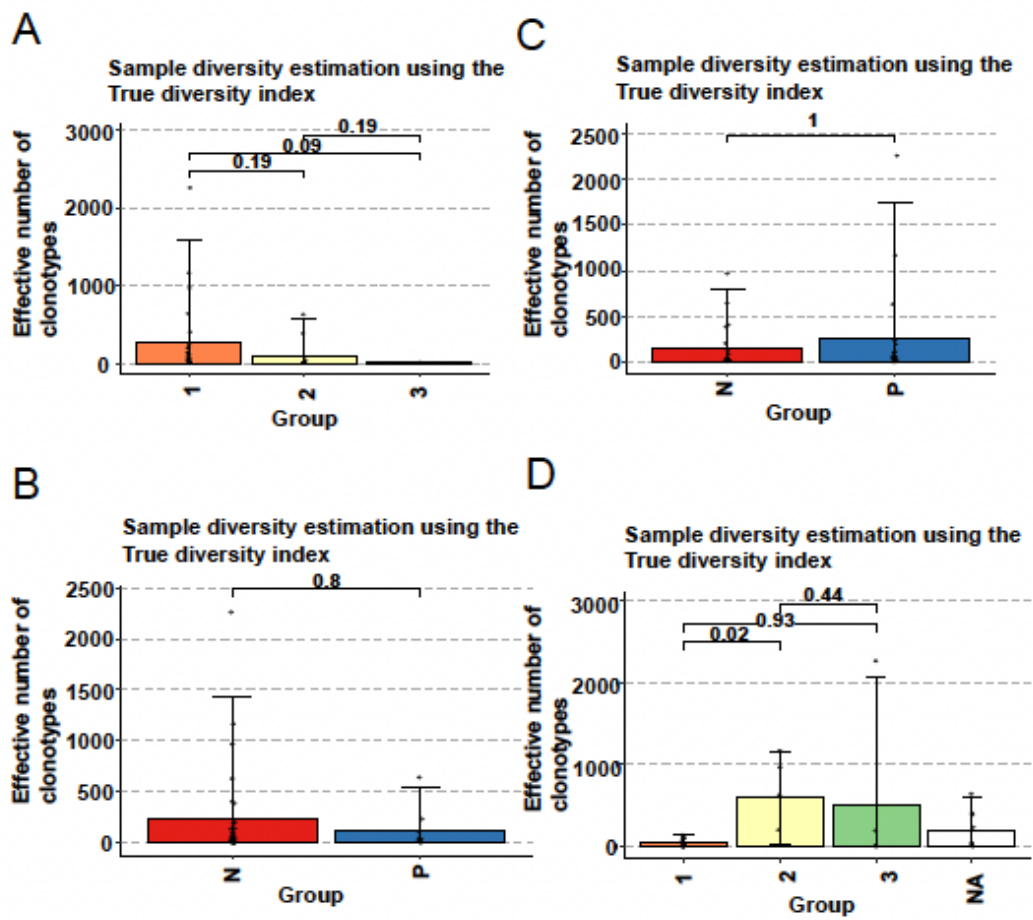


**Supplemental information**

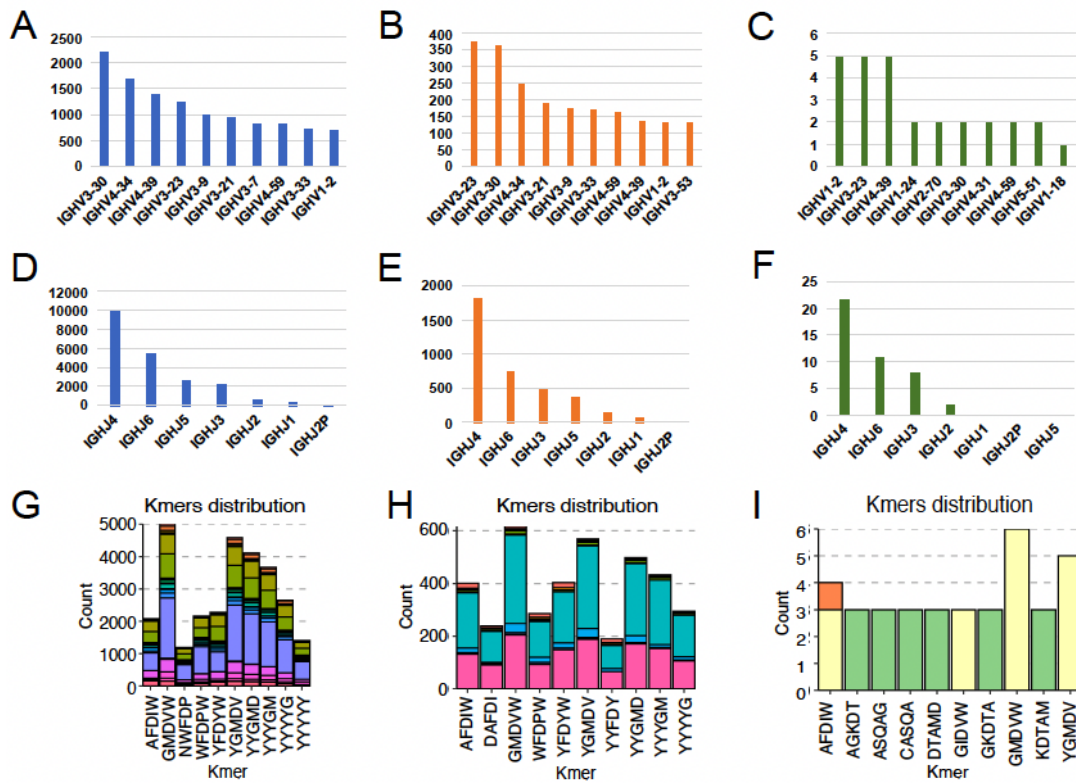
**IGH rod-like tracer: An AlphaFold2 structural  
similarity extraction-based predictive biomarker  
for MRD monitoring in pre-B-ALL**

**Zhongling Zhuo, Qingchen Wang, Chang Li, Lili Zhang, Lanxin Zhang, Ran You, Yan Gong, Ying Hua, Linzi Miao, Jiefei Bai, Chunli Zhang, Ru Feng, Meng Chen, Fei Su, Chenxue Qu, and Fei Xiao**



**Supplement Figure 1 Summary of clonotypes with diversity. Related to Figure 5**

The relationship between the diversity of IGH clonotypes and relapse frequency (A), gene mutation status (B), FCM-MRD status (C), and disease risk classification (D).



**Supplement Figure 2 Summary of clonotypes with gene usage, and motifs. Related to Figure 5**

The most frequent V gene usage in 1<sup>st</sup> relapse samples (A), 2<sup>nd</sup> relapse samples (B), and 3<sup>rd</sup> relapse samples (C). The most frequent J gene usage in 1<sup>st</sup> relapse samples (D), 2<sup>nd</sup> relapse samples (E), and 3<sup>rd</sup> relapse samples (F). The most frequent motifs in 1<sup>st</sup> relapse samples (G), 2<sup>nd</sup> relapse samples (H), and 3<sup>rd</sup> relapse samples (I).