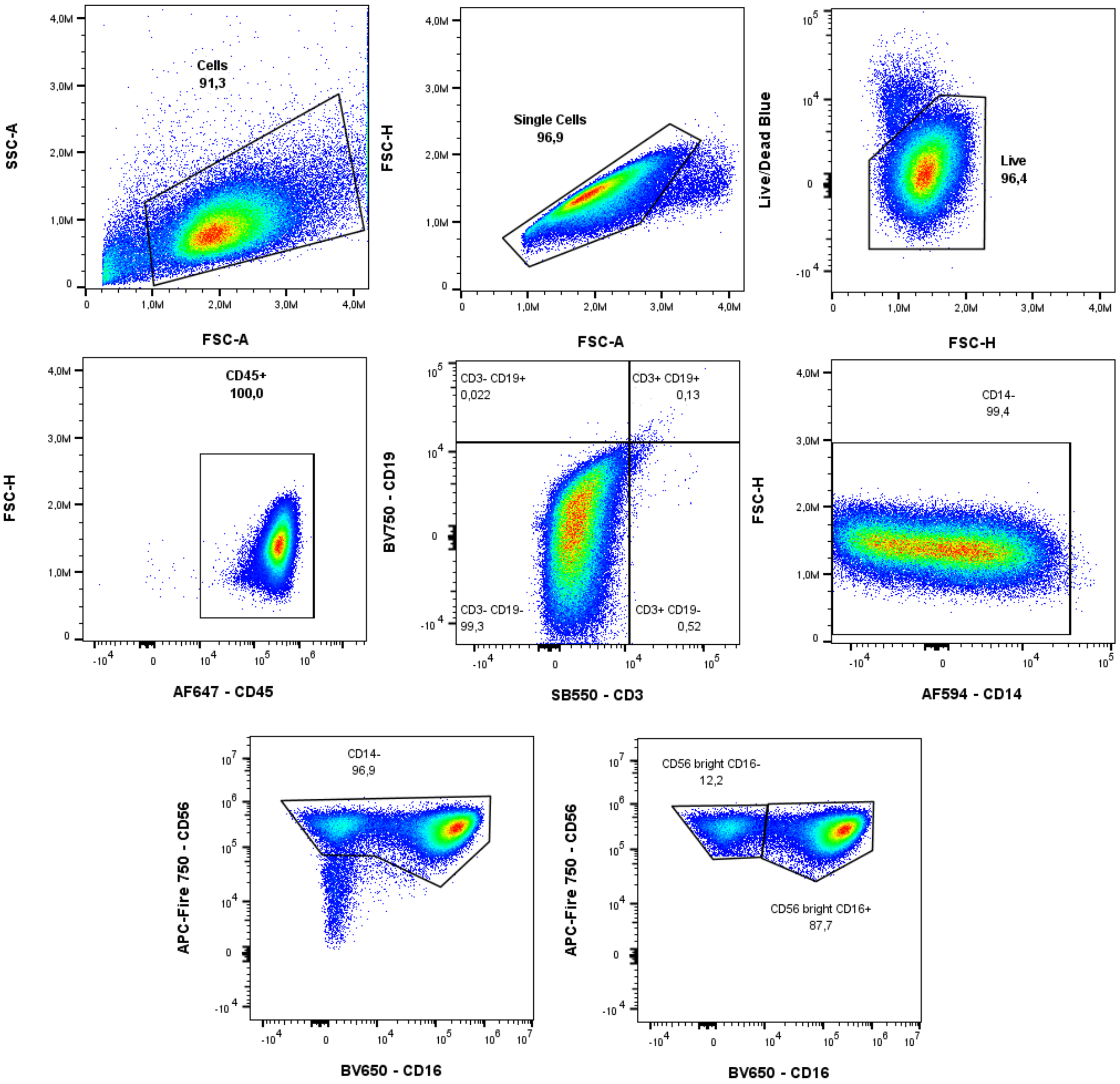
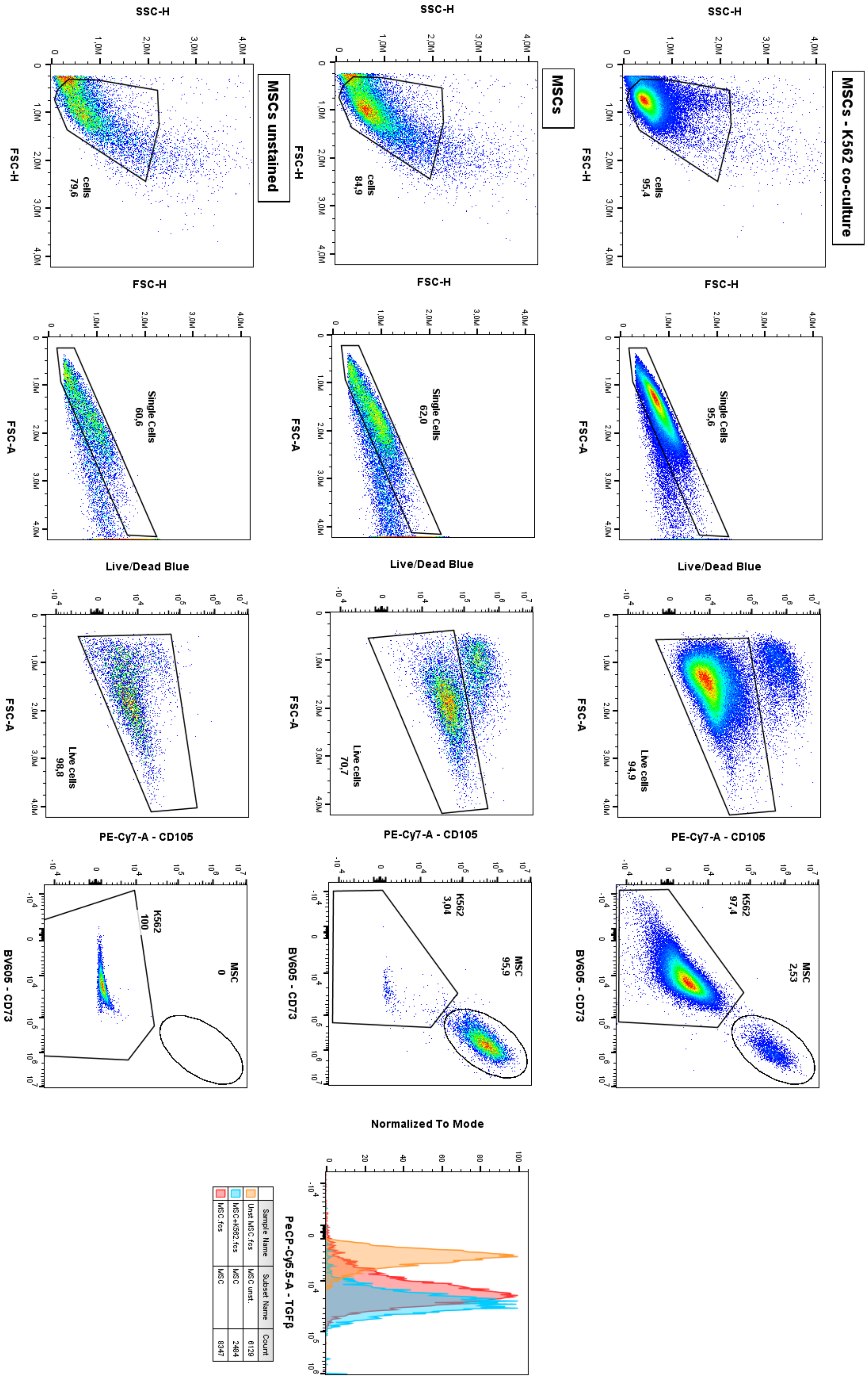
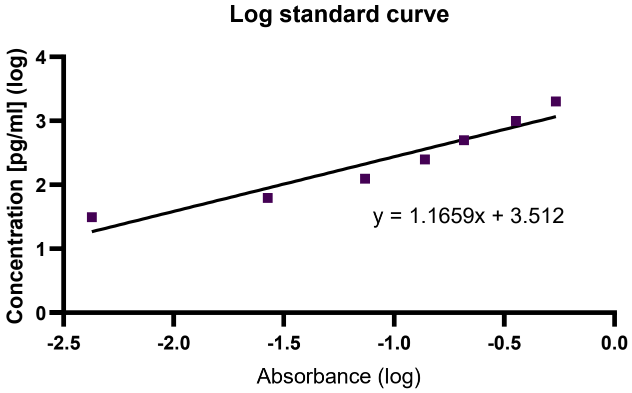


Figure S1 (above) – Gating strategy for NK cell purity evaluation and subset ratio assessment
From the Live cell population, NK cells are defined as CD45+ CD3- CD19- CD14- CD56+
The subpopulations are then further defined as CD56 dim/bright CD16+/-

Figure S2 (bellow) – Gating strategy for analysis of TGF-β content in MSCs co-cultured with K562 cells
From the Live cell population, MSCs were defined as CD105; CD73+ (K562 cells are the negative population)
In the third row, the MSCs were only stained with Live/Dead blue and thus are negative for CD105, CD73 and TGF-β
TGF-β was stained intracellularly.


