



Mémoire de Maîtrise en médecine no 6879

Functional Analysis of Immunocompromised Patients' Leucocytes by Single-cell Mass Cytometry

APPENDIX

Lausanne, 31.01.2020

List of Figures

1	General overview of the interactions between the innate and the adap- tive immune systems in response to a bacterial skin infection - This fig- ure highlights the essential role of dendritic cells in order to assure the proper interaction between the two parts of the immune system, by pre- senting the bacterial antigen at its surface to T lymphocytes after its migra- tion to the skin lymphnodes. This triggers the downstream activation of the adaptive system in order to fight against the microorganism invasion of the skin by T and B lymphocytes. It also illustrates the importance of the different mediators of the immune response, among others cytokines. Modified from (61).	A8
2	Overview of the main actors of the immune system - Principal actors of different nature involved in the immune system	A9
3	I- Cytokines characteristics and functions - Type I cytokine familiy members: cell sources, related receptors and biological effects of the principal members. Modified from (7).	A10
3	II- Cytokines characteristics and functions - Type I and II cytokine familiy members: cell sources, related receptors and biological effects of the principal members. Modified from (7).	A11
3	III- Cytokines characteristics and functions - TNF superfamily cytokines, IL-1 family cytokines and other cytokines: cell sources, related receptors and biological effects of the principal members. Modified from (7)	A12
4	I- Overview of the principal pathogen recognition receptors of the innate immune system. - Cell-associated PRRs (1)	A13
4	II- Overview of the principal pathogen recognition receptors of the in- nate immune system Cell-associated PRRs (2)	A14

- 4 III- Overview of the principal pathogen recognition receptors of the innate immune system. - Soluble PRRs. PAMP, pathogen-associated molecular pattern; DAMP, Damaged-associated molecular pattern; PRR, Pattern recognition receptor; DC, Dendritic cell; TLR, Toll-like receptor; TIR, Toll/interleukin-1 receptor; NF-κB, Nuclear factor-κB; NLR, NOD-like receptors; NOD, Nucleotide oligomerization domain; NLRP, NACHT, NALP, LRR and PYD domains-containing protein 3; RLR, RIG-like receptors; MDA, Melanoma differentiation-associated protein; CDSs, Cytosolic DNA sensors; CLRs, C-type lectin-like receptors; AIM, Absent in melanoma; SP, Surfactant protein; STING, Stimulator of IFN genes; MD2, Myeloid differenitation protein 2; EC, Extracellular; IC, Intracellular; NF-*k*B, Nuclear factor κB; AP-1, Activation protein 1; IRF, Interferon response factor; BIR, Baclovirus inhibition of apoptosis protein repeat; CARDs, Caspase recruitment and activation domains; DAP, Diaminopimelic acid; MDP, Muramyl dipeptide; K+, Potassium ion; STING, Stimulator of IFN genes; cGAS, Cyclic GMP-AMP synthase; cGAMP, Cyclic GMP-AMP; DAI, DNA-dependent activator of IFN-regulatory factors; IFI16, Interferon inducible protein 16; ER, Endoplasmic reticulum; MAVS, Mitochondrial antiviral-signalling; ITAM, Immunoreceptor ryrosine-based activation motif; DC-SIGN, Dendritic cellspecific intercellular adhesion molecule 3-grabbing nonintegrin; Mincle, Macrophage inducible Ca2+ dependent lectin; SRA, Scavenger receptor A; FPRs, Formyl-peptide receptor; FPRL, Formyl-peptide receptor-like; GPCR, GTP-binding G protein-coupled receptor; CRP, C-reactive protein; SAP, Serum amyloid P; MBL, Mannose-binding lectin; MASP, Mannose/mannanassociated serine proteases; DAF, Decay accelerating factor; MCP, Mem-
- 5 Overview of the principal PAMPs and DAMPs. - Type, subtype and origin of the principal molecular patterns recognized by the innate immunity. PAMP, Pathogen-associated molecular pattern; DAMP, Damagedassociated molecular pattern; ATP, Adenosine triphosphate; CpG, Cytosineguanine-rich oligonucleotide; dsRNA, Double-stranded RNA; HMGB1, Highmobility group box 1; HSP, Heat shock protein; LPS, Lipopolysaccharide; ssRNA, Single-stranded RNA; TLR, Toll-like receptor; RSV, Respiratory syncytial virus; AIM2, Absent in melanoma-2; cGAS, Cyclic GMP-AMP synthase; DAI, DNA-dependent activator of IFN-regulatory factors; IFI16, Interferon inducible protein 16; NLR, NOD-like receptor; NOD, Nucleotide oligomerization domain; DC-SIGN, Dendritic cell-specific intercellular adhesion molecule 3-grabbing nonintegrin; SRs, Scavenger receptors; FPRs, Formyl peptide receptors; CRP, C-reactive protein; SAP, Serum amyloid P; MBL, Mannose-binding lectin. Sources: (7), (62), (63) and (64). A16

7	Overview of the different hematopoietic stem cell-derived innate im- mune cells - Innate immune cells are the products of differentiation from two different haematopoietic lineages: the myeloid and lymphoid progen- itors. Sources: (7), (65), (67), (68) and (69).	A18
8	I- CD molecules characteristics and functions - CD molecules characteristics: structure, main cellular expression and functions. Modified from (7), (70) and (71).	A19
8	II- CD molecules characteristics and functions - CD molecules character- istics (following): structure, main cellular expression and functions. Mod- ified from (7), (70) and (71).	A20
8	III- CD molecules characteristics and functions - CD molecules character- istics (following): structure, main cellular expression and functions. Mod- ified from (7), (70) and (71).	A21
9	Major immune cells molecular characterization - This non-exhaustive table illustrates the phenotypic molecular signatures characterizing the major known human immune cells subsets. Blue means an absence of expression, whereas orange means that the molecule is expressed. Sources: (2) and (7).	A22
10	Main DCs subsets molecular characterization - Surface molecules, intra- cellular PRRs, expressed genes and released cytokines by plasmacytoid DCs, type 1 and type 2 conventional DCs. Sources: (5).	A23
11	Primary immunodeficiencies classification - Classification of PID based on the side of immunity that is disturbed, and the mechanism responsible for this defect. Sources: (12)	A24
12	Mass Cytometry Workflow - General outlook of mass cytometry workflow, from single-cell suspension to data analysis. Modified from (33)	A25
13	General Analysis Pipeline - General data processing pipeline starting with data acquisition through a mass cytometer, then cluster identifications and finally intra-clusters evaluation.	A26
14	Innate immune functional panel - Panel of antibodies used in this project, with the corresponding heavy metal isotope, marker, clone and source. In, Indium; Pr, Praseodymium; Nd, Neodymium; Sm, Samarium; Eu, Europium; Gd, Gadolinium; Tb, Terbium; Dy, Dysprosium; Er, Erbium; Yb, Ytterbium; Bi, Bismuth; Ho, Holmium; Lu, Lutetium.	A27
15	Initial gating strategy to individualize each condition for each patient and healthy donor - Gating strategy using FlowJo, allowing to get indi- vidualized FCS files for each samples condition, illustrated for the batched data acquired containing the healthy donors 1 to 5. At the end, this means that 60 FCS files will be created (15 patients, 15 healthy donors, with each of them having 2 conditions)	A28
16	I- Manual gating strategy for the major known immune cells popula- tions - Manual gating using Cytobank, plotting two-dimension scatter- plots to iteratively cluster cells groups according to their surface markers. It can be seen as an iterative selection process of different markers expres- sions which at the end will define the corresponding cells populations	A29
16	II- Manual gating strategy for the major known immune cells popula- tions - Following.	A30
	-	

17	Clustering surface markers - Surface markers used to discriminate cells subpopulations when automatically clustering them, for all cells and mDC	
18	population	A31
	tinguished by color. The y-axis indicates the cell counts for each of the sample, and is written on the top of each barplot. HD, healthy donor; P, patient; US, unstimulated; S, stimulated	A32
19	Non-redundancy scores for all samples and all surface markers - Surface markers are arranged according to their NRS from the statistically most to the least discriminative, for all samples. This should be used as a help to identify the markers that will be used for the downstream clustering, but	
	should not be taken as an absolute verity as it does not take into account biological meanings.	A33
20	FlowSOM minimal spanning tree - Minimal spanning tree representing 100 clusters, or nodes, resulting from a FlowSOM algorithm. 10 markers	1.24
21	intensities are presented for each node	A34
22	culated and are represented with the corresponding color on this heatmap. Heatmap of the median intensities of each surface markers the major	A35
	known immune cells populations - Each known identified immune cell population is represented with its signature of surface molecular expression	.A36
23 24	tSNE plot of all cells - Each cell is coloured according to the cluster it has been assigned to	A37
24	playing the final result of clustering after the manual step, highlighting the different immune cells populations that could be isolated and identified	.A38
25	tSNE plot stratified by samples and conditions - tSNE plot displaying the meta-clustering for each of the samples and conditions, allowing a quick overview of the presence or absence of each immune cell population. US,	
26	unstimulated; S, stimulated	A39
27	lated; S, stimulated	A40 tic
	clustering methods - The mean manual and semi-automatic obtained proportion of each cell population is represented for healthy donors and patients in the unstimulated condition. HD, healthy donor; P, patient; US, unstimulated.	A41
28	Median activation markers intensities for each of the groups and condi- tions - Visual representation of the activation markers intensities in each of the populations for the healthy donors and patients groups, compared	
29	by conditions. US, unstimulated; S, stimulated	A42
	populations for the healthy donors and patients groups, compared by con- ditions. US, unstimulated; S, stimulated	A43

30	Boxplots with jittered points representing the immune cells relative abundance between healthy donors and patients in the unstimulated condition - General overview of the immune cells relative abundance distribution between patients and healthy donors. HD, healthy donor	- A44
31	Boxplots with jittered points representing the cytokines expression in the different immune cells populations - Comparison for each of the populations the difference in cytokines expression between the unstimulated and stimulated conditions. HD, healthy donor.	A45
32	Normalized activation markers expression comparison between the health donors and patients group in the unstimulated condition - Heatmap il- lustrating the differences in the activation markers expressions that are statistically significant in the identified immune cells populations between the patients and healthy donors groups. HD, healthy donor; P, patient; US, unstimulated; S, stimulated	ny A46
33	Normalized activation markers expression comparison between the health donors and patients group in the stimulated condition - Heatmap illus- trating the differences in the activation markers expressions that are statis- tically significant in the identified immune cells populations between the patients and healthy donors groups. HD, healthy donor; P, patient; US, unstimulated; S, stimulated	n y A47
34	Barplot displaying the number of acquired events for each samples and conditions in the mDC population - The x-axis represents the different samples and conditions, distinguished by color. The y-axis indicates the cell counts for each of the sample, and is written on the top of each barplot. HD, healthy donor; P, patient; US, unstimulated; S, stimulated	A48
35	Non-redundancy scores for all samples and all surface markers in the mDC population - Surface markers are arranged according to their NRS from the statistically most to the least discriminative, for all samples. This should be used as a help to identify the markers that will be used for the downstream clustering, but should not be taken as an absolute verity as it does not take into account biological meanings	A49
36	Minimal spanning tree obtained with FlowSOM on the mDC popula- tion - (A) Minimal spanning tree displaying the intensity in some marker expressions of the 100 identified clusters. (B) CD1c expression intensities among the 100 clusters.	A50
37	Heatmap of the median intensities of each surface markers in each population for all samples in the mDC population - Median intensities for each cluster have been calculated and are represented with the corresponding color on this heatmap.	A51
38	Median markers intensities of the mDC family 20 meta-clusters - Surface markers intensities are represented for each of the clusters obtained with FlowSOM and ConsensusClusterPlus metaclustering.	A52
39	Median cytokines intensities of the mDC family 20 meta-clusters - Cy- tokines intensities are represented for each of the clusters obtained with FlowSOM and ConsensusClusterPlus metaclustering	A53
40	tSNE plot of all myeloid dendritic cells - Each cell is coloured according to the cluster it has been assigned to	A54

41	tSNE plot comparison between healthy donors and patients in the mDC population - tSNE plot displaying the identified immune cells populations for the healthy donors group, compared to the one obtained for the pa- tients group. US, unstimulated; S, stimulated	A55
42	tSNE plot stratified by samples and conditions in the mDC population - tSNE plot displaying the meta-clustering for each of the samples and conditions, allowing a quick overview of the presence or absence of each clustered mDC subpopulation. HD, healthy donor; P, patient; US, unstim- ulated; S, stimulated.	A56
43	mDC tSNE graph of patient 02 and healthy donor 13 - tSNE graphs fo- cusing on patient 02 and healthy donor 13. HD, healthy donor; P, patient; US, unstimulated; S, stimulated.	A57
44	Normalized activation markers expression comparison between the health donors and patients group in the stimulated condition of all mDCs - Heatmap illustrating the differences in the activation markers expressions that are statistically significant in the overall mDCs between the patients and healthy donors groups. HD, healthy donor; P, patient; US, unstimu- lated; S, stimulated.	y A58
45	Normalized cytokines expression comparison between the healthy donors and patients group in the stimulated condition of all mDCs - Heatmap illustrating the differences in the cytokines expressions that are statistically significant in the overall mDCs between the patients and healthy donors groups. HD, healthy donor; P, patient; US, unstimulated; S, stimulated	A59
46	Median activation markers expressions intensities for each of the clus- ters and conditions among mDCs - Visual representation of the activation markers expressions in each of the mDCs clusters for the healthy donors and patients groups, compared by conditions. US, unstimulated; S, stimu- lated.	A60
47	Median cytokines expressions intensities for each of the clusters and conditions among mDCs - Visual representation of the cytokines expressions in each of the mDCs clusters for the healthy donors and patients groups, compared by conditions. US, unstimulated; S, stimulated	A61
48	Normalized proportions of mDC subpopulations that are significantly different between the healthy donors and patients groups in the unstimulated condition - HD, healthy donor; P, patient; US, unstimulated; S, stimulated.	A62
49	Boxplots with jittered points representing the mDC subpopulations rel- ative abundance between healthy donors and patients in the unstimu- lated condition - General overview of the mDC subpopulations relative abundance distribution between patients and healthy donors in the un- stimulated condition. HD, healthy donor; P, patient	A63
50	Normalized cytokines expression comparison between the healthy donors and patients group in the unstimulated condition of mDCs subpopula- tions - Heatmap illustrating the differences in the cytokines expressions that are statistically significant in the identified mDC subpopulations be- tween the patients and healthy donors groups. HD, healthy donor; P, pa-	
	tient; US, unstimulated.	A64

51	Normalized cytokines expression comparison between the healthy donors	
	and patients group in the stimulated condition of mDCs subpopulations	
	- Heatmap illustrating the differences in the cytokines expressions that are	
	statistically significant in the identified mDC subpopulations between the	
	patients and healthy donors groups. HD, healthy donor; P, patient; S, stim-	
	ulated	A65
52	Normalized activation markers expression comparison between the health	y
	donors and patients group in the unstimulated condition of mDCs sub-	
	populations - Heatmap illustrating the differences in the activation mark-	
	ers expressions that are statistically significant in the identified mDCs sub-	
	populations between the patients and healthy donors groups. HD, healthy	
	donor; P, patient; US, unstimulated.	A66
53	Normalized activation markers expression comparison between the health	y
	donors and patients group in the stimulated condition of mDCs subpop-	
	ulations - Heatmap illustrating the differences in the activation markers	
	expressions that are statistically significant in the identified mDCs sub-	
	populations between the patients and healthy donors groups. HD, healthy	
	donor; P, patient; S, stimulated.	A67

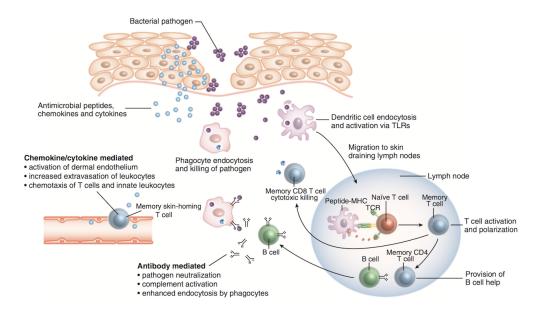


Figure 1: General overview of the interactions between the innate and the adaptive immune systems in response to a bacterial skin infection - This figure highlights the essential role of dendritic cells in order to assure the proper interaction between the two parts of the immune system, by presenting the bacterial antigen at its surface to T lymphocytes after its migration to the skin lymphnodes. This triggers the downstream activation of the adaptive system in order to fight against the microorganism invasion of the skin by T and B lymphocytes. It also illustrates the importance of the different mediators of the immune response, among others cytokines. Modified from (61).

