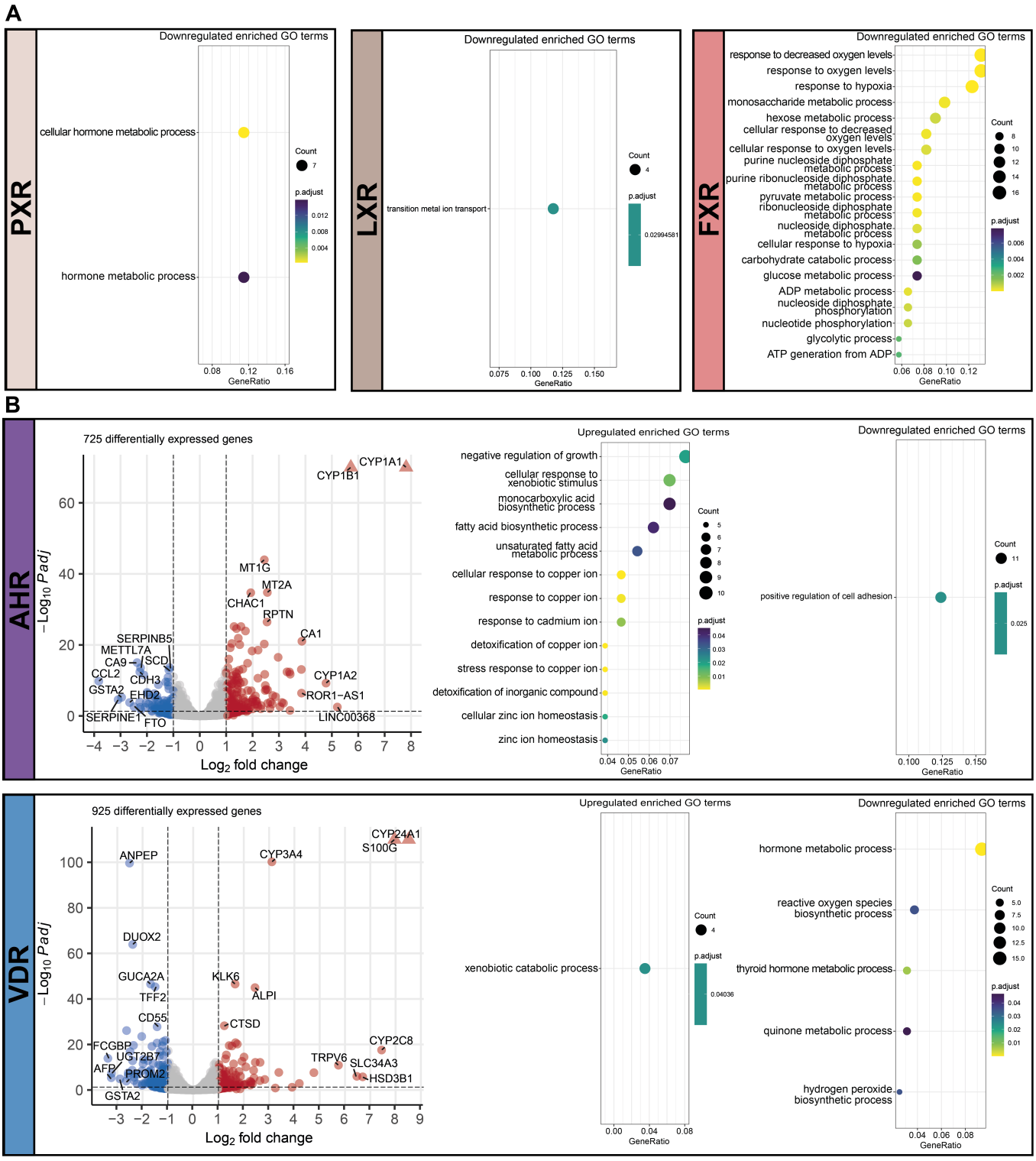
