

Differential Pattern of Resistance and Sensitivity to Different Classes of MET Inhibitors for *MET*-Amplified Tumors With *MET*-D1228X or *MET*-Y1230X Mutations



To the Editor:

We thank Drs. Fujino and Mitsudomi¹ for their interest in our description of *MET* mutations as a mechanism of resistance to dual EGFR-MET inhibition in *EGFR*-mutated plus *MET*-amplified lung cancer.² The ongoing approvals and late-stage development of multiple type I *MET* tyrosine kinase inhibitors—such as capmatinib, tepotinib, savolitinib, and crizotinib—have paved the way for the use of these therapies in the clinical care of patients with tumors driven by *MET* aberrations.^{1,3-5}

However, the widespread use of type I *MET* inhibitors will also highlight the inherited vulnerability of tumor adaptation mediated by on-target resistance through *MET* kinase domain mutations, including *MET*-D1228X and *MET*-Y1230X mutations.² Some type II *MET* inhibitors (i.e., cabozantinib, merestinib, and glesatinib) have preclinical activity against *MET*-amplified tumors co-harboring *MET*-D1228X or *MET*-Y1230X mutations.^{1,2} Fujino and Mitsudomi¹ eloquently highlighted the preclinical differences in the inhibitory profiles of these two mutations and pointed toward the need for the development of more potent *MET* inhibitors with an enhanced pattern of activity against *MET* kinase domain mutations.

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