Quanterix™
The Science of Precision Health

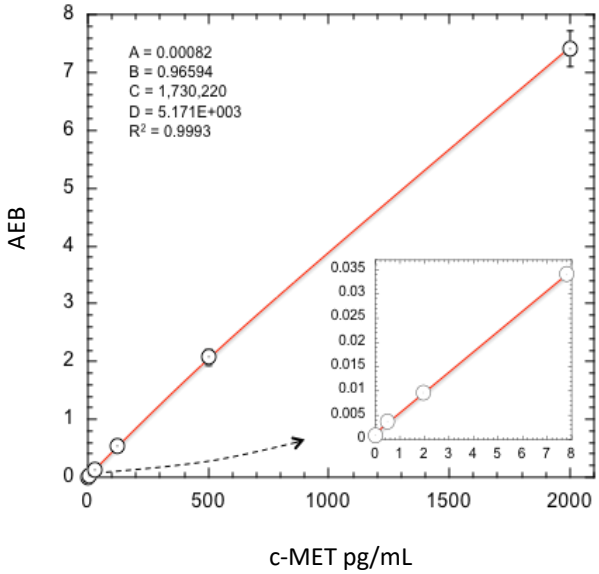
Simoa® c-MET Discovery Kit
HD-1/HD-X Data Sheet

Item 102073

Description

c-MET, also known as MET, is a receptor tyrosine kinase that, after binding with its ligand, hepatocyte growth factor, activates a wide range of different cellular signaling pathways, including those involved in proliferation, motility, migration and invasion. c-MET is encoded by the MET gene, and it transduces signals from the extracellular matrix into the cytoplasm by binding to hepatocyte growth factor/HGF ligand. c-MET is a heterodimer made of an alpha chain (50 kDa) and a beta chain (145 kDa), which are disulfide linked. Ligand binding at the cell surface induces autophosphorylation of MET on its intracellular domain that provides docking sites for downstream signaling molecules. Following activation by ligand, MET interacts with the PI3-kinase subunit PIK3R1, PLCG1, SRC, GRB2, STAT3 or the adapter GAB1. Recruitment of these downstream effectors by MET leads to the activation of several signaling cascades, including the RAS-ERK, PI3 kinase-AKT, or PLCgamma-PKC. In its inactive state, the C-terminal tail interacts with the catalytic domain and inhibits the kinase activity. Upon ligand binding, the C-terminal tail is displaced and becomes phosphorylated, thus increasing the kinase activity. Genetic polymorphisms, chromosomal translocation, overexpression, and additional splicing and proteolytic cleavage of c-MET have been described in a wide range of cancers.

Calibration Curve: Four-parameter curve fit parameters are depicted.



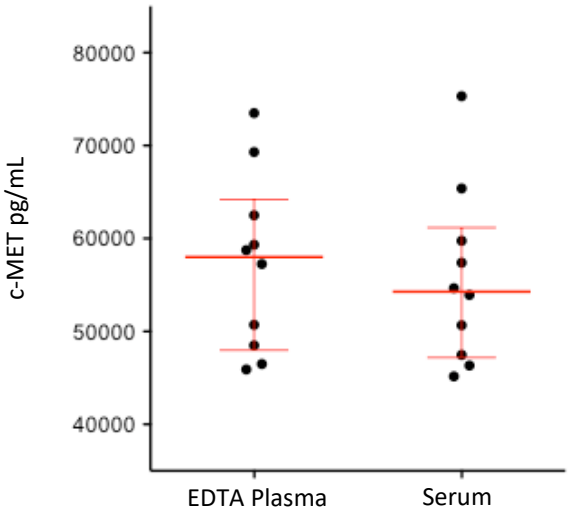
Lower Limit of Quantification (LLOQ): Triplicate measurements of serially diluted calibrator were read back on the calibration curve over 1 reagent lot on 1 instrument (6 runs total).

Limit of Detection (LOD): Calculated as 2.5 standard deviations from the mean of background signal read back on each calibration curve over 1 reagent lot on 1 instrument (6 runs total).

LLOQ	**0.244 pg/mL** pooled CV 16% mean recovery 122%
LOD	**0.036 pg/mL** range 0.024–0.049 pg/mL
Dynamic range (serum and plasma)	800 ng/mL
Diluted Sample volume*	100 µL per measurement
Tests per kit	192

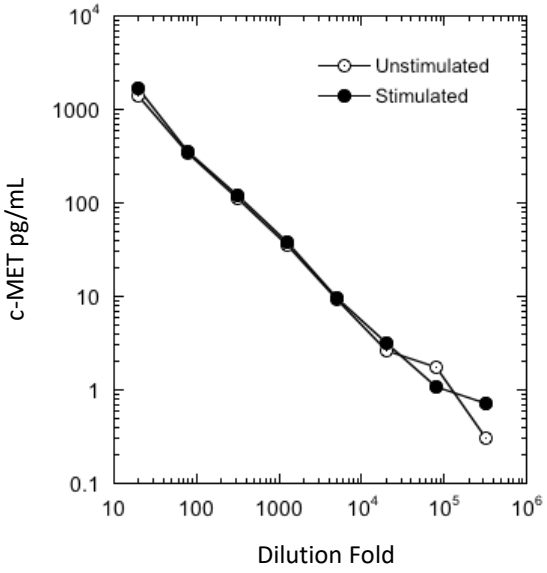
***See Kit Instruction for details**

Endogenous Sample Reading: Healthy donor EDTA plasma (n=10) and serum (n=10) were measured. Error bars depict median with interquartile range.



Sample Type	Median c-MET pg/mL	% Above LOD
Serum	54,283	100%
Plasma	58,012	100%

Dilution Fold: c-MET measured from unstimulated and stimulated A549 cell lysates.



Precision: Representative precision was estimated with repeated assay of serum panels using one instrument and one reagent lot. Within-run and between-run CVs are depicted in the following table. Within-run CVs reflect average CVs across 5 experiments of 3 replicates each.

Sample	Mean (pg/mL)	Within run CV	Between run CV
Panel 1	35.493	3.8%	9.3%
Panel 2	43,727	3.6%	8.3%
Panel 3	42,547	2.9%	5.8%

Dilution Linearity: 100x diluted serum sample diluted 2x serially to 6400x with sample diluent.

Dilution Linearity (6400x)	**Mean = 96%** Range: 94-98%