Supplemental Figure 12. CB^2 detects essential genes missed by other leading methods: the case of *COPS8*. sgRNA quantification for *COPS8* in cell line (A) RT112, (B) UMUC3 using CRISPRn and (C) RT112 using the CRISPRi library. The top panels show CPM (count per million) of sgRNAs that target *COPS8* for each group (T_0 and T_1), and the bottom panels indicate the reported FDR for *COPS8* in each screen across all the methods. A horizontal line at FDR = 0.01 is used as a threshold for statistical cutoff. CB^2 outperforms all other methods of identifying *COPS8* as an essential gene across all benchmark datasets.