Supplementary Information for

Translational profiling in childhood acute lymphoblastic leukemia: no evidence for glucocorticoid regulation of mRNA translation.
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Supplementary Figure 1: Distribution of biotypes in pools 1 (left panel) and 3 (middle panel) for the top 1% of genes with the highest relative expression in the corresponding pool compared to the total number of genes on the microarray. A) CEM-C7H2 cell line, ethanol-treated, B) CEM-C7H2 cell line, GC-treated, C) NALM6 cell line, ethanol-treated, D) NALM6 cell line, GC-treated. Table 1 presents a list of all biotypes on the microarray.

Supplementary Figure 2: Comparison of the genes’ relative expressions in pool 3 in EtOH- treated control samples between C7H2 and NALM6 cells. Left: all genes detectable on the Exon microarray, middle: protein coding genes, and right: genes from all other biotypes. The colors of the data points represent the differential expression of a gene between the C7H2 and the NALM6 cell lines, with red and blue indicating higher expression in C7H2 and NALM6 cells, respectively, and white corresponding to same expression in both cell lines.

Supplementary Table 1: Average expression and relative expression in the various pools of all genes detected on the Exon microarray in C7H2 cells. Columns “transcript_id”, “gene_id”, “probe_count”, “gene_name”, “gene_biotyp ete” and “chromosome_name” contain annotations for the respective probe set id on the microarray. Columns “RE.p1”, “RE.p2”, “RE.p3” contain averaged relative expression across the 3 biological replicates of each gene in pools 1, 2 and 3 respectively.
tively. Columns "exprs.p1", "exprs.p2" and "exprs.p3" contain averaged expression of a gene across the 3 biological replicates (log2 scale). Suffix "GC" and "EtOH" indicate the treatment.

**Supplementary Table 2**: Average expression and relative expression in the various pools of all genes detected on the Exon microarray in NALM6 cells. For a description of the content, see Supplementary Table 1.
**GO-analysis on genes with similar translational efficiency**

Genes were sorted based on their translational efficiency and grouped into 5 similar-sized groups of genes. A Gene Ontology (Biological Function) analysis was performed on each of these groups using the complete set of genes as background gene set.

