



Figure AS5. Turnover of predicted transcription factor binding sites (TFBS) and genes between *Z. mays* and other Andropogoneae species by genomic divergence. A single representative subgenome was used for TFBS turnover calculations in polyploid species. Loess smooth regression lines with 95% confidence intervals are shown. Genomic divergence was calculated using alignments to all fourfold degenerate sites in *Z. mays*.