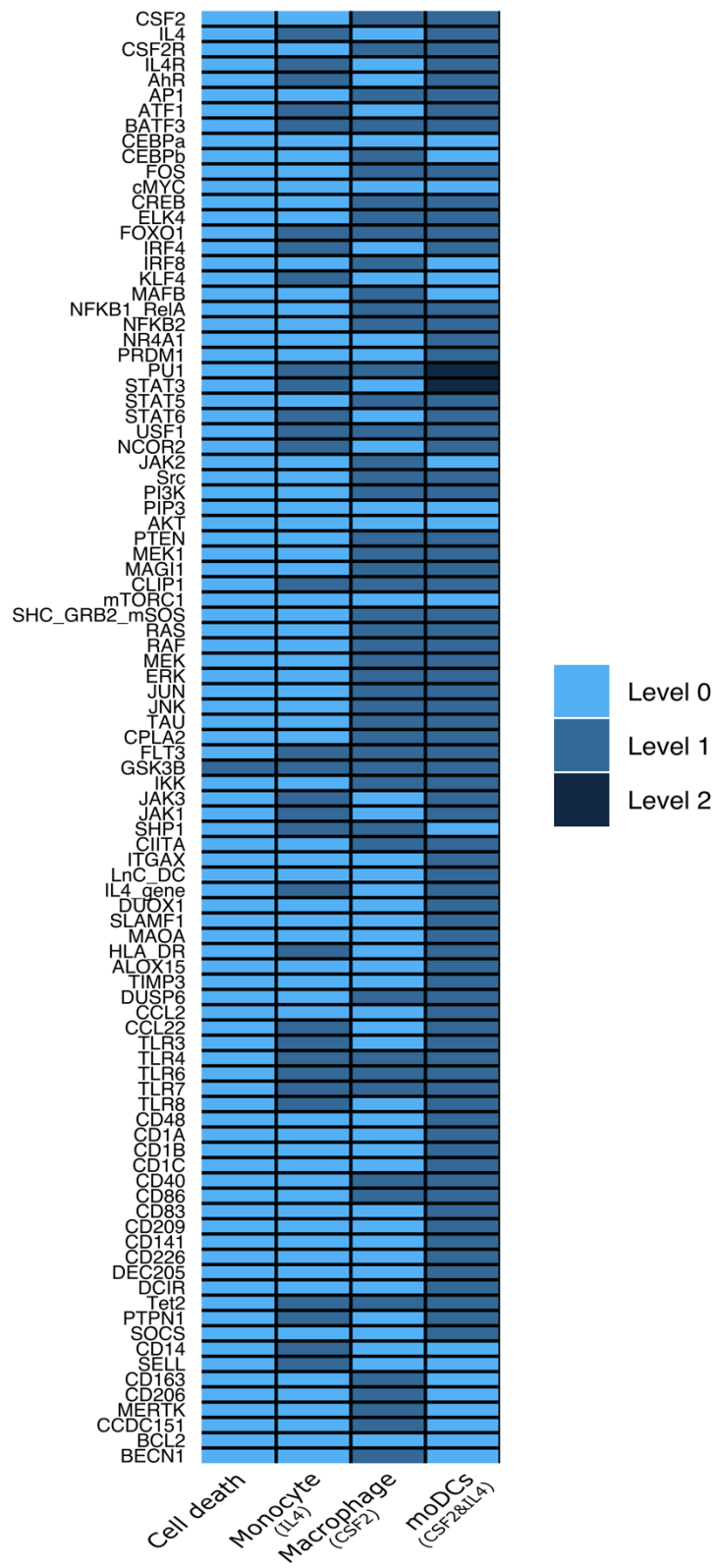# SupplementatyFigure1

Supplementary Figure 1. Stables states of the logical model of monocytes to dendritic cells differentiation *in vitro*. Displays the complete set of nodes, every column corresponds to a specific cell type according with each input. The first column corresponds to the final outcome in the absence of both IL4 and CSF2, *i.e.* cell-death of the monocytes. The second column corresponds to the stimulation of monocytes by IL4. The third column corresponds to the macrophage outcome, in the presence of the sole CSF2. Finally, the fourth column corresponds to moDCs commitment, in the presence of both IL4 and CSF2, where STAT3 reaches the level 2 in the presence of the long non-coding RNA LnC-DC, and PU.1 reaches the level 2, which is required to turn-off MAFB during moDCs commitment.

