Supplementary Information

Mediation analysis reveals common mechanisms of RUNX1 point mutations and
RUNX1/RUNX1T1 fusions influencing survival of patients with acute myeloid leukemia

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**Details on the procedure followed to test for mediation effects**

In order to adjust for the (possibly) confounding variables sex, age, and cytogenetics, we considered these variables as baseline covariates, both in the regression model that relates the mediator to the exposure and in the regression model that relates survival to the mediator (see Lange and Hansen\(^1\) for details on these two models). The influences of exposure and mediators were modeled time-independent, because the estimation of time-independent influences is generally much more robust as opposed to the estimation of time-dependent influences. The robustness of the time-independent model is associated with a greater power of the corresponding tests. The advantage of time-dependent effects that the true dependencies can be better rendered is important for descriptive analyses, but less in this analysis in which the greater power achieved from using time-independent effects is much more important. We used the simulation approach by Lange and Hansen\(^1\) to calculate \(p\) values. This approach is more accurate than the less computationally intensive alternative presented in the same paper that uses a delta rule approximation.

**Pre-selection data sets and validation data sets**

As validation data set, for all three comparisons we chose AMLCG Cohort 1. For the comparison t(8;21)+ vs. t(8;21)- we used the HOVON as pre-selection data set. The AMLCG Cohort 1 data had 17,389 gene expression variables that were all contained in the HOVON data set, the latter having 19,204 gene expression variables. Thus we used the 17,389 gene expression variables common to both data sets for this comparison. For both, the \(RUNX1^+\) vs. \(RUNX1^-\) and t(8;21)+ vs. \(RUNX1^{++}\) comparison we combined the TCGA and the AMLCG Cohort 2 data set to obtain a pre-selection data set. After combining the two data sets, ComBat\(^2\) was used to remove batch effects. Combining the data sets enabled us to use a much larger sample size for the pre-selection. Here, 13,808 gene expression variables appeared both in the pre-selection data set as well as in the AMLCG Cohort 1 data set. Consequently, these 13,808 gene expression variables were used in the respective comparisons. The combined pre-selection data set is referred to as “AMLCG Cohort 2 with TCGA”. We note that combining different data sets for analysis, as performed in our analysis in the cases of the preselections for the comparisons \(RUNX1^+\) vs. \(RUNX1^-\) and t(8;21)+ vs. \(RUNX1^{++}\), can lead to less precise results than if using a single data set of the same size as the combined data set. In the case of the comparison t(8;21)+ vs. t(8;21)- a large (single) data set, the HOVON data set, was available for the pre-selection, which is why, for this comparison, we did not deem it necessary to use a combined data set.
Mediation analysis for the t(8;21)++ vs. RUNX1++ comparison of genes used in LSC17

The LSC17 is a prognostic score for AML patients that features 17 genes\(^3\). It seems interesting to study, whether some of these genes show indications for mediation activity with respect to the t(8;21)++ vs. RUNX1++ comparison. In the main analysis presented in the paper, we were not able to identify any candidates for mediator genes in this direct comparison of RUNX1 point mutations and RUNX1/RUNX1T1 fusions. As also stated in the paper, the latter can likely be explained by the limited sample size available for that comparison.

In this supplementary section, we present the results of an additional mediation analysis in which we only considered genes that are featured in LSC17. This restriction to only a few promising genes greatly alleviates the multiple testing problem in comparison to the main analysis. Due to this restriction, only a small number of \(p\) values have to be adjusted for multiple testing instead of – as in the main analysis - hundreds of \(p\) values. Moreover, given the prognostic power of LSC17, it seems much more likely that there are mediator genes among the genes considered in this prognostic score than among genes for which there is no known (strong) relation to the outcome of AML patients. Given the small number of considered genes and the small sample size in this analysis, we did not use a part of the data for pre-selecting promising genes here. Instead, we combined the data sets AMLCG Cohort 1 and AMLCG Cohort 2 with TCGA to a single data set in order to increase the statistical power of the analysis. Again, ComBat was used to remove batch effects between these two data sets. This combined data set featured 16 of the 17 genes considered in LSC17. Using the combined data, each of these 16 genes was tested for mediation activity with respect to the t(8;21)++ vs. RUNX1++ comparison. For this task, the testing framework by Lange and Hansen was employed in exactly the same way as described in section ‘Definition of mediator effects and testing procedure’ of the paper. The \(p\) values from these tests were again adjusted for multiple comparisons using the Benjamini-Hochberg procedure. The results are presented in Supplementary Table S3. Three of the 16 genes show a
statistically significant mediation activity in this analysis: \textit{GPR56}, \textit{KIAA0125}, and \textit{NGFRAP1}. Also in the main analysis presented in the paper, \textit{KIAA0125} was among the three genes identified as candidates for mediation activity with respect to \(t(8;21)^{++}\) vs. \textit{RUNX1}^{++}. The other two of the three genes discussed in the paper, \textit{CD109} and \textit{HOPX}, were not considered in the current analysis, because these two genes are not among the 16 genes from LSC17 studied here.

Summarizing, by considering a more robust analysis flow in this supplementary subsection, we were able to identify two further genes that are promising with respect to mediation activity for the comparison \(t(8;21)^{++}\) vs. \textit{RUNX1}^{++}. Note, however, that we used the same data sets, AMLCG Cohort 1 and AMLCG Cohort 2 with TCGA, for this analysis as for the main analysis. Thus, there is a higher danger that the results obtained from this analysis are over-optimistic than there would be, if we would have had independent data available for this second analysis.
### Supplementary Tables

| Variable    | BH-adjusted p value | Variable    | BH-adjusted p value |
|-------------|---------------------|-------------|---------------------|
| FAM92A1     | <0.001              | ADRM1       | 0.031               |
| FADS1       | <0.001              | ATP13A2     | 0.034               |
| PHGDH       | 0.001               | CALCRL     | 0.035               |
| **CD109**   | 0.001               | ADRBK1     | 0.035               |
| GALNT12     | 0.001               | KDELC1     | 0.035               |
| GPR56       | 0.001               | C16orf93   | 0.035               |
| CLU         | 0.001               | MBTPS1     | 0.035               |
| DDIT4       | 0.001               | ZNF334     | 0.035               |
| B3GNT1      | 0.001               | SCHIP1     | 0.035               |
| NGFRAP1     | 0.002               | SEL1L3     | 0.035               |
| DOCK1       | 0.002               | BEX2       | 0.035               |
| NRBP1       | 0.003               | GOLGA8A    | 0.036               |
| SH3BP4      | 0.003               | IGF2BP3    | 0.037               |
| IRX1        | 0.003               | TPK1       | 0.037               |
| WBP5        | 0.003               | BIVM       | 0.037               |
| **KIAA0125**| 0.003               | NYNRIN     | 0.037               |
| SYNJ2       | 0.004               | MPO        | 0.037               |
| F12         | 0.007               | PCTP       | 0.037               |
| DLC1        | 0.007               | NCRNA00205 | 0.037               |
| HDAC4       | 0.010               | HTR1F      | 0.038               |
| MICALL2     | 0.011               | CYB5A      | 0.038               |
| DNMT3B      | 0.011               | RFTN1      | 0.038               |
| ZC3H12C     | 0.013               | TRAT1      | 0.040               |
| HOPX        | 0.017               | TSC22D4    | 0.040               |
| Variable       | BH-adjusted p value | Variable       | BH-adjusted p value |
|----------------|---------------------|----------------|---------------------|
| GPR114         | 0.017               | CCNG2          | 0.042               |
| GC18M052797_at | 0.017               | RAB27A         | 0.042               |
| TANC1          | 0.018               | YPEL2          | 0.042               |
| ACOT7          | 0.019               | TMEM163        | 0.042               |
| TM4SF1         | 0.026               | WDR54          | 0.043               |
| MMRN1          | 0.026               | PCCA           | 0.043               |
| ALDH2          | 0.026               | PYGB           | 0.043               |
| ARHGAP22       | 0.027               | KIAA1274       | 0.044               |
| SAP30L         | 0.028               | HMGN5          | 0.048               |
| HOMER3         | 0.028               | KCTD15         | 0.048               |

**Supplementary Table S1:** Significant mediator genes for the comparison t(8;21)+ vs. t(8;21)-
Genes which also appear in Supplementary Table S2 are printed in bold.
| Variable      | BH-adjusted $p$ value |
|---------------|-----------------------|
| C10orf58      | <0.001                |
| BEND4         | 0.001                 |
| CD109         | 0.002                 |
| SCRN1         | 0.005                 |
| IFITM3        | 0.015                 |
| KIAA0125      | 0.015                 |
| SLITRK5       | 0.020                 |
| HOPX          | 0.022                 |
| CHRDLD1       | 0.036                 |
| FAM171B       | 0.038                 |
| FHL1          | 0.038                 |
| CCDC85C       | 0.040                 |

**Supplementary Table S2: Significant mediator genes for the comparison $RUNX1^+$ vs. $RUNX1^-$**

Genes which also appear in Supplementary Table S1 are printed in bold.
| Variable      | BH-adjusted p value |
|---------------|---------------------|
| **GPR56**     | 0.040               |
| **KIAA0125**  | 0.040               |
| **NGFRAP1**   | 0.040               |
| **DPYSL3**    | 0.081               |
| **MMRN1**     | 0.081               |
| **NYNRIN**    | 0.210               |
| **ARHGAP22**  | 0.673               |
| **DNMT3B**    | 0.693               |
| **CDK6**      | 0.795               |
| **EMP1**      | 0.795               |
| **SOCS2**     | 0.795               |
| **AKR1C3**    | 0.979               |
| **CD34**      | 0.979               |
| **LAPTM4B**   | 0.979               |
| **ZBTB46**    | 0.979               |
| **CPXM1**     | 0.992               |

**Supplementary Table S3:** Results of the additional mediation analysis performed for the comparison t(8;21)++ vs. RUNX1++ in which only LSC17 genes were considered. Genes with significant results are printed in bold.
Supplementary Table S4: Results of univariate Cox proportional hazards regression analyses using AMLCG Cohort 1 Note that we do not report p values here, because these genes were determined to be significant mediators and mediators influence the outcome by definition.

| Gene    | Hazard ratio | Harrel’s concordance index |
|---------|--------------|----------------------------|
| CD109   | 1.312        | 0.587                      |
| KIAA0125| 1.281        | 0.552                      |
| HOPX    | 1.259        | 0.556                      |
Supplementary Figure S1: Reasons for exclusion of patients

**AMLCG Cohort 1**
- 488 patients
- Exclusion of missing information on t(8;21)
- 471 patients
- Exclusion of missing information on RUNX1
- 469 patients

**HOVON**
- 462 patients
- Exclusion of missing information on survival
- 461 patients

**TCGA**
- 179 patients
- Exclusion of missing information on cytogenetics
- 151 patients
- Exclusion of patients with non-intensive induction treatment
- 109 patients
- Exclusion of missing information on survival
- 100 patients

