

Supplementary Materials for

A functional genomic approach to actionable gene fusions for precision oncology

Jun Li, Hengyu Lu, Patrick Kwok-Shing Ng, Angeliki Pantazi, Carman Ka Man Ip, Kang Jin Jeong, Bianca Amador, Richard Tran, Yiu Huen Tsang, Lixing Yang, Xingzhi Song, Turgut Dogruluk, Xiaojia Ren, Angela Hadjipanayis, Christopher A. Bristow, Semin Lee, Melanie Kucherlapati, Michael Parfenov, Jiabin Tang, Sahil Seth, Harshad S. Mahadeshwar, Kamalika Mojumdar, Dong Zeng, Jianhua Zhang, Alexei Protopopov, Jonathan G. Seidman, Chad J. Creighton, Yiling Lu, Nidhi Sahni, Kenna R. Shaw, Funda Meric-Bernstam, Andrew Futreal, Lynda Chin, Kenneth L. Scott, Raju Kucherlapati*, Gordon B. Mills*, Han Liang*

*Corresponding author. Email: hliang1@mdanderson.org (H. Liang); millsg@ohsu.edu (G.B.M.); rkucherlapati@bwh.harvard.edu (R.K.)

Published 9 February 2022, *Sci. Adv.* **8**, eabm2382 (2022)
DOI: 10.1126/sciadv.abm2382

The PDF file includes:

Figs. S1 and S2

Other Supplementary Material for this manuscript includes the following:

Tables S1 and S2

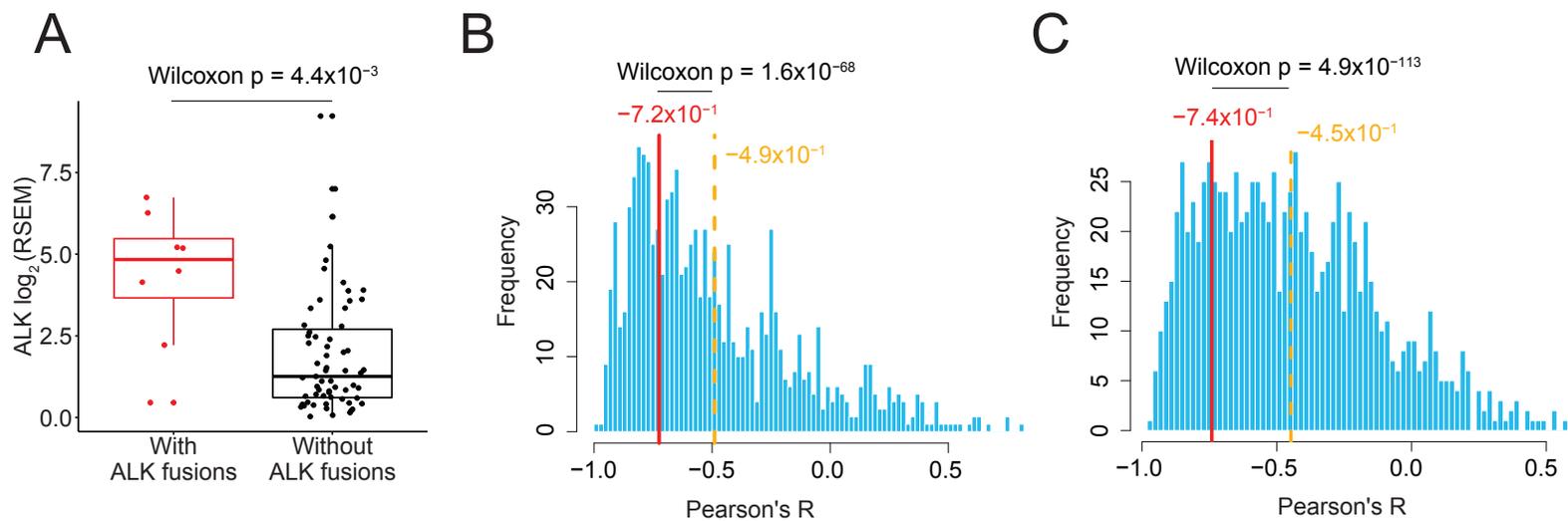


Figure S1. Differential expression analysis between cell lines with and without *ALK* fusions.

