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PARTICIPATING INSTITUTIONS

The following CALGB/Alliance institutions participated in this study. For each of these institutions, the current or last principal investigator and the cytogeneticists who analyzed the cases are listed as follows:

Dana Farber Cancer Institute, Boston, MA: Harold J. Burstein, Ramana Tantravahi, Cynthia C. Morton and Paola Dal Cin (grant no. U10CA032291); Roswell Park Cancer Institute, Buffalo, NY: Ellis G. Levine and AnneMarie W. Block (grant no. U10CA059518); The Ohio State University Medical Center, Columbus, OH: Richard M. Goldberg, Karl S. Theil and Nyla A. Heerema (grant no. U10CA180850); University of Chicago Medical Center, Chicago, IL: Hedy L. Kindler, Diane Roulston, Katrin M. Carlson and Michelle M. LeBeau (grant no. U10CA041287); Duke University Medical Center, Durham, NC: Jeffrey Crawford, Sandra H. Bigner and Barbara K. Goodman (grant no. U10CA047577); North Shore University Hospital, Manhasset, NY: Daniel R. Budman, Prasad R. K. Koduru and Chandrika Sreekantaiah (grant no. U10CA035279); Washington University School of Medicine, St. Louis, MO: Nancy L. Bartlett, Jaime Garcia-Heras and Shashikant Kulkarni (grant no. U10CA077440); University of Alabama at Birmingham: Robert Diasio and Andrew J. Carroll; Georgetown University Medical Center, Washington, DC: Minnetta C. Liu and Jeanne M. Meck; Long Island Jewish Medical Center, Lake Success, NY: Daniel R. Budman and Prasad R. K. Koduru; Vermont Cancer Center, Burlington, VT: Steven M. Grunberg and Mary Tang; University of Missouri/Ellis Fischel Cancer Center, Columbia, MO: Clint Kingsley and Tim Hui-Ming Huang; Mount Sinai School of Medicine, New York, NY: Lewis R. Silverman and Vesna Najfeld; Rhode Island Hospital, Providence, RI: Howard Safran, and Aurelia Meloni-Ehrig; University of Tennessee Cancer Center, Memphis, TN: Harvey B. Niell and Sugandhi A. Tharapel; University of Illinois, Chicago, IL: Arkadiusz Z. Dudek and Valerie Lindgren; Moores University of California San Diego Cancer Center, San Diego, CA: Barbara A. Parker and E. Robert Wassman, Jr.; University of Maryland Cancer Center, Baltimore, MD: Martin J. Edelman and Judith Stamberg.

TREATMENT PROTOCOLS

Patients in this study received intensive cytarabine/daunorubicin-based therapy on one of the following Cancer and Leukemia Group B (CALGB) frontline treatment protocols: 8525 (n=5),[1] 8923 (n=1),[2] 9120 (n=1),[3] 9222 (n=4),[4] 9621 (n=5),[5] 19808 (n=3),[6] 10503 (n=5),[7] 9720 (n=2),[8] 10201 (n=3),[9] 10603 (n=1),[10] 11002 (n=2) or 10102 (n=3).[11] CALGB 11002 evaluated clinical benefit from primary therapy with decitabine-based chemotherapy, given either alone or in combination with bortezomib.

Patients who enrolled on the treatment protocols also provided written informed consent to participate in the companion protocols CALGB 8461[12] (prospective cytogenetic companion), CALGB 9665 (leukemia tissue bank), which involved collection and preservation of pretreatment bone marrow (BM) aspirates, blood samples, and buccal swabs and CALGB 20202 (molecular studies in AML). Study protocols were in accordance with the Declaration of Helsinki and approved by the institutional review boards at each center, and all patients provided written informed consent.

DEFINITION OF CLINICAL END POINTS

Complete remission (CR) required an absolute neutrophil count ≥1,500/μL, platelet count ≥100,000/μL, no leukemic blasts in the blood, BM cellularity ≥ 20% with maturation of all cell lines, no Auer rods, <5% BM blast cells, and no evidence of extramedullary leukemia, all of which had persisted for at least 1 month. Relapse was defined by ≥5% BM blasts, circulating leukemic blasts, or the development of extramedullary leukemia. Disease-free survival (DFS) was measured from the date of CR until the date of relapse or death; patients alive and relapse-free at last follow-up were censored. Overall survival (OS) was measured from the date on study

until the date of death, and patients alive at last follow-up were censored.[13]

SUPPLEMENTARY METHODS

We reviewed the CALGB/Alliance database, which contains 4,455 AML and ALL patients consecutively, and identified 35 adults with translocations between chromosomes 11 and 19. Nineteen patients, all diagnosed with AML, harbored t(11;19)(q23;p13.1). Among 16 patients with t(11;19)(q23;p13.3), 12 were diagnosed with AML, three with ALL, and one with ambiguous lineage acute leukemia (who received AML-type therapy and is, for the purposes of this study, grouped with AML patients). All patients with t(11;19) received treatment on CALGB protocols and provided Institutional Review Board-approved, protocol-specific informed consent in accordance with federal and institutional guidelines. Pretreatment BM and/or blood samples were analyzed cytogenetically in CALGB-designated institutional laboratories using short-term (24-48 hours) unstimulated cultures, a direct method or both. At least 20 G- or Q-banded metaphases were analyzed in all but one patient. The karyotypes were interpreted according to the International System for Human Cytogenetic Nomenclature.[14] A minimum of two karyotypes from each abnormal clone were centrally reviewed by the CALGB Karyotype Review Committee.[15]

Baseline characteristics were compared between t(11;19)(q23;p13.1) and t(11;19)(q23;p13.3) AML patients using Fisher's exact test for categorical variables and the Wilcoxon rank-sum test for continuous variables.[16] For time-to-event analyses, we calculated survival estimates using the Kaplan-Meier method, and compared groups by the log-rank test.[17] Statistical analyses were performed by the Alliance Statistics and Data Center. Results analyzed were available in the database as of February 9, 2015.

Molecular analyses

Viable cryopreserved BM or blood cells of patients enrolled onto the CALGB 9665 tissue bank protocol were stored for future analyses prior to starting treatment. Mononuclear cells from BM or blood were enriched by Ficoll-Hypaque gradient and cryopreserved in liquid nitrogen until thawed at 37^{o}C for analysis. DNA extractions were performed using the DNeasy Blood and Tissue Kit (QIAGEN, Hilden, Germany). The mutational status of 32 genes (*ASXL1*, *BCOR*, *BCORL1*, *CBL*, *DNMT3A*, *ETV6*, *EZH2*, *FLT3* for tyrosine kinase domain mutations [*FLT3*-TKD], *GATA2*, *IDH1*, *IDH2*, *KIT*, *KRAS*, *NPM1*, *NRAS*, *PHF6*, *PTPN11*, *RAD21*, *RUNX1*, *SF1*, *SF3A1*, *SF3B1*, *SMC1A*, *SMC3*, *SRSF2*, *STAG2*, *TET2*, *TP53*, *U2AF1*, *U2AF2*, *WT1* and *ZRSR2*) was determined by targeted amplicon sequencing using the Miseq platform (Illumina, San Diego, CA). The variant allele frequency (VAF) cut-off for reporting mutations was set to 0.3. Testing for the presence or absence of *FLT3* internal tandem duplication (*FLT3*-ITD) and mutations in *CEBPA* was performed as previously described.[18,19] Only double *CEBPA* mutations were considered as clinically relevant. Molecular analyses were performed at The Ohio State University, Columbus, OH.

Gene- and microRNA-expression profiling

Total RNA was extracted from BM or blood blast cells using the Trizol extraction method kit (QIAGEN). For each sample with adequate quantity and quality of RNA, the RNA was used to make two sets of libraries. Gene expression libraries were constructed with the Illumina Truseq stranded mRNA library preparation kit, while small RNA libraries were constructed with the NEBNext small RNA library prep kit (New England Biolabs, Ipswich, MA). Both libraries were sequenced on an Illumina HiSeq 2500 targeting 40x10^{6} and 25x10^{6} reads for mRNA and small RNA libraries, respectively.

DNA library preparations were performed according to the manufacturer's instructions. Samples were pooled and run on the Miseq machine using the Illumina Miseq Reagent Kit v3. Sequenced reads were aligned to the hg19 genome build using the Illumina Isis Banded Smith-Waterman aligner. Single nucleotide variant and indel calling was performed using MuTect and GATK SomaticIndelDetector (Broad Institute, Cambridge, MA), respectively.[20,21] Aggregate putative variant reports were produced with Mucor.[22] All called variants underwent visual inspection of the aligned reads using the Integrative Genomics Viewer (Broad Institute).[23]

Protein-coding gene expression was quantitated by estimating abundances for protein-coding isoforms from GENCODE21[24] with Sailfish,[25] then using custom bioinformatics scripts to collapse isoforms into genes. Estimated gene-level counts were input into DESeq2[26] and genes were tested for differential expression between groups using the negative binomial test. Raw reads were also aligned to GRCh38 using STAR,[27] and chimeric/fusion transcripts were called using custom bioinformatics scripts.

Alignments of microRNAs from the Illumina FASTQ files were obtained using Novoalign (Novocraft, Selangor, Malaysia). Quality control was performed with FastQC (Babraham Institute, Cambridge, UK), and the adaptor stripping option in Novoalign was used to remove any residual terminal adaptor sequences left in the reads. The microRNAs were normalized as reads per million, thresholded at 10, and invariant microRNAs were removed using standard conditions (<20% of expression data have at least a 1.5-fold change in either direction from microRNA's median value or percent of data missing or filtered out exceeds 50%). MicroRNAs differentially expressed between the two cytogenetic groups with a *P*-value <0.05 and false discovery rate (FDR) <0.1 were used to define the microRNA signature.

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Supplementary Table S1. Cytogenetic, hematologic and clinical characteristics and treatment outcomes of AML patients with t(11;19)(q23;p13.1)

Patient no.	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
Patients with t(11;19)(q23;p13.1) as a sole chromosome abnormality												
1	63/F	B	46,XX,t(11;19)(q23;p13.1)[2]/46,XX[5]	M1	10.4	110	4.1	25/43	No	CR	74.1+	75.4+
2	28/F	W	46,XX,t(11;19)(q23;p13.1)[20]	M4	10.3	111	71.3	22/33	No	NE[a]	NA	11
3	47/M	W	46,XY,t(11;19)(q23;p13.1)[7]/ 46,XY[13]	M2	8.9	22	3.2	4/26	No	CR	5.5	10.4[b]
4	54/M	W	46,XY,t(11;19)(q23;p13.1)[30]	M5a	8.9	19	52.5	1/NR	No	NE[c]	NA	0.1
5	58/F	Native Ameri-can	46,XX,t(11;15;19)(q23;q15;p13.1) [20]	M5b	8.6	74	71.8	26/51	No	CR	3.6	11.4[d]
6	43/M	W	46,XY,t(11;19)(q23;p13.1)[15]/ 46,XY[5]	M4	15.8	163	37.7	8/55	NR	CR	37.5+	38.4+[d]
7	67/M	NR	46,XY,t(11;19)(q23;p13.1)[24]/ 46,XY[8]	NR	8.9	34	2.1	14/34	No	No CR	NA	3.8
8	41/F	W	46,XX,t(11;19)(q23;p13.1)[28]	M4	8.2	19	90	11/85	No	No CR	NA	1.5
9	60/F	W	46,XX,t(11;19)(q23;p13.1)[20]	M2	8.6	16	4.6	41/68	Skin, gums	No CR	NA	2
10	64/F	W	46,XX,t(11;19)(q23;p13.1)[42]	M5b	11.1	49	25.4	2/86	Liver	CR	5.5	11
11	20/F	W	46,XX,t(11;19)(q23;p13.1)[26]	M4	2.8	29	97.5	51/77	Gums, lymph nodes	No CR	NA	7.5

Patient no.	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
12	54/M	W	46,XY,t(11;19)(q23;p13.1)[22]	M5b	10.2	88	59.3	5/76	No	CR	6.3	8.2
13	24/F	W	46,XX,t(11;19)(q23;p13.1)[20]	M4	7.8	42	71.6	0/50	Heart, lung, liver and colon	NE[e]	NA	0
14	58/M	W	46,XY,t(11;19)(q23;p13.1)[19]]/ 46,XY[1]	M4	9.1	117	21.5	6/58	No	No CR	NA	9.4
Patients with t(11;19)(q23;p13.1) and secondary chromosome abnormalities												
15	70/F	W	46,XX,t(11;19)(q23;p13.1)[1]/ 46,XX,add(5)(q33),add(10)(p11.2), der(11)add(11)(p11.2)add(11)(q12),der(19)t(11;19)(q23;p13.1)[17]/ 46,XX[2]	M5a	8.8	28	40.6	5/46	Skin	No CR	NA	0.5
16	35/M	W	47,XY,+8,t(11;19)(q23;p13.1)[30]	M5a	9.8	59	29.4	75/93	No	CR	4.1	7.7[b]
17	66/F	W	46,XX,t(11;19)(q23;p13.1)[3]/ 47,XX,idem,+21[2]/46,XX[25]	M2	10	97	2.8	21/64	No	CR	17.9	28.5
18	33/M	W	46,XY,t(11;19)(q23;p13.1)[17]/ 46,idem,inv(12)(p12p13)[3]	M5b	10.3	111	25.9	10/63	No	No CR	NA	7.6
19	49/F	His-panic	46,XX,t(11;19)(q23;p13.1)[25]/ 46,idem,del(20)(q11)[3]	M4	10.7	42	7.6	2/44	No	CR	5.6	23.5

Abbreviations: B,African American; BM, bone marrow; CR, complete remission; DFS, disease-free survival; FAB, French-American-British classification; F, female; Hb, hemoglobin; M, male; NA, not applicable; NE, not evaluable; NR, not reported, OS, overall survival; PB, peripheral blood; Plts, platelet count; W, Caucasian; WBC, white blood count.

[a] No bone marrow examination after treatment was performed.
[b] Patient underwent autologous hematopoietic stem cell transplant in first complete remission.
[c] Patient died of acute renal failure on day one of treatment.
[d] Patient underwent allogeneic hematopoietic stem cell transplant in first complete remission.
[e] Patient died of cardiac arrest one day after receiving chemotherapy.

Supplementary Table S2. Cytogenetic, hematologic and clinical characteristics and treatment outcomes of AML patients with t(11;19)(q23;p13.3)

Patient no.	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
Patients with AML and t(11;19)(q23;p13.3) as a sole chromosome abnormality												
20	40/F	W	46,XX,t(11;19)(q23;p13.3)[20]	Other[a]	7.8	65	10	13/45	No	NE[b]	NA	0.4
21	34/F	W	46,XX,t(11;19)(q23;p13.3)[20]	M1	8.5	21	36.5	72/86	No	No CR	NA	9.2
22	25/F	W	46,XX,t(11;19)(q23;p13.3)[32]/ 46,XX[2]	M5a	10.7	86	29.7	85/92	Gums, lymph nodes	CR	10.8	20.3
23	26/F	W	46,XX,t(11;19)(q23;p13.3)[22]	M5b	9.6	45	8.3	44/87	No	CR	9.5	17.8
24	84/F	W	46,XX,t(11;19)(q23;p13.3)[15]/ 46,XX[5]	M5a	10	29	20.2	76/90	No	CR	2.7	5.6
Patients with AML and t(11;19)(q23;p13.3) and secondary chromosome abnormalities												
25	67/F	W	46,XX,t(11;19)(q23;p13.3)[16]/ 47,idem,+8[4]	Other[c]	10.4	140	10.4	6/72	No	CR	89.3+	90.7+[d]
26	27/M	Native Ameri-can	46,XY,t(11;19)(q23;p13.3)[1]/ 47,idem,+8[22]]/46,XY[6]	M5b	7.5	56	3.6	61/88	No	CR	2.2	7.6
27	34/F	B	47,XX,+8,t(11;19)(q23;p13.3)[13]/ 46,XX[7]	M5a	12	21	2.6	45/96	Gums	CR	10	15.1
28	31/F	W	46,XX,+8,t(11;19)(q23;p13.3), +13[20]	M5a	9.5	66	52.7	73/94	No	NE[e]	NA	1.3

Patient no.	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-pons e*	*DFS (mo)*	*OS (mo)*
29	43/F	W	46,XX,+8,dic(10;12)(p11.2;p11.2), t(11;19)(q23;p13.3)[21]	M5b	7.4	88	6.4	45/90	NR	CR	6.0	10.0
30	38/M	W	46,XY,t(11;19)(q23;p13.3)[15]/ 47,idem,+X,del(12)(p12p13)[5]	M0	9.6	184	2.3	2/60	No	CR	133+	134.3+[f]
31	62/M	W	46,XY,+9,t(11;19)(q23;p13.3),-14, i(14)(q10)[20]	Other[c]	8.9	34	80.7	86/85	Spleen	No CR	NA	12.5
32	70/M	W	46,XY,del(7)(q11.2q36),t(11;19) (q23;p13.3),del(20)(q11.2q13.3) [18]/46,idem,add(5)(q31), add(6)(q12)[3]	NR	6.2	20	2.6	55/84	No	NE[g]	NA	1.1

Abbreviations: B, African American; BM, bone marrow; CR, complete remission; CRi, complete remission with incomplete count recovery, DFS, disease-free survival; FAB, French-American-British classification; F, female; Hb, hemoglobin; M, male; mo, months; NA, not applicable; NE, not evaluable; NR, not reported, OS, overall survival; PB, peripheral blood; Plts, platelet count; W, Caucasian; WBC, white blood count.

[a] Ambiguous lineage acute leukemia.
[b] Patient died on day 11 of treatment.
[c] Therapy-related AML.
[d] Patient underwent allogeneic hematopoietic stem cell transplant in first complete remission.
[e] Patient died of cardiopulmonary arrest before disease response assessment.
[f] Patient underwent autologous hematopoietic stem cell transplant in first complete remission.
[g] Patient died of massive subdural hemorrhage on day 2 of second induction cycle of treatment.

Supplementary Table S3. Cytogenetic, hematologic and clinical characteristics and treatment outcomes of ALL patients with t(11;19)(q23;p13.3)

Patient no.	*Age/ Sex*	*Race*	*Karyotype*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
33	79/F	W	46,XX,t(11;19)(q23;p13.3)[20]	12.5	165	92.5	10/90	No	CRi	2.1	5.2
34	79/F	W	BM: 46,XX,t(11;19)(q23;p13.3)[20] Blood: 46,XX,t(11;19)(q23; p13.3)[20]	13.8	11	231.9	98/94	NR	No CR	NA	0.8
35	30/F	B	86<4n>,XXXX,add(1)(p36.1)x2,-9, -11,t(11;19)(q23;p13.3),-12,-15, -17, -18,der(19)t(11;19)(q23; p13.3)[20]	7.7	66	11.8	46/65	No	CR	7.9	8.8[a]

Abbreviations: B, African American; BM, bone marrow; CR, complete remission; CRi, complete remission with incomplete count recovery, DFS, disease-free survival; F, female; Hb, hemoglobin; mo, months; NA, not applicable; NR, not reported, OS, overall survival; PB, peripheral blood; Plts, platelet count; W, Caucasian; WBC, white blood count.

[a] Patient underwent allogeneic hematopoietic stem cell transplant in first complete remission.