MSCs unstained
MSCs
MSCs - K562 co-culture
SSC-H
FSC-H
cells 79,6
cells 84,9
cells 95,4
FSC-A
Single Cells 60,6
Single Cells 62,0
Single Cells 95,6
Live/Dead Blue
Live cells 98,8
Live cells 70,7
Live cells 94,9
PE-Cy7-A - CD105
BV605 - CD73
K562 100
MSC 0
K562 3,04
MSC 95,9
K562 97,4
MSC 2,53
0
1,0M
2,0M
3,0M
4,0M
-10^4
10^4
10^5
10^6
10^7
Normalized To Mode
0
20
40
60
80
100
PeCP-Cy5.5-A - TGFβ
Sample Name
Subset Name
Count
Unst MSC.fcs
MSC unst.
6129
MSC+K562.fcs
MSC
2484
MSC.fcs
MSC
8347

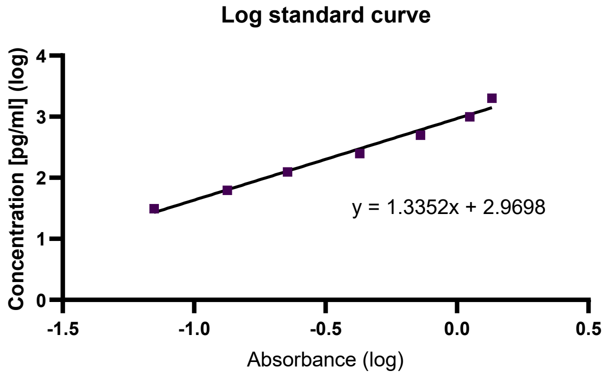
Standard average (NK cultures)							
Concentration [pg/ml]	2000	1000	500	250	125	62.5	31.3
Optical density	0.54265	0.35785	0.20765	0.13815	0.07405	0.02665	0.00425
Log standard							
Concentration [pg/ml]	3.30103	3	2.69897	2.39794	2.09691	1.79588	1.495544
Optical density	-0.2655	-0.4463	-0.68267	-0.85965	-1.13047	-1.5743	-2.37161



Optical density	**Ctrl**	**TGFb**	**K562**
Culture 1	0.26375	0.4395	0.13435
Culture 2	0.05645	0.6863	0.15845
Culture 3	0.0273	0.4483	0.0965

Figure S3 – ELISA data for TGF-β content assessment in NK cell cultures
Upper table: Raw data for standard curve definition
Middle: Standard curve with equation for concentration calculation
Lower table: Measured optical densities of individual samples (n=3)

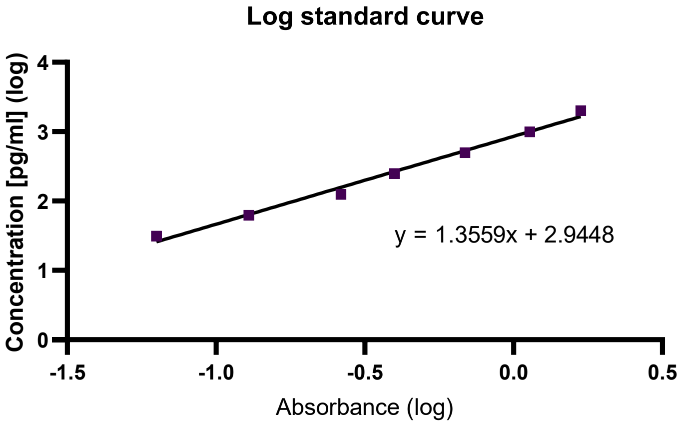
Standard average (Leukemic cell lines)							
Concentration [pg/ml]	2000	1000	500	250	125	62.5	31.3
Optical density	1.35895	1.1177	0.72605	0.42715	0.2268	0.1337	0.07045
Log standard							
Concentration [pg/ml]	3.30103	3	2.69897	2.39794	2.09691	1.79588	1.495544
Optical density	0.133203	0.048325	-0.13903	-0.36942	-0.64436	-0.87387	-1.15212



Optical density	**U937**	**MOLM13**	**K562**	**THP-1**
Control	1.330604	1.996477	2.59704	1.002168
Stimulated	1.71388	2.109966	2.635338	1.4533

Figure S4 – ELISA data for TGF-β production in leukemic cell lines U937, MOLM13, K562 and THP-1
Upper table: Raw data for standard curve definition
Middle: Standard curve with equation for concentration calculation
Lower table: Measured optical densities of individual samples

Standard average (Co-cultivation of leukemic cells with MSC)							
Concentration [pg/ml]	2000	1000	500	250	125	62.5	31.3
Optical density	1.6807	1.13315	0.6872	0.3977	0.2628	0.12885	0.06305
Log standard							
Concentration [pg/ml]	3.30103	3	2.69897	2.39794	2.09691	1.79588	1.495544
Optical density	0.22549	0.054287	-0.16292	-0.40044	-0.58037	-0.88992	-1.20031



Optical density	**Blast**	**MSC**	**Blast + MSC**
-	0.26525	0.89395	0.99665

Figure S5 – ELISA data for TGF-β content in supernatants of blast cells, MSCs and their co-cultivation
Upper table: Raw data for standard curve definition
Middle: Standard curve with equation for concentration calculation
Lower table: Measured optical densities of individual samples

