SUPPLEMENTARY APPENDIX

Knockdown of *Hnrnpa0*, a del(5q) gene, alters myeloid cell fate in murine cells through regulation of AU-rich transcripts

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Supplementary Materials for D. Young *et al.*

Purification of hematopoietic populations from mice.

Cells from the spleens, thymi, and bone marrow of C57BL/6J mice were harvested as appropriate for each population. For primitive populations including Lin^{-}Sca-1^{+}Kit^{+} (LSK), common lymphoid (CLP) and myeloid (CMP) progenitors, and granulocyte-monocyte progenitors (GMP), the cells were depleted of mature cells using the Mouse Hematopoietic Progenitor Cell Enrichment Kit (StemCell Technologies). The cells were stained for appropriate lineage markers, as described in Supplementary Figure S1, and sorted using a FACSAria fluorescence activated cell sorter (BD Biosciences).

Real-time RT-PCR analysis

Total RNA was purified from cells using Stat-60 (Tel-Test), according to the manufacturer's protocols. First-strand cDNA was synthesized using SuperScript III SuperMix for qRT-PCR (Invitrogen) containing both random hexamers and oligo(dT)$_{20}$ for priming. Real-time PCR reactions were run on a StepOne Plus Real-Time PCR System (Applied Biosystems) using the Fast SYBR Green Master Mix (Applied Biosystems). See Supplementary Table S6 for primer design. Samples were quantified by the standard curve method with *Gapdh* (or *Rn18S,* where indicated) as an internal control. cDNA standards were generated from total RNA isolated from total mouse bone marrow.

Gene expression profiling-PUER cells

Expression data were analyzed using two separate analysis platforms. The data were entered into the LIMMA package developed for the R statistical platform and validated using the GeneSpring GX 10 software (Agilent). The data were cross-array normalized using quantile normalization. Linear models were fit for genes in the dataset using construct (control or hairpin) and differentiation status (un-differentiated or differentiated) as predictors to identify genes whose expression showed a significant ($p < 0.05$) dependence upon the construct or differentiation state, or both. The multiple comparison method of Benjamini and Hochberg was used to correct for predicted false discovery.

To look for preferential changes in AU-rich genes, a list of all known AU-rich genes in the mouse genome was obtained from the AU-rich element containing mRNA database (ARED Organism, March 2008 release)[1]. The complete set of genes was classified as either AU-rich or non AU-rich. The fraction of AU-rich genes with a fold-difference between hairpin-expressing and controls above a given cutoff was calculated. The fold-differences were randomly reassigned across the entire geneset 10,000 times. For each permutation, the fraction of AU-rich genes randomly assigned a fold-difference above the cutoff was calculated. These permutations were used to define a null set. AU-rich genes were said to be significantly enriched or depleted at a given cutoff if the fraction of AU-rich genes above the cutoff was less than 2.5% or greater than 97.5% of the null set (two-tailed test).

To determine AU-rich gene enrichment, we implemented a simplified gene set enrichment analysis (GSEA) algorithm [2-4]. The data were ranked according to the Bayesian moderated *t*-statistic for the base-2 log-transformed fold-difference between the hairpin-expressing and control cells. An enrichment profile was generated by "walking" across the data, increasing the score when the gene encountered is AU-rich; decreasing the score when it is not. As such, the enrichment profile represents a "random walk". If a particular area of the dataset is enriched for AU-rich genes, the profile will be deflected upwards. The weighting of the step at gene x_i is given by:

$$\Delta ES(x_i, s) = \begin{cases} \dfrac{N - n_s}{n_s} & x_i \in s \\ \dfrac{n_s}{N - n_s} & x_i \notin s \end{cases}$$

given a geneset, s, made of n_s genes of a total N genes. This weighting is such that the total increases and decreases are equal, giving the random walk a net displacement of zero. The overall enrichment score is the maximum deviation of the walk, negative or positive, from zero. This algorithm differs from the more recently developed GSEA algorithms in that the genes were not weighted according to the test statistic. As a result, the enrichment score represents a Kolmogorov-Smirnov statistic. To test for significant enrichment, the six samples were permuted for each gene and the t-statistic and enrichment score recalculated. This was repeated 1,000 times to generate a null distribution of enrichment scores. An enrichment score greater than the fraction of null enrichment scores set by $1 - \alpha$ is considered significant.

Gene expression profiling-t-MN patient samples

We performed gene expression profiling on leukemia cells from 38 patients with t-MN using Affymetrix GeneChip HT HG-U133+ PM microarrays according to the manufacturer's instructions. Signals from all samples were normalized using the Robust Multichip Average (RMA) algorithm implemented in the Bioconductor R package[5].

Differential expression analysis of t-MN patients with and without del(5q) was performed using limma (linear models for microarray data)[6] with estimation of false discovery rate (FDR)[7]. Probesets with FDR <0.3 were considered to be differentially expressed. Among these genes, 515 genes appear in the list of AU-rich genes from the ARED database (ARED Organism, March 2008 release). A heatmap of 515 genes AU-rich genes was then generated using Spotfire Decision Site 9.1.1 (Tibco).

To examine expression of human *HNRNPA0*, we performed gene expression analysis of the human hematopoietic stem cell lineages using previously published data[8] (GEO accession GSE24759). N. Novershtern and B. Ebert, Boston MA, kindly provided expression arrays of a control cell line (HeLa cells) for the human HSC lineages to enable us to renormalize and process the raw data. Expression signals were normalized by RMA and batch-corrected by the ComBat method[9], without the HeLa dataset. (Batch effects were more properly adjusted without the HeLa dataset.) The resulting probe expression signals were z-transformed for visualization. In the study by Novershtern et al., cell populations representing hematopoietic stem and progenitor cells, terminally differentiated cells and intermediate states were purified by cell sorting, from 4 to 7 independent donors. They were designated as follows: Hematopoietic stem cell (HSC1,2), common myeloid progenitor (CMP), megakaryocyte/erythroid progenitor (MEP). Erythroid cells (ERY1–5). CFU-MK (MEGA1) and megakaryocyte (MEGA2). Granulocyte/monocyte progenitor (GMP), CFU-G (GRAN1), neutrophilic metamyelocyte (GRAN2), neutrophil (GRAN3), CFU-M (MONO1), monocytes (MONO2), eosinophil (EOS), and basophil (BASO). Myeloid dendritic cell (DENDa2) and plasmacytoid dendritic cell (DENDa1). Early B cell (Pre-BCELL2), pro-B cell (Pre-

BCELL3), naive B cell (BCELLa1), mature B cell, class able to switch (BCELLa2), mature B cell (BCELLa3), and mature B cell, class switched (BCELLa4). Mature NK cell (NK1–4). Naive CD8+ T cell (TCELL2), CD8+ effector memory RA (TCELL1), CD8+ effector memory (TCELL3), CD8+ central memory (TCELL4), naive CD4+ T cell (TCELL6), CD4+ effector memory (TCELL7), and CD4+ central memory (TCELL8). For easier visualization, populations within the same lineage were merged, as indicated in the figure.

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Supplementary Tables for D. Young *et al.*

Supplementary Table S1. Differential expression of *HNRNPA0* and other AUBPs in t-MN del(5q) patients.

Gene	RefSeq ID	Fold change in del(5q) vs. non-del(5q)	FDR	P value	Role in mRNA decay[1]
HNRNPA0	**NM_006805**	**-2.02**	**0.016**	**0.000121**	**Stabilizing**
TIA1	NM_022037 NM_022173	-1.99	0.028	0.000375	Translational Silencing
HNRNPU	NM_004501 NM_031844	-1.62	0.109	0.005143	Stabilizing
AUH	NM_001698	-1.53	0.168	0.014030	
HNRNPA3	NM_194247	-1.50	0.040	0.000692	
PAIP2	NM_001033112 NM_016480	-1.44	0.007	0.000025	Stabilizing
ELAVL1 (HuR)	NM_001419	-1.38	0.134	0.008295	Stabilizing[2]
HNRNPA1	NM_002136 NM_031157	-1.33	0.019	0.000178	Destabilizing
CUGBP1	NM_001025596 NM_006560 NM_198700	-1.25	0.102	0.004601	Stabilizing and Destabilizing
HNRNPH1	NM_005520	-1.25	0.050	0.001088	
HNRNPUL1	NM_007040 NM_144732	1.29	0.192	0.018844	
ZFP36L1	NM_004926	2.53	0.122	0.006709	Destabilizing

[1] Predicted role in mRNA stability obtained from Journal of Interferon & Cytokine Research 25:1-10 (2005), Nature Reviews Molecular Cell Biology 3: 195-205, *RNA 1: 171-182* (2002).

[2] An increasing number of AUBPs, such as HuR, are recently being recognized for their ability to both stabilize and destabilize, depending on the target gene and cellular context. *Blood* 118: 5732-5740 (2011)

Supplementary Table S2. Contingency analysis of differentially expressed ARE-containing genes in PUER cells.

Undifferentiated[1]	**≥ 1.5-fold change**	**≥ 2-fold change**	**≥ 2.5-fold change**
Mis-regulated (Total)	205 (199) $p = 0.6$	45 (38) $p = 0.3$	10 (12) $p = 0.4$
Up-regulated	89 (87) $p = 0.8$	16 (17) $p = 0.7$ 3	3 (6) $p = 0.9$
Down-regulated	116 (112) $p = 0.7$	29 (21) $p = 0.1$	7 (6) $p = 0.9$
Differentiated[1]	**≥ 1.5-fold change**	**≥ 2-fold change**	**≥ 2.5-fold change**
Mis-regulated (Total)	250 (203) $p = 0.0006$	54 (38) $p = 0.01$	13 (11) $p = 0.7$
Up-regulated	100 (93) $p = 0.5$	17 (16) $p = 0.9$	1 (5) $p = 0.01$
Down-regulated	150 (110) $p < 0.0002$	37 (22) $p = 0.002$	12 (7) $p = 0.05$

[1] Permutation analysis of all 21,087 genes represented on the arrays (10,000 permutations) was used to determine the expected number of differentially-expressed AU-rich genes (in parentheses), and the significance of the deviation of the observed number of differentially expressed AU-rich genes from the expected number (two-tailed test). At increasing fold-change cutoffs, the down-regulated AU-rich genes become increasingly overrepresented (1.5-fold: 36% overrepresented, $p < 0.0002$; 2-fold: 68% overrepresented, $p = 0.002$; 2.5-fold: 71% overrepresented, $p = 0.05$).

Supplementary Table S3. Leading edge analysis of AU-rich genes in PUER cells.

Undifferentiated – Up-regulated in hairpin-expressing cells (72 genes)

Gene[a]	Rank	Δ[b]	Gene	Rank	Δ	Gene	Rank	Δ
Tia1 [1]	5	1.879	***Pax6***	903	1.566	***Hmbox1***	2365	1.544
Pacs2	6	1.510	***Sv2b***	904	2.004	***Lhfpl1***	2430	1.636
Atg16l1	25	1.646	***Fyn***	928	1.667	***Jmjd1c***	2472	1.521
Mbnl1	48	1.509	***Fgfr2***	1019	2.250	***Wdr72***	2535	2.095
Klra2	72	1.539	***Slco4c1*** [1]	1052	1.560	***Pdgfb***	2584	1.685
Pik3cd	101	1.592	***Lgi1***	1093	1.931	***Serpinb5***	2699	1.513
Lancl1 [1]	138	1.670	***Il12b***	1191	1.731	***Vnn1***	2759	1.685
Rps6kb1 [1]	141	1.698	***Shprh***	1200	1.543	***Insm1***	2838	2.126
Hhip	183	2.987	***Bdnf***	1279	1.613	***Otud7b***	2865	1.607
Pias3	188	1.570	***Glt25d2***	1365	1.694	***Ebf1***	2981	1.542
Kcnh1	211	1.721	***Tnfrsf10b***	1426	1.781	***Gpm6b*** [1]	3023	1.566
Gria4	331	1.706	***Olfr77***	1434	1.541	***Col8a1***	3058	1.617
Neurog2	343	2.176	***Crb3***	1446	1.675	***Leprel1***	3096	1.515
Lrrc3b	354	1.911	***Cyfip2***	1469	1.902	***Ncald***	3197	1.752
Axud1	357	2.108	***Snx10*** [1]	1483	1.933	***Pabpc5***	3210	2.436
Il2	413	1.954	***Aldh1a3*** [1]	1702	1.749	***Lrrtm4***	3213	1.938
Prrx1	568	2.498	***Smarce1***	1732	1.585	***C1qtnf3***	3254	2.619
Sv2a [1]	627	1.517	***Gpr158***	1804	1.500	***Hs3st3b1***	3425	1.574
Il4	686	1.611	***Slc2a13***	2036	1.733	***Slc35d1***	3484	1.570
Mmp12	707	1.864	***Ccnb3***	2091	2.272	***Neurl*** [1]	3521	1.814
Sox9	757	2.115	***Ccl22***	2201	1.592	***Shroom2***	3587	1.874
Hapln1	799	1.842	***Slc14a1***	2203	1.584	***Zfp532*** [1]	3745	1.539
Npy2r	809	4.522	***Rsad1***	2213	1.581	***Cobll1***	4006	1.668
Yipf7 [1]	871	1.525	***Asah2***	2224	2.348	***Kcna1***	4331	1.519

(continued)

[a] Genes shown are members of the "leading edge" and show a 1.5-fold or greater difference in expression between hairpin-expressing and control cells.

[b] Fold-change (hairpin-expressing cells relative to control cells).

[1] Genes positively enriched in both undifferentiated and differentiated cells.

[2] Genes negatively enriched in both undifferentiated and differentiated cells.

Table S3. (Continued)

Undifferentiated – Down-regulated in hairpin-expressing cells (100 genes)

Gene	Rank	Δ	Gene	Rank	Δ	Gene	Rank	Δ
Itga6	11	-2.026	***Foxj3***	574	-1.575	***Lrch2***	2068	-1.610
Tcfap2e[2]	23	-2.631	***Kcng3***	586	-5.155	***Rab39b***	2082	-2.018
Tial1[2]	31	-1.732	***Gatad1***[2]	652	-1.579	***Edn1***	2138	-1.838
Hnrnpl[2]	75	-1.659	***Dmxl1***	682	-1.768	***Slc16a1***[2]	2165	-1.611
Camk2d[2]	76	-1.517	***Shoc2***[2]	724	-1.687	***Wnt3***	2176	-1.551
Homez	78	-1.727	***Icam1***	741	-1.746	***Irx2***	2180	-2.206
Nudcd1	80	-1.530	***Angpt1***[2]	744	-1.617	***Il6st***	2209	-2.113
Adrbk2	81	-1.551	***Htr4***	763	-1.897	***Dpp4***	2463	-1.565
Creb5[2]	95	-1.909	***Tmem67***	788	-2.324	***Srd5a2l2***	2567	-1.523
Fut9	102	-2.246	***Cbfb***[2]	793	-2.013	***Ntrk1***	2591	-2.706
Atp2b1[2]	114	-1.520	***Veph1***	905	-1.817	***Ndg1***	2629	-1.629
AU042671	129	-1.639	***Lypla1***[2]	915	-1.608	***Tnfsf11***	2723	-2.833
Sftpa1	146	-1.890	***Osbpl8***[2]	967	-1.658	***Slc13a1***	2785	-1.620
Unkl	163	-1.658	***Cadps***[2]	1026	-2.138	***Fat4***	2800	-1.862
Cxadr	190	-1.585	***Sp3***[2]	1143	-1.542	***Rnf180***[2]	2971	-2.090
Il20	197	-1.591	***Ptp4a1***[2]	1182	-1.548	***Kynu***[2]	2999	-2.002
Vsnl1	221	-2.921	***Ccne2***[2]	1200	-1.735	***Hivep2***	3032	-2.093
Actr2[2]	244	-1.512	***Efnb2***	1246	-2.497	***Cacnb4***[2]	3052	-1.517
Csf2	279	-1.848	***Tmem163***	1271	-1.653	***Pxdn***	3147	-1.864
AK129128	286	-1.787	***Ank2***[2]	1291	-2.024	***Adam12***	3173	-1.733
D4Bwg0951e	314	-2.490	***Nr0b1***	1331	-2.187	***St18***[2]	3177	-1.520
Egr2[2]	337	-1.509	***Lrrc39***	1339	-1.574	***Prdm1***	3396	-1.602
Setd5[2]	365	-1.626	***Cck***	1410	-1.586	***AI504432***	3460	-2.302
Mgat5	396	-1.613	***Syt13***	1452	-1.574	***AU021034***	3528	-1.515
Tmod2	402	-2.269	***Twist1***	1514	-1.911	***Col12a1***	3535	-2.176
Lpp[2]	407	-1.758	***Foxred2***	1528	-1.578	***Gpr3***	3664	-2.019
Zfhx1b[2]	409	-1.605	***Mtap2***[2]	1542	-1.942	***Mal2***	3680	-1.677
Vti1a[2]	425	-1.864	***Cage1***	1650	-1.864	***Gdf6***	3874	-2.019
Tmem44	464	-1.770	***Emcn***	1766	-2.995	***Frem2***	4014	-1.647
Stambpl1	466	-1.580	***Sox30***	1783	-1.573	***Kcnv2***	4015	-1.801
BC018371[2]	475	-1.665	***Scn2b***	1785	-1.822	***Areg***	4087	-1.643
Kcnj6	488	-2.929	***Brsk2***	1987	-2.427	***Col5a2***	4088	-1.862
Cwf19l2	516	-1.573	***P2ry10***	1993	-1.815			
Dap3	525	-1.546	***Gje1***	2033	-1.542			

(continued)

Table S3. (Continued)

Differentiated – Up-regulated in hairpin-expressing cells (80 genes)

Gene	Rank	Δ	Gene	Rank	Δ	Gene	Rank	Δ
Tia1[1]	6	1.973	***Tmc7***	539	1.758	***Kcnj3***	2074	1.892
Six4	15	1.903	***Sema6a***	549	1.945	***Lypd6***	2185	1.545
Rgs8	43	1.976	***Sp6***	578	1.755	***Cep170***	2308	1.953
Txndc13	60	1.504	***AB112350***	592	1.526	***Gpr33***	2374	2.172
Rps6kb1[1]	64	2.004	***Lamp3***	596	2.190	***Aldh1a3***[1]	2497	1.700
BC053440	67	1.623	***Ide***	653	1.731	***Neurl***[1]	2499	2.251
Top2a	70	1.548	***Yipf7***[1]	692	1.719	***Spdyb***	2512	1.531
Myo1b	71	1.746	***Ufd1l***	716	1.508	***Gabrg1***	2552	1.641
Dnajc6	74	1.751	***Xpo1***	787	1.517	***B3galt2***	2588	1.886
Cpe	85	1.530	***Il6***	993	1.661	***B3gnt5***	2616	1.769
Cep350	100	1.687	***Ercc6***	1016	1.618	***Ric8b***	2657	1.691
Ccrn4l	115	1.797	***Cenpa***	1038	1.699	***Hivep2***	2692	2.560
Xpo5	155	1.510	***Sv2a***[1]	1083	1.526	***Zfp532***[1]	2705	1.798
Zfp275	164	1.584	***Ccl7***	1144	2.202	***Slit2***	2810	2.303
Zfp609	177	1.619	***Polr3f***	1147	1.569	***Adamts16***	2838	2.120
Pmpca	181	1.501	***Slc16a12***	1167	1.736	***Fn3k***	2921	1.637
Cacna1b	184	2.020	***Kbtbd8***	1276	1.574	***Xlkd1***	2999	1.550
D15Wsu169e	189	1.557	***Hip1***	1339	1.669	***Plscr2***	3237	1.710
Atf2	194	1.744	***Rasl11b***	1404	1.910	***Akr1c14***	3335	2.500
Fancm	204	1.604	***Capn3***	1568	1.720	***Adam12***	3412	1.844
Gca	205	1.575	***Cd109***	1592	1.893	***Zbtb7c***	3435	2.350
Rhbdd2	263	1.563	***Slco4c1***[1]	1717	1.548	***Rfxdc1***	3471	1.798
Tiparp	277	1.589	***Ankrd52***	1720	1.594	***Gpm6b***[1]	3558	1.551
Slmap	288	1.550	***BC013481***	1776	1.542	***Slc2a12***	3684	1.516
Lancl1[1]	416	1.634	***Sgip1***	1815	1.886	***Zfp352***	3702	1.805
Pcgf3	501	1.541	***Fbn1***	1932	1.853	***Snx10***[1]	3724	1.569
Crb1	533	1.560	***Dst***	2055	2.457			