Supplementary Table S4. Cytogenetic, hematologic and clinical characteristics and treatment outcomes of previously reported adult patients with t(11;19)(q23;p13.1) for whom outcome data are available

Study/Case no.[a]	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*AML type*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
Patients with t(11;19)(q23;p13.1) as a sole chromosome abnormality													
Cerveira[28]/5	47/F	NR	46,XX,t(11;19)(q23;p13.1)[22]	M5	t-AML	9	83	107	1/44	No	No CR	NA	4
De Braekeleer[29]/P9	50/F	NR	46,XX,t(11;19)(q23;p13)[25]/ 46,XX[3][b]	M2	t-AML	8.8	162	6.1	22/38	No	No CR	NA	5
De Braekeleer[29]/ P10	51/F	NR	46,XX,t(11;19)(q23;p13.1)[19]/ 46,XX[4][b]	M2	s-AML	7.1	84	68	8/20	No	CR	35	38
Huh[30]/S13	57/F	Asian	46,XX,t(11;19)(q23;p13.1)[16]/ 46,XX[4]	NR	t-AML	NR	NR	NR	NR	NR	CR	10	NR
Huret[31]/11	53/F	NR	46,XX,t(11;19)(q23;p13.1)	M4	t-AML	10.1	51	1	0/NR	No	CR	12+	15+
Huret[31]/14	63/F	NR	46,XX,t(11;19)(q23;p13.1)	M1/M2	t-AML	10	50	24	45/NR	No	PR	NA	3
Kakihana[32]/1	77/M	Asian	46,XY,t(11;19)(q23;p13.1)	NR	s-AML	NR	NR	NR	NR/20	NR	CR	NR	15
Kondo[33]/33	42/M	Asian	46,XY,t(11;19)(q23;p13.1)	NR	*de novo*	NR	NR	NR	NR	NR	No CR	NA	49.8+
Manola[34]/1	46/F	NR	Diagnosis: 46,XX,t(11;19)(q23;p13.1)[10]/ 46,XX[13] Relapse: 46,XX,t(11;19)(q23;p13.1)[5]/ 46,idem,t(12;12)(p13;q13)[15]	M2	t-AML	8.8	40	1.06	0/35	No	CR	8	14+
Moorman[35]/128	50/M	NR	46,XY,t(11;19)(q23;p13.1)	M2	*de novo*	NR	NR	3	NR	NR	CR	NR	26.5
Moorman[35]/129	63/M	NR	46,XY,t(11;19)(q23;p13.1)	M4	*de novo*	NR	NR	16	NR	NR	CR	NR	14.1
Moorman[35]/136	36/M	NR	46,XY,t(11;19)(q23;p13.1)	M4	*de novo*	NR	NR	10	NR	NR	CR	NR	13.4+
Moorman[35]/279	17/M	NR	46,XY,t(11;19)(q23;p13.1)	M1	*de novo*	NR	NR	56	NR	NR	CR	NR	5.4
Moorman[35]/313	30/F	NR	46,XX,t(11;19)(q23;p13.1)	M4	*de novo*	NR	NR	NR	NR	NR	CR	NR	3.4+
Moorman[35]/365	53/F	NR	46,XX,t(11;19)(q23;p13.1)	M4	s-AML	NR	NR	3	NR	NR	CR	NR	52.9
Moorman[35]/372	66/M	NR	46,XY,t(11;19)(q23;p13.1)	M4	s-AML	NR	NR	28	NR	NR	No CR	NA	7.2

Study/Case no.[a]	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*AML type*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
Moorman[35]/378	63/F	NR	46,XX,t(11;19)(q23;p13.1)	M4	*de novo*	NR	NR	6	NR	NR	CR	NR	7.3
Moorman[35]/382	60/F	NR	46,XX,t(11;19)(q23;p13.1)	M2	s-AML	NR	NR	1	NR	NR	CR	NR	19.3
Moorman[35]/383	32/F	NR	46,XX,t(11;19)(q23;p13.1)	M5	*de novo*	NR	NR	5	NR	NR	CR	NR	36.2+
Moorman[35]/388	60/M	NR	46,XY,t(11;19)(q23;p13.1)	NR	*de novo*	NR	NR	12	NR	NR	CR	NR	12.5+
Moorman[35]/466	61/F	NR	46,XX,t(11;19)(q23;p13.1)	M2	s-AML	NR	NR	161	NR	NR	CR	NR	16.5
Moorman[35]/468	18/M	NR	46,XY,t(11;19)(q23;p13.1)	M1	*de novo*	NR	NR	7	NR	NR	CR	NR	6.6
Moorman[35]/470	60/F	NR	46,XX,t(11;19)(q23;p13.1)	M5a	*de novo*	NR	NR	55	NR	NR	CR	NR	35+
Muto[36]/1	35/F	Asian	46,XX,t(11;19)(q23;p13.1)	M5b	*de novo*	NR	NR	56.5	NR	NR	CR	NR	15.8[c]
Muto[36]/2	31/M	Asian	46,XY,t(11;19)(q23;p13.1)	M5b	*de novo*	NR	NR	136.2	NR	NR	CR	NR	9[c]
Muto[36]/3	33/M	Asian	46,XY,t(11;19)(q23;p13.1)	M4	*de novo*	NR	NR	27.9	NR	NR	CR	NR	156.6+[c]
Muto[36]/5	33/M	Asian	46,XY,t(11;19)(q23;p13.1)	M4	*de novo*	NR	NR	4.4	NR	NR	CR	NR	6.3[c]
Muto[36]/6	16/F	Asian	46,XX,t(11;19)(q23;p13.1)	M1	*de novo*	NR	NR	4.6	NR	NR	CR	NR	5+[c]
Muto[36]/7	24/F	Asian	46,XX,t(11;19)(q23;p13.1)	M1	*de novo*	NR	NR	0.5	NR	NR	CR	NR	127.6+[c]
Muto[36]/8	34/M	Asian	46,XY,t(11;19)(q23;p13.1)	M4	*de novo*	NR	NR	9.7	NR	NR	CR	NR	88.4[c]
Parkin[37]/ MI-AML-036	55/M	NR	Diagnosis: 46,XY,t(11;19)(q23;p13.1)[20] Relapse: 46,XY,t(11;19)(q23;p13.1)[19]/ 46,XY[1]	M4	*de novo*	NR	NR	NR	NR	NR	CR	1.3	NR
Parkin[37]/ MI-AML-068	58/F	NR	Diagnosis: 46,XX,t(11;19)(q23;p13.1)[20] Relapse: 46,XX,t(11;19)(q23;p13.1)[18]/ 46,XY[2]	M4	t-AML	NR	NR	NR	NR	NR	CR	21.6	NR

Study/Case no.[a]	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*AML type*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
Sarova[38]/36	36/F	NR	46,XX,t(11;19)(q23;p13.1)	NR	*de novo*	NR	NR	NR	NR	NR	NR	NR	13.5
Yamamoto[39]/1	75/F	Asian	Diagnosis: 46,XX,t(11;19)(q23;p13.1)[18]/ 46,XX[2][b] Second relapse: 46,XX,t(11;19)(q23;p13.1)[16]/ 46,idem,t(8;12)(q13;p13)[4]	M4	*de novo*	5.7	43	38.9	58/49	NR	CR	8	21
Patients with t(11;19)(q23;p13.1) and secondary chromosome abnormalities													
Huret[31]/10	49/F	NR	47,XX,+8,t(11;19)(q23;p13.1), del(13q)	M5a	*de novo*	4.9	17	47	71/NR	No	NE	NA	0.5
Huret[31]/12	56/M	NR	45,XY,-7,+t(7q;10q),-10, t(11;19)(q23;p13.1)	M5b	*de novo*	12	30	66	61/NR	Yes	CR	NR	12+
Huret[31]/13	59/M	NR	46,XY,t(11;19)(q23;p13.1)/ 46,idem,del(6)(p21)	M2	*de novo*	9.1	67	2	6/NR	No	CR	NR	39
Huret[31]/16	75/F	NR	46,XX,t(11;19)(q23;p13.1)/ 47,idem,+8	M4	*de novo*	8.1	20	321	74	Yes	CR	2	5
Muto[36]/4	32/F	Asian	47,XX,t(11;19)(q23;p13.1),+8	M1	*de novo*	NR	NR	0.8	NR	NR	CR	NR	135.8+[c]
Moorman[35]/ 142	38/M	NR	46,XY,t(11;19)(q23;p13.1), del(17)(p12)	M5b	*de novo*	NR	NR	59	NR	NR	?CR	NR	0.5+
Takeuchi[40]/1	32/F	Asian	47,XX,+8,t(11;19)(q23;p13.1) [20][d]	M1	*de novo*	Pan-cyto-penic	Pan-cytope-nic	Pan-cytope-nic	NR/90	NR	CR	16+	NR
Vermaelen[41]/6	81/M	NR	BM: 47,XY,+8,t(11;19)(q23;p13.1) [10][e] Blood: 46,XY,t(11;19)(q23;p13.1)[2]/ 47,idem,+8[9][e]	M4	*de novo*	NR	NR	24.3	50	No	No CR	NA	0.75

Abbreviations: BM, bone marrow; CR, complete remission; DFS, disease-free survival; FAB, French-American-British classification; F, female; Hb, hemoglobin; M, male; mo, months; NA, not applicable; NE, not evaluable; NR, not reported; OS, overall survival; Plts, platelet count; PB, peripheral blood; PR, partial remission; s-AML, secondary AML evolving from antecedent hematologic malignancy; t-AML, therapy-related AML; WBC, white blood count.

[a] For each case from the literature, the first author's name and superscript reference number of the study reporting them is followed by the case number in this study.

[b] This patient is positive for the *MLL*/*ELL* gene fusion detected using long distance inverse PCR.
[c] For these cases, this is survival after transplantation.
[d] This patient is positive for the *MLL*/*ELL* gene fusion detected using RT-PCR.
[e] Translocation (11;19) reported as t(11;19)(q22;p11). The presence of t(11;19)(q23;p13.1) determined based on the Figure 1d in this report.[41]

Supplementary Table S5: Cytogenetic, hematologic and clinical characteristics and treatment outcomes of previously reported adult patients with t(11;19)(q23;p13.3) for whom outcome data are available

Study/ Case no. [a]	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*AML/ ALL type*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
Patients with AML and t(11;19)(q23;p13.3) as a sole chromosome abnormality													
Blanco[42]/1	18/M	NR	46,XY,t(11;19)(q23;p13.3)	M4	t-AML	NR	NR	NR	NR	NR	NR	NR	7
Cerveira[28]/21	61/M	NR	46,XX,t(11;19)(q23;p13.3)[15]/ 46,XX[15]	M5	t-AML	8.6	36	65.9	93/83	Yes	No CR	NA	1+
Naghashpour[43]/1	37/M	NR	46,XY,t(11;19)(q23;p13.3)[9]/ 46,XY[11]	NA	MPAL	8.6	179	10.6	3/NR	No	CR	7.5+	9+
Moorman[35]/117	17/F	NR	46,XX,t(11;19)(q23;p13.3)	M4	*de novo*	NR	NR	NR	NR	NR	CR	NR	9.8
Moorman[35]/556	30/F	NR	46,XX,t(11;19)(q23;p13.3)	M4	*de novo*	NR	NR	9	NR	NR	CR	NR	10.6+
Sarova[38]/28	43/M	NR	46,XY,t(11;19)(q23;p13.3)[19]/ 46,XY[3]	M1	s-AML	NR	NR	NR	NR	NR	NR	NR	0.7
Sarova[38]/34	42/M	NR	46,XY,t(11;19)(q23;p13.3)[18]/ 46,XY[4]	M5a	*de novo*	NR	NR	NR	NR	NR	NR	NR	21+
Sarova[38]/35	31/M	NR	46,XY,t(11;19)(q23;p13.3)[18]/ 46,XY[3]	NR	*de novo*	NR	NR	NR	NR	NR	NR	NR	14.3
Shen[44]/1	18/M	Asian	46,XY,t(11;19)(q23;p13.3)	M5b	t-AML	10.3	54	202.6	90	Gums, Skin	No CR	NA	3
Suehiro[45]/1	76/M	Asian	46,XY,t(11;19)(q23;p13.3)[20]	M0	t-AML	8.2	26	3.2	51/84	NR	NR	NR	3
Zhang[46]/1	37/M	NR	46,XY,t(11;19)(q23;p13.3)[7]/ 46,XY[5]	M5a	t-AML	NR	NR	74.6	92/NR	No	NR	NA	2
Cerveira[28]/22	59/M	NR	46,XY,t(11;19)(q23;p13.3), add(12)(p12)[10]/46,XY[10]	NA	AMDCL	11.6	136	1.2	NA/81	Yes	CR	11	13
Cerveira[28]/23	68/M	NR	47,XY,der(2)t(1;2)(q21;q37), +i(8)(q10),t(11;19)(q23;p13.3) 47,idem,+8,-i(8)(q10)[3]	M5	*de novo*	8.1	9	0.1	NA/37.5	No	No CR	NA	23
Chin[47]/1	24/F	NR	46,XX,t(11;19)(q23;p13.3), der(22)(22pter→22q13: :19p11→19p13.3::11q23→ 11qter)[3]/45,idem,-X[19]	NR	t-AML	8.9	31	NR	NR/90	NR	CR	NR	NR

Study/ Case no. [a]	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*AML/ ALL type*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
Patients with AML and t(11;19)(q23;p13.3) and secondary chromosome abnormalities													
Cigudosa[48]/1	73/ M	NR	37~58,XX,der(3)t(3;21)(q11.2; q11.2),del(5)(q12q33),+8, der(8)t(8;11)(p21;p11.2)t(8;12) (q22;q13),t(11;19)(q23;p13.3), der(12)t(12;18)(q24;q11.2), der(16)t(3;16)(?;p11.2),der(18) t(3;18)(?;q21),der(19)ins(19; 17)(p13.1;?)t(3;19)(q11.2; p13.3),r(11)x2amp(MLL)	M6	*de novo*	NR	NR	NR	NR	NR	NR	NR	1
De Braekeleer[29]/P8	44/F	NR	49,XX,+8,+8,+8,t(11;19)(q23; p13)[25][b]	M5	*de novo*	NR	NR	NR	NR	NA	CR	NR	16+
Moorman[35]/64	25/F	NR	46,XX,t(11;19)(q23;p13.3)/ 47,idem,+8/47,idem,+mar	M2	*de novo*	NR	NR	8	NR	NR	CR	NR	55.4
Moorman[35]/ 373	74/ M	NR	46,XY,t(11;19)(q23;p13.3)/ 46,XY,-7,der(11)t(11;19),-19, +mar,+r	M5a	*de novo*	NR	NR	20	NR	NR	CR	NR	3.6
Moorman[35]/ 402	23/ M	NR	47,XY,t(11;19)(q23;p13.3),+21	M1	*de novo*	NR	NR	94	NR	NR	CR	NR	5.4+
Moorman[35]/ 578	20/F	NR	48,XX,add(6)(q23),+8,t(11;19) (q23;p13.3),+der(19)t(11;19)	M6	*de novo*	NR	NR	92	NR	NR	CR	NR	106.1+
Moorman[35]/ 604	75/ M	NR	45,XY,-7,t(11;19)(q23;p13.3)	NA	AL	NR	NR	1	NR	NR	CR	NR	3.8+
Ninomiya[49]/1	34/F	Asian	46,XX,t(11;19)(q23;p13), add(12)(p11)[10]/46,idem,i(21) (q10)[5]/46,idem,add(21) (q22)[5][c]	NA	t-AML	NR	NR	NR	NR	NR	CR	2	6
Vendrame-Goloni[50]/1	18/F	NR	Diagnosis: 43~46,XX,t(5;16)(q13;q22), t(11;19)(q23;p13.3)[cp11]/ 46,XX[8] Second relapse: 33~46,XX,-X[4],del(1)(q21) [16],t(5;16)(q13;q22)[17],-8[5], -10[3],t(11;19)(q25;p13.3)[17], del(12)(p12)[17],-15[4], der(17)t(1;17)(q21; q21)[17], i(17)(q10)[17],-18[5],-20[4], -21[3],-22[6][cp17]	M4eo	*de novo*	9.4	41	63.4	64/NR	No	CR	7	24

Study/ Case no.[a]	*Age/ Sex*	*Race*	*Karyotype*	*FAB*	*AML/ ALL type*	*Hb (g/dL)*	*Plts ($x10^9$/ L)*	*WBC ($x10^9$/ L)*	*PB/BM blasts (%)*	*Organ involve-ment*	*Res-ponse*	*DFS (mo)*	*OS (mo)*
Patients with ALL and t(11;19)(q23;p13.3) as a sole chromosome abnormality													
Moorman[35]/ 336	67/F	NR	46,XX,t(11;19)(q23;p13.3)	NR	Pro-B ALL	NR	NR	257	NR	NR	CR	NR	4.2+
Moorman[35]/ 420	19/M	NR	46,XY,t(11;19)(q23;p13.3)	NR	T-ALL	NR	NR	218	NR	NR	CR	NR	53.8+
Rubnitz[51]/9	15.2/M	B	46,XY,t(11;19)(q23;p13.3)	NR	T-ALL	NR	NR	496	NR	NR	CR	NR	24+
Wright[52]/1	33/M	W	Diagnosis: 46,XY,t(11;19)(q23;p13.3) Relapse: 46,XY,t(11;19)(q23;p13.3), t(3;16)(q23;p13)	L2	T-ALL	NR	NR	173	86/NR	Lymph nodes	PR	NA	38+
Patients with ALL and t(11;19)(q23;p13.3) and secondary chromosome abnormalities													
Finke[53]/P1	31/M	NR	47,XY,+X,i(7)(q10),t(11;19)(q23;p13)[d]	NR	AL	NR	NR	NR	NR	NR	CR	NR	36+
Moorman[35]/122	17/F	NR	47,XX,t(11;19)(q23;p13.3), +17,?add(21)(q22)	NR	T-ALL	NR	NR	117	NR	NR	CR	NR	6.1+
Rubnitz[51]/10	17/M	W	46,XY,del(4)(q21),del(9)(p13), dic(9;13)(p12;p12),t(11;19)(q23;p13.3),+19,+20,-22	NR	T-ALL	NR	NR	6	NR	NR	? lineage switch to AML	14.4	NR
Rubnitz[51]/11	16.6/M	B	47,XY,+8,t(11;19)(q23;p13.3)	NR	B-ALL	NR	NR	73	NR	NR	CR	12	NR
Rubnitz[51]/11	18/F	W	46,XX,add(10)(q24),t(11;19)(q23;p13.3)	NR	T-ALL	NR	NR	80	NR	NR	CR	NR	22.8+
Yoo[54]/1	41/F	Asian	47,XX,+X,t(11;19)(q23;p13.3)[4]/46,XX[16]	NR	t-B-ALL	5.8	31	3.5	15/95	No	CR	3	NR

Abbreviations: AL, acute leukemia; AMDCL, acute myeloid dendritic cell leukemia; BM, bone marrow; CR, complete remission; DFS, disease-free survival; FAB, French-American-British classification; F, female; Hb, hemoglobin; M, male; MPAL, mixed phenotype acute leukemia; mo, months; NR, not reported; NA, not applicable; OS, overall survival; PB, peripheral blood; Plts, platelet count; PR, partial remission; s-AML, secondary AML evolving from antecedent hematologic malignancy; t-B-ALL, therapy-related B-ALL; t-AML, therapy-related AML; WBC, white blood count.

[a] For each case from the literature, the first author's name and superscript reference number of the study reporting them is followed by the case number in this study.
[b] This patient is positive for the *MLL*/*MLLT1* gene fusion detected using long distance inverse PCR.
[c] This patient is positive for the *MLL*/*MLLT1* gene fusion detected using RT-PCR.
[d] The presence of t(11;19)(q23;p13.3) was determined based on Figure 1 in Finke *et al.*[53]

Supplementary Table S6. Comparison of selected genetic changes between AML patients with t(11;19)(q23;p13.1) and those with t(11;19)(q23;p13.3)[a]

Characteristic	*t(11;19)(q23;p13.1) (n=13)*	*t(11;19)(q23;p13.3) (n=8)*	P-*value*[b]
ASXL1, n (%)			0.38
Mutated	0 (0)	1 (13)	
Wild type	13 (100)	7 (87)	
ETV6, n (%)			0.38
Mutated	0 (0)	1 (13)	
Wild type	13 (100)	7 (87)	
FLT3-TKD, n (%)			0.50
Present	2 (15)	0 (0)	
Absent	11 (85)	8 (100)	
GATA2, n (%)			0.38
Mutated	0 (0)	1 (13)	
Wild type	13 (100)	7 (87)	
KIT, n (%)			0.38
Mutated	0 (0)	1 (13)	
Wild type	13 (100)	7 (87)	
KRAS, n (%)			1.00
Mutated	1 (8)	0 (0)	
Wild type	12 (92)	8 (100)	
NRAS, n (%)			1.00
Mutated	1 (8)	0 (0)	
Wild type	12 (92)	8 (100)	
SF1, n (%)			0.38
Mutated	0 (0)	1 (13)	
Wild type	13 (100)	7 (87)	
SMC3, n (%)			0.38
Mutated	0 (0)	1 (13)	
Wild type	13 (100)	7 (87)	
TET2, n (%)			1.00
Mutated	3 (23)	1 (13)	
Wild type	10 (77)	7 (87)	
U2AF1, n (%)			0.38
Mutated	0 (0)	1 (13)	
Wild type	13 (100)	7 (87)	

Abbreviation: *FLT3*-TKD, tyrosine kinase domain mutation in the *FLT3* gene.
[a] Only those genes mutated in at least one patient are listed in this Table. No mutations were detected in the *BCOR*, *BCORL1*, *CBL*, *CEBPA*, *DNMT3A*, *EZH2*, *IDH1*, *IDH2*, *NPM1*, *PHF6*, *PTPN11*, *RAD21*, *RUNX1*, *SF3A1*, *SF3B1*, *SMC1A*, *SRSF2*, *STAG2*, *TP53*, *U2AF2*, *WT1* or *ZRSR2* genes. No patient was found to harbor *FLT3*-ITD. Specific nucleotide and amino acid changes are given in Supplementary Table S7.
[b] *P*-values for categorical variables are from Fisher's exact test.

