Supplementary Materials: Early Assessment of Colorectal Cancer by Quantifying Circulating Tumor Cells in Peripheral Blood: ECT2 in Diagnosis of Colorectal Cancer

Chih-Jung Chen, Wen-Wei Sung, Hung-Chang Chen, Yi-Jye Chern, Hui-Ting Hsu, Yueh-Min Lin, Shu-Hui Lin, Konan Peck, Kun-Tu Yeh

Figure S1. Candidate marker genes examined for detection of circulating tumor cells by nested real-time polymerase chain reaction (PCR). (A) Tumor cells undergoing the epithelial to mesenchymal transition (EMT) acquire motile propensities and enter the blood. A 1.5 mL sample of peripheral blood from colorectal cancer patients was directly taken for candidate marker gene determination. (B) RNA was extracted from cells isolated from the peripheral blood. After reverse transcription of RNA, expression of candidate marker genes was quantified by nested real-time PCR. (C) Nested real-time PCR diagram. First, a target sequence is amplified by an outer primer set with a few rounds. The PCR products from the first PCR reaction are subjected to real-time PCR using a hydrolysable fluorescent probe for detection. Two rounds of PCR as well as sequence-based probe detection ensure the sensitivity and specificity of this method.