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MicroRNA and transcription factor co-regulatory network analysis reveals miR-19 inhibits CYLD in T-cell acute lymphoblastic leukemia

T-cell acute lymphoblastic leukemia (T-ALL) is an aggressive hematological malignancy accounting for about 15 and 25% of pediatric and adult acute lymphoblastic leukemia, respectively. T-ALL is usually characterized by proliferation of thymocytes at various stages of development with high white blood cell counts, mediastinal lymph nodes enlargement and central nervous system involvement. Although this neoplastic disorder originates from the thymus, it will spread throughout all organs and will be fatal rapidly without therapy. Compared with the common B-cell lineage ALL, T-ALL has a worse prognosis in patients historically. Current multi-agent combination chemotherapy provides an overall survival rate of 60%-70% in children and only 30–40% in adults. Currently, understanding of the etiology of T-ALL has largely come from the studies of gene abnormalities. Although the oncogenicity of these genes is well established, understanding of the transformational programs and multi-step pathogenesis of T-ALL remains limited. Especially the regulatory networks of T-ALL genes expression are still elusive.