### Enriched processes in both cell lines

| Term                                                                 | Size | Pvalue | Count | Pvalue | Count |
|----------------------------------------------------------------------|------|--------|-------|--------|-------|
| GO:0000398 mRNA splicing, via spliceosome                             | 190  | 0.0000 | 85    | 0.0000 | 88    |
| GO:0000375 RNA splicing, via transesterification reactions            | 195  | 0.0000 | 85    | 0.0000 | 88    |
| GO:0043436 oxoacid metabolic process                                  | 577  | 0.0000 | 207   | 0.0000 | 207   |
| GO:0016671 mRNA metabolic process                                     | 531  | 0.0000 | 175   | 0.0000 | 176   |
| GO:0006396 RNA processing                                             | 573  | 0.0000 | 194   | 0.0000 | 182   |
| GO:0044281 small molecule metabolic process                           | 1226 | 0.0000 | 343   | 0.0000 | 399   |
| GO:0022613 ribonucleoprotein complex biogenesis                       | 215  | 0.0000 | 79    | 0.0000 | 76    |
| GO:0046395 carboxylic acid catabolic process                          | 119  | 0.0000 | 54    | 0.0000 | 51    |
| GO:0002474 antigen processing and presentation of peptide antigen via MHC class I | 74   | 0.0000 | 42    | 0.0000 | 34    |
| GO:0044282 small molecule catabolic process                           | 154  | 0.0000 | 63    | 0.0000 | 60    |
| GO:0002478 antigen processing and presentation of exogenous peptide antigen | 60   | 0.0000 | 37    | 0.0000 | 29    |
| GO:0050878 regulation of body fluid levels                            | 307  | 0.0000 | 106   | 0.0000 | 110   |
| GO:0000084 S phase of mitotic cell cycle                              | 129  | 0.0000 | 52    | 0.0000 | 50    |
| GO:1901606 alpha-amino acid catabolic process                         | 45   | 0.0000 | 23    | 0.0000 | 26    |
| GO:0002479 antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent | 59   | 0.0000 | 36    | 0.0000 | 28    |
| GO:0065200 cellular amino acid metabolic process                      | 198  | 0.0000 | 67    | 0.0000 | 115   |
| GO:0019886 antigen processing and presentation of exogenous peptide antigen via MHC class II | 63   | 0.0000 | 30    | 0.0001 | 30    |
| GO:0016192 vesicle-mediated transport                                 | 551  | 0.0000 | 162   | 0.0001 | 174   |
| GO:0007596 blood coagulation                                          | 265  | 0.0000 | 92    | 0.0001 | 94    |
| GO:0000216 M/G1 transition of mitotic cell cycle                      | 75   | 0.0000 | 35    | 0.0001 | 31    |
| GO:0044248 cellular catabolic process                                 | 1192 | 0.0001 | 318   | 0.0001 | 332   |
| GO:0002504 antigen processing and presentation of peptide or polysaccharide antigen via MHC class II | 65   | 0.0000 | 30    | 0.0001 | 30    |
| GO:0044403 symbiosis, encompassing mutualism through parasitism       | 336  | 0.0000 | 112   | 0.0002 | 107   |
| GO:0009068 aspartate family amino acid catabolic process              | 9    | 0.0000 | 8     | 0.0002 | 7     |
| GO:0019048 virus-host interaction                                     | 304  | 0.0000 | 102   | 0.0001 | 97    |
| GO:0019885 antigen processing and presentation of endogenous peptide antigen via MHC class I | 6    | 0.0000 | 6     | 0.0007 | 6     |
| GO:0019221 cytokine-mediated signaling pathway                        | 201  | 0.0000 | 73    | 0.0003 | 69    |
| GO:0006732 coenzyme metabolic process                                 | 136  | 0.0000 | 53    | 0.0004 | 51    |
| GO:0034097 response to cytokine stimulus                              | 301  | 0.0000 | 104   | 0.0004 | 96    |
| GO:0016643 cellular component organization                            | 2612 | 0.0005 | 642   | 0.0000 | 709   |
| GO:0006221 cellular component disassembly involved in execution phase of apoptosis | 51   | 0.0001 | 24    | 0.0005 | 23    |
| GO:0072524 pyridine-containing compound metabolic process             | 34   | 0.0000 | 19    | 0.0006 | 18    |
| GO:0000278 mitotic cell cycle                                         | 651  | 0.0007 | 179   | 0.0001 | 182   |
| GO:0043555 regulation of translation in response to stress           | 13   | 0.0004 | 9     | 0.0004 | 9     |
| GO:0048205 COPI coating of Golgi vesicle                              | 13   | 0.0004 | 9     | 0.0004 | 9     |
| GO:0019883 antigen processing and presentation of endogenous antigen | 7    | 0.0007 | 6     | 0.0002 | 7     |
| GO:0019882 antigen processing and presentation                        | 79   | 0.0000 | 42    | 0.0009 | 31    |
| GO:0051437 positive regulation of ubiquitin-protein ligase activity involved in mitotic cell cycle | 67   | 0.0000 | 30    | 0.0005 | 27    |
| GO:0033554 cellular response to stress                                 | 913  | 0.0002 | 246   | 0.0008 | 247   |
| GO:0032057 negative regulation of translational initiation in response to stress | 5   | 0.0006 | 5     | 0.0005 | 6     |
| GO:0071702 organic substance transport                                | 1248 | 0.0002 | 328   | 0.0010 | 336   |
| GO:0048194 Golgi vesicle budding                                      | 14   | 0.0009 | 9     | 0.0009 | 9     |

**Supplementary Table 3:** Significantly enriched Biological Process GO-terms in both cell lines; analysis using genes with the highest translational efficiencies in each cell line. "Size": total number of genes annotated to the GO-term, "Size": number of genes from those tested for enrichment that are annotated to the GO-term. Columns with suffix "C" and "N" contain values for C7H2 and NALM6 cells, respectively.
**Supplementary Table 4:** Significantly enriched Biological Process GO-terms in both cell lines; analysis using genes with the lowest translational efficiencies in each cell line. "Size": total number of genes annotated to the GO-term, "Count": number of genes from those tested for enrichment that are annotated to the GO-term. Columns with suffix "C" and "N" contain values for C7H2 and NALM6 cells, respectively.