(continued)

Table S3. (Continued)

Differentiated – Down-regulated in hairpin-expressing cells (142 genes)

Gene	Rank	Δ	Gene	Rank	Δ	Gene	Rank	Δ
Slc2a1	4	-1.658	***Rnf103***	556	-1.768	***Ntrk2***	2227	-2.109
Atp2b1[2]	17	-1.861	***Stt3a***	567	-1.546	***Klf8***	2231	-1.780
Calcrl	22	-1.603	***Isl1***	572	-4.177	***Dner***	2246	-1.661
Uevld	28	-1.575	***Slc35a5***	575	-2.133	***Dgkb***	2253	-1.514
Camk2d[2]	45	-1.696	***Sp3***[2]	578	-1.856	***Sox9***	2265	-1.724
Kras	56	-1.548	***Klrc1***	734	-2.153	***Cxcl15***	2283	-1.589
Creb5[2]	59	-2.199	***Il1r1***	814	-1.632	***Kynu***[2]	2331	-2.447
Egr2[2]	69	-1.890	***Ank2***[2]	828	-2.565	***Mmp12***	2352	-1.542
Pdcl3	74	-1.608	***Slc2a3***	861	-2.381	***Whrn***	2356	-1.686
Dusp1	75	-1.566	***Tcfap2e***[2]	864	-1.725	***Fank1***	2401	-1.709
Bcl9	86	-2.393	***Scrt1***	866	-1.689	***Pitx2***	2474	-1.645
Edem1	93	-2.046	***Ptp4a1***[2]	880	-1.739	***Eva1***	2535	-1.538
Rala	96	-1.542	***Ncoa7***	882	-1.836	***Arhgap29***	2595	-1.545
Shoc2[2]	115	-2.454	***C5ar1***	895	-2.014	***Peli2***	2688	-1.593
Trp53inp1	121	-2.073	***Svil***	901	-1.652	***Bmp5***	2716	-1.545
Hnrnpl[2]	131	-1.718	***Insm1***	910	-3.763	***Arpp21***	2739	-2.396
Cul5	134	-1.610	***Slc16a1***[2]	933	-2.158	***St18***[2]	2781	-1.650
Ccl3	152	-1.654	***Zfhx1b***[2]	980	-1.546	***Srpx***	2873	-1.791
Pdcl	162	-1.730	***Txndc10***	1008	-1.659	***Nhlh2***	2915	-1.626
Tmtc4	171	-1.572	***Dynlt3***	1014	-1.633	***Ildr1***	3199	-2.569
Tial1[2]	181	-1.627	***Tacc1***	1017	-1.634	***Foxp2***	3285	-1.532
Lypla1[2]	184	-2.243	***Ugt2b1***	1040	-1.796	***Cacnb4***[2]	3291	-1.551
Sertad2	188	-1.694	***Gatad1***[2]	1099	-1.565	***Oprm1***	3343	-1.898
Ube3a	192	-1.502	***Rad21***	1121	-1.682	***Sox21***	3347	-1.650
Fer1l3	195	-1.828	***Eno2***	1146	-1.561	***ORF34***	3373	-1.646
Actr2[2]	205	-1.658	***Angpt1***[2]	1152	-1.612	***Rnf180***[2]	3411	-2.098
Rbbp4	210	-1.533	***Irs1***	1201	-3.632	***Prrx1***	3412	-1.608
BC052328	258	-2.144	***Nxt2***	1246	-1.575	***Chodl***	3439	-1.506
Wsb1	277	-1.812	***Slc25a26***	1280	-1.825	***Cobll1***	3449	-1.787
Tob2	291	-1.603	***Wdr44***	1285	-2.020	***Sypl2***	3498	-2.031
BC018371[2]	294	-1.953	***Lpp***[2]	1309	-1.591	***Mmp3***	3503	-1.982
Ccne2[2]	295	-2.554	***Fbxl3***	1332	-1.773	***Pde8b***	3679	-3.145
Inpp4b	299	-2.142	***Ints6***	1389	-2.531	***Gpr12***	3699	-1.578
Ccl4	302	-1.568	***Lep***	1422	-1.573	***Slc5a7***	3706	-1.837
Pftk1	306	-2.065	***Cacna2d1***	1524	-2.557	***Il5***	3847	-1.654
Taf13	318	-1.501	***Adamts19***	1582	-2.087	***Cadps***[2]	3866	-1.535
Cd163	342	-1.966	***Vasn***	1603	-1.581	***St8sia6***	4000	-1.798
Cbfb[2]	348	-2.743	***Gng2***	1695	-1.924	***Mtap2***[2]	4053	-1.516
Rab18	380	-1.552	***Chst3***	1737	-1.676	***Fgf12***	4253	-1.524
Setd5[2]	383	-1.772	***Osbpl8***[2]	1745	-1.580	***Chrnb4***	4331	-2.727
Chmp5	389	-1.531	***Egr1***	1750	-1.616	***V1rc15***	4434	-1.722
Il1b	413	-1.609	***Dtl***	1786	-2.255	***Hnmt***	4447	-1.502
Hisppd1	443	-1.576	***Vti1a***[2]	1814	-1.565	***Akap14***	4471	-1.575
Bcl10	483	-2.143	***Zdhhc21***	1977	-1.566	***Tspan3***	4495	-3.153
Net1	485	-2.059	***Baalc***	2040	-1.546	***Colec10***	4527	-1.669
Trim23	493	-1.754	***Grem2***	2093	-1.535	***Bmpr1b***	4563	-1.551
Chsy1	532	-1.514	***Rab39***	2167	-1.518			
Tpd52	538	-1.502	***Plekha5***	2183	-2.188			

Supplementary Table S4. ARE genes differentially expressed (FDR <0.3) in t-MN del(5q) vs. non-del(5q) t-MN patients.

ProbesetID	Gene_Symbol	Refseq	Fold Change	Mean non del(5q)	Mean del(5q)	FDR	T.Statistic	P.Value	Annotation
225326_PM_at	RBM27	NM_018989	-2.26339786	215.436109	95.18260683	2.39E-07	-9.67714127	8.74E-12	RNA binding motif protein 27
201769_PM_at	CLINT1	NM_014666	-2.12935293	309.304459	145.2574889	3.14E-05	-7.37745477	7.79E-09	clathrin interactor 1
202164_PM_s_at	CNOT8	NM_004779	-2.38325278	175.652825	73.70297725	0.000118925	-6.74039419	5.63E-08	CCR4-NOT transcription complex, subunit 8
221257_PM_x_at	FBXO38	NM_030793 ///	-1.83890762	144.261314	78.44946207	0.000118925	-6.72729207	5.86E-08	F-box protein 38
218307_PM_at	RSAD1	NM_018346	-2.30859306	79.1333233	34.27772734	0.001595415	-5.52583179	2.57E-06	radical S-adenosyl methionine domain containing 1
202892_PM_at	CDC23	NM_004661	-2.2792176	74.9170842	32.86964974	0.002294478	-5.35421236	4.41E-06	cell division cycle 23 homolog (S. cerevisiae)
211671_PM_s_at	NR3C1	NM_000176 ///	-1.8000649	313.760465	174.3050847	0.002916479	-5.25163944	6.09E-06	nuclear receptor subfamily 3, group C, member 1 (glucocorticoid receptor)
213026_PM_at	ATG12	NM_004707	-1.763981	158.334618	89.75982054	0.003156664	-5.2047783	7.05E-06	ATG12 autophagy related 12 homolog (S. cerevisiae)
205097_PM_at	SLC26A2	NM_000112	-2.8545579	72.3166548	25.33374953	0.003521817	-5.14227763	8.58E-06	solute carrier family 26 (sulfate transporter), member 2
226949_PM_at	GOLGA3	NM_005895	1.584765426	18.4380994	29.22006248	0.003550503	5.130218955	8.91E-06	golgi autoantigen, golgin subfamily a, 3
231002_PM_s_at	RABEP1	NM_001083585	-1.49299132	24.9536995	16.71389456	0.00411776	-5.06467322	1.09E-05	Rabaptin, RAB GTPase binding effector protein 1
238783_PM_at	hCG_25653	NM_153354 ///	-1.90006097	46.3419293	24.38970645	0.005159209	-4.91949073	1.72E-05	hCG25653 /// transmembrane protein 161B
211200_PM_s_at	EFCAB2	NM_001143943	-2.57298208	56.5819243	21.99079606	0.006507421	-4.80174816	2.48E-05	EF-hand calcium binding domain 2
222984_PM_at	PAIP2	NM_001033112	-1.43708744	500.513984	348.283598	0.006507421	-4.80281832	2.47E-05	poly(A) binding protein interacting protein 2
232865_PM_at	AFF4	NM_014423	-2.97375828	100.954757	33.94854173	0.00776738	-4.72312626	3.16E-05	AF4/FMR2 family, member 4
229240_PM_at	ZDHHC21	NM_178566	-2.31352201	43.0004212	18.58656241	0.00776738	-4.72206271	3.17E-05	Zinc finger, DHHC-type containing 21
226797_PM_at	MBTD1	NM_017643	-1.83949392	143.432401	77.97383836	0.008157408	-4.67064434	3.72E-05	mbt domain containing 1
1558143_PM_a_at	BCL2L11	NM_006538 ///	3.331233187	30.4109319	101.3059055	0.00860781	4.635274489	4.15E-05	BCL2-like 11 (apoptosis facilitator)
205148_PM_s_at	CLCN4	NM_001830	2.606522766	5.61890938	14.64581521	0.009383322	4.581102737	4.90E-05	chloride channel 4
201037_PM_at	PFKP	NM_002627	-2.46453189	177.690141	72.09894158	0.009494858	-4.57153848	5.04E-05	phosphofructokinase, platelet
228540_PM_at	QKI	NM_006775 ///	1.650047911	8.60091431	14.1919207	0.009594306	4.556986301	5.27E-05	quaking homolog, KH domain RNA binding (mouse)
1554067_PM_at	C12orf66	NM_152440	-2.5822919	17.9571075	6.953941789	0.01038851	-4.51260293	6.04E-05	chromosome 12 open reading frame 66
200768_PM_s_at	MAT2A	NM_005911	-1.8693688	608.740004	325.6393299	0.010807193	-4.49070145	6.46E-05	methionine adenosyltransferase II, alpha
212406_PM_s_at	PCMTD2	NM_001104925	-1.73633292	195.124505	112.3773575	0.011299515	-4.46571053	6.97E-05	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 2
202430_PM_s_at	PLSCR1	NM_021105	2.453027219	193.186362	473.8914042	0.013293552	4.371533839	9.29E-05	phospholipid scramblase 1
225633_PM_at	DPY19L3	NM_207325	-2.30513901	62.4527657	27.09284141	0.014050434	-4.34147921	0.000101777	dpy-19-like 3 (C. elegans)
211814_PM_s_at	CCNE2	NM_057749	1.566472023	6.27034084	9.822313499	0.016374945	4.255020663	0.000132209	cyclin E2
1554453_PM_at	HNRPLL	NM_001142650	1.374068627	6.06424966	8.332695204	0.016424983	4.25145664	0.000133638	heterogeneous nuclear ribonucleoprotein L-like
213557_PM_at	CRKRS	NM_015083 ///	-1.95776692	40.0083275	20.43569498	0.016424983	-4.25096999	0.000133835	Cdc2-related kinase, arginine/serine-rich
203791_PM_at	DMXL1	NM_005509	-1.93489116	83.3908593	43.09847556	0.016792241	-4.23993279	0.000138365	Dmx-like 1
234967_PM_at	IL6ST	NM_002184 ///	1.313201084	4.51994641	5.935598534	0.017125671	4.231938118	0.000141739	interleukin 6 signal transducer (gp130, oncostatin M receptor)
226496_PM_at	ZCCHC7	NM_032226	-1.83320812	188.25878	102.693621	0.01802411	-4.19972682	0.000156171	zinc finger, CCHC domain containing 7
225611_PM_at	MAST4	NM_015183 ///	-3.29498168	52.5247444	15.94083046	0.018174896	-4.19076919	0.000160433	microtubule associated serine/threonine kinase family member 4
206861_PM_s_at	CGGBP1	NM_001008390	1.719005839	91.4377457	157.1820186	0.018508357	4.175955371	0.000167733	CGG triplet repeat binding protein 1
201133_PM_s_at	PJA2	NM_014819	-1.62014248	261.521075	161.4185659	0.018508357	-4.1777601	0.000166826	praja ring finger 2
226687_PM_at	PRPF40A	NM_017892	-1.61288955	128.476973	79.65639905	0.019281662	-4.15231316	0.000180061	PRP40 pre-mRNA processing factor 40 homolog A (S. cerevisiae)
235526_PM_at	SOX6	NM_001145811	-1.71109767	163.735186	95.69014622	0.020921378	-4.10718106	0.000206099	SRY (sex determining region Y)-box 6
225425_PM_s_at	MRPL41	NM_032477	-1.5545145	41.9525966	26.98758784	0.022576254	-4.04957059	0.000244725	mitochondrial ribosomal protein L41
225295_PM_at	SLC39A10	NM_001127257	-2.49550321	109.326893	43.80955793	0.022576254	-4.05103977	0.000243657	solute carrier family 39 (zinc transporter), member 10
202872_PM_at	ATP6V1C1	NM_001695	2.356060909	9.61830806	22.66131964	0.022608847	4.046258591	0.000247148	ATPase, H+ transporting, lysosomal 42kDa, V1 subunit C1
1555137_PM_a_at	FGD6	NM_018351	1.546823301	5.18822803	8.025272	0.025103205	3.987563285	0.00029418	FYVE, RhoGEF and PH domain containing 6
207433_PM_at	IL10	NM_000572	1.624177801	4.98113781	8.090253457	0.026033058	3.970032745	0.000309844	interleukin 10
212171_PM_x_at	VEGFA	NM_001025366	2.018945862	23.4195154	47.28273365	0.026309135	3.962326363	0.000316983	vascular endothelial growth factor A
1570156_PM_s_at	FMN1	NM_001103184	1.311466754	4.91707028	6.448574202	0.026506387	3.95166474	0.000327125	formin 1
225764_PM_at	ETV6	NM_001987	-2.58516716	249.939561	96.68216633	0.027951577	-3.91638706	0.000362985	ets variant 6
201447_PM_at	TIA1	NM_022037 ///	-1.98996812	72.7688164	36.5678302	0.028405348	-3.9049229	0.000375439	TIA1 cytotoxic granule-associated RNA binding protein
225209_PM_s_at	UBE2J2	NM_058167 ///	1.539372698	74.5084693	114.6963035	0.02980933	3.88004378	0.000403913	ubiquitin-conjugating enzyme E2, J2 (UBC6 homolog, yeast)
221050_PM_s_at	GTPBP2	NM_019096	1.827192507	20.0498089	36.63486063	0.029863869	3.877520795	0.000406915	GTP binding protein 2
230359_PM_at	KNDC1	NM_152643	1.190514953	4.94692378	5.889386732	0.031000786	3.858483809	0.000430275	kinase non-catalytic C-lobe domain (KIND) containing 1
203685_PM_at	BCL2	NM_000633 ///	-3.47806946	167.252195	48.08765241	0.031920039	-3.84269467	0.000450632	B-cell CLL/lymphoma 2
202362_PM_at	RAP1A	NM_001010935	1.549302943	652.897396	1011.535857	0.032694814	3.827674672	0.000470862	RAP1A, member of RAS oncogene family
231967_PM_at	PHF20L1	NM_016018 ///	1.782793273	18.1492917	32.35643513	0.034914218	3.78682639	0.000530435	PHD finger protein 20-like 1
217930_PM_s_at	TOLLIP	NM_019009	1.735970468	29.5994742	51.38381308	0.036446514	3.754552344	0.000582605	toll interacting protein
225178_PM_at	TTC14	NM_001042601	-2.04090064	91.5816729	44.87316589	0.036871527	-3.74701173	0.000595491	tetratricopeptide repeat domain 14
200080_PM_s_at	H3F3A	NM_002107 ///	1.173720618	4601.33978	5400.687371	0.039316113	3.709527501	0.000663751	H3 histone, family 3A /// H3 histone, family 3B (H3.3B) /// H3 histone, family 3A pseudogene
200972_PM_at	TSPAN3	NM_005724 ///	-1.77196363	175.416068	98.99529799	0.039917463	-3.69245449	0.000697293	tetraspanin 3
204194_PM_at	BACH1	NM_001011545	1.831546616	95.3597544	174.6558354	0.040595081	3.672014155	0.000739606	BTB and CNC homology 1, basic leucine zipper transcription factor 1
200083_PM_at	USP22	NM_015276	-1.45877608	227.581272	156.0083658	0.041498658	-3.65521363	0.00077623	ubiquitin specific peptidase 22
224359_PM_s_at	HOOK3	NM_032410	1.50605243	7.9805083	12.01906392	0.042335721	3.641488855	0.000807443	hook homolog 3 (Drosophila)
202948_PM_at	IL1R1	NM_000877	3.312117046	15.6784505	51.928863	0.043544394	3.624253672	0.000848355	interleukin 1 receptor, type I
226975_PM_at	RNPC3	NM_017619	-1.76333981	234.117793	132.7695269	0.046578934	-3.57963447	0.000963767	RNA-binding region (RNP1, RRM) containing 3
216598_PM_s_at	CCL2	NM_002982	5.513090278	8.59653037	47.39344799	0.046894002	3.576340392	0.000972862	chemokine (C-C motif) ligand 2
228418_PM_at	EXOC5	NM_006544	1.843010897	16.9074824	31.16067432	0.047799043	3.561968519	0.001013519	exocyst complex component 5
216115_PM_at	NF1	NM_000267 ///	-1.97045524	23.2266233	11.78744019	0.048376361	-3.55532979	0.001032846	neurofibromin 1
218215_PM_s_at	NR1H2	NM_007121	1.586112482	32.0081994	50.76860459	0.04858342	3.553526705	0.001038157	nuclear receptor subfamily 1, group H, member 2
225666_PM_at	TMTC4	NM_001079669	-2.27253064	51.6584102	22.73166722	0.049266442	-3.54293275	0.001069892	transmembrane and tetratricopeptide repeat containing 4
200608_PM_s_at	RAD21	NM_006265	1.407029127	656.937816	924.330642	0.050782382	3.522869187	0.001132568	RAD21 homolog (S. pombe)
205569_PM_at	LAMP3	NM_014398	1.47453459	4.91036284	7.240499861	0.051271917	3.517659656	0.00114941	lysosomal-associated membrane protein 3
225835_PM_at	SLC12A2	NM_001046	-2.7499573	22.7520744	8.273610064	0.052934591	-3.49586945	0.001222501	solute carrier family 12 (sodium/potassium/chloride transporters), member 2
242508_PM_at	KIAA2018	NM_001009899	1.179226147	4.89715672	5.774855252	0.053090109	3.490944716	0.001239628	KIAA2018
222991_PM_s_at	UBQLN1	NM_013438 ///	1.767765805	80.9955808	143.1812181	0.053518206	3.478809707	0.001282819	ubiquilin 1
202786_PM_at	STK39	NM_013233	-1.72569817	71.435756	41.3952782	0.053862802	-3.47331307	0.001302854	serine threonine kinase 39 (STE20/SPS1 homolog, yeast)

Supplementary Table S4. ARE genes differentially expressed (FDR <0.3) in t-MN del(5q) vs. non-del(5q) t-MN patients.

