

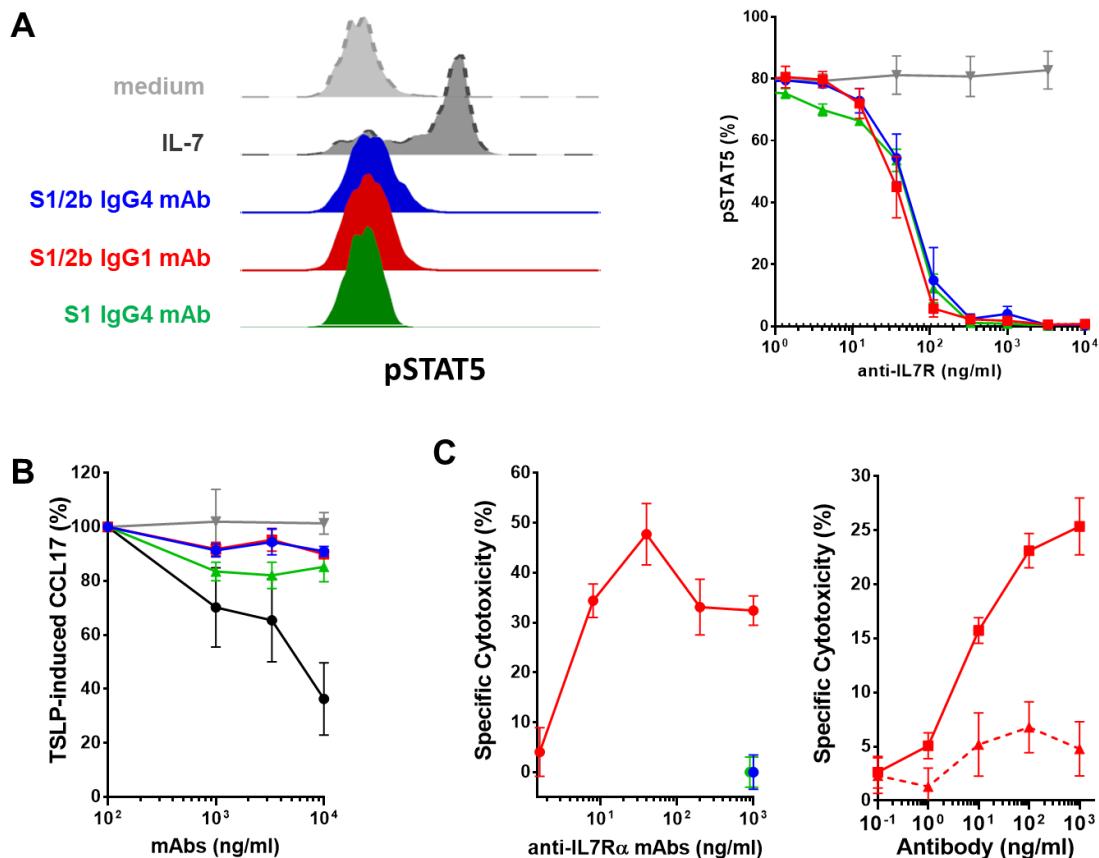
**Supplementary figures and tables**

**IL-7 receptor blockade blunts antigen-specific memory T cell responses and  
chronic inflammation in primates**

by Belarif et al.

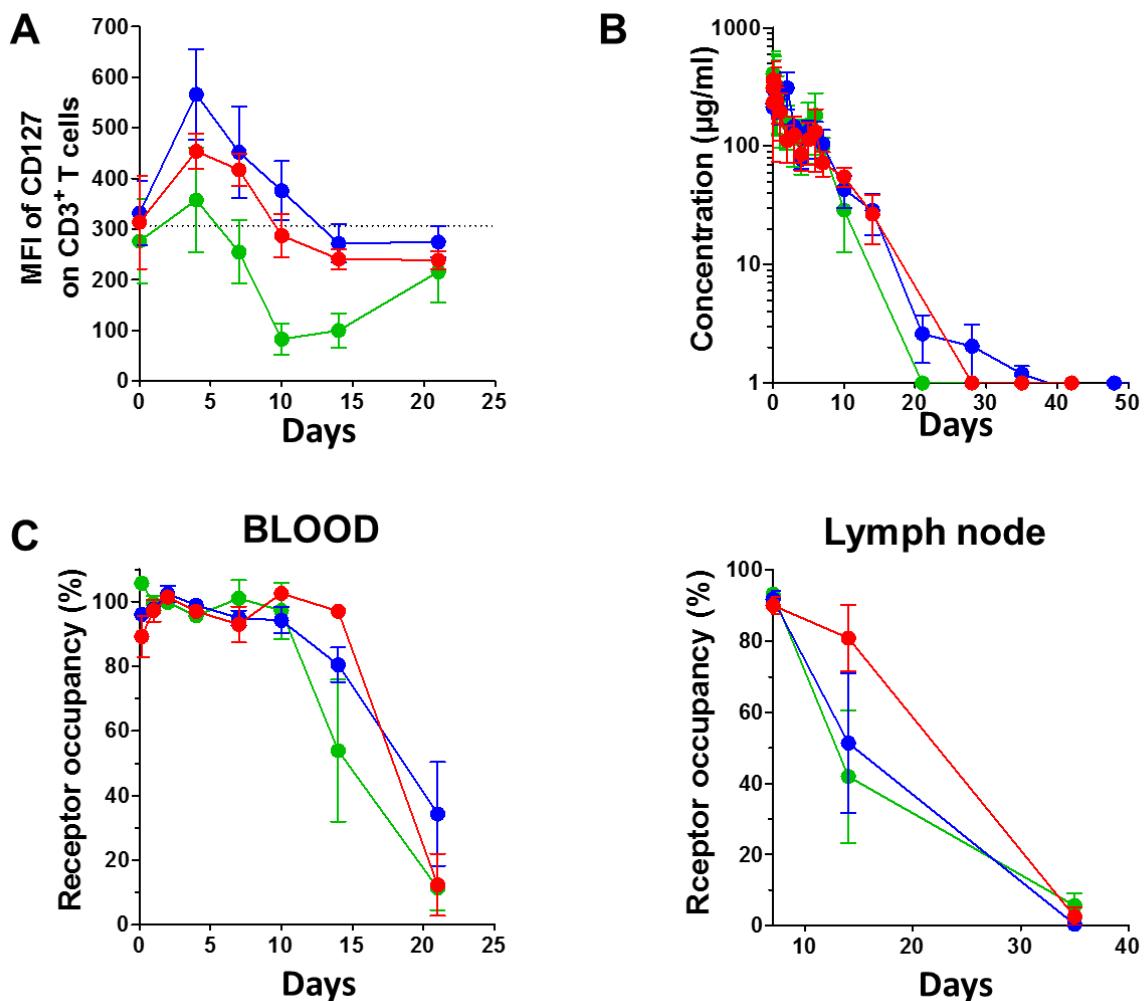
**Supplementary Figure 1:** *In vitro* functional characterization of anti-IL7R $\alpha$  mAbs.