Actors o	of the immune system
Family	Actors
Physical and Chemical Barriers	Epithelia (skin) Mucosa (gut, lungs, nose, eyes) Antimicrobial products Enzymes (pepsine, lysozyme) Fatty acid Low pH Endogenous microbial flora
Hematopoietic Stem Cell-Derived Immune Cells	Innate immunity Phagocytic cells Neutrophils Macrophages Monocytes Eosinophils Basophils Dendritic cells (DCs) Mast cells Natural killer (NK cells) NKT cells Innate lymphoid cells (ILC) Adaptive immunity B cells T cells T cells
Blood Molecules	Complement system Mediators of inflammation Cytokines Chemokines Proteases Lipid mediators Peptides, amines Nitric oxyde Adhesion molecules Acute-phase proteins (CRP) Antibodies
Lymphoid Tissues	Primary Thymus Bone marrow Secondary Lymph nodes Tonsils Spleen Mucosa-Associated Lymphoid Tissue (MALT) Tertiary Bronchus-Associated Lymphoid Tissues (BALTs) Inducible Lymphoid Follicles (ILFs)

Figure 2: **Overview of the main actors of the immune system -** Principal actors of different nature involved in the immune system.

				acteristics and function	
Cytokine	and Subunits	Principal Cell Source	Cytokine Receptor and Subunits		Principal Cellular Targets and Biologic Effects
Type I Cytokine F	amiliy Members	·			
IL-2		T cells	CD25 (IL-2Ra) CD122 (IL-2Rß) CD132 (yc)	NK cells B cells	 Proliferation and differentiation into effector and memory cells Promotes regulatory T cell development, survival and function Proliferation Activation Proliferation
IL-4		CD4+ T cells (Th2, Tfh)	CD124 (IL-4Ra)		Ab synthesis (in vitro) Isotype switching to IgE and IgG4
		Mast cells Macrophages M2	CD132 (yc)	T cells Macrophages	Th2 differentiation Troifferentiation Troifferention (growth factor) Alternative activation (M2) Inhibition of IFNy-mediated classical activation Stimulate persistalsis Promotes the expression of adhesion molecules and secretion of chemokines
IL-5		CD4+ T cells (Th2) ILCs group 2	CD125 (IL-5Rα) CD131 (βc)	Eosinophils	Activation Increased growth and differentiation
IL-6		Macropages Endothelial cells T cells	CD126 (IL-6Ra) CD130 (gp130)	Liver B cells T cells	- Synthesis of acute-phase protein - Proliferation of antibody-producing cells - Th17 differentiation
IL-9		CD4+ T cells	CD129 (IL-9R) CD132 (yc)	Mast cells, B cells,	T cells and tissue cells: - Survival and activation
11-10		T cells Macrophages M2 DC B cells Eosinophils Mast cells Keratinocytes Epithelial cells	ILIOR1 ILIOR2 Stimulation is dose- dependent	DC Macrophages Immature T cells B cells	Potent inhibitor of Ag presentation Inhibits MHC class II and upregulation of CD80 and CD86 Inhibits MHC class II and upregulation of CD80 and CD86 Inhibits MHC class II and upregulation of CD80 and CD86 Inhibits of CC and CXC Inhibits DC maturation Inhibits DC maturation Inhibits DC maturation Inhibits OT matrophage matrix metalloproteases Increase secretion of I-LRA Inhibits of C 28 pathway Costimulation of C 28 pathway Costimulation of B cells activation Prolonged B survival Class switching
	1. 404 (. OF)			T cells	Co-stimulation of NK cells proliferation and cytokines production Growth factor to stimulate the proliferation of certain subsets of CD8+ T cells
IL-12	IL-12A (p35) IL-12B (p40	Macrophage Dendritic cells	CD212 (IL-12Rß1) IL-12Rß2	T and NK cells	- Th1 differentiation - IFN-y synthesis - Increased cytotoxic activity
IL-13		CD4+ T cells (Th2) NKT cells ILCs group 2 Mast cells Macrophages M2	CD213a1 (IL-13Ra1) CD213a2 (IL-13Ra2) CD132 (yc)	Macrophages Epithelial cells GI tract	 Isotype switching to IgE and IgG4 Isotypes Alternative activation (M2) Increased mucus production from airway and gut epithelial cells Stimulates peristalsis Promotes the expression of adhesion molecules and secretion of chemokines
IL-15		Macrophages Other cell types	IL-15Rα CD122 (IL-2Rβ) CD132 (γc)		 Proliferation Survival and proliferation of memory CD8+ cells
IL-17	IL-17A IL-17F	CD4+ T cells (Th17) ILCs group 3 γδ T cells CD8+ T cells	CD217 (IL-17RA) IL-17RC		scrophages, and other cell types - Increased chemokine and cytokine production to recruit neutrophils and monocytes - GM-CSF and G-CSF production to enhance neutrophils production
IL-21		Th2 cells Th17 cells Tfh cells	CD360 (IL-21R) CD132 (yc)	NK cells	Activation, proliferation, differentiation in germinal centers Development Increased generation (differentiation) (amplification) Increased proliferation, differentiation and effector function Increased proliferation, differentiation and effector function
IL-23	IL-23A (p19) IL-12B (p40)	Macrophages DCs	IL-23R CD212 (IL-12Rβ1)	T cells	- Differentiation and expansion of Th17

Figure 3: **I- Cytokines characteristics and functions** - Type I cytokine familiy members: cell sources, related receptors and biological effects of the principal members. Modified from (7).

		Cytokines characteris	tics and functions (following)
Cytokine and Subunits	Principal Cell Source	Cytokine Receptor and Subunits	Principal Cellular Targets and Biologic Effects
Type I Cytokine Familiy Members (fol	llowing)	·	
c-Kit Ligand (Stem cell factor)	Bone marrow stromal cells	CD117 (KIT)	Pluripotent hematopoietic stem cells
GM-CSF (Granulocyte-monocyte CSF)	T cells Macrophages Endothelial cells Fibroblasts	CD116 (GM-CSFRa) CD131 (ßc)	Immature and committed progenitors, mature macrophages - Maturation of granulocytes and monocytes - Macrophage activation
M-CSF, CSF1 (Monocyte CSF)	Macrophages Endothelial cells Bone marrow cells Fibroblasts	CD115 (CSF1R)	Committed hematopoletic progenitors - Maturation of monocytes
G-CSF (Granulocyte CSF)	Macrophages Fibroblasts Endothelial cells	CD114 (CSF3R)	Committed hematopoietic progenitors - Maturation of granulocytes
TSLP (Thymic stromal lymphopoletin)	Keratinocytes Bronchial epithelial cells Fibroblasts Smooth muscle cells Endothelial cells Mast cells Macrophages Granulocytes Dendritic cells	TSLP-receptor CD127 (IL-7R)	DC - Activation Eosinophils - Activation Mast cells - Cytokine production T cells - Th2 differentiation
Type II Cytokine Familiy Members	·	•	
IFN-a Type I interferon	pDC Macrophages	IFNAR1 CD118 (IFNAR2)	All cells - Antiviral state - Increased class I MHC expression NK cells - Activation
IFN-B Type I interferon	pDC Fibroblasts	IFNAR1 CD118 (IFNAR2)	All cells - AntiViral state - Increased class I MHC expression NK cells - Activation
I FN-Y Type II interferon	T cells (Th1, CD8+ T cells) NK cells	CD119 (IFNGR1) IFNGR2	Macrophages - Classical activation Increased microbicidal functions B cells - Isotype switching to gosonizing and complement-fixing IgG subclasses T cells - Th1 differentiation; inhibition of Th2 and Th17 differentiation APCs - Increased expression of PZ costimulators at their surface Various cells - Increased expression of Class I and II MHC - Increased antigen processing and presentation to T cells
IFN-λ1-3 Type III interferon	DCs	IFNLR1 (IL-28Rα) CD210B (IL-10Rβ2)	Epithelial cells - Antiviral state
IL-10	Macrophages T cells (mainly Treg)	CD210 (IL-10Ra) IL-10Rß	Macrophages, DC - Inhibition of expression of IL-12, costimulators and class II MHC
IL-22	Th17 cells NK cells ILCs group 3	IL-22Ra1 IL-22Ra2 IL-10Rß2	Epithelial cells - Production of defensins (antimicrobial peptides) - Increased barrier function (repair reactions) - Increased production of chemokines Hepatocytes - Survival

Figure 3: **II- Cytokines characteristics and functions** - Type I and II cytokine familiy members: cell sources, related receptors and biological effects of the principal members. Modified from (7).

			Cytokines characteris	tics and functions (fo	llowing)
Cytokine a	and Subunits	Principal Cell Source	Cytokine Receptor and Subunits		Principal Cellular Targets and Biologic Effects
TNF Superfamily	Cytokines		Suburno		
TNFa		Macrophages NK cells T cells Neutrophils	CD120a (TNFRSF1) CD120b (TNFRSF2)	Endothelial cells Neutrophils Hypothalamus Muscle, fat	- Activation (inflammation, coagulation) - Activation - Fever - Catabolsm (cachexia)
Lymphotoxin-a	LTa TNFSF1	T cells B cells	CD120a (TNFRSF1) CD120b (TNFRSF2)	Same as TNF	
Lymphotoxin-aß	LTaß	T cells NK cells Follicula B cells Lymphoid inducer cells	LTBR	Lymphoid tissue s	tromal cells and follicular dendritic cells (FDC) - Chemokine expression - Lymphold organogenesis
BAFF	CD257 TNFSF13B	DC Monocytes Follicular dendritic cells B cells	BAFF-R (TNFRSF13C) TACI (TNFRSF13B) BCMA (TNFRSF17)	B cells	- Surwal - Proliferation
APRIL	CD256 TNFSF13	T cells DC Monocytes Follicular dendritic cells	TACI (TNFRSF13B) BCMA (TNFRSF17)	B cells	- Survival - Proliferation
Osteoprotegerin	OPG TNFRSF11B	Osteoblasts	RANKL	Osteoclast precur	sor cells - Inhibits osteoclast differentiation
IL-1 Family Cytok	ines				
IL-1a		Macrophages DC Fibroblasts Endothelial cells Keratinocytes Hepatocytes Neutrophils	CD121a (IL-1R1) IL-1RAP CD121b (IL-1R2)	Endothelial cells Hypothalamus	- Activation (inflammation, coagulation) - Fever
IL-1b		Macrophages DC Fibroblasts Endothelial cells Keratinocytes Neutrophils	CD121a (IL-1R1) IL-1RAP CD121b (IL-1R2)	Endothelial cells Hypothalamus Liver T cells	- Activation (inflammation, coagulation) - Fever - Synthesis of acute-phase proteins - Th17 differentiation
IL-1RA		Macrophages	CD121a (IL-1R1) IL-1RAP	Various cells	- Competitive antagonist of IL-1
IL-18		Monocytes Macrophages DC Kupffer cells Keratinocytes Chondrocytes Synovial fibroblasts Osteoblasts	CD218a (IL-18Ra) CD218b (IL-18Rb)	NK cells, T cells Monocytes Neutrophils	- IFN-y synthesis - Expression of GM-CSF, TNF, IL-1b - Activation - Cytokine release
IL-33		Endothelial cells Smooth muscle cells Keratinocytes Fibroblasts	ST2 (IL1RL1) IL-1RAP	T cells ILCs	- Th2 development - Activation of group 2 ILCs
Other Cytokines				1	
TGF-ß		T cells (Tregs) Macrophages Other cell types	TGF-8 R1 TGF-8 R2 TGF-8 R3	T cells B cells Macrophages Fibroblasts Neutrophils	Inhibition of proliferation and effector functions Differentiation of Th12 and Treg Inhibition of proliferation IgA production IgA production Inhibition of activation Stimulation of anglogenic factors Increased collagen synthesis and matrix-modifying enzymes Inhibition of activation

Figure 3: **III- Cytokines characteristics and functions** - TNF superfamily cytokines, IL-1 family cytokines and other cytokines: cell sources, related receptors and biological effects of the principal members. Modified from (7).