**AMLCG Cohort 2**
- 260 patients
- Exclusion of missing information on t(8;21)
- 252 patients
Supplementary Figure S2: Heatmap of the genes selected for comparison $t(8;21)^+$ vs. $t(8;21)^-$ (data set HOVON) The heatmap shows the expression values of each of the genes selected for comparison $t(8;21)^+$ vs. $t(8;21)^-$ for each sample in data set HOVON with $t(8;21)^-$. The genes are in the rows and the observations are in the columns. The dendrogram on the left hand side shows the result of agglomerative hierarchical clustering using the Euclidian distance and complete linkage, where the dendrogram was reordered based on the mean expression values of the genes. The genes that were selected both from the comparison $t(8;21)^+$ vs. $t(8;21)^-$ and from the comparison $RUNX1^+$ vs. $RUNX1^-$ are marked in red on the left margin.
Supplementary Figure S3: Heatmap of the genes selected for comparison t(8;21)+ vs. t(8;21)- (data set AMLCG Cohort 1) The heatmap shows the expression values of each of the genes selected for comparison t(8;21)+ vs. t(8;21)- for each sample in data set AMLCG Cohort 1 with t(8;21)- and at the same time RUNX1-. The genes are in the rows and the observations are in the columns. The dendrogram on the left hand side shows the result of agglomerative hierarchical clustering using the Euclidian distance and complete linkage, where the dendrogram was reordered based on the mean expression values of the genes. The genes that were selected both from the comparison t(8;21)+ vs. t(8;21)- and from the comparison RUNX1+ vs. RUNX1- are marked in red on the left margin.
Supplementary Figure S4: Heatmap of the genes selected for comparison *RUNX1*+ vs. *RUNX1*-
(data set AMLCG Cohort 2 with TCGA) The heatmap shows the expression values of each of the
genes selected for comparison *RUNX1*+ vs. *RUNX1*- for each sample in data set AMLCG Cohort 2
with TCGA with t(8;21)- and at the same time *RUNX1*-. The genes are in the rows and the
observations are in the columns. The dendrogram on the left hand side shows the result of
agglomerative hierarchical clustering using the Euclidian distance and complete linkage, where the
dendrogram was reordered based on the mean expression values of the genes. The genes that were
selected both from the comparison t(8;21)+ vs. t(8;21)- and from the comparison *RUNX1*+ vs. *RUNX1*-
are marked in red on the left margin.
Supplementary Figure S5: Heatmap of the genes selected for comparison \textit{RUNX1+} vs. \textit{RUNX1-} (data set AMLCG Cohort 1) The heatmap shows the expression values of each of the genes selected for comparison \textit{RUNX1+} vs. \textit{RUNX1-} for each sample in data set AMLCG Cohort 1 with t(8;21)- and at the same time \textit{RUNX1-}. The genes are in the rows and the observations are in the columns. The dendrogram on the left hand side shows the result of agglomerative hierarchical clustering using the Euclidian distance and complete linkage, where the dendrogram was reordered based on the mean expression values of the genes. The genes that were selected both from the comparison t(8;21)+ vs. t(8;21)- and from the comparison \textit{RUNX1+} vs. \textit{RUNX1-} are marked in red on the left margin.
**Supplementary Figure S6: RUNX1- with t(8;21)-: Survival differences between patients with high and low gene expression values**

Each subplot shows the Kaplan Meier curves of patients with expression values higher/lower than the median expression value for one of the three genes selected both from the comparison t(8;21)+ vs. t(8;21)- and from the comparison RUNX1+ vs. RUNX1-. In each case one of the data sets AMLCG Cohort 2 with TCGA and AMLCG Cohort 1 was used. For this plot only patients without RUNX1 mutations and without a RUNX1 fusion (t(8;21)-) were considered. The medians were in all cases taken across the data sets AMLCG Cohort 2 with TCGA and AMLCG Cohort 1. Censorings are indicated as plus signs in the subplots. The p values are the results of log-rank tests used to test for survival differences between the two groups associated with the respective Kaplan Meier curves.
Supplementary Figure S7: Validation cohort: standardized RPKM values for the three genes selected as mediators both for the RUNX1+ vs. RUNX1- comparison and the t(8;21)+ vs. t(8;21)- comparison. Standardized RPKM values in validation cohort for the three genes that appear in both, Supplementary Table S1 and Supplementary Table S2, separated by whether only mutations (RUNX1+), only fusion (t(8;21)+) or neither of these two (RUNX1- and t(8;21)-) are present in the respective patients. The p values are the results of Wilcoxon tests. For each gene, we tested ‘RUNX1+’ against ‘RUNX1- and t(8;21)-’ and ‘t(8;21)+’ against ‘RUNX1- and t(8;21)-’.

Supplementary Figure S8: Validation cohort: patients with RUNX1- and t(8;21)-: Survival differences between patients with high and low gene expression values. Each subplot shows the Kaplan Meier curves of patients in the validation cohort with expression values higher/lower than the median expression value for one of the three genes selected both from the comparison t(8;21)+ vs. t(8;21)- and from the comparison RUNX1+ vs. RUNX1-. For this plot only patients without RUNX1 mutations and without a RUNX1 fusion (t(8;21)-) were considered. Censorings are indicated as plus signs in the subplots. The p values are the results of log-rank tests used to test for survival differences between the two groups associated with the respective Kaplan Meier curves.
References

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List of genes pre-selected for the comparison t(8;21)++ vs. RUNX1++ together with corresponding (unadjusted) p values obtained in the pre-selection

| Variable | p value from pre-selection analysis |
|----------|-------------------------------------|
| PPCDC    | 0.000588                            |
| PDIA3    | 0.000678                            |
| ABCA2    | 0.000954                            |
| PTGES    | 0.001043                            |
| MAPRE1   | 0.001254                            |
| GALNT7   | 0.001277                            |
| HTRA3    | 0.001481                            |
| LMO4     | 0.001893                            |
| NRIP3    | 0.001941                            |
| FAM125B  | 0.002256                            |
| HTT      | 0.002778                            |
| SLITRK5  | 0.002834                            |
| BTBD11   | 0.003208                            |
| ANKRD39  | 0.004207                            |
| GALR3    | 0.004363                            |
| LPHN1    | 0.004394                            |
| PDIA6    | 0.004416                            |
| CBX6     | 0.004488                            |
| SCN8A    | 0.004839                            |
| CATSPERG | 0.004884                            |
| BEX2     | 0.005852                            |
| MAFG     | 0.005943                            |
| MGAT3    | 0.006255                            |
| CD59     | 0.006481                            |
| PGM2     | 0.006783                            |
| RAB4A    | 0.007271                            |
| MED12L   | 0.007618                            |
| SLC48A1  | 0.007703                            |
| ARHGAP5  | 0.007916                            |
| DLAT     | 0.007923                            |
| EPB49    | 0.008318                            |
| MLLT6    | 0.008384                            |
| KIAA0182 | 0.008736                            |
| RPAP2    | 0.008783                            |
| SLC25A37 | 0.008911                            |
| SLC24A6  | 0.008973                            |
| HOXA9    | 0.009422                            |
| CLCN2    | 0.009432                            |
| Gene          | Value   |
|--------------|---------|
| ST6GALNAC3   | 0.009711|
| HSP90B1      | 0.010094|
| TUFT1        | 0.010294|
| KLHDC8A      | 0.010402|
| CHST12       | 0.010407|
| CTNNBL1      | 0.010429|
| SETBP1       | 0.010894|
| C9orf142     | 0.010925|
| PANX2        | 0.01105  |
| OSGIN1       | 0.011146|
| DPPA4        | 0.01115  |
| NGFRAP1      | 0.011466|
| DPYSL3       | 0.011651|
| C21orf63     | 0.011683|
| NYNRIN       | 0.011686|
| NAPA         | 0.011809|
| TRIM2        | 0.012051|
| SLC25A13     | 0.012054|
| SLC9A5       | 0.012107|
| SLC45A4      | 0.01212  |
| ANKH         | 0.012508|
| ARHGAP31     | 0.012684|
| MRS2         | 0.012724|
| ST6GALNAC4   | 0.012863|
| GRK6         | 0.012878|
| LTBP3        | 0.013008|
| SYNJ2        | 0.013061|
| IGF2R        | 0.013256|
| DVL3         | 0.013382|
| BEND4        | 0.013591|
| SLC6A8       | 0.013636|
| TTTY14       | 0.013771|
| NPDC1        | 0.01386  |
| WNK1         | 0.01437  |
| EIF3A        | 0.014429|
| SLC6A9       | 0.014945|
| ABCB6        | 0.015081|
| PAPSS1       | 0.015163|
| FAM169A      | 0.015398|
| PHF2         | 0.015472|
| PAFAH1B1     | 0.015606|
| TSPAN32      | 0.015721|
| SNAP23       | 0.015949|
| PVRL1        | 0.015979|
| HDAC5        | 0.016157|
| SWAP70       | 0.016194|
| MMRN1        | 0.016336|
| Gene  | Value  |
|-------|--------|
| PDE8B | 0.016714 |
| PHKA1 | 0.016845 |
| PAWR  | 0.016983 |
| ANKMY2| 0.017478 |
| SEPT11| 0.017498 |
| SPRED2| 0.01752  |
| C1QTNF6| 0.017549 |
| DNAH10| 0.017919 |
| PHGDH | 0.018195 |
| GNPNAT1| 0.018515 |
| CDC123| 0.018671 |
| TSN   | 0.018675 |
| CDKL5 | 0.019006 |
| ADH5  | 0.019059 |
| C1QBP | 0.019068 |
| OPTN  | 0.019204 |
| BZW2  | 0.019736 |
| PMM1  | 0.019999 |
| FUT7  | 0.020124 |
| YWHAE | 0.020402 |
| RASSF7| 0.020695 |
| NFKBID| 0.020781 |
| C7orf50| 0.020819 |
| FGFRL1| 0.020947 |
| ANK1  | 0.021499 |
| PINK1 | 0.022045 |
| TWSG1 | 0.022057 |
| BMPR2 | 0.022116 |
| C9orf103| 0.022151 |
| GPN3  | 0.022332 |
| TMCC2 | 0.022469 |
| IPO11 | 0.022491 |
| GFI1B | 0.022497 |
| CPNE8 | 0.023057 |
| GPATCH8| 0.023262 |
| TIA1  | 0.023358 |
| CCT2  | 0.023428 |
| ITPR3 | 0.023692 |
| ULK1  | 0.023926 |
| NOTCH1| 0.023972 |
| MAGED1| 0.024448 |
| ZNF135| 0.024541 |
| PTPN1 | 0.024653 |
| HAT1  | 0.024854 |
| SHROOM4| 0.024913 |
| FAM160A1| 0.025083 |
| CCND3 | 0.025144 |
| Gene    | Value   |
|---------|---------|
| RAP1GAP | 0.025221|
| MTM1    | 0.025255|
| PITPNB  | 0.02561 |
| OSBP2   | 0.025643|
| HPCAL1  | 0.025672|
| SLC2A1  | 0.025681|
| GRM2    | 0.025747|
| SLC25A39| 0.026246|
| TM6SF1  | 0.02634 |
| EFNA1   | 0.026531|
| ACVR2A  | 0.026789|
| ANKRD2  | 0.026948|
| PHAX    | 0.027133|
| GPR35   | 0.027157|
| CTXN1   | 0.027213|
| SLC25A24| 0.027333|
| SLC4A1  | 0.027568|
| CTSC    | 0.027676|
| ABCG1   | 0.027828|
| CHST11  | 0.027874|
| MAP6D1  | 0.02788 |
| MTCH1   | 0.027897|
| STAP1   | 0.028266|
| HOPX    | 0.028348|
| FKB1P1B | 0.028377|
| ADARB1  | 0.02859 |
| CLIC2   | 0.028703|
| PIM2    | 0.028802|
| OBSL1   | 0.028946|
| SMOX    | 0.029006|
| KCNA3   | 0.029524|
| PRDX4   | 0.029541|
| F12     | 0.02955 |
| KLC2    | 0.02961 |
| ASB2    | 0.029663|
| PUS7    | 0.029753|
| CHD3    | 0.029772|
| TSPAN17 | 0.029954|
| LARP6   | 0.030141|
| PSTPIP1 | 0.03022 |
| THAP10  | 0.030357|
| CYYR1   | 0.030539|
| ATG4D   | 0.030858|
| ARL1    | 0.030926|
| PRKD2   | 0.031301|
| RNF208  | 0.03143 |
| PDCD4   | 0.03155 |
| Gene      | Score |
|-----------|-------|
| NTSC3L    | 0.031632 |
| BRF1      | 0.031847 |
| TMEM63B   | 0.031868 |
| CUEDC1    | 0.03211 |
| COMMD8    | 0.032142 |
| GRHL1     | 0.03221 |
| TANC1     | 0.032433 |
| DNAJB11   | 0.032514 |
| SPNS3     | 0.032694 |
| FBXO7     | 0.033263 |
| NFE2      | 0.033539 |
| C5orf4    | 0.033607 |
| RG9MTD2   | 0.033671 |
| JOSD2     | 0.033732 |
| ZNF664    | 0.033897 |
| UGT8      | 0.034034 |
| PRDX3     | 0.034198 |
| INF2      | 0.034239 |
| TMOD1     | 0.034318 |
| TRAF4     | 0.034561 |
| ALAS2     | 0.034754 |
| LOC388588 | 0.034865 |
| LYPLA1    | 0.035065 |
| SLC7A5    | 0.035307 |
| NBEAL2    | 0.03534 |
| TP53I11   | 0.035473 |
| TNS1      | 0.035719 |
| POLR1B    | 0.035858 |
| NOL8      | 0.035981 |
| DAB1      | 0.036349 |
| SETMAR    | 0.036533 |
| TFE3      | 0.036618 |
| KBTBD3    | 0.03666 |
| AGPS      | 0.036846 |
| IDS       | 0.037093 |
| CYB5R4    | 0.037245 |
| SPIB      | 0.03731 |
| ZFAND2B   | 0.037348 |
| ELF1      | 0.037412 |
| SELO      | 0.037617 |
| PLEKHM1   | 0.037646 |
| INPP5K    | 0.037736 |
| KLF12     | 0.03795 |
| SERPINB1  | 0.037965 |
| SPSB1     | 0.038111 |
| SDK2      | 0.038162 |
| C5orf56   | 0.038344 |
| Gene      | Value  |
|-----------|--------|
| ABHD10    | 0.039459 |
| YARS2     | 0.039568 |
| RCN1      | 0.03958 |
| ZNF295    | 0.039657 |
| KLHL3     | 0.039682 |
| ANKS6     | 0.039952 |
| RBM38     | 0.040262 |
| MFAP3L    | 0.040313 |
| FAM32A    | 0.040398 |
| FTL       | 0.04047 |
| SLC41A1   | 0.04082 |
| VDAC3     | 0.040864 |
| SPTB      | 0.041069 |
| CSPP1     | 0.041191 |
| CD7       | 0.041467 |
| C10orf10  | 0.041555 |
| TFB2M     | 0.041619 |
| HOXA7     | 0.041683 |
| SPON2     | 0.041688 |
| RFTN1     | 0.041839 |
| TMEM86A   | 0.041862 |
| ERLIN2    | 0.041967 |
| ADAM17    | 0.041991 |
| ZNF85     | 0.042183 |
| RTN1      | 0.042199 |
| CD109     | 0.042824 |
| APOLD1    | 0.042844 |
| ICAM2     | 0.0432 |
| KRTAP5-9  | 0.04328 |
| CAV1      | 0.043486 |
| SFXN4     | 0.043807 |
| SIPA1     | 0.04386 |
| ARID5A    | 0.04403 |
| SPATC1    | 0.044306 |
| SCML1     | 0.044407 |
| MRPL3     | 0.044427 |
| GALNT1    | 0.044544 |
| SLC29A2   | 0.044946 |
| PFKM      | 0.044963 |
| ITGA4     | 0.045045 |
| DMKN      | 0.045152 |
| PRKCZ     | 0.045162 |
| SNX14     | 0.04522 |
| SLC25A28  | 0.045237 |
| C10orf88  | 0.046025 |
| CRBN      | 0.046101 |
| SIAH2     | 0.046297 |
| Gene   | Score  |
|--------|--------|
| ERMAP  | 0.046533 |
| THBD   | 0.046592 |
| ZNFS32 | 0.046641 |
| SCARB2 | 0.046846 |
| EXPH5  | 0.046981 |
| ERCC1  | 0.047007 |
| DEPDC7 | 0.04708  |
| NCOR2  | 0.047087 |
| RHAG   | 0.047222 |
| USF2   | 0.047384 |
| ANKMY1 | 0.047512 |
| NMI    | 0.047668 |
| ID2    | 0.047983 |
| AUTS2  | 0.047986 |
| UGP2   | 0.048065 |
| GLA    | 0.048107 |
| EPS8L2 | 0.048192 |
| SIAE   | 0.048305 |
| HAGH   | 0.048417 |
| RABEP1 | 0.048632 |
| DEDD2  | 0.048647 |
| EMILIN1| 0.048813 |
| YWHAH  | 0.049201 |
| CRISP3 | 0.049338 |
| SEPT9  | 0.049362 |
| GPR108 | 0.049365 |
| PDIA4  | 0.049739 |
| PNPT1  | 0.049918 |
List of genes found to be differentially expressed using limma for the comparison t(8;21)++ vs. *RUNX1*++ together with p values after Benjamini-Hochberg adjustment obtained in the validation analysis