(A) *Left:* Representative phosphorylated STAT5 (pSTAT5) staining by flow cytometry of unstimulated baboon PBMCs or incubated 15min with 0.1ng/ml of human IL-7  $\pm$  10 $\mu$ g/ml of anti-IL7R $\alpha$  mAbs. *Right:* IL-7-induced pSTAT5 inhibition with increasing concentration of site-1/2b IgG4 mAb (blue), site-1/2b IgG1 mAb (red), site-1 IgG4 (green) mAbs, or Ig control (grey). (B) TSLP-induced CCL17 secretion (normalized to control condition without mAb) by CD1c $^+$  dendritic cells with increasing concentration of anti-IL7R $\alpha$  mAbs (same colors as in (A)) or anti-TSLPR mAb (black). (C) *Left:* Specific cytotoxicity (%) induced by anti-IL7R $\alpha$  mAbs (same colors as in (A)) on transfected IL-7R $\alpha^+$  Ba/F3 cell line cultured 4 hours with NK cells (ratio 1:10). *Right:* Specific cytotoxicity (%) induced with increasing concentration of site-1/2b IgG1 on human T cell leukemia expressing high level of CD127 (DND-41 cell line, solid red line) or low level of CD127 (Jurkat cell line, dotted red line) cultured 4 hours with NK cells (ratio 1:10). Data are mean  $\pm$  SEM.



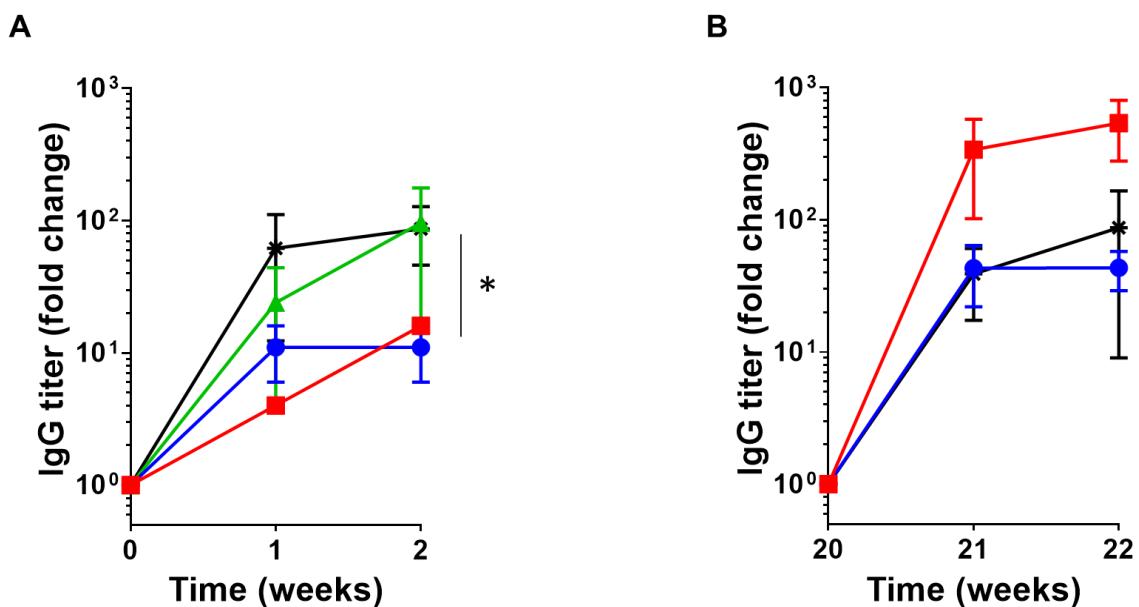
**Supplementary Figure 2: Pharmacological evaluation following intravenous administration of anti-IL7R $\alpha$  mAbs in baboons.**

(A) Total CD127 expression represented by the Mean Fluorescence Intensity (MFI) measured by flow cytometry on peripheral blood CD3 $^{+}$  baboon T lymphocytes after a single intravenous injection of 10mg/kg of the site-1/2b IgG1 mAb (red, n= 3), site-1/2b IgG4 mAb (blue, n = 3) or site-1 IgG4 mAb (green, n = 3). Dotted line represents the mean basal level of expression before administration of mAbs. (B) Serum concentration of anti-IL7R $\alpha$  mAbs after injection in same animals as in (A). (C) CD127 receptor occupancy determined by flow cytometry on peripheral CD3 $^{+}$  T lymphocytes purified from the blood (*left*) or lymph nodes (*right*) of the same animals as in (A). Data are mean  $\pm$  SEM.



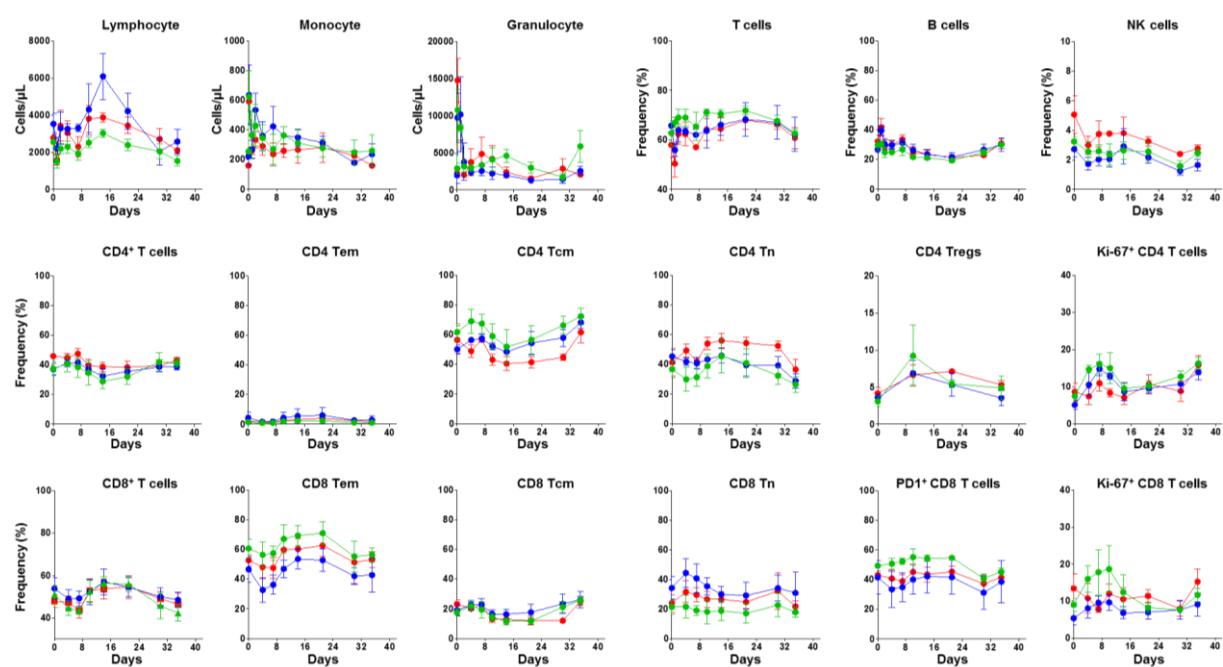
**Supplementary Figure 3: Sheep red blood cell (SRBC) immunization.**

(A) Anti-SRBC IgG fold-change serum titers in baboons treated with a single intravenous injection of 10mg/kg of the site-1/2b IgG1 mAb (red, n= 3), site-1/2b IgG4 mAb (blue, n = 3) or site-1 IgG4 mAb (green, n = 3), and challenged 24 hours later with intravenous injection of 1.5ml/kg of SRBC at 10%. Historical placebo-treated animals (black, n= 3) following the same protocol were used as controls <sup>50</sup>. (B) Same as in (A) after secondary SRBC challenge performed 20 weeks following anti-IL7R $\alpha$  mAb administration. Data are mean  $\pm$  SEM. \* p<0.05 one-way ANOVA and Dunn's test comparison between the site1/2b IgG4 mAb and control group at 2 weeks post-SRBC challenge.