General overview of the principal Pattern Recognition Receptors (PRR) with their characteristics	Location Ligands (PAMPs or DAMPs) Transcription factors Effects associated	-	Plasma membrane Various microbial molecules Nr-48 Inflammetry reponse Endosomal membrane - US - US - Colonics: Th, IL CL Findosomal membrane - US - Reptdospycans - Claimetry reponse - Nucleic cidds RF7 APL ChemoRes: CL2, CCL3 CL3 - Nucleic cidds RF7 Artheision mecules: Exelectin - Proteins - Proteins	Cytosol NURA NURA FFV NURA NURA FFV MURA Corrol of Legionella preumophila infection NOD2 NOD2 Corrol of Legionella preumophila infection NOD3 NOD3 NOD3 NURA NURA NOD3 NURA NURA NOD3 NURA NURA NURA NURA NURA Control of Legionella preunophila infection NURA NURA NURA NURA NURA NURA NURA Control of Legionella preunophila infection Control of Legionella preunophila infection NURA NURA NURA NURA NURA Control of Legionella retrol on Control of Legionella retrol on NURA NURA Control of Legionella retrol on NURA Cont	Crosol RNA (vrua) IRF3 Crosol ANA (vrua) IRF3 Crosolmes productions (FN-a, IFN-g) as NA As NA http://www.name.org/astronomeses NR-bush http://wwww.name.org/astronomeses NR-bush http://www.name.org/astronomeses NR-bush http://wwwwwwwwwwwwwwwww	Cytosol dcDNA (bacteria and virus) 5TING pathwary 5TING-pathwary Cytokine production: IFN-q. IFN-9, IFN-1, IC-16, IRN-1, IC-16, IL-33, IRN-1, IC-16, IL-33, IRN-1, IC-16, IL-33, IRN-1, IC-16, IL-34, IRN-1, IC-16, IRN-1,
General overview of the principal Pattern R	structure Associated molecules Distribution		teins TLR 2,TLR DCs odules TLR 2, Rescores TLR 4 8 etils MD2 Many other cells CD14 Many other cells	addi Phageortes ds Phageortes ers Other cells aing domain protests protests	spare recruitment domains MAVS Phageopres Threact why signaling proteins MAVS Other cells deheticase domain STAA recognition semital domain > STAA recognition	TING pathway Phagoores adapto protein CGAMP CCAMP CGAMP CCAMP CCAMP CCAMP CCAMP CCAMP CCAMP CCAM
	Subtypes Molecular structure		TLRs 1-9 Tarsementane proteins EC: Leuch-rich modules IC: TR domain	MLRA Lacch-rich repeat domain NRC DOI NODI - 5- Fond soligenes NODI - 5- Fond soligenes NOD NRCA NURA Transactivating domain NLRA NURA NURA - Transactivating domain NLRA - Anton domains NLRA - Anton domains NLRA - CACRS NLRA - CACRS - Signalling complexes	RIG-1 Caspace recruitment domains MON-5 - Caspace recruitment domains MON-5 - Caspace recruitment domains - RNA-heliciase domain - RNA-recognition - SNA recognition	STING-independent STING AM2 Transmembrane aduptor protein RIA polymerase 3 on ER membrane GGAS DA1 FI16
	PRR class	Cell-associated	TLRs (TIR superfamily)	Se la compara de la compara	RLPS	053

Figure 4: I- Overview of the principal pathogen recognition receptors of the innate immune system. - Cell-associated PRRs (1).

			General overview of the principal Pattern Recognition Receptors (PRR) with their characteristics (following)	ipal Pattern Recognition R	eceptors (PRR) with their cha	iracteristics (following)		
PRR class	Subtypes	Molecular structure	Associated molecules	Distribution	Location	Ligands (PAMPs or DAMPs)	Transcription factors associated	Effects
Cell-associated (following)								
CLRs	Mannose receptor (CD206)	Transmembrane receptor	Dectins	Macrophages	Plasma membrane	Mannose receptor (CD206)	Dectins	Mannose receptor (CD206)
	Dectins Dectin-1 (CD369)	Dectin-1	SYK	DCs Somme tissue cells		D-mannose L-fucose	NF-KB	Phagocytosis of microbes Antifungal immunity
	Dectin-2	Cytoplasmic tail: ITAM	CARD9	Blood		N-acetyl-D-glucosamine		Dectins
	Mincle	Dectin-2		EC fluid		Dectins		Antifungal immunity
	Langerin (CD207)	Cytoplasmic tail: ITAM				Dectin-1		Mycobacterial immunity
	DC-SIGN (CD209)	Relies on FcRy				β-glucans (bacteria and fungi)		Inflammatory response
						Dectin-2		Antigen presentation
						High-mannose oligosaccharides		Third cell induction
						(tungi, bacteria)		Langerin
						Mannose		Antigen presentation
						DC-SIGN		DC-SIGN
						Mannose		Adhesion
						Fucose		Pathogenic role in disseminating infections
								HBV
								HIV-1
Scavenger receptors	SR-A		CD36	Phagocytes	Plasma membrane	Diacylglycerides		SR-A
	CD36		TLR2, TLR 6			Oxidized lipoproteins		Mediate phagocytosis of microorganisms
						Lipoteichoic acid		CD36
						LPS		Mediate phagocytosis of microorganisms
						Nucleic acids		Coreceptor in TLR2/6 pathway
						β-glucans Proteins		
FPRs	FPR1	GPCR	G proteins	Phagocytes	Plasma membrane	Peptides with N-formylmethionyl residues		Increased cell motility
	FPRL1					 Act as chemoattractants 		Phagocytosis

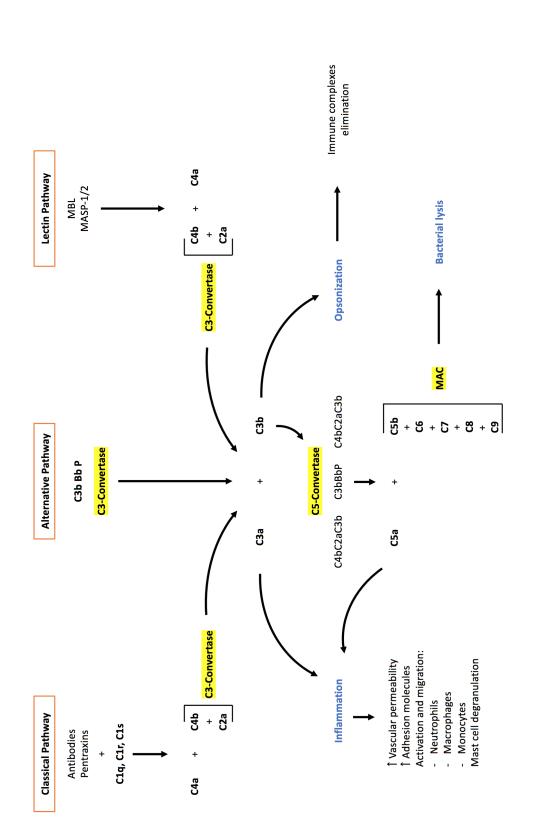
Figure 4: II- Overview of the principal pathogen recognition receptors of the innate immune system. - Cell-associated PRRs (2).

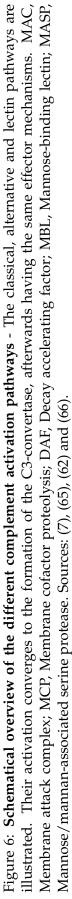
		0	General overview of the principal Pattern Recognition Receptors (PRR) with their characteristics (following)	pal Pattern Recognition Re	ceptors (PRR) with their cha	racteristics (following)		
PRR class	Subtypes	Molecular structure	Associated molecules	Distribution	Location	Ligands (PAMPs or DAMPs)	Transcription factors associated	Effects
Soluble								
Pentraxins	Short pentradins CRP 5.AP Long pentradins PTY3	Pentameric proteins		Produced by CRP, SAP Liver Liver DCS Macrophages Endothelium Neutrophils	Plasma	CRP, SAP ProsphoryCholine Prosphatofychtandamine Amyloid fibrils Bacteria Virus Virus Apoptotic cells Apoptotic cells		Complement activation by binding Ctq Complement activation by binding Ctq Pethogenic responses Autoimmunity Amyoidosis
Collectins	Mamose-binding lectin Surfactorit proteins SP-D SP-D	Trimeric or heameric proteins Collagen-like tail Calcium-dependent (C-type) lectin head	MBL Careeptor -> Internalization MASP1/2 MASP1/2		MBL Plasma SP _A SP-D Alveoli	MBL Carbohydrates with terminal mamose or fucose SP-A, SP-D Various microbial structures		MBL Complement activation by binding MASP1/2 -> Letch pathway initiation Opsonization Opsonization SFA SFD Reduction of alveol to expand upon inhelation -> MBN of alveoly to expand upon inhelation Opsonization -> Ingestion by alveolar macrophages
Ficolins	Ficolin	Collagen-like domain Fibrinogen-tpe carbohydrate recognition domain	MASP1/2		Plasma	N -acetyglucosamine (Gram+ bacteria) Lipoteichoic acid (Gram+ bacteria)		Opsonization -> Enhancing phagocytosis Complement activation by binding MASP1/2 -> Lectin pathway initiation
Complement	Various complement protein Cla, Clr, Cls Cla, Cl, Cl Cl, Cl, Cl Cl, Cl, Cl Cl, Cl Cl, Cl Cl, Cl Cl, Cl Cl Cl Cl Cl Cl Cl Cl Cl Cl Cl Cl Cl C	Serine proteases	Inhibitors C4-binhibitor C4-binhibitor C4-binhig protein C81 Ifactor MCP ACHORS ACHORS B protein P B protein P Protein P Protein P Protein		Plasma	Microbial surfaces		Approving the second se

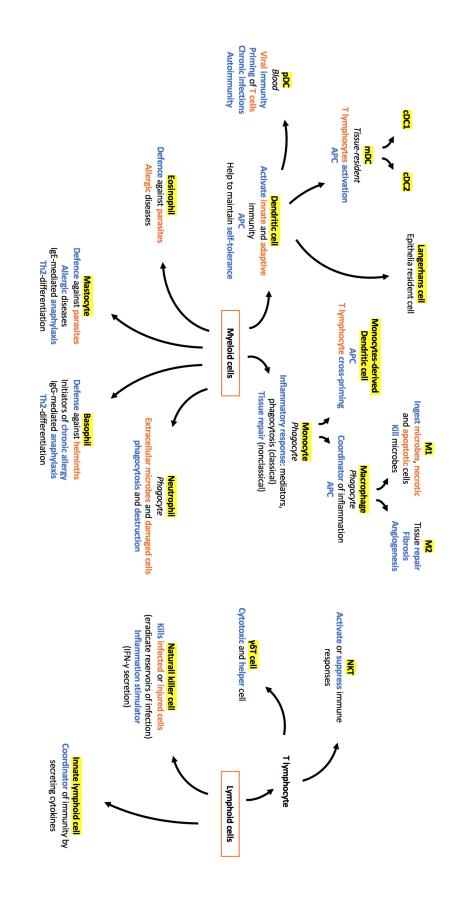
dependent lectin; SRA, Scavenger receptor A; FPRs, Formyl-peptide receptor; FPRL, Formyl-peptide receptor-like; GPCR, GTP-binding associated molecular pattern; DAMP, Damaged-associated molecular pattern; PRR, Pattern recognition receptor; DC, Dendritic cell; TLR, foll-like receptor; TIR, Toll/interleukin-1 receptor; NF-kB, Nuclear factor-kB; NLR, NOD-like receptors; NOD, Nucleotide oligomerization domain; NLRP, NACHT, NALP, LRR and PYD domains-containing protein 3; RLR, RIG-like receptors; MDA, Melanoma differentiationassociated protein; CDSs, Cytosolic DNA sensors; CLRs, C-type lectin-like receptors; AIM, Absent in melanoma; SP, Surfactant protein; STING, Stimulator of IFN genes; MD2, Myeloid differenitation protein 2; EC, Extracellular; IC, Intracellular; NF-kB, Nuclear factor kB; AP-1, Activation protein 1; IRF, Interferon response factor; BIR, Baclovirus inhibition of apoptosis protein repeat; CARDs, Caspase recruitment and activation domains; DAP, Diaminopimelic acid; MDP, Muramyl dipeptide; K+, Potassium ion; STING, Stimulator of IFN genes; cGAS, Cyclic GMP-AMP synthase; cGAMP, Cyclic GMP-AMP; DAI, DNA-dependent activator of IFN-regulatory factors; IF116, Interferon inducible protein 16; ER, Endoplasmic reticulum; MAVS, Mitochondrial antiviral-signalling; ITAM, Immunoreceptor ryrosine-based activation motif; DC-SIGN, Dendritic cell-specific intercellular adhesion molecule 3-grabbing nonintegrin; Mincle, Macrophage inducible Ca2+ G protein-coupled receptor; CRP, C-reactive protein; SAP, Serum amyloid P; MBL, Mannose-binding lectin; MASP, Mannose/mannan-Figure 4: III- Overview of the principal pathogen recognition receptors of the innate immune system. - Soluble PRRs. PAMP, pathogenassociated serine proteases; DAF, Decay accelerating factor; MCP, Membrane co-factor proteolysis. Sources: (7), (62) and (63).

