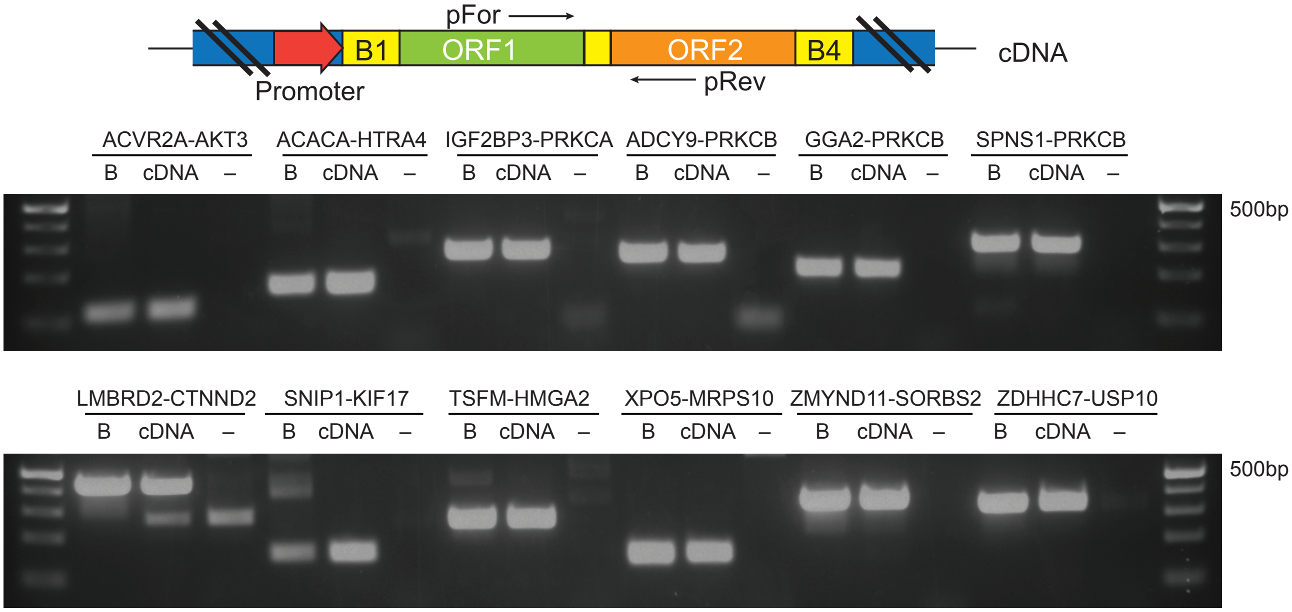
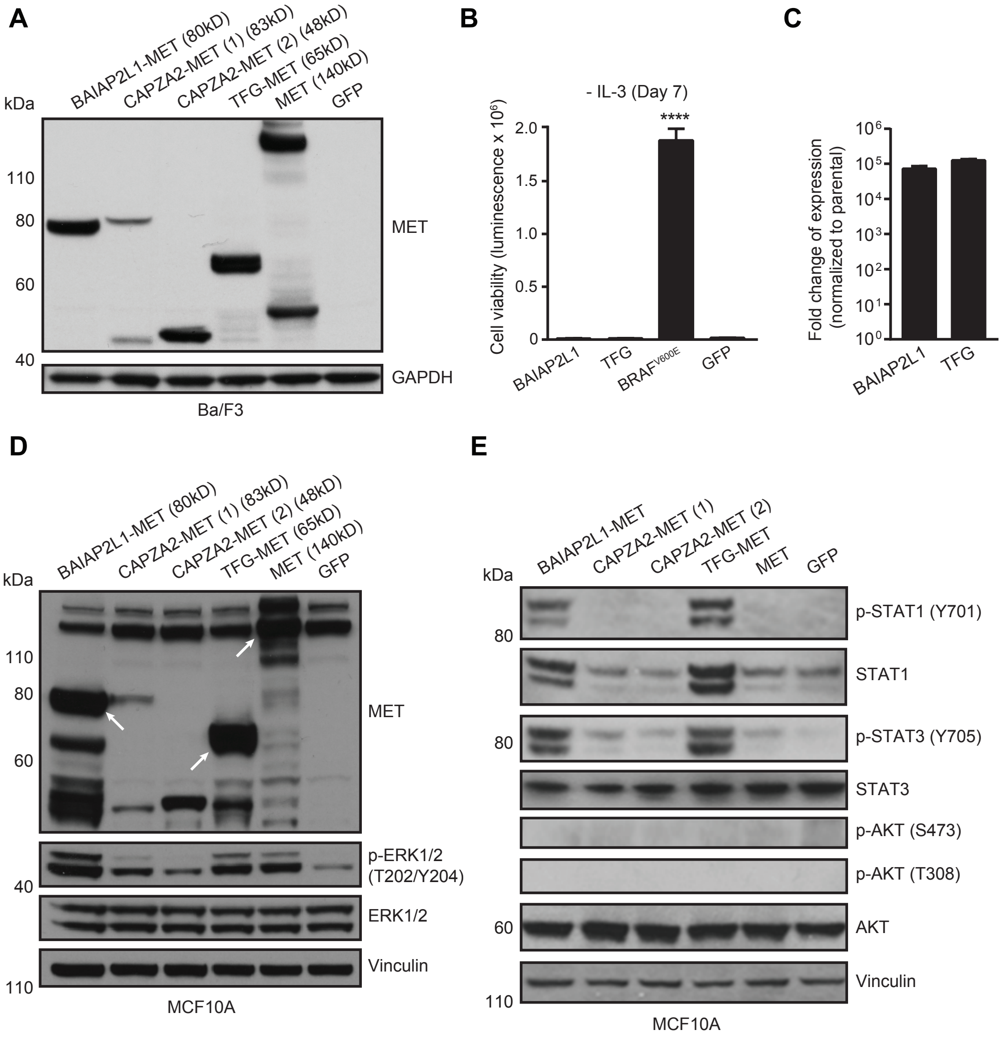
Supplementary Figure 1



