Supplemental Figures

Aberrant *ARID5B* expression and its association with Ikaros dysfunction in acute lymphoblastic leukemia

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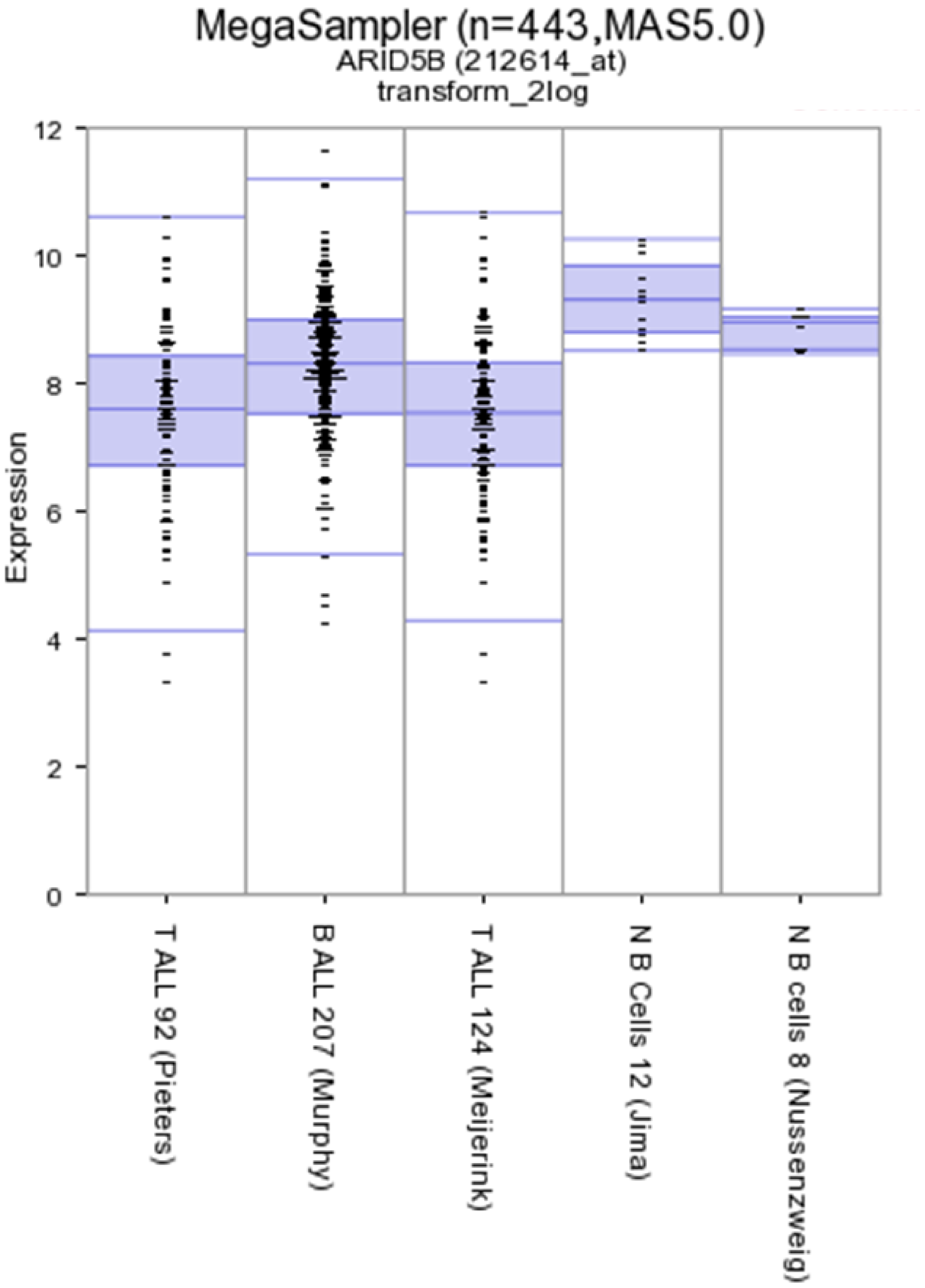

Fig. S1 *ARID5B* expression in the reported ALL microarray cohort studies. Leukemia types are as indicated as well as normal (N) B cells. Data generated from human oncogenomics server (https://hgserver1.amc.nl/cgi-bin/r2/main.cgi) with GEO database (GSE7440, GSE11877, GSE10609, GSE26713 and GSE28491). The default one way Analysis of Variance (ANOVA) in the server was used for statistical analysis.

