Supplementary Table 1. Selection of significantly differentiated genes for RT-qPCR validation. Taken from Peeters and colleagues.[13]

			Patiens		***Filteres read counts***		**Controls**						
Gene symbol	**Ensembl ID**	**Gene name**	**IV.10**	**IV.11**	**IV.10**	**IV.5**	**III.9**	**IV.8**	**Method**	**Basemean/cpm**	**fc**	**adj_pval**	**mean fc**
ADD2	ENSG000000 75340	*Adducin 2 (beta)*	112	169	114	371	861	467	DESeq2 edgeR	290.91 3.42	−0.72 −1.20	.00 .01	−0.96
C12orf55	ENSG000001 88596	*Cilia- and flagella-associated protein 54*	184	192	323	535	1029	971	DESeq2 edgeR	456.81 4.07	−0.81 −1.05	.00 .00	−0.93
C12orf79	ENSG000002 57242	*Chromosome 12 open reading frame 79*	675	1304	1693	470	912	589	DESeq2 edgeR	1010.88 5.19	1.19 1.69	.00 .00	1.44
CCDC126	ENSG000001 69193	*Coiled-coil domain containing 126*	86	98	143	173	666	456	DESeq2 edgeR	219.14 3.03	−0.59 −1.09	.01 .05	−0.84
CCDC74A	ENSG000001 63040	*Coiled-coil domain containing 74A*	154	308	340	592	1594	1667	DESeq2 edgeR	627.79 4.52	−0.83 −1.42	.00 .00	−1.12
CCL22	ENSG000001 02962	*Chemokine (C-C motif) ligand 22*	5329	8440	9969	6426	6301	6660	DESeq2 edgeR	7579.37 8.10	0.73 1.02	.00 .00	0.87
CDH24	ENSG000001 39880	*Cadherin 24, type 2*	163	172	238	127	207	207	DESeq2 edgeR	190.34 2.78	0.64 0.89	.00 .05	0.77
CEP70	ENSG000001 14107	*Centrosomal protein 70kDa*	175	315	321	117	398	243	DESeq2 edgeR	262.03 3.24	0.56 0.99	.02 .07	0.77
CLLU1OS	**ENSG000002 05057**	***Chronic lymphocytic leukemia up-regulated 1 opposite strand***	**376**	**213**	**362**	**27**	**22**	**62**	**DESeq2 edgeR**	**224.48 2.98**	**0.65 3.88**	**.00 .00**	**2.27**
CTSC	ENSG000001 09861	***Cathepsin C***	**2256**	**2665**	**3093**	**4880**	**10595**	**10493**	**DESeq2 edgeR**	**4870.05 7.46**	**−0.68 −0.84**	**.00 .00**	**−0.76**
DACT1	ENSG000001 65617	*Dishevelled-binding antagonist of beta-catenin 1*	1572	1508	2346	1381	2290	1641	DESeq2 edgeR	1821.14 6.04	0.73 0.84	.00 .00	0.78
GIMAP5	ENSG000001 96329	*GTPase, IMAP family member 5*	92	104	128	242	394	784	DESeq2 edgeR	244.87 3.19	−0.61 −1.32	.00 .03	−0.96
GRAMD1B	ENSG000000 23171	***GRAM domain containing 1B***	**28**	**55**	**92**	**132**	**262**	**238**	**DESeq2 edgeR**	**112.66 2.09**	**−0.55 −1.07**	**.03 .10**	**−0.81**