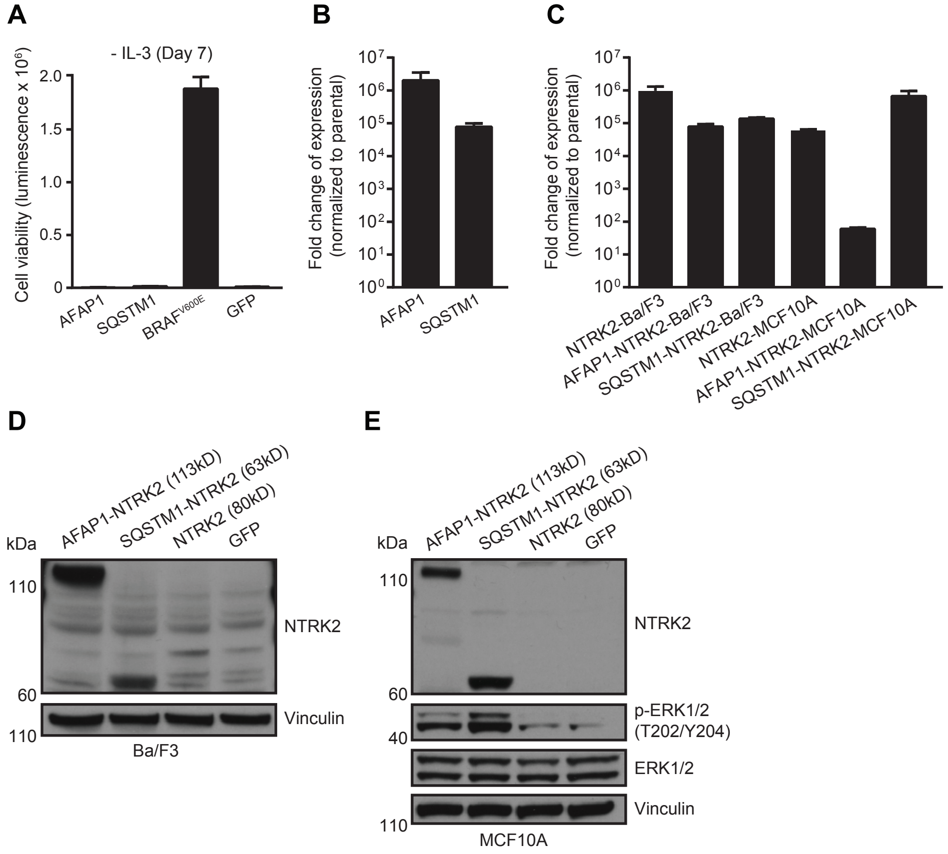
**Supplementary Figure 1**. PCR detection of the indicated fusion transcripts from Ba/F3 RNA/cDNA extracts. B = fusion DNA backbone (positive control); - = cDNA from GFP-expressing cells as negative control.