Sample ID	TechnicalReplicate	#RawReads	#MappedReads	%Mapped	#UniquelyMappedReads	%UniquelyMapped	PBC	NRF	NSC	RSC
EGAR00001085103	none	36270988	34556576	95.27	34429873	94.92	0.62	0.61	1.213468	4.973275
EGAR00001088389	none	59464947	58507187	98.39	58195238	97.86	0.54	0.5	1.193545	3.120265
EGAR00001402942	none	61298322	58636670	95.66	58494233	95.43	0.72	0.72	1.12851	2.988048
EGAR00001402945	none	53792767	50450609	93.79	50276262	93.46	0.72	0.72	1.096921	2.880922
EGAR00001096292	none	43643430	43124385	98.81	42914833	98.33	0.62	0.6	1.144857	2.705355
EGAR00001088409	none	34883406	34269455	98.24	34089818	97.73	0.75	0.75	1.122595	2.300364
EGAR00001305774	none	62396291	52634872	84.36	52526559	84.18	0.71	0.71	1.673187	1.496055
EGAR00001402937	none	48107687	46457099	96.57	46352205	96.35	0.71	0.71	1.638107	1.480712
EGAR00001402975	none	53756793	52000602	96.73	51916823	96.58	0.7	0.68	2.603013	1.158121
EGAR00001402944	none	46489075	45459055	97.78	45336634	97.52	0.94	0.94	1.06705	1.153417
EGAR00001080465	none	58927868	57311046	97.26	56365411	95.65	0.59	0.52	1.155807	1.144716
EGAR00001305771	none	50554614	49043003	97.01	48942079	96.81	0.94	0.93	1.169745	1.077844
EGAR00001085095	none	26253843	25776307	98.18	25671563	97.78	0.72	0.72	1.051644	0.8222461
EGAR00001402946	none	49647095	47554723	95.79	46817138	94.3	0.89	0.84	1.052285	0.4493812
EGAR00001320582	none	35464413	34464338	97.18	34301686	96.72	0.98	0.97	1.012696	0.3588252
EGAR00001402965	none	34302091	33342092	97.2	33187744	96.75	0.98	0.98	1.008811	0.2364044
EGAR00001402963	none	33958907	33557992	98.82	33394119	98.34	0.98	0.98	1.008083	0.2085872
EGAR00001228104	none	25945154	25256088	97.34	25189608	97.09	0.88	0.88	1.176624	1.884106
EGAR00001080466	none	44148235	40264959	91.2	40082521	90.79	0.58	0.56	1.718232	1.886858
EGAR00001100410	none	44271422	43530938	98.33	43305088	97.82	0.88	0.87	1.047842	1.455561
EGAR00001231891	none	36632043	36058094	98.43	35867916	97.91	0.73	0.73	1.140675	2.899751
EGAR00001132113	none	40076490	27355246	68.26	27213222	67.9	0.84	0.83	1.130482	2.327079
EGAR00001100397	none	44848605	43388220	96.74	43164756	96.25	0.87	0.87	1.103035	1.438625
EGAR00001143021	none	28239437	24486109	86.71	24400038	86.4	0.79	0.78	1.154481	3.878428
EGAR00001132117	none	56770007	50780835	89.45	50022736	88.11	0.76	0.73	1.096564	0.9502099
EGAR00001132116	none	52456200	41300163	78.73	41112241	78.37	0.76	0.75	1.120459	2.763786

Supplementary table 1. QC table results after alignment. QC results of the samples used for ChIP-seq data analysis.

TF	JASPAR ID
AHR	MA0006.1
AP1	MA0940.1
ATF1	MA0604.1
BATF3	MA0835.1
CEBPA	MA0102.3
CEBPB	MA0466.2
CREB1	MA0018.3
ELK4	MA0076.1
FOXO1	MA0480.1
IRF4	MA1419.1
IRF8	MA0652.1
KLF4	MA0039.2
MAFB	MA0117.2
NFKB1	MA0105.4
NFKB2	MA0778.1
NR4A1	MA1112.1
SPI1	MA0080.4
STAT3	MA0144.2
STAT5	MA0519.1
STAT6	MA0520.1
USF1	MA0093.3
PRDM1	MA0508.3

Supplementary table 2. Transcription factors JASPAR ID. List of the transcription factors and their corresponding ID from the JASPAR database that were used in this study to find transcription factors binding sites.