Supplementary Table S7. Gene mutations in patients with t(11;19) rearrangements

Gene	*Chromosome*	*Base change (GRCh37)*[a]	*Mutation*[b]
ASXL1	20	31022441 A>AG	p.G643G
ETV6	12	12037393 TG>T	p.W342*
FLT3	13	28592640 A>C 28592640 A>T	p.D835E
GATA2	3	128202792 CG>C	p.D309
KIT	4	55599321 A>T	p.D816V
KRAS	12	25380275 T>G	p.Q61H
NRAS	1	115258747 C>T	p.G12D
SF1	11	64534502 AGGC>A	p.PP457P
SMC3	10	112361552 GAAGA>G	p.KK935
TET2	4	106158364 GAA>G[c] 106164832 GA>G[c] 106156458 TA>T 106156446 GA>G 106164914 G>A	p.E1089* p.E1234* p.K454* p.K450* p.R1261H
U2AF1	21	44514777 T>G	Q84P
No mutations were detected in the *BCOR*, *BCORL1*, *CBL*, *CEBPA*, *DNMT3A*, *EZH2*, *IDH1*, *IDH2*, *NPM1*, *PHF6*, *PTPN11*, *RAD21*, *RUNX1*, *SF3A1*, *SF3B1*, *SMC1A*, *SRSF2*, *STAG2*, *TP53*, *U2AF2*, *WT1* or *ZRSR2* genes. No patient was found to harbor *FLT3*-ITD.			

[a] Each line corresponds to a separate patient

[b] Asterisk indicates introduction of stop codon.

[c] Both mutations were found in the same patient

Supplementary Table S8. Comparison between results of cytogenetic analysis and RNA sequencing

Patient no.	*Cytogenetic Group*	*RNA sequencing*		
		11q23 gene	*19p13 gene (TPG)*	*TPG location*
5	t(11;19)(q23;p13.1)	*KMT2A*	*ELL*	19p13.1
6	t(11;19)(q23;p13.1)	ND	ND	ND
14	t(11;19)(q23;p13.1)	*KMT2A*	*ELL*	19p13.1
15	t(11;19)(q23;p13.1)	*KMT2A*	*ELL*	19p13.1
16	t(11;19)(q23;p13.1)	*KMT2A*	*ELL*	19p13.1
18	t(11;19)(q23;p13.1)	*KMT2A*	*ELL*	19p13.1
20	t(11;19)(q23;p13.3)	*KMT2A*	*MLLT1*	19p13.3
21	t(11;19)(q23;p13.3)	*KMT2A*	*MLLT1*	19p13.3
24	t(11;19)(q23;p13.3)	*KMT2A*	*MLLT1*	19p13.3
27	t(11;19)(q23;p13.3)	*KMT2A*	*MLLT1*	19p13.3
28	t(11;19)(q23;p13.3)	*KMT2A*	*MLLT1*	19p13.3
30	t(11;19)(q23;p13.3)	*KMT2A*	*MLLT1*	19p13.3
31	t(11;19)(q23;p13.3)	*KMT2A*	*MLLT1*	19p13.3

Abbreviations: TPG, translocation partner gene; ND, none detected.

The two cases with gene expression profiles reminiscent of the other translocation group are shaded with colors used in the PCA plot [yellow for t(11;19)(q23;p13.1) and blue for t(11;19)(q23;p13.3)].

In case no. 6, no fusion between *KMT2A* and any gene located between 19p13.1 and 19p13.3 could be detected likely due to sampling.

Supplementary Table S9. Genes differentially expressed between t(11;19)(q23;p13.1) and t(11;19)(q23;p13.3) with two aberrant cases removed from analysis

281 Genes upregulated in t(11;19)(q23;p13.3) compared to t(11;19)(q23;p13.1)					
Symbol	*Chrom.*	*Band*	*log2FC*	*q-value*	*Description*
RP11-245G13.2	2	p25.1	5.38	0.00531	
LINC00086	X	q26.3	5.17	0.00875	long intergenic non-protein coding RNA 86 [Source:HGNC Symbol;Acc:HGNC:34499]
ADCY1	7	p12.3	5.15	0.00932	adenylate cyclase 1 (brain) [Source:HGNC Symbol;Acc:HGNC:232]
MSX2	5	q35.2	3.60	0	msh homeobox 2 [Source:HGNC Symbol;Acc:HGNC:7392]
THNSL2	2	p11.2	3.20	0.00002	threonine synthase-like 2 (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:25602]
HRC	19	q13.33	3.20	0.00009	histidine rich calcium binding protein [Source:HGNC Symbol;Acc:HGNC:5178]
GOLGA8J	15	q13.2	2.85	0.00001	golgin A8 family, member J [Source:HGNC Symbol;Acc:HGNC:38650]
GATM	15	q21.1	2.84	0.00001	glycine amidinotransferase (L-arginine:glycine amidinotransferase) [Source:HGNC Symbol;Acc:HGNC:4175]
ZNF300	5	q33.1	2.82	0	zinc finger protein 300 [Source:HGNC Symbol;Acc:HGNC:13091]
C10orf35	10	q22.1	2.81	0	chromosome 10 open reading frame 35 [Source:HGNC Symbol;Acc:HGNC:23519]
CTD-2376I4.2	5	q13.2	2.67	0.00104	
PPAPDC3	9	q34.13	2.65	0.00074	phosphatidic acid phosphatase type 2 domain containing 3 [Source:HGNC Symbol;Acc:HGNC:28174]
DNAH10	12	q24.31	2.65	0.00117	dynein, axonemal, heavy chain 10 [Source:HGNC Symbol;Acc:HGNC:2941]
CYP2F1	19	q13.2	2.63	0.00007	cytochrome P450, family 2, subfamily F, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:2632]
OTOF	2	p23.3	2.62	0.00203	otoferlin [Source:HGNC Symbol;Acc:HGNC:8515]
LAMA3	18	q11.2	2.61	0	laminin, alpha 3 [Source:HGNC Symbol;Acc:HGNC:6483]
MAPK15	8	q24.3	2.58	0.00075	mitogen-activated protein kinase 15 [Source:HGNC Symbol;Acc:HGNC:24667]
RP3-388E23.2	6	q23.3	2.50	0	
GOLGA8M	15	q13.1	2.42	0	golgin A8 family, member M [Source:HGNC Symbol;Acc:HGNC:44404]
APOC4-APOC2	19	q13.32	2.42	0.00005	APOC4-APOC2 readthrough (NMD candidate) [Source:HGNC Symbol;Acc:HGNC:44426]
DISC1FP1	11	q14.3	2.42	0.00949	DISC1 fusion partner 1 (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:33625]
MYOZ1	10	q22.2	2.26	0.00436	myozenin 1 [Source:HGNC Symbol;Acc:HGNC:13752]
CAMK2B	7	p13	2.21	0.00491	calcium/calmodulin-dependent protein kinase II beta [Source:HGNC Symbol;Acc:HGNC:1461]
APOC2	19	q13.32	2.19	0.00032	apolipoprotein C-II [Source:HGNC Symbol;Acc:HGNC:609]
TRPM4	19	q13.33	2.18	0	transient receptor potential cation channel, subfamily M, member 4 [Source:HGNC Symbol;Acc:HGNC:17993]

OVOL1	11	q13.1	2.17	0.00022	ovo-like zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:8525]
RP11-114J13.1	5	q23.2	2.16	0.00672	
LA16c-349E10.1	16	p13.3	2.14	0	
KLHDC9	1	q23.3	2.12	0.00009	kelch domain containing 9 [Source:HGNC Symbol;Acc:HGNC:28489]
ANKRD20A1	9	q21.11	2.11	0	ankyrin repeat domain 20 family, member A1 [Source:HGNC Symbol;Acc:HGNC:23665]
GOLGA6D	15	q24.2	2.11	0.00024	golgin A6 family, member D [Source:HGNC Symbol;Acc:HGNC:32204]
ZNF532	18	q21.32	2.10	0	zinc finger protein 532 [Source:HGNC Symbol;Acc:HGNC:30940]
TUSC1	9	p21.2	2.08	0.00183	tumor suppressor candidate 1 [Source:HGNC Symbol;Acc:HGNC:31010]
EDA2R	X	q12	2.04	0.00506	ectodysplasin A2 receptor [Source:HGNC Symbol;Acc:HGNC:17756]
LINC00475	9	q22.31	2.03	0.00363	long intergenic non-protein coding RNA 475 [Source:HGNC Symbol;Acc:HGNC:23569]
NEO1	15	q24.1	2.03	0.00631	neogenin 1 [Source:HGNC Symbol;Acc:HGNC:7754]
ALPK3	15	q25.3	2.01	0.00002	alpha-kinase 3 [Source:HGNC Symbol;Acc:HGNC:17574]
RP11-757G1.6	11	q13.3	2.00	0	
DNAAF3	19	q13.42	1.99	0.00755	dynein, axonemal, assembly factor 3 [Source:HGNC Symbol;Acc:HGNC:30492]
SPIN3	X	p11.21	1.98	0.00333	spindlin family, member 3 [Source:HGNC Symbol;Acc:HGNC:27272]
CCNB3	X	p11.22	1.97	0.00278	cyclin B3 [Source:HGNC Symbol;Acc:HGNC:18709]
DUSP15	20	q11.21	1.96	0.00077	dual specificity phosphatase 15 [Source:HGNC Symbol;Acc:HGNC:16236]
SYT17	16	p12.3	1.92	0.00008	synaptotagmin XVII [Source:HGNC Symbol;Acc:HGNC:24119]
RP11-497G19.1	12	q24.22	1.92	0.00363	
C19orf84	19	q13.41	1.91	0.00027	chromosome 19 open reading frame 84 [Source:HGNC Symbol;Acc:HGNC:27112]
MIR17HG	13	q31.3	1.90	0	miR-17-92 cluster host gene (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:23564]
GAS1	9	q21.33	1.87	0.00079	growth arrest-specific 1 [Source:HGNC Symbol;Acc:HGNC:4165]
NMUR1	2	q37.1	1.87	0.00086	neuromedin U receptor 1 [Source:HGNC Symbol;Acc:HGNC:4518]
GOLGA8O	15	q13.3	1.86	0	golgin A8 family, member O [Source:HGNC Symbol;Acc:HGNC:44406]
CYP2E1	10	q26.3	1.86	0.00479	cytochrome P450, family 2, subfamily E, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:2631]
RP11-465B22.8	1	p36.33	1.86	0.00517	
LINC00899	22	q13.31	1.80	0.00001	long intergenic non-protein coding RNA 899 [Source:HGNC Symbol;Acc:HGNC:48583]
AC027601.1	17	q25.3	1.79	0.00883	
ARHGAP32	11	q24.3	1.78	0.00356	Rho GTPase activating protein 32 [Source:HGNC Symbol;Acc:HGNC:17399]
EPHX2	8	p21.2	1.75	0.00042	epoxide hydrolase 2, cytoplasmic [Source:HGNC Symbol;Acc:HGNC:3402]

PSD	10	q24.32	1.75	0.00198	pleckstrin and Sec7 domain containing [Source:HGNC Symbol;Acc:HGNC:9507]
GRAMD3	5	q23.2	1.74	0.00011	GRAM domain containing 3 [Source:HGNC Symbol;Acc:HGNC:24911]
GRHL1	2	p25.1	1.73	0.00042	grainyhead-like 1 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:17923]
RP11-566K19.6	15	q11.2	1.72	0	
MMP14	14	q11.2	1.71	0.00008	matrix metallopeptidase 14 (membrane-inserted) [Source:HGNC Symbol;Acc:HGNC:7160]
RP11-338N10.3	1	p36.23	1.71	0.00844	
CAMKV	3	p21.31	1.69	0.00045	CaM kinase-like vesicle-associated [Source:HGNC Symbol;Acc:HGNC:28788]
PTPRF	1	p34.2	1.69	0.00377	protein tyrosine phosphatase, receptor type, F [Source:HGNC Symbol;Acc:HGNC:9670]
DBH-AS1	9	q34.2	1.66	0.00001	DBH antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:24155]
DOCK6	19	p13.2	1.66	0.00309	dedicator of cytokinesis 6 [Source:HGNC Symbol;Acc:HGNC:19189]
RP11-47L3.1	17	q12	1.66	0.00718	
CTD-2035E11.4	5	p12	1.65	0.00452	
RP11-146D12.2	9	p11.2	1.65	0.00715	
LPAR5	12	p13.31	1.64	0.00002	lysophosphatidic acid receptor 5 [Source:HGNC Symbol;Acc:HGNC:13307]
SLC2A10	20	q13.12	1.62	0.00092	solute carrier family 2 (facilitated glucose transporter), member 10 [Source:HGNC Symbol;Acc:HGNC:13444]
HECTD2	10	q23.32	1.59	0	HECT domain containing E3 ubiquitin protein ligase 2 [Source:HGNC Symbol;Acc:HGNC:26736]
RP11-159N11.4	11	q23.2	1.59	0.00623	
MRC2	17	q23.2	1.58	0.00787	mannose receptor, C type 2 [Source:HGNC Symbol;Acc:HGNC:16875]
CDC14B	9	q22.33	1.57	0	cell division cycle 14B [Source:HGNC Symbol;Acc:HGNC:1719]
SLC2A14	12	p13.31	1.57	0.00012	solute carrier family 2 (facilitated glucose transporter), member 14 [Source:HGNC Symbol;Acc:HGNC:18301]
FAM83H	8	q24.3	1.56	0.00123	family with sequence similarity 83, member H [Source:HGNC Symbol;Acc:HGNC:24797]
ZFYVE9	1	p32.3	1.56	0.0062	zinc finger, FYVE domain containing 9 [Source:HGNC Symbol;Acc:HGNC:6775]
PNMA3	X	q28	1.55	0.00019	paraneoplastic Ma antigen 3 [Source:HGNC Symbol;Acc:HGNC:18742]
ADAMTS10	19	p13.2	1.55	0.00038	ADAM metallopeptidase with thrombospondin type 1 motif, 10 [Source:HGNC Symbol;Acc:HGNC:13201]
SERHL	22	q13.2	1.54	0.00019	serine hydrolase-like (pseudogene) [Source:HGNC Symbol;Acc:HGNC:14408]
FAM169A	5	q13.3	1.54	0.00407	family with sequence similarity 169, member A [Source:HGNC Symbol;Acc:HGNC:29138]
OBSCN	1	q42.13	1.53	0.00076	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF [Source:HGNC Symbol;Acc:HGNC:15719]
RP11-578F21.6	15	q13.1	1.52	0.00825	

GSTM3	1	p13.3	1.51	0.001	glutathione S-transferase mu 3 (brain) [Source:HGNC Symbol;Acc:HGNC:4635]
PHLDA3	1	q32.1	1.50	0.00004	pleckstrin homology-like domain, family A, member 3 [Source:HGNC Symbol;Acc:HGNC:8934]
KRT8	12	q13.13	1.49	0.00002	keratin 8 [Source:HGNC Symbol;Acc:HGNC:6446]
RP4-695O20__B.10	22	q13.31	1.47	0	
SOCS2-AS1	12	q22	1.47	0.00424	SOCS2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:27054]
CLCNKA	1	p36.13	1.45	0.0057	chloride channel, voltage-sensitive Ka [Source:HGNC Symbol;Acc:HGNC:2026]
SNPH	20	p13	1.44	0.00011	syntaphilin [Source:HGNC Symbol;Acc:HGNC:15931]
PRDM5	4	q27	1.43	0.00666	PR domain containing 5 [Source:HGNC Symbol;Acc:HGNC:9349]
C15orf38	15	q26.1	1.42	0.00005	
CCND2	12	p13.32	1.42	0.00029	cyclin D2 [Source:HGNC Symbol;Acc:HGNC:1583]
CHPF	2	q35	1.40	0.0006	chondroitin polymerizing factor [Source:HGNC Symbol;Acc:HGNC:24291]
AC004381.7	7	p15.2	1.40	0.00462	
SARDH	9	q34.2	1.39	0.00007	sarcosine dehydrogenase [Source:HGNC Symbol;Acc:HGNC:10536]
LPHN1	19	p13.12	1.39	0.0001	latrophilin 1 [Source:HGNC Symbol;Acc:HGNC:20973]
SATB1-AS1	3	p24.3	1.39	0.00051	SATB1 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:50687]
FZD3	8	p21.1	1.39	0.00797	frizzled class receptor 3 [Source:HGNC Symbol;Acc:HGNC:4041]
MYEF2	15	q21.1	1.39	0.00986	myelin expression factor 2 [Source:HGNC Symbol;Acc:HGNC:17940]
LGR4	11	p14.1	1.38	0.00254	leucine-rich repeat containing G protein-coupled receptor 4 [Source:HGNC Symbol;Acc:HGNC:13299]
GALM	2	p22.1	1.38	0.00419	galactose mutarotase (aldose 1-epimerase) [Source:HGNC Symbol;Acc:HGNC:24063]
CCDC155	19	q13.33	1.37	0.00228	coiled-coil domain containing 155 [Source:HGNC Symbol;Acc:HGNC:26520]
RP11-803P9.1	3	q29	1.37	0.00825	
U91328.22	6	p22.2	1.35	0.00796	
RP11-44N21.1	14	q32.33	1.34	0.00106	
TPM2	9	p13.3	1.33	0	tropomyosin 2 (beta) [Source:HGNC Symbol;Acc:HGNC:12011]
MEIS1	2	p14	1.32	0	Meis homeobox 1 [Source:HGNC Symbol;Acc:HGNC:7000]
FCHO2	5	q13.2	1.32	0.00007	FCH domain only 2 [Source:HGNC Symbol;Acc:HGNC:25180]
MMP15	16	q21	1.32	0.00062	matrix metallopeptidase 15 (membrane-inserted) [Source:HGNC Symbol;Acc:HGNC:7161]
PACSIN3	11	p11.2	1.31	0.00049	protein kinase C and casein kinase substrate in neurons 3 [Source:HGNC Symbol;Acc:HGNC:8572]
CACNA1A	19	p13.13	1.31	0.00178	calcium channel, voltage-dependent, P/Q type, alpha 1A subunit [Source:HGNC Symbol;Acc:HGNC:1388]

TTC12	11	q23.2	1.31	0.00242	tetratricopeptide repeat domain 12 [Source:HGNC Symbol;Acc:HGNC:23700]
HSPG2	1	p36.12	1.31	0.00312	heparan sulfate proteoglycan 2 [Source:HGNC Symbol;Acc:HGNC:5273]
FKBP14	7	p14.3	1.31	0.00796	FK506 binding protein 14, 22 kDa [Source:HGNC Symbol;Acc:HGNC:18625]
SENP6	6	q14.1	1.30	0	SUMO1/sentrin specific peptidase 6 [Source:HGNC Symbol;Acc:HGNC:20944]
MTX3	5	q14.1	1.30	0.00007	metaxin 3 [Source:HGNC Symbol;Acc:HGNC:24812]
AC009495.3	2	q24.2	1.29	0.00898	
PPFIA3	19	q13.33	1.28	0	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 3 [Source:HGNC Symbol;Acc:HGNC:9247]
C14orf79	14	q32.33	1.28	0.00012	chromosome 14 open reading frame 79 [Source:HGNC Symbol;Acc:HGNC:20126]
PON2	7	q21.3	1.28	0.00619	paraoxonase 2 [Source:HGNC Symbol;Acc:HGNC:9205]
RANBP17	5	q35.1	1.28	0.00811	RAN binding protein 17 [Source:HGNC Symbol;Acc:HGNC:14428]
RP11-353N4.5	1	q21.2	1.28	0.00898	
CABP4	11	q13.2	1.27	0.00027	calcium binding protein 4 [Source:HGNC Symbol;Acc:HGNC:1386]
RP11-329B9.4	3	q27.1	1.27	0.00185	
AC007392.3	7	q21.2	1.26	0.00015	
H1F0	22	q13.1	1.26	0.0039	H1 histone family, member 0 [Source:HGNC Symbol;Acc:HGNC:4714]
LINC00477	12	p12.1	1.26	0.00421	long intergenic non-protein coding RNA 477 [Source:HGNC Symbol;Acc:HGNC:26557]
HESX1	3	p14.3	1.26	0.00579	HESX homeobox 1 [Source:HGNC Symbol;Acc:HGNC:4877]
TTC28	22	q12.1	1.25	0	tetratricopeptide repeat domain 28 [Source:HGNC Symbol;Acc:HGNC:29179]
TMEM136	11	q23.3	1.25	0.00017	transmembrane protein 136 [Source:HGNC Symbol;Acc:HGNC:28280]
ETV5	3	q27.2	1.25	0.00421	ets variant 5 [Source:HGNC Symbol;Acc:HGNC:3494]
LTC4S	15	q15.1	1.25	0.00815	leukocyte receptor tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:6721]
RP11-1000B6.3	15	q13.3	1.24	0	
FZD7	2	q33.1	1.24	0.00035	frizzled class receptor 7 [Source:HGNC Symbol;Acc:HGNC:4045]
CCDC40	17	q25.3	1.23	0	coiled-coil domain containing 40 [Source:HGNC Symbol;Acc:HGNC:26090]
ZNF334	20	q13.12	1.23	0.00617	zinc finger protein 334 [Source:HGNC Symbol;Acc:HGNC:15806]
ACRBP	12	p13.31	1.22	0.00066	acrosin binding protein [Source:HGNC Symbol;Acc:HGNC:17195]
ZNF853	7	p22.1	1.22	0.00075	zinc finger protein 853 [Source:HGNC Symbol;Acc:HGNC:21767]
KLHL3	5	q31.2	1.21	0	kelch-like family member 3 [Source:HGNC Symbol;Acc:HGNC:6354]
GOLGA8F	15	q13.1	1.20	0	golgin A8 family, member F [Source:HGNC Symbol;Acc:HGNC:32378]

