Supplemental Materials

Muscarinic receptor agonist-induced β Pix binding to β -catenin promotes colon neoplasia

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Supplemental Table 1. PCR primers used in this work.

Genes	Earward primar assurance 5' 2'	Reverse primer sequence 5'-3'	
Human	Forward primer sequence 5 - 5		
ARHGEF7	TTCATGCGCCTGGATAAATA	CCTCTTCCGGACTTCTTGAC	
CHRM3	TGGTTTGATGCTCCTACCTG	AGGACAGAGGAGTGGACCAG	
c-MYC	CATACATCCTGTCCGTCCAAG	GAGTTCCGTAGCTGTTCAAGT	
CCND1	AAGCTGTGCATCTACACCGA	CTTGAGCTTGTTCACCAGGA	
PTGS2	AGCACTTCACGCATCAGTTT	CGCAGTTTACGCTGTCTAGC	
B2M	GAGGCTATCCAGCGTACTCC	ATGGATGAAACCCAGACACA	
Murine			
Axin2	CAGAGGGACAGGAACCACTC	TGCCAGTTTCTTTGGCTCTT	
с-Мус	CAGCAGCGACTCTGAAGAAG	GACTCCGACCTCTTGGCA	
CcnD1	CAACGCACTTTCTTTCCAGA	GACTCCAGAAGGGCTTCAAT	
Ptgs2	AGCCTTCTCCAACCTCTCCT	CAGGGATGAACTCTCTCCGT	
B2m	CCAAGACCGTCTACTGGGAT	TCTTTCTGCGTGCATAAATTG	

Supplemental Figure 1



Supplemental Fig. 1. Muscarinic receptor antibody specificity. (**a**) Normal colon tissue sections obtained from WT, *Chrm1*, *Chrm3*, and dual *Chrm1/Chrm3* knockout mice were immunostained with anti-M₁R and anti-M₃R antibodies. Representative images confirm that M₁R and M₃R immunostaining, respectively, was absent in tissues from M₁R- and M₃R-deficient mice. Size bars, 50 µm. (**b**) Basal CD133 and M₁R staining in normal colon epithelial cells. Images show H&E (left panels) and immunofluorescent staining with DAPI (nuclear stain, blue), CD133 (red-Alexa Fluor 594), M₁R, and merged images. Size bars in H&E image, 50 µm. (**c**) Basal CD133 and M₃R staining in normal colon epithelial cells. Images show H&E (left panels) and immunofluorescent staining with DAPI (nuclear stain, blue), CD133 (red-Alexa Fluor 594), M₁R, and merged images. Size bars in H&E image, 50 µm. (**c**) Basal CD133 and M₃R staining in normal colon epithelial cells. Images show H&E (left panels) and immunofluorescent staining with DAPI (nuclear stain, blue), CD133 (red-Alexa Fluor 594), M₃R, and merged images. Arrows indicate epithelial lining. Size bars in H&E image, 50 µm.



Supplemental Fig. 2. Expression levels of CHRM3 and ARHGEF7 in colorectal adenocarcinoma. (a) Effect of CHRM3 expression levels on patient survival. Lower levels of CHRM3 expression were associated with prolonged survival (p=0.031). Image downloaded from UALCAN server. Survival probability was examined by Kaplan-Meier analysis and statistical significance determined using the log rank test. (b) Relationship between gene amplification and transcriptional upregulation of ARHGEF7 in CRC. (cBioPortal analysis of the TCGA PanCancer Atlas dataset, www.cBioportal.org). (c) ARHGEF7 copy number alterations in colon tumor samples obtained from 526 patients (333 colon adenocarcinomas; 137 rectal adenocarcinomas; 56 mucinous colorectal adenocarcinomas) reveal 15 missense mutations in 13 patients with an overall frequency of ARHGEF7 mutation of 2.4%. (d) Although there is no apparent difference in ARHGEF7 mRNA expression between colon adenocarcinoma, colorectal mucinous adenocarcinoma, and rectal adenocarcinoma, ARHGEF7 missense mutations were more common in colon compared to rectal adenocarcinoma. (e) CHRM3 copy number

alterations in colon tumor samples obtained from 526 patients (333 colon adenocarcinomas; 137 rectal adenocarcinomas; 56 mucinous colorectal adenocarcinomas) reveal 11 missense and 5 truncating mutations in 16 patients with an overall frequency of *CHRM3* mutation of 3.0%. (f) There is no apparent difference in *CHRM3* mRNA expression and mutations between colon, colorectal mucinous, and rectal adenocarcinomas.

Supplemental Figure 3



Supplemental Fig. 3. Lack of correlation between *ARHGEF7* and *CHRM3* mRNA expression levels with *PTGS2* mRNA expression levels in human colon adenocarcinomas. Univariate mixed models incorporating participant ID as a random effect were employed to compare (**a**) *ARHGEF7* and (**b**) *CHRM3* expression levels as a function of *PTGS2* levels in colon adenocarcinomas and paired adjacent normal tissue samples (n=78 for each). Values are expressed as 'normalized read counts' as described in Methods. No correlation was found between *PTGS2* and *ARHGEF7* (*p*=0.471) or *CHRM3* (*p*=0.869) mRNA expression levels.

Original uncut gels for immunoblots (the following images show the respective regions of the original blots, labelled using red boxes delineating the cropped versions shown in the manuscript figures). In red, we also indicated the proteins that was targeted for analysis. To ascertain that equal amounts of cytoplasmic and nuclear proteins were included in the extracted protein *input* for immunoprecipitation, in preliminary gels we used β -actin and H2A loading controls, respectively. Then, we immunoblotted immunoprecipitates for expression of the *bait* protein as a second loading control (e.g., immunoblotting for β Pix following immunoprecipitation with anti- β Pix antibody).

Fig. 2d



Fig. 3a









Fig. 3c



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Fig. 3e











Fig. 3g





Fig. 3i



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Fig. 4a

















Fig. 5c





Fig. 5e



Fig. 6g

Fig. 6g_Ctl & CKO1,2



Fig. 6g_Ctl & CKO 3,4,5,6