	Pathogens structures recognized by PRR					
Туре	Structure	Source	PRR recognition			
Pathogen-Associated Molecular Patterns (PAMPs)						
Nucleic acids	ssRNA	Virus	TLR 7, 8			
	dsRNA	Virus	TLR 3, RNA polymerase 3, AIM2, cGAS, DAI, IFI16, RIG-I, MDA-			
	CpG	Virus, bacteria	TLR 9			
Proteins	Pilin	Bacteria	TLR 2			
	Flagellin	Bacteria	TLR 5, NLRB, NLRC4			
	F protein	Virus (RSV)	TLR 4			
	N-formylmethionine	Bacteria	FPRs			
Cell wall lipids	LPS	Gram- bacteria	TLR 4, NLRP7, SRs			
	Lipoteichoic acid	Gram+ bacteria	TLR 2, SRs, Ficolin			
	Phosphorylcholine	Bacteria	CRP, SAP			
	Phosphatidylethanolamine	Bacteria	CRP, SAP			
	rnosphaticylethanolamme	Bacteria	CRF, SAF			
Cell wall polymers	Peptidoglycan	Bacteria	TLR 2, TLR 6, NOD 1, NOD 2			
Carbohydrates	Mannan	Fungi, bacteria	CD206, Dectin-2, Langerin, DC-SIGN, MBL			
-	Fucose	Bacteria	CD206, DC-SIGN, MBL			
	N-acetyl-D-glucosamine	Bacteria	CD206, Ficolin			
	Glucans	Fungi	TLR 2, TLR 6, Dectin-1, SRs			
stress-induced proteins	HSPs	Damaged cells	TLR 2, TLR 4			
itress-induced proteins Crystals	Monosodium urate	Damaged cells Damaged cells	NLRP3			
			· · · · · · · · · · · · · · · · · · ·			
Crystals	Monosodium urate Silica	Damaged cells	NLRP3 NLRP3			
	Monosodium urate		NLRP3			
rystals Proteolytically cleaved extracellular matrix	Monosodium urate Silica Proteoglycan peptides	Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3			
Proteolytically cleaved	Monosodium urate Silica	Damaged cells	NLRP3 NLRP3			
rystals Proteolytically cleaved extracellular matrix	Monosodium urate Silica Proteoglycan peptides Phosphorylcholine	Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3			
Proteolytically cleaved extracellular matrix Cell wall lipid	Monosodium urate Silica Proteoglycan peptides Phosphorylcholine Phosphatidylethanolamine	Damaged cells Damaged cells Apoptotic cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP			
rystals Proteolytically cleaved extracellular matrix Cell wall lipid Vlitochondria and	Monosodium urate Silica Proteoglycan peptides Phosphory/choline Phosphatidy/ethanolamine Formylated peptides	Damaged cells Damaged cells Apoptotic cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP			
Proteolytically cleaved extracellular matrix cell wall lipid Vitochondria and mitochondrial components	Monosodium urate Silica Proteoglycan peptides Phosphory/choline Phosphatidylethanolamine Formylated peptides and ATP	Damaged cells Damaged cells Apoptotic cells Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP NLRP3			
Proteolytically cleaved extracellular matrix cell wall lipid Vitochondria and mitochondrial components	Monosodium urate Silica Proteoglycan peptides Phosphorylcholine Phosphatidylethanolamine Formylated peptides and ATP HMGB1	Damaged cells Damaged cells Apoptotic cells Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP NLRP3			
Proteolytically cleaved extracellular matrix cell wall lipid Witochondria and mitochondrial components Nuclear proteins	Monosodium urate Silica Proteoglycan peptides Phosphorylcholine Phosphatidylethanolamine Formylated peptides and ATP HMGB1 Histones	Damaged cells Damaged cells Apoptotic cells Damaged cells Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP NLRP3 TLR 2, TLR 4			
Proteolytically cleaved extracellular matrix cell wall lipid Witochondria and mitochondrial components Nuclear proteins Nucleic acids ysosomal damage	Monosodium urate Silica Proteoglycan peptides Phosphorylcholine Phosphatidylethanolamine Formylated peptides and ATP HMGB1 Histones Extracellular ATP ROS	Damaged cells Damaged cells Apoptotic cells Damaged cells Damaged cells Damaged cells Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP NLRP3 TLR 2, TLR 4 NLRP3 NLRP3			
rystals Proteolytically cleaved extracellular matrix Cell wall lipid Viltochondria and mitochondrial components Nuclear proteins	Monosodium urate Silica Proteoglycan peptides Phosphory/choline Phosphatidylethanolamine Formylated peptides and ATP HMGB1 Histones Extracellular ATP ROS Alum	Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP NLRP3 TLR 2, TLR 4 NLRP3 NLRP3 NLRP3			
Proteolytically cleaved extracellular matrix cell wall lipid Witochondria and mitochondrial components Nuclear proteins Nucleic acids ysosomal damage	Monosodium urate Silica Proteoglycan peptides Phosphorylcholine Phosphatidylethanolamine Formylated peptides and ATP HMGB1 Histones Extracellular ATP ROS	Damaged cells Damaged cells Apoptotic cells Damaged cells Damaged cells Damaged cells Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP NLRP3 TLR 2, TLR 4 NLRP3 NLRP3			
Proteolytically cleaved extracellular matrix cell wall lipid Witochondria and mitochondrial components Nuclear proteins Nucleic acids ysosomal damage	Monosodium urate Silica Proteoglycan peptides Phosphory/choline Phosphatidylethanolamine Formylated peptides and ATP HMGB1 Histones Extracellular ATP ROS Alum	Damaged cells Damaged cells Apoptotic cells Damaged cells Damaged cells Damaged cells Damaged cells	NLRP3 NLRP3 TLR 2, TLR 4, NLRP3 CRP, SAP NLRP3 TLR 2, TLR 4 NLRP3 NLRP3 NLRP3			

Figure 5: **Overview of the principal PAMPs and DAMPs.** - Type, subtype and origin of the principal molecular patterns recognized by the innate immunity. PAMP, Pathogen-associated molecular pattern; DAMP, Damaged-associated molecular pattern; ATP, Adenosine triphosphate; CpG, Cytosine-guanine-rich oligonucleotide; dsRNA, Double-stranded RNA; HMGB1, High-mobility group box 1; HSP, Heat shock protein; LPS, Lipopolysaccharide; ssRNA, Single-stranded RNA; TLR, Toll-like receptor; RSV, Respiratory syncytial virus; AIM2, Absent in melanoma-2; cGAS, Cyclic GMP-AMP synthase; DAI, DNA-dependent activator of IFN-regulatory factors; IFI16, Interferon inducible protein 16; NLR, NOD-like receptor; NOD, Nucleotide oligomerization domain; DC-SIGN, Dendritic cell-specific intercellular adhesion molecule 3-grabbing nonintegrin; SRs, Scavenger receptors; FPRs, Formyl peptide receptors; CRP, C-reactive protein; SAP, Serum amyloid P; MBL, Mannose-binding lectin. Sources: (7), (62), (63) and (64).







differentiation from two different haematopoietic lineages: the myeloid and lymphoid progenitors. Sources: (7), (65), (67), (68) and (69). Figure 7: Overview of the different hematopoietic stem cell-derived innate immune cells - Innate immune cells are the products of

CD Molecules					
CD Number (Other Names)		Molecular Structure, Family	Main Cellular Expression	Known or Proposed Function(s)	
CD1a-d		Class MHC-like g superfamily ß2-microglobulin associated	Thymocytes DC (including Langerhans cells)	- Presentaion of nonpeptid (lipid and gylcolipid) antigens to some T cells	
СDЗуу		Associated with CD3d and CD3e in TCR complex Ig superfamily ITAM in cytoplasmic tail	T cells	 Cell surface expression of and signal transduction by the T cell antigen receptor 	
CD 3d		Associated with CD3y and CD3e in TCR complex Ig superfamily ITAM in cytoplasmic tail	T cells	 Cell surface expression of and signal transduction by the T cell antigen receptor 	
D3e		Associated with CD3d and CD3y in TCR complex lg superfamily ITAM in cytoplasmic tail	T cells	 Cell surface expression of and signal transduction by the T cell antigen receptor 	
CD4		lg superfamily	Class II MHC-restricted T cells Some macrophages	Coreceptor in class II MHC-restricted antigen-induced T cell activation (binds to class II MHC molecules) Thymocyte development Receptor for HIV	
	;p40 ;P41	Associated to PI3-Kinase	T cells NK cells Stem cell/Precursor	- T cell interactions	
D8a		Expressed as a homodimer or heterodimer with CD8ß	Class I MHC-restricted T cells Subset of DC	Coreceptor in class MHC-restricted antigen-induced T or activation (binds to class MHC molecules) Thymocyte development	
D8ßß		Expressed as a heterodimer with CD8a Ig superfamily	Class I MHC-restricted T cells	Coreceptor in class I MHC-restricted antigen-induced T c activation (binds to class I MHC molecules) Thymocyte development	
D11a L	FA-1 a chain	Noncovalently linked to CD18 to form LFA-1 integrin	Leukocytes	Cell-cell adhesion Binds to ICAM-1 (CD54), ICAM-2 (CD102), ICAM-3(CD50)	
	Иас-1 R3	Noncovalently linked to CD18 to form Mac-1 integrin	Granulocytes Monocytes Macrophages DC NK cells	Phagocytosis of iC3b-coated particles Neutrophil and monocyte adhesion to endothelium (binds CD54) and extracellular matrix proteins	
	0150, 95 CR4aa chain	Noncovalently linked to CD18 to form p150, 95 integrin	Monocytes Macrophages Granulocytes NK cells	Phagocytosis of iC3b-coated particles Neutrophil and monocyte adhesion to endothelium (binds CD54) and extracellular matrix proteins	
D14		GPI linked	DC Monocytes Macrophages Granulocytes	Binds complex of LPS and LPS-binding protein and displays LPS to TLR4 Required for LPS-induced macrophage activation	
D15		Carbohydrate largely used for Dx of Hodgkin Lymphoma	Stem cell/Precursor Macrophages Monocytes Granulocytes	- Adhesion - Granulocyte activation	
D16a F	cyyRIIIA	Transmembrane protein Ig superfamily	NK cells Macrophages	 Binds FC region of IgG Phagocytosis and Ab-dependent cellular cytotoxicity 	
D16b F	cyyRIIIB	GPI linked Ig superfamily	Neutrophils	 Binds Fc region of IgG Synergy with FcyyRII in immune complex-mediated neutrophil activation 	
D19		lg superfamily	Most B cells	B cell activation Forms a coreceptor complex with CD21 and CD81 that delivers signals that synergize with signals from B cell antigen receptor complex	
D20		Tetraspan (TM4SF) family	B cells	 Possible role in B cell activation or regulation Calcium ion channel 	
	CR2 C3d receptor	Regulators of complement activation	Mature B cells Follicular DCs	Receptor for complement fragment C3d Forms a coreceptor complex with CD19 and CD81 that delivers activating signals in B cells Receptor for Epstein-Bar virus	

Figure 8: **I- CD molecules characteristics and functions -** CD molecules characteristics: structure, main cellular expression and functions. Modified from (7), (70) and (71).

		CD Molect	ules (following)		
CD Nur	mber (Other Names)	Molecular Structure, Family	Main Cellular Expression	Known or Proposed Function(s)	
CD23	FceRIIB	C-type lectin	Activated B cells Monocytes Macrophages	Low-affinity Fce receptor, induced by IL-4 Function is not clear	
CD25	IL-2 receptor a chain	Noncovalently associated with IL-2Rß (CD122) and IL-2Ry (CD132) chains to form a high-affinity IL-2 receptor	Activated T cells Activated B cells Regulatory T cells (Treg)	Binds IL-2 and promotes responses to low concentrations of IL-2	
CD26	DPP4	Dipeptidyl peptidase	T cells B cells NK cells Macrophages Epithlial cells	 Exopeptidase Régulation immunitaire Transduction signal Apoptose Métabolisme glucose (augmente GLP-1 et GIP) 	
CD27		TNF receptor superfamily	T cells B cells NK cells	Generation and long term maintenance of T cell immunity Regulation of B cell activation and Ig synthesis	
CD28		lg superfamily	CD4+ T cells >50% of CD8+ cells	- T cell receptor for costimulatory molecues CD80 (B7.1) and CD86 (B7.2)	
CD 30	TNFRSF8	TNFR superfamily	Activated T and B cells NK cells Monocytes Reed-Sternberg cells in HL	- Not established	
CD31	PECAM-1	Ig superfamily	Platelets Monocytes Granulocytes B cells Endothelial cells	 Adhesion molecule involved in leukocyte transmigration through endothelium 	
CD33		Sialoahesin Ig superfamily	DC Macrophages Monocytes Granulocytes Stem cell/Precursor Mast cells	Cell adhesion Cell-cell signaling Inhibitory receptor Apoptosis Granulocytes: decreasing expression with maturation	
CD 38		Type II transmembrane glycoprotein Synthesizes and hydrolyzes ADP (IC Ca2+ messenger)	T cells B cells DC NK cells Marcophages Monocytes Stem cell/Precursors	- Cell adhesion - Signal transduction	
CD40		TNFR superfamily	B cells Macrophages DC Endothelial cells	Binds CD154 (CD40L) Role in T cell-mediated activation of B cells, macrophages and DC	
CD45	LCA	Protein tyrosine phosphatase receptor family Fibronectin type III family	Hematopoietic cells	- Tyrosine phosphatase that regulates T and B cells activatio	
CD56	NCAM	lg superfamily	T cells NK cells DC	Cell adhesion NK activation: upregulation Neural plasticity NK suppression: downregulation	
CD62L	L-Selectin	Selectin famíly	B cells T cells Monocytes Granulocytes Some NK cells	 Leukocyte-endotheliai adhesion Homing of naive T cells to peripheral lymph nodes 	
CD 66b		Carcinoembryonic antigen family	Granulocytes	 Cell adhesion Cellular migration Pathogen binding and activation of signaling pathways 	
CD 69		C-type lectin	Activated B cells T cells NK cells Neutrophils	 Binds to and impairs surface expression of S1PR1, thereby promoting retention of recently activated lymphocytes in lymphoid tissues (Transient marker) 	

Figure 8: **II- CD molecules characteristics and functions** - CD molecules characteristics (following): structure, main cellular expression and functions. Modified from (7), (70) and (71).

CD Molecules (following)					
CD Num	nber (Other Names)	Molecular Structure, Family Main Cellular Expression		Known or Proposed Function(s)	
CD86	B7-2	lg superfamily	B cells Monocytes DC Some T cells	Costimulator for T lymphocyte activation Ligand for CD28 and CD152 (CTLA-4)	
CD94		C-type lectin On NK cells covalently assembles with other C-type lectin molecules (NKG2)	NK cells Subset of CD8+ T cells	CD94/NKG2 complex functions as an NK cell inhibitory receptor Binds HLA-E class I MHC molecules	
CD123	IL-3RA	Beta common (ßc) family of cytokines	DC Granulocytes Stem cell/Precursor Endothelial cells	 Hematopoletic progenitor cell growth and differentiation 	
CD141	BDCA-3 CLEC9A Thrombomodulin	EGF-like domains	Cross-presenting DC Monocytes Endothelial cells	 Binds thrombin and prevents blood coagulation 	
CD154	CD40L	TNFR superfamily	Activated CD4+ T cells	 Activation of B cells, macrophages, and endothelial cells Ligand for CD40 	
CD159a	NKG2A	C-type lectin Forms heterodimer with CD94	NK cells T cell subset	 Inhibition or activation of NK cells on interation with class I HLA molecules 	
CD159c	NKG2C	C-type lectin Forms heterodimer with CD94	NK cells	 Activation of NK cells on interaction with the appropriate class I HLA molecules 	
CD314	NKG2D	C-type lectin	NK cells Activated CD8+ T cells NK-T cells Some myeloid cells	 Binds MHC class I, and the class I-like molecules MIC-A, MIC-B, Rae1, and ULBP4 Role in NK cell and CTL activation 	
CD337	NKp30	I-type Ig-like fold	NK cells	- Immune surveillance in anti-tumor immunity	

Figure 8: **III- CD molecules characteristics and functions -** CD molecules characteristics (following): structure, main cellular expression and functions. Modified from (7), (70) and (71).