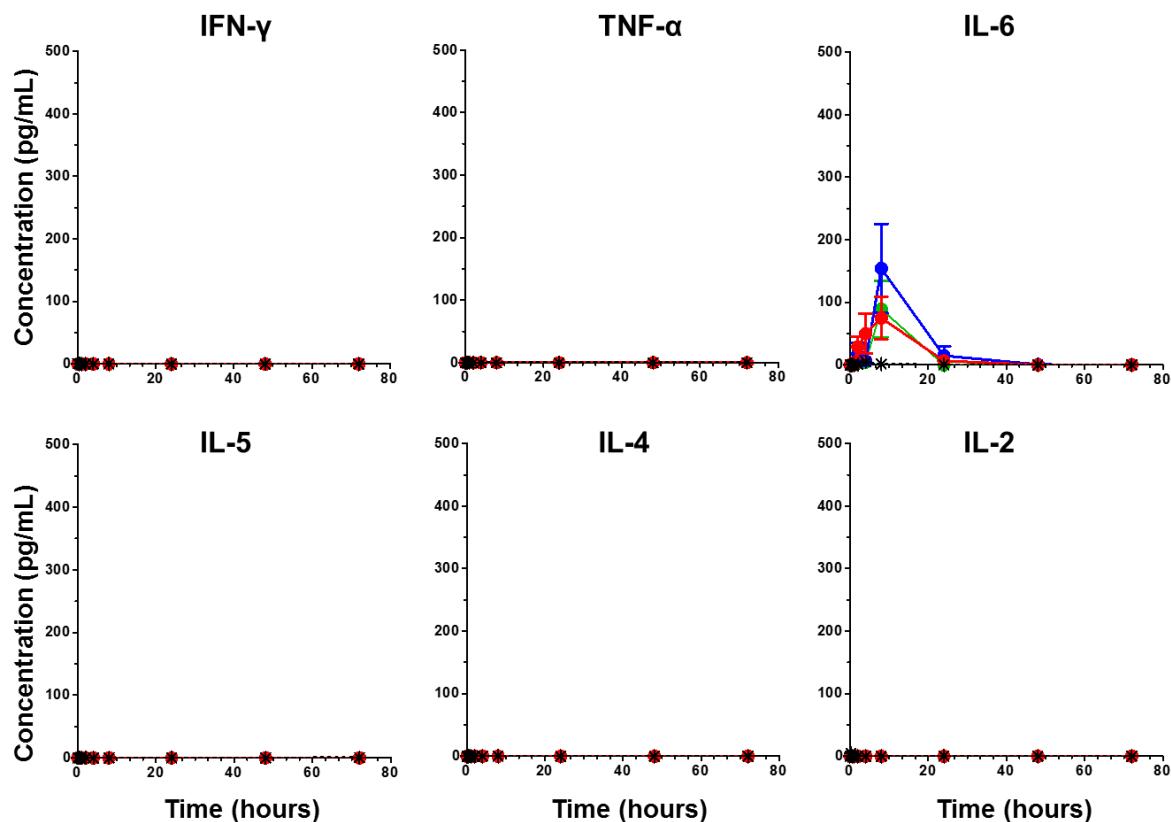
**Supplementary Figure 4: Anti-IL-7R $\alpha$  mAbs in primates do not induce modification of peripheral blood cells.**

Peripheral blood immune cell enumeration and T cell subset frequency determined by flow cytometry for baboons treated with a single intravenous injection of 10mg/kg of the site-1/2b IgG1 mAb (red, n= 3), site-1/2b IgG4 mAb (blue, n = 3) or site-1 IgG4 mAb (green, n = 3). T cell sub-populations were defined using the following gating strategy CD3 $^{+}$  CD4 $^{+}$  or CD8 $^{+}$  cells for Tem: effector memory T cells (CD95 $^{+}$  CD28 $^{-}$ ), Tcm: central memory T cells (CD95 $^{+}$  CD28 $^{+}$ ), Tn: naïve T cells (CD95 $^{-}$  CD28 $^{+}$ ), Tregs: regulatory T cells (CD4 $^{+}$  CD25 $^{\text{high}}$  Foxp3 $^{+}$ ) as previously described <sup>76</sup>. Data are mean  $\pm$  SEM of the indicated population.



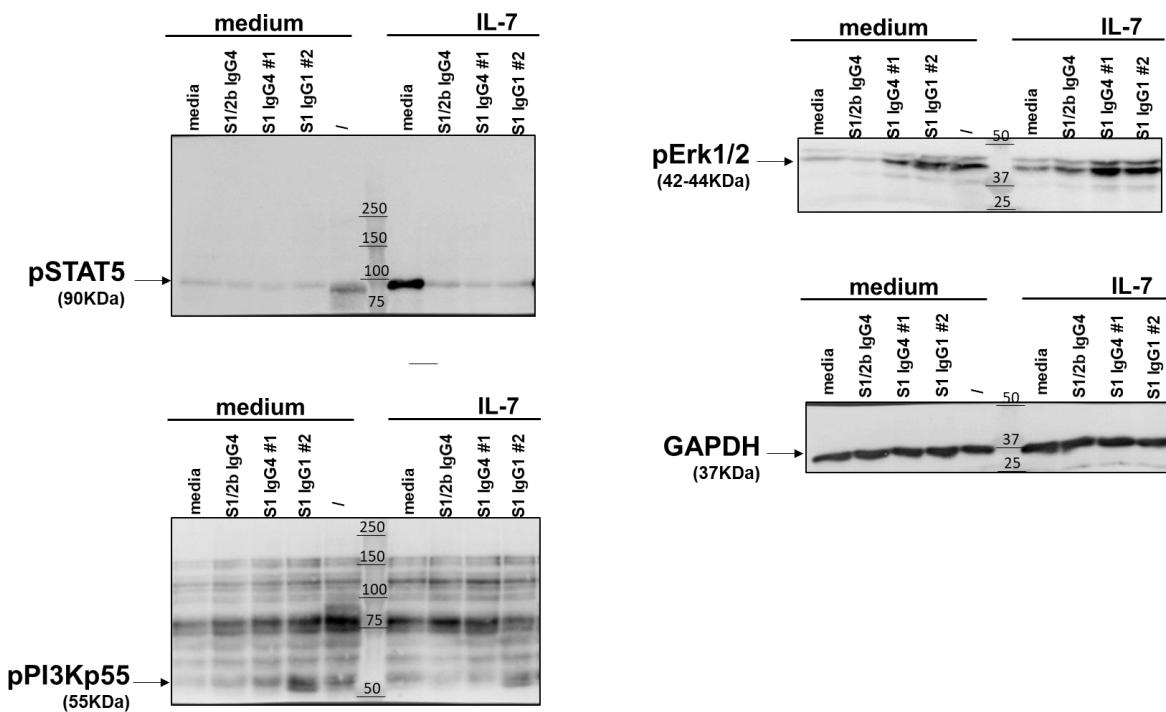
**Supplementary Figure 5:** Anti-IL7R $\alpha$  mAb administration does not induce significant peripheral cytokine release.

