Figure S1. Expression of *RIZ1* (PRDM2-001) and *RIZ2* (PRDM2-003) transcripts in COAD and its subtypes on GEPIA2. Differentially expressed *RIZ1* and *RIZ2* transcripts in COAD samples (A). *RIZ1* and *RIZ2* overexpression in tumor samples compared to normal tissues (B). *RIZ2* expression in COAD subtypes with microsatellite instability-high (MSI-H), microsatellite instability-low (MSI-L), or microsatellite stability (MSS) (C). Histograms represent the *PRDM2* gene expression by qRT-PCR in colon cancer cell lines with MSI (DLD1, HCT116, SW48) and with MSS (SW620). Their expression was verified using two sets of primers recognizing sequences *RIZ1* specific or a common region to both *RIZ1* and *RIZ2* (and indicated as *RIZex8*) (D).
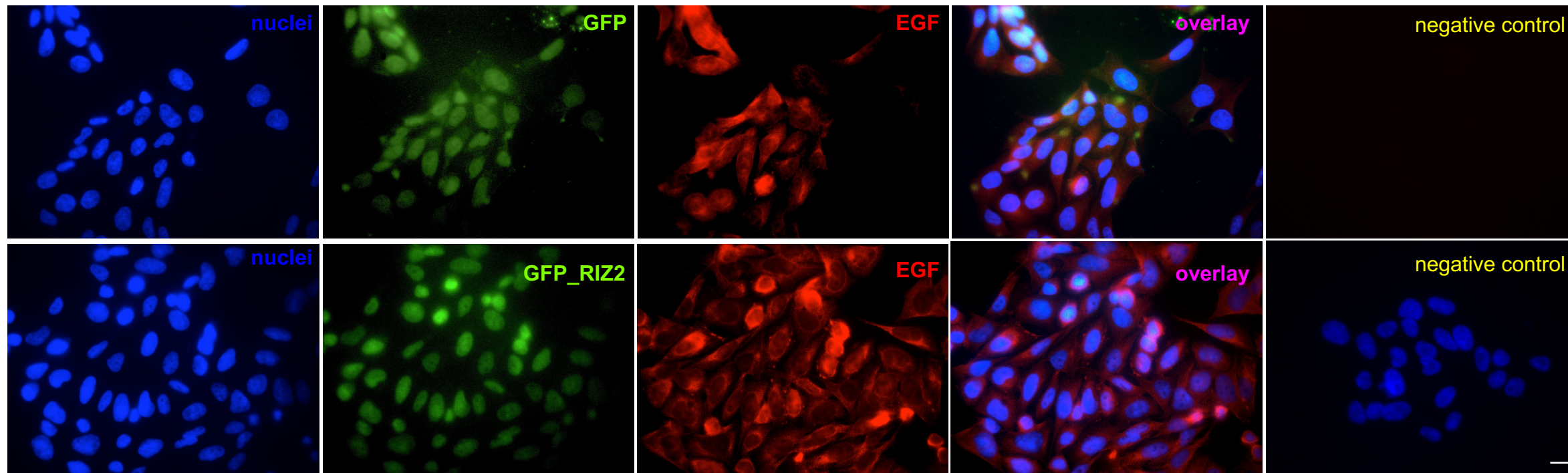
