

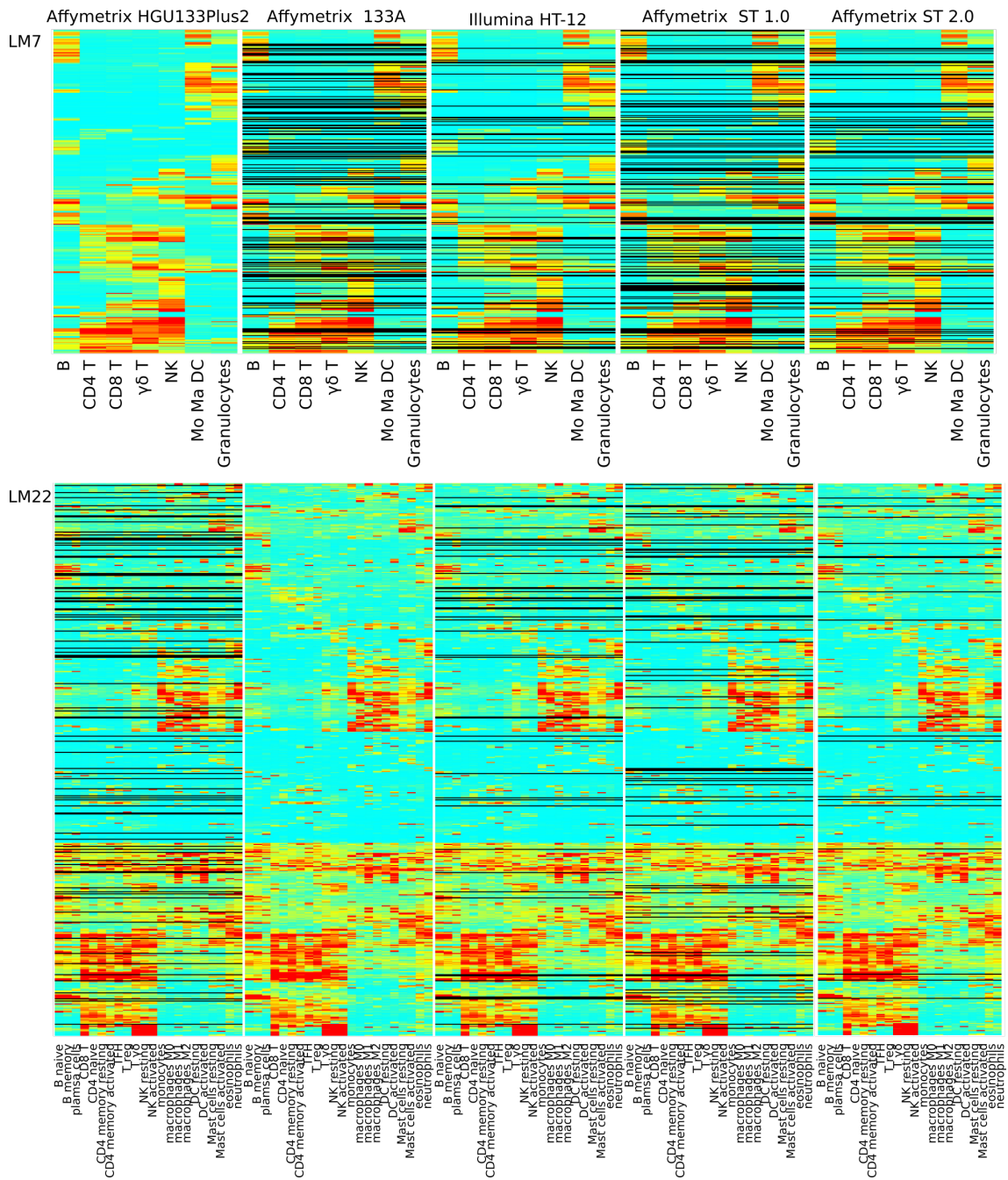
## Supplemental Information

# Assessment of tumor-infiltrating TCRV $\gamma$ 9V $\delta$ 2 $\gamma\delta$ lymphocyte abundance by deconvolution of human cancers microarrays

### Authors:

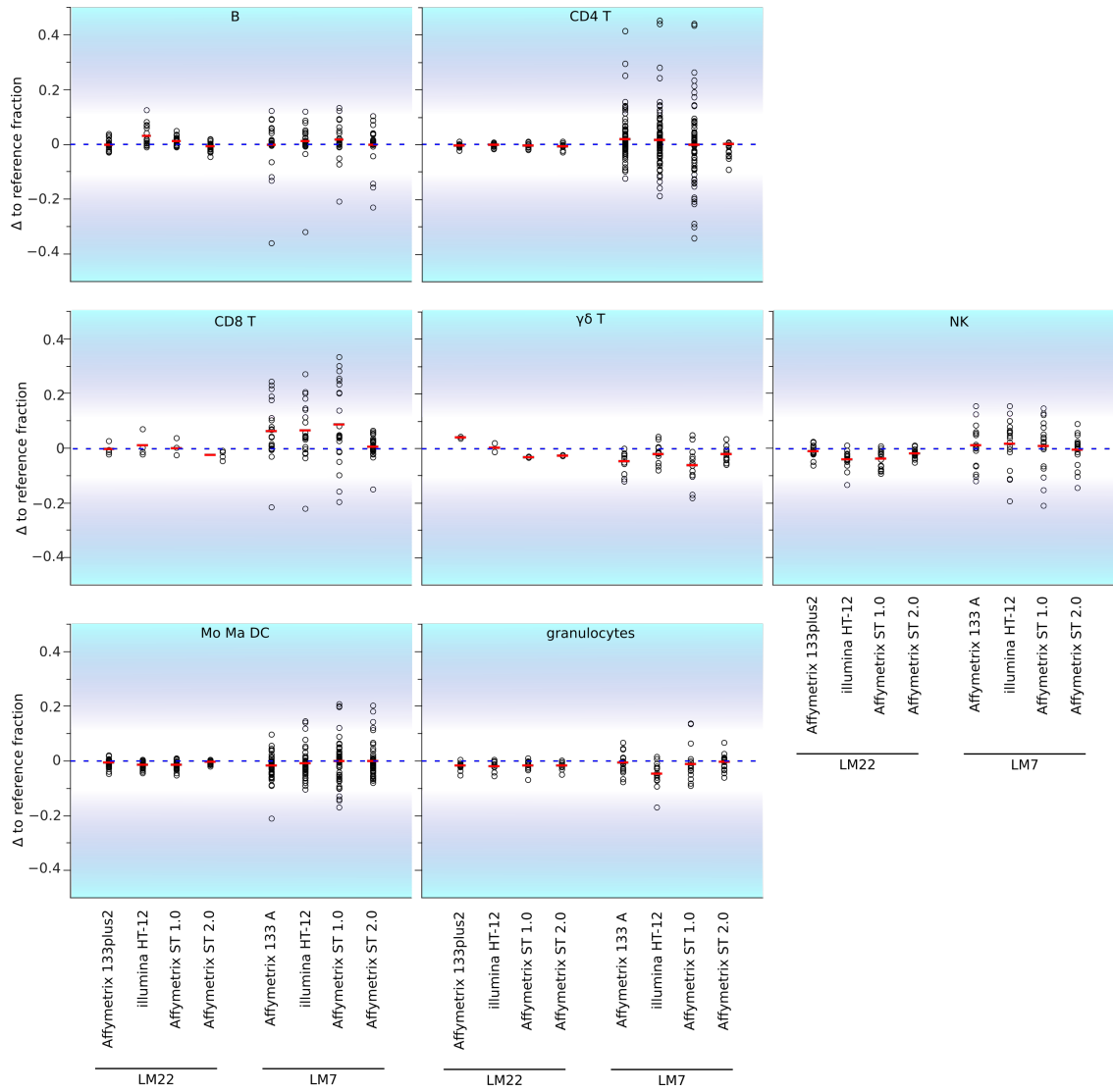
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## **Supplemental Figures**



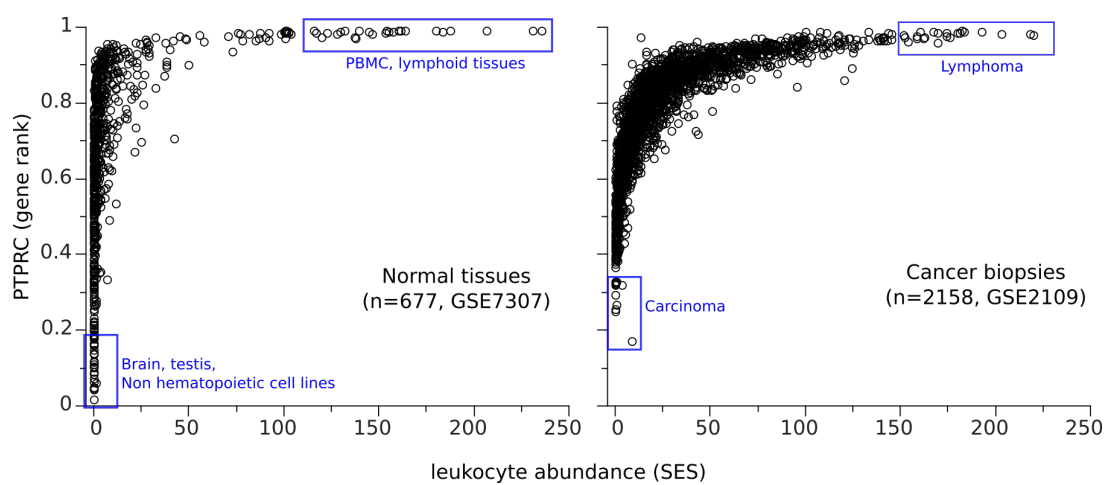
**Supplemental Figure 1: Gene coverage of LM7 and LM22 by various microarray platforms**

LM7 and LM22 are represented as genes (lines), cell subsets (columns) and expression levels (shown by a color gradient scale, blue: expression levels < 200, yellow : 200-1000, red: >1000). Black lines: missing genes. Of the 375 genes from LM7, the HGU133A platform lacks 117 genes, Illumina HT-12 lacks 50 genes, Affymetrix ST1.0 lacks 95 genes and Affymetrix ST2.0 lacks 85 genes. Of the 547 genes from LM22, the HGU133 Plus2.0 platform lacks 82 genes, Illumina HT-12 lacks 43 genes, Affymetrix ST1.0 lacks 111 genes and Affymetrix ST2.0 lacks 71 genes.



**Supplemental Figure 2: Deviation introduced by different microarray platforms**

Cell subsets were enumerated with CIBERSORT-LM7 and LM22 in all reference samples (Supplemental Table 1 for LM7, listed in<sup>1</sup> for LM22) and these reference rates were compared to those produced when removing the LM7 and LM22 genes missing from the other platforms. Shown are deviations from results with the learning platform (Affymetrix HGU-133A for LM22, Affymetrix HGU133Plus 2.0 for LM7) by the specified platform, for each LM7 cell subset. Red bar: group means. Note the figure does not reflect the platform quality but stability of its results across platforms.



**Supplemental Figure 3: Metrics for leukocyte abundance in samples**

The CIBERSORT reference matrix LM7 was used to define 7 cell subset-specific gene sets by filtering out those LM7 genes which expression was  $<1000$  in the respective cell subset. This produced 7 gene sets: B; T CD4<sup>+</sup>; T CD8<sup>+</sup>; T  $\gamma\delta$ ; NK; Mo-Ma-DC Granulocytes. For each sample from the specified data sets, the sample enrichment scores (SES) of these 7 gene sets were computed as described elsewhere.<sup>2</sup> These 7 SES were adjusted to equivalent weights for each cell subset and summed. In parallel, each transcriptome from the specified data sets was rank-ordered (increasing order of expression level) and each gene rank was divided by the total number of ranks. CD45 is the leucocyte-defining marker expressed by all LM7 lineages, hence the rank of the CD45-encoding gene PTPRC was a surrogate gene marker of leukocyte abundance. Each sample from the specified dataset was analyzed for leukocyte abundance (based on SES) and for CD45 gene expression levels.

