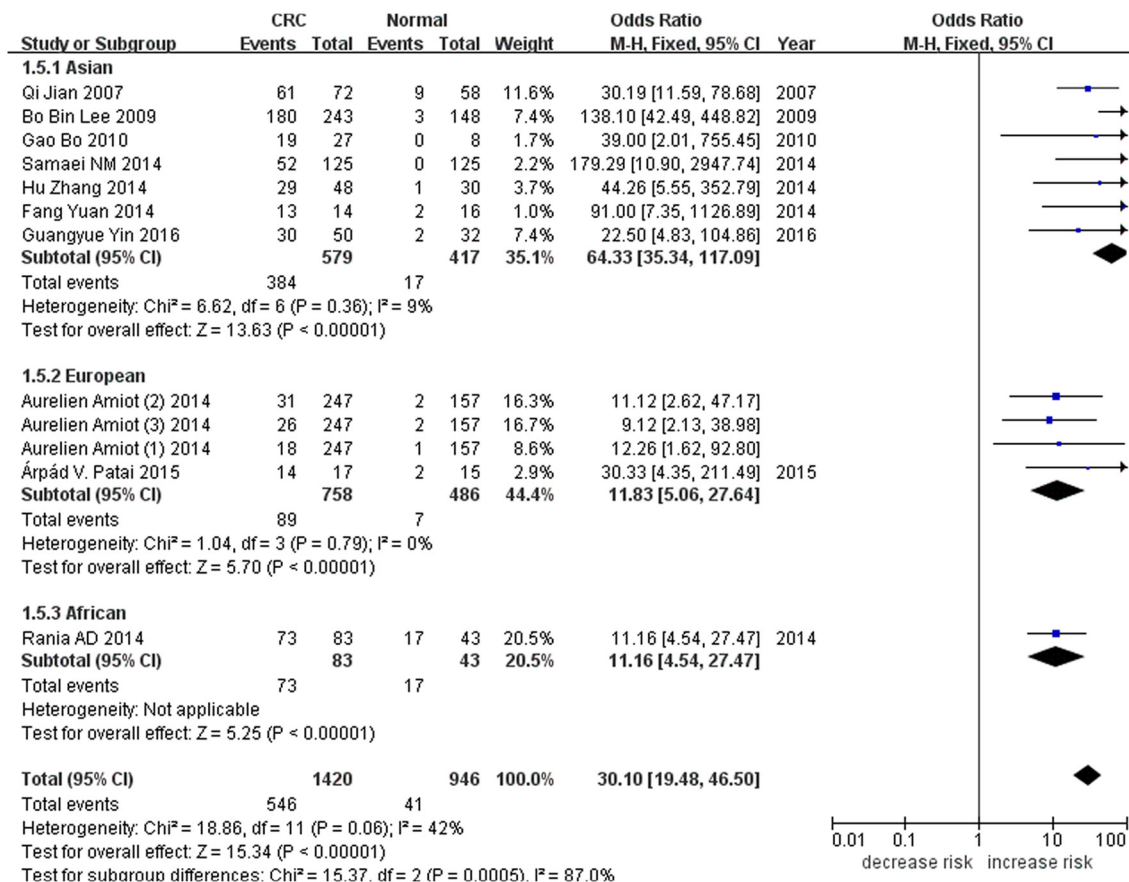
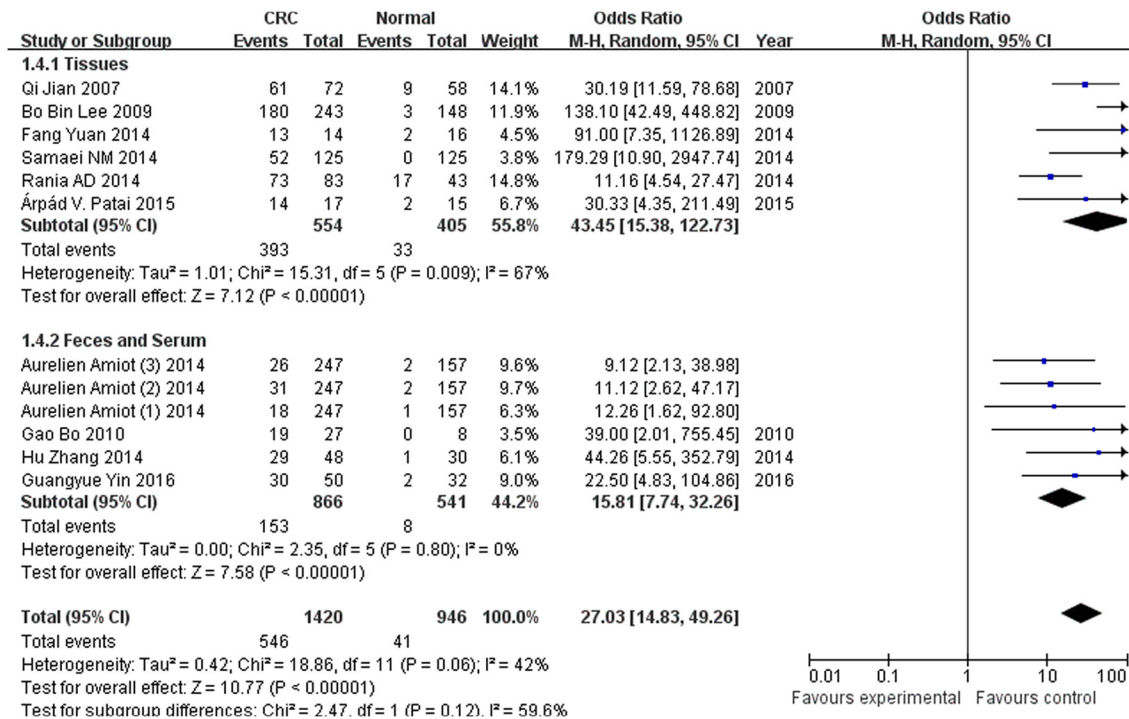