# Supplementary Figure 2



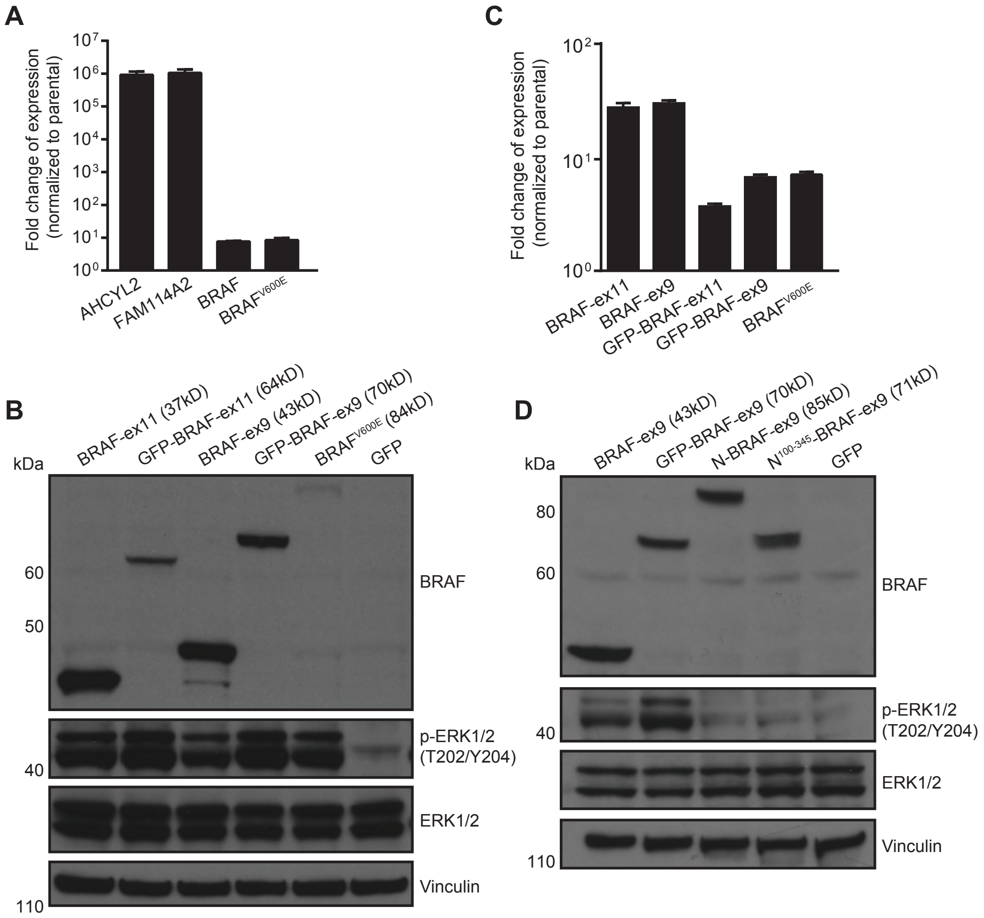
**Supplementary Figure 2.** (**A**) Immunoblots of *MET* fusions expression in Ba/F3. (**B**) Ba/F3 cell survival assay for full-length *BAIAP2L1* and *TFG* (mean luminescence, error bars denote standard deviation, N=3 respectively) compared to *BRAF*$^{V600E}$ (positive control). GFP = negative control. (**C**) Quantitative PCR of over-expression of *BAIAP2L1* and *TFG* in Ba/F3. (**D-E**) Immunoblots of *MET* fusions expression and MAPK and STAT signaling activation in MCF-10A cells. Arrow denotes the correct size of BAIAP2L1-MET, TFG-MET, and wild-type MET.

Supplementary Figure 3



**Supplementary Figure 3**. (**A**) Ba/F3 cell survival assay for full-length *AFAP1* and *SQSTM1* (mean luminescence, error bars denote standard deviation, N=3, respectively) compared to *BRAF*$^{V600E}$ (positive control). GFP = negative control. Quantitative PCR of over-expression of (**B**) *AFAP1* and *SQSTM1* in Ba/F3 and (**C**) both *NTRK2* fusions and wild-type *NRKT2* in Ba/F3 and MCF-10A cells. (**D-E**) Immunoblots of *NTRK2* fusions expression and MAPK signaling activation in Ba/F3 and MCF-10A cells.

Supplementary Figure 4



**Supplementary Figure 4**. Quantitative PCR of expression of (**A**) full-length wild-type genes as indicated in Ba/F3 and (**C**) *BRAF* kinase domains and GFP-BRAF fusions in Ba/F3. Immunoblots of expression of and MAPK signaling activation by (**B**) *BRAF* kinase domains and GFP-BRAF fusions and (**D**) *BRAF* fusion kinase domain (Exons 9-18) only (BRAF-ex9), fused to GFP (GFP-BRAF-ex9), fused to WT N-terminus (N-BRAF-ex9), and fused to AA100-345 fragment (N$^{100-345}$-BRAF-ex9) in Ba/F3 cells.