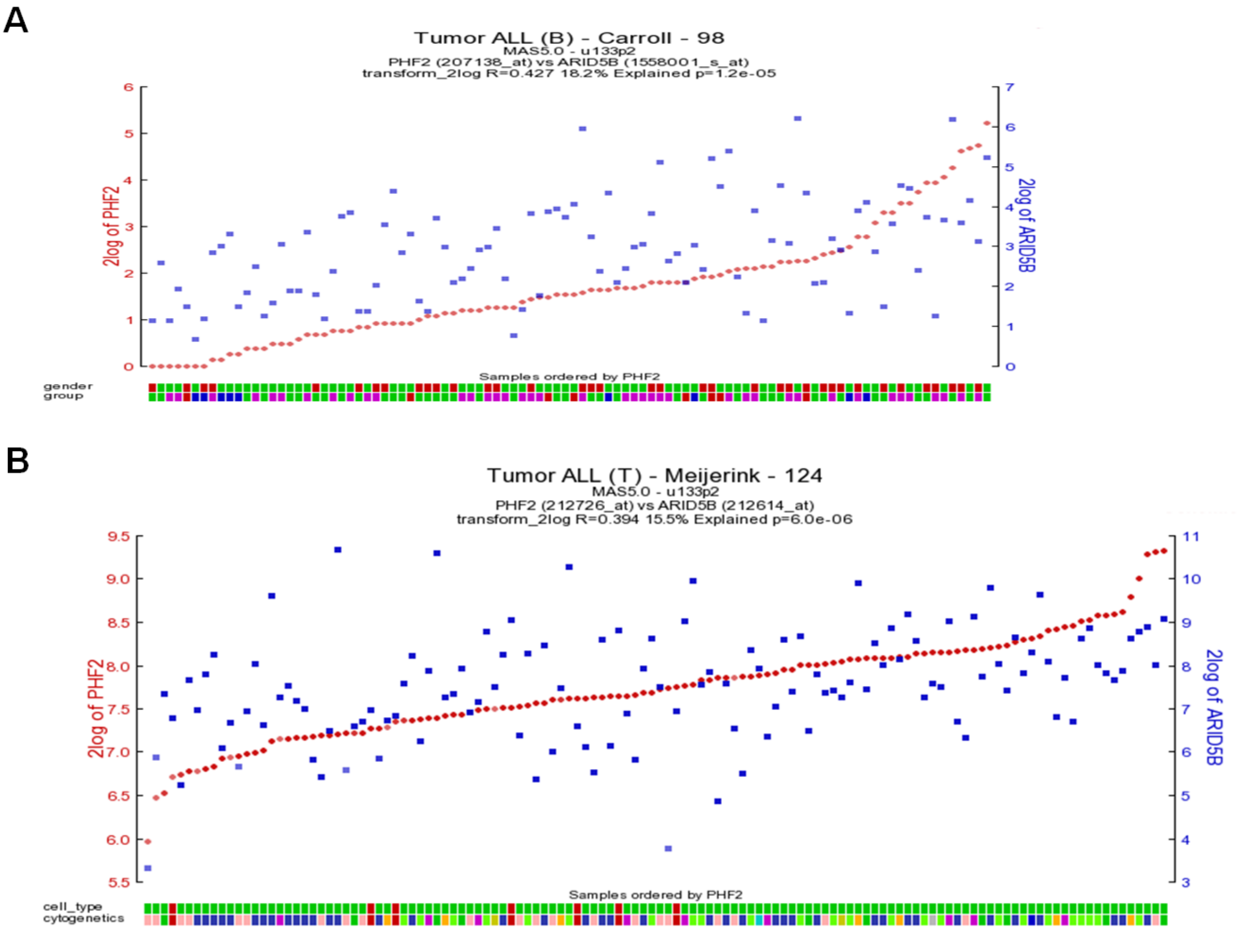

Fig. S2 Correlation of *ARID5B* expression with *PHF2* in the cohort of (A) B-ALL and (B) T-ALL patients. Data generated from human oncogenomics server (https://hgserver1.amc.nl/cgi-bin/r2/main.cgi) with GEO database (GSE11877 and GSE26713). The default Pearson correlation in the server was used to calculate the statistics.