Ctrl vs. D-14d	logFC	logCPM	logCPM_CTRL	logCPM_d0	F	PValue	FDR	UP	DOWN
CRYBG2	8.356	4.939	-2.432	5.430	651.760	1.20747E-06	0.002284536	1	0
ZNF683	9.507	5.836	-2.580	6.161	913.252	5.06934E-07	0.002284536	1	0
CD300A	-5.754	6.142	7.065	1.342	1306.285	2.01529E-07	0.002284536	0	1
LDLRAD4	3.416	7.560	4.971	8.385	712.881	9.58936E-07	0.002284536	1	0
RAB27B	-4.275	4.695	5.598	1.349	616.752	1.39152E-06	0.002284536	0	1
TNFRSF11A	4.254	4.660	1.223	5.440	790.851	7.34225E-07	0.002284536	1	0
ITGAE	6.274	8.647	3.218	9.475	499.033	2.39671E-06	0.003428491	1	0
TNFSF4	4.407	6.679	3.149	7.551	433.760	3.4329E-06	0.003928608	1	0
PTGDR	-3.403	4.199	5.049	1.667	450.801	3.11019E-06	0.003928608	0	1
PIK3R6	2.726	5.052	3.078	5.793	394.049	4.38954E-06	0.004566722	1	0
IL12RB2	-2.025	7.068	7.726	5.703	321.201	7.40114E-06	0.00487891	0	1
UBASH3B	-2.141	6.865	7.416	5.278	327.927	7.01977E-06	0.00487891	0	1
BMF	2.180	5.822	4.329	6.506	329.248	6.94809E-06	0.00487891	1	0
CCR7	7.726	3.049	-3.062	3.427	337.952	6.50019E-06	0.00487891	1	0
ADAP1	-2.129	5.309	5.947	3.825	316.678	7.67392E-06	0.00487891	0	1
DMD	4.134	3.219	-0.010	4.035	341.063	6.34984E-06	0.00487891	1	0
CRIM1	-2.237	6.979	7.696	5.461	302.153	8.65038E-06	0.004923056	0	1
NCR3	-2.684	6.116	6.867	4.189	304.154	8.50597E-06	0.004923056	0	1
RGS3	-2.534	6.635	7.266	4.733	297.056	9.03392E-06	0.004923056	0	1
CFH	-2.941	3.925	4.551	1.614	244.865	1.47738E-05	0.005407344	0	1
FCMR	-2.470	3.851	4.595	2.143	237.814	1.59124E-05	0.005407344	0	1
VSTM4	4.879	3.056	-0.827	3.868	275.472	1.09485E-05	0.005407344	1	0
KRT81	2.197	5.310	3.446	5.636	256.343	1.31494E-05	0.005407344	1	0
PXN	-2.207	6.258	6.871	4.667	275.657	1.09298E-05	0.005407344	0	1
ZNF551	2.772	4.197	2.179	4.928	247.984	1.43059E-05	0.005407344	1	0
PRKD3	1.884	7.114	5.878	7.761	256.210	1.31667E-05	0.005407344	1	0
RAB3GAP1	3.046	5.907	3.672	6.713	235.487	1.63147E-05	0.005407344	1	0
PMEPA1	8.012	4.961	-1.975	5.956	251.452	1.38096E-05	0.005407344	1	0
NECTIN3	2.002	5.237	3.918	5.916	242.003	1.52218E-05	0.005407344	1	0
ANKH	3.558	4.598	1.834	5.381	245.131	1.4733E-05	0.005407344	1	0
CLIC5	4.072	3.651	0.521	4.556	245.538	1.4671E-05	0.005407344	1	0
CD109	2.314	4.768	3.131	5.441	229.985	1.73242E-05	0.005407344	1	0
RADIL	7.391	3.781	-2.368	4.744	230.733	1.7182E-05	0.005407344	1	0
NCS1	2.105	6.637	5.078	7.184	230.602	1.72067E-05	0.005407344	1	0
WIPF3	14.461	5.415	-3.991	6.272	1805.279	1.74827E-05	0.005407344	1	0
IRF8	-2.389	7.505	7.899	5.517	224.697	1.83777E-05	0.00553458	0	1
IL9RP3	3.871	2.773	-0.115	3.674	213.740	2.08622E-05	0.005684466	1	0
CYS1	5.832	4.340	-0.646	5.188	217.116	2.00495E-05	0.005684466	1	0
HSPA4L	3.771	2.291	-0.681	2.962	214.022	2.07926E-05	0.005684466	1	0
GNPDA1	-3.485	4.244	4.870	1.458	213.859	2.08328E-05	0.005684466	0	1
MYO5B	9.248	5.686	-2.539	6.608	207.546	2.24762E-05	0.005981809	1	0
SMOX	2.603	4.910	3.061	5.659	204.596	2.33062E-05	0.00606174	1	0
NSMCE1	1.840	5.375	4.147	5.982	198.767	2.50759E-05	0.006321205	1	0
TRPM2	-2.007	4.736	5.124	3.133	197.735	2.54085E-05	0.006321205	0	1
MIR124-1HG	-1.881	4.622	5.231	3.357	195.154	2.62675E-05	0.006395859	0	1
ECE1	2.231	6.904	5.330	7.563	183.298	3.07781E-05	0.006593908	1	0
CNR2	-1.604	5.068	5.329	3.728	183.144	3.08434E-05	0.006593908	0	1
FGR	-2.363	6.636	7.272	4.906	186.852	2.93201E-05	0.006593908	0	1
ANK3	2.478	3.801	2.038	4.494	191.162	2.76772E-05	0.006593908	1	0
SMAD3	-4.826	5.683	6.526	1.693	183.114	3.08561E-05	0.006593908	0	1
BCL2A1	-2.000	4.930	5.600	3.606	182.511	3.11142E-05	0.006593908	0	1
ERICD	4.699	3.055	-0.669	3.865	184.291	3.03606E-05	0.006593908	1	0
UNC5B	13.566	4.509	-3.991	4.985	1212.814	3.28406E-05	0.006833229	1	0
TSC22D3	-1.822	5.213	5.681	3.864	174.830	3.46825E-05	0.007087618	0	1
TMEM229B	-1.996	4.708	5.282	3.286	168.045	3.83241E-05	0.00720937	0	1
CYBRD1	3.381	2.268	-0.254	3.039	169.351	3.75834E-05	0.00720937	1	0
ETS2	2.518	5.953	4.190	6.705	166.279	3.93585E-05	0.00720937	1	0
PXYLP1	2.389	3.689	2.037	4.409	168.932	3.78189E-05	0.00720937	1	0
GFOD1	-2.161	6.383	7.023	4.868	172.323	3.59695E-05	0.00720937	0	1
GIMAP7	-1.695	5.940	6.525	4.832	167.712	3.85161E-05	0.00720937	0	1
MYORG	2.033	4.490	3.077	5.102	165.729	3.96881E-05	0.00720937	1	0
PLP2	1.393	6.646	5.787	7.179	162.876	4.14631E-05	0.007221284	1	0
IL9R	5.972	5.828	0.785	6.723	162.591	4.16467E-05	0.007221284	1	0
IL9R	5.972	5.828	0.785	6.723	162.591	4.16467E-05	0.007221284	1	0
MRC2	6.160	4.484	-0.731	5.418	161.106	4.262E-05	0.007279756	1	0
ITGA1	3.100	8.486	6.219	9.318	159.784	4.35137E-05	0.007323104	1	0
TIMP1	1.928	3.898	2.602	4.518	157.303	4.52625E-05	0.007507022	1	0

YPEL2	3.582	2.045	-0.745	2.673	156.143	4.61131E-05	0.007538841	1	0
ITM2C	3.131	6.291	3.931	7.064	154.009	4.77378E-05	0.007694526	1	0
CLNK	2.120	3.595	1.762	3.860	149.059	5.18235E-05	0.008237063	1	0
PTGER3	2.858	4.071	1.502	4.352	148.000	5.27606E-05	0.008271134	1	0
RCBTB2	-3.238	6.897	7.713	4.484	146.881	5.37758E-05	0.008316357	0	1
FBXO2	-1.664	4.563	4.851	3.191	146.003	5.45917E-05	0.00832962	0	1
MYBL1	-1.603	6.213	6.785	5.181	144.484	5.60452E-05	0.00832962	0	1
NHS	4.587	4.379	0.691	5.227	145.086	5.54629E-05	0.00832962	1	0
CTBP2	-1.372	5.732	6.229	4.858	142.360	5.81677E-05	0.008347693	0	1
PITPNM2	-2.924	4.290	5.019	2.120	141.356	5.92095E-05	0.008347693	0	1
SETBP1	-1.319	6.057	6.563	5.245	140.106	6.05434E-05	0.008347693	0	1
LINC00299	-1.564	4.662	5.126	3.571	140.373	6.02551E-05	0.008347693	0	1
LTA	-2.310	4.553	5.161	2.873	142.591	5.7931E-05	0.008347693	0	1
WNT7B	9.716	3.928	-3.573	4.205	142.066	5.84702E-05	0.008347693	1	0
GPR25	8.534	3.432	-3.385	4.368	139.274	6.14544E-05	0.008372435	1	0
FAM3C	-1.526	7.350	7.912	6.387	136.234	6.49504E-05	0.00874461	0	1
SKI	2.096	7.040	5.576	7.668	127.660	7.64294E-05	0.00912061	1	0
AMOTL1	1.720	5.320	3.784	5.512	132.571	6.95398E-05	0.00912061	1	0
KCNMB4	5.962	2.480	-2.182	3.319	129.883	7.31996E-05	0.00912061	1	0
PTGER2	-1.241	7.225	7.692	6.452	128.646	7.49725E-05	0.00912061	0	1
PLEK	-2.516	7.757	8.469	5.956	129.618	7.35738E-05	0.00912061	0	1
CHROMR	1.699	4.649	3.545	5.239	131.403	7.10978E-05	0.00912061	1	0
ABCG1	4.390	4.967	1.444	5.824	130.341	7.25567E-05	0.00912061	1	0
DUSP1	-1.635	4.670	5.171	3.541	127.606	7.65098E-05	0.00912061	0	1
PPARD	1.807	5.764	4.536	6.337	128.493	7.51957E-05	0.00912061	1	0
GIMAP1	-1.550	5.318	5.868	4.320	128.927	7.45639E-05	0.00912061	0	1
STRBP	1.967	5.221	3.901	5.867	131.932	7.03864E-05	0.00912061	1	0
DRAXIN	1.372	7.767	6.701	8.073	124.526	8.13294E-05	0.009124842	1	0
VAV3	-1.535	5.347	5.905	4.375	124.674	8.10875E-05	0.009124842	0	1
INAVA	6.467	5.402	-0.189	6.326	126.940	7.75188E-05	0.009124842	1	0
PIK3AP1	-2.020	7.141	7.797	5.780	125.381	7.99499E-05	0.009124842	0	1
SIGLEC10-AS1	-3.165	1.852	2.607	-0.437	125.520	7.97283E-05	0.009124842	0	1

Table 1S (above) – List of differentially expressed genes in D-14d NK cells (compared to Ctrl)
Top 100 differentially expressed genes D-14d NK cells compared to untreated Ctrl NK cells. Among provided data: logFC – log fold change; logCPM – log count per million; FDR – false discovery rate; relative upregulation is marked by "1" in "UP" column, relative downregulation is marked by "1" in "DOWN" column.

