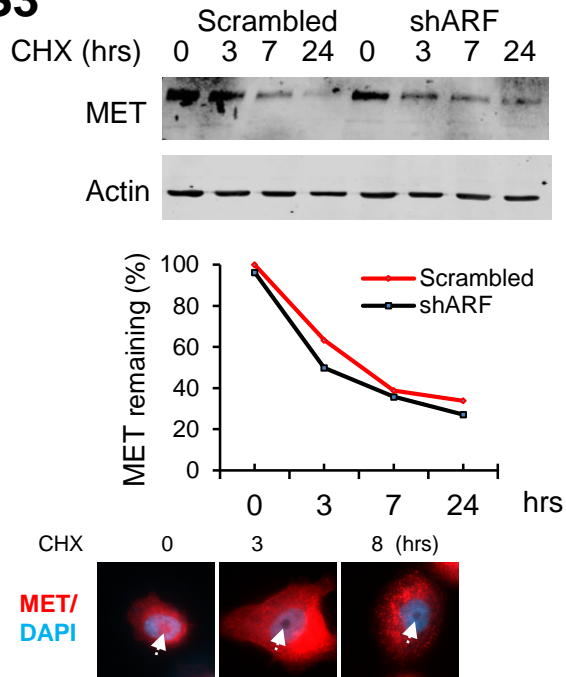


**Figure legend**

S1: IHC of MET in wild type prostate tissues.

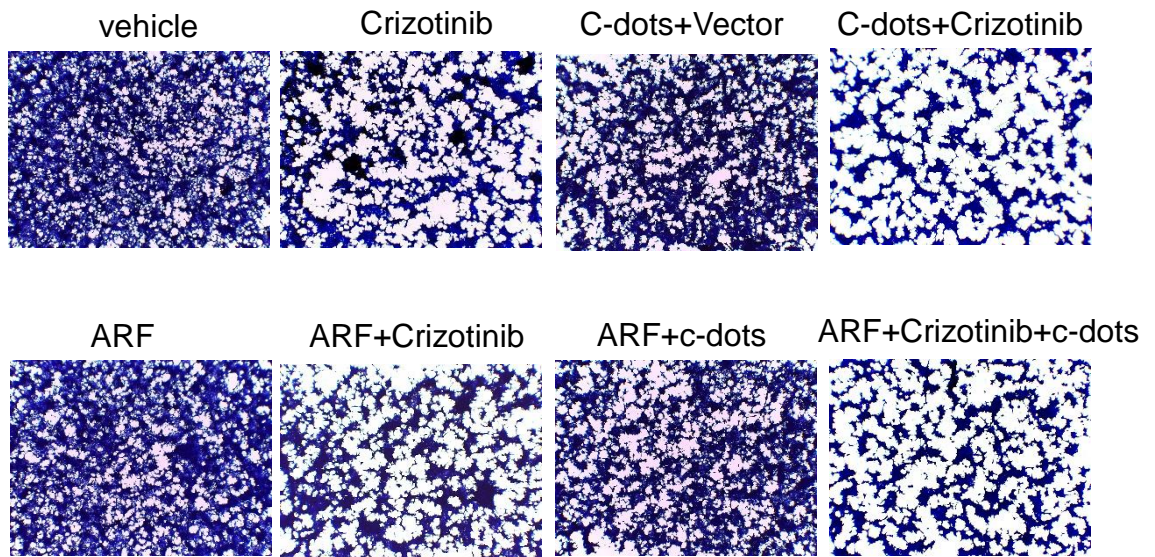
S2A: IF images showing ARF and MET colocalization in nucleus of DU145 cells.

S2B: Western blot showing MET knockdown in PC3 cells. Below images, the input of nuclear MET of 65kDa and Pim-1 in nuclear extract compared to cytosol extract.