**Enriched processes in C7H2 cells**

| Term                                                                 | Size  | Pvalue C | Count C | Pvalue N | Count N |
|----------------------------------------------------------------------|-------|----------|---------|----------|---------|
| GO:0009083 viral transcription                                       | 130   | 0.0000   | 51      | 0.0000   | 70      |
| GO:0006415 translational termination                                 | 78    | 0.0000   | 35      | 0.0000   | 59      |
| GO:0006614 SRP-dependent translational protein targeting to membrane | 92    | 0.0000   | 36      | 0.0000   | 59      |
| GO:0027599 establishment of protein localization to endoplasmic reticulum | 94    | 0.0000   | 36      | 0.0000   | 59      |
| GO:0006414 translational elongation                                  | 91    | 0.0000   | 35      | 0.0000   | 59      |
| GO:0034324 protein complex disassembly                               | 121   | 0.0000   | 43      | 0.0000   | 66      |
| GO:0039058 viral infectious cycle                                     | 187   | 0.0000   | 59      | 0.0000   | 82      |
| GO:0006402 mRNA catabolic process                                    | 163   | 0.0000   | 53      | 0.0000   | 78      |
| GO:0006413 translational initiation                                 | 132   | 0.0000   | 44      | 0.0000   | 71      |
| GO:0034267 cellular protein metabolic process                        | 2303  | 0.0001   | 488     | 0.0000   | 522     |
| GO:0033365 protein localization to organelle                          | 398   | 0.0002   | 103     | 0.0000   | 117     |
| GO:0034265 cellular macromolecule catabolic process                  | 590   | 0.0003   | 143     | 0.0000   | 177     |
**Supplementary Table 5:** GO-terms (Biological Process) significantly enriched with genes with the highest translational efficiency in C7H2 cells. 2078 genes were tested against the background gene set of 10344 genes. GO-terms with a single associated gene were excluded.

| Pvalue   | Count | Size | Term                                                   |
|----------|-------|------|--------------------------------------------------------|
| 0.000    | 6     | 7    | positive regulation of cholesterol transport          |
| 0.001    | 11    | 20   | negative regulation of viral genome replication       |

**Supplementary Table 6:** GO-terms (Biological Process) significantly enriched with genes with high translational efficiency in C7H2 cells. 2081 genes were tested against the background gene set of 10344 genes. GO-terms with a single associated gene were excluded.

| Pvalue   | Count | Size | Term                                                   |
|----------|-------|------|--------------------------------------------------------|
| 0.000    | 6     | 6    | regulation of endocrine process                        |
| 0.000    | 5     | 5    | regulation of dopamine metabolic process               |
**Supplementary Table 7:** GO-terms (Biological Process) significantly enriched with genes with medium translational efficiency in C7H2 cells. 2082 genes were tested against the background gene set of 10344 genes. GO-terms with a single associated gene were excluded.

| Pvalue | Count | Size | Term                                         |
|--------|-------|------|----------------------------------------------|
| GO:0042130 | 0.001 | 9    | negative regulation of T cell proliferation |

**Supplementary Table 8:** GO-terms (Biological Process) significantly enriched with genes with low translational efficiency in C7H2 cells. 2080 genes have been tested against the background gene set of 10334 genes. GO-terms with a single associated gene were excluded.

| Pvalue | Count | Size | Term                                         |
|--------|-------|------|----------------------------------------------|
| GO:0019083 | 0.000 | 51   | viral transcription                            |
| GO:0006415 | 0.000 | 35   | translational termination                      |
| GO:0006614 | 0.000 | 36   | SRP-dependent cotranslational protein targeting to membrane |
| GO:0006614 | 0.000 | 36   | establishment of protein localization to endoplasmic reticulum |
| GO:0006614 | 0.000 | 35   | translational elongation                       |
| GO:0043241 | 0.000 | 43   | protein complex disassembly                    |
| GO:0019058 | 0.000 | 59   | viral infectious cycle                          |
| GO:0006460 | 0.000 | 53   | mRNA catabolic process                         |
| GO:0006641 | 0.000 | 44   | translational initiation                       |
| GO:0006612 | 0.000 | 43   | protein targeting to membrane                  |
| GO:0000184 | 0.000 | 35   | nuclear-transcribed mRNA catabolic process, nonsense-mediated decay |
| GO:0044267 | 0.000 | 488  | cellular protein metabolic process             |
| GO:0033365 | 0.000 | 103  | protein localization to organelle              |
| GO:0044265 | 0.000 | 143  | cellular macromolecule catabolic process       |
| GO:0006355 | 0.000 | 388  | regulation of transcription, DNA-dependent     |
| GO:0010556 | 0.001 | 431  | regulation of macromolecule biosynthetic process |
| GO:0051252 | 0.001 | 399  | regulation of RNA metabolic process            |
| GO:0032091 | 0.000 | 11   | negative regulation of protein binding         |

