

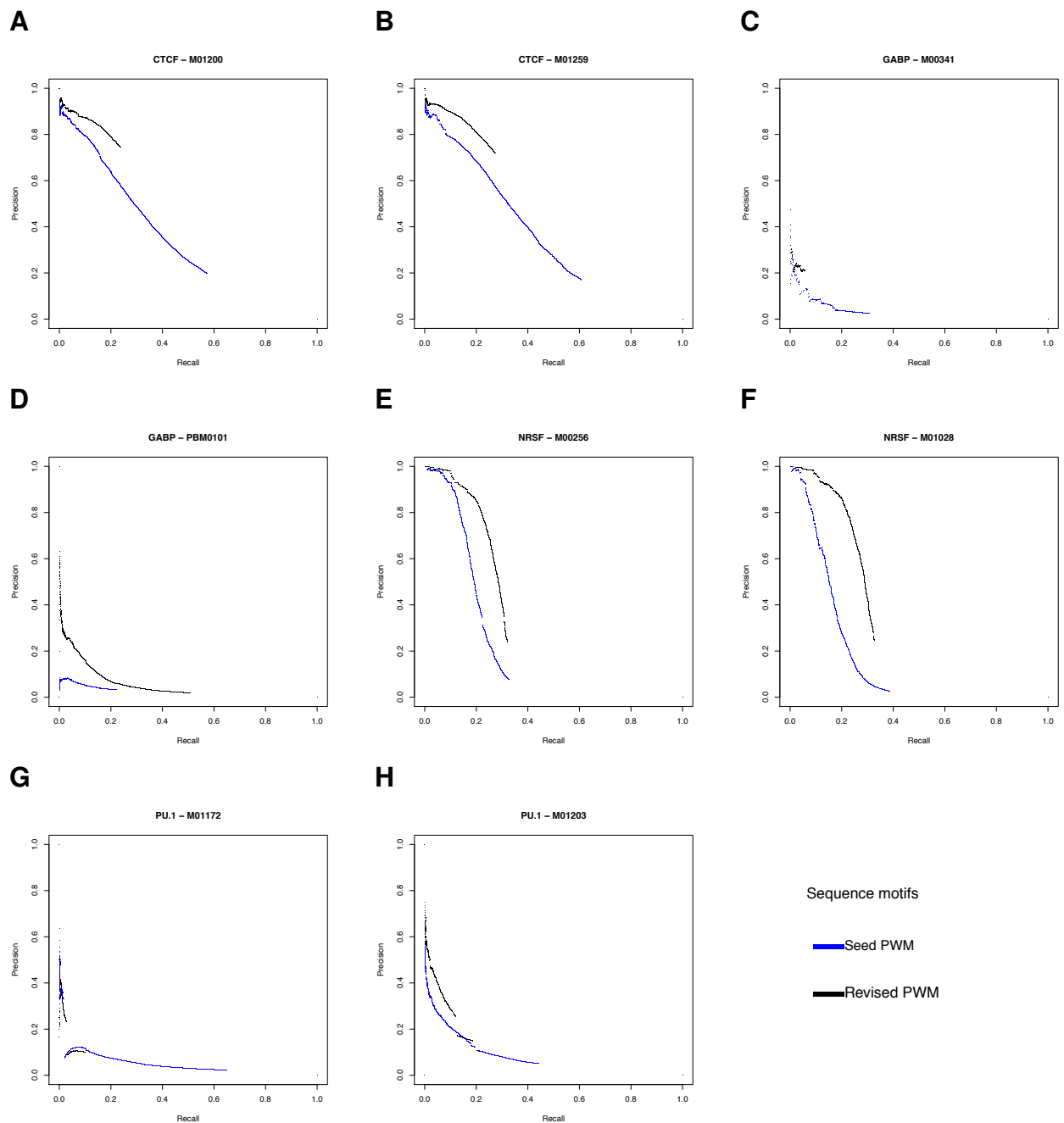


Figure S7: Precision-recall curves for seed (blue) and revised (black) sequence models. For each TF binding motif, CENTIPEDE-predicted footprints in GM12878 cells were compared using ENCODE ChIP-seq data as a gold standard. (A & B) CTCF (C & D) GABP (E & F) NRSF (G & H) PU.1