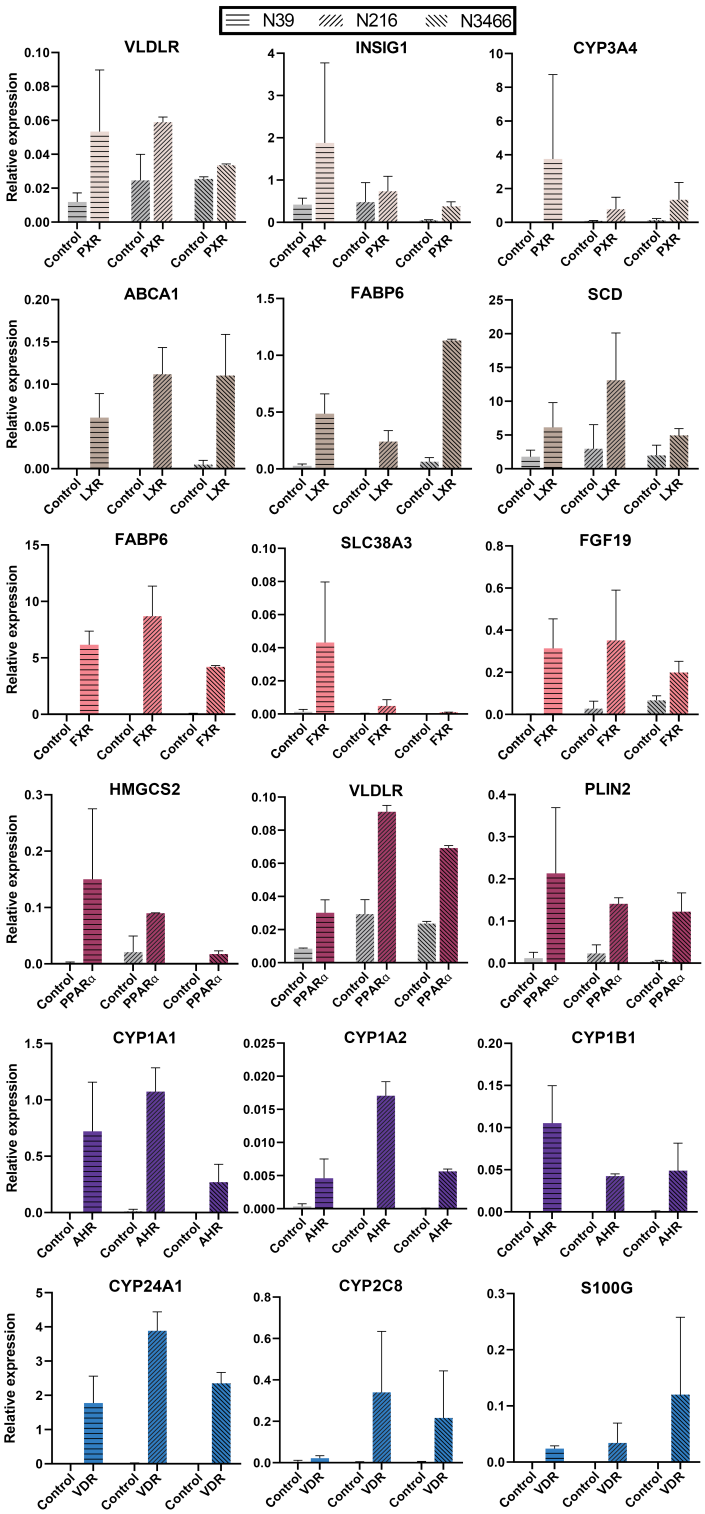
Figures S1 to S3

