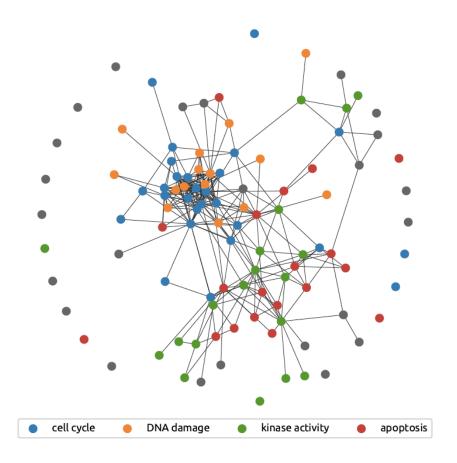
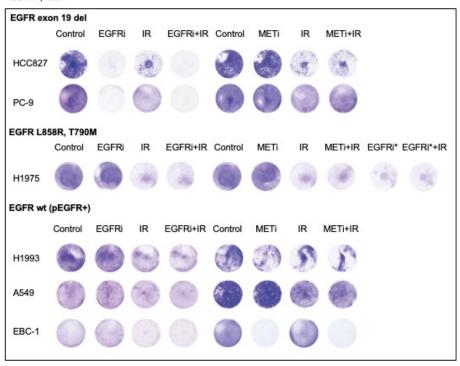
## **Supplementary figures**

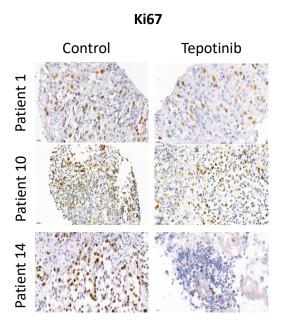


**Supplementary figure 1.** STRING-based visualization of relationships and functional GO terms of the 104 unique proteins, whose phosphopeptides were analyzed by SRM.

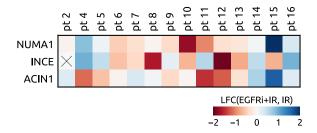
## EGFR+, MET+

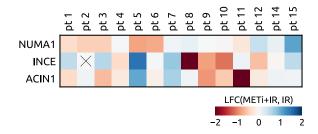


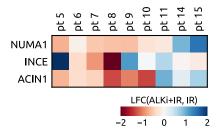
**Supplementary figure 2.** Representative pictures of viability of a panel of EGFR-positive cells towards EGFR inhibition by gefitinib (EGFRi), AZD9291 (EGFRi\*) or EMD1214063 (METi), IR and their combination. Note that parts of the figure have been reproduced from Figure 3A.



**Supplementary figure 3.** Representative pictures of immunohistochemical staining (*Ki67* – cell proliferation marker) of selected tepotinib-treated patient tissues (*control* – untreated tissues (OTCs) collected and stained at day 3, *tepotinib* – tepotinib-treated OTCs collected and stained at day 3 (48 hrs upon the start of MET inhibition).







**Supplementary figure 4.** Heat maps visualizing NUMA1, INCE a ACIN1 phosphorylation levels ratios of EGFRi (gefitinib)+IR- (top panel), METi+IR- (middle panel) or ALKi+IR- (low panel) versus IR-treated patients' tissues.