Table 2S (bellow) – Pathway enrichment analysis results of differentially expressed genes in D-14d NK cells
The pathway enrichment analysis was performed via Gene Ontology database with differentially expressed genes of D-14d NK cells compared to untreated Ctrl NK cells. Top 50 biological pathways are listed here.

Analysis Type: PANTHER Overrepresentation Test (Released 20221013) Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.7709866 Released 2023-03-06 Analyzed List: upload_1 (Homo sapiens) Reference List: Homo sapiens (all genes in database) Test Type: FISHER Correction: FDR GO biological process complete	Homo sapiens - REFLIST	Ctrl vs. D-14d	Expected	Over/under	Fold enrichment	Raw P-value	FDR
cellular response to ionomycin (GO:1904637)	4	3	0.12	+	24.43	8.41E-04	2.70E-02
response to ionomycin (GO:1904636)	4	3	0.12	+	24.43	8.41E-04	2.70E-02
positive regulation of microglial cell mediated cytotoxicity (GO:1904151)	4	3	0.12	+	24.43	8.41E-04	2.69E-02
regulation of microglial cell mediated cytotoxicity (GO:1904149)	5	3	0.15	+	19.55	1.32E-03	3.82E-02
adherens junction maintenance (GO:0034334)	7	4	0.21	+	18.62	2.18E-04	8.96E-03
platelet degranulation (GO:0002576)	8	4	0.25	+	16.29	3.19E-04	1.23E-02
positive regulation of natural killer cell cytokine production (GO:0002729)	8	4	0.25	+	16.29	3.19E-04	1.23E-02
regulation of natural killer cell cytokine production (GO:0002727)	9	4	0.28	+	14.48	4.50E-04	1.61E-02
positive regulation of CD4-positive, alpha-beta T cell proliferation (GO:2000563)	10	4	0.31	+	13.03	6.15E-04	2.08E-02
granzyme-mediated programmed cell death signaling pathway (GO:0140507)	10	4	0.31	+	13.03	6.15E-04	2.07E-02
immune response-regulating cell surface receptor signaling pathway involved in phagocytosis (GO:0002433)	21	7	0.64	+	10.86	1.38E-05	9.01E-04
Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)	21	7	0.64	+	10.86	1.38E-05	8.97E-04
regulation of neutrophil activation (GO:1902563)	15	5	0.46	+	10.86	2.47E-04	9.97E-03
positive regulation of inflammatory response to antigenic stimulus (GO:0002863)	13	4	0.4	+	10.02	1.36E-03	3.93E-02
Fc receptor mediated stimulatory signaling pathway (GO:0002431)	23	7	0.71	+	9.91	2.25E-05	1.36E-03
positive regulation of glial cell proliferation (GO:0060252)	18	5	0.55	+	9.05	4.97E-04	1.75E-02
Fc-gamma receptor signaling pathway (GO:0038094)	29	8	0.89	+	8.99	1.06E-05	7.19E-04
regulation of CD4-positive, alpha-beta T cell proliferation (GO:2000561)	22	6	0.68	+	8.88	1.47E-04	6.47E-03
positive regulation of myeloid leukocyte mediated immunity (GO:0002888)	22	6	0.68	+	8.88	1.47E-04	6.45E-03
positive regulation of bone resorption (GO:0045780)	19	5	0.58	+	8.57	6.12E-04	2.08E-02
defense response to protozoan (GO:0042832)	27	7	0.83	+	8.45	5.37E-05	2.85E-03
regulation of B cell receptor signaling pathway (GO:0050855)	20	5	0.61	+	8.14	7.47E-04	2.45E-02
chloride ion homeostasis (GO:0055064)	20	5	0.61	+	8.14	7.47E-04	2.44E-02
natural killer cell mediated cytotoxicity (GO:0042267)	33	8	1.01	+	7.9	2.37E-05	1.42E-03
response to protozoan (GO:0001562)	29	7	0.89	+	7.86	7.91E-05	3.88E-03
positive regulation of alpha-beta T cell proliferation (GO:0046641)	29	7	0.89	+	7.86	7.91E-05	3.87E-03
leukocyte migration involved in inflammatory response (GO:0002523)	21	5	0.64	+	7.76	9.02E-04	2.85E-02
stimulatory C-type lectin receptor signaling pathway (GO:0002223)	21	5	0.64	+	7.76	9.02E-04	2.84E-02
cellular response to lectin (GO:1990858)	21	5	0.64	+	7.76	9.02E-04	2.83E-02
response to lectin (GO:1990840)	21	5	0.64	+	7.76	9.02E-04	2.83E-02
regulation of inflammatory response to antigenic stimulus (GO:0002861)	43	10	1.32	+	7.58	3.14E-06	2.59E-04
negative regulation of T cell receptor signaling pathway (GO:0050860)	26	6	0.8	+	7.52	3.19E-04	1.23E-02
positive regulation of leukocyte degranulation (GO:0043302)	26	6	0.8	+	7.52	3.19E-04	1.22E-02
regulation of glial cell proliferation (GO:0060251)	35	8	1.07	+	7.45	3.42E-05	1.91E-03
natural killer cell mediated immunity (GO:0002228)	35	8	1.07	+	7.45	3.42E-05	1.90E-03