Other supporting materials for this manuscript include the following:

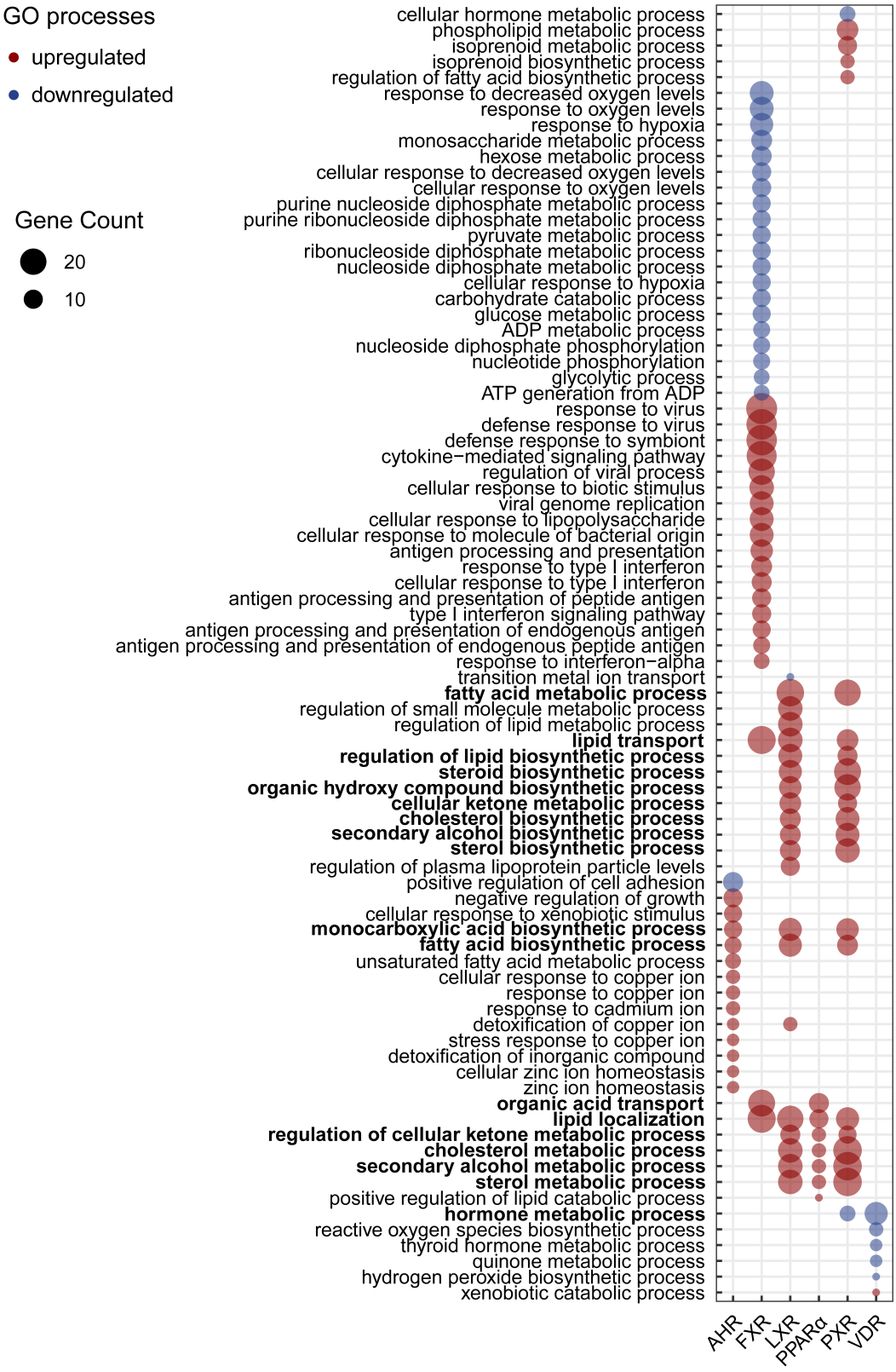
Datasets S1 to S2



Supplementary figure 1. Transcriptional targets of nuclear receptors in human intestinal organoids. A) Downregulated GO processes of PXR, LXR and FXR agonists. PPAR agonist did not lead to enriched downregulated GO processes. B) Volcano plots and enriched GO processes showing transcriptional profiles induced by AHR agonist and VDR agonist. Labelled genes are the top 10 differentially up- or down-regulated genes with the highest log_2 fold change. Triangles indicate $–log_{10}$ P-adjusted value higher then y-axis.



Supplementary figure 2. Nuclear receptor transcriptional responses are conserved across donors. Quantitative PCR analysis of the top three induced genes per nuclear agonist in human small intestinal organoids differentiated in the presence of the specified nuclear receptor agonists for 7 days. Shown are the original donor (N39) and two additional donors, n=2, Error bars =SD.



Supplementary figure 3. Enrichment of multiple lipid GO terms is shared by different nuclear receptors. An overview of enriched GO terms from each nuclear receptor characterisation is shown, depicted previously in Fig.2 and Fig. S1. GO terms in bold indicate terms enriched in multiple NR conditions.

Dataset S1 (separate file).

Lists of all significant differentially expressed genes for each nuclear receptor condition.

Dataset S2 (separate file).

Lists of all genes in enriched GO processes based on top for each nuclear receptor condition. Input for GO term enrichment analysis was all differentially expressed genes with a logFC of at least 1 and an adjusted P value lower than 0.05.