| Variable | p value from validation analysis (using AMLCG Cohort 1) |
|----------|---------------------------------------------------------|
| RUNX1T1  | 1.26E-41                                                |
| POU4F1   | 1.94E-35                                                |
| CAV1     | 6.84E-17                                                |
| PALM     | 8.29E-15                                                |
| ILSRA    | 1.12E-14                                                |
| HYAL3    | 1.95E-14                                                |
| HOXA9    | 1.07E-13                                                |
| TRH      | 1.16E-13                                                |
| LAMAS    | 1.94E-13                                                |
| VOPP1    | 4.78E-13                                                |
| KIAA0125 | 5.41E-13                                                |
| PRAME    | 2.98E-12                                                |
| KDM4B    | 1.42E-11                                                |
| LAT2     | 1.71E-11                                                |
| SIPA1L2  | 2.89E-11                                                |
| GDF11    | 3.23E-11                                                |
| SPINK2   | 3.31E-11                                                |
| HOPX     | 7.07E-11                                                |
| CACNA2D2 | 7.34E-11                                                |
| NTNG2    | 7.34E-11                                                |
| CD19     | 1.73E-10                                                |
| PRKD3    | 1.79E-10                                                |
| LOXL3    | 1.9E-10                                                 |
| NGFRAP1  | 2.33E-10                                                |
| WFDC1    | 3.17E-10                                                |
| CDH26    | 4.37E-10                                                |
| ADRM1    | 5.94E-10                                                |
| SLC28A3  | 8.77E-10                                                |
| SLC25A1  | 1E-09                                                   |
| SSX2IP   | 1.21E-09                                                |
| C15orf39 | 1.28E-09                                                |
| ROBO1    | 1.93E-09                                                |
| SLC24A3  | 2.88E-09                                                |
| WBP5     | 3.78E-09                                                |
| CD38     | 4.79E-09                                                |
| TRAF7    | 4.93E-09                                                |
| Gene      | Expression  |
|-----------|-------------|
| TNS3      | 5.07E-09    |
| SLC5A10   | 5.08E-09    |
| ARHGAP21  | 5.37E-09    |
| ZG16B     | 1.12E-08    |
| MEIS1     | 1.29E-08    |
| SCCPDH    | 1.32E-08    |
| OPTN      | 1.32E-08    |
| STXBPS    | 1.38E-08    |
| GLT25D1   | 1.38E-08    |
| KCNE1L    | 1.5E-08     |
| NAT6      | 1.88E-08    |
| TSPAN32   | 1.88E-08    |
| NIPA1     | 1.88E-08    |
| PPBP      | 1.89E-08    |
| CMTM4     | 2.47E-08    |
| CBX6      | 2.47E-08    |
| PXK       | 2.51E-08    |
| MSI2      | 2.52E-08    |
| VEGFA     | 3.14E-08    |
| HPGDS     | 3.46E-08    |
| STAR      | 3.46E-08    |
| HSPG2     | 3.59E-08    |
| TMEM44    | 3.83E-08    |
| CLIC2     | 3.83E-08    |
| PLTP      | 4.21E-08    |
| PURA      | 5.54E-08    |
| TPK1      | 5.54E-08    |
| USP6NL    | 5.54E-08    |
| CLEC11A   | 6.08E-08    |
| CLEC5A    | 7.03E-08    |
| FNIP2     | 8.29E-08    |
| NIT2      | 8.43E-08    |
| FNDC3B    | 9.7E-08     |
| SLC48A1   | 9.84E-08    |
| KCTD6     | 1.11E-07    |
| IGLL1     | 1.11E-07    |
| HAL       | 1.32E-07    |
| CALR      | 1.4E-07     |
| SHC1      | 1.44E-07    |
| BMPR2     | 1.44E-07    |
| LOC374443 | 1.51E-07    |
| LAMC3     | 1.61E-07    |
| DSE       | 1.77E-07    |
| ADCY7     | 1.98E-07    |
| GPM6B     | 1.98E-07    |
| MAGED2    | 1.98E-07    |
| DAGLB     | 2.29E-07    |
| Gene    | Log2FoldChange |
|---------|----------------|
| CORO2A  | 2.96E-07       |
| HOXB4   | 3.12E-07       |
| PKIG    | 3.27E-07       |
| RWDD2A  | 3.33E-07       |
| DEPDC7  | 3.38E-07       |
| RETN    | 3.48E-07       |
| HYAL2   | 3.82E-07       |
| CD109   | 4.19E-07       |
| ANGPTL6 | 4.2E-07        |
| FBXO21  | 4.21E-07       |
| SRXN1   | 4.21E-07       |
| HOXA3   | 4.43E-07       |
| CD96    | 4.78E-07       |
| PHYHD1  | 4.83E-07       |
| MPO     | 4.97E-07       |
| HOMER3  | 4.97E-07       |
| TIE1    | 5.06E-07       |
| VLDLR   | 5.96E-07       |
| EPCAM   | 6.79E-07       |
| SERPINB1| 7.26E-07       |
| ABCA1   | 7.26E-07       |
| VAT1    | 7.38E-07       |
| ZC3H12C | 8.36E-07       |
| ZNF664  | 8.36E-07       |
| EEF2K   | 8.4E-07        |
| TP53I3  | 8.41E-07       |
| ITGA9   | 9.45E-07       |
| DPY19L3 | 9.45E-07       |
| FBLN5   | 1.02E-06       |
| TPSAB1  | 1.08E-06       |
| IRX1    | 1.09E-06       |
| BTBD11  | 1.14E-06       |
| PON2    | 1.18E-06       |
| CPVL    | 1.21E-06       |
| C16orf93| 1.26E-06       |
| CD36    | 1.34E-06       |
| LPCAT4  | 1.36E-06       |
| ALCAM   | 1.37E-06       |
| CD59    | 1.38E-06       |
| HDAC4   | 1.53E-06       |
| PIAS3   | 1.54E-06       |
| SCHIP1  | 1.74E-06       |
| ALDH2   | 1.81E-06       |
| HOXA7   | 1.82E-06       |
| THBS3   | 1.95E-06       |
| CHIC1   | 1.95E-06       |
| CMTM7   | 2.01E-06       |
| Gene   | Value  |
|--------|--------|
| SCMH1  | 2.04E-06 |
| MLLT3  | 2.12E-06 |
| NXF3   | 2.14E-06 |
| CAMKK2 | 2.14E-06 |
| SLC41A1| 2.15E-06 |
| GPR56  | 2.21E-06 |
| RUNX3  | 2.21E-06 |
| CTNND1 | 2.24E-06 |
| SLC46A3| 2.35E-06 |
| BEX4   | 2.48E-06 |
| P2RX5  | 2.48E-06 |
| DNM1   | 2.8E-06  |
| DHCR7  | 2.83E-06 |
| SRPRB  | 2.87E-06 |
| SLC45A3| 2.88E-06 |
| PTPN7  | 2.9E-06  |
| SGMS1  | 2.9E-06  |
| ACCS   | 3.08E-06 |
| TMEM43 | 3.22E-06 |
| C11orf21| 3.22E-06|
| ACVR1  | 3.31E-06 |
| GALNT2 | 3.56E-06 |
| WIPF3  | 3.68E-06 |
| MAFA   | 3.69E-06 |
| PHF19  | 4.36E-06 |
| PCGF5  | 4.38E-06 |
| IL17RB | 4.43E-06 |
| SYNGR1 | 4.61E-06 |
| NTRK1  | 4.8E-06  |
| ZC3H3  | 5.03E-06 |
| NARFL  | 5.25E-06 |
| CLIP4  | 5.31E-06 |
| LRWD1  | 5.33E-06 |
| ACP5   | 5.33E-06 |
| GPR153 | 5.51E-06 |
| CTNNBL1| 5.52E-06 |
| BEND4  | 5.6E-06  |
| LAIR1  | 5.6E-06  |
| ARHGAP5| 5.6E-06  |
| LFNG   | 5.96E-06 |
| GCLM   | 6.26E-06 |
| PLXNC1 | 6.51E-06 |
| TM6SF1 | 6.51E-06 |
| CRIM1  | 6.65E-06 |
| PF4    | 6.65E-06 |
| SLC12A7| 6.65E-06 |
| CPNE8  | 6.65E-06 |
| Gene       | Log2 Fold Change |
|------------|------------------|
| ZNF238     | 7.01E-06         |
| SDPR       | 7.23E-06         |
| HOXB3      | 7.45E-06         |
| BDH1       | 7.6E-06          |
| EDEM1      | 7.88E-06         |
| ALOX12     | 7.9E-06          |
| GRAMD1A    | 7.9E-06          |
| GSDMD      | 8.42E-06         |
| BLVRB      | 8.46E-06         |
| TMC4       | 8.46E-06         |
| CTSC       | 8.63E-06         |
| CAPRIN2    | 8.63E-06         |
| TMEM216    | 9.35E-06         |
| ATP1B1     | 9.55E-06         |
| SMAD3      | 9.73E-06         |
| DOK1       | 1.07E-05         |
| GSN        | 1.08E-05         |
| HOXB2      | 1.14E-05         |
| PLBD2      | 1.18E-05         |
| SLC25A29   | 1.18E-05         |
| GNB5       | 1.18E-05         |
| EGLN1      | 1.22E-05         |
| ACP6       | 1.3E-05          |
| EDEM2      | 1.3E-05          |
| TM7SF3     | 1.3E-05          |
| F2RL1      | 1.34E-05         |
| POLE       | 1.34E-05         |
| TMEM38B    | 1.4E-05          |
| TUSC1      | 1.42E-05         |
| ESYT1      | 1.42E-05         |
| ASL        | 1.43E-05         |
| TSPAN17    | 1.49E-05         |
| CSF3R      | 1.57E-05         |
| CXXC5      | 1.63E-05         |
| ABCG1      | 1.78E-05         |
| CAV2       | 1.84E-05         |
| C3AR1      | 1.84E-05         |
| TM4SF1     | 1.87E-05         |
| RASSF1     | 2.12E-05         |
| C1QTNF4    | 2.19E-05         |
| NAT14      | 2.44E-05         |
| DNMT3A     | 2.48E-05         |
| TMEM161A   | 2.51E-05         |
| JAZF1      | 2.57E-05         |
| GPR114     | 2.57E-05         |
| SMOX       | 2.61E-05         |
| C6orf192   | 2.71E-05         |
| Gene   | P-Value  |
|--------|----------|
| TTC7B  | 2.72E-05 |
| PGAP2  | 2.95E-05 |
| IFFO2  | 3E-05    |
| SLC18A2| 3.04E-05 |
| CRIP2  | 3.1E-05  |
| ACOT13 | 3.14E-05 |
| WNK1   | 3.34E-05 |
| PRKCH  | 3.57E-05 |
| CLINT1 | 3.58E-05 |
| LPAR5  | 3.58E-05 |
| HEBP1  | 3.58E-05 |
| GF1B   | 3.71E-05 |
| TRIO   | 3.84E-05 |
| CRELD1 | 3.86E-05 |
| TMOD1  | 3.91E-05 |
| DAD1   | 3.93E-05 |
| ANKRD37| 4.12E-05 |
| WWP1   | 4.23E-05 |
| RALGAPA2| 4.24E-05 |
| RBM38  | 4.62E-05 |
| GPR146 | 4.66E-05 |
| ARHGAP12| 4.78E-05 |
| FKB1P1B| 4.79E-05 |
| LPCAT2 | 4.79E-05 |
| EVC2   | 4.86E-05 |
| CHST12 | 4.99E-05 |
