SUPPLEMENTAL FIGURE LEGENDS

Figure S1: Schematic representation of the index patient’s treatment history. A timeline detailing the index patient’s diagnosis and subsequent systemic therapies is depicted. Time in months is shown below the arrow. The timeline starts at the patient’s initial diagnosis.

Figure S2: Schematic representation of the study design. 37 IMT tumor samples from 33 patients were collected under IRB approved protocols. ALK immunohistochemistry (IHC) was performed on each of the 37 cases as standard of clinical care. Targeted next-generation sequencing (NGS) using the FoundationOne™ was completed in each case. 22/26 ALK IHC+ and 11/11 ALK IHC- samples were evaluable. ALK kinase fusions were detected in 20/22 (91%) of the ALK IHC+ cases. In the ALK IHC- cases, 2/11 (18%) harbored ALK fusions, 2/11 (18%) harbored PDGFRβ fusions, and 4/11 (36%) harbored ROS1 fusions. Overall, therapeutically actionable kinase fusions were detected in 28/33 (85%) of cases.

SUPPLEMENTAL TABLE LEGENDS

Supplemental Table 1: Changes in the indicated laboratory parameters after 3 cycles of crizotinib. HgB: hemoglobin, Hct: hematocrit, MCV: mean corpuscular volume, ESR: erythrocyte sedimentation rate, LDH: lactate dehydrogenase.

Supplemental Table 2: FoundationOne™ panel. This targeted next generation sequencing platform evaluates for 3769 exons of 236 cancer genes and 47 introns of 19 commonly rearranged genes, including 8 tyrosine kinases.
**Supplemental Table 3: Summary of genomic coordinates for the kinase fusions identified in this study.** The sample number is depicted in the far left column. For tumor samples in which a kinase fusion was identified, the genomic coordinates for of each of the fusion genes is indicated. There were no other recurrent alterations. *The FN1-ALK fusion was detected with RNA sequencing. #Sufficient material was available to verify these kinase fusions with RNA sequencing.