ProbesetID	Gene_Symbol	Refseq	Fold Change	Mean non del(5q)	Mean del(5q)	FDR	T.Statistic	P.Value	Annotation
202118_PM_s_at	CPNE3	NM_003909	2.414019135	27.6880953	66.83959191	0.05421451	3.468860605	0.001319303	copine III
1558338_PM_at	SEMA6A	NM_020796	-1.61367858	8.51254362	5.275241132	0.054707421	-3.46406369	0.001337247	Sema domain, transmembrane domain (TM), and cytoplasmic domain, (semaphorin) 6A
212600_PM_s_at	UQCRC2	NM_003366	-1.33504921	664.966472	498.0838648	0.055830539	-3.45022907	0.00139032	ubiquinol-cytochrome c reductase core protein II
217433_PM_at	TACC1	NM_001122824	1.239197391	6.0640534	7.514559156	0.056481653	3.443755423	0.001415842	transforming, acidic coiled-coil containing protein 1
244721_PM_at	TP53INP1	NM_001135733	1.183816321	6.77613658	8.021701071	0.056481653	3.443933815	0.001415133	tumor protein p53 inducible nuclear protein 1
201552_PM_at	LAMP1	NM_005561	1.478858206	222.461433	328.9889151	0.057723242	3.431869284	0.001463877	lysosomal-associated membrane protein 1
224743_PM_at	IMPAD1	NM_017813	-1.4709439	111.709043	75.94378201	0.059669872	-3.40895785	0.001560906	inositol monophosphatase domain containing 1
225222_PM_at	HIAT1	NM_033055	1.311982941	181.374016	237.9596152	0.059991978	3.404922148	0.001578623	hippocampus abundant transcript 1
226083_PM_at	TMEM70	NM_001040613	1.191458846	5.9666694	7.109041042	0.061093379	3.393567711	0.001629508	transmembrane protein 70
202227_PM_s_at	BRD8	NM_001164326	-1.94141983	168.514512	86.79962462	0.061211756	-3.39229963	0.001635287	bromodomain containing 8
238694_PM_at	DGKE	NM_003647	-2.29123989	31.4421631	13.72277221	0.061953621	-3.38358766	0.001675526	diacylglycerol kinase, epsilon 64kDa
214876_PM_s_at	TUBGCP5	NM_001102610	-1.60992698	17.8138857	11.06502714	0.062974344	-3.37361822	0.001722734	tubulin, gamma complex associated protein 5
208103_PM_s_at	ANP32E	NM_001136478	2.103953947	53.6766734	112.9332488	0.063059964	3.372410138	0.00172854	acidic (leucine-rich) nuclear phosphoprotein 32 family, member E
242974_PM_at	CD47	NM_001025079	-1.97363197	29.4349848	14.91412038	0.063232162	-3.37119108	0.001734418	CD47 molecule
200056_PM_s_at	C1D	NM_006333 ///	1.534131009	192.756799	295.7141829	0.06416352	3.361500649	0.001781827	C1D nuclear receptor co-repressor
227861_PM_at	TMEM161B	NM_153354	-1.48698792	97.2571231	65.40545633	0.065990641	-3.34680693	0.001856082	transmembrane protein 161B
203917_PM_at	CXADR	NM_001338	1.972114353	9.63872901	19.00867582	0.06600959	3.345549115	0.001862574	coxsackie virus and adenovirus receptor
205770_PM_at	GSR	NM_000637	1.62977493	17.7646524	28.95238512	0.06600959	3.345702536	0.001861781	glutathione reductase
219104_PM_at	RNF141	NM_016422	1.845626354	26.8755562	49.60223487	0.067469631	3.328873519	0.001950718	ring finger protein 141
201565_PM_s_at	ID2	NM_002166	2.267678058	691.644136	1568.426231	0.067476612	3.32792269	0.001955862	inhibitor of DNA binding 2, dominant negative helix-loop-helix protein
203418_PM_at	CCNA2	NM_001237	2.906282969	17.2423747	50.11121996	0.06780454	3.324002723	0.001977206	cyclin A2
225383_PM_at	ZNF275	NM_001080485	-1.77836461	82.82834	46.57556706	0.067837237	-3.32349651	0.001979978	zinc finger protein 275
227094_PM_at	DHTKD1	NM_018706	-2.07313826	91.5997943	44.18412232	0.067925647	-3.32279937	0.001983803	dehydrogenase E1 and transketolase domain containing 1
225119_PM_at	CHMP4B	NM_176812	1.774539038	36.7850064	65.27642994	0.06799016	3.32200357	0.001988177	chromatin modifying protein 4B
225756_PM_at	CSNK1E	NM_001894 ///	-1.56407144	13.3635176	8.544058292	0.069405301	-3.30938271	0.002058788	casein kinase 1, epsilon
223236_PM_at	CCDC55	NM_032141	-1.30369071	112.347202	86.17626964	0.069536119	-3.30758564	0.002069035	coiled-coil domain containing 55
220707_PM_s_at	FOXRED2	NM_001102371	1.242464575	6.03981002	7.504249996	0.0698025	3.304629763	0.002085995	FAD-dependent oxidoreductase domain containing 2
237469_PM_at	TOP2A	NM_001067	1.972043033	6.28547301	12.39522327	0.069929959	3.302654952	0.002097399	Topoisomerase (DNA) II alpha 170kDa
1554599_PM_x_at	GTF2H3	NM_001516	-1.73974801	39.1752281	22.51776006	0.070166426	-3.3012109	0.002105777	general transcription factor IIH, polypeptide 3, 34kDa
1558249_PM_s_at	STX16	NM_001001433	-1.42222954	39.1863927	27.55279067	0.070310136	-3.29936581	0.002116527	syntaxin 16
223588_PM_at	THAP2	NM_031435	-1.20915138	5.21598397	4.313755958	0.070680465	-3.2942536	0.002146586	THAP domain containing, apoptosis associated protein 2
220081_PM_x_at	HSD17B7	NM_016371	-1.41150162	101.94216	72.2224891	0.070737838	-3.29084733	0.002166839	hydroxysteroid (17-beta) dehydrogenase 7
207791_PM_s_at	RAB1A	NM_004161 ///	1.775344877	107.128527	190.1900818	0.071113202	3.286135056	0.002195159	RAB1A, member RAS oncogene family
1558691_PM_a_at	DOCK4	NM_014705	1.427872204	4.11880577	5.881128273	0.075310513	3.246913509	0.002444941	dedicator of cytokinesis 4
218193_PM_s_at	GOLT1B	NM_016072	1.438758929	53.6948984	77.25401455	0.077529033	3.223832899	0.00260433	golgi transport 1 homolog B (S. cerevisiae)
230885_PM_at	SPG7	NM_003119 ///	-1.71708828	131.099422	76.3498441	0.07938991	-3.20950107	0.002708221	spastic paraplegia 7 (pure and complicated autosomal recessive)
200720_PM_s_at	ACTR1A	NM_005736	1.563324539	70.6560262	110.4582996	0.080089691	3.204123093	0.002748212	ARP1 actin-related protein 1 homolog A, centractin alpha (yeast)
224947_PM_at	RNF26	NM_032015	1.521707369	43.8243579	66.68784839	0.080505189	3.196970299	0.00280227	ring finger protein 26
221806_PM_s_at	SETD5	NM_001080517	-1.49295567	200.892465	134.5602349	0.080621139	-3.19580514	0.002811171	SET domain containing 5
222399_PM_s_at	TM9SF3	NM_020123	1.43855368	111.263904	160.0590993	0.080621139	3.195669223	0.002812211	transmembrane 9 superfamily member 3
1554396_PM_at	UEVLD	NM_001040697	1.191615279	5.0617749	6.031688306	0.081667879	3.188043263	0.002871154	UEV and lactate/malate dehyrogenase domains
209653_PM_at	KPNA4	NM_002268	1.659908712	8.96931546	14.88824487	0.081975303	3.185895377	0.002887966	karyopherin alpha 4 (importin alpha 3)
1552619_PM_a_at	ANLN	NM_018685	1.899341806	8.97255014	17.04193959	0.082540331	3.179907244	0.002935331	anillin, actin binding protein
225711_PM_at	ARL6IP6	NM_152522 ///	1.609518152	26.0476517	41.92416818	0.082540331	3.179554943	0.002938141	ADP-ribosylation-like factor 6 interacting protein 6
1558934_PM_a_at	GTF2H5	NM_207118	-1.16292822	4.94837452	4.255098824	0.082540331	-3.17899778	0.002942589	general transcription factor IIH, polypeptide 5
203746_PM_s_at	HCCS	NM_001122608	2.210177095	63.5268111	140.4055028	0.082540331	3.180730252	0.002928778	holocytochrome c synthase (cytochrome c heme-lyase)
1570627_PM_at	TCEB3	NM_003198	1.191758567	6.43836847	7.672980788	0.082540331	3.181122912	0.002925656	transcription elongation factor B (SIII), polypeptide 3 (110kDa, elongin A)
230637_PM_at	SFXN4	NM_213649	-1.48925733	25.3067325	16.99285405	0.083382194	-3.17036401	0.003012343	sideroflexin 4
227783_PM_at	CCDC57	NM_198082	-1.40123014	57.4618937	41.00817702	0.084389053	-3.16184402	0.003082712	coiled-coil domain containing 57
218184_PM_at	TULP4	NM_001007466	-1.9049199	16.844653	8.842709366	0.085762168	-3.15241971	0.003162365	tubby like protein 4
1552719_PM_at	CASC4	NM_138423 ///	-1.40290906	21.7132686	15.47731725	0.086426095	-3.14678335	0.00321093	cancer susceptibility candidate 4
225002_PM_s_at	SUMF2	NM_001042469	-1.58762079	43.945686	27.68021571	0.086583997	-3.14383651	0.003236602	sulfatase modifying factor 2
209103_PM_s_at	UFD1L	NM_001035247	1.428959129	221.904816	317.0929128	0.086583997	3.143532369	0.003239263	ubiquitin fusion degradation 1 like (yeast)
202370_PM_s_at	CBFB	NM_001755 ///	-1.60225922	328.13051	204.7923999	0.087111522	-3.13806588	0.003287438	core-binding factor, beta subunit
224621_PM_at	MAPK1	NM_002745 ///	1.274804	539.91205	688.2820411	0.087111522	3.138212118	0.00328614	mitogen-activated protein kinase 1
212959_PM_s_at	GNPTAB	NM_024312	-1.74787329	273.978188	156.7494561	0.087323772	-3.13505309	0.003314278	N-acetylglucosamine-1-phosphate transferase, alpha and beta subunits
221889_PM_at	KCTD13	NM_178863	-1.4459488	15.2837423	10.57004388	0.087323772	-3.13481799	0.003316381	potassium channel tetramerisation domain containing 13
212620_PM_at	ZNF609	NM_015042	-1.78230566	157.905065	88.59595119	0.087602443	-3.13240445	0.003338046	zinc finger protein 609
201695_PM_s_at	NP	NM_000270	2.357080836	331.885181	782.2801989	0.089545407	3.11722985	0.003477354	nucleoside phosphorylase
219133_PM_at	OXSM	NM_001145391	-1.50033312	56.0276674	37.34348512	0.089932808	-3.11192983	0.003527293	3-oxoacyl-ACP synthase, mitochondrial
206336_PM_at	CXCL6	NM_002993	1.322113439	5.57445211	7.370058048	0.090127066	3.110433628	0.003541514	chemokine (C-X-C motif) ligand 6 (granulocyte chemotactic protein 2)
212731_PM_at	ANKRD46	NM_198401	-1.76828318	15.7533026	8.908812132	0.090471475	-3.10690657	0.00357525	ankyrin repeat domain 46
222589_PM_at	NLK	NM_016231	-1.68921017	119.687409	70.85406634	0.090471475	-3.10590484	0.003584887	nemo-like kinase
213270_PM_at	MPP2	NM_005374	1.25245866	8.57707265	10.74242892	0.091092521	3.102098773	0.003621727	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)
205246_PM_at	PEX13	NM_002618	1.394865838	14.777397	20.61248626	0.092270307	3.092595895	0.003715277	peroxisomal biogenesis factor 13
57703_PM_at	SENP5	NM_152699	1.23445456	6.27506916	7.746287736	0.092367155	3.091063457	0.003730575	SUMO1/sentrin specific peptidase 5
214718_PM_at	GATAD1	NM_021167	-1.80063447	50.3067532	27.93834838	0.093478225	-3.0800144	0.003842649	GATA zinc finger domain containing 1
224880_PM_at	RALA	NM_005402	-1.78395541	152.745897	85.62203708	0.094142532	-3.07467063	0.003897987	v-ral simian leukemia viral oncogene homolog A (ras related)
228054_PM_at	TMEM44	NM_001011655	-1.27167144	7.42843967	5.841477163	0.096140326	-3.06137115	0.004038996	transmembrane protein 44
209307_PM_at	SWAP70	NM_015055	-2.31422842	56.7135237	24.50645027	0.096847426	-3.0567304	0.004089322	SWAP switching B-cell complex 70kDa subunit
232065_PM_x_at	CENPL	NM_001127181	1.870614945	14.01998	26.22598407	0.101216987	3.023878491	0.004462866	centromere protein L
215548_PM_s_at	SCFD1	NM_016106 ///	1.276720094	166.413233	212.4631181	0.102150952	3.018075466	0.004532103	sec1 family domain containing 1
216504_PM_s_at	SLC39A8	NM_001135146	1.208323032	4.86299683	5.876071075	0.10241166	3.014244573	0.004578363	solute carrier family 39 (zinc transporter), member 8
209489_PM_at	CUGBP1	NM_001025596	-1.25473992	452.993202	361.025575	0.10241166	-3.01239394	0.00460087	CUG triplet repeat, RNA binding protein 1

Supplementary Table S4. ARE genes differentially expressed (FDR <0.3) in t-MN del(5q) vs. non-del(5q) t-MN patients.

