DioSensAITM

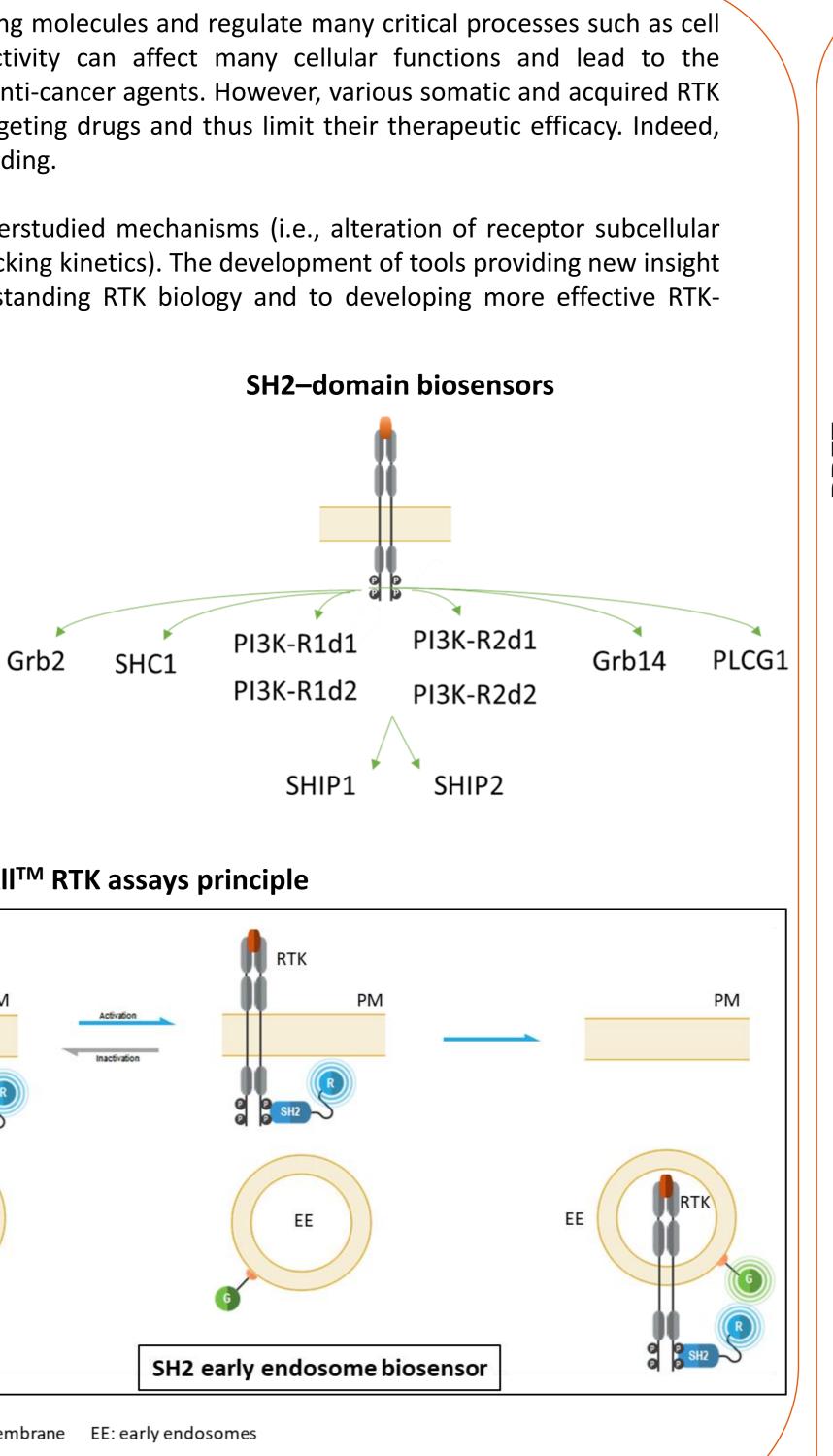


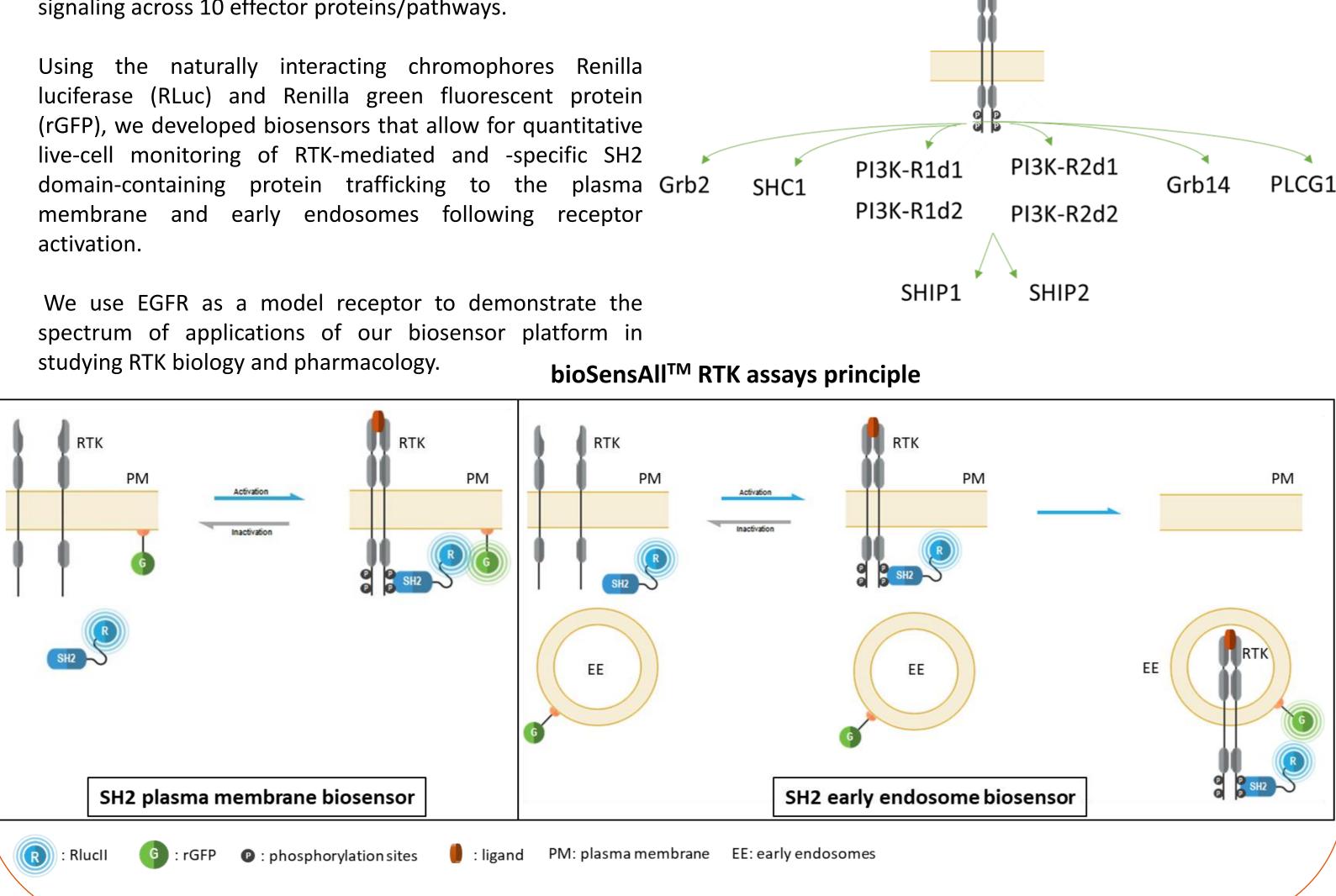
Abstract number: #3160 Session: Innovative Assay Technologies Poster number: 6304

Receptor Tyrosine Kinases (RTKs) bind to a variety of signaling molecules and regulate many critical processes such as cell growth, differentiation and survival. Dysregulated RTK activity can affect many cellular functions and lead to the development of cancer, making RTKs prime targets for new anti-cancer agents. However, various somatic and acquired RTK mutations have been shown to confer resistance to RTK-targeting drugs and thus limit their therapeutic efficacy. Indeed, RTK mutations may alter receptor activity or prevent drug binding.

Additionally, mutations may act via more complex and understudied mechanisms (i.e., alteration of receptor subcellular localization, dimerization, signaling bias, and signaling / trafficking kinetics). The development of tools providing new insight into these complex mechanisms is crucial to better understanding RTK biology and to developing more effective RTKtargeting drugs.

We present herein a live-cell BRET-based biosensor platform allowing for real-time spatiotemporal monitoring of RTK signaling across 10 effector proteins/pathways.





Conclusion : technology advantages

This study highlights the applicability of our biosensor platform to perform in depth characterization of RTK biology and pharmacology. The bioSensAll[™] RTK platform represents a tool for the development and characterization of novel TKIs, effective against various mutations involved in drug resistance.

