

Supplementary Materials

A proteomic approach to better understand the role of human neutrophil peptides in the NSCLC microenvironment

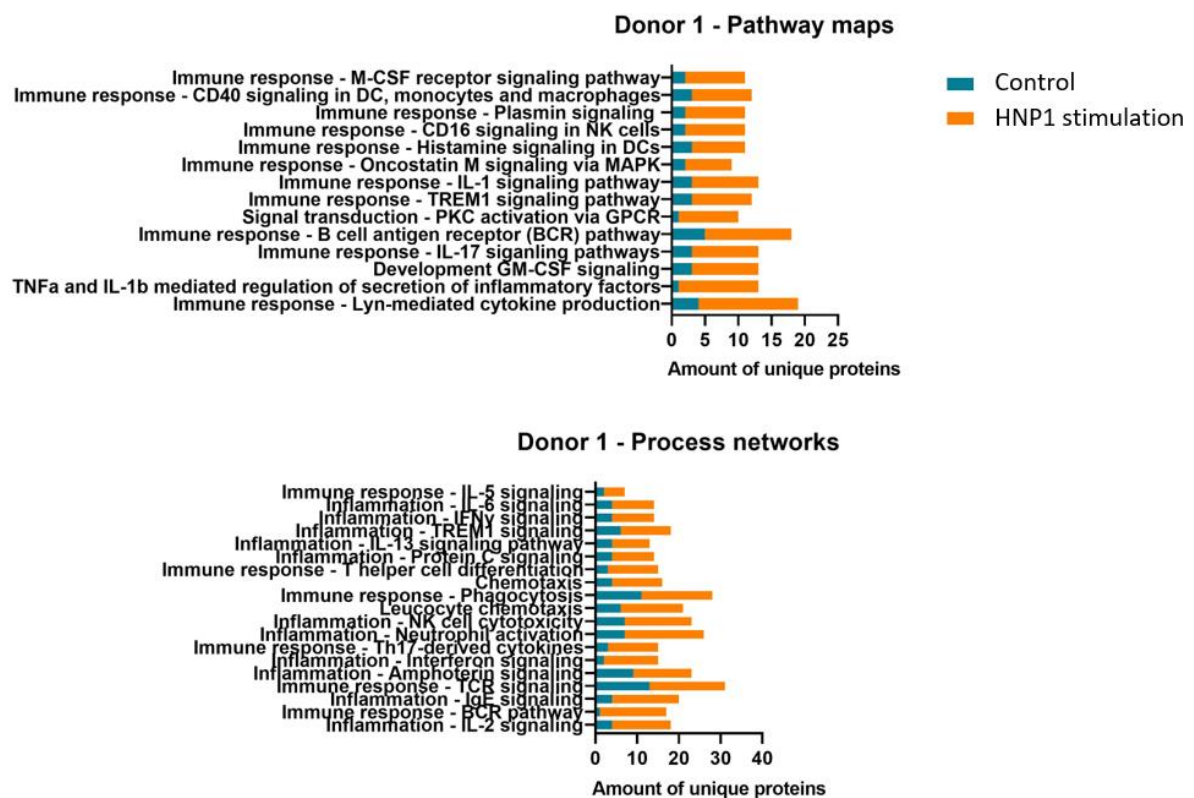


Figure S1. Overview of immune-related pathway maps (**upper**) and process networks (**lower**) in *in vitro* cocultures of A549 and PBMCs for donor 1, with (orange) and without (blue) treatment with human neutrophil peptide 1 (HNP1), after proteomic and MetaCore™ analyses.