				Mean	Mean				
ProbesetID	**Gene_Symbol**	**Refseq**	**Fold Change**	**non del(5q)**	**del(5q)**	**FDR**	**T.Statistic**	**P.Value**	**Annotation**
205931_PM_s_at	CREB5	NM_001011666	3.316602991	10.6797171	35.42038162	0.102776509	3.009191503	0.004640062	cAMP responsive element binding protein 5
224479_PM_s_at	MRPL45	NM_032351	-1.64746935	97.5033727	59.18372479	0.103228854	-3.00594569	0.004680106	mitochondrial ribosomal protein L45
205976_PM_at	FASTKD2	NM_001136193	-1.68514695	15.7540997	9.348798752	0.103431837	-3.00435597	0.004699837	FAST kinase domains 2
242600_PM_at	FRMD3	NM_174938	1.38165272	4.89574415	6.764218227	0.103431837	3.004198366	0.004701798	FERM domain containing 3
209222_PM_s_at	OSBPL2	NM_014835 ///	1.449082202	65.8768638	95.46099085	0.104476758	2.996477387	0.004798784	oxysterol binding protein-like 2
204393_PM_s_at	ACPP	NM_001099 ///	2.38828714	13.7233794	32.7753706	0.104555478	2.995321606	0.004813463	acid phosphatase, prostate
201919_PM_at	SLC25A36	NM_001104647	-1.57521168	363.204163	230.5748284	0.104580885	-2.99455916	0.00482317	solute carrier family 25, member 36
1554086_PM_at	TUBGCP3	NM_006322	1.401094108	7.60156474	10.65050757	0.1062863	2.983010093	0.00497247	tubulin, gamma complex associated protein 3
225207_PM_at	PDK4	NM_002612	2.815627388	13.8458017	38.9846185	0.106378723	2.981790985	0.004988481	pyruvate dehydrogenase kinase, isozyme 4
205174_PM_s_at	QPCT	NM_012413	3.588867827	18.3442047	65.83492592	0.107257804	2.977485455	0.005045416	glutaminyl-peptide cyclotransferase
222517_PM_at	AP3M1	NM_012095 ///	-1.52119765	39.8930194	26.2247443	0.108685193	-2.96716373	0.005184404	adaptor-related protein complex 3, mu 1 subunit
215101_PM_s_at	CXCL5	NM_002994	1.485982987	4.53927343	6.745283095	0.108685193	2.967513342	0.005179638	chemokine (C-X-C motif) ligand 5
219356_PM_s_at	CHMP5	NM_016410	1.416760206	224.466161	318.0147246	0.109434043	2.961803338	0.005257996	chromatin modifying protein 5
225862_PM_at	SLC25A26	NM_173471	-1.4629522	34.9737509	23.90628411	0.109625642	-2.95997934	0.00528326	solute carrier family 25, member 26
212753_PM_at	PCGF3	NM_006315	-1.62386098	107.977806	66.49448911	0.11013528	-2.95605015	0.005338071	polycomb group ring finger 3
226217_PM_at	SLC30A7	NM_001144884	-1.38425788	166.86453	120.5443959	0.112647031	-2.9405998	0.005558818	solute carrier family 30 (zinc transporter), member 7
201368_PM_at	ZFP36L2	NM_006887	-1.45898949	1355.68758	929.1962652	0.113135887	-2.93674527	0.00561521	zinc finger protein 36, C3H type-like 2
243246_PM_at	NAT12	NM_001011713	1.199941965	7.35568163	8.826391069	0.113482456	2.934461472	0.005648874	N-acetyltransferase 12 (GCN5-related, putative)
225240_PM_s_at	MSI2	NM_138962 ///	-2.36748896	211.985208	89.5401038	0.113544481	-2.93383305	0.00565817	musashi homolog 2 (Drosophila)
205966_PM_at	TAF13	NM_005645	1.385222204	6.27183623	8.687886805	0.113761588	2.932048884	0.005684642	TAF13 RNA polymerase II, TATA box binding protein (TBP)-associated factor, 18kDa
222514_PM_at	RRAGC	NM_022157	1.337112411	182.816876	244.4467139	0.114384887	2.926563178	0.005766764	Ras-related GTP binding C
207375_PM_s_at	IL15RA	NM_002189 ///	1.844064648	16.3306727	30.11481613	0.114525015	2.923899218	0.005807043	interleukin 15 receptor, alpha
230058_PM_at	LOC646891	NM_001039707	-1.5626879	11.5511462	7.391844641	0.114552624	-2.92284385	0.005823073	similar to Serologically defined colon cancer antigen 3 /// serologically defined colon cancer antigen 3
221795_PM_at	NTRK2	NM_001007097	1.188744037	3.70453501	4.403743898	0.115627885	2.916498744	0.005920328	neurotrophic tyrosine kinase, receptor, type 2
225830_PM_at	PDZD8	NM_173791	1.954577571	18.4385529	36.03958193	0.11572949	2.915592406	0.005934344	PDZ domain containing 8
1554021_PM_a_at	ZNF12	NM_006956 ///	-1.61684033	65.2929482	40.38305254	0.115786707	-2.91464114	0.005949087	zinc finger protein 12
227075_PM_at	ELP3	NM_018091	-1.58273165	71.359911	45.0865508	0.116171796	-2.91050814	0.006013544	elongation protein 3 homolog (S. cerevisiae)
206448_PM_at	ZNF365	NM_014951 ///	1.311407575	6.31366379	8.27978652	0.116503134	2.909143986	0.006034962	zinc finger protein 365
222522_PM_x_at	MRPS10	NM_018141	1.636403025	111.283081	182.1039709	0.11678767	2.907117949	0.006066904	mitochondrial ribosomal protein S10
226688_PM_at	C3orf23	NM_001029839	-1.66300309	9.95792051	5.987914613	0.1174186	-2.9036044	0.006122673	chromosome 3 open reading frame 23
221803_PM_s_at	NRBF2	NM_030759	1.672625267	26.4834896	44.29695393	0.117421201	2.903156283	0.00612982	nuclear receptor binding factor 2
220088_PM_at	C5AR1	NM_001736	3.722069646	46.9367957	174.7020227	0.117828892	2.89990027	0.006181986	complement component 5a receptor 1
203758_PM_at	CTSO	NM_001334	-2.10001187	52.5661239	25.03134609	0.118045171	-2.89870129	0.0062013	cathepsin O
209865_PM_at	SLC35A3	NM_012243	-1.43037746	18.9813141	13.27014343	0.118269453	-2.89761373	0.006218868	solute carrier family 35 (UDP-N-acetylglucosamine (UDP-GlcNAc) transporter), member A3
227658_PM_s_at	PLEKHA3	NM_019091	1.251665197	8.0073963	10.02257927	0.120248677	2.885456885	0.006418441	pleckstrin homology domain containing, family A (phosphoinositide binding specific) member 3
1563646_PM_a_at	TMEM67	NM_001142301	-1.15706932	6.99539973	6.045791403	0.120248677	-2.88571713	0.006414106	transmembrane protein 67
224797_PM_at	ARRDC3	NM_020801	-1.69863906	118.090087	69.52041177	0.120312953	-2.88320829	0.006456005	arrestin domain containing 3
220999_PM_s_at	CYFIP2	NM_001037332	-2.53999041	61.1625906	24.07985099	0.120312953	-2.88378655	0.006446325	cytoplasmic FMR1 interacting protein 2
225312_PM_at	COMMD6	NM_203495 ///	-1.42950216	1094.85887	765.9022167	0.120798206	-2.87923543	0.006522878	COMM domain containing 6
205333_PM_s_at	RCE1	NM_001032279	1.264133014	14.8560978	18.78008369	0.121642839	2.873030097	0.006628625	RCE1 homolog, prenyl protein peptidase (S. cerevisiae)
213302_PM_at	PFAS	NM_012393	-1.90005156	86.9211176	45.74671526	0.121764833	-2.87134277	0.006657655	phosphoribosylformylglycinamidine synthase
222918_PM_at	RAB9B	NM_016370	-1.33792951	12.1122245	9.052961627	0.121953355	-2.87036249	0.006674575	RAB9B, member RAS oncogene family
211962_PM_s_at	ZFP36L1	NM_004926	2.528068704	220.964192	558.6126582	0.122248623	2.868355874	0.006709336	zinc finger protein 36, C3H type-like 1
206409_PM_at	TIAM1	NM_003253	1.170934034	6.20741619	7.268474879	0.122485305	2.865975653	0.006750788	T-cell lymphoma invasion and metastasis 1
222819_PM_at	CTPS2	NM_001144002	-1.8510258	37.7711194	20.40550669	0.123926259	-2.85650697	0.006918067	CTP synthase II
207941_PM_s_at	RBM39	NM_004902 ///	-1.36138779	806.146054	592.1502034	0.123926259	-2.85634438	0.006920973	RNA binding motif protein 39
213100_PM_at	UNC5B	NM_170744	1.178966155	5.09639793	6.00848067	0.124222511	2.854785581	0.006948891	Unc-5 homolog B (C. elegans)
226512_PM_at	ZMYM2	NM_003453 ///	-1.49512375	21.3258404	14.26359548	0.126203557	-2.84202516	0.007181414	zinc finger, MYM-type 2
206183_PM_s_at	HERC3	NM_014606	1.204117185	14.1497636	17.03797348	0.126233746	2.838854656	0.007240303	hect domain and RLD 3
212442_PM_s_at	LASS6	NM_203463	-1.75624273	297.666237	169.4903738	0.126233746	-2.84025396	0.007214257	LAG1 homolog, ceramide synthase 6
219399_PM_at	LIN7C	NM_018362	1.529514959	14.3926561	22.01378274	0.126233746	2.839114774	0.007235455	lin-7 homolog C (C. elegans)
229908_PM_s_at	UNKL	NM_001037125	-1.72244602	138.401639	80.35180068	0.126411429	-2.83720954	0.007271037	unkempt homolog (Drosophila)-like
202094_PM_at	BIRC5	NM_001012270	2.052746879	13.5751662	27.86637998	0.126531525	2.836503913	0.007284257	baculoviral IAP repeat-containing 5
219342_PM_at	CASD1	NM_022900	-1.77841667	26.2726401	14.77305093	0.126992655	-2.8316998	0.007374858	CAS1 domain containing 1
219859_PM_at	CLEC4E	NM_014358	1.657778489	6.21632123	10.30528362	0.128023201	2.824015528	0.007521964	C-type lectin domain family 4, member E
214537_PM_at	HIST1H1D	NM_005320	1.682138458	10.1754369	17.11649374	0.128713069	2.818897833	0.007621448	histone cluster 1, H1d
225121_PM_at	TBC1D23	NM_018309	1.472139212	102.285386	150.578328	0.128713069	2.818649105	0.007626315	TBC1 domain family, member 23
212071_PM_s_at	SPTBN1	NM_003128 ///	-1.88202168	386.612067	205.4238119	0.128714721	-2.81850538	0.007629128	spectrin, beta, non-erythrocytic 1
223664_PM_x_at	BCL2L13	NM_015367	1.520255598	36.2734057	55.14484814	0.129108384	2.815512891	0.007687922	BCL2-like 13 (apoptosis facilitator)
230836_PM_at	ST8SIA4	NM_005668 ///	-2.21911517	30.7922416	13.87590968	0.129226759	-2.81491581	0.007699703	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 4
223373_PM_s_at	PLA2G12A	NM_030821	1.963171997	28.9190107	56.77299204	0.129646076	2.811806077	0.007761335	phospholipase A2, group XIIA
204633_PM_s_at	RPS6KA5	NM_004755 ///	-1.60953058	108.556133	67.44583436	0.129646076	-2.81199203	0.007757637	ribosomal protein S6 kinase, 90kDa, polypeptide 5
218378_PM_s_at	PRKRIP1	NM_024653	-1.57992049	78.0196228	49.38199312	0.129827526	-2.80985817	0.007800175	PRKR interacting protein 1 (IL11 inducible)
223470_PM_at	PIGM	NM_145167	-1.78512305	23.7168054	13.28580986	0.132495388	-2.79475116	0.008107599	phosphatidylinositol glycan anchor biosynthesis, class M
235061_PM_at	PPM1K	NM_152542	-1.74035644	27.559456	15.8355239	0.134194845	-2.78219448	0.008371667	protein phosphatase 1K (PP2C domain containing)
212522_PM_at	PDE8A	NM_002605 ///	-1.90013514	31.3586014	16.50335321	0.135215884	-2.77555107	0.008514592	phosphodiesterase 8A
236007_PM_at	AKAP10	NM_007202	-1.57439676	141.357896	89.78543376	0.135618417	-2.77239405	0.008583304	A kinase (PRKA) anchor protein 10
201749_PM_at	ECE1	NM_001113347	1.812947948	24.7781692	44.92153095	0.135618417	2.772112681	0.008589453	endothelin converting enzyme 1
205018_PM_s_at	MBNL2	NM_144778 ///	1.45094992	7.52666116	10.9208084	0.137157052	2.761901667	0.008815389	muscleblind-like 2 (Drosophila)
227980_PM_at	ZNF322A	NM_024639	-1.53433342	36.8275047	24.00228277	0.138345093	-2.75371862	0.009000423	zinc finger protein 322A
219098_PM_at	MYBBP1A	NM_001105538	-1.40257662	28.8602486	20.57659326	0.13855895	-2.75192562	0.009041445	MYB binding protein (P160) 1a
225610_PM_at	UHRF2	NM_152896	-1.30195121	235.436749	180.8337732	0.138952292	-2.74965399	0.009093667	ubiquitin-like with PHD and ring finger domains 2
215049_PM_x_at	CD163	NM_004244 ///	3.561971253	48.2304193	171.7953671	0.139819837	2.744443559	0.009214507	CD163 molecule
213262_PM_at	SACS	NM_014363	-1.92520594	79.0968864	41.08489637	0.139828376	-2.74399668	0.00922494	spastic ataxia of Charlevoix-Saguenay (sacsin)
225037_PM_at	SLC35C2	NM_015945 ///	-1.43511611	43.3832364	30.22977457	0.140978536	-2.73651938	0.009401142	solute carrier family 35, member C2
202900_PM_s_at	NUP88	NM_002532	-1.47010623	153.575061	104.4652813	0.14427711	-2.71820364	0.009846022	nucleoporin 88kDa
202080_PM_s_at	TRAK1	NM_001042646	-1.5220914	86.4892519	56.82264004	0.145088127	-2.71297944	0.009976444	trafficking protein, kinesin binding 1
201682_PM_at	PMPCB	NM_004279	-1.27900116	251.754346	196.8366825	0.145251602	-2.71182039	0.010005597	peptidase (mitochondrial processing) beta
242916_PM_at	CEP110	NM_007018	-1.51390032	315.643312	208.4967608	0.145757417	-2.71010324	0.01004893	centrosomal protein 110kDa

Supplementary Table S4. ARE genes differentially expressed (FDR <0.3) in t-MN del(5q) vs. non-del(5q) t-MN patients.

				Mean	Mean				
ProbesetID	Gene_Symbol	Refseq	**Fold Change**	**non del(5q)**	**del(5q)**	**FDR**	**T.Statistic**	**P.Value**	**Annotation**
1569617_PM_at	OSBP2	NM_030758	3.676666423	13.0730836	48.06536759	0.146262995	2.705861361	0.010156724	oxysterol binding protein 2
223229_PM_at	UBE2T	NM_014176	2.76182976	48.4775065	133.8866201	0.146663426	2.702306485	0.010247883	ubiquitin-conjugating enzyme E2T (putative)
223336_PM_s_at	RAB18	NM_021252	1.434705311	124.868901	179.150075	0.147068501	2.700602804	0.010291839	RAB18, member RAS oncogene family
220671_PM_at	CCRN4L	NM_012118	1.275621759	11.4484603	14.6039051	0.147426484	2.698956423	0.010334482	CCR4 carbon catabolite repression 4-like (S. cerevisiae)
223073_PM_at	HIATL1	NM_032558	1.423104394	116.446875	165.7160601	0.147442061	2.698532644	0.010345485	hippocampus abundant transcript-like 1
239177_PM_at	IRGQ	NM_001007561	1.136925067	4.67765071	5.318138355	0.147513261	2.698236441	0.010353182	immunity-related GTPase family, Q
225576_PM_at	C6orf72	NM_138785	1.387099994	80.4688195	111.618299	0.147990475	2.694256011	0.01045713	chromosome 6 open reading frame 72
1557836_PM_at	ELMOD2	NM_153702	1.359718878	4.69555166	6.384630234	0.148055468	2.693700521	0.010471713	ELMO/CED-12 domain containing 2
222581_PM_at	XPR1	NM_001135669	1.399045783	74.1353077	103.7186896	0.148480233	2.690158486	0.010565144	xenotropic and polytropic retrovirus receptor
210807_PM_s_at	SLC16A7	NM_004731	1.291930189	16.9279595	21.86974193	0.148883897	2.688211394	0.010616831	solute carrier family 16, member 7 (monocarboxylic acid transporter 2)
214980_PM_at	UBE3A	NM_000462 ///	-1.51342304	22.8525159	15.09988634	0.149046517	-2.68740836	0.010638216	Ubiquitin protein ligase E3A
210462_PM_at	BLZF1	NM_003666	1.289904369	5.18831602	6.692431494	0.149102924	2.686854222	0.010652997	basic leucine zipper nuclear factor 1
209042_PM_s_at	UBE2G2	NM_003343 ///	-1.35374347	285.463409	210.8696479	0.149948104	-2.68173653	0.010790399	ubiquitin-conjugating enzyme E2G 2 (UBC7 homolog, yeast)
202531_PM_at	IRF1	NM_002198	-1.61484498	185.607536	114.9382992	0.149993477	-2.68141237	0.010799157	interferon regulatory factor 1
1556151_PM_at	ITFG1	NM_030790	-1.29757394	134.602216	103.7337547	0.15013697	-2.68039668	0.010826641	Integrin alpha FG-GAP repeat containing 1
211171_PM_s_at	PDE10A	NM_001130690	1.1268584	4.66893939	5.261233566	0.150256488	2.679595846	0.010848357	phosphodiesterase 10A
218335_PM_x_at	TNIP2	NM_001161527	1.39348988	74.4860514	103.7955588	0.150479391	2.678350018	0.01088222	TNFAIP3 interacting protein 2
212984_PM_at	ATF2	NM_001880	-1.33382296	192.100539	144.0225159	0.150650681	-2.67720038	0.010913555	activating transcription factor 2
203011_PM_at	IMPA1	NM_001144878	-1.33712256	250.149618	187.0805452	0.150872222	-2.67588653	0.010949468	inositol(myo)-1(or 4)-monophosphatase 1
227607_PM_at	STAMBPL1	NM_020799	-2.07820872	34.4849827	16.59360893	0.15095349	-2.67379812	0.011006777	STAM binding protein-like 1
215063_PM_x_at	LRRC40	NM_017768	-1.29313987	201.408677	155.7516573	0.151335767	-2.67077839	0.011090133	leucine rich repeat containing 40
1568913_PM_at	NSUN3	NM_022072	1.339900404	6.499417	8.708571463	0.151335767	2.671028245	0.011083214	NOL1/NOP2/Sun domain family, member 3
228305_PM_at	ZNF565	NM_001042474	-1.40536709	10.5743178	7.524238951	0.151823335	-2.66810479	0.011164421	zinc finger protein 565
232007_PM_at	AGPAT5	NM_018361	-1.9005055	34.8103577	18.31636779	0.153478106	-2.66067705	0.011373224	1-acylglycerol-3-phosphate O-acyltransferase 5 (lysophosphatidic acid acyltransferase, epsilon)
228662_PM_at	SOCS7	NM_014598	-1.64390182	57.7745749	35.14478432	0.15411917	-2.65663159	0.011488458	Suppressor of cytokine signaling 7
238164_PM_at	USP6NL	NM_001080491	1.640387898	25.6964282	42.15210985	0.155525327	2.650327856	0.011670166	USP6 N-terminal like
202321_PM_at	GGPS1	NM_001037277	-1.40868883	15.7205989	11.15973845	0.155809991	-2.64861294	0.011720056	geranylgeranyl diphosphate synthase 1
223852_PM_s_at	STK40	NM_032017	1.314583601	32.387903	42.5766062	0.156112652	2.645976647	0.011797135	serine/threonine kinase 40
206708_PM_at	FOXN2	NM_002158	1.262687076	7.70890449	9.733934073	0.156166844	2.645644811	0.01180687	forkhead box N2
224336_PM_s_at	DUSP16	NM_030640	1.177668848	5.04067817	5.936249653	0.156730935	2.642462503	0.011900606	dual specificity phosphatase 16
214700_PM_x_at	RIF1	NM_018151	1.349253129	22.7549892	30.7022404	0.157672529	2.637704774	0.012042027	RAP1 interacting factor homolog (yeast)
202804_PM_at	ABCC1	NM_004996 ///	-1.79457493	381.356208	212.5050346	0.158049918	-2.63334657	0.012172929	ATP-binding cassette, sub-family C (CFTR/MRP), member 1
219439_PM_at	C1GALT1	NM_020156	1.589316871	45.9774108	73.07267459	0.158049918	2.633515898	0.012167819	core 1 synthase, glycoprotein-N-acetylgalactosamine 3-beta-galactosyltransferase, 1
217837_PM_s_at	RNF103	NM_001005753	1.353748625	167.755825	227.0992178	0.158717099	2.628390366	0.012323386	ring finger protein 103 /// vacuolar protein sorting 24 homolog (S. cerevisiae)
241017_PM_at	RPL31	NM_000993 ///	-1.77086587	19.144997	10.8110938	0.159125016	-2.625518	0.012411365	ribosomal protein L31 /// TBC1 domain family, member 8 (with GRAM domain)
53076_PM_at	B4GALT7	NM_007255	-1.24901352	19.2983982	15.45091217	0.159496469	-2.62388271	0.012461711	xylosylprotein beta 1,4-galactosyltransferase, polypeptide 7 (galactosyltransferase I)
1555431_PM_a_at	IL31RA	NM_139017	-1.10881651	4.31117195	3.888084195	0.159537509	-2.62366872	0.012468313	interleukin 31 receptor A
1562259_PM_at	TEX9	NM_198524	1.19760297	8.77328374	10.50691066	0.159593878	2.622879186	0.0124927	testis expressed 9
235374_PM_at	MDH1	NM_005917	-1.51434344	87.4967469	57.77866806	0.159857611	-2.62098395	0.012551419	Malate dehydrogenase 1, NAD (soluble)
204341_PM_at	TRIM16	NM_006470	-1.77866094	13.6235571	7.659445788	0.161649902	-2.61159614	0.012846036	tripartite motif-containing 16
202378_PM_s_at	LEPROT	NM_017526	1.429706482	278.77999	398.573559	0.162447667	2.608296947	0.012951077	leptin receptor overlapping transcript
239884_PM_at	CADPS	NM_003716 ///	1.166788009	4.57585733	5.339055461	0.162950976	2.605203043	0.013050298	Ca++-dependent secretion activator
228696_PM_at	SLC45A3	NM_033102	-2.21035541	34.9591911	15.816095	0.162950976	-2.60548141	0.013041342	solute carrier family 45, member 3
203375_PM_s_at	TPP2	NM_003291	-1.49429865	147.119193	98.45367435	0.163065164	-2.60462292	0.01306898	tripeptidyl peptidase II
208075_PM_s_at	CCL7	NM_006273	2.246779964	4.88989779	10.98652438	0.163072646	2.604329909	0.013078426	chemokine (C-C motif) ligand 7
242356_PM_at	VTI1A	NM_145206	1.517879396	29.0165473	44.04361936	0.164483435	2.597768371	0.013291592	Vesicle transport through interaction with t-SNAREs homolog 1A (yeast)
204097_PM_s_at	RBMX2	NM_016024	-1.37781008	36.5313653	26.51407894	0.166269744	-2.58808907	0.013611881	RNA binding motif protein, X-linked 2
225343_PM_at	TMED8	NM_213601	-1.39914629	232.851364	166.4238877	0.166269744	-2.58790606	0.013618005	transmembrane emp24 protein transport domain containing 8
205452_PM_at	PIGB	NM_004855	-1.45046747	39.2498428	27.06013315	0.166278655	-2.58733632	0.013637084	phosphatidylinositol glycan anchor biosynthesis, class B
218603_PM_at	HECA	NM_016217	1.459931376	177.809221	259.5892607	0.166656317	2.584787784	0.013722732	headcase homolog (Drosophila)
210821_PM_x_at	CENPA	NM_001042426	1.806233011	8.49373909	15.34167193	0.166941251	2.583722581	0.013758676	centromere protein A
235925_PM_at	TCF12	NM_003205 ///	-1.68366929	53.1764678	31.58367754	0.167765129	-2.57964027	0.01389723	Transcription factor 12
229770_PM_at	GLT1D1	NM_144669	2.193422414	11.2554221	24.68789504	0.167985545	2.578564803	0.013933945	glycosyltransferase 1 domain containing 1
204252_PM_at	CDK2	NM_001798 ///	1.595360258	39.5258479	63.05796691	0.168053615	2.577902848	0.013956587	cyclin-dependent kinase 2
205052_PM_at	AUH	NM_001698	-1.52927445	67.102012	43.87833188	0.168449885	-2.5757564	0.014030238	AU RNA binding protein/enoyl-Coenzyme A hydratase
206075_PM_s_at	CSNK2A1	NM_001895 ///	1.38484155	27.5094582	38.09624079	0.168937189	2.571770356	0.014167958	casein kinase 2, alpha 1 polypeptide
223240_PM_at	FBXO8	NM_012180	1.509043372	18.0782596	27.28087776	0.170287713	2.562478617	0.01449382	F-box protein 8
226186_PM_at	TMOD2	NM_001142885	-1.68763868	26.3272681	15.60006208	0.170287713	-2.56293929	0.014477504	tropomodulin 2 (neuronal)
224334_PM_s_at	MRPL51	NM_006415 ///	1.429765645	35.0906002	50.17133465	0.170287713	2.563625788	0.01445322	mitochondrial ribosomal protein L51 /// serine palmitoyltransferase, long chain base subunit 1
213820_PM_s_at	STARD5	NM_181900	1.375913221	7.77301749	10.69499753	0.170387639	2.561210785	0.014538812	StAR-related lipid transfer (START) domain containing 5
211220_PM_s_at	HSF2	NM_001135564	1.140979824	4.8222265	5.502063148	0.170669629	2.559920915	0.014584717	heat shock transcription factor 2
210119_PM_at	KCNJ15	NM_002243 ///	2.380374412	8.14196597	19.38092745	0.170989697	2.557219655	0.014681283	potassium inwardly-rectifying channel, subfamily J, member 15
225026_PM_at	CHD6	NM_032221	-1.55522169	41.0193062	26.37521482	0.171159075	-2.5564744	0.014708028	chromodomain helicase DNA binding protein 6
225961_PM_at	KLHDC5	NM_020782	-1.57214124	23.2961857	14.8181252	0.1723755	-2.55156225	0.014885429	kelch domain containing 5
203414_PM_at	MMD	NM_012329	1.868802615	96.339758	180.0399916	0.172895361	2.549119769	0.014974366	monocyte to macrophage differentiation-associated
205394_PM_at	CHEK1	NM_001114121	1.746031769	12.6614545	22.10730175	0.173390713	2.546042346	0.015087116	CHK1 checkpoint homolog (S. pombe)
208398_PM_s_at	TBPL1	NM_004865	1.863693078	147.446599	274.795205	0.173605119	2.543939166	0.015164618	TBP-like 1
218009_PM_s_at	PRC1	NM_003981 ///	2.571425228	132.685214	341.1901066	0.173988799	2.542130849	0.015231546	protein regulator of cytokinesis 1
235879_PM_at	MBNL1	NM_021038 ///	-1.55843269	599.671553	384.7914352	0.174490461	-2.53946666	0.015330644	Muscleblind-like (Drosophila)
210358_PM_x_at	GATA2	NM_001145661	-2.05732389	23.8372926	11.58655318	0.174766268	-2.53790819	0.015388886	GATA binding protein 2
204379_PM_s_at	FGFR3	NM_000142 ///	1.913709051	7.88164757	15.0831803	0.175282871	2.533380793	0.015559232	fibroblast growth factor receptor 3
203952_PM_at	ATF6	NM_007348	1.222084643	56.643367	69.22298891	0.175327935	2.532853331	0.01557919	activating transcription factor 6
1565698_PM_at	HECTD2	NM_173497 ///	1.097185171	3.64220316	3.996171297	0.175533994	2.530138507	0.015682283	HECT domain containing 2
204586_PM_at	BSN	NM_003458	1.135337083	4.2841083	4.863907019	0.175637753	2.529250014	0.015716158	bassoon (presynaptic cytomatrix protein)
1570200_PM_at	HELB	NM_033647	-1.32474845	21.6564316	16.34758023	0.176572158	-2.52358976	0.015933539	helicase (DNA) B
242050_PM_at	LRRC7	NM_020794	1.2919254	6.31157128	8.15407925	0.176973426	2.521836212	0.016001439	Leucine rich repeat containing 7

