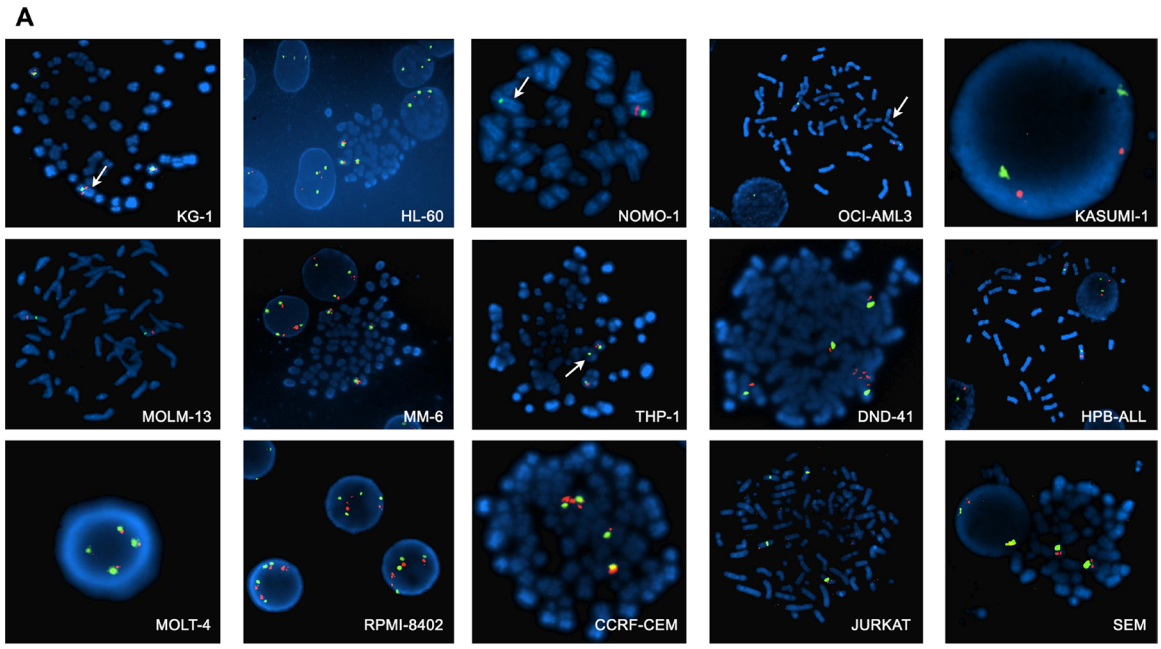
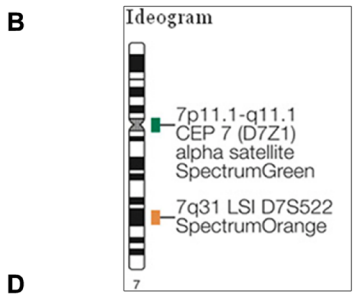
# Identification of cytogenetic and molecular subgroup of acute myeloid leukemias showing sensitivity to L-Asparaginase