## **Supplemental Tables**

**CIBERSORT-LM7 fraction (%)**

	B cells	T CD4	T CD8	T $\gamma\delta$	NK	MoMaDC	granulocytes	
Sample annotation	B cells	88,97%	4,51%	0,56%	3,07%	0,69%	0,84%	1,37%
	T CD4	0,85%	84,06%	7,01%	2,74%	3,83%	0,54%	0,97%
	T CD8	0,90%	13,56%	77,22%	3,04%	3,36%	0,60%	1,32%
	T $\gamma\delta$	0,49%	1,20%	2,73%	91,69%	2,39%	1,19%	0,32%
	NK	0,57%	3,00%	7,53%	4,59%	80,38%	2,68%	1,25%
	MoMaDC	5,31%	0,24%	1,32%	1,19%	0,55%	86,98%	4,41%
	granulocytes	0,65%	0,70%	0,38%	1,50%	0,37%	8,72%	87,68%

**CIBERSORT-LM22 fraction (%)**

	B cells	T CD4	T CD8	T $\gamma\delta$	NK	MoMaDC	granulocytes	
Sample annotation	B cells	92,38%	2,86%	1,08%	0,75%	1,04%	1,45%	0,44%
	T CD4	1,25%	81,84%	0,26%	8,23%	5,44%	1,14%	1,84%
	T CD8	0,89%	32,51%	46,10%	12,67%	4,49%	1,32%	2,03%
	T $\gamma\delta$	2,60%	31,10%	2,53%	31,60%	23,52%	3,12%	5,53%
	NK	1,44%	14,75%	3,76%	4,66%	68,70%	2,14%	4,55%
	MoMaDC	4,42%	5,68%	0,37%	1,02%	2,04%	80,87%	5,59%
	granulocytes	0,98%	3,72%	0,23%	0,93%	2,90%	2,98%	88,27%

**Supplemental table 1: Comparison of LM7 and LM22 for leucocyte composition of reference samples**

The (n=265) reference samples used for CIBERSORT learning were analyzed by CIBERSORT-LM7 and CIBERSORT-LM22. Table shows their respective results for each lineage according to the sample annotation specified in each GSM file. The fractions were normalized to 100% of total leucocyte content. The rates of correct identifications of most lineages are significantly improved with CIBERSORT-LM7.

GSE number	Number of samples	Cell type	First author	reference
GSE11430	10	monocytes, macrophages	Maouche S	3
GSE12195	10	B cells	Compagno M	4
GSE13738	8	CD4 T cells	Bangs SC	5
GSE14879	36	NK, CD8, CD4 T cells	Eckerle S	6
GSE22282	3	DC	Bosco MC	7
GSE27291	12	$\gamma\delta$ T cells	Pont F	8
GSE28490	32	DC, eosinophils, monocytes, neutrophils, CD8 T cells	Allantaz F	9
GSE28491	18	eosinophils, monocytes, neutrophils, CD8 T cells	Allantaz F	9
GSE28726	15	CD4 T cells	Constantinides MG	10
GSE30536	11	macrophages	Sirois M	11
GSE42088	3	DC	Favila MA	12
GSE43769	12	CD4 T cells	Cousins DJ	
GSE45535	4	B cells, monocytes	Morehouse CA	
GSE56314	12	B cells	Dybkr K	13
GSE56464	8	B cells	Mei HE	14
GSE61697	24	CD4 T cells	Takeshita M	15
GSE65010	12	CD4 T cells	Walter GJ	16
GSE66384	7	CD4 T cells	Amé-Thomas P	17
GSE71566	6	CD4 T cells	Kanduri K	18
GSE72642	7	monocytes, NK, CD8 T cells	Du X	19
GSE8059	3	NK, CD8 T cells	Dybkaer K	20
GSE83920	3	mast cells	Leerkes M	
NA	9	NK	Poupot M	unpublished data from our lab

**Supplemental table 2: List of reference studies**

Gene	B cells	T CD4	T CD8	T $\gamma\delta$	NK	MoMaDC	granulocytes
ABCB1	212.07	37.14	64.54	516.28	190.63	27.32	19.20
ABCB4	212.15	37.15	64.56	516.82	190.70	27.32	19.21
ADRB2	107.31	26.83	129.07	614.81	975.45	73.89	75.59
AIM2	725.77	126.46	35.17	105.86	39.67	77.17	20.27
ALOX5	720.88	18.64	97.85	14.94	43.99	1828.00	3686.10
ANKRD55	10.89	105.60	17.56	15.25	13.94	16.76	34.61
ANPEP	15.88	14.65	15.43	12.05	18.80	429.67	419.37
APOBEC3A	9.09	10.49	11.82	10.79	15.53	449.15	440.20
AQP9	18.78	17.86	24.33	23.48	29.13	671.83	875.33
ARRDC4	17.10	19.54	25.35	16.09	51.28	347.85	254.19
AYTL1	14.96	20.88	23.82	27.34	23.69	102.93	324.43
B3GNT5	9.22	16.43	13.55	17.66	14.40	190.69	803.19
BANK1	3060.15	26.23	25.01	36.09	32.74	46.49	36.16
BCL11A	1439.09	38.74	61.85	43.51	51.98	165.30	173.86
BCL11B	16.31	1398.82	1789.13	1336.53	650.40	24.67	52.69
BCL2A1	398.71	136.47	138.36	88.46	215.86	1276.95	6703.52
BCNP1	1146.03	29.02	50.98	28.22	25.80	29.83	53.87
BCOR	247.07	135.08	199.00	758.20	178.57	67.94	56.17
BLNK	436.36	15.17	30.19	15.06	20.03	27.12	20.38
BPGM	65.21	70.04	28.74	372.19	353.71	73.99	44.75
BRDG1	1049.45	40.13	16.68	19.19	159.65	19.97	49.67
BTBD11	12.49	89.63	124.57	392.85	26.08	45.08	44.56
BTBD5	220.48	167.44	74.41	1025.77	154.30	110.28	59.88
BTK	1208.27	23.19	43.34	29.31	44.48	320.10	236.49
C16ORF30	29.90	277.29	587.98	146.72	125.04	32.58	35.00
C5AR1	8.27	9.98	9.20	8.23	13.34	324.93	476.22
C5ORF29	740.73	7.40	8.33	7.77	9.02	199.50	338.20
C6ORF105	16.04	219.24	21.29	10.94	13.21	16.02	14.22
C6ORF190	14.52	195.76	214.06	189.44	23.89	13.50	52.86
CACNA2D3	9.02	8.64	8.96	8.60	9.59	208.66	8.08
CAMK4	23.86	111.90	60.75	44.69	21.23	19.28	27.85
CAPG	390.67	93.02	69.40	48.54	115.91	1187.96	240.55
CCDC64	80.93	323.39	395.60	145.44	128.85	47.19	56.49
CCL4	65.42	54.61	708.83	2306.39	6074.61	92.97	2394.10
CCL5	52.85	311.33	4397.70	4043.25	4397.70	116.11	95.79
CCR3	21.05	23.13	28.08	24.41	25.60	21.72	877.58
CCR5	110.81	153.11	411.77	3349.60	580.22	648.82	110.25
CCR6	1142.65	24.75	26.64	31.47	17.60	9.44	8.58
CCR7	251.43	765.02	1299.25	444.04	189.79	31.51	17.88
CD14	22.53	19.65	16.01	17.09	20.46	2567.76	222.95
CD160	16.25	14.72	187.37	83.31	414.27	14.17	11.11
CD163	23.34	23.79	32.66	23.86	25.36	1094.75	56.80
CD180	804.01	54.11	67.07	52.24	70.05	202.43	151.99
CD19	762.42	12.77	16.58	13.60	14.66	18.54	12.91
CD1C	1654.02	51.01	61.99	57.41	55.53	320.09	69.00
CD2	24.14	2083.27	2029.52	1670.19	1567.94	41.54	25.24
CD200	93.47	67.63	17.74	20.52	16.21	12.05	13.73
CD22	1316.25	23.53	29.44	25.73	26.14	34.36	20.22
CD226	24.12	151.76	23.73	126.56	370.23	15.30	10.32
CD244	37.56	31.78	164.89	92.01	847.30	151.05	56.77
CD247	36.71	870.48	1632.35	1906.60	2540.90	53.92	52.23
CD28	9.42	665.68	386.24	200.79	12.91	11.76	10.33
CD300A	136.60	51.44	344.61	519.86	2283.85	1153.54	1636.99
CD300LF	12.78	15.25	20.11	21.78	31.65	985.88	748.99
CD3D	104.30	3769.34	4327.44	2500.19	380.90	93.64	73.30
CD3E	34.23	438.19	133.95	233.17	84.25	34.18	42.51
CD3G	31.39	1085.63	1225.53	577.62	89.93	37.93	28.18
CD40LG	45.71	277.66	63.68	71.50	53.55	44.75	98.34
CD5	49.95	534.41	329.61	388.13	42.24	44.68	62.56
CD6	184.55	1435.53	2341.06	2011.64	331.01	125.53	151.14
CD69	948.70	1461.99	1149.83	2950.16	1392.53	17.36	540.07
CD72	666.89	36.19	25.11	26.41	62.96	43.88	16.21
CD79A	4206.50	73.16	96.00	98.43	65.70	83.49	127.19
CD79B	1206.08	91.09	74.50	38.97	87.81	47.77	35.82
CD8A	21.51	23.20	3810.17	216.22	561.28	31.41	23.20
CD8B	38.48	52.25	1512.13	55.90	74.82	46.13	70.51