NIPA1	15	q11.2	1.20	0	non imprinted in Prader-Willi/Angelman syndrome 1 [Source:HGNC Symbol;Acc:HGNC:17043]
WWC1	5	q34	1.20	0.00179	WW and C2 domain containing 1 [Source:HGNC Symbol;Acc:HGNC:29435]
SGK2	20	q13.12	1.20	0.00822	serum/glucocorticoid regulated kinase 2 [Source:HGNC Symbol;Acc:HGNC:13900]
MEF2C-AS1	5	q14.3	1.19	0.00066	MEF2C antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:48908]
RP1-32B1.4	6	q23.3	1.19	0.00798	
EFEMP2	11	q13.1	1.19	0.00998	EGF containing fibulin-like extracellular matrix protein 2 [Source:HGNC Symbol;Acc:HGNC:3219]
NRSN2	20	p13	1.18	0.00311	neurensin 2 [Source:HGNC Symbol;Acc:HGNC:16229]
RPS6KL1	14	q24.3	1.16	0.0077	ribosomal protein S6 kinase-like 1 [Source:HGNC Symbol;Acc:HGNC:20222]
PRR34	22	q13.31	1.15	0.00008	proline rich 34 [Source:HGNC Symbol;Acc:HGNC:25606]
PPAN-P2RY11	19	p13.2	1.15	0.00773	PPAN-P2RY11 readthrough [Source:HGNC Symbol;Acc:HGNC:33526]
GOLGA6A	15	q24.1	1.14	0.0007	golgin A6 family, member A [Source:HGNC Symbol;Acc:HGNC:13567]
CTC-510F12.2	19	p13.2	1.13	0.00029	
TMPRSS9	19	p13.3	1.13	0.00064	transmembrane protease, serine 9 [Source:HGNC Symbol;Acc:HGNC:30079]
CIB2	15	q25.1	1.12	0.00006	calcium and integrin binding family member 2 [Source:HGNC Symbol;Acc:HGNC:24579]
AC026150.8	15	q13.2	1.11	0.0096	
RHPN1-AS1	8	q24.3	1.10	0.00008	RHPN1 antisense RNA 1 (head to head) [Source:HGNC Symbol;Acc:HGNC:28457]
TBX1	22	q11.21	1.10	0.00255	T-box 1 [Source:HGNC Symbol;Acc:HGNC:11592]
REEP6	19	p13.3	1.09	0.00027	receptor accessory protein 6 [Source:HGNC Symbol;Acc:HGNC:30078]
PAOX	10	q26.3	1.07	0.00041	polyamine oxidase (exo-N4-amino) [Source:HGNC Symbol;Acc:HGNC:20837]
GOLGA8H	15	q13.2	1.07	0.00242	golgin A8 family, member H [Source:HGNC Symbol;Acc:HGNC:37443]
CTD-3092A11.2	15	q13.2	1.06	0.00001	
ZBTB38	3	q23	1.06	0.00042	zinc finger and BTB domain containing 38 [Source:HGNC Symbol;Acc:HGNC:26636]
PCSK4	19	p13.3	1.06	0.00346	proprotein convertase subtilisin/kexin type 4 [Source:HGNC Symbol;Acc:HGNC:8746]
MEF2C	5	q14.3	1.06	0.00374	myocyte enhancer factor 2C [Source:HGNC Symbol;Acc:HGNC:6996]
GOLGA8N	15	q13.3	1.05	0	golgin A8 family, member N [Source:HGNC Symbol;Acc:HGNC:44405]
AL133493.2	21	q22.3	1.05	0.00017	
RUNDC3A	17	q21.31	1.05	0.0031	RUN domain containing 3A [Source:HGNC Symbol;Acc:HGNC:16984]
SATB1	3	p24.3	1.05	0.00336	SATB homeobox 1 [Source:HGNC Symbol;Acc:HGNC:10541]
RGAG4	X	q13.1	1.05	0.00983	retrotransposon gag domain containing 4 [Source:HGNC Symbol;Acc:HGNC:29430]
PHLDB1	11	q23.3	1.04	0.00005	pleckstrin homology-like domain, family B, member 1 [Source:HGNC Symbol;Acc:HGNC:23697]

AC016757.3	2	q13	1.04	0.00185	
ZFP82	19	q13.12	1.03	0.00001	ZFP82 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:28682]
RP11-588H23.3	12	q15	1.03	0.00452	
GOLGA6L19	15	q25.2	1.02	0	
NKD1	16	q12.1	1.02	0.00013	naked cuticle homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:17045]
ECHDC2	1	p32.3	1.02	0.0006	enoyl CoA hydratase domain containing 2 [Source:HGNC Symbol;Acc:HGNC:23408]
MOK	14	q32.31	1.02	0.00495	MOK protein kinase [Source:HGNC Symbol;Acc:HGNC:9833]
RHBDF1	16	p13.3	1.01	0.00192	rhomboid 5 homolog 1 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:20561]
RP11-89K11.1	15	q26.3	1.01	0.0048	
GOLGA8R	15	q13.2	1.00	0.00622	golgin A8 family, member R [Source:HGNC Symbol;Acc:HGNC:44407]
PLTP	20	q13.12	1.00	0.00636	phospholipid transfer protein [Source:HGNC Symbol;Acc:HGNC:9093]
FAM95B1	9	q21.11, p11.2	0.99	0.00014	family with sequence similarity 95, member B1 [Source:EntrezGene;Acc:100133036]
CTF1	16	p11.2	0.98	0.00002	cardiotrophin 1 [Source:HGNC Symbol;Acc:HGNC:2499]
CAND2	3	p25.2	0.98	0.00779	cullin-associated and neddylation-dissociated 2 (putative) [Source:HGNC Symbol;Acc:HGNC:30689]
RP11-242F4.2	8	p22	0.98	0.00796	
PTGR1	9	q31.3	0.97	0.00847	prostaglandin reductase 1 [Source:HGNC Symbol;Acc:HGNC:18429]
RP5-884M6.1	7	q22.3	0.97	0.00987	
C19orf57	19	p13.12	0.96	0.00036	chromosome 19 open reading frame 57 [Source:HGNC Symbol;Acc:HGNC:28153]
FGFR4	5	q35.2	0.95	0.00045	fibroblast growth factor receptor 4 [Source:HGNC Symbol;Acc:HGNC:3691]
NUMBL	19	q13.2	0.93	0	numb homolog (Drosophila)-like [Source:HGNC Symbol;Acc:HGNC:8061]
FAM213A	10	q23.1	0.93	0.00017	family with sequence similarity 213, member A [Source:HGNC Symbol;Acc:HGNC:28651]
MYB	6	q23.3	0.92	0	v-myb avian myeloblastosis viral oncogene homolog [Source:HGNC Symbol;Acc:HGNC:7545]
TARBP1	1	q42.2	0.92	0.00004	TAR (HIV-1) RNA binding protein 1 [Source:HGNC Symbol;Acc:HGNC:11568]
CCDC62	12	q24.31	0.92	0.00437	coiled-coil domain containing 62 [Source:HGNC Symbol;Acc:HGNC:30723]
DFNB59	2	q31.2	0.92	0.00655	deafness, autosomal recessive 59 [Source:HGNC Symbol;Acc:HGNC:29502]
TXK	4	p12	0.91	0.00077	TXK tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:12434]
NMB	15	q25.2	0.90	0.00113	neuromedin B [Source:HGNC Symbol;Acc:HGNC:7842]
PCP2	19	p13.2	0.90	0.00221	Purkinje cell protein 2 [Source:HGNC Symbol;Acc:HGNC:30209]
NUTM2D	10	q23.2	0.90	0.00411	NUT family member 2D [Source:HGNC Symbol;Acc:HGNC:23447]

ARL2	11	q13.1	0.90	0.00481	ADP-ribosylation factor-like 2 [Source:HGNC Symbol;Acc:HGNC:693]
PLEKHA7	11	p15.1	0.89	0.00883	pleckstrin homology domain containing, family A member 7 [Source:HGNC Symbol;Acc:HGNC:27049]
CACNA1F	X	p11.23	0.88	0.00017	calcium channel, voltage-dependent, L type, alpha 1F subunit [Source:HGNC Symbol;Acc:HGNC:1393]
TMEM102	17	p13.1	0.88	0.00188	transmembrane protein 102 [Source:HGNC Symbol;Acc:HGNC:26722]
LINC00863	10	q23.2	0.87	0.00042	long intergenic non-protein coding RNA 863 [Source:HGNC Symbol;Acc:HGNC:45162]
RP11-308K2.1	4	q35.2	0.85	0.00001	
ADSSL1	14	q32.33	0.85	0.00493	adenylosuccinate synthase like 1 [Source:HGNC Symbol;Acc:HGNC:20093]
TEC	4	p11	0.84	0.00102	tec protein tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:11719]
GPC1	2	q37.3	0.84	0.00796	glypican 1 [Source:HGNC Symbol;Acc:HGNC:4449]
CDNF	10	p13	0.83	0.00237	cerebral dopamine neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:24913]
RP11-1136G4.2	16	q12.2	0.82	0.00079	
WDR35	2	p24.1	0.81	0.00098	WD repeat domain 35 [Source:HGNC Symbol;Acc:HGNC:29250]
RP11-320M2.1	2	p25.1	0.81	0.0022	
MBNL1-AS1	3	q25.1	0.81	0.0027	MBNL1 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:44584]
CDK6	7	q21.2	0.81	0.00886	cyclin-dependent kinase 6 [Source:HGNC Symbol;Acc:HGNC:1777]
DEXI	16	p13.13	0.79	0.0001	Dexi homolog (mouse) [Source:HGNC Symbol;Acc:HGNC:13267]
KCNMB3	3	q26.32	0.79	0.00576	potassium large conductance calcium-activated channel, subfamily M beta member 3 [Source:HGNC Symbol;Acc:HGNC:6287]
HSPA2	14	q23.3	0.78	0.00055	heat shock 70kDa protein 2 [Source:HGNC Symbol;Acc:HGNC:5235]
RP5-1159O4.1	7	p21.3	0.78	0.00062	
TNPO1	5	q13.2	0.77	0.00001	transportin 1 [Source:HGNC Symbol;Acc:HGNC:6401]
RP1-155G6.4	20	q13.13	0.77	0.00029	
LINC00997	7	p14.3	0.77	0.00309	long intergenic non-protein coding RNA 997 [Source:HGNC Symbol;Acc:HGNC:48952]
LINC00526	18	p11.31	0.76	0.00745	long intergenic non-protein coding RNA 526 [Source:HGNC Symbol;Acc:HGNC:28278]
CCDC120	X	p11.23	0.75	0.00002	coiled-coil domain containing 120 [Source:HGNC Symbol;Acc:HGNC:28910]
MAGED2	X	p11.21	0.75	0.0008	melanoma antigen family H, 1 [Source:HGNC Symbol;Acc:HGNC:24092]
RNF220	1	p34.1	0.74	0	ring finger protein 220 [Source:HGNC Symbol;Acc:HGNC:25552]
C11orf95	11	q13.1	0.74	0.0004	chromosome 11 open reading frame 95 [Source:HGNC Symbol;Acc:HGNC:28449]
CTD-2366F13.1	5	q11.2	0.73	0.00797	
ARMCX4	X	q22.1	0.73	0.00856	armadillo repeat containing, X-linked 4 [Source:HGNC Symbol;Acc:HGNC:28615]

AC007566.10	19	q13.42	0.70	0.00156	
KIAA1161	9	p13.3	0.70	0.00563	KIAA1161 [Source:HGNC Symbol;Acc:HGNC:19918]
ZNF768	16	p11.2	0.70	0.00832	zinc finger protein 768 [Source:HGNC Symbol;Acc:HGNC:26273]
MYO15A	17	p11.2	0.69	0.00025	myosin XVA [Source:HGNC Symbol;Acc:HGNC:7594]
CHRNB4	15	q25.1	0.69	0.00093	cholinergic receptor, nicotinic, beta 4 (neuronal) [Source:HGNC Symbol;Acc:HGNC:1964]
CTD-2630F21.1	19	q13.12	0.68	0.00001	
RP11-166D19.1	11	q24.1	0.67	0.00145	
DECR2	16	p13.3	0.67	0.00155	2,4-dienoyl CoA reductase 2, peroxisomal [Source:HGNC Symbol;Acc:HGNC:2754]
TARSL2	15	q26.3	0.67	0.00443	threonyl-tRNA synthetase-like 2 [Source:HGNC Symbol;Acc:HGNC:24728]
RP3-327A19.5	X	q24	0.67	0.00603	
SPIN1	9	q22.1	0.66	0.00103	spindlin 1 [Source:HGNC Symbol;Acc:HGNC:11243]
GATSL2	7	q11.23	0.66	0.00165	GATS protein-like 2 [Source:HGNC Symbol;Acc:HGNC:37073]
ZNF582	19	q13.43	0.66	0.00278	zinc finger protein 582 [Source:HGNC Symbol;Acc:HGNC:26421]
TVP23C	17	p12	0.66	0.00918	trans-golgi network vesicle protein 23 homolog C (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:30453]
WDR6	3	p21.31	0.65	0	WD repeat domain 6 [Source:HGNC Symbol;Acc:HGNC:12758]
RP11-95P2.1	16	p13.3	0.65	0.00082	
FGF11	17	p13.1	0.65	0.00343	fibroblast growth factor 11 [Source:HGNC Symbol;Acc:HGNC:3667]
RP1-179N16.6	6	p21.31	0.64	0.00815	
BMP1	8	p21.3	0.63	0.00183	bone morphogenetic protein 1 [Source:HGNC Symbol;Acc:HGNC:1067]
XXbac-BPG308K3.6	6	p22.1	0.60	0.00604	
BBS5	2	q31.1	0.59	0.00125	Bardet-Biedl syndrome 5 [Source:HGNC Symbol;Acc:HGNC:970]
ZNF569	19	q13.12	0.57	0.00247	zinc finger protein 569 [Source:HGNC Symbol;Acc:HGNC:24737]
DPH1	17	p13.3	0.56	0.00001	diphthamide biosynthesis 1 [Source:HGNC Symbol;Acc:HGNC:3003]
CTD-2349P21.5	17	q11.2	0.56	0.00146	
ZSCAN12	6	p22.1	0.56	0.00203	zinc finger and SCAN domain containing 12 [Source:HGNC Symbol;Acc:HGNC:13172]
FAM221A	7	p15.3	0.55	0.00666	family with sequence similarity 221, member A [Source:HGNC Symbol;Acc:HGNC:27977]
ENO3	17	p13.2	0.54	0.00144	enolase 3 (beta, muscle) [Source:HGNC Symbol;Acc:HGNC:3354]
RP11-481J2.4	16	q21	0.54	0.00326	
LINC00641	14	q11.2	0.54	0.00348	long intergenic non-protein coding RNA 641 [Source:HGNC Symbol;Acc:HGNC:27511]

TASP1	20	p12.1	0.54	0.00365	taspase, threonine aspartase, 1 [Source:HGNC Symbol;Acc:HGNC:15859]
CRAMP1L	16	p13.3	0.54	0.00499	Crm, cramped-like (Drosophila) [Source:HGNC Symbol;Acc:HGNC:14122]
CTC-360G5.9	19	q13.2	0.51	0.00636	
PATZ1	22	q12.2	0.51	0.00754	POZ (BTB) and AT hook containing zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:13071]
ZNF582-AS1	19	q13.43	0.50	0.00717	ZNF582 antisense RNA 1 (head to head) [Source:HGNC Symbol;Acc:HGNC:25213]
THAP7-AS1	22	q11.21	0.48	0.00175	THAP7 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:41013]
CCDC97	19	q13.2	0.47	0.00536	coiled-coil domain containing 97 [Source:HGNC Symbol;Acc:HGNC:28289]
FUBP3	9	q34.11	0.45	0.00085	far upstream element (FUSE) binding protein 3 [Source:HGNC Symbol;Acc:HGNC:4005]
NAT10	11	p13	0.44	0.0001	N-acetyltransferase 10 (GCN5-related) [Source:HGNC Symbol;Acc:HGNC:29830]
DDHD2	8	p11.23	0.44	0.00563	DDHD domain containing 2 [Source:HGNC Symbol;Acc:HGNC:29106]
DCAF4	14	q24.2	0.43	0.00158	DDB1 and CUL4 associated factor 4 [Source:HGNC Symbol;Acc:HGNC:20229]
RP11-159F24.6	5	p12	0.41	0.00466	
CTB-131B5.5	5	q31.3	0.40	0.00862	
CDC14A	1	p21.2	0.39	0.00258	cell division cycle 14A [Source:HGNC Symbol;Acc:HGNC:1718]
AC005562.1	19	p13.11	0.36	0.00499	
TMEM192	4	q32.3	0.34	0.00064	transmembrane protein 192 [Source:HGNC Symbol;Acc:HGNC:26775]
RPS6KA5	14	q32.11	0.34	0.00563	ribosomal protein S6 kinase, 90kDa, polypeptide 5 [Source:HGNC Symbol;Acc:HGNC:10434]
PDCD6IP	3	p22.3	0.33	0.0027	programmed cell death 6 interacting protein [Source:HGNC Symbol;Acc:HGNC:8766]
MYBBP1A	17	p13.2	0.31	0.0049	MYB binding protein (P160) 1a [Source:HGNC Symbol;Acc:HGNC:7546]
YLPM1	14	q24.3	0.31	0.00636	YLP motif containing 1 [Source:HGNC Symbol;Acc:HGNC:17798]
AC074117.10	2	p23.3	0.29	0.00422	
APOOL	X	q21.1	0.27	0.00234	apolipoprotein O-like [Source:HGNC Symbol;Acc:HGNC:24009]
SMG6	17	p13.3	0.27	0.00346	SMG6 nonsense mediated mRNA decay factor [Source:HGNC Symbol;Acc:HGNC:17809]
409 Genes downregulated in t(11;19)(q23;p13.3) compared to t(11;19)(q23;p13.1)					
AC017002.4			-5.45	0.00376	
NECAB2	16	q23.3	-3.03	0.0005	N-terminal EF-hand calcium binding protein 2 [Source:HGNC Symbol;Acc:HGNC:23746]
TRBV13	7	q34	-2.98	0.00002	T cell receptor beta variable 13 [Source:HGNC Symbol;Acc:HGNC:12188]
RP11-545N8.3	12	q13.3	-2.76	0.00003	
LYVE1	12	q15	-2.63	0.00014	lysozyme [Source:HGNC Symbol;Acc:HGNC:6740]
CD14	5	q31.3	-2.62	0.00053	CD14 molecule [Source:HGNC Symbol;Acc:HGNC:1628]