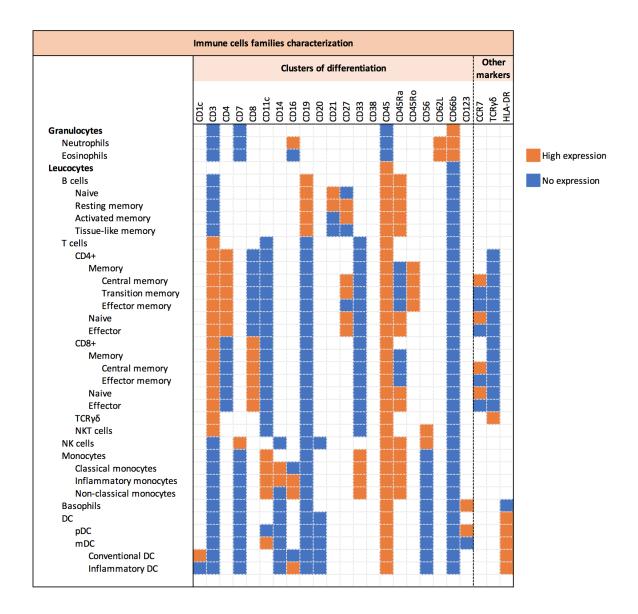


Figure 9: **Major immune cells molecular characterization** - This non-exhaustive table illustrates the phenotypic molecular signatures characterizing the major known human immune cells subsets. Blue means an absence of expression, whereas orange means that the molecule is expressed. Sources: (2) and (7).

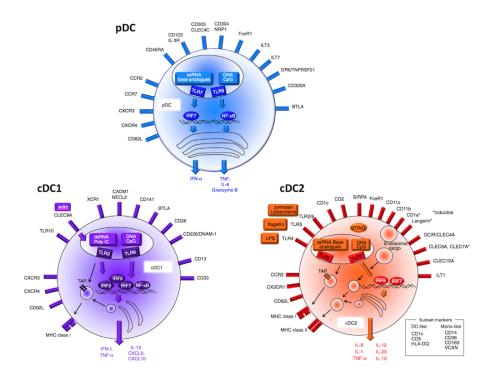


Figure 10: **Main DCs subsets molecular characterization** - Surface molecules, intracellular PRRs, expressed genes and released cytokines by plasmacytoid DCs, type 1 and type 2 conventional DCs. Sources: (5).

Classification of primary immune deficiency diseases					
Deficiencies of the innate immune system					
Phagocytic cells	Impaired production: severe congenital neutropenia (SCN) Asplenia				
	Impaired adhesion: leukocyte adhesion deficiency (LAD) Impaired killing: chronic granulomatous disease (CGD)				
Innate immunity receptors and	Defects in Toll-like receptor signalling				
signal transduction	Mendelian susceptibility to mycobacterial disease				
Complement deficiencies	Classical, alternative, and lectin pathways				
	Lytic phase				
Deficiencies of the adaptive immu	une system				
T lymphocytes					
Impaired development	Severe combined immune deficiencies (SCIDs) DiGeorge syndrome				
Impaired survival, migration,	Combined immunodeficiencies				
function	Hper-IgE syndrome (Job syndrome)				
	DOCK8 deficiency				
	CD40 ligand deficiency				
	Wiskott-Aldrich syndrome				
	Ataxia-telangiectasia and other DNA repair deficiencies				
B lymphocytes					
Impaired development	XL and AR agammaglobulinemia				
Impaired function	Hyper-IgM syndrome				
	Common variable immunodeficiency (CVID)				
	IgA deficiency				
Regulatory defects					
Innate immunity	Autoinflammatory syndromes				
	Severe colitis				
Adaptive immunity	Hemophagocytic lymphohistiocytosis (HLH)				
	Autoimmune lymphoproliferation syndrome (ALPS)				
	Autoimmunity and inflammatory diseases (IPEX, APECED)				

Figure 11: **Primary immunodeficiencies classification** - Classification of PID based on the side of immunity that is disturbed, and the mechanism responsible for this defect. Sources: (12).

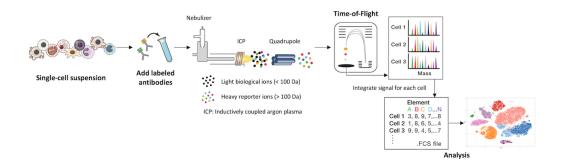


Figure 12: Mass Cytometry Workflow - General outlook of mass cytometry workflow, from single-cell suspension to data analysis. Modified from (33).

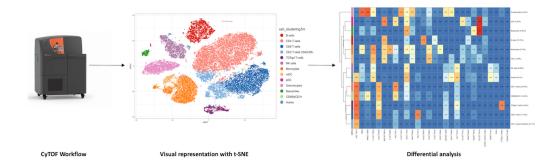


Figure 13: **General Analysis Pipeline** - General data processing pipeline starting with data acquisition through a mass cytometer, then cluster identifications and finally intraclusters evaluation.

Immunodeficiency panel used in this project						
Isotope	Marker	Clone	Source	Titration [µL]		
Extracellular markers						
89 Y	CD45 #1	HI30	DVS	0.50		
113 In	CD8	RPA-T8	CHUV	0.25		
115 In	CD4	RPA-T4	CHUV	0.30		
141 Pr	CD45 #2	HI30	DVS	0.70		
142 Nd	CD19	HIB19	DVS	0.80		
143 Nd	HLADR	L243	DVS	0.75		
144 Nd	CD69	FN50	DVS	0.50		
145 Nd 146 Nd	CD31	WM59 IT2.2	DVS CHUV	0.60		
146 No 147 Sm	CD86 CD7	CD7-6B7	DVS	0.25		
147 Sm 148 Nd	CD16	3G8	DVS	0.45		
148 Nu 151 Eu	CD123	6H6	DVS	0.72		
155 Gd	CD27	L128	DVS	0.50		
155 Gd	ΤCRγδ	B1	CHUV	0.80		
158 Gd	CD33	WM53	DVS	0.50		
150 Cu 159 Tb	CD337/NKp30	Z25	DVS	0.50		
160 Gd	CD14	M5E2	DVS	0.97		
161 Dy	CD1c	L161	CHUV	0.61		
162 Dy	CD11c	Bu15	DVS	0.96		
163 Dy	CD62L	DREG-56	CHUV	0.25		
166 Er	CD314/NKG2D	ON72	DVS	0.50		
167 Er	CD38	HIT2	DVS	0.30		
168 Er	CD66b	G10F5	CHUV	0.80		
169 Er	CD159a/NKG2A	Z199	DVS	0.50		
170 Er	CD3	UCHT1	DVS	0.40		
172 Yb	CD15	W6D3	DVS	0.50		
173 Yb	CD141	1A4	DVS	0.75		
174 Yb	CD94/NKG2	HP-3D9	DVS	0.50		
176 Yb	CD56	HCD56	DVS	0.96		
209 Bi	CD11b	ICRF44	DVS	0.40		
	Intracellular markers					
149 Sm	IL12p40	C11.5	CHUV	0.50		
150 Nd	IFNα	LT27:295	CHUV	0.60		
152 Sm	ΤΝFα	Mab11	DVS	0.50		
153 Eu	IL1b	AS10	CHUV	0.50		
154 Sm	IL6	MQ2-13A5	DVS	0.80		
164 Dy	IL17a	N49-653	DVS	0.80		
165 Ho	IFNγ	B27	DVS	0.50		
171 Yb	Granzyme B	GB11	DVS	0.50		
175 Lu	Perforin	B-D48	DVS	0.60		

Figure 14: **Innate immune functional panel** - Panel of antibodies used in this project, with the corresponding heavy metal isotope, marker, clone and source. In, Indium; Pr, Praseodymium; Nd, Neodymium; Sm, Samarium; Eu, Europium; Gd, Gadolinium; Tb, Terbium; Dy, Dysprosium; Er, Erbium; Yb, Ytterbium; Bi, Bismuth; Ho, Holmium; Lu, Lutetium.

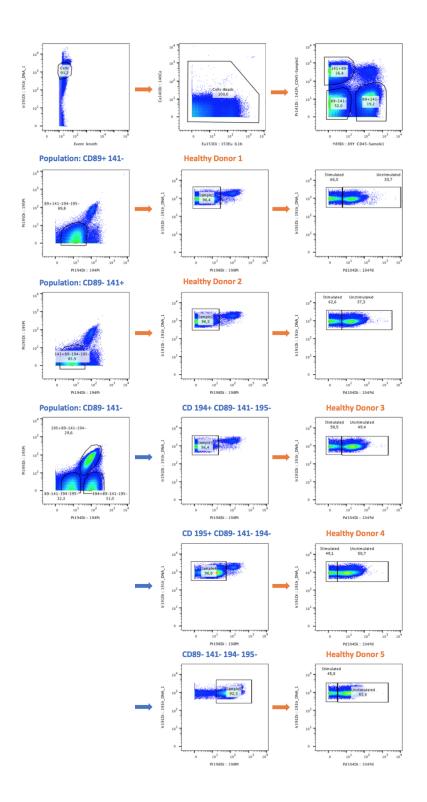
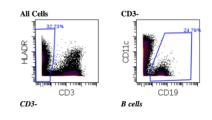


Figure 15: **Initial gating strategy to individualize each condition for each patient and healthy donor** - Gating strategy using FlowJo, allowing to get individualized FCS files for each samples condition, illustrated for the batched data acquired containing the healthy donors 1 to 5. At the end, this means that 60 FCS files will be created (15 patients, 15 healthy donors, with each of them having 2 conditions).

B cells



CD4+

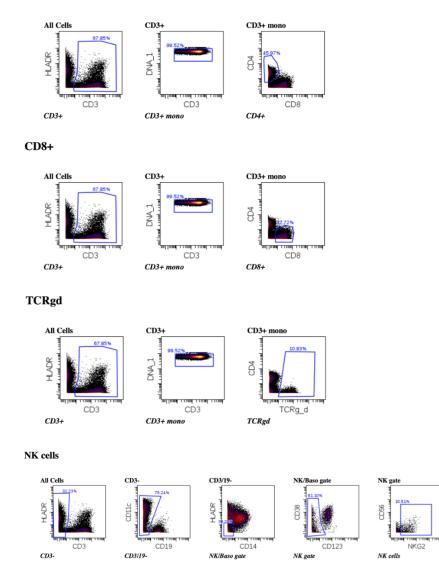


Figure 16: I- Manual gating strategy for the major known immune cells populations -Manual gating using Cytobank, plotting two-dimension scatterplots to iteratively cluster cells groups according to their surface markers. It can be seen as an iterative selection process of different markers expressions which at the end will define the corresponding cells populations.

Mono gate 2

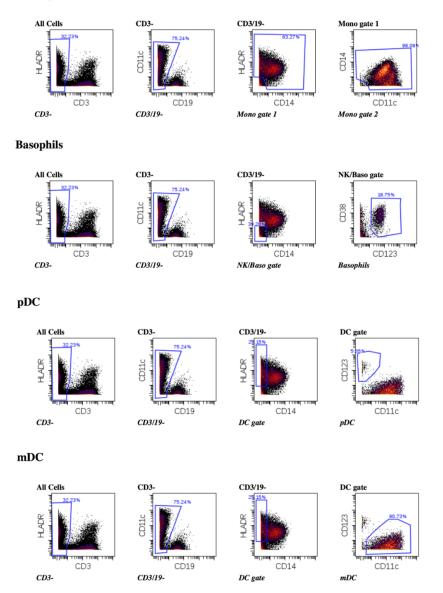
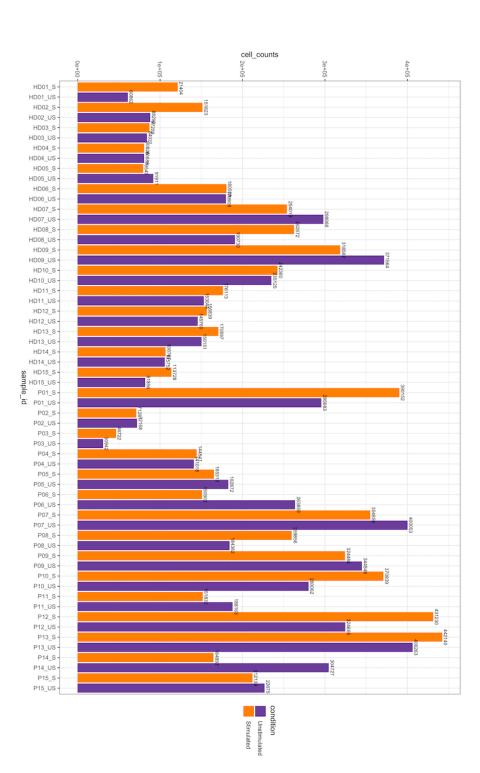


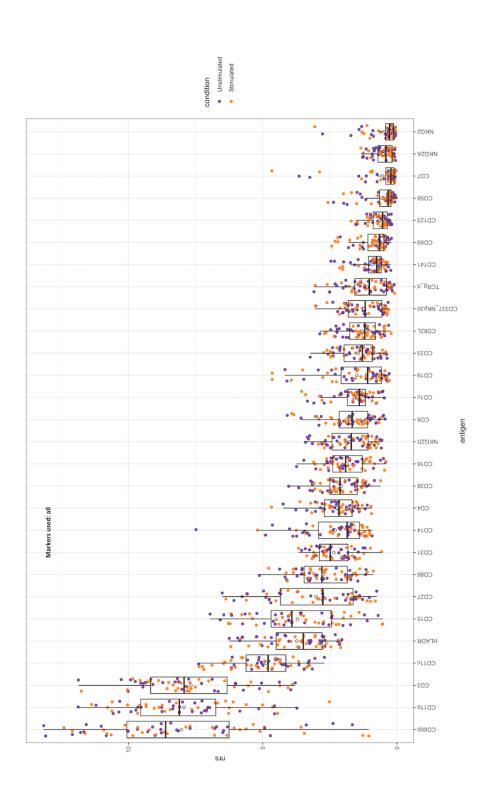
Figure 16: **II- Manual gating strategy for the major known immune cells populations** - Following.

Clustering Suface Markers				
All cells	mDCs			
CD1c	CD1c			
CD3	CD11b			
CD4	CD11c			
CD7	CD16			
CD8	CD31			
CD11c	CD38			
CD14	CD62L			
CD16	CD69			
CD19	CD86			
CD56	CD123			
CD66b	CD141			
CD123	HLA-DR			
HLA-DR				
TCRγ				

Figure 17: **Clustering surface markers** - Surface markers used to discriminate cells subpopulations when automatically clustering them, for all cells and mDC population.



and conditions, distinguished by color. The y-axis indicates the cell counts for each of the sample, and is written on the top of each barplot. HD, healthy donor; P, patient; US, unstimulated; S, stimulated. Figure 18: Barplot displaying the number of acquired events for each sample and condition - The x-axis represents the different samples



the statistically most to the least discriminative, for all samples. This should be used as a help to identify the markers that will be used for Figure 19: Non-redundancy scores for all samples and all surface markers - Surface markers are arranged according to their NRS from the downstream clustering, but should not be taken as an absolute verity as it does not take into account biological meanings.