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Gene	B cells	T CD4	T CD8	T $\gamma\delta$	NK	MoMaDC	granulocytes
CD93	13.67	19.01	24.09	25.35	94.70	2082.88	207.23
CD96	65.83	401.97	784.37	272.69	808.16	20.12	26.32
CDR2	47.27	549.95	591.81	361.37	137.80	105.41	30.61
CHRM3	10.69	138.96	127.05	21.98	51.28	10.73	14.05
CLC	22.43	16.28	29.03	15.29	35.03	23.77	718.28
CLEC12A	11.57	10.15	14.36	10.69	22.53	339.54	599.31
CLEC2D	575.83	857.36	361.77	263.14	325.39	56.62	39.84
CLEC4A	76.32	37.19	32.21	62.70	33.65	1707.31	107.65
CLEC7A	14.71	22.60	34.71	24.72	32.28	2620.69	605.89
CLU1	130.32	9.96	10.71	8.89	9.33	8.94	9.15
CMTM2	9.97	13.30	14.29	13.75	13.25	14.67	303.27
CPNE5	1464.85	27.66	40.20	46.43	40.09	30.42	28.93
CPNE8	12.52	28.70	12.12	22.20	31.89	310.91	11.47
CPVL	14.85	12.30	17.60	35.71	16.06	2122.84	10.86
CR1	740.58	32.90	42.00	26.26	29.04	43.09	248.23
CR2	511.08	10.92	32.95	14.48	11.18	11.55	20.72
CREM	83.28	214.57	144.63	4115.03	659.42	129.84	126.21
CRTAM	9.81	23.63	907.39	94.90	461.92	171.21	10.28
CSF2RB	411.22	65.01	49.75	80.52	177.18	1349.78	4327.44
CST7	29.88	382.43	1844.11	1220.08	3210.07	60.31	669.86
CTLA4	13.19	1117.57	63.89	102.76	14.34	11.35	10.26
CTSW	64.02	146.84	358.48	743.72	4702.82	62.09	87.65
CXCR3	84.85	139.08	298.66	1314.40	135.49	39.77	34.22
CXCR6	43.76	162.29	368.84	1296.69	75.63	27.26	35.35
CYBB	1093.45	24.44	31.00	30.29	38.88	2113.04	478.93
DAPK1	28.45	22.26	58.46	43.68	138.02	1121.41	900.14
DEFA1	27.39	21.69	64.45	15.36	569.07	38.51	918.26
DEFA3	27.39	21.68	64.43	15.36	568.28	38.51	915.84
DENND2D	530.01	877.81	2130.27	413.80	1207.26	210.75	49.42
DMXL2	13.69	26.35	18.02	19.63	51.69	1494.51	549.67
DOK3	1204.76	20.91	34.10	21.83	35.80	764.56	1170.69
DSCR1L2	16.56	43.78	21.43	18.38	12.26	16.41	10.24
EAF2	996.46	64.97	50.24	35.24	71.38	290.06	197.98
EDG8	25.29	26.07	151.54	1306.74	1532.62	23.61	22.74
ELOVL6	11.61	19.94	12.20	18.90	366.78	12.41	9.74
EMILIN2	33.20	68.86	67.03	138.45	112.88	1578.29	62.02
EMR2	10.50	11.73	13.22	11.28	15.59	285.80	1217.33
EMR3	25.99	18.31	18.52	16.87	16.95	47.53	604.45
ENPP5	6.29	5.86	8.00	6.40	92.45	5.99	5.69
EOMES	18.47	69.97	1201.29	790.67	1869.33	28.16	25.58
F13A1	20.34	22.49	41.05	42.32	30.86	996.80	69.25
FAM125B	44.93	69.51	384.48	499.81	93.42	159.92	74.73
FAM30A	578.51	45.94	63.40	35.15	54.96	45.13	73.66
FAM46C	1104.98	664.63	316.51	5751.26	563.33	27.88	177.15
FASLG	21.91	29.88	53.01	152.56	667.82	19.94	20.41
FBP1	37.01	42.26	71.76	39.53	83.74	552.81	71.98
FCER1G	29.32	37.70	102.39	53.17	2405.93	3421.76	1252.18
FCGBP	39.70	60.81	361.14	146.22	133.81	34.75	34.49
FCGR2A	55.75	15.37	18.76	17.06	36.98	822.90	1332.45
FCGR2B	568.20	16.61	19.17	23.13	35.64	129.30	240.90
FCGR3A	16.32	11.47	13.41	32.31	1827.14	87.63	187.67
FCGR3B	16.33	11.47	13.42	32.32	1841.93	87.65	187.76
FCN1	23.65	21.30	37.62	21.54	27.93	1707.31	127.35
FCRL1	508.97	12.48	18.45	10.30	12.64	12.22	34.85
FCRL2	712.80	27.17	57.38	22.51	31.05	26.62	313.56
FCRL3	1034.58	80.07	1201.17	115.95	1763.79	37.36	53.32
FCRL5	1284.81	53.35	90.76	52.11	54.41	52.51	99.73
FCRLA	1174.39	30.30	36.52	51.11	37.46	57.58	39.17
FFAR2	14.67	16.06	14.92	17.61	16.04	21.70	1056.95
FGD4	19.59	10.22	11.73	11.20	15.73	334.05	325.40
FGF7	8.04	9.50	10.32	9.16	9.25	9.00	308.67
FGL2	84.17	41.57	26.18	26.84	132.34	2355.58	1209.10
FGR	163.23	43.41	253.45	97.93	1327.95	2907.33	2186.79
FLJ22662	25.02	22.45	32.20	24.70	21.71	3484.77	291.63
FLJ22814	249.89	13.25	16.22	11.13	14.71	12.77	10.36

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Gene	B cells	T CD4	T CD8	T $\gamma\delta$	NK	MoMaDC	granulocytes
FLJ25967	417.31	420.38	522.79	2367.74	207.13	70.74	245.02
FLJ42562	219.91	17.19	14.32	30.78	20.46	14.65	10.43
FLJ44635	9.11	14.84	18.00	18.44	58.26	71.59	487.35
FPR1	34.69	40.60	62.93	54.20	60.28	646.19	4761.88
GALNAC4S-6ST	650.91	18.44	17.96	20.74	27.59	1296.69	1537.10
GCA	478.00	82.89	26.89	59.51	58.00	746.75	2499.17
GGTA1	20.56	19.06	31.26	23.44	23.49	541.12	32.31
GIMAP1	14.44	629.39	1217.01	551.16	498.77	171.09	7.29
GIMAP6	15.86	626.71	1279.59	459.68	1856.69	125.14	27.37
GIMAP7	9.53	1363.89	2092.95	692.48	1458.26	186.45	7.01
GNG2	271.03	936.07	1346.76	4622.74	2969.15	791.71	1138.40
GNLY	38.13	54.86	955.91	3521.14	9010.54	43.62	30.83
GPR109B	11.32	15.36	16.15	12.63	33.34	60.25	371.34
GPR132	82.33	66.09	64.04	467.80	62.36	57.99	120.68
GPR171	11.44	571.33	1397.55	2370.45	710.73	19.26	44.77
GPR97	42.55	36.12	50.40	47.64	100.77	38.78	716.13
GZMA	16.29	239.75	1925.89	880.92	6074.61	21.50	11.41
GZMB	18.00	29.47	1071.31	4764.47	7088.56	38.11	15.82
GZMH	22.08	36.81	2588.25	710.44	2378.04	33.20	19.21
GZMK	21.41	111.25	1936.64	1797.89	301.92	26.83	22.99
HCK	88.94	26.29	22.53	27.35	45.93	1803.65	1811.00
HIP1	23.60	21.47	23.22	25.59	69.63	81.78	332.78
HLA-DMB	1337.29	61.73	202.73	126.55	265.98	1626.75	141.38
HLA-DOB	2102.11	44.61	61.29	67.78	76.18	58.21	65.13
HLA-DQA1	5914.52	35.30	108.02	86.27	330.61	2038.15	14.50
HLA-DQA2	5636.81	35.30	107.99	86.25	330.41	2020.08	14.50
HLA-DRB4	459.17	40.29	55.72	45.73	45.58	2511.40	60.49
ICOS	25.16	741.28	183.59	390.37	62.85	21.86	22.96
IFI30	2534.95	111.47	191.96	234.55	280.07	8219.82	2149.04
IFNG	23.01	58.10	93.46	317.34	668.84	16.90	15.69
IGHD	1163.73	43.18	50.99	36.87	46.30	41.32	80.54
IGSF6	11.78	13.39	12.93	9.65	16.03	1611.53	198.50
IL18RAP	27.29	117.83	265.79	2102.11	3157.17	36.93	773.46
IL2RA	30.66	250.06	22.11	104.14	89.08	18.49	23.14
IL2RB	93.23	1770.01	1769.51	2382.87	4155.82	55.33	119.14
IL32	36.53	1369.03	207.55	291.98	1913.51	29.86	20.81
IL7R	43.20	3014.31	2973.84	2970.72	325.39	103.17	77.57
IL8RB	11.88	11.19	11.83	12.19	147.48	36.19	585.41
ITGAM	59.54	61.86	191.34	670.15	1458.26	2259.00	1190.37
ITGAX	39.46	32.15	32.28	32.75	128.34	472.94	963.59
ITK	14.44	1984.40	1849.33	1331.07	1814.08	26.27	16.20
KCNE3	17.74	20.57	37.76	21.10	31.35	1227.11	940.09
KCNJ2	8.87	10.05	13.65	12.04	13.62	103.44	169.47
KIAA0125	686.06	21.95	30.82	20.17	35.02	25.97	36.04
KIAA0746	2977.44	400.43	290.72	537.63	349.16	406.08	41.39
KIAA0748	149.81	421.68	154.67	93.00	168.88	37.58	31.25
KIAA1212	39.66	28.89	23.96	12.12	19.01	864.48	36.11
KIAA1324	32.99	133.03	64.18	60.32	43.79	26.53	89.73
KIAA1913	22.04	33.52	16.46	180.56	39.43	10.98	9.46
KIR2DL1	44.63	46.21	87.03	93.66	590.20	42.12	73.50
KIR2DL2	37.57	31.43	62.13	98.56	620.09	32.18	45.04
KIR2DL4	31.37	34.31	45.13	60.07	432.00	35.15	61.58
KIR2DL5A	35.22	27.13	48.89	67.95	510.62	27.41	36.16
KIR2DS2	14.04	12.09	27.68	61.68	539.73	10.68	13.98
KIR2DS5	50.07	46.53	98.66	101.23	766.12	45.76	85.62
KIR3DL1	29.11	28.68	43.48	135.14	678.38	24.29	22.47
KIR3DL2	32.23	33.66	37.35	97.65	510.62	30.14	31.98
KIR3DL3	27.99	25.40	39.79	71.00	506.16	26.54	39.80
KIT	19.81	21.22	44.39	55.66	260.63	23.65	373.76
KLRB1	24.11	354.78	1856.26	2590.73	2969.15	46.27	26.65
KLRC1	9.27	8.90	108.84	2941.33	1814.08	9.12	14.32
KLRC2	9.27	8.89	108.81	2898.76	1800.90	9.12	14.32
KLRC3	7.35	7.62	54.36	102.02	758.59	8.43	8.61
KLRC4	264.69	39.08	1223.75	565.08	1959.78	26.64	47.26
KLRD1	22.16	26.94	409.83	518.18	2481.89	26.19	27.72

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Gene	B cells	T CD4	T CD8	T $\gamma\delta$	NK	MoMaDC	granulocytes
KLRF1	13.88	14.69	61.28	138.26	2775.54	30.57	11.82
KLRK1	80.44	46.04	2931.04	1775.10	3673.52	51.82	60.57
KMO	390.29	14.79	23.22	18.40	21.19	254.11	39.16
KSP37	15.52	20.18	827.94	1203.46	2432.84	19.47	11.22
LAT	92.69	2167.56	1731.45	1545.47	730.06	140.90	46.58
LCK	174.21	3060.72	3851.44	1809.37	2083.27	32.95	34.72
LEF1	18.48	1249.05	1904.68	155.33	150.88	38.44	171.47
LENG10	9.85	125.61	151.09	712.23	76.46	21.50	60.62
LEPREL1	31.36	47.33	56.34	922.39	48.14	66.85	67.68
LOC144571	13.09	29.75	270.02	147.54	167.20	24.92	28.71
LOC202134	19.74	50.14	379.81	23.11	20.62	23.46	26.00
LOC283027	8.69	8.58	10.76	8.81	10.47	9.44	635.97
LOC284262	351.34	14.73	34.52	72.77	191.87	35.85	16.34
LOC285382	7.35	7.24	7.92	7.06	7.58	8.27	120.20
LOC339562	738.59	68.55	139.92	77.22	70.97	77.94	231.90
LOC360030	7.09	21.45	9.04	94.91	7.34	11.74	11.95
LOC391427	789.16	34.18	58.17	33.57	46.80	39.73	95.65
LOC400509	115.49	11.01	9.75	18.10	15.57	12.41	8.05
LOC401131	10.63	11.78	16.37	13.49	13.20	13.51	297.18
LOC439949	30.80	1012.09	894.57	290.16	909.69	24.18	22.72
LOC440607	14.02	15.51	17.02	13.30	19.03	615.67	145.97
LOC642083	13.04	186.58	2496.90	5323.30	2329.29	27.83	34.61
LOC642103	12.25	10.18	11.31	8.89	37.23	16.80	756.22
LOC643675	31.93	56.78	2006.72	36.07	82.65	58.08	767.68
LOC643930	96.42	49.09	158.70	1860.11	2103.82	338.57	777.27
LOC645022	77.77	112.54	359.66	312.36	39.63	27.57	22.12
LOC647134	417.88	48.40	67.86	44.21	62.43	52.87	63.06
LOC647353	1855.63	5131.25	4197.05	1601.81	2887.52	41.48	11.03
LOC647460	107.49	13.24	15.61	11.71	15.14	12.67	11.85
LOC649805	163.68	22.88	25.38	17.94	24.69	18.71	16.76
LOC650946	6222.95	35.36	108.05	86.29	330.81	2056.15	14.54
LOC652106	418.20	48.42	67.88	44.22	62.44	52.89	63.08
LOC652494	693.11	76.04	128.10	50.74	71.23	70.58	167.18
LOC652651	692.02	76.02	128.06	50.73	71.21	70.57	167.12
LOC652745	715.39	24.00	28.50	21.23	23.85	24.94	34.06
LOC652758	14.02	15.51	17.02	13.30	19.04	616.58	146.02
LOC653117	12.21	17.55	33.39	13.68	14.50	15.88	904.59
LOC653506	44.43	55.22	91.06	1216.86	281.87	351.77	560.37
LOC653600	27.38	21.68	64.42	15.35	567.59	38.50	913.60
LOC653725	110.78	153.06	411.42	3289.81	579.51	647.88	110.22
LOC653757	31.36	34.31	45.12	60.05	431.66	35.15	61.55
LOC90925	1385.84	24.92	22.69	20.94	27.40	22.01	22.21
LPAAT-THETA	13.59	44.47	26.81	163.85	22.50	642.62	357.10
LRRK2	152.33	10.18	11.98	9.67	11.93	306.86	232.53
LRRN3	18.84	75.83	159.74	34.40	26.72	18.60	16.99
LY86	1195.48	37.26	64.89	53.41	49.45	1885.94	85.14
LY9	341.84	309.87	965.53	218.83	135.24	111.68	48.00
LY96	572.15	93.54	23.18	10.05	16.39	1188.35	1340.33
MAG	1115.37	35.00	51.74	38.40	44.57	49.92	73.29
MANSC1	11.10	10.79	9.17	7.25	7.74	20.68	291.35
MARCH1	172.25	7.96	9.07	8.33	8.26	345.17	61.73
MEFV	14.99	27.80	25.41	21.60	17.88	34.72	689.77
METRNL	44.44	55.24	91.09	1221.95	282.00	351.99	560.98
MGAM	12.25	10.18	11.30	8.89	37.23	16.80	754.75
MGC24103	9.12	9.00	19.73	9.84	131.64	9.86	17.04
MGC61571	100.45	143.99	434.38	173.76	1303.06	189.78	9.81
MNDA	92.31	11.06	17.98	12.52	15.95	3132.15	2294.15
MPEG1	1008.43	14.28	15.26	20.08	26.04	3851.44	188.22
MS4A1	5796.90	19.12	32.78	21.06	27.03	21.02	40.73
MS4A6A	67.23	31.09	38.20	51.86	35.28	1952.48	210.45
MS4A7	283.94	25.81	28.61	39.26	46.37	590.17	42.68
MTAC2D1	21.03	412.27	290.20	579.26	77.52	16.08	18.13
MXD1	101.89	128.64	104.32	326.27	250.98	473.18	3293.00
MYBL1	12.84	67.57	438.57	309.81	3210.07	14.36	14.83
NAPSB	654.45	19.72	21.80	32.42	19.16	667.29	14.60