Serum concentration (pg/mL) of indicated cytokines (IL-2, IL-4, IL-5, IL-6, TNF $\alpha$  and INF $\gamma$ ) in baboons after a single intravenous injection of 10mg/kg of the site-1/2b IgG1 mAb (red, n=3), site-1/2b IgG4 mAb (blue, n = 3) or site-1 IgG4 mAb (green, n = 3). Data are mean  $\pm$  SEM.



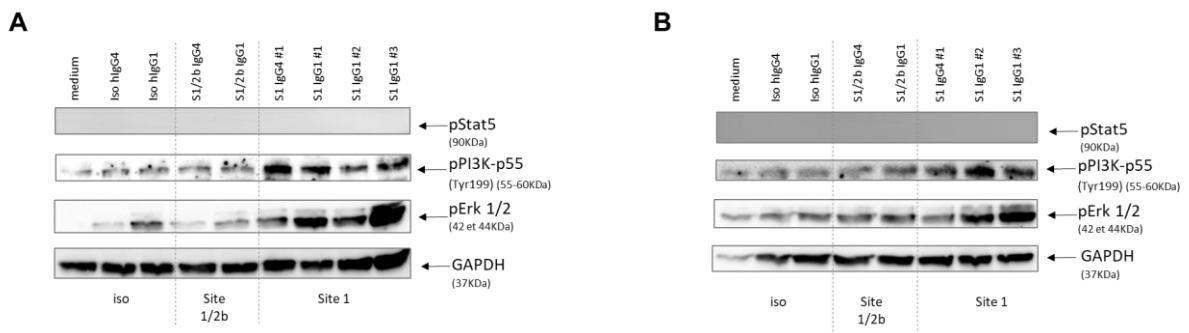
**Supplementary Figure 6: Comparison of anti-IL-7R $\alpha$  site-1 and site1/2b mAbs agonist signals on human cell by western blot.**

Raw data of the representative phospho-STAT5, phospho-PI3k-p55, phospho-ERK1/2 and GAPDH western blot of one out of seven representative human donor cells illustrated in Figure 3C. PBMCs were pretreated with 10 $\mu$ g/mL of one anti-IL-7R $\alpha$  mAb and then incubated for 10 min at 37°C with or without 5ng/ml of human IL-7.

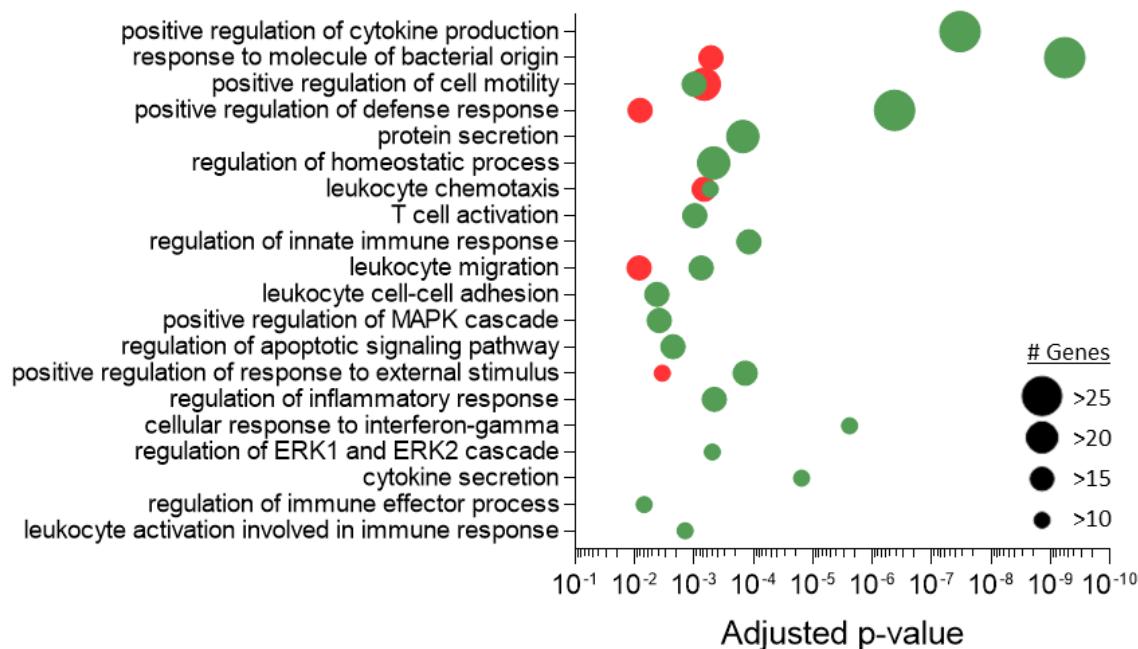


**Supplementary Figure 7: Comparison of anti-IL-7R $\alpha$  site-1 and site1/2b mAbs agonist signals on human and baboon PBMC.**

Phospho-STAT5, phospho-PI3k-p55, phospho-ERK1/2 and GAPDH western blot on human (**A**) or baboon cells (**B**). PBMCs were pretreated with 10 $\mu$ g/mL of anti-IL-7R $\alpha$  mAbs (Site 1/2b IgG4, Site 1/2b IgG1, Site 1 IgG4 #1, Site 1 IgG1 #1, Site 1 IgG1 #2 and Site 1 IgG1 #3) or human isotype control (Iso hIgG4 and Iso hIgG1) and then incubated for 10 min at 37°C before protein lysates analysis.

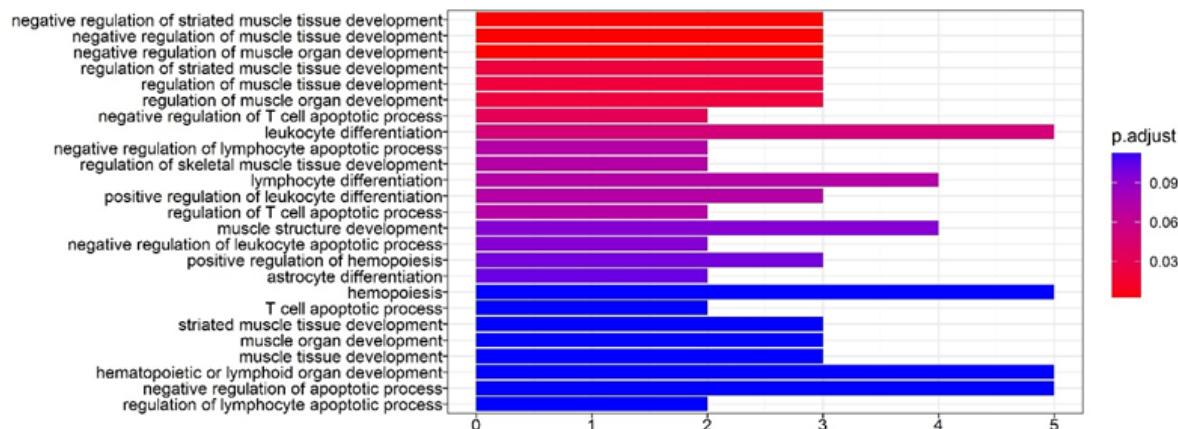


**Supplementary Figure 8: Gene Ontology (GO) identified in the signature for each anti-IL-7R $\alpha$  mAb (blue: site-1/2b IgG4, red: site-1 IgG4#1, green: site-1 IgG1#2) versus control. Circle size is proportional to the number of genes for each category.**