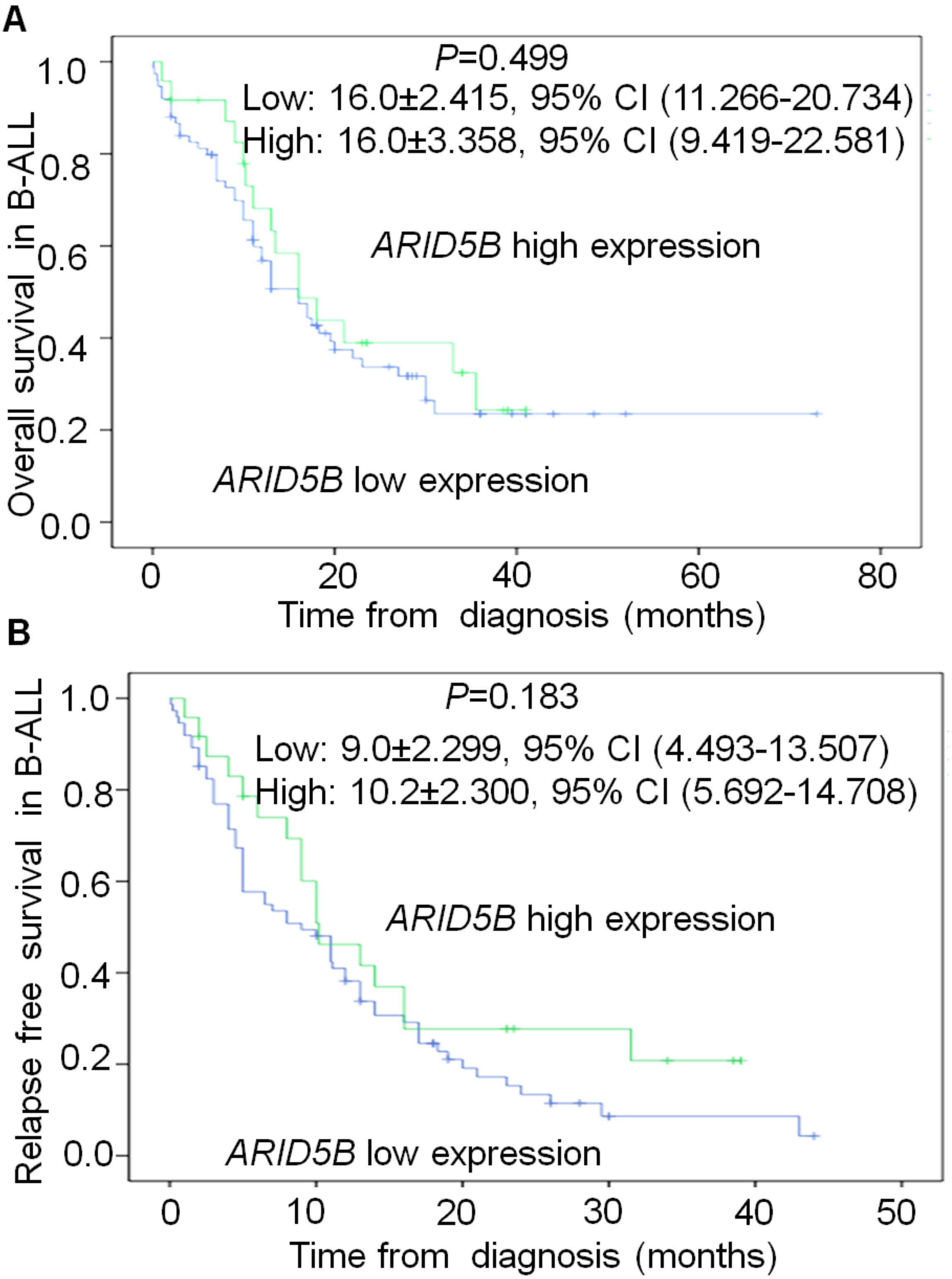

Fig. S3 Association of *ARID5B* low expression with **(A)** overall survival and **(B)** relapse free survival in B-ALL