**Supplementary Table 9:** GO-terms (Biological Process) significantly enriched with genes with the lowest translational efficiency in C7H2 cells. 2101 genes have been tested against the background gene set of 10344 genes. GO-terms with a single associated gene were excluded.

| Pvalue | Count | Size | Term                                         |
|--------|-------|------|----------------------------------------------|
| GO:0000398 | 0.000 | 88   | mRNA splicing, via spliceosome              |
| GO:0000375 | 0.000 | 88   | RNA splicing, via transestification reactions |
| GO:0043436 | 0.000 | 207  | oxoacid metabolic process                   |
| GO:0006520 | 0.000 | 115  | cellular amino acid metabolic process        |
| GO:0016071 | 0.000 | 176  | mRNA metabolic process                      |
| GO:0006396 | 0.000 | 182  | RNA processing                              |
| GO:0051276 | 0.000 | 182  | chromosome organization                      |
| GO:0016568 | 0.000 | 126  | chromatin modification                       |
| GO:0048281 | 0.000 | 399  | small molecule metabolic process             |
| GO:0016043 | 0.000 | 709  | cellular component organization              |
| GO:1901606 | 0.000 | 26   | alpha-amino acid catabolic process           |
| GO:0071704 | 0.000 | 1351 | organic substance metabolic process          |
| GO:0022613 | 0.000 | 76   | ribonucleoprotein complex biosynthesis       |
| GO:0046395 | 0.000 | 51   | carboxylic acid catabolic process            |
| GO:1901607 | 0.000 | 21   | alpha-amino acid biosynthetic process        |
| GO:0002474 | 0.000 | 34   | antigen processing and presentation of peptide antigen via MHC class I |
| GO:0044282 | 0.000 | 60   | small molecule catabolic process             |
| GO:0002478 | 0.000 | 29   | antigen processing and presentation of exogenous peptide antigen |
| GO:0009084 | 0.000 | 50   | S phase of mitotic cell cycle                |
| GO:0058878 | 0.000 | 110  | regulation of body fluid levels              |
| GO:0044711 | 0.000 | 94   | single-organism biosynthetic process         |
| GO:0007016 | 0.000 | 7    | cytoskeletal anchoring at plasma membrane    |
| GO:0008214 | 0.000 | 12   | protein dealkylation                         |
| GO:0016577 | 0.000 | 11   | histone demethylation                        |
| GO:0002479 | 0.000 | 28   | antigen processing and presentation of exogenous peptide antigen via MHC class I, TAP-dependent |

**Enriched processes in NALM6 cells**

| Pvalue | Count | Size | Term                                         |
|--------|-------|------|----------------------------------------------|
| GO:0002478 | 0.000 | 29   | antigen processing and presentation of exogenous peptide antigen |