Supplementary Table S4. ARE genes differentially expressed (FDR <0.3) in t-MN del(5q) vs. non-del(5q) t-MN patients.

ProbesetID	Gene_Symbol	Refseq	Fold Change	Mean non del(5q)	Mean del(5q)	FDR	T.Statistic	P.Value	Annotation
217428_PM_s_at	COL10A1	NM_000493	1.129734656	5.00143095	5.650289875	0.17781935	2.518280385	0.01613994	collagen, type X, alpha 1
36994_PM_at	ATP6V0C	NM_001694	1.367732968	396.194835	541.8887381	0.177901622	2.517563601	0.016167991	ATPase, H+ transporting, lysosomal 16kDa, V0 subunit c
200974_PM_at	ACTA2	NM_001141945	-2.32528088	19.0352564	8.186218071	0.179640591	-2.50984222	0.016473002	actin, alpha 2, smooth muscle, aorta
221563_PM_at	DUSP10	NM_007207 ///	-2.12538214	145.151235	68.2941818	0.17964662	-2.50908045	0.016503377	dual specificity phosphatase 10
203301_PM_s_at	DMTF1	NM_001142326	-1.43749895	255.795912	177.9451121	0.180466903	-2.50563749	0.0166413	cyclin D binding myb-like transcription factor 1
203680_PM_at	PRKAR2B	NM_002736	2.536795836	123.326574	312.8543387	0.181561164	2.501657533	0.016802046	protein kinase, cAMP-dependent, regulatory, type II, beta
219761_PM_at	CLEC1A	NM_016511	1.190336861	5.56442792	6.623543661	0.182650798	2.497116095	0.016987199	C-type lectin domain family 1, member A
204010_PM_s_at	KRAS	NM_004985 ///	-1.12791053	5.02781049	4.457632384	0.182696751	-2.49670261	0.017004149	v-Ki-ras2 Kirsten rat sarcoma viral oncogene homolog
223321_PM_s_at	FGFRL1	NM_001004356	1.246726641	8.81791232	10.9935262	0.182884429	2.49558146	0.017050185	fibroblast growth factor receptor-like 1
219269_PM_at	HMBOX1	NM_001135726	-1.38401428	310.057516	224.0276856	0.182884429	-2.49567742	0.017046241	homeobox containing 1
201634_PM_s_at	CYB5B	NM_030579	-1.47576065	33.423344	22.64821468	0.183291911	-2.49307191	0.017153644	cytochrome b5 type B (outer mitochondrial membrane)
244118_PM_at	GABRA1	NM_000806 ///	1.093054158	4.53005295	4.95159321	0.183291911	2.492993846	0.017156872	gamma-aminobutyric acid (GABA) A receptor, alpha 1
212612_PM_at	RCOR1	NM_015156	1.418278892	127.149002	180.332745	0.183291911	2.493226849	0.01714724	REST corepressor 1
223086_PM_x_at	MRPL51	NM_016497	1.34991107	470.28174	634.8385268	0.183392139	2.492309123	0.017185205	mitochondrial ribosomal protein L51
218168_PM_s_at	CABC1	NM_020247	-1.39096427	108.222126	77.80367056	0.183392139	-2.49249273	0.017177603	chaperone, ABC1 activity of bc1 complex homolog (S. pombe)
218531_PM_at	TMEM134	NM_001078650	-1.48439018	32.7811857	22.08394139	0.184280836	-2.48870896	0.017334876	transmembrane protein 134
1561297_PM_at	WARS2	NM_015836 ///	1.299345757	5.61221918	7.292213184	0.184373158	2.487638282	0.017379617	Tryptophanyl tRNA synthetase 2, mitochondrial
212274_PM_at	LPIN1	NM_145693	-1.93866497	108.773112	56.10722529	0.18484466	-2.48352032	0.017552678	lipin 1
203142_PM_s_at	AP3B1	NM_003664	-1.32576462	87.1622818	65.74491451	0.185837512	-2.47897223	0.01774564	adaptor-related protein complex 3, beta 1 subunit
1552798_PM_a_at	TLR4	NM_138554 ///	1.588017884	9.05487487	14.37930322	0.185877575	2.478483653	0.017766483	toll-like receptor 4
204008_PM_at	DNAL4	NM_005740	-1.29334861	18.6899685	14.45083587	0.186727833	-2.47507347	0.017912589	dynein, axonemal, light chain 4
229287_PM_at	PCNX	NM_014982	-1.71413089	84.3054165	49.18260156	0.187045379	-2.47355855	0.017977844	pecanex homolog (Drosophila)
224661_PM_at	PIGY	NM_001042616	1.461630907	132.530471	193.7106322	0.187902249	2.469682381	0.018145798	phosphatidylinositol glycan anchor biosynthesis, class Y
1560116_PM_a_at	NEDD1	NM_001135175	1.25389393	154.750486	194.0406953	0.188296525	2.468186525	0.018210994	neural precursor cell expressed, developmentally down-regulated 1
204618_PM_s_at	GABPB1	NM_002041 ///	-1.37153861	107.935428	78.69660128	0.189369772	-2.46399065	0.018395009	GA binding protein transcription factor, beta subunit 1
210048_PM_at	NAPG	NM_003826	1.541332196	22.418881	34.55494301	0.189809263	2.462707899	0.018451603	N-ethylmaleimide-sensitive factor attachment protein, gamma
203478_PM_at	NDUFC1	NM_002494	1.299130374	474.734809	616.7424099	0.190094614	2.461215825	0.01851763	NADH dehydrogenase (ubiquinone) 1, subcomplex unknown, 1, 6kDa
205701_PM_at	IPO8	NM_006390	1.092245674	4.88198363	5.332325499	0.190461436	2.45923372	0.018605676	importin 8
227692_PM_at	GNAI1	NM_002069	-2.51537858	31.5455458	12.54107277	0.190488578	-2.45909583	0.018611815	guanine nucleotide binding protein (G protein), alpha inhibiting activity polypeptide 1
201824_PM_at	RNF14	NM_004290 ///	-1.73661453	42.3932435	24.41142971	0.190865855	-2.45748598	0.018683626	ring finger protein 14
209098_PM_s_at	JAG1	NM_000214	1.609149017	5.79463981	9.324438959	0.191166614	2.456269669	0.01873805	jagged 1 (Alagille syndrome)
205652_PM_s_at	TTLL1	NM_001008572	-1.59410234	17.1256124	10.74310728	0.191166614	-2.45612415	0.01874457	tubulin tyrosine ligase-like family, member 1
211114_PM_x_at	SIP1	NM_001009182	1.417572543	10.430806	14.78642416	0.191577795	2.454444937	0.018819967	survival of motor neuron protein interacting protein 1
201830_PM_s_at	NET1	NM_001047160	2.04690107	69.1134705	141.4684367	0.192159638	2.452007389	0.018929904	neuroepithelial cell transforming 1
233813_PM_at	PPP1R16B	NM_015568	-2.8312232	58.3210878	20.59925468	0.192334492	-2.45077147	0.018985869	protein phosphatase 1, regulatory (inhibitor) subunit 16B
242730_PM_at	MYRIP	NM_015460	-1.0970238	4.69849243	4.28294485	0.192641541	-2.44971525	0.019033815	myosin VIIA and Rab interacting protein
209838_PM_at	COPS2	NM_001143887	1.448709184	39.9933982	57.93880329	0.193391065	2.445456237	0.01922827	COP9 constitutive photomorphogenic homolog subunit 2 (Arabidopsis)
229173_PM_at	KIAA1715	NM_030650	1.431171605	21.3356273	30.53494394	0.193963215	2.442275332	0.019374676	KIAA1715
215485_PM_s_at	ICAM1	NM_000201	1.311912987	7.51621804	9.860624069	0.194160924	2.440865012	0.019439912	intercellular adhesion molecule 1
226795_PM_at	LRCH1	NM_001164211	-1.50869641	57.1357321	37.87092742	0.194351494	-2.43958138	0.019499462	leucine-rich repeats and calponin homology (CH) domain containing 1
1560145_PM_at	MKLN1	NM_001145354	-1.45561982	78.9881849	54.26429589	0.194589068	-2.43839974	0.019554426	Muskelin 1, intracellular mediator containing kelch motifs
227425_PM_at	REPS2	NM_001080975	1.739643405	9.61143977	16.72047781	0.194945019	2.436570652	0.019639783	RALBP1 associated Eps domain containing 2
205899_PM_at	CCNA1	NM_001111045	-2.82660108	63.0011417	22.28865695	0.200804133	-2.41322154	0.020759529	cyclin A1
204887_PM_s_at	PLK4	NM_014264	1.891142774	26.6595768	50.41706594	0.201593088	2.410892983	0.020874314	polo-like kinase 4 (Drosophila)
228619_PM_x_at	TIPRL	NM_001031800	-1.38580207	221.368646	159.7404497	0.203220024	-2.40473875	0.021180458	TIP41, TOR signaling pathway regulator-like (S. cerevisiae)
209921_PM_at	SLC7A11	NM_014331	1.661193749	11.10082	18.44061273	0.204545415	2.399688768	0.021434702	solute carrier family 7, (cationic amino acid transporter, y+ system) member 11
210074_PM_at	CTSL2	NM_001333	1.195411043	5.60037014	6.694744309	0.20471264	2.398603297	0.021489711	cathepsin L2
202498_PM_s_at	SLC2A3	NM_006931	2.296575426	25.7695941	59.18181645	0.206193781	2.393152679	0.021767867	solute carrier family 2 (facilitated glucose transporter), member 3
206301_PM_at	TEC	NM_003215	-1.9087275	15.076293	7.898609448	0.206379119	-2.39258717	0.021796912	tec protein tyrosine kinase
202228_PM_s_at	NPTN	NM_001161363	1.411009745	202.161563	285.2519354	0.206502841	2.392112413	0.021821323	neuroplastin
209298_PM_s_at	ITSN1	NM_001001132	2.33010924	6.47739355	15.09303456	0.207674497	2.387446541	0.02206255	intersectin 1 (SH3 domain protein)
211434_PM_s_at	CCRL2	NM_001130910	2.072508764	19.2131227	39.8193651	0.207979819	2.386089124	0.02213318	chemokine (C-C motif) receptor-like 2
227361_PM_at	HS3ST3B1	NM_006041	-2.28572882	30.3939603	13.29727307	0.20817979	-2.38475382	0.022202859	heparan sulfate (glucosamine) 3-O-sulfotransferase 3B1
220021_PM_at	TMC7	NM_001160364	1.118700007	4.78971375	5.35825281	0.208976315	2.382240723	0.022334537	transmembrane channel-like 7
229825_PM_at	PLK3	NM_004073	1.092090608	4.23012414	4.619678839	0.210528754	2.377319202	0.022594454	Polo-like kinase 3 (Drosophila)
224967_PM_at	UGCG	NM_003358	2.387029573	107.235582	255.9745062	0.212010077	2.371574761	0.022901286	UDP-glucose ceramide glucosyltransferase
201732_PM_s_at	CLCN3	NM_001829 ///	2.042491893	30.9954421	63.30793915	0.212370461	2.36963115	0.023005951	chloride channel 3
234561_PM_at	SLC2A13	NM_052885	1.094317839	4.33563071	4.74455803	0.212740636	2.368254035	0.02308037	solute carrier family 2 (facilitated glucose transporter), member 13
203080_PM_s_at	BAZ2B	NM_013450	-1.51038619	133.19789	88.18796861	0.212985524	-2.36713901	0.023140786	bromodomain adjacent to zinc finger domain, 2B
205426_PM_s_at	HIP1	NM_005338	1.153963436	5.22544855	6.029976558	0.214315916	2.361876331	0.023427866	huntingtin interacting protein 1
221582_PM_at	HIST3H2A	NM_033445	2.582969332	20.5864997	53.1742973	0.214442502	2.361481068	0.023449556	histone cluster 3, H2a
218252_PM_at	CKAP2	NM_001098525	1.761138345	84.7654269	149.2836436	0.214573676	2.360520099	0.023502367	cytoskeleton associated protein 2
239352_PM_at	SLC6A15	NM_001146335	1.138957814	5.12033807	5.831849048	0.214821478	2.359519743	0.023557456	solute carrier family 6 (neutral amino acid transporter), member 15
203989_PM_x_at	F2R	NM_001992	-1.92340926	45.6684486	23.74348996	0.214927545	-2.359016	0.023585241	coagulation factor II (thrombin) receptor
201881_PM_s_at	ARIH1	NM_005744	1.390612085	48.1934792	67.01843456	0.214986156	2.358120869	0.023634687	ariadne homolog, ubiquitin-conjugating enzyme E2 binding protein, 1 (Drosophila)
200899_PM_s_at	MGEA5	NM_001142434	-1.28279411	321.438408	250.5767735	0.215019263	-2.35792365	0.023645594	meningioma expressed antigen 5 (hyaluronidase)

Supplementary Table S4. ARE genes differentially expressed (FDR <0.3) in t-MN del(5q) vs. non-del(5q) t-MN patients.