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Gene	B cells	T CD4	T CD8	T $\gamma\delta$	NK	MoMaDC	granulocytes
NCF1	618.29	57.47	61.04	40.25	46.49	628.89	2027.10
NCF2	63.11	36.59	29.60	13.23	40.17	3322.76	4542.67
NDFIP2	18.46	149.30	42.95	465.47	403.11	10.77	93.26
NKG7	36.32	63.59	1478.18	2606.00	5519.19	79.84	29.03
NOD3	481.56	868.46	1576.16	1511.26	1751.13	23.70	22.07
NPL	19.97	33.05	40.36	52.35	49.94	548.01	421.18
NR4A3	36.33	33.17	28.77	1132.07	68.18	66.13	88.99
OASL	40.89	64.85	116.44	565.54	255.07	81.70	247.47
P2RY13	10.91	10.22	12.21	9.90	12.22	122.56	393.99
P2RY14	15.36	19.23	15.38	94.83	42.38	24.00	523.59
PACAP	339.04	49.95	75.53	43.09	72.97	45.15	58.04
PADI4	10.91	13.36	38.96	13.75	14.37	37.38	692.14
PASK	131.65	349.83	1119.41	155.52	80.75	44.43	56.72
PBX4	45.06	298.30	232.81	501.13	75.42	28.16	20.50
PCSK5	16.21	78.22	448.43	17.02	198.98	161.63	36.10
PDE4B	871.34	618.29	618.81	3231.54	295.90	233.78	1029.84
PDE4D	51.02	488.27	326.19	1126.19	564.79	43.65	169.85
PDGFD	36.34	16.95	101.45	110.03	410.37	17.30	29.59
PGAP1	11.00	124.01	72.19	287.27	44.61	24.30	37.51
PLA2G7	8.25	8.66	9.05	8.24	10.30	183.62	8.08
PLAUR	46.41	42.72	46.03	74.44	54.45	600.25	1253.57
PLCG2	2354.68	42.47	183.87	144.54	687.01	613.49	591.31
PLCXD2	42.12	98.87	168.14	423.88	249.32	13.25	12.17
PLEKHK1	5.94	23.92	7.34	46.29	7.13	6.11	5.85
PLXDC2	10.96	10.11	10.76	9.32	22.16	321.22	81.46
PNOC	472.02	20.64	21.38	17.85	23.23	29.05	17.18
POU2AF1	5115.30	164.40	88.42	11.83	22.39	18.52	18.04
PRF1	47.41	517.35	2542.05	7146.19	9010.54	85.24	92.48
PRKCH	33.03	2588.25	2948.14	3108.66	3014.31	154.99	75.33
PRKCQ	18.95	538.09	473.93	679.22	984.36	33.72	42.16
PRKX	338.05	527.97	461.64	2378.04	830.36	340.18	184.85
PRKY	338.25	528.54	462.10	2405.93	832.10	340.38	184.91
PRO1268	47.13	50.52	48.46	39.07	34.55	48.07	1369.92
PROK2	7.39	9.69	11.76	23.00	8.53	11.70	256.77
PRSS33	41.21	35.63	38.39	44.43	37.76	43.74	203.04
PTGDR	13.29	14.05	41.26	17.78	331.21	13.40	59.06
PTGS2	10.49	10.53	9.28	10.33	13.94	49.45	1217.23
PYGL	14.75	13.43	16.29	12.68	20.69	248.17	632.97
PYHIN1	18.31	192.19	261.25	225.73	1138.35	18.25	10.02
QPCT	77.49	13.11	13.15	71.23	14.49	524.43	238.06
RAB27B	16.47	28.55	34.75	106.07	476.48	30.40	22.11
RAB30	788.45	85.04	53.48	134.95	49.79	40.36	87.92
RALGPS2	1701.79	36.00	69.64	58.76	44.34	86.12	300.83
RASGEF1A	11.31	28.63	163.88	49.36	160.74	53.24	39.05
RASGRP1	393.64	1663.83	1595.32	1350.94	1577.93	62.27	25.05
RASGRP3	327.37	27.24	17.23	60.98	21.29	27.03	12.25
RGS13	64.35	7.06	7.15	9.71	7.74	6.67	6.37
RGS18	7.09	9.86	13.22	13.33	25.46	475.12	1092.06
RNASE6	1121.34	23.47	23.90	17.85	36.03	2445.14	327.09
RORA	26.63	489.00	669.37	2624.65	468.89	29.67	26.12
SI00A12	10.45	11.51	19.76	10.91	11.59	153.83	469.27
SAMD3	18.99	121.52	355.44	331.76	1800.90	16.69	16.57
SART2	170.38	18.60	20.57	82.84	26.88	690.95	123.69
SCML4	41.41	114.73	514.49	120.70	78.57	22.30	21.99
SH2D1B	12.63	14.97	21.90	49.73	2604.32	21.43	36.95
SIGLEC10	600.98	64.16	88.39	35.15	53.32	582.59	1350.89
SIRPG	20.78	287.61	289.99	28.46	18.54	17.46	16.02
SKAP1	109.08	606.00	530.15	222.36	701.97	35.23	35.98
SLAMF1	550.77	301.77	103.18	263.12	21.21	20.57	18.22
SLAMF7	253.12	21.01	347.49	647.91	2237.20	886.00	24.67
SLC15A2	439.83	24.87	19.70	19.71	23.73	60.61	30.02
SLC7A7	183.85	38.11	45.66	30.20	56.04	2703.18	98.66
SLCO4C1	12.04	15.36	14.63	48.14	426.22	33.69	110.87
SOCS1	111.11	114.86	97.73	758.80	206.88	27.46	45.64
SPIB	265.50	29.75	43.31	37.35	38.66	37.41	36.81

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Gene	B cells	T CD4	T CD8	T $\gamma\delta$	NK	MoMaDC	granulocytes
SPINLW1	10.03	10.28	10.49	8.59	9.22	8.75	267.75
ST3GAL6	13.38	8.94	8.94	9.03	9.02	166.10	166.11
STAT4	39.56	558.90	1102.95	1721.77	1856.69	74.47	58.45
STYK1	7.44	8.34	23.01	46.52	97.96	7.70	7.73
SYK	1263.83	35.67	68.61	42.59	502.43	1993.03	697.56
SYTL2	18.68	142.53	564.72	1117.84	869.19	39.61	114.95
SYTL3	73.28	335.97	442.08	1776.01	679.48	216.47	244.23
TARP	13.04	186.52	2469.67	5131.25	2306.52	27.83	34.60
TBC1D4	18.39	662.57	510.91	35.77	32.93	174.37	46.02
TBC1D8	30.81	36.03	30.10	38.78	43.53	555.81	91.97
TCL1A	413.03	31.45	27.36	37.74	33.29	37.86	23.49
TFEC	11.03	6.13	7.25	9.44	8.67	414.01	8.14
TLR10	215.83	14.86	21.47	15.51	16.01	27.12	40.08
TLR8	10.82	9.89	9.56	8.74	13.78	1039.76	203.20
TM6SF1	11.30	17.36	16.13	35.38	399.18	356.29	494.32
TMEM154	491.02	186.97	146.41	125.53	71.81	646.27	3135.11
TNFAIP2	32.84	27.68	43.49	32.63	54.03	495.27	938.69
TNFRSF17	395.81	10.52	11.14	10.71	10.94	11.29	9.68
TNFSF12-TNFSF13	85.59	46.45	70.62	41.03	69.68	1183.32	168.74
TNFSF13	85.56	46.44	70.61	41.02	69.67	1178.65	168.61
TNFSF13B	51.93	79.06	83.67	27.90	177.00	2356.22	543.97
TRA@	501.10	2149.04	1000.88	224.92	202.86	96.14	137.21
TRAC	337.54	2381.98	2317.90	586.75	322.34	48.09	30.17
TRAT1	9.99	833.96	268.75	278.16	21.05	11.96	11.31
TRAV20	515.87	3484.77	1095.28	189.23	163.58	88.17	103.23
TRBC1	546.61	5227.27	5131.25	2415.60	3263.25	68.57	48.56
TRBV19	545.97	5019.27	4907.29	2389.05	3210.07	68.55	48.55
TRBV21-1	1883.48	5519.19	4475.27	1621.90	2969.15	41.50	11.04
TRBV3-1	1870.36	5323.30	4324.82	1611.40	2927.13	41.49	11.03
TRBV5-4	1898.76	5754.42	4643.54	1631.57	3014.31	41.51	11.04
TRD@	26.59	55.53	143.02	7146.19	6371.28	30.51	18.69
TRDV2	515.27	3414.55	1091.46	189.15	163.52	88.15	103.20
TRGC2	13.05	186.64	2526.41	5519.19	2354.68	27.84	34.61
TRGV2	13.05	186.80	2588.25	6074.61	2405.93	27.85	34.63
TRGV9	13.05	186.74	2556.55	5754.42	2378.04	27.84	34.62
TSHZ2	33.03	100.56	18.84	15.88	15.11	15.27	16.75
TXK	13.54	158.68	174.99	109.69	875.53	13.53	16.46
TYROBP	52.39	35.57	96.81	145.31	2604.32	5421.25	5323.30
UBASH3A	29.70	316.56	511.62	160.25	38.58	17.19	13.80
UPP1	40.71	306.72	277.36	1637.88	449.54	478.81	354.95
USP6NL	230.42	17.89	15.72	13.12	19.21	63.82	14.18
VPREB3	216.88	21.97	24.96	21.26	23.63	22.50	19.36
XCL1	31.51	28.28	203.87	109.50	6074.61	16.68	15.42
XCL2	35.22	32.83	336.66	175.12	6371.28	24.38	26.84
ZAP70	37.63	481.05	775.80	179.54	613.07	26.00	15.87
ZC3H12D	589.58	753.96	232.69	69.83	33.48	113.01	9.54
ZNF101	158.06	523.65	504.85	151.24	139.99	66.40	22.85
ZNF528	34.01	38.65	29.42	25.07	27.94	46.12	904.49
ZNF595	30.56	18.25	27.04	10.54	25.34	24.57	862.71

**Supplemental table 3: LM7 matrix.** Genes specifically expressed (i.e.  $\log_2(\text{expression}) > 9$ ) by a specific subtype are colored as follows:

B cells, CD4, CD8,  $\gamma\delta$ , NK, MoMaDC and granulocytes.

