

Cancer Immunology, Immunotherapy (submitted in 2018)- Hakimeh Ebrahimi-Nik et. al

Supplementary Table 1. Pathways that are significantly upregulated in P6 compared to P5 sub-populations by IPA

Pathways	Genes	Log ₂ Fold Change (P6/P5)	P5 (TPM ^a)	P6 (TPM ^a)
Acute Phase Response Signaling (25/158 genes)	C3	1.1	335.9	747
	C1rb	1.4	5.9	15.4
	C1s1	2.9	1.3	10
	Cebpb	1.7	109	349.8
	Cfb	2.1	27.7	123.8
	Cp	1.4	3.3	8.7
	Fn1	1.3	123.3	307.4
	Fos	2.2	15.6	74.3
	Hp	2.5	54.9	304.4
	Il18	2.1	4.1	17.6
	Il1a	2.5	10.5	58.3
	Il1b	1.6	51.2	155.9
	Il1r1	-1.1	5.3	2.5
	Il1rn	1.1	136	298.8
	Il1f9	2.5	4	23.3
	Jak2	-1.8	439.4	125.6
	Map3k14	-1.7	40.5	12.1
	Mras	-1.6	78.1	26.2
	Pik3cg	-1.3	110.3	45
	Saa3	1.1	54.6	116.8
	Serpine1	2.6	1.2	7.9
	Serpinf1	-3.7	3.8	0.3
	Socs2	-1.5	390.7	139.3
	Tcf4	-1.4	14.2	5.3
	Vwf	1.4	8.2	22.4
TLR Signaling (12/72 genes)	Fos	2.2	15.6	74.3
	Il18	2.1	4.1	17.6
	Il1a	2.5	10.5	58.3
	Il1b	1.6	51.2	155.9
	Il1r1	-2.7	73.1	11.1
	Il1rn	1.1	136	298.8
	Il1f9	2.5	4	23.3
	Map3k14	-1.7	40.5	12.1
	Tlr2	1.4	107.6	282.3
	Tlr7	1.6	7.9	24.8
	Tlr9	-2.4	29.7	5.5
	Traf1	-1.4	10.6	4

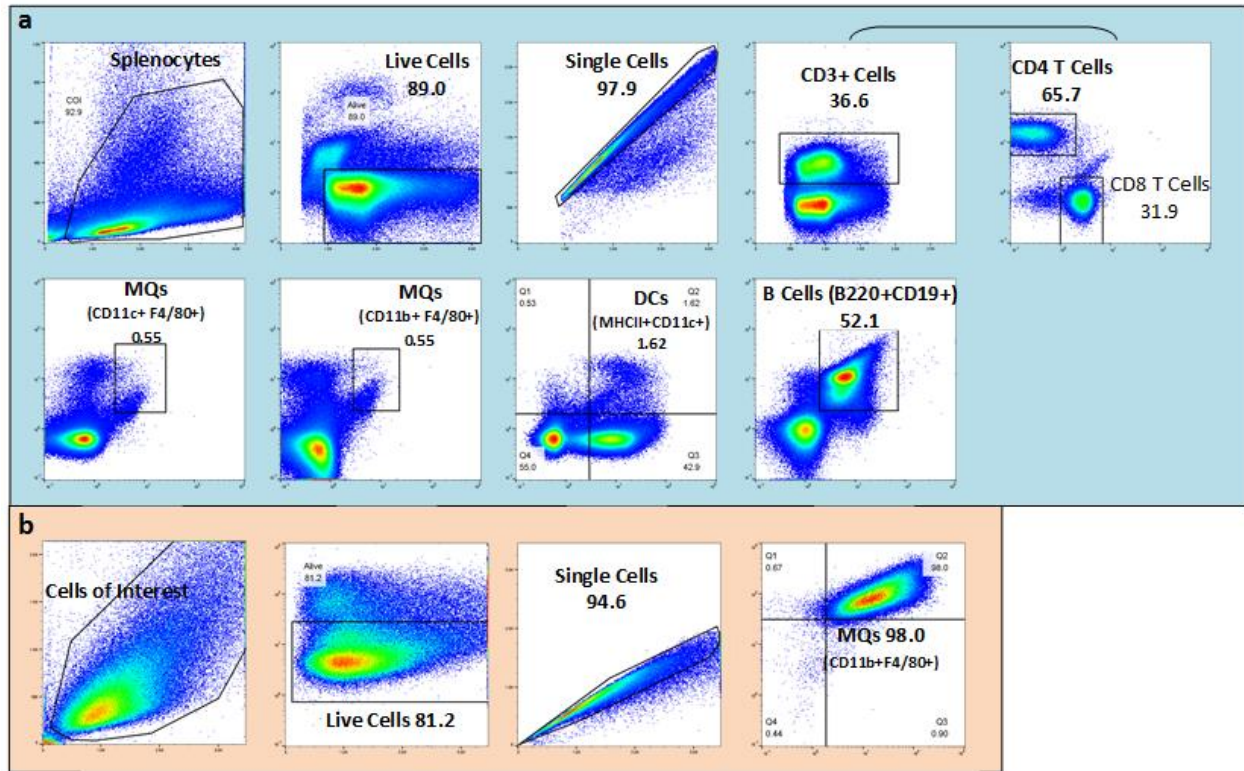
^a Transcripts per Million

Supplementary Table 2. Pathways that are significantly downregulated in P6 compared to P5 sub-populations by IPA