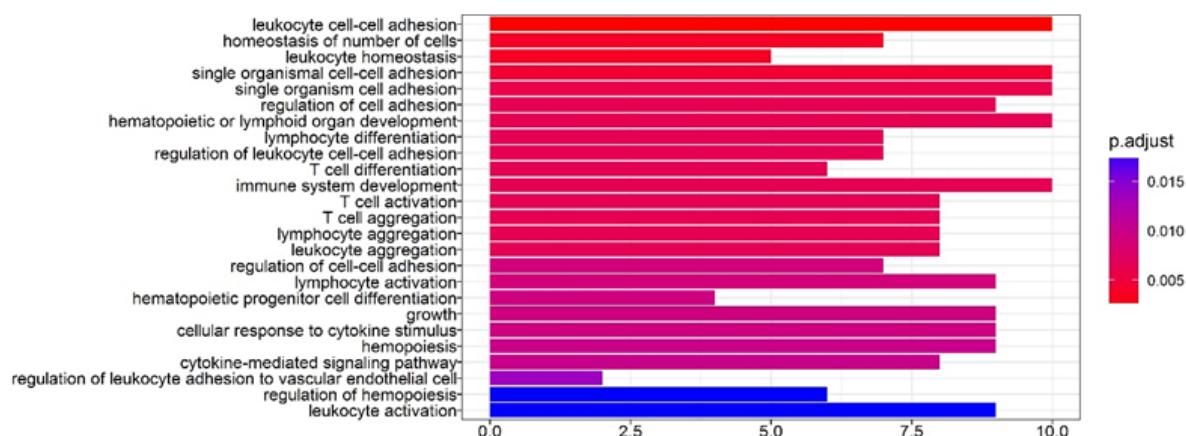


**Supplementary Figure 9:** GoMiner gene ontology enrichment of the three clusters identified for the 93 most differentially expressed genes (FDR 5%, FC > 2) between IL-7 stimulation and control medium condition.

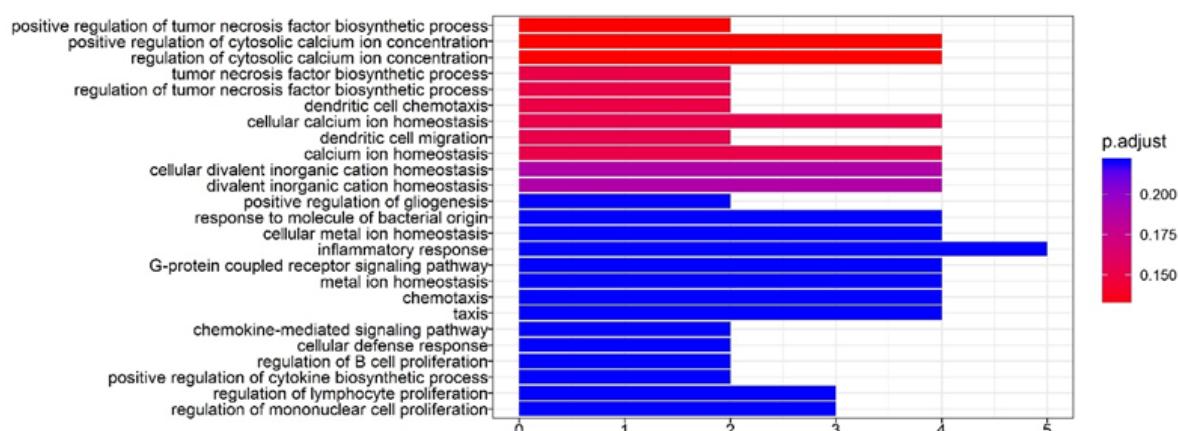
### Cluster 1



### Cluster 2

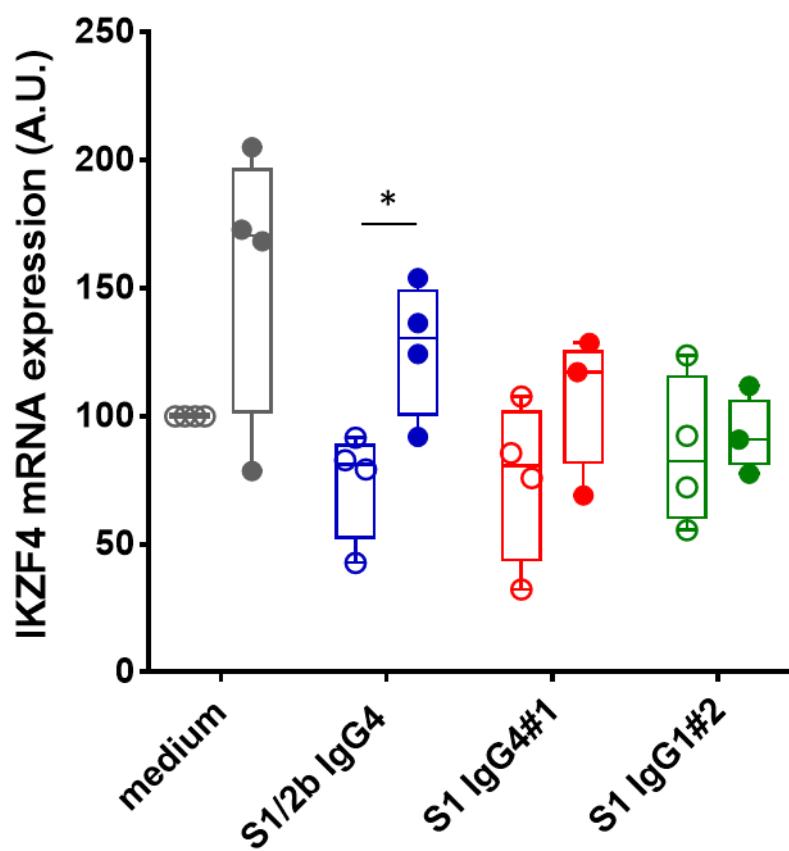


### Cluster 3



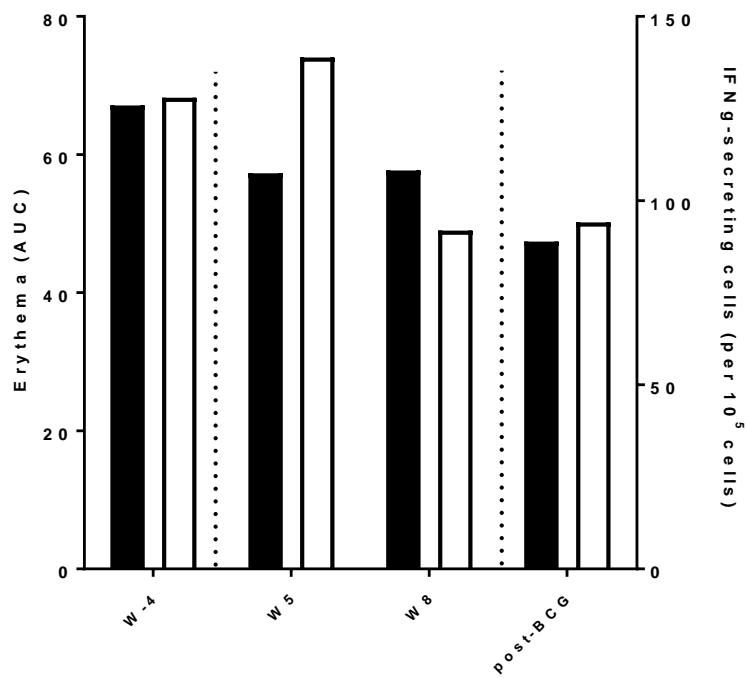
**Supplementary Figure 10: IKZF4 gene expression.**