GSE number	Number of samples	Cell type	First author	reference
GSE11103	41	monocytes, B cells	Abbas AR	21
GSE13906	4	$\gamma\delta$ T cells	Zhang Y	22
GSE15743	4	NK	Stegmann KA	23
GSE16020	20	granulocytes	Vinh DC	24
GSE20300	24	monocytes, eosinophils, neutrophils	Shen-Orr SS	25
GSE49877	36	CD4, CD8 T cells	Raine T	26
GSE53166	113	DC	Lee MN	27
GSE65133	20	B cells, CD4, CD8, $\gamma\delta$ T cells, NK, monocytes	Newman AM	28
GSE65134	7	CD4 T cells	Newman AM	28
GSE65135	28	B cells, CD4, CD8 T cells	Newman AM	28
GSE6740	40	CD4, CD8 T cells	Hyrca MD	29
GSE7307	677	normal (non cancer) tissues	Roth R	
E-MEXP-2055	6	fetal $\gamma\delta$ T cells	Vermijlen D	30

**Supplemental table 4: List of validation studies**

<b>cancer</b>	<b>B cells</b>	<b>T CD4</b>	<b>T CD8</b>	<b>T <math>\gamma\delta</math></b>	<b>NK</b>	<b>MoMaDC</b>	<b>granulocytes</b>
B-ALL	32.88	4.42	17.40	9.16	3.14	17.32	17.54
BL	62.67	7.76	10.44	0.38	2.02	11.67	1.92
CLL	95.07	14.11	10.73	3.44	4.55	14.23	10.87
DLBCL	76.12	11.69	15.21	0.94	4.67	29.77	2.73
FL	92.40	32.81	12.88	0.22	2.30	9.75	1.52
MCL	115.21	10.01	9.07	1.29	0.88	6.56	2.30
SMZL	128.39	16.86	9.60	0.13	1.95	6.16	1.90
THRBL	29.41	48.12	26.97	0.14	14.10	45.91	3.20
T-ALL	4.33	58.32	17.66	6.45	2.29	11.98	11.41
ALCL	27.30	27.09	15.26	2.89	6.61	35.00	2.17
AITL	36.65	62.17	17.97	0.81	5.40	22.48	2.27
PTCL-NOS	31.06	50.35	20.61	2.36	10.29	32.08	1.25
PTCL NK	19.19	21.95	9.88	1.22	43.27	30.32	4.96
CML	1.26	1.16	11.00	13.83	2.11	36.86	56.59
Lung Squamous Cell	25.80	10.29	7.84	2.83	1.32	46.13	4.16
Lung Non Small Cell	28.73	9.24	6.35	3.59	0.95	45.38	0.78
Lung Adenocarcinoma	18.27	8.93	5.39	2.47	0.61	42.17	0.80
Pancreas	15.18	12.34	4.39	2.35	0.52	45.56	2.49
Prostate	5.99	6.40	5.84	9.58	0.34	17.19	1.65
Breast Inflammatory	17.23	12.68	6.82	2.49	0.92	32.35	0.05
Breast Ductal	10.56	8.53	5.90	1.80	0.54	33.94	0.31
Breast Lobular Carcinoma	7.04	7.45	6.93	1.91	0.41	33.67	0.39
Stomach	10.71	9.51	5.78	1.42	1.56	30.13	0.52
Kidney Pap & Cc	5.92	5.23	6.92	1.19	0.79	37.21	0.59
Colorectal	10.94	8.00	3.17	2.17	0.32	30.08	3.59
Bladder	7.51	7.45	4.24	1.88	0.93	28.95	3.23
Liver	6.30	7.26	3.57	1.49	0.52	32.83	1.18
Esophagus	12.92	4.21	2.94	5.90	0.07	21.64	3.18
Uterus	8.81	7.35	3.97	1.68	0.86	24.24	2.88
Thyroid	10.30	5.87	3.88	1.86	0.20	25.56	0.39
Head & Neck	7.79	4.95	5.19	3.97	0.51	21.34	0.68
Melanoma Primary	5.66	12.32	2.49	1.20	1.82	19.76	1.14
Melanoma Metastasis	5.99	4.83	1.93	0.71	0.77	17.57	1.40
Sarcoma	3.37	2.65	2.28	1.63	0.41	21.89	0.67
Ovary	4.37	2.36	1.66	0.98	0.34	18.06	0.86
Endometrium	3.85	4.14	1.78	1.35	0.51	16.30	0.89
Cervix	4.37	1.85	2.98	4.22	0.22	11.34	0.57
Kidney Chromophobe	2.51	0.87	3.87	1.65	0.16	13.58	0.01
Kidney Oncocytoma	1.35	0.18	2.04	0.83	0.01	5.56	0.00
Sarcoma Ewing	0.86	2.42	0.48	0.35	0.19	10.19	1.14
Pilocytic Astrocytoma	0.63	0.27	0.20	2.17	0.00	18.11	0.91
Glioblastoma	0.57	0.60	0.20	1.29	0.02	12.27	0.67
Low Grade Glioma	0.61	0.27	0.22	1.38	0.01	7.18	0.42
PNET	0.41	0.66	0.22	0.77	0.02	6.12	0.39
Ependymoma	0.26	0.60	0.00	0.55	0.02	6.00	0.18
Medulloblastoma	0.09	1.63	0.03	0.38	0.00	2.07	0.03

<b>AML subtype</b>	<b>B cells</b>	<b>T CD4</b>	<b>T CD8</b>	<b>T <math>\gamma\delta</math></b>	<b>NK</b>	<b>MoMaDC</b>	<b>granulocytes</b>
RAEB	7.56	48.19	25.66	2.81	8.09	48.47	38.35
RAEB-t	5.27	24.66	10.28	7.15	3.19	59.85	18.91
M0	12.72	18.51	8.92	7.42	2.63	33.28	8.33
M1	9.31	8.97	8.17	9.23	1.09	19.88	10.34
M2	10.53	10.95	11.08	8.90	1.94	28.49	19.68
M3	6.17	6.00	11.56	17.43	0.46	11.44	16.84
M4	4.41	4.11	5.87	4.14	0.75	71.06	12.95
M5	4.75	4.29	5.32	3.33	0.86	68.16	8.96
M6	9.64	20.26	10.94	8.94	3.97	28.98	19.05
M7	14.31	33.26	17.01	7.61	12.35	39.48	12.11

**Supplemental table 5: Abundance of leukocytes infiltrating cancers.** Data are group means for each malignancy

<b>GSE number</b>	<b>Number of samples</b>	<b>Cancer type</b>	<b>First author</b>	<b>reference</b>
E-TABM-783	35	AITL, PTCL	Leval L	<sup>31</sup>

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GSE number	Number of samples	Cancer type	First author	reference
E-TABM-791	8	PTCL, PTCL-NK	Huang Y	32
GSE10139	108	CCL	Friedman DR	33
GSE10358	304	AML	Tomasson MH	34
GSE10524	80	DLBCL	Booman M	35
GSE10846	420	DLBCL	Lenz G	36
GSE11151	67	kidney	Yusenko MV	37
GSE11318	406	DLBCL	Lenz G	38
GSE11877	207	ALL	Kang H	39
GSE12195	136	DLBCL, FL	Compagno M	4
GSE12417	405	AML	Metzeler KH	40
GSE12453	67	BL, DLBCL, FL, HL, THRBL	Brune V	41
GSE12734	14	CLL	Stamatopoulos B	42
GSE13041	27	GBM	Lee Y	43
GSE13159	2011	ALL, AML, B-ALL, CLL, CML, MDS, T-ALL	Kohlmann A	44
GSE13996	73	HL, THRBL	Chetaille B	45
GSE14468	526	AML	Wouters BJ	46
GSE14973	14	CLL	Stamatopoulos B	47
GSE15471	78	pancreas	Badea L	48
GSE15490	50	CLL	Shehata M	49
GSE15605	74	melanoma	Raskin L	50
GSE15913	40	CLL	Giannopoulos K	51
GSE16024	26	FL, MCL	Hamoudi R	
GSE16455	55	CCL, FL, HCL, MCL, SMZL	Fernández V	52
GSE17189	17	BL, DLBCL	Deffenbacher KE	53
GSE17920	130	HL	Steidl C	54
GSE17951	154	prostate	Wang Y	55
GSE46602	50	prostate	Mortensen MM	56
GSE19067	44	PTCL, PTCL-NK	Iqbal J	57
GSE19069	147	AITL, ALCL, PTCL	Iqbal J	58
GSE19982	30	kidney	Tan MH	59
GSE21029	62	CLL	Herishanu Y	60
GSE2109	2158	ALCL, bladder, Breast, colorectal, DLBCL, endometrium, esophagus, FL, head & neck, kidney, liver, lung, melanoma, ovary, pancreas, prostate, sarcoma, stomach, thyroid, uterus	Curley E	
GSE21452	64	MCL	Hartmann EM	61
GSE21554	69	FL, MCL, SMZL	Watkins AJ	62
GSE22762	195	CLL	Herold T	63
GSE23720	370	breast	Bekhouché I	64
GSE25571	109	CLL	Herold T	65
GSE26673	16	BL	Piccaluga PP T	66
GSE26713	109	CLL	Herold T	65
GSE25571	117	T-ALL	Homminga I	67
GSE27858	56	CLL	Dürig J	68
GSE28654	112	CLL	Trojani A	69
GSE29605	22	CLL	Davidson-Mocada JK	
GSE31048	221	CLL	Wang L	70
GSE32701	40	esophagus	Aoyagi K	71
GSE33075	27	CML	Benito R	72
GSE33135	24	CLL	Baptista MJ	73
GSE34171	510	DLBCL	Monti S	74
GSE34620	117	ewing sarcoma	Postel-Vinay S	75
GSE35935	62	CLL	Bonina S	
GSE36000	38	MCL	Navarro A	76
GSE37168	13	CLL	Landau DA	77
GSE38816	18	FL	Green MR	78
GSE39133	34	HL	Steidl C	79
GSE42038	79	T-ALL	Horstmann MA	
GSE44971	58	pilocytic astrocytoma	Lambert SR	80
GSE46170	38	T-ALL	Hatirnaz Ng O	
GSE4732	303	BL, DLBCL	Dave SS	81
GSE4845	45	melanoma	Hoek KS	82
GSE50161	130	ependymoma, GBM, MB, pilocytic astrocytoma	Griesinger AM	83
GSE50570	6	pancreas	Seqq V	

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<b>GSE number</b>	<b>Number of samples</b>	<b>Cancer type</b>	<b>First author</b>	<b>reference</b>
GSE53117	10	DLBCL	Chapman J	84
GSE53786	5	DLBCL	Scott DW	85
GSE53820	81	DLBCL, FL	Brodtkorb M,	86
GSE55267	69	FL	Guo S	87
GSE57303	70	stomach	Qian Z	88
GSE58445	193	PTCL	Iqbal J	89
GSE6338	60	AITL, ALCL, PTCL	Piccaluga PP	90
GSE64086	12	BL	Ferreiro JF	91
GSE64905	11	BL	Lee S	
GSE65135	26	DLBCL, FL	Newman AM	28
GSE65823	31	ALCL, PTCL	Scarfò I	92
GSE6791	84	Cervix, head & neck	Pyeon D	93
GSE68848	580	GBM, low grade glioma	Fine H	
GSE69049	93	BL, DLBCL	Barrans SL	
GSE69051	250	BL, DLBCL	Barrans SL	
GSE73038	182	GBM, MB, PNET	Sturm D	94
GSE7307	677	breast, cervix, melanoma, prostate	Roth R	
GSE7553	87	melanoma	Riker AI	95
GSE7788	21	NLPHL, THRBL	Van Loo P	96
GSE8271	34	kidney	Koeman JM	97