Pathways	Genes	Log ₂ Fold Change (P6/P5)	P5 (TPM ^a)	P6 (TPM ^a)
Dendritic Cell Maturation (28/168 genes)	Ccr7	-4.5	79.1	3.5
	Cd40	-2.5	10.4	1.8
	Cd83	-3.2	74.2	7.8
	Cd86	-2.7	109.3	16.4
	Fcgr4	1.5	11.1	31.7
	Fgfr1	-4.1	34.2	2
	Fscn1	-5.1	40.1	1.2
	H2-Q6	-1.1	17.2	8
	H2-DMb2	-2.6	1495	242.9
	H2-Oa	-2.5	65.7	11.6
	H2-Ob	-4.8	60.4	2.1
	H2-Aa	-3.8	5337.3	385.1
	H2-Ab1	-3.5	3715.8	323.6
	H2-Ea-ps	-4.1	5228.8	294.1
	H2-Eb1	-4.2	2511.4	135.4
	Il18	2.1	4.1	17.6
	Il1a	2.5	10.5	58.3
	Il1b	1.6	51.2	155.9
	Il1rn	1.1	136	298.8
	Il1f9	2.5	4	23.3
	Jak2	-1.8	439.4	125.6
	Lepr	-1.5	39.1	13.7
	Map3k14	-1.7	40.5	12.1
	Pik3cg	-1.3	110.3	45
	Plcl1	-1.2	7.3	3.1
	Stat4	-3.4	4.1	0.4
	Tlr2	1.4	107.6	282.3
	Tlr9	-2.4	29.7	5.5
Integrin Signaling (20/211 genes)	Cav1	1.6	1	3.2
	Ctnn	-1.1	11.9	5.4
	Fgfr1	-4.1	34.2	2
	Fyn	-3.1	62.3	7.1
	Itga2b	-1.1	4	1.9
	Itgae	-2.6	11.1	1.8
	Itgax	-1.2	780.5	328.4
	Itgb7	-1.1	261.3	125.1
	Mras	-1.6	78.1	26.2
	Mylk	-3.6	2.6	0.2
	Pak1	-1.5	15.8	5.6
	Pdgfb	-1.7	10.3	3.1
	Pik3cg	-1.3	110.3	45
	Ppp1r12a	-1.1	64.6	30.4
	Ptk2	-1.9	9.9	2.6
	Tln2	2	2.2	8.8
	Tlr9	-2.4	29.7	5.5
	Tspan2	-3.1	11.8	1.3
	Tspan4	1.1	9.7	21.4
	Tspan7	-1.3	1.1	0.4
ERK/MAPK Signaling (16/191 genes)	Esr1	-1	29	14.2
	Fgfr1	-4.1	34.2	2
	Fos	2.2	15.6	74.3
	Fyn	-3.1	62.3	7.1
	Mras	-1.6	78.1	26.2
	Pak1	-1.5	15.8	5.6
	Pik3cg	-1.3	110.3	45
	Pparg	1.5	18.2	52.4
	Ppm1j	-1.6	4.4	1.4
	Ppp1r14a	-3.5	7.4	0.6
	Prkar2a	-1.2	71.1	31.8
	Prkcb	-1.3	107.7	43.6
	Prkcg	-1.1	3.2	1.4
	Ptk2	-1.9	9.9	2.6
	Tln2	2	2.2	8.8
	Tlr9	-2.4	29.7	5.5

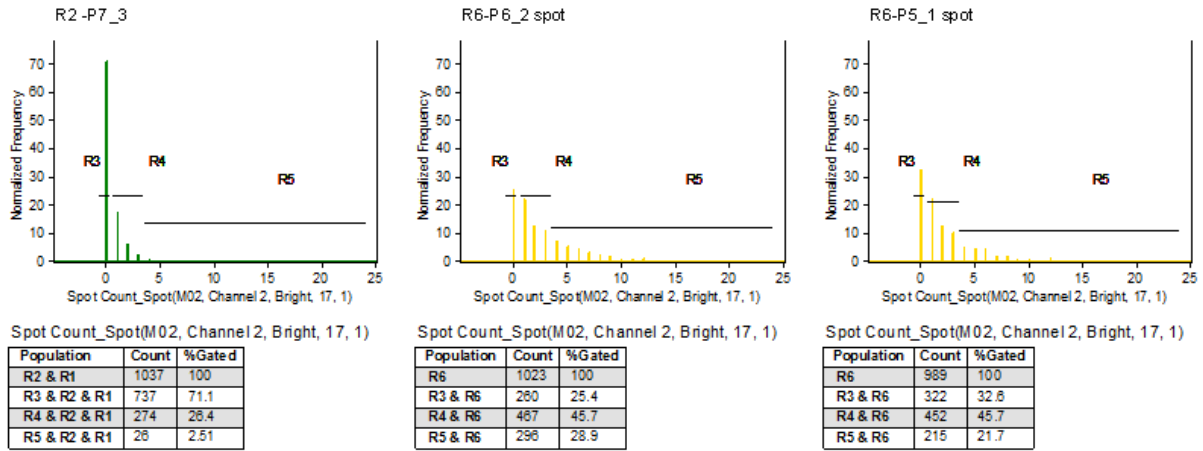
^a Transcripts per Million

Supplementary Figure 1.



The phenotype of BALB/cJ splenocytes (a) and bone marrow derived macrophages (b). Boxes represents gates and percentage of cells in each gate.

Supplementary Figure 2.



Using ImageStreamX Mark II Imaging Flow Cytometer the number of the beads in each sub population were quantified. X-axis shows the number of beads and Y-axis indicates the percentage of the cells. R3 gate is representative of the cells that were not able to take up any beads. R4 shows the percentage of the cells that took up 1-3 beads and R5 represents the percentage of the cells that had more than 3 beads. The tables shows the statistics for each graph.