Capacity to:

- Identify signaling and trafficking bias
- Analyze trafficking to cellular compartments
- Detect mutation-induced variations in the signaling of RTKs
- Study untagged receptors
- Adapt assays to a HTS compatible format
- Characterize small molecules and biologics-based therapeutics

Decrypting EGFR signaling with BRET biosensors: A novel approach to study RTK mutations and the effects of inhibitors

Florence Gross^{1*}, Guilhem Dugast¹, Arturo D. Mancini¹, Stephan Schann², Xavier Leroy² ¹Domain Therapeutics NA Inc., Montréal, Canada / ²Domain Therapeutics, Strasbourg-Illkirch, France

<u>Figure 1</u>: Profiling of EGFR ligands – recruitment of **PLCG1** Dose response curves and real-time kinetics upon EGF and Epiregulin stimulation ⁸⁰⁰⁰1 → EGF 🗕 Epiregul 6000-<u>2</u> 4000 2000 - EC50 **EGF** : 0,06nM **Epiregulin**: 3,3nM -12 -10 -14 log [ligands] (M) 8000-<u>2</u> 4000 - No stim. 2000-EGF (EC80) Epiregulin (EC80) n= 4 1000 2000 3000 Time (s)

EGF, Compared to Epiregulin is less potent in promoting the recruitment of PLCG1 effector at the plasma membrane.

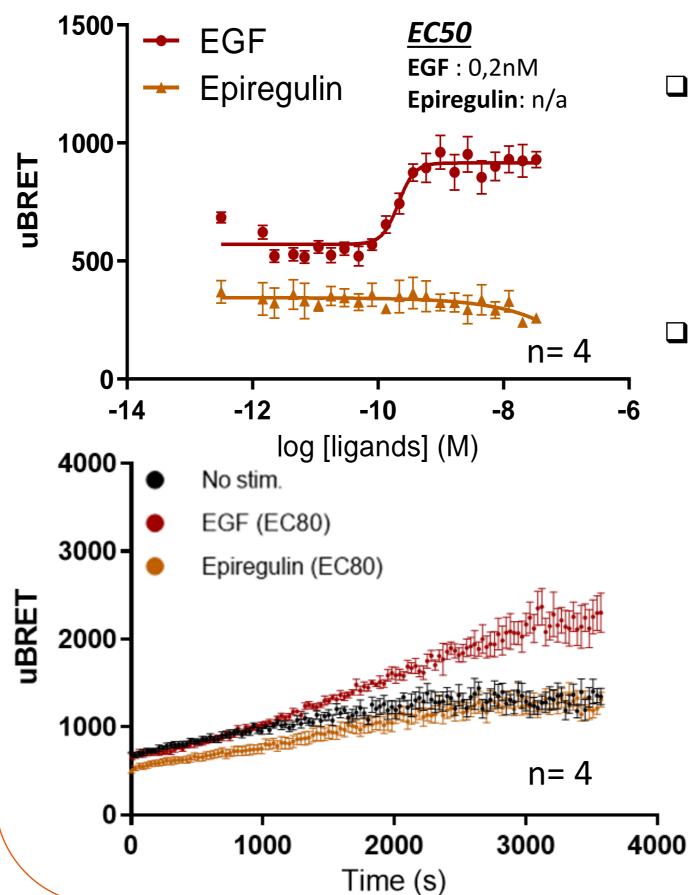
- PLCG1 EGF-induced effector recruitment was more efficacious compared Epiregulin, but Epiregulin-induced PLCG1 recruitment effector displayed faster kinetics relative to that observed with EGF.
- RTK biosensor enables to platform discriminate the effects of different agonists and to assess signaling kinetics timescales ranging on milliseconds to from hours.