**Supplemental table 6: List of cancers studies**

## **Supplemental References**

## References

- [1] A. J. Gentles, A. M. Newman, C. L. Liu, S. V. Bratman, W. Feng, D. Kim, V. S. Nair, Y. Xu, A. Khuong, C. D. Hoang *et al.*, The prognostic landscape of genes and infiltrating immune cells across human cancers, *Nature medicine* 2015; 21:938–945.
- [2] M. Tosolini, C. Algans, F. Pont, B. Ycart, and J.-J. Fournié, Large scale microarray profiling reveals four stages of immune escape in non-hodgkin lymphomas, *OncoImmunology* 2016; 5:e1188246.
- [3] S. Maouche, O. Poirier, T. Godefroy, R. Olasso, I. Gut, J.-P. Collet, G. Montalescot, and F. Cambien, Performance comparison of two microarray platforms to assess differential gene expression in human monocyte and macrophage cells, *BMC genomics* 2008; 9:1.
- [4] M. Compagno, W. K. Lim, A. Grunn, S. V. Nandula, M. Brahmachary, Q. Shen, F. Bertoni, M. Ponzoni, M. Scandurra, A. Califano *et al.*, Mutations of multiple genes cause deregulation of  $\text{nf}\kappa\text{b}$  in diffuse large b-cell lymphoma, *Nature* 2009; 459:717–721.
- [5] S. C. Bangs, D. Baban, H. J. Cattani, C. K.-F. Li, A. J. McMichael, and X.-N. Xu, Human  $\text{cd4}^+$  memory t cells are preferential targets for bystander activation and apoptosis, *The Journal of Immunology* 2009; 182:1962–1971.
- [6] S. Eckerle, V. Brune, C. Döring, E. Tiacchi, V. Bohle, C. Sundström, R. Kodet, M. Paulli, B. Falini, W. Klapper *et al.*, Gene expression profiling of isolated tumour cells from anaplastic large cell lymphomas: insights into its cellular origin, pathogenesis and relation to hodgkin lymphoma, *Leukemia* 2009; 23:2129–2138.
- [7] M. C. Bosco, D. Pierobon, F. Blengio, F. Raggi, C. Vanni, M. Gattorno, A. Eva, F. Novelli, P. Cappello, M. Giovarelli *et al.*, Hypoxia modulates the gene expression profile of immunoregulatory receptors in human mature dendritic cells: identification of  $\text{trem-1}$  as a novel hypoxic marker in vitro and in vivo, *Blood* 2011; 117:2625–2639.
- [8] F. Pont, J. Familiades, S. Déjean, S. Fruchon, D. Cendron, M. Pouput, R. Pouput, F. L'Faqihi-Olive, N. Prade, B. Ycart *et al.*, The gene expression profile of phosphoantigen-specific human  $\gamma\delta$  t lymphocytes is a blend of  $\alpha\beta$  t-cell and nk-cell signatures, *European journal of immunology* 2012; 42:228–240.
- [9] F. Allantaz, D. T. Cheng, T. Bergauer, P. Ravindran, M. F. Rossier, M. Ebeling, L. Badi, B. Reis, H. Bitter, M. D'Asaro *et al.*, Expression profiling of human immune cell subsets identifies mirna-mrna regulatory relationships correlated with cell type specific expression, *PLoS one* 2012; 7:e29979.
- [10] M. G. Constantinides, D. Picard, A. K. Savage, and A. Bendelac, A naive-like population of human  $\text{cd1d}$ -restricted t cells expressing intermediate levels of promyelocytic leukemia zinc finger, *The Journal of Immunology* 2011; 187:309–315.
- [11] M. Sirois, L. Robitaille, R. Allary, M. Shah, C. H. Woelk, J. Estaquier, and J. Corbeil,  $\text{traf6}$  and  $\text{irf7}$  control hiv replication in macrophages, *PLoS one* 2011; 6:e28125.
- [12] M. A. Favila, N. S. Geraci, E. Zeng, B. Harker, D. Condon, R. N. Cotton, A. Jayakumar, V. Tripathi, and M. A. McDowell, Human dendritic cells exhibit a pronounced type i ifn signature following leishmania major infection that is required for  $\text{il-12}$  induction, *The Journal of Immunology* 2014; 192:5863–5872.
- [13] K. Dybkær, M. Bøgsted, S. Falgreen, J. S. Bødker, M. K. Kjeldsen, A. Schmitz, A. E. Bilgrau, Z. Y. Xu-Monette, L. Li, K. S. Bergkvist *et al.*, Diffuse large b-cell lymphoma classification system that associates normal b-cell subset phenotypes with prognosis, *Journal of Clinical Oncology* 2015; 33:1379–1388.
- [14] H. E. Mei, I. Wirries, D. Frölich, M. Brisslert, C. Giesecke, J. R. Grün, T. Alexander, S. Schmidt, K. Luda, A. A. Köhl *et al.*, A unique population of  $\text{igg}$ -expressing plasma cells lacking  $\text{cd19}$  is enriched in human bone marrow, *Blood* 2015; 125:1739–1748.
- [15] M. Takeshita, K. Suzuki, Y. Kassai, M. Takiguchi, Y. Nakayama, Y. Otomo, R. Morita, T. Miyazaki, A. Yoshimura, and T. Takeuchi, Polarization diversity of human  $\text{cd4}^+$  stem cell memory t cells, *Clinical Immunology* 2015; 159:107–117.
- [16] G. J. Walter, V. Fleskens, K. S. Frederiksen, M. Rajasekhar, B. Menon, J. G. Gerwien, H. G. Evans, and L. S. Taams, Phenotypic, functional, and gene expression profiling of peripheral  $\text{cd45ra}^+$  and  $\text{cd45ro}^+$   $\text{cd4}^+$   $\text{cd25}^+$   $\text{cd127}^{\text{low}}$   $\text{treg}$  cells in patients with chronic rheumatoid arthritis, *Arthritis & Rheumatology* 2016; 68:103–116.
- [17] P. Amé-Thomas, S. Hoeller, C. Artchounin, J. Misiak, M. S. Braza, R. Jean, J. Le Priol, C. Monvoisin, N. Martin, P. Gaulard *et al.*,  $\text{Cd10}$  delineates a subset of human  $\text{il-4}$  producing follicular helper t cells involved in the survival of follicular lymphoma b cells, *Blood* 2015; 125:2381–2385.
- [18] K. Kanduri, S. Tripathi, A. Larjo, H. Mannerström, U. Ullah, R. Lund, R. D. Hawkins, B. Ren, H. Lähdesmäki, and R. Lahesmaa, Identification of global regulators of t-helper cell lineage specification, *Genome medicine* 2015; 7:1.
- [19] X. Du, Y. Tang, H. Xu, L. Lit, W. Walker, P. Ashwood, J. P. Gregg, and F. R. Sharp, Genomic profiles for human peripheral blood t cells, b cells, natural killer cells, monocytes, and polymorphonuclear cells: comparisons to ischemic stroke, migraine, and tourette syndrome, *Genomics* 2006; 87:693–703.
- [20] K. Dybkaer, J. Iqbal, G. Zhou, H. Geng, L. Xiao, A. Schmitz, F. d'Amore, and W. C. Chan, Genome wide transcriptional analysis of resting and  $\text{il2}$  activated human natural killer cells: gene expression signatures indicative of novel molecular signaling pathways, *BMC genomics* 2007; 8:1.
- [21] A. R. Abbas, K. Wolslegel, D. Seshasayee, Z. Modrusan, and H. F. Clark, Deconvolution of blood microarray data identifies cellular activation patterns in systemic lupus erythematosus, *PLoS one* 2009; 4:e6098.
- [22] Y. Zhang, J. H. Ohyashiki, N. Shimizu, and K. Ohyashiki, Aberrant expression of nk cell receptors in epstein-barr virus-positive  $\gamma\delta$  t-cell lymphoproliferative disorders, *Hematology* 2013; .
- [23] K. A. Stegmann, N. K. Björkström, H. Veber, S. Ciesek, P. Riese, J. Wiegand, J. Hadem, P. V. Suneetha, J. Jaroszewicz, C. Wang *et al.*, Interferon- $\alpha$ -induced  $\text{trail}$  on natural killer cells is associated with control of hepatitis c virus infection, *Gastroenterology* 2010; 138:1885–1897.
- [24] D. C. Vinh, S. Y. Patel, G. Uzel, V. L. Anderson, A. F. Freeman, K. N. Olivier, C. Spalding, S. Hughes, S. Pittaluga, M. Raffeld *et al.*, Autosomal dominant and sporadic monocytopenia with susceptibility to mycobacteria, fungi, papillomaviruses, and myelodysplasia, *Blood* 2010; 115:1519–1529.