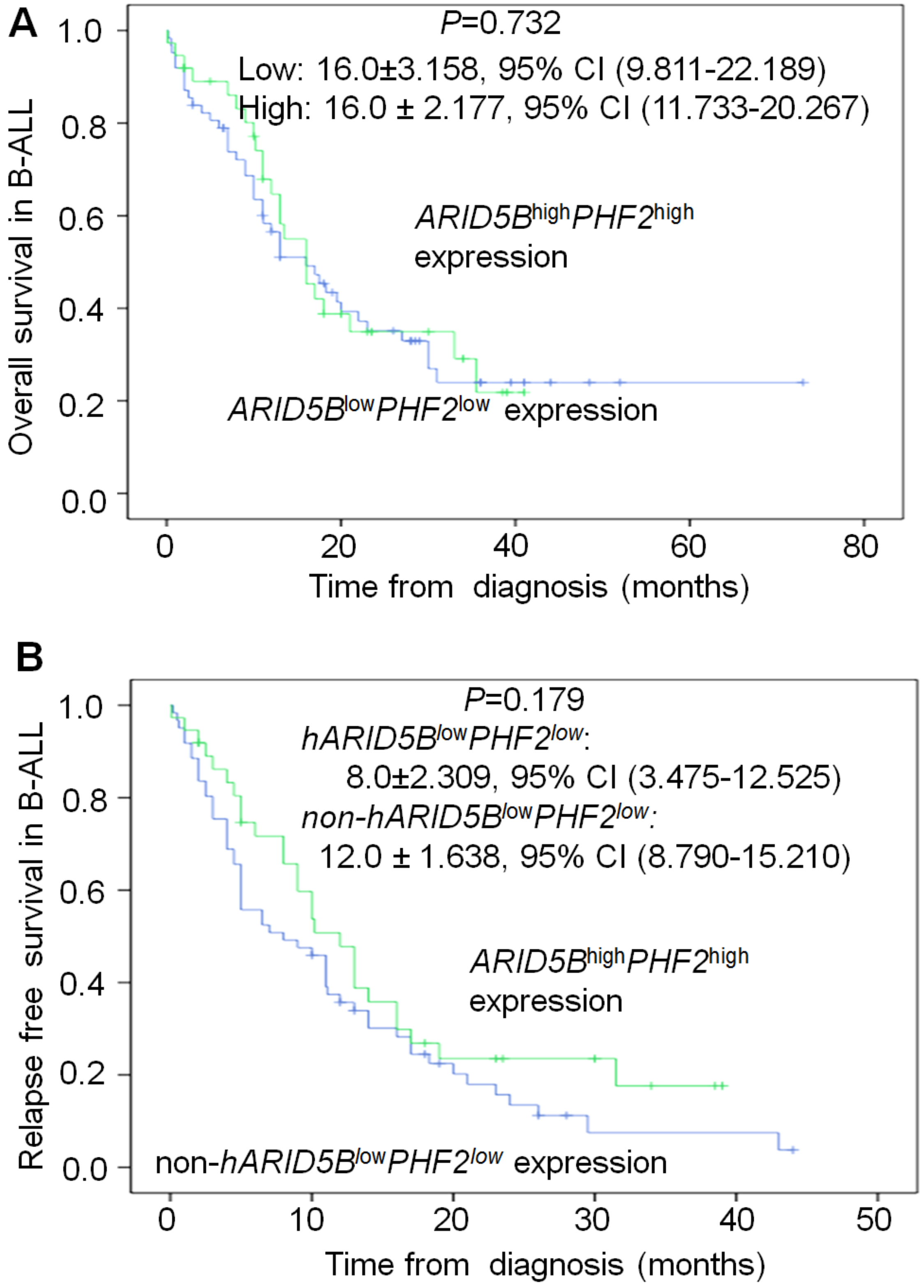

Fig. S4 Association of *ARID5B*$^{\text{low}}$*PHF2*$^{\text{low}}$ expression with **(A)** overall survival and **(B)** relapse free survival in B-ALL