IKZF4 mRNA expression confirmed by RT-qPCR on human PBMC cultured for 3.5 hours with (empty round) or without (full symbols) 5 ng/ml of IL-7 and 10  $\mu$ g/ml of anti-human IL-7R $\alpha$  mAbs (blue: site-1/2b IgG4, red: site-1 IgG4#1, green: site-1 IgG1#2). Data were normalized to basal expression in the absence of IL-7 and mAbs. \* p<0.05 between indicated groups.



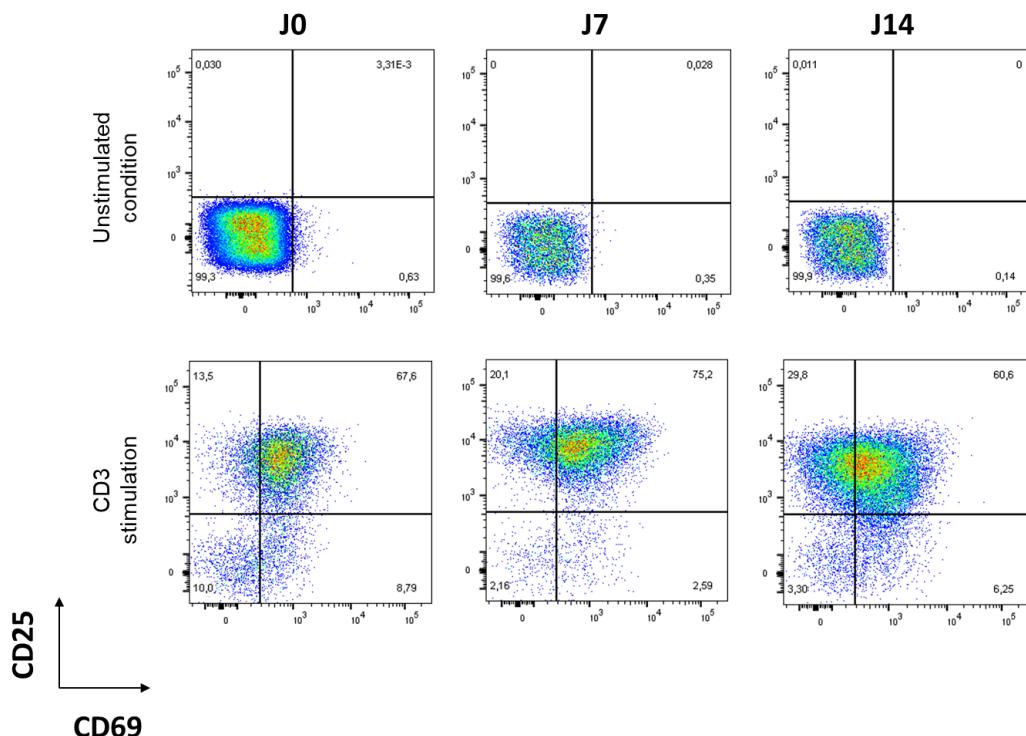
**Supplementary Figure 11: Erythema and Elispot response in the non-responder animal.**

Cutaneous erythema response (black histograms, *left-axis*) at indicated time-points, represented with area under the curve (AUC) of daily erythema diameters, after tuberculin intradermal injection in the non-responder baboon (1 out of 10) treated with a single intravenous injection of 10mg/Kg of the humanized site-1/2b IgG4 mAb. IFN- $\gamma$ -secreting cell frequencies (white histograms, *right-axis*) in PBMCs of the same animal after *ex-vivo* tuberculin restimulation at the indicated time-point.



**Supplementary Figure 12: CD25 and C69 expression on baboon CD3<sup>+</sup> T cells population before and after stimulation.**

Representative expression of CD25 and CD69 analyzed by flow cytometry on peripheral blood T-cell (CD3+) at the indicated time-point after treatment with a single intravenous injection of 10 mg/kg of a humanized site-1/2b IgG4 mAb. CD25 and CD69 expression was analyzed on T cells in unstimulated or after 48 hours of anti-CD3 polyclonal stimulation.



**Supplementary Table 1:** List of genes significantly (FDR 5%) and differentially (fold-change >1.5) expressed after incubation of human PBMCs (n=7) with anti-IL7R $\alpha$  mAbs compared to unstimulated cells.