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| GO:0016125 | 0.000 | 35 | 83 | sterol metabolic process |
|-------------|-------|----|----|------------------------|
| GO:0043085 | 0.000 | 172 | 592 | positive regulation of catalytic activity |
| GO:0016192 | 0.000 | 73 | 211 | vesicle-mediated transport |
| GO:0016570 | 0.000 | 76 | 227 | histone modification |
| GO:0044248 | 0.000 | 332 | 1248 | cellular catabolic process |
| GO:000278 | 0.000 | 182 | 636 | mitotic cell cycle |
| GO:002867 | 0.000 | 980 | 4056 | nitrogen compound metabolic process |
| GO:003125 | 0.000 | 106 | 341 | interphase |
| GO:0007596 | 0.000 | 94 | 296 | blood coagulation |
| GO:0016615 | 0.000 | 71 | 211 | organic hydroxy compound metabolic process |
| GO:000216 | 0.000 | 31 | 73 | M/G1 transition of mitotic cell cycle |
| GO:0051325 | 0.000 | 106 | 341 | interphase |
| GO:0006807 | 0.000 | 98 | 296 | nitrogen compound metabolic process |
| GO:0000278 | 0.000 | 182 | 636 | mitotic cell cycle |
| GO:0006921 | 0.000 | 23 | 53 | cellular component disassembly involved in execution phase of apoptosis |
| GO:0065003 | 0.000 | 200 | 731 | macromolecular complex assembly |
| GO:0032370 | 0.000 | 156 | 544 | positive regulation of cellular protein metabolic process |
| GO:0019048 | 0.000 | 97 | 312 | virus-host interaction |
| GO:0046394 | 0.000 | 61 | 180 | carboxylic acid biosynthetic process |
| GO:0003219 | 0.000 | 29 | 70 | positive regulation of viral reproduction |
| GO:0006749 | 0.000 | 29 | 71 | protein methylation |
| GO:0019221 | 0.000 | 69 | 212 | cytokine-mediated signaling pathway |
| GO:0006139 | 0.000 | 879 | 3640 | nucleobase-containing compound metabolic process |
| GO:0006901 | 0.000 | 17 | 34 | vesicle coating |
| GO:0006732 | 0.000 | 51 | 147 | coenzyme metabolic process |
| GO:0006800 | 0.000 | 13 | 23 | retrograde vesicle-mediated transport, Golgi to ER |
| GO:0006744 | 0.000 | 9 | 13 | regulation of translation in response to stress |
| GO:0048205 | 0.000 | 9 | 13 | COPI coating of Golgi vesicle |
| GO:0034079 | 0.000 | 96 | 315 | response to cytokine stimulus |
| GO:0044764 | 0.000 | 162 | 575 | multi-organism cellular process |
| GO:0006260 | 0.000 | 73 | 229 | DNA replication |
| GO:0006913 | 0.000 | 78 | 248 | nucleocytoplasmic transport |
| GO:0006984 | 0.000 | 34 | 89 | ER-nucleus signaling pathway |
| GO:0006921 | 0.000 | 23 | 53 | cellular component disassembly involved in execution phase of apoptosis |
| GO:0065003 | 0.000 | 200 | 731 | macromolecular complex assembly |
| GO:0051656 | 0.000 | 36 | 96 | establishment of organelle localization |
| GO:0005214 | 0.000 | 16 | 32 | DNA strand elongation involved in DNA replication |
| GO:0030521 | 0.000 | 21 | 47 | androsten receptor signaling pathway |
| GO:0002444 | 0.000 | 5 | 5 | assembly of spliceosomal tri-snRNP |
| GO:0051246 | 0.000 | 5 | 5 | negative regulation of transcriptional initiation in response to stress |
| GO:0051291 | 0.000 | 5 | 5 | L-proline biosynthetic process |
| GO:0006271 | 0.000 | 16 | 32 | DNA strand elongation involved in DNA replication |
| GO:0006984 | 0.000 | 34 | 89 | ER-nucleus signaling pathway |
| GO:0006921 | 0.000 | 23 | 53 | cellular component disassembly involved in execution phase of apoptosis |
| GO:0051656 | 0.000 | 36 | 96 | establishment of organelle localization |
| GO:0005214 | 0.000 | 16 | 32 | DNA strand elongation involved in DNA replication |
| GO:0030521 | 0.000 | 21 | 47 | androsten receptor signaling pathway |
| GO:0002444 | 0.000 | 5 | 5 | assembly of spliceosomal tri-snRNP |
| GO:0051246 | 0.000 | 5 | 5 | negative regulation of transcriptional initiation in response to stress |
| GO:0051291 | 0.000 | 5 | 5 | L-proline biosynthetic process |
| GO:0006271 | 0.000 | 16 | 32 | DNA strand elongation involved in DNA replication |
| GO:0006984 | 0.000 | 34 | 89 | ER-nucleus signaling pathway |
| GO:0006921 | 0.000 | 23 | 53 | cellular component disassembly involved in execution phase of apoptosis |
| GO:0051656 | 0.000 | 36 | 96 | establishment of organelle localization |
| GO:0005214 | 0.000 | 16 | 32 | DNA strand elongation involved in DNA replication |
| GO:0030521 | 0.000 | 21 | 47 | androsten receptor signaling pathway |
| GO:0002444 | 0.000 | 5 | 5 | assembly of spliceosomal tri-snRNP |
| GO:0051246 | 0.000 | 5 | 5 | negative regulation of transcriptional initiation in response to stress |
| GO:0051291 | 0.000 | 5 | 5 | L-proline biosynthetic process |
| GO:0006271 | 0.000 | 16 | 32 | DNA strand elongation involved in DNA replication |
| GO:0006984 | 0.000 | 34 | 89 | ER-nucleus signaling pathway |
| GO:0006921 | 0.000 | 23 | 53 | cellular component disassembly involved in execution phase of apoptosis |
| GO:0051656 | 0.000 | 36 | 96 | establishment of organelle localization |
| GO:0005214 | 0.000 | 16 | 32 | DNA strand elongation involved in DNA replication |
| GO:0030521 | 0.000 | 21 | 47 | androsten receptor signaling pathway |
| GO:0002444 | 0.000 | 5 | 5 | assembly of spliceosomal tri-snRNP |
| GO:0051246 | 0.000 | 5 | 5 | negative regulation of transcriptional initiation in response to stress |
| GO:0051291 | 0.000 | 5 | 5 | L-proline biosynthetic process |