| TANC1  | 5E-05    |
| SYNJ2  | 5E-05    |
| SOX15  | 5.02E-05 |
| ANKRD13B| 5.34E-05 |
| FAM92A1| 5.49E-05 |
| SECTM1 | 5.49E-05 |
| XK     | 5.57E-05 |
| C10orf125| 5.57E-05 |
| GANAB  | 5.57E-05 |
| SLC6A8 | 5.66E-05 |
| AEBP1  | 5.8E-05  |
| TUBA1A | 5.8E-05  |
| EFNA1  | 5.8E-05  |
| INTU   | 6.03E-05 |
| PRKAR2B| 6.12E-05 |
| GALNT1 | 6.2E-05  |
| ITPKA  | 6.35E-05 |
| TPPP3  | 6.47E-05 |
| CD300A | 6.51E-05 |
| MXRA7  | 6.58E-05 |
| EPS15L1| 6.58E-05 |
| Gene      | Score  |
|-----------|--------|
| PI4K2A    | 6.8E-05|
| SBF2      | 6.96E-05|
| HOXB5     | 6.97E-05|
| FBXO7     | 7.51E-05|
| CA1       | 7.62E-05|
| ANXA6     | 7.69E-05|
| BEX2      | 7.93E-05|
| ARHGEF6   | 8.14E-05|
| CSRP2     | 8.17E-05|
| GUSB      | 8.17E-05|
| CPXM1     | 8.31E-05|
| EPB49     | 8.35E-05|
| DBN1      | 8.44E-05|
| NOC2L     | 8.66E-05|
| HK2       | 8.77E-05|
| ATP6V1A   | 8.95E-05|
| COMT      | 9.21E-05|
| IGF2BP3   | 9.37E-05|
| MAP4K2    | 9.43E-05|
| AP1B1     | 9.43E-05|
| ZCCHC2    | 9.44E-05|
| PODXL2    | 9.83E-05|
| RXRA      | 9.83E-05|
| PTPN4     | 9.9E-05 |
| C21orf56  | 9.92E-05|
| SLC40A1   | 0.000101|
| SUCNR1    | 0.000101|
| BTK       | 0.000101|
| PTX3      | 0.000102|
| ZCCHC24   | 0.000103|
| HTR1F     | 0.000104|
| LTBP1     | 0.000104|
| TPM1      | 0.000107|
| CD244     | 0.000108|
| ABR       | 0.000108|
| MSLN      | 0.000109|
| C10orf10  | 0.000114|
| HOMER2    | 0.000114|
| SPNS3     | 0.000114|
| MBP       | 0.000114|
| GALNT12   | 0.000117|
| NPHP4     | 0.000117|
| CDK5RAP2  | 0.000118|
| FSCN1     | 0.000118|
| DOCK11    | 0.000118|
| PRMT1     | 0.000121|
| STAP1     | 0.000123|
| Gene   | Score  |
|--------|--------|
| ELANE  | 0.000127|
| CYYR1  | 0.000127|
| PLAU   | 0.000131|
| SNCA   | 0.000132|
| ACVR2A | 0.000134|
| IDS    | 0.000134|
| TSTD1  | 0.000135|
| HOXA5  | 0.000136|
| DHRS3  | 0.000137|
| NPW    | 0.000137|
| LRP3   | 0.000144|
| CTSW   | 0.000147|
| PRTFDC1| 0.000147|
| KLHDC8A| 0.000154|
| FAM46A | 0.000154|
| GALC   | 0.000154|
| MANF   | 0.000156|
| RFXANK | 0.000157|
| EPB42  | 0.000159|
| SMARCA4| 0.000167|
| DVL3   | 0.000167|
| C16orf5| 0.000167|
| PGM2   | 0.000168|
| QPRT   | 0.00017  |
| PCTP   | 0.000172 |
| KIAA0182| 0.000172|
| TUBB1  | 0.000172 |
| KBTBD7 | 0.000181 |
| JUP    | 0.000185 |
| ISYNA1 | 0.000188 |
| HTT    | 0.000192 |
| ABCA5  | 0.000193 |
| RNF187 | 0.000194 |
| TCEAL3 | 0.000194 |
| TKTL1  | 0.000194 |
| PDLIM1 | 0.000194 |
| ATXN1  | 0.000197 |
| KIAA1274| 0.0002  |
| KCNQ5  | 0.000204 |
| CALCRL | 0.000204 |
| CDC47L | 0.000208 |
| RPUSD3 | 0.000213 |
| SH2D3C | 0.000218 |
| TRIM58 | 0.000218 |
| AVEN   | 0.000218 |
| UTY    | 0.000227 |
| FYN    | 0.000229 |
| Gene       | Score  |
|------------|--------|
| DHX33      | 0.000229 |
| PLD1       | 0.000231 |
| CD58       | 0.000232 |
| CLEC2L     | 0.000237 |
| PSMF1      | 0.000238 |
| TMIGD2     | 0.000242 |
| DCBLD1     | 0.000242 |
| CMTM5      | 0.00025  |
| DEF8       | 0.000255 |
| DOCK1      | 0.000257 |
| ARHGEF3    | 0.00026  |
| PGRMC1     | 0.00026  |
| CCDC125    | 0.000262 |
| CYTL1      | 0.000262 |
| CEBPE      | 0.000262 |
| RIN2       | 0.000262 |
| HSP90B1    | 0.000264 |
| VSTM1      | 0.000267 |
| SLC2A1     | 0.00027  |
| ANK1       | 0.00027  |
| NOTCH1     | 0.000275 |
| EMR1       | 0.000278 |
| ZNF652     | 0.000278 |
| SORL1      | 0.000281 |
| USP10      | 0.000286 |
| CD72       | 0.00029  |
| DTX3       | 0.000298 |
| FNDC3A     | 0.000305 |
| SLC35B2    | 0.000308 |
| ITGAE      | 0.000312 |
| CCDC86     | 0.000313 |
| CD84       | 0.000315 |
| SLC44A1    | 0.000319 |
| NME4       | 0.000333 |
| SFXN3      | 0.000334 |
| RHBD1      | 0.000338 |
| BAIIAP3    | 0.000338 |
| IL1RL1     | 0.000343 |
| NUDT13     | 0.000345 |
| PLXNB2     | 0.000349 |
| ITGB4      | 0.000362 |
| LDHA       | 0.000376 |
| AGPS       | 0.000383 |
| FAM125B    | 0.000383 |
| LSP1       | 0.000392 |
| LRP11      | 0.000396 |
| PAPSS1     | 0.000399 |
| Gene   | Value   |
|--------|---------|
| PCNX   | 0.000403|
| L3MBTL4| 0.000409|
| NEDD4L | 0.000416|
| FNBP1  | 0.000424|
| ZEB1   | 0.000424|
| NRBPI  | 0.000426|
| XYLTI  | 0.000426|
| CCDC102A| 0.000428|
| SELENBP1| 0.000436|
| ST6GALNAC4| 0.000436|
| SPTLC2 | 0.000436|
| GPATCH8| 0.000444|
| TSPAN4 | 0.000447|
| UBA1   | 0.000456|
| ZNF711 | 0.000456|
| CYP4F2 | 0.000456|
| IQCE   | 0.000462|
| QSOX1  | 0.000465|
| GABARAPL1| 0.000479|
| TARBP2 | 0.000479|
| NFE2   | 0.000479|
| GPI    | 0.00048 |
| KDM5D  | 0.000487|
| AKAP2  | 0.000488|
| GBE1   | 0.000498|
| PGM3   | 0.000502|
| RAB40C | 0.000517|
| MAPKAPK3| 0.000524|
| KBTBD8 | 0.000524|
| FBXW9  | 0.000525|
| ITGA2B | 0.000531|
| PITPNM2| 0.000538|
| SDCCAG8| 0.000542|
| CAMK2D | 0.000542|
| DLL1   | 0.000542|
| PGD    | 0.000546|
| DUSP7  | 0.000554|
| CHST2  | 0.000554|
| EXT2   | 0.000554|
| ADRA2C | 0.000561|
| NRZF6  | 0.000568|
| PRSS21 | 0.000568|
| ANKH   | 0.000568|
| PDLIM2 | 0.000569|
| GCNT2  | 0.000574|
| ACADSB | 0.000577|
| RHAG   | 0.000585|
| Gene   | P-value |
|--------|---------|
| GATM   | 0.000588|
| HPGD   | 0.000588|
| C11orf63 | 0.000588 |
| HOXB6  | 0.000588|
| PYGB   | 0.000591|
| ARC    | 0.000597|
| C19orf76 | 0.000599 |
| DACT1  | 0.000606|
| ANPEP  | 0.000621|
| FSTL3  | 0.000625|
| PTPN12 | 0.000632|
| AHSP   | 0.000634|
| HEXA   | 0.000645|
| C2orf18| 0.000649|
| WIPF1  | 0.000651|
| SELS   | 0.000652|
| SH2B3  | 0.000655|
| INO80C | 0.000657|
| SPRED1 | 0.000671|
| PPP1R16B | 0.000673 |
| ATP2B4 | 0.000674|
| METRNL | 0.000675|
| IL15   | 0.000679|
| NOTCH2 | 0.000684|
| TNS1   | 0.000684|
| OSGEP  | 0.000684|
| MRS2   | 0.000691|
| KCTD15 | 0.000695|
| FAM169A| 0.000698|
| SIAE   | 0.000698|
| SMYD2  | 0.000708|
| ALAS2  | 0.000713|
| FRMD4B | 0.000722|
| STIM2  | 0.000724|
| BSPRY  | 0.000727|
| SORD   | 0.000731|
| C1orf174 | 0.000736 |
| ZNF804A| 0.000736|
| CCDC92 | 0.000736|
| ARSD   | 0.000758|
| TRIM8  | 0.000775|
| YWHAH  | 0.000784|
| DISC1  | 0.000785|
| MYLK   | 0.000799|
| MTMR1  | 0.000799|
| KCTD5  | 0.000799|
| NUAK2  | 0.000816|
| Gene       | p-value |
|------------|---------|
| UBE2QL1    | 0.000818|
| CHD4       | 0.000829|
| FUT4       | 0.000855|
| E2F7       | 0.000855|
| CPA3       | 0.000857|
| METTL9     | 0.000866|
| NFE2L3     | 0.00087 |
| SH3BP4     | 0.000881|
| ATP13A2    | 0.000915|
| DOPEY1     | 0.000915|
| PCCA       | 0.000924|
| FNBP1L     | 0.000927|
| CPEB4      | 0.000927|
| RASA3      | 0.000927|
| PALLD      | 0.000929|
| KEL        | 0.000929|
| SLC4A1     | 0.000929|
| SPINK4     | 0.000943|
| GCNT1      | 0.00095 |
| HTATIP2    | 0.00095 |
| TSLP       | 0.000973|
| ECHS1      | 0.000976|
| TK2        | 0.000981|
| WASL       | 0.000982|
| DDIT4L     | 0.000994|
| GNA11      | 0.000994|
| FAM60A     | 0.000994|
| C20orf194  | 0.000996|
| RAP1GAP2   | 0.001008|
| KIAA1549   | 0.001017|
| PLXDC2     | 0.001017|
| C12orf29   | 0.001017|
| AHCY       | 0.001027|
| ALAS1      | 0.001032|
| MED12      | 0.001053|
| KLF11      | 0.001084|
| PTPN1      | 0.001096|
| GTF3C5     | 0.001128|
| IGSF1      | 0.001128|
| VASN       | 0.001128|
| CEACAM4    | 0.001128|
| PAWR       | 0.001131|
| NCAM1      | 0.001151|
| TBC1D1     | 0.001167|
| SEL1L3     | 0.001169|
| FHDC1      | 0.001173|
| FGD6       | 0.001173|
| Gene   | Value  |
|--------|--------|
| DSG2   | 0.001173 |
| ALS2   | 0.001195 |
| TRIM6  | 0.001199 |
| MYCT1  | 0.001214 |
| UBP1   | 0.001217 |
| MEST   | 0.001224 |
| SH3TC1 | 0.001236 |
| LYPLA1 | 0.001236 |
| SIDT2  | 0.001236 |
| SLCO4A1| 0.001236 |
| C9orf25| 0.001237 |
| DDIT4  | 0.001237 |
| UBE2F  | 0.001247 |
| OSBPL3 | 0.00127  |
| ASGR2  | 0.00127  |
| TNFRSF1B| 0.001278 |
| MTL5   | 0.001311 |
| PIGB   | 0.001326 |
| HEMK1  | 0.001332 |
| LPIN1  | 0.001341 |
| GBGT1  | 0.001342 |
| PRKCZ  | 0.001342 |
| FAM159A| 0.001342 |
| MYL4   | 0.001351 |
| MAFB   | 0.001365 |
| MAN1A1 | 0.001386 |
| MYH10  | 0.001411 |
| FBXO3  | 0.001418 |
| SNAP23 | 0.001434 |
| MAPRE1 | 0.001482 |
| HMBS   | 0.001502 |
| HSF5   | 0.001502 |
| ADD2   | 0.001503 |
| KCNK17 | 0.001503 |
| NOD2   | 0.001503 |
| CDCA7  | 0.001533 |
| DUSP28 | 0.001533 |
| HAGH   | 0.001549 |
| BCL3   | 0.001568 |
| PANX2  | 0.001575 |
| SLC22A18| 0.001613 |
| MLEC   | 0.001613 |
| EMR2   | 0.001627 |
| ABCB6  | 0.001631 |
| CNN3   | 0.001634 |
| ERMAP  | 0.00166  |
| BCL2L11| 0.001687 |
| Gene   | Value  |
|--------|--------|
| IKZF2  | 0.001691 |
| MEX3A  | 0.001703 |
| TXNIP  | 0.001723 |
| RTCD1  | 0.001727 |
| RMND5B | 0.001727 |
| SIGLECP3 | 0.00178 |
| BCR    | 0.001785 |
| TMEM158 | 0.001805 |
| ZYG11B | 0.001809 |
| RAB5B  | 0.001849 |
| FAM81A | 0.001896 |
| ZBTB38 | 0.001897 |
| C1orf186 | 0.001898 |
| CASP2 | 0.001949 |
| FAM129B | 0.001954 |
| PLIN2  | 0.001955 |
| Pdia6  | 0.001965 |
| SFXN4  | 0.001965 |
| LYSMD4 | 0.001974 |
| MICAL2 | 0.001984 |
| CCT2   | 0.002032 |
| TRAK2  | 0.002059 |