			Patiens		*Filteres read counts*		Controls						
Gene symbol	**Ensembl ID**	**Gene name**	**IV.10**	**IV.11**	**IV.10**	**IV.5**	**III.9**	**IV.8**	**Method**	**Basemean/cpm**	**fc**	**adj_pval**	**mean fc**
HSPA1L	ENSG00000204390	*Heat shock 70kDa protein 1-like*	449	330	319	289	338	313	DESeq2 edgeR	368.47 3.73	0.60 1.06	.01 .03	0.83
HSPA6	ENSG00000173110	*Heat shock 70kDa protein 6 (HSP70B′)*	434	221	258	195	273	260	DESeq2 edgeR	300.17 3.43	0.59 1.20	.02 .04	0.89
IFITM3	ENSG00000142089	*Interferon induced transmembrane protein 3*	664	828	1101	570	646	869	DESeq2 edgeR	820.59 4.89	0.78 1.07	.00 .00	0.93
IL17RB	ENSG00000056736	*Interleukin 17 receptor B*	2074	2053	2575	1434	2227	2270	DESeq2 edgeR	2197.23 6.31	0.84 0.99	.00 .00	0.92
LFNG	ENSG00000106003	*LFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyl transferase*	142	122	209	130	163	102	DESeq2 edgeR	151.73 2.45	0.60 1.03	.01 .07	0.81
MB21D2	ENSG00000180611	***Mab-21 domain containing 2***	**810**	**793**	**698**	**558**	**693**	**509**	**DESeq2** **edgeR**	**739.07** **4.74**	**0.79** **1.21**	**.00** **.00**	**1.00**
MDGA1	ENSG00000112139	*MAM domain containing glycosylphosphatidylinositol anchor 1*	215	327	319	8	6	9	DESeq2 edgeR	190.05 2.73	2.86 6.00	.00 .00	4.43
NDUFA4L2	ENSG00000185633	***NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 4-like 2***	**133**	**109**	**227**	**120**	**117**	**133**	**DESeq2** **edgeR**	**147.17** **2.41**	**0.58** **1.07**	**.02** **.08**	**0.82**
NEDD4L	ENSG00000049759	***Neural precursor cell expressed, developmentally down-regulated 4-like, e3 ubiquitin protein ligase***	**1187**	**873**	**1481**	**740**	**1277**	**1189**	**DESeq2** **edgeR**	**1162.32** **5.39**	**0.75** **0.97**	**.00** **.00**	**0.86**
PARD3	ENSG00000148498	*Par-3 partitioning defective 3 homolog (C. elegans)*	1265	1113	1557	717	1648	699	DESeq2 edgeR	1223.41 5.47	0.85 1.23	.00 .00	1.04
PEX5L	ENSG00000114757	*Peroxisomal biogenesis factor 5-like*	119	241	274	502	840	1142	DESeq2 edgeR	439.64 4.01	−0.69 −1.18	.00 .01	−0.94
PLA2G4C	ENSG00000105499	***Phospholipase A2, group IVC (cytosolic, calcium-independent)***	**395**	**414**	**420**	**259**	**332**	**508**	**DESeq2** **edgeR**	**409.46** **3.89**	**0.60** **0.98**	**.01** **.04**	**0.79**

			Patiens		*Filteres read counts*		Controls						
Gene symbol	**Ensembl ID**	**Gene name**	**IV.10**	**IV.11**	**IV.10**	**IV.5**	**III.9**	**IV.8**	**Method**	**Basemean/cpm**	**fc**	**adj_pval**	**mean fc**
PRKCH	ENSG000000 27075	*Protein kinase C, eta*	172	161	258	339	1158	995	DESeq2 edgeR	417.46 3.94	−0.70 −1.19	.00 .00	−0.95
PRLR	ENSG000001 13494	*Prolactin receptor*	207	501	384	264	356	224	DESeq2 edgeR	342.71 3.63	0.63 1.16	.01 .02	0.89
PTK2	ENSG000001 69398	*PTK2 protein tyrosine kinase 2*	57	56	77	197	271	434	DESeq2 edgeR	153.62 2.53	−0.75 −1.45	.00 .00	−1.10
PTK7	ENSG000001 12655	*PTK7 protein tyrosine kinase 7*	112	236	262	124	168	147	DESeq2 edgeR	184.37 2.73	0.73 1.24	.00 .01	0.98
RAB31	ENSG000001 68461	*RAB31, member RAS oncogene family*	243	385	286	693	2316	1195	DESeq2 edgeR	688.62 4.65	−0.75 −1.27	.00 .00	−1.01
SPIRE1	ENSG000001 34278	*Spire homolog 1 (Drosophila)*	125	119	271	109	192	100	DESeq2 edgeR	156.40 2.50	0.62 1.13	.01 .04	0.88
TIGIT	ENSG000001 81847	*T cell immunoreceptor with Ig and ITIM domains*	288	222	636	216	316	347	DESeq2 edgeR	346.43 3.65	0.65 1.12	.00 .02	0.88
TMEM51	ENSG000001 71729	*Transmembrane protein 51*	184	157	252	123	242	191	DESeq2 edgeR	195.55 2.82	0.66 0.92	.00 .04	0.79
TNFRSF21	ENSG000001 46072	***Tumor necrosis factor receptor superfamily, member 21***	**178**	**264**	**325**	**146**	**344**	**146**	**DESeq2** **edgeR**	**239.61** **3.11**	**0.68** **1.12**	**.00** **.01**	**0.90**
TOX	ENSG000001 98846	*Thymocyte selection-associated high mobility group box*	43	71	64	153	391	211	DESeq2 edgeR	128.11 2.27	−0.67 −1.20	.00 .02	−0.94

cpm = counts per million; fc = log-transformed fold change; adj_pval = adjusted *P*-value