COMMOD8	-0.33	0.165	-0.59	0.002	*	-0.40	0.034	*	VNN2	-0.47	0.086	-0.60	0.008	*	-0.41	0.074
CPO58	0.52	0.055	0.46	0.043	*	0.64	0.004	*	WBP5	-0.97	0.205	-1.42	0.020	*	-0.70	0.288
CYB5R1	-0.25	0.327	-0.51	0.013	*	-0.73	0.000	*	XPT0	0.78	0.061	0.78	0.026	*	0.57	0.108
DUSP6	-0.45	0.129	-0.61	0.013	*	-0.48	0.049	*	ZDHHC3	0.56	0.095	0.73	0.008	*	0.30	0.328
ENVY2	-0.45	0.067	-0.46	0.026	*	-0.59	0.004	*	ZER1	0.58	0.161	0.78	0.019	*	0.36	0.333
FCER1G	-0.45	0.165	0.75	0.004	*	-0.51	0.049	*	ZNFS89	0.27	0.504	0.73	0.012	*	0.25	0.474
FRMD8	0.52	0.053	0.72	0.001	*	0.49	0.028	*	ZNF71	0.55	0.100	0.65	0.020	*	0.23	0.487
GSR	0.43	0.086	0.71	0.001	*	0.50	0.014	*	ZNF792	0.70	0.100	0.95	0.008	*	0.67	0.063
KIF1B	0.45	0.092	0.59	0.007	*	0.57	0.006	*	ARHGAP4A	-0.24	0.527	0.00	1.000	*	-0.02	0.018
MER2D	0.53	0.103	0.60	0.028	*	0.57	0.035	*	ACSL1	0.07	0.273	0.08	0.023	*	0.52	0.114
MPZL1	0.38	0.220	0.58	0.020	*	0.75	0.002	*	AGO2	0.21	0.547	0.31	0.259	*	0.71	0.003
NF1	-0.3	0.005	0.50	0.000	*	-0.60	0.000	*	POPBC3D	0.20	0.573	0.12	0.201	*	0.68	0.024
NDUFA5	-0.25	0.247	-0.60	0.000	*	-0.35	0.037	*	ARHGAP31	0.22	0.582	0.28	0.364	*	0.60	0.026
NDUFB7	-0.37	0.213	-0.49	0.043	*	-0.62	0.007	*	ATF3	0.18	0.771	0.04	0.949	*	0.89	0.017
NUP153	0.34	0.228	0.57	0.009	*	0.62	0.005	*	B3GNT5	0.11	0.855	-0.01	0.985	*	0.81	0.013
S100A4	-0.41	0.120	-0.54	0.014	*	-0.82	0.000	*	BACH2	0.26	0.352	0.25	0.296	*	0.71	0.001
S100A8	-0.38	0.266	-0.56	0.043	*	-0.77	0.004	*	C19orf43	-0.57	0.055	-0.30	0.285	*	-0.59	0.014
SERPIN1A	-0.46	0.067	-0.69	0.001	*	-0.47	0.021	*	C9orf69	0.34	0.319	0.40	0.153	*	0.64	0.012
SLC17A5	-0.33	0.173	-0.51	0.010	*	-0.72	0.004	*	CCL4	-0.15	0.757	-0.39	0.248	*	0.94	0.002
SLC7A7	-0.47	0.076	-0.68	0.002	*	-0.52	0.016	*	CCL8	-0.28	0.813	-0.94	0.214	*	2.02	0.003
SNRK-A51	0.59	0.079	0.57	0.042	*	0.59	0.031	*	CCRL2	-0.02	0.514	0.00	1.000	*	-1.02	0.002
STAT5A	0.34	0.166	0.66	0.001	*	0.49	0.012	*	CD360	-0.64	0.258	-0.74	0.443	*	2.02	0.000
TBX5A1	-0.27	0.390	-0.49	0.043	*	-0.64	0.007	*	CD374	-0.28	0.494	-0.36	0.285	*	0.78	0.008
TPH2	-0.52	0.079	-0.40	0.006	*	-0.49	0.002	*	CD36	-0.77	0.172	-0.72	0.129	*	-1.26	0.005
TMEM184B	0.42	0.245	0.63	0.013	*	0.55	0.007	*	CD52	-0.08	0.769	-0.25	0.155	*	-0.61	0.000
TYRD9B	-0.35	0.212	-0.56	0.012	*	-0.84	0.000	*	CD69	0.02	0.974	-0.06	0.770	*	0.82	0.000
USAG5	-0.39	0.120	-0.49	0.018	*	-0.68	0.001	*	CD72	-0.30	0.499	-0.29	0.431	*	0.65	0.038
USP19	0.48	0.145	0.76	0.005	*	0.54	0.044	*	CHKA	-0.41	0.410	-0.56	0.156	*	-0.76	0.039
USP38	0.44	0.105	0.49	0.029	*	0.61	0.006	*	CLIC3	0.05	0.939	-0.05	0.913	*	-0.67	0.041
XYLT2	0.27	0.329	0.60	0.005	*	0.57	0.006	*	COMM3-BM1	0.34	0.655	0.21	0.771	*	-1.41	0.005
ACTR5	0.56	0.137	0.74	0.018	*	0.53	0.009	*	COX17	-0.21	0.616	-0.45	0.133	*	-0.17	0.015
ADAMDEC1	-0.88	0.095	-1.24	0.004	*	-0.63	0.176	*	CRTAM	0.03	0.581	0.03	0.581	*	1.05	0.002
ARHGAP18	-0.55	0.094	-0.63	0.021	*	-0.51	0.050	*	CSF3	0.11	0.939	0.79	0.337	*	1.61	0.024
AU1	1.01	0.101	1.14	0.026	*	0.67	0.223	*	CSF3RB	0.04	0.930	0.01	0.989	*	0.73	0.004
BAG2	0.29	0.548	0.70	0.042	*	0.42	0.200	*	CX3CR1	-0.19	0.662	-0.24	0.493	*	-0.64	0.023
BAMBI	-0.44	0.067	0.67	0.003	*	-0.32	0.074	*	CX1L10	-0.55	0.511	-0.36	0.648	*	1.58	0.007
BLOC153	-0.54	0.180	0.71	0.029	*	-0.37	0.289	*	CXK19	-0.32	0.687	-0.05	0.956	*	1.61	0.002
C16orf4	0.44	0.128	0.63	0.008	*	0.30	0.077	*	DUSP1	0.85	0.133	0.82	0.088	*	0.93	0.043
C1orf216	0.25	0.669	0.82	0.042	*	0.55	0.193	*	DVL2	0.54	0.143	0.58	0.058	*	0.61	0.040
C2orf149	-0.47	0.455	-0.97	0.040	*	-0.44	0.047	*	EGR2	-0.67	0.094	-0.45	0.210	*	0.85	0.008
C3orf158	0.46	0.182	0.60	0.032	*	0.43	0.144	*	EIF4EBP1	-0.46	0.260	-0.15	0.737	*	-0.81	0.010
CANK1D	0.47	0.228	0.64	0.040	*	0.48	0.136	*	EPST1	0.09	0.874	0.16	0.728	*	0.75	0.021
CCL2	-0.33	0.522	-0.86	0.019	*	0.52	0.186	*	FAM104A1	0.03	0.338	0.05	0.338	*	0.59	0.004
CCL7	-0.48	0.282	-0.90	0.010	*	0.36	0.355	*	FASLG	0.05	0.513	0.05	0.881	*	0.76	0.007
CCR12	-0.42	0.263	-0.76	0.011	*	0.09	0.848	*	FBXO30	0.27	0.586	0.63	0.077	*	0.24	0.024
CD33	-1.08	0.261	-1.61	0.039	*	-1.28	0.103	*	FGFBP2	-0.16	0.647	-0.23	0.384	*	-0.77	0.001
CD6	0.12	0.833	0.67	0.029	*	-0.49	0.119	*	FUS	0.30	0.429	0.37	0.238	*	0.61	0.029
CD6B	-0.35	0.184	-0.66	0.002	*	-0.36	0.000	*	GBP1	-0.22	0.716	-0.34	0.475	*	1.07	0.005
CD6CAE2P	-0.39	0.050	-0.65	0.037	*	0.08	0.654	*	GBP1P1	-0.19	0.820	-0.02	0.579	*	1.11	0.019
CLEC4E	-0.61	0.086	-0.94	0.001	*	0.53	0.069	*	GBP2	0.04	0.924	0.02	0.956	*	0.61	0.004
CLECT7A	-0.35	0.521	-0.83	0.034	*	-0.51	0.223	*	GBP3	0.00	0.997	0.08	0.823	*	0.74	0.002
CPNE8	-0.52	0.422	-1.02	0.036	*	-0.32	0.601	*	GHCR	-0.03	0.952	-0.16	0.574	*	0.59	0.035
CSF3	0.03	0.959	-0.63	0.030	*	0.30	0.353	*	GMAP8	0.37	0.298	0.45	0.692	*	0.59	0.000
CTSF	0.32	0.628	1.25	0.006	*	0.88	0.051	*	CD28	0.28	0.268	-0.29	0.194	*	-0.61	0.003
DAB2	-0.62	0.089	-0.67	0.029	*	-0.49	0.119	*	IGF2R	0.15	0.664	0.37	0.199	*	0.66	0.003
DFNA5	-0.63	0.080	-0.89	0.002	*	-0.33	0.311	*	IRG1	-0.36	0.567	-0.45	0.380	*	1.41	0.002
EC11	0.62	0.167	0.78	0.031	*	0.45	0.249	*	ISOC2	0.30	0.564	0.07	0.898	*	0.74	0.036
ELAVL1	0.56	0.120	0.74	0.013	*	0.51	0.065	*	JAC1	0.63	0.087	0.53	0.098	*	0.06	0.001
EROL1	-0.52	0.086	-0.65	0.001	*	-0.31	0.252	*	JUN	0.56	0.070	0.45	0.688	*	0.59	0.018
EXOC4	-0.51	0.130	-0.69	0.013	*	-0.23	0.244	*	JNIP	-0.08	0.885	-0.24	0.549	*	0.89	0.005
FAM115A	0.69	0.090	0.76	0.001	*	0.44	0.064	*	INTS3	0.55	0.092	0.49	0.079	*	0.67	0.010
FAM483G	0.39	0.431	0.82	0.029	*	0.71	0.055	*	IRF1	0.40	0.414	0.71	0.056	*	0.72	0.046
FCAR	-0.32	0.280	-0.71	0.002	*	-0.31	0.211	*	IRF4	0.36	0.256	0.41	0.113	*	1.03	0.000
FGFR	-0.41	0.067	-0.67	0.000	*	-0.27	0.169	*	IRFB	-0.09	0.790	0.01	0.982	*	0.71	0.000
FHL3	0.57	0.180	0.72	0.035	*	0.24	0.572	*	IRG1	-0.32	0.512	-0.36	0.181	*	-0.68	0.005
FKBP8	0.39	0.166	0.68	0.002	*	0.28	0.250	*	IHWCR2	0.07	0.858	-0.19	0.435	*	0.66	0.001
FL11	0.63	0.053	1.01	0.000	*	0.51	0.065	*	HIST1H2BK8	-0.29	0.391	-0.47	0.076	*	-0.71	0.005
FPR2	-0.36	0.529	-0.88	0.032	*	0.11	0.867	*	HIVEP1	0.36	0.213	0.09	0.783	*	0.65	0.005
G05	-0.40	0.231	-0.65	0.015	*	0.02	0.973	*	HSPBP1	0.53	0.153	0.49	0.120	*	0.78	0.007
GEMIN2	-0.13	0.855	-0.85	0.041	*	-0.38	0.420	*	HSPH1	0.40	0.414	0.71	0.056	*	0.72	0.046
GGH	-0.45	0.302	-0.73	0.004	*	-0.59	0.091	*	IFNG	0.32	0.706	-0.32	0.654	*	1.21	0.024
GMAP1	0.39	0.256	-0.85	0.006	*	-0.39	0.241	*	IGF2R	0.16	0.809	-0.07	0.901	*	1.09	0.004
HECTD3	-0.02	0.982	-0.61	0.048	*	-0.38	0.249	*	IRNF19A	0.27	0.457	0.02	0.579	*	0.57	0.002
NC1C1	-0.48	0.214	-0.85	0.005	*	-0.53	0.198	*	IP21	-0.54	0.412	-0.10	0			

