



Supplementary Figure 3 WaferGen SmartChIP QRTPCR analysis of false-negative RNA-Seq genes. Official gene symbols are indicated in upper left corner with the number of RNA-Seq aligned reads in parentheses () and number of samples with C_t values lower than background in brackets [] for vehicle control samples. Bars represent mean fold-change determined by WaferGen technology (\pm SEM), the red line represents RNA-Seq fold-change, and the green line represents Agilent fold change. Significant differences within WaferGen data were determined by one-way ANOVA followed by Dunnett's *post-hoc* test and indicated by an asterisk (*). Red (RNA-Seq) and green (Agilent) dots represent $P_1(t)$ values with size indicating level of significance (small \sim 0.8, large \sim 1). Labels on the X-axis indicate the dose of TCDD (μ g/kg), number of aligned RNA-Seq reads, and number of samples with C_t values lower than background. Dashed lines indicate 1.5 and 2.0 |fold-change| thresholds to identify DEGs.