| DLC1   | 0.002077 |
| ARRB1  | 0.002077 |
| PEA15  | 0.002111 |
| CCDC109B | 0.002122 |
| H2AFJ  | 0.002139 |
| LCMT1  | 0.002139 |
| ID2    | 0.002141 |
| MAP3K14 | 0.002141 |
| SYTL4  | 0.002146 |
| EGFL7  | 0.002148 |
| TXLNA  | 0.002163 |
| RCN1   | 0.002163 |
| SPTB   | 0.002192 |
| CLU    | 0.002197 |
| IFNAR2 | 0.002197 |
| CECR6  | 0.002197 |
| ZCCHC6 | 0.002198 |
| FRMD4A | 0.002202 |
| C5orf25 | 0.002226 |
| ADAMTS4L4 | 0.002267 |
| SMARCD2 | 0.002272 |
| NCEH1  | 0.002272 |
| ARL4C  | 0.002337 |
| LAG3   | 0.002354 |
| AKT3   | 0.002378 |
| Gene      | Score |
|-----------|-------|
| GLIS3     | 0.002378 |
| MST4      | 0.002378 |
| ZNF518A   | 0.002411 |
| TGFB1     | 0.002411 |
| STXBP1    | 0.00242 |
| PIM2      | 0.00242 |
| SAP3OL    | 0.002434 |
| GDPDS     | 0.002441 |
| DOPEY2    | 0.002441 |
| ORAI2     | 0.002446 |
| ZFY       | 0.00246 |
| KPTN      | 0.00248 |
| DPPA4     | 0.002492 |
| LMO4      | 0.002504 |
| UGP2      | 0.00253 |
| LAPTM5    | 0.002544 |
| ARFGAP2   | 0.002557 |
| RCBTB1    | 0.002581 |
| LTBP3     | 0.002588 |
| ANGPT1    | 0.002626 |
| C14orf101 | 0.002677 |
| LPPR3     | 0.002677 |
| MAN1B1    | 0.002699 |
| EFHC2     | 0.002712 |
| DNAJB11   | 0.002727 |
| INPP5J    | 0.002745 |
| IRF8      | 0.00277 |
| C5orf4    | 0.002776 |
| COPG2     | 0.002786 |
| F11R      | 0.002807 |
| ACSM3     | 0.002812 |
| CDAN1     | 0.002822 |
| SKP2      | 0.00283 |
| E2F2      | 0.002858 |
| SNX9      | 0.002866 |
| ZBTB42    | 0.002882 |
| SLC23A2   | 0.002887 |
| SETBP1    | 0.002971 |
| SLC22A16  | 0.002992 |
| ALS2CL    | 0.003024 |
| CPNE7     | 0.003024 |
| TBXA2R    | 0.003024 |
| RFTN1     | 0.003028 |
| PMP22     | 0.003028 |
| MMRN1     | 0.003037 |
| MEIS2     | 0.003063 |
| LPHN1     | 0.003081 |
| Gene   | Value |
|--------|-------|
| OLIG1  | 0.003084 |
| PPAP2A | 0.003094 |
| PRR5L  | 0.003108 |
| JAM3   | 0.003117 |
| TBL1X  | 0.003119 |
| MED21  | 0.003172 |
| PTPRM  | 0.0032  |
| CLCN3  | 0.003229 |
| PDIA4  | 0.003295 |
| TREX1  | 0.003298 |
| KIAA1211 | 0.003313 |
| TNFRSF4| 0.003343 |
| TMEM163| 0.003364 |
| SGSH   | 0.003364 |
| CDKN2C | 0.003439 |
| MTMR9  | 0.003465 |
| DFFB   | 0.003491 |
| C9orf72| 0.003491 |
| TUBB6  | 0.003542 |
| CYP1B1 | 0.003557 |
| FAM82A1| 0.003557 |
| MTHFD1L| 0.003557 |
| C9orf9 | 0.003557 |
| ELK3   | 0.003561 |
| KAT2B  | 0.003625 |
| LOC642852| 0.003688 |
| SORBS3 | 0.003706 |
| FBXL19 | 0.003712 |
| TMEM150A| 0.003742 |
| BZW2   | 0.003763 |
| DDOST  | 0.003833 |
| SMARCC1| 0.00384 |
| CALU   | 0.003842 |
| ATG4D  | 0.003842 |
| PROS1  | 0.003866 |
| THOC5  | 0.003866 |
| CEP135 | 0.003868 |
| FAM54B | 0.00387 |
| CYTH4  | 0.00387 |
| C6orf162| 0.003883 |
| HERPUD2| 0.003901 |
| PORCN  | 0.003901 |
| S100A16| 0.00392 |
| RERE   | 0.003947 |
| FXYD6  | 0.003951 |
| DPYS1L2| 0.00396 |
| ULK1   | 0.003963 |
| Gene     | p-value   |
|----------|-----------|
| SLC23A1  | 0.003974  |
| ANXA5    | 0.003977  |
| CCM2     | 0.003996  |
| ARNTL    | 0.004034  |
| CHST10   | 0.004038  |
| SLC16A7  | 0.004058  |
| DOK3     | 0.004138  |
| NEFH     | 0.004164  |
| FAM53C   | 0.004181  |
| SLC25A37 | 0.004203  |
| B3GNT1   | 0.004255  |
| TMCC2    | 0.004307  |
| SH3BP5   | 0.004313  |
| KIAA1598 | 0.00439   |
| NT5DC3   | 0.004426  |
| MED12L   | 0.004435  |
| TCF3     | 0.004435  |
| PLIN3    | 0.004435  |
| ZNF135   | 0.004479  |
| MCCC1    | 0.004494  |
| PBX3     | 0.004494  |
| MAGED1   | 0.004494  |
| MLLT1    | 0.004548  |
| IGSF10   | 0.004602  |
| PES1     | 0.004632  |
| NPDC1    | 0.004647  |
| CHN2     | 0.00468   |
| STK32B   | 0.004699  |
| HYOU1    | 0.00474   |
| PPCDC    | 0.00474   |
| C1QBP    | 0.00474   |
| ZNF662   | 0.004758  |
| RUVBL2   | 0.004758  |
| IQSEC1   | 0.004796  |
| MRPL44   | 0.004805  |
| MMS19    | 0.004844  |
| CERCAM   | 0.004853  |
| DDX3Y    | 0.004853  |
| ETS2     | 0.004853  |
| CCDC6    | 0.004901  |
| FAF1     | 0.004917  |
| CSNK1E   | 0.004917  |
| C9orf40  | 0.004928  |
| PPIP5K2  | 0.004936  |
| LRRC34   | 0.004959  |
| SYNE2    | 0.004997  |
| PTGR1    | 0.005012  |
| Gene    | Probability |
|---------|-------------|
| LARP6   | 0.00504     |
| DDAH1   | 0.005069    |
| SPP1    | 0.005094    |
| BCL7A   | 0.005094    |
| NINJ1   | 0.005097    |
| ELF4    | 0.005097    |
| ADAMTS3 | 0.005114    |
| LAMB2   | 0.005148    |
| PADI2   | 0.005154    |
| TTL4    | 0.005154    |
| ACOX2   | 0.005156    |
| ATP6V0A1| 0.005166    |
| FARSA   | 0.00518     |
| SLC39A8 | 0.005364    |
| KLHDC3  | 0.005364    |
| RAP1GAP | 0.005377    |
| TOB2    | 0.005377    |
| DNAJB6  | 0.0054      |
| GPR183  | 0.005432    |
| TNFAIP2 | 0.005457    |
| TUBG2   | 0.005483    |
| RWDD1   | 0.005519    |
| DLL3    | 0.005608    |
| KIAA0226| 0.005611    |
| C7orf58 | 0.005635    |
| TES     | 0.005704    |
| IL6R    | 0.005712    |
| MAP7    | 0.005728    |
| ZNF184  | 0.005798    |
| CYB5R4  | 0.005822    |
| SELL    | 0.005829    |
| AGPAT9  | 0.005829    |
| PHKA1   | 0.005909    |
| CCND3   | 0.005973    |
| NME1    | 0.005976    |
| ANKLE2  | 0.006007    |
| MRPL1   | 0.006052    |
| ZMYM4   | 0.006072    |
| RUNDC3A | 0.006072    |
| LGALS3  | 0.006157    |
| TMEM2   | 0.006195    |
| LGALS2  | 0.006353    |
| ALDH1A1 | 0.006396    |
| ICA1    | 0.006413    |
| DLGAP3  | 0.006426    |
| EIF3A   | 0.006456    |
| ARHGEF7 | 0.006499    |
| Gene  | Value |
|-------|-------|
| OBSL1 | 0.006574 |
| PRDM1 | 0.006685 |
| GDF15 | 0.006693 |
| SLC7A5 | 0.006716 |
| Pdia3 | 0.00672 |
| F3 | 0.006747 |
| HNRNPF | 0.006835 |
| UX51 | 0.006852 |
| Ncald | 0.006863 |
| STK24 | 0.006924 |
| PINK1 | 0.006935 |
| SLC6A19 | 0.007068 |
| ALDH18A1 | 0.007068 |
| TMEM50B | 0.007068 |
| E2F8 | 0.007178 |
| TSPAN31 | 0.00719 |
| RASD1 | 0.007216 |
| SLC25A39 | 0.007216 |
| TMEM88 | 0.007243 |
| TDRKH | 0.007253 |
| BAG3 | 0.007446 |
| GNA12 | 0.007456 |
| TET1 | 0.00754 |
| APEX1 | 0.00754 |
| SDSL | 0.007719 |
| FBXO15 | 0.007833 |
| EIF4E3 | 0.00787 |
| ARMCX2 | 0.007903 |
| CBR3 | 0.007904 |
| PDRG1 | 0.007947 |
| ZNF318 | 0.007985 |
| HCFC2 | 0.00799 |
| PRDM16 | 0.008001 |
| ITFG3 | 0.008001 |
| SMAD7 | 0.008007 |
| UNG | 0.008009 |
| ZNF574 | 0.008009 |
| OSBP2 | 0.008009 |
| CYR61 | 0.008123 |
| CABLES2 | 0.008153 |
| JHDM1D | 0.008155 |
| USP9Y | 0.008177 |
| MATN2 | 0.008245 |
| SLITRK5 | 0.008276 |
| AP152 | 0.00828 |
| GNGT2 | 0.008306 |
| EMILIN1 | 0.008309 |
| Gene      | Score |
|-----------|-------|
| CREB3L2   | 0.008309 |
| HEPACAM2  | 0.008313 |
| SLC43A3   | 0.008337 |
| KIAA0247  | 0.008368 |
| HMGAA2    | 0.008479 |
| CDK2AP1   | 0.008484 |
| CCNJ      | 0.008537 |
| MRPL3     | 0.008545 |
| PLAGL1    | 0.008545 |
| NACC2     | 0.008545 |
| ABI3      | 0.008545 |
| TNFRSF10B | 0.008550 |
| BCAR3     | 0.008605 |
| GAS2L1    | 0.008605 |
| KIAA0090  | 0.008624 |
| PPARD     | 0.008632 |
| ME1       | 0.008675 |
| SLC9A6    | 0.008701 |
| PELI1     | 0.008969 |
| SNX24     | 0.008996 |
| EVPL      | 0.009021 |
| PARP3     | 0.009046 |
| PITPNA    | 0.009046 |
| C19orfJ51 | 0.009046 |
| F12       | 0.009051 |
| BRP44     | 0.009204 |
| SPON1     | 0.009274 |
| PDCD4     | 0.009290 |
| KIAA1383  | 0.009311 |
| LRRG42    | 0.009384 |
| SDC2      | 0.009384 |
| FAM131A   | 0.009467 |
| MTCH1     | 0.009467 |
| WDR35     | 0.009505 |
| HEXB      | 0.009505 |
| MACROD2   | 0.009672 |
| NTN1      | 0.009694 |
| NECAB3    | 0.009806 |
| PRNP      | 0.009816 |
| ZNF786    | 0.009827 |
| DEK       | 0.009853 |
| INPP5D    | 0.009936 |
| TSKS      | 0.009950 |
| NEGR1     | 0.010026 |
| SLC9A9    | 0.010151 |
| CCNG2     | 0.010158 |
| SMPDL3A   | 0.010363 |
| Gene     | Log2 Fold Change |
|----------|------------------|
| COCH     | 0.010363         |
| ATP1B2   | 0.01037          |
| SOX4     | 0.01038          |
| EXOG     | 0.010407         |
| DACH1    | 0.01044          |
| GTF2H4   | 0.010469         |
| HDAC1    | 0.010489         |
| TUFT1    | 0.010489         |
| AAK1     | 0.010602         |
| ANKRD35  | 0.010694         |
| MARCKSL1 | 0.010709         |
| AASS     | 0.010737         |
| CUL7     | 0.010784         |
| CR1L     | 0.010832         |
| GAS2L3   | 0.010865         |
| GTSF1    | 0.010923         |
| NBN      | 0.010991         |
| FAM69B   | 0.011125         |
| ADARB1   | 0.011189         |
| LRRC32   | 0.011211         |
| KIAA0020 | 0.011387         |
| DECR2    | 0.011493         |
| SNAI1    | 0.011493         |
| CAPG     | 0.011616         |
| TXNDC5   | 0.011741         |
| COBLL1   | 0.011754         |
| SRPK1    | 0.011754         |
| PNMT     | 0.011801         |
| RBM47    | 0.011931         |
| RAPGEOF | 0.012055         |
| STAT5A   | 0.012056         |
| TRAF3IP2 | 0.012211         |
| SLC6A9   | 0.012275         |
| C9orf89  | 0.012305         |
| LAYN     | 0.012405         |
| CCDC24   | 0.012513         |
| APOI3    | 0.012552         |
| HSDL1    | 0.012584         |