ProbesetID	Gene_Symbol	Refseq	Fold Change	Mean non del(5q)	Mean del(5q)	FDR	T.Statistic	P.Value	Annotation
212804_PM_s_at	GAPVD1	NM_015635	1.601112015	164.352237	263.1463407	0.215123585	2.35650252	0.02372432	GTPase activating protein and VPS9 domains 1
216939_PM_s_at	HTR4	NM_000870 ///	1.127005382	5.87231599	6.618131725	0.215265111	2.355571779	0.023776008	5-hydroxytryptamine (serotonin) receptor 4
2028_PM_s_at	E2F1	NM_005225	1.151914399	5.5521249	6.395572623	0.216294141	2.351832077	0.023984716	E2F transcription factor 1
222071_PM_s_at	SLCO4C1	NM_180991	1.858178935	7.40292731	13.75596358	0.218267393	2.345402498	0.024347407	solute carrier organic anion transporter family, member 4C1
225022_PM_at	GOPC	NM_001017408	-1.44424963	57.7034313	39.95391816	0.218451814	-2.34414789	0.024418753	golgi associated PDZ and coiled-coil motif containing
203018_PM_s_at	SSX2IP	NM_014021	1.551213996	10.7537232	16.68132598	0.218622262	2.343358594	0.024463735	synovial sarcoma, X breakpoint 2 interacting protein
225586_PM_at	WDR85	NM_138778	-1.20639488	46.0746452	38.19201003	0.219458739	-2.34005016	0.024653093	WD repeat domain 85
205085_PM_at	ORC1L	NM_004153	1.797949227	12.5819427	22.6216941	0.220275675	2.336150821	0.024877966	origin recognition complex, subunit 1-like (yeast)
205959_PM_at	MMP13	NM_002427	1.161437146	5.56787975	6.466742368	0.221082607	2.333661367	0.025022496	matrix metallopeptidase 13 (collagenase 3)
219637_PM_at	ARMC9	NM_025139	-1.20319981	6.55256478	5.445948983	0.221418265	-2.33211896	0.025112423	armadillo repeat containing 9
208705_PM_s_at	EIF5	NM_001969 ///	1.247058979	1089.9832	1359.273343	0.224126418	2.322894636	0.025656321	eukaryotic translation initiation factor 5
213292_PM_s_at	SNX13	NM_015132	1.465398241	20.2472048	29.67021827	0.22413538	2.322718122	0.025666831	sorting nexin 13
202777_PM_at	SHOC2	NM_007373	1.180173212	220.719181	260.4868645	0.224978605	2.320135319	0.025821066	soc-2 suppressor of clear homolog (C. elegans)
229116_PM_at	CNKSR2	NM_014927	-1.49696263	6.74273837	4.504279705	0.225466516	-2.31779773	0.025961376	connector enhancer of kinase suppressor of Ras 2
215288_PM_at	TRPC2	NR_002720	-1.55044576	7.22938001	4.66277517	0.225796719	-2.31637238	0.026047266	transient receptor potential cation channel, subfamily C, member 2 (pseudogene)
226183_PM_at	GSK3B	NM_001146156	-1.37003209	33.4439421	24.41106469	0.225947573	-2.31558142	0.026095039	glycogen synthase kinase 3 beta
210415_PM_s_at	ODF2	NM_002540 ///	-1.27843466	16.1320524	12.61859743	0.225947573	-2.31549123	0.026100491	outer dense fiber of sperm tails 2
223342_PM_at	RRM2B	NM_015713	-1.47677001	53.8897397	36.49162652	0.226370842	-2.31381114	0.026202246	ribonucleotide reductase M2 B (TP53 inducible)
215223_PM_s_at	SOD2	NM_000636 ///	2.208698752	148.850391	328.7656725	0.226872507	2.31119252	0.026361554	superoxide dismutase 2, mitochondrial
239835_PM_at	KBTBD8	NM_032505	1.725645061	40.2557374	69.46711443	0.227604648	2.307318829	0.026598812	kelch repeat and BTB (POZ) domain containing 8
220115_PM_s_at	CDH10	NM_006727	1.213901261	5.39572754	6.549880458	0.229879664	2.297168509	0.027229626	cadherin 10, type 2 (T2-cadherin)
209510_PM_at	RNF139	NM_007218	1.244153044	345.320339	429.6313505	0.231846599	2.289730786	0.027700347	ring finger protein 139
205227_PM_at	IL1RAP	NM_002182 ///	-2.03068473	100.27691	49.38083621	0.232301185	-2.28629027	0.02792055	interleukin 1 receptor accessory protein
214553_PM_s_at	ARPP19	NM_006628	1.509243977	25.6678154	38.73899577	0.232690919	2.284647321	0.028026256	cAMP-regulated phosphoprotein, 19kDa
226716_PM_at	PRR12	NM_020719	-1.31620907	18.0419644	13.70752171	0.232690919	-2.28459722	0.028029485	proline rich 12
202980_PM_s_at	SIAH1	NM_001006610	-1.30022538	13.9122613	10.69988446	0.232690919	-2.28455127	0.028032447	seven in absentia homolog 1 (Drosophila)
1560101_PM_at	SYDE2	NM_032184	1.094487374	3.99871113	4.376538843	0.232911353	2.28357974	0.028095135	synapse defective 1, Rho GTPase, homolog 2 (C. elegans)
201599_PM_at	OAT	NM_000274	2.083653883	375.269826	781.9324294	0.233483641	2.280517761	0.028293533	ornithine aminotransferase (gyrate atrophy)
213140_PM_s_at	SS18L1	NM_198935	-1.49837494	65.5901849	43.77421368	0.233856569	-2.27888269	0.02839999	synovial sarcoma translocation gene on chromosome 18-like 1
208093_PM_s_at	NDEL1	NM_001025579	1.434571298	173.88136	249.4452077	0.234400991	2.27703711	0.028520583	nudE nuclear distribution gene E homolog (A. nidulans)-like 1
202561_PM_at	TNKS	NM_003747	-1.37088179	40.0490114	29.2140517	0.234409785	-2.27682412	0.028534529	tankyrase, TRF1-interacting ankyrin-related ADP-ribose polymerase
204492_PM_at	ARHGAP11A	NM_014783 ///	1.418070022	5.95939867	8.450844604	0.235368636	2.27311029	0.028778694	Rho GTPase activating protein 11A
202020_PM_s_at	LANCL1	NM_001136574	-1.56622321	144.07671	91.98989584	0.236034532	-2.27038886	0.0289588	LanC lantibiotic synthetase component C-like 1 (bacterial)
225867_PM_at	VASN	NM_138440	1.173929798	8.23672842	9.669340927	0.236124383	2.269988706	0.028985367	vasorin
202432_PM_at	PPP3CB	NM_001142353	-1.21717347	217.611098	178.7839648	0.236418994	-2.26776323	0.029133521	protein phosphatase 3 (formerly 2B), catalytic subunit, beta isoform
212907_PM_at	SLC30A1	NM_021194	2.027740329	94.4536825	191.5275413	0.236418994	2.267676185	0.029139329	Solute carrier family 30 (zinc transporter), member 1
227740_PM_at	UHMK1	NM_175866	1.221092676	67.5689206	82.50791415	0.236418994	2.26847864	0.029085821	U2AF homology motif (UHM) kinase 1
217959_PM_s_at	TRAPPC4	NM_016146	1.405478829	152.566381	214.4288179	0.237254049	2.265228407	0.029303094	trafficking protein particle complex 4
207719_PM_x_at	CEP170	NM_001042404	-1.42944013	274.62638	192.121639	0.237272693	-2.26469884	0.029338631	centrosomal protein 170kDa
232756_PM_at	KALRN	NM_001024660	-1.1105303	5.92916218	5.339036822	0.237272693	-2.26466936	0.029340611	kalirin, RhoGEF kinase
208940_PM_at	SEPHS1	NM_012247	-1.47876869	50.8298931	34.37311972	0.238264378	-2.26106644	0.029583433	selenophosphate synthetase 1
202293_PM_at	STAG1	NM_005862	1.266934241	32.9786407	41.78176916	0.23919705	2.257224612	0.029844336	stromal antigen 1
226368_PM_at	CHST11	NM_018413	-1.43204328	143.99778	100.5540701	0.239561788	-2.25604383	0.029924936	Carbohydrate (chondroitin 4) sulfotransferase 11
1554329_PM_x_at	STXBP4	NM_178509	-1.15810786	5.07661012	4.383538262	0.240188431	-2.25419408	0.030051591	syntaxin binding protein 4
207050_PM_at	CACNA2D1	NM_000722	1.205254285	7.32407766	8.827375976	0.240634615	2.252528241	0.030166063	calcium channel, voltage-dependent, alpha 2/delta subunit 1
217798_PM_at	CNOT2	NM_014515	-1.25194887	323.012486	258.0077299	0.240854435	-2.25169999	0.030223123	CCR4-NOT transcription complex, subunit 2
202670_PM_at	MAP2K1	NM_002755	1.409019561	96.3536054	135.7641148	0.242407269	2.244174683	0.030745994	mitogen-activated protein kinase kinase 1
225263_PM_at	HS6ST1	NM_004807	-1.873465	62.4900668	33.35534263	0.242443769	-2.24378537	0.030773263	heparan sulfate 6-O-sulfotransferase 1
218901_PM_at	PLSCR4	NM_001128304	2.125940753	13.9676774	29.69445461	0.242574334	2.242979017	0.030829811	phospholipid scramblase 4
204639_PM_at	ADA	NM_000022	-2.57340497	238.357796	92.62350808	0.24263586	-2.24266225	0.03085205	adenosine deaminase
202129_PM_s_at	RIOK3	NM_003831	2.418042627	58.935982	142.5097167	0.242697372	2.240775089	0.030984841	RIO kinase 3 (yeast)
222703_PM_s_at	YRDC	NM_024640	1.329600735	32.9029013	43.74772173	0.242697372	2.240839386	0.030980308	yrdC domain containing (E. coli)
203566_PM_s_at	AGL	NM_000028 ///	-1.46210306	54.1913235	37.06395612	0.242777053	-2.24024262	0.0310224	amylo-1, 6-glucosidase, 4-alpha-glucanotransferase
1555317_PM_at	POLK	NM_016218	-1.22676724	5.32182277	4.338086787	0.242777053	-2.2401586	0.031028331	polymerase (DNA directed) kappa
53912_PM_at	SNX11	NM_013323 ///	1.172709056	36.0847233	42.31688181	0.245090326	2.231272065	0.031661306	sorting nexin 11
202871_PM_at	TRAF4	NM_004295	-1.58940843	22.3758292	14.07808636	0.245912662	-2.22911244	0.031816862	TNF receptor-associated factor 4
212893_PM_at	ZZZ3	NM_015534	-1.42612716	60.3993985	42.35204269	0.247707922	-2.22180085	0.032348578	zinc finger, ZZ-type containing 3
203360_PM_s_at	MYCBP	NM_012333	1.663027464	36.3126045	60.38885861	0.248326561	2.219771254	0.032497573	c-myc binding protein
207160_PM_at	IL12A	NM_000882	-1.55153174	12.067221	7.777617888	0.250178023	-2.21386663	0.032934517	interleukin 12A (natural killer cell stimulatory factor 1, cytotoxic lymphocyte maturation factor 1, p35)
242482_PM_at	PRKAR1A	NM_002734 ///	-1.2203617	5.46458127	4.477837414	0.250374889	-2.21337665	0.03297101	protein kinase, cAMP-dependent, regulatory, type I, alpha (tissue specific extinguisher 1)
224209_PM_s_at	GDA	NM_004293	1.145526706	5.32386966	6.098634872	0.250820425	2.211778169	0.033090311	guanine deaminase
203373_PM_at	SOCS2	NM_003877	-2.45194665	216.463701	88.2823862	0.250966194	-2.21118836	0.033134428	suppressor of cytokine signaling 2
225570_PM_at	SLC41A1	NM_173854	1.691599013	24.3310347	41.15835421	0.251987337	2.206475811	0.033488805	solute carrier family 41, member 1
201249_PM_at	SLC2A1	NM_006516	2.139046264	7.68817691	16.4453661	0.25279038	2.204088789	0.033669588	solute carrier family 2 (facilitated glucose transporter), member 1
235521_PM_at	HOXA3	NM_030661 ///	-2.5130913	24.3545415	9.691069132	0.2529355	-2.20338688	0.033722913	homeobox A3
227945_PM_at	TBC1D1	NM_015173	-1.50694193	29.2524661	19.41180717	0.253599395	-2.20114896	0.033893432	TBC1 (tre-2/USP6, BUB2, cdc16) domain family, member 1
226056_PM_at	CDGAP	NM_020754	1.416728679	5.70933317	8.088576045	0.257520136	2.187377697	0.034959704	Cdc42 GTPase-activating protein
202195_PM_s_at	TMED5	NM_016040	1.589337278	28.7202062	45.64609435	0.258368477	2.184712258	0.035169488	transmembrane emp24 protein transport domain containing 5
221905_PM_at	CYLD	NM_001042355	-1.43327152	100.049881	69.80525276	0.259063806	-2.18125926	0.035442918	cylindromatosis (turban tumor syndrome)
209593_PM_s_at	TOR1B	NM_014506	1.449399666	51.547515	74.71295111	0.259063806	2.180970625	0.03546586	torsin family 1, member B (torsin B)
204387_PM_x_at	MRP63	NM_024026	-1.31556603	110.508481	84.00070989	0.25946994	-2.17960148	0.035574862	mitochondrial ribosomal protein 63

Supplementary Table S4. ARE genes differentially expressed (FDR <0.3) in t-MN del(5q) vs. non-del(5q) t-MN patients.

ProbesetID	Gene_Symbol	Refseq	Fold Change	Mean non del(5q)	Mean del(5q)	FDR	T.Statistic	P.Value	Annotation
224453_PM_s_at	ETNK1	NM_001039481	1.339521369	8.98418741	12.03451102	0.259581309	2.179038511	0.035619767	ethanolamine kinase 1
228523_PM_at	NANOS1	NM_199461	1.150789353	3.99664343	4.599294712	0.260446729	2.176641697	0.035811514	nanos homolog 1 (Drosophila)
223931_PM_s_at	CHFR	NM_001161344	1.343794301	58.0726829	78.03774033	0.261280393	2.173628718	0.036053852	checkpoint with forkhead and ring finger domains
212441_PM_at	KIAA0232	NM_001100590	1.361889049	208.753578	284.2992121	0.262806014	2.165849292	0.036686299	KIAA0232
1552943_PM_at	GABRG1	NM_173536	1.560809251	5.72453741	8.934910946	0.263719154	2.163006791	0.036919826	gamma-aminobutyric acid (GABA) A receptor, gamma 1
237761_PM_at	NEK6	NM_001145001	1.11231322	5.33813295	5.937675854	0.265057079	2.158435485	0.037298146	NIMA (never in mitosis gene a)-related kinase 6
1559624_PM_at	STK32A	NM_001112724	1.098429618	5.57439018	6.123075278	0.265634212	2.156118369	0.037491217	serine/threonine kinase 32A
205519_PM_at	WDR76	NM_024908	1.310719144	10.6981068	14.02221342	0.265770423	2.155766616	0.037520604	WD repeat domain 76
204346_PM_s_at	RASSF1	NM_007182 ///	-1.41742573	66.0484437	46.59746355	0.266570484	-2.15240185	0.037802739	Ras association (RalGDS/AF-6) domain family member 1
216060_PM_s_at	DAAM1	NM_014992	1.797164488	60.2069833	108.2018523	0.268143147	2.147668942	0.038202768	dishevelled associated activator of morphogenesis 1
208653_PM_s_at	CD164	NM_001142401	1.778588731	25.5793994	45.49523149	0.26999899	2.140229458	0.038839126	CD164 molecule, sialomucin
238427_PM_at	GRPEL2	NM_152407	1.212838611	6.39275984	7.753385971	0.270453819	2.138505185	0.038987946	GrpE-like 2, mitochondrial (E. coli)
206066_PM_s_at	RAD51C	NM_002876 ///	1.410010828	39.5551945	55.77325256	0.2704956	2.13751261	0.039073843	RAD51 homolog C (S. cerevisiae)
206669_PM_at	GAD1	NM_000817 ///	1.428768334	7.50880012	10.72833583	0.270668386	2.136995875	0.039118627	glutamate decarboxylase 1 (brain, 67kDa)
240873_PM_x_at	DAB2	NM_001343	1.178138731	4.78995268	5.643228767	0.271303963	2.13468137	0.039319775	disabled homolog 2, mitogen-responsive phosphoprotein (Drosophila)
241453_PM_at	PTK2	NM_005607 ///	1.110234474	4.10943548	4.562436935	0.272077366	2.132312126	0.039526625	PTK2 protein tyrosine kinase 2
223915_PM_at	BCOR	NM_001123383	-1.92614296	77.0904665	40.02323204	0.272339649	-2.13165039	0.03958457	BCL6 co-repressor
210377_PM_at	ACSM3	NM_005622 ///	-1.99037188	22.2829473	11.19536881	0.274376285	-2.12545367	0.040130837	acyl-CoA synthetase medium-chain family member 3
219996_PM_at	ASB7	NM_024708 ///	1.23428876	10.7349347	13.25000925	0.274376285	2.125474209	0.040129016	ankyrin repeat and SOCS box-containing 7
206015_PM_s_at	FOXJ3	NM_014947	-1.20002757	132.840633	110.6979835	0.274849557	-2.12391772	0.040267261	forkhead box J3
215014_PM_at	KCND3	NM_004980 ///	1.080269052	3.62691638	3.918045519	0.275497788	2.122125203	0.040426991	potassium voltage-gated channel, Shal-related subfamily, member 3
219547_PM_at	COX15	NM_004376 ///	-1.40671545	60.4530337	42.97460008	0.275780024	-2.12109253	0.040519265	COX15 homolog, cytochrome c oxidase assembly protein (yeast)
202822_PM_at	LPP	NM_005578	-1.49544158	57.1203465	38.19630752	0.276184946	-2.11919109	0.040689654	LIM domain containing preferred translocation partner in lipoma
211071_PM_s_at	MLLT11	NM_006818	-1.83055333	85.5801977	46.75099944	0.276522614	-2.11829933	0.040769782	myeloid/lymphoid or mixed-lineage leukemia (trithorax homolog, Drosophila); translocated to, 11
227846_PM_at	GPR176	NM_007223	1.239525049	6.30961753	7.82092898	0.277241289	2.116270029	0.04095264	G protein-coupled receptor 176
204715_PM_at	PANX1	NM_015368	1.439755694	14.5988747	21.0188129	0.277399844	2.115402533	0.04103103	pannexin 1
222671_PM_s_at	JMJD4	NM_001161465	-1.15281463	7.13553163	6.189660871	0.277931308	-2.1135222	0.041201396	jumonji domain containing 4
1569729_PM_a_at	ASZ1	NM_130768 ///	1.134551814	4.41673411	5.01101369	0.278871738	2.11097999	0.041432723	ankyrin repeat, SAM and basic leucine zipper domain containing 1
202576_PM_s_at	DDX19A	NM_001014449	-1.29150217	66.4835605	51.47769934	0.281446326	-2.10206193	0.042253281	DEAD (Asp-Glu-Ala-As) box polypeptide 19A /// DEAD (Asp-Glu-Ala-As) box polypeptide 19B
226952_PM_at	EAF1	NM_033083	1.676314911	62.0247604	103.9730307	0.281975271	2.100152767	0.042430791	ELL associated factor 1
202067_PM_s_at	LDLR	NM_000527	1.562875268	13.9962555	21.87440161	0.28209279	2.099630476	0.042479467	low density lipoprotein receptor
226651_PM_at	HOMER1	NM_004272	-1.5147626	33.2581716	21.95602902	0.283430536	-2.09476567	0.042935214	homer homolog 1 (Drosophila)
226326_PM_at	PCGF5	NM_032373	1.783064387	91.2367522	162.6810037	0.283605591	2.094263478	0.042982504	polycomb group ring finger 5
1566722_PM_a_at	SVEP1	NM_153366	1.065849739	4.17431457	4.449192094	0.283937454	2.093178917	0.043084791	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
215886_PM_x_at	USP12	NM_182488	1.563369797	7.89034327	12.33552436	0.284553536	2.091254095	0.043266852	ubiquitin specific peptidase 12
228257_PM_at	ANKRD52	NM_173595	1.13262612	17.6132528	19.94923016	0.285188922	2.089568532	0.043426837	ankyrin repeat domain 52
220009_PM_at	LONRF3	NM_001031855	1.322699116	5.61494528	7.426883151	0.285204294	2.089222499	0.043459744	LON peptidase N-terminal domain and ring finger 3
222642_PM_s_at	TMEM33	NM_018126	1.304948987	8.83860293	11.53392594	0.285204294	2.0892219	0.043459801	transmembrane protein 33
204641_PM_at	NEK2	NM_002497	2.052141999	33.0030347	67.72691356	0.286434545	2.084625338	0.043899019	NIMA (never in mitosis gene a)-related kinase 2
207952_PM_at	IL5	NM_000879	1.094660609	3.98303563	4.36007221	0.286876465	2.083100915	0.044045542	interleukin 5 (colony-stimulating factor, eosinophil)
219030_PM_at	TPRKB	NM_016058	1.345006023	176.453476	237.3309873	0.289368528	2.074355625	0.044894431	TP53RK binding protein
211553_PM_x_at	APAF1	NM_001160 ///	1.122076403	4.90311605	5.50167082	0.289602537	2.073822463	0.044946645	apoptotic peptidase activating factor 1
209096_PM_at	UBE2V2	NM_003350	1.321730837	102.334549	135.2587294	0.289986203	2.07229572	0.045096457	ubiquitin-conjugating enzyme E2 variant 2
223659_PM_at	TMPRSS13	NM_001077263	1.140562205	5.91543468	6.746921222	0.290849403	2.070445212	0.045278626	transmembrane protease, serine 13
222490_PM_at	POLR3E	NM_018119	-1.47967649	86.3868967	58.38228644	0.290938849	-2.07013027	0.045309694	polymerase (RNA) III (DNA directed) polypeptide E (80kD)
1562391_PM_at	B3GALNT2	NM_152490	1.221954851	9.65534378	11.79839417	0.291331895	2.068240773	0.045496479	beta-1,3-N-acetylgalactosaminyltransferase 2
222646_PM_s_at	ERO1L	NM_014584	1.66097347	30.9182315	51.3543623	0.291405787	2.067949652	0.045525318	ERO1-like (S. cerevisiae)
226871_PM_s_at	ATG4D	NM_032885	1.415800915	18.8189152	26.64383733	0.291901271	2.066630694	0.045656174	ATG4 autophagy related 4 homolog D (S. cerevisiae)
211164_PM_at	EPHA3	NM_005233 ///	1.104600239	4.09523698	4.523599751	0.293192846	2.062451987	0.046072931	EPH receptor A3
212341_PM_at	YIPF6	NM_173834	1.524004919	125.643848	191.4818424	0.293533936	2.061434576	0.046174904	Yip1 domain family, member 6
231791_PM_at	ASAH2	NM_001079516	1.138129971	4.48746131	5.107314209	0.294656003	2.058072611	0.046513273	N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2 /// N-acylsphingosine amidohydrolase (non-lysosomal ceramidase) 2B
227305_PM_s_at	SMCR8	NM_144775	-1.26169098	369.612451	292.9500614	0.296797828	-2.05105705	0.047226359	Smith-Magenis syndrome chromosome region, candidate 8
221516_PM_s_at	SMCR7L	NM_019008	1.208832491	93.4777012	112.9988823	0.297485604	2.049245303	0.047412057	Smith-Magenis syndrome chromosome region, candidate 7-like
1566515_PM_at	CWF19L2	NM_152434	1.148320273	4.24227308	4.871488184	0.297804352	2.048114406	0.047528294	CWF19-like 2, cell cycle control (S. pombe)
213394_PM_at	MAPKBP1	NM_001128608	-1.6471855	10.9634612	6.655875274	0.297928245	-2.04768709	0.04757228	mitogen-activated protein kinase binding protein 1
213548_PM_s_at	CDV3	NM_001134422	1.58054852	12.8819227	20.36050392	0.298010677	2.047141728	0.047628468	CDV3 homolog (mouse)
231121_PM_at	HPS3	NM_032383	1.182486925	5.91104653	6.989735233	0.298563006	2.045668175	0.047780577	Hermansky-Pudlak syndrome 3

Supplementary Table S5. Ingenuity Pathway Analysis (IPA®) of differentially expressed AU-rich genes predicts downstream biological processes in t-MN del(5q) versus non-del(5q) patients.