Diagnostic value of *WIF1* methylation for colorectal cancer: a meta-analysis

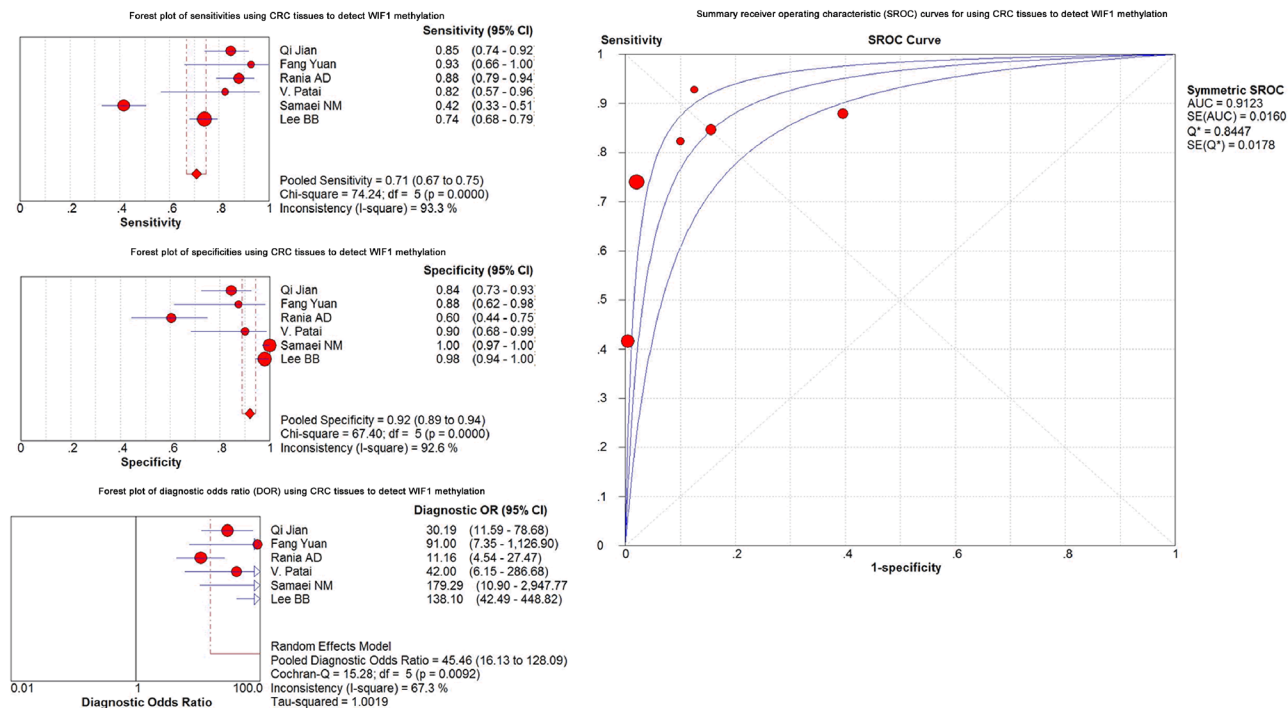
SUPPLEMENTARY MATERIALS



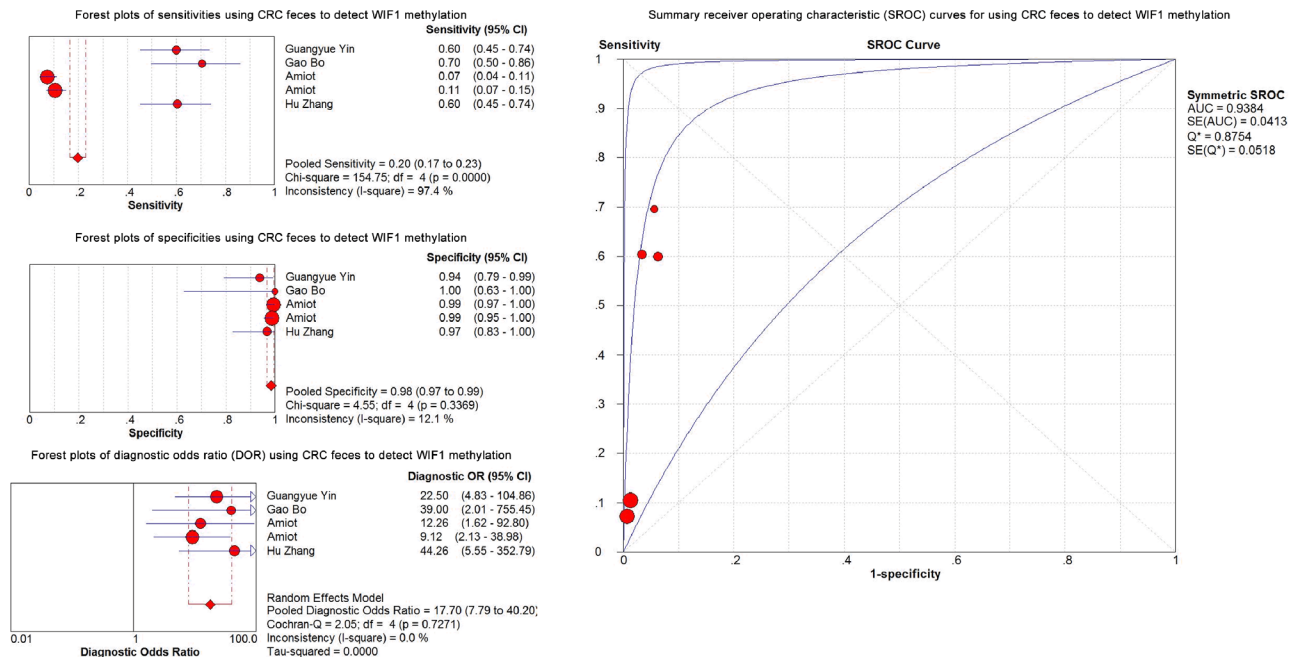
Supplementary Figure 1: Subgroup meta-analysis by ethnicity of *WIF1* methylation in CRC.



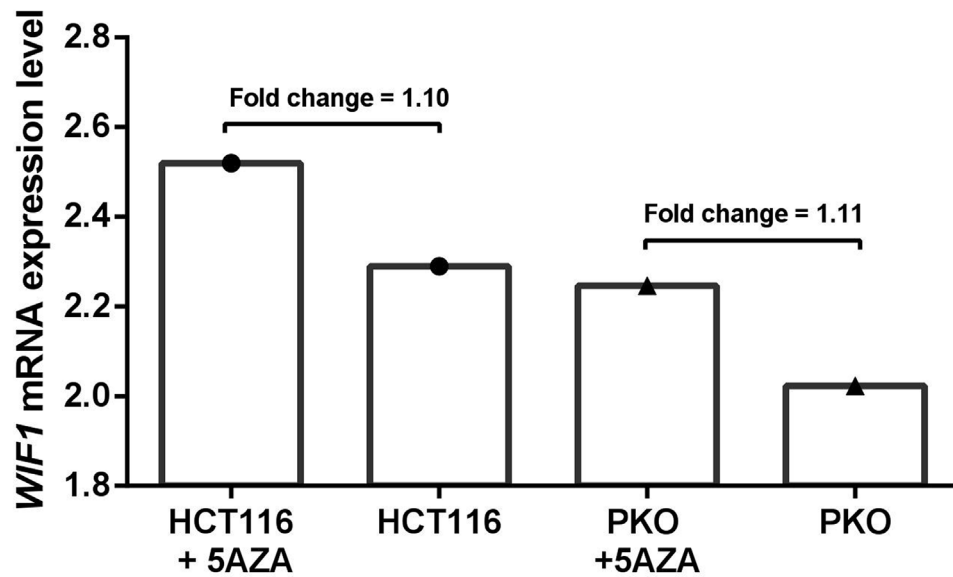
Supplementary Figure 2: Subgroup meta-analyses by sample type of *WIFI* methylation in CRC.



Supplementary Figure 3: Forest plots of sensitivities, specificities diagnostic odds ratio (DOR), and summary receiver operating characteristic (SROC) curves of *WIF1* hypermethylation as a diagnostic biomarker for CRC in tissues. AUC stands for area under the curve.



Supplementary Figure 4: Forest plots of sensitivities, specificities diagnostic odds ratio (DOR), and summary receiver operating characteristic (SROC) curves of *WIF1* hypermethylation as a diagnostic biomarker for CRC in feces. AUC stands for area under the curve.



Supplementary Figure 5: The expression value changes with and without 5AZA treatment in CRC cell lines (HCT116 and PKO) derive from the GEO database (GSE32323). *WIF1* expression profiles for two CRC cell lines were measured by Affymetrix HG-U133 Plus 2.0 arrays. And the normalized gene expression levels were presented as log₂-transformed values by robust multi-array average. 5AZA: cell line with 5-AZA-deoxycytidine treatment.