Ctrl vs. D-7d	logFC	logCPM	logCPM_CTRL	logCPM_d7	F	PValue	FDR	UP	DOWN
CRYBG2	8.532	5.157	-2.397	5.426	835.940	6.72144E-07	0.002561093	1	0
ZNF683	9.393	5.759	-2.545	6.146	886.625	5.78055E-07	0.002561093	1	0
ITGAE	5.732	8.008	3.252	8.979	960.127	4.71335E-07	0.002561093	1	0
SKI	2.280	7.171	5.610	7.889	452.030	3.23608E-06	0.004651487	1	0
UBXN10	-3.502	4.485	5.336	1.855	386.650	4.81837E-06	0.004651487	0	1
VSTM4	6.021	4.268	-0.792	5.000	360.007	5.77842E-06	0.004651487	1	0
ACTN1	-6.830	5.408	6.309	-0.533	518.818	2.27671E-06	0.004651487	0	1
BMF	2.754	6.321	4.364	7.114	320.844	7.74365E-06	0.004651487	1	0
SMAD3	-3.062	5.823	6.561	3.504	366.906	5.50598E-06	0.004651487	0	1
LRRC28	2.386	4.893	3.217	5.595	314.231	8.16429E-06	0.004651487	1	0
ITGAX	-3.045	7.383	8.149	5.107	354.802	5.99646E-06	0.004651487	0	1
ZFHX3	2.396	6.981	4.534	6.931	308.636	8.54529E-06	0.004651487	1	0
PIK3R6	3.116	5.386	3.113	6.223	447.547	3.31937E-06	0.004651487	1	0
PRKD3	2.168	7.400	5.912	8.079	311.123	8.37295E-06	0.004651487	1	0
ZBTB20	3.646	4.917	2.170	5.797	367.114	5.49807E-06	0.004651487	1	0
LTB	-2.282	6.638	7.263	4.983	368.492	5.44591E-06	0.004651487	0	1
ERICD	4.810	3.101	-0.634	4.046	461.938	3.06199E-06	0.004651487	1	0
TSC22D3	-2.009	5.213	5.716	3.712	316.583	8.01112E-06	0.004651487	0	1
IL9R	5.797	5.625	0.819	6.592	342.570	6.556E-06	0.004651487	1	0
IL9R	5.797	5.625	0.819	6.592	342.570	6.556E-06	0.004651487	1	0
WNT7B	11.349	5.435	-3.537	6.200	499.424	2.50926E-06	0.004651487	1	0
VSIG10L	4.322	3.014	-0.304	3.915	297.757	9.36015E-06	0.004863449	1	0
RAB3GAP1	3.210	6.097	3.706	6.912	289.874	1.00194E-05	0.004900701	1	0
GPR35	2.087	6.012	4.579	6.664	286.852	1.02893E-05	0.004900701	1	0
KRT86	2.355	5.934	3.724	6.058	271.406	1.18391E-05	0.004938111	1	0
KRT81	3.018	6.187	3.481	6.470	271.064	1.1877E-05	0.004938111	1	0
CYS1	5.846	4.386	-0.611	5.214	265.415	1.25278E-05	0.004938111	1	0
PGAP1	2.022	4.853	3.516	5.532	266.356	1.24161E-05	0.004938111	1	0
FAM102A	2.745	6.284	4.300	7.043	271.483	1.18306E-05	0.004938111	1	0
NECTIN1	-5.204	2.506	3.286	-1.681	225.869	1.8841E-05	0.004948685	0	1
FOS	-2.358	4.632	5.370	3.019	254.929	1.3874E-05	0.004948685	0	1
NSMCE1	1.867	5.424	4.181	6.044	225.326	1.89558E-05	0.004948685	1	0
MRC2	6.292	4.630	-0.696	5.571	246.433	1.51164E-05	0.004948685	1	0
CD300A	-3.571	6.263	7.100	3.538	224.892	1.90484E-05	0.004948685	0	1
PDE6G	-3.900	3.057	3.560	-0.162	242.157	1.58007E-05	0.004948685	0	1
RAB27B	-3.675	4.766	5.633	1.974	244.895	1.53577E-05	0.004948685	0	1
PLEK	-2.066	7.847	8.504	6.439	229.289	1.81392E-05	0.004948685	0	1
DUSP2	-1.734	6.035	6.638	4.905	237.103	1.66661E-05	0.004948685	0	1
NECTIN3	1.963	5.246	3.953	5.912	231.781	1.76505E-05	0.004948685	1	0
ITGA1	3.094	8.512	6.254	9.347	261.037	1.30668E-05	0.004948685	1	0
CSF2	-3.163	6.279	7.106	3.944	240.273	1.61159E-05	0.004948685	0	1
NCR3	-2.509	6.170	6.901	4.397	235.058	1.70351E-05	0.004948685	0	1
WIPF3	14.769	5.768	-3.956	6.693	2199.338	1.37646E-05	0.004948685	1	0
UNC5B	14.852	5.832	-3.956	6.287	2059.249	1.52661E-05	0.004948685	1	0
GZMK	-6.727	6.661	7.355	0.742	220.964	1.99149E-05	0.005058824	0	1
IFIT3	3.273	4.989	2.522	5.773	218.770	2.04229E-05	0.005075087	1	0
TJP1	14.155	5.133	-3.956	5.099	1580.688	2.31411E-05	0.005087028	1	0
GRB2	1.681	7.449	6.373	8.054	210.615	2.24775E-05	0.005087028	1	0
LDLRAD4	3.618	7.746	5.005	8.626	208.235	2.31307E-05	0.005087028	1	0
ETS2	2.278	5.784	4.225	6.500	212.109	2.20801E-05	0.005087028	1	0
RADIL	7.495	3.970	-2.333	4.957	211.549	2.2228E-05	0.005087028	1	0
AGO2	1.809	8.410	7.230	9.039	215.156	2.12999E-05	0.005087028	1	0
POLR1E	1.578	5.774	4.779	6.355	205.787	2.38309E-05	0.005139821	1	0
PMEPA1	7.973	5.013	-1.940	5.981	202.052	2.49567E-05	0.005282968	1	0
TSPAN14	1.606	8.019	6.941	8.546	190.230	2.90488E-05	0.005628078	1	0
KIR2DL4	-1.492	6.254	6.747	5.257	190.574	2.8917E-05	0.005628078	0	1
PHACTR1	-3.194	3.703	3.967	0.885	190.844	2.88141E-05	0.005628078	0	1
MYORG	1.846	4.401	3.111	4.949	190.844	2.88142E-05	0.005628078	1	0
NCS1	2.358	6.995	5.113	7.467	195.028	2.72832E-05	0.005628078	1	0
AQP3	2.253	4.647	3.035	5.285	185.096	3.11187E-05	0.005928635	1	0
P2RY2	13.556	4.526	-3.956	5.126	1283.298	3.21142E-05	0.006017987	1	0
DRAXIN	1.707	8.018	6.736	8.442	179.477	3.36263E-05	0.00619972	1	0
MMP14	1.918	7.710	5.900	7.816	176.804	3.49182E-05	0.006218171	1	0
IRF8	-1.650	7.711	7.934	6.284	174.859	3.59023E-05	0.006218171	0	1

ERFL	3.183	2.275	-0.015	3.083	175.605	3.55204E-05	0.006218171	1	0
ANKH	3.371	4.556	1.869	5.223	175.997	3.53222E-05	0.006218171	1	0
SMOX	3.432	5.663	3.095	6.525	173.749	3.6481E-05	0.006224101	1	0
FCMR	-2.357	3.904	4.629	2.285	172.045	3.73951E-05	0.006241648	0	1
NETO2	2.647	3.374	1.524	4.142	171.533	3.76759E-05	0.006241648	1	0
USP46	2.401	5.651	3.997	6.396	168.276	3.95331E-05	0.006455752	1	0
FAM43A	1.964	5.634	4.262	6.225	166.311	4.07151E-05	0.006555139	1	0
MXRA7	1.731	6.624	5.511	7.240	163.799	4.22993E-05	0.006715605	1	0
CARD19	2.247	5.728	4.205	6.448	162.129	4.34002E-05	0.00679599	1	0
MYADM	-1.443	6.300	6.774	5.331	160.242	4.46923E-05	0.006903753	0	1
GLUL	1.457	6.654	5.743	7.198	159.216	4.54178E-05	0.006922279	1	0
RAB37	-2.973	5.142	5.904	2.937	158.167	4.61763E-05	0.006945276	0	1
MYO5B	9.410	6.070	-2.504	6.787	153.952	4.94077E-05	0.007334801	1	0
CHROMR	1.615	4.620	3.580	5.190	152.826	5.0324E-05	0.00737504	1	0
WDFY2	1.851	6.647	5.376	7.224	147.417	5.50705E-05	0.007584466	1	0
BCL2A1	-1.650	5.040	5.635	3.989	148.468	5.41005E-05	0.007584466	0	1
ITGAM	-1.732	6.744	7.344	5.613	148.631	5.39523E-05	0.007584466	0	1
DUSP1	-1.837	4.632	5.206	3.376	149.398	5.32627E-05	0.007584466	0	1
BSPRY	-1.783	4.046	4.641	2.866	147.927	5.45971E-05	0.007584466	0	1
RFX2	2.470	4.021	2.239	4.690	146.548	5.58904E-05	0.007605752	1	0
SPRY4	-2.138	3.807	4.015	1.902	142.968	5.94536E-05	0.007995461	0	1
IL12RB2	-1.349	7.261	7.760	6.412	142.199	6.02604E-05	0.008009732	0	1
MIB1	1.671	8.457	7.386	9.057	141.037	6.15075E-05	0.008081514	1	0
VDR	1.606	6.228	5.168	6.773	138.156	6.47597E-05	0.008328115	1	0
IL9RP3	3.778	2.840	-0.080	3.610	136.049	6.729E-05	0.008328115	1	0
P2RY11	-2.822	3.099	3.799	1.026	136.259	6.70313E-05	0.008328115	0	1
SAMHD1	-1.208	7.015	7.487	6.279	136.822	6.63465E-05	0.008328115	0	1
TRPM2	-1.494	4.879	5.158	3.674	135.674	6.77556E-05	0.008328115	0	1
DMTN	2.357	6.684	4.798	7.162	136.401	6.68582E-05	0.008328115	1	0
ITGA4	-1.750	8.042	8.496	6.746	133.987	6.99028E-05	0.008500628	0	1
PGGHG	-1.901	5.075	5.454	3.563	131.522	7.32135E-05	0.008809509	0	1
HSPA6	-2.571	4.614	5.331	2.762	129.984	7.53893E-05	0.008976826	0	1
INAVA	6.099	5.067	-0.154	6.001	126.028	8.14194E-05	0.009155476	1	0
STX3	-1.387	6.727	7.256	5.870	121.848	8.85416E-05	0.009155476	0	1
PAK1	1.276	5.748	4.949	6.224	120.777	9.05055E-05	0.009155476	1	0

Table 3S (above) – List of differentially expressed genes in D-14d NK cells (compared to Ctrl)
Top 100 differentially expressed genes D-14d NK cells compared to untreated Ctrl NK cells. Among provided data: logFC – log fold change; logCPM – log count per million; FDR – false discovery rate; relative upregulation is marked by "1" in "UP" column, relative downregulation is marked by "1" in "DOWN" column.