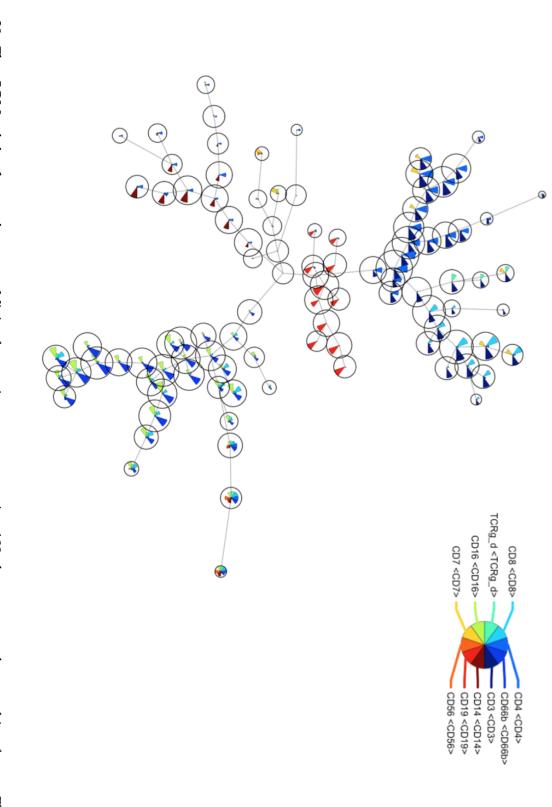


Figure 20: FlowSOM minimal spanning tree - Minimal spanning tree representing 100 clusters, or nodes, resulting from a FlowSOM algorithm. 10 markers intensities are presented for each node.

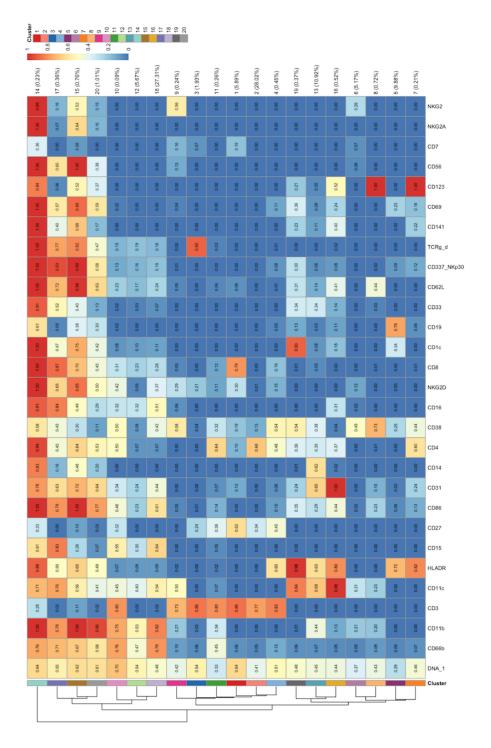
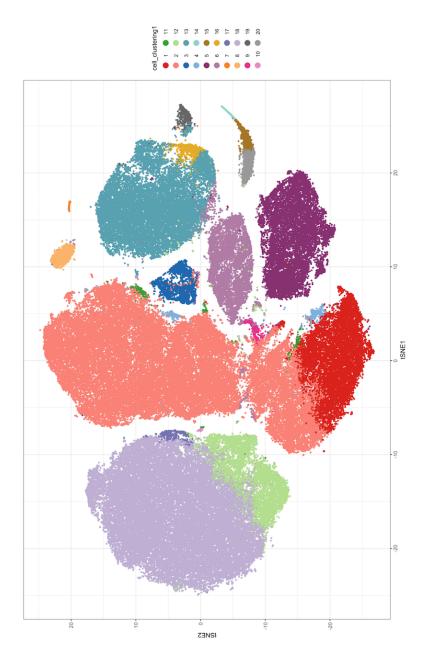


Figure 21: Heatmap of the median intensities of each surface markers in each population for all samples - Median intensities for each cluster have been calculated and are represented with the corresponding color on this heatmap.

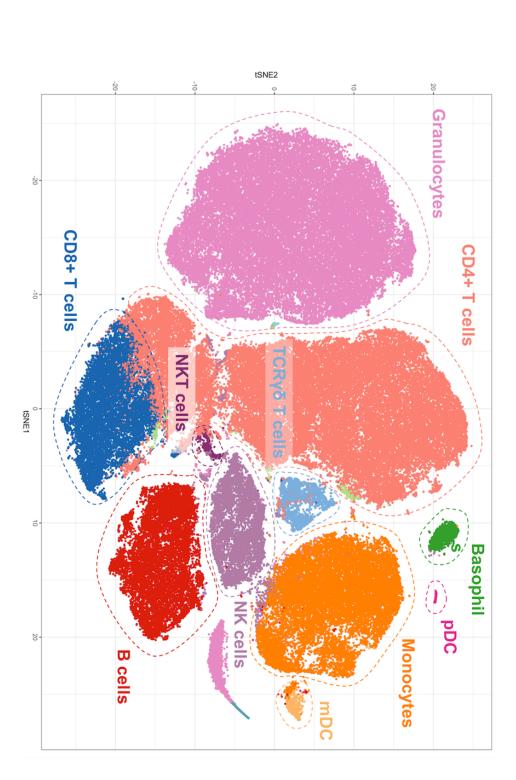
Cluster											
CD66b	0.09	0.74	0.07	0.06	0.07	0.05	0.10	0.06	0.06	0.05	0.05
CD11P	0.20	0.81	0.00	0.01	0.43	0.21	0.21	0.02	0.00	80	0.00
CD3	0.00	0.01	0.00	8	0.00	0.00	0.73	0.86	0.86	0.78	8
SCD11c	0.23	0.52	0.00	0.84	0.70	0.31	0.50	0.00	0.00	0.00	0.00
AD-AJH	0.00	0.10	0.82	ŝ	0.64	0.00	0.02	000	000	0.00	0.72
CD12	0.00	0.57	00	8	0.00	8	00	8	80	80	8
CD27	0.00	0.00	0.00	000	0.00	0.00	000	0.24	0.62	0.34	0.00
CD86	0.23	0.57	0.13	0.35	0.30	0.02	0.05	0.01	0.00	0.00	0.06
CD31	0.15	0.43	0.24	0.24	0.67	0.00	0.00	0.00	0.13	0.00	0.03
CD14	0.00	0.00	0.00	0.01	0.59	0.00	0.00	0.00	0.00	00	.00
CD4	0.01	0.09	0.60	0.36	0.35	000	0.00	00	0.15	0.68	8
CD38	0.73	0.35	0.44	0.54	0.36	0.49	0.58	0.04	0.19	0.14	0.25
CD16	0.00	0.48	0.00	0.00	0.00	0.02	0.06	0.00	0.00	0.00	0.00
NKG2D	0.00	0.32	0.00	8	0.00	0.12	0.29	0.21	0.30	0.02	8
CD8	0.01	0.29	0.01	0.01	0.05	8	0.05	8	0.79	8	8
CD1c	0.00	0.12	8	8	0.08	8	0.00	8	8	8	0.34
CD19	0.00	8	0.06	0.13	0.03	8	0.00	8	8	8	0.76
CD33	0.03	0.07	8	0.34	0.32	8	8	8	8	8	8
CD62L	0.44	0.25	8	0.31	0.15	0.00	0.05	0.00	0.06	0.00	8
NKp30	0.00	0.20	0.12	0.30	0.06	0.00	0.01	0.00	0.00	0.00	0.09
бүярт	0.00	0.19	0.00	0.00	0.01	0.00	0.00	.90	0.00	0.00	0.00
CD141	0.00	.00	0.22	0.23	0.12	0.00	0.00	8	8	8	8
CD69	8	0.02	0.18	0.36	0.09	8	0.04	8	8	8	0.23
CD123	1.00	0.00	1.00	0.21	0.06	0.00	0.00	0.00	0.00	0.00	0.00
CD26	0.00	0.00	0.00	0.00	0.00	0.06	0.13	0.00	0.00	0.00	0.00
202	0.00	.00	0.00	.00	0.00	0.07	0.16	0.07	0.19	0.00	0.00
NKG2A	0.00	0.00	00	8	0.00	8	00	8	8	8	8
NKG2	0.00	0.00	0.00	0.00	0.00	0.26	0.56	0.00	0.00	0.00	0.00
	Basophils	Granulocytes	pDC	mDC	Monocytes	NK cells	NKT cells	TCRγδ T cells	CD8+ T cells	CD4+ T cells	B cells
	0 0 0 0 0 0 1										

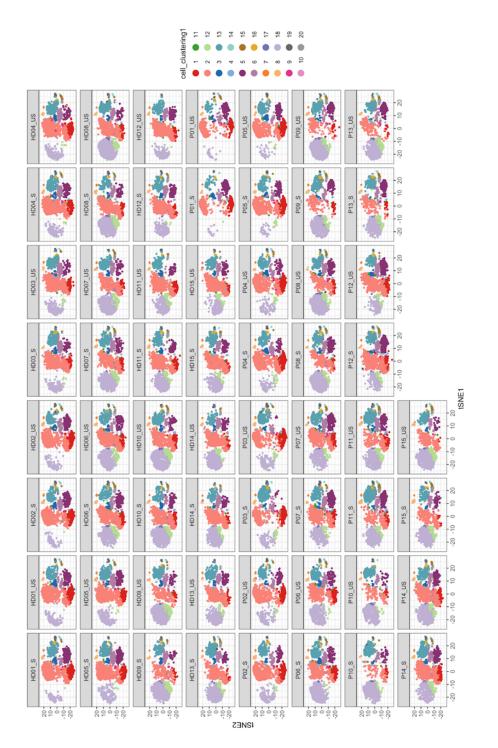
fied immune cell population is represented with its signature of surface molecular expression. Figure 22: Heatmap of the median intensities of each surface markers the major known immune cells populations - Each known identi-



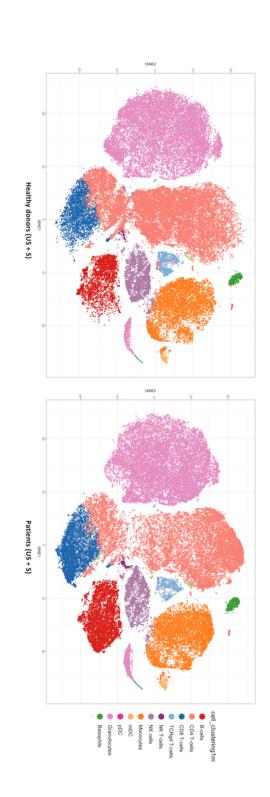


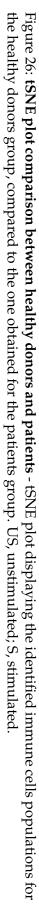


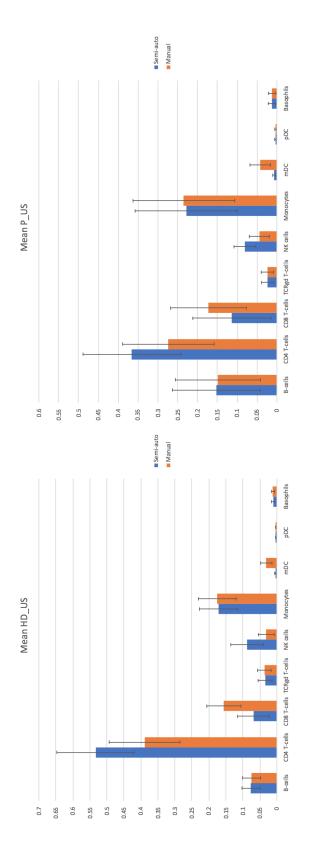


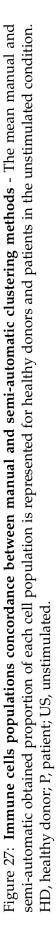


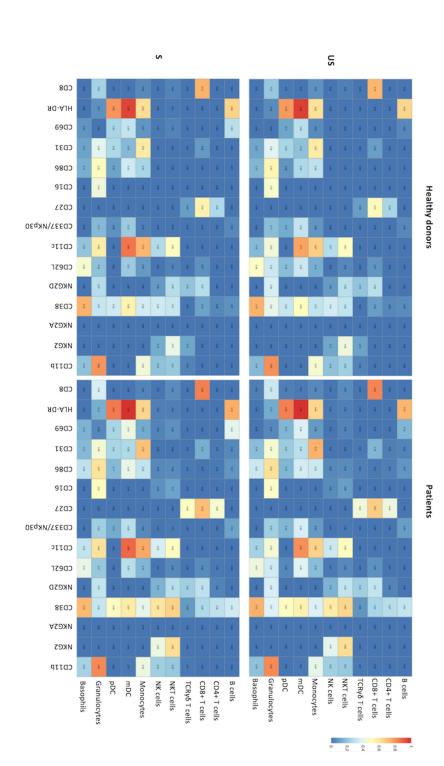












intensities in each of the populations for the healthy donors and patients groups, compared by conditions. US, unstimulated; S, stimulated. Figure 28: Median activation markers intensities for each of the groups and conditions - Visual representation of the activation markers

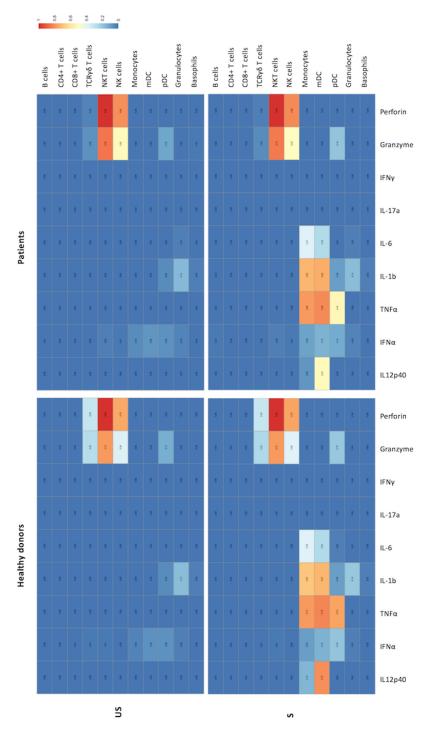


Figure 29: Median cytokines expressions intensities for each of the groups and conditions - Visual representation of the cytokines ex-pressions in each of the populations for the healthy donors and patients groups, compared by conditions. US, unstimulated; S, stimulated.