Endosomes

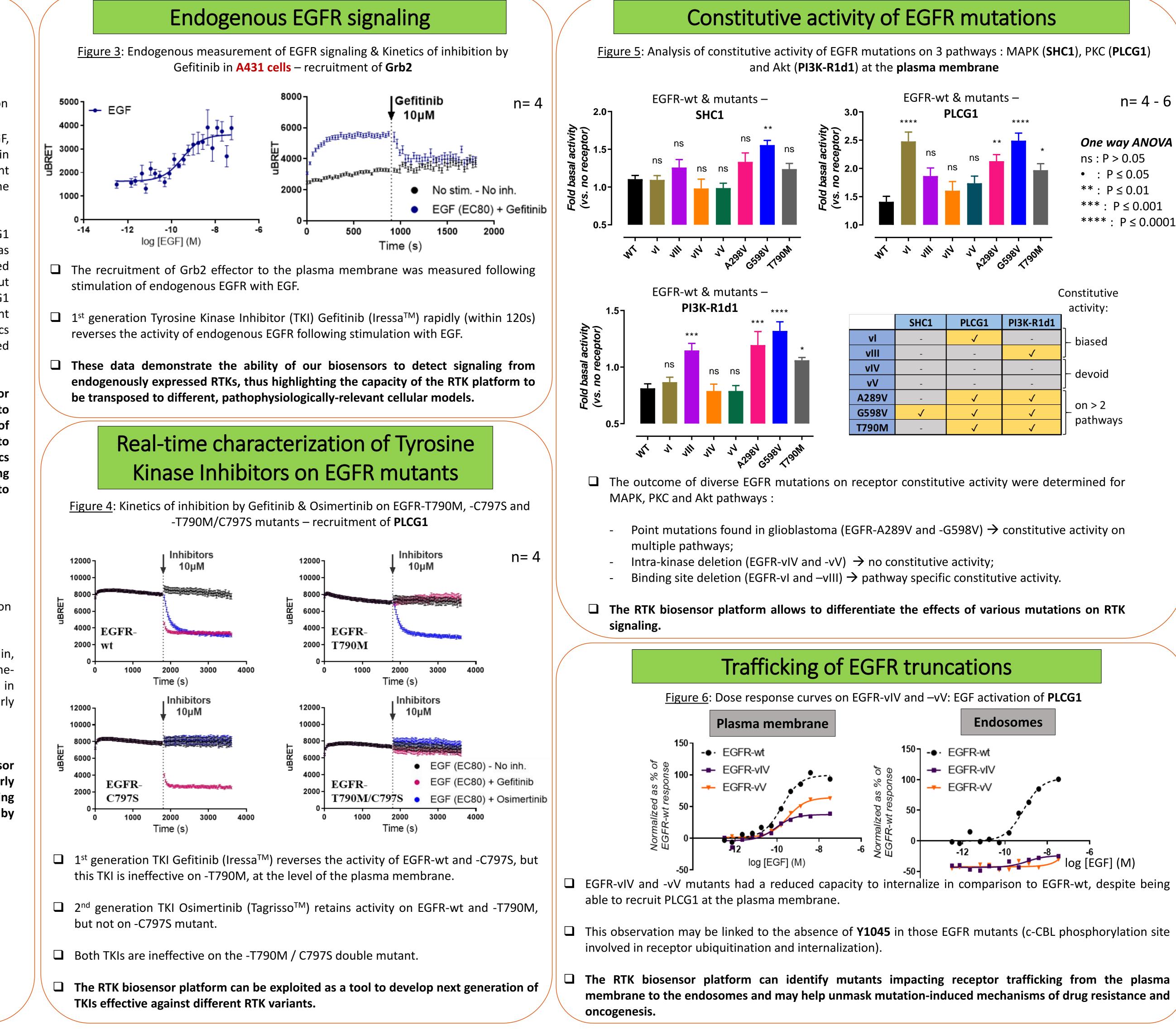
Characterization of EGFR

Plasma membrane

Figure 2: Ligand-biased trafficking of the recruitment of **PLCG1** to EGFR Dose response curves and real-time kinetics upon EGF and Epiregulin stimulation



- **G** EGF, but not Epiregulin, promoted a gradual timedependent increase in PLCG1 levels in the early endosome compartment
- 🛛 The biosensor RTK platform permits to clearly depict the unique signaling signature induced by different EGFR ligands.





^{*}Presenter information: Florence Gross fgross@domaintherapeutics.com

Figure 5: Analysis of constitutive activity of EGFR mutations on 3 pathways : MAPK (SHC1), PKC (PLCG1)

ns : P > 0.05 • : P ≤ 0.05 **: P≤0.01 ***: P ≤ 0.001 ****: P ≤ 0.0001

- Point mutations found in glioblastoma (EGFR-A289V and -G598V) → constitutive activity on

GEFR-vIV and -vV mutants had a reduced capacity to internalize in comparison to EGFR-wt, despite being

This observation may be linked to the absence of **Y1045** in those EGFR mutants (c-CBL phosphorylation site

□ The RTK biosensor platform can identify mutants impacting receptor trafficking from the plasma membrane to the endosomes and may help unmask mutation-induced mechanisms of drug resistance and