Table 4S (bellow) – Pathway enrichment analysis results of differentially expressed genes in D-14d NK cells
The pathway enrichment analysis was performed via Gene Ontology database with differentially expressed genes of D-14d NK cells compared to untreated Ctrl NK cells. Top 50 biological pathways are listed here.

Analysis Type: PANTHER Overrepresentation Test (Released 20221013) **Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.7709866 Released 2023-03-06** **Analyzed List: upload_1 (Homo sapiens)** **Reference List: Homo sapiens (all genes in database)** **Test Type: FISHER** **Correction: FDR** **GO biological process complete**	**Homo sapiens - REFLIST**	**Ctrl vs. D-7d**	**Expected**	**over/under**	**Fold enrichment**	**Raw P-value**	**FDR**
regulation of lung blood pressure (GO:0014916)	3	3	0.11	+	27.09	8.29E-04	2.62E-02
negative regulation of tau-protein kinase activity (GO:1902948)	3	3	0.11	+	27.09	8.29E-04	2.61E-02
actomyosin contractile ring assembly actin filament organization (GO:2000689)	4	3	0.15	+	20.32	1.41E-03	3.97E-02
positive regulation of monocyte extravasation (GO:2000439)	4	3	0.15	+	20.32	1.41E-03	3.96E-02
adherens junction maintenance (GO:0034334)	7	4	0.26	+	15.48	4.30E-04	1.54E-02
granzyme-mediated programmed cell death signaling pathway (GO:0140507)	10	5	0.37	+	13.55	1.26E-04	5.45E-03
positive regulation of natural killer cell cytokine production (GO:0002729)	8	4	0.3	+	13.55	6.27E-04	2.08E-02
positive regulation of heat generation (GO:0031652)	9	4	0.33	+	12.04	8.81E-04	2.73E-02
regulation of natural killer cell cytokine production (GO:0002727)	9	4	0.33	+	12.04	8.81E-04	2.73E-02
negative regulation of platelet aggregation (GO:0090331)	12	5	0.44	+	11.29	2.44E-04	9.63E-03
regulation of heat generation (GO:0031650)	12	5	0.44	+	11.29	2.44E-04	9.61E-03
negative regulation of pathway-restricted SMAD protein phosphorylation (GO:0060394)	13	5	0.48	+	10.42	3.28E-04	1.23E-02
regulation of T-helper 2 cell differentiation (GO:0045628)	11	4	0.41	+	9.85	1.59E-03	4.33E-02
intracellular chloride ion homeostasis (GO:0030644)	11	4	0.41	+	9.85	1.59E-03	4.32E-02
protein folding in endoplasmic reticulum (GO:0034975)	11	4	0.41	+	9.85	1.59E-03	4.31E-02
intracellular monoatomic anion homeostasis (GO:0030002)	11	4	0.41	+	9.85	1.59E-03	4.31E-02
negative regulation of T cell cytokine production (GO:0002725)	11	4	0.41	+	9.85	1.59E-03	4.30E-02
regulation of vascular wound healing (GO:0061043)	11	4	0.41	+	9.85	1.59E-03	4.29E-02
negative regulation of homotypic cell-cell adhesion (GO:0034111)	14	5	0.52	+	9.68	4.33E-04	1.55E-02
Fc receptor mediated stimulatory signaling pathway (GO:0002431)	23	8	0.85	+	9.42	9.47E-06	5.89E-04
immune response-regulating cell surface receptor signaling pathway involved in phagocytosis (GO:0002433)	21	7	0.78	+	9.03	4.34E-05	2.26E-03
regulation of neutrophil activation (GO:1902563)	15	5	0.55	+	9.03	5.60E-04	1.90E-02
Fc-gamma receptor signaling pathway involved in phagocytosis (GO:0038096)	21	7	0.78	+	9.03	4.34E-05	2.25E-03
T cell chemotaxis (GO:0010818)	15	5	0.55	+	9.03	5.60E-04	1.89E-02
myeloid dendritic cell differentiation (GO:0043011)	21	6	0.78	+	7.74	3.11E-04	1.18E-02
myeloid dendritic cell activation (GO:0001773)	25	7	0.92	+	7.59	1.09E-04	4.83E-03
negative regulation of T-helper cell differentiation (GO:0045623)	18	5	0.66	+	7.53	1.11E-03	3.26E-02
positive regulation of endothelial cell apoptotic process (GO:2000353)	18	5	0.66	+	7.53	1.11E-03	3.25E-02
negative regulation of platelet activation (GO:0010544)	19	5	0.7	+	7.13	1.36E-03	3.87E-02
regulation of platelet aggregation (GO:0090330)	31	8	1.14	+	6.99	5.74E-05	2.86E-03
positive regulation of amyloid-beta formation (GO:1902004)	20	5	0.74	+	6.77	1.66E-03	4.41E-02
regulation of catecholamine metabolic process (GO:0042069)	20	5	0.74	+	6.77	1.66E-03	4.41E-02
regulation of dopamine metabolic process (GO:0042053)	20	5	0.74	+	6.77	1.66E-03	4.40E-02
positive regulation of natural killer cell mediated immunity (GO:0002717)	32	8	1.18	+	6.77	6.96E-05	3.36E-03
dendritic cell differentiation (GO:0097028)	37	9	1.37	+	6.59	2.96E-05	1.62E-03
Fc-gamma receptor signaling pathway (GO:0038094)	29	7	1.07	+	6.54	2.39E-04	9.48E-03
response to protozoan (GO:0001562)	29	7	1.07	+	6.54	2.39E-04	9.45E-03
positive regulation of amino acid transport (GO:0051957)	25	6	0.92	+	6.5	6.86E-04	2.24E-02
regulation of homotypic cell-cell adhesion (GO:0034110)	38	9	1.4	+	6.42	3.54E-05	1.89E-03
regulation of T cell cytokine production (GO:0002724)	38	9	1.4	+	6.42	3.54E-05	1.89E-03
regulation of T-helper 1 type immune response (GO:0002825)	30	7	1.11	+	6.32	2.85E-04	1.09E-02
positive regulation of amyloid precursor protein catabolic process (GO:1902993)	26	6	0.96	+	6.25	8.19E-04	2.60E-02
positive regulation of T cell cytokine production (GO:0002726)	26	6	0.96	+	6.25	8.19E-04	2.60E-02

