Figure S1

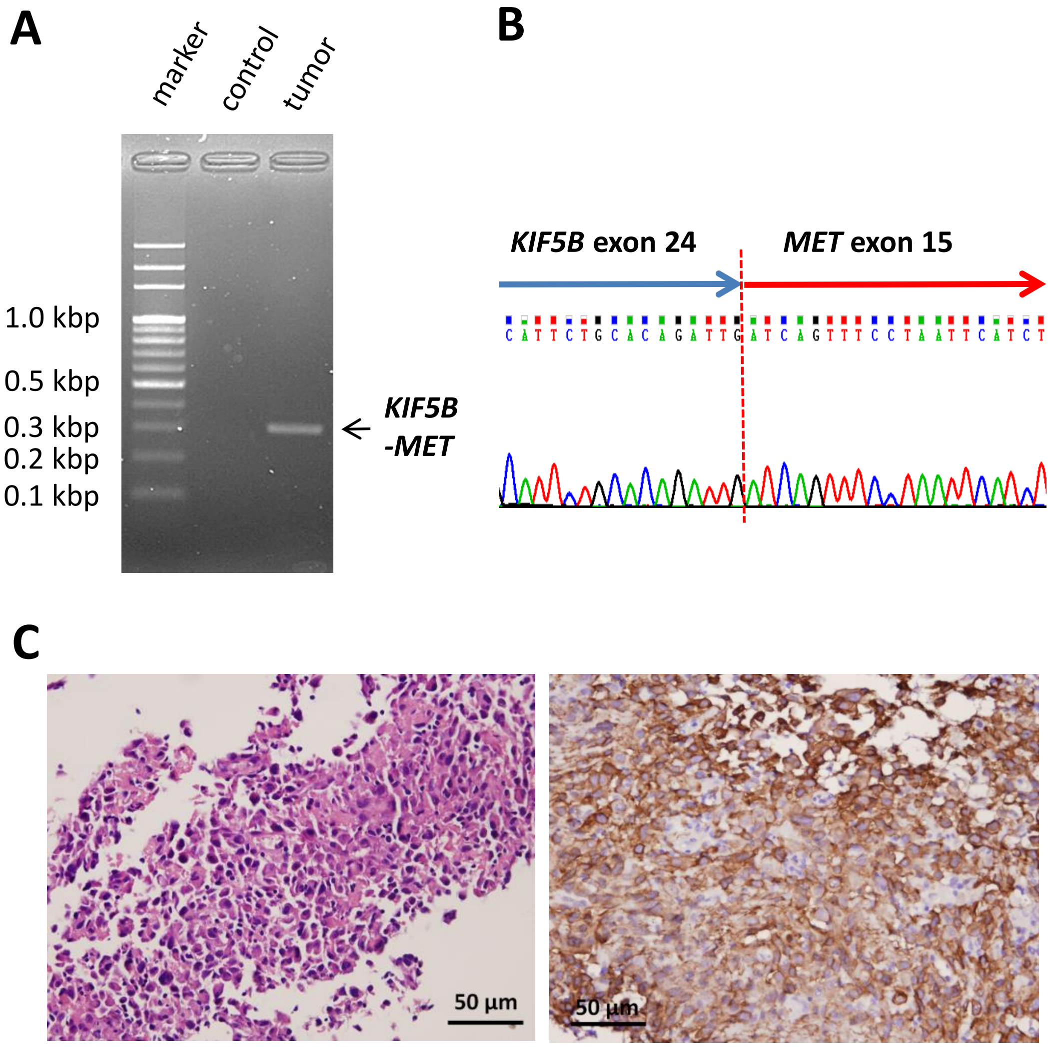

Figure S1. Identification of the *KIF5B-MET*(K24;M15) in a pulmonary sarcomatoid carcinoma patient. **(A)** An amplification product of 298 base pairs from one step RT-PCR. The control sample was from another individual with lung adenocarcinoma individual. **(B)** cDNA sequencing chromatograms showing the conjoined regions. **(C)** Pathologic examination showing a sarcomatoid features (left panel, hematoxylin-eosin stain, original magnification 400×). Immunohistochemical staining for c-MET showing strong positivity (right panel) (original magnification 400×).