Category	**Functions Annotation**[1]	**p-Value**	**Predicted Activation State**[2]	**Activation z-score**	**Genes**[3]
Cellular Growth and Proliferation	Proliferation of tumor cell lines	1.17E-04	Increased	2.35	***ACPP, APAF1***, *ARRDC3, ATF2, BCL2*, ***BCL2L11, BIRC5, CCL2, CCNA2, CCNE2, CDK2, CHEK1, COPS2, CSNK2A1, CXADR, DAB2***, *DMTF1*, ***E2F1, ENC1***, *ETV6*, ***FGFR3, FGFRL1***, *GATA2, GSK3B, HK2*, ***ID2, IL10***, *IL12A*, ***IL15RA, IL5, IL6ST***, *IRF1*, ***JAG1***, *KRAS*, ***MAP2K1, MAPK1***, *MYBBP1A*, ***MYCBP, NEK2***, *NF1*, ***NR1H2***, *NR3C1*, ***NTRK2***, *PFKP, PRKAR1A*, ***PRKAR2B, PTK2***, *RALA, RASSF1*, ***RCE1***, *RNF14, SIAH1, SLC26A2*, ***SLC2A1, SLC7A11, SOD2***, *SOX6*, ***TIAM1, TLR4***, *TPP2*, ***TRIB2, UBE2J2, UGCG, VEGFA***
Cellular Growth and Proliferation	Stimulation of cells	3.94E-03	Increased	2.588	*BCL2*, ***C5AR1, CCL2, CCL7, CCNA2, CLEC4E, CXCL5, HTR4, IL10***, *IL12A*, ***IL1R1, IL5, NTRK2***, *SLC12A2*, ***TLR4, VEGFA***
Cell Cycle	Interphase	4.25E-04	Increased	2.113	*ATF2, BCL2*, ***BCL2L11, BIRC5***, *CCNA1*, ***CCNA2, CCNE2***, *CDC23*, ***CDK2, CHEK1, COPS2, CSNK2A1***, *CYLD, DMTF1*, ***E2F1***, *ETV6, GSK3B*, ***ID2, IL10***, *IRF1, KRAS*, ***MAP2K1, MAPK1, NEK6***, *NR3C1*, ***PLK3***, *POLK*, ***PTK2***, *RASSF1, RRM2B, SIAH1*, ***SOD2, TBPL1***, *TPP2*, ***VEGFA***
Cell Cycle	S phase	1.09E-03	Increased	2.46	*BCL2*, ***BCL2L11, BIRC5, CCNA2, CDK2, CHEK1***, *DMTF1*, ***E2F1, ID2***, *KRAS*, ***MAP2K1, PLK3***, *POLK, RASSF1*, ***SOD2, TBPL1, VEGFA***

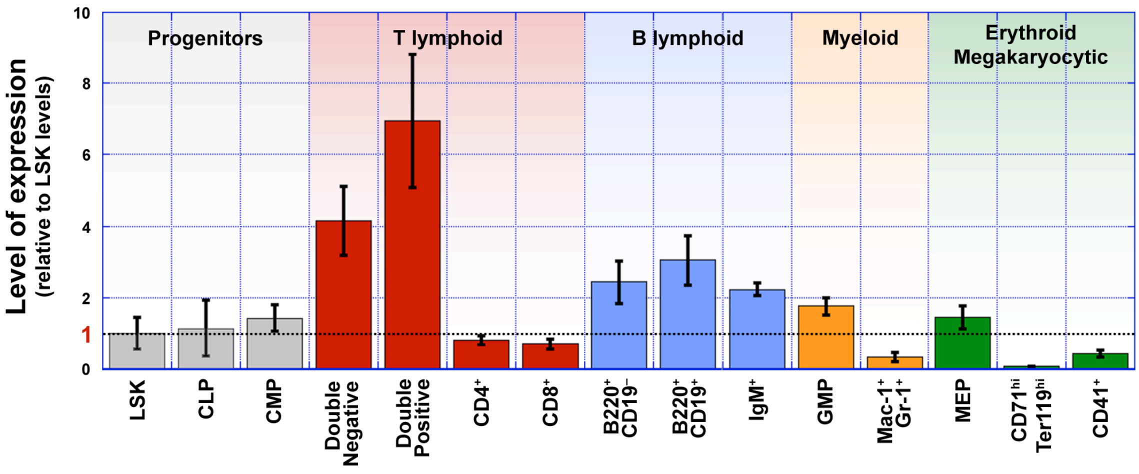
[1] IPA® was used to identify functional annotations that attach biological information to genomic elements.

[2] Predicts the increases or decreases to downstream biological processes using the direction of change in the gene expression data.

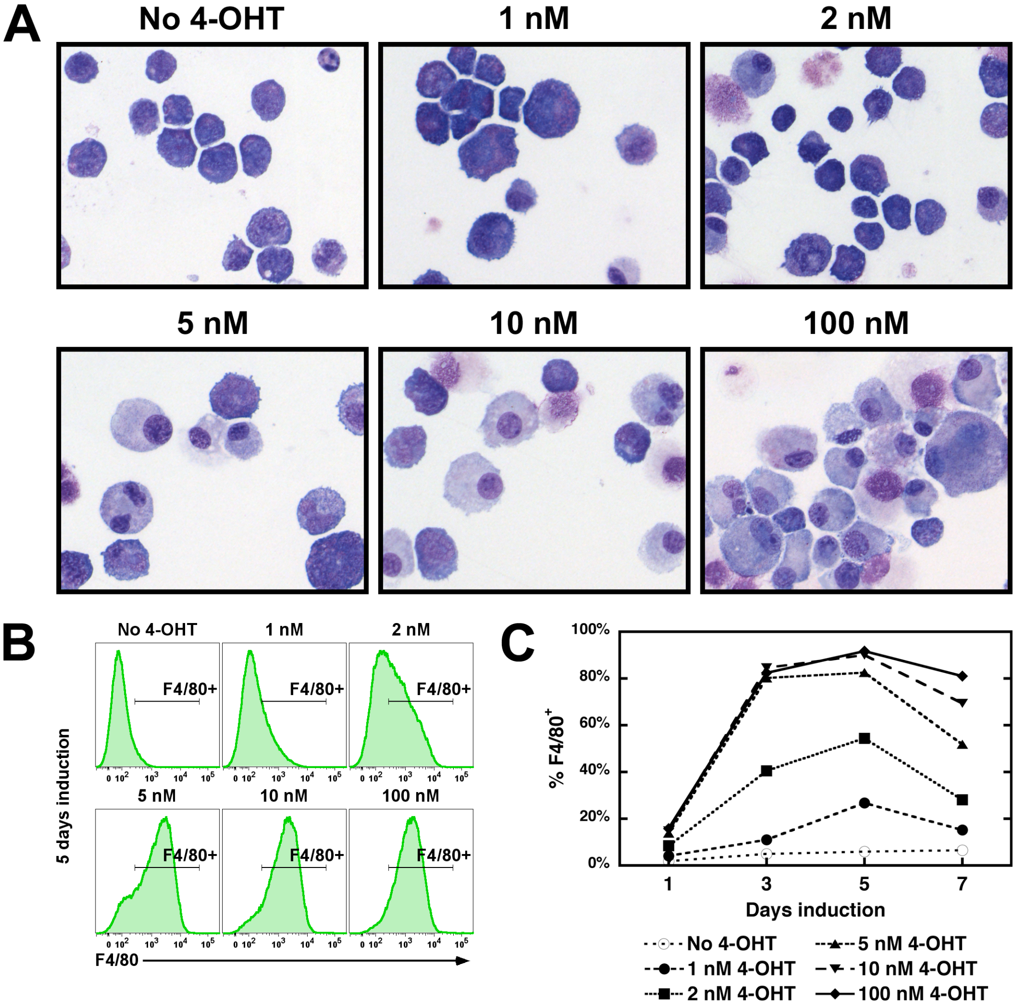
[3] Genes upregulated are in bold; genes downregulated are in regular font.

Supplementary Table S6. Primers used for real-time RT-PCR analysis.

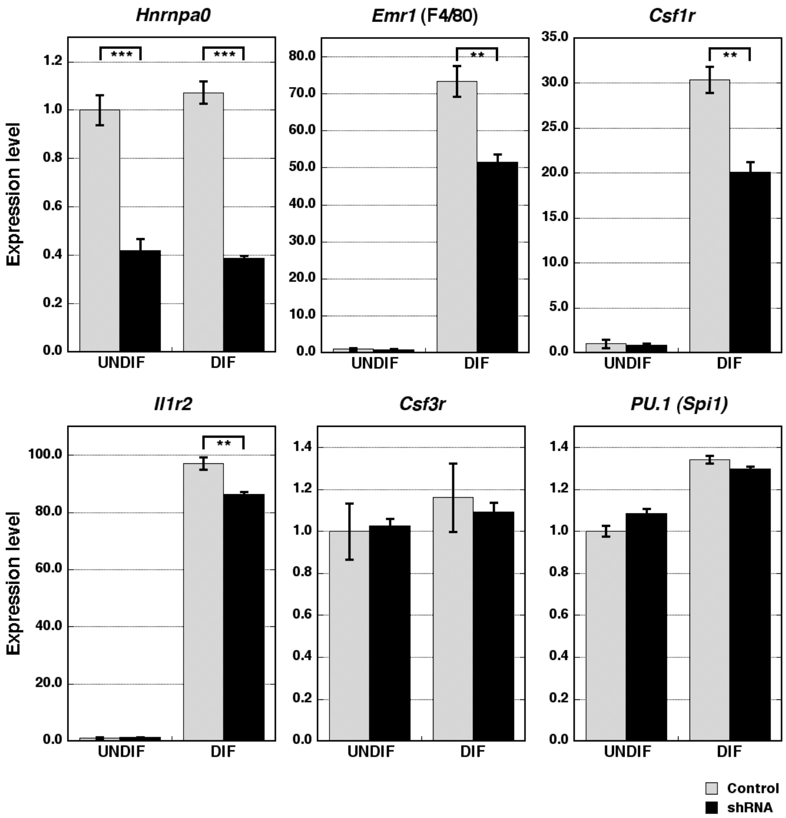
Target	Sequence		Size
Bmi1	Forward	TAC ACG CTA ATG GAC ATT GCC TAC A	141 bp
	Reverse	TTC CAG CTC TCC AGC ATT CGT CAG T	
Cebpa	Forward	TTC GGG TCG CTG GAT CTC TAG GCT	148 bp
	Reverse	ACG GCC TGA CTC CCT CAT CTT AGA C	
Csf1r (Fms)	Forward	CTC CAA CCT GCA TCG GCT CAC GCT A	148 bp
	Reverse	GTT TCA CCC GGC TCT ACA ACC AGT	
Csf3r (Gcsfr)	Forward	AGG AGT GTG AAC TTC GCT ACC AG	138 bp
	Reverse	TGC ATC GCA TCT GTA GGG TGT AGA C	
Egr1	Forward	GGA GCC GAG CGA ACA ACC CTA TGA G	106 bp
	Reverse	GAT GGG AGG CAA CCG AGT CGT TTG G	
Egr2	Forward	GCG GGA GAT GGC ATG ATC AAC	93 bp
	Reverse	AGG TGC AGA GAT GGG AGC GAA GCT A	
Emr1 (F4/80)	Forward	TCA TTG AAT GAC TGC CAC AGT ACG A	155 bp
	Reverse	GCT GGG CAA GTG GTA GTA TCT T	
Gapdh	Forward	TGT GTC CGT CGT GGA TCT GA	77 bp
	Reverse	CCT GCT TCA CCA CCT TCT TGA	
Gfi1	Forward	AAG ACC CTT TGC GTG CGA GAT G	148 bp
	Reverse	ATG TGT GGA CAG CGT GGA TGA C	
Hnrnpa0	Forward	GGC GGC CTC AAT GTG CAG ACG AGT GA	207 bp
	Reverse	CTT CAG CTC CAC CGT GTT GCC GTC CAC	
Il1R (II)	Forward	TGG CCA GGA ATA CAA CAT CAC TAG G	143 bp
	Reverse	GAA ACA CTT TGC ACG GGA CTA TCA	
Irf8 (Icsbp)	Forward	AAG GGC AGG CCC AAC AA	78 bp
	Reverse	CTG CAG CTC TCG GAT GAA CTG	
Maf	Forward	AGC AGT TGG TGA CCA TGT CG	216 bp
	Reverse	TGG AGA TCT CCT GCT TGA GG	
Myc	Forward	CCT CTG CCC GCG ATC AGC TC	118 bp
	Reverse	GAA GTT CAC GTT GAG GGG CAT CGT C	
Nab2	Forward	CGG GAG GGC AAA CAG CTT AGC TT	140 bp
	Reverse	TAG GTG CTC TCT CGG GCT ACT TGT C	
Spi1 (PU.1)	Forward	GGA GAA GCT GAT GGC TTG G	75 bp
	Reverse	CAG GCG AAT CTT TTT CTT GC	
Rn18s	Forward	GCG ATT TGT CTG GTT AAT TCC GAT A	110 bp
	Reverse	AAC GCC ACT TGT CCC TCT AAG AAG	



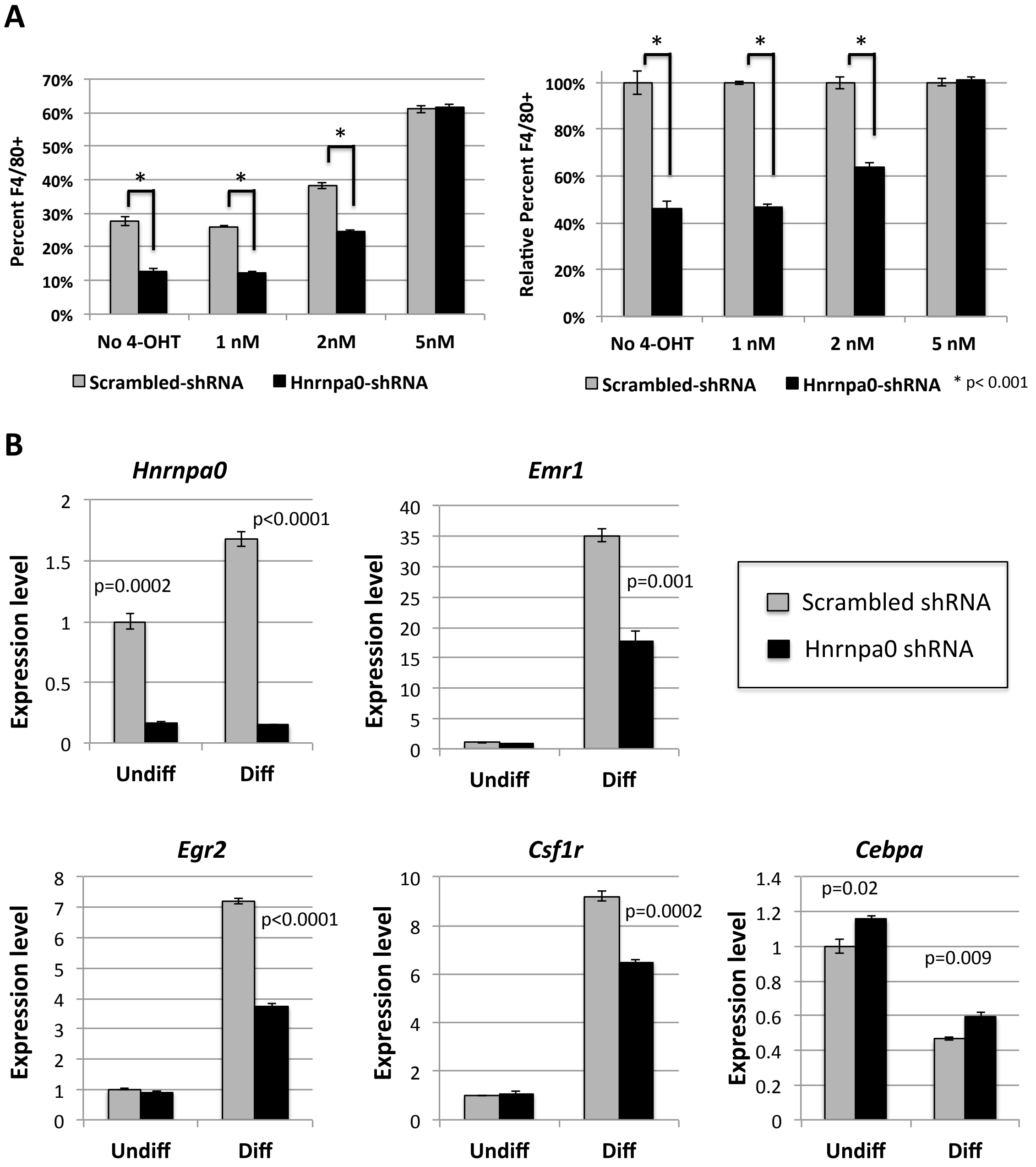
Supplementary Figure S1. Expression profile of *Hnrnpa0* in mouse haematopoietic populations. *Hnrnpa0* expression was measured by RT-PCR in sorted hematopoietic cells from C57BL/6J mice. *Hnrnpa0* expression was normalized against *Rn18s* expression and reported relative to the expression levels found in LSK (Lin$^-$ Sca-1$^+$ Kit$^+$) cells, which includes primitive hematopoietic stem cells that possess the capacity of self-renewal and can give rise to all mature cell types found in the blood. CLP: common lymphoid progenitors (Lin$^-$ Sca-1^{lo} Kit^{lo} IL-7R$^+$) give rise to B and T lineage cells; CMP: common myeloid progenitors (Lin$^-$ Sca-1$^-$ Kit$^+$ CD34$^+$ FcγRIII$^-$) give rise to all myeloid lineages. Shaded areas in different colors indicate various stages of maturation within each lineage. T cell maturation proceeds from a CD4$^-$CD8$^-$ double negative stage, to a CD4$^+$CD8$^+$ double positive stage and then to a mature CD4$^+$ or CD8$^+$ T cell. B cell maturation proceeds from a B220$^+$ CD19$^-$ IgM$^-$ pro-B cell stage, to a B220$^+$ CD19$^+$ IgM$^-$ pre-B cell stage and then to a more mature B220$^+$ CD19$^+$ IgM$^+$ B cell. GMP: granulocyte-monocyte progenitors (Lin$^-$ Sca-1$^-$ Kit$^+$ CD34$^+$ FcγRIII$^+$) give rise to mature Mac1$^+$ Gr1$^+$ myeloid cells; MEP: megakaryocyte-erythroid progenitors (Lin$^-$ Sca-1$^-$ Kit$^+$ CD34$^-$ FcγRIII$^-$) give rise to CD71^{hi} Ter119^{hi} erythroid cells as well as CD41$^+$ megakaryocytes. In all lineages, *Hnrnpa0* expression drops as cells terminally differentiate.