(A) Differential expression analysis between cell lines with and without *ALK* fusions. (B-C) The distribution of Pearson's Rs calculated based on the correlation analysis between the *ALK* expression of randomly sampled cell lines that do not have *ALK* fusions and Crizotinib (B) or NVP-TAE684 (C) drug sensitivity. The orange dashed line indicates the mean of randomly sampled Pearson's Rs. The red solid line indicates the Pearson's R calculated based on correlation analysis between drug sensitivity and *ALK* expression in cell lines with *ALK* fusions. One sample Wilcoxon test was performed to calculate the p-value.

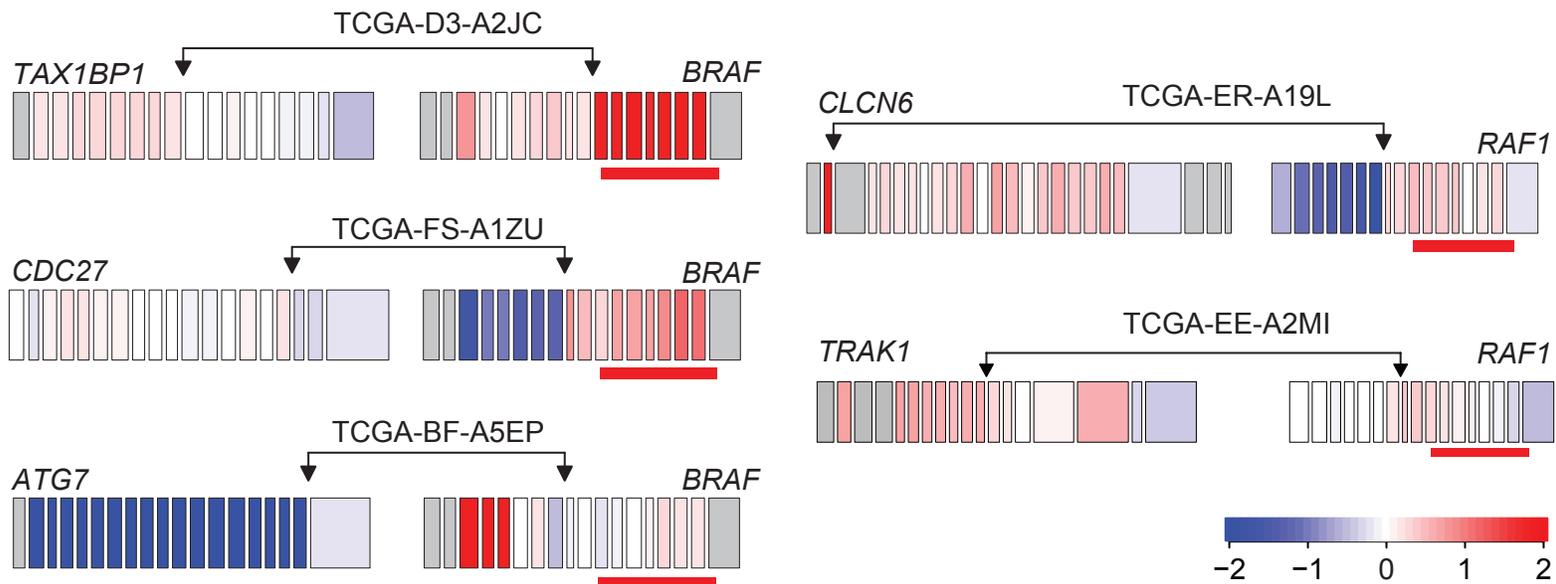


Figure S2. Structural details and exon expression profiles of *BRAF* (*TAX1BP1-BRAF*, *CDC27-BRAF*, and *ATG7-BRAF*, left) and *RAF1* (*CLCN6-RAF1* and *TRAK1-RAF1*, right) fusions.

Breakpoints are indicated by linked arrows. The mRNA expression (Z-normalized) levels relative to expression levels for each exon in the respective tumor type are shown. Red and blue colors depict high and low expression levels, respectively. Exons that code for protein tyrosine kinase domains are marked with red bars.