Supplementary Information

Prognostic significance of high GFI1 expression in AML of normal karyotype and its association with a FLT3-ITD signature

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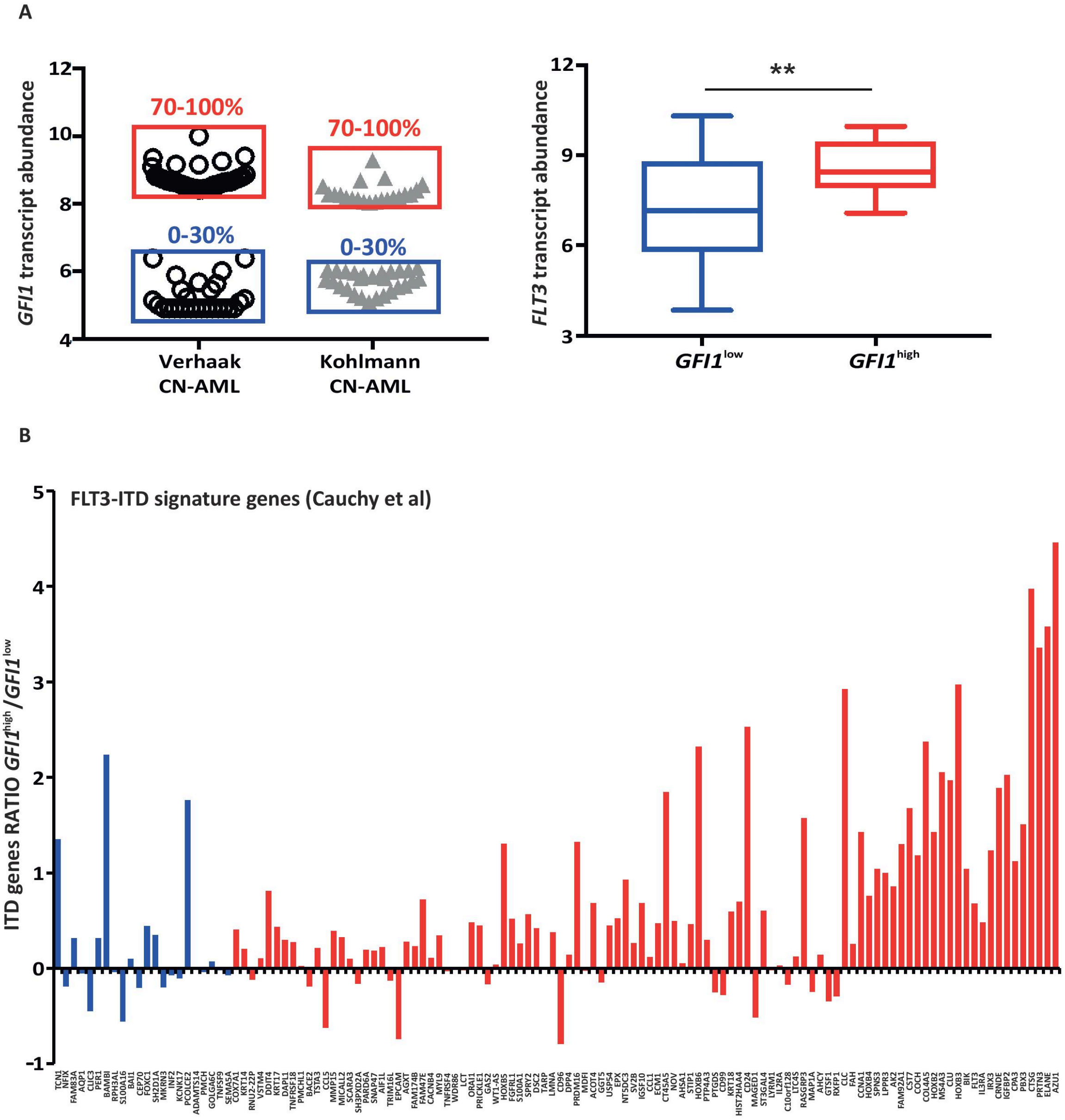

Figure S1. Analysis of FLT3-ITD genes in an independent CN-AML dataset

(A) Representation of the 0-30% *GFI1*^{low} and 70-100% *GFI1*^{high} expression boundaries comparing samples from the Verhaak et al[19] and the Kohlmann et al datasets. Boxplots in the right panel represent the abundance of the *FLT3* transcript in *GFI1*^{low} versus *GFI1*^{high} CN-AML patient samples from the Kohlmann dataset. (B) Histogram representing expression of FLT3-ITD molecular signature genes in *GFI*^{high} versus *GFI1*^{low} FLT3-WT CN-AML patient samples from the Kohlmann dataset. The ranking of the genes is the same as that depicted in FIG2A.