Ctrl vs. D-18h	logFC	logCPM	logCPM_CTRL	logCPM_d13	F	PValue	FDR	UP	DOWN
NXPH4	6.615	4.988	-0.547	5.902	1061.408	4.37759E-08	0.000497863	1	0
KRT81	3.311	6.237	3.406	6.705	627.308	2.1601E-07	0.001228342	1	0
KRT86	3.018	6.365	3.649	6.655	472.583	5.08883E-07	0.001251546	1	0
KIAA0513	3.382	4.485	1.879	5.234	509.952	4.04319E-07	0.001251546	1	0
SOX4	2.976	6.570	3.493	6.438	460.519	5.50227E-07	0.001251546	1	0
PMEPA1	7.066	3.916	-1.964	4.724	406.793	8.00079E-07	0.001500471	1	0
ITGA1	2.635	8.087	6.177	8.811	387.844	9.23823E-07	0.001500471	1	0
LTB	-2.813	6.476	7.187	4.380	371.069	1.05546E-06	0.001500471	0	1
ZBTB20	3.179	4.402	2.096	5.256	316.197	1.70808E-06	0.002158445	1	0
ITGA5	2.379	7.639	5.995	8.373	287.734	2.26721E-06	0.002578501	1	0
ITM2C	2.876	6.110	3.890	6.760	259.281	3.09743E-06	0.002709777	1	0
PIK3IP1	2.472	5.478	3.745	6.212	261.848	3.00741E-06	0.002709777	1	0
AMZ1	7.272	4.053	-2.217	4.854	263.884	2.93849E-06	0.002709777	1	0
LDLRAD4	3.425	7.489	4.929	8.355	252.673	3.34627E-06	0.002718367	1	0
GPR35	2.122	5.988	4.503	6.622	246.141	3.61896E-06	0.002743897	1	0
FAM102A	3.286	6.847	4.224	7.498	233.533	4.23482E-06	0.003010166	1	0
BMP8A	5.817	4.542	-0.444	4.971	189.225	7.92629E-06	0.003279781	1	0
TSPAN14	1.994	8.211	6.865	8.859	219.171	5.11814E-06	0.003279781	1	0
BMF	2.599	6.144	4.288	6.883	195.257	7.22026E-06	0.003279781	1	0
SMAD3	-2.293	5.846	6.485	4.197	180.125	9.17548E-06	0.003279781	0	1
MFGE8	2.264	5.025	3.332	5.580	177.135	9.64249E-06	0.003279781	1	0
IL21R	2.889	6.059	3.946	6.835	187.275	8.17396E-06	0.003279781	1	0
PIK3R6	3.115	5.398	3.038	6.139	216.619	5.30004E-06	0.003279781	1	0
VSIG10L	3.818	2.528	-0.365	3.300	179.715	9.23764E-06	0.003279781	1	0
ADCY3	2.562	7.096	5.306	7.868	203.284	6.40457E-06	0.003279781	1	0
PLEK	-1.628	7.868	8.428	6.800	182.547	8.81879E-06	0.003279781	0	1
KLHL6	1.771	6.702	5.490	7.258	198.803	6.84388E-06	0.003279781	1	0
LDB2	2.959	5.147	2.492	5.493	188.195	8.05581E-06	0.003279781	1	0
PPARD	1.649	5.564	4.494	6.140	176.591	9.7309E-06	0.003279781	1	0
CLIC5	3.767	3.312	0.488	4.209	205.906	6.16482E-06	0.003279781	1	0
PRKAR2B	2.875	3.807	1.471	4.283	201.327	6.59174E-06	0.003279781	1	0
PIM2	-1.972	6.749	7.393	5.423	181.793	8.92785E-06	0.003279781	0	1
APLN	4.091	4.297	0.958	4.946	176.140	9.80503E-06	0.003279781	1	0
SRM	2.031	5.664	4.303	6.329	173.311	1.02871E-05	0.003313884	1	0
APOL4	2.299	6.232	4.654	6.952	170.476	1.08024E-05	0.003313884	1	0
PLXNA1	-4.887	5.787	6.595	1.723	171.750	1.05667E-05	0.003313884	0	1
HBEGF	-1.883	4.656	5.170	3.293	167.584	1.13639E-05	0.003313884	0	1
ERICD	3.433	1.700	-0.692	2.600	167.833	1.13141E-05	0.003313884	1	0
SKI	2.369	7.224	5.534	7.900	163.052	1.23245E-05	0.003359297	1	0
VSTM4	4.821	2.878	-0.847	3.801	162.690	1.24057E-05	0.003359297	1	0
ETS2	1.604	5.192	4.149	5.750	162.723	1.23983E-05	0.003359297	1	0
MYO5B	7.370	3.683	-2.493	4.672	158.686	1.33545E-05	0.003492637	1	0
F2RL3	1.731	4.612	2.993	4.709	156.859	1.38195E-05	0.003492637	1	0
RAB3GAP1	1.964	4.941	3.631	5.591	157.443	1.36685E-05	0.003492637	1	0
GIT1	1.495	7.393	6.455	7.949	154.142	1.45515E-05	0.00359771	1	0
ECE1	1.911	6.614	5.289	7.200	145.858	1.71271E-05	0.003728039	1	0
NBPF10	1.906	5.064	3.815	5.715	149.471	1.5935E-05	0.003728039	1	0
LHX4	6.843	2.006	-3.032	3.022	148.461	1.62569E-05	0.003728039	1	0
KDM5B	1.824	7.367	6.060	7.884	143.736	1.7883E-05	0.003728039	1	0
ERFL	3.585	2.586	-0.079	3.393	146.974	1.67467E-05	0.003728039	1	0
ZNF551	2.484	3.900	2.140	4.601	147.941	1.6426E-05	0.003728039	1	0
SUSD3	5.553	2.973	-1.514	3.898	148.196	1.63427E-05	0.003728039	1	0
IL9R	3.339	3.181	0.750	4.051	143.340	1.80289E-05	0.003728039	1	0
IL9R	3.339	3.181	0.750	4.051	143.340	1.80289E-05	0.003728039	1	0
ADGRG3	2.562	8.439	5.672	8.246	140.411	1.91592E-05	0.003822756	1	0
EIF4EBP1	1.974	5.773	4.471	6.443	141.198	1.88465E-05	0.003822756	1	0
FAM83D	2.519	5.599	3.800	6.315	137.981	2.01691E-05	0.003954875	1	0
GRB2	1.435	7.190	6.297	7.732	137.162	2.05251E-05	0.003956472	1	0

CDA	7.924	2.956	-3.038	3.729	136.196	2.09562E-05	0.003972241	1	0
CTSA	1.685	6.303	5.195	6.878	133.680	2.21366E-05	0.004071898	1	0
LTA	-2.028	4.564	5.119	3.105	133.554	2.2198E-05	0.004071898	0	1
DDI2	1.564	6.709	5.719	7.282	132.191	2.28772E-05	0.004102569	1	0
BCAR3	2.640	4.438	2.247	4.850	131.402	2.32828E-05	0.004102569	1	0
SLAMF7	-1.481	8.907	9.452	7.972	130.407	2.38081E-05	0.004102569	0	1
SELPLG	1.564	7.922	6.937	8.500	130.858	2.35683E-05	0.004102569	1	0
NOTCH2NLA	1.704	5.541	4.446	6.148	127.691	2.53248E-05	0.004235574	1	0
POLR1E	1.783	5.863	4.703	6.483	128.254	2.5E-05	0.004235574	1	0
ITGAM	-1.747	6.665	7.268	5.521	126.960	2.5755E-05	0.00424509	0	1
TOR1A	1.600	7.562	6.524	8.123	124.941	2.6994E-05	0.004385756	1	0
HNRNPUL2-BSCL2	11.233	2.442	-3.855	3.291	411.144	2.82211E-05	0.004430922	1	0
ITGB2	-1.885	9.655	10.298	8.413	122.734	2.84408E-05	0.004430922	0	1
MARCHF3	2.287	3.476	1.442	3.664	123.005	2.82575E-05	0.004430922	1	0
LMO7	2.281	3.520	1.908	4.171	119.967	3.04038E-05	0.004610425	1	0
GAS7	1.461	7.364	6.300	7.759	120.120	3.02903E-05	0.004610425	1	0
NOTCH2NLB	1.895	4.980	3.734	5.623	116.913	3.27839E-05	0.004724607	1	0
HVCN1	1.743	4.559	3.303	5.041	116.369	3.32339E-05	0.004724607	1	0
LAIR2	-2.018	3.826	4.370	2.364	116.628	3.30187E-05	0.004724607	0	1
SCARB2	1.756	5.140	3.966	5.715	118.084	3.18432E-05	0.004724607	1	0
CARD19	2.085	5.519	4.129	6.210	117.538	3.22777E-05	0.004724607	1	0
OASL	2.052	6.386	4.986	7.037	115.377	3.40754E-05	0.004784433	1	0
CCL3	-1.401	9.149	9.682	8.282	113.759	3.55098E-05	0.004865697	0	1
PGAP1	1.925	4.709	3.441	5.357	114.047	3.52485E-05	0.004865697	1	0
PDCD4	1.281	6.146	5.354	6.633	112.022	3.71401E-05	0.004911559	1	0
QPCT	4.702	3.604	-0.414	4.433	112.115	3.70512E-05	0.004911559	1	0
SLC6A6	1.495	8.433	7.487	8.982	112.307	3.68661E-05	0.004911559	1	0
ANXA1	-1.303	7.588	8.037	6.734	111.178	3.79687E-05	0.004963429	0	1
AUTS2	1.279	6.131	5.283	6.560	109.870	3.93018E-05	0.005079313	1	0
ARHGAP31	-1.403	5.461	5.911	4.512	109.092	4.01232E-05	0.005127206	0	1
PINK1	1.450	5.157	4.242	5.688	100.687	5.06565E-05	0.005366967	1	0
GALNT2	2.769	7.269	5.152	7.912	103.276	4.70569E-05	0.005366967	1	0
PPP1R14B	1.850	7.566	6.342	8.193	101.569	4.93901E-05	0.005366967	1	0
TPCN1	1.888	5.148	3.640	5.523	98.926	5.33168E-05	0.005366967	1	0
RHOF	1.329	7.763	6.908	8.236	97.087	5.62964E-05	0.005366967	1	0
ABAT	1.757	4.220	3.090	4.841	99.764	5.20281E-05	0.005366967	1	0
NKD1	4.837	2.848	-0.964	3.720	103.022	4.73952E-05	0.005366967	1	0
ZNRF1	2.241	4.575	3.002	5.247	98.775	5.35538E-05	0.005366967	1	0
ZDHHC7	1.756	6.374	5.198	6.950	97.657	5.53491E-05	0.005366967	1	0
ITGAE	2.393	4.956	3.177	5.547	96.738	5.68858E-05	0.005366967	1	0