Figure S2: Immunofluorescence analysis with the anti-EGF antibody (red) on DLD1-pEGFP and DLD1-pEGFP_hRIZ2 positive cells (green). Nuclei are stained in blue. Cells stained with the secondary antibody alone, as negative control, are reported.
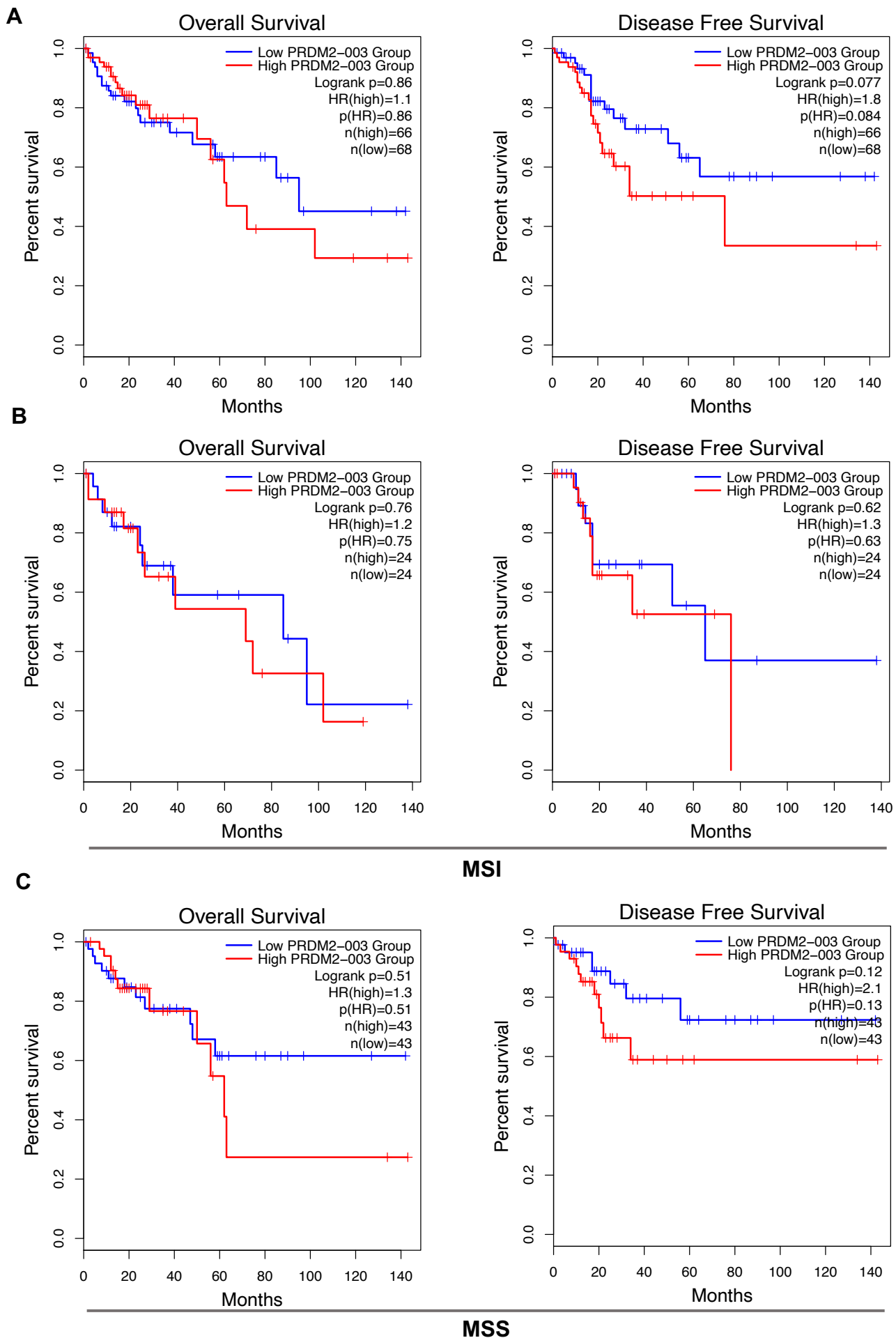
Figure S3: Analysis of Overall Survival and Disease-Free Survival correlation with *RIZ2* (PRDM2-003) expression in TCGA-COAD patients. Analysis was carried out on GEPIA2 platform using either the whole COAD dataset (A) and on patients grouped according to the MSI status (B and C).
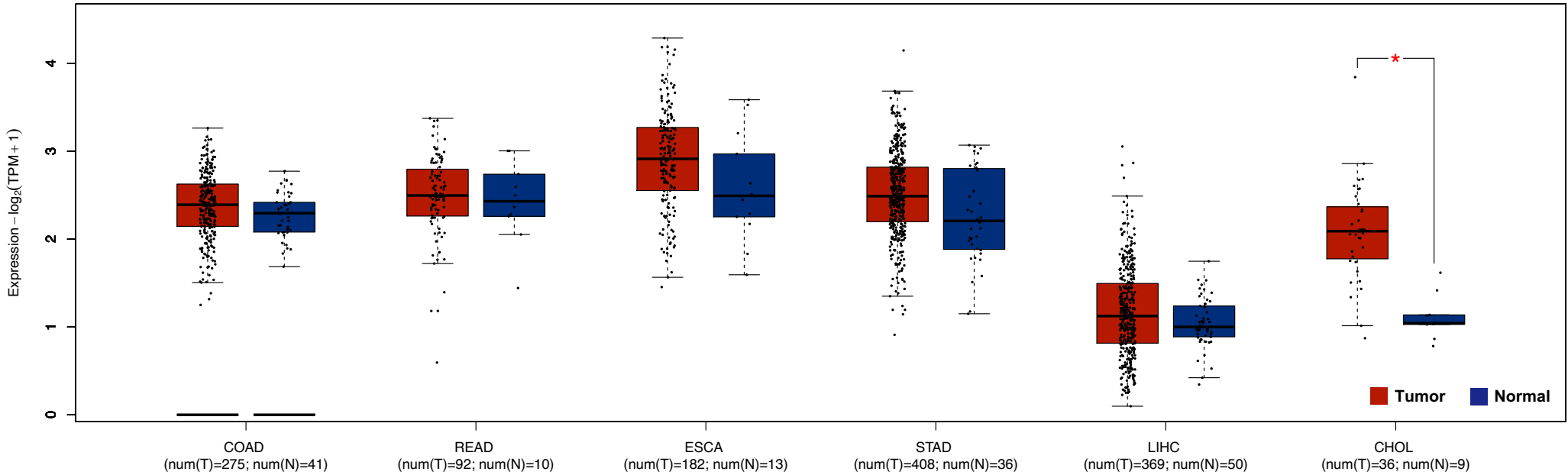
PRDM2-003

Figure S4: Expression of PRDM2-003 in tumors of the gastroenterological system. GEPIA2 analysis of *RIZ2* (PRDM2-003) transcript in tumor samples compared to normal tissues of the following TCGA datasets: COAD (Colon adenocarcinoma), READ (Rectum adenocarcinoma), ESCA (Esophageal carcinoma), STAD (Stomach adenocarcinoma), LIHC (Liver hepatocellular carcinoma) and CHOL (Cholangio carcinoma).