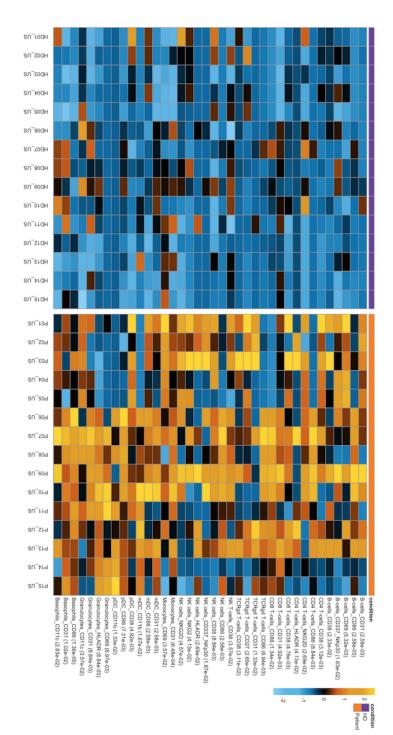


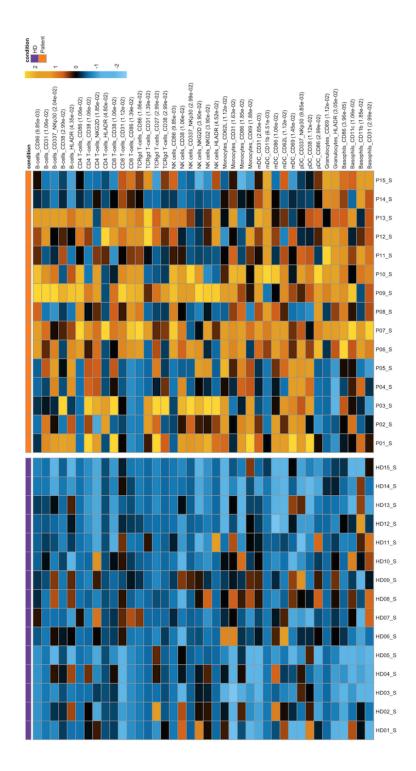


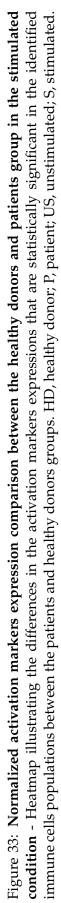


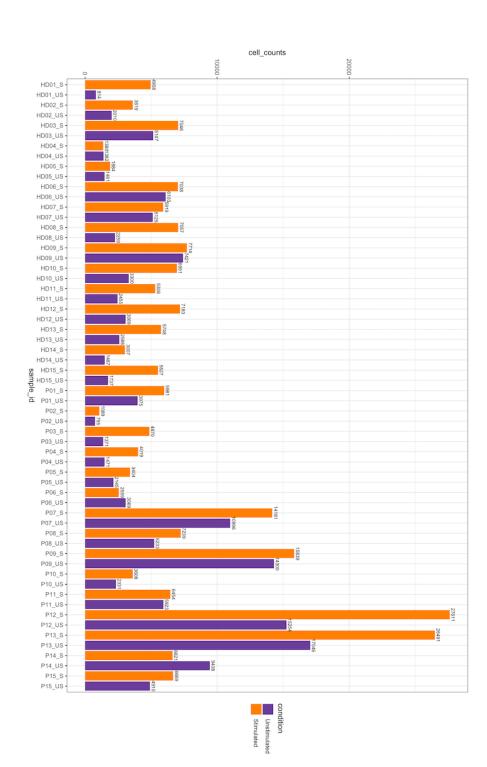
Figure 31: **Boxplots with jittered points representing the cytokines expression in the different immune cells populations** - Comparison for each of the populations the difference in cytokines expression between the unstimulated and stimulated conditions. HD, healthy donor.

immune cells populations between the patients and healthy donors groups. HD, healthy donor; P, patient; US, unstimulated; S, stimulated. condition - Heatmap illustrating the differences in the activation markers expressions that are statistically significant in the identified Figure 32: Normalized activation markers expression comparison between the healthy donors and patients group in the unstimulated

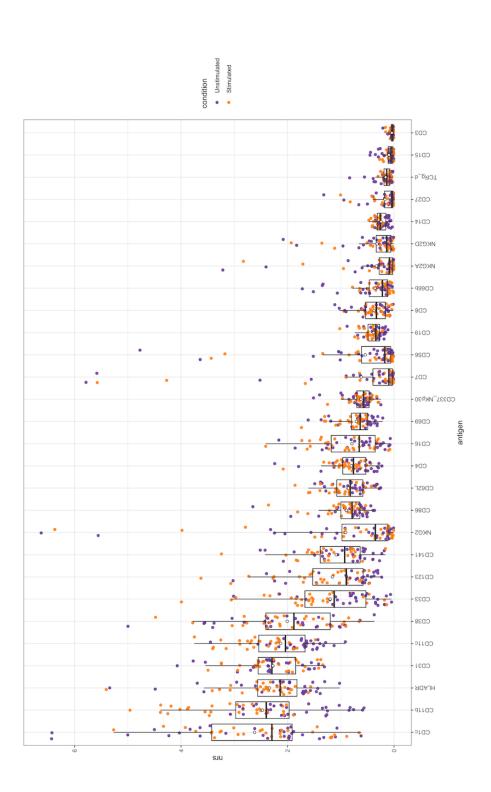








represents the different samples and conditions, distinguished by color. The y-axis indicates the cell counts for each of the sample, and is written on the top of each barplot. HD, healthy donor; P, patient; US, unstimulated; S, stimulated. Figure 34: Barplot displaying the number of acquired events for each samples and conditions in the mDC population - The x-axis



according to their NRS from the statistically most to the least discriminative, for all samples. This should be used as a help to identify the Figure 35: Non-redundancy scores for all samples and all surface markers in the mDC population - Surface markers are arranged markers that will be used for the downstream clustering, but should not be taken as an absolute verity as it does not take into account biological meanings.

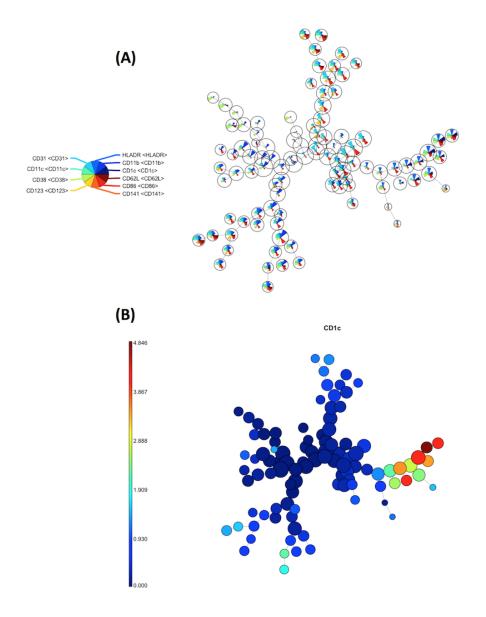


Figure 36: **Minimal spanning tree obtained with FlowSOM on the mDC population** - (A) Minimal spanning tree displaying the intensity in some marker expressions of the 100 identified clusters. (B) CD1c expression intensities among the 100 clusters.

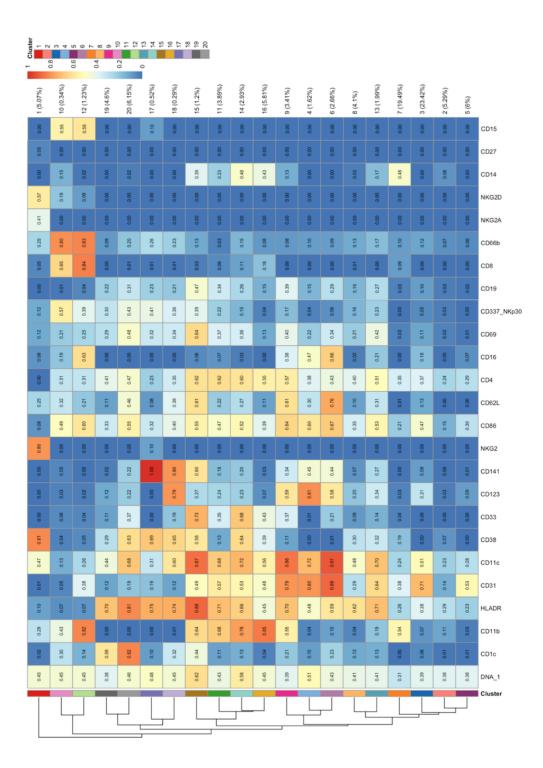


Figure 37: Heatmap of the median intensities of each surface markers in each population for all samples in the mDC population -Median intensities for each cluster have been calculated and are represented with the corresponding color on this heatmap.

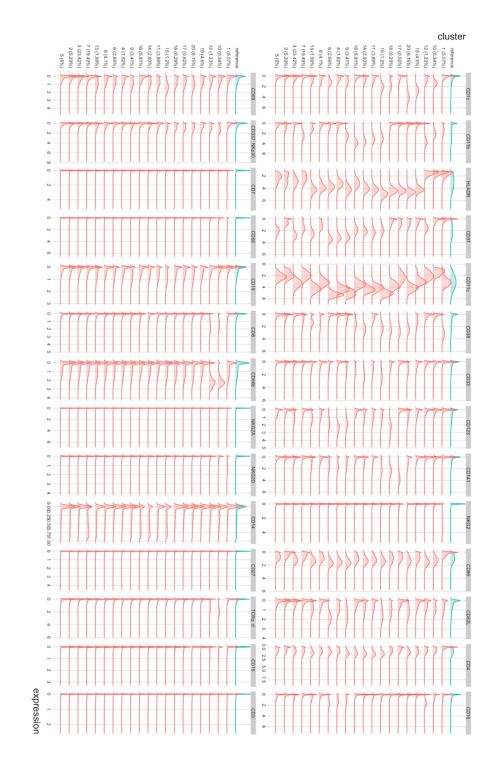
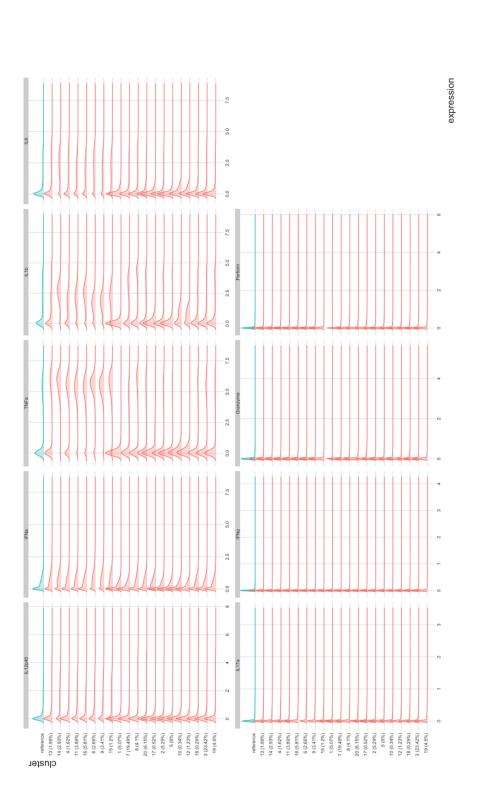


Figure 38: Median markers intensities of the mDC family 20 meta-clusters - Surface markers intensities are represented for each of the clusters obtained with FlowSOM and ConsensusClusterPlus metaclustering.





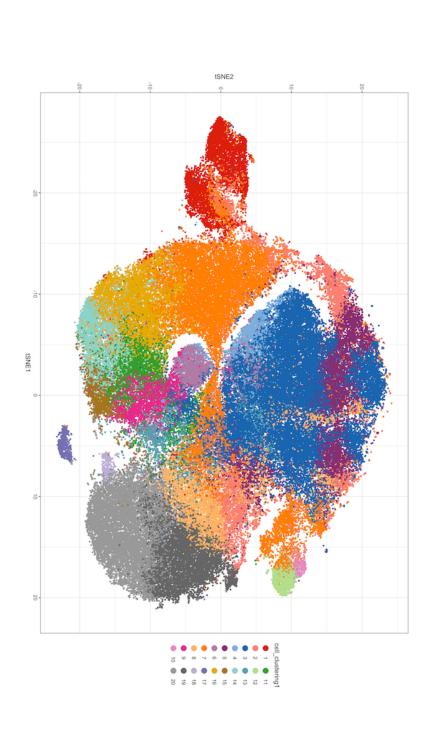
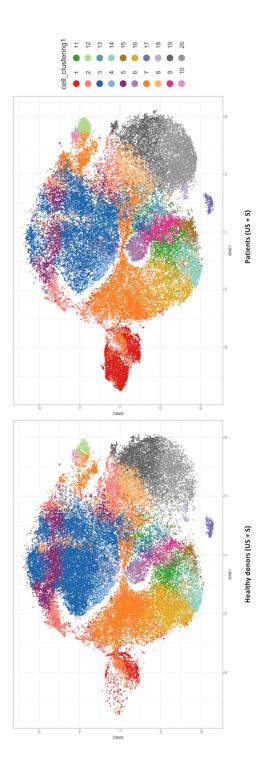
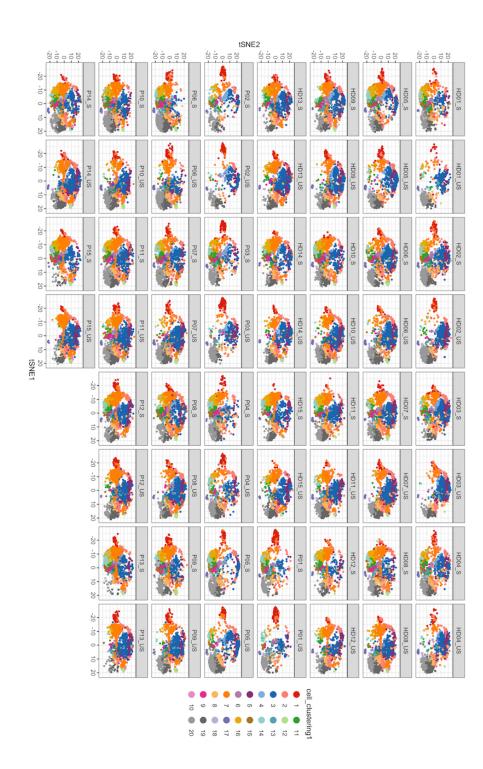