- [25] S. S. Shen-Orr, R. Tibshirani, P. Khatri, D. L. Bodian, F. Staedtler, N. M. Perry, T. Hastie, M. M. Sarwal, M. M. Davis, and A. J. Butte, Cell type-specific gene expression differences in complex tissues, *Nature methods* 2010; 7:287–289.
- [26] T. Raine, J. Z. Liu, C. A. Anderson, M. Parkes, and A. Kaser, Generation of primary human intestinal t cell transcriptomes reveals differential expression at genetic risk loci for immune-mediated disease, *Gut* 2014; gutjnl–2013.
- [27] M. N. Lee, C. Ye, A.-C. Villani, T. Raj, W. Li, T. M. Eisenhaure, S. H. Imboya, P. I. Chipendo, F. A. Ran, K. Slowikowski *et al.*, Common genetic variants modulate pathogen-sensing responses in human dendritic cells, *Science* 2014; 343:1246980.
- [28] A. M. Newman, C. L. Liu, M. R. Green, A. J. Gentles, W. Feng, Y. Xu, C. D. Hoang, M. Diehn, and A. A. Alizadeh, Robust enumeration of cell subsets from tissue expression profiles, *Nature methods* 2015; 12:453–457.
- [29] M. D. Hycza, C. Kovacs, M. Loutfy, R. Halpenny, L. Heisler, S. Yang, O. Wilkins, M. Ostrowski, and S. D. Der, Distinct transcriptional profiles in ex vivo cd4+ and cd8+ t cells are established early in human immunodeficiency virus type 1 infection and are characterized by a chronic interferon response as well as extensive transcriptional changes in cd8+ t cells, *Journal of virology* 2007; 81:3477–3486.
- [30] D. Vermijlen, M. Brouwer, C. Donner, C. Liesnard, M. Tackoen, M. Van Rysselberge, N. Twité, M. Goldman, A. Marchant, and F. Willems, Human cytomegalovirus elicits fetal  $\gamma\delta$  t cell responses in utero, *The Journal of experimental medicine* 2010; 207:807–821.
- [31] L. de Leval, D. S. Rickman, C. Thielen, A. de Reynies, Y.-L. Huang, G. Delsol, L. Lamant, K. Leroy, J. Briere, T. Molina *et al.*, The gene expression profile of nodal peripheral t-cell lymphoma demonstrates a molecular link between angioimmunoblastic t-cell lymphoma (aitl) and follicular helper t (tfh) cells, *Blood* 2007; 109:4952–4963.
- [32] Y. Huang, A. De Reynies, L. De Leval, B. Ghazi, N. Martin-Garcia, M. Travert, J. Bosq, J. Brière, B. Petit, E. Thomas *et al.*, Gene expression profiling identifies emerging oncogenic pathways operating in extranodal nk/t-cell lymphoma, nasal type, *Blood* 2010; 115:1226–1237.
- [33] D. R. Friedman, J. B. Weinberg, W. T. Barry, B. K. Goodman, A. D. Volkheimer, K. M. Bond, Y. Chen, N. Jiang, J. O. Moore, J. P. Gockerman *et al.*, A genomic approach to improve prognosis and predict therapeutic response in chronic lymphocytic leukemia, *Clinical Cancer Research* 2009; 15:6947–6955.
- [34] M. H. Tomasson, Z. Xiang, R. Walgren, Y. Zhao, Y. Kasai, T. Miner, R. E. Ries, O. Lubman, D. H. Fremont, M. D. McLellan *et al.*, Somatic mutations and germline sequence variants in the expressed tyrosine kinase genes of patients with de novo acute myeloid leukemia, *Blood* 2008; 111:4797–4808.
- [35] M. Booman, K. Szuhai, A. Rosenwald, E. Hartmann, H. C. Kluin-Nelemans, D. de Jong, E. Schuurings, and P. Kluin, Genomic alterations and gene expression in primary diffuse large b-cell lymphomas of immune-privileged sites: the importance of apoptosis and immunomodulatory pathways, *The Journal of pathology* 2008; 216:209–217.
- [36] G. Lenz, G. Wright, S. Dave, W. Xiao, J. Powell, H. Zhao, W. Xu, B. Tan, N. Goldschmidt, J. Iqbal *et al.*, Stromal gene signatures in large-b-cell lymphomas, *New England Journal of Medicine* 2008; 359:2313–2323.
- [37] M. V. Yusenko, R. P. Kuiper, T. Boethe, B. Ljungberg, A. G. van Kessel, and G. Kovacs, High-resolution dna copy number and gene expression analyses distinguish chromophobe renal cell carcinomas and renal oncocytomas, *BMC cancer* 2009; 9:1.
- [38] G. Lenz, G. W. Wright, N. T. Emre, H. Kohlhammer, S. S. Dave, R. E. Davis, S. Carty, L. T. Lam, A. Shaffer, W. Xiao *et al.*, Molecular subtypes of diffuse large b-cell lymphoma arise by distinct genetic pathways, *Proceedings of the National Academy of Sciences* 2008; 105:13520–13525.
- [39] H. Kang, I.-M. Chen, C. S. Wilson, E. J. Bedrick, R. C. Harvey, S. R. Atlas, M. Devidas, C. G. Mullighan, X. Wang, M. Murphy *et al.*, Gene expression classifiers for relapse-free survival and minimal residual disease improve risk classification and outcome prediction in pediatric b-precursor acute lymphoblastic leukemia, *Blood* 2010; 115:1394–1405.
- [40] K. H. Metzeler, M. Hummel, C. D. Bloomfield, K. Spiekermann, J. Braess, M.-C. Sauerland, A. Heinecke, M. Radmacher, G. Marcucci, S. P. Whitman *et al.*, An 86-probe-set gene-expression signature predicts survival in cytogenetically normal acute myeloid leukemia, *Blood* 2008; 112:4193–4201.
- [41] V. Brune, E. Tiacci, I. Pfeil, C. Döring, S. Eckerle, C. J. van Noesel, W. Klapper, B. Falini, A. von Heydebreck, D. Metzler *et al.*, Origin and pathogenesis of nodular lymphocyte-predominant hodgkin lymphoma as revealed by global gene expression analysis, *The Journal of experimental medicine* 2008; 205:2251–2268.
- [42] B. Stamatopoulos, B. Haibe-Kains, C. Equeter, N. Meuleman, A. Sorée, C. De Bruyn, D. Hanosset, D. Bron, P. Martiat, and L. Lagneaux, Gene expression profiling reveals differences in microenvironment interaction between patients with chronic lymphocytic leukemia expressing high versus low zap70 mrna, *haematologica* 2009; 94:790–799.
- [43] Y. Lee, A. C. Scheck, T. F. Cloughesy, A. Lai, J. Dong, H. K. Farooqi, L. M. Liau, S. Horvath, P. S. Mischel, and S. F. Nelson, Gene expression analysis of glioblastomas identifies the major molecular basis for the prognostic benefit of younger age, *BMC medical genomics* 2008; 1:1.
- [44] A. Kohlmann, T. J. Kipps, L. Z. Rassenti, J. R. Downing, S. A. Shurtleff, K. I. Mills, A. F. Gilkes, W.-K. Hofmann, G. Basso, M. C. Dell’Orto *et al.*, An international standardization programme towards the application of gene expression profiling in routine leukaemia diagnostics: the microarray innovations in leukemia study prephase, *British journal of haematology* 2008; 142:802–807.
- [45] B. Chetaille, F. Bertucci, P. Finetti, B. Esterni, A. Stamatoullas, J. M. Picquetot, M. C. Copin, F. Morschhauser, O. Casasnovas, T. Petrella *et al.*, Molecular profiling of classical hodgkin lymphoma tissues uncovers variations in the tumor microenvironment and correlations with ebv infection and outcome, *Blood* 2009; 113:2765–3775.
- [46] B. J. Wouters, B. Löwenberg, C. A. Erpelinck-Verschueren, W. L. van Putten, P. J. Valk, and R. Delwel, Double cebpa mutations, but not single cebpa mutations, define a subgroup of acute myeloid leukemia with a distinctive gene expression profile that is uniquely associated with a favorable outcome, *Blood* 2009; 113:3088–3091.
- [47] B. Stamatopoulos, N. Meuleman, C. De Bruyn, P. Mineur, P. Martiat, D. Bron, and L. Lagneaux, Antileukemic activity of valproic acid in chronic lymphocytic leukemia b cells defined by microarray analysis, *Leukemia* 2009; 23:2281–2289.

- [48] L. Badea, V. Herlea, S. O. Dima, T. Dumitrascu, I. Popescu, et al., Combined gene expression analysis of whole-tissue and microdissected pancreatic ductal adenocarcinoma identifies genes specifically overexpressed in tumor epithelia—the authors reported a combined gene expression analysis of whole-tissue and microdissected pancreatic ductal adenocarcinoma identifies genes specifically overexpressed in tumor epithelia, *Hepato-gastroenterology* 2008; 55:2016.
- [49] M. Shehata, D. Demirtas, S. Schnabl, M. Hilgarth, R. Hubmann, C. Fonatsch, I. Schwarzingler, G. Hopfinger, K. Eigenberger, D. Heintel *et al.*, Sequential gene expression profiling during treatment for identification of predictive markers and novel therapeutic targets in chronic lymphocytic leukemia, *Leukemia* 2010; 24:2122–2127.
- [50] L. Raskin, D. R. Fullen, T. J. Giordano, D. G. Thomas, M. L. Frohm, K. B. Cha, J. Ahn, B. Mukherjee, T. M. Johnson, and S. B. Gruber, Transcriptome profiling identifies *hmg2* as a biomarker of melanoma progression and prognosis, *Journal of Investigative Dermatology* 2013; 133:2585–2592.
- [51] K. Giannopoulos, A. Dmoszynska, M. Kowal, E. Wkasik-Szczepanek, A. Bojarska-Junak, J. Rolinski, H. Döhner, S. Stilgenbauer, and L. Bullinger, Thalidomide exerts distinct molecular antileukemic effects and combined thalidomide/fludarabine therapy is clinically effective in high-risk chronic lymphocytic leukemia, *Leukemia* 2009; 23:1771–1778.
- [52] V. Fernández, O. Salamero, B. Espinet, F. Solé, C. Royo, A. Navarro, F. Camacho, S. Beà, E. Hartmann, V. Amador *et al.*, Genomic and gene expression profiling defines indolent forms of mantle cell lymphoma, *Cancer research* 2010; 70:1408–1418.
- [53] K. E. Deffenbacher, J. Iqbal, Z. Liu, K. Fu, and W. C. Chan, Recurrent chromosomal alterations in molecularly classified aids-related lymphomas: an integrated analysis of dna copy number and gene expression, *JAIDS Journal of Acquired Immune Deficiency Syndromes* 2010; 54:18–26.
- [54] C. Steidl, T. Lee, S. P. Shah, P. Farinha, G. Han, T. Nayar, A. Delaney, S. J. Jones, J. Iqbal, D. D. Weisenburger *et al.*, Tumor-associated macrophages and survival in classic hodgkin’s lymphoma, *New England Journal of Medicine* 2010; 362:875–885.
- [55] Y. Wang, X.-Q. Xia, Z. Jia, A. Sawyers, H. Yao, J. Wang-Rodriguez, D. Mercola, and M. McClelland, In silico estimates of tissue components in surgical samples based on expression profiling data, *Cancer research* 2010; 70:6448–6455.
- [56] M. M. Mortensen, S. Høyer, A.-S. Lynnerup, T. F. Ørntoft, K. D. Sørensen, M. Borre, and L. Dyrskjøt, Expression profiling of prostate cancer tissue delineates genes associated with recurrence after prostatectomy, *Scientific reports* 2015; 5.
- [57] J. Iqbal, D. Weisenburger, A. Chowdhury, M. Y. Tsai, G. Srivastava, T. C. Greiner, C. Kucuk, K. Deffenbacher, J. Vose, L. Smith *et al.*, Natural killer cell lymphoma shares strikingly similar molecular features with a group of non-hepatosplenic  $\gamma\delta$  t-cell lymphoma and is highly sensitive to a novel aurora kinase a inhibitor in vitro, *Leukemia* 2011; 25:348–358.
- [58] J. Iqbal, D. D. Weisenburger, T. C. Greiner, J. M. Vose, T. McKeithan, C. Kucuk, H. Geng, K. Deffenbacher, L. Smith, K. Dybkaer *et al.*, Molecular signatures to improve diagnosis in peripheral t-cell lymphoma and prognostication in angioimmunoblastic t-cell lymphoma, *Blood* 2010; 115:1026–1036.
- [59] M.-H. Tan, C. F. Wong, H. L. Tan, X. J. Yang, J. Ditlev, D. Matsuda, S. K. Khoo, J. Sugimura, T. Fujioka, K. A. Furge *et al.*, Genomic expression and single-nucleotide polymorphism profiling discriminates chromophobe renal cell carcinoma and oncocytoma, *BMC cancer* 2010; 10:1.
- [60] Y. Herishanu, P. Pérez-Galán, D. Liu, A. Biancotto, S. Pittaluga, B. Vire, F. Gibellini, N. Njuguna, E. Lee, L. Stennett *et al.*, The lymph node microenvironment promotes b-cell receptor signaling, *nf- $\kappa$ b* activation, and tumor proliferation in chronic lymphocytic leukemia, *Blood* 2011; 117:563–574.
- [61] E. M. Hartmann, E. Campo, G. Wright, G. Lenz, I. Salaverria, P. Jares, W. Xiao, R. M. Braziel, L. M. Rimsza, W.-C. Chan *et al.*, Pathway discovery in mantle cell lymphoma by integrated analysis of high-resolution gene expression and copy number profiling, *Blood* 2010; 116:953–961.
- [62] A. J. Watkins, R. A. Hamoudi, N. Zeng, Q. Yan, Y. Huang, H. Liu, J. Zhang, E. Braggio, R. Fonseca, L. de Leval *et al.*, An integrated genomic and expression analysis of 7q deletion in splenic marginal zone lymphoma, *PLoS ONE* 2012; 7.
- [63] T. Herold, V. Jurinovic, K. Metzeler, A.-L. Boulesteix, M. Bergmann, T. Seiler, M. Mulaw, S. Thoene, A. Dufour, Z. Pasalic *et al.*, An eight-gene expression signature for the prediction of survival and time to treatment in chronic lymphocytic leukemia, *Leukemia* 2011; 25:1639–1645.
- [64] I. Bekhouche, P. Finetti, J. Adelaïde, A. Ferrari, C. Tarpin, E. Charafe-Jauffret, C. Charpin, G. Houvenaeghel, J. Jacquemier, G. Bidaut *et al.*, High-resolution comparative genomic hybridization of inflammatory breast cancer and identification of candidate genes, *PLoS One* 2011; 6:e16950.
- [65] T. Herold, V. Jurinovic, M. Mulaw, T. Seiler, A. Dufour, S. Schneider, P. M. Kakadia, M. Feuring-Buske, J. Braess, K. Spiekermann *et al.*, Expression analysis of genes located in the minimally deleted regions of 13q14 and 11q22-23 in chronic lymphocytic leukemia—unexpected expression pattern of the rho gtpase activator *arhgap20*, *Genes, Chromosomes and Cancer* 2011; 50:546–558.
- [66] P. P. Piccaluga, G. De Falco, M. Kustagi, A. Gazzola, C. Agostinelli, C. Tripodo, E. Leucci, A. Onnis, A. Astolfi, M. R. Sapienza *et al.*, Gene expression analysis uncovers similarity and differences among burkitt lymphoma subtypes, *Blood* 2011; 117:3596–3608.
- [67] I. Homminga, R. Pieters, A. W. Langerak, J. J. de Rooi, A. Stubbs, M. Verstegen, M. Vuerhard, J. Buijs-Gladdines, C. Kooi, P. Klous *et al.*, Integrated transcript and genome analyses reveal *nkx2-1* and *mf2c* as potential oncogenes in t cell acute lymphoblastic leukemia, *Cancer cell* 2011; 19:484–497.
- [68] J. Dürig, U. Dührsen, L. Klein-Hitpass, J. Worm, J. R. Hansen, H. Ørum, and M. Wissenbach, The novel antisense *bcl-2* inhibitor *spc2996* causes rapid leukemic cell clearance and immune activation in chronic lymphocytic leukemia, *Leukemia* 2011; 25:638–647.
- [69] A. Trojani, B. Di Camillo, A. Tedeschi, M. Lodola, S. Montesano, F. Ricci, E. Vismara, A. Greco, S. Veronese, A. Orlicchio *et al.*, Gene expression profiling identifies *arsd* as a new marker of disease progression and the sphingolipid metabolism as a potential novel metabolism in chronic lymphocytic leukemia., *Cancer biomarkers: section A of Disease markers* 2010; 11:15–28.
- [70] L. Wang, A. K. Shalek, M. Lawrence, R. Ding, J. T. Gaublomme, N. Pochet, P. Stojanov, C. Sougnez, S. A. Shukla, K. E. Stevenson *et al.*, Somatic mutation as a mechanism of *wnt/ $\beta$ -catenin* pathway activation in cll, *Blood* 2014; blood–2014.