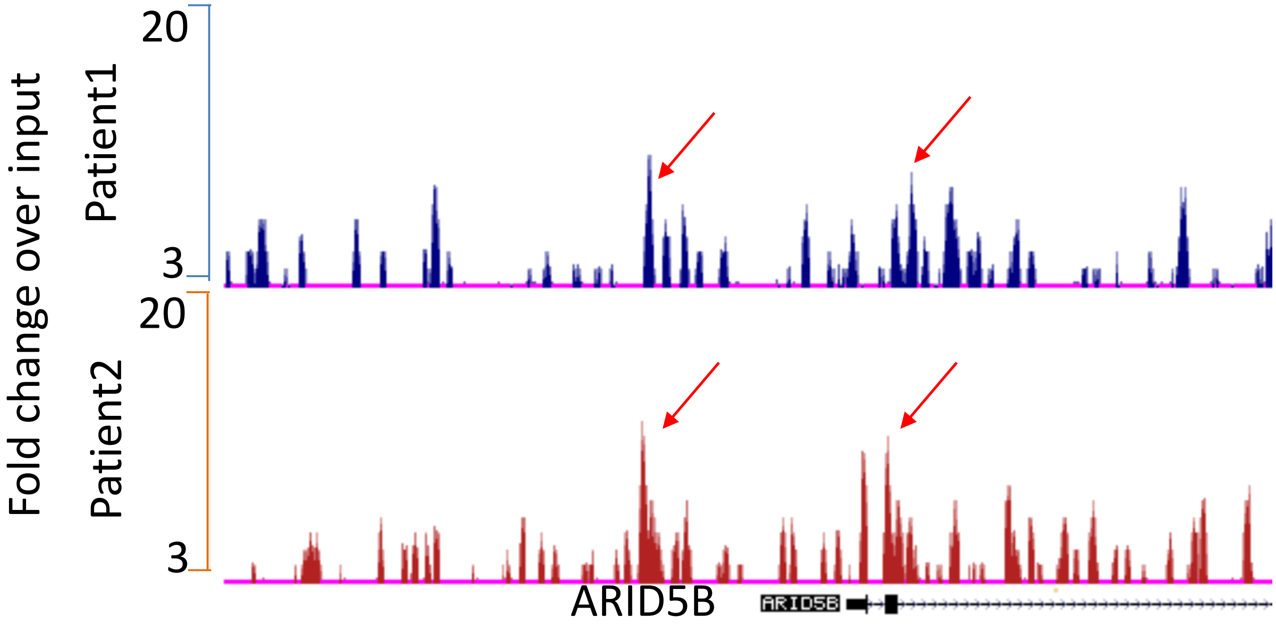

Fig S5 Ikaros binds to the promoter of ARID5B in primary B-ALL from different patients identified by ChIP-seq.