Figure 40: **tSNE plot of all myeloid dendritic cells** - Each cell is coloured according to the cluster it has been assigned to.







donor; P, patient; US, unstimulated; S, stimulated. of the samples and conditions, allowing a quick overview of the presence or absence of each clustered mDC subpopulation. HD, healthy Figure 42: tSNE plot stratified by samples and conditions in the mDC population - tSNE plot displaying the meta-clustering for each

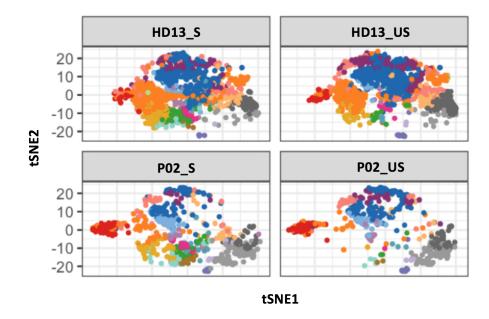
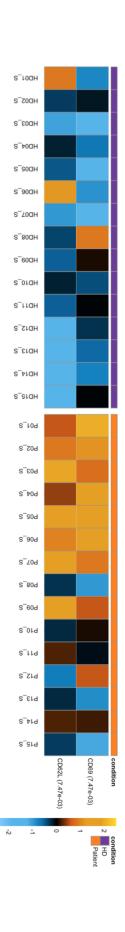


Figure 43: **mDC tSNE graph of patient 02 and healthy donor 13** - tSNE graphs focusing on patient 02 and healthy donor 13. HD, healthy donor; P, patient; US, unstimulated; S, stimulated.



overall mDCs between the patients and healthy donors groups. HD, healthy donor; P, patient; US, unstimulated; S, stimulated. condition of all mDCs - Heatmap illustrating the differences in the activation markers expressions that are statistically significant in the Figure 44: Normalized activation markers expression comparison between the healthy donors and patients group in the stimulated

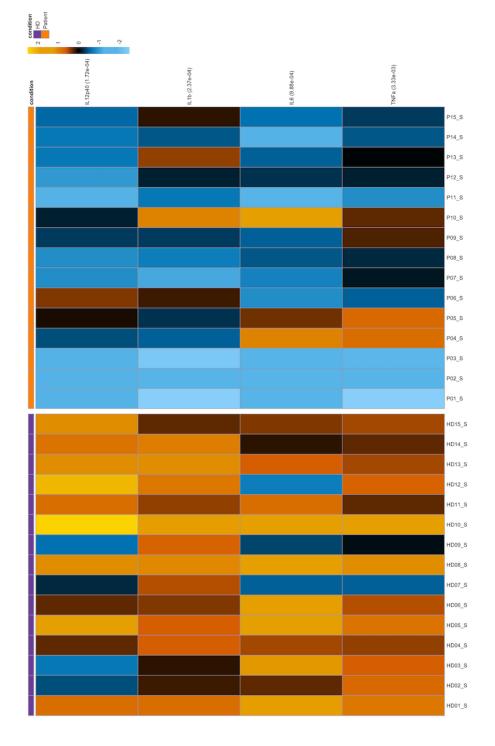
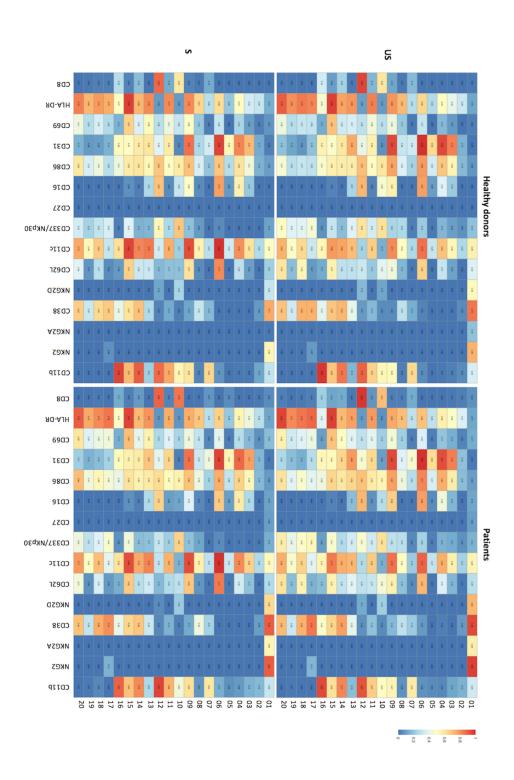
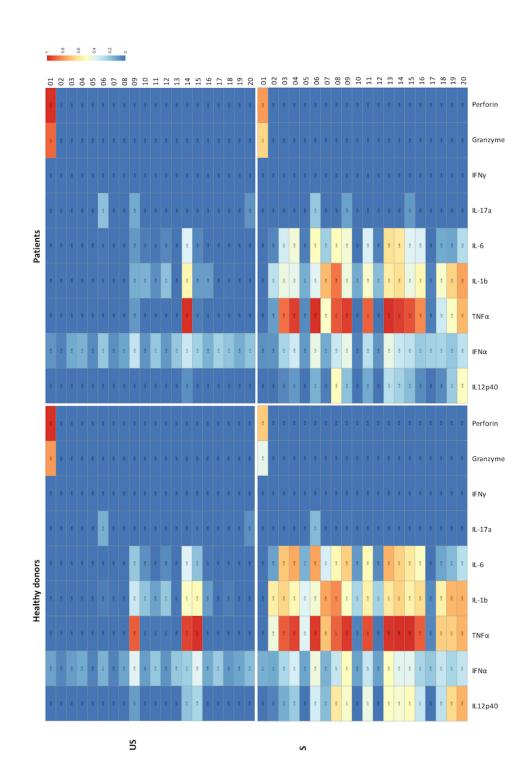


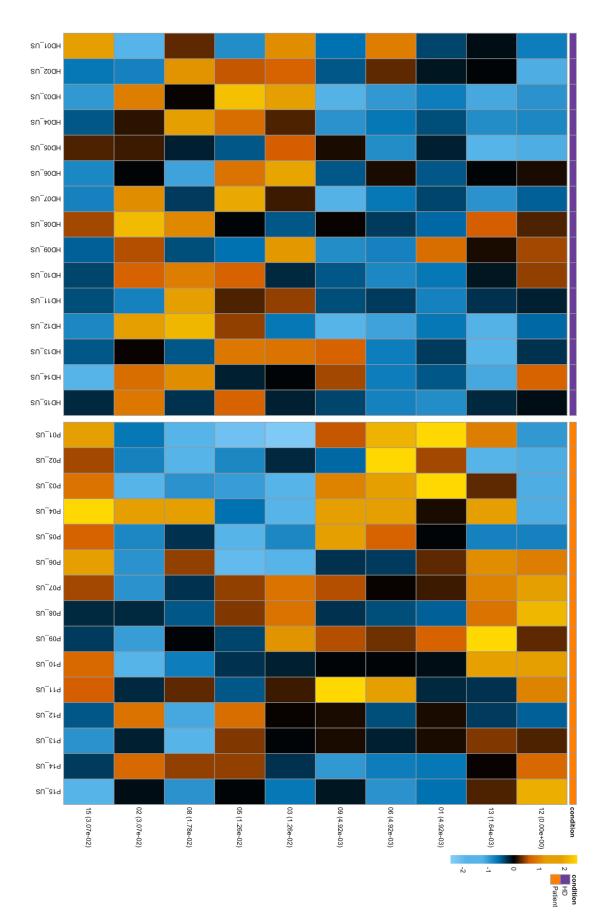
Figure 45: Normalized cytokines expression comparison between the healthy donors and patients group in the stimulated condition of all mDCs - Heatmap illustrating the differences in the cytokines expressions that are statistically significant in the overall mDCs between the patients and healthy donors groups. HD, healthy donor; P, patient; US, unstimulated; S, stimulated.



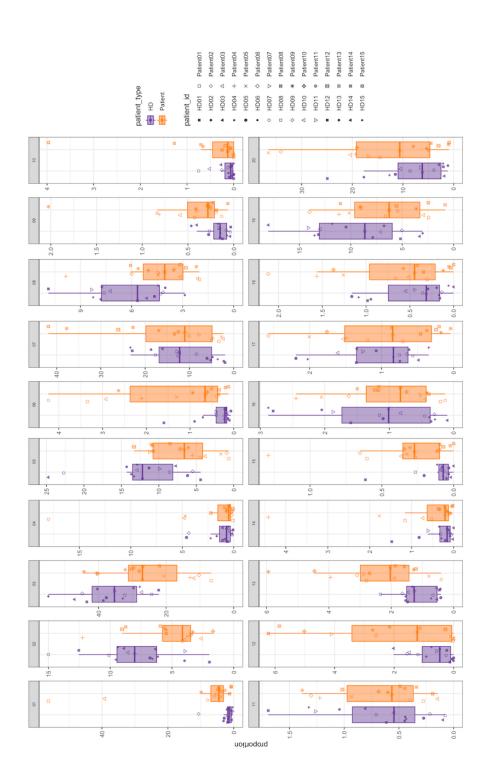
of the activation markers expressions in each of the mDCs clusters for the healthy donors and patients groups, compared by conditions. Figure 46: Median activation markers expressions intensities for each of the clusters and conditions among mDCs - Visual representation US, unstimulated; S, stimulated.



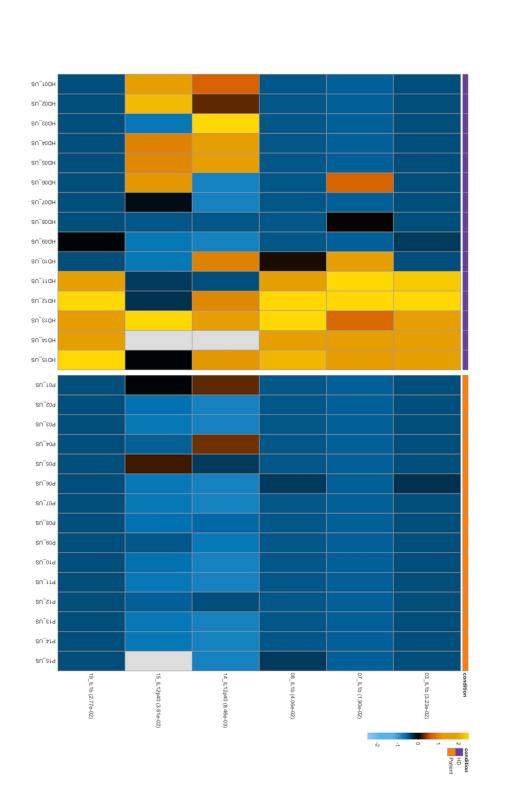




groups in the unstimulated condition - HD, healthy donor; P, patient; US, unstimulated; S, stimulated. Figure 48: Normalized proportions of mDC subpopulations that are significantly different between the healthy donors and patients

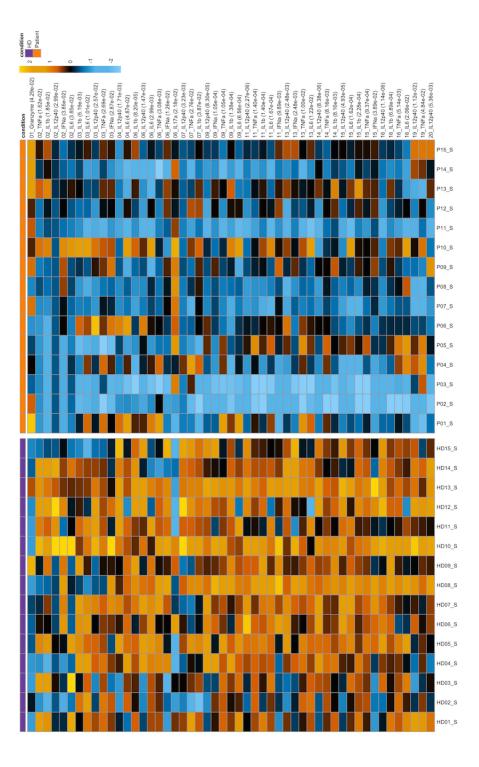


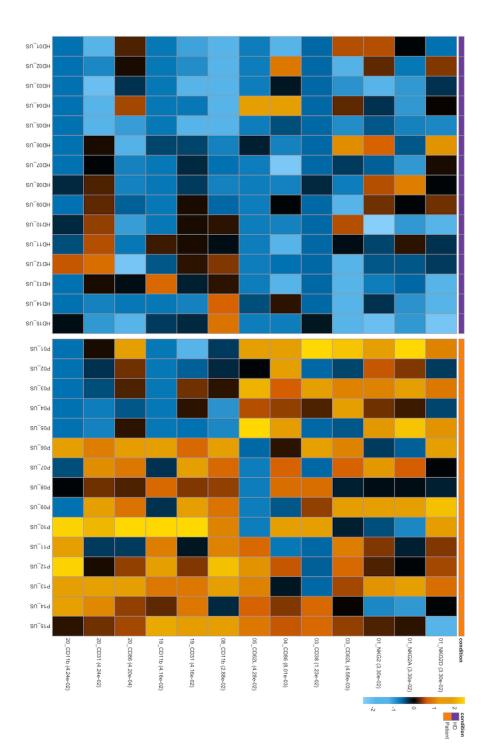
in the unstimulated condition - General overview of the mDC subpopulations relative abundance distribution between patients and healthy donors in the unstimulated condition. HD, healthy donor; P, patient. Figure 49: Boxplots with jittered points representing the mDC subpopulations relative abundance between healthy donors and patients



of mDCs subpopulations - Heatmap illustrating the differences in the cytokines expressions that are statistically significant in the identified Figure 50: Normalized cytokines expression comparison between the healthy donors and patients group in the unstimulated condition mDC subpopulations between the patients and healthy donors groups. HD, healthy donor; P, patient; US, unstimulated.

Figure 51: Normalized cytokines expression comparison between the healthy donors and patients group in the stimulated condition of mDCs subpopulations - Heatmap illustrating the differences in the cytokines expressions that are statistically significant in the identified mDC subpopulations between the patients and healthy donors groups. HD, healthy donor; P, patient; S, stimulated.





significant in the identified mDCs subpopulations between the patients and healthy donors groups. HD, healthy donor; P, patient; US, lated condition of mDCs subpopulations - Heatmap illustrating the differences in the activation markers expressions that are statistically Figure 52: Normalized activation markers expression comparison between the healthy donors and patients group in the unstimuunstimulated.