SERPINA1	14	q32.13	-2.57	0.00004	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 1 [Source:HGNC Symbol;Acc:HGNC:8941]
EMR3	19	p13.12	-2.52	0.00851	egf-like module containing, mucin-like, hormone receptor-like 3 [Source:HGNC Symbol;Acc:HGNC:23647]
OR52K1	11	p15.4	-2.51	0.00117	olfactory receptor, family 52, subfamily K, member 1 [Source:HGNC Symbol;Acc:HGNC:15222]
AC008984.2	2	q24.3	-2.46	0	
MPO	17	q22	-2.45	0.00019	myeloperoxidase [Source:HGNC Symbol;Acc:HGNC:7218]
RP11-597D13.9	4	q32.1	-2.42	0.00121	
FFAR2	19	q13.12	-2.41	0	free fatty acid receptor 2 [Source:HGNC Symbol;Acc:HGNC:4501]
VCAN	5	q14.2	-2.41	0.00128	versican [Source:HGNC Symbol;Acc:HGNC:2464]
FCGR3A	1	q23.3	-2.38	0.00001	Fc fragment of IgG, low affinity IIIa, receptor (CD16a) [Source:HGNC Symbol;Acc:HGNC:3619]
CLEC4E	12	p13.31	-2.37	0	C-type lectin domain family 4, member E [Source:HGNC Symbol;Acc:HGNC:14555]
RP11-351I24.1	11	p15.4	-2.37	0.00328	
APOBEC3A	22	q13.1	-2.33	0	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3A [Source:HGNC Symbol;Acc:HGNC:17343]
SLC11A1	2	q35	-2.33	0	solute carrier family 11 (proton-coupled divalent metal ion transporter), member 1 [Source:HGNC Symbol;Acc:HGNC:10907]
RP11-156K13.3	8	p22	-2.33	0.00175	
STK32B	4	p16.2	-2.33	0.00363	serine/threonine kinase 32B [Source:HGNC Symbol;Acc:HGNC:14217]
FCN1	9	q34.3	-2.32	0.00007	ficolin (collagen/fibrinogen domain containing) 1 [Source:HGNC Symbol;Acc:HGNC:3623]
TRBV20-1	7	q34	-2.32	0.00007	T cell receptor beta variable 20-1 [Source:HGNC Symbol;Acc:HGNC:12196]
CPAMD8	19	p13.11	-2.26	0.00044	C3 and PZP-like, alpha-2-macroglobulin domain containing 8 [Source:HGNC Symbol;Acc:HGNC:23228]
TRIM7	5	q35.3	-2.25	0.00101	tripartite motif containing 7 [Source:HGNC Symbol;Acc:HGNC:16278]
DPYD	1	p21.3	-2.24	0.00001	dihydropyrimidine dehydrogenase [Source:HGNC Symbol;Acc:HGNC:3012]
BCL2A1	15	q25.1	-2.22	0	BCL2-related protein A1 [Source:HGNC Symbol;Acc:HGNC:991]
TRBV14	7	q34	-2.22	0.00006	T cell receptor beta variable 14 [Source:HGNC Symbol;Acc:HGNC:12189]
CFH	1	q31.3	-2.21	0	complement factor H [Source:HGNC Symbol;Acc:HGNC:4883]
PKLR	1	q22	-2.19	0.00246	pyruvate kinase, liver and RBC [Source:HGNC Symbol;Acc:HGNC:9020]
CD96	3	q13.13	-2.15	0	CD96 molecule [Source:HGNC Symbol;Acc:HGNC:16892]
LYZ	3	q13.33	-2.14	0	MYCBP-associated, testis expressed 1 [Source:HGNC Symbol;Acc:HGNC:24010]
AC017002.1	2	q13	-2.14	0.00053	
VIPR1	3	p22.1	-2.13	0	vasoactive intestinal peptide receptor 1 [Source:HGNC Symbol;Acc:HGNC:12694]

WASF1	6	q21	-2.13	0.00005	WAS protein family, member 1 [Source:HGNC Symbol;Acc:HGNC:12732]
LINC01272	20	q13.13	-2.12	0	long intergenic non-protein coding RNA 1272 [Source:HGNC Symbol;Acc:HGNC:50328]
CA1	8	q21.2	-2.11	0.00185	carbonic anhydrase I [Source:HGNC Symbol;Acc:HGNC:1368]
VNN2	6	q23.2	-2.08	0.00298	vanin 2 [Source:HGNC Symbol;Acc:HGNC:12706]
PLBD1	12	p13.1	-2.06	0.004	phospholipase B domain containing 1 [Source:HGNC Symbol;Acc:HGNC:26215]
S100A9	1	q21.3	-2.06	0.00487	S100 calcium binding protein A9 [Source:HGNC Symbol;Acc:HGNC:10499]
SLC7A7	14	q11.2	-2.05	0.00017	solute carrier family 7 (amino acid transporter light chain, y+L system), member 7 [Source:HGNC Symbol;Acc:HGNC:11065]
MYL4	17	q21.32	-2.04	0.00077	myosin, light chain 4, alkali; atrial, embryonic [Source:HGNC Symbol;Acc:HGNC:7585]
CDA	1	p36.12	-2.02	0.00305	cytidine deaminase [Source:HGNC Symbol;Acc:HGNC:1712]
ARG1	6	q23.2	-2.02	0.0034	arginase 1 [Source:HGNC Symbol;Acc:HGNC:663]
S100A8	1	q21.3	-2.02	0.00529	S100 calcium binding protein A8 [Source:HGNC Symbol;Acc:HGNC:10498]
ADORA2A	22	q11.23	-2.01	0.00014	adenosine A2a receptor [Source:HGNC Symbol;Acc:HGNC:263]
C19orf38	19	p13.2	-1.97	0	chromosome 19 open reading frame 38 [Source:HGNC Symbol;Acc:HGNC:34073]
IER3	6	p21.33	-1.97	0	immediate early response 3 [Source:HGNC Symbol;Acc:HGNC:5392]
FPR1	19	q13.41	-1.96	0.00421	formyl peptide receptor 1 [Source:HGNC Symbol;Acc:HGNC:3826]
FCN2	9	q34.3	-1.96	0.0054	ficolin (collagen/fibrinogen domain containing lectin) 2 [Source:HGNC Symbol;Acc:HGNC:3624]
ADM	11	p15.4	-1.95	0.00001	adrenomedullin [Source:HGNC Symbol;Acc:HGNC:259]
CLEC7A	12	p13.2	-1.95	0.00026	C-type lectin domain family 7, member A [Source:HGNC Symbol;Acc:HGNC:14558]
RHAG	6	p12.3	-1.95	0.00481	Rh-associated glycoprotein [Source:HGNC Symbol;Acc:HGNC:10006]
CYBB	X	p21.1	-1.92	0.00327	cytochrome b-245, beta polypeptide [Source:HGNC Symbol;Acc:HGNC:2578]
CAMK1	3	p25.3	-1.91	0.00129	calcium/calmodulin-dependent protein kinase I [Source:HGNC Symbol;Acc:HGNC:1459]
CD36	7	q21.11	-1.90	0.00006	CD36 molecule (thrombospondin receptor) [Source:HGNC Symbol;Acc:HGNC:1663]
SLC2A3	12	p13.31	-1.89	0	solute carrier family 2 (facilitated glucose transporter), member 3 [Source:HGNC Symbol;Acc:HGNC:11007]
CECR1	22	q11.1	-1.89	0	cat eye syndrome chromosome region, candidate 1 [Source:HGNC Symbol;Acc:HGNC:1839]
CLMN	14	q32.13	-1.88	0	calmin (calponin-like, transmembrane) [Source:HGNC Symbol;Acc:HGNC:19972]
LILRB2	19	q13.42	-1.88	0	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 2 [Source:HGNC Symbol;Acc:HGNC:6606]
FAM178B	2	q11.2	-1.88	0.00368	family with sequence similarity 178, member B [Source:HGNC Symbol;Acc:HGNC:28036]
HBD	11	p15.4	-1.87	0.00595	hemoglobin, delta [Source:HGNC Symbol;Acc:HGNC:4829]

RP11-256L6.3	12	q23.1	-1.84	0.00017	
CRISPLD2	16	q24.1	-1.83	0	cysteine-rich secretory protein LCCL domain containing 2 [Source:HGNC Symbol;Acc:HGNC:25248]
CLEC12A	12	p13.31	-1.83	0.00068	C-type lectin domain family 12, member A [Source:HGNC Symbol;Acc:HGNC:31713]
RHCE	1	p36.11	-1.83	0.00883	Rh blood group, CcEe antigens [Source:HGNC Symbol;Acc:HGNC:10008]
GYPC	2	q14.3	-1.78	0	glycophorin C (Gerbich blood group) [Source:HGNC Symbol;Acc:HGNC:4704]
EPB42	15	q15.2	-1.78	0.00278	erythrocyte membrane protein band 4.2 [Source:HGNC Symbol;Acc:HGNC:3381]
CLEC12B	12	p13.2	-1.77	0.00002	C-type lectin domain family 12, member B [Source:HGNC Symbol;Acc:HGNC:31966]
AKR1C3	10	p15.1	-1.76	0.00026	aldo-keto reductase family 1, member C3 [Source:HGNC Symbol;Acc:HGNC:386]
PTGER2	14	q22.1	-1.75	0.00035	prostaglandin E receptor 2 (subtype EP2), 53kDa [Source:HGNC Symbol;Acc:HGNC:9594]
CTD-2105E13.14	19	q13.42	-1.75	0.00363	
FAM65C	20	q13.13	-1.75	0.0077	family with sequence similarity 65, member C [Source:HGNC Symbol;Acc:HGNC:16168]
ANK1	8	p11.21	-1.74	0.00183	ankyrin 1, erythrocytic [Source:HGNC Symbol;Acc:HGNC:492]
HP	16	q22.2	-1.74	0.00666	haptoglobin [Source:HGNC Symbol;Acc:HGNC:5141]
SELL	1	q24.2	-1.73	0.00001	selectin L [Source:HGNC Symbol;Acc:HGNC:10720]
S1PR3	9	q22.1	-1.72	0	sphingosine-1-phosphate receptor 3 [Source:HGNC Symbol;Acc:HGNC:3167]
CKAP4	12	q23.3	-1.70	0	cytoskeleton-associated protein 4 [Source:HGNC Symbol;Acc:HGNC:16991]
SLC16A6	17	q24.2	-1.69	0.00137	solute carrier family 16, member 6 [Source:HGNC Symbol;Acc:HGNC:10927]
CPNE7	16	q24.3	-1.69	0.00338	copine VII [Source:HGNC Symbol;Acc:HGNC:2320]
PTGS2	1	q31.1	-1.67	0	prostaglandin-endoperoxide synthase 2 (prostaglandin G/H synthase and cyclooxygenase) [Source:HGNC Symbol;Acc:HGNC:9605]
BCAT1	12	p12.1	-1.67	0.0001	branched chain amino-acid transaminase 1, cytosolic [Source:HGNC Symbol;Acc:HGNC:976]
P2RY13	3	q25.1	-1.66	0.00075	purinergic receptor P2Y, G-protein coupled, 13 [Source:HGNC Symbol;Acc:HGNC:4537]
PADI4	1	p36.13	-1.65	0.00588	peptidyl arginine deiminase, type IV [Source:HGNC Symbol;Acc:HGNC:18368]
TRBV12-4	7	q34	-1.65	0.00691	T cell receptor beta variable 12-4 [Source:HGNC Symbol;Acc:HGNC:12186]
NME8	7	p14.1	-1.63	0.00563	NME/NM23 family member 8 [Source:HGNC Symbol;Acc:HGNC:16473]
CTSS	1	q21.3	-1.62	0	cathepsin S [Source:HGNC Symbol;Acc:HGNC:2545]
TNFRSF1B	1	p36.22	-1.62	0.00098	tumor necrosis factor receptor superfamily, member 1B [Source:HGNC Symbol;Acc:HGNC:11917]
GPR183	13	q32.3	-1.61	0.0006	G protein-coupled receptor 183 [Source:HGNC Symbol;Acc:HGNC:3128]
SLA	8	q24.22	-1.61	0.00657	Src-like-adaptor [Source:HGNC Symbol;Acc:HGNC:10902]
FXYD6	11	q23.3	-1.61	0.00946	FXYD domain containing ion transport regulator 6 [Source:HGNC Symbol;Acc:HGNC:4030]

CD300LB	17	q25.1	-1.60	0.00007	CD300 molecule-like family member b [Source:HGNC Symbol;Acc:HGNC:30811]
MCEMP1	19	p13.2	-1.60	0.00427	mast cell-expressed membrane protein 1 [Source:HGNC Symbol;Acc:HGNC:27291]
MNDA	1	q23.1	-1.60	0.00544	myeloid cell nuclear differentiation antigen [Source:HGNC Symbol;Acc:HGNC:7183]
TNFSF8	9	q33.1	-1.59	0	tumor necrosis factor (ligand) superfamily, member 8 [Source:HGNC Symbol;Acc:HGNC:11938]
CEBPB	20	q13.13	-1.59	0.00001	CCAAT/enhancer binding protein (C/EBP), beta [Source:HGNC Symbol;Acc:HGNC:1834]
MZB1	5	q31.2	-1.59	0.0023	marginal zone B and B1 cell-specific protein [Source:HGNC Symbol;Acc:HGNC:30125]
FCAR	19	q13.42	-1.58	0.00023	Fc fragment of IgA, receptor for [Source:HGNC Symbol;Acc:HGNC:3608]
HAL	12	q23.1	-1.57	0.00021	histidine ammonia-lyase [Source:HGNC Symbol;Acc:HGNC:4806]
RP4-753P9.3	X	q26.1	-1.56	0.00035	
DAGLA	11	q12.2	-1.55	0.00002	diacylglycerol lipase, alpha [Source:HGNC Symbol;Acc:HGNC:1165]
NCF2	1	q25.3	-1.54	0	neutrophil cytosolic factor 2 [Source:HGNC Symbol;Acc:HGNC:7661]
CMTM2	16	q21	-1.53	0.00077	CKLF-like MARVEL transmembrane domain containing 2 [Source:HGNC Symbol;Acc:HGNC:19173]
ITGB2-AS1	21	q22.3	-1.53	0.00104	ITGB2 antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:44304]
CTB-61M7.2	19	q13.42	-1.52	0.00115	
IFI30	19	p13.11	-1.52	0.00983	interferon, gamma-inducible protein 30 [Source:HGNC Symbol;Acc:HGNC:5398]
S100A11	1	q21.3	-1.50	0.00004	S100 calcium binding protein A11 [Source:HGNC Symbol;Acc:HGNC:10488]
LILRA4	19	q13.42	-1.50	0.00126	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 4 [Source:HGNC Symbol;Acc:HGNC:15503]
IGLV1-40	22	q11.22	-1.50	0.00808	immunoglobulin lambda variable 1-40 [Source:HGNC Symbol;Acc:HGNC:5877]
FYN	6	q21	-1.49	0	FYN proto-oncogene, Src family tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:4037]
TAL1	1	p33	-1.49	0.00499	T-cell acute lymphocytic leukemia 1 [Source:HGNC Symbol;Acc:HGNC:11556]
PTAFR	1	p35.3	-1.48	0.00019	platelet-activating factor receptor [Source:HGNC Symbol;Acc:HGNC:9582]
IGHA2	14	q32.33	-1.48	0.00366	immunoglobulin heavy constant alpha 2 (A2m marker) [Source:HGNC Symbol;Acc:HGNC:5479]
XXbac-B33L19.4	22	q11.21	-1.48	0.00388	
DMTN	8	p21.3	-1.48	0.00733	dematin actin binding protein [Source:HGNC Symbol;Acc:HGNC:3382]
SERPINB10	18	q21.33	-1.47	0.00119	serpin peptidase inhibitor, clade B (ovalbumin), member 10 [Source:HGNC Symbol;Acc:HGNC:8942]
IGLV2-14	22	q11.22	-1.47	0.00437	immunoglobulin lambda variable 2-14 [Source:HGNC Symbol;Acc:HGNC:5888]
CYTIP	2	q24.1	-1.46	0.00156	cytohesin 1 interacting protein [Source:HGNC Symbol;Acc:HGNC:9506]
GIMAP4	7	q36.1	-1.46	0.00233	GTPase, IMAP family member 4 [Source:HGNC Symbol;Acc:HGNC:21872]
LLNLR-470E3.1	19	q13.41	-1.46	0.00343	

C1QTNF4	11	p11.2	-1.46	0.00622	C1q and tumor necrosis factor related protein 4 [Source:HGNC Symbol;Acc:HGNC:14346]
CTB-31N19.3	16	p12.2	-1.45	0	
ACSL1	4	q35.1	-1.45	0.00061	acyl-CoA synthetase long-chain family member 1 [Source:HGNC Symbol;Acc:HGNC:3569]
FAM134B	5	p15.1	-1.44	0.00002	family with sequence similarity 134, member B [Source:HGNC Symbol;Acc:HGNC:25964]
TMEM56	1	p21.3	-1.44	0.00056	transmembrane protein 56 [Source:HGNC Symbol;Acc:HGNC:26477]
HBEGF	5	q31.3	-1.44	0.00155	heparin-binding EGF-like growth factor [Source:HGNC Symbol;Acc:HGNC:3059]
CRHBP	5	q13.3	-1.44	0.00331	corticotropin releasing hormone binding protein [Source:HGNC Symbol;Acc:HGNC:2356]
CD48	1	q23.3	-1.43	0.0001	CD48 molecule [Source:HGNC Symbol;Acc:HGNC:1683]
IGLV1-44	22	q11.22	-1.43	0.00897	immunoglobulin lambda variable 1-44 [Source:HGNC Symbol;Acc:HGNC:5879]
AC073254.1	2	q37.1	-1.42	0	
FCER1G	1	q23.3	-1.42	0	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide [Source:HGNC Symbol;Acc:HGNC:3611]
REEP5	5	q22.2	-1.42	0.00639	receptor accessory protein 5 [Source:HGNC Symbol;Acc:HGNC:30077]
ST3GAL6	3	q12.1	-1.41	0	ST3 beta-galactoside alpha-2,3-sialyltransferase 6 [Source:HGNC Symbol;Acc:HGNC:18080]
LILRB3	19	q13.42	-1.41	0.00062	leukocyte immunoglobulin-like receptor, subfamily B (with TM and ITIM domains), member 3 [Source:HGNC Symbol;Acc:HGNC:6607]
IGSF6	16	p12.2	-1.41	0.00064	immunoglobulin superfamily, member 6 [Source:HGNC Symbol;Acc:HGNC:5953]
IQSEC1	3	p25.2	-1.41	0.00152	IQ motif and Sec7 domain 1 [Source:HGNC Symbol;Acc:HGNC:29112]
XXbac-BPG252P9.10	6	p21.33	-1.41	0.00261	
RRAS	19	q13.33	-1.39	0.00003	related RAS viral (r-ras) oncogene homolog [Source:HGNC Symbol;Acc:HGNC:10447]
NAMPT	7	q22.3	-1.39	0.00007	nicotinamide phosphoribosyltransferase [Source:HGNC Symbol;Acc:HGNC:30092]
SRD5A1	5	p15.31	-1.38	0.00006	steroid-5-alpha-reductase, alpha polypeptide 1 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 1) [Source:HGNC Symbol;Acc:HGNC:11284]
CCRL2	3	p21.31	-1.38	0.0057	chemokine (C-C motif) receptor-like 2 [Source:HGNC Symbol;Acc:HGNC:1612]
LGI4	19	q13.12	-1.38	0.00806	leucine-rich repeat LGI family, member 4 [Source:HGNC Symbol;Acc:HGNC:18712]
ITGAM	16	p11.2	-1.37	0.00075	integrin, alpha M (complement component 3 receptor 3 subunit) [Source:HGNC Symbol;Acc:HGNC:6149]
RP11-373D23.2	2	p23.2	-1.36	0.00117	
MME	3	q25.2	-1.36	0.00427	membrane metallo-endopeptidase [Source:HGNC Symbol;Acc:HGNC:7154]
FGR	1	p35.3	-1.34	0.00013	FGR proto-oncogene, Src family tyrosine kinase [Source:HGNC Symbol;Acc:HGNC:3697]
THEMIS2	1	p35.3	-1.34	0.00075	thymocyte selection associated family member 2 [Source:HGNC Symbol;Acc:HGNC:16839]
LILRA1	19	q13.42	-1.34	0.00473	leukocyte immunoglobulin-like receptor, subfamily A (with TM domain), member 1 [Source:HGNC Symbol;Acc:HGNC:6602]

