



Figure S1 Concordance of MBD-seq and Jiang *et al.* whole genome bisulfite-seq (WGBS) at the MBT time point in zebrafish. (A) Histogram of methylation enriched reads overlapping Jiang *et al.* identified methylated CpGs. Over 70% of the 19.4×10^6 CpGs with a methylation of greater than 0.5 (1 being fully methylated, 0 being unmethylated) have at least one overlapping MBD-seq read. (B) Average MBD-seq read ratio scores at Jiang *et al.* CpGs with methylation less than 0.5 and greater than 0.5. Standard error shown.