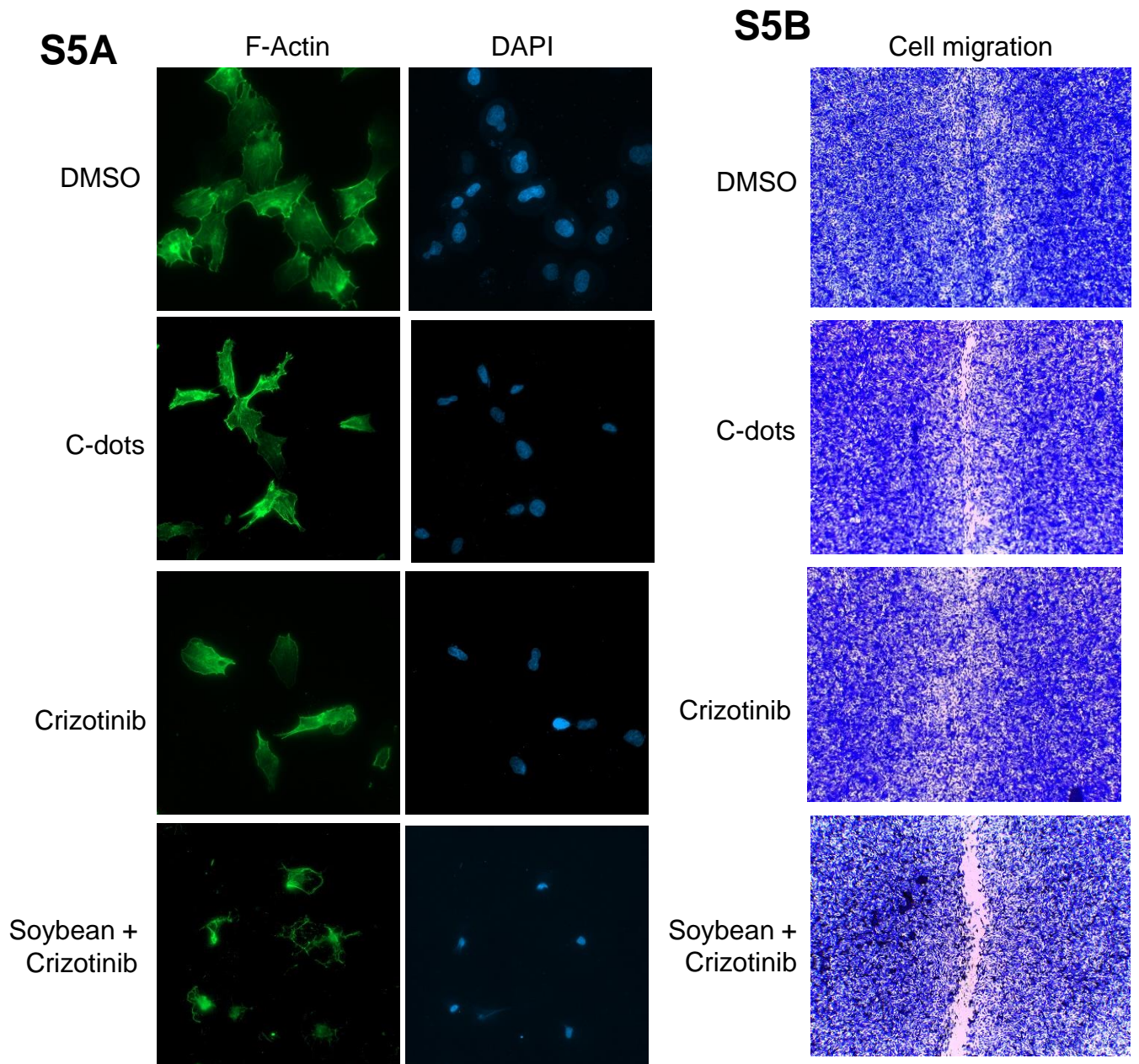
**S3****Figure legend**

S3: Cycloheximide (CHX) chase assay showing ARF knockdown decreases MET half-life from about 6.5hrs to 3 hrs in PC3 cells. 50 $\mu$ g/ml of CHX was used to chase MET protein degradation. IF analysis of nuclear MET suggests nMET is faster degraded than cytosolic MET.

