***MET* copy number assay**

Genomic DNA (gDNA) was prepared using the DNeasy® Blood and Tissue DNA kit (Qiagen, catalog #69504) according to the manufacturer’s protocol. Briefly, frozen tumor chunks were weighed on an analytical balance and 20.0-25.0 mg of tissue per sample was subjected to the gDNA isolation protocol. gDNA was eluted in 200.0 µL of elution buffer (provided with kit) and gDNA concentration quantified using a NanoDrop 1000 spectrophotometer (NanoDrop Products). All gDNAs were diluted to 5.0 ng/µL in nuclease-free H2O. *MET* copy number was determined by multiplexed quantitative PCR (qPCR) using a FAM-labeled Taqman probe targeting human *MET* (Hs05018546\_cn) and a VIC-labeled probe targeting human *RNAse P1* to act as an internal normalization control gene. qPCR was carried out in 384-well format (ABI, part #4309849) sealed with optically clear adhesive film (ABI, part # 4311971), and included the following components per 10.0 µL reaction:

5.0 µL - Taqman Gene Expression Master Mix (ABI, part #4369016).

0.5 µL - FAM-labeled *MET* CN assay probe (ABI, part #4400291).

0.5 µL - VIC-labeled *RNAse P1* CN assay probe (ABI, part #4401631).

2.0 µL - nuclease-free H2O (Ambion, part #AM9906).

2.0 µL - gDNA template (10.0 ng total)

Thermocycling conditions on an ABI 7900HT Sequence Detection System run in Standard Mode were as follows: (50°C, 2 min, 1 cycle); (95°C, 10 sec, 1 cycle); (95°C, 15 sec followed by 60°C, 1 min two-step cycle, 40 cycles). A standard curve ranging from 80.0 to 0.3125 ng/well was employed, allowing for *MET* and *RNAse P1* ng values to be calculated for each well using the Absolute Quantification (AQ) method. The *MET:RNAse P1* ng ratio was calculated for each tumor sample and normalized to that of a diploid fibroblast control sample with a *MET:RNAse P1* ratio of 1.0. All ratios were multiplied by two to obtain actual *MET* CN values (diploid control harbors two copies of *MET*).

**small-molecule MET inhibitor sensitivity (IC50 determination) assay**

AGS and GTL16 gastric cancer cell lines were obtained from an in-house repository and grown in F12/Ham’s (Gibco) and RPMI-1640 (Sigma-Aldrich) medium respectively, each supplemented with 10% calf serum and Pen/Strep antibiotic. For viability assays, 2,000 cells/well were seeded in 96-well plates in complete RPMI-1640 media lacking Phenol Red 24 hours prior to dosing. The following compounds were purchased as lyophilized powders from Selleck Chemical: SGX-523 (catalog #S1112), JNJ-38877605 (catalog #S1114), PHA-665752 (catalog #S1070). INC280, AZD6094, Sunitinib and Crizotinib were obtained from an in-house compound collection. All compounds were prepared in 100% DMSO and final [DMSO] in culture was 0.1%. Following dosing, cells were incubated at 37°C for five days and cell viability was determined using the CellTiter-Glo reagent (Promega, catalog #G7571) according to manufacturer’s instructions and luminescence measured on a Tecan plate reader instrument using Magellan software (v6.6). In order to determine cell viability relative to start of the experiment, a single plate containing quadruplicate wells of each cell line was subjected to CellTiter-Glo analysis immediately prior to dosing of all other plates (~24 hours after seeding); this plate served as a ‘Day0’ control. Cell viability data were converted into ‘viability inhibition, VI’ using the following equation:

% VI = 100-(((Day5drug-Day0)/(Day5DMSO-Day0))\*100)

Day5DMSO and Day5drug represent the luminescence signals for vehicle and drug-treated cells at the end of the experiment, respectively. Day0 represents the signal for untreated cells at the start of the experiment. Relative viability (RV) = 100-VI. RV was plotted against the log [drug] (µM) and IC50 values for each compound computed using GraphPad Prism® software (v5.00).

**Mutation analysis**

PDX mutation status was analyzed by performing targeted next generation sequencing of the genes indicated in Supplemental Table 2. NimbleGen capture platform was used to capture gene exons. The captured DNA fragments were sequenced by Illumina’s HiSeq technology and at least 50 X effective mean depths was generated for all samples. All mutations detected were manually verified using the CLC software.

**Gene expression analysis**

Gene expression data was generated using the Affymetrix platform. RNA extracted from a pool of three tumors obtained from the same PDX model at the same passage were hybridized to the Affymetrix HG-U133 Plus 2.0 Array (Affymetrix, Santa Clara, California) following the manufacturer’s guideline. The probe level intensities from the resulting raw Affymetrix CEL files were background corrected, log2 transformed and quantile normalized using the Robust Multiarray Analysis (RMA) method.