- [71] K. Aoyagi, K. Minashi, H. Igaki, Y. Tachimori, T. Nishimura, N. Hokamura, A. Ashida, H. Daiko, A. Ochiai, M. Muto *et al.*, Artificially induced epithelial-mesenchymal transition in surgical subjects: its implications in clinical and basic cancer research, *PLoS One* 2011; 6:e18196.
- [72] R. Benito, E. Lumbreras, M. Abáigar, N. C. Gutierrez, M. Delgado, C. Robledo, J. L. García, A. E. Rodríguez-Vicente, M. C. Cañizo, and J. M. H. Rivas, Imatinib therapy of chronic myeloid leukemia restores the expression levels of key genes for dna damage and cell-cycle progression, *Pharmacogenetics and genomics* 2012; 22:381–388.
- [73] M. J. Baptista, A. Muntañola, E. Calpe, P. Abrisqueta, O. Salamero, E. Fernández, C. Codony, E. Giné, S. G. Kalko, M. Crespo *et al.*, Differential gene expression profile associated to apoptosis induced by dexamethasone in cll cells according to ighv/zap-70 status, *Clinical Cancer Research* 2012; 18:5924–5933.
- [74] S. Monti, B. Chapuy, K. Takeyama, S. J. Rodig, Y. Hao, K. T. Yeda, H. Inguilizian, C. Mermel, T. Currie, A. Dogan *et al.*, Integrative analysis reveals an outcome-associated and targetable pattern of p53 and cell cycle deregulation in diffuse large b cell lymphoma, *Cancer cell* 2012; 22:359–372.
- [75] S. Postel-Vinay, A. S. Véron, F. Tirode, G. Pierron, S. Reynaud, H. Kovar, O. Oberlin, E. Lapouble, S. Ballet, C. Lucchesi *et al.*, Common variants near *tardbp* and *egr2* are associated with susceptibility to ewing sarcoma, *Nature genetics* 2012; 44:323–327.
- [76] A. Navarro, G. Clot, C. Royo, P. Jares, A. Hadzidimitriou, A. Agathangelidis, V. Bikos, N. Darzentas, T. Papadaki, I. Salaverria *et al.*, Molecular subsets of mantle cell lymphoma defined by the ighv mutational status and *sox11* expression have distinct biologic and clinical features, *Cancer research* 2012; 72:5307–5316.
- [77] D. A. Landau, S. L. Carter, P. Stojanov, A. McKenna, K. Stevenson, M. S. Lawrence, C. Sougnez, C. Stewart, A. Sivachenko, L. Wang *et al.*, Evolution and impact of subclonal mutations in chronic lymphocytic leukemia, *Cell* 2013; 152:714–726.
- [78] M. R. Green, A. J. Gentles, R. V. Nair, J. M. Irish, S. Kihira, C. L. Liu, I. Kela, E. S. Hopmans, J. H. Myklebust, H. Ji *et al.*, Hierarchy in somatic mutations arising during genomic evolution and progression of follicular lymphoma, *Blood* 2013; 121:1604–1611.
- [79] C. Steidl, A. Diepstra, T. Lee, F. C. Chan, P. Farinha, K. Tan, A. Telenius, L. Barclay, S. P. Shah, J. M. Connors *et al.*, Gene expression profiling of microdissected hodgkin reed-sternberg cells correlates with treatment outcome in classical hodgkin lymphoma, *Blood* 2012; 120:3530–3540.
- [80] S. R. Lambert, H. Witt, V. Hovestadt, M. Zucknick, M. Kool, D. M. Pearson, A. Korshunov, M. Ryzhova, K. Ichimura, N. Jabado *et al.*, Differential expression and methylation of brain developmental genes define location-specific subsets of pilocytic astrocytoma, *Acta neuropathologica* 2013; 126:291–301.
- [81] S. S. Dave, K. Fu, G. W. Wright, L. T. Lam, P. Kluin, E.-J. Boerma, T. C. Greiner, D. D. Weisenburger, A. Rosenwald, G. Ott *et al.*, Molecular diagnosis of burkitt's lymphoma, *New England Journal of Medicine* 2006; 354:2431–2442.
- [82] K. S. Hoek, N. C. Schlegel, P. Brafford, A. Sucker, S. Ugurel, R. Kumar, B. L. Weber, K. L. Nathanson, D. J. Phillips, M. Herlyn *et al.*, Metastatic potential of melanomas defined by specific gene expression profiles with no *braf* signature, *Pigment Cell Research* 2006; 19:290–302.
- [83] A. M. Griesinger, D. K. Birks, A. M. Donson, V. Amani, L. M. Hoffman, A. Waziri, M. Wang, M. H. Handler, and N. K. Foreman, Characterization of distinct immunophenotypes across pediatric brain tumor types, *The Journal of Immunology* 2013; 191:4880–4888.
- [84] J. Chapman, A. Gentles, V. Sujoy, F. Vega, C. Dumur, T. Blevins, L. Bernal-Mizrachi, M. Mosunjac, A. Pimentel, D. Zhu *et al.*, Gene expression analysis of plasmablastic lymphoma identifies downregulation of b-cell receptor signaling and additional unique transcriptional programs, *Leukemia* 2015; .
- [85] D. W. Scott, G. W. Wright, P. M. Williams, C.-J. Lih, W. Walsh, E. S. Jaffe, A. Rosenwald, E. Campo, W. C. Chan, J. M. Connors *et al.*, Determining cell-of-origin subtypes of diffuse large b-cell lymphoma using gene expression in formalin-fixed paraffin-embedded tissue, *Blood* 2014; 123:1214–1217.
- [86] M. Brodtkorb, O. C. Lingjærde, K. Huse, G. Trøen, M. Hystad, V. I. Hilden, J. H. Myklebust, E. Leich, A. Rosenwald, J. Delabie *et al.*, Whole-genome integrative analysis reveals expression signatures predicting transformation in follicular lymphoma, *Blood* 2014; 123:1051–1054.
- [87] S. Guo, J. K. Chan, J. Iqbal, T. McKeithan, K. Fu, B. Meng, Y. Pan, W. Cheuk, D. Luo, R. Wang *et al.*, *Ezh2* mutations in follicular lymphoma from different ethnic groups and associated gene expression alterations, *Clinical Cancer Research* 2014; 20:3078–3086.
- [88] Z. Qian, G. Zhu, L. Tang, M. Wang, L. Zhang, J. Fu, C. Huang, S. Fan, Y. Sun, J. Lv *et al.*, Whole genome gene copy number profiling of gastric cancer identifies *pak1* and *kras* gene amplification as therapy targets, *Genes, Chromosomes and Cancer* 2014; 53:883–894.
- [89] J. Iqbal, G. Wright, C. Wang, A. Rosenwald, R. D. Gascoyne, D. D. Weisenburger, T. C. Greiner, L. Smith, S. Guo, R. A. Wilcox *et al.*, Gene expression signatures delineate biological and prognostic subgroups in peripheral t-cell lymphoma, *Blood* 2014; 123:2915–2923.
- [90] P. P. Piccaluga, C. Agostinelli, A. Califano, M. Rossi, K. Basso, S. Zupo, P. Went, U. Klein, P. L. Zinzani, M. Baccarani *et al.*, Gene expression analysis of peripheral t cell lymphoma, unspecified, reveals distinct profiles and new potential therapeutic targets, *Journal of Clinical Investigation* 2007; 117:823.
- [91] J. F. Ferreira, J. Morscio, D. Dierickx, L. Marcelis, G. Verhoef, P. Vandenberghe, T. Tousseyn, and I. Wlodarska, Post-transplant molecularly defined burkitt lymphomas are frequently myc-negative and characterized by the 11q-gain/loss pattern, *haematologica* 2015; 100:e275–e279.
- [92] I. Scarfò, E. Pellegrino, E. Mereu, I. Kwee, L. Agnelli, E. Bergaggio, G. Garaffo, N. Vitale, M. Caputo, R. Machiorlatti *et al.*, Identification of a new subclass of alk-negative *alcl* expressing aberrant levels of *erbb4* transcripts, *Blood* 2016; 127:221–232.
- [93] D. Pyeon, M. A. Newton, P. F. Lambert, J. A. Den Boon, S. Sengupta, C. J. Marsit, C. D. Woodworth, J. P. Connor, T. H. Haugen, E. M. Smith *et al.*, Fundamental differences in cell cycle deregulation in human papillomavirus-positive and human papillomavirus-negative head/neck and cervical cancers, *Cancer research* 2007; 67:4605–4619.
- [94] D. Sturm, B. A. Orr, U. H. Toprak, V. Hovestadt, D. T. Jones, D. Capper, M. Sill, I. Buchhalter, P. A. Northcott, I. Leis *et al.*, New brain tumor entities emerge from molecular classification of cns-pnets, *Cell* 2016; 164:1060–1072.

- [95] A. I. Riker, S. A. Enkemann, O. Fodstad, S. Liu, S. Ren, C. Morris, Y. Xi, P. Howell, B. Metge, R. S. Samant *et al.*, The gene expression profiles of primary and metastatic melanoma yields a transition point of tumor progression and metastasis, *BMC medical genomics* 2008; 1:1.
- [96] P. Van Loo, T. Tousseyn, V. Vanhentenrijk, D. Dierickx, A. Malecka, I. V. Bempt, G. Verhoef, J. Delabie, P. Marynen, P. Matthys *et al.*, T cell/histiocyte rich large b-cell lymphoma shows transcriptional features suggestive of a tolerogenic host immune response, *Haematologica* 2009; haematol-2009.
- [97] J. M. Koeman, R. C. Russell, M.-H. Tan, D. Petillo, M. Westphal, K. Koelzer, J. L. Metcalf, Z. Zhang, D. Matsuda, K. J. Dykema *et al.*, Somatic pairing of chromosome 19 in renal oncocytoma is associated with deregulated elgn2-mediated oxygen-sensing response, *PLoS Genet* 2008; 4:e1000176.