| TRIM46   | 0.012613         |
| PRKD2    | 0.012693         |
| CALML4   | 0.012735         |
| YARS2    | 0.012891         |
| ALPK3    | 0.012927         |
| TMEM25   | 0.013065         |
| MN1      | 0.013066         |
| TMCO3    | 0.013179         |
| RHOH     | 0.013188         |
| Gene      | Score   |
|-----------|---------|
| CDK9      | 0.013188|
| DFNA5     | 0.013244|
| KCNA3     | 0.013341|
| DPYSL3    | 0.013341|
| RPS6KL1   | 0.013341|
| P2RX4     | 0.013381|
| SLC16A6   | 0.013386|
| CBFA2T3   | 0.013403|
| PTK2      | 0.013452|
| C21orf7   | 0.013467|
| MRPS24    | 0.013479|
| SLC26A11  | 0.013579|
| LOC388588 | 0.013732|
| TMEM65    | 0.013911|
| CASZ1     | 0.013924|
| TARS      | 0.013984|
| SPRYD4    | 0.014076|
| MCAM      | 0.014105|
| FAM20C    | 0.014167|
| FBP1      | 0.014222|
| PDGFA     | 0.014222|
| NCOR2     | 0.014303|
| GLB1L     | 0.014303|
| KRI1      | 0.014303|
| PYCR1     | 0.014353|
| BCL2      | 0.014475|
| BPGM      | 0.014516|
| GRAMD3    | 0.014536|
| ELMO1     | 0.014605|
| MYB       | 0.014621|
| KDM1A     | 0.014635|
| SLC25A42  | 0.014635|
| DNAJB2    | 0.014688|
| LSM14B    | 0.01477 |
| CLCN5     | 0.01479 |
| TUBA4B    | 0.014809|
| CERK      | 0.014849|
| FZD2      | 0.014883|
| TPCN1     | 0.015036|
| CDC123    | 0.01521 |
| MYO1C     | 0.015264|
| LOC146880 | 0.015266|
| CD320     | 0.015313|
| MPEG1     | 0.015331|
| SLC25A24  | 0.015537|
| TOP1MT    | 0.015539|
| VAMP2     | 0.015607|
| Gene     | Value  |
|----------|--------|
| TNFSF14  | 0.015607 |
| SETDB2   | 0.015649 |
| DCAF12   | 0.015769 |
| MBTPS1   | 0.015811 |
| RAB33A   | 0.01584  |
| COMMD8   | 0.015849 |
| SAMD8    | 0.015859 |
| N4BP2L1  | 0.015933 |
| FAM40B   | 0.015989 |
| KIAA0664 | 0.016004 |
| PRKCE    | 0.01601  |
| KLRG2    | 0.016116 |
| AR       | 0.016207 |
| PIP4K2A  | 0.016272 |
| VWF      | 0.016291 |
| ULBP2    | 0.016354 |
| TRIM62   | 0.01636  |
| LDLRAP1  | 0.01636  |
| PTPLAD1  | 0.016437 |
| ITGA4    | 0.016519 |
| CDK4     | 0.016663 |
| SLC20A1  | 0.016905 |
| PSD3     | 0.016934 |
| KIAA0556 | 0.016956 |
| KCNJ2    | 0.017019 |
| AIFM2    | 0.017063 |
| PLEKHM1  | 0.017067 |
| HMGN3    | 0.0172   |
| LARP1    | 0.017261 |
| PPFIBP2  | 0.017261 |
| GCDH     | 0.017538 |
| CDK6     | 0.017666 |
| LITAF    | 0.017724 |
| HTR7     | 0.017794 |
| BTG2     | 0.017897 |
| DNAJC12  | 0.017927 |
| ADM      | 0.017992 |
| MYO1F    | 0.018077 |
| MLLT6    | 0.018205 |
| MS4A2    | 0.018659 |
| CDKN2A   | 0.018784 |
| ZBTB16   | 0.018845 |
| SLC29A1  | 0.019083 |
| RLTPR    | 0.019083 |
| RAB40B   | 0.01952  |
| IL12A    | 0.019529 |
| KCTD7    | 0.019539 |
| Gene      | Value  |
|-----------|--------|
| SCARA3    | 0.019712 |
| SH3BP2    | 0.01978 |
| SVIL      | 0.01978 |
| BLNK      | 0.019807 |
| TCTN3     | 0.019834 |
| TICAM1    | 0.01993 |
| GNPDA1    | 0.020247 |
| RABGAP1   | 0.020316 |
| RPAP1     | 0.020389 |
| BASP1     | 0.020425 |
| AOAH      | 0.020445 |
| RAC3      | 0.020469 |
| SLC46A2   | 0.020534 |
| IL11RA    | 0.020546 |
| SLC27A5   | 0.020584 |
| PANK1     | 0.020605 |
| SULF2     | 0.02075 |
| C1orf54   | 0.020948 |
| GF1       | 0.021131 |
| OBFC1     | 0.021131 |
| CLECL1    | 0.021249 |
| SPSB1     | 0.02154 |
| STAB1     | 0.021544 |
| AIF1      | 0.021553 |
| CD48      | 0.02168 |
| RECK      | 0.021739 |
| AARS1D1   | 0.022084 |
| HOXA4     | 0.02211 |
| LCAT      | 0.022142 |
| KDM5B     | 0.022183 |
| FAM70A    | 0.022325 |
| MAP1A     | 0.022337 |
| KCTD12    | 0.022362 |
| DEAF1     | 0.02239 |
| SOD1      | 0.022397 |
| ARHGAP6   | 0.022418 |
| UPK3A     | 0.022422 |
| SLC44A3   | 0.022498 |
| CORO1C    | 0.022568 |
| NMD3      | 0.022703 |
| LDLRAD3   | 0.022888 |
| PAFAH2    | 0.022949 |
| IL10RA    | 0.022986 |
| LTK       | 0.023013 |
| TSC22D2   | 0.023044 |
| SSBP2     | 0.023357 |
| CHST15    | 0.023357 |
| Gene   | Value  |
|--------|--------|
| TRIM38 | 0.023443 |
| LOXHD1 | 0.023461 |
| TMEM111 | 0.023832 |
| NDRG2 | 0.023832 |
| CXCL16 | 0.023878 |
| ARHGEF5 | 0.024163 |
| RAPH1 | 0.02424 |
| PLVP | 0.024418 |
| TFEB | 0.024633 |
| TP53BP1 | 0.024673 |
| TRUB2 | 0.024792 |
| TTTY15 | 0.024797 |
| ART4 | 0.024797 |
| HOXC4 | 0.024807 |
| SEMA4D | 0.024837 |
| COX10 | 0.024914 |
| MMP28 | 0.024949 |
| WDR92 | 0.025063 |
| CD86 | 0.025082 |
| GPC6 | 0.025105 |
| IPO4 | 0.025418 |
| FAM65A | 0.025418 |
| ARHGEF10L | 0.026184 |
| SMARCA2 | 0.026184 |
| ATP5H | 0.026624 |
| C1orf43 | 0.02673 |
| ZCCHC7 | 0.026783 |
| TBC1D12 | 0.027163 |
| TFB2M | 0.027251 |
| YWHAEX | 0.027342 |
| ZNF532 | 0.027342 |
| ITPK1 | 0.027517 |
| CCR5 | 0.027757 |
| PHLDA1 | 0.027791 |
| GTF2IRD1 | 0.028108 |
| NANOS1 | 0.028108 |
| GRIK5 | 0.02814 |
| HES1 | 0.028186 |
| THBD | 0.028407 |
| ACHE | 0.028472 |
| AMFR | 0.028472 |
| GABBR1 | 0.028501 |
| RNF168 | 0.028829 |
| GLMN | 0.028863 |
| SCAMP5 | 0.02908 |
| OGG1 | 0.029097 |
| ABCA2 | 0.02932 |
| Gene   | Score |
|--------|-------|
| ZMYM6  | 0.029569 |
| TNFSF10| 0.029673 |
| CD69   | 0.029673 |
| DSC2   | 0.029874 |
| UBQLN4 | 0.029915 |
| ABHD12B| 0.030026 |
| DENR   | 0.030103 |
| C18orf1| 0.0302  |
| DPM2   | 0.030359 |
| TNFRSF11A| 0.030515 |
| TMEM40 | 0.030613 |
| KIF21A | 0.030613 |
| B4GALT2| 0.030734 |
| MAFG   | 0.030734 |
| CDC42EP1| 0.030842 |
| ST14   | 0.031036 |
| NBEA   | 0.031036 |
| CRHBP  | 0.031138 |
| CARHSP1| 0.03122  |
| PGM2L1 | 0.031262 |
| LRP1   | 0.031292 |
| ATG16L2| 0.031543 |
| LDOC1  | 0.031652 |
| ELAVL4 | 0.031817 |
| NOTCH2NL| 0.031893 |
| EPB41L3| 0.031893 |
| PDZD8  | 0.032158 |
| KLHDC9 | 0.032498 |
| INE1   | 0.032601 |
| ZFYVE9 | 0.032607 |
| SLC05A1| 0.032677 |
| MICALCL| 0.03293  |
| LAX1   | 0.033053 |
| RAB4A  | 0.033053 |
| ACN9   | 0.033067 |
| ABCC3  | 0.033135 |
| GRPEL1 | 0.033176 |
| FAM196A| 0.033339 |
| WSB1   | 0.033493 |
| NYNRIN | 0.033495 |
| NRIP3  | 0.033517 |
| B3GALTL| 0.033883 |
| C21orf63| 0.033883 |
| HIVEP3 | 0.034055 |
| CDKN1B | 0.034055 |
| ERBB2IP| 0.034104 |
| INPP4B | 0.034179 |
| Gene   | Score |
|--------|-------|
| LOC728819 | 0.03463 |
| BEX1 | 0.03463 |
| ZNF419 | 0.03463 |
| CCDC159 | 0.034841 |
| CCDC149 | 0.035029 |
| FKBPI5 | 0.035129 |
| PHF2 | 0.035129 |
| PLCG1 | 0.035129 |
| ZFP36 | 0.035149 |
| LY96 | 0.035305 |
| SAMD13 | 0.035365 |
| TRIM2 | 0.035381 |
| FAM176B | 0.035792 |
| TPP2 | 0.035999 |
| LGSN | 0.036257 |
| MTS51 | 0.036335 |
| GAS6 | 0.036371 |
| KIAA1958 | 0.036472 |
| ANK6 | 0.036743 |
| RPL17 | 0.036779 |
| TMEM102 | 0.036829 |
| HLX | 0.036857 |
| PHF7 | 0.036857 |
| FAM179B | 0.036895 |
| TNFAIP1 | 0.036895 |
| PTRF | 0.036994 |
| ATP10A | 0.037162 |
| MGC12982 | 0.037164 |
| MINA | 0.037679 |
| ZNF334 | 0.037679 |
| MLLT4 | 0.037718 |
| PKIB | 0.037774 |
| XPO6 | 0.037774 |
| ARID5A | 0.037877 |
| SLC25A28 | 0.038128 |
| ZNF597 | 0.038138 |
| BEND6 | 0.038358 |
| HOXA6 | 0.03864 |
| STX12 | 0.038728 |
| NDFIP2 | 0.038761 |
| LOC149134 | 0.038875 |
| C3orf45 | 0.03903 |
| FAM198B | 0.03903 |
| SPATA13 | 0.039381 |
| ARHGEF11 | 0.039562 |
| C20orf29 | 0.039562 |
| ENTPD7 | 0.039602 |
| Gene       | Value   |
|------------|---------|
| HMOX1      | 0.040033|
| TRANK1     | 0.040318|
| LNP1       | 0.04044 |
| MYC        | 0.040569|
| KIAA1462   | 0.040569|
| RPS6KA1    | 0.040613|
| COL5A1     | 0.040613|
| SASH3      | 0.040957|
| FAM101B    | 0.040962|
| TARSL2     | 0.041075|
| NAPSB      | 0.041176|
| TBC1D8     | 0.042136|
| WDR12      | 0.042136|
| COPZ2      | 0.042136|
| ZNF74      | 0.042287|
| HEG1       | 0.042358|
| TRIP10     | 0.042678|
| AFMID      | 0.042881|
| ZFP36L1    | 0.0429  |
| PTPN9      | 0.043366|
| ABCA7      | 0.04338 |
| GGT5       | 0.043545|
| CCDC78     | 0.043552|
| CORO2B     | 0.044141|
| ARHGAP22   | 0.044202|
| TCP11L1    | 0.044563|
| MFNG       | 0.044742|
| NTSC2      | 0.044956|
| NUP93      | 0.045285|
| ABCC1      | 0.04533 |
| LIMD1      | 0.045679|
| HIP1R      | 0.04576 |
| LRRC16A    | 0.045858|
| HPSE       | 0.045948|
| TMEM63B    | 0.045967|
| UCHL1      | 0.046243|
| SIPA1L1    | 0.046262|
| AADAT      | 0.046546|
| DHCR24     | 0.046785|
| ABCC4      | 0.047058|
| NHS        | 0.04707 |
| FADS1      | 0.047266|
| MALT1      | 0.047499|
| ABTB1      | 0.047657|
| UBA6       | 0.047657|
| SLC24A6    | 0.047657|
| ASB12      | 0.047817|
| Gene      | Value   |
|-----------|---------|
| TBC1D13   | 0.048115|
| HSPA5     | 0.048246|
| PDGFC     | 0.048264|
| APOLD1    | 0.048286|
| GALNT7    | 0.048616|
| SKIL      | 0.04866 |
| GLCE      | 0.04866 |
| SEMA3C    | 0.048688|
| MLLT10    | 0.048865|
| RPAIN     | 0.049456|
| CLASP2    | 0.049544|
| TGFBI1I1  | 0.049909|
List of genes used in the over-representation analysis that were significant to significance level 0.10 in the validation analysis of the comparison *RUNX1*+ vs. *RUNX1*- together with the corresponding (unadjusted) $p$ values obtained in the validation analysis