## SUPPLEMENTARY MATERIALS

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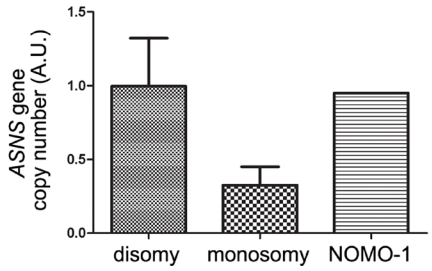
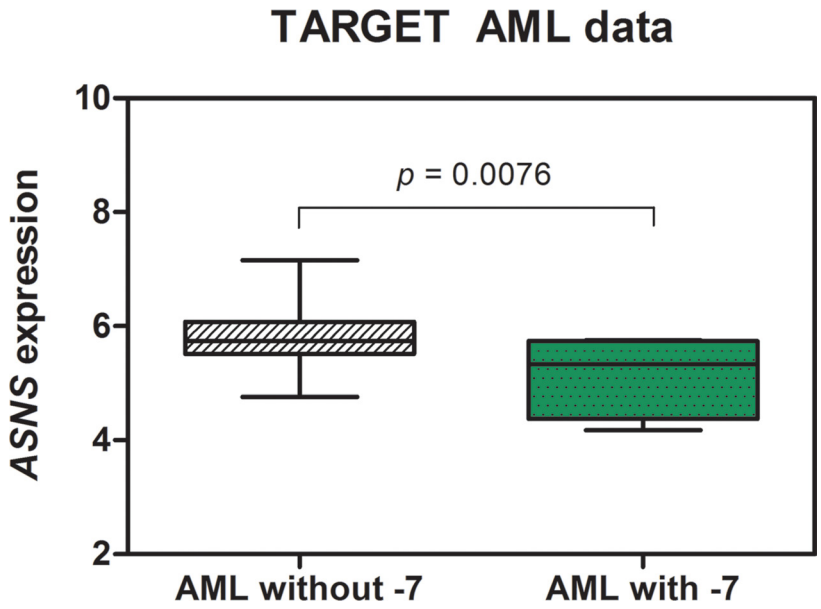
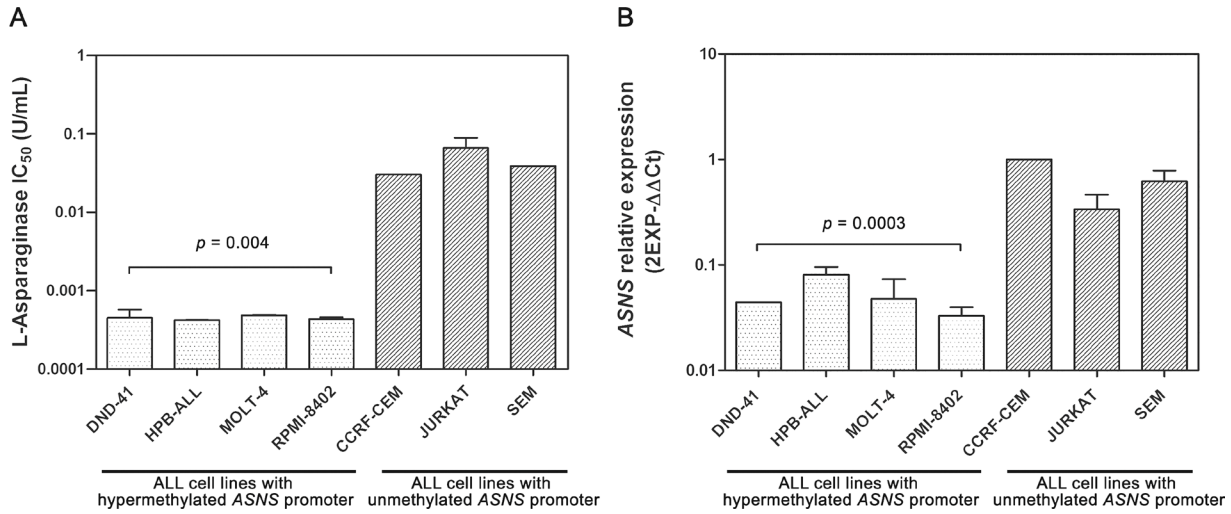
| Cell line | Leukemia subtype | Cytogenetic status of chromosome 7 |
|---|---|---|
| KG-1 | AML | ish + der(7)t(7q;?) |
| HL-60 | AML | trisomy |
| NOMO-1 | AML | ish der(7)t(7q;?) |
| OCI-AML3 | AML | ish dup(7)(qter->q31?) and translocation |
| KASUMI-1 | AML | disomy |
| MOLM-13 | AML | disomy |
| MM-6 | AML | trisomy/tetrasomy |
| THP-1 | AML | ish + 7/ish + der(7)t(7q;?) or i(7p) |
| DND-41 | T-ALL | tetrasomy |
| HPB-ALL | T-ALL | disomy |
| MOLT-4 | T-ALL | tetrasomy |
| RPMI-8402 | T-ALL | tetrasomy |
| CCRF-CEM | T-ALL | tetrasomy |
| JURKAT | T-ALL | tetrasomy |
| SEM | B-ALL | disomy |




**Supplementary Figure 1: FISH analysis of AML and ALL cell lines without -7, using LSI D7S522/CEP 7 probe, a mixture of Spectrum Orange (7q31) and Spectrum Green (7p11.1-q11.1) probes.** Normal diploid chromosome 7 have two signals for both centromeric (green) and telomeric (orange) probes. (**A**) Interphase or metaphase FISH results of 8 AML (KG-1, HL-60, NOMO-1, OCI-AML3, KASUMI-1, MOLM-13, MM-6, THP-1) and 7 ALL (DND-41, HPB-ALL, MOLT-4, RPMI-8402, CCRF-CEM, JURKAT, SEM) cell lines. Arrows indicates complex aberrations involving chromosome 7. (**B**) Ideogram of LSI D7S522/CEP 7 probe. (**C**) Summary of cytogenetic status of chromosome 7 in both AML and ALL cell lines. (**D**) Copy number analysis by qPCR of ASNS locus in NOMO-1 cells, compared with disomic (SEM, KASUMI-1, MOLM-13) and monosomic (UCSD-AML1, FKH-1) cell lines.




**Supplementary Figure 2: ASNS expression in pediatric TARGET AML database.** Boxplots show ASNS normalized expression of samples from the NCI-COG TARGET AML project (https://ocg.cancer.gov/programs/target/acute-myeloid-leukemia), classified by chromosome 7 status.




**Supplementary Figure 3:** (**A**) $IC_{50}$ of ALL cell lines after 48 h of treatment with increasing concentrations of L-Asp. DND41, HPB-ALL, MOLT-4 and RPMI-8402, which have *ASNS* promoter methylation, were more sensitive than other ALL cell lines (Unpaired *t* test, $p = 0.004$). (**B**) ALL cell lines sensitive to L-Asp treatment showed lower amount of *ASNS* transcript (Unpaired *t* test, $p = 0.0004$). *ASNS* relative expression is calculated as $2^{-\Delta\Delta Ct}$. Gene expression was normalized to *GAPDH* and *ATP5B* housekeeping genes. Data are expressed as mean ± SD of three independent experiments.