**Supplementary Table 10:** GO-terms (Biological Process) significantly enriched with genes with the highest translational efficiency in NALM6 cells. 2245 genes were tested for enrichment against the background gene set of 11096 genes. GO-terms with a single associated gene were excluded.

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### Supplementary Table 11: GO-terms (Biological Process) significantly enriched with genes with medium translational efficiency in NALM6 cells. 2238 genes were tested for enrichment against the background gene set of 11096 genes. GO-terms with a single associated gene were excluded.

| Pvalue | Count | Size | Term                                           |
|--------|-------|------|------------------------------------------------|
| 0.000  | 8     | 11   | regulation of dendritic spine development      |
| 0.000  | 484   | 2194 | multicellular organismal development           |
| 0.000  | 230   | 974  | nervous system development                     |
| 0.000  | 18    | 42   | formation of primary germ layer                |
| 0.000  | 63    | 219  | sensory organ development                      |

### Supplementary Table 12: GO terms (Biological Process) significantly enriched with genes with high translational efficiency in NALM6 cells. 2269 genes were tested for enrichment against the background gene set of 11096 genes. GO-terms with a single associated gene were excluded.

| Pvalue | Count | Size | Term                                           |
|--------|-------|------|------------------------------------------------|
| 0.000  | 29    | 74   | nucleosome assembly                            |
| 0.000  | 44    | 129  | nucleobase-containing compound transport       |
| 0.000  | 12    | 21   | negative regulation of viral genome replication|
| 0.000  | 39    | 112  | RNA transport                                  |
| 0.000  | 5     | 5    | peptidyl-proline hydroxylation to 4-hydroxy-L-proline |
| 0.000  | 5     | 5    | semaphorin-plexin signaling pathway            |
| 0.001  | 40    | 118  | RNA localization                               |

### Supplementary Table 13: GO-terms (Biological Process) significantly enriched with genes with low translational efficiency in NALM6 cells. 2219 genes were tested for enrichment against the background gene set of 11096 genes. GO-terms with a single associated gene were excluded.

| Pvalue | Count | Size | Term                                           |
|--------|-------|------|------------------------------------------------|
| 0.000  | 59    | 82   | translational termination                      |
| 0.000  | 59    | 94   | translational elongation                       |
| 0.000  | 59    | 96   | SRP-dependent cotranslational protein targeting to membrane |
Supplementary Table 14: GO-terms (Biological Process) significantly enriched with genes with the lowest translational efficiency in NALM6 cells. 2257 genes were tested for enrichment against the background gene set of 11096 genes. GO-terms with a single associated gene were excluded.
Analysis of microRNA target genes

miRNA (family) target gene predictions base on Targetscan version 6.2 [1] (target genes have been defined using the file Predicted_Targets_Info.txt that contains all predicted conserved targets of conserved miRNA families).