E2F2	1	p36.12	-1.33	0.00007	E2F transcription factor 2 [Source:HGNC Symbol;Acc:HGNC:3114]
JAZF1	7	p15.1	-1.33	0.00027	JAZF zinc finger 1 [Source:HGNC Symbol;Acc:HGNC:28917]
RHD	1	p36.11	-1.33	0.00446	Rh blood group, D antigen [Source:HGNC Symbol;Acc:HGNC:10009]
NAMPTL	10	p11.21	-1.32	0.00026	nicotinamide phosphoribosyltransferase pseudogene 1
PITPNC1	17	q24.2	-1.31	0	phosphatidylinositol transfer protein, cytoplasmic 1 [Source:HGNC Symbol;Acc:HGNC:21045]
PNPLA1	6	p21.31	-1.31	0.00029	patatin-like phospholipase domain containing 1 [Source:HGNC Symbol;Acc:HGNC:21246]
SYN2	3	p25.2	-1.31	0.00278	synapsin II [Source:HGNC Symbol;Acc:HGNC:11495]
IL1RL1	2	q12.1	-1.30	0.00521	interleukin 1 receptor-like 1 [Source:HGNC Symbol;Acc:HGNC:5998]
OSM	22	q12.2	-1.29	0	oncostatin M [Source:HGNC Symbol;Acc:HGNC:8506]
TFR2	7	q22.1	-1.29	0.00006	transferrin receptor 2 [Source:HGNC Symbol;Acc:HGNC:11762]
HLA-G	6	p22.1	-1.29	0.0001	major histocompatibility complex, class I, G [Source:HGNC Symbol;Acc:HGNC:4964]
MRVI1	11	p15.4	-1.29	0.00014	murine retrovirus integration site 1 homolog [Source:HGNC Symbol;Acc:HGNC:7237]
HCAR3	12	q24.31	-1.28	0	hydroxycarboxylic acid receptor 3 [Source:HGNC Symbol;Acc:HGNC:16824]
TRBV28	7	q34	-1.28	0.00001	T cell receptor beta variable 28 [Source:HGNC Symbol;Acc:HGNC:12209]
APCDD1	18	p11.22	-1.28	0.00377	adenomatosis polyposis coli down-regulated 1 [Source:HGNC Symbol;Acc:HGNC:15718]
IGLV7-46	22	q11.22	-1.28	0.00609	immunoglobulin lambda variable 7-46 (gene/pseudogene) [Source:HGNC Symbol;Acc:HGNC:5930]
RP11-295G20.2	1	q42.2	-1.27	0	
BLVRB	19	q13.2	-1.27	0	biliverdin reductase B (flavin reductase (NADPH)) [Source:HGNC Symbol;Acc:HGNC:1063]
SASH3	X	q26.1	-1.27	0.00012	SAM and SH3 domain containing 3 [Source:HGNC Symbol;Acc:HGNC:15975]
RASGEF1B	4	q21.22	-1.26	0.00005	RasGEF domain family, member 1B [Source:HGNC Symbol;Acc:HGNC:24881]
GCH1	14	q22.2	-1.26	0.00008	GTP cyclohydrolase 1 [Source:HGNC Symbol;Acc:HGNC:4193]
TRBC2	7	q34	-1.26	0.0002	T cell receptor beta constant 2 [Source:HGNC Symbol;Acc:HGNC:12157]
IVNS1ABP	1	q25.3	-1.25	0	influenza virus NS1A binding protein [Source:HGNC Symbol;Acc:HGNC:16951]
PSTPIP1	15	q24.3	-1.25	0.0027	proline-serine-threonine phosphatase interacting protein 1 [Source:HGNC Symbol;Acc:HGNC:9580]
PLK3	1	p34.1	-1.24	0.00035	polo-like kinase 3 [Source:HGNC Symbol;Acc:HGNC:2154]
DGUOK-AS1	2	p13.1	-1.24	0.00156	DGUOK antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:43441]
PLEK	2	p14	-1.23	0	pleckstrin [Source:HGNC Symbol;Acc:HGNC:9070]
CYFIP2	5	q33.3	-1.23	0.00001	cytoplasmic FMR1 interacting protein 2 [Source:HGNC Symbol;Acc:HGNC:13760]
LSP1	6	p21.33	-1.23	0.00003	leukocyte specific transcript 1 [Source:HGNC Symbol;Acc:HGNC:14189]
MBOAT2	2	p25.1	-1.23	0.00007	membrane bound O-acyltransferase domain containing 2 [Source:HGNC Symbol;Acc:HGNC:25193]

OR52K2	11	p15.4	-1.23	0.0002	olfactory receptor, family 52, subfamily K, member 2 [Source:HGNC Symbol;Acc:HGNC:15223]
ANKRD22	10	q23.31	-1.23	0.00185	ankyrin repeat domain 22 [Source:HGNC Symbol;Acc:HGNC:28321]
CUEDC1	17	q22	-1.23	0.00481	CUE domain containing 1 [Source:HGNC Symbol;Acc:HGNC:31350]
PILRA	7	q22.1	-1.22	0.0002	paired immunoglobin-like type 2 receptor alpha [Source:HGNC Symbol;Acc:HGNC:20396]
IFI27L2	14	q32.12	-1.22	0.00134	interferon, alpha-inducible protein 27-like 2 [Source:HGNC Symbol;Acc:HGNC:19753]
DLGAP5	14	q22.3	-1.21	0.00068	discs, large (Drosophila) homolog-associated protein 5 [Source:HGNC Symbol;Acc:HGNC:16864]
LINC00877	3	p13	-1.20	0.00883	long intergenic non-protein coding RNA 877 [Source:HGNC Symbol;Acc:HGNC:27706]
TLR2	4	q31.3	-1.19	0.00109	toll-like receptor 2 [Source:HGNC Symbol;Acc:HGNC:11848]
NPL	1	q25.3	-1.19	0.0054	N-acetylneuraminate pyruvate lyase (dihydrodipicolinate synthase) [Source:HGNC Symbol;Acc:HGNC:16781]
KIAA0513	16	q24.1	-1.19	0.00687	KIAA0513 [Source:HGNC Symbol;Acc:HGNC:29058]
GLIPR1	12	q21.2	-1.19	0.00933	GLI pathogenesis-related 1 [Source:HGNC Symbol;Acc:HGNC:17001]
EPOR	19	p13.2	-1.18	0.00019	erythropoietin receptor [Source:HGNC Symbol;Acc:HGNC:3416]
AK4	1	p31.3	-1.18	0.00038	adenylate kinase 4 [Source:HGNC Symbol;Acc:HGNC:363]
EHD4	15	q15.1	-1.18	0.00875	EH-domain containing 4 [Source:HGNC Symbol;Acc:HGNC:3245]
CSF1	1	p13.3	-1.18	0.0091	colony stimulating factor 1 (macrophage) [Source:HGNC Symbol;Acc:HGNC:2432]
SAT1	X	p22.11	-1.17	0	spermidine/spermine N1-acetyltransferase 1 [Source:HGNC Symbol;Acc:HGNC:10540]
NLRP1	17	p13.2	-1.17	0.00035	NLR family, pyrin domain containing 1 [Source:HGNC Symbol;Acc:HGNC:14374]
SORL1	11	q24.1	-1.17	0.00797	sortilin-related receptor, L(DLR class) A repeats containing [Source:HGNC Symbol;Acc:HGNC:11185]
PPAP2A	5	q11.2	-1.16	0.00214	phosphatidic acid phosphatase type 2A [Source:HGNC Symbol;Acc:HGNC:9228]
AGFG1	2	q36.3	-1.16	0.00914	ArfGAP with FG repeats 1 [Source:HGNC Symbol;Acc:HGNC:5175]
KIAA0040	1	q25.1	-1.15	0	KIAA0040 [Source:HGNC Symbol;Acc:HGNC:28950]
GLIPR2	9	p13.3	-1.15	0.00004	GLI pathogenesis-related 2 [Source:HGNC Symbol;Acc:HGNC:18007]
LINC00936	12	q21.33	-1.15	0.00028	long intergenic non-protein coding RNA 936 [Source:HGNC Symbol;Acc:HGNC:27883]
CP	3	q25.1	-1.14	0.00399	ceruloplasmin (ferroxidase) [Source:HGNC Symbol;Acc:HGNC:2295]
DUSP1	5	q35.1	-1.13	0.00185	dual specificity phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:3064]
ATP1B2	17	p13.1	-1.13	0.00781	ATPase, Na+/K+ transporting, beta 2 polypeptide [Source:HGNC Symbol;Acc:HGNC:805]
ENTPD1	10	q24.1	-1.12	0	ectonucleoside triphosphate diphosphohydrolase 1 [Source:HGNC Symbol;Acc:HGNC:3363]
OAT	10	q26.13	-1.12	0	ornithine aminotransferase [Source:HGNC Symbol;Acc:HGNC:8091]
TKT	3	p21.1	-1.12	0.00017	transketolase [Source:HGNC Symbol;Acc:HGNC:11834]

HIST1H2AL	6	p22.1	-1.12	0.00221	histone cluster 1, H2al [Source:HGNC Symbol;Acc:HGNC:4730]
CTSD	11	p15.5	-1.12	0.00778	cathepsin D [Source:HGNC Symbol;Acc:HGNC:2529]
PIF1	15	q22.31	-1.12	0.00797	PIF1 5'-to-3' DNA helicase [Source:HGNC Symbol;Acc:HGNC:26220]
RP11-1157N2__B.2	18	p11.21	-1.11	0	
TMEM170B	6	p24.2	-1.11	0.00631	transmembrane protein 170B [Source:HGNC Symbol;Acc:HGNC:34244]
TMEM120A	7	q11.23	-1.10	0	transmembrane protein 120A [Source:HGNC Symbol;Acc:HGNC:21697]
MEGF9	9	q33.2	-1.10	0.00013	multiple EGF-like-domains 9 [Source:HGNC Symbol;Acc:HGNC:3234]
EAF1	3	p25.1	-1.09	0.00002	ELL associated factor 1 [Source:HGNC Symbol;Acc:HGNC:20907]
HLA-F	6	p22.1	-1.09	0.00009	major histocompatibility complex, class I, F [Source:HGNC Symbol;Acc:HGNC:4963]
PITPNM1	11	q13.2	-1.09	0.00016	phosphatidylinositol transfer protein, membrane-associated 1 [Source:HGNC Symbol;Acc:HGNC:9003]
BST1	4	p15.32	-1.09	0.00019	bone marrow stromal cell antigen 1 [Source:HGNC Symbol;Acc:HGNC:1118]
EHD1	11	q13.1	-1.09	0.0082	EH-domain containing 1 [Source:HGNC Symbol;Acc:HGNC:3242]
AC074289.1	2	p14	-1.08	0.00012	
CD300LF	17	q25.1	-1.08	0.00228	CD300 molecule-like family member f [Source:HGNC Symbol;Acc:HGNC:29883]
RP3-426I6.5	1	p35.3	-1.07	0.0001	
TMEM71	8	q24.22	-1.07	0.00281	transmembrane protein 71 [Source:HGNC Symbol;Acc:HGNC:26572]
CCDC69	5	q33.1	-1.06	0.00117	coiled-coil domain containing 69 [Source:HGNC Symbol;Acc:HGNC:24487]
TICAM1	19	p13.3	-1.05	0.00469	toll-like receptor adaptor molecule 1 [Source:HGNC Symbol;Acc:HGNC:18348]
NFKBIA	14	q13.2	-1.04	0.00019	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, alpha [Source:HGNC Symbol;Acc:HGNC:7797]
RP11-542M13.3	16	q24.1	-1.04	0.00185	
TMEM255B	13	q34	-1.04	0.00847	transmembrane protein 255B [Source:HGNC Symbol;Acc:HGNC:28297]
RP11-568J23.4	16	q24.1	-1.03	0.00017	
HIST1H2AI	6	p22.1	-1.03	0.00091	histone cluster 1, H2ai [Source:HGNC Symbol;Acc:HGNC:4725]
ANXA6	5	q33.1	-1.03	0.00311	annexin A6 [Source:HGNC Symbol;Acc:HGNC:544]
RP3-453C12.14	20	q13.12	-1.02	0.00541	
C9orf72	9	p21.2	-1.01	0	chromosome 9 open reading frame 72 [Source:HGNC Symbol;Acc:HGNC:28337]
CTD-2540B15.13	19	q13.11	-1.01	0.00228	
C10orf54	10	q22.1	-1.01	0.00437	chromosome 10 open reading frame 54 [Source:HGNC Symbol;Acc:HGNC:30085]
STEAP4	7	q21.12	-1.01	0.00556	STEAP family member 4 [Source:HGNC Symbol;Acc:HGNC:21923]

FOSB	19	q13.32	-1.01	0.00604	FBJ murine osteosarcoma viral oncogene homolog B [Source:HGNC Symbol;Acc:HGNC:3797]
RP11-65J3.1	9	q34.11	-1.01	0.00851	
RP11-629O1.2	8	q24.22	-0.99	0.00012	
PC	11	q13.2	-0.99	0.00099	pyruvate carboxylase [Source:HGNC Symbol;Acc:HGNC:8636]
ESPL1	12	q13.13	-0.99	0.00255	extra spindle pole bodies homolog 1 (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:16856]
MGAT3	22	q13.1	-0.99	0.00983	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase [Source:HGNC Symbol;Acc:HGNC:7046]
KLF6	10	p15.2	-0.98	0.00091	Kruppel-like factor 6 [Source:HGNC Symbol;Acc:HGNC:2235]
S100A6	1	q21.3	-0.98	0.00103	S100 calcium binding protein A6 [Source:HGNC Symbol;Acc:HGNC:10496]
EPHB2	1	p36.12	-0.98	0.00106	EPH receptor B2 [Source:HGNC Symbol;Acc:HGNC:3393]
RIPK2	8	q21.3	-0.98	0.00175	receptor-interacting serine-threonine kinase 2 [Source:HGNC Symbol;Acc:HGNC:10020]
PSAP	10	q22.1	-0.98	0.00228	prosaposin [Source:HGNC Symbol;Acc:HGNC:9498]
NLRP3	1	q44	-0.98	0.0091	NLR family, pyrin domain containing 3 [Source:HGNC Symbol;Acc:HGNC:16400]
NPC2	14	q24.3	-0.97	0	Niemann-Pick disease, type C2 [Source:HGNC Symbol;Acc:HGNC:14537]
ITGB2	21	q22.3	-0.97	0	integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) [Source:HGNC Symbol;Acc:HGNC:6155]
VIM-AS1	10	p13	-0.97	0.00156	VIM antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:44879]
BTG1	12	q21.33	-0.97	0.00309	B-cell translocation gene 1, anti-proliferative [Source:HGNC Symbol;Acc:HGNC:1130]
UBXN11	1	p36.11	-0.96	0	UBX domain protein 11 [Source:HGNC Symbol;Acc:HGNC:30600]
MALAT1	11	q13.1	-0.96	0.00025	metastasis associated lung adenocarcinoma transcript 1 (non-protein coding) [Source:HGNC Symbol;Acc:HGNC:29665]
CEACAM1	19	q13.2	-0.96	0.00622	carcinoembryonic antigen-related cell adhesion molecule 1 (biliary glycoprotein) [Source:HGNC Symbol;Acc:HGNC:1814]
ADORA2A-AS1	22	q11.23	-0.94	0.00179	ADORA2A antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:37122]
HCAR2	12	q24.31	-0.94	0.00199	hydroxycarboxylic acid receptor 2 [Source:HGNC Symbol;Acc:HGNC:24827]
PXYLP1	3	q23	-0.94	0.00473	2-phosphoxylose phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:26303]
GLUL	1	q25.3	-0.93	0.00078	glutamate-ammonia ligase [Source:HGNC Symbol;Acc:HGNC:4341]
NRGN	11	q24.2	-0.93	0.0023	neurogranin (protein kinase C substrate, RC3) [Source:HGNC Symbol;Acc:HGNC:8000]
ZFP36	19	q13.2	-0.93	0.00851	ZFP36 ring finger protein [Source:HGNC Symbol;Acc:HGNC:12862]
SLC9A3R1	17	q25.1	-0.92	0.00001	solute carrier family 9, subfamily A (NHE3, cation proton antiporter 3), member 3 regulator 1 [Source:HGNC Symbol;Acc:HGNC:11075]
GNS	12	q14.3	-0.92	0.00007	glucosamine (N-acetyl)-6-sulfatase [Source:HGNC Symbol;Acc:HGNC:4422]

RP11-670E13.6	17	q22	-0.92	0.00111	
BRI3	7	q21.3	-0.92	0.00157	brain protein I3 [Source:HGNC Symbol;Acc:HGNC:1109]
SCPEP1	17	q22	-0.92	0.00883	serine carboxypeptidase 1 [Source:HGNC Symbol;Acc:HGNC:29507]
ASAP1	8	q24.22	-0.91	0.00003	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1 [Source:HGNC Symbol;Acc:HGNC:2720]
LINC00671	17	q21.31	-0.91	0.00233	long intergenic non-protein coding RNA 671 [Source:HGNC Symbol;Acc:HGNC:44339]
DOK3	5	q35.3	-0.91	0.00714	docking protein 3 [Source:HGNC Symbol;Acc:HGNC:24583]
FTH1	11	q12.3	-0.91	0.00755	ferritin, heavy polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:3976]
S100A4	1	q21.3	-0.90	0	S100 calcium binding protein A4 [Source:HGNC Symbol;Acc:HGNC:10494]
AC116035.1	3	p24.1	-0.90	0.00066	
DHX34	19	q13.32	-0.90	0.00255	DEAH (Asp-Glu-Ala-His) box polypeptide 34 [Source:HGNC Symbol;Acc:HGNC:16719]
DEPDC1B	5	q12.1	-0.90	0.00681	DEP domain containing 1B [Source:HGNC Symbol;Acc:HGNC:24902]
TMIGD2	19	p13.3	-0.90	0.00932	transmembrane and immunoglobulin domain containing 2 [Source:HGNC Symbol;Acc:HGNC:28324]
MBD2	18	q21.2	-0.89	0	methyl-CpG binding domain protein 2 [Source:HGNC Symbol;Acc:HGNC:6917]
CD2	1	p13.1	-0.89	0.00125	CD2 molecule [Source:HGNC Symbol;Acc:HGNC:1639]
SNX22	15	q22.31	-0.88	0.0002	sorting nexin 22 [Source:HGNC Symbol;Acc:HGNC:16315]
AGTRAP	1	p36.22	-0.88	0.00098	angiotensin II receptor-associated protein [Source:HGNC Symbol;Acc:HGNC:13539]
NFKBIZ	3	q12.3	-0.88	0.00257	nuclear factor of kappa light polypeptide gene enhancer in B-cells inhibitor, zeta [Source:HGNC Symbol;Acc:HGNC:29805]
TAGAP	6	q25.3	-0.88	0.00987	T-cell activation RhoGTPase activating protein [Source:HGNC Symbol;Acc:HGNC:15669]
TRIB1	8	q24.13	-0.87	0.0003	tribbles pseudokinase 1 [Source:HGNC Symbol;Acc:HGNC:16891]
CTD-3252C9.4	19	p13.12	-0.87	0.00118	
DDIT3	12	q13.3	-0.87	0.00458	DNA-damage-inducible transcript 3 [Source:HGNC Symbol;Acc:HGNC:2726]
H1FX	3	q21.3	-0.86	0	H1 histone family, member X [Source:HGNC Symbol;Acc:HGNC:4722]
LST1	12	q23.1	-0.86	0.00003	leukotriene A4 hydrolase [Source:HGNC Symbol;Acc:HGNC:6710]
HK2	2	p12	-0.86	0.00008	hexokinase 2 [Source:HGNC Symbol;Acc:HGNC:4923]
HK1	10	q22.1	-0.86	0.00048	hexokinase 1 [Source:HGNC Symbol;Acc:HGNC:4922]
ATP6V1B2	8	p21.3	-0.85	0.00019	ATPase, H+ transporting, lysosomal 56/58kDa, V1 subunit B2 [Source:HGNC Symbol;Acc:HGNC:854]
JUNB	19	p13.13	-0.85	0.00085	jun B proto-oncogene [Source:HGNC Symbol;Acc:HGNC:6205]
GLRX	5	q15	-0.85	0.00393	glutaredoxin (thioltransferase) [Source:HGNC Symbol;Acc:HGNC:4330]
GABARAPL1	12	p13.2	-0.85	0.00599	GABA(A) receptor-associated protein like 1 [Source:HGNC Symbol;Acc:HGNC:4068]

MESDC1	15	q25.1	-0.85	0.00654	mesoderm development candidate 1 [Source:HGNC Symbol;Acc:HGNC:13519]
CD55	1	q32.2	-0.85	0.00797	CD55 molecule, decay accelerating factor for complement (Cromer blood group) [Source:HGNC Symbol;Acc:HGNC:2665]
PTTG1	5	q33.3	-0.84	0.00077	pituitary tumor-transforming 1 [Source:HGNC Symbol;Acc:HGNC:9690]
RP3-402G11.26	22	q13.33	-0.84	0.0096	
NAAA	4	q21.1	-0.83	0.00017	N-acylethanolamine acid amidase [Source:HGNC Symbol;Acc:HGNC:736]
FOSL2	2	p23.2	-0.83	0.00309	FOS-like antigen 2 [Source:HGNC Symbol;Acc:HGNC:3798]
FTL	19	q13.33	-0.83	0.00347	ferritin, light polypeptide [Source:HGNC Symbol;Acc:HGNC:3999]
HIST1H1C	6	p22.2	-0.83	0.00702	histone cluster 1, H1c [Source:HGNC Symbol;Acc:HGNC:4716]
NETO2	16	q12.1	-0.83	0.00705	neuropilin (NRP) and tolloid (TLL)-like 2 [Source:HGNC Symbol;Acc:HGNC:14644]
MCL1	1	q21.2	-0.82	0.00036	myeloid cell leukemia 1 [Source:HGNC Symbol;Acc:HGNC:6943]
BTN2A2	6	p22.2	-0.82	0.00961	butyrophilin, subfamily 2, member A2 [Source:HGNC Symbol;Acc:HGNC:1137]
SCARNA9	11	q21	-0.81	0.00008	small Cajal body-specific RNA 9 [Source:HGNC Symbol;Acc:HGNC:32566]
FAM45A	10	q26.11	-0.81	0.00051	family with sequence similarity 45, member A [Source:HGNC Symbol;Acc:HGNC:31793]
GLTP	12	q24.11	-0.81	0.00179	glycolipid transfer protein [Source:HGNC Symbol;Acc:HGNC:24867]
CLEC1A	12	p13.2	-0.81	0.00604	C-type lectin domain family 1, member A [Source:HGNC Symbol;Acc:HGNC:24355]
ZNF438	10	p11.23	-0.81	0.00828	zinc finger protein 438 [Source:HGNC Symbol;Acc:HGNC:21029]
CTSB	8	p23.1	-0.81	0.00874	cathepsin B [Source:HGNC Symbol;Acc:HGNC:2527]
AMPD2	1	p13.3	-0.80	0.00003	adenosine monophosphate deaminase 2 [Source:HGNC Symbol;Acc:HGNC:469]
KIF21B	1	q32.1	-0.80	0.00375	kinesin family member 21B [Source:HGNC Symbol;Acc:HGNC:29442]
FKBP15	9	q32	-0.80	0.00923	FK506 binding protein 15, 133kDa [Source:HGNC Symbol;Acc:HGNC:23397]
FBXL5	4	p15.32	-0.79	0	F-box and leucine-rich repeat protein 5 [Source:HGNC Symbol;Acc:HGNC:13602]
LYAR	11	p15.4	-0.79	0.00536	lymphatic vessel endothelial hyaluronan receptor 1 [Source:HGNC Symbol;Acc:HGNC:14687]
C20orf24	20	q11.23	-0.78	0	chromosome 20 open reading frame 24 [Source:HGNC Symbol;Acc:HGNC:15870]
TREX1	3	p21.31	-0.78	0.00388	three prime repair exonuclease 1 [Source:HGNC Symbol;Acc:HGNC:12269]
CARD16	11	q22.3	-0.78	0.00755	caspase recruitment domain family, member 16 [Source:HGNC Symbol;Acc:HGNC:33701]
ABHD5	3	p21.33	-0.77	0.00048	abhydrolase domain containing 5 [Source:HGNC Symbol;Acc:HGNC:21396]
PTGS1	9	q33.2	-0.77	0.00086	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase) [Source:HGNC Symbol;Acc:HGNC:9604]
SHKBP1	19	q13.2	-0.77	0.00266	SH3KBP1 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:19214]
PECAM1	17	q23.3	-0.77	0.00348	platelet/endothelial cell adhesion molecule 1 [Source:HGNC Symbol;Acc:HGNC:8823]