Table 5S (above) – List of differentially expressed genes in D-14d NK cells (compared to Ctrl)
Top 100 differentially expressed genes D-14d NK cells compared to untreated Ctrl NK cells. Among provided data: logFC – log fold change; logCPM – log count per million; FDR – false discovery rate; relative upregulation is marked by "1" in "UP" column, relative downregulation is marked by "1" in "DOWN" column.

Table 6S (bellow) – Pathway enrichment analysis results of differentially expressed genes in D-14d NK cells
The pathway enrichment analysis was performed via Gene Ontology database with differentially expressed genes of D-14d NK cells compared to untreated Ctrl NK cells. Top 50 biological pathways are listed here.

Inhibitory NK cell receptors and possibilities of manipulation of cytotoxic properties

(SUPPLEMENT)

Bc. Veronika Švubová

Analysis Type: PANTHER Overrepresentation Test (Released 20221013)	**Homo sapiens - REFLIST**	**Ctrl vs. D-18h**	**Expected**	**over/under**	**Fold enrichment**	**Raw P-value**	**FDR**
Annotation Version and Release Date: GO Ontology database DOI: 10.5281/zenodo.7709866 Released 2023-03-06							
Analyzed List: upload_1 (Homo sapiens)							
Reference List: Homo sapiens (all genes in database)							
Test Type: FISHER							
Correction: FDR							
GO biological process complete							
regulation of prostaglandin-E synthase activity (GO:2000361)	3	3	0.14	+	22.07	1.47E-03	4.33E-02
macrophage derived foam cell differentiation (GO:0010742)	7	4	0.32	+	12.61	9.07E-04	3.03E-02
DNA cytosine deamination (GO:0070383)	9	5	0.41	+	12.26	2.19E-04	9.58E-03
cytidine metabolic process (GO:0046087)	12	6	0.54	+	11.03	7.74E-05	4.14E-03
cytidine catabolic process (GO:0006216)	12	6	0.54	+	11.03	7.74E-05	4.12E-03
cytidine deamination (GO:0009972)	12	6	0.54	+	11.03	7.74E-05	4.11E-03
foam cell differentiation (GO:0090077)	8	4	0.36	+	11.03	1.31E-03	4.06E-02
positive regulation of isomerase activity (GO:0010912)	8	4	0.36	+	11.03	1.31E-03	4.05E-02
regulation of isomerase activity (GO:0010911)	8	4	0.36	+	11.03	1.31E-03	4.04E-02
positive regulation of extracellular matrix assembly (GO:1901203)	11	5	0.5	+	10.03	4.44E-04	1.71E-02
regulation of vascular wound healing (GO:0061043)	11	5	0.5	+	10.03	4.44E-04	1.70E-02
pyrimidine ribonucleoside catabolic process (GO:0046133)	14	6	0.63	+	9.46	1.50E-04	7.07E-03
pyrimidine ribonucleoside metabolic process (GO:0046131)	14	6	0.63	+	9.46	1.50E-04	7.05E-03
semaphorin-plexin signaling pathway involved in axon guidance (GO:1902287)	14	6	0.63	+	9.46	1.50E-04	7.03E-03
cytidine to uridine editing (GO:0016554)	12	5	0.54	+	9.19	6.06E-04	2.19E-02
negative regulation of pathway-restricted SMAD protein phosphorylation (GO:0060394)	13	5	0.59	+	8.49	8.09E-04	2.75E-02
DNA deamination (GO:0045006)	13	5	0.59	+	8.49	8.09E-04	2.74E-02
pyrimidine nucleoside catabolic process (GO:0046135)	16	6	0.73	+	8.28	2.68E-04	1.13E-02
semaphorin-plexin signaling pathway involved in neuron projection guidance (GO:1902285)	16	6	0.73	+	8.28	2.68E-04	1.12E-02
nucleotide-binding oligomerization domain containing signaling pathway (GO:0070423)	14	5	0.63	+	7.88	1.06E-03	3.42E-02
regulation of neutrophil activation (GO:1902563)	15	5	0.68	+	7.36	1.36E-03	4.13E-02
regulation of nitric-oxide synthase biosynthetic process (GO:0051769)	21	7	0.95	+	7.36	1.50E-04	7.08E-03
nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway (GO:0035872)	15	5	0.68	+	7.36	1.36E-03	4.12E-02
retina vasculature development in camera-type eye (GO:0061298)	19	6	0.86	+	6.97	5.69E-04	2.09E-02
regulation of extracellular matrix assembly (GO:1901201)	16	5	0.73	+	6.9	1.73E-03	4.90E-02
regulation of extracellular matrix disassembly (GO:0010715)	16	5	0.73	+	6.9	1.73E-03	4.90E-02
hyaluronan catabolic process (GO:0030214)	16	5	0.73	+	6.9	1.73E-03	4.89E-02
negative regulation of single stranded viral RNA replication via double stranded DNA intermediate (GO:0045869)	16	5	0.73	+	6.9	1.73E-03	4.88E-02
leukocyte tethering or rolling (GO:0050901)	20	6	0.91	+	6.62	7.13E-04	2.51E-02
ribonucleoside catabolic process (GO:0042454)	20	6	0.91	+	6.62	7.13E-04	2.50E-02
leukocyte cell-cell adhesion (GO:0007159)	56	16	2.54	+	6.31	5.75E-08	7.54E-06
heterotypic cell-cell adhesion (GO:0034113)	36	10	1.63	+	6.13	2.20E-05	1.42E-03
negative regulation of CD4-positive, alpha-beta T cell differentiation (GO:0043371)	22	6	1	+	6.02	1.08E-03	3.49E-02
leukocyte adhesion to vascular endothelial cell (GO:0061756)	22	6	1	+	6.02	1.08E-03	3.49E-02
positive regulation of myeloid leukocyte mediated immunity (GO:0002888)	22	6	1	+	6.02	1.08E-03	3.48E-02
DNA demethylation (GO:0080111)	22	6	1	+	6.02	1.08E-03	3.47E-02
negative regulation of viral genome replication (GO:0045071)	56	15	2.54	+	5.91	3.02E-07	3.20E-05
response to fluid shear stress (GO:0034405)	34	9	1.54	+	5.84	7.76E-05	4.11E-03
cellular extravasation (GO:0045123)	42	11	1.9	+	5.78	1.37E-05	9.35E-04
regulation of superoxide anion generation (GO:0032928)	23	6	1.04	+	5.76	1.32E-03	4.05E-02
pyrimidine nucleoside metabolic process (GO:0006213)	24	6	1.09	+	5.52	1.59E-03	4.58E-02
regulation of type 2 immune response (GO:0002828)	33	8	1.5	+	5.35	3.23E-04	1.30E-02