Figure S22: **Correlation of CENTIPEDE predictions and mutated enhancers in HepG2 and K562 cells.** For each point, plotted is the difference in the change in probability of binding (mutated prior log ratio - reference prior log ratio, x-axis) versus the log_2(fold change) between mutated and wild type reporter constructs expression (y-axis). The black line represents the best-fit line from a linear model fit on all 22 points.