| Variable  | $p$ value from validation analysis (using AMLCG Cohort 1) |
|-----------|--------------------------------------------------------|
| C10orf58  | 1.5E-06                                                |
| BEND4     | 1.53E-05                                               |
| CD109     | 0.000031                                               |
| SCRN1     | 8.67E-05                                               |
| KIAA0125  | 0.0003                                                 |
| IFITM3    | 0.000351                                               |
| SLITRK5   | 0.000551                                               |
| HOPX      | 0.000702                                               |
| CHRDL1    | 0.00129                                                |
| FAM171B   | 0.001593                                               |
| FHL1      | 0.001643                                               |
| CCDC85C   | 0.001881                                               |
| SH3BP4    | 0.002814                                               |
| C21orf63  | 0.003149                                               |
| CYP2E1    | 0.004187                                               |
| H1F0      | 0.004898                                               |
| HMGA2     | 0.005262                                               |
| ARHGEF10  | 0.006078                                               |
| HTR1F     | 0.006274                                               |
| TRPS1     | 0.007286                                               |
| CCNA1     | 0.007855                                               |
| IL12RB2   | 0.009275                                               |
| SEMA3C    | 0.014794                                               |
| ZNF135    | 0.018876                                               |
| CMTCM4    | 0.021011                                               |
| GPR34     | 0.021433                                               |
| FAM169A   | 0.022676                                               |
| KIAA1804  | 0.023177                                               |
| FRMD4B    | 0.023434                                               |
| SLC12A7   | 0.024127                                               |
| KLHL3     | 0.024173                                               |
| USP18     | 0.024434                                               |
| CLCN5     | 0.025957                                               |
| BAI3      | 0.026028                                               |
| OSBPL5    | 0.026974                                               |
| Gene       | Value  |
|------------|--------|
| ACSL3      | 0.02754|
| PIWIL4     | 0.029474|
| RASD1      | 0.035128|
| PLXNC1     | 0.035261|
| LRRC16A    | 0.036575|
| RFTN1      | 0.037568|
| PSRC1      | 0.039053|
| LOC283663  | 0.039097|
| AMOT       | 0.040024|
| HDC        | 0.041078|
| ANKMY2     | 0.042015|
| MLLT3      | 0.04233|
| SLC16A1    | 0.042495|
| PEAR1      | 0.05266|
| IGF2BP3    | 0.055242|
| ADM        | 0.056334|
| COBL       | 0.05785|
| AAK1       | 0.062933|
| ZNF193     | 0.06578|
| FTO        | 0.069394|
| ARHGAP31   | 0.071813|
| ABCG1      | 0.073791|
| MYEF2      | 0.075051|
| SLC41A1    | 0.079714|
| INHBA      | 0.09547|
| KLF9       | 0.096034|
| CDCP1      | 0.096192|
List of genes used in the over-representation analysis that were significant to significance level 0.10 in the validation analysis of the comparison t(8;21)+ vs. t(8;21)- together with the corresponding (unadjusted) \( p \) values obtained in the validation analysis

