

G₁/S transcriptional networks modulated by the *HOX11/TLX1* oncogene of T-cell acute lymphoblastic leukemia

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Description of Supplementary Information

1. The complete dataset is contained in the files “[PivotData human.xls](#)” and “[PivotData murine.xls](#)”:
 - JHH1 - Jurkat cells transduced with HOX11 and Hyg genes, Experiment 1
 - JHH2 - Jurkat cells transduced with HOX11 and Hyg genes, Experiment 2
 - JHH3 - Jurkat cells transduced with HOX11 and Hyg genes, Experiment 3
 - JH1,2,3 - Jurkat cells transduced with the Hyg gene alone, Experiment 1,2,3
 - J - Jurkat cells
 - K - K3P cells
 - S - Sil cells
 - JHH-JH is the relative expression data for JHH normalized to JH
 - K-J and S-J are the relative expression data for K3P and SIL normalized to J
 - TH - murine HOX11-positive THY137 cells
 - TC - murine HOX11-negative THY112.2C cells
 - TH-TC is the relative expression data for TH normalized to TC
2. The file “[Filtered data.xls](#)” contains the following information on separate sheets:
 - [Ferrando](#) – HOX11 “signature” genes from Ferrando *et al.* (2002)
 - [K3P and Sil vs Jurkat >4](#) – the complete list of genes expressed at least 4-fold higher (signal log₂ ratio >2) in K3P and Sil versus Jurkat cells. Authors’ comments are provided in columns AF and AG.
 - [E2F](#) – E2F targets
 - [Myc](#) – Set I and Set II c-Myc targets (plus calculated correlation coefficients for Set II c-Myc targets)
 - [CREB](#) – CREB targets
 - [Mitochondrial](#) – mitochondrial genes
 - [IFN](#) – interferon-induced genes
 - [Wnt](#) – Wnt-related genes
 - [HOX11 groups](#) – gene list used to generate HOX11 functional groups
 - [HOX11 all >2](#) – all the genes expressed in human and murine HOX11-positive cell lines at least 2-fold higher (signal log₂ ratio >1) than in the corresponding HOX11-negative control cell lines.
3. The file “[HOX11 groups.jpg](#)” shows HOX11 functional groups. Genes associated with the HOX11-positive phenotype were selected to meet the following criteria: the median values of the signal log₂ ratio from three experiments in HOX11-transduced Jurkat cells versus empty vector-transduced Jurkat cells were >1 and all values for the corresponding K3P/Jurkat and Sil/Jurkat signal log₂ ratios were >1 (see file “[Filtered data.xls](#)”, [HOX11 groups](#) sheet). A total of 112 genes were uploaded into the NetAffx Gene Ontology Data tool and 65 genes were annotated. The graph shows all functional groups containing at least three genes. The color scheme is based on the percentage of total genes representing a given functional group.
4. The file “[Supplementary Fig 1.pdf](#)” contains Supplementary Figure 1 showing Western blot and RT-PCR analyses of HOX11 expression in K3P, Sil and Jurkat/MSCVhyg-HOX11 cells.