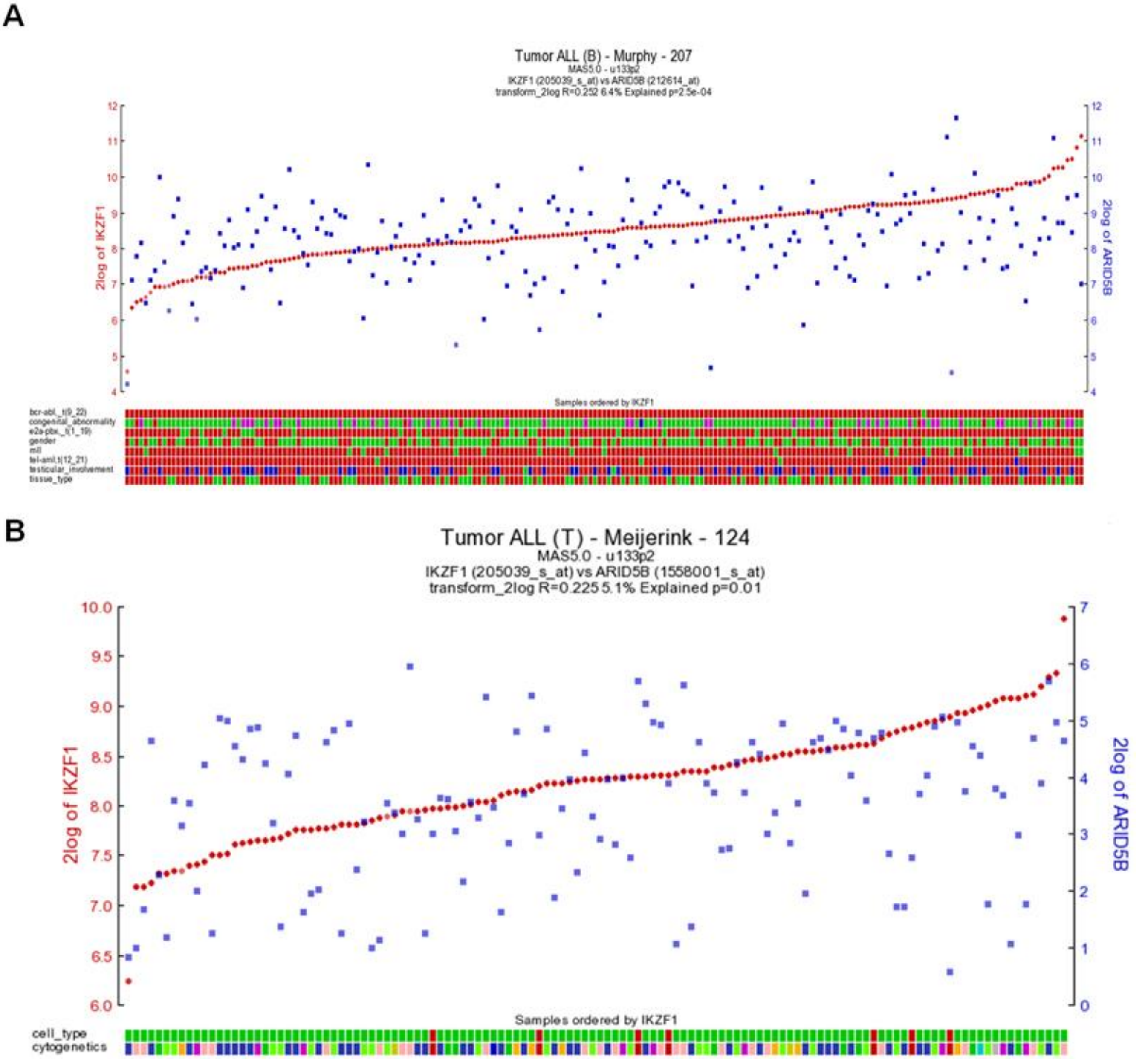

Fig. S6 Correlation of *ARID5B* expression with *Ikaros* in the cohort of (A) B-ALL and (B) T-ALL patients. Data generated from human oncogenomics server with GEO database (GSE11877 and GSE26713). Pearson correlation is used to calculate the statistics.