| Variable    | \( p \) value from validation analysis (using AMLCG Cohort 1) |
|-------------|---------------------------------------------------------------|
| FAM92A1     | 3E-07                                                         |
| FADS1       | 2.4E-06                                                       |
| GALNT12     | 1.17E-05                                                      |
| CD109       | 0.000013                                                      |
| PHGDH       | 1.32E-05                                                      |
| GPR56       | 1.38E-05                                                      |
| DDIT4       | 2.05E-05                                                      |
| B3GNT1      | 2.36E-05                                                      |
| CLU         | 2.54E-05                                                      |
| NGFRAP1     | 3.09E-05                                                      |
| DOCK1       | 3.99E-05                                                      |
| SH3BP4      | 6.19E-05                                                      |
| IRX1        | 6.33E-05                                                      |
| NRBP1       | 0.000066                                                      |
| WBP5        | 8.22E-05                                                      |
| KIAA0125    | 8.89E-05                                                      |
| SYNJ2       | 0.000116                                                      |
| F12         | 0.000196                                                      |
| DLC1        | 0.000202                                                      |
| HDAC4       | 0.000328                                                      |
| MICALL2     | 0.000354                                                      |
| DNMT3B      | 0.000382                                                      |
| ZC3H12C     | 0.000472                                                      |
| GPR114      | 0.000653                                                      |
| HOPX        | 0.000653                                                      |
| GC18M052797\_at | 0.000669                      |
| TANC1       | 0.000769                                                      |
| ACOT7       | 0.000805                                                      |
| MMRN1       | 0.001215                                                      |
| TM4SF1      | 0.001237                                                      |
| ALDH2       | 0.001252                                                      |
| ARHGAP22    | 0.001342                                                      |
| HOMER3      | 0.001414                                                      |
| SAP30L      | 0.001452                                                      |
| ADRM1       | 0.001667                                                      |
| Gene      | P-value  |
|-----------|----------|
| ATP13A2   | 0.001891 |
| CALCRL    | 0.001994 |
| KDELC1    | 0.002079 |
| ZNF334    | 0.002149 |
| ADRBK1    | 0.00215  |
| MBTPS1    | 0.002194 |
| C16orf93  | 0.002224 |
| SCHIP1    | 0.002277 |
| BEX2      | 0.002348 |
| SEL1L3    | 0.002396 |
| GOLGA8A   | 0.002537 |
| IGF2BP3   | 0.002735 |
| PCTP      | 0.002863 |
| BIVM      | 0.002913 |
| TPK1      | 0.002956 |
| NYNRIN    | 0.002968 |
| NCRNA00205| 0.002999 |
| MPO       | 0.003017 |
| CYB5A     | 0.003148 |
| HTR1F     | 0.003168 |
| RFTN1     | 0.00325  |
| TRAT1     | 0.003447 |
| TSC22D4   | 0.003516 |
| CCNG2     | 0.003836 |
| YPEL2     | 0.003849 |
| RAB27A    | 0.00386  |
| TMEM163   | 0.004003 |
| PCCA      | 0.00411  |
| WDR54     | 0.00422  |
| PYGB      | 0.004234 |
| KIAA1274  | 0.004376 |
| HMGN5     | 0.004837 |
| KCTD15    | 0.004962 |
| PRKCZ     | 0.005653 |
| CCDC102A  | 0.005822 |
| SLC25A12  | 0.005867 |
| HOXA9     | 0.005902 |
| TSEN15    | 0.006206 |
| TSPAN2    | 0.006244 |
| C7orf23   | 0.0069   |
| C1orf186  | 0.007715 |
| HAVCR2    | 0.008576 |
| SPATS2L   | 0.008752 |
| ZMIZ1     | 0.008816 |
| RAB40B    | 0.008917 |
| PCNX      | 0.009224 |
| RAB43     | 0.009387 |
| Gene       | Value   |
|------------|---------|
| CUL9       | 0.009712|
| RNF44      | 0.010195|
| RDX        | 0.010657|
| FUT4       | 0.010907|
| CMTM4      | 0.010989|
| DPP9       | 0.011267|
| PLXNC1     | 0.011481|
| FRMD4B     | 0.011514|
| ZNF532     | 0.012205|
| SOLH       | 0.012648|
| MEF2C      | 0.012655|
| RAB5B      | 0.013157|
| VSTM1      | 0.013759|
| P2RX4      | 0.013967|
| NCRNA00173 | 0.013989|
| SH3BP5     | 0.014296|
| CPT1B      | 0.014386|
| CFD        | 0.014626|
| PHKA1      | 0.014888|
| STARD9     | 0.015106|
| TAF1C      | 0.0152  |
| TMEM25     | 0.015291|
| NOTCH1     | 0.0155  |
| INO80C     | 0.015745|
| CHIC1      | 0.016284|
| TMEM38B    | 0.016289|
| GC19P054794_at | 0.016569   |
| RPS6KL1    | 0.017649|
| ARL8A      | 0.017722|
| KPTN       | 0.018534|
| ITPKA      | 0.018739|
| ZC3HAV1    | 0.018852|
| MXRA7      | 0.019704|
| VAV1       | 0.020113|
| SREBF2     | 0.020437|
| NPDC1      | 0.020891|
| CPNE8      | 0.021398|
| MAP7       | 0.02142 |
| HEXA       | 0.021736|
| CDR2       | 0.02223 |
| ATP2B4     | 0.022364|
| RUNX3      | 0.022376|
| GNB5       | 0.022561|
| LAMAS      | 0.022773|
| SNAP47     | 0.024273|
| TXNIP      | 0.024731|
| TSC2       | 0.024971|
| Gene   | Value  |
|--------|--------|
| ZEB1   | 0.024989 |
| STAR   | 0.025573 |
| CD82   | 0.025908 |
| MLX    | 0.026422 |
| TMEM216| 0.026846 |
| HSDL1  | 0.027065 |
| FAM169A| 0.027211 |
| SLC12A7| 0.027524 |
| RNF130 | 0.028187 |
| HERPUD2| 0.028296 |
| DEAF1  | 0.028393 |
| MKNK2  | 0.028701 |
| MAP1A  | 0.029185 |
| PPAP2A | 0.029774 |
| TES    | 0.029914 |
| NRD1   | 0.029939 |
| WHAMML1| 0.029956 |
| ATP11A | 0.030406 |
| ANKS6  | 0.031032 |
| GOLGA8B| 0.031628 |
| LARP1  | 0.033764 |
| COMMD7 | 0.034099 |
| MSI2   | 0.034108 |
| GPR157 | 0.034981 |
| MED12L | 0.035056 |
| AKT3   | 0.035454 |
| AGTPBP1| 0.0356  |
| EDC4   | 0.036809 |
| LPHN1  | 0.037045 |
| PABPC4 | 0.037284 |
| HSF5   | 0.037428 |
| STARD10| 0.038102 |
| CLCN5  | 0.038108 |
| LGSN   | 0.039505 |
| USP45  | 0.039586 |
| SFXN3  | 0.039598 |
| TRIO   | 0.040723 |
| PSMD5  | 0.040883 |
| ETFB   | 0.041513 |
| EI24   | 0.042518 |
| ERMP1  | 0.042574 |
| CTSF   | 0.042703 |
| CRLF3  | 0.043431 |
| TGF1   | 0.045136 |
| OBSL1  | 0.045233 |
| ATL3   | 0.045892 |
| ABCG1  | 0.04659 |
| Gene          | Value   |
|--------------|---------|
| TNNT1        | 0.046813|
| ZNF438       | 0.046832|
| LY6G5C       | 0.048107|
| TSC22D1      | 0.048203|
| SC5DL        | 0.048415|
| GC17M016189_at | 0.04873 |
| ARMCK2       | 0.048768|
| SPP1         | 0.049073|
| CAMKK2       | 0.049337|
| FYCO1        | 0.04953 |
| CCND3        | 0.049906|
| MID1IP1      | 0.050136|
| MAP3K1       | 0.051883|
| CLIP2        | 0.052332|
| AKAP2        | 0.054482|
| FAM100A      | 0.05491 |
| TMEM9        | 0.055033|
| DPPA4        | 0.055653|
| ZNF711       | 0.055849|
| DNM3         | 0.055933|
| PRDM16       | 0.057061|
| VPS28        | 0.057344|
| CD59         | 0.057912|
| ENO2         | 0.058316|
| CLEC12B      | 0.05893 |
| RABGAP1      | 0.058987|
| DCP2         | 0.059096|
| ABCA2        | 0.059188|
| SORBS3       | 0.060154|
| C11orf63     | 0.060297|
| PCGF1        | 0.060377|
| BSDC1        | 0.060389|
| IL7          | 0.061242|
| MARCKSL1     | 0.061864|
| PLSCR3       | 0.062599|
| CALR         | 0.063182|
| CD164        | 0.064037|
| STK10        | 0.064995|
| HARS         | 0.066741|
| TRIP10       | 0.067294|
| COL18A1      | 0.068721|
| CDK12        | 0.068921|
| PRKX         | 0.069385|
| EIF5A2       | 0.06941 |
| LY75         | 0.070135|
| TLR2         | 0.070154|
| TNFRSF4      | 0.07084 |
| Gene   | Expression Value |
|--------|------------------|
| REXO1  | 0.071105         |
| MRPS22 | 0.071235         |
| ESYT1  | 0.071678         |
| RAB27B | 0.072945         |
| DTD1   | 0.073146         |
| LPIN1  | 0.074487         |
| SAMD9  | 0.076723         |
| RASGRP2| 0.081639         |
| PPFIBP1| 0.081791         |
| PDE2A  | 0.082398         |
| GUSB   | 0.082546         |
| EFCAB2 | 0.082922         |
| LCT    | 0.083932         |
| TRAF7  | 0.085182         |
| PTPRA  | 0.085931         |
| RNF8   | 0.08624          |
| MOGS   | 0.086471         |
| SERPING1| 0.086497        |
| TNFSF4 | 0.086749         |
| RNF31  | 0.086831         |
| CNOT8  | 0.086993         |
| GC14P100990_at | 0.087777     |
| ENSG00000227403| 0.089545   |
| SSPN   | 0.090212         |
| PPCDC  | 0.093091         |
| RNASET2| 0.096315         |
| GC11P003833_at | 0.09694     |
| UBE2I  | 0.097697         |
| ANKRD50| 0.099775         |