Figure S2

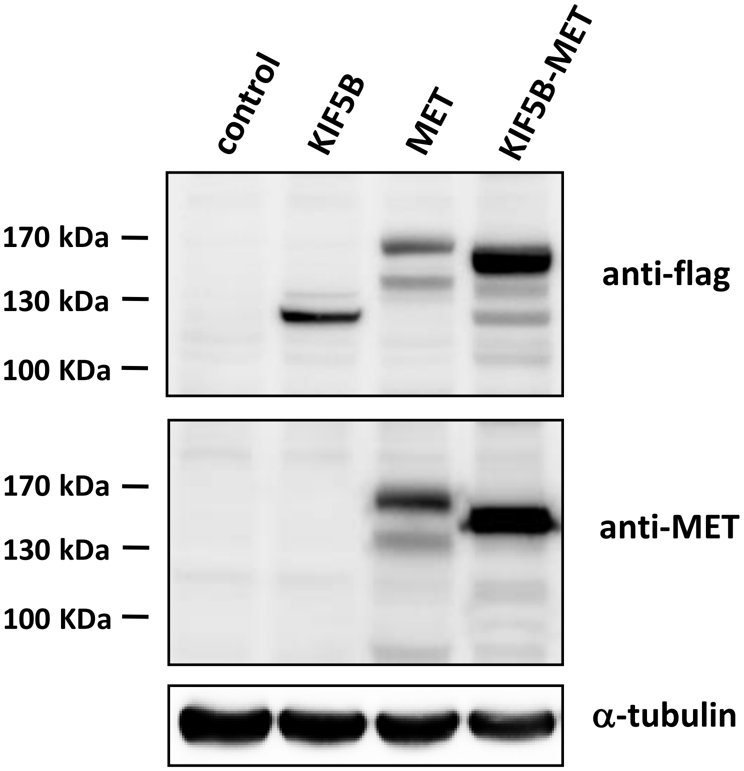

Figure S2. Expression of fusion protein in *KIF5B-MET*-positive cells. 293T cells were transfected with an empty vector (control), *KIF5B*, *MET*, or *KIF5B-MET*. The expression levels of transfected proteins in cell lysates were analyzed by western blotting. The detected protein size in *KIF5B-MET*-positive cells was corresponded to the predicted value of KIF5B-MET (149kDa), which was different from the wild-type MET or KIF5B, inferring the expression of KIF5B-MET fusion protein.

Figure S3

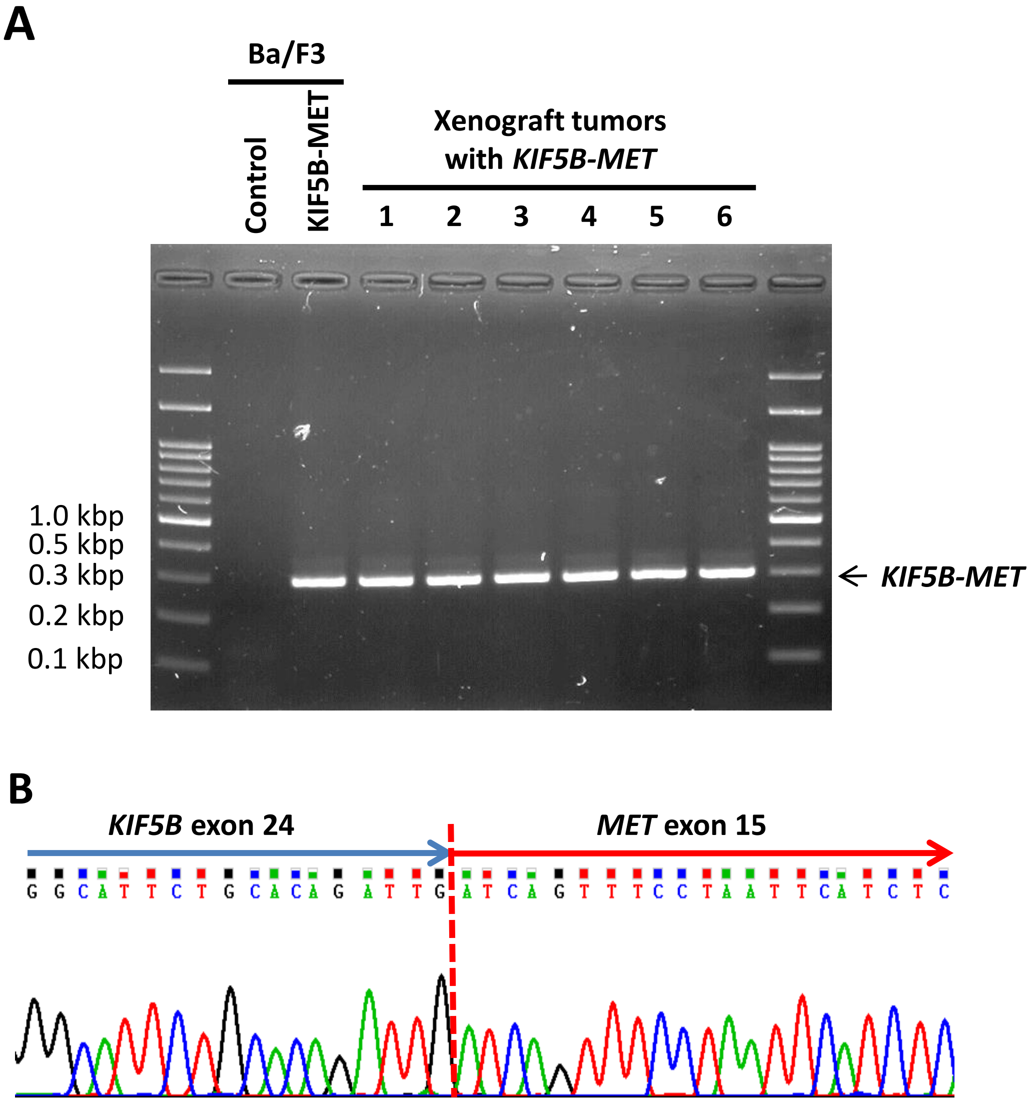

Figure S3. Confirmation of KIF5B-MET fusion transcript in xenograft tumors. **(A)** Identical amplification products of 298 base pairs by one step RT-PCR from KIF5B-MET-positive Ba/F3 cells and xenograft tumors. **(B)** cDNA sequencing chromatograms showing the conjoined regions from a xenograft tumor.