**Supplementary Table 2:** List of genes significantly (FDR 5%) and differentially (fold-change > 2) expressed after incubation of human PBMCs (n=7) with IL-7 compared to unstimulated cells.

Gene ID	logFC /Unstim	adj.P.Val	Gene ID	logFC /Unstim	adj.P.Val
CISH	3,24	1,8E-16	NOG	-1,92	1,4E-03
SOC52	2,91	7,8E-12	MAP3K14-AS1	-1,74	1,4E-02
MEOX1	2,56	2,5E-07	S100B	-1,61	1,6E-02
DPP4	2,42	1,1E-14	PASK	-1,55	1,9E-15
BCL2	2,28	3,4E-10	TSC22D3	-1,52	1,2E-15
TAF4B	2,27	9,9E-13	TCF7	-1,43	3,2E-12
FRMD4B	1,96	5,4E-08	HPCAL4	-1,38	1,5E-04
AFAP1	1,87	4,1E-08	GIMAP2	-1,34	1,1E-12
PTGER2	1,85	1,5E-12	AVP1	-1,32	2,7E-03
IGFBP3	1,84	9,3E-07	PF4	-1,32	2,3E-02
IRF4	1,82	5,6E-12	FAM102A	-1,13	2,1E-09
IFNG	1,66	1,4E-03	CBR3	-1,12	1,4E-03
AHR	1,64	2,3E-07	GPA33	-1,11	1,4E-03
DNLZ	1,63	1,2E-04	PHF19	-1,11	1,4E-03
CMAHP	1,57	2,8E-08	ZCCHC18	-1,10	3,7E-02
ALDH16A1	1,54	2,5E-04	IL7R	-1,10	1,4E-09
TXK	1,46	8,3E-08	CD27	-1,09	1,4E-09
ADAM19	1,46	5,8E-11	AQP3	-1,08	1,6E-04
RGS1	1,44	4,3E-09	SNHG7	-1,08	3,7E-02
PSMD3	1,44	1,8E-04	LOC100507206	-1,07	4,7E-02
CDK6	1,44	4,7E-07	TMEM204	-1,06	3,4E-10
PDE4B	1,43	1,2E-11	FAIM3	-1,03	4,4E-11
LTA	1,42	2,8E-06	NCAPH	-1,02	3,4E-04
MB21D2	1,39	1,2E-06	LY9	-1,01	6,6E-08
BHLHE40	1,39	2,5E-07	SELL	-1,00	6,4E-13
TNFRSF4	1,38	1,2E-03			
SOS1	1,37	6,1E-09			
ETS1	1,37	5,2E-05			
FAM101B	1,36	4,7E-06			
FAM13A	1,30	2,7E-04			
TAF10	1,29	4,9E-03			
CCR2	1,29	3,3E-05			
AP3M2	1,28	3,1E-09			
DDRGK1	1,28	7,0E-03			
DOHH	1,26	4,9E-02			
IKZF4	1,26	3,8E-05			
SLC4A10	1,26	5,9E-05			
KLC2	1,23	3,6E-03			
COTL1	1,23	2,9E-04			
CYLD	1,21	6,4E-13			
SYNE3	1,19	9,6E-04			
DUSP2	1,19	1,4E-02			
CD88	1,17	1,5E-09			
ITGA4	1,16	1,2E-11			
ST3GAL5	1,15	2,8E-02			
IL2RA	1,15	1,8E-07			
GNPDA1	1,15	2,8E-09			
CCR5	1,15	2,1E-04			
MAF1	1,14	2,0E-02			
SLC37A3	1,14	1,7E-04			
SPINT1	1,14	1,8E-02			
FKBP5	1,14	2,7E-07			
DDI2	1,13	2,9E-03			
HSBP1L1	1,12	3,8E-03			
MTA2	1,12	5,8E-04			
UGCG	1,10	2,2E-03			
TLR1	1,10	5,2E-05			
C17orf59	1,07	1,4E-02			
RNF149	1,07	5,3E-05			
GNA15	1,07	7,9E-04			
POLRMT	1,06	5,3E-05			
HSPA1L	1,06	4,2E-03			
CMTM6	1,04	7,3E-13			
TRPC4AP	1,03	2,9E-04			
PITRM1	1,03	2,5E-07			
B3GNT2	1,03	1,1E-02			
KLF7	1,02	5,7E-05			
TAZ	1,01	3,2E-02			