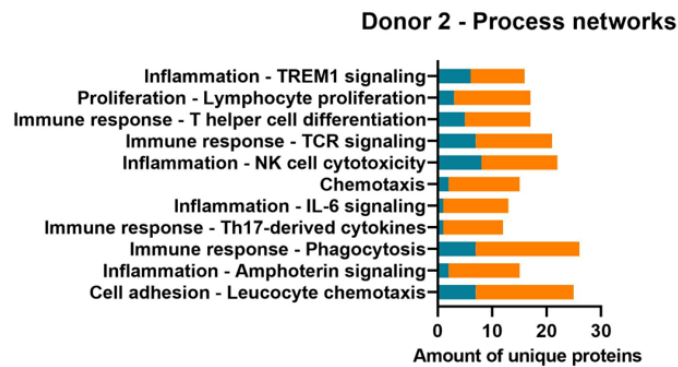
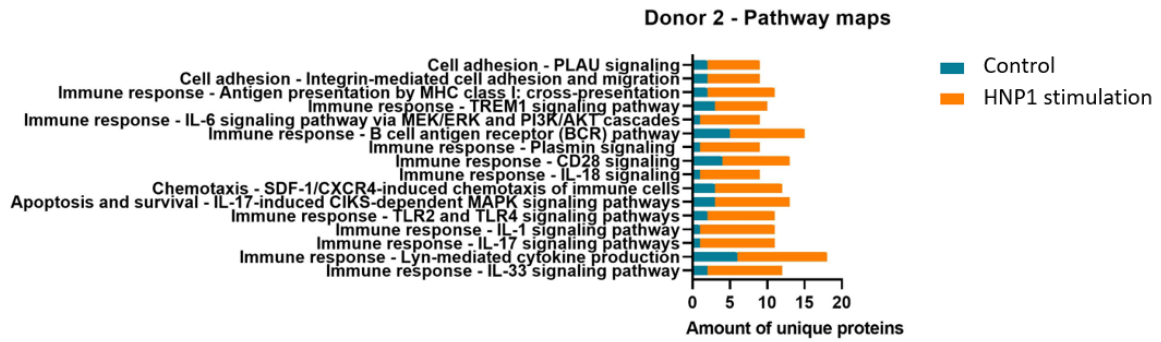


Figure S2. Overview of immune-related pathway maps (**upper**) and process networks (**lower**) in *in vitro* cocultures of A549 and PBMCs for donor 2, with (orange) and without (blue) treatment with human neutrophil peptide 1 (HNP1), after proteomic and MetaCore™ analyses.

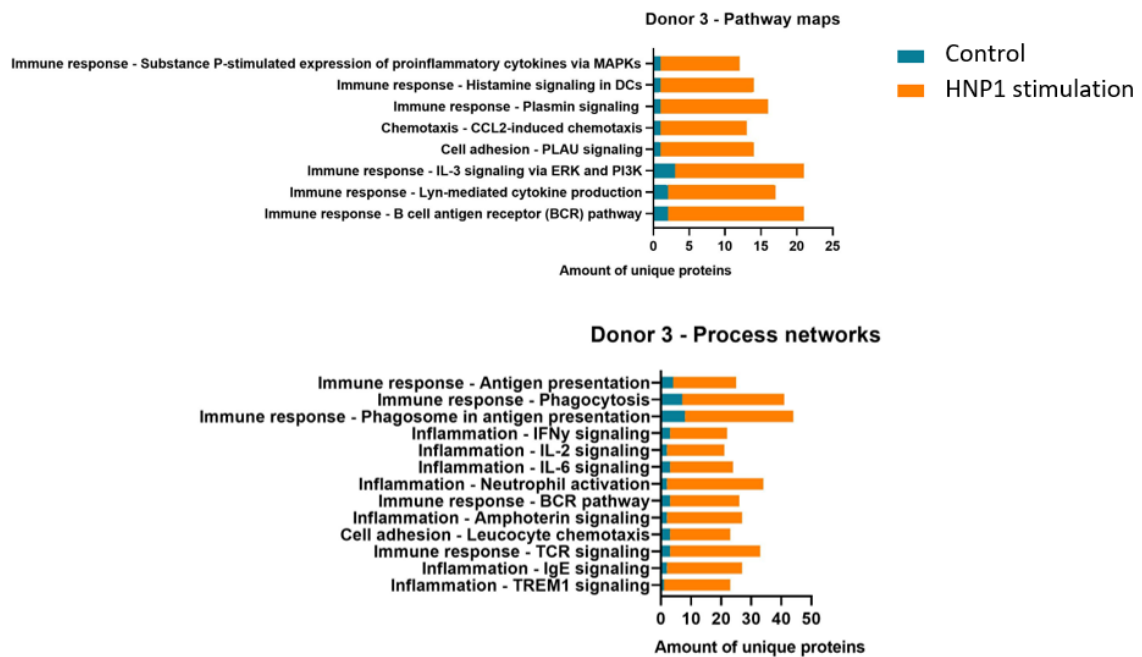


Figure S3. Overview of immune-related pathway maps (**upper**) and process networks (**lower**) in *in vitro* cocultures of A549 and PBMCs for donor 3, with (orange) and without (blue) treatment with human neutrophil peptide 1 (HNP1), after proteomic and MetaCore™ analyses.