S4

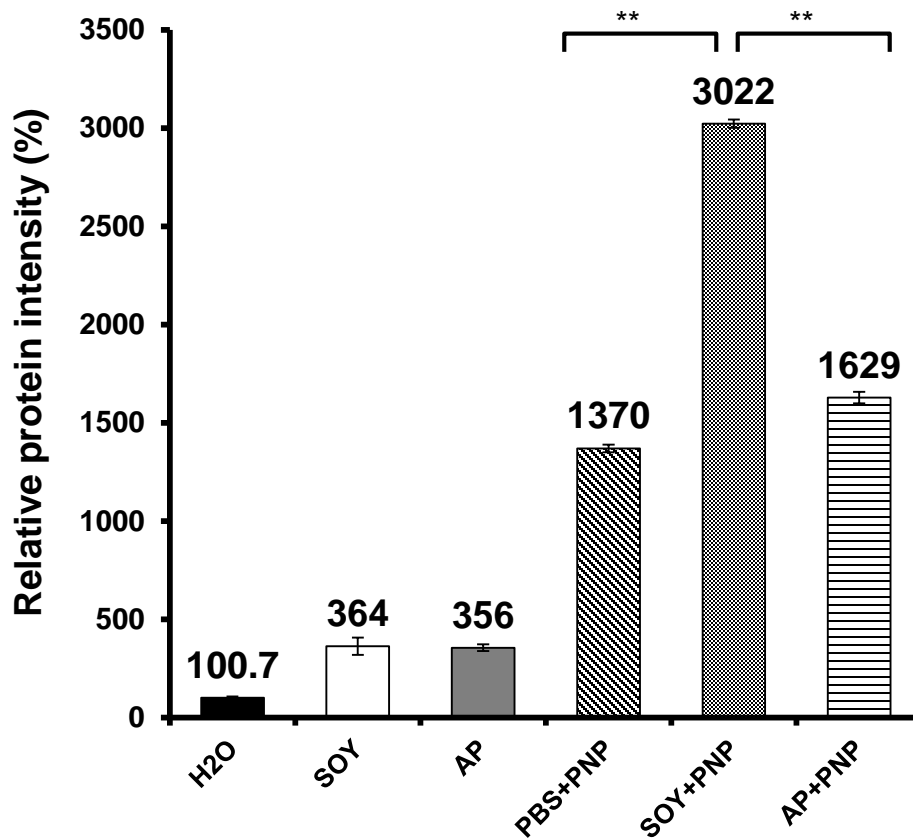
**Figure legend**

S4: ARF overexpression allow cells to resistant the efficiency of drug combination of MET inhibitor Crizotinib ( 10 $\mu$ M) with c-dots at low dose in HEK 293 cells.

**Figure legend**

S: Soybean c-dots enhanced of MET inhibitor Crizotinib efficiency to disrupt cytoskeleton F-actin and inhibit cell migration in PC3 cells. Scratch assay was used to measure cell migration and F-actin was stained by Phalloidin.

S6

**Figure legend**

Phosphatase assay of carbon nanodots using alkaline phosphatase as control and pNP as substrate. For protocols, refer to <https://www.mblintl.com/assets/JM-K412.pdf>.

## Additional Materials and Methods

**Theoretical calculation method** Protomers and rotamers of acetamide, phosphorylated tyrosine and their dimers (read main text) were investigated at Density Functional Theory (DFT) level. The (electronic ground state) molecular geometry of the investigated systems was fully optimized, both *in vacuo* and in the aqueous solution. The results were obtained by employing hybrid (*viz.* B3LYP[1], and M06-2X[2]) and long-range corrected functionals (*viz.* CAM-B3LYP[3] and  $\omega$ -B97X[4]), coupled with the Pople triple- $\zeta$  6-311++G\*\* basis set. The D3 version of Grimme's semi-empirical dispersion with Becke-Johnson damping GD3BJ[5] was also included in the case of the B3LYP, CAM-B3LYP, and  $\omega$ -B97X functionals. Solvent effects were taken into account via the implicit polarizable continuum model in its integral equation formalism (IEF-PCM).[6] The molecular cavity was built using the SMD parameterization.[7] The standard values for dielectric constant and refractive index were always assumed. The vibrational frequencies and thermochemicals were computed in harmonic approximation at  $T = 298.15$  K and  $p = 1$  atm, in high precision mode, and no imaginary frequencies were found.

The atomic charge population analysis, electric multiple moments, electronic density, and electrostatic potential were also computed using Mulliken's and the CHelpG procedure[8].

To investigate the presence and nature of possible intramolecular H-bonding interactions, two different approaches were used: (1) topological analysis based on Bader's atoms in molecules (AIM) theory[9] and (2) the non-covalent interaction (NCI) index combined with the second derivative of the reduced density gradient along the second main axis of variation [10]. Hessian of electron density was additionally calculated at along RDG isosurface with  $|\text{isovalue}| = 0.5$ :

$$s = \frac{1}{2(3\pi^2)^{1/3}} |\nabla\rho|/\rho^{4/3}, \quad (1)$$

where  $\rho$  is the electron density.

The integration grid for the electronic density for topological and RDG analysis was set to 150 radial shells and 974 angular points. For the rest of the calculations, the integration grid was set as 99 radial shells and 590 angular points. The convergence criteria of the self-consistent field were set to  $10^{-12}$  for the RMS change in the density matrix and  $10^{-10}$  for the maximum change in the density matrix. The convergence criteria for optimizations were set to  $2 \times 10^{-6}$  a.u. for maximum force,  $1 \times 10^{-6}$  a.u. for RMS force,  $6 \times 10^{-6}$  a.u. for maximum displacement and  $4 \times 10^{-6}$  a.u. for RMS displacement.

All optimization and frequency calculations were performed using the GAUSSIAN G09.E01 software package.[10] The location of BCPs and subsequent calculation of SF values were performed using a modified version of the PROAIMV program.[12] The calculation of the RDG and its derivatives were performed using homemade code.

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