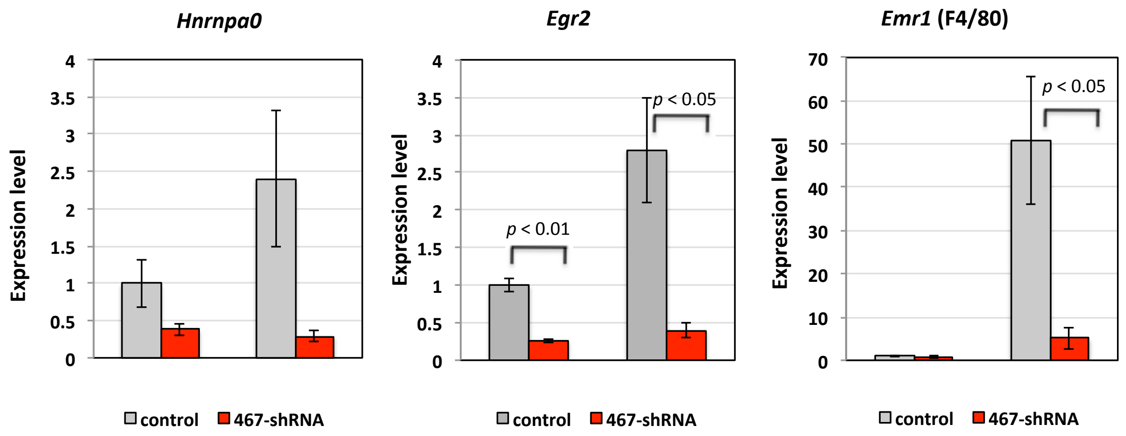
Supplementary Figure S2. PUER cells differentiate into macrophages in a dose-dependent manner. PUER cells were grown with or without different doses of 4-OHT (1 nM, 2 nM, 5 nM, 10 nM, 100 nM) for seven days, and assessed for macrophage differentiation. **A.** The morphology of PUER cells after treatment with differing concentrations of 4-OHT. The cells were grown in the presence or absence of the drug for five days, collected and prepared by cytocentrifuge preparation. The cells were fixed and stained with Wright-Giemsa stain. Beginning after one day of treatment with 4-OHT, the cells were sampled every two days for six days and analyzed by flow cytometry for the expression of the F4/80 macrophage surface marker. **B**. Representative flow cytometry histogram taken after 5 days of treatment, illustrating the gating used to determine F4/80 positive cells. **C.** Plot of F4/80 analysis. The percentage of cells staining positive for F4/80 is displayed as a function of time from the beginning of treatment. Empty circles indicate cells grown without 4-OHT. Filled symbols indicate cells treated with 4-OHT at the indicated concentrations.



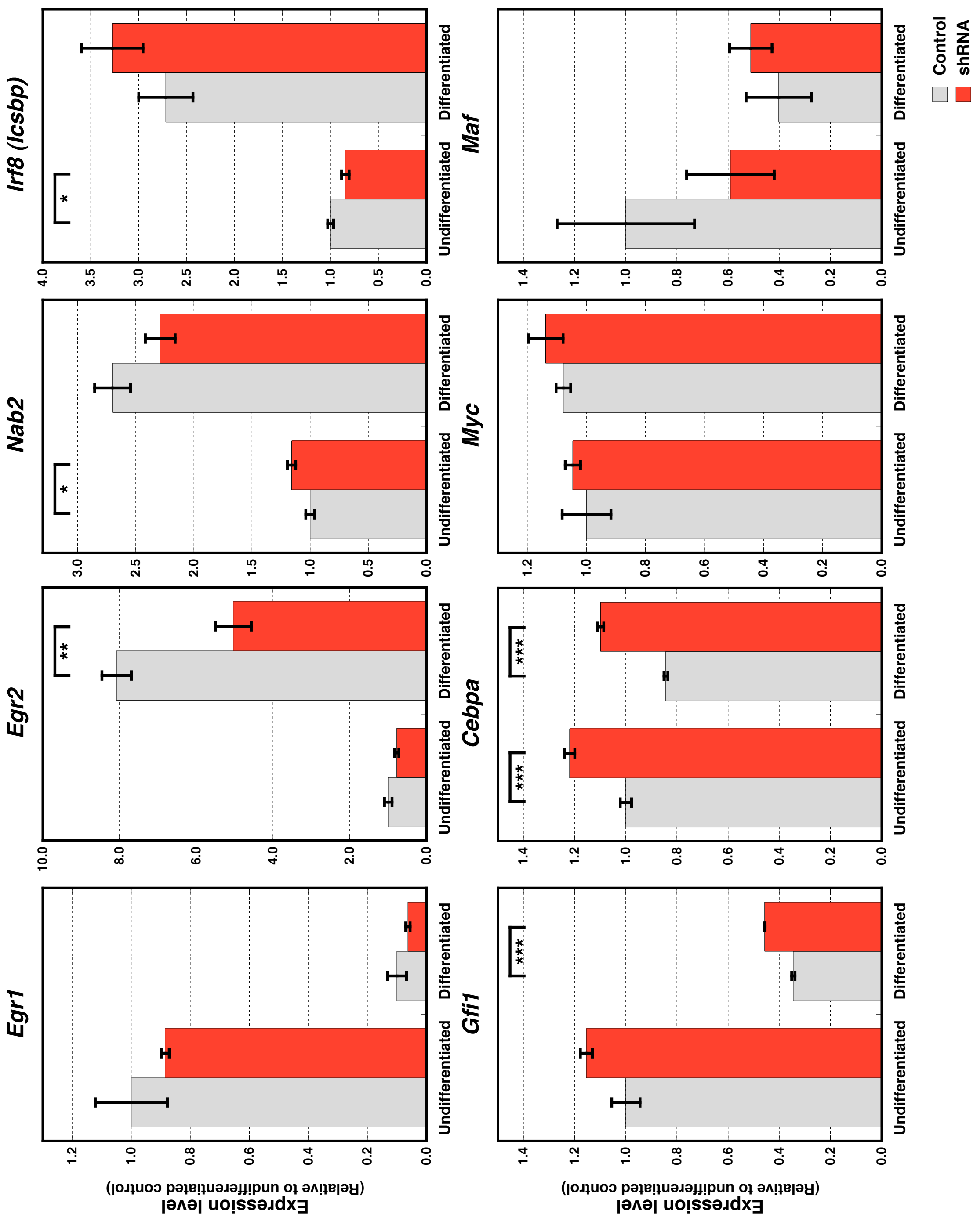
Supplementary Figure S3. Validation of the PUER system prior to microarray analysis. Samples of PUER cells expressing an empty (Control) or *Hnrnpa0* hairpin-expressing (shRNA) retroviral construct were induced to undergo differentiation. The expression of a select group of genes was measured by RT-PCR analysis in undifferentiated (UNDIF) and differentiated (DIF) PUER cells to confirm *Hnrnpa0* KD and induction of differentiation. Gene expression is reported relative to the expression observed in undifferentiated control cells. The average of three independent experiments with standard error of the mean is shown. Significant differences are indicated (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$). There was a comparable induction of *Spi1*/*PU.1* expression upon exposure to 4-OHT (27% increase, $p << 0.0001$) in control and *Hnrnpa0* hairpin-expressing cells, indicating that the phenotype is a consequence of changes to targets other than *Spi1/Pu.1*.



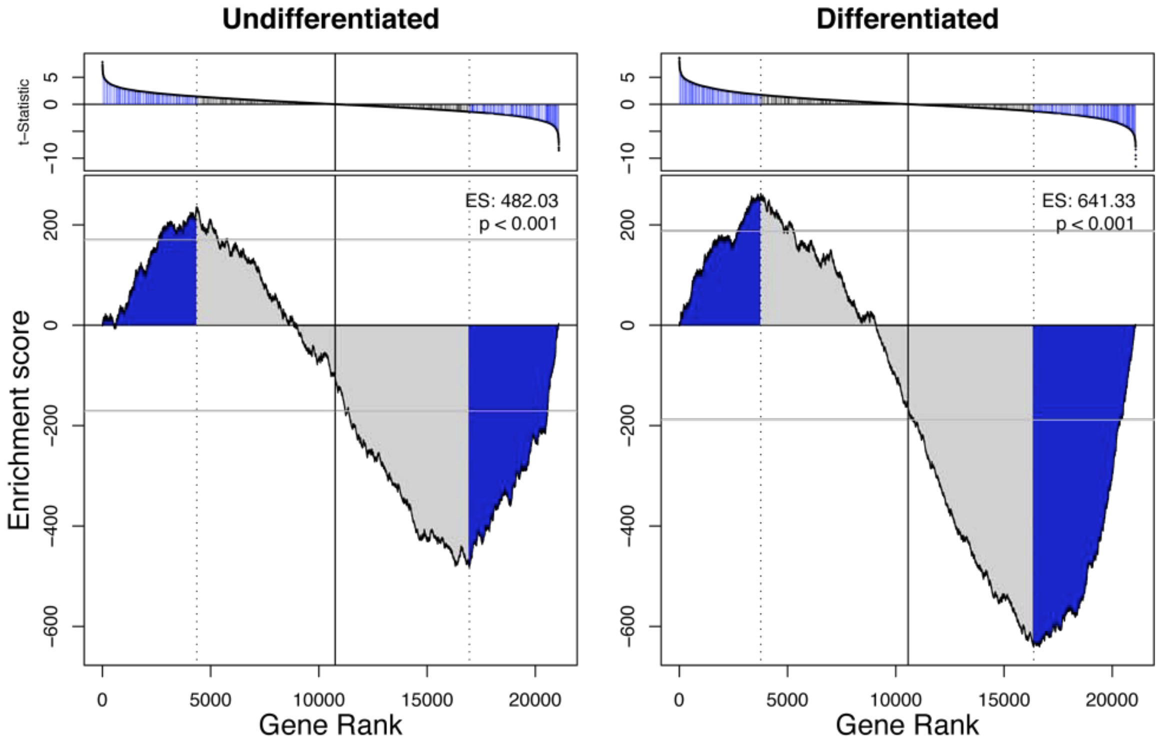
Supplementary Figure S4. Validation of *Hnrnpa0* knockdown using a scrambled shRNA as a control. PUER cells were retrovirally-transduced with either scrambled or *Hnrnpa0* hairpin-expressing (shRNA) vector. PUER cells expressing the two constructs were differentiated using different doses of 4-OHT as indicated. After 4 days of induction, the cells were labeled to detect F4/80 expression (marker of monocytes) and analyzed by flow cytometry. **A.** The histograms depict the percent or fraction of F4/80^{+} cells after *Hnrnpa0* shRNA treatment, relative to the scrambled control. **B.** The expression of a select group of genes was measured by real-time RT-PCR analysis in undifferentiated (Undiff) and differentiated (Diff) PUER cells to confirm *Hnrnpa0* KD and effects upon myeloid lineage specification. Gene expression is reported relative to the expression observed in undifferentiated control cells. The average of three independent experiments with standard error of the mean is shown. Significant differences are indicated.



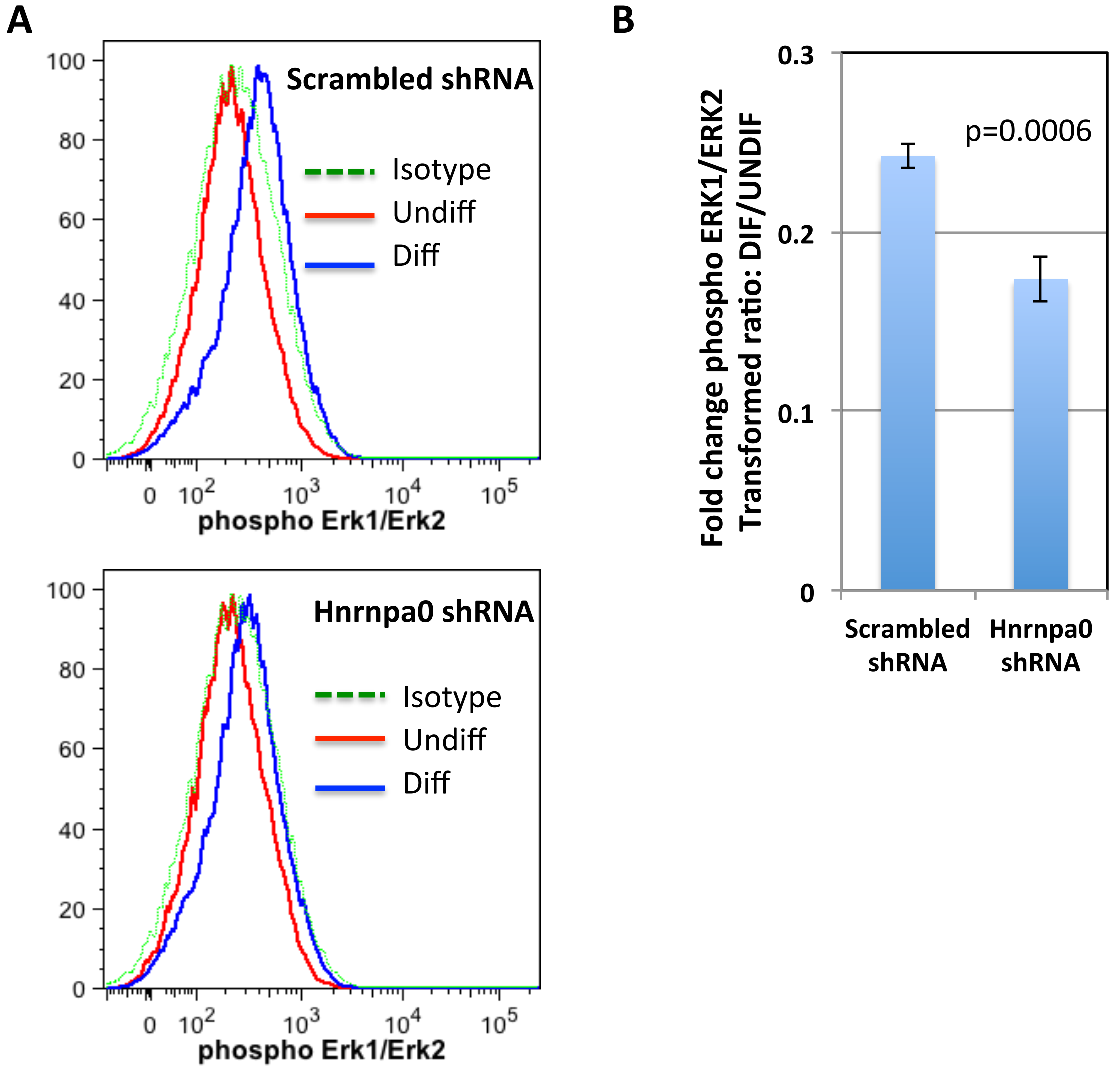
Supplementary Figure S5. Real-time RT-PCR of select myeloid genes after *Hnrnpa0* knockdown using a second shRNA. PUER cells were transduced with a second *Hnrnpa0* shRNA. Gene expression is reported relative to the expression observed in undifferentiated (Undiff) control cells ($n = 3$). Shown is the average of three independent experiments. Bars indicate the standard error of the mean. Significant differences are indicated (Control: empty-vector; 467-shRNA: second hairpin-expressing vector).



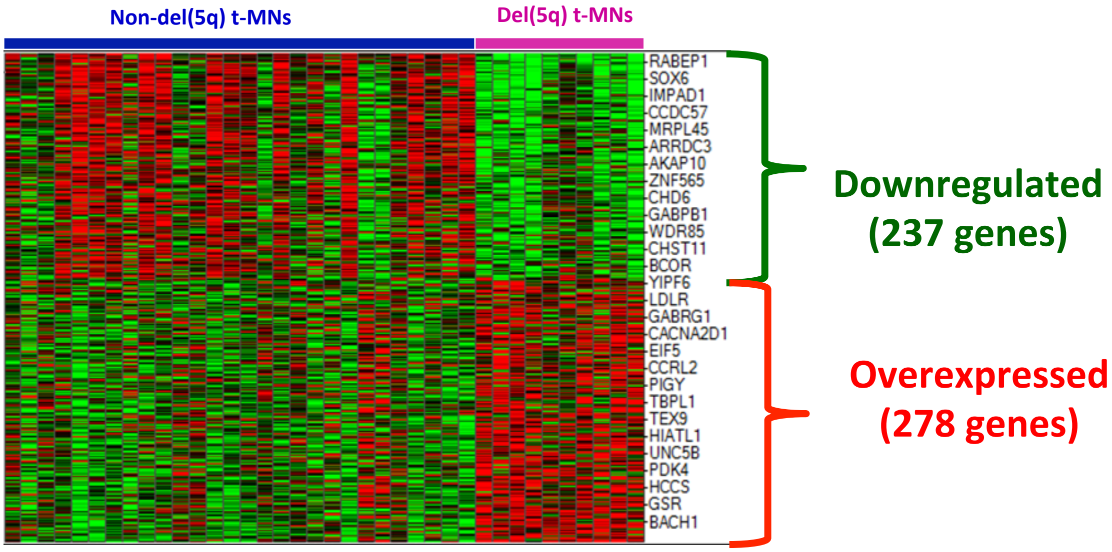
Supplementary Figure S6. Real-time RT-PCR validation of the expression of select myeloid genes in PUER cells. The results of the microarray expression profiling were validated by real-time RT-PCR using cDNA templates prepared from the same RNA samples. Gene expression is reported relative to the expression observed in undifferentiated control cells (*n* = 3). Shown is the average of three independent experiments. Bars indicate the standard error of the mean. Significant differences are indicated (*, $p < 0.05$; **, $p < 0.01$; ***, $p < 0.001$). (Control: empty-vector; shRNA: hairpin-expressing vector)



Supplementary Figure S7. Gene enrichment analysis of AU-rich element-containing genes. All unique transcripts were ranked according the Bayesian modeled *t*-statistic of the fold difference between hairpin-expressing cells and control construct-expressing cells (upper panels). The *t*-statistic is equal in direction and similar in magnitude to the base-2 log-transformed fold change. The enrichment profiles (lower panels) were created by walking along the ranked genes. The score was increased when an ARE-containing gene was encountered and decreased when a non-ARE-containing gene was encountered to create the random walk as plotted. Enrichment is indicated by an upwards deflection of random walk. The size of the increase and decrease was weighted according to the total number of each class gene such that the random walk has an overall displacement of zero. The overall enrichment score is the maximum deviation of the random walk from zero. Significant enrichment was determined by randomly permuting the samples for each gene, re-calculating and re-ranking the modeled *t*-statistic to generate a new enrichment score. 1,000 cycles of permutation were used to generate a null distribution of enrichment scores. The actual enrichment scores were compared to this distribution to determine significance level (one-tailed). The regions in blue indicate the "leading edge": those ARE-containing genes whose enrichment at either end of the distribution lead to the significant enrichment score.



Supplementary Figure S8. Erk1/2 is less activated upon differentiation after *Hnrnpa0* knockdown. PUER cells transduced with *Hnrnpa0* shRNA or scrambled shRNA were induced with 2nM 4-OHT for 48 hours. **A.** Activated Erk1/2 was assessed by phospho-flow cytometric analysis using a phospho-specific Erk1/2 rabbit mAb conjugated to Alexa 647 (Cell Signaling). A non-specific rabbit mAb was used as an isotype control. **B.** To calculate fold change between undifferentiated and differentiated cells, the transformed ratio: $\log_{10}$ (Diff MFI)-$\log_{10}$ (Undiff MFI), where MFI= mean fluorescent intensity was used. Two biological repeats, each done in triplicate were averaged with the standard error of the mean. Erk1/2 was less activated upon differentiation in *Hnrnpa0* shRNA cells than in scrambled shRNA PUER cells (p=0.006).



Supplementary Figure S9. Gene expression signature of AU-rich genes in del(5q) vs. other t-MNs. Significantly (FDR<0.3) differentially expressed genes (515 genes) are shown. A partial list of genes with greatest fold difference is shown. Please refer to Table S4 for the complete list of genes.