In this analysis we evaluated whether genes with low translational efficiency harbor similar miRNA target sites. Similar to a GO analysis, we thus performed hypergeometric tests to analyse for significant over-representation of predicted miRNA target sites in the 3' UTR of the 5% or genes with the lowest translational efficiency.

Of the in total 536 genes constituting the 5% of genes with lowest translational efficiency in C7H2 341 are also predicted target of at least one miRNA. These genes have been analysed for enrichment against the background gene set consisting of 6899 genes also predicted to be target of at least one miRNA (out of in total 10318 expressed protein coding genes). For NALM6 cells 363 genes have been tested against 7192 background genes (of in total 577 and 11129 test and background genes, respectively).

An enrichment analysis has also been performed on the 5% of the genes with the highest translational efficiency. Some of the miRNA families below (indicated by ‡) have also been found significant in that analysis and thus most likely represent false positive findings.

### Supplementary Table 15: miRNA families with a significant over-representation of predicted target sites in the 3’ UTR of the 5% of genes with the lowest translational efficiency. C7H2 cell line. Count: number of tested genes being a predicted target of the miRNA. Size: total number of predicted target genes for the miRNA detectable on the microarray, %: percentage of predicted target genes being among the genes with the lowest translational efficiency. †: highest expression of any of the miRNAs host genes detected in the respective cell line. For miRNA host gene prediction see [2]. ‡: target sites for that miRNA are also significantly over-represented in 3’ UTRs of genes with the highest translational efficiencies.
Supplementary Table 16: miRNA families with a significant over-representation of predicted target sites in the 3' UTR of the 5% of genes with the lowest translational efficiency. NALM6 cell line. Count: number of tested genes being a predicted target of the miRNA, Size: total number of predicted target genes for the miRNA detectable on the microarray, %: percentage of predicted target genes being among the genes with the lowest translational efficiency. †: highest expression of any of the miRNAs host genes detected in the respective cell line. ‡: target sites for that miRNA are also significantly over-represented in 3' UTRs of genes with the highest translational efficiencies.

Detailed information on some miRNA families

Here we list some more information for some of the miRNA families identified in the analysis above. In addition to the expression of their target genes across all 3 pools we add information about the expression of these miRNAs in the analysed cell lines or the lymphoid tissue. Specifically, we evaluate expression of the mature miRNA in C7H2 cells [2], tissue specific expression according to www.microrna.org and information from the literature.

miR-30abcdef/30abe-5p/384-5p

- Host gene: host gene relatively high expressed in C7H2 and NALM6 cells.
- Mature miRNA expression in C7H2 cells [2]: miR-30a-5p, miR-30c, miR-30d, miR-30e-5p high expressed.
- Expression profile from microrna.org: miR-30e high in lymphoid tissue.
- Literature: high in ALL [3].

Supplementary Figure 3: Expression of target genes for the miRNA family miR-30abcdef/30abe-5p/384-5p across pools in both cell lines. The boxplot represents expression of all target genes for the miRNA, expression of target genes among the 5% of genes with the lowest translational efficiency are draw in red. The horizontal blue line indicates the (highest) expression of any of the potential host genes for that miRNA in the respective cell line.
miR-93/93a/105/106a/291a-3p/294/295/302abcde/372/373/428/519a/520be/520acd-3p/1378/1420ac

miR-93 is encoded in the miR-106b∼25 cluster, miR-106a in the miR-106a∼363 cluster.

- Host gene: not detectable.
- Mature miRNA expression in C7H2 cells [2]: miR-93, miR-106a very high expressed, miR-105, miR-302abcd, miR-372, miR-373, miR-520be low, not detectable: miR-291a, miR-294, miR-295, miR-302e, miR-428, miR-519a and others.
- Expression profile from microrna.org: miR-93, miR-106a high in lymphoid tissue (B, and T).
- Literature: miR-93, miR-106a high in lymphoid malignancies [3].

Supplementary Figure 4: Expression of target genes for the miRNA family miR-93/93a/105/106a/291a-3p/294/295/302abcde/372/373/428/519a/520be/520acd-3p/1378/1420ac across pools in both cell lines. The boxplot represents expression of all target genes for the miRNA, expression of target genes among the 5% of genes with the lowest translational efficiency are draw in red. The horizontal blue line indicates the (highest) expression of any of the potential host genes for that miRNA in the respective cell line.

miR-181abcd/4262

miR-181a and miR-181b are both processed from 2 precursors, both clustered together (i.e. miR-181a-1 and miR-181b-1 as well as miR-181a-2 and miR-181b-2). miR-181c and miR-181d are also processed from the same primary transcript.

