An anchoring protein ZFYVE9 (SARA) does not recruit SMAD2/3 to TGFB1:TGFBR2:p-TGFBR1 KD Mutants

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Introduction

Reactome is open-source, open access, manually curated and peer-reviewed pathway database. Pathway annotations are authored by expert biologists, in collaboration with Reactome editorial staff and cross-referenced to many bioinformatics databases. A system of evidence tracking ensures that all assertions are backed up by the primary literature. Reactome is used by clinicians, geneticists, genomics researchers, and molecular biologists to interpret the results of high-throughput experimental studies, by bioinformaticians seeking to develop novel algorithms for mining knowledge from genomic studies, and by systems biologists building predictive models of normal and disease variant pathways.

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Literature references

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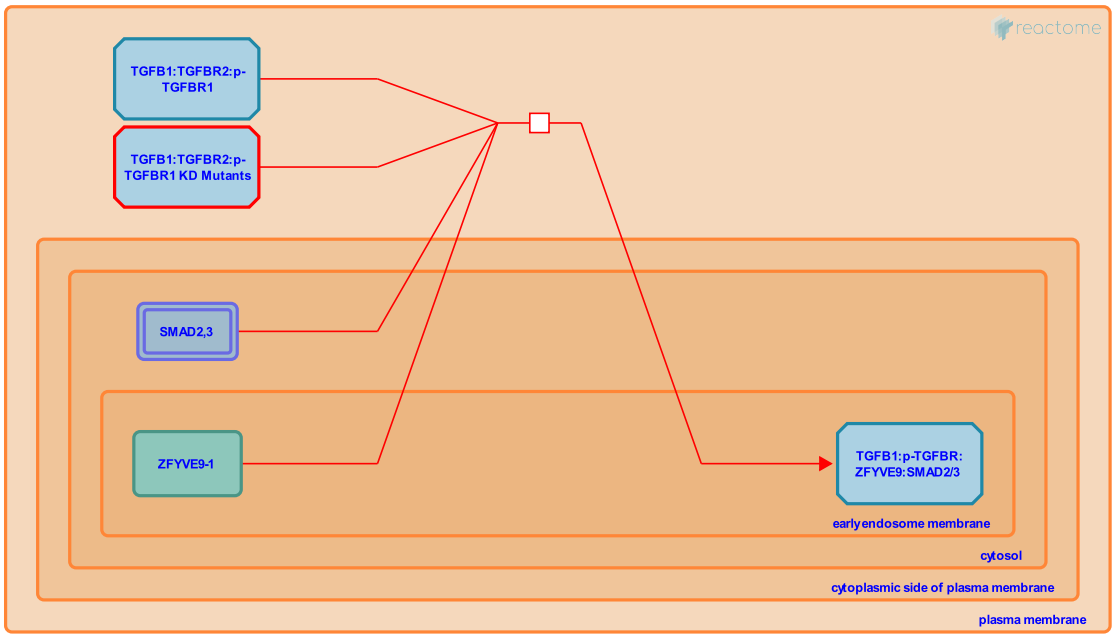
Stable identifier: R-HSA-3656523

Type: transition

Compartments: cytosol, early endosome membrane, plasma membrane

Diseases: cancer



It is assumed that TGFBR1 kinase domain (KD) mutants found in Ferguson-Smith tumor (multiple self-healing squamous epithelioma, MSSE), which have truncated KD or internal deletions in the KD (Goudie et al. 2011), cannot bind SMAD2 and SMAD3, but this has not been experimentally examined. The interaction with R-SMADs requres the presence of the L45 loop in the TGFBR1 kinase domain (amino acid residues 265-273), which is missing in some of the TGFBR1 KD truncation mutants (Chen et al. 1998). Other kinase domain regions may also be involved in the interaction with SMAD2/3 or the conformation and presentation of the L45 loop.

As TGFBR1 residues phosphorylated by TGFBR2 are upstream of kinase domain (KD) mutations that cause truncations or internal deletions in the TGFBR1 KD (Goudie et al. 2011), it is assumed that TGFBR1 KD mutants can still bind to TGF-beta (TGFB1)-activated TGFBR2 and undergo TGFBR2-mediated phosphorylation, but this has not been experimentally examined.

Literature references

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Editions

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