

Figure S8: Comparison of prior Pr(binding) derived from PWM scores to ChIP-seq read data across all motif matches using seed (blue) and revised (black) sequence models. Due to thresholds on the match score (see Section S3.2), few models have data Pr(binding) < 0.2. For ease of display data is binned in 10% increments. Points represent the average number of ChIP-seq reads within that bin and vertical lines represent the 95% confidence interval. Spearman correlation (legend) is calculated using the full data set without binning. (A & B) CTCF, (C & D) NRSF, (E & F) PU.1