- Host gene: average expression of one of the host genes.
- Mature miRNA expression in C7H2 cells [2]: miR-181a and miR-181b very high expressed, miR-181c low expressed, miR-181d and miR-4262 not detectable.
- Expression profile from microrna.org: miR-181a, miR-181b high in lymphoid tissue
- Literature: miR-181a, b high in ALL [3].

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**Supplementary Figure 5**: Expression of target genes for the miRNA family miR-181abcd/4262 across pools in both cell lines. The boxplot represents expression of all target genes for the miRNA, expression of target genes among the 5% of genes with the lowest translational efficiency are drawn in red. The horizontal blue line indicates the (highest) expression of any of the potential host genes for that miRNA in the respective cell line.

**miR-19ab**

miR-19a and miR-19b-1 are part of the miR-17 92 cluster, miR-19b-2 of the miR-106a 363 cluster.

- Host gene: moderate expression of the host gene in NALM6.
- Mature miRNA expression in C7H2 cells [2]: miR-19a intermediate and miR-19b high expressed.
- Expression profile from microrna.org: high in lymphoma.
- Literature: miR-19a and b from miR-17 92 cluster high in ALL [3].
**Supplementary Figure 6**: Expression of target genes for the miRNA miR-19ab family across pools in both cell lines. The boxplot represents expression of all target genes for the miRNA, expression of target genes among the 5% of genes with the lowest translational efficiency are draw in red. The horizontal blue line indicates the (highest) expression of any of the potential host genes for that miRNA in the respective cell line.

**miR-17/17-5p/20a-5p/20b-5p/93/106a/427/518a-3p/519d**

- **Host gene**: high expression of the host gene in NALM6.
- **Mature miRNA expression in C7H2 cells** [2]: miR-17-5p, miR-106a very high expressed, miR-20a, miR-93, miR-106b high expressed, not detectable: miR-20b, miR-427 etc.
- **Expression profile from microrna.org**: miR-17, miR-106a and b, miR-20a, miR-93 high in lymphoid tissue
- **Literature**: miR-17, part of miR-17 92 cluster overexpressed in ALL [3]. miR-106a, 20b high in lymphoid malignancies. miR-106b, 93 high in lymphoid malignancies.
Supplementary Figure 7: Expression of target genes for the miRNA family miR-17/17-5p/20ab/20b-5p/93/106ab/427/518a-3p/519d across pools in both cell lines. The boxplot represents expression of all target genes for the miRNA, expression of target genes among the 5% of genes with the lowest translational efficiency are drawn in red. The horizontal blue line indicates the (highest) expression of any of the potential host genes for that miRNA in the respective cell line.

miR-26ab/1297/4465

- Host gene: high expression of the host gene in NALM6.
- Mature miRNA expression in C7H2 cells [2]: miR-26a high expressed, miR-26b low; others not detectable
- Expression profile from microrna.org: miR-26a and b high in lymphoid tissue, specifically B-cells
- Literature: miR-26a high in ALL [3].
Supplementary Figure 8: Expression of target genes for the miRNA family miR-26ab/1297/4465 across pools in both cell lines. The boxplot represents expression of all target genes for the miRNA, expression of target genes among the 5% of genes with the lowest translational efficiency are draw in red. The horizontal blue line indicates the (highest) expression of any of the potential host genes for that miRNA in the respective cell line.
RNA fractions from sucrose gradient separation

**Supplementary Figure 9:** Representative example of Agilent gel electrophoresis of RNA fractions obtained by sucrose gradient separation from C7H2 cells. Fractions 1-6 (pool 1) encompass non-ribosome bound RNAs, as suggested by the absence of 28S RNA. Fractions 7-9 form an intermediate pool mostly containing translationally-initiated mRNAs (pool 2). Fractions 10-23 (pool 3) contain mRNAs bound to multiple ribosomes, as evidenced by the presence of ribosomal subunits 18S and 28S.
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