PSMB9	6	p21.32	-0.77	0.00464	proteasome (prosome, macropain) subunit, beta type, 9 [Source:HGNC Symbol;Acc:HGNC:9546]
HMGB2	4	q34.1	-0.77	0.00609	high mobility group box 2 [Source:HGNC Symbol;Acc:HGNC:5000]
FYB	5	p13.1	-0.77	0.00897	FYN binding protein [Source:HGNC Symbol;Acc:HGNC:4036]
DUSP2	2	q11.2	-0.76	0	dual specificity phosphatase 2 [Source:HGNC Symbol;Acc:HGNC:3068]
RP11-802E16.3	11	q13.2	-0.76	0.00008	
LIME1	20	q13.33	-0.76	0.00042	Lck interacting transmembrane adaptor 1 [Source:HGNC Symbol;Acc:HGNC:26016]
CORO1A	16	p11.2	-0.76	0.0007	coronin, actin binding protein, 1A [Source:HGNC Symbol;Acc:HGNC:2252]
SBF2	11	p15.4	-0.76	0.00685	SET binding factor 2 [Source:HGNC Symbol;Acc:HGNC:2135]
POR	7	q11.23	-0.75	0.00462	P450 (cytochrome) oxidoreductase [Source:HGNC Symbol;Acc:HGNC:9208]
TCIRG1	11	q13.2	-0.74	0.00027	T-cell, immune regulator 1, ATPase, H+ transporting, lysosomal V0 subunit A3 [Source:HGNC Symbol;Acc:HGNC:11647]
NLRC5	16	q13	-0.74	0.00691	NLR family, CARD domain containing 5 [Source:HGNC Symbol;Acc:HGNC:29933]
P2RX4	12	q24.31	-0.74	0.00986	purinergic receptor P2X, ligand-gated ion channel, 4 [Source:HGNC Symbol;Acc:HGNC:8535]
TMEM256-PLSCR3	17	p13.1	-0.73	0.00077	TMEM256-PLSCR3 readthrough (NMD candidate) [Source:HGNC Symbol;Acc:HGNC:49186]
IL6R	1	q21.3	-0.73	0.00796	interleukin 6 receptor [Source:HGNC Symbol;Acc:HGNC:6019]
RAB24	5	q35.3	-0.72	0	RAB24, member RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9765]
SLC36A1	5	q33.1	-0.72	0.00155	solute carrier family 36 (proton/amino acid symporter), member 1 [Source:HGNC Symbol;Acc:HGNC:18761]
DEF8	16	q24.3	-0.71	0.00076	differentially expressed in FDCP 8 homolog (mouse) [Source:HGNC Symbol;Acc:HGNC:25969]
CLCN5	X	p11.23	-0.71	0.00315	chloride channel, voltage-sensitive 5 [Source:HGNC Symbol;Acc:HGNC:2023]
C1orf162	1	p13.2	-0.71	0.00328	chromosome 1 open reading frame 162 [Source:HGNC Symbol;Acc:HGNC:28344]
JDP2	14	q24.3	-0.71	0.00727	Jun dimerization protein 2 [Source:HGNC Symbol;Acc:HGNC:17546]
TSPO	22	q13.2	-0.71	0.00892	translocator protein (18kDa) [Source:HGNC Symbol;Acc:HGNC:1158]
EVI2B	17	q11.2	-0.70	0	ecotropic viral integration site 2B [Source:HGNC Symbol;Acc:HGNC:3500]
C14orf80	14	q32.33	-0.70	0.00185	chromosome 14 open reading frame 80 [Source:HGNC Symbol;Acc:HGNC:20127]
DGKA	12	q13.2	-0.70	0.00713	diacylglycerol kinase, alpha 80kDa [Source:HGNC Symbol;Acc:HGNC:2849]
C6orf1	6	p21.31	-0.69	0.00029	chromosome 6 open reading frame 1 [Source:HGNC Symbol;Acc:HGNC:1340]
MXD3	5	q35.3	-0.69	0.00079	MAX dimerization protein 3 [Source:HGNC Symbol;Acc:HGNC:14008]
RPS6KA1	1	p36.11	-0.69	0.00628	ribosomal protein S6 kinase, 90kDa, polypeptide 1 [Source:HGNC Symbol;Acc:HGNC:10430]
SEMA4A	1	q22	-0.69	0.0077	sema domain, immunoglobulin domain (Ig), transmembrane domain (TM) and short cytoplasmic domain, (semaphorin) 4A [Source:HGNC Symbol;Acc:HGNC:10729]

SHROOM1	5	q31.1	-0.69	0.00962	shroom family member 1 [Source:HGNC Symbol;Acc:HGNC:24084]
SELK	3	p21.1	-0.68	0.00001	selenoprotein K [Source:RefSeq peptide;Acc:NP_067060]
TMEM167A	5	q14.2	-0.68	0.00026	transmembrane protein 167A [Source:HGNC Symbol;Acc:HGNC:28330]
SEC14L4	22	q12.2	-0.68	0.00294	SEC14-like 4 (S. cerevisiae) [Source:HGNC Symbol;Acc:HGNC:20627]
HLA-C	6	p21.33	-0.68	0.00847	major histocompatibility complex, class I, C [Source:HGNC Symbol;Acc:HGNC:4933]
ZNF281	1	q32.1	-0.67	0.00098	zinc finger protein 281 [Source:HGNC Symbol;Acc:HGNC:13075]
SNX27	1	q21.3	-0.67	0.00266	sorting nexin family member 27 [Source:HGNC Symbol;Acc:HGNC:20073]
POLE4	2	p12	-0.67	0.00369	polymerase (DNA-directed), epsilon 4, accessory subunit [Source:HGNC Symbol;Acc:HGNC:18755]
RP11-375N15.2	8	p23.1	-0.67	0.00779	
MXD1	2	p13.3	-0.66	0.00609	MAX dimerization protein 1 [Source:HGNC Symbol;Acc:HGNC:6761]
AP3S1	5	q22.3	-0.66	0.00666	adaptor-related protein complex 3, sigma 1 subunit [Source:HGNC Symbol;Acc:HGNC:2013]
FLT4	5	q35.3	-0.66	0.00683	fms-related tyrosine kinase 4 [Source:HGNC Symbol;Acc:HGNC:3767]
TBC1D7	6	p24.1	-0.65	0.00406	TBC1 domain family, member 7 [Source:HGNC Symbol;Acc:HGNC:21066]
KIF13B	8	p12	-0.64	0.0006	kinesin family member 13B [Source:HGNC Symbol;Acc:HGNC:14405]
FCHO1	19	p13.11	-0.64	0.00102	FCH domain only 1 [Source:HGNC Symbol;Acc:HGNC:29002]
MTRNR2L9	6	q11.1	-0.64	0.00233	MT-RNR2-like 9 (pseudogene) [Source:HGNC Symbol;Acc:HGNC:37166]
TMSB4X	X	p22.2	-0.63	0.00377	thymosin beta 4, X-linked [Source:HGNC Symbol;Acc:HGNC:11881]
GK5	3	q23	-0.63	0.00433	glycerol kinase 5 (putative) [Source:HGNC Symbol;Acc:HGNC:28635]
B2M	15	q21.1	-0.62	0	beta-2-microglobulin [Source:HGNC Symbol;Acc:HGNC:914]
LRRN2	11	p15.5	-0.62	0.00413	lymphocyte-specific protein 1 [Source:HGNC Symbol;Acc:HGNC:6707]
LPPR2	19	p13.2	-0.62	0.00453	Lipid phosphate phosphatase-related protein type 2 [Source:UniProtKB/Swiss-Prot;Acc:Q96GM1]
AC135048.13	16	p11.2	-0.62	0.0063	
MTRNR2L1	17	p11.2	-0.62	0.00679	MT-RNR2-like 1 [Source:HGNC Symbol;Acc:HGNC:37155]
STK10	5	q35.1	-0.62	0.00758	serine/threonine kinase 10 [Source:HGNC Symbol;Acc:HGNC:11388]
PLAGL2	20	q11.21	-0.62	0.00897	pleiomorphic adenoma gene-like 2 [Source:HGNC Symbol;Acc:HGNC:9047]
ADCY7	16	q12.1	-0.61	0.00556	adenylate cyclase 7 [Source:HGNC Symbol;Acc:HGNC:238]
LINC00115	1	p36.33	-0.59	0.00761	long intergenic non-protein coding RNA 115 [Source:HGNC Symbol;Acc:HGNC:26211]
ATP6AP2	X	p11.4	-0.58	0.00007	ATPase, H+ transporting, lysosomal accessory protein 2 [Source:HGNC Symbol;Acc:HGNC:18305]
EIF1	17	q21.2	-0.58	0.00288	eukaryotic translation initiation factor 1 [Source:HGNC Symbol;Acc:HGNC:3249]
GABARAP	17	p13.1	-0.58	0.00298	GABA(A) receptor-associated protein [Source:HGNC Symbol;Acc:HGNC:4067]

ZFAND5	9	q21.13	-0.58	0.00609	zinc finger, AN1-type domain 5 [Source:HGNC Symbol;Acc:HGNC:13008]
GADD45A	1	p31.3	-0.57	0.00012	growth arrest and DNA-damage-inducible, alpha [Source:HGNC Symbol;Acc:HGNC:4095]
RNF130	5	q35.3	-0.57	0.00025	ring finger protein 130 [Source:HGNC Symbol;Acc:HGNC:18280]
PFKM	12	q13.11	-0.57	0.00259	phosphofructokinase, muscle [Source:HGNC Symbol;Acc:HGNC:8877]
DENND1A	9	q33.3	-0.56	0.00208	DENN/MADD domain containing 1A [Source:HGNC Symbol;Acc:HGNC:29324]
SMS	X	p22.11	-0.55	0.00379	spermine synthase [Source:HGNC Symbol;Acc:HGNC:11123]
TIFA	4	q25	-0.54	0.00027	TRAF-interacting protein with forkhead-associated domain [Source:HGNC Symbol;Acc:HGNC:19075]
MSL3	X	p22.2	-0.52	0.00266	male-specific lethal 3 homolog (Drosophila) [Source:HGNC Symbol;Acc:HGNC:7370]
RP11-51J9.5	8	p12	-0.52	0.0053	
ARHGAP27	17	q21.31	-0.52	0.00596	Rho GTPase activating protein 27 [Source:HGNC Symbol;Acc:HGNC:31813]
LDHA	11	p15.1	-0.51	0.00076	lactate dehydrogenase A [Source:HGNC Symbol;Acc:HGNC:6535]
NDUFA2	5	q31.3	-0.51	0.00447	NADH dehydrogenase (ubiquinone) 1 alpha subcomplex, 2, 8kDa [Source:HGNC Symbol;Acc:HGNC:7685]
SLC26A6	3	p21.31	-0.51	0.00686	solute carrier family 26 (anion exchanger), member 6 [Source:HGNC Symbol;Acc:HGNC:14472]
LAMTOR5	1	p13.3	-0.50	0.00017	late endosomal/lysosomal adaptor, MAPK and MTOR activator 5 [Source:HGNC Symbol;Acc:HGNC:17955]
MANF	3	p21.2	-0.50	0.00406	mesencephalic astrocyte-derived neurotrophic factor [Source:HGNC Symbol;Acc:HGNC:15461]
RAP1A	1	p13.2	-0.50	0.00718	RAP1A, member of RAS oncogene family [Source:HGNC Symbol;Acc:HGNC:9855]
OAZ1	19	p13.3	-0.49	0.00401	ornithine decarboxylase antizyme 1 [Source:HGNC Symbol;Acc:HGNC:8095]
UBQLN2	X	p11.21	-0.48	0.00183	ubiquilin 2 [Source:HGNC Symbol;Acc:HGNC:12509]
CAPZB	1	p36.13	-0.48	0.00797	capping protein (actin filament) muscle Z-line, beta [Source:HGNC Symbol;Acc:HGNC:1491]
ATP1B3	3	q23	-0.48	0.00876	ATPase, Na+/K+ transporting, beta 3 polypeptide [Source:HGNC Symbol;Acc:HGNC:806]
MIIP	1	p36.22	-0.46	0.00437	migration and invasion inhibitory protein [Source:HGNC Symbol;Acc:HGNC:25715]
PSMA2	7	p14.1	-0.43	0.00016	proteasome (prosome, macropain) subunit, alpha type, 2 [Source:HGNC Symbol;Acc:HGNC:9531]
COMMD9	11	p13	-0.43	0.00018	COMM domain containing 9 [Source:HGNC Symbol;Acc:HGNC:25014]
PSMB8	6	p21.32	-0.43	0.00797	proteasome (prosome, macropain) subunit, beta type, 8 [Source:HGNC Symbol;Acc:HGNC:9545]
C15orf61	15	q23	-0.42	0.0006	chromosome 15 open reading frame 61 [Source:HGNC Symbol;Acc:HGNC:34453]
MT-ND1	MT	n/a	-0.42	0.00252	mitochondrially encoded NADH dehydrogenase 1 [Source:HGNC Symbol;Acc:HGNC:7455]
NDUFS5	1	p34.3	-0.39	0.00679	NADH dehydrogenase (ubiquinone) Fe-S protein 5, 15kDa (NADH-coenzyme Q reductase) [Source:HGNC Symbol;Acc:HGNC:7712]
FAM73B	9	q34.11	-0.36	0.00287	family with sequence similarity 73, member B [Source:HGNC Symbol;Acc:HGNC:23621]

GAK	4	p16.3	-0.31	0.00011	cyclin G associated kinase [Source:HGNC Symbol;Acc:HGNC:4113]
PSMA7	20	q13.33	-0.29	0.00788	proteasome (prosome, macropain) subunit, alpha type, 7 [Source:HGNC Symbol;Acc:HGNC:9536]

Abbreviations: Chrom., chromosome; log2FC, $\log_2$ (base 2 logarithm) transformed fold change; q-value, false discovery rate adjusted p-value.

Genes without a description are clone-based and/or are of unknown function.

Supplementary Table S10A. Genes differentially expressed between patients who achieved CR versus those who did not

Genes upregulated in patients who did not achieve CR					
Gene symbol	*Chrom.*	*Band*	*log2FC*	*q-value*	*Description*
CEACAM6	19	q13.2	-3.04	0.00004	carcinoembryonic antigen-related cell adhesion molecule 6 (non-specific cross reacting antigen) [Source:HGNC Symbol;Acc:HGNC:1818]
TRBV27	7	q34	-2.82	0.00060	T cell receptor beta variable 27 [Source:HGNC Symbol;Acc:HGNC:12208]
ZNF827	4	q31.22	-2.33	0.02048	zinc finger protein 827 [Source:HGNC Symbol;Acc:HGNC:27193]
ZSCAN18	19	q13.43	-2.28	0.00514	zinc finger and SCAN domain containing 18 [Source:HGNC Symbol;Acc:HGNC:21037]
AL122127.25	14	q32.33	-2.08	0.08548	
NPM2	8	p21.3	-2.07	0.03818	nucleophosmin/nucleoplasmin 2 [Source:HGNC Symbol;Acc:HGNC:7930]
GPR114	16	q21	-2.03	0.01526	G protein-coupled receptor 114 [Source:HGNC Symbol;Acc:HGNC:19010]
TIE1	1	p34.2	-2.02	0.08017	tyrosine kinase with immunoglobulin-like and EGF-like domains 1 [Source:HGNC Symbol;Acc:HGNC:11809]
SH2D1A	X	q25	-1.98	0.06969	SH2 domain containing 1A [Source:HGNC Symbol;Acc:HGNC:10820]
ARHGAP22	10	q11.23	-1.95	0.06969	Rho GTPase activating protein 22 [Source:HGNC Symbol;Acc:HGNC:30320]
SPNS2	17	p13.2	-1.95	0.09794	spinster homolog 2 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:26992]
EMID1	22	q12.2	-1.94	0.08117	EMI domain containing 1 [Source:HGNC Symbol;Acc:HGNC:18036]
RP4-666F24.3	1	p13.2	-1.88	0.08548	
JUP	17	q21.2	-1.87	0.03818	junction plakoglobin [Source:HGNC Symbol;Acc:HGNC:6207]
SSBP2	5	q14.1	-1.83	0.03818	single-stranded DNA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:15831]
SEPP1	5	p12	-1.81	0.05451	selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:HGNC:10751]
NEDD4	15	q21.3	-1.80	0.09794	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:7727]
C9orf43	9	q32	-1.79	0.09794	chromosome 9 open reading frame 43 [Source:HGNC Symbol;Acc:HGNC:23570]
DNMT3B	20	q11.21	-1.78	0.09876	DNA (cytosine-5-)-methyltransferase 3 beta [Source:HGNC Symbol;Acc:HGNC:2979]
MACC1	7	p21.1	-1.76	0.06969	metastasis associated in colon cancer 1 [Source:HGNC Symbol;Acc:HGNC:30215]
RLTPR	16	q22.1	-1.75	0.09876	RGD motif, leucine rich repeats, tropomodulin domain and proline-rich containing [Source:HGNC Symbol;Acc:HGNC:27089]
CTA-984G1.5	22	q12.2	-1.74	0.09794	
SCARF1	17	p13.3	-1.70	0.06969	scavenger receptor class F, member 1 [Source:HGNC Symbol;Acc:HGNC:16820]
MN1	22	q12.1	-1.69	0.06969	meningioma (disrupted in balanced translocation) 1 [Source:HGNC Symbol;Acc:HGNC:7180]
AF127936.7	21	q11.2	-1.69	0.08967	
ZEB1	10	p11.22	-1.67	0.09794	zinc finger E-box binding homeobox 1 [Source:HGNC Symbol;Acc:HGNC:11642]

GUCY2D	17	p13.1	-1.67	0.09794	guanylate cyclase 2D, membrane (retina-specific) [Source:HGNC Symbol;Acc:HGNC:4689]
LINC01150	11	p15.5	-1.62	0.08967	long intergenic non-protein coding RNA 1150 [Source:HGNC Symbol;Acc:HGNC:49469]
SPNS3	17	p13.2	-1.58	0.09080	spinster homolog 3 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:28433]
RP11-93H24.3	13	q14.3	-1.55	0.04531	
VN1R1	19	q13.43	-1.53	0.06622	vomeronasal 1 receptor 1 [Source:HGNC Symbol;Acc:HGNC:13548]
ZNF772	19	q13.43	-1.43	0.06969	zinc finger protein 772 [Source:HGNC Symbol;Acc:HGNC:33106]
ZNF443	19	p13.2	-1.40	0.00199	zinc finger protein 443 [Source:HGNC Symbol;Acc:HGNC:20878]
ZNF550	19	q13.43	-1.29	0.09794	zinc finger protein 550 [Source:HGNC Symbol;Acc:HGNC:28643]
MAPKBP1	15	q15.1	-1.11	0.07035	mitogen-activated protein kinase binding protein 1 [Source:HGNC Symbol;Acc:HGNC:29536]
JMJD7	15	q15.1	-0.90	0.08017	jumonji domain containing 7 [Source:HGNC Symbol;Acc:HGNC:34397]
ODF2L	1	p22.3	-0.68	0.05451	outer dense fiber of sperm tails 2-like [Source:HGNC Symbol;Acc:HGNC:29225]
Genes downregulated in patients who did not achieve CR					
Gene symbol	*Chrom.*	*Band*	*log2FC*	*q-value*	*Description*
AMIGO2	12	q13.11	2.80	0.00018	adhesion molecule with Ig-like domain 2 [Source:HGNC Symbol;Acc:HGNC:24073]
RAB11FIP5	2	p13.2	2.37	0.01469	RAB11 family interacting protein 5 (class I) [Source:HGNC Symbol;Acc:HGNC:24845]
KCTD1	18	q11.2	2.18	0.00590	potassium channel tetramerization domain containing 1 [Source:HGNC Symbol;Acc:HGNC:18249]
KCNC3	19	q13.33	2.10	0.05451	potassium voltage-gated channel, Shaw-related subfamily, member 3 [Source:HGNC Symbol;Acc:HGNC:6235]
CD276	15	q24.1	2.02	0.03818	CD276 molecule [Source:HGNC Symbol;Acc:HGNC:19137]
FAM110B	8	q12.1	1.87	0.08017	family with sequence similarity 110, member B [Source:HGNC Symbol;Acc:HGNC:28587]
TEF	22	q13.2	1.75	0.09876	thyrotrophic embryonic factor [Source:HGNC Symbol;Acc:HGNC:11722]
PCED1B	12	q13.11	1.66	0.09876	PC-esterase domain containing 1B [Source:HGNC Symbol;Acc:HGNC:28255]
RP13-977J11.2	12	q24.33	1.54	0.09794	
CTC-428G20.6	5	q22.3	1.51	0.06969	
TMEM104	17	q25.1	1.46	0.09876	transmembrane protein 104 [Source:HGNC Symbol;Acc:HGNC:25984]
AIFM2	10	q22.1	1.42	0.05778	apoptosis-inducing factor, mitochondrion-associated, 2 [Source:HGNC Symbol;Acc:HGNC:21411]
RP11-106D4.2	16	q24.2	1.38	0.07035	
CTD-2538C1.2	19	q13.11	1.33	0.07035	
ULBP1	6	q25.1	1.13	0.09794	UL16 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:14893]
RP11-159D12.5	17	q22	1.13	0.09794	Uncharacterized protein {ECO:0000313|Ensembl:ENSP00000463235} [Source:UniProtKB/TrEMBL;Acc:J3QKU1]
POMGNT2	3	p22.1	0.70	0.00199	protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-) [Source:HGNC Symbol;Acc:HGNC:25902]

Supplementary Table S10B. Genes differentially expressed between those who achieved CR versus those who did not controlling for translocation partner

Genes upregulated in patients who did not achieve CR					
Gene symbol	*Chrom.*	*Band*	*log2FC*	*q-value*	*Description*
ZNF827	4	q31.22	-2.56	0.01437	zinc finger protein 827 [Source:HGNC Symbol;Acc:HGNC:27193]
TRBV20-1	7	q34	-2.36	0.01519	T cell receptor beta variable 20-1 [Source:HGNC Symbol;Acc:HGNC:12196]
ANO7	2	q37.3	-2.33	0.06018	anoctamin 7 [Source:HGNC Symbol;Acc:HGNC:31677]
KIAA0125	14	q32.33	-2.32	0.07618	KIAA0125 [Source:HGNC Symbol;Acc:HGNC:19955]
MDGA1	6	p21.2	-2.31	0.03439	MAM domain containing glycosylphosphatidylinositol anchor 1 [Source:HGNC Symbol;Acc:HGNC:19267]
GPR114	16	q21	-2.29	0.00230	G protein-coupled receptor 114 [Source:HGNC Symbol;Acc:HGNC:19010]
IL17RE	3	p25.3	-2.11	0.08722	interleukin 17 receptor E [Source:HGNC Symbol;Acc:HGNC:18439]
SEPP1	5	p12	-2.10	0.00230	selenoprotein P, plasma, 1 [Source:HGNC Symbol;Acc:HGNC:10751]
JUP	17	q21.2	-2.03	0.01388	junction plakoglobin [Source:HGNC Symbol;Acc:HGNC:6207]
C9orf43	9	q32	-2.03	0.05130	chromosome 9 open reading frame 43 [Source:HGNC Symbol;Acc:HGNC:23570]
ARHGAP22	10	q11.23	-2.03	0.05566	Rho GTPase activating protein 22 [Source:HGNC Symbol;Acc:HGNC:30320]
EMID1	22	q12.2	-1.97	0.05130	EMI domain containing 1 [Source:HGNC Symbol;Acc:HGNC:18036]
SERPING1	11	q12.1	-1.96	0.03342	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1 [Source:HGNC Symbol;Acc:HGNC:1228]
CTA-984G1.5	22	q12.2	-1.95	0.00685	
NPM2	8	p21.3	-1.92	0.09670	nucleophosmin/nucleoplasmin 2 [Source:HGNC Symbol;Acc:HGNC:7930]
NEDD4	15	q21.3	-1.91	0.09916	neural precursor cell expressed, developmentally down-regulated 4, E3 ubiquitin protein ligase [Source:HGNC Symbol;Acc:HGNC:7727]
MACC1	7	p21.1	-1.88	0.05130	metastasis associated in colon cancer 1 [Source:HGNC Symbol;Acc:HGNC:30215]
ZNF439	19	p13.2	-1.88	0.09916	zinc finger protein 439 [Source:HGNC Symbol;Acc:HGNC:20873]
RP13-714J12.1	12	q24.33	-1.85	0.05676	
MN1	22	q12.1	-1.84	0.03525	meningioma (disrupted in balanced translocation) 1 [Source:HGNC Symbol;Acc:HGNC:7180]
AF127936.7	21	q11.2	-1.80	0.07618	
SPNS3	17	p13.2	-1.79	0.01757	spinster homolog 3 (Drosophila) [Source:HGNC Symbol;Acc:HGNC:28433]
SSBP2	5	q14.1	-1.79	0.03525	single-stranded DNA binding protein 2 [Source:HGNC Symbol;Acc:HGNC:15831]
SCARF1	17	p13.3	-1.79	0.05327	scavenger receptor class F, member 1 [Source:HGNC Symbol;Acc:HGNC:16820]
SV2A	1	q21.2	-1.76	0.06188	synaptic vesicle glycoprotein 2A [Source:HGNC Symbol;Acc:HGNC:20566]
VSIG10	12	q24.23	-1.76	0.07177	V-set and immunoglobulin domain containing 10 [Source:HGNC Symbol;Acc:HGNC:26078]

RP11-93H24.3	13	q14.3	-1.61	0.03342	
ZNF772	19	q13.43	-1.53	0.02058	zinc finger protein 772 [Source:HGNC Symbol;Acc:HGNC:33106]
USP53	4	q26	-1.49	0.09916	ubiquitin specific peptidase 53 [Source:HGNC Symbol;Acc:HGNC:29255]
ZNF443	19	p13.2	-1.41	0.00230	zinc finger protein 443 [Source:HGNC Symbol;Acc:HGNC:20878]
ZFP30	19	q13.12	-1.36	0.09916	ZFP30 zinc finger protein [Source:HGNC Symbol;Acc:HGNC:29555]
ZNF550	19	q13.43	-1.26	0.09691	zinc finger protein 550 [Source:HGNC Symbol;Acc:HGNC:28643]
TXNDC16	14	q22.1	-1.22	0.02816	thioredoxin domain containing 16 [Source:HGNC Symbol;Acc:HGNC:19965]
ZNF85	19	p12	-1.18	0.00895	zinc finger protein 85 [Source:HGNC Symbol;Acc:HGNC:13160]
ZNF528	19	q13.41	-1.12	0.00230	zinc finger protein 528 [Source:HGNC Symbol;Acc:HGNC:29384]
MAPKBP1	15	q15.1	-1.10	0.02055	mitogen-activated protein kinase binding protein 1 [Source:HGNC Symbol;Acc:HGNC:29536]
JMJD7	15	q15.1	-0.95	0.00230	jumonji domain containing 7 [Source:HGNC Symbol;Acc:HGNC:34397]
PHLPP1	18	q21.33	-0.92	0.09916	PH domain and leucine rich repeat protein phosphatase 1 [Source:HGNC Symbol;Acc:HGNC:20610]
EFHC1	6	p12.2	-0.91	0.09777	EF-hand domain (C-terminal) containing 1 [Source:HGNC Symbol;Acc:HGNC:16406]
TRPV1	17	p13.2	-0.80	0.00584	transient receptor potential cation channel, subfamily V, member 1 [Source:HGNC Symbol;Acc:HGNC:12716]
ODF2L	1	p22.3	-0.64	0.00685	outer dense fiber of sperm tails 2-like [Source:HGNC Symbol;Acc:HGNC:29225]
Genes downregulated in patients who did not achieve CR					
Gene symbol	*Chrom.*	*Band*	*log2FC*	*q-value*	*Description*
AMIGO2	12	q13.11	3.05	0.00029	adhesion molecule with Ig-like domain 2 [Source:HGNC Symbol;Acc:HGNC:24073]
TUBB3	16	q24.3	2.66	0.00206	tubulin, beta 3 class III [Source:HGNC Symbol;Acc:HGNC:20772]
KCTD1	18	q11.2	2.64	0.00009	potassium channel tetramerization domain containing 1 [Source:HGNC Symbol;Acc:HGNC:18249]
RAB11FIP5	2	p13.2	2.64	0.00685	RAB11 family interacting protein 5 (class I) [Source:HGNC Symbol;Acc:HGNC:24845]
CLDN23	8	p23.1	2.36	0.05676	claudin 23 [Source:HGNC Symbol;Acc:HGNC:17591]
C10orf35	10	q22.1	2.34	0.00450	chromosome 10 open reading frame 35 [Source:HGNC Symbol;Acc:HGNC:23519]
CDR2L	17	q25.1	2.30	0.00230	cerebellar degeneration-related protein 2-like [Source:HGNC Symbol;Acc:HGNC:29999]
PDE4A	19	p13.2	2.19	0.05130	phosphodiesterase 4A, cAMP-specific [Source:HGNC Symbol;Acc:HGNC:8780]
HNRNPLL	2	p22.1	2.18	0.00996	heterogeneous nuclear ribonucleoprotein L-like [Source:HGNC Symbol;Acc:HGNC:25127]
DCHS1	11	p15.4	2.12	0.03342	dachsous cadherin-related 1 [Source:HGNC Symbol;Acc:HGNC:13681]
PLCD1	3	p22.2	2.11	0.00685	phospholipase C, delta 1 [Source:HGNC Symbol;Acc:HGNC:9060]
CEP170B	14	q32.33	2.04	0.00685	centrosomal protein 170B [Source:HGNC Symbol;Acc:HGNC:20362]
C17orf96	17	q12	2.04	0.01528	chromosome 17 open reading frame 96 [Source:HGNC Symbol;Acc:HGNC:34493]

CDC42BPB	14	q32.32	1.88	0.06679	CDC42 binding protein kinase beta (DMPK-like) [Source:HGNC Symbol;Acc:HGNC:1738]
MSX2	5	q35.2	1.88	0.09587	msh homeobox 2 [Source:HGNC Symbol;Acc:HGNC:7392]
TEF	22	q13.2	1.88	0.09691	thyrotrophic embryonic factor [Source:HGNC Symbol;Acc:HGNC:11722]
ZNF503	10	q22.2	1.87	0.03342	zinc finger protein 503 [Source:EntrezGene;Acc:84858]
PCED1B	12	q13.11	1.76	0.09916	PC-esterase domain containing 1B [Source:HGNC Symbol;Acc:HGNC:28255]
SOX13	1	q32.1	1.71	0.01519	SRY (sex determining region Y)-box 13 [Source:HGNC Symbol;Acc:HGNC:11192]
CTD-2357A8.3	17	q25.3	1.55	0.09587	
SNPH	20	p13	1.49	0.02055	syntaphilin [Source:HGNC Symbol;Acc:HGNC:15931]
AIFM2	10	q22.1	1.44	0.05130	apoptosis-inducing factor, mitochondrion-associated, 2 [Source:HGNC Symbol;Acc:HGNC:21411]
CTD-2538C1.2	19	q13.11	1.40	0.05140	
RP11-106D4.2	16	q24.2	1.40	0.05297	
RP11-159D12.5	17	q22	1.27	0.00664	Uncharacterized protein {ECO:0000313|Ensembl:ENSP00000463235} [Source:UniProtKB/TrEMBL;Acc:J3QKU1]
PCED1B-AS1	12	q13.11	1.27	0.09916	PCED1B antisense RNA 1 [Source:HGNC Symbol;Acc:HGNC:44166]
ULBP1	6	q25.1	1.16	0.09916	UL16 binding protein 1 [Source:HGNC Symbol;Acc:HGNC:14893]
GAA	17	q25.3	1.03	0.09928	glucosidase, alpha; acid [Source:HGNC Symbol;Acc:HGNC:4065]
LTBP4	19	q13.2	0.95	0.07618	latent transforming growth factor beta binding protein 4 [Source:HGNC Symbol;Acc:HGNC:6717]
NKRF	X	q24	0.74	0.09916	NFKB repressing factor [Source:HGNC Symbol;Acc:HGNC:19374]
POMGNT2	3	p22.1	0.70	0.00450	protein O-linked mannose N-acetylglucosaminyltransferase 2 (beta 1,4-) [Source:HGNC Symbol;Acc:HGNC:25902]

Abbreviations: Chrom., chromosome; log2FC, $\log_2$ (base 2 logarithm) transformed fold change; q-value, false discovery rate adjusted p-value.

Genes without a description are clone-based and/or are of unknown function.

Supplementary Figure S1. Outcome of AML patients with t(11;19)(q23;p13.1) and AML patients plus one with ambiguous lineage acute leukemia with t(11;19)(q23;p13.3) for whom survival data are available. (**a**) Disease-free survival. (**b**) Overall survival.

Figure S1a

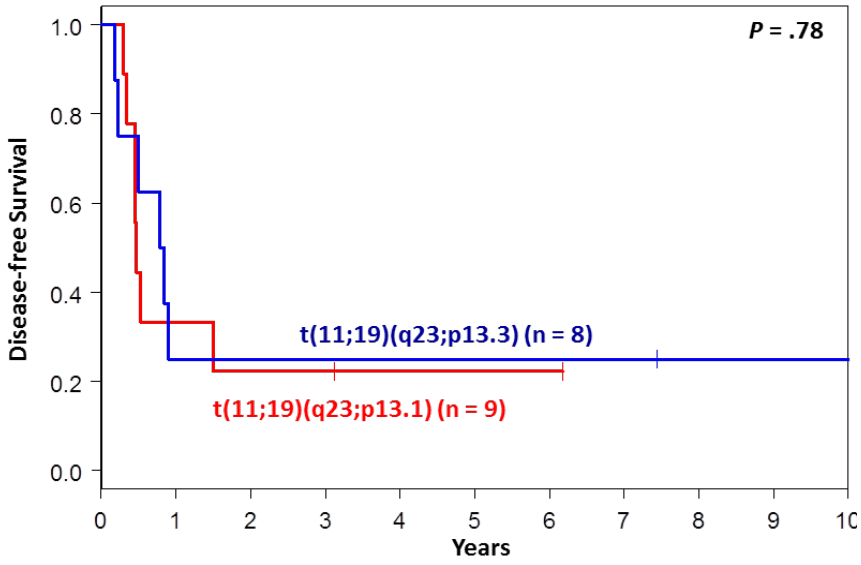
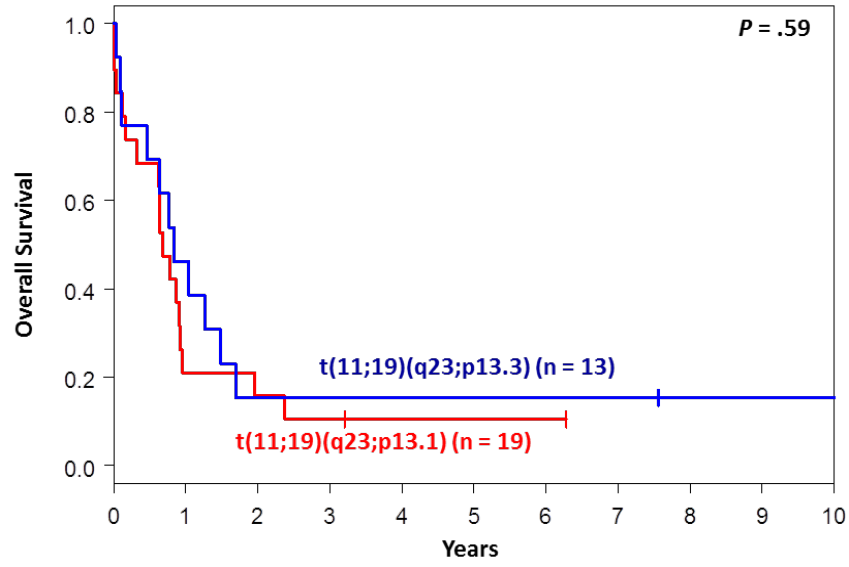
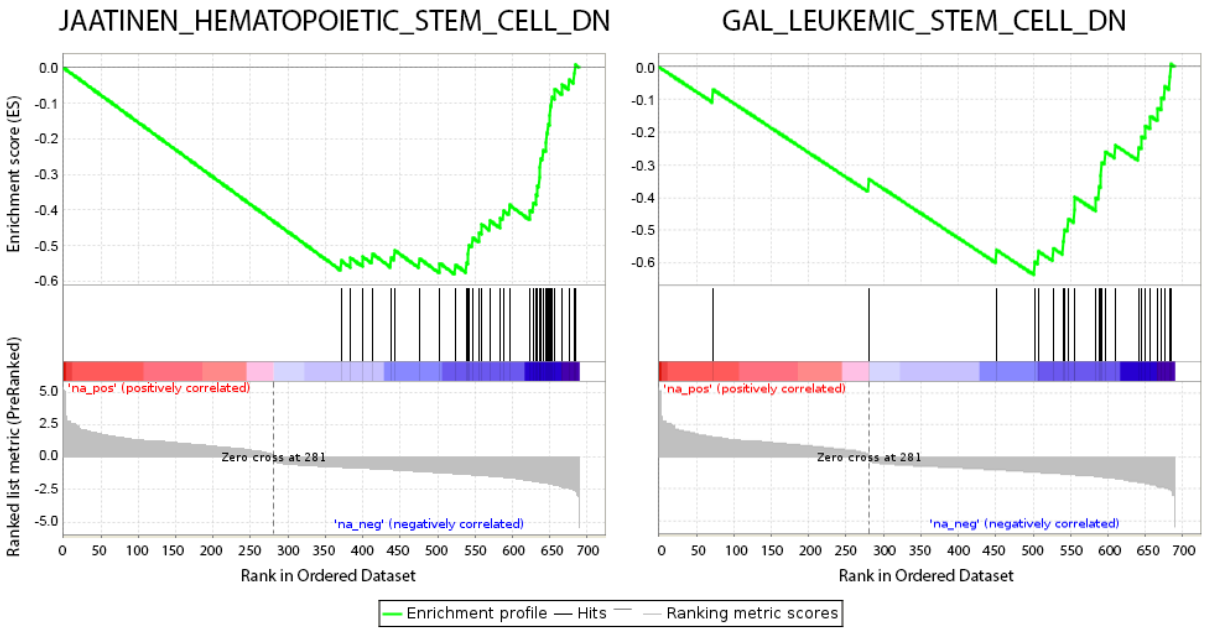


Figure S1b



Supplementary Figure S2. Gene set enrichment analysis of 690 genes differentially expressed between patients with t(11;19)(q23;p13.3) and those with t(11;19)(q23;p13.1). The figure depicts significant (FDR < 0.001 for both gene sets) overlap between genes downregulated in t(11;19)(q23;p13.3) cases and genes downregulated in two stem cell signatures. Each vertical black tick in the middle of the figure represents a "hit" or an overlap between the two gene sets. Hits occurring in the red portion labeled 'na_pos' are genes upregulated in t(11;19)(q23;p13.3) cases whereas hits in the blue portion labeled 'na_neg' are genes downregulated. Gene sets JAATINEN_HEMATOPOIETIC_STEM_CELL_DN and GAL_LEUKEMIC_STEM_CELL_DN reflect genes downregulated in hematopoietic stem cells and leukemia stem cells, respectively, and are available at The Broad Institute's MSigDB (http://www.broadinstitute.org/sea/msigdb/).



Supplementary Figure S3. Principal component analysis plot as in the main text, but colored for both translocation cytogenetic band and whether the translocation exists as a sole cytogenetic abnormality. As seen here, absence or presence of multiple cytogenetic abnormalities does not adequately